GENE PRECURSOR-SEQUENCE P-SEQID GENE-SEQ G-SEQID FOLDED PRECURSOR
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GAM24 CTGGTTAACTTCTTGAGCTA 1 GTTAACTTCT 2638 TTA TTGA ATTTC AAC- GA
TTTCGTGGAACTTGGAACAC TGAGCTATTT CTGG ACTTC GCT GTGG TTG A
AGCCTGCCACCCAGTGAAGT CGTG |||| ||||| ||| |||| |||
GTCCAG GACC TGAAG TGA CACC GAC /
TG- ---- CC--- GTCC AC

GAM25 TCACCATCTGCAGCCTTGAA 2 AAGGAGCTTT 2640 CA C- CC A TT GGAG- - AA
GGAGCTTTGGTTCGGAGACA GGTTCGGAGA TCAC TCTG AG TTGA GGAGCT GGTTC ACA
GGC A
GGCAAAGGAGCCATGTGTGG CAGG |||| |||| || |||| |||||| ||||| ||| |||
AGAGCCTGGTTTCTCAGTAC AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G
TTCCAGACCGTGA CC CT AT - T- AGGTG A AG

GAM26 GACTATGGCAAGGACCTGAT 3 TATGGCAAGG 2639 A AA- A T AGAA- CA
GGAGAAGGTCAAGAGCCCAG ACCTGATGGA GACT TGGC GG CCTGA GG GGT A
AGCTTCAGGCCGAGGCCAAG GAAG |||| |||| || ||||| || |||
TC CTGA ACCG CC GGACT TC CCG /
- GAG - - GAGAC AG

GAM27 GGCTCCCAATGTTGACGTTG 4 CCAGGCCAAA 4707 CTCCC CG---- AG TGC
GCCAGGGCTTTGCAAACAAG AAGGCTCAAC GG AATGTTGA TTGGCC GGCTT A
CCAGGCCAAAAAGGCTCAAC ATTT || |||||||| |||||| ||||| |||
ATTTACACC CC TTACAACT AACCGG CCGAA /
ACAT- CGGAAA A- CAA

GAM28 GCATTGATCTTATCCTCCGT 5 TTGATCTTAT 4706 GAT AT TC GA T CTCA
GACTGTCACCTCATCGTCGT CCTCCGTGAC GCATT CTT CC CGT CTG CAC T
GCAGAATGAGGGCCGAGTAG TGTC ||||| ||| || ||| ||| |||
ATGC CGTAG GAG GG GTA GAC GTG /
AT- CC GA A- - CTGC

GAM29 GCAGTGGAGGGGGCAGGACC 6 GAGCAGGTCC 4705 GA A ACCT GGTG C
TCCTGCTGGTGCAGCACCAG ACCGGCCCCT GCAGTG GGGGGC GG CCTGCT CAGCA C
TGCTGGAGCAGGTCCACCGG ACAT |||||| |||||| || |||||| |||||
CCCCTACATTGC CGTTAC TCCCCG CC GGACGA GTCGT A
A- G ACCT G--- G

GAM30 GGTCATTGTGCCCTGCCAAG 7 TGGCTGGTCA 4585 T TTG G- A A G G C --- AG
GCACAGCGTAGATCTGGAAA TGGAAGGGGC GG CA TGCCCT CCA GGC CAGC TA AT
TGGAAAG AGC A
GAGCAGAATGCTTTCCTTTT AGTT || || |||||| ||| ||| |||| || || ||||||| |||

CATATGTGGCTGGTCATGGA CC GT ACGGGG GGT CTG GTCG GT TA ACTTTTC TCG
/
AGGGGCAGTTGTCC T TG- AA A - - G T CTT TA

GAM31 GCGCGGCTGTGGCACATGTC 8 TGTGGCACAT 4584 - - T C AT- TCT--- TT
GTCTCTTGCTTTGTTGTACT GTCGTCTCTT GCG CG GC GTGG AC GTCGTC TGC T
CGCCGACGGCTAAGTCCATT GCTT ||| || || |||| || |||||| |||
GCACGCCGC CGC GC CG TACC TG CGGCAG ATG G
C A T - AAT CCGCTC TT

GAM32 AGTTGGGCTGGGTCTTGGTA 9 TCCAAGAACT 4583 ----- G TAC TTCCG
CACGTGGTTCCGCCCATCTC AGTTCACCCC AGTTGGG CTGG TCTTGG ACGTGG C
CACGTCCAAGAACTAGTTCA AGCT ||||||| |||| |||||| ||||||
CCCCAGCT TCGACCC GATC AGAACC TGCACC C
CACTT A --- TCTAC

GAM33 AACCCAGACGCCATGAAAGC 10 ACGCCATGAA 2909 AC C A CTG T- C AGAAAA
TGCCATGGCCCTGGAGAAAA AGCTGCCATG AACCCAG GC ATGAA G CCA GG CCTGG A
AGCTGAACCAGGCCCTTTGG GCCC ||||||| || ||||| | ||| || |||||
ATCTTCATGCCTGGGTT TTGGGTC CG TACTT C GGT CC GGACC /
-- - - TA- TT C AAGTCG

GAM34 GGCGGTCCCGCGGGTCTGTC 11 CCGCGGGTCT 2911 C G C T C A
TCTTGCTTCAACAGTGTTGG GTCTCTTGCT GG GGTCCC CGGGTCTGT TCT G TTCAAC G
ACGGAACAGATCCGGGGACT TCAA || |||||| ||||||||| ||| | ||||||
CTC CT TCAGGG GCCTAGACA AGG C AGGTTG /
C - - - - T

GAM35 CCCATCTCTGTGACTTCCTG 12 AGTGAAGCTT 2910 - TGACTTCCTG AC AG
GAGACTCACTTCTAGATGAG ATCAGAAGAT CCCATCT CTG GAG TCACTTCT A
GAAGTGAAGCTTATCAGAAG GGG ||||||| ||| ||| ||||||||
ATGGG GGGTAGA GAC TTC AGTGAAGG T
A TA-------- GA AG

GAM36 GGGACTCACTGCTGCAGGAT 13 TTCGTACCAA 2957 A C A--- - A TA
GGGGAATTTAGCATGGATCT GAGCACCGGT GGG CTCACTG TGC GG ATGGGGA TT G
TCGTACCAAGAGCACCGGTG GGGG ||| ||||||| ||| || ||||||| ||
GGGCCC CCC GGGTGGC ACG CC TGCTTCT GG C
G C AGAA A A TA

GAM37 CACCTTCAATGTCACTGTCA 14 AATGTCACTG 2956 AA CA C ACAA
CCAAGACTGACAAGACGCTA TCACCAAGAC CACCTTC TGT CTGTCA CAAGACTG G
GTCTTGCTGATGGGCAAAGA TGAC ||||||| ||| |||||| ||||||||

AGGTG GTGGAAG ACG GGTAGT GTTCTGAT /
AA -- C CGCA

GAM38 TGGCGGACGGGACCTGTCAG 15 TCCCCGGGAA 2958 GGA- TCA - AT-- T- TACAA
GACGCGGCCATCGTGGGCTA AACGTTCGTC TGGCGGACG CCTG GGACG CGGCC CG
GGGC G
CAAGGACTCGCCCTCCGTCT A |||||||||| |||| ||||| ||||| || ||||
GGGCCGCCGTCCCCGGGAAA ACTGCTTGC GGGC CCTGC GCCGG GC CCCG /
ACGTTCGTCA AAAA C-- C GTCT CT CTCAG

GAM39 TTCTGCATACAAGTTGGCAG 16 GATTCTGTGG 3882 ACAAG G A ATAC
GAACATTATACATGGCAGTG AGAGTGCAGA TTCTGCAT TT GCAGGA CATT A
ATTCTGTGGAGAGTGCAGAG G |||||||| || |||||| ||||
GAGACGTG AG TGTCTT GTGA /
AG--- G A CGGT

GAM40 CGTTTCGGGTGCTGGCGGCT 17 AAGGAACCAT 3880 TTC-- -- G C CA GA AAA TAAG
GCAGCCGGAGTTCAAACCTA GGCCAACTGT CGT GGGT GCT GCGG TG GCCG GTTC CC
C
AGCAGCTGGAAGGAACCATG GAGC ||| |||| ||| |||| || |||| |||| ||
GCCAACTGTGAGCGTACCTT GCG TCCA CGA TGTC AC CGGT CAAG GG /
CATTGCG TTACT TG G A -- AC GAA TCGA

GAM41 CACTACGTTGACCTGAAGGA 18 AAGGACCGTC 3879 GA-- GAA- CCATTCT --
AAAT
CCGTCCATTCTTTGCCGGCC CATTCTTTGC CACTACGTT CCT GGACCGT
TTGCCGGCCT GGTG A
TGGTGAAATACATGCACTCA CGGC |||||||| ||| ||||||| |||||||||| ||||
GGGCCGGTAGTTGCCATGGT GTGGTGTAA GGG TCTGGTA GATGGCCGGG
TCAC /
CTGGGAGGGGCTGAATGTGG GTCG AGGG CCGTT-- AC GTAC
TG

GAM42 GAACACAAGTGTGTTGTTGT 19 TAGCATAGTG 4447 C G - TG CTT T TTCATG-- A C
CTTCTATCTTCTTCATGGCA GTCAAGCTTG GAA ACAAGT TG T TTGT CTATC TC GC
GACT A
GACTCAGTGGTCAGCGGAAA TTTC ||| |||||| || | |||| ||||| || || ||||
CTTGATGATAGCATAGTGGT CTT TGTTCG AC G GATA GATAG AG CG CTGG G
CAAGCTTGTTTC - A T GT C-- T TTCAAAGG A T

GAM43 GTGTCTTCGGCCGCCGGAAG 20 TTCTTCTTTT 4449 T CG T- TGACG
GGTGGGTGACGTGCGGATCT TGTGGCTGTG GTGTCT CGGCCGC GAAGGG GGG T
TCTTCTTTTTGTGGCTGTGG GACA |||||| ||||||| |||||| |||
ACAC CACAGG GTCGGTG TTTCTT TCT /
T TT CT AGGCG

GAM44 GGGTGTTGACCTTGGCCACA 21 GTGCTTGTTG 4448 CCTT ----- ATGTCAT - TCT
TCAATGTCATACAGCTTCTT GCTTTAACAT GGGTGTTGA GGCCA CATCA ACAG CT T
CACAGCCTGTTTAATCTGGT CC |||||||||| ||||| ||||| |||| ||
GCTTGTTGGCTTTAACATCC CCTACAATT TCGGT GTGGT TGTC GA /
---- TGTTC CTAATT- C CAC

GAM45 CGGCTCCGAGAGCAGGTTCT 22 TACACATTGA 3296 - AGAG C A TC GCAG C
TCGTGAGTTCCTCGCAGGGC GAACCTGAAC CGGC TCCG CAGGTTCTT GTG GT CTC GG
C
CGGTCAGAGCTACACATTGA ATGG |||| |||| ||||||||| ||| || ||| ||
GAACCTGAACATGGAGGCCG GCCG AGGT GTCCAAGAG TAC CA GAG CT G
G ACAA T A TC A--- G

GAM46 AGGAGGACGCGCTGCCCGGC 23 GAGAGTACTC 3295 ------ G- G CAGAAAA AA
CAGAAAACGGAGTTCAAGGT CTGCGTCTTC AGGAGGACGC GCT CCC GC CGGAGTTC
G
GGACTCCGACGACCAGTGGG CT |||||||||| ||| ||| || ||||||||
GAGAGTACTCCTGCGTCTTC TCCTTCTGCG TGA GGG TG GCCTCAGG /
CT TCCTCA GA G ACCAGCA TG

GAM47 TCTACAAAGTGCCGTCCACT 24 TCCAATCTGA 2616 A - - CACTG CT- C
GAGACTGAGGCCTTGGCTTC TGGGCATGTT TCT CAAA GTGCC GTC AGA GAGGC T
CAATCTGATGGGCATGTTTG TGAG ||| |||| ||||| ||| ||| |||||
AGA AGA GTTT TACGG TAG TCT CTTCG T
- G G ----- AAC G

GAM48 GATCCAAGCTGCCTGGAGGG 25 TTCCTCCGGG 2617 CAAGCT C ACTG
GCTTTCACTGGCGGCAGAAA TGAAGAGATC GATC GCCTGGAGGGG TTTC G
TTCCTCCGGGTGAAGAGATC |||| ||||||||||| ||||
CTAG TGGGCCTCCTT AAAG C
AGAAG- - ACGG

GAM49 CCGGTGTAAATGTTGAGCCT 26 TAAATGTTGA 2618 AA GA TTTTT G- TT
TTTTGGCCTGGCTTGTTTGC GCCTTTTTGG CCGGTGT ATGTT GCC GGCCT GC G
AAAGGCCCTGGCAAACGTCA CCTG ||||||| ||||| ||| ||||| ||
ACATTGG GGTTACA TGCAA CGG CCGGA CG T
AC A- TC--- AA TT

GAM50 TTGAGAAGCGCCGACGAGAC 27 TGAGAAGGCT 2621 G CGACGAG A AATAA G
CGGATCAATAACAGTTTGTC GGTACCCAGT TT AGAAGCGC ACCGG TC CAGTTT T
TGAGCTGAGAAGGCTGGTAC GCTT || |||||||| ||||| || ||||||
CCAGTGCTTTTGAG GA TTTTCGTG TGGTC GG GTCGAG C

G ACCCA-- - AAGA- T

GAM51 TGGAGAAGGAGAGTGCGGAC 28 TAGGTTCCAT 2620 A AG- GC- GAGA A T TT
GAGAATGGAAACTTGAGTTC GTCCCCAACT TGG GAAGG AGT GGAC ATGGAA CT GAG C
GGCTCTAGGTTCCATGTCCC ACAT ||| ||||| ||| |||| |||||| || |||
CAACTACATCTTCCCA ACC CTTCT TCA CCTG TACCTT GA CTC /
- ACA ACC ---- G T GG

GAM52 TGACGCGCACGCCCCTGCTA 29 GGGAATGCCT 2619 C CC T ACTA- T
TGGACTATCGGAGTTTGGGA GGCAGAAGTT TGACGCGCA GC CTGCTA GG TCGGAGTT G
TTTCGGGAATGCCTGGCAGA GCGC ||||||||| || |||||| || ||||||||
AGTTGCGCGTTA ATTGCGCGT TG GACGGT CC GGCTTTAG /
- AA - GTAAG G

GAM53 TCCAGAAAGCTGATGGTGTG 30 AGAAAGCTGA 2622 AG- TGA --- -- - CTAC
CCCGTCTACCTGAAACGAGG TGGTGTGCCC TCC AAAGC TGGT GT GCC CGT C
CCTGCCTGACCAAATGCTTT GTCT ||| ||||| |||| || ||| |||
ACCGGA AGG TTTCG ACCA CG CGG GCA /
CCA TAA GTC TC A AAGT

GAM54 GTATGGTACAGAGGAGGCCA 31 TGGAATTTTC 2623 -- TA GG ACAGAAGC
TTACAGAAGCAAGCACCAAG TGGGCCGAAT GTAT GG CAGAGGA CCATT A
ATGGAATTTTCTGGGCCGAA AC |||| || ||||||| |||||
TAC CATA CC GTCTTTT GGTAG /
AG GG AA AACCACGA

GAM55 TCTTGTGTTGAGACTTCGTG 32 TACACCACTC 2624 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM56 GGATGACATCCAGAGGGCAG 33 TGTCACAGCC 2625 TG CAGAG A-- AT A - A- GG
AATGCATGCTGCAGCAGGCG ACAGATGTTG GGA ACATC GGC GA GC TGCTG CAGC
GGC A
GAGAGGCTGGGCTGCCGGCA TCC ||| ||||| ||| || || ||||| |||| |||
GTTGTCACAGCCACAGATGT CCT TGTAG CCG CT TG ACGGC GTCG TCG G
TGTCC GT ACA-- ACA GT - C GG GA

GAM57 TCTTGTGTTGAGACTTCGTG 34 TACACCACTC 2626 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G

ATAA AACCC - GAAGAA

GAM58 CCATACTGGTATGTGTTTCT 35 ATGGAACAAC 2627 T T-- - TC - ACA
CCTGGACAAGACATCATGGA CACTCCTATC CCATAC GGTA GTG TT TCC TGG A
ACAACCACTCCTATCTGTAT TGTA |||||| |||| ||| || ||| |||
GG GGTATG CTAT CAC AA AGG ACT G
T CCT C CA T ACA

GAM59 GGCCTTTCAGCTAACATTCA 36 CCTTTCAGCT 2628 CT TA A- G AACC
TGGATGCAAACCACTACTGG AACATTCATG GGC TTCAGC AC TTCATGGAT CA A
TCTGTGGACGGTCTGCTGAA GATG ||| |||||| || ||||||||| ||
TGCC CCG AAGTCG TG AGGTGTCTG GT /
T- TC GC - CATC

GAM60 TTCACCACCATGGAGAAGGC 37 CTGCCCCCTC 2629 CA GA GGC CT T A CAAA TCA
TGGGGCTCATTTGCAGGGGG TGCTGATGCC TTCAC CCATG GAA TGGGG CATT GCAGGGGGG GC AGGG T
GAGCCAAAAGGGTCATCATC CCCA ||||| ||||| ||| ||||| |||| ||||||||| || ||||
TCTGCCCCCTCTGCTGATGC AAGTG GGTAC CTT ACCCC GTAG CGTCTCCCC CG TCTC /
CCCCATGTTCGTCATGGGTG TG TG GT- C- T - ---- TAC
TGAA

GAM61 CTGGCCAACAGCCTTGCCTG 38 TCAGGCTGGG 2630 CAA - - AA-- AAG
TCAAGGAAAGTACACTCCGA GCTGCTGCCA CTGGC CAGCCTT GCCTG TC GGA T
GCGGTCAGGCTGGGGCTGCT G ||||| ||||||| ||||| || |||
GCCAG GACCG GTCGGGG CGGAC GG CCT A
TC- T T CGAG CAC

GAM62 TCTACAAAGTGCCGTCCACT 39 TCCAATCTGA 2631 A - - CACTG CT- C
GAGACTGAGGCCTTGGCTTC TGGGCATGTT TCT CAAA GTGCC GTC AGA GAGGC T
CAATCTGATGGGCATGTTTG TGAG ||| |||| ||||| ||| ||| |||||
AGA AGA GTTT TACGG TAG TCT CTTCG T
- G G ----- AAC G

GAM63 CAAACAAGAGGACTGTGTTG 40 TGTGTTGTGG 2632 AA - A T T TG C - - T
TGGTCTGGGGAGAATGTAAT TCTGGGGAGA CA CA AG GGAC GTGT G GT TG GGGAG AATG A
CATTCCTTCCACAACTGCTG ATGT || || || |||| |||| | || || ||||| ||||
CATGTCCCTGTGGGTG GT GT TC CCTG TACG C CA AC CCTTC TTAC A
GG G - - T GT - A C T

GAM64 TCTTGTGTTGAGACTTCGTG 41 TACACCACTC 2633 GAGA GT--- C AAAGGA

GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM65 GCCCTGCCAAGCACAGCGTA 42 TGTGGCTGGT 2634 G- A- A G G --- AG
GATCTGGAAAGAGCAGAATG CATGGAAGGG GCCCT CCA GC CAGC TA ATCTGGAAAG AGC
A
CTTTCCTTTTCAGATGTGGC GC ||||| ||| || |||| || |||||||||| |||
TGGTCATGGAAGGGGC CGGGG GGT TG GTCG GT TAGACTTTTC TCG /
AA AC - - G CTT TA

GAM66 TGCTACTATTTTATTGCAGG 43 TATTTTATTG 2635 ACTA T AGGA GG- T
AGGTGGGGGTGTATGCACCG CAGGAGGTGG TGCT TTTTAT GC GGTG GGTG A
CACACCGGGGCTATGAGAAG GGGT |||| |||||| || |||| ||||
CA ACGA AGAGTA CG CCAC CCAC T
---- T GGG- ACG G

GAM67 AAACAGACTGGGCCAATGTC 44 TATCAAGGAA 2636 C -- CACAAAGAA - CA-
ACCGAT
CACAAAGAATTCCTGGTCAG GGGCAGGCGT AAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
CACCACCGATGTCCAAAGGT GATG ||||||| ||||||| ||||| ||||| ||| |||||
GCAATATCAAGGAAGGGCAG TTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GCGTGATGGCTTATTTGTTT - AG ACGGG---- A TAA AAACCT

GAM68 CTAGGGGTCTGTACCGGGCT 45 TCCCAACCCC 2637 CT-- C- C CC-- C TCA
GGCCTGTGCCTATCACCTCT TGTATTCCCA CTAGGGGT GTAC GGG TGG TGTGC TA C
TATGCACACCTCCCAACCCC CCCC |||||||| |||| ||| ||| ||||| ||
TGTATTCCCACCCCTGG GGTCCCCA TATG CCC ACC ACACG AT C
CCCT TC A CTCC T TCT

GAM69 TCACCATCTGCAGCCTTGAA 46 AAGGAGCTTT 2642 CA C- CC A TT GGAG- - AA
GGAGCTTTGGTTCGGAGACA GGTTCGGAGA TCAC TCTG AG TTGA GGAGCT GGTTC ACA
GGC A
GGCAAAGGAGCCATGTGTGG CAGG |||| |||| || |||| |||||| ||||| ||| |||
AGAGCCTGGTTTCTCAGTAC AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G
TTCCAGACCGTGA CC CT AT - T- AGGTG A AG

GAM70 GACTATGGCAAGGACCTGAT 47 TATGGCAAGG 2641 A AA- A T AGAA- CA
GGAGAAGGTCAAGAGCCCAG ACCTGATGGA GACT TGGC GG CCTGA GG GGT A
AGCTTCAGGCCGAGGCCAAG GAAG |||| |||| || |||||| || |||
TC CTGA ACCG CC GGACT TC CCG /

- GAG - - GAGAC AG

GAM71 GACTATGGCAAGGACCTGAT 48 TATGGCAAGG 2643 A AA- A T AGAA- CA
GGAGAAGGTCAAGAGCCCAG ACCTGATGGA GACT TGGC GG CCTGA GG GGT A
AGCTTCAGGCCGAGGCCAAG GAAG |||| |||| || ||||| || |||
TC CTGA ACCG CC GGACT TC CCG /
- GAG - - GAGAC AG

GAM72 TCACCATCTGCAGCCTTGAA 49 AAGGAGCTTT 2644 CA C- CC A TT GGAG- - AA
GGAGCTTTGGTTCGGAGACA GGTTCGGAGA TCAC TCTG AG TTGA GGAGCT GGTTC ACA
GGC A
GGCAAAGGAGCCATGTGTGG CAGG |||| |||| || |||| |||||| ||||| ||| |||
AGAGCCTGGTTTCTCAGTAC AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G
TTCCAGACCGTGA CC CT AT - T- AGGTG A AG

GAM73 ATCCATTGCCATTTGGTACA 50 CAAATGACAT 2645 ATTGCCA - G ------- T
AATGACATTTGTTCTTTCTG TTGTTCTTTC ATCC TTTG GTACAAAT ACATTTG TTCTTTC
G
TGAAAGAGATGCCCTCGAGT TGTG |||| |||| |||||||| ||||||| |||||||
GTGTTTGTACACAAACCCTT TAGG AAAC CATGTTTG TGTGAGC GAGAAAG /
AGGAT ATTCCC- A - TCCCGTA T

GAM74 CCCGCCAGGCCTCCATAGAG 51 TGGCCAGTAC 2646 A C CATAGA - - A
CTGCCCAGCATGGCTGTGGC CAAGAGTCGG CCCGCC GGC TC GCTG CC CAGC T
CAGTACCAAGAGTCGGTGGG TGGG |||||| ||| || |||| || ||||
GGGTGG CTG AG TGAC GG GTCG /
- - AACCA- C T G

GAM75 GCAAAATCACTCGTTTTGTA 52 TCACTCGTTT 2647 A-- TT TG AAA CT
GGGAAAGGTTGCTTTGTTAA TGTAGGGAAA GCA AATCACTCG T TAGGG GGTTG T
TCATGCCCTATGGTGGGTGA GGTT ||| ||||||||| | ||||| |||||
TTAACTGC CGT TTAGTGGGT G ATCCC CTAAT T
CAA -- GT GTA TG

GAM76 TCTTGTGTTGAGACTTCGTG 53 TACACCACTC 2648 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM77 GCTGATCTCCTGCCTGATGT 54 CCTGCCTGAT 2649 CCT AT -- CAGAGCCAA A
TTCTGTCTCAGAGCCAAGGC GTTTCTGTCT GCTGATCT GCCTG GT TTCTGTCT GGCC A
CAAGAGGCCCAGACAGAGTT CAGA |||||||| ||||| || |||||||| ||||

GCCCCAGGCCCGGATCAGC CGACTAGG CGGAC CG GAGACAGA CCGG G
CC- CC TT C-------- A

GAM78 GATTCCCCTGTCCATGGTGG 55 CACAGCGTTC 2650 T - T CAT T AA C AA-- TGC
TCGGAAACTGCGCATTGAAC GGCTCTTTGA GAT CC CC GTC GG GGTCGGA CTG GCATTG
CAGGGTG A
AGGGTGTGCAAGTCATCCTG CTGG ||| || || ||| || ||||||| ||| |||||| |||||||
GACCCAGTGCACAGCGTTCG CTA GG GG CAG TC TCGGCTT GAC CGTGAC
GTCCTAC /
GCTCTTTGACTGGTGGCATC C T T TT- - GC A CCAG TGA

GAM79 CCAAGACCAACAGGATGCCA 56 CACTCGGTGT 2651 ---- -- AA CC CC TATTTC
CGCTGGGCCGAGCGACTATT ACGTCCTGGA CCA AGA CC CAGGATG ACGCTGGG
GAGCGAC C
TCCTGCCAATGTTGCTCACT GGAC ||| ||| || ||||||| |||||||| |||||||
CGGTGTACGTCCTGGAGGAC GGT TCT GG GTCCTGC TGTGGCTC CTCGTTG T
TCTATTGTGG GTTA CA AG A- A- TAACCG

GAM80 TCTGGCAGCGGTACCCGAAT 57 CACCGGGAGG 2652 - C - CGAA TATAGCAA - GA
CCCTATAGCAAACATGTCTT TGACCCCTGA TCTGG CAG GGT ACC TCCC AC ATGTCTT
C
GACGGAAGACATAGTACACC CCAG ||||| ||| ||| ||| |||| || |||||||
GGGAGGTGACCCCTGACCAG AGACC GTC CCA TGG AGGG TG TACAGAA /
A A C G ---- CCACA--- A GG

GAM81 GGCCAATTGAAACAAACAGT 58 TATTAGGGAT 2653 C T ACAAACAG G GTT T A GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM82 TCTTTGCTTTAAATAATACT 59 AGAGGTCCTT 2655 TG AA T- A A
ACTGGGCTGATTACAGTTCA AGATAGAGAG TCTT CTTTA TAA ACT CTGGGCTG T
GAGGTCCTTAGATAGAGAGG GAGA |||| ||||| ||| ||| ||||||||
AGA AGAG GAGAT ATT TGG GACTTGAC T
GA AG CC A A

GAM83 GTGACAGTGCTGGCTAGTGA 60 CTCGAGCAAC 2654 --- C AG A- - CTC
CGGCAGCTCCACTCCTGCTC GGTTACCATC GTGACA GTG TGGCT TG CG GCAG C
GAGCAACGGTTACCATCAAT AATG |||||| ||| ||||| || || ||||
GTCAC CACTGT TAC ATTGG AC GC CGTC A
AAC C CA GA T CTC

GAM84 AGCACATGGTATTCCTGGGT 61 TGACCCGACA 2656 TAT GGG-- AGT AG- A- A ACAA
GGTGCAGTTCTAGCGGATAT AGAGTACCAA AGCACATGG TCCT TGGTGC TCT CGG TATC TGAAAG A
CATGAAAGACAAAGACAACT GAAA |||||||||| |||| |||||| ||| ||| |||| |||||| TTTGGATGACCCGACAAGAG TCGTGTGCC GGGA ACCATG AGA GCC GTAG GTTTTC G
TACCAAGAAAAGGGTGTCCG TGT AAAGA --- ACA CA - AACA TGTGCT

GAM85 TCTTGTGTTGAGACTTCGTG 62 TACACCACTC 2657 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG |||||||||| |||| ||||||| ||||| CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM86 GCGGCGAACTTCTGCACACA 63 TAGCGTGGCC 2658 CT C - TC T TG T TCTC TG
GCTCCAGTGTTTGCTCTGGA ACTGCGTTGA GCGGCGAA TCTG ACA CAGC CAGTG T C CTGGA GA A
TCTCGATGACTTTCTCTAGC TGTT |||||||| |||| ||| |||| ||||| | | ||||| || GTGGCCACTGCGTTGATGTT CGTCGTTT GGGT TGT GTTG GTCAC G G GATCT CT C
GGGCTTTTGCTGC TC - A C- C GT C ---- TT

GAM87 GCATCTTCTACTAGTGTGTT 64 TTCAAATAAC 2660 TCT AGTG GTA T C
AGTAGATGGATTCACAGATC AAAAGTAGAT GCA TCTACT TGTTA GA GGATT A
CTTCAAATAACAAAAGTAGA TCTG ||| |||||| ||||| || ||||| TTCTGC CGT AGATGA ACAAT CT CCTAG C
CTT AA-- AAA T A

GAM88 CCACTGTCTGTAAGATTCCC 65 TTGCTCAGCT 2659 C TC TA C-- C C -- AAA TT
AGCAGCTGCAGCCTCAAAAT TCTGGCTCAA CCA TG TG AGATT CCAG AGCTG AGC CTC ATT T
TTTTAACAATCAGGAGTTGC TCTG ||| || || ||||| |||| ||||| ||| ||| ||| TCAGCTTCTGGCTCAATCTG GGT AC AC TCTAA GGTC TCGAC TCG GAG TAA A
TCAACCATGG - CA TG CTC T - TT GAC CA

GAM89 AAACATCTCCAGGCTTTGAT 66 TCTCCAGGCT 2661 CT - - -- TT C G
TTTTGTACCATGGAAATTGT TTGATTTTTG AAACAT CCAGG CTTTG AT TT GTAC AT G
ATTTAACCATACAGGGTTTT TACC |||||| ||||| ||||| || || |||| || GGTATGTTT TTTGTA GGTTT GGGAC TA AA TATG TA A
T- T A CC TT T A

GAM90 GCATCAGAGTAATCTTCAGT 67 TATACTGTAT 2662 G ATCTT-- - A
GTGGAATGTTAAATAACGCT TTTGTACTAT GCATCA AGTA CAGTGTGGAA TGTT A

TTTATACTGTATTTTGTACT GATG |||||| |||| |||||||||| ||||
ATGATGT TGTAGT TCAT GTCATATTTT GCAA A
A GTTTTAT C T

GAM91 TTCAGTGACGTACATGGCTC 68 TACTGGAGAG 2664 GAC A GG--- TG TCT CAC
TGGTTCTGGACACAAAATCT GAAATGACTG TTCAGT GT CAT CTC GT GGA A
GTACTGGAGAGGAAATGACT CTGA |||||| || ||| ||| || |||
GCTGAA AAGTCG CA GTA GAG CA TCT /
T-- - AAGGA GT TG- AAA

GAM92 CTGTGGGATGATTGCCACAT 69 TGGGATCGAA 2663 G TT - ATA-- GGAACA GGG
TGG
ACATGGAACACCTGGGAGTG GTGACAAAGT CTGTGG ATGA GC CAC CAT CCT AGTGC
A
CTGGAAATGTACTGGGATCG GTGT |||||| |||| || ||| ||| ||| |||||
AAGTGACAAAGTGTGTTTTC GACACT TACT TG GTG GTG GGG TCATG /
ATTCACAG - TT T AAACA AAGCTA --- TAA

GAM93 GGGGCTAGCAGGACTTCTCG 70 AGCAGGACTT 2665 AG G TTCTCG A- AAC
GCGAGGGAGTTTTTAACTTT CTCGGCGAGG GGGGCT CAG AC GCG GGGAGTTTTT T
GGAGAACTCCTCATGCACCC GAGT |||||| ||| || ||| ||||||||||
TGTGCTGGAGTCCC CCCTGA GTC TG CGT TCCTCAAGAG /
G- G TCCCA- AC GTT

GAM94 GCTCTTGCAATCAAGTCTGT 71 TTTGTAGTCA 2666 T A CAAGTCT G T CCT
GATGTATTAATAATGCCTTA TTTTAAGTAG GCTC TGC AT GTGAT TAT AATAATG T
TATATTGTTTGTAGTCATTT CATG |||| ||| || ||||| ||| |||||||
TAAGTAGCATGAGC CGAG ACG TG TACTG ATG TTGTTAT /
T A AATTT-- - T ATA

GAM95 CAGGGAGAGGCTCTTCTGCG 72 ACGGAGCATG 2667 A GC G AG GTT GAG
TGTAGTGGTTGTGCAGAGCC AGAAGACGTT CAGGG GAG TCTTCT CGTGT TG GTGCA C
TCATGCATCACGGAGCATGA CCCC ||||| ||| |||||| ||||| || |||||
GAAGACGTTCCCCTG GTCCC CTT AGAAGA GTACG GC TACGT C
- GC - AG AC- ACT

GAM96 TGGCCGGGCGCGGTGGCTCA 73 TCACAAGGTC 2670 CGCG - ------- - A CAG G
AGCCTGTAATCCCAGCACTT CGGAGATTGA TGGCCGGG GTGG CTCAA GCCT GT ATCC
CACTTTGG A
TGGGAGGCCGAGGTGGGTGG GACC |||||||| |||| ||||| |||| || |||| ||||||||
ATCACAAGGTCCGGAGATTG ATCGGTCC TACC GAGTT TGGA CA TAGG
GTGGAGCC G
AGACCATCCTGGCTA ---- A AGAGGCC A C TGG G

GAM97 GTGAACCCGGGAGGCAGAGC 74 CACTGCACTC 2669 GA AGGCA CT A CAAG
TTGCAGTGAGCCAAGATCAT CAGCCTGGGT GT ACCCGGG GAG TGCAGTG GC A
GCCACTGCACTCCAGCCTGG GAC || ||||||| ||| ||||||| ||
GTGAC CA TGGGTCC CTC ACGTCAC CG /
G- GAC-- -- - TACT

GAM98 CACGGTGAAACCCCGTCTCT 75 CCGGGCACAG 2668 - AAAC T A-- AAAA CAA
ACTAAAACTACAAAAAATTA TGGCGGGCGC CAC GGTG CCCGTC CT CT CTA A
GCCGGGCACAGTGGCGGGCG CTGT ||| |||| |||||| || || |||
CCTGTG GTG CCGC GGGCGG GA GG GAT A
T ---- T CAC GCC- TAA

GAM99 TCGTTCTGCAGATTGACAAT 76 TGGCATGCGC 2671 -- ACA- C----- C GA T
GCCCGTCTTGCTGCTGATGA CAGTCTGTGG TCGTTCT GCAGATTG ATGCC GTCTTG
TGCT TGACT T
CTTTAGAGTCAAGTATGAGA AGAA ||||||| |||||||| ||||| |||||| |||| |||||
CAGAGCTGGCATGCGCCAGT AGCAAGA TGTCTGAC TACGG CAGAGT ATGA
ACTGA A
CTGTGGAGAACGA GG CGCG TCGAGA - -- G

GAM100 AAGATAGAGGCAGAACTGCA 77 TGTTCTGGAG 2672 GA----- AA G TG
GGACATCTGCAATGATGTTC CTGTTGGACA AAGATA GGCAG CT CAGGACATC C
TGGAGCTGTTGGACAAATAT AATA |||||| ||||| || |||||||||
CTT TTCTAT TTGTC GA GTCTTGTAG A
AAACAGG -- G TA

GAM101 GGCAGAGGGCTCTCAGGGTC 78 CTCCCTACGT 2673 -- - A - CC- CA TCC CGT
CACGTCAAGGGTCCAGCAGT CACACTCCGG GGCA GAGG GCTCTC GG GT ACGT AGGG
AGCAGT C
CGTCACCATTGCTCCCTACG AGGG |||| |||| |||||| || || |||| |||| ||||||
TCACACTCCGGAGGGTGTCT CCGT CTCT TGGGAG CC CA TGCA TCCC TCGTTA /
CAATGCC AA G G T CAC -- --- CCA

GAM102 CTTAGATGGCCAATTGAAAC 79 TATTAGGGAT 2674 T C T ACAAACAG G GTT T A
GAT
AAACAGTTCTGAGACCGTTC AATATTCATT CTTAGA GGC AA TGAA TTCTGA ACC CT CC
CCACT T
TTCCACCACTGATTAAGAGT TAGC |||||| ||| || |||| |||||| ||| || || |||||
GGGGTGGCAGGTATTAGGGA GAGTCT CCG TT ACTT GGGATT TGG GG GG
GGTGA /
TAATATTCATTTAGCCTTCT T A T ATAATA-- A AC- T - GAA
GAG

GAM103 TTCTTTCTCTTGTGCTTATT 80 TTAGCACCAC 2675 C CTTATT T GAG - CTTCTT

CTTCTTGGGAGTGGTGTAAG CACGAAGTCT TTCTTT TCTTGTG CTTC TGG TGGTGT AAGA
C
ACTTCTTCTTCCTTTTCTTA CGAC |||||| ||||||| |||| ||| |||||| ||||
GCACCACCACGAAGTCTCGA GAGAAG AGAGCGC GAAG ACC ACCACG TTCT T
CGCGAGATGAAGAG T AGCTCT C --- A TTTCCT

GAM104 GGCCAATTGAAACAAACAGT 81 TATTAGGGAT 2676 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAAAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - AAA

GAM105 TTTTCTTCCTATTACTTGTC 82 TTCCAAAGAA 2677 - AC ---- TGCCAC
TCTGCCACCAGAAATGAGAA TGGGATAGAA TTTTCT TCCTATT TTG TCTC C
TTCCAAAGAATGGGATAGAA AA |||||| ||||||| ||| ||||
AA AAAAGA AGGGTAA AAC AGAG /
T GA CTTA TAAAGA

GAM106 CTTTTGGCAGAGCTCCCACT 83 TTGAAGGAGC 2679 AGA CACTATTTG GA
ATTTGCAATGGATTTTGGAT GCCAAAAG CTTTTGGC GCTCC CAATGGATTTTG T
AAACAAGATCTGTTGAAGGA |||||||| ||||| ||||||||||
GCGCCAAAAG GAAAACCG CGAGG GTTGTCTAGAAC A
--- AA------- AA

GAM107 ACAAGTTATTGCCACTGCTA 84 TACGGTATAT 2678 A TATT C C ---- CA- TT- AT
CGGTATATTTCAAGAGATTC TTCAAGAGAT ACA GT GCCA TG TACGG TATATTT AGAGA
CT G
TATGCCAGGTATTCTCTGAA TCTA ||| || |||| || ||||| ||||||| ||||| ||
AAGTATAGATCCTGTATTAA TGT CA CGGT AT ATGTC ATATGAA TCTCT GG C
TGGCTCCTACATGT A TCCT A T CTAG AAG TAT AC

GAM108 TTGTTTTCCCTAACATCAAG 85 TGCCTTGATG 2680 CC- --- -- AGAG
AATGTGAGAGAACCACCACC TTAGACAAAA TTGTTTT CTAACATCAAG AAT GTG A
AATTTGCCTTGATGTTAGAC ACAG ||||||| |||||||||| ||| |||
AAAAACAG GACAAAA GATTGTAGTTC TTA CAC A
ACA CGT AC CACC

GAM109 GAACATCTTGTAAGATACTC 86 TAAGATACTC 2681 C A-- T C-- - CT T
CTGACATCTTGCTTTAGCAC CTGACATCTT GAACAT TTGT AGA ACT CTG ACAT TGC T
ATGTACAGTACAGTTTCTAT GCTT |||||| |||| ||| ||| ||| |||| |||
GATAATGTGTTT TTTGTG AATA TCT TGA GAC TGTA ACG T
T GTA T CAT A C- A

GAM110 TCTACAAAGTGCCGTCCACT 87 TCCAATCTGA 2682 A - - CACTG CT- C
GAGACTGAGGCCTTGGCTTC TGGGCATGTT TCT CAAA GTGCC GTC AGA GAGGC T
CAATCTGATGGGCATGTTTG TGAG ||| |||| ||||| ||| ||| |||||
AGA AGA GTTT TACGG TAG TCT CTTCG T
- G G ----- AAC G

GAM111 TCTGGACTGCCCAAATTTGT 88 GGACTGCCCA 2684 G -------- AAA TCAT
CCTCATCAACTGGACAGGCG AATTTGTCCT TCTG AC TGCCC TTTGTCC C
AGGGCGTGAACGATGTGCGG CATC |||| || ||||| |||||||
A AGGC TG GCGGG GGACAGG /
G TAGCAAGT AGC TCAA

GAM112 GCACCATGGCCAGCTTCCTG 89 CACGGGCCGA 2683 - T CA- T GAAGGG A ACC
AAGGGGGCCCATGTGACCAT GGAGGATGTG GCAC CA GGC GC TCCT GGCCC TGTG A
CAACGCACGGGCCGAGGAGG GAGC |||| || ||| || |||| ||||| ||||
ATGTGGAGCCTGAGTGC CGTG GT CCG TG AGGA CCGGG ACGC T
A - AGG T GGAG-- C AAC

GAM113 GCCTCCCTCGAGGAAGCCCA 90 TTGGTAATCT 2685 C- A ----- C - A
CACATAACATGTTGTTGGTA TTCCACGGTA GCCTCC TCG GGAA GCC ACA CAT A
ATCTTTCCACGGTAGGAGGC GGAG |||||| ||| |||| ||| ||| |||
CGGAGG GGC CCTT TGG TGT GTA /
AT A TCTAA T T C

GAM114 TTGGTGTAGACTCCAGGCCT 91 TTCCTTGGAG 2686 TG T - CC-- T - ACA
GTTCTTCTGGGCACAGCATA CTCTCCATTG T GTG AGA CTCCAGG TGT CTTCTGGG C G
GCCCCAGGAGACAATTCCTT G | ||| ||| ||||||| ||| |||||||| |
GGAGCTCTCCATTGG G TAC TCT GAGGTTC ACA GAGGACCC G C
GT C C CTTA - C ATA

GAM115 TCTTGTGTTGAGACTTCGTG 92 TACACCACTC 2687 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM116 CCCTGCCTGCTAGCTGGGGA 93 ATCCATGAGA 2688 TGCCT - CCG CT CA G
CCGCTCCTTGGCAGATGTCA TCTCCCACAG CCC GCTAGCTG GGGA CTC TGG GAT T
TCATCCATGAGATCTCCCAC TTGG ||| |||||||| |||| ||| ||| |||
AGTTGGTTTGGG GGG TGGTTGAC CCCT GAG ACC CTA /
TT--- A CTA T- TA C

GAM117 GGCCAATTGAAACAAACAGT 94 TATTAGGGAT 2689 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM118 ATTGTGAATAGTGCCGCAAT 95 TAGCAGCATG 2690 A C A C G
AAACATACGTGTGCATGTGT ATTTATAAT ATTGTGAAT GTGC GC ATAAA ATACGT T
CTTTATAGCAGCATGATTTA ||||||||| |||| || ||||| ||||||
TAAT TAATATTTA TACG CG TATTT TGTGTA G
G A A C C

GAM119 CTTCTTCAGTGAGACGGGCG 96 TTTGTAGACT 2691 T GAC- CG ----- T C
CTGGCAAGCACGTGCCCCGG TGGAACCCAC CTTC TCAGTGA GGG CTG GCAAGCACG
GCC C
GCTGTGTTTGTAGACTTGGA AGTC |||| ||||||| ||| ||| ||||||||| |||
ACCCACAGTCATTGATGAAG GAAG AGTTACT CCC GGT TGTTTGTGT CGG /
T GACA AA TCAGA - G

GAM120 GGCCAATTGAAACAAACAGT 97 TATTAGGGAT 2692 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM121 ATTTGAGAAGGAGGCTGCTG 98 CTTCAAGTAT 2693 TG AGG - GA T AAA
AGATGGGAAAGGGCTCCTTC GCCTGGGTCT ATT AGA AGGC TGCT GA GGG G
AAGTATGCCTGGGTCTTGGA TGGA ||| ||| |||| |||| || |||
T TAG TCT TCCG ATGA CT CCT /
GT GGG T A- T CGG

GAM122 AACGTGTCTGTGCAGGGTAT 99 TGCAGGGTAT 2694 G- G G ATTATCATC CCG
TATCATCTACCGAGCCGCTA TATCATCTAC AACGT TCT TGCAG GT TACCGAG C
CTTCGGTATCTATGACACTG CGAG ||||| ||| ||||| || |||||||
CAAAGGGAATGTT TTGTA GGA ACGTC CA ATGGCTT /
AG A A GTATCT--- CAT

GAM123 GGCCTCGGTGACTGCCTGGT 100 GATTAAGGGC 2695 C ACT GG GA - A
TAAGATCTACAAATCTGATG CTGTACCAAG GGCCT GGTG GCCT TTAA TCTA CA A
GGATTAAGGGCCTGTACCAA GCT ||||| |||| |||| |||| |||| ||
GGCT TCGGA CCAT CGGG AATT GGGT GT T
A GTC -- A- A C

GAM124 GCTATAAAGGAACAAGGATT 101 GAGGACCTAA 2696 T AA- CA A- TGCTATT
CCGTGCTATTATCATCTCTG TTCTGTGTAT GC ATA GGAA AGG TTCCG A
GAGGACCTAATTCTGTGTAT GC || ||| |||| ||| |||||
GC CG TAT TCTT TCC GAGGT /
- GTG AA AG CTCTACT

GAM125 GCCCAGGCAGAGTCTCTGCG 102 CTTGCTGTGC 2697 - - AG TA A-- C
TTACAAACTCCTAGGAGGGC GGAGGGCCTG GC CCA GGCAG TCTCTGCGT CAA CTC T
TTGCTGTGCGGAGGGCCTGC CTAT || ||| ||||| ||||||||| ||| |||
TATGGTGT TG GGT TCGTC GGAGGCGTG GTT GAG A
T A CG TC CGG G

GAM126 GGTCTACGCCATCTGTTATT 103 TGTTATTGTC 2698 AC CTG T - ---- TC
GTCCCCTGCCTCGCCTGGCA CCCTGCCTCG GGTCT GCCAT TTA TGTC CC CTGCC G
GATCTGGAGGCGCTGAAAGT CCTG ||||| ||||| ||| |||| || |||||
GGCAGACT TCAGA CGGTG AGT GCGG GG GACGG C
-- AA- C A TCTA TC

GAM127 AGAGTGACAAAATGGTGACA 104 TATCTTACCA 2699 TG AAA- AC GGG
GGTAGCTGGGACCTAGGCTA TGAAGGTTGT AGAG AC ATGGTG AGGTAGCT A
TCTTACCATGAAGGTTGTTT TTT |||| || |||||| ||||||||
T TTTT TG TACCAT TCTATCGG C
GT GAAG -- ATC

GAM128 GGTAGTTGATGCCAACCTTG 105 TAGTTGATGC 2700 A A A - - G - A CA
AAGCCAGTGGGGCACCAATC CAACCTTGAA GGT GTTG TGCCA CC TTGAAGCCA GTG GGCA
CCA TC C
CACAAGACTGGATGCTGCGC GCCA ||| |||| ||||| || ||||||||| ||| |||| ||| ||
TTGGTTTCGATGGTGGCAAT CCG CGGT ACGGT GG AGCTTTGGT CGC TCGT GGT AG /
GGCAGCC A A - T T G A C AA

GAM129 TTGTGGTCCATGGCGAGCCC 106 CATGCACACA 2701 - C- C A C --- AT - ---
GC
AGGCCTCAGACAATGGCTGT GCTCTCTGTA TTGTGGT CCATGG GAG CC GGC TCAG ACA G
GCTGTG GTGTT T
GGTGTTGCTCAGACATGCAC CCTT ||||||| |||||| ||| || ||| |||| ||| | |||||| |||||
ACAGCTCTCTGTACCTTGAG GACACCA GGTACC CTC GG CCG AGTT TGT C CGACAC
TACAG /
CCAGGTCTCCACCATGGCAC C AC T A - CCA CT T ACG AC
CACAG

GAM130 CGGCTCCGAGAGCAGGTTCT 107 TACACATTGA 2702 - AGAG C A TC GCAG C
TCGTGAGTTCCTCGCAGGGC GAACCTGAAC CGGC TCCG CAGGTTCTT GTG GT CTC GG
C

CGGTCAGAGCTACACATTGA ATGG |||| |||| ||||||||| ||| || ||| ||
GAACCTGAACATGGAGGCCG GCCG AGGT GTCCAAGAG TAC CA GAG CT G
G ACAA T A TC A--- G

GAM131 TTCCACCCATGGCAAATTCC 108 TGAGAACGGG 2704 CCC A- ATGG-- - GT
ATGGCACCGTCAAGGCTGAG AAGCTTGTCA TTCCA ATGGCAA TTCC CA CC C
AACGGGAAGCTTGTCATCAA TCAA ||||| ||||||| |||| || ||
TGGAA AAGGT TACTGTT AAGG GT GG /
AAC CG GCAAGA C AA

GAM132 TTCACCACCATGGAGAAGGC 109 CTGCCCCCTC 2703 CA GA GGC CT T A
CAAA TCA
TGGGGCTCATTTGCAGGGGG TGCTGATGCC TTCAC CCATG GAA TGGGG CATT
GCAGGGGGG GC AGGG T
GAGCCAAAAGGGTCATCATC CCCA ||||| ||||| ||| ||||| |||| ||||||||| || ||||
TCTGCCCCCTCTGCTGATGC AAGTG GGTAC CTT ACCCC GTAG CGTCTCCCC CG
TCTC /
CCCCATGTTCGTCATGGGTG TG TG GT- C- T - ---- TAC
TGAA

GAM133 CCAGAAGACTGTGGATGGCC 110 TGGATGGCCC 2705 A CT T CCC C - AA- GT
CTCCGGGAAACTGTGGCGTG TCCGGGAAAC CCAG AGA G GGATGG TC GG GA CTGTGGC
G
ATGGCCGCGGGGCTCTCCAG TGTG |||| ||| | |||||| || || || |||||||
AACATCATCCCTGCTCTACT GGTC TCT T CCTACT AG CC CT GGCGCCG A
GG A CG C ACA A T CGG GT

GAM134 GCTGTGGGCAGGTCATCCCT 111 TCACTGGATG 2706 T - ---- C- GAA
GAGCTGAACGGGAAGCTCAC GCTTCCGTGT GC GTGGG CA GGTCATCC TGAGCT C
TGGATGGCTTCCGTGTCCCA CCCA || ||||| || |||||||| ||||||
CTGC CG CACCC GT TCGGTAGG ACTCGA G
T T GCCT TC AGG

GAM135 AAGATAGAGGCAGAACTGCA 112 TGTTCTGGAG 2707 GA----- AA G TG
GGACATCTGCAATGATGTTC CTGTTGGACA AAGATA GGCAG CT CAGGACATC C
TGGAGCTGTTGGACAAATAT AATA |||||| ||||| || |||||||||
CTT TTCTAT TTGTC GA GTCTTGTAG A
AAACAGG -- G TA

GAM136 CGAGCACATGATGGCGATAC 113 CGGGAGCTCA 2708 G GC- ACGGG AA G T
GGGAGCTCAAAGTGTGCCTT AAGTGTGCCT CGA CACATGATG GAT AGCTC AGTGT CCT C
CTCGGGGACACTGGGGTTGG TCTC ||| ||||||||| ||| ||||| ||||| |||
GAAATCAAGCATCGTGTGTC GCT GTGTGCTAC CTA TTGGG TCACA GGG T
G - GAA AAGGG G- G C

GAM137 AATTGATAAAGCCAGAGTGG 114 TGTGACCCAA 2709 A G GA AACCACT - - A A AGAC
AGACACAGAACCACTGGTTC GCTGTGTCCA AATTG TAAAGCCAGA TGGA CACAG GGTT CAC CT CA TG A
ACCTACAATGAGACAATGAC ATCT ||||| |||||||||| |||| ||||| |||| ||| || || ||
AGTGGAGAGTGTGACCCAAG TTGAC GTTTCGGTCT ACCT GTGTC CCAG GTG GA GT AC /
CTGTGTCCAATCTGGCTTTG - A -- GAAC--- T A G G AGTA
CAGTT

GAM138 CTCTCGGGGGCGGAGGGGGT 115 TCCCTCCCAA 2710 - GC- - C TGA
GCCTGTGAGCTCTCAGCCAC CCCTGGTGAG CTC TCGGGG GGAGGGG GTG CTG G
TTCCCTCCCAACCCTGGTGA ||| |||||| ||||||| ||| |||
G GAG GGTCCC CCTCCCT CAC GAC C
T AAC T C TCT

GAM139 AGACGCTCGTTTTCTCAGGA 116 TCAAGGGTCG 2711 T TT CA CAA C A
CCCAAGGAACCAAAATTGCT TGTGTTT AGACGC CG TTCT GGACC GGAA CA A
TCTGATGGTCTCAAGGGTCG |||||| || |||| ||||| |||| ||
TGTGTTT TTTGTG GC GGGA TCTGG TCTT GT A
T T- AC TAG C T

GAM140 GGTCACTCGTATAGAACAGT 117 TAGAACAGTA 2712 --- A GAA TATT TAT
ATTGTTTCTATAATTTGAAG TTGTTTCTAT GGTC ACTCGT TA CAG GTTTC A
CTCCCTGAATGGACGGGTTC AATT |||| |||||| || ||| |||||
AGGCC CCGG TGGGCA GT GTC CGAAG A
ACT G AA- CCT- TTT

GAM141 AACTTGAAAGTGAACAGTAT 118 TGGCCCACAT 2713 T AG- T ACTTTCC AT A
GACTTTCCTGATCCAGAACA CTGTTTAATC AACT GAA TGAACAG ATG TG CCAGA C
GTTTGGCCCACATCTGTTTA TTCC |||| ||| ||||||| ||| || |||||
ATCTTCCAGTT TTGA CTT ATTTGTC TAC AC GGTTT A
C CTA - ------- CC G

GAM142 TCCCCCGACGGGCGGCTCAT 119 TTAAGCTGTG 2715 CCGACG G ATCG GC GA A
CGTGTCTGCCAGTGATGACA GGACAAGAGC TCCC GGC GCTC TGTCT CAGT TGACA G
AGACTGTTAAGCTGTGGGAC AGCC |||| ||| |||| ||||| |||| |||||
AAGAGCAGCCGGGA AGGG CCG CGAG ACAGG GTCG ATTGT A
------ A A--- GT A- C

GAM143 CACCTATGTGGACTTCCAGC 120 CGGCATGGAC 2714 A--- GACT - - G ACG
CCAGTGGGACGTGCATTGCG AACACAGTGA CACCT TGTG TCCA GCC CAGTG G T
CTGCGGCATGGACAACACAG AGGT ||||| |||| |||| ||| ||||| |
TGAAGGTG GTGGA ACAC AGGT CGG GTCGC T G

AGTG AAC- A C G TAC

GAM144 CAGTGAGACCAGTGTCCTGA 121 CACAGACTAT 2716 AC TCC CGA-- C G
ATCGACTCTGCCGGCTCGGC ATTCGCTTCA CAGTGAG CAGTG TGAAT CT TGCCG C
ACAGACTATATTCGCTTCAC CTGA ||||||| ||||| ||||| || |||||
TGAGTTCATTG GTTACTT GTCAC GCTTA GA ACGGC /
GA TTC TATCA C T

GAM145 GAGAAGATCAAAGGTGGAAT 122 TCTCAATGCC 2717 AT- T ATC A -- T AAGA G
GA G
CCACACAGCAGATACCAAGA GTGTGTTCTC GAGAAG CAAAGG GGA CACAC GCA GA ACC
CA CAGG GT T
CAGCAGGGAGTGTGTGCCTC TTTG |||||| |||||| ||| ||||| ||| || ||| || |||| ||
TTGATGCAGGTCTCAATGCC CTCTTC GTTTCT CTT GTGTG CGT CT TGG GT GTTC
CG G
GTGTGTTCTCTTTGCTGCTT GTC - --- C AA C AC-- A TC T
CTC

GAM146 CTTCAGGAGCCAGCTGTAGG 123 CAGGAGCCAG 2718 - - GTG T TC
TGTCCTTGTCCTGCAGGAGC CTGTAGGTGT CTTCAGGAG CCA GCTGTAG TCCT G C
TGCAGCATGGCCTTCTGAAG CCTT ||||||||| ||| ||||||| |||| |
GAAGTCTTC GGT CGACGTC AGGA C /
C A G-- - GT

GAM147 GTAGTATGGCATCGAGGAGA 124 TCAAAACCCT 2719 T CATC AATG-- CAAACCTG
ATGGAGACCAAACCTGTGAT CCTCATCATC GTAG ATGG GAGGAG GAGAC T
AACCTGTCTCAAAACCCTCC TAC |||| |||| |||||| |||||
TCATCATCTAC CATC TACT CTCCTC CTCTG /
- A--- CCAAAA TCCAATAG

GAM148 CCACCATTAAGCAGTTCATG 125 AGATGCTCTG 2721 TAA TT - - TCG
GACATCTTCTCGCTACCGGA CTGTCCTGTG CCACCAT GCAG CA TGGA CATCTTC C
GATGCTCTGCTGTCCTGTGT TGGT ||||||| |||| || |||| |||||||
GGTGG GGTGGTG TGTC GT GTCT GTAGAGG T
--- CT C C CCA

GAM149 ACCAGTGGATCGAGCAGGAC 126 AGCAGGACAT 2720 - ATCGAG TG AAGTA GA
ATGGAGAAGTACATCCTGAG GGAGAAGTAC ACCAG TGG CAGGACA GAG CATCCT G
AGGGGATGAGACGTTTGCTG ATCC ||||| ||| ||||||| ||| ||||||
TCCTGAGCCGCCTGGT TGGTC GCC GTCCTGT TTT GTAGGG /
C GA---- CG GCAGA GA

GAM150 GAAGAAGGGACCCCAGGTCA 127 AGGGACCCCA 2722 A-- A - A-- - - - CC
GAGACTGGAGCCATTACTTC GGTCAGAGAC GAAGA GGG CCC CAGGTC GA GA CT GGAG
A

AAGATCATCGAGGACCTGAG TGGA ||||| ||| ||| |||||| || || || ||||
GGCTCAGATCTTC CTTCT CTC GGG GTCCAG CT CT GA CTTC T
AGA - A GAG A A A AT

GAM151 GTGTGGCCGATGTGTCTATT 128 TCAGGAGACC 2723 - CTAT AAGA T TC
GAAGATTCTGTGATCTCACT ATTGCATCAT GTGTGGCCGATG TGT TG TTCTG GA T
CTCAGGAGACCATTGCATCA TGGC |||||||||||| ||| || ||||| ||
TTGGCCGCAC CACGCCGGTTAC ACG AC AGGAC CT C
T TT-- CAG- T CA

GAM152 GGTACAGAGAATGCAAGCGC 129 AAGCGCACGC 2725 A-- - A AA G CA GG CC
ACGCAAGGGGTGTCCACCAC AAGGGGTGTC GGT CAG AG ATGC GC CACG AGG TGT A
AGACCTCGTGGGCCGCATGC CACC ||| ||| || |||| || |||| ||| |||
TGCTGGTAACC CCA GTC TC TACG CG GTGC TCC ACA /
ATG G G C- G -- AG CC

GAM153 GCCCATCACAGCAGCCAGGA 130 CAGCAGCCAG 2724 CA --- GATG C A CG
GATGTCCTCTGAGTACCGGG GAGATGTCCT GCCCATCA GCA GCCAGGA TC TCTG GTAC
G
AGTATGCAGACGAGTTTTGG CTGA |||||||| ||| ||||||| || |||| ||||
CAAGTGCCCTGGTGGGC CGGGTGGT CGT CGGTTTT AG AGAC TATG /
CC GAA G--- C G AG

GAM154 GAAACAGACTGGGCCAATGT 131 TATCAAGGAA 2726 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM155 CTCTCGGGGGCGGAGGGGGT 132 TCCCTCCCAA 2727 - GC- - C TGA
GCCTGTGAGCTCTCAGCCAC CCCTGGTGAG CTC TCGGGG GGAGGGG GTG CTG G
TTCCCTCCCAACCCTGGTGA ||| |||||| ||||||| ||| |||
G GAG GGTCCC CCTCCCT CAC GAC C
T AAC T C TCT

GAM156 GGTGAGGTGGGTGGATCACC 133 TGAGGTGGGT 2728 - TGGA - A- A-- C
TGAGGTCAGGAGTTCAAGAC GGATCACCTG GGT GAGGTGGG TCACC TG GGTCAGG GTT
A
CAGCCTGGCCAACATGGTGA AGGT ||| |||||||| ||||| || ||||||| |||
AACCCCATCTCTACT TCA CTCTACCC AGTGG AC CCGGTCC CAG /
T CAA- T AA GAC A

GAM157 TCCACGAGCCTGGAGAGCTC 134 GCAACAGTGG 2729 A- A A- CGGA GA C
GGACTGCGAGTCCCTGGACA CTTCGGGCCG TCC CG GCCTGGAG GCT CTGC GTC C
GCAGCAACAGTGGCTTCGGG GAGG ||| || |||||||| ||| |||| |||
CCGGAGGA AGG GC CGGGCTTC TGA GACG CAG T
AG - GG CAAC A- G

GAM158 GGCCAATTGAAACAAACAGT 135 TATTAGGGAT 2730 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM159 GTAGAGCTTTATGCTGAAAA 136 GAGCTTTATG 2732 - TA GAAAA - T A
GGTGGCCACTAGAGGTCTGT CTGAAAAGGT GTAGAG CTT TGCT GGTGGC CAC AG G
GTGCCATTGCCCAGGCAGAG GGCC |||||| ||| |||| |||||| ||| ||
TCTCTGC CGTCTC GAG ACGG TTACCG GTG TC G
T -- ACCCG T - T

GAM160 GGGAAACTCCGAGGACAGAG 137 TGGCCTGATG 2731 AAA A--- - GA AA TG A
GGCTAAATCCATGAAGTTTG ATCCACAGCG GGG CTCCG GGA CA GGGCT ATCCA A G
TGGATGGCCTGATGATCCAC GAGA ||| ||||| ||| || ||||| ||||| |
AGCGGAGACCC CCC GAGGC CCT GT TCCGG TAGGT T /
A-- GACA A AG -- GT T

GAM161 AGCAGGGCCTCATACTCCTG 138 TGCCCGGGTC 2733 - CT- CT CT- CGC
GGCCTGGCGCTGTCCCTCTG TGTGCCAGCT AG CAGGGC CATA CCTGGGC GG T
CCCGGGTCTGTGCCAGCTCT CTGA || |||||| |||| ||||||| ||
GACT TC GTCTCG GTGT GGGCCCG CC /
A ACC CT TCT CTG

GAM162 TGGTAGTGGGTGAATCTGGA 139 TCACAGATTT 2734 T TGG TG GATT ----- C CA
TTGGGAAAGTCGACATTAAT GTATTCTCCA TGG AG G AATCTG GGGAA AGT GA T
CAACTCATTATTCCTCACAG ||| || | |||||| ||||| ||| ||
ATTTGTATTCTCCA ACC TC T TTAGAC TCCTT TCA CT T
- TTA GT AC-- ATTAC A AA

GAM163 GACTATGGCAAGGACCTGAT 140 TATGGCAAGG 2735 A AA- A T AGAA- CA
GGAGAAGGTCAAGAGCCCAG ACCTGATGGA GACT TGGC GG CCTGA GG GGT A
AGCTTCAGGCCGAGGCCAAG GAAG |||| |||| || ||||| || |||
TC CTGA ACCG CC GGACT TC CCG /
- GAG - - GAGAC AG

GAM164 TCACCATCTGCAGCCTTGAA 141 AAGGAGCTTT 2736 CA C- CC A TT GGAG- - AA
GGAGCTTTGGTTCGGAGACA GGTTCGGAGA TCAC TCTG AG TTGA GGAGCT GGTTC ACA
GGC A
GGCAAAGGAGCCATGTGTGG CAGG |||| |||| || |||| |||||| ||||| ||| |||
AGAGCCTGGTTTCTCAGTAC AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G
TTCCAGACCGTGA CC CT AT - T- AGGTG A AG

GAM165 GAAACAGACTGGGCCAATGT 142 TATCAAGGAA 2737 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM166 TCTTGTGTTGAGACTTCGTG 143 TACACCACTC 2738 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM167 TCTTGTGTTGAGACTTCGTG 144 TACACCACTC 2739 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM168 GGCCCAGGATCGGCAGGGCT 145 TTCCCATGCC 2740 - - G- - GC- GA A
GCTGGCAGAGGAATCCCAGC ACCAGGCTCC GGCCCAG GA TC GCAGG GCT TGGCA
GGAATCCC G
TGGGGTTCCCATGCCACCAG TGCA ||||||| || || ||||| ||| ||||| ||||||||
GCTCCTGCAGGACTTGCTGG CCGGGTC TT AG CGTCC CGG ACCGT CCTTGGGG C
GCC G C GA T ACC AC T

GAM169 CCACCACCTGGAGCCCGAGG 146 TTCTTCACGG 2741 C GGA- AG T AAGT
AGGTGCTCAAGTACAGCGAG GCAGCAAGCT CCACCA CT GCCCG GAGG GCTC A
TTCTTCACGGGCAGCAAGCT GGTG |||||| || ||||| |||| ||||
GGTGG GGTGGT GA CGGGC CTTC TGAG /
C ACGA A- T CGAC

GAM170 TGTTCTTGGTGAGAAGGGCC 147 AGTTCAGAAG 2743 - T AA GGCGGA GG A T

GGCGGATTCGGGAACTGACT AGGTTTGGCT TGTTCT TGG GAG GGGCC TTC GAACTG C
G
GCTGTAGTTCAGAAGAGGTT TTCC ||||||| ||| ||| ||||| ||| |||||| |
TGGCTTTCCAGAGGGCA ACGGGA ACC TTC TTTGG AAG CTTGAT G C
G T GG AG---- A- - T

GAM171 GTAGAGCTTTATGCTGAAAA 148 GAGCTTTATG 2742 - TA GAAAA - T A
GGTGGCCACTAGAGGTCTGT CTGAAAAGGT GTAGAG CTT TGCT GGTGGC CAC AG G
GTGCCATTGCCCAGGCAGAG GGCC |||||| ||| |||| |||||| ||| ||
TCTCTGC CGTCTC GAG ACGG TTACCG GTG TC G
T -- ACCCG T - T

GAM172 AGGGGCTCACGCGCACGCTG 149 GCTCACGCGC 2744 C--- C C CA- TTCTT
CTCACCTTCTTCGACCTGGC ACGCTGCTCA AGGGG TCA GCGCA GCTGCT CC C
CTGGCGGCTGCGCATGAACT CCTT ||||| ||| ||||| |||||| ||
TCCCCT TCCCC AGT CGCGT CGGCGG GG /
TTCA A - TCC TCCAG

GAM173 TCTTGTGTTGAGACTTCGTG 150 TACACCACTC 2745 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM174 GTGAAGGAACAGTTTGCCTG 151 TATCCAGTAT 2747 AACAGT TG CT CATTTC -
ACC
GAGACATTTCTACTGGTACC CTCCGTGATT GTGAAGG T C GGAGA TACTGG TACCTT
A
TTACCAATGAGGGTATCCAG ACCT ||||||| | | ||||| |||||| ||||||
TATCTCCGTGATTACCTTCA TACTTCC A G CCTCT ATGACC ATGGGA /
T ATT--- GT -- ------ T GTA

GAM175 CAAGAAAGCCGAGGCTGGGG 152 TTTGGTCGTG 2746 GAAA C C -- G A A T A T
CTGGGTCAGCAACCGAATTC GACGTGGTCA CAA GC GAGG TGG GGCTG GTC GC
ACCGAAT CC GTT A
CAGTTTAGAGGCGGATTTGG GCCA ||| || |||| ||| ||||| ||| || ||||||| || |||
TCGTGGACGTGGTCAGCCAC GTT TG CTCC ACC CTGGT CAG TG TGGTTTA GG CGG
G
CTCAGTAAAATTG AAAA A - GA G G C - - A

GAM176 CAAGAAAGCCGAGGCTGGGG 153 TTTGGTCGTG 2746 GAAA C C -- G A A T A T
CTGGGTCAGCAACCGAATTC GACGTGGTCA CAA GC GAGG TGG GGCTG GTC GC
ACCGAAT CC GTT A
CAGTTTAGAGGCGGATTTGG GCCA ||| || |||| ||| ||||| ||| || ||||||| || |||

TCGTGGACGTGGTCAGCCAC GTT TG CTCC ACC CTGGT CAG TG TGGTTTA GG CGG
G
CTCAGTAAAATTG AAAA A - GA G G C - - A

GAM177 GACTATCCAGTTGATGGGCT 154 ATCCAGTTGA 2748 T- GG C GA - T GGA T
GCCAGATCTGGGGCATGCCC TGGGCTGCCA GACTA CCAGTTGAT GCTG CA TCTGG GGCA
GCCCA CC C
AGGACCTCATGGATGGGCTG GATC ||||| ||||||||| |||| || ||||| |||| ||||| ||
CCTCCAGGTGACAGCAATCA TTGGT GGTCGACTA CGAC GT GGACC CCGT CGGGT
GG A
GCTGGCCTGGTT CC A- A -- T - A-- T

GAM178 CAGTGCACCGCCATCAGCAG 155 TACACGGTGG 2749 T AC TCAG - TTA C - G- C T
G A
GATTTACACGGTGGGGCGCA GGCGCAGCTT AG GC CGCCA CA GGAT CA GGT G GG
GCAGCT CGA GGCCGGG G
GCTTCGAGGGCCGGGAGCTC CGAG || || ||||| || |||| || ||| | || |||||| ||| |||||||
CTGGTCATCGAGCTGTCCGA TC CG GTGGT GT CCTG GT CCA C CC TGTCGA GCT
CTGGTCC C
CAACCCTGGCGTCCATGAGC - A- CCGA A CG- C A AG - - A T
CTGGTGAGCCTG

GAM179 TGCATGGGAATGAGGCTGTT 156 CTTGGCCCAG 2750 AA- A TT- C AA
GGACGAGAACTGCTCATTTT TACCTATGCA TGCATGGG TG GGCTG GGA GAG C
CTTGGCCCAGTACCTATGCA |||||||| || ||||| ||| |||
ACGTATCC AC CCGGT TTT CTC /
ATG - TCT A GT

GAM180 CACCTTTACGGCCAAACCGT 157 TGTGGATATA 2751 TT C CC C-- C--- G
CCACCTCGACCGATTCTGTG GTTTTCCCTG CACC TA GG AAAC GTCCAC TC A
GATATAGTTTTCCCTGTTGG TTGG |||| || || |||| |||||| ||
TG GTGG GT CC TTTG TAGGTG AG C
TT - CT ATA TCTT C

GAM181 CTTGTGGGAGAGATTATCAA 158 TGGGAGAGAT 2753 T GA ATC -------- - G A AT
GCGTTTTGAGCAGAAAGGAT TATCAAGCGT CTTG GGGAGA TT AAGC GTTTT GA CAG
AAGG T
TCCGCCTTGTTGGTCTGAAA TTTG |||| |||||| || |||| ||||| || ||| ||||
TTCATGCAAGCTTCCGAAGA GAAC TCTTCT AA TTCG TAAAG CT GTT TTCC C
TCTTCTCAAG - AG GCC AACGTACT T G G GC

GAM182 CACTACGTTGACCTGAAGGA 159 AAGGACCGTC 2752 GA-- GAA- CCATTCT --
AAAT
CCGTCCATTCTTTGCCGGCC CATTCTTTGC CACTACGTT CCT GGACCGT
TTGCCGGCCT GGTG A

TGGTGAAATACATGCACTCA CGGC ||||||||| ||| ||||||| |||||||||| ||||
GGGCCGGTAGTTGCCATGGT GTGGTGTAA GGG TCTGGTA GATGGCCGGG
TCAC /
CTGGGAGGGGCTGAATGTGG GTCG AGGG CCGTT-- AC GTAC
TG

GAM183 TGCTCAGACAGGGTGTGCTG 160 ATGCTGCCCT 2754 T ACA G T T A G
GGCATCAAGGTGAAGATCAT GTGACCCAAC TGC CAG GGGT TGC GGGCA CA GGT A
GCTGCCCTGTGACCCAACTG TGGT ||| ||| |||| ||| ||||| || |||
GTA ATG GTC CCCA GTG CCCGT GT CTA A
- AA- - T C A G

GAM184 GAATTTCCGCTGCCTGTGCA 161 CCACCGCATC 2755 T T T TC AA CTT CTTTAAG
C
CTCATGAAAAGGGCTTTGGC ATCCCCCAGT GAATT CCGC GCCTG GCAC ATGAA GGG TGG
GGAAG A
TTTAAGGGAAGCAGCTTCCA TCAT ||||| |||| ||||| |||| ||||| ||| ||| |||||
CCGCATCATCCCCCAGTTCA TTTAG GGCG CGGAC CGTG TACTT CCC ACT
CCTTC /
TGTGCCAGGCGCGGTGATTT T - - -- GA CCT ACGCCA- G

GAM185 GGCCAATTGAAACAAACAGT 162 TATTAGGGAT 2756 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM186 TCTCCGGGGGCTGGCAGATG 163 TGGCAGATGG 2758 G CTG AGA AG AT
GAGGAGGCCGATGACTGGCT AGGAGGCCGA TCTCC GGGG GC TGG GAGGCCG G
TCGCTACGGCAACCCCTGGG TGAC ||||| |||| || ||| |||||||
AGA AGAGG TCCC CG ATC CTTCGGT /
G CAA GC- G- CA

GAM187 GCTACCTGTGCACTTCTACG 164 TGCCAAGTGG 2757 CACT GG G GA A AG
GCCATGTGGAGCACACCAGC GTGGACACAC GCTACCTGTG TCTAC CCAT TG GCAC CC C
CAGGGTGCCAAGTGGGTGGA AGGT |||||||||| ||||| |||| || |||| ||
CACACAGGTGGT TGGTGGACAC AGGTG GGTG AC CGTG GG /
AC-- -- A -- - AC

GAM188 TCTTGTGTTGAGACTTCGTG 165 TACACCACTC 2759 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM189 TGAATTCAGTGATATCCCTA 166 GTGGATAGGT 2760 TC- ATATC- A CC
TACACTGCCATTTAGTGGAT TATTGTACTT TGAAT AGTG CCTAT CACTG A
AGGTTATTGTACTTCCATTC CCAT ||||| |||| ||||| |||||
A ACTTA TCAT GGATA GTGAT /
CCT GTTATT G TT

GAM190 TCTTGTGTTGAGACTTCGTG 167 TACACCACTC 2761 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM191 GAAGAAGGGACCCCAGGTCA 168 AGGGACCCCA 2762 A-- A - A-- - - - CC
GAGACTGGAGCCATTACTTC GGTCAGAGAC GAAGA GGG CCC CAGGTC GA GA CT GGAG
A
AAGATCATCGAGGACCTGAG TGGA ||||| ||| ||| |||||| || || || ||||
GGCTCAGATCTTC CTTCT CTC GGG GTCCAG CT CT GA CTTC T
AGA - A GAG A A A AT

GAM192 AGGTCCAGGCAGTGACCTCA 169 TTTGCAGCTT 2763 TC CA- C A------ AG
CAAGGACAGCACAGTTTTTG AGAGATCACC AGG CAGG GTGA CTC CAAGGAC C
CAGCTTAGAGATCACCCACC CACC ||| |||| |||| ||| |||||||
TGCCCCT TCC GTCC CACT GAG GTTTTTG A
CC ACC A ATTCGAC AC

GAM193 GGGGCCTCTATCCACGAGTT 170 AGCCGCAAGT 2764 TAT CG TCT TC C AG- T
CTGCATCAACCTGCGGCAGC TCCTGCTGCT GGGGCCTC CCA AGT GCA AAC TGCGGC
CTC A
TCTACGGGGACAGCCGCAAG TGGT |||||||| ||| ||| ||| ||| |||||| |||
TTCCTGCTGCTTGGTCTGAG TCCCGGAG GGT TCG CGT TTG ACGCCG GGG C
GCCCT TCT -- T-- CC A ACA G

GAM194 CTCGATTTGAAGACTCTCCC 171 TTGAAGACTC 2765 - A - ------ ATG
TCGTATGTAAAATGGGGTAA TCCCTCGTAT CTCG ATTTGA GA CTCTC CCTCGT T
ACTGAGAGATTATCAGGTCC GTAA |||| |||||| || ||||| ||||||
GAG GAGC TGGACT TT GAGAG GGGGTA /
C A A TCAAAT AAA

GAM195 TCTGACCAGCACCCACACTC 172 GACCAGCACC 2766 T A ACACT CT - C TC
AGGCTCTGGCCGCAGTGTCC CACACTCAGG TC GACCAGC CCC CAGG CTGGC CG AGTG
C
TGTCATTCGAGTCAGGTTCT CTCT || ||||||| ||| |||| ||||| || ||||

GGGGGCTGGTTTGA AG TTGGTCG GGG GTCT GACTG GC TTAC T
T - ----- TG A - TG

GAM196 GCTTGGCCAAGTATGCAGAC 173 TGGGGTGTGT 2767 T AAGTAT G - - AC
CCTGTGGCTGACCTCCTAGA TCCGGGCCCG GCT GGCC GCA ACCCT GTGG CTG C
CCGCTGGGGTGTGTTCCGGG GC ||| |||| ||| ||||| |||| |||
CCCGGC CGG CCGG TGT TGGGG CGCC GAT T
C GCCT-- G T A CC

GAM197 ATTCTATAATGAAGATGTTT 174 TGTCAAGAAA 2768 TATA- ----- A AC GG GCA
CATGAACTGGGGCACGTATT CTTCTTATCT ATTC ATGAAGAT GTTTC TGA T G C
TGTCAAGAAACTTCTTATCT TCAT |||| |||||||| ||||| ||| | |
TCATGAACTGAAT TAAG TACTTCTA CAAAG ACT G T /
TCAAG TTCTT A -- TT ATG

GAM198 CCTGCGCGCCCTCGACGTCA 175 CTGAAGCCAG 2769 CC GAC AATG C C AATC
ATGTGGCCTTGCGCAAAATC ACAAAGAGAT CCTGCGCG CTC GTC TGGC TTG GCAA G
GCCAACTTGCTGAAGCCAGA CGTG |||||||| ||| ||| |||| ||| ||||
CAAAGAGATCGTGCAGG GGACGTGC GAG CAG ACCG AGT CGTT C
TA AAA ---- A - CAAC

GAM199 TGGTAGTGGGTGAATCTGGA 176 TCACAGATTT 2770 T TGG TG GAT ----- C CA
TGGGAAAGTCGACATTAATC GTATTCTCCA TGG AG G AATCTG GGGAA AGT GA T
AACTCATTATTCCTCACAGA ||| || | |||||| ||||| ||| ||
TTTGTATTCTCCA ACC TC T TTAGAC TCCTT TCA CT T
- TTA GT AC- ATTAC A AA

GAM200 GCTCCAGTCAACGTTTACAC 177 TCAACGTTTA 2771 C G C A C AA AAA TG
GGGAAGTAAAATCTGTCCGA CACGGGAAGT GCT CA TCAA GTTT CA GGG GTA TC T
AATGCACCCTGAAAGCTTTG AAAA ||| || |||| |||| || ||| ||| ||
AGTGAAGC CGA GT AGTT CGAA GT CCC CGT AG /
A G T A - A- AA- CC

GAM201 GGTGACAACATGCTGGAGCC 178 TTGGTTCAAG 2772 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM202 CTCGTCGATCTCGTTCTCCA 179 TACACTGGCA 2773 GATCTC - - CT TG
TGTCTTCCGTGTGCTGGATA GAGCTCACAG CTCGTC GTTCT CCA TGT TCCG T
CACTGGCAGAGCTCACAGAT ATGA |||||| ||||| ||| ||| ||||
GAG GAGTAG CGAGA GGT ACA AGGT /

ACACT- C C T- CG

GAM203 TCACCATCTGCAGCCTTGAA 180 AAGGAGCTTT 2775 CA C- CC A TT GGAG- - AA
GGAGCTTTGGTTCGGAGACA GGTTCGGAGA TCAC TCTG AG TTGA GGAGCT GGTTC ACA
GGC A
GGCAAAGGAGCCATGTGTGG CAGG |||| |||| || |||| |||||| ||||| ||| |||
AGAGCCTGGTTTCTCAGTAC AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G
TTCCAGACCGTGA CC CT AT - T- AGGTG A AG

GAM204 GACTATGGCAAGGACCTGAT 181 TATGGCAAGG 2774 A AA- A T AGAA- CA
GGAGAAGGTCAAGAGCCCAG ACCTGATGGA GACT TGGC GG CCTGA GG GGT A
AGCTTCAGGCCGAGGCCAAG GAAG |||| |||| || ||||| || |||
TC CTGA ACCG CC GGACT TC CCG /
- GAG - - GAGAC AG

GAM205 GCCTTATTGGAGGAATTGTT 182 TGTCAAGAGT 2776 - G C- T TTGTCCTG
CCATCTTCTGTTGTCCTGAC TTTTCTAATA GCCT TATTGGAGGAATT TT CATC TCTG A
TTCTTTCCAGGTGATGTCAA TGGG |||| |||||||||||| || |||| ||||
GAGTTTTTCTAATATGGGC CGGG ATAATCTTTTTGA AA GTAG GGAC /
T G CT T CTTTCTTC

GAM206 CGGCGGCAAGATGGCAGTGC 183 AAGTTTGTCG 2778 GGC- G--- - A AAG
AAATATCCAAGAAGAGGAAG CTGATGGCAT CGGC AAGATG CAGTG CAAAT TCC A
TTTGTCGCTGATGGCATCTT CTTC |||| |||||| ||||| ||||| |||
CAAAGCTG GTCG TTCTAC GTCGC GTTTG AGG /
AAAC GGTA T A AGA

GAM207 AATGAGTTTCTTACTCGGGA 184 TACTCTGGAG 2777 GA T - G C GA
GCTGGCTGAAGATGGCTACT TTGAGGTGCG AAT GT TCTTA CTC GGAG TGGCT A
CTGGAGTTGAGGTGCGAGTT AGTT ||| || ||||| ||| |||| |||||
TTG CG GGAGT GAG TCTC ATCGG G
AG T T G - TA

GAM208 GTAGAGCTTTATGCTGAAAA 185 GAGCTTTATG 2780 - TA GAAAA - T A
GGTGGCCACTAGAGGTCTGT CTGAAAAGGT GTAGAG CTT TGCT GGTGGC CAC AG G
GTGCCATTGCCCAGGCAGAG GGCC |||||| ||| |||| |||||| ||| ||
TCTCTGC CGTCTC GAG ACGG TTACCG GTG TC G
T -- ACCCG T - T

GAM209 GGGAAACTCCGAGGACAGAG 186 TGGCCTGATG 2779 AAA A--- - GA AA TG A
GGCTAAATCCATGAAGTTTG ATCCACAGCG GGG CTCCG GGA CA GGGCT ATCCA A G
TGGATGGCCTGATGATCCAC GAGA ||| ||||| ||| || ||||| ||||| |
AGCGGAGACCC CCC GAGGC CCT GT TCCGG TAGGT T /

A-- GACA A AG -- GT T

GAM210 TGGTGGCTGGGGGCCAGCTG 187 TCCGCCAGTT 2781 TG G - TG---- AG G A-- GGG
GGCGAGCTGCACAACGGGAC CTGCTCGGGC TGGTGGC GGG CC AGC GGCG CT CAC
AC A
ACAGTATCGTGAGGTCCGCC TCTG ||||||| ||| || ||| |||| || ||| ||
AGTTCTGCTCGGGCTCTGGC ACCACCG CTC GG TCG CCGC GG GTG TG C
CACCA GT G C TCTTGA CT A CTA ACA

GAM211 GTAGAGCTTTATGCTGAAAA 188 GAGCTTTATG 2783 - TA GAAAA - T A
GGTGGCCACTAGAGGTCTGT CTGAAAAGGT GTAGAG CTT TGCT GGTGGC CAC AG G
GTGCCATTGCCCAGGCAGAG GGCC |||||| ||| |||| |||||| ||| ||
TCTCTGC CGTCTC GAG ACGG TTACCG GTG TC G
T -- ACCCG T - T

GAM212 GGGAAACTCCGAGGACAGAG 189 TGGCCTGATG 2782 AAA A--- - GA AA TG A
GGCTAAATCCATGAAGTTTG ATCCACAGCG GGG CTCCG GGA CA GGGCT ATCCA A G
TGGATGGCCTGATGATCCAC GAGA ||| ||||| ||| || ||||| ||||| |
AGCGGAGACCC CCC GAGGC CCT GT TCCGG TAGGT T /
A-- GACA A AG -- GT T

GAM213 CAAGAAGGTTATCTCCTCAG 190 TGTGGTGGCT 2784 GAA TC A GA GT
CCAACAGAGCTGTGGTTGGT GGAGGTGGCC CAA GGTTATCTCC AGCCA CA GCT G
GTGGTGGCTGGAGGTGGCCG GAAT ||| |||||||||| ||||| || |||
AATTG GTT CCGGTGGAGG TCGGT GT TGG G
AAG -- G G- TT

GAM214 CTTCTCCTCAGCTGGAGCAG 191 TGCAGCACCA 2785 T T- A A G - GGG
CAGCAGTGGAGGGGGCAGGA GCTGCTGGAG CT CTCC CAGCTGG GC GCA CAGT GGAGG C
CCTCCTGCTGGTGCAGCACC CAG || |||| ||||||| || ||| |||| |||||
AGCTGCTGGAGCAG GA GAGG GTCGACC CG CGT GTCG CCTCC A
C TC A A G T AGG

GAM215 GCATTGATCTTATCCTCCGT 192 TTGATCTTAT 2786 GAT AT TC GA T CTCA
GACTGTCACCTCATCGTCGT CCTCCGTGAC GCATT CTT CC CGT CTG CAC T
GCAGAATGAGGGCCGAGTAG TGTC ||||| ||| || ||| ||| |||
ATGC CGTAG GAG GG GTA GAC GTG /
AT- CC GA A- - CTGC

GAM216 GTCCCGAAACAAGCTTTCAC 193 CCAGGGCCTC 2787 GAA TT A CGT A CC
CGACGTGGCCACTGGCTCCC GGGGCCGCTT GTCCC ACAAGC TC CCGA GGCC CTGGCT
C
TGGGCCAGGGCCTCGGGGCC GTGG ||||| |||||| || |||| |||| ||||||

GCTTGTGGGAT TAGGG TGTTCG GG GGCT CCGG GACCGG /
--- CC - --- - GT

GAM217 GACTGAAGGAGGAATATCAG 194 AGAATGCTGA 2788 GA GA AT CCTTATC G-- GAG
TCCCTTATCCGGTATGTGGA CAACGATTGG GACT AG GGA ATCAGTC CGGTAT TG A
GAACAACAAGAATGCTGACA TTCC |||| || ||| ||||||| |||||| ||
ACGATTGGTTCCGACTGGAG CTGA TC CCT TGGTTAG GTCGTA AC A
TC GG AG -- CAACA-- AGA AAC

GAM218 GCTTTATTATGGCTGCTGTT 195 TATTATGGCT 2789 TT -- C - AA GA AC- TTT
GTCCAACAGAACGACCTAGT GCTGTTGTCC GCT ATTAT GGCTG TGTT GTCC CA ACG
CTAGTA G
ATTTGAATTTGCTAGTAACG AACA ||| ||||| ||||| |||| |||| || ||| ||||||
TCATGGAGGATGAACGACAG CGA TAGTG TCGAC GCAA TAGG GT TGC GATCGT A
CTTGGTGATCCAGC CC GT A G AG AC AAT TTA

GAM219 ACCGTGTTAGCCAGGATGGT 196 TCCACCCACC 2790 CG TT - A TCTC TCCTG
CTCGATCTCCTGACCTTGTG TCGGCTCCCA AC TG AGCC AGG TGG GATC A
ATCCACCCACCTCGGCTCCC AAGT || || |||| ||| ||| ||||
AAAGT TG AC TCGG TCC ACC CTAG C
AA CC C - CAC- TGTTC

GAM220 ATCTTCATGGTGCTGGGCGC 197 CTGCATCCTG 2791 T GTG --- --- -- T- A
CAGGGCGGTGGATCTCCTTC TCAGCAATGC ATC TCATG CTGGGC GC CAGG GCGG GG T
TGCATCCTGTCAGCAATGCC CCGG ||| ||||| |||||| || |||| |||| ||
CGGATACATGGTGGT TGG GGTAC GGCCCG CG GTCC CGTC CC C
T ATA TAA ACT TA TT T

GAM221 ATGCAGCACAAGTTCTCATA 198 ATCAGGTTTT 2793 C TT CATATCC TTTTT
TCCTTGCTTTTTCCATTTTG TGTCTGCAT ATGCAG ACAAG CT TTGC C
CAATCAGGTTTTTGTCTGCA |||||| ||||| || ||||
T TACGTC TGTTT GG AACG C
- TT ACT---- TTTTA

GAM222 GTGCACTCGATGATGCGGCC 199 TTCGTCCCGA 2794 C AT CC CTT TGCTT C
CG-- A
CACTTCCAGCTTGCTTTTGG AGTTGGTGTC GTGCA TCG GATGCGG CA CCAGCT TTGGG
ACG GC G
GCACGCGGCAGATGCAGTTC CCGT ||||| ||| ||||||| || |||||| ||||| ||| ||
GTCCCGAAGTTGGTGTCCCG CACGT AGT CTGTGCC GT GGTTGA AGCCC TGC
CG A
TGTCTGAATGCAC A -- CT --- ----- - TTGA T

GAM223 AAGATGTAGCGGGTTTTCTG 200 TAGCGGGTTT 2792 TGT- C GT G GG C
GTGGTGGATCCGAAGATGGG TCTGGTGGTG AAGA AG GG TTTCTG TGGT ATC G
CCACAGAGATTCCACTTTCC GATC |||| || || |||||| |||| |||
TCTT TTCT TC CC AGAGAC ACCG TAG A
CCTT A TT - GG A

GAM224 GATGCCGACTGGGAGCTACT 201 AGCTACTGGG 2795 CGA- GAGCTA GGT A
GGGTGAGCTGGACTACCAGC TGAGCTGGAC GATGC CTGG CTG GAGCTGG C
TTCAGGACCAGGACAGCGTC TACC ||||| |||| ||| |||||||
CTGCG GACC GAC TTCGACC T
ACAG AG---- --- A

GAM225 GAGCAGCTACGAGGAGCAGC 202 TGCTGCTCGT 2796 - G G GACC CGCT
CGACCGTGCGCTTCCAACAC GGCCTGCTC GAGCAG CTACGAG AGCA CC GTG T
CAGGTGCTGCTCGTGGCCTG |||||| ||||||| |||| || |||
CTC CTCGTC GGTGCTC TCGT GG CAC /
C G - AC-- AACC

GAM226 CACCTTTACGGCCAAACCGT 203 TGTGGATATA 2797 TT C CC C-- C--- G
CCACCTCGACCGATTCTGTG GTTTTCCCTG CACC TA GG AAAC GTCCAC TC A
GATATAGTTTTCCCTGTTGG TTGG |||| || || |||| |||||| ||
TG GTGG GT CC TTTG TAGGTG AG C
TT - CT ATA TCTT C

GAM227 TTGGTCCATATCTCCATGCA 204 TCCATATCTC 2798 TC ATCTCC- G- - ACA
TGGCGGATACAGTGAAATCT CATGCATGGC TTGG CAT ATGCATG CG GAT G
CGAGCATGCATCTTCTCGGT GGAT |||| ||| ||||||| || |||
GAGCCAG GACC GTG TACGTAC GC CTA T
GA GCTCTTC GA T AAG

GAM228 AGCCATCCAGCGTCGCTGTA 205 TGAAGTACCA 2799 - GTC- GTA T CTG
AGTTCCTCTGTCTCAGGGCT GCTGAGGTGG AGCCATC CAGC GCT AGT CCT T
GAAGTACCAGCTGAGGTGGC CT ||||||| |||| ||| ||| |||
T TCGGTGG GTCG TGA TCG GGA /
A ACCA AG- - CTC

GAM229 CCGTTCCAGTTCGAGATCAC 206 TTCCAGTTCG 2800 - CG- CAC- GT
CTTCGAGTGCATCGAGGACC AGATCACCTT CCGTTCCA GTT AGAT CTTCGA G
TGTCTGAAGACTTGGAATGG CGAG |||||||| ||| |||| ||||||
GGTAAGGT CAG TCTG GGAGCT /
T AAG TCCA AC

GAM230 GAGACGGGCGGATCACGAGG 207 TTGGCTAACA 2801 CGGA GA---- GATCG

TCAGGAGATCGAGACCATCT CGGTGAAACC GAGACGGG TCAC GGTCAGGA A
TGGCTAACACGGTGAAACCC CCGT |||||||| |||| ||||||||
CGTTTC CTTTGCCC AGTG TCGGTTCT /
CAA- GCACAA ACCAG

GAM231 GGACCAGTGGGCCAGAGATG 208 TGTTAAGTAT 2802 - GT GA-- CCT TT
ACCCTGCTTTCTTGGTCCTG CTGGCTCTGT GGAC CA GGGCCAGA TGAC GCT C
TTAAGTATCTGGCTCTGTGT GTGT |||| || |||||||| |||| |||
GTCC CCTG GT CTCGGTCT ATTG TGG /
T GT ATGA TCC TT

GAM232 CCATGTCATCAGCGTGGACC 209 CGTGCTATGA 2803 TCAG - - T AGACC
CTTCAGACCAGAAGAAGACG CATTGACGTG CCATGTCA CGTGG AC CC TC A
GCGTGCTATGACATTGACGT G |||||||| ||||| || || ||
GG GGTGCAGT GTATC TG GG AG G
TACA G C C AAGAA

GAM233 AGGAGAAGCTGTGCTCCGTC 210 TGGCAACCGC 2804 AA-- T GCT G GAAC
GCCTGGAACTTCGAGCAGGA GATCCTCCT AGGAG GC GT CCGTC CCTG T
GATGGCAACCGCGATCCTCC ||||| || || ||||| ||||
T TCCTC CG CA GGTAG GGAC T
CTAG C AC- A GAGC

GAM234 GGAGGTGGTGGAGGCTGTGA 211 CATTGTGGGC 2805 GG G ------ T AG- CAA
GGT
CCATTGTAGAGACAACAACC TACGTGGAAA GGAGGT TGGAGGCT TGA CCAT GTAG
ACAA CCAT G
ATGGTGGTAGTGGGCATTGT CCCT |||||| |||||||| ||| |||| |||| |||| ||||
GGGCTACGTGGAAACCCTCG CTTCCA GCCTCCGG GCT GGTG CATC TGTT GGTG
/
AGGCCTCCGGACCTTC G- A CCCAAA - GGG ACG ATG

GAM235 TCACAGACTTCCTGGGATAC 212 GTGCGGGAAG 2806 AGACT- G CAAA G--- CT
AAAGGCTGGCATGACTCACA TCGACATGTG TCAC TCCTGG ATA GGCT GCATGA C
TCGTGCGGGAAGTCGACATG CCGG |||| |||||| ||| |||| ||||||
TGCCGGGATCCAAGGTGA AGTG AGGGCC TGT CTGA CGTGCT A
GAACCT G ACAG AGGG AC

GAM236 TTGTCGTCATTGGACACGTA 213 TAAATGCGGT 2808 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM237 GGTGACAACATGCTGGAGCC 214 TTGGTTCAAG 2807 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM238 GGTTTTCAAGGTGTCATGAA 215 TCAAACGAAA 2809 CA G A AAAAGA GA AAA- -
CTG
AAGATGGGGATTTAAAGGCC ACCCACAGGA GGTTTT AGGT TC TG TGGG TTT GGCCA
GC C
AGCCTGCTACGCATGGTCAA GACC |||||| |||| || || |||| ||| ||||| ||
ACGAAAACCCACAGGAGACC TCGAGG TCCA AG AC ACCC AAG CTGGT CG /
TGGAGCT -- G G ------ AA CAAA A CAT

GAM239 AGGAGAAGCTGTGCTACGTC 216 GGAGATGGCC 2810 GAA- T CTA GC GACT
GCCCTGGACTTCGAGCAGGA ACCGCCGCAT AGGA GC GTG CGTC CCTG T
GATGGCCACCGCCGCATCCT CCT |||| || ||| |||| ||||
TCCT CG CAC GTAG GGAC /
ACGC C CG- A- GAGC

GAM240 GGTGACAACATGCTGGAGCC 217 TTGGTTCAAA 2811 AA-- G G-- T TA
AAGTGCTAACATGCCTTGGT GGGATGGAAA GGTGAC CAT CT GAGCCAAG GC A
TCAAAGGGATGGAAAGTCAC GTCA |||||| ||| || |||||||| ||
C CCACTG GTA GG CTTGGTTC CG C
AAAG G AAA - TA

GAM241 TGCTTCTCATGTAGGGCGCC 218 TCTGTTGCAG 2812 T-- -- -- C TT TC TG
GACAGCATATTCTGAATCAG CAGGCTCTGC TGCTTC CATGTAGGGC GC CGACAG ATA
CTGAA AGC G
CTGGGGGTTTTCAGTTATCT ATGC |||||| |||||||||| || |||||| ||| ||||| |||
GTTGCAGCAGGCTCTGCATG ATGGGG GTACGTCTCG CG GTTGTC TAT GACTT TTG
/
CCTGGGGTA TCC GA AC - T- -- GG

GAM242 TGGGAGAGTATTTTAGAGAC 219 TTTGATCATC 2813 A ATTT- - - T A
AATGGCAAACATGCTTTGAT TATGACGACT TGGG GAGT TAGA GA CAA GGCA A
CATCTATGACGACTTATCCA TATC |||| |||| |||| || ||| ||||
ACCT TTCA ATCT CT GTT TCGT C
A GCAGT A A - A

GAM243 TGGCTTCTCCTGCAGTGATA 220 CTGCAGTGAT 2814 CTCC- A - T AC
TTGATGAGTGTAGCTACTCC ATTGATGAGT TGGCTT TGCAGTG TATTGAT GAG GTAGCT T
AGCTACCTCTGTCAGTACCG GTAG |||||| ||||||| ||||||| ||| ||||||

CTGCGTCAACGAGCCA ACCGAG GCGTCGC ATGACTG CTC CATCGA /
CAACT C T - CC

GAM244 GATTAAGCCATGCATGTCTA 221 TAAGCCATGC 2816 A---- -- TG- TAA GCAC
AGTACGCACGGCCGGTACAG ATGTCTAAGT GATT AGCCAT GCA TC GTAC G
TGAAACTGCGAATGGCTCAT ACGC |||| |||||| ||| || ||||
TAAATC CTAA TCGGTA CGT AG CATG /
ATTAC AG CAA TGA GCCG

GAM245 GAGCTAATACATGCCGACGG 222 GGATGCGTGC 2815 G A C CGACGG TGA C
GCGCTGACCCCCTTCGCGGA ATTTATCAGA GA CT ATA ATGC GCGC CCCCCTT G
GGGGGATGCGTGCATTTATC TC || || ||| |||| |||| |||||||
AGATC CT GA TAT TACG TGCG GGGGGAG C
A C T ------ TA- G

GAM246 GGGGGTGCGGTGCGCCGGCG 223 TCGGGCCGAT 2817 G C- GGA TT GACTC
GACTTTGGTGACTCTAGATA CGCACGCACC GGGGGTGCG TGCG CGGC CT GGT T
ACCTCGGGCCGATCGCACGC CCC ||||||||| |||| |||| || |||
ACCCCC CCCCCACGC ACGC GCCG GG CCA /
- TA --- CT ATAGA

GAM247 TCTTGCGGCATCCACGAGAC 224 TGACGTGGAC 2818 - CA- AGAC - ACTC
CACCTTCAACTCCATCATGA ATCCGCAAAG TCTT GCGG TCCACG CAC CTTCA C
AGTGTGACGTGGACATCCGC A |||| |||| |||||| ||| |||||
AAAGA AGAA CGCC AGGTGC GTG GAAGT /
A TAC A--- T ACTA

GAM248 TTGTCGTCATTGGACACGTA 225 TAAATGCGGT 2819 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM249 CGTGAAGAAGGCGGCCCGGG 226 ACGCGCCTGG 2820 AA G -- CATCA AAA
TCATCATAGAAAAGTACTAC GCAACGACTT CGTG GAAG CG GCCCGGGT TAG A
ACGCGCCTGGGCAACGACTT CCAC |||| |||| || |||||||| |||
CCACACG GCAC CTTC GC CGGGTCCG ATC /
AC A AA CGCAC ATG

GAM250 TTGTCGTCATTGGACACGTA 227 TAAATGCGGT 2822 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C

CTA GTAAA TCTA G TCA

GAM251 GGTGACAACATGCTGGAGCC 228 GGTCAAGGGA 2821 AA-- G G- G T TA
AAGTGCTAACATGCCTTGGG TGGAAAGTCA GGTGAC CAT CT GA CCAAG GC A
TCAAGGGATGGAAAGTCACC CC |||||| ||| || || ||||| ||
CCACTG GTA GG CT GGTTC CG C
AAAG G AA G - TA

GAM252 TTGTCGTCATTGGACACGTA 229 TAAATGCGGT 2824 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM253 GGTGACAACATGCTGGAGCC 230 TTCAAGGGAA 2823 AA-- G- G- T TA
AAGTGCTAACATGCCTTGGT TGGAAAGTCA GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGAATGGAAAGTCAC CC |||||| ||| || |||||||| ||
C CCACTG GTA GG CTTGGTTC CG C
AAAG AG AA - TA

GAM254 GGTGACAACATGCTGGGAGC 231 TTCAAGGGAT 2825 AA--- G GG - T TA
CAAGTGCTAACATGCCTTGG GGGAAAGTCA GGTGAC CAT CT GAGCC AAG GC A
GTTCAAGGGATGGGAAAGTC CC |||||| ||| || ||||| ||| ||
ACC CCACTG GTA GG CTTGG TTC CG C
AAAGG G AA G - TA

GAM255 TTGTCGTCATTGGACACGTA 232 TAAATGCGGT 2826 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM256 CAGGTGAAAATGGCAGGTTT 233 TGGAAGGTGG 2827 T ATG -- TT - T- - A A
TTGTTTGGAAGGTGGGGGGA GGGGAGATGC CAGG GAAA GCAGGTT TTTGT GG AAGG GG
GGGGAG TGCC C
GATGCCACAAGGTGACTCCC CACA |||| |||| ||||||| ||||| || |||| || |||||| ||||
CACCTCCCTTGCCTCACAGA GTCC CTTT TGTCCGG AGACA CC TTCC CC CCCCTC
GTGG A
TTGGCCTGTTTTCCCTG - --- TT CT G CT A A A

GAM257 GTTGTTATTGGTGCAGGAGT 234 TTTGGCAAAG 2829 TG-- TG AG AATAGG A G
AATAGGTGTAGAATTGGGTT ACTTGGTGCA GTTGTTAT G C GAGT TGT GAATTG G
CAGTTTGGCAAAGACTTGGT GATG |||||||| | | |||| ||| ||||||

GCAGATGTGACAGC CGACAGTG C G TTCA ACG TTTGAC T
TAGA GT G- GAA--- G T

GAM258 CTGGTGCTACCAAGAAGTCA 235 TTCTATTGAA 2828 GG A T ----- AT
GATGGAAACAATTGATGTTT GCTGCTTCTG CT TGCTACCA GAAG CAG ATGGAAACA T
CTATTGAAGCTGCTTCTGGT GTGG || |||||||| |||| ||| |||||||||
GGTAAAG GA ATGGTGGT CTTC GTC TATCTTTGT /
A- - - GAAGT AG

GAM259 TCTTGTGTTGAGACTTCGTG 236 TACACCACTC 2830 GAGA GT--- C AAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGAA A
AAGAATTCTTACACCACTCC TAAG ||||||||| |||| ||||||| ||||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCTT G
ATAA AACCC - AAGAA

GAM260 TCTTGTGTTGAGACTTCGTG 237 TACACCACTC 2831 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM261 CTCCTGTGAGCCCACATTCA 238 TCTACAGAAG 2833 - G CACA AA A CATTT T- T
ACATTTTTTGATACATTTGA ATGAAGAAGA CTC CT TGAGCC TTC CATTTTTTG TA GA CCA
C
TCCATCTTTGGTTTCTACAG TAGG ||| || |||||| ||| ||||||||| || || |||
AAGATGAAGAAGATAGGCTT GAG GA ATTCGG AAG GTAGAAGAC AT CT GGT T
AGAGAGAG A G ATAG AA - ----- TT T

GAM262 ATGCTTGAGAAATGCCCTTT 239 AGCCCAAAAA 2832 --- G- C CCT CTC
TCCTGCTGGCTCAGATTTAG TGGCATTTGA ATGCT TGA AAATGCC TTTT GCTGG A
CCCAAAAATGGCATTTGATT TTAA ||||| ||| ||||||| |||| |||||
AAACAGCAT TACGA ATT TTTACGG AAAA CGATT /
CAA AG T ACC TAG

GAM263 CTCGGCCTCCCCTTCAGCAG 240 TGATGAGCAG 2834 TCCC --- C TG CA TAA--
CCACT
CTTTGACCACTCTAAAGCCC TTGAACCTGT CTCGGCC CTTCAG CAG TT AC CTC AGC
A
ACTACTATCGCTATGATGAG GCCT ||||||| |||||| ||| || || ||| |||
CAGTTGAACCTGTGCCTGGA GAGTCGG GAGGTC GTC AA TG GAG TCG /
GCGGCTGAG C--- CGT C GT AC TAGTA CTATC

GAM264 TCACATGACAATGAAGCAGA 241 CAAGCCATCC 2835 GACAAT--- T--- CTC CT

TATGGCTCTCCCGCTGGTTC CCTTTGCTTT TCACAT GAAGCAGA ATGGCT CCG G
GGCAAGCCATCCCCTTTGCT TACA |||||| |||||||| |||||| |||
TTTACAATACAGTGTGA AGTGTG TTTCGTTT TACCGA GGC G
ACATAACAT CCCC AC- TT

GAM265 ACCAGTGGATCGAGCAGGAC 242 AGCAGGACAT 2836 ATCGAG TG AAGTA GA
ATGGAGAAGTACATCCTGAG GGAGAAGTAC ACCAGTGG CAGGACA GAG CATCCT G
AGGGGATGAGACGTTTGCTG ATCC |||||||| ||||||| ||| ||||||
TCCTGAGCCGCTGGT TGGTCGCC GTCCTGT TTT GTAGGG /
GA---- CG GCAGA GA

GAM266 GCCCATGGGAAACAGCTGTT 243 GCACATGGTG 2837 - -- AA GC- T T A AACA
CTTTCA
CCTCATCACCAACAGTCCTT GGTCCCGATT GC CCA TGGGA CA TGT CC CATC CC GTC
G
TCAGCTTCGTAGACAAGGGG GGCG || ||| ||||| || ||| || |||| || |||
ATGCGGCACATGGTGGGTCC CG GGT GCCCT GT ACA GG GTAG GG CAG C
CGATTGGCGC C TA GG GGT C C - GAA- ATGCTT

GAM267 CCTAAGTATTGCTGCCTTGT 244 TTGCTGCCTT 2838 TA T T T - T TT
GTATTTTATTTAGTGTACAG GTGTATTTTA CC AGTAT GC GCCT GT GTATT TAT A
TACTACAGGTGCATACTCTG TTTA || ||||| || |||| || ||||| |||
G GG TCATA CG TGGA CA CATGA ATG /
TC - - - T C TG

GAM268 GTTCTGGCTGCTGAGGTGCT 245 TGAGGTGCTT 2839 T CT C CC- CA G
TGTCCATGGCATCGAGAGAC GTCCATGGCA G TCTGGCTG GAGGTG TTGT ATGG TC A
CCATACCGCGATATTTCTTT TCGA | |||||||| |||||| |||| |||| ||
AGCCGGATC C AGGCCGAT CTTTAT AGCG TACC AG G
T TT - CCA C- A

GAM269 GGTGACAACATGCTGGAGCC 246 TTGGTTCAAG 2840 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM270 GGTGACAACATGCTGGAGCC 247 TTGGTTCAAG 2841 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM271 ATTTGAGAAGGAGGCTGCTG 248 TTCAAGTATG 2842 TG AGG - GA AA
AGATGGGAAAGGGCTCATTC CCTGGGTCTT ATT AGA AGGC TGCT GATGGG A
AAGTATGCCTGGGTCTTGGA GGAT ||| ||| |||| |||| ||||||
T TAG TCT TCCG ATGA TTACTC G
GT GGG T AC GG

GAM272 GGTGACAACATGCTGGAGCC 249 TTGGTTCAAG 2843 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM273 GGTGACAACATGCTGGAGCC 250 TTGGTTCAAG 2844 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM274 GTGAGAAACTGGAGGACATG 251 AACTGGAGGA 2845 - AA TG A TGCT GA A
CTGGAGAGTGGGAACCCCGC CATGCTGGAG GTGA GA C GAGG CA GGA GTGGG A
CATCTTTGCCTCTGGGATCA AGTG |||| || | |||| || ||| |||||
TCAT TACT CT G CTCC GT TCT CGCCC /
A AG GT - T--- AC C

GAM275 TAATTGTGGTTTCCAACCCA 252 TTACCTGGAA 2846 G--- ACCCA G TCT
GTGGACATTCTTACGTATGT ACTAAGTGGA TAATT TGGTTTCCA GTG ACAT T
TACCTGGAAACTAAGTGGAT TTA ||||| ||||||||| ||| ||||
TA ATTAG ATCAAAGGT CAT TGTA A
GTGA C---- - TGC

GAM276 GGTGACAACATGCTGGAGCC 253 TTGGTTCAAG 2847 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM277 TTGTCGTCATTGGACACGTA 254 TAAATGCGGT 2848 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM278 GGTGACAACATGCTGGAGCC 255 TTGGTTCAAG 2849 AA-- G G- T TA

AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM279 GTGGAAGCTTGTTTAATATC 256 AAGCTTGTTT 2850 GA T- A C T AC TC
GCTCTACCATCATCCTGAAA AATATCGCTC GTG AGCTTG TTA TAT GC CT CA A
GGCATAATAATTTGAGTTAC TACC ||| |||||| ||| ||| || || ||
AC CAC TTGAGT AAT ATA CG GA GT T
A- TT A - - AA CC

GAM280 GGTGACAACATGCTGGAGCC 257 TTGGTTCAAG 2851 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM281 GGTGACAACATGCTGGAGCC 258 TTGGTTCAAG 2852 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM282 TTGTCGTCATTGGACACGTA 259 TAAATGCGGT 2854 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM283 GGTGACAACATGCTGGAGCC 260 TTGGTTCAAG 2853 AA--- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGCAAA GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGCAAAGTCAC GTCA |||||| ||| || |||||||| ||
C CCACTG GTA GG CTTGGTTC CG C
AAACG G AA - TA

GAM284 TTGTCGTCATTGGACACGTA 261 TAAATGCGGT 2855 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM285 TTGTCGTCATTGGACACGTA 262 TAAATGCGGT 2856 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C

TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM286 TTGTCGTCATTGGACACGTA 263 TAAATGCGGT 2857 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM287 CGGAGTGTCGGTGGTGATGG 264 TCGGTGGTGA 2858 -- AT - C A GT
GCATCCCGAGCGTGCGGCGC TGGGCATCCC CGGAGTGTCGGT GGTG GG GCATC CG GC G
GAGGTGCACTCGTACCTGAC GAGC |||||||||||| |||| || ||||| || ||
TGACACTCTG GTCTCACAGTCA CCAT TC CGTGG GC CG /
GT GC A A G GC

GAM288 CTTCTACCCTGACTTCTCCC 265 TGGGGACCCC 2859 C - CG----- C A
GCCTCCGAGAGTCCTTTGGG AAGGAGAGAG CTTCTACC TGACT TCTCC CCTC GAG G
GACCCCAAGGAGAGAGTCAG TCAG |||||||| ||||| ||||| |||| |||
GTGGAGG GGAGGTGG ACTGA AGAGG GGGG TTC T
- G AACCCCA T C

GAM289 TCCCGCAGCAGCAAAGTCTC 266 CAGCAGCAAA 2860 CA CAAA TC G AC GT
TCGCGACACCCTGTACGAGG GTCTCTCGCG TCCCG GCAG G TCTCGC AC CCT A
CGGTGCGGGAAGTCCTGCAC ACAC ||||| |||| | |||||| || |||
GGGA AGGGC CGTC T AGGGCG TG GGA /
A- C--- GA - GC GC

GAM290 GGTGACAACATGCTGGAGCC 267 TTGGTTCAAG 2861 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM291 GGTGACAACATGCTGGAACC 268 TTGGTTCAAG 2862 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAACCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM292 ATTTGAGAAGGAGGCTGCTG 269 CTTCAAGTAT 2863 TG AGG - GA T AAA
AGATGGGAAAGGGCTCCTTC GCCTGGGTCT ATT AGA AGGC TGCT GA GGG G
AAGTATGCCTGGGTCTTGGA TGGA ||| ||| |||| |||| || |||

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     T                              TAG  TCT   TCCG ATGA  CT CCT   /
                                     GT   GGG    T    A-  T  CGG

GAM293  GGTGACAACATGCTGGAGCC 270    TTGGTTCAAG 2864        AA--   G  G-       T  TA
     AAGTGCTAACATGCCTTGGT       GGATGGAAAG       GGTGAC    CAT CT  GAGCCAAG GC  A
     TCAAGGGATGGAAAGTCACC       TCAC             ||||||    ||| ||  |||||||| ||
                                CCACTG    GTA GG  CTTGGTTC CG  C
                                   AAAG   G  AA      -  TA

GAM294  TTGTCGTCATTGGACACGTA 271    TAAATGCGGT 2865       ---      GACAC      CG--  A  CCA
     GATTCGGGCAAGTCCACCAC       GGCATCGACA       TTGTC   GTCATTG    GTAGATT    GGC AGT   C
     TACTGGCCATCTGATCTATA       A                |||||   |||||||    |||||||    ||| |||
     AATGCGGTGGCATCGACAA                         AACAG   CGGTGGC    TATCTAG    CCG TCA   C
                                  CTA      GTAAA      TCTA   G   TCA

GAM295  GGTGACTAGCATGCTGGAGC 272    TTGGTTCAAG 2866        AG-   G  G-       T  TA
     CGAGTGCTAACATGCCTTGG       GGATGGAAAG       GGTGACT   CAT CT  GAGCCGAG GC  A
     TTCAAGGGATGGAAAGTCAC       TCAC             |||||||   ||| ||  |||||||| ||
     C                          CCACTGA   GTA GG  CTTGGTTC CG  C
                                   AAG   G  AA      -  TA

GAM296  TGGGTATGGAATCTTGCGGC 273    TGGAATCTTG 2867      -     AA   -   CA-     AGAC   -   ACGT
     ATCCACGAGACCACCTTCAA       CGGCATCCAC       TGG GTATGG  TCTT GCGG   TCCACG    CAC
CTTCA   C
     CGTCCATCATGAAGTGTGAC       GAGA             |||  ||||||  ||||  ||||   ||||||    |||  |||||
     GTGGACATCCGCAAAGACCT                        ACC CATGTC  AGAA CGCC   AGGTGC    GTG GAAGT    C
     GTACGCCA                      G     C-    A    TAC     A---   T     ACTA

GAM297  CCGGGTTGGCCTGAACCTGC 274    GGCCTGAACC 2868     G-   T    T-  A  T    T       ACGGTA
     TTTATGCTCAGACGGTATCA       TGCTTTATGC       CC  GGT GGCC  GA CC GCTT ATGCTCAG      T
     GATATTGAGCGTGGGTGGAT       TCAG             ||  ||| ||||  || || |||| ||||||||
     CTTGGTCACCAAGG                    GG  CCA CTGG  CT GG TGGG TGCGAGTT     /
                                AA   -   TT  A  -   -       ATAGAC

GAM298  GGCGAACCTGAAAAGTTAGG 275    TATGCCAAGG 2869       AACC   AA    --   A-    T  T
     TCAGGCGTTGACTGAAGTCT       CCAATAGCTT       GGCG    TGA  AGTTA  GGTC  GGCGT GAC G
     ATGCCAAGGCCAATAGCTTC       CACC             ||||    |||  |||||  ||||  ||||| |||
     ACCGTC                        CTGC    ACT  TCGAT  CCGG  CCGTA CTG A
                                  C---   --    AA   AA    T   A

GAM299  GGGTGACAACATGCTGGAGC 276    GTTCAAGGGC 2870       -   AA--      G--      A T  TT
     CAAGTGCTTACATGCCTGGT       ATGGAAAGTC       GGGT GAC    CATGCT   GAGCCA G GC  A
     TCAAGGGCATGGAAAGTCAA       AACC             ||||  |||    ||||||   |||||| | ||
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     CCC                          CCCA CTG   GTACGG  CTTGGT C CG  C
                                  A  AAAG    GAA    - -  TA

GAM300  TTGTCGTCATTGGACACGTA 277   TAAATGCGGT 2871      ---     GACAC     CG--  A  CCA
     GATTCGGGCAAGTCCACCAC      GGCATCGACA      TTGTC  GTCATTG   GTAGATT   GGC AGT  C
     TACTGGCCATCTGATCTATA      A           |||||  |||||||   |||||||   ||| |||
     AATGCGGTGGCATCGACAA                   AACAG  CGGTGGC   TATCTAG   CCG TCA  C
                               CTA    GTAAA    TCTA  G  TCA

GAM301  GAAGCTGAAGAAGCCGCCCT 278   AAGAAGCCGC 2872      CTG   A    - TG TT  C   C   G
     GGTTGCACATGCCGTCGGCC      CCTGGTTGCA      GAAG  AAGA GCCGCC C  G  GCA ATGC GTCG C
     ATGACTGTGTATGCTCTGGT      CATG          ||||  |||| |||||| |  |  ||| |||| ||||
     GGTGGTGTCTTACTTC                  CTTC  TTCT TGGTGG G  C  CGT TGTG CAGT C
                               A--   G    T GT T-  A   T   A

GAM302  GGTGACAACATGCTGGAGCC 279   TTGGTTCAAG 2873       AA--  G  G-      T  TA
     AAGTGCTAACATGCCTTGGT      GGATGGAAAG      GGTGAC   CAT CT  GAGCCAAG GC  A
     TCAAGGGATGGAAAGTCACC      TCAC          ||||||   ||| ||  |||||||| ||
                           CCACTG   GTA GG  CTTGGTTC CG  C
                              AAAG  G  AA     -  TA

GAM303  GGTGACAACATGCTGGAGCC 280   TTGGTTCAAG 2874       AA--  G  G-      T  TA
     AAGTGCTAACATGCCTTGGT      GGATGGAAAG      GGTGAC   CAT CT  GAGCCAAG GC  A
     TCAAGGGATGGAAAGTCACC      TCAC          ||||||   ||| ||  |||||||| ||
                           CCACTG   GTA GG  CTTGGTTC CG  C
                              AAAG  G  AA     -  TA

GAM304  TTGTCGTCATTGGACACGTA 281   TAAATGCGGT 2875      ---     GACAC     CG--  A  CCA
     GATTCGGGCAAGTCCACCAC      GGCATCGACA      TTGTC  GTCATTG   GTAGATT   GGC AGT  C
     TACTGGCCATCTGATCTATA      A           |||||  |||||||   |||||||   ||| |||
     AATGCGGTGGCATCGACAA                   AACAG  CGGTGGC   TATCTAG   CCG TCA  C
                               CTA    GTAAA    TCTA  G  TCA

GAM305  TTGTCGTCATTGGACACGTA 282   TAAATGCGGT 2877      ---     GACAC     CG--  A  CCA
     GATTCGGGCAAGTCCACCAC      GGCATCGACA      TTGTC  GTCATTG   GTAGATT   GGC AGT  C
     TACTGGCCATCTGATCTATA      A           |||||  |||||||   |||||||   ||| |||
     AATGCGGTGGCATCGACAA                   AACAG  CGGTGGC   TATCTAG   CCG TCA  C
                               CTA    GTAAA    TCTA  G  TCA

GAM306  GGTGACAACATGCTGGAGCC 283   TTGGTTCAAG 2876       AA--  G  G-      T  TA
     AAGTGCTAACATGCCTTGGT      GGATGGAAAG      GGTGAC   CAT CT  GAGCCAAG GC  A
     TCAAGGGATGGAAAGTCACC      TCAC          ||||||   ||| ||  |||||||| ||
                           CCACTG   GTA GG  CTTGGTTC CG  C
```

AAAG G AA - TA

GAM307 CTTCCTTTTTCCAGAATTTG 284 TGCCTGAGGT 2878 T G GAAATT AGAAA GA
AAATTGTAATAGAAACAGAA TGTGGAAAAG CTTCCTTTT CCA AATTT GTAAT CA A
GATGAGATTATGCCTGAGGT GAAG ||||||||| ||| ||||| ||||| ||
TGTGGAAAAGGAAG GAAGGAAAA GGT TTGGA TATTA GT /
- G GTCCG- GA--- AG

GAM308 GGTGACAACATGCTGGAGCC 285 TTGGTTCAAG 2879 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM309 CAAGCTGGTGATGCCCAACT 286 AGCTGGTGAT 2880 AG T TGCCCA - C- AAC
ACCCATTCATCAACATTCGG GCCCAACTAC CA CTGG GA ACTAC CCATT ATC A
TCAAGTGGTGTGGTTCCTCA CCAT || |||| || ||||| ||||| |||
GAGTG GT GACT CT TGGTG GGTGA TGG /
GA C ------ T AC CTT

GAM310 TAGTTCAGTTCTTTCAAGGG 287 GATAACATTG 2881 GTTCTT GG GAAA GC
TTGGAAATCGTGCCAAATGG ACGATGGACT TAGTTCA TCAA GTTG TCGT C
GATAACATTGACGATGGACT A ||||||| |||| |||| ||||
A ATCAGGT AGTT CAAT GGTA /
AGC--- A- AG-- AA

GAM311 GAAACAGACTGGGCCAATGT 288 TATCAAGGAA 2882 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM312 CAGGGGGGTGCGAGCTGGTA 289 TGGTATGGAT 2883 GT- TA-- ------- T T G
TGGATGCCCTCCTGGGGGTTC GCCCTCCTGG CAGGGGG GCGAGCTGG TGGAT GCCC
CC GG G
CTGGGGGCTCTGCACATCCA GGTT ||||||| ||||||||| ||||| |||| || ||
GACTCCAGTTTGTCCACCCC GTCCCCC TGTTTGACC ACCTA CGGG GG CC T
CTG ACC TCAG CACGTCT - T T

GAM313 ATGGTTGTCACTTTCAGATT 290 TCTAGCTTGC 2884 TT T- - TCT T G T AACA

CTAGCTTGCTTGGACTTTCA TTGGACTTTC ATGG GTCACT TCA GAT AGCT GCTTG ACT TCAGTGGC A
GTGGCAACAAATGGAGCCAC AGTG |||| |||||| ||| ||| |||| ||||| ||| |||||||| TGACAGTACAGGTGGCTTCA TACT CAGTGG AGT CTA TCGG TGGAC TGA AGTCACCG A
TCTTGACTGGTGACCTCAT C- TC T CT- - A C AGGT

GAM314 CAAGGAGAGAGCTGGGCTTT 291 CTGAAGCTGT 2885 - AG- TTTCCA TAC GAC
CCAAGTTACCTGACCTTAAA TCAGAAGTTC CAAGGA GAG CTGGGC AGT CT C
GATGCTGAAGCTGTTCAGAA TTCC |||||| ||| |||||| ||| ||
GTTCTTCCTTG GTTCCT CTT GACTTG TCG GA T
T GAA TCGAAG TA- AAT

GAM315 TCTTGTGTTGAGACTTCGTG 292 TACACCACTC 2886 T GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TC TGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG || |||||| |||| ||||||| ||||| CAAGAAGAATAAGCACATGA AG ACACGA GAAG TCACCAC ATTCT G
T ATAA AACCC - GAAGAA

GAM316 GGTCTCTTCAGAGCTGCTGT 293 TATGAGGCCC 2887 CT -------- G T- - GT TC
GCCCAGTGGTGCTTCAACTG TAGAGCTCCG GGTCT TCA GAGCT CTG GCC CA GGTGCT A
GTATCTATGAGGCCCTAGAG GGAC ||||| ||| ||||| ||| ||| || |||||| CTCCGGGACAATGATAAGAC TCAGA AGT CTCGA GAT CGG GT CTATGG A
T AT AACAGGGC - CC A AT TC

GAM317 GCACTCTCCGAGTCGCTGAA 294 TGCTGCGGCC 2888 CC T - -- T T T GAC
GCCGCTGCTGTCGCTGACAC TTTCATGCGC GCACTCT GAG CGC TGAA GCCGC GC G CGCT A
TGGGCGCTGCTGCGGCCTTT TCCA ||||||| ||| ||| |||| ||||| || | |||| CATGCGCTCCAGGGTGC CGTGGGA CTC GCG ACTT CGGCG CG C GCGG /
C- - T TC T T - GTC

GAM318 GGCCTGGGAGGGCATGGGTC 295 GGGCATGGGT 2889 T G - TC G G
AAGGGCGTCCGGGAAGCTGG CAAGGGCGTC GGCC GGGAGG CA TGGG AAGGGC TCCGG A
AGCTCTTCCTGCTGACCTTC CGGG |||| |||||| || |||| |||||| ||||| CGGCC CCGG CCTTCC GT GTCC TTCTCG AGGTC A
- A C -- - G

GAM319 AGAGTCCCACTTTGTTGCCC 296 CACTTTGTTG 2890 CCAC TT C-- -- - G TG
AGGCTGGAGTGCAGTAGGCA CCCAGGCTGG AGAGTC TTTG GCCCAGG TGGAG TGCAGT AG CA A
TGATCTTGGCTCACTGCAAC AGTG |||||| |||| ||||||| ||||| |||||| || || CTCCACCTCCTGGGTTCAAG TCTTAG GAAC TGGGTCC ACCTC ACGTCA TC GT T

CGATTCT C--- T- TCC CA C G TC

GAM320 GAGATGGGGTTTCACCATGT 297 TTTCACCATG 2891 A GTT- A TT C CT CT
TGGCCAGGCTGGTCTTGAAC TTGGCCAGGC GAG TGGG TCACC TG GG CAGG GGT T
TCCTGACCTCAGGTGATCCA TGGT ||| |||| ||||| || || |||| |||
CCCACCTC CTC ACCC AGTGG AC CC GTCC TCA /
C ACCT - T- A -- AG

GAM321 TATTGGCTAGCTTGTGCCCT 298 AAGCTTGCTG 2893 TG - TG - CT-- GT-- AT
CAAGTGTTTGGAATGTATCT TGGCCATGGT TAT GCTAGC T TG CC CAAGT TTGGA G
AGTAAAGCTTGCTGTGGCCA GCTG ||| |||||| | || || ||||| |||||
TGGTGCTGGCTGGTG GTG CGGTCG G AC GG GTTCG GATCT /
GT T GT C TGTC AAAT AT

GAM322 GCACAGGGAAATCTCAGTTC 299 TGTGCTGACC 2892 A GAA T CAAATATG A ACA
CTCAAATATGCAGCAAAGAT ACAGGAATTG GCAC GG ATC CAGTTCCT CAGCA AGATT
C
TACACCAAGATCTGTGCTGA GATC |||| || ||| |||||||| ||||| |||||
CCACAGGAATTGGATCTACT CGTG TC TAG GTTAAGGA GTCGT TCTAG /
AGTGC A ATC - CACCA--- G AAC

GAM323 AAGATAGAGGCAGAACTGCA 300 TGTTCTGGAG 2894 GA----- AA G TG
GGACATCTGCAATGATGTTC CTGTTGGACA AAGATA GGCAG CT CAGGACATC C
TGGAGCTGTTGGACAAATAT AATA |||||| ||||| || |||||||||
CTT TTCTAT TTGTC GA GTCTTGTAG A
AAACAGG -- G TA

GAM324 CAGCTCTCCGGTCATCTTTG 301 TTCCACAGCC 2895 CTCC TC CAG TCA C A-- AT
CAGGTGGTCAGGCCTATACC AGATTTGACC CAGCT GGTCA TTTG GTGG GGC TAT CC T
ATTCAAGGACAGTATGCCAT AAGC ||||| ||||| |||| |||| ||| ||| ||
TCCACAGCCAGATTTGACCA GTCGA CCAGT AGAC CACC CCG ATG GG C
AGCTG A--- TT CGA TTA T ACA AA

GAM325 GATGTCTGGGGCGCAGATCA 302 TCACTGGATC 2896 T GC AAAAT- CG ------- A
AAATTGCGAACCCAGTGGAA TGCTGCCCAG GATG CTGGG GCAGATC TG AACC
CAGTGGA G
GGATCTACTGATAGGCAGGT CATT |||| ||||| ||||||| || |||| |||||||
TACCATCACTGGATCTGCTG TTAC GACCC CGTCTAG AC TTGG GTCATCT G
CCCAGCATT - GT GTCACT CA ACGGATA A

GAM326 CGGCTCCGAGAGCAGGTTCT 303 TACACATTGA 2897 - AGAG C A TC GCAG C
TCGTGAGTTCCTCGCAGGGC GAACCTGAAC CGGC TCCG CAGGTTCTT GTG GT CTC GG
C

CGGTCAGAGCTACACATTGA ATGG |||| |||| ||||||||| ||| || ||| ||
GAACCTGAACATGGAGGCCG GCCG AGGT GTCCAAGAG TAC CA GAG CT G
G ACAA T A TC A--- G

GAM327 GTGGAGGTGACTGGTGATGA 304 ATTGATGGTC 2898 GA - GA A GG
ATACAATGTGGAAAGCATTG AGCCAGGTGC GTGGAGGT CTGG TGAT AT CAATGT A
ATGGTCAGCCAGGTGCCTTC CTTC |||||||| |||| |||| || ||||||
AC CACTTCCG GACC ACTG TA GTTACG /
TG G G- - AA

GAM328 GCATAATCGGTCACTCGTAT 305 TGAATGGACG 2899 AATC --- A GAA TATT TAT
AGAACAGTATTGTTTCTATA GGTTCAGGCC GCAT GGTC ACTCGT TA CAG GTTTC A
ATTTGAAGCTTTCTGAATGG TGAT |||| |||| |||||| || ||| |||||
ACGGGTTCAGGCCTGATGC CGTA CCGG TGGGCA GT GTC CGAAG A
GT-- ACT G AA- TTT- TTT

GAM329 GGTGTCCTGGAGCCTCTGTA 306 CTGGAGCCTC 2900 T C TCT-- C- T - A
CCTGTGCCCAAATGGTGCCC TGTACCTGTG GG GTC TGGAGCC GTAC TG GC CC A
GCTGTGCCACCTGGTTTCAA CCCA || ||| ||||||| |||| || || ||
GACCC CC CAG ACTTTGG CGTG GC CG GG A
- A TCCAC TC C T T

GAM330 ATGGTGCTAAGGAAATTTGC 307 TTGACCCATC 2901 G ATT T CTTCG C - T CT
TATGCTCTTCGAGCTGAGGG ATCTGGTTTG ATGGT CTAAGGAA TGCTA GCT AG TGA
GGGTTA TGGG G
TTATTGGGCTGACTTTATTG GCAT ||||| |||||||| ||||| ||| || ||| |||||| ||||
ACCCATCATCTGGTTTGGCA TACCA GGTTTTTT ACGGT TGG TC ACT CCCAGT ATTT
/
TTTTTTGGACCAT - --- T ----- T A T CA

GAM331 ATGGTGACAACATGCTGGAG 308 GTCAAGGGAT 2902 AA- - G GGA GTA
CCAAGTGTAACATGGCTTGG TGGAAGTCAC ATGGTGAC CA T CT GCCAAGT A
TCAAGGGATTGGAAGTCACC CGT |||||||| || | || |||||||
GT TGCCACTG GT A GG TGGTTCG C
AAG T G AAC GTA

GAM332 AGGTCATTGCTCCCTGGAGG 309 ACGGTTCAAG 2903 T- G GA C AAT
ATGCCTGAATTCTACAGACG GGCCGCAATG AGGTCATTGC CCCT GAG TG CTG T
GTTCAAGGGCCGCAATGACC ACCT |||||||||| |||| ||| || |||
T TCCAGTAACG GGGA CTT GC GAC /
CC A G- A ATC

GAM333 ATCAGACAGATCACAGCTAC 310 GATCACAGCT 2904 A CAGCT T C GCCA

GGTGACATTTCTGCCACTGT ACGGTGACAT ATCAG CAGATCA ACGG GA ATTTCT C
TGGAAGTTTCTTGTTCATTT TTCT ||||| ||||||| |||| || ||||||
GATCTGCTGAT TAGTC GTCTAGT TGTT CT TGAAGG /
\- TTACT - T TTGT

GAM334 CTCCGCCACCATGTTCGAGG 311 CACCATGTTC 2905 C ATG C CGC-- GG
CGCGCCTGGTCCAGGGCTCC GAGGCGCGCC CTCCG CACC TT GAGG GCCT T
ATCCTCAAGAAGGTGTTGGA TGGT ||||| |||| || |||| ||||
G GAGGT GTGG GA CTCC CGGG C
T AA- A TACCT AC

GAM335 CTGCAGGAGAAGATGGCGGT 312 CAGGAGAAGA 2906 TG A G GTCTCCAC TT
CTCCACAGGAGTTAAAGTTC TGGCGGTCTC C CAGG GAAGAT GCG AGGAG A
CTCGTAATTTTCGCTTGTGG CACA | |||| |||||| ||| |||||
G GTTC CTTTTA TGC TCCTT A
GT G A -------- GA

GAM336 CTTTGTAAGATGCAAAGAGG 313 CTGTGCTGCC 2907 TAAGA C A TT ATCA TA
TTGGATCAAGTTTAAATGAC CCTTTCACAT CTTTG TG AAAG GG GG AGTT A
TGTGCTGCCCCTTTCACATC CAAA ||||| || |||| || || ||||
AAAG GAAAC AC TTTC CC TC TCAG /
TAC-- - - CG GTG- TA

GAM337 TAAGGAAGTCAGCACTTACA 314 AGGAAGTCAG 2908 CA TTACA- GAAAA TA
TTACGAAAATTGGGTACAAC CACTTACATT TAAGGAAGT GCAC TTAC TTGGG C
CCCGACAAAGTAGCATTTTG ACGA ||||||||| |||| |||| |||||
TGCCATTTTCTTG GTTCTTTTA CGTG GATG AGCCC A
C- TTTTAC AAAC- CA

GAM338 CCATGCCGTTAGTAACGAGG 315 CGAGGAACAT 2912 T - AG -- - A GA CAA C
AACATCGAGCCAAGGCACCT CGAGCCAAGG CCA GC CGTT TAACG AGG AAC TC GC GGCA
C
GTGCCAGTCAGACGTTGCCT CACC ||| || |||| ||||| ||| ||| || || ||||
AGCGTTAGAAGCGAGCTGG GGT CG GCGA ATTGC TCC TTG AG TG CCGT T
\- A AG GA G C AC A-- G

GAM339 TTCTGGGGGACTATGTGGAC 316 TAAGATCAAG 2913 G - A TGGACAG A CCTT - AC
AGGGGCAAGCAGTCCTTGGA TACCCCGAGA TTCT GGGG ACT TG GGGC AGCAGT GG
AG C
GACCATCTGCCTGCTGCTGG A |||| |||| ||| || |||| |||||| || ||
CCTATAAGATCAAGTACCCC AAGA CCCC TGA AC TCCG TCGTCG CC TC /
GAGAA G A - TAGAATA G T--- G TA

GAM340 ACACTGCTTCAAGGTTTCTT 317 TCAAGGTTTC 2914 A TTC G A- TTCTTAGAAT CT
TTGTATATAATTCTTAGAAT TTTTGTATAT AC CTGC AA GTTTCTTTTGT TATAA GCTCATTT T
GCTCATTTCTTTTAAATGGG AATT || |||| || |||||||||||| ||||| |||||||||
TTAATTTGTACAGCAGAGGG TG GATG TT TAAGGGAGACG ATGTT TGGGTAAA /
AATGTTATTGTAGGT - TTA G AC TAAT------ TT

GAM341 GGTGACAACATGCTGGAGCC 318 TTGGTTCAAG 2915 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM342 CGGAGTGTCGGTGGTGATGG 319 TCGGTGGTGA 2916 -- AT C A T
TGCATCCCGAGCGTGCGTGC TGGTGCATCC CGGAGTGTCGGT GGTG GGTGCATC CG GCG G
GCGAGGTGCACTCGTACCTG CGAG |||||||||||| |||| |||||||| || |||
ACTGACACTCTG GTCTCACAGTCA CCAT TCACGTGG GC CGT C
GT GC A G G

GAM343 CTTCTACCCTGACTTCTCCC 320 TGGGGACCCC 2917 C - CG----- C A
GCCTCCGAGAGTCCTTTGGG AAGGAGAGAG CTTCTACC TGACT TCTCC CCTC GAG G
GACCCCAAGGAGAGAGTCAG TCAG |||||||| ||||| ||||| |||| |||
GTGGAGG GGAGGTGG ACTGA AGAGG GGGG TTC T
- G AACCCCA T C

GAM344 TTGTCGTCATTGGACACGTA 321 TAAATGCGGT 2918 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM345 AGGTCATTGCTCCCTGGAGG 322 CAAGGGCCGC 2919 T- G GGAT TGAATT
ATGCCTGAATTCTACAACCG AATGACCT AGGTCATTGC CCCT GA GCC C
GTTCAAGGGCCGCAATGACC |||||||||| |||| || |||
T TCCAGTAACG GGGA CT TGG T
CC A ---- CCAACA

GAM346 TTGTCGTCATTGGACACGTA 323 TAAATGCGGT 2920 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM347 GGTGACAACATGCTGGGAGC 324 TTGGTTCAAG 2921 AA-- G GG T TA
CAAGTGCTAACATGCCTTGG GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TTCAAGGGATGGAAAGTCAC TCAC |||||| ||| || |||||||| ||
C CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM348 AGTCCAACGTCTCTGATGCG 325 TATCATTTAT 2922 - AC ------ TG TC
GTGGCTCAGAGCACCCGTAT GGAGGCTCTG AGTC CA GTCTCT GATGCGG GC A
CATTTATGGAGGCTCTGTGA TGAC |||| || |||||| ||||||| ||
CT TCAG GT CGGAGG CTATGCC CG /
T CT TATTTA CA AG

GAM349 GGCAGAAGAATTTAAGAAAC 326 GATTGGGTGC 2923 ---- - -- CT C
TCAACTGCCAAGTGATTGGG TTCTGTGGAT GGCAGA AGAATTTA AGAA ACTCAA GC A
TGCTTCTGTGGATTCTCACT TCTC |||||| |||||||| |||| |||||| ||
TCTGTC CTGTCT TCTTAGGT TCTT TGGGTT TG /
TCAC G CG AG A

GAM350 TCCGAAAGAAGCTGGTGATC 327 AAGAAGCTGG 2924 AAA GATC CCT-- TG A
GTTGGGGATGGTGCCTGTGG TGATCGTTGG TCCG GAAGCTGGT GTTGGGGATGGTG G
GG A
GAAGACCTGCCTCCTCATCG GGAT |||| ||||||||| |||||||||||| | ||
TCTTCAGCAAGGATCAGTTT AGGC CTTTGACTA CGACTTCTGCTAC C CC G
CCGGA --- GGAA TCCTC GT A

GAM351 GGAGCACATGTGCCGCCTGG 328 CACAGCCCGG 2925 A C - ----- T ACAT TCAC
ACATTGATTCACCACCCATC AACACTGGCA GG GCA ATG TGCCG CC GG TGAT C
ACAGCCCGGAACACTGGCAT TCAT || ||| ||| ||||| || || ||||
CATCTGTACC CC TGT TAC ACGGT GG CC ACTA /
A C T CACAA C GAC- CCCA

GAM352 GGTGACAACATGCTGGAGCC 329 TTGGTTCAAG 2926 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM353 TTGTCGTCATTGGACACGTA 330 TAAATGCGGT 2927 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM354 TTGTCGAGCTCATCAGGTGG 331 AACCTTATTT 2929 AT --------- T G -- A G TT CT

TGGAAGATGGATATGAATTT TCAGCCCCAA TTGTCGAGCTC CA GG GGT GAAGAT GG TAT AATT TTG A

TTTGCTAAACGACAGTTGGT ATTA |||||||||| || || ||| |||||| || ||| |||| |||

AACCTTATTTTCAGCCCCAA AATAGTTTGAG GT CC CCG CTTTTA CC ATG TTGA AGC /

ATTACTGTGGCGAGTTTGAT CG GTCATTAAA - A TT A G C- AA

AA

GAM355 ATTTGACACCCTTTATGATG 332 ACCCTTTATG 2928 CAC GA ACA TA

TCACACCTTTAACTTAAGGA ATGTCACACC ATTTGA CCTTTAT TGTC CCTT A

GACGGGTAAAGGATCTTAAA TTTA |||||| ||||||| |||| ||||

T TAAATT GGAAATG GCAG GGAA C

CTA G- A-- TT

GAM356 GGTGACAACATGCTGGAGCC 333 TTGGTTCAAG 2930 AA-- G G- T TA

AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A

TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||

CCACTG GTA GG CTTGGTTC CG C

AAAG G AA - TA

GAM357 TCTACAAAGTGCCGTCCACT 334 TCCAATCTGA 2931 A - - CACTG CT- C

GAGACTGAGGCCTTGGCTTC TGGGCATGTT TCT CAAA GTGCC GTC AGA GAGGC T

CAATCTGATGGGCATGTTTG TGAG ||| |||| ||||| ||| ||| |||||

AGA AGA GTTT TACGG TAG TCT CTTCG T

- G G ----- AAC G

GAM358 GCGGCTGGGACCCTGTACAC 335 TCTCATCGCT 2932 -- A ACAC TC AAACTG-- TT

GTATCCTGAAAACTGGAGGG GCTCAGTACA GCGG CTGGG CCCTGT GTA CTGA GAGGGCC C

CCTTCAAGGCTCTCATCGCT GCGG |||| ||||| |||||| ||| |||| |||||||

GCTCAGTACAGCGGGGCTCA CGCC GACTC GGGGCG CAT GACT CTCTCGG /

GGTCCGC TG - A--- -- CGTCGCTA AA

GAM359 GTAGAAGAAGATGAATACAA 336 ATGACCCCAT 2933 AA A CA TTCTACAA A

AGCTTTCTACAAATCATTTT GGCTTATATT GTAG GAAG TGAATA AAGCT ATCATTTTC A

CAAAGGAAAGTGATGACCCC CACT |||| |||| |||||| ||||| |||||||||

ATGGCTTATATTCACTTTAC CGTC TTTC ACTTAT TTCGG TAGTGAAAG A

TGC A- - A- TACCCCAG G

GAM360 GGCCACTCCTGCATCTTTAC 337 TCCTGCATCT 2934 CT CT C A CTTC- T

CGTCTCAGGGACTTCCAGTT TTACCGTCTC GGCCA CCTGCAT TTAC GTCTC GGGA CAG T
GCTGCCCCTTCCCAGAGGCC AGGG ||||| ||||||| |||| ||||| |||| ||| |
GTGGCATGCGGGGATGGCC CCGGT GGGCGTA GGTG CGGAG CCCT GTC /
AG C- C A TCCCC G

GAM361 AAGATAGAGGCAGAACTGCA 338 TGTTCTGGAG 2935 GA----- AA G TG
GGACATCTGCAATGATGTTC CTGTTGGACA AAGATA GGCAG CT CAGGACATC C
TGGAGCTGTTGGACAAATAT AATA |||||| ||||| || |||||||||
CTT TTCTAT TTGTC GA GTCTTGTAG A
AAACAGG -- G TA

GAM362 TCTTGTGTTGAGACTTCGTG 339 TACACCACTC 2936 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| ||||| |
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM363 GGTGACAACATGCTGGAGCC 340 TTGGTTCAAG 2937 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM364 GGTGACAACATGCTGGAGCC 341 TTGGTTCAAG 2938 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM365 CTGGTTCTCGCCGCCTCACG 342 AAGCAGAAGC 2939 TT GC- A - C ACAAA A
AGAA
CGAACTCTACAAATGCATCA AGATTCGGCG CTGG CTC CGCCTC CGC GAA TCT TGC TCA
A
AGAAAGCGGTGAAGCAGAAG CGGG |||| ||| |||||| ||| ||| ||| ||| |||
CAGATTCGGCGCGGGGTGAA GACT GAG GTGGGG GCG CTT AGA ACG AGT /
AGAGGTTCAG TG AAA C G - CGAAG A GGCG

GAM366 TAGCATGAAGTCCCTCTGGA 343 ATGGATCTTA 2940 T AG C--- CT CTG - TC
TCTTGAGCTGGTTTATGGAC CTGTCCAGAG TAGCA GA TC CTCTGGAT TGAG GTTTATG
GAC A
TCAATCGTCTCATGGATCTT CACT ||||| || || |||||||| |||| ||||||| |||
ACTGTCCAGAGCACTGATCT GTCGT CT AG GAGACCTG ATTC TAGGTAC CTG A
CCTGCTG C CT TCAC TC --- T CT

GAM367 GGTGACAACATGCTGGAGCC 344 TTGGTTCAAG 2941 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM368 GTCCGCTTCTCGCCCAACAG 345 TCCTGTGGGT 2942 - -- A - AACCC
GAGCAACCCTATCATCGTCT GGGACAAGCT GTCC GCT TCTCGCCCA CAGGAG C T
CCTGTGGGTGGGACAAGCTG GGGC |||| ||| ||||||||| |||||| |
GGC CGGG CGA AGGGTGGGT GTCCTC G A
T AC - T CTACT

GAM369 TGTGGGTATCTCCTCAGATG 346 TGGAACCCTG 2943 TATC T T - TTTG C G
GGCAGTTTGCCCTCTCAGGC CGCCTCTGGG TGTGGG TCC CAGA GG GCAG CC TCTCAG
C
TCCTGGGATGGAACCCTGCG ATCT |||||| ||| |||| || |||| || ||||||
CCTCTGGGATCTCACA ACACTC AGG GTCT CC CGTC GG AGGGTC T
T--- - - G CCAA T C

GAM370 AGATGCTGACAATACTTGGG 347 TGACAATACT 2944 GA AC--- AAC- GA
AACCTGAAGAAAATTTAGAT TGGGAACCTG AGATGCT CAAT TTGGG CTGAA A
TGTCCAGAATTGATTGAAGC AAGA ||||||| |||| ||||| |||||
GTTT TTTGCGA GTTA GACCT GATTT /
A- GTTAA GTTA AA

GAM371 CTGGGACCCTGTACACGTAT 348 TCTCATCGCT 2945 A ACAC TC AAACTG-- TT
CCTGAAAACTGGAGGGCCTT GCTCAGTACA CTGGG CCCTGT GTA CTGA GAGGGCC C
CAAGGCTCTCATCGCTGCTC GCGG ||||| |||||| ||| |||| |||||||
AGTACAGCGGGGCTCAG GACTC GGGGCG CAT GACT CTCTCGG /
- A--- -- CGTCGCTA AA

GAM372 CTTGTGGGAGAGATTATCAA 349 TGGGAGAGAT 2947 T GA ATC -------- - G A AT
GCGTTTTGAGCAGAAAGGAT TATCAAGCGT CTTG GGGAGA TT AAGC GTTTT GA CAG
AAGG T
TCCGCCTTGTTGGTCTGAAA TTTG |||| |||||| || |||| ||||| || ||| ||||
TTCATGCAAGCTTCCGAAGA GAAC TCTTCT AA TTCG TAAAG CT GTT TTCC C
TCTTCTCAAG - AG GCC AACGTACT T G G GC

GAM373 CACTACGTTGACCTGAAGGA 350 AAGGACCGTC 2946 GA-- GAA- CCATTCT --
AAAT
CCGTCCATTCTTTGCCGGCC CATTCTTTGC CACTACGTT CCT GGACCGT
TTGCCGGCCT GGTG A
TGGTGAAATACATGCACTCA CGGC ||||||||| ||| ||||||| |||||||||| ||||

GGGCCGGTAGTTGCCATGGT GTGGTGTAA GGG TCTGGTA GATGGCCGGG TCAC /
CTGGGAGGGGCTGAATGTGG GTCG AGGG CCGTT-- AC GTAC TG

GAM374 GTGGGGTAAAAGCCCAGACG 351 ACGCCATGAA 2948 AA AC C A C CTT- C GAGAAC
CCATGAAAGCTGCCTTGGCC AGCTGCCTTG GTGGGGTA AGCCCAG GC ATGAA G TGC GGCC TGG A
CTGGGAGAACAAGCTGAACC GCCC |||||||| ||||||| || ||||| | ||| |||| |||
AGGCCTTTTGCATCTTCATG CGCCCCGT TTGGGTC CG TACTT C ACG CCGG ACC A
CCCTGGGTTCTGCCCCGC C- C- - - T TTTT - AAGTCG

GAM375 TCTTGTGTTGAGACTTCGTG 352 TACACCACTC 2949 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM376 GGTGTCCTGGAGCCTCTGTA 353 CTGGAGCCTC 2950 T C TCT-- C- T - A
CCTGTGCCCAAATGGTGCCC TGTACCTGTG GG GTC TGGAGCC GTAC TG GC CC A
GCTGTGCCACCTGGTTTCAA CCCA || ||| ||||||| |||| || || ||
GACCC CC CAG ACTTTGG CGTG GC CG GG A
- A TCCAC TC C T T

GAM377 GCTCTTGCAATCAAGTCTGT 354 TTTGTAGTCA 2951 T A CAAGTCT G T CCT
GATGTATTAATAATGCCTTA TTTTAAGTAG GCTC TGC AT GTGAT TAT AATAATG T
TATATTGTTTGTAGTCATTT CATG |||| ||| || ||||| ||| |||||||
TAAGTAGCATGAGC CGAG ACG TG TACTG ATG TTGTTAT /
T A AATTT-- - T ATA

GAM378 TCTTGTGTTGAGACTTCGTG 355 TACACCACTC 2952 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM379 GGAGGGGCTGGGCTCTACCC 356 ACCCCTTTCT 2953 G - ACCC T TTCC CA CT
CTTTCTTCTTTCCATCCAGT TCTTTCCATC GGAGGG CTGGGCT CT CTTTCT CT ATC GT A
CTATTGCCAGATCCAGAGAA CAGT |||||| ||||||| || |||||| || ||| ||
AGCGCGGAAGCCCAGCTCTC CCTCTC GACCCGA GG GAAAGA GA TAG CG /
C - A CGC- - CC-- AC TT

GAM380 TGGTGGCATGTGCCTGTAGT 357 TGCCTGTAGT 2954 --- TGTG- AGTCC ACT
CCCAGCTACTCAGGAGGCTG CCCAGCTACT TGGT GGCA CCTGT CAGCT C
AGGCAGGAGAATTGCTTGAA CAGG |||| |||| ||||| |||||
CCA ACCA TCGT GGACG GTCGG A
AGT TAAGA GA--- AGG

GAM381 TGTCCACAGCTGGCAAATTC 358 ATGGCTGAAG 2955 A- G AAA GCAG AAT
AGTGCAGATCAGAATCAAAC GCGAGTTGAA TGTCC CAGCT GC TTCAGT ATCAG C
TGATGGCTGAAGGCGAGTTG GGAT ||||| ||||| || |||||| |||||
AAGGATA ATAGG GTTGA CG AAGTCG TAGTC /
AA G G-- G--- AAA

GAM382 GGCGGATCACCTGAGGTCAG 359 GATCACCTGA 2959 A--- TGA-- AGT A
GAGTTTGAGACCAGCCTGAC GGTCAGGAGT GGCGG TCACC GGTCAGG TTG G
CAATGTGGTGAAACCCCGTC TTGA ||||| ||||| ||||||| |||
CTGCC AGTGG CCAGTCC GAC A
CCAA TGTAA --- C

GAM383 AGGCGGGCGGATCACGAGGT 360 AACACGGTGA 2960 CGGA GA---- GATCG
CAGGAGATCGAAACCATCCT AACCCCGTCT AGGCGGG TCAC GGTCAGGA A
GGCTAACACGGTGAAACCCC ||||||| |||| ||||||||
GTCT TCTGCCC AGTG TCGGTCCT /
CAA- GCACAA ACCAA

GAM384 GGTGTCCTGGAGCCTCTGTA 361 CTGGAGCCTC 2961 T C TCT-- C- T - A
CCTGTGCCCAAATGGTGCCC TGTACCTGTG GG GTC TGGAGCC GTAC TG GC CC A
GCTGTGCCACCTGGTTTCAA CCCA || ||| ||||||| |||| || || ||
GACCC CC CAG ACTTTGG CGTG GC CG GG A
- A TCCAC TC C T T

GAM385 ATAGAGAAAACACTGATTGA 362 GAGAAAACAC 2962 - C TT- AA- GC
TAATAGGCATTTTAGTGGTC TGATTGATAA ATAG AGAAAACA TGA GAT TAG A
TTTTTAATGTTTTCTGCTGT TAGG |||| |||||||| ||| ||| |||
TGTC TCTTTTGT ATT CTG ATT /
G A TTT GTG TT

GAM386 GCACTCTGTTCTTCCGCCGC 363 ACTCTGTTCT 2963 AC G CC TCC TC TT
TCCGCCGTCGCGTTTCTCTG TCCGCCGCTC GC TCT TTCTTCCG GC GCCG GCG T
CCGGTCGCAATGGAAGAAGA CGCC || ||| |||||||| || |||| |||
GATCGC CG AGA AAGAAGGT CG TGGC CGT C
CT G AA C-- -- CT

GAM387 TTTGTGCTGAAGGAGGGTGT 364 TAGTGTCCGG 2964 TGAAGGA GA-- A AAA
TTC GT

GGAGTACCGGATAAAAATCT CATGAAGTAC TTTGTGC GGGTGTG GT CCGGATA
ATCTCT CGG T
CTTTCCGGGTTAACCGAGAG ATCC ||||||| ||||||| || ||||||| |||||| |||
ATAGTGTCCGGCATGAAGTA GGACATG CCTACAT TA GGCCTGT TAGAGA GCC
/
CATCCAGCATACGTACAGG CATACGA GAAG C GA- --- AA

GAM388 GAGGCCGTCAAAGTGCACAG 365 CAACGGGGAA 2965 AA ACAGC ACAC--- GTT T
CCAG
CTTCCCCACACTCAAGTTCT CGCACGCTGA GAGGCCGTCA GTGC TTCCCC TCAA CT
TCCTG T
TTCCTGCCAGTGCCGACAGG TGGT |||||||||| |||| |||||| |||| || |||||
ACGGTCATTGATTACAACGG TTTTGGTAGT CACG AAGGGG AGTT GG AGGAC
G
GGAACGCACGCTGATGGTTT CG C---- CAACATT ACT C AGCC
T

GAM389 GGTCCTTGCCATCTCCTTCC 366 AAGTGCCTCC 2966 CC- C------ TC CCATT
ATCTGCCCATTAACTCTCGC GTGAGGAGAT GGTCCTTG ATCTCCTT CA TGC A
AAGTGCCTCCGTGAGGAGAT TCAC |||||||| |||||||| || |||
TCACAAGGACC CCAGGAAC TAGAGGAG GT ACG A
ACT TGCCTCC GA CTCTC

GAM390 CCCTGGGGTTGGGGCCTCAC 367 AGGCAGGAGG 2967 GGG ACC A
CCCTCTGGAGGGCCGGAGGC TGGAAACCCC CCCTGGGGTT GCCTC CCTCTGG G
AGGAGGTGGAAACCCCAGGG AGGG |||||||||| ||||| |||||||
GGGACCCCAA TGGAG GGAGGCC G
AGG GAC G

GAM391 TCTTGTGTTGAGACTTCGTG 368 TACACCACTC 2968 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM392 GCCATCTTGGCTCCTGTGGA 369 AAAGGAACTA 2969 A T ----- G- - CTG
GGCCTGCTGGGAACGGGACT TGTCTGGAAG GCC TCT GGC TCCT TGGAGG CCTG G
TCTAAAAGGAACTATGTCTG GC ||| ||| ||| |||| |||||| ||||
GAAGGC CGG AGG CTG AGGA ATCTTC GGGC /
A T TATCA AA A AAG

GAM393 CCAGACTGCATGTTATTGCG 370 TGCATGTTAT 2970 CT- TATT ----- - ACA
AGCAGGAACAAAGATCCTGA TGCGAGCAGG CCAGA GCATGT GC GAG CAGGA A
CTTTTCTAGTTTTTATATGC AACA ||||| |||||| || ||| |||||
TCTTCTGG GGTCT CGTATA TG TTC GTCCT /

TCT TTTT ATCTT A AGA

GAM394 GCTGGACGAGCTGACCTTGG 371 TGACCTTGGA 2971 TG G C C - A G G- CCG A
AAGGGGTGGCCCGGTACATG AGGGGTGGCC GC GAC AG TGAC TTG GA GG GT GC GT C
CAGAGCGAACGCTGTCGCAG CGGT || ||| || |||| ||| || || || || ||
AGTCATCTGTTTGGT TG TTG TC ACTG GAC CT TC CA CG CG A
GT - T A G G G AG AGA T

GAM395 GGCTTCCGTGATGGTCTACG 372 CTTCCGTGAT 2972 --- G A TAC--- GACA-- GTA
ATGACACCAGTAAGAAATGG GGTCTACGAT GGCT TCC TG TGGTC GAT CCA A
GTACCAATCAAACCTGGCCA GACA |||| ||| || ||||| ||| |||
GCAGGGATTCAGCC CCGA AGG AC ACCGG CTA GGT G
CTT G G TCCAAA ACCATG AAA

GAM396 CAGAAATGCTTCCTGGAATA 373 TGACAGTTTA 2973 AAAT -- AATATT-- - TT
TTACGTCAGCTTGGTGCTGA ACAAGCCTTA CAG GCTTCCT GG AC GTCAGC G
CAGTTTAACAAGCCTTAGGA GGAA ||| ||||||| || || ||||||
AGTTAGCTG GTC TGAAGGA CC TG CAGTCG /
GAT- TT GAACAATT A TG

GAM397 CCGAGGAAGCTAAGGCTGCG 374 AGGAAGCTAA 2974 GAA TAA C -- CC
TTGGGGTGAGGCCCTCACTT GGCTGCGTTG CCGAG GC GGCTG GTTG GGGTGAGG C
CATCCGGCGACTAGCTACCG GGGT ||||| || ||||| |||| ||||||||
CGCTCGG GGCTC CG TCGAT CAGC CCTACTTC T
G-- CCA - GG AC

GAM398 GTCCCGAAACAAGCTTTCAC 375 CCAGGGCCTC 2975 GAA TT A CGT A CC
CGACGTGGCCACTGGCTCCC GGGGCCGCTT GTCCC ACAAGC TC CCGA GGCC CTGGCT
C
TGGGCCAGGGCCTCGGGGCC GTGG ||||| |||||| || |||| |||| ||||||
GCTTGTGGGAT TAGGG TGTTCG GG GGCT CCGG GACCGG /
--- CC - --- - GT

GAM399 GGTGACAACATGCTGGAGCC 376 TTGGTTCAAG 2976 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM400 GGTGACAACATGCTGGAGCC 377 TTGGTTCAAG 2977 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C

AAAG G AA - TA

GAM401 CCATGCCTATCCAGGTGCTG 378 CTCCTGGTGT 2979 TAT- TGC A CTGA A A ATTA
AAGGGCCTGACCATCACTCA TGGCGTGG CCATGCC CCAGG TGA GGGC CC TC CTC A
TTAAGAACAGAGGAGGCTGC ||||||| ||||| ||| |||| || || |||
CTGTTACTCCTGGTGTTGGC GGTGCGG GGTCC ATT TCCG GG AG GAG G
GTGG TTGT TC- G TC-- - - ACAA

GAM402 CAGGGACACTGAGCTGGCTA 379 TCTCCTGGGG 2978 ACA A GC - C CA A- C
TCTCGGCGCTTCGGGCAAGA TCCTGCAGGT CAGGG CTG GCTG TATCT CGG GCTTCGGG
AGA CTG A
ACTGCAACAGGCTCTCCTGG GTAC ||||| ||| |||| ||||| ||| |||||||| ||| |||
GGTCCTGCAGGTGTACAGCC GTCCC GGC CGAC GTGGA GTC TGGGGTCC TCT GAC
/
GGGCCCCTG CG- - AT C C -- CG A

GAM403 GTGGAGCGAGCCAAATGAAG 380 AAAGCAGTTC 2980 G- AG AAATGA A ATCAAG GT
AAGAGCTGATCAAGTTCATG TCTGAGGAGC GTGGA CG CC AGA GAGCTG TTCAT G
TGTGGTGAAAAGCAGTTCTC GAAT ||||| || || ||| |||||| |||||
TGAGGAGCGAATCCGC CGCCT GC GG TCT CTTGAC AAGTG /
AA GA AG---- - GAA--- GT

GAM404 TCTCCTGCTTCTGGGACCTG 381 ACCGTGTTTT 2981 CC CT CCTGCCA AC TTG A
TCCG
CCAGCACCGTGTTTTGTGGT GTGGTTAGCT TCT TG TCTGGGA GC CGTGTT TGGTT GC
T
TAGCTCCGTTCTTGCCAACC CCGT ||| || ||||||| || |||||| ||||| ||
AAGCATGAGCTCCCAGATTC AGA GC AGACCCT CG GTACGA ACCAA CG /
GTCAGA CT TT ------- A- --- C TTCT

GAM405 TCTTGTGTTGAGACTTCGTG 382 TACACCACTC 2982 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM406 TCAGCCTGCTGAACAGTTCC 383 TATCCTTGTT 2983 CT - CCTTTTTC TA C
TCCAAA
TTTTTCAAAGACATAGATAC TTTAACTGTT TCAGC GCTG AACAGTT AAAGACA GATA CA
A
CATCCAAAAATTTCCTGATA GTGG ||||| |||| ||||||| ||||||| |||| ||
TCCTTGTTTTTAACTGTTGT AGTCG CGGT TTGTCAA TTTTTGT CTAT GT /
GGCTTGCTGA TT G -------- TC A CCTTTA

GAM407 GTAGAGCTTTATGCTGAAAA 384 GAGCTTTATG 2985 - TA GAAAA - T A
GGTGGCCACTAGAGGTCTGT CTGAAAAGGT GTAGAG CTT TGCT GGTGGC CAC AG G
GTGCCATTGCCCAGGCAGAG GGCC |||||| ||| |||| |||||| ||| ||
TCTCTGC CGTCTC GAG ACGG TTACCG GTG TC G
T -- ACCCG T - T

GAM408 GGGAAACTCCGAGGACAGAG 385 TGGCCTGATG 2984 AAA A--- - GA AA GA
GGCTAAATCCATGAAGTTGT ATCCACAGCG GGG CTCCG GGA CA GGGCT ATCCAT A
GGATGGCCTGATGATCCACA GAGA ||| ||||| ||| || ||||| ||||||
GCGGAGACCC CCC GAGGC CCT GT TCCGG TAGGTG G
A-- GACA A AG -- TT

GAM409 TGGCACTCCTAGGCTCTATC 386 TGCCATAGGC 2986 TA T CAGAC A CC CAT
AGACTGACCCCTCGGGCACA CGGGGTGCCA TGGCACTCC GGC CTAT TG CC TCGGGCA
A
TACCATGCCTGGAAGGCCAA ||||||||| ||| |||| || || |||||||
TGCCATAGGCCGGGGTGCCA ACCGTGGGG CCG GATA AC GG GGTCCGT /
-- - CCGTA C AA ACC

GAM410 GGAGCACATGTGCCGCCTGG 387 CACAGCCCGG 2987 A C - ----- T ACAT TCAC
ACATTGATTCACCACCCATC AACACTGGCA GG GCA ATG TGCCG CC GG TGAT C
ACAGCCCGGAACACTGGCAT TCAT || ||| ||| ||||| || || ||||
CATCTGTACC CC TGT TAC ACGGT GG CC ACTA /
A C T CACAA C GAC- CCCA

GAM411 CTCTCCCTTGACCCAAGCCA 388 TGAGCAGTTA 2988 C GAC AAG CG GA G GAATC
CGAACGAGCTGGAGGGAATC TTGGAGGAAG CTCTC CTT CC CCA AAC GCT GAGG T
TGCGGTACTTTGAGCAGTTA AGAG ||||| ||| || ||| ||| ||| ||||
TTGGAGGAAGAGAGAG GAGAG GAA GG GGT TTG CGA TTTC G
A --- A-- TA A- G ATGGC

GAM412 TGTCACCATCCTCTGCATTG 389 TCCCTGGCTT 2989 CA C- AT- C TG CACT C T
ACTTGGGCACTGACATGGTT ATGAGCAGGC TGTCAC TC TCTGC TGA T GG GA ATGGT C
CCTGCCATCTCCCTGGCTTA TGAG |||||| || ||||| ||| | || || |||||
TGAGCAGGCTGAGAGTGACA ACAGTG AG GGACG ATT G CC CT TACCG C
AG TC AGT C GT ---- C T

GAM413 GTAGAGCTTTATGCTGAAAA 390 GAGCTTTATG 2991 - TA GAAAA - T A
GGTGGCCACTAGAGGTCTGT CTGAAAAGGT GTAGAG CTT TGCT GGTGGC CAC AG G
GTGCCATTGCCCAGGCAGAG GGCC |||||| ||| |||| |||||| ||| ||
TCTCTGC CGTCTC GAG ACGG TTACCG GTG TC G
T -- ACCCG T - T

GAM414 GGGAAACTCCGAGGACAGAG 391 TGGCCTGATG 2990 AAA A--- - GA AA TG A
GGCTAAATCCATGAAGTTTG ATCCACAGCG GGG CTCCG GGA CA GGGCT ATCCA A G
TGGATGGCCTGATGATCCAC GAGA ||| ||||| ||| || ||||| ||||| |
AGCGGAGACCC CCC GAGGC CCT GT TCCGG TAGGT T /
A-- GACA A AG -- GT T

GAM415 ATGGTGCTAAGGAAATTTGC 392 TTGACCCATC 2992 G ATT T CTTCG C - T CT
TATGCTCTTCGAGCTGAGGG ATCTGGTTTG ATGGT CTAAGGAA TGCTA GCT AG TGA
GGGTTA TGGG G
TTATTGGGCTGACTTTATTG GCAT ||||| |||||||| ||||| ||| || ||| |||||| ||||
ACCCATCATCTGGTTTGGCA TACCA GGTTTTTT ACGGT TGG TC ACT CCCAGT ATTT
/
TTTTTTGGACCAT - --- T ----- T A T CA

GAM416 AGGAGGACGCGCTGCCCGGC 393 GAGAGTACTC 2993 ------ G- G CAGAAAA AA
CAGAAAACGGAGTTCAAGGT CTGCGTCTTC AGGAGGACGC GCT CCC GC CGGAGTTC
G
GGACTCCGACGACCAGTGGG CT |||||||||| ||| ||| || ||||||||
GAGAGTACTCCTGCGTCTTC TCCTTCTGCG TGA GGG TG GCCTCAGG /
CT TCCTCA GA G ACCAGCA TG

GAM417 CGGCTCCGAGAGCAGGTTCT 394 TACACATTGA 2994 - AGAG C A TC GCAG C
TCGTGAGTTCCTCGCAGGGC GAACCTGAAC CGGC TCCG CAGGTTCTT GTG GT CTC GG
C
CGGTCAGAGCTACACATTGA ATGG |||| |||| ||||||||| ||| || ||| ||
GAACCTGAACATGGAGGCCG GCCG AGGT GTCCAAGAG TAC CA GAG CT G
G ACAA T A TC A--- G

GAM418 TCTTGTGTTGAGACTTCGTG 395 TACACCACTC 2995 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM419 TCTTGTGTTGAGACTTCGTG 396 TACACCACTC 2996 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM420 GCGTGCGGCCGCAAGCTTAT 397 CTTGGCACTG 2997 T ---- TATT---- T
TCCCTTTAGTGAGGGTTAAT GCCGTCGT GCG GCGGCCG CAAGCT CCCTT A
TTTAGCTTGGCACTGGCCGT ||| ||||||| |||||| |||||

CGT TGC TGCCGGT GTTCGA GGGAG G
- CACG TTTTAATT T

GAM421 ACGATTCGCAGTTATATAAG 398 TAAGGGAATC 2998 G ---- AGG C TC T
GGAATCAGTGTTCACGTCTC AGTGTTCACG ACGATTC CA GTTATATA GAAT AGTGT ACG C
TGTATATATTTATTTATGTG TCTC ||||||| || |||||||| |||| ||||| |||
TAATTTAATGGGAATTGT TGTTAAG GT TAATGTGT TTTA TTATA TGT T
G AATT A-- T TA C

GAM422 CTGCGCTCCTGTCTTCTGGC 399 GCTCCTGTCT 2999 CGC- CTTC TTCA AAG
TTCAGTCTGGAAGATCCCCA TCTGGCTTCA CTG TCCTGT TGGC GTCTGG A
GACACATGCTAACAGGATCT GTCT ||| |||||| |||| ||||||
ACAG GAC AGGACA ATCG CAGACC /
ATCT ---- TACA CCT

GAM423 GCAACATCCAGACTCCAGAA 400 TGTTATGCTG 3000 AA T A AGAAT TGCCA A
TACAGCTGCCAAGGAGACCC TGGGGACTGG GC CA CCAG CTCC ACAGC AGG G
TGTTATGCTGTGGGGACTGG CTGG || || |||| |||| ||||| |||
CTGGGGC CG GT GGTC GGGG TGTCG TCC A
GG C A ----- TATTG C

GAM424 CACCAAGAAGTTGACAGCCA 401 AGAAGTTGAC 3001 CAA T CCA A-- TA
GGTGAATGTTATACACAAGC AGCCAGGTGA CAC GAAG TGACAG GGTGA TGT T
TCATCGTCTGTCATCTTCAC ATGT ||| |||| |||||| ||||| |||
GTG GTG CTTC ACTGTC CTACT ACA /
CA- T TG- CGA CA

GAM425 GGTGTGCCCGATGTGCAGCG 402 TTTGAAAGGC 3002 G CCG AG-- GTTC C ACT
AGCAGTTCCCTCCTGACTAT ATGTGCAGAC GGT TGC ATGTGC CGAGCA CCT CTG A
GACCAGCAGGTGTTTGAAAG C ||| ||| |||||| |||||| ||| |||
GCATGTGCAGACC CCA ACG TGTACG GTTTGT GGA GAC T
G --- GAAA ---- C CAG

GAM426 TCTTGTGTTGAGACTTCGTG 403 TACACCACTC 3003 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM427 TTGCGGCATCCACGAGACCA 404 TGACGTGGAC 3004 CA- AGAC - ACTC
CCTTCAACTCCATCATGAAG ATCCGCAA TTGCGG TCCACG CAC CTTCA C
TGTGACGTGGACATCCGCAA |||||| |||||| ||| |||||
AACGCC AGGTGC GTG GAAGT /

TAC A--- T ACTA

GAM428 GCATTGATCTTATCCTCCGT 405 TTGATCTTAT 3005 TGAT AT TC GA T CTCA
GACTGTCACCTCATCGTCGT CCTCCGTGAC GCAT CTT CC CGT CTG CAC T
GCAGAATGAGGGCCGAGTAT TGTC |||| ||| || ||| ||| |||
ATGC CGTA GAG GG GTA GAC GTG /
TAT- CC GA A- - CTGC

GAM429 GGCTCCCAATGTTGACGTTG 406 CAATGTTGAC 3006 CTCCC CG---- AG GTTTG
GCCAGGGCGTTTGCAAACAA GTTGGCCAGG GG AATGTTGA TTGGCC GGC C
GCCAGGCCAAAAAGGCTCAA GCGT || |||||||| |||||| |||
CATTTACACC CC TTACAACT AACCGG CCG A
ACAT- CGGAAA A- AACAA

GAM430 GGTGTCCTGGAGCCTCTGTA 407 CTGGAGCCTC 3007 T C TCT-- C- T - A
CCTGTGCCCAAATGGTGCCC TGTACCTGTG GG GTC TGGAGCC GTAC TG GC CC A
GCTGTGCCACCTGGTTTCAA CCCA || ||| ||||||| |||| || || ||
GACCC CC CAG ACTTTGG CGTG GC CG GG A
- A TCCAC TC C T T

GAM431 CAGGGACAGAAGGCAGCTCC 408 GGAGCAGGTG 3008 A- --- - C CA
CTTCCCCCAGGAAGGGCAAG CCTGGCTGTC CAGGGACAG AGGCA GCTCC CTT CCC G
AGGAGCAGGTGCCTGGCTGT CCTG ||||||||| ||||| ||||| ||| |||
CCCTG GTCCCTGTC TCCGT CGAGG GAA GGG G
GG GGA A C AA

GAM432 GCAACAGACTCTTTATTTAA 409 TCAAGTCCCT 3009 ACT---- T A- GTT
TGTGGTTTAAAATACATCAA GGCTGTTGT GCAACAG CTT ATTT ATGTG T
AATCAAGTCCCTGGCTGTTG ||||||| ||| |||| |||||
T TGTTGTC GAA TAAA TACAT A
GGTCCCT C AC AAA

GAM433 TGCTATTGTGAATAGTGCTG 410 TAGCAGGATG 3011 ------ A G A A G
CAATAAACATAAGTGTGCAT ATTTATAATC TGCT ATTGTGAAT GT CTGC ATAAACATA GT T
GTGTGTTTATAGCAGGATGA CTTT |||| ||||||||| || |||| ||||||||| ||
TTTATAATCCTTTGGGTA ATGG TAATATTTA TA GACG TATTTGTGT TA G
GTTTCC G G A G C

GAM434 GTATTTCTAGTTCTAGATCC 411 TCCACAATGG 3010 TTT TA CC A - CC
CTGAGGAATCACCACACTGA TTGAACTAGT GTA CTAGTTC GATC TG GGAA TCA A
CTTCCACAATGGTTGAACTA TTAC ||| ||||||| |||| || |||| |||
GTTTAC CAT GATCAAG TTGG AC CCTT AGT C
TT- -- TA A C CA

GAM435 TCTTTAACACAGTGTCCCAT 412 CACAGTGTCC 3012 T C TCC TG AATT
TGAAATTTTAATTTTTAGAG CATTGAAATT TCTT AA ACAGTG CAT AAATTTT T
AATTTATGAATCACTGTTTC TTAA |||| || |||||| ||| |||||||
AAGA AGAA TT TGTCAC GTA TTTAAGA /
C - TAA -- GATT

GAM436 CACAGGCCAGGGAGAAAGAG 413 TCCCTAGATC 3013 AG --- AG GAC A - C A G
GAGACAGAGGAAGCACCGAG AATTTTCTTC CAC GCCA GGGAGAAAG GA AG GGAAG CA
CG GG T
GGTGGCTACGTTGTCTTCCC TGGA ||| |||| ||||||||| || || ||||| || || ||
TAGATCAATTTTCTTCTGGA GTG CGGT TCTTCTTTT CT TC CCTTC GT GC TC G
TGGCTCGTG CT AGG AA AGA - T T A G

GAM437 TCAGCCTGCTGAACAGTTCC 414 TATCCTTGTT 3014 T - CCTTTTTC TA C
TCCAAA
TTTTTCAGAGACATAGATAC TTTAACTGTT TCAGCC GCTG AACAGTT AGAGACA GATA CA
A
CATCCAAAAATTTCCTGATA GTGG |||||| |||| ||||||| ||||||| |||| ||
TCCTTGTTTTTAACTGTTGT AGTCGG CGGT TTGTCAA TTTTTGT CTAT GT /
GGCTGGCTGA T G -------- TC A CCTTTA

GAM438 GGCCAATTGAAACAAACAGT 415 TATTAGGGAT 3015 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM439 CAGGGAGCTCCCAGTCCTGG 416 GAGCTCCCAG 3016 --- C GGGAGAG AAGG
GAGAGGCTGAAGGCAAAGCA TCCTGGGAGA CAGG GAGCTCC AGTCCT GCTG C
GCAGAGGACTCGGAGCTCAC GGCT |||| ||||||| |||||| ||||
ACTTG GTTC CTCGAGG TCAGGA CGAC /
ACA C GA----- GAAA

GAM440 GTAGAGCTTTATGCTGAAAA 417 GAGCTTTATG 3018 - TA GAAAA - T A
GGTGGCCACTAGAGGTCTGT CTGAAAAGGT GTAGAG CTT TGCT GGTGGC CAC AG G
GTGCCATTGCCCAGGCAGAG GGCC |||||| ||| |||| |||||| ||| ||
TCTCTGC CGTCTC GAG ACGG TTACCG GTG TC G
T -- ACCCG T - T

GAM441 GGGAAACTCCGAGGACAGAG 418 TGGCCTGATG 3017 AAA A--- - GA AA TG A
GGCTAAATCCATGAAGTTTG ATCCACAGCG GGG CTCCG GGA CA GGGCT ATCCA A G

TGGATGGCCTGATGATCCAC GAGA ||| ||||| ||| || ||||| ||||| |
AGCGGAGACCC CCC GAGGC CCT GT TCCGG TAGGT T /
A-- GACA A AG -- GT T

GAM442 TCTTGTGTTGAGACTTCGTG 419 TACACCACTC 3019 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM443 GGGAAACTCCGAGGACAGAG 420 TGGCCTGATG 3020 AAA A--- - GA AA GA
GGCTAAATCCATGAAGTTGT ATCCACAGCG GGG CTCCG GGA CA GGGCT ATCCAT A
GGATGGCCTGATGATCCACA GAGA ||| ||||| ||| || ||||| ||||||
GCGGAGACCC CCC GAGGC CCT GT TCCGG TAGGTG G
A-- GACA A AG -- TT

GAM444 ACTTACGGCAAGCCTGTCCA 421 GCAGAGGAGC 3021 A CA TGT CA AA AAA G
GA- CTTC
TCATGGTGTTAACCAGCTAA GAGCTGGAAC CTT CGG AGCC CCAT TGGTGTT CCAGCT
GTTT CTC AGC A
AGTTTGCTCGAAGCCTTCAG GCCA ||| ||| |||| |||| ||||||| |||||| |||| ||| |||
TCCGTTGCAGAGGAGCGAGC GAG GTC TCGG GGTG ACCGCAA GGTCGA CGAG
GAG TTG /
TGGAACGCCACTGTGGGGCT A -- --- TC -- G-- - ACG CCTG
CTGAGAGT

GAM445 CTGAATTCTTACTGGGTTGG 422 TATCCTCATT 3022 A-- C---- TG A T- A TACCA
TGAAGATTCCACATACCAAA GATCCATTCC CTGA TTCTTA TGGGT GTGA GAT CC CA A
TTTTTTGAGGTTATCCTCAT ATAA |||| |||||| ||||| |||| ||| || ||
TGATCCATTCCATAAGAGCT GACT GAGAAT ACCTA TACT CTA GG GT A
ATCAG ATC ACCTT GT C TT A TTTTT

GAM446 GAGGTGGGTACTGGCATCAC 423 GATTGCAGGC 3023 - ----- G TCA GACAA GAT
TGATGACAATGAAGATGAAA AAAATACCCA GAGGT GGGTA CT GCA CTGAT TGAA G
ATTCAGCCAATCAGATTGCA ACTT ||||| ||||| || ||| ||||| ||||
GGCAAAATACCCAACTTT TTTCA CCCAT GG CGT GACTA ACTT A
A AAAAC A TA- ACCG- AAA

GAM447 TCCTTGGCGTGGCACCCAAC 424 TGGGTTCCAA 3024 TT CA---- AACTC-- - AC
TCACCCCAGCACCGTGGCTG AGGGGGAGAT TCC GGCGTGG CCC ACCC CAGC C
TGGGTTCCAAAGGGGGAGAT ATCA ||| ||||||| ||| |||| ||||
ATCATGCTCTGGA AGG TCGTACT GGG TGGG GTCG G
TC ATAGAG GAAACCT T GT

GAM448 TCTTGTGTTGAGACTTCGTG 425 TACACCACTC 3025 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG |||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM449 TCTTGTGTTGAGACTTCGTG 426 TACACCACTC 3026 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG |||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM450 TCCGTGTTCTGCACCAGTAT 427 TACCATGGTC 3027 T C -- T- - AAGA
TGTGGCTCAAGACTCCAGAG GGAATTTGGA TCCG GTTCTG ACCA GTA TGTGGC TC C
GCCACATTTACCATGGTCGG |||| |||||| |||| ||| |||||| ||
AATTTGGA AGGT TAAGGC TGGT CAT ACACCG AG /
T - AC TT G ACCT

GAM451 GGGAACTGGGCATCATCGAC 428 GGGCATCATC 3028 AC - C ATC AG - GG
AGTGCCTTCGGCCAGAGCGG GACAGTGCCT GGGA TG GG ATC GAC TGCC TTC C
CAAGTTCAAGATCCACATCC TCGG |||| || || ||| ||| |||| |||
C CCCT AC CC TAG TTG ACGG GAG /
-- A - AAC A- C AC

GAM452 CTGGAGCAGCTGCGTAAAAC 429 GAGCAGCTGC 3029 --- G AAAACATAC - G AT A
ATACAGGCCGGAGCTTATCA GTAAAACATA CTGGA GCA CTGCGT AGGC C GAGCTT CA
A
AAGATGGCAAGTTTGGGGCC CAGG ||||| ||| |||||| |||| | |||||| ||
TACATGCAGGTGCACATTCA GACTT CGT GACGTA TCCG G TTTGAA GT G
G ACA G CA------- G G CG A

GAM453 TGCTCTGGTGTGTGAAGGTC 430 TCTGGTGTGT 3030 TCT - GA------- - TAAC
GGTGGGTTAACTGTGTGCCT GAAGGTCGGT TGC GGTG TGT AGGT CGGTGGGT T
ACTGAACCTGGCAAATAAAC GGGT ||| |||| ||| |||| ||||||||
ATCACCCTGCA ACG CCAC ACA TCCA GTCATCCG /
TC- T AATAAACGG A TGTG

GAM454 TCACCATCTGCAGCCTTGAA 431 AAGGAGCTTG 3032 CA C- CC A T GGAG- - AA
GGAGCTTGGTTCGGAGACAG GTTCGGAGAC TCAC TCTG AG TTGA GGAGCT GGTTC ACA
GGC A
GCAAAGGAGCCATGTGTGGA AGGC |||| |||| || |||| |||||| ||||| ||| |||
GAGCCTGGTTTCTCAGTACT AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G
TCCAGACCGTGA CC CT AT - T AGGTG A AG

GAM455 GACTATGGCAAGGACCTGAT 432 TATGGCAAGG 3031 A AA- A T AGAA- CA
GGAGAAGGTCAAGAGCCCAG ACCTGATGGA GACT TGGC GG CCTGA GG GGT A
AGCTTCAGGCCGAGGCCAAG GAAG |||| |||| || ||||| || |||
TC CTGA ACCG CC GGACT TC CCG /
- GAG - - GAGAC AG

GAM456 GCGAGGTGGACGGGCTCCTG 433 CATTCCATGC 3033 GGAC- CT- C AGG
CGGCAAGGGGACATGCTTCG AGCCTTGC GCGAGGT GGG CCTG GGCA G
GGCATTCCATGCAGCCTTGC ||||||| ||| |||| ||||
CGTTCCG CCT GGGC TCGT G
ACGTA TAC T ACA

GAM457 GACTATCCACCTTGGGTCGC 434 CAGACAGTTG 3034 T TTGG C TTG - G
TTTGCTGTTCGTGATATGAG CGGTGGGTGT GAC ATCCACC GT GCT CTGT TCGT A
ACAGACAGTTGCGGTGGGTG C ||| ||||||| || ||| |||| ||||
TC CTG TGGGTGG CG TGA GACA AGTA /
- ---- T CA- G T

GAM458 CTGCAGCAGCAATAATTTCC 435 CAGCAGCAAT 3035 CA A AAT-- C- T TAG C CCA
CAGATGCTCTGATTAGGGCA AATTTCCCAG CTG GC GCAAT TTCC AGATGC CTGAT
GGCA TG T
CTGCCATCATACATGCCATT ATGC ||| || ||||| |||| |||||| ||||| |||| ||
AGGCATCTTAGGAGCTCCCA GAC CG CGTTA GAGG TCTACG GATTA CCGT AC C
TTGCAGCCACAG AC A CCCTC AT - --- - ATA

GAM459 GGCCCAGGGATCGGCAGGGC 436 TTCCCATGCC 3036 G - G- - GCT GA A
TGCTGGCAGAGGAATCCCAG CCAGGCTCCT GGCCCAG GA TC GCAGG GCT GGCA
GGAATCCC G
CTGGGGTTCCCATGCCCCAG GCAG ||||||| || || ||||| ||| |||| ||||||||
GCTCCTGCAGGACTTGCTGG CCGGGTC TT AG CGTCC CGG CCGT CCTTGGGG C
GCC G C GA T ACC AC T

GAM460 CTTTGTAAGATGCAAAGAGG 437 CTGTGCTGCC 3037 TAAGA C A TT ATCA TA
TTGGATCAAGTTTAAATGAC CCTTTCACAT CTTTG TG AAAG GG GG AGTT A
TGTGCTGCCCCTTTCACATC CAAA ||||| || |||| || || ||||
AAAG GAAAC AC TTTC CC TC TCAG /
TAC-- - - CG GTG- TA

GAM461 CTCGCTATATGGGGAAGGGT 438 TATGGGGAAG 3038 C TA AA CT A GC- GC
GTCTCAAAGGCTGTTGAGCA GGTGTCTCAA CT GCTA TGGGG GGGTGT CA AG TGTTGA A
CATCAATAAAACTATGTGCG AGGC || |||| ||||| |||||| || || ||||||
CCTGCCCTGGTTAGCAAG GA CGAT GTCCC TCCGCG GT TC ATAACT /
A TG G- T- A AAA AC

GAM462 TTGCCGTCTGCCAAAGCTGG 439 TACGCCACAT 3039 T TG CAA- TG- C TGAGA G
TGCCGTTGAGAAGGGGGTCC CGCTGACTGT TTGCCG C C AGC GTG CGT AGGG G
CCTGTACGCCACATCGCTGA GGTG |||||| | | ||| ||| ||| |||| |
CTGTGGTGGCAA AACGGT G G TCG CAC GCA TCCC T
- GT TCAG CTA C TG--- C

GAM463 GGGTCAAGCCAGCACCTGAT 440 TGAAGAGGAA 3040 TCA CA GAAA C TG G
GAAACTTCCTTCAGTGAGGC TCAGGACCTG GGG AGCCAG CCTGAT CTTC TTCAG A G
CTTGCTGAAGAGGAATCAGG GCTC ||| |||||| |||||| |||| ||||| |
ACCTGGCTCCC CCC TCGGTC GGACTA GGAG AAGTC T C
--- CA A--- - GT C

GAM464 GGTGACAACATGCTGGAGCC 441 TTGGTTCAGG 3041 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGGAAG GGTGAC CAT CT GAGCCAAG GC A
TCAGGGGATGGGAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAGG G GA - TA

GAM465 GGCTGGGGCTCATTTGCAGG 442 GCTCATTTGC 3042 - CT T A CAAA TCA
GGGGAGCCAAAAGGGTCATC AGGGGGGAGC GGC TGGGG CATT GCAGGGGGG GC AGGG
T
ATCTCTGCCCCCTCTGCTGA CAAA ||| ||||| |||| ||||||||| || ||||
TGCCCCCATGTT TTG ACCCC GTAG CGTCTCCCC CG TCTC /
T C- T - ---- TAC

GAM466 GCTCATTATTGACTACTTAG 443 TACAATGATA 3043 ---- ACTACT A TCAA
CTGAGTTCAATTCCACACCA ACTGAGC GCTCA TTATTG TAGCTG GT T
GCTGTCTTTACAATGATAAC ||||| |||||| |||||| ||
TGAGC CGAGT AGTAAC GTCGAC CA T
CAAT ATTTCT - CACC

GAM467 GTGCTGTGTGTCACCAACTG 444 TGAAAAGTTG 3044 TG G CA GG T T TT AG G
GTCTTCTAATTTGGAAGGAG GAAACAGTGG GTGC T TGT CCAACT TC TC AAT GGAAGG TT
G
TTGGAAAGGCCTTTTTGTTG CAC |||| | ||| |||||| || || ||| |||||| ||
ATGAAAAGTTGGAAACAGTG CACG G ACA GGTTGA AG AG TTG TTTTCC GA A
GCAC GT - AA AA T - T- G- A

GAM468 TTTGTTAAACCAATCACAGC 445 TCGGCAGTGG 3045 AA ATCACAG T T GCA
GGTGGGTGGAAAGCATGAAT GGTAACGGA TTTGTTA CCA CGG GGG GGAAA T
TTTCCCCTCGGCAGTGGGGT ||||||| ||| ||| ||| |||||
AACGGA AGGCAAT GGT GCT CCC CTTTT /

GG GACG--- - - AAG

GAM469 ATGGTCGTTCTACTGGGCTG 446 TACTGGGCTG 3046 CTAC ATT GA AGCCA
ATTTTGGACAGTGGAGCCAC ATTTTGGACA ATGGTCGTT TGGGCTG TTG CAGTGG C
TCATACCACTGCAATTCCAG GTGG |||||||||| ||||||| ||| ||||||
TCCACGATGGCTAT TATCGGTAG ACCTGAC AAC GTCACC /
C--- CTT -- ATACT

GAM470 GGGGCAGGAGGGTGTCAAGT 447 TGTCTTGGTT 3047 G ---- TG AGTG---- TG
GGTCTGAACTGATAAAAATT CGTGTCCC GGGGCA GA GGG TCA GTC A
GTGATGTCTTGGTTCGTGTC |||||| || ||| ||| |||
CC CCCTGT CT TCT AGT TAG A
G TGGT GT GTTAAAAA TC

GAM471 TTGTCGTCATTGGACACGTA 448 TAAATGCGGT 3049 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM472 GGTGACAACATGCTGGAGCC 449 TTGGTTCAAG 3048 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM473 TTGTCGTCATTGGACACGTA 450 TAAATGCGGT 3051 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM474 GGTGACAACATGCTGGAGCC 451 TTGGTTCAAG 3050 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM475 GAGGCGGAGCTTGCAGTGAG 452 ACTCCAGCCT 3052 - AG A- G AT----- C
CCGAGATTGCACCACTGCAC GGGCGACAGA GAGGCGGAG CTTGC TG GCC AG TGCA C
TCCAGCCTGGGCGACAGAGC GCAA ||||||||| ||||| || ||| || |||| |||
AAGACTCCGTCTC CTCTGCCTC GAACG AC CGG TC ACGT A
A AG AG G CGACCTC C

GAM476 GCCCAAGATGTGCAGCTTCC 453 TATGCCAGCC 3053 AA - TTCCT GAC CAAAGT AT

TGGAGTGGAGGGACCTCAAA TCTACTTCTG GCCC GATG TGCAGC GGAGTGGAGG CT TGTCT A

GTTGTCTATAAGAGATATGC CTGC |||| |||| |||||| |||||||||| || |||||

CAGCCTCTACTTCTGCTGCG CGGG CTAC GCGTCG CTTCATCTCC GA ATAGA /

CCATCGAGGGC AG C T---- --- CCGT-- GA

GAM477 ATTTGAGAAGGAGGCTGCTG 454 CTTCAAGTAT 3054 TG AGG - GA T AAA

AGATGGGAAAGGGCTCCTTC GCCTGGGTCT ATT AGA AGGC TGCT GA GGG G

AAGTATGCCTGGGTCTTGGA TGGA ||| ||| |||| |||| || |||

T TAG TCT TCCG ATGA CT CCT /

GT GGG T A- T CGG

GAM478 CATTGTCGTCATTGGACACG 455 CGTCATTGGA 3055 GTC-- T- A C ATTC C

TAGATTCGGGCAAGTCCACC CACGTAGATT CATT GTCA TGG CA GTAG GGG A

ACTACTGGCCATCTGATCTA CGGG |||| |||| ||| || |||| |||

TAAATG GTAA TAGT ACC GT CATC CCT A

ATATC CT G - ACCA G

GAM479 GTCAGGCAGAGGTGACGCCA 456 CACCCCTCAA 3056 C TGAC AGA TTTAAA A GA

GGAGATGATTTAAAGGTGAA ACCTTGGCTC GTCAGG AGAGG GCCAGG TGA GGTG AAAT C

AATGACAAGGTTTCCACCCC CTTT |||||| ||||| |||||| ||| |||| ||||

TCAAACCTTGGCTCCTTTTC CAGTCT TTTCC CGGTTC ACT CCAC TTTG A

TGAC - T--- CAA CC---- C GA

GAM480 GGCTCACGCCTGTAATCCCA 457 AAGAGGCGGG 3057 C C AA A T AG A

GCTCTCAGGGAGGCTAAGAG AGGATAGCTT GGCTCA GC TGT TCCC GC CTC GG G

GCGGGAGGATAGCTTGAGCC GAGC |||||| || ||| |||| || ||| ||

CCGAGT CG ATA AGGG CG GAG TC /

T - GG - - AA G

GAM481 TCTGGCGCTGGCGCGGCTCC 458 CTACCAGCGG 3058 G G - AAGAA- TCC

AAGAAGGCATCCGCATTTGC CGGCCGCGGC TCTGGC CTG CGCGGCT CC GGCA G

TACCAGCGGCGGCCGCGGCG GGAG |||||| ||| ||||||| || ||||

GAGCCAGG GGACCG GGC GCGCCGG GG TCGT C

A G C CGACCA TTA

GAM482 GCCTGATCATCCTACTGCAG 459 GTGGACCTGC 3059 CTGA ACT GCC G CC G

GGCCTCCAGGGCCGGGTAAC GGGATGAGAG GC TCATCCT GCAGG TCCA GG GG T

CACTGTGGACCTGCGGGATG C || ||||||| ||||| |||| || ||
AGAGC CG AGTAGGG CGTCC AGGT TC CC A
AG-- --- --- G A- A

GAM483 GAACGACCTGAACCTCTGTC 460 AAGCACAGAG 3060 A GAAC - ACCAAC AAC TG ATT
TTCGACCAACTGAAGCAACT ATAAGGTCGC GA CGACCT CTCTGT CTTCG TGAAGC T GG A
TGGGATTAATTGCTTGATTA TC || |||||| |||||| ||||| |||||| | ||
GCTTCACGAAGCACAGAGAT CT GCTGGA GAGACA GAAGC ACTTCG A TC A
AAGGTCGCTC C ATA- C ------ ATT GT GTT

GAM484 TTATGTTATTAGGTGTAAAG 461 TACTGCGAGC 3061 - AG GTA AG A T TG
AAAGTGTATGCTGTGCCTGT AGTTCTTCCA TTATGT TATT GT AAGAA TGT TGC GTGCC T
TTTGGTACTGCGAGCAGTTC ATTC |||||| |||| || ||||| ||| ||| |||||
TTCCAATTCGATGAATATAA AATATA GTAG TA TTCTT ACG GCG CATGG T
A CT ACC G- A T TT

GAM485 TTGTCGTCATTGGACACGTA 462 TAAATGCGGT 3063 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM486 GGTGACAACATGCTGGAGCC 463 GTTCAAGGGC 3062 AA-- G-- T TA
AAGTGCTAACATGCCTTGGT ATGGAAAGTC GGTGAC CATGCT GAGCCAAG GC A
TCAAGGGCATGGAAAGTCAC ACC |||||| |||||| |||||||| ||
C CCACTG GTACGG CTTGGTTC CG C
AAAG GAA - TA

GAM487 GTGAGAGCGGTAAGATGGCG 464 TCAGCACCGA 3064 A C AA- C GG-- - G G TCC GC
GCGGCGGCGGTGGTGGAGTT CCGGGAGGCC GTG GAG GGT GATGG GGC CGG CGGTG TG AGT AGAGA C
CCAGAGAGCCCAGTCTCTAC TCCA ||| ||| ||| ||||| ||| ||| ||||| || ||| |||||
TCAGCACCGACCGGGAGGCC CAC CTC CTA CTACC CCG GCC GCCAC AC TCA TCTCT C
TCCATCGACATCCTCCAC - - CAG T GAGG A G - --- GA

GAM488 GGTGACAACATGCTGGAGCC 465 TTGGTTCAAG 3065 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM489 TTGTCGTCATTGGACACGTA 466 TAAATGCGGT 3066 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM490 GGTGACAACATGCTGGAGCC 467 TTGGTTCAAG 3067 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM491 TTTAGGGGAAGTCAGACTAA 468 TAGGGGAAGT 3068 G A A AA C G TG
TCCCTGGGTGCACTTCGAGA CAGACTAATC TTTAGG GA GTC GACT TC CT GG C
GAAAGGTTGGACCTCGCCTG CCTG ||||||| || ||| |||| || || ||
AG GAGTCC CT CAG TTGG AG GA CT A
G C G AA A G TC

GAM492 GATGAGTGGCTTTTCGAGGG 469 CGAGGGACCT 3069 A TTC G C GG T A C--- G
ACCTGGCACGTACATCCCCC GGCACGTACA GATG GTGGCTT GAG GA CT CACG AC TCC
CC G
GGAAGGAAGTGGAGGTCGTG TCCC |||| ||||||| ||| || || |||| || ||| ||
GAGATCATTCAGGCCACCAT CTAC CACCGGA CTT CT GA GTGC TG AGG GG A
C - --- A A G- - G TGAA A

GAM493 TCCGTGTTCTGCACCAGTAT 470 TACCATGGTC 3070 T C -- T- - AAGA
TGTGGCTCAAGACTCCAGAG GGAATTTGGA TCCG GTTCTG ACCA GTA TGTGGC TC C
GCCACATTTACCATGGTCGG |||| |||||| |||| ||| |||||| ||
AATTTGGA AGGT TAAGGC TGGT CAT ACACCG AG /
T - AC TT G ACCT

GAM494 TCCTCAAGTTCCTCCAGCTT 471 ATGAAGCAGA 3071 ---- C C TATG - TAT CAA
TTTATGTCTGATATGCCAAA ACCTGGATGA TCCT CAAGTTC TCCAG TTTT TC TGA GC A
GCCTGCCTTCATGAAGCAGA GCTT |||| ||||||| ||||| |||| || ||| ||
ACCTGGATGAGCTTGGAATA AGGA GTTCGAG AGGTC AAGA AG ACT CG G
GGA TAAG T C CGA- T TC- TCC

GAM495 GCATTGATCTTATCCTCCGT 472 TTGATCTTAT 3072 GAT AT TC GA T CTCA
GACTGTCACCTCATCGTCGT CCTCCGTGAC GCATT CTT CC CGT CTG CAC T
GCAGAATGAGGGCCGAGTAG TGTC ||||| ||| || ||| ||| |||
ATGC CGTAG GAG GG GTA GAC GTG /
AT- CC GA A- - CTGC

GAM496 GGCTCCCAATGTTGACGTTG 473 CCAGGCCAAA 3073 CTCCC CG---- AG TGC
GCCAGGGCTTTGCAAACAAG AAGGCTCAAC GG AATGTTGA TTGGCC GGCTT A
CCAGGCCAAAAAGGCTCAAC ATTT || |||||||| |||||| ||||| /
ATTTACACC CC TTACAACT AACCGG CCGAA /
ACAT- CGGAAA A- CAA

GAM497 TCTTGTGTTGAGACTTCGTG 474 TACACCACTC 3074 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| ||||| /
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM498 ATGAACTATGTGGTTTGAAT 475 TATGTGGTTT 3075 --- AA AT- - CA
CGGATGTAGACCATTAGTAC GAATCGGATG ATGAACTATGT GGTTTG TCGG GTAG AC T
TACTACTTGAGCTAAACTTC TAGA |||||||||| |||||| |||| |||| || /
TGCATGGTTCAT TACTTGGTACG TCAAAT AGTT CATC TG /
TCT CG CAT A AT

GAM499 GCACCTGGGGAAGTTTGGCG 476 GGGAAGTTTG 3076 A-- AGTTT --- TTGCTT A
TCATTTGCTTGGAAGACCTC GCGTCATTTG GC CCTGGGGA GGCG TCAT GG A
ATTCATGAAATTGCCTTCCC CTTG || |||||||| |||| |||| || /
AGGGAAGC CG GGACCCTT CCGT AGTA CC G
AAG ----- TAA CTTACT A

GAM500 CCCCAGAGTGGATTTCCCTC 477 AGTGGATTTC 3077 G ATTT ATCTCGA- GCT
GATCTCGACTCCGCTTCAAG CCTCGATCTC CCCCAGA TGG CCCTCG CTCC T
GAGAAGCTTGGCGAGGGCCA GACT ||||||| ||| |||||| |||| /
GTTTGGGG GGGGTTT ACC GGGAGC GAGG /
G ---- GGTTCGAA AAC

GAM501 GCCGCGCTGTTGCCGCGGCT 478 GACCTGGACA 3078 G - ATTCTTAAAA G
TGTTATTCTTAAAATGGCGC AGTATGTGGA GCCGCGCTGTT CCGCG GCTTGTT TGGC C
CGCTAGACCTGGACAAGTAT AATA |||||||||| ||||| ||||||| |||| /
GTGGAAATAGCGCGGC CGGCGCGATAA GGTGT TGAACAG ATCG /
A A GTCCAG---- C

GAM502 CCATGAAGCTGGTGACCATG 479 AGCTGGTGAC 3079 GAA - CA GACAAG
TTTGACAAGCTCTCCAGGAA CATGTTTGAC CCAT GCTGG TGAC TGTTT C
CAGAGTCATCCAGCCAATGG AAGC |||| ||||| |||| ||||| /
GGTA CGACC ACTG ACAAG T
AC- T AG GACCTC

GAM503 GGCAGAGTTCCAAGACAGGA 480 TGGCTTGGCA 3080 -- AGA------- ATATC CT GAA
TATCGGGTGCATCTGAGAAA TACACAATGG GGCAGA GTTCCA CAGG GGGTGCAT GA
A
GACATCGTGCACTCTGGCTT AGCG |||||| |||||| |||| |||||||| ||
GGCATACACAATGGAGCGTT CCGTCT CGAGGT GTTC CTCACGTG CT G
CTGCC TG AACACATACG GGT-- -- ACA

GAM504 GGTCTGTTTACAGAGTGTGG 481 TAAAGAAAGA 3081 GTTTA--- AG AA G -- G
TAATTTCGTTCTTTAGATTT AAATTACAGC GGTCT CAG TGTGGT TTTC TTCTTTA GATTT
C
GCAGAATTTATAAAGAAAGA CTGC ||||| ||| |||||| |||| |||||||| |||||
AAATTACAGCCTGCACACCC CCAGA GTC ACATTA AAAG AAGAAAT TTAAG /
AAGACC ACCCACAC CG -- A AT A

GAM505 CTTGTGGGAGAGATTATCAA 482 TGGGAGAGAT 3083 T GA ATC -------- - G A AT
GCGTTTTGAGCAGAAAGGAT TATCAAGCGT CTTG GGGAGA TT AAGC GTTTT GA CAG
AAGG T
TCCGCCTTGTTGGTCTGAAA TTTG |||| |||||| || |||| ||||| || ||| ||||
TTCATGCAAGCTTCCGAAGA GAAC TCTTCT AA TTCG TAAAG CT GTT TTCC C
TCTTCTCAAG - AG GCC AACGTACT T G G GC

GAM506 CACTACGTTGACCTGAAGGA 483 AAGGACCGTC 3082 GA-- GAA- CCATTCT --
AAAT
CCGTCCATTCTTTGCCGGCC CATTCTTTGC CACTACGTT CCT GGACCGT
TTGCCGGCCT GGTG A
TGGTGAAATACATGCACTCA CGGC ||||||||| ||| ||||||| |||||||||| ||||
GGGCCGGTAGTTGCCATGGT GTGGTGTAA GGG TCTGGTA GATGGCCGGG
TCAC /
CTGGGAGGGGCTGAATGTGG GTCG AGGG CCGTT-- AC GTAC
TG

GAM507 TATACATATATACATATTAT 484 TATACATATT 3084 TAT A - T AA
GTATGGTTGTAAATTCATAC ATGTATGGTT TATACA ATACAT TTATGT ATGG TGTA T
ACTTATCACATGAATGTGTT GTAA |||||| |||||| |||||| |||| ||||
ACTGTATA ATATGT TGTGTA AGTACA TATT ACAT T
CAT - C C AC

GAM508 CAAGGAACTTCAGGCACATG 485 AAGAGGGTGT 3085 AG- ATGGTG GA G
GTGCTGATGAGTTATTAAAG ACGGGAGTTT CAAGGAACTTC GCAC CT TGA T
AGGGTGTACGGGAGTTTCTT CTTG |||||||||| |||| || |||
G GTTCTTTGAGG TGTG GA ATT T
GCA GGA--- A- A

GAM509 CCACAGGTCCTCTTTAGCCA 486 TGGAGCTGAA 3086 ---- C--- - CA AA

CAGGGAACCTCCTCTGGAGC AGACACAGAC CCACAG GTC TCTT TAGC CAGGG C
TGAAAGACACAGACGCCGCT GCCG |||||| ||| |||| |||| |||||
GTGG GGTGTC CAG AGAA GTCG GTCTC C
GCCG ACAC A AG CT

GAM510 CTTCTTCAGTGAAACGGGTG 487 TTTGTAGACT 3087 T AAC- G ----- G C
CTGGCAAGCATGTGCCCCGG TGGAACCCAC CTTC TCAGTGA GGGT CTG GCAAGCAT
TGCC C
GCAGTGTTTGTAGACTTGGA AGTC |||| ||||||| |||| ||| |||||||| ||||
ACCCACAGTCATTGATGAAG GAAG AGTTACT CCCA GGT TGTTTGTG ACGG /
T GACA A TCAGA - G

GAM511 GTAACAGGTGGGGCTGGCTA 488 GAGCTGCTGG 3088 TA TG -- TG ACA TG CA CG
CATTGGCAGCCACACGGTGC AGGCTGGCTA G ACAGG GG GC GCT T GCAGC CA G
TGGAGCTGCTGGAGGCTGGC CTTG | ||||| || || ||| | ||||| ||
TACTTGCCTGTGGT T TGTCC TC CG CGG G CGTCG GT T
GG GT AT GT A-- GT AG CG

GAM512 TTTTGGGAAGGGGGACCTGC 489 GGGAAGGGGG 3089 GG GA TG -- AATTTA
TGTTTGGCCAATTTATCCTA ACCTGCTGTT TTTT GAAGGGG CC CTGTTT GGCC T
CAGGTCTTGGACGGTGGGAC TGGC |||| ||||||| || |||||| ||||
CTCTTCAGAGAA AAGA CTTCTCC GG GGCAGG CTGG /
GA A- GT TT ACATCC

GAM513 TGGACATGGACATGAGCCCC 490 CGACAAAGAT 3090 GA GGA G - C CCCCA ACT -
GTGTGA
CTGAGGCCCCAGAACTATCT TATCACTTTA TG CAT CAT AGCC CC TGAGG GA ATCTTT
TCGGT A
TTTCGGTGTGTGAACTAAAG AGGT || ||| ||| |||| || ||||| || |||||| |||||
GCCGACAAAGATTATCACTT AC GTA GTA TCGG GG ATTTC CT TAGAAA AGCCG
/
TAAGGTGGCTAATGATGAAC AA --- A T A A---- AT- C GAAATC
A

GAM514 TCCTTGGGCTCATCCAAGAA 491 TCCAAGAACT 3091 TCATC ACTCTTC CTA
CTCTTCTGTATCTAAAACAA CTTCTGTATC TCCTTGGGC CAAGA TGTAT A
TACATCTCAAATCTTGGCCC TAAA ||||||||| ||||| |||||
AGGGA AGGGACCCG GTTCT ACATA A
----- AAACTCT ACA

GAM515 TCTTGTGTTGAGACTTCGTG 492 TACACCACTC 3092 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM516 GAGGGGTCCATACGGCGTCG 493 GAAACTTTCA 3093 G ATAC C TCT A GTCGTA
TTCTGGATTCCCGTCGTAAC CAATGTCCGG GAGGG TCC GGCGT GT GG TTCCC A
TTAAAGGGAAACTTTCACAA AGCC ||||| ||| ||||| || || |||||
TGTCCGGAGCCCTT TTCCC AGG CTGTA CA TC AAGGG /
G C--- A CTT A AAATTC

GAM517 GTGTACTTTTCAATCCTGTG 494 TTAAATTATG 3094 TTCAA T- ---- CTT A AAT
TAATGTTTAATTCTTGCAAC GCAATATTGC GTGTACTT TCC GTGTAATGTT TAATT GCA
CTG C
TGAATCAAAACAGTGTTAAA ACTT |||||||| ||| |||||||||| ||||| ||| |||
TTATGGCAATATTGCACTTG TACATGAG GGG CACGTTATAA ATTAA TGT GAC A
GGGAATGAGTACAT TAAG- TT CGGT AT- - AAA

GAM518 GGCTTTTATGTTTTTGTTGC 495 TTGCATTTAT 3095 TAT-- T -- TA TT-- TG GT
ATTTATGTTTTTGCAGTCAA GTTTTTGCAG GGCTTT GTTT TGTTG CATT TG TT CA C
TGTGAATTCTTACGAATGTA TCAA |||||| |||| ||||| |||| || || ||
CAACACAAACTGTATGAAGC CCGAAG CAAA ACAAC GTAA AT AA GT /
C TATGT C AT GC TCTT GT AA

GAM519 GATGAGTTTCTGAGGATCAG 496 TTCACCTGCG 3096 AGT G GA AG T - TG C
CACT
CACTGCCAGTGGAGATGGGC CTGTGGACAC GATG TTCT AG TC CAC GC CAG GAGATGGG
GT A
GTCACTACTGCTACCCTCAT TGAG |||| |||| || || ||| || ||| |||||||| ||
TTCACCTGCGCTGTGGACAC CTAC AAGA TC AG GTG CG GTC CTTTACTC CA C
TGAGAACATC --- G AC -- T C CA C TCGT

GAM520 CTTCTTCAGTGAGACGGGCG 497 TTTGTAGACT 3097 T GAC- CG ----- T C
CTGGCAAGCACGTGCCCCGG TGGAACCCAC CTTC TCAGTGA GGG CTG GCAAGCACG
GCC C
GCTGTGTTTGTAGACTTGGA AGTC |||| ||||||| ||| ||| ||||||||| |||
ACCCACAGTCATTGATGAAG GAAG AGTTACT CCC GGT TGTTTGTGT CGG /
T GACA AA TCAGA - G

GAM521 GGAGATCATTGACCTTGTGT 498 CACCGGTCTT 3098 TT - TGTT AATTC AA C
TGGACCGAATTCGCAAGCTG CAGGGCTTCT GGAGATCA GA CCTTG GGACCG GC
GCTGG T
GCTGACCAGTGCACCGGTCT TGGT |||||||| || ||||| |||||| || |||||
TCAGGGCTTCTTGGTTTTC CTTTTGGT TT GGGAC TCTGGC CG TGACC G
TC C T--- CA--- -- A

GAM522 TCTTGTGTTGAGACTTCGTG 499 TACACCACTC 3099 GAGA GT--- C AAAGGA

GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM523 CCATGTTGGATAAGGGATCA 500 AGGGATCAGC 3100 TGTT TAA-- TCAG G CCC
GCCGTTGATGCCCAACCCAT CGTTGATGCC CCA GGA GGGA CC TTGATG A
CAAAGGATTTTCCCATCGCT CAAC ||| ||| |||| || ||||||
CCCTGG GGT CCT CCCT GG AACTAC /
C--- CGCTA TTTA A CCA

GAM524 ATGTAAGCGCTGGTCATTTT 501 TTAGTAATTA 3101 - CT CATTTT -- TCA T
GAT
TCTTCTGGGGTTTACTGATC CTCTAGGAGA ATGTAAG CG GGT TCTTCTGGGGT TTACTGA
GTG GGT T
AGTGTGGTGATTTTAACTTC TTTT ||||||| || ||| |||||||||| ||||||| ||| |||
ATTTAGTAATTACTCTAGGA TATATTC GT CCA AGAGGATCTCA AATGATT TAC TCA
/
GATTTTACCTTGACTTATAT A T- TTTT-- TT --- T ATT

GAM525 GCATAATCGGTCACTCGTAT 502 TGAATGGACG 3102 AATC --- A GAA TATT TAT
AGAACAGTATTGTTTCTATA GGTTCAGGCC GCAT GGTC ACTCGT TA CAG GTTTC A
ATTTGAAGCTTTCTGAATGG TGAT |||| |||| |||||| || ||| |||||
ACGGGTTCAGGCCTGATGC CGTA CCGG TGGGCA GT GTC CGAAG A
GT-- ACT G AA- TTT- TTT

GAM526 TCTTGTGTTGAGACTTCGTG 503 TACACCACTC 3103 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM527 CTGGACTTGGATGGGCCCGA 504 GGGCATTGGG 3104 - C-- T G - G CA
GTTGGGGGCAACACCCCGGG GCTTTCCAGC CTG GA TTGGA GG CCCGA GTT GGGG A
CATTGGGGCTTTCCAGCTCT TCTC ||| || ||||| || ||||| ||| ||||
CACAG GAC CT GACCT TC GGGTT CGG CCCC /
A CTC T G A G AC

GAM528 GAGCAAGAAAAGTGCTGGGC 505 TGTTCCGGAG 3105 AAGTG CTC TTATTT
TCCCACTTATTTTCTCCCTG TTCTTGCTC GAGCAAGAA CTGGG CCAC T
TGGTGTTCCGGAGTTCTTGC ||||||||| ||||| ||||
TC CTCGTTCTT GGCCT GGTG /
GA--- TGT TCCCTC

GAM529 GAGAATGGGAAGATTGTGGG 506 TGATGTGCCC 3106 AA GAAGA TG -- -- AAAAT
GTATGTCCTGGCCAAAATGG CATGGACATA GAG TGG T TGGGGTATGTC CTGG CC G
AAGAGGACCCAGATGATGTG TCAC ||| ||| | |||||||||| |||| ||
CCCCATGGACATATCACCTC CTC ACT G ACCCCGTGTAG GACC GG /
C- ATACA GT TA CA AGAAG

GAM530 CAGGACACAGCATTGTTGGT 507 CAGCATTGTT 3107 C CA-- TG TTTG TAC TTT
TTTGCCATGTACTATTTTAC GGTTTTGCCA CAGGA ACAG TTGT GT CCATG TAT A
CTATGACCCGTGGATTGGCA TGTA ||||| |||| |||| || ||||| |||
AGTTATTGTATCTTG GTTCT TGTT AACG TA GGTGC GTA /
A ATTG GT ---- CCA TCC

GAM531 TCGCTGCAGCAGCATGCACT 508 CTGCAGCAGC 3108 -- -- CAT G---- C A-- ATG
TCTTGGTAGCAGAATGGAAT ATGCACTTCT TCGCTG CAG CAG GCACTTCTT GTAG AG
ATGGA A
GAACCATCCATCAACTTCTA TGGT |||||| ||| ||| ||||||||| |||| || |||||
TAAAAGAAGAGGTGCTTCTG AGTGAC GTC GTC CGTGGAGAA TATC TC TACCT A
ATCTGTCCAGTGA CT TA TT- GAAAA T AAC ACC

GAM532 GTTTTTCATCTGCACTGCCA 509 CATCTGCACT 3110 CA T AC G A G GA
AGACTGAGTGGTTGGATGGC GCCAAGACTG GTTTTT TC GC TGCCAA ACTG GTG TTG T
AAGCATGTGGTGTTGGCAAA AGTG |||||| || || |||||| |||| ||| |||
GTGAAAGAAGGC CGGAAG AG TG ACGGTT TGGT TAC AAC /
AA - AA G G G GG

GAM533 GTTGGACTTGTGTTTATCTT 510 TAGCTCAGGA 3109 CTT A AACCAC TCA
AACCACCAGATCATTCCTTC GAGCACCCCT GTTGGA GTGTTT TCTT CAGA T
TGTAGCTCAGGAGAGCACCC CCAA |||||| |||||| |||| ||||
CTCCAAC CAACCT CACGAG AGGA GTCT T
CCC - CTCGAT TCC

GAM534 CTGTGGCCTACCAGGTGAAT 511 TACCAGGTGA 3111 -- - A ATA TGGAAAT
ATTGGCTTGGAAATGATAAA ATATTGGCTT CTGTGG CCTA CC GGTGA TTGGCT G
ATTAGCCAGCTTACCAGGAT GGAA |||||| |||| || ||||| ||||||
GGGACCCACAG GACACC GGGT GG CCATT GACCGA A
CA A A C-- TTAAAAT

GAM535 TCTTGTGTTGAGACTTCGTG 512 TACACCACTC 3112 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM536 TCTTGTGTTGAGACTTCGTG 513 TACACCACTC 3113 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM537 AATGAAACCATCTGAGCGAG 514 TCCCTGGAGC 3114 AAA TGA--- G TC- AT TT
TCCCTGGAGCAACTATGCTT AACTATGCTT AATG CCATC GC AG CCTGGAGCAACT GC
C
CTTGCTAAGTTGCTCCAGGA CTTG |||| ||||| || || |||||||||||| ||
TTCTGGTGCCCCTGATGGAA TTAC GGTAG TG TC GGACCTCGTTGA CG /
CATT AA- TCCCCG G TTA AT TT

GAM538 TTAGCTGGGGCCTTGAAGAT 515 TGGACAGGCA 3115 -- - TGAA G AAGATA A- TA
GATGAAGATATGACACTTAC TGATTATTGG TTAGCT GG GGCCT GAT ATG TG CACT C
AAGGTGGACAGGCATGATTA GCCA |||||| || ||||| ||| ||| || ||||
TTGGGCCACCAAGGCTGG GGTCGG CC CCGGG TTA TAC AC GTGG /
AA A TTA- G GG---- AG AA

GAM539 TAAGGTGGATGAGAATGGCA 516 TGGCAAAATT 3116 A- AGAAT AAA T --- AG T
AAATTAGTCGCCTTCGTCGA AGTCGCCTTC TAAGGTGG TG GGCA TTAG CGCC
TTCGTCG AG G
GAGTGCCCTTCTGATGAATG GTCG |||||||| || |||| |||| |||| ||||||| ||
TGGTGCTGGGGTGTTTATGG GTTTCACT AC TTGT GGTC GTGG AAGTAGT TC C
CAAGTCACTTTG GA GGTAT GG- - TGT CT C

GAM540 TCTTGTGTTGAGACTTCGTG 517 TACACCACTC 3117 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM541 TTGTCGTCATTGGACACGTA 518 CATCTGATCT 3119 --- GACAC T CAA CCA
GATTCGGGCAAGTCCACCAC ATAAATGCGG TTGTC GTCATTG GTAGAT CGGG GTCCA C
TACTGGGCATCTGATCTATA TGGC ||||| ||||||| |||||| |||| |||||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTA GTCT CGGGT /
CTA GTAAA - A-- CAT

GAM542 CCATTGAAAAATTTGAGAAG 519 TTTCAAGTAT 3118 TTGAAA TG AGG -- - T AAA
GAGGCTGCTGAGATGGGAAA TGCCTGGGTC CCA AATT AGA AGGC TGCT GAGA GGG
G
GGGCTCCTTTCAAGTATTGC TTGG ||| |||| ||| |||| |||| |||| |||
CTGGGTCTTGGATTAAACTG GGT TTAG TCT TCCG ATGA CTTT CCT /

G CAAA-- GT GGG TT A - CGG

GAM543 CACCTGGGCCTGCCCCAGTG 520 TTAGCCCACA 3120 G CCCCAGT AAT TTCAC
GCAATATGCCTTCACCAGCT GGCCAAGGTG CACCT GGCCTG GGC ATGCC C
ATGGCATTAGCCCACAGGCC ||||| |||||| ||| |||||
AAGGTG GTGGA CCGGAC CCG TACGG A
A AC----- AT- TATCG

GAM544 GTGTGGCCGATGTGTCTATT 521 TCAGGAGACC 3121 - CTAT AAGA T TC
GAAGATTCTGTGATCTCACT ATTGCATCAT GTGTGGCCGATG TGT TG TTCTG GA T
CTCAGGAGACCATTGCATCA TGGC |||||||||||| ||| || ||||| ||
TTGGCCGCAC CACGCCGGTTAC ACG AC AGGAC CT C
T TT-- CAG- T CA

GAM545 GCTGCTGCTGATGGACTGCC 522 TCGGCCATCA 3122 T - GA CC-- AG- GCTATA G
TCG
GGCCGCAGGAGCTATACGAG ACGTGGCCAT GCTGC GC TGATG CTG GGCCGC GA
CGA TCG C
TCGTCGCACATCGAGTCGGC CCCG ||||| || ||||| ||| |||||| || ||| |||
CATCAACGTGGCCATCCCGG CGGCG CG ACTAC GGC CCGGTG CT GCT AGC A
GCATCATGCTGCGGC T T G- CCTA CAA ACCG-- G TAC

GAM546 GACTATGGCAAGGACCTGAT 523 TATGGCAAGG 3123 A AA- A T AGAA- CA
GGAGAAGGTCAAGAGCCCAG ACCTGATGGA GACT TGGC GG CCTGA GG GGT A
AGCTTCAGGCCGAGGCCAAG GAAG |||| |||| || ||||| || |||
TC CTGA ACCG CC GGACT TC CCG /
- GAG - - GAGAC AG

GAM547 GACAAGGGTGCCTCTAAAAG 524 AAGGGTGCCT 3124 T CTCTAAA ------ GGC
CTTGACAGGGCCTTGACTGC CTAAAAGCTT GACAAGGG GC AGCTTGA CAG C
ACAATTCGAGCTGAATTTGC GACA |||||||| || ||||||| |||
CCCTTGTC CTGTTCCC CG TCGAGCT GTC T
- TTTAAG- TAACAC AGT

GAM548 CCATTAAGTCAGTTTCGATC 525 TAAGATGCTA 3125 AGT C TC AAACT GC T
TTCAAACTGTGCCTTGTTTT GAAATTCAAT CCATTAAGTC TT GA TTC GT CTTGTTTT T
TTAAAAGATAAGATGCTAGA GGGA |||||||||| || || ||| || ||||||||
AATTCAATGGGATTTGGTGG GGTGGTTTAG AA CT AAG CG GAATAGAA A
GGT - TA AT--- TA A

GAM549 CTTTGCAAGCACAGCAAGTC 526 AGCAAGTCCC 3126 A ACA- AA C TAATA GC
CCTGTAATAAGATAGGCACA TGTAATAAGA CTTTGC AGC GC GT CCTG AGATAG A
ACTGTCTGATCCAGGTACGC TAGG |||||| ||| || || |||| ||||||

ACGAGTTGGCAAAG GAAACG TTG CG CA GGAC TCTGTC C
G AGCA -- T CTAG- AA

GAM550 CCACCACCTGGAGCCCGAGG 527 TTCTTCACGG 3127 C GGA- AG T AAGT
AGGTGCTCAAGTACAGCGAG GCAGCAAGCT CCACCA CT GCCCG GAGG GCTC A
TTCTTCACGGGCAGCAAGCT GGTG |||||| || ||||| |||| ||||
GGTGG GGTGGT GA CGGGC CTTC TGAG /
C ACGA A- T CGAC

GAM551 CCGGTTGCCAATGTATGCTT 528 TGCCAATGTA 3128 GTT ATG --- C
GTACTCCAGGCTCCTTGGAG TGCTTGTACT CCG GCCA TATGCTTGT ACTCCAGG T
TTATACAGGTATGAAATGGC CCAG ||| |||| ||||||||| ||||||||
CATGG GGT CGGT GTATGGACA TGAGGTTC /
AC- AAA TAT C

GAM552 CGGCGGCAAGATGGCAGTGC 529 TCGCTGATGG 3129 GGC- G--- - ATA AAG
AAATATCCAAGAAGAGGAAG CATCTTCAAA CGGC AAGATG CAGTG CAA TCC A
TTGTCGCTGATGGCATCTTC GCTG |||| |||||| ||||| ||| |||
AAAGCTG GTCG TTCTAC GTCGC GTT AGG /
AAAC GGTA T GA- AGA

GAM553 GTAGAGCTTTATGCTGAAAA 530 GAGCTTTATG 3131 - TA GAAAA - T A
GGTGGCCACTAGAGGTCTGT CTGAAAAGGT GTAGAG CTT TGCT GGTGGC CAC AG G
GTGCCATTGCCCAGGCAGAG GGCC |||||| ||| |||| |||||| ||| ||
TCTCTGC CGTCTC GAG ACGG TTACCG GTG TC G
T -- ACCCG T - T

GAM554 GGGAAACTCCGAGGACAGAG 531 TGGCCTGATG 3130 AAA A--- - GA AA TG A
GGCTAAATCCATGAAGTTTG ATCCACAGCG GGG CTCCG GGA CA GGGCT ATCCA A G
TGGATGGCCTGATGATCCAC GAGA ||| ||||| ||| || ||||| ||||| |
AGCGGAGACCC CCC GAGGC CCT GT TCCGG TAGGT T /
A-- GACA A AG -- GT T

GAM555 GGGAAACTCCGAGGACAGAG 532 TGGCCTGATG 3132 AAA A---- - GA AA TG A
GGCTAAATCCATGAAGTTTG ATCCACAGCT GGG CTCCG GGA CA GGGCT ATCCA A G
TGGATGGCCTGATGATCCAC GGAG ||| ||||| ||| || ||||| ||||| |
AGCTGGAGACCC CCC GAGGT CCT GT TCCGG TAGGT T /
A-- CGACA A AG -- GT T

GAM556 ATGTGAACCTTTGTATTTTT 533 TCAGTGAAAG 3133 CTT TG ---- TAA
GCTCCTAATTTTGGACTCAG TGTACTGTTT ATGTGAAC TGTATTTT C TCC T
TGAAAGTGTACTGTTTACAT ACAT |||||||| |||||||| | |||
TACATTTG ATGTGAAA G AGG /

TC- GT ACTC TTT

GAM557 TTGGTCCATATCTCCATGCA 534 TCCATATCTC 3135 TC ATCTCC- G- - ACA
TGGCGGATACAGTGAAATCT CATGCATGGC TTGG CAT ATGCATG CG GAT G
CGAGCATGCATCTTCTCGGT GGAT |||| ||| ||||||| || |||
GAGCCAG GACC GTG TACGTAC GC CTA T
GA GCTCTTC GA T AAG

GAM558 CACCTTTACGGCCAAACCGT 535 TGTGGATATA 3134 TT C CC C-- C--- G
CCACCTCGACCGATTCTGTG GTTTTCCCTG CACC TA GG AAAC GTCCAC TC A
GATATAGTTTTCCCTGTTGG TTGG |||| || || |||| |||||| ||
TG GTGG GT CC TTTG TAGGTG AG C
TT - CT ATA TCTT C

GAM559 GACTCTTCAGGGAAAAGGTC 536 TATACTGCTC 3136 TCAG AA GT A AA
AGTGAAGTTTAACAAGGGCT TTAGCCAGAG GACTCT GG AAG CAGTG AGTTT C
ATACTGCTCTTAGCCAGAGT TC |||||| || ||| ||||| |||||
C CTGAGA CC TTC GTCAT TCGGG /
---- GA TC A AA

GAM560 TCTGAAAACTACACCGCTGT 537 TGGCCGAGTG 3137 AACTACA G -- ACTG
GGCCCAGACTGTGAACCTGC GCTCATTCAG TCTGAA CCGCT TGGCC CAG T
TGGCCGAGTGGCTCATTCAG A |||||| ||||| ||||| |||
A AGACTT GGTGA GCCGG GTC /
ACTC--- - TC CAAG

GAM561 GGAGTCTTCTGCTGGAGGTT 538 TGAGCCCATT 3139 AGT TG A TTCC C G
CCTTCACTGTGCGTGCTGAC GGCAGGGGTA GG CTTCTGC G GG TTCACTGTG GT C
CATGGTGAGCCCATTGGCAG CC || ||||||| | || |||||||| ||
GGGTACC CC GGGGACG T CC GAGTGGTAC CA T
AT- GT A C--- - G

GAM562 GACTTTGGTAGACACAGGCA 539 TGGGAACCAT 3138 A AG A A TGA---- GCTGATCT
TTGGCATGACCAAAGCTGAT TGCCAAGTCT G CTTTGGT AC CAGGC TTGGCA CCAAA
C
CTCATAAATAATTTGGGAAC GGTA | ||||||| || ||||| |||||| |||||
CATTGCCAAGTCTGGTACTA C GAAATCA TG GTCTG AACCGT GGTTT /
AAGC - -- - - TACCAAG AATAAATA

GAM563 TTCACCACCATGGAGAAGGC 540 CTGCCCCCTC 3140 CA GA GGC CT T A
CAAA TCA
TGGGGCTCATTTGCAGGGGG TGCTGATGCC TTCAC CCATG GAA TGGGG CATT
GCAGGGGGG GC AGGG T

GAGCCAAAAGGGTCATCATC CCCA ||||| ||||| ||| ||||| |||| ||||||||| || ||||
TCTGCCCCCTCTGCTGATGC AAGTG GGTAC CTT ACCCC GTAG CGTCTCCCC CG
TCTC /
CCCCATGTTCGTCATGGGTG TG TG GT- C- T - ---- TAC
TGAA

GAM564 AATGAGTTTCTTACTCGGGA 541 TACTCTGGAG 3141 GA T - G C GA
GCTGGCTGAAGATGGCTACT TTGAGGTGCG AAT GT TCTTA CTC GGAG TGGCT A
CTGGAGTTGAGGTGCGAGTT AGTT ||| || ||||| ||| |||| |||||
TTG CG GGAGT GAG TCTC ATCGG G
AG T T G - TA

GAM565 GTAGAGCTTTATGCTGAAAA 542 GAGCTTTATG 3144 - TA GAAAA - T A
GGTGGCCACTAGAGGTCTGT CTGAAAAGGT GTAGAG CTT TGCT GGTGGC CAC AG G
GTGCCATTGCCCAGGCAGAG GGCC |||||| ||| |||| |||||| ||| ||
TCTCTGC CGTCTC GAG ACGG TTACCG GTG TC G
T -- ACCCG T - T

GAM566 GCCACGTGTTGCTCAGACAG 543 ATGCTGCCCT 3142 G T ACAG GTG - T A G
GGTGTGCTGGGCATCAAGGT GGGGAACCAA GCCACGT TTGC CAG GGT CT GGGCA CA
GGT A
GAAGATCATGCTGCCCTGGG CTGG ||||||| |||| ||| ||| || ||||| || |||
GAACCAACTGGTAAGATGTG CGGTGTA AATG GTC CCA GG CCCGT GT CTA A
GC G - AA-- AGG T C A G

GAM567 GGGAAACTCCGAGGACAGAG 544 TGGCCTGATG 3143 AAA A--- - GA AA TG A
GGCTAAATCCATGAAGTTTG ATCCACAGCG GGG CTCCG GGA CA GGGCT ATCCA A G
TGGATGGCCTGATGATCCAC GAGA ||| ||||| ||| || ||||| ||||| |
AGCGGAGACCC CCC GAGGC CCT GT TCCGG TAGGT T /
A-- GACA A AG -- GT T

GAM568 CTGTATCGATATGGTTCCTT 545 TTGAAAGTGC 3145 TC AT-- TCC C C A A
TTCCGTCACCACTGGACATT CTGAGATCCT CTGTA GAT GGT TTTTC GT ACC CTGGAC T
GTCCAGGGTATTGAAAGTGC GCAG ||||| ||| ||| ||||| || ||| ||||||
CTGAGATCCTGCAG GACGT CTA CCG GAAAG TA TGG GACCTG /
C- GAGT T-- T - - T

GAM569 GGACTCAGTGGCCTTTGAGG 546 TCAGTGGCCT 3146 -- TTGAGGATG CT AA
ATGTGGCTGTGAACTTCACC TTGAGGATGT GGACTCAGT GGCCT TGG GTG C
CAGGAGGAGTGGGCTTTGCT GGCT ||||||||| ||||| ||| |||
GAGTCC CCTGAGTCG TCGGG ACC CAC /
TT TGAGGAGG- -- TT

GAM570 GCGGGGCGGAGGCACTCGCG 547 CACTGCGTGA 3147 G G CAC G AAT T--- ---
TC

CGGGGGGTAATTCGGGGTCT CCTTGGTTCA GC GGGC GAGG TCGCGCGG GGGT TCGGGG CTG GGT T
GGGTTCTGGTGCCGCGCAGC GC || |||| |||| |||||||| |||| |||||| ||| |||
TTTCCCCGATGGCCCACTGC CG CTTG TTCC AGTGCGTC CCCG AGCCCC GAC CCG G
GTGACCTTGGTTCAGC A G --- A GT- TTTC GCG TG

GAM571 TCAGAGTCTCCTAAAGAGCC 548 TCATTGGAGG 3148 T CTAAAG GAA C AA
CGAACAGCTGAGGAAGCTCT GTTGAGCTTT TCAGAG CTC AGCCC CAG TGAGG G
TCATTGGAGGGTTGAGCTTT GA |||||| ||| ||||| ||| |||||
GA AGTTTC GAG TTGGG GTT ACTTC /
- ------ AG- - TC

GAM572 TTGTCACATATGCCACTGTG 549 CAAGGCCACA 3149 A A AC GA AGG G G
GAGGAGGTGGATGCAGCTAT CAAGGTGGAT TTGTC CAT TGCC TGTG GG TG ATGCA C
GCATGCAAGGCCACACAAGG GGAC ||||| ||| |||| |||| || || |||||
TGGATGGACAG GACAG GTA GTGG ACAC CC AC TACGT T
- G A- A- GGA G A

GAM573 CCCCGGCAGCGGTTGGCGAG 550 TTCTCCATGA 3150 - TTGGCGA - AA
TGGGGACCGAACCCCCGGTT TCCCGCTGGC CCCCGGC AGCGG GTGG GGACCG C
CTCCATGATCCCGCTGGCCG CGGG ||||||| ||||| |||| ||||||
GGG GGGGCCG TCGCC TACC CTTGGC C
G CTAG--- T CC

GAM574 GCGGAGAGGTATCTGCTGCG 551 CGGGCGCGGG 3151 A--- TA ---- GTA
CCTGAGATGAGTAAACTGTC CGCTAGACGC GCGG GAGG TCTG CTGCGCCTGAGATGA A
GTTTCGGGCGCGGGCGCTAG CTCG |||| |||| |||| ||||||||||||||
ACGCCTCGAAGCCGC CGCC CTCC AGAT GGCGCGGGCTTTGCT A
GAAG GC CGCG GTC

GAM575 AGATGTGGGATGTCAGTACT 552 TCATGATAAC 3152 T TGT T GG ------ T
GGCATGTGCCTTATGACCCT TGGGTACGTG AGA GTGGGA CAG ACT CATGTGCCT TATGACCC C
CGTGGGTCATGATAACTGGG GAGT ||| |||||| ||| ||| ||||||||| ||||||||
TACGTGGAGTTCTGTTCCAT TCT TACCTT GTC TGA GTGCATGGG GTACTGGG G
TCT - --- T G- TCAATA T

GAM576 GTTTCAGAGCCCAGAGTTTT 553 AAGACTTTGT 3153 TCAG --- - ACA
CTGTTACAAGGCAACATGAA GTGGCTACAT GTT AGCC CAGAGTTTTC TGTT A
GACTTTGTGTGGCTACATGA GAC ||| |||| |||||||||| ||||
C CAG TCGG GTTTCAGAAG ACAA /
TACA TGT T CGG

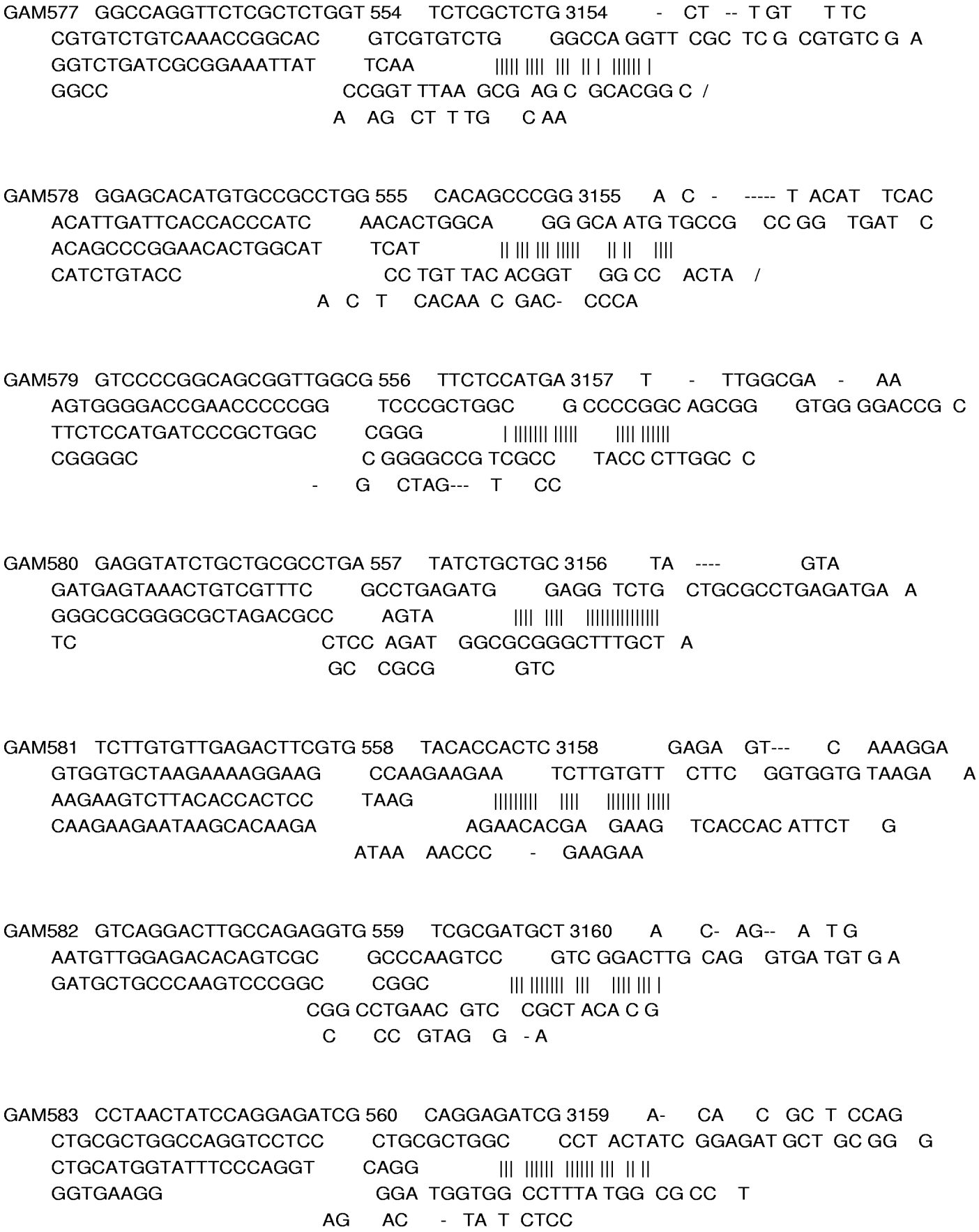
GAM577 GGCCAGGTTCTCGCTCTGGT 554 TCTCGCTCTG 3154 - CT -- T GT T TC
CGTGTCTGTCAAACCGGCAC GTCGTGTCTG GGCCA GGTT CGC TC G CGTGTC G A
GGTCTGATCGCGGAAATTAT TCAA
GGCC CCGGT TTAA GCG AG C GCACGG C /
A AG CT T TG C AA
GAM578 GGAGCACATGTGCCGCCTGG 555 CACAGCCCGG 3155 A C - ----- T ACAT TCAC
ACATTGATTCACCACCCATC AACACTGGCA GG GCA ATG TGCCG CC GG TGAT C
ACAGCCCGGAACACTGGCAT TCAT
CATCTGTACC CC TGT TAC ACGGT GG CC ACTA /
A C T CACAA C GAC- CCCA
GAM579 GTCCCCGGCAGCGGTTGGCG 556 TTCTCCATGA 3157 T - TTGGCGA - AA
AGTGGGGACCGAACCCCCGG TCCCGCTGGC G CCCCGGC AGCGG GTGG GGACCG C
TTCTCCATGATCCCGCTGGC CGGG
CGGGGC C GGGGCCG TCGCC TACC CTTGGC C
- G CTAG--- T CC
GAM580 GAGGTATCTGCTGCGCCTGA 557 TATCTGCTGC 3156 TA ---- GTA
GATGAGTAAACTGTCGTTTC GCCTGAGATG GAGG TCTG CTGCGCCTGAGATGA A
GGGCGCGGGCGCTAGACGCC AGTA
TC CTCC AGAT GGCGCGGGCTTTGCT A
GC CGCG GTC
GAM581 TCTTGTGTTGAGACTTCGTG 558 TACACCACTC 3158 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA
GAM582 GTCAGGACTTGCCAGAGGTG 559 TCGCGATGCT 3160 A C- AG-- A T G
AATGTTGGAGACACAGTCGC GCCCAAGTCC GTC GGACTTG CAG GTGA TGT G A
GATGCTGCCCAAGTCCCGGC CGGC
CGG CCTGAAC GTC CGCT ACA C G
C CC GTAG G - A
GAM583 CCTAACTATCCAGGAGATCG 560 CAGGAGATCG 3159 A- CA C GC T CCAG
CTGCGCTGGCCAGGTCCTCC CTGCGCTGGC CCT ACTATC GGAGAT GCT GC GG G
CTGCATGGTATTTCCCAGGT CAGG
GGTGAAGG GGA TGGTGG CCTTTA TGG CG CC T
AG AC - TA T CTCC

GAM584 GTGTGGCCGATGTGTCTATT 561 TCAGGAGACC 3161 - CTAT AAGA T TC
GAAGATTCTGTGATCTCACT ATTGCATCAT GTGTGGCCGATG TGT TG TTCTG GA T
CTCAGGAGACCATTGCATCA TGGC ||||||||||||| ||| || ||||| ||
TTGGCCGCAC CACGCCGGTTAC ACG AC AGGAC CT C
T TT-- CAG- T CA

GAM585 GGGCTGTGGTGTCTGTCCGC 562 TGTGGTGTCT 3162 - TC TC TT GAAGACA AA
TTTCAGGAAGACATTATTTC GTCCGCTTTC GGGCTGTGGT G TG CGCT CAG TTATTTC T
AATATGGAATAAGACTGCCA AGGA |||||||||| | || |||| ||| |||||||
GTGACCAAGCAACCACAGCC CCCGACACCA C AC GTGA GTC AATAAGG /
C A GA CA CC AG----- TA

GAM586 CCCAGGCTGAGAGCGCCCAG 563 ATGCTTCGGA 3163 G T GA-- C AG A GA
AGCAACAGACTGATGATGCT TGCACAATCT CCCA GC GA GCG CC AGCA CA C
TCGGATGCACAATCTGCATG GCAT |||| || || ||| || |||| ||
GG GGGT CG CT CGT GG TCGT GT T
A T AACA A CT A AG

GAM587 GTGGTTAATGTTTGAAAAAG 564 TAATGTTTGA 3164 A --- AA CTT T GTC T A
CTCTTGCAATCAAGTCTGTG AAAAGCTCTT GTGGTT ATGT TTGAAA GCT GCAA CAA
TGTGA GTATT A
ATGTATTAATAATGCCTTAT GCAA |||||| |||| |||||| ||| |||| ||| ||||| |||||
ATATTGTTTGTAGTCATTTT TACCGA TACG AATTTT TGA TGTT GTT ATATT CGTAA /
AAGTAGCATGAGCCAT G ATG AC --- T AT- C T

GAM588 GGGAGCCAGCAAGCAGGATG 565 TCGAAGAGCT 3165 AGCAA AGGA A A--- G
CCAA ---- A
ATATCGAAGAGCTGGAGACC GGAGACCAAG GGAGCC GC TGAT TCGA GAGCT GAGA
GGCCGT GGG A
AAGGCCGTGGGAATGTCTAA GCCG |||||| || |||| |||| ||||| |||| |||||| |||
CGATGGCCGCTTTCTCAAGT CCTCGG CG GCTA AGCT TTTGA CTCT CCGGTA
TCT T
TTGACATCGAAATCGGCAGA AGA-- ---- A ACAG A TTCG GCAA G
GGCTCCT

GAM589 GCCGTCGGAGTCCATCATGG 566 TGCCCATTGC 3166 C CCATCAT T TG CTT TT
GAGGTGTGGTCTTGTAGTTG TCTCCCACTC GCCGT GGAGT GGGAGG G GT GTAGTTG C
TTCTCCGGCTGCCCATTGCT CACG ||||| ||||| |||||| | || |||||||
CTCCCACTCCACGGC CGGCA CCTCA CCCTCT C TA CGTCGGC /
- ------- - GT CC- CT

GAM590 TTTGACCCTTTTGAGATGGA 567 TTCAAATAAA 3167 CCTT TG AAC TA- C- C TT
ACTTTCATAAAGTTTCTTGG CTTATTTGAA TTTGAC TTGAGA G TTTCA AAGTTT TTGG
AGTAG T
CAGTAGTTTATTTGCTTCAA AAGT |||||| |||||| | ||||| |||||| |||| |||||

ATAAACTTATTTGAAAAGTT AAACTG AACTCT T AAAGT TTCAAA AACT TCGTT /
GTCTCAAGTCAAA ---- GT GA- TTA TA - TA

GAM591 TCTTGTGTGAGACTTCGTGG 568 TACACCACTC 3168 GAGA- GT--- C AAAGGA
TGGTGCTAAGAAAAGGAAGA CCAAGAAGAA TCTTGTGT CTTC GGTGGTG TAAGA A
AGAAGTCTTACACCACTCCC TAAG |||||||| |||| ||||||| |||||
AAGAAGAATAAGCACAAGA AGAACACG GAAG TCACCAC ATTCT G
AATAA AACCC - GAAGAA

GAM592 GAGGAGAAGCGCGAGGGCTA 569 TGCAAAACCA 3169 A AGG A------- CC
CGAGCGTCTCCTGAAGATGC GCGTGGCGGC GAGGAGA GCGCG GCTACG GCGTCT T
AAAACCAGCGTGGCGGCGCG GCGC ||||||| ||||| |||||| ||||||
CTCTCTTC CTTCTCT CGCGC CGGTGC CGTAGA /
- GG- GACCAAAA AG

GAM593 GTGGGGTAAAACCCCAGACG 570 TGCCCTGGGG 3170 - - AC AG- TG T- C
AGAAAA
CATGAAAGCTGCATGGCCCT TTTCTGCCCG GTG GGGTA AAACCCCAG GCATGAA C CA GG
CCTGG A
GGAGAAAAAGCTGAACCAGG CAC ||| ||||| |||||||| ||||||| | || || |||||
CCCTTTGTGGATCTTCATGC CAC CCCGT TTTGGGGTC CGTACTT G GT CC GGACC
/
CCTGGGGTTTCTGCCCGCAC G C C- CTA GT TT C AAGTCG

GAM594 ATTTGAGAAGGAGGCTGCTG 571 CTTCAAGTAT 3171 TG AGG - GA T AAA
AGATGGGAAAGGGCTCCTTC GCCTGGGTCT ATT AGA AGGC TGCT GA GGG G
AAGTATGCCTGGGTCTTGGA TGGA ||| ||| |||| |||| || |||
T TAG TCT TCCG ATGA CT CCT /
GT GGG T A- T CGG

GAM595 GGTGACAACATGCTGGAGCC 572 TTCCAAGGGA 3172 AA-- G -- T TA
AAGTGCTAACATGCCTTGGT TGGACAGTCA GGTGAC CAT CT GGAGCCAAG GC A
TCCAAGGGATGGACAGTCAC CC |||||| ||| || |||||||| ||
C CCACTG GTA GG CCTTGGTTC CG C
ACAG G AA - TA

GAM596 GGTGACAACATGCTGGAGCC 573 TTGGTTCAGG 3173 AA---- G G GCT
AAGTGCTAACATGCTTGGTT GATGGCACAC GGTGAC CAT CT GAGCCAAGT A
CAGGGATGGCACACGTCACC GTCA |||||| ||| || |||||||||
CCACTG GTA GG CTTGGTTCG A
CACACG G A TAC

GAM597 AGTACAAGGGCTATCTGGTA 574 TACAGAAGAA 3174 T GG - ---- GAT--- A G

TCTGTAGATGGCTACATGAA TACATAGATG AG ACAAG CTATCTG GTA TCTGTA GGCT CAT A
CATGCAGCTTGCAAATACAG GAGC || ||||| ||||||| ||| |||||| |||| |||
AAGAATACATAGATGGAGCT TC TGTTC GGTAGAT CAT AGACAT TCGA GTA A
TGTCT - GA A AAGA AAACGT C C

GAM598 GTGCTTAAGGGCTTCCGGAA 575 TAAGGGCTTC 3175 TTA CT ACGG GTC
CGGGGCTGTCTATGGAGCCA CGGAACGGGG GTGC AGGG TCCGGA GGCT T
AAATCCGGGCCCCTCACGCG CTGT |||| |||| |||||| ||||
C CGCG TCCC GGGCCT CCGA A
CAC C- AAAA GGT

GAM599 GGTGACAACATGCTGGAGCC 576 GTGGTTCAGG 3176 AA-- G G - T TA
AAGTGCTAACATGCCTGTGG GATGGAAAGT GGTGAC CAT CT GAGCCA AG GC A
TTCAGGGATGGAAAGTCACC CACC |||||| ||| || |||||| || ||
CCACTG GTA GG CTTGGT TC CG C
AAAG G A G - TA

GAM600 TGGTGGAAAAGGGTGTATTG 577 CATGACAACA 3177 AAAA A A A-- AAC AA
ACAACAGAGAAACAGAACTT CATCCCCTCA TGGTGG GGGTGT TTG CA CAGAGA AG C
CCTACTTTTTGACATGACAA CCA |||||| |||||| ||| || |||||| ||
CACATCCCCTCACCA ACCACT CCTACA AAC GT GTTTTT TC T
CC-- C A ACA CA- CT

GAM601 TGCTAATTGTTCCTCTAAAG 578 TCTAAAGTAA 3178 AA TG C TAATC ATG TT
TAATCGCCATGCGTTCTTCG TCGCCATGCG TGCT T TTCCT TAAAG GCC CG C
GGCTTCATCTTTAAAGGAAT TTCT |||| | ||||| ||||| ||| ||
GAAGCA ACGA A AAGGA ATTTC CGG GC /
-- GT A TACTT --- TT

GAM602 GAGTCTATCCAAAATCACCA 579 TCCAAAATCA 3179 A AAAAT CA C G CTAA
CCACCGTGGGCCTAAACATC CCACCACCGT GAGTCT TCC CAC CCAC GTG GC A
GCGCACTGTGGATGTGGGAA GGGC |||||| ||| ||| |||| ||| ||
AGGCTC CTCGGA AGG GTG GGTG CAC CG /
A ----- TA T G CTAC

GAM603 GGATTGAAACTGTCTCAGGA 580 TACCTGGCCA 3180 A A C- ACCTT T TCTT
CCTTGATGATCTTGCTATTC CAGTTCAAGC GG TTGAA CTGT TCAGG GA GA G
TCTACCTGGCCACAGTTCAA C || ||||| |||| ||||| || ||
GCC CC AACTT GACA GGTCC CT CT /
G - CC AT--- - TATC

GAM604 ATCCTGGCCCATCGTGCTGC 581 GCGCTGCCGG 3181 - - GT- CT CCA T CCA GA

TGCCCCACGGTTCGGTACCA CCGCGGCTTC ATCCTG GC CCATC GCTG GCC CGGT
CGGTA CAC A
CACGAATGGTGCGCTGCCGG AGCC |||||| || ||||| |||| ||| |||| ||||| |||
CCGCGGCTTCAGCCTGGATG TGGGAC CG GGTAG CGAC CGG GCCG GCCGT GTG
/
GAGCTCAGGGT T A GTC TT C-- - CGC GT

GAM605 CCTTCGCTAGTCTCCGTATG 582 TCGCTAGTCT 3182 C AGTC--- G CGT-- AAC
GCCCGTGCCAACGCCCGGCT CCGTATGGCC CCTT GCT TCCGTATG CC GCC G
CTTCGGCATACGGGCAAAAA CGTG |||| ||| |||||||| || |||
GAGCCAAGG GGAA CGA GGGCATAC GG CGG /
C GAAAAAC - CTTCT CCC

GAM606 GGTGTAAATGTTGAGCCTTT 583 TAAATGTTGA 3183 GTA- ---- TTTTT G- TT
TTGGCCTGGCTTGTTTGCAA GCCTTTTTGG GGT AATGTTGA GCC GGCCT GC G
AGGCCCTGGCAACGTCAACA CCTG ||| |||||||| ||| ||||| ||
TTGGGAGCC CCG TTACAACT CGG CCGGA CG T
AGGG GCAA TC--- AA TT

GAM607 GCGACGTCCTGTTTCTGGCT 584 TGAGATTGGG 3184 CGTCC T - AA--- A TA- CCTT
GTGAAGCCACATATCATCCC GCCGACGTGC GCGA TGT TCTGGCT GTG GCC CA
TCATCC C
CTTCATCCTGGATGAGATTG AAGC |||| ||| ||||||| ||| ||| || ||||||
GGGCCGACGTGCAAGCCAGA TGCT ACA AGACCGA CGT CGG GT AGTAGG A
CACATCGT ----- C A GCAGC G TAG TCCT

GAM608 GATCAGACTGAGGATGTCCT 585 TTGGATACTT 3186 TC A ---------- CTG G
GGAGGCTGTAGCTGCAAAGC TAGTCTATTC GA AGACTGAGG TGTCC TGGAGG
TAGCT C
TGGATCTTCCAGATGACTTG || ||||||||| ||||| |||||| |||||
ATTGGATACTTTAGTCTATT CT TCTGATTTC ATAGG ACCTTC GTCGA A
C TA - TTAGTTCAGTAG TAG A

GAM609 GACAGCGGCGGCTCCGCCTA 586 TGAATGGAGT 3185 -- C CC CCTA
CGTGGCCTATAACATTCACG CCTGCACTGT GACA GCGG GGCTCCG TACGTGG T
TGAATGGAGTCCTGCACTGT C |||| |||| ||||||| |||||||
C CTGT CGTC CTGAGGT GTGCACT A
CA - AA TACA

GAM610 TCACCATCTGCAGCCTTGAA 587 AAGGAGCTTT 3188 CA C- CC A TT GGAG- - AA
GGAGCTTTGGTTCGGAGACA GGTTCGGAGA TCAC TCTG AG TTGA GGAGCT GGTTC ACA
GGC A
GGCAAAGGAGCCATGTGTGG CAGG |||| |||| || |||| |||||| ||||| ||| |||
AGAGCCTGGTTTCTCAGTAC AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G

TTCCAGACCGTGA CC CT AT - T- AGGTG A AG

GAM611 GACTATGGCAAGGACCTGAT 588 TATGGCAAGG 3187 A AA- A T AGAA- CA
GGAGAAGGTCAAGAGCCCAG ACCTGATGGA GACT TGGC GG CCTGA GG GGT A
AGCTTCAGGCCGAGGCCAAG GAAG |||| |||| || ||||| || |||
TC CTGA ACCG CC GGACT TC CCG /
- GAG - - GAGAC AG

GAM612 CTCAGTTCTGCCTCCTGACT 589 TGTGGCAGTT 3189 T- G - C A- A C- - GCTC
ATGACAGTAATCCCACCCAG ACTGATGTGG CTCAG TCT CC TC TG CTATG CAGTAAT CCAC
CCA A
CTCAACTATGGTGTGGCAGT ACCA ||||| ||| || || || ||||| ||||||| |||| |||
TACTGATGTGGACCATGATG GAGTT AGG GG AG AC GGTGT GTCATTG GGTG GGT /
GGGACTTTGAG TC - T T CA A AC T ATCA

GAM613 GGCCACGTACACCGACAAGT 590 GGAAGACATC 3190 AC GACAA AG------ AAT
TGTTCAAGTTCCGCAATAAC CTGAGCGATG GGCCACGT ACC GTTGTTCA TTCCGC A
CGGTGGGAAGACATCCTGAG AGGT |||||||| ||| |||||||| ||||||
CGATGAGGTCAACGTGGCC CCGGTGCA TGG TAGCGAGT AGGGTG A
AC AG--- CCTACAGA GCC

GAM614 CGGCTCCGAGAGCAGGTTCT 591 TACACATTGA 3191 - AGAG C A TC GCAG C
TCGTGAGTTCCTCGCAGGGC GAACCTGAAC CGGC TCCG CAGGTTCTT GTG GT CTC GG
C
CGGTCAGAGCTACACATTGA ATGG |||| |||| ||||||||| ||| || ||| ||
GAACCTGAACATGGAGGCCG GCCG AGGT GTCCAAGAG TAC CA GAG CT G
G ACAA T A TC A--- G

GAM615 CTCCGAGCAGATTATGAGAT 592 TTGAATTAGA 3192 CA ATGAG AG AGA C
TGCAAGTAAAGAAAGAGACC TGCAATGGAT CTCCGAG GATT ATTGCA TAA AAGAGA C
TGTTTTTTGAATTAGATGCA CACT ||||||| |||| |||||| ||| ||||||
ATGGATCACTTGGAG GAGGTTC CTAG TAACGT ATT TTTTTT T
A- G---- AG AAG G

GAM616 GTTTGATCCTCGCCCTGTTT 593 GCCCTGTTTC 3193 TT TCC - T---- AAAC- GT
CCAAAAACGCGTACAGGCTC CAAAAACGCG GT GA TCG CCCTGTT CCAA GC A
ATCTTGGCAGCCAACAGGGA TACA || || ||| ||||||| |||| ||
TGAATTCTAC CA CT AGT GGGACAA GGTT CG C
T- TA- A CCGAC CTACT GA

GAM617 GATGTGATCGCCAACCAGCC 594 AAGCTGGTTT 3194 G ----- CTGTCG G A G
TGTCGTGATCGACAACGGAT TGCTGGTGAT GAT TGATCGCCA ACCAGC TGATC ACA CG
A

CCGGTGTGATTAAAGCTGGT CAGA ||| |||||||||| |||||| ||||| ||| ||
TTTGCTGGTGATCAGATC CTA ACTAGTGGT TGGTCG ATTAG TGT GC T
G CGTTT AA---- - G C

GAM618 CAAGAACACTCCTTGGGCGT 595 TCCTTGGGCG 3195 A CCTT CCTT- GTTTTG
CCTTGCTGTTTTGTTTGTGA TCCTTGCTGT CA GAACACT GGGCGT GCT T
AGCTTTCTATGCCCAGTGTT TTTG || ||||||| |||||| |||
CCTG GT CTTGTGA CCCGTA CGA /
C ---- TCTTT AGTGTT

GAM619 TCTACTTTTACTACTGTGCC 596 TCAAAGCATG 3196 TT- A GT T AT-- TTA
TTGCTTATGTTTGTTAGGAC GCTAAGAGTG TCTACT TACT CT GCC TGCTT GTTTG G
CAAACCTCAAAGCATGGCTA TTCA |||||| |||| || ||| ||||| |||||
AGAGTGTTCAGTAGA AGATGA GTGA GA CGG ACGAA CAAAC /
CTT - AT T ACTC CAG

GAM620 TCTTGTGTTGAGACTTCGTG 597 TACACCACTC 3197 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM621 TCTTGTGTTGAGACTTCGTG 598 TACACCACTC 3198 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM622 GCCGGCCTGGGTGCTTACCA 599 TTTTCCTAGC 3199 T TACC-- TCTC GA
GCTGTCTCAGGATCCAAGGA TACATCTGGT GCCGGCC GGGTGCT AGCTG AGGATCCAAG
A
ACGTTTGGGTTTTCCTAGCT ACCT ||||||| ||||||| ||||| ||||||||||
ACATCTGGTACCTTGGCTGG CGGTCGG TCCATGG TCGAT TTTTGGGTTT /
C T TCTACA CC-- GC

GAM623 CTTGTGGGAGAGATTATCAA 600 TGGGAGAGAT 3202 T GA ATC -------- - G A AT
GCGTTTTGAGCAGAAAGGAT TATCAAGCGT CTTG GGGAGA TT AAGC GTTTT GA CAG
AAGG T
TCCGCCTTGTTGGTCTGAAA TTTG |||| |||||| || |||| ||||| || ||| ||||
TTCATGCAAGCTTCCGAAGA GAAC TCTTCT AA TTCG TAAAG CT GTT TTCC C
TCTTCTCAAG - AG GCC AACGTACT T G G GC

GAM624 CACTACGTTGACCTGAAGGA 601 AAGGACCGTC 3200 GA-- GAA- CCATTCT --
AAAT

CCGTCCATTCTTTGCCGGCC CATTCTTTGC CACTACGTT CCT GGACCGT
TTGCCGGCCT GGTG A
TGGTGAAATACATGCACTCA CGGC |||||||||| ||| ||||||| |||||||||| ||||
GGGCCGGTAGTTGCCATGGT GTGGTGTAA GGG TCTGGTA GATGGCCGGG
TCAC /
CTGGGAGGGGCTGAATGTGG GTCG AGGG CCGTT-- AC GTAC
TG

GAM625 CGTTTCGGGTGCTGGCGGCT 602 AAGGAACCAT 3201 TTC-- -- G C CA GA AAA
TAAG
GCAGCCGGAGTTCAAACCTA GGCCAACTGT CGT GGGT GCT GCGG TG GCCG GTTC CC
C
AGCAGCTGGAAGGAACCATG GAGC ||| |||| ||| |||| || |||| |||| ||
GCCAACTGTGAGCGTACCTT GCG TCCA CGA TGTC AC CGGT CAAG GG /
CATTGCG TTACT TG G A -- AC GAA TCGA

GAM626 CCCCGGAGCCCCAAGGAGCC 603 CTACATGGCA 3203 - A---- - AGG CA--- - T CTC
CCTCATCAGTGGCTGGCTCT ATCGGGGGCT CCC CGG GC CCCA AGCCCCT TCA
GTGGC GG T
TCTTCCGCTACATGGCAATC ATGT ||| ||| || |||| ||||||| ||| ||||| ||
GGGGGCTATGTGGGTGCAGC GGG GCC CG GGGT TCGGGGG GGT CATCG CC T
CACCGTGGG T ACCGA T GTA CTAAC A - TTC

GAM627 CCACCAACACAGTTTTCGAT 604 TGTCCAGTCT 3205 ACAC TTT CCAAAC T - - T
GCCAAACGTCTGATTGGACG GATATGAAAC CCACCA AG TCGATG GTC GATTGGACG
CAG ATT G
CAGATTTGATGATGCTGTTG ATTG |||||| || |||||| ||| ||||||||| ||| |||
TCCAGTCTGATATGAAACAT GGTGGT TC GGTTAC TAG CTGACCTGT GTC TAG A
TGGCCCTTTATGGTGG ATT- CC- AAAGTA T T G T

GAM628 ACAGTGCCAGCTTACTTTAA 605 CTGGAACTAT 3204 GT--- TTACTTT AC T AGGCT
TGACTCTCAGCGTCAGGCTA TGCTGGTCTC ACA GCCAGC AATG TC CAGCGTC A
CCAAAGATGCTGGAACTATT AATG ||| |||||| |||| || |||||||
GCTGGTCTCAATGT TGT TGGTCG TTAT AG GTCGTAG /
AACTC ------- CA - AAACC

GAM629 CCCTGGGGTTGGGGCCTCAC 606 AGGCAGGAGG 3206 GGG ACC A
CCCTCTGGAGGGCCGGAGGC TGGAAACCCC CCCTGGGGTT GCCTC CCTCTGG G
AGGAGGTGGAAACCCCAGGG AGGG |||||||||| ||||| |||||||
GGGACCCCAA TGGAG GGAGGCC G
AGG GAC G

GAM630 TTCTTAAAGAATAACAGTAA 607 TTGCTTGGAT 3207 AG A T- T T CCAAATCT TTA
ACATTCCAATGTCCAAATCT GTTTCTTTGG TTCTTAA AATA CAG AAACAT CCAA GT TGG
G

TGGTTAGTCTTCCACTATAT TGTT ||||||| |||| ||| |||||| |||| || ||| TGCTTGGATGTTTCTTTGGT AGGAATT TTGT GTT TTTGTA GGTT CG ACC T GTTGGTTAAGGA GG G TC - - TTATATC- TTC

GAM631 GGGGCTGCTTACTATAGGGT 608 TTAAGAGTTA 3208 GG T T- G ATGT TT TAACTATGTATATTCATTGT ACTTGTGGTT G GC GCT ACTATAGG TTAACT ATA C TAAGAGTTAACTTGTGGTTT TGGC | || ||| |||||||| |||||| ||| GGCTGTTTC C TG CGG TGGTGTTC AATTGA TGT / TT T TT - GAAT TA

GAM632 CACGCCATGACCTTCACTGC 609 GTGCTTTCAC 3209 G CC A TG G T GA---- - G C TGTCTCAGAGAAGGATGATC AAAATGGAGA CAC CCATGA TTC C CT TC CA GAAGG AT AT A AGGATGGTGCTTTCACAAAA GTGG ||| |||||| ||| | || || || ||||| || || TGGAGAGTGGAGAATTCATG GTG GGTACT AAG G GA AG GT CTTTC TG TA G GGGTG G T- A GT G - AAAACA G G G

GAM633 GGAACATTAGTCTGAACTGC 610 CACTGCGTTC 3210 A CT-- T --- ACCT AGTTGGACCTCCTGACCAAG TCACACTAGT GG ACATTAGT GAAC GCAGT TGG C CACTGCGTTCTCACACTAGT GTGC || |||||||| |||| ||||| ||| GTGCC CC TGTGATCA CTTG CGTCA ACC / G CACT - CGA AGTC

GAM634 CGGCGACATTGTGGACTTGG 611 CGACATTGTG 3211 G GTGG GG GTGA AG CTTCAGTGAGGTAGAAGACC GACTTGGCTT CGGC ACATT ACTT CTTCA GGT A ATGATGGAGAAGGTGATGTG CAGT |||| ||||| |||| ||||| ||| GCTG GTCG TGTAG TGGA GAGGT CCA / G ---- A- AGTA GA

GAM635 CCCACTGATGGAGCCCAGCA 612 TGATGCTCAC 3213 G AGCC AGCAT AA-- GT GCATTGAGAAAATTGTAGAG ATAGGTTGTG CCCACT ATGG CAGC TGAG AATT A ATTGATGCTCACATAGGTTG CCAT |||||| |||| |||| |||| |||| TGCCATGAGTGGG GGGTGA TACC GTTG ACTC TTAG / G GT-- GATAC GTAG AG

GAM636 AATTGATAAAGCCAGAGTGG 613 TGTGACCCAA 3212 A G GA AACCACT - - A A AGAC AGACACAGAACCACTGGTTC GCTGTGTCCA AATTG TAAAGCCAGA TGGA CACAG GGTT CAC CT CA TG A ACCTACAATGAGACAATGAC ATCT ||||| |||||||||| |||| ||||| |||| ||| || || || AGTGGAGAGTGTGACCCAAG TTGAC GTTTCGGTCT ACCT GTGTC CCAG GTG GA GT AC / CTGTGTCCAATCTGGCTTTG - A -- GAAC--- T A G G AGTA CAGTT

GAM637 GAAACAGACTGGGCCAATGT 614 TATCAAGGAA 3214 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM638 ATCCGCCTCACAGACAGTTG 615 TTCCTCAGGC 3215 ACAGA G T A C- GAAATC
G
CGTCCAGAGGCTTTTGGAAA TGCAAGTGGA ATCCGCCTC CA TTGCG CC GAGG TTTTG
ACC A
TCACCGAAGGGTCAGAATTC GGGA |||||||||| || ||||| || |||| ||||| |||
CTCAGGCTGCAAGTGGAGGG TAGGTGGAG GT AACGT GG CTCC AAGAC TGG A
AGGTGGAT GGAG- G C A TT ------ G

GAM639 GGAAGTCTCAACCTGGAGAA 616 TGCCTTAGTA 3216 A AC-- GAAGA TACAAT A GT
GATGCTATACAATGCAAGAG AAATCCAGCT GGA GTCTCA CTGGA TGCTA GCA GAG G
GTGAACTCTGCCTTAGTAAA GGTG ||| |||||| ||||| ||||| ||| |||
ATCCAGCTGGTGGGATATTC CTT TAGGGT GACCT ATGAT CGT CTC /
A GGTC AAA-- TC---- - AA

GAM640 CAGGTTCAGCCTATGACCCA 617 TATGACCCAG 3217 TC- - A C GT AA CC CTTC
CCA
GGTCCAAAAGTTCCAGCCTT GTCCAAAAGT CAGGT AGC CT TGACC AG CC AAGTT AGC
TCTG C
CTCTGCCACCTCCAGAGCTA TCCA ||||| ||| || ||||| || || ||||| ||| ||||
GCTTCAGGTTCTGGTCAAAG GTCCA TCG GA ACTGG TC GG TTCGA TCG AGAC /
AGCTCACACCTG CAC A A - TT AC -- ---- CTC

GAM641 GCGCTACTTCGGCGGCACCG 618 TCCCCCGCCG 3218 G GG ACCGA C T C TT
AGGACCGCCTGTCCTGCTTC AGAAGTGGAG GC CTACTTC CGGC GGAC GCC GTC TGC C
GCGCAGACGGTGTCCCCCGC C || ||||||| |||| |||| ||| ||| |||
CGAGAAGTGGAGC CG GGTGAAG GCCG CCTG TGG CAG ACG /
A A- CCC-- - - - CG

GAM642 TTGAGACAAGAGTCTCGCTC 619 TCTCGCTCTG 3219 A TC C TT C--- C -- A -
CAA
TGTTGCCCAGGCTGGAGTGC TTGCCCAGGC TTGAGACA GAG TCGCT TG GCC AGG
TGGAG TGCA TG GCT T
AATGGCTCAATCTCAGCTCA TGGA |||||||| ||| ||||| || ||| ||| ||||| |||| || |||
CTGCATCCTCCACCTCCCAG GACTCTGT CTC AGTGA AC TGG TCC ACCTC ACGT
AC CGA /

GTTCAAGTGATTCTCATGTC A TT - T- ACCC - CT C T CTC
TCAG

GAM643 TCTTGTGTTGCGACTTCGTG 620 TACACCACTC 3220 GCGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG |||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM644 AGAAACAAAAGCAGGTGCTG 621 TAGCATGCCT 3221 CAA- C -- TCA--- AA
AATCATGAAAACCTCAATTA CTTAATTTTT AGAAA AAG AGGT GCTGAA TGA A
TTTTTAGCATGCCTCTTAAT CT ||||| ||| |||| |||||| |||
TTTTCT TCTTT TTC TCCG CGATTT ACT /
TTAA - TA TTATTA CC

GAM645 CCATGCCTATCCAGGTGCTG 622 CTCCTGGTGT 3222 TAT- TGC A CTGA A A ATTA
AAGGGCCTGACCATCACTCA TGGCGTGG CCATGCC CCAGG TGA GGGC CC TC CTC A
TTAAGAACAGAGGAGGCTGC ||||||| ||||| ||| |||| || || |||
CTGTTACTCCTGGTGTTGGC GGTGCGG GGTCC ATT TCCG GG AG GAG G
GTGG TTGT TC- G TC-- - - ACAA

GAM646 GAAGCTGAAGAAGCCGCCCT 623 AAGAAGCCGC 3223 CTG A - TG TT C C G
GGTTGCACATGCCGTCGGCC CCTGGTTGCA GAAG AAGA GCCGCC C G GCA ATGC GTCG C
ATGACTGTGTATGCTCTGGT CATG |||| |||| |||||| | | ||| |||| ||||
GGTGGTGTCTTACTTC CTTC TTCT TGGTGG G C CGT TGTG CAGT C
A-- G T GT T- A T A

GAM647 TGGGAGGAGCAGTGCTTGGC 624 TTGGAGTCAT 3224 A A G CT CTGC - G
TCCCTGCAGTTTGGCTACAA CAATGCCCCC TGGG GG GCA TG TGGCTCC AGT TTG C
CACTTGGAGTCATCAATGCC CA |||| || ||| || ||||||| ||| |||
CCCCA ACCC CC CGT AC ACTGAGG TCA AAC T
- - A T- T--- C A

GAM648 GAAGAAAGGACCCCAGGTCA 625 AAGGACCCCA 3225 AAG - - A-- - - - CC
GAGACTGGAGCCATTACTTC GGTCAGAGAC GAAGA GA CCC CAGGTC GA GA CT GGAG A
AAGATCATCGAGGACCTGAG TGGA ||||| || ||| |||||| || || || ||||
GGCTCAGATCTTC CTTCT CT GGG GTCCAG CT CT GA CTTC T
AGA C A GAG A A A AT

GAM649 TCATCGGTGGCGGAGTCTTC 626 CAATGCCCCT 3226 - G G TC C- CAA G
CAGGCCATCAAGGGTTTCCG GTTGGAATTC TCA TCGGTG CGGA TCT CAGG CAT GG T
CAATGCCCCTGTTGGAATTC GGCA ||| |||||| |||| ||| |||| ||| ||
GGCACCGGTTGA AGT GGCCAC GCTT AGG GTCC GTA CC T
T G A TT CC ACG T

GAM650 AGCAAGAAAATGGCTGGAAG 627 TGGCAAGACA 3227 AA-- A- TG --- TG --- A
AGCTGTCTTGTTGGCAGGAC GCTCTGGCTC AGC GA AATGGC GA AGAGCTGTCTTGT G
CAGG C
CTCCTGGAACTGGCAAGACA TGGC ||| || |||||| || |||||||||||| | ||||
GCTCTGGCTCTGGCTATTGC TCG CT TTATCG CT TCTCGACAGAACG C GTCC C
TCAGGAGCT AGGA CG GT CGG GT AAG T

GAM651 GATCAGACAGATCACAGCTA 628 GATCACAGCT 3228 A CAGCT T C GCCA
CGGTGACATTTCTGCCACTG ACGGTGACAT GATCAG CAGATCA ACGG GA ATTTCT C
TTGGAAGTTTCTTGTTCATT TTCT |||||| ||||||| |||| || ||||||
TGATCTGCTGATT TTAGTC GTCTAGT TGTT CT TGAAGG /
- TTACT - T TTGT

GAM652 CTTGGGTCGCTTGCTGTTCG 629 TCAGGAGCAG 3229 GG G C GA----- AG
TGATATGAGACAGACAGTTG GTGGACAAG CTTG TCGCTTGCT TT GTGATAT GAC A
CGGTGGGTGTCATCAGGAGC |||| ||||||||| || ||||||| |||
AGGTGGACAAG GAAC GGTGGACGA GA TACTGTG TTG /
A- G C GGTGGCG AC

GAM653 GCTTTGAACGTACTGTTGAA 630 CCGCAGTGAA 3230 -- T-------- G TGTAC
GCACTGTACAAGTTTGTGGT TGTTCAAAGC GCTTTGAACGT ACTGT GAA CAC A
TCCTAAGCCCCGCAGTGAAT |||||||||| ||||| ||| |||
GTTCAAAGC CGAAACTTGTA TGACG CTT GTG /
AG CCCCGAATC G TTTGA

GAM654 GGGCGGCATTGACAAGCTGG 631 CGGCATTGAC 3231 C CAT ACA CG ACAT
GCGAGTACATGGAGAAGCTG AAGCTGGGCG GGG GG TG AGCTGGG AGT G
TCCCGGCTGGCGTACCACCC AGTA ||| || || ||||||| |||
CCC CC GC TCGGCCC TCG G
A AT- GG- TG AAGA

GAM655 GACTATGGCAAGGACCTGAT 632 TATGGCAAGG 3232 A AA- A T AGAA- CA
GGAGAAGGTCAAGAGCCCAG ACCTGATGGA GACT TGGC GG CCTGA GG GGT A
AGCTTCAGGCCGAGGCCAAG GAAG |||| |||| || ||||| || |||
TC CTGA ACCG CC GGACT TC CCG /
- GAG - - GAGAC AG

GAM656 TCACCATCTGCAGCCTTGAA 633 AAGGAGCTTG 3233 CA C- CC A T GGAG- - AA
GGAGCTTGGTTCGGAGACAG GTTCGGAGAC TCAC TCTG AG TTGA GGAGCT GGTTC ACA
GGC A
GCAAAGGAGCCATGTGTGGA AGGC |||| |||| || |||| |||||| ||||| ||| |||
GAGCCTGGTTTCTCAGTACT AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G

TCCAGACCGTGA CC CT AT - T AGGTG A AG

GAM657 CACCTTTACGGCCAAACCGT 634 TGTGGATATA 3234 TT C CC C-- C--- G
CCACCTCGACCGATTCTGTG GTTTTCCCTG CACC TA GG AAAC GTCCAC TC A
GATATAGTTTTCCCTGTTGG TTGG |||| || || |||| |||||| ||
TG GTGG GT CC TTTG TAGGTG AG C
TT - CT ATA TCTT C

GAM658 TTGGTCCATATCTCCATGCA 635 TCCATATCTC 3235 TC ATCTCC- G- - ACA
TGGCGGATACAGTGAAATCT CATGCATGGC TTGG CAT ATGCATG CG GAT G
CGAGCATGCATCTTCTCGGT GGAT |||| ||| ||||||| || |||
GAGCCAG GACC GTG TACGTAC GC CTA T
GA GCTCTTC GA T AAG

GAM659 GTGGGGTAAAACCCCAGACG 636 TTGGATCTTC 3238 A C AC C A CTG T-- C
AGAAAA
CCATGAAAGCTGCCATGGCC ATGCCCTGGG GTGGGGTA AACCC AG GC ATGAA G CCA GG
CCTGG A
CTGGAGAAAAAGCTGAACCA TTCT |||||||| ||||| || || ||||| | ||| || |||||
GGCCCTTTTGGATCTTCATG CGCCCCGT TTGGG TC CG TACTT C GGT CC GGACC
/
CCCTGGGTTCTGCCCCGC C - C- - - TA- TTT C AAGTCG

GAM660 GGAGAAGCGCGAGGGCTACG 637 TGCAAAACCA 3237 A AGG A------- CC
AGCGTCTCCTGAAGATGCAA GCGTGGCGGC GGAGA GCGCG GCTACG GCGTCT T
AACCAGCGTGGCGGCCGCGC CGCG ||||| ||||| |||||| ||||||
TCTCT TCTCT CGCGC CGGTGC CGTAGA /
- CGG GACCAAAA AG

GAM661 GGACCCCCATCTCTGTGACT 638 TATCACAGAA 3236 AC- - - CTTCC ACC - AG
TCCTGGAGCACCTCACTTCC GCATGGGGTG GG CCCCAT CT CTGTGA TGGAGC TCAC
TTCCT C
TAGCATGAGGAACGTGAAGC ACC || |||||| || |||||| |||||| |||| |||||
TTTATCACAGAAGCATGGGG CC GGGGTA GA GACACT ATTTCG AGTG AAGGA A
TGACC AGT C A ----- A-- C GT

GAM662 TTGTCGTCATTGGACACGTA 639 TAAATGCGGT 3240 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM663 ATTTGAGAAGGAGGCTGCTG 640 CTTCAAGTAT 3239 TG AGG - GA T AAA

AGATGGGAAAGGGCTCCTTC GCCTGGGTCT ATT AGA AGGC TGCT GA GGG G
AAGTATGCCTGGGTCTTGGA TGGA ||| ||| |||| |||| || |||
T TAG TCT TCCG ATGA CT CCT /
GT GGG T A- T CGG

GAM664 CTGATCCCTCCCCCAGCTCT 641 GATCCCTCCC 3241 A- - - A C-- - C
GCTGGGTCCCGGGGCCACAG CCAGCTCTGC CTG TCC CTCCC CC GCT TGCTG GGTC C
CGTCAGGCCGGTGGGGGTGG TGGG ||| ||| ||||| || ||| ||||| ||||
AGGTAG GAT AGG GGGGG GG CGG GCGAC CCGG G
GG T T C ACT A G

GAM665 TCACCATCTGCAGCCTTGAA 642 AAGGAGCTTT 3243 CA C- CC A TT GGAG- - AA
GGAGCTTTGGTTCGGAGACA GGTTCGGAGA TCAC TCTG AG TTGA GGAGCT GGTTC ACA
GGC A
GGCAAAGGAGCCATGTGTGG CAGG |||| |||| || |||| |||||| ||||| ||| |||
AGAGCCTGGTTTCTCAGTAC AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G
TTCCAGACCGTGA CC CT AT - T- AGGTG A AG

GAM666 GACTATGGCAAGGACCTGAT 643 TATGGCAAGG 3242 A AA- A T AGAA- CA
GGAGAAGGTCAAGAGCCCAG ACCTGATGGA GACT TGGC GG CCTGA GG GGT A
AGCTTCAGGCCGAGGCCAAG GAAG |||| |||| || ||||| || |||
TC CTGA ACCG CC GGACT TC CCG /
- GAG - - GAGAC AG

GAM667 TCACCATCTGCAGCCTTGAA 644 AAGGAGCTTG 3245 CA C- CC A T GGAG- - AA
GGAGCTTGGTTCGGAGACAG GTTCGGAGAC TCAC TCTG AG TTGA GGAGCT GGTTC ACA
GGC A
GCAAAGGAGCCATGTGTGGA AGGC |||| |||| || |||| |||||| ||||| ||| |||
GAGCCTGGTTTCTCAGTACT AGTG AGAC TC GACT CTTTGG CCGAG TGT CCG G
TCCAGACCGTGA CC CT AT - T AGGTG A AG

GAM668 GACTATGGCAAGGACCTGAT 645 TATGGCAAGG 3244 A AA- A T AGAA- CA
GGAGAAGGTCAAGAGCCCAG ACCTGATGGA GACT TGGC GG CCTGA GG GGT A
AGCTTCAGGCCGAGGCCAAG GAAG |||| |||| || ||||| || |||
TC CTGA ACCG CC GGACT TC CCG /
- GAG - - GAGAC AG

GAM669 GGATGACTACATGGAGGCTT 646 TCTAAAGCCT 3247 A ACA G ACA TTCAC
TAACAAGACTTCACATTACT ACAAAGTTAA GG TGACT TG AGGCTTTA AGAC A
GTTTCTAAAGCCTACAAAGT CC || ||||| || |||||||| ||||
TAACC CC ATTGA AC TCCGAAAT TTTG /
A A-- A C-- TCATT

GAM670 GAGGTTTTTATTCACAAAGT 647 TCAAAGGGCC 3246 T CACAAAG --- G A A- ACA
TGATGGTCTGTCTGATGATC AATGATGACC GAGGTT TTATT TTGATG GTCT TCTG TG TC
A
ACAAAATAGAAACACAGAGG TT |||||| ||||| |||||| |||| |||| || ||
GACATTCATCAAAGGGCCAA TTCCAG AGTAA AACTAC CAGG AGAC AC AG A
TGATGACCTT T CCGGGA- TTA G - AA ATA

GAM671 GGTGGACAAGTCAGACTATG 648 CAAGTCAGAC 3248 GGA T A ATGA GG AT
ACATGGTGGATTATCTGAAT TATGACATGG GGT CAAG CAG CT CATGGT ATT C
GAGCTATGGGAAAGCTGCTT TGGA ||| |||| ||| || |||||| |||
GGAAGCC CCG GTTC GTC GA GTATCG TAA /
AAG - - AAGG AG GT

GAM672 CCTGCATGGGGTGTTTGTGG 649 TGCCAAGGGT 3249 - - TGT GAGG - G
CCGAGGTGGAGGATGACAGT CCTGACGGCC CCTG CATGGGGT GTT GGCC TGG AGGAT A
CCTGCCAAGGGTCCTGACGG TCGT |||| |||||||| ||| |||| ||| |||||
CCTCGTGCCAGG GGAC GTGCTCCG CAG CTGG ACC TCCTG C
C G TC- GA-- G A

GAM673 GCTAAATGGCCGGACCATGG 650 CACATGTATG 3251 AAT C --- - TTGAG
AGATTGAGTCTACCTTTCAC TCCAGCCTGT GCTA GGC GGAC CATG GAGA T
ATGTATGTCCAGCCTGTAGT AGT |||| ||| |||| |||| ||||
TGAT CCG CCTG GTAC CTTT /
GT- A TAT A CCATC

GAM674 CATCCACAGCTTACCCCATT 651 TCCACAGCTT 3250 A--- ACCCC TACAG
CTGTACAGAGCTCACCGGGA ACCCCATTCT CATCCAC GCTT ATTCTG A
TTATTCAAGCCATGGTGGAT GTAC ||||||| |||| ||||||
G GTAGGTG CGAA TAGGGC G
GTAC CTTAT CACTC

GAM675 GGGCCTCACTTGTCCACCTT 652 TCACTTGTCC 3252 C CACC A AGA GG
CCAGCAGATGTGGATTAGCA ACCTTCCAGC GGGCCT ACTTGTC TTCC GC TGT A
AGCAGGAGTACAGACGAGTC AGAT |||||| ||||||| |||| || |||
GGGCCC CCCGGG TGAGCAG GAGG CG ACG T
C ACAT A A-- AT

GAM676 GGGTATGGAATCTTGCGGCA 653 TGGAATCTTG 3253 - AA - CA- AGAC - ACTC
TCCACGAGACCACCTTCAAC CGGCATCCAC GG GTATGG TCTT GCGG TCCACG CAC
CTTCA C
TCCATCATGAAGTGTGACGT GAGA || |||||| |||| |||| |||||| ||| |||||
GGACATCCGCAAAGACCTGT CC CATGTC AGAA CGCC AGGTGC GTG GAAGT /
ACGCC G C- A TAC A--- T ACTA

GAM677 TGTCACCATCCTCTGCATTG 654 TCCCTGGCTT 3254 CA C- AT- C TG CACT C T
ACTTGGGCACTGACATGGTT ATGAGCAGGC TGTCAC TC TCTGC TGA T GG GA ATGGT C
CCTGCCATCTCCCTGGCTTA TGAG |||||| || ||||| ||| | || || |||||
TGAGCAGGCTGAGAGTGACA ACAGTG AG GGACG ATT G CC CT TACCG C
AG TC AGT C GT ---- C T

GAM678 AGATGGGTGGATCACCTGAG 655 TGGCAACATG 3255 TGGA - AG AGTTCT
GTCAGGAGTTCTAGATCAGC GTGAAACCCC AGATGGG TCACC TG GTCAGG A
CTGGCAACATGGTGAAACCC ATCT ||||||| ||||| || ||||||
CATCT TCTACCC AGTGG AC CGGTCC /
CAA- T AA GACTAG

GAM679 GAGGTATCTGCTGCGCCTGA 656 TATCTGCTGC 3258 TA ---- GTA
GATGAGTAAACTGTCGTTTC GCCTGAGATG GAGG TCTG CTGCGCCTGAGATGA A
GGGCGCGGGCGCTAGACGCC AGTA |||| |||| ||||||||||||||
TC CTCC AGAT GGCGCGGGCTTTGCT A
GC CGCG GTC

GAM680 ACCTGGCCACTTGTACCCGG 657 GGGCCCGAAA 3256 C AC- A ---- G GA
GTCCCGCGGAGATCGGGGGC GGGCACAAAG AC TGGCC TTGT CCC GGGTCCC CG G
CCGAAAGGGCACAAAGGGGT GGGT || ||||| |||| ||| ||||||| ||
CACGT TG ACTGG AACA GGG CCCGGGG GC /
C GGA C AAAG - TA

GAM681 CCCCGGCAGCGGTTGGCGAG 658 TTCTCCATGA 3257 - TTGGCGA - AA
TGGGGACCGAACCCCCGGTT TCCCGCTGGC CCCCGGC AGCGG GTGG GGACCG C
CTCCATGATCCCGCTGGCCG CGGG ||||||| ||||| |||| ||||||
GGG GGGGCCG TCGCC TACC CTTGGC C
G CTAG--- T CC

GAM682 GGCGTCTGACCAAACACACC 659 TGATTCGGGA 3259 TCTGA A A- AAGT CG
AAGTTCGTGCGGGACATGAT GGTGTGTGGC GGCG CCA ACAC CC TCGTG G
TCGGGAGGTGTGTGGCTTTG TTTG |||| ||| |||| || |||||
CC CCGT GGT TGTG GG AGTAC /
TTC-- G GA GCTT AG

GAM683 CAGGTCGAGGTGGTGCATCT 660 AGGTGGTGCA 3260 GA TG-- A TA-- GC
ATCTATGGCAAACAGTTTGA TCTATCTATG CAGGTC GGTGG CATCT TC TG A
AGATGAACTTCATCCAGACT GCAA |||||| ||||| ||||| || ||
TG GTTCAG CTACT GTAGA AG AC /
AC TCAA - TTTG AA

GAM684 TCTTGTGTTGAGACTTCGTG 661 TACACCACTC 3261 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG |||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM685 TCAGAACCAATAATTAGGAT 662 AACCAATAAT 3262 GAA T - TT TCT--- TA
AGATTTTATGCTCTCTTCAT TAGGATAGAT TCA CCAATAAT AGGATA GAT TATGC CTTCAT
C
TACATTGTGAAGTGTCTTGT TTTA ||| |||||||| |||||| ||| ||||| ||||||
GTAGTCATATTCTATTGTTG AGT GGTTGTTA TCTTAT CTG ATGTG GAAGTG A
GAATGA AA- - A -- TTCTGT TT

GAM686 TCTTGTGTTGAGACTTCGTG 663 TACACCACTC 3263 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG |||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM687 GATGAGTGGCTTTTCGAGGG 664 CGAGGGACCT 3264 A TTC G C GG T A C--- G
ACCTGGCACGTACATCCCCC GGCACGTACA GATG GTGGCTT GAG GA CT CACG AC TCC
CC G
GGAAGGAAGTGGAGGTCGTG TCCC |||| ||||||| ||| || || |||| || ||| ||
GAGATCATTCAGGCCACCAT CTAC CACCGGA CTT CT GA GTGC TG AGG GG A
C - --- A A G- - G TGAA A

GAM688 ACCAGCTGGATAAGGACATC 665 TATCACTTTC 3265 -- T - C AA - - G
AATACCTTCTCTATGCGTGT CGGAGCTGGT ACCAGCT GGA AAG GA ATC TACC TTCTCT AT C
CAGGGAGTGGTACGGGTATC ||||||| ||| ||| || ||| |||| |||||| ||
ACTTTCCGGAGCTGGT TGGTCGA CCT TTC CT TGG ATGG GAGGGA TG G
GG - A A GC T C T

GAM689 TTAGTTGGTGGAGCGATTTG 666 GTGGAGCGAT 3267 GA GATTT G AATTCC
TCTGGTTAATTCCGATAACG TTGTCTGGTT TTAGTTGGTG GC GTCT GTT G
AACGAGACTCTGGCATGCTA AATT |||||||||| || |||| |||
ACTAG GATCAATCGT CG CAGA CAA /
A- GTCT- G GCAATA

GAM690 AGTGGCGTTCAGCCACCCGA 667 TGTCCGGGGC 3266 - T A C G GA--- ATA G
GATTGAGCAATAACAGGTCT TGCACGCGCG AGTG GCGT CAGCC CC GA ATT GCA ACA G
GTGATGCCCTTAGATGTCCG CT |||| |||| ||||| || || ||| ||| |||
GGGCTGCACGCGCGCT TCGC CGCA GTCGG GG CT TAG CGT TGT T
G C - C G ATTCC AG- C

GAM691 AACTGGTGATTGTTGGTGAT 668 CTTGCTCATA 3268 GA T G-- CT GAA
GGAGCCTGTGGAAAGACATG GTCTTCAGCA AACTGGT TTGTTGG GAT GAGC GTG A
CTTGCTCATAGTCTTCAGCA AGGA ||||||| ||||||| ||| |||| |||
AGGACCAGTT TTGACCA AACGACT CTG CTCG CGT G
GG T ATA TT ACA

GAM692 TGTGCCCACAGTGTTTGAGA 669 TGGAAAGCAG 3269 - T TGAGAA G GCAGA GA
ACTATGTGGCAGATATCGAG GTAGAGTTGG TGTG CCCACAG GTT CTAT TG TATC G
GTGGATGGAAAGCAGGTAGA CTTT |||| ||||||| ||| |||| || ||||
GTTGGCTTTGTGGGACACA ACAC GGGTGTT CGG GATG AC GTAG G
A T TTGA-- G GAAAG GT

GAM693 TCTTGTGTTGAGACTTCGTG 670 TACACCACTC 3270 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM694 CGTTTCGGGTGCTGGCGGCT 671 AAGGAACCAT 3272 TTC-- -- G C CA GA AAA
TAAG
GCAGCCGGAGTTCAAACCTA GGCCAACTGT CGT GGGT GCT GCGG TG GCCG GTTC CC
C
AGCAGCTGGAAGGAACCATG GAGC ||| |||| ||| |||| || |||| |||| ||
GCCAACTGTGAGCGTACCTT GCG TCCA CGA TGTC AC CGGT CAAG GG /
CATTGCG TTACT TG G A -- AC GAA TCGA

GAM695 CTTGTGGGAGAGATTATCAA 672 TGGGAGAGAT 3273 T GA ATC -------- - G A AT
GCGTTTTGAGCAGAAAGGAT TATCAAGCGT CTTG GGGAGA TT AAGC GTTTT GA CAG
AAGG T
TCCGCCTTGTTGGTCTGAAA TTTG |||| |||||| || |||| ||||| || ||| ||||
TTCATGCAAGCTTCCGAAGA GAAC TCTTCT AA TTCG TAAAG CT GTT TTCC C
TCTTCTCAAG - AG GCC AACGTACT T G G GC

GAM696 TTCTGCATACAAGTTGGCAG 673 GATTCTGTGG 3274 ACAAG G A ATAC
GAACATTATACATGGCAGTG AGAGTGCAGA TTCTGCAT TT GCAGGA CATT A
ATTCTGTGGAGAGTGCAGAG G |||||||| || |||||| ||||
GAGACGTG AG TGTCTT GTGA /
AG--- G A CGGT

GAM697 CACTACGTTGACCTGAAGGA 674 AAGGACCGTC 3271 GA-- GAA- CCATTCT --
AAAT
CCGTCCATTCTTTGCCGGCC CATTCTTTGC CACTACGTT CCT GGACCGT
TTGCCGGCCT GGTG A

TGGTGAAATACATGCACTCA CGGC ||||||||| ||| ||||||| |||||||||| ||||
GGGCCGGTAGTTGCCATGGT GTGGTGTAA GGG TCTGGTA GATGGCCGGG
TCAC /
CTGGGAGGGGCTGAATGTGG GTCG AGGG CCGTT-- AC GTAC
TG

GAM698 ACTTCAATCCCCTCTGCGCT 675 CCCCTCTGCG 3275 ATCCC GCGC G AA-- A
AATGC
TCTGATGGGAAATCTTATGA CTTCTGATGG ACTTCA CTCT TTCTGATG GA TCTT TGAT
A
TAATGCATGCCAAATCAAAG GAAA |||||| |||| |||||||| || |||| ||||
AAGCATCGTGTCAGAAACAG TGAAGT GAGG AAGACTGT CT AGAA ACTA T
GAGAAAATGAAGT AAAA- ACA- G ACGA - AACCG

GAM699 GTCCCTCCGAACAAGTGAAA 676 GCCCTGTTTG 3276 --- A AGTGA G T TA
AGAGGTCCTTGTATGTCAGG ATTATGATCG GTCCC TCCGA CA AAA AGG CCTTG T
GCCCTGTTTGATTATGATCG GACT ||||| ||||| || ||| ||| |||||
GACTCGGGAC CAGGG AGGCT GT TTT TCC GGGAC /
CTC A ATTAG G C TG

GAM700 CGCTCGTCACCAGGACCCAA 677 TCAAGGGTCG 3277 - T- C G AA GA AAATTG
GGAACCAAAATTGCATCTGA TGTGTTTGAA CGCT CG CAC A GACCC G ACCA C
TGGTCTCAAGGGTCGTGTGT GTG |||| || ||| | ||||| | ||||
TTGAAGTG GTGA GT GTG T CTGGG C TGGT /
A TT - G AA TC AGTCTA

GAM701 GGTGTGGCTCACGGCCATCG 678 TGGCATGAAG 3278 CTCAC-- A TG CTA TCTA
TGCTGTTCTGCTAGGTTCTA GTCTACAACT GGTGTGG GGCC TCGTGC TTCTG GGT T
TGTGTACCGCTCAGAGTGGC CCAC ||||||| |||| |||||| ||||| |||
ATGAAGGTCTACAACTCCAC TCACACC CTGG AGTACG GAGAC CCA /
ACT TCAACAT A GT TCG TGTG

GAM702 TCGCGCGGGGGGTAATTCGG 679 TCCCCGATGG 3279 G AAT T--- --- TC
GGTCTGGGTTCTGGTGCCGC CCCACTGCGT TCGCGCGG GGGT TCGGGG CTG GGT T
GCAGCTTTCCCCGATGGCCC GA |||||||| |||| |||||| ||| |||
ACTGCGTGA AGTGCGTC CCCG AGCCCC GAC CCG G
A GT- TTTC GCG TG

GAM703 TCGGCTCCAAGTCTGACCCA 680 TGGGAGGGGG 3280 T A T A AC TG TT
CTCTGCGTCCTTTTACAGGA CAGCTGGGCT TCGGC CCA G CTG CCC TC CGTCCT T
TGTGGGAGGGGGCAGCTGGG GA ||||| ||| | ||| ||| || ||||||
CTGA AGTCG GGT C GAC GGG GG GTAGGA /
- - - G GA GT CA

GAM704 GGTGTCCTGGAGCCTCTGTA 681 CTGGAGCCTC 3281 T C TCT-- C- T - A
CCTGTGCCCAAATGGTGCCC TGTACCTGTG GG GTC TGGAGCC GTAC TG GC CC A
GCTGTGCCACCTGGTTTCAA CCCA || ||| ||||||| |||| || || ||
GACCC CC CAG ACTTTGG CGTG GC CG GG A
- A TCCAC TC C T T

GAM705 GTGAAGAATGGCATTCCTTC 682 TCAGGGAGGA 3282 AT- AT AAC TTAT G
TAACAGAATTATTTCGGGAG GCTTTATCTT GTGAAGA GGC TCCTTCT AGAA TTC G
GGTTTTCTCAGGGAGGAGCT TAT ||||||| ||| ||||||| |||| |||
TTATCTTTAT TATTTCT TCG AGGAGGG TCTT GGG G
ATT -- AC- TT-- A

GAM706 GATGTGACCTACCAGATTTC 683 TATGCCACTG 3283 T-- CC A AA- TAA
AGAACATGTGTTAATAGTAT AAAACTTAGG GATG GACCTA AG TTTCAG CATGTGT T
ATATGCCACTGAAAACTTAG TCCT |||| |||||| || |||||| |||||||
GTCCTGTATC CTAT CTGGAT TC AAAGTC GTATATA /
GTC -- A ACC TGA

GAM707 TCTTGTGTTGAGACTTCGTG 684 TACACCACTC 3284 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM708 CGGCTCCGAGAAGCAGGTTC 685 AGCAGGTTCT 3285 - AGAAG C-- - ------- G
TTCGTGAGTTCCTCGCAAGG TCGTGAGTTC CGGC TCCG CAGGTTCTT GTG AGTTC
CTC C
GCCGGTCAGAGCTACACATT CTCG |||| |||| ||||||||| ||| ||||| |||
GAGAACCTGAACATGGAGGC GCCG AGGT GTCCAAGAG CAC TCGAG GGG A
CG G ACAA- TTA A ACTGGCC A

GAM709 CTTCTTCAGTGAGACGGGCG 686 TTTGTAGACT 3286 T GAC- CG ----- T C
CTGGCAAGCACGTGCCCCGG TGGAACCCAC CTTC TCAGTGA GGG CTG GCAAGCACG
GCC C
GCTGTGTTTGTAGACTTGGA AGTC |||| ||||||| ||| ||| ||||||||| |||
ACCCACAGTCATTGATGAAG GAAG AGTTACT CCC GGT TGTTTGTGT CGG /
T GACA AA TCAGA - G

GAM710 GGAGATCATTGACCTTGTGT 687 CACCGGTCTT 3287 TT - TGTT AATTC AA C
TGGACCGAATTCGCAAGCTG CAGGGCTTCT GGAGATCA GA CCTTG GGACCG GC
GCTGG T
GCTGACCAGTGCACCGGTCT TGGT |||||||| || ||||| |||||| || |||||
TCAGGGCTTCTTGGTTTTC CTTTTGGT TT GGGAC TCTGGC CG TGACC G
TC C T--- CA--- -- A

GAM711 TCATGGGCACGGCTCGGGAC 688 CACCTTCTGG 3288 CA -- G C A GAAAC GAG
AGTT
GGAGACGAAACCAGACAGAG ACTGCTGCCC TCATGGG CGGC TC GGA GG GAC CAGACA
GGTCA T
GGTCAAGTTTACAGATGACC CCAT ||||||| |||| || ||| || ||| |||||| |||||
GTGTCTGCAAGAGTCACCTT AGTACCC GTCG AG TCT CC CTG GTCTGT CCAGT
A
CTGGACTGCTGCCCCCATGA CC TC G T A AGAAC G-- AGAC

GAM712 CAATGTGCAACTGACATCTG 689 TGTCCAGTAG 3289 T-- - ACA T G AT CT AAT
CTAGTGATGATCTGGTAATA CCGAACAGTT CAATG GCAA CTG TC GCTA TG GAT GGT A
TACAACCTGTCCAGTAGCCG TGTT ||||| |||| ||| || |||| || ||| |||
AACAGTTTGTTTTTATTG GTTAT TGTT GAC AG CGAT AC CTG CCA T
TTT T A-- C G -- T- ACA

GAM713 GGCCAATTGAAACAAACAGT 690 TATTAGGGAT 3290 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM714 TGGGTATGGAATCTTGCGGC 691 TGGAATCTTG 3291 - AA - CA- AG C ACTC
ATCCACGAGACACCTTCAAC CGGCATCCAC TGG GTATGG TCTT GCGG TCCACG ACAC
TTCA C
TCCACTCATGAAGTGTGACG GAGA ||| |||||| |||| |||| |||||| |||| ||||
TGGACATCCGCAAAGACCTG ACC CATGTC AGAA CGCC AGGTGC TGTG AAGT A
TACGCCA G C- A TAC AG - ACTC

GAM715 CAGCTCTTATCTGAAAACTA 692 TATCTGAAAA 3292 T A AACTACA G -- ACTG
CACCGCTGTGGCCCAGACTG CTACACCGCT CAGC CTT TCTGAA CCGCT TGGCC CAG T
TGAACCTGCTGGCCGAGTGG GTGG |||| ||| |||||| ||||| ||||| |||
CTCATTCAGACAGGTGTTG GTTG GGA AGACTT GGTGA GCCGG GTC /
T C ACTC--- - TC CAAG

GAM716 CTTTTCGACTGCAGGATCAT 693 TGCAGGATCA 3293 T CT GG- ATC T ATG TC
CAGGTTCGGATGAGTCTCAT TCAGGTTCGG CT TTCGA GCA ATC AGGT CGG AGTC A
GTGGCTGCTGCACCTCCAGA ATGA || ||||| ||| ||| |||| ||| ||||
TATATGCTCTCGAACAG GA AAGCT CGT TAG TCCA GTC TCGG T
C CT ATA ACC C G-- TG

GAM717 GAGTCCTCCGTGTTCTGCAC 694 TACCATGGTC 3294 GTCC T C -- T- - AAGA

CAGTATTGTGGCTCAAGACT GGAATTTGGA GA TCCG GTTCTG ACCA GTA TGTGGC TC C
CCAGAGGCCACATTTACCAT TTAT || |||| |||||| |||| ||| |||||| ||
GGTCGGAATTTGGATTATC CT AGGT TAAGGC TGGT CAT ACACCG AG /
ATT- T - AC TT G ACCT

GAM718 GTCTTAGCAGTGGACGCGAG 695 TAGCAGTGGA 3297 T- A C A------- AA
GTACAACGCGTACCGACACC CGCGAGGTAC GTCT AGC GTGGA GCG GGTAC C
AACGTTTCCACAGTTTCGGA AACG |||| ||| ||||| ||| |||||
C CAGG TTG CACCT TGC CCATG /
CT A T AACCACAG CG

GAM719 CATCCGGATTTCCCACCAGA 696 TCCGGATTTC 3298 TC TTTC AG GAAC A
TGCACA
GTGTGGAACCCGGGGTCATG CCACCAGAGT CA CGGA CCACCAG TGTG CCGGGGTC
TGA C
ATGCACACTGAACATTCAAG GTGG || |||| ||||||| |||| |||||||| |||
ATTCTGGCACACAGCCTGGT GT GCCT GGTGGTC ACAC GGTCTTAG ACT T
GGTGTTCCGAGTG GA TGT- CG AC-- A TACAAG

GAM720 GGGGCTGCTGCACCGCGTTT 697 CGGAAACCCA 3299 G - C----- A CAGC
CCATAGCAGCATGTCCTACG GCACGTGTGT GGGGCT CTGCAC CG GTTTCC TAG A
GAAACCCAGCACGTGTGTAG AGAG |||||| |||||| || |||||| |||
AGCCTC CTCCGA GATGTG GC CAAAGG ATC /
- T ACGACC C CTGT

GAM721 GGATGGATAACATAGTTGTT 698 TAACATAGTT 3300 ATA T TG ------ GG
TCTCTGGGGACCACCAGACT GTTTCTCTGG GGATGG ACA AGT TTTC TCTGG A
TCTTGAAGTGACTTGTGTCC GGAC |||||| ||| ||| |||| |||||
CATCT TCTACC TGT TCA GAAG AGACC C
CTG - GT TTCTTC AC

GAM722 GTGGATCGGCGGCTCCATCC 699 TCAGCAAGCA 3302 TC - - CA----- GC C - CT CA
TGGCCTCGCTGTCCACCTTC GGAGTATGAC GTGGA GGC GG CTC TCCTG CT GCTG
TCCAC TC G
CAGCAGATGTGGATCAGCAA GAGT ||||| ||| || ||| ||||| || |||| ||||| ||
GCAGGAGTATGACGAGTCCG TACCT CCG CC GAG AGGAC GA CGAC AGGTG AG
/
GCCCCTCCAT CC G T CAGTATG -- A T T- AC

GAM723 ACGTGGACATCCGCAAAGAC 700 CTGTCTGGCG 3301 ACAT- AA CT GCCA
CTGTACGCCAACACAGTGCT GCACCACCAT ACGTGG CCGC AGAC GTAC A
GTCTGGCGGCACCACCATGT GT |||||| |||| |||| ||||
TGTACC GGCG TCTG CGTG /
ACCAC G- T- ACAC

GAM724 GTAGAGCTTTATGCTGAAAA 701 GAGCTTTATG 3304 - TA GAAAA - T A
GGTGGCCACTAGAGGTCTGT CTGAAAAGGT GTAGAG CTT TGCT GGTGGC CAC AG G
GTGCCATTGCCCAGGCAGAG GGCC |||||| ||| |||| |||||| ||| ||
TCTCTGC CGTCTC GAG ACGG TTACCG GTG TC G
T -- ACCCG T - T

GAM725 GGGAAACTCCGAGGACAGAG 702 TGGCCTGATG 3303 AAA A--- - GA AA TG A
GGCTAAATCCATGAAGTTTG ATCCACAGCG GGG CTCCG GGA CA GGGCT ATCCA A G
TGGATGGCCTGATGATCCAC GAGA ||| ||||| ||| || ||||| ||||| |
AGCGGAGACCC CCC GAGGC CCT GT TCCGG TAGGT T /
A-- GACA A AG -- GT T

GAM726 TCTCTGTAATGTGCCTGTGC 703 TGTAATGTGC 3305 - - GTG TG ----- A G
CTGTGGCCAGAGGGGAGCCC CTGTGCCTGT TCTCTGT AATGTGC CT CCTG GC CAG GGG
A
CCTGACCGTGCTGTGGGAGA GGCC ||||||| ||||||| || |||| || ||| |||
GCACATTGACAGAGA AGAGACA TTACACG GA GGGT CG GTC CCC G
G A --- GT TGCCA - C

GAM727 GAGTTCTGAATCCAAATACA 704 TCTTGTACAT 3306 TT- AAT --- A G C
AAGATGACATCCGGTGTGGT TTTGGCTAGT GAG CTG CCAAA TACAA GAT ACAT C
CTTGTACATTTTGGCTAGTT TTTT ||| ||| ||||| ||||| ||| ||||
TTTC CTT GAT GGTTT ATGTT CTG TGTG /
TTT C-- TAC - G G

GAM728 GGCCAATTGAAACAAACAGT 705 TATTAGGGAT 3307 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM729 GCCGTGGCTGGCATCAAGGG 706 TCGGCCCCTG 3308 T AT A - AAG AA
CGACAAGGCTGACAAGGCGT CGCCGGCCTC GCCG GGCTGGC CA GGGC GAC GCTGAC G
CGGCGTCGGCCCCTGCGCCG GGC |||| ||||||| || |||| ||| ||||||
GCCTCGGC CGGC CCGGCCG GT CCCG CTG CGGCTG /
T C- C G --- CG

GAM730 AGTGGCGTTCAGCCACCCGA 707 TGTCCGGGGC 3309 - T A C G GA--- ATA G
GATTGAGCAATAACAGGTCT TGCACGCGCG AGTG GCGT CAGCC CC GA ATT GCA ACA G
GTGATGCCCTTAGATGTCCG CT |||| |||| ||||| || || ||| ||| |||
GGGCTGCACGCGCGCT TCGC CGCA GTCGG GG CT TAG CGT TGT T

G C - C G ATTCC AG- C

GAM731 GATGGTTTAGTGAGGCCCTC 708 TGAGAAGACG 3310 T GA C GGA C-- GC
GGATCGGCCCCGCCGGGGTC GTCGAACTTG GATGGTT AGT GGCC TC TCGGC
CCGCCGGGGTCG C
GGCCCACGGCCCTGGCGGAG ACTA ||||||| ||| |||| || ||||| ||||||||||
CGCTGAGAAGACGGTCGAAC CTATCAG TCA CTGG AG AGTCG GGCGGTCCCGGC /
TTGACTATC T AG C AAG CGA AC

GAM732 GGGAGGCATTGATCATGGGC 709 AGGCATTGAT 3311 ATTGA TG-- CCA T- TT
CCAGAAGACACCTGCTTTGA CATGGGCCCA GGGAGGC TCA GGC GAAGACACC GC T
GTTTGGTGTTTTTCCTGCCA GAAG ||||||| ||| ||| ||||||||| ||
TCCTGAGTTTCCC CCCTTTG AGT CCG TTTTTGTGG TG /
----- CCTA TCC TT AG

GAM733 GGCAGCTCTTCGGCCGCATC 710 TGCAGATGCG 3312 T C- CC -- T
CCCATGCGCTTCTCGGTGCT TTTCGACGGG GGCAGCTC TCGG CGCATC CAT GCGCT C
GATGCAGATGCGTTTCGACG CTGC |||||||| |||| |||||| ||| |||||
GGCTGCT TCGTCGGG AGCT GCGTAG GTA CGTGG T
C TT AC GT C

GAM734 GCTAAATGGCCGGACCATGG 711 CACATGTATG 3314 AAT C --- - TTGAG
AGATTGAGTCTACCTTTCAC TCCAGCCTGT GCTA GGC GGAC CATG GAGA T
ATGTATGTCCAGCCTGTAGT AGT |||| ||| |||| |||| ||||
TGAT CCG CCTG GTAC CTTT /
GT- A TAT A CCATC

GAM735 CATCCACAGCTTACCCCATT 712 TCCACAGCTT 3313 A--- ACCCC TACAG
CTGTACAGAGCTCACCGGGA ACCCCATTCT CATCCAC GCTT ATTCTG A
TTATTCAAGCCATGGTGGAT GTAC ||||||| |||| ||||||
G GTAGGTG CGAA TAGGGC G
GTAC CTTAT CACTC

GAM736 GAGGAAGCGGACCGAGCCCG 713 CCGCCGCGGG 3315 AGC C C CT G AT
TCGCCTTGGAGCATGAGCGC CTCGTCCTCC GAGGA GGAC GAGCCCGT GC TG AGC G
TGCGCCGCCGCGGGCTCGTC TC ||||| |||| |||||||| || || |||
CTCCTC CTCCT CCTG CTCGGGCG CG GC TCG A
--- - C CC G CG

GAM737 GTGGAGCTGCTCACTCTGCC 714 AGCCTGGATG 3316 - -- T C T CC - TGA- AG
ATG
ATGTGCTCCCTGACCTGAAG GTGCAGACAG GTG GAGCT GC CACT TGCCA GTGCT CTG ACC
AGG GAGG G

GAGGAGGATGGCAGCCTCAG CACT ||| ||||| || |||| ||||| ||||| ||| ||| ||| ||||
CCTGGATGGTGCAGACAGCA CAC CTCGA CG GTGG GCGGT CACGA GAC TGG TCC
CTCC /
CTGGCGTGGTGGCCAAGCTC T AC - T - CA G TAGG GA GAC
TCAC

GAM738 ATGATTGGAGACAAAGTTTA 715 TCAAATGGAA 3317 A G ATG -- AGG
TGTCCATTACAAAGGAAAAT AGAAGTTTGA ATGATTGGAG CAAA TTT TCCATT ACAA A
TGTCAAATGGAAAGAAGTTT TTCC |||||||||| |||| ||| |||||| ||||
GATTCCAGTCAT TACTGACCTT GTTT AAG AGGTAA TGTT /
A G AA- AC AAA

GAM739 CCCCAAAATGGAGGACTTTG 716 CCTGGACAAC 3318 A A - CTA A T GGC
CTACCAGGACCTACGGCACC AGACCTCTGT CCCCAAA TGGAGG CT TTG CCAGG CC AC A
AGTGGCCTGGACAACAGACC TTGG ||||||| |||||| || ||| ||||| || ||
TCTGTTTGGGG GGGGTTT GTCTCC GA AAC GGTCC GG TG /
- A C A-- - - ACC

GAM740 TCATATTTTCTATCATCATG 717 TCTATCATCA 3319 A T TTGT T G
TTGTGTATATGTGCAAACCT TGTTGTGTAT TCAT TTTTCTA CATCATG GTATA GT C
GTACTTCCATGATGTGGGAA ATGT |||| ||||||| ||||||| ||||| ||
GGTGA AGTG GAAGGGT GTAGTAC CATGT CA A
- - CTT- C A

GAM741 TTTGGATGTATAATAGTTTA 718 TGGATGTATA 3320 AATAG T A-- -- T
GCAAGATGTTACTTTTGTAA ATAGTTTAGC TTTGGATGTAT TT AGCA GATGTT AC T
GACATCAGATGTTCAAAAAA AAGA |||||||||| || |||| |||||| ||
GTGCATCCGAA AAGCCTACGTG AA TTGT CTACAG TG T
AAAA- C AGA AA T

GAM742 GTTCTTAAGGTTGAAGTGTG 719 AGTGGACAGC 3321 AA- -- G G- CCAGT
GTTCAGGGCCAGTGCAATAT ACTTAGTAGC GTTCTT GGTTG AAGTGT GTTCA GG G
TAGTGGACAGCACTTAGTAG TGTG |||||| ||||| |||||| ||||| ||
CTGTGGAGGAC CAGGAG TCGAT TTCACG CAGGT TT /
GTG GA A GA ATAAC

GAM743 TCTTGTGTTGAGACTTCGTG 720 TACACCACTC 3322 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM744 CCGGGTTGGCCTGAACCTGC 721 GGCCTGAACC 3323 G- T T- A T T ACGGTA
TTTATGCTCAGACGGTATCA TGCTTTATGC CC GGT GGCC GA CC GCTT ATGCTCAG T

GATATTGAGCGTGGGTGGAT TCAG || ||| |||| || || |||| ||||||||
CTTGGTCACCAAGG GG CCA CTGG CT GG TGGG TGCGAGTT /
AA - TT A - - ATAGAC

GAM745 CCCAGGGCATGAAGATCACA 722 GGGCATGAAG 3324 - - ATCACA G TTC T
ATGGGCCTGGTTCAGATTTT ATCACAATGG CCCAGG GC ATGAAG ATGG CCTGG AGA T
TCTCCAGGGCCGTGGCAGCT GCCT |||||| || |||||| |||| ||||| |||
TTCATGGCATCTGGG GGGTCT CG TACTTT TGCC GGACC TCT T
A G CGACGG G --- T

GAM746 GAGAGCGCGGCCGCACGCTG 723 AAGCTCGTAG 3325 - --- CG AC GG CA
GTTTTGCATCTTCAGGAAAG CCATCGCGCT GAGA GCGC GGC C GCT TTTTG T
CTCGTAGCCATCGCGCTTCT TCTC |||| |||| ||| | ||| |||||
C CTCT CGCG CCG G CGA AGGAC C
T CTA AT CT A- TT

GAM747 TCAAGTCTGACGTGTGGTCT 724 CTGGTCACCA 3326 A AC ------ AAT TA A
TTTGGAATCTTACTCACAGA AAGGAAGAGT TCA GTCTG GTGTGGT CTTTTGG CT CTC C
GCTGGTCACCAAAGGAAGAG GCCA ||| ||||| ||||||| ||||||| || |||
TGCCATACCCAGGCATGA AGT CGGAC CATACCG GGAAACC GG GAG /
A C- TGAGAA ACT TC A

GAM748 GGCTGTGGGAAGCGATTTGC 725 TGGATTCTTG 3327 TG AGC TT - C AC- TATTT T
GATGTTCACCTCCACGATAT GGAGCTGGAT GGCTG GGA GAT GCGA TGTTCA CTCC GA
GC G
TTGCTGTGGTTGGATTCTTG ACTC ||||| ||| ||| |||| |||||| |||| || ||
GGAGCTGGATACTCGTTTAT CCGAC TCT CTA TGCT ATAGGT GAGG CT TG T
CATCTCAGCC -- A-- TT C C GTT TAGGT G

GAM749 TGATGAGAGCCTGAGGAGCC 726 TAATGAGAGA 3328 A G GAG ATTT AA- ----- ACG
CGG G
ATTTGAGCAATGGGGAACGC TCCAAACACC TG TGA AGCCT GAGCC GAGC TGG GGA
CTCA ACT T
TCACGGACTGTGTGGTAATG AAGC || ||| ||||| ||||| |||| ||| ||| |||| |||
AGAGATCCAAACACCAAGCG AC ACT TTGGG TTCGG CTCG ACC CCT GAGT
TGG G
CTCCAGGGGCTTGGGTTGTC - G --- GGAC CGA ACAAA AGA AA- T
ACA

GAM750 TTGGGGACCACGTCACCACG 727 TACCATGGCA 3330 GG AC CCAC C- - AG
GTACAACAGGCAGCAAGCCC GGGTCACAA TTG GACC GTCA GGTA AACAGG C C
TGTTTTTACCATGGCAGGGT ||| |||| |||| |||| |||||| |
CACAA AAC CTGG CGGT CCAT TTGTCC G /
A- GA A--- TT C AA

GAM751 GCCAACCTTGAAGCCAGTGG 728 TTGAAGCCAG 3329 A - TG - G - ATTC
GGCACCAATTCACAAACTGG TGGGGCACCA GCCA CC T AAGCCA GTG GGCA CCA A
ATGCTGCGCTTGGTTTTGAT ATTC |||| || | ||||||| ||| |||| |||
GGTGGC CGGT GG A TTTGGT CGC TCGT GGT C
- T GT T G A CAAA

GAM752 GGCCAATTGAAACAAACAGT 729 TATTAGGGAT 3331 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM753 CACAATCTGGAGACATGGAG 730 TGACATCGTC 3332 T GACA GG- C T-- ---- G
GCAGCTGTGGCGGGTGTTAG CTGCTTATCA CACAA CTGGA TGGA CAG TG GGCGGG
TGTTAGA A
AGATGTCTGACATCGTCCTG CTGA ||||| ||||| |||| ||| || |||||| |||||||
CTTATCACTGATATCCGACA GTGTT GACCT GCCT GTC AC TCGTCC ACAGTCT T
TCCAGTTGTG - ACA- ATA - TAT TGCT G

GAM754 GGCAGCTCTTCGGCCGCATC 731 TGCAGATGCG 3333 T C- CC -- T
CCCATGCGCTTCTCGGTGCT TTTCGACGGG GGCAGCTC TCGG CGCATC CAT GCGCT C
GATGCAGATGCGTTTCGACG CTGC |||||||| |||| |||||| ||| |||||
GGCTGCT TCGTCGGG AGCT GCGTAG GTA CGTGG T
C TT AC GT C

GAM755 CTTGTGGGAGAGATTATCAA 732 TGGGAGAGAT 3335 T GA ATC -------- - G A AT
GCGTTTTGAGCAGAAAGGAT TATCAAGCGT CTTG GGGAGA TT AAGC GTTTT GA CAG
AAGG T
TCCGCCTTGTTGGTCTGAAA TTTG |||| |||||| || |||| ||||| || ||| ||||
TTCATGCAAGCTTCCGAAGA GAAC TCTTCT AA TTCG TAAAG CT GTT TTCC C
TCTTCTCAAG - AG GCC AACGTACT T G G GC

GAM756 CACTACGTTGACCTGAAGGA 733 AAGGACCGTC 3334 GA-- GAA- CCATTCT --
AAAT
CCGTCCATTCTTTGCCGGCC CATTCTTTGC CACTACGTT CCT GGACCGT
TTGCCGGCCT GGTG A
TGGTGAAATACATGCACTCA CGGC ||||||||| ||| ||||||| |||||||||| ||||
GGGCCGGTAGTTGCCATGGT GTGGTGTAA GGG TCTGGTA GATGGCCGGG
TCAC /
CTGGGAGGGGCTGAATGTGG GTCG AGGG CCGTT-- AC GTAC
TG

GAM757 TTCTGCATACAAGTTGGCAG 734 GATTCTGTGG 3336 ACAAG G A ATAC

GAACATTATACATGGCAGTG AGAGTGCAGA TTCTGCAT TT GCAGGA CATT A
ATTCTGTGGAGAGTGCAGAG G |||||||| || |||||| |||| GAGACGTG AG TGTCTT GTGA /
AG--- G A CGGT

GAM758 TCTACAAAGTGCCGTCCACT 735 TCCAATCTGA 3337 A - - CACTG CT- C
GAGACTGAGGCCTTGGCTTC TGGGCATGTT TCT CAAA GTGCC GTC AGA GAGGC T
CAATCTGATGGGCATGTTTG TGAG ||| |||| ||||| ||| ||| |||||
AGA AGA GTTT TACGG TAG TCT CTTCG T
- G G ----- AAC G

GAM759 GGGGGAACGTGGTCATCAGT 736 TAAAACTCAT 3338 ACGT - C GGTC T TTCCA
GGTCAGTGGGGTTCCAAGAT AGACCCAGGT GGGGGA GGTC AT AGT AG GGGG A
TATCCCCTAAAACTCATAGA CTCC |||||| |||| || ||| || ||||
CCCAGGTCTCCC CCCTCT CCAG TA TCA TC CCCT /
GGAC A C AAA- - ATTAG

GAM760 TCTTGTGTTGAGACTTCGTG 737 TACACCACTC 3339 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM761 GAATATTTCCACAATGTCTG 738 TACACGGTCG 3340 CACA T AAC G TTCA
TGAACTGGACCTGGTGTTCA TGGACGAGAT GAATATTTC ATG CTGTG TGGACCT GTG A
ACTTCTACAAGGTTTACACG GTTC ||||||||| ||| ||||| ||||||| |||
GTCGTGGACGAGATGTTC CTTGTAGAG TGC GGCAC ATTTGGA CAT /
CAGG T --- A CTTC

GAM762 CTCCGAGCAGATTATGAGAT 739 TTGAATTAGA 3341 CA ATGAG AG AGA C
TGCAAGTAAAGAAAGAGACC TGCAATGGAT CTCCGAG GATT ATTGCA TAA AAGAGA C
TGTTTTTTGAATTAGATGCA CACT ||||||| |||| |||||| ||| ||||||
ATGGATCACTTGGAG GAGGTTC CTAG TAACGT ATT TTTTTT T
A- G---- AG AAG G

GAM763 GCAAGGAAGATGCTGCCAAT 740 CACTACACCA 3343 AA ----- - AACTA-- C
AACTATGCCCGAGGGCACTA TTGGCAAGGA GCAAGG GATG CT GCCAAT TGCC G
CACCATTGGCAAGGAGATCA GATC |||||| |||| || |||||| ||||
TTGACCTTGT TGTTCC TTAC GA CGGTTA ACGG A
AG TAGAG A CCACATC G

GAM764 CTTCTTCAGTGAGACGGGCG 741 TTTGTAGACT 3342 T GAC- CG ----- T C
CTGGCAAGCACGTGCCCCGG TGGAACCCAC CTTC TCAGTGA GGG CTG GCAAGCACG
GCC C

GCTGTGTTTGTAGACTTGGA AGTC |||| ||||||| ||| ||| ||||||||| |||
ACCCACAGTCATTGATGAAG GAAG AGTTACT CCC GGT TGTTTGTGT CGG /
T GACA AA TCAGA - G

GAM765 GGAGATCATTGACCTTGTGT 742 CACCGGTCTT 3344 TT - TGTT AATTC AA C
TGGACCGAATTCGCAAGCTG CAGGGCTTCT GGAGATCA GA CCTTG GGACCG GC
GCTGG T
GCTGACCAGTGCACCGGTCT TGGT |||||||| || ||||| |||||| || |||||
TCAGGGCTTCTTGGTTTTC CTTTTGGT TT GGGAC TCTGGC CG TGACC G
TC C T--- CA--- -- A

GAM766 CCTGAAGCAGCACTACATTG 743 TTCCCTGGGC 3346 AG- GC- A GA A-- CG
ACCTGAAAGAACGACCATTC TGGTGAAGTA CCTGA CA ACT CATT CCTG AAGAA A
TTCCCTGGGCTGGTGAAGTA CATG ||||| || ||| |||| |||| |||||
CATGAACTCAGG GGACT GT TGA GTGG GGGT TTCTT C
CAA ACA A TC CCC AC

GAM767 CTTGTGGGAGAGATTATCAA 744 TGGGAGAGAT 3347 T GA ATC -------- - G A AT
GCGTTTTGAGCAGAAAGGAT TATCAAGCGT CTTG GGGAGA TT AAGC GTTTT GA CAG
AAGG T
TCCGCCTTGTTGGTCTGAAA TTTG |||| |||||| || |||| ||||| || ||| ||||
TTCATGCAAGCTTCCGAAGA GAAC TCTTCT AA TTCG TAAAG CT GTT TTCC C
TCTTCTCAAG - AG GCC AACGTACT T G G GC

GAM768 CACTACGTTGACCTGAAGGA 745 AAGGACCGTC 3345 GA-- GAA- CCATTCT --
AAAT
CCGTCCATTCTTTGCCGGCC CATTCTTTGC CACTACGTT CCT GGACCGT
TTGCCGGCCT GGTG A
TGGTGAAATACATGCACTCA CGGC ||||||||| ||| ||||||| |||||||||| ||||
GGGCCGGTAGTTGCCATGGT GTGGTGTAA GGG TCTGGTA GATGGCCGGG
TCAC /
CTGGGAGGGGCTGAATGTGG GTCG AGGG CCGTT-- AC GTAC
TG

GAM769 GGAGCGCACCTTCATCGCCA 746 CGGCCTGGTG 3348 ACCT--- A - A GACG GT
TCAAGCCGGACGGCGTGCAG GGCGAGATCA GGAGCGC TC TCGCC ATCA GCCG GC G
CGCGGCCTGGTGGGCGAGAT TCAA ||||||| || ||||| |||| |||| ||
CATCAAGCGCTTC CTTCGCG AG AGCGG TGGT CGGC CG /
AACTACT - G C G--- AC

GAM770 GCGGGGCGGAGGCACTCGCG 747 CACTGCGTGA 3349 G G CAC G AAT T--- ---
TC
CGGGGGGTAATTCGGGGTCT CCTTGGTTCA GC GGGC GAGG TCGCGCGG GGGT TCGGGG
CTG GGT T
GGGTTCTGGTGCCGCGCAGC GC || |||| |||| |||||||| |||| |||||| ||| |||

TTTCCCCGATGGCCCACTGC CG CTTG TTCC AGTGCGTC CCCG AGCCCC GAC CCG G
GTGACCTTGGTTCAGC A G --- A GT- TTTC GCG TG

GAM771 GAGATGCAGCAGAAGTTGGT 748 TGCAGCAGAA 3350 A AG GAA G G- GCT
GGAGCTGTCGGCTGAGAACG GTTGGTGGAG GAG TGC CA GTTGGTG AGCT TCG G
AGAAGCTGCACCAGCGCGTG CTGT ||| ||| || ||||||| |||| |||
GAGCAGCTC CTC ACG GT CGACCAC TCGA AGC A
G AG GCG G AG AAG

GAM772 GGGGATTGTGGGGATATAGT 749 TTACTACATG 3351 A GT- GG - GC G
GGGCGAGGTGCCTTTACTAC TGTGATCTGA GGGG TT GG ATATA GTGG GAG T
ATGTGTGATCTGAAAACCCT AAAC |||| || || ||||| |||| |||
TCCC AA CT TGTGT CATC TTC G
A AGT AG A AT C

GAM773 GCATTTCTCATTTTTATTTG 750 TGTACAGATT 3352 CTCA --- - AAA TT
ACAGAAAAAGTTGCTCTTGC TTAAAAAACC GCATTT TTTTTA TTTG ACAG AAG G
TGTACAGATTTTAAAAAACC AAAA |||||| |||||| |||| |||| |||
AAAATGC CGTAAA AAAAAT AGAC TGTC TTC /
ACCA TTT A G-- TC

GAM774 CACCTTTACGGCCAAACCGT 751 TGTGGATATA 3353 TT C CC C-- C--- G
CCACCTCGACCGATTCTGTG GTTTTCCCTG CACC TA GG AAAC GTCCAC TC A
GATATAGTTTTCCCTGTTGG TTGG |||| || || |||| |||||| ||
TG GTGG GT CC TTTG TAGGTG AG C
TT - CT ATA TCTT C

GAM775 GCTGTTGAAGAGGCATTCGT 752 AGGCATTCGT 3354 C AGAG TT TACCAGT A TG
ACCAGTTATTAAACTCTGTT ACCAGTTATT G TGTTGA GCA CG TATTAA CTCTGTTT A
TTGATGGGATAGAGATTGAT AAAC | |||||| ||| || |||||| ||||||||
ATTTTGTTTGCAAGATTAGC C ACGATT CGT GT ATAGTT GAGATAGG /
AC - AGAA TT TTT---- A GT

GAM776 TATAAGATGTATAAGAAGTC 753 TAAGATGTAT 3355 A TAAG C A A
TTAACGGTTGCAGGGTAACC AAGAAGTCTT TAT AGATGTA AAGT TTA CGGTTGC G
GATGAAATTTTACATCTAGT AACG ||| ||||||| |||| ||| |||||||
A ATG TCTACAT TTTA AGT GCCAATG /
A ---- A A G

GAM777 TATGGGCCAAACGCCACAAC 754 TCGGTGGTGT 3356 G --- AAC---- TTCCA
ATCTATTCCAATATATTAGG TTCCTGGGCT TATGG CCA AACGCCAC ATCTA A
TTTCCTCGGTGGTGTTTCCT ATG ||||| ||| |||||||| |||||

GGGCTATG GTATC GGT TTGTGGTG TGGAT /
G CCT GCTCCTT TATAT

GAM778 AAGATAGAGGCAGAACTGCA 755 TGTTCTGGAG 3357 GA----- AA G TG
GGACATCTGCAATGATGTTC CTGTTGGACA AAGATA GGCAG CT CAGGACATC C
TGGAGCTGTTGGACAAATAT AATA |||||| ||||| || |||||||||
CTT TTCTAT TTGTC GA GTCTTGTAG A
AAACAGG -- G TA

GAM779 TCTGGCAGCTGGTACCCGAA 756 CACCGGGAGG 3358 - CT - CGAA TATAGCAA -
GA
TCCCTATAGCAAACATGTCT TGACCCCTGA TCTGG CAG GGT ACC TCCC AC ATGTCTT
C
TGACGGAAGACATAGTACAC CCAG ||||| ||| ||| ||| |||| || |||||||
CGGGAGGTGACCCCTGACCA AGACC GTC CCA TGG AGGG TG TACAGAA /
GA A C- G ---- CCACA--- A GG

GAM780 TCTCCTGCTTCTGGGACCTG 757 ACCGAACCAT 3359 CC CT CCT - GCACC TTG T
CT
CCAGCACCGTTTTTGTGGTT GAGCTCCCAG TCT TG TCTGGGA GC CA GTTT TGGT AG
C
AGCTCCTTCTTGCCAACCGA ATTC ||| || ||||||| || || |||| |||| ||
ACCATGAGCTCCCAGATTCG AGA GC AGACCCT CG GT CAAG ACCG TC C
TCAGA CT TT --- A AC--- CCA T TT

GAM781 TGTGAGCCCGAGTGGTGTGA 758 TGGCTCCACA 3360 - AG-- T GA A C CTTCATC
TGCCTGAGGACCCACTCTTC GGCAAACCCA TGTGAGCC CG TGG GT TGCCTG GGA CCACT
C
ATCCTGTACACCAGTGGCTC AGGG |||||||| || ||| || |||||| ||| |||||
CACAGGCAAACCCAAGGGTG ACACTTGG GT ACC CA ACGGAC CCT GGTGA T
TGGTTCACA T GGGA - A- A C CCACATG

GAM782 AAGATAGAGGCAGAACTGCA 759 TGTTCTGGAG 3361 GA----- AA G TG
GGACATCTGCAATGATGTTC CTGTTGGACA AAGATA GGCAG CT CAGGACATC C
TGGAGCTGTTGGACAAATAT AATA |||||| ||||| || |||||||||
CTT TTCTAT TTGTC GA GTCTTGTAG A
AAACAGG -- G TA

GAM783 TCTGGCAGCGGTACCCGAAT 760 CACCGGGAGG 3363 - C - CGAA TATAGCAA - GA
CCCTATAGCAAACATGTCTT TGACCCCTGA TCTGG CAG GGT ACC TCCC AC ATGTCTT
C
GACGGAAGACATAGTACACC CCAG ||||| ||| ||| ||| |||| || |||||||
GGGAGGTGACCCCTGACCAG AGACC GTC CCA TGG AGGG TG TACAGAA /
A A C G ---- CCACA--- A GG

GAM784 CCAACAGGATGCCACGCTGG 761 CACTCGGTGT 3362 AA CC CC TATTTC
GCCGAGCGACTATTTCCTGC ACGTCCTGGA CC CAGGATG ACGCTGGG GAGCGAC C
CAATGTTGCTCACTCGGTGT GG || ||||||| |||||||| |||||||
ACGTCCTGGAGG GG GTCCTGC TGTGGCTC CTCGTTG T
AG A- A- TAACCG

GAM785 TCTTGTGTTGAGACTTCGTG 762 TACACCACTC 3364 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM786 GAGGCGGGCAGATCACAAGG 763 AACACAGTGA 3365 GC CAGA AA---- GATCG
TCAGGAGATCGAGACCATCC AACCCCATCT GAG GGG TCAC GGTCAGGA A
TGGCTAACACAGTGAAACCC C ||| ||| |||| ||||||||
CATCTC CTC CCC AGTG TCGGTCCT /
TA CAA- ACACAA ACCAG

GAM787 GAAGCTGAAGAAGCCGCCCT 764 AAGAAGCCGC 3366 CTG A - TG TT C C G
GGTTGCACATGCCGTCGGCC CCTGGTTGCA GAAG AAGA GCCGCC C G GCA ATGC GTCG C
ATGACTGTGTATGCTCTGGT CATG |||| |||| |||||| | | ||| |||| ||||
GGTGGTGTCTTACTTC CTTC TTCT TGGTGG G C CGT TGTG CAGT C
A-- G T GT T- A T A

GAM788 GGCGGTCCCGCGGGTCTGTC 765 CCGCGGGTCT 3368 C G C T C A
TCTTGCTTCAACAGTGTTGG GTCTCTTGCT GG GGTCCC CGGGTCTGT TCT G TTCAAC G
ACGGAACAGATCCGGGGACT TCAA || |||||| ||||||||| ||| | ||||||
CTC CT TCAGGG GCCTAGACA AGG C AGGTTG /
C - - - - T

GAM789 GCTGGGCGAGTATCTCTTTC 766 TAAGAGCCTT 3367 G- TAT- TCGAAA ACTCT
GAAAGGTCACTCTCAAGCAC CTGAGCCCAG GCTGGGC AG CTCTT GGTC C
GACTAAGAGCCTTCTGAGCC C ||||||| || ||||| ||||
CAGC CGACCCG TC GAGAA TCAG A
AG TTCC ------ CACGA

GAM790 ATTTGAGAAGGAGGCTGCTG 767 CTTCAAGTAT 3369 TG AGG - GA T AAA
AGATGGGAAAGGGCTCCTTC GCCTGGGTCT ATT AGA AGGC TGCT GA GGG G
AAGTATGCCTGGGTCTTGGA TGGA ||| ||| |||| |||| || |||
T TAG TCT TCCG ATGA CT CCT /
GT GGG T A- T CGG

GAM791 TCCTGGCTGCAGATGAGTCC 768 TCCATTGGCA 3370 - C CAGA A - C A- TT A
ACTGGGAGCATTGCCAAGCG CCGAGAACAC TCCT GG TG TG GT CCA TGGG GCA GCC A
GCTGCAGTCCATTGGCACCG CGAG |||| || || || || ||| |||| ||| |||
AGAACACCGAGGA AGGA CC AC GC CA GGT ACCT CGT CGG G
G - AAGA - C T GA -- C

GAM792 GGCCGTGCTCTTTGGAATTT 769 GATCCAGTTC 3371 GT TT T-- ACAT T
TCCTGTACATGGGAGTCACC TATGAGCGGC GGCC GCTC TGGAATT TCCTGT GGGAG C
TCCCTTAACGGGATCCAGTT T |||| |||| ||||||| |||||| |||||
CTATGAGCGGCT TCGG CGAG ATCTTGA AGGGCA CCCTC A
-- T- CCT ATT- C

GAM793 AATGGGCCGAGGAGATGGAT 770 ATAGGCCTAG 3372 CC GG GA CGT- AAA- TG
TGATTCTCGTGGCAAACGTG TGGAAGTGAT AATGGG GAGGAGAT ATT TTCT GGC CG A
AATTTGATAGGCCTAGTGGA AGAT |||||| |||||||| ||| |||| ||| ||
AGTGATAGATCTTCTTTTCC TTACCC TTCTTCTA TAG AAGG CCG GT A
CATT TT GA TG TGAT GATA TT

GAM794 TTCGGTGCTTTTACCTACCT 771 GCTCATCGTG 3373 T--- - TAC-- AC-- - AG
ACAACGAGCGCGAGAACCTG TGGCTGCTGG TTCGG GCTTT TACC CTACA GAGCG CG
A
CCGCTCATCGTGTGGCTGCT TGAA ||||| ||||| |||| ||||| ||||| ||
GGTGAAAAGCTTCTCCGAG GAGCC CGAAA GTGG GGTGT CTCGC GT A
TCTT A TCGTC GCTA C CC

GAM795 GAGCTCATATTTTATGCAGA 772 TTGACACTGT 3374 TT-- A ATGATCA ATA
TGATCAGTCAACACATAAGC ACAATCCCTA GAGCTCATA TT TGCAG GTCAACAC A
AAGTGTTGACACTGTACAAT TGAG ||||||||| || ||||| ||||||||
CCCTATGAGTTT TTTGAGTAT AA ATGTC CAGTTGTG G
CCCT C A------ AAC

GAM796 GGTGACAACATGCTGGAGCC 773 TTGGTTCAAC 3375 AA-- G -- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CTG GAGCCAAG GC A
TCAACGGATGGAAAGTCACC TCAC |||||| ||| ||| |||||||| ||
CCACTG GTA GGC CTTGGTTC CG C
AAAG - AA - TA

GAM797 CTTCCAGCCTTAAGGCATGT 774 TAAAGGTCAT 3376 C A ATGTA-- TAAGG
ATTTGATAAGGCAAAATTCA GAGGCTGAAG CTTC AGCCTTA GGC TTTGA C
AAGGTAAAGGTCATGAGGCT |||| ||||||| ||| |||||
GAAG GAAG TCGGAGT CTG AAACT /
- A GAAATGG TAAAA

GAM798 GCCATCACTGCCACCAGAAG 775 TCACTGCCAC 3378 T C AAGA G TGG
ACTGTGGATGGCCCCTCCGG CAGAAGACTG GCCATCAC GCCAC AG CT TGGA C
GGAAAACTGTGGCGTGATGG TGGA ||||||||| ||||| || || ||||
C CGGTAGTG CGGTG TC GG GCCT /
- - AAAA G CCC

GAM799 CAACGAGATTTGGTCGTAGT 776 ACGAGATTTG 3377 GA----- G T -- - T
GGGGCGCCTTGGTCACCAGG GTCGTAGTGG CAACGA TTTG TCG AGT GGGGC GCCTTGG
C
GCTGCTTTTAACTCTGGGTA GGCG |||||| |||| ||| ||| ||||| |||||||
AAGTGGATATTGTTG GTTGTT AAAT GGT TCA TTTCG CGGGACC /
ATAGGTG G C AT T A

GAM800 GCCTCTGAGAGAAGCAGCTG 777 TGAGAGAAGC 3379 - TG A ------- T GGC
GGGGCCCTCACCCTGCATCG AGCTGGGGGC GCCT C AGAGA GCA GC GGG C
TCTTGCGTCTCTTGGCAGGC CCTC |||| | ||||| ||| || |||
CGGA G TCTCT CGT CG CCC C
C GT G TCTGCTA T ACT

GAM801 CCACCACCTGGAGCCCGAGG 778 TTCTTCACGG 3380 C GGA- AG T AAGT
AGGTGCTCAAGTACAGCGAG GCAGCAAGCT CCACCA CT GCCCG GAGG GCTC A
TTCTTCACGGGCAGCAAGCT GGTG |||||| || ||||| |||| ||||
GGTGG GGTGGT GA CGGGC CTTC TGAG /
C ACGA A- T CGAC

GAM802 GGCCAATTGAAACAAACAGT 779 TATTAGGGAT 3381 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM803 GGCCAATTGAAACAAACAGT 780 TATTAGGGAT 3382 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM804 GAAACAGACTGGGCCAATGT 781 TATCAAGGAA 3383 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G

GCACCACCGATGTCCAAAGG GATG ||||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM805 CCGGAACCTGCTCATCTGGA 782 AGAGTTGTTC 3384 GA - - A CAA G -- AAA
TCAAGAAGAATTTGCTAAAA ATCCAGGGAG CCG AC CTG CTC TCTGGAT GAA AATTT GCT
A
GAGCGGCCAGAGTTGTTCAT ACAG ||| || ||| ||| ||||||| ||| ||||| |||
CCAGGGAGACAGCGTGCGG GGC TG GAC GAG GGACCTA CTT TTGAG CGG G
G- C A - --- G AC CGA

GAM806 GATGCCGACTGGGAGCTACT 783 AGCTACTGGG 3385 CGA- GAGCTA GGT A
GGGTGAGCTGGACTACCAGC TGAGCTGGAC GATGC CTGG CTG GAGCTGG C
TTCAGGACCAGGACAGCGTC TACC ||||| |||| ||| |||||||
CTGCG GACC GAC TTCGACC T
ACAG AG---- --- A

GAM807 TTCACTTCTGATCCAGCACT 784 CAAGCCAACT 3386 AC-- G--- TTC TCA T T
TCTGTCATTTGCTGAATATT GTGAACATGG TTC TTCTGATCCA CAC TG TTTGC GAA A
TCTGCAAGCCAACTGTGAAC GTCA ||| |||||||||| ||| || ||||| |||
ATGGGTCAGAAACAGGAA AAG AAGACTGGGT GTG AC GAACG CTT /
GACA ACAA TCA C-- T T

GAM808 TGTGGTGCCTGGTGGAGACC 785 CATTGCTGAG 3387 G T G A - AA CAGAGA -
CA T
TGGCCAAGGTACAGAGAGCT GCCTGGGCTC TGTGGT CC GGTG AG CCT GGCC GGTA
GCTGTG TG TGC G
GTGTGCATGCTGAGCAACAC GCCT |||||| || |||| || ||| |||| |||| |||||| || |||
CACAGCCATTGCTGAGGCCT ACACCA GG CCGC TC GGG CCGG TCGT CGACAC AC
ACG /
GGGCTCGCCTGGACCACA - T - - T AG TAC--- C A- A

GAM809 AACTGGTGATTGTTGGTGAT 786 TTGGTGATGG 3388 GA ------ TG C - G
GGAGCCTGTGGAAACGACAT AGCCTGTGGA AACTGGT TTGTTG GTGA GAGC TGT G A
GCTTGCTCATAGTCTTCAGC AACG ||||||| |||||| |||| |||| ||| |
AAGGACCAGTT TTGACCA AACGAC TACT TTCG ACA C A
GG TTCTGA CG T G A

GAM810 GTTTTCTAACTTGTCTTGGT 787 TAACTTGTCT 3389 T GTCT A A TA
AATTGCAATTTAACTAGGTG TGGTAATTGC GTTTTC AACTT TGGT ATTGCA TT A
CGGTGGCTACTAAAGTTCGA AATT |||||| ||||| |||| |||||| ||
AGGC CGGAAG TTGAA ATCG TGGCGT GA /
C ATC- G G TC

GAM811 GCTCAACCTCTTTGTTCAGT 788 TACTACTGGA 3390 AACC TT- T GTA TTGAA
ATGTGTAACCTTGAAGCTAA TATCTGACTG GCTC TC TGTTCAGTA GT ACC G
TTGGTACTACTGGATATCTG GAGC |||| || ||||||||| || |||
ACTGGAGC CGAG AG ATAGGTCAT CA TGG C
GTC- TCT - --- TTAAT

GAM812 TTTTCCTTATCCAATGTACT 789 TATAGTGTGG 3391 T A-- CA ATTAT
CACGGGATTATGTTTATGTT ATCAGGAAAA TTTTCCT ATCCA TGTACT CGGG G
CGGCGGTATAGTGTGGATCA ||||||| ||||| |||||| ||||
GGAAAA AAAAGGA TAGGT ATATGG GCTT T
C GTG CG GTATT

GAM813 GGCGACACAGGTGTTGGTAA 790 TACAGTTTAC 3392 - C AGG- G CAT- TT
ATCATGCTTATTGCTACAGT AGACAAGAGG GGC GA AC TGTT GTAAAT GC A
TTACAGACAAGAGGTTTCAG TTTC ||| || || |||| |||||| ||
CC CCG CT TG ACAG CATTTG CG /
A T GAGA A ACAT TT

GAM814 GAATCGCTCCTGCAGCAGAG 791 TGCGCATGAG 3393 CGCTC GCAG- A----- C AC
CCAACATGCCCATCACTCGG ACCCTGGCTA GAAT CTGCA AGCCA CATGC CATC T
ATGCGCATGAGACCCTGGCT GAGA |||| ||||| ||||| ||||| |||| /
AGAGATGCAGATTAATTC CTTA GACGT TCGGT GTACG GTAG /
ATTA- AGAGA CCCAGA C GC

GAM815 GTAGGATTAGATCATTAGCT 792 TAGATCATTA 3394 T T T T GT-- C
CAGTGACCTCCTAGGGTTTC GCTCAGTGAC GTAGGAT AGA CAT AGC CA GACCT C
GATGTGCTATGTTCTCATCC CTCC ||||||| ||| ||| ||| || |||||
TAC CATCCTA TCT GTA TCG GT TTGGG T
C T - T AGCT A

GAM816 CTTGGTTCTACAGCCATTGG 793 AGCCATTGGG 3397 GG CAT ATC G A
GATCCAGACATCAGAGGGTG ATCCAGACAT CTT TTCTACAGC TGGG CA ACATC G
TGTGCCTAGCTGTGGAGAAG CAGA ||| ||||||||| |||| || |||||
AG GAG GAGGTGTCG ATCC GT TGTGG A
AA --- --- G G

GAM817 GGTGCCATGTCTCGTCCCTT 794 GGAGTTGATG 3398 G ATG ---- TG GTAGC
TGGAGTAGCATTATTATTTG AGAAAGGACC GGT CC TCTCGTC CCTT GA A
GAGGAGTTGATGAGAAAGGA ||| || ||||||| |||| ||
CC CCA GG AGAGTAG GGAG TT T
- AA- TTGA GT ATTAT

GAM818 AATTGATAAAGCCAGAGTGG 795 TGTGACCCAA 3395 A G GA AACCACT - - A A AGAC
AGACACAGAACCACTGGTTC GCTGTGTCCA AATTG TAAAGCCAGA TGGA CACAG GGTT CAC CT CA TG A
ACCTACAATGAGACAATGAC ATCT ||||| |||||||||| |||| ||||| |||| ||| || || ||
AGTGGAGAGTGTGACCCAAG TTGAC GTTTCGGTCT ACCT GTGTC CCAG GTG GA GT AC /
CTGTGTCCAATCTGGCTTTG - A -- GAAC--- T A G G AGTA
CAGTT

GAM819 CCCACTGATGGAGCCCAGCA 796 TGATGCTCAC 3396 G AGCC AGCAT AA-- GT
GCATTGAGAAAATTGTAGAG ATAGGTTGTG CCCACT ATGG CAGC TGAG AATT A
ATTGATGCTCACATAGGTTG CCAT |||||| |||| |||| |||| ||||
TGCCATGAGTGGG GGGTGA TACC GTTG ACTC TTAG /
G GT-- GATAC GTAG AG

GAM820 CGGACACATCACAGGTATTG 797 GTGGGGCAGA 3399 CATCAC ACTGG- T A C CG
ACTGGGCTCCCAAGAGCGAC CCGCAATGCC CGGACA AGGTATTG GC CCCA GAG GAC C
CGCATTGTCACTTGTGGGGC TATG |||||| |||||||| || |||| ||| |||
AGACCGCAATGCCTATGTCT GTCTGT TCCGTAAC CG GGGT TTC CTG A
G A----- GCCAGA - G A TT

GAM821 TGATGCGCAAGGCCATCCGA 798 TCTGGAGAAA 3400 T - A GCCA G ACC AAA
GGGCACCTGGAAAACAACCC CTGCTGCCTC TGA GC GCA G TCC AGGGC TGG A
AGCTCTGGAGAAACTGCTGC A ||| || ||| | ||| ||||| |||
CTCA ACT CG CGT C AGG TCTCG ACC C
C T - AAAG - --- CAA

GAM822 CTGGAGCAGCTGCGTAAAAC 799 GAGCAGCTGC 3401 --- G AAAACATAC - G AT A
ATACAGGCCGGAGCTTATCA GTAAAACATA CTGGA GCA CTGCGT AGGC C GAGCTT CA A
AAGATGGCAAGTTTGGGGCC CAGG ||||| ||| |||||| |||| | |||||| ||
TACATGCAGGTGCACATTCA GACTT CGT GACGTA TCCG G TTTGAA GT G
G ACA G CA------- G G CG A

GAM823 GGCCCAGGGATCGGCAGGGC 800 TTCCCATGCC 3402 G - G- - GCT GA A
TGCTGGCAGAGGAATCCCAG CCAGGCTCCT GGCCCAG GA TC GCAGG GCT GGCA GGAATCCC G
CTGGGGTTCCCATGCCCCAG GCAG ||||||| || || ||||| ||| |||| ||||||||
GCTCCTGCAGGACTTGCTGG CCGGGTC TT AG CGTCC CGG CCGT CCTTGGGG C
GCC G C GA T ACC AC T

GAM824 GACAAGTTTCAAAGGAAGAA 801 TTTATAGATG 3403 AGTT - AA CTCAT CAC

CATTTATGACTCATGCCACA GCTTCTTTCT GACA TCA AAGGAAG CATTTATGA GC A
AAAGCTATTTATAGATGGCT GATT |||| ||| ||||||| ||||||||| ||
TCTTTCTGATTATGTC CTGT AGT TTTCTTC GTAGATATT CG /
ATT- C G- TAT-- AAA

GAM825 GCATGGACAAAATTGAAACT 802 AGTTGCGGGA 3404 ACAAA TG AT------- ATGA
ATCAACTTTCATGAAGTTAA ATCAAGTTTT GCATGG AT AAACT CAACTTTC A
GGAAGTTGCGGGAATCAAGT GGTG |||||| || ||||| |||||||
TTTGGTGTTACCATGC CGTACC TG TTTGA GTTGAAGG G
ATTG- GT ACTAAGGGC AATT

GAM826 TGGAGGTAGAGCTCATCACC 803 GAGCTCATCA 3405 AG C - TTCCTCCC GC
AGGTTCCTCCCGATGCTCAT CCAGGTTCCT TGGAGGT AG TCATC ACCAGG GAT T
GTCCTTCCTGGTGGATGACT CCCG ||||||| || ||||| |||||| |||
ACACTTTCA ACTTTCA TC AGTAG TGGTCC CTG C
CA - G TTC----- TA

GAM827 TGATGATGCACAGTTTGATG 804 TAACAGGAAA 3406 GA---- - G TG GC CAT G TGA
G GAAT
CTTCCCATTGTGACAGTGAC AATTGAATGT TGAT TG CACA TT AT TTCC TGT ACAG
CAAGG T T
AAGGGTGAATTTGGTGGCTT GACA |||| || |||| || || |||| ||| |||| ||||| |
TGGTTCTGTAACAGGAAAAA ACTA AC GTGT AA TA AAGG ACA TGTC GTTTC G /
TTGAATGTGACAATTAAAAT AAATTA A - GT AA --- A TTG G TGGT
CA

GAM828 TGCTGCTTCTTGGCTGGCTT 805 GCCACTGGCC 3407 - - - --- TT- T- T
GCTTTGGCAGTCACTGCCAC TTGCCTTTGG TGC TGCTTCT TG GCT GGC GCT TGGCAG C
TGGCCTTGCCTTTGGCACAT CACA ||| ||||||| || ||| ||| ||| ||||||
GGAAGCATGCA ACG ACGAAGG AC CGG CCG CGG ACCGTC /
T T A TTT TTC TC A

GAM829 GCTGGAACTGAAGCTGGGGC 806 TGGGGCTGCA 3408 AA TG - TG CA T TT TT
TGCAGCCTGGGCCTTGGTTT GCCTGGGCCT GCTGG C AAG C GGGCTG GCC GGGCC GG
T
GATCCTTGGCCTTGGCCTTG TGGT ||||| | ||| | |||||| ||| ||||| ||
GCCTTGGCCTTTGGCCGGC CGGCC G TTC G TCCGGT CGG TCCGG CC G
-- GT C GT TC T TT TA

GAM830 GCCCTATTACCTGAACCTGA 807 TATCAGACTG 3409 T ACCTGAAC C- TC
TCGAGCTCTTCCTGCAGAGT AGATTGGGC GCCC ATT CTGAT GAGCTCT C
TCCTATCAGACTGAGATTGG |||| ||| ||||| |||||||
GC CGGG TAG GACTA CTTGAGA T
T AGTCA--- TC CG

GAM831 GTCCCGGGAGCGTGTGTTCT 808 AGCCCTGGAC 3410 GA---- GTG GAC CCCGCT
T C GAT
CCGAGGACCGGGCCCGCTTC TACCTGCACT GTCCCGG GCGT TTCTCCGAG CGGG
TCTA GG GCTGA T
TATGGCGCTGAGATTGTGTC CGGA ||||||| |||| ||||||||| |||| |||| || |||||
AGCCCTGGACTACCTGCACT CAGGGCC TGCA AAGAGGCTC GTCC AGGT CC
CGACT /
CGGAGAAGAACGTGGTGTAC ATGTGG AG- AC- ATC--- - - GTG
CGGGAC

GAM832 GTGGACTGGTGGGGGCTGGG 809 TGATGTGCGG 3411 CT TG - G G ATG
CGTGGTCATGTACGAGATGA TCGCCTGCCC GTGGA GG GG GGCTG GCGT GTC T
TGTGCGGTCGCCTGCCCTTC TTCT ||||| || || ||||| |||| |||
TAC CATCT CC CC CTGGC TGTA TAG A
TC GT G G G AGC

GAM833 GGCTGGGGCTCATTTGCAGG 810 GCTCATTTGC 3412 - CT T A CAAA TCA
GGGGAGCCAAAAGGGTCATC AGGGGGGAGC GGC TGGGG CATT GCAGGGGGG GC AGGG
T
ATCTCTGCCCCCTCTGCTGA CAAA ||| ||||| |||| ||||||||| || ||||
TGCCCCCATGTT TTG ACCCC GTAG CGTCTCCCC CG TCTC /
T C- T - ---- TAC

GAM834 TGGGTATGGAATCTTGCGGC 811 TGGAATCTTG 3413 - AA - CA- AGAC - ACTC
ATCCACGAGACCACCTTCAA CGGCATCCAC TGG GTATGG TCTT GCGG TCCACG CAC
CTTCA C
CTCCATCATGAAGTGTGACG GAGA ||| |||||| |||| |||| |||||| ||| |||||
TGGACATCCGCAAAGACCTG ACC CATGTC AGAA CGCC AGGTGC GTG GAAGT /
TACGCCA G C- A TAC A--- T ACTA

GAM835 TTGTCGTCATTGGACACGTA 812 TAAATGCGGT 3415 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM836 GGTGACAACATGCTGGAGCC 813 TTGGTTCAAG 3414 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM837 AGGCCCTATTGGACAAATTT 814 TATTGGACAA 3416 CTA TG CAAAT - GC
GGTGGGGAGCATAATCCACC ATTTGGTGGG AGGCC T GA TTGGTGG GGA A

ATCAATATATCTGGAGGCCT GAGC ||||| | || ||||||| |||
TCCGG G CT AACTACC CCT T
A-- GT ATAT- A AA

GAM838 GGTGACAACATGCTGGAGCC 815 TTGGTTCAAG 3417 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM839 TTGTCGTCATTGGACACGTA 816 TAAATGCGGT 3418 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM840 GGTGACAACATGCTGGAGCC 817 TTGGTTCAAG 3419 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM841 ATTTGAGAAGGAGGCTGCTG 818 CTTCAAGTAT 3420 TG AGG - GA T AAA
AGATGGGAAAGGGCTCCTTC GCCTGGGTCT ATT AGA AGGC TGCT GA GGG G
AAGTATGCCTGGGTCTTGGA TGGA ||| ||| |||| |||| || |||
T TAG TCT TCCG ATGA CT CCT /
GT GGG T A- T CGG

GAM842 CATTGTCGTCATTGGACACG 819 CGTCATTGGA 3421 GTC-- T- A C ATTC C
TAGATTCGGGCAAGTCCACC CACGTAGATT CATT GTCA TGG CA GTAG GGG A
ACTACTGGCCATCTGATCTA CGGG |||| |||| ||| || |||| |||
TAAATG GTAA TAGT ACC GT CATC CCT A
ATATC CT G - ACCA G

GAM843 GGTGACAACATGCTGGAGCC 820 TTGGTTCAAG 3422 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM844 GGTGACAACATGCTGGAGCC 821 TTGGTTCAAG 3423 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||

CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM845 TTGTCGTCATTGGACACGTA 822 TAAATGCGGT 3425 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM846 GTCAGCACTTACATTAAGAA 823 TACATTAAGA 3424 G CTTA A A CCCCG A
AATTGGTACAACCCCGACAC AAATTGGTAC GTCA CA CATTA GAAA TTGGTACAA AC C
AGTAGCATTTGTGCCAATTT AACC |||| || ||||| |||| ||||||||| ||
CTGGTGGAATGGTGAC CAGT GT GTGGT CTTT AACCGTGTT TG /
G AAG- - - TACGA A

GAM847 TGAAGCACTACGGGCCTGGC 824 AAGACACCAA 3426 C AC GCTG AGCATG AA
TGGGTGAGCATGGCCAACGC CGGGTCCCAG TGAAG ACT GGGCCTG GGTG GCC C
AGGCAAAGACACCAACGGGT TTCT ||||| ||| ||||||| |||| |||
CCCAGTTCTTCA ACTTC TGA CCTGGGC CCAC CGG G
T C- AA-- AGAAA- AC

GAM848 GGCGACACAGGTGTTGGTAA 825 TACAGTTTAC 3427 - C AGG- G CAT- TT
ATCATGCTTATTGCTACAGT AGACAAGAGG GGC GA AC TGTT GTAAAT GC A
TTACAGACAAGAGGTTTCAG TTTC ||| || || |||| |||||| ||
CC CCG CT TG ACAG CATTTG CG /
A T GAGA A ACAT TT

GAM849 GGTGACAACATGCTGGAGCC 826 TTGGTTCAAG 3428 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM850 GGCCATCTGATCTATCAAAT 827 AGCCCATTGA 3429 A GATCTA G--- - A GACA
GCGGTGGCATCGACAGAAGA AAAATTTGAG GGCC TCT TCAAAT CGGTGG C TC G
GAAGCCCATTGAAAAATTTG AAGG |||| ||| |||||| |||||| | ||
AGAAGGAGGCT TCGG AGG AGTTTA GTTACC G AG /
- AAG--- AAAA C A AGAA

GAM851 TGTGGAAGTCCAGGGGCCCC 828 TGGAAGTCCA 3430 --- - CCCCATGAA- GA
ATGAAGCCCGAGATGGGCAG GGGGCCCCAT TGTGG AAGTCCAGG GG GCCC G
CTCCTTATCCGCCTGGATTT GAAG ||||| ||||||||| || ||||
GAACCGCA ACGCC TTTAGGTCC CC CGGG /

AAG G TATTCCTCGA TA

GAM852 GAAGATGGTAACTGGGATCT 829 GATCCCATAT 3431 T ---- GTT--- TAACA
CGTTGGAAATAACACCCCCA TGTTTCCATC GAAGATGG AAC TGGGATCTC GGAAA C
TTTTCTTCATCAGGGATCCC TTT |||||||| ||| ||||||||| |||||
ATATTGTTTCCATCTTT TTTCTACC TTG ACCCTAGGG TCTTT C
T TTAT ACTACT TACCC

GAM853 AACTGAAGGACATCGCATGT 830 CATCGCATGT 3432 AA-- - TT AA TG GA
TTAAAATGTGGGAACATTGT TTAAAATGTG AACTG GGACA TCGCATG TAA TG G A
AGGTTATCATGTGATTGTTC GGAA ||||| ||||| ||||||| ||| || |
CATGTAGTT TTGAT CTTGT AGTGTAC ATT AT T /
GTAC T T- GG GT AC

GAM854 TGATGCGCAAGGCCATCCGA 831 TCTGGAGAAA 3433 T - A GCCA G ACC AAA
GGGCACCTGGAAAACAACCC CTGCTGCCTC TGA GC GCA G TCC AGGGC TGG A
AGCTCTGGAGAAACTGCTGC A ||| || ||| | ||| ||||| |||
CTCA ACT CG CGT C AGG TCTCG ACC C
C T - AAAG - --- CAA

GAM855 CCGGAACCTGCTCATCTGGA 832 AGAGTTGTTC 3434 GA - - A CAA G -- AAA
TCAAGAAGAATTTGCTAAAA ATCCAGGGAG CCG AC CTG CTC TCTGGAT GAA AATTT GCT
A
GAGCGGCCAGAGTTGTTCAT ACAG ||| || ||| ||| ||||||| ||| ||||| |||
CCAGGGAGACAGCGTGCGG GGC TG GAC GAG GGACCTA CTT TTGAG CGG G
G- C A - --- G AC CGA

GAM856 AAGATAGAGGCAGAACTGCA 833 TGTTCTGGAG 3435 GA----- AA G TG
GGACATCTGCAATGATGTTC CTGTTGGACA AAGATA GGCAG CT CAGGACATC C
TGGAGCTGTTGGACAAATAT AATA |||||| ||||| || |||||||||
CTT TTCTAT TTGTC GA GTCTTGTAG A
AAACAGG -- G TA

GAM857 GCGACCGGGACCATATGATA 834 TATTATGGAG 3436 A GA - AGA AATAGG
GACCAATAGGAGGAAGAGGG CTGGGCGT GCG CCGG CCATA TGAT CC A
GGTTATTATGGAGCTGGGCG ||| |||| ||||| |||| ||
T TGC GGTC GGTAT ATTG GG /
G GA T GG- AGAAGG

GAM858 ATGATGAACAGTATGCTTGG 835 AGGTTCCTTC 3437 G AA TT----- GT T
GAGTCTTCTGCTGGAGGTTC ACTGTGCGTG AT ATG CAGTATGC GGGA CTTC G
CTTCACTGTGCGTGCTGACC CTGA || ||| |||||||| |||| ||||
ATGGT TG TAC GTCGTGCG TCCT GAGG C

G CA TGTCACT TG T

GAM859 TTCTCAGTTCATAGGCTATC 836 TATCCCATCA 3438 A ATAG A C- ------ A GAGA
CCATCACCCTTTATTTGGAG CCCTTTATTT TTCTC GTTC GCT TC CATCAC CCTTT TTTG
A
AAGGAACGAGAGAAGGAAAT GGAG ||||| |||| ||| || |||||| ||||| ||||
TAGTGATGATGAGGCAGAGG AAGAG CAAG CGG AG GTAGTG GGAAG GAGC /
AACGAGAA - GAGA - TA ATTAAA A AAGG

GAM860 AGGAGGACGCGCTGCCCGGC 837 GAGAGTACTC 3439 ------ G- G CAGAAAA AA
CAGAAAACGGAGTTCAAGGT CTGCGTCTTC AGGAGGACGC GCT CCC GC CGGAGTTC
G
GGACTCCGACGACCAGTGGG CT |||||||||| ||| ||| || ||||||||
GAGAGTACTCCTGCGTCTTC TCCTTCTGCG TGA GGG TG GCCTCAGG /
CT TCCTCA GA G ACCAGCA TG

GAM861 GACGGCCATGCTGGTCTGCA 838 TACAAGATCA 3441 C ATGCTG G - A- C- -- - A
AGTCAGAGTCCGTGCCACCT CTGACTCTGA GA GGCC GTCT CA AGTCAG GTC GTGCCA
CCT GTC C
GTCACTGACTGGGCCTGGTA GGAC || |||| |||| || |||||| ||| |||||| ||| |||
CAAGATCACTGACTCTGAGG CT CCGG CAGG GT TCAGTC TAG CATGGT GGG CAG
/
ACAAGGCCCTC C AA---- A C AC AA CC T T

GAM862 CGGCTCCGAGAGCAGGTTCT 839 TACACATTGA 3440 - AGAG C A TC GCAG C
TCGTGAGTTCCTCGCAGGGC GAACCTGAAC CGGC TCCG CAGGTTCTT GTG GT CTC GG
C
CGGTCAGAGCTACACATTGA ATGG |||| |||| ||||||||| ||| || ||| ||
GAACCTGAACATGGAGGCCG GCCG AGGT GTCCAAGAG TAC CA GAG CT G
G ACAA T A TC A--- G

GAM863 TCTTGTGTTGAGACTTCGTG 840 TACACCACTC 3442 GAGA GT--- C AAAGGAT
GTGGTGCTAAGAAAAGGATA CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
GAAGAAGTCTTACACCACTC TAAG ||||||||| |||| ||||||| |||||
CCAAGAAGAATAAGCACAAG AGAACACGA GAAG TCACCAC ATTCT /
A ATAA AACCC - GAAGAAG

GAM864 ACCTGGTGCCTGAGCTCGAT 841 TGCCTGAGCT 3443 G CT A - CC ATCT
GGGGTCCGCATCTTCTCCCG CGATGGGGTC ACCT GTGC GAGCTCG TGGG GT GC T
CAGCACCCACGAGTTCCTGC CGCA |||| |||| ||||||| |||| || ||
ATGAGGT TGGA TACG CTTGAGC ACCC CG CG C
G TC - A A- CCCT

GAM865 GGCCGTGCAGCAGTGCATTG 842 GTGCATTGAG 3444 G C T A GAGG GGACA A A
AGGCTGCAGGACATGAGCAC GCTGCAGGAC GGCC TG AGCAG GC TT CTGCA TG GC C
CAGCCAGACATGCAGAAGAG ATGA |||| || ||||| || || ||||| || ||
TCTGCTCAGGGCC CCGG AC TCGTC TG AG GACGT AC CG C
G - - - AA-- ACAG- - A

GAM866 CGCTCGTCACCAGGACCCAA 843 TCAAGGGTCG 3445 - T- C G AA GA AAATTG
GGAACCAAAATTGCATCTGA TGTGTTTGAA CGCT CG CAC A GACCC G ACCA C
TGGTCTCAAGGGTCGTGTGT GTG |||| || ||| | ||||| | ||||
TTGAAGTG GTGA GT GTG T CTGGG C TGGT /
A TT - G AA TC AGTCTA

GAM867 GCATAATCGGTCACTCGTAT 844 TGAATGGACG 3446 AATC --- A GAA TATT TAT
AGAACAGTATTGTTTCTATA GGTTCAGGCC GCAT GGTC ACTCGT TA CAG GTTTC A
ATTTGAAGCTTTCTGAATGG TGAT |||| |||| |||||| || ||| |||||
ACGGGTTCAGGCCTGATGC CGTA CCGG TGGGCA GT GTC CGAAG A
GT-- ACT G AA- TTT- TTT

GAM868 GAAACAGACTGGGCCAATGT 845 TATCAAGGAA 3447 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM869 TCTTGTGTTGAGACTTCGTG 846 TACACCACTC 3448 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| ||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM870 ATGGTGAACAACCATGCTGG 847 GTTCAAGGGG 3449 ACAA G G-- A T TA
AGCCAAAGTGCTAACATGCC ATGGAAAGTC ATGGTGA CCAT CT GAGCCAA G GC A
TTGGTTCAAGGGGATGGAAA ACCG ||||||| |||| || ||||||| | ||
GTCACCGT TGCCACT GGTA GG CTTGGTT C CG C
GAAA G GAA - - TA

GAM871 GGCCAATTGAAACAAACAGT 848 TATTAGGGAT 3450 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /

CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM872 GAAGCGGGTGTTGGCCCTGC 849 GGGTGTTGGC 3452 T T CC CC- CC
CTGGGAAGCCGCCCTTCCTG CCTGCCTGGG GAAGCGGG GT GG CTG TGGGAAG G
ACCCAGCTCCACTCCTGCTT AAGC ||||||||| || || ||| |||||||
C CTTCGTCC CA CC GAC GTCCTTC /
T - TC CCA CC

GAM873 CCATGGACCGCCTGTACTTT 850 TATCACATCC 3451 A C T -- T GA ATGG G
GTGATGGAGTACGTGAATGG AGCAAGTCGG CC TGGACCG CTG ACTT TG GATG GTACGTGA
GG C
GGGCGACCTCATGTATCACA CCGG || ||||||| ||| |||| || |||| |||||||| ||
TCCAGCAAGTCGGCCGGTTC GG ACTTGGC GGC TGAA AC CTAC TATGTACT CC G
AAGG A C - CG - AC ---- A

GAM874 AGATAAAGATTGTGATGTGC 851 TGCCATGGCC 3453 TTGT T GT TAT TGTA
TGGTTGGTTATAAAGCTGTG ATCTTTTTCT AGATAAAGA GATG GCTG TGGT AAAGCTG T
TATCGGATCAGCTTTGCCAT TTGT ||||||||| |||| |||| |||| |||||||
GGCCATCTTTTTCTTTGTCT TCTGTTTCT CTAC CGGT ACCG TTTCGAC C
TTTT - -- --- TAGG

GAM875 TCTTGTGTTGAGACTTCGTG 852 TACACCACTC 3454 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM876 CCCTACCAGAGGAGGTACCG 853 TGTGAAGAGC 3456 - A -- A GGA--- TGACAGC
GGAGCGCCGTGACAGCGATA GGAGCCCATC CC CT CCAGAGGA GGT CCG GCGCCG G
CATACCGGTGTGAAGAGCGG CTTT || || |||||||| ||| ||| ||||||
AGCCCATCCTTTGGAGAGG GG GA GGTTTCCT CCG GGC TGTGGC A
A - AC A GAGAAG CATACAT

GAM877 GATCGTGGGGAACCTGGGTG 854 GGGAACCTGG 3457 - - TGAAGGCA A --- GG
AAGGCACCTTTGGCAAGGTG GTGAAGGCAC GATCGT GGGG AACCTGGG CCTTTGGCA
GGT GGT A
GTGGAGTGCTTGGACCATGC CTTT |||||| |||| |||||||| ||||||||| ||| |||
CAGAGGGAAGTCTCAGGTTG CTAGCA TCCC TTGGACTC GGAGACCGT CCA TCG
/
CCCTGACGATC G G TGAAG--- A GGT TG

GAM878 CCAGGTCTTGTAGCAGCGCC 855 CAGCAGCCGG 3455 G - T A A --- C GAGAA
TCCTCGAGAAGCCAACAGAG AGTGTGG CCA G TCT GT GC GCGC CT CTC G

CAGTAAGCGCAGCAGCCGGA ||| | ||| || || |||| || |||
GTGTGG GGT T AGG CG CG CGCG GA GAG C
G G C A A AAT C ACAAC

GAM879 TCTTGTGTTGAGACTTCGTG 856 TACACCACTC 3458 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM880 CGGGAGTCGAGCAGTGATTC 857 GAGCAGTGAT 3459 TC TGATTC --- T CA
TTGGGAGCTGCTCATTTTAG TCTTGGGAGC CGGGAG GAGCAG TTGGGA GC GCT T
CTGCCTGTCCCAGCTCTGCT TGCT |||||| |||||| |||||| || |||
CCCTCCCG GCCCTC CTCGTC GACCCT CG CGA T
C- TC---- GTC T TT

GAM881 AGCTTCCTGAGCAGCGAGGT 858 TTCCTGAGCA 3460 T TG AG GGT T TT
GTTGGTGGGGGACTTGATGT GCGAGGTGTT AGCT CC AGC CGA GTTGG GGGGGAC G
CCCCCTTCGACCAGTCGGGT GGTG |||| || ||| ||| ||||| |||||||
TTGGGGGCT TCGG GG TTG GCT CAGCT CCCCCTG /
- GT G- GAC T TA

GAM882 AGGAGGACGCGCTGCCCGGC 859 GAGAGTACTC 3461 ------ G- G CAGAAAA AA
CAGAAAACGGAGTTCAAGGT CTGCGTCTTC AGGAGGACGC GCT CCC GC CGGAGTTC
G
GGACTCCGACGACCAGTGGG CT |||||||||| ||| ||| || ||||||||
GAGAGTACTCCTGCGTCTTC TCCTTCTGCG TGA GGG TG GCCTCAGG /
CT TCCTCA GA G ACCAGCA TG

GAM883 GACGGCCATGCTGGTCTGCA 860 TACAAGATCA 3462 C ATGCTG G - A- C- -- - A
AGTCAGAGTCCGTGCCACCT CTGACTCTGA GA GGCC GTCT CA AGTCAG GTC GTGCCA
CCT GTC C
GTCACTGACTGGGCCTGGTA GGAC || |||| |||| || |||||| ||| |||||| ||| |||
CAAGATCACTGACTCTGAGG CT CCGG CAGG GT TCAGTC TAG CATGGT GGG CAG
/
ACAAGGCCCTC C AA---- A C AC AA CC T T

GAM884 GCATAATCGGTCACTCGTAT 861 TGAATGGACG 3463 AATC --- A GAA TATT TAT
AGAACAGTATTGTTTCTATA GGTTCAGGCC GCAT GGTC ACTCGT TA CAG GTTTC A
ATTTGAAGCTTTCTGAATGG TGAT |||| |||| |||||| || ||| |||||
ACGGGTTCAGGCCTGATGC CGTA CCGG TGGGCA GT GTC CGAAG A
GT-- ACT G AA- TTT- TTT

GAM885 TCTACAAAGTGCCGTCCACT 862 TCCAATCTGA 3464 A - - CACTG CT- C
GAGACTGAGGCCTTGGCTTC TGGGCATGTT TCT CAAA GTGCC GTC AGA GAGGC T
CAATCTGATGGGCATGTTTG TGAG ||| |||| ||||| ||| ||| |||||
AGA AGA GTTT TACGG TAG TCT CTTCG T
- G G ----- AAC G

GAM886 GGGGTGGGGGGTCTGTTTGG 863 TGTTTGGCAA 3465 - TCTG TG ACT T A A
CAACTGGGGTGAAGGGATTG CTGGGGTGAA GGGGT GGGGGG TT GCA GGGG GA GGG T
CCCTCCCCCTGCTGGGATCC GGGA ||||| |||||| || ||| |||| || |||
CCCCAACCCC CCCCA CCCCCC GG CGT CCCC CT CCC T
A TA-- GT --- - - G

GAM887 GGCTCCCAATGTTGACGTTG 864 CCAGGCCAAA 3466 CTCCC CG---- AG TGC
GCCAGGGCTTTGCAAACAAG AAGGCTCAAC GG AATGTTGA TTGGCC GGCTT A
CCAGGCCAAAAAGGCTCAAC ATTT || |||||||| |||||| |||||
ATTTACACC CC TTACAACT AACCGG CCGAA /
ACAT- CGGAAA A- CAA

GAM888 AAGATAGAGGCAGAACTGCA 865 TGTTCTGGAG 3467 GA----- AA G TG
GGACATCTGCAATGATGTTC CTGTTGGACA AAGATA GGCAG CT CAGGACATC C
TGGAGCTGTTGGACAAATAT AATA |||||| ||||| || |||||||||
CTT TTCTAT TTGTC GA GTCTTGTAG A
AAACAGG -- G TA

GAM889 GGCCAATTGAAACAAACAGT 866 TATTAGGGAT 3468 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAAAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - AAA

GAM890 CTAACTGTACTGTTTTTTCT 867 ATGTAACATG 3470 AACTG TT TCACG TG AGC
ATTCACGTGTGTCTAGCTGC GAAAACAGTA CT TACTGTTT TCTAT TG TCT T
AGGATGTAACATGGAAAACA ACTA || |||||||| ||||| || |||
GTAACTAAAG GA ATGACAAA AGGTA AT AGG /
AATCA -- CA--- GT ACG

GAM891 ATTGCTTTGCTAAAAATAAG 868 GACAGTATTT 3469 G CT- AGC AG G- AAA
CTCCCAGGGTGTTTCAAACT TTTATCAAAG ATT CTTTG AAAAATA TCCC GGT TTTC C
TAGAGAAGACCAAGGGACAG GAAT ||| ||||| ||||||| |||| ||| ||||
TATTTTTTATCAAAGGAAT TAA GAAAC TTTTTAT AGGG CCA AGAG /
G TAT GAC AA GA ATT

GAM892 TCTTGTGTTGAGACTTCGTG 869 TACACCACTC 3471 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG |||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM893 CAGGGACAGAAGGCAGCTCC 870 GGAGCAGGTG 3472 A- --- - C CA
CTTCCCCCAGGAAGGGCAAG CCTGGCTGTC CAGGGACAG AGGCA GCTCC CTT CCC G
AGGAGCAGGTGCCTGGCTGT CCTG |||||||||| ||||| ||||| ||| |||
CCCTG GTCCCTGTC TCCGT CGAGG GAA GGG G
GG GGA A C AA

GAM894 CCAGGAGCTACACACCTTCG 871 TCGCCCAGAT 3473 - - CA-- --- GA GCCA
AGGTGACCGGCCAGGAAACG CAAGGCTCAT CCAG GAG CTACA CCT TC GGTGACCG G
GTCGCCCAGATCAAGGCTCA GTAG |||| ||| ||||| ||| || |||||||||
TGTAGCCTCACTGG GGTC CTC GATGT GGA AG CCGCTGGC /
A C ACTC ACT AC AAAG

GAM895 GCATTGCCCGGAAGATCAAG 872 GCCCGGAAGA 3474 AGATCAAG G T- AG
TCGTGCTCCTGGCAGGCGCG TCAAGTCGTG GCATTGCCCGGA TCGT CTCC GGC G
CCCTGGAGGATGAGGCCACT CTCC |||||||||||| |||| |||| |||
CTGGGCAGTGC CGTGACGGGTCT AGTA GAGG CCG C
CACCGG-- G TC CG

GAM896 GTGATTTTACCTTTATTTCC 873 TGGGGTGGGA 3475 -- CTTTA AC AA AA T TCA
TTCACTTTAAGCCAATCATG GCAGAAGGAA GTGATTTT AC TTTCCTTC TTT GCC TCA
GAAATT C
AAATTTCACAGTGATTTCTG GGCT |||||||| || |||||||| ||| ||| ||| ||||||
GGGTGGGAGCAGAAGGAAGG TACTAAGA TG GAAGGAAG GAG TGG GGT CTTTAG
/
CTGTGTTAAGAATCAT AT TGTCG AC GG -- - TGA

GAM897 CCTCGAGTGGCTCCGAATGT 874 GTGCACAAGT 3476 GAGT CC--- GT AT G A CAG
TTGATCAGCAAGAAATTCAG TCCCATAAGC CCTC GGCT GAAT TTG CA CA GAAATT G
GTATTAATTTCTGGTGCACA CTAG |||| |||| |||| ||| || || ||||||
AGTTCCCATAAGCCTAGAGG GGAG CCGA CTTG AAC GT GT CTTTAA T
AT-- ATACC -- AC G - TTA

GAM898 TCCATTAAGCAGTTCATGGA 875 AAGCAGTTCA 3477 A TT - -- TCG
CATCTTCTCGCTACCGGAGA TGGACATCTT TCCATTA GCAG CA TGGA CATCTTC C
TGGCTCTGCTGTCCTGTGTG CTCG ||||||| |||| || |||| |||||||
GTGGA AGGTGGT TGTC GT GTCT GTAGAGG T
G CT C CG CCA

GAM899 CGCGGCTACTACAACCAGAG 876 CTCCAGTGGA 3478 C A AGA GA CC CT
CGAGGCCGGGTCTCACACCC TGTATGGCTG CGCGGCTA TACA CC GC GG GGGT C
TCCAGTGGATGTATGGCTGC CG |||||||| |||| || || || ||||
G GCGTCGGT ATGT GG TG CC CCCA /
- A --- A- T- CA

GAM900 GGCCAATTGAAACAAACAGT 877 TATTAGGGAT 3479 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM901 GCTTTTAACTTGGACTAGTG 878 AAAGAGCCAT 3481 TAAC T AA C- TGCA
TAACTCCTTCATGCAATAAA GCTGTCTAGT GCTTT TTGGAC AGTGT CTC TTCA A
CTGAAAAGAGCCATGCTGTC CTTG ||||| |||||| ||||| ||| ||||
TAGTCTTGAAGT TGAAG GATCTG TCGTA GAG AAGT T
TTCT - CC AA CAAA

GAM902 AAGCTTAAGTGAGGATTTCC 879 TCCCTTGTCA 3480 TAA A ---- - - T- T TT
TTGCAATGAGTAGAATTTCC CAGGTTTAAA AAGCT GTGAGG TTT CCT TG CAA GAG AGAA
T
CTTCTCTCCCTTGTCACAGG AACC ||||| |||||| ||| ||| || ||| ||| ||||
TTTAAAAACCTCACAGCTT TTCGA CACTCC AAA GGA AC GTT CTC TCTT C
--- A ATTT C T CC - CC

GAM903 AAGAGTAGGATGTCTGCTGA 880 TGAGAAAGAG 3482 G G GCTGAAG C-- T AA
AGTCATCCATCAAGTTGAAG ATGCTGCTCT AAGAGTAG AT TCT TCATC ATCAAGT G G
AAGCACTTGATACAGATGAG T |||||||| || ||| ||||| ||||||| |
AAAGAGATGCTGCTCTT TTCTCGTC TA AGA AGTAG TAGTTCA C A
G G AAG---- ACA - GA

GAM904 TCTTGTGTTGAGACTTCGTG 881 TACACCACTC 3483 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM905 TAAAGCTGATGATCCAACAA 882 AAGCTGATGA 3484 GA ACAA------- AGG CAG
TGGGGGAGGGCCCAGACAAG TCCAACAATG TAAAGCT TGATCCA TGGGGG GCC A
GCACGCTCCCAGCTCCTGAT GGGG ||||||| ||||||| |||||| |||
CCTGGATCGAGGCTTTG GTTTCGG GCTAGGT ACCCTC CGG /
A- CCTAGTCCTCG GCA AAC

GAM906 GTGGGCGACTAGGCCCATAG 883 GCCCATAGCA 3485 G TAG CATA- --- G A CTG
CAAGCGTGGCATCCTGACCC AGCGTGGCAT GT GGCGAC GCC GCAA GCGTG C TC A
TGAAGTACGCCCATTGCAGC CCTG || |||||| ||| |||| ||||| | ||
ATGGCATCGTCGCCGAC CA CCGCTG CGG CGTT CGCAT G AG C
G CTA TACGA ACC - A TCC

GAM907 AAATGCAGGTTTACAAAGAT 884 TACCATTGGC 3486 C A-- G AG GG ATAAA-- ATA
GAGCAGGTGGTGGTGATAAA TGGTCTTACC AAATG AGGTTTAC AAGAT AGC GTGGT TG
GG A
GGATAAATACCCAAAGGCCC GTGG ||||| |||||||| ||||| ||| ||||| || ||
GTTACCATTGGCTGGTCTTA TTTAC TCCAGGTG TTCTG TCG TACCA GC CC A
CCGTGGACCTCCATTT C CCA G GT TT CCGGAAA CAT

GAM908 GGCCAATTGAAACAAACAGT 885 TATTAGGGAT 3487 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM909 CTTCTTCAGTGAGACGGGCG 886 TTTGTAGACT 3488 T GAC- CG ----- T C
CTGGCAAGCACGTGCCCCGG TGGAACCCAC CTTC TCAGTGA GGG CTG GCAAGCACG
GCC C
GCTGTGTTTGTAGACTTGGA AGTC |||| ||||||| ||| ||| ||||||||| |||
ACCCACAGTCATTGATGAAG GAAG AGTTACT CCC GGT TGTTTGTGT CGG /
T GACA AA TCAGA - G

GAM910 GGAGATCATTGACCTTGTGT 887 CACCGGTCTT 3489 TT - TGTT AATTC AA C
TGGACCGAATTCGCAAGCTG CAGGGCTTCT GGAGATCA GA CCTTG GGACCG GC
GCTGG T
GCTGACCAGTGCACCGGTCT TGGT |||||||| || ||||| |||||| || |||||
TCAGGGCTTCTTGGTTTTC CTTTTGGT TT GGGAC TCTGGC CG TGACC G
TC C T--- CA--- -- A

GAM911 ATACAGGATGATAGTTCGTG 888 TCAGATTGCT 3490 A ATGAT TC G CACAG
TGACAAACACAGATATCATT TATGCCCGTA ATAC GG AGT GT TGACAAA A
TGTCAGATTGCTTATGCCCG T |||| || ||| || |||||||
TAT TATG CC TCG TA ACTGTTT /
C GTAT- T- G ACTAT

GAM912 ATCTATGAAGGCCAAGTGGA 889 TGGTCAGCCA 3491 AA CAA GA - GA A AG
GGTGACTGGTGATGAATACA GGTGCCTTCA ATCTATG GGC GTGGAGGT CTGG TGAT AT
CAATGT A

ATGTAGAAAGCATTGATGGT CCTG ||||||| ||| |||||||| |||| |||| || ||||||
CAGCCAGGTGCCTTCACCTG TAGGTAT TCG CACTTCCG GACC ACTG TA GTTACG /
CTATATGGAT A- TC- TG G G- - AA

GAM913 GGCCAATTGAAACAAACAGT 890 TATTAGGGAT 3492 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || ||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM914 AGAAACAAAAGCAGGTGCTG 891 TAGCATGCCT 3493 CAA- C -- TCA--- AA
AATCATGAAAACCTCAATTA CTTAATTTTT AGAAA AAG AGGT GCTGAA TGA A
TTTTTAGCATGCCTCTTAAT CT ||||| ||| |||| |||||| |||
TTTTCT TCTTT TTC TCCG CGATTT ACT /
TTAA - TA TTATTA CC

GAM915 AAGATAGAGGCAGAACTGCA 892 TGTTCTGGAG 3494 GA----- AA G TG
GGACATCTGCAATGATGTTC CTGTTGGACA AAGATA GGCAG CT CAGGACATC C
TGGAGCTGTTGGACAAATAT AATA |||||| ||||| || |||||||||
CTT TTCTAT TTGTC GA GTCTTGTAG A
AAACAGG -- G TA

GAM916 TCTTGTGTTGAGACTTCGTG 893 TACACCACTC 3495 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM917 GGAGGGGAGGCCGGATGTGA 894 TGAGTGGAGC 3497 GG G GAG - TT TTTCT
C TT
GTGGAGCGGCCATTTCCTGT GGCCATTTCC GGA GGAGGCCG ATGT TGG AGCGGCCAT
CCTG CTG AG T
TTCTCTGCAGTTTTCCTCAG TGTT ||| |||||||| |||| ||| ||||||||| |||| ||| ||
CTTTGGGTGGTGGCCGCTGC CCT CCTTCGGC TACG GCC TCGCCGGTG GGGT
GAC TC /
CGGGCATCGGCTTCCAGTCC GA - G-- G GT TTC-- - CT

GAM918 AAGTGTGTGGTGGTGGGAGA 895 TACACAACCA 3496 - G GGA G GCT A
CGGAGCTGTAGGTAAAACTT ATGCATTT AAGTGTGT GGT GTG GAC GA GTAGGTAA A
GCCTACTGATCAGTTACACA |||||||| ||| ||| ||| || ||||||||
ACCAATGCATTT TTTACGTA CCA CAC TTG CT CATCCGTT /
A A A-- A AGT C

GAM919 TCTTGTGTTGAGACTTCGTG 896 TACACCACTC 3498 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM920 GAAACAGACTGGGCCAATGT 897 TATCAAGGAA 3499 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM921 TGTGCCCACAGGTTGAGAAC 898 TGGAAAGCAG 3500 - TG GAA G GCAGA GA
TATGTGGCAGATATCGAGGT GTAGAGTTGG TGTG CCCACAGGT A CTAT TG TATC G
GGATGGAAAGCAGGTAGAGT CTTG |||| ||||||||| | |||| || ||||
TGGCTTGTGGGACACA ACAC GGGTGTTCG T GATG AC GTAG G
A GT GA- G GAAAG GT

GAM922 AGAAACAAAAGCAGGTGCTG 899 TAGCATGCCT 3501 CAA- C -- TCA--- AA
AATCATGAAAACCTCAATTA CTTAATTTTT AGAAA AAG AGGT GCTGAA TGA A
TTTTTAGCATGCCTCTTAAT CT ||||| ||| |||| |||||| |||
TTTTCT TCTTT TTC TCCG CGATTT ACT /
TTAA - TA TTATTA CC

GAM923 GGCCAATTGAAACAAACAGT 900 TATTAGGGAT 3502 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM924 GGCCAATTGAAACAAACAGT 901 TATTAGGGAT 3503 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM925 GGGGCTGTGGTTACCTCTCT 902 GTGAAGGTTC 3504 - T- CTC T A C
CTTCATGACACCCCTGTGAC GCCTGCAGTC GGGGCTGT GGT ACCT TC TCATG CAC C

GTGGTGAAGGTTCGCCTGCA TC |||||||| ||| |||| || ||||| |||
GTCTC CTCTGACG CCG TGGA AG GGTGC GTG C
T CT --- T A T

GAM926 GTGGAGCGAGCCAAATGAAG 903 AAAGCAGTTC 3505 G- AG AAATGA A ATCAAG GT
AAGAGCTGATCAAGTTCATG TCTGAGGAGC GTGGA CG CC AGA GAGCTG TTCAT G
TGTGGTGAAAAGCAGTTCTC GAAT ||||| || || ||| |||||| |||||
TGAGGAGCGAATCCGC CGCCT GC GG TCT CTTGAC AAGTG /
AA GA AG---- - GAA--- GT

GAM927 TGGTGCTGACTATCCAGTTG 904 CTGCCTCCAG 3506 CT- T- GG C GA - T
GGA T
ATGGGCTGCCAGATCTGGGG GTGACAGCAA TGGTG GACTA CCAGTTGAT GCTG CA
TCTGG GGCA GCCCA CC C
CATGCCCAGGACCTCATGGA TCAG ||||| ||||| |||||||||| |||| || ||||| |||| ||||| ||
TGGGCTGCCTCCAGGTGACA GTCAT TTGGT GGTCGACTA CGAC GT GGACC CCGT
CGGGT GG A
GCAATCAGCTGGCCTGGTTT AGT CC A- A -- T - A-- T
GATACTG

GAM928 GGGTATGGAATCTGGCGGCA 905 TGACGTGGAC 3507 - AA G- CA- AG C ACTC
TCCACGAGACACCTTCAACT ATCCGCAAAG GG GTATGG TCT GCGG TCCACG ACAC TTCA
C
CCATCATGAAGTGTGACGTG ACCG || |||||| ||| |||| |||||| |||| ||||
GACATCCGCAAAGACCGTAC CC CATGCC AGA CGCC AGGTGC TGTG AAGT /
GCC G -- AA TAC AG - ACTA

GAM929 GAAACAGACTGGGCCAATGT 906 TATCAAGGAA 3508 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM930 GACCACCATATGTTCTTTGA 907 TGGGATAGGA 3509 - A TAT TTGA TTA CA
CTATAATTATGGACAATATT TTGGCGGCTC GA CC CCA GTTCT CTATAA TGGA A
TCACTTTGTGGGATAGGATT || || ||| ||||| |||||| ||||
GGCGGCTC CT GG GGT TAGGA GGTGTT ACTT T
C C --- TAG- TC- TA

GAM931 GCGAGGCTGAACGCCTGACG 908 AGGCTGAACG 3510 GA- A----- C AA CATCG
TCAAGGCGACATCGCCAAAC CCTGACGTCA GC GGCTG ACGCCTGA GTC GGCGA C
CTCGCCCAGATTCAGGCGTG AGGC || ||||| |||||||| ||| |||||

TAAACCAGCCGGAGC CG CCGAC TGCGGACT TAG CCGCT C
AGG CAAATG - AC CCAAA

GAM932 GTAGAGCTTTATGCTGAAAA 909 GAGCTTTATG 3512 - TA GAAAA - T A
GGTGGCCACTAGAGGTCTGT CTGAAAAGGT GTAGAG CTT TGCT GGTGGC CAC AG G
GTGCCATTGCCCAGGCAGAG GGCC ||||||| ||| |||| |||||| ||| ||
TCTCTGC CGTCTC GAG ACGG TTACCG GTG TC G
T -- ACCCG T - T

GAM933 CTCCGAGGACAGAGGGCTAA 910 TGGCCTGATG 3511 A--- - GA AAA TGA
AATCCATTGAAGTTTGTGGA ATCCACAGCG CTCCG GGA CA GGGCT ATCCAT A
TGGCCTGATGATCCACAGCG GAG ||||| ||| || ||||| ||||||
GAG GAGGC CCT GT TCCGG TAGGTG G
GACA A AG --- TTT

GAM934 GGAGTTGAAGCCAAACAGCC 911 TTGAAGCCAA 3514 AG AA------ CAA - - A
AAATTCTGCCATTAGGAAGT ACAGCCAAAT GG TTGAAGCCA CAGC ATTCT GC CATT G
GTGTAAGGGTCCAGCTGATC TCTG || ||||||||| |||| ||||| || ||||
AAGAATGGCTTTAAAATC CT AATTTCGGT GTCG TGGGA TG GTGA G
AA AAGAACTA ACC A T A

GAM935 GCCTTTGTACCCAATGACGG 912 ACCCAATGAC 3513 AC TGA T T GAGG
TTGCTTGAACTTTATTGAGG GGTTGCTTGA GCCTTTGT CCAA CGGT GCT GAACTTTATT A
AAAATGATGAAGTTCTGGTT ACTT |||||||| |||| |||| ||| ||||||||||
GCTGGATTTGGTCGCAAAGG TGGAAACG GGTT GTCG TGG CTTGAAGTAG /
T CT TAG T T TAAA

GAM936 TCACTGATGTCTCCTTAGGG 913 CAGGACCAAG 3515 GA --- A GA C A
ATCTCTTCAAATGAGCAGGA GATCAGACAA TCACT TGTC TCCTT GG TCT TTC A
CCAAGGATCAGACAAAGGTG AGGT ||||| |||| ||||| || ||| |||
A AGTGG ACAG AGGAA CC GGA GAG A
AA ACT - A- C T

GAM937 GCTCACAATCTCTGTCATCG 914 TGGCATGAAG 3516 ACAA - G -- AT CC C
GCTGATCCAACCGTTCCTTG AAGGAATAGA GCTC TCT CT TCAT CGGCTG CCAA GTTC T
AGCTTGGCAGCTGGCATGAA GC |||| ||| || |||| |||||| |||| ||||
GAAGGAATAGAGC CGAG GGA GA AGTA GTCGAC GGTT CGAG /
ATAA A - CG -- -- T

GAM938 TCTACAAAGTGCCGTCCACT 915 TCCAATCTGA 3517 A - - CACTG CT- C
GAGACTGAGGCCTTGGCTTC TGGGCATGTT TCT CAAA GTGCC GTC AGA GAGGC T
CAATCTGATGGGCATGTTTG TGAG ||| |||| ||||| ||| ||| |||||
AGA AGA GTTT TACGG TAG TCT CTTCG T

- G G ----- AAC G

GAM939 TGAAGTCACACATGAAAGAA 916 TTGCTCTGCT 3518 TCAC A CAT T CT T
GCCATGATCAAGCTTGGTTT TCTTCATGTA TGAAG ACATGAA GAAGC GA CAAG TGG T
CCACTTGCTCTGCTTCTTCA TCTT ||||| ||||||| ||||| || |||| |||
TGTATCTTTA ATTTC TGTACTT CTTCG CT GTTC ACC /
TA-- - T-- C -- T

GAM940 ACATCAAGACAATGTATACT 917 TAGCTGTAGT 3519 - C A TTCAAA CCATAC
ATTTCAAATATATCCATACA ACATGTTTTC ACATCAA GA AATGT TACTAT TATAT A
TAATCAAATATAGCTGTAGT ATTG ||||||| || ||||| |||||| |||||
ACATGTTTTCATTGGTGT TGTGGTT CT TTGTA ATGATG ATATA T
A T C TCG--- AACTAA

GAM941 TCGAGACCATCGCCAATGAG 918 TATCATTGGG 3520 ACC--- G - CGACA T
TACAGCGACAGGTGTACCCC ATCAAGAACT TCGAG ATC CCAATGA GTACAG GG G
GGCCTGTATATCATTGGGAT CGA ||||| ||| ||||||| |||||| ||
CAAGAACTCGA AGCTC TAG GGTTACT TATGTC CC T
AAGAAC - A CGGCC A

GAM942 GCATTGGTGATCTCTGCTAC 919 TCAGCAGAGA 3521 ATTG G AC GTTC
AGAAAGCTGTTCATGGTAGG TGACAGGC GC GT ATCTCTGCT AGAAAGCT A
CTTTCTCAGCAGAGATGACA || || ||||||||| ||||||||
GGC CG CA TAGAGACGA TCTTTCGG T
GA-- G C- ATGG

GAM943 TGCCAACCTTGAAGCCAGTG 920 TTGAAGCCAG 3522 A - TG - G - ATCC
GGGCACCAATCCACAAACTG TGGGGCACCA TGCCA CC T AAGCCA GTG GGCA CCA A
GATGCTGCGCTTGGTTTTGA ATCC ||||| || | |||||| ||| |||| |||
TGGTGGCA ACGGT GG A TTTGGT CGC TCGT GGT C
- T GT T G A CAAA

GAM944 ACTGTGATTCATGGTATCAA 921 TACCCTTGGA 3523 -- A--- ACA TACT
GACAGTGTCTACTATATTGA AGAATTATGA ACTGT GATTCATGGT TCAAG GTGTC A
TACCCTTGGAAGAATTATGA ATTT ||||| |||||||||| ||||| |||||
ATTTAACAGT TGACA TTAAGTATTA GGTTC CATAG /
AT AGAA C-- TTAT

GAM945 AGTCCGCACCATGCTGGTTA 922 AGGAAGATCC 3524 C--- CA GTTAG TCCA A A AC
GGAAGATCCAGGAAGAGTCA AGGAAGAGTC AGTC GCAC TGCTG GAAGA GG AG GTC
T
CTGAGGACCTACCTCTTCAC ACTG |||| |||| ||||| ||||| || || |||
CTACAGCAGTGTCTATGACT TCAG TGTG ACGAC CTTCT CC TC CAG G

TATC -- ATCCA ---- A - GA

GAM946 GAGATGGGGTTTCACCATGT 923 TTTCACCATG 3525 GTT- A TT C C-- T
TGGCCAGGCTCGTCTCGAAC TTGGCCAGGC GAGATGGG TCACC TG GG CAGG TCG C
TCCTGACTTCAGGTGATCCA TCGT |||||||| ||||| || || |||| |||
CCCATCTC CTCTACCC AGTGG AC TC GTCC AGC /
ACCT - T- A TCA T

GAM947 TCTACAAAGTGCCGTCCACT 924 TCCAATCTGA 3526 A - - CACTG CT- C
GAGACTGAGGCCTTGGCTTC TGGGCATGTT TCT CAAA GTGCC GTC AGA GAGGC T
CAATCTGATGGGCATGTTTG TGAG ||| |||| ||||| ||| ||| |||||
AGA AGA GTTT TACGG TAG TCT CTTCG T
- G G ----- AAC G

GAM948 CTGTAATCCCAGCTACTCGG 925 TTGAACCTGA 3527 - A A AGGCTG AA
GAGGCTGAGGCAGAAGAATT GAGGCGGAGG CTGTAATC CC GCT CTCGGG AGGCAG G
GCTTGAACCTGAGAGGCGGA TTAC |||||||| || ||| |||||| ||||||
GGTTACAG GACATTGG GG CGG GAGTCC TTCGTT /
A - A AAG--- AA

GAM949 TTTCCTGCTTGTATTGGCGT 926 CAGCAACCCA 3528 TAT C ATATC CT
ATATCGTTCCTCCTGAGCAG CAGTAGGTAG TTTCCTGCTTG TGG GT GTTC C
CAACCCACAGTAGGTAGGAA GAAA |||||||||| ||| || ||||
A AAAGGATGGAT ACC CA CGAG /
GAC - ACGA- TC

GAM950 CGGCTCCGAGAGCAGGTTCT 927 TACACATTGA 3530 - AGAG C A TC ACAG C
TCGTGAGTTCCTCACAGGGC GAACCTGAAC CGGC TCCG CAGGTTCTT GTG GT CTC GG C
CGGTCAGAGCTACACATTGA ATGG |||| |||| ||||||||| ||| || ||| ||
GAACCTGAACATGGAGGCCG GCCG AGGT GTCCAAGAG TAC CA GAG CT G
G ACAA T A TC A--- G

GAM951 AGGAGGACGCGCTGCCCGGC 928 GAGAGTACTC 3529 ------ G- G CAGAAAA AA
CAGAAAACGGAGTTCAAGGT CTGCGTCTTC AGGAGGACGC GCT CCC GC CGGAGTTC
G
GGACTCCGACGACCAGTGGG CT |||||||||| ||| ||| || ||||||||
GAGAGTACTCCTGCGTCTTC TCCTTCTGCG TGA GGG TG GCCTCAGG /
CT TCCTCA GA G ACCAGCA TG

GAM952 GAAACAGACTGGGCCAATGT 929 TATCAAGGAA 3531 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G

GCACCACCGATGTCCAAAGG GATG ||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM953 TGGGGCTCATTTGCAGGGGG 930 GCTCATTTGC 3533 CT T A CAAA TCA
GAGCCAAAAGGGTCATCATC AGGGGGGAGC TGGGG CATT GCAGGGGGG GC AGGG T
TCTGCCCCCTCTGCTGATGC CAAA ||||| |||| |||||||| || ||||
CCCCA ACCCC GTAG CGTCTCCCC CG TCTC /
C- T - ---- TAC

GAM954 CATGACCACAGTCCATGCCA 931 ATGGCCCCTC 3532 A CCATG ATCACT- - - A
TCACTGCCACCCAGAAGACT CGGGAAACTG CATG CCACAGT CC GCCA CC CAG A
GTGGATGGCCCCTCCGGGAA TGGC |||| ||||||| || |||| || |||
ACTGTGGCGTG GTGC GGTGTCA GG CGGT GG GTC G
- AA--- GCCTCCC A T A

GAM955 CCAATCCCAGCCAAAGAATG 932 ATGGAGCAGT 3534 T- A- GAAT C A - AT
CTCCTGTTACCTTCATTGTG AGTCAAGTTT CCAA CCC GCCAAA GCT CTGTT CC TTC T
GATGGAGCAGTAGTCAAGTT GGCC |||| ||| |||||| ||| ||||| || |||
TGGCCAGGGTTTTGG GGTT GGG CGGTTT TGA GACGA GG AGG /
TT AC GAAC T - T TG

GAM956 CTTCTTCAGTGAGACGGGCG 933 TTTGTAGACT 3535 T GAC- CG ----- T C
CTGGCAAGCACGTGCCCCGG TGGAACCCAC CTTC TCAGTGA GGG CTG GCAAGCACG
GCC C
GCTGTGTTTGTAGACTTGGA AGTC |||| ||||||| ||| ||| ||||||||| |||
ACCCACAGTCATTGATGAAG GAAG AGTTACT CCC GGT TGTTTGTGT CGG /
T GACA AA TCAGA - G

GAM957 CACCTTTACGGCCAAACCGT 934 TGTGGATATA 3536 TT C CC C-- C--- G
CCACCTCGACCGATTCTGTG GTTTTCCCTG CACC TA GG AAAC GTCCAC TC A
GATATAGTTTTCCCTGTTGG TTGG |||| || || |||| |||||| ||
TG GTGG GT CC TTTG TAGGTG AG C
TT - CT ATA TCTT C

GAM958 TTGGTCCATATCTCCATGCA 935 TCCATATCTC 3537 TC ATCTCC- G- - ACA
TGGCGGATACAGTGAAATCT CATGCATGGC TTGG CAT ATGCATG CG GAT G
CGAGCATGCATCTTCTCGGT GGAT |||| ||| ||||||| || |||
GAGCCAG GACC GTG TACGTAC GC CTA T
GA GCTCTTC GA T AAG

GAM959 GGCCAATTGAAACAAACAGT 936 TATTAGGGAT 3538 C T ACAAACAG G GTT T A
GAT

TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM960 GAAACAGACTGGGCCAATGT 937 TATCAAGGAA 3539 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM961 CTGTGGATAATGGTACTTCA 938 GTCCCAGCTG 3540 TG A A-- C CAAGC AG
GCCTGGGGCAAGCCCATAGA GGGAGAACCA CTG G TAATGGT CTTCAGC TGGGG CCAT
A
CAGTGGTCCCAGCTGGGGAG TTAC ||| | ||||||| ||||||| ||||| ||||
AACCATTACTGCAG GAC C ATTACCA GGGGTCG ACCCT GGTG /
GT - AGA - ----- AC

GAM962 AGGTGGGTGGATCGCCTGAG 939 CCTGGCCAAC 3541 - GGA - A- A-- C
GTCAGGAGTTCAAGACCAGC ATGGTGAAAC AGGTGG GT TCGCC TG GGTCAGG GTT A
CTGGCCAACATGGTGAAACT TCCA |||||| || ||||| || ||||||| |||
CCATCT TCTACC CA AGTGG AC CCGGTCC CAG /
T A-- T AA GAC A

GAM963 GGCCAATTGAAACAAACAGT 940 TATTAGGGAT 3542 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM964 TGGCGCTGACTGTGGGAGGG 941 GCCCTCTACA 3543 C A---- - ACC TAC
ACCATCTACTGCCTGATCGC TGGCTTCGCA TGG GCTG CTGTG GGAGGG ATC T
CCTCTACATGGCTTCGCAGC GCCC ||| |||| ||||| |||||| |||
CCA ACC CGAC GGTAC TCTCCC TAG G
- GCTTC A GC- TCC

GAM965 CACCTTTACGGCCAAACCGT 942 TGTGGATATA 3544 TT C CC C-- C--- G
CCACCTCGACCGATTCTGTG GTTTTCCCTG CACC TA GG AAAC GTCCAC TC A
GATATAGTTTTCCCTGTTGG TTGG |||| || || |||| |||||| ||
TG GTGG GT CC TTTG TAGGTG AG C

TT - CT ATA TCTT C

GAM966 TTGGTCCATATCTCCATGCA 943 TCCATATCTC 3545 TC ATCTCC- G- - ACA
TGGCGGATACAGTGAAATCT CATGCATGGC TTGG CAT ATGCATG CG GAT G
CGAGCATGCATCTTCTCGGT GGAT |||| ||| ||||||| || |||
GAGCCAG GACC GTG TACGTAC GC CTA T
GA GCTCTTC GA T AAG

GAM967 TCACAGACAACAGCCTGGTG 944 CTGCTTCCCG 3546 C AC- - T- - GG
GCAGCGGGCCACGACTGCTT GTGCTGTTCA TCA AG AACAGC CTGG GGCAG CG C
CCCGGTGCTGTTCACCTATG CCTA ||| || |||||| |||| ||||| ||
A AGT TC TTGTCG GGCC TCGTC GC /
A CAC T CT A AC

GAM968 CCCGCCAGGCCTCCATAGAG 945 TGGCCAGTAC 3547 A C CATAGA - - A
CTGCCCAGCATGGCTGTGGC CAAGAGTCGG CCCGCC GGC TC GCTG CC CAGC T
CAGTACCAAGAGTCGGTGGG TGGG |||||| ||| || |||| || ||||
GGGTGG CTG AG TGAC GG GTCG /
- - AACCA- C T G

GAM969 TTGACATTGTAGGCTGGCGC 946 TTCATGCCCT 3549 AT CT CT C GTT
TGGCATCAGGTTCACACTCA CTTGCATCGT TTGAC TGTAGG GGCG GGCAT AG C
TGTTCATGCCCTCTTGCATC TAA ||||| |||||| |||| ||||| ||
GTTAA AATTG ACGTTC CCGT TTGTA TC /
CT TC AC C ACA

GAM970 TAGCCGTGATGTCCGGGGGC 947 TCTGCATTGG 3548 A G - C ATG G
CGTGTACATCATGTTACCGT CTGCTGGGCA TAGCCGTG TGTCCGG GGCCG TGTA ATC
TTACC T
GGGGTGGGGTCTGCATTGGC TATG |||||||| ||||||| ||||| |||| ||| |||||
TGCTGGGCATATGGCTG GTCGGTAT ACGGGTC TCGGT ACGT TGG GGTGG G
- G T C --- G

GAM971 GCCGGGTCACCTTCGAGGCG 948 ACCGTGGTGA 3550 CA AG ACGAGAA GA
GACGAGAATGAGAACATCAC AGGGCATCCG GCCGGGT CCTTCG GCGG TGA A
CGTGGTGAAGGGCATCCGGC GC ||||||| |||||| |||| |||
CGGCCTA GGAAGT TGCC ACT /
CG GG ------- AC

GAM972 ACTGCTTCAAGGACATCGTG 949 TTTGCAGACT 3551 TTCA ACA AACA TGAT A CA
AACATGCTGATGCACCATGA ATGAAGCCTA ACTGC AGG TCGTG TGC GCACC TGA G
CAGGTTCAAGGTGTTTGCAG CATG ||||| ||| ||||| ||| ||||| |||
ACTATGAAGCCTACATGCAG TGACG TCC AGTAT ACG TGTGG ACT /

T TACA GA- CAG- TT-- A TG

GAM973 GAGTGGACCAAGAAGGTCAT 950 TCTCCAGTGA 3552 G A AAGAA CA- ATC G
CAGGAACATCGCCTGCTCGG CCGGACCATC GA TGG CC GGTCAT GGAAC GCCT C
GCAAGTTCTCCAGTGACCGG || ||| || |||||| ||||| ||||
ACCATC CT ACC GG CCAGTG TCTTG CGGG T
- A ----- ACC AA- C

GAM974 GATGGGTGTAATGCCTGAGA 951 TGAGATTGCA 3554 GTAAT A TGCACA C T A
ATGG
TTGCACAAGCTGTGGAAGAG CAAGCTGTGG GATGGGT GCCTG GAT AG TG GGA GAG
A
ATGGATTGGCTCCTCCCAAC AAGA ||||||| ||||| ||| || || ||| |||
TGATATCCAGGCTGAATCTA CTATCTA CGGAC CTA TC AC CCT CTC /
TC AGT-- - TAG--- A - C GGTT

GAM975 CTGGTGCTTCAGTGCTGAAC 952 TTTGCAATTG 3553 GG AG GA- AT-- AGA- A TA A
AT
AAATGGCAGATGAACCCATA GGTCAGATGG CT TGCTTC TGCT ACAA GGC TGA CCCA
TG CAGAGG C
TGACAGAGGATCTGCTTTTG TCTT || |||||| |||| |||| ||| ||| |||| || ||||||
CAATTGGGTCAGATGGTCTT GG ATGAAG ACGA TGTT CTG ACT GGGT AC
GTTTTC /
TGTTGTCAAAGCAGAGAAGT AA AG AAC GTTT GTAG - TA - GT
AAAGG

GAM976 TCTACCATGCAGGCCTTTTT 953 TTGGATTTGG 3555 TGC TT- TG CTAG A
GGACCTAGGTACTGACAAGT CTTTGGTGGA TCTACCA AGGCC TT GAC GT C
TTGGATTTGGCTTTGGTGGA ||||||| ||||| || ||| ||
AGGTGGT TTCGG AG TTG CA T
--- TTT GT AA-- G

GAM977 GGCCCAGGGATCGGCAGGGC 954 TTCCCATGCC 3556 G - G- - GCT GA A
TGCTGGCAGAGGAATCCCAG CCAGGCTCCT GGCCCAG GA TC GCAGG GCT GGCA
GGAATCCC G
CTGGGGTTCCCATGCCCCAG GCAG ||||||| || || ||||| ||| |||| ||||||||
GCTCCTGCAGGACTTGCTGG CCGGGTC TT AG CGTCC CGG CCGT CCTTGGGG C
GCC G C GA T ACC AC T

GAM978 GGCTCCCAATGTTGACGTTG 955 CCAGGCCAAA 3557 CTCCC CG---- AG CT C
GCCAGGGCCTTTGCAAACAA AAAGCTCAAC GG AATGTTGA TTGGCC GGC TTG A
GCCAGGCCAAAAAAGCTCAA ATTT || |||||||| |||||| ||| |||
CATTTACACC CC TTACAACT AACCGG CCG AAC A
ACAT- CGAAAA A- -- A

GAM979 GTTGTTATTGGTGCAGGAGT 956 TTTGGCAAAG 3558 TG-- TG AG AATAGG A G
AATAGGTGTAGAACTGGGTT ACTTGGTGCA GTTGTTAT G C GAGT TGT GAACTG G
CAGTTTGGCAAAGACTTGGT GATG |||||||| | | |||| ||| ||||||
GCAGATGTGACAGC CGACAGTG C G TTCA ACG TTTGAC T
TAGA GT G- GAA--- G T

GAM980 CTCAGTGTGGGCCATCCATC 957 TAGCAAAGGT 3559 GC C TCTGA- T - GA GA T
TGAGGTTGATGAGATATTTG GCATCTGTCA CTCAGTGTGG CAT CA GG TGAT GA TATTT TGCTATA C
ATGCTATATCATATAGCAAA TCCG |||||||||| ||| || || |||| || ||||| ||||||| GGTGCATCTGTCATCCGAAT GGGTTACATC GTA GT CC ACTG CT GTGGA ACGATAT /
GCTGCATGACTACATTGGG A- C CGTAAG T T AC A- A

GAM981 CTGTGATGAATACCTGGACC 958 ATTTATGTGG 3560 G GAA- GA------ AAC ATT
AAACAAATGGGATTTCCCCT AAGCTGAACA CTGT AT TACCTG CCA AAATGGG T
CATTTATGTGGAAGCTGAAC GGTA |||| || |||||| ||| |||||||
AGGTAGAAGATGACAG GACA TA ATGGAC GGT TTTACTC /
G GAAG AAGTCGAA GTA CCC

GAM982 GGAGAAGGGGGAGATGTTGA 959 TCGCTGGCTC 3561 G - AT- T - TC
GCATGTTCAGCAGCGTGGCT CCACTTTGTC GGA AAGG GGGAG GT GAGC ATGT A
TCGCTGGCTCCCACTTTGTC T ||| |||| ||||| || |||| ||||
T TCT TTTC CCCTC CG TTCG TGCG G
G A GGT C G AC

GAM983 GCTGGTTTCCTGGCCGAGGC 960 ATCAGCTCCG 3562 TTT G - CTGAA T
GGAGCTGCTGAACCTGAGGA ACTTTGGACG GCTGG CCTG CCGAGG CGGAGCTG CC G
AGATCAGCTCCGACTTTGGA GGCA ||||| |||| |||||| |||||||| ||
CGGGCACCCGGT TGGCC GGGC GGTTTC GCCTCGAC GG /
CAC A A TAGAA A

GAM984 TTCTTTTTGGTTTTGACATC 961 TTTTTGGTTT 3563 TT A TTC A
ATTCATTTCCACCTGGGAAT TGACATCATT TTCTTTTTGGT TG CATCA ATTTCC C
TTCTGGTGCCATGCCAGAAA CATT |||||||||| || ||||| ||||||
GAA AAGAAAGACCG AC GTGGT TAAGGG C
T- C CTT T

GAM985 CTAGCCAAAATGTACAAGAC 962 TCAGAACTCA 3564 - AAA ACAAGA - TCA TT AT
CACACCGGATGTCATCTTTG TTTGGTGGTG CTA GCCA TGT CCAC ACCGGATG TCT GT T
TATTTGGATTCAGAACTCAT GCAA ||| |||| ||| |||| |||||||| ||| ||

TTGGTGGTGGCAAGACAACT GAT CGGT ACA GGTG TGGTTTAC AGA TA T
GGCTTAG T CA- GAAC-- G TCA CT GG

GAM986 TGTTGGTGCTGGCAAAAAGC 963 TTGGTGCTGG 3565 -- G A - A GA AAA GCT A
CGAAGGAGTAAAGGTGCTGC CAAAAAGCCG TGTTGGTG CT GC AAAAG CCG AG GT GGT
GCA T
AATGATGTTAGCTGTGGCCA AAGG |||||||| || || ||||| ||| || || ||| |||
CTGTGGATTTTTCGCAAGAA ATAATTAC GA CG TTTTT GGT TC CG TCG TGT G
CATTAATA AA A C A G AC GTG AT- A

GAM987 TCTTGTGTTGAGACTTCGTG 964 TACACCACTC 3566 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM988 TCTTGTGTTGAGACTTCGTG 965 TACACCACTC 3567 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM989 CTGGATCTATGAATGACAGG 966 TGAATGACAG 3569 A AAT C C CCACAT T
AGGGCAGACCACATTGTTTT GAGGGCAGAC CTGG TCTATG GA AGGAGGG AGA TGT T
CACATCCATTTCCCCTCCTT CACA |||| |||||| || ||||||| ||| |||
CCCATGGGCCAG GACC GGGTAC CT TCCTCCC TTT ACA T
- C-- - C ACCT-- C

GAM990 CTTGTGGGAGAGATTATCAA 967 TGGGAGAGAT 3570 T GA ATC -------- - G A AT
GCGTTTTGAGCAGAAAGGAT TATCAAGCGT CTTG GGGAGA TT AAGC GTTTT GA CAG
AAGG T
TCCGCCTTGTTGGTCTGAAA TTTG |||| |||||| || |||| ||||| || ||| ||||
TTCATGCAAGCTTCCGAAGA GAAC TCTTCT AA TTCG TAAAG CT GTT TTCC C
TCTTCTCAAG - AG GCC AACGTACT T G G GC

GAM991 CACTACGTTGACCTGAAGGA 968 AAGGACCGTC 3568 GA-- GAA- CCATTCT --
AAAT
CCGTCCATTCTTTGCCGGCC CATTCTTTGC CACTACGTT CCT GGACCGT
TTGCCGGCCT GGTG A
TGGTGAAATACATGCACTCA CGGC ||||||||| ||| ||||||| |||||||||| ||||
GGGCCGGTAGTTGCCATGGT GTGGTGTAA GGG TCTGGTA GATGGCCGGG
TCAC /
CTGGGAGGGGCTGAATGTGG GTCG AGGG CCGTT-- AC GTAC
TG

GAM992 TCTTGTGTTGAGACTTCGTG 969 TACACCACTC 3571 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG |||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM993 TGCTGCTGCTTGGCCTCTGC 970 TCGTGCGCGG 3573 C - - CT C CT
ATCTTCCTGCTCTACAAGAT GGACCAGCCG TGCTGCTG TTGG CCTC TGCAT TC TG C
CGTGCGCGGGGACCAGCCGG GCGG |||||||| |||| |||| ||||| || ||
CGGCA ACGGCGGC GACC GGGG GCGTG AG AC /
C A C CT A AT

GAM994 CCGGATCCCTGCCTAGCGCG 971 TGCCGAGGAT 3572 C ------ - - G - A TACT- GAG
GCCCAACCTTTACTCCAGAG GTGGTGGCGA CCGGATC CT GC CTAG CGC GCC CA CCTT
CCA A
ATCATGGCTGCCGAGGATGT CTGG ||||||| || || |||| ||| ||| || |||| |||
GGTGGCGACTGGCGCGACCC GGTCTAG GA CG GGTC GCG TGG GT GGAG GGT
/
AAGCGATCTGG C ACCCAG C A G T A CCGTC ACT

GAM995 GGCCAATTGAAACAAACAGT 972 TATTAGGGAT 3574 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM996 GTCCCTGCTTCCCGACACCA 973 TACCCCAGTC 3575 T C- AGCCTCA AATA ACA
GCCTCATGGAATATGCAACA CACGGTGTTC GTCCCTGCT CC GACACC TGG TGCA A
ACTCCTGTACCCCAGTCCAC TGGC |||||||| || |||||| ||| ||||
GGTGTTCTGGCAGCAGGGAC CAGGGACGA GG TTGTGG ACC ATGT C
C TC CACCTG- CC-- CCT

GAM997 TTCTGTGAGGCTGTGGCCAT 974 CGGCATCATC 3576 TGA - A----- AC CATCAT
AATT TAG
CTACGGCATCATCATGGCAA ATGGCAATTG TTCTG GGCTG TGGCC TCT GGCAT GGC
GTCAT C
TTGTCATTAGCAACATGGCT TCAT ||||| ||||| ||||| ||| ||||| ||| |||||
GAGCCTTTCAGTGCCACAGA AAGGC CCGGC ACCGG AGA CCGTG CCG
CGGTA /
CCCCAAGGCCATCGGCCATC TA- T AACCCC CA ACTTT- AGT- CAA
GGAA

GAM998 TCTTGTGTTGAGACTTCGTG 975 TACACCACTC 3577 GAGA GT--- C AAAGGA

GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM999 GGCCAATTGAAACAAACAGT 976 TATTAGGGAT 3578 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1000 GGCCAATTGAAACAAACAGT 977 TATTAGGGAT 3579 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1001 GACAAGTTTCAAAGGAAGAA 978 TTTATAGATG 3580 AGTT - AA CTCAT CAC
CATTTATGACTCATGCCACA GCTTCTTTCT GACA TCA AAGGAAG CATTTATGA GC A
AAAGCTATTTATAGATGGCT GATT |||| ||| ||||||| ||||||||| ||
TCTTTCTGATTATGTC CTGT AGT TTTCTTC GTAGATATT CG /
ATT- C G- TAT-- AAA

GAM1002 GATATGTGTGTAGTTTGTGG 979 TCAGTGTGGT 3582 - TAGTTT GTT AG-- CAGA -
A
CAGTTTTGGCCAAGGAGCAG CAGTGTTACC GATAT GTGTG GTGGCA TTGGCCA GAG
AGG AAG T
AAGGAAGATTACTTGCCTGT ATCC ||||| ||||| |||||| ||||||| ||| ||| |||
TCTCAGTGTGGTCAGTGTTA CTGTG CATAC CATTGT GACTGGT CTC TCC TTC T
CCATCCATACTGTGTC T CTAC-- --- GTGA TTG- G A

GAM1003 CTGCCTAGACCCTCCATTGC 980 CTGGAAGTGC 3581 - CCT - GA-- TC A
AGACAGTTCCCAAAGGAGGC AAATGGTGTG CTGC CTAGAC CCATT GCA CAGT CC A
TGGAAGTGCAAATGGTGTGT TTTG |||| |||||| ||||| ||| |||| ||
TTGGTGCAG GACG GGTTTG GGTAA CGT GTCG GG /
T TGT A GAAG GA A

GAM1004 GATGACGTGGCCTTTCGAGG 981 TGACGTGGCC 3583 C- TTC G C GG T A C--- G
GACCTGGCACGTACATCCCC TTTCGAGGGA GATGA GTGGCCT GAG GA CT CACG AC TCC
CC G
CGGAAGGAAGTGGAGGTCGT CCTG ||||| ||||||| ||| || || |||| || ||| ||
GGAGATCATTCAGGCCACCC CTACT CACCGGA CTT CT GA GTGC TG AGG GG A

TCATC CC --- A A G- - G TGAA A

GAM1005 ACGTGGTGAAACCCCATCTC 982 TGAAACCCCA 3584 GTGAA - A- AAATA
TACTAAAAATACAAAAATTA TCTCTACTAA ACGTG ACC CCATCTCT CTAA C
GCCAGGGGTGGTGGTGCACG AAAT ||||| ||| |||||||| ||||
T TGCAC TGG GGTGGGGA GATT /
G---- T CC AAAAA

GAM1006 TCTTGTGTTGAGACTTCGTG 983 TACACCACTC 3585 GAGA GT--- C AAAGGAA
GTGGTGCTAAGAAAAGGAAC CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA C
GAAGAAGTCTTACACCACTC TAAG ||||||||| |||| ||||||| |||||
CCAAGAAGAATAAGCACAAG AGAACACGA GAAG TCACCAC ATTCT /
A ATAA AACCC - GAAGAAG

GAM1007 TCTTGTGTTGAGACTTCGTG 984 TACACCACTC 3586 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM1008 CGTCGGGCCCGGTTCGAGGT 985 CTGCGCTACC 3587 GG-- C GA TGA-- A AA
GGCTGACGAGGACAAGCAGT AGAACCTGGA CGTCG CC GGTTC GGTGGC CG GGAC G
CCCGGCTGCGCTACCAGAAC GAAC ||||| || ||||| |||||| || ||||
CTGGAGAACGATG GTAGC GG CCAAG CCATCG GC CCTG /
AAGA T A- CGTCG - AC

GAM1009 GGCCCAGGATCGGCAGGGCT 986 TTCCCATGCC 3588 - - G- - GCT GA A
GCTGGCAGAGGAATCCCAGC CCAGGCTCCT GGCCCAG GA TC GCAGG GCT GGCA
GGAATCCC G
TGGGGTTCCCATGCCCCAGG GCAG ||||||| || || ||||| ||| |||| ||||||||
CTCCTGCAGGACTTGCTGGG CCGGGTC TT AG CGTCC CGG CCGT CCTTGGGG C
CC G C GA T ACC AC T

GAM1010 GGCCAATTGAAACAAACAGT 987 TATTAGGGAT 3589 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAAAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - AAA

GAM1011 AAGATGATTCTGACAGTGAA 988 TCTGACAGTG 3590 A A T- AAAGCA-- - A ATCA
AAGCAGCAACAAATTCATCA AAAAGCAGCA AAGATG TTCTG CAG GA GCA ACAA TTC C
CATCAAGAACTTGTATGCCT ACAA |||||| ||||| ||| || ||| |||| |||

TCAACCTCTTCTGCCAGAAG TTTTGC AAGAC GTC CT CGT TGTT AAG A
CGTTTT G C TT CCAACTTC A C AACT

GAM1012 GGCCAATTGAAACAAACAGT 989 TATTAGGGAT 3591 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1013 CTACAGGACACAATGTGGCT 990 CAGGACACAA 3592 TA A - - GG TG C- TG T ACT
GACCTGGTGGTGATACTCAA TGTGGCTGAC C CAGG CA CAAT GT C AC TGG G GAT C
GATTCTGCCAACGTTGGAAG CTGG | |||| || |||| || | || ||| | |||
CTGTTGCTGCCCTGGGG G GTCC GT GTTG CG G TG ACC C TTA /
GG C C T AA GT CA GT - GAA

GAM1014 GGGTCAAGCCAGCACCTGAT 991 TGAAGAGGAA 3593 TCA CA GAAA C TG G
GAAACTTCCTTCAGTGAGGC TCAGGACCTG GGG AGCCAG CCTGAT CTTC TTCAG A G
CTTGCTGAAGAGGAATCAGG GCTC ||| |||||| |||||| |||| ||||| |
ACCTGGCTCCC CCC TCGGTC GGACTA GGAG AAGTC T C
--- CA A--- - GT C

GAM1015 GCTACTATTTTATTGCAGGA 992 TATTTTATTG 3594 ACTA T AGGA GG- T
GGTGGGGGTGTATGCACCGC CAGGAGGTGG GCT TTTTAT GC GGTG GGTG A
ACACCGGGGCTATGAGAAGC GGGT ||| |||||| || |||| ||||
CGA AGAGTA CG CCAC CCAC T
---- T GGG- ACG G

GAM1016 AAGTTGCCCGCTGTGTAAGA 993 TGTAAGAAAA 3595 CC --- AAAAA - A
AAAAGCCAAGAGACTGCTTT AGCCAAGAGA AAGTTGC GCTGT GTAAG GC CAAGAG C
TGAGTGACATTTATTTAGCA CTGC ||||||| ||||| ||||| || ||||||
GCTAGTAACTT TTCAATG CGACG TATTT TG GTTTTC T
AT ATT ACAG- A G

GAM1017 CAGGGGGGTGCGAGCTGGTA 994 TGGTATGGAT 3596 GT- TA-- -- C--- TG T
TGGATGCCCTCCTGGGTTTC GCCCTCCTGG CAGGGGG GCGAGCTGG TGGA TGC CTCC
GG T
CTGGGGGCTCTGCACTTCCA GTTT ||||||| |||||||| |||| ||| |||| ||
GACTCCAGTTTGTCCACCCC GTCCCCC TGTTTGACC ACCT ACG GGGG CC /
CTG ACC TCAG TC TCTC GT T

GAM1018 TGCATGGTTTCCAGCAGCTG 995 TTCAATCGAT 3598 GTTTCC GC GTTCT CAG
AGTTCTTCAACAGATCCATT GCTTTACATG TGCATG AGCA TGA TCAA A

GATTCAATCGATGCTTTACA CA |||||| |||| ||| ||||
TGCA ACGTAC TCGT GCT AGTT T
ATT--- A- AACTT ACC

GAM1019 CCCATTGGGCGCCAACTACT 996 TTCGTATTAT 3597 G CGC A -- ACTGCCAT - CC - AGA
GTGTGGAACTGCCATAAGCG TGTCTTTATT CCCATT GG CA CT ACTGTGTGGA AAG CGA GTGC AGCC G
ACCGTGCAGCCAGAGAGGGG TCGT |||||| || || || |||||||||| ||| ||| |||| ||||
TTCGTATTATTGTCTTTATT GGGTAA CT GT GA TGACACACTT TTC GTT TATG TTGG /
TCGTTCACACAGTACAGCTG G TTA C CA GCTTTAT- T AT C GGA
ATTTCGAATGGG

GAM1020 AGGCTAAGTCAGAGTCTCCT 997 TTGAGCTTTG 3600 AA- A- C CT --- GAA C AA
AAAGAGCCCGAACAGCTGAG AAACAACTGA AGGCT GTCAG GT TC AAAG AGCCC CAG TGAGG G
GAAGCTCTTCATTGGAGGGT TGAG ||||| ||||| || || |||| ||||| ||| |||||
TGAGCTTTGAAACAACTGAT TCCGA TAGTC CA AG TTTC TTGGG GTT ACTTC /
GAGAGCCT GAG AA A -- GAG AG- - TC

GAM1021 AGGAGCCATTTTGAGCAATG 998 CTCCAGGGGC 3599 G ATTTT AA- AA CAC AC G TAATG
GGGAACGCTCACGGACTGTG TTTGGGTTTG A GAGCC GAGC TGGGG CGCT GG TGT TGG A
TGGTAATGAGAGATCCAAAC T | ||||| |||| ||||| |||| || ||| |||
ACCAAGCGCTCCAGGGGCTT T TTTGG TTCG ACCTC GCGA CC ACA ACC /
TGGGTTTGT G GT--- GGG -- A-- -- A TAGAG

GAM1022 CTTCTTCAGTGAGACGGGCG 999 TTTGTAGACT 3601 T GAC- CG ----- T C
CTGGCAAGCACGTGCCCCGG TGGAACCCAC CTTC TCAGTGA GGG CTG GCAAGCACG GCC C
GCTGTGTTTGTAGACTTGGA AGTC |||| ||||||| ||| ||| ||||||||| |||
ACCCACAGTCATTGATGAAG GAAG AGTTACT CCC GGT TGTTTGTGT CGG /
T GACA AA TCAGA - G

GAM1023 TCTTGTGTTGAGACTTCGTG 1000 TACACCACTC 3602 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM1024 GCAGATGATCGAGACGTACT 1001 ACTTTGACTT 3603 ATGATCGA ACT TG CT T A CC - AAG
TTGACTTCCGGTTGTATCGC CCGGTTGTAT GCAG GACGT T A TCCGGT GT TCG TG TGG A

CTGTGGAAGAGCCGCCAGCA CGCC |||| ||||| | | |||||| || ||| || |||
CTCGAAGCTGCTGGACTTTG TGTC CTGCA A T AGGTCG CG AGC AC ACC G
ACGACGTCCTGT -------- GC- GT TC T A TC G GCC

GAM1025 TCTACAAAGTGCCGTCCACT 1002 TCCAATCTGA 3604 A - - CACTG CT- C
GAGACTGAGGCCTTGGCTTC TGGGCATGTT TCT CAAA GTGCC GTC AGA GAGGC T
CAATCTGATGGGCATGTTTG TGAG ||| |||| ||||| ||| ||| |||||
AGA AGA GTTT TACGG TAG TCT CTTCG T
- G G ----- AAC G

GAM1026 GGGAAACTCCGAGGACAGAG 1003 TGGCCTGATG 3605 AAA A--- - GA AA TG A
GGCTAAATCCATGAAGTTTG ATCCACAGCG GGG CTCCG GGA CA GGGCT ATCCA A G
TGGATGGCCTGATGATCCAC GAGA ||| ||||| ||| || ||||| ||||| |
AGCGGAGACCC CCC GAGGC CCT GT TCCGG TAGGT T /
A-- GACA A AG -- GT T

GAM1027 AGGAGGACGCGCTGCCCGGC 1004 GAGAGTACTC 3606 ------ G- G CAGAAAA AA
CAGAAAACGGAGTTCAAGGT CTGCGTCTTC AGGAGGACGC GCT CCC GC CGGAGTTC
G
GGACTCCGACGACCAGTGGG CT |||||||||| ||| ||| || |||||||
GAGAGTACTCCTGCGTCTTC TCCTTCTGCG TGA GGG TG GCCTCAGG /
CT TCCTCA GA G ACCAGCA TG

GAM1028 CGGCTCCGAGAGCAGGTTCT 1005 TACACATTGA 3607 - AGAG C A TC GCAG C
TCGTGAGTTCCTCGCAGGGC GAACCTGAAC CGGC TCCG CAGGTTCTT GTG GT CTC GG
C
CGGTCAGAGCTACACATTGA ATGG |||| |||| ||||||||| ||| || ||| ||
GAACCTGAACATGGAGGCCG GCCG AGGT GTCCAAGAG TAC CA GAG CT G
G ACAA T A TC A--- G

GAM1029 GACGGCCATGCTGGTCTGCA 1006 TACAAGATCA 3608 C ATGCTG G - A- C- -- - A
AGTCAGAGTCCGTGCCACCT CTGACTCTGA GA GGCC GTCT CA AGTCAG GTC GTGCCA
CCT GTC C
GTCACTGACTGGGCCTGGTA GGAC || |||| |||| || |||||| ||| |||||| ||| |||
CAAGATCACTGACTCTGAGG CT CCGG CAGG GT TCAGTC TAG CATGGT GGG CAG
/
ACAAGGCCCTC C AA---- A C AC AA CC T T

GAM1030 AAGATAGAGGCAGAACTGCA 1007 TGTTCTGGAG 3609 GA----- AA G TG
GGACATCTGCAATGATGTTC CTGTTGGACA AAGATA GGCAG CT CAGGACATC C
TGGAGCTGTTGGACAAATAT AATA |||||| ||||| || |||||||||
CTT TTCTAT TTGTC GA GTCTTGTAG A
AAACAGG -- G TA

GAM1031 CTTTCTGGGCAGAAGATGGC 1008 TCATGTGGAG 3610 AAGATGG - TT ATAA
CACTGTTCAATAAAAGACTG CCCTGTCCAG CTTTCTGGGCAG CCAC TG CA A
TCATGTGGAGCCCTGTCCAG AGAG |||||||||||| |||| || ||
AGAG GAGAGACCTGTC GGTG AC GT /
CCGA--- T T- CAGA

GAM1032 CTCGGGCTAAGCAGATTGTG 1009 AAGCAGATTG 3611 T- AGA TG GTG G T
TGGAATGGTCCTGTGGGGGT TGTGGAATGG CTCGGGC AAGC T T GAATG TCC G
ATTTGAATGGGAAGCTTTTG TCCT ||||||| |||| | | ||||| |||
CCCGGG GGGCCCG TTCG G A TTTAT GGG T
TT AAG GT AG- G G

GAM1033 GGCTTCTGGCATACCTGCTG 1010 TGAAAGCAGC 3612 T C--- G GGAT TGG
GCTGGATGGGCTTGGACTGT AAGAAGTATG GGCTTC GGCATAC TGCTG CT GGGCT A
GGTCCTGAAAGCAGCAAGAA CTGA |||||| ||||||| ||||| || |||||
GTATGCTGAGGCT TCGGAG TCGTATG ACGAC GA CCTGG C
- AAGA - AAGT TGT

GAM1034 TCTTGTGTTGAGACTTCGTG 1011 TACACCACTC 3613 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM1035 GGAGGGCACGTGCGTGGAGT 1012 ACGCTGCAGC 3614 A CA - G G GCAGATA GA
GGCTCCGCAGATACCTGGAG GCACGGACCC GG GGG CGTGCG TG AGTG CTCC CCTG G
AACGGGAAGGAGACGCTGCA CCC || ||| |||||| || |||| |||| ||||
GCGCACGGACCCCCC CC CCC GCACGC AC TCGC GAGG GGGC /
C AG G G A AA----- AA

GAM1036 CCTGCGCGCCCTCGACGTCA 1013 CTGAAGCCAG 3615 CC GAC AATG C C AATC
ATGTGGCCTTGCGCAAAATC ACAAAGAGAT CCTGCGCG CTC GTC TGGC TTG GCAA G
GCCAACTTGCTGAAGCCAGA CGTG |||||||| ||| ||| |||| ||| ||||
CAAAGAGATCGTGCAGG GGACGTGC GAG CAG ACCG AGT CGTT C
TA AAA ---- A - CAAC

GAM1037 GCACTTTTAGGAACTACATC 1014 TAGGAACTAC 3616 A T AA ACA TGGA- AG
ATGGACTTCCAGGTTGGGAA ATCATGGACT GC CT TTAGG CT TCA CTTCC G
GGAGTTTGAGGAGGATCTGA TCCA || || ||||| || ||| |||||
CAGGC CG GA AGTCT GA AGT GAAGG T
- C AG GG- TTGAG GT

GAM1038 GGAGCTGTTGGGTCGTGTAG 1015 TGGCAACAGG 3617 - GT G AGTTGA C TG A
TTGATGCCCTTGGTAATGCT GTCCAATTGG GGAGCTG TTGG C TGT TGCC T GTA T
ATTGATGGCAACAGGGTCCA TTCC ||||||| |||| | ||| |||| | |||
ATTGGTTCC CCTTGGT AACC G ACA ACGG A TAT G
T TG G ------ T GT C

GAM1039 AGCCGCTCCACTCGCATGTC 1016 TGACATGGAG 3618 C CG CACTG A- TCGC
CACTGTCTCAGAGCTTCGCA GTGGAGCTGC AGC GCTCCACT CATGTC TCTC GAGCT A
TCACGGCTCAGGAGAATGAC T ||| |||||||| |||||| |||| |||||
ATGGAGGTGGAGCTGCT TCG CGAGGTGG GTACAG AGAG CTCGG /
T AG TA--- GA CACT

GAM1040 CGTCTGGGATGTGAGGAGCC 1017 TGGGAAGTGA 3619 T TGT A C TG-- - G
CCTCTGCCCGGCTGCCCAGT GGAGCGCCTC CG CTGGGA GAGG GC CCTC CCCGG CT C
CTGGGAAGTGAGGAGCGCCT TTCC || |||||| |||| || |||| ||||| ||
CTTCCCGGCCG GC GGCCCT CTCC CG GGAG GGGTC GA C
C T-- G A TGAA T C

GAM1041 TAGCCGTGATGTCCGGGGGC 1018 TCTGCATTGG 3620 A G - C ATG G
CGTGTACATCATGTTACCGT CTGCTGGGCA TAGCCGTG TGTCCGG GGCCG TGTA ATC
TTACC T
GGGGTGGGGTCTGCATTGGC TATG |||||||| ||||||| ||||| |||| ||| |||||
TGCTGGGCATATGGCTG GTCGGTAT ACGGGTC TCGGT ACGT TGG GGTGG G
- G T C --- G

GAM1042 TTGACATTGTAGGCTGGCGC 1019 TTCATGCCTC 3621 AT CT CT C GTT
TGGCATCAGGTTCACACTCA TTTGCATCGT TTGAC TGTAGG GGCG GGCAT AG C
TGTTCATGCCTCTTTGCATC TAA ||||| |||||| |||| ||||| ||
GTTAA AATTG ACGTTT CCGT TTGTA TC /
CT CT AC C ACA

GAM1043 AGAAACAAAAGCAGGTGCTG 1020 TAGCATGCCT 3622 CAA- C -- TCA--- AA
AATCATGAAAACCTCAATTA CTTAATTTTT AGAAA AAG AGGT GCTGAA TGA A
TTTTTAGCATGCCTCTTAAT CT ||||| ||| |||| |||||| |||
TTTTCT TCTTT TTC TCCG CGATTT ACT /
TTAA - TA TTATTA CC

GAM1044 GGCCAATTGAAACAAACAGT 1021 TATTAGGGAT 3623 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1045 AGAAACAAAAGCAGGTGCTG 1022 TAGCATGCCT 3624 CAA- C -- TCA--- AA
AATCATGAAAACCTCAATTA CTTAATTTTT AGAAA AAG AGGT GCTGAA TGA A
TTTTTAGCATGCCTCTTAAT CT ||||| ||| |||| |||||| |||
TTTTCT TCTTT TTC TCCG CGATTT ACT /
TTAA - TA TTATTA CC

GAM1046 GAAACAGACTGGGCCAATGT 1023 TATCAAGGAA 3625 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM1047 TGGCATCCCAGATGTTGCAG 1024 TTGCAGTCGA 3626 - AGA AG GAAG T CA A A
TCGAAGTCGTCGTAGCCAGC AGTCGTCGTA TGGCATC CC TGTTGC TC TCG CGTAGC
GCG GC G
GAGCAGCAGCCGTCCGCTGC GCCA ||||||| || |||||| || ||| |||||| ||| ||
GCGAGAAGGCAACAGAGGTG ACCGTAG GG ACAACG AG AGC GCGTCG TGC CG C
ATGCCA T AG- GA ---- - CC - A

GAM1048 GGTTTTGTATGTCAAGGAGG 1025 GTGTTCCCCT 3627 T TGTC A TT CCTTT
AGTTTAAGGCCTTTCCGACC TTTCTGCGCA GGTT TGTA AAGG GGAG TAAGG C
ACCTTGTGTTCCCCTTTTCT GCC |||| |||| |||| |||| |||||
GCGCAGCC CCGA GCGT TTCC CCTT GTTCC C
C CTT- - GT ACCAG

GAM1049 AGTGTCGTGGACTCTTCTGT 1026 GGGCATCAGG 3628 C ---- - A-- AGGC
AGC
GGCAGGACTTGGAGGCTGTC AAACTTGGCC AGTGT GTGGAC TCTTCTGTGGC AGG
CTTGG TGTCCCT G
CCTAGCGCACAGGGGGCATC ACAG ||||| |||||| |||||||||| ||| ||||| |||||||
AGGAAACTTGGCCACAGAAG TCGTA CATCTG AGAAGACACCG TTC GGACT
ACGGGGG C
ACCTGGTCTACATGCT - GTCC G AAA ---- ACA

GAM1050 GTGGACGAATATGATCCAAC 1027 GAGGATTCCT 3629 G C TGA CAATAG A - - GAA
AA
AATAGAGGATTCCTACAGGA ACAGGAAGCA GT GA GAATA TCCAA AGG TTC CTA CAG
GC G
AGCAAGTAGTAATTGATGGA AGTA || || ||||| ||||| ||| ||| ||| ||| ||
GAAACCTGTCTCTTGGATAT CA CT CTTAT AGGTT TCC AAG GGT GTT TG /
TCTCGAC G - --- CTCTG- A A A AA- AT

GAM1051 GATACAAGACAGGCAAGAAC 1028 TACAAGACAG 3631 A - --- AA TG - TT
AAGTGGTTCTTCCAGAAACT GCAAGAACAA GAT CAAGACAG GCA AGAAC G GTT C C
GCGGTTTTAGATGCTTTGTT GTGG ||| |||||||| ||| ||||| | ||| |
TTGATC CTA GTTTTGTT CGT TTTTG C CAA G /
- T AGA G- GT A AC

GAM1052 GGGCGGCCGCTCTAGAGGAT 1029 TAGAGGATCC 3632 C C C TCCAA T-- A T
CCAAGCTTACGTACGCGTGC AAGCTTACGT GGG GGC GCT TAGAGGA GCT ACGT CGCG
G
ATGCGACGTCATAGCTCTTC ACGC ||| ||| ||| ||||||| ||| |||| ||||
TATAGTGTCACCT TCC CTG TGA ATCTTCT CGA TGCA GCGT C
A - T ----- TAC - A

GAM1053 AGGTACTCTGTGGATATCCC 1030 TCGTCAATAA 3630 TA T CC- -- A
CTTGGACAAAACTGTCGTCA GGATGTCTTC AGG CTCTG GGATATCC TTG GACA A
ATAAGGATGTCTTCAGAGAT AGAG ||| ||||| |||||||| ||| ||||
CCT TCC GAGAC TCTGTAGG AAC CTGT A
TA T AAT TG C

GAM1054 TGGGTATGGAATCTTGCGGC 1031 TGGAATCTTG 3635 - AA - CA- AGAC - ACTC
ATCCACGAGACCACCTTCAA CGGCATCCAC TGG GTATGG TCTT GCGG TCCACG CAC
CTTCA C
CTCCATCATGAAGTGTGACG GAGA ||| |||||| |||| |||| |||||| ||| |||||
TGGACATCCGCAAAGACCTG ACC CATGTC AGAA CGCC AGGTGC GTG GAAGT /
TACGCCA G C- A TAC A--- T ACTA

GAM1055 TGCGTAGCATTTGCTGCATG 1032 TTTGCCCCTG 3634 C A CAT T GAGA
GGTTAATTGAGAATAGAAAT GCAAATGCAC TG GT GCATTTGCTG GGGT AATT A
TTGCCCCTGGCAAATGCACA ACA || || |||||||||| |||| ||||
CA AC CA CGTAAACGGT CCCG TTAA /
A - C-- T AGAT

GAM1056 GGTGCTGTCGGGCGGACCAC 1033 AGGATGCAGA 3633 T T ACCA-- A-- GGG T
CATGTATCCGGGCATTGCTG AGGAGATCAC GG GC GTCGGGCGG CC TGTATCC CA T
ACAGGATGCAGAAGGAGATC CGCC || || ||||||||| || ||||||| ||
ACCGCCTGGCGCCC CC CG CGGTCCGCC GG ACGTAGG GT G
- - ACTAGA AAG ACA C

GAM1057 GGTTCCGTCATCATCAAAGT 1034 TCCGTCATCA 3636 TC T- A AAAG- GG
CAAAGATGCGGAAGGCATAA TCAAAGTCAA GGT CGTCA CATCAA GTC ATGC A
TGGGACTTGATGTCTGGCGT AGAT ||| ||||| |||||| ||| ||||
GGCT TCG GCGGT GTAGTT CAG TACG /

GT CT - GGTAA GA

GAM1058 GGGCCCGGGCAGGACTGGGC 1035 TGGTGAGCCC 3637 C AGGA --- TC TGA
CTCCCTCTGATCGATGAGGT AGAGCCCGAG GGGC CGGGC CTGGGC C CCTC T
GGTGAGCCCAGAGCCCGAGC CCC |||| ||||| |||||| | ||||
CC CCCG GCCCG GACCCG G GGAG C
A A--- AGT GT TAG

GAM1059 TCTACAAAGTGCCGTCCACT 1036 TCCAATCTGA 3638 A - - CACTG CT- C
GAGACTGAGGCCTTGGCTTC TGGGCATGTT TCT CAAA GTGCC GTC AGA GAGGC T
CAATCTGATGGGCATGTTTG TGAG ||| |||| ||||| ||| ||| |||||
AGA AGA GTTT TACGG TAG TCT CTTCG T
- G G ----- AAC G

GAM1060 GGATCACTGCTGGCCTACTC 1037 TGCCATAGCC 3640 CAC C CTC TA G A AC
TGGTTACGGGGACACTGACG AGTAACATCT GGAT TGCTGGC TA TGGT CGG GAC CTG G
CCCGGGTCACCGCTGCCATA |||| ||||||| || |||| ||| ||| |||
GCCAGTAACATCT TCTA ATGACCG AT ACCG GCC CTG GGC /
CA- - --- TC A - CC

GAM1061 ATCTGGGTGCAAAAGCCCAG 1038 TGCAAAAGCC 3639 G A CA TTAGGAAC GC
GGTTAGGAACCGTAGGCATG CAGGGTTAGG ATCTGGGT CAAA GCC GGG CGTAG A
CTGCGCCCCAAGGCTTTGAC AACC |||||||| |||| ||| ||| |||||
CCAGGT TGGACCCA GTTT CGG CCC GCGTC /
- - AA C------- GT

GAM1062 TTGCAGGAATTGAAGCTTTT 1039 TTGAAGCTTT 3641 TG AA TG CT C G C AGAA
ACAGCTGGAGACTGAGAAGT TACAGCTGGA T CAGG T AAG TTTACAG TG AGA TG G
AGGCATCTGTACTGTAAACC GACT | |||| | ||| ||||||| || ||| ||
TTTGACCTGTGA A GTCC A TTC AAATGTC AT TCT AC /
GT -- GT C- - G - GGAT

GAM1063 GGAGGCGGAGCTTGCAGTGA 1040 CACCTGGGCC 3642 - A-- A G AT----- C
GCCGAGATTGCGCCACTGCA ACAGAGCGAG GGAGGCGGAG CTTGC GTG GCC AG TGCG
C
CTTCCACCTGGGCCACAGAG ACTC |||||||||| ||||| ||| ||| || |||| |||| ||||

CGCAGCCTGAATGGCGAATG GG AAGCGGT CGAC GCGTTG CTTC CCG /
G T AAGTC - ACAACC - CTAGC

GAM1065 AGCCTTCATCGTCTGGCTGG 1042 GATGACCAAG 3644 G G - C AC-- CC
CCAACGGGGACACCCTCCGT CGGGAGGATG AGCCTTCATC TCT GCT GG CA GGGGACAC T
GTCTTCAAGATGACCAAGCG GGGG |||||||||| ||| ||| || || ||||||||
GGAGGATGGGGGCT TCGGGGGTAG AGG CGA CC GT CTTCTGTG /
G G A A AGAA CC

GAM1066 TCTTGTGTTGAGACTTCGTG 1043 TACACCACTC 3645 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| ||||| |
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM1067 GCTCCCCTTTGGTGCTCACT 1044 CCTTTGGTGC 3646 CTTT T- A CCT -- T
ACCTGGTTGTCGATGTATCG TCACTACCTG GCTCCC GG GCTC CTA GGTTG TCGA G
GATCAGCTTCTTGGGGGCCT GTTG |||||| || |||| ||| ||||| |||| |
CCTTGGGAGC CGAGGG CC CGGG GGT TCGAC GGCT T
TT-- TC - TCT TA A

GAM1068 GGCCGCATGCTGGAGGTAAA 1045 TGGAAAACGT 3647 ATGCT GTAAAG- - G- CT CC
GTCCATGGTTCCCTGGCCCC GAGAGGTCAG GGCCGC GGAG TC CATG TTCC GGC C
GTGCTGGAAAACGTGAGAGG ACTC |||||| |||| || |||| |||| |||
TCAGACTCCTAAGGTGGCC CCGGTG CCTC AG GTGC AAGG TCG /
GAAT- AGACTGG A AA -- TG

GAM1069 GAGGAGGTGTACTTTGAGAA 1046 TCAGACGCAG 3648 AG TTT AA TCA AG -- GAG
CCTCATGCAGCTGGTGGAGC ATGGACTCTG GAGG GTGTAC GAG CC TGC CT GGTG C
ACTACACCTCAGACGCAGAT TACG |||| |||||| ||| || ||| || ||||
GGACTCTGTACGCGCCTC CTCC CGCATG CTC GG ACG GA CCAC A
G- T-- A- TAG CA CT ATC

GAM1070 TCTGATCTGGTGGAATATAG 1047 TGGAATATAG 3650 --- GGAA TAT GA
TAGTATGGAGACCATCCTTC TAGTATGGAG TCTG ATCTGGT TATAGTAG GGA C
CTATTATGAACCAGGTATAC ACCA |||| ||||||| |||||||| |||
AGA AGAC TGGACCA GTATTATC CCT /
ATA A--- CTT AC

GAM1071 CTGCTGGTGGGAGAACCTAG 1048 AGTGAAGAAT 3649 - T GA AGAG GACA TG
AGTTGGGAAGACATCACTGA TTCCAGAAGA CTGCT GG GG GAACCT TTGGGAA
TCACTGATTA T
TTATGTCTCTGGTCAGTGAA GGTT ||||| || || |||||| ||||||| ||||||||||

GAATTTCCAGAAGAGGTTCC GACGG CC CC CTTGGA GACCTTT AGTGACTGGT C
TCCCCGGGCAG G - TC GAA- AAGA CT

GAM1072 GAAACAGACTGGGCCAATGT 1049 TATCAAGGAA 3651 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM1073 GAGCTTTCTGGGCAGACTTG 1050 ACTTGGTGAC 3652 TTCT AC- ACCT C GC C
TTCTT
GTGACCTTGCCAGCTCCAGC CTTGCCAGCT GAGCT GGGCAG TTGGTG TG CA TCCAG
AGCC G
AGCCTTCTTGTCCACTGGCT CCAG ||||| |||||| |||||| || || ||||| ||||
TTGGATGACACCCACCGGCA CTCGG TCTGTC GGCCAC AC GT AGGTT TCGG T
ACTGTCTGGCTC ---- AAC CC-- A -- - TCACC

GAM1074 TTTTGAAAGTTATCAGGAAG 1051 TTAGAACTCT 3653 AA TA - A-- T AA
AATTGGGTCAAAGAAATGCT TTACTGAACT TTTTG AGT TCAG GAAGA TTGGG CA G
TAGAACTCTTTACTGAACTG GGCG ||||| ||| |||| ||||| ||||| ||
GCGGAA AAGGC TCA AGTC TTTCT GATTC GT A
GG -- A CAA - AA

GAM1075 CAACTCGACGGCGCGCAACG 1052 ACGGACCCAG 3654 C A C- A- G C AAG GG G
TGACCTGGAAGCTGGGCAGG CTCAGTGAGC CAA TCG CGGCG GC AC TGA CTGG CTG
CAG C
CGACTGTACGGACCCAGCTC TTCG ||| ||| ||||| || || ||| |||| ||| |||
AGTGAGCTTCGCTGATGACT GTT AGT GTCGC CG TG ACT GACC GGC GTC G
TG C A TT AG - C CA- AT A

GAM1076 GTGTCTTCGGCCGCCGGAAG 1053 TTCTTTTTGT 3655 T CG TGCGT
GGGGGTGCGTCCGGATCTTC GGCTGTGGAC GTGTCT CGGCCGC GAAGGGGGG C
TTCTTTTTGTGGCTGTGGAC AC |||||| ||||||| |||||||||
AC CACAGG GTCGGTG TTTCTTCTT C
T TT CTAGG

GAM1077 GTAGAGATGGGGTTTCACCA 1054 CCTGACCTCG 3656 A A GTT- CAT TAGC T C
TGTTAGCCAGGATGGTCTCG TGATCCACCC GT GAG TGGG TCAC GT CAGGA GGT T
ATCTCCTGACCTCGTGATCC ACCT || ||| |||| |||| || ||||| |||
ACCCACCTCAGC CG CTC ACCC AGTG CA GTCCT CTA C
A C ACCT CTC ---- - G

GAM1078 GACGGCGCTACGCACGGACC 1055 ACGCACGGAC 3657 GG TA-- CG CC G G
GACGGGAAGGTTTTCCAGTT CGACGGGAAG GAC CGC CGCA GA GAC GGAA G
TCTTAATGCGAAATGCGAGT GTTT ||| ||| |||| || ||| ||||
C CTG GCG GCGT TT TTG CCTT T
A- TAAA AA CT A T

GAM1079 GATTGGACTCTATCATATGT 1056 TCTATCATAT 3658 TG CTCT G CCAAGC
GTCAAATCCAAGCTTAAACA GTGTCAAATC GAT GA ATCATAT TGTCAAAT T
ATTTGACAGTGTGGTTCATC CAAG ||| || ||||||| ||||||||
TGATC CTA CT TGGTGTG ACAGTTTA /
GT ACT- - ACAAAT

GAM1080 GAGGTGGTGGTGCAGAGACT 1057 GTGCAGAGAC 3659 TG G G ------ A T A - GG T
C
CTTCCAGGTCAAAGGGCGGC TCTTCCAGGT GAGG GT GT CA GAG CTCTTCCAGG CA AGG
GC CG GTGGT C
GTGTGGTCCGTGCCACCGAG CAAA |||| || || || ||| |||||||||| || ||| || || |||||
GTACCTGTGTCCTGGGAGAG CTTC CA CG GT TTC GAGAGGGTCC GT TCC TG GC
CACCG G
CTTCAACAATGGCGACTGCT GT G - AACAAC - T G A GA - T
TC

GAM1081 GCTTCGAGTCGGCCACCTTC 1058 TGAAGTACAA 3660 C G---- - AGGC-- A TC
CTAGGCTACTTCAAGTCTGG GAAAGGAGGT GCTT GAGTC GCCAC CTTCCT TACTTCA G
T
CCTGAAGTACAAGAAAGGAG GTGG |||| ||||| ||||| |||||| ||||||| |
GTGTGGCATCAGGATTCAAG CGAA CTTAG CGGTG GGAGGA ATGAAGT C /
C - GACTA T AAGAAC C GG

GAM1082 GGCCAATTGAAACAAACAGT 1059 TATTAGGGAT 3661 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1083 GGCCAATTGAAACAAACAGT 1060 TATTAGGGAT 3662 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1084 GGCCAATTGAAACAAACAGT 1061 TATTAGGGAT 3663 C T ACAAACAG G GTT T A GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1085 GGCCAATTGAAACAAACAGT 1062 TATTAGGGAT 3664 C T ACAAACAG G GTT T A GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1086 AGATGCTGACAATACTTGGG 1063 TGACAATACT 3665 GA AC--- AAC- GA
AACCTGAAGAAAATTTAGAT TGGGAACCTG AGATGCT CAAT TTGGG CTGAA A
TGTCCAGAATTGATTGAAGC AAGA ||||||| |||| ||||| |||||
GTTT TTTGCGA GTTA GACCT GATTT /
A- GTTAA GTTA AA

GAM1087 GCTCACAATCTCTGTCATCG 1064 TGGCATGAAG 3666 ACAA - G -- AT CC C
GCTGATCCAACCGTTCCTTG AAGGAATAGA GCTC TCT CT TCAT CGGCTG CCAA GTTC T
AGCTTGGCAGCTGGCATGAA GC |||| ||| || |||| |||||| |||| ||||
GAAGGAATAGAGC CGAG GGA GA AGTA GTCGAC GGTT CGAG /
ATAA A - CG -- -- T

GAM1088 GAGGTGGAGATCATCGTGGA 1065 ACCTGCTGGT 3667 AGA GTGGAGG T A GA
GGAGCTGGAGCTGAAGAAGC GAACCACTTC GAGGTGG TCATC AGC GG GCT A
ACCTGCTGGTGAACCACTTC ||||||| ||||| ||| || |||
CTTCACC AGTGG TCG CC CGA /
A-- ------- T A AG

GAM1089 AGGCTTGGCTTTGTTACTTT 1066 TACCATACCA 3668 TT G- ---- -- CC A AAA GTA
TGATGACCATGATCCTGTGG TCAAATGGTC AGGC GGCTTT TTACTTTTG ATGACCA TGAT TGTGG TA TC T
ATAAAATCGTATTGCAGAAA ATAA |||| |||||| ||||||||| ||||||| |||| ||||| || ||
TACCATACCATCAAATGGTC TCTG TCGGAA AATGAAGAC TACTGGT ACTA ATACC AT AG T
ATAATGCAGAAGTAAGAAAG TT AG GTAA AA CC - AA- ACG
GCTTTGTCT

GAM1090 GTGCACTCAACAGAACGGCC 1067 TCGCCACGAA 3669 A AA AA GC AAAT AA TG
CTTCAAATGTGAGAAATGTG GGATCGGCTG GTGC CTC CAG CG CCTTC GTGAGA TG A
AGGCAGCTTTCGCCACGAAG CGGG |||| ||| ||| || ||||| |||||| ||

GATCGGCTGCGGGCGCAC CACG GGG GTC GC GGAAG CGCTTT AC /
C C- G- TA CAC- CG GG

GAM1091 GGGGCGCGCAAAGCCACGAA 1068 TGTTTCTGGT 3670 AAA---- C AG- C
AAGCAAACTTTTTGATGTTT CCATGGGGTG GGGGCGCGC GCCA GAAA CAAA T
CTGGTCCATGGGGTGCGCCC CGCC ||||||||| |||| |||| ||||
C CCCCGCGTG TGGT CTTT GTTT /
GGGTACC - GTA T

GAM1092 ACTTTTTTAATGGGTCTCAA 1069 TAATGGGTCT 3671 T TCT ATTCTG AAAT
ATTCTGTGACAAATTTTTGG CAAATTCTGT ACTTTTT AATGGG CAA TGAC T
TCAAGTTGTTTCCATTAAAA GACA ||||||| |||||| ||| ||||
AGT TGAAAAA TTACCT GTT ACTG /
- TT- GA---- GTTT

GAM1093 GTCGGCCTGCAAGGAAGACA 1070 AGGAAGACAT 3673 C - G A ACATCC - AAA-- -
GG
TCCCCAGCGAAAAGAGTGAG CCCCAGCGAA GT GGC CT CA GGAAG CCAG CG AG
AGTGA A
GAGATCACTACTGGCAGTGC AAGA || ||| || || ||||| |||| || || |||||
CTGGTTTAGCTTCCTGGAGA CA CCG GA GT CCTTC GGTC GT TC TCACT /
GCCAC - A G - GATTT- C GACGG A AG

GAM1094 CCTCTCCTACATTGAGCACA 1071 ACTATGGTGG 3672 TCCTACA G C--- - A TC CC
CC
TCTTTGAGATCTCCCGCCGT TTGACTACAG CCTC TT AGCACAT TTTG AG TC CCGCCGT
TGA T
CCTGACCTACTCACTATGGT AACC |||| || ||||||| |||| || || ||||||| |||
GGTTGACTACAGAACCCGTG GGAG AA TCGTGTG AGAC TC AG GGTGGTA ACT /
TGCTGAAGATCTCTGAGG TCTCTAG G CCCA A - TT TC CA

GAM1095 GACGGCCATGCTGGTCTGCA 1072 TACAAGATCA 3675 C ATGCTG G - A- C- -- - A
AGTCAGAGTCCGTGCCACCT CTGACTCTGA GA GGCC GTCT CA AGTCAG GTC GTGCCA
CCT GTC C
GTCACTGACTGGGCCTGGTA GGAC || |||| |||| || |||||| ||| |||||| ||| |||
CAAGATCACTGACTCTGAGG CT CCGG CAGG GT TCAGTC TAG CATGGT GGG CAG
/
ACAAGGCCCTC C AA---- A C AC AA CC T T

GAM1096 CGGCTCCGAGAGCAGGTTCT 1073 TACACATTGA 3674 - AGAG C A TC GCAG C
TCGTGAGTTCCTCGCAGGGC GAACCTGAAC CGGC TCCG CAGGTTCTT GTG GT CTC GG
C
CGGTCAGAGCTACACATTGA ATGG |||| |||| ||||||||| ||| || ||| ||
GAACCTGAACATGGAGGCCG GCCG AGGT GTCCAAGAG TAC CA GAG CT G

G ACAA T A TC A--- G

GAM1097 GGGAAACTCCGAGGACAGAG 1074 TGGCCTGATG 3676 AAA A--- - GA AA GAA
GGCTAAATCCATGAAGTCTG ATCCACAGCG GGG CTCCG GGA CA GGGCT ATCCAT G
TGGATGGCCTGATGATCCAC GAGA ||| ||||| ||| || ||||| ||||||
AGCGGAGACCC CCC GAGGC CCT GT TCCGG TAGGTG /
A-- GACA A AG -- TCT

GAM1098 GTAGAGCTTTATGCTGAAAA 1075 GAGCTTTATG 3677 - TA GAAAA - T A
GGTGGCCACTAGAGGTCTGT CTGAAAAGGT GTAGAG CTT TGCT GGTGGC CAC AG G
GTGCCATTGCCCAGGCAGAG GGCC |||||| ||| |||| |||||| ||| ||
TCTCTGC CGTCTC GAG ACGG TTACCG GTG TC G
T -- ACCCG T - T

GAM1099 GCCCAGGGAGAACCCCTTGG 1076 ACTCTGGTGG 3679 AGAACCC -- - GA TCCT
T
ATATCGCCAGGATGATCCTA ATATGGCCAG GCCCAGGG CTTGG ATATC GCCAG TGA
AGC A
GCTATCGTTCTTTTCACTCT GATG |||||||| ||||| ||||| ||||| ||| |||
GGTGGATATGGCCAGGATGC TGGGTTCC GGACC TATAG TGGTC ACT TTG T
CTTGGGT GTA---- GG G TC TTTC C

GAM1100 CAGTTGATGGGCTGCCAGAT 1077 CTGCCTCCAG 3678 GG C GA - T GGA T
CTGGGGCATGCCCAGGACCT GTGACAGCAA CAGTTGAT GCTG CA TCTGG GGCA GCCCA
CC C
CATGGATGGGCTGCCTCCAG TCAG |||||||| |||| || ||||| |||| ||||| ||
GTGACAGCAATCAGCTG GTCGACTA CGAC GT GGACC CCGT CGGGT GG A
A- A -- T - A-- T

GAM1101 CGGCTGCGCGGGTCGCGGTG 1078 TGGCAGTGCC 3680 G GGTC G G - G G G
AA GG
CTGTGAGGTCTGCGGGCGCT TGACGGCGCG CGGCT CGCG GCG TGCTGT AGGT CTGC
GGC CTG CA TCC C
GGCAAATCCGGCCCAGGATG TCTG ||||| |||| ||| |||||| |||| |||| ||| ||| || |||
TAGAGCTGGCAGTGCCTGAC GTTGA GCGC TGC GCGGCA TCCG GACG TCG GAT GT
AGG C
GGCGCGTCTGACGCGGAGTT G AGTC - G T G A - -- AC
G

GAM1102 GAAACAGACTGGGCCAATGT 1079 TATCAAGGAA 3681 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/

GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM1103 GCTCCCCTTTGGTGCTCACT 1080 CCTTTGGTGC 3682 CTTT T- A CCT -- T
ACCTGGTTGTCGATGTATCG TCACTACCTG GCTCCC GG GCTC CTA GGTTG TCGA G
GATCAGCTTCTTGGGGGCCT GTTG |||||| || |||| ||| ||||| ||||
CCTTGGGAGC CGAGGG CC CGGG GGT TCGAC GGCT T
TT-- TC - TCT TA A

GAM1104 TGGGTGTGTTGAAGAAGAGG 1081 TTGAAGAAGA 3683 A AG ATC- TGG-- CAG
ATCCGGGTGGCCTCAGTGAA GGATCCGGGT TGGGTGTGTTGA GA AGG CGGG CCT T
AAGGATTTTCTCGTAGGCCT GGCC |||||||||||| || ||| |||| |||
TCTCAATGCACCCA ACCCACGTAACT CT TCC GCTC GGA G
- -- GGAT TTTTA AAA

GAM1105 GTGCACCTGAGCCGTGGAGG 1082 TTGCTCCTGA 3684 C C-- GG T TCC
GGCTGAAGTCCAGATCTTTG CGTCCCTCAG GTGCA CTGAG CGT AGGGGC GAAG A
CTCCTGACGTCCCTCAGATG ATGC ||||| ||||| ||| |||||| ||||
CAC CACGT GACTC GCA TCCTCG TTTC /
A CCT G- - TAG

GAM1106 CCCCTCCTTGAAGCTGATGG 1083 TGATGGTGAA 3685 C- GAA T G TG ACA- TC
TGAATGTGTGCGGACACACT TGTGTGCGGA CC CTCCTT GC GATGGTGAAT TG CGG CAC
T
CTCTGTGAAAGTTGTGTAGA CACA || |||||| || |||||||||| || ||| |||
TTTACTGTTTGTGAGAGGAG GG GAGGAG TG TTGTCATTTA AT GTT GTG /
CTGG TC AG- T G GT GAAA TC

GAM1107 CTGGGATAGAAGCCTTTGAC 1084 TAGAAGCCTT 3686 A A CTT --- AG
CAGGCAGGTCAGGCTGACCT TGACCAGGCA CTGGGAT GA GC TGACCAGG CAGGTC G
GGTTCTTGGTCAGCTCATCC GGTC ||||||| || || |||||||| ||||||
CGG GGCCCTA CT CG ACTGGTTC GTCCAG /
- - --- TTG TC

GAM1108 GGAGACAGGGAGAGGCTCTT 1085 ACGGAGCATG 3687 - A A GC G AG GTT GAG
CTGCGTGTAGTGGTTGTGCA AGAAGACGTT GG AG CAGGG GAG TCTTCT CGTGT TG
GTGCA C
GAGCCTCATGCATCACGGAG CCCC || || ||||| ||| |||||| ||||| || |||||
CATGAGAAGACGTTCCCCTG CC TC GTCCC CTT AGAAGA GTACG GC TACGT C
CTGCC G - - GC - AG AC- ACT

GAM1109 GGCCAATTGAAACAAACAGT 1086 TATTAGGGAT 3688 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T

ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1110 CCTGGCTGACCTGGTGTTTG 1087 TGACCTGGTG 3689 --- --- TT CTCT T
TCTGCACTCTGCCCTTCTGG TTTGTCTGCA CCTGGCTG ACCTG GTG TGTCTGCA GCCC T
GCCTATGCAGGCATCCATGA CTCT |||||||| ||||| ||| |||||||| ||||
ATGGGTGTTTGGCCAGG GGACCGGT TGGGT TAC ACGGACGT CGGG C
TTG AAG CT ATC- T

GAM1111 GCTCCTTCATCTGTCCTGCA 1088 TGTGCTGCAG 3690 T TCT - AAGGT AAA
GAAGGTTGTGGGAAAAGCTT AGGCTGAAGG GC CCTTCA GTC CTGCAG TGTGGG A
CTATGTGCTGCAGAGGCTGA TGC || |||||| ||| |||||| ||||||
AGGTGC CG GGAAGT CGG GACGTC GTATCT /
T --- A GT--- TCG

GAM1112 TCTTGTGTTGAGACTTCGTG 1089 TACACCACTC 3691 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM1113 GGCCAATTGAAACAAACAGT 1090 TATTAGGGAT 3692 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1114 CTTCCTGGCGGAACTTATTC 1091 AAGGAGCGTC 3694 T- - AA TA TCC AGC G
TCCCAGACGCTCAGCCTGGG TGCTGGACGA CTTCC GG CGG CT TTC CAGACGCTC CTGG
C
CAGCCAGAAGGAGCGTCTGC GCTG ||||| || ||| || ||| ||||||||| ||||
TGGACGAGCTGACCTTGGAA GAAGG CC GTC GA AGG GTCTGCGAG GACC A
G TT A -- GC TC- GAA G

GAM1115 CGGTACATGCAGAGCGAACG 1092 TCGCAGAGTC 3693 AC C CGCT CA GTCA TT
- CTG
CTGTCGCAGAGTCATCTGTT ATCTGTTTGG CGGT ATG AGAGCGAA GTCG GA TCTGT
GGTG GGAG G
TGGTGGGAGCTGGAATCTCC TGGG |||| ||| |||||||| |||| || ||||| |||| ||||
ACATCCGCAGGCATCCCCGA GCCA TAC TCTCGCTT CAGC CT GGACG CTAC
CCTC /
CTTTCGCTCTCCATCCACCG CC C T--- CC AC-- C- A TAA

GAM1116 TTTGGGTGGCATAGAGGTTT 1093 AGAGGTTTTG 3695 TA TTT TG GC- G
TGTATTGAGGGCCAGTGATG TATTGAGGGC TTTGGGTGGCA GAGGT GTAT AGG CA T
ATGTTTTGATATTTATTTCC CAGT |||||||||| ||||| |||| ||| ||
TGCTACTTAAA AAATTCATCGT CTTTA TATA TTT GT G
C- TT- GT GTA A

GAM1117 GCAGCTCCAGCGTCAAATTT 1094 TTCAAGAGCT 3696 TCC C CAAA T CACC C T
GTCTCCACCAGCTCCTCCTC AAGAACCTGC GCAGC AG GT TTTG CTC AGCTC TCC C
CCGGAAGAGCTTCAAGAGCT TGC ||||| || || |||| ||| ||||| |||
AAGAACCTGCTGC CGTCG TC CA GAAT GAG TCGAG AGG C
--- - A--- C AACT A C

GAM1118 GAGGCCGCCACCGGCAAGGG 1095 CTGCATCCCC 3697 CCG AC --- - - - GG
GTGCGCGCTGGGGAGCGGAC TTTCTGCTGC GAGG CC CGGCA AGGGG TGC GCG CTG G
GCTGCATCCCCTTTCTGCTG AGGA |||| || ||||| ||||| ||| ||| |||
CAGGAACCTC CTCC GG GTCGT TCCCC ACG CGC GGC /
AA- AC CTT T T A GA

GAM1119 GGACATCCACCTCTTCCCTG 1096 TGAGTTCCTG 3698 A AC CTTCC C AC A - --- A
CTCGTCACTGAACGGAGCTT CTCGCCGATG GG CATCC CT CTG TCGTC TGA C GGAGCTT
GATG C
GATGACCCCATCCTTGAGTT ATAG || ||||| || ||| ||||| ||| | ||||||| ||||
CCTGCTCGCCGATGATAGCC CC GTAGG GA GAT AGTAG GCT G CCTTGAG CTAC
C
ACCAGTGGGATGCC - GT CCACC - CC C T TTC C

GAM1120 GGCCAATTGAAACAAACAGT 1097 TATTAGGGAT 3699 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1121 TCGGCTCCAAGTCTGACCCA 1098 TGGGAGGGGG 3700 T A T A AC TG TT
CTCTGCGTCCTTTTACAGGA CAGCTGGGCT TCGGC CCA G CTG CCC TC CGTCCT T
TGTGGGAGGGGGCAGCTGGG GA ||||| ||| | ||| ||| || ||||||
CTGA AGTCG GGT C GAC GGG GG GTAGGA /
- - - G GA GT CA

GAM1122 TGTCTGGTGATTAGTTCTGT 1099 TGGAATGCCA 3701 TA- A---- T TA
GACTGTGTTTTACCTGGGCC TCACCGGATA TGTCTGGTGAT GTTCTGTG CTG GTTT C
AGCATGCCATGGAATGCCAT |||||||||| |||||||| ||| ||||

CACCGGATA ATAGGCCACTA TAAGGTAC GAC CGGG /
CCG CGTAC - TC

GAM1123 GAGGCAGAGTTGGAGCTCAC 1100 TGATTAGTCT 3702 C -- - T C TA C- T AATCC
AGTAACTGCCAGTTGAATCC CTTGGCTCCT GAGG AGA GTT GGAGC CA AG ACTG CAG TG
A
AAATAACATCTGATTAGTCT AGCA |||| ||| ||| ||||| || || |||| ||| ||
CTTGGCTCCTAGCAATCTCT CTTC TCT CGA CCTCG GT TC TGAT GTC AC /
TC - AA T - - TC TA T AATAA

GAM1124 GACTCAATGTGCAACTGACA 1101 TGTCCAGTAG 3703 T T-- - ACA T G AT CT AAT
TCTGCTAGTGATGATCTGGT CCGAACAGTT GAC CAATG GCAA CTG TC GCTA TG GAT
GGT A
AATATACAACCTGTCCAGTA TGTT ||| ||||| |||| ||| || |||| || ||| |||
GCCGAACAGTTTGTTTTTAT TTG GTTAT TGTT GAC AG CGAT AC CTG CCA T
TGTGTT T TTT T A-- C G -- T- ACA

GAM1125 GGCCAATTGAAACAAACAGT 1102 TATTAGGGAT 3704 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1126 GGCCAATTGAAACAAACAGT 1103 TATTAGGGAT 3705 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1127 GGCCAATTGAAACAAACAGT 1104 TATTAGGGAT 3706 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1128 GCCCCCCTACTTCCGCTTCC 1105 TGCCACTGGT 3707 - TACT TGAC CA CT- G-
CCT
TGACACTCATGGCCTTCCAC GGAGGTGGGC GCCCC CC TCCGCTTCC ACT TGGC
TCCAC TCTT C
GTCTTCCTCCAAGAGAAGGT ATTG ||||| || ||||||||| ||| |||| ||||| ||||
GGACCTGCCACTGGTGGAGG CGGGG GG GGGTGGAGG TGG ACCG AGGTG
AGAG /

TGGGCATTGGCGGGGC C TTAC ---- TC TCC GA AAC

GAM1129 GATGTCAATGCTGCCATTGC 1106 TCAATGCTGC 3708 --- CT T C-- - AAAAC GCAC
CACCATCAAAACCAAGCGCA CATTGCCACC GATGTCAA TG GCCA TG CACCA TC CAAGC
A
CATCCAGTTTGTGGATTGGT ATCA |||||||| || |||| || ||||| || |||||
GCCCCACTGGCTTCAAGGTT CTACGGTT AC CGGT AC GTGGT AG GTTTG /
GGCATC GGA TT C CCC T GT--- ACCT

GAM1130 TGTGGTGCCTGGTGGAGACC 1107 CATTGCTGAG 3709 G T G A - AA CAGAGA -
CA T
TGGCCAAGGTACAGAGAGCT GCCTGGGCTC TGTGGT CC GGTG AG CCT GGCC GGTA
GCTGTG TG TGC G
GTGTGCATGCTGAGCAACAC GCCT |||||| || |||| || ||| |||| |||| |||||| || |||
CACAGCCATTGCTGAGGCCT ACACCA GG CCGC TC GGG CCGG TCGT CGACAC AC
ACG /
GGGCTCGCCTGGACCACA - T - - T AG TAC--- C A- A

GAM1131 AACTTGAAAGTGAACAGTAT 1108 TGGCCCACAT 3710 T AG- T ACTTTCC AT A
GACTTTCCTGATCCAGAACA CTGTTTAATC AACT GAA TGAACAG ATG TG CCAGA C
GTTTGGCCCACATCTGTTTA TTCC |||| ||| ||||||| ||| || |||||
ATCTTCCAGTT TTGA CTT ATTTGTC TAC AC GGTTT A
C CTA - ------- CC G

GAM1132 TCCTGACTTTTTAATGATTG 1109 TATCTCATTG 3711 CT TTT T- T A T
CCATTCTAACTGGCGTGAGA TGGTTTTGA TC GACT TAATGA TGCCAT CT AC G
TGGTATCTCATTGTGGTTTT || |||| |||||| |||||| || ||
GA AG TTGG GTTACT ATGGTA GA TG G
TT T-- CT - G C

GAM1133 GAAACAGACTGGGCCAATGT 1110 TATCAAGGAA 3712 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM1134 GTTACTGGAGTACGGGGCCA 1111 AAAGACCAAG 3713 - C - - CCAGG CA- A AC-
AC
GGTGCCACCCTTAGTCACTA GGAATGCAAG GT TA TGGA GTA CGGGG TGC CCCTT GTC
TACCA T
CCAACTTCCTGGTGAAAGAC TCCC || || |||| ||| ||||| ||| ||||| ||| |||||

CAAGGGAATGCAAGTCCCCG CA GT GCCT CAT GCCCC ACG GGGAA CAG GTGGT
T
ATACATCCGATGTAC T A A A TGA-- TAA C AAA CC

GAM1135 TCTTGTGTTGAGACTTCGTG 1112 TACACCACTC 3714 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM1136 GGTGTTAAGTGCTCCAAGGA 1113 TAAGTGCTCC 3715 TTA T --- A - A G A
GGTGGCCACCGACATCCGTG AAGGAGGTGG GGTG AG GCT CCA GGA GGTGGCC CC AC T
GGGCCATCATCCTGGCCAAG CCAC |||| || ||| ||| ||| ||||||| || ||
CTCTCCATC CTAC TC CGA GGT CCT CTACCGG GG TG C
C-- T ACC - A - - C

GAM1137 GGACCCTTGACTCTGTTCCC 1114 TCACCACTGG 3716 A C CT TTCAA- ACAC
TTCAAGATCACACACATAGG GGACCAGTCA GG CC TTGACT GTTCCC GATC A
TCACCACTGGGGACCAGTCA AAGG || || |||||| |||||| ||||
AAGGCC CC GG AACTGA CAGGGG CTGG /
- A C- TCACCA ATAC

GAM1138 GGCCAATTGAAACAAACAGT 1115 TATTAGGGAT 3717 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1139 GGCCAATTGAAACAAACAGT 1116 TATTAGGGAT 3718 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1140 GTATCTGGGGATGAAAAAGG 1117 CAGCCAGCAC 3719 A GATGAAA TA TT --- GT
AGTAGTTTTCTGTTACTGGT CTCTTTATAG GT TCTGGG AAGGAG GTT CTGTTA CTG T
TTAACAGAAATGACAGCCAG AACC || |||||| |||||| ||| |||||| |||
CACCTCTTTATAGAACCCAG CA GGACCC TTTCTC CGA GACAGT GAC T
GAC - AAGATA- CA CC AAA AA

GAM1141 GGCCAATTGAAACAAACAGT 1118 TATTAGGGAT 3720 C T ACAAACAG G GTT T A
GAT

TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1142 GGCCAATTGAAACAAACAGT 1119 TATTAGGGAT 3721 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1143 TGTAGATTGTCAACATCGAA 1120 TAGATTGTCA 3722 TT C GAAT - A- TA
TTGATGGGATCATACTTTTG ACATCGAATT TGTAGA GT AACATC TG ATGGG TCA C
AGCTCCATACATGGGTGTTA GATG |||||| || |||||| || ||||| |||
TTTCTGCA ACGTCT TA TTGTGG AC TACCT AGT T
T- - GT-- A CG TT

GAM1144 GAAACAGACTGGGCCAATGT 1121 TATCAAGGAA 3723 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM1145 CACCTTTACGGCCAAACCGT 1122 TGTGGATATA 3724 TT C CC C-- C--- G
CCACCTCGACCGATTCTGTG GTTTTCCCTG CACC TA GG AAAC GTCCAC TC A
GATATAGTTTTCCCTGTTGG TTGG |||| || || |||| |||||| ||
TG GTGG GT CC TTTG TAGGTG AG C
TT - CT ATA TCTT C

GAM1146 TTGGTCCATATCTCCATGCA 1123 TCCATATCTC 3725 TC ATCTCC- G- - ACA
TGGCGGATACAGTGAAATCT CATGCATGGC TTGG CAT ATGCATG CG GAT G
CGAGCATGCATCTTCTCGGT GGAT |||| ||| ||||||| || |||
GAGCCAG GACC GTG TACGTAC GC CTA T
GA GCTCTTC GA T AAG

GAM1147 GCATAATCGGTCACTCGTAT 1124 TGAATGGACG 3726 AATC --- A GAA TATT TAT
AGAACAGTATTGTTTCTATA GGTTCAGGCC GCAT GGTC ACTCGT TA CAG GTTTC A
ATTTGAAGCTTTCTGAATGG TGAT |||| |||| |||||| || ||| |||||
ACGGGTTCAGGCCTGATGC CGTA CCGG TGGGCA GT GTC CGAAG A
GT-- ACT G AA- TTT- TTT

GAM1148 GGCCAATTGAAACAAACAGT 1125 TATTAGGGAT 3727 C T ACAAACAG G GTT T A GAT

TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1149 GCCGGCCTGGGTGCTTACCA 1126 TTTTCCTAGC 3728 T TACC-- TCTC GA
GCTGTCTCAGGATCCAAGGA TACATCTGGT GCCGGCC GGGTGCT AGCTG AGGATCCAAG A
ACGTTTGGGTTTTCCTAGCT ACCT ||||||| ||||||| ||||| ||||||||||
ACATCTGGTACCTTGGCTGG CGGTCGG TCCATGG TCGAT TTTTGGGTTT /
C T TCTACA CC-- GC

GAM1150 AACTTGAAAGTGAACAGTAT 1127 TGGCCCACAT 3729 T AG- T ACTTTCC AT A
GACTTTCCTGATCCAAAACA CTGTTTAATC AACT GAA TGAACAG ATG TG CCAAA C
GTTTGGCCCACATCTGTTTA TTCC |||| ||| ||||||| ||| || |||||
ATCTTCCAGTT TTGA CTT ATTTGTC TAC AC GGTTT A
C CTA - ------- CC G

GAM1151 CACCTTTACGGCCAAACCGT 1128 TGTGGATATA 3730 TT C CC C-- C--- G
CCACCTCGACCGATTCTGTG GTTTTCCCTG CACC TA GG AAAC GTCCAC TC A
GATATAGTTTTCCCTGTTGG TTGG |||| || || |||| |||||| ||
TG GTGG GT CC TTTG TAGGTG AG C
TT - CT ATA TCTT C

GAM1152 TTGGTCCATATCTCCATGCA 1129 TCCATATCTC 3731 TC ATCTCC- G- - ACA
TGGCGGATACAGTGAAATCT CATGCATGGC TTGG CAT ATGCATG CG GAT G
CGAGCATGCATCTTCTCGGT GGAT |||| ||| ||||||| || |||
GAGCCAG GACC GTG TACGTAC GC CTA T
GA GCTCTTC GA T AAG

GAM1153 CACCTTTACGGCCAAACCGT 1130 TGTGGATATA 3732 TT C CC C-- C--- G
CCACCTCGACCGATTCTGTG GTTTTCCCTG CACC TA GG AAAC GTCCAC TC A
GATATAGTTTTCCCTGTTGG TTGG |||| || || |||| |||||| ||
TG GTGG GT CC TTTG TAGGTG AG C
TT - CT ATA TCTT C

GAM1154 TTGGTCCATATCTCCATGCA 1131 TCCATATCTC 3733 TC ATCTCC- G- - ACA
TGGCGGATACAGTGAAATCT CATGCATGGC TTGG CAT ATGCATG CG GAT G
CGAGCATGCATCTTCTCGGT GGAT |||| ||| ||||||| || |||
GAGCCAG GACC GTG TACGTAC GC CTA T

GA GCTCTTC GA T AAG

GAM1155 GGACGAGCTCTTTGACCACA 1132 CGAGTACATG 3734 A ACCACAT - A C A
TTGTCCAGTGCATCGCGGAC GGCATGAAGG GGACG GCTCTTTG TGTCCA GTGC TCG GG
C
TTCCTCGAGTACATGGGCAT GCGT ||||| ||||||||| |||||| |||| ||| ||
GAAGGGCGTGTCC CCTGT CGGGAAGT ACGGGT CATG AGC CC T
G ------- A - T T

GAM1156 GTTGATGCCAACCTTGAAGC 1133 TTGAAGCCAG 3736 A A - TG - G - ATCC
CAGTGGGGCACCAATCCACA TGGGGCACCA GTTG TGCCA CC T AAGCCA GTG GGCA CCA
A
AACTGGATGCTGCGCTTGGT ATCC |||| ||||| || | |||||| ||| |||| |||
TTTGATGGTGGCAATGGC CGGT ACGGT GG A TTTGGT CGC TCGT GGT C
A - T GT T G A CAAA

GAM1157 GCATTGGTGATCTTTGCTAC 1134 TCAGCAGAGA 3735 ATTG G AC GTTC
AGAAAGCTGTTCATGGTAGG TGACAGGGGC GC GT ATCTTTGCT AGAAAGCT A
CTTTCTCAGCAGAGATGACA || || ||||||||| ||||||||
GGGGC CG CA TAGAGACGA TCTTTCGG T
GGGA G C- ATGG

GAM1158 GGCCAATTGAAACAAACAGT 1135 TATTAGGGAT 3737 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1159 AGGCCTGCCGTCATGTCTAA 1136 TCTTCATTGG 3738 C C -- CT-- CA G TA-- --
GAAC
GTCAGAGTCTCCTAAAGAGC AGGGTTGAGC AGGC TG CGTCA TGT AAGT GA TCTCC
AAGAGC CC A
CCGAACAGCTAAGGAAGCTC TTTG |||| || ||||| ||| |||| || ||||| |||||| ||
TTCATTGGAGGGTTGAGCTT TCCG AC GTAGT ACA TTCG TT GGAGG TTCTCG GG
G
TGAAACAACTGATGACAGCC - A CA AAGT AG G TTAC AA AATC
T

GAM1160 AGAGGACTGTGTTGTGGTCT 1137 TGTGTTGTGG 3739 A T T TG C - - T
GGGGAGAATGTAATCATTCC TCTGGGGAGA AG GGAC GTGT G GT TG GGGAG AATG A
TTCCACAACTGCTGCATGTC ATGT || |||| |||| | || || ||||| ||||
CCT TC CCTG TACG C CA AC CCTTC TTAC A
- - T GT - A C T

GAM1161 TCAGTCTTTGACCAACTGGG 1138 TAGAGGATTA 3740 - TGAC--- A G-- ATAC ACA
ATCATACAGAGGGACAAAAG TACAGATGAT TCAGT CTT CA CTG GATC AGAGGG A
CTCCTCTAGAGGATTATACA GATT ||||| ||| || ||| |||| ||||||
GATGATGATTTAAGCACTGA AGTCA GAA GT GAC TTAG TCTCCT A
C TTTAGTA A ATA GAGA CGA

GAM1162 TTGGTCCATATCTCCATGCA 1139 TCCATATCTC 3742 TC ATCTCC- G- - ACA
TGGCGGATACAGTGAAATCT CATGCATGGC TTGG CAT ATGCATG CG GAT G
CGAGCATGCATCTTCTCGGT GGAT |||| ||| ||||||| || |||
GAGCCAG GACC GTG TACGTAC GC CTA T
GA GCTCTTC GA T AAG

GAM1163 CACCTTTACGGGCAAACCGT 1140 TGTGGATATA 3741 TT C C C-- C--- G
CCACCTCGACCGATTCTGTG GTTTTCCCTG CACC TA GGG AAAC GTCCAC TC A
GATATAGTTTTCCCTGTTGG TTGG |||| || ||| |||| |||||| ||
TG GTGG GT CCC TTTG TAGGTG AG C
TT - T ATA TCTT C

GAM1164 AGAAACAAAAGCAGGTGCTG 1141 TAGCATGCCT 3743 CAA- C -- TCA--- AA
AATCATGAAAACCTCAATTA CTTAATTTTT AGAAA AAG AGGT GCTGAA TGA A
TTTTTAGCATGCCTCTTAAT CT ||||| ||| |||| |||||| |||
TTTTCT TCTTT TTC TCCG CGATTT ACT /
TTAA - TA TTATTA CC

GAM1165 GGTGTAAATGTTGAGCCTTT 1142 TAAATGTTGA 3744 GTA-- ----- TTTTT G- TT
TTGGCCTGGCTTGTTTGCAA GCCTTTTTGG GGT AATGTTGA GCC GGCCT GC G
AGGCCCTGGCAAACGTCAAC CCTG ||| |||||||| ||| ||||| ||
ATTGGGAAGCC CCG TTACAACT CGG CCGGA CG T
AAGGG GCAAA TC--- AA TT

GAM1166 GGCCAATTGAAACAAACAGT 1143 TATTAGGGAT 3745 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1167 GGCCAATTGAAACAAACAGT 1144 TATTAGGGAT 3746 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1168 CTTGGTTCTACAGCCATGGG 1145 TGTGCCTAGC 3749 GG CA GATC G A
GATCCAGACATCAGAGGGTG TGTGGAGAAG CTT TTCTACAGC TGGG CA ACATC G
TGTGCCTAGCTGTGGAGAAG AG ||| ||||||||| |||| || |||||
AG GAG GAGGTGTCG ATCC GT TGTGG A
AA -- ---- G G

GAM1169 GGACCCATCTGGGACCTTTG 1146 CAGAGGGTGC 3750 CCCA - GT- T GA-- T
TACAGTGTGATGCTCGAGCA CCAGAGCTCC GGA TCTGGG ACCTTT ACAG GT TGC C
ATTGGCTCTGTTCAGAGGGT ||| |||||| |||||| |||| || |||
GCCCAGAGCTCC CCT AGACCC TGGGAG TGTC CG ACG G
CG-- G ACT T GTTA A

GAM1170 AATTGATAAAGCCAGAGTGG 1147 TGTGACCCAA 3747 A G GA AACCACT - - A
A AGAC
AGACACAGAACCACTGGTTC GCTGTGTCCA AATTG TAAAGCCAGA TGGA CACAG GGTT
CAC CT CA TG A
ACCTACAATGAGACAATGAC ATCT ||||| |||||||||| |||| ||||| |||| ||| || || ||
AGTGGAGAGTGTGACCCAAG TTGAC GTTTCGGTCT ACCT GTGTC CCAG GTG GA
GT AC /
CTGTGTCCAATCTGGCTTTG - A -- GAAC--- T A G G AGTA
CAGTT

GAM1171 CCCACTGATGGAGCCCAGCA 1148 TGATGCTCAC 3748 G AGCC AGCAT AA-- GT
GCATTGAGAAAATTGTAGAG ATAGGTTGTG CCCACT ATGG CAGC TGAG AATT A
ATTGATGCTCACATAGGTTG CCAT |||||| |||| |||| |||| ||||
TGCCATGAGTGGG GGGTGA TACC GTTG ACTC TTAG /
G GT-- GATAC GTAG AG

GAM1172 AACTTGAAAGTGAACAGTAT 1149 TGGCCCACAT 3751 T AG- T ACTTTCC AT A
GACTTTCCTGATCCAGAACA CTGTTTAATC AACT GAA TGAACAG ATG TG CCAGA C
GTTTGGCCCACATCTGTTTA TTCC |||| ||| ||||||| ||| || |||||
ATCTTCCAGTT TTGA CTT ATTTGTC TAC AC GGTTT A
C CTA - ------- CC G

GAM1173 AATGACTGGGTGTATTTTCT 1150 TCTCTGATGA 3752 A TG A ATGCAAT TG- A
TGGC
CTGATGATGCAATCCAGGTG TGCAATCCAG AATG C GGTGT TTTTCTCTGATG CCAGG
GC TGCC A
GCATGCCTGGCATAACTGGT GTGG |||| | ||||| |||||||||||| ||||| || ||||
GGCATTCCTGGCATCAGAGG TTAC G CCACA GGAGGAGACTAC GGTCC CG GTGG
T
AGGAACACCTGGCATT - GT A ------- TTA - TCAA

GAM1174 ATGGTGACAACATGCTGGAG 1151 AGGGATGGAA 3753 AA-- G G T TA
CCAAGTGCTAACATGCCTTG CGTCACCGT ATGGTGAC CAT CT GAGCCAAG GC A
GTTCAGGGATGGAACGTCAC |||||||| ||| || |||||||| ||
CGT TGCCACTG GTA GG CTTGGTTC CG C
CAAG G A - TA

GAM1175 GGGAGCTGGAAGGCGTGATC 1152 TGACAGGTCT 3754 GA AA CGT- T G- A
CTGGAGCTGCAGGAGCAGCT GATCCCCAGT GG GCTGG GG GA CCTG AGCTGC G
GACAGGTCTGATCCCCAGTG GACC || ||||| || || |||| ||||||
ACC CC TGACC CC CT GGAC TCGACG G
AG -- TAGT - AG A

GAM1176 GATTGTACTGTATGGGGACT 1153 ACTCCAATTG 3755 - TAT- AC ATT TG TGA
ACCGA
CCAATTGCTTGGATGACAGT CTTGGATGAC GAT TGTACTG GGGG TCCA GCT GA CAGTC
C
CACCGACAGAAGGACTGCTT AGTC ||| ||||||| |||| |||| ||| || |||||
TGGGCTTCTGGATGCCCTCC CTA ACATGAC TCCC AGGT CGG TT GTCAG /
TCCAGTACACATC C CTCC GT CTT GT C-- GAAGA

GAM1177 TCTTGTGTTGAGACTTCGTG 1154 TACACCACTC 3756 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM1178 GGAGCACATGTGCCGCCTGG 1155 CACAGCCCGG 3757 A C - ----- T ACAT TCAC
ACATTGATTCACCACCCATC AACACTGGCA GG GCA ATG TGCCG CC GG TGAT C
ACAGCCCGGAACACTGGCAT TCAT || ||| ||| ||||| || || ||||
CATCTGTACC CC TGT TAC ACGGT GG CC ACTA /
A C T CACAA C GAC- CCCA

GAM1179 GGCCAATTGAAACAAACAGT 1156 TATTAGGGAT 3758 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1180 GGCCAATTGAAACAAACAGT 1157 TATTAGGGAT 3759 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /

CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1181 GGCCAATTGAAACAAACAGT 1158 TATTAGGGAT 3760 C T ACAAACAG G GTT T A GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1182 TGGCATCCCAGATGTTGCAG 1159 TTGCAGTTGA 3761 - AGA AG GAAG T CA A A
TTGAAGTCGTCGTAGCCAGC AGTCGTCGTA TGGCATC CC TGTTGC TT TCG CGTAGC GCG GC G
GAGCAGCAGCCGTCCGCTGC GCCA ||||||| || |||||| || ||| |||||| ||| ||
GCGAGAAGGCAACAGAGGTG ACCGTAG GG ACAACG AG AGC GCGTCG TGC CG C
ATGCCA T AG- GA ---- - CC - A

GAM1183 GAGCTGGAGAGATGTTAGAA 1160 TATCAAGTGG 3762 - GAGA GAA CT- G CT
GATGGCTCTGAGAGATTCCT CATCCACGCT GAGC TGGA TGTTA GATGGCT GA AGATTC C
CTGCGAATCTGTTTTTAGCT T |||| |||| ||||| ||||||| || ||||||
ATCAAGTGGCATCCACGCTT TTCG ACCT ACGGT CTATCGA TT TCTAAG T
C ---- GAA TTT G CG

GAM1184 TGGTGGGGTCAGTGGAAGTT 1161 TGTCTCAGAC 3763 T T AAGT T-- TC
CTGTCACTGGATCTGGTTTC CTTGCCCCAC TGGTGGGG CAG GG TCTG CACTGGA T
AGTGTCTCAGACCTTGCCCC CA |||||||| ||| || |||| |||||||
ACCA ACCACCCC GTT CC AGAC GTGACTT G
- - ---- TCT TG

GAM1185 GCTGGAACTGAAGCTGGGGC 1162 TGGGGCTGCA 3764 AA TG - TG CA T TT TT
TGCAGCCTGGGCCTTGGTTT GCCTGGGCCT GCTGG C AAG C GGGCTG GCC GGGCC GG T
GATCCTTGGCCTTGGCCTTG TGGT ||||| | ||| | |||||| ||| ||||| ||
GCCTTGGCCTTTGGCCGGC CGGCC G TTC G TCCGGT CGG TCCGG CC G
-- GT C GT TC T TT TA

GAM1186 GAAACAGACTGGGCCAATGT 1163 TATCAAGGAA 3765 C -- CACAAAGAA - CA- ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG /
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT

TT

GAM1187 GCCAACCTTGAAGCCAGTGG 1164 TTGAAGCCAG 3766 A - TG - G - ATCC
GGCACCAATCCACAAACTGG TGGGGCACCA GCCA CC T AAGCCA GTG GGCA CCA A
ATGCTGCGCTTGGTTTTGAT ATCC |||| || | |||||| ||| |||| |||
GGTGGC CGGT GG A TTTGGT CGC TCGT GGT C
- T GT T G A CAAA

GAM1188 CTTCTTCAGTGAGACGGGCG 1165 TTTGTAGACT 3767 T GAC- CG ----- T C
CTGGCAAGCACGTGCCCCGG TGGAACCCAC CTTC TCAGTGA GGG CTG GCAAGCACG
GCC C
GCTGTGTTTGTAGACTTGGA AGTC |||| ||||||| ||| ||| |||||||| |||
ACCCACAGTCATTGATGAAG GAAG AGTTACT CCC GGT TGTTTGTGT CGG /
T GACA AA TCAGA - G

GAM1189 GGGGGAACTGGTTCTGGGGT 1166 CAAGCAGTCC 3768 AA - TC- TC T CA AC CTC
GTG
CACTCCTGCTCATGGAACGT AAGCGGAGTC GGGGG CT GGT TGGGG ACTCC GCT TGGA
GT TCA A
CTCTCAGTGATTATGGCAAG TCCA ||||| || ||| ||||| ||||| ||| |||| || |||
CAGTCCAAGCGGAGTCTCCA CCCCC GA CCA ACCTC TGAGG CGA ACCT CG GGT
/
TTTACCAAGCGCCCCC GC A TTT -- - -- GA AAC ATT

GAM1190 GAGTATGGGGTGACAAAAAT 1167 CACTGATTTT 3769 CA--- TCCT GCTTAATG
TAGTTCCTGGTGCTTAATGA ATATATTACC GAGTATGGGGTGA AAAATTAGT GGT A
AACTTTCTGCCACTGATTTT CCGT |||||||||||| ||||||||| |||
ATATATTACCCCGTGCTT TTCGTGCCCCATT TTTTAGTCA CCG /
ATATA ---- TCTTTCAA

GAM1191 GAAACAGACTGGGCCAATGT 1168 TATCAAGGAA 3770 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM1192 GGCCGTGCAGCAGTGCATTG 1169 GTGCATTGAG 3771 G C T A GAGG GGACA A A
AGGCTGCAGGACATGAGCAC GCTGCAGGAC GGCC TG AGCAG GC TT CTGCA TG GC C
CAGCCAGACATGCAGAAGAG ATGA |||| || ||||| || || ||||| || ||
TCTGCTCAGGGCC CCGG AC TCGTC TG AG GACGT AC CG C
G - - - AA-- ACAG- - A

GAM1193 GACTTTGATGGCACTCCTAG 1170 TGCCATAGGC 3773 TTGA TA T CAGAC A CC CAT
GCTCTATCAGACTGACCCCT CGGGGTGCCA GACT TGGCACTCC GGC CTAT TG CC TCGGGCA A
CGGGCACATACCATGCCTGG AGTC |||| ||||||||| ||| |||| || || ||||||| AAGGCCAATGCCATAGGCCG CTGA ACCGTGGGG CCG GATA AC GG GGTCCGT / GGGTGCCAAGTC ---- -- - CCGTA C AA ACC

GAM1194 CTGACGAAGCCATTGAAACA 1171 ACGAAGCCAT 3772 GA GAAA A------- TG TT GATGATCTGACCATTAAGCT TGAAACAGAT CTGAC AGCCATT CAG TGATC ACCA A GGTGATCAAGGCACTCCTGG GATC ||||| ||||||| ||| ||||| |||| AAGTGGTTCAGTCAG GACTG TTGGTGA GTC ACTAG TGGT A AC AG-- CTCACGGA -- CG

GAM1195 TGGCATCCCAGATGTTGCAG 1172 TTGCAGTTGA 3774 - AGA AG GAAG T CA A A TTGAAGTCGTCGTAGCCAGC AGTCGTCGTA TGGCATC CC TGTTGC TT TCG CGTAGC GCG GC G
GAGCAGCAGCCGTCCGCTGC GCCA ||||||| || |||||| || ||| |||||| ||| || GCGAGAAGGCAACAGAGGTG ACCGTAG GG ACAACG AG AGC GCGTCG TGC CG C ATGCCA T AG- GA ---- - CC - A

GAM1196 AGGCACTGGAGAGATATTCT 1173 AGAGATATTC 3775 - - - GTGTACA-- A GTGTACATTTCATTTGAGAC TGTGTACATT AGGCAC TGG AGAGATATT CT TTTC T TCCTTCCAAGTAGTATTTCT TCAT |||||| ||| ||||||||| || |||| GCCATGTGTCT TCTGTG ACC TCTTTATGA GA AGAG T T G T ACCTTCCTC T

GAM1197 GTTTGTGACTTTGGTGTTTC 1174 ACTTTGGTGT 3776 T ACTTT TCGGC A C GGCATGGAGACCGAAGTCCC TTCGGCATGG GTT GTG GGTGTT ATGG GAC G ATTGACACCTTTCCCACTGA AGAC ||| ||| |||||| |||| ||| C CAG CAC CCACAG TACC CTG A T CCTTT T---- - A

GAM1198 TCTCTGTAATGTGCCTGTGC 1175 TGTAATGTGC 3777 - - GTG TG ----- A G CTGTGGCCAGAGGGGAGCCC CTGTGCCTGT TCTCTGT AATGTGC CT CCTG GC CAG GGG A
CCTGACCGTGCTGTGGGAGA GGCC ||||||| ||||||| || |||| || ||| ||| GCACATTGACAGAGA AGAGACA TTACACG GA GGGT CG GTC CCC G G A --- GT TGCCA - C

GAM1199 GAAAGGTCGAAGATATGAGG 1176 TCGAAGATAT 3778 --- ---- G - A TGGA G CGGTGAAGTGGATGGTGGTG GAGGCGGTGA GAAAGGTC GAAGA TAT AGGC GGTG AG TGGTGGT T

TTTGCCATTGGAGTCTGCAC AGTG |||||||| ||||| ||| |||| |||| || |||||||
TGGCCTGGTGGGTCTCTTTG TTTTTCAG TTTCT GTG TCCG TCAC TC GTTACCG T
TGGACTTTTT GTG CTGG G G G TGAG T

GAM1200 GGAAAGATTGTGCAGATGAC 1177 TATCAAGTCT 3780 GTGCA T - A G TC
TGAAGCAGAAGTTCGAGGCT CGGGAGATCT GGAAAGATT GA GACT GA GCA AAGT G
TATGTATCAAGTCTCGGGAG TTCT ||||||||| || |||| || ||| ||||
ATCTTTCT TCTTTCTAG CT CTGA CT TGT TTCG /
AGGG- - A A A GA

GAM1201 GAGGAAAGCAGTCTTTGGAA 1178 TTATAAAATC 3779 - C - AACCA--- TT TA
ACCATTTGTTTGCTATTGGC AAATATCCAG GAG GAAAG AGT CTTTGGA TTTGT GC T
TTATAAAATCAAATATCCAG AGAA ||| ||||| ||| ||||||| ||||| ||
AGAACTTCTTTCTCTT TTC CTTTC TCA GAGACCT AAATA CG /
T T A ATAAACTA TT GT

GAM1202 TCTTGTGTTGAGACTTCGTG 1179 TACACCACTC 3781 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| ||||| |||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM1203 CTTGAACTTCAGAAAGTATC 1180 AGATTGCTAT 3782 T- AAAGT- ----- C A T A
AGGTAATCAGCAGATTGTAG TACTGGACAT CTTGAACT CAG ATCA GGTAAT AGCAG TTG
AGG C
GACAGCCTCAGATTGCTATT GATC |||||||| ||| |||| |||||| ||||| ||| |||
ACTGGACATGATCAGGGGCT GAACTTGA GTC TAGT TCATTA TCGTT GAC TCC A
GTTAGTTCAAG TT GGGGAC ACAGG - A - G

GAM1204 GACACTCTTGATGACCTGAT 1181 TTCCAACAGT 3783 T A AC T- C GAGT AGT
AGCAGCTGTGAGTACCAGAG TCTTCTCAGA GACACTCT G TG CTGA AG AGCTGT ACCAG
G
TGCCCACTGGTTCCAACAGT CCAC |||||||| | || |||| || |||||| |||||
TCTTCTCAGACCACAGAGTG CTGTGAGA C AC GACT TC TTGACA TGGTC C
TC - - CA CT - ACCT ACC

GAM1205 TGCTGACAGGCCAGTGGGAA 1182 GGCCAGTGGG 3784 ACAGG--- GA A AGATT
GGATCAGATTTTATTAAGAC AAGGATCAGA TGCTG CCAGTGG AGG TC T
CTCTACTGGAAAAGAAACAG TTTT ||||| ||||||| ||| ||
TA ATGAC GGTCATC TCC AG T
AAAGAAAA -- - AATTA

GAM1206 CACTTGTTGTGGTGTCAAGG 1183 TGACTGTTGT 3785 T G A AAT AAA - CT

CAAATGCAAAACAGGTTTCT CTGATGCTAG CACT GTT TGGTGTCA GGCA GCA CAG GTTT C
CGAAAGCGCTGACTGTTGTC ACTG |||| ||| |||||||| |||| ||| ||| ||||
TGATGCTAGACTGGTG GTGG CAG ATCGTAGT CTGT TGT GTC CGAA /
T - - --- CA- G AG

GAM1207 GCTCCCTGGGTGACTCTGAT 1184 TCCCTGGGTG 3786 TC G GA------ CAA TG
GGCAAGCATGAGACTGTGAA ACTCTGATGG GC CCTGGGT ACTCT TGG GCA A
CCAGGAAGAGAAGAGTGGCC CAAG || ||||||| ||||| ||| |||
CAGGTGC CG GGACCCG TGAGA ACC TGT G
T- G AGAGAAGG AAG CA

GAM1208 TCCTGCGAGTTCCCCTAAGT 1185 AAGTTCCCTA 3787 T TT CCTAA - A CT -- GA
TCTTAGAGGACTGCTTTGCC AAGAATGGCC TCC GCGAG CC GTTCTT AG GGA GCTTTGC
CTTTT T
TTTTGATCTGAGAGTTGCAA CTTG ||| ||||| || |||||| || ||| ||||||| |||||
AGTTCCCTAAAGAATGGCCC AGG TGTTC GG TAAGAA TC CCT TGAAACG GAGAG /
TTGTGGA - CC ----- A - -- TT TC

GAM1209 GGCTGAGGCAGGGGGATCAT 1186 AACACTGAAA 3788 CT A GA - A- GATCG
GAGGTCAGGAGATCGAGACC CCCCGTCTCT GG GAGGC GGGG TCA TG GGTCAGGA A
ATCCTGGCTAACACTGAAAC ACC || ||||| |||| ||| || ||||||||
CCCGTCTCTACC CC CTCTG CCCC AGT AC TCGGTCCT /
AT - AA C AA ACCAG

GAM1210 ACTCTGAAGATGATCAGACA 1187 AACACTGCCC 3789 A--- GA-- CA- ----- AATTG
GGGCAAGCGAAATTGGTCAT AGCTTTGAGG ACTCTG AGAT TCAGA GGGCA AGCGA
G
TCTCGCTAACACTGCCCAGC AGAT |||||| |||| ||||| ||||| |||||
TTTGAGGAGATCTGAAATAG TGAGAT TCTA AGTTT CCCGT TCGCT T
AGT AAAG GAGG CGA CACAA CTTAC

GAM1211 GCATTGATCTTATCCTCCGT 1188 CAGAATTGAG 3790 GAT A- C GA T CTCA
GACTGTCACCTCATCGTCGT GGCCGAGTAG GCATT CTT TCCTC GT CTG CAC T
GCAGAATTGAGGGCCGAGTA ATGC ||||| ||| ||||| || ||| |||
GATGC CGTAG GAG GGGAG TA GAC GTG /
AT- CC T A- - CTGC

GAM1212 GGCTCCCAATGTTGACGTTG 1189 CCAGGCCAAA 3791 CTCCC CG---- AG TGC
GCCAGGGCTTTGCAAACAAG AAGGCTCAAC GG AATGTTGA TTGGCC GGCTT A
CCAGGCCAAAAAGGCTCAAC ATTT || |||||||| |||||| |||||
ATTTACACC CC TTACAACT AACCGG CCGAA /
ACAT- CGGAAA A- CAA

GAM1213 ATAGGGAACAGTTTTGCCCT 1190 CTCGGGGTCT 3792 - --- AA G- TAC T AAT
GGAACAGAGTTACAGATACA GAAGACTGTC ATAGGGA ACAGTTTT GCCCTGG CA AGT
AGA ACAC C
CAATCAAGAGTGTTCTTGCT TTCC ||||||| |||||||| ||||||| || ||| ||| ||||
GATGCTCGGGGTCTGAAGAC TATCCTT TGTCAGAA TGGGGCT GT TCG TCT TGTG
A
TGTCTTCCTAT C GTC C- AG T-- - AGA

GAM1214 CTCTGCACAGCAGCCCAGCA 1191 CAGCAGCCCA 3793 GCACA C- G A- TAGAG
TT CA
GGGATGTCCTCTCTAGAGAT GCAGGGATGT CTCT GCAGC CA CAGGG TGTCCTCTC
ATGG TAT A
GGTTTATCAAGGGTACCCCA CCTC |||| ||||| || ||||| ||||||||| |||| |||
TGAGAGGGCAGCTCCTGATG GAGA CGTCG GT GTCCT ACGGGAGAG TACC ATG
/
CAGCTGCCGGAAGAG AGGC- AC A CG ----- CC GG

GAM1215 ATGGTGAAACATGCTGGAGC 1192 TTCACGGATG 3794 - AA--- G - A T TA
CAAGTGCTAACATGCCTGGT GAAAGTCAGC ATGG TGA CAT CTG GAGCCA G GC A
TCACGGATGGAAAGTCAGCC CGT |||| ||| ||| ||| |||||| | ||
GT TGCC ACT GTA GGC CTTGGT C CG C
G GAAAG - A - - TA

GAM1216 TCTTGTGTTGAGACTTCGTG 1193 TACACCACTC 3795 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM1217 TCTACAAAGTGCCGTCCACT 1194 TCCAATCTGA 3796 A - - CACTG CT- C
GAGACTGAGGCCTTGGCTTC TGGGCATGTT TCT CAAA GTGCC GTC AGA GAGGC T
CAATCTGATGGGCATGTTTG TGAG ||| |||| ||||| ||| ||| |||||
AGA AGA GTTT TACGG TAG TCT CTTCG T
- G G ----- AAC G

GAM1218 GAGATGCAGCAGAAGTTGGT 1195 TGCAGCAGAA 3797 A AG GAA G G- GCT
GGAGCTGTCGGCTGAGAACG GTTGGTGGAG GAG TGC CA GTTGGTG AGCT TCG G
AGAAGCTGCACCAGCGCGTG CTGT ||| ||| || ||||||| |||| |||
GAGCAGCTC CTC ACG GT CGACCAC TCGA AGC A
G AG GCG G AG AAG

GAM1219 GCATCTTCTACTAGTGTGTT 1196 TTCAAATAAC 3798 TCT AGTG GTA T C
AGTAGATGGATTCACAGATC AAAAGTAGAT GCA TCTACT TGTTA GA GGATT A
CTTCAAATAACAAAAGTAGA TCTG ||| |||||| ||||| || |||||

TTCTGC CGT AGATGA ACAAT CT CCTAG C
CTT AA-- AAA T A

GAM1220 GCGATATGAGATTGTGGGGA 1197 TTGGACCATG 3801 AT GA GT G TGAAGGCA
A --- GG
ACCTGGGTGAAGGCACCTTT CCAGAGGGAA GCG ATGA TT GGG AACCTGGG
CCTTTGGCA GGT GGT A
GGCAAGGTGGTGGAGTGCTT GTCT ||| |||| || ||| |||||||| ||||||||| ||| |||
GGACCATGCCAGAGGGAAGT CGC TACT AA CCC TTGGACTC GGAGACCGT CCA
TCG /
CTCAGGTTGCCCTGAAGATC C- AG GT G TGAAG--- A GGT TG
ATCCGC

GAM1221 CCCTACCAGAGGAGGTACCG 1198 TGTGAAGAGC 3800 - A -- A GGA--- TGACAGC
GGAGCGCCGTGACAGCGATA GGAGCCCATC CC CT CCAGAGGA GGT CCG GCGCCG G
CATACCGGTGTGAAGAGCGG CTTT || || |||||||| ||| ||| ||||||
AGCCCATCCTTTGGAGAGG GG GA GGTTTCCT CCG GGC TGTGGC A
A - AC A GAGAAG CATACAT

GAM1222 CCAGGTCTTGTAGCAGCGCC 1199 CAGCAGCCGG 3799 G - T A A --- C GAGAA
TCCTCGAGAAGCCAACAGAG AGTGTGG CCA G TCT GT GC GCGC CT CTC G
CAGTAAGCGCAGCAGCCGGA ||| | ||| || || |||| || |||
GTGTGG GGT T AGG CG CG CGCG GA GAG C
G G C A A AAT C ACAAC

GAM1223 GTTTCAGAGCCCAGAGTTTT 1200 AAGACTTTGT 3803 TCAG --- - ACA
CTGTTACAAGGCAACATGAA GTGGCTACAT GTT AGCC CAGAGTTTTC TGTT A
GACTTTGTGTGGCTACATGA GAC ||| |||| |||||||||| ||||
C CAG TCGG GTTTCAGAAG ACAA /
TACA TGT T CGG

GAM1224 CTGTGGACCTGAATGTTGAT 1201 CGTTCAGTGA 3802 CC ATG A- C TCA T A AC
CCCTCGCTTCAGATTGACAT GAGAGACAAA CTGTGGA TGA TTG TC CTCGCT GA TG CAT
C
ACCTGATGCGTTCAGTGAGA GTCA ||||||| ||| ||| || |||||| || || |||
GAGACAAAGTCAAATTTACA GACATTT ACT AAC AG GAGTGA CT GC GTA /
G AA GA- AG A --- T - GT

GAM1225 GGCCAATTGAAACAAACAGT 1202 TATTAGGGAT 3804 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1226 GAAACAGACTGGGCCAATGT 1203 TATCAAGGAA 3805 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM1227 GGTAGGTGGATCACCTGAGG 1204 TGGATCACCT 3807 T TG A--- - A- AGT A
TCAGGAGTTTGAGACCAGCC GAGGTCAGGA GG AGG G TCACC TG GGTCAGG TTG G
TGACCAACATGGTGAAACCC GTTT || ||| | ||||| || ||||||| |||
TGTCTCC CC TCT C AGTGG AC CCAGTCC GAC A
- GT CCAA T AA --- C

GAM1228 GGGCGGCCGCTCTAGAGGAT 1205 TAGAGGATCC 3806 C C C TCCAA T-- A T
CCAAGCTTACGTACGCGTGC AAGCTTACGT GGG GGC GCT TAGAGGA GCT ACGT CGCG
G
ATGCGACGTCATAGCTCTTC ACGC ||| ||| ||| ||||||| ||| |||| ||||
TATAGTGTCACCT TCC CTG TGA ATCTTCT CGA TGCA GCGT C
A - T ----- TAC - A

GAM1229 GGGCGGCCGCTCTAGAGGAT 1206 TAGAGGATCC 3808 C C C TCCAA T-- A T
CCAAGCTTACGTACGCGTGC AAGCTTACGT GGG GGC GCT TAGAGGA GCT ACGT CGCG
G
ATGCGACGTCATAGCTCTTC ACGC ||| ||| ||| ||||||| ||| |||| ||||
TATAGTGTCACCT TCC CTG TGA ATCTTCT CGA TGCA GCGT C
A - T ----- TAC - A

GAM1230 GAAACAGACTGGGCCAATGT 1207 TATCAAGGAA 3809 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM1231 TGCGCATCACTGTGGGCGTG 1208 AAGGAGCGGT 3810 CACT G - G G TAC CA
GATGGCTCCGTGTACAAGCT TCCATGCCAG TGCGCAT GT GGCGTGGA T GCTCC TG
AAGCTG C
GCACCCCAGCTTCAAGGAGC CGTG ||||||| || |||||||| | ||||| || ||||||
GGTTCCATGCCAGCGTGCGC ACGCGTG CG CCGTACCT G CGAGG AC TTCGAC /
A ---- A T G A --- CC

GAM1232 GAAACAGACTGGGCCAATGT 1209 TATCAAGGAA 3811 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM1233 ATGATGAACAGTATGCTTGG 1210 AGGTTCCTTC 3812 G AA TT----- GT T
GAGTCTTCTGCTGGAGGTTC ACTGTGCGTG AT ATG CAGTATGC GGGA CTTC G
CTTCACTGTGCGTGCTGACC CTGA || ||| |||||||| |||| ||||
ATGGT TG TAC GTCGTGCG TCCT GAGG C
G CA TGTCACT TG T

GAM1234 TTCTCAGTTCATAGGCTATC 1211 TATCCCATCA 3814 AG ATAG A C- ------ A GAGA
CCATCACCCTTTATTTGGAG CCCTTTATTT TTCTC TTC GCT TC CATCAC CCTTT TTTG
A
AAGGAACGAGAGAAGGAAAT GGAG ||||| ||| ||| || |||||| ||||| ||||
TAGTGATGATGAGGCAGAGG AAGAG AAG CGG AG GTAGTG GGAAG GAGC /
AAGAGAA -- GAGA - TA ATTAAA A AAGG

GAM1235 GAATTCTACAAGAGCCTCAC 1212 TCAAGCACTT 3813 A- A CCTCA AA GG A
TAATGACTGGGAAGACCACT TTCTGTAGAA GA TTCTACA GAG CT TGACTG AAG C
TGGCAGTCAAGCACTTTTCT GGTC || ||||||| ||| || |||||| |||
GTAGAAGGTC CT AAGATGT CTT GA ACTGAC TTC C
GG - TTCAC -- GG A

GAM1236 GGTTGTACTTGGCCAAGCGC 1213 AAGCGCTCAG 3815 ACTT CAA --- -- AA G
TCAGATCGGCAAGGGGCACC ATCGGCAAGG GGTTGT GGC GCGCT CAGATC GGC GG G
AGTCTTGATCTGCCCAGTGC GGCA |||||| ||| ||||| |||||| ||| ||
ACAGCCCCACAACC CCAACA CCG CGTGA GTCTAG CTG CC C
CC-- ACA CCC TT A- A

GAM1237 GACACAGAACCACTGGTTCA 1214 GAGAGTGTGA 3816 AACCACT - - A A AGAC
CCTACAATGAGACAATGACA CCCAAGCTGT GACACAG GGTT CAC CT CA TG A
GTGGAGAGTGTGACCCAAGC GTC ||||||| |||| ||| || || ||
TGTGTC CTGTGTC CCAG GTG GA GT AC /
GAAC--- T A G G AGTA

GAM1238 CCACCACCTGGAGCCCGAGG 1215 TTCTTCACGG 3817 C GGA- AG T AAGT
AGGTGCTCAAGTACAGCGAG GCAGCAAGCT CCACCA CT GCCCG GAGG GCTC A

TTCTTCACGGGCAGCAAGCT GGTG |||||| || ||||| |||| ||||
GGTGG GGTGGT GA CGGGC CTTC TGAG /
C ACGA A- T CGAC

GAM1239 GTTAAAGCTTACCGGGAGAA 1216 TACCGGGAGA 3818 A TTAC- GAAG AGAAG G
GATTGAGAAGGAGCTGGAGA AGATTGAGAA GTTAA GC CGGGA ATTG GAGCTG A
CAGTTTGCAATGATGTCCTG GGAG ||||| || ||||| |||| ||||||
TCTCTGCTTGAC CAGTT CG GTCCT TAAC TTTGAC G
- TCTCT GTAG G---- A

GAM1240 GGCCAATTGAAACAAACAGT 1217 TATTAGGGAT 3819 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1241 TCTTGTGTTGAGACTTCGTG 1218 TACACCACTC 3820 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM1242 GGGTGTTGAACTTGGCCACA 1219 TTGAACTTGG 3821 C TG CA- ATGTCAT - TCT
TCAATGTCATACAGCTTCTT CCACATCAAT GGGTGTTGAA T GC CATCA ACAG CT T
CACAGCCTGTTTAATCTGGT GTCA |||||||||| | || ||||| |||| ||
GCTTGTTGGCTTTAACATCC CCTACAATTT G TG GTGGT TGTC GA /
C GT TTC CTAATT- C CAC

GAM1243 GCTTCCCCACACTCAAGTTC 1220 ACTCAAGTTC 3822 - ACAC--- GTT T CCAG
TTTCCTGCCAGTGCCGACAG TTTCCTGCCA GC TTCCCC TCAA CT TCCTG T
GACGGTCATTGATTACAACG GTGC || |||||| |||| || |||||
GGGAACGC CG AAGGGG AGTT GG AGGAC G
C CAACATT ACT C AGCC

GAM1244 GCAGCACGTCATCTGCGACA 1221 TCCCCAAGGT 3823 AC- A GC AGG -- GC
AGGTGGGGCTGCAGAAGATC GTCAGAGAAG GCAGC GTC TCT GACA TGGGG CT A
CCCAAGGTGTCAGAGAAGAC ACCA ||||| ||| ||| |||| ||||| ||
CAAGCTGC CGTCG CAG AGA CTGT ACCCC GA /
AAC A GA GGA TA AG

GAM1245 AAAGCTGGTACGCCTGCAGG 1222 TGGTACGCCT 3824 T T C CA AC GT AA
TACCGGTCCGGAATTCCCGG GCAGGTACCG AAAGC GG ACGC TG GGT CG CCGG T

GTCGACCCACGCGTCCGTTT GTCC ||||| || |||| || ||| || ||||
T TTTTG CC TGCG AC CCA GC GGCC /
- - C -- -- TG CT

GAM1246 AACTTGAAAGTGAACAGTAT 1223 TGGCCCACAT 3825 T AG- T ACTTTCC AT A
GACTTTCCTGATCCAGAACA CTGTTTAATC AACT GAA TGAACAG ATG TG CCAGA C
GTTTGGCCCACATCTGTTTA TTCC |||| ||| ||||||| ||| || |||||
ATCTTCCAGTT TTGA CTT ATTTGTC TAC AC GGTTT A
C CTA - ------- CC G

GAM1247 GGAAGGACTTTCTGTTATTG 1224 TCTGTTATTG 3826 A CT ---- TTGC AG AAT
CAAAGTTGGTAAATAAAGAT CAAAGTTGGT GGA GGA TTC TGTTA AA TTGGTA A
GCCAAGGTTACTAACATCAC AAAT ||| ||| ||| ||||| || ||||||
GAATTTCCTCC CCT CCT AAG ACAAT TT AACCGT A
- TT CACT CA-- GG AGA

GAM1248 GGCCAATTGAAACAAACAGT 1225 TATTAGGGAT 3827 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1249 ATTTGAGAAGGAGGCTGCTG 1226 CTTCAAGTAT 3828 TG AGG - GA T AAA
AGATGGGAAAGGGCTCCTTC GCCTGGGTCT ATT AGA AGGC TGCT GA GGG G
AAGTATGCCTGGGTCTTGGA TGGA ||| ||| |||| |||| || |||
T TAG TCT TCCG ATGA CT CCT /
GT GGG T A- T CGG

GAM1250 TCAAAAACATGATTACAGGG 1227 TACAGGGACA 3829 AA GATTA G TC - TGAC
ACATCTCAGGCTGACTGTGC TCTCAGGCTG TCA AACAT CAG GACA TCAGG C T
TGTCCTGATTGTTGCTGCTG ACTG ||| ||||| ||| |||| ||||| |
GTGTTGGTGA AGT TTGTG GTC TTGT AGTCC G G
GG GTC-- G T- T TCGT

GAM1251 CTGGAGCAGCTGCGTAAAAC 1228 GAGCAGCTGC 3830 --- G AAAACATAC - G AT A
ATACAGGCCGGAGCTTATCA GTAAAACATA CTGGA GCA CTGCGT AGGC C GAGCTT CA
A
AAGATGGCAAGTTTGGGGCC CAGG ||||| ||| |||||| |||| | |||||| ||
TACATGCAGGTGCACATTCA GACTT CGT GACGTA TCCG G TTTGAA GT G
G ACA G CA------- G G CG A

GAM1252 CATTGTCGTCATTGGACACG 1229 CGTCATTGGA 3831 GTC-- T- A C ATTC C

TAGATTCGGGCAAGTCCACC CACGTAGATT CATT GTCA TGG CA GTAG GGG A
ACTACTGGCCATCTGATCTA CGGG |||| |||| ||| || |||| |||
TAAATG GTAA TAGT ACC GT CATC CCT A
ATATC CT G - ACCA G

GAM1253 GCGACCGGGACCATATGATA 1230 TATTATGGAG 3832 A GA - AGA AATAGG
GACCAATAGGAGGAAGAGGG CTGGGCGT GCG CCGG CCATA TGAT CC A
GGTTATTATGGAGCTGGGCG ||| |||| ||||| |||| ||
T TGC GGTC GGTAT ATTG GG /
G GA T GG- AGAAGG

GAM1254 CTTCATCTGGTGTTGAGACT 1231 TACACCACTC 3833 A G GAGA --- C AAAGGA
TCGGGGTGGTGCTAAGAAAA CCAAGAAGAA CTTC TCT GTGTT CTTC GGGGTGGTG TAAGA
A
GGAAGAAGAAGTCTTACACC CAAG |||| ||| ||||| |||| |||||||||| |||||
ACTCCCAAGAAGAACAAGCA GAAG AGA TACGA GAAG CCTCACCAC ATTCT G
TAAGAGGAAG G A ACAA AAC - GAAGAA

GAM1255 GTTTTCATGGGAAGCCACTT 1232 CATGGGAAGC 3834 A ------ CACTTTGA T GT
TGACAGGCATTACTGTGGCA CACTTTGACA GTTTTC TGG GAAGC CAGGCA TACT G
AGTGTTGTCTGACTTACTGC GGCA |||||| ||| ||||| |||||| ||||
TTCAACAAACCAGAAGAC CAGAAG ACC CTTCG GTCTGT GTGA G
- AAACAA TCATTCA- T AC

GAM1256 CATGGCCAAGCGGCTGAGCC 1233 TACCGCCAGT 3835 C -- G CAAAT G AAAAC A-
AGA
AAATTGGGGTGGAAAACACA CCATGTTCAG CATGG CA AGCG CTGAGC TGGG TGG
ACAG GG A
GAGGAGAACCGCCGGCTGTA TGCT ||||| || |||| |||||| |||| ||| |||| ||
CCGCCAGTCCATGTTCAGTG GTGCC GT TCGT GACTTG ACCT ACC TGTC CC /
CTGATGACCGTG A AG - T---- G GCCA- GG GCC

GAM1257 GATGATAATGGTGTTCCCTT 1234 AATGGTGTTC 3836 ATA GT TT- C GAAC
CGTCCGAACCATCCAGGATA CCTTCGTCCG GATG ATG G CCCTT GTCC C
AGGGCATCGTCGTGGGCATC AACC |||| ||| | ||||| ||||
CTAC TGC C GGGAA TAGG A
GGG TG TAC - ACCT

GAM1258 CATTGTCGTCATTGGACACG 1235 CGTCATTGGA 3837 GTC-- T- A C ATTC C
TAGATTCGGGCAAGTCCACC CACGTAGATT CATT GTCA TGG CA GTAG GGG A
ACTACTGGCCATCTGATCTA CGGG |||| |||| ||| || |||| |||
TAAATG GTAA TAGT ACC GT CATC CCT A
ATATC CT G - ACCA G

GAM1259 GGTGACAACATGCTGGAGCC 1236 TTGGTTCAAG 3838 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1260 TGTTCTTGGTGAGAAGGGCC 1237 TTCAGAAGAG 3841 GG A G GGA GG A T
GGCGGATTCGGGAACTGACT GTTGGCTTTC TGTTCTT TG GAAGG CCGGC TTC GAACTG C
G
GCTGTAGTTCAGAAGAGGTT CAGA ||||||| || ||||| ||||| ||| |||||| |
GGCTTTCCAGAGGGCA ACGGGAG AC CTTTC GGTTG AAG CTTGAT G C
-- - - GAG A- - T

GAM1261 CGAGGTTGTGGTGTCTGGGA 1238 GACCCTGTTA 3839 G T GTCT- AAA A--- - GAG
AA TG A
AACTCCGAGGACAGAGGGCT ACTACTACGT CGA GT GTGGT GGG CTCCG GGA CA
GGCT ATCCA A G
AAATCCATGAAGTTTGTGGA TG ||| || ||||| ||| ||||| ||| || |||| ||||| |
TGGCTGATGATCCACAGCGG GTT CA CATCA CCC GAGGC CCT GT TCGG
TAGGT T /
AGACCCTGTTAACTACTACG G T ATTGT A-- GACA A AG- -- GT T
TTG

GAM1262 GTAGAGCTTTATGCTGAAAA 1239 GAGCTTTATG 3840 - TA GAAAA - T A
GGTGGCCACTAGAGGTCTGT CTGAAAAGGT GTAGAG CTT TGCT GGTGGC CAC AG G
GTGCCATTGCCCAGGCAGAG GGCC |||||| ||| |||| |||||| ||| ||
TCTCTGC CGTCTC GAG ACGG TTACCG GTG TC G
T -- ACCCG T - T

GAM1263 CCAGTTGATGGGCTGCCAGA 1240 CTGCCTCCAG 3842 GG C GA - T GGA T
TCTGGGGCATGCCCAGGACC GTGACAGCAA CCAGTTGAT GCTG CA TCTGG GGCA GCCCA
CC C
TCATGGATGGGCTGCCTCCA TCAG ||||||||| |||| || ||||| |||| ||||| ||
GGTGACAGCAATCAGCTGG GGTCGACTA CGAC GT GGACC CCGT CGGGT GG A
A- A -- T - A-- T

GAM1264 TTGGTGCCCAGGGAGAACCC 1241 ACTCTGGTGG 3843 G AGAACCC -- - GA
TCCT T
CTTGGATATCGCCAGGATGA ATATGGCCAG TT GTGCCCAGGG CTTGG ATATC GCCAG
TGA AGC A
TCCTAGCTATCGTTCTTTTC GATG || |||||||||| ||||| ||||| ||||| ||| |||
ACTCTGGTGGATATGGCCAG AG TATGGGTTCC GGACC TATAG TGGTC ACT TTG
T
GATGCCTTGGGTATGGA G GTA---- GG G TC TTTC C

GAM1265 GGTGACAACATGCTGGCAGC 1242 CTTCAAGGGC 3844 AA---- --- C T TA
CAAGTGCTAACATGCCTTGG ATGGAACACG GGTGAC CATGCT GG AGCCAAG GC A
CTTCAAGGGCATGGAACACG TCAC ||||||| ||||||| || ||||||| ||
TCACC CCACTG GTACGG CT TCGGTTC CG C
CACAAG GAA - - TA

GAM1266 GGCTTGCAGGAGCTTTCGGG 1243 TGTCAAGGAC 3845 TTGC G TC CA GA -- G AT
ACACTTTGAGAACCAGAAGG TCCCAAGCTG GGC AG AGCTT GGGA CTTTGA AC CAGAAG
TG G
TGATGTACGGCTTCTGCAGT CTCT ||| || ||||| |||| |||||| || |||||| ||
GTCAAGGACTCCCAAGCTGC CCG TC TCGAA CCCT GGAACT TG GTCTTC GC /
TCTGCC TC-- G -- CA G- AC G AT

GAM1267 GGTCTTGTCAATTCTGTTAC 1244 TTCACACAGA 3846 G ----- TACTA CTG
TAGAGGACTGGCTTATCTTC ATTACCACGA GGTCTT TC AATTCTGT GAGGA G
ACACAGAATTACCACGAGGA GGAG ||||||| || |||||||| |||||
GATC CTAGAG AG TTAAGACA CTTCT C
G CACCA CA--- ATT

GAM1268 TTGTCGTCATTGGACACGTA 1245 TAAATGCGGT 3847 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM1269 CATTGTCGTCATTGGACACG 1246 CGTCATTGGA 3848 GTC-- T- A C ATTC C
TAGATTCGGGCAAGTCCACC CACGTAGATT CATT GTCA TGG CA GTAG GGG A
ACTACTGGCCATCTGATCTA CGGG |||| |||| ||| || |||| |||
TAAATG GTAA TAGT ACC GT CATC CCT A
ATATC CT G - ACCA G

GAM1270 GTTCCCGCATCTGGAGTTCA 1247 TCAACACCCG 3850 -- - A CA A A C G
GGAGTATTCGGGGAAACCTC GCTTCGGAAG GTTC CC GC TCTGGAGTT GG GT TT GGG A
AACACCCGGCTTCGGAAGCT CTGG |||| || || ||||||||| || || || |||
GGACGAGC CGAG GG CG AGGCTTCGG CC CA AA TCC A
CA T A -- - C C A

GAM1271 CAAGATTCTTGATACTGCAC 1248 AGAGAAAAGC 3849 A AT-- T- A--- A
TCTCTAAGATTGGAGAGAAA CTGTTTACCA CAAG TTCTTG AC GC CTCTCTA G
AGCCTGTTTACCAAGGAGCT AGGA |||| |||||| || || |||||||
TG GTTC AGGAAC TG CG GAGAGGT A
G CATT TC AAAA T

GAM1272 CCCTGGAGGAGATCTATCTC 1249 AGAGATCATT 3851 T T--- TCTG GCC
TTCTGCCTGCCCATTAAGGA GATTTCTTCC CCC GGAGGAGATC ATCTCT CCT C
ATCAGAGATCATTGATTTCT TGGG ||| |||||||||| |||||| |||
TCCTGGG GGG CCTTCTTTAG TAGAGA GGA A
T TTAC CTAA ATT

GAM1273 GAGACTGGATGGCTTTTCAT 1250 TGGCTTTTCA 3852 CT TC GA - A GAG AA
TGACATGGTAGAGAGGAAAT TTGACATGGT GAGA GGATGGCTTT ATT CAT GGT GA GA T
GGATCAAATCCACCAATGAA AGAG |||| |||||||||| ||| ||| ||| || ||
ATCAAAGCTGTCCTCTT TTCT CCTGTCGAAA TAA GTA CCA CT CT G
-- C- A- A C AAA AG

GAM1274 GCAAATGCTTCTAAACGGAC 1251 CTGCATGGGT 3853 GC--- AAACG ---- G
TCAGCAGATGCGTAGCATTT TAATTGAGAA GCAAAT TTCT GACT CAGCAGATGC T
GCTGCATGGGTTAATTGAGA TAGA |||||| |||| |||| ||||||||||
ATAGAAATTTGC CGTTTA AAGA TTGG GTCGTTTACG /
AAGAT GTTAA GTAC A

GAM1275 CAGGTGAAGGCACCTGGCTG 1252 TTCATCACCA 3854 A CAC C CCAT-- CTT
ACCATCAATGCTTTCCACAT GTCACCTCCA CAGGTG AGG CTGG TGA CAATG T
TGTATTCATCACCAGTCACC CTTG |||||| ||| |||| ||| |||||
TCCACTTG GTTCAC TCC GACC ACT GTTAC /
C ACT - ACTTAT ACC

GAM1276 GGCCAATTGAAACAAACAGT 1253 TATTAGGGAT 3855 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1277 GGCCAATTGAAACAAACAGT 1254 TATTAGGGAT 3856 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1278 GGCCAATTGAAACAAACAGT 1255 TATTAGGGAT 3857 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /

CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1279 CCCCAGCCAAAGATGACAGC 1256 TTTATCTTTT 3858 - C- CA- AACAACA
AGAACAACATAATTTACACT TGCTGAGGG CCC CAGC AAAGATGA GCAG T
GTGATTTATCTTTTTGCTGA ||| |||| |||||||| ||||
GGG GGG GTCG TTTCTATT TGTC A
A TT TAG ACATTTA

GAM1280 GGCCAATTGAAACAAACAGT 1257 TATTAGGGAT 3859 C T ACAAACAG G GTT T A GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1281 GACTATCCAGTTGATGGGCT 1258 CTGCCTCCAG 3861 - GG C GA - T GGA T
GCCAGATCTGGGGCATGCCC GTGACAGCAA GACTA TCCAGTTGAT GCTG CA TCTGG GGCA GCCCA CC C
AGGACCTCATGGATGGGCTG TCAG ||||| |||||||||| |||| || ||||| |||| ||||| ||
CCTCCAGGTGACAGCAATCA TTGGT GGGTCGACTA CGAC GT GGACC CCGT CGGGT GG A
GCTGGGCTGGTT C A- A -- T - A-- T

GAM1282 CGCCAGGATGATCCTAGCTA 1259 TATCGTTCTT 3860 A ATC- G GTTCT C - T A- G A
TCGTTCTTTTCACTCTGGTG TTCACTCTGG CGCCAGG TG CTA CTATC TTTCA TC TGG GG TATG CCAGG T
GATATGGCCAGGATGCCTTG TGGA ||||||| || ||| ||||| ||||| || ||| || |||| |||||
GGTATGGACCCCATGATGGA GTGGTCC AC GGT GGTAG AAGGT AG ACC CC GTAT GGTTC G
ACATGAGATGGGTGGCCACC C CACC G AGTAC - T - AG G C
ACCCTGGTG

GAM1283 GGAGGGGCTGGGCTCTACCC 1260 ACCCCTTTCT 3862 G - ACCC T TTCC CA CT
CTTTCTTCTTTCCATCCAGT TCTTTCCATC GGAGGG CTGGGCT CT CTTTCT CT ATC GT A
CTATTGCCAGATCCAGAGAA CAGT |||||| ||||||| || |||||| || ||| ||
AGCGCGGAAGCCCAGCTCTC CCTCTC GACCCGA GG GAAAGA GA TAG CG /
C - A CGC- - CC-- AC TT

GAM1284 TCTTGTGTTGAGACTTCGTG 1261 TACACCACTC 3863 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM1285 GGAGTGGGGTGCAGTGAGTG 1262 GTGCAGTGAG 3864 TG--- - AG CTCAA T AGA
C CGA
GCCTCAAAGTTGTGCAGATG TGGCCTCAAA GGAG GGGTGCAG TG TGGC AGTTG GC
TG TTC G
CTTCCGAGCCAGAAACAAAG GTTG |||| |||||||| || |||| ||||| || || |||
CCAGCTGCCGCCGTCCATCT CCTC CTCACGTC AC GCCG TCGAC CG AC AAG /
GCACTCATGTCCTCC CTGTA T CT CCG-- - AA- A ACC

GAM1286 GGCCAATTGAAACAAACAGT 1263 TATTAGGGAT 3865 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1287 GAAGGTTAAGCTGGCTGTCC 1264 TGAGAATGGC 3866 TAA ---- C GAAA A
TGAAATATTATAAGGTGGAT AAATTAGTCG GAAGGT GCTG GCTGT CT TATT T
GAGAATGGCAAATTAGTCGC CCTT |||||| |||| ||||| || ||||
CTTC CTTCCG TGAT CGGTA GA GTGG A
C-- TAAA A GTAG A

GAM1288 TCTTGTGTTGAGACTTCGTG 1265 TACACCACTC 3867 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| ||||| G
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM1289 CCACCTGCTCTTGTCCACGG 1266 TCCACGGTGA 3868 A - CTTG - GAG-- G G
TGAGCTTGCTGTAGAGGAAG GCTTGCTGTA CC CC TGCT TCC ACGGT CTT CT T
AAGGAGCCGTCGGAGTCCAG GAGG || || |||| ||| ||||| ||| ||
CACGGGG GG GG ACGA AGG TGCCG GAA GA A
- C CCTG C AGGAA G G

GAM1290 TTGCCGGCCGTCGCACTCAT 1267 TGCGTGTAGT 3869 - TC T ATTTA------- GGA
TTACCCGGAGACAGGGAGAG GGTTGTGCAG TTGC CGGCCG GCAC C CCC G
GCTCTTCTGCGTGTAGTGGT |||| |||||| |||| | |||
TGTGCAG GACG GTTGGT TGTG G GGG /
T GA C TCTTCTCGGAGA ACA

GAM1291 GCCGGCCTGGGTGCTTACCA 1268 TTTTCCTAGC 3870 T TACC-- TCTC GA
GCTGTCTCAGGATCCAAGGA TACATCTGGT GCCGGCC GGGTGCT AGCTG AGGATCCAAG
A
ACGTTTGGGTTTTCCTAGCT ACCT ||||||| ||||||| ||||| ||||||||||

ACATCTGGTACCTTGGCTGG CGGTCGG TCCATGG TCGAT TTTTGGGTTT /
C T TCTACA CC-- GC

GAM1292 GCTGCTTGAGTCATGCTGAA 1269 TAAGAAGTTG 3871 - AG GCT - - G A T
GAGATAGGCTTCATAGATTA TCATCATTCT GCTGCT TG TCAT GAA GA GATAG CTTC TAGAT
A
TATTTAAGAAGTTGTCATCA GAAT |||||| || |||| ||| || ||||| |||| |||||
TTCTGAATGAGGTACAGCAG TGACGA AT AGTA CTT CT CTGTT GAAG ATTTA /
T C GG AGT A A - A T

GAM1293 GAAACAGACTGGGCCAATGT 1270 TATCAAGGAA 3872 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM1294 GCCAACCTTGAAGCCAGTGG 1271 TTGAAGCCAG 3873 A - TG - G - ATCC
GGCACCAATCCACAAACTGG TGGGGCACCA GCCA CC T AAGCCA GTG GGCA CCA A
ATGCTGCGCTTGGTTTTGAT ATCC |||| || | |||||| ||| |||| |||
GGTGGC CGGT GG A TTTGGT CGC TCGT GGT C
- T GT T G A CAAA

GAM1295 GGCCAATTGAAACAAACAGT 1272 TATTAGGGAT 3874 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1296 GCCTGGGCCATGAAGAGCTT 1273 TGGCAGTAAG 3875 CT T A ----- TA TT TG C T
GCCTAAGTTTTGGGCAGTGA TGTTTATCTG GC GGGCCA GA GAGC TTGCC AG T GG AG
G
ACTCCTTGATGTTCTGGCAG GCCT || |||||| || |||| ||||| || | || ||
TAAGTGTTTATCTGGCCTGC CG TCCGGT CT TTTG GACGG TT A TC TC A
-- - A TGAAT TC GT GT C A

GAM1297 GAAACAGACTGGGCCAATGT 1274 TATCAAGGAA 3876 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||

TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM1298 TGGGGCTCATTTGCAGGGGG 1275 GCTCATTTGC 3877 CT T A CAAA TCA
GAGCCAAAAGGGTCATCATC AGGGGGGAGC TGGGG CATT GCAGGGGGG GC AGGG T
TCTGCCCCCTCTGCTGATGC CAAA ||||| |||| ||||||||| || ||||
CCCCA ACCCC GTAG CGTCTCCCC CG TCTC /
C- T - ---- TAC

GAM1299 AGTACAAGGGCTATCTGGTA 1276 TACAGAAGAA 3878 T GG - ---- GAT--- A G
TCTGTAGATGGCTACATGAA TACATAGATG AG ACAAG CTATCTG GTA TCTGTA GGCT
CAT A
CATGCAGCTTGCAAATACAG GAGC || ||||| ||||||| ||| |||||| |||| |||
AAGAATACATAGATGGAGCT TC TGTTC GGTAGAT CAT AGACAT TCGA GTA A
TGTCT - GA A AAGA AAACGT C C

GAM1300 CTTGTGGGAGAGATTATCAA 1277 TGGGAGAGAT 3881 T GA ATC -------- - G A AT
GCGTTTTGAGCAGAAAGGAT TATCAAGCGT CTTG GGGAGA TT AAGC GTTTT GA CAG
AAGG T
TCCGCCTTGTTGGTCTGAAA TTTG |||| |||||| || |||| ||||| || ||| ||||
TTCATGCAAGCTTCCGAAGA GAAC TCTTCT AA TTCG TAAAG CT GTT TTCC C
TCTTCTCAAG - AG GCC AACGTACT T G G GC

GAM1301 TCTTGTGTTGAGACTTCGTG 1278 TACACCACTC 3883 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM1302 TCCACAATGAACACAAGTGT 1279 TCAGTGGTCA 3884 A AA-- - GTG T T A-- T T
GTTGTTGTCTTCTATCTTCT GCGGAAACTT TCCAC ATG CA CAAGT TTGTTG CT CT TCT CT
C
TCATGGCAGACTCAGTGGTC GATG ||||| ||| || ||||| |||||| || || ||| ||
AGCGGAAACTTGATGATAGC GGGTG TAC GT GTTCA GGCGAC GG GA AGA GG A
ATAGTGGG A GATA A AA- T T CTC C T

GAM1303 ACATCAAGACAATGTATACT 1280 TAGCTGTAGT 3885 - C A TTCAAA CCATAC
ATTTCAAATATATCCATACA ACATGTTTTC ACATCAA GA AATGT TACTAT TATAT A
TAATCAAATATAGCTGTAGT ATTG ||||||| || ||||| |||||| |||||
ACATGTTTTCATTGGTGT TGTGGTT CT TTGTA ATGATG ATATA T
A T C TCG--- AACTAA

GAM1304 AGAATAGGGAGTTTTCACAC 1281 TTTGCCATCT 3886 A - TT ------ TT TT TTTT
GTTTCTTGATCTTTTCACCT TGTGTTGACT AGA TAGG GAGTT CACA CG TC GATC C
GATCCTGATTTGCCATCTTG CACC ||| |||| ||||| |||| || || ||||
TGTTGACTCACCTATCT TCT ATCC CTCAG GTGT GT AG CTAG /
- A TT TCTACC TT TC TCCA

GAM1305 GGAATGCTGCAAAAATACTC 1282 TACTCTAGTT 3887 - G CAA C TTCAACA GATC
TAGTTCAACAAAGAGTTATG CAACAAAGAG GG AAT CTG AAATACT TAG AAGAGTTAT A
ATCACAAAATAATTTTTATC TTAT || ||| ||| ||||||| ||| |||||||||
CATTCTACAGTGTTTCAGAA CC TTA GAC TTTGTGA ATC TTTTTAATA /
TTACC A A --- C TTACCTA AAAC

GAM1306 GGGCGGCCGCTCTAGAGGAT 1283 TAGAGGATCC 3888 C C C TCCAA T-- A T
CCAAGCTTACGTACGCGTGC AAGCTTACGT GGG GGC GCT TAGAGGA GCT ACGT CGCG
G
ATGCGACGTCATAGCTCTTC ACGC ||| ||| ||| ||||||| ||| |||| ||||
TATAGTGTCACCT TCC CTG TGA ATCTTCT CGA TGCA GCGT C
A - T ----- TAC - A

GAM1307 GGGCGGCCGCTCTAGAGGAT 1284 TAGAGGATCC 3889 C C C TCCAA T-- A T
CCAAGCTTACGTACGCGTGC AAGCTTACGT GGG GGC GCT TAGAGGA GCT ACGT CGCG
G
ATGCGACGTCATAGCTCTTC ACGC ||| ||| ||| ||||||| ||| |||| ||||
TATAGTGTCACCT TCC CTG TGA ATCTTCT CGA TGCA GCGT C
A - T ----- TAC - A

GAM1308 CTTGGTTCTACAGCCATTGG 1285 AGCCATTGGG 3892 GG CAT ATC G A
GATCCAGACATCAGAGGGTG ATCCAGACAT CTT TTCTACAGC TGGG CA ACATC G
TGTGCCTAGCTGTGGAGAAG CAGA ||| ||||||||| |||| || |||||
AG GAG GAGGTGTCG ATCC GT TGTGG A
AA --- --- G G

GAM1309 AATTGATAAAAGCCAGAGTT 1286 TAAAAGCCAG 3890 ATA G GA AACCAC T - A-
A AGAC
GGAGACACAGAACCACTGGT AGTTGGAGAC ATTG AAAGCCAGA TTGGA CACAG TGG
TCAC CT CCA TG A
TCACCTACCAATGAGACAAT ACAG |||| ||||||||| ||||| ||||| ||| |||| || ||| ||
GACAGTGGAGAGTGTGACCC TGAC TTTCGGTCT AACCT GTGTC ACC AGTG GA
GGT AC /
AAGCTGTGTCCAATCTGGCT G-- - -- GA---- C T GA G AGTA
TTGCAGTT

GAM1310 CCCACTGATGGAGCCAGCAG 1287 TGATGCTCAC 3891 G AGC AGCAT AA-- GT
CATTGAGAAAATTGTAGAGA ATAGGTTGTG CCCACT ATGG CAGC TGAG AATT A
TTGATGCTCACATAGGTTGT CCAT |||||| |||| |||| |||| ||||

GCCATGAGTGGG GGGTGA TACC GTTG ACTC TTAG /
G GT- GATAC GTAG AG

GAM1311 TCTGTGTGAGACTTCGTGGT 1288 TACACCACTC 3893 - GAGA- GT--- C AAAGGAA
GGTGCTAAGAAAAGGAACGA CCAAGAAGAA TCT GTGT CTTC GGTGGTG TAAGA C
AGAAGTCTTACACCACTCCC TAAG ||| |||| |||| ||||||| |||||
AAGAAGAATAAGCACAAGA AGA CACG GAAG TCACCAC ATTCT /
A AATAA AACCC - GAAGAAG

GAM1312 TCTTGTGTTGAGACTTCGTG 1289 TACACCACTC 3894 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM1313 GCATAATCGGTCACTCGTAT 1290 TGAATGGACG 3895 AATC --- A GAA TATT TAT
AGAACAGTATTGTTTCTATA GGTTCAGGCC GCAT GGTC ACTCGT TA CAG GTTTC A
ATTTGAAGCTTTCTGAATGG TGAT |||| |||| |||||| || ||| |||||
ACGGGTTCAGGCCTGATGC CGTA CCGG TGGGCA GT GTC CGAAG A
GT-- ACT G AA- TTT- TTT

GAM1314 GGTGTGAGAGCGGTAAGATG 1291 TCAGCACCGA 3896 T A C AA- C GG-- - G G
TCC GC
GCGGCGGCGGCGGTGGTGGA CCGGGAGGCC GG GTG GAG GGT GATGG GGC CGG
CGGTG TG AGT AGAGA C
GTTCCAGAGAGCCCAGTCTC TCCA || ||| ||| ||| ||||| ||| ||| ||||| || ||| |||||
TACTCAGCACCGACCGGGAG CC CAC CTC CTA CTACC CCG GCC GCCAC AC TCA
TCTCT C
GCCTCCATCGACATCCTCCA T - - CAG T GAGG A G - --- GA
CTCC

GAM1315 TTATGCTGCAGCATATTGTA 1292 CAGCATATTG 3898 C A TACT TGCT
CTGGCCTGCTGCTGGCCCGC TACTGGCCTG TTATGCTG AGC TATTG GGCCTGC G
AGGCTTCTCAATAGGTTTGG CTGC |||||||| ||| ||||| |||||||
CATGG GGTACGGT TTG ATAAC TCGGACG /
- G TCT- CCCG

GAM1316 ATCTATGAAGGCCAAGTGGA 1293 TGGTCAGCCA 3897 TGAA CAA GA - GA A
GG
GGTGACTGGTGATGAATACA GGTGCCTTCA ATCTA GGC GTGGAGGT CTGG TGAT AT
CAATGT A
ATGTGGAAAGCATTGATGGT CCTG ||||| ||| |||||||| |||| |||| || ||||||
CAGCCAGGTGCCTTCACCTG TAGGT TCG CACTTCCG GACC ACTG TA GTTACG /
CTATTTGGAT TTA- TC- TG G G- - AA

GAM1317 CTTGGTTCTACAGCCATTGG 1294 AGCCATTGGG 3900 GG CAT ATC G A
GATCCAGACATCAGAGGGTG ATCCAGACAT CTT TTCTACAGC TGGG CA ACATC G
TGTGCCTAGCTGTGGAGAAG CAGA ||| ||||||||| |||| || |||||
AG GAG GAGGTGTCG ATCC GT TGTGG A
AA --- --- G G

GAM1318 CCCACTGATGGAGCCCAGCA 1295 TGATGCTCAC 3899 G AGCC AGCAT AA-- GT
GCATTGAGAAAATTGTAGAG ATAGGTTGTG CCCACT ATGG CAGC TGAG AATT A
ATTGATGCTCACATAGGTTG CCAT |||||| |||| |||| |||| ||||
TGCCATGAGTGGG GGGTGA TACC GTTG ACTC TTAG /
G GT-- GATAC GTAG AG

GAM1319 GGCCAATTGAAACAAACAGT 1296 TATTAGGGAT 3901 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1320 GGCCAATTGAAACAAACAGT 1297 TATTAGGGAT 3902 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1321 CCAGGAGCTACACACCTTCG 1298 TCGCCCAGAT 3903 - - CA-- --- GA GCCA
AGGTGACCGGCCAGGAAACG CAAGGCTCAT CCAG GAG CTACA CCT TC GGTGACCG G
GTCGCCCAGATCAAGGCTCA GTAG |||| ||| ||||| ||| || ||||||||
TGTAGCCTCACTGG GGTC CTC GATGT GGA AG CCGCTGGC /
A C ACTC ACT AC AAAG

GAM1322 GCATTGCCCGGAAGATCAAG 1299 GCCCGGAAGA 3904 AGATCAAG G T CA C
TCGTGCTCCTGGCAGGCGCG TCAAGTCGTG GCATTGCCCGGA TCGT CTCC GG GG G
CCCCTGGAGGATGAGGCCAC CTCC |||||||||||| |||| |||| || ||
TCTGGGCAGTGC CGTGACGGGTCT AGTA GAGG CC CC C
CACCGG-- G T -- G

GAM1323 GAAACAGACTGGGCCAATGT 1300 TATCAAGGAA 3905 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG ||||||| ||||||| ||||| ||||| ||| |||||

TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM1324 TGGCATCCCAGATGTTGCAG 1301 TTGCAGTTGA 3906 - AGA AG GAAG T CA A A
TTGAAGTCGTCGTAGCCAGC AGTCGTCGTA TGGCATC CC TGTTGC TT TCG CGTAGC
GCG GC G
GAGCAGCAGCCGTCCGCTGC GCCA ||||||| || |||||| || ||| |||||| ||| ||
GCGAGAAGGCAACAGAGGTG ACCGTAG GG ACAACG AG AGC GCGTCG TGC CG C
ATGCCA T AG- GA ---- - CC - A

GAM1325 TCTTGTGTTGAGACTTCGTG 1302 TACACCACTC 3907 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM1326 TAGGAAGTAATGTAGAAGAG 1303 TTGGTGGCCA 3910 TAATGTA A---- G ATA T
ATAGTGATTAATAATACACG AGAATCTCTT TAGGAAG GAAGAGAT GT ATTAATA
CACGTT C
TTTCCTAATGTGGGATATTG CGTT ||||||| |||||||| || ||||||| ||||||
GTGGCCAAGAATCTCTTCGT GTCCTTC CTTCTCTA CG TGGTTAT GTGTAA C
TCTTCCTG TTG---- AGAAC G AGG T

GAM1327 AAAAGCTGGATTGCTGATTT 1304 ATGACTGTAG 3908 ATTGCT ATAAACAAG TAA
TTGCTAATAAACAAGATGTT CAGAAATCTC AAAAGCTGG GATTTTTGCTA ATGT A
AAAGAATGCATGACTGTAGC CCAG ||||||||| |||||||||| ||||
AGAAATCTCCCAGTTTTT TTTTTGACC CTAAAGACGAT TACG G
CT---- GTCAG---- TAA

GAM1328 GTGGCATATCCAGGCATGCT 1305 GGACTTGAAT 3909 - GG TGCT G CTAAC AGG
GTGCTCTAACTGGCGAGGGA GGATGATGTC GTGGCAT ATCCA CA GT CT TGGCG G
TTGTGCCAAGGACTTGAATG AC ||||||| ||||| || || || |||||
GATGATGTCAC CACTGTA TAGGT GT CA GA ACCGT A
G AA T--- G ----- GTT

GAM1329 GAAACAGACTGGGCCAATGT 1306 TATCAAGGAA 3911 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT

TT

GAM1330 TCTATCTGGTCTTTGCAAGC 1307 TATCTGGTCT 3912 TC A TCTTC TT GA TC C
AGTCTTCAGGTTAAAGATAC TTGCAAGCAG TCTATCTGG TTTGCA GCAG AGG AAA TACT
TAA A
TTCTAACAGGTTACAGTACA TCTT ||||||||| |||||| |||| ||| ||| |||| |||
TTTCCTCTGTATGTAAATTC GGGTAGACT AAATGT TGTC TCC TTT ATGA ATT G
AGATGGG T- A ----- -- AC C- G

GAM1331 CTTTACTGCAGGTAGCCAGA 1308 CACCAGGTGC 3913 A TG -- C GACA TA- GCC
CAGCCTTAGGAGCCACATAT CATGCCTATT CTTT C CAGG TAG CA GCCT GGA A
CCACCAGGTGCCATGCCTAT CCTG |||| | |||| ||| || |||| |||
TCCTGTGGAGAG GAGA G GTCC ATC GT TGGA CCT C
- GT TT C ACCG CCA ATA

GAM1332 CAAAGTGCAGCTGGCCATGC 1309 CGAAGGCTTG 3914 - A TG CCA GA--- A A- GG
AGACCTACGAGATGGTGGAT ATGCAGACCT CA AAGTGC GC G TGCA CCT CGAG TGGT
A
AAACCACATTCGAAGGCTTG GGCG || |||||| || | |||| ||| |||| ||||
ATGCAGACCTGGCGCGCTTG GT TTCGCG CG C ACGT GGA GCTT ACCA T
TG G - GT CAG AGTTC A AC AA

GAM1333 CATTAGATAAATCAATTGAC 1310 TAAATCAATT 3915 GATA A CAAAAG TT
TGCAAAAGCATTTTTCATGA GACTGCAAAA CATTA AATCAATTG CTG CAT T
AGTCAGCCAGTTGATTAGTA GCAT ||||| ||||||||| ||| |||
GTG GTGAT TTAGTTGAC GAC GTA /
GA-- C TGAA-- CT

GAM1334 AGCGGAAGATGGAGAACCGT 1311 TGGAGAACCG 3916 AAGA C TTA GGA - G T
GATTACCGGGATGCACAGGA TGATTACCGG AGCGG TGGAGAAC GTGA CCG TGCA CAG
AG T
GTTTGCTGCTGATGTACGGC GATG ||||| |||||||| |||| ||| |||| ||| ||
TTATGTTCTCCAACTGCT TCGTC ACCTCTTG TATT GGC ATGT GTC TC T
A--- - C-- --- A G G

GAM1335 GAAACAGACTGGGCCAATGT 1312 TATCAAGGAA 3917 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM1336 GGCCAATTGAAACAAACAGT 1313 TATTAGGGAT 3918 C T ACAAACAG G GTT T A GAT

TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T

ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||

CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /

CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1337 TGAAACAGACTGGGCCAATG 1314 TATCAAGGAA 3919 C -- CACAAAGAA - CA- ACCGAT

TCCACAAAGAATTCCTGGTC GGGCAGGCGT TGAAACAGA TGGGCCA ATGTC TTCCT GGT GCACC G

AGCACCACCGATGTCCAAAG GATG ||||||||| ||||||| ||||| ||||| ||| |||||

GTGCAATATCAAGGAAGGGC GTTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG /

AGGCGTGATGGCTTATTTGT - AG ACGGG---- A TAA AAACCT

TTTG

GAM1338 GGCCAATTGAAACAAACAGT 1315 TATTAGGGAT 3920 C T ACAAACAG G GTT T A GAT

TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T

ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||

CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /

CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1339 CCGGAACCTGCTCATCTGGA 1316 AGAGTTGTTC 3921 GA - - A CAA G -- AAA

TCAAGAAGAATTTGCTAAAA ATCCAGGGAG CCG AC CTG CTC TCTGGAT GAA AATTT GCT A

GAGCGGCCAGAGTTGTTCAT ACAG ||| || ||| ||| ||||||| ||| ||||| |||

CCAGGGAGACAGCGTGCGG GGC TG GAC GAG GGACCTA CTT TTGAG CGG G

G- C A - --- G AC CGA

GAM1340 CCGGAACCTGCTCATCTGGA 1317 AGAGTTGTTC 3922 GA - - A CAA G -- AAA

TCAAGAAGAATTTGCTAAAA ATCCAGGGAG CCG AC CTG CTC TCTGGAT GAA AATTT GCT A

GAGCGGCCAGAGTTGTTCAT ACAG ||| || ||| ||| ||||||| ||| ||||| |||

CCAGGGAGACAGCGTGCGG GGC TG GAC GAG GGACCTA CTT TTGAG CGG G

G- C A - --- G AC CGA

GAM1341 TTCACAGTTCCGGCTTCCCG 1318 CAAATGCCAG 3923 TCC-- T ---- G CA- GTCTTTG

GCTGCTGTCATATTTGCCGT CAGAGGCCTT TTCACAGT GGC TCCC GGCT CTGT TATTTGCC T

CTTTGTCATCACAGGCAAAT TTGG |||||||| ||| |||| |||| |||| ||||||||

GCCAGCAGAGGCCTTTTGGG AAGTGTCA CCG GGGG CCGG GACG GTAAACGG /

GTGCCACGCCACTGTGAA CCGCA T TTTT A ACC ACACTAC

GAM1342 GTGGCTTCTATGGCAAGGGT 1319 TCTGCTGTCC 3924 CTAT C - CT TAA TT - -- TCG
CCCTCCATTAAGCAGTTCAT TGTGTGGTGG GTGGCTT GG AAG GGTCC CCAT GCAG CA TGGA CATCTTC C
GGACATCTTCTCGCTACCGG ACTA ||||||| || ||| ||||| |||| |||| || |||| |||||||
AGATGGCTCTGCTGTCCTGT CACCGGG TC TTC TCAGG GGTG TGTC GT GTCT GTAGAGG T
GTGGTGGACTACTTTCTGGG ---- T A T- --- CT C CG CCA
CCAC

GAM1343 GCCCCCCTACTTCCGCTTCC 1320 TGGCAGTGGT 3925 - TACT TGA CATG T-- G-CCT
TGACACTCATGGCCTTCCAC GGAGGTGGGC GCCCC CC TCCGCTTCC CACT GCC TCCAC TCTT C
GTCTTCCTCCAAGAGAAGGT ATTG ||||| || ||||||||| |||| ||| ||||| ||||
GGACCTGGCAGTGGTGGAGG CGGGG GG GGGTGGAGG GTGA CGG AGGTG AGAG /
TGGGCATTGGCGGGGC C TTAC TG- ---- TCC GA AAC

GAM1344 CCCTGGAGGAGATCTATCTC 1321 AGAGATCATT 3927 T T--- TCTC GCC
TTCTCCCTGCCCATTAAGGA GATTTCTTCC CCC GGAGGAGATC ATCTCT CCT C
ATCAGAGATCATTGATTTCT TGGG ||| |||||||||| |||||| |||
TCCTGGG GGG CCTTCTTTAG TAGAGA GGA A
T TTAC CTAA ATT

GAM1345 ACCCGTGCCGGCCAGCGCAC 1322 GGGGACTACA 3926 T CA- CCA- AA--- TT
CAGGTTCAAGGCATTTGTTG ATGTGCCACG ACCCG GCCGGC GCGCA GGTTC GGCA T
CTATCGGGGACTACAATGTG TCGG ||||| |||||| ||||| ||||| ||||
CCACGTCGGTCTGGGT TGGGT TGGCTG CGTGT TCAGG TCGT /
C CAC AACA GGCTA TG

GAM1346 TGCTCCTTCATCAGCTTTGC 1323 GGACACGAAG 3928 CT CA CCAA T GA
CAACTCTCGGAGCTCGGAGG CAAATGATGA TGCTC TCAT GCTTTG CTC CG G
ACACGAAGCAAATGATGAGT GTA ||||| |||| |||||| ||| ||
A ATGAG AGTA CGAAGC GAG GC /
T- AA ACAG - TC

GAM1347 TGCTACGAGGAGGTCAAGGA 1324 AGGAGGTCAA 3929 A-- A CAA AC A TG AG
CCGCTGCACCCTGGCAGAGA GGACCGCTGC TGCT CG GGAGGT GG CGCTGC CCC GC A
AGCTGGGGGGGCAGTGCCGTC ACCC |||| || |||||| || |||||| ||| ||
ATCTCCCTGGAGGGCA ACGG GT CCTCTA CC GTGACG GGG CG G
GAG C CTG -- G GT AA

GAM1348 GTGCCCTGGGGCTTTCCAAA 1325 TTGGAGCCTG 3930 CC TTCCAA A TC T
GGCACCTCGCATGCCTGTTT TCAGCCCCAG GTGC TGGGGCT AGGC CC GCA G
GGAGCCTGTCAGCCCCAGCA CAC |||| ||||||| |||| || |||
C CACG ACCCCGA TCCG GG TGT C
-- CTG--- A TT C

GAM1349 AGTAGTTCTTTGATGTGAAA 1326 TGAAAGGGGC 3931 A --- ---- G CAGCACA TTT
GGGGCAGCACAGTCATTTAA AGCACAGTCA AGT GTT CTTT GATGT AAAGGGG GTCA
A
ACTTGATCCAACCTCTTTGC TTTA ||| ||| |||| ||||| ||||||| ||||
ATCTTACAAAGTTAAACAGC TCG CAA GAAA CTACG TTTCTCC TAGT A
T A ATT CATT - AACC--- TCA

GAM1350 CTTCTACCCTGACTTCTCCC 1327 TGGGGACCCC 3932 C - GC----- AG
GCCTCCGAGAGTCCTTTGGG AAGGGAGAGA CTTCTACC TGACT TCTCCC CTCCGAG T
GACCCCAAGGGAGAGAGTCA GTCA |||||||| ||||| |||||| |||||||
GGTGGAGG GGAGGTGG ACTGA AGAGGG GGGGTTT /
- G AACCCCA CC

GAM1351 ATTGCTTTCAGTTTCTTCTT 1328 TCCCCAGAAA 3933 - TC- TTA TT TTTTTT
TAGGTTCTTGATTTTTTTGT TTGACTGAGA ATTG CTTTCAGTT TTCT GG CTTGA T
CTATCTCAGGGTCCCCAGAA GACA |||| ||||||||| |||| || |||||
ATTGACTGAGAGACAGT TGAC GAGAGTCAG AAGA CC GGACT G
A TTA CC- TG CTATCT

GAM1352 TCTTCCAGAAGTGTGATTGG 1329 TTCCAGAAGT 3934 - --- TT ATAAAT
GAATAAATATGCCTCTCCTT GTGATTGGGA TCTTCC AGAA GTGTGA GGGA A
TTTATATTATTTCTAGGAAG ATAA |||||| |||| |||||| ||||
A AGAAGG TCTT TATATT TCCT /
A TAT TT CTCCGT

GAM1353 ACCAGCTGGATAAGGACATC 1330 TATCACTTTC 3935 -- T - C AA - - G
AATACCTTCTCTATGCGTGT CGGAGCTGGT ACCAGCT GGA AAG GA ATC TACC TTCTCT AT C
CAGGGAGTGGTACGGGTATC ||||||| ||| ||| || ||| |||| |||||| ||
ACTTTCCGGAGCTGGT TGGTCGA CCT TTC CT TGG ATGG GAGGGA TG G
GG - A A GC T C T

GAM1354 GGCGCCATGGTGCTGTTGCA 1331 CATGGTGCTG 3936 - T-- - A- GT
CGTGCTGTTTGAGCACGCGG TTGCACGTGC GGCGCCA TGGTGC GTTG C CGTGCT T
TCGGCTACGCGCTGCTGGCG TGTT ||||||| |||||| |||| | ||||||
CT TCGCGGT GTCGCG CGGC G GCACGA /
C CAT T GC GT

GAM1355 GGCTCCCAATGTTGACGTTG 1332 CCAGGCCAAA 3938 CTCCC CG---- AG TGC
GCCAGGGCTTTGCAAACAAG AAGGCTCAAC GG AATGTTGA TTGGCC GGCTT A
CCAGGCCAAAAAGGCTCAAC ATTT || |||||||| |||||| ||||| /
ATTTACACC CC TTACAACT AACCGG CCGAA
ACAT- CGGAAA A- CAA

GAM1356 GCATTGATCTTATCCTCCGT 1333 TTGATCTTAT 3937 GAT AT TC GA T CTCA
GACTGTCACCTCATCGTCGT CCTCCGTGAC GCATT CTT CC CGT CTG CAC T
GCAGAATGAGGGCCGAGTAG TGTC ||||| ||| || ||| ||| |||
ATGC CGTAG GAG GG GTA GAC GTG /
AT- CC GA A- - CTGC

GAM1357 GACTTTGGTAGACACAGGCA 1334 TGGGAACCAT 3939 A AG A A TGA----
GCTGATCT
TTGGCATGACCAAAGCTGAT TGCCAAGTCT G CTTTGGT AC CAGGC TTGGCA CCAAA
C
CTCATAAATAATTTGGGAAC GGTA | ||||||| || ||||| |||||| |||||
CATTGCCAAGTCTGGTACTA C GAAATCA TG GTCTG AACCGT GGTTT /
AAGC - -- - - TACCAAG AATAAATA

GAM1358 GGAGTCTTCTGCTGGAGGTT 1335 TGAGCCCATT 3940 AGT TG A TTCC C G
CCTTCACTGTGCGTGCTGAC GGCAGGGGTA GG CTTCTGC G GG TTCACTGTG GT C
CATGGTGAGCCCATTGGCAG CC || ||||||| | || |||||||||
GGGTACC CC GGGGACG T CC GAGTGGTAC CA T
AT- GT A C--- - G

GAM1359 CCTAATCGACTTCTTCCATG 1336 CCTCGAGAGG 3941 A C CT ATG- AC ATCC
CGAGACGCATCCTCATCGCC GGGGATCTCA CCT AT GA TCTTCC CGAG GC T
CTCGAGAGGGGGGATCTCAT TCAG ||| || || |||||| |||| ||
CAGG GGA TA CT AGGGGG GCTC CG /
C - CT GAGA C- CTAC

GAM1360 TTGCGGCATCCACGAGACCA 1337 TGACGTGGAC 3942 CA- AGAC - ACTC
CCTTCAACTCCATCATGAAG ATCCGCAA TTGCGG TCCACG CAC CTTCA C
TGTGACGTGGACATCCGCAA |||||| |||||| ||| |||||
AACGCC AGGTGC GTG GAAGT /
TAC A--- T ACTA

GAM1361 GCTGTGGGCAAGGTCATCCC 1338 TGGCATGGGC 3944 T - ---- G - C- GAA
TGAGCTGAACGGGAAGCTCA TTTCGTGTCC GC GTGGG CA AG TCAT CC TGAGCT C
CTGGCATGGGCTTTCGTGTC CACT || ||||| || || |||| || ||||||
CCACTGC CG CACCC GT TC GGTA GG ACTCGA G
T T GCTT G C TC AGG

GAM1362 CATGACCACAGTCCATGCCA 1339 ATGGCCCCTC 3943 A CCATG ATCACT- - - A
TCACTGCCACCCAGAAGACT CGGGAAACTG CATG CCACAGT CC GCCA CC CAG A
GTGGATGGCCCCTCCGGGAA TGGC |||| ||||||| || |||| || |||
ACTGTGGCGTG GTGC GGTGTCA GG CGGT GG GTC G
\- AA--- GCCTCCC A T A

GAM1363 GCTGCTCACAATAGTTGATA 1340 GATAATAGTA 3945 T AG A C AGGATTG
CCCCAGGATTGGAGATGCAG ATTGTGGCAG GCTGC CACAAT TTG TA CCC G
GGATAATAGTAATTGTGGCA C ||||| |||||| ||| || |||
GC CGACG GTGTTA GAT AT GGG /
\- AT A A ACGTAGA

GAM1364 CACCTTTACGGCCAAACCGT 1341 TGTGGATATA 3946 TT C CC C-- C--- G
CCACCTCGACCGATTCTGTG GTTTTCCCTG CACC TA GG AAAC GTCCAC TC A
GATATAGTTTTCCCTGTTGG TTGG |||| || || |||| |||||| ||
TG GTGG GT CC TTTG TAGGTG AG C
TT - CT ATA TCTT C

GAM1365 TTGGTCCATATCTCCATGCA 1342 TCCATATCTC 3947 TC ATCTCC- G- - ACA
TGGCGGATACAGTGAAATCT CATGCATGGC TTGG CAT ATGCATG CG GAT G
CGAGCATGCATCTTCTCGGT GGAT |||| ||| ||||||| || |||
GAGCCAG GACC GTG TACGTAC GC CTA T
GA GCTCTTC GA T AAG

GAM1366 CGGAAAACAGCTGGAAGATG 1343 AAGAGTCCAC 3948 AAA- G A TCGT C G ACTAC
GTCGTACCCTGTCTGACTAC CTTGCAGCTG CGGA CAGCTG AAG TGG AC CT TCTG A
AACATCCAGAAAGAGTCCAC GTGC |||| |||||| ||| ||| || || ||||
CTTGCAGCTGGTGCTCCG GCCT GTCGAC TTC ACC TG GA AGAC /
CGTG G C ---- A A CTACA

GAM1367 CAGAGACTGTCCTTTGCAAA 1344 TTCCTGGAAG 3949 A GT GCAA AT --- CAT
GGAAATGACCAGCATTTCAA GGTAGATTCT CAGAG CT CCTTT AGGAA GAC CAG T
CTGTATGTCTTCCTGGAAGG G ||||| || ||||| ||||| ||| |||
GTAGATTCTG GTCTT GA GGAAG TCCTT CTG GTC T
A TG G--- -- TAT AAC

GAM1368 CTGGTTTGTTGAAACAGTAA 1345 TGTCAAAGTG 3950 TT GAAACA ---- - TGCC
GTCAGACAACATTTGCCACA ACTTGCCATA CTGG TGTT GTAAGTCA GACA ACATT A
ATAATGTCTGTCAAAGTGAC AACA |||| |||| |||||||| |||| |||||
TTGCCATAAACACCCCAG GACC ACAA CGTTCAGT CTGT TGTAA /
CC ATAC-- GAAA C TAAC

GAM1369 TTCTTTCTCTTGTGCTTATT 1346 TCTCTTGTGC 3951 C CTTATT T GAG --
CTTCTT
CTTCTTGGGAGTGGTGTAAG TTATTCTTCT TTCTTT TCTTGTG CTTC TGG TGGTGT AAGA
C
ACTTCTTCTTCCTTTTCTTA TGGG |||||| ||||||| |||| ||| |||||| ||||
AGCACCACCACGAAGTCTCA GAGAAG AGAACAC GAAG ACC ACCACG TTCT T
ACACAAGATGAAGAG T AACTCT C --- AA TTTCCT

GAM1370 GGCCAATTGAAACAAACAGT 1347 TATTAGGGAT 3952 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1371 GCAGATGAGTTACTAGAAAG 1348 TGAGTTACTA 3953 - ACTAGAAA TT AGG AC
CTTCCTGGAGGGTTTTCACG GAAAGCTTCC GCAGA TGAGTT GC CCTGG GTTTTC G
ATGAAAGCACCCAGGTGCAG TGGA ||||| |||||| || ||||| ||||||
CTCACTCTGC CGTCT ACTCGA CG GGACC CGAAAG /
C -------- T- CA- TA

GAM1372 GACAGAACTCTGCTTCCAGC 1349 CCACCGAGCT 3954 AA ------ T C -- - CA
GCTGTGTGCCAGCTTGCACC CTGGACGCTG GACAG CTCT GC TCCAG GCT GTG TGC G
ACCGAGCTCTGGACGCTGAG AGGA ||||| |||| || ||||| ||| ||| |||
GAGGAGGCCTGTC CTGTC GAGG CG AGGTC CGA CAC ACG C
CG AGGAGT C T GC C TT

GAM1373 AAGGATACCAGGATGGTTAC 1350 TACCAGGATG 3955 A - - A T --- G T
CAGGATGACTACCGTCATCA GTTACCAGGA AAGG TA CCA GG TGGT AC CA GATGAC A
TGAGAGTTATCACCATGGAT TGAC |||| || ||| || |||| || || ||||||
ACCCTT TTCC AT GGT CC ACTA TG GT CTACTG C
C A A - T AGA A C

GAM1374 TGATGTCTTTGACCTGAGGT 1351 TTTGCATAAG 3956 A- GAG T G GTC
ATAGAGTTGTCCTCTAAAAT GCATAGGGAC TGATGTCTTTG CCT GTA AGA TT C
CTTTGCATAAGGCATAGGGA ATCA |||||||||| ||| ||| ||| ||
CATCA ACTACAGGGAT GGA CGT TCT AA T
AC ATA T A ATC

GAM1375 TTGGCGATGCTGTCGGGGAT 1352 ATGCTGTCGG 3957 GAT --- TT C CAAC---- AC
TCTGCTGGGCAACTGGGCAC GGATTCTGCT TTGGC GCTGTCGG GGA CTG TGGG
TGGGC C
CCTGCCCGCCACCATCCTCA GGGC ||||| |||||||| ||| ||| |||| |||||
CCAGTCTCTTCACCGACAGC AACTG CGACAGCC TCT GAC ACTC GCCCG /

TTAGTCAA ATT ACT CT C CTACCACC TC

GAM1376 GCCGACAAGGAGCGCCTGGC 1353 TGTCCAAGAT 3958 ----- AA - CGC - C C - AC
CATCCTGGGCATCCACAATG TGTCCAGACC GCC GAC GG AG CTGG C ATC TGGGCATC C
A
AGGTGTCCAAGATTGTCCAG TACC ||| ||| || || |||| | ||| |||||||| |
ACCTACCACGTCAATATGGC CGG CTG CC TC GACC G TAG ACCTGTGG G /
TATAA CA A CA- T T A A TA

GAM1377 TTCCACCCATGGCAAATTCC 1354 TGAGAACGGG 3959 CCC A- ATGG-- - GT
ATGGCACCGTCAAGGCTGAG AAGCTTGTCA TTCCA ATGGCAA TTCC CA CC C
AACGGGAAGCTTGTCATCAA TCAA ||||| ||||||| |||| || ||
TGGAA AAGGT TACTGTT AAGG GT GG /
AAC CG GCAAGA C AA

GAM1378 GGCCAATTGAAACAAACAGT 1355 TATTAGGGAT 3960 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1379 GCCCTGCTGGCTGATGAGCT 1356 TGATGAGCTC 3961 - G G TG CA CT CA TG
CATCACTGTCTACAGCCTGC ATCACTGTCT GCC CT CT GC ATGAGCT TCA GTCTA GCC C
CTGGCATGGACCCTGACTGG ACAG ||| || || || ||||||| ||| ||||| |||
CTCATTGGCGAGAGAGGC CGG GA GA CG TACTCGG AGT CAGGT CGG /
A - G GT TC CC A- TC

GAM1380 GGTGACAACATGCTGGAGCC 1357 TTGGTTCAAG 3962 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1381 AGAAGATTCCTGTATCTGGC 1358 TTCCTGTATC 3963 ATTCC ATCT - - TG
TATGTAGCTGCTGGCTATAT TGGCTATGTA AGAAG TGT GG C TATGTAGC C
GTGTCCTGTGGCATTCCTTC GCTG ||||| ||| || | ||||||||
T TCTTC ACG CC G GTATATCG /
CTT-- GTGT T T GT

GAM1382 TCTTGTGTTGAGACTTCGTG 1359 TACACCACTC 3964 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||

CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM1383 CATGGGATGGGGAAGTACGG 1360 TTGGACAACC 3965 AT AGTA - -- G A CTTCA
CAGGTGTCTAAGCATGCCTT CTGCTCGAAT CATGGG GGGGA CG GCAGG TGTCTAA C TGC
G
CAGCCTCAAGCAGTTGGACA CCCT |||||| ||||| || ||||| ||||||| | |||
ACCCTGCTCGAATCCCTCCC GTGTCC TCCCT GC CGTCC ACAGGTT G ACG C
TGTG C- AA-- T CA - - AACTC

GAM1384 TGTGCTCTGTGCAAGGTGGC 1361 TAACAAAGGT 3966 CT AAG- GGC AA C-- T
TGTGAACTCCCTGTCCCAGC ACTAAGCACA TGTGCT GTGC GT TGTG CTC CTG C
TTGAGGCACATAACAAAGGT |||||| |||| || |||| ||| |||
ACTAAGCACA ACACGA CATG CA ACAC GAG GAC /
AT GAAA AT- G- TTC C

GAM1385 GGCCAATTGAAACAAACAGT 1362 TATTAGGGAT 3967 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1386 GGTTCGGTACCACACGAAGG 1363 AGCTCAGGGT 3968 TA ACGAAG CGC ----
AGC
TGCGCGCCGGCCGCGGCTTC GGCCGGCATT GGTTCGG CCAC GTG GCCGGCCGC
GGCTTC C
AGCCTGGAGGAGCTCAGGGT CACA ||||||| |||| ||| ||||||||| ||||||
GGCCGGCATTCACAAGAAGG CCAGGCC GGTG CAC CGGCCGGTG TCGAGG T
TGGCCCGGACC C- GAAGAA TTA GGAC AGG

GAM1387 GTCCAGGCCATGTATATCTG 1364 TATCTGGATC 3969 CCATGTATA A GATG C G AA
GATCGATGGTACTGGAGAAG GATGGTACTG GTCCAGG TCTGG TC GTA TG AG G
GACTGCGCTGCAAGACCCGG GAGA ||||||| ||||| || ||| || ||
ACCCTGGAC CAGGTCC AGGCC AG CGT GC TC /
C-------- C AA-- C G AG

GAM1388 GCCAACTTGAAAGTGAACAG 1365 TGGCCCACAT 3970 C- T AG- T ACTTTCC AT A
TATGACTTTCCTGATCCAGA CTGTTTAATC GC AACT GAA TGAACAG ATG TG CCAGA C
ACAGTTTGGCCCACATCTGT TTCC || |||| ||| ||||||| ||| || |||||
TTAATCTTCCAGTTTAGC CG TTGA CTT ATTTGTC TAC AC GGTTT A
AT C CTA - ------- CC G

GAM1389 GGGCCGAGATTAGAGCTCGA 1366 TAGAGCTCGA 3971 - G AGC AA- -- TT TCGGA
ATGGGCATTGGGCTCGGCTC ATGGGCATTG GGG CCGA ATTAG TCG TGG GCA
GGGCTCGGC G
GGAGAATGCTGCCGGGCCCT GGCT ||| |||| ||||| ||| ||| ||| |||||||||
GCAACTGGGACGAAGCTGAT CCC GGCT TAGTC AGC GTC CGT CCCGGGCCG A
ATCGGACCC A A GA- AGG AA -- TCGTA

GAM1390 TTTGGTGAAGTACCTTTTGG 1367 GTGAAGTACC 3972 A A T TG TAAAGA - A AA- T
CTAAAGACCAGACGAAGATT TTTTGGCTAA TTTGGTGA GT CCT T GC CC AG CG GAT C
CCCATCAAGCGCTCGGACAT AGAC |||||||| || ||| | || || || || ||| |||
GCTGAAGGACATCATCAAA AAACTACT CA GGA A CG GG TC GC CTA C
A - - GT TACA-- C - GAA C

GAM1391 TGTGGAACAAGTTCGCATCC 1368 TGGAACAAGT 3973 TG AACAA A GAGG A CG
TGAGGGGACTGGGCGCCATC TCGCATCCTG TG G GTTCGC TCCT GG CTGGG C
CAGCCAGGAGTGAACCGCTG AGGG || | |||||| |||| || |||||
CA AC C CAAGTG AGGA CC GACCT /
GT GC--- - ---- - AC

GAM1392 TTGTCGTCATTGGACACGTA 1369 TAAATGCGGT 3974 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM1393 GGTGACAACATGCTGGAGCC 1370 TTGGTTCAAG 3975 AA--- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAA GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAAGTCAC GTCA |||||| ||| || |||||||| ||
C CCACTG GTA GG CTTGGTTC CG C
AAAAG G AA - TA

GAM1394 GAATCTCATTAATCCATTCA 1371 TGACGAGGCA 3976 A A T---- TTC G- - A
TGCGCGTCACTAATTAGATG TTTGGCTACC GA TCTC TTAA CCA ATGC CGTCA CT A
ACGAGGCATTTGGCTACCTT TTAA || |||| |||| ||| |||| ||||| ||
AAGAGAGTC CT AGAG AATT GGT TACG GCAGT GA T
G - CCATC T-- GA A T

GAM1395 GTACTGGAGAGACATTAAGA 1372 TCCTGCTGCT 3977 GA GACATT A ACT T T G
AGACTGGAGTGGTGTTTGGT TTCATTGACA GTACTG GA AAG AG GGAGTGG GTT G T
GCCAGCCTATTCCTGCTGCT GTAT |||||| || ||| || ||||||| ||| |
TTCATTGACAGTAT TATGAC TT TTC TC CCTTATC CGA C G
AG ACT--- G GT- - - C

GAM1396 AGCTCCAGTGGACAAAAGAA 1373 TCTAGATTTG 3978 ------- A AGAA C
GGAATCCACGTTCTAGATTT GCCATTTGAT AGCTCCA GTGG CAAA GGAAT C
GGCCATTTGATGATGGAGCT GATG ||||||| |||| |||| |||||
TCGAGGT TACC GTTT TCTTG A
AGTAGTT G AGA- C

GAM1397 GTTCACAGAGGAACTTAAGA 1374 AGAGGAACTT 3979 AGA A AAGAA G ---- TG
AGTATGGAGTGACGACTTGT AAGAAGTATG GTTCAC GGA CTT GTATG AGTG ACGACTTG
G
GGTTCGAGTTGTGTGATGCT GAGT |||||| ||| ||| ||||| |||| ||||||||
ACATATGATAAAGCTCCAGT CAGGTG CCT GAA TATAC TCGT TGTTGAGC /
GGAC A-- C ATAG- A AGTG TT

GAM1398 GGCCAATTGAAACAAACAGT 1375 TATTAGGGAT 3980 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1399 GGCCAATTGAAACAAACAGT 1376 TGGCAGGTAT 3981 C T ACAAACAG GTT T A
GAT
TCTGATACCGTTCTTCCACC TAGGGATAAT GGC AA TGAA TTCTGATACC CT CC CCACT
T
ACTGATTAAGAGTGGGGTGG ATTC ||| || |||| |||||||||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATTATGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- AC- T - GAA

GAM1400 GGCCAATTGAAACAAACAGT 1377 TATTAGGGAT 3982 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1401 CCATCTGATTTTGAGCACAC 1378 TGTTACTGGA 3983 T A A CA -------- - TT TT
CATCCATGTTGGCTTTGATG GAATTCACTG CCA CTG TTTTG GCA CCA TCCA TG GGC T
CTGTTACTGGAGAATTCACT GCAT ||| ||| ||||| ||| ||| |||| || |||
GGCATGCCAGAACAGTGG GGT GAC AAGAC CGT GGT AGGT AT TCG G
- - - AC CACTTAAG C TG TA

GAM1402 GGTGACAACATGCTGGAGCC 1379 TTGGTTCAAG 3984 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||

CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1403 GTCATCCAGGAGGCGGCAAC 1380 TGGCCAGGCA 3985 T A -- -- A GACAG
ACGACAGGTACCCAGTGTGG GCTCCCGGCT GTCA CC GGAG GC GGC ACAC G
CCAGGCAGCTCCCGGCTGAC GAC |||| || |||| || ||| ||||
CAGT GG CCTC CG CCG TGTG T
C C GA GA G ACCCA

GAM1404 GGCCTGATCCTGGCCTGTGG 1381 TGGGAGCTCG 3986 GA CC AGC AT CC
GAGCTCGGATGGGGCCATCT GATGGGGCCA GGCCT TCCTGG TGTGGG TCGG GGGG A
CCCTGCTGACTTACACCGGG TCTC ||||| |||||| |||||| |||| ||||
GAAGGCC CCGGA GGGGCC ACATTC AGTC CCCT /
A- -- --- GT CT

GAM1405 CCTGCCGGCAAACTTAGCCT 1382 GCAAACTTAG 3987 - CAAA T - ---- -- TTCA
TGCTGCCCAGCTCCTCTTCA CCTTGCTGCC CCT GCCGG CT AGC CTTGCT GC
CCAGCTCCTC A
ATTCTGAGGAGCTGGTTGTA CAGC ||| ||||| || ||| |||||| || ||||||||||
CTTGGCAAGCGCTCAGATCG GGA CGGCT GA TCG GAACGG TG GGTCGAGGAG /
GCAAGG A A--- C C TTCA TT TCTT

GAM1406 GGCCCAGGGATCGGCAGGGC 1383 TTCCCATGCC 3988 G - G- - GCT GA A
TGCTGGCAGAGGAATCCCAG CCAGGCTCCT GGCCCAG GA TC GCAGG GCT GGCA
GGAATCCC G
CTGGGGTTCCCATGCCCCAG GCAG ||||||| || || ||||| ||| |||| ||||||||
GCTCCTGCAGGACTTGCTGG CCGGGTC TT AG CGTCC CGG CCGT CCTTGGGG C
GCC G C GA T ACC AC T

GAM1407 CATTGTCGTCATTGGACACG 1384 CGTCATTGGA 3989 GTC-- T- A C ATTC C
TAGATTCGGGCAAGTCCACC CACGTAGATT CATT GTCA TGG CA GTAG GGG A
ACTACTGGCCATCTGATCTA CGGG |||| |||| ||| || |||| |||
TAAATG GTAA TAGT ACC GT CATC CCT A
ATATC CT G - ACCA G

GAM1408 GGTGACAACCATGCTGGAGC 1385 TTGGTTCAAG 3990 AA- G G- T TA
CAAGTGCTAACATGCCTTGG GGATGGAAAG GGTGAC CCAT CT GAGCCAAG GC A
TTCAAGGGATGGAAAGTCAC TCAC |||||| |||| || |||||||| ||
C CCACTG GGTA GG CTTGGTTC CG C
AAA G AA - TA

GAM1409 CATTGTCGTCATTGGACACG 1386 CGTCATTGGA 3991 GTC-- T- A C ATTC C
TAGATTCGGGCAAGTCCACC CACGTAGATT CATT GTCA TGG CA GTAG GGG A

ACTACTGGCCATCTGATCTA CGGG |||| |||| ||| || |||| |||
TAAATG GTAA TAGT ACC GT CATC CCT A
ATATC CT G - ACCA G

GAM1410 TTGTCGTCATTGGACACGTA 1387 TAAATGCGGT 3992 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM1411 GCACTCTGTTCTTCCGCCGC 1388 ACTCTGTTCT 3993 AC G CC TCC TC TT
TCCGCCGTCGCGTTTCTCTG TCCGCCGCTC GC TCT TTCTTCCG GC GCCG GCG T
CCGGTCGCAATGGAAGAAGA CGCC || ||| |||||||| || |||| |||
GATCGC CG AGA AAGAAGGT CG TGGC CGT C
CT G AA C-- -- CT

GAM1412 GGTGACAACATGCTGGAGCC 1389 TTGGTTCAAG 3994 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1413 GTATGGAATCTTGCGGGATC 1390 TGGAATCTTG 3995 AA G -- AGGAGA C ACTC
CAAGGAGACCACCTTCAACT CGGGATCCAA GTATGG TCTTGC GGA TCCA CCAC TTCA
C
CCATCATGAAGTGGGACGTG GGAG |||||| |||||| ||| |||| |||| ||||
GACATCCGGCAAGGACTGTA CATGTC GGAACG CCT AGGT GGTG AAGT /
C A- G AC GCAG-- - ACTA

GAM1414 AGTCCAACGTCTCTGATGCG 1391 TATCATTTAT 3996 - AC ------ TG TC
GTGGCTCAGAGCACCCGTAT GGAGGCTCTG AGTC CA GTCTCT GATGCGG GC A
CATTTATGGAGGCTCTGTGA TGAC |||| || |||||| ||||||| ||
CT TCAG GT CGGAGG CTATGCC CG /
T CT TATTTA CA AG

GAM1415 GGTGACAACATGCTGGAGCC 1392 TTGGTTCAAG 3997 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1416 GGTGGTGATGGGCTTCTGGT 1393 TGACCATGCA 3998 - A C - G G A
GGGCAGTGAGACGGTGACCA GAACCTCAAC GGTGGT G TGGG TTCTG GTGG CA TG G

TGCAGAACCTCAACGACCGC GACC ||||||| | ||||| ||||| |||| || ||
C CCGCCA C ACTC AAGAC TACC GT GC /
G A C G A G A

GAM1417 GGTCAAGCTGTAACCGGGTC 1394 AAGCTGTAAC 3999 - A ---- GT
AATGTGTGGAATATTGGGGG CGGGTCAATG GGTCAAG CTGTA CCGGGT CAATGT G
GCTCGGCTGCAGACTTGGCC TGTG ||||||| ||||| |||||| ||||||
CCGGTTC GACGT GGCTCG GTTATA /
A C GGGG AG

GAM1418 GAGACTTTCTAAAGTGTACT 1395 TTACAAGAAT 4000 AAA----- - T- G TACCT
CA
TAAAACATAGTAGTTTTTTA ACTTTTGTTT GAGACTTTCT GTGTACT TAAAACA AGTA
TTTTT TTCA A
CCTTTCACAAAACTGAGTTA TACA |||||||||| ||||||| ||||||| |||| ||||| ||||
CAAGAATACTTTTGTTTTAC CTCTGAAGGA TACGTGA ATTTTGT TCAT AAGAA
GAGT A
AGTGCATCCCTTCCGAGGAA GCCTTCCC C TT - CATT- CA
GTCTC

GAM1419 TCTGTTCTTCCGCCGCTCCG 1396 CGCGGTCGCG 4001 G C T- C T CGT
CCGTCAGCGTTCTACTGCGC ATGGAAGAAG TCT TTCTTCCG CGC CCGC G CAG T
GGTCGCGATGGAAGAAGAGA AGA ||| |||||||| ||| |||| | |||
AGA AAGAAGGT GCG GGCG C GTC /
G A CT - - ATC

GAM1420 TCCTTCTCTGGGAAATCTAC 1397 TGGGAAATCT 4002 T CT AATCT - TG C GC A
TCCTTTGGGCGAGTGCCTTA ACTCCTTTGG TCC TCT GGGA AC TCCTT GG GAGT CTT T
TCCAAGAATTCCCCTGAAGG GCGA ||| ||| |||| || ||||| || |||| |||
ACGTCGTCCCTCGGGTGGA AGG GGG CCCT TG AGGAA CC CTTA GAA C
T CT GC--- C GT C A- C

GAM1421 TTGTCGTCATTGGACACGTA 1398 TAAATGCGGT 4004 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM1422 GGTGACAACATGCTGGAGCC 1399 TTGGTTCAAG 4003 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1423 GCAGCCAAGCATTTGATACT 1400 AAGCATTTGA 4005 CCA- GATA AAAG GA
GGAGAAAGTTTCAGAAGATG TACTGGAGAA GCAG AGCATTT CTGGAG TTTCA A
AAGAACTTCGGAAGAGAATG AGTT |||| ||||||| |||||| |||||
CTCATTCTGC CGTC TCGTAAG GGCTTC GAAGT /
TTAC AGAA AA-- AG

GAM1424 GATCAACAGGCTTATTAGAA 1401 TAGAAGAATG 4006 A A TAT A A G
GAATGAATAAGGTGTCTACC AATAAGGTGT GATC AC GGCT TAGAAGAATGA TA GGT T
ATGATTATTTTTCTAAGCTG CTAC |||| || |||| |||||||||| || |||
GTGGGTT TTGG TG TCGA ATCTTTTTATT GT CCA C
G G --- A A T

GAM1425 GGTGACAACATGCTGGAGCC 1402 TTGGTTCAAG 4007 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1426 GGTGACAACATGCTGGAGCC 1403 TTGGTTCAAG 4008 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1427 TCGGTTGCACGCAGCTGAGC 1404 CTCCAAGGAG 4010 GTT- G C- A---- A CT
AGGAGAGCCTCAAGCGCTCC CTCAACCTGG TCG GCAC CAG TGAGC GGAG GC C
AAGGAGCTCAACCTGGTGCT TGCT ||| |||| ||| ||||| |||| ||
GGACGA AGC CGTG GTC ACTCG CCTC CG /
AGGT - CA AGGAA G AA

GAM1428 CGGAGTGTCGGTGGTGATGG 1405 TCGGTGGTGA 4009 -- AT - C A GT
GCATCCCGAGCGTGCGGCGC TGGGCATCCC CGGAGTGTCGGT GGTG GG GCATC CG GC G
GAGGTGCACTCGTACCTGAC GAGC |||||||||||| |||| || ||||| || ||
TGACACTCTG GTCTCACAGTCA CCAT TC CGTGG GC CG /
GT GC A A G GC

GAM1429 TCTACCCTGACTTCTCCCGC 1406 ACCCTGACTT 4011 A - - CG---- AG
TCCGAGAGTCCTTTGGGGAC CTCCCGCTCC TCT CC CTGACT TCTCC CTCCGAG T
CCCAGGAGAGAGTCAGTGGA GAGA ||| || |||||| ||||| |||||||
GGA AGG GG GACTGA AGAGG GGGGTTT /
A T G ACCCCA CC

GAM1430 TTGCGGCATCCACGAGACCA 1407 TGACGTGGAC 4012 CA- AGAC - ACTC

CCTTCAACTCCATCATGAAG ATCCGCAA TTGCGG TCCACG CAC CTTCA C
TGTGACGTGGACATCCGCAA |||||| |||||| ||| |||||
AACGCC AGGTGC GTG GAAGT /
TAC A--- T ACTA

GAM1431 CGCGGCTACTACAACCAGAG 1408 CTCCAGTGGA 4013 C A AGA GA C CT
CGAGGACGGGTCTCACACCC TGTATGGCTG CGCGGCTA TACA CC GC GGA GGGT C
TCCAGTGGATGTATGGCTGC CG |||||||| |||| || || ||| ||||
G GCGTCGGT ATGT GG TG CCT CCCA /
- A --- A- - CA

GAM1432 CTTTGATGATATGAGTTTAA 1409 CTTACGGTTT 4014 A TATG TTA AG TCCT - T
AGGAGTCTCTCCTTCGTGGC GAGAAGCCTT CTTTG TGA AGT AAGG TCTC TCGTG GCA
C
ATCTATGCTTACGGTTTGAG CCGC ||||| ||| ||| |||| |||| ||||| |||
AAGCCTTCCGCTATTCAGCA GAGAC ACT TCG TTCC AGAG GGCAT CGT T
GAG G TA-- CC- GA TTT- T A

GAM1433 TTTCCTGGGCACAGACCGGG 1410 GTGCTGCCCA 4016 G CAGA G- A TG AAG
GACAGTGCAGAAGGTCATTG AGGATGACCA TTTCCTGG CA CC GGG CAG CAG G
TGCTGCCCAAGGATGACCAG GGAG |||||||| || || ||| ||| |||
GAGA AGAGGACC GT GG CCC GTC GTT /
A A--- AA - GT ACT

GAM1434 GCCTGCACCGTTGCCAGGCG 1411 TGCCTGGGAT 4015 CA G - CTG T TGACTG
TATGGGGCTGCCTGTGCTGA GGCCAGGC GCCTG CCGTT CCAGGCGTA TGGGG CCTG GC
C
CTGCTGCCTTGCCCGGGACC ||||| ||||| ||||||||| ||||| |||| ||
CTTACTGTGCCTGGGATGGC CGGAC GGTAG GGTCCGTGT ATTCC GGGC CG /
CAGGC C- - C CA- C TTCCGT

GAM1435 TCTTGTGTTGAGACTTCGTG 1412 TACACCACTC 4018 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAATCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - AAAGAA

GAM1436 GAAGGTTAACGCTGGCTGTC 1413 TGACGAATGG 4017 TAAC C-- TGAAA- ATA
CTGAAATATTATAAGGTGGA GCAAAATTAG GAAGGT GCTGG TGTCC TATT A
TGACGAATGGGCAAAATTAG TCGC |||||| ||||| ||||| ||||
TCGCCTTC CTTCCG TGATT ACGGG GTAG G
C--- AAA TAAGCA GTG

GAM1437 CTTCTTCAGTGAGACGGGCG 1414 TTTGTAGACT 4019 T GAC- CG ----- T C
CTGGCAAGCACGTGCCCCGG TGGAACCCAC CTTC TCAGTGA GGG CTG GCAAGCACG
GCC C
GCTGTGTTTGTAGACTTGGA AGTC |||| ||||||| ||| ||| ||||||||| |||
ACCCACAGTCATTGATGAAG GAAG AGTTACT CCC GGT TGTTTGTGT CGG /
T GACA AA TCAGA - G

GAM1438 TCATGGGCACGGCTCGGGAC 1415 CACCTTCTGG 4020 CA -- G C A GAAAC GAG
AGTT
GGAGACGAAACCAGACAGAG ACTGCTGCCC TCATGGG CGGC TC GGA GG GAC CAGACA
GGTCA T
GGTCAAGTTTACAGATGACC CCAT ||||||| |||| || ||| || ||| |||||| |||||
GTGTCTGCAAGAGTCACCTT AGTACCC GTCG AG TCT CC CTG GTCTGT CCAGT
A
CTGGACTGCTGCCCCCATGA CC TC G T A AGAAC G-- AGAC

GAM1439 CATGGAATATGAGAAAATAG 1416 TGGAATATGA 4021 AA - AGAAAC- AG
CAGAAACAGATTTTGAGAAG GAAAATAGCA CATGG TATG AGAAAATAGC AGATTTTG A
CGAGATTTTCGGAAGGTTGT GAAA ||||| |||| |||||||||| ||||||||
TTTCTGCATGGACCGTG GTGCC GTAC TCTTTTGTTG TTTAGAGC /
AG G GAAGGCT GA

GAM1440 GTAGAGCTTTATGCTGAAAA 1417 GAGCTTTATG 4023 - TA GAAAA - T A
GGTGGCCACTAGAGGTCTGT CTGAAAAGGT GTAGAG CTT TGCT GGTGGC CAC AG G
GTGCCATTGCCCAGGCAGAG GGCC |||||| ||| |||| |||||| ||| ||
TCTCTGC CGTCTC GAG ACGG TTACCG GTG TC G
T -- ACCCG T - T

GAM1441 GGGAAACTCCGAGGACAGAG 1418 TGGCCTGATG 4022 AAA A--- - GA AA TG A
GGCTAAATCCATGAAGTTTG ATCCACAGCG GGG CTCCG GGA CA GGGCT ATCCA A G
TGGATGGCCTGATGATCCAC GAGA ||| ||||| ||| || ||||| ||||| |
AGCGGAGACCC CCC GAGGC CCT GT TCCGG TAGGT T /
A-- GACA A AG -- GT T

GAM1442 TGCCAACCTTGAAGCCAGTG 1419 TTGAAGCCAG 4024 A - TG - G - ATCC
GGGCACCAATCCACAAACTG TGGGGCACCA TGCCA CC T AAGCCA GTG GGCA CCA A
GATGCTGCGCTTGGTTTTGA ATCC ||||| || | |||||| ||| |||| |||
TGGTGGCA ACGGT GG A TTTGGT CGC TCGT GGT C
- T GT T G A CAAA

GAM1443 TCTTGTGTTGAGACTTCGTG 1420 TACACCACTC 4025 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G

ATAA AACCC - GAAGAA

GAM1444 TCCATCGGGCAGCCAGAGGC 1421 ACTGAGCACC 4026 G A---- AG C C TC
CCAGCGTCTCCGATGACACT TGGTGAATGG TCCATC GGC GCCAG GC CAG GTC C
GAGCACCTGGTGAATGGCCG CCGG |||||| ||| ||||| || ||| |||
GATGGA AGGTAG CCG TGGTC CG GTC CAG G
G GTAAG CA A A TA

GAM1445 CATCATGGATTCATCCCTTA 1422 TACCCGCCGG 4027 G T- CTTA - G ACAGA CTG
CCCGCCGGGACAGATCTGCT GACAGATCTG CATCAT GAT CATCC CC CGCC GG TCTG
G
GGTATCAGAAGCCGGGCGTG CTGG |||||| ||| ||||| || |||| || ||||
GGTTTGGATGCCATCAATGA GTAGTA CTA GTAGG GG GCGG CC AGAC /
TG A CC TTTG T G GA--- TAT

GAM1446 GCCCTATTACCTGAACCTGA 1423 TATCAGACTG 4029 T ACCTGAAC C-- TC
TCGAGCTCTTCCTGCAGAGT AGATTGGGC GCCC ATT CTGAT GAGCTCT C
TCCCTATCAGACTGAGATTG |||| ||| ||||| |||||||
GGC CGGG TAG GACTA CTTGAGA T
T AGTCA--- TCC CG

GAM1447 GCCAAGGAAACAGGATGCTG 1424 TGATAGTCTC 4028 -- AC A TGA C - G- GGA
ATAGTCTCCAGCAGGGCCTG CAGCAGGGCC GCCA AGGAA AGG TGC TAGT TCCA GCA
GGCCT C
GACATGTGGGCTGGTGTGTG TGGA |||| ||||| ||| ||| |||| |||| ||| |||||
GAACTGCTGCAACTTTCTTC CGGT TCCTT TTC ACG GTCA AGGT TGT TCGGG A
CTGGTGGC GG CT A TC- - G GG TGT

GAM1448 TGACATGTTGCCAACACCTT 1425 TTTCTAATAA 4030 TGTT AC CTTG--- TT
GAGAAGCATTATTTGTTTCT AAGTAATGGC TGACA GCCA AC AGAAGCA A
AATAAAAGTAATGGCTTTGT TTTG ||||| |||| || |||||||
CA ACTGT CGGT TG TCTTTGT /
TT-- AA AAAATAA TT

GAM1449 GGCCAATTGAAACAAACAGT 1426 TATTAGGGAT 4031 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1450 GGCCAATTGAAACAAACAGT 1427 TATTAGGGAT 4032 C T ACAAACAG G GTT T A
GAT

TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1451 CCGGAACCTGCTCATCTGGA 1428 AGAGTTGTTC 4033 GA - - A CAA G -- AAA
TCAAGAAGAATTTGCTAAAA ATCCAGGGAG CCG AC CTG CTC TCTGGAT GAA AATTT GCT
A
GAGCGGCCAGAGTTGTTCAT ACAG ||| || ||| ||| ||||||| ||| ||||| |||
CCAGGGAGACAGCGTGCGG GGC TG GAC GAG GGACCTA CTT TTGAG CGG G
G- C A - --- G AC CGA

GAM1452 TCTTGTGTTGAGACTTCGTG 1429 TACACCACTC 4034 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM1453 GGCCAATTGAAACAAACAGT 1430 TATTAGGGAT 4035 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1454 GGCCAATTGAAACAAACAGT 1431 TATTAGGGAT 4036 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1455 GGCCAATTGAAACAAACAGT 1432 TATTAGGGAT 4037 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1456 TTAAGACAAAGCAATTTTAA 1433 CCTTGCTGCA 4038 C A TAATACT T CAC
TACTAGGTGCACACCACATG AACTGCTTTT TTAAGA AAAGCA TTT AGG GCA C
CCCTTGCTGCAAACTGCTTT CTTG |||||| |||||| ||| ||| |||
TCTTGA AGTTCT TTTCGT AAA TCC CGT /
- C CGTCGT- - ACA

GAM1457 TTGTCGTCATTGGACACGTA 1434 TAAATGCGGT 4040 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM1458 AAGCTGGTACGCCTGCAGGT 1435 GCTGGTACGC 4039 T C CA AC GT AA
ACCGGTCCGGAATTCCCGGG CTGCAGGTAC AAGCTGG ACGC TG GGT CG CCGG T
TCGACCCACGCGTCCGGTTT CGGT ||||||| |||| || ||| || ||||
TTTGGCC TGCG AC CCA GC GGCC /
- C -- -- TG CT

GAM1459 CGGCTCCGAGAGCAGGTTCT 1436 TACACATTGA 4041 - AGAG C A TC GCAG C
TCGTGAGTTCCTCGCAGGGC GAACCTGAAC CGGC TCCG CAGGTTCTT GTG GT CTC GG
C
CGGTCAGAGCTACACATTGA ATGG |||| |||| ||||||||| ||| || ||| ||
GAACCTGAACATGGAGGCCG GCCG AGGT GTCCAAGAG TAC CA GAG CT G
G ACAA T A TC A--- G

GAM1460 GTGTCTGGAAAAATTCACCG 1437 GCCATGCGGA 4042 AAA AC A C AA CA
TGAGCCTGAACCACAAGCTG GCTTCTAGAT GTGTCTGGAA TTC CGTG GC TG CCA A
GACAGCCATGCGGAGCTTCT GC |||||||||| ||| |||| || || |||
AGATGC CGTAGATCTT GAG GTAC CG AC GGT /
C-- GC - - A- CG

GAM1461 TCTTGTGTTGAGACTTCGTG 1438 TACACCACTC 4043 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM1462 GAACTTGATTTTCATTAATC 1439 ACTTGATTTT 4044 AC T TTA-- A-- - G C TAATTT
CAGAGCTGCAGCACCAGAGA CATTAATCCA GA TTGAT TTCA ATCC GAGCTG CA CAC
AGAGA C
TAATTTCAATCAACTCTTTT GAGC || ||||| |||| |||| |||||| || ||| |||||
GTGATGACAGCTTGGCGGGT CT AACTG AAGT TGGG TTCGAC GT GTG TTTCT A
ACGGTTGAATGTCAATGTC GT T TGGCA CGG A A T CAACTA

GAM1463 GTGCGGCTCAGTGAGACTCT 1440 TCAGTGAGAC 4045 T T A CT-- C TC
TGGTGGGGCGGGTCCGCTTC TCTTGGTGGG GTGCGGC CAG GAG CT TGGTGGGG GGG C
CTCTTCACCATCACAGGCTT GCGG ||||||| ||| ||| || |||||||| |||
CTGGCTGCGC CGCGTCG GTC TTC GA ACCACTTC CCT G

- - G CACT T TC

GAM1464 GAAACAGACTGGGCCAATGT 1441 TATCAAGGAA 4046 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM1465 GGCCCAGGGATCGGCAGGGC 1442 TTCCCATGCC 4047 G - G- - GCT GA A
TGCTGGCAGAGGAATCCCAG CCAGGCTCCT GGCCCAG GA TC GCAGG GCT GGCA
GGAATCCC G
CTGGGGTTCCCATGCCCCAG GCAG ||||||| || || ||||| ||| |||| ||||||||
GCTCCTGCAGGACTTGCTGG CCGGGTC TT AG CGTCC CGG CCGT CCTTGGGG C
GCC G C GA T ACC AC T

GAM1466 CCCACTCCACGGGGATGTCG 1443 TCGTTGGGAT 4048 C A G TC GGATAAAA TTT
- GT
TTGGGATAAAAGCCTTTGAC AAAAGCCTTT CCCA TCC CGGG ATG GTTG GCC
GACCAGG CAG A
CAGGCAGGTAAGGCTGACCT GACC |||| ||| |||| ||| |||| ||| ||||||| |||
GGTTTTTGGTCAACTCATCC GGGT AGG GCCC TAC CAAC TGG TTGGTCC GTC A
CGGGATGGG - - - T- -------- TTT A GG

GAM1467 GCCCTCAGGGAACTTTGTGG 1444 TCTACAGCCT 4049 A- AAC T C - TT CA
CCTGTGGGGGGTTGGACAAC CAAGACCCGC GCCCTC GGG TTTG GGC TGTGGG GGG GGA
A
ATCTGCTCCATCTACAGCCT GAGG |||||| ||| |||| ||| |||||| ||| |||
CAAGACCCGCGAGGGC CGGGAG CCC GAAC CCG ACATCT CCT TCT /
CG A-- T - A CG AC

GAM1468 GGTGCAGAAGCAGACCCGTG 1445 AAGCAGACCC 4050 T GA- AG T CA- G CCA-
AA--- TT
CCGGCCAGCGCACCAGGTTC GTGCCGGCCA GG GCA AGC ACCCG GCCGGC GC CA
GGTTC GGCA T
AAGGCATTTGTTGCTATCGG GCGC || ||| ||| ||||| |||||| || || ||||| ||||
GGACTACAATGGCCACGTCG CC CGT TTG TGGGT TGGCTG CG GT TCAGG
TCGT /
GTCTGGGTGTTAAGTGCTCC T GAA -- C CAC - AACA GGCTA TG

GAM1469 CGGGTCTTCGCCAACATCCT 1446 AGGACCAAGA 4051 - GCC C ------ AC
CCTCTACATCCAGAGGACCA GCATGTTCCA CG GGTCTTC AACAT C TCCTCT A

AGAGCATGTTCCAGAGGACC GAGG || ||||||| ||||| | ||||||
ACG GC CCAGGAG TTGTA G AGGAGA T
A ACC C AGAACC CC

GAM1470 TCTTGTGTTGAGACTTCGTG 1447 TACACCACTC 4052 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM1471 TCTGCAATGGCTGCCAGGCG 1448 GAGCATTGGC 4053 G- - GGA A CCT- C CA
GATCACTCCTCCACTGGAGC AGTGAATTGC TCTGCAAT GCTGCCAG GC TC CT CCA
TGGAGC T
CATCCCGCTCCATGGCCAAA AGA |||||||| |||||||| || || ||| ||||||
GCGAGAGCATTGGCAGTGAA AGACGTTA TGACGGTT CG AG GA GGT ACCTCG C
TTGCAGA AG A AG- C AACC - CC

GAM1472 GTAGAGCTTTATGCTGAAAA 1449 GAGCTTTATG 4055 - TA GAAAA - T A
GGTGGCCACTAGAGGTCTGT CTGAAAAGGT GTAGAG CTT TGCT GGTGGC CAC AG G
GTGCCATTGCCCAGGCAGAG GGCC |||||| ||| |||| |||||| ||| ||
TCTCTGC CGTCTC GAG ACGG TTACCG GTG TC G
T -- ACCCG T - T

GAM1473 GGGAAACTCCGAGGACAGAG 1450 TGGCCTGATG 4054 AAA A--- - GA AA TG A
GGCTAAATCCATGAAGTTTG ATCCACAGCG GGG CTCCG GGA CA GGGCT ATCCA A G
TGGATGGCCTGATGATCCAC GAGA ||| ||||| ||| || ||||| ||||| |
AGCGGAGACCC CCC GAGGC CCT GT TCCGG TAGGT T /
A-- GACA A AG -- GT T

GAM1474 TGGCTAAGTTGGTTGCTTTT 1451 TAAGTTGGTT 4056 CTA T CTTTT- T A- AA
TGGTGATTAGTCAAAGAGAC GCTTTTTGGT TGG AGTTGG TG TGG GATT GTC A
CAAATCCCATATCCTCGTCC GATT ||| |||||| || ||| |||| |||
GACTCCTCCG GCC TCAGCC GC ACC CTAA CAG /
TCC T TCCTAT - AC AG

GAM1475 AGGGTTAGTTTTTGTAGCCT 1452 TGGCACGCTC 4057 --- TT A- TC- C
CGGCTGGCCCGTCGGCCTCT GAACTTCCGG AGGGTT AGTTT GT GCC GGCTGG C
GGCACGCTCGAACTTCCGGC CCCT |||||| ||||| || ||| ||||||
CCT TCCCGG TCAAG CG CGG CCGGCT C
CCT CT CA TCT G

GAM1476 GGTGACAACATGCTGGAGCC 1453 TTGGTTCAAG 4058 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A

TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1477 CATGACCACAGTCCATGCCA 1454 ATGGCCCCTC 4059 A CCATG ATCACT- - - A
TCACTGCCACCCAGAAGACT CGGGAAACTG CATG CCACAGT CC GCCA CC CAG A
GTGGATGGCCCCTCCGGGAA TGGC |||| ||||||| || |||| || |||
ACTGTGGCGTG GTGC GGTGTCA GG CGGT GG GTC G
- AA--- GCCTCCC A T A

GAM1478 GTGCACCTGAGCCGTGGAGG 1455 TTGCTCCTGA 4060 C C-- GG T TCC
GGCTGAAGTCCAGATCTTTG CGTCCCTCAG GTGCA CTGAG CGT AGGGGC GAAG A
CTCCTGACGTCCCTCAGATG ATGC ||||| ||||| ||| |||||| ||||
CAC CACGT GACTC GCA TCCTCG TTTC /
A CCT G- - TAG

GAM1479 CATTGTCGTCATTGGACACG 1456 CGTCATTGGA 4061 GTC-- T- A C ATTC C
TAGATTCGGGCAAGTCCACC CACGTAGATT CATT GTCA TGG CA GTAG GGG A
ACTACTGGCCATCTGATCTA CGGG |||| |||| ||| || |||| |||
TAAATG GTAA TAGT ACC GT CATC CCT A
ATATC CT G - ACCA G

GAM1480 TGCGGATCTCCTCCCGGGGG 1457 GTCCAGTTTG 4062 A CC---- -- --- C ACG
AAGCTGGCTGAACGCGACAT TACCCTTCCG TGCGG TCT TCCCGG GGG AAGCTGG TGA
C
CGTCCAGTTTGTACCCTTCC GGAC ||||| ||| |||||| ||| ||||||| |||
GGGACTACGTGGACCGCA ACGCC AGG AGGGCC CCC TTTGACC GCT G
- TGCATC TT ATG T ACA

GAM1481 TTCAGAGCTGGTATCGGAGC 1458 AGCTGGTATC 4063 AG ---- G - A- C---- ATA
GGGGAGACCTGGGATAGCAA GGAGCGGGGA TTCAG CTGGTA TCG AGC GGGG GA
CTGGG G
GTTCAGCACCATCGCCTCCA GACC ||||| |||||| ||| ||| |||| || |||||
GCTACGAAGAGTGCCGGGCT GAGTC GGCCGT AGC TCG CCTC CT GACTT C
GAG G- GAGA A A CG ACCAC GAA

GAM1482 AAGATGCTGCGGAATCTGCT 1459 CGATAAGCAC 4064 - AATCT TG- CT AGATTG
GGCTCTTCGTCAGATTGGGC TGCTTCCCGC AAGATGC TGCGG GC GCT TCGTC G
AGAGGACGATAAGCACTGCT AGGC ||||||| ||||| || ||| |||||
TCCCGCAGGCATTTT TTTTACG ACGCC CG CGA AGCAG /
G CTT-- TCA AT GAGACG

GAM1483 TTGTCGTCATTGGACACGTA 1460 TAAATGCGGT 4066 --- GACAC CG-- A CCA

GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM1484 GGTGACAACATGCTGGAGCC 1461 TTGGTTCAAG 4065 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1485 TTGTCGTCATTGGACACGTA 1462 TAAATGCGGT 4067 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM1486 CATTGTCGTCATTGGACACG 1463 CGTCATTGGA 4068 GTC-- T- A C ATTC C
TAGATTCGGGCAAGTCCACC CACGTAGATT CATT GTCA TGG CA GTAG GGG A
ACTACTGGCCATCTGATCTA CGGG |||| |||| ||| || |||| |||
TAAATG GTAA TAGT ACC GT CATC CCT A
ATATC CT G - ACCA G

GAM1487 GGCCCAGGGATCGGCAGGGC 1464 TTCCCATGCC 4069 G - G- - GCT GA A
TGCTGGCAGAGGAATCCCAG CCAGGCTCCT GGCCCAG GA TC GCAGG GCT GGCA
GGAATCCC G
CTGGGGTTCCCATGCCCCAG GCAG ||||||| || || ||||| ||| |||| ||||||||
GCTCCTGCAGGACTTGCTGG CCGGGTC TT AG CGTCC CGG CCGT CCTTGGGG C
GCC G C GA T ACC AC T

GAM1488 ATTTGAGAAGGAGGCTGCTG 1465 CTTCAAGTAT 4070 TG AGG - GA T AAA
AGATGGGAAAGGGCTCCTTC GCCTGGGTCT ATT AGA AGGC TGCT GA GGG G
AAGTATGCCTGGGTCTTGGA TGGA ||| ||| |||| |||| || |||
T TAG TCT TCCG ATGA CT CCT /
GT GGG T A- T CGG

GAM1489 GGTGACAACATGCTGGAGCC 1466 TTGGTTCAAG 4071 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1490 CTTTATCAAAAACATGATTA 1467 TCAAAAACAT 4072 --- AA GATTA G TC - TGAC

CAGGGACATCTCAGGCTGAC GATTACAGGG CTTTA TCA AACAT CAG GACA TCAGG C T
TGTGCTGTCCTGATTGTTGC ACAT ||||| ||| ||||| ||| |||| ||||| |
TGCTGGTGTTGGTGAATTTG GAAGT AGT TTGTG GTC TTGT AGTCC G G
AAG TTA GG GTC-- G T- T TCGT

GAM1491 GGTGACAACATGCTGGAGCC 1468 TTGGTTCAAG 4073 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1492 GGTGACAACATGCTGGAGCC 1469 TTGGTTCAAG 4074 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1493 TTGTCGTCATTGGACACGTA 1470 TAAATGCGGT 4075 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM1494 TTGTCGTCATTGGACACGTA 1471 TAAATGCGGT 4076 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM1495 CATTGTCGTCATTGGACACG 1472 CGTCATTGGA 4077 GTC-- T- A C ATTC C
TAGATTCGGGCAAGTCCACC CACGTAGATT CATT GTCA TGG CA GTAG GGG A
ACTACTGGCCATCTGATCTA CGGG |||| |||| ||| || |||| |||
TAAATG GTAA TAGT ACC GT CATC CCT A
ATATC CT G - ACCA G

GAM1496 GGTGACAACATGCTGGAGCC 1473 TTGGTTCAAG 4078 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1497 GGCATCTCTGAGGAGACCAC 1474 TCTGAGGAGA 4080 C GA CGACTGG T - A CT
GACTGGGGTCCACAACTCTA CCACGACTGG GGCATCT TGAGGA CCA GG CCA CA CT A

CAAGATGATGGCCAATGGGA GGTC ||||||| |||||| ||| || ||| || ||
TCCTCAAGGTGCC CCGTGGA ACTCCT GGT CC GGT GT GA /
- AG AA----- - A A AC

GAM1498 GCCATCAATGTCAATGACTC 1475 AATGACTCCG 4079 A TCAAT - T - - CA T
CGTCACCAAGAGCAGTTTGA TCACCAAGAG GCCATC ATG GACTCC G CA CCA AGAG GTT
G
CAACCTCTATGGCTGCCGGG CAGT |||||| ||| |||||| | || ||| |||| |||
AGTCCCTCATAGATGGC CGGTAG TAC CTGAGG C GT GGT TCTC CAA A
A TCC-- G C C A -- C

GAM1499 TACGGGCTCTGAAATTGCCA 1476 TGGAATTGAT 4081 - A- G CAA C-- TGA
GACAAAACCCTCATTGACCT AGAGCTCCGT TACGG GCTCTG AATT CCAGA AACC TCAT C
CTATGAACAGGTTGTTCTGG G ||||| |||||| |||| ||||| |||| ||||
AATTGATAGAGCTCCGTG GTGCC CGAGAT TTAA GGTCT TTGG AGTA C
T AG - TG- ACA TCT

GAM1500 GGTGACAACATGCTGGAGCC 1477 TTGGTTCAAG 4082 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1501 TTGTCGTCATTGGACACGTA 1478 TAAATGCGGT 4083 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM1502 GGTGACAACATGCTGGAGCC 1479 TTGGTTCAAG 4084 AA--- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAA GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAAGTCAC GTCA |||||| ||| || |||||||| ||
C CCACTG GTA GG CTTGGTTC CG C
AAAAG G AA - TA

GAM1503 GTGTGGCCGATGTGTCTATT 1480 TCAGGAGACC 4085 - CTAT AAGA T TC
GAAGATTCTGTGATCTCACT ATTGCATCAT GTGTGGCCGATG TGT TG TTCTG GA T
CTCAGGAGACCATTGCATCA TGGC |||||||||||| ||| || ||||| ||
TTGGCCGCAC CACGCCGGTTAC ACG AC AGGAC CT C
T TT-- CAG- T CA

GAM1504 CGCTCGTCACCAGGACCCAA 1481 TCAAGGGTCG 4086 - T- C G AA GA AAATTG
GGAACCAAAATTGCATCTGA TGTGTTTGAA CGCT CG CAC A GACCC G ACCA C

TGGTCTCAAGGGTCGTGTGT GTG |||| || ||| | ||||| | ||||
TTGAAGTG GTGA GT GTG T CTGGG C TGGT /
A TT - G AA TC AGTCTA

GAM1505 GCTCTCCGCCGCAGCTTCAG 1482 CAATGCTAAA 4087 CC C TC--- CC-- GG
CACCTCGGCCCAGAACAATG GTAGCTGTGC GCTCT GC GCAGCT AGCA TC C
CTAAAGTAGCTGTGCTAGGG TAGG ||||| || |||||| |||| ||
GC CGGGG CG TGTCGA TCGT AG C
AT - TGAAA AACA AC

GAM1506 GGTGACAACATGCTGGAGCC 1483 TTGGTTCAAG 4088 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1507 TTGTCGTCATTGGACACGTA 1484 TAAATGCGGT 4089 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM1508 GGCCAATTGAAACAAACAGT 1485 TATTAGGGAT 4090 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1509 TCCAGAAAGCTGATGGTGTG 1486 AGGCTGCCTG 4091 AG- TGA --- - - CTAC
CCCGTCTACCTGAAACGAGG ACCAAATGCT TCC AAAGC TGGT GT GCC CGT C
CTGCCTGACCAAATGCTTTA TTAC ||| ||||| |||| || ||| |||
CCGGA AGG TTTCG ACCA CG CGG GCA /
CCA TAA GTC T A AAGT

GAM1510 ATTTGAGAAGGAGGCTGCTG 1487 CTTCAAGTAT 4092 TG AGG - GA T AAA
AGATGGGAAAGGGCTCCTTC GCCTGGGTCT ATT AGA AGGC TGCT GA GGG G
AAGTATGCCTGGGTCTTGGA TGGA ||| ||| |||| |||| || |||
T TAG TCT TCCG ATGA CT CCT /
GT GGG T A- T CGG

GAM1511 GGCCAATTGAAACAAACAGT 1488 TATTAGGGAT 4093 C T ACAAACAG G GTT T A
GAT

TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1512 GCCAACCTTGAAGCCAGTGG 1489 TTGAAGCCAG 4094 A - TG - G - ATCC
GGCACCAATCCACAAACTGG TGGGGCACCA GCCA CC T AAGCCA GTG GGCA CCA A
ATGCTGCGCTTGGTTTTGAT ATCC |||| || | |||||| ||| |||| |||
GGTGGC CGGT GG A TTTGGT CGC TCGT GGT C
- T GT T G A CAAA

GAM1513 AACTTGAAAGTGAACAGTAT 1490 TGGCCCACAT 4095 T AG- T ACTTTCC AT A
GACTTTCCTGATCCAGAACA CTGTTTAATC AACT GAA TGAACAG ATG TG CCAGA C
GTTTGGCCCACATCTGTTTA TTCC |||| ||| ||||||| ||| || |||||
ATCTTCCAGTT TTGA CTT ATTTGTC TAC AC GGTTT A
C CTA - ------- CC G

GAM1514 GGCCAATTGAAACAAACAGT 1491 TATTAGGGAT 4096 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1515 TCTTGTGTTGAGACTTCGTG 1492 TACACCACTC 4097 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM1516 TCTTGTGTTGAGACTTCGTG 1493 TACACCACTC 4098 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM1517 GGGGGAGCTCATCGGCTACT 1494 CGACACCGAG 4099 T TC TC AACG AAG
CTGAACGCGGCCAAGGTGCC GTGGTTTGTG GGGGGAGC CA GGCTAC TG CGGCC G
GGCCGACACCGAGGTGGTTT CTCC |||||||| || |||||| || |||||
GTGCTCCCCC CCCCCTCG GT TTGGTG GC GCCGG T
T -- GA CACA CCG

GAM1518 GGGGTGAGCTGGGGAGGCTT 1495 ATGGCCCCAG 4100 GA G TCT G - A

CTGCGGTTCTGGAGTCCCGG TTCCCCAGCA GGGGT GCTGGGGAG CT GC GTT CTGG G
CAATGGCCCCAGTTCCCCAG AACC ||||| ||||||||| || || ||| ||||
CAAACCCC CCCCA CGACCCCTT GA CG TAA GGCC T
AA - CCC G C C

GAM1519 GCCCAGGTGGTGCAGTGGGT 1496 GTGCAGTGGG 4101 G CAG TGA - C A
GAGCTTGTGCTGATTCCGAT TGAGCTTGTG GCCCAGGTG TG TGGG GC TTGTG TG T
ATAGTGCCCCCCAGCCAGTA CTGA ||||||||| || |||| || ||||| ||
CCTGGGT TGGGTCCAT AC ACCC CG GATAT GC T
G CG- CC- T A C

GAM1520 GCGGCTGGGACCCTGTACAC 1497 TCTCATCGCT 4102 -- A ACAC TC AAACTG--
TT
GTATCCTGAAAACTGGAGGG GCTCAGTACA GCGG CTGGG CCCTGT GTA CTGA
GAGGGCC C
CCTTCAAGGCTCTCATCGCT GCGG |||| ||||| |||||| ||| |||| |||||||
GCTCAGTACAGCGGGGCTCA CGCC GACTC GGGGCG CAT GACT CTCTCGG /
GGTCCGC TG - A--- -- CGTCGCTA AA

GAM1521 TGAAGCACTACGGGCCTGGC 1498 AGACACCAAC 4103 C AC GCTG AGCATG AA
TGGGTGAGCATGGCCAACGC GGGTCCAGTT TGAAG ACT GGGCCTG GGTG GCC C
AGGCAAAGACACCAACGGGT CTTC ||||| ||| ||||||| |||| |||
CCAGTTCTTCA ACTTC TGA CCTGGGC CCAC CGG G
T -- AA-- AGAAA- AC

GAM1522 TCTTGTGTTGAGACTTCGTG 1499 TACACCACTC 4104 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM1523 TGAAGATCCTCACTGAGCGA 1500 CAGCTTCACC 4106 A TCAC G A T A ACCA-- - -
GCG
GGCTACAGCTTCACCACCAC ACCACGGCCG TGAAG TCC TGA CG GGC ACAGCTTC CC
CG GC CGA G
GGCCGAGCGGGAAATCGTGC AGCG ||||| ||| ||| || ||| |||||||| || || || |||
GCGACATCAGGAGAAGCTGT GCTTC AGG GCT GC TCG TGTCGAAG GG GC CG
GCT G
GCTACGTCGCCCTGGACTTC - TCCC - A - A ACTACA G T AAA
G

GAM1524 GCACTCTGTTCTTCCGCCGC 1501 ACTCTGTTCT 4105 AC G CC TCC TC TT
TCCGCCGTCGCGTTTCTCTG TCCGCCGCTC GC TCT TTCTTCCG GC GCCG GCG T
CCGGTCGCAATGGAAGAAGA CGCC || ||| |||||||| || |||| |||
GATCGC CG AGA AAGAAGGT CG TGGC CGT C

CT G AA C-- -- CT

GAM1525 GGTGACAACATGCTGGAGCC 1502 CCTTGGTTCA 4107 AA-- G G- T AA
AAGTGCTAACATGGCCTTGG AGGGATGGAA GGTGAC CAT CT GAGCCAAG GCT C
TTCAAGGGATGGAAAGTCAC AGTC |||||| ||| || |||||||| |||
C CCACTG GTA GG CTTGGTTC CGG /
AAAG G AA - TA

GAM1526 GAGACAATGATCATAGACAA 1503 TAGACAACTG 4108 CAA AT AG CT T GC- C A
CTGCTGCATGCACTGGTGCA CTGCATGCAC GAGA TG CAT ACAA GC GCAT ACTGGTG AG
A
GAATCCTTACCAGTTTGATG TGGT |||| || ||| |||| || |||| |||||||| ||
TGCTTGTGATGCCCAATCTC CTCT AC GTA TGTT CG TGTA TGACCAT TC T
A-- CC G- -- - GTT - C

GAM1527 TCTTGAGTATCACTCCAGCA 1504 ATCAAAGTTG 4109 AT- --- A- AGATGCG
TGATCGCAGATGCGGTGAAG GCAAGGTGCG TCTTGAGT CACT CCAGC TGATCGC G
AAGGTGATCAAAGTTGGCAA GACT |||||||| |||| ||||| |||||||
GGTGCGGACTCGAGA AGAGCTCA GTGG GGTTG ACTAGTG T
GGC AAC AA GAAGAAG

GAM1528 GGCCAATTGAAACAAACAGT 1505 TATTAGGGAT 4110 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1529 TTGTCGTCATTGGACACGTA 1506 TAAATGCGGT 4111 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM1530 CTGCATAGTATTTGGGCTCC 1507 TAGTATTTGG 4112 AG- G T A C GAT
ACTTCACTGATCTGAAAGTT GCTCCACTTC CTGCAT TATTT GGC CC CTT ACT C
GAGGGTGTTGGAATAGAGGT ACTG |||||| ||||| ||| || ||| |||
GCAG GACGTG ATAAG TTG GG GAG TGA T
GAG G T - T AAG

GAM1531 GTATCTGCCAGCAGAATGGC 1508 TGGCATGGTG 4114 T C AGAAT- - G T CCTG
ATGGTGCCCATCGTGGAGCC CCCATCGTGG GTA CTG CAGC GG CATGGT CCCATCG
GGAG A

TGAGATCCTCCCTGATGGGG AGCC ||| ||| |||| || |||||| ||||||| ||||
ACCATGACTTGAAGCGCTGC TAT GAC GTCG TC GTACCA GGGTAGT CCTC /
CAGTAT - C CGAAGT A G C CTAG

GAM1532 ATGGTCACCCCAGGCCATGC 1509 GGAGATGGCC 4113 A CCA G GCA GA T
TTGCACTCAGAAGTTTTCTC ATGGCGACCG ATGGTC CC GGCCAT CTT CTCA AG T
ATGAGGAGATGGCCATGGCG T |||||| || |||||| ||| |||| ||
ACCGT TGCCAG GG CCGGTA GAG GAGT TC T
C TA- - --- AC T

GAM1533 GGTGACAACATGCTGGAGCC 1510 TTGGTTCAAG 4115 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1534 GGTGACAACATGCTGGAGCC 1511 GGTCACAGGG 4117 AA-- G - - G T TA
AAGTGCTAACATGCCTTGGG ATGGAAAGTC GGTGAC CAT C TG GA CCAAG GC A
TCACAGGGATGGAAAGTCAC ACC |||||| ||| | || || ||||| ||
C CCACTG GTA G AC CT GGTTC CG C
AAAG G G A G - TA

GAM1535 CATTGTCGTCATTGGACACG 1512 CGTCATTGGA 4116 GTC-- T- A C ATTC C
TAGATTCGGGCAAGTCCACC CACGTAGATT CATT GTCA TGG CA GTAG GGG A
ACTACTGGCCATCTGATCTA CGGG |||| |||| ||| || |||| |||
TAAATG GTAA TAGT ACC GT CATC CCT A
ATATC CT G - ACCA G

GAM1536 ATGGTGACAACATGCTGGAG 1513 TTGGTTCAAG 4118 AA-- G G- T TA
CCAAGTGCTAACATGCCTTG GGATGGAAAG ATGGTGAC CAT CT GAGCCAAG GC A
GTTCAAGGGATGGAAAGTCA TCAC |||||||| ||| || |||||||| ||
CCGT TGCCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1537 GACTTCGCCCGGCAGAAGCT 1514 TACAAAGTGA 4120 C G C TAGAT -- A TG --
TGCGC
AGATCCCAAGATTGCTGTGG CTAATGGGGC GA TTC CCCGG AGAAGC CCCA AG T CT
GTGGC A
CTGCGCAGAACTGCTACAAA TTTT || ||| ||||| |||||| |||| || | || |||||
GTGACTAATGGGGCTTTTAC CT GAG GGGTC TTTTCG GGGT TC A GA CATCG /
TGGGGAGATC A - A ----- AA - GT AA TCAAG

GAM1538 CTCGGAGTAATCGCCTGCAT 1515 CATCACTGAG 4119 TAAT GCA TG G GAA ATGAA

TGGGGAGAAGCTAGATGAAA AAGGTGTTTT CTCGGAG CGCCT T G GA GCTAG A
GGGAAGCTGGCATCACTGAG CGAG ||||||| ||||| | | || |||||
AAGGTGTTTTCGAG GAGCTTT GTGGA A C CT CGGTC G
T--- AG- GT A A-- GAAGG

GAM1539 TCCCCCCTCCGCCCCCGCCG 1516 TGAAGAGGGG 4121 ----- CG- GCCG AAG
CGGAAAGTTAAGTTTGAAGA GGAAGAGGGG TCC CCCCTC CCCCC CGGA T
GGGGGGAAGAGGGGAACATG AACA ||| |||||| ||||| ||||
GA AGG GGGGAG GGGGG GTTT T
TACAA AAG AGAA GAA

GAM1540 TCTTTTCAGTAATTTCATCC 1517 GAACAGGTTG 4122 CA A CCT ATCT TTTTG
TCTTTATCTACCTGTTCTAT GAAGTGTGGA TCTTTT GT ATTTCAT CTTT ACCTGTTCTA C
TTTGCGTTTTTTAGAACAGG GTCA |||||| || ||||||| |||| ||||||||||
TTGGAAGTGTGGAGTCACCA AGGAAG CA TGAGGTG GAAG TGGACAAGAT G
GAAGGA AC C T-- GT-- TTTTT

GAM1541 TTGGTGATATTGCCCTTGCT 1518 TATTGCCCTT 4123 T TATT CT ATG A AAAAT T
ATGGAGGAGAGTTTAAAAAA GCTATGGAGG TTGG GA GCC TGCT GAGGAG GTTTAA
ACT A
TACTTAGAGGTTGTATTGAA AGAG |||| || ||| |||| |||||| |||||| |||
TACTCTTCAGCAGGCCTCCC AACC CT CGG ACGA CTTCTC TAAGTT TGG G
AA - C--- -- --- A ATGT- A

GAM1542 CTGCAGGAGAAGATGGCGGT 1519 CAGGAGAAGA 4124 TG A G GTCTCCAC TT
CTCCACAGGAGTTAAAGTTC TGGCGGTCTC C CAGG GAAGAT GCG AGGAG A
CTCGTAATTTTCGCTTGTGG CACA | |||| |||||| ||| |||||
G GTTC CTTTTA TGC TCCTT A
GT G A -------- GA

GAM1543 TGATGCGCAAGGCCATCCGA 1520 TCTGGAGAAA 4125 T - A GCCA G ACC AAA
GGGCACCTGGAAAACAACCC CTGCTGCCTC TGA GC GCA G TCC AGGGC TGG A
AGCTCTGGAGAAACTGCTGC A ||| || ||| | ||| ||||| |||
CTCA ACT CG CGT C AGG TCTCG ACC C
C T - AAAG - --- CAA

GAM1544 GTAGAGCTTTATGCTGAAAA 1521 GAGCTTTATG 4126 - TA GAAAA - T A
GGTGGCCACTAGAGGTCTGT CTGAAAAGGT GTAGAG CTT TGCT GGTGGC CAC AG G
GTGCCATTGCCCAGGCAGAG GGCC |||||| ||| |||| |||||| ||| ||
TCTCTGC CGTCTC GAG ACGG TTACCG GTG TC G
T -- ACCCG T - T

GAM1545 TCTTGTGTTGAGACTTCGTG 1522 TACACCACTC 4127 GAGA GT--- C AAAGGA

GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| ||||| CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM1546 GTGCACCTGAGCCGTGGAGG 1523 TTGCTCCTGA 4128 C C-- GG T TCC
GGCTGAAGTCCAGATCTTTG CGTCCCTCAG GTGCA CTGAG CGT AGGGGC GAAG A
CTCCTGACGTCCCTCAGATG ATGC ||||| ||||| ||| |||||| |||| CAC CACGT GACTC GCA TCCTCG TTTC /
A CCT G- - TAG

GAM1547 TCTTGTGTTGAGACTTCGTG 1524 TACACCACTC 4129 GAGA GT--- C AAAGGAA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA G
AAGAAAGTCTTACACCACTC TAAG ||||||||| |||| ||||||| ||||| CCAAGAAGAATAAGCACAAG AGAACACGA GAAG TCACCAC ATTCT /
A ATAA AACCC - GAAAGAA

GAM1548 GGCCAATTGAAACAAACAGT 1525 TATTAGGGAT 4130 C T ACAAACAG G GTT T A GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || ||||| CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1549 TCAAGCCCCGGACAGGGTCT 1526 ACGCGGCCAA 4131 A - GACAG TTACA ACTAT
TACATCAACTATTACGACAT TGTGGGCTGG TC AGCCC CG GGTC TCA T
GAACGCGGCCAATGTGGGCT A || ||||| || |||| ||| GGA AG TCGGG GT CCGG AGT A
G T AA--- CGCA- ACAGC

GAM1550 GGTGACAACATGCTGGAGCC 1527 TTGGTTCAAG 4132 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| || CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1551 TTGTCGTCATTGGACACGTA 1528 TAAATGCGGT 4133 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| ||| AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM1552 CAAGATTCTTGATACTGCAC 1529 AGAGAAAAGC 4134 A AT-- T- A--- A

TCTCTAAGATTGGAGAGAAA CTGTTTACCA CAAG TTCTTG AC GC CTCTCTA G
AGCCTGTTTACCAAGGAGCT AGGA |||| |||||| || || |||||||
TG GTTC AGGAAC TG CG GAGAGGT A
G CATT TC AAAA T

GAM1553 GTTCCCGCATCTGGAGTTCA 1530 TCAACACCCG 4135 -- - A CA A A C G
GGAGTATTCGGGGAAACCTC GCTTCGGAAG GTTC CC GC TCTGGAGTT GG GT TT GGG A
AACACCCGGCTTCGGAAGCT CTGG |||| || || ||||||||| || || || |||
GGACGAGC CGAG GG CG AGGCTTCGG CC CA AA TCC A
CA T A -- - C C A

GAM1554 TAGCATTTTGTGCCAATATC 1531 TTTGTGCCAA 4136 T CAATA - TGGAA G
TGGTTGGAATGGTGACAACA TATCTGGTTG TAGCATTTTG GC TCTG GT TG T
TGCTCGGAGCCAAAGTGCTA GAAT |||||||||| || |||| || ||
ATCGTGAAAC CG AGGC CG AC G
- ----- T TACA- A

GAM1555 GGTGACAACATGCTGGAGCC 1532 TTGGTTCAAG 4137 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1556 GGTGACAACATGCTGGAGCC 1533 TTGGTTCAAG 4138 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1557 GCCAACATCGACCAGGAGAC 1534 GACCAGGAGA 4139 CATC AGACCTA T AC-- C
CTACCGCTGTGAACTCATTC CCTACCGCTG GCCAA GACCAGG CCGC GTGA TCATT A
AAGGATGGAACATTACTGTG TGAA ||||| ||||||| |||| |||| ||||
GACCTGGTCATTGGC CGGTT CTGGTCC GGTG CATT GGTAG A
A--- A------ T ACAA G

GAM1558 CATTGTCGTCATTGGACACG 1535 CGTCATTGGA 4140 GTC-- T- A C ATTC C
TAGATTCGGGCAAGTCCACC CACGTAGATT CATT GTCA TGG CA GTAG GGG A
ACTACTGGCCATCTGATCTA CGGG |||| |||| ||| || |||| |||
TAAATG GTAA TAGT ACC GT CATC CCT A
ATATC CT G - ACCA G

GAM1559 GGTGACAACATGCTGGAGCC 1536 TTCAAGGGAT 4141 AA-- G G- C T TA
CAGTGCTAACATGCCTTGGT GGAAAGTCAC GGTGAC CAT CT GAGCC AG GC A

TCAAGGGATGGAAAGTCACC C |||||| ||| || ||||| || ||
CCACTG GTA GG CTTGG TC CG C
AAAG G AA T - TA

GAM1560 GGTGACAACATGCTGGAGCC 1537 TTGGTTCAAG 4142 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1561 GGTGAACAACATGCTGGAGC 1538 TTGGTTCAAG 4143 ACAA- G G- T TA
CAAGTGCTAACATGCCTTGG GGATGGAAAG GGTGA CAT CT GAGCCAAG GC A
TTCAAGGGATGGAAAGTCAC TCAC ||||| ||| || |||||||| ||
C CCACT GTA GG CTTGGTTC CG C
GAAAG G AA - TA

GAM1562 TTGTCGTCATTGGACACGTA 1539 TAAATGCGGT 4144 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM1563 GGTGACAACATGCTGGAGCC 1540 TTGGTTCAAG 4145 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1564 ATTTGAGAAGGAGGCTGCTG 1541 CTTCAAGTAT 4146 TG AGG - GA T AAA
AGATGGGAAAGGGCTCCTTC GCCTGGGTCT ATT AGA AGGC TGCT GA GGG G
AAGTATGCCTGGGTCTTGGA TGGA ||| ||| |||| |||| || |||
T TAG TCT TCCG ATGA CT CCT /
GT GGG T A- T CGG

GAM1565 GGTGACAACATGCTGGAGCC 1542 TTGGTTCAAG 4147 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1566 GGTGACAACATGCTGGAGCC 1543 TTGGTTCAAG 4148 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||

CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1567 TTGTCGTCATTGGACACGTA 1544 TAAATGCGGT 4150 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM1568 GGTGACAACATGCTGGAGCC 1545 TTGGTTCAAG 4149 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1569 GGTGACAACATGCTGGAGCC 1546 TTGGTTCAAG 4152 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1570 ATTTGAGAAGGAGGCTGCTG 1547 CTTCAAGTAT 4151 TG AGG - GA T AAA
AGATGGGAAAGGGCTCCTTC GCCTGGGTCT ATT AGA AGGC TGCT GA GGG G
AAGTATGCCTGGGTCTTGGA TGGA ||| ||| |||| |||| || |||
T TAG TCT TCCG ATGA CT CCT /
GT GGG T A- T CGG

GAM1571 TTGTCGTCATTGGACACGTA 1548 TAAATGCGGT 4153 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM1572 GGTGACAACATGCTGGAGCC 1549 TTGGTTCAAG 4154 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1573 TTGTCGTCATTGGACACGTA 1550 TGGCCATCTG 4156 T GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC ATCTATAAAT TTG CGTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA GCGG ||| |||||||| ||||||| ||| |||
AATGCGGTGGCGTCGA AGC GCGGTGGC TATCTAG CCG TCA C

```
                                T      GTAAA     TCTA   G   TCA


GAM1574  GGTGACAACATGCTGGAGCC 1551    TTGGTTCAAG 4155       AA--   G  G-      T  TA
     AAGTGCTAACATGCCTTGGT       GGATGGAAAG       GGTGAC   CAT CT  GAGCCAAG GC  A
     TCAAGGGATGGAAAGTCACC       TCAC          ||||||   ||| ||  |||||||| ||
                                CCACTG   GTA GG  CTTGGTTC CG  C
                                   AAAG   G  AA      -  TA


GAM1575  GGTGACAACATGCTGGAGCC 1552    TTGGTTCAAG 4157       AA--   G  G-      T  TA
     AAGTGCTAACATGCCTTGGT       GGATGGAAAG       GGTGAC   CAT CT  GAGCCAAG GC  A
     TCAAGGGATGGAAAGTCACC       TCAC          ||||||   ||| ||  |||||||| ||
                                CCACTG   GTA GG  CTTGGTTC CG  C
                                   AAAG   G  AA      -  TA


GAM1576  TTGTCGTCATTGGACACGTA 1553    TAAATGCGGT 4159       ---      GACAC     CG--   A   CCA
     GATTCGGGCAAGTCCACCAC       GGCATCGACA       TTGTC   GTCATTG    GTAGATT    GGC AGT   C
     TACTGGCCATCTGATCTATA       A             |||||  |||||||    |||||||   ||| |||
     AATGCGGTGGCATCGACAA                      AACAG   CGGTGGC    TATCTAG    CCG TCA   C
                                CTA     GTAAA     TCTA   G   TCA


GAM1577  GGTGACAACATGCTGGAGCC 1554    TTGGTTCAAG 4158       AA--   G  G-      T  TA
     AAGTGCTAACATGCCTTGGT       GGATGGAAAG       GGTGAC   CAT CT  GAGCCAAG GC  A
     TCAAGGGATGGAAAGTCACC       TCAC          ||||||   ||| ||  |||||||| ||
                                CCACTG   GTA GG  CTTGGTTC CG  C
                                   AAAG   G  AA      -  TA


GAM1578  GGTGACAACATGCTGGAGCC 1555    TTGGTTCAAG 4160       AA--   G  G-      T  TA
     AAGTGCTAACATGCCTTGGT       GGATGGAAAG       GGTGAC   CAT CT  GAGCCAAG GC  A
     TCAAGGGATGGAAAGTCACC       TCAC          ||||||   ||| ||  |||||||| ||
                                CCACTG   GTA GG  CTTGGTTC CG  C
                                   AAAG   G  AA      -  TA


GAM1579  GGTGACAACATGCTGGAGCC 1556    TTGGTTCAAG 4161       AA--   G  G-      T  TA
     AAGTGCTAACATGCCTTGGT       GGATGGAAAG       GGTGAC   CAT CT  GAGCCAAG GC  A
     TCAAGGGATGGAAAGTCACC       TCAC          ||||||   ||| ||  |||||||| ||
                                CCACTG   GTA GG  CTTGGTTC CG  C
                                   AAAG   G  AA      -  TA


GAM1580  GCTCGGAACTGCCGACCCGA 1557    GGAGCGGAGT 4162       AA   -    AG-   T    AGAGG
     GTGCTTCCCGCAGAGGGCTG       GGGTCGGGCG       GCTCGG  CTGCC GACCCG   TGCT CCCGC    G
     GTGGTGGGAGCGGAGTGGGT       GGGC          ||||||  ||||| ||||||   |||| |||||
     CGGGCGGGGCCGAGC                       CGAGCC  GGCGG CTGGGT   GCGA GGGTG    C
                                GG    G     GAG   -    GTGGT
```

GAM1581 GGTGACAACATGCTTGGAGC 1558 GTCAAGGGAT 4163 AA-- G GGA T TA
CAAGTGCTAACATGCCTTGG GGAAAGTCAC GGTGAC CAT CTT GCCAAG GC A
TCAAGGGATGGAAAGTCACC C |||||| ||| ||| |||||| ||
CCACTG GTA GGA TGGTTC CG C
AAAG G AC- - TA

GAM1582 TTCTGGTGTATCAAAGCACA 1559 TGGTATCTGT 4164 G C G- T C AA A
TGACTAAAATGAAATCATGG GAATTTTATA TTCTGGT TAT AAA CACA GA TA ATG A
TATCTGTGAATTTTATAAGC AGCT ||||||| ||| ||| |||| || || |||
TAGAA AAGATCG ATA TTT GTGT CT AT TAC A
A T AA - - GG T

GAM1583 TCTTGTGTTGAGACTTCGTG 1560 TACACCATCC 4166 GAGA G T C- AAAGGA
GTGGTGGCTAAGAAAAGGAA CAAGAAGAAT TCTTGTGTT CTTC TGG GGTGG TAAGA A
GAAGAAGTCTTACACCATCC AAGC ||||||||| |||| ||| ||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG ACC CTACC ATTCT G
ATAA A - AC GAAGAA

GAM1584 GAAGGTTAAGCTGGTGTCCT 1561 TGAGAATGGA 4165 TAA G- TGAAA ATA
GAAATATTATAAGGTGGATG AAATTAGTCG GAAGGT GCTGGT TCC TATT A
AGAATGGAAAATTAGTCGCC CCTT |||||| |||||| ||| ||||
TTC CTTCCG TGATTA AGG GTAG G
C-- AA TAAGA GTG

GAM1585 GCTTTCCTTTCCAAGAGGAA 1562 TGGACTGTCC 4167 T CCA A-- T GCAG
TCCTCGGCAGATAAACGTGG TCTACAGAAG GCTT CCTTT AGAGGA TCC CG A
ACTGTCCTCTACAGAAGGAA GAAG |||| ||||| |||||| ||| ||
GC CGAA GGAAG TCTCCT AGG GC /
- ACA GTC T AAAT

GAM1586 CGTCATGTCTAAGTCAGAGT 1563 TGTCTAAGTC 4170 TG---- CA G -- -- GAAC
CTCCTAAAGAGCCCGAACAG AGAGTCTCCT CGTCA TCTAAGT GA TCTCCTA AAGAGC CC
A
CTGAGGAAGCTCTTCATGGG AAAG ||||| ||||||| || ||||||| |||||| ||
AGGGTTGAGCTTGGAAACAA GTAGT AGGTTCG TT GGAGGGT TTCTCG GG G
CTGATG CAACAA AG G AC AA AGTC

GAM1587 AGCCTGAGGAGCCATTTGGA 1564 TAATGAGAGA 4168 GA A AA- ----- ACG CGG
G
GCAATGGGGAACGCTCACGG TCCAAACACC AGCCT GGAGCC TTTGGAGC TGG GGA
CTCA ACT T
ACTGTGTGGTAATGAGAGAT AAGC ||||| |||||| |||||||| ||| ||| |||| |||

CCAAACACCAAGCGCTCCAG TTGGG TTTCGG GGACCTCG ACC CCT GAGT TGG
G
GGGCTTTGGGTT -- - CGA ACAAA AGA AA- T

GAM1588 AGTTGTGGACACAAAGAGAG 1565 CAGATTCTCA 4169 -- A AAA------ - C
CTGTCTCCAGAGACAGATTC AAGACCAGGT AGTT GTGG CAC GAGAG CTGTCT C
TCAAAGACCAGGTGCCCACT GCCC |||| |||| ||| ||||| ||||||
TAACT TCAA CACC GTG CTCTT GACAGA A
TT C GACCAGAAA A G

GAM1589 GAGGAGAAGTACTAAAACTT 1566 TAAAAGGAGC 4171 - A --- AA A A-- GTATC
CGA
TATAAAAATCTGCTGTATCT AGACTATTTT GAGGAGAA GT CT AA CTTT TAAAA TCTGCT
TTGGA G
TGGACGAGACTATCTAAAAG AAAA |||||||| || || || |||| ||||| |||||| |||||
GAGCAGACTATTTTAAAAAG TTCCTTTT CA GA TT GAAA ATTTT AGACGA AATCT
A
CGTTTGAAGAACATTTTCCT A A AGT GC A ATC GGAA- ATC
T

GAM1590 TTGTCGTCATTGGACACGTA 1567 TAAATGCGGT 4172 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM1591 TTCTCAGATGGGCGGGTGTC 1568 TGTGAAGGTG 4173 TG- -- TCT TGC AA G AA
TGTCTCTGCTCGAATTGACA ATGAGATTTC TTCTCAGA GGC GGGTG GTCTC TCG TT
ACAGAA G
GAAAAGGATTCTGTGAAGGT CATC |||||||| ||| ||||| ||||| ||| || ||||||
GATGAGATTTCCATCCATGC AAGAGTTT TCG CCTAC TAGAG AGT AA TGTCTT /
TGACTTTGAGAA CAG TA CTT T-- GG G AG

GAM1592 GGCCTCGGTGACTGCCTGGT 1569 CAAGGGCCTG 4174 C ACT GGTTAA TA AAT
TAAGATCTACAAATCTGATG TACCAAGGCT GGCCT GGTG GCCT GATC CA C
CGGATCAAGGGCCTGTACCA ||||| |||| |||| |||| ||
AGGCT TCGGA CCAT CGGG CTAG GT /
A GTC AA---- GC AGT

GAM1593 TGTTGCTATTTCCTAACCTG 1570 TTGGCTCCGG 4175 G TT TAA---- C G -- G
CAGGCAGAACCTGAAAGGGC GGCATCCTGG TGTT CTA TCC CCTG AG CAGAA CCT A
ATTTTGGCTCCGGGGCATCC ATTT |||| ||| ||| |||| || ||||| |||
TGGATTTAGAACA ACAA GAT AGG GGGC TC GTTTT GGG A
- TT TCCTACG C G AC A

GAM1594 CATTGTCGTCATTGGACACG 1571 CGTCATTGGA 4176 GTC-- T- A C ATTC C
TAGATTCGGGCAAGTCCACC CACGTAGATT CATT GTCA TGG CA GTAG GGG A
ACTACTGGCCATCTGATCTA CGGG |||| |||| ||| || |||| |||
TAAATG GTAA TAGT ACC GT CATC CCT A
ATATC CT G - ACCA G

GAM1595 GGTGACAACATGCTGGAGCC 1572 TTGGTTCAAG 4177 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC ||||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1596 CTTGTGGGAGAGATTATCAA 1573 TGGGAGAGAT 4180 T GA ATC -------- - G A AT
GCGTTTTGAGCAGAAAGGAT TATCAAGCGT CTTG GGGAGA TT AAGC GTTTT GA CAG
AAGG T
TCCGCCTTGTTGGTCTGAAA TTTG |||| |||||| || |||| ||||| || ||| ||||
TTCATGCAAGCTTCCGAAGA GAAC TCTTCT AA TTCG TAAAG CT GTT TTCC C
TCTTCTCAAG - AG GCC AACGTACT T G G GC

GAM1597 CACTACGTTGACCTGAAGGA 1574 AAGGACCGTC 4178 GA-- GAA- CCATTCT --
AAAT
CCGTCCATTCTTTGCCGGCC CATTCTTTGC CACTACGTT CCT GGACCGT
TTGCCGGCCT GGTG A
TGGTGAAATACATGCACTCA CGGC ||||||||| ||| ||||||| |||||||||| ||||
GGGCCGGTAGTTGCCATGGT GTGGTGTAA GGG TCTGGTA GATGGCCGGG
TCAC /
CTGGGAGGGGCTGAATGTGG GTCG AGGG CCGTT-- AC GTAC
TG

GAM1598 CGTTTCGGGTGCTGGCGGCT 1575 AAGGAACCAT 4179 TTC-- -- G C CA GA AAA
TAAG
GCAGCCGGAGTTCAAACCTA GGCCAACTGT CGT GGGT GCT GCGG TG GCCG GTTC CC
C
AGCAGCTGGAAGGAACCATG GAGC ||| |||| ||| |||| || |||| |||| ||
GCCAACTGTGAGCGTACCTT GCG TCCA CGA TGTC AC CGGT CAAG GG /
CATTGCG TTACT TG G A -- AC GAA TCGA

GAM1599 TTCTGCATACAAGTTGGCAG 1576 GATTCTGTGG 4181 ACAAG G A ATAC
GAACATTATACATGGCAGTG AGAGTGCAGA TTCTGCAT TT GCAGGA CATT A
ATTCTGTGGAGAGTGCAGAG G |||||||| || |||||| ||||
GAGACGTG AG TGTCTT GTGA /
AG--- G A CGGT

GAM1600 GACATGGAGGTCAGCGCCAC 1577 TCTGAAGACT 4182 GAG C A A T GAA T - ATA-
T GA

AGAACTCATGAACATTCTCA GATGGTTTGG GACATG GTCAG GCC CAGA C CAT CA TCT CA AGG TGT C
ATAAGGTTGTGACGCGACAC GCAT |||||| ||||| ||| |||| | ||| || ||| || ||| |||
CCTGATCTGAAGACTGATGG CTGTAC CAGTT CGG GTTT G GTA GT AGA GT TCC ACA G
TTTGGGCATTGACACATGTC A-- A - - - --- C A CTAG C GC

GAM1601 TACCGAACTTTTGTTCCCAT 1578 TTATAAGCTA 4183 TTGTT CCA- TT TT
ACCAGTTTGGTTTCGCTACC TGGGGAGTTT TACCGAACTT CCCATA GT GGT C
TTATAAGCTATGGGGAGTTT GGTA |||||||||| |||||| || |||
GGTA ATGGTTTGAG GGGTAT TA CCA G
----- CGAA TT TC

GAM1602 TGAGATGGAGTCTCGCTCTG 1579 TCTCGCTCTG 4184 AT- TC C TT C-- C-- C - ATGA
TTGCCCAGGCTGGACTGCAG TTGCCCAGGC TGAG GGAG TCGCT TG GCCCAGG TGGA TGCAG G GC T
CGGCATGATCTTGGCTCACT TGGA |||| |||| ||||| || ||||||| |||| ||||| | ||
GCAACCTCCGCCTCCTGGGT ACTC CTTC AGCGA AC TGGGTCC GCCT ACGTC C CG /
TCAAGCGATTCTTCTGCCTC CGT TT - T- TCC CCA A T GTTC
A

GAM1603 GGCCAATTGAAACAAACAGT 1580 TATTAGGGAT 4185 C T ACAAACAG G GTT T A GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1604 CATCCGCAGGGTTCGGATGA 1581 TGTTCAGTAT 4186 CGCA- C - A- C TG
GACCAGGTGTTGCTTGTTCA CTCAAGCCCA CATC GGGTT G GATG GA CAGG T
GTATCTCAAGCCCAGAAAGA GAAA |||| ||||| | |||| || ||||
TG GTAG CCCGA C CTAT CT GTTC /
AAAGA A T GA T GT

GAM1605 GTGGACTGGTGGGGGCTGGG 1582 TGATGTGCGG 4187 CT TG - G G ATG
CGTGGTCATGTACGAGATGA TCGCCTGCCC GTGGA GG GG GGCTG GCGT GTC T
TGTGCGGTCGCCTGCCCTTC TTCT ||||| || || ||||| |||| |||
TAC CATCT CC CC CTGGC TGTA TAG A
TC GT G G G AGC

GAM1606 GGCCCAGGGATCGGCAGGGC 1583 TTCCCATGCC 4188 G - G- - GCT GA A
TGCTGGCAGAGGAATCCCAG CCAGGCTCCT GGCCCAG GA TC GCAGG GCT GGCA GGAATCCC G

CTGGGGTTCCCATGCCCCAG GCAG ||||||| || || ||||| ||| |||| ||||||||
GCTCCTGCAGGACTTGCTGG CCGGGTC TT AG CGTCC CGG CCGT CCTTGGGG C
GCC G C GA T ACC AC T

GAM1607 GTAGAGCTTTATGCTGAAAA 1584 GAGCTTTATG 4190 - TA GAAAA - T A
GGTGGCCACTAGAGGTCTGT CTGAAAAGGT GTAGAG CTT TGCT GGTGGC CAC AG G
GTGCCATTGCCCAGGCAGAG GGCC |||||| ||| |||| |||||| ||| ||
TCTCTGC CGTCTC GAG ACGG TTACCG GTG TC G
T -- ACCCG T - T

GAM1608 CGAGGTTGTGGTGTCTGGGA 1585 GACCCTGTTA 4189 G T GTCT- AAA A--- - GAG
AA GA
AACTCCGAGGACAGAGGGCT ACTACTACGT CGA GT GTGGT GGG CTCCG GGA CA
GGCT ATCCAT A
AAATCCATGAAGTTGTGGAT TG ||| || ||||| ||| ||||| ||| || |||| ||||||
GGCTGATGATCCACAGCGGA GTT CA CATCA CCC GAGGC CCT GT TCGG
TAGGTG G
GACCCTGTTAACTACTACGT G T ATTGT A-- GACA A AG- -- TT
TG

GAM1609 GACACATCGCTGACTTGGCT 1586 CATCGCTGAC 4191 CAT-- ACTT ACTC A
GGCAACTCTGAAGTCATCCT TTGGCTGGCA GACA CGCTG GGCTGGCA TG A
GCCAGTCCCGGCGTTCAATG ACTC |||| ||||| |||||||| ||
TC CTGT GCGGC CTGACCGT AC G
AACTT C--- CCT- T

GAM1610 CTGTGAGGCTGTGGCCATCT 1587 TTAGCAACAT 4192 T G CTACG ATCATC A
ACGGCATCATCATGGCAATT GGCTGAGCCT CTG GAGGCT TGGCCAT GC ATGGC A
GTCATTAGCAACATGGCTGA TTCA ||| |||||| ||||||| || |||||
GCCTTTCAG GAC TTCCGA GTCGGTA CG TACTG T
T - CAA-- AT---- T

GAM1611 GGCCAATTGAAACAAACAGT 1588 TATTAGGGAT 4193 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1612 GCCAGTGGCCGTGCAACCCA 1589 AGAGAAAAGC 4194 -- - AACCCA AAAG-- ATA
ACG
GAGAAAAGCCTGATAGGTCA CTGATAGGTC GCCA GTGGCCG TGC GAGA CCTG GGTC
T
CGTGCCCGACCAGCGGGAGA ACGT |||| ||||||| ||| |||| |||| ||||
TCATCTCCTTCGGCAGCGGC CGGT TATCGGC ACG CTCT GGGC CCAG G

TATGGTGGC GG G GCTTC- ACTAGA GA- CCC

GAM1613 GTATGTGCTTCCATTCAGCA 1590 TGACTCAGCC 4195 -- T TCA- A CT --- C TC
TGGGTCCTGTGGGCTCCCCG TATGTGGTGG GTATGT GCT CCAT GC TGGGTC GTGGGCT
CCCCG TG C
CTGTCCCGCATCGGGGTGCA CAAG |||||| ||| |||| || |||||| ||||||| ||||| ||
GCTCACTGACTCAGCCTATG CGTACG CGG GGTG CG ACTCAG CACTCGA GGGGC
AC /
TGGTGGCAAGCATGC AA T TATC - T- CGT T GC

GAM1614 TCGCGCGGGGGGTAATTCGG 1591 TCCCCGATGG 4196 G AAT TCT TCTG C
GGTCTGGGTTCTGGTGCCGC CCCACTGCGT TCGCGCGG GGGT TCGGGG GGGT GTGC G
GCATGCTTTCCCCGATGGCC GA |||||||| |||| |||||| |||| ||||
CACTGCGTGA AGTGCGTC CCCG AGCCCC TTCG TACG /
A GT- T-- ---- C

GAM1615 AGGAGGACGCGCTGCCCGGC 1592 GAGAGTACTC 4197 ------ G- G CAGAAAA AA
CAGAAAACGGAGTTCAAGGT CTGCGTCTTC AGGAGGACGC GCT CCC GC CGGAGTTC
G
GGACTCCGACGACCAGTGGG CT |||||||||| ||| ||| || |||||||
GAGAGTACTCCTGCGTCTTC TCCTTCTGCG TGA GGG TG GCCTCAGG /
CT TCCTCA GA G ACCAGCA TG

GAM1616 TGGTGAAATGTGACCTCGCC 1593 TACCGTGGTG 4199 T GTG C AAT T TT
ATGGTAAATACATGGCTTGC ACGTGGTTTC TGG GAAAT AC TCGCCATGGTA ACA GGC G
TGCCTGTTGTACCGTGGTGA CCA ||| ||||| || |||||||||| ||| |||
CGTGGTTTCCCA ACC CTTTG TG AGTGGTGCCAT TGT CCG /
- G-- C GT- - TC

GAM1617 CTGGCCACATATGCCCCTGT 1594 TAGCAGAGAT 4198 - CATAT- CCCT C - CTACC
CATCTCTGCTGAGAAAGCCT TACCAATGCT CTGGC CA GC GT ATCTCTGCTG AGAAAGC
A
ACCATGAACAGCTTTCTGTA TGCT ||||| || || || |||||||||| |||||||
GCAGAGATTACCAATGCTTG GACCG GT CG CA TAGAGACGAT TCTTTCG T
CTTTGAGCCAG A TTCGTT TAAC T G ACAAG

GAM1618 GTAGAGCTTTATGCTGAAAA 1595 GAGCTTTATG 4201 - TA GAAAA - T A
GGTGGCCACTAGAGGTCTGT CTGAAAAGGT GTAGAG CTT TGCT GGTGGC CAC AG G
GTGCCATTGCCCAGGCAGAG GGCC |||||| ||| |||| |||||| ||| ||
TCTCTGC CGTCTC GAG ACGG TTACCG GTG TC G
T -- ACCCG T - T

GAM1619 CTCCGAGGACAGAGGGCTAA 1596 TGGCCTGATG 4200 A--- - GA AA TG A

ATCCATGAAGTTTGTGGATG ATCCACAGCG CTCCG GGA CA GGGCT ATCCA A G
GCCTGATGATCCACAGCGGA GAG ||||| ||| || ||||| ||||| |
G GAGGC CCT GT TCCGG TAGGT T /
GACA A AG -- GT T

GAM1620 GGACCTCAGGTGGCTGAAGG 1597 TGAAGGAGAC 4203 CTC GC-- GA T TT G
AGACGAATGTATTTGGTGTC GAATGTATTT GGAC AGGTG TGAAGGA CGAA GTA TGGT T
TGCCATATCTTTGCATCCTT GGTG |||| ||||| ||||||| |||| ||| ||||
CAATGACACTTTTGTCC CCTG TTCAC ACTTCCT GTTT TAT ACCG C
TT- AGTA AC C -- T

GAM1621 CCATCTGCCGTGTGACTGGT 1598 ATGAATCCTC 4202 TCT-- C AC - GAA--- AAA
GGGATGAACGGTAAAGGCAG ACCATATGCT CCA GC GTGTG TGGTG GGAT CGGT G
ACCGAGATGAATCCTCACCA GCTA ||| || ||||| ||||| |||| ||||
TATGCTGCTATGTTGG GGT CG CGTAT ACCAC CCTA GCCA G
TGTAT T -- T AGTAGA GAC

GAM1622 TGAGACGGAGTCTCGCTTTG 1599 TTCAAGTGAT 4204 A - TC T TC T--- T -- - A
A
TCACCCTGGCTGGAGTGCAG TCTCCCGCCT TGAG CGG AG TCGCTT G ACCC GGC GGAG
TGCAGTG GC TG T
TGGCATGATCTCAGCTCACT CA |||| ||| || |||||| | |||| ||| |||| ||||||| || ||
GCAACCTCTGCCTCCCGGGT ACTC GCC TC AGTGAA C TGGG CCG TCTC ACGTCAC
CG AC C
TCAAGTGATTCTCCCGCCTC C C TT - T- CCCT - CA T - T
A

GAM1623 GGCCAATTGAAACAAACAGT 1600 TATTAGGGAT 4205 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1624 TAAGTCAACACCGTTCTTCA 1601 GTCAACACCG 4206 CA GTTCTTCATGT - -- AG
TGTAGTACTTCTCCAGCTTG TTCTTCATGT TAAGT ACACC AGTAC TTCT CC C
GCCAGAATGTGCTTGCCATA AGTA ||||| ||||| ||||| |||| ||
GGTGTACTTA ATTCA TGTGG TCGTG AAGA GG /
-- ATACCGT---- T CC TT

GAM1625 GGTGACAACATGCTGGAGCC 1602 TTGGTTCACC 4207 AA--- -- T TA
AAGTGCTAACATGCCTTGGT GGCATGGACA GGTGAC CATGCTGG AGCCAAG GC A
TCACCGGCATGGACAAGTCA AGTC |||||| |||||||| ||||||| ||
CC CCACTG GTACGGCC TTGGTTC CG C
AACAG AC - TA

GAM1626 GTGTTCCATGGTCAAAAAAT 1603 TGTCAAGACT 4208 TT - CAAAAAA GA AT AA
GGCAGACAATGATTGAAGCT ACCGATGGTT GTG CCAT GGT TGGCA CAATG TG G
CACGTTGATGTCAAGACTAC AC ||| |||| ||| ||||| ||||| ||
CGATGGTTAC CAT GGTA CCA ACTGT GTTGC AC /
T- G TCAGA-- A- -- TC

GAM1627 TGCATTTAGAAAATTCAAGC 1604 TGGCATGGAT 4209 - TTAG A A GATTACT A T GTAA
TGATTACTGAAGATGTTCAG CTTACCCGTG TG CAT AA ATTCA GCT GAAG TG TCAGG A
GGTAAAAACTGCCTGACTAA ACA || ||| || ||||| ||| |||| || |||||
CTTCCATGGCATGGATCTTA AC GTG TT TAGGT CGG CTTC AT AGTCC A
CCCGTGACA A CCCA C A TAC---- A C GTCA

GAM1628 GAGTCTCGCTCTGTTGCCCA 1605 TCTCGCTCTG 4210 TC C TT C-- -- - A A
GGCTGGAGTGCAGTGGCATG TTGCCCAGGC GAG TCGCT TG GCCCAGG TGGAG TGCAGTG GC TG T
ATCTCGGCTCACTGCAACCT TGGA ||| ||||| || ||||||| ||||| ||||||| || ||
CTGCCTCCTGGGTTCAAGCG CTC AGCGA AC TGGGTCC GTCTC ACGTCAC CG GC C
ATTCTC TT - T- TCC CA T - T

GAM1629 GAAACAGACTGGGCCAATGT 1606 TATCAAGGAA 4211 C -- CACAAAGAA - CA- ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| ||||| /
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM1630 GCCAAAATGTCTGTCAATGT 1607 TGCCCCGTCT 4212 AAAA GTCAATG GCA T CAGTTC GCT
CAACCGCAGCGTGTCAGACC GATTGCCAAG GCC TGTCT TCAACC GCG GTCAGAC TATC A
AGTTCTATCGCTACAAGATG GTTG ||| ||||| |||||| ||| ||||||| |||| /
CCCCGTCTGATTGCCAAGGT CGG ACGGG AGTTGG CGT TAGTCTG GTAG
TGAGGGCAAAGGC AA-- ------- AAC - CCCC-- AAC

GAM1631 GGTTGAGGGCAAAGGCAATG 1608 AGGCAATGGA 4213 G AAAG G- A--- AGT
GAATCAAGACAGTTATAGTC ATCAAGACAG GGTTGAG GC GCAATG AATCA GAC T
AACATGGTTGACGTTGCAAA TTAT ||||||| || |||||| ||||| |||
GGCGCTTAATC CTAATTC CG CGTTGC TTGGT CTG /
G GAAA AG ACAA ATA

GAM1632 CATGTCTGTAAAACTTGACG 1609 TGTAAAACTT 4214 T AAA - AT---- GC- T AT
TATTTTGTGTATGCATGTTT GACGTATTTT CATGTC GT ACTTG ACGT TTTGTGTAT
ATGTTT C T
TCATTTTGCAAATATTTAAT GTGT |||||| || ||||| |||| ||||||||| |||||| |
ATATAGACCTATGATGTACA GTACAG CA TGGAC TGTA AGATATATA TATAAA G /
GGTACGACATG - --- A GTATCC ATT C TT

GAM1633 TCTGCAAGGTGGTGGAAGTG 1610 GTGGAAGTGG 4215 AAGG-- T- AG AG A
GGCAGCAAGATCTACGTGGA GCAGCAAGAT TCTGC TGG GGAAGTGGGC CA ATCT C
TGATGGGCTTATTTCTCTCC CTAC ||||| ||| |||||||||| || ||||
AGGTGAAGCAGA AGACG ACC TCTTTATTCG GT TAGG G
AAGTGG TC G- AG T

GAM1634 AGATTACTCTGTTTTATAAG 1611 TTCCTCACTT 4216 T T TATAA TT- TCTT CT
TAATA
CCTTTTTGATCTTGAACTTC AAGGCAGGCA AGA TAC CTGTTT GCCTT TGA GAA TCG
G
GTAATAGCACTTTGATTTCC GTGT ||| ||| |||||| ||||| ||| ||| |||
TCACTTAAGGCAGGCAGTGT TCT ATG GACGGA CGGAA ACT CTT AGT /
ACTCT C T ----- TTC C--- T- TTCAC

GAM1635 GCTGATGATATGATAAAGCT 1612 TCCCCATAGG 4217 - - T TAAAGCT A GAA CC T
GC
CAGCATAGAAGGCCCTCAGG CTGCCTCATC GC TGA TGA ATGA CAGC TA GG CTCAGG
CCA A
TCCAGCACCATGGCCCTGAG TCGC || ||| ||| |||| |||| || || |||||| |||
CTCCCCATAGGCTGCCTCAT CG ACT GCT TACT GTCG AT CC GAGTCC GGT C
CTCGCTCATGC T C C CC----- G ACC TC C AC

GAM1636 GGGAAACTCCGAGGACAGAG 1613 TGGCCTGATG 4218 AAA A--- - GA AA TG A
GGCTAAATCCATGAAGTTTG ATCCACAGCG GGG CTCCG GGA CA GGGCT ATCCA A G
TGGATGGCCTGATGATCCAC GAGA ||| ||||| ||| || ||||| ||||| |
AGCGGAGACCC CCC GAGGC CCT GT TCCGG TAGGT T /
A-- GACA A AG -- GT T

GAM1637 GTAGAGCTTTATGCTGAAAA 1614 GAGCTTTATG 4219 - TA GAAAA - T A
GGTGGCCACTAGAGGTCTGT CTGAAAAGGT GTAGAG CTT TGCT GGTGGC CAC AG G
GTGCCATTGCCCAGGCAGAG GGCC |||||| ||| |||| |||||| ||| ||
TCTCTGC CGTCTC GAG ACGG TTACCG GTG TC G
T -- ACCCG T - T

GAM1638 CCTTTCGCCAGCTGGCGTAA 1615 TGGCGTAATA 4220 T ----- G AGC--- A CCGCA
TAGCGAAGAGGCCCGCACCG GCGAAGAGGC CC TTCGCCA GCTG CGTAAT GAAG GGC
C

ATCGCCCTTCCCAACAGTTG CCGC || ||||||| |||| |||||| |||| |||
CGCAGCCTGAATGGCGAATG GG AAGCGGT CGAC GCGTTG CTTC CCG /
G T AAGTC - ACAACC - CTAGC

GAM1639 GGCCAATTGAAACAAACAGT 1616 TATTAGGGAT 4221 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1640 TTTGGGTGGCATAGAGGTTT 1617 AGAGGTTTTG 4222 TA TTT TG GC- G
TGTATTGAGGGCCAGTGATG TATTGAGGGC TTTGGGTGGCA GAGGT GTAT AGG CA T
ATGTTTTGATATTTATTTCC CAGT |||||||||| ||||| |||| ||| ||
TGCTACTTAAA AAATTCATCGT CTTTA TATA TTT GT G
C- TT- GT GTA A

GAM1641 GCCATGTGCTCCCTGACCTG 1618 AGCCTGGATG 4223 T CC - TGA- AG ATG
AAGGAGGAGGATGGCAGCCT GTGCAGACAG GCCA GTGCT CTG ACC AGG GAGG G
CAGCCTGGATGGTGCAGACA CACT |||| ||||| ||| ||| ||| ||||
GCACTGGC CGGT CACGA GAC TGG TCC CTCC /
- CA G TAGG GA GAC

GAM1642 GGGATCATTGATTGTGTGGT 1619 TCATTGATTG 4224 TC-- T TG - G A-- ---- C G
GAGAATCCCTAAGGAGCAGG TGTGGTGAGA GGGA AT GAT TGT GGT AG ATCCCT
AAGGAG AGG C
GCTTCCTCTCCTTCTGGAGG ATCC |||| || ||| ||| ||| || |||||| |||||| |||
GGTAACCTGGCCAACGTGAT CCCT TG CTA GCA CCG TC TGGGGA TTCCTC TCC T
CCGTTACTTCCC TCAT C GT A G CAA GGTC - T

GAM1643 TCCGCATGTCCCTTCGCGGG 1620 CATGTCCCTT 4225 CA T CGCG A GTG TG-
GCAA
AAGGCTGTGGTGCTGATGGG CGCGGGAAGG TCCG TG CCCTT GGA GGCT GTGC ATGG
G
CAAGAACACCATGATGCGCA CTGT |||| || ||||| ||| |||| |||| ||||
AGGCCATCCGAGGGCACCTG AGGT AC GGGAG CCT CCGG CGCG TACC /
GA CC - ---- A AA- TAG ACAA

GAM1644 TGATGCGCAAGGCCATCCGA 1621 TCTGGAGAAA 4226 T - A GCCA G ACC AAA
GGGCACCTGGAAAACAACCC CTGCTGCCTC TGA GC GCA G TCC AGGGC TGG A
AGCTCTGGAGAAACTGCTGC A ||| || ||| | ||| ||||| |||
CTCA ACT CG CGT C AGG TCTCG ACC C
C T - AAAG - --- CAA

GAM1645 GAGGCAGGAGAATGGTGTTA 1622 CCACTGCACT 4227 A AA - TAA- AGGC CT A
- A
ACCCAGGAGGCGGAGCTTGC CCAGCCTGGG GAGGC GGAG TGG TGT CCCAGG GGAG
TGCAGTG GC CG G
AGTGAGCCGAGATCGCGCCA AGAC ||||| |||| ||| ||| |||||| |||| ||||||| || ||
CTGCACTCCAGCCTGGGAGA CTCTG CCTC ACC ACA GGGTCC CCTC ACGTCAC
CG GC A
CACAGCCAGACTCCGTCTC - AG G CAGA GA-- -- - C T

GAM1646 GGTTCTTCATCTTGTGTTTG 1623 GGTCCAGGAA 4228 T - TG AAGA AA- A- - A
CTGC
AAGACAAGAAGCTGGATCCG GCCAGCCAGC GGTTCT CATC T TGTTTG CAAG GCTGG
TCC GGA CTC T
GAACTCCTGCTCTGTGAGGT TTGG |||||| |||| | |||||| |||| ||||| ||| ||| |||
CCAGGAAGCCAGCCAGCTTG TCGAGA GTGG G ACGGAC GTTC CGACC AGG CCT
GAG /
GCCACAGGCATGGTGGTGTA T T GT ACCG GAC GA A G TGTC
GAGCT

GAM1647 GCCAGTATGAGAGCCTGGAA 1624 TGAGAGCCTG 4229 TAT - - ---- CA AC
CACATGACCCTCACCTGTTC GAACACATGA GCCAG GAG AG CCT GGAACA TG C
CTCCAAGGTCTGCTCTTTTG CCCT ||||| ||| || ||| |||||| ||
GC CGGTT CTC TC GGA CCTTGT AC /
TT- G T ACCT CC TC

GAM1648 TCTTGTGTTGAGACTTCGTG 1625 TACACCACTC 4230 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM1649 GGCCAATTGAAACAAACAGT 1626 TATTAGGGAT 4231 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1650 TGATGCGCAAGGCCATCCGA 1627 TCTGGAGAAA 4234 T - A GCCA G ACC AAA
GGGCACCTGGAAAACAACCC CTGCTGCCTC TGA GC GCA G TCC AGGGC TGG A
AGCTCTGGAGAAACTGCTGC A ||| || ||| | ||| ||||| |||
CTCA ACT CG CGT C AGG TCTCG ACC C
C T - AAAG - --- CAA

GAM1651 CGAGTCCTGGCCTTGTCTGT 1628 GAACAGGTCA 4232 TCCT - GG AC--- TTA
GGAGACGGATTACACCTTCC AGGCCTTCTT CGAG GGCCTTG TCTGT AG GGA C
ACTTGCTGAACAGGTCAAGG G |||| ||||||| ||||| || |||
CCTTCTTG GTTC CCGGAAC GGACA TC CCT A
TT-- T AG GTTCA TCC

GAM1652 TCCGCATGTCCCTTCGCGGG 1629 CATGTCCCTT 4233 CA T CGCG A GTG TG-
GCAA
AAGGCTGTGGTGCTGATGGG CGCGGGAAGG TCCG TG CCCTT GGA GGCT GTGC ATGG
G
CAAGAACACCATGATGCGCA CTGT |||| || ||||| ||| |||| |||| ||||
AGGCCATCCGAGGGCACCTG AGGT AC GGGAG CCT CCGG CGCG TACC /
GA CC - ---- A AA- TAG ACAA

GAM1653 GACCAAACACTGTGACAAAG 1630 TGAAAATGTT 4235 - G AAG- TTC
CAGAGTTCTTCAGTTCTGAA AAAGTGTTTG GAC CAAACACT TGACA CAGAG T
AATGTTAAAGTGTTTGAGTC AGTC ||| |||||||| ||||| |||||
CTG GTTTGTGA ATTGT GTCTT T
A A AAAA GAC

GAM1654 GCACTCTGTTCTTCCGCCGC 1631 ACTCTGTTCT 4236 AC G CC TCC TC TT
TCCGCCGTCGCGTTTCTCTG TCCGCCGCTC GC TCT TTCTTCCG GC GCCG GCG T
CCGGTCGCAATGGAAGAAGA CGCC || ||| |||||||| || |||| |||
GATCGC CG AGA AAGAAGGT CG TGGC CGT C
CT G AA C-- -- CT

GAM1655 GATGGTGTTAAGCTGTACAC 1632 TGAGGAGTAA 4237 G TG TAAGC ----- CA TT
CCCAGGACAGTTTATCCTGT GTGTACAATG GAT G T TGTACAC CC GGACAG T
CTGAGGAGTAAGTGTACAAT TGAT ||| | | ||||||| || ||||||
GTGATC CTA T A ACATGTG GG TCTGTC A
G GT ----- AATGA AG CT

GAM1656 TTAAGACAAAGCAATTTTAA 1633 CCTTGCTGCA 4238 C A TAATACT T CAC
TACTAGGTGCACACCACATG AACTGCTTTT TTAAGA AAAGCA TTT AGG GCA C
CCCTTGCTGCAAACTGCTTT CTTG |||||| |||||| ||| ||| |||
TCTTGA AGTTCT TTTCGT AAA TCC CGT /
- C CGTCGT- - ACA

GAM1657 GGCCAATTGAAACAAACAGT 1634 TATTAGGGAT 4239 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1658 GAAACAGACTGGGCCAATGT 1635 TATCAAGGAA 4240 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM1659 CAGCGCCAGGTGGCCCAGCT 1636 TGTCGAAGTT 4241 AG--- G TT C C TTC --
TC
TGGCCACCACCTGGTTGTTC GGCCGCGTCG CAGCGCC GT GCCCAGC GGCCAC AC
TGGTTG TCGA GC G
TCGAGCTCGTTGTTGTCGAA TGGC ||||||| || ||||||| |||||| || |||||| |||| ||
GTTGGCCGCGTCGTGGCTGC GTCGCGG CG CGGGTCG TCGGTG TG GCCGGT
AGCT TG /
TGGGCGGCAGGCAGGCGCTG ACGGA G -- C C TGA GT TT

GAM1660 GGATTGTTGAACTGTTACCA 1637 GGAGTTGGAA 4242 A- ---- C A A AT TTCAGC
GCACCATGCTTTCAGCAACA ACATTTTTTA GG TTGTTG AA TGTT CCAGC CC GCT A
TTTCAGCGGAGTTGGAAACA CAGC || |||||| || |||| ||||| || |||
TTTTTTACAGCAAAACC CC AACGAC TT ACAA GGTTG GG CGA A
AA ATTT T A A -- CTTTAC

GAM1661 GGAGAAGGGGGAGATGTTGA 1638 TCGCTGGCTC 4243 -- - AT- T - C
GCATGTTCAGCAACGTGGCT CCACTTTGTC GGAGA AGG GGGAG GT GAGC ATGTT A
TCGCTGGCTCCCACTTTGTC TCC ||||| ||| ||||| || |||| |||||
TCC CCTCT TTC CCCTC CG TTCG TGCAA G
GT A GGT C G C

GAM1662 TCGTTCTGCAGATTGACAAT 1639 TGAGACAGAG 4245 -- ACA- ------ C GA T
GCCCGTCTTGCTGCTGATGA CTGGGCATGC TCGTTCT GCAGATTG ATGCCC GTCTTG
TGCT TGACT T
CTTTAGAGTCAAGTATGAGA GCCA ||||||| |||||||| |||||| |||||| |||| |||||
CAGAGCTGGGCATGCGCCAG AGCAAGA TGTCTGAC TACGGG CAGAGT ATGA
ACTGA A
TCTGTGGAGAACGA GG CGCG TCGAGA - -- G

GAM1663 GCGAAGAAGGGACCCCAGGT 1640 AGGGACCCCA 4244 A-- A - A-- - - - CC
CAGAGACTGGAGCCATTACT GGTCAGAGAC GCGAAGA GGG CCC CAGGTC GA GA CT
GGAG A
TCAAGATCATCGAGGACCTG TGGA ||||||| ||| ||| |||||| || || || ||||
AGGGCTCAGATCTTCGC CGCTTCT CTC GGG GTCCAG CT CT GA CTTC T

AGA - A GAG A A A AT

GAM1664 TGAGGCAGGAGAATTGCTTG 1641 CAGAGCAAGA 4246 A AA GAA-- AGG GTTT AGCCGA
AACCCGGGAGGTGGAGGTTT CTCCGTCTCA TGAGGC GGAG TTGCTT CCCGGG TGGAG CAGTG G
CAGTGAGCCGAGATCACACC |||||| |||| |||||| |||||| ||||| |||||
ACTGCACTCCAGCCTGGGCA ACTCTG CCTC AACGAG GGGTCC ACCTC GTCAC A
ACAGAGCAAGACTCCGTCTC - AG ACAAC G-- AC-- CACACT
A

GAM1665 CGCTCGTCACCAGGACCCAA 1642 TCAAGGGTCG 4247 - T- C G AA GA AAATTG
GGAACCAAAATTGCATCTGA TGTGTTTGAA CGCT CG CAC A GACCC G ACCA C
TGGTCTCAAGGGTCGTGTGT GTG |||| || ||| | ||||| | ||||
TTGAAGTG GTGA GT GTG T CTGGG C TGGT /
A TT - G AA TC AGTCTA

GAM1666 GCTGGTAAACATGACCTGGG 1643 TATGTACCCC 4248 T CCT - T AG TA
ACATTGTAAGAATATATTTA CATTATGTTT GCTGG AAACATGA GGG ACAT GTA AA T
ATATATGTACCCCCATTATG TCCG ||||| |||||||| ||| |||| ||| ||
TTTTCCGGT TGGCC TTTGTATT CCC TGTA TAT TT /
T ACC A - AA TA

GAM1667 GGCCAATTGAAACAAACAGT 1644 TATTAGGGAT 4249 C T ACAAACAG G GTT T A GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1668 GGAGTTGCCAGCGTCCCTGG 1645 TGCCAGCGTC 4250 TT GCG - AA- CCTGCA
TGAATGGCCTGCAGCCTCTC CCTGGTGAAT GGAG GCCA TC CCTGGTG TGG G
CCAGCACACCAGGAGAATGG GGCC |||| |||| || ||||||| |||
CTTCTCC CCTC CGGT AG GGACCAC ACC /
TT A-- A ACG CTCTCC

GAM1669 TCTTGTGTTGAGACTTCGTG 1646 TACACCACTC 4251 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM1670 CCCCCATCTCTGTGACTTTC 1647 TCTGTGACTT 4252 C C CTTTCCTG AC AG

CTGGAGACTCACTTCCTAGA TCCTGGAGAC CC CCATCT TGTGA GAG TCACTTCCT A
TGAGGAAGTGAAGCTTATCA TCAC || |||||| ||||| ||| |||||||||
CGAAGATGGTGG GG GGTAGA GCACT TTC AGTGAAGGA /
T A A------- GA GT

GAM1671 GTGGGGTAAAACCCCAGACG 1648 ACGCCATGAA 4253 G A AC C A CTG TGT-
AGAAAA
CCATGAAAGCTGCCATGTGC AGCTGCCATG GTG GGTA AACCCCAG GC ATGAA G CCA
GCCTGG A
CTGGAGAAAAAGCTGAACCA TGCC ||| |||| |||||||| || ||||| | ||| ||||||
GGCCCTTTGGATCTTCATGC CAC CCGT TTGGGGTC CG TACTT C GGT CGGACC /
CCTGGGGTTCTGCCGCAC G C C- - - TA- TTCC AAGTCG

GAM1672 GGCCAATTGAAACAAACAGT 1649 TATTAGGGAT 4254 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1673 GGAGTGGTGATGCACACATT 1650 TGTCACACTG 4255 - T ACA TT- G A CA
TGGGGGTTATGCCAACAGCA GAGGCTTCAT GGAGTGG TGA GC CA TGG GGTT TGC A
AAGCTGTCACACTGGAGGCT TTAC ||||||| ||| || || ||| |||| |||
TCATTTACTCC CCTCATT ACT CG GT ACT TCGA ACG /
T T GAG CAC G A AC

GAM1674 ATGGCCGAGGAGAAGCGCGA 1651 TGCAAAACCA 4256 G -- A AGG A------- CC
GGGCTACGAGCGTCTCCTGA GCGTGGCGGC ATG CC GAGGAGA GCGCG GCTACG
GCGTCT T
AGATGCAAAACCAGCGTGGC CGCG ||| || ||||||| ||||| |||||| ||||||
GGCCGCGCTCTCTTCCAGGA TAC GG CTTCTCT CGCGC CGGTGC CGTAGA /
CAT A AC - CGG GACCAAAA AG

GAM1675 CCCAGAGCCATGAAAGCTGC 1652 AGGCCTTTGT 4257 A C AG- TG T- AGAAAA
ATGGCCTGGAGAAAAAGCTG GGATCTTCAT CCCAG GC ATGAA C CA GGCCTGG A
AACCAGGCCTTTGTGGATCT GCCC ||||| || ||||| | || |||||||
TCATGCCCTGGG GGGTC CG TACTT G GT CCGGACC /
C - CTA GT TT AAGTCG

GAM1676 TCCATCGGGCAGCCAGAGGC 1653 ACTGAGCACC 4258 G A---- AG C C TC
CCAGCGTCTCCGATGACACT TGGTGAATGG TCCATC GGC GCCAG GC CAG GTC C
GAGCACCTGGTGAATGGCCG CCGG |||||| ||| ||||| || ||| |||
GATGGA AGGTAG CCG TGGTC CG GTC CAG G
G GTAAG CA A A TA

GAM1677 GACATAGCACCTGAGCAGGC 1654 TGACCGGCAC 4259 A ACCTGA A - - AGTC
ACCTCAGTCCGTGTAGAGTG CAAGGCATGT GACAT GC GC GG CAC CTC C
TGACCGGCACCAAGGCATGT C ||||| || || || ||| |||
C CTGTA CG CG CC GTG GAG G
- GAACCA G A T ATGT

GAM1678 GTAGAGCTTTATGCTGAAAA 1655 GAGCTTTATG 4261 - TA GAAAA - T A
GGTGGCCACTAGAGGTCTGT CTGAAAAGGT GTAGAG CTT TGCT GGTGGC CAC AG G
GTGCCATTGCCCAGGCAGAG GGCC |||||| ||| |||| |||||| ||| ||
TCTCTGC CGTCTC GAG ACGG TTACCG GTG TC G
T -- ACCCG T - T

GAM1679 GGGAAACTCCGAGGACAGAG 1656 TGGCCTGATG 4260 AAA A--- - GA AA TG A
GGCTAAATCCATGAAGTTTG ATCCACAGCG GGG CTCCG GGA CA GGGCT ATCCA A G
TGGATGGCCTGATGATCCAC GAGA ||| ||||| ||| || ||||| ||||| |
AGCGGAGACCC CCC GAGGC CCT GT TCCGG TAGGT T /
A-- GACA A AG -- GT T

GAM1680 GCCCTACAGCTCCCAGGATG 1657 CAGCTCCCAG 4262 - A --- GA GGGAA TA
TGTTCGGGAACCTACAGCGG GATGTGTTCG GCC CTAC GCT CCCAG TGTGTTC CC C
GAACACGGACTGGGCAAGGC GGAA ||| |||| ||| ||||| ||||||| ||
GGTGGTGGT TGG GGTG CGG GGGTC GCACAAG GG A
T G AAC AG ----- CG

GAM1681 AGAGGCGGGCGGATCACGAG 1658 AACACGGTGA 4263 CGGA GA---- GATCG
GTCAGGAGATCGAGACCATC AACCCCGTCT AGAGGCGGG TCAC GGTCAGGA A
CTGGCTAACACGGTGAAACC CT ||||||||| |||| ||||||||
CCGTCTCT TCTCTGCCC AGTG TCGGTCCT /
CAA- GCACAA ACCAG

GAM1682 AGGACGCGGCCGCAAGCTTA 1659 CTTGGCACTG 4264 - ---- TATT---- T
TTCCCTTTAGTGAGGGTTAA GCCGTCGTTT AGGACG CGGCCG CAAGCT CCCTT A
TTTTAGCTTGGCACTGGCCG T |||||| |||||| |||||| |||||
TCGTTTT TTTTGC GCCGGT GTTCGA GGGAG G
T CACG TTTTAATT T

GAM1683 AACTGGTGATTGTTGGTGAT 1660 CTTGCTCATA 4265 GA T G-- CT GAA
GGAGCCTGTGGAAAGACATG GTCTTCAGCA AACTGGT TTGTTGG GAT GAGC GTG A
CTTGCTCATAGTCTTCAGCA AGGA ||||||| ||||||| ||| |||| |||
AGGACCAGTT TTGACCA AACGACT CTG CTCG CGT G
GG T ATA TT ACA

GAM1684 GGGCGAGATGGGCGGATCAC 1661 TAACATGGTG 4266 GC CGGA AA---- GA A
AAGGTCAGGAGATGGAGACC AAACCCCGTC GG GAGATGGG TCAC GGTCAGGA TGG G
ATCCTGGCTAACATGGTGAA TCTA || |||||||| |||| |||||||| |||
ACCCCGTCTCTACT TC CTCTGCCC AGTG TCGGTCCT ACC /
AT CAA- GTACAA -- A

GAM1685 GGCTATGGGAGGTGCTATGG 1662 TATGGGAGGT 4267 T GGT TAT AA- AAC
GCATAAACAACAGAGGTGCC GCTATGGGCA GGC ATGGGA GC GGGCAT AC A
ATGCCCCCTGCTCCTGTGCC TAAA ||| |||||| || |||||| ||
CCG TGTCCT CG CCCGTA TG /
- --- TCC CCG GAG

GAM1686 CTTCTCCTCAGCTGGAGCAG 1663 TGCAGCACCA 4268 T T- A A G - GGG
CAGCAGTGGAGGGGGCAGGA GCTGCTGGAG CT CTCC CAGCTGG GC GCA CAGT GGAGG C
CCTCCTGCTGGTGCAGCACC CAG || |||| ||||||| || ||| |||| |||||
AGCTGCTGGAGCAG GA GAGG GTCGACC CG CGT GTCG CCTCC A
C TC A A G T AGG

GAM1687 GCTCCCAATGTTGACGTTGG 1664 TCCCAATGTT 4269 TC AA T C - AG--- TT AA
CCAGGGCCTTTGCAAACAAG GACGTTGGCC GC CC TGT GA GTTG GCC GGCCT GC A
CCAGGCCAAAAAGGCTCAAC AGGG || || ||| || |||| ||| ||||| ||
ATTTACACCGGCTGC CG GG ACA TT CAAC CGG CCGGA CG C
TC CC T A T AAAAA C- AA

GAM1688 GTAGACAAGTCCTCCAGCAC 1665 GCTGACATCT 4270 CAA C CA-- TA GA
AGCCTATATGGAGCTCACTA GAGGACTCTG GTAGA GTCCTC AG CAGCCTA TG G
GGCTGACATCTGAGGACTCT C ||||| |||||| || ||||||| ||
GC CGTCT CAGGAG TC GTCGGAT AC /
--- - TACA C- TC

GAM1689 GCACTCTGTTCTTCCGCCGC 1666 ACTCTGTTCT 4271 AC G CC TCC TC TT
TCCGCCGTCGCGTTTCTCTG TCCGCCGCTC GC TCT TTCTTCCG GC GCCG GCG T
CCGGTCGCAATGGAAGAAGA CGCC || ||| |||||||| || |||| |||
GATCGC CG AGA AAGAAGGT CG TGGC CGT C
CT G AA C-- -- CT

GAM1690 AGCCGCACCAACGAGACAGG 1667 TACATCGACA 4272 C AA-- GACA--- TG- GGAG
TGGAGCTGCAGGAGCTGAAT AGGTGCGCT AGC GCACC CGA GGTGGAGC CA C
GACCGCTTCGCCAACTACAT ||| ||||| ||| |||||||| ||
CGACAAGGTGCGCT TCG CGTGG GCT CCGCTTCG GT /
- AACA ACATCAA CCA AAGT

GAM1691 GCAGGATCTGCCCAACGTTG 1668 AAAGAAATTA 4273 TC C GTTG GG AG- A
AAGGTCAGTGTGATGGCATA GAGTTGGCAC GCAGGA TGCC AAC AA TC TGTG T
AAAGAAATTAGAGTTGGCAC TTCC |||||| |||| ||| || || ||||
TTCCTGC CGTCCT ACGG TTG TT AG ATAC G
TC - AGA- AA AAA G

GAM1692 AGCTGTCTTGCGCACAATCA 1669 TGCCAGTAGC 4274 T - AAT A CACA G
AAGCTGCCACAGGGTTCCTC GCAAGCAGCT AGCTG CTTGCGC AC CA AGCTGC GG T
GCAGCAGCTCTGCCAGTAGC ||||| ||||||| || || |||||| ||
GCAAGCAGCT TCGAC GAACGCG TG GT TCGACG TC T
- A ACC C ACGC C

GAM1693 GAGTATGGGGTGACAAAAAT 1670 CACTGATTTT 4275 CA--- TCCT GCTTAATG
TAGTTCCTGGTGCTTAATGA ATATATTACC GAGTATGGGGTGA AAAATTAGT GGT A
AACTTTCTGCCACTGATTTT CCGT |||||||||||| ||||||||| |||
ATATATTACCCCGTGCTT TTCGTGCCCCATT TTTTAGTCA CCG /
ATATA ---- TCTTTCAA

GAM1694 TACAGCCATGTCACTCCTGG 1671 CTCCCAGACT 4276 - TGTCAC TG G - GG - T
ACA
CGACCCTGGGGCTGGAGCTG AGTGGTGCTG TAC AGCCA TCC GC ACC CTGG CTGG AGC
GG G
GACAGTGGCCCTGCTCCCAG GGAT ||| ||||| ||| || ||| |||| |||| ||| ||
ACTAGTGGTGCTGGGATGGC ATG TCGGT AGG CG TGG GATC GACC TCG CC T
TCGTA C ------ GT - T A- C T CGG

GAM1695 GACGGCCATGCTGGTCTGCA 1672 TACAAGATCA 4279 C ATGCTG G - A- C- -- - A
AGTCAGAGTCCGTGCCACCT CTGACTCTGA GA GGCC GTCT CA AGTCAG GTC GTGCCA
CCT GTC C
GTCACTGACTGGGCCTGGTA GGAC || |||| |||| || |||||| ||| |||||| ||| |||
CAAGATCACTGACTCTGAGG CT CCGG CAGG GT TCAGTC TAG CATGGT GGG CAG
/
ACAAGGCCCTC C AA---- A C AC AA CC T T

GAM1696 CTCCTCACCTGCTCCTTGAA 1673 CACCTGCTCC 4278 ---- - GAATGA --- ACAGAG
TGACAGCGCCACAGAGGTCA TTGAATGACA CTCCT CACC TGCTCCTT CAGC GCC G
CAGGGCACCGCTGGCTGAAG GCGC ||||| |||| |||||||| |||| |||
GGGGGCGTGGTGCTGAAGGA GAGGA GTGG GCGGGGGG GTCG CGG /
G AGTC T AAGTCG CCA GACACT

GAM1697 CGGCTCCGAGAGCAGGTTCT 1674 TACACATTGA 4277 - AGAG C A TC GCAG C
TCGTGAGTTCCTCGCAGGGC GAACCTGAAC CGGC TCCG CAGGTTCTT GTG GT CTC GG
C
CGGTCAGAGCTACACATTGA ATGG |||| |||| ||||||||| ||| || ||| ||

GAACCTGAACATGGAGGCCG GCCG AGGT GTCCAAGAG TAC CA GAG CT G
G ACAA T A TC A--- G

GAM1698 GCCCTGCTGGCTGATGAGCT 1675 TGATGAGCTC 4280 - G G TG CA CT CA TG
CATCACTGTCTACAGCCTGC ATCACTGTCT GCC CT CT GC ATGAGCT TCA GTCTA GCC C
CTGGCATGGACCCTGACTGG ACAG ||| || || || ||||||| ||| ||||| |||
CTCATTGGCGAGAGAGGC CGG GA GA CG TACTCGG AGT CAGGT CGG /
A - G GT TC CC A- TC

GAM1699 GATCTCGGACACATCTGTGG 1676 TGTGGTGCTG 4281 A CATCT GA AACAG
TGCTGTCCATGGACAAACAG TCCATGGACA GATCTCGG CA GTGGTGCTGTCCATG CA C
CGCTCCCTGGACATGGACAG AACA |||||||| || |||||||||||||| ||
CATCATTGCTGAGGTC CTGGAGTC GT TACTACGACAGGTAC GT G
- ----- AG CCCTC

GAM1700 GCAGCCGGGCCTGAGGCTGA 1677 GCTGCAGAGC 4282 AG G G GAGA T A AGA A
GAGCATGTACCAGATCAAGT CTGGGCTGGG GC CC GGCCT AGGCT GCA GT CC TCA G
ATGAGGAGCTGCAGAGCCTG AAGC || || ||||| ||||| ||| || || |||
GGCTGGGAAGC CG GG TCGGG TCCGA CGT CG GG AGT T
AA G - GA-- - A --- A

GAM1701 AGCCGGGCATGGTGGCTCAC 1678 TCACAAGGTC 4283 C --- - AC- - A CAG G
ACCTGTAATCCCAGCACTTT AGGAGATCGA AGCCGGG ATGGT GG CTC ACCT GT ATCC
CACTTTGG A
GGGAGGCCAAGGTGGGTGGA GACC ||||||| ||||| || ||| |||| || |||| ||||||||
TCACAAGGTCAGGAGATCGA TCGGTCC TACCA CT GAG TGGA CA TAGG
GTGGAACC G
GACCATCCTGGCT - GAG A GAC A C TGG G

GAM1702 TCCAGGGTTAGTTTTTGTAG 1679 TGGCACGCTC 4284 - --- TT A- TC- C
CCTCGGCTGGCCCGTCGGCC GAACTTCCGG TCCA GGGTT AGTTT GT GCC GGCTGG C
TCTGGCACGCTCGAACTTCC CCCT |||| ||||| ||||| || ||| ||||||
GGCCCTTGGA AGGT CCCGG TCAAG CG CGG CCGGCT C
T CCT CT CA TCT G

GAM1703 GAATTGGTGAACGGAAGAGT 1680 TATAGTAATG 4285 TT - AACG A C GT T
CCTTATGTTGCAGTATGCTG GCCTTCAGCA GAA GG TG GAAG GTC TTAT TGCAG A
TATAGTAATGGCCTTCAGCA TCCT ||| || || |||| ||| |||| |||||
TCCTCTTC CTT CC AC CTTC CGG AATG ATGTC T
CT T GA-- - T AT G

GAM1704 GGCCACAGGCCGCTACTACG 1681 TACTACGCCA 4287 AGGC CTA AC A -- CA
CCATGAAGATCCTCAAGAAG TGAAGATCCT GGCCAC CG CT GCCATGA GA TCCT A

GAAGTCATCGTGGCCAAGGA CAAG |||||| || || ||||||| || ||||
CGAGGTGGCC CCGGTG GC GA CGGTGCT CT AGGA /
GA-- AG- AC A GA AG

GAM1705 ACTTCGGGCTGTGCAAGGAG 1682 AAGACCTTTT 4286 T C AA- GA- A ACGG
GGGATCAAGGACGGTGCCAC GCGGCACACC ACT CGGG TGTGC GGAGGG TCA GG T
CATGAAGACCTTTTGCGGCA TGAG ||| |||| ||||| |||||| ||| ||
CACCTGAGT TGA GTCC ACACG TTTTCC AGT CC /
- - GCG AGA A ACCG

GAM1706 TTGGAGAAGGCATTTGAAGA 1683 AGGCATTTGA 4288 A A T AAT AA
TGAAATGAAAAAGCTTCTAC AGATGAAATG TTGGAGAAGGC TTTGA GA GA GAA A
TCTTCCTTAAAGCCTTTTCC AAAA |||||||||| ||||| || || |||
GA AGCCTTTTCCG AAATT CT CT CTT /
- C T CAT CG

GAM1707 GACTTTTAAATATTTTGAAG 1684 TTGAAGCCCA 4289 T ---- TG C- TT - AA
CCCATTTCAGTTAAATAATG TTTCAGTTAA GAC TTTAAAT ATTT AAG CCAT CA GTTA T
ACATGTCATGGTCCTTTGGA ATAA ||| ||||||| |||| ||| |||| || ||||
ATCTTCATTTAAATGTT TTG AAATTTA TAAG TTC GGTA GT CAGT /
T CTTC GT CT CT A AA

GAM1708 GCCCATGGGAAACAGCTGTT 1685 GCACATGGTG 4291 - -- AA GC- T T A AACA
CTTTCA
CCTCATCACCAACAGTCCTT GGTCCCGATT GC CCA TGGGA CA TGT CC CATC CC GTC
G
TCAGCTTCGTAGACAAGGGG GGCG || ||| ||||| || ||| || |||| || |||
ATGCGGCACATGGTGGGTCC CG GGT GCCCT GT ACA GG GTAG GG CAG C
CGATTGGCGC C TA GG GGT C C - GAA- ATGCTT

GAM1709 ACCAGTGGATCGAGCAGGAC 1686 AGCAGGACAT 4290 - ATCGAG TG AAGTA GA
ATGGAGAAGTACATCCTGAG GGAGAAGTAC ACCAG TGG CAGGACA GAG CATCCT G
AGGGGATGAGACGTTTGCTG ATCC ||||| ||| ||||||| ||| ||||||
TCCTGAGCCGCCTGGT TGGTC GCC GTCCTGT TTT GTAGGG /
C GA---- CG GCAGA GA

GAM1710 TTGTGAACAGATTAAGGATA 1687 TTGTGTGTGT 4292 GA A ----- G T- GTT
AATATATGCAGAATCGGTTG GTTTCTCCAA TTGT AC GATTAAGGAT AAATATATGCA AA CG
G
GTGCGTCTTGTGTGTGTGTT TCCT |||| || |||||||||| |||||||||| || ||
TCTCCAATCCTTGATCCGTA AACA TG CTAGTTCCTA TTTGTGTGTGT TT GC /
ACAA A- C ACCTC G CT GTG

GAM1711 ACCAGATCCTTCTCATCCGT 1688 CATCCGTACG 4293 - CC - ACG TTTTC --
ATTTCTT
ACGGATTTTCAAATATGCGC GATTTTCAAA ACCA GAT TTCT CATCCGT GA AAATAT
GCGCTAT C
TATATTTCTTCGCTAATTAG TATG |||| ||| |||| ||||||| || |||||| |||||||
TGGTGTTGGTATTTTCATGA TGGT CTA AGGA GTGGGTA CT TTTATG TGTGGTG
G
TGGGTGCAGGACTATCTTGG T TC C GTA ----- GT ATTAATC
T

GAM1712 GTCCTGTGAGTTTACTGGGG 1689 TGAGGATATG 4295 TG TT--- TG G C A C
ATATTCTCCGAACACCGGTG CTTGGTCGGG GTCC TGAGT AC GG ATATTCTC GA CA C
TCTGAGGATATGCTTGGTCG TATT |||| ||||| || || |||||||| || ||
GGTATTCAATGGAT TAGG ACTTA TG TC TATAGGAG CT GT G
TA TGGGC GT G T - G

GAM1713 TTCTCTGCTGCTGGGCTACC 1690 TGGTTTGGTA 4296 T C G C CAA- A GCA-- T T
G
ACACAATGAGATTGCAGCTC AAGAAATCCA TTCTC GCTG TGG CTAC ACA TG GATT GC
CAGATC GTC C
AGATCTGTCGCCAGGCTGGT AAGA ||||| |||| ||| |||| ||| || |||| || |||||| |||
TTGGTAAAGAAATCCAAAGA AGGAG TGAC ATC GATG TGT AC CTAA TG GTTTGG
CGG C
TGTAGTAGACTACAGTGAGG - - A A AGAA - AGAAA - T A
A

GAM1714 ATCCAAAGATGTAGTAGACT 1691 TAGTAGACTA 4294 AAGAT C GA- A
ACAGTGAGGAAAATTTTGCA CAGTGAGGAA ATCCA GTAGTAGA TACAGT GGA A
ATTGTATTTGCTGCTATGGG AATT ||||| |||||||| |||||| |||
T TGGGT CGTCGTTT ATGTTA TTT A
AT--- - ACG T

GAM1715 CGCTCGTCACCAGGACCCAA 1692 TCAAGGGTCG 4297 - TC - G AA GA AA TG
GGAACCAAAAGTGCATCTGA TGTGTTGTGA CGCT CG AC CA GACCC G ACCA AG C
TGGTCTCAAGGGTCGTGTGT AGTG |||| || || || ||||| | |||| ||
TGTGAAGTG GTGA GT TG GT CTGGG C TGGT TC /
A GT T G AA TC AG TA

GAM1716 TGCATTTAGAAAGATTCAAG 1693 AAGCTGATTA 4299 - TTAGA A G TACT A T
GTAA
CTGATTACTGAAGATGTTCA CTGAAGATGT TG CAT AAGATTCA GCT AT GAAG TG TCAGG
A
GGGTAAAAACTGCCTGACTA TCAG || ||| |||||||| ||| || |||| || |||||
ACTTCCATGGGCATGGATCT AC GTG TTCTAGGT CGG TA CTTC AT AGTCC A
TACCCGTGACA A CCCA- A G C--- A C GTCA

GAM1717 GTGTTCCATGGTCAAAAAAT 1694 TGTCAAGACT 4298 TT - CAAAAAA GA AT AA
GGCAGACAATGATTGAAGCT ACCGATGGTT GTG CCAT GGT TGGCA CAATG TG G
CACGTTGATGTCAAGACTAC AC ||| |||| ||| ||||| ||||| ||
CGATGGTTAC CAT GGTA CCA ACTGT GTTGC AC /
T- G TCAGA-- A- -- TC

GAM1718 TCGCAAGGCTGGCTGACCAG 1695 TATCTTGGTT 4301 G - GCT-- TT-- A GGT
TTGCACCGGTCTTCAGGGCT TTCCACAGCT TC CAA GGCTG GACCAG GC CC C
ATCTTGGTTTTCCACAGCTA ATTG || ||| ||||| |||||| || ||
TTGGGA AG GTT TCGAC TTGGTT CG GG T
G A ACCTT CTAT - ACT

GAM1719 GCAAGGAATGATGCTAGCCA 1696 CACTACACCA 4300 -- G-- A AACTA-- C
ATAACTATGCCCGAGGGCAC TTGGCAAGGA GCAAGG AATGAT CT GCCAAT TGCC G
TACACCATTGGCAAGGAGAT GATC |||||| |||||| || |||||| ||||
CATTGACCTTGT TGTTCC TTACTA GA CGGTTA ACGG A
AG GAG A CCACATC G

GAM1720 GCTGATGGGGTACACACGGT 1697 ACTACAAGCT 4302 T A-- --- GG-- - AA A
GGAGCCAACGGAGGCCGGGG GTGCTTTGAC GCTGA GGGGT CA CACGGT AG CC CGG G
ACTACAAGCTGTGCTTTGAC AACT ||||| ||||| || |||||| || || |||
AACTCCTTCAGC CGACT CCTCA GT GTGTCG TC GG GCC /
T ACA TTC AACA A G- G

GAM1721 GAAACAGACTGGGCCAATGT 1698 TATCAAGGAA 4303 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM1722 TCTTGTGTGAGACTTCGTGG 1699 TACACCACTC 4304 GAGA- GT--- C AAAGGA
TGGTGCTAAGAAAAGGAAGA CCAAGAAGAA TCTTGTGT CTTC GGTGGTG TAAGA A
AGAAGTCTTACACCACTCCC TAAG |||||||| |||| ||||||| |||||
AAGAAGAATAAGCACAAGA AGAACACG GAAG TCACCAC ATTCT G
AATAA AACCC - GAAGAA

GAM1723 GTGGTGAAGACAGGCCGAGT 1700 CAGCAGATTC 4306 AAGACA C-- GA T GAG
GATGCTTGGGGAGACCAATC AAAGCCAGGC GTGGTG GGC GAGT TGCT GGG A
CAGCAGATTCAAAGCCAGGC ACCA |||||| ||| |||| |||| |||
ACCAT TACCAC CCG CTTA ACGA CCT C
GGA--- AAA G- - AAC

GAM1724 CCTGAAAGACCGACCATTCT 1701 TGAAAGACCG 4305 GAA- A-- T- T- CTG AA
TCCCTGGGCTGGTGAAGTAC ACCATTCTTC CCT AGACCG CCAT CT CCCTGGG GTG G
ATGAACTCAGGGCCGGTTGT CCTG ||| |||||| |||| || ||||||| |||
GGCCATGGTCTGGGAGGG GGG TCTGGT GGTG GG GGGACTC TAC /
AGGG ACC TT CC AAG AT

GAM1725 GCCAACCTTGAAGCCAGTGG 1702 TTGAAGCCAG 4307 A - TG - G - ATCC
GGCACCAATCCACAAACTGG TGGGGCACCA GCCA CC T AAGCCA GTG GGCA CCA A
ATGCTGCGCTTGGTTTTGAT ATCC |||| || | |||||| ||| |||| |||
GGTGGC CGGT GG A TTTGGT CGC TCGT GGT C
- T GT T G A CAAA

GAM1726 GAAACAGACTGGGCCAATGT 1703 TATCAAGGAA 4308 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM1727 TCTGTGTGTGGAGACTTCGT 1704 TACACCATTC 4309 G- GGAGA G --- C AAAGGA
GGTGGTGCTAAGAAAAGGAA CCAAGAAGAA TCT TGTGT CTTC TGG TGGTG TAAGA A
GAAGAAGTCTTACACCATTC TAAG ||| ||||| |||| ||| ||||| |||||
CCAAGAAGAATAAGCACAAG AGA ACACG GAAG ACC ACCAC ATTCT G
AGA GA AATAA A CTT - GAAGAA

GAM1728 ACTTTCAGGGTAATGATGCA 1705 AGTGCAGAAA 4310 TGA-- C TGAACA
CCTGTTGAACAAGACATTAC CTTACTTTGA ACTTTCAGGGTAA TGCAC TGT A
AGTGCAGAAACTTACTTTGA AAGT |||||||||||| ||||| |||
AAGT TGAAAGTTTCATT ACGTG ACA /
CAAAG - TTACAG

GAM1729 TCAGAGTCTTCTCATCTGTG 1706 AAGTTTGTCG 4311 ---------- A G A CC C GG
CCAGCACCCTTCATGGATTT GCAAAGAAGA TCAGAGT CTTCTC TCT TGCC GCA CTT AT
A
GTAAAGTTTGTCGGCAAAGA GAGG ||||||| |||||| ||| |||| ||| ||| ||
AGAGAGGCTTGTTCTTGACA AGTTTCA GGAGAG AGA ACGG TGT GAA TG T
CTTTGA CAGTTCTTGTTC A A C TT A TT

GAM1730 TCCAGGGTTAGTTTTTGTAG 1707 TGGCACGCTC 4312 - --- TT A- TC- C
CCTCGGCTGGCCCGTCGGCC GAACTTCCGG TCCA GGGTT AGTTT GT GCC GGCTGG C

TTTGGCACGCTCGAACTTCC CCCT |||| ||||| ||||| || ||| ||||||
GGCCCTTGGA AGGT CCCGG TCAAG CG CGG CCGGCT C
T CCT CT CA TTT G

GAM1731 CAGGTGAAGGCACCTGGCTG 1708 TTCATCACCA 4313 A CAC C CCAT-- CTT
ACCATCAATGCTTTCCACAT GTCACCTCCA CAGGTG AGG CTGG TGA CAATG T
TGTATTCATCACCAGTCACC CTTG |||||| ||| |||| ||| |||||
TCCACTTG GTTCAC TCC GACC ACT GTTAC /
C ACT - ACTTAT ACC

GAM1732 ACATAGTGGAGGCCGCAGCA 1709 TGAAGCGAGC 4314 ---- C A- AG A
GTCAGGGACATTTCTGAAGC GTCTTCGATG ACATAG TGGAGGC GC GC TCAGGG C
GAGCGTCTTCGATGCCTATG CCTA |||||| ||||||| || || ||||||
T TGTATC GCTTCTG CG CG AGTCTT A
CGTA - AG A- T

GAM1733 TCTTGTGTTGAGACTTCGTG 1710 TACACCACTC 4315 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM1734 AGGCAAACGAGAAGAAGGAG 1711 CTTCGTGTCC 4316 GA-- A-- AACC-- AGT T
GAACCCAAGTAGCTTTTTGG AACCCTCTTG AGGCAAAC GAAG AGGAGG CA AGCT T
CTTCGTGTCCAACCCTCTTG CCCT |||||||| |||| |||||| || ||||
CCCTTCGCCTGTTTGCCT TCCGTTTG CTTC TTCTCC GT TCGG T
TCCG CCG CAACCT GCT T

GAM1735 GCTGCGTTTATAAACCATGA 1712 ACCATGATTG 4317 CG ATAA -- T C A
TTGCAGACCTAATTGTAAGT CAGACCTAAT GCTG TTT ACCA TGAT GCAGAC TA T
TTGTGTCAACTGGTCGAGAT TGTA |||| ||| |||| |||| |||||| ||
ACAGC CGAC AGA TGGT ACTG TGTTTG AT T
AT GC-- CA - A G

GAM1736 GTGTGAAGGCTCTAAGAGAC 1713 TAAGAGACAT 4318 AG TA A- AAC--- TG GAA
TGTT
ATTGAACCTGGAGAAGAAAT TGAACCTGGA GTGTGA GCTC AGAG CATTG C GAGAA
ATTTCT A
TTCTTGTTATTATGGAGATG GAAG |||||| |||| |||| ||||| | ||||| ||||||
GGTTCTTTGGAGAAAATAAT CACATT TGAG TCTT GTAAT G TTCTT TAGAGG /
GAGTTCTGCGAGTGTTACAC G- CG GA AAAAGA GT GGG TATT

GAM1737 TGCGAAAGACGGGGCACTGG 1714 TGCCTGCGCC 4319 GAAA--- - CT TTTTAAA AG

TGCTTTTAAATCCAGAGTGG TGCTCCTGTT TGC GACGGG GCA GGTGC TCC A
GACTGCCTGCGCCTGCTCCT ATCA ||| |||||| ||| ||||| |||
GTTATCAATAGCA ACG TTGTCC CGT CCGCG AGG G
ATAACTA T -- TCCGTC- GT

GAM1738 TTGAGGAGAACATGCTACTT 1715 GAACATGCTA 4320 A A C TAGACAT AAA
AGACATGGAGAAAACGACTT CTTAGACATG TTG GGAG ACATG TACT GGAG A
CAGTGTCATGTACTCCACAA GAGA ||| |||| ||||| |||| ||||
AAC CCTC TGTAC GTGA CTTC /
A A T ------- AGC

GAM1739 GGAGTGGAGCTGCTCACTCT 1716 AGCCTGGATG 4321 A-- - -- T C T CC - TGA-
AG ATG
GCCATGTGCTCCCTGACCTG GTGCAGACAG GTG GAGCT GC CACT TGCCA GTGCT CTG
ACC AGG GAGG G
AAGGAGGAGGATGGCAGCCT CACT ||| ||||| || |||| ||||| ||||| ||| ||| ||| ||||
CAGCCTGGATGGTGCAGACA CAC CTCGA CG GTGG GCGGT CACGA GAC TGG
TCC CTCC /
GCACTGGCGTGGTGGCCAAG GAC T AC - T - CA G TAGG GA GAC
CTCTCACCAGCC

GAM1740 GGCCAATTGAAACAAACAGT 1717 TATTAGGGAT 4322 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1741 TTGAGAAGGAGTCTCGCTCT 1718 TCTCGCTCTG 4323 A- TC C TC C-- -- A - A
A
GTCACCCAGGCTGGAGTGCA TCACCCAGGC TTGAG AGGAG TCGCT TG ACCCAGG TGGAG
TGCA TG GC CG T
ATGGCACGATCTCGGCTCAC TGGA ||||| ||||| ||||| || ||||||| ||||| |||| || || ||
TGCAACCTCTGCCTCCTGGG GACTC TTCTC AGCGA AC TGGGTCC GTCTC ACGT
AC CG GC C
TTCAAGCGATTCTCTTGCCT CG TT - T- TCC CA C T - T
CAG

GAM1742 GGCCAATTGAAACAAACAGT 1719 TATTAGGGAT 4324 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1743 TACAGCGGCTGCGTCTCTCT 1720 GTAGCGGAAC 4325 ------ - TAC A-- GA G T

GTGTACTTGACCGTGATGGG CAGATTGCAG TACAGC GGCTGCGTC TCTCTGTG TTG
CCGT TG GGC G
GCTGAGGTCGTAGCGGAACC GGAT |||||| |||||||| |||||||| ||| |||| || |||
AGATTGCAGGGATGATGCGG ATGTCG CCGGCGTAG AGGGACGT GAC GGCG AT
CTG A
CCCGTGTGGCTGTA GTGTGC T TA- CAA -- G G

GAM1744 GGGTTTTTCAGAGTCGGAGA 1721 TTTTTCAGAG 4326 T G- GA AA CTAT
GGAACAAGCTAGCTATGTTG TCGGAGAGGA GGGT TTTCA AGTCGGA GGAAC GCTAG G
ACTGGTGTTCTTCTGGCTAA ACAA |||| ||||| ||||||| ||||| |||||
TGGAACACTT TTCA AAGGT TCGGTCT TCTTG TGGTC /
C AA -- -- AGTT

GAM1745 GGTCGCAGAGGAGACACCGC 1722 GGGGATTTCT 4327 T C CACC T- G T
CGTAGTTGCCGGTACATCGG GGCTCTTTCC GG CG AGAGGAGA GCCG AGTT CCGG A
GGATTTCTGGCTCTTTCCTC TCTT || || |||||||| |||| |||| ||||
TTCGCC CC GC TCTCCTTT CGGT TTAG GGCT C
- T CT-- CT G A

GAM1746 CCCACTGGTGCGCATGGTGG 1723 ACTGGTGCGC 4328 CGCAT TG ------ C- AG
CCACGCCTCCATTAGCAAAG ATGGTGGCCA CCCACTGGTG GG GCCA CGCCT CATT C
TGAAGGGTGATCATTTGGCT CGCC |||||||||| || |||| ||||| ||||
GCTTTTACTAGTGGG GGGTGATCAT TC CGGT GTGGG GTGA /
TT--- GT TTACTA AA AA

GAM1747 GATGATAGTTACTGATATAT 1724 TGGAACGGGA 4329 A AC CA- AGAT A G C
T ATG
ACAATCATAGATTTCACAGA TGATATTTAT GATG TAGTT TGATATATA ATCAT TTC CA
AATATT GCTA GG A
ATATTCGCTATGGATGAAAA GTGT |||| ||||| ||||||||| ||||| ||| || |||||| |||| ||
CCTTAGTAGTATTATGGAAC CTAC ATTAA GCTGTGTAT TAGTA AAG GT TTATGA
TGAT CC /
GGGATGATATTTATGTGTCG A A- TTA GGGC - A - T AAA
AAATTAACATC

GAM1748 GTCCCTGACACTGCCCGCTA 1725 CCTGACACTG 4330 C - TG ACTA-- AGA
CTACAAGAAACATGGCATCA CCCGCTACTA GTC CTGA CAC CCCGCT CA A
GGTGGGTGGTGATCGGAGAC CAAG ||| |||| ||| |||||| ||
CAG GGCT GTG GGGTGG GT /
A A GT ACTACG ACA

GAM1749 TGTGGCCCGGAGTTTGATGT 1726 GCCCGGAGTT 4332 TTTGAT C GAT
GTAGGGCGGTGATACCCAGC TGATGTGTAG TGTGGCCCGGAG GTGTAGGG GGT A
TCCTTGCACCTCTGGGCCAC GGCG |||||||||||| |||||||| |||
A ACACCGGGTCTC CACGTTCC TCG C

------ - ACC

GAM1750 CCTGCGAGTGCTGTCAAAGG 1727 TGTCAAAGGG 4331 GA---- CT- AAA - TG
GGATGGGGGTGACATCCTCA GATGGGGGTG CCTGC GTG GTC GGGGAT GGGGG A
ATCCCCCCGATCTTCATACC ACAT ||||| ||| ||| |||||| |||||
CGAGCGGG GGGCG TAC TAG CCCCTA CTCCT /
AGCCCA TTC CC- A AC

GAM1751 ATCAATGAGATCCGTCAGAT 1728 AACCCAGTGG 4333 ATG G AGATGT G- ATC
GTCTGGGGCGCAGATCAAAA AAGGATCTAC ATCA AGATCC TC CTGGG CGCAG A
TTGCGAACCCAGTGGAAGGA TGAT |||| |||||| || ||||| |||||
TCTACTGAT TAGT TCTAGG AG GACCC GCGTT /
CA- A GT---- AA AAA

GAM1752 GCCGTCCAGCTCTCCGGTCA 1729 TTCCACAGCC 4334 ----- C CTCC TC CAG TCA C
A-- AT
TCTTTGCAGGTGGTCAGGCC AGATTTGACC GCC GT CAGCT GGTCA TTTG GTGG GGC
TAT CC T
TATACCATTCAAGGACAGTA AAGC ||| || ||||| ||||| |||| |||| ||| ||| ||
TGCCATTCCACAGCCAGATT CGG CA GTCGA CCAGT AGAC CACC CCG ATG
GG C
TGACCAAGCTGCACCAGTTG TTGAC C A--- TT CGA TTA T ACA AA
GC

GAM1753 CGGAGTGGTGGCCAGCCAGC 1730 GGAGCAGATG 4335 GT- G ------ GC G AGTG
CTGCTCGTGTAGTGGACGAA GCCATCAGTG CGGA GGT GCCA GCCA CTGCTC TGT G
CGGGAGCAGATGGCCATCAG GCGG |||| ||| |||| |||| |||||| |||
TGGCGGCTTCATCCG GCCT TCG CGGT CGGT GACGAG GCA /
ACT G GACTAC A- G AGCA

GAM1754 GGTGACAACATGCTGGAGCC 1731 TTGGTTCAAG 4336 AA-- G G- C T TA
CAAGTGCTAACATGCCTTGG GGATGGAAAG GGTGAC CAT CT GAGCC AAG GC A
TTCAAGGGATGGAAAGTCAC TCAC |||||| ||| || ||||| ||| ||
C CCACTG GTA GG CTTGG TTC CG C
AAAG G AA - - TA

GAM1755 GCAGTGGAGGGGGCAGGACC 1732 CAGGTCCACC 4337 GA A--- C GG CA
TCCTCTGGTGCAGCACCACT GGCCCCTACA GCAGTG GGGGGC GGACCT CTCT TGCAG C
GTAGGAGCAGGTCCACCGGC TTGC |||||| |||||| |||||| |||| |||||
CCCTACATTGC CGTTAC TCCCCG CCTGGA GAGG ATGTC /
A- GCCA C -- AC

GAM1756 GGCTCCCAATGTTGACGTTG 1733 CAATGTTGAC 4338 CTCCC CG---- AG GTTTG
GCCAGGGCGTTTGCAAACAA GTTGGCCAGG GG AATGTTGA TTGGCC GGC C

GCCAGGCCAAAAAGGCTCAA GCGT || |||||||| |||||| |||
CATTTACACC CC TTACAACT AACCGG CCG A
ACAT- CGGAAA A- AACAA

GAM1757 CTGCTCCAGCAGCTGGTGCT 1734 TCCACTGGCT 4339 G AG T T CA TCC
GCAGCCAGCAGGAGGTCCTG GCTGCTCCAG CT CTCC CAGCTGG GC GCAGCCAG GGAGG
T
CCCCCTCCACTGGCTGCTGC CTGA || |||| ||||||| || |||||||| |||||
TCCAGCTGAGGAGAAG GA GAGG GTCGACC CG CGTCGGTC CCTCC G
A A- T T A- CCC

GAM1758 GTGAAGAACTCGCAGTCCTT 1735 ACTCGCAGTC 4340 A AC GTC CT-------- T
CTTCTCTGGCCTCTTTGGAG CTTCTTCTCT GTG AGA TCGCA CTTCTTCT GGCCTC T
GCTCATCCAAAATAGAGGAA GGCC ||| ||| ||||| |||||||| ||||||
GCATGCGAAATCTACGC CGC TCT AGCGT GAAGGAGA TCGGAG T
A AA AC- TAAAACCTAC G

GAM1759 TCTTGTGTTGAGACTTCGTG 1736 TACACCACTC 4341 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM1760 TGTGCCCACAGTGTTTGAGA 1737 TGGAAAGCAG 4342 - T TGAGAA G GCAGA GA
ACTATGTGGCAGATATCGAG GTAGAGTTGG TGTG CCCACAG GTT CTAT TG TATC G
GTGGATGGAAAGCAGGTAGA CTTT |||| ||||||| ||| |||| || ||||
GTTGGCTTTGTGGGACACA ACAC GGGTGTT CGG GATG AC GTAG G
A T TTGA-- G GAAAG GT

GAM1761 CCTGTCGGCAATGCCAGGGT 1738 AGACAGCACT 4343 - G C G ACA- G
ACATGGTGGTGCCGCCAGAC GTGTTGGCGT CCTGT CG CAATGC AG GT TGGTG T
AGCACTGTGTTGGCGTACAG ACAG ||||| || |||||| || || |||||
G GGACA GC GTTGTG TC CG ACCGC G
T G - A ACAG C

GAM1762 TGGAGGGGCCGGACTCGTCA 1739 GTGGACAGCG 4344 GG C A GT TAC -- A A-
TG
TACTCCTGCTTGCTGATCCA AGGCCAGGAT TGGA GGC GG CTC CA TCCTG CTTGCTG
TCCAC TC C
CATCTGCTGGAAGGTGGACA GGAG |||| ||| || ||| || ||||| ||||||| ||||| ||
GCGAGGCCAGGATGGAGCCG ACCT CCG CC GAG GT AGGAC GAGCGAC AGGTG
AG /
CCGATCCA AG - - -- --- CG - GA GT

GAM1763 GCCTTGAACCTGAGGGGGAT 1740 TGTTGATACT 4345 GA TGAGGG - C TGGA A
TCCACAGCTGTTTGGAGGCA GCTGGAATCC GCCTT ACC GGATTCCA CAG TGTT GGC T
TCTGCTGTTGATACTGCTGG AGAG ||||| ||| |||||||| ||| |||| |||
AATCCAGAGTGGTGAGGC CGGAG TGG CCTAAGGT GTC ATAG TCG C
-- TGAGA- C - TTG- T

GAM1764 GCACTCTGTTCTTCCGCCGC 1741 ACTCTGTTCT 4346 AC G CC TCC TC TT
TCCGCCGTCGCGTTTCTCTG TCCGCCGCTC GC TCT TTCTTCCG GC GCCG GCG T
CCGGTCGCAATGGAAGAAGA CGCC || ||| |||||||| || |||| |||
GATCGC CG AGA AAGAAGGT CG TGGC CGT C
CT G AA C-- -- CT

GAM1765 TGGGTATGGAATCTTGCGGC 1742 TGGAATCTTG 4347 - AA - CA- AGAC - ACTC
ATCCACGAGACCACCTTCAA CGGCATCCAC TGG GTATGG TCTT GCGG TCCACG CAC
CTTCA C
CTCCATCATGAAGTGTGACG GAGA ||| |||||| |||| |||| |||||| ||| |||||
TGGACATCCGCAAAGACCTG ACC CATGTC AGAA CGCC AGGTGC GTG GAAGT /
TACGCCA G C- A TAC A--- T ACTA

GAM1766 AAGATAGAGGCAGAACTGCA 1743 TGTTCTGGAG 4348 GA----- AA G TG
GGACATCTGCAATGATGTTC CTGTTGGACA AAGATA GGCAG CT CAGGACATC C
TGGAGCTGTTGGACAAATAT AATA |||||| ||||| || |||||||||
CTT TTCTAT TTGTC GA GTCTTGTAG A
AAACAGG -- G TA

GAM1767 CACTACGTTGACCTGAAGGA 1744 AAGGACCGTC 4349 GA-- GAA- CCATTCT --
AAAT
CCGTCCATTCTTTGCCGGCC CATTCTTTGC CACTACGTT CCT GGACCGT
TTGCCGGCCT GGTG A
TGGTGAAATACATGCACTCA CGGC ||||||||| ||| ||||||| |||||||||| ||||
GGGCCGGTAGTTGCCATGGT GTGGTGTAA GGG TCTGGTA GATGGCCGGG
TCAC /
CTGGGAGGGGCTGAATGTGG GTCG AGGG CCGTT-- AC GTAC
TG

GAM1768 GTAGAGCTTTATGCTGAAAA 1745 GAGCTTTATG 4351 - TA GAAAA - T A
GGTGGCCACTAGAGGTCTGT CTGAAAAGGT GTAGAG CTT TGCT GGTGGC CAC AG G
GTGCCATTGCCCAGGCAGAG GGCC |||||| ||| |||| |||||| ||| ||
TCTCTGC CGTCTC GAG ACGG TTACCG GTG TC G
T -- ACCCG T - T

GAM1769 GGGAAACTCCGAGGACAGAG 1746 TGGCCTGATG 4350 AAA A--- - GA AA TG A
GGCTAAATCCATGAAGTTTG ATCCACAGCG GGG CTCCG GGA CA GGGCT ATCCA A G
TGGATGGCCTGATGATCCAC GAGA ||| ||||| ||| || ||||| ||||| |

AGCGGAGACCC CCC GAGGC CCT GT TCCGG TAGGT T /
A-- GACA A AG -- GT T

GAM1770 GAATCACATAAAATTGTGTG 1747 TGCACACATG 4352 TAAAAT- TCAT
TGCACGTTCATGTACACATG TAACCTCTGT GAATCACA TGTGTGTGCACGT G
TGCACACATGTAACCTCTGT GATT |||||||| ||||||||||||
GATTC CTTAGTGT GTACACACGTGTA T
CTCCAAT CACA

GAM1771 CGGCTCCGAGAGCAGGTTCT 1748 TACACATTGA 4353 - AGAG C A TC GCAG C
TCGTGAGTTCCTCGCAGGGC GAACCTGAAC CGGC TCCG CAGGTTCTT GTG GT CTC GG
C
CGGTCAGAGCTACACATTGA ATGG |||| |||| ||||||||| ||| || ||| ||
GAACCTGAACATGGAGGCCG GCCG AGGT GTCCAAGAG TAC CA GAG CT G
G ACAA T A TC A--- G

GAM1772 TTCCACACCTTCACAATCCC 1749 GCCCTGTGTG 4354 C TT ATCC-- TCTAGAA
ATCTCTAGAAGCAGTTACGA GTCTGGAA TTCCA ACC CACA CATC G
TGAAGCCCTGTGTGGTCTGG ||||| ||| |||| ||||
AA AAGGT TGG GTGT GTAG /
C T- CCCGAA CATTGAC

GAM1773 TTAGCATGAAGTCCCTCTGG 1750 ATGGATCTTA 4355 T AG C--- CT CTG - TC
ATCTTGAGCTGGTTTATGGA CTGTCCAGAG TTAGCA GA TC CTCTGGAT TGAG GTTTATG
GAC A
CTCAATCGTCTCATGGATCT CACT |||||| || || |||||||| |||| ||||||| |||
TACTGTCCAGAGCACTGATC GGTCGT CT AG GAGACCTG ATTC TAGGTAC CTG A
TCCTGCTGG C CT TCAC TC --- T CT

GAM1774 TTTGGGACCTTTGTACAGTT 1751 GTCTGGTTCA 4356 G GTA-- TTGTGAT G
GTGATGCTCGAGCAATTGGG GAGGGTGCCA TTTGG ACCTTT CAG GCTCGA C
TCTGGTTCAGAGGGTGCCAG GA ||||| |||||| ||| ||||||
A AGACC TGGGAG GTC TGGGTT A
G ACTTG ------- A

GAM1775 ATTTGAGAAGGAGGCTGCTG 1752 CTTCAAGTAT 4357 TG AGG - GA T AAA
AGATGGGAAAGGGCTCCTTC GCCTGGGTCT ATT AGA AGGC TGCT GA GGG G
AAGTATGCCTGGGTCTTGGA TGGA ||| ||| |||| |||| || |||
T TAG TCT TCCG ATGA CT CCT /
GT GGG T A- T CGG

GAM1776 GGTGACAACATGCTGGAGCC 1753 TTGGTTCAAC 4358 AA-- G -- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CTG GAGCCAAG GC A

TCAACGGATGGAAAGTCACC TCAC |||||| ||| ||| |||||||| ||
CCACTG GTA GGC CTTGGTTC CG C
AAAG - AA - TA

GAM1777 TTGTCGTCATTGGACACGTA 1754 TAAATGCGGT 4360 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM1778 GGTGACAACATGCTGGAGCC 1755 TTGGTTCAAG 4359 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1779 TGATGCGCAAGGCCATCCGA 1756 TCTGGAGAAA 4361 T - A GCCA G ACC AAA
GGGCACCTGGAAAACAACCC CTGCTGCCTC TGA GC GCA G TCC AGGGC TGG A
AGCTCTGGAGAAACTGCTGC A ||| || ||| | ||| ||||| |||
CTCA ACT CG CGT C AGG TCTCG ACC C
C T - AAAG - --- CAA

GAM1780 CTTCTTCAGTGAGACGGGCG 1757 TTTGTAGACT 4362 T GAC- CG ----- T C
CTGGCAAGCACGTGCCCCGG TGGAACCCAC CTTC TCAGTGA GGG CTG GCAAGCACG
GCC C
GCTGTGTTTGTAGACTTGGA AGTC |||| ||||||| ||| ||| ||||||||| |||
ACCCACAGTCATTGATGAAG GAAG AGTTACT CCC GGT TGTTTGTGT CGG /
T GACA AA TCAGA - G

GAM1781 GGTGACAACATGCTGGAGCC 1758 TTGGTTCAAG 4363 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1782 TCGGCTCCAAGTCTGACCCA 1759 TGGGAGGGGG 4365 T A T A AC TG TT
CTCTGCGTCCTTTTACAGGA CAGCTGGGCT TCGGC CCA G CTG CCC TC CGTCCT T
TGTGGGAGGGGGCAGCTGGG GA ||||| ||| | ||| ||| || ||||||
CTGA AGTCG GGT C GAC GGG GG GTAGGA /
- - - G GA GT CA

GAM1783 TCGCGCGGGGGGTAATTCGG 1760 TCCCCGATGG 4364 G AAT T--- --- TC
GGTCTGGGTTCTGGTGCCGC CCCACTGCGT TCGCGCGG GGGT TCGGGG CTG GGT T

GCAGCTTTCCCCGATGGCCC GA ||||||||| |||| |||||| ||| |||
ACTGCGTGA AGTGCGTC CCCG AGCCCC GAC CCG G
A GT- TTTC GCG TG

GAM1784 CGGCTCCGAGAGCAGGTTCT 1761 TACACATTGA 4366 - AGAG C A TC GCAG C
TCGTGAGTTCCTCGCAGGGC GAACCTGAAC CGGC TCCG CAGGTTCTT GTG GT CTC GG
C
CGGTCAGAGCTACACATTGA ATGG |||| |||| ||||||||| ||| || ||| ||
GAACCTGAACATGGAGGCCG GCCG AGGT GTCCAAGAG TAC CA GAG CT G
G ACAA T A TC A--- G

GAM1785 GTCTGCAAGTCAGAGTCCGT 1762 TACAAGATCA 4367 G - A- C- -- - A
GCCACCTGTCACTGACTGGG CTGACTCTGA GTCT CA AGTCAG GTC GTGCCA CCT GTC C
CCTGGTACAAGATCACTGAC GGAC |||| || |||||| ||| |||||| ||| |||
TCTGAGGAC CAGG GT TCAGTC TAG CATGGT GGG CAG /
A C AC AA CC T T

GAM1786 GTTCCCGCATCTGGAGTTCA 1763 TCAACACCCG 4368 T C A CA A A C G
GGAGTATTCGGGGAAACCTC GCTTCGGAAG GT CC GC TCTGGAGTT GG GT TT GGG A
AACACCCGGCTTCGGAAGCT CTGG || || || ||||||||| || || || |||
GGAC CA GG CG AGGCTTCGG CC CA AA TCC A
- T A -- - C C A

GAM1787 GAGCTTCTCCTTGCCAGTTT 1764 TCTCCTTGCC 4369 TTCTC TTTCTCC AG C - TTG
CTCCCAGCAGGACCCTCTTC AGTTTCTCCC GAGC CTTGCCAG CAGC GACC TCTT C T
TTGTTTTGAAAGATGGTCGG AGCA |||| |||||||| |||| |||| |||| |
CTGCTTTTGGTAGGCACGCT CTCG GGATGGTT GTCG CTGG AGAA G /
C CAC-- TTC---- G- T A TTT

GAM1788 GGCCAATTGAAACAAACAGT 1765 TATTAGGGAT 4370 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1789 GAAGGAACAGTTTGCCTGGA 1766 TATCCAGTAT 4372 AACAGT TG CT CATTTC -
ACC
GACATTTCTACTGGTACCTT CTCCGTGATT GAAGG T C GGAGA TACTGG TACCTT A
ACCAATGAGGGTATCCAGTA ACCT ||||| | | ||||| |||||| ||||||
TCTCCGTGATTACCTTC CTTCC A G CCTCT ATGACC ATGGGA /
ATT--- GT -- ------ T GTA

GAM1790 CCGACAAGAAAGCCGAGGCT 1767 TTTGGTCGTG 4371 GA--- GAAA C C -- G A A T A T

GGGGCTGGGTCAGCAACCGA GACGTGGTCA CC CAA GC GAGG TGG GGCTG GTC GC ACCGAAT CC GTT A

ATTCCAGTTTAGAGGCGGAT GCCA || ||| || |||| ||| ||||| ||| || ||||||| || |||

TTGGTCGTGGACGTGGTCAG GG GTT TG CTCC ACC CTGGT CAG TG TGGTTTA GG CGG G

CCACCTCAGTAAAATTGGAC AGCAG AAAA A - GA G G C - - A

GAGG

GAM1791 GGGCTGTAGTGCACTTTGAG 1768 TAGTGCACTT 4373 G TA- ACTT G G-- G GG

CGAGGGCGGCCTGGGGACCG TGAGCGAGGG G GCTG GTGC TGA CGA GGC GCCTGG A

CCGGGTGGCTGTGTCGTCAT CGGC | |||| |||| ||| ||| ||| ||||||

TAGCATCATTGGCGC C CGGT TACG ACT GCT TCG TGGGCC C

G TAC ATT- - GTG G GC

GAM1792 CACCATTGATATTGTATTTA 1769 TATTGTATTT 4374 A ATAT TATT A GG

GAAGGTTTCAGGTGGGTGAA AGAAGGTTTC CACC TTG TG TAG AGGTTTCA T

ACCTCCTATTCCATGCGTAA AGGT |||| ||| || ||| ||||||||

GGTG GTGG AAT AC ATC TCCAAAGT G

- GCGT CTT- C GG

GAM1793 TCCTCCGAACCAGCATCCCC 1770 TCTGTGGACA 4375 GA A CCAC TCAA- AAGAC

ACCATCAACATGGAGAACAA TTGACTCGGA TCCTCC ACCAGC TCC CA CATGGAGAAC C

GACCACGTGGTTCTCTGTGG GCTG |||||| |||||| ||| || ||||||||||

ACATTGACTCGGAGCTGGTG AGGAGG TGGTCG AGG GT GTGTCTCTTG /

GAGGA -- - CTCA TACAG GTGCA

GAM1794 CCACCACCTGGAGCCCGAGG 1771 TTCTTCACGG 4376 C GGA- AG T AAGT

AGGTGCTCAAGTACAGCGAG GCAGCAAGCT CCACCA CT GCCCG GAGG GCTC A

TTCTTCACGGGCAGCAAGCT GGTG |||||| || ||||| |||| ||||

GGTGG GGTGGT GA CGGGC CTTC TGAG /

C ACGA A- T CGAC

GAM1795 CACAGAGGCGAGTTTGTGGG 1772 GGGCCATACC 4377 G G CATAC AG TGT- GAG

CCATACCAAGGGATGTGCTG AAGGGATGTG CACAGAGGC AGTTTGT GGC CA GGA GCT C

AGCTGTGGCCTTCTCCTCTG CTGA ||||||||| ||||||| ||| || ||| |||

ACAAGCCGGCAGATTGTCTC GTGTCTCTG TTAGACG CCG GT CCT CGG /

TGTG - G AACA- CT CTTC TGT

GAM1796 GCAGGGACCCCTGCAAGTGT 1773 TGACACGAGG 4378 G GCAA-- TG - - CT

TGGTCGGGGGCCTCGAGCTG GGAGGGGTCT GCA GGACCCCT GTGT G TCGGG GGC C

CCTGAGCTGACACGAGGGGA GTGT ||| |||||||| |||| | ||||| |||

GGGGTCTGTGT TGT TCTGGGGA CACA C AGTCC TCG /
G GGGGAG GT G G AG

GAM1797 TTTTGAGCACAAAACCACCG 1774 TGGAAAGTGA 4379 AG- AAAA GA CC--- CA C
GAGA
GGGATCTAGCCTGTGGCACC GGCGAGA TTTTG CAC CCACCGGG TCTAG TGTGG CC
CG T
CCGGAGATGACACGAGGCTC ||||| ||| |||||||| ||||| ||||| || ||
ACATGACTCTAGACACTTGG AGAGC GTG GGTGGTTC AGATC ACACT GG GC /
TGGAAAGTGAGGCGAGA GGA AAA- AC TCAGT C- A ACAG

GAM1798 GTCTTTGTATTAAAAGTAAG 1775 TTAAAAGTAA 4380 T A A AG - TAC
CCTTATTGTTACAATGCACA GCCTTATTGT GTCT TGT TTA AAGTA CCTT ATTGT A
GTGGAGGACTGCTTATAGAG TACA |||| ||| ||| ||||| |||| |||||
CACAGAC CAGA ACG GAT TTCGT GGAG TGACA A
C A A CA G CGT

GAM1799 TGTCACCATCCTCTGCATTG 1776 TCCCTGGCTT 4381 CA C- AT- C TG CACT C T
ACTTGGGCACTGACATGGTT ATGAGCAGGC TGTCAC TC TCTGC TGA T GG GA ATGGT C
CCTGCCATCTCCCTGGCTTA TGAG |||||| || ||||| ||| | || || |||||
TGAGCAGGCTGAGAGTGACA ACAGTG AG GGACG ATT G CC CT TACCG C
AG TC AGT C GT ---- C T

GAM1800 GGCTGCCAGATGGGACCTCA 1777 GACCTCACTG 4382 G G GA TGAC- ACG- G
CTGACCCAGACGTTCCGGGC ACCCAGACGT GGCT CCA ATGG CCTCAC CCAG TTCCG G
CCGGGAACAGCTGGCAGCTG TCCG |||| ||| |||| |||||| |||| |||||
TGAGGCTCTATGTGGAGCT TCGA GGT TATC GGAGTG GGTC AGGGC C
- G TC TCGAC GACA C

GAM1801 TGGGACTCGTGCCTTCTGCT 1778 TGTCCCAGCT 4383 TCGT T TTCT GTGG
GTTCTCATTGTGGCCAAGAA GAGGGCCTTT TGGGAC GCCTTC GCTG CATT C
ATGTCCCAGCTGAGGGCCTT GTCC |||||| |||||| |||| ||||
TGTCCCA ACCCTG CGGGAG CGAC GTAA C
TTTC T CCT- AGAA

GAM1802 GTGCATCAGCCGGCTTGAGT 1779 AAACTAGCGA 4384 T - G- TG GT ATAT
TTGTTCAATATCAAAGCTGA GGTCTGCTGT GTGCA CAG CC GCT AGTTT TCA C
AAACTAGCGAGGTCTGCTGT AC ||||| ||| || ||| ||||| |||
AC CATGT GTC GG CGA TCAAA AGT A
C T AG -- -- CGAA

GAM1803 CATTGTCGTCATTGGACACG 1780 CGTCATTGGA 4385 GTC-- T- A C ATTC C
TAGATTCGGGCAAGTCCACC CACGTAGATT CATT GTCA TGG CA GTAG GGG A

ACTACTGGCCATCTGATCTA CGGG |||| |||| ||| || |||| |||
TAAATG GTAA TAGT ACC GT CATC CCT A
ATATC CT G - ACCA G

GAM1804 GAAGTTTATTGTCCATAGAG 1781 TTGGATGCTT 4386 A T CATA ACTTA - AA
ACTTAAAGGCAGAAAACCTG GATATGAACA GA GTTTAT GTC GAG AAG GCAG A
CTCTTGGATGCTTGATATGA TC || |||||| ||| ||| ||| ||||
ACATC CT CAAGTA TAG TTC TTC CGTC /
A - ---- GTAGG T CA

GAM1805 GCTAACTAGCAGGGACCCCT 1782 TGAGCTGACA 4387 AACTA G -- AA- G G ACC
GCAAGTGTTAGGTCGGGGGG CGAGGCGGAG GCT GCA GGACCCCT GC GTGTTAG
TCGGG GG T
ACCTCGAGCTGCCTGAGCTG GGGT ||| ||| |||||||| || ||||||| ||||| ||
ACACGAGGCGGAGGGGTCTG CGA TGT TCTGGGGA CG CACAGTC AGTCC TC C
TGTAGC ----- G GG GAG G G GAG

GAM1806 ATGGTGACACACATGCTGGA 1783 TTGGTTCAAG 4388 - ACA- G G- T TA
GCCAAGTGCTAACATGCCTT GGATGGAAAG ATGGT GAC CAT CT GAGCCAAG GC A
GGTTCAAGGGATGGAAAGTC TCAA ||||| ||| ||| || |||||||| ||
AACCGT TGCCA CTG GTA GG CTTGGTTC CG C
A AAAG G AA - TA

GAM1807 TTGTCGTCATTGGACACGTA 1784 TAAATGCGGT 4389 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM1808 GGTGACAACATGCTGGAGCC 1785 TTGGTTCAAG 4390 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1809 TTGTCGTCATTGGACACGTA 1786 TAAATGCGGT 4391 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM1810 GGCAGCGAGTCAGTAACTTT 1787 AGTCAGTAAC 4392 - G A TTAA AG GT
AAGCCAGGTGTATATGCGGT TTTAAGCCAG GGCAG CGA TCAGT ACT GCC GT A

GTCAGTCACTGGTCGCCTGC GTGT ||||| ||| ||||| ||| ||| ||
C CCGTC GCT GGTCA TGA TGG CG T
C - C CTG- -- TA

GAM1811 TGTCTCTTATCATGTTGGTG 1788 CATTGCTGGC 4393 TAT-- - TG GGA C
GAGGTGGCCGCAGCCATTGC TATGTGTTTA TGTCTCT CAT GT GT GGTGGC G
TGGCTATGTGTTTAGAGATA GAGA ||||||| ||| || || ||||||
ATAGAGA GTA CG CG TTACCG C
TTTGT T GT --- A

GAM1812 TTGTCGTCATTGGACACGTA 1789 TAAATGCGGT 4395 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM1813 GGTGACAACATGCTGGAGCC 1790 TTGGTTCAAG 4394 AA--- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAA GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAAGTCAC GTCA |||||| ||| || |||||||| ||
C CCACTG GTA GG CTTGGTTC CG C
AAAAG G AA - TA

GAM1814 GGTGACAACATGCTGGAGCC 1791 TTGGTTCAAG 4396 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1815 GGTGACAACATGCTGGAGCC 1792 TTGGTTCAAG 4397 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1816 TTGTCGTCATTGGACACGTA 1793 TAAATGCGGT 4398 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM1817 TTGTCGTCATTGGACACGTA 1794 TAAATGCGGT 4399 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||

AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM1818 TTCAGGCCTTCCAGTTCACT 1795 TGTCCAGCTG 4400 GC T CACT AA GG
GACAAACATGGGGAACGTGT GTGGAACTGG TTCAG CT CCAGTT GAC ACATG G
GTCCAGCTGGTGGAACTGGA A ||||| || |||||| ||| |||||
AGGTC GG GGTCGA CTG TGTGC /
AA T C--- -- AA

GAM1819 GGTGACAACATGCTGGAGCC 1796 TTGGTTCAAG 4401 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC ||||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1820 GGCCAATTGAAACAAACAGT 1797 TATTAGGGAT 4402 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1821 GGCCAATTGAAACAAACAGT 1798 TATTAGGGAT 4403 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1822 TGAAGCTGACGAAATGTTAA 1799 ACGAAATGTT 4404 A GAC- - - CCG A C
GCCGTGGATTCAAGGACCAG AAGCCGTGGA TGA GCT GAA ATGTTA AG TGG TT A
ATCTATGACATATTCCAAAA TTCA ||| ||| ||| |||||| || ||| ||
GCTCA ACT CGA CTT TACAGT TC ACC AG A
- AAAC A A TAG - G

GAM1823 GCGAGCAGTCTGAATGCCAG 1800 TTTTGCTACA 4405 CT- ----- A
AATGGATAACCGTTTTGCTA GCATTTGTAA GCGAGCAGT GAATGC CAGAATGG T
CAGCATTTGTAATTGCTTGT TTGC ||||||||| |||||| ||||||||
TGTTCGTTA TTTACG GTTTTGCC A
ATG ACATC A

GAM1824 GCCAGCACGCCAAGTACACT 1801 TGAAGAGACG 4406 CACG AAG - - CTG- CA
TGCTCTTTCTGTGGCAAAAC AGCTGTGGGG GCCAG CC TACA CTTG CTCTTT TGG A

CAAGATGAAGAGACGAGCTG ATCT ||||| || |||| |||| |||||| |||
TGGGGATCTGGC CGGTC GG GTGT GAGC GAGAAG ACC /
TA-- G-- C A TAGA AA

GAM1825 TTGTCGTCATTGGACACGTA 1802 TAAATGCGGT 4407 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM1826 CAGGAAGAGCTGGTGTCCAA 1803 CCAGATCGGG 4408 A GG - AAC- G AC
CCTGGGGACGATTGCCAGAT GTCAAAGGCC CAGGAAG GCT TG TCC CTGG G G
CGGGGTCAAAGGCCTTCCTG TTCC ||||||| ||| || ||| |||| |
GTCCTTC CGG AC GGG GACC T /
- AA T GCTA G TA

GAM1827 CTGCTGTTCTTGCCCAAGAG 1804 TGTTCTTGCC 4409 C----- CCA AG - TGA
TGTGTCTGACTATGACGGCA CAAGAGTGTG CTGCTGTT TTGC AG TGT GTC C
AACTGAGCAACTTCAAAACA TCTG |||||||| |||| || ||| |||
GCAG GACGACAA AACG TC ACG CAG /
AACTTC AG- AA G TAT

GAM1828 CGAAAAGGGGGAGTCATCTG 1805 AGGGGGAGTC 4410 A ---- - TCT AAT
GCAAAAATGTCACTTTGCCT ATCTGGCAAA CGAA AGGGG GAGT CA GGCAAA G
GCTGTATTCAAGGCTCCTAT AATG |||| ||||| |||| || ||||||
TCG GCTT TCCTC CTTA GT CCGTTT T
A GGAA T CGT CAC

GAM1829 TCCATCGGGCAGCCAGAGGC 1806 ACTGAGCACC 4411 G A---- AG - C TC
CAGCGTCTCCGATGACACTG TGGTGAATGG TCCATC GGC GCCAG GC CAG GTC C
AGCACCTGGTGAATGGCCGG CCGG |||||| ||| ||||| || ||| |||
ATGGA AGGTAG CCG TGGTC CG GTC CAG G
G GTAAG CA A A TA

GAM1830 CTGGGGGCTTTAGCTGTTGG 1807 GACCTTGGTG 4412 G TTA --- G GTGTTCTTA
CAGCTATGGTGTTCTTAATC TAGACTCCAG CTGGGG CT GCT GTT GCAGCTATG A
CATTTCACATAGTTGTAGAC |||||| || ||| ||| |||||||||
CTTGGTGTAGACTCCAG GACCTC GA TGG CAG TGTTGATAC /
A TG- TTC A ACTTTACCT

GAM1831 GAACATGTTGCTGGTAATCT 1808 TGCTGGTAAT 4413 AT G - AATCTTT G AGGC
TTCCAGGGTAGGAGGCTTCA CTTTCCAGGG GAAC GTT CTG GT CCAGG TAGG T
CACTTAGCCTGGCTCAGCAC TAGG |||| ||| ||| || ||||| ||||

AGGAACGTTC CTTG CAA GAC CG GGTCC ATTC T
-- G A ACTC--- G ACAC

GAM1832 TGAAACAGACTGGGCCAATG 1809 TATCAAGGAA 4414 C -- CACAAAGAA - CA-
ACCGAT
TCCACAAAGAATTCCTGGTC GGGCAGGCGT TGAAACAGA TGGGCCA ATGTC TTCCT
GGT GCACC G
AGCACCACCGATGTCCAAAG GATG |||||||| ||||||| ||||| ||||| ||| |||||
GTGCAATATCAAGGAAGGGC GTTTTGTTT ATTCGGT TGCGG AAGGA CTA
CGTGG /
AGGCGTGATGGCTTATTTGT - AG ACGGG---- A TAA AAACCT
TTTG

GAM1833 TGCAGGAGTCTTGGAGGGTC 1810 CGTGGCGGAA 4416 GA T G --------- GG G
GGATGCGGCGCCGGATGAGG GATGCGTTTG TGCAG GTCT G AGGGTCGGATGCG
GCGCC AT A
ATGAGGCGTGGCGGAAGATG GCTC ||||| |||| | |||||||||||| ||||| ||
CGTTTGGCTCTGCAGACACT ACGTC CAGA C TCTCGGTTTGCGT TGCGG TA G
GCA A- - G AGAAGGCGG AG G

GAM1834 GGGGACTCTGGGAGGCTGGT 1811 TGACAGCCTT 4415 -- - GTGC- GAA
GCAGCCAGAAGGCATGGCTC CTAGTAGAAT GGGGA CT CTGGGAGGCTG AGCCA G
TTGACAGCCTTCTAGTAGAA CTCT ||||| || |||||||||| |||||
TCTCT TCTCT GA GATCTTCCGAC TCGGT /
AA T AGTTC ACG

GAM1835 CGCTTCCGCCGGGTGGACAT 1812 TGTGGACGAG 4417 G GG GGACA G G ACG
CGACGAATTTGACGAGAACA CAGGAGGAGG CGCTTCC CC GT TC AC AATTTG A
AATTGTGGACGAGCAGGAGG CG ||||||| || || || || |||||
AGGCG GCGGAGG GG CG AG TG TTAAAC /
A A- AGC-- G - AAG

GAM1836 GGCCAATTGAAACAAACAGT 1813 TATTAGGGAT 4418 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1837 GGCCAATTGAAACAAACAGT 1814 TATTAGGGAT 4419 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1838 TTTGATGTGGTCCCTACGTT 1815 TGAGCCCGTT 4420 TG -- CCCT-- TT CCAGT
TTCGTTCCAGTGCATTATGA TGTCAGCCGC TT A TGTGGT ACG TTCGTT G
TGAGCCCGTTTGTCAGCCGC AGAT || | |||||| ||| ||||||
AGATTGAA AA T ACGCCG TGC GAGTAG C
GT AG ACTGTT CC TATTA

GAM1839 GGTGACAACATGCTGGAGCC 1816 TTGGTTCAAG 4421 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1840 GCTGCTGCTGGAAATGCTGA 1817 TGCTGGAAAT 4422 T-- G T T CT AACCCA
CTTTTAACCCACACAAGCGA GCTGACTTTT GCTGC GCT GAAA GC GA TTT C
ATCTCTGCCTTTCGAGCTCT AACC ||||| ||| |||| || || |||
GCAGC CGACG CGA CTTT CG CT AAG /
TCT G C T CT CGAACA

GAM1841 GGTGACAACATGCTGGAGCC 1818 TTGGTTCAAG 4423 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1842 GGGTACGTGCCAAGCATCCT 1819 AAGCATCCTC 4425 C---- ----- TC G GA AG
CGCGCGACCCGAGAGCCTGG GCGCGACCCG GGGTA GTGCCA AGCA CTC CGC CCCG
A
GGAGCGGGGGTTTGCTGGCC AGAG ||||| |||||| |||| ||| ||| ||||
GTGGCACTCATTTACCC CCCAT CACGGT TCGT GGG GCG GGGT G
TTACT GCCGG TT G AG CC

GAM1843 GGAGACAGGGAGAGGCTCTT 1820 ACGGAGCATG 4424 - A A GC - GTA GTT GAG
CTGTGTGTAGTGGTTGTGCA AGAAGACGTT GG AG CAGGG GAG TCTTCT GTGT GTG
GTGCA C
GAGCCTCATGCATCACGGAG CCCC || || ||||| ||| |||||| |||| ||| |||||
CATGAGAAGACGTTCCCCTG CC TC GTCCC CTT AGAAGA TACG CAC TACGT C
CTGCC G - - GC G AGG --- ACT

GAM1844 GAAACAGACTGGGCCAATGT 1821 TATCAAGGAA 4426 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G

GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM1845 GAAACAGACTGGGCCAATGT 1822 TATCAAGGAA 4427 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM1846 GCTGCCATCTTCCCAGTATT 1823 TGGCTCCCAG 4428 CCA C--- ATT G A C G
TCTTGGACAGTCCCAGGAAC GAGGACATCA GCTG TCTTCC AGT TCTTG AC GTC CAG A
TTGAGGCGGTGCAGGGTGGC GC |||| |||||| ||| ||||| || ||| |||
TCCCAGGAGGACATCAGC CGAC AGGAGG TCG GGGAC TG CGG GTT A
TAC ACCC GT- G G A C

GAM1847 TCTTGTGTTGAGACTTCGTG 1824 TACACCACTC 4429 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM1848 ACCGCTCCACGAGCCTGGAG 1825 GCAACAGTGG 4430 GC A- A A- CGGA GA C
AGCTCGGACTGCGAGTCCCT CTTCGGGCCG ACC TCC CG GCCTGGAG GCT CTGC GTC C
GGACAGCAGCAACAGTGGCT GAGG ||| ||| || |||||||| ||| |||| |||
TCGGGCCGGAGGAAGGT TGG AGG GC CGGGCTTC TGA GACG CAG T
A- AG - GG CAAC A- G

GAM1849 GCAGGTATGTGATGACATCA 1826 TGACATCAGC 4431 G TG A----- G G--- G C
GCCGACGCCTGGCACTGCTG CGACGCCTGG GCAGGTAT TGA AC TCAGCC AC CCTG CA
T
CAGGAACAGTGGGCTGGAGG CACT |||||||| ||| || |||||| || |||| ||
AAAGTTGTCAATACCTGT TGTCCATA ACT TG GGTCGG TG GGAC GT G
- GT AAAGGA G ACAA - C

GAM1850 GGTCATTGTGCCCTGCCAAG 1827 TTCCTTTTCA 4432 T TTG G- A A G G - GA
GCACAGCGTAGATCTGGAAA GATGTGGCTG GG CA TGCCCT CCA GGC CAGC TA
ATCTGGAAAG AGCA A
GAGCAGAATGTGTTCCTTTT GTCA || || |||||| ||| ||| |||| || |||||||||| ||||
CAGATGTGGCTGGTCATGGA CC GT ACGGGG GGT CTG GTCG GT TAGACTTTTC
TTGT /

AGGGGCAGTTGTCC T TG- AA A - - G C GT

GAM1851 TGCTACTATTTTATTGCCCG 1828 TATTTTATTG 4433 ACTA T GA GG- T
AGGTGGGGGTGTATGCACCG CCCGAGGTGG TGCT TTTTAT GCCC GGTG GGTG A
CACACCGGGGCTATGAGAAG GGGT |||| |||||| |||| |||| ||||
CA ACGA AGAGTA CGGG CCAC CCAC T
---- T G- ACG G

GAM1852 GTTGCACAGCCACAGACTTC 1829 CATTGTGAAG 4434 AGCCAC T GCACAGA AC
TCAGCACAGAGTGGGGACTG TCTCTTATGG GTTGCAC AGACTTC CA GTGGGG T
CCTTCCATTGTGAAGTCTCT TGCA ||||||| ||||||| || ||||||
TATGGTGCAGC CGACGTG TCTGAAG GT TACCTT G
GTATTC T ------- CC

GAM1853 TCTACAAAGTGCCGTCCACT 1830 TCCAATCTGA 4435 A - - CACTG CT- C
GAGACTGAGGCCTTGGCTTC TGGGCATGTT TCT CAAA GTGCC GTC AGA GAGGC T
CAATCTGATGGGCATGTTTG TGAG ||| |||| ||||| ||| ||| |||||
AGA AGA GTTT TACGG TAG TCT CTTCG T
- G G ----- AAC G

GAM1854 GGTGCCGGCAACCTTGGTGA 1831 TGTCTTGCTC 4436 AAC T -- CT A ACG
CCTTGAGCACGTTGAAGCGC AGAGGCCGGC GGTGCCGGC CT GGT GAC TG GC T
ACTGTCTTGCTCAGAGGCCG ACT ||||||||| || ||| ||| || ||
GCACT TCACGGCCG GA TCG CTG AC CG T
GA- C TT TC G AAG

GAM1855 TTAGTTGATATATCCTATGG 1832 TATTGAGTTA 4437 T TA CT GG---- AA
TGGTGAAAATGGATTCAACG TCTACTGA TTAGT GATA TC ATGGT TGAA T
CAAGCTATTGAGTTATCTAC ||||| |||| || ||||| ||||
TGA AGTCA CTAT AG TATCG ACTT G
T TG T- AACGCA AG

GAM1856 ATGGTGACAACATGCTGGAG 1833 TGGGTCCAAG 4438 AA-- G -- G T TA
CCAAGTGCTAACATGCCTTG GGATGGAAAG ATGGTGAC CAT CT GGA CCAAG GC A
GGTCCAAGGGATGGAAAGTC TCAC |||||||| ||| || ||| ||||| ||
ACCGT TGCCACTG GTA GG CCT GGTTC CG C
AAAG G AA G - TA

GAM1857 GTGACAACATGCTGGAGCCA 1834 TTTCAAGGGA 4439 AA--- G -- T TA
AGTGCTAACATGCCTTGGTT TGGAAAAGTC GTGAC CAT CT GGAGCCAAG GC A
TCAAGGGATGGAAAAGTCAC AC ||||| ||| || ||||||||| ||
CACTG GTA GG CTTTGGTTC CG C
AAAAG G AA - TA

GAM1858 TTGTCGTCATTGGACACGTA 1835 TAAATGCGGT 4440 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM1859 GGTGACAACATGCTGGAGCC 1836 TTGGTTCAAG 4441 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGCAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGCAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AACG G AA - TA

GAM1860 ATTTGAGAAGGAGGCTGCTG 1837 CTTCAAGTAT 4443 TG AGG - GA T AAA
AGATGGGAAAGGGCTCCTTC GCCTGGGTCT ATT AGA AGGC TGCT GA GGG G
AAGTATGCCTGGGTCTTGGA TGGA ||| ||| |||| |||| || |||
T TAG TCT TCCG ATGA CT CCT /
GT GGG T A- T CGG

GAM1861 ATGGTGACAACATGCTGGAG 1838 TTGGTTCAAG 4442 AA-- G G- T TA
CCAAGTGCTAACATGCCTTG GGATGGCAAG ATGGTGAC CAT CT GAGCCAAG GC A
GTTCAAGGGATGGCAAGTCA TCAC |||||||| ||| || |||||||| ||
CCGT TGCCACTG GTA GG CTTGGTTC CG C
AACG G AA - TA

GAM1862 GGTGACAACATGCTGGAGCC 1839 CTTGGCTTCC 4444 AA-- G - - T TA
AAGTGCTAACATGCCTTGGC AAGGATGGAA GGTGAC CAT CT GGA GCCAAG GC A
TTCCAAGGATGGAAAGTCAC AGTC |||||| ||| || ||| |||||| ||
C CCACTG GTA GA CCT CGGTTC CG C
AAAG G A T - TA

GAM1863 ATGGTGACAACATGCTGGAA 1840 TTGGTTCAGG 4445 AA-- G G- G T TCA
GCCAAGTGCTCAACATGCCT GGATGGAAAG ATGGTGAC CAT CT GAA CCAAG GC A
TGGTTCAGGGGATGGAAAGT TCAC |||||||| ||| || ||| ||||| ||
CACCGT TGCCACTG GTA GG CTT GGTTC CG /
AAAG G GA - - TAC

GAM1864 GAAGCTGAAGAAGCCGCCCT 1841 AAGAAGCCGC 4446 CTG A - TG TT C C G
GGTTGCACATGCCGTCGGCC CCTGGTTGCA GAAG AAGA GCCGCC C G GCA ATGC GTCG C
ATGACTGTGTATGCTCTGGT CATG |||| |||| |||||| | | ||| |||| ||||
GGTGGTGTCTTACTTC CTTC TTCT TGGTGG G C CGT TGTG CAGT C
A-- G T GT T- A T A

GAM1865 GCCATCCCGGGCAGTGGGCA 1842 GCACGGTGGT 4450 GGG CAAA ATACC CCA
CCGTCAAAGTATACCTGCCC GACTGTCCGG GCCATCCCGGGCAGT CACCGT GT TGC A
AACAAGCAACGCACGGTGGT GATG |||||||||||||| |||||| || |||
GACTGTCCGGGATGGC CGGTAGGGCCTGTCA GTGGCA CA ACG /
GTG CG-- ----- AAC

GAM1866 AGGAGGACGCGCTGCCCGGC 1843 GAGAGTACTC 4451 ------ G- G CAGAAAA AA
CAGAAAACGGAGTTCAAGGT CTGCGTCTTC AGGAGGACGC GCT CCC GC CGGAGTTC
G
GGACTCCGACGACCAGTGGG CT |||||||||| ||| ||| || ||||||||
GAGAGTACTCCTGCGTCTTC TCCTTCTGCG TGA GGG TG GCCTCAGG /
CT TCCTCA GA G ACCAGCA TG

GAM1867 CGGCTCCGAGAGCAGGTTCT 1844 TACACATTGA 4452 - AGAG C A TC GCAG C
TCGTGAGTTCCTCGCAGGGC GAACCTGAAC CGGC TCCG CAGGTTCTT GTG GT CTC GG
C
CGGTCAGAGCTACACATTGA ATGG |||| |||| ||||||||| ||| || ||| ||
GAACCTGAACATGGAGGCCG GCCG AGGT GTCCAAGAG TAC CA GAG CT G
G ACAA T A TC A--- G

GAM1868 TGATGCGCAAGGCCATCCGA 1845 TCTGGAGAAA 4453 T - A GCCA G ACC AAA
GGGCACCTGGAAAACAACCC CTGCTGCCTC TGA GC GCA G TCC AGGGC TGG A
AGCTCTGGAGAAACTGCTGC A ||| || ||| | ||| ||||| |||
CTCA ACT CG CGT C AGG TCTCG ACC C
C T - AAAG - --- CAA

GAM1869 GTAGAGCTTTATGCTGAAAA 1846 GAGCTTTATG 4454 - TA GAAAA - T A
GGTGGCCACTAGAGGTCTGT CTGAAAAGGT GTAGAG CTT TGCT GGTGGC CAC AG G
GTGCCATTGCCCAGGCAGAG GGCC |||||| ||| |||| |||||| ||| ||
TCTCTGC CGTCTC GAG ACGG TTACCG GTG TC G
T -- ACCCG T - T

GAM1870 GATGCCAGAAGTCCGGGGAG 1847 CAACAGGAAG 4455 T- CAGA G GC- GC
CCTTGTTGGTGCAAATGCCA TTTTGGGACT GA GC AGTCC GGGA CTTGTTGGT A
ACAGGAAGTTTTGGGACTAA AAGC || || ||||| |||| |||||||||
GCCTTC CT CG TCAGG TTTT GGACAACCG A
TC AA-- G GAA TA

GAM1871 TCCTGTAGTGTTCCTGGAGA 1848 CATCAATTAA 4456 - T- CCTG GA C - A
AGCTAGAGCCTGATTGTAGG CTTCTACAGT TC CTGTAG GTT GA AG TAG AGCCTG T
CTACTACTCATCAATTAACT GG || |||||| ||| || || ||| ||||||
TCTACAGTGG GG GACATC CAA CT TC ATC TCGGAT T
T TT TTAA AC - A G

GAM1872 GGTGACAACATGCTGGAGCC 1849 TTGGTTCAAG 4457 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1873 TTGTCGTCATTGGACACGTA 1850 TAAATGCGGT 4458 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM1874 TGTCACCATCCTCTGCATTG 1851 TCCCTGGCTT 4459 CA C- AT- C TG CACT C T
ACTTGGGCACTGACATGGTT ATGAGCAGGC TGTCAC TC TCTGC TGA T GG GA ATGGT C
CCTGCCATCTCCCTGGCTTA TGAG |||||| || ||||| ||| | || || |||||
TGAGCAGGCTGAGAGTGACA ACAGTG AG GGACG ATT G CC CT TACCG C
AG TC AGT C GT ---- C T

GAM1875 GGTGACAACATGCTGGAGCC 1852 TTGGTTCAAG 4461 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1876 ATTTGAGAAGGAGGCTGCTG 1853 CTTCAAGTAT 4460 TG AGG - GA T A
AGATGGGAGAGGGCTCCTTC GCCTGGGTCT ATT AGA AGGC TGCT GA GGGAG G
AAGTATGCCTGGGTCTTGGA TGGA ||| ||| |||| |||| || |||||
T TAG TCT TCCG ATGA CT TCCTC G
GT GGG T A- - G

GAM1877 GAGGAGGGGAGATTCAGTGT 1854 CAGCAGTGAG 4462 ---- G - T GA GA TG
GGTGGGGGACTGAGTGTGGC GGTCTCTCTC GAGGAGGGGAGA TTCA TG TGG GGGG CT G
T
AGGGACTCCCCAGCAGTGAG TTCC |||||||||||| |||| || ||| |||| || |
GGTCTCTCTCTTCCTC CTCCTTCTCTCT GAGT AC ACC CCTC GG C /
CTGG G G - AG A- GG

GAM1878 GGCCAATTGAAACAAACAGT 1855 TATTAGGGAT 4463 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /

CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1879 AGGTCTAGTGCATCTTTTAA 1856 GTGCATCTTT 4464 CT TCTTTTAACC A- - CCTT
CCAGCCGAATGGAGTCCTTT TAACCAGCCG AGGT AGTGCA AGCCGA TGG AGT T
ACAAACTGCCGACTTGGCTC AATG |||| |||||| |||||| ||| |||
AACAAACTGCATTACCT TCCA TTACGT TCGGTT GCC TCA /
-- CAAACAAC-- CA G AACA

GAM1880 GCCAGCACGCCAAGTACACT 1857 TGAAGAGACG 4465 CACG A CA - CTG- CA
TGCTCTTTCTGTGGCAAAAC AGCTGCGTGG GCCAG CCA GTA CTTG CTCTTT TGG A
CAAGATGAAGAGACGAGCTG ATCT ||||| ||| ||| |||| |||||| |||
CGTGGATCTGGC CGGTC GGT CGT GAGC GAGAAG ACC /
TA-- G C- A TAGA AA

GAM1881 GTGGATCCTGCATGAAGACA 1858 TGTCACGGTA 4466 CC ATGAA CTGAC CC GA
GTGGCTGACGGTGCCTGGAC AAGTCCGC GTGGAT TGC GACAGTGG GGTG TG C
GTACAATACCACTTCCGCTG |||||| ||| |||||||| |||| ||
TCACGGTAAAGTCCGC CGCCTG ATG CTGTCGCC CCAT AC G
AA GCA-- TTCA- A- AT

GAM1882 GAGTCTCGCTCTGTTGCCCA 1859 TCTCGCTCTG 4467 TC C TT C-- -- - A A
GGCTGGAGTGCAGTGGCATG TTGCCCAGGC GAG TCGCT TG GCCCAGG TGGAG
TGCAGTG GC TG T
ATCTCGGCTCACTGCAACCT TGGA ||| ||||| || ||||||| ||||| ||||||| || ||
CTGCCTCCTGGGTTCAAGCG CTC AGCGA AC TGGGTCC GTCTC ACGTCAC CG GC C
ATTCTC TT - T- TCC CA T - T

GAM1883 GTGTGTTGTTGTGGGCGATG 1860 TGTTGTGGGC 4468 G T CGAT-- T- - GG
GTGCTGTTGGTAAAACATGT GATGGTGCTG GT TGTTGT GTGGG GG GC TGTT T
CTCCTGATATCCTACACAAC TTGG || |||||| ||||| || || ||||
AAAC CA ACAACA CATCC CC TG ACAA /
A - TATAGT TC T AA

GAM1884 TTGCGGCATCCACGAGACCA 1861 TGACGTGGAC 4469 CA- AGAC - ACTC
CCTTCAACTCCATCATGAAG ATCCGCAA TTGCGG TCCACG CAC CTTCA C
TGTGACGTGGACATCCGCAA |||||| |||||| ||| |||||
AACGCC AGGTGC GTG GAAGT /
TAC A--- T ACTA

GAM1885 TCTTGTGTTGAGACTTCGTG 1862 TACACCACTC 4470 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G

ATAA AACCC - GAAGAA

GAM1886 TGGAGCCACTCCCTGACTAC 1863 TCCATGGGTT 4471 GCCA ----- A A - C- GGA
AAGGACCCCCGGCGGACAGA ATACACGGGA TGGA CTCCC TGACT CA GGAC CC CGGC
C
GCTGATGGTGTCCATGGGTT GGAG |||| ||||| ||||| || |||| || ||||
ATACACGGGAGGAGATCCA ACCT GAGGG ATTGG GT CCTG GG GTCG /
AGAG CACAT - A T TA AGA

GAM1887 CCCTACCAGAGGAGGTACCG 1864 TGTGAAGAGC 4473 - A -- A GGA--- TGACAGC
GGAGCGCCGTGACAGCGATA GGAGCCCATC CC CT CCAGAGGA GGT CCG GCGCCG G
CATACCGGTGTGAAGAGCGG CTTT || || |||||||| ||| ||| ||||||
AGCCCATCCTTTGGAGAGG GG GA GGTTTCCT CCG GGC TGTGGC A
A - AC A GAGAAG CATACAT

GAM1888 CCAGGTCTTGTAGCAGCGCC 1865 CAGCAGCCGG 4472 G - T A A --- C GAGAA
TCCTCGAGAAGCCAACAGAG AGTGTGG CCA G TCT GT GC GCGC CT CTC G
CAGTAAGCGCAGCAGCCGGA ||| | ||| || || |||| || |||
GTGTGG GGT T AGG CG CG CGCG GA GAG C
G G C A A AAT C ACAAC

GAM1889 GATTGTGGGGAACCTGGGTG 1866 GGGAACCTGG 4474 --- - TGAAGGCA A ---
GG
AAGGCACCTTTGGCAAGGTG GTGAAGGCAC GATTGTG GGG AACCTGGG CCTTTGGCA
GGT GGT A
GTGGAGTGCTTGGACCATGC CTTT ||||||| ||| |||||||| ||||||||| ||| |||
CAGAGGGAAGTCTCAGGTTG CTAGCAC CCC TTGGACTC GGAGACCGT CCA TCG
/
CCCTGACACGATC AGT G TGAAG--- A GGT TG

GAM1890 TCTGGAGGAGCAGTTGTCTG 1867 GAGGAGCAGT 4475 - A GT TC GAGAAG - GT
ATGAAGAGAAGGTGCGTATA TGTCTGATGA TCT GGAGG GCA TG TGATGAA G TGC A
GCAGCAAAATTCATCATTCA AGAG ||| ||||| ||| || ||||||| | |||
TGCCCCTCCTGGA AGG CCTCC CGT AC ACTACTT C ACG /
T C -- TT AAAA-- G AT

GAM1891 TTTCAGGGTAATGATGCACC 1868 AGTGCAGAAA 4476 TGA-- C TGAACA
TGTTGAACAAGAAATTACAG CTTACTTTGA TTTCAGGGTAA TGCAC TGT A
TGCAGAAACTTACTTTGAAA AA |||||||||| ||||| |||
AAAGTTTCATT ACGTG ACA /
CAAAG - TTAAAG

GAM1892 TGGTAAAATTGCATGGGTTT 1869 AATTGCATGG 4477 G GGG G A TT

GTAGGTACTTTTGGAATCTA GTTTGTAGGT TGGTAAAATT CAT TTT TAGGT C T
GAAGAAATGAAATTTTACCA ACTT |||||||||| ||| ||| ||||| |
ACCATTTTAA GTA GAA ATCTA G /
A AA- G A GT

GAM1893 TCCCAGCTCACTCAGCTGGA 1870 ACTCAGCTGG 4478 CA- CA A A- - AA G
GCTGAAGGGGAACTGCTTGG AGCTGAAGGG TCC GCT CTCAGCTGG GCTG AGG GG CT C
ACCGCCTGCCAGCCCAGCTG GAAC ||| ||| ||||||||| |||| ||| || ||
GGCCAGTGTCGGA AGG TGA GGGTCGACC CGAC TCC CC GG T
CTG CC - CG G A- T

GAM1894 TGTGGTTATCTCCTCAGATG 1871 ATGGAACCCT 4479 TTATC T T - TTG- C G
GCCAGTTGCCCTCTCAGGCT GCGCCTCTGG TGTGG TCC CAGA GGC CAG CC TCTCAG C
CCTGGGATGGAACCCTGCGC GATC ||||| ||| |||| ||| ||| || ||||||
CTCTGGGATCTCACA ACACT AGG GTCT CCG GTC GG AGGGTC T
CT--- - - C CCAA T C

GAM1895 TGGGGTGGCAGGTATTAGGG 1872 TGGGCAGACT 4480 -- - GATAATA T CTT
ATAATATTCATATAGCCTTC TGGTGACCTG TGGGGT GGCAGGT ATTAGG TTCA ATAGC C
TGAGCTATCTGGGCAGACTT TCGA |||||| ||||||| |||||| |||| |||||
GGTGACCTGTCGAACTCCA ACCTCA CTGTCCA TGGTTC GGGT TATCG /
AG G AGAC--- C AGT

GAM1896 AGATGCTGACAATACTTGGG 1873 TGACAATACT 4481 GA AC--- AAC- GA
AACCTGAAGAAAATTTAGAT TGGGAACCTG AGATGCT CAAT TTGGG CTGAA A
TGTCCAGAATTGATTGAAGC AAGA ||||||| |||| ||||| |||||
GTTT TTTGCGA GTTA GACCT GATTT /
A- GTTAA GTTA AA

GAM1897 TGCTGCTGACAAACCAAGAG 1874 ACCAAGAGGA 4482 - ACAA GAGG GC- A C
GATTTGCCAGAGGTCTTGAT TTTGCCAGAG TGCTG CTG ACCAA ATTT CAG GGT T
CCTGAAAGAATAATTGGTGC GTCT ||||| ||| ||||| |||| ||| |||
CACAGACAGCA ACGAC GAC TGGTT TAAG GTC CTA T
A ACCG AA-- AAA - G

GAM1898 AAGATAGAGGCAGAACTGCA 1875 TGTTCTGGAG 4483 GA----- AA G TG
GGACATCTGCAATGATGTTC CTGTTGGACA AAGATA GGCAG CT CAGGACATC C
TGGAGCTGTTGGACAAATAT AATA |||||| ||||| || |||||||||
CTT TTCTAT TTGTC GA GTCTTGTAG A
AAACAGG -- G TA

GAM1899 CAGTGCTGGCCTGGAAGCCC 1876 AAGGAGCTGG 4484 - GG-- ---- C- AAG G
CTCAAGTCGGGTATGAAGGA CCGTGTTCCG CAGTG CT CCTGGAA GCC CTC TCG G

GCTGGCCGTGTTCCGGGAGA GGAG ||||| || ||||||| ||| ||| |||
AGGTCACTG GTCAC GG GGGCCTT CGG GAG AGT T
T AAGA GTGC TC GA- A

GAM1900 CAGAGAAACTATGGGACACA 1877 TTGAAGCATA 4485 A AA G- A A GA GT AA-
A
GATATGTTGAAGTATTCAAG CTGGTCCAAA CAG GA CTAT GGAC CAG TATGTT AGTATTCAA
CA CA C
TCAAACAACGTTGAAATGGA TAGT ||| || |||| |||| ||| |||||| ||||||||| || ||
TTGGGTGTTGAAGCATACTG GTC CT GATA CCTG GTC ATACGA TTGTGGGTT GT GT
G
GTCCAAATAGTCCTG - -- AA - - AG AG AAA T

GAM1901 GGCCAATTGAAACAAACAGT 1878 TATTAGGGAT 4486 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1902 CCTGCCAAAAGAGCTCATGT 1879 AAGAGCTCAT 4487 - AGAG ATG G A A- A
TGTGCCACCACCAAGAGGAA GTTGTGCCAC CCTG CCAAA CTC TT TGCC CC CC A
GGGGCAGGGGAGGATTTGGA CACC |||| ||||| ||| || |||| || ||
CAGG GGAC GGTTT GAG GG ACGG GG GG G
A AG-- --- G - AA A

GAM1903 GATGGTAATATTCTATCCTT 1880 TAGAAGACAA 4488 TAT C-- ATG- A CAA AT CT
ATGACACTATTGCAACCAAA TGGATTACCA GATGGTAA TCTAT CTT AC CTATTG CCAA
TGG T
TTGGCTTTACCATCTTGGCT TC |||||||| ||||| ||| || |||||| |||| |||
TTAGTAGGTATAGAAGACAA CTACCATT AGGTA GAA TG GATGAT GGTT ACC /
TGGATTACCATC --- ACA GATA - TTC CT AT

GAM1904 ATGGTGACAACATGCTGGAG 1881 TTCACAGGAT 4489 T AA-- G - GCT
CCAAGTGCTACATGGCTTGG GGCAAGTCCC ATGG GAC CAT CTG GAGCCAAGT A
TTCACAGGATGGCAAGTCCC CGT |||| ||| ||| ||| |||||||||
CGT TGCC CTG GTA GAC CTTGGTTCG C
C AACG G A GTA

GAM1905 CCAGCTATCCGGAGGGGTTT 1882 CGGAGGGGTT 4490 - ATCC-- - TT- G AT
CCAGGTATATAAGCATGGTG TCCAGGTATA CCA GCT GGAGGG GT CCA GT A
TGCGCCTTCCTGCCACAGCA TAAG ||| ||| |||||| || ||| ||
TGG GGT CGA CCTTCC CG GGT CG T
A CACCGT G TGT A AA

GAM1906 GGGGTTTGTGGAGCGCTGTG 1883 GTGAAGCTAC 4491 GT A CTG - GTCCA - T
TA
GGAGCGTCCAGCCTGGGTGT TCAATACGCG GGG TTGTGG GCG TGGG AGC GCC TGGG
GTCGT C
CGTTACTTGCGGCTCCGTGG CCAC ||| |||||| ||| |||| ||| ||| |||| |||||
TGAAGCTACTCAATACGCGC CCT AACACC CGC ACTC TCG TGG GCCT CGGCG /
CACAACGTCC GC G ATA A AAG-- T - TT

GAM1907 GTGCCTCTTGTCCGTGGCCG 1884 TCGAAGGTCA 4492 TT C- G- T AG G
TGACGTTCAGGATGCCGTTG CTCGATCTGG GTGCCTC GTC GTGGCC TGACG TC GATGCC
T
GCATCGATTGTCGAAGGTCA GGCA ||||||| ||| |||||| ||||| || ||||||
CTCGATCTGGGGCAC CACGGGG TAG CACTGG GCTGT AG CTACGG /
TC CT AA T -- T

GAM1908 GAGACTCTTCCAGGTCAAAG 1885 AGGTACCTGT 4493 GA T A - GG T C
GGCGGCGTGTGGTCCGTGCC GTCCTGGGAG GA CTCTTCCAGG CA AGG GC CG GTGGT C
ACCGAGGTACCTGTGTCCTG AGCT || |||||||||| || ||| || || |||||
GGAGAGCTTC CT GAGAGGGTCC GT TCC TG GC CACCG G
TC T G A GA - T

GAM1909 CTTGTGGGAGAGATTATCAA 1886 TGGGAGAGAT 4495 T GA ATC -------- - G A AT
GCGTTTTGAGCAGAAAGGAT TATCAAGCGT CTTG GGGAGA TT AAGC GTTTT GA CAG
AAGG T
TCCGCCTTGTTGGTCTGAAA TTTG |||| |||||| || |||| ||||| || ||| ||||
TTCATGCAAGCTTCCGAAGA GAAC TCTTCT AA TTCG TAAAG CT GTT TTCC C
TCTTCTCAAG - AG GCC AACGTACT T G G GC

GAM1910 CACTACGTTGACCTGAAGGA 1887 AAGGACCGTC 4494 GA-- GAA- CCATTCT --
AAAT
CCGTCCATTCTTTGCCGGCC CATTCTTTGC CACTACGTT CCT GGACCGT
TTGCCGGCCT GGTG A
TGGTGAAATACATGCACTCA CGGC ||||||||| ||| ||||||| |||||||||| ||||
GGGCCGGTAGTTGCCATGGT GTGGTGTAA GGG TCTGGTA GATGGCCGGG
TCAC /
CTGGGAGGGGCTGAATGTGG GTCG AGGG CCGTT-- AC GTAC
TG

GAM1911 GCGATGACTTCTGTTTCTTC 1888 GATGACTTCT 4496 G - TTCTTCC A --- GG G T
A
CAGATGCTCATGGGTGGGGG GTTTCTTCCA GC ATGACTTC TGT AG TGCT CATG TGGGG
TG GTGTCGC C
TGTGTGTCGCACAGTGACAC GATG || |||||||| ||| || |||| |||| ||||| || |||||||
TCAACTTCAACATGCCAGGC TG TACTGAAG ACG TC GCGG GTAC ACTTC AC
CACAGTG /

GCCTTTGTGCATGAAGTCAT G T TGTT--- C ACC A- A T A
GGT

GAM1912 GGTGTGACCCTCGCCATGGT 1889 TACCGTGGTG 4497 TGT C-- AAT T TT
AAATACATGGCTTGCTGCCT ACGTGGTTCC GG GACC TCGCCATGGTA ACA GGC G
GTTATACCGTGGTGACGTGG C || |||| |||||||||| ||| |||
TTCCC CC TTGG AGTGGTGCCAT TGT CCG /
C-- TGC AT- - TC

GAM1913 TGCCACCATCAAAACCAAGC 1890 TTGGTGCCCC 4498 - ATCAAAA AGC-- - GT
GTACCATCCAGTTTGTGGAT ACTGGCTTCA TGCCA CC CCA GTACCA TCCA T
TGGTGCCCCACTGGCTTCAA AGGT ||||| || ||| |||||| ||||
GGTTGGCA ACGGT GG GGT CGTGGT AGGT /
T AACTTC- CACCC T GT

GAM1914 TGTGGTGCCTGGCGGAGACC 1891 TACCACAGCT 4499 G T G A - AA ACA G ----
ATG
TGGCCAAGGTACAGAGAGCT GTTGCCGAGG TGTGGT CC GGCG AG CCT GGCC GGT GA
AGCTGTG TGC C
GTGTGCATGCTGAGCAATAC CCTG |||||| || |||| || ||| |||| ||| || ||||||| |||
CACAGCTGTTGCCGAGGCCT ACACCA GG CCGC TC GGG CCGG CCG TT TCGACAC
ACG /
GGGCTCGCCTGGACCACA - T - - T AG --- G CATA AGT

GAM1915 TTATGCTGCAGCATATTGTA 1892 CAGCATATTG 4501 C A TACT TGCT
CTGGCCTGCTGCTGGCCCGC TACTGGCCTG TTATGCTG AGC TATTG GGCCTGC G
AGGCTTCTCAATAGGTTTGG CTGC |||||||| ||| ||||| |||||||
CATGG GGTACGGT TTG ATAAC TCGGACG /
- G TCT- CCCG

GAM1916 ATCTATGAAGGCCAAGTGGA 1893 TGGTCAGCCA 4500 TGAA CAA GA - GA A
GG
GGTGACTGGTGATGAATACA GGTGCCTTCA ATCTA GGC GTGGAGGT CTGG TGAT AT
CAATGT A
ATGTGGAAAGCATTGATGGT CCTG ||||| ||| |||||||| |||| |||| || ||||||
CAGCCAGGTGCCTTCACCTG TAGGT TCG CACTTCCG GACC ACTG TA GTTACG /
CTATTTGGAT TTA- TC- TG G G- - AA

GAM1917 CATCCGCAGGGTTCGGATGA 1894 TGTTCAGTAT 4502 CGCA- C - A- C TG
GACCAGGTGTTGCTTGTTCA CTCAAGCCCA CATC GGGTT G GATG GA CAGG T
GTATCTCAAGCCCAGAAAGA GAAA |||| ||||| | |||| || ||||
TG GTAG CCCGA C CTAT CT GTTC /
AAAGA A T GA T GT

GAM1918 GCATCTGTTTTCTGGTTTTC 1895 TTACTTGTCC 4503 ---- C TTTTC- CTTA C
AATCTCTCTTACAACTTCTT AAAAACAACA GCATC TGTTTT TGG AATCTCT CAA T
GACCAGAGATTACTTGTCCA TGAT ||||| |||||| ||| ||||||| |||
AAAACAACATGATGC CGTAG ACAAAA ACC TTAGAGA GTT T
TACA - TGTTCA CCA- C

GAM1919 GAAACAGACTGGGCCAATGT 1896 TATCAAGGAA 4504 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM1920 AGATGGATGGGACAGAAAAT 1897 TGGGACAGAA 4505 AT- GAAAATAAA A- TT C
AAATCTAAGTTTGGTGCGAA AATAAATCTA AGATGG GGGACA TCT AG TGGTG G
CGCCATTCTGGGGGTGTCCC AGTT |||||| |||||| ||| || |||||
TTGCCGTCT TCTGCC CCCTGT GGG TC ACCGC A
GTT --------- GG TT A

GAM1921 GGAGAAGCTGAAGAGAGATG 1898 AGCTGAAGAG 4506 AAG GA GA- GTT CA-- A
ATC
TGGAGTTTCTAGTGCAGCTG AGATGTGGAG GGAG CTGAA GA TGTGGA TCTAGTG
GCTG AG A
AAGATCATGGACTACAGCCT TTTC |||| ||||| || |||||| ||||||| |||| ||
TCTGCTAGGCATCCACGACA TCTC GGCTT CT GCACCT GGATCGT CGAC TC T
TCATTCGGGGCTCT GG- A- ACA AC- CTTC A AGG

GAM1922 TGCGCTGAATGATGTCACGG 1899 TGAATGATGT 4508 AAT TG CAC- GT AA
CAGTCGTTGAACACACGGCG CACGGCAGTC TGCGCTG GA T GGCA CGTTG C
GATGTTCTCAGTGTCCACAG GTTG ||||||| || | |||| |||||
CGCA ACGCGAC CT G TTGT GCGGC A
AC- GT ACTC AG AC

GAM1923 GTGAAATGAGGGTAGCAGTA 1900 TAGCAGTAGT 4507 GAAA AG G ACGC TCT
GTGACGCCCATCTCCACTGG GACGCCCATC GT TGAGGGT CAGTA TG CCA C
CAGTGCTGATCCTCAGAAAC TCCA || ||||||| ||||| || |||
CA ACTCCTA GTCGT AC GGT /
AAG- -- G ---- CAC

GAM1924 TTGGAGGCTTGAAGTGAATT 1901 TGAAGTGAAT 4509 CT AA T- C GTTCATTAA
CGGCAGCGTTCATTAAACAC TCGGCAGCGT TTGGAGG TG GTGAAT CGG AGC A
CTTCCAGCTCCTGTCATTTA TCAT ||||||| || |||||| ||| |||

CCACTTCTTCAA AACTTCT AC CATTTA GTC TCG /
TC -- CT C ACCTTCCAC

GAM1925 CCTGGCACGGTGACTCACGC 1902 AGGCAGGCAG 4510 ACG C AC AATCC A T
CTGTAATCCCAGCACTTTGT ATCACAAGGT CCTGGC GTGA TC GCCTGT CAGC CTT G
GAGGCTGAGGCAGGCAGATC CAGG |||||| |||| || |||||| |||| |||
ACAAGGTCAGG GGACTG CACT AG CGGACG GTCG GAG /
GAA - A- GA--- - T

GAM1926 AGTGATGGTCAGTATTTCTT 1903 ACTTCAGGCA 4511 G- TC--- A A
TGAAATTCTACAAGGAACTT CATGGTGCTG AGTGAT GTCAGTATT TTTGAA TTCT C
CAGGCACATGGTGCTGATGA ATGA |||||| ||||||||| |||||| ||||
GTTATT TTATTG TAGTCGTGG GGACTT AAGG A
AG TACAC C A

GAM1927 GGTGAAATGAGGGTAGCAGT 1904 TAGCAGTAGT 4512 AA--- AG G ACGC TCT
AGTGACGCCCATCTCCACTG GACGCCCATC GGTGA TGAGGGT CAGTA TG CCA C
GCAGTGCTGATCCTCAGAAA TCCA ||||| ||||||| ||||| || |||
CTCATC CTACT ACTCCTA GTCGT AC GGT /
CAAAG -- G ---- CAC

GAM1928 AGGCAACAGAAGATGCTGCC 1905 AGATGCTGCC 4513 - CA AGA -- AACTA-- C
AATAACTATGCCCGAGGGCA AATAACTATG AGG CAA GA TGCT GCCAAT TGCC G
CTACACCATTGGCAAGGCAG CCCG ||| ||| || |||| |||||| ||||
ATCATTGACCT TCC GTT CT ACGG CGGTTA ACGG A
A A- AG- AA CCACATC G

GAM1929 GGCCAATTGAAACAAACAGT 1906 TATTAGGGAT 4514 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1930 TTGGTCCATATCTCCATGCA 1907 TCCATATCTC 4515 TC ATCTCC- G- - ACA
TGGCGGATACAGTGAAATCT CATGCATGGC TTGG CAT ATGCATG CG GAT G
CGAGCATGCATCTTCTCGGT GGAT |||| ||| ||||||| || |||
GAGCCAG GACC GTG TACGTAC GC CTA T
GA GCTCTTC GA T AAG

GAM1931 TCTTGTGTTGAGACTTCGTG 1908 TACACCACTC 4516 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||

CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM1932 GGCCAATTGAAACAAACAGT 1909 TATTAGGGAT 4517 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1933 AATGGTGACAACATGCTGGG 1910 CATGGCAACG 4518 AA--- GG - T TA
AGCCAAGTGCTAACATGCCT TCACCGTT AATGGTGAC CATGCT GAGCC AAG GC A
TGGGTTCAAGGCATGGCAAC ||||||||| |||||| ||||| ||| ||
GTCACCGTT TTGCCACTG GTACGG CTTGG TTC CG C
CAACG AA G - TA

GAM1934 GGTGACAACATGCTGGAGCC 1911 TTCACAGGAT 4519 AA--- G - A T TA
AAGTGCTAACATGCCTGGTT GGGACAGTCA GGTGAC CAT CTG GAGCCA G GC A
CACAGGATGGGACAGTCACC CC |||||| ||| ||| |||||| | ||
CCACTG GTA GAC CTTGGT C CG C
ACAGG G A - - TA

GAM1935 TCTACAAAGTGCCGTCCACT 1912 TCCAATCTGA 4520 A - - CACTG CT- C
GAGACTGAGGCCTTGGCTTC TGGGCATGTT TCT CAAA GTGCC GTC AGA GAGGC T
CAATCTGATGGGCATGTTTG TGAG ||| |||| ||||| ||| ||| |||||
AGA AGA GTTT TACGG TAG TCT CTTCG T
- G G ----- AAC G

GAM1936 AGAAACAAAAGCAGGTGCTG 1913 TAGCATGCCT 4521 CAA- C -- TCA--- AA
AATCATGAAAACCTCAATTA CTTAATTTTT AGAAA AAG AGGT GCTGAA TGA A
TTTTTAGCATGCCTCTTAAT CT ||||| ||| |||| |||||| |||
TTTTCT TCTTT TTC TCCG CGATTT ACT /
TTAA - TA TTATTA CC

GAM1937 CGAGATGAGTTTCTGAGGAT 1914 TTCACCTGCG 4522 A AGT G GA AG T - TG C
CACT
CAGCACTGCCAGTGGAGATG CTGTGGACAC CG GATG TTCT AG TC CAC GC CAG
GAGATGGG GT A
GGCGTCACTACTGCTACCCT TGAG || |||| |||| || || ||| || ||| |||||||| ||
CATTTCACCTGCGCTGTGGA GC CTAC AAGA TC AG GTG CG GTC CTTTACTC CA C
CACTGAGAACATCCG - --- G AC -- T C CA C TCGT

GAM1938 GTCGGGCTTGTGCGTATGGG 1915 TGGGTGGTGT 4523 - GG G G T GATG GGG -
-- G

TGGTGTGATGTCTGGGGCTG GATGTCTGGG GTC G CTT TGC TATGGG GGTGT TCT GCTGTC CCT GCT C

TCCCTGCTGCACAGCCCAGG GCTG ||| | ||| ||| |||||| ||||| ||| |||||| ||| |||

AGGCGGTGGAAGAAGATATC CAG C GAA GCG ATACCC CTATA AGA TGGCGG GGA CGA A

CCCATAGCGAAAGAACGGAC G AA A - - GA-- AGG A CC C

GAM1939 TGCGCTGAATGATGTCACGG 1916 TGAATGATGT 4524 AAT TG CAC- GT AA

CAGTCGTTGAACACACGGCG CACGGCAGTC TGCGCTG GA T GGCA CGTTG C

GATGTTCTCAGTGTCCACAG GTTG ||||||| || | |||| |||||

CGCA ACGCGAC CT G TTGT GCGGC A

AC- GT ACTC AG AC

GAM1940 GAAGCAATTTCTCTACAGAT 1917 AAGCAGTCTG 4526 AATT--- T G AAAAT G

GGTAAAATGCAAGGAATTGC TGAGATCCTT GAAGC TCTC ACAGAT GT GCAA G

CACAAGCAGTCTGTGAGATC GGGC ||||| |||| |||||| || ||||

CTTGGGCTTC CTTCG AGAG TGTCTG CG CGTT A

GGTTCCT - A AACAC A

GAM1941 ATCTCAGGACTCTGGATACC 1918 TCTGGATACC 4525 C CT A TTAT CT A GGC

TTTATTTTTGCTTCAGGTGG TTTATTTTTG ATCT AGGA CTGGAT CCT TTTTG TC GGT T

CTTTTAATCAGATTCAAAAG CTTC |||| |||| |||||| ||| ||||| || |||

GGAATTTAGTTTTCTAGAT TAGA TCTT GATTTA GGG AAAAC AG CTA T

- TT A ---- TT A ATT

GAM1942 GGCGGGTGGGGGGCCTTTGG 1919 GCCCAAGGCA 4527 C - AA-- T- AA- A C

AAGGTTTGCAAGGAGTTGCT TCACCAAGAT GG GGGTGG GGGGCCTTTGG GGT TGC GG GTTG T

GCGGCCCAAGGCATCACCAA TAAA || |||||| |||||||||| ||| ||| || ||||

GATTAAAGGCCTCGCCATCT CC TCTACC CTCCGGAAATT CCA ACG CC CGGC /

TCC T G AGAA CT GAA - G

GAM1943 AACTGGTGATTGTCGGTGAT 1920 TGATGGAGCC 4528 GA CGGTGA C A- AC

GGAGCCTGTGGAAAGACATG TGTGGAAAGA AACTGGT TTGT TGGAG CTGTGG AAG A

CTTGCTCATAGTCTTCAGCA CATG ||||||| |||| ||||| |||||| |||

AGGACCAGTT TTGACCA AACG ACTTC GATACT TTC /

GG ------ T CG GT

GAM1944 TCTTGTGTTTGAGACTTCGT 1921 TACACCACTC 4529 AGA GT--- C AAAGGA

GGTGGTGCTAAGAAAAGGAA CCAAGAAGAA TCTTGTGTTTG CTTC GGTGGTG TAAGA A

GAAGAAGTCTTACACCACTC TAAG |||||||||| |||| ||||||| |||||

CCAAGAAGAATAAGCACAAG AGAACACGAAT GAAG TCACCAC ATTCT G

A AA- AACCC - GAAGAA

GAM1945 GGAGATGAAACGGAAGATGC 1922 AACTTTCTCA 4530 A AA-- A ATG A T TCTC A
GCGAGGATGTGATCTCTTCC TCTACGTGGC GGAG TGA CGG AG CGCG GGATG GA TTCC
T
ATACGGAACTTTCTCATCTA CCTC |||| ||| ||| || |||| ||||| || ||||
CGTGGCCCTCCTGCGAGTCA CCTC ACT GTC TC GTGC TCTAC CT AAGG A
CTCC - GAGC C CCG A T TTC- C

GAM1946 CATCCACACCTAATGTCCAC 1923 CCTGTGGACA 4531 A ----- AA T T CAC
ATGGTCAGCACCACCCTGCC GCAGGATGAT CATCC CA CCT TGTCCACA GG CAG C
TGTGGACAGCAGGATGATTG TGAG ||||| || ||| |||||||| || |||
AGGATG GTAGG GT GGA ACAGGTGT CC GTC /
A TAGTA CG - - CCA

GAM1947 GCAGGATGATTGAGGATGCA 1924 TGATTGAGGA 4532 A- T-- A CA AAGT
ATTCGAAGTCACAGCGAATC TGCAATTCGA GCAGG TGA TGAGG TG ATTCG C
AGCCTCACCTTCAGCCCTGT AGTC ||||| ||| ||||| || |||||
TGTCC ACT ACTCC AC TAAGC /
CG TCC G -- GACA

GAM1948 TGTGGTGCCTGGTGGAGACC 1925 CATTGCTGAG 4533 G T G A - AA CAGAGA -
CA T
TGGCCAAGGTACAGAGAGCT GCCTGGGCTC TGTGGT CC GGTG AG CCT GGCC GGTA
GCTGTG TG TGC G
GTGTGCATGCTGAGCAACAC GCCT |||||| || |||| || ||| |||| |||| |||||| || |||
CACAGCCATTGCTGAGGCCT ACACCA GG CCGC TC GGG CCGG TCGT CGACAC AC
ACG /
GGGCTCGCCTGGACCACA - T - - T AG TAC--- C A- A

GAM1949 AGCAAGAGTAGGGTGCATGG 1926 TTCACCCAAC 4534 ------ C TGAATAA
CTTGAATAAGAGGAAACAGC ATTTGCTTTT AGCAAGAGTA GGGTG ATGGCT G
CGTTCACCCAACATTTGCTT GCT |||||||||| ||||| ||||||
TTGCT TCGTTTTCGT CCCAC TGCCGA /
TTACAA T CAAAGGA

GAM1950 GCTGTTGCATTGTAACTTGT 1927 TTGCATTGTA 4535 - AA TG CATTAA - TTG
GGTGTGCATTAAGATGTGCT ACTTGTGGTG GCTGTT GCATTGT CT TGGTGTG
GATGTGCTG AGGA C
GAGGATTGCGAACTCCTGCA TGCA |||||| ||||||| || ||||||| ||||||||| ||||
GCATATTTATACTGTGGGAC CGACAG CGTGGCA GG GTCATAT TTATACGAC TCCT
G
GGTGCGGACAGC G -- GT ------ G CAA

GAM1951 TCTTGTGTTGAGACTTCGTG 1928 TACACCACTC 4536 GAGA GT--- C AAAGGA

GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM1952 CACCTTTACGGCCAAACCGT 1929 TGTGGATATA 4537 TT C CC C-- C--- G
CCACCTCGACCGATTCTGTG GTTTTCCCTG CACC TA GG AAAC GTCCAC TC A
GATATAGTTTTCCCTGTTGG TTGG |||| || || |||| |||||| ||
TG GTGG GT CC TTTG TAGGTG AG C
TT - CT ATA TCTT C

GAM1953 TTGGTCCATATCTCCATGCA 1930 TCCATATCTC 4538 TC ATCTCC- G- - ACA
TGGCGGATACAGTGAAATCT CATGCATGGC TTGG CAT ATGCATG CG GAT G
CGAGCATGCATCTTCTCGGT GGAT |||| ||| ||||||| || |||
GAGCCAG GACC GTG TACGTAC GC CTA T
GA GCTCTTC GA T AAG

GAM1954 AGCTGCCCTCCTCTTCTCCC 1931 GGAGAAGGGG 4539 T - TCA CA
CTCACACTACAGCCCTGGTG GTGGGTGCT AGC GCCC TCCTCTTCTCCCC CACTA G
GGGGAGAAGGGGGTGGGTGC ||| |||| |||||||||||| |||||
T TCG TGGG GGGGGAAGAGGGG GTGGT C
- T --- CC

GAM1955 GGTCTGGTCCCCGTGTTGCC 1932 TCCCCGTGTT 4540 T ---- CCTATTA CCTTT
TATTAGCCCTTTACCCTGAG GCCTATTAGC GG CTGGTCCCCG TGTTG GC A
CACCACCCCAACAGACTTGG CCTT || |||||||||| ||||| ||
GGACCAGCC CC GACCAGGGGT ACAAC CG C
- TCAG CCCACCA AGTCC

GAM1956 GAAGTTGATCTACTTCCAGC 1933 GTGGATCCCG 4541 G- ACTT ---- G C GC T GA
TGCACCGGGCCCTCAAGATG TGGAGCCACA GAAGTT ATCT CCA GCT CAC GG CC CAA T
ATTGTGGATCCCGTGGAGCC TGGC |||||| |||| ||| ||| ||| || || |||
ACATGGCGAGATGAAATTTC CTTTAA TAGA GGT CGA GTG CC GG GTT /
AG GC-- ACAC G C TA T AG

GAM1957 GGGACCTCAATGCCTGGACC 1934 GCAGAGCGTC 4542 ----- AT GACCAAG A - G
AG
AAGAGTGCCGAGGCCTTTGG CTGGCACTAA GGGACC TCA GCCTG AGTGCCG GGC
CTTTG CA A
CAAGATTGTGGCAGAGCGTC CTCA |||||| ||| ||||| ||||||| ||| ||||| ||
CTGGCACTAACTCAACAGGC CCCTGG AGT CGGAC TCACGGT CTG GAGAC GT T
CCTGACCCATGGTCCC TACCC CC AACTCAA C C G GT

GAM1958 GATGAGAAAAGTCCCAGGCT 1935 TGTGTTGTGG 4543 AAA C CTA- TG G TT TTTG
AATGGCAGAAATTTGCACTT AACCTGAGAT GATGAG AGTC CAGG A GCA AAA TGCAC A
TGAACATGTGTGTTTTTGTG TCCT |||||| |||| |||| | ||| ||| |||||
TTGTGGAACCTGAGATTCCT TTATTC TTAG GTCC T TGT TTT GTGTG /
TATT C-- A AAGG GT G TT TACA

GAM1959 GGTGACAACATGCTGGAGCC 1936 TTGGTTCAAG 4544 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC ||||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM1960 TGTTTTGCCTCTGTCTTTGA 1937 AGAGGGCAAG 4546 C--- G AAAAATA CAAT
AAAATACTTCCAATTCCAAG GAAGGAGAGA TGTTTTG CTCT TCTTTG CTTC T
AAGAGGGCAAGGAAGGAGAG ACAG ||||||| |||| |||||| ||||
AACAGAGCA ACGAGAC GAGG AGGAAC GAAG /
AAGA A GGGA--- AACC

GAM1961 AGTGATGGTCAGTATTTCTT 1938 ACTTCAGGCA 4545 G- TTC-- A A
TGAAATTCTACAAGGAACTT CATGTGCTGA AGTGAT GTCAGTAT TTTGAA TTCT C
CAGGCACATGTGCTGATGAG TGAG |||||| |||||||| |||||| ||||
TTATT TTATTG TAGTCGTG GGACTT AAGG A
AG TACAC C A

GAM1962 TCTTGTGTTGAGACTTCGTG 1939 TACACCACTC 4547 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM1963 CTTGGTTCTACAGCCATTGG 1940 AGCCATTGGG 4549 GG CAT ATC G A
GATCCAGACATCAGAGGGTG ATCCAGACAT CTT TTCTACAGC TGGG CA ACATC G
TGTGCCTAGCTGTGGAGAAG CAGA ||| ||||||||| |||| || |||||
AG GAG GAGGTGTCG ATCC GT TGTGG A
AA --- --- G G

GAM1964 CCCACTGATGGAGCCCAGCA 1941 TGATGCTCAC 4548 G AGCC AGCAT AA-- GT
GCATTGAGAAAATTGTAGAG ATAGGTTGTG CCCACT ATGG CAGC TGAG AATT A
ATTGATGCTCACATAGGTTG CCAT |||||| |||| |||| |||| ||||
TGCCATGAGTGGG GGGTGA TACC GTTG ACTC TTAG /
G GT-- GATAC GTAG AG

GAM1965 GGAAGACTTGAAGAGGTTAT 1942 TGGGACAATT 4550 --- T - ATCAC TAA T ----- T
AC

CACGACATTTAAGGAATCTG TCAGTTCTAA AA GACT GAA GAGGTT GACATT GGAA CTGA
TCC CAGA T
ATCCTCAGAACTTCTCTGGG TAAT || |||| ||| |||||| |||||| |||| |||| ||| ||||
ACAATTTCAGTTCTAATAAT TT CTGA CTT TTTTAA CTGTAA TCTT GACT AGG
GTCT /
GTCTTAAATTTTATTCCAGT GTC C A ATT-- TAA - TTAAC - CT
CCTGTTCT

GAM1966 CGTCCCTGACACTGCCCGCT 1943 CCTGACACTG 4551 C - TG ACTA-- AGA
ACTACAAGAAACATGGCATC CCCGCTACTA CGTC CTGA CAC CCCGCT CA A
AGGTGGGTGGTGATCGGAGA CAAG |||| |||| ||| |||||| ||
CG GCAG GGCT GTG GGGTGG GT /
A A GT ACTACG ACA

GAM1967 TCTCTGTCCTTCTACAGGAG 1944 TCTGTCCTTC 4552 - T TACAG TTCC TGCC
GTGTTCCGCTTTGCCTACTA TACAGGAGGT TC TCTG CCTTC GAGGTG GCTT T
CAAGCTGCTTCACGAAGGCA GTTC || |||| ||||| |||||| ||||
GATGA AG AGAC GGAAG CTTCGT CGAA A
T - CA--- ---- CATC

GAM1968 TGGCATCCCAGATGTTGCAG 1945 TTGCAGTTGA 4553 - AGA AG GAAG T CA A A
TTGAAGTCGTCGTAGCCAGC AGTCGTCGTA TGGCATC CC TGTTGC TT TCG CGTAGC
GCG GC G
GAGCAGCAGCCGTCCGCTGC GCCA ||||||| || |||||| || ||| |||||| ||| ||
GCGAGAAGGCAACAGAGGTG ACCGTAG GG ACAACG AG AGC GCGTCG TGC CG C
ATGCCA T AG- GA ---- - CC - A

GAM1969 ATCTATGAAGGCCAAGTGGA 1946 TGGTCAGCCA 4554 TGAA CAA GA - GA A
GG
GGTGACTGGTGATGAATACA GGTGCCTTCA ATCTA GGC GTGGAGGT CTGG TGAT AT
CAATGT A
ATGTGGAAAGCATTGATGGT CCTG ||||| ||| |||||||| |||| |||| || ||||||
CAGCCAGGTGCCTTCACCTG TAGGT TCG CACTTCCG GACC ACTG TA GTTACG /
CTATTTGGAT TTA- TC- TG G G- - AA

GAM1970 TTATGCTGCAGCATATTGTA 1947 CAGCATATTG 4555 C A TACT TGCT
CTGGCCTGCTGCTGGCCCGC TACTGGCCTG TTATGCTG AGC TATTG GGCCTGC G
AGGCTTCTCAATAGGTTTGG CTGC |||||||| ||| ||||| |||||||
CATGG GGTACGGT TTG ATAAC TCGGACG /
- G TCT- CCCG

GAM1971 CCACCATATGTTCTTTGACT 1948 TGGGATAGGA 4556 A TAT TTGA TTA CA
ATAATTATGGACAATATTTC TTGGCGG CC CCA GTTCT CTATAA TGGA A
ACTTTGTGGGATAGGATTGG || ||| ||||| |||||| ||||
CGG GG GGT TAGGA GGTGTT ACTT T

C --- TAG- TC- TA

GAM1972 CGGAGCACCAGGTGCAAGGT 1949 AGACAGGGTA 4557 CAC G C ---- T ATGT
GGACTCTTTCTGGATGTTGT CGACCATCTT CGGAG CAG TG AAGGTGG ACTCT TCTGG T
AGTCAGACAGGGTACGACCA CCAG ||||| ||| || ||||||| ||||| |||||
TCTTCCAGCTGTTTTCCG GCCTT GTC AC TTCTACC TGGGA AGACT /
TT- G C AGCA C GATG

GAM1973 CCTCCGTGACTGTCACCTCA 1950 TAGATGCAGG 4558 C G --- - GT-- T AGAA
TCGTCGTGCAGAATGAAGGC TGAGCTCGGT CCTC GT ACTG TCACCT CATC CG GC T
CGTGTAGATGCAGGTGAGCT GACA |||| || |||| |||||| |||| || ||
CGGTGACAGAGG GGAG CA TGGC AGTGGA GTAG GC CG /
A G TCG C ATGT - GAAG

GAM1974 GTCCAGGGGTGGGAATACAG 1951 AGGGGGTGGG 4559 C GGGAA AG G GAGG A
AGA
GGGGTGGGAGGTGTGCATAA AGGTGTGCAT GTC AGGGGT TAC GGG TGG TGTGC TA G
GAGGTGATAGGCACAGGCCA AAGA ||| |||||| ||| ||| ||| ||||| ||
GCCCGGTACAGACCCCTAGG CGG TCCCCA ATG CCC ACC ACACG AT G
C A GAC-- G- G GG-- G AGT

GAM1975 GAGAAGGCAGCAGGCGGCCT 1952 CAAGGTGCTC 4560 C C - ------ G
TTGTTGCTCAGCAAGGTGCT TGCTCGCCTA GAGAAGG AG AGGCG GC CTTTGTT C
CTGCTCGCCTACTTCCTTCT CTTC ||||||| || ||||| || |||||||
T TTCTTCC TC TCCGC CG GGAACGA T
T A T TCTCGT C

GAM1976 TGTTGACCTCCTGTACTGGA 1953 CTGCTGCTTT 4561 CCTCCT GA GACATT A ACT
T G
GAGACATTAAGAAGACTGGA CATTGACAGT TGTTGA GTACTG GA AAG AG GGAGTGG
GTTG T
GTGGTGTTGGTGCCAGCCTA ATTC |||||| |||||| || ||| || ||||||| ||||
TTCCTGCTGCTTTCATTGAC ACGACT TATGAC TT TTC TC CCTTATC CGAC G
AGTATTCAGCA ------ AG ACT--- G GT- - C

GAM1977 GGATTTCCACAAGACGGCAC 1954 TAAAAGTGTG 4562 TTTC -- - TG CGTC
GCAGCGT
CCTATGTCGTCACTGGCAGC GGAGTGCCGT GGA CACAA GACGGCAC CCTA T ACTG
A
GTAGATCAAACAGTAAAAGT TGAT ||| ||||| |||||||| |||| | ||||
GTGGGAGTGCCGTTGATTGT CCT GTGTT TTGCCGTG GGGT G TGAC /
GTCTCC CT-- AG A GT AAAA AAACTAG

GAM1978 GGTGACAACATGCTGGAGCC 1955 GGTCAAGGGA 4563 AA-- G G- G T TA
AAGTGCTAACATGCCTTGGG TGGCAAGTCA GGTGAC CAT CT GA CCAAG GC A
TCAAGGGATGGCAAGTCACC CC |||||| ||| || || ||||| ||
CCACTG GTA GG CT GGTTC CG C
AACG G AA G - TA

GAM1979 GTCATCTTTGGCTTGCAACA 1956 TGAGGAGAAT 4564 GG- T AA GC G T CAAG
TTGCCCTGGATGCTGTCAAG GGTCGGAAAA GTCATCTTT CT GC CATT CCT GA GCTGT A
ATGGTACAGTTTGAGGAGAA GAGA |||||||||| || || |||| ||| || |||||
TGGTCGGAAAAGAGATGGC CGGTAGAGA GG TG GTAA GGA TT TGACA /
AAA C -- GA G - TGGT

GAM1980 GTTCCACCCTGAAGTTGGCC 1957 TAGCTGGATG 4565 CC AAG TG CT - GA T
AGTAATA
TTACAGAAAATGGAAAAGTA CAGTGGAAC GTTCCAC TG T GC TA CA AAA GGAAA C
ATACTGAAGAATTTCCTTTA ||||||| || | || || || ||| |||||
TGATATAGCTGGATGCAGTG CAAGGTG AC G CG AT GT TTT CCTTT /
GAAC -- GTA GT AT A A- - AAGAAGT

GAM1981 GGTCTCTTCAGAGCTGCTGG 1958 TATGAGGCCC 4566 CT -------- G T - GT TCA
TGCCCAGTGGTGCTTCAACG TAGAGCTCCG GGTCT TCA GAGCT CTGG GCC CA
GGTGCT A
TGGTATCTATGAGGCCCTAG GGAC ||||| ||| ||||| |||| ||| || ||||||
AGCTCCGGGACAATGATAAG TCAGA AGT CTCGA GATC CGG GT CTATGG /
ACT AT AACAGGGC - C A AT TGC

GAM1982 TTGCCGTCTGCCACAGCTGG 1959 TAGCAGCACA 4567 TCT --- TG- C T AGA G
TGCCGTCTGAGAAGGGGGTC TCGCTGACTT TTGCCG GCCA CAGC GTGC G CTG AGGGG
T
CCCCTGTAGCAGCACATCGC GGCT |||||| |||| |||| |||| | ||| |||||
TGACTTGGCTCGGCAA AACGGC CGGT GTCG CACG C GAT TCCCC /
T-- TCA CTA A - G-- C

GAM1983 GGCTCCCAATGTTGACGTTG 1960 CCAGGCCAAA 4569 CTCCC CG---- AG TGC
GCCAGGGCTTTGCAAACAAG AAGGCTCAAC GG AATGTTGA TTGGCC GGCTT A
CCAGGCCAAAAAGGCTCAAC ATTT || |||||||| |||||| |||||
ATTTACACC CC TTACAACT AACCGG CCGAA /
ACAT- CGGAAA A- CAA

GAM1984 GCAGTGGAGGGGGCAGGACC 1961 TGAGCAGGTC 4568 GA A ACCT G TG - A
TCCTGCTGGTGCAGCACCAG CACCGGCCCC GCAGTG GGGGGC GG CCTGCT G C AGC C
CTCGTGTGAGCAGGTCCACC TACA |||||| |||||| || |||||| | | |||
GGCCCCTACATTGC CGTTAC TCCCCG CC GGACGA T G TCG C
A- G ACCT G GT C A

GAM1985 TTTGGAGCGCCGGGAGCGAG 1962 TCTTCATTCC 4570 AGCGC- C- - AAC
AGTGTGAACATGGCTACGCC CGTCCATGCC TTTGG CGGGAG GAGAG TGTG A
TCTTCATTCCCGTCCATGCC GAG ||||| |||||| ||||| ||||
GAG GAGCC GCCCTT TTCTC GCAT T
GTACCT AC C CGG

GAM1986 GGCATCTCTGAGCGAGACCA 1963 TGGGATCCTC 4572 C C GA CGAC G T - ACC TA
CGACTGGGGTCCACAACCTC ACAGGTGCC GGCATCT TGAG GA CCA TG GG CCA CA TC
C
TACAAGATGATGGCCACATG ||||||| |||| || ||| || || ||| || ||
GGATCCTCACAGGTGCC CCGTGGA ACTC CT GGT AC CC GGT GT AG /
C - AG ---- A - A --- AA

GAM1987 GCCATCAATGTCAATGACTC 1964 TGGCTGCGGG 4571 A TCAAT - CA - CAA T
CGTCACCAAGAGCAAGTTTG AGTCCTCATA GCCATC ATG GACTCC GT CCA AGAG GTT G
ACAACCTCTATGGCTGCGGG GATG |||||| ||| |||||| || ||| |||| |||
AGTCCTCATAGATGGC CGGTAG TAC CTGAGG CG GGT TCTC CAA A
A TC--- G TC A --- C

GAM1988 GAATATGTCACCACTTCTTG 1965 TATGTCACCA 4573 T C CT----- C -- AA
AACTAAGTTCAGAAAATCTT CTTCTTGAAC GAA ATGT ACCA TCTTGAA TAAGTTC AG A
AGAACTTGCTTTAAGATCAT TAAG ||| |||| |||| ||||||| ||||||| ||
CAATGGTTATATCTTT TTT TATA TGGT AGAATTT GTTCAAG TC /
C T AACTACT C AT TA

GAM1989 GAAACAGACTGGGCCAATGT 1966 TATCAAGGAA 4574 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM1990 AAACAGACTGGGCCAATGTC 1967 TATCAAGGAA 4575 C -- CACAAAGAA - CA-
ACCGAT
CACAAAGAATTCCTGGTCAG GGGCAGGCGT AAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
CACCACCGATGTCCAAAGGT GATG ||||||| ||||||| ||||| ||||| ||| |||||
GCAATATCAAGGAAGGGCAG TTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GCGTGATGGCTTATTTGTTT - AG ACGGG---- A TAA AAACCT

GAM1991 GGCCAATTGAAACAAACAGT 1968 TATTAGGGAT 4576 C T ACAAACAG G GTT T A GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM1992 ACCATGCTATATATTATTCA 1969 TATTATTCAG 4577 TATATAT GG GAT AGAA
GGTTAGATTCTCAGAATGCC GTTAGATTCT ACCATGC TATTCA TTA TCTC T
CAGGGATATGAATGGATATT CAGA ||||||| |||||| ||| ||||
CATTGCATGGT TGGTACG ATAGGT AGT AGGG G
TTACTT- A- AT- ACCC

GAM1993 TCTTGTGTTGAGACTTCGTG 1970 TACACCACTC 4578 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM1994 TGTGGTGCCTGGTGGAGACC 1971 CATTGCTGAG 4579 G T G A - AA CAGAGA - CA T
TGGCCAAGGTACAGAGAGCT GCCTGGGCTC TGTGGT CC GGTG AG CCT GGCC GGTA GCTGTG TG TGC G
GTGTGCATGCTGAGCAACAC GCCT |||||| || |||| || ||| |||| |||| |||||| || |||
CACAGCCATTGCTGAGGCCT ACACCA GG CCGC TC GGG CCGG TCGT CGACAC AC ACG /
GGGCTCGCCTGGACCACA - T - - T AG TAC--- C A- A

GAM1995 GATGAGGGGTTAGCATCGCT 1972 TAGCATCGCT 4581 G TT - -- AG C - CC-- CT- CG
GAGTGAGGACGGAAGATCAC GAGTGAGGAC TGA GGG AG CATCGCTGA GTG GA GGA AGATCA CAT CCATC C
CCATCTCCATCCGCCAGATG GGAA ||| ||| || ||||||||| ||| || ||| |||||| ||| |||||
GCCTATGTTTCTGGTCTCTC ATT TCT TC GTGGTGACT TAT CT CCT TCTGGT GTA GGTAG /
CTTCGGTATCATCAGTGGTG G CT T AC GG T C CTTT TCC AC
TCTTCTCTGTTATC

GAM1996 CTGGGCTTTGGGCCTGGTGG 1973 GGGCCTGGTG 4580 G TGG T T - -- CCTA A
TTGGGAGTCACCTACTGACA GTTGGGAGTC CTGG CTT GCC GG GGTT GGGA GTCA CTG C
TCGGGACTGACATTCCTGAA ACCT |||| ||| ||| || |||| |||| |||| |||
CCCCTGGTATGAGGCCAG GACC GAG TGG CC CCAA TCCT CAGT GGC A
G TA- T - G TA CAG- T

GAM1997 GTGCGCTCGGGGCCCTTCGG 1974 TTCGGTCAGA 4582 GG ------ G GAT CC C T
GCAGATCTTCCGGCCGGACA GTGGTGCTGG GTGCGCTC GGCCC TTC GGCA CTT
GGCCGGA AAC T
ACTTCGTTTTCGGTCAGAGT GAAC |||||||| ||||| ||| |||| ||| ||||||| |||
GGTGCTGGGAACAACTGGGC CACGTGGG CCGGG AGG TCGT GAG CTGGCTT
TTG /
CAAGGGTGCAC AA TCAACA G GGT A- - C

GAM1998 TGGCATCCCAGATGTTGCAG 1975 TTGCAGTTGA 4586 - AGA AG GAAG T C A A
TTGAAGTCGTCGTAGCCAGC AGTCGTCGTA TGGCATC CC TGTTGC TT TCG CGTAGC
AGCG GC G
GAGCAGCAGCCGTTCGCTGC GCCA ||||||| || |||||| || ||| |||||| |||| ||
GCGAGAAGGCAACAGAGGTG ACCGTAG GG ACAACG AG AGC GCGTCG TTGC CG C
ATGCCA T AG- GA ---- - C - A

GAM1999 GTCACCATCCTCTGCATTGA 1976 TCCCTGGCTT 4587 CA C- AT- C TG CACT C T
CTTGGGCACTGACATGGTTC ATGAGCAGGC GTCAC TC TCTGC TGA T GG GA ATGGT C
CTGCCATCTCCCTGGCTTAT TGAG ||||| || ||||| ||| | || || |||||
GAGCAGGCTGAGAGTGAC CAGTG AG GGACG ATT G CC CT TACCG C
AG TC AGT C GT ---- C T

GAM2000 CAGCTCAGAAAATAGACAAC 1977 TGCCAGTATT 4588 - AG A G T--- - C
GGAATATTTGGGATTTCCTG ATGATGTGAT CAGCTCAGA AAAT ACA CG AATATT GGGATT
TC T
GGATGATCTCTGCCAGTATT TTAT ||||||||| |||| ||| || |||||| |||||| ||
ATGATGTGATTTATTTGAGT GTTGAGTTT TTTA TGT GT TTATGA CTCTAG AG G
TG A G- A A CCGT T G

GAM2001 GTGAGGATTCCTTGCAATGA 1978 TCTCCTTGTC 4589 GATT--- - - T T TT
GTAGAATTCCCTTCTCTCCT ACAGGTTTAA GTGAG CCT TG CAA GAG AGAA C
TGTCACAGGTTTAAAACTCA AACT ||||| ||| || ||| ||| ||||
C CACTC GGA AC GTT CTC TCTT /
AAAATTT C T C - CC

GAM2002 GATGCCGACTGGGAGCTACT 1979 AGCTACTGGG 4591 CGA- GAGCTA GGT A
GGGTGAGCTGGACTACCAGC TGAGCTGGAC GATGC CTGG CTG GAGCTGG C
TTCAGGACCAGGACAGCGTC TACC ||||| |||| ||| |||||||
CTGCG GACC GAC TTCGACC T
ACAG AG---- --- A

GAM2003 CCGGAACCTGCTCATCTGGA 1980 AGAGTTGTTC 4590 GA - - A CAA G -- AAA
TCAAGAAGAATTTGCTAAAA ATCCAGGGAG CCG AC CTG CTC TCTGGAT GAA AATTT GCT
A

GAGCGGCCAGAGTTGTTCAT ACAG ||| || ||| ||| ||||||| ||| ||||| |||
CCAGGGAGACAGCGTGCGG GGC TG GAC GAG GGACCTA CTT TTGAG CGG G
G- C A - --- G AC CGA

GAM2004 GCTCTCCGCCGCAGCTTCAG 1981 CTAAAGTAGC 4592 CC - A C CC-- GG
CACCTCGGCCCAGAACAATG GTGCTAGGGG GCTCT GC CGC GCTT AGCA TC C
CTAAAGTAGCGTGCTAGGGG C ||||| || ||| |||| |||| ||
C CGGGG CG GCG TGAA TCGT AG C
AT T A A AACA AC

GAM2005 CCAGTGGACGGCTTTTCTGC 1982 TACCGATGGG 4593 AC-- TT TGCA TTAAT GAC
AGGTTTAATAGATGACAATG AAGTCCTTAT CCAGTGG GGCTT C GGT AGAT A
ATCTCTACCGATGGGAAGTC TATT ||||||| ||||| | ||| ||||
CTTATTATTGG GGTTATT CTGAA G CCA TCTA /
ATTC GG TAG- TC--- GTA

GAM2006 GCTCTTCTGTGATCTTGGCC 1983 TGGGTTAGTG 4594 T TCT T---- - CA
TCCCGGAGCAGTTCCTCCTG GCCGCTCACA GCTCT CTGTGA TGGCC CCC GGAG G
GGTTAGTGGCCGCTCACAGT GTGG ||||| |||||| ||||| ||| ||||
GGGGC CGGGG GACACT GCCGG GGG CCTC T
T C-- TGATT T CT

GAM2007 TGCGCTGAATGATGTCACGG 1984 TGTCTCAGTG 4595 AAT TG CAC GT AA
CAGTCGTTGAACACACGGCG TCCACAGCGC TGCGCTG GA T GGCA CGTTG C
GATGTCTCAGTGTCCACAGC A ||||||| || | |||| |||||
GCA ACGCGAC CT G CTGT GCGGC A
AC- GT ACT AG AC

GAM2008 GGGTGCGGAGGCAGCAAATG 1985 AGGCAGCAAA 4596 G AG- A AATG AG C -- T
TTACAGGTCCTGGTGGTGTT TGTTACAGGT GG TGCGG GC GCA TTAC GTC TGG TGG G
CCAGTTCAAGGCAGTAAATA CCTG || ||||| || ||| |||| ||| ||| |||
TGCAGCAGACCGTAACC CC ATGCC CG CGT AATG CGG ACT ACC T
A AGA A ATA- A- A TG T

GAM2009 AATATTGGTCATCTAAAAAC 1986 ATAGAACATA 4597 TC AAAAACT GGG
TTTCTGTTTTCTGGGGTCTG AGATTTCCAA AATATTGG ATCT TTCTGTTTTCT G
GGAAAATAGAACATAAGATT TATT |||||||| |||| ||||||||||
TCCAATATT TTATAACC TAGA AAGATAAAAGG T
TT ATAC--- GTC

GAM2010 CCCTGGAGGAGATCTATCTC 1987 AGAGATCATT 4598 T T--- TCTC GCC
TTCTCCCTGCCCATTAAGGA GATTTCTTCC CCC GGAGGAGATC ATCTCT CCT C
ATCAGAGATCATTGATTTCT TGGG ||| |||||||||| |||||| |||

TCCTGGG GGG CCTTCTTTAG TAGAGA GGA A
T TTAC CTAA ATT

GAM2011 GGTGTTAAGTGCTCCAAGGA 1988 TAAGTGCTCC 4599 TTA T --- A - A CA
GGTGGCCACCGCCATCCGTG AAGGAGGTGG GGTG AG GCT CCA GGA GGTGGCC CCGC T
GGGCCATCATCCTGGCCAAG CCAC |||| || ||| ||| ||| ||||||| ||||
CTCTCCATC CTAC TC CGA GGT CCT CTACCGG GGTG /
C-- T ACC - A - CC

GAM2012 GGCCTGGTGAAAGGAGCCTG 1989 TGCCAGAAGA 4600 T -- - CCTG AAGACAC GAC
CCAGAAGACACTCAGCGACC CACTCAGCGA GGCC GGTGAA AGG AG CCAG TCAGC C
TGAAGCTGGACTACCTGGAC CCTG |||| |||||| ||| || |||| |||||
CTCTACCTTATTCACTGGCC CCGG TCACTT TCC TC GGTC GGTCG T
- AT A TCCA CATCA-- AAG

GAM2013 TGTGGCTTGGGACAAGCTGG 1990 TGGCTTGGGA 4601 C GACA-- ------- AT
TCAGGTATGGAACCTGGCTA CAAGCTGGTC TGTGG TTGG AGCT GGTCAGGT G
ACTGCAAGCTGAAAGACCAA AGGT ||||| |||| |||| ||||||||
CCACA ACACC AACC TCGA TCGGTCCA /
- AGAAAG ACGTCAA AG

GAM2014 TCTTGTGTTGAGACTTCGTG 1991 TACACCACTC 4602 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM2015 CCTAATCGACTTCTTCCATG 1992 CCTCGAGAGG 4603 A C CT ATG- AC ATCC
CGAGACGCATCCTCATCGCC GGGGATCTCA CCT AT GA TCTTCC CGAG GC T
CTCGAGAGGGGGGATCTCAT TCAG ||| || || |||||| |||| ||
CAGG GGA TA CT AGGGGG GCTC CG /
C - CT GAGA C- CTAC

GAM2016 TGTGGTGGCTGGAGGTTGGC 1993 TTGAAGGCTG 4604 - GGA TG GAATT CAA
CGAATTGACAAACCCATCTT GCCGGGCGTA TGTGGTG GCT GGT GCC GA A
GAAGGCTGGCCGGGCGTACC CCAC ||||||| ||| ||| ||| ||
ACA ACACCAT CGG CCG CGG CT C
G G-- GT AAGTT ACC

GAM2017 GCTTGCTCATGATGTACGCG 1994 CTCATGATGT 4605 ACGCGCAG AAG CTA
CAGTCCAAAGGCATCTACTA ACGCGCAGTC GCTTGCTCATGATGT TCCA GCAT C
CGTGCAGTGGAGGATGACAT CAAA |||||||||||||| |||| ||||
CGTGGGCAAGC CGAACGGGTGCTACA AGGT CGTG /

GTAGG--- GA- CAT

GAM2018 GACATCTGTCACCCCATTGA 1995 TGATCTGGCT 4606 ACC TT-- - A T
TCGCCAGGGTTGATTCGGCT GGCTAGGCGG GACATCTGTC CCA GATC GCC GGG T
GATCTGGCTGGCTAGGCGGG GTGT |||||||||| ||| |||| ||| |||
TGTC CTGTGGGCGG GGT CTAG CGG CTT G
ATC CGGT T - A

GAM2019 CTTCTCCTCAGCTGGAGCAG 1996 TGCAGCACCA 4607 T T- A A G - GGG
CAGCAGTGGAGGGGGCAGGA GCTGCTGGAG CT CTCC CAGCTGG GC GCA CAGT GGAGG C
CCTCCTGCTGGTGCAGCACC CAG || |||| ||||||| || ||| |||| |||||
AGCTGCTGGAGCAG GA GAGG GTCGACC CG CGT GTCG CCTCC A
C TC A A G T AGG

GAM2020 CCTAATCGACTTCTTCCATG 1997 CCTCGAGAGG 4608 A C CT ATG- AC ATCC
CGAGACGCATCCTCATCGCC GGGGATCTCA CCT AT GA TCTTCC CGAG GC T
CTCGAGAGGGGGGATCTCAT TCAG ||| || || |||||| |||| ||
CAGG GGA TA CT AGGGGG GCTC CG /
C - CT GAGA C- CTAC

GAM2021 GAGGTGGGTGGATCACCTGA 1998 AACACGGTGA 4609 TGGA - A- A-- C
GGTCAGGAGTTCGAGACCAG AACCCCATCT GAGGTGGG TCACC TG GGTCAGG GTT G
CCTGGCCAACACGGTGAAAC C |||||||| ||||| || ||||||| |||
CCCATCTC CTCTACCC AGTGG AC CCGGTCC CAG /
CAA- C AA GAC A

GAM2022 TTGTCGTCATTGGACACGTA 1999 TAAATGCGGT 4611 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM2023 ATGGTGACACATGCTGGAGC 2000 TTCACGGATG 4610 A--- G - T TA
CAGTGCTAACATGCCTGGTT GCAAGTCACC ATGGTGAC CAT CTG GAGCCAG GC A
CACGGATGGCAAGTCACCGT GT |||||||| ||| ||| ||||||| ||
TGCCACTG GTA GGC CTTGGTC CG C
AACG - A - TA

GAM2024 CAACAGGCCTATTAGAAGAA 2001 TATTAGAAGA 4612 A CTATT ACTAA C
TGAACTAACGTGTCTACGCA ATGAACTAAC CAAC GGC AGAAGAATGA CGTGT T
TGATTATTTTTCTTAAGCTG GTGT |||| ||| |||||||||| |||||
GTTG GTTG TCG TCTTTTTATT GTACG A
G AAT-- A---- C

GAM2025 TCTTGTGTTGAGACTTCGTG 2002 TACACCACTC 4613 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM2026 GGGTGACCCTCGCCATGGTA 2003 TTGTACCGTG 4614 T C-- AAT T TT
AATACATGGCTTGCTGCCTG GTGACGTGGT GGG GACC TCGCCATGGTA ACA GGC G
TTGTACCGTGGTGACGTGGT TCCC ||| |||| |||||||||| ||| |||
TCCC CCC TTGG AGTGGTGCCAT TGT CCG /
- TGC GT- - TC

GAM2027 GTGGTGCCTGGTGGAGACCT 2004 CATTGCTGAG 4615 G T G A - AA CAGAGA -
CA T
GGCCAAGGTACAGAGAGCTG GCCTGGGCTC GTGGT CC GGTG AG CCT GGCC GGTA
GCTGTG TG TGC G
TGTGCATGCTGAGCAACACC GCCT ||||| || |||| || ||| |||| |||| |||||| || |||
ACAGCCATTGCTGAGGCCTG CACCA GG CCGC TC GGG CCGG TCGT CGACAC AC
ACG /
GGCTCGCCTGGACCAC - T - - T AG TAC--- C A- A

GAM2028 CAGAGACCCCGAGTTCTACA 2005 CTAAACTTCA 4616 ACC- CTAC CCT AGAATG
AGTTCCTGCAGGAGAATGAC GCGACTCGGA CAGAG CCGAGTT AAGTT GCAGG A
CAGAGCCTGCTAAACTTCAG CAGC ||||| ||||||| ||||| |||||
CGACTCGGACAGCTCTG GTCTC GGCTCAG TTCAA CGTCC /
GACA CGAC AT- GAGACC

GAM2029 CTGTCGCCCAGGCTGGAGTG 2006 TCGCCCAGGC 4617 GTC --- C -- TCA A
CAGTGTCATGATCTCAGCTC TGGAGTGCAG CT GCCC AGG TGGAGT GCAGTG TG T
ACTGCAAGCTCCACCTCCCG TGTC || |||| ||| |||||| |||||| ||
GGTTCAAG GA TGGG TCC ACCTCG CGTCAC AC C
ACT CCC - AA TCG T

GAM2030 CACTATGTTGGCCAGGCTGG 2007 ATGATCCACC 4618 A TT- - T CTC TC A
TCTCGATCTCCTGATCTCAG TGCCTCGGCC CACT TG GGCC AGGC GGT GATC CTG T
ATGATCCACCTGCCTCGGCC TCCC |||| || |||| |||| ||| |||| |||
TCCCAAAGTG GTGA AC CCGG TCCG CCA CTAG GAC C
A CCT C T C-- TA T

GAM2031 CTTTCTGGGCAGAAGATGGC 2008 TCATGTGGAG 4619 AAGATGG - TT ATAA
CACTGTTCAATAAAACGACT CCCTGTCCAG CTTTCTGGGCAG CCAC TG CA A
GTCATGTGGAGCCCTGTCCA AGAG |||||||||||| |||| || ||

GAGAG GAGAGACCTGTC GGTG AC GT A
CCGA--- T T- CAGC

GAM2032 CCGGAACCTGCTCATCTGGA 2009 AGAGTTGTTC 4620 GA - - A CAA G -- AAA
TCAAGAAGAATTTGCTAAAA ATCCAGGGAG CCG AC CTG CTC TCTGGAT GAA AATTT GCT
A
GAGCGGCCAGAGTTGTTCAT ACAG ||| || ||| ||| ||||||| ||| ||||| |||
CCAGGGAGACAGCGTGCGG GGC TG GAC GAG GGACCTA CTT TTGAG CGG G
G- C A - --- G AC CGA

GAM2033 GATGCCGACTGGGAGCTACT 2010 AGCTACTGGG 4621 CGA- GAGCTA GGT A
GGGTGAGCTGGACTACCAGC TGAGCTGGAC GATGC CTGG CTG GAGCTGG C
TTCAGGACCAGGACAGCGTC TACC ||||| |||| ||| |||||||
CTGCG GACC GAC TTCGACC T
ACAG AG---- --- A

GAM2034 GGCCAATTGAAACAAACAGT 2011 TATTAGGGAT 4622 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM2035 GTCCTTAAGGTTCAGCACAG 2012 GTGGAGCCCT 4623 - A- GT A---- C--- T CACG
CCTTCATCAGGCACGTCTTA CTGTGTATTC GT CCTTA G TC GCACAG CTTCA CAGG T
CCTGTGGAGCCCTCTGTGTA CGAG || ||||| | || |||||| ||||| ||||
TTCCGAGTCGGTGAGGTAC CA GGAGT C AG TGTGTC GAGGT GTCC /
T GG TG CCTTA TCCC - ATTC

GAM2036 AGCTGAAGTCACACATGAAA 2013 TGAAAGAAGC 4624 AG C ATG A C TC TT TTC
GAAGCCATGATCAAGCTTGG CATGATCAAG AGCTGA TCA AC AAAGA GC ATGA AAGC GGT
C
TTTCCACTTGCTCTGCTTCT CTTG |||||| ||| || ||||| || |||| |||| |||
TCATGTATCTTTATAGTATG TCGATT AGT TG TTTCT TG TACT TTCG TCG A
ATCTTAGCT CT A ATA A - TC TC TTC

GAM2037 AAGCTTAAGTGAGGATTTCC 2014 TCCCTTGTCA 4625 TAA A ---- - - T- T TT
TTGCAATGAGTAGAATTTCC CAGGTTTAAA AAGCT GTGAGG TTT CCT TG CAA GAG AGAA
T
CTTCTCTCCCTTGTCACAGG AACC ||||| |||||| ||| ||| || ||| ||| ||||
TTTAAAAACCTCACAGCTT TTCGA CACTCC AAA GGA AC GTT CTC TCTT C
--- A ATTT C T CC - CC

GAM2038 GGTCTACGCCATCTGTTATT 2015 TGTTATTGTC 4626 AC CTG T - ---- TC
GTCCCCTGCCTCGCCTGGCA CCCTGCCTCG GGTCT GCCAT TTA TGTC CC CTGCC G
GATCTGGAGGCGCTGAAAGT CCTG ||||| ||||| ||| |||| || |||||
GGCAGACT TCAGA CGGTG AGT GCGG GG GACGG C
-- AA- C A TCTA TC

GAM2039 ACGAACGGTTAAGCTGGCTG 2016 TGAGAATGGC 4627 -- GT GCTG C GAA-- ATT
TCCTGAACACTATTATAACG AAAATTAGTC ACGAA CG TAA GCTGT CT CACT A
GTGGACTGAGAATGGCAAAA GCCT ||||| || ||| ||||| || ||||
TTAGTCGCCTTCGT TGCTT GC ATT CGGTA GA GTGG T
CC TG AAAA A GTCAG CAA

GAM2040 TCTTGTGTCGAGACTTCGTG 2017 TACACCACTC 4628 CGAGA GT--- C - AAACAGG
GTGGTGCTAAGCAAACAGGA CCAAGAAGAA TCTTGTGT CTTC GGTGGTG TAAG C A
AGAAGAAGTCTTACACCACT TAAG |||||||| |||| ||||||| |||| |
CCCAAGAAGAATAAGCACAA AGAACACG GAAG TCACCAC ATTC G /
GA AATAA AACCC - T AAGAAGA

GAM2041 GCCAACCTTGAAGCCAGTGG 2018 TTGAAGCCAG 4629 A - TG - G - ATCC
GGCACCAATCCACAAACTGG TGGGGCACCA GCCA CC T AAGCCA GTG GGCA CCA A
ATGCTGCGCTTGGTTTTGAT ATCC |||| || | |||||| ||| |||| |||
GGTGGC CGGT GG A TTTGGT CGC TCGT GGT C
- T GT T G A CAAA

GAM2042 GGAGCTCGAGGCCCCTGGAG 2019 GTCAGCTTCT 4631 TC---- CCC AATT -- CC
GAATTGCTACACCCCCAGTG AGCTTTATAT GGAGC GAGGC TGGAGG GCT ACAC C
TATGGTCAGCTTCTAGCTTT TTGC ||||| ||||| |||||| ||| ||||
ATATTTGCTCC CCTCG TTTCG ATCTTC TGG TGTG /
TTTATA --- GAC- TA AC

GAM2043 GAACTTGGGGGAATTTGGTC 2020 TGGGGGAATT 4630 A TG TG--- TAGGAC
AGTAGGACAAAGAATCTGGC TGGTCAGTAG GA CT GGGGAATT GTCAG A
AGAGAGATTTCCCTGGGATC GACA || || |||||||| |||||
CT GG CCCTTTAG CGGTC /
A GT AGAGA TAAGAA

GAM2044 TGCCGGTGACAAATTAACAG 2021 AACACTCTGT 4632 - T AATT---- - --- G
AGGTCCTTGAAGAGGCTAAC TTAATGAAGT TGC CGG GACA AACAGAG GT CCTT A
ACTCTGTTTAATGAAGTGTC GTCC ||| ||| |||| ||||||| || ||||
CCGAGCA ACG GCC CTGT TTGTCTC CA GGAG /
A - GAAGTAAT A ATC A

GAM2045 TGGCATCCCAGATGTTGCAG 2022 TTGCAGTTGA 4633 AGA AG GAAG T CA A A

TTGAAGTCGTCGTAGCCAGC AGTCGTCGTA TGGCATCCC TGTTGC TT TCG CGTAGC GCG GC G
GAGCAGCAGCCGTCCGCTGC GCCA ||||||||| |||||| || ||| |||||| ||| ||
GCGAGAAGGCAACAGAGGGA ACCGTAGGG ACAACG AG AGC GCGTCG TGC CG C
TGCCA AG- GA ---- - CC - A

GAM2046 TCTGTGGGTTACGCCATCTT 2023 GGTTACGCCA 4634 GG - - A T G AAA
TAAGGTTCTAAATGAGAAGA TCTTTAAGGT TCTGTG TTA CG CC TCTT AAG TTCT T
AACTTCAAGAGGTTGATAGT TCTA |||||| ||| || || |||| ||| ||||
TTATGGA AGGTAT GAT GT GG AGAA TTC AAGA G
TT A T - C A AGA

GAM2047 GGGAAACTCCGAGGACAGAG 2024 TGGCCTGATG 4636 AAA A--- - GA AA TG A
GGCTAAATCCATGAAGTTTG ATCCACAGCG GGG CTCCG GGA CA GGGCT ATCCA A G
TGGATGGCCTGATGATCCAC GAGA ||| ||||| ||| || ||||| ||||| |
AGCGGAGACCC CCC GAGGC CCT GT TCCGG TAGGT T /
A-- GACA A AG -- GT T

GAM2048 GCCACGTGTTGCTCAGACAG 2025 ATGCTGCCCT 4635 C G T ACAG T G - T A G
GGTGTGCTGGGCATCAAGGT GGGACCCAAC GCCA GT TTGC CAG GG GT CT GGGCA CA GGT A
GAAGATCATGCTGCCCTGGG TGGT |||| || |||| ||| || || || ||||| || |||
ACCCAACTGGTAAGATTGGC CGGT TA AATG GTC CC CA GG CCCGT GT CTA A
- G - AA-- - G T C A G

GAM2049 TTGTCGTCATTGGACACGTA 2026 TAAATGCGGT 4637 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM2050 GGCTCCTCTGTTCCGACCTT 2027 CCTCTGTTCC 4638 C TC- - TCCC CAG
TCCCGTGCCCTGCAGATTTC GACCTTTCCC GGCTC TCTGT CGA CCTT GTGCCCTG A
TAGGGCGCACTGAGGCTCGA GTGC ||||| ||||| ||| |||| ||||||||
CCACGGAAGGGCC CCGGG AGGCA GCT GGAG CGCGGGAT T
A CCA C TCA- CTT

GAM2051 CTTCTTCAGTGAGACGGGCG 2028 TTTGTAGACT 4639 T GAC- CG ----- T C
CTGGCAAGCACGTGCCCCGG TGGAACCCAC CTTC TCAGTGA GGG CTG GCAAGCACG GCC C
GCTGTGTTTGTAGACTTGGA AGTC |||| ||||||| ||| ||| ||||||||| |||
ACCCACAGTCATTGATGAAG GAAG AGTTACT CCC GGT TGTTTGTGT CGG /
T GACA AA TCAGA - G

GAM2052 GCAAGGAAGATGCTGCCAAT 2029 CACTACACCA 4640 AA ----- - AACTA-- C
AACTATGCCCGAGGGCACTA TTGGCAAGGA GCAAGG GATG CT GCCAAT TGCC G
CACCATTGGCAAGGAGATCA GATC |||||| |||| || |||||| ||||
TTGACCTTGT TGTTCC TTAC GA CGGTTA ACGG A
AG TAGAG A CCACATC G

GAM2053 GGAGATCATTGACCTTGTGT 2030 CACCGGTCTT 4641 TT - TGTT AATTC AA C
TGGACCGAATTCGCAAGCTG CAGGGCTTCT GGAGATCA GA CCTTG GGACCG GC
GCTGG T
GCTGACCAGTGCACCGGTCT TGGT |||||||| || ||||| |||||| || |||||
TCAGGGCTTCTTGGTTTTC CTTTTGGT TT GGGAC TCTGGC CG TGACC G
TC C T--- CA--- -- A

GAM2054 TTTTTGATGAGAATGAGCTT 2031 CTTCAAAGCC 4643 -- AGA TG- T A AC- ACA
TG
GAGCTGCTGATGTGTGGGAC CATGCAGTAG TTTTTGA TG ATGAGCT AGC GCTG
TGTGTGGG TGGAG TCAG T
TGGAGACATCAGTGTGTCTG TTGT ||||||| || ||||||| ||| |||| |||||||| ||||| ||||
ACTTCAAAGCCCATGCAGTA AGAGACT AC TACTCGG TTG TGAT ACGTACCC
ACTTC AGTC /
GTTGTTGGTGGCTCATGGCA TT GG- TGG T G GAA --- TG
TTTCAGAGA

GAM2055 AGAGGTGCACAGGATGCTGC 2032 TCTGACCACT 4642 T CA T TG CCAT C TG- G
TTT
AGCTGGCCATCAGCGAGGGT CTCCTGTCAT AGAGG GCA GGA GC CAGCTGG CAG
GAGGGT C AGGGC G
TGCGAGGGCTTTGGCATGCT CCAG ||||| ||| ||| || ||||||| ||| |||||| | |||||
CTGACCACTCTCCTGTCATC TCTCT CGT CCT CG GTTGACC GTC CTCTCA G
TCTCG G
CAGTTGGCTCCCATGCTCTC - AC - -- TACT - CCA - TAC
T

GAM2056 GTATGGTACGGAGGAGGCCA 2033 TGGAATTTTC 4644 -- TA GG ACAGAAGC
TTACAGAAGCAAGCACCAAG TGGGCCGAAT GTAT GG CGGAGGA CCATT A
ATGGAATTTTCTGGGCCGAA AC |||| || ||||||| |||||
TAC CATA CC GTCTTTT GGTAG /
AG GG AA AACCACGA

GAM2057 TTCAGTGGGTTCTTCTTTAG 2034 TTGCGTGGTG 4645 T TTTA - C T A
GACTCTGCGATGGATCTTCT CCCGAAGGGC TTCAG GGGTTCTTC GG ACT TGCGA GG T
TGCGTGGTGCCCGAAGGGCT TCTT ||||| ||||||||| || ||| ||||| ||
CTTTGGA AGGTT CTCGGGAAG CC TGG GCGTT CT C
T C--- G T - T

GAM2058 ATGGCCGAGGAGAAGCGCGA 2035 TGCAAAACCA 4646 G -- A AGG A------- CC
GGGCTACGAGCGTCTCCTGA GCGTGGCGGC ATG CC GAGGAGA GCGCG GCTACG
GCGTCT T
AGATGCAAAACCAGCGTGGC GCGC ||| || ||||||| ||||| |||||| ||||||
GGCGCGCTCTCTTCCAGGAC TAC GG CTTCTCT CGCGC CGGTGC CGTAGA /
AT A AC - GG- GACCAAAA AG

GAM2059 GTGCAGATCTCAGTGGGCTG 2036 TCAGTGGGCT 4647 TG A CT TG TGGAT CA T
GATGCATGCAGGGTACCCCA GGATGCATGC G C GAT CAG GGC GCATG GGG A
TCATGTGCCATCTGGAGTCA AGGG | | ||| ||| ||| ||||| |||
GTGC C G CTG GTC CCG TGTAC CCC /
GT A AG TA ----- TA C

GAM2060 TCTTGTGTTGAGACTTCGTG 2037 TACACCACTC 4648 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM2061 GGTCTACGCCATCTGTTATT 2038 TGTTATTGTC 4649 AC CTG T - ---- TC
GTCCCCTGCCTCGCCTGGCA CCCTGCCTCG GGTCT GCCAT TTA TGTC CC CTGCC G
GATCTGGAGGCGCTGAAAGT CCTG ||||| ||||| ||| |||| || |||||
GGCAGACT TCAGA CGGTG AGT GCGG GG GACGG C
-- AA- C A TCTA TC

GAM2062 GTGGAGCGAGCCAAATGAAG 2039 AAAGCAGTTC 4650 G- AG AAATGA A ATCAAG
GT
AAGAGCTGATCAAGTTCATG TCTGAGGAGC GTGGA CG CC AGA GAGCTG TTCAT G
TGTGGTGAAAAGCAGTTCTC GAAT ||||| || || ||| |||||| |||||
TGAGGAGCGAATCCGC CGCCT GC GG TCT CTTGAC AAGTG /
AA GA AG---- - GAA--- GT

GAM2063 GTTCCCTGCCGAAGACTGGG 2040 TGGGAGGATA 4651 TG--- GAAGA TG - TTAGATGA
CGTGGCTTAGATGAAGATGA ATGGGGAT GTTCCC CC C GGCGTG GC A
AGATGCACATGTCTGGGAGG |||||| || | |||||| ||
ATAATGGGGAT TAGGGG GG G CTGTAC CG G
TAATA AG--- GT A TAGAAGTA

GAM2064 TTGTCGTCATTGGACACGTA 2041 TAAATGCGGT 4652 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM2065 GAAACAGACTGGGCCAATGT 2042 TATCAAGGAA 4653 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM2066 GAAACAGACTGGGCCAATGT 2043 TATCAAGGAA 4654 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM2067 GGCCAATTGAAACAAACAGT 2044 TATTAGGGAT 4655 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM2068 GGCCAATTGAAACAAACAGT 2045 TATTAGGGAT 4656 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM2069 CTTCACGCTGGGGCTAGCAG 2046 TGAGAACTCC 4657 - T - TAGC C G GAGT
GACTTCTCGGCGAGGGAGTT TCATGCACCC CTTCA CGC GGG GC AGGA TTCTCG CGAGG
T
TTTAACTTTGTGAGAACTCC TGTG ||||| ||| ||| || |||| |||||| |||||
TCATGCACCCTGTGCTGGAG GAGGT GTG CCC CG TCCT AAGAGT GTTTC T
C T A TAC- C - AATT

GAM2070 GAAACAGACTGGGCCAATGT 2047 TATCAAGGAA 4658 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||

TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM2071 GGCCAATTGAAACAAACAGT 2048 TATTAGGGAT 4659 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM2072 CTTGTGGGAGAGATTATCAA 2049 TCTGAAATTC 4660 T GA ATC -- T --- ---- AT
GCGTTTGAGCAGAAAGGATT ATGCAAGCTT CTTG GGGAGA TT AAGC GT TGAG CAGA
AAGG T
CCGCCTTGTGGTCTGAAATT CCGA |||| |||||| || |||| || |||| |||| ||||
CATGCAAGCTTCCGAAGATC GAAC TCTTCT AA TTCG CG ACTT GTCT TTCC C
TTCTCAAG - AG GCC AA T AAA GGTG GC

GAM2073 AACCCAGACGCCATGAAAGC 2050 ACGCCATGAA 4661 AC C AG- GCAT- AGAAAA
TGCATGGCCTGGAGAAAAAG AGCTGCATGG AACCCAG GC ATGAA CT GGCCTGG A
CTGAACCAGGCCCTTTTGGA CCTG ||||||| || ||||| || |||||||
TCTTCATGCCCTGGGTT TTGGGTC CG TACTT GG CCGGACC /
C- - CTA TTTTC AAGTCG

GAM2074 TGATGCGCAAGGCCATCCGA 2051 TCTGGAGAAA 4662 T - A GCCA G ACC AAA
GGGCACCTGGAAAACAACCC CTGCTGCCTC TGA GC GCA G TCC AGGGC TGG A
AGCTCTGGAGAAACTGCTGC A ||| || ||| | ||| ||||| |||
CTCA ACT CG CGT C AGG TCTCG ACC C
C T - AAAG - --- CAA

GAM2075 TGGAGGGGCCGGACTCGTCA 2052 GTGGACAGCG 4663 GG C A GT TAC -- A A-
TG
TACTCCTGCTTGCTGATCCA AGGCCAGGAT TGGA GGC GG CTC CA TCCTG CTTGCTG
TCCAC TC C
CATCTGCTGGAAGGTGGACA GGAG |||| ||| || ||| || ||||| ||||||| ||||| ||
GCGAGGCCAGGATGGAGCCG ACCT CCG CC GAG GT AGGAC GAGCGAC AGGTG
AG /
CCGATCCA AG - - -- --- CG - GA GT

GAM2076 GGTGACAACATGCTGGAGCC 2053 TTGGTTCAAG 4664 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM2077 TCTTGTGTTGAGACTTCGTG 2054 TACACCACTC 4665 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG |||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM2078 TATGCAGAAGCGAGAGAAGC 2055 TTGTTTGGCT 4666 AGAAGCG G CG AG ATA
TCGGCGGCCAGTCATATCTC TGTTTAACAG TATGC AGA AAGCT GCGGCC TC T
GAAGGTTGTTTGGCTTGTTT CATA ||||| ||| ||||| |||||| ||
AACAGCATA ATACG TTT TTCGG TGTTGG AG /
ACAA--- G TT A- CTC

GAM2079 GAGACTCTTCCAGGTCAAAG 2056 AGGTACCTGT 4667 GA T A - GG T C
GGCGGCGTGTGGTCCGTGCC GTCCTGGGAG GA CTCTTCCAGG CA AGG GC CG GTGGT C
ACCGAGGTACCTGTGTCCTG AGCT || |||||||||| || ||| || || |||||
GGAGAGCTTC CT GAGAGGGTCC GT TCC TG GC CACCG G
TC T G A GA - T

GAM2080 CAGGTGATCTGCCCACCTTG 2057 AATTACAGGT 4668 ATC - - GCCTC AA
GCCTCCCAAAGTGCTGGAAT GTGAGGCACA CAGGTG TGCC CAC CTTG CCA G
TACAGGTGTGAGGCACAACG ACGC |||||| |||| ||| |||| |||
CCTG GTCCGC ACGG GTG GGAC GGT T
AAC A T ATTAA CG

GAM2081 TAGCATTGGGTGCCAATTTC 2058 TGGGTGCCAA 4669 G G ATTT G GGAA
GTGGTGTGGAATGGTGACAA TTTCGTGGTG TAGCATT GGT CCA CGTG TGT T
CATGCGTGGAGCCAAGTGCT TGGA ||||||| ||| ||| |||| |||
A ATCGTGA CCG GGT GTAC ACA /
A A GC-- A GTGG

GAM2082 GGCGGCCAATAGTGTCTCTG 2059 AGTGTCTCTG 4670 G ATA CTC- T TT A-- TC
GTAGTTAGCAGCTTCACCGG GTAGTTAGCA GGCG CCA GTGT TGG AG AGC GCT A
CAAAGTTCTCTTCCATTTCA GCTT |||| ||| |||| ||| || ||| |||
CGCATCTGGCGTC CTGC GGT CGCA ACC TC TTG CGG /
- CTA CTTT T TC AAA CC

GAM2083 GAAACTGGTGATTGTTGGTG 2060 CTTGCTCATA 4671 A GA T G-- CT GAA
ATGGAGCCTGTGGAAAGACA GTCTTCAGCA GAA CTGGT TTGTTGG GAT GAGC GTG A
TGCTTGCTCATAGTCTTCAG AGGA ||| ||||| ||||||| ||| |||| |||
CAAGGACCAGTTC CTT GACCA AACGACT CTG CTCG CGT G
- GG T ATA TT ACA

GAM2084 GTATGGTACAGAGGAGGCCA 2061 TGGAATTTTC 4672 -- TA GG ACAGAAGC
TTACAGAAGCAAGCACCAAG TGGGCCGAAT GTAT GG CAGAGGA CCATT A
ATGGAATTTTCTGGGCCGAA AC |||| || ||||||| |||||
TAC CATA CC GTCTTTT GGTAG /
AG GG AA AACCACGA

GAM2085 GTAACAGGTACATAGGTAAC 2062 ACAGGTACAT 4673 C- TACAT A- GTATA
CAAAGTATATAGCTTATTTG AGGTAACCAA GTAA AGG AGGT ACCAAA T
GTGAATCTTCATCCTCATTA AGTA |||| ||| |||| ||||||
C CATT TCC TCTA TGGTTT A
AC TACT- AG ATTCG

GAM2086 GGCCAGGTTCTCGCTCTGTC 2063 CGGCACGGTC 4674 G CT C- TG- T T
GTGTCTGTTCAAACCGGCAC TGATCCGGAA GGCCA GTT CG TC TCGTGTC GT C
GGTCTGATCCGGAAATATGG ATAT ||||| ||| || || ||||||| ||
CC CCGGT TAA GC AG GGCACGG CA A
A AG CT TCT C A

GAM2087 CCAAGGAGCTAGAGGACTTT 2064 AAGGAGCTAG 4675 A - AG -- ATGA A
GAGATGAAGAAAGCTGCTGC AGGACTTTGA CCA GGA GCTAG GAC TTTGAG AG A
TCGAGCTGTCACTGGCGTCC GATG ||| ||| ||||| ||| |||||| ||
TGG GGT CCT CGGTC CTG GAGCTC TC A
- G A- TC GTCG G

GAM2088 CAGCTCTCCGGTCATCTTTG 2065 TTCCACAGCC 4677 CTCC TC CAG TCA C A-- AT
CAGGTGGTCAGGCCTATACC AGATTTGACC CAGCT GGTCA TTTG GTGG GGC TAT CC T
ATTCAAGGACAGTATGCCAT AAGC ||||| ||||| |||| |||| ||| ||| ||
TCCACAGCCAGATTTGACCA GTCGA CCAGT AGAC CACC CCG ATG GG C
AGCTG A--- TT CGA TTA T ACA AA

GAM2089 ATCAATGAGATCCGTCAGAT 2066 AACCCAGTGG 4676 ATG G AGATGT G- ATC
GTCTGGGGCGCAGATCAAAA AAGGATCTAC ATCA AGATCC TC CTGGG CGCAG A
TTGCGAACCCAGTGGAAGGA TGAT |||| |||||| || ||||| |||||
TCTACTGAT TAGT TCTAGG AG GACCC GCGTT /
CA- A GT---- AA AAA

GAM2090 GCACTCTGTTCTTCCGCCGC 2067 ACTCTGTTCT 4678 AC G CC TCC TC TT
TCCGCCGTCGCGTTTCTCTG TCCGCCGCTC GC TCT TTCTTCCG GC GCCG GCG T
CCGGTCGCAATGGAAGAAGA CGCC || ||| |||||||| || |||| |||
GATCGC CG AGA AAGAAGGT CG TGGC CGT C
CT G AA C-- -- CT

GAM2091 AAGATAGAGGCAGAACTGCA 2068 TGTTCTGGAG 4679 GA----- AA G TG
GGACATCTGCAATGATGTTC CTGTTGGACA AAGATA GGCAG CT CAGGACATC C
TGGAGCTGTTGGACAAATAT AATA |||||| ||||| || |||||||||
CTT TTCTAT TTGTC GA GTCTTGTAG A
AAACAGG -- G TA

GAM2092 AGGACGCGGCCGCAAGCTTA 2069 CTTGGCACTG 4680 - ---- TATT---- T
TTCCCTTTAGTGAGGGTTAA GCCGTCGTTT AGGACG CGGCCG CAAGCT CCCTT A
TTTTAGCTTGGCACTGGCCG T |||||| |||||| |||||| |||||
TCGTTTT TTTTGC GCCGGT GTTCGA GGGAG G
T CACG TTTTAATT T

GAM2093 ATGGTGACAACATGCTGGAG 2070 AGGGATGGAA 4681 AA-- G G T TA
CCAAGTGCTAACATGCCTTG AGTCACCGT ATGGTGAC CAT CT GAGCCAAG GC A
GTTCAGGGATGGAAAGTCAC |||||||| ||| || |||||||| ||
CGT TGCCACTG GTA GG CTTGGTTC CG C
AAAG G A - TA

GAM2094 TTGTCGTCATTGGACACGTA 2071 TAAATGCGGT 4682 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM2095 TGATCTGGAAGCCAACCTGG 2072 TGGAAGCCAA 4685 A CCAACCT TCC G T
CTGTCCTGAAGCTGTACCAG CCTGGCTGTC TG TCTGGAAG GGCTG TGAA CTG A
TTCAACCCAGCCTTCTTTCA CTGA || |||||||| ||||| |||| |||
GACCA AC AGACTTTC CCGAC ACTT GAC /
C TT----- CCA - C

GAM2096 GGATGAAAACATGGACCTCT 2073 CTTTGAAGAC 4684 AACA C--- G G T
TGGAAGGTATAACTGGCTTT TCTGTCCGAA GGATGAA TGGAC TCTT GAAG TA A
GAAGACTCTGTCCGAAAGTT AGTT ||||||| ||||| |||| |||| ||
TATCT TCTATTT GCCTG AGAA TTTC GT A
GAAA TCTC G G C

GAM2097 GAGAGCATTAGACCCAAGAC 2074 GAGCATTAGA 4683 GACCCAA - G AAG
CATTGTGGAGAAGATTGACT CCCAAGACCA GAGAGCATTA GAC CATTGT GAG A
TGACAGTGTGTCCAGCATAA TTGT |||||||||| ||| |||||| |||
TGCTCTC CTCTCGTAAT CTG GTGACA TTC T
ACGAC-- T G AGT

GAM2098 GGCCAATTGAAACAAACAGT 2075 TATTAGGGAT 4686 C T ACAAACAG G GTT T A
GAT

TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM2099 GAAACAGACTGGGCCAATGT 2076 TATCAAGGAA 4687 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM2100 GGTTTCAGCATGTCCTTCTC 2077 GACAACATTA 4688 T TCCTT CTG A AATACTT TA
TGAATGATGAATACTTTTAC ACGGTCCTCA GGT TCAGCATG CT AATG TG TTAC C
TACTTGTGACAACATTAACG TGCT ||| |||||||| || |||| || ||||
GTCCTCATGCTGATACC CCA AGTCGTAC GG TTAC AC AGTG /
T TCCT- CAA A ------- TT

GAM2101 GCTGGGGTGCTAGGACTTGG 2078 TACGATGTTC 4689 - ACT T- - TT-- T
TGCATGTGTTCTTTCTAGTC CCACCTGGAT GCTGGGGTG CTAGG TGG GCAT GTG CT T
CTTACGATGTTCCCACCTGG GCCC ||||||||| ||||| ||| |||| ||| ||
ATGCCCCAGC CGACCCCGT GGTCC ACC TGTA CAT GA C
A --- CT G TCCT T

GAM2102 GTGGGAACGGGTGGCCCGGC 2079 TAGCAAGCAG 4690 - GG-- CG - GT TAA
TGTGTGACTTTAACCCCAAG GCCAAAGATG GTGGGA ACG TGGCC GCT GT GACTT C
TCTAGCAAGCAGGCCAAAGA TCTC |||||| ||| ||||| ||| || |||||
TGTCTCCCGC CGCCCT TGT ACCGG CGA CG CTGAA /
C AGAA A- A AT CCC

GAM2103 TCGAATGCAACTCTCTTTTT 2080 TTTCAAAGGA 4691 C CT TG C
TGAGATTGAGCTCCTTGATT GAGGATTTAT TCGAATG AA CTCTTTTTTGAGAT AG T
TCAAAGGAGAGGATTTATTT TTGA ||||||| || |||||||||||||| ||
GA AGTTTAT TT GAGAGGAAACTTTA TC /
- AG GT C

GAM2104 TGCGCTGAATGATGTCACGG 2081 TGAATGATGT 4692 AAT TG CAC- GT AA
CAGTCGTTGAACACACGGCG CACGGCAGTC TGCGCTG GA T GGCA CGTTG C
GATGTTCTCAGTGTCCACAG GTTG ||||||| || | |||| |||||
CGCA ACGCGAC CT G TTGT GCGGC A
AC- GT ACTC AG AC

GAM2105 AAGGGGTTTTCGCAAAATCA 2082 ATGCCCTATG 4693 G TTCGCAA GGGGA AAA
CT
CTCGGGGGAAGGGAAAGGTT GTGGGTGATT AAG GGTT AATCACTCG AGGG GGTTG T
GCTTTGTTAATCATGCCCTA AACT ||| |||| ||||||||| |||| |||||
TGGTGGGTGATTAACTGCTT TTC TCAA TTAGTGGGT TCCC CTAAT T
G ------- GGTA- GTA TG

GAM2106 GGTGAAATGAGGGTAGCAGT 2083 TAGCAGTAGT 4694 AA--- AG G ACGC TCT
AGTGACGCCCATCTCCACTG GACGCCCATC GGTGA TGAGGGT CAGTA TG CCA C
GCAGTGCTGATCCTCAGAAA TCCA ||||| ||||||| ||||| || |||
CTCATC CTACT ACTCCTA GTCGT AC GGT /
CAAAG -- G ---- CAC

GAM2107 GGTGACAAACATGCTGGAGA 2084 TTGGTTCAAG 4695 AAA-- G GGA GCT
CCAAGTGCTACATGCTTGGT GGATGGACAA GGTGAC CAT CT GACCAAGT A
TCAAGGGATGGACAAGTCAC GTCA |||||| ||| || ||||||||
C CCACTG GTA GG TTGGTTCG /
AACAG G AAC TAC

GAM2108 CATTGTCGTCATTGGACACG 2085 CGTCATTGGA 4696 GTC-- T- A C ATTC C
TAGATTCGGGCAAGTCCACC CACGTAGATT CATT GTCA TGG CA GTAG GGG A
ACTACTGGCCATCTGATCTA CGGG |||| |||| ||| || |||| |||
TAAATG GTAA TAGT ACC GT CATC CCT A
ATATC CT G - ACCA G

GAM2109 GGTGACAACATGCTGGAGCC 2086 TTGGTTCAAG 4697 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM2110 ATGATGAACAGTATGCTTGG 2087 AGGTTCCTTC 4698 G AA TT----- GT T
GAGTCTTCTGCTGGAGGTTC ACTGTGCGTG AT ATG CAGTATGC GGGA CTTC G
CTTCACTGTGCGTGCTGACC CTGA || ||| |||||||| |||| ||||
ATGGT TG TAC GTCGTGCG TCCT GAGG C
G CA TGTCACT TG T

GAM2111 TTTCTCAGTTCATAGGCTAT 2088 TATCCCATCA 4699 AG ATAG A C- ------ A GAGA
CCCATCACCCTTTATTTGGA CCCTTTATTT TTTCTC TTC GCT TC CATCAC CCTTT TTTG
A
GAAGGAACGAGAGAAGGAAA GGAG |||||| ||| ||| || |||||| ||||| ||||
TTAGTGATGATGAGGCAGAG AAAGAG AAG CGG AG GTAGTG GGAAG GAGC /
GAAGAGAAA -- GAGA - TA ATTAAA A AAGG

GAM2112 GAATATTTCCACAATGTCTG 2089 TACACGGTCG 4700 CACA T AAC G TTCA
TGAACTGGACCTGGTGTTCA TGGACGAGAT GAATATTTC ATG CTGTG TGGACCT GTG A
ACTTCTACAAGGTTTACACG GTTC |||||||||| ||| ||||| ||||||| |||
GTCGTGGACGAGATGTTC CTTGTAGAG TGC GGCAC ATTTGGA CAT /
CAGG T --- A CTTC

GAM2113 GTAGTGGGTGTTGAGATTGA 2090 TTGAATTTTT 4701 T T T- G TCTTAAT - GCT
ACGCTTTCTTAATTGGTGGC TACTCTCTCT GTAG GGG GT GAGATT AACGCTT TGGT
GGCT T
TGCTTTTAGGCCTACTATGG AC |||| ||| || |||||| ||||||| |||| ||||
GTGTTGAATTTTTTACTCTC CATC CTC CA TTTTAA TTGTGGG ATCA CCGG /
TCTAC T T TT G T------ T ATT

GAM2114 GGCCAATTGAAACAAACAGT 2091 TATTAGGGAT 4702 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM2115 TTGTCGTCATTGGACACGTA 2092 TAAATGCGGT 4703 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM2116 GTGTGTCATCGATATCCTCA 2093 TACGAGTTTG 4704 ATC--- AT TT TA ACC
TTTTCTATGGCACCTTCAGC GGGCAGTCTC GTGTGTC GAT CCTCA TTC TGGC T
TACGAGTTTGGGGCAGTCTC CTCA ||||||| ||| ||||| ||| ||||
CTCAGACACAC CACACAG CTG GGGGT GAG ATCG /
ACTCCT AC TT C- ACT

GAM2117 GACATCTGTCACCCCAGTGA 2094 TGATCTGGCT 4709 ACC -- - ATGGT
TCGCCATGGTTGATTCGGCT GGCTAGGCGG GACATCTGTC CCAGT GATC GCC T
GATCTGGCTGGCTAGGCGGG GTGT |||||||||| ||||| |||| |||
TGTC CTGTGGGCGG GGTCG CTAG CGG /
ATC GT T CTTAG

GAM2118 CGAGTAGCTGCGCTCCCCTG 2095 TAGGAGAACG 4708 - ------ GC C TAGAA C CAA
CT
CTAGAACCTCCAAACAAGCT TAGGGTAGTC CGA GT AGCT GCT CCCTGC CCT CAAA
GCT C

CTCAAGGTCCATTTGTAGGA AAGC ||| || |||| ||| |||||| ||| |||| |||
GAACGTAGGGTAGTCAAGCT GCT CA TCGA TGA GGGATG GGA GTTT TGG /
TCCAAGACGTCG G GAACCT AC T CAAGA T ACC AA

GAM2119 GGCTGGGGCTCATTTGCAGG 2096 GCTCATTTGC 4711 - CT T A CAAA TCA
GGGGAGCCAAAAGGGTCATC AGGGGGGAGC GGC TGGGG CATT GCAGGGGGG GC AGGG
T
ATCTCTGCCCCCTCTGCTGA CAAA ||| ||||| |||| ||||||||| || ||||
TGCCCCCATGTT TTG ACCCC GTAG CGTCTCCCC CG TCTC /
T C- T - ---- TAC

GAM2120 CATGACCACAGTCCATGCCA 2097 ATGGCCCCTC 4710 A CCATG ATCACT- - - A
TCACTGCCACCCAGAAGACT CGGGAAACTG CATG CCACAGT CC GCCA CC CAG A
GTGGATGGCCCCTCCGGGAA TGGC |||| ||||||| || |||| || |||
ACTGTGGCGTG GTGC GGTGTCA GG CGGT GG GTC G
- AA--- GCCTCCC A T A

GAM2121 TCTTGTGTTGAGACTTCGTG 2098 TACACCACTC 4712 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM2122 GAAGAATGTGGATCAGTTTT 2099 TTTCATCGAC 4713 A--- C TT CT GA
GATGGAACTTGGAGTACGTT TTATCTATGA GAAGA TGTGGAT AGTT GATGGAA TG G
TTCATCGACTTATCTATGAG GCAT ||||| ||||||| |||| ||||||| ||
CATCTTC CTTCT GTATCTA TCAG CTACTTT GC /
ACGA T -- T- AT

GAM2123 CTGTACGCTCCCACGGTGGC 2100 ACGCTCCCAC 4714 A - G TG AT- ACT TTCCAC
ACATGAACGACTTCTTCCAC GGTGGCACAT CTGT CGCTC CCAC G GCAC GAACG TC T
TCCTTCCTGATTGTGTTCCG GAAC |||| ||||| |||| | |||| ||||| ||
CGTGCTGTGTGGAGAGTGGA GATA GTGAG GGTG T CGTG CTTGT AG C
TAG G A - GT CGC GTT TCCTTC

GAM2124 GTTTGCCACATGTAGCCAGG 2101 TAATCAGGCC 4715 - AC-- AG T TGTG C A G
GGTCCTTGTGGATCACTATC CAGGCTGCGT GTTT GCC ATGTAGCC GGG CCT GAT ACT
TCTG A
TGGAGTCAGAGGTAATCAGG TGAA |||| ||| |||||||| ||| ||| ||| ||| ||||
CCCAGGCTGCGTTGAAGGCT CAAG CGG TGCGTCGG CCC GGA CTA TGG AGAC G
GAAC T AAGT A- - ---- A - T

GAM2125 CACCATGTTGGCCAGGCTGG 2102 GGGGATCCGC 4716 CA TT- C- T CTC A A

TCTCGAACTCCTGACTCAGG CCGCCTCAGC CAC TG GGC AGGC GGT GA CTCCTG C
GGATCCGCCCGCCTCAGCCT CTCT ||| || ||| |||| ||| || ||||||
CTCAAAGTG GTG AC CCG TCCG CCG CT GGGGAC /
AA TCT AC C C-- A T

GAM2126 GGTCCGGGGAGCAGCCCAGA 2103 GGGGAGCAGC 4718 GG GC- A - ACCAGC - GC
GGCGGGGGGCCCACCAGCTC CCAGAGGCGG GGTCC GGA AGCCC GAGGCGGG GGGCCC TC TGA A
TGAGCAGATCATGAAGACAG GGGG ||||| ||| ||||| |||||||| |||||| || |||
GGGCCCTTTTGCTTCAGGGT CTAGG CCT TTGGG CTTCGTTT CCCGGG AG ACT /
TTCATCCAGGATC A- ACT A T GACAGA T AG

GAM2127 GCTGCAGAGGATGATTGCCG 2104 TTTTTCCGAG 4717 - GA----- CG CAC CCCC
CCGTGGACACAGACTCCCCC TGGCAACTGA GCTG CAGAGGAT TTGCCGC TGGA AGACT C
CGAGAGGTCTTTTTCCGAGT CATG |||| |||||||| ||||||| |||| |||||
GGCAACTGACATGTTTTCTG CGGC GTCTTTTG AACGGTG GCCT TCTGG C
ACGGC A TACAGTC A- TTT AGAG

GAM2128 GGCCAATTGAAACAAACAGT 2105 TATTAGGGAT 4719 C T ACAAACAG G GTT T A GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM2129 CCAGTCAGGGTCTTCACGAA 2106 TCAGGGTCTT 4721 TC TT GAAGA CCA- AA
GATCTGCATCCCACCTCTAA CACGAAGATC CCAG AGGGTC CAC TCTGCATC CCTCT G
GACGGAGGACCAGGTGCAGG TGCA |||| |||||| ||| |||||||| |||||
GTGGACTCTTTCTGG GGTC TCTCAG GTG GGACGTGG GGAGG /
TT -- ----- ACCA CA

GAM2130 CAGGTGCAGGGTGGACTCTT 2107 TGCGTCCATC 4720 G C TCT GA TTG
TCTGGATGTTGTAGTCAGAC TTCCAGCTG CAG TG AGGGTGGAC TTCTG TG T
AGGGTGCGTCCATCTTCCAG ||| || ||||||||| ||||| ||
CTG GTC AC TTCTACCTG GGGAC AC /
G C CGT AG TGA

GAM2131 ACCTGCGCCCTCCTGCCTCC 2108 GGTCAAGCTG 4722 C C G TC GT C A--- T T
TGTGACCTCGAGATCTCTCT AGTCTGAGCG AC TG GCCCTCCT CC CT GAC TCG GATCTC C T
TCGGGGGGTCAAGCTGAGTC GAGG || || |||||||| || || ||| ||| |||||| |
TGAGCGGAGGAGGGCCCGAG TG GC CGGGAGGA GG GA CTG AGT CTGGGG G C

T A C - C- GT - CGAA - G

GAM2132 GTGGCGCAGAGTGTGGGCCG 2109 GCGCAGAGTG 4723 C A G CGCC C AGT
CGCCTTCCTGGAGTACTACC TGGGCCGCGC GTGG GCAG GTGTG GCCG TTC TGG A
AAGAGCACCTGGCGTACGCC CTTC |||| |||| ||||| |||| ||| |||
TGCCCCAC CACC CGTC CGCAT CGGT GAG ACC /
C - G CCAC A ATC

GAM2133 CCCATCTCTGTGACTTCCTG 2110 TGGGAAGGGA 4724 - -- GGAGA T
GAGACTCATTTCTAGATGGG AGTTATCAAG CCCATC TCT GTGACTTCCT CTCATT C
AAGGGAAGTTATCAAGACGA ACGA |||||| ||| |||||||||| ||||||
TGGG GGGTAG AGA TATTGAAGGG GGGTAG T
C AC AA--- A

GAM2134 GAAACAGACTGGGCCAATGT 2111 TATCAAGGAA 4725 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM2135 GGCCAATTGAAACAAACAGT 2112 TATTAGGGAT 4726 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM2136 GGATCTCTGAAGACATCCTT 2113 TCCAAGGGGA 4727 AT AA C ATT CA
ATTGACGACAGTTTTGTCCA TATCCACAGA GG CTCTG GA ATCCTT GACGA G
AGGGGATATCCACAGAGTAC GTAC || ||||| || |||||| |||||
C CC GAGAC CT TAGGGG CTGTT /
AT AC A AAC TT

GAM2137 GGCCAATTGAAACAAACAGT 2114 TATTAGGGAT 4728 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM2138 CCTTAGATGTTCTGACAGCA 2115 TAGATGTTCT 4730 TAG- GA - C- TTT
CTGCACCTTTGGCTTGGTTT GACAGCACTG CCT ATGTTCT CAGC ACTG ACC G
CAGTGGTTGGTGGAACATGA CACC ||| ||||||| |||| |||| |||
ATAGG GGA TACAAGG GTTG TGAC TGG G
TAAG TG G TT TTC

GAM2139 ACCACATTGTTGCTTGGAGA 2116 CACATTGTTG 4729 A G TG GA -- TTTTCG
CATGTCATTTTCGCGTCTGT CTTGGAGACA ACC CATTGTT CT GA CA TGTCA C
CTGACATTTGCGTCTGAGAA TGTC ||| ||||||| || || || |||||
ACAATGCGGT TGG GTAACAA GA CT GT ACAGT G
C A GT GC TT CTGTCT

GAM2140 GGAGATCATTGACCTTGTGT 2117 CACCGGTCTT 4733 TT - TGTT AATTC AA C
TGGACCGAATTCGCAAGCTG CAGGGCTTCT GGAGATCA GA CCTTG GGACCG GC
GCTGG T
GCTGACCAGTGCACCGGTCT TGGT |||||||| || ||||| |||||| || |||||
TCAGGGCTTCTTGGTTTTC CTTTTGGT TT GGGAC TCTGGC CG TGACC G
TC C T--- CA--- -- A

GAM2141 CTTCTTCAGTGAGACGGGCG 2118 TTTGTAGACT 4732 T GAC- CG ----- T C
CTGGCAAGCACGTGCCCCGG TGGAACCCAC CTTC TCAGTGA GGG CTG GCAAGCACG
GCC C
GCTGTGTTTGTAGACTTGGA AGTC |||| ||||||| ||| ||| ||||||||| |||
ACCCACAGTCATTGATGAAG GAAG AGTTACT CCC GGT TGTTTGTGT CGG /
T GACA AA TCAGA - G

GAM2142 CAGTTGATTATGGCAAGAAG 2119 TATGGCAAGA 4731 ATTA - AAGTCCAA A CTC
TCCAAGCTGGAGTTCTCCAT AGTCCAAGCT CAGTTG TGG CAAG GCTGG GTT C
TTAACCCAGCACCCCAGGTT GGAG |||||| ||| |||| ||||| |||
TGTCCACAGCTG GTCGAC ACC GTTT CGACC CAA A
---- T GGACCCCA - TTT

GAM2143 TGCTGGCCTTGGGAAGGCCG 2120 GAACTGCGAG 4734 CT GGAA -- AG T
CGGAGCTGGTGACCCAGAAC GCTTATGAGG TG GGCCTTG GGCC GCGG CTGG G
TGCGAGGCTTATGAGGCCCA CCCA || ||||||| |||| |||| ||||
CA AC CCGGAGT TCGG CGTC GACC A
AC AT-- AG AA C

GAM2144 GCCATCCCGGGCAGTGGGCA 2121 GCACGGTGGT 4735 GGG CAAA ATACC CCA
CCGTCAAAGTATACCTGCCC GACTGTCCGG GCCATCCCGGGCAGT CACCGT GT TGC A
AACAAGCAACGCACGGTGGT GATG |||||||||||||| |||||| || |||
GACTGTCCGGGATGGC CGGTAGGGCCTGTCA GTGGCA CA ACG /
GTG CG-- ----- AAC

GAM2145 TTGTCGTCATTGGACACGTA 2122 TAAATGCGGT 4736 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM2146 TGACTTGGAAGGTGCCCTGT 2123 TCACATGCCA 4738 GGAA C T T CGT TG A
CACG
GCTATGTCGTGCCTGCAGGG GGTCACCAGG TGACTT GGTG CCTG GC ATGT GCC C
GGGA T
ACACGTCGGATCCCGTGGGC TCA |||||| |||| |||| || |||| ||| | ||||
CTCACATGCCAGGTCACCAG ACTGGA CCAC GGAC CG TACA CGG G CCCT /
GTCA ---- T - - CTC GT - AGGC

GAM2147 GCAGACTCATGCAGCCCTAT 2124 CAACTATCAG 4737 CTCAT A - CC AGACCA
GGCCGCTCAGACCAAGGCGC GGCAGCTCTG GCAGA GC GCCCT ATGG GCTC A
AGAGCAACTATCAGGGCAGC C ||||| || ||||| |||| ||||
TCTGC CGTCT CG CGGGA TATC CGAG /
----- A C AA ACGCGG

GAM2148 GTAGAGCTTTATGCTGAAAA 2125 GAGCTTTATG 4740 - TA GAAAA - T A
GGTGGCCACTAGAGGTCTGT CTGAAAAGGT GTAGAG CTT TGCT GGTGGC CAC AG G
GTGCCATTGCCCAGGCAGAG GGCC |||||| ||| |||| |||||| ||| ||
TCTCTGC CGTCTC GAG ACGG TTACCG GTG TC G
T -- ACCCG T - T

GAM2149 GGGAAACTCCGAGGACAGAG 2126 TGGCCTGATG 4739 AAA A--- - GA AA TG A
GGCTAAATCCATGAAGTTTG ATCCACAGCG GGG CTCCG GGA CA GGGCT ATCCA A G
TGGATGGCCTGATGATCCAC GAGA ||| ||||| ||| || ||||| ||||| |
AGCGGAGACCC CCC GAGGC CCT GT TCCGG TAGGT T /
A-- GACA A AG -- GT T

GAM2150 TCTTGTGTTGAGACTTCGTG 2127 TACACCACTC 4741 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM2151 TCTTGTGTTGAGACTTCGTG 2128 TACACCACTC 4742 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM2152 GGCGTTCAGCAGAGTCAGGG 2129 CAGCAGAGTC 4743 ---- - - C GATG C TATA
ATGGGTCCATTATATGATCC AGGGATGGGT GGCGTT CAGCA GA GT AGG GGT CAT T
ATGAACCAGAACCTCACATC CCAT |||||| ||||| || || ||| ||| |||
TTGCTGTTCCGGCGCC CCGCGG GTCGT CT CA TCC CCA GTA G
CCTT T A C AAGA A CCTA

GAM2153 CCCTGGAGGAGATCTATCTC 2130 AGAGATCATT 4744 T T--- TCTC GCC
TTCTCCCTGCCTATTAAGGA GATTTCTTCC CCC GGAGGAGATC ATCTCT CCT T
ATCAGAGATCATTGATTTCT TGGG ||| |||||||||| |||||| |||
TCCTGGG GGG CCTTCTTTAG TAGAGA GGA A
T TTAC CTAA ATT

GAM2154 GGTTCCGGTTCTGTGGTGAT 2131 TGGCAGAAAT 4745 TT TCT G -- GACTGT G
CTGGACTGTCCCGACTGGGT CAGCACGCTG GG CCGGT GTG TGA TCTG CCC A
CCTGGCAGAAATCAGCACGC GCC || ||||| ||| ||| |||| |||
TGGCC CC GGTCG CAC ACT AGAC GGG C
-- --- G AA GGTCCT T

GAM2155 GACGGCCATGCTGGTCTGCA 2132 TACAAGATCA 4747 C ATGCTG G - A- C- -- - A
AGTCAGAGTCCGTGCCACCT CTGACTCTGA GA GGCC GTCT CA AGTCAG GTC GTGCCA
CCT GTC C
GTCACTGACTGGGCCTGGTA GGAC || |||| |||| || |||||| ||| |||||| ||| |||
CAAGATCACTGACTCTGAGG CT CCGG CAGG GT TCAGTC TAG CATGGT GGG CAG
/
ACAAGGCCCTC C AA---- A C AC AA CC T T

GAM2156 CGGCTCCGAGAGCAGGTTCT 2133 TACACATTGA 4746 - AGAG C-- - -- CA
TCGTGAGTTCCTCGCAGGGC GAACCTGAAC CGGC TCCG CAGGTTCTT GTG AGTTCC TCG
G
CGGTCGGAGCTACACATTGA ATGG |||| |||| |||||||| ||| |||||| |||
GAACCTGAACATGGAGGCCG GCCG AGGT GTCCAAGAG CAC TCGAGG GGC G
G ACAA TTA A CT CG

GAM2157 GTGGATCGGCGGCTCCATCC 2134 TCAGCAAGCA 4748 TC - - CA----- GC C - CT
CA
TGGCCTCGCTGTCCACCTTC GGAGTATGAC GTGGA GGC GG CTC TCCTG CT GCTG
TCCAC TC G
CAGCAGATGTGGATCAGCAA GAGT ||||| ||| || ||| ||||| || |||| ||||| ||
GCAGGAGTATGACGAGTCCG TACCT CCG CC GAG AGGAC GA CGAC AGGTG AG
/
GCCCCTCCAT CC G T CAGTATG -- A T T- AC

GAM2158 TGTCCAATGATTGAAGCCAG 2135 AAGAATCATG 4750 - G TG GGAA A G--- TG - AA

GAAGAATCATGGGCTGGTAT GGCTGGTATT TGTCCA AT AT AAGCCA GA TCAT GGC GTATTT GT A

TTGTAAAAGACAAGATATTT TGTA ||||||| || || |||||| || |||| ||| |||||| ||

GCTGTGGGTGGTCAGAATGG ACAGGT TG TG TTTGGT CT GGTG TCG TATAGA CA /

TTTAGGTGGTCTGGACA C G GA AAGA - GGTG TT A GA

GAM2159 AGTTTAGGAAACAATGTTTC 2136 ATCCTGCCTC 4749 GAAACA - - AG ----- A T

TGGGAGAGTGCTTAATTCCT AGAAACATGG AGTTTAG ATGTTTCTG GG AG T GCTT AT C

GTGAAGTTTATGATCCTGCC ACTG ||||||| ||||||||| || || | |||| ||

TCAGAAACATGGACTGAGCT TCGAGTC TACAAAGAC CC TC A TGAA TG C

AGG--- T G CT GTATT G T

GAM2160 GCCTGAAGACGTACACTGGC 2137 TTACTGGTGG 4751 T AG TA- GG A - - ACT T

CACAAGAATGAGAAATACTG GAAGTGGATT GCC GA ACG CACT CCAC AG AAT GAGAAAT GCA A

CATATTTGCCAATTTCTCTG GTGT ||| || ||| |||| |||| || ||| ||||||| |||

TTACTGGTGGGAAGTGGATT CGG CT TGT GTGA GGTG TC TTG CTCTTTA CGT T

GTGTCTGGC T G- TAG AG G A T AC- T

GAM2161 CCGTGGTTCCTCACCTGCAT 2138 TGTCTTGGGG 4752 GG CT C-- AA ------- CAG

TAACCAGCCCCAGTTCCGGG GAAGTGCAAC CCGT TTC CAC TGCATT CC AGCCC T

CTGTCTTGGGGGAAGTGCAA TGTG |||| ||| ||| |||||| || |||||

CTGTGGAGAAAGATGG GGTA AAG GTG ACGTGA GG TCGGG /

GA AG TCA AG GGTTCTG CCT

GAM2162 GCTCATCCTCCGTCCTGTCG 2139 TGAAACTTGC 4753 C-- TG G CT A T- GAG T

TTCTGAAACTTGCTGAGGAA TGAGGAACTC GCTCATCCT CGTCC TC TT GAA CT GCT GAACTC A

CTCTATGAGTTTGGCCTGGT TATG ||||||||| ||||| || || ||| || ||| ||||||

TCTTGAGGAGGATGTCTAGG CGGGTAGGA GTAGG AG AG CTT GG CGG TTTGAG /

ATGGGC TCT -- G TT - TC --- T

GAM2163 CAAACAAGAGGACTGTGTTG 2140 TGTGTTGTGG 4754 AA - A T T TG C - - T

TGGTCTGGGGAGAATGTAAT TCTGGGGAGA CA CA AG GGAC GTGT G GT TG GGGAG AATG A

CATTCCTTCCACAACTGCTG ATGT || || || |||| |||| | || || ||||| ||||

CATGTCCCTGTGGGTG GT GT TC CCTG TACG C CA AC CCTTC TTAC A

GG G - - T GT - A C T

GAM2164 GTCTACAAGCATTTTGAAAT 2141 TACAAGCATT 4755 A AG--- TT- AT C

ATTCTGTGCCTTCGCAGAAT TTGAAATATT GTCT CA CAT TGAAAT TCTGTG C

TTCGTGTGTGATCACTGAGG CTGT |||| || ||| |||||| ||||||
AC CAGG GT GTG GCTTTA AGACGC T
A CACTA TGT -- T

GAM2165 CAGTTGGTCTTGGCACTCAG 2142 TGTCAGGGAG 4756 CT A - C --- C G AT
CCAGCTTCGCCTCCGTGATC CTGCTGCAGG CAGTTGGT TGGC CT CAGC AGCTTC GC TCC
TG C
TTCAGGATGTCAGGGAGCTG TCAG |||||||| |||| || |||| |||||| || ||| ||
CTGCAGGTCAGCCAGCTG GTCGACCG ACTG GA GTCG TCGAGG TG AGG AC /
-- - C - GAC T - TT

GAM2166 GGGCTGCGGGCGACCTTTAC 2143 TACCATAGGA 4757 TGCGGG TT ATAGG A-- -
T
CATAGGACGAAGTAACCTTG CGAAGTAACC GGGC CGACC TACC ACG AGTA
ACCTTGCAT C
CATTCGGATGCAAGGTGTAC TTGC |||| ||||| |||| ||| |||| |||||||||
TGTACGTACACAGGTGCTGG CCTG GCTGG GTGG TGC TCAT TGGAACGTA G
TCGATGTCC TA---- TC ACACA ATG G G

GAM2167 CCTTCGCTAGTCTCCGTATG 2144 TCGCTAGTCT 4758 C AGT--- G CGT-- AAC
GCCCGTGCCAACGCCCGGCT CCGTATGGCC CCTT GCT CTCCGTATG CC GCC G
CTTCGGCATACGGGGCAAAA CGTG |||| ||| ||||||||| || |||
GAGCCAAGG GGAA CGA GGGGCATAC GG CGG /
C GAAAAC - CTTCT CCC

GAM2168 TCTTGTGTTGAGACTTCGTG 2145 TACACCACTC 4759 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM2169 AACTGGTGATTGTTGGTGAT 2146 CTTGCTCATA 4760 GA T G-- CT GAA
GGAGCCTGTGGAAAGACATG GTCTTCAGCA AACTGGT TTGTTGG GAT GAGC GTG A
CTTGCTCATAGTCTTCAGCA AGGA ||||||| ||||||| ||| |||| |||
AGGACCAGTT TTGACCA AACGACT CTG CTCG CGT G
GG T ATA TT ACA

GAM2170 TGTGCCCACAGTGTTGAGAA 2147 TGGAAAGCAG 4761 - T TG GAA G GCAGA GA
CTATGTGGCAGATATCGAGG GTAGAGTTGG TGTG CCCACAG GT A CTAT TG TATC G
TGGATGGAAAGCAGGTAGAG CTTT |||| ||||||| || | |||| || ||||
TTGGCTTTGTGGGACACA ACAC GGGTGTT CG T GATG AC GTAG G
A T GT GA- G GAAAG GT

GAM2171 CTGACGAAGCCATTGAAACA 2148 ACGAAGCCAT 4762 GA GAAA A------- TG TT
GATGATCTGACCATTAAGCT TGAAACAGAT CTGAC AGCCATT CAG TGATC ACCA A
GGTGATCAAGGCACTCCTGG GATC ||||| ||||||| ||| ||||| ||||
AAGTGGTTCAGTCAG GACTG TTGGTGA GTC ACTAG TGGT A
AC AG-- CTCACGGA -- CG

GAM2172 ATAGGGAACAGTTTTGCCCT 2149 CTCGGGGTCT 4763 - --- AA G- TAC T AAT
GGAACAGAGTTACAGATACA GAAGACTGTC ATAGGGA ACAGTTTT GCCCTGG CA AGT
AGA ACAC C
CAATCAAGAGTGTTCTTGCT TTCC ||||||| |||||||| ||||||| || ||| ||| ||||
GATGCTCGGGGTCTGAAGAC TATCCTT TGTCAGAA TGGGGCT GT TCG TCT TGTG
A
TGTCTTCCTAT C GTC C- AG T-- - AGA

GAM2173 GTTTTTCGATGTTTAGATAT 2150 ATGGTCCCTG 4764 T - TATTTTTCT AG CA TT
TTTTCTTCGGGGAAGCACAA ATCAATTTTA GT TTTCGA TGTTTAGA TCGGGGA CA AG T
GTTTCTTTTCATGGTCCCTG AACA || |||||| |||||||| ||||||| || ||
ATCAATTTTAAACAGTTGGA CA AAGGTT ACAAATTT AGTCCCT GT TT C
ACAC C G TAACT---- G- AC TT

GAM2174 GGTGACAACATGCTGGAGCC 2151 GTTCAAGGGT 4765 AA-- G-- T TA
AAGTGCTAACATGCCTTGGT ATGGAAAGTC GGTGAC CATGCT GAGCCAAG GC A
TCAAGGGTATGGAAAGTCAC ACC |||||| |||||| |||||||| ||
C CCACTG GTATGG CTTGGTTC CG C
AAAG GAA - TA

GAM2175 ATGGTGACAACATGCTGGAG 2152 TTGGTTCACG 4766 AA-- G - GCT
CCAAGTGCTAAATGGCTTGG GATGGCAAGT ATGGTGAC CAT CTG GAGCCAAGT A
TTCACGGATGGCAAGTCACC CACC |||||||| ||| ||| |||||||||
GT TGCCACTG GTA GGC CTTGGTTCG A
AACG - A GTA

GAM2176 GGAAGCGAGCGAGCGCTTCG 2153 CACGAGGTGC 4767 A A-- C CG T AT
CTGCCGGCTACATCCAGTGC ACACGTTCGT GGA GCGAGCG GCGCTTCG TGC GC AC C
ATGCACGAGGTGCACACGTT GTCC ||| ||||||| |||||||| ||| || ||
CGTGTCC CCT TGCTTGC CGTGGAGC ACG CG TG /
G ACA - TA - AC

GAM2177 TTTGAGATGTACGACCTGGA 2154 TGGAGATCAT 4768 - - A- CCTGGA- A--- AT
CGGCGACGGGCGCATCACGC CGAGGCAATC TTTG AGAT GT CGA CGGCG CGGGCGC
C
GCCTGGAGATGCTGGAGATC TACA |||| |||| || ||| ||||| |||||||
ATCGAGGCAATCTACAAG GAAC TCTA CG GCT GTCGT GTCCGCG /
A A GA ACTAGAG AGAG CA

GAM2178 GGCCAATTGAAACAAACAGT 2155 TATTAGGGAT 4769 C T ACAAACAG G GTT T A GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM2179 GGGAAACTCCGAGGACAGAG 2156 TGGCCTGATG 4770 AAA A--- - GA AA GAA
GGCTAAATCCATGAAGTCTG ATCCACAGCG GGG CTCCG GGA CA GGGCT ATCCAT G
TGGATGGCCTGATGATCCAC GAGA ||| ||||| ||| || ||||| ||||||
AGCGGAGACCC CCC GAGGC CCT GT TCCGG TAGGTG /
A-- GACA A AG -- TCT

GAM2180 ACCTGCGACTGAGCGATGCC 2157 TAACGGGTCC 4771 TG G - C G CGG - A
GTCGGGGACCAGGTACTGGC TGCGGTGGTG ACC C ACTG AG GAT CCGT GGACCA GGT C
CGTGGTTTAACGGGTCCTGC GGT ||| | |||| || ||| |||| |||||| |||
GGTGGTGGGT TGG G TGGC TC CTG GGCA TTTGGT CCG T
GT G G - - A-- G G

GAM2181 GTCCTGTGAGTTTACTGGGG 2158 TGAGGATATG 4772 TG TT--- TG G CGTA C
ATATTCTCCGTAACACCGGT CTTGGTCGGG GTCC TGAGT AC GG ATATTCTC ACA C
GTCTGAGGATATGCTTGGTC TATT |||| ||||| || || |||||||| |||
GGGTATTCAATGGAT TAGG ACTTA TG TC TATAGGAG TGT G
TA TGGGC GT G TC-- G

GAM2182 GGCTTGCAGGAGCTTTCGGG 2159 TGTCAAGGAC 4773 TTGC G TC CA GA -- G AT
ACACTTTGAGAACCAGAAGG TCCCAAGCTG GGC AG AGCTT GGGA CTTTGA AC CAGAAG TG G
TGATGTACGGCTTCTGCAGT CTCT ||| || ||||| |||| |||||| || |||||| ||
GTCAAGGACTCCCAAGCTGC CCG TC TCGAA CCCT GGAACT TG GTCTTC GC /
TCTGCC TC-- G -- CA G- AC G AT

GAM2183 GCGGTACTTTCTGGCTGGCT 2160 TGGCTGGCTT 4774 T CT CTT T T- AT
TGAGGTTGATGTATGTGGCC GAGGTTGATG GCGG ACTTT GGCTGG GAGG TGA GT G
TTCATCTTCTCGGCCTCAGG TATG |||| ||||| |||||| |||| ||| ||
GTTCCGC CGCC TGGGA CCGGCT CTTC ACT CG /
T CT --- T TC GT

GAM2184 GAGCTCTTTTTGGACTCCAA 2161 TGCACGTCTT 4775 ----- TCCAAAA T
AAATGGTATCCCTACTATGC AATAAGAAGG GAGCTCTTTTT GGAC ATGGTA C
ACGTCTTAATAAGAAGGGGC GGCT |||||||||| |||| ||||||
TT TTCGGGGAAGA TCTG TATCAT C

ATAAT CACG--- C

GAM2185 ACGTGGTGAAACCCCATCTC 2162 TGAAACCCCA 4776 GTGAA - A- AAATA
TACTAAAAATACAAAAATTA TCTCTACTAA ACGTG ACC CCATCTCT CTAA C
GCCAGGGGTGGTGGTGCACG AAAT ||||| ||| |||||||| ||||
T TGCAC TGG GGTGGGGA GATT /
G---- T CC AAAAA

GAM2186 AGCGCCGGCTATGCCCCTGT 2163 GTCACATTGC 4777 GC TA--- CCC T - TG A
ATTGGATTGCCACACGGGTC ATGCAAGTTT AGC CGGC TGC TGTA TG GAT CC C
ACATTGCATGCAAGTTTGCT GCTG ||| |||| ||| |||| || ||| ||
GAGCT TCG GTCG ACG ACGT AC CTG GG A
A- TTTGA T-- T A -- C

GAM2187 TTCTTGAAGTCTGGGTGATG 2164 TGGCAAGCCC 4778 AGTC-- GA ---- TG
CTGCCATTGTGATATGGTTC ATGTGTGTCG TTCTTGA TGGGT TGCT GCCAT T
CTGGCAAGCCCATGTGTGTC AGAG ||||||| ||||| |||| |||||
GAGAG GAGAGCT ACCCG ACGG TGGTA G
GTGTGT A- TCCT TA

GAM2188 GACAGTGAAGGATTCTTATC 2165 TTTGCGCAAA 4779 AAGGA- A AA -- T GCC
ACATAATGTGCAGGCCATGT ATGTGGAAAG GACAGTG TTCTT TCACAT TGTGCAGGC CA
GT T
GCCTGTGAACTTGAAGTTTG AAAG ||||||| ||||| |||||| ||||||||| || ||
CGCAAAATGTGGAAAGAAAG TTGTTAC AAGAA GGTGTA ACGCGTTTG GT CA G
AAGACATTGTT AGAAGA A AA AA T AGT

GAM2189 TCATTGCTGATGGAGGAATC 2166 CTTGGCCCTT 4780 T A AA AATGT TATT G
CAAAATGTGGGTCATATTGC GGGGCCTCCA TCAT GCTG TGGAGG TCCAA GGGTCA GC A
GAAAGCCTTGGCCCTTGGGG CAGT |||| |||| |||||| ||||| |||||| ||
CCTCCACAGTCATGA AGTA TGAC ACCTCC GGGTT CCCGGT CG A
C - G- ----- TC-- A

GAM2190 TTGTCGTCATTGGACACGTA 2167 TAAATGCGGT 4781 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM2191 ATGGTGACAACATGCTGGAG 2168 TTGGTTCAAG 4782 - AA- G G- GCT
CCAAGTGCTAACATGCTTGG GGATGGAAGT ATGGT GAC CAT CT GAGCCAAGT A
TTCAAGGGATGGAAGTCAAC CAAC ||||| ||| ||| || |||||||||
CGT TGCCA CTG GTA GG CTTGGTTCG A

A AAG G AA TAC

GAM2192 GTGGATTCCCACTTTAGCCA 2169 TAGCCATCTG 4783 ATT TTTA - GTGCC ATAA
TCTGTGCCTGGATAAATACA TGCCTGGATA GTGG CCCAC GCCAT CT TGG A
CCAAGAAAGAATGGTGGTTG AATA |||| ||||| ||||| || |||
TGGGCCAC CACC GGGTG TGGTA GA ACC /
--- TTGG A AAGA- ACAT

GAM2193 TTGTCGTCATTGGACACGTA 2170 TAAATGCGGT 4785 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM2194 ATGGTGACAAACATGCTGGA 2171 TTCAAGGGAT 4784 AAA G G- A T TA
GCCAAGTGCTAAATGCCTGG GGAAGTCACC ATGGTGAC CAT CT GAGCCA G GC A
TTCAAGGGATGGAAGTCACC GT |||||||| ||| || |||||| | ||
GT TGCCACTG GTA GG CTTGGT C CG /
AAG G AA - - TA

GAM2195 TTGTCGTCATTGGACACGTA 2172 TAAATGCGGT 4787 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM2196 GGAATGGTGACAACATGCTT 2173 TTGGTTCCAG 4786 GA AA-- G T TA
GGAGCCAAGTGCTAACATGC GGATGGCAAG G ATGGTGAC CAT CTTGGAGCCAAG GC A
CTTGGTTCCAGGGATGGCAA TCAC | |||||||| ||| |||||||||||| ||
GTCACCGTAAC C TGCCACTG GTA GGACCTTGGTTC CG C
AA AACG G - TA

GAM2197 GCATCCAGGACTGCGGGACA 2174 TGAGAACTCC 4788 CCA- A ----- - TG C
AGATTCTTGGTGCCACCATT AGGATTGTCC GCAT GG CTGCGGGACAA GA TTCT GTG C
GAGAACTCCAGGATTGTCCT TGCA |||| || |||||||||| || |||| |||
GCAGATCGACAATGC CGTA CT GACGTCCTGTT CT AAGA TAC A
ACAG A AGGAC C GT C

GAM2198 GCTGTGTGCTATCGGATAAA 2175 TATCGGATAA 4789 - A G--- T C GAG
ATCTCTAAGAGCTACATTAC AATCTCTAAG GCTGTG TGCT TC GA AAAATCT TAA C
AGATTTTTTCAACAGGAAGT AGCT |||||| |||| || || ||||||| |||
ATCACAGT TGACAC ATGA GG CT TTTTAGA ATT T
T A ACAA T C ACA

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GAM2199  ATTCTATAATGAAGATGTTT 2176    TGTCAAGAAA 4790       TATA-       -----     A   AC GG GCA
         CATGAACTGGGGCATGTATT        CTTCTTATCT        ATTC     ATGAAGAT     GTTTC TGA  T  G   T
         TGTCAAGAAACTTCTTATCT        TCAT           ||||    ||||||||    ||||| |||  |  |
         TCATGAACTGAAT                      TAAG    TACTTCTA    CAAAG ACT  G  T  /
                                  TCAAG       TTCTT     A  -- TT ATG

GAM2200  CAGCACACTACCAGAAGACA 2177    TGGCTGGATT 4791       CAC   CAG-  GA   ---- -    AA
         GCAGAAATGAAAAGCATTTA        ATTTGTAATG        CAGCA   TAC    AA  CAGC    AG AAATG  A
         CTTGTGGCTGGATTATTTGT        CTG           |||||   |||    ||  ||||    || |||||
         AATGCTG                       GTCGT   ATG    TT  GTCG    TC TTTAC  /
                                  A--   TTTA  AG    GTGT  A     GA

GAM2201  GTGCTTCAACTGGTATCTAT 2178    TATGAGGCCC 4792       T    T   AT  A     -  AGAG     GGACAA
TA
         GAGGCCCTAGAGCTCCGGGA        TAGAGCTCCG        GTGCT CAAC GGT  CT TGAGGC CCT    CTCCG
  TGA  A
         CAATGATAAGACTCGCTATA        GGAC           ||||| |||| |||  || ||||||  |||    |||||      |||
         TGGGGAAGGGTGTCTCAAAG                    CACGA GTTG TCG  GA ACTCTG GGG    GGGGT     GCT
G
         GCTGTTGAGCAC                        -   -   --  A     T   AA--     ATATC-   CA

GAM2202  TCCGCATGTCCCTTCGCGGG 2179    CATGTCCCTT 4793       CA  T    CGCG   A    GTG    TG-
GCAA
         AAGGCTGTGGTGCTGATGGG        CGCGGGAAGG        TCCG  TG CCCTT    GGA GGCT   GTGC   ATGG
 G
         CAAGAACACCATGATGCGCA        CTGT           ||||  ||  |||||    ||| ||||   ||||   ||||
         AGGCCATCCGAGGGCACCTG                    AGGT  AC GGGAG    CCT CCGG   CGCG   TACC    /
         GA                          CC  -    ----   A    AA-    TAG    ACAA

GAM2203  GACTTTGGTAGACACAGGCA 2180    TGGGAACCAT 4794     A      AG  A     A     TGA----
GCTGATCT
         TTGGCATGACCAAAGCTGAT        TGCCAAGTCT        G CTTTGGT  AC CAGGC TTGGCA      CCAAA
C
         CTCATAAATAATTTGGGAAC        GGTA           | |||||||  || ||||| ||||||       |||||
         CATTGCCAAGTCTGGTACTA                    C GAAATCA  TG GTCTG AACCGT      GGTTT       /
         AAGC                           -      --  -    -     TACCAAG     AATAAATA

GAM2204  GGAGTCTTCTGCTGGAGGTT 2181    TGAGCCCATT 4795     AGT      TG A  TTCC        C  G
         CCTTCACTGTGCGTGCTGAC        GGCAGGGGTA        GG   CTTCTGC  G GG    TTCACTGTG GT C
         CATGGTGAGCCCATTGGCAG        CC             ||   |||||||  | ||    |||||||||  ||
         GGGTACC                       CC   GGGGACG  T CC    GAGTGGTAC CA T
                                  AT-      GT A  C---        -  G
```

GAM2205 TCATCGATGGCAAGGGTGTC 2182 AAGGGTGTCC 4796 G CAAG TCGC- CTG
CTTCGCCAGATCACTGTTAA TTCGCCAGAT TCATC ATGG GGTGTCCT CAGATCA T
TGATTTGCCTGTGGGACGCT CACT ||||| |||| |||||||| |||||||
CCGTGGATGA AGTAG TGCC TCGCAGGG GTTTAGT /
G ---- TGTCC AAT

GAM2206 TTGCGGCATCCACGAGACCA 2183 TGACGTGGAC 4797 CA- AGAC - ACTC
CCTTCAACTCCATCATGAAG ATCCGCAA TTGCGG TCCACG CAC CTTCA C
TGTGACGTGGACATCCGCAA |||||| |||||| ||| |||||
AACGCC AGGTGC GTG GAAGT /
TAC A--- T ACTA

GAM2207 GAACTTGATTTTCATTAATC 2184 ACTTGATTTT 4798 AC T TTA-- A-- - G C TAATTT
CAGAGCTGCAGCACCAGAGA CATTAATCCA GA TTGAT TTCA ATCC GAGCTG CA CAC
AGAGA C
TAATTTCAATCAACTCTTTT GAGC || ||||| |||| |||| |||||| || ||| |||||
GTGATGACAGCTTGGCGGGT CT AACTG AAGT TGGG TTCGAC GT GTG TTTCT A
ACGGTTGAATGTCAATGTC GT T TGGCA CGG A A T CAACTA

GAM2208 TCTCGTTCATCCATTCATGC 2185 TGACGAGGCA 4799 GTTCAT--- TTC G- - A
GCGTCACTAATTAGATGACG TTTGGCTACC TCTC CCA ATGC CGTCA CT A
AGGCATTTGGCTACCTTAAG TTAA |||| ||| |||| ||||| ||
AGA AGAG GGT TACG GCAGT GA T
AATTCCATC T-- GA A T

GAM2209 TCCTGGTCTGTTCTGTGAGT 2186 AGGTGGTTCC 4800 T T TGGTTT CA AGCA
GGTTTCTATCCAGGCAGCAT GGAATGGCCA TCCTGGTC GTTCTG GAG CTATC GGC T
TGAAGTCAGGTGGTTCCGGA GGA |||||||| |||||| ||| ||||| |||
ATGGCCAGGA AGGACCGG TAAGGC CTT GGTGG CTG /
- - ------ A- AAGT

GAM2210 GGTGACAACATGCTGGAGCC 2187 TTGGTTCAAG 4801 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM2211 GGTGACAACATGCTGGAGCC 2188 TTGGTTCAAG 4802 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM2212 CAAGATTCTTGATACTGCAC 2189 AGAGAAAAGC 4803 A AT-- T- A--- A
TCTCTAAGATTGGAGAGAAA CTGTTTACCA CAAG TTCTTG AC GC CTCTCTA G
AGCCTGTTTACCAAGGAGCT AGGA |||| |||||| || || |||||||
TG GTTC AGGAAC TG CG GAGAGGT A
G CATT TC AAAA T

GAM2213 GCCGCATCTTCTTGTGCGTC 2190 AGACACCATG 4805 G- - TG C- GC C GC
GCCAGCCGAGCCACATCGCT GGGAAGGTGA GCC CATCTTC T TG GTC CAGC GA C
GAGACACCATGGGGAAGGTG AGGT ||| ||||||| | || ||| |||| ||
AAGGT TGG GTGGAAG G AC CAG GTCG CT A
AA G GT CA A- - AC

GAM2214 ACTGGCGCTGCAAGGCTGTG 2191 TGGCATGGCC 4804 TGCAA T - ---- - CT
GAA
GGCAAGGTCATCCCTTGAGC TTCCGTGTCC ACTGGCGC GGC GTGGG CA AGGTCAT CC
TGAGCT C
TGAACGGGAAGCTCACTGGC CACT |||||||| ||| ||||| || ||||||| || ||||||
ATGGCCTTCCGTGTCCCACT TGACTGTG CCG CACCC GT TCCGGTA GG ACTCGA
G
GCCAACGTGTCAGT CAA-- T T GCCT C TC AGG

GAM2215 CAAGAAGGTTATCTCCTCAG 2192 TGTGGTGGCT 4806 GAA TC A GA GT
CCAACAGAGCTGTGGTTGGT GGAGGTGGCC CAA GGTTATCTCC AGCCA CA GCT G
GTGGTGGCTGGAGGTGGCCG GAAT ||| |||||||||| ||||| || |||
AATTG GTT CCGGTGGAGG TCGGT GT TGG G
AAG -- G G- TT

GAM2216 TATCTTTAAATACTGCAAAG 2193 GTGCATTGCC 4807 AAATACT A T-- GC
CATTGTGAGCTGCATCACTT ACAGGAGATA TATCTTT GCAA GCAT GTGA T
TGTGCATTGCCACAGGAGAT ||||||| |||| |||| ||||
A ATAGAGG CGTT CGTG CACT G
ACAC--- A TTT AC

GAM2217 GGTTCATTCTCTGGATCAGA 2194 TTCATTGTCA 4808 -- C G - C GT TCA --- TA
GTCAGTGGTGTCAGAATATC CTAACATCTG GGTTCA TTCT TG ATCAGA GT AGTG G GAAT
ATC T
TATAATGATCAGGTTCATTG GTGT |||||| |||| || |||||| || |||| | |||| |||
TCACTAACATCTGGTGTACA TCAAGT AAGA AT TGGTCT CA TCAC T CTTG TAG A
GAAGTTGAACT TG C G A A TG TA- GAC TA

GAM2218 GACTGGAAGGTGCCCTGTGC 2195 TGGAAGGTGC 4809 GGAA C T T CGT TG A
CACG
TATGTCGTGCCTGCAGGGAC CCTGTGCTAT GACT GGTG CCTG GC ATGT GCC C GGGA
T

ACGTCGGATCCCGTGGGCCT GTCG |||| |||| |||| || |||| ||| | ||||
CACATGCCAGGTCACCAGGT CTGG CCAC GGAC CG TACA CGG G CCCT /
C A--- T - - CTC GT - AGGC

GAM2219 CCCGGTATTGCCAGGCGGCT 2196 TCACAGCAAC 4810 G A- CG A AT CTCT
GAGAATGTTACGCTCTGACA TGGGGGAATA CCCGGTATT CC GG GCTG GA GTTACG G
TCTGTAACCTCACAGCAACT TCGG ||||||||| || || |||| || ||||||
GGGGGAATATCGGG GGGCTATAA GG TC CGAC CT CAATGT A
G GG AA A C- CTAC

GAM2220 GGACTCTCAGGAATCTTTCA 2197 AGGAAGGGAT 4811 C - - GA-- G AA
GATTGCTGCAACTAAGCAGG GGAAGGTCTC GGA TCTCA GGA ATCTTTCA TT CTGC C
AAGGGATGGAAGGTCTCCTT CTTG ||| ||||| ||| |||||||| || ||||
GGGACTCT TCT AGGGT CCT TGGAAGGT AA GACG T
C T C AGGG G AA

GAM2221 TCATCTCGGGTGGGATGTGC 2198 TGGTTCTTGG 4812 CGGG G TTT GT CCT
GAGGTTTCTGTGCCCTTATC TATGTCCCAG TCATCT TGGGATGTGC AGG CT GC T
GTCTGGTTCTTGGTATGTCC GATG |||||| |||||||||| ||| || ||
CAGGATGA AGTAGG ACCCTGTATG TTC GG TG /
---- G TT- TC CTA

GAM2222 GCTTATGGTAGTGGGTGAAT 2199 TCACAGATTT 4813 A T TGG TG GATT ----- C CA
CTGGATTGGGAAAGTCGACA GTATTCTCCA GCTT TGG AG G AATCTG GGGAA AGT GA
T
TTAATCAACTCATTATTCCT GAGT |||| ||| || | |||||| ||||| ||| ||
CACAGATTTGTATTCTCCAG TGAG ACC TC T TTAGAC TCCTT TCA CT T
AGT - - TTA GT AC-- ATTAC A AA

GAM2223 TCCTTATGCGCGTAACCGTC 2200 CAACCTGGAC 4814 G C TCC CTTT CA CT
CTCCCTTTGGTCAGGGCTAT CTGGTTATCG TCCTTAT CG GTAACCG TCC GGT GGG A
ACCCAACCTGGACCTGGTTA ATAA ||||||| || ||||||| ||| ||| |||
TCGATAAGGA AGGAATA GC TATTGGT AGG CCA CCC /
- - CC- T--- A- AT

GAM2224 TGTCACCATCCTCTGCATTG 2201 TCCCTGGCTT 4815 CA C- AT- C TG CACT C T
ACTTGGGCACTGACATGGTT ATGAGCAGGC TGTCAC TC TCTGC TGA T GG GA ATGGT C
CCTGCCATCTCCCTGGCTTA TGAG |||||| || ||||| ||| | || || |||||
TGAGCAGGCTGAGAGTGACA ACAGTG AG GGACG ATT G CC CT TACCG C
AG TC AGT C GT ---- C T

GAM2225 GCTCTCCGCGCAGCTTCAGC 2202 CAATGCTAAA 4816 CC TC--- CC-- GG
ACCTCGGCCAGAACAATGCT GTAGCTGTGC GCTCT GCGCAGCT AGCA TC C

AAAGTAGCTGTGCTAGGGGC TAGG ||||| ||||||||| |||| ||
CGGGG CGTGTCGA TCGT AG /
AT TGAAA AACA AC

GAM2226 CGTCATGTCTAAGTCAGAGT 2203 TCTAAGTCAG 4817 -- C- CA G TA- -- GAAC
CTCCTAAAGAGCCCGAACAG AGTCTCCTAA CGTCA TGT TAAGT GA TCTCC AAGAGC CC
A
CTGAGGAAGCTCTTCATGGA AGAG ||||| ||| ||||| || ||||| |||||| ||
GGGTTGAGCTTGAAACAACT GTAGT ACA GTTCG TT GGAGG TTCTCG GG G
GATG CA AA AG G TAC AA AGTC

GAM2227 GGTGACAACATGCTGGAGCC 2204 TTGGTTCAAG 4818 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM2228 GTTTTTTCCAGCCAGCTTTC 2205 TTCCAGCCAG 4820 TT CC CCAAATC - A
CAAATCGACAGTACCAGCTG CTTTCCAAAT GTTTT CCAG AGCTTT GA CAGT C
CTCTTCACACAGGGTTCTGG CGAC ||||| |||| |||||| || ||||
GGAAAAC CAAAA GGTC TTGGGA CT GTCG C
GG -- CACACTT C A

GAM2229 GCCTGGGCCTGAGCAGCATC 2206 GAGCAGCATC 4819 T T C CATC - TG ACCT GA
GTTGGCGTCTGGTACCTGCT GTTGGCGTCT GCC GGGCC GAG AG GTTGGCG TC GT GCT
G
GAGGAAGCACTGGATTGCCA GGTA ||| ||||| ||| || ||||||| || || |||
ACAACCTTTTTGGCCTGGC CGG TCCGG TTT TC CAACCGT AG CA CGA /
- T - CAA- T GT ---- AG

GAM2230 GATGGGATGGAAATGAAATG 2207 TGGGATGGAA 4821 T TG AA--- - AAAAG
GCCAAAAGAGCAAAGGCTTA ATGAAATGGC GA GGGA GA TGAAATG GCC A
TTTCAAAACCTTTGTCCCTC CAAA || |||| || ||||||| |||
CT CCCT TT ACTTTAT CGG /
- GT CCAAA T AAACG

GAM2231 TCCTCCGCGGGCATGACCAG 2208 TACATCGCCC 4822 CG- - - ACC -- TA
TCCGCCTACGACGGCAAGGA TGAACGAGGA TCCTC C GGGC ATG AGTCC GCC C
TTACATCGCCCTGAACGAGG ||||| | |||| ||| ||||| |||
A AGGAG G CCCG TAC TTAGG CGG G
CAA T C A-- AA CA

GAM2232 CCGGAACCTGCTCATCTGGA 2209 AGAGTTGTTC 4823 GA - - AT CAA G -- AAA

TCAAGAAGAATTTGCTAAAA ATCCAGGAGA CCG AC CTG CTC CTGGAT GAA AATTT GCT A
GAGCGGCCAGAGTTGTTCAT CAGC ||| || ||| ||| |||||| ||| ||||| |||
CCAGGAGACAGCGTGCGG GGC TG GAC GAG GACCTA CTT TTGAG CGG G
G- C A -- --- G AC CGA

GAM2233 GTCCTGTGAGTTTACTGGGG 2210 TGAGGATATG 4824 TG TT--- TG G C A C
ATATTCTCCGAACACCGGTG CTTGGTCGGG GTCC TGAGT AC GG ATATTCTC GA CA C
TCTGAGGATATGCTTGGTCG TATT |||| ||||| || || |||||||| || ||
GGTATTCAATGGAT TAGG ACTTA TG TC TATAGGAG CT GT G
TA TGGGC GT G T - G

GAM2234 GCGCGCGGTGGTGGTGGGCT 2211 TACATGAAGC 4825 C GG GACCC AC
TTGACCCGCACTTCAGCTAC TCACCAAGGC GCGCG GGT TGGTGGGCTTT GC T
ATGAAGCTCACCAAGGCCCT CCTG ||||| ||| |||||||||| ||
GCGC CGCGT CCG ACCACTCGAAG CG T
C GA TACAT AC

GAM2235 GCAGGATCTCCAACTATAAT 2212 AAAGCAGGTG 4826 A T- ATAA- C T
GCTTCTGTCCTTAAAAGCAG GAGTTGGTTG GCAGG TC CCAACT TGCTT TG C
GTGGAGTTGGTTGAATCTGT AATC ||||| || |||||| ||||| ||
TGTCT AG GGTTGA ACGAA AT C
A TT GGTGG A T

GAM2236 CATTGTCGTCATTGGACACG 2213 CGTCATTGGA 4827 GTC-- T- A ATTC C
TAGATTCGGGCAAGTCCACC CACGTAGATT CATT GTCA TGG CACGTAG GGG A
ACTACGTGGCCATCTGATCT CGGG |||| |||| ||| ||||||| |||
ATAAATG GTAA TAGT ACC GTGCATC CCT A
ATATC CT G ACCA G

GAM2237 TCATGTCTAAGTCAGAGTCT 2214 TCTAAGTCAG 4828 -- C- CA G TA- -- GAAC
CCTAAAGAGCCCGAACAGCT AGTCTCCTAA TCA TGT TAAGT GA TCTCC AAGAGC CC A
GAGGAAGCTCTTCATGGAGG AGAG ||| ||| ||||| || ||||| |||||| ||
GTTGAGCTTGAAACAACTGA AGT ACA GTTCG TT GGAGG TTCTCG GG G
CA AA AG G TAC AA AGTC

GAM2238 CAGCTCAAGTCGGCCTGCAA 2215 AGGAAGACAT 4830 CAA- C - G A ACATCC - AAA-
- - GG
GGAAGACATCCCCAGCGAAA CCCCAGCGAA CAGCT GT GGC CT CA GGAAG CCAG CG
AG AGTGA A
AGAGTGAGGAGATCACTACT AAGA ||||| || ||| || || ||||| |||| || || |||||
GGCAGTGCCTGGTTTAGCTT GTCGA CA CCG GA GT CCTTC GGTC GT TC
TCACT /
CCTGGAGAGCCACAACAAGC ACAA - A G - GATTT- C GACGG A AG
TG

GAM2239 AGCACATCTTTGAGATCTCC 2216 ACTATGGTGG 4829 C--- - A TC CC CC
CGCCGTCCTGACCTACTCAC TTGACTACAG AGCACAT TTTG AG TC CCGCCGT TGA T
TATGGTGGTTGACTACAGAA AACC ||||||| |||| || || ||||||| |||
CCCGTGTGCT TCGTGTG AGAC TC AG GGTGGTA ACT /
CCCA A - TT TC CA

GAM2240 GAGGGTGTCTATGGAGAGGC 2217 AGGCAGTGGC 4831 GT ------- - G G G GA G
GGCGGCGCGGCTGCTGAGGC GATGGCGCCC GAGG GTCTAT GGAGAGG CG CG CGC
GCTGCT GGC G
GGAGGCTGAGGCAGTGGCGA TTTC |||| |||||| ||||||| || || ||| |||||| |||
TGGCGCCCTTTCCTGAAGAA CTTC CAGGTG CCTTTCC GC GT GCG TGACGG TCG
A
GTGGACGTCTTC TG AAGAAGT C G A G AG G

GAM2241 GTTCCAAGAAAGACAGTTCT 2218 AGAAAGACAG 4832 GA CA C TCA CT
GGTCAGGCCTAAAGCTCTTC TTCTGGTCAG GTTCCAA AAGA GTT TGG GGC A
CGCAATATTCTTCTTTGGAA GCCT ||||||| |||| ||| ||| |||
T TAAGGTT TTCT TAA GCC TCG /
TC TA C TTC AA

GAM2242 CCGGAACCTGCTCATCTGGA 2219 AGAGTTGTTC 4833 GA - - A CAA G -- AAA
TCAAGAAGAATTTGCTAAAA ATCCAGGGAG CCG AC CTG CTC TCTGGAT GAA AATTT GCT
A
GAGCGGCCAGAGTTGTTCAT ACAG ||| || ||| ||| ||||||| ||| ||||| |||
CCAGGGAGACAGCGTGCGG GGC TG GAC GAG GGACCTA CTT TTGAG CGG G
G- C A - --- G AC CGA

GAM2243 TCTTGTGTTGAGACTTCGTG 2220 TACACCACTC 4834 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM2244 AAGCTGAAGGTGCTGGAGGT 2221 AAGGTGCTGG 4835 AA- - TG CA ----- T
GCCAAGTGAAGTGTGTGCAT AGGTGCCAAG AAGCTG GGT GC GAGGTGC AGT GAAGTG
G
TTTTGATAACTGTGTACTTC TGAA |||||| ||| || ||||||| ||| ||||||
TGGTGACTGTACAGTTT TTTGAC TCA TG CTTCATG TCA TTTTAC T
ATG G GT TG ATAGT G

GAM2245 ACCTTCGGGTCCACTGGTTT 2222 TGGCATATCA 4836 C CACTG--- A CACCCA AC
GATGACACCCACCGCAACTG CGAACAGCAA ACCTT GGGTC GTTTG TGA CCGCA T
TCTGTGGCATATCACGAACA AGCG ||||| ||||| ||||| ||| |||||

GCAAAGCGACCCAAAGGT TGGAA CCCAG CAAGC ACT GGTGT G
A CGAAACGA - ATAC-- CT

GAM2246 GGAACTTGTAACTTTATGCA 2223 TTTGACAAAC 4837 C A TA----- CA TGT
AGAGTCTGTTCTTGACTTTG CTTCAAGTGC GGAA TTGTA CTT TG AGAGTC T
ACAAACCTTCAAGTGCAATT AATT |||| ||||| ||| || ||||||
CC CCTT AACGT GAA AC TTTCAG /
- - CTTCCAA AG TTC

GAM2247 GAGCCAGGCTCCAGTCTGGT 2224 TGGCCATGGA 4838 A T---- TC - A C G
GTCCAGGACCCGTGTGAAGA TACCATCCTG GAGCC GGC CCAG TGGTGTCCA GG CC
GTGT A
CGCTGGCCATGGATACCATC GCCA ||||| ||| |||| ||||||||| || || ||||
CTGGCCAATGCTAGGTTC CTTGG TCG GGTC ACCATAGGT CC GG CGCA A
A TAACC CT A - T G

GAM2248 GGCCTATTGAAGACACCTGC 2225 TTGAAGACAC 4839 ATT---- ACACCT TATG
TCAGTATGACGCTTCTGAGC CTGCTCAGTA GGCCT GAAG GCTCAG A
TAAAAGCTTCCATGAAGGGG TGAC ||||| |||| ||||||
CT TCGGG CTTC CGAGTC C
GAAGTAC GAAAAT TTCG

GAM2249 TCTTGTGTTGAGACTTCGTG 2226 TACACCACTC 4840 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM2250 GGTTTTGTATGTCAAGGAGG 2227 GTGTTCCCCT 4841 T TGTC A TT CCTTT
AGTTTAAGGCCTTTCCGACC TTTCTGCGCA GGTT TGTA AAGG GGAG TAAGG C
ACCTTGTGTTCCCCTTTTCT GCC |||| |||| |||| |||| |||||
GCGCAGCC CCGA GCGT TTCC CCTT GTTCC C
C CTT- - GT ACCAG

GAM2251 TCTTGTGTTGAGACTTCGTG 2228 TACACCACTC 4842 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM2252 TCTTGTGTTGAGACTTCGTG 2229 TACACCACTC 4843 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||

CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM2253 ATTTGAGAAGGAGGCTGCTG 2230 CTTCAAGTAT 4844 TG AGG - GA T AAA
AGATGGGAAAGGGCTCCTTC GCCTGGGTCT ATT AGA AGGC TGCT GA GGG G
AAGTATGCCTGGGTCTTGGA TGGA ||| ||| |||| |||| || |||
T TAG TCT TCCG ATGA CT CCT /
GT GGG T A- T CGG

GAM2254 CTTTATCAAAAACATGATTA 2231 TCAAAAACAT 4845 --- AA GATTA G TC - TGAC
CAGGGACATCTCAGGCTGAC GATTACAGGG CTTTA TCA AACAT CAG GACA TCAGG C T
TGTGCTGTCCTGATTGTTGC ACAT ||||| ||| ||||| ||| |||| ||||| |
TGCTGGTGTTGGTGAATTTG GAAGT AGT TTGTG GTC TTGT AGTCC G G
AAG TTA GG GTC-- G T- T TCGT

GAM2255 TTGTCGTCATTGGACACGTA 2232 TAAATGCGGT 4846 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM2256 TGAGGCAGGAGAATCACTTG 2233 CCACTGCACT 4847 A AA GAACC AGGC GT
A - A
AACCCCAGGAGGCGGAGGTT CCAGCCTGGC TGAGGC GGAG TCACTT CCAGG GGAG
TGCAGTG GC TG G
GCAGTGAGCTGAGATCACGC GACT |||||| |||| |||||| ||||| |||| ||||||| || ||
CACTGCACTCCAGCCTGGCG ACTCTG CCTC AGTGAG GGTCC CCTC ACGTCAC
CG AC A
ACTGAGTGAGACTCCGTCTC - AG TCAGC GA-- -- - C T
A

GAM2257 AAGAGTAGGATGTCTGCTGA 2234 TGAGAAGGAG 4848 GAT G GAAG C-- T AA
AGTCATCCATCAGGTTGAAG ATGCTGCTCT AAGAGTAG GTCT CT TCATC ATCAGGT G G
AAGCACTTGATACAGATGAG T |||||||| |||| || ||||| ||||||| |
AAGGAGATGCTGCTCTT TTCTCGTC TAGA GA AGTAG TAGTTCA C A
G-- G AG-- ACA - GA

GAM2258 TGGTATATGTGTATTAGTGA 2235 TATGTGTATT 4849 GTA TGAA TT- A T
AACATTGTAAAGGTGAACTT AGTGAAACAT TGGTATATGT TTAG ACA GTA AGG G
CTACCTCTGTATCTAAATGT TGTA |||||||||| |||| ||| ||| |||
ATACCA ACCATATGTA AATC TGT CAT TTC A
--- TA-- CTC C A

GAM2259 TCAGGCCGTTGCTGAGCTCA 2236 CGTTGCTGAG 4851 A C-- - -- CA AC A

ACGGGACCCAGGTGGAGTCT CTCAACGGGA TC GGC GTTG CT GAGCT ACGGG CC G
GTACAGCTCAAAGTCAACAT CCCA || ||| |||| || ||||| ||||| ||
AGCCCGA AG CCG CAAC GA CTCGA TGTCT GG G
C ATA T AA CA GA T

GAM2260 CGCTACTGGCAAGTCTGTCT 2237 GTTGCCACCG 4850 ACT AGTCT GCTC GC
AGAA-- T
GGGGCTCCCTCGCTGTCCAG GGACAAGAGG CGCT GGCA GTCTGGG CCTC TGTCC
CAGCCC A
AACAGCCCTAAGGGTTGCCA ACCC |||| |||| ||||||| |||| ||||| ||||||
CCGGGACAAGAGGACCCAGA GTGA CTGT TAGACCC GGAG ACAGG GTTGGG /
TTGTCTACAGTG CAT ----- A--- A- GCCACC A

GAM2261 TCCATGTGACTGTCGGCGGG 2238 GGGCTTTGTC 4852 A CGGCGG GTC - TC C
C
CTTTGTCTCTGGATTCGATG TCTGGATTCG TCCATGTG CTGT GCTTT TCTG GAT
GATGGCT TG G
GCTCTGCGGGCACAGCCATC ATGG |||||||| |||| ||||| |||| ||| ||||||| ||
ATCACAGAAGAGCATGCAGC AGGTGTAC GACG CGAGA AGAC CTA CTACCGA AC
G
CATGTGGA C TA---- --- A -- C G

GAM2262 GGCCAATTGAAACAAACAGT 2239 TATTAGGGAT 4853 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM2263 CACTACGTTGACCTGAAGGA 2240 AAGGACCGTC 4854 GA-- GAA- CCATTCT --
AAAT
CCGTCCATTCTTTGCCGGCC CATTCTTTGC CACTACGTT CCT GGACCGT
TTGCCGGCCT GGTG A
TGGTGAAATACATGCACTCA CGGC ||||||||| ||| ||||||| |||||||||| ||||
GGGCCGGTAGTTGCCATGGT GTGGTGTAA GGG TCTGGTA GATGGCCGGG
TCAC /
CTGGGAGGGGCTGAATGTGG GTCG AGGG CCGTT-- AC GTAC
TG

GAM2264 TCTTGTGGGAGAGATTATCA 2241 TGGGAGAGAT 4856 T GA ATC -------- - G A AT
AGCGTTTTGAGCAGAAAGGA TATCAAGCGT TCTTG GGGAGA TT AAGC GTTTT GA CAG
AAGG T
TTCCGCCTTGTTGGTCTGAA TTTG ||||| |||||| || |||| ||||| || ||| ||||
ATTCATGCAAGCTTCCGAAG GGAAC TCTTCT AA TTCG TAAAG CT GTT TTCC C
ATCTTCTCAAGG - AG GCC AACGTACT T G G GC

GAM2265 CGTTACGGGTGCTGGCGGCT 2242 AAGGAACCAT 4855 TAC-- -- G C CA GA AAA TAAG
GCAGCCGGAGTTCAAACCTA GGCCAACTGT CGT GGGT GCT GCGG TG GCCG GTTC CC C
AGCAGCTGGAAGGAACCATG GAGC ||| |||| ||| |||| || |||| |||| ||
GCCAACTGTGAGCGTACCTT GCG TCCA CGA TGTC AC CGGT CAAG GG /
CATTGCG TTACT TG G A -- AC GAA TCGA

GAM2266 ATGATCCATCTGTGTAGTTT 2243 TCTGAACAGT 4857 CCATC TTT C CA CCAGGT
CTGAACAGTCAGCGATTCCA CAGCGATTCC ATGAT TGTGTAG CTGAA AGT GCGATT T
GGTTTTAAATAGTTGTAAAT AGGT ||||| ||||||| ||||| ||| ||||||
TTTCAGTTTCTACACACTTT TACTA ACACATC GACTT TTA TGTTGA /
ATCAT TTTC- TTT - AA TAAATT

GAM2267 ATTTGAGAAGGAGGCTGCTG 2244 CTTCAAGTAT 4858 TG AGG - GA T AAA
AGATGGGAAAGGGCTCCTTC GCCTGGGTCT ATT AGA AGGC TGCT GA GGG G
AAGTATGCCTGGGTCTTGGA TGGA ||| ||| |||| |||| || |||
T TAG TCT TCCG ATGA CT CCT /
GT GGG T A- T CGG

GAM2268 GGTGACAACATGCTGGAGCC 2245 GTGGTTCAAG 4859 AA-- G G- - T TA
AAGTGCTAACATGCCTGTGG GGATGGAAAG GGTGAC CAT CT GAGCCA AG GC A
TTCAAGGGATGGAAAGTCAC TCAC |||||| ||| || |||||| || ||
C CCACTG GTA GG CTTGGT TC CG C
AAAG G AA G - TA

GAM2269 GGTGCTGGCGGGCGGTACCA 2246 AGGATGCAGA 4860 - ---- A---- ACCA GGG T
CCATGTATCCGGGCATTGCT AGGAGATCAC GGTGCTGG C GGGCGGT CC TGTATCC CA T
GACAGGATGCAGAAGGAGAT CGCC |||||||| | ||||||| || ||||||| ||
CACCGCCCTGGCGCCCAGCA CCACGACC G CCCGCCA GG ACGTAGG GT G
CC C CGGT CTAGA AAG- ACA C

GAM2270 TGGCATCCCAGATGTTGCAG 2247 TTGCAGTTGA 4861 - AGA AG GAAG T CA A A
TTGAAGTCGTCGTAGCCAGC AGTCGTCGTA TGGCATC CC TGTTGC TT TCG CGTAGC GCG GC G
GAGCAGCAGCCGTCCGCTGC GCCA ||||||| || |||||| || ||| |||||| ||| ||
GCGAGAAGGCAACAGAGGTG ACCGTAG GG ACAACG AG AGC GCGTCG TGC CG C
ATGCCA T AG- GA ---- - CC - A

GAM2271 AGGAGGACGCGCTGCCCGGC 2248 GAGAGTACTC 4862 ------ G- G CAGAAAA AA
CAGAAAACGGAGTTCAAGGT CTGCGTCTTC AGGAGGACGC GCT CCC GC CGGAGTTC G

GGACTCCGACGACCAGTGGG CT |||||||||| ||| ||| || ||||||||
GAGAGTACTCCTGCGTCTTC TCCTTCTGCG TGA GGG TG GCCTCAGG /
CT TCCTCA GA G ACCAGCA TG

GAM2272 CGGCTCCGAGAGCAGGTTCT 2249 TACACATTGA 4863 - AGAG C A TC GCAG C
TCGTGAGTTCCTCGCAGGGC GAACCTGAAC CGGC TCCG CAGGTTCTT GTG GT CTC GG
C
CGGTCAGAGCTACACATTGA ATGG |||| |||| ||||||||| ||| || ||| ||
GAACCTGAACATGGAGGCCG GCCG AGGT GTCCAAGAG TAC CA GAG CT G
G ACAA T A TC A--- G

GAM2273 TCTTGTGTTGAGACTTCGTG 2250 TACACCACTC 4864 GAGA GT--- C ACAAGGA
GTGGTGCTAAGAACAAGGAA CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
GAAGAAGTCTTACACCACTC TAAG ||||||||| |||| ||||||| |||||
CCAAGAAGAATAAGCACAAG AGAACACGA GAAG TCACCAC ATTCT /
A ATAA AACCC - GAAGAAG

GAM2274 GACTATCCACCTTTGGGTCG 2251 TGAGACCGAC 4865 T TTTG- C GC C
CTTTGCTGTCGTGATATGAG CGTTGCGGTG GAC ATCCACC GGTCG TTT TGT G
ACCGACCGTTGCGGTGGGTG GGTG ||| ||||||| ||||| ||| |||
TC CTG TGGGTGG CCAGC AGA ATA T
- CGTTG C GT G

GAM2275 GTGGGCAAGGTCATCCCTGA 2252 TCACCTGGAT 4866 - --- C-- GAA
GCTGAACGGAAAGCTCACCT GGCTTTCGTG GTGGG CA AGGTCATCC TGAGCT C
GGATGGCTTTCGTGTCCCAT TCCC ||||| || ||||||||| ||||||
TACCC GT TTCGGTAGG ACTCGA G
T GCT TCC AAG

GAM2276 GATCTCGGACACATCTGTGG 2253 TGTGGTGCTG 4868 A CATCT GA ACAGC
TGCTGTCCATGGACAACAGC TCCATGGACA GATCTCGG CA GTGGTGCTGTCCATG CA C
CGCTCCCTGGACATGGACAG ACAG |||||||| || |||||||||||||| ||
CATCATTGCTGAGGTC CTGGAGTC GT TACTACGACAGGTAC GT G
- ----- AG CCCTC

GAM2277 CCGCAGCCGGGCTGAGGCTG 2254 TGAGGAGCTG 4867 G GAGG AG A--- CAG
AGAGCATGTACCAGATCAAG CAGAGCCTGG CC CAGCCGGGCT CTG AGC TGTAC A
TATGAGGAGCTGCAGAGCCT CTGG || |||||||||| ||| ||| |||||
GGCTGGG GG GTCGGTCCGA GAC TCG GTATG T
- ---- G- AGGA AAC

GAM2278 ACATGCCTTGGTTCACGGAT 2255 TGGCATGCCC 4869 T CTTG ATG- AA CC
GGCAAGTCCCCCGTAGGATG GTGGACACGC ACA GC GTTCACGG GC GTCC C

GCATGCCCGTGGACACGCTG TGT ||| || |||||||| || ||||
T TGT CG CAGGTGCC CG TAGG G
- CA-- CGTA G- AT

GAM2279 TTGTCGTCATTGGACACGTA 2256 TAAATGCGGT 4870 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM2280 GCGGCCTCGGTGATGTGGAT 2257 CCTCGGTGAT 4871 CC GTGA T A G
GTGAATGACTGGAGACAGCA GTGGATGTGA GCGG TCG TGTGGATG GAATG CTG A
TTCTATTTACAAGAACGGTA ATGA |||| ||| |||||||| ||||| |||
CTGC CGTC GGC ACATTTAT CTTAC GAC G
AT AAGA - - A

GAM2281 TACGAAAACCTCACGGCCAA 2258 CTGGACGAGC 4872 AAC AC- AG GG- T GG
GGTGCTGGCCATGCTGGCCT ACGTGGCCTT TACGAA CTC GGCCA GTGCT CCA GCT C
GGCTGGACGAGCACGTGGCC CGAG |||||| ||| ||||| ||||| ||| |||
TTCGAGTTCGTG GTGCTT GAG CCGGT CACGA GGT CGG /
--- CTT G- GCA - TC

GAM2282 GTGGAGGTGACTGGTGATGA 2259 ATTGATGGTC 4873 GA - GA A GG
ATACAATGTGGAAAGCATTG AGCCAGGTGC GTGGAGGT CTGG TGAT AT CAATGT A
ATGGTCAGCCAGGTGCCTTC CTTC |||||||| |||| |||| || ||||||
AC CACTTCCG GACC ACTG TA GTTACG /
TG G G- - AA

GAM2283 GGCTGGGATTGGAACTGTGT 2260 TGGAACTGTG 4874 - TT A - G- CCTCATCA TT
TGGGAGCCTCATCATTGGTT TTGGGAGCCT GGC TGGGA GGA CTGT GTT GGAG TTGG
A
ATGCCAGGAACCCTTCTCTG CATC ||| ||||| ||| |||| ||| |||| |||| /
AAGCAACAGCTCTTCTCCTA CCG ATCCT TCT GACA CGA TCTC GACC /
CGCC C CT C A AG TTCCCAAG GT

GAM2284 TCCCTGCTGATTCCGCCTAA 2261 TGAGGTTTCG 4875 GAT-- ------ A CGTA
GCCCGTACCCCTTGGCTGAG CTGGATAGTA TCCCTGCT TCC GCCT AGCC C
GTTTCGCTGGATAGTAGGTA GGTA |||||||| ||| |||| ||||
GGGA AGGGATGG AGG TGGA TCGG C
ATGAT TCGCTT G TTCC

GAM2285 GGCTCCCAATGTTGACGTTG 2262 CCAGGCCAAA 4876 CTCCC CG---- AG AT C
GCCAGGGCATTTGCAAACAA AAGGCTCAAC GG AATGTTGA TTGGCC GGC TTG A

GCCAGGCCAAAAAGGCTCAA ATTT || |||||||| |||||| ||| |||
CATTTACACC CC TTACAACT AACCGG CCG AAC A
ACAT- CGGAAA A- -- A

GAM2286 TGGCACCCCGGCCTATGGCA 2263 TCAGTCTGAT 4877 - C- - - C CCA GG
TTGGCCTTCCAGGCATGGTA AGAGCCTAGG TGGCAC CC GGC CTAT GG ATTGGCCTT
GGCAT T
TGTGCCCGAGGGGTCAGTCT AGTG |||||| || ||| |||| || ||||||||| |||||
GATAGAGCCTAGGAGTGCCA ACCGTG GG CCG GATA TC TGACTGGGG CCGTG /
A AT A G - AGC TA

GAM2287 CTCTCGGGGGCGGAGGGGGT 2264 TCCCTCCCAA 4878 - GC- - C TGA
GCCTGTGAGCTCTCAGCCAC CCCTGGTGAG CTC TCGGGG GGAGGGG GTG CTG G
TTCCCTCCCAACCCTGGTGA ||| |||||| ||||||| ||| |||
G GAG GGTCCC CCTCCCT CAC GAC C
T AAC T C TCT

GAM2288 CCTGAAGCCTTGAAGCCTCT 2265 TTGAAGCCTC 4879 AA TTG CTTC - T C- A- AG
TCGGGATGTCTTCCAGCGTA TTCGGGATGT CCTG GCC AAGCCT GG GA GTCTTCCAG GT
ATC C
ATCAGCAGGATGGGCAATTG CTTC |||| ||| |||||| || || ||||||||| || |||
GAGGACTCACCAGGCTTGTG GGAC CGG TTCGGA CC CT CAGGAGGTT CG TAG /
GCCAGG -- TG- ---- A - AA GG GA

GAM2289 TCTTGTGTTGAGACTTCGTG 2266 TACACCACTC 4880 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM2290 GATGGCGGTGGCCACCTCCT 2267 CGACGTGGCC 4881 G C C-- AGCAC
TGGAGCACTTAACACCCAGA ATTGTAGTC GAT GCGGTGGCCAC TC TTGG T
CCGACGTGGCCATTGTAGTC ||| |||||||||| || ||||
CTG TGTTACCGGTG AG GACC T
A C CCA CACAA

GAM2291 CTCCAACGATGCCTTTGTTC 2268 CAGGAGCCAG 4882 CAACGA T--- GAAAA - T CCG
TGAAAACCCCCTCAGCCGCC CGAGGCAGAG CTC TGCCTT GTTCT CC CCC CAG C
TACCTGTGGGTGGGTACAGG ||| |||||| ||||| || ||| |||
AGCCAGCGAGGCAGAG GAG ACGGAG CGAGG GG GGG GTC C
------ CGAC ACATG T T CAT

GAM2292 CAAGAAGGTTATCTCCTCAG 2269 TGTGGTGGCT 4883 GAA TC GA GT

CCATCAGAGCTGTGGTTGGT GGAGGTGGCC CAA GGTTATCTCC AGCCATCA GCT G
GTGGTGGCTGGAGGTGGCCG GAAT ||| |||||||||| |||||||| |||
AATTG GTT CCGGTGGAGG TCGGTGGT TGG G
AAG -- G- TT

GAM2293 CAGCATTGGATCAACTATTT 2270 TATTTCTTCA 4884 GGA- ACT AGA A
CTTCAGATCGTTCTGATTCA GATCGTTCTG CAGCATT TCA ATTTCTTC TCGTTCTG T
GAGCGAGAGGAGATTGAAGT ATTC ||||||| ||| |||||||| ||||||||
GGATGTTG GTTGTAG AGT TAGAGGAG AGCGAGAC /
GTGA --- --- T

GAM2294 AGTTTAGTGGCAAGTTCTTT 2271 TGGCAAGTTC 4885 A AA TCTTTA TTT CTT
AGCCTTTGCCTTTTCGAGCT TTTAGCCTTT AGTTT GTGGC GT GCC GC T
TGGCGATACGAGCCACAGAC GCCT ||||| ||||| || ||| ||
T TCAGA CACCG CA CGG CG T
- AG TAG--- TT- AGC

GAM2295 GGTGTCCTGGAGCCTCTGTA 2272 CTGGAGCCTC 4886 T C TCT-- C- T - A
CCTGTGCCCAAATGGTGCCC TGTACCTGTG GG GTC TGGAGCC GTAC TG GC CC A
GCTGTGCCACCTGGTTTCAA CCCA || ||| ||||||| |||| || || ||
GACCC CC CAG ACTTTGG CGTG GC CG GG A
- A TCCAC TC C T T

GAM2296 CTTAATCTTGTGGATTTTGT 2273 ATCTTGTGGA 4887 AAT --- AT- TC
AGATGGTTTCAAATGACTGA TTTTGTAGAT CTT CTTGTGGATTT TGTAG GGTT A
ACTGCATTCAGATTTACGAG GGTT ||| |||||||||| ||||| ||||
TGAAAG GAA GAGCATTTAGA ACGTC TCAG A
AGT CTT AAG TA

GAM2297 GCTGAGAAGGAGCTGGGGAT 2274 TCTCCATGAG 4888 AAGG CT TCCC TCC CC AT
CCCCGCTCTCCTGGACCCCA CGTCCCTGAC GCTGAG AG GGGGA CGCTC TGGA CCA G
ATGACATGGTCTCCATGAGC TGCC |||||| || ||||| ||||| |||| |||
GTCCCTGACTGCCTCAGC CGACTC TC TCCCT GCGAG ACCT GGT A
CG-- AG ---- T-- CT AC

GAM2298 GCAATTCGGACAGATGATAA 2275 TACCTTGTTT 4889 - AGAT CT T ATT
CTGTATTGTATTAAAGACAT GGTTCGAATG GCA ATTCGGAC GATAA GTA TGT A
TACCTTGTTTGGTTCGAATG TGC ||| |||||||| ||||| ||| |||
TGC CGT TAAGCTTG TTGTT CAT ACA /
G GT-- C- T GAA

GAM2299 TAAAATTCAAGCTGATTACT 2276 TGACTAACTT 4890 A A GATTACT A T GTAA
GAAGATGTTCAGGGTAAAAA CCATGGCATG TAA ATTCA GCT GAAG TG TCAGG A

CTGCCTGACTAACTTCCATG GATC ||| ||||| ||| |||| || |||||
GCATGGATCTTA ATT TAGGT CGG CTTC AT AGTCC A
C A TAC---- A C GTCA

GAM2300 GGCCGTGTCTCAAGTAACCA 2277 AAGTACGTGC 4891 - G T AA-- - AA A GT CG
CCAAGTACGTGCTGTGGGTG TGTGGGTGGA GGC CGT TC CAAGT CCA CC GT
CGTGCTGTGG GGACGA A
GACGACGACTTCGTCTTCAC CGAC ||| ||| || ||||| ||| || || |||||||||| ||||||
GGCGCGGACGCGGCTGGAGA TCG GCA GG GTTCG GGT GG CA GCGCGGCACT
TCTGCT /
GGCTTGTGGACGTGCT T - T GAGA C CG G -- TC

GAM2301 GCAAGAAGGAAGGAGGGAGG 2278 AGAAGGAAGG 4893 AGA --- - - C T GAGC
GCAGAGCGTTGTCTGAGCAA AGGGAGGGCA GCA AGGA AGG AGGGAGGGCAG AG GT
GTCT A
CAAAGGCCGCCTGCTGCCTT GAGC ||| |||| ||| |||||||||| || || ||||
CTCTGTCTGTCTCCTGGTGC CGT TCCT TCT TCTCTTCCGTC TC CG CGGA /
GG- CTG G G - C AACA

GAM2302 CCACCAGTCCAGGGGTGGGA 2279 AGGGGGTGGG 4892 A C - --- AA--- AG G GAG
GC G
ATACAGGGGGTGGGAGGTGT AGGTGTGCAT CCACC GTC AGGG GT GGG TAC GGG TGG
GTGT ATAA A
GCATAAGAGGTTATAGGCAC AAGA ||||| ||| |||| || ||| ||| ||| ||| |||| ||||
AGGCCAGCCCGGTACAGAAC GGTGG CAG TCCT CG CCC ATG CCC ACC CACG
TATT G
CCTAGGCGTCCTGACAGGTG A - G GAT AAGAC G- G GGA GA G
G

GAM2303 GGTCATTGTGTCCTGCCAAG 2280 AGCCGTAGAT 4894 T TTG G- A A TAG ---
AG
GCACAGCCGTAGATCTGGAA CTGGAAAGAG GG CA TGTCCT CCA GGC CAGCCG
ATCTGGAAAG AGC A
AGAGCAGAATGCTTTCCTTT CAGA || || |||||| ||| ||| |||||| |||||||||| |||
TCAGATGTGGCTGGTCATGG CC GT ACGGGG GGT CTG GTCGGT TAGACTTTTC
TCG /
AAGGGGCAGTTGTCC T TG- AA A - G-- CTT TA

GAM2304 TCTTGTGTTGAGACTTCGTG 2281 TACACCACTC 4895 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM2305 GATACTGGAAACTTTGGTTT 2282 TATCAAATAT 4896 TG AAA T ---- GG AACA

TGGGATCCAGGAACACATCG GACCCAAGCA GATAC G CTT GGTT TTG ATCCAGG C
ATCTGGGTATCAAATATGAC TTGG ||||| | ||| |||| ||| |||||||
CCAAGCATTGGTATC CTATG T GAA CCAG AAC TGGGTCT A
GT AC- C TATA TA AGCT

GAM2306 GAATTCTACAAGAGCCTCAC 2283 TCAAGCACTT 4897 A- A CCTCA AA GG A
TAATGACTGGGAAGACCACT TTCTGTAGAA GA TTCTACA GAG CT TGACTG AAG C
TGGCAGTCAAGCACTTTTCT GGTC || ||||||| ||| || |||||| |||
GTAGAAGGTC CT AAGATGT CTT GA ACTGAC TTC C
GG - TTCAC -- GG A

GAM2307 AGGCCCACATGGTCACTCAC 2284 ACCACGAGTG 4898 - T --- ACAGCAG G
AGCAGCCGCAAGGACCACGA CAAGCTCTGT AGGCCC ACA GGT CACTC CC C
GTGCAAGCTCTGTGGGGCCT GGGG |||||| ||| ||| ||||| ||
TCCGGG TGT TCG GTGAG GG A
G C AAC CACCA-- A

GAM2308 GATCGCCATGTTCATGGTGA 2285 TTCATGGTGA 4899 C ATGG CCA CAA A AT
ACACCATTCAACAATCTATC ACACCATTCA GAT GCCATGTTC TGAACA TTCAA TCT TCC C
CATCTCCGGAGGAACCTTGA ACAA ||| ||||||||| |||||| ||||| ||| |||
AGCTGTTCAGAATATGGTAT CTA TGGTATAAG ACTTGT AAGTT AGG AGG T
C - ---- CG- CCA - CC

GAM2309 CTTTGGTAGACACAGGCATT 2286 TGGGAACCAT 4900 AG A A TGA---- GCTGATCT
GGCATGACCAAAGCTGATCT TGCCAAGTCT CTTTGGT AC CAGGC TTGGCA CCAAA C
CATAAATAATTTGGGAACCA GGTA ||||||| || ||||| |||||| |||||
TTGCCAAGTCTGGTACTAAA GAAATCA TG GTCTG AACCGT GGTTT /
G -- - - TACCAAG AATAAATA

GAM2310 AAGCTTTATTCCCATTGGGT 2287 TGCCTATGGG 4901 AT A G - T AAGGATA
CCAAGGCTGGTAAGGATAGT CTGGAGGGAG AAGCTTT TCCC TT GGTCCA AGGC GGT G
TAAAAAAGCTGCCTATGGGC AGGC ||||||| |||| || |||||| |||| |||
TGGAGGGAGAGGCTT TTCGGAG AGGG AG TCGGGT TCCG TCG T
-- - G A - AAAAAAT

GAM2311 GCTGGGCTCAAAAGGCTCTG 2288 TCGAAGAGAT 4902 ---------- A TGGG T
GGTCGTGCTTGAAAGTGAGC ACTCGCCCAG GCTGGGC TC AAAGGCTC TCG G
CTTTCGAAGAGATACTCGCC C ||||||| || |||||||| |||
CAGC CGACCCG AG TTTCCGAG AGT C
CTCATAGAGA C TGAA T

GAM2312 GAGAGGAGCAGGTGCAGTGA 2289 TGTGATGGCC 4903 CA CA G T C - C
TTCATACCCACTCTAAAGCT ACCCTTCTCT GAGAGGAG GGTG GT AT CATA CCA CT T

GGCTGTGATGGCCACCCTTC T |||||||| |||| || || |||| ||| ||
TCTT TTCTCTTC CCAC CG TA GTGT GGT GA A
-- -- G - C C A

GAM2313 GGATTGGAAAGGGGACAGAG 2290 TCTCCAGGTG 4904 T AA- G A-- - - AA
AGGTGGACAAGCAAGTCCAG CTCATCTCCA GGAT GGA GGG AC GAGA GG TGGAC G
CCTTCTCCAGGTGCTCATCT TCC |||| ||| ||| || |||| || |||||
CCATCC CCTA CCT CTC TG CTCT CC ACCTG C
- CTA G GAC T G AA

GAM2314 CCCACTGATGGAGCCCAGCA 2291 TGATGCTCAC 4906 G AGCC AGCAT AA-- GT
GCATTGAGAAAATTGTAGAG ATAGGTTGTG CCCACT ATGG CAGC TGAG AATT A
ATTGATGCTCACATAGGTTG CCAT |||||| |||| |||| |||| ||||
TGCCATGAGTGGG GGGTGA TACC GTTG ACTC TTAG /
G GT-- GATAC GTAG AG

GAM2315 AATTGATAAAGCCAGAGTGG 2292 TGTGACCCAA 4905 A G GA AACCACT - - A A AGAC
AGACACAGAACCACTGGTTC GCTGTGTCCA AATTG TAAAGCCAGA TGGA CACAG GGTT CAC CT CA TG A
ACCTACAATGAGACAATGAC ATCT ||||| |||||||||| |||| ||||| |||| ||| || || ||
AGTGGAGAGTGTGACCCAAG TTGAC GTTTCGGTCT ACCT GTGTC CCAG GTG GA GT AC /
CTGTGTCCAATCTGGCTTTG - A -- GAAC--- T A G G AGTA
CAGTT

GAM2316 GTGATGCTCGAGCAATTGGC 2293 GCTCGAGCAA 4908 AT-- - GA TT CTT GA
TCTGCTTCAGAGGGTGCCCA TTGGCTCTGC GTG GCT C GCAA GGCTCTG CA G
GAGCTCCTTGCAAGAAGTTT TTCA ||| ||| | |||| ||||||| ||
ACCAC CAC TGA G CGTT TCGAGAC GT /
CATT A AA CC CC- GG

GAM2317 CTTGGTTCTACAGCCATTGG 2294 AGCCATTGGG 4907 GG CAT ATC G A
GATCCAGACATCAGAGGGTG ATCCAGACAT CTT TTCTACAGC TGGG CA ACATC G
TGTGCCTAGCTGTGGAGAAG CAGA ||| ||||||||| |||| || |||||
AG GAG GAGGTGTCG ATCC GT TGTGG A
AA --- --- G G

GAM2318 CCCATTTGGCTTATAAAGAC 2295 AGGAACCGCG 4909 G ATAAAGA - ACA- TT
TCGGTTACAGCTTGATGCAA GGGAAAGGCG CCCATTTG CTT CT CGGTT GC G
GGAACCGCGGGGAAAGGCGA AATG |||||||| ||| || ||||| ||
ATGGG GGGTAAGC GAA GG GCCAA CG /
G AGG---- C GGAA TA

GAM2319 CTGCAAGGAAAAGTTGAATG 2296 TACATATGAT 4910 AAGGAAA TG--- ATCCTG
ATGTATTTGATCCTGATTCT TTCAGCTGCA CTGC AGTTGAA ATGTATTTG A
ACCCAAGTACATATGATTTC ATGG |||| ||||||| |||||||||
AGCTGCAATGGCAG GACG TCGACTT TACATGAAC T
GTAACG- TAGTA CCATCT

GAM2320 GTGGATTGGTGGAGTTTGGG 2297 TGACTGGAGC 4911 T T A G -- TAATG
AGCATTAATGTATGACATGC ACCCCCATTC GTGGAT GG GG GTTT GG AGCAT T
TGACTGGAGCACCCCCATTC AC |||||| || || |||| || |||||
AC CACTTA CC CC CGAG TC TCGTA /
C - A G AG CAGTA

GAM2321 GATGTCAATGCTGCCATTGC 2298 TGGATTGGTG 4912 A-- CT T C-- TCAAA GCAG
CACCATCAAAACAAGCGCAG CCCCACTGGC GATGTCA TG GCCA TG CACCA ACAAGC
C
CATCCAGTTTGTGGATTGGT TTCA ||||||| || |||| || ||||| ||||||
GCCCCACTGGCTTCAAGGTG CTACGGT AC CGGT AC GTGGT TGTTTG A
GCATC GGA TT C CCC TAGG- ACCT

GAM2322 GAGGTGGGTGGATCACCTGA 2299 TGACCAACAT 4913 GGA - A- T TCA
GGTCAGGTGTTCAAGACCAC GGTGAAACCC GAGGTGGGT TCACC TG GGTCAGG GT A
CCTGACCAACATGGTGAAAC ATCT ||||||||| ||||| || ||||||| ||
CCATCTC CTCTACCCA AGTGG AC CCAGTCC CA G
A-- T AA - CCA

GAM2323 GGTCATTCTGGGCTTTCCCT 2300 AGGAACCAGG 4914 AT C - CAA AAT G
GCAACCAATTTGGAAAACAG AGAGAACTCA GGTC TCTGGG TTTC CCTG CC TT G
GAACCAGGAGAGAACTCAGA GAGA |||| |||||| |||| |||| || ||
GATC CTAG AGACTC AGAG GGAC GG AA A
-- A A CAA AC- A

GAM2324 GCTGGAACTGAAGCTGGGGC 2301 TGGGGCTGCA 4915 AA TG - TG CA T TT TT
TGCAGCCTGGGCCTTGGTTT GCCTGGGCCT GCTGG C AAG C GGGCTG GCC GGGCC GG
T
GATCCTTGGCCTTGGCCTTG TGGT ||||| | ||| | |||||| ||| ||||| ||
GCCTTGGCCTTTGGCCGGC CGGCC G TTC G TCCGGT CGG TCCGG CC G
-- GT C GT TC T TT TA

GAM2325 GAATATTTCCACAATGTCTG 2302 TACACGGTCG 4916 CACA T AAC G TTCA
TGAACTGGACCTGGTGTTCA TGGACGAGAT GAATATTTC ATG CTGTG TGGACCT GTG A
ACTTCTACAAGGTTTACACG GTTC ||||||||| ||| ||||| ||||||| |||
GTCGTGGACGAGATGTTC CTTGTAGAG TGC GGCAC ATTTGGA CAT /
CAGG T --- A CTTC

GAM2326 TCTTGTGTTGAGACTTCGTG 2303 TACACCACTC 4917 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG |||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM2327 TGGCACTCCTAGGCTCTATC 2304 TGCCATAGGC 4919 TA T CAGAC A CC CAT
AGACTGACCCCTCGGGCACA CGGGGTGCCA TGGCACTCC GGC CTAT TG CC TCGGGCA
A
TACCATGCCTGGAAGGCCAA |||||||||| ||| |||| || || |||||||
TGCCATAGGCCGGGGTGCCA ACCGTGGGG CCG GATA AC GG GGTCCGT /
-- - CCGTA C AA ACC

GAM2328 CTGACGAAGCCATTGAAACA 2305 ACGAAGCCAT 4918 GA GAAA A------- TG TT
GATGATCTGACCATTAAGCT TGAAACAGAT CTGAC AGCCATT CAG TGATC ACCA A
GGTGATCAAGGCACTCCTGG GATC ||||| ||||||| ||| ||||| ||||
AAGTGGTTCAGTCAG GACTG TTGGTGA GTC ACTAG TGGT A
AC AG-- CTCACGGA -- CG

GAM2329 TAATTTAGTGAGGTGAACGA 2306 TTAGTGAGGT 4920 TT GAACG - TTAC
CTTCAGATTTCATTACTGGA GAACGACTTC TAAT AGTGAGGT ACTTCAGAT TTCA T
TTGGATATTTGAGGTAAAAT AGAT |||| |||||||| ||||||||| ||||
TTCATTTGGTTA ATTG TTACTTTA TGGAGTTTA AGGT /
GT AAA-- T TAGG

GAM2330 TCTTGTGTTGAGACTTCGTG 2307 TACACCACTC 4921 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG |||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM2331 TCAGATGATGGGAAAACTCG 2308 ACTCGAGTAA 4922 ATGA AAA AAAG GC GA
GACA
AGTAAAGCTGCTGTTTCAGA AGCTGCTGTT TCAG TGGG ACTCGAGT CT TGTTTCA
ATCTG C
ATCTGGACACCAAACAGATT TCAG |||| |||| |||||||| || ||||||| |||||
GAGATGAAGGAACTCGAGTT AGTC ACCT TGAGCTCA GG GTAGAGT TAGAC /
CCAGGACCTGA CAGG --- A--- AA -- AAAC

GAM2332 TGCAGTGGCCGGTACAGCTG 2309 TACACATTAC 4923 G CC- C----- AG
GGAGGAGCGCCCCTTCCGGC CATTCCGGTG TGCA TGG GGTA AGCTGGGAGG C
TACACATTACCATTCCGGTG CA |||| ||| |||| ||||||||||
CA ACGT GCC CCAT TCGGCCTTCC G

G TTA TACACA CC

GAM2333 CTGGGCCAAGTGGCCATTCT 2310 AAGTGGCCAT 4924 CCAA - T TC CAAATC
TCTGTTCAAATCTGGTTAAA TCTTCTGTTC CTGGG GTGGC CA TCT TGTT T
AGCATGGACTGTGCCACACA AAAT ||||| ||||| || ||| ||||
CCCAG GACCC CACCG GT AGG ACGA G
ACA- T C T- AAATTG

GAM2334 TTGAGATGGAGTATTGCTCT 2311 TTACTGCAAG 4925 AT- T T TCT - C-- -- -
ACAA
GTGGCCCAGGCTGGAGTGCA CTCCGCCTCC TTGAG GGAG AT GC GTGG CCCAGG
TGGAGT GCAGTG GC T
GTGGCACAATCTCGGCTTAC TGGG ||||| |||| || || |||| |||||| |||||| |||||| ||
TGCAAGCTCCGCCTCCTGGG GACTC CCTC TA CG CACT GGGTCC GCCTCG
CGTCAT CG /
TTCACGCCATTCTCCTACCT CAT T C --- T TCC AA T GCTC
CAG

GAM2335 CACTACGTTGACCTGAAGGA 2312 AAGGACCGTC 4926 GA-- GAA- CCATTCT --
AAAT
CCGTCCATTCTTTGCCGGCC CATTCTTTGC CACTACGTT CCT GGACCGT
TTGCCGGCCT GGTG A
TGGTGAAATACATGCACTCA CGGC ||||||||| ||| ||||||| |||||||||| ||||
GGGCCGGTAGTTGCCATGGT GTGGTGTAA GGG TCTGGTA GATGGCCGGG
TCAC /
CTGGGAGGGGCTGAATGTGG GTCG AGGG CCGTT-- AC GTAC
TG

GAM2336 TTCTGCATACAAGTTGGCAG 2313 GATTCTGTGG 4927 ACAAG G A ATAC
GAACATTATACATGGCAGTG AGAGTGCAGA TTCTGCAT TT GCAGGA CATT A
ATTCTGTGGAGAGTGCAGAG G ||||||||| || |||||| ||||
GAGACGTG AG TGTCTT GTGA /
AG--- G A CGGT

GAM2337 TCTTGTGTTGAGACTTCGTG 2314 TACACCACTC 4928 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM2338 AGGAACCATCCCAGGTGCGG 2315 TGTTGGGAAG 4929 A - GG G A- - - TC
GCGGCACCCAGAGACTCACC TCGCTGGCGA AGGA CCATC CCA TGC GGCGGC CCCAG AG
AC A
CGTGCTGTTGGGAAGTCGCT TGGA |||| ||||| ||| ||| |||||| ||||| || ||
GGCGATGGAGATGGTCCT TCCT GGTAG GGT GCG TCGCTG GGGTT TC TG C
- A A- G AA G G CC

GAM2339 TGGGTGTGCAGGCTGTAATT 2316 TACCACACTC 4930 G ---- GC AAT-- T TAAATTC
TTCTTTCTTTATAAATTCTG TGTAAACAGA TGGGT TG CAG TGT TTTC TTCTTTA T
CAAATCTAAAGAACGAAATT CCCA ||||| || ||| ||| |||| |||||||
ACCACACTCTGTAAACAGAC ACCCA AC GTC ACA AAAG AAGAAAT /
CCA G AAAT TC CCATT C CTAAACG

GAM2340 GGCTCCACAGTGTGCACAGA 2317 CTCAAGTTTC 4931 - CAGTGTG CGA G AT CA
AGCT
TGAACGAAGTTATGGCAGAG ATTTGTGAAG GGCT CCA CACAGATGAA A TT GG GAGTT
A
TTAGCTAACAGAACTCCCTC TTGG |||| ||| |||||||||| | || || |||||
AAGTTTCATTTGTGAAGTTG TCGA GGT GTGTTTACTT T AA CC CTCAA /
GAAGCT A TGAA--- --- G CT -- GACA

GAM2341 GTGAGGCATGACGGCTCCGA 2318 TGTTCGGAGA 4932 G - A- G CC T
GCCCTGCGTGGACGTGCTGT CGGGCATCGC GT AGGC ATG CG CTCCGAGC TGCG G
TCGGAGACGGGCATCGCCTG CTGA || |||| ||| || |||||||| ||||
AT TA TCCG TAC GC GAGGCTTG GTGC G
G C GG A TC A

GAM2342 GTAGTGCTCCTGGAGAAGCT 2319 GAGAAGCTAG 4933 G GG- C GCC T GCT
AGAGCCTGATGTAGGCTACA AGCCTGATGT GTAGT CTCCT AGAAG TAGA TGATG AG A
TACTCATCATTTACTTCTAC AGGC ||||| ||||| ||||| |||| ||||| ||
AGGGAGACTAC CATCA GAGGG TCTTC ATTT ACTAC TC C
- ACA - --- - ATA

GAM2343 GAACAGAATCTTGTGGAAGA 2320 TGGAAGAAGA 4934 ATC--- --- AA T GAT
AGAATGAAGTTGCTGATTAT ATGAAGTTGC GAACAGA TTGTGGAAGA AGAATG GT GCT T
GAAGCTACAACATTTTCCAT TGAT ||||||| |||||||||| |||||| || |||
CTTCTATAACAACACTCTGT CTTGTCT AATATCTTCT TTTTAC CA CGA A
TC CACAAC ACC AA T AGT

GAM2344 GGTGACAACATGCTGGAGCC 2321 TGGGTTCAAG 4935 AA-- G G- A T TA
AAGTGCTAACATGCCTGGGT GGATGGAAAG GGTGAC CAT CT GAGCC AG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || ||||| || ||
CCACTG GTA GG CTTGG TC CG C
AAAG G AA G - TA

GAM2345 AACAGAGATTTACCGCATTG 2322 TACCGCATTG 4936 GA TT-- T CA AG AA
GACAGA
TTTCTCAGAAGCAAATGTCA TTTCTCAGAA AACA GAT ACCGCATTGTT CT GA CA TGTCA
C

GACAGACGCGAAAATGACAT GCAA |||| ||| |||||||||| || || || |||||
GTCTCCAAGCAACAATGTGG TTGT TTA TGGTGTAACAA GA CT GT ACAGT G
TTCCTATTCATGTT AC TCCT C AC CT -- AAAAGC

GAM2346 TCTTGTGTTGAGACTTCGTG 2323 TCACACCACT 4937 GAGA GT--- CTA AAAGGA
GTGGTGCTAAGAAAAGGAAG CCCAAGAAGA TCTTGTGTT CTTC GGTGGTG AGA A
AAGAAGTCTCACACCACTCC ATAA ||||||||| |||| ||||||| |||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC TCT G
ATAA AACCC AC- GAAGAA

GAM2347 GAGGCAGGTGGATCACCTGA 2324 TGGATCACCT 4938 A T A- - A- A- C
GGTCAGGAGTTCAGGAGCAG GAGGTCAGGA GAGGC GG GG TCACC TG GGTCAGG GTT A
CCTGGCCAACATGGTGAAAC GTTC ||||| || || ||||| || ||||||| |||
CCCGTCTC CTCTG CC CC AGTGG AC CCGGTCC CGA G
- - AA T AA GA G

GAM2348 GCATAGCTTTCAAGAAATTG 2325 TTCAAGAAAT 4939 A T - TT-- --- TTT
TCACAAAAGGTTTTATTCTC TGTCACAAAA GCAT GCTT CAA GAAA GTCACAA AAGG T
TTTGCTTGTGACTATTTTTC GGTT |||| |||| ||| |||| ||||||| ||||
ATTGAAGCATGC CGTA CGAA GTT CTTT CAGTGTT TTCT A
- - A TTAT CGT CTT

GAM2349 GGGGGGCAAGATCTACAAAG 2326 TCCAATCTGA 4940 - AAGA A - - CACTG CT- C
TGCCGTCCACTGAGACTGAG TGGGCATGTT GGGGG GC TCT CAAA GTGCC GTC AGA
GAGGC T
GCCTTGGCTTCCAATCTGAT TGAG ||||| || ||| |||| ||||| ||| ||| |||||
GGGCATGTTTGAGAAACGGC CCTTC CG AGA GTTT TACGG TAG TCT CTTCG T
GCTTCC G GCAA - G G ----- AAC G

GAM2350 CATGTGATGATAATGGTCTT 2327 TTGGCAGCCA 4941 TG T A T TCTC T AA
CTCGCCATCCCAAGATGGGT TGATCTTTGC CATG A GAT ATGG CT GCCA CCC G
TGGCAGCCATGATCTTTGCA ATG |||| | ||| |||| || |||| |||
TG GTAC T CTA TACC GA CGGT GGG /
GT T G - ---- T TA

GAM2351 GAAAGATTGTGCAGATGACT 2328 TATCAAGTCT 4942 GTGCA T - A G TC
GAAGCAGAAGTTCGAGGCTT CGGGAGATCT GAAAGATT GA GACT GA GCA AAGT G
ATGTATCAAGTCTCGGGAGA TTC |||||||| || |||| || ||| ||||
TCTTTC CTTTCTAG CT CTGA CT TGT TTCG /
AGGG- - A A A GA

GAM2352 GAGGAAAGCAGTCTTTGGAA 2329 TTATAAAATC 4943 - C - AACCA--- TT TA
ACCATTTGTTTGCTATTGGC AAATATCCAG GAG GAAAG AGT CTTTGGA TTTGT GC T

```
     TTATAAAATCAAATATCCAG       AGAA          ||| |||||| ||| |||||||       |||||  ||
     AGAACTTCTTTCTCTT                    TTC CTTTC TCA GAGACCT       AAATA  CG  /
                                 T    T  A     ATAAACTA    TT  GT


GAM2353  TCTTGAATTACAGGGGGGTT 2330    TAGCTAATAA 4944     T      C  GG GG    -   TC   T
     TGTAGCTTCTCTTTGTAGAT       AATCACTTAA       TC TGAATTA AG  G  TTTGT AGCT  TCT T
     AGCTAATAAAATCACTTAAT       TTCA          || |||||||  ||  |  ||||| ||||  |||
     TCACGG                          GG ACTTAAT TC  C  AAATA TCGA  AGA G
                                C      -  A- TA     A    T-   T


GAM2354  GCAGGTTTTTTCTTCTTCAA 2331    TAGCAGAGTG 4945     A     T       AAA  A   T  -   ATTA   --
AGC   T
     AACCATTCTACCTCATTAGC       TGAGGGCACT       GC GGTTTT TCTTCTTCA   CC TTC AC CTC
GCAT  TCA   GAGC G
     ATTCAAGCGAGCTGTGGCTC       GAGG          || |||||| |||||||||   || ||| || |||    ||||  |||   ||||
     TGATGATCATGTAGCAGAGT                 CG TCAAAA GGGAGGAGT   GG GAG TG GAG    TGTA  AGT
 CTCG T
     GTGAGGGCACTGAGGAGGGC                   G     C       CAC  -   -  T   ACGA    CT   AGT    G
     AAAACTGGC

GAM2355  GCCAACCTTGAAGCCAGTGG 2332    TTGAAGCCAG 4946      A  - TG     -   G    -   ATCC
     GGCACCAATCCACAAACTGG       TGGGGCACCA       GCCA CC T  AAGCCA GTG GGCA CCA    A
     ATGCTGCGCTTGGTTTTGAT       ATCC          |||| || |  |||||| ||| |||| |||
     GGTGGC                          CGGT GG A  TTTGGT CGC TCGT GGT    C
                               -  T GT     T   G    A   CAAA


GAM2356  TGGCACCCCGGCCTATGGCA 2333    TCAGTCTGAT 4947        -  C-  -   -  C       CCA     GG
     TTGGCCTTCCAGGCATGGTA       AGAGCCTAGG       TGGCAC CC  GGC CTAT GG ATTGGCCTT
GGCAT  T
     TGTGCCCGAGGGGTCAGTCT       AGTG          |||||| ||  ||| |||| || |||||||||   |||||
     GATAGAGCCTAGGAGTGCCA                 ACCGTG GG  CCG GATA TC TGACTGGGG   CCGTG  /
                                A  AT   A    G  -       AGC     TA


GAM2357  TCTTGTGTTGAGACTTCGTG 2334    TACACCACTC 4948          GAGA    GT---      C     AAAGGA
     GTGGTGCTAAGAAAAGGAAG       CCAAGAAGAA       TCTTGTGTT    CTTC     GGTGGTG TAAGA     A
     AAGAAGTCTTACACCACTCC       TAAG          |||||||||    ||||     ||||||| |||||
     CAAGAAGAATAAGCACAAGA                 AGAACACGA    GAAG     TCACCAC ATTCT     G
                                   ATAA    AACCC      -    GAAGAA


GAM2358  TTGCGGCATCCACGAGACCA 2335    TGACGTGGAC 4949        CA-     AGAC   -    ACTC
     CCTTCAACTCCATCATGAAG       ATCCGCAA         TTGCGG   TCCACG    CAC CTTCA    C
     TGTGACGTGGACATCCGCAA                 ||||||   ||||||    ||| |||||
                               AACGCC   AGGTGC    GTG GAAGT    /
                                  TAC     A---   T     ACTA
```

GAM2359 GCTCCCCTTTGGTGCTCACT 2336 CCTTTGGTGC 4950 CTTT T- A CCT -- T
ACCTGGTTGTCGATGTATCG TCACTACCTG GCTCCC GG GCTC CTA GGTTG TCGA G
GATCAGCTTCTTGGGGGCCT GTTG |||||| || |||| ||| ||||| ||||
CCTTGGGAGC CGAGGG CC CGGG GGT TCGAC GGCT T
TT-- TC - TCT TA A

GAM2360 TGTGTCGTGGAGGCGAATGT 2337 TGGCATCGTA 4951 - GGAG A T--- A ACCA
TTGCACCAACCAAAACCTGG GAGTGAACAC TGTGT CGT GCGA TGTT GC CCA A
CGCCGTTGGCATCGTAGAGT A ||||| ||| |||| |||| || |||
GAACACA ACACA GTG TGCT ACGG CG GGT /
A AGA- - TTGC C CCAA

GAM2361 GGTGACAACATGCTGGAGCC 2338 TTCAAGGGAT 4952 AA-- G G- A T A
AAGTGCTAACTATGGCCTGG GGAAAGTCAC GGTGAC CAT CT GAGCCA G GCTA C
TTCAAGGGATGGAAAGTCAC C |||||| ||| || |||||| | ||||
C CCACTG GTA GG CTTGGT C CGGT T
AAAG G AA - - A

GAM2362 CATTGTCGTCATTGGACACG 2339 CGTCATTGGA 4953 GTC-- T- A C ATTC C
TAGATTCGGGCAAGTCCACC CACGTAGATT CATT GTCA TGG CA GTAG GGG A
ACTACTGGCCATCTGATCTA CGGG |||| |||| ||| || |||| |||
TAAATG GTAA TAGT ACC GT CATC CCT A
ATATC CT G - ACCA G

GAM2363 GTGACAACATGCTGGAGACC 2340 TTCCACGGGA 4954 AA--- G GA- T TA
AAGTGCTAACATGCCTTGGT TGGGAAAGTC GTGAC CAT CTG GACCAAG GC A
TCCACGGGATGGGAAAGTCA AC ||||| ||| ||| ||||||| ||
C CACTG GTA GGC TTGGTTC CG C
AAAGG G ACC - TA

GAM2364 CATTGTCGTCATTGGACACG 2341 CGTCATTGGA 4955 GTC-- T- A C ATTC C
TAGATTCGGGCAAGTCCACC CACGTAGATT CATT GTCA TGG CA GTAG GGG A
ACTACTGGCCATCTGATCTA CGGG |||| |||| ||| || |||| |||
TAAATG GTAA TAGT ACC GT CATC CCT A
ATATC CT G - ACCA G

GAM2365 GTGGAGGTGACTGGTGATGA 2342 ATTGATGGTC 4956 GA - GA A GG
ATACAATGTGGAAAGCATTG AGCCAGGTGC GTGGAGGT CTGG TGAT AT CAATGT A
ATGGTCAGCCAGGTGCCTTC CTTC |||||||| |||| |||| || ||||||
AC CACTTCCG GACC ACTG TA GTTACG /
TG G G- - AA

GAM2366 CCGGAAGCTGCCCTTCCAGA 2343 AAGCTGCCCT 4957 AA C ----- AG GAGG GC
GGTTGGTGAGGGAGATCGCG TCCAGAGGTT CCGG GCTGC CTT CC AGGTTGGT
GAGATC G
CAGGATTTCAAAACCGACCT GGTG |||| ||||| ||| || |||||||| ||||||
GAGGTTTCAGAGCGCAGCCA GGCT CGACG GAG GG TCCAGCCA CTTTAG C
TCGG AC C ACTTT AG AAA- GA

GAM2367 CATTGTCGTCATTGGACACG 2344 CGTCATTGGA 4958 GTC-- T- A C ATTC C
TAGATTCGGGCAAGTCCACC CACGTAGATT CATT GTCA TGG CA GTAG GGG A
ACTACTGGCCATCTGATCTA CGGG |||| |||| ||| || |||| |||
TAAATG GTAA TAGT ACC GT CATC CCT A
ATATC CT G - ACCA G

GAM2368 GGGCATCCTGGCTGCAGATG 2345 TCCATTGGCA 4959 GCA - C CAGA A - C A- TT A
AGTCCACTGGGAGCATTGCC CCGAGAACAC GG TCCT GG TG TG GT CCA TGGG GCA
GCC A
AAGCGGCTGCAGTCCATTGG CGAG || |||| || || || || ||| |||| ||| |||
CACCGAGAACACCGAGGAGA CC AGGA CC AC GC CA GGT ACCT CGT CGG G
ACC AAG G - AAGA - C T GA -- C

GAM2369 GGTGACAACATGCTGGAGCC 2346 TTGGTTCAAG 4960 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM2370 ACATCATTGTCTATCATGAA 2347 TGTGAAGAAG 4961 ATTG-- A AA-- G G TCAGG
CTTGTACAGCCATCAGGTAA ACATGGAGAA ACATC TCT TCATG CTT TACA CCA T
AAATTGGTGTGAAGAAGACA TGGA ||||| ||| ||||| ||| |||| |||
TGGAGAATGGAGGATGT TGTAG AGA GGTAC GAA GTGT GGT A
GAGGTA - AGAA - - TAAAA

GAM2371 GTTGACCTCCACGGTGATGC 2348 ATGCTGTGGC 4963 A AC GATGCT C - - ACA
TGTGGCTGCAGACCAACAAA TGCAGACCAA GTTG CCTCC GGT GTGG TGC AGA CCA A
TCTGGCTCTGGCACCATGAA CAAA |||| ||||| ||| |||| ||| ||| |||
CCTCGGAGGCAGC CGAC GGAGG CCA TACC ACG TCT GGT /
- CT AG---- - G C CTA

GAM2372 CTGGAGGTGGAAGCCAACAA 2349 TTGAAGGTGG 4962 TG AGCCAACA TTTG AGTA
CC
TGCCTTTGACCAGTATCGAG CGTCTCATCT C GAGGTGGA ATGCC ACC TCGAGA T
ACCTGTATTTTGAAGGTGGC GTCT | |||||||| ||||| ||| ||||||
GTCTCATCTGTCTACCTCTG G CTCCATCT TGCGG TGG AGTTTT G
G GT GTCTACTC ---- A--- AT

GAM2373 TTGTCGTCATTGGACACGTA 2350 TAAATGCGGT 4964 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM2374 TGTTCTCTAGGCCTTTGTAG 2351 TATTATGCGA 4965 GGCC GAAAAC GA TT
AAAACATGGACGTTGTTCCT ATCTATAGAG TGTTCTCTA TTTGTA ATG CGTTG C
TGGCGCACATATTATGCGAA AATA ||||||||| |||||| ||| |||||
TCTATAGAGAATA ATAAGAGAT AAGCGT TAC GCGGT /
ATCT ATTA-- AC TC

GAM2375 GTGCTTCAACTGGTATCTAT 2352 TATGAGGCCC 4966 T T AT A - AGAG GGACAA
TA
GAGGCCCTAGAGCTCCGGGA TAGAGCTCCG GTGCT CAAC GGT CT TGAGGC CCT CTCCG
TGA A
CAATGATAAGACTCGCTATA GGAC ||||| |||| ||| || |||||| ||| ||||| |||
TGGGGAAGGGTGTCTCAAAG CACGA GTTG TCG GA ACTCTG GGG GGGGT GCT
G
GCTGTTGAGCAC - - -- A T AA-- ATATC- CA

GAM2376 TTGAACTCATTCTGGCTGCA 2353 TGTTACATGC 4967 AC TC T AA ACTTA-- AGG
AACTACTTAGACATCAAAGG AAGACTGTTG TTGA TCAT TGGC GCA CT GACATCAA T
TTTGCTTGATGTTACATGCA CCAA |||| |||| |||| ||| || ||||||||
AGACTGTTGCCAATATGATC AACT AGTA ACCG TGT GA TTGTAGTT T
AA -- TA T CA ACGTACA CGT

GAM2377 TTTCAGGGTAATGATGCACC 2354 ACAGTGCAGA 4968 ATGA-- C ACA
TGTTGAACAAGAAATTAACA AACATACTTT TTTCAGGGTA TGCAC TGTTGA A
GTGCAGAAACATACTTTGAA GAAA |||||||||| ||||| ||||||
A AAAGTTTCAT ACGTG ACAATT G
ACAAAG - AAA

GAM2378 TTGTCGTCATTGGACACGTA 2355 TAAATGCGGT 4969 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM2379 GTCTCTTCAGAGCTGCTTGT 2356 TATGAGGCCC 4970 TTCA G TGT - GT TC
GCCCAGTGGTGCTTCAACTG TAGAGCTCCG GTCTC GAGCT CT GCC CA GGTGCT A
GTATCTATGAGGCCCTAGAG GGAC ||||| ||||| || ||| || ||||||

CTCCGGGAC CAGGG CTCGA GA CGG GT CTATGG A
C--- - TCC A AT TC

GAM2380 GGTGTTAAGTGCTCCAAGGA 2357 TAAGTGCTCC 4971 TTA T --- A - A CA
GGTGGCCACCGCCATCCGTG AAGGAGGTGG GGTG AG GCT CCA GGA GGTGGCC CCGC T
GGGCCATCATCCTGGCCAAG CCAC |||| || ||| ||| ||| ||||||| ||||
CTCTCCATC CTAC TC CGA GGT CCT CTACCGG GGTG /
C-- T ACC - A - CC

GAM2381 ATGGTGACAACATGCTGGAG 2358 TTGGTTCAAG 4972 AA-- G G- T TA
CCAAGTGCTAACATGCCTTG GGATGGAAAG ATGGTGAC CAT CT GAGCCAAG GC A
GTTCAAGGGATGGAAAGTCA TCAC |||||||| ||| || |||||||| ||
CCGT TGCCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM2382 ATGGTGACAACATGCTGGAG 2359 TTGGTTCCAC 4973 AA-- G -- T TA
CCAAGTGCTAACATGCCTTG GGGATGGAAA ATGGTGAC CAT CT GGAGCCAAG GC A
GTTCCACGGGATGGAAAGTC GTCA |||||||| ||| || ||||||||| ||
ACCGT TGCCACTG GTA GG CCTTGGTTC CG C
AAAG G CA - TA

GAM2383 GGCTCATGAGGATGCGGAGT 2360 ATGGAGCTCT 4974 ATGA ---- --- A
GTGAGAAGCTCATGGAGCTC ACGAGCGTCT GGCTC GGATGC GGAGT GTGAG A
TACGAGCGTCTGGAGGAGCT GGAG ||||| |||||| ||||| |||||
TCGAG TCTGCG TCTCG TACTC /
GAGG AGCA AGG G

GAM2384 CATGACCACAGTCCATGCCA 2361 ATGGCCCCTC 4975 A CCATG ATCACT- - - A
TCACTGCCACCCAGAAGACT CGGGAAACTG CATG CCACAGT CC GCCA CC CAG A
GTGGATGGCCCCTCCGGGAA TGGC |||| ||||||| || |||| || |||
ACTGTGGCGTG GTGC GGTGTCA GG CGGT GG GTC G
- AA--- GCCTCCC A T A

GAM2385 GCGACTGCAGCTCTGGGACA 2362 CATCCGGGAC 4976 G C-- C G CAC TCA G- TC
CAGCTGGTCAGGAGAGGTTC TCCACGGTGG GC ACTG AG TCT GGA AGCTGG GGA AGGT
C
CGCAGCCTGATCCCCAGCTA C || |||| || ||| ||| |||||| ||| ||||
CATCCGGGACTCCACGGTGG CG TGGC TC AGG CCT TCGACC CCT TCCG G
C G ACC - G ACA --- AG AC

GAM2386 GCGCGCCAAAGAACTGAGCG 2363 AAGCAGCTTT 4977 CC- A AGCG CATTG A GC
TCATGTTCATTGAGACCAGT TTCGACGTGT GCGCG AAAGA CTG TCATGTT AG CCAGT G
GCGAAGACTGGCTACAACGT ||||| ||||| ||| ||||||| || |||||

GAAGCAGCTTTTTCGACGTG TGTGC TTTTT GAC AGTGCAA TC GGTCA A
T AGC C GA-- CA--- - GA

GAM2387 GTGTAAAATTATTGCTTATG 2364 TTAAAAGAAG 4978 ATTAT TAT A C G TG
TCATTTCTTAAGCAGTTATG GCTAGCATTG GTGTAAA TGCT GTC TTT TTAAGCA TTA C
CTCTTAATGCTTAAAAGAAG TTTG ||||||| |||| ||| ||| ||||||| |||
GCTAGCATTGTTTGCAC CACGTTT ACGA CGG AGA AATTCGT AAT T
GTT-- T-- A A - TC

GAM2388 CATTGTCGTCATTGGACACG 2365 CGTCATTGGA 4979 GTC-- T- A C ATTC C
TAGATTCGGGCAAGTCCACC CACGTAGATT CATT GTCA TGG CA GTAG GGG A
ACTACTGGCCATCTGATCTA CGGG |||| |||| ||| || |||| |||
TAAATG GTAA TAGT ACC GT CATC CCT A
ATATC CT G - ACCA G

GAM2389 AGCATGATCAAGAAGCCCCG 2366 CAATGCAGTC 4980 - AGAA C C CTC AA-- AGTG
CCCACTCGGGCTGAAGGCAG CTGGATGGAG AGCATGAT CA GC CCG CCA GGGCTG
GGC A
TGATTTTGGCCAATGCAGTC CCGA |||||||| || || ||| ||| |||||| |||
CTGGATGGAGCCGACTGCAT TCGTACTA GT CG GGT GGT CCTGAC CCG T
CATGCT C CAGC A A --- GTAA GTTT

GAM2390 GGGTTGTGTCTCCAGTCCTC 2367 TGTGTCTCCA 4981 TG T CTC A TAT GG
GGG
TCTGGAGGGTATGTTCTGGG GTCCTCTCTG GGGT TG CTCCAGTCCT TGG GGG GTTCT
GCGGA G
CGGAGGGGCCATCTGCATGG GAGG |||| || |||||||||| ||| ||| ||||| |||||
AACTTCTCACCAAACAGGGC TCCG AC GAGGTCGGGA ACC CTC CAAGG CGTCT /
TGGAGCAGTGCCT TG - CAA A TT- TA ACC

GAM2391 TTCGGGCTGTGCAAGGAGGG 2368 AAGACCTTTT 4982 C AA- GA- A ACGG
GATCAAGGACGGTGCCACCA GCGGCACACC TTCGGG TGTGC GGAGGG TCA GG T
TGAAGACCTTTTGCGGCACA TGAG |||||| ||||| |||||| ||| ||
CCTGAG GAGTCC ACACG TTTTCC AGT CC /
- GCG AGA A ACCG

GAM2392 CCGATTCTGGTTTCCTGGGG 2369 AGGCGGCGGC 4983 A G C ---- G A GAC
CTGCGGCCACTTCGGTGGAC GGCGAGGCCC CCG TTCT GTTTC TGGG GCTGC GCC
CTTCGGTG C
CCAGCGCTGAGGCGGCGGCG AAGA ||| |||| ||||| |||| ||||| ||| ||||||||
GCGAGGCCCAAGAAATAAGA GGC AAGA TAAAG ACCC CGGCG CGG GGAGTCGC /
AGCGG G A A GGAG G C GAC

GAM2393 TTCCACCCATGGCAAATTCC 2370 TGAGAACGGG 4985 CCC A- ATGG-- - GT
ATGGCACCGTCAAGGCTGAG AAGCTTGTCA TTCCA ATGGCAA TTCC CA CC C
AACGGGAAGCTTGTCATCAA TCAA ||||| ||||||| |||| || ||
TGGAA AAGGT TACTGTT AAGG GT GG /
AAC CG GCAAGA C AA

GAM2394 CATGACCACAGTCCATGCCA 2371 ATGGCCCCTC 4984 A CCATG ATCACT- - - A
TCACTGCCACCCAGAAGACT CGGGAAACTG CATG CCACAGT CC GCCA CC CAG A
GTGGATGGCCCCTCCGGGAA TGGC |||| ||||||| || |||| || |||
ACTGTGGCGTG GTGC GGTGTCA GG CGGT GG GTC G
- AA--- GCCTCCC A T A

GAM2395 TTCCACCCATGGCAAATTCC 2372 TGAGAACGGG 4986 CCC A- ATGG-- - GT
ATGGCACCGTCAAGGCTGAG AAGCTTGTCA TTCCA ATGGCAA TTCC CA CC C
AACGGGAAGCTTGTCATCAA TCAA ||||| ||||||| |||| || ||
TGGAA AAGGT TACTGTT AAGG GT GG /
AAC CG GCAAGA C AA

GAM2396 GAAGTCCCGTGTTGCCATCC 2373 TGCCAAGGAT 4987 G CGT GC CAA T CT--- G
TCAAGGCTAACCTGCGCAAG GTGGACTTGG GAA TCC GTT CATCCT GGC AAC GC C
TCCCCAGTTGCCAAGGATGT AGTT ||| ||| ||| |||||| ||| ||| ||
GGACTTGGAGTTC CTT AGG CAG GTAGGA CCG TTG TG A
G TT- GT A-- - ACCCC A

GAM2397 TGATGCGCAAGGCCATCCGA 2374 TCTGGAGAAA 4988 T - A GCCA G ACC AAA
GGGCACCTGGAAAACAACCC CTGCTGCCTC TGA GC GCA G TCC AGGGC TGG A
AGCTCTGGAGAAACTGCTGC A ||| || ||| | ||| ||||| |||
CTCA ACT CG CGT C AGG TCTCG ACC C
C T - AAAG - --- CAA

GAM2398 GGCTGGGATTGGAACTGTGT 2375 AGGAACCCTT 4989 - TT A - G CCTCATCA TT
TTGGGAGCCTCATCATTGGT CTCTGAAGCA GGC TGGGA GGA CTGT GTTT GGAG TTGG
A
TATGCCAGGAACCCTTCTCT ACAG ||| ||||| ||| |||| |||| |

GAM2400 GATGCATTTGTTGGAGGTTT 2377 TGCAAGCCTC 4991 - TG TCTGTC- A
TCTGTCTCAACTGGTCTCTG TGACTGAATG GATGCATTT GT GAGGTTT TC A
CAAGCCTCTGACTGAATGTA TATC |||||||||| || ||||||| ||
TC CTATGTAAG CA CTCCGAA GG C
T GT CGTCTCT T

GAM2401 ATCAGGTAATGCAGTTTGTT 2378 ACTCCATTCG 4992 AA-- G GTTG A C--- GT
GAGCCAAGTCGGCAGTTTGT GCTGGTTAAA ATCAGGT TGCA TTT AGCCA GTCGG AGTTT
A
AAAGGACTCCATTCGGCTGG AGAT ||||||| |||| ||| ||||| ||||| |||||
TTAAAAGATGCACTAAACCT TAGTCCA ACGT GAA TTGGT CGGCT TCAGG /
GAT AATC A AA-- - TACC AA

GAM2402 TTTAGATTTGAACTTCTCGA 2379 TCAGCTTTGG 4993 AACT GA ACC AC
AGAGCTACCAACACCCAAGT AGGCAGATCT TTTAGATTTG TCTC AGAGCT AAC C
TCAGCTTTGGAGGCAGATCT GGA |||||||||| |||| |||||| |||
GGA AGGTCTAGAC GGAG TTTCGA TTG C
---- G- C-- AA

GAM2403 TCTTGTGTTGAGACTTCGTG 2380 TACACCACTC 4994 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM2404 GCCGTGTGGACAGGGGACAA 2381 CTATGTGTCT 4995 G TG C GG CAA- - -- - - TT
GAT
CACTGCCGAGTGGGACCATT CAGCTTGGGG GCC TG GA AGG A CACT GCC GAG TGGGAC
CAT GAA C
TGAAGATCTCTATTCCTATG CTGG ||| || || ||| | |||| ||| ||| |||||| ||| |||
TGTCTCAGCTTGGGGCTGGT CGG GT CT TCC T GTGG CGG TTC ACTCTG GTA CTT
T
GGGACTTTCCTTCTGTGGGG G GT - TT CAGG T GG G T TC ATC
C

GAM2405 TCCGATGCTACTATTTTATT 2382 TATTTTATTG 4996 GA-- ACTA T AGGA GG- T
GCAGGAGGTGGGGGTGTATG CAGGAGGTGG TCC TGCT TTTTAT GC GGTG GGTG A
CACCGCACACCGGGGCTATG GGGT ||| |||| |||||| || |||| ||||
AGAAGCAAGAAGGA AGG ACGA AGAGTA CG CCAC CCAC T
AAGA ---- T GGG- ACG G

GAM2406 GTTCATGCAGCTGTGGCAGA 2383 TACTGTGTAA 4997 T- GCT- G- -- T- -- TTCAT
GTTACAGTTCTGTGGTTTCA TTAGTGCCAC GT CATGCA GTGGCA AGT TACAGT CTGT
GGT G

TGTTAGTTACCTTATAGTTA TTAA || |||||| |||||| ||| |||||| |||| |||
CTGTGTAATTAGTGCCACTT CA GTATGT CACCGT TTA GTGTCA GATA CCA T
AATGTATGTTAC TT AATT GA AT TT TT TTGAT

GAM2407 GGGTGGATCACCTGAGGTCA 2384 TGGATCACCT 4998 TG A- - A- A-- C
GGAGTTCAAGACCAGCCTGG GAGGTCAGGA GGG G TCACC TG GGTCAGG GTT A
CCAACATGGTGAAACTCCCC GTTC ||| | ||||| || ||||||| |||
CCC C AGTGG AC CCGGTCC CAG /
CT AA T AA GAC A

GAM2408 GTGGGTGCATCACATGAGGT 2385 TGGCCAACAT 4999 TGCA - A- AGTTCG
CAGGAGTTCGAGATCAGCCT GGTGAAATCC GTGGG TCAC ATG GGTCAGG A
GGCCAACATGGTGAAATCCC CAT ||||| |||| ||| |||||||
AT TACCC AGTG TAC CCGGTCC /
TAA- G AA GACTAG

GAM2409 TCTTGTGTTGAGACTTCGTG 2386 TACACCACTC 5000 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM2410 GTACATGGGCTGAGGAATGT 2387 GTAGAGTTTT 5001 AT---- G TG AAG GAA
TCAAGCAGAAGAAATGGTAG CTTCAGGCTT GTAC GG CTGAGGAA TTC CA G
AGTTTTCTTCAGGCTTAAAG AAAG |||| || |||||||| ||| ||
GGTAT TATG TC GACTTCTT GAG GT /
GGAAAT G TT ATG AAA

GAM2411 TTGAGACAGAGTTTCGCTCT 2388 TCACTGCAAA 5002 A - TT CT TT --- C -- A T
GAT
TGTTGCCCAGGCTGGAGTGC CTCCACCTCC TTGAG CAG AG TCGCT TG GCCC AGG
TGGAGT GCA TGG GC C
AATGGTGCGATCTCAGCTCA CGGG ||||| ||| || ||||| || |||| ||| |||||| ||| ||| ||
CTGCAAACTCCACCTCCCGG GACTC GTC TC AGCGA AC TGGG TCC ACCTCA CGT
ACT CG /
GTTCAAGCGATTCTCCTGCC C C TT -- T- CCC - AA C - ACT
TCAG

GAM2412 GGCAGAAGGCTTTTACACCA 2389 AGGCTTTTAC 5003 AGA ----- C - AA GA
CAAGTGCAGTGAAAGAACTG ACCACAAGTG GGC AGGC TTTTA AC CAC GTGCAGT A
CACGGTGAGTTTAAAACAAC CAGT ||| |||| ||||| || ||| |||||||
CGCTTGTGGCC CCG TTCG AAAAT TG GTG CACGTCA A
GTG CCAAC T A G- AG

GAM2413 GTGGAGGCTGTGGAGCTGCT 2390 TGTGGAGCTG 5005 CT GA TAATTCGC A
AATTCGCAATCATTTGGTTA CTAATTCGCA GTGGAGG GTG GCTGC AATC T
ATATGCAGCAGTATGATCTT ATCA ||||||| ||| ||||| ||||
CAC CACTTCT TAT CGACG TTGG T
AG GA TATAA--- T

GAM2414 CAATGCTCCAGAAGGATTGC 2391 TAGTGCGATC 5004 A C GAA-- CCCA GA
CCCAGCTGATGGAAGTAGTG CAACTATGAA CA TGCT CA GGATTGC GCT T
CGATCCAACTATGAAGCAAT GCAA || |||| || ||||||| |||
G GT ACGA GT CCTAGCG TGA G
A A ATCAA TGA- AG

GAM2415 CAGGACAGAAATCATTATCT 2392 TTCTTGGTGA 5006 GA- A A--- AGC - CA
TAGCCACCAGAACACAGAAT GAAGGGCCGG CAG CAGAA TCATT TCTT CACCA GAACA G
GTTCTTGGTGAGAAGGGCCG ATGA ||| ||||| ||||| |||| ||||| |||||
GATGATTCTGGAACTG GTC GTCTT AGTAG GGAA GTGGT CTTGT /
AAG - GCCG GA- T AA

GAM2416 GCTGTAGTTCAGATGAGGTT 2393 TGTAGTTCAG 5007 TG AG- - G T - A
TGGCTTTCCAGAGGGCAGTG ATGAGGTTTG GC T TTCAG ATGAGGTTT GC TT CC G
TAGAGCTTTATGCTGAAAAG GCTT || | ||||| ||||||||| || || ||
GTGGC CG G AAGTC TATTTCGAG TG GA GG A
GT GAA G A T C G

GAM2417 GAGATGGGTTTCACCATGTT 2394 GATGGGTTTC 5008 A TTCAC TT CT CT
GGTCAGGCTGGTCTCGAACT ACCATGTTGG GAG TGGGT CATG GGTCAGG GGT C
CCTGACCTCATGATCCGCCC TCAG ||| ||||| |||| ||||||| |||
ACCTC CTC ACCCG GTAC CCAGTCC TCA /
C CCTA- T- -- AG

GAM2418 TCTACAAAGTGCCGTCCACT 2395 TCCAATCTGA 5009 A - - CACTG CT- C
GAGACTGAGGCCTTGGCTTC TGGGCATGTT TCT CAAA GTGCC GTC AGA GAGGC T
CAATCTGATGGGCATGTTTG TGAG ||| |||| ||||| ||| ||| |||||
AGA AGA GTTT TACGG TAG TCT CTTCG T
- G G ----- AAC G

GAM2419 TTGTCGTCATTGGACACGTA 2396 TAAATGCGGT 5010 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM2420 ATCTGATCTCTCGGTCCCTT 2397 GATCTCTCGG 5011 A - TCCT A ATAA

CCTTAACCCCATAAAAAGAA TCCCTTCCTT ATCTG TCTC TCGGTCCCT TA CCCC A
GGGGATATTTGGGGACCGAC AACC ||||| |||| ||||||||| || ||||
GGGAACAGGT TGGAC AGGG AGCCAGGGG AT GGGG A
A C TTT- A AAGA

GAM2421 CCTATCAGTAGATCCTTCCA 2398 TATCAGTAGA 5012 T-- - T CA---- TT ATTT
CTGGGTTCGCAATTTTGATC TCCTTCCACT CC ATCAGT AGATCC TC CTGGG CGCA T
TGCGCCCCAGACATCTGACG GGGT || |||||| |||||| || ||||| ||||
GATCTCATTGATTTTGG GG TAGTTA TCTAGG AG GACCC GCGT /
TTT C C TCTACA C- CTAG

GAM2422 ATTTGAGAAGGAGGCTGCTG 2399 CTTCAAGTAT 5014 TG AGG - GA T AAA
AGATGGGAAAGGGCTCCTTC GCCTGGGTCT ATT AGA AGGC TGCT GA GGG G
AAGTATGCCTGGGTCTTGGA TGGA ||| ||| |||| |||| || |||
T TAG TCT TCCG ATGA CT CCT /
GT GGG T A- T CGG

GAM2423 ATGGTGACAACATGCTGGAG 2400 TTGGTTCAAG 5013 AA-- G G- T TA
CCAAGTGCTAACATGCCTTG GGATGGAAAG ATGGTGAC CAT CT GAGCCAAG GC A
GTTCAAGGGATGGAAAGTCA TCAC |||||||| ||| || |||||||| ||
CCGT TGCCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM2424 ACAAGTTATTGCCACTGCTA 2401 TACGGTATAT 5015 A TATT C C ---- CA- TT- AT
CGGTATATTTCAAGAGATTC TTCAAGAGAT ACA GT GCCA TG TACGG TATATTT AGAGA
CT G
TATGCCAGGTATTCTCTGAA TCTA ||| || |||| || ||||| ||||||| ||||| ||
AAGTATAGATCCTGTATTAA TGT CA CGGT AT ATGTC ATATGAA TCTCT GG C
TGGCTCCTACATGT A TCCT A T CTAG AAG TAT AC

GAM2425 CTTTTGGCAGAGCTCCCACT 2402 TCTGTTGGAG 5016 AGA CACTATT G GA
ATTTGCAATGGATTTTGGAT GAGCGCCAAA CTTTTGGC GCTCC T CAATGGATTTTG T
AAACAAGATCTGTTGGAGGA AG |||||||| ||||| | ||||||||||
GCGCCAAAAG GAAAACCG CGAGG A GTTGTCTAGAAC A
--- ------- G AA

GAM2426 CTAAAACGGCTTTTGATGAG 2403 ATACAAAGAC 5017 AA TT- CCAT AA GATACAC
A A
GCCATTGCTGAACTTGATAC AGCACCCTCA CTAA CGGCT TGATGAGG TGCTG CTT TG
ATGA G
ACTGAATGAAGACTCATACA TCAT |||| ||||| |||||||| ||||| ||| || ||||
AAGACAGCACCCTCATCATG GATT GTTGA ACTACTCC ACGAC GAA AC TACT A
CAGTTGCTTAG C- CGT C--- A- ------- A C

GAM2427 GCAAGAAAGAGATGCAACCC 2404 CTTGCTCTTA 5018 AG --- T - A CACCCA
ACACACCCAATCCGCCTGGG ACTTTTCTGT GCA AAAG AGA GCAA CCC CA A
GCTTGCTCTTAACTTTTCTG ||| |||| ||| |||| ||| ||
T TGT TTTC TCT CGTT GGG GT /
CT AAT - C - CCGCCT

GAM2428 GAATATTTCCACAATGTCTG 2405 TACACGGTCG 5019 CACA T AAC G TTCA
TGAACTGGACCTGGTGTTCA TGGACGAGAT GAATATTTC ATG CTGTG TGGACCT GTG A
ACTTCTACAAGGTTTACACG GTTC ||||||||| ||| ||||| ||||||| |||
GTCGTGGACGAGATGTTC CTTGTAGAG TGC GGCAC ATTTGGA CAT /
CAGG T --- A CTTC

GAM2429 TCTTGTGTTGAGACTTCGTG 2406 TACACCATCC 5020 GAGA G -- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CAAGAAGAAT TCTTGTGTT CTTC TGG TGGTG TAAGA A
AAGAAGTCTTACACCATCCC AAGC ||||||||| |||| ||| ||||| |||||
AAGAAGAATAAGCACAAGA AGAACACGA GAAG ACC ACCAC ATTCT G
ATAA A CT - GAAGAA

GAM2430 GGTGACAACATGCTGGAGCC 2407 TTGGTTCAAG 5021 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM2431 GCCCAGGTGGTGCAGTGGGT 2408 GTGCAGTGGG 5022 G CAG TGA T C A
GAGCTTTGCTGATTCCGATA TGAGCTTTGC GCCCAGGTG TG TGGG GCT TG TG T
TAGTGCCCCCAGCCAGTACC TGAT ||||||||| || |||| ||| || ||
TGGGT TGGGTCCAT AC ACCC TGA AT GC T
G CG- CCG T A C

GAM2432 ATGGTGACAACATGCTGGAG 2409 TTGGTTCAAG 5023 AA-- G G- T TA
CCAAGTGCTAACATGCCTTG GGATGGCAAG ATGGTGAC CAT CT GAGCCAAG GC A
GTTCAAGGGATGGCAAGTCA TCAC |||||||| ||| || |||||||| ||
CCGT TGCCACTG GTA GG CTTGGTTC CG C
AACG G AA - TA

GAM2433 GGCCAATTGAAACAAACAGT 2410 TATTAGGGAT 5024 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM2434 CTTCTTCAGTGAGACGGGCG 2411 TTTGTAGACT 5025 - GAC- CG ----- T C
CTGGCAAGCACGTGCCCCGG TGGAACCCAC CTTCT TCAGTGA GGG CTG GCAAGCACG
GCC C
GCTGTGTTTGTAGACTTGGA AGTC ||||| ||||||| ||| ||| |||||||||| |||
ACCCACAGTCATTGATAGAA GAAGA AGTTACT CCC GGT TGTTTGTGT CGG /
G T GACA AA TCAGA - G

GAM2435 GGTCTCTTCAGAGCTGCTGT 2412 TATGAGGCCC 5026 CT -------- G T- - GT TC
GCCCAGTGGTGCTTCAACTG TAGAGCTCCG GGTCT TCA GAGCT CTG GCC CA GGTGCT
A
GTATCTATGAGGCCCTAGAG GGAC ||||| ||| ||||| ||| ||| || ||||||
CTCCGGGACAATGATAAGAC TCAGA AGT CTCGA GAT CGG GT CTATGG A
T AT AACAGGGC - CC A AT TC

GAM2436 TCTTGTGTTGAGACTTCGTG 2413 TACACCACTC 5027 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCGCAAGA AGAACGCGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM2437 GAGCTTCTCCTTGCCAGTTT 2414 TCTCCTTGCC 5028 TTCTC TTTCTCC AG C - TTG
CTCCCAGCAGGACCCTCTTC AGTTTCTCCC GAGC CTTGCCAG CAGC GACC TCTT C T
TTGTTTTGAAAGATGGTCGG AGCA |||| |||||||| |||| |||| |||| |
CTGCTTTTGGTAGGCACGCT CTCG GGATGGTT GTCG CTGG AGAA G /
C CAC-- TTC---- G- T A TTT

GAM2438 ATGGTGACAACATGCTGGAG 2415 TTCACGGGAT 5029 AA- G - C T TA
CCCAGTGCTACATGCCTTGG GGAAGTCACC ATGGTGAC CAT CTG GAGCC AG GC C
TTCACGGGATGGAAGTCACC GT |||||||| ||| ||| ||||| || ||
GT TGCCACTG GTA GGC CTTGG TC CG /
AAG G A T - TA

GAM2439 ACCTTATCTCTGTGCTTCGT 2416 TCTGTGCTTC 5030 T- G TGAA C- AAT
GAAGCTAATCAAGCAATTAA GTGAAGCTAA ACCT ATCTCTGT CTTCG GCTAAT AAGCAATT
C
TCCCAAGTTGCTTCAGTTGG TCAA |||| |||||||| ||||| |||||| ||||||||
TCGAAGACAGAGGTTCAGGT TGGA TGGAGACA GAAGC TGGTTG TTCGTTGA /
CT - ---- AC ACC

GAM2440 GGCCAATTGAAACAAACAGT 2417 TATTAGGGAT 5031 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||

CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM2441 GGCCAATTGAAACAAACAGT 2418 TATTAGGGAT 5032 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM2442 CCATCATGGCTCAGATTGGC 2419 GAAGAAGCGA 5033 - TG - A -- C A- T
TCCTATGTTCCTGCAGAAGA CAATTGGGAT CCATC A G CTCAG TTG GCT CT TGT C
AGCGACAATTGGGATTGTGG TGTG ||||| | | ||||| ||| ||| || |||
ATGG GGTAG T T GGGTT AAC CGA GA ACG C
G GT A - AG A AG T

GAM2443 AAGATAGAGGCAGAACTGCA 2420 TGTTCTGGAG 5034 GA----- AA G TG
GGACATCTGCAATGATGTTC CTGTTGGACA AAGATA GGCAG CT CAGGACATC C
TGGAGCTGTTGGACAAATAT AATA |||||| ||||| || |||||||||
CTT TTCTAT TTGTC GA GTCTTGTAG A
AAACAGG -- G TA

GAM2444 TCTGGTGTGGAGACTTCGTG 2421 TACACCACTC 5035 G GGAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCT GTGT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||| |||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGA CACG GAAG TCACCAC ATTCT G
A AATAA AACCC - GAAGAA

GAM2445 TTTTAAGAAGAGCTGTGTGC 2422 CCTTGGACCA 5037 A G CC---- T T A CC----
TAT
TCCCTTTGGTTCCGGGGACC CAGCCTTCCA TTTTAAGA GAGCTGTGT CT CT TGGT
CCGGGG CC GCT A
CCGCTTATAGCCAGCAAAAA GACA |||||||| ||||||||| || || |||| |||||| || |||
TGGCCTTGGACCACAGCCTT AAGATTTT CTTGATACA GA GA ACCA GGTTCC GG
CGA /
CCAGACATAGTTCCTTTTAG C - CCTTCC C - - TAAAAA CCG
AA

GAM2446 TTTGGCACGAACCATGCCAC 2423 GCCACTGTTT 5036 A- T----- CT TCCA CCC TT
TGTTTCCATGGGCCCGAGTT CCATGGGCCC TTTGGC CGAACCA GCCA GTT TGGG
GAG A
ACTTTTCCCCAGATGACTCT GAGT |||||| ||||||| |||| ||| |||| |||
GGTTTTGTTTGGTTTGCCGC AGACCG GTTTGGT TGGT CAG ACCC CTT C
CAGA CC TTGTTT CT TAG- --- TT

GAM2447 TCTTGTGTTGAGACTTCGTG 2424 TACACCACTC 5038 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG |||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM2448 GGCCGCTCTAGAGGATCCAA 2425 TAGAGGATCC 5039 C-- C TCCAA T-- A T
GCTTACGTACGCGTGCATGC AAGCTTACGT GG CGCT TAGAGGA GCT ACGT CGCG G
GACGTCATAGCTCTTCTATA ACGC || |||| ||||||| ||| |||| ||||
GTGTCACC CC GTGA ATCTTCT CGA TGCA GCGT C
ACT T ----- TAC - A

GAM2449 AAGATAGAGGCAGAACTGCA 2426 TGTTCTGGAG 5040 GA----- AA G TG
GGACATCTGCAATGATGTTC CTGTTGGACA AAGATA GGCAG CT CAGGACATC C
TGGAGCTGTTGGACAAATAT AATA |||||| ||||| || |||||||||
CTT TTCTAT TTGTC GA GTCTTGTAG A
AAACAGG -- G TA

GAM2450 CTCTCGGGGGCGGAGGGGGT 2427 TCCCTCCCAA 5041 - GC- - C TGA
GCCTGTGAGCTCTCAGCCAC CCCTGGTGAG CTC TCGGGG GGAGGGG GTG CTG G
TTCCCTCCCAACCCTGGTGA ||| |||||| ||||||| ||| |||
G GAG GGTCCC CCTCCCT CAC GAC C
T AAC T C TCT

GAM2451 GCCTGGCGATTGAGAGTGAC 2428 TTCATGTATT 5042 CG- G CG A GGAG
GGCAAGAAGGGGAGCAAAGT ACTTCGATAA GCCTGG ATTGA AGTGA GCA GAAGG C
TTTCATGTATTACTTCGATA CCCG |||||| ||||| ||||| ||| |||||
ACCCGGGT TGGGCC TAGCT TCATT TGT CTTTT /
CAA - A- A GAAA

GAM2452 GACTTTGGTAGACACAGGCA 2429 TGGGAACCAT 5043 A AG A A TGA----
GCTGATCT
TTGGCATGACCAAAGCTGAT TGCCAAGTCT G CTTTGGT AC CAGGC TTGGCA CCAAA
C
CTCATAAATAATTTGGGAAC GGTA | ||||||| || ||||| |||||| |||||
CATTGCCAAGTCTGGTACTA C GAAATCA TG GTCTG AACCGT GGTTT /
AAGC - -- - - TACCAAG AATAAATA

GAM2453 GGAGTCTTCTGCTGGAGGTT 2430 TGAGCCCATT 5044 AGT TG A TTCC C G
CCTTCACTGTGCGTGCTGAC GGCAGGGGTA GG CTTCTGC G GG TTCACTGTG GT C
CATGGTGAGCCCATTGGCAG CC || ||||||| | || |||||||| ||
GGGTACC CC GGGGACG T CC GAGTGGTAC CA T
AT- GT A C--- - G

GAM2454 CTGAAAACAAACAAGAGGAC 2431 TGTGTTGTGG 5045 AAA- AA A A T T TG C - - T
TGTGTTGTGGTCTGGGGAGA TCTGGGGAGA CTG AC ACA G GGAC GTGT G GT TG GGGAG
AATG A
ATGTAATCATTCCTTCCACA ATGT ||| || ||| | |||| |||| | || || ||||| ||||
ACTGCTGCATGTCCCTGTGG GAC TG TGT C CCTG TACG C CA AC CCTTC TTAC A
GTGAAACAG AAAG GG - - - T GT - A C T

GAM2455 CCACCGGGGATCTAGCCTGT 2432 TAGCCTGTGG 5046 GA CC--- CA C GAGA
GGCACCCCGGAGATGACACG CACCCCGGAG CCACCGGG TCTAG TGTGG CC CG T
AGGCTCACATGACTCTAGAC ATGA |||||||| ||||| ||||| || ||
ACTTGGTGG GGTGGTTC AGATC ACACT GG GC /
AC TCAGT C- A ACAG

GAM2456 GCAGGGACCCCTGAAGTGTT 2433 TGACACGAGG 5047 G GAA--- TG - - CT
GGTCGGGGGCCTCGAGCTGC GGAGGGGTCT GCA GGACCCCT GTGT G TCGGG GGC C
CTGAGCTGACACGAGGGGAG GTGT ||| |||||||| |||| | ||||| |||
GGGTCTGTGT TGT TCTGGGGA CACA C AGTCC TCG /
G GGGGAG GT G G AG

GAM2457 TCCCTGCTGATTCCGCCTAA 2434 TGAGGTTTCG 5048 GAT-- ------ A CGTA
GCCCGTACCCCTTGGCTGAG CTGGATAGTA TCCCTGCT TCC GCCT AGCC C
GTTTCGCTGGATAGTAGGTA GGTA |||||||| ||| |||| ||||
GGGA AGGGATGG AGG TGGA TCGG C
ATGAT TCGCTT G TTCC

GAM2458 GCCGCACCAGGTCTTGTAGC 2435 CAGCAGCCGG 5049 CAGG T A A --- C GAGAA
AGCGCCTCCTCGAGAAGCCA AGTGTGGC GCCGCAC TCT GT GC GCGC CT CTC G
ACAGAGCAGTAAGCGCAGCA ||||||| ||| || || |||| || |||
GCCGGAGTGTGGC CGGTGTG AGG CG CG CGCG GA GAG C
---- C A A AAT C ACAAC

GAM2459 ACACAAAACTATGAGAGTGA 2436 TTACCATGAA 5050 --- T --- TG AAA- AC GGG
CAAAATGGTGACAGGTAGCT GGTTGTTTTG ACACAAA AC ATGAG AG AC ATGGTG
AGGTAGCT A
GGGACCTAGGCTATCTTACC CTTA ||||||| || ||||| || || |||||| ||||||||
ATGAAGGTTGTTTTGCTTAT TGTGTTT TG TATTC TT TG TACCAT TCTATCGG C
TGTATATTTGTGT ATA T GTT GT GAAG -- ATC

GAM2460 TTGAGACAGAGTCTTGCTCT 2437 TCTTGCTCTG 5051 A - TC C TC --- T -- -
ACGA
GTCACCCAGGCTGGAGTGCA TCACCCAGGC TTGAG CAG AG TTGCT TG ACCC AGGC
GGAG TGCAGTG GC T

GTGGCACGATCTCAGCTCAC TGGA |||||| ||| || |||||| || |||| |||| |||| ||||||| ||
TGCAACCTCCGTCTCCCGGG GACTC GTC TC AACGA AC TGGG TCTG CCTC
ACGTCAC CG /
TTCAAGCAATTCTCCTGCCT C C TT - T- CCC - CA T ACTC
CAG

GAM2461 TCTTGTGTTGAGACTTCGTG 2438 TACACCACTC 5052 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM2462 GTATTTGGAGAAGGCATTTG 2439 AGGCATTTGA 5054 A A A T AAT AA
AAGATGAAATGAAAAAGCTT AGATGAAATG GT TTTGGAGAAGGC TTTGA GA GA GAA A
CTCCTCTTCCTTAAAGCCTT AAAA || |||||||||||| ||||| || || |||
TTCCGAAAC CA AAGCCTTTTCCG AAATT CT CT CTT /
- - C T CCT CG

GAM2463 GCTGTCGGGGATTCTGCTGG 2440 TCGGGGATTC 5053 --- TT C CAA-- ACCC
GCAATGGCACCCTGCCCGCC TGCTGGGCAA GCTGTCGG GGA CTG TGGG TGGC T
ACCATCCTCACCAGTCTCTT TGGC |||||||| ||| ||| |||| ||||
CACCGACAGC CGACAGCC TCT GAC ACTC ACCG /
ACT CT C CTACC CCCG

GAM2464 TCTTGTGTGGAGACTTCGTG 2441 TACACCACTC 5055 GGAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG |||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACG GAAG TCACCAC ATTCT G
AATAA AACCC - GAAGAA

GAM2465 CCCACAGACGAATACCTGGA 2442 ACCTGGAGGG 5056 A AATACCTG - A C-- -- C
GGGCATGATGAGCGAGGCCC CATGATGAGC CCC CAGACG GAGGG CATG TGAG GA
GGCC C
CGGGGCCCATCAACTTCACC GAGG ||| |||||| ||||| |||| |||| || ||||
ATGTTCCTCACCATGTTTGG GGG GTTTGT CTCCT GTAC ACTT CT CCGG G
GG - ACCA---- T C CAA AC G

GAM2466 GATGCCGACTGGGAGCTACT 2443 AGCTACTGGG 5058 CGA- GAGCTA GGT A
GGGTGAGCTGGACTACCAGC TGAGCTGGAC GATGC CTGG CTG GAGCTGG C
TTCAGGACCAGGACAGCGTC TACC ||||| |||| ||| |||||||
CTGCG GACC GAC TTCGACC T
ACAG AG---- --- A

GAM2467 CCGGAACCTGCTCATCTGGA 2444 AGAGTTGTTC 5057 GA - - AT CAA G -- AAA

TCAAGAAGAATTTGCTAAAA ATCCAGGAGA CCG AC CTG CTC CTGGAT GAA AATTT GCT A
GAGCGGCCAGAGTTGTTCAT CAGC ||| || ||| ||| |||||| ||| ||||| |||
CCAGGAGACAGCGTGCGG GGC TG GAC GAG GACCTA CTT TTGAG CGG G
G- C A -- --- G AC CGA

GAM2468 CCGCACCGATCGCCTTTCCC 2445 GCGAATGGCA 5059 AC- C- T - A- T G
AACAGTGCGCAGCCTGAATG AATTGTAAGC CCGC CGAT GCC TTC CCA CAG GC C
GCGAATGGCAAATTGTAAGC GG |||| |||| ||| ||| ||| ||| ||
GG GGCG GTTA CGG AAG GGT GTC CG /
AAT AA T C AA - A

GAM2469 GGTGGGTGGATCACCTGAGG 2446 TGGATCACCT 5060 TGGA - A- A-- C
TCAGGAGTTCGAGACCAGCC GAGGTCAGGA GGTGGG TCACC TG GGTCAGG GTT G
TGGCCAACACGGTGAAACCC GTTC |||||| ||||| || ||||||| |||
CATC CTACCC AGTGG AC CCGGTCC CAG /
CAA- C AA GAC A

GAM2470 TCTTCCCAGTATTTCTTGGA 2447 CGGTGCAGGG 5061 C--- ATT G A C G
CAGTCCCAGGAACTTGAGGC TGGCTCCCAG TCTTCC AGT TCTTG AC GTC CAG A
GGTGCAGGGTGGCTCCCAGG GAGG |||||| ||| ||||| || ||| |||
AGGA AGGAGG TCG GGGAC TG CGG GTT A
ACCC GT- G G A C

GAM2471 TCTTCCCAGTATTTCTTGGA 2448 CGGTGCAGGG 5062 C--- ATT G A C G
CAGTCCCAGGAACTTGAGGC TGGCTCCCAG TCTTCC AGT TCTTG AC GTC CAG A
GGTGCAGGGTGGCTCCCAGG GAGG |||||| ||| ||||| || ||| |||
AGGA AGGAGG TCG GGGAC TG CGG GTT A
ACCC GT- G G A C

GAM2472 GAAACAGACTGGGCCAATGT 2449 TATCAAGGAA 5063 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM2473 CCTTGGCTTCAACCTTAGCT 2450 TGTGGTGGCA 5064 TCAACCTTA GG TG A ACA
GGGGCTGCAGCAGCACAGAG GCAGCCAAGG CCTTGGCT GCTG GC CAGC GC G
AGCAGCTGTGGTGGCAGCAG |||||||| |||| || |||| ||
CCAAGG GGAACCGA CGAC TG GTCG CG /
--------- GG GT A AGA

GAM2474 GGAGAAGGGGGGAGATGTTG 2451 TCGCTGGCTC 5065 G G AT- T - TC
AGCATGTTCAGCAGCGTGGC CCACTTTGTC GGA AAGG GGGAG GT GAGC ATGT A
TTCGCTGGCTCCCACTTTGT T ||| |||| ||||| || |||| ||||
CT TCT TTTC CCCTC CG TTCG TGCG G
G A GGT C G AC

GAM2475 TTGATTTTCATTAATCCAGA 2452 TTTTGTGATG 5066 T TTA-- A-- - G C TAATTT
GCTGCAGCACCAGAGATAAT ACAGCTTGGC TTGAT TTCA ATCC GAGCTG CA CAC AGAGA
C
TTCAATCAACTCTTTTGTGA GGGT ||||| |||| |||| |||||| || ||| |||||
TGACAGCTTGGCGGGTACGG AACTG AAGT TGGG TTCGAC GT GTG TTTCT A
TTGAATGTCAA T TGGCA CGG A A T CAACTA

GAM2476 TCTTGTGTTGAGACTTCGTG 2453 TACACCACTC 5067 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM2477 GAGGCGGGCGGATCACCGGA 2454 CCTGACCAAC 5068 GC CGGA A GA-- AGT A
GGTCGGGAGTTTGAGACCAG ATGGAGAAAC GAG GGG TC CCG GGTCGGG TTG G
CCTGACCAACATGGAGAAAC CCCA ||| ||| || ||| ||||||| |||
CCCATCTC CTC CCC AG GGT CCAGTCC GAC A
TA CAA- A ACAA --- C

GAM2478 GCCCATGGGAAACAGCTGTT 2455 GCACATGGTG 5070 - -- AA GC- T T - AACA
CTTTCA
CCTCATCACCAACAGTCCTT GGTCCCGATT GC CCA TGGGA CA TGT CC CATC ACC GTC
G
TCAGCTTCGTAGACAAGGTG GGCG || ||| ||||| || ||| || |||| ||| |||
GATGCGGCACATGGTGGGTC CG GGT GCCCT GT ACA GG GTAG TGG CAG C
CCGATTGGCGC C TA GG GGT C C G AA-- ATGCTT

GAM2479 ACCAGTGGATCGAGCAGGAC 2456 AGCAGGACAT 5069 - ATCGAG TG AAGTA GA
ATGGAGAAGTACATCCTGAG GGAGAAGTAC ACCAG TGG CAGGACA GAG CATCCT G
AGGGGATGAGACGTTTGCTG ATCC ||||| ||| ||||||| ||| ||||||
TCCTGAGCCGCCTGGT TGGTC GCC GTCCTGT TTT GTAGGG /
C GA---- CG GCAGA GA

GAM2480 GTCCTTCTTTCAGACCAAAG 2457 TGAGATAGCC 5072 -- T A AAA TGGA G C
CTTGGACGTCAGTGCCAGCG AGGCTGAAGA GTC CTTCTT CAG CC GCT CGTCA TG C
ATGATGAGATAGCCAGGCTG AGCA ||| |||||| ||| || ||| ||||| ||
AAGAAGCAGAC CAG GAAGAA GTC GG CGA GTAGT GC A

AC - - AC- TAGA A G

GAM2481 CTGGGCCCGGAGGTCACCAC 2458 ACGCAGTTAC 5071 TG - GGA- CA G TA- G G AA
GCAGTTACGGCGTGCCAATA GGCGTGCCAA C GG CCC GGT CCAC CAGT CG CGT CC T
CCGGACGGTGCACACTGAGT TACC | || ||| ||| |||| |||| || ||| ||
GGACCCAGAGGGACCTGG G CC GGG CCA GGTG GTCA GT GCA GG A
GT A AGAC -- A CAC G - CC

GAM2482 TCTTGTGTTGAGACTTCGTG 2459 TACACCACTC 5073 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM2483 TCCGCATGTCCCTTCGCGGG 2460 CATGTCCCTT 5074 CA T CGCG A GTG TG-
GCAA
AAGGCTGTGGTGCTGATGGG CGCGGGAAGG TCCG TG CCCTT GGA GGCT GTGC ATGG
G
CAAGAACACCATGATGCGCA CTGT |||| || ||||| ||| |||| |||| ||||
AGGCCATCCGAGGGCACCTG AGGT AC GGGAG CCT CCGG CGCG TACC /
GA CC - ---- A AA- TAG ACAA

GAM2484 CTTCTTCAGTGAGACGGGCG 2461 TTTGTAGACT 5076 T GAC- CG ----- T C
CTGGCAAGCACGTGCCCCGG TGGAACCCAC CTTC TCAGTGA GGG CTG GCAAGCACG
GCC C
GCTGTGTTTGTAGACTTGGA AGTC |||| ||||||| ||| ||| ||||||||| |||
ACCCACAGTCATTGATGAAG GAAG AGTTACT CCC GGT TGTTTGTGT CGG /
T GACA AA TCAGA - G

GAM2485 CAGGCAAGGAAGATGCTGCC 2462 CACTACACCA 5075 G AA ----- - AACTA-- C
AATAACTATGCCCGAGGGCA TTGGCAAGGA CA GCAAGG GATG CT GCCAAT TGCC G
CTACACCATTGGCAAGGAGA GATC || |||||| |||| || |||||| ||||
TCATTGACCTTGTGTG GT TGTTCC TTAC GA CGGTTA ACGG A
G AG TAGAG A CCACATC G

GAM2486 GTGGAGCAGCAGGGGGCTGA 2463 TACCAGTTCA 5077 AG - - A - A
TGCCTTTGATCCCGAGGAGT CTTGCTTGAC GTGG CA GCAGG GGGCTG TGC CTTTG T
ACCAGTTCACTTGCTTGACC CTAC |||| || ||||| |||||| ||| |||||
TAC CATC GT CGTTC CTTGAC ATG GGAGC C
CA T A C A C

GAM2487 GTTCCTGAGTGGGAAGGGCT 2464 TTGGTGATCT 5079 C AG AAG TT CTA AAAA G
TGGTGATCTATCCGAAAATT ATCCGAAAAT GTT CTG TGGG GGC GGTGAT TCCG TTG A

GGAGACAAGCTGGACATCAT TGGA ||| ||| |||| ||| |||||| |||| |||
CTGCCCCCGAGCAGAAGC CGA GAC GCCC CCG CTACTA AGGT AAC G
A GA --- T- C-- CG-- A

GAM2488 CCTGGGTGACTCTGATGGCA 2465 AACCAGGAAG 5078 G GA------ CAA TG
AGCATGAGACTGTGAACCAG AGAAGAGTGG CCTGGGT ACTCT TGG GCA A
GAAGAGAAGAGTGGCCCAGG CCCA ||||||| ||||| ||| |||
GGACCCG TGAGA ACC TGT G
G AGAGAAGG AAG CA

GAM2489 TTAAGCAAGGGATTCGTGAA 2466 TGGAAAAATT 5080 AA A TGAAG- TGTA
GTCATTTTGTGTAAGGATCA GGACTCAGGC TTAAGC GGG TTCG TCATTTTG A
AGATGGAAAAATTGGACTCA TTAA |||||| ||| |||| ||||||||
GGCTTAA AATTCG CTC AGGT GGTAGAAC /
GA - TAAAAA TAGG

GAM2490 ATGGTGACAACATGCTGGAG 2467 TTGGTTCAGG 5081 AA-- G G T TA
CCAAGTGCTAACCTGCCTTG ATGGAGAGTC ATGGTGAC CAT CTG AGCCAAG GC A
GTTCAGGATGGAGAGTCACC ACCG |||||||| ||| ||| ||||||| ||
GT TGCCACTG GTA GAC TTGGTTC CG C
AGAG G - - TC

GAM2491 AACCCGACACAGTAGCATTT 2468 CTGGAGCCAA 5082 - CAG T CAATT TG TGGAA
G
GTGCCAATTTCTGGTTGGAA GTGCTAACAT AACCC GACA TAGCATTTG GC TC GT TG T
TGGTGACAACATGCTGGAGC GTCT ||||| |||| ||||||||| || || || ||
CAAGTGCTAACATGTCTGGG TTGGG CTGT ATCGTGAAC CG AG CG AC G
TT T ACA - ----- GT TACA- A

GAM2492 GGTGACAACATGCTGAGAGC 2469 CCTGGCTCCA 5083 AA--- G GA A T AA
CAAGTGCTAACATGGCCTGG GGGATGGCAA GGTGAC CAT CT GAGCCA G GCT C
CTCCAGGGATGGCAAAGTCA AGTC |||||| ||| || |||||| | |||
CC CCACTG GTA GG CTCGGT C CGG /
AAACG G AC - - TA

GAM2493 AGACCATGACTACCTTCACC 2470 TACCTTCACC 5084 - GACTA TGGAA A AC
TGGAACATCAACCACGCCCG TGGAACATCA AGAC CAT CCTTCACC CATCA CC G
GCTGATGGTGGTGGAGGAAC ACCA |||| ||| |||||||| ||||| ||
GATGTGTTT TTTG GTA GGAGGTGG GTAGT GG C
T GCAA- TG--- C CC

GAM2494 CCAACAGGATGCCACGCTGG 2471 CACTCGGTGT 5085 AA CC CC TATTTC
GCCGAGCGACTATTTCCTGC ACGTCCTGGA CC CAGGATG ACGCTGGG GAGCGAC C

CAATGTTGCTCACTCGGTGT GG || ||||||| |||||||| |||||||
ACGTCCTGGAGG GG GTCCTGC TGTGGCTC CTCGTTG T
AG A- A- TAACCG

GAM2495 TTGTCGTCATTGGACACGTA 2472 TAAATGCGGT 5086 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| |||
AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM2496 GTGCTTCAACTGGTATCTAT 2473 TATGAGGCCC 5087 T T AT A - AGAG GGACAA
TA
GAGGCCCTAGAGCTCCGGGA TAGAGCTCCG GTGCT CAAC GGT CT TGAGGC CCT CTCCG
TGA A
CAATGATAAGACTCGCTATA GGAC ||||| |||| ||| || |||||| ||| ||||| |||
TGGGGAAGGGTGTCTCAAAG CACGA GTTG TCG GA ACTCTG GGG GGGGT GCT
G
GCTGTTGAGCAC - - -- A T AA-- ATATC- CA

GAM2497 GGTCATGATGTTGGATTCTG 2474 TGATGTTGGA 5088 TG T- GG G G ACCA A
TTGCCTGGGTACCACCAGAG TTCTGTTGCC GGTCA ATG T ATTCT TTGCCT GGT CC G
GGAAAGCTGGGGCGGAGGGA TGGG ||||| ||| | ||||| |||||| ||| ||
TTTGTTCGTGTTGACC CCAGT TGC G TAGGG GGCGGG TCG GG A
TG TT TT A G AAA- G

GAM2498 GTTCCATGACGGGGACTCAG 2475 TGACGGGGAC 5089 ATGA GA- - G G G
TGGTGTTTGCAGGACCTGCA TCAGTGGTGT GTTCC CGGG CT CA TG TGTTTGCAG A
GGCAACAGTGTGGAGACCCG TTGC ||||| |||| || || || |||||||||
GGGGGAAC CAAGG GCCC GG GT AC ACGGACGTC /
GGG- AGA T G A C

GAM2499 GGAGGGGTCCCTGCAGAAGC 2476 CTGTACCAGC 5090 TCCCT A ---- TG TG
GTGGCATTGTGGAACAATGC ATCTGCTCCC GGAGGGG GCAGA GC G GCATTG G
TGTACCAGCATCTGCTCCCT TCT ||||||| ||||| || | ||||||
CT TCTCCCT CGTCT CG T CGTAAC /
----- A ACCA GT AA

GAM2500 GGAGAAGGGGGAGATGTTGA 2477 TCGCTGGCTC 5091 -- - AT- T - TC
GCATGTTCAGCAGCGTGGCT CCACTTTGTC GGAGA AGG GGGAG GT GAGC ATGT A
TCGCTGGCTCCCACTTTGTC TCC ||||| ||| ||||| || |||| ||||
TCC CCTCT TTC CCCTC CG TTCG TGCG G
GT A GGT C G AC

GAM2501 TCTTCCGGCAGACCGATTGC 2478 TTCCTGGCTC 5092 T - - CT-- T T
CTTCATGAAGGCTTCAAAGT TGCAGTTGGT TCT CCGGCA G ACCGATTGC TCA GAAGGCT C
TTTCCTGGCTCTGCAGTTGG ACTT ||| |||||| | |||||||||| ||| |||||||
TACTTGCCGGAGA AGA GGCCGT C TGGTTGACG GGT CTTTTGA A
- T A TCTC C A

GAM2502 CTTCTCCTCAGCTGGAGCAG 2479 TGCAGCACCA 5093 T T- A A G - GGG
CAGCAGTGGAGGGGGCAGGA GCTGCTGGAG CT CTCC CAGCTGG GC GCA CAGT GGAGG C
CCTCCTGCTGGTGCAGCACC CAG || |||| ||||||| || ||| |||| |||||
AGCTGCTGGAGCAG GA GAGG GTCGACC CG CGT GTCG CCTCC A
C TC A A G T AGG

GAM2503 GCATAATCGGTCACTCGTAT 2480 TGAATGGACG 5094 AATC --- A GAA TATT TAT
AGAACAGTATTGTTTCTATA GGTTCAGGCC GCAT GGTC ACTCGT TA CAG GTTTC A
ATTTGAAGCTTTCTGAATGG TGAT |||| |||| |||||| || ||| |||||
ACGGGTTCAGGCCTGATGC CGTA CCGG TGGGCA GT GTC CGAAG A
GT-- ACT G AA- TTT- TTT

GAM2504 CAGTATCTGAACACAGTCAT 2481 AGTCATTCCT 5095 AACACA A TTAC--- A AA
TCCTTACGAGAAGAAAGCCT TACGAGAAGA CAGTATCTG GTC TTCC GAG AGA G
CTCCTCCCTCAGTGGAAGAC AAGC ||||||||| ||| |||| ||| |||
CTGCAGATGCTG GTCGTAGAC CAG AAGG CTC TCT /
GTC--- - TGACTCC C CC

GAM2505 CCAGAATGTTTTGAGCTACT 2482 TCCAAGTACG 5096 AA-- GAGC GGGA TAAAG
ATG
TCGGGATACTTGGTAAAGGG AGAAGTAACA CCAG TGTTTT TACTTC TACTTGG
GGGGCT G
GGCTATGGAAAGGTTCTCCA GGAG |||| |||||| |||||| ||||||| ||||||
AGTACGAGAAGTAACAGGAG GGTC ACGAGG ATGAAG ATGAACC TCTTGG /
CAAATACTGG ATAA ACA- AGC- ----- AAA

GAM2506 GGTGACAACATGCTGGAGCC 2483 TTGGTTCAAG 5097 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| ||
CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM2507 CATGACCACAGTCCATGCCA 2484 ATGGCCCCTC 5098 A CCATG ATCACT- - - A
TCACTGCCACCCAGAAGACT CGGGAAACTG CATG CCACAGT CC GCCA CC CAG A
GTGGATGGCCCCTCCGGGAA TGGC |||| ||||||| || |||| || |||
ACTGTGGCGTG GTGC GGTGTCA GG CGGT GG GTC G
- AA--- GCCTCCC A T A

GAM2508 TCATGACCACAGTCCATGCC 2485 ATGGCCCCTC 5099 A CCATG ATCACT- - - A
ATCACTGCCACCCAGAAGAC CGGGAAACTG TCATG CCACAGT CC GCCA CC CAG A
TGTGGATGGCCCCTCCGGGA TGGC ||||| ||||||| || |||| || |||
AACTGTGGCGTGA AGTGC GGTGTCA GG CGGT GG GTC G
- AA--- GCCTCCC A T A

GAM2509 TCTCTAACAAGGTGCAGAGC 2486 TTCACAGTGG 5100 AACA ATTG TGAT T
TTAGCTGATTGGTGAACAGT CTAAGTTCTG TCTCT AGGTGCAGAGCTTAGCTG GTGAACAG
TGG T
GATTGGTTTCCGCTTTGTTC CACC ||||| |||||||||||||||| |||||||| |||
ACAGTGGCTAAGTTCTGCAC AGAGA TCCACGTCTTGAATCGGT CACTTGTT GCC /
CTGAAGAGA AG-- GA-- TC-- T

GAM2510 GGACGGCGTGCTGGCTGACT 2487 AGGAAGTTCC 5101 C - CT -- CG
TCGAGGGCGGATTCCTCAGG GCGCGCGCTT GGA GGCGTGC TGG GACTTC GAGGG G
AAGTTCCGCGCGCGCTTTCC TCC ||| ||||||| ||| |||||| |||||
CCT TCGCGCG GCC TTGAAG CTCCT /
T C -- GA TA

GAM2511 GCTCTCCGCCGCAGCTTCAG 2488 CAATGCTAAA 5102 CC C TC--- CC-- GG
CACCTCGGCCCAGAACAATG GTAGCTGTGC GCTCT GC GCAGCT AGCA TC C
CTAAAGTAGCTGTGCTAGGG TAGG ||||| || |||||| |||| ||
GC CGGGG CG TGTCGA TCGT AG C
AT - TGAAA AACA AC

GAM2512 CGTCATGTCTAAGTCAGAGT 2489 AGTCAGAGTC 5103 T CTAAG T CTAAAG GAA C
AA
CTCCTAAAGAGCCCGAACAG TCCTAAAGAG CGTCA GT TCAGAG CTC AGCCC CAG
TGAGG G
CTGAGGAAGCTCTTCATTGG CCCG ||||| || |||||| ||| ||||| ||| |||||
AGGGTTGAGCTTTGAAACAA GTAGT CA AGTTTC GAG TTGGG GTT ACTTC /
CTGATG - ACAA- - ------ AG- - TC

GAM2513 ATTTGAGAAGGAGGCTGCTG 2490 CTTCAAGTAT 5104 TG AGG - GA T AAA
AGATGGGAAAGGGCTCCTTC GCCTGGGTCT ATT AGA AGGC TGCT GA GGG G
AAGTATGCCTGGGTCTTGGA TGGA ||| ||| |||| |||| || |||
T TAG TCT TCCG ATGA CT CCT /
GT GGG T A- T CGG

GAM2514 GGTGACAACATGCTGGAGCC 2491 TTGGTTCAAG 5105 AA--- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAA GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAAGTCAC GTCA |||||| ||| || |||||||| ||
C CCACTG GTA GG CTTGGTTC CG C

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                                    AAAAG  G  AA      -  TA


GAM2515  TTGTCGTCATTGGACACGTA 2492   TAAATGCGGT 5106       ---     GACAC     CG--  A  CCA
     GATTCGGGCAAGTCCACCAC      GGCATCGACA      TTGTC  GTCATTG   GTAGATT   GGC AGT  C
     TACTGGCCATCTGATCTATA      A            |||||  |||||||   |||||||   ||| |||
     AATGCGGTGGCATCGACAA                    AACAG  CGGTGGC   TATCTAG   CCG TCA  C
                               CTA     GTAAA     TCTA  G  TCA


GAM2516  GGTGACAACATGCTGGCAGC 2493   TCACGGGATG 5107       AA--  G  GC  -   T  TA
     CAAGTGCTAACATGCCCTTG      GAACGTCACC      GGTGAC   CAT CTG  AG CCAAG GC  A
     GTCTCACGGGATGGAACGTC                   ||||||   ||| |||  || ||||| ||
     ACC                       CCACTG   GTA GGC  TC GGTTC CG  C
                                CAAG  G  AC  T   C  TA


GAM2517  GACTCAATGTGCAACTGACA 2494   TGCTAGTGAT 5108         TGC  TG  ATCT--  G  AT  CT  AAT
     TCTGCTAGTGATGATCTGGT      GATCTGGTAA      GACTCAATG   AAC  AC    GCTA TG  GAT  GGT  A
     AATATACAACCTGTCCAGTA      TATA          |||||||||  |||  ||    |||| ||  |||  |||
     GCCAAACAGTTGGTTTTTAT                   TTGAGTTAT   TTG  TG    CGAT AC  CTG  CCA  T
     TGAGTT                        TT-  GT  ACAAAC   G  --  T-  ACA


GAM2518  GTGTGTAGTGGTTGTGCAGA 2495   TGAGAAGACA 5109     T   T--  TT   CAGAGC     ATC
     GCCTCATGCATCACGGAGCA      TTCCCCTCCT      GTG GTAG  GG  GTG    CTCATGC  A
     TGAGAAGACATTCCCCTCCT      GCCA          ||| ||||  ||  |||    |||||||
     GCCAC                       CAC CGTC  CC  TAC    GAGTACG  C
                              -  CTC  CT  AGAA--     AGG


GAM2519  GCTCTCCGCCGCAGCTTCAG 2496   CAATGCTAAA 5110       CC  C    TC---   CC--  GG
     CACCTCGGCCCAGAACAATG      GTAGCTGTGC      GCTCT  GC GCAGCT   AGCA   TC  C
     CTAAAGTAGCTGTGCTAGGG      TAGG          |||||  || ||||||    ||||   ||
     GC                        CGGGG  CG TGTCGA   TCGT   AG  C
                                AT  -    TGAAA   AACA  AC


GAM2520  AACGGGAGATGCAGTTTATT 2497   AGGGAATACA 5111     GGG--    A  T    ACA  AGCA  AT
     TACACCAGCAGCCATGGGGG      CAGCGTTTAC      AAC    AGATGC GT TATTT  CC   GCC  G
     CAGAGGGAATACACAGCGTT      AAAG          |||    |||||| || |||||  ||   |||
     TACAAAGTT                  TTG    TTTGCG CA ATAAG   GG   CGG  /
                               AAACA    A  C    ---  AGA-  GG


GAM2521  CGATAACCTGAAGCTGTTCT 2498   AACCTGAAGC 5112       AC   A  G--     A-  TC    C
CCTCTCCT
     GTTACCTCTGGGCTCTCATC      TGTTCTGTTA      CGATA  CTGA GCT   TTCTGTT  CC  TGGGCT TCAT
    A
     CTCTCCTATTTATACAGTGA      CCTC          |||||  |||| |||   |||||||  ||  |||||| ||||
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AGCCCATGGCAAATAGGAAG GCTAT GACT CGA AGGATAA GG ACCCGA AGTG /
AAGCTCAGTATCG -- - AGA AC T- - ACATATTT

GAM2522 GAAACAGACTGGGCCAATGT 2499 TATCAAGGAA 5113 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM2523 GAGACGGGTGGATCACAAGG 2500 AACACGGTGA 5115 - GGA AA---- GA A
TCAGGAGATCGAGACGATCC AACTCCGTCT GAGACGG GT TCAC GGTCAGGA TCG G
TGGCTAACACGGTGAAACTC C ||||||| || |||| |||||||| |||
CGTCTC CTCTGCC CA AGTG TCGGTCCT AGC /
T A-- GCACAA -- A

GAM2524 AGGCAGGAGAATGGTGTTAA 2501 CCACTGCACT 5114 A AA - TAA- AGGC CT A
- A
CCCAGGAGGCGGAGCTTGCA CCAGCCTGGG AGGC GGAG TGG TGT CCCAGG GGAG
TGCAGTG GC CG G
GTGAGCCGAGATCGCGCCAC AGAC |||| |||| ||| ||| |||||| |||| ||||||| || ||
TGCACTCCAGCCTGGGAGAC TCTG CCTC ACC ACA GGGTCC CCTC ACGTCAC CG
GC A
ACAGCCAGACTCCGTCT - AG G CAGA GA-- -- - C T

GAM2525 GAAACAGACTGGGCCAATGT 2502 TATCAAGGAA 5116 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM2526 GGCCAATTGAAACAAACAGT 2503 TATTAGGGAT 5117 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM2527 CTCTGCATGACTTGGGCACT 2504 TGAGCAGGCT 5118 G CT GG GA TG-- CT-- TC

GACATGGTTCCTGCCATCTC GAGAGTGACA CTCT CATGA TG CACT CA GTTC GCCA T
CCTGGCTTATGAGCAGGCTG TCAT |||| ||||| || |||| || |||| ||||
AGAGTGACATCATGAAGAG GAGA GTACT AC GTGA GT CGAG CGGT C
A -- A- GA CGGA TATT CC

GAM2528 AGTCTTTGCTACTGTGAATA 2505 TGCATGTGTC 5119 TTTG TA--- - AATAA
GTGCCGCAATAAACATACGT TTTATAGTAG AGTC CTACTGTGAA GTGC CGC A
GTGCATGTGTCTTTATAGTA AATG |||| |||||||||| |||| |||
GAATGATT TTAG GATGATATTT TACG GTG /
TAA- CTGTG T CATAC

GAM2529 AAGTCTTTGCTATTGTGAAT 2506 TCTTTGCTAT 5120 -- TGT ATA - AATAA
AGTGCCGCAATAAACATACG TGTGAATAGT AAGTC TTTGCTAT GA GTGC CGC A
TGTGCATGTGTCTTTATAGT GCCG ||||| |||||||| || |||| |||
AGAATGATTT TTTAG AGATGATA CT TACG GTG /
TA TTT GTG T CATAC

GAM2530 GTTCCTGGGGCCTTGCCGAA 2507 GGCCCTTGCG 5121 - GG CGAAAT TAC
ATGCCGGTACACCTCTCGGC AGGACCGGAG GTTC CTGG CCTTGC GCCGG A
CCTTGCGAGGACCGGAGAGC AGC |||| |||| |||||| |||||
CGAG GGCC GGAGCG CGGCT C
A A- TTCC-- CTC

GAM2531 GAAACAGACTGGGCCAATGT 2508 TATCAAGGAA 5122 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM2532 CATGCGCTGAATGATGTCAC 2509 TGAATGATGT 5123 AAT TG CAC- GT AA
GGCAGTCGTTGAACACACGG CACGGCAGTC CATGCGCTG GA T GGCA CGTTG C
CGGATGTTCTCAGTGTCCAC GTTG ||||||||| || | |||| |||||
AGCGCATG GTACGCGAC CT G TTGT GCGGC A
AC- GT ACTC AG AC

GAM2533 CCACTGCAGTGCTGATCCTC 2510 GCCCCGGTCA 5124 T A - ATCC AA CT
AGAAACTCATCTCGAATGAG CGCGTGG CCAC GC GTG CTG TCAG ACTCAT C
TACTTGGCCCCGGTCACGCG |||| || ||| ||| |||| ||||||
TGG GGTG CG CAC GGC GGTT TGAGTA /
- - T CCC- CA AG

GAM2534 AGCCTCCAAGGGAGAATTGC 2511 CCTCCAAGGG 5125 CC G AGAA A-- CCTGA
AGAATTGGCCTGACCTCTTA AGAATTGCAG AG TCCAA GG TTGCAGA TTGG C
CCAAAACTCTGTAGCCTGTT AATT || ||||| || ||||||| ||||
GGATTCT TC AGGTT TC GATGTCT AACC C
TT G C--- CAA ATTCT

GAM2535 CCGGTGTAAATGTTGAGCCT 2512 TAAATGTTGA 5126 AA A TTTTT G- TT
TTTTGGCCTGGCTTGTTTGC GCCTTTTTGG CCGGTGT ATGTTG GCC GGCCT GC G
AAAGGCCCTGGCCAACGTCA CCTG ||||||| |||||| ||| ||||| ||
ACATTGG GGTTACA TGCAAC CGG CCGGA CG T
AC - TC--- AA TT

GAM2536 CTGCTCCAGCAGCTGGTGCT 2513 CCACTGCTGC 5127 G AG T T C CA TCC
GCACCAGCAGGAGGTCCTGC TGCTCCAGCT CT CTCC CAGCTGG GC GCA CAG GGAGG T
CCCCTCCACTGCTGCTGCTC GAGG || |||| ||||||| || ||| ||| |||||
CAGCTGAGGAGAAG GA GAGG GTCGACC CG CGT GTC CCTCC G
A A- T T C A- CCC

GAM2537 CAGTTGAATTATACTATTGG 2514 GTGGATCGTG 5128 - A A TG A - TA
CGAGGTTCCAATATCATTTG TTTATGGTGA CAG TTG ATT TACTAT GCG GGTTC CAA T
TGGATCGTGTTTATGGTGAA ATCC ||| ||| ||| |||||| ||| ||||| |||
TCCAAGTTG GTT AAC TAA GTGGTA TGT CTAGG GTT C
G C - TT G T TA

GAM2538 GAAACAGACTGGGCCAATGT 2515 TATCAAGGAA 5129 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM2539 GTTCAGTTCGAGCGCCAAGA 2516 CGGCATCTCC 5130 G G G A TCGTGA CAA C A
GAG
TCGTGAAGCCCAATGGCGAG CAGGCTCTTC GTTCA TTC AGC CCA GA AGCC TGG GAGA
GCCGGAC T
AAGCCGGACGAGTTCGAGTC TGGA ||||| ||| ||| ||| || |||| ||| |||| |||||||
CGGCATCTCCCAGGCTCTTC CAAGT GAG TCG GGT CT TCGG ACC CTCT
CGGCCTG T
TGGAGCTGGAGATGAAC A G A - TC---- --- - A AGC

GAM2540 TTCACCACCATGGAGAAGGC 2517 CTGCCCCCTC 5131 CA GA AG C CT T A
CAAA TCA

CTGGGGCTCATTTGCAGGGG TGCTGATGCC TTCAC CCATG GA GC TGGGG CATT
GCAGGGGGG GC AGGG T
GGAGCCAAAAGGGTCATCAT CCCA ||||| ||||| || || ||||| |||| ||||||||| || ||||
CTCTGCCCCCTCTGCTGATG AAGTG GGTAC CT TG ACCCC GTAG CGTCTCCCC CG
TCTC /
CCCCCATGTTCGTCATGGGT TG TG -- T C- T - ---- TAC
GTGAA

GAM2541 ACTGGTGATTGTTGGTGATG 2518 CTTGCTCATA 5132 GA T G-- CT GAA
GAGCCTGTGGAAAGACATGC GTCTTCAGCA ACTGGT TTGTTGG GAT GAGC GTG A
TTGCTCATAGTCTTCAGCAA AGGA |||||| ||||||| ||| |||| |||
GGACCAGT TGACCA AACGACT CTG CTCG CGT G
GG T ATA TT ACA

GAM2542 TGTGCCCACAGTGTTTGAGA 2519 TGGAAAGCAG 5133 - T TGAGAA G GCAGA GA
ACTATGTGGCAGATATCGAG GTAGAGTTGG TGTG CCCACAG GTT CTAT TG TATC G
GTGGATGGAAAGCAGGTAGA CTTT |||| ||||||| ||| |||| || ||||
GTTGGCTTTGTGGGACACA ACAC GGGTGTT CGG GATG AC GTAG G
A T TTGA-- G GAAAG GT

GAM2543 CGTCGTCGGCGCTGGGCAGG 2520 TGTGGCCAGC 5134 G GGC - A A GGCGG A
GGA
CACACGGCGGACACTGTCTG TCCAGCAGGG CGTC TC GCTGG GC GGC CAC AC
CTGTCTG G
GGAGAAGCGGACAGGTGTGG GGAT |||| || ||||| || ||| ||| || |||||||
CCAGCTCCAGCAGGGGGATG GTAG GG CGACC CG CCG GTG TG GACAGGC /
G GA- T A - ----- - GAA

GAM2544 GAACTTGGGGTTCTTGAAAA 2521 TGGGGTTCTT 5135 AC TG C AAACATT TC- AG
CATTGGAGATCTTCAAGACC GAAAACATTG GA T GGGTT TTGA GGAGA TTCA A
TGAATGTTCTCCTCGTCAAA GAGA || | ||||| |||| ||||| ||||
GCCCTGGTC CT G CCCGA AACT CCTCT AAGT /
-- GT - GCT---- TGT CC

GAM2545 GGGGCAGGGCTGCCTGCTGC 2522 CGTTGTACTT 5136 GCCTGC TT GGG
AGCTTGCCAGGGGTCTTGTT GGTCTTGCCC GGGGCAGGGCT TGCAGC GCCAG T
GGCGTTGTACTTGGTCTTGC C |||||||||| |||||| |||||
CCC CCCCGTTCTGG ATGTTG CGGTT C
TTC--- -- GTT

GAM2546 GAGACGGGGTTTCACCATGT 2523 ACGGGGTTTC 5137 ACG TTCAC TT CT CT
TGGTTAGGCTGGTCTCGAAC ACCATGTTGG GAG GGGT CATG GGTTAGG GGT C
TCCTGACCTCATGATCCACC TTAG ||| |||| |||| ||||||| |||
CACCTC CTC CCCA GTAC CCAGTCC TCA /
CA- CCTA- T- -- AG

GAM2547 CTGCCCATTGAAGCGGTAGT 2524 AGGCATAGAA 5138 - GA G TG TA AGAA GAA AGAGA

GATAGGCATAGAAGGCGAAG GGCGAAGTGG CTGCC CATT AGCG TAG A GGCAT GGC GTGGT T

TGGTAGAGATAGAAGAACCG TAGA ||||| |||| |||| ||| | ||||| ||| |||||

CAGCCAATGCCGCTTGCTGG GACGG GTGG TCGT GTC T CCGTA CCG CGCCA A

TGCTGGTGTGGCAG T -- G GT CG A--- A-- AGAAG

GAM2548 GCTGGAACTGAAGCTGGGGC 2525 TGGGGCTGCA 5139 AA TG - TG CA T TT TT

TGCAGCCTGGGCCTTGGTTT GCCTGGGCCT GCTGG C AAG C GGGCTG GCC GGGCC GG T

GATCCTTGGCCTTGGCCTTG TGGT ||||| | ||| | |||||| ||| ||||| ||

GCCTTGGCCTTTGGCCGGC CGGCC G TTC G TCCGGT CGG TCCGG CC G

-- GT C GT TC T TT TA

GAM2549 GGTTACAGTCTCTAGCTTCG 2526 TACATGGATG 5140 AG A CG CC

CCATGTACATGGCCCTTCCG GGCGGGGAGG GGTTAC TCTCT GCTT CCATGTACATGG C

TGTACATGGATGGGCGGGGA TAAC |||||| ||||| |||| ||||||||||||

GGTAACT TCAATG AGGGG CGGG GGTACATGTGCC /

G- - TA TT

GAM2550 CCGTCTTTGTGCATCTATCC 2527 TCAGATGGAA 5142 CTT A T T TCT CT G

ATTTCTCATCTTCTACCTGG CTGGAAGATG CCGT TGTGCATCT TCCA TTC CATCT AC GG T

GTTACCTTGTCAGATGGAAC TATG |||| ||||||||| |||| ||| ||||| || ||

TGGAAGATGTATGTCATGG GGTA GTATGTAGA AGGT AAG GTAGA TG CC T

CT- - C - C-- TT A

GAM2551 ACTGTGATTCATGGTATCAA 2528 TACCCTTGGA 5141 -- A--- ACA TACT

GACAGTGTCTACTATATTGA AGAATTATGA ACTGT GATTCATGGT TCAAG GTGTC A

TACCCTTGGAAGAATTATGA ATTT ||||| |||||||||| ||||| |||||

ATTTAACAGT TGACA TTAAGTATTA GGTTC CATAG /

AT AGAA C-- TTAT

GAM2552 ATCTGTTTTCTGGGTTTCAA 2529 TTACTTGTCC 5143 ---- C TTTC- CTTA C

TCTCTCTTACAACTTCTTGA AAAAACAACA ATC TGTTTT TGGG AATCTCT CAA T

CCAGAGATTACTTGTCCAAA TGAT ||| |||||| |||| ||||||| |||

AACAACATGAT TAG ACAAAA ACCT TTAGAGA GTT T

TACA - GTTCA CCA- C

GAM2553 GGCCCAGGGATCGGCAGGGC 2530 TTCCCATGCC 5144 G - G- - GCT GA A

TGCTGGCAGAGGAATCCCAG CCAGGCTCCT GGCCCAG GA TC GCAGG GCT GGCA GGAATCCC G

CTGGGGTTCCCATGCCCCAG GCAG |||||||| || || ||||| ||| |||| ||||||||
GCTCCTGCAGGACTTGCTGG CCGGGTC TT AG CGTCC CGG CCGT CCTTGGGG C
GCC G C GA T ACC AC T

GAM2554 TCGCCCGTCCCTTACCTACA 2531 TCCCTTACCT 5145 - TC T CAT - A TG--- G CTG
TTGTTCCAACATGCCAGAGG ACATTGTTCC TCGC CCG CC TACCTA TGTTC CA CA CCA
AGG T
CTGTTAACCTTGGAGACCTG AACA |||| ||| || |||||| ||||| || || ||| |||
CTGCGGATATGGGTACGGCC AGCG GGC GG ATGGGT ATAGG GT GT GGT TCC /
CGGCGCGA C CC C --- C C CCAGA - AAT

GAM2555 CACCTTTACGGCCAAACCGT 2532 TGTGGATATA 5146 TT C CC C-- C--- G
CCACCTCGACCGATTCTGTG GTTTTCCCTG CACC TA GG AAAC GTCCAC TC A
GATATAGTTTTCCCTGTTGG TTGG |||| || || |||| |||||| ||
TG GTGG GT CC TTTG TAGGTG AG C
TT - CT ATA TCTT C

GAM2556 TTGGTCCATATCTCCATGCA 2533 TCCATATCTC 5147 TC ATCTCC- G- - ACA
TGGCGGATACAGTGAAATCT CATGCATGGC TTGG CAT ATGCATG CG GAT G
CGAGCATGCATCTTCTCGGT GGAT |||| ||| ||||||| || |||
GAGCCAG GACC GTG TACGTAC GC CTA T
GA GCTCTTC GA T AAG

GAM2557 CCAGGGGTGGACGATGCTGA 2534 TGACTGGGTC 5148 GG GGA - G AT GG C
GTCAGAATGTGGCCTGGACA ATCGAGAACC CCA GGT CGATG CT AGTCAGA GT CCTGGA
A
ACTTCGGGGACTTTGACTGG ATGG ||| ||| ||||| || ||||||| || ||||||
GTCATCGAGAACCATGG GGT CCA GCTAC GG TCAGTTT CA GGGCTT A
A- AGA T G -- G- C

GAM2558 AGTACATCATAATCGGCGAC 2535 TACAGTTTAC 5149 CA- A- C - C AGG- G CAT- TT
ACAGGTGTTGGTAAATCATG AGACAAGAGG AGTA TCAT AT GGC GA AC TGTT GTAAAT
GC A
CTTATTGCTACAGTTTACAG TTTC |||| |||| || ||| || || |||| |||||| ||
ACAAGAGGTTTCAGCCAGTG TCAT AGTA TG CCG CT TG ACAG CATTTG CG /
CATGACCTTACT TCC CG A A T GAGA A ACAT TT

GAM2559 GTATGGTACAGAGGAGGCCA 2536 TGGAATTTTC 5150 -- TA GG ACAGAAGC
TTACAGAAGCAAGCACCAAG TGGGCCGAAT GTAT GG CAGAGGA CCATT A
ATGGAATTTTCTGGGCCGAA AC |||| || ||||||| |||||
TAC CATA CC GTCTTTT GGTAG /
AG GG AA AACCACGA

GAM2560 TTTGAACTTGTCCCCTGAAT 2537 TGAGTTAGAA 5151 --- C CTGAAT ACA T AG A
A- T
AGCTACAGGTTTTGGAAGCT TCCAAACCAG TTTGAAC TTGT CC AGCT GGTTT GGA
CTGA TCA TG T
GAATCAATGTTATCAGATGA AGCT ||||||| |||| || |||| ||||| ||| |||| ||| ||
GTTAGAATCCAAACCAGAGC AGACTTG GACA GG TCGA CCAAA CCT GATT AGT
AC A
TCCTGGTACAGTTTGTTCAG TTT T TCC--- GA- - AA G AG T
A

GAM2561 AGTGACGAAAAATAACAATA 2538 TAATTGGAAT 5152 - GAAAA AA - A- T
CAGGACTCTTTCGAGGCCCT GAGTCCACT AGTG AC AT CAAT ACAGG CTC T
GTAATTGGAATGAGTCCACT |||| || || |||| ||||| |||
TCAC TG TA GTTA TGTCC GAG T
C AG--- AG A CG C

GAM2562 CGGCTCCGAGAGCAGGTTCT 2539 TACACATTGA 5153 - AGAG C A TC GCAG C
TCGTGAGTTCCTCGCAGGGC GAACCTGAAC CGGC TCCG CAGGTTCTT GTG GT CTC GG
C
CGGTCAGAGCTACACATTGA ATGG |||| |||| ||||||||| ||| || ||| ||
GAACCTGAACATGGAGGCCG GCCG AGGT GTCCAAGAG TAC CA GAG CT G
G ACAA T A TC A--- G

GAM2563 GAGACGGCCATGCTGGTCTG 2540 TACAAGATCA 5154 AC ATGCTG G - A- C- - --
A
CAAGTCAGAGTCCGTGCCAG CTGACTCTGA GAG GGCC GTCT CA AGTCAG GTC
GTGCCAG CT GTC C
CTGTCACTGACTGGGCCTGG GGAC ||| |||| |||| || |||||| ||| ||||||| || |||
TACAAGATCACTGACTCTGA CTC CCGG CAGG GT TCAGTC TAG CATGGTC GG
CAG /
GGACAAGGCCCTC -- AA---- A C AC AA C GT T

GAM2564 TTGGAGCAGTTTCTGACCAT 2541 GAGCAGTTTC 5155 - A AC - GC G
CCTGCCTGGGGAGATCCAGA TGACCATCCT TTGGA GC GTTTCTG CATCC T CTGGG A
TGTGGGTGCGGAAACAGTGT GCCT ||||| || ||||||| ||||| | |||||
CCAG GACCT TG CAAAGGC GTGGG G GACCT G
G A -- T TA A

GAM2565 GGCCAATTGAAACAAACAGT 2542 TATTAGGGAT 5156 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM2566 GGCCAATTGAAACAAACAGT 2543 TATTAGGGAT 5157 C T ACAAACAG G GTT T A GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM2567 TCAGCCTGCTGAACAGTTCC 2544 TATCCTTGTT 5158 CT - G CCTTTTTC TA C TCCAAA
TTTTTCAAAAACATAGATAC TTTAACTGTT TCAGC GC T AACAGTT AAAAACA GATA CA A
CATCCAAAAATTTCCTGATA GGGG ||||| || | ||||||| ||||||| |||| ||
TCCTTGTTTTTAACTGTTGG AGTCG CG G TTGTCAA TTTTTGT CTAT GT /
GGCTTGCTGA TT G G -------- TC A CCTTTA

GAM2568 AATGCTAATATGATGGTCTT 2545 GTCACTTAAA 5159 AATAT- C--- ACA A A CAAACA
AGGACATGAACCAAGACAAA CAAGCCATCT AATGCT GATGGT TTAGG TGA CC AGA A
CAACTTCGAATCTGGGTCAC ATCC |||||| |||||| ||||| ||| || |||
TTAAACAAGCCATCTATCCA TTACGG CTACCG AATTC ACT GG TCT C
GGCATT ACCTAT AACA --- - G AAGCTT

GAM2569 GAAATTTTAGTTCATATGTA 2546 TACTTGGTGT 5160 TT ATATG CC- T
CACTAGCCAGTGGTTGTGGA AAAGAACTTA GAAATT AGTTC TACACTAG AGTGGTTG G
CAACCATTTACTTGGTGTAA ATTT |||||| ||||| |||||||| ||||||||
AGAACTTAATTTC CTTTAA TCAAG ATGTGGTT TTACCAAC G
T- AA--- CAT A

GAM2570 TTTACATTGTTTACCAAGCT 2547 AAAAAGCAAA 5161 CAT TT C- AG -- AAC
GTAGTGCTTTAAGAACACTA ATAAACTTGG TTTA TGT ACCAAG TGT TGCTT TAAG A
CTTAAAAAGCAAAATAAACT TTTA |||| ||| |||||| ||| ||||| ||||
TGGTTTACATTTAAA AAAT ACA TGGTTC ATA ACGAA ATTC /
TT- TT AA AA AA ATC

GAM2571 GTCGCTGGGATAGAAGCCTT 2548 TAGAAGCCTT 5162 G A A CTT --- AG
TGACCAAGCAGGTCAGGCTG TGACCAAGCA GTC CTGGGAT GA GC TGACCAAG CAGGTC G
ACCTGGTTCTTGGTCAGCTC GGTC ||| ||||||| || || |||||||| ||||||
ATCCCGGGAT TAG GGCCCTA CT CG ACTGGTTC GTCCAG /
- - - --- TTG TC

GAM2572 GCACTCTGTTCTTCCGCCGC 2549 ACTCTGTTCT 5163 AC G CC TCC TC TT
TCCGCCGTCGCGTTTCTCTG TCCGCCGCTC GC TCT TTCTTCCG GC GCCG GCG T
CCGGTCGCAATGGAAGAAGA CGCC || ||| |||||||| || |||| |||
GATCGC CG AGA AAGAAGGT CG TGGC CGT C

```
                                CT  G      AA  C--   --  CT

GAM2573  GCATTGATCTTATCCTCCGT 2550   TTGATCTTAT 5164       GAT  AT  TC  GA  T  CTCA
         GACTGTCACCTCATCGTCGT       CCTCCGTGAC       GCATT  CTT  CC  CGT  CTG CAC  T
         GCAGAATGAGGGCCGAGTAG       TGTC          |||||  |||  ||  |||  ||| |||
         ATGC                              CGTAG  GAG  GG  GTA  GAC GTG   /
                                          AT-  CC  GA  A-  -  CTGC

GAM2574  GATTTGGTATTGGACTTGCA 2551   TTGGCACATC 5165     -   ATT---   T-    TC---- TT   GA
         AGTCTCTTTACAGAAAATGT       CTTGCATTGT       GAT TTGGT    GGAC  TGCAAG    TC  TACA  A
         ATTGGCACATCCTTGCATTG       TCTA          ||| |||||     ||||  ||||||     ||  ||||
         TTCTACGCCGCCAATGTC                    CTG AACCG    CTTG  ACGTTC    GG  ATGT  /
                                   T    CCGCAT   TT    CTACAC  TT   AA

GAM2575  TTGTCGTCATTGGACACGTA 2552   TAAATGCGGT 5167       ---      GACAC     CG--  A  CCA
         GATTCGGGCAAGTCCACCAC       GGCATCGACA       TTGTC  GTCATTG    GTAGATT   GGC AGT  C
         TACTGGCCATCTGATCTATA       A             |||||  |||||||    |||||||   ||| |||
         AATGCGGTGGCATCGACAA                    AACAG  CGGTGGC    TATCTAG   CCG TCA  C
                                   CTA     GTAAA     TCTA  G  TCA

GAM2576  GGTGACAACATGCTGGAGCC 2553   TTTCAAGGGA 5166       AA--  G  --       T  TA
         AAGTGCTAACATGCCTTGGT       TGGAAAGTCA       GGTGAC   CAT CT  GGAGCCAAG GC  A
         TTCAAGGGATGGAAAGTCAC       CC            ||||||   ||| ||  |||||||||  ||
         C                                CCACTG   GTA GG  CTTTGGTTC CG  C
                                    AAAG  G  AA       -  TA

GAM2577  AAGATAGAGGCAGAACTGCA 2554   TGTTCTGGAG 5168       GA-----    AA  G       TG
         GGACATCTGCAATGATGTTC       CTGTTGGACA       AAGATA     GGCAG  CT CAGGACATC  C
         TGGAGCTGTTGGACAAATAT       AATA          ||||||      |||||  ||  |||||||||
         CTT                              TTCTAT     TTGTC  GA GTCTTGTAG  A
                                    AAACAGG    --  G       TA

GAM2578  CTTCCTCCTCTCTGACCGGT 2555   CCTCTCTGAC 5169       CC   T  C     GC--     CT   CAG
         TGGCCAGGGACTATGCAGCC       CGGTTGGCCA       CTTCCT  TCTC GA CGGTTG   CAGGGA  ATG   C
         ATCGTCTTCTTTGCTAACAA       GGGA          ||||||  |||| ||  ||||||   ||||||  |||
         CCGCTTTGAGACAGGGAAG                     GAAGGG  AGAG TT GCCAAC   GTTTCT  TGC   /
                                    AC   T  C     AATC     TC   TAC

GAM2579  AGGAGCTTGTTTCATATCGT 2556   GCTTGTTTCA 5170       C    TCA  C  -   T    G--  GATA  ACA
         GCCATTAACAGGCCAGATAT       TATCGTGCCA       AGGAG TTGTT   TAT GTG CCAT AACAG   CCA
TC   G
         CACAGACACGGAAATGGAAA       TTAA          |||||  |||||   |||  |||  ||||  |||||   |||    ||
         CTGTTATGGACACTATAGTT                    TTCTC GACAG   ATA CAC GGTA TTGTC   GGT    GG   A
```

GACAGCCTCTT C TTG T A - AAA AAA- CAC

GAM2580 ACCTACTTTGAGATGGCAAG 2557 GATGGCAAGA 5171 C T G GAAC C CAC
AACTGCTGGAGACACACTGG ACTGCTGGAG AC TACTT GAGATG CAA TG TGGAGACA T
ATGTTTTTACCATGATTGAC ACAC || ||||| |||||| ||| || ||||||||
ATCTTTAAGTATGT TG ATGAA TTCTAC GTT AC ATTTTTGT /
T T A AGT- C AGG

GAM2581 CCAAAGAGCTGAATGTTATG 2558 AAGCAGCTCT 5172 AA-- AA TG TTA A T AAAA
GG AC
TTTATTGAAAAGTGCAAAAG TTCGACGTGT CC AGAGCTG TGTTA T TTGAAA G GC GCT
AT A
CTGGATACAATGTAAAGCAG AGCA || ||||||| ||||| | |||||| | || ||| ||
CTCTTTCGACGTGTAGCAGC GG TTTCGAC ACGAT G AGCTTT C CG CGA TG /
AGCTTTGCCGGG GCCG G- GT C-- - T A--- AA TA

GAM2582 GCATTGATCTTATCCTCCGT 2559 TTGATCTTAT 5173 GAT AT TC GA T CTCA
GACTGTCACCTCATCGTCGT CCTCCGTGAC GCATT CTT CC CGT CTG CAC T
GCAGAATGAGGGCCGAGTAG TGTC ||||| ||| || ||| ||| |||
ATGC CGTAG GAG GG GTA GAC GTG /
AT- CC GA A- - CTGC

GAM2583 GGCTCCCAATGTTGACGTTG 2560 CAATGTTGAC 5174 CTCCC CG---- AG GTTTG
GCCAGGGCGTTTGCAAACAA GTTGGCCAGG GG AATGTTGA TTGGCC GGC C
GCCAGGCCAAAAAGGCTCAA GCGT || |||||||| |||||| |||
CATTTACACC CC TTACAACT AACCGG CCG A
ACAT- CGGAAA A- AACAA

GAM2584 GCCGCATCTTCTTTTGCGTC 2561 AGACACCATG 5175 G- - C- GCC C GC
GCCAGCCGAGCCACATCGCT GGGAAGGTGA GCC CATCTTCTTT TG GTC AGC GA C
CAGACACCATGGGGAAGGTG AGGT ||| |||||||||| || ||| ||| ||
AAGGT TGG GTGGAAGGGG AC CAG TCG CT A
AA T CA AC- - AC

GAM2585 GGCTGGGGCTCATTTGCAGG 2562 GCTCATTTGC 5176 - CT T A CAAA TCA
GGGGAGCCAAAAGGGTCATC AGGGGGGAGC GGC TGGGG CATT GCAGGGGGG GC AGGG
T
ATCTCTGCCCCCTCTGCTGA CAAA ||| ||||| |||| ||||||||| || ||||
TGCCCCCATGTT TTG ACCCC GTAG CGTCTCCCC CG TCTC /
T C- T - ---- TAC

GAM2586 CTTGTGGGAGAGATTATCAA 2563 TGGGAGAGAT 5179 T GA ATC -------- - G A AT
GCGTTTTGAGCAGAAAGGAT TATCAAGCGT CTTG GGGAGA TT AAGC GTTTT GA CAG
AAGG T

TCCGCCTTGTTGGTCTGAAA TTTG |||| |||||| || |||| ||||| || ||| ||||
TTCATGCAAGCTTCCGAAGA GAAC TCTTCT AA TTCG TAAAG CT GTT TTCC C
TCTTCTCAAG - AG GCC AACGTACT T G G GC

GAM2587 CACTACGTTGACCTGAAGGA 2564 AAGGACCGTC 5177 GA-- GAA- CCATTCT --
AAAT
CCGTCCATTCTTTGCCGGCC CATTCTTTGC CACTACGTT CCT GGACCGT
TTGCCGGCCT GGTG A
TGGTGAAATACATGCACTCA CGGC ||||||||| ||| ||||||| |||||||||| ||||
GGGCCGGTAGTTGCCATGGT GTGGTGTAA GGG TCTGGTA GATGGCCGGG
TCAC /
CTGGGAGGGGCTGAATGTGG GTCG AGGG CCGTT-- AC GTAC
TG

GAM2588 CGTTTCGGGTGCTGGCGGCT 2565 AAGGAACCAT 5178 TTC-- -- G C CA GA AAA
TAAG
GCAGCCGGAGTTCAAACCTA GGCCAACTGT CGT GGGT GCT GCGG TG GCCG GTTC CC
C
AGCAGCTGGAAGGAACCATG GAGC ||| |||| ||| |||| || |||| |||| ||
GCCAACTGTGAGCGTACCTT GCG TCCA CGA TGTC AC CGGT CAAG GG /
CATTGCG TTACT TG G A -- AC GAA TCGA

GAM2589 TCTACAAAGTGCCGTCCACT 2566 TCCAATCTGA 5180 A - - CACTG CT- C
GAGACTGAGGCCTTGGCTTC TGGGCATGTT TCT CAAA GTGCC GTC AGA GAGGC T
CAATCTGATGGGCATGTTTG TGAG ||| |||| ||||| ||| ||| |||||
AGA AGA GTTT TACGG TAG TCT CTTCG T
- G G ----- AAC G

GAM2590 GATCAACAGGCTTATTAGAA 2567 TAGAAGAATG 5181 A TAT ACTAA G
GAATGAACTAAGGTGTCTAC AACTAAGGTG GATCAAC GGCT TAGAAGAATGA GGT T
CATGATTATTTTTCTAAGCT TCTA ||||||| |||| |||||||||| |||
GGTTGGTT TTGGTTG TCGA ATCTTTTTATT CCA C
G --- AGTA- T

GAM2591 GAGGAAGACGGTGCCCGATC 2568 TAATGTCGGG 5182 -- C - TC CCAC AA
CATCCACAGAAAAACCTTCT ACATCATCTT GAGG AAGA GGTG CCCGA CAT AGAA A
AATGTCGGGACATCATCTTC CACC |||| |||| |||| ||||| ||| ||||
ACCTC CTCC TTCT CTAC GGGCT GTA TCTT /
AC A A -- A--- CC

GAM2592 TATTCCACGTGGATTGGGGG 2569 TAAGAAGATG 5183 ACGTGGA - GCCTCCCT A
CTCCATCTTTGCCTCCCTGG TGGGTCTCCA TATTCC TTGGGGGCTC CATCTTT GG C
ACACCTTTAAGAAGATGTGG AAAA |||||| |||||||||| ||||||| ||
GTCTCCAAAAAGGAATA ATAAGG AACCTCTGGG GTAGAAG CC /
AAA---- T AATTT--- A

GAM2593 GAGTCCTGGCCTTGTCTGTG 2570 CCACTTGCTG 5184 C ---- CT A C AT
GAGACGGATTACACCTTCCC AAAAGGTCAA GAGTC TGGCCTT GT GTGG GA GG T
ACTTGCTGAAAAGGTCAAGG GGCT ||||| ||||||| || |||| || ||
CTT TTCGG ACTGGAA CG CACC CT CC A
A AAGT TT - T AC

GAM2594 TTGCAATTATTTGAGGAACT 2571 TGCCGTGGAG 5185 AT ACTCC G - TACACA
GACCC
CCGCCGCCTGGCGCCCATTA GCCTCTTCAA TTGCA TATTTGAGGA GCC CC TGGCGCCCAT
GC C
CACAGCGACCCCACAGAAGC GTGC ||||| |||||||||| ||| || |||||||||| ||
CACCGCGTGGGTGCCGTGGA GACGT GTGAACTTCT CGG GG GCCGTGGGTG CG
A
GGCCTCTTCAAGTGCTGCAG C- C---- A T CGCCAC AAGAC

GAM2595 CCGCGTGCAGTACCAGTTCG 2572 CGTGCAGTAC 5186 - -- TT A- AGC
AGATGGAGAGCTTCGACTCC CAGTTCGAGA CCGCGT GCAGT ACCAG CG GATGGAG T
ATCCCCGGCCTGGTGCGCTG TGGA |||||| ||||| ||||| || |||||||
CTACGTGG GGTGCA CGTCG TGGTC GC CTACCTC T
T CG CG CC AGC

GAM2596 GAGAAGGTCCCCTTCACCAA 2573 TAAGTCGTCT 5187 AA C C AA C - C C-- AA
GGTCCAGGAGCCATTCTAGA TCTGACCGGT GAG GGT CCCTT ACC GGTC AGGAG C ATT
TAG A
AACTCTGATAAGTCGTCTTC CAAG ||| ||| ||||| ||| |||| ||||| | ||| |||
TGACCGGTCAAGGGCGCTCC CTC TCG GGGAA TGG CCAG TCTTC G TGA GTC /
TC C- C C -- - T C ATA TC

GAM2597 TCATGCTGCAGCATATTGTA 2574 CAGCATATTG 5188 C A TACT TGCT
CTGGCCTGCTGCTGGCCCGC TACTGGCCTG TCATGCTG AGC TATTG GGCCTGC G
AGGCTTCTCAATAGGTTCGG CTGC |||||||| ||| ||||| |||||||
CATGG GGTACGGC TTG ATAAC TCGGACG /
- G TCT- CCCG

GAM2598 CCACCGGGTATCTAGCCTGT 2575 TATCTAGCCT 5189 A CC--- - ACCC GAGA
GGCCACCCCGGAGATGACAC GTGGCCACCC CCACCGGGT TCTAG TGTG GCC CG T
GAGGCTCACATGACTCTAGA CGGA ||||||||| ||||| |||| ||| ||
CACTTGGTGG GGTGGTTCA AGATC ACAC CGG GC /
C TCAGT T A--- ACAG

GAM2599 AGAAACAAAAGCAGGTGCTG 2576 TAGCATGCCT 5190 CAA- C -- TCA--- AA
AATCATGAAAACCTCAATTA CTTAATTTTT AGAAA AAG AGGT GCTGAA TGA A

TTTTTAGCATGCCTCTTAAT CT ||||| ||| |||| |||||| |||
TTTTCT TCTTT TTC TCCG CGATTT ACT /
TTAA - TA TTATTA CC

GAM2600 GCTTCTATTTTATTGCAGGA 2577 GCACACCGGG 5191 ATTT T AGGA GG- T
GGTGGGGGTGTATGCACCGC GCTATGAGAA GCTTCT TAT GC GGTG GGTG A
ACACCGGGGCTATGAGAAGC GC |||||| ||| || |||| ||||
CGAAGA GTA CG CCAC CCAC T
---- T GGG- ACG G

GAM2601 CAAAGCGACCAGCTACATTT 2578 AAGCGACCAG 5192 AA A ------ AAG TGGG
ACCAAAGCCTGGGTGATGTG CTACATTTAC CA GCGACCAGCT CATT TACCA CC T
GAGTGGTACATAGAGATGAA CAAA || |||||||||| |||| ||||| ||
GCTGGTCGTCATG GT TGCTGGTCGA GTAG ATGGT GG G
AC A AGATAC GA- TGTA

GAM2602 GGCCAATTGAAACAAACAGT 2579 TATTAGGGAT 5193 C T ACAAACAG G GTT T A
GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGC AA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TAGC ||| || |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCG TT ACTT GGGATT TGG GG GG GGTGA /
CATTTAGCC A T ATAATA-- A AC- T - GAA

GAM2603 ACGGCCGAGGGGGTAGCTTT 2580 TAGCTTTAAC 5194 G GTAG AA GACG G- C
AACTGTGACGGGTGTCGCCC TGTGACGGGT ACGGCC AGGGG CTTT CTGT GGT TCGC C
AGGTGAAGATCATGACGGAG GTCG |||||| ||||| |||| |||| ||| ||||
AAGGAACTCCTGGCCGT TGCCGG TCCTC GGAA GGCA CTA AGTG A
- AA-- GA GTA- GA G

GAM2604 TCTTGTGTTGAGACTTCGTG 2581 TACACCACTC 5195 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM2605 CCACCACCTGGAGCCCGAGG 2582 TTCTTCACGG 5196 C GGA- AG T AAGT
AGGTGCTCAAGTACAGCGAG GCAGCAAGCT CCACCA CT GCCCG GAGG GCTC A
TTCTTCACGGGCAGCAAGCT GGTG |||||| || ||||| |||| ||||
GGTGG GGTGGT GA CGGGC CTTC TGAG /
C ACGA A- T CGAC

GAM2606 CCAACAGGATGCCACGCTGG 2583 CACTCGGTGT 5197 AA CC CC TATTTC
GCCGAGCGACTATTTCCTGC ACGTCCTGGA CC CAGGATG ACGCTGGG GAGCGAC C

CAATGTTGCTCACTCGGTGT GG || ||||||| |||||||| |||||||
ACGTCCTGGAGG GG GTCCTGC TGTGGCTC CTCGTTG T
AG A- A- TAACCG

GAM2607 TCTGGCAGCGGTACCCGAAT 2584 CACCGGGAGG 5198 - C - CGAA TATAGCAA - GA
CCCTATAGCAAACATGTCTT TGACCCCTGA TCTGG CAG GGT ACC TCCC AC ATGTCTT C
GACGGAAGACATAGTACACC CCAG ||||| ||| ||| ||| |||| || ||||||| GGGAGGTGACCCCTGACCAG AGACC GTC CCA TGG AGGG TG TACAGAA / A A C G ---- CCACA--- A GG

GAM2608 AGGACTAGAGCTCATGCTGA 2585 TGGCAGAGTA 5199 AG TCAT - CA G
TCATGTCGGTCAGGGGTTTG CGGCTGCTGT AGGACT AGC GCTG AT TGTCGGTCAG G
ACTGGCAGAGTACGGCTGCT TGGA |||||| ||| |||| || |||||||||| GTTGGAGTTTT TTTTGA TTG CGGC TG ACGGTCAGTT G
GG TCGT A AG T

GAM2609 GTTTTGAAAGCTGTACAATT 2586 TACAATTTGG 5200 TT TG-- A- GA - TGA
TGGTGAATGGAGTGACCAAC TGAATGGAGT GT TGAAAGC TACA TTTGGT ATG GAG C
CTCGCATAACCAAAGATGTG GACC || ||||||| |||| |||||| ||| ||| ATTTGTTTTCATGC CG ACTTTTG GTGT AAACCA TAC CTC C
T- TTTA AG A- G CAA

GAM2610 GGTGACAACATGCTGGAGCC 2587 TTGGTTCAAG 5201 AA-- G G- T TA
AAGTGCTAACATGCCTTGGT GGATGGAAAG GGTGAC CAT CT GAGCCAAG GC A
TCAAGGGATGGAAAGTCACC TCAC |||||| ||| || |||||||| || CCACTG GTA GG CTTGGTTC CG C
AAAG G AA - TA

GAM2611 TTGTCGTCATTGGACACGTA 2588 TAAATGCGGT 5202 --- GACAC CG-- A CCA
GATTCGGGCAAGTCCACCAC GGCATCGACA TTGTC GTCATTG GTAGATT GGC AGT C
TACTGGCCATCTGATCTATA A ||||| ||||||| ||||||| ||| ||| AATGCGGTGGCATCGACAA AACAG CGGTGGC TATCTAG CCG TCA C
CTA GTAAA TCTA G TCA

GAM2612 CTGGGCGGCGGCACGGGCTC 2589 TCATCAGCAA 5203 C GG-- C AG -- AC
AGGCATGGGCACGCTGCTCA GATCCGTGAG CTGGG GGC CACGGG TC GC ATGGGC G
TCAGCAAGATCCGTGAGGAG GAGT ||||| ||| |||||| || || |||||| TTCCCGG GGCCC TTG GTGCCT AG CG TACTCG /
- AGGA - AA AC TC

GAM2613 GCTGGTGGTGGGCGGGGACG 2590 AGGAGGCCAT 5204 T GG C GG- TA

GCCGGTTCTACATGAAGGAG CCAGCTCATC GC GGTGGTGGGC GGA GGCC TTC C
GCCATCCAGCTCATCGCTCG GCTC || |||||||||| ||| |||| |||
C CG TCGCTACTCG CCT CCGG AAG /
C A- A AGG TA

GAM2614 GAAACAGACTGGGCCAATGT 2591 TATCAAGGAA 5205 C -- CACAAAGAA - CA-
ACCGAT
CCACAAAGAATTCCTGGTCA GGGCAGGCGT GAAACAGA TGGGCCA ATGTC TTCCT GGT
GCACC G
GCACCACCGATGTCCAAAGG GATG |||||||| ||||||| ||||| ||||| ||| |||||
TGCAATATCAAGGAAGGGCA TTTTGTTT ATTCGGT TGCGG AAGGA CTA CGTGG
/
GGCGTGATGGCTTATTTGTT - AG ACGGG---- A TAA AAACCT
TT

GAM2615 TGCATGGGAATGAGGCTGTT 2592 CTTGGCCCAG 5206 AA- A TT- C AA
GGACGAGAACTGCTCATTTT TACCTATGCA TGCATGGG TG GGCTG GGA GAG C
CTTGGCCCAGTACCTATGCA |||||||| || ||||| ||| |||
ACGTATCC AC CCGGT TTT CTC /
ATG - TCT A GT

GAM2616 AGGGTTAGTTTTTGTAGCCT 2593 TGGCACGCTC 5207 --- TT A- TTC C
TCGGCTGGCCCGTCGGCCTC GAACTTCCGG AGGGTT AGTTT GT GCC GGCTGG C
TGGCACGCTCGAACTTCCGG CCCT |||||| ||||| || ||| ||||||
CCCT TCCCGG TCAAG CG CGG CCGGCT C
CCT CT CA TCT G

GAM2617 AGGAGGCGGAGGCAGCTGGG 2594 CATCGCTCGT 5208 - C CTG TCC - ACC
GAGGTCCTGAGCGATGTGAC CTCTTCCTAC AGGAGGCGG AGG AG GGGAGG TGAGCGATG
TG A
CAGGCCGCCATCGCTCGTCT TCTC ||||||||| ||| || |||||| ||||||||| ||
CTTCCTACTCTCCTGCCGCC TCCTCCGCC TCC TC TCCTTC GCTCGCTAC GC /
TCCT G - TCA TCT C CGG

GAM2618 GCTGGGCTGGGCGAGTATCT 2595 AAGCACGACT 5209 G C TA CT- AAAG- TC
CTTCGAAAGGGTCACTCTCA AAGAGCCTTC GCTGGGCT GG GAG TCT TCG GG A
AGCACGACTAAGAGCCTTCT TGAG |||||||| || ||| ||| ||| ||
GAGCCCAGC CGACCCGA TC TTC AGA AGC CT C
G - CG ATC ACGAA CT

GAM2619 GTGGGGTAAAACCCAGACGC 2596 ACGCCATGAA 5210 G - AC C GCGG T--- T
AG AA
CATGAAAGCGGCCATGGCCT AGCGGCCATG GTG GGTAA AACCCAG GC ATGAAA CCA
GGCCT GG AA A
TGGAGAAAAAGCTTAACCAG GCCT ||| ||||| ||||||| || |||||| ||| ||||| || ||

GCCCTTTTGGATTTTCATGC CAC CCGTT TTGGGTC CG TACTTT GGT CCGGA CC
TT /
CCTGGGTTCTTGCCGCAC G C C- - TA-- TTTC - AA CG

GAM2620 AGGCTGGAGTGCAATGGCAT 2597 TCCCAGGTTC 5211 T TGCAATG A T CTCACT AC
GATCTTGGCTCACTGCAACC AAGCAATTCT AGGC GGAG GC TGA CTTGG GCA C
TCTGCCTCCCAGGTTCAAGC CCTG |||| |||| || ||| ||||| |||
AATTCTCCTGCCT TCCG CCTC CG ACT GGACC CGT /
T TTAA--- A T CTC--- CT

GAM2621 TATTTCAAAACGATGTGGGG 2598 TAAGTCTTCG 5212 AA A- GT TTT G
GCTTTTTACGAAAGTTAAGT TGGATGGCTT TATTTCAA CG T GGGGGCTT AC A
CTTCGTGGATGGCTTGGAGT GGAG |||||||| || | |||||||| ||
G GTGAGGTT GT G CTTCTGAA TG A
CG AG TG T-- A

GAM2622 GGACATTCAGCTGGTGGCCG 2599 AGTGGAGCTG 5213 C AGCT-- TG -- - CACCCTG
CGCTCTCTGTCACCCTGGGC GCGGTTTCCT GGA ATTC GG GCCGC GCTCT CTGT G
CTCTTTGCAGTGGAGCTGGC CTCA ||| |||| || ||||| ||||| ||||
GGTTTCCTCTCAGGAGTCTC CCT TGAG CC TGGCG CGAGG GACG G
C C GACTCT TT GT T TTTCTCC

GAM2623 ATAGCGCCAGTTCCCCAGCA 2600 GGGCTTGGGA 5214 GCC- C-- CAAA AGAG
CCCCC
AACCCCCTCCAGAGCTGCCC GTGACTTGAA ATAGC AGTT CCCAG CCCCCTCC CTG
G
CCGGATGCACAGACAAGGAG GCTG ||||| |||| ||||| |||||||| |||
GGGGCTTGGGAGTGACTTGA TGTCG TCAG GGGTT GGGGGAGG GAC G
AGCTGT AAGT TGA C--- AACA ACGTA

GAM2624 GGGCAAATGAGTCCTCTGTG 2601 TCGAACACAG 5215 AA A CTC GCCAA GG AA T
GCCAAGAGGTCAGAATCGTC ACCCATGGCC GGGC ATG GTC TGTG GA TCAG TCG C
CCTGAGGCTGAATCGAACAC C |||| ||| ||| |||| || |||| |||
AGACCCATGGCCC CCCG TAC CAG ACAC CT AGTC AGT C
G- C --- AAG-- A- GG C

GAM2625 TCTTGTGTTGAGACTTCGTG 2602 TACACCACTC 5216 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM2626 CCCGCCAGGCCTCCATAGAG 2603 TGGCCAGTAC 5217 A C CATAGA - - A

CTGCCCAGCATGGCTGTGGC CAAGAGTCGG CCCGCC GGC TC GCTG CC CAGC T
CAGTACCAAGAGTCGGTGGG TGGG |||||| ||| || |||| || ||||
GGGTGG CTG AG TGAC GG GTCG /
- - AACCA- C T G

GAM2627 TCTTGTGTTGAGACTTCGTG 2604 TACACCACTC 5218 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM2628 GAGCGATCTTATCTCTGTGC 2605 TCTGTGCTTC 5219 T- G TGAA C- AAT
TTCGTGAAGCTAATCAAGCA GTGAAGCTAA GAGCGATCT ATCTCTGT CTTCG GCTAAT
AAGCAATT C
ATTAATCCCAAGTTGCTTCA TCAA ||||||||| |||||||| ||||| |||||| ||||||||
GTTGGTCGAAGACAGAGGTT CTTGCTGGA TGGAGACA GAAGC TGGTTG TTCGTTGA
/
CAGGTCGTTC CT - ---- AC ACC

GAM2629 TCTTGTGTTGAGACTTCGTG 2606 TACACCACTC 5220 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM2630 GATATCGAAGAGCTGGAGAC 2607 TCGAAGAGCT 5221 A A--- G CCAA ---- A
CAAGGCCGTGGGAATGTCTA GGAGACCAAG GAT TCGA GAGCT GAGA GGCCGT GGG A
ACGATGGCCGCTTTCTCAAG GCCG ||| |||| ||||| |||| |||||| |||
TTTGACATCGAAATC CTA AGCT TTTGA CTCT CCGGTA TCT T
A ACAG A TTCG GCAA G

GAM2631 ATCAGGTAATGCAGTTTGTT 2608 ACTCCATTCG 5222 AA-- G GTTG A C--- GT
GAGCCAAGTCGGCAGTTTGT GCTGGTTAAA ATCAGGT TGCA TTT AGCCA GTCGG AGTTT
A
AAAGGACTCCATTCGGCTGG AGAT ||||||| |||| ||| ||||| ||||| |||||
TTAAAAGATGCACTAAACCT TAGTCCA ACGT GAA TTGGT CGGCT TCAGG /
GAT AATC A AA-- - TACC AA

GAM2632 TCTTGTGTTGAGACTTCGTG 2609 TACACCACTC 5223 GAGA GT--- C AAAGGA
GTGGTGCTAAGAAAAGGAAG CCAAGAAGAA TCTTGTGTT CTTC GGTGGTG TAAGA A
AAGAAGTCTTACACCACTCC TAAG ||||||||| |||| ||||||| |||||
CAAGAAGAATAAGCACAAGA AGAACACGA GAAG TCACCAC ATTCT G
ATAA AACCC - GAAGAA

GAM2633 CGTTTCGGGTGCTGGCGGCT 2610 AAGGAACCAT 5225 TTC-- -- G C CA GA AAA TAAG
GCAGCCGGAGTTCAAACCTA GGCCAACTGT CGT GGGT GCT GCGG TG GCCG GTTC CC C
AGCAGCTGGAAGGAACCATG GAGC ||| |||| ||| |||| || |||| |||| ||
GCCAACTGTGAGCGTACCTT GCG TCCA CGA TGTC AC CGGT CAAG GG /
CATTGCG TTACT TG G A -- AC GAA TCGA

GAM2634 CTTGTGGGAGAGATTATCAA 2611 TGGGAGAGAT 5226 T GA ATC -------- - G A AT
GCGTTTTGAGCAGAAAGGAT TATCAAGCGT CTTG GGGAGA TT AAGC GTTTT GA CAG AAGG T
TCCGCCTTGTTGGTCTGAAA TTTG |||| |||||| || |||| ||||| || ||| ||||
TTCATGCAAGCTTCCGAAGA GAAC TCTTCT AA TTCG TAAAG CT GTT TTCC C
TCTTCTCAAG - AG GCC AACGTACT T G G GC

GAM2635 CACTACGTTGACCTGAAGGA 2612 AAGGACCATC 5224 GA-- GAA- CCATTCT -- AAAT
CCATCCATTCTTTGCCGGCC CATTCTTTGC CACTACGTT CCT GGACCAT TTGCCGGCCT GGTG A
TGGTGAAATACATGCACTCA CGGC ||||||||| ||| ||||||| |||||||||| ||||
GGGCCGGTAGTTGCCATGGT GTGGTGTAA GGG TCTGGTA GATGGCCGGG TCAC /
CTGGGAGGGGCTGAATGTGG GTCG AGGG CCGTT-- AC GTAC TG

GAM2636 GGAGCGCACCTTCATCGCCA 2613 CGGCCTGGTG 5227 ACCT--- A - A GACG GT
TCAAGCCGGACGGCGTGCAG GGCGAGATCA GGAGCGC TC TCGCC ATCA GCCG GC G
CGCGGCCTGGTGGGCGAGAT TCAA ||||||| || ||||| |||| |||| ||
CATCAAGCGCTTC CTTCGCG AG AGCGG TGGT CGGC CG /
AACTACT - G C G--- AC

GAM2637 GGCCAATTGAAACAAACAGT 2614 TATTAGGGAT 5228 T ACAAACAG G GTT T A GAT
TCTGAGACCGTTCTTCCACC AATATTCATT GGCCAA TGAA TTCTGA ACC CT CC CCACT T
ACTGATTAAGAGTGGGGTGG TGGC |||||| |||| |||||| ||| || || |||||
CAGGTATTAGGGATAATATT CCGGTT ACTT GGGATT TGG GG GG GGTGA /
CATTTGGCC T ATAATA-- A AC- T - GAA

GAM2638 TGAGAGGTCGGCTTGGAAGT 2615 TCCAACAGTC 5229 A GG- G ------- A T
GTGGACAGTTTTGAACGGTC TTGCTTCAGA TGAG GGTC CTT GAAGTG TGGAC GTT T
CAACAGTCTTGCTTCAGAGA GAAG |||| |||| ||| |||||| ||||| |||
AGGACTACTCA ACTC TCAG GAG CTTCGT ACCTG CAA /
A GAA A TCTGACA G G

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GENE    TARGET    UTR SEQUENCE            SEQID   BINDING-SITE
======== ========= === ===================== ======= ==========================
GAM24   MAGEA3    3'  CATGAGATAACTCAAGAA    19314         C
                          TTCTTGAG TATTTCGTG
                          |||||||| |||||||||
                          AAGAACTC ATAGAGTAC
                               A
GAM24   GENX-3414 3'  CACATTTTATGCTTAAAAAGTT 15456         C     TATTTC_
          AAC                   GTTAACTT TTGAGC      GTG
                          |||||||| ||||||      |||
                          CAATTGAA AATTCG      CAC
                               A     TATTTTA
GAM24   KIAA0376  3'  CACGAAGTCTCCAAGAAG    66212         _ CT
                          CTTCTTG AG  ATTTCGTG
                          ||||||| ||  ||||||||
                          GAAGAAC TC  TGAAGCAC
                               C __
GAM24   LOC152343 3'  CACGAAATGCTTAAAAGCTAAC 81421      A  C     T
                          GTTA CTT TTGAGC ATTTCGTG
                          |||| ||| |||||| ||||||||
                          CAAT GAA AATTCG TAAAGCAC
                            C  _     _
GAM24   LOC154877 3'  CACAAAATAAAGCTCAAG    87530         __    C
                          CTTGAGCT  ATTT GTG
                          ||||||||  |||| |||
                          GAACTCGA  TAAA CAC
                               AA   A
GAM24   LOC158510 3'  CATGAGATAACTCAAGAA    82832         C
                          TTCTTGAG TATTTCGTG
                          |||||||| |||||||||
                          AAGAACTC ATAGAGTAC
                               A
GAM25   APBA1     3'  TCTCTGGAAGGCCCCTT     70476      A    TGG
                          AAGG GCTT   TTCGGAGA
                          |||| ||||   ||||||||
                          TTCC CGGA   AGGTCTCT
                            C   ____
GAM25   CA7       3'  CCAGTCACCAAAGCCACCT    60828      A_       TCGGA   A
                          AGG  GCTTTGGT    GAC GG
                          |||  ||||||||    ||| ||
                          TCC  CGAAACCA    CTG CC
                            AC       _____   A
GAM25   E2F3      3'  CTGTCTCCATGAACCACTC    10467     CTT     __
                          GAG   TGGTTC  GGAGACAG
                          |||   ||||||  ||||||||
                          CTC   ACCAAG  CCTCTGTC
                            ___      TA
GAM25   HD        3'  CCTATCCCCAGGACAGGTCCCT 10911     AG   TG   _  A  C
                          AGG  CTT  GTTC GG GA AGG
                          |||  |||  |||| || || |||
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                                TCC  GGA  CAGG CC CT TCC
                                  CT   __    A  C  A
GAM25   LZTR1    3'  CTGTCACCCAAGGCTCCT    23170          TTCG A
                                AGGAGCTTTGG    G GACAG
                                ||||||||||    | |||||
                                TCCTCGGAACC    C CTGTC
                                      ____ A
GAM25   MECP2    3'  CCCGTCTAACCACAGCTCCTT  18394        T    CGG    A
                                AAGGAGCT TGGTT   AGAC GG
                                |||||||| |||||   |||| ||
                                TTCCTCGA ACCAA   TCTG CC
                                     C     ___    C
GAM25   PLA2G2A  5'  CTGTCTCCAAACAGCCTT    6110      A   TTG   C
                                AGG GCT   GTT GGAGACAG
                                ||| |||   ||| ||||||||
                                TTC CGA   CAA CCTCTGTC
                                  _   ___    A
GAM25   PLOD     3'  CCTGAAAAACCAAGGCCCC    6114     A       CGGAGA
                                GG GCTTTGGTT     CAGG
                                || |||||||||      ||||
                                CC CGGAACCAA     GTCC
                                 C        AAA___
GAM25   POLR2A   3'  CCTGTCCCCAAATTGAAGATCC 8128       G   TG   C  A
           TT                     AAGGA CTT  GTT GG GACAGG
                                |||||| |||  ||| || ||||||
                                TTCCT GAA  TAA CC CTGTCC
                                   A   GT   A  C
GAM25   RAB36    3'  CCTGTCTCCAACACCGCCTCCT 18163      CTT    TC_
                                AGGAG   TGGT   GGAGACAGG
                                |||||   ||||   |||||||||
                                TCCTC   GCCA   CCTCTGTCC
                                   C__    CAA
GAM25   RAP1     3'  CCTGTCCTTTGGCAGAAGCTCC 39111          G  T    _
           TT                     AAGGAGCTTT GT CGGAG ACAGG
                                |||||||||| || ||||| |||||
                                TTCCTCGAAG CG GTTTC TGTCC
                                      A  _     C
GAM25   SFRP5    3'  CCTGCCCCAAGGCCCAGAGCTC 13032          TT __  AGA
           C                      GGAGCTTTGG  C  GG   CAGG
                                ||||||||||  |  ||   ||||
                                CCTCGAGACC  G  CC   GTCC
                                      CG AA  CC_
GAM25   SORCS2   3'  CCTGTCCCCCAGACCCAAAGCT 40800          T  _  A_
           CT                     GGAGCTTTGG TC GG  GACAGG
                                |||||||||| || ||  ||||||
                                TCTCGAAACC AG CC  CTGTCC
                                      C  A  CC
GAM25   TFR2     3'  CCCGTCCCCCAGTCAAGAGCTC 13698          _ GT C  A   A
           CT                     AGGAGCTTT G  T GG GAC GG
                                |||||||||  |  | || ||| ||
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                                TCCTCGAGA C  A CC CTG CC
                                     A TG C  C   C
GAM25   C1orf35   3'  CTGCCTCGGAAGCTCCTT    44480        TTGGT  G   A
                                AAGGAGCT    TC GAG CAG
                                ||||||||    || ||| |||
                                TTCCTCGA    AG CTC GTC
                                     _____  G   C
GAM25   DKFZp434J1015 3'  CCGCCTCCACCTGAAAAGCTCC 94209          ___  TC   ACA
          TT                     AAGGAGCTTT   GGT  GGAG   GG
                                ||||||||||   |||  ||||   ||
                                TTCCTCGAAA   CCA  CCTC   CC
                                     AGT   __    CG_
GAM25   EFS2      3'  CTGCCTGCCAAAGCCCC     20773    A      TC  AGA
                                GG GCTTTGGT  GG   CAG
                                || ||||||||  ||   |||
                                CC CGAAACCG  CC   GTC
                                 C       T_  ___
GAM25   FLJ10350  5'  CCGCCTCCGAGTCGCTACTT   97248     G   TTT GT     ACA
                                AAG AGC   G  TCGGAG   GG
                                ||| |||   |  ||||||   ||
                                TTC TCG   C  AGCCTC   CC
                                  A   ___ TG     CG_
GAM25   HRI       3'  CTGCCCCACAAGCTCCTT    27738         _   TT
                                AAGGAGCTT TGG  CGG
                                |||||||| |||  |||
                                TTCCTCGAA ACC  GTC
                                     C   CC
GAM25   KIAA0057  3'  CCTGTCTCTTGCAAGCTCC    25409        TG  TC
                                GGAGCTT  GT  GGAGACAGG
                                |||||||  ||  |||||||||
                                CCTCGAA  CG  TCTCTGTCC
                                    __  T_
GAM25   KIAA0189  3'  CCTGTCCCCTTTCCTAAAGCTC 28941           TTC_  A
          CT                     AGGAGCTTTGG    GG GACAGG
                                ||||||||||    || ||||||
                                TCCTCGAAATC    CC CTGTCC
                                      CTTT  C
GAM25   KIAA1203  3'  CCTGCCCTCCCACCAAAGCCTC 72087       _      TC    A_
          CT                     AGGAG CTTTGGT  GGAG  CAGG
                                ||||| |||||||  ||||  ||||
                                TCCTC GAAACCA  CCTC  GTCC
                                   C      C_   CC
GAM25   KIAA1533  5'  CCTGCCCCCAAGCCGGCCCC   74140    A   TT    C  AGA
                                GG GCT  GGTT GG   CAGG
                                || |||  |||| ||   ||||
                                CC CGG  CCGA CC   GTCC
                                 C   __    A  CCC
GAM25   SAMHD1    3'  CCTGCCCCCGTGAAGAGTTCC  61981         GGTT   AGA
                                GGAGCTTT   CGG   CAGG
                                ||||||||   |||   ||||
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                                CCTTGAGA   GCC   GTCC
                                    AGT_   CCC
GAM25   SCGN    3'  CCTGTCTCACTGAAAGCCCCT  23775    A   _  TCG
                                AGG GCTTT GGT   GAGACAGG
                                ||| ||||| |||   ||||||||
                                TCC CGAAA TCA   CTCTGTCC
                                  C    G  ___
GAM25   SYT6    3'  CTCTCCGAAACCACCTC    79519    CTT   _    CA
                                GAG   TGGTT CGGAGA  G
                                |||   ||||| ||||||  |
                                CTC   ACCAA GCCTCT  C
                                  C__    A     A
GAM25   UBXD2   3'  CTGCCTCCATCAGCTTCTT   68892       TT   TC   A
                                AAGGAGCT  GGT  GGAG CAG
                                ||||||||  |||  |||| |||
                                TTCTTCGA  CTA  CCTC GTC
                                    __  __   C
GAM25   LOC113146 3'  CCTAAAATGGAACCAAAGCTTC 73334           GGAGAC
                                GGAGCTTTGGTTC    AGG
                                ||||||||||||     |||
                                CTTCGAAACCAAG    TCC
                                      GTAAAA
GAM25   LOC113521 5'  CCCGTCTCCGAGCTGCTCC   73402      TTT        A
                                GGAGC   GGTTCGGAGAC GG
                                |||||   |||||||||| ||
                                CCTCG   TCGAGCCTCTG CC
                                  ___         C
GAM25   LOC115704 3'  CCTGCAGCGGAAACCAAAGTCC 73906    AG     __  GAGA
          C                      GG  CTTTGGT  TCG   CAGG
                                ||  |||||||  |||   ||||
                                CC  GAAACCA  GGC   GTCC
                                 CT     AA   GAC_
GAM25   LOC136345 3'  CCTACCCCACCCAAAGCTGCCT 76712    _      TTC  AGAC
                                AGG AGCTTTGG   GG   AGG
                                ||| ||||||||   ||   |||
                                TCC TCGAAACC   CC   TCC
                                  G      CA_  CCA_
GAM25   LOC144231 5'  CCTGTCTTCCTTGACCAAAGCT 83938          C__
          CT                     GGAGCTTTGGTT   GGAGACAGG
                                ||||||||||||   |||||||||
                                TCTCGAAACCAG   CTTCTGTCC
                                      TTC
GAM25   LOC146856 5'  CTGTCTCCATGAACCACTC   83700    CTT    __
                                GAG   TGGTTC  GGAGACAG
                                |||   ||||||  ||||||||
                                CTC   ACCAAG  CCTCTGTC
                                  ___     TA
GAM25   LOC147669 5'  CCGCCTCCTGGGCAAGCTCC   85180       TG   _   ACA
                                GGAGCTT  GTTC GGAG   GG
                                |||||||  |||| ||||   ||
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                                CCTCGAA  CGGG CCTC   CC
                                   __   T   CG_
GAM25   LOC148021 5'  CTACCTCCAGAGCTACTT    79316     G      TTC  _
                                AAG AGCTTTGG   GG AG
                                ||| ||||||||   || ||
                                TTC TCGAGACC   CC TC
                                  A       T__  A
GAM25   LOC153688 3'  CCTGCCCCCAAACCAAGGCCT  87307    A       C  AGA
                                GG GCTTTGGTT GG   CAGG
                                || |||||||| ||   ||||
                                TC CGGAACCAA CC   GTCC
                                 _       A  CCC
GAM25   LOC155032 5'  CCTACCCCACCCAAAGCTGCCT 87592     _      TTC  AGAC
                                AGG AGCTTTGG   GG    AGG
                                ||| ||||||||   ||    |||
                                TCC TCGAAACC   CC    TCC
                                  G       CA_  CCA_
GAM25   LOC157349 5'  CCGTCTCCGGCAGCCCCT    82335    A   TTG  T     A
                                AGG GCT   GT CGGAGAC GG
                                ||| |||   || ||||||| ||
                                TCC CGA   CG GCCTCTG CC
                                  C  ___  _      C
GAM25   LOC157349 5'  CCGTCTCCGGCAGCCCCT    82336    A   TTG  T     A
                                AGG GCT   GT CGGAGAC GG
                                ||| |||   || ||||||| ||
                                TCC CGA   CG GCCTCTG CC
                                  C  ___  _      C
GAM25   LOC199991 3'  CCTGTCCACCCTCAAAGCCCT  91515    A     TTC  A_
                                AGG GCTTTGG   GG  GACAGG
                                ||| |||||||   ||  ||||||
                                TCC CGAAACT   CC  CTGTCC
                                  _     C__  AC
GAM26   AGRP     5'  CTTCATTAGGCCCTGCCATA   24616       A  A
                                TATGGCA GG CCTGATGGAG
                                ||||||| || ||||||||||
                                ATACCGT CC GGATTACTTC
                                    C  _
GAM26   CGTHBA    3'  CTTCCCTCCAGTCCTTGCCG   24890         C  AT  A
                                TGGCAAGGAC TG  GG GAAG
                                |||||||||| ||  || ||||
                                GCCGTTCCTG AC  CC CTTC
                                      _ CT  _
GAM26   COL5A3    3'  CTCCCCAGGCTCACCTTGCCAT 32318         A___   AT
           G                     TATGGCAAGG    CCTG  GGAG
                                ||||||||||    ||||  ||||
                                GTACCGTTCC    GGAC  CCTC
                                      ACTC    C_
GAM26   FGF23     3'  CTTCTCTGGGGTCCCTTCCA   40557     CAA     GA
                                TGG   GGACCT  TGGAGAAG
                                |||   ||||||  ||||||||
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                                ACC  CCTGGG  GTCTCTTC
                                 TTC    __
GAM26  FUT3    3' CTCCCAGAGACCTTGCCA   5621       AC_  AT
                                TGGCAAGG  CTG  GGAG
                                ||||||||  |||  ||||
                                ACCGTTCC  GAC  CCTC
                                    AGA  __
GAM26  FUT5    3' CTCCCAGAGACCTTGCCA   10726      AC_  AT
                                TGGCAAGG  CTG  GGAG
                                ||||||||  |||  ||||
                                ACCGTTCC  GAC  CCTC
                                    AGA  __
GAM26  TCF12   3' TCTCCTATCCTCTTGCCATA  13639       ACCT  _
                                TATGGCAAGG   GAT GGAGA
                                ||||||||||   ||| |||||
                                ATACCGTTCT   CTA CCTCT
                                     C___  T
GAM26  WSX1    3' CTCCCCCACATCCTTTCCTTGC 17915      CCT  _____
           C                     GGCAAGGA  GAT   GGAG
                                ||||||||  |||   ||||
                                CCGTTCCT  CTA   CCTC
                                    TTC  CACCC
GAM26  ZAP70   3' CTTCCCCACCCTCAGCCCCACC 71375    CAA  AC   ___  A
           CCA                   TGG  GG  CTGA  TGG GAAG
                                |||  ||  ||||  ||| ||||
                                ACC  CC  GACT  ACC CTTC
                                 CCA  CC   CCC  C
GAM26  C1orf34 3' CCTCTGGCCATTGCCATA   61303       _  A  T  T
                                TATGGCAA GG CC GA GG
                                |||||||| || || || ||
                                ATACCGTT CC GG CT CC
                                    A  _  T  _
GAM26  CLSTN1  3' CTCCCCAGAGCACCCCCTGCCA 30787      A  AC____  AT
           T                    ATGGCA GG    CTG  GGAG
                                ||||||  ||    |||  ||||
                                TACCGT CC    GAC  CCTC
                                   C  CCACGA  C_
GAM26  DKFZP434J193 3' CTTCTCCACCACTCTCCTTGCC 71562         CC_  A
           ATG                   TATGGCAAGGA  TG TGGAGAAG
                                ||||||||||  || ||||||||
                                GTACCGTTCCT  AC ACCTCTTC
                                     CTC  C
GAM26  DNAJC6  3' CTCCAAAGTTCCCACCATA  29492      CAA  C  GA
                                TATGG  GGA CT  TGGAG
                                |||||  ||| ||  |||||
                                ATACC  CCT GA  ACCTC
                                   AC_  T  A_
GAM26  FLJ12122 5' CTGCCAGCTCAGGTCCCTGCCA 47092      A     __  _
                                TGGCA GGACCTGA  TGG AG
                                ||||| ||||||||  ||| ||
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                                ACCGT CCTGGACT  ACC TC
                                  C       CG   G
GAM26   FLJ14642 3' CTTCTCCGTAGTCCCCGCC   52575     AA    CTG
                                GGC  GGAC   ATGGAGAAG
                                |||  ||||   |||||||||
                                CCG  CCTG   TGCCTCTTC
                                  CC    A__
GAM26   FLJ20275 3' CTGTCAGATCCTTGCCAT    35308          C
                                ATGGCAAGGA CTGATGG
                                |||||||||| |||||||
                                TACCGTTCCT GACTGTC
                                      A
GAM26   FLJ21369 3' CTTCTCCATCAAGTTTCACCA 46051     CAA    C
                                TGG   GGAC TGATGGAGAAG
                                |||   |||| ||||||||||
                                ACC   TTTG ACTACCTCTTC
                                  AC_    A
GAM26   HSPC016  3' TCTCTATTCCCTGCCATA    32503        A   CCTG
                                TATGGCA GGA    ATGGAGA
                                |||||||  |||    |||||||
                                ATACCGT CCT    TATCTCT
                                   C  _____
GAM26   HT014    3' CTTCCTAATAAATCCTTGCCA  40153         CC  A   A
                                TGGCAAGGA  TG TGG GAAG
                                |||||||||  ||  ||| ||||
                                ACCGTTCCT  AT ATC CTTC
                                      AA  A  _
GAM26   KIAA0773 3' CTTCTCCACGACCTCACC    28722    CA   ACC  A
                                GG  AGG   TG TGGAGAAG
                                ||  |||   || ||||||||
                                CC  TCC   GC ACCTCTTC
                                 AC   A__  _
GAM26   KIAA1181 3' CTCCATCAGCTGGTCA      68911      A  GAC
                                TGGC AG   CTGATGGAG
                                ||||  ||   |||||||||
                                ACTG TC   GACTACCTC
                                  G  ___
GAM26   KIAA1348 3' CTTCTTAGGTCTTGCCA     69122        G     T
                                TGGCAAG ACCTGA GGAG
                                |||||||  ||||||  ||||
                                ACCGTTC TGGATT CTTC
                                      _     _
GAM26   KIAA1493 3' CTTCTCCACCTAGTCTGCC   64840      AG   CTGA
                                GGCA  GAC    TGGAGAAG
                                ||||  |||    ||||||||
                                CCGT  CTG    ACCTCTTC
                                  __  ATCC
GAM26   KIAA1535 3' CTCTGTGGTCCTTGCC      80212          TG
                                GGCAAGGACC  ATGGAG
                                ||||||||||  ||||||
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                                CCGTTCCTGG  TGTCTC
                                    __
GAM26   KIAA1819 5' CTTCTCCACGGCTCCCCCA   70252    CAA   C   A
                                TGG   GGA CTG TGGAGAAG
                                |||   ||| ||| ||||||||
                                ACC   CCT GGC ACCTCTTC
                                  C__   C   _
GAM26   LAT1-3TM 3' CTCCATCAGTGTCATCACCA  49143    CAAG  _
                                TGG    GAC CTGATGGAG
                                |||    ||| |||||||||
                                ACC    CTG GACTACCTC
                                  ACTA   T
GAM26   LAT1-3TM 5' CTCCATCAGTGTCATTACCA  49144    CAAG  _
                                TGG    GAC CTGATGGAG
                                |||    ||| |||||||||
                                ACC    CTG GACTACCTC
                                  ATTA   T
GAM26   OS4      3' CTTCCCCATCATCCCTTCCATT 20389      _  CC___    A
            GCCA                  TGGCAA GGA    TGATGG GAAG
                                |||||| |||    |||||| ||||
                                ACCGTT CCT    ACTACC CTTC
                                   A   TCCCT    C
GAM26   RASSF2   3' CTTCTCCACCTTCTCTCCA   29097    CA   CCTGA
                                TGG  AGGA    TGGAGAAG
                                |||  ||||    ||||||||
                                ACC  TCTT    ACCTCTTC
                                  TC    CC___
GAM26   SARM     3' CTCCCCCAGGCCCTGCCAT   31285      A  A   AT
                                ATGGCA GG CCTG  GGAG
                                |||||| || ||||  ||||
                                TACCGT CC GGAC  CCTC
                                   C  _   CC
GAM26   SELB     3' CTCCCCCAGGGCCTCCTTGCC  62591       ___   AT
                                GGCAAGGA   CCTG  GGAG
                                ||||||||   ||||  ||||
                                CCGTTCCT   GGAC  CCTC
                                     CCG    CC
GAM26   SERPING1 3' CTTCTCCATGGCCCTGCCATG  5348       A  A  TG
                                TATGGCA GG CC  ATGGAGAAG
                                ||||||| || ||  |||||||||
                                GTACCGT CC GG  TACCTCTTC
                                   C  _  __
GAM26   ZDHHC8   3' TCCCCACCAACTTCTCTGCC   64622     _   CC  A   A
                                GGCA AGGA  TG TGG GA
                                |||| ||||  || ||| ||
                                CCGT TCTT  AC ACC CT
                                  C    CA  C   C
GAM26   LOC142946 3' CCATGGTCCTTGCCATA     83783           TG
                                TATGGCAAGGACC  ATGG
                                ||||||||||||  ||||
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                                ATACCGTTCCTGG  TACC
                                       __
GAM26   LOC150319 3'  CTTCTCCATCCTCCTGCCAT   80471       A   CCT
                                ATGGCA GGA   GATGGAGAAG
                                |||||| |||   ||||||||||
                                TACCGT CCT   CTACCTCTTC
                                   _   C__
GAM26   LOC197423 5'  CTCCATCAGTGTCATTACCA   78424     CAAG  _
                                TGG    GAC CTGATGGAG
                                |||    ||| |||||||||
                                ACC    CTG GACTACCTC
                                  ATTA   T
GAM26   LOC199923 5'  CTTCTCCACCTCCTGCCA    89871      A   CCTGA
                                TGGCA GGA    TGGAGAAG
                                ||||| |||    ||||||||
                                ACCGT CCT    ACCTCTTC
                                   _  CC___
GAM26   LOC220565 5'  CTCCATCAGTGTCATCACCA   92441     CAAG  _
                                TGG    GAC CTGATGGAG
                                |||    ||| |||||||||
                                ACC    CTG GACTACCTC
                                  ACTA   T
GAM26   LOC221975 5'  CTTCTCCATGGAGCCTGCC    94192      A  AC  G
                                GGCA GG  CT ATGGAGAAG
                                |||| ||  || |||||||||
                                CCGT CC  GG TACCTCTTC
                                   _ GA  _
GAM26   LOC257239 5'  CTTCTCCACCTCAACCACCA   98844     CAA  ACC  __
                                TGG   GG   TGA  TGGAGAAG
                                |||   ||   |||  ||||||||
                                ACC   CC   ACT  ACCTCTTC
                                  A__  A__   CC
GAM26   LOC90499  3'  CTTCTCCATGGCCCCCTCCA   63741     CAA  A  TG
                                TGG   GG CC  ATGGAGAAG
                                |||   || ||  |||||||||
                                ACC   CC GG  TACCTCTTC
                                  TCC  C  __
GAM27   HRH1     3'  AAATGTGCCCTTTTGGCCGG   7812     A      A   TCA
                                CC GGCCAAAA GGC   ACATTT
                                || |||||||| |||   ||||||
                                GG CCGGTTTT CCG   TGTAAA
                                  _       C   ___
GAM27   POLD2    5'  TTGAACCTCCTTGGCCTGG    21721         AA   C
                                CCAGGCCAA  AGG TCAA
                                |||||||||  ||| ||||
                                GGTCCGGTT  TCC AGTT
                                      CC   A
GAM27   SCN7A    3'  AAATGTTGAAAGCCTAAGCC   12947     CAAAA   __
                                GGC    AGGC  TCAACATTT
                                |||    ||||  |||||||||
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                                CCG    TCCG  AGTTGTAAA
                                  AA___   AA
GAM27   SHANK2   3'  GTTGAACTTCTTCTTTGGCCTC 25531   C      _   C__
            A                    C AGGCCAAA AAGG   TCAAC
                                | |||||||| ||||   |||||
                                A TCCGGTTT TTCT   AGTTG
                                 C       C    TCA
GAM27   SIAT8E   3'  TGAGCCTCCTGGCCTGG     60552        AAA
                                CCAGGCCA   AGGCTCA
                                ||||||||   |||||||
                                GGTCCGGT   TCCGAGT
                                     CC_
GAM27   SLC7A8   3'  GAGCCCTTCCTGGCCTGG    25304        AA   _
                                CCAGGCCA  AAGG CTC
                                ||||||||  |||| |||
                                GGTCCGGT  TTCC GAG
                                     CC    C
GAM27   TFAP2C   3'  TGGGAACCCCTCCTGGCCTGG  13687        AAA  ____
                                CCAGGCCA   AGG    CTCA
                                ||||||||   |||    ||||
                                GGTCCGGT   TCC    GGGT
                                     CC_   CCAA
GAM27   TRPM2    3'  GAGCCTTGCCTGGCCTGG    13864        AA_
                                CCAGGCCA   AAGGCTC
                                ||||||||   |||||||
                                GGTCCGGT   TTCCGAG
                                     CCG
GAM27   FLJ13189 3'  TTGAACCTTTTTTGCCTGG   46498       C      C
                                CCAGGC AAAAAGG TCAA
                                |||||| ||||||| ||||
                                GGTCCG TTTTTCC AGTT
                                   T      A
GAM27   FLJ20208 3'  AAATGCAGGCTTTTTAGCC   35240     C     G  CAA
                                GGC AAAAAG CT   CATTT
                                ||| |||||| ||   |||||
                                CCG TTTTTC GA   GTAAA
                                  A     G  C__
GAM27   FLJ22944 3'  AAATGTTGGGATTTGAACCC  47866    CCAA   GG
                                GG    AAA  CTCAACATTT
                                ||    |||  ||||||||||
                                CC    TTT  GGGTTGTAAA
                                 CAAG   A_
GAM27   HPRP8BP  3'  AAATGTTGGATGTCCAGGCT   60060     AAAAA  __
                                GGCC    GGC  TCAACATTT
                                ||||    |||  |||||||||
                                TCGG    CTG  GGTTGTAAA
                                  AC___   TA
GAM27   KIAA0872 3'  AAATGTTAAGCCTTTTGTTATT 30731     GCCA       C
            G                    CAG    AAAAGGCT AACATTT
                                |||    |||||||| |||||||
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                                GTT    TTTTCCGA TTGTAAA
                                  ATTG       A
GAM27   KIAA1843  3'  AAATGTTGACTGAACCTGACCT 62880      C  AAAA_  C
            G                      CAGG CA     GG TCAACATTT
                                   |||| ||     || |||||||||
                                   GTCC GT     TC AGTTGTAAA
                                     A  CCAAG  _
GAM27   KIAA1975  3'  AAATGTTGATTTTTCTGACC   74407    C  A    C
                                   GG CA AAAGG TCAACATTT
                                   || || ||||| |||||||||
                                   CC GT TTTTT AGTTGTAAA
                                    A  C    _
GAM27   MRIP2     3'  AAATGTTGATTTTTCTGACC   56789    C  A    C
                                   GG CA AAAGG TCAACATTT
                                   || || ||||| |||||||||
                                   CC GT TTTTT AGTTGTAAA
                                    A  C    _
GAM27   SLC26A10  5'  TTGAACCCCTTTGGCCTG    56851         AA  C
                                   CAGGCCAAA  GG TCAA
                                   |||||||||  || ||||
                                   GTCCGGTTT  CC AGTT
                                        CC  A
GAM27   THEG      3'  TGAGCTTTTTGGCCTGG     33892           G
                                   CCAGGCCAAAAAAG CTCA
                                   |||||||||||||| ||||
                                   GGTCCGGTTTTTC GAGT
                                                 _
GAM27   LOC118704 3'  AAATGTTGATTTTTCTGACC   74359    C  A    C
                                   GG CA AAAGG TCAACATTT
                                   || || ||||| |||||||||
                                   CC GT TTTTT AGTTGTAAA
                                    A  C    _
GAM27   LOC118706 3'  AAATGTTGATTTTTCTGACC   74361    C  A    C
                                   GG CA AAAGG TCAACATTT
                                   || || ||||| |||||||||
                                   CC GT TTTTT AGTTGTAAA
                                    A  C    _
GAM27   LOC123036 3'  AAATGTTTGCAGTTTTGGCT   74645         AG  TC
                                   GGCCAAAA  GC  AACATTT
                                   ||||||||  ||  |||||||
                                   TCGGTTTT  CG  TTGTAAA
                                        GA  T_
GAM27   LOC123624 3'  AAATGTTGGGCTTCTGTGCCT  76134      _  AAA
                                   AGGC CA   AGGCTCAACATTT
                                   |||| ||   ||||||||||||
                                   TCCG GT   TTCGGGTTGTAAA
                                     T  C__
GAM27   LOC128338 3'  AAATATTGAGCCTTTTTAATAG 75250    AGGCC          C
            G                      CC     AAAAAGGCTCAA ATTT
                                   ||     |||||||||||| ||||
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                                GG    TTTTTCCGAGTT TAAA
                                 ATAA_          A
GAM27   LOC143158 3'  AAATGTTGATTTTTCTGACC   76997    C  A    C
                                GG CA AAAGG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM27   LOC195979 3'  AAATGTTGATTTTTCTGACC   88928    C  A    C
                                GG CA AAAGG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM27   LOC219672 5'  AATGGTGCTTTTTGGCTGG    92963      G       G TCAA
                                CCAG CCAAAAAG C    CATT
                                |||| |||||||| |    ||||
                                GGTC GGTTTTTC G    GTAA
                                  _       _ TG__
GAM27   LOC220466 3'  AAATGTTGATTTTTCTGACC   74398    C  A    C
                                GG CA AAAGG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM27   LOC254105 3'  AGGTGTGGCCCCCTTGGCCTGG 96416          AAA    CA
                                CCAGGCCAA   GGCT  ACATTT
                                |||||||||   ||||  ||||||
                                GGTCCGGTT   CCGG  TGTGGA
                                      CCC   __
GAM27   LOC255319 3'  AAATGTTGATTTTTCTGACC   96152    C  A    C
                                GG CA AAAGG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM27   LOC91300  5'  GTTGAGCTTTTCTGGCCCGG   96238    A    A
                                CC GGCCA AAAGGCTCAAC
                                || ||||| ||||||||||
                                GG CCGGT TTTTCGAGTTG
                                 C    C
GAM27   LOC91300  5'  GTTGAGCTTTTCTGGCCCGG   96239    A    A
                                CC GGCCA AAAGGCTCAAC
                                || ||||| ||||||||||
                                GG CCGGT TTTTCGAGTTG
                                 C    C
GAM27   LOC91660  5'  AAATGTTTATCTTCTTTTTGGC 67399           CTC__
           TT                    AGGCCAAAAAGG    AACATTT
                                 ||||||||||||    |||||||
                                 TTCGGTTTTTCT    TTGTAAA
                                       TCTAT
GAM28   AQP7     5'  GACAGTCACGGAGGAACAAGAT 8605          A_
           CAA                     TTGATCTT  TCCTCCGTGACTGTC
                                 ||||||||  ||||||||||||||||
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                                AACTAGAA  AGGAGGCACTGACAG
                                    CA
GAM28   MMP14    5'  GACTAAGCAGAAGAAAGATCAA 18428        A  C  C  GACT
                                TTGATCTT TC TC GT    GTC
                                |||||||| || || ||    |||
                                AACTAGAA AG AG CG    CAG
                                    _  A  A  AAT_
GAM28   KIAA0433 5'  ACAGTCATCATAATATCAA    31498      C    CCTCC
                                TTGAT TTAT    GTGACTGT
                                ||||| ||||    ||||||||
                                AACTA AATA    TACTGACA
                                   T   C____
GAM28   KIAA1915 5'  GACAGTATTTTAAAAATAAGGT 73667         CCTCCGTG_
            CAA                   TTGATCTTAT       ACTGTC
                                ||||||||||       ||||||
                                AACTGGAATA       TGACAG
                                     AAAATTTTA
GAM28   MGC5370   3'  CAGTTGAAAAGATCAA      52193        A  CTCCGT
                                TTGATCTT TC     GACTG
                                |||||||| ||     |||||
                                AACTAGAA AG     TTGAC
                                    A  _______
GAM28   TREX1    5'  GACAGCTGGAGACAGAGATCAA 54382        ATC    TGA
                                TTGATCTT   CTCCG   CTGTC
                                ||||||||   |||||   |||||
                                AACTAGAG   GAGGT   GACAG
                                    ACA    C__
GAM28   TREX1    5'  GACAGCTGGAGACAGAGATCAA 54388        ATC    TGA
                                TTGATCTT   CTCCG   CTGTC
                                ||||||||   |||||   |||||
                                AACTAGAG   GAGGT   GACAG
                                    ACA    C__
GAM28   LOC127534 3'  ACAGCAGATAAGATCAA     75963          CTCCG  A  _
                                TTGATCTTATC    TG CTG T
                                ||||||||||    || ||| |
                                AACTAGAATAG    AC GAC A
                                     _____  _  T
GAM28   LOC150480 5'  GACAGTCACGGAGGAAGAAGAT 61025         A_
            CAA                   TTGATCTT  TCCTCCGTGACTGTC
                                ||||||||  ||||||||||||||||
                                AACTAGAA  AGGAGGCACTGACAG
                                    GA
GAM28   LOC158279 5'  GACAGTCACAGAGGAACAAGAT 60330        A_    C
            CAA                   TTGATCTT  TCCTC GTGACTGTC
                                ||||||||  ||||| |||||||||
                                AACTAGAA  AGGAG CACTGACAG
                                    CA    A
GAM28   LOC201522 3'  GACCTTCGGGAGAACGAGATCA 89637        ATC   G   CT
            A                    TTGATCTT   CTCC TGA  GTC
                                ||||||||   |||| |||  |||
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                                AACTAGAG  GAGG GCT  CAG
                                    CAA   _  TC
GAM28  LOC220864 5'  GACAGTCACAGAGGAACAAGAT 92487        A_   C
          CAA                    TTGATCTT  TCCTC GTGACTGTC
                                |||||||| |||||| |||||||||
                                AACTAGAA  AGGAG CACTGACAG
                                    CA    A
GAM28  LOC254381 5'  GACAGTCACGACAGCAGACCAA 99328     A  TATCCTC
                                TTG TCT      CGTGACTGTC
                                ||| |||      ||||||||||
                                AAC AGA      GCACTGACAG
                                  C  CGACA__
GAM29  HOXB6    3'  GGAGCCAGGAGACCTGCTC   60540        CA  _  C
                                GAGCAGGTC  CC GGC CC
                                |||||||||  || ||| ||
                                CTCGTCCAG  GG CCG GG
                                     A_  A  A
GAM29  RXRB     3'  TGTAGGAACCGATCTGCT    42034        CACC  CC
                                AGCAGGTC   GG  CCTACA
                                ||||||||   ||  ||||||
                                TCGTCTAG   CC  GGATGT
                                    _____  AA
GAM29  ZNFN2A1  3'  ATGCAGGGGCCGTGCTGTCC  61390   AG  GTC  C     A
                                G  CAG   CAC GGCCCCT CAT
                                |  |||   ||| ||||||| |||
                                C  GTC   GTG CCGGGGA GTA
                                 CT  ___  _     C
GAM29  DKFZP434P211 3'  ATGTAGGGCACCTTGGACCTCT 28023     C     CC  C_
          C                      GAG AGGTCCA  GG  CCCTACAT
                                ||| |||||||  ||  ||||||||
                                CTC TCCAGGT  CC  GGGATGTA
                                  _     T_  AC
GAM29  HSPC072  3'  GGGTGCCAGTGGACCTGCTC  27172          C  _
                                GAGCAGGTCCAC GGC CCC
                                |||||||||||| ||| |||
                                CTCGTCCAGGTG CCG GGG
                                      A  T
GAM29  KIAA1183  3'  ATGTAGAAGCTGACTGAGACCT 63188        _ C_   CC
          GCT                    AGCAGGTC CA  CGGC  CTACAT
                                ||||||| ||  ||||  ||||||
                                TCGTCCAG GT  GTCG  GATGTA
                                    A  CA   AA
GAM29  LOC142949 5'  TGTAAGTCGGACCTGC     83784        ACC  CCC
                                GCAGGTCC   GGC   TACA
                                ||||||||   |||   ||||
                                CGTCCAGG   CTG   ATGT
                                    ___   A__
GAM29  LOC150174 3'  ATGTAGGGCACCTTGGACCTCT 80429     C     CC  C_
          C                      GAG AGGTCCA  GG  CCCTACAT
                                ||| |||||||  ||  ||||||||
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                                CTC TCCAGGT  CC  GGGATGTA
                                  _     T_  AC
GAM29   LOC150213 3'  ATGTAGGGCACCTTGGACCTCT 75348     C      CC  C_
            C                    GAG AGGTCCA  GG  CCCTACAT
                                 ||| |||||||  ||  ||||||||
                                CTC TCCAGGT  CC  GGGATGTA
                                  _     T_  AC
GAM29   LOC155032 3'  ATGTAGGGGCCAGCCCATCTC  87590     CA_  CCACC
                                GAG  GGT    GGCCCCTACAT
                                |||  |||    ||||||||||
                                CTC  CCG    CCGGGGATGTA
                                  TAC  A____
GAM29   LOC203286 3'  AGTGGCCGATGGACCTGC    92142         C    C
                                GCAGGTCCA CGGCC CT
                                ||||||||| ||||| ||
                                CGTCCAGGT GCCGG GA
                                     A    T
GAM29   LOC219513 5'  GGGGGCAGGTGGACCCGGC   95991    A_      G
                                GC  GGTCCACC GCCCCT
                                ||  |||||||| ||||||
                                CG  CCAGGTGG CGGGGG
                                 GC       A
GAM29   LOC221968 3'  AGGATGCTAGACCTGCTC    94140         CACC  C_
                                GAGCAGGTC   GGC  CCT
                                |||||||||   |||  |||
                                CTCGTCCAG   TCG  GGA
                                     A___   TA
GAM29   LOC254182 5'  AGGAACTTGTCAATCTGCTC  97745        CC  C  CC
                                GAGCAGGT  AC GG  CCT
                                ||||||||  || ||  |||
                                CTCGTCTA  TG TC  GGA
                                    AC  T  AA
GAM30   ADAM2    5'  ACTGCCCTGTAACCACCA    9398      C   CATGGAA
                                TGG TGGT     GGGGCAGT
                                ||| ||||     ||||||||
                                ACC ACCA     TCCCGTCA
                                  _   ATG____
GAM30   CD68     3'  AACTGCCCCCCCCCCCCCCAG 60496      TCAT_  AA
            C                    GCTGG    GG  GGGGCAGTT
                                 |||||    ||  |||||||||
                                 CGACC    CC  CCCCGTCAA
                                   CCCCC  CC
GAM30   MUCDHL   3'  AACAGCACCTCCCACCAACCAG 88631        CA_  A  G  A
            CCA                    TGGCTGGT   TGG AGG GC GTT
                                   ||||||||   ||| ||| || |||
                                   ACCGACCA   ACC TCC CG CAA
                                      ACC   C   A  A
GAM30   MUCDHL   3'  GCACCTCCCACCAACCAGCCA  88640        CA_  A  G
                                TGGCTGGT   TGG AGG GC
                                ||||||||   ||| ||| ||
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                                ACCGACCA  ACC TCC CG
                                    ACC  C  A
GAM30   MUCDHL   3' GCACCTCCCACCAACCAGCCA 88641       CA_  A  G
                                TGGCTGGT  TGG AGG GC
                                ||||||||  ||| ||| ||
                                ACCGACCA  ACC TCC CG
                                    ACC  C  A
GAM30   MUCDHL   3' AACAGCACCTCCCACCAACCAG 49198       CA_  A  G  A
          CCA                   TGGCTGGT  TGG AGG GC GTT
                                ||||||||  ||| ||| || |||
                                ACCGACCA  ACC TCC CG CAA
                                    ACC  C  A  A
GAM30   MUCDHL   3' GCACCTCCCACCAACCAGCCA 49205       CA_  A  G
                                TGGCTGGT  TGG AGG GC
                                ||||||||  ||| ||| ||
                                ACCGACCA  ACC TCC CG
                                    ACC  C  A
GAM30   MUCDHL   3' GCACCTCCCACCAACCAGCCA 49206       CA_  A  G
                                TGGCTGGT  TGG AGG GC
                                ||||||||  ||| ||| ||
                                ACCGACCA  ACC TCC CG
                                    ACC  C  A
GAM30   RAB30    3' CCTTTACCCATGACCAACA  27938   GC      __
                                TG  TGGTCATGG  AAGGG
                                ||  |||||||||  |||||
                                AC  ACCAGTACC  TTTCC
                                 A_       CA
GAM30   TRIM34   3' ACCACCCCCATGACCACCA  41508   C      AA  GCA
                                TGG TGGTCATGG  GGG  GT
                                ||| |||||||||  |||  ||
                                ACC ACCAGTACC  CCC  CA
                                  _       __  AC_
GAM30   TRIM34   3' ACCACCCCCATGACCACCA  56110   C      AA  GCA
                                TGG TGGTCATGG  GGG  GT
                                ||| |||||||||  |||  ||
                                ACC ACCAGTACC  CCC  CA
                                  _       __  AC_
GAM30   AFAP     3' ACCGCCCCTTCCCCAAGC   41602   _ TCAT      A
                                GCT GG   GGAAGGGGC GT
                                ||| ||   ||||||||| ||
                                CGA CC   CCTTCCCCG CA
                                  A ____       C
GAM30   KIAA0562 3' ACAGTCTCCTAACCAGCCA  28812       CA  AA   A
                                TGGCTGGT  TGG  GGGGC GT
                                ||||||||  |||  ||||| ||
                                ACCGACCA  ATC  CTCTG CA
                                    __  __    A
GAM30   MGC4707  3' ACAGCCCCAAGACCAGCCA  44360       ATGGAA   A
                                TGGCTGGTC    GGGGC GT
                                |||||||||    ||||| ||
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                                ACCGACCAG     CCCCG CA
                                    AA____    A
GAM30   ZER6     3'  AACTGCTTGTCATGACCAGACA 64113    G        AAGG
                                TG CTGGTCATGG   GGCAGTT
                                || ||||||||||   |||||||
                                AC GACCAGTACT   TCGTCAA
                                 A        GT__
GAM30   LOC138130 5'  AACTGCCCCCTCGGTTCAGTCC 76479    _   TC  G  A
           A                     TGG CTGG  AT GA GGGGCAGTT
                                ||| ||||  || || |||||||||
                                ACC GACT  TG CT CCCCGTCAA
                                  T   __  G  C
GAM30   LOC149296 5'  AACTGCCCCCCAGGCATACAGC 80018      ___   A   AA
           CA                     TGGCTG   GTC TGG  GGGGCAGTT
                                ||||||   ||| |||  |||||||||
                                ACCGAC   CGG ACC  CCCCGTCAA
                                   ATA  _  __
GAM30   LOC219654 3'  CCTCCCCAGACCAGCCA     92929         A   AA
                                TGGCTGGTC TGG  GGGG
                                |||||||||  |||  ||||
                                ACCGACCAG ACC  CTCC
                                     _  C_
GAM30   LOC253782 5'  CTACCCCTATCAGCCA      97398         CATGGA    C
                                TGGCTGGT     AGGGG AG
                                ||||||||     ||||| ||
                                ACCGACTA     TCCCC TC
                                     _______    A
GAM30   LOC257359 5'  GCTCCCAGAACCAGCCA     97976         CA   AAG
                                TGGCTGGT  TGG   GGGC
                                ||||||||  |||   ||||
                                ACCGACCA  ACC   CTCG
                                     AG   ___
GAM31   DGKG     3'  AAGCAAGAAACTATAATGCACA 9040       G  CA   C  C
                                TGTG CA  TGT GT TCTTGCTT
                                |||| ||  ||| || ||||||||
                                ACAC GT  ATA CA AGAACGAA
                                  _ A_   T  A
GAM31   PIN      3'  AGCATGGACTGTGCCACA     14985          TGTC    CT
                                TGTGGCACA    GTCT  TGCT
                                |||||||||    ||||  ||||
                                ACACCGTGT    CAGG  ACGA
                                     ____    T_
GAM31   TGFB3    3'  AGCTGCACATGTGCCACA     13715           C  CTCTT
                                TGTGGCACATGT GT     GCT
                                ||||||||||||| ||     |||
                                ACACCGTGTACA CG     CGA
                                       _  T_____
GAM31   LOC118987 3'  AAGCAAAAAATGTGGATGCCAT 74391        CA  T   CTC
           A                     TGTGGCA  TG CGT   TTGCTT
                                |||||||  || |||   ||||||
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                                ATACCGT  GT GTA   AACGAA
                                    AG  _   AAA
GAM31   LOC123443 3'  AAGCAAGACGGGCCCACGCCAC 74661       ACAT   GTC
            A                    TGTGGC   GTC   TCTTGCTT
                                 ||||||   |||   ||||||||
                                 ACACCG   CGG   AGAACGAA
                                    CACC   GC_
GAM31   LOC126823 5'  AGCAAGAAGGCTGCCACA    75079       CATGTC   _
                                 TGTGGCA     GTCT CTTGCT
                                 |||||||     |||| ||||||
                                 ACACCGT     CGGA GAACGA
                                    _______   A
GAM31   LOC152742 3'  AGCAAAAGACAGTAGCCA    87045     ACA  TC    C
                                 TGGC   TG  GTCT TTGCT
                                 ||||   ||  |||| |||||
                                 ACCG   AT  CAGA AACGA
                                   ___  GA    A
GAM31   LOC199982 3'  AAGCAAGAAATACTCTACATCA 89896      CACAT_  C  C
            CA                    TGTGG     GT GT TCTTGCTT
                                  |||||     || || ||||||||
                                  ACACT     CA TA AGAACGAA
                                     ACATCT  _  A
GAM31   LOC199982 3'  AGCAAGAGACAACCCATA    89898      CACAT  C
                                 TGTGG     GT GTCTCTTGCT
                                 |||||     || ||||||||||
                                 ATACC     CA CAGAGAACGA
                                    ______  A
GAM31   LOC253634 5'  AAGTCCTCACGACATGTGCCCA 98415    T          CTCTT
                                 TG GGCACATGTCGT     GCTT
                                 || ||||||||||||     ||||
                                 AC CCGTGTACAGCA     TGAA
                                  _          CTCC_
GAM32   ACCN2    3'  AGCTGGGGATTGGCGACTCCTG 39623    A  ACTA   CA_
                                 CA GA    GTT   CCCCAGCT
                                 || ||    |||   ||||||||
                                 GT CT    CGG   GGGGTCGA
                                  C  CAG_   TTA
GAM32   HD       3'  AGCTGGGGCCGGAGCCTTTGGA 10905       AACTA    A__
                                 TCCAAG     GTTC   CCCCAGCT
                                 ||||||     ||||   ||||||||
                                 AGGTTT     CGAG   GGGGTCGA
                                    C_____    GCC
GAM32   JRK      3'  AGCTGGGACTCAGTTCTTGG   87816         _   TCAC
                                 CCAAGAACT AGT    CCCAGCT
                                 |||||||||  |||    |||||||
                                 GGTTCTTGA TCA    GGGTCGA
                                       C  _____
GAM32   PCM1     5'  AGCTGCAAAAACTAGTTTCT   21671      _     CACCC
                                 AGAA CTAGTT     CAGCT
                                 |||| ||||||     |||||
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                                TCTT GATCAA    GTCGA
                                  T     AAAC_
GAM32   PTPRA    5'  AGCTGGGGGGCCAGTTC     55947      A   CA
                                GAACT GTT  CCCCAGCT
                                |||||| |||  ||||||||
                                CTTGA CGG  GGGGTCGA
                                  C   __
GAM32   CECR2    3'  AGCTATCAAGAACAAGTTCTTG 49429          A    ACCCC
           GA                     TCCAAGAACT GTTC     AGCT
                                |||||||||| ||||    ||||
                                AGGTTCTTGA CAAG     TCGA
                                     A    AACTA
GAM32   CMG2     3'  AGCTGGGGCTACAGAACTCTTG 55197      ACTA    A____
                                CAAGA    GTTC    CCCCAGCT
                                |||||    ||||    ||||||||
                                GTTCT    CAAG    GGGGTCGA
                                  _____   ACATC
GAM32   DCOHM    3'  GCTGGGGGCACTTCTTG     50530      ACT   TCA
                                CAAGA   AGT   CCCCAGC
                                |||||   |||   |||||||
                                GTTCT   TCA   GGGGTCG
                                  ___   CG_
GAM32   DKFZP564B167 3'  CTGGTAGCTAGTTCTTG     31837          CACC
                                CAAGAACTAGTT    CCAG
                                ||||||||||||    ||||
                                GTTCTTGATCGA    GGTC
                                     T___
GAM32   DOC2B    3'  AGCTGGGGTGGGGGGCTCT    14559     A  AG
                                AGA CT  TTCACCCCAGCT
                                ||| ||  ||||||||||||
                                TCT GG  GGGTGGGGTCGA
                                  C  G_
GAM32   FBP17    5'  AGCTGGGGCACCGAGCTCTGGG 73145     A   A  AGTTCA
           A                     TCC AGA CT     CCCCAGCT
                                ||| ||| ||     ||||||||
                                AGG TCT GA     GGGGTCGA
                                  G   C  GCCAC_
GAM32   FLJ12994  3'  AGCTAGGGTGAACCGTAG     77946     __      C
                                CTA  GTTCACCC AGCT
                                |||  |||||||| ||||
                                GAT  CAAGTGGG TCGA
                                  GC       A
GAM32   KIAA1318  3'  CTGGAGGACTGGTTCCTGGA   67874      A        ACC
                                TCCA GAACTAGTTC   CCAG
                                |||| ||||||||||   ||||
                                AGGT CTTGGTCAGG   GGTC
                                  C        A__
GAM32   MAGEB1    5'  AGCCGAGGGTGAATTCTCAGGA 11425     A_   ACTA       CA_
                                TCC  AGA    GTTCACCC   GCT
                                |||  |||    ||||||||   |||
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                                AGG  TCT    TAAGTGGG   CGA
                                  AC   ____       AGC
GAM32   MAGEB2   5'  AGCCAGGGGTGAATTCTCAGGA 11429     A_   ACTA       A_
                                TCC  AGA    GTTCACCCC  GCT
                                |||  |||    |||||||||  |||
                                AGG  TCT    TAAGTGGGG  CGA
                                  AC   ____       AC
GAM32   SB52     5'  GCTGGGGTCGCTCTCGGG    57175     A   ACTA  TC
                                TCC AGA    GT  ACCCCAGC
                                |||  |||    ||  ||||||||
                                GGG TCT    CG  TGGGGTCG
                                  C   ____  C_
GAM32   LOC145622 3'  AGTGTGTGAACTAATTCATG   77803     A   C       CCCA
                                CA GAA TAGTTCAC    GCT
                                ||  |||  ||||||||    |||
                                GT CTT ATCAAGTG    TGA
                                 A   A       TG__
GAM32   LOC146733 5'  AGCTAGGGGTGAGCTTCTTAGA 84782     C    ACT        _
                                TC AAGA   AGTTCACCCC AGCT
                                ||  ||||   ||||||||||  ||||
                                AG TTCT   TCGAGTGGGG TCGA
                                 A   ___         A
GAM32   LOC151162 5'  AGCTGAGGGTGAGTTCCTGTGA 86425    _  A    TAGT     _
                                TC CA GAAC    TCACCC CAGCT
                                ||  ||  ||||    ||||||  |||||
                                AG GT CTTG    AGTGGG GTCGA
                                 T  C    ____      A
GAM32   LOC203377 5'  AGCTGAGGGTGAGTTCCTGTGA 92254    _  A    TAGT     _
                                TC CA GAAC    TCACCC CAGCT
                                ||  ||  ||||    ||||||  |||||
                                AG GT CTTG    AGTGGG GTCGA
                                 T  C    ____      A
GAM32   LOC256524 5'  AGCTGGGCCGCCAGTTCCGGGA 97316     AA     A  TCAC
                                TCC  GAACT GT    CCCAGCT
                                |||  |||||  ||    |||||||
                                AGG  CTTGA CG    GGGTCGA
                                  GC    C  CC__
GAM32   LOC257538 5'  AGCCAAGGAGATGTTGTTCTTG 99603         TAGT  A  CCA
           GA                     TCCAAGAAC    TC CC   GCT
                                |||||||||    ||  ||   |||
                                AGGTTCTTG    AG GG   CGA
                                      TTGT  A  AAC
GAM32   LOC51083  5'  AGCTGGGGTGACTTTTC     32558     CT   T
                                GAA  AGT CACCCCAGCT
                                |||  |||  ||||||||||
                                CTT  TCA GTGGGGTCGA
                                  T_   _
GAM32   LOC51195  3'  AGCTGGGGTGGGGTGGATC    33404     A   G
                                GA CTA TTCACCCCAGCT
                                ||  |||  ||||||||||||
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                                CT GGT GGGTGGGGTCGA
                                 A  G
GAM33   BAPX1    3' GGCCACACTAGTTCATGGT   8646       AA   CCA
                                GCCATGA  GCTG  TGGCC
                                |||||||  ||||  |||||
                                TGGTACT  TGAT  ACCGG
                                   __   CAC
GAM33   C1QBP    3' GCCATAGTTTCATGGC     60857        G  GCC
                                GCCATGAAA CT  ATGGC
                                |||||||||  ||  |||||
                                CGGTACTTT GA  TACCG
                                   _ ___
GAM33   DNASE1   5' GGGCCACAGAGCAGTCATGGC 19073       AA  GCCA
                                GCCATGA  GCT   TGGCCC
                                |||||||  |||   ||||||
                                CGGTACT  CGA   ACCGGG
                                    GA  GAC_
GAM33   HMOX1    3' GGGCCATGGCAATTTTTA    10944      C
                                TGAAAG TGCCATGGCCC
                                ||||||  ||||||||||
                                ATTTTT ACGGTACCGGG
                                   A
GAM33   HTR2C    3' CCATGAAAAGTTTTCAAGC   7869     CA      GC_
                                GC  TGAAAGCT   CATGG
                                ||  ||||||||   |||||
                                CG  ACTTTTGA   GTACC
                                 A_      AAA
GAM33   PPARGC1  3' GGGCCATTGCCTTCATGCCGT 26083    C     A  TGCC
                                ACG CATGAA GC   ATGGCCC
                                |||  ||||||  ||   |||||||
                                TGC GTACTT CG   TACCGGG
                                  C     C  T___
GAM33   RERE     3' GGCCCTGACCTTCATGGTGT  25017        AGCTGC  T
                                ACGCCATGAA     CA GGCC
                                ||||||||||     ||  ||||
                                TGTGGTACTT     GT CCGG
                                     CCA___  C
GAM33   SCML2    3' GCTTATAAGCTTTCATGAAGT 21428    GC       GCCAT
                                AC  CATGAAAGCT    GGC
                                ||  ||||||||||    |||
                                TG  GTACTTTCGA    TCG
                                 AA        ATAT_
GAM33   TBX3     3' GGGCCCGCCATGGCGT     33809       AAAGCT  CAT
                                ACGCCATG     GC  GGCCC
                                ||||||||     ||  |||||
                                TGCGGTAC     CG  CCGGG
                                   _______ C__
GAM33   ABLIM    3' GGCCATATCATTCATGGC    11324       AGC  CC
                                GCCATGAA   TG  ATGGCC
                                ||||||||   ||  ||||||
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                              CGGTACTT  AC  TACCGG
                                  ___  TA
GAM33  ABLIM   3' GGCCATATCATTCATGGC   22982       AGC  CC
                              GCCATGAA  TG  ATGGCC
                              ||||||||  ||  ||||||
                              CGGTACTT  AC  TACCGG
                                  ___  TA
GAM33  ABT1    3' GCCATGGCAGGTCATAGAGT  26301   GCC   AAG
                              AC  ATGA  CTGCCATGGC
                              ||  ||||  ||||||||||
                              TG  TACT  GACGGTACCG
                               AGA   G__
GAM33  CDC14B  3' GGACGACAGCCCTCATCGGCGT 54007     _   AA   CCA  G
                              ACGCC ATGA  GCTG  TG CC
                              ||||| ||||  ||||  || ||
                              TGCGG TACT  CGAC  GC GG
                                 C   CC   A__  A
GAM33  DKFZP434H0820 5' GGCCGGGCTCCATGGCG    64584       AAAGCT  A
                              CGCCATG    GCC TGGCC
                              |||||||    ||| |||||
                              GCGGTAC    CGG GCCGG
                                  CT____  _
GAM33  FLJ20034  3' GGCCATGGCCCCTCATGAAGT  34850   GC   AAGCT
                              AC  CATGA   GCCATGGCC
                              ||  |||||   |||||||||
                              TG  GTACT   CGGTACCGG
                               AA   CCC__
GAM33  FLJ20464  5' GCCCCGCTTTCATGCGT    35696    C      TGCCAT
                              ACGC ATGAAAGC    GGC
                              |||| ||||||||    |||
                              TGCG TACTTTCG    CCG
                                _      CC____
GAM33  KIAA0172  3' GGCTGAAGCTTTCACAGTG   65598    CA     GCCAT
                              CGC  TGAAAGCT   GGCC
                              |||  ||||||||   ||||
                              GTG  ACTTTCGA   TCGG
                                AC      AG___
GAM33  KIAA0318  3' GGACCTTTGCTTCTCATGGC  69530       _   TGCCAT  _
                              GCCATGA AAGC    GG CC
                              ||||||| ||||    || ||
                              CGGTACT TTCG    CC GG
                                  C   TTT___  A
GAM33  MGC12538  3' GGCCATGGACAGGTCCATG   52205    AAAG  _
                              CATG   CTG CCATGGCC
                              ||||   ||| ||||||||
                              GTAC   GAC GGTACCGG
                                CTG_  A
GAM33  MGC23280  3' GGCCAGGATGCTTGCCATGGC  59054      A_   TG  A
                              GCCATG  AAGC  CC TGGCC
                              ||||||  ||||  || |||||
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                                CGGTAC  TTCG  GG ACCGG
                                   CG    TA  _
GAM33   MGC2508   3'  GGGCCATGGCACTAGATGGC   44506      GAA  C
                                GCCAT   AG TGCCATGGCCC
                                |||||   || ||||||||||
                                CGGTA   TC ACGGTACCGGG
                                  GA_  _
GAM33   NICE-3    3'  TGTGTTGCAGCTTTCCTG    31886    T      __
                                CA GAAAGCTGC  CATG
                                || |||||||||  ||||
                                GT CTTTCGACG  GTGT
                                 C        TT
GAM33   PANX1     5'  GGCGCCGCGCAGCTTTCCCGAC 60804    CCAT       CA   _
          G                      CG    GAAAGCTGC  TGGC CC
                                ||    |||||||||  |||| ||
                                GC    CTTTCGACG  GCCG GG
                                 AGCC        C_   C
GAM33   PCDH20    3'  GGTTTGCAGCTTTCAT     43424          CAT
                                ATGAAAGCTGC   GGCC
                                ||||||||||   ||||
                                TACTTTCGACG   TTGG
                                      T__
GAM33   SARM      3'  GGACCAGGCAGCCCCCATGGC  31297       AAA     A  _
                                GCCATG   GCTGCC TGG CC
                                ||||||   |||||| ||| ||
                                CGGTAC   CGACGG ACC GG
                                   CCC     _  A
GAM33   LOC115219 3'  GGCCATGGAAGCCCATGG    73699       AAA   G
                                CCATG   GCT CCATGGCC
                                |||||   ||| ||||||||
                                GGTAC   CGA GGTACCGG
                                  C__   A
GAM33   LOC143920 5'  GCCATGGCGCTTCTCAGGGC   77114     A  _   T
                                GCC TGA AAGC GCCATGGC
                                ||| ||| |||| ||||||||
                                CGG ACT TTCG CGGTACCG
                                  G   C   _
GAM33   LOC146657 5'  GCCATGGCGCTTCCCACGGC   61079     A  A_   T
                                GCC TG  AAGC GCCATGGC
                                ||| ||  |||| ||||||||
                                CGG AC  TTCG CGGTACCG
                                  C  CC   _
GAM33   LOC147341 3'  GCCATGGCCATAGCGT      85120      C   AAAGCT
                                ACGC ATG     GCCATGGC
                                ||||  |||     ||||||||
                                TGCG TAC     CGGTACCG
                                  A  _______
GAM33   LOC149386 5'  GCCCCGCGACTCTCATGGC    85560        A  C   CAT
                                GCCATGA AG TGC   GGC
                                ||||||| || |||   |||
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                                CGGTACT TC GCG   CCG
                                    C  A   CC_
GAM33   LOC149657 3'  GGGCCATGGCCCAGCCCTGGC  85717      TGAAA  __
                                GCCA    GCT  GCCATGGCCC
                                ||||    |||  ||||||||||
                                CGGT    CGA  CGGTACCGGG
                                  CC___   CC
GAM33   LOC150397 3'  CCATGGCAGCCTTCAGGG    80657    A   A
                                CC TGAA GCTGCCATGG
                                || |||| ||||||||||
                                GG ACTT CGACGGTACC
                                 G   C
GAM33   LOC257185 5'  GGCCATGGGGGTCCGGCG    98021     ATGAAA   G
                                CGCC     GCT CCATGGCC
                                ||||     ||| ||||||||
                                GCGG     TGG GGTACCGG
                                  CC____   G
GAM33   LOC257319 3'  GCCTGTTACTTTCATGACGT   97473    C      CT  CAT
                                ACG CATGAAAG  GC   GGC
                                ||| ||||||||  ||   |||
                                TGC GTACTTTC  TG   CCG
                                  A       AT  T__
GAM33   LOC257408 3'  GGGCCATGCCTGCTTCATGC   97798    C    A  TGC
                                GC ATGAA GC   CATGGCCC
                                || ||||| ||   ||||||||
                                CG TACTT CG   GTACCGGG
                                 _    _ TCC
GAM34   FSTL1    3'  TTGAAAGAGGAACAGACCC    24008       CT   GC
                                GGGTCTGT  CTT  TTCAA
                                ||||||||  |||  |||||
                                CCCAGACA  GAG  AAGTT
                                    AG   A_
GAM34   MTMR6    5'  GGCAGACAGACCCGCGG     95199           CTT
                                CCGCGGGTCTGTCT   GCT
                                ||||||||||||||   |||
                                GGCGCCCAGACAGA   CGG
                                                 ___
GAM34   MYO3A    3'  GAAACAAGAGACCTGGG     60769    G     TGTC    C
                                CC CGGGTC    TCTTG TTC
                                || ||||||    ||||| |||
                                GG GTCCAG    AGAAC AAG
                                 _     _____     A
GAM34   SLC6A6   3'  TTGTACAAAAAGAAAACCCACG 13187     C   CTG   C  GCTT
          G                      CCG GGGT   TCT TT    CAA
                                ||| ||||   ||| ||    |||
                                GGC CCCA   AGA AA    GTT
                                  A   AA_   A  ACAT
GAM34   BANP     5'  AAGCAAGAAACTTGAGG     66797    G    CTGTC
                                CC CGGGT    TCTTGCTT
                                || |||||    ||||||||
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                                GG GTTCA    AGAACGAA
                                 A    A____
GAM34   GBA2     5'  TGAAGCAAGAGCTCCCCGG   71579    C   TCTGT
                                CCG GGG    CTCTTGCTTCA
                                ||| |||    ||||||||||
                                GGC CCC    GAGAACGAAGT
                                  _  TC___
GAM34   KIAA1318 5'  GAGTCAGACAGACCCG     67876         CTT
                                CGGGTCTGTCT   GCTT
                                ||||||||||   ||||
                                GCCCAGACAGA   TGAG
                                      C__
GAM34   KIAA1817 3'  TGAAGCAAGCGGACCC     68783       TCT
                                GGGTCTG   CTTGCTTCA
                                |||||||   |||||||||
                                CCCAGGC   GAACGAAGT

                                   ___
GAM34   MST4     3'  AAGCAAGATCATTTACCCAAGG 33741    GC    CT  C_
                                CC  GGGT  GT  TCTTGCTT
                                ||  ||||  ||  ||||||||
                                GG  CCCA  TA  AGAACGAA
                                 AA    TT  CT
GAM34   ZIC5     3'  GAGCCTGAGACAAACCCGTG   53614       C     TT
                                CGCGGGT TGTCTC  GCTT
                                ||||||| ||||||  ||||
                                GTGCCCA ACAGAG  CGAG
                                    A     TC
GAM34   LOC150174 3'  TGAAACACAGACCCAGG     80442    GC       CTCTT C
                                CC  GGGTCTGT    G TTCA
                                ||  ||||||||    | ||||
                                GG  CCCAGACA    C AAGT
                                 A_       _____ A
GAM34   LOC150213 3'  TGAAACACAGACCCAGG     75361    GC       CTCTT C
                                CC  GGGTCTGT    G TTCA
                                ||  ||||||||    | ||||
                                GG  CCCAGACA    C AAGT
                                 A_       _____ A
GAM34   LOC152762 5'  GAGAAGAAAACAGACCCAGG   81534    GC       C_   G
                                CC  GGGTCTGT  TCTT CTT
                                ||  ||||||||  |||| |||
                                GG  CCCAGACA  AGAA GAG
                                 A_       AA   _
GAM34   LOC220021 5'  GAAGCAAGTCACAACCCAGC   95022    _   C   CT
                                GC GGGT TGT  CTTGCTTC
                                || |||| |||  ||||||||
                                CG CCCA ACA  GAACGAAG
                                 A    _   CT
GAM34   LOC254835 3'  TTGAAGCAAGAGACAGACCC   98713
                                GGGTCTGTCTCTTGCTTCAA
                                ||||||||||||||||||||
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                                CCCAGACAGAGAACGAAGTT

GAM34   LOC257364 3'  GAAGCAGGTCCAAACCCAGG  96644    GC   C  TCT
                                CC  GGGT TG   CTTGCTTC
                                ||  |||| ||   ||||||||
                                GG  CCCA AC   GGACGAAG
                                 A_   A  CT_
GAM35   ASGR1    5'  CCCATTCTCCAAGCTTCA    9805        ATCA  AG
                                TGAAGCTT   GA  ATGGG
                                ||||||||   ||  |||||
                                ACTTCGAA   CT  TACCC
                                     C___  CT
GAM35   CDC23    3'  CCCATCTTAATTAAGCCTTAC  17408     A    TCAG
                                GTGA GCTTA   AAGATGGG
                                |||| |||||   ||||||||
                                CATT CGAAT   TTCTACCC
                                  C    TAA_
GAM35   LZTR1    5'  CCCATCTTGCTGCAACTTC   23166     CTTAT  _
                                GAAG    CAG AAGATGGG
                                ||||    ||| ||||||||
                                CTTC    GTC TTCTACCC
                                  AAC__   G
GAM35   NEURL    3'  CCCATCTTCTCGGGCTTCA   16128       ATC
                                TGAAGCTT   AGAAGATGGG
                                ||||||||   ||||||||||
                                ACTTCGGG   TCTTCTACCC
                                     C__
GAM35   PSMC3    5'  CCCATCTTCTGCCCGCTCCT   12515    T  A  TTAT
                                AG GA GC    CAGAAGATGGG
                                || || ||    ||||||||||
                                TC CT CG    GTCTTCTACCC
                                 _ _  CCC_
GAM35   STX1A    3'  CCCACCCTCCCTCGGCTTTACT 17208        TATCA  AGA
                                AGTGAAGCT    GA   TGGG
                                |||||||||    ||   ||||
                                TCATTTCGG    CT   ACCC
                                     CTCC_  CCC
GAM35   SYT5     3'  CCACCCTTAAGCTTCCT     13502    T      TC  AAGA
                                AG GAAGCTTA  AG    TGG
                                || ||||||||  ||    |||
                                TC CTTCGAAT  TC    ACC
                                 _       ___  CC__
GAM35   DKFZp434F142 3'  CCATCTTCTGCCTCAC     51032     A  TTATC
                                GTGA GC    AGAAGATGG
                                |||| ||    |||||||||
                                CACT CG    TCTTCTACC
                                  C  _____
GAM35   FLJ10737  3'  CCCATCCTCTGCGTTTCATT   37052        TTAT   A
                                AGTGAAGC   CAGA GATGGG
                                ||||||||   |||| ||||||
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                                TTACTTTG   GTCT CTACCC
                                    C___   C
GAM35   FLJ13449  3'  CTGTTGATAAGCCCCACT    44928     AA       A
                                AGTG  GCTTATCAG AG
                                ||||  |||||||||| ||
                                TCAC  CGAATAGTT TC
                                  CC       G
GAM35   G2        3'  CCCATCTTCCATTGTCCTCA   67240     A CT  TCA
                                TGA G  TA   GAAGATGGG
                                ||| |  ||   |||||||||
                                ACT C  GT   CTTCTACCC
                                  _ CT  TAC
GAM35   KIAA0285  5'  CCCACCCCTGGGCAGCTTCACT 29682         TA    AAGA
                                AGTGAAGCT  TCAG    TGGG
                                |||||||||  ||||    ||||
                                TCACTTCGA  GGTC    ACCC
                                     CG    CCC_
GAM35   SCYB10    3'  CCATCTTCCAAGGGTACT    9601      AAG   ATCA
                                AGTG   CTT    GAAGATGG
                                ||||   |||    ||||||||
                                TCAT   GAA    CTTCTACC
                                  GG_   C___
GAM35   LOC118978 5'  CCCATCTTCTGACTTTTCCT   76504    T    CTTA
                                AG GAAG    TCAGAAGATGGG
                                || ||||    ||||||||||||
                                TC CTTT    AGTCTTCTACCC
                                 _    TC__
GAM35   LOC128582 5'  CCCTGTGACAAGGCTTCAC    76290         A_   GAAGAT
                                GTGAAGCTT  TCA     GGG
                                |||||||||  |||     |||
                                CACTTCGGA  AGT     CCC
                                     AC   GT____
GAM35   LOC148930 3'  CCCATCTTCTCACTGCTCCCT  79841    T  A  TTATC
                                AG GA GC    AGAAGATGGG
                                || || ||    ||||||||||
                                TC CT CG    TCTTCTACCC
                                 C  _  TCAC_
GAM35   LOC158835 3'  CCCATCTTCTGATAACTGC    82878    __
                                GC  TTATCAGAAGATGGG
                                ||  ||||||||||||||
                                CG  AATAGTCTTCTACCC
                                 TC
GAM35   LOC203504 5'  CCACCTGGAGCTTCAC      92321         AT   AAGA
                                GTGAAGCTT  CAG    TGG
                                |||||||||  |||    |||
                                CACTTCGAG  GTC    ACC
                                     __   C___
GAM35   LOC254835 5'  CCCATCTTCTTGATGAGCTTCA 98708            _
            CT                    AGTGAAGCTTATCA GAAGATGGG
                                ||||||||||||| |||||||||
```

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                                TCACTTCGAGTAGT CTTCTACCC
                                        T
GAM36   GRIN2B   3'  CCCAGAGTGAACACTCTTGGTA 7730      G       ____   CGG
            GAA                   TTC TACCAAGAG    CAC   TGGG
                                |||  |||||||||    |||   ||||
                                AAG ATGGTTCTC    GTG   ACCC
                                  _       ACAA   AG_
GAM36   RGS3     3'  CCCACTGCCCCGGTACGAG    56313        AAGA   CCG
                                TTCGTACC    GCA   GTGGG
                                ||||||||    |||   |||||
                                GAGCATGG    CGT   CACCC
                                     CCC_   ___
GAM36   PRDM7    3'  CTGATGCTCCTGGCCGAA     54845      TA   A    C
                                TTCG  CCA GAGCA CGG
                                ||||  ||| ||||| |||
                                AAGC  GGT CTCGT GTC
                                  C_   C    A
GAM36   LOC158364 5'  CCCTTGCTGCTCCTGATGC    82754     C  A    C   T
                                GTA CA GAGCA CGG GGG
                                ||| ||  ||||| ||| |||
                                CGT GT CTCGT GTT CCC
                                  A  C    C   _
GAM37   ADAR     3'  GTCCCTTGATAACAGTGAC    32364        CAC    ACT
                                GTCACTGT   CAAG   GAC
                                ||||||||   ||||   |||
                                CAGTGACA   GTTC   CTG
                                     ATA    C__
GAM37   C1D      3'  GTCAGTCTTGCAAGTACCATT  22013      TC   GTCAC
                                AATG  ACT    CAAGACTGAC
                                ||||  |||    ||||||||||
                                TTAC  TGA    GTTCTGACTG
                                  CA   AC___
GAM37   EPB41    5'  CAGTCTTGATGAAGAGATCATT 16689      _  A  G   C
                                AATG TC CT TCA CAAGACTG
                                |||| ||  ||  ||| ||||||||
                                TTAC AG GA AGT GTTCTGAC
                                  T  A  _   A
GAM37   FPGS     3'  CAGAACTTCACAGTGACA     18264        CACC   A_
                                TGTCACTGT    AAG  CTG
                                |||||||||    |||  |||
                                ACAGTGACA    TTC  GAC
                                     C___    AA
GAM37   GRB10    3'  GTCAGTCTACCGTATAGTAACA 19198     C    C  CA_
                                TGT ACTGT AC   AGACTGAC
                                ||| |||||  ||   ||||||||
                                ACA TGATA TG   TCTGACTG
                                  A    _  CCA
GAM37   HHEX     3'  GTTTTGATAAAGTGACATT    12264        GTCAC
                                AATGTCACT    CAAGAC
                                |||||||||    ||||||
```

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                                TTACAGTGA    GTTTTG
                                     AATA_
GAM37   WWOX    3' CAGTGAGGATGACAGTGACA  33489         _ AAG
                                TGTCACTGTCA CC   ACTG
                                |||||||||||  ||   ||||
                                ACAGTGACAGT GG   TGAC
                                     A  AG_
GAM37   WWOX    3' CAGTGAGGATGACAGTGACA  33490         _ AAG
                                TGTCACTGTCA CC   ACTG
                                |||||||||||  ||   ||||
                                ACAGTGACAGT GG   TGAC
                                     A  AG_
GAM37   ADMP    5' CGGAGGTGACAGCGACG     59511     A      AAGA
                                TGTC CTGTCACC    CTG
                                |||| ||||||||    |||
                                GCAG GACAGTGG    GGC
                                  C       A___
GAM37   DHODH   3' TCAGTCTTGCAAGGACATT   9068       A  GTCAC
                                AATGTC CT    CAAGACTGA
                                ||||||  ||    |||||||||
                                TTACAG GA    GTTCTGACT
                                  _  AC___
GAM37   FLJ14327 3' GTCAGAGCCATAATAGTGACAT 46687          CACCAAGA
            T                    AATGTCACTGT       CTGAC
                                ||||||||||        |||||
                                TTACAGTGATA       GACTG
                                     ATACCGA_
GAM37   FLJ21839 5' GTCAGCCCTGACCAGTGGCATT 41837          _  CCAAGA
                                AATGTCACTG TCA     CTGAC
                                |||||||||| |||     |||||
                                TTACGGTGAC AGT     GACTG
                                     C   CCC___
GAM37   FLJ31762 3' CAGCCACTTTGGTGACAATGAC 58758     C        A___
                                GTCA TGTCACCAAG    CTG
                                |||| ||||||||||    |||
                                CAGT ACAGTGGTTT    GAC
                                  A        CACC
GAM37   ICB-1   3' TCAACCTTGGTGACAGCAGCG  17935     CA        AC
                                TGT  CTGTCACCAAG  TGA
                                |||  ||||||||||  |||
                                GCG  GACAGTGGTTC  ACT
                                  AC         CA
GAM37   KIAA0100 5' GTCAGTCTTAAGTTTCAGCAAC 28653     CA   TC  C_
            A                    TGT  CTG  AC  AAGACTGAC
                                |||  |||  ||  |||||||||
                                ACA  GAC  TG  TTCTGACTG
                                  AC   TT  AA
GAM37   KIAA0125 3' GTGGGTGGTGACAGTGAC    29576          AAG  G
                                GTCACTGTCACC   ACT AC
                                ||||||||||||   ||| ||
```

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                                CAGTGACAGTGG  TGG TG
                                    ___  G
GAM37  KIAA0266 5' TCAGGAATTTGAAGTGACATT 41643       G  CCAAGA
                                AATGTCACT TCA    CTGA
                                ||||||||| |||    ||||
                                TTACAGTGA AGT    GACT
                                   _  TTAAG_
GAM37  KIAA0408 3' TTTGAAAACAGTGACATT   28803        CAC
                                AATGTCACTGT  CAAG
                                ||||||||||  ||||
                                TTACAGTGACA  GTTT
                                     AAA
GAM37  KIAA1140 3' GTCAGGGTGGGGCAACAGTGGC 63443       CA__  AGA
          AT                  ATGTCACTGT   CCA  CTGAC
                              ||||||||||   |||  |||||
                              TACGGTGACA   GGT  GACTG
                                   ACGG  GG_
GAM37  KIAA1582 5' CAGCATTCCAACAGTGACAT  65986       CACC  GA
                                ATGTCACTGT   AA  CTG
                                ||||||||||   ||  |||
                                TACAGTGACA   TT  GAC
                                   ACC_  AC
GAM37  LSM1     3' GTCACTGAGTGAAAGTGACAT  27842       G   CA  AC
                                ATGTCACT TCAC  AG  TGAC
                                |||||||| ||||  ||  ||||
                                TACAGTGA AGTG  TC  ACTG
                                   A   AG  __
GAM37  SLC11A2  3' GTCAGTCTCAGATTTACAAGCA 7051      CACT__  ACCA
          TT                   AATGT    GTC   AGACTGAC
                               |||||    |||   ||||||||
                               TTACG    TAG   TCTGACTG
                                  AACATT  AC__
GAM37  SLC19A3  3' CAGCCTGGGCAACACAGTGACA 48239       CA__  A  A
                                TGTCACTGT   CC AG CTG
                                |||||||||   || || |||
                                ACAGTGACA   GG TC GAC
                                   CAAC  G  C
GAM37  LOC138389 3' GTCTGGGTGACAGCACAT   76743     CA      A
                                ATGT  CTGTCACC AGAC
                                ||||  |||||||| ||||
                                TACA  GACAGTGG TCTG
                                  C_      G
GAM37  LOC254635 3' GTGGGGCAGGGACAGTGACATT 96042          A  AAGA  G
                                AATGTCACTGTC CC   CT AC
                                |||||||||||| ||   || ||
                                TTACAGTGACAG GG   GG TG
                                      _ ACG_  G
GAM37  LOC255974 5' CAGCCTCAGCCACAGTGACAT  99341        CACCA  A
                                ATGTCACTGT    AG CTG
                                ||||||||||    || |||
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                                TACAGTGACA    TC GAC
                                     CCGAC  C
GAM37   LOC91145 3'  TCAGTCTGGCCAGAACA    65682    CA  TCA  A
                                TGT  CTG   CCA GACTGA
                                |||  |||   ||| ||||||
                                ACA  GAC   GGT CTGACT
                                  A_   C__   _
GAM38   ADAMTS8  5'  TGATTCCGCTTTTCCTGGAGA  23856    C       _  TTC
                                TC CCGGGAAAA CG   GTCA
                                || |||||||| ||   ||||
                                AG GGTCCTTTT GC   TAGT
                                 A        C  CT_
GAM38   EXT1     5'  TGAAGTTGCCTTCCCGGGG   5524          ___   G
                                CCCCGGGAA   AAC TTCG
                                |||||||||   ||| ||||
                                GGGGCCCTT   TTG AAGT
                                     CCG   _
GAM38   FXR2     3'  TGACAAGGTCCCCCTGGGGA  17961        AAA  G  C
                                TCCCCGGG   AC TT GTCA
                                ||||||||   || || ||||
                                AGGGGTCC   TG AA CAGT
                                     CCC  G  _
GAM38   HEPH     5'  TGACTCTGTTCCCCCGGGGG  29653        AA    TTC
                                TCCCCGGG  AACG   GTCA
                                ||||||||  ||||   ||||
                                GGGGGCCC  TTGT   CAGT
                                     CC    CT_
GAM38   KCNC4    5'  TGACGCTGCCTCCTCGGGA   18335     C   AAAC  T_
                                TCCC GGGA    GT  CGTCA
                                |||| ||||    ||  |||||
                                AGGG TCCT    CG  GCAGT
                                  C    C___  TC
GAM38   MNT      3'  TGAGTGGGCCCTGCCCGGGGA  40091        AAAAC    _
                                TCCCCGGG     GTTCG TCA
                                ||||||||     ||||| |||
                                AGGGGCCC     CGGGT AGT
                                     GTCC_    G
GAM38   NLGN2    3'  TGACCGCTTCCCCGGGGA    89537        A  A  TTC
                                TCCCCGGG AA CG   GTCA
                                ||||||| || ||   ||||
                                AGGGGCCC TT GC   CAGT
                                     C  C  ___
GAM38   PSMB9    3'  TGAACGTTTCCCTGGAGA    12512    C    A
                                TC CCGGG AAACGTTCG
                                || ||||| |||||||||
                                AG GGTCC TTTGCAAGT
                                 A    C
GAM38   RENT1    3'  TGACGGCTTTTTCCCGGGGG  12819          C  T
                                TCCCCGGGAAAA GT CGTCA
                                |||||||||||| || |||||
```

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                                GGGGGCCCTTTT CG GCAGT
                                      T  _
GAM38   SLC20A2   3'  TGACAAACATTTTCTTGG    23121        C   C
                                CCGGGAAAA GTT GTCA
                                ||||||||| ||| ||||
                                GGTTCTTTT CAA CAGT
                                     A   A
GAM38   WHSC1     3'  TGACATCGTTCCCTGGGGA   56702        AA    TTC
                                TCCCCGGG  AACG   GTCA
                                ||||||||  ||||   ||||
                                AGGGGTCC  TTGC   CAGT
                                    C_    TA_
GAM38   C11orf21  3'  TGACACCCACTCCTGGGGA   27110        AAAC  TC
                                TCCCCGGGA    GT  GTCA
                                |||||||||    ||  ||||
                                AGGGGTCCT    CA  CAGT
                                     CACC  __
GAM38   C20orf12  3'  GACTTGCCTTTCCCGGGG    36848        AC  TC
                                CCCCGGGAAA  GT  GTC
                                ||||||||||  ||  |||
                                GGGGCCCTTT  CG  CAG
                                     C_  TT
GAM38   DKFZp762K222 5'  TGAAGACTGTCTCCCGGGGA   71675        AA   T  G
                                TCCCCGGGA  ACG TC TCA
                                |||||||||  ||| || |||
                                AGGGGCCCT  TGT AG AGT
                                     C_  C  A
GAM38   FLJ00001  3'  TGACACCCCGGCCTCCCTGGGG 82718      _   AAA  TTC_
           A                    TCCCC GGGA   CG    GTCA
                                |||||  ||||   ||    ||||
                                AGGGG CCCT   GC    CAGT
                                   T    CCG  CCCA
GAM38   FLJ10719  3'  TGGCTTCGTTTTTCCAAGGA   63208     CC       TTC
                                TCC  GGGAAAACG   GTCA
                                |||  |||||||||   ||||
                                AGG  CCTTTTTGC   CGGT
                                  AA        TT_
GAM38   FLJ12700  3'  TGAGCGTTCCCACAGGGA    46662     C__    AA
                                TCCC   GGGA  ACGTTCG
                                ||||   ||||  |||||||
                                AGGG   CCCT  TGCGAGT
                                   ACA   __
GAM38   FLJ20464  5'  CGAGCTTTGTCCCCGGGGA   35695        AA_  C
                                TCCCCGGG   AA GTTCG
                                ||||||||   || |||||
                                AGGGGCCC   TT CGAGC
                                     CTG  T
GAM38   GNG11     5'  TGACAAGCGTCCCGGAGA    15943    C     AAA    C
                                TC CCGGGA   CGTT GTCA
                                || ||||||   |||| ||||
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                                AG GGCCCT   GCGA CAGT
                                 A     ___    A
GAM38   KIAA0882  3'  CGGGCGCCTTCCCGGGGG    83533          AA
                                TCCCCGGGAA  CGTTCG
                                ||||||||||  ||||||
                                GGGGGCCCTT  GCGGGC
                                      CC
GAM38   KIAA0931  3'  TGAGTGCTGTTTTCCAGGAGA  68021    C  G      _  TCG
                                TC CC GGAAAAC GT   TCA
                                || || ||||||| ||   |||
                                AG GG CCTTTTG CG   AGT
                                 A  A      T  TG_
GAM38   KIAA1280  5'  TGACGGTGTCCTCGGGGA     70291       _   AAACGT
                                TCCCCG GGA     TCGTCA
                                |||||| |||     ||||||
                                AGGGGC CCT     GGCAGT
                                    T   GT____
GAM38   KIAA1357  3'  TGAAAGTGCTTCCCGGGGA    72434          A_  G
                                TCCCCGGGAA  AC TTCG
                                ||||||||||  || ||||
                                AGGGGCCCTT  TG AAGT
                                      CG  A
GAM38   P66       3'  TGAGTATTTTTCCGGGGA     40744           CG
                                TCCCCGGGAAAA  TTCG
                                ||||||||||||  ||||
                                AGGGGCCTTTTT  GAGT
                                       AT
GAM38   RAI       5'  TGGGTGTCTTCCTGGGGA     22858          A   TT
                                TCCCCGGGAA ACG  CG
                                |||||||||| |||  ||
                                AGGGGTCCTT TGT  GT
                                      C   GG
GAM38   SHANK3    5'  GACGAGCGCCTCCTGGGGA    66106          AAA
                                TCCCCGGGA   CGTTCGTC
                                |||||||||   ||||||||
                                AGGGGTCCT   GCGAGCAG
                                      CC_
GAM38   LOC169611 3'  TGGGGGATTTTCCTGGG      83667          AC    G
                                CCCGGGAAA  GTTC TCA
                                |||||||||  |||| |||
                                GGGTCCTTT  TAGG GGT
                                      __    G
GAM38   LOC200269 3'  TGACAGCCATGTTTTCCCGGAG 90078    C          TC__
           A                     TC CCGGGAAAACGT    GTCA
                                || ||||||||||||    ||||
                                AG GGCCCTTTTGTA    CAGT
                                 A          CCGA
GAM38   LOC204823 5'  TGGACGTTTCCCAGAGGA     91060     CC_     A
                                TCC   GGGAAA CGTTCG
                                |||   |||||| ||||||
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                                AGG   CCCTTT GCAGGT
                                  AGA     _
GAM38   LOC221504 5'  TGACCGCGGCTTCCCGGG    94022        AA   TC
                                CCCGGGAA  CGT  GTCA
                                ||||||||  |||  ||||
                                GGGCCCTT  GCG  CAGT
                                    CG   C_
GAM38   LOC257079 5'  TGAGGATTCTTCCCGGGGA   97624         AACGT  G
                                TCCCCGGGAA    TC TCA
                                ||||||||||    || |||
                                AGGGGCCCTT    AG AGT
                                     CTT__  G
GAM38   LOC81537  5'  GGCCCGCCTTCCCGGGGG    48636         AA  TTC
                                TCCCCGGGAA  CG   GTC
                                ||||||||||  ||   |||
                                GGGGGCCCTT  GC   CGG
                                     CC  C__
GAM38   LOC83690  5'  TGGAGATTTTCCTGGGGA    49597          CG
                                TCCCCGGGAAAA  TTCG
                                ||||||||||||  ||||
                                AGGGGTCCTTTT  AGGT
                                      AG
GAM38   LOC90485  5'  GACAGCAGTTCCCGGAGG    63698    _     AAC   C
                                CC CCGGGAA   GTT GTC
                                || |||||||   ||| |||
                                GG GGCCCTT   CGA CAG
                                 A      GA_  _
GAM39   ARHA      3'  CTCTGCACTCCCACCTGA    71232    T_   A
                                TC  GTGG GAGTGCAGAG
                                ||  |||| ||||||||||
                                AG  CACC CTCACGTCTC
                                 TC   _
GAM39   ASGR2     5'  CTCCACACCTTTCACAGATC   56046     T      A   CA
                                GAT CTGTGGAG GTG  GAG
                                ||| ||||||| |||  |||
                                CTA GACACTTT CAC  CTC
                                  _      C   AC
GAM39   GZMM      3'  CTCGCTGTCTCCACAGGA     19213          GT  A
                                TTCTGTGGAGA  GC GAG
                                ||||||||||  || |||
                                AGGACACCTCT  CG CTC
                                      GT  _
GAM39   IFNAR2    3'  CTCTGCCACCTCTACAGAATC  7899           A  _
                                GATTCTGTGGAG GTG CAGAG
                                ||||||||||| ||| |||||
                                CTAAGACATCTC CAC GTCTC
                                      _  C
GAM39   KAL1      3'  CTCTGCATAGATACAAAAT    5835      C    GAGA
                                ATT TGTG    GTGCAGAG
                                ||| ||||    ||||||||
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                                TAA ACAT    TACGTCTC
                                  A    AGA_
GAM39   LIF      3'  CTGCACAGCATCACTGAATC   11303      T    AGA_
                                GATTC GTGG    GTGCAG
                                ||||| ||||    ||||||
                                CTAAG CACT    CACGTC
                                   T    ACGA
GAM39   MTMR1    5'  CTGGACAGTCCCACAGGATC   70724          A __  G
                                GATTCTGTGG GA  GT CAG
                                |||||||||| ||  || |||
                                CTAGGACACC CT  CA GTC
                                      _  GA  G
GAM39   PKIG     3'  CTCATGGAGCTCCACAGATC   23927     T       AGTG  _
                                GAT CTGTGGAG    CA GAG
                                ||| ||||||||    || |||
                                CTA GACACCTC    GT CTC
                                  _       GAG_  A
GAM39   PPP1R3C  3'  CTCTGCAGTGACAGAATT    19423        GGAGAG
                                GATTCTGT     TGCAGAG
                                ||||||||     |||||||
                                TTAAGACA     ACGTCTC
                                     GTG___
GAM39   PTPRH    3'  CTCTGCACCCCACCATC     12616     TCT    AGA
                                GAT   GTGG   GTGCAGAG
                                |||   ||||   ||||||||
                                CTA   CACC   CACGTCTC
                                  C__    C__
GAM39   RFX2     3'  CTCTGCACTCAACTGGAACC   7156    A   _  GGA
                                G TTCT GT   GAGTGCAGAG
                                | |||| ||   ||||||||||
                                C AAGG CA   CTCACGTCTC
                                 C    T  A__
GAM39   SHMT2    3'  CTCCTTATTCCCTACAGAATC  19435          A     CA
                                GATTCTGTGG GAGTG  GAG
                                |||||||||| |||||  |||
                                CTAAGACATC CTTAT  CTC
                                      C     TC
GAM39   STK4     3'  CTCTGTCGTCTCTCCACAG   21864          _  _
                                CTGTGGAGAG TG CAGAG
                                |||||||||| || |||||
                                GACACCTCTC GC GTCTC
                                      T  T
GAM39   TEM8     3'  CTCTAGCTTTCCACAAATC   50826      C        GC
                                GATT TGTGGAGAGT  AGAG
                                |||| ||||||||||  ||||
                                CTAA ACACCTTTCG  TCTC
                                  _        A_
GAM39   USH3A    3'  CTGCACTCTTATTGGATTC   54842    T   GTG
                                GA TCT   GAGAGTGCAG
                                || |||   ||||||||||
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                                CT AGG   TTCTCACGTC
                                 T   TTA
GAM39   ZNF219   5' CTGCACTTCCCAGAACC    33554   A    T   G
                                G TTCTG GGA AGTGCAG
                                | ||||| ||| |||||||
                                C AAGAC CCT TCACGTC
                                 C    _  _
GAM39   ASB13    3' CTGCGCTGTTCTACAGAA    45546         _
                                TTCTGTGGAG AGTGCAG
                                |||||||||| |||||||
                                AAGACATCTT TCGCGTC
                                      G
GAM39   Di-Ras2  3' CTCTGGAGTCACAGAATC    34611          AGAGTG
                                GATTCTGTGG     CAGAG
                                ||||||||||     |||||
                                CTAAGACACT     GTCTC
                                      GAG___
GAM39   DKFZP434N014 3' CTCTGCACCCCCAGCCTATC   61229     T__   T  AGA
                                GAT   CTG GG   GTGCAGAG
                                |||   ||| ||   ||||||||
                                CTA   GAC CC   CACGTCTC
                                  TCC   _  C__
GAM39   FLJ10432 3' CTCTGCACTCCATGATGAA   39351     T__    GA
                                TTC   GTGGA  GTGCAGAG
                                |||   |||||  ||||||||
                                AAG   TACCT  CACGTCTC
                                  TAG     __
GAM39   FLJ12505 3' CTCTGCACTTTACCCAGCATC  45714     T   T  _
                                GAT CTG GG AGAGTGCAGAG
                                ||| ||| || ||||||||||
                                CTA GAC CC TTTCACGTCTC
                                  C   _  A
GAM39   KIAA1854 3' CTCCGACCTCCCTACAGAATC  72205          A   TGCA
                                GATTCTGTGG GAG    GAG
                                |||||||||| |||    |||
                                CTAAGACATC CTC    CTC
                                      C   CAGC
GAM39   KIF13B   3' CTTTCTCTCCACAAAGTC    31562      C       TGC
                                GATT TGTGGAGAG   AG
                                |||| |||||||||   ||
                                CTGA ACACCTCTC   TC
                                   A        TT_
GAM39   KIF13B   3' CTTTCTCTCCACAAAGTC    31563      C       TGC
                                GATT TGTGGAGAG   AG
                                |||| |||||||||   ||
                                CTGA ACACCTCTC   TC
                                   A        TT_
GAM39   MAP      3' CTCTTCAGGTTCACAGAA    43367          GAG  C
                                TTCTGTGGA   TG AGAG
                                |||||||||   || ||||
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                                AAGACACTT   AC TCTC
                                     GG_  T
GAM39   PRKRI    5'  CTCTTCCCTCCACAGATC    21828     T      AGTGC
                                GAT CTGTGGAG    AGAG
                                ||| ||||||||    ||||
                                CTA GACACCTC    TCTC
                                  _      CCT__
GAM39   PRO0650  5'  CTGTGACGCTCCACAGAA    27071          A  _
                                TTCTGTGGAG GT GCAG
                                |||||||||| || ||||
                                AAGACACCTC CA TGTC
                                     G  G
GAM39   RASSF2   3'  CTCCACCTTCTCTCCACAGAAT 29096            TGCA__
                                ATTCTGTGGAGAG     GAG
                                ||||||||||||      |||
                                TAAGACACCTCTC     CTC
                                       TTCCAC
GAM39   TRIM26   3'  CTCTGCACTCTCTGGAAT    14347      GT
                                ATTCT  GGAGAGTGCAGAG
                                |||||  ||||||||||||||
                                TAAGG  TCTCTCACGTCTC
                                  __
GAM39   TTTY11   3'  CTGGACCCAGCAGAATC     50025       _  AGA  G
                                GATTCTG TGG   GT CAG
                                ||||||| |||   || |||
                                CTAAGAC ACC   CA GTC
                                    G   ___  G
GAM39   LOC143326 3'  CTCTGCCAACACAGGATC    77055         GAGAGT
                                GATTCTGTG     GCAGAG
                                |||||||||     ||||||
                                CTAGGACAC     CGTCTC
                                     AAC___
GAM39   LOC144058 5'  CTCTGAGGGCCACAGAATT    77181          AGAGTG
                                GATTCTGTGG     CAGAG
                                ||||||||||     |||||
                                TTAAGACACC     GTCTC
                                     GGGA__
GAM39   LOC146443 3'  CTCTTGGACCCCACAGAAT    78446         AGA  G  _
                                ATTCTGTGG   GT CA GAG
                                |||||||||   || || |||
                                TAAGACACC   CA GT CTC
                                     C__  G  T
GAM39   LOC146756 3'  CTCTGAGAAGCCTCCACAGAAT 84801           A  G___
          C                      GATTCTGTGGAG GT    CAGAG
                                ||||||||||||| ||    |||||
                                CTAAGACACCTC CG    GTCTC
                                       _ AAGA
GAM39   LOC165246 5'  CTCCCACTGCCCACAGAA    83365         AG   CA
                                TTCTGTGG  AGTG  GAG
                                ||||||||  ||||  |||
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                                AAGACACC  TCAC  CTC
                                    CG    C_
GAM39   LOC201304 3'  CTCTGCACTCCAGAA       89604       TGGA
                                TTCTG    GAGTGCAGAG
                                |||||    ||||||||||
                                AAGAC    CTCACGTCTC
                                  _____
GAM39   LOC202052 3'  CTCTGCAGGCATTCCACAGAGT 91898           A  __
          C                      GATTCTGTGGAG GT  GCAGAG
                                ||||||||||||  ||  ||||||
                                CTGAGACACCTT CG  CGTCTC
                                      A  GA
GAM39   LOC206426 3'  CTCCATCCTCTCCACAGCATC  91098     T        TGCA
                                GAT CTGTGGAGAG    GAG
                                ||| ||||||||||    |||
                                CTA GACACCTCTC    CTC
                                  C         CTAC
GAM39   LOC219920 5'  CTCCGCACTCTCCTGGGTC    94949       TGT        A
                                GATTC   GGAGAGTGC GAG
                                |||||   ||||||||| |||
                                CTGGG   CCTCTCACG CTC
                                   T__        C
GAM39   LOC221354 3'  CTCCAGAACCTCACACAGAATC 94012          _   A  GCA_
                                GATTCTGTG GAG GT    GAG
                                |||||||| ||| ||    |||
                                CTAAGACAC CTC CA    CTC
                                      A   _  AGAC
GAM39   LOC255423 5'  CTCTTACTGCCCACAGAA    99439         AG    C
                                TTCTGTGG  AGTG AGAG
                                ||||||||  |||| ||||
                                AAGACACC  TCAT TCTC
                                    CG    _
GAM39   LOC257464 5'  CTCTTGCTTTCCCCAAAATC   91242      C  T       C
                                GATT TG GGAGAGTG AGAG
                                |||| || |||||||| ||||
                                CTAA AC CCTTTCGT TCTC
                                  A  C       _
GAM39   LOC257494 3'  CTCTGCACTCTCTGGAAT    99632       GT
                                ATTCT  GGAGAGTGCAGAG
                                |||||  ||||||||||||||
                                TAAGG  TCTCTCACGTCTC
                                   __
GAM39   LOC92840  3'  CTCCCAGGCCTCCACAGAGTC  57246           A  GCA_
                                GATTCTGTGGAG GT    GAG
                                ||||||||||||  ||    |||
                                CTGAGACACCTC CG    CTC
                                      _  GACC
GAM40   ADCY8     5'  GCTCACAGCGCTGCGGCTCCT  8501       A  AT   CAA
                                AGGA CC  GGC   CTGTGAGC
                                ||||  ||  |||   ||||||||
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                                TCCT GG  TCG   GACACTCG
                                  C  CG   C__
GAM40   CIT     5'  GCTCACAGAGCTACAGCTCTCC 70304     ACCA__    CAA
                                GGA     TGGC   CTGTGAGC
                                |||     ||||   ||||||||
                                CCT     ATCG   GACACTCG
                                  CTCGAC   A__
GAM40   FAAH    5'  GCGGTCTCCGGCCATGGCCCC  97238    AA      A___
                                GG  CCATGGCC    ACTGT
                                ||  ||||||||    |||||
                                CC  GGTACCGG    TGGCG
                                 CC       CCTC
GAM40   GSTM3   5'  GCTCACAGTTTCCCTAGTCCT  68638     ACCAT  CC
                                AGGA    GG  AACTGTGAGC
                                ||||    ||  ||||||||||
                                TCCT    CC  TTGACACTCG
                                  GAT__  CT
GAM40   HMX1    3'  GCGGTCGGCCATGGCC     38947    AA      A
                                GG  CCATGGCC ACTGT
                                ||  |||||||| |||||
                                CC  GGTACCGG TGGCG
                                 __       C
GAM40   HSD11B2  3'  GCTCCGTGAGCCTTGGTTCCT  5771         T   CA  T T
                                AGGAACCA GGC  AC G GAGC
                                |||||||| |||  || | ||||
                                TCCTTGGT CCG  TG C CTCG
                                     T   AG  _ _
GAM40   HYAL1   5'  CTCCAGTGGCCATGCTCC    53703     AC      A   T
                                GGA  CATGGCCA CTG GAG
                                |||  |||||||| ||| |||
                                CCT  GTACCGGT GAC CTC
                                  C_       _   _
GAM40   NPTX2   3'  GCTGGAGTGGCCATGTCCCTT  94085      AAC       A  G G
                                AAGG   CATGGCCA CT T AGC
                                ||||   |||||||| || | |||
                                TTCC   GTACCGGT GA G TCG
                                  CT_       _  G _
GAM40   RFX2    3'  GCCCCACCAGACCATGGGTTCC 7158          _   CCAA   _  A_
           TT                    AAGGAACC ATGG    CTG TG  GC
                                |||||||| ||||    ||| ||  ||
                                TTCCTTGG TACC    GAC AC  CG
                                     G    A___    C  CC
GAM40   SMAP    5'  GCCCCACAGAGCCATGGTCC   22932     A      CAA     A_
                                GGA CCATGGC   CTGTG  GC
                                ||| |||||||   |||||  ||
                                CCT GGTACCG   GACAC  CG
                                  _      A__     CC
GAM40   SMURF1  3'  GCTCACAGCCCTGAGCTCTTT  94049       AC_  T   CAAC
                                AAGGA   CA GGC    TGTGAGC
                                |||||   || |||    |||||||
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                                TTTCT  GT CCG   ACACTCG
                                  CGA  C  ____
GAM40   SORCS2   3'  CAGTGCCCATGGTTCCT    40798         CCA
                                AGGAACCATGG  ACTG
                                ||||||||||  ||||
                                TCCTTGGTACC  TGAC
                                     CG_
GAM40   DC-TM4F2 3'  ACTGTTGGCCAGGGCTCCT   48895    A  A     T
                                AGGA CC TGGCCAAC GT
                                |||| || |||||||| ||
                                TCCT GG ACCGGTTG CA
                                  C  G      T
GAM40   DKFZp566H0824 5'  GCTCACAAACCCCATAGTTGCC 34488    _  C   CCAAC
            T                    AGG AAC ATGG    TGTGAGC
                                ||| ||| ||||    |||||||
                                TCC TTG TACC    ACACTCG
                                  G  A   CCAA_
GAM40   FLJ10292 3'  GCCCACAGTTGTTGGTTGTTCC 36432      C  GGC      A
            T                    AGGAAC AT   CAACTGTG GC
                                |||||| ||  |||||||| ||
                                TCCTTG TG   GTTGACAC CG
                                   T  GTT      C
GAM40   FLJ20085 3'  GCTCATGGTGCCACAGCCCCT  35009    AACCA   CA
                                AGG    TGGC  ACTGTGAGC
                                |||    ||||  |||||||||
                                TCC    ACCG  TGGTACTCG
                                  CCGAC   __
GAM40   FLJ22690 3'  GCTCACAGCCGACCTGTGGCCT 45575    AA    CCAA_
                                AGG  CCATGG    CTGTGAGC
                                |||  ||||||    ||||||||
                                TCC  GGTGTC    GACACTCG
                                  __     CAGCC
GAM40   FLJ32449 3'  GCATTTGGCCATGGTTCCTT   59378            C
                                AAGGAACCATGGCCAA TGT
                                |||||||||||||||| |||
                                TTCCTTGGTACCGGTT ACG
                                          T
GAM40   HPIP     3'  GCTCACAGCTGCCTTGGCCCC  40425    AA  T   CAA
                                GG  CCA GGC   CTGTGAGC
                                ||  ||| |||   ||||||||
                                CC  GGT CCG   GACACTCG
                                  CC   T   TC_
GAM40   ILF3     3'  GCTCACAGTCGAACTACAGCTC 25234    ACCA   CCA_
            C                    GGA   TGG   ACTGTGAGC
                                |||   |||   |||||||||
                                CCT   ATC   TGACACTCG
                                  CGAC   AAGC
GAM40   KIAA1190 3'  GCTCACAGAGCACCCCAGTTCC 71651      CAT  CCAA
            T                    AGGAAC   GG   CTGTGAGC
                                ||||||   ||   ||||||||
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                                TCCTTG  CC   GACACTCG
                                   ACC  ACGA
GAM40   MGC11266 3' GCTCACAGTGGTCAGGGCCC  44488   AA A    A
                                GG  CC TGGCCA CTGTGAGC
                                ||  || |||||| ||||||||
                                CC  GG ACTGGT GACACTCG
                                 CG  _    _
GAM40   MGC11352 5' ACTGTTGGCCAGGGCTCCT   65424    A A     T
                                AGGA CC TGGCCAAC GT
                                |||| || |||||||| ||
                                TCCT GG ACCGGTTG CA
                                  C  G      T
GAM40   MGC5590  3' CACAACTTTGGTTTCTT    44149        T  CCAAC
                                AAGGAACCA GG    TGTG
                                ||||||||| ||    ||||
                                TTCTTTGGT TC    ACAC
                                      T  A____
GAM40   MKP-7    3' GCTTCTCTTGGCCATGGTCCC 67015   A        CTGT
                                GG ACCATGGCCAA   GAGC
                                || ||||||||||   ||||
                                CC TGGTACCGGTT   TTCG
                                 C         CTC_
GAM40   MSP      3' GCTCAGGCAGGCCATGGCC   50245   AA      AA  G
                                GG  CCATGGCC  CT TGAGC
                                ||  ||||||||  || |||||
                                CC  GGTACCGG  GG ACTCG
                                 __       AC  _
GAM40   PGR1     3' CTCACAGTTGGAGTTCTCC   53905   A    CATGG
                                A GGAAC    CCAACTGTGAG
                                | |||||    ||||||||||
                                C TCTTG    GGTTGACACTC
                                 C    A____
GAM40   PTPRT    3' GCTTCGTGTTGGCCAAGACTCC 56502      ACCA       TGT
           TT                    AAGGA   TGGCCAAC   GAGC
                                |||||   ||||||||  ||||
                                TTCCT   ACCGGTTG   TTCG
                                   CAGA       TGC
GAM40   TRF4-2   3' CTCAAACAAGCCATGGTTCCTT 42611          CAACTG
                                AAGGAACCATGGC     TGAG
                                ||||||||||||     ||||
                                TTCCTTGGTACCG     ACTC
                                      AACAA_
GAM40   LOC122786 3' GCCTTTGGCCATGATTCT    74622      C       CT
                                GGAA CATGGCCAA  GT
                                |||| |||||||||  ||
                                TCTT GTACCGGTT  CG
                                  A       TC
GAM40   LOC138428 3' TAGTGGCCATGGCTGCCT    75862     AA_       A
                                AGG   CCATGGCCA CTG
                                |||   ||||||||| |||
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                                TCC   GGTACCGGT GAT
                                  GTC       _
GAM40   LOC145581 3'  GCTCCATTAGACCATGGTTC   77794         CCAAC  T
                                GAACCATGG     TG GAGC
                                |||||||||     || ||||
                                CTTGGTACC     AC CTCG
                                     AGATT  _
GAM40   LOC146268 5'  GCTCACAGTCGGCTTGCTGCCT 78342     AAC  T    A
                                AGG   CA GGCC ACTGTGAGC
                                |||   || |||| |||||||||
                                TCC   GT TCGG TGACACTCG
                                  GTC  _    C
GAM40   LOC147299 3'  GCTGTGAGCCGCCATGGTCCC  78981    A       CAA  GTG
                                GG ACCATGGC   CT   AGC
                                || ||||||||   ||   |||
                                CC TGGTACCG   GA   TCG
                                 C       CC_  GTG
GAM40   LOC159199 3'  GCTCACAGCTGGCGGCCCT    83062     AA  ATG    A
                                AGG  CC   GCCA CTGTGAGC
                                |||  ||   |||| ||||||||
                                TCC  GG   CGGT GACACTCG
                                  C_  ____    C
GAM40   LOC200982 5'  AGTTGGCCATGGCTCTTT     91807       A
                                AAGGA CCATGGCCAACT
                                ||||| ||||||||||||
                                TTTCT GGTACCGGTTGA
                                   C
GAM40   LOC221495 5'  CCACAGCTTGGTTCCT       95493         T   CAAC    A
                                AGGAACCA GGC    TGTG G
                                |||||||| |||    |||| |
                                TCCTTGGT TCG    ACAC C
                                     _   _____    C
GAM40   LOC253842 3'  GCTCATAGAAGCCTGGTCCCT  99238     A    T   CAA
                                AGG ACCA GGC   CTGTGAGC
                                ||| |||| |||   ||||||||
                                TCC TGGT CCG   GATACTCG
                                  C    _   AA_
GAM40   LOC254778 3'  GCCCTGTGTTGGCCAAGGTTCC 97831       A       TGTGA
                                GGAACC TGGCCAAC     GC
                                |||||| ||||||||     ||
                                CCTTGG ACCGGTTG     CG
                                    A       TGTCC
GAM40   LOC255231 3'  CTCACAGTTAGCCAGCTGACC  97119    AACCA    C
                                GG     TGGC AACTGTGAG
                                ||     |||| |||||||||
                                CC     ACCG TTGACACTC
                                 AGTCG    A
GAM40   LOC257358 5'  GCTCGTGAAGAGCATGGTTCCT 98900          G CAACTG
          T                      AAGGAACCATG C      TGAGC
                                ||||||||||| |      |||||
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                                TTCCTTGGTAC G     GCTCG
                                      _ AGAAGT
GAM40   LOC90190  3'  CGCCCACAGAGCAATTGGCCAT 62422     AC       _____    A ___
            GCCTCC                  GGA  CATGGCCAA    CTGTG GC   G
                                |||  |||||||||    |||||  ||   |
                                CCT  GTACCGGTT    GACAC CG   C
                                  CC        AACGA    C ___
GAM40   LOC90495  3'  GCTCACAGTCAACTGCTTTCTT 63737       CCAT   CA___
            T                    AAGGAA    GGC    ACTGTGAGC
                                ||||||   |||    |||||||||
                                TTTCTT    TCG    TGACACTCG
                                    ____  TCAAC
GAM40   LOC90750  3'  GCTCACAGCCCTGCCCTGCCCC 64630    AAC  T   CAA_
            C                    GG   CA GGC    CTGTGAGC
                                ||   || |||    ||||||||
                                CC   GT CCG    GACACTCG
                                 CCC  C   TCCC
GAM41   ADAT1     3'  CCAGCAAAGAATGAAGGC    24914     __        C
                                GTC  CATTCTTTGC GG
                                |||  ||||||||||  ||
                                CGG  GTAAGAAACG CC
                                  AA        A
GAM41   M17S2     5'  CCGGTAGCGGACGGTCCTT    20910          ATTCT
                                AAGGACCGTCC    TTGCCGG
                                ||||||||||    |||||||
                                TTCCTGGCAGG    GATGGCC
                                      C_____
GAM41   ST14      5'  CCGGCAGGGACGACGCCT    42042     AC    CAT
                                AGG  CGTC   TCTTTGCCGG
                                |||  ||||   ||||||||||
                                TCC  GCAG   AGGGACGGCC
                                  __    C__
GAM41   HTGN29    5'  GCCAACTGTGTGGCGGTCC    39885        _   TC  T
                                GGACCGTC CAT  TT GC
                                |||||||| |||  || ||
                                CCTGGCGG GTG  AA CG
                                     T   TC  C
GAM41   PMAIP1    3'  GCAAGAATGGAAGACCCTT    41211      ACCG       T
                                AAGG    TCCATTCTT GC
                                ||||    ||||||||| ||
                                TTCC    AGGTAAGAA CG
                                  CAGA       _
GAM41   LOC144278 3'  GCCAGCAAAGACTGCTCGATGG 77274          ___  T      C
            TCCT                    AGGACCGTC   CA TCTTTGC GGC
                                |||||||||   || ||||||| |||
                                TCCTGGTAG   GT AGAAACG CCG
                                     CTC  C      A
GAM41   LOC147976 3'  CCGGTGAATGAAGACCCT    79287     ACC   CA   _  TG
                                AGG   GTC  TTC TT  CCGG
                                |||   |||  ||| ||  ||||
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                                TCC   CAG  AAG AA  GGCC
                                 ___   __   T  GT
GAM41   LOC254263 5'  GCCGGCAGCGGACGCGCC    96367    AC     ATTCT
                                GG  CGTCC    TTGCCGGC
                                ||  |||||    ||||||||
                                CC  GCAGG    GACGGCCG
                                 GC    C____
GAM42   ARHGAP6   3'  AAACAAGCTGAACCTACTA    26430     _   CA
                                TAGT GGT  AGCTTGTTT
                                |||| |||  |||||||||
                                ATCA CCA  TCGAACAAA
                                  T   AG
GAM42   CLASP1    5'  AAGTTCTCAACCACTGTGCTA  65889          CA__
                                TAGCATAGTGGT    AGCTT
                                ||||||||||||    |||||
                                ATCGTGTCACCA    TTGAA
                                       ACTC
GAM42   GIF       3'  AAACATGGAGAACCACTATGT  18912          CAAG  _
                                GCATAGTGGT    CT TGTTT
                                ||||||||||    || |||||
                                TGTATCACCA    GG ACAAA
                                      AGA_  T
GAM42   FLJ20396  3'  AAACAAGCTTTGACCACT     35579          _
                                AGTGGTCAA GCTTGTTT
                                |||||||| ||||||||
                                TCACCAGTT CGAACAAA
                                      T
GAM42   GNB4      3'  AAACAAGCTTTCAGTAAACTA  41560     CA  G   TC
                                TAG  TA TGG  AAGCTTGTTT
                                |||  || |||  ||||||||||
                                ATC  AT ACT  TTCGAACAAA
                                  AA  G   __
GAM42   MUC17     3'  GAAACAAGCCCTGTACTTAC   95927     _  _  A_
                                GTG GT CA  GCTTGTTTC
                                ||| || ||  |||||||||
                                CAT CA GT  CGAACAAAG
                                  T  T  CC
GAM42   LOC129642 3'  GAAACAAGCCCTCCCATGC    57924      AGT  TCAA
                                GCAT   GG    GCTTGTTTC
                                ||||   ||    |||||||||
                                CGTA   CC    CGAACAAAG
                                  C__  TCC_
GAM42   LOC146485 5'  AAACAAGCTTATGGATGCT    60490      AGTG  C
                                AGCAT    GT AAGCTTGTTT
                                |||||    || ||||||||||
                                TCGTA    TA TTCGAACAAA
                                   GG__  _
GAM42   LOC148266 3'  GAAACAAACTTGACAAAGC    79509     ATAGTG     C
                                GC     GTCAAG TTGTTTC
                                ||     |||||| |||||||
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                                CG     CAGTTC AACAAAG
                                 AAA___     A
GAM43   DTNA    3'  TCCACATCAAAAGAAGAA    9143        TTG   C
                                TTCTTCTTT   TGG TGTGGA
                                |||||||||   ||| ||||||
                                AAGAAGAAA   ACT ACACCT
                                   ___   _
GAM43   DTNA    3'  TCCACATCAAAAGAAGAA    9144        TTG   C
                                TTCTTCTTT   TGG TGTGGA
                                |||||||||   ||| ||||||
                                AAGAAGAAA   ACT ACACCT
                                   ___   _
GAM43   SCN3A   5'  TCCACAGAGAAAGAAAGAA   23619       GTGG
                                TTCTTTTT    CTGTGGA
                                ||||||||    |||||||
                                AAGAAAGA    GACACCT
                                     AAGA
GAM43   TTC3    3'  CCCACCACAAAAAGAGAA    13883     T       C  T
                                TTCT CTTTTTGTGG TG GG
                                |||| |||||||||| || ||
                                AAGA GAAAAACACC AC CC
                                  _       _ _
GAM43   C1orf16 3'  CGCAGTGCAACAAAAAGAA   29912         _ _
                                TTCTTTTTGT G GCTGTG
                                |||||||||| | ||||||
                                AAGAAAAACA C TGACGC
                                     A G
GAM43   C8orf17 5'  CCACAGCCCTAGAAAGAA    39992        T
                                TTCTTTTTG GGCTGTGG
                                ||||||||| ||||||||
                                AAGAAAGAT CCGACACC
                                     C
GAM43   CSNK1G1 3'  TCCAAACTAAAAAGAAGAA   42131          TGGCTG
                                TTCTTCTTTTTG     TGGA
                                ||||||||||||     ||||
                                AAGAAGAAAAAT     ACCT
                                     CAA___
GAM43   DIO2    3'  CACAAGGCCAGAAAAAGAAGAA 26548         G    __
                                TTCTTCTTTTT TGGCT  GTG
                                |||||||||| |||||  |||
                                AAGAAGAAAAA ACCGG  CAC
                                     G     AA
GAM43   FLJ13031 5' TCCACAGCTCAGAGAAGAA   45515       TT  T
                                TTCTTCTT  TG GGCTGTGGA
                                ||||||||  || |||||||||
                                AAGAAGAG  AC TCGACACCT
                                   __  _
GAM43   HSPC195 3'  GTCCCTAGCATAAAAAGAA   81868         G   T
                                TTCTTTTTGTG CTG GGAC
                                |||||||||| ||| ||||
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                                AAGAAAAATAC GAT CCTG
                                      _  C
GAM43   KIAA0420  3'  GTCTCAAAAAAAGAAGAA    64094          G  GCTGT
                                TTCTTCTTTTT TG    GGAC
                                |||||||||| ||    ||||
                                AAGAAGAAAAA AC    TCTG
                                      A _____
GAM43   KIAA1726  3'  TGTTTAACCACAAAAAAAAG  67836    C       CTG
                                CTT TTTTTGTGG  TGGACA
                                ||| |||||||||  ||||||
                                GAA AAAAACACC  ATTTGT
                                  A       A__
GAM43   PDZD2     5'  GTCCACAACCAAGAGGAA    81732       TTTTG  C
                                TTCTTCT    TGG TGTGGAC
                                |||||||    ||| |||||||
                                AAGGAGA    ACC ACACCTG
                                     _____  A
GAM43   SIAT8C    5'  GTCCACAACCACACAGA     32449    TTT    C
                                TCT   TGTGG TGTGGAC
                                |||   ||||| |||||||
                                AGA   ACACC ACACCTG
                                  C__    A
GAM43   LOC144563 5'  CAGAGGCCACAAGAAGAA    77393          G_
                                TTCTTTTTGTGGCT  TG
                                ||||||||||||||  ||
                                AAGAAGAACACCGG  AC
                                      AG
GAM43   LOC147837 3'  TGTCACACACACAAAAA     79213       GC   _
                                TTTTTGTG  TGTG GACA
                                ||||||||  |||| ||||
                                AAAAACAC  ACAC CTGT
                                     __   A
GAM43   LOC149863 3'  CCTCTGTCTCAAAAAAAAGAA  85877      C    T   TGT
                                TTCTT TTTTTG GGC   GG
                                ||||| |||||| |||   ||
                                AAGAA AAAAAC CTG   CC
                                   A     T   TCT
GAM43   LOC151632 5'  CAGAGGCCACAAGAAGAA    86640          G_
                                TTCTTTTTGTGGCT  TG
                                ||||||||||||||  ||
                                AAGAAGAACACCGG  AC
                                      AG
GAM43   LOC157247 5'  CACCTCTACAAAAAAAGAA   82287      C       CT
                                TTCTT TTTTTGTGG  GTG
                                ||||| |||||||||  |||
                                AAGAA AAAAACATC  CAC
                                   _       TC
GAM43   LOC200904 5'  CAGAGGCCACAAGAAGAA    91774          G_
                                TTCTTTTTGTGGCT  TG
                                ||||||||||||||  ||
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                                AAGAAGAACACCGG  AC
                                      AG
GAM43   LOC201853 5'  CCCAGACACCAAAAGAAGAA  90507        T  G  T
                                TTCTTCTTTT GTG CTG GG
                                |||||||||| ||| ||| ||
                                AAGAAGAAAA CAC GAC CC
                                     C   A  _
GAM43   LOC203078 3'  CACCACTACAAAAAAAAAAGAA 90787     C__      CT
                                TTCTT  TTTTTGTGG  GTG
                                |||||  |||||||||  |||
                                AAGAA  AAAAACATC  CAC
                                   AAA       AC
GAM43   LOC219919 5'  CAGAGGCCACAAGAAGAA   94920          G_
                                TTCTTTTTGTGGCT  TG
                                ||||||||||||||  ||
                                AAGAAGAACACCGG  AC
                                      AG
GAM43   LOC221795 5'  CAGAGGCCACAAGAAGAA   94070          G_
                                TTCTTTTTGTGGCT  TG
                                ||||||||||||||  ||
                                AAGAAGAACACCGG  AC
                                      AG
GAM43   LOC256515 5'  CAGAGGCCACAAGAAGAA   98206          G_
                                TTCTTTTTGTGGCT  TG
                                ||||||||||||||  ||
                                AAGAAGAACACCGG  AC
                                      AG
GAM43   LOC257354 3'  GTCTCAAAAAAAGAAGAA   96796         G  GCTGT
                                TTCTTCTTTTT TG    GGAC
                                |||||||||| ||    ||||
                                AAGAAGAAAAA AC    TCTG
                                      A  _____
GAM43   LOC90110  5'  CATCTCACAAAAAAGAGAA  62176     TC       CT
                                TTCT  TTTTTGTGG  GTG
                                ||||  |||||||||  |||
                                AAGA  AAAAACACT  TAC
                                   GA       C_
GAM44   B29     3'  ATGTTAAAAACAAAGCA    50037     GT  GC
                                TGCTT  TG  TTTAACAT
                                |||||  ||  ||||||||
                                ACGAA  AC  AAATTGTA
                                   __  AA
GAM44   DLEU2   3'  ATGTTAATGTTCAACAAGCA  21206        _ T
                                TGCTTGTTGG C TTAACAT
                                |||||||||| | |||||||
                                ACGAACAACT G AATTGTA
                                      T T
GAM44   EDN2    5'  GGACGCTGGCAACAGGCAC   10483         G  TTAACA
                                GTGCTTGTTG CT     TCC
                                |||||||||| ||     |||
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                                CACGGACAAC GG     AGG
                                     _ TCGC__
GAM44   FCMD    3' ATGTAGGCACAATAAGCAC   23027        _   TA
                                GTGCTTGTTG GCTT  ACAT
                                |||||||||| ||||  ||||
                                CACGAATAAC CGGA  TGTA
                                     A   __
GAM44   FGFR2   3' GATATTAATGTTAACAAG    43635        T   C
                                CTTGTTGGC TTAA ATC
                                ||||||||| |||| |||
                                GAACAATTG AATT TAG
                                     T   A
GAM44   FGFR2   3' GATATTAATGTTAACAAG    43644        T   C
                                CTTGTTGGC TTAA ATC
                                ||||||||| |||| |||
                                GAACAATTG AATT TAG
                                     T   A
GAM44   FGFR2   3' GATATTAATGTTAACAAG    43765        T   C
                                CTTGTTGGC TTAA ATC
                                ||||||||| |||| |||
                                GAACAATTG AATT TAG
                                     T   A
GAM44   FGFR2   3' GATATTAATGTTAACAAG    43768        T   C
                                CTTGTTGGC TTAA ATC
                                ||||||||| |||| |||
                                GAACAATTG AATT TAG
                                     T   A
GAM44   FGFR2   3' GATATTAATGTTAACAAG    43776        T   C
                                CTTGTTGGC TTAA ATC
                                ||||||||| |||| |||
                                GAACAATTG AATT TAG
                                     T   A
GAM44   FGFR2   3' GATATTAATGTTAACAAG    5563         T   C
                                CTTGTTGGC TTAA ATC
                                ||||||||| |||| |||
                                GAACAATTG AATT TAG
                                     T   A
GAM44   MECP2   3' GGATGTTTTTCTTACCGACAAG 18408          CTTT___
           CAC                   GTGCTTGTTGG      AACATCC
                                ||||||||||       |||||||
                                CACGAACAGCC      TTGTAGG
                                     ATTCTTT
GAM44   PAFAH1B1 3' GATGTTAGAGACAAACAC    6475      C   TGG
                                GTG TTGT   CTTTAACATC
                                ||| ||||   ||||||||||
                                CAC AACA   GAGATTGTAG
                                  A   ___
GAM44   PNUTL2  3' GATGCAGTCAACAACAC      55380     C       TTAA
                                GTG TTGTTGGCT    CATC
                                ||| |||||||||    ||||
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                                CAC AACAACTGA   GTAG
                                  _       C___
GAM44   SOCS4    3' GGATGTTAAAAGTAACAA    55992       GC
                                TTGTTG  TTTAACATCC
                                ||||||  ||||||||||
                                AACAAT  AAATTGTAGG
                                   GA
GAM44   TDG      3' GATATTAAAGCTGGGTAC    13646       GTT       C
                                GTGCTT   GGCTTTAA ATC
                                ||||||   |||||||| |||
                                CATGGG   TCGAAATT TAG
                                   ___       A
GAM44   APOARGC  3' GGATACTTCCAAACAAGCAC  44678         _ CTTTAAC
                                GTGCTTGTT GG      ATCC
                                |||||||||  ||      ||||
                                CACGAACAA CC      TAGG
                                      A  TTCA___
GAM44   C3AR1    3' ATGTGGAGCAGCCAACAAGCA  15764          TTA__
                                TGCTTGTTGGCT    ACAT
                                ||||||||||||    ||||
                                ACGAACAACCGA    TGTA
                                      CGAGG
GAM44   CENTA2   3' ATGTTAGAGAAACAGAGCAC  37864      _   GG
                                GTGCT TGTT  CTTTAACAT
                                |||||  ||||  |||||||||
                                CACGA ACAA  GAGATTGTA
                                   G    A_
GAM44   DKFZP564G092 5' GATGTTAAAAGTAGGAAGCAT  32161       G   GC
                                GTGCTT TTG  TTTAACATC
                                ||||||  |||  |||||||||
                                TACGAA GAT  AAATTGTAG
                                   G   GA
GAM44   DNAJB6   3' ATGTTAAACTATAACAAGCAC  19717         GC_
                                GTGCTTGTTG   TTTAACAT
                                ||||||||||   ||||||||
                                CACGAACAAT   AAATTGTA
                                      ATC
GAM44   FLJ10517 3' TTAAAGCCAATCATGAGTAC  36784       ___
                                GTGCTT   GTTGGCTTTAA
                                ||||||   ||||||||||||
                                CATGAG   TAACCGAAATT
                                   TAC
GAM44   FLJ11000 3' GGACATTAAAAGAGCGAGCAC  37527         GGC    CA
                                GTGCTTGTT   TTTAA  TCC
                                |||||||||   |||||  |||
                                CACGAGCGA   AAATT  AGG
                                      GA_    AC
GAM44   FLJ14084 3' GATGGACTCCAACAAGCAT   41593          CTTTAA
                                GTGCTTGTTGG     CATC
                                ||||||||||      ||||
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                                TACGAACAACC     GTAG
                                      TCAG__
GAM44   FLJ20619 3' ATGTTGTCAACAGACAC     35889     CT      TTT
                                GTG  TGTTGGC   AACAT
                                |||  |||||||   |||||
                                CAC  ACAACTG   TTGTA
                                  AG      ___
GAM44   FLJ22659 3' GGATGCTACTGTCAACAAG   46829         TT  A
                                CTTGTTGGC  TA CATCC
                                |||||||||  || |||||
                                GAACAACTG  AT GTAGG
                                     TC  C
GAM44   KCNH7    3' ATGTTAAAACTGCCAGCA    53837        ___
                                TGTTGGC   TTTAACAT
                                |||||||   ||||||||
                                ACGACCG   AAATTGTA
                                    TCA
GAM44   KIAA0276 3' ATGTTAATGGCAAGCA      71520         GCT
                                TGCTTGTTG   TTAACAT
                                |||||||||   |||||||
                                ACGAACGGT   AATTGTA
                                      ___
GAM44   KIAA1393 3' GGATGCTAAAGGAGATAAAGC 72573      _  GG    A
                                GCTT GTT  CTTTA CATCC
                                |||| |||  ||||| |||||
                                CGAA TAG  GAAAT GTAGG
                                  A  AG    C
GAM44   KIAA1644 3' ATGTTAAAGTTAAGCA      86216       TTG
                                TGCTTG   GCTTTAACAT
                                ||||||   ||||||||||
                                ACGAAT   TGAAATTGTA
                                     ___
GAM44   MGC14161 5' GATGCCAAAGGCCAGTAC    52910      TGTT     AA_
                                GTGCT    GGCTTT   CATC
                                |||||    ||||||   ||||
                                CATGA    CCGGAA   GTAG
                                   _____     ACC
GAM44   PP1044   3' ATGTTAAAACGCAGCGC     41674      T  T GC
                                GTGCT GT G  TTTAACAT
                                ||||| || |  ||||||||
                                CGCGA CG C  AAATTGTA
                                  _ _ A_
GAM44   STAF65(gamma) 3'  ATGTTAAACTGCATAACAGGCA 30062          _  __
            C                    GTGCTTGTTG GC  TTTAACAT
                                 ||||||||||  ||  ||||||||
                                 CACGGACAAT CG  AAATTGTA
                                       A  TC
GAM44   ZNF313   3' GATGCCGAGAAGCCAGCAAACA 38564     C         AA__
            C                    GTG TTGTTGGCTTT    CATC
                                 |||  ||||||||||    ||||
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                                CAC AACGACCGAAG   GTAG
                                  A         AGCC
GAM44   LOC123775 5'  GATGTTAAAAACTTTAAGCA  76142       TTGGC
                                TGCTTG    TTTAACATC
                                ||||||    |||||||||
                                ACGAAT    AAATTGTAG
                                   TTCAA
GAM44   LOC143828 3'  ATGTTAAACTATAACAAGCAC  73185         GC_
                                GTGCTTGTTG   TTTAACAT
                                ||||||||||   ||||||||
                                CACGAACAAT   AAATTGTA
                                      ATC
GAM44   LOC145317 3'  GGATGGTCGCCAAGCAAGCAC  84281         _   TTTAA
                                GTGCTTGTT GGC    CATCC
                                ||||||||| |||    |||||
                                CACGAACGA CCG    GTAGG
                                      A   CTG__
GAM44   LOC150418 3'  GGATGTTAAAGCCAACAAGCAC 66116
                                GTGCTTGTTGGCTTTAACATCC
                                ||||||||||||||||||||||
                                CACGAACAACCGAAATTGTAGG

GAM44   LOC151196 5'  GATATTTCAACAAGCA      86452         CTTT  C
                                TGCTTGTTGG    AA ATC
                                ||||||||||    || |||
                                ACGAACAACT    TT TAG
                                      _____  A
GAM44   LOC154089 3'  GGATGTTAATATCTCAAACA   81943    C   TT  CT
                                TG TTG  GG  TTAACATCC
                                || |||  ||  |||||||||
                                AC AAC  CT  AATTGTAGG
                                 A   T_  AT
GAM44   LOC199957 3'  GGATGTTAAAGCCAACAAGCAC 89890
                                GTGCTTGTTGGCTTTAACATCC
                                ||||||||||||||||||||||
                                CACGAACAACCGAAATTGTAGG

GAM44   LOC200273 5'  GGACACCAAAAGCCAGCAGC   71335     T       AACA_
                                GCT GTTGGCTTT     TCC
                                ||| |||||||||     |||
                                CGA CGACCGAAA     AGG
                                  _        ACCAC
GAM44   LOC206463 3'  GGATGTTAAAGCCAACAAGCAC 91104
                                GTGCTTGTTGGCTTTAACATCC
                                ||||||||||||||||||||||
                                CACGAACAACCGAAATTGTAGG

GAM44   LOC222484 5'  ATGTGGCCAACAGCAC      95999       T      TTA
                                GTGCT GTTGGCT   ACAT
                                ||||| |||||||   ||||
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                                CACGA CAACCGG   TGTA
                                  _     ____
GAM44   LOC255030 5'  GGATGCCAAAGCCAGAGGG   99085    TG       AA
                                CT  TTGGCTTT  CATCC
                                ||  ||||||||  |||||
                                GG  GACCGAAA  GTAGG
                                 GA       CC
GAM44   LOC92578  5'  TGTAATACCAACAAGCAC    70398          CT   A
                                GTGCTTGTTGG  TTA CA
                                ||||||||||  ||| ||
                                CACGAACAACC  AAT GT
                                      AT   _
GAM45   IRS1      3'  CCATAGATGGTTCTCAATTGTA 19874      C         TGAAC
                                TACA ATTGAGAACC    ATGG
                                |||| ||||||||||    ||||
                                ATGT TAACTCTTGG    TACC
                                  _        TAGA_
GAM45   SERPINF1  3'  CCTGTAAGGTTTCAATG     12038        A   GA   T
                                CATTGAGA CCT  ACA GG
                                |||||||| |||  ||| ||
                                GTAACTTT GGA  TGT CC
                                    _   A_   _
GAM45   HSA243396 3'  CCATGTTCAGCAATGTCAATG  37844       GAAC_
                                CATTGA    CTGAACATGG
                                ||||||    ||||||||||
                                GTAACT    GACTTGTACC
                                   GTAAC
GAM45   KIAA1387  3'  CAGGAATTTTCAATATGTA    71444      C       __
                                TACA ATTGAGAA  CCTG
                                |||| ||||||||  ||||
                                ATGT TAACTTTT  GGAC
                                  A       AA
GAM45   MGC16063  3'  TTCAAATTCCAATGTGTA     54930         A   CC
                                TACACATTG GAA  TGAA
                                |||||||| |||  ||||
                                ATGTGTAAC CTT  ACTT
                                      _   AA
GAM45   SMCR8     3'  CCATGCTCAGGTTTGACTATGT 59253      TGA_      A
                                ACAT    GAACCTGA CATGG
                                ||||    |||||||| |||||
                                TGTA    TTTGGACT GTACC
                                  TCAG       C
GAM45   UPLC1     3'  CCATGCTAGGCCCCAATGT    35227       AGAA    AA
                                ACATTG    CCTG  CATGG
                                ||||||    ||||  |||||
                                TGTAAC    GGAT  GTACC
                                   CCC_    C_
GAM45   ZNF334    3'  CCATAAGTCAACCCTCAATGT  36637        AACC   AC_
                                ACATTGAG    TGA   ATGG
                                ||||||||    |||   ||||
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                                TGTAACTC   ACT  TACC
                                    CCA_  GAA
GAM45   LOC145082 3'  TATGGAATGCCCTTAATGTGTA 84196          AACCTGAA
                                TACACATTGAG      CATG
                                ||||||||||      ||||
                                ATGTGTAATTC      GTAT
                                     CCGTAAG_
GAM45   LOC157723 3'  CCAAGTAAGGTTCTCAAATGT  82465     _     GA  A
                                ACATT GAGAACCT  AC TGG
                                ||||| ||||||||  || |||
                                TGTAA CTCTTGGA  TG ACC
                                   A      A_  A
GAM45   LOC219988 5'  CCATGTTCGGCCCCCAATG   93262     AGAAC
                                CATTG    CTGAACATGG
                                |||||    ||||||||||
                                GTAAC    GGCTTGTACC
                                   CCCC_
GAM46   CHAD    3'  GGAAGGCTGAGCCTCTC    8855      TA  CTGC
                                GAGAG  CTC   GTCTTCC
                                |||||  |||   |||||||
                                CTCTC  GAG   CGGAAGG
                                   C_  T___
GAM46   DSG1    5'  AGGAAGGCAGAAACACCTC   10449    A  ACTC   GT
                                GAG GT   CTGC  CTTCCT
                                ||| ||   ||||  ||||||
                                CTC CA   GACG  GAAGGA
                                  _ CAAA   __
GAM46   MID1    3'  AAGATGTAGAAGTCCCTC    6351     T_  C
                                GAG  ACT CTGCGTCTT
                                |||  ||| |||||||||
                                CTC  TGA GATGTAGAA
                                  CC   A
GAM46   OTOF    3'  AGGAAGACTCCTGAAACCCTC  17828    A  AC  CTGC
                                GAG GT  TC   GTCTTCCT
                                ||| ||  ||   ||||||||
                                CTC CA  AG   CAGAAGGA
                                  C  A_  TCCT
GAM46   RNMT    3'  AGGACATCCAAGGGTACTCTC  15047       T  GCGTCT
                                GAGAGTAC CCT     TCCT
                                |||||||| |||     ||||
                                CTCTCATG GGA     AGGA
                                     _  ACCTAC
GAM46   SCN3A   5'  AGGAAGACACGTTATACCCT  23612   A  CTCC  C
                                AG GTA   TG GTCTTCCT
                                || |||   || ||||||||
                                TC CAT   GC CAGAAGGA
                                 C  ATT_  A
GAM46   SFRS7   3'  GGAAGGCGATACTCTC     60148      CTCCTG
                                GAGAGTA    CGTCTTCC
                                |||||||    ||||||||
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                                CTCTCAT     GCGGAAGG
                                   A_____
GAM46   SLC13A4  5' AAGACGAAGGAGGACTCTC   25857       A    G
                                GAGAGT CTCCT CGTCTT
                                |||||| ||||| ||||||
                                CTCTCA GAGGA GCAGAA
                                   G    A
GAM46   SSX2     3' AGGAAGATGACGAGTAACTC  97962     _   CTG
                                GAGT ACTC  CGTCTTCCT
                                |||| ||||  |||||||||
                                CTCA TGAG  GTAGAAGGA
                                  A   CA_
GAM46   TGFBR2   3' AAGATTCAAGAGTATTCTC   13725         C  C
                                GAGAGTACTC TG GTCTT
                                |||||||||| || |||||
                                CTCTTATGAG AC TAGAA
                                      A  T
GAM46   TNFRSF11A 3' AGGAAGACCACCCGGCATTCTC 15187       A  CC_  C
                                GAGAGT CT   TG GTCTTCCT
                                |||||| ||   || ||||||||
                                CTCTTA GG   AC CAGAAGGA
                                   C  CCC  _
GAM46   AP3M2    3' AGGAAGACCCGTACTCTC    23299        TCCT C
                                GAGAGTAC    G GTCTTCCT
                                ||||||||    | ||||||||
                                CTCTCATG    C CAGAAGGA
                                     _____ C
GAM46   CALN1    3' AGGAAGACACAGAATTCTTTC  49658      TACTC   C
                                GAGAG     CTG GTCTTCCT
                                |||||     ||| ||||||||
                                CTTTC     GAC CAGAAGGA
                                   TTAA_   A
GAM46   DAMS     5' AGGAAATTCAAGTACTCT    42084        CC  C  C
                                AGAGTACT  TG GT TTCCT
                                ||||||||  || || |||||
                                TCTCATGA  AC TA AAGGA
                                     __  T  _
GAM46   DKFZP727M111 5' AGGCCAGGAGGACCCTC     32055     A  A     C
                                GAG GT CTCCTG GTCT
                                ||| || |||||| ||||
                                CTC CA GAGGAC CGGA
                                  C  G     _
GAM46   FLJ14486 5' AGGAAGGTTCAAGTCTCTC   52434       T   CC  CG
                                GAGAG ACT  TG  TCTTCCT
                                ||||| |||  ||  |||||||
                                CTCTC TGA  AC  GGAAGGA
                                   _  __  TT
GAM46   FUSIP1   3' AGGAAGACAGCCATAGTCTC  22780     T   CCT  _
                                GAG ACT   GC GTCTTCCT
                                ||| |||   || ||||||||
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                                CTC TGA   CG CAGAAGGA
                                  _   TAC  A
GAM46   HIC      3'  GAAGATTGAGTACTCT      68048          CTGC
                                AGAGTACTC    GTCTTC
                                |||||||||    ||||||
                                TCTCATGAG    TAGAAG
                                     T___
GAM46   IL22R    3'  AGGAAATGCAGGGAAACTC    41467      AC       C
                                GAGT  TCCTGCGT TTCCT
                                ||||  |||||||| |||||
                                CTCA  GGGACGTA AAGGA
                                  AA       _
GAM46   KIAA0472 3'  AGGAGGGGTAAGTACTCTC    72334         CC   G
                                GAGAGTACT  TGC TCTTCCT
                                |||||||||  ||| |||||||
                                CTCTCATGA  ATG GGGAGGA
                                     __   _
GAM46   KIAA1229 3'  AGGATGTAAAAGTTCTCTC    62750       T   CC
                                GAGAG ACT  TGCGTCTT
                                ||||| |||  ||||||||
                                CTCTC TGA  ATGTAGGA
                                   T   AA
GAM46   LAK-4P   3'  AGGAAGACAGTTTCGCCTCTC  24394       TACTCCT  _
                                GAGAG      GC GTCTTCCT
                                |||||      || ||||||||
                                CTCTC      TG CAGAAGGA
                                   CGCTT__  A
GAM46   MRPS35   3'  AGGTCCTCAGGAGTATTCTC   41819           CGTCTT
                                GAGAGTACTCCTG     CCT
                                ||||||||||||      |||
                                CTCTTATGAGGAC     GGA
                                       TCCT__
GAM46   OBTP     5'  AGGATCTGCAAGGAGGACCCTC 34663     A  A    _   TCT
                                GAG GT CTCCT GCG   TCCT
                                ||| || ||||| |||   ||||
                                CTC CA GAGGA CGT   AGGA
                                  C  G    A   CT_
GAM46   RI58     3'  AGATCAGGAATACTCTT     25774        C    C
                                GAGAGTA TCCTG GTCT
                                ||||||| ||||| ||||
                                TTCTCAT AGGAC TAGA
                                   A    _
GAM46   SMBP     3'  AAGACAGAAGTGTACTCTC    72620        TC  GC_
                                GAGAGTAC  CT   GTCTT
                                ||||||||  ||   |||||
                                CTCTCATG  GA   CAGAA
                                     T_  AGA
GAM46   SNTG1    5'  AGGACTCTGAGGAGTACTCTT  39099           G  TCT
                                GAGAGTACTCCT CG   TCCT
                                ||||||||||| ||   ||||
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                                TTCTCATGAGGA GT   AGGA
                                      _ CTC
GAM46   SNX11    3' AGGACCAGGAGTATCTC     26169      G      C
                                GAGA TACTCCTG GTCTT
                                |||| |||||||| |||||
                                CTCT ATGAGGAC CAGGA
                                  _       _
GAM46   TTY7     3' AGGAAGACACAGGTAGCT    50015     ACT    C
                                AGT   CCTG GTCTTCCT
                                |||   |||| ||||||||
                                TCG   GGAC CAGAAGGA
                                  AT_    A
GAM46   LOC123872 5' GGAAAGAGGGTACTCTC     74710          _ GCGTC
                                GAGAGTACTC CT     TTCC
                                |||||||||| ||     ||||
                                CTCTCATGGG GA     AAGG
                                      A ______
GAM46   LOC138389 3' AGGAAGACTTGCAAGTCTCTC 76725      T   CC   __
                                GAGAG ACT  TGC  GTCTTCCT
                                ||||| |||  |||  ||||||||
                                CTCTC TGA  ACG  CAGAAGGA
                                   _  __   TT
GAM46   LOC143943 3' AGGAAGATCAGCAGCCTCTC   83911      TA  C   C
                                GAGAG  CT CTG GTCTTCCT
                                |||||  || ||| ||||||||
                                CTCTC  GA GAC TAGAAGGA
                                   C_  C   _
GAM46   LOC145009 5' AAGAAACAAAGGAGTACTTTC  60965           GCG__
                                GAGAGTACTCCT     TCTT
                                ||||||||||||     ||||
                                CTTTCATGAGGA     AGAA
                                      AACAA
GAM46   LOC147976 5' AGGAAGACTGGGGTACCCTC   79285     A      TGC
                                GAG GTACTCC   GTCTTCCT
                                ||| |||||||   ||||||||
                                CTC CATGGGG   CAGAAGGA
                                  C      T__
GAM46   LOC151512 3' AGGAAGACAATGCTTGTACCTC 86611     A   TCCT  ___
                                GAG GTAC    GC   GTCTTCCT
                                ||| ||||    ||   ||||||||
                                CTC CATG    CG   CAGAAGGA
                                  _    TT__  TAA
GAM46   LOC158801 3' GAAAACACAAGAAGTATTCT   88255        _ C  C  C
                                AGAGTACT C TG GT TTC
                                |||||||| | || || |||
                                TCTTATGA G AC CA AAG
                                     A A  A  A
GAM46   LOC206426 3' GAAGCGAGGTGCACTCTC    91099       ACT   G  T
                                GAGAGT   CCT CG CTTC
                                ||||||   ||| || ||||
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                                CTCTCA   GGA GC GAAG
                                   CGT   _ _
GAM46   LOC254337 5'  GGAAAGGGGAGTATCTC     98012      G      GCGTC
                                GAGA TACTCCT     TTCC
                                |||| |||||||     ||||
                                CTCT ATGAGGG     AAGG
                                  _      GA___
GAM46   LOC256790 5'  AGTGCAGGAGTGCCCTC     96489     A         T
                                GAG GTACTCCTGCG CT
                                ||| |||||||||| ||
                                CTC CGTGAGGACGT GA
                                  C         _
GAM46   LOC256946 3'  AGGAAGACAGCCATAGTCTC   96182     T   CCT  _
                                GAG ACT   GC GTCTTCCT
                                ||| |||   || ||||||||
                                CTC TGA   CG CAGAAGGA
                                  _   TAC  A
GAM46   LOC257396 5'  GAAATGTAGGAGCATCTC     98922      GTA       C
                                GAGA   CTCCTGCGT TTC
                                ||||   ||||||||| |||
                                CTCT   GAGGATGTA AAG
                                   AC_       _
GAM46   LOC257408 3'  AGGGCACCAGGAGTACCTC    97797     A       C  CT
                                GAG GTACTCCTG GT  TCCT
                                ||| |||||||| ||  ||||
                                CTC CATGAGGAC CA  GGGA
                                  _       _ C_
GAM46   LOC257453 3'  AGGAAGATGACGAGTAACTC   82927      _    CTG
                                GAGT ACTC   CGTCTTCCT
                                |||| ||||   |||||||||
                                CTCA TGAG   GTAGAAGGA
                                   A   CA_
GAM46   LOC51066  3'  AGGAAGATGGCCGACACTCTC  32500       AC  CTG
                                GAGAGT  TC   CGTCTTCCT
                                ||||||  ||   |||||||||
                                CTCTCA  AG   GTAGAAGGA
                                   C_  CCG
GAM47   HRH1      3'  CTCAAACATGTTTAGAGTGGA  7819       A    TGG
                                TCCA TCTGA   GCATGTTTGAG
                                |||| |||||   ||||||||||
                                AGGT AGATT   TGTACAAACTC
                                   G    ___
GAM47   TRIM37    3'  CTCAAATTTGTCATCAG     31625        G  T
                                CTGATGG CA GTTTGAG
                                ||||||| || |||||||
                                GACTACT GT TAAACTC
                                    _ T
GAM47   HTMP10    3'  CTCAAAAAAGCCATCAGATCTG 53758    CA        G ATG
            A                    TC  ATCTGATGG C   TTTGAG
                                ||  |||||||| |   ||||||
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                                AG  TAGACTACC G   AAACTC
                                 TC        _ AAA
GAM47   PAK2     5'  CTCAAATATCACCAAACTAGA  67140      A__   GC
                                TCTG   TGG  ATGTTTGAG
                                ||||   |||  |||||||||
                                AGAT   ACC  TATAAACTC
                                  CAA   AC
GAM47   SEMA6A   3'  CTCGAGTACCCACCAGA     40818      A    CA
                                TCTG TGGG  TGTTTGAG
                                |||| ||||  ||||||||
                                AGAC ACCC  ATGAGCTC
                                  C   __
GAM47   TTY7     3'  TCAAACATGCAGGCTGGA     50019      AT  GATGG
                                TCCA  CT    GCATGTTTGA
                                ||||  ||    ||||||||||
                                AGGT  GA    CGTACAAACT
                                  CG  _____
GAM47   LOC144766 3'  CTCAAACATGAGAAGACTGGG  77481      A   GATGGG
                                TCCA TCT     CATGTTTGAG
                                |||| |||     ||||||||||
                                GGGT AGA     GTACAAACTC
                                  C   AGA___
GAM47   LOC201685 5'  TAAACACCCATCAGATGGA    91845      A       CA
                                TCCA TCTGATGGG  TGTTTG
                                |||| |||||||||  ||||||
                                AGGT AGACTACCC  ACAAAT
                                  _       __
GAM47   LOC221596 5'  CTCAAACAAAACTCAGATT    93623       TG GCA
                                AATCTGA  G   TGTTTGAG
                                |||||||  |   ||||||||
                                TTAGACT  C   ACAAACTC
                                   __ AAA
GAM47   LOC93622  3'  CTCTGCAGACCATCAGAT     57729        GCA   TT
                                ATCTGATGG   TGT  GAG
                                |||||||||   |||  |||
                                TAGACTACC   ACG  CTC
                                     AG_   T_
GAM48   ATRN     3'  CGATCCCCTGAGCTAACCCGGA 58445          GA____  A_   ___
           GGAA                   TTCCTCCGGGT     AG  GATC   G
                                ||||||||||      ||  ||||   |
                                AAGGAGGCCCA     TC  CTAG   C
                                     ATCGAG  CC   ___
GAM48   CTSH     3'  ATCCTGCCCTGGAGGAA     16526          TGA  A
                                TTCCTCCGGG   AG GAT
                                ||||||||||   || |||
                                AAGGAGGTCC   TC CTA
                                     CG_  _
GAM48   EHF      3'  GATTTGTACTCAGAGGAA    25124       C    AAGA
                                TTCCTC GGGTG    GATC
                                ||||||  |||||   ||||
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                                AAGGAG CTCAT    TTAG
                                   A    GT__
GAM48   HPS1    3'  GATCTCTTCCTTGCAGGGA   5763       C   T
                                TTCCT CGGG GAAGAGATC
                                ||||| |||| |||||||||
                                AGGGA GTTC CTTCTCTAG
                                   C   _
GAM48   WEE1    5'  GATCCCCCAGCACCGGAGGAG  14109         _  GAAGA
                                TTCCTCCGG GT    GATC
                                ||||||||| ||    ||||
                                GAGGAGGCC CG    CTAG
                                      A  ACCCC
GAM48   BTN2A1  3'  GATCTCTTCCTGTCAGAGGA   55301      C  GT_
                                TCCTC GG   GAAGAGATC
                                ||||| ||   |||||||||
                                AGGAG CT   CTTCTCTAG
                                   A  GTC
GAM48   CG018   5'  ATCCTGACTTCCTGGAGGAA   54484         TGA__  A
                                TTCCTCCGGG    AG GAT
                                ||||||||||    || |||
                                AAGGAGGTCC    TC CTA
                                      TTCAG  _
GAM48   DKFZP434L1435 5'  GATCTCCCATCTCCCGGAGGAA 93789          T  A__
                                TTCCTCCGGG GA   GAGATC
                                |||||||||| ||   ||||||
                                AAGGAGGCCC CT   CTCTAG
                                      T  ACC
GAM48   DKFZP434P0721 3'  ATCTCTTCTTCAAGAAGAA   64457     C  CG  T
                                TTC TC  GG GAAGAGAT
                                ||| ||  || ||||||||
                                AAG AG  CT CTTCTCTA
                                  A  AA  T
GAM48   GABARAPL1 3'  GATCTCTTACCTTTGGAA    49418      TCC     A
                                TTCC   GGGTGA GAGATC
                                ||||   |||||| ||||||
                                AAGG   TCCATT CTCTAG
                                   TT_     _
GAM48   GABARAPL3 3'  GATCTCTTATCTTTGGAA    51782      TCC     A
                                TTCC   GGGTGA GAGATC
                                ||||   |||||| ||||||
                                AAGG   TCTATT CTCTAG
                                   TT_     _
GAM48   JM5     3'  GATCCCTAACCTGGAGGAA   23958          GA  A
                                TTCCTCCGGGT  AG GATC
                                ||||||||||  || ||||
                                AAGGAGGTCCA  TC CTAG
                                      A_  C
GAM48   KIAA0390  3'  GATCCCTTCACCTGTGGA    28871     TC        A
                                TCC  CGGGTGAAG GATC
                                |||  ||||||||| ||||
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                                AGG  GTCCACTTC CTAG
                                  T_       C
GAM48   KIAA1280  5'  GATCTCTTTCTGGAAGAA    70279    C    GT
                                TTC TCCGG  GAAGAGATC
                                ||| |||||  |||||||||
                                AAG AGGTC  TTTCTCTAG
                                  A    __
GAM48   ORCTL3    3'  GATCTCCTCAATCTGGAG    16192       _  A
                                CTCCGGGT GA GAGATC
                                |||||||| || ||||||
                                GAGGTCTA CT CTCTAG
                                     A  C
GAM48   SERHL     3'  ATCTCCAGCCAGCTGGAGGAA  97349        G  AA__
                                TTCCTCCGG TG    GAGAT
                                ||||||||| ||    |||||
                                AAGGAGGTC AC    CTCTA
                                      G  CGAC
GAM48   LOC132203 5'  ATCTCTCCACTTGGAAGGA   75541     _     A
                                TCCT CCGGGTG AGAGAT
                                |||| ||||||| ||||||
                                AGGA GGTTCAC TCTCTA
                                  A      C
GAM48   LOC136306 3'  GATCTCTTCCTTGAGGAA    75769      C   T
                                TTCCTC GGG GAAGAGATC
                                |||||| ||| |||||||||
                                AAGGAG TTC CTTCTCTAG
                                       _  _
GAM48   LOC147136 5'  GATCCCATCCGGAAGAA     78863    C      AAGA
                                TTC TCCGGGTG    GATC
                                ||| ||||||||    ||||
                                AAG AGGCCTAC    CTAG
                                  A       C___
GAM48   LOC152464 3'  GATCCCTAACCTGGAGGAA   60648         GA  A
                                TTCCTCCGGGT  AG GATC
                                ||||||||||  || ||||
                                AAGGAGGTCCA  TC CTAG
                                       A_  C
GAM48   LOC154089 3'  GATCTTTTTCCAAAGGAA    81942      CCG  T
                                TTCCT   GG GAAGAGATC
                                |||||   || |||||||||
                                AAGGA   CC TTTTTCTAG
                                   AA_  _
GAM48   LOC196559 5'  GATCTCTTGCACTGGTAGAA  91211    CT   _  G
                                TTC  CCGG GT AAGAGATC
                                |||  |||| || ||||||||
                                AAG  GGTC CG TTCTCTAG
                                  AT    A  _
GAM48   LOC199957 5'  TCTCATCATCCGGATGAA    89891    C       A
                                TTC TCCGGGTGA GAGA
                                ||| ||||||||| ||||
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                                AAG AGGCCTACT CTCT
                                  T       A
GAM48   LOC204275 3'  GATCTCTGGCAGTGGAGGAA  91006       G_  GA
                                TTCCTCCG  GT  AGAGATC
                                ||||||||  ||  |||||||
                                AAGGAGGT  CG  TCTCTAG
                                    GA  G_
GAM48   LOC253782 3'  GATCTCTTAGTAGGGGGAA   97401       GGGTG
                                TTCCTCC    AAGAGATC
                                |||||||    ||||||||
                                AAGGGGG    TTCTCTAG
                                   ATGA_
GAM48   LOC254268 3'  GATCATGCCTGGAAGAA    97144    C      AAGA
                                TTC TCCGGGTG   GATC
                                ||| ||||||||   ||||
                                AAG AGGTCCGT   CTAG
                                  A       A___
GAM48   LOC256446 5'  GATCTCTTCACGGAGTGAA   98999    _   GG
                                TTC CTCC  GTGAAGAGATC
                                ||| ||||  ||||||||||
                                AAG GAGG  CACTTCTCTAG
                                  T   __
GAM48   LOC256715 3'  ATCCCAGGTCAACCCGGGGAA  99091    T    _  AGA__
                                TTCC CCGGGT GA    GAT
                                |||| |||||| ||    |||
                                AAGG GGCCCA CT    CTA
                                  _     A  GGACC
GAM48   LOC90843  3'  GATCTCTTAGCCAGAGGAA   64876      CG   G
                                TTCCTC  GGT AAGAGATC
                                ||||||  ||| ||||||||
                                AAGGAG  CCG TTCTCTAG
                                   A_   A
GAM49   COL19A1   3'  CAGACCAAAGAGTTCACA    10261    T   C     C
                                TGT GAGC TTTTTGG CTG
                                ||| |||| ||||||| |||
                                ACA CTTG AGAAACC GAC
                                  _   _      A
GAM49   RRM2B    3'  CAAAAACTTAACATTTA     68431         CC
                                TAAATGTTGAG  TTTTTG
                                ||||||||||  ||||||
                                ATTTACAATTC  AAAAAC
                                            __
GAM49   TCF2     3'  CAGGCTGGAGCCCAGCATT   22402       A  CTT  TG
                                AATGTTG GC   TT  GCCTG
                                ||||||| ||   ||  |||||
                                TTACGAC CG   AG  CGGAC
                                   C  ___  GT
GAM49   BY55     3'  AGACAGACCTCAACATT     60061        CCTT   GC
                                AATGTTGAG    TTTG  CT
                                |||||||||    ||||  ||
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                                TTACAACTC   AGAC  GA
                                     C___   A_
GAM49   C8orf2   3'  CAAGTCAGGCTGAACATT    24145      G    T_
                                AATGTT AGCCT  TTTG
                                |||||| |||||  ||||
                                TTACAA TCGGA  GAAC
                                   G    CT
GAM49   FLJ13409 3'  CAGGCTTCAACTTAACATTTA 45194          CCTTTTT
                                TAAATGTTGAG      GGCCTG
                                ||||||||||       ||||||
                                ATTTACAATTC      TCGGAC
                                      AACT___
GAM49   FLJ22774 3'  CTAAAAAGGCTGAACATTTA   64471        G
                                TAAATGTT AGCCTTTTTGG
                                |||||||| ||||||||||
                                ATTTACAA TCGGAAAAATC
                                     G
GAM49   HSOBRGRP 3'  CAGACCAAGAGCCTCAACATTT 34462         C    T  C
                                AAATGTTGAG CTTTT GG CTG
                                |||||||||| ||||| || |||
                                TTTACAACTC GAGAA CC GAC
                                      C    _  A
GAM49   KIAA0435 3'  GCTAGAACTCAGCATT      29661         CCT
                                AATGTTGAG   TTTTGGC
                                |||||||||   |||||||
                                TTACGACTC   AAGATCG
                                     ___
GAM49   MGC10940 3'  CAAAAAGTAAAAAAAGCTCAAC 51183        _________
            A                    TGTTGAGC       CTTTTTG
                                |||||||||       |||||||
                                ACAACTCG       GAAAAAC
                                     AAAAAAAT
GAM49   ZIN      3'  CAGGCCAGGGATTGCCCAACA  26391      A  C_
                                TGTTG GC  TTTTTGGCCTG
                                ||||| ||  ||||||||||
                                ACAAC CG  AGGGACCGGAC
                                   C  TT
GAM49   LOC256158 5'  CAGGCCACTGGAGAGCCCACA  99482     T A  _    T_
                                TGT G GC CTTT  TGGCCTG
                                ||| | || ||||  |||||||
                                ACA C CG GAGG  ACCGGAC
                                  _ C  A    TC
GAM50   FACL5    3'  AAGCACTGAATAAAAACCTCCT 64856    A   CTGG  CC
                                AG AGG    TA  CAGTGCTT
                                || |||    ||  ||||||||
                                TC TCC    AT  GTCACGAA
                                 C   AAAA  AA
GAM50   OTP      3'  AAGCATTGCTACCAACCGCCTC 50404      AA  C     CC
            A                    TGAG  GG TGGTA  CAGTGCTT
                                ||||  || |||||  ||||||||
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                                ACTC  CC ACCAT  GTTACGAA
                                  CG  A    C_
GAM50   ASB13    3'  AAGCACTGGGTTCTGCCCTTTC 45539      A  T  T
            A                    TGAGA GGC GG ACCCAGTGCTT
                                 |||||| ||| || ||||||||||
                                 ACTTT CCG TC TGGGTCACGAA
                                   C  _  T
GAM50   BTBD3    3'  AAGCGTTCCACCACCCTCTCA  31026      A  C   ACCCAG
                                 TGAGA GG TGGT     TGCTT
                                 ||||| || ||||     |||||
                                 ACTCT CC ACCA     GCGAA
                                   C  _   CCTT__
GAM50   C22orf2  3'  AGCAAGCACCAGCCTTCCA   96087    A       ACCCAG
                                 TG GAAGGCTGGT     TGCT
                                 || ||||||||||     ||||
                                 AC CTTCCGACCA     ACGA
                                  _        CGA___
GAM50   CMG2     3'  CACACCAGCCTCCTCA      55198     A      ACCCA
                                 TGAG AGGCTGGT     GTG
                                 |||| ||||||||     |||
                                 ACTC TCCGACCA     CAC
                                   C       _____
GAM50   DDX18    3'  AAGCACTGAGCACTGTTACTTC 23195      GC_   ACC
            T                    AGAAG   TGGT   CAGTGCTT
                                 |||||   ||||   ||||||||
                                 TCTTC   GTCA   GTCACGAA
                                    ATT    CGA
GAM50   FLJ11560 3'  AAGCACTGGGGTGCCTCCTCTC 48005      A  CT     _
            A                    TGAGA GG  GGTACCC AGTGCTT
                                 ||||| ||  ||||||| |||||||
                                 ACTCT CC  CCGTGGG TCACGAA
                                   _ T_     G
GAM50   FLJ30058 3'  CACTGCCAGCCCCTTCA     59302     AA     TACC
                                 TGAG  GGCTGG    CAGTG
                                 ||||  ||||||    |||||
                                 ACTT  CCGACC    GTCAC
                                   CC     _____
GAM50   GMPPB    3'  AAGCTGTTGGACACCTGCCTTC 26212        T  AC  GT_
            TCA                    TGAGAAGGC GGT  CCA   GCTT
                                 |||||||||  |||  |||   ||||
                                 ACTCTTCCG CCA  GGT   CGAA
                                      T   CA   TGT
GAM50   GMPPB    5'  AAGCTGTTGGACACCTGCCTTC 26213        T  AC  GT_
            TCA                    TGAGAAGGC GGT  CCA   GCTT
                                 |||||||||  |||  |||   ||||
                                 ACTCTTCCG CCA  GGT   CGAA
                                      T   CA   TGT
GAM50   KIAA0217 3'  AAGCAAGTAACCAGCTTCTCA  67593       G    ACCCAG
                                 TGAGAAG CTGGT     TGCTT
                                 ||||||| |||||     |||||
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                                ACTCTTC GACCA     ACGAA
                                   _    ATGA__
GAM50   KIAA0478  3'  AAGCACTGAGAAATTCTTTCTC 30168        CTGGTACC
           A                     TGAGAAGG       CAGTGCTT
                                 ||||||||       ||||||||
                                 ACTCTTTC       GTCACGAA
                                     TTAAAGA_
GAM50   MGC4832   3'  TGTATACCAGCCTTTCA     59661      A      CC
                                 TGAGA GGCTGGTA  CA
                                 ||||| ||||||||  ||
                                 ACTTT CCGACCAT  GT
                                   _       AT
GAM50   PRO1483   3'  AAGCACTGAAGGAGCCGCC    38329     T   A __
                                 GGC GGT CC  CAGTGCTT
                                 ||| ||| ||  ||||||||
                                 CCG CCG GG  GTCACGAA
                                  _  A  AA
GAM50   LOC124222 3'  CTGCATACCAGCCCTCCCA    74748    A  A      CC
                                 TG GA GGCTGGTA  CAG
                                 || || ||||||||  |||
                                 AC CT CCGACCAT  GTC
                                  C  C       AC
GAM50   LOC148114 5'  AGCACTGGGCATATTCT     79359      GGC  GTA
                                 AGAA   TG   CCCAGTGCT
                                 ||||   ||   |||||||||
                                 TCTT   AC   GGGTCACGA
                                   AT_ ____
GAM50   LOC197003 3'  AAGCACAACCAGACCTTCTCA  89210         _    ACCCA
                                 TGAGAAGG CTGGT    GTGCTT
                                 |||||||| |||||    ||||||
                                 ACTCTTCC GACCA    CACGAA
                                     A    A_____
GAM50   LOC255158 3'  GGGATACTAGCCCTCTCA    97883       A      _
                                 TGAGA GGCTGGTA CCC
                                 ||||| |||||||| |||
                                 ACTCT CCGATCAT GGG
                                    C       A
GAM50   LOC92170  3'  AAGCACTGGCTTCGCCCCTCA  68907      AA   T  TAC
                                 TGAG  GGC GG   CCAGTGCTT
                                 ||||  ||| ||   |||||||||
                                 ACTC  CCG CT   GGTCACGAA
                                   C_   _  TC_
GAM51   CA3       3'  ATGTAGTTGGAATTTATCCTA  18996      TTCCAT  CC
                                 TAGG     GT  CCAACTACAT
                                 ||||     ||  ||||||||||
                                 ATCC     TA  GGTTGATGTA
                                   TATT__  A_
GAM51   HNF3B     3'  TGTAGTTTTAACAGAACC    41715       CA   CCCC
                                 GGTTC  TGT    AACTACA
                                 |||||  |||    |||||||
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                                CCAAG  ACA    TTGATGT
                                  __   ATT_
GAM51   TGFBR2   5'  TTGAGGAAGACATGGAACC   13737          __ _
                                GGTTCCATGTC  CC CAA
                                ||||||||||  || |||
                                CCAAGGTACAG  GG GTT
                                      AA  A
GAM51   C7orf14  5'  GGGGAAAGACATGGACCCTA  74291      T    ____
                                TAGG TCCATG   TCCCC
                                |||| ||||||   |||||
                                ATCC AGGTAC   AGGGG
                                  C     AGAA
GAM51   DEFCAP   3'  TAGGAGGGACATGGAACC    53388          CAA
                                GGTTCCATGTCCC  CTA
                                ||||||||||||  |||
                                CCAAGGTACAGGG  GAT
                                      AG_
GAM51   DEFCAP   3'  TAGGAGGGACATGGAACC    53391          CAA
                                GGTTCCATGTCCC  CTA
                                ||||||||||||  |||
                                CCAAGGTACAGGG  GAT
                                      AG_
GAM51   DEFCAP   3'  TAGGAGGGACATGGAACC    30615          CAA
                                GGTTCCATGTCCC  CTA
                                ||||||||||||  |||
                                CCAAGGTACAGGG  GAT
                                      AG_
GAM51   DIS3     3'  TGTAGTTACACAAACCTA    30927       CCA  CCCC
                                TAGGTT  TGT   AACTACA
                                ||||||  |||   |||||||
                                ATCCAA  ACA   TTGATGT
                                   AC_  ____
GAM51   LOC89919 3'  GTGGCCAGGGAGATGGAACC  61379        G   CAA
                                GGTTCCAT TCCC  CTAC
                                |||||||| ||||  ||||
                                CCAAGGTA AGGG  GGTG
                                     G   ACC
GAM52   DLST     3'  GCGTTCCTGCCAGGCTCTCCC  10416     AT       AAGTT
                                GGGA  GCCTGGCAG    GCGC
                                ||||  |||||||||    ||||
                                CCCT  CGGACCGTC    TGCG
                                  CT       CT___
GAM52   KRTHA1   5'  GTCTTCAGCCAGGCACTCCC   11238     A      A   TT
                                GGGA TGCCTGGC GAAG  GC
                                |||| |||||||| ||||  ||
                                CCCT ACGGACCG CTTC  TG
                                  C       A   __
GAM52   NRXN3    5'  GCAGCCTGCCAGGCACCTCC   58073     A_       AA
                                GGA  TGCCTGGCAG  GTTGC
                                |||  ||||||||||  |||||
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                                CCT  ACGGACCGTC  CGACG
                                  CC        __
GAM52   PFKL     3'  GCCACCTGCCAGGCCTCCC    12059      AT        AA  T
                                GGGA  GCCTGGCAG  GT GC
                                ||||  |||||||||  || ||
                                CCCT  CGGACCGTC  CA CG
                                  C_        __  C
GAM52   PKD1     3'  GCACAGCTGTCTGCCAGGCACT 6104       A         _    C
            CTC                   GGGA TGCCTGGCAGA AGTTG GC
                                ||||  |||||||||||  |||||  ||
                                CTCT ACGGACCGTCT TCGAC CG
                                  C         G    A
GAM52   C20orf59  3'  GCGTGGTTCCCGCCAAACCTCC 42234      ATGCC    A_   G TG
            C                    GGGA     TGGC  GAA T  CGC
                                ||||     ||||  |||  |  |||
                                CCCT     ACCG  CTT G  GCG
                                  CCAA_    CC   _ GT
GAM52   FLJ11286  3'  GCTTTTGCCAGGCATCCC     37795      A
                                GGGA TGCCTGGCAGAAGT
                                ||||  ||||||||||||||
                                CCCT ACGGACCGTTTTCG
                                  _
GAM52   FLJ22671  3'  CTTCCCCAGGCATCCC       46313      A      CA
                                GGGA TGCCTGG  GAAG
                                ||||  |||||||  ||||
                                CCCT ACGGACC  CTTC
                                  _      C_
GAM52   KCNMB2    3'  CTTCTGACAAGCATTCCC     20685        C  G
                                GGGAATGC TG CAGAAG
                                ||||||||  ||  ||||||
                                CCCTTACG AC GTCTTC
                                     A  A
GAM52   KIAA0375  3'  GCACTGGGCTGCCAGGATTCCC 71577        G       AAGT_
                                GGGAAT CCTGGCAG     TGC
                                ||||||  ||||||||     |||
                                CCCTTA GGACCGTC     ACG
                                  _       GGGTC
GAM52   KIAA1138  3'  GCCCCTCCTGCCAGGCCCTCCC 62819      AT        A  TT
                                GGGA  GCCTGGCAG AG  GC
                                ||||  |||||||||  ||  ||
                                CCCT  CGGACCGTC TC  CG
                                  CC        C  CC
GAM52   KIAA1729  3'  GCACAACCCCGAGGCAGCCCC  90590     AA    _  CAGAA    C
                                GGG  TGCCT GG     GTTG GC
                                |||  |||||  ||     ||||  ||
                                CCC  ACGGA CC     CAAC CG
                                  CG     G  C____    A
GAM52   LOC150372 5'  GCGGGCCCTGCCAGGCCTCCC  80616      AT        AAG
                                GGGA  GCCTGGCAG   TTGC
                                ||||  |||||||||   ||||
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                                CCCT  CGGACCGTC   GGCG
                                  C_       CCG
GAM52   LOC51337  3'  GCATCTGCCAGGCAGCCCC   34083     AA        AGT
                                GGG  TGCCTGGCAGA   TGC
                                |||  ||||||||||   |||
                                CCC  ACGGACCGTCT   ACG
                                  CG         ___
GAM52   LOC90906  3'  GCGGGGACTTCCAGGCACTCCC 64953      A      CAG   _ G
                                GGGA TGCCTGG   AAGT T CGC
                                ||||  |||||||   |||| | |||
                                CCCT ACGGACC   TTCA G GCG
                                  C      ___    G G
GAM53   AGER      3'  AGACAGATCCCATCCATCAGCT 8532     AA       _  TGCCC_
            CCCT                    AG  AGCTGATGG TG     GTCT
                                ||  |||||||||  ||      ||||
                                TC  TCGACTACC AC     CAGA
                                 CC        T  CCTAGA
GAM53   CRIM1     3'  AGACGAGCACATCAGAACCCTT 33600      CTGA_       C
            T                    AAAG     TGGTGTGC CGTCT
                                ||||     ||||||||  |||||
                                TTTC     ACTACACG GCAGA
                                  CCAAG       A
GAM53   PLAU      3'  ACGGGCACCACCCGCTTTCT   69539        TGAT   _
                                AGAAAGC    GGTG TGCCCGT
                                |||||||    ||||  |||||||
                                TCTTTCG    CCAC ACGGGCA
                                    C___    C
GAM53   PODXL     3'  AGACAGTTTATCATCAACTCTT 19411     A  C       T  CC
            T                    AGA AG TGATGGTG GC  GTCT
                                ||| ||  ||||||||  ||  ||||
                                TTT TC ACTACTAT TG  CAGA
                                  C  A       T  A_
GAM53   RAPSN     5'  AGACGGGCTGAACCAGCTTT   51971       GAT   GT_
                                AAAGCT   GGT   GCCCGTCT
                                ||||||   |||   ||||||||
                                TTTCGA   CCA   CGGGCAGA
                                   ___   AGT
GAM53   RASA1     3'  AGACAACCTCATCAGCTGCCT  42955    AA       T  GCCC
                                AG  AGCTGATGG GT    GTCT
                                ||  |||||||||  ||    ||||
                                TC  TCGACTACT CA    CAGA
                                 CG        C  A___
GAM53   C1QR1     3'  ACAGGAAAACACAGCTTTCT   24863         A  GTGTG  C
                                AGAAAGCTG TG     CC GT
                                |||||||||  ||     || ||
                                TCTTTCGAC AC     GG CA
                                      _  AAAA_  A
GAM53   C20orf129 3'  GGACATCATCAGCTTCCT    62043    A          G
                                AG AAGCTGATGGTGT CC
                                ||  ||||||||||||  ||
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                                TC TTCGACTACTACA GG
                                 C          _
GAM53   FLJ20514  5'  GCAACCATCAGCTCTCT     35787     A        G
                                AGA AGCTGATGGT TGC
                                ||| |||||||||| |||
                                TCT TCGACTACCA ACG
                                  C        _
GAM53   KIAA0534  3'  ACGGGCACTGGACCCAGCTTTC 71929         AT   ___
                                GAAAGCTG  GGT   GTGCCCGT
                                ||||||||  |||   ||||||||
                                CTTTCGAC  CCA   CACGGGCA
                                     __  GGT
GAM53   KIAA1029  3'  GGGACACCATCAGGCCTCT   24431     AAG        G
                                AGA   CTGATGGTGT CCC
                                |||   |||||||||| |||
                                TCT   GACTACCACA GGG
                                  CCG        _
GAM53   RASGRP4   3'  AGACGAGATCTATGAGCTTTCT 54741         G    TGTGCC
                                AGAAAGCT ATGG     CGTCT
                                |||||||| ||||     |||||
                                TCTTTCGA TATC     GCAGA
                                     G    TAGA__
GAM53   LOC142941 5'  GACAAATACCAGGCTTTCT    83767         GA     GCCC
                                AGAAAGCT  TGGTGT    GTC
                                ||||||||  ||||||    |||
                                TCTTTCGG  ACCATA    CAG
                                     __     AA__
GAM53   LOC158187 3'  GACAAACCTATCAGTTTCT    87993       G      T  GCCC
                                AGAAA CTGATGG GT    GTC
                                |||||  ||||||| ||    |||
                                TCTTT GACTATC CA    CAG
                                  _      _ AA__
GAM53   LOC255019 3'  GGATGGGCCACCAGCCACCT   96781     C  A_    T
                                AG TG  TGGTG GCCCGTCT
                                || ||  ||||| ||||||||
                                TC AC  ACCAC CGGGTAGG
                                 C  CG    _
GAM53   LOC51285  3'  AGAACCTCAGCATCAGCTCCCT 33799     AA       G  TGCCCG
                                AG  AGCTGATG TG     TCT
                                ||  |||||||| ||     |||
                                TC  TCGACTAC AC     AGA
                                 CC       G  TCCA__
GAM54   BRCA1     3'  GTTTGCCAGAAAACACCA    24573     AA       GC
                                TGG  TTTTCTGG  CGAAT
                                |||  ||||||||  |||||
                                ACC  AAAAGACC  GTTTG
                                  AC       __
GAM54   EYA4      3'  TATTTGGAATAAAAATTCCA   15886         C  GG
                                TGGAATTTT TG  CCGAATA
                                |||||||| ||  |||||||
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                                ACCTTAAAA AT  GGTTTAT
                                     _ AA
GAM54   MECP2    3' ATTTGGCAGAAAATTACA    18385    G      GG
                                TG AATTTTCT  GCCGAAT
                                || ||||||||  |||||||
                                AC TTAAAAGA  CGGTTTA
                                 A      __
GAM54   CG012    3' TGGCTACCCAGAAAATTTCA   84171           ___
                                TGGAATTTTCTGG  GCCG
                                ||||||||||||  ||||
                                ACTTTAAAAGACC  CGGT
                                       CAT
GAM54   HBXAP    3' ATTTTTCCTAGAAAACTCCA   33880     A       CC
                                TGGA TTTTCTGGG  GAAT
                                |||| |||||||||  ||||
                                ACCT AAAAGATCC  TTTA
                                  C       TT
GAM54   KIAA0997 3' TCAACCCAAAAAGTTCCA    30889        C    CC
                                TGGAATTTT TGGG  GA
                                ||||||||| ||||  ||
                                ACCTTGAAA ACCC  CT
                                     A    AA
GAM54   KIAA1014 3' GTATTCTCCATAAAATTCCA  65961        C    CC
                                TGGAATTTT TGGG  GAATAC
                                ||||||||| ||||  ||||||
                                ACCTTAAAA ACCT  CTTATG
                                     T   __
GAM54   MAGEH1   3' GTATTCGTTTTAAAATTCC   26771        CT   C
                                GGAATTTT  GGGC GAATAC
                                ||||||||  |||| ||||||
                                CCTTAAAA  TTTG CTTATG
                                     T_   _
GAM54   PSK      5' TATTCGGGGTTCAGACCCCA  32882     AATTT      __
                                TGG    TCTGGGCC  GAATA
                                |||    ||||||||  |||||
                                ACC    AGACTTGG  CTTAT
                                  CC___       GG
GAM54   SDF1     3' TATTCCCTAGAAACTTCCA   92520      T      CC
                                TGGAA TTTCTGGG  GAATA
                                ||||| ||||||||  |||||
                                ACCTT AAAGATCC  CTTAT
                                   C       __
GAM54   TAO1     5' TATTCGGGGTTCAGACCCCA  17720     AATTT      __
                                TGG    TCTGGGCC  GAATA
                                |||    ||||||||  |||||
                                ACC    AGACTTGG  CTTAT
                                  CC___       GG
GAM54   VMP      3' GTACCCGGCCACCAGAAAACCC 55765    AA      __   AA
            C                    GG  TTTTCTGG  GCCG  TAC
                                ||  ||||||||  ||||  |||
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                                CC  AAAAGACC  CGGC  ATG
                                 CC       AC    CC
GAM54   LOC126295 3'  GTATAATGCTCCAGAAAATTC  74975          _  CGA
                                GAATTTTCTGG GC   ATAC
                                |||||||||||  ||   ||||
                                CTTAAAAGACC CG   TATG
                                      T  TAA
GAM54   LOC146184 5'  ATTCAACCAGAAAATTTCA   84596           GCC
                                TGGAATTTTCTGG   GAAT
                                ||||||||||||   ||||
                                ACTTTAAAAGACC   CTTA
                                       AA_
GAM54   LOC150407 3'  GTATTCCAAGAAAATTTCA   80643          GGGCC
                                TGGAATTTTCT    GAATAC
                                ||||||||||    ||||||
                                ACTTTAAAAGA    CTTATG
                                      AC___
GAM54   LOC91496  5'  TTTGGCAGAAAATGCCA    66813    A     GG
                                TGG ATTTTCT  GCCGAA
                                ||| |||||||  ||||||
                                ACC TAAAAGA  CGGTTT
                                  G      __
GAM55   CDH12     3'  CTTATCATTTAAAGTGGTGTA  15777        CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM55   GOCAP1    3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM55   DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090      T   AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                   _   GTCA_
GAM55   DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
            A                    TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM55   FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126        CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM55   HMP19     3'  CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
            TA                    TACA   TCC   GAAGAATAAG
                                ||||   |||   ||||||||||
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                              ATGT   AGG   TTTCTTATTC
                                AAA_  ATTG
GAM55   KIAA1719 3' TCTGTCTTGGGAGTGGTGTA  68742           _
                              TACACCACTCCCAAGA AGA
                              |||||||||||||||| |||
                              ATGTGGTGAGGGTTCT TCT
                                       G
GAM55   KIAA1853 3' TTTTTCTTGGAAGCAGTG   69929    CA  C
                              CAC  CT CCAAGAAGAA
                              |||  || ||||||||||
                              GTG  GA GGTTCTTTTT
                                AC  A
GAM55   KIAA1877 3' CTTATTCTTCTGCCATGAGT  66748    CCA__
                              ACTC    AGAAGAATAAG
                              ||||    ||||||||||
                              TGAG    TCTTCTTATTC
                                TACCG
GAM55   KIAA1906 3' CTTATTCTTCTTGACTTTTGG 73571    CTCC_
                              CCA    CAAGAAGAATAAG
                              |||    ||||||||||||
                              GGT    GTTCTTCTTATTC
                                TTTCA
GAM55   OSBPL11  3' CTTAATTTCCCAAGAGTGGTG 43206       CCAA   AA
                              CACCACTC   GAAG  TAAG
                              ||||||||   ||||  ||||
                              GTGGTGAG   CTTT  ATTC
                                   AACC   A_
GAM55   YME1L1   3' TCATTCTTGATGTGGTGTA   58438       TCC    _
                              TACACCAC   CAAGAA GA
                              ||||||||   ||||||  ||
                              ATGTGGTG   GTTCTT CT
                                   TA_    A
GAM55   ZNF262   3' CTTATTTTGTTTGGGAGT    18723       A
                              ACTCCCAAG AGAATAAG
                              ||||||||| ||||||||
                              TGAGGGTTT TTTTATTC
                                   G
GAM55   LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_   AAGA
                              TACACCAC   CCAAG   ATA
                              ||||||||   |||||   |||
                              ATGTGGTG   GGTTC   TGT
                                   CAA    GG__
GAM56   ADAM2    3' GGACAACAGAGATGCCATGATA 9399      CA  CACAGA
                              TGTCA  GC    TGTTGTCC
                              |||||  ||    ||||||||
                              ATAGT  CG    ACAACAGG
                                AC  TAGAG_
GAM56   ADRB3    3' GATTCCCCGGCTGTGACA    5249        ACA  TGTT
                              TGTCACAGCC   GA   GTC
                              ||||||||||   ||   |||
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                                ACAGTGTCGG  CT   TAG
                                     CCC  ____
GAM56  CAPZA1   3' GAACTCAAGTGTAACTGTGATA 73025       CC  GA  TTG
                                TGTCACAG  ACA  TG   TC
                                ||||||||  |||  ||   ||
                                ATAGTGTC  TGT  AC   AG
                                     AA   GA   TCA
GAM56  CYP19    3' GATAACTGTAAATGTGACA   5440       GCC   A
                                TGTCACA   ACAG TGTT
                                |||||||   |||| ||||
                                ACAGTGT   TGTC ATAG
                                    AAA   A
GAM56  GGA3     3' GGCACCTGTGGCTGGACA    26590     A      A
                                TGTC CAGCCACAG TGTT
                                |||| ||||||||| ||||
                                ACAG GTCGGTGTC ACGG
                                  _       C
GAM56  ITGB1    3' GAAGTTATACTGTGGCTATGCA 11052    T  C     _  TTG
                                TG CA AGCCACAG ATG   TC
                                || || |||||||| |||   ||
                                AC GT TCGGTGTC TAT   AG
                                 _ A      A   TGA
GAM56  MN1      5' GACCCACCCGCGGCTGTGACA  11653        ACAGA  TT
                                TGTCACAGCC    TG  GTC
                                ||||||||||    ||  |||
                                ACAGTGTCGG    AC  CAG
                                     CGCCC  C_
GAM56  NPHS2    3' GACAACATGTTTCCGTGAC   28278     AGCC   GA
                                GTCAC    ACA  TGTTGTC
                                |||||    |||  |||||||
                                CAGTG    TGT  ACAACAG
                                   CCTT   __
GAM56  PCTK1    3' GACAGCATGGCCGTGCCA    53418    T  A   CAGA
                                TG CAC GCCA    TGTTGTC
                                || ||| ||||    |||||||
                                AC GTG CGGT    ACGACAG
                                 C   C   _____
GAM56  PTK2B    3' GGACACAGGGTGACGGTGACA  15907      AGC   AGA   T
                                TGTCAC   CAC   TGT GTCC
                                ||||||   |||   ||| ||||
                                ACAGTG   GTG   ACA CAGG
                                    GCA   GG_   _
GAM56  RBBP9    3' GGACAACATTGGTCTAGGACA  70692     AC  _   CAG
                                TGTC  AG CCA   ATGTTGTCC
                                ||||  || |||   |||||||||
                                ACAG  TC GGT   TACAACAGG
                                  GA  T   ____
GAM56  SULT1C1  3' GACAGGATGGCTGTCAACA   8319     C_      CAGA G
                                TGT  ACAGCCA    T TTGTC
                                |||  |||||||    | |||||
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                                ACA  TGTCGGT   A GACAG
                                  AC      ____ G
GAM56   TRIP12   3'  ACAATAAATGTGGCTGTGCA  16179    T       GA
                                TG CACAGCCACA  TGTTGT
                                || ||||||||||  ||||||
                                AC GTGTCGGTGT  ATAACA
                                  _        AA
GAM56   AF9Q34   3'  GACTCTGTGTGGCTGTGCA   51715    T       GATGTT
                                TG CACAGCCACA     GTC
                                || ||||||||||     |||
                                AC GTGTCGGTGT     CAG
                                  _        GTCT__
GAM56   CLDN1    3'  GATGCTTTCTGTGGCTAAACA  41186     CAC       TGT
                                TGT   AGCCACAGA   TGTC
                                |||   |||||||||   ||||
                                ACA   TCGGTGTCT   GTAG
                                  AA_       TTC
GAM56   DKFZp434E0519 3'  GACAAAGTGGCTGTATCA    50990    TC      AGATG
                                TG  ACAGCCAC    TTGTC
                                ||  ||||||||    |||||
                                AC  TGTCGGTG    AACAG
                                  TA       A____
GAM56   DKFZP564G2022 5'  GGCACTCCACGGCTGTGA    31936        ACA  T  T
                                TCACAGCC   GA GT GTC
                                ||||||||   || || |||
                                AGTGTCGG   CT CA CGG
                                     CAC  _  _
GAM56   DNAJC5   3'  AGCTCTGTGGCTAGAACA    62132     CAC       T
                                TGT   AGCCACAGA GTT
                                |||   ||||||||| |||
                                ACA   TCGGTGTCT CGA
                                  AGA       _
GAM56   FLJ14100  3'  GGACAAAGCTCTCCGTGGCTGT 47337          __   TG_
            GGCA                    TGTCACAGCCAC  AGA   TTGTCC
                                ||||||||||||  |||   ||||||
                                ACGGTGTCGGTG  TCT   AACAGG
                                       CC   CGA
GAM56   HSPC049   3'  GACTGGTATTGTGGCTGTGCCA 72412    T        ATGTT
                                TG CACAGCCACAG    GTC
                                || ||||||||||     |||
                                AC GTGTCGGTGTT    CAG
                                  C         ATGGT
GAM56   KIAA0620  3'  GGACAACATCTACGAGTGCT   62811     C  ____
                                AGC AC    AGATGTTGTCC
                                ||| ||    ||||||||||
                                TCG TG    TCTACAACAGG
                                  _ AGCA
GAM56   KIAA0763  3'  ACAGCTGGCAATGTGACA    30163        __    CAGAT
                                TGTCACA  GCCA    GTTGT
                                |||||||  ||||    |||||
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                                ACAGTGT  CGGT    CGACA
                                   AA   _____
GAM56   KIAA1010  3' GACAACATAACACCTGTGAC  72541       CCACAG
                                GTCACAG     ATGTTGTC
                                |||||||     ||||||||
                                CAGTGTC     TACAACAG
                                   CACAA_
GAM56   KIAA1054  3' AGTATCTGTGACTGTGGCA   68960       C
                                TGTCACAG CACAGATGTT
                                |||||||| ||||||||||
                                ACGGTGTC GTGTCTATGA
                                   A
GAM56   KIAA1130  3' GGACAGTGGGTGATGTGACA  63097       GC   AGATG
                                TGTCACA  CAC    TTGTCC
                                |||||||  |||    ||||||
                                ACAGTGT  GTG    GACAGG
                                   A_   GGT__
GAM56   KIAA1265  3' AACTTCTGTGGCTATGCA    71336    T  C       T
                                TG CA AGCCACAGA GTT
                                || || |||||||||| |||
                                AC GT TCGGTGTCT CAA
                                 _ A        T
GAM56   KIAA1754  3' GACACACGGGGTGACTGTGGCA 63929        C   AGA   _
                                TGTCACAG CAC   TGT TGTC
                                |||||||| |||   ||| ||||
                                ACGGTGTC GTG   GCA ACAG
                                   A   GG_   C
GAM56   KIAA1775  3' GGACAATAAATGGATGTGACA  53545       G   CAGA
                                TGTCACA CCA    TGTTGTCC
                                ||||||| |||    ||||||||
                                ACAGTGT GGT    ATAACAGG
                                   A   AA__
GAM56   MANBAL    3' GATCCCACTAGCTGTGACA    42217       CAC  A  TT
                                TGTCACAGC   AG TG  GTC
                                |||||||||   || ||  |||
                                ACAGTGTCG   TC AC  TAG
                                    A__  _  CC
GAM56   MAPK8IP3  3' GACACCAGGTGCCTGTGACA   54140       C   AGA  T
                                TGTCACAG CAC   TG TGTC
                                |||||||| |||   || ||||
                                ACAGTGTC GTG   AC ACAG
                                   C   G__  C
GAM56   PCDH17    3' ACGACCCTGTGGCTGTGA     27833         AT
                                TCACAGCCACAG  GTTGT
                                ||||||||||||  |||||
                                AGTGTCGGTGTC  CAGCA
                                     C_
GAM56   PRO0159   5' GGATGTTCTCTGTGGCTGTGA  26949          TGT
                                TCACAGCCACAGA   TGTCC
                                ||||||||||||   |||||
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                                AGTGTCGGTGTCT  GTAGG
                                       CTT
GAM56   SCDGF-B  3'  GACAATGTATAAGCTGTAACA  53633    C    CACAG
                                TGT ACAGC    ATGTTGTC
                                ||| |||||    ||||||||
                                ACA TGTCG    TGTAACAG
                                  A    AATA_
GAM56   STARD7   3'  GATTTCACTCCTAACTGTGACA 39742       CCAC_ A  TT
                                TGTCACAG    AG TG  GTC
                                ||||||||    || ||  |||
                                ACAGTGTC    TC AC  TAG
                                     AATCC  _  TT
GAM56   LOC125893 3'  AATATCATGACTGTGACA    76171       C  CA
                                TGTCACAG CA  GATGTT
                                |||||||| ||  ||||||
                                ACAGTGTC GT  CTATAA
                                     A  A_
GAM56   LOC130355 5'  AACATCTGTGACTGTGACA   75433       C
                                TGTCACAG CACAGATGTT
                                |||||||| ||||||||||
                                ACAGTGTC GTGTCTACAA
                                     A
GAM56   LOC130536 5'  GGACAACGAGAGGGACTGCAAC 76245    CA  _  ACAGA
          A                      TGT  CAG CC    TGTTGTCC
                                |||  ||| ||    ||||||||
                                ACA  GTC GG    GCAACAGG
                                  AC   A  GAGA_
GAM56   LOC130902 3'  GGCCACCAATGGCTATGACA  75486     C    CAGAT  T
                                TGTCA AGCCA    GT GTC
                                ||||| |||||    || |||
                                ACAGT TCGGT    CA CGG
                                   A    AAC__  C
GAM56   LOC145693 3'  GACAGCAGGTGACATGACA   77854     CA__  ACAGA
                                TGTCA   GCC    TGTTGTC
                                |||||   |||    |||||||
                                ACAGT   TGG    ACGACAG
                                   ACAG  _____
GAM56   LOC146237 3'  GGGCCTGTGGCTGCAGCA    84613    CA       ATGTT
                                TGT  CAGCCACAG    GTCC
                                |||  |||||||||    ||||
                                ACG  GTCGGTGTC    CGGG
                                  AC       _____
GAM56   LOC146784 5'  GGACAGCAGTAGGCATGACA  78716     CA  ACAGA
                                TGTCA  GCC    TGTTGTCC
                                |||||  |||    ||||||||
                                ACAGT  CGG    ACGACAGG
                                   A_  ATG__
GAM56   LOC147160 3'  AACTCTGTGGCCAAGACA    85064     ACA      T
                                TGTC   GCCACAGA GTT
                                ||||   |||||||| |||
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                                ACAG   CGGTGTCT CAA
                                  AAC      _
GAM56   LOC152445 5'  GGACAACATCCCGCAAACGACA 86954      ACA_  CACA
                                TGTC   GC   GATGTTGTCC
                                ||||   ||   ||||||||||
                                ACAG   CG   CTACAACAGG
                                  CAAA  CC__
GAM56   LOC200178 3'  GGACAAAAGGTGGACCATGACA 89999      CAG_   AGATG
                                TGTCA   CCAC    TTGTCC
                                |||||   ||||    ||||||
                                ACAGT   GGTG    AACAGG
                                  ACCA   GAA__
GAM56   LOC200197 3'  GGCCCCTCTGTAGCCTGTGACA 90019        _ C    TGTT
                                TGTCACAG C ACAGA   GTC
                                |||||||| | |||||   |||
                                ACAGTGTC G TGTCT   CGG
                                     C A    CCC_
GAM56   LOC221410 3'  GGACAATTATGGCTGTGAC   93697         CAGAT
                                GTCACAGCCA    GTTGTCC
                                ||||||||||    |||||||
                                CAGTGTCGGT    TAACAGG
                                      AT____
GAM56   LOC253299 5'  AGCATCCTGTGGCTGCACA   98194     CA       _
                                TGT  CAGCCACAG ATGTT
                                |||  ||||||||| |||||
                                ACA  GTCGGTGTC TACGA
                                  C_       C
GAM56   LOC255623 3'  AATATCATGACTGTGACA    96497        C  CA
                                TGTCACAG CA  GATGTT
                                |||||||| ||  ||||||
                                ACAGTGTC GT  CTATAA
                                     A  A_
GAM56   LOC56891  5'  AACATCTATGGTTGTGACA   39685          C
                                TGTCACAGCCA AGATGTT
                                |||||||||| |||||||
                                ACAGTGTTGGT TCTACAA
                                       A
GAM56   LOC90326  3'  ACATCTGTGAGCATGACA    62951       CA  _
                                TGTCA  GC CACAGATGT
                                |||||  || |||||||||
                                ACAGT  CG GTGTCTACA
                                   A_  A
GAM56   LOC90580  3'  GGACAGCAGAACGACTTGACA  64109       C  CCACAGA
                                TGTCA AG       TGTTGTCC
                                ||||| ||       ||||||||
                                ACAGT TC       ACGACAGG
                                   _  AGCAAG_
GAM56   LOC92181  3'  ATATCTGTAATTGTAACA    68942     C    CC
                                TGT ACAG  ACAGATGT
                                ||| ||||  ||||||||
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                                ACA TGTT  TGTCTATA
                                  A   AA
GAM57   CDH12    3'  CTTATCATTTAAAGTGGTGTA  15777        CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM57   GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM57   DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090      T   AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                   _   GTCA_
GAM57   DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
            A                    TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM57   FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126        CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM57   HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
            TA                    TACA   TCC   GAAGAATAAG
                                ||||   |||   ||||||||||
                                ATGT   AGG   TTTCTTATTC
                                  AAA_   ATTG
GAM57   KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68742            _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                          G
GAM57   KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM57   KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748     CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM57   KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
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                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM57   OSBPL11  3' CTTAATTTCCCAAGAGTGGTG 43206       CCAA   AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                    AACC   A_
GAM57   YME1L1   3' TCATTCTTGATGTGGTGTA   58438       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                    TA_    A
GAM57   ZNF262   3' CTTATTTTGTTTGGGAGT    18723       A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                    G
GAM57   LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_    AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
                                ATGTGGTG   GGTTC   TGT
                                    CAA    GG__
GAM58   DMRT2    3' TACAGATGGAAATTGCCCA   22654    AA   CCAC   T
                                TGG  CAA   TCC ATCTGTA
                                |||  |||   ||| |||||||
                                ACC  GTT   AGG TAGACAT
                                  C_   AA__   _
GAM58   EPHB1    3' CAGAAGCAGTGTTCCAT     16693      AACC   C  A
                                ATGGAAC    ACT CT TCTG
                                |||||||    ||| || ||||
                                TACCTTG    TGA GA AGAC
                                   ____   C  _
GAM58   FRK      3' TACTGATTAGAGTGGTTATTC 10719    C      CT   T
                                GAA AACCACTC  ATC GTA
                                ||| ||||||||  ||| |||
                                CTT TTGGTGAG  TAG CAT
                                  A       AT   T
GAM58   ONECUT1  3' CAGAAATGGTTGTTCTAT    62817         CTCCTA
                                ATGGAACAACCA     TCTG
                                ||||||||||||     ||||
                                TATCTTGTTGGT     AGAC
                                    AA____
GAM58   SORBS1   3' ACAAATAGGAGTAGCAATTCT 31801     CAACC      C
                                GGAA     ACTCCTAT TGT
                                ||||     |||||||| |||
                                TCTT     TGAGGATA ACA
                                  AACGA       A
GAM58   TMEPAI   3' ATGGGAGTGGCTTTCCAT    39825      CAA
                                ATGGAA   CCACTCCTAT
                                ||||||   ||||||||||
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                                TACCTT   GGTGAGGGTA
                                   TC_
GAM58   caspr5   3' TAGGAAGTAGATGTTCCAT   56254        ACC  _
                                ATGGAACA   ACT CCTA
                                ||||||||   ||| ||||
                                TACCTTGT   TGA GGAT
                                     AGA   A
GAM58   KIAA0515 5' CAGTGGGAGTGGCCACTCC   64545    ACAA       T
                                GGA   CCACTCCTA CTG
                                |||   ||||||||| |||
                                CCT   GGTGAGGGT GAC
                                  CACC       _
GAM58   KIAA0594 3' TACATAGGCCAACAACTGTTCC 65518        ACCACT__   TC
           AT                    ATGGAACA      CCTA  TGTA
                                ||||||||      ||||  ||||
                                TACCTTGT      GGAT  ACAT
                                     CAACAACC   __
GAM58   TOMM34   3' ACAGACATGGTTGTTGCA    23313    G      CTCCTA
                                TG AACAACCA     TCTGT
                                || |||||||      |||||
                                AC TTGTTGGT     AGACA
                                 G       AC____
GAM58   LOC149821 3' TACAGATAAGCAGTCTTCCA   85937      CAACC   C  _
                                TGGAA    ACT CT ATCTGTA
                                |||||    ||| || |||||||
                                ACCTT    TGA GA TAGACAT
                                   C_____   C  A
GAM58   LOC199899 3' TACAGATAAAAGTCTAGTTCCA 91470       AACC   CC
                                TGGAAC    ACT  TATCTGTA
                                ||||||   |||  ||||||||
                                ACCTTG   TGA  ATAGACAT
                                   ATC_   AA
GAM58   LOC199923 3' CAGGTGGACTGACTGCCCCAT  89867     AA  AC  C   T
                                ATGG  CA  CA TCC ATCTG
                                ||||  ||  || ||| |||||
                                TACC  GT  GT AGG TGGAC
                                  CC  CA  C  _
GAM58   LOC92697  5' ACAGATAGGGTTTCTCCAT   70801      AC    ACTC
                                ATGGA  AACC   CTATCTGT
                                |||||  ||||   ||||||||
                                TACCT  TTGG   GATAGACA
                                   CT   _____
GAM59   BCKDHB   3' TCATGATATTGGCTGAAA    5342          CAT
                                TTTCAGCTAA   TCATGG
                                ||||||||||   ||||||
                                AAAGTCGGTT   AGTACT
                                     AT_
GAM59   CLCN6    3' CCACCAAAGTTAGCTGAAAG   8902           A  CA
                                CTTTCAGCTAAC TT  TGG
                                |||||||||||| ||  |||
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                                GAAAGTCGATTG AA  ACC
                                      A  CC
GAM59   CLCN6    3' CCACCAAAGTTAGCTGAAAG  41694          A  CA
                                CTTTCAGCTAAC TT  TGG
                                |||||||||||| ||  |||
                                GAAAGTCGATTG AA  ACC
                                      A  CC
GAM59   CLCN6    3' CCACCAAAGTTAGCTGAAAG  41701          A  CA
                                CTTTCAGCTAAC TT  TGG
                                |||||||||||| ||  |||
                                GAAAGTCGATTG AA  ACC
                                      A  CC
GAM59   EGFL6    3' CATTTTAGAATTACTAGCTGAA 31938        AC_   AT
           A                     TTTCAGCTA   ATTC  GGATG
                                |||||||||   ||||  |||||
                                AAAGTCGAT   TAAG  TTTAC
                                     CAT    AT
GAM59   IRS2     3' CATATAATGTTAGCTGGAAGG  60438           C_
                                CCTTTCAGCTAACATT  ATG
                                |||||||||||||||  |||
                                GGAAGGTCGATTGTAA  TAC
                                         TA
GAM59   NR2E3    3' CTTTGAATGCCAGCCAAAGG  33418      CA  AA     T
                                CCTTT  GCT  CATTCA GG
                                |||||  |||  |||||| ||
                                GGAAA  CGA  GTAAGT TC
                                   C_   CC     T
GAM59   WTAP     3' CTTTGAATGTTGCTAAAAGG  18139      C  T      T
                                CCTTT AGC AACATTCA GG
                                ||||| ||| |||||||| ||
                                GGAAA TCG TTGTAAGT TC
                                   A  _       T
GAM59   BIRC1    3' CATCCATGTTGTACAACTGAAA 16988      CTA_  TT
                                TTTCAG   ACA  CATGGATG
                                ||||||   |||  ||||||||
                                AAAGTC   TGT  GTACCTAC
                                    AACA  T_
GAM59   DKFZP434F091 3' ATCCTGGTTAGCAAAAGG   31892      CA    ATTCAT
                                CCTTT  GCTAAC     GGAT
                                |||||  ||||||     ||||
                                GGAAA  CGATTG     CCTA
                                   A_     GT____
GAM59   HSJ001348 3' CATCCATGGGGAGCTGAGA   62856       AACAT
                                TTTCAGCT    TCATGGATG
                                ||||||||    |||||||||
                                AGAGTCGA    GGTACCTAC
                                     GG___
GAM59   KIAA1069  3' CCATAATGAGAGTTGAAAGG  68529         AA   C
                                CCTTTCAGCT  CATT ATGG
                                ||||||||||  |||| ||||
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                                GGAAAGTTGA  GTAA TACC
                                      GA   _
GAM59   MGC13159  3'  ATCCAGCTAGCTGAAAG     53036          ACATTCA
                                CTTTCAGCTA      TGGAT
                                ||||||||||      |||||
                                GAAAGTCGAT      ACCTA
                                      CG_____
GAM59   MGC26766  3'  CATCCATGAAGAGCTGAAGG   59468         AACA
                                CTTTCAGCT    TTCATGGATG
                                |||||||||    ||||||||||
                                GGAAGTCGA    AAGTACCTAC
                                      G___
GAM59   MGC5528   3'  CATCCATGAAATTGGCTGAA   44273         CA
                                TTCAGCTAA  TTCATGGATG
                                |||||||||  ||||||||||
                                AAGTCGGTT  AAGTACCTAC
                                      A_
GAM59   NAPG      5'  CTATGAAAACTTAGCTGAAAGG 98536          CA_
                                CCTTTCAGCTAA   TTCATGG
                                ||||||||||||   |||||||
                                GGAAAGTCGATT   AAGTATC
                                       CAA
GAM59   SIAT8D    3'  CATCCACCAATGAACTGAAAGG 20231        CTAA    CA
                                CCTTTCAG    CATT  TGGATG
                                ||||||||    ||||  ||||||
                                GGAAAGTC    GTAA  ACCTAC
                                      AA__    CC
GAM59   SMC2L1    3'  CATGATAAATGTAGCTGAAA   22245         A   ___
                                TTTCAGCTA CAT   TCATG
                                ||||||||| |||   |||||
                                AAAGTCGAT GTA   AGTAC
                                      _   AAT
GAM59   LOC115286 3'  CATTCTCATGTCAGACTGAAAG 73763         _  A    TCAT
            G                    CCTTTCAG CT ACAT    GGATG
                                ||||||||  || ||||    |||||
                                GGAAAGTC GA TGTA    CTTAC
                                      A  C    CT__
GAM59   LOC121838 5'  GTGAATGTTAGCAAAAG     76516      CA
                                CTTT  GCTAACATTCAT
                                ||||  ||||||||||||
                                GAAA  CGATTGTAAGTG
                                  A_
GAM60   ADCY6     3'  GGGAGCAGGGGAGGGGTCAG   31590     C      G   ATG
                                CTG CCCCTCT CTG   CCC
                                ||| ||||||| |||   |||
                                GAC GGGGAGG GAC   GGG
                                  T      G   GA_
GAM60   ADCY6     3'  GGGAGCAGGGGAGGGGTCAG   40959     C      G   ATG
                                CTG CCCCTCT CTG   CCC
                                ||| ||||||| |||   |||
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                                GAC GGGGAGG GAC   GGG
                                  T     G  GA_
GAM60   AGRN    3'  GGGGCAGGTGCAGAGGTGGCAG 79588      C     TGA
                                CTGCC CCTCTGC   TGCCCC
                                ||||| |||||||   ||||||
                                GACGG GGAGACG   ACGGGG
                                   T     TGG
GAM60   AKAP2   3'  TGGGGGCATTTTTAGAGCGGCA 24231     CC    CT
                                TGCC  CTCTG  GATGCCCCCA
                                ||||  |||||  ||||||||||
                                ACGG  GAGAT  TTACGGGGGT
                                  C_    TT
GAM60   AQP6    3'  GGGACAGAGCAGAGGAAGGCAG 55009      C_      GA  _
                                CTGCC  CCTCTGCT  TG CCC
                                |||||  ||||||||  || |||
                                GACGG  GGAGACGA  AC GGG
                                   AA       G_  A
GAM60   AQP6    3'  TGGGGACAGGGGGCAGGGGCAG  55018       CTC   GA  C
                                CTGCCCC   TGCT  TG CCCCA
                                |||||||   ||||  || |||||
                                GACGGGG   ACGG  AC GGGGT
                                    ___    GG  A
GAM60   AQP6    3'  GGGACAGAGCAGAGGAAGGCAG 9731       C_      GA  _
                                CTGCC  CCTCTGCT  TG CCC
                                |||||  ||||||||  || |||
                                GACGG  GGAGACGA  AC GGG
                                   AA       G_  A
GAM60   ASIC4   5'  GCGGCAGCAGAGGCAGCAG   38537     CC       A
                                CTGC  CCTCTGCTG TGC
                                ||||  ||||||||| |||
                                GACG  GGAGACGAC GCG
                                  AC       G
GAM60   ATOX1   3'  GGATGGACCAAAGGGGGCAG   15749        C  CTGATG  C_
                                CTGCCCCCT TG     CC  CC
                                ||||||||| ||     ||  ||
                                GACGGGGGA AC     GG  GG
                                     A  CA____  TA
GAM60   ATP1A2  3'  GGGTAGCAGCAGAGGCAG    7367       CCC      A
                                CTGCC   TCTGCTG TGCCC
                                |||||   ||||||| |||||
                                GACGG   AGACGAC ATGGG
                                   ___      G
GAM60   ATRN    3'  TGAGGACACAGCCAGGACGGCA 58447      C_  CT   A  C  C
          G                      CTGCC  CCT  GCTG TG CC CA
                                |||||  |||  |||| || || ||
                                GACGG  GGA  CGAC AC GG GT
                                   CA  C_   _ A  A
GAM60   AVP     5'  GCCAGCAGAGGCAGCAG     6675      CC       AT
                                CTGC  CCTCTGCTG  GC
                                ||||  |||||||||  ||
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                                GACG  GGAGACGAC  CG
                                  AC       __
GAM60   B3GNT3   3'  TGGAGGTGTGGGCAGAGGAGGG 27306    _      G    C
                                CCC CCTCTGCT ATGCC CCA
                                ||| |||||||| ||||| |||
                                GGG GGAGACGG TGTGG GGT
                                  A       G    A
GAM60   CBFA2T2  3'  GGAGTCGGCAGAGAAGCAG   18712     CCC        G
                                CTGC   CTCTGCTGAT CC
                                ||||   |||||||||| ||
                                GACG   GAGACGGCTG GG
                                  AA_        A
GAM60   CDS2     3'  GGAACAGAACTGAGCAGGGGCA 15108        __   TG__   ATG
           G                     CTGCCCC  CTC    CTG   CC
                                |||||||  |||    |||   ||
                                GACGGGG  GAG    GAC   GG
                                    AC   TCAA   AA_
GAM60   CEP2     3'  TGGGGGCAGGGGAAGAGACAG  23250    CCCC    G  GA
                                CTG    CTCT CT  TGCCCCCA
                                |||    |||| ||  ||||||||
                                GAC    GAGA GG  ACGGGGGT
                                  A___    A  GG
GAM60   COPA     5'  GGGGGGACAGAGGGGCAG    16479        C    CTGATG
                                CTGCCCC TCTG     CCCCC
                                ||||||| ||||     |||||
                                GACGGGG AGAC     GGGGG
                                    _   AG_____
GAM60   DAG1     3'  TGGGGGCACCTGGGAGGTCA   16557    T   _   TCTGCTGA
                                C GCC CCC       TGCCCCCA
                                | ||| |||       ||||||||
                                A TGG GGG       ACGGGGGT
                                 C   A   TCC_____
GAM60   DBCCR1   5'  GGGAGGCAGAGGGAGTAG    28243      C        GATG
                                CTGC CCCTCTGCT    CCC
                                |||| |||||||||    |||
                                GATG GGGAGACGG    GGG
                                  A       A___
GAM60   DDB2     3'  TGGGTGGTAGCAGAGGGATCA  5458     CC        GAT   _
                                TG  CCCTCTGCT   GCC CCCA
                                ||  |||||||||   ||| ||||
                                AC  GGGAGACGA   TGG GGGT
                                  TA        ___   T
GAM60   DTNA     3'  GCCAGCAGGGGGGAGCAG     9146       C         AT
                                CTGC CCCTCTGCTG  GC
                                |||| ||||||||||  ||
                                GACG GGGGGACGAC  CG
                                  A        __
GAM60   DTNA     3'  GCCAGCAGGGGGGAGCAG     53270      C         AT
                                CTGC CCCTCTGCTG  GC
                                |||| ||||||||||  ||
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                                GACG GGGGGACGAC  CG
                                  A        __
GAM60   DTNA    3'  GCCAGCAGGGGGAGCAG    53272     C        AT
                                CTGC CCCTCTGCTG  GC
                                |||| ||||||||||  ||
                                GACG GGGGGACGAC  CG
                                  A        __
GAM60   DTNA    3'  GCCAGCAGGGGGAGCAG    53277     C        AT
                                CTGC CCCTCTGCTG  GC
                                |||| ||||||||||  ||
                                GACG GGGGGACGAC  CG
                                  A        __
GAM60   DTR     3'  GGGGTCAGTGCAGCAGAGGACA 10457    CCC       AT___
            G                    CTG   CCTCTGCTG    GCCCC
                                |||   |||||||||    |||||
                                GAC   GGAGACGAC    TGGGG
                                  A__       GTGAC
GAM60   DUSP3   3'  GGGGGCTCAGAGGGGG     15837        CTGAT
                                CCCCCTCTG    GCCCCC
                                |||||||||    ||||||
                                GGGGGAGAC    CGGGGG
                                     T_____
GAM60   EGFL4   3'  GGGGATCCAGGAGGAGCAG   62470     CC    GCT   G
                                CTGC  CCTCT   GAT CCCC
                                ||||  |||||   ||| ||||
                                GACG  GGAGG   CTA GGGG
                                  A_    AC_  _
GAM60   EHD2    3'  TGGAAGCATTTAGAGGGG    28231        CT    CC
                                CCCCTCTG  GATGC  CCA
                                ||||||||  |||||  |||
                                GGGGAGAT  TTACG  GGT
                                     __    AA
GAM60   EIF2B5  3'  GGGAACAGCAGAGAGCAG    62205     CCC      ATG
                                CTGC   CTCTGCTG   CCC
                                ||||   ||||||||   |||
                                GACG   GAGACGAC   GGG
                                  A__       AA_
GAM60   EPHA8   3'  TGGAGGCATCATGGCAGAG   40441        __     C
                                CTCTGCT  GATGCC CCA
                                |||||||  |||||| |||
                                GAGACGG  CTACGG GGT
                                     TA     A
GAM60   EZH1    3'  TGGGAGTGTTACAGTAGGGAGC 10558     C   _  C     C
            AG                    CTGC CCCT CTG TGATGC CCCA
                                |||| |||| ||| |||||| ||||
                                GACG GGGA GAC ATTGTG GGGT
                                  A   T  _     A
GAM60   FGFR4   5'  GGAGGAGCCAGGAAGGCAG   10637      C_  CT   GATG  C
                                CTGCC  CCT  GCT   CC CC
                                |||||  |||  |||   || ||
```

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                                GACGG  GGA  CGA    GG GG
                                  AA   C_   ____   A
GAM60   FGFR4    5'  GGAGGAGCCAGGAAGGCAG   43630      C_   CT   GATG  C
                                CTGCC  CCT  GCT    CC CC
                                |||||  |||  |||    || ||
                                GACGG  GGA  CGA    GG GG
                                  AA   C_   ____   A
GAM60   GCNT2    5'  GGGGAGGCAGAGGGAGG     9455     _       GATG
                                CC CCCTCTGCT    CCCC
                                || |||||||||    ||||
                                GG GGGAGACGG    GGGG
                                 A        A___
GAM60   GDF5     3'  GGAATCACAGAGGGGTCAG   6896      C       C    G
                                CTG CCCCTCTG TGAT CC
                                ||| |||||||| |||| ||
                                GAC GGGGAGAC ACTA GG
                                  T       _    A
GAM60   GRLF1    3'  TGGGGACAGAGGCAGGGGCA   79263       CTC    GA  C
                                TGCCCC   TGCT  TG CCCCA
                                ||||||   ||||  || |||||
                                ACGGGG   ACGG  AC GGGGT
                                   ___    AG  A
GAM60   H1F0     5'  GGCAGAGGCAGAGGCAG     19219       CCC     GA
                                CTGCC   TCTGCT  TGCC
                                |||||   ||||||  ||||
                                GACGG   AGACGG  ACGG
                                   ___     AG
GAM60   H1F0     5'  TGGGAAAAGGGAGGCAGAGGAG 19220       C       GATG  ____
            GCAG                    CTGCC CCTCTGCT    CC    CCCA
                                |||||  ||||||||    ||    ||||
                                GACGG GGAGACGG    GG    GGGT
                                   A       AG__  AAAA
GAM60   HMG20A   3'  TGGGGGCAGAGAAAGAGTGCAG 37072      CCC    GCTGA
                                CTGC   CTCT    TGCCCCCA
                                ||||   ||||    ||||||||
                                GACG   GAGA    ACGGGGGT
                                  T__    AAGAG
GAM60   HNRPD    5'  GGGAGGCGAAGGGGGCAG    49389         CTGCTGA   _
                                CTGCCCCCT      TGCC CCC
                                |||||||||      |||| |||
                                GACGGGGGA      GCGG GGG
                                    A_______    A
GAM60   HNRPD    5'  GGGAGGCGAAGGGGGCAG    10950         CTGCTGA   _
                                CTGCCCCCT      TGCC CCC
                                |||||||||      |||| |||
                                GACGGGGGA      GCGG GGG
                                    A_______    A
GAM60   HOXB3    5'  GGGGGGCAGAGAGGGG      10955      _     TGATG
                                CCCC CTCTGC    CCCCC
                                |||| ||||||    |||||
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                                GGGG GAGACG    GGGGG
                                  A    _____
GAM60   ISG20    5'  GGCAGCAGAGAGGCAG     11022      CC     GAT
                                CTGCC  CTCTGCT   GCC
                                |||||  |||||||   |||
                                GACGG  GAGACGA   CGG
                                  A_     ___
GAM60   ITIH1    3'  GGGGCCAAGGCAGAGGAGG   11058    C      GAT
                                CC CCTCTGCT   GCCCC
                                || ||||||||   |||||
                                GG GGAGACGG   CGGGG
                                 A       AAC
GAM60   JRK      5'  GGATCAGCAGAGCAGGCAG   87829      CC       G
                                CTGCC  CTCTGCTGAT CC
                                |||||  |||||||||| ||
                                GACGG  GAGACGACTA GG
                                  AC        _
GAM60   LEP      3'  GGGGTGATTTCAGAGAGGGCAG 5866       C    CT  _
                                CTGCCC CTCTG  GAT GCCCC
                                ||||||| |||||  ||| |||||
                                GACGGG GAGAC  TTA TGGGG
                                   A    T_  G
GAM60   LMO2     5'  GGAGGCCGAGCAAGCGGAGGCA 19938      _ _ C   GAT   C
           G                     CTGCC CC CT TGCT   GCC CC
                                |||||  ||  ||  ||||   |||  ||
                                GACGG GG GA ACGA   CGG GG
                                   A  C  _   GC_   A
GAM60   LUZP1    5'  GGGGCCGCAGAGGGGACA    54404    C       TGAT
                                TG CCCCTCTGC    GCCCC
                                ||  |||||||||   |||||
                                AC GGGGAGACG    CGGGG
                                 A       C___
GAM60   MAP3K9   3'  GGGGCGGGCAAGGGGGACAG   61365    _     C    GA
                                CTG CCCCCT TGCT  TGCCCC
                                |||  ||||||  ||||  ||||||
                                GAC GGGGGA ACGG  GCGGGG
                                  A     _   __
GAM60   MGEA5    5'  GGAGGGCAGCAGAGGCAG    25220      CCC     GAT   _
                                CTGCC   TCTGCT   GCCC CC
                                |||||   ||||||   |||| ||
                                GACGG   AGACGA   CGGG GG
                                   ___     ___    A
GAM60   MMP14    3'  GGCAGAACAGCCAGAGGGGGCA 18430          _   A__
           G                     CTGCCCCCTCTG CTG   TGCC
                                ||||||||||||  |||   ||||
                                GACGGGGGAGAC GAC   ACGG
                                       C   AAG
GAM60   MSL3L1   3'  GGAAGTCAGCAGCAGGGGAGGC 55322      _   __      GC
           AG                     CTGCC CCCT  CTGCTGAT  CC
                                |||||  ||||  ||||||||  ||
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                                GACGG GGGG  GACGACTG  GG
                                  A   AC      AA
GAM60   NCOA6IP  5' GGGGGCAGGGGCAGGGGCAG  46155      CTC   GA
                                CTGCCCC  TGCT  TGCCCCC
                                |||||||  ||||  |||||||
                                GACGGGG  ACGG  ACGGGGG
                                   ___   GG
GAM60   NCSTN    5' GCTCAGCAGAGAGGCA     74136     CC      T
                                TGCC  CTCTGCTGA GC
                                ||||  |||||||| ||
                                ACGG  GAGACGACT CG
                                  A_      _
GAM60   NR4A2    3' TGGAAACTGTCAAGAGGGGGCA 21647       GC   GCCC_
                                TGCCCCCTCT  TGAT   CCA
                                ||||||||||  ||||   |||
                                ACGGGGGAGA  ACTG   GGT
                                     __   TCAAA
GAM60   P2RY6    3' GGAAGCTTCTTAGAAGAGGCAG 15999     CCC   CT  T  CC
                                CTGCC  TCTG  GA GC  CC
                                |||||  ||||  || ||  ||
                                GACGG  AGAT  CT CG  GG
                                   AGA   T_  T  AA
GAM60   PCSK5    5' GGGCCAGCAGAGGGGGC    21676          AT
                                GCCCCCTCTGCTG  GCCC
                                ||||||||||||  ||||
                                CGGGGGGAGACGAC  CGGG
                                              __
GAM60   PEX13    5' GGGAGCCGAGAGGAGGCGG   12043     C    GCTGAT  C
                                CTGCC CCTCT     GC CCC
                                ||||| |||||     || |||
                                GGCGG GGAGA     CG GGG
                                   A    GC____  A
GAM60   PGF      3' TGAAGGCAGTGGCAGGGGAGCA 12067     C  T    GA   CC
           G                     CTGC CCC CTGCT  TGCC  CA
                                ||||  ||| |||||  ||||  ||
                                GACG GGG GACGG  ACGG  GT
                                  A  _    TG   AA
GAM60   PHLDA3   5' GGAGGCATCTGGCAGAGGCGG  25694    _      _     C
                                CC CCTCTGCT GATGCC CC
                                || |||||||| |||||| ||
                                GG GGAGACGG CTACGG GG
                                 C      T     A
GAM60   PLAB     5' TGGGGGCACCCTGAGGGGGCA  66428        TGCTGA
                                TGCCCCCTC     TGCCCCCA
                                |||||||||     ||||||||
                                ACGGGGGAG     ACGGGGGT
                                     TCCC__
GAM60   PPP2R2B  5' GGGCAGCGGAGGCAG      17122      CCC     GAT   C
                                CTGCC   TCTGCT   GCC C
                                |||||   ||||||   ||| |
```

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                                GACGG  AGGCGA  CGG G
                                  ___    ___  A
GAM60   PROK1    3' TGGGAGCAAGGGACAGGGAGCA 51571    C   CTG  GA  C
          G                     CTGC CCCT  CT  TGC CCCA
                                |||| ||||  ||  ||| ||||
                                GACG GGGA  GG  ACG GGGT
                                  A   CA_  GA  A
GAM60   PSCD3    3' GGAAGGCGTGGCAGGGAGGCAG 16164     C T   G   C_
                                CTGCC CC CTGCT ATGCC  CC
                                ||||| || ||||| |||||  ||
                                GACGG GG GACGG TGCGG  GG
                                  A _   _    AA
GAM60   PTCRA    3' GGGGCATTTAGGGAGCAG    57154    C   CTGCT
                                CTGC CCCT    GATGCCCC
                                |||| ||||    ||||||||
                                GACG GGGA    TTACGGGG
                                  A   T____
GAM60   PTGS1    3' GCATACAACAGAGGGGGCA   55474        C _
                                TGCCCCCTCTG TG ATGC
                                |||||||||| || ||||
                                ACGGGGGAGAC AC TACG
                                      A  A
GAM60   PTGS1    3' GCATACAACAGAGGGGGCA   8242         C _
                                TGCCCCCTCTG TG ATGC
                                |||||||||| || ||||
                                ACGGGGGAGAC AC TACG
                                      A  A
GAM60   RAP1GA1  3' GGGATTGCTCAGTGGAAGCAG  12774    CCCC  TG   T  C__
                                CTGC   TC  CTGA GC   CCC
                                ||||   ||  |||| ||   |||
                                GACG   AG  GACT CG   GGG
                                  A___  GT   _  TTA
GAM60   RIMS1    5' GCGAGCAGAGGGGGCGG    73030          GA
                                CTGCCCCCTCTGCT  TGC
                                ||||||||||||||  |||
                                GGCGGGGGAGACGA  GCG
                                          __
GAM60   RPA2     5' GGAGCATGGGCAGAGGAGACAG 12899    CCC      G   C
                                CTG  CCTCTGCT ATGC CC
                                |||  |||||||| |||| ||
                                GAC  GGAGACGG TACG GG
                                  AGA      G   A
GAM60   RPS6KA2  3' GGCACAGGTGGGAGGGCAG  41225     C  TG  A
                                CTGCCC CTC  CTG TGCC
                                |||||| |||  ||| ||||
                                GACGGG GGG  GAC ACGG
                                   A  TG  _
GAM60   S100A10  5' GGGGGCAGGAAGAGGGGG   60048       GCTGA
                                CCCCCTCT    TGCCCCC
                                ||||||||    |||||||
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                                GGGGGAGA    ACGGGGG
                                    AGG__
GAM60   SIRT1    5' GGGAGCAGAGGAGGCG     25289     C      GATG
                                TGCC CCTCTGCT    CCC
                                |||| ||||||||    |||
                                GCGG GGAGACGA    GGG
                                  A      _____
GAM60   SLC12A4  5' GGGGACAGCGGCGGGGACAG  18629    C   T    ATG
                                CTG CCCC CTGCTG   CCCC
                                ||| |||| ||||||   ||||
                                GAC GGGG GGCGAC   GGGG
                                  A   C     A__
GAM60   SLC22A12 3' GGAGAGCAGAGGGGTCAG    58690    C       GATG
                                CTG CCCCTCTGCT    CC
                                ||| ||||||||||    ||
                                GAC GGGGAGACGA    GG
                                  T        GA__
GAM60   SLC5A5   5' GGGGCGGACGCAGAGACAG   6597     CCCC     TGA
                                CTG    CTCTGC   TGCCCC
                                |||    ||||||   ||||||
                                GAC    GAGACG   GCGGGG
                                  A___     CAG
GAM60   SOX11    3' CAAAGGCAGAGGGGGCGG    13310          GA
                                CTGCCCCCTCTGCT  TG
                                ||||||||||||||  ||
                                GGCGGGGGGAGACGG  AC
                                        AA
GAM60   SPAG8    3' GGGGGCAGAGCGGGGCAG    25841       CTCT   GA
                                CTGCCCC    GCT  TGCCCCC
                                |||||||    |||  |||||||
                                GACGGGG    CGA  ACGGGGG
                                    _____  G_
GAM60   STK11    3' GGGCCGGGCAGGGGGACAG   6599     C    T    GAT
                                CTG CCCC CTGCT   GCCC
                                ||| |||| |||||   ||||
                                GAC GGGG GACGG   CGGG
                                  A    _    GC_
GAM60   STX1A    3' GGGAAGAGGCAGAGGGAGGCAG 17214      _       GATG
                                CTGCC CCCTCTGCT    CCC
                                ||||| |||||||||    |||
                                GACGG GGGAGACGG    GGG
                                   A        AGAA
GAM60   TTYH1    3' GGGAGTAGCTGAGGGGGCAG   40685         T   ATG
                                CTGCCCCCTC GCTG   CCC
                                |||||||||| ||||   |||
                                GACGGGGGAG CGAT   GGG
                                      T   GA_
GAM60   UBE2G2   3' GGGAGGCAGAGGTAGCAG    65490     CC      GATG
                                CTGC  CCTCTGCT    CCC
                                ||||  ||||||||    |||
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                                GACG  GGAGACGG   GGG
                                  AT      A___
GAM60   USP5    3'  GGGCAGAGCAGAGGGGCAG   14448       C     GA
                                CTGCCCC TCTGCT  TGCCC
                                ||||||| ||||||  |||||
                                GACGGGG AGACGA  ACGGG
                                   _     G_
GAM60   WHSC1   3'  TGGGGACATTGGGAAGGTGGGC 56703       _  CTG TG   C
          AG                      CTGCCC CCT   C  ATG CCCCA
                                ||||||| |||   |  ||| |||||
                                GACGGG GGA   G  TAC GGGGT
                                   T   AG_ GT   A
GAM60   ZNF219  3'  GCCAGCAGGGGGCAG      33555         CT    AT
                                CTGCCCCCT  GCTG  GC
                                |||||||||  ||||  ||
                                GACGGGGGA  CGAC  CG
                                     __    __
GAM60   20D7-FC4 3'  GGACCCACCAGCAGGGAGCAG  61564     CC  T     A  CCC
                                CTGC  CC CTGCTG TG   CC
                                ||||  || ||||||  ||   ||
                                GACG  GG GACGAC AC   GG
                                  A_ _     C  CCA
GAM60   ABIN-2  3'  GGAACATCTGGCAGAGGG    44461         _   CC
                                CCCTCTGCT GATG  CC
                                |||||||||  ||||  ||
                                GGGAGACGG CTAC  GG
                                     T    AA
GAM60   AIP     5'  GGAAGTTGCCGAAAGGGAGCAG 15615     _  C_  T  T   GC
                                CTGC CCC  TC GC GAT  CC
                                |||| |||  || || |||  ||
                                GACG GGG  AG CG TTG  GG
                                  A   AA  C  _   AA
GAM60   ASB13   3'  TGGGGAGCACAGAGGAGGC   45547     C     CTGA  _
                                GCC CCTCTG    TGC CCCCA
                                |||  ||||||    ||| |||||
                                CGG GGAGAC    ACG GGGGT
                                  A      ____   A
GAM60   BATF    5'  GGGCAGGCAGAGGAGGCA    22147      C       GA
                                TGCC CCTCTGCT  TGCCC
                                |||| ||||||||  |||||
                                ACGG GGAGACGG  ACGGG
                                  A       __
GAM60   BCDO2   3'  TGAGGACTCCAAAAGGGGGGCA 50036        T  GC  ATGC  C
                                TGCCCCC CT  TG    CC CA
                                ||||||| ||  ||    || ||
                                ACGGGGG GA  AC    GG GT
                                   _ AA  CTCA  A
GAM60   BRP44I  5'  TGGGAAGCGGCAGCAGAGGCAG 32740       CCC      A   C_
                                CTGCC   TCTGCTG TGC  CCCA
                                |||||   ||||||| |||  ||||
```

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                                GACGG  AGACGAC GCG  GGGT
                                  ___     G  AA
GAM60   C12orf22  3'  GGAGGCAGTAGGGAGCA    48708    C   CT  GAT  C
                                TGC CCCT  GCT  GCC CC
                                ||| ||||  |||  ||| ||
                                ACG GGGA  TGA  CGG GG
                                  A  __  ___  A
GAM60   C12orf3   3'  GGGGTCTTGAAGAGGGGGCAG  40166         GC  T
                                CTGCCCCCTCT  TGA GCCCC
                                ||||||||||  ||| |||||
                                GACGGGGGAGA  GTT TGGGG
                                      A_  C
GAM60   C17orf31  5'  TGAAGGTGGCAGAGGATGCAG  34545    CC      GAT  CC
                                CTGC  CCTCTGCT  GCC  CA
                                ||||  ||||||||  |||  ||
                                GACG  GGAGACGG  TGG  GT
                                  TA       ___  AA
GAM60   C20orf110 3'  TGGGGGAGACAGAAGGGGCAG  80367       C  _ GATG
                                CTGCCCC TCTG CT   CCCCCA
                                ||||||| |||| ||   ||||||
                                GACGGGG AGAC GA   GGGGGT
                                    A   A ____
GAM60   C20orf39  5'  TGAGGGGAGGGCAGAGGAGG  46579   C      GATG  _
                                CC CCTCTGCT   CCCC CA
                                || ||||||||   |||| ||
                                GG GGAGACGG   GGGG GT
                                 A      GA__   A
GAM60   C8orf13   3'  GGGGTGTCAGAGGAAGC    82481   CC   GCT
                                GC  CCTCT  GATGCCCC
                                ||  |||||  ||||||||
                                CG  GGAGA  CTGTGGGG
                                 AA   ___
GAM60   CAMTA1    3'  GGAAATTTGCAGAGGGGCAG  68506       C   T  GC
                                CTGCCCC TCTGC GAT  CC
                                ||||||| ||||| |||  ||
                                GACGGGG AGACG TTA  GG
                                    _   T  AA
GAM60   CBLN1     5'  GGGAACACAGCGCGGAGGGG  16369       __  A  CC
                                CCCCTCT  GCTG TG  CCC
                                |||||||  |||| ||  |||
                                GGGGAGG  CGAC AC  GGG
                                    CG   _  AA
GAM60   CENTG3    3'  GGAAGAGGGCAGAGGGGCCAG  50047    C       GATG_
                                CTG CCCCTCTGCT    CC
                                ||| ||||||||||    ||
                                GAC GGGGAGACGG    GG
                                  C        GAGAA
GAM60   cerk      3'  TGGGGGCAGTCAGGAGGAAGC  43172    CC   TG  _
                                GC  CCTC  CTGA TGCCCCCA
                                ||  ||||  |||| ||||||||
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                                CG  GGAG  GACT ACGGGGGT
                                 AA   __   G
GAM60   COASTER   3'  TGGGGGCAGGGCAAGAGGAGAC 32083    CCC    _  GA
          AG                     CTG   CCTCT GCT  TGCCCCCA
                                |||   ||||| |||  ||||||||
                                GAC   GGAGA CGG  ACGGGGGT
                                  AGA    A  G_
GAM60   CXYorf1   3'  TGGGGGCATCGGCAAGG     82925     C
                                CCT TGCTGATGCCCCCA
                                ||| ||||||||||||||
                                GGA ACGGCTACGGGGGT
                                 _
GAM60   DIO2      3'  TGGAGAAATGAAGCAGAGGAAG 26558    C_      G_  GCCC
          G                      CC  CCTCTGCT  AT   CCA
                                ||  ||||||||  ||   |||
                                GG  GGAGACGA  TA   GGT
                                 AA       AG  AAGA
GAM60   DIO2      3'  TGGAGAAATGAAGCAGAGGAAG 7668     C_      G_  GCCC
          G                      CC  CCTCTGCT  AT   CCA
                                ||  ||||||||  ||   |||
                                GG  GGAGACGA  TA   GGT
                                 AA       AG  AAGA
GAM60   DKFZP564B1162 5'  GGGGGTGCTATAAAAGAAGCAG 49350     CCCC   GC__  AT
                                CTGC    TCT    TG  GCCCCC
                                ||||    |||    ||  ||||||
                                GACG    AGA    AT  TGGGGG
                                  A___   AAAT  CG
GAM60   DKFZP564C103 3'  GGGGGCACTGAGGAAGCAG   32241     CC    TGCTGA
                                CTGC  CCTC     TGCCCCC
                                ||||  ||||     |||||||
                                GACG  GGAG     ACGGGGG
                                  AA   TC____
GAM60   DKFZP667O116 3'  CAGAAGCAGAGGAGGCAG    95939      C      GA
                                CTGCC CCTCTGCT  TG
                                ||||| ||||||||  ||
                                GACGG GGAGACGA  AC
                                   A       AG
GAM60   DKFZP761C169 5'  GGGGCACCTCTGGTGGGGCAG  68424       C  TGCTGA
                                CTGCCCC TC     TGCCCC
                                ||||||| ||     ||||||
                                GACGGGG GG     ACGGGG
                                    T  TCTCC_
GAM60   DKFZp762K222 5'  GGGGACTGCAGCGGAGGCAG   71671      CCC      ATG_
                                CTGCC   TCTGCTG   CCCC
                                |||||   |||||||   ||||
                                GACGG   AGGCGAC   GGGG
                                   ___     GTCA
GAM60   DKFZp762O076 5'  GGCAGCAGAGGCAGCAG     73957      CC       GAT
                                CTGC  CCTCTGCT   GCC
                                ||||  ||||||||   |||
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                                GACG  GGAGACGA   CGG
                                  AC       ___
GAM60   DPCR1    3'  TGGGGGCACCAATGCAGA    56000       __ A
                                TCTGC  TG TGCCCCCA
                                ||||||  || ||||||||
                                AGACG  AC ACGGGGGT
                                   TA  C
GAM60   DRF1     3'  TGGAGGAGGCAGTGGGGGCAG  47762         T    GATG  C
                                CTGCCCCC CTGCT    CC CCA
                                |||||||| |||||    || |||
                                GACGGGGG GACGG    GG GGT
                                     T    A___  A
GAM60   FAM3D    3'  GGGGCTGAGGAGGAGGAGCAG  57947      _ _    GCTGAT
                                CTGC CC CCTCT     GCCCC
                                |||| || |||||     |||||
                                GACG GG GGAGG     CGGGG
                                  A  A    AGT___
GAM60   FBP17    3'  TGGGAGCATCTGGCAGGCAGGG 73163          ___    _    C
            GGGCAG                  CTGCCCCCT   CTGCT GATGC CCCA
                                |||||||||   ||||| ||||| ||||
                                GACGGGGGG   GACGG CTACG GGGT
                                     ACG    T    A
GAM60   FBXO9    5'  GGGGGCGGTGCAGAGGGGGCA  54251           TGA
                                TGCCCCCTCTGC   TGCCCCC
                                ||||||||||||   |||||||
                                ACGGGGGAGACG   GCGGGGG
                                       TG_
GAM60   FLJ10415 3'  CAGCAGCAGAGGCAGCAG    36586      CC       A
                                CTGC  CCTCTGCTG TG
                                ||||  ||||||||| ||
                                GACG  GGAGACGAC AC
                                  AC        G
GAM60   FLJ10415 3'  GGGAGGAACAGCAGCAGAGGCA 36588       CC  _     ATG  _
            G                    CTGCC  CT CTGCTG   CC CCC
                                |||||  || ||||||   || |||
                                GACGG  GA GACGAC   GG GGG
                                   A_  C     AA_  A
GAM60   FLJ10468 3'  ATCAGCAGAGCAGGACAG    36631     _ CC
                                CTG CC  CTCTGCTGAT
                                ||| ||  ||||||||||
                                GAC GG  GAGACGACTA
                                  A  AC
GAM60   FLJ11126 3'  GGCAGCAGAGAGGCCAG     37652     C  C      GAT
                                CTG CC CTCTGCT   GCC
                                ||| || |||||||   |||
                                GAC GG GAGACGA   CGG
                                  C  A      ___
GAM60   FLJ12242 3'  GGGGAGAGGCAGCAGAAGGGGC 45504       C      ATG__
                                GCCCC TCTGCTG    CCCC
                                ||||| |||||||     ||||
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                                CGGGG AGACGAC    GGGG
                                  A      GGAGA
GAM60   FLJ12547 3' TGGAAGCACAGCGTGAGGGGGC 47136        _    A  CC
           A                    TGCCCCCTC TGCTG TGC  CCA
                                |||||||| ||||| |||  |||
                                ACGGGGGAG GCGAC ACG  GGT
                                     T    _  AA
GAM60   FLJ12577 3' GGTGAGCAGGGGAGCA     48886    C  T    GA
                                TGC CCC CTGCT  TGCC
                                ||| ||| |||||  ||||
                                ACG GGG GACGA  GTGG
                                  A  _    __
GAM60   FLJ12700 5' GGGGCAGTCAGGGAGCAG    46658     C   CTGCT  _
                                CTGC CCCT    GA TGCCCC
                                |||| ||||    || ||||||
                                GACG GGGA    CT ACGGGG
                                  A  _____ G
GAM60   FLJ12770 3' GGGGCAGTTGATGAGGCAG   50680     CCC  T  GAT
                                CTGCC   TC GCT   GCCCC
                                |||||   || |||   |||||
                                GACGG   AG TGA   CGGGG
                                   AGT  T  ___
GAM60   FLJ12998 3' TGGAGGGACAGAGCAGAGGGGC 43152    C       GA  _  _
           CAG                    CTG CCCCTCTGCT  TG CCC CCA
                                ||| ||||||||||  || ||| |||
                                GAC GGGGAGACGA  AC GGG GGT
                                  C        G_  A  A
GAM60   FLJ13111 3' TGAGGGACACACAGAGGTGACA 47629    CCC    C  A  _  C
           G                     CTG   CCTCTG TG TG CCC CA
                                |||   |||||| || || ||| ||
                                GAC   GGAGAC AC AC GGG GT
                                  AGT     _  _  A  A
GAM60   FLJ13114 3' GGAGCTTGGGCAGCAGGGGCAG 44905       CT    GAT  C
                                CTGCCCC  CTGCT   GC CC
                                |||||||  |||||   || ||
                                GACGGGG  GACGG   CG GG
                                     AC    GTT  A
GAM60   FLJ14249 3' TGGGGACATCGGTGTGAAGGG  42647    C  _      C
                                CCC TC TGCTGATG CCCCA
                                ||| || |||||||| |||||
                                GGG AG GTGGCTAC GGGGT
                                  A  T       A
GAM60   FLJ14594 3' GGAGCAGGCTAGGGGGCAG   52507        CT   GA   C
                                CTGCCCCCT  GCT  TGC CC
                                |||||||||  |||  ||| ||
                                GACGGGGGA  CGG  ACG GG
                                     T_   __   A
GAM60   FLJ14642 3' GGGAAGCAGAGGTGGCAG    52577      C       GATG
                                CTGCC CCTCTGCT    CCC
                                ||||| ||||||||    |||
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                                GACGG GGAGACGA    GGG
                                  T       A___
GAM60   FLJ14810  3'  TGGGGACAGAGAGCAGGGGGCA 52705         CT   GA_  C
          G                    CTGCCCCCT  GCT   TG CCCCA
                               |||||||||  |||   || |||||
                               GACGGGGGA  CGA   AC GGGGT
                                    __   GAG  A
GAM60   FLJ20296  3'  GGGCACAGCAGGGGACAG    35366     CC   T     A
                               CTG  CCC CTGCTG TGCCC
                               |||  ||| |||||| |||||
                               GAC  GGG GACGAC ACGGG
                                 A_  _     _
GAM60   FLJ20619  5'  GGGTGAGGCCAGGGGAGCAG   35894      _    CT   GAT
                               CTGC CCCCT  GCT   GCCC
                               |||| |||||  |||   ||||
                               GACG GGGGA  CGG   TGGG
                                 A    C_   AG_
GAM60   FLJ20700  3'  GGGAGGCCAAGGGGGCAG    36013         C  CTGAT  _
                               CTGCCCCCT TG     GCC CCC
                               |||||||||  ||     ||| |||
                               GACGGGGGA AC     CGG GGG
                                    _ ______   A
GAM60   FLJ22160  3'  GGGCATCAGGGACGCAG     45034      CCCC   G
                               CTGC    TCT CTGATGCCC
                               ||||    ||| |||||||||
                               GACG    AGG GACTACGGG
                                 C___   _
GAM60   FLJ23058  5'  GGCATCTCGGGGCAGGGGGCAG 45527          ___   CT
                               CTGCCCCCT   CTG  GATGCC
                               |||||||||   |||  ||||||
                               GACGGGGGA   GGC  CTACGG
                                    CGG   T_
GAM60   FLJ23403  3'  CAACAGCAATAGGGGGCAG   42204         C_    A
                               CTGCCCCCT  TGCTG TG
                               |||||||||  |||||  ||
                               GACGGGGGA  ACGAC AC
                                    TA    A
GAM60   FLJ32818  5'  GGGGGTGCCAGGGAAGCAG   59074     C_   CT  TGAT
                               CTGC  CCCT  GC    GCCCCC
                               ||||  ||||  ||    ||||||
                               GACG  GGGA  CG    TGGGGG
                                 AA    C_  _____
GAM60   FREQ     3'  TGGGAGCTGGAAGAAGGGGCA  27378       C   G  GAT  C
                               TGCCCC TCT CT   GC CCCA
                               ||||||  ||| ||   ||  ||||
                               ACGGGG AGA GG   CG GGGT
                                  A   A  T__  A
GAM60   GMPPB    5'  GGGCATAGCAGATGGGGCAG   97455        C      A
                               CTGCCCC TCTGCTG TGCCC
                               |||||||  |||||||  |||||
```

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                                GACGGGG AGACGAT ACGGG
                                    T     _
GAM60   HIC2     3' GGTGATGCAGCAGCAGGGGCA 65873      CT     AT__
                                TGCCCC CTGCTG   GCC
                                |||||| ||||||   |||
                                ACGGGG GACGAC   TGG
                                   AC     GTAG
GAM60   KBRAS2   3' TGAGGGCAAAGTAGAGG    34631       GA    C
                                CCTCTGCT TGCCC CA
                                |||||||| ||||| ||
                                GGAGATGA ACGGG GT
                                    A_    A
GAM60   KIAA0057 3' TGGGGGCCGAGCAGGGGGCA 25426       CT   GAT
                                TGCCCCCT GCT  GCCCCCA
                                |||||||| |||  |||||||
                                ACGGGGGA CGA  CGGGGGT
                                    __  GC_
GAM60   KIAA0265 5' GGGCTGGGACAGTGGGGGCAG 70442       T  _ GAT
                                CTGCCCCC CTG CT  GCCC
                                |||||||| ||| ||  ||||
                                GACGGGGG GAC GG  CGGG
                                    T  A GT_
GAM60   KIAA0280 3' GGGAATCCAGAGAGGGGCAG  93307      _   CT  G
                                CTGCCCC CTCTG  GAT CCC
                                ||||||| |||||  ||| |||
                                GACGGGG GAGAC  CTA GGG
                                    A   __  A
GAM60   KIAA0321 5' GGGTCTTTGCAGCAGGGGCAG 63059      CT   T T
                                CTGCCCC  CTGC GA GCCC
                                |||||||  |||| || ||||
                                GACGGGG  GACG TT TGGG
                                    AC   T C
GAM60   KIAA0329 3' GGTGGCAGCAGAGGCAG    29941     CCC     AT
                                CTGCC  TCTGCTG  GCC
                                |||||  |||||||  |||
                                GACGG  AGACGAC  TGG
                                  ___     GG
GAM60   KIAA0540 3' GGGAACACCCCGGGGTGGGCAG 64616     C   CTGA  CC
                                CTGCCC CTCTG   TG  CCC
                                |||||| |||||   ||  |||
                                GACGGG GGGGC   AC  GGG
                                   T   CCC_  AA
GAM60   KIAA0557 3' GGGCAGCGTATGGGGGCAG   78572      TC   TGA
                                CTGCCCCC  TGC  TGCCC
                                |||||||| |||  |||||
                                GACGGGGG  ATG  ACGGG
                                    T_  CG_
GAM60   KIAA0620 3' GGGGGCTGGAGGGGGGCAG   62813      T  G  GAT
                                CTGCCCCC CT CT  GCCCCC
                                |||||||| || ||  ||||||
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                                GACGGGGG GA GG   CGGGGG
                                    _ _  T__
GAM60   KIAA0720  3' GGCCGAGCAGAGGGGGCA    62988          GAT
                                TGCCCCCTCTGCT   GCC
                                |||||||||||||   |||
                                ACGGGGGAGACGA   CGG
                                    GC_
GAM60   KIAA0769  3' GGAGCAAAGAGGGGGGCAG   29758       T  G  GA   C
                                CTGCCCCC CT CT  TGC CC
                                |||||||| || ||  ||| ||
                                GACGGGGG GA GA  ACG GG
                                    _ _  A_   A
GAM60   KIAA0836  3' GCATCAAAGGGGGCAG     65167         CTGC
                                CTGCCCCCT   TGATGC
                                |||||||||   ||||||
                                GACGGGGGA   ACTACG
                                    A___
GAM60   KIAA0913  5' TGGGGGCGAGGAAGAGAAGGC  69535    CC   G  GA
                                GCC  CTCT CT  TGCCCCCA
                                |||  |||| ||  ||||||||
                                CGG  GAGA GG  GCGGGGGT
                                  AA   A  A_
GAM60   KIAA0945  3' TGGGGGCGGGAAGGAGGGGCA  30907       CT  GCTGA
                                TGCCCC  CT    TGCCCCCA
                                ||||||  ||    ||||||||
                                ACGGGG  GA    GCGGGGGT
                                   AG  AGG__
GAM60   KIAA0980  3' TGGGAGCTGTCAGCAAGGAGCA 47999     CC   C     _  C
          G                      CTGC  CCT TGCTGAT GC CCCA
                                ||||  ||| |||||||  || ||||
                                GACG  GGA ACGACTG CG GGGT
                                  A_  _     T  A
GAM60   KIAA1130  3' GGGAGGCAGAGGTAGCAG    63099     CC      GATG
                                CTGC  CCTCTGCT   CCC
                                ||||  ||||||||   |||
                                GACG  GGAGACGG   GGG
                                  AT       A___
GAM60   KIAA1136  3' GGCATGGGTAGAAGAGGACCAG 92959    CC  _  _    G
                                CTG  CC CT CTGCT ATGCC
                                |||  || || ||||| |||||
                                GAC  GG GA GATGG TACGG
                                  CA  A  A    G
GAM60   KIAA1193  3' GGGGCACAGAGGGCAG     68275       CC   CTGA    C
                                CTGCCC  TCTG   TGCCC C
                                ||||||  ||||   ||||| |
                                GACGGG  AGAC   ACGGG G
                                   __   _____    A
GAM60   KIAA1199  3' GGCCCAGCAGAGGGAGTAG   72931     C        AT
                                CTGC CCCTCTGCTG  GCC
                                ||||  ||||||||||  |||
```

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                                GATG GGGAGACGAC  CGG
                                  A        C_
GAM60   KIAA1259 3' GGGCGGAGAGAGGGGGCAG   50800          G  GA
                                CTGCCCCCTCT CT  TGCCC
                                |||||||||| ||  |||||
                                GACGGGGGAGA GA  GCGGG
                                      _ G_
GAM60   KIAA1277 3' GCTGTCCTGCAGCGGGGACAG  65079     C   T   T_  _
                                CTG CCCC CTGC  GAT GC
                                ||| |||| ||||  ||| ||
                                GAC GGGG GACG  CTG CG
                                  A   C   TC  T
GAM60   KIAA1277 3' GGGACAGCGGGGAGGCAG    65080      C  T     ATG
                                CTGCC CC CTGCTG   CCC
                                ||||| || ||||||   |||
                                GACGG GG GGCGAC   GGG
                                   A _     A__
GAM60   KIAA1277 3' GGGGACAGTGGGGACAG     65082     C   TCT   ATG
                                CTG CCCC   GCTG   CCCC
                                ||| ||||   ||||   ||||
                                GAC GGGG   TGAC   GGGG
                                  A   ____   A__
GAM60   KIAA1363 5' GGACACCGTAGAGGGGGCA   69791          T A  _
                                TGCCCCCTCTGC G TG CC
                                |||||||||||| | || ||
                                ACGGGGGAGATG C AC GG
                                      _ C  A
GAM60   KIAA1399 3' GGAGCCAACAGAGGGAGCAG  70793     C     C  AT  C
                                CTGC CCCTCTG TG  GC CC
                                |||| ||||||| ||  || ||
                                GACG GGGAGAC AC  CG GG
                                  A      A __ A
GAM60   KIAA1610 5' GGGAGCGGCAGAGACGGCAG  67739      CC       ATG
                                CTGCC  CTCTGCTG   CCC
                                |||||  ||||||||   |||
                                GACGG  GAGACGGC   GGG
                                   CA       GA_
GAM60   KIAA1879 5' TGGAGGACGTGCAGAGGGTGCA 73949     C       TG  _  C
          G                      CTGC CCCTCTGC  ATG CC CCA
                                |||| ||||||||  ||| || |||
                                GACG GGGAGACG  TGC GG GGT
                                  T       __  A  A
GAM60   KIAA1957 3' GGTGGGCGCGGAGGGAGCAG  76217     C       TGAT   _
                                CTGC CCCTCTGC    GCCC CC
                                |||| ||||||||    |||| ||
                                GACG GGGAGGCG    CGGG GG
                                  A       _____   T
GAM60   KIF13B   3' CAGCAGCAGAGGGGACAG    83713     C         A
                                CTG CCCCTCTGCTG TG
                                ||| ||||||||||| ||
```

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                                GAC GGGGAGACGAC AC
                                  A         G
GAM60   KIF13B   3'  CAGCAGCAGAGGGGACAG    31557     C         A
                                CTG CCCCTCTGCTG TG
                                ||| |||||||||| ||
                                GAC GGGGAGACGAC AC
                                  A         G
GAM60   KRTHB2   3'  TGGGGACAGACGGCAGAG    53454        A_  C
                                CTCTGCTG  TG CCCCA
                                ||||||||  || |||||
                                GAGACGGC  AC GGGGT
                                     AG  A
GAM60   LIN-28   3'  TGGGGGCAACCAGGAGGGGGG  45473        G   A_
                                CCCCTCT CTG  TGCCCCCA
                                ||||||| |||  ||||||||
                                GGGGGGA GAC  ACGGGGGT
                                    G   CA
GAM60   MESDC2   3'  GGCAGGCAGAGGAAACAG    72918     CCC       GA
                                CTG   CCTCTGCT  TGCC
                                |||   ||||||||  ||||
                                GAC   GGAGACGG  ACGG
                                  AAA       __
GAM60   MGC10334 5'  GGGTGCGGTGCAGAGCAGAGCA 48321      CCC_     TGA   C
            G                    CTGC    CTCTGC   TGC CCC
                                ||||    ||||||   ||| |||
                                GACG    GAGACG   GCG GGG
                                  AGAC     TG_   T
GAM60   MGC10765 3'  GGGAGGCAGAGGGTGCAG    44564     C        GATG
                                CTGC CCCTCTGCT    CCC
                                |||| |||||||||    |||
                                GACG GGGAGACGG    GGG
                                  T        A___
GAM60   MGC13010 5'  TGGAGGCACGGCAGAGGAGGCA 52062       C        A    C
            G                    CTGCC CCTCTGCTG TGCC CCA
                                ||||| ||||||||| |||| |||
                                GACGG GGAGACGGC ACGG GGT
                                  A        _    A
GAM60   MGC15416 5'  TGGGGGCAGCCAGGGAGAGGGC 57349       C    G   A_
            A                    TGCCC CTCT CTG  TGCCCCCA
                                ||||| |||| |||  ||||||||
                                ACGGG GAGG GAC  ACGGGGGT
                                  A    _  CG
GAM60   MGC16025 3'  TGGAAGGTTTTAGCAGAAAAAG 53029    CCC_       T   C_
            G                    CC    TCTGCTGA GCC  CCA
                                ||    |||||||| |||  |||
                                GG    AGACGATT TGG  GGT
                                 AAAA       T   AA
GAM60   MGC21688 3'  GTGTTTGGAGAGGAGGCAG    58917       C    GCT
                                CTGCC CCTCT   GATGC
                                ||||| |||||   |||||
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                                GACGG GGAGA   TTGTG
                                  A     GGT
GAM60   MGC35558  3'  TGAGGGCATCGTGGAAGGG   59422     C  TG T      C
                                CCC TC  C GATGCCC CA
                                ||| ||  | ||||||| ||
                                GGG AG  G CTACGGG GT
                                  A  GT _      A
GAM60   MGC5566   3'  TGGAAGCATTGCCAGAGGGG   44125        CT    CC
                                CCCCTCTG  GATGC  CCA
                                ||||||||  |||||  |||
                                GGGGAGAC  TTACG  GGT
                                     CG    AA
GAM60   NOPAR     5'  GGGGGGAGCAGAGGAGGCAG   54860      C       GATG
                                CTGCC CCTCTGCT    CCCCC
                                ||||| ||||||||    |||||
                                GACGG GGAGACGA    GGGGG
                                  A       G___
GAM60   NOPAR     5'  TGGAGACAAGGTAGGGGGGAGC 54861      _        GA  CCC
              AG                  CTGC CCCCTCTGCT  TG   CCA
                                ||||| ||||||||||  ||   |||
                                GACG GGGGGGATGG  AC   GGT
                                  A         A_  AGA
GAM60   OBTP      3'  GGAAGCCTCCAAGCAGAGGACA 34667     CCC       __  T  CC
              G                   CTG   CCTCTGCT  GA GC  CC
                                |||   ||||||||  || ||  ||
                                GAC   GGAGACGA  CT CG  GG
                                  A__       AC  C  AA
GAM60   P114-RHO-GEF 3'  GGGGGCATGGGCAGAGAGGGC  31674      C      G
                                GCCC CTCTGCT ATGCCCCC
                                |||| ||||||| ||||||||
                                CGGG GAGACGG TACGGGGG
                                  A      G
GAM60   p25       3'  TGGGGGTGACAAGAGGAGACAG 23839     CCC     GC  A
                                CTG   CCTCT  TG TGCCCCCA
                                |||   |||||  || ||||||||
                                GAC   GGAGA  AC GTGGGGGT
                                  AGA     __  A
GAM60   P2RXL1    3'  TGGAGGTCTGGGAGAGAGAGCA 19565      CCC    G  GAT   C
              G                   CTGC   CTCT CT   GCC CCA
                                ||||   |||| ||   ||| |||
                                GACG   GAGA GG   TGG GGT
                                  AGA    G  TC_   A
GAM60   P2RXL1    3'  TGGGAGAGAGAGCAGAGGGCGG 19566       _       GATGCC
              CAG                   CTGCC CCCTCTGCT      CCCA
                                ||||| |||||||||      ||||
                                GACGG GGGAGACGA      GGGT
                                  C        GAGAGA
GAM60   PP591     5'  TGGAGGGCCTTGCAGAGGGGCA 48152        C     TGAT   _
              G                   CTGCCCC TCTGC    GCCC CCA
                                ||||||| |||||    |||| |||
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                                GACGGGG AGACG   CGGG GGT
                                   _    TTC_   A
GAM60   PRO1257  5'  TGAGGGCATGAGCAGAGG    38327        G     C
                                CCTCTGCT ATGCCC CA
                                |||||||| |||||| ||
                                GGAGACGA TACGGG GT
                                     G     A
GAM60   REPRIMO  3'  TGGGGGCAGGTGGAGAGGGCGG 39532       C   TG  GA
                                CTGCCC CTC  CT  TGCCCCCA
                                |||||| |||  ||  ||||||||
                                GGCGGG GAG  GG  ACGGGGGT
                                   A  GT  __
GAM60   RINZF    5'  GGGGGCGAGACAGAGGGGG   43939         _  GA
                                CCCCCTCTG CT  TGCCCCC
                                ||||||||| ||  |||||||
                                GGGGGAGAC GA  GCGGGGG
                                     A  __
GAM60   RP4-622L5 3'  GGATATACAGACGGGGGCAG   39428        _   CTG  G
                                CTGCCCCC TCTG   AT CC
                                |||||||| ||||   || ||
                                GACGGGGG AGAC   TA GG
                                     C    ATA  _
GAM60   SIAT8A   5'  GGAGCATCGCTCGGAGGGGACA 13144    C       C_     C
                                TG CCCCTCTG  TGATGC CC
                                || ||||||||  |||||| ||
                                AC GGGGAGGC  GCTACG GG
                                  A       TC     A
GAM60   SKIP     3'  TGGGGGCAGGCAGAAGGG    33713    C     GA
                                CCC TCTGCT  TGCCCCCA
                                ||| ||||||  ||||||||
                                GGG AGACGG  ACGGGGGT
                                  A     __
GAM60   SKIP     3'  TGGGGGCAGGCAGAAGGG    56248    C     GA
                                CCC TCTGCT  TGCCCCCA
                                ||| ||||||  ||||||||
                                GGG AGACGG  ACGGGGGT
                                  A     __
GAM60   SLC16A6  3'  GGGGACACAAGGAGGCAG    17441      C   CTGC  A  C
                                CTGCC CCT    TG TG CCCC
                                ||||| |||    || || ||||
                                GACGG GGA    AC AC GGGG
                                   A  _____  _  A
GAM60   SLC2A10  5'  GGAGGGCAGGGCAGGAGGGACA 48556     C   CT    GA    _
           G                     CTG CCC  CTGCT  TGCCC CC
                                ||| |||  |||||  ||||| ||
                                GAC GGG  GACGG  ACGGG GG
                                  A  AG    G_    A
GAM60   SLC37A1  3'  GGCCAGCAGAGAAGCAG     39092      CCC       AT
                                CTGC   CTCTGCTG  GCC
                                ||||   ||||||||  |||
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                                GACG  GAGACGAC  CGG
                                  AA_      __
GAM60   SPRY4   3' GGATAGCAGGGGAGGCAG   49021     C      ATG
                                CTGCC CCTCTGCTG  CC
                                ||||| |||||||||  ||
                                GACGG GGGGACGAT  GG
                                   A       A__
GAM60   SPRY4   3' GGGCATCATCAGGCAG     49027     CCCTC  C
                                CTGCC    TG TGATGCCC
                                |||||    || ||||||||
                                GACGG    AC ACTACGGG
                                   _____ T
GAM60   SSH-3   3' GGAGCAGGAGCAGGGGCAG  37418      CTC   GA  C
                                CTGCCCC  TGCT  TGC CC
                                |||||||  ||||  ||| ||
                                GACGGGG  ACGA  ACG GG
                                   ___   GG  A
GAM60   SSH-3   3' GGAGCAGGGGCAGGGGCAG  37419      CTC   GA  C
                                CTGCCCC  TGCT  TGC CC
                                |||||||  ||||  ||| ||
                                GACGGGG  ACGG  ACG GG
                                   ___   GG  A
GAM60   SSH-3   3' GGGGCAGGGGCAGGGGCAG  37420      CTC   GA
                                CTGCCCC  TGCT  TGCCCC
                                |||||||  ||||  ||||||
                                GACGGGG  ACGG  ACGGGG
                                   ___   GG
GAM60   STAT2   3' GGGTACAGAGGGGACA     19454   C     CTGA
                                TG CCCCTCTG   TGCCC
                                || ||||||||   |||||
                                AC GGGGAGAC   ATGGG
                                 A     _____
GAM60   STC2    3' GGAGAAGGGTGGAGAGGAGGCA 14934     C   G  GAT   _____
          G                      CTGCC CCTCT CT  GCCC   CC
                                ||||| ||||| ||  ||||   ||
                                GACGG GGAGA GG  TGGG   GG
                                   A   _ ___   AAGA
GAM60   STX1B2  5' GGAGCAGCAGCAGAGGCAG  54619     CCC    A  C
                                CTGCC  TCTGCTG TGC CC
                                |||||  ||||||| ||| ||
                                GACGG  AGACGAC ACG GG
                                   ___     G  A
GAM60   SYT13   3' GGCTGGCAGAGTAGGCAG   95102     CC     GAT
                                CTGCC  CTCTGCT  GCC
                                |||||  |||||||  |||
                                GACGG  GAGACGG  CGG
                                   AT     T__
GAM60   TED     3' GGGGGCACAGAGGGG      32273       CTGA
                                CCCCTCTG   TGCCCCC
                                ||||||||   |||||||
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                                GGGGAGAC   ACGGGGG
                                    ____
GAM60   TGIF2    3' GCCACAGCAGGGGGCAG    41751        CT   AT
                                CTGCCCCCT GCTG GC
                                ||||||||| |||| ||
                                GACGGGGGA CGAC CG
                                     __   AC
GAM60   THTPA    5' TGAGGACATCAGCAGCAGTGG 44511   C _      C C
                                CC CT CTGCTGATG CC CA
                                || || |||||||| || ||
                                GG GA GACGACTAC GG GT
                                 T C       A A
GAM60   TM4-B    5' GGACACAGAGGGGCAG     25889       C   C ATG
                                CTGCCCC TCTG TG  CC
                                ||||||| |||| ||  ||
                                GACGGGG AGAC AC  GG
                                   _  _ A__
GAM60   YKT6     3' GGTAGCTGCAGAGGGGGGAG  22642   G       TGA
                                CT CCCCCTCTGC  TGCC
                                || ||||||||||  ||||
                                GA GGGGGAGACG  ATGG
                                 G        TCG
GAM60   ZIC5     5' TGAAGGCGGGCAGAGGG    53615        GA   CC
                                CCCTCTGCT TGCC CA
                                ||||||||| |||| ||
                                GGGAGACGG GCGG GT
                                     __   AA
GAM60   ZNF263   3' GGAATTGGCAGAGGAAGTAG  20427    CC     TG G
                                CTGC CCTCTGC AT CC
                                |||| ||||||| || ||
                                GATG GGAGACG TA GG
                                  AA     GT A
GAM60   ZNF263   3' GGGAGGTGCAGAGGCAGCAG  20428    CC     TGAT _
                                CTGC CCTCTGC   GCC CCC
                                |||| |||||||   ||| |||
                                GACG GGAGACG   TGG GGG
                                  AC     ____  A
GAM60   LOC116173 3' GCCAGCCAGAGAGGACAG   57427    C C   _ AT
                                CTG CC CTCTG CTG GC
                                ||| || ||||| |||  ||
                                GAC GG GAGAC GAC CG
                                  A A   C __
GAM60   LOC124470 3' TGGAAAGGCAGGCAGAGGG   76149       GA   C__
                                CCCTCTGCT TGCC  CCA
                                ||||||||| ||||  |||
                                GGGAGACGG ACGG  GGT
                                     __   AAA
GAM60   LOC124590 3' TGGAGGCACCAGAGGGGCA   76153      C   CTGA   C
                                TGCCCC TCTG   TGCC CCA
                                |||||| ||||   |||| |||
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                                ACGGGG AGAC    ACGG GGT
                                   _   C___    A
GAM60   LOC124997 3'  GCCTTCAGCTGAGGGGGCAG   74848          T    T_
                                CTGCCCCCTC GCTGA  GC
                                |||||||||| |||||  ||
                                GACGGGGGAG CGACT  CG
                                     T    TC
GAM60   LOC127841 5'  GCCCAGGCAGAGAGGGCAG    75188       C      GAT
                                CTGCCC CTCTGCT   GC
                                |||||| |||||||   ||
                                GACGGG GAGACGG   CG
                                   A      ACC
GAM60   LOC129181 5'  TGGGGGCTGCAGCAGGGAGGCA 76315      C  T     AT
                                TGCC CC CTGCTG  GCCCCCA
                                |||| || ||||||  |||||||
                                ACGG GG GACGAC  CGGGGGT
                                  A _     GT
GAM60   LOC129303 3'  GGGAACAGCAGAGGGGATAG   75375     C         ATG
                                CTG CCCCTCTGCTG   CCC
                                ||| ||||||||||   |||
                                GAT GGGGAGACGAC   GGG
                                  A          AA_
GAM60   LOC130940 5'  GGGGGTGGCGGAGAGGACAG   57939     C  C      GAT
                                CTG CC CTCTGCT   GCCCCC
                                ||| || |||||||   ||||||
                                GAC GG GAGGCGG   TGGGGG
                                  A  A      ___
GAM60   LOC143437 5'  TGGGGATACAGCAGGGAGCA   83861     CC  T     A  C
                                TGC  CC CTGCTG TG CCCCA
                                |||  || |||||| || |||||
                                ACG  GG GACGAC AT GGGGT
                                  A_ _     _ A
GAM60   LOC145241 5'  TGAAGGTGATCAGCAGGGGCAG 63529         CTC      _   CC
                                CTGCCCC   TGCTGAT GCC  CA
                                |||||||   ||||||| |||  ||
                                GACGGGG   ACGACTA TGG  GT
                                     ___      G   AA
GAM60   LOC146802 3'  GCAGCAGCAGAGAGCAG     78726      CCC       A
                                CTGC   CTCTGCTG TGC
                                ||||   |||||||| |||
                                GACG   GAGACGAC ACG
                                  A__       G
GAM60   LOC147043 5'  GGCATCAGAAGGGGAGC     88504    _    CTG
                                GC CCCCT   CTGATGCC
                                || |||||   ||||||||
                                CG GGGGA   GACTACGG
                                 A    A__
GAM60   LOC147645 5'  CACGGTTGGGGGAGGCAG     79066       _    T    A
                                CTGCC CCCTC GCTG TG
                                ||||| ||||| |||| ||
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                                GACGG GGGGG TGGC AC
                                  A    T   _
GAM60   LOC147912 5'  TGGGGGCGAAAAGGGGGGACAG 79266     C      GCTGA
                                CTG CCCCTCT    TGCCCCCA
                                ||| |||||||    ||||||||
                                GAC GGGGGGA    GCGGGGGT
                                  A      AAA__
GAM60   LOC148413 3'  GGGGCATCGGGGGGCAG     79581         CTGCT
                                CTGCCCCCT    GATGCCCC
                                |||||||||    ||||||||
                                GACGGGGGG    CTACGGGG
                                             _____
GAM60   LOC149386 5'  TGGGGGCGTCAGCAGAGGGGCA 85565        C
          G                      CTGCCCC TCTGCTGATGCCCCCA
                                |||||||| ||||||||||||||||
                                GACGGGG AGACGACTGCGGGGGT
                                  _
GAM60   LOC150481 3'  TGAGGGGATGGGCAGAGGAGGC 80717     C      G  G   _
                                GCC CCTCTGCT AT CCCC CA
                                ||| |||||||| || |||| ||
                                CGG GGAGACGG TA GGGG GT
                                  A       G  _   A
GAM60   LOC152220 3'  TGGGACTAGCAGCAGAGGCAG  86771      CCC      ATGCC
                                CTGCC   TCTGCTG    CCCA
                                |||||   |||||||    ||||
                                GACGG   AGACGAC    GGGT
                                   ___      GATCA
GAM60   LOC152627 3'  GGGAGGCAGAGGGTGCAG    81512      C       GATG
                                CTGC CCCTCTGCT    CCC
                                |||| |||||||||    |||
                                GACG GGGAGACGG    GGG
                                  T       A___
GAM60   LOC155066 5'  GGACCCGGCCAGAGGGACAG   82210     CC     _   ATG
                                CTG  CCCTCTG CTG   CC
                                |||  ||||||| |||   ||
                                GAC  GGGAGAC GGC   GG
                                  A_      C   CCA
GAM60   LOC157860 3'  GGGGCATCTGGGCGCAG     87880      C   TCTGCT
                                CTGC CCC     GATGCCCC
                                |||| |||     ||||||||
                                GACG GGG     CTACGGGG
                                  C   T_____
GAM60   LOC158062 3'  GGGGAGAGCCACAGAGGAGCAG 87964      CC     C  AT  ___
                                CTGC  CCTCTG TG  GC   CCCC
                                ||||  |||||| ||  ||   ||||
                                GACG  GGAGAC AC  CG   GGGG
                                  A_     _  __  AGA
GAM60   LOC158191 3'  TGAGGGGATGGGCAGAGGAGGC 82686     C      G  G   _
                                GCC CCTCTGCT AT CCCC CA
                                ||| |||||||| || |||| ||
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                                CGG GGAGACGG TA GGGG GT
                                  A       G _    A
GAM60   LOC159121 3'  TGGGGGCAAGGGCAAGAGG    88389       _   GA
                                CCTCT GCT  TGCCCCCA
                                ||||| |||  ||||||||
                                GGAGA CGG  ACGGGGGT
                                   A   GA
GAM60   LOC159199 5'  GGGCAGCAGAGTGAGCAG    83066     CCC      GAT
                                CTGC   CTCTGCT   GCCC
                                ||||   |||||||   ||||
                                GACG   GAGACGA   CGGG
                                  AGT      ___
GAM60   LOC162083 3'  GGAAAGCTGAGGGGGCAG    83208          T   GATG
                                CTGCCCCCTC GCT    CC
                                |||||||||| |||    ||
                                GACGGGGGAG CGA    GG
                                      T   AA__
GAM60   LOC163682 3'  GGGGGCACAGGGGGCAG     88412         CTGCT A
                                CTGCCCCCT    G TGCCCCC
                                |||||||||    | |||||||
                                GACGGGGGA    C ACGGGGG
                                     _____ _
GAM60   LOC164714 3'  GGCAGCAGGGGGGGCAG     88586            GAT
                                CTGCCCCCTCTGCT   GCC
                                ||||||||||||||   |||
                                GACGGGGGGGGACGA   CGG
                                      ___
GAM60   LOC169693 5'  GGGAAGCAGAGGAGCAG     88630      CC       GATG
                                CTGC  CCTCTGCT    CCC
                                ||||  ||||||||    |||
                                GACG  GGAGACGA    GGG
                                  A_       A___
GAM60   LOC196214 5'  GTACAGCAAGGGGGGCAG     91183          C     A
                                CTGCCCCCT TGCTG TGC
                                ||||||||| ||||| |||
                                GACGGGGGA ACGAC ATG
                                     _    _
GAM60   LOC196410 3'  TGGGGGCACCAGGGAGAATCAG 89034     CCCC    G   A
                                CTG    CTCT CTG TGCCCCCA
                                |||    |||| ||| ||||||||
                                GAC    GAGG GAC ACGGGGGT
                                  TAA_    _   C
GAM60   LOC196955 5'  TGAGGGCATTGTAAAAGG    77876     C_   T      C
                                CCT  TGC GATGCCC CA
                                |||  ||| ||||||| ||
                                GGA  ATG TTACGGG GT
                                  AA   _      A
GAM60   LOC200093 3'  TGGGGGCATCGGCAAGG     63781     C
                                CCT TGCTGATGCCCCCA
                                ||| ||||||||||||||
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                                GGA ACGGCTACGGGGGT
                                  _
GAM60   LOC200563 5'  GCATCAGTCAGTGGACAG    91656     CCC  T  _
                                CTG   CC CTG CTGATGC
                                |||   || ||| |||||||
                                GAC   GG GAC GACTACG
                                  A__  T  T
GAM60   LOC200734 3'  TGAAGGCATCGGTTAAGGGCA  90284      CCTCT       CC
                                TGCCC    GCTGATGCC  CA
                                |||||    |||||||||  ||
                                ACGGG    TGGCTACGG  GT
                                   AAT__       AA
GAM60   LOC201685 5'  GCCAGCAGACAGGGCAG     91842       CC      AT
                                CTGCCC  TCTGCTG  GC
                                ||||||  |||||||  ||
                                GACGGG  AGACGAC  CG
                                   AC     __
GAM60   LOC203238 3'  GTTTCAGCAGAAGTGGCAG    90824       CCC       T
                                CTGCC   TCTGCTGA GC
                                |||||   |||||||| ||
                                GACGG   AGACGACT TG
                                   TGA       T
GAM60   LOC203554 5'  GGGAGGCAGCAGAGGGG     92328         GAT  _
                                CCCCTCTGCT   GCC CCC
                                ||||||||||   ||| |||
                                GGGGAGACGA   CGG GGG
                                     ___  A
GAM60   LOC220024 5'  GGGAGCTGAGCGCAGCAGAGAG 95032      CCC       AT____  C
           CAG                    CTGC   CTCTGCTG     GC CCC
                                ||||   ||||||||     || |||
                                GACG   GAGACGAC     CG GGG
                                  A__       GCGAGT  A
GAM60   LOC221184 5'  TGGGGGTGCCCCAGCAGCGGGG 93411         T     A__
           GCAG                    CTGCCCCC CTGCTG   TGCCCCCA
                                |||||||| ||||||   ||||||||
                                GACGGGGG GACGAC   GTGGGGGT
                                     C     CCC
GAM60   LOC221922 5'  GGGAGGGTCAGGAGGGCAG    94255       CCTC G     G  _
                                CTGCCC    T CTGAT CC CCC
                                ||||||    | ||||| || |||
                                GACGGG    A GACTG GG GGG
                                   ____ G     _  A
GAM60   LOC221922 5'  GGGGGAGCAGGAGGGCAG     94258       C T     GATG
                                CTGCCC C CTGCT    CCCCC
                                |||||| | |||||    |||||
                                GACGGG G GACGA    GGGGG
                                   A _     _____
GAM60   LOC221922 5'  GGGGGAGCAGGAGGGCAG     94259       C T     GATG
                                CTGCCC C CTGCT    CCCCC
                                |||||| | |||||    |||||
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                                GACGGG G GACGA   GGGGG
                                   A _   _____
GAM60   LOC221964 3'  GGGGCAGGGGCAGGGGCAG   95607       CTC   GA
                                CTGCCCC  TGCT  TGCCCC
                                |||||||  ||||  ||||||
                                GACGGGG  ACGG  ACGGGG
                                    ___   GG
GAM60   LOC253367 3'  GGGGAGTTTCGAGGGGGCA   99438        TGCT  T  _
                                TGCCCCCTC   GA GC CCCC
                                |||||||||   || || ||||
                                ACGGGGGAG   CT TG GGGG
                                     _____  T  A
GAM60   LOC253531 5'  TGGGGATACAGCAGGGAGCA  98227    CC  T    A  C
                                TGC  CC CTGCTG TG CCCCA
                                |||  || |||||| || |||||
                                ACG  GG GACGAC AT GGGGT
                                  A_  _    _  A
GAM60   LOC253974 3'  TGGGGGCATCAGCAGAGGGGGC 99284
          AG                    CTGCCCCCTCTGCTGATGCCCCCA
                                |||||||||||||||||||||||||
                                GACGGGGGGAGACGACTACGGGGGT

GAM60   LOC254050 3'  GGAAGGCAGAGGTGGCAG   96562      C      GATG
                                CTGCC CCTCTGCT   CC
                                ||||| ||||||||   ||
                                GACGG GGAGACGG   GG
                                   T      AA__
GAM60   LOC254181 5'  GGGCCCCAGCAGAGCAGGCAG  99442     CC      AT
                                CTGCC  CTCTGCTG  GCCC
                                |||||  ||||||||  ||||
                                GACGG  GAGACGAC  CGGG
                                   AC      CC
GAM60   LOC254263 3'  GGCTCAGCAGGGGGGCAG   96369       T     T
                                CTGCCCCC CTGCTGA GCC
                                |||||||| ||||||| |||
                                GACGGGGG GACGACT CGG
                                     _     _
GAM60   LOC255394 5'  TGAGGGCCCCAGAGGGGG   96544       CTGAT   C
                                CCCCCTCTG    GCCC CA
                                |||||||||    |||| ||
                                GGGGGAGAC    CGGG GT
                                     CC___   A
GAM60   LOC256073 5'  GGAAGCTCCAAGAGGGCAG   98487     CC   GCT  T  CC
                                CTGCCC  TCT   GA GC  CC
                                ||||||  |||   || ||  ||
                                GACGGG  AGA   CT CG  GG
                                   __  AC_  _  AA
GAM60   LOC256254 3'  GTTTCAGCAGAAGTGGCAG   97902     CCC      T
                                CTGCC   TCTGCTGA GC
                                |||||   |||||||| ||
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                                GACGG   AGACGACT TG
                                   TGA       T
GAM60   LOC256530 3'  GGGAGTTCAGTGGGGACAG   98622    C   TCT    T  C
                                CTG CCCC   GCTGA GC CCC
                                ||| ||||   ||||| || |||
                                GAC GGGG   TGACT TG GGG
                                  A   ___    _ A
GAM60   LOC256949 5'  GGCTGCGGAGGAGGCAG     96985      C      TGAT
                                CTGCC CCTCTGC    GCC
                                ||||| |||||||    |||
                                GACGG GGAGGCG    CGG
                                   A      T___
GAM60   LOC257095 5'  GGGCAGCGGGGGCAG       98721        TCT   GAT   C
                                CTGCCCCC   GCT   GCC C
                                ||||||||   |||   ||| |
                                GACGGGGG   CGA   CGG G
                                     ___   ___   A
GAM60   LOC257450 3'  GGGGTCAAGCAGAGGAGG    91451    C      GAT
                                CC CCTCTGCT   GCCCC
                                || ||||||||   |||||
                                GG GGAGACGA   TGGGG
                                 A       AC_
GAM60   LOC51125  5'  GGAGGGCAGAGGAGGCGG    32743      C    GCTGAT   _
                                CTGCC CCTCT     GCCC CC
                                ||||| |||||     |||| ||
                                GGCGG GGAGA     CGGG GG
                                   A    _______    A
GAM60   LOC56832  3'  GGCTATCAGCAGAAGGATCAG  65447     CC  C       _
                                CTG  CC TCTGCTGAT GCC
                                |||  || |||||||| |||
                                GAC  GG AGACGACTA CGG
                                  TA  A        T
GAM60   LOC56964  5'  GGACAGTCAGTGGGAGCAG    63252     C   T   _   ATG
                                CTGC CCC CTG CTG   CC
                                |||| ||| ||| |||   ||
                                GACG GGG GAC GAC   GG
                                  A   T   T   A__
GAM60   LOC90119  5'  GGGGAGGGCAGAGGGGTCAG   62211     C        GATG
                                CTG CCCCTCTGCT    CCCC
                                ||| ||||||||||    ||||
                                GAC GGGGAGACGG    GGGG
                                  T         GA__
GAM60   LOC90462  3'  GGCCCAGCAGAGGGCAG     63572       CC      AT
                                CTGCCC  TCTGCTG  GCC
                                ||||||  |||||||  |||
                                GACGGG  AGACGAC  CGG
                                   __       C_
GAM60   LOC90494  5'  GGAGTAGGCAGAGGGATCAG  63734     CC       GA   C
                                CTG  CCCTCTGCT  TGC CC
                                |||  |||||||||  ||| ||
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                                GAC  GGGAGACGG  ATG GG
                                  TA       __   A
GAM60   LOC91040  3'  TGGGGGCATCGGCAAGG     65356     C
                                CCT TGCTGATGCCCCCA
                                ||| ||||||||||||||
                                GGA ACGGCTACGGGGGT
                                  _
GAM60   LOC91974  5'  TGGGAGCAAACTTCAGAGAAGG 68365      CC    CTGA_  C
           CAG                    CTGCC  CTCTG    TGC CCCA
                                ||||||  |||||    ||| ||||
                                GACGG  GAGAC    ACG GGGT
                                   AA    TTCAA  A
GAM60   LOC92230  5'  GGGGGCAAAAGGGGCAG     69087       CTCTGC GA
                                CTGCCCC     T  TGCCCCC
                                |||||||     |  |||||||
                                GACGGGG     A  ACGGGGG
                                   _______ AA
GAM60   LOC92340  3'  TGGGGACCTCAGTGGGGGCAG  69570       TCT    TGC
                                CTGCCCCC   GCTGA   CCCCA
                                ||||||||   |||||   |||||
                                GACGGGGG   TGACT   GGGGT
                                    ___    CCA
GAM60   LOC92710  3'  GGGTGCAGAGAGGCAG      70866      CC     TGAT
                                CTGCC  CTCTGC   GCCC
                                |||||  ||||||   ||||
                                GACGG  GAGACG   TGGG
                                   A_     _____
GAM61   ADAM19    3'  GCAGCAGCTGCACTGG      53842      GC  G
                                TCAG  TG GGCTGCTGC
                                ||||  ||  |||||||||
                                GGTC  AC TCGACGACG
                                  __  G
GAM61   APOB48R   3'  CTGGTTCCTCCCCAGCCTGA   38585         CTGCT
                                TCAGGCTGGGG    GCCAG
                                ||||||||||     |||||
                                AGTCCGACCCC    TGGTC
                                      TCCT_
GAM61   B3GAT1    3'  CTGAGAGAGCCCAGCCTGA    55054         G  G  GC
                                TCAGGCTGGG CT CT  CAG
                                |||||||||| ||  ||  |||
                                AGTCCGACCC GA GA  GTC
                                    _  _  GA
GAM61   B3GAT1    3'  CTGAGAGAGCCCAGCCTGA    38453         G  G  GC
                                TCAGGCTGGG CT CT  CAG
                                |||||||||| ||  ||  |||
                                AGTCCGACCC GA GA  GTC
                                    _  _  GA
GAM61   BBS4      3'  TGGCAGCAAGGCTTGA      53448        GGGGC
                                TCAGGCT    TGCTGCCA
                                |||||||    ||||||||
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                                AGTTCGG    ACGACGGT
                                   A____
GAM61   CA7     3' TGGCAGCAGCCCCACCCCGA  60829    A  C
                                TC GG TGGGGCTGCTGCCA
                                || || ||||||||||||||
                                AG CC ACCCCGACGACGGT
                                 C  C
GAM61   CAPN2    5' CTGGCCGCGCCCCAGCC    10012        T  T
                                GGCTGGGGC GC GCCAG
                                ||||||||| || |||||
                                CCGACCCCG CG CGGTC
                                      _ C
GAM61   COLQ    3' CTGGCAGCAGCTTCTCC    55410    CT
                                GG  GGGGCTGCTGCCAG
                                ||  ||||||||||||||
                                CC  CTTCGACGACGGTC
                                 T_
GAM61   COLQ    3' CTGGCAGCAGCTTCTCC    55412    CT
                                GG  GGGGCTGCTGCCAG
                                ||  ||||||||||||||
                                CC  CTTCGACGACGGTC
                                 T_
GAM61   COLQ    3' CTGGCAGCAGCTTCTCC    55414    CT
                                GG  GGGGCTGCTGCCAG
                                ||  ||||||||||||||
                                CC  CTTCGACGACGGTC
                                 T_
GAM61   COLQ    3' CTGGCAGCAGCTTCTCC    55416    CT
                                GG  GGGGCTGCTGCCAG
                                ||  ||||||||||||||
                                CC  CTTCGACGACGGTC
                                 T_
GAM61   COLQ    3' CTGGCAGCAGCTTCTCC    55424    CT
                                GG  GGGGCTGCTGCCAG
                                ||  ||||||||||||||
                                CC  CTTCGACGACGGTC
                                 T_
GAM61   COLQ    3' CTGGCAGCAGCTTCTCC    20258    CT
                                GG  GGGGCTGCTGCCAG
                                ||  ||||||||||||||
                                CC  CTTCGACGACGGTC
                                 T_
GAM61   CYBB    3' GCAGCCAGCTGCCAGCCT    76848       _    _
                                AGGCTGG GGCTG CTGC
                                ||||||| ||||| ||||
                                TCCGACC TCGAC GACG
                                    G    C
GAM61   CYP39A1  3' CTGGCAGCACCTAGACCTGA  33920      _    GC
                                TCAGG CTGGG  TGCTGCCAG
                                ||||| |||||  |||||||||
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                                AGTCC GATCC  ACGACGGTC
                                  A    __
GAM61   DDX11    3' GGCAGCAGCTGCTGGCCTG   48391      TG _
                                CAGGC  G GGCTGCTGCC
                                |||||  | ||||||||||
                                GTCCG  C TCGACGACGG
                                   GT G
GAM61   DGCR2    5' GGTTCAGCCCCGCCTGA     18908      T     CT
                                TCAGGC GGGGCTG  GCC
                                ||||||| |||||||  |||
                                AGTCCG CCCCGAC  TGG
                                   _     T_
GAM61   DRD4     3' GGACGCCCCCCGGCCTGA    7680         CT  TG
                                TCAGGCTGGGG  GC  CC
                                ||||||||||  ||  ||
                                AGTCCGGCCCC  CG  GG
                                      C_  CA
GAM61   DTNA     3' CTGGCAGCAGCCTCACC     53207    C
                                GG TGGGGCTGCTGCCAG
                                || ||||||||||||||
                                CC ACTCCGACGACGGTC
                                 _
GAM61   DTNA     3' CTGGCAGCAGCCTCACC     53275    C
                                GG TGGGGCTGCTGCCAG
                                || ||||||||||||||
                                CC ACTCCGACGACGGTC
                                 _
GAM61   EDN3     3' CTGTAAAGACAGCCCCAGCT   5481         _ GC_
                                GGCTGGGGCTG CT   CAG
                                |||||||||| ||   |||
                                TCGACCCCGAC GA   GTC
                                      A  AAT
GAM61   ENIGMA   3' GCGGTGGCCCCTAGCCTGA   62869      _    TG
                                TCAGGCT GGGGC  CTGC
                                ||||||| |||||  ||||
                                AGTCCGA CCCCG  GGCG
                                    T    GT
GAM61   F2RL3    3' CAGGAGTTCAACACCAGCCTGA 15503       _____   G
                                TCAGGCTGG    GGCT CTG
                                |||||||||    |||| |||
                                AGTCCGACC    TTGA GAC
                                     ACAAC   G
GAM61   FLOT2    3' CTGGCCCTGCCCCAGCCTG   16798        TGCT
                                CAGGCTGGGGC   GCCAG
                                ||||||||||   |||||
                                GTCCGACCCCG   CGGTC
                                      TCC_
GAM61   FMR2     3' CTGAAGAATGCCCCAGCTGA  10690     G     TG_  GC
                                TCAG CTGGGGC  CT  CAG
                                |||| |||||||  ||  |||
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                                AGTC GACCCCG   GA  GTC
                                  _      TAA  A_
GAM61   FPGS    3'  CTGGAGTGCCCCCAGCC     18266        CT   G
                                GGCTGGGG  GCT CCAG
                                ||||||||  ||| ||||
                                CCGACCCC  TGA GGTC
                                    CG  _
GAM61   FUT7    3'  GGGGGCACCCCAGCCTGA    16806          C   G
                                TCAGGCTGGGG TGCT CC
                                |||||||||||| |||| ||
                                AGTCCGACCCC ACGG GG
                                      _   G
GAM61   FZD10   5'  GCAGCAGCCCGTGCCCGG    24213    A   TG
                                TC GGC  GGGCTGCTGC
                                || |||  ||||||||||
                                GG CCG  CCCGACGACG
                                 C   TG
GAM61   GM2A    3'  CTGGCAATACTCCAGCCTGG   68379          C  C
                                TCAGGCTGGGG TG TGCCAG
                                |||||||||||| || ||||||
                                GGTCCGACCTC AT ACGGTC
                                      _ A
GAM61   GPRK5   5'  GGCAGCAGCGGCGGCAGCCCGA 19185    A    GG___
                                TC GGCTG    GCTGCTGCC
                                || |||||    |||||||||
                                AG CCGAC    CGACGACGG
                                 C    GGCGG
GAM61   HBZ     3'  CTGGAGGTTCCCCAGCC     19234        CT   G
                                GGCTGGGG  GCT CCAG
                                ||||||||  ||| ||||
                                CCGACCCC  TGG GGTC
                                    T_  A
GAM61   HSPG2   3'  GGCCACGCCCCAGCCCGA    19840    A       _ CT
                                TC GGCTGGGGC TG  GCC
                                || |||||||| ||  |||
                                AG CCGACCCCG AC  CGG
                                 C       C __
GAM61   IGF2    5'  CTGGCCCGCCCCAGCCCGA   7035     A       TGCT
                                TC GGCTGGGGC   GCCAG
                                || |||||||||   |||||
                                AG CCGACCCCG   CGGTC
                                 C       CC__
GAM61   IRAK1   3'  CTGGCAGCAGCTCTTTGCC   9612     T_
                                GGC  GGGGCTGCTGCCAG
                                |||  ||||||||||||||
                                CCG  TCTCGACGACGGTC
                                  TT
GAM61   ITGA4   3'  CTGGCAAACTTCAGACTGA   7955      G     CTGC
                                TCAG CTGGGG   TGCCAG
                                |||| ||||||   ||||||
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                                AGTC GACTTC   ACGGTC
                                  A     AA__
GAM61   JUP     5'  GGCTCCCACCCCGGCCCGA   11111    A      C  CT_
                                TC GGCTGGGG TG   GCC
                                || |||||||| ||   |||
                                AG CCGGCCCC AC   CGG
                                 C       _  CCT
GAM61   KMO     3'  CTGGCAGAGTTTACAGCCTGG  14844         _    G
                                TCAGGCTG GGGCT CTGCCAG
                                |||||||| ||||| |||||||
                                GGTCCGAC TTTGA GACGGTC
                                     A    _
GAM61   KRTHA8  5'  CTGTGCAGCCTCAGCC      23192           TGC
                                GGCTGGGGCTGC   CAG
                                ||||||||||||   |||
                                CCGACTCCGACG   GTC
                                       T__
GAM61   MAML1   3'  CTGGCAGCAGGACCCCAG    29275       __
                                CTGGGG  CTGCTGCCAG
                                ||||||  ||||||||||
                                GACCCC  GACGACGGTC
                                   AG
GAM61   MAT2A   3'  CAGTTGGAGCTCCAGCCTGA  20968           ___
                                TCAGGCTGGGGCT   GCTG
                                ||||||||||||   ||||
                                AGTCCGACCTCGA   TGAC
                                      GGT
GAM61   MPL     3'  CTGCGCACAGCCCCAGCT    19353          C  _
                                GGCTGGGGCTG TGC CAG
                                |||||||||| ||| |||
                                TCGACCCCGAC ACG GTC
                                      _  C
GAM61   MYBBP1A 3'  CTGGCAAGCACAGCCTGA   27996        GG   GC
                                TCAGGCTG  GCT  TGCCAG
                                ||||||||  |||  ||||||
                                AGTCCGAC  CGA  ACGGTC
                                     A_  __
GAM61   NPTX1   5'  GTCGCGAGCCACAGCCCGA   11841    A    G   _ T
                                TC GGCTG GGCT GC GC
                                || ||||| |||| || ||
                                AG CCGAC CCGA CG TG
                                 C    A   G  C
GAM61   OAS3    3'  GCAGCAGAGTGGCCCTGG    21654      _  GGG
                                TCAGG CTG   CTGCTGC
                                ||||| |||   |||||||
                                GGTCC GGT   GACGACG
                                   C   GA_
GAM61   OVOL1   3'  CTGGCAGCAGACCCCCC     17068    CT   _
                                GG  GGGG CTGCTGCCAG
                                ||  |||| ||||||||||
```

```
                                CC  CCCC GACGACGGTC
                                 __   A
GAM61   PHEMX    3'  CAGCAGGTCGCCTCCAGCCTGA 58140        _  _____
                                TCAGGCTGG GGC   TGCTG
                                |||||||||  |||   |||||
                                AGTCCGACC CCG   ACGAC
                                     T  CTGG
GAM61   PIK3R2   3'  GCGCGGCCCCAGCCTGG    18515           T
                                TCAGGCTGGGGCTGC GC
                                |||||||||||||||  ||
                                GGTCCGACCCCGGCG CG
                                                _
GAM61   PKD1     5'  GCGGGCCCCGCCTGA      6105       T    TG
                                TCAGGC GGGGC  CTGC
                                ||||||  |||||  ||||
                                AGTCCG CCCCG  GGCG
                                  _    __
GAM61   PODXL    5'  CTGGCTCTGCGCCCCAGCCCGG 19416    A      T  T__
                                TC GGCTGGGGC GC   GCCAG
                                ||  |||||||||  ||   |||||
                                GG CCGACCCCG CG   CGGTC
                                 C       _  TCT
GAM61   PSMD9    3'  CTGTTGTCACCCCAGCTGA   12525     G     CT  TGC
                                TCAG CTGGGG  GC   CAG
                                ||||  ||||||  ||   |||
                                AGTC GACCCC  TG   GTC
                                  _     AC  TT_
GAM61   PTPN7    5'  CTGGCAAGAGGCAGCCTGG   12594       GGG  GC
                                TCAGGCTG   CT  TGCCAG
                                ||||||||   ||  ||||||
                                GGTCCGAC   GA  ACGGTC
                                     G__  GA
GAM61   PTPN7    5'  CTGGCAAGAGGCAGCCTGG   55467       GGG  GC
                                TCAGGCTG   CT  TGCCAG
                                ||||||||   ||  ||||||
                                GGTCCGAC   GA  ACGGTC
                                     G__  GA
GAM61   RAB36    3'  CTGCGGCCCCCAGCCTGG    18168         CT    C
                                TCAGGCTGGGG  GCTGC AG
                                ||||||||||  |||||  ||
                                GGTCCGACCCC  CGGCG TC
                                                __    _
GAM61   SEPN1    3'  GGCAGCAGCCCCATGATGG   66977     GGC
                                TCA   TGGGGCTGCTGCC
                                |||   ||||||||||||
                                GGT   ACCCCGACGACGG
                                  AGT
GAM61   SH3BP2   3'  CTGGCTCAGGCCCAGCC     13067       G   CT
                                GGCTGGG CTG  GCCAG
                                |||||||  |||  |||||
```

```
                                CCGACCC GAC  CGGTC
                                    G   T_
GAM61   SLC16A2  3'  CTGGCAACAGTCTTACTGA   22524     GC       C
                                TCAG  TGGGGCTG TGCCAG
                                ||||  |||||||| ||||||
                                AGTC  ATTCTGAC ACGGTC
                                  __       A
GAM61   SMS      5'  CAGCCGGCCGCAGCCTGA    17184       G    _
                                TCAGGCTG GGCTG CTG
                                |||||||| ||||| |||
                                AGTCCGAC CCGGC GAC
                                    G    C
GAM61   SOX10    3'  CAGCCCCTGCCCCCAGCCTG  23667         _ T___
                                CAGGCTGGGG C    GCTG
                                |||||||||| |    ||||
                                GTCCGACCCC G    CGAC
                                      C TCCC
GAM61   SPINT2   3'  CTGGCAGCAGCCCCGAGTT   63850     _
                                GGCT GGGGCTGCTGCCAG
                                |||| ||||||||||||||
                                TTGA CCCCGACGACGGTC
                                  G
GAM61   SPON1    5'  CTGGCAGCCTCTCAACGTGA  63120     GGC    CT
                                TCA   TGGGG  GCTGCCAG
                                |||   |||||  ||||||||
                                AGT   ACTCT  CGACGGTC
                                  GCA    C_
GAM61   STAT6    5'  TAGCAGGGCCAGCCTTGA    13452    _    GG
                                TCA GGCTGG  CTGCTG
                                ||| ||||||  ||||||
                                AGT CCGACC  GACGAT
                                  T     GG
GAM61   STIM1    5'  CTGACAGCAGCCCCGCAGCC   60780     __       C
                                GGCT  GGGGCTGCTG CAG
                                ||||  |||||||||| |||
                                CCGA  CCCCGACGAC GTC
                                  CG        A
GAM61   STIM1    3'  CTGGACAAGGCCCACAGCCTGA 60781       _    GC  _
                                TCAGGCTG GGGCT  TG CCAG
                                |||||||| |||||  || ||||
                                AGTCCGAC CCCGG  AC GGTC
                                    A    A_ A
GAM61   TBL1X    3'  CTGGCTTCCCCAGCCTG     20132         CTGCT
                                CAGGCTGGGG    GCCAG
                                ||||||||||    |||||
                                GTCCGACCCC    CGGTC
                                      TT____
GAM61   TNP2     5'  CTGAGAGCTGCCCCAGCCTGG  19457          T   GC
                                TCAGGCTGGGGC GCT  CAG
                                |||||||||||| |||  |||
```

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                                GGTCCGACCCCG CGA  GTC
                                      T   GA
GAM61   TRPV3    3'  GCAGCAGTCTGGAGCCTG    96814       G_
                                CAGGCT  GGGCTGCTGC
                                ||||||  ||||||||||
                                GTCCGA  TCTGACGACG
                                   GG
GAM61   UBQLN3   3'  CTGGGGGGCCCCAGTCT     34371          G TG
                                AGGCTGGGGCT C  CCAG
                                |||||||||||  |  ||||
                                TCTGACCCCGG G  GGTC
                                      G __
GAM61   WBSCR1   3'  GGCAGCAGGAGCCTGG      50086       GGGG
                                TCAGGCT    CTGCTGCC
                                |||||||    ||||||||
                                GGTCCGA    GACGACGG
                                   G___
GAM61   WBSCR1   3'  GGCAGCAGGAGCCTGG      42484       GGGG
                                TCAGGCT    CTGCTGCC
                                |||||||    ||||||||
                                GGTCCGA    GACGACGG
                                   G___
GAM61   WFS1     3'  CAGTGTGGCCCCAGCCCGA    21164    A        __
                                TC GGCTGGGGCT  GCTG
                                || ||||||||||  ||||
                                AG CCGACCCCGG  TGAC
                                 C         TG
GAM61   WISP1    3'  CTGGACTACACCCAAGCCTGA  15280        G   C  CTG_
                                TCAGGCT GGG TG    CCAG
                                ||||||| ||| ||    ||||
                                AGTCCGA CCC AC    GGTC
                                   A  _  ATCA
GAM61   XT3      3'  CTGACTGTCCCCCAGCCCGA   39909    A       CT  TGC
                                TC GGCTGGGG  GC   CAG
                                || ||||||||  ||   |||
                                AG CCGACCCC  TG   GTC
                                 C       C_  TCA
GAM61   AGS3     5'  GCAGCAGTGCCAGCCTGG     73509         G
                                TCAGGCTGG GCTGCTGC
                                |||||||||  ||||||||
                                GGTCCGACC TGACGACG
                                      G
GAM61   ASB10    3'  CTGGCAGCAGGAGGCCCAG    56001       G___
                                CTGGG    CTGCTGCCAG
                                |||||    ||||||||||
                                GACCC    GACGACGGTC
                                   GGAG
GAM61   ATP6V1H  5'  CTGACGCGGCGCCCCAGCCCGG 32515    A       T    __
                                TC GGCTGGGGC GCTGC  CAG
                                || |||||||| |||||  |||
```

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                                GG CCGACCCCG CGGCG  GTC
                                 C        _    CA
GAM61   C17orf31  3'  GTGGACAGCCCAGCCTGA    34541         G  _ TG
                                TCAGGCTGGG CTG C  C
                                |||||||||| ||| |  |
                                AGTCCGACCC GAC G  G
                                      _  A GT
GAM61   C1orf29   3'  CTGACATTTGGCCCAGCCTG  23339         G  GC_  C
                                CAGGCTGGG CT  TG CAG
                                ||||||||| ||  || |||
                                GTCCGACCC GG  AC GTC
                                      _ TTT  A
GAM61   C1orf34   3'  CTGGCAGCCTAGAGGCTGA   61306     G  GG  CT
                                TCAG CT  GG  GCTGCCAG
                                |||| ||  ||  ||||||||
                                AGTC GA  TC  CGACGGTC
                                  G  GA  __
GAM61   C20orf183 5'  CAGAAGCCCCAGCCTCGA    48529    _        G
                                TC AGGCTGGGGCT CTG
                                || ||||||||||| |||
                                AG TCCGACCCCGA GAC
                                 C         A
GAM61   CACNG4    3'  GGTAGCGGCCCCAGCTGA    27709     G
                                TCAG CTGGGGCTGCTGCC
                                |||| ||||||||||||||
                                AGTC GACCCCGGCGATGG
                                  _
GAM61   CD84-H1   3'  TTGGGAACCCCAGTCCTGA   54226      _     CTGCTG
                                TCAGG CTGGGG     CCAG
                                ||||| ||||||     ||||
                                AGTCC GACCCC     GGTT
                                   T     AAG___
GAM61   CDC14B    3'  GGCAGCAGTGTGTCCAGCCTG  54008         ___
                                CAGGCTGGG   GCTGCTGCC
                                |||||||||   |||||||||
                                GTCCGACCT   TGACGACGG
                                      GTG
GAM61   CLDN15    5'  CTGATTCCACCCCAGCCTG    57370         C  CTGC
                                CAGGCTGGGG TG    CAG
                                |||||||||| ||    |||
                                GTCCGACCCC AC    GTC
                                      _ CTTA
GAM61   CLDN15    5'  CTGATTCCACCCCAGCCTG    27565         C  CTGC
                                CAGGCTGGGG TG    CAG
                                |||||||||| ||    |||
                                GTCCGACCCC AC    GTC
                                      _ CTTA
GAM61   CRF       3'  CAGCCCACCCCAGCCTGG     22911         CT_
                                TCAGGCTGGGG   GCTG
                                ||||||||||   ||||
```

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                                GGTCCGACCCC  CGAC
                                      ACC
GAM61   CYP2E    5' CTGGCAGCAGGGCCCCAG   7579        __
                                CTGGGGCT GCTGCCAG
                                |||||||| ||||||||
                                GACCCCGG CGACGGTC
                                    GA
GAM61   DDX37    5' CTGGCAGCAGCCTGTC     51987    TG
                                GGC GGGCTGCTGCCAG
                                ||| ||||||||||||
                                CTG TCCGACGACGGTC
                                  __
GAM61   DKFZP586A011 3' CTGGCAGCAGCCTCTACTGG 31841     GCT
                                TCAG  GGGGCTGCTGCCAG
                                ||||  ||||||||||||||
                                GGTC  CTCCGACGACGGTC
                                  AT_
GAM61   DKFZP586J0619 3' GGCAGCAGAACCACCTGA   82320     C  GG
                                TCAGG TGG CTGCTGCC
                                ||||| ||| ||||||||
                                AGTCC ACC GACGACGG
                                   _  AA
GAM61   DKFZP586M1120 3' GCAGCAGCCCTGTGGTCCTG  49282     _ __
                                CAGG CT  GGGGCTGCTGC
                                |||| ||  ||||||||||
                                GTCC GG  TCCCGACGACG
                                  T  TG
GAM61   FBXO21   3' CTGGCTCCTCCAGCCTGA   54349         CTGCT
                                TCAGGCTGGGG   GCCAG
                                ||||||||||    |||||
                                AGTCCGACCTC   CGGTC
                                      CT___
GAM61   FKHL18   5' CAGCAGCCTGGCAGCCCGG  80369   A   __
                                TC GGCTG GGGCTGCTG
                                || |||||  |||||||||
                                GG CCGAC  TCCGACGAC
                                 C    GG
GAM61   FLJ00007 3' CTGAGGCCCCCAGCCTGA   71777        CT  GC
                                TCAGGCTGGGG GCT CAG
                                |||||||||| |||  |||
                                AGTCCGACCCC CGG GTC
                                      __  A_
GAM61   FLJ10450 3' CTGACAGTAGGCCAGCCTG  36600      G G    C
                                CAGGCTG G CTGCTG CAG
                                ||||||| | |||||| |||
                                GTCCGAC C GATGAC GTC
                                   _ G    A
GAM61   FLJ11726 3' CTGGAGTTAAAACCCCAGCC  47019      CT___  G
                                GGCTGGGG   GCT CCAG
                                ||||||||   ||| ||||
```

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                                CCGACCCC    TGA GGTC
                                    AAAAT  _
GAM61   FLJ12089  3' CTGGGGGGAGCCCCAGGCTGA  44951     G      G  G
                                TCAG CTGGGGCT CT CCAG
                                |||| |||||||| || ||||
                                AGTC GACCCCGA GG GGTC
                                  G       G  G
GAM61   FLJ12190  3' GGGAAGACCCCAGCCTGG    47568          _  GCTG
                                TCAGGCTGGGG CT   CC
                                |||||||||| ||   ||
                                GGTCCGACCCC GA   GG
                                      A  AG__
GAM61   FLJ12800  3' TGGCAGGCCAGCTTGA      43536         GGCTG
                                TCAGGCTGG    CTGCCA
                                |||||||||    ||||||
                                AGTTCGACC    GACGGT
                                    G____
GAM61   FLJ13072  5' GCAGAGCCCCCAGCCTGA    91392          _  G
                                TCAGGCTGGGG CT CTGC
                                |||||||||| || ||||
                                AGTCCGACCCC GA GACG
                                      C  _
GAM61   FLJ13769  3' TAGCAGTTTGAGCCCAGCCT  47262        _____
                                AGGCTGGG    GCTGCTG
                                ||||||||    |||||||
                                TCCGACCC    TGACGAT
                                    GAGTT
GAM61   FLJ13798  3' CTGGACGCCACAGCCTGA    88473        G   TGCTG
                                TCAGGCTG GGC    CCAG
                                |||||||| |||    ||||
                                AGTCCGAC CCG    GGTC
                                    A   CA___
GAM61   FLJ20019  5' CTGATGCAGACCCCAGCT    34815        _   TGC
                                GGCTGGGG CTGC   CAG
                                |||||||| ||||   |||
                                TCGACCCC GACG   GTC
                                    A    TA_
GAM61   FLJ20195  3' CAGCACCCCCGCCCCAGCCT  35214         _____
                                AGGCTGGGGC    TGCTG
                                ||||||||||    |||||
                                TCCGACCCCG    ACGAC
                                      CCCCC
GAM61   FLJ20296  3' CTGGCAGTGTTGTCAGCT    35365       _  T
                                GGCTGG GGC GCTGCCAG
                                |||||| ||| ||||||||
                                TCGACT TTG TGACGGTC
                                   G  _
GAM61   FLJ21135  5' GGGAGCCCCCAGCCCGG     46351    A      CT  G
                                TC GGCTGGGG  GCT CC
                                || ||||||||  ||| ||
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                                GG CCGACCCC  CGA GG
                                 C       __  G
GAM61   FLJ21865  3'  CAGCCCAGCCCCAGCCTGA   43110          __
                                TCAGGCTGGGGCT  GCTG
                                ||||||||||||  ||||
                                AGTCCGACCCCGA  CGAC
                                     CC
GAM61   FLJ23604  3'  CTGGCAACATATTTCCCAGCC  47547       C___  C
                                GGCTGGGG   TG TGCCAG
                                ||||||||   || ||||||
                                CCGACCCT   AC ACGGTC
                                    TTAT  A
GAM61   FLJ31164  3'  CTGTGTCGGCCCCAGCTGA   59395     G       CT  _
                                TCAG CTGGGGCTG  GC CAG
                                ||||  |||||||||  ||  |||
                                AGTC GACCCCGGC  TG GTC
                                  _       __  T
GAM61   GBTS1     3'  CTGGGGTGTCCCCAGCC     59723       C   G
                                GGCTGGGG TGCT CCAG
                                ||||||||  ||||  ||||
                                CCGACCCC GTGG GGTC
                                    T   _
GAM61   GIPC3     3'  GCACAGCCCCAGCCCGG     56533    A       C
                                TC GGCTGGGGCTG TGC
                                ||  ||||||||||  |||
                                GG CCGACCCCGAC ACG
                                 C         _
GAM61   GMPPB     3'  CTGGCACTGGTCTCAGCCT   97445         GC
                                AGGCTGGGGCT  TGCCAG
                                ||||||||||  ||||||
                                TCCGACTCTGG  ACGGTC
                                      TC
GAM61   GPR88     5'  CTGGCACTGATCCCAGCTGA  42136     G    GC GC
                                TCAG CTGGG  T  TGCCAG
                                ||||  |||||  |  ||||||
                                AGTC GACCC  G  ACGGTC
                                  _    TA TC
GAM61   HEMK      3'  CTGGAGTCATACCCAGCCT   32955       GC  _  G
                                AGGCTGGG  TG CT CCAG
                                ||||||||  ||  ||  ||||
                                TCCGACCC  AC GA GGTC
                                    AT  T  _
GAM61   HOMER-3   5'  GCCCATCCCAGCCTGA     17906         C  CT
                                TCAGGCTGGGG TG  GC
                                ||||||||||| ||  ||
                                AGTCCGACCCT AC  CG
                                      _ C_
GAM61   HSA250839 3'  CTGGCAGGCCACAGTCCTGA  37851      _  G  TG
                                TCAGG CTG GGC  CTGCCAG
                                |||||  |||  |||  |||||||
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                                AGTCC GAC CCG  GACGGTC
                                  T  A  __
GAM61   HSPC065  3' CTGGCAACTGCTTACCAGCCTG 27150        __  TGC
          G                    TCAGGCTGG  GGC  TGCCAG
                               |||||||||  |||  ||||||
                               GGTCCGACC  TCG  ACGGTC
                                    AT  TCA
GAM61   HUMZD58C02 3' CTGGTTGACCCCAGCCTGG  80576         CTGCT
                               TCAGGCTGGGG   GCCAG
                               ||||||||||    |||||
                               GGTCCGACCCC   TGGTC
                                     AGT__
GAM61   IL18BP   3' GCAGCAGCACAACCTTGA   20311    _ C  GG
                               TCA GG TG  GCTGCTGC
                               ||| || ||  ||||||||
                               AGT CC AC  CGACGACG
                                 T  A  A_
GAM61   KIAA0057 3' CTGGCATCTTGCCAGCCTGG  25412       GGCTGC
                               TCAGGCTGG    TGCCAG
                               |||||||||    ||||||
                               GGTCCGACC    ACGGTC
                                    GTTCT_
GAM61   KIAA0063 3' CAGCAGCAAAGCCAGCCTGG  30254       G___
                               TCAGGCTGG   GCTGCTG
                               |||||||||   |||||||
                               GGTCCGACC   CGACGAC
                                    GAAA
GAM61   KIAA0140 3' CTGGCAGAAAGCCCCCAGCC  28513       _ G_
                               GGCTGGGG CT  CTGCCAG
                               |||||||| ||  |||||||
                               CCGACCCC GA  GACGGTC
                                    C  AA
GAM61   KIAA0211 3' CTGGGTATCCCCCAGCC    28285       C_  TG
                               GGCTGGGG  TGC  CCAG
                               ||||||||  |||  ||||
                               CCGACCCC  ATG  GGTC
                                    CT  __
GAM61   KIAA0417 3' CAGCATGCCCAGCCCTGA   71759     _   G _
                               TCAGG CTGGG C TGCTG
                               ||||| ||||| | |||||
                               AGTCC GACCC G ACGAC
                                  C   _ T
GAM61   KIAA0935 3' CTGACGCATGCCACAGCCTGA 73097       G  _  T C
                               TCAGGCTG GGC TGC G CAG
                               |||||||| ||| ||| | |||
                               AGTCCGAC CCG ACG C GTC
                                    A  T  _ A
GAM61   KIAA0953 3' GGGAGCTCCCAGCCTGA    67329         CT  G
                               TCAGGCTGGGG  GCT CC
                               ||||||||||  ||| ||
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                                AGTCCGACCCT  CGA GG
                                      __   G
GAM61   KIAA1036 3' CTGGGGTTGTCCCCAGCCTG   30490         _ T   G
                                CAGGCTGGGG C GCT CCAG
                                |||||||||| | ||| ||||
                                GTCCGACCCC G TGG GGTC
                                     T T   _
GAM61   KIAA1091 3' GCTCACATCCCAGCCTGA    70264          C  CT_
                                TCAGGCTGGGG TG   GC
                                |||||||||| ||   ||
                                AGTCCGACCCT AC   CG
                                      _  ACT
GAM61   KIAA1100 3' CTGGAGGGCGTCCCAGCCT   30441          T   G_
                                AGGCTGGGGC GCT  CCAG
                                |||||||||| |||  ||||
                                TCCGACCCTG CGG  GGTC
                                      _   GA
GAM61   KIAA1280 5' GCAGCAGCTGGCCCGG     70281    A    GG
                                TC GGCT  GGCTGCTGC
                                || ||||  |||||||||
                                GG CCGG  TCGACGACG
                                 C   __
GAM61   KIAA1364 3' CTGACATGTCCCCAGCT     64346        CT  _  C
                                GGCTGGGG  GC TG CAG
                                ||||||||  || || |||
                                TCGACCCC  TG AC GTC
                                     __  T  A
GAM61   KIAA1691 3' CAGCTCTGCCCCAGCCCTGA  94124      _      T__
                                TCAGG CTGGGGC   GCTG
                                ||||| |||||||   ||||
                                AGTCC GACCCCG   CGAC
                                   C      TCT
GAM61   KIAA1784 3' CAGCCACCGCCAGCCTGA    65743         _  CT
                                TCAGGCTGG GG  GCTG
                                ||||||||| ||  ||||
                                AGTCCGACC CC  CGAC
                                      G  AC
GAM61   KIAA1828 5' CAGCATGGCCCTGCCCGA    74202    A  T     __
                                TC GGC GGGGCT  GCTG
                                || ||| ||||||  ||||
                                AG CCG TCCCGG  CGAC
                                 C  _     TA
GAM61   KIAA1924 3' GGGGCCCCCCCCAGCCTG    74056         CT  G
                                CAGGCTGGGG  GCT CC
                                ||||||||||  ||| ||
                                GTCCGACCCC  CGG GG
                                      CC  _
GAM61   KIAA1978 3' GGACAGCCCCCAGCTCTGA   74894      _     CT   _
                                TCAG GCTGGGG  GCTG CC
                                |||| |||||||  |||| ||
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                                AGTC CGACCCC  CGAC GG
                                  T      __    A
GAM61   KLK15    3'  CTGGCCAGCAGCCCCGCCTGA  57514       T        _
                                TCAGGC GGGGCTGCTG CCAG
                                |||||| |||||||||| ||||
                                AGTCCG CCCCGACGAC GGTC
                                   _         C
GAM61   KLK15    3'  CTGGCCAGCAGCCCCGCCTGA  57517       T        _
                                TCAGGC GGGGCTGCTG CCAG
                                |||||| |||||||||| ||||
                                AGTCCG CCCCGACGAC GGTC
                                   _         C
GAM61   KLK15    3'  CTGGCCAGCAGCCCCGCCTGA  43712       T        _
                                TCAGGC GGGGCTGCTG CCAG
                                |||||| |||||||||| ||||
                                AGTCCG CCCCGACGAC GGTC
                                   _         C
GAM61   KLK15    3'  CTGGCCAGCAGCCCCGCCTGA  34419       T        _
                                TCAGGC GGGGCTGCTG CCAG
                                |||||| |||||||||| ||||
                                AGTCCG CCCCGACGAC GGTC
                                   _         C
GAM61   MAP3K3   3'  CTGGGAGCCCCCAGCCTG    11539         CT   G
                                CAGGCTGGGG  GCT CCAG
                                ||||||||||  ||| ||||
                                GTCCGACCCC  CGA GGTC
                                   __   G
GAM61   MGC13033 3'  TAGCAGCCCGGCAGCCTGA   49546         __
                                TCAGGCTG  GGGCTGCTG
                                ||||||||  |||||||||
                                AGTCCGAC  CCCGACGAT
                                     GG
GAM61   MGC13047 5'  TAGCAAGGCCCAGCCTGG    52090         G  _
                                TCAGGCTGGG CT GCTG
                                |||||||||| || ||||
                                GGTCCGACCC GA CGAT
                                      G  A
GAM61   MGC19556 3'  CAGCCGTGCCCCAGCCTGG   54337           T__
                                TCAGGCTGGGGC   GCTG
                                ||||||||||||   ||||
                                GGTCCGACCCCG   CGAC
                                       TGC
GAM61   MGC23244 3'  CTGTCAGCCCCATCCTGA    58831       C       CTGC
                                TCAGG TGGGGCTG    CAG
                                ||||| ||||||||    |||
                                AGTCC ACCCCGAC    GTC
                                   T       T___
GAM61   MGC2668  3'  CTGACAAGGCGCTCCAGCC   61193         T   GC__
                                GGCTGGGGC GCT    CAG
                                ||||||||| |||    |||
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                                CCGACCTCG CGG   GTC
                                     _  AACA
GAM61   MGC2749  3'  CTGAGTTCACCCCAGCC    44169       C  CT  _
                                GGCTGGGG TG  GC CAG
                                |||||||| ||  || |||
                                CCGACCCC AC  TG GTC
                                     _  T_  A
GAM61   MKP-7    5'  CAGTCACCACCAGCCTGA    67011        _  CT
                                TCAGGCTGG GG  GCTG
                                ||||||||| ||  ||||
                                AGTCCGACC CC  TGAC
                                     A  AC
GAM61   NIFU     5'  CTGTCGGCCCCGGCCCGA    67880    A       CTGC
                                TC GGCTGGGGCTG   CAG
                                || ||||||||||   |||
                                AG CCGGCCCCGGC   GTC
                                 C        T___
GAM61   PDZ-     5'  CTGGCAGCCGGGCACCCG    65628    _  __
                                TGGG GCT  GCTGCCAG
                                |||| |||  ||||||||
                                GCCC CGG  CGACGGTC
                                  A  GC
GAM61   PFDN1    3'  CTGGCTCATCCCAGCC      12048       C  CT
                                GGCTGGGG TG  GCCAG
                                |||||||| ||  |||||
                                CCGACCCT AC  CGGTC
                                     _  T_
GAM61   PLAGL2   3'  CAGTTGGCACCAGCCTGA    70955       G   _
                                TCAGGCTGG GCTG CTG
                                ||||||||| |||| |||
                                AGTCCGACC CGGT GAC
                                     A   T
GAM61   PTPRT    3'  CTGGCCTTCCCCAGCCTG    56491        CTGCT
                                CAGGCTGGGG    GCCAG
                                ||||||||||    |||||
                                GTCCGACCCC    CGGTC
                                     TTC__
GAM61   RAI1     3'  CTGACGCAGCCCCCAGCC    60952       _   T C
                                GGCTGGGG CTGC G CAG
                                |||||||| |||| | |||
                                CCGACCCC GACG C GTC
                                     C   _ A
GAM61   SARM     3'  CTGGCTGCGCCCCCAGCC    31287       C   T
                                GGCTGGGG TGC GCCAG
                                |||||||| ||| |||||
                                CCGACCCC GCG CGGTC
                                     C   T
GAM61   SCAMP5   3'  CTGGCAGTTGAGCTGCCTGA  58058      TGG   __
                                TCAGGC   GGCT  GCTGCCAG
                                ||||||   ||||  ||||||||
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                                AGTCCG  TCGA  TGACGGTC
                                   ___   GT
GAM61   SH3BGRL3  3'  CTGGCTGCCCCCAGCC     49261       CT  T
                                GGCTGGGG  GC GCCAG
                                ||||||||  || |||||
                                CCGACCCC  CG CGGTC
                                   __  T
GAM61   SHANK3    3'  CAGAGCCTCACCCAGCCTGA  66100        ____  G
                                TCAGGCTGGG   GCT CTG
                                ||||||||||   ||| |||
                                AGTCCGACCC   CGA GAC
                                     ACTC  _
GAM61   SLC6A13   5'  CTGGCAGCAGCTTCACT    34001    C
                                GG TGGGGCTGCTGCCAG
                                || ||||||||||||||
                                TC ACTTCGACGACGGTC
                                 _
GAM61   SUI1      3'  CTGGCAGTGTCAAGCCTGA   20537      GG  T
                                TCAGGCT  GGC GCTGCCAG
                                |||||||  ||| ||||||||
                                AGTCCGA  CTG TGACGGTC
                                   A_  _
GAM61   TOR1B     3'  CTGGTATCAGCCCCAGCCTG  27971         C
                                CAGGCTGGGGCTG TGCCAG
                                |||||||||||| ||||||
                                GTCCGACCCCGAC ATGGTC
                                      T
GAM61   TRPM3     3'  GGCAGCAAGCAGTTCTACCT  65526    C       ____
                                AGG TGGGGCTGCT   GCC
                                ||| ||||||||||   |||
                                TCC ATCTTGACGA   CGG
                                  _       ACGA
GAM61   ZDHHC8    3'  GGCCACCCCAGCCTGG     64621         C  CT
                                TCAGGCTGGGG TG  GCC
                                |||||||||| ||  |||
                                GGTCCGACCCC AC  CGG
                                      _ __
GAM61   ZNF238    3'  CTGAAAAAGCCCCAGGCTGA  22027     G      GCTGC
                                TCAG CTGGGGCT    CAG
                                |||| ||||||||    |||
                                AGTC GACCCCGA    GTC
                                  G       AAAA_
GAM61   LOC115399 3'  CTGGCAGCAGCTCCCC     73813    CT
                                GG  GGGGCTGCTGCCAG
                                ||  ||||||||||||||
                                CC  CCTCGACGACGGTC
                                  __
GAM61   LOC122704 3'  CTGGCCAACCCAGCCTGG    74605        GC  CT
                                TCAGGCTGGG  TG  GCCAG
                                |||||||||  ||  |||||
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                                GGTCCGACCC  AC  CGGTC
                                     A_  __
GAM61   LOC123096 3'  GCAGCAGCCAGCACCTGG    74653      C  G_
                                TCAGG TG  GGCTGCTGC
                                ||||| ||  |||||||||
                                GGTCC AC  CCGACGACG
                                   _  GA
GAM61   LOC123242 5'  CTGGCAGCAGGCCCAGCTGA   76116     G    G
                                TCAG CTGGG CTGCTGCCAG
                                |||| ||||| ||||||||||
                                AGTC GACCC GACGACGGTC
                                   _    G
GAM61   LOC125144 3'  CTGGCAGCAGCATCTCAGCC   74853       __
                                GGCTGGG  GCTGCTGCCAG
                                |||||||  ||||||||||
                                CCGACTC  CGACGACGGTC
                                     TA
GAM61   LOC130576 3'  CTGGCAACTAGTCCCACCTGA  75458      C       C_
                                TCAGG TGGGGCTG  TGCCAG
                                ||||| ||||||||  ||||||
                                AGTCC ACCCTGAT  ACGGTC
                                   _       CA
GAM61   LOC130612 3'  GTAAAGCCACCAGCCTGA    75472         _   GC
                                TCAGGCTGG GGCT  TGC
                                ||||||||| ||||  |||
                                AGTCCGACC CCGA  ATG
                                     A    A_
GAM61   LOC131377 3'  CTGGCCCTGCCCCAGCCT    76779          TGCT
                                AGGCTGGGGC    GCCAG
                                ||||||||||    |||||
                                TCCGACCCCG    CGGTC
                                     TCC_
GAM61   LOC143909 5'  CTGGCAGCGGCAGCC       83924      GGG
                                GGCT   GCTGCTGCCAG
                                ||||   ||||||||||
                                CCGA   CGGCGACGGTC
                                   ___
GAM61   LOC144501 3'  GGTTGTTCCCAGCCTGA     84032          CT  T
                                TCAGGCTGGGG  GC GCC
                                ||||||||||  || |||
                                AGTCCGACCCT  TG TGG
                                     __  T
GAM61   LOC146268 3'  CTGGAAGGCCCAGCCTGA    78339          G  GCTG
                                TCAGGCTGGG CT    CCAG
                                |||||||||| ||    ||||
                                AGTCCGACCC GG    GGTC
                                     _  AA__
GAM61   LOC146452 3'  CTGGGGCAGGACCCCAGCCTG  78472          __    G
                                CAGGCTGGGG  CTGCT CCAG
                                |||||||||  ||||| ||||
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                                GTCCGACCCC  GACGG GGTC
                                      AG    _
GAM61   LOC146774 3' CAGAAGGCCCCGGCCTGA    78693          G_
                                TCAGGCTGGGGCT  CTG
                                |||||||||||||  |||
                                AGTCCGGCCCCGG  GAC
                                       AA
GAM61   LOC148078 3' CTGGCTGGGCCCAGCCTG    85251        G  GCT
                                CAGGCTGGG CT   GCCAG
                                |||||||||  ||   |||||
                                GTCCGACCC GG   CGGTC
                                     G  T__
GAM61   LOC148113 3' GTTCAACCCTAGCCTGA     79375          C  CT
                                TCAGGCTGGGG TG  GC
                                ||||||||||| ||  ||
                                AGTCCGATCCC AC  TG
                                       A  T_
GAM61   LOC150445 3' GGCAGCAGCGCTCGCTGA    80680     G T  G
                                TCAG C GG GCTGCTGCC
                                |||| | || |||||||||
                                AGTC G TC CGACGACGG
                                  _ C  G
GAM61   LOC150622 5' CTGGCACATACCCCAGCC    80762        C_  C
                                GGCTGGGG  TG TGCCAG
                                ||||||||  || ||||||
                                CCGACCCC  AC ACGGTC
                                     AT  _
GAM61   LOC151632 5' CTGGGATGCGTCCCCAGCC    86644        C   TG_
                                GGCTGGGG TGC   CCAG
                                |||||||| |||   ||||
                                CCGACCCC GCG   GGTC
                                     T   TAG
GAM61   LOC151723 5' CTGGCAGCAGCCCTCCAGC    83496      __
                                GCTGG  GGCTGCTGCCAG
                                |||||  ||||||||||||
                                CGACC  CCGACGACGGTC
                                   TC
GAM61   LOC152274 3' CTGGGATGGAGCCCCAGCC    81341         G  G__
                                GGCTGGGGCT CT   CCAG
                                |||||||||| ||   ||||
                                CCGACCCCGA GG   GGTC
                                      _  TAG
GAM61   LOC158314 5' GGCTGCGCCCCCCAGCCCGG   88098    A      C_   T
                                TC GGCTGGGG  TGC GCC
                                || ||||||||  ||| |||
                                GG CCGACCCC  GCG CGG
                                 C       CC   T
GAM61   LOC164668 3' CAGTTCCTTGCCCCAACCTGG  83426      C     T____
                                TCAGG TGGGGC    GCTG
                                ||||| ||||||    ||||
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                                GGTCC ACCCCG    TGAC
                                   A     TTCCT
GAM61   LOC164691 5' CTGGCAGCAACAGAGCCTG   83428      GGGGC
                                CAGGCT    TGCTGCCAG
                                ||||||    |||||||||
                                GTCCGA    ACGACGGTC
                                   GACA_
GAM61   LOC165246 3' CTGGCTGCCCCTGCCCGA    83366    A  T    TGCT
                                TC GGC GGGGC    GCCAG
                                || ||| |||||    |||||
                                AG CCG CCCCG    CGGTC
                                 C  T    T___
GAM61   LOC170221 3' CTGGCAGTAGCAACCTG     83467     CTGGG
                                CAGG    GCTGCTGCCAG
                                ||||    ||||||||||
                                GTCC    CGATGACGGTC
                                  AA___
GAM61   LOC196485 3' CTGACTGTCCCCCAGCCTGA  89071         CT  TGC
                                TCAGGCTGGGG  GC   CAG
                                ||||||||||  ||   |||
                                AGTCCGACCCC  TG   GTC
                                      C_  TCA
GAM61   LOC196955 5' CTGGCAGCAGGCCCAGCTGA  77866     G    G
                                TCAG CTGGG CTGCTGCCAG
                                |||| ||||| ||||||||||
                                AGTC GACCC GACGACGGTC
                                  _    G
GAM61   LOC197273 5' GGCAGCAGAAGCAGCCCGG   67993    A    GGG
                                TC GGCTG   CTGCTGCC
                                || |||||   ||||||||
                                GG CCGAC   GACGACGG
                                 C    GAA
GAM61   LOC197358 3' CTGGCAAATGCAGCCTCA    89429         ___
                                TGGGGCTGC   TGCCAG
                                |||||||||   ||||||
                                ACTCCGACG   ACGGTC
                                     TAA
GAM61   LOC200138 3' CTGGCAGCAAATCCAAACTGA 91542     GC   GC
                                TCAG  TGGG  TGCTGCCAG
                                ||||  ||||  |||||||||
                                AGTC  ACCT  ACGACGGTC
                                  AA   AA
GAM61   LOC202986 3' CTGACTGTCCCCCAGCCTGA  92064         CT  TGC
                                TCAGGCTGGGG  GC   CAG
                                ||||||||||  ||   |||
                                AGTCCGACCCC  TG   GTC
                                      C_  TCA
GAM61   LOC219653 3' CTGGCAGCAGCTGGCC      92916     GG
                                GGCT  GGCTGCTGCCAG
                                ||||  ||||||||||||
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                                CCGG  TCGACGACGGTC
                                  __
GAM61   LOC220021 3'  CAGCATCTGGCCCAGCCTG    95019         ___ C
                                CAGGCTGGG   G TGCTG
                                |||||||||   | |||||
                                GTCCGACCC   C ACGAC
                                     GGT T
GAM61   LOC220064 3'  CTGGTCTTGAACTCCCAGCCTG 95065          CTGCT__
          A                      TCAGGCTGGGG      GCCAG
                                ||||||||||       |||||
                                AGTCCGACCCT      TGGTC
                                      CAAGTTC
GAM61   LOC220567 3'  CTGGTTCCTCCCCAGCCTGA   92434          CTGCT
                                TCAGGCTGGGG     GCCAG
                                ||||||||||     |||||
                                AGTCCGACCCC     TGGTC
                                      TCCT_
GAM61   LOC221354 3'  CTGACCGTCCCCCAGCCCGA   94013    A      CT  TGC
                                TC GGCTGGGG  GC   CAG
                                || ||||||||  ||   |||
                                AG CCGACCCC  TG   GTC
                                 C       C_  CCA
GAM61   LOC221410 3'  CAGCAACCTAAGACCAGTCTGA 93692         _____  C
                                TCAGGCTGG     GG TGCTG
                                |||||||||     || |||||
                                AGTCTGACC     CC ACGAC
                                      AGAAT  A
GAM61   LOC222166 3'  CTGACAGTTACCACCTGA    95736      C   GGCT    C
                                TCAGG TGG    GCTG CAG
                                ||||| |||    |||| |||
                                AGTCC ACC    TGAC GTC
                                   _   AT__    A
GAM61   LOC222166 3'  CTGGTTTCCGCAGCCTGA    95737        G  CTGCT
                                TCAGGCTG GG     GCCAG
                                |||||||| ||     |||||
                                AGTCCGAC CC     TGGTC
                                     G  TT___
GAM61   LOC222967 5'  GGCAACACCTCAGCCCGA    94457    A      C  C
                                TC GGCTGGGG TG TGCC
                                || |||||||| || ||||
                                AG CCGACTCC AC ACGG
                                 C       _  A
GAM61   LOC254268 5'  CTGACAGCAGCCAGCT      97142      GG       C
                                GGCT  GGCTGCTG CAG
                                ||||  |||||||| |||
                                TCGA  CCGACGAC GTC
                                   __       A
GAM61   LOC254532 5'  CTGGCCCTCCCCAGCCCGG   98453    A      CTGCT
                                TC GGCTGGGG     GCCAG
                                || ||||||||     |||||
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                                GG CCGACCCC    CGGTC
                                 C       TCC__
GAM61   LOC254556 3' CTGACAGCACAGGGCCTGG   96259       GGGGC    C
                                TCAGGCT    TGCTG CAG
                                |||||||    ||||| |||
                                GGTCCGG    ACGAC GTC
                                    GAC__    A
GAM61   LOC255043 3' CAGCCCAGCCCAGCCTGA    97067        G  __
                                TCAGGCTGGG CT  GCTG
                                |||||||||| ||  ||||
                                AGTCCGACCC GA  CGAC
                                      _  CC
GAM61   LOC255065 3' CTGGCAGCAGATCTCCAG    98371       __
                                CTGGGG  CTGCTGCCAG
                                ||||||  ||||||||||
                                GACCTC  GACGACGGTC
                                    TA
GAM61   LOC256158 5' CAGCAGCACCGTCAGCCTG   99481       __ _
                                CAGGCTG  GG GCTGCTG
                                |||||||  || |||||||
                                GTCCGAC  CC CGACGAC
                                    TG  A
GAM61   LOC256227 5' GGCAGCAGCGGCAGCTGA    97762     G   GG
                                TCAG CTG  GCTGCTGCC
                                |||| |||  |||||||||
                                AGTC GAC  CGACGACGG
                                  _  GG
GAM61   LOC256940 5' CTGACAACAGCCACTCCTGG   98246      CTGG    C  C
                                TCAGG    GGCTG TG CAG
                                |||||    ||||| || |||
                                GGTCC    CCGAC AC GTC
                                   TCA_    A  A
GAM61   LOC257481 3' CTGGCCTCGTCTCCAGCCCGA  61761    A       C  CT
                                TC GGCTGGGG TG  GCCAG
                                || |||||||| ||  |||||
                                AG CCGACCTC GC  CGGTC
                                 C       T  TC
GAM61   LOC51246  3' CTGGCAGCAGGGACACCTGG   33639      C  GGG
                                TCAGG TG   CTGCTGCCAG
                                ||||| ||   ||||||||||
                                GGTCC AC   GACGACGGTC
                                  _  AGG
GAM61   LOC56912  5' CTGGAGTGAGACCCCAGCC    39749        _ _  G
                                GGCTGGGG CT GCT CCAG
                                |||||||| || ||| ||||
                                CCGACCCC GA TGA GGTC
                                    A  G  _
GAM61   LOC56912  3' CTGGCCCCTCTGCCCCAGCTGA 39750      G      TGCT__
                                TCAG CTGGGGC     GCCAG
                                |||| |||||||     |||||
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                                AGTC GACCCCG     CGGTC
                                  _      TCTCCC
GAM61   LOC90120  5'  CTGGCCCCAGCCCCAGCC    62214          CT
                                GGCTGGGGCTG  GCCAG
                                ||||||||||  |||||
                                CCGACCCCGAC  CGGTC
                                      CC
GAM61   LOC90381  3'  CTGTCACAGCCCCAACC     63213    C      C  C
                                GG TGGGGCTG TG CAG
                                || ||||||| || |||
                                CC ACCCCGAC AC GTC
                                 A       _ T
GAM61   LOC91179  3'  CTGGTTGACCCCAGCCTGG   65765          CTGCT
                                TCAGGCTGGGG    GCCAG
                                ||||||||||    |||||
                                GGTCCGACCCC    TGGTC
                                      AGT__
GAM61   LOC91409  3'  GCAGCAGCCCTGCTTGG     66571       T
                                TCAGGC GGGGCTGCTGC
                                |||||| ||||||||||
                                GGTTCG TCCCGACGACG
                                  _
GAM61   LOC91960  3'  CTGTGGGCAGCCCCACCTGA   68282      C        GC
                                TCAGG TGGGGCTGCT  CAG
                                ||||| ||||||||||  |||
                                AGTCC ACCCCGACGG  GTC
                                  _        GT
GAM61   LOC92345  5'  CAGGGGCCCCAATCCTGA    57240      C_     G
                                TCAGG  TGGGGCT CTG
                                |||||  ||||||| |||
                                AGTCC  ACCCCGG GAC
                                   TA      G
GAM61   LOC96652  3'  CTGGCTGGCCCGGCCT      66078        G  GCT
                                AGGCTGGG CT   GCCAG
                                |||||||| ||   |||||
                                TCCGGCCC GG   CGGTC
                                     _ T__
GAM62   HRH1      3'  CTCAAACATGTTTAGAGTGGA  7819       A    TGG
                                TCCA TCTGA   GCATGTTTGAG
                                |||| |||||   ||||||||||
                                AGGT AGATT   TGTACAAACTC
                                  G    ___
GAM62   TRIM37    3'  CTCAAATTTGTCATCAG     31625        G  T
                                CTGATGG CA GTTTGAG
                                ||||||| || |||||||
                                GACTACT GT TAAACTC
                                     _ T
GAM62   HTMP10    3'  CTCAAAAAAGCCATCAGATCTG 53758    CA        G ATG
            A                    TC  ATCTGATGG C   TTTGAG
                                ||  |||||||| |   ||||||
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                                AG  TAGACTACC G   AAACTC
                                 TC        _ AAA
GAM62   PAK2     5'  CTCAAATATCACCAAACTAGA  67140      A__   GC
                                TCTG   TGG  ATGTTTGAG
                                ||||   |||  |||||||||
                                AGAT   ACC  TATAAACTC
                                  CAA   AC
GAM62   SEMA6A   3'  CTCGAGTACCCACCAGA     40818      A    CA
                                TCTG TGGG  TGTTTGAG
                                |||| ||||  ||||||||
                                AGAC ACCC  ATGAGCTC
                                  C   __
GAM62   TTY7     3'  TCAAACATGCAGGCTGGA     50019      AT  GATGG
                                TCCA  CT    GCATGTTTGA
                                ||||  ||    ||||||||||
                                AGGT  GA    CGTACAAACT
                                  CG  _____
GAM62   LOC144766 3'  CTCAAACATGAGAAGACTGGG  77481      A   GATGGG
                                TCCA TCT     CATGTTTGAG
                                |||| |||     ||||||||||
                                GGGT AGA     GTACAAACTC
                                  C   AGA___
GAM62   LOC201685 5'  TAAACACCCATCAGATGGA    91845      A       CA
                                TCCA TCTGATGGG  TGTTTG
                                |||| |||||||||  ||||||
                                AGGT AGACTACCC  ACAAAT
                                  _       __
GAM62   LOC221596 5'  CTCAAACAAAACTCAGATT    93623        TG GCA
                                AATCTGA  G   TGTTTGAG
                                |||||||  |   ||||||||
                                TTAGACT  C   ACAAACTC
                                   __ AAA
GAM62   LOC93622  3'  CTCTGCAGACCATCAGAT     57729         GCA   TT
                                ATCTGATGG   TGT  GAG
                                |||||||||   |||  |||
                                TAGACTACC   ACG  CTC
                                     AG_   T_
GAM63   CDO1     3'  ACATGATCCCCAGACCACAACA 10162              GA
                                TGTTGTGGTCTGGGGA  ATGT
                                ||||||||||||||||  ||||
                                ACAACACCAGACCCCT  TACA
                                          AG
GAM63   SMTN     3'  ACACCCTCCCCCCCCACATACAC 23651      _    TCT     AA
          A                      TGTGT TGTGG   GGGGAG  TGT
                                 |||||  |||||   ||||||  |||
                                 ACACA ACACC   CCCCTC  ACA
                                   T     C__      CC
GAM63   SMTN     3'  ACACCCTCCCCCCCCACATACAC 23652      _    TCT     AA
          A                      TGTGT TGTGG   GGGGAG  TGT
                                 |||||  |||||   ||||||  |||
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                                ACACA ACACC   CCCCTC  ACA
                                  T    C__     CC
GAM63   HB-1    5'  TCCTCTGCCACACCACA    41317     T     CT
                                TGTG TGTGGT  GGGGA
                                |||| ||||||  |||||
                                ACAC ACACCG  CTCCT
                                  C     T_
GAM64   CDH12   3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM64   GOCAP1  3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM64   DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090      T   AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                  _   GTCA_
GAM64   DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
          A                      TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM64   FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM64   HMP19   3'  CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
          TA                     TACA   TCC   GAAGAATAAG
                                ||||   |||   ||||||||||
                                ATGT   AGG   TTTCTTATTC
                                  AAA_  ATTG
GAM64   KIAA1579  3'  TACTCTTAGTGGTGTA     37154         CCCAAG   A
                                TACACCACT     AAGA TA
                                |||||||||     |||| ||
                                ATGTGGTGA     TTCT AT
                                     _______   C
GAM64   KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA  68742            _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                          G
GAM64   KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
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                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM64   KIAA1877 3' CTTATTCTTCTGCCATGAGT   66748     CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM64   KIAA1906 3' CTTATTCTTCTTGACTTTTGG  73571    CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM64   OSBPL11  3' CTTAATTTCCCAAGAGTGGTG  43206       CCAA   AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                     AACC   A_
GAM64   YME1L1   3' TCATTCTTGATGTGGTGTA   58438       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                     TA_    A
GAM64   YME1L1   3' TCATTCTTGATGTGGTGTA   27323       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                     TA_    A
GAM64   ZNF262   3' CTTATTTTGTTTGGGAGT    18723        A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                     G
GAM64   LOC91960 3' TGTGGCTTGGAACGTGGTGTA  68294       TC_   AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
                                ATGTGGTG   GGTTC   TGT
                                     CAA    GG__
GAM65   B4GALT2  3' CCCCCTCCCCCTAGCCCA    48344    T    TCAT   A
                                TG GGCTGG   GGA GGGG
                                || ||||||   ||| ||||
                                AC CCGATC   CCT CCCC
                                  _    CC__   C
GAM65   B4GALT2  3' CCCCCTCCCCCTAGCCCA    48345    T    TCAT   A
                                TG GGCTGG   GGA GGGG
                                || ||||||   ||| ||||
                                AC CCGATC   CCT CCCC
                                  _    CC__   C
GAM65   BHMT2    3' GCCCCTTCCCTTCCAGCCCACA 34735      _   TCAT
                                TGTGG CTGG   GGAAGGGGC
                                ||||| ||||   |||||||||
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                                ACACC GACC    CCTTCCCCG
                                  C    TTC_
GAM65   CACNA1A  3'  CCCCCTCCACCCCCCGGCCACA 5357          TCA_   A
                                TGTGGCTGG    TGGA GGGG
                                |||||||||    |||| ||||
                                ACACCGGCC    ACCT CCCC
                                     CCCC    C
GAM65   DDX11    3'  GCCCCTTCTACAACCACG    48389      C  GTCA
                                TGTGG TG    TGGAAGGGGC
                                ||||| ||    ||||||||||
                                GCACC AC    ATCTTCCCCG
                                  A  _____
GAM65   DEDD     3'  CCCTTCCAACCAATCACA    53376      GC    CA
                                TGTG  TGGT  TGGAAGGG
                                ||||  ||||  ||||||||
                                ACAC  ACCA  ACCTTCCC
                                  TA   __
GAM65   FMNL     3'  GCCCCCTCCAAATAGCCATA   20870        GTCA    A
                                TGTGGCTG    TGGA GGGGC
                                ||||||||    |||| |||||
                                ATACCGAT    ACCT CCCCG
                                     AA__    C
GAM65   GA       5'  GCCCCTCCTTCCCAGCCACA   26089         TCAT   A
                                TGTGGCTGG    GGA GGGGC
                                |||||||||    ||| |||||
                                ACACCGACC    CCT CCCCG
                                     CTT_   _
GAM65   HUNK     3'  CCCCTTCCACTTCCCAC     28183      CT   CAT
                                GTGG  GGT   GGAAGGGG
                                ||||  |||   ||||||||
                                CACC  TCA   CCTTCCCC
                                  CT   ___
GAM65   IL20RA   3'  CCCCTTTGATCCCAGCCATA   27801         TC  G
                                TGTGGCTGG  AT GAAGGGG
                                |||||||||  || |||||||
                                ATACCGACC  TA TTTCCCC
                                     C_  G
GAM65   MKI67    3'  TCCCAGTGACCAGCCACA    11599           GGAA
                                TGTGGCTGGTCAT    GGGG
                                ||||||||||||    ||||
                                ACACCGACCAGTG    CCCT
                                       A___
GAM65   MUCDHL   3'  TCCCACCAACCAGCCACA    88649         CA   AA
                                TGTGGCTGGT  TGG  GGGG
                                ||||||||||  |||  ||||
                                ACACCGACCA  ACC  CCCT
                                     __   A_
GAM65   MUCDHL   3'  TCCCACCAACCAGCCACA    88650         CA   AA
                                TGTGGCTGGT  TGG  GGGG
                                ||||||||||  |||  ||||
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                                ACACCGACCA  ACC  CCCT
                                      __   A_
GAM65   NT5M     3'  GCCCCTCTTGGTCTCAGCCACA 39893        _ _  T   A
                                TGTGGCTG G TCA GGA GGGGC
                                |||||||| | ||| ||| |||||
                                ACACCGAC C GGT TCT CCCCG
                                     T T  _  _
GAM65   NUCB1    3'  GCCCCTTCCCCACACAGCCCCA 21644    T    _ CAT
                                TG GGCTG GT   GGAAGGGGC
                                || ||||| ||   |||||||||
                                AC CCGAC CA   CCTTCCCCG
                                 C    A  CC_
GAM65   PDGFB    3'  CCCCTCCCACGGTGCCCA    12023    T   TGG  A   A
                                TG GGC   TC TGG AGGGG
                                || |||   || ||| |||||
                                AC CCG   GG ACC TCCCC
                                 _   T__  C   C
GAM65   PDK4     5'  GCCCCTCAAGCCAGCCACA   99090         CATG  A
                                TGTGGCTGGT    GA GGGGC
                                ||||||||||    || |||||
                                ACACCGACCG    CT CCCCG
                                     AA__  _
GAM65   PXN      3'  CCCCTTCCCCAGCCA      12669        TCAT
                                TGGCTGG    GGAAGGGG
                                |||||||    ||||||||
                                ACCGACC    CCTTCCCC
                                     ____
GAM65   SLC6A5   5'  GCCCCCTCCCGCTGGAGCGACA 16141     G   __   CAT   A
                                TGT GCT  GGT   GGA GGGGC
                                ||| |||  |||   ||| |||||
                                ACA CGA  TCG   CCT CCCCG
                                  G   GG   C__   C
GAM65   SLC9A1   5'  CCCCTTCCTTTAGCCCACA   70922      _    TCAT
                                TGTGG CTGG    GGAAGGGG
                                ||||| ||||    ||||||||
                                ACACC GATT    CCTTCCCC
                                   C    T___
GAM65   SORCS2   3'  CCCCTTCCACCTGTCCCCCA   40799     CT  T  __
                                TGG  GG CA  TGGAAGGGG
                                |||  || ||  |||||||||
                                ACC  CC GT  ACCTTCCCC
                                  C_  T  CC
GAM65   SOX11    3'  GCCCCTTCCTGTGGAGCCTACA 13320     _    GG    _
                                TGT GGCT  TCAT GGAAGGGGC
                                ||| ||||  |||| |||||||||
                                ACA CCGA  GGTG CCTTCCCCG
                                  T    __    T
GAM65   TACR1    5'  GCCCCAGGCGCCAGCCACA   8328          CATGGAA
                                TGTGGCTGGT      GGGGC
                                ||||||||||      |||||
```

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                                ACACCGACCG      CCCCG
                                     CGGA___
GAM65   ZNF236   3' GCCCCGGGCAACCAGCCA    24736        CA  GAA
                                TGGCTGGT  TG   GGGGC
                                ||||||||  ||   |||||
                                ACCGACCA  AC   CCCCG
                                     __  GGG
GAM65   BRUNOL6  3' CTTTCACTGACCAGCCACA   54521          _
                                TGTGGCTGGTCA TGGAAG
                                |||||||||||| ||||||
                                ACACCGACCAGT ACTTTC
                                       C
GAM65   C20orf124 3' GCCCCTCCCTGCTGAGCCA   45840      _ T T   A
                                TGGCT GG CA GGA GGGGC
                                ||||| || || ||| |||||
                                ACCGA TC GT CCT CCCCG
                                   G  _  C   _
GAM65   C20orf139 5' CCCCTCTCACCAGCTACA    85916         CAT GA
                                TGTGGCTGGT   G  AGGGG
                                ||||||||||   |  |||||
                                ACATCGACCA   C  TCCCC
                                     ___ TC
GAM65   C20orf44  3' CCCCCTCCAGCAACTACA    37309      CTG  CA    A
                                TGTGG   GT  TGGA GGGG
                                |||||   ||  |||| ||||
                                ACATC   CG  ACCT CCCC
                                   AA_  __    C
GAM65   CBX6     3' GCCCCTTCCACATCCCAC    27416     CT   CA
                                GTGG  GGT  TGGAAGGGGC
                                ||||  |||  ||||||||||
                                CACC  CTA  ACCTTCCCCG
                                   __   C_
GAM65   CSEN     3' GCCCCTCCCATGGCCCAGC    26460      _     A
                                GCTGG TCATGG AGGGGC
                                ||||| |||||| ||||||
                                CGACC GGTACC TCCCCG
                                   C     C
GAM65   CXYorf1   3' GCCCCCACCGCAACAGCCACA  82916        GTCA   AA
                                TGTGGCTG    TGG  GGGGC
                                ||||||||    |||  |||||
                                ACACCGAC    GCC  CCCCG
                                     AAC_   AC
GAM65   DKFZP434N014 5' CCCCCTAGGATCCAGCCAC    61228         _ A   AA
                                GTGGCTGG TC TGG  GGGG
                                |||||||| || |||  ||||
                                CACCGACC AG ATC  CCCC
                                     T  G   __
GAM65   DKFZP566K1924 5' GCCCCTCGCGCTCCAGCCAC   74197         TCA  GA
                                GTGGCTGG   TG  AGGGGC
                                ||||||||   ||  ||||||
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                                CACCGACC  GC  TCCCCG
                                    TC_  GC
GAM65   DKFZp761O132 3' CCCCTTCTGTTCGCCACA   51167      T  TC
                                TGTGGC GG  ATGGAAGGGG
                                |||||| ||  ||||||||||
                                ACACCG CT  TGTCTTCCCC
                                  _  __
GAM65   FLJ10156 3' GCCCCCTGCTCCAGCCACA   39204        TCAT  AA_
                                TGTGGCTGG   GG  GGGGC
                                |||||||||   ||  |||||
                                ACACCGACC   TC  CCCCG
                                    ____ GTC
GAM65   FLJ12587 3' GCCCCTTCCACAAAGCTGTA  42781   TG  GGTCA
                                TG  GCT   TGGAAGGGGC
                                ||  |||   ||||||||||
                                AT  CGA   ACCTTCCCCG
                                 GT  AAC__
GAM65   FLJ12876 3' CCCCTTCCAAAAGTCAGTCACA 43088        TCA_
                                TGTGGCTGG   TGGAAGGGG
                                |||||||||   |||||||||
                                ACACTGACT   ACCTTCCCC
                                    GAAA
GAM65   FLJ13055 3' GCCCCCCAAGCCAGCCA    43018       CA  AA
                                TGGCTGGT  TGG  GGGGC
                                ||||||||  |||  |||||
                                ACCGACCG  ACC  CCCCG
                                    A_  __
GAM65   FLJ21438 5' GCCCCTTCCACTCTACCCA   62196    C  TCA
                                TGG TGG   TGGAAGGGGC
                                ||| |||   ||||||||||
                                ACC ATC   ACCTTCCCCG
                                  C  TC_
GAM65   FLJ23058 3' GCCCCCTTTTCCACCAGCCA  45525       CAT  ___
                                TGGCTGGT  GGAA  GGGGC
                                ||||||||  ||||  |||||
                                ACCGACCA  CCTT  CCCCG
                                    ___   TTC
GAM65   FLJ23588 3' GCCCAGCGGGACGACAGCCACA 43272        __  ATGGAAG
                                TGTGGCTG  GTC     GGGC
                                ||||||||  |||     ||||
                                ACACCGAC  CAG     CCCG
                                    AG  GGCGA__
GAM65   GBTS1    3' CCCCCGGGACCAGCCACA    59722         A  AA
                                TGTGGCTGGTC TGG  GGG
                                |||||||||||  |||  |||
                                ACACCGACCAG GCC  CCC
                                    G  __
GAM65   KIAA0152 3' CCCCTTCCATGTCCCACCCCA  28970    T  CT  T
                                TG GG  GG CATGGAAGGGG
                                || ||  || ||||||||||
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                                AC CC  CC GTACCTTCCCC
                                 C  AC  T
GAM65   KIAA0222 3' GCCCCTTCCCTGAGCCAC    28397      TGG   T
                                GTGGC   TCA GGAAGGGGC
                                |||||   ||| |||||||||
                                CACCG   AGT CCTTCCCCG
                                  ___   C
GAM65   KIAA0377 3' CCCCTTCCACCAGCAACA    28500     G     CAT
                                TGT GCTGGT   GGAAGGGG
                                ||| ||||||   ||||||||
                                ACA CGACCA   CCTTCCCC
                                  A     ___
GAM65   KIAA0444 3' CCCCTTTCCCCAGGCACA    62996     G    TCAT
                                TGTG CTGG    GGAAGGGG
                                |||| ||||    ||||||||
                                ACAC GACC    CTTTCCCC
                                  G    C___
GAM65   KIAA0478 3' CCCCTTCCTTCCAGGCACA   30176     G    TCAT
                                TGTG CTGG    GGAAGGGG
                                |||| ||||    ||||||||
                                ACAC GACC    CCTTCCCC
                                  G    TT__
GAM65   KIAA0789 5' GCCCCTTCCATCCTCTCCCA  64431     CT  TC
                                TGG  GG  ATGGAAGGGGC
                                |||  ||  ||||||||||
                                ACC  CT  TACCTTCCCCG
                                  CT  CC
GAM65   KIAA0967 3' GCCCCTTCCACTCTCCCAC   30478     CT  TCA
                                GTGG  GG   TGGAAGGGGC
                                ||||  ||   ||||||||||
                                CACC  CT   ACCTTCCCCG
                                  CT  C__
GAM65   KIAA1130 3' CTGGCATGACCAGCCTCA    63093    T        GA
                                TG GGCTGGTCATG  AG
                                || ||||||||||  ||
                                AC CCGACCAGTAC  TC
                                 T         GG
GAM65   KSR      5' GCCCCCCCCACCCAGCCGCA  64738        TCA   AA
                                TGTGGCTGG   TGG  GGGGC
                                |||||||||   |||  |||||
                                ACGCCGACC   ACC  CCCCG
                                     C__    CC
GAM65   LYPLA3   3' CCCTTCCCACACACCAGCCACA 25559         CAT__
                                TGTGGCTGGT    GGAAGGG
                                ||||||||||    |||||||
                                ACACCGACCA    CCTTCCC
                                      CACAC
GAM65   MGC16491 3' GCCCCTTCCAGGGTGCCAC   54739      T G  A
                                GTGGC G TC TGGAAGGGGC
                                ||||| | || ||||||||||
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                                CACCG T GG ACCTTCCCCG
                                  _ G  _
GAM65   NPTXR    3'  CCCCTTTCCCAGCCCACA    27430      _    TCAT
                                TGTGG CTGG   GGAAGGGG
                                ||||| ||||   ||||||||
                                ACACC GACC   CTTTCCCC
                                  C   ____
GAM65   PME-1    3'  GCCCCCTCCACCTTTCCAC   32869     CT_  CAT  A
                                GTGG  GGT  GGA GGGGC
                                ||||  |||  ||| |||||
                                CACC  CCA  CCT CCCCG
                                  TTT  ___  C
GAM65   PRDM12   3'  GCCCCTTCCAACACACACA   41512     GCTG  CA
                                TGTG   GT  TGGAAGGGGC
                                ||||   ||  ||||||||||
                                ACAC   CA  ACCTTCCCCG
                                  ACA_  __
GAM65   TED      3'  CCCCTGGCTCAGACCAGCCCA  32265    T      A  _ A_
                                TG GGCTGGTC TG G  AGGGG
                                || |||||||| || |  |||||
                                AC CCGACCAG AC C  TCCCC
                                 _       _  T GG
GAM65   TREX1    3'  GCCCTGAGTGTCCAGCCACA   50605        T   GGAA
                                TGTGGCTGG CAT    GGGGC
                                ||||||||| |||    |||||
                                ACACCGACC GTG    TCCCG
                                     T   AG__
GAM65   TREX1    5'  GCCCTGAGTGTCCAGCCACA   50606        T   GGAA
                                TGTGGCTGG CAT    GGGGC
                                ||||||||| |||    |||||
                                ACACCGACC GTG    TCCCG
                                     T   AG__
GAM65   TREX1    5'  GCCCTGAGTGTCCAGCCACA   50607        T   GGAA
                                TGTGGCTGG CAT    GGGGC
                                ||||||||| |||    |||||
                                ACACCGACC GTG    TCCCG
                                     T   AG__
GAM65   TREX1    5'  GCCCTGAGTGTCCAGCCACA   50608        T   GGAA
                                TGTGGCTGG CAT    GGGGC
                                ||||||||| |||    |||||
                                ACACCGACC GTG    TCCCG
                                     T   AG__
GAM65   LOC145314 3'  CCTGAGAAATGACCAGTCACA  77611           GGAA_
                                TGTGGCTGGTCAT    GGG
                                ||||||||||||     |||
                                ACACTGACCAGTA    TCC
                                       AAGAG
GAM65   LOC145919 3'  GCCCCTCCTCCTCAGCCAC    78027        TCAT  A
                                GTGGCTGG   GGA GGGGC
                                ||||||||   ||| |||||
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                                CACCGACT    CCT CCCCG
                                    CCT_  _
GAM65   LOC146243 3'  GCCCCTTCCACCTAACCCCCA  84621     CT   CA__
                                TGG  GGT    TGGAAGGGGC
                                |||  |||    ||||||||||
                                ACC  CCA    ACCTTCCCCG
                                  C_   ATCC
GAM65   LOC147229 3'  GCCCCTTTGCCCCAACACA   78922     GC   TCATG
                                TGTG  TGG    GAAGGGGC
                                ||||  |||    ||||||||
                                ACAC  ACC    TTTCCCCG
                                  A_   CCG__
GAM65   LOC148529 5'  GCCCCTGTCTACAGCCACA   85321       GTCA   _
                                TGTGGCTG    TGGA AGGGGC
                                ||||||||    |||| ||||||
                                ACACCGAC    ATCT TCCCCG
                                    _____   G
GAM65   LOC149302 5'  CCCCTCCGTGGCAGCCCA    80039    T    G      A
                                TG GGCTG TCATGGA GGGG
                                || ||||| ||||||| ||||
                                AC CCGAC GGTGCCT CCCC
                                 _    _     _
GAM65   LOC158983 3'  CCCCCCACGAAATCAGCCACA  82948         __ A   AA
                                TGTGGCTGG  TC TGG  GGGG
                                |||||||||  || |||  ||||
                                ACACCGACT  AG ACC  CCCC
                                     AA  C  __
GAM65   LOC162417 3'  CCCCAGGCAGCCAGCCACA   83213         CA  GAA
                                TGTGGCTGGT  TG   GGGG
                                ||||||||||  ||   ||||
                                ACACCGACCG  AC   CCCC
                                     __  GGA
GAM65   LOC200014 5'  GCCCCCCAGGAACCAGCCA   89938        _ A   AA
                                TGGCTGGT C TGG  GGGGC
                                |||||||| | |||  |||||
                                ACCGACCA G ACC  CCCCG
                                    A G   __
GAM65   LOC254182 3'  GCCCCTTCCATGAAGGGCCCA  97750    T   GG
                                TG GGCT  TCATGGAAGGGGC
                                || ||||  ||||||||||||||
                                AC CCGG  AGTACCTTCCCCG
                                 _    GA
GAM65   LOC55971  5'  CCCCATCCCCTGACCAGCTACA 38732          T_   A
                                TGTGGCTGGTCA  GGA GGGG
                                ||||||||||||  ||| ||||
                                ACATCGACCAGT  CCT CCCC
                                      CC   A
GAM65   LOC90133  3'  GCCCCTCCCGTGGCTGCCACA  62291       T      A
                                TGTGGC GGTCATGG AGGGGC
                                |||||| |||||||| ||||||
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                                ACACCG TCGGTGCC TCCCCG
                                   _       C
GAM65   LOC91012 5' CCCCTCTTTCCCCAGACACA  65244      G   TCAT  A
                                TGTG CTGG   GGA GGGG
                                |||| ||||   ||| ||||
                                ACAC GACC   TCT CCCC
                                  A   CCTT  _
GAM66   ADCY2    3' ACCCCCATCTCTGCAAAAAAAT 65641       A     G
           A                     TATTTT TTGCAG AGGTGGGGGT
                                 |||||| |||||| ||||||||||
                                 ATAAAA AACGTC TCTACCCCCA
                                    A     _
GAM66   CST1     3' CCCCCACCTCCTGCAATTAAA  10329     T
                                TTT ATTGCAGGAGGTGGGGG
                                ||| |||||||||||||||
                                AAA TAACGTCCTCCACCCCC
                                  T
GAM66   CST2     3' ACCCCCACCTCCTGCAATTAAA 8995      T
                                TTT ATTGCAGGAGGTGGGGGT
                                ||| |||||||||||||||||
                                AAA TAACGTCCTCCACCCCCA
                                  T
GAM66   CST3     3' ACCCCCACCTCCTGCAATAAAA 5432
           TA                     TATTTTATTGCAGGAGGTGGGGGT
                                  ||||||||||||||||||||||||
                                  ATAAAATAACGTCCTCCACCCCCA

GAM66   CST4     3' ACCCCCACCTCCTGCAATTAAA 10332     T
                                TTT ATTGCAGGAGGTGGGGGT
                                ||| |||||||||||||||||
                                AAA TAACGTCCTCCACCCCCA
                                  T
GAM66   ICA1     3' ACCCCCATCTCTACAAAAAATA 42514       A   CA
                                TATTTT TTG  GGAGGTGGGGGT
                                |||||| |||  ||||||||||||
                                ATAAAA AAC  TCTCTACCCCCA
                                   _   A_
GAM66   IL10RA   3' ACCCCCACCCCTCTGCCAAAGT 60377       ATT   _ A
           A                     TATTTT   GCAG G GGTGGGGGT
                                 ||||||   |||| | |||||||||
                                 ATGAAA   CGTC C CCACCCCCA
                                    C__    T C
GAM66   PRG2     3' ACCTCCCTGCAATAAAATG   12259            _
                                TATTTTATTGCAGG AGGT
                                |||||||||||||| ||||
                                GTAAAATAACGTCC TCCA
                                          C
GAM66   C20orf139 3' CGCCTCCTGCAATAAAA     85918             TG
                                TTTTATTGCAGGAGG  G
                                |||||||||||||||  |
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                                AAAATAACGTCCTCC  C
                                       GT
GAM66   DC13     3'  CTTATCTCCTTCAATAAAATA  39879          C
                                TATTTTATTG AGGAGGTGGG
                                |||||||||| ||||||||||
                                ATAAAATAAC TCCTCTATTC
                                      T
GAM66   DKFZp761N1114 3'  CCTTTCCTAAAATAAAATA   79781          GC     T
                                TATTTTATT  AGGAGG GG
                                |||||||||  ||||||  ||
                                ATAAAATAA  TCCTTT CC
                                     AA     _
GAM66   FBXO27   3'  ACCCCCATCGCTACAAAAAATA 74997        A   C  GA
                                TATTTT TTG AG  GGTGGGGGT
                                |||||| ||| ||  |||||||||
                                ATAAAA AAC TC  CTACCCCCA
                                   _   A  G_
GAM66   FLJ20013  3'  ACCCCCATCTCTACAAAAAATA 34791        A   CA
                                TATTTT TTG  GGAGGTGGGGGT
                                |||||| |||  ||||||||||||
                                ATAAAA AAC  TCTCTACCCCCA
                                   _   A_
GAM66   HGC6.2   5'  ACCCCCACCTCACTTACAA   27618     C_  _
                                TTG  AG GAGGTGGGGGT
                                |||  || ||||||||||
                                AAC  TC CTCCACCCCCA
                                  AT  A
GAM66   MGC4840   3'  CCCCATTTCTACAAAAAATA   72021       A   CA
                                TATTTT TTG  GGAGGTGGGG
                                |||||| |||  ||||||||||
                                ATAAAA AAC  TCTTTACCCC
                                   _   A_
GAM66   TSA1902   3'  CCTAAAGTCCTGCAATAAAAT  41722            GG_
                                ATTTTATTGCAGGA   TGGG
                                ||||||||||||||   ||||
                                TAAAATAACGTCCT   ATCC
                                       GAA
GAM66   LOC130507 3'  CCTATCGTTCTACAATAAAATA 75455          C   _
                                TATTTTATTG AGGA GGTGGG
                                |||||||||| |||| ||||||
                                ATAAAATAAC TCTT CTATCC
                                     A   G
GAM66   LOC143188 3'  ACCCCCACCTCCTCATTA    83789    T  C
                                TA TG AGGAGGTGGGGGT
                                || || ||||||||||||
                                AT AC TCCTCCACCCCCA
                                 T  _
GAM66   LOC91191  3'  ACCCCCACCCCAAATTAAAATG 65800        TTGCA  A
                                TATTTTA    GG GGTGGGGGT
                                |||||||    || |||||||||
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                                GTAAAAT    CC CCACCCCCA
                                   TAAA_  _
GAM67   PIP5K1A  3'  TATCCCACCCTGCCTTGATA  14520       A   CA  C
                                TATCAAGG AGGG  GG GTG
                                |||||||| ||||  || |||
                                ATAGTTCC TCCC  CC TAT
                                   G   A_  C
GAM67   SOX11    3'  ACCCACCCCCCCTTGGTA   13308       AA  CA  C
                                TATCAAGG  GGG  GG GT
                                ||||||||  |||  || ||
                                ATGGTTCC  CCC  CC CA
                                   CC   A_  _
GAM67   CHL1     3'  TGTTACCTTTCCTCAATA   22768    CA      CA
                                TAT  AGGAAGGG  GGCG
                                |||  ||||||||  ||||
                                ATA  TCCTTTCC  TTGT
                                  AC       A_
GAM67   EPB41L1  3'  CATTCTGCCCTTCCCTGA   71104    A        C
                                TCA GGAAGGGCAGG GTG
                                ||| ||||||||||| |||
                                AGT CCTTCCCGTCT TAC
                                  C         _
GAM67   FLJ00060 3'  CATACCCCCTGCCCTCCTCTGA 61741    _   A      CGTG
                                TCA AGGA GGGCAGG   ATG
                                ||| |||| |||||||   |||
                                AGT TCCT CCCGTCC   TAC
                                  C   _      CCCA
GAM67   FLJ10898 5'  CACCACAGCCCTTTCTCAATA  60126    CA       AGGC
                                TAT  AGGAAGGGC   GTG
                                |||  |||||||||   |||
                                ATA  TCTTTCCCG   CAC
                                  AC       ACAC
GAM67   FLJ22557 3'  ATCATCCCATCCTTAATA   45581    C    A  CAGGC
                                TAT AAGGA GGG    GTGAT
                                ||| ||||| |||    |||||
                                ATA TTCCT CCC    TACTA
                                  A    A  _____
GAM67   KIAA0574 3'  CATCCCCTGCCCTCCCCTGA  69808    A  A      CGT
                                TCA GG AGGGCAGG   GATG
                                ||| || ||||||||   ||||
                                AGT CC TCCCGTCC   CTAC
                                  C  C       C__
GAM67   KIAA0632 3'  CACCTCAGAAACCCTTCCTTGA 32071         CA___  C
                                TCAAGGAAGGG    GG GTG
                                ||||||||||    || |||
                                AGTTCCTTCCC    CT CAC
                                      AAAGA  C
GAM67   KIAA1354 5'  CAGTGACTGCCTTCCCTTGATA 61572        A      G  _
                                TATCAAGG AGGGCAG CG TG
                                |||||||| ||||||| || ||
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                                ATAGTTCC TTCCGTC GT AC
                                    C      A  G
GAM67   MGC20460  5'  CACCGCCTCCTACCCTTCTT   54901        C___    _
                                AGGAAGGG    AGGCG TG
                                ||||||||    ||||| ||
                                TTCTTCCC    TCCGC AC
                                    ATCC     C
GAM67   LOC158476 3'  CACGCCCGCCCCCCCCATTGA  88186     _ AA_   A
                                TCAA GG   GGGC GGCGTG
                                |||| ||   |||| ||||||
                                AGTT CC   CCCG CCGCAC
                                  A  CCC    C
GAM67   LOC90459  3'  CACACCCGCCTAATTTTTG    63550       A_   A  C
                                CAAGGA  GGGC GG GTG
                                ||||||  |||| || |||
                                GTTTTT  TCCG CC CAC
                                    AA    C  A
GAM68   ADARB1    3'  GGGTGGGAAAATAGAGGTAGG  32339    A   C    A
                                CC ACC CTGT TTCCCACCC
                                || ||| |||| |||||||||
                                GG TGG GATA AAGGGTGGG
                                 A   A    A
GAM68   AES       3'  GGGACAGGGAGGTTGGGA     8524          _  GTAT
                                TCCCAACC CCT    TCCC
                                |||||||| |||    ||||
                                AGGGTTGG GGG    AGGG
                                    A   AC__
GAM68   ANXA6     3'  GGGGTGGGGGGAGGGGTTGGG  15740          GTA
                                CCCAACCCCT   TTCCCACCCC
                                ||||||||||   ||||||||||
                                GGGTTGGGGA   GGGGGTGGGG
                                     G__
GAM68   ARF4L     3'  GGGGTGGGGATGGGAGATGGGA 70391       AC_  TGT
                                TCCCA   CCC   ATTCCCACCCC
                                |||||   |||   ||||||||||
                                AGGGT   GGG   TAGGGGTGGGG
                                   AGA   ___
GAM68   ARHGDIA   3'  GGGGTGGAGCTGGGGTGTGGGA 16297       _    T  ATTC
                                TCCCA ACCCC GT    CCACCCC
                                ||||| ||||| ||    |||||||
                                AGGGT TGGGG CG    GGTGGGG
                                   G     T  A___
GAM68   BCL11B    3'  GGGATGGGTGGGGTGGGGA   57578     A    TGTATT   _
                                TCCC ACCCC      CCCA CCC
                                |||| |||||      |||| |||
                                AGGG TGGGG      GGGT GGG
                                  G    T_____    A
GAM68   BCL2      5'  GGGGTGGGAGCTGGGG      7238       T  AT
                                CCCC GT  TCCCACCCC
                                |||| ||  |||||||||
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                                GGGG CG  AGGGTGGGG
                                  T __
GAM68   CABC1    3'  GGGTGGGAGCAGCGGAACAGGG 40042     AAC_ _   AT
             A                   TCCC   CC CTGT  TCCCACCC
                                 ||||   || ||||  ||||||||
                                 AGGG   GG GACG  AGGGTGGG
                                   ACAA  C   __
GAM68   CDC42    3'  GGGGTAGGGTGGGGGTGGGGA  10142     A     TATT  _
                                 TCCC ACCCCTG   CCC ACCCC
                                 |||| |||||||   ||| |||||
                                 AGGG TGGGGGT   GGG TGGGG
                                   G      ____  A
GAM68   CDK10    3'  GGGACAAGGTATGGGGTGGGA  14791      A   T   ____
                                 TCCCA CCCC GTAT   TCCC
                                 ||||| |||| ||||   ||||
                                 AGGGT GGGG TATG   AGGG
                                   _   _   GAAC
GAM68   CDK10    3'  GGGACAAGGTATGGGGTGGGA  14792      A   T   ____
                                 TCCCA CCCC GTAT   TCCC
                                 ||||| |||| ||||   ||||
                                 AGGGT GGGG TATG   AGGG
                                   _   _   GAAC
GAM68   CDK10    3'  GGGACAAGGTATGGGGTGGGA  54835      A   T   ____
                                 TCCCA CCCC GTAT   TCCC
                                 ||||| |||| ||||   ||||
                                 AGGGT GGGG TATG   AGGG
                                   _   _   GAAC
GAM68   CDKN2B   5'  GGGGCGGAGCCTAAGGGGGTGG 55313      A    GTATTC  A
             GA                    TCCCA CCCCT     CC CCCC
                                   |||||  |||||     || ||||
                                   AGGGT GGGGA     GG GGGG
                                     G    ATCCGA  C
GAM68   CPO      3'  TGGCTGTGCAGGGGTTTGGA   5416     C        TC
                                   TCC AACCCCTGTAT  CCA
                                   ||| ||||||||||  |||
                                   AGG TTGGGGACGTG  GGT
                                     T         TC
GAM68   DES      3'  GGTGGGAGCAGGAGATTGAGA  72592    C  CC_    AT
                                   TC CAA   CCTGT  TCCCACC
                                   || |||   |||||  |||||||
                                   AG GTT   GGACG  AGGGTGG
                                    A  AGA    __
GAM68   DHCR24   3'  GGAATGGAAAGAATGTGGGATT 29301      CC  TG    ___   CC
             TGG                     CCAA  CC  TATTC   CCA  CC
                                     ||||  ||  |||||   |||  ||
                                     GGTT  GG  GTAAG   GGT  GG
                                       TA  GT    AAA   AA
GAM68   DLG4     3'  GGGATGGGTCTAGGGAGTGGGA 9084       AC    TATT   _
                                   TCCCA  CCCTG   CCCA CCC
                                   |||||  |||||   |||| |||
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                                AGGGT  GGGAT    GGGT GGG
                                   GA    CT__    A
GAM68   DLG4    3'  GGGTGGGGCAGGGGTCGGGG  9085      A      ATT
                                TCCC ACCCCTGT   CCCACCC
                                |||| ||||||||   |||||||
                                GGGG TGGGGACG   GGGTGGG
                                  C       ___
GAM68   DOCK1   3'  GGAGCAAGGTGGGTCTGGGA  9106       _   _ GTA
                                TCCCA ACCC CT   TTCC
                                ||||| |||| ||   ||||
                                AGGGT TGGG GG   GAGG
                                   C    T  AAC
GAM68   DPP6    5'  GGGGTGGGGAGTGGGAACCGGA 56322    CAAC   TGTA
                                TCC    CCC    TTCCCACCCC
                                |||    |||    ||||||||||
                                AGG    GGG    AGGGGTGGGG
                                  CCAA   TG__
GAM68   EGLN2   5'  GGGCAAGGAGGGGTGGGA    54918      A   TGTAT   CA_
                                TCCCA CCCC    TCC   CCC
                                ||||| ||||    |||   |||
                                AGGGT GGGG    AGG   GGG
                                   _   _____  AAC
GAM68   EIF2C1  3'  GATGGGGTGGGGGTGGGA    25196      A   TG ATT   CC
                                TCCCA CCCC  T   CCCA  C
                                ||||| ||||  |   ||||  |
                                AGGGT GGGG  G   GGGT  G
                                   _   GT ___    AA
GAM68   EIF4G1  5'  GGGTGGGAGCTGGGGCAGGGA  18256     AA    T  AT
                                TCCC  CCCC GT  TCCCACCC
                                ||||  |||| ||  ||||||||
                                AGGG  GGGG CG  AGGGTGGG
                                  AC    T  __
GAM68   ENC1    3'  GGGGCGAGGGAGGGGGGTGGGA 14648      A    GTA    A__
                                TCCCA CCCCT   TTCCC   CCCC
                                ||||| |||||   |||||   ||||
                                AGGGT GGGGG   GAGGG   GGGG
                                   _    ___     AGC
GAM68   EP300   5'  GGGTGGGGGCGCAGGCCCGGGA 9286      AACC    TA
                                TCCC    CCTG  TTCCCACCC
                                ||||    ||||  |||||||||
                                AGGG    GGAC  GGGGGTGGG
                                   CCC_    GC
GAM68   ETF1    3'  GGGTGGGAAGGGATGGGA    17590      A  CTGTA
                                TCCCA CCC    TTCCCACCC
                                ||||| |||    |||||||||
                                AGGGT GGG    AAGGGTGGG
                                   A  _____
GAM68   FCN2    3'  GGTGGGGGTGACACTGGGA   15921      ACCCCTG
                                TCCCA      TATTCCCACC
                                |||||      ||||||||||
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                                AGGGT     GTGGGGGTGG
                                  CACA___
GAM68   FOSB    3'  GGGACGGGGGTGGGA      23057      A     TAT
                                TCCCA CCCCTG   TCCC
                                ||||| ||||||   ||||
                                AGGGT GGGGGC   AGGG
                                  _     ___
GAM68   FUT7    3'  GGCTGGGCACAGAGGTCAGGA  16805    CA   C    ATT    C
                                TCC  ACC CTGT   CCCA CC
                                |||  ||| ||||   |||| ||
                                AGG  TGG GACA   GGGT GG
                                  AC   A    C__    C
GAM68   FY      5'  GGGTGAGTATGGGGCCAGG   10739    AAC        CC
                                CC   CCCTGTATTC  ACCC
                                ||   ||||||||||  ||||
                                GG   GGGGTATGAG  TGGG
                                 ACC         __
GAM68   GALNT2   3'  GGGGTGGGTGTGGGGACTGGGA 16819      AC   TG  TT
                                TCCCA  CCC  TA  CCCACCCC
                                |||||  |||  ||  ||||||||
                                AGGGT  GGG  GT  GGGTGGGG
                                   CA   GT  __
GAM68   GARP    3'  GGGGTGAGATTGGGGGTTGG   19785         GTAT  C
                                CCAACCCCT    TC CACCCC
                                |||||||||    || ||||||
                                GGTTGGGGGG    AG GTGGGG
                                      TT__  A
GAM68   GAS7    3'  GGGTGGGGTGAGGTTGGGG   20858        CCTGTAT
                                TCCCAACC      TCCCACCC
                                ||||||||      ||||||||
                                GGGGTTGG      GGGGTGGG
                                    AGT____
GAM68   GLI     3'  GGGATGGGAGGTATGGGCTGGG 19168      A   CTGTA     _
           G                     TCCCA CCC     TTCCCA CCC
                                ||||| |||     |||||| |||
                                GGGGT GGG     GAGGGT GGG
                                   C   TATG_     A
GAM68   GPC4    3'  GGGATGGGGTGGGGTGGGA   9354       A   TGTAT    _
                                TCCCA CCCC    TCCCA CCC
                                ||||| ||||    ||||| |||
                                AGGGT GGGG    GGGGT GGG
                                   _   T_____    A
GAM68   HDAC5   3'  GGGATGGGGATGGGGCCAGG   58300    CAA    TGT     _
                                CC   CCCC   ATTCCCA CCC
                                ||   ||||   ||||||| |||
                                GG   GGGG   TAGGGGT GGG
                                 ACC    ___      A
GAM68   HIP12   3'  GGGGTGGGACCAGGCTGGGA   66819      ACC    TAT
                                TCCCA   CCTG   TCCCACCCC
                                |||||   ||||   |||||||||
```

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                                AGGGT  GGAC  AGGGTGGGG
                                  C__  C__
GAM68  HOXB5   3' GGGTGGGAAGGGGCTAGGGA  10957    AA_   GTAT
                                TCCC  CCCCT  TCCCACCC
                                ||||  |||||  ||||||||
                                AGGG  GGGGA  AGGGTGGG
                                  ATC   ____
GAM68  HPCAL1  3' GGGTGGGGACGAGGCGTCGGGA 10969    A C  GTA
                                TCCC AC CCT  TTCCCACCC
                                |||| || |||  |||||||||
                                AGGG TG GGA  AGGGGTGGG
                                  C C  GC_
GAM68  INHA    5' GGGTAGAAGAGGGTGGGTGTGG 10999     _  _ GTA  CC
           GA                   TCCCA ACCC CT  TTC  ACCC
                                ||||| |||| ||  |||  ||||
                                AGGGT TGGG GG  AAG  TGGG
                                  G  T  GAG  A_
GAM68  INHA    5' GGGTGGGTGTGGGATGGGG   11000     A  CTGT  T
                                TCCCA CCC   AT CCCACCC
                                ||||| |||   || |||||||
                                GGGGT GGG   TG GGGTGGG
                                  A  _____ T
GAM68  ITGA4   5' GTGGGTATAGAAGGGTGCTGA  7958    CCA  __   TT
                                TC  ACCC  CTGTA  CCCAC
                                ||  ||||  |||||  |||||
                                AG  TGGG  GATAT  GGGTG
                                 TCG   AA   __
GAM68  ITPR2   5' GGAGTGGACACGAGGTGGGA  11082     A  CC  ATTC  _
                                TCCCA CC  TGT   CCAC CC
                                |||||  ||  |||  |||| ||
                                AGGGT GG  GCA   GGTG GG
                                  _ A_  CA__   A
GAM68  KCNJ4   3' GGTGGGGGTTTCAAAGACTGGG 18359    ACCCC  T_
                                CCCA   TG  ATTCCCACC
                                ||||   ||  |||||||||
                                GGGT   AC  TGGGGGTGG
                                  CAGAA  TT
GAM68  KLHL3   3' GGGATGAGGCTGGGGTTGGGA  88850        T  AT__
                                TCCCAACCCC GT   TCCC
                                ||||||||||  ||   ||||
                                AGGGTTGGGG CG   AGGG
                                     T  GAGT
GAM68  KLK3    3' GGGATGGGGATGAAGTAAGGA  9709    CA  CCCTG     _
                                TCC  AC   TATTCCCA CCC
                                |||  ||   |||||||| |||
                                AGG  TG   GTAGGGGT GGG
                                  AA  AA___     A
GAM68  KRTHA1  3' GGAGCAAGGATGCAGGGCCCAG 11236    CAAC       CCAC_
           GA                   TCC   CCCTGTATTC   CC
                                |||   ||||||||||   ||
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                                AGG   GGGACGTAGG    GG
                                  ACCC        AACGA
GAM68   KRTHA7   5'  GGATGGGGTATAAAAGGGTTGG 15017        CTG  _    C
             GA                    TCCCAACCC   TAT TCCCA CC
                                   |||||||||   ||| ||||| ||
                                   AGGGTTGGG   ATA GGGGT GG
                                       AAA   T    A
GAM68   LRP1     5'  GGGGTGGGGTGAAGGGTTTGG  11362     C    GTAT
                                   CCAA CCCT    TCCCACCCC
                                   |||| ||||    |||||||||
                                   GGTT GGGA    GGGGTGGGG
                                     T    AGT_
GAM68   MADH2    5'  GGGGCGGGAAGACGGCGGCCGG 20917     AA  C    A    A
             GA                    TCCC  CC CTGT TTCCC CCCC
                                   ||||  || |||| ||||| ||||
                                   AGGG  GG GGCA AAGGG GGGG
                                     CC  C    G    C
GAM68   MADH6    5'  GGAGTAAGAAGGGAGCTGGGG  19976      AC_   G__
                                   TCCCA   CCCT   TATTCC
                                   |||||   ||||   ||||||
                                   GGGGT   GGGA   ATGAGG
                                      CGA    AGA
GAM68   MAML1    5'  GGCGGTGGGGAGAGGCCGAGG  29279    AACC   GTA      _
                                   CC    CCT   TTCCCACC CC
                                   ||    |||   |||||||| ||
                                   GG    GGA   AGGGGTGG GG
                                     AGCC   G__       C
GAM68   MAP3K7IP1 3'  GGGTAGCAAGCAGGGGTTGTGA 21490    C        ATTCCC
                                   TC CAACCCCTGT      ACCC
                                   || ||||||||||      ||||
                                   AG GTTGGGGACG      TGGG
                                    T         AACGA_
GAM68   MAP3K9   3'  GGGACGGGGATGTTAGGA    61364     C  __    TAT
                                   TCC AAC  CCCTG   TCCC
                                   ||| |||  |||||   ||||
                                   AGG TTG  GGGGC   AGGG
                                     A   TA    ___
GAM68   MGAT3    5'  GGGGTGGGGGGAGGGGATCGGG 11564      AA_    GTA
             G                     TCCC   CCCCT   TTCCCACCCC
                                   ||||   |||||   ||||||||||
                                   GGGG   GGGGA   GGGGGTGGGG
                                     CTA    G__
GAM68   NAV2     3'  GGGTGGGGTGGGAGTGGGA   60796      AC   TGTAT
                                   TCCCA  CCC    TCCCACCC
                                   |||||  |||    ||||||||
                                   AGGGT  GGG    GGGGTGGG
                                     GA   T____
GAM68   NDRG1    3'  GGGGTGGGGGTGGAATTGGGG  60310       CC  TGT
                                   TCCCAA  CC   ATTCCCACCCC
                                   ||||||  ||   ||||||||||
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                                GGGGTT  GG   TGGGGGTGGGG
                                  AA  ___
GAM68   NEDD4L   5'  GGGTAGGGTGCGGGACCGGGG  31606     AACC     TT  _
                                CCC    CCTGTA  CCC ACCC
                                |||    ||||||  ||| ||||
                                GGG    GGGCGT  GGG TGGG
                                  GCCA     __   A
GAM68   NIPSNAP1  3'  GGGGTGGGAAGAGAGGAGGCCA 14662    CAA  _  GTA
           GG                     CC   CC CCT   TTCCCACCCC
                                ||   || |||   ||||||||||
                                GG   GG GGA   AAGGGTGGGG
                                 ACC  A   GAG
GAM68   NPR1     3'  GGGGTGGCGCAGAAGGGTTGGG 88741          __    ATTC
           G                     TCCCAACCC  CTGT    CCACCCC
                                |||||||||  ||||    |||||||
                                GGGGTTGGG  GACG    GGTGGGG
                                     AA    C___
GAM68   NR4A1    3'  GGTGGGAGCGGGGCTGGGA    10946       A    T  AT
                                TCCCA CCCC GT  TCCCACC
                                ||||| |||| ||  |||||||
                                AGGGT GGGG CG  AGGGTGG
                                  C    _ __
GAM68   OXTR     3'  GGGGTAAGCAGTGGGGTTGGGA 8081           __   AT_
                                TCCCAACCCC  TGT   TCCC
                                ||||||||||  |||   ||||
                                AGGGTTGGGG  ACG   GGGG
                                     TG   AAT
GAM68   PABPN1   3'  GTGGGAACAGGGAGGTGGGA   17358       AC_     AT
                                TCCCA   CCCTGT  TCCCAC
                                |||||   ||||||  ||||||
                                AGGGT   GGGACA  AGGGTG
                                  GGA     __
GAM68   PAX7     5'  GGGGTGGGGGGTGGGGGTAGGG 11974      A     TG A
           A                     TCCC ACCCC  T TTCCCACCCC
                                |||| |||||  | ||||||||||
                                AGGG TGGGG  G GGGGGTGGGG
                                  A     GT _
GAM68   PBX2     3'  GGGGTGGGAGGCATGGGCCGGG 11981      AA   C   A
           G                     TCCC  CCC TGT TTCCCACCCC
                                ||||  ||| ||| ||||||||||
                                GGGG  GGG ACG GAGGGTGGGG
                                  CC   T  _
GAM68   PCDH1    3'  GGGGTAGGGACGGGGGTGGGA  51578       A      TAT   _
                                TCCCA CCCCTG   TCCC ACCCC
                                ||||| ||||||   |||| |||||
                                AGGGT GGGGGC   AGGG TGGGG
                                  _     ___    A
GAM68   PCTK1    3'  GGGGTGGGAGGGCAGGGGTGGG 53420       A      A
           A                     TCCCA CCCCTGT TTCCCACCCC
                                ||||| ||||||| ||||||||||
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                                AGGGT GGGGACG GAGGGTGGGG
                                  _     G
GAM68   PIK3C2B  3'  GGTTGGGGAGGGTTGGGG   12108        CTGTA    C
                                TCCCAACCC    TTCCCA CC
                                |||||||||    |||||| ||
                                GGGGTTGGG    AGGGGT GG
                                     _____     T
GAM68   PLAG1    3'  GGGATGGGGGCAAGGGTGGGA  12149      A  C  AT   _
                                TCCCA CCC TGT  TCCCA CCC
                                ||||| ||| |||  ||||| |||
                                AGGGT GGG ACG  GGGGT GGG
                                  _  A  __    A
GAM68   POU2AF1  3'  GAGTAGTAAGGGGTGGGA   21744      A    G__
                                TCCCA CCCCT   TATTC
                                ||||| |||||   |||||
                                AGGGT GGGGA   ATGAG
                                  _    ATG
GAM68   PPOX     5'  GGGGTGGGAGTAGCGGATTTG  6130     CC  TG
                                CAA  CC  TATTCCCACCCC
                                |||  ||  ||||||||||||
                                GTT  GG  ATGAGGGTGGGG
                                  TA  CG
GAM68   PPP1CB   5'  GGGGTGGGGGGGAGGGCCCGGGA 12227     AAC   GTA
                                TCCC   CCCT   TTCCCACCCC
                                ||||   ||||   ||||||||||
                                AGGG   GGGA   GGGGGTGGGG
                                  CCC   G__
GAM68   PPP1R12B 3'  GGGATGGGGTGGGGTTGGGG   50361        TGTAT   _
                                TCCCAACCCC    TCCCA CCC
                                ||||||||||    ||||| |||
                                GGGGTTGGGG    GGGGT GGG
                                     T____    A
GAM68   PPP1R8   3'  GGGTGGGATTGGGTGGGA    57510      A  CTGTAT
                                TCCCA CCC     TCCCACCC
                                ||||| |||     ||||||||
                                AGGGT GGG     AGGGTGGG
                                  _  TT____
GAM68   PPP2R4   3'  GGGTGGGTGGGGTCGGG     61182     A    TGTATT
                                CCC ACCCC     CCCACCC
                                ||| |||||     |||||||
                                GGG TGGGG     GGGTGGG
                                  C    T_____
GAM68   PRKY     3'  GGCAGGAGAATATGGAACTCAG 12379     CAACCC      _ AC
           GA                    TCC     CTGTATTC CC  CC
                                |||     |||||||| ||  ||
                                AGG     GGTATAAG GG  GG
                                  ACTCAA       A  AC
GAM68   PROK1    3'  GGGGTGGGAGCAAGGGACAGGG 51568     AAC   GTA
           A                     TCCC   CCCT   TTCCCACCCC
                                ||||   ||||   ||||||||||
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                                AGGG  GGGA  GAGGGTGGGG
                                  ACA   AC_
GAM68  PRSS8   3' GGGGTGGGAGTAACAGGG   12422      _
                                CCCTGT ATTCCCACCCC
                                |||||| ||||||||||
                                GGGACA TGAGGGTGGGG
                                   A
GAM68  PRX     3' GGAGTGGGAGTGGGGACCAGGA 40899    CAA_   TGT     _
                                TCC   CCCC  ATTCCCAC CC
                                |||   ||||  |||||||| ||
                                AGG   GGGG  TGAGGGTG GG
                                  ACCA  ____      A
GAM68  PRX     3' GGTGGCAGCAGGGGTCAGGG  40901    A_     ATTC
                                CCC  ACCCCTGT   CCACC
                                |||  ||||||||   |||||
                                GGG  TGGGGACG   GGTGG
                                  AC      AC__
GAM68  PTGS1   3' GGGGTAAGATGAGGGGTTGAGG 55477   _     G   CCC
                                CC CAACCCCT TATT  ACCCC
                                || |||||||| ||||  |||||
                                GG GTTGGGGA GTAG  TGGGG
                                 A       _   AA_
GAM68  PTK7    3' GGGGTGGGCCCTGGAGATGAGG 12551    _ ACC  TGTATT
          A                      TCC CA  CC    CCCACCCC
                                |||  ||  ||    ||||||||
                                AGG GT  GG    GGGTGGGG
                                  A  AGA  TCCC__
GAM68  PYGM    3' GGGTGGGGTACTGGAGTT   20036    C  T   T
                                AAC CC GTAT CCCACCC
                                ||| || |||| |||||||
                                TTG GG CATG GGGTGGG
                                  A  T   _
GAM68  RABIF   3' TGAGAGTGGAGGGTGTAGG   12732   A _   G   C
                                CC AC CCCT TATTC CA
                                || || |||| ||||| ||
                                GG TG GGGA GTGAG GT
                                 A  T   G    A
GAM68  RAD51L1 3' GGAATGAGAGCAAGGGTTGGG  56877       C  ____
                                CCCAACCC TGT   ATTCC
                                |||||||| |||   |||||
                                GGGTTGGG ACG   TAAGG
                                     A  AGAG
GAM68  RANBP2L1 5' GGGGTGGGAACTTGTGGCTTG  51051    C  C  TA
                                CAA CC TG  TTCCCACCCC
                                ||| || ||  ||||||||||
                                GTT GG GT  AAGGGTGGGG
                                  C  T  TC
GAM68  RAP1GA1 3' GGAGTGAGCACTGGGTTGGGA  12773       C_  __
                                TCCCAACCC  TGT  ATTCC
                                |||||||||  |||  |||||
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                                AGGGTTGGG  ACG  TGAGG
                                     TC   AG
GAM68   RAP1GA1  3'  GGTGGGAGAGAGAGTTTGAGA  12775    C   CCC  GTA
                                TC CAA   CT   TTCCCACC
                                || |||   ||   ||||||||
                                AG GTT   GA   GAGGGTGG
                                 A   TGA  GA_
GAM68   RHEB2    5'  GGCGGCGGAAGAAGGTGGGA   20048      ACC   GTA    CA  _
                                TCCCA   CCT   TTCC  CC CC
                                |||||   |||   ||||  || ||
                                AGGGT   GGA   AAGG  GG GG
                                   ___   AG_   C_  C
GAM68   RXRB     3'  GGGGTGAGAAGTACAGGG    42031         _ C
                                CCCTGTATT C CACCCC
                                ||||||||| | ||||||
                                GGGACATGA G GTGGGG
                                     A A
GAM68   SCA1     3'  GGGGTAAGGGGGGTTGGGG   6182           GTAT
                                TCCCAACCCCT   TCCC
                                ||||||||||   ||||
                                GGGGTTGGGGG   GGGG
                                      GAAT
GAM68   SGCA     3'  GGGTGGGGTGGGGTGAGA    5247     CCA    TGTAT
                                TC   ACCCC    TCCCACCC
                                ||   |||||    ||||||||
                                AG   TGGGG    GGGGTGGG
                                 AG_    T____
GAM68   SIAT4C   3'  GGGCAGGGGCATTGGGA     21859       __     TATT
                                TCCCAA  CCCCTG   CCC
                                ||||||  ||||||   |||
                                AGGGTT  GGGGAC   GGG
                                   AC     ____
GAM68   SLC20A1  3'  GGGATGGATGAATGAAGTGG   60097    C  G    __  _
                                CC CT TATTC  CCA CCC
                                || || |||||  ||| |||
                                GG GA GTAAG  GGT GGG
                                 T  A    TA   A
GAM68   SLC21A9  3'  GGGTGGGGGGAAGCTGGGG   24380     T  A__
                                CCCC GT   TTCCCACCC
                                |||| ||   |||||||||
                                GGGG CG   GGGGGTGGG
                                  T  AAG
GAM68   SLC25A15 3'  GGAACGGAAACTTAGGTTGGGA 27295         CCT  A    CAC
                                TCCCAACC   GT TTCC   CC
                                ||||||||   || ||||   ||
                                AGGGTTGG   CA AAGG   GG
                                     ATT  _    CAA
GAM68   SLC2A1   3'  GGGTAGGAGGTTTGGATGGGA  22518      A  CCTGTA    C
                                TCCCA CC     TTCC ACCC
                                ||||| ||     |||| ||||
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                                AGGGT GG     GAGG TGGG
                                  A  TTTG__   A
GAM68   SLC2A3   5' GGGTGGGGTGGGGCTGGGG  23644      A   TGTAT
                                TCCCA CCCC    TCCCACCC
                                ||||| ||||    ||||||||
                                GGGGT GGGG    GGGGTGGG
                                  C   T____
GAM68   SLC7A6   3' GGGTGGGGGGAAGATTGGGG  15643      CCC  GTA
                                TCCCAA  CT  TTCCCACCC
                                ||||||  ||  |||||||||
                                GGGGTT  GA  GGGGGTGGG
                                  A__  AG_
GAM68   SLC8A2   3' GGGATGGGTGGGGGGATGGGA 66937     A    GTATT   _
                                TCCCA CCCCT    CCCA CCC
                                ||||| |||||    |||| |||
                                AGGGT GGGGG    GGGT GGG
                                  A    GT___   A
GAM68   SMN1     3' GGGGTGGGGGTGGGAGG    43462   _  GT
                                CC CCT  ATTCCCACCCC
                                || |||  ||||||||||||
                                GG GGG  TGGGGGTGGGG
                                 A  __
GAM68   SPR      3' GGAATAGAACTTAAGGGGTGGG 13386     A    G_______
           A                     TCCCA CCCCT      TATTCC
                                ||||| |||||      ||||||
                                AGGGT GGGGA      ATAAGG
                                  _    ATTCAAG
GAM68   SYNGR1   3' GGGACAGGGAGGTATGGGA   17508     _  _  GTAT
                                TCCCA ACC CCT   TCCC
                                ||||| ||| |||   ||||
                                AGGGT TGG GGG   AGGG
                                  A  A  AC__
GAM68   SYT5     5' GGGGTGGGAATGGGGGACTAGG 13504    AA__    GT
           G                     CCC   CCCCT  ATTCCCACCCC
                                |||   |||||  ||||||||||
                                GGG   GGGGG  TAAGGGTGGGG
                                 ATCA   __
GAM68   TACSTD2  5' GGGACGGGGAGGGGGGCGGGA  11407     AA   GTA   AC
                                TCCC  CCCCT   TTCCC  CCC
                                ||||  |||||   |||||  |||
                                AGGG  GGGGG   AGGGG  GGG
                                  CG    ___    CA
GAM68   TCEB3    3' GGCAGGAATACAAGGACAGTGG 13609     AC__  C      CA
           GG                    TCCCA   CC TGTATTCC  CC
                                |||||   || ||||||||  ||
                                GGGGT   GG ACATAAGG  GG
                                  GACA  A      AC
GAM68   TFCP2    5' GGAGTGGGAGTGCGGGAGTCCA 20166   CCA  C         _
           GA                    TC   AC CCTGTATTCCCAC CC
                                ||   || ||||||||||||| ||
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                                AG   TG GGGCGTGAGGGTG GG
                                 ACC  A           A
GAM68   TGFA     3'  GGAATAAAGGTAGGGGTTCAGA 13713    CC      ____
                                TC  AACCCCTG    TATTCC
                                ||  ||||||||    ||||||
                                AG  TTGGGGAT    ATAAGG
                                 AC       GGAA
GAM68   TNC      3'  GGGATGGGAGAGGGGTAGG   10978    A     GTA     _
                                CC ACCCCT   TTCCCA CCC
                                || ||||||   |||||| |||
                                GG TGGGGA   GAGGGT GGG
                                 A      ___      A
GAM68   TPST2    3'  GGGTAGAGAATGAAGGGTATGG 14582     AC    G     CC_
                                CCA  CCCT TATTC   ACCC
                                |||  |||| |||||   ||||
                                GGT  GGGA GTAAG   TGGG
                                  AT    A     AGA
GAM68   UNC13    3'  GGACTGTGGTACTAGGGGCTGG 22098      A    _   TTC    ___
           GA                     TCCCA CCCCT GTA   CCAC   CC
                                |||||| ||||| |||   ||||   ||
                                AGGGT GGGGA CAT   GGTG   GG
                                   C     T    ___    TCA
GAM68   ZAP70    3'  GGAGCAGGGAGGTCCGGGA    71376     A_   __    AT
                                TCCC  ACC  CCTGT  TCC
                                ||||  |||  |||||  |||
                                AGGG  TGG  GGACG  AGG
                                  CC   AG    __
GAM68   ZNF137   3'  GGGTGGGGGAGAGGGGCAGGGA 14312      AA    GTA
                                TCCC  CCCCT   TTCCCACCC
                                ||||  |||||   |||||||||
                                AGGG  GGGGA   GGGGGTGGG
                                  AC    GA_
GAM68   ZNF146   3'  GGATGGGAGTGAGGATGGGA   24077      ACC   G      CC
                                TCCCA   CCT TATTCCCA  CC
                                |||||   ||| ||||||||  ||
                                AGGGT   GGA GTGAGGGT  GG
                                   A__   _       AA
GAM68   ABLIM    3'  GGTGGGATGTGGAGGTCAGA   22983    CCA   C TG   T
                                TC   ACC C  TAT CCCACC
                                ||   ||| |  ||| ||||||
                                AG   TGG G  GTA GGGTGG
                                 AC_   A GT   _
GAM68   ABT1     3'  GGGTGGACTGGGTTGGGA    26303         CT  ATTC
                                TCCCAACCC  GT    CCACCC
                                |||||||||  ||    ||||||
                                AGGGTTGGG  CA    GGTGGG
                                      T_  _____
GAM68   ALS2CR3  3'  TGGGTAGAGGGTGGGA     31185      AC    G  TT
                                TCCCA  CCCT TA  CCCA
                                |||||  |||| ||  ||||
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                                AGGGT  GGGA AT  GGGT
                                  __   G  __
GAM68   AP1G2    5' GGGGTGGGCGCGGAATTTGG  15353     CCC   ATT
                                CCAA  CTGT  CCCACCCC
                                ||||  ||||  ||||||||
                                GGTT  GGCG  GGGTGGGG
                                  TAA   C__
GAM68   APCL     3' GGGGTGGGACTCGCAGGGGCCG 20820     AA     AT_
           GG                     CCC  CCCCTGT  TCCCACCCC
                                ||| |||||||  |||||||||
                                GGG  GGGGACG  AGGGTGGGG
                                  CC     CTC
GAM68   BRD2     3' GGGCAGGGCAAGGGTGGGA   18796      A  C  ATT  CA
                                TCCCA CCC TGT  CC  CCC
                                ||||| ||| |||  ||  |||
                                AGGGT GGG ACG  GG  GGG
                                  _  A  ___  AC
GAM68   C20orf35 3' GGTGGGAAGGATGGTGGGA   38075      A __  GTAT
                                TCCCA CC  CCT   TCCCACC
                                ||||| ||  |||   |||||||
                                AGGGT GG  GGA   AGGGTGG
                                  _ TA  ____
GAM68   C9orf9   3' GGATGGAGTGGGGGTCGG   39026    A    GT   CA
                                CC ACCCCT  ATTCC  CC
                                || ||||||  |||||  ||
                                GG TGGGGG  TGAGG  GG
                                 C     __    TA
GAM68   CCR7     3' GGGTGAGTGCAAGGGGCGTGGG 10226      A_   _    CC
           A                     TCCCA  CCCCT GTATTC  ACCC
                                |||||  ||||| ||||||  ||||
                                AGGGT  GGGGA CGTGAG  TGGG
                                  GC    A    __
GAM68   CDC16    5' GGGGCGGGGTGCTTAGGGTGCA 15337    CA_  CT_  T  A
           GGA                    TCC   ACCC   GTAT CCC CCCC
                                |||   ||||  |||| ||| ||||
                                AGG   TGGG   CGTG GGG GGGG
                                  ACG   ATT   _  C
GAM68   CECR2    3' GTGGGAAGGGTGGGTGGGGA  49438     A   _ GTA
                                TCCC ACCC CT   TTCCCAC
                                |||| |||| ||   |||||||
                                AGGG TGGG GG   AAGGGTG
                                  G   T  G__
GAM68   CLSTN3   3' GGGGCAGGGGCGGGGGGTTGGG 28879         GTAT   A_
                                CCCAACCCCT   TCCC  CCCC
                                ||||||||||   ||||  ||||
                                GGGTTGGGGG   GGGG  GGGG
                                     GC__   AC
GAM68   CRMP5    3' GGGATGGGGGTGGCTGGGA   39705      A  _  G
                                TCCCA CC CCT TATTCC
                                ||||| || ||| ||||||
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                                AGGGT GG GGG GTAGGG
                                  C  T   G
GAM68   DAPK2    3'  GGGGTGGGAGTGTGGACTTAGG 27515     CAACCC TG
           A                     TCC     C  TATTCCCACCCC
                                 |||     |  ||||||||||||
                                 AGG     G  GTGAGGGTGGGG
                                   ATTCA_ GT
GAM68   Di-Ras2  3'  GGTGGGAGGGAGGACTGG    34614     A_ _  GTAT
                                 CCA  CC CCT    TCCCACC
                                 |||  || |||    |||||||
                                 GGT  GG GGG    AGGGTGG
                                   CA  A  ____
GAM68   DKFZP434C171 3'  GGGTGGATCACAAGGTTGGGA  32196        CC   AT   C
                                 TCCCAACC  TGT  TCC ACCC
                                 ||||||||  |||  ||| ||||
                                 AGGGTTGG  ACA  AGG TGGG
                                      A_   CT   _
GAM68   DKFZP586C1324 3'  GGTGGATCACAAGGTTGGGA   70360        CC   AT   C
                                 TCCCAACC  TGT  TCC ACC
                                 ||||||||  |||  ||| |||
                                 AGGGTTGG  ACA  AGG TGG
                                      A_   CT   _
GAM68   DKFZP727G051 5'  TGGGAGTGGGGGTGGAGA    70012    _  A    GT
                                 TC CCA CCCCT  ATTCCCA
                                 || ||| |||||  |||||||
                                 AG GGT GGGGG  TGAGGGT
                                   A  _    __
GAM68   DKFZp761O17121 3'  GAGTAGGGGAGAAGGTTGGGG  51132         ____  G
                                 TCCCAACC    CCT TATTC
                                 ||||||||    ||| |||||
                                 GGGGTTGG    GGG ATGAG
                                      AAGA   G
GAM68   DKFZP762D096 5'  GGGGTGGGCCAGGACCGGGGA  66181      AACC    TATT
                                 TCCC    CCTG    CCCACCCC
                                 ||||    ||||    ||||||||
                                 AGGG    GGAC    GGGTGGGG
                                   GCCA    C___
GAM68   DNAJB5   3'  GGAGTGGGAGGGAGGTGGGGA  25355      A  _  GTAT     _
                                 TCCC ACC CCT    TCCCAC CC
                                 |||| ||| |||    |||||| ||
                                 AGGG TGG GGG    AGGGTG GG
                                   G  A  _____     A
GAM68   DNAL4    3'  GGGTAGAGGAGGTGGGA     20422      A _  G  TT
                                 TCCCA CC CCT TA  CCC
                                 ||||| || ||| ||  |||
                                 AGGGT GG GGA AT  GGG
                                   _ A  G  __
GAM68   DUSP9    3'  GGGGTGGGGAAGGGG       9157       GTA
                                 CCCCT   TTCCCACCCC
                                 |||||   ||||||||||
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                              GGGGA  AGGGGTGGGG
                                     ___
GAM68  ELOVL1   3' GGGTGGGCGGGGGCCTGGGA  43372     A_    TATT
                              TCCCA  CCCCTG   CCCACCC
                              |||||  ||||||   |||||||
                              AGGGT  GGGGGC   GGGTGGG
                                CC    ____
GAM68  ENDO180  3' GGGTGGGAGCTGGGCCGGG   21269    AAC   T  AT
                              CCC   CCC GT  TCCCACCC
                              |||   ||| ||  ||||||||
                              GGG   GGG CG  AGGGTGGG
                                CC_   T  __
GAM68  EPB41L1  3' GGTGGGAGGGGAGGGCGG    71114   _ AA   TGTAT
                              TC CC  CCCC    TCCCACC
                              || ||  ||||    |||||||
                              GG GG  GGGG    AGGGTGG
                               C  GA   _____
GAM68  ERG-1    5' GGGTAGGTGGAGGTGGGA    42101     A _  TGTATT  C
                              TCCCA CC CC     CC ACCC
                              ||||| || ||     || ||||
                              AGGGT GG GG     GG TGGG
                                 _  A  T_____  A
GAM68  ESM1     3' TGGGGAGGGGGTGGGA     23851     A    GTA
                              TCCCA CCCCT   TTCCCA
                              ||||| |||||   ||||||
                              AGGGT GGGGG   AGGGGT
                                     _    ___
GAM68  EZFIT    3' GGGGTGGGGACTCGGGGTCAGG 41381    AAC    TA
          G                    CCC   CCCTG  TTCCCACCCC
                              |||   |||||  ||||||||||
                              GGG   GGGGC  AGGGGTGGGG
                                ACT    TC
GAM68  FLJ00024 3' GGGTGGGGACAGGGCTGGGA  64498     AC     AT
                              TCCCA  CCCTGT  TCCCACCC
                              |||||  ||||||  ||||||||
                              AGGGT  GGGACA  GGGGTGGG
                                 C_     __
GAM68  FLJ00024 3' GGTGGAGGGAGGGTTGGGG   64500       CTGTAT   A _
                              TCCCAACCC     TCCC CC CC
                              |||||||||     |||| || ||
                              GGGGTTGGG     AGGG GG GG
                                     _______   A  T
GAM68  FLJ10702 3' GGATACTTTTTTAAGGGGTTGA 36970    C      ________
          GA                   TC CAACCCCT      GTATTC
                              || ||||||||      ||||||
                              AG GTTGGGGA      CATAGG
                               A       ATTTTTT
GAM68  FLJ11274 3' GGAGCAGGAGAGGTGGGA    37780      A ___    AT
                              TCCCA CC   CCTGT  TCC
                              ||||| ||   |||||  |||
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                                AGGGT GG   GGACG  AGG
                                  _  AGA    __
GAM68   FLJ12221  3' GGGTGGGCTCAGGGTTGGGG  63223        C  TATT
                                TCCCAACCC TG    CCCACCC
                                |||||||||  ||    |||||||
                                GGGGTTGGG AC    GGGTGGG
                                     _  TC__
GAM68   FLJ12242  3' GGGGTGGGCCCCGGGCCTGAGA 45505    C  AC   TGTATT
                                TC CA  CCC     CCCACCCC
                                ||  ||  |||     ||||||||
                                AG GT  GGG     GGGTGGGG
                                 A  CC   CCCC__
GAM68   FLJ12526  3' GAATGGAAGGGGGTGGGG    45927      A    G_
                                TCCCA CCCCT  TATTC
                                |||||  |||||  |||||
                                GGGGT GGGGA  GTAAG
                                   G    AG
GAM68   FLJ12526  3' GGAGTGGGTGAGGGTGGGA    45929      AC    GTATT    _
                                TCCCA  CCCT    CCCAC CC
                                |||||  ||||    ||||| ||
                                AGGGT  GGGA    GGGTG GG
                                   __   GT___    A
GAM68   FLJ12592  3' GGTGGGGTGGAGGTGGGGA    50653     A  _  TGTAT
                                TCCC ACC CC    TCCCACC
                                ||||  ||| ||    |||||||
                                AGGG TGG GG    GGGGTGG
                                  G   A  T____
GAM68   FLJ12806  5' GGGGCGGGAGGGGACGGGGTGG 43393     A    TGTA_    A
           GGA                   TCCC ACCCC    TTCCC CCCC
                                ||||  |||||    ||||| ||||
                                AGGG TGGGG    GAGGG GGGG
                                  G    CAGGG    C
GAM68   FLJ13659  3' GGGTGAATTACATGAGGTTGGG 48035        CC_   TTCC
           A                    TCCCAACC   TGTA   CACCC
                                ||||||||   ||||   |||||
                                AGGGTTGG   ACAT   GTGGG
                                     AGT    TAA_
GAM68   FLJ14129  3' GGGGTGGGGGGGCAGTTAGG   48811    C__   A
                                CC   CTGT TTCCCACCCC
                                ||   |||| ||||||||||
                                GG   GACG GGGGGTGGGG
                                 ATT    G
GAM68   FLJ14490  3' GGGTGGGAGCCTGGGCTGGG   52447     A   CT  AT
                                CCCA CCC  GT  TCCCACCC
                                ||||  |||  ||  ||||||||
                                GGGT GGG  CG  AGGGTGGG
                                  C   TC  __
GAM68   FLJ14708  3' GGGGTGCCTGGGCGGGGCTGGG 52607      A   T  ATTCC
           A                    TCCCA CCCC GT    CACCCC
                                |||||  |||| ||    ||||||
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                                AGGGT GGGG CG    GTGGGG
                                  C   _ GGTCC
GAM68   FLJ20128 3' GGGGCGGGTGGGGGGAGCCTGG 35082    A___    GTATT  A
                                CCA   CCCCT    CCC CCCC
                                |||   |||||    ||| ||||
                                GGT   GGGGG    GGG GGGG
                                  CCGA    GT___   C
GAM68   FLJ20330 3' GGGTGGGATGGGCTGGTGA   39144   _  A  CTGTAT
                                TC CCA CCC     TCCCACCC
                                || ||| |||     ||||||||
                                AG GGT GGG     AGGGTGGG
                                 T  C  T_____
GAM68   FLJ20378 3' GGTGGGGTGGGGGGCTGG    35560    A    GTAT
                                CCA CCCCT    TCCCACC
                                ||| |||||    |||||||
                                GGT GGGGG    GGGGTGG
                                  C    GT__
GAM68   FLJ20508 3' GGAGTAGCCGCAGGGGTGGGA  35755      A     _____
                                TCCCA CCCCTGT    ATTCC
                                ||||| |||||||    |||||
                                AGGGT GGGGACG    TGAGG
                                   _      CCGA
GAM68   FLJ20531 3' GGGTGGGGGGCAAGACTGGG   35801     ACCCC   AT
                                CCCA    TGT  TCCCACCC
                                ||||    |||  ||||||||
                                GGGT    ACG  GGGGTGGG
                                  CAGA_  __
GAM68   FLJ20695 3' GGGTGGGGGGAGAGGGGTGG   35986    A    GTA
                                CCA CCCCT   TTCCCACCC
                                ||| |||||   |||||||||
                                GGT GGGGA   GGGGGTGGG
                                  _    GA_
GAM68   FLJ20701 3' GGGTGGGAGTGTGGATGGGGA  36024     AACCC TG
                                TCCC    C  TATTCCCACCC
                                ||||    |  ||||||||||
                                AGGG    G  GTGAGGGTGGG
                                  GTA__ GT
GAM68   FLJ20856 3' GGGGTGGGATCGGGGAGCAGGA 47864    CAAC    TAT
                                TCC   CCCTG   TCCCACCCC
                                |||   |||||   |||||||||
                                AGG   GGGGC   AGGGTGGGG
                                  ACGA    T__
GAM68   FLJ21135 3' GGGCAGGGCAGGGCTGGG    46352     AC     ATT  CA
                                CCCA  CCCTGT   CC  CCC
                                ||||  ||||||   ||  |||
                                GGGT  GGGACG   GG  GGG
                                  C_     ___  AC
GAM68   FLJ21290 5' GGTAGGACAGGGTTGGG     47398        C  TAT   C
                                CCCAACCC TG   TCC ACC
                                |||||||| ||   ||| |||
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                                GGGTTGGG AC   AGG TGG
                                   _ ___   A
GAM68   FLJ21777 5' GGGGCGAGGAGAAGGTGGGA  50845     ACC  GTAT  CA_
                                TCCCA  CCT   TCC  CCCC
                                |||||  |||   |||  ||||
                                AGGGT  GGA   AGG  GGGG
                                  ___  AG__  AGC
GAM68   FLJ21916 3' TGGAAAATGCAGGGTGTGG  43898    AC      C_
                                CCA  CCCTGTATT  CCA
                                |||  |||||||||  |||
                                GGT  GGGACGTAA  GGT
                                  GT       AA
GAM68   FLJ21988 3' GGTGGGAAACAGAGCTGG   42854    ACCC   A
                                CCA   CTGT TTCCCACC
                                |||   |||| ||||||||
                                GGT   GACA AAGGGTGG
                                  CGA_   _
GAM68   FLJ22282 3' GGGGTGGGATCGGTGGACCAGG 45965    AAC_ _  TAT
           G                     CCC   CC CTG  TCCCACCCC
                                |||   || |||  |||||||||
                                GGG   GG GGC  AGGGTGGGG
                                  ACCA  T  T__
GAM68   FLJ22282 3' GGTGGAAGCATGGGGTGGGA  45966     A  _  A  C
                                TCCCA CCCC TGT TTCC ACC
                                ||||| |||| ||| |||| |||
                                AGGGT GGGG ACG AAGG TGG
                                  _   T  _  _
GAM68   FLJ22635 3' GGTGGGGGGAGTGGGAAGTGGGA 47673     ACC  TG A
                                TCCCA  CC  T TTCCCACC
                                |||||  ||  | ||||||||
                                AGGGT  GG  G GGGGGTGG
                                   GAA  GT A
GAM68   FLJ23185 3' GGGGTGGGCGCTGGGCAGTCGG 47521     A  __  T  ATT
           GA                    TCCC AC  CCC GT  CCCACCCC
                                |||| ||  ||| ||  ||||||||
                                AGGG TG  GGG CG  GGGTGGGG
                                  C  AC  T  C__
GAM68   FLJ23309 3' GGGGTAGAAGGAAGGCTGGGA  46592     ACC  GTA  CC
                                TCCCA  CCT  TTC  ACCCC
                                |||||  |||  |||  |||||
                                AGGGT  GGA  AAG  TGGGG
                                  C__  AGG  A_
GAM68   FLJ31168 3' GGGATGGGAGTGGGGTAGG   59184   A   TGT    _
                                CC ACCCC  ATTCCCA CCC
                                || |||||  ||||||| |||
                                GG TGGGG  TGAGGGT GGG
                                 A    ___     A
GAM68   GABARAPL1 3' GGGGTGGGAGTGGGGAGCAGGA 49422    CAA_   TGT
                                TCC   CCCC  ATTCCCACCCC
                                |||   ||||  ||||||||||
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                                AGG   GGGG  TGAGGGTGGGG
                                  ACGA   ___
GAM68   GABARAPL3 3'  GGGGTGGGAGTGGGGAGCAGGA 51786    CAA_   TGT
                                TCC   CCCC  ATTCCCACCCC
                                |||   ||||  ||||||||||
                                AGG   GGGG  TGAGGGTGGGG
                                  ACGA   ___
GAM68   GK001    3'  GGGATGGGTAAGGGTTGGG   39882       CTGTATT   _
                                CCCAACCC     CCCA CCC
                                ||||||||     |||| |||
                                GGGTTGGG     GGGT GGG
                                     AAT____   A
GAM68   GPA33    3'  GGGCGGCGGAGGAAGGGTTAGG 20571    _    CTGTA   _  A
            G                    CCC AACCC    TTC CC CCC
                                ||| |||||    ||| || |||
                                GGG TTGGG    AGG GG GGG
                                  A    AAGG_   C  C
GAM68   HIC      5'  GGGGCGGAGTGCGCGGAGT   68051    _ C      CA
                                AC CC TGTATTCC  CCCC
                                || || ||||||||  ||||
                                TG GG GCGTGAGG  GGGG
                                 A  C       C_
GAM68   HSJ001348 3'  GGGATGGGAGAGTGGGGATCAG 62859    CAAC   TG A    _
            G                    CC    CCC  T TTCCCA CCC
                                ||   |||  | |||||| |||
                                GG    GGG  G GAGGGT GGG
                                 ACTA   GT A     A
GAM68   HSPC182   5'  GGGTGGGAACCCAAGCGGG   27201    _ _ TA
                                CCC CT G  TTCCCACCC
                                ||| || |  |||||||||
                                GGG GA C  AAGGGTGGG
                                  C  A CC
GAM68   HSPF2    5'  GGTGGGGAGGGGGAGCAGGA   19837    CAA_    GTA
                                TCC   CCCCT   TTCCCACC
                                |||   |||||  ||||||||
                                AGG   GGGGG   AGGGGTGG
                                  ACGA   ___
GAM68   HSU79274  3'  GGTGAGGGTAAGGGGTTGTGA  26149    C      GTAT   _
                                TC CAACCCCT    TCC CACC
                                || ||||||||    ||| ||||
                                AG GTTGGGGA    GGG GTGG
                                 T       AT__   A
GAM68   HXCP2    3'  GGGATGGGAAGTTAGGAAAGAT 51804      ACC____    TA    _
            ATGGGA                 TCCCA      CCTG  TTCCCA CCC
                                |||||      ||||  |||||| |||
                                AGGGT      GGAT  AAGGGT GGG
                                   ATAGAAA    TG     A
GAM68   IL-17RC   3'  GGGGTGGGACCAGGGGCGGGA  52180      AA     TAT
                                TCCC  CCCCTG   TCCCACCCC
                                ||||  ||||||   |||||||||
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                                AGGG  GGGGAC   AGGGTGGGG
                                  C_     C__
GAM68   KIAA0125 3' GGGTGGGGTGGGGCTGAGG   29574    _ A   TGTAT
                                CC CA CCCC    TCCCACCC
                                || || ||||    ||||||||
                                GG GT GGGG    GGGGTGGG
                                 A  C   T____
GAM68   KIAA0427 3' GGGATGAGGGTGGGGGGTGTGG 29388      AC   G    C _
           GA                     TCCCA  CCCT TATTC CA CCC
                                |||||  |||| ||||| || |||
                                AGGGT  GGGG GTGGG GT GGG
                                   GT   G    A A
GAM68   KIAA0429 5' GGGTGGGACAAGGCTGAGA   29244    C  ACC   GTAT
                                TC CA   CCT    TCCCACCC
                                || ||   |||   ||||||||
                                AG GT   GGA    AGGGTGGG
                                 A  C__   AC__
GAM68   KIAA0430 3' GGGTAGGCGAGGGGTTCGGA   39355     C      _ ATT
                                TCC AACCCCT GT   CCC
                                ||| ||||||| ||   |||
                                AGG TTGGGGA CG   GGG
                                  C      G  GAT
GAM68   KIAA0481 3' GGTGGACATGGGGTTGG     72323         _  ATTC
                                CCAACCCC TGT    CCACC
                                |||||||| |||    |||||
                                GGTTGGGG ACA    GGTGG
                                     T  ____
GAM68   KIAA0537 3' GAGTGCAGGGGGTTGGGA    29928          _
                                TCCCAACCCC TGTATTC
                                |||||||||| |||||||
                                AGGGTTGGGG ACGTGAG
                                      G
GAM68   KIAA0672 3' GGGGTAAGGGTGGGGGTTG    30050         TATT  __
                                CAACCCCTG    CCC  ACCCC
                                |||||||||    |||  |||||
                                GTTGGGGGT    GGG  TGGGG
                                     ____   AA
GAM68   KIAA0694 5' GGGGTGGGAAGAGTGGGGGT   72973      TG A_
                                ACCCC  T  TTCCCACCCC
                                |||||  |  ||||||||||
                                TGGGG  G  AAGGGTGGGG
                                   GT AG
GAM68   KIAA0720 3' GGGGCGAGAGTCGGGGTGGGGA 62989      A    T T   CCA
                                TCCC ACCCC G ATTC   CCCC
                                |||| ||||| | ||||   ||||
                                AGGG TGGGG C TGAG   GGGG
                                  G    _ _    AGC
GAM68   KIAA0775 3' GGTGGGGACTTGGGCTGGGA   28957      A   CT  AT
                                TCCCA CCC  GT  TCCCACC
                                ||||| |||  ||  |||||||
```

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                                AGGGT GGG  CA  GGGGTGG
                                  C   TT __
GAM68   KIAA0792 3' GGGGCGGGATGGGGGTGTGGA 28768    CA     TAT   A
                                TCC  ACCCCTG   TCCC CCCC
                                |||  |||||||   |||| ||||
                                AGG  TGGGGGT   AGGG GGGG
                                  TG      ___   C
GAM68   KIAA1018 3' GGACAAGAATATAGCAGTCAGG 31058    CA  CC      CCAC
          A                      TCC  AC  CTGTATTC   CC
                                |||  ||  ||||||||   ||
                                AGG  TG  GATATAAG   GG
                                  AC  AC       AACA
GAM68   KIAA1075 3' GGGATGGGAGAGGGGTGGGGA  62387     A    GTA    _
                                TCCC ACCCCT   TTCCCA CCC
                                ||||  ||||||   ||||||  |||
                                AGGG TGGGGA   GAGGGT GGG
                                  G     ___     A
GAM68   KIAA1181 3' GGGCAGGGTGGGGTGGGGA   68912     A    TGTATT   A_
                                TCCC ACCCC     CCC  CCC
                                |||| |||||     |||  |||
                                AGGG TGGGG     GGG  GGG
                                  G    T_____   AC
GAM68   KIAA1181 3' GGGTGGGGTGGGGATGG     68913     A   TGTAT
                                CCA CCCC     TCCCACCC
                                |||  ||||    ||||||||
                                GGT GGGG     GGGGTGGG
                                  A   T____
GAM68   KIAA1183 3' GATAGAAGGCGGTTGGGA    63195        _   G_
                                TCCCAACC CCT  TATT
                                ||||||||  |||  ||||
                                AGGGTTGG GGA  ATAG
                                     C   AG
GAM68   KIAA1196 3' GGAGTGGGTGTGGAGACCCGGA 62151     CAACCC  G   T    _
                                TCC      CT TAT CCCAC CC
                                |||      || ||| ||||| ||
                                AGG      GA GTG GGGTG GG
                                  CCCA__  G   T    A
GAM68   KIAA1280 5' GGGTGAATACAGCAGTTAGGA  70285     C   CC      CC
                                TCC AAC  CTGTATTC  ACCC
                                |||  |||  ||||||||  ||||
                                AGG TTG  GACATAAG  TGGG
                                  A   AC       __
GAM68   KIAA1336 3' GGAGTGGGGGAAGCATGGG    72786     C   A_     _
                                CCC TGT  TTCCCAC CC
                                |||  |||  |||||||  ||
                                GGG ACG  GGGGGTG GG
                                  T   AA      A
GAM68   KIAA1522 3' GGGGCAGGTGTGGGGCTGTGGA 65608     _  A    TGTATT  CA
                                TCC CA CCCC     CC  CCCC
                                |||  ||  ||||     ||  ||||
```

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                                AGG GT GGGG     GG  GGGG
                                  T  C    TGT___  AC
GAM68   KIAA1553  3'  GTGGGGGTGAGGGCCAAGG   93569    CAAC    G
                                CC    CCCT TATTCCCAC
                                ||    |||| |||||||||
                                GG    GGGA GTGGGGGTG
                                 AACC    _
GAM68   KIAA1577  3'  GGGGTGGGGGGGTGGGGATGGGA 65101       A    TGTA
                                TCCCA CCCC    TTCCCACCCC
                                ||||| ||||    ||||||||||
                                AGGGT GGGG    GGGGGTGGGG
                                   A    TG__
GAM68   KIAA1579  3'  GGAAAAATATGGGTTGGG    37150         C   A_
                                CCCAACCC TGT  TTCC
                                |||||||| |||  ||||
                                GGGTTGGG ATA  AAGG
                                     T   AA
GAM68   KIAA1655  3'  GGGGCAGAGGCAGGGGTACAGG 67192     CA_      A   CCA
            A                    TCC   ACCCCTGT TTC   CCCC
                                |||   |||||||| |||   ||||
                                AGG   TGGGGACG GAG   GGGG
                                  ACA       _   AC_
GAM68   KIAA1811  3'  GGGTGGGGGGAGGGACGGGA   65420     AAC    GTA
                                TCCC   CCCT   TTCCCACCC
                                ||||   ||||   |||||||||
                                AGGG   GGGA   GGGGGTGGG
                                  CA_   ____
GAM68   KIAA1949  5'  GGGGTGGGGGCTGGGG     99699     T  AT
                                CCCC GT  TCCCACCCC
                                |||| ||  |||||||||
                                GGGG CG  GGGGTGGGG
                                  T  __
GAM68   LIMR      3'  GGGTGGGGTAGGGGCAGGGA   36676     AA     TAT
                                TCCC  CCCCTG   TCCCACCC
                                ||||  ||||||   ||||||||
                                AGGG  GGGGAT   GGGGTGGG
                                  AC     ____
GAM68   LYPLA3    3'  GGATGAGAGCAGGGGTTGG   25563          AT  C  C
                                CCAACCCCTGT  TC CA CC
                                ||||||||||  || || ||
                                GGTTGGGGACG  AG GT GG
                                       __  A  A
GAM68   MADHIP    3'  GGGTGGGAGTGGGGGTTTGGGA 17817       _    GT
                                TCCCAA CCCCT  ATTCCCACCC
                                ||||||  |||||  ||||||||||
                                AGGGTT GGGGG  TGAGGGTGGG
                                   T    __
GAM68   MADHIP    3'  GGGTGGGAGTGGGGGTTTGGGA 17818       _    GT
                                TCCCAA CCCCT  ATTCCCACCC
                                ||||||  |||||  ||||||||||
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                                AGGGTT GGGGG  TGAGGGTGGG
                                   T    __
GAM68   MAP1LC3A  3'  GGGATGGGGGAGGGTGGGGA  51682     AAC   GTA    _
                                TCCC  CCCT  TTCCCA CCC
                                ||||  ||||  |||||| |||
                                AGGG  GGGA  GGGGGT GGG
                                  GT_   ___    A
GAM68   MAP3K3   3'  GGAATGGCAGCAGGGGTTGGGG 11542          ____
                                TCCCAACCCCTGT   ATTCC
                                ||||||||||||   |||||
                                GGGGTTGGGGACG   TAAGG
                                       ACGG
GAM68   MGC10772  5'  GGAGTGAGTGCAGGACCAGG  48294   AACC      CC  _
                                CC   CCTGTATTC  AC CC
                                ||   |||||||||  || ||
                                GG   GGACGTGAG  TG GG
                                 ACCA       __ A
GAM68   MGC10814  3'  GGGTGGGTCACATGAGGTTGGG 52023       CC_  ATT
           A                     TCCCAACC  TGT  CCCACCC
                                ||||||||  |||  |||||||
                                AGGGTTGG  ACA  GGGTGGG
                                    AGT  CT_
GAM68   MGC1203  3'  TGGGAGACCGGGGTGGGA   44411     A   T  A
                                TCCCA CCCC GT TTCCCA
                                ||||| |||| || ||||||
                                AGGGT GGGG CA GAGGGT
                                  _   C  _
GAM68   MGC15875  3'  GGAATGGGGTAGGGTGGGA   53017     A  __  G
                                TCCCA CCC  CT TATTCC
                                ||||| |||  || ||||||
                                AGGGT GGG  GG GTAAGG
                                  _  AT  G
GAM68   MGC21854  5'  GGCAGAAAATAGGTGTGGGA  54603     ACC   A  __
                                TCCCA  CCTGT TTC  CC
                                |||||  ||||| |||  ||
                                AGGGT  GGATA AAG  GG
                                  GT_    A  AC
GAM68   MGC22014  3'  GGGGCGGGTTGGGGGTGCAGA  65116   CCA    GTATT  A
                                TC  ACCCCT   CCC CCCC
                                ||  ||||||   ||| ||||
                                AG  TGGGGG   GGG GGGG
                                 ACG    TT___  C
GAM68   MGC2654  5'  GGGAGTCGGGTGGGA     44350     ACC   T
                                TCCCA  CCTG ATTCCC
                                |||||  |||| ||||||
                                AGGGT  GGGC TGAGGG
                                  ___   _
GAM68   MGC35521  3'  GGGGTGGAGCAAAAGGTTGGGA 59667       CC_  ATTC
                                TCCCAACC  TGT  CCACCCC
                                ||||||||  |||  |||||||
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                                AGGGTTGG  ACG   GGTGGGG
                                    AAA  A___
GAM68   MGC4251  3' GGAGTATGGCAGGGCTGGGA  51468     A  __
                                TCCCA CCC  CTGTATTCC
                                ||||| |||  |||||||||
                                AGGGT GGG  GGTATGAGG
                                   C  AC
GAM68   MGC4342  3' TGGGAGAGGGGGTGGGGA   44520    A    GTAT
                                TCCC ACCCCT   TCCCA
                                |||| ||||||   |||||
                                AGGG TGGGGG   AGGGT
                                  G    AG__
GAM68   MGC8407  3' GGGATGGGCAGGAGGGTGGGA 44115     A _   AT_
                                TCCCA CC CCTGT  TCCC
                                ||||| || |||||  ||||
                                AGGGT GG GGACG  AGGG
                                   G A   GGT
GAM68   MGC955   3' GGGATGGGAATAATCATTGAGA 44281   C  CCCCTG     _
                                TC CAA    TATTCCCA CCC
                                || |||    |||||||| |||
                                AG GTT    ATAAGGGT GGG
                                 A  ACTA__     A
GAM68   MOST2    5' GGTGGGCACAGGGCTGG    40071    AC    ATT
                                CCA  CCCTGT  CCCACC
                                |||  ||||||  ||||||
                                GGT  GGGACA  GGGTGG
                                  C_    C__
GAM68   MSTP031  3' GGGTGGATAGGTACAGGATTGG 50167      CC      C__
           GA                    TCCCAA  CCTGTATT  CCACCC
                                ||||||  ||||||||  ||||||
                                AGGGTT  GGACATGG  GGTGGG
                                   A_      ATA
GAM68   MVD      3' GGGATGGGGAGGGGGTATGAGA 11718   C _    GTA    _
                                TC CA ACCCCT  TTCCCA CCC
                                || || ||||||  |||||| |||
                                AG GT TGGGGG  AGGGGT GGG
                                 A A    ___     A
GAM68   NBR2     3' GGGGTGGGGAGCAGAGCTGG  20622    ACCC   A
                                CCA   CTGT TTCCCACCCC
                                |||   |||| ||||||||||
                                GGT   GACG AGGGGTGGGG
                                  CGA_  _
GAM68   OSBPL10  5' GGTGGATAAGGGGTGGGGA   35525    A    GTATTC
                                TCCC ACCCCT     CCACC
                                |||| ||||||     |||||
                                AGGG TGGGGA     GGTGG
                                  G    ATA___
GAM68   P8       3' GGGAGTGAGAGGCTGGGA    25675      A  C  G
                                TCCCA CC CT TATTCCC
                                ||||| || || |||||||
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                                AGGGT GG GA GTGAGGG
                                  C  A  _
GAM68   PADI1    3'  GGGGTGTGAGCTGGGGTTGGGA 62703          T  AT  C
                                TCCCAACCCC GT  TC CACCCC
                                |||||||||| ||  || ||||||
                                AGGGTTGGGG CG  AG GTGGGG
                                     T  __  T
GAM68   PANK     3'  GGGTCATGTACAAATATTGGGA 57160       CCCC    TCCC
                                TCCCAA   TGTAT   ACCC
                                ||||||   |||||   ||||
                                AGGGTT   ACATG   TGGG
                                   ATAA    TAC_
GAM68   PCAF     5'  GGGGTGGGCGAAGGGGGCGGGA 15286     AA    GTATT
                                TCCC  CCCCT    CCCACCCC
                                ||||  |||||    ||||||||
                                AGGG  GGGGA    GGGTGGGG
                                  CG    AGC__
GAM68   PCDH19   3'  GGGGTGGGGCTGGGACCGGG   64447    AAC   T  ATT
                                CCC   CCC GT   CCCACCCC
                                |||   ||| ||   ||||||||
                                GGG   GGG CG   GGGTGGGG
                                 CCA   T  ___
GAM68   PIP5K2B  3'  GGGTGGGAGCAGAGTCGGG   57698    A  CC    AT
                                CCC AC  CTGT  TCCCACCC
                                ||| ||  ||||  ||||||||
                                GGG TG  GACG  AGGGTGGG
                                 C  A_   __
GAM68   POMT2    3'  GGATGGGTGCCAGAGGGTGGGA 26319      A  _  TATT   C
                                TCCCA CCC CTG    CCCA CC
                                ||||| ||| |||    |||| ||
                                AGGGT GGG GAC    GGGT GG
                                  _  A  CGT_   A
GAM68   PPP1R16B 3'  GGGGTGGATTCGGGAGCTGGGA 62040      ACC    TATTC
                                TCCCA   CCTG    CCACCCC
                                |||||   ||||    |||||||
                                AGGGT   GGGC    GGTGGGG
                                   CGA   TTA__
GAM68   PRO1048  3'  GGATGGGAATGATGGTTTGAGA 38117    C   C  CTG      C
                                TC CAA CC   TATTCCCA CC
                                || ||| ||   |||||||| ||
                                AG GTT GG   GTAAGGGT GG
                                 A   T  TA_       A
GAM68   PRO1584  5'  GGGTGGGGTGGGGTGGAGA   38335    _  A   TGTAT
                                TC CCA CCCC    TCCCACCC
                                || ||| ||||    ||||||||
                                AG GGT GGGG    GGGGTGGG
                                 A   _    T____
GAM68   PRO1855  3'  GGAGTAGGCTTGGGGGTGGGGA 38145      A     ____
                                TCCC ACCCCTG    TATTCC
                                |||| |||||||    ||||||
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```
                                AGGG TGGGGGT   ATGAGG
                                  G     TCGG
GAM68   PSKH1   3' GGGCAGGACAGGGGGTTTGGA 68800    C     GTAT  CA
                                TCC AACCCCT   TCC  CCC
                                ||| |||||||   |||  |||
                                AGG TTGGGGG   AGG  GGG
                                  T     AC__  AC
GAM68   RAB35   3' GGGGTGGGGACTCAGGGCTGG 23418    AC    TA
                                CCA  CCCTG  TTCCCACCCC
                                |||  |||||  ||||||||||
                                GGT  GGGAC  AGGGGTGGGG
                                  C_    TC
GAM68   RAB6B   3' GGAGTAGGGTGGGATGGGG   33875     A  _  G
                                TCCCA CCC CT TATTCC
                                ||||| ||| || ||||||
                                GGGGT GGG GG ATGAGG
                                   A  T  G
GAM68   RPIA    3' GGGGTGGGGGGAAGAGTGGGA 58594     ACCC  GTA
                                TCCCA   CT   TTCCCACCCC
                                |||||   ||   ||||||||||
                                AGGGT   GA   GGGGGTGGGG
                                   GA__  AG_
GAM68   SFXN2   3' GGGTAGATTGGGGGGTGGGA  74381     A    GTAT  CC
                                TCCCA CCCCT   TC  ACCC
                                ||||| |||||   ||  ||||
                                AGGGT GGGGG   AG  TGGG
                                   G    TT__  A_
GAM68   SHARP   3' GGGATATGCAGAACTTGGGA  31104     CCC    _
                                TCCCAA  CTGTAT TCCC
                                ||||||  |||||| ||||
                                AGGGTT  GACGTA AGGG
                                    CAA    T
GAM68   SLC4A9  3' GGAGTAGGAGTCTGGGAGTGGA 66807   _  AC  TGT   C  _
          GA                    TC CCA  CCC  ATTCC AC CC
                                || |||  |||  ||||| || ||
                                AG GGT  GGG  TGAGG TG GG
                                 A  GA  TC_   A  A
GAM68   SRF     3' GGCAGGAATGGGGGTCAGA   13396   CCA    GT    CA
                                TC  ACCCCT  ATTCC  CC
                                ||  ||||||  |||||  ||
                                AG  TGGGGG  TAAGG  GG
                                 AC_     __    AC
GAM68   SRp25   3' GGGGCAGGGGGGTGGAGGTTGGG 38610       _ TGT    A_
          G                     TCCCAACC CC  ATTCCC  CCCC
                                |||||||| ||  ||||||  ||||
                                GGGGTTGG GG  TGGGGG  GGGG
                                    A ____    AC
GAM68   SRp25   3' GGGGCAGGGGGGTGGAGGTTGGG 38611       _ TGT    A_
          G                     TCCCAACC CC  ATTCCC  CCCC
                                |||||||| ||  ||||||  ||||
```

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                                GGGGTTGG GG   TGGGGG  GGGG
                                    A ___     AC
GAM68   STX6     5'  GGGGTGGGCGGAGGGAGACCGG 20612      AA___  _  TATT
            GA                    TCCC    CCC CTG   CCCACCCC
                                  ||||    ||| |||   ||||||||
                                  AGGG    GGG GGC   GGGTGGGG
                                    CCAGA  A  _____
GAM68   SYNE-2   3'  GGGGTGGGGGCGGGGGGTTGG  31476         GTA
                                  CCAACCCCT   TTCCCACCCC
                                  |||||||||   ||||||||||
                                  GGTTGGGGG   GGGGGTGGGG
                                       GC_
GAM68   TA-PP2C  3'  GGGGCGGGGTGGGGGGTCTGGA 58406     CA     GTAT   A
                                  TCC  ACCCCT   TCCC CCCC
                                  |||  ||||||   |||| ||||
                                  AGG  TGGGGG   GGGG GGGG
                                    TC     GT__   C
GAM68   TRIAD3   3'  GGGGTAGGAGTGTGGATGGAGA 96137    _  ACCC TG     C
                                  TC CCA   C  TATTCC ACCCC
                                  || |||   |  |||||| |||||
                                  AG GGT   G  GTGAGG TGGGG
                                   A  A___ GT     A
GAM68   TRIM29   3'  GGGTGAGATAGGTTGGGG    25011         CCTGTAT  C
                                  TCCCAACC      TC CACCC
                                  ||||||||      || |||||
                                  GGGGTTGG      AG GTGGG
                                       AT_____  A
GAM68   TRPV6    3'  GGGGTGGGAAGTGGGGCTAGG  38463    CAA    TGTA
                                  CC   CCCC    TTCCCACCCC
                                  ||   ||||    ||||||||||
                                  GG   GGGG    AAGGGTGGGG
                                   ATC    TG__
GAM68   UNC5D    3'  GGAATGGGGGAGGTGGGGA   56006      A  _  G
                                  TCCC ACC CCT TATTCC
                                  |||| ||| ||| ||||||
                                  AGGG TGG GGG GTAAGG
                                    G   A   G
GAM68   WASPIP   3'  GGTGGGAGGGGGAGTGGGA   14085      A_    GTAT
                                  TCCCA  CCCCT   TCCCACC
                                  |||||  |||||   |||||||
                                  AGGGT  GGGGG   AGGGTGG
                                     GA    _____
GAM68   ZDHHC3   3'  GGGGTGGGGGTAGGAGTT    33934     C   GT
                                  AAC CCT  ATTCCCACCCC
                                  ||| |||  ||||||||||
                                  TTG GGA  TGGGGGTGGGG
                                    A  __
GAM68   ZFP95    3'  GGGGTGGGAGTTTTGAGTGGGA 28121       ACCCCTGT
                                  TCCCA       ATTCCCACCCC
                                  |||||       ||||||||||
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                                AGGGT      TGAGGGTGGGG
                                  GAGTTT__
GAM68   ZNF237   5' GAGTGGGGGTGGCTGGGA   27269      A _  G
                                TCCCA CC CCT TATTC
                                ||||| || ||| |||||
                                AGGGT GG GGG GTGAG
                                  C  T   G
GAM68   LOC114987 3' GGAGTGGGATGTAGGGCTGG  59798    AC      T   _
                                CCA  CCCTGTAT CCCAC CC
                                |||  |||||||| ||||| ||
                                GGT  GGGATGTA GGGTG GG
                                  C_      _    A
GAM68   LOC124470 3' GGGGTGGGGGGATTAGGAACTGG 76148      ACC   TA
            GG                    TCCCA   CCTG  TTCCCACCCC
                                |||||   ||||  ||||||||||
                                GGGGT   GGAT  GGGGGTGGGG
                                  CAA   TA
GAM68   LOC126299 3' GGGGTGGGAGGAGGGGGCTGAG 74980    _ A    GTA
            GA                    TCC CA CCCCT   TTCCCACCCC
                                ||| || |||||   ||||||||||
                                AGG GT GGGGG   GAGGGTGGGG
                                  A  C    AG_
GAM68   LOC130535 3' GGTGGGAAAATGGCTTG    76654    C  CT  A
                                CAA CC  GT TTCCCACC
                                ||| ||  || ||||||||
                                GTT GG  TA AAGGGTGG
                                  C  __  A
GAM68   LOC132870 5' TGGGGTATGCAGGGTCTGG   75580    AC      _
                                CCA  CCCTGTAT TCCCA
                                |||  |||||||| |||||
                                GGT  GGGACGTA GGGGT
                                  CT       T
GAM68   LOC134288 3' GGTGAGAGTCGGGTGGGA    75660      ACC   T   C
                                TCCCA   CCTG ATTC CACC
                                |||||   |||| |||| ||||
                                AGGGT   GGGC TGAG GTGG
                                  ____   _   A
GAM68   LOC135892 5' GGGGCACTTACAGGGGCCGGA  75762    CAA      TTCCCA
                                TCC   CCCCTGTA     CCCC
                                |||   ||||||||     ||||
                                AGG   GGGGACAT     GGGG
                                  CC_       TCAC__
GAM68   LOC138429 5' GGGGTGGGATCGGGTCGGGA   75865    A   CTGTAT
                                TCCC ACCC     TCCCACCCC
                                |||| ||||     |||||||||
                                AGGG TGGG     AGGGTGGGG
                                  C   CT____
GAM68   LOC138639 3' GGAGTGACTGTGAAGTGGTTGG 75883        C  G   TCC  _
            GA                    TCCCAACC CT TAT   CAC CC
                                |||||||| || |||   ||| ||
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                                AGGGTTGG GA GTG   GTG GG
                                     T  A   TCA   A
GAM68   LOC142893 5'  GGTGGGAAGGATGGGTTGGG   83761        CTGTA
                                CCCAACCC    TTCCCACC
                                ||||||||    ||||||||
                                GGGTTGGG    AAGGGTGG
                                     TAGG_
GAM68   LOC142927 3'  GGGCAGAACTGGGTTGGGA    76948        CT  A  _
                                TCCCAACCC  GT TT CCC
                                |||||||||  || || |||
                                AGGGTTGGG  CA GA GGG
                                     T_  A  C
GAM68   LOC142927 3'  GGTGGGAATGGACGGTGCAGGA 76950     CA_   CCTG
                                TCC   ACC    TATTCCCACC
                                |||   |||    ||||||||||
                                AGG   TGG    GTAAGGGTGG
                                  ACG   CAG_
GAM68   LOC145501 3'  GGGATGTGCAGGGCTGGGA    77773      AC       _
                                TCCCA  CCCTGTAT TCCC
                                |||||  |||||||| ||||
                                AGGGT  GGGACGTG AGGG
                                   C_       T
GAM68   LOC145693 3'  GGCAAAGTGCAGAGGTGGGA   77856      A  C      C__
                                TCCCA CC CTGTATT   CC
                                ||||| || |||||||   ||
                                AGGGT GG GACGTGA   GG
                                   _  A       AAC
GAM68   LOC146429 5'  GGGGTGGGGGCAGAGATGAGGA 84670     _  ACCC    AT
                                TCC CA    CTGT  TCCCACCCC
                                |||  ||    ||||  |||||||||
                                AGG GT    GACG  GGGGTGGGG
                                  A  AGA_    __
GAM68   LOC146517 3'  GGGGTGGAGAAAGGATGGGA   78511      ACC   GTA  _
                                TCCCA   CCT   TTC CCACCCC
                                |||||   |||   ||| |||||||
                                AGGGT   GGA   AAG GGTGGGG
                                   A__   ____   A
GAM68   LOC146667 5'  GGGGCGGGGGGTGAGGGTGGGA  84716      AC   G      A
                                TCCCA  CCCT TATTCCC CCCC
                                |||||  |||| ||||||| ||||
                                AGGGT  GGGA GTGGGGG GGGG
                                   __   _      C
GAM68   LOC146728 5'  GGGGTGGGGGGGTGGGGGT    84771      TG A
                                ACCCC  T TTCCCACCCC
                                |||||  | ||||||||||
                                TGGGG  G GGGGGTGGGG
                                   GT _
GAM68   LOC147054 5'  GAAACAGAACTCGGTTGGGA   85005        C_____    A
                                TCCCAACC    CTGT TTC
                                ||||||||    |||| |||
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                                AGGGTTGG    GACA AAG
                                    CTCAA   _
GAM68   LOC147229 5'  GGTGAGGCCGGGGGTATGGGA  78926      _     TATT  _
                                TCCCA ACCCCTG   CC CACC
                                ||||| |||||||   || ||||
                                AGGGT TGGGGGC   GG GTGG
                                   A      C___  A
GAM68   LOC148114 5'  GGGGTGGGAGAAGAGGGGGT  79363      GTA_
                                ACCCCT   TTCCCACCCC
                                ||||||   ||||||||||
                                TGGGGG   GAGGGTGGGG
                                   AGAA
GAM68   LOC149076 3'  GGAGTGGGAATCCCCAGCCGAG 79880    AACCC  T__      _
            G                    CC    CTG   ATTCCCAC CC
                                ||    |||   |||||||| ||
                                GG    GAC   TAAGGGTG GG
                                 AGCC_  CCC       A
GAM68   LOC149127 3'  GGTGGGGAGGAGGTCAGA    85503    CCA  _  GTAT
                                TC   ACC CCT    TCCCACC
                                ||   ||| |||    |||||||
                                AG   TGG GGA    GGGGTGG
                                 AC_   A  _____
GAM68   LOC149506 3'  GGGGTGGGGCGAGGGCTAGG   85640    AAC   _  ATT
                                CC   CCCT GT   CCCACCCC
                                ||   |||| ||   ||||||||
                                GG   GGGA CG   GGGTGGGG
                                 ATC    G  ___
GAM68   LOC149506 3'  GTGGGGGAAAAGGAGGTGGGA  85645      A  _   GTA
                                TCCCA CC CCT   TTCCCAC
                                ||||| || |||   |||||||
                                AGGGT GG GGA   GGGGGTG
                                   _  A   AAA
GAM68   LOC149606 3'  GGAGTAAATGGAGGTGGGA   80265      A  _  TG_
                                TCCCA CC CC   TATTCC
                                ||||| || ||   ||||||
                                AGGGT GG GG   ATGAGG
                                   _  A  TAA
GAM68   LOC150245 5'  GGTGGGGACAAGGCCGGGA   86117     AACC   GTA
                                TCCC    CCT   TTCCCACC
                                ||||    |||   ||||||||
                                AGGG    GGA   AGGGGTGG
                                  CC__    AC_
GAM68   LOC150271 3'  GGAGCAGAGAGGTATGGGA   86143      _   C__    AT
                                TCCCA ACC   CTGT  TCC
                                ||||| |||   ||||  |||
                                AGGGT TGG   GACG  AGG
                                   A   AGA   __
GAM68   LOC150368 3'  GGGGTGGGAAGATTGGGGATGG 80517      A    TGTA
            GA                    TCCCA CCCC    TTCCCACCCC
                                ||||| ||||    ||||||||||
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                                AGGGT GGGG    AAGGGTGGGG
                                  A    TTAG
GAM68   LOC150372 3' GGTGGGGGCAAGGGTCAGGG   80620     A_   C   AT
                                CCC  ACCC TGT  TCCCACC
                                |||  |||| |||  |||||||
                                GGG  TGGG ACG  GGGGTGG
                                  AC    A  __
GAM68   LOC150468 3' GGGGCAGGGGAGAGGGGTGGGG 80687      A     GTA    A_
          A                      TCCC ACCCCT   TTCCC  CCCC
                                |||| ||||||   |||||  ||||
                                AGGG TGGGGA   AGGGG  GGGG
                                  G     G__    AC
GAM68   LOC150481 3' GGTGAGTGCAGAGTGGGA    80712       ACCC       _
                                TCCCA    CTGTATTC CC
                                |||||    |||||||| ||
                                AGGGT    GACGTGAG GG
                                   GA__       T
GAM68   LOC151005 5' GGGCGGATGCAGGGACTG    80898    AC       TC  A
                                CA  CCCTGTAT  CC CCC
                                ||  ||||||||  || |||
                                GT  GGGACGTA  GG GGG
                                 CA       __ C
GAM68   LOC151057 3' GGCAGGAACAGTGGTGGGGA   86389      A   C    AT   CA
                                TCCC ACC CTGT  TCC  CC
                                |||| ||| ||||  |||  ||
                                AGGG TGG GACA  AGG  GG
                                  G   T    __   AC
GAM68   LOC151178 5' GTGGGGAGGAGGGTTGGGA    80961         _ GTA
                                TCCCAACCC CT   TTCCCAC
                                |||||||| ||   |||||||
                                AGGGTTGGG GG   AGGGGTG
                                     A ___
GAM68   LOC153711 5' GGGGTGCGGGGGGTGGGGA    87344      A
                                TCCC ACCCCTGTATTCC
                                |||| ||||||||||||
                                AGGG TGGGGGCGTGGGG
                                  G
GAM68   LOC154789 5' GGGCAGGGTGGGGTGTGGGA   82031       _    TGTATT   A_
                                TCCCA ACCCC     CCC  CCC
                                |||||| |||||     |||  |||
                                AGGGT TGGGG     GGG  GGG
                                   G     T_____   AC
GAM68   LOC155032 3' GGTGGGAAGGAAGGATTGG    87598      CC   GTA
                                CCAA  CCT   TTCCCACC
                                ||||  |||   ||||||||
                                GGTT  GGA   AAGGGTGG
                                  A_   AGG
GAM68   LOC158191 3' GGTGAGTGCAGAGTGGGA    82681       ACCC       _
                                TCCCA    CTGTATTC CC
                                |||||    |||||||| ||
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                                AGGGT   GACGTGAG GG
                                  GA__      T
GAM68   LOC158230 5' GGAGTGGGAAGGTAGGTGGGA 82701     ACC   TA    _
                                TCCCA  CCTG  TTCCCAC CC
                                |||||  ||||  ||||||| ||
                                AGGGT  GGAT  AAGGGTG GG
                                  ____  GG     A
GAM68   LOC169436 5' GGGGTAGATGTGGGGGTGG   83619    A   TG   CCC
                                CCA CCCC  TATT  ACCCC
                                ||| ||||  ||||  |||||
                                GGT GGGG  GTAG  TGGGG
                                  _   GT   A__
GAM68   LOC196746 3' GGGGCGGGCTGGGAGGTGGGA 88901     A _   TATT  A
                                TCCCA CC CCTG   CCC CCCC
                                ||||| || ||||   ||| ||||
                                AGGGT GG GGGT   GGG GGGG
                                  _ A   C___  C
GAM68   LOC196957 3' GGAGTGGGAGTTGGAGTTG   89191     C  TGT     _
                                CAAC CC   ATTCCCAC CC
                                |||| ||   |||||||| ||
                                GTTG GG   TGAGGGTG GG
                                  A  T__      A
GAM68   LOC199799 3' GGGTGAGGGTGGGGCTGGAGA  79252   _  A   TGTAT  _
                                TC CCA CCCC    TCC CACCC
                                || ||| ||||    ||| |||||
                                AG GGT GGGG    GGG GTGGG
                                 A  C   T____  A
GAM68   LOC199958 3' GGAGTGGAGAAGGGGCCAGGG  91492    AA_   GTAT  _   _
                                CCC   CCCCT   TC CCAC CC
                                |||   |||||   || |||| ||
                                GGG   GGGGA   AG GGTG GG
                                 ACC    ____  A   A
GAM68   LOC200058 3' GGATGGGAAGCCAGGAAGTGGG 89963     ACC   TA    C
        A                        TCCCA  CCTG  TTCCCA CC
                                |||||  ||||  |||||| ||
                                AGGGT  GGAC  AAGGGT GG
                                  GAA   CG    A
GAM68   LOC201294 3' GGCGGAGGGGGAGGTTGGGG  89588       _ TGTATT  A _
                                TCCCAACC CC    CCC CC CC
                                |||||||| ||    ||| || ||
                                GGGGTTGG GG    GGG GG GG
                                    A ______  A  C
GAM68   LOC201294 3' GGGTGGGAGGAGCTGGGG   89592    T  A_
                                CCCC GT  TTCCCACCC
                                |||| ||  |||||||||
                                GGGG CG  GAGGGTGGG
                                  T  AG
GAM68   LOC203260 3' GGAATGGGGACATAGGTTGGGA 90850       CC   AT   CC
                                TCCCAACC  TGT  TCCCA  CC
                                ||||||||  |||  |||||  ||
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                                AGGGTTGG  ACA  GGGGT  GG
                                    AT   __    AA
GAM68   LOC203668 5'  GGGTAAGAAGGCAAGGTGGGGA 90985     A   CC   A   CC
                                TCCC ACC  TGT TTC  ACCC
                                |||| |||  ||| |||  ||||
                                AGGG TGG  ACG AAG  TGGG
                                  G   A_   G   AA
GAM68   LOC203668 5'  GGTGGGGAGCCGGAGCTGG    90986     ACC  T  A
                                CCA   CC GT TTCCCACC
                                |||   || || ||||||||
                                GGT   GG CG AGGGGTGG
                                  CGA  C  _
GAM68   LOC205100 3'  GGGCGGAGAGGAGGTGGGA    92390      A  _   GTA    CA
                                TCCCA CC CCT   TTCC  CCC
                                ||||| || |||   ||||  |||
                                AGGGT GG GGA   GAGG  GGG
                                  _  A   ____    C_
GAM68   LOC221393 3'  GGAGTGGGAGTGTGGGTTGG   93908       CTG       _
                                CCAACCC   TATTCCCAC CC
                                |||||||   |||||||||  ||
                                GGTTGGG   GTGAGGGTG GG
                                    T__        A
GAM68   LOC221393 3'  GGGGTAGGGTTGGGGGTGGGA  93909      A    GTATT   _
                                TCCCA CCCCT    CCC ACCCC
                                ||||| |||||    ||| |||||
                                AGGGT GGGGG    GGG TGGGG
                                  _    TT___   A
GAM68   LOC221922 5'  GGAATAGGAGGGCAGGGGTGAG 94248     CA      A    CAC_
          GA                      TCC  ACCCCTGT TTCC    CC
                                |||  |||||||| ||||    ||
                                AGG  TGGGGACG GAGG    GG
                                  AG       G    ATAA
GAM68   LOC221922 5'  GGAGAGCAGGGGTGAGGA    94249     CA      A
                                TCC  ACCCCTGT TTCC
                                |||  |||||||| ||||
                                AGG  TGGGGACG GAGG
                                  AG       A
GAM68   LOC221922 5'  GGAGCAGGAGGGCAGGGGTCAG 94250     CA      A    CAC_
          GA                      TCC  ACCCCTGT TTCC    CC
                                |||  |||||||| ||||    ||
                                AGG  TGGGGACG GAGG    GG
                                  AC       G    ACGA
GAM68   LOC221922 5'  GGAGCAGGAGGGCAGGGGTGAG 94251     CA      A    CAC_
          GA                      TCC  ACCCCTGT TTCC    CC
                                |||  |||||||| ||||    ||
                                AGG  TGGGGACG GAGG    GG
                                  AG       G    ACGA
GAM68   LOC221922 5'  GGGACAGGAGGGCAGGGGTGAG 94253    CCA      A    CA_
          A                       TC   ACCCCTGT TTCC   CCC
                                ||   |||||||| ||||   |||
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                                AG   TGGGGACG GAGG   GGG
                                 AG_       G    ACA
GAM68   LOC221922 5'  GGGCAGGAGTTGGGGGAGCAGG 94256     CAA_     T     CA
           A                      TCC    CCCCTG ATTCC  CCC
                                  |||    |||||| |||||  |||
                                  AGG    GGGGGT TGAGG  GGG
                                    ACGA     _     AC
GAM68   LOC221922 5'  GGGGCAGGAAGGCAGGGGTGGG 94257       A      A    CA
           A                      TCCCA CCCCTGT TTCC  CCCC
                                  ||||| ||||||| ||||  ||||
                                  AGGGT GGGGACG AAGG  GGGG
                                     _      G    AC
GAM68   LOC245744 3'  GGGGTGGGGAGAGGTTGAGGA  92790     _     CCTGTA
                                  TCC CAACC      TTCCCACCCC
                                  ||| |||||      ||||||||||
                                  AGG GTTGG      AGGGGTGGGG
                                    A     AG____
GAM68   LOC254057 3'  GGAATGAGGGAATGAGGA     98784     _ AC    G
                                  TCC CA  CCCT TATTCC
                                  ||| ||  |||| ||||||
                                  AGG GT  GGGA GTAAGG
                                    A  AA   _
GAM68   LOC254228 3'  GGGACAGAACAGGGATTAGGGA 97653      _ C     AT__
                                  TCCC AA CCCTGT    TCCC
                                  |||| || ||||||    ||||
                                  AGGG TT GGGACA    AGGG
                                     A  A     AGAC
GAM68   LOC254866 5'  GGGTAGGGTGCGGGACCGGGG  98569     AACC     TT   _
                                  CCC    CCTGTA  CCC ACCC
                                  |||    ||||||  ||| ||||
                                  GGG    GGGCGT  GGG TGGG
                                    GCCA      __   A
GAM68   LOC255042 5'  GGGATGAGGCGGGGTGGGA    97053       A    T  AT__
                                  TCCCA CCCC GT    TCCC
                                  ||||| |||| ||    ||||
                                  AGGGT GGGG CG    AGGG
                                     _    _  GAGT
GAM68   LOC255170 3'  GGGATAAAGGGGTGTGGGA    99381       _     GTAT
                                  TCCCA ACCCCT    TCCC
                                  ||||| ||||||    ||||
                                  AGGGT TGGGGA    AGGG
                                     G      AAT_
GAM68   LOC256021 3'  GGAATGGGGATGGGGCTGG    98277     A    TGT      CC
                                  CCA CCCC   ATTCCCA  CC
                                  ||| ||||   |||||||  ||
                                  GGT GGGG   TAGGGGT  GG
                                    C    ____       AA
GAM68   LOC256073 3'  GGGCGAGTATAGAGAGTGAGA  98488    C  ACCC       CCA
                                  TC CA    CTGTATTC   CCC
                                  || ||    ||||||||   |||
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                                AG GT   GATATGAG   GGG
                                 A  GAGA      C__
GAM68   LOC256158 5' GGGGTGGGCAGAGGCTGGAGA 99511   _  A  C   TATT
                                TC CCA CC CTG   CCCACCCC
                                || ||| || |||   ||||||||
                                AG GGT GG GAC   GGGTGGGG
                                 A   C  A  ____
GAM68   LOC256867 5' GGGCGGAGGGGGGGGTTGGG  96515        GTA   CA
                                CCCAACCCCT   TTCC  CCC
                                ||||||||||   ||||  |||
                                GGGTTGGGGG   GAGG  GGG
                                      GG_   C_
GAM68   LOC257364 3' GTGGGGCACAGCAGGGGTGAGA 96647    CCA      AT__
                                TC   ACCCCTGT   TCCCAC
                                ||   ||||||||   ||||||
                                AG   TGGGGACG   GGGGTG
                                 AG_      ACAC
GAM68   LOC257484 3' GGGGCGGGTTGGGGGTGCAGA  90244    CCA    GTATT   A
                                TC   ACCCCT    CCC CCCC
                                ||   ||||||    ||| ||||
                                AG   TGGGGG    GGG GGGG
                                 ACG     TT___   C
GAM68   LOC51061  3' GGTGAAAATTGTACATTGGGA  32484      CCCC    TCC___
                                TCCCAA   TGTAT     CACC
                                ||||||   |||||     ||||
                                AGGGTT   ACATG     GTGG
                                   ____    TTAAAA
GAM68   LOC51301  3' GGGGTGAGGATGTGGGTTGGGA 33909        CTGTAT  _
                                TCCCAACCC     TCC CACCCC
                                |||||||||     ||| ||||||
                                AGGGTTGGG     AGG GTGGGG
                                      TGT___   A
GAM68   LOC51337  3' GGAATAGAGTGGGGGTGGGA   34085      A_  _ G
                                TCCCA  CCC CT TATTCC
                                |||||  ||| || ||||||
                                AGGGT  GGG GA ATAAGG
                                   GG   T  G
GAM68   LOC51725  3' GGGACAGGAAATGCAGGATGGG 70427      ACC      _ CA_
           A                     TCCCA   CCTGTATT CC   CCC
                                |||||   |||||||| ||   |||
                                AGGGT   GGACGTAA GG   GGG
                                   A__       A  ACA
GAM68   LOC58525  3' GGGTGGGGTTGGGGGGTGGGA  79351      A    GTAT
                                TCCCA CCCCT    TCCCACCC
                                ||||| |||||    ||||||||
                                AGGGT GGGGG    GGGGTGGG
                                   G     TT__
GAM68   LOC63928  5' GGAGCGCCCTGGGGTTGGGA   42272         T__ TA
                                TCCCAACCCC   G  TTCC
                                ||||||||||   |  ||||
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                                AGGGTTGGGG  C  GAGG
                                     TCC GC
GAM68   LOC84548 3' GTGTGAGAACAGGGGTGGGA  71767     A     A  C
                                TCCCA CCCCTGT TTC CAC
                                ||||| ||||||| ||| |||
                                AGGGT GGGGACA GAG GTG
                                  _     A  T
GAM68   LOC89919 3' GGGTGGGAACATGTGGGG    61377     _  A
                                CCCC TGT TTCCCACCC
                                |||| ||| |||||||||
                                GGGG GTA AAGGGTGGG
                                  T  C
GAM68   LOC90190 3' GGTGGGAAGAGGATGAGGA   62430    _  A  C  GTAT
                                TCC CA CC CT   TCCCACC
                                ||| || || ||   |||||||
                                AGG GT GG GA   AGGGTGG
                                 A  A  A  ____
GAM68   LOC90342 5' GGGCGAGGAGGAGGGCTGGGA  63015     A  CTGTA   CA_
                                TCCCA CCC    TTCC   CCC
                                ||||| |||    ||||   |||
                                AGGGT GGG    GAGG   GGG
                                   C  AG___   AGC
GAM68   LOC90499 3' GGTAGAATGCAGCTTGAGA   63744   C  CCC      CC
                                TC CAA   CTGTATTC  ACC
                                || |||   ||||||||  |||
                                AG GTT   GACGTAAG  TGG
                                 A  C__      A_
GAM68   LOC91050 3' GGACATGATACAGGGATGGGA  65376     AC      CCCA
                                TCCCA  CCCTGTATT   CC
                                |||||  |||||||||   ||
                                AGGGT  GGGACATAG   GG
                                   A_       TACA
GAM68   LOC91409 3' GGGTGGGCAGGACCAGGGA   66572    AACC   TATT
                                TCCC   CCTG   CCCACCC
                                ||||   ||||   |||||||
                                AGGG   GGAC   GGGTGGG
                                  ACCA   ____
GAM68   LOC91461 3' GGGGCGGGGGTGGGGCCGGGG 66705    AA   TGT    A
                                TCCC  CCCC   ATTCCC CCCC
                                ||||  ||||   |||||| ||||
                                GGGG  GGGG   TGGGGG GGGG
                                  CC   ___     C
GAM68   LOC92078 3' GGAGTGTCAAGGGCTGGG    68606    A  C  _
                                CCCA CCC TG TATTCC
                                |||| ||| || ||||||
                                GGGT GGG AC GTGAGG
                                  C  A  T
GAM68   LOC92162 5' GGATAAGGGGGGTGGGGA    68905    A    G_
                                TCCC ACCCCT  TATTC
                                |||| ||||||  |||||
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                                AGGG TGGGGG  ATAGG
                                  G     GA
GAM68   LOC92162 5'  GGGTGGGGAGAGGCTGGG    68906     A  CCTGTA
                                CCCA CC     TTCCCACCC
                                |||| ||     |||||||||
                                GGGT GG     AGGGGTGGG
                                  C  AG____
GAM68   LOC93380 3'  GGATGAGGATACAGAGTTG   72655     CC      C  C
                                CAAC  CTGTATTC CA CC
                                ||||  |||||||| || ||
                                GTTG  GACATAGG GT GG
                                  A_      A  A
GAM69   CA7      3'  CCAGTCACCAAAGCCACCT   60828     A_      TCGGA   A
                                AGG  GCTTTGGT    GAC GG
                                |||  ||||||||    ||| ||
                                TCC  CGAAACCA    CTG CC
                                  AC       _____   A
GAM69   E2F3     3'  CTGTCTCCATGAACCACTC   10467     CTT     __
                                GAG   TGGTTC  GGAGACAG
                                |||   ||||||  ||||||||
                                CTC   ACCAAG  CCTCTGTC
                                  ___     TA
GAM69   HD       3'  CCTATCCCCAGGACAGGTCCCT 10911     AG   TG   _  A  C
                                AGG  CTT  GTTC GG GA AGG
                                |||  |||  |||| || || |||
                                TCC  GGA  CAGG CC CT TCC
                                  CT   __    A  C  A
GAM69   LZTR1    3'  CTGTCACCCAAGGCTCCT    23170          TTCG A
                                AGGAGCTTTGG    G GACAG
                                ||||||||||    | |||||
                                TCCTCGGAACC    C CTGTC
                                       ____ A
GAM69   MECP2    3'  CCGTCTAACCACAGCTCCTT   18395        T    CGG    A
                                AAGGAGCT TGGTT   AGAC GG
                                |||||||| |||||   |||| ||
                                TTCCTCGA ACCAA   TCTG CC
                                     C     ___    C
GAM69   PLA2G2A  5'  CTGTCTCCAAACAGCCTT    6110      A   TTG   C
                                AGG GCT   GTT GGAGACAG
                                ||| |||   ||| ||||||||
                                TTC CGA   CAA CCTCTGTC
                                  _   ___   A
GAM69   PLOD     3'  CCTGAAAAACCAAGGCCCC    6114     A       CGGAGA
                                GG GCTTTGGTT     CAGG
                                || |||||||||     ||||
                                CC CGGAACCAA     GTCC
                                  C        AAA___
GAM69   POLR2A   3'  CCTGTCCCCAAATTGAAGATCC 8128       G   TG   C  A
            TT                    AAGGA CTT  GTT GG GACAGG
                                |||||| |||  ||| || ||||||
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                                TTCCT GAA  TAA CC CTGTCC
                                   A   GT   A  C
GAM69   RAB36    3'  CCTGTCTCCAACACCGCCTCCT 18163      CTT    TC_
                                AGGAG   TGGT   GGAGACAGG
                                |||||   ||||   |||||||||
                                TCCTC   GCCA   CCTCTGTCC
                                   C__    CAA
GAM69   RAP1     3'  CCTGTCCTTTGGCAGAAGCTCC 39111          G  T    _
           TT                    AAGGAGCTTT GT CGGAG ACAGG
                                ||||||||||  ||  |||||  |||||
                                TTCCTCGAAG CG GTTTC TGTCC
                                      A  _    C
GAM69   SFRP5    3'  CCTGCCCCAAGGCCCAGAGCTC 13032          TT __  AGA
           C                     GGAGCTTTGG  C  GG   CAGG
                                ||||||||||  |  ||   ||||
                                CCTCGAGACC  G  CC   GTCC
                                      CG AA  CC_
GAM69   SORCS2   3'  CCTGTCCCCCAGACCCAAAGCT 40800          T  _  A_
           CT                    GGAGCTTTGG TC GG  GACAGG
                                ||||||||||  ||  ||  ||||||
                                TCTCGAAACC AG CC  CTGTCC
                                      C  A  CC
GAM69   TFR2     3'  CCCGTCCCCCAGTCAAGAGCTC 13698          _ GT C  A   A
           CT                    AGGAGCTTT G  T GG GAC GG
                                |||||||||  |  | ||  ||| ||
                                TCCTCGAGA C  A CC CTG CC
                                      A TG C  C   C
GAM69   C1orf35  3'  CTGCCTCGGAAGCTCCTT    44480        TTGGT  G   A
                                AAGGAGCT    TC GAG CAG
                                ||||||||    || ||| |||
                                TTCCTCGA    AG CTC GTC
                                     _____  G   C
GAM69   DKFZp434J1015 3'  CCGCCTCCACCTGAAAAGCTCC 94209          ___   TC    ACA
           TT                    AAGGAGCTTT   GGT  GGAG   GG
                                ||||||||||   |||  ||||   ||
                                TTCCTCGAAA   CCA  CCTC   CC
                                      AGT   __    CG_
GAM69   FLJ10350  5'  CCGCCTCCGAGTCGCTACTT   97248     G   TTT GT     ACA
                                AAG AGC   G  TCGGAG   GG
                                |||  |||   |  ||||||   ||
                                TTC TCG   C  AGCCTC   CC
                                  A   ___ TG     CG_
GAM69   HRI      3'  CTGCCCCACAAGCTCCTT    27738          _   TT
                                AAGGAGCTT TGG  CGG
                                |||||||||  |||  |||
                                TTCCTCGAA ACC  GTC
                                      C   CC
GAM69   KIAA0057  3'  CCTGTCTCTTGCAAGCTCC   25409        TG  TC
                                GGAGCTT  GT  GGAGACAGG
                                |||||||  ||  |||||||||
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                                CCTCGAA  CG  TCTCTGTCC
                                   __ T_
GAM69   KIAA0189  3'  CCTGTCCCCTTTCCTAAAGCTC 28941          TTC_  A
            CT                   AGGAGCTTTGG   GG GACAGG
                                 ||||||||||    || ||||||
                                 TCCTCGAAATC   CC CTGTCC
                                      CTTT  C
GAM69   KIAA1203  3'  CCTGCCCTCCCACCAAAGCCTC 72087      _      TC   A_
            CT                   AGGAG CTTTGGT  GGAG  CAGG
                                 ||||| |||||||  ||||  ||||
                                 TCCTC GAAACCA  CCTC  GTCC
                                   C      C_   CC
GAM69   KIAA1533  5'  CCTGCCCCCAAGCCGGCCCC  74140    A  TT   C  AGA
                                 GG GCT  GGTT GG   CAGG
                                 || |||  |||| ||   ||||
                                 CC CGG  CCGA CC   GTCC
                                  C  __   A  CCC
GAM69   SAMHD1   3'  CCTGCCCCCGTGAAGAGTTCC  61981        GGTT   AGA
                                 GGAGCTTT   CGG   CAGG
                                 ||||||||   |||   ||||
                                 CCTTGAGA   GCC   GTCC
                                      AGT_   CCC
GAM69   SCGN    3'  CCTGTCTCACTGAAAGCCCCT  23775    A   _  TCG
                                 AGG GCTTT GGT   GAGACAGG
                                 ||| ||||| |||   ||||||||
                                 TCC CGAAA TCA   CTCTGTCC
                                   C    G  ___
GAM69   SYT6    3'  CTCTCCGAAACCACCTC    79519    CTT   _    CA
                                 GAG   TGGTT CGGAGA  G
                                 |||   ||||| ||||||  |
                                 CTC   ACCAA GCCTCT  C
                                   C__    A     A
GAM69   UBXD2   3'  CTGCCTCCATCAGCTTCTT   68892       TT   TC   A
                                 AAGGAGCT  GGT  GGAG CAG
                                 ||||||||  |||  |||| |||
                                 TTCTTCGA  CTA  CCTC GTC
                                      __  __   C
GAM69   LOC113146 3'  CCTAAAATGGAACCAAAGCTTC 73334          GGAGAC
                                 GGAGCTTTGGTTC     AGG
                                 ||||||||||||      |||
                                 CTTCGAAACCAAG     TCC
                                       GTAAAA
GAM69   LOC113521 5'  CCGTCTCCGAGCTGCTCC    73404      TTT        A
                                 GGAGC   GGTTCGGAGAC GG
                                 |||||   |||||||||||| ||
                                 CCTCG   TCGAGCCTCTG CC
                                    ___         C
GAM69   LOC115704 3'  CCTGCAGCGGAAACCAAAGTCC 73906    AG     __  GAGA
            C                    GG  CTTTGGT  TCG   CAGG
                                 ||  |||||||  |||   ||||
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                                CC  GAAACCA  GGC    GTCC
                                 CT      AA   GAC_
GAM69   LOC136345 3' CCTACCCCACCCAAAGCTGCCT 76712     _      TTC  AGAC
                                AGG AGCTTTGG   GG    AGG
                                ||| ||||||||   ||    |||
                                TCC TCGAAACC   CC    TCC
                                  G       CA_  CCA_
GAM69   LOC144231 5' CCTGTCTTCCTTGACCAAAGCT 83938          C__
           CT                    GGAGCTTTGGTT   GGAGACAGG
                                 ||||||||||||   ||||||||||
                                 TCTCGAAACCAG   CTTCTGTCC
                                        TTC
GAM69   LOC146856 5' CTGTCTCCATGAACCACTC    83700     CTT     __
                                GAG   TGGTTC  GGAGACAG
                                |||   ||||||  ||||||||
                                CTC   ACCAAG  CCTCTGTC
                                  ____     TA
GAM69   LOC147669 5' CCGCCTCCTGGGCAAGCTCC   85180       TG   _   ACA
                                GGAGCTT  GTTC GGAG   GG
                                |||||||  |||| ||||   ||
                                CCTCGAA  CGGG CCTC   CC
                                    __   T    CG_
GAM69   LOC148021 5' CTACCTCCAGAGCTACTT     79316     G       TTC  _
                                AAG AGCTTTGG   GG AG
                                ||| ||||||||   || ||
                                TTC TCGAGACC   CC TC
                                  A       T__  A
GAM69   LOC153688 3' CCTGCCCCCAAACCAAGGCCT  87307    A       C  AGA
                                GG GCTTTGGTT GG   CAGG
                                || |||||||| ||   ||||
                                TC CGGAACCAA CC   GTCC
                                 _       A  CCC
GAM69   LOC155032 5' CCTACCCCACCCAAAGCTGCCT 87592     _      TTC  AGAC
                                AGG AGCTTTGG   GG    AGG
                                ||| ||||||||   ||    |||
                                TCC TCGAAACC   CC    TCC
                                  G       CA_  CCA_
GAM69   LOC157349 5' CCGTCTCCGGCAGCCCCT    82335     A   TTG  T      A
                                AGG GCT   GT CGGAGAC GG
                                ||| |||   || ||||||| ||
                                TCC CGA   CG GCCTCTG CC
                                  C  ___  _      C
GAM69   LOC157349 5' CCGTCTCCGGCAGCCCCT    82336     A   TTG  T      A
                                AGG GCT   GT CGGAGAC GG
                                ||| |||   || ||||||| ||
                                TCC CGA   CG GCCTCTG CC
                                  C  ___  _      C
GAM69   LOC199991 3' CCTGTCCACCCTCAAAGCCCT  91515     A      TTC  A_
                                AGG GCTTTGG   GG  GACAGG
                                ||| |||||||   ||  ||||||
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                                TCC CGAAACT  CC  CTGTCC
                                  _     C__  AC
GAM70   AGRP    5'  CTTCATTAGGCCCTGCCATA  24616       A  A
                                TATGGCA GG CCTGATGGAG
                                ||||||| || ||||||||||
                                ATACCGT CC GGATTACTTC
                                    C  _
GAM70   CGTHBA  3'  CTTCCCTCCAGTCCTTGCCG  24890        C  AT  A
                                TGGCAAGGAC TG  GG GAAG
                                |||||||||| ||  || ||||
                                GCCGTTCCTG AC  CC CTTC
                                      _ CT  _
GAM70   COL5A3  3'  CTCCCCAGGCTCACCTTGCCAT 32318        A___   AT
          G                      TATGGCAAGG   CCTG  GGAG
                                ||||||||||   ||||  ||||
                                GTACCGTTCC   GGAC  CCTC
                                     ACTC   C_
GAM70   FGF23   3'  CTTCTCTGGGGTCCCTTCCA  40557    CAA    GA
                                TGG  GGACCT  TGGAGAAG
                                |||  ||||||  ||||||||
                                ACC  CCTGGG  GTCTCTTC
                                  TTC    __
GAM70   FUT3    3'  CTCCCAGAGACCTTGCCA    5621       AC_  AT
                                TGGCAAGG  CTG  GGAG
                                ||||||||  |||  ||||
                                ACCGTTCC  GAC  CCTC
                                    AGA  __
GAM70   FUT5    3'  CTCCCAGAGACCTTGCCA    10726      AC_  AT
                                TGGCAAGG  CTG  GGAG
                                ||||||||  |||  ||||
                                ACCGTTCC  GAC  CCTC
                                    AGA  __
GAM70   TCF12   3'  TCTCCTATCCTCTTGCCATA  13639       ACCT  _
                                TATGGCAAGG   GAT GGAGA
                                ||||||||||   ||| |||||
                                ATACCGTTCT   CTA CCTCT
                                     C___  T
GAM70   WSX1    3'  CTCCCCCACATCCTTTCCTTGC 17915      CCT  _____
          C                     GGCAAGGA  GAT   GGAG
                                ||||||||  |||   ||||
                                CCGTTCCT  CTA   CCTC
                                    TTC  CACCC
GAM70   ZAP70   3'  CTTCCCCACCCTCAGCCCCACC 71375    CAA  AC   ___  A
          CCA                     TGG  GG  CTGA  TGG GAAG
                                |||  ||  ||||  ||| ||||
                                ACC  CC  GACT  ACC CTTC
                                  CCA  CC   CCC  C
GAM70   C1orf34 3'  CCTCTGGCCATTGCCATA   61303       _  A  T  T
                                TATGGCAA GG CC GA GG
                                |||||||| || || || ||
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                                ATACCGTT CC GG CT CC
                                    A  _  T  _
GAM70   CLSTN1   3'  CTCCCCAGAGCACCCCCTGCCA 30787       A  AC____   AT
           T                    ATGGCA GG     CTG  GGAG
                                ||||||  ||     |||  ||||
                                TACCGT CC     GAC  CCTC
                                   C  CCACGA   C_
GAM70   DKFZP434J193 3'  CTTCTCCACCACTCTCCTTGCC 71562          CC_  A
           ATG                    TATGGCAAGGA   TG TGGAGAAG
                                ||||||||||   ||  ||||||||
                                GTACCGTTCCT   AC ACCTCTTC
                                      CTC  C
GAM70   DNAJC6   3'  CTCCAAAGTTCCCACCATA   29492      CAA   C  GA
                                TATGG   GGA CT  TGGAG
                                |||||   |||  ||  |||||
                                ATACC   CCT GA  ACCTC
                                   AC_   T  A_
GAM70   FLJ12122  5'  CTGCCAGCTCAGGTCCCTGCCA 47092      A      __  _
                                TGGCA GGACCTGA  TGG AG
                                ||||| ||||||||  |||  ||
                                ACCGT CCTGGACT  ACC TC
                                   C       CG   G
GAM70   FLJ14642  3'  CTTCTCCGTAGTCCCCGCC   52575    AA    CTG
                                GGC  GGAC   ATGGAGAAG
                                |||  ||||   |||||||||
                                CCG  CCTG   TGCCTCTTC
                                  CC    A__
GAM70   FLJ20275  3'  CTGTCAGATCCTTGCCAT    35308          C
                                ATGGCAAGGA CTGATGG
                                |||||||||| |||||||
                                TACCGTTCCT GACTGTC
                                      A
GAM70   FLJ21369  3'  CTTCTCCATCAAGTTTCACCA  46051    CAA    C
                                TGG   GGAC TGATGGAGAAG
                                |||   |||| ||||||||||
                                ACC   TTTG ACTACCTCTTC
                                  AC_    A
GAM70   HSPC016   3'  TCTCTATTCCCTGCCATA    32503       A   CCTG
                                TATGGCA GGA    ATGGAGA
                                |||||||  |||    |||||||
                                ATACCGT CCT    TATCTCT
                                   C  ____
GAM70   HT014    3'  CTTCCTAATAAATCCTTGCCA  40153         CC  A   A
                                TGGCAAGGA  TG TGG GAAG
                                |||||||||  ||  ||| ||||
                                ACCGTTCCT  AT ATC CTTC
                                      AA  A   _
GAM70   KIAA0773  3'  CTTCTCCACGACCTCACC    28722    CA   ACC  A
                                GG  AGG   TG TGGAGAAG
                                ||  |||   || ||||||||
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                                CC  TCC   GC ACCTCTTC
                                 AC   A__  _
GAM70   KIAA1181  3' CTCCATCAGCTGGTCA      68911      A  GAC
                                TGGC AG   CTGATGGAG
                                |||| ||   |||||||||
                                ACTG TC   GACTACCTC
                                  G  ___
GAM70   KIAA1321  3' CTCCTTAGGTCCTCACA     62899    GCA       T
                                TG   AGGACCTGA GGAG
                                ||   ||||||||| ||||
                                AC   TCCTGGATT CCTC
                                 AC_        _
GAM70   KIAA1348  3' CTTCTTAGGTCTTGCCA     69122       G     T
                                TGGCAAG ACCTGA GGAG
                                ||||||| |||||| ||||
                                ACCGTTC TGGATT CTTC

                                   _     _
GAM70   KIAA1493  3' CTTCTCCACCTAGTCTGCC    64840     AG   CTGA
                                GGCA  GAC    TGGAGAAG
                                ||||  |||    ||||||||
                                CCGT  CTG    ACCTCTTC
                                  __  ATCC
GAM70   KIAA1535  3' CTCTGTGGTCCTTGCC      80212          TG
                                GGCAAGGACC  ATGGAG
                                ||||||||||  ||||||
                                CCGTTCCTGG  TGTCTC

                                    __
GAM70   KIAA1819  5' CTTCTCCACGGCTCCCCCA   70252    CAA   C   A
                                TGG   GGA CTG TGGAGAAG
                                |||   ||| ||| ||||||||
                                ACC   CCT GGC ACCTCTTC
                                  C__   C  _
GAM70   LAT1-3TM  3' CTCCATCAGTGTCATCACCA  69155     CAAG  _
                                TGG    GAC CTGATGGAG
                                |||    ||| |||||||||
                                ACC    CTG GACTACCTC
                                  ACTA   T
GAM70   LAT1-3TM  5' CTCCATCAGTGTCATTACCA  49144     CAAG  _
                                TGG    GAC CTGATGGAG
                                |||    ||| |||||||||
                                ACC    CTG GACTACCTC
                                  ATTA   T
GAM70   OS4      3' CTTCCCCATCATCCCTTCCATT 20389       _  CC___     A
           GCCA                    TGGCAA GGA    TGATGG GAAG
                                |||||| |||    |||||| ||||
                                ACCGTT CCT    ACTACC CTTC
                                   A  TCCCT     C
GAM70   RASSF2    3' CTTCTCCACCTTCTCTCCA   29097    CA   CCTGA
                                TGG  AGGA    TGGAGAAG
                                |||  ||||    ||||||||
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                                ACC  TCTT    ACCTCTTC
                                  TC   CC___
GAM70   SARM     3'  CTCCCCCAGGCCCTGCCAT   31285       A  A   AT
                                ATGGCA GG CCTG  GGAG
                                |||||| || ||||  ||||
                                TACCGT CC GGAC  CCTC
                                   C  _   CC
GAM70   SELB     3'  CTCCCCCAGGGCCTCCTTGCC  62591         ___   AT
                                GGCAAGGA   CCTG  GGAG
                                ||||||||   ||||  ||||
                                CCGTTCCT   GGAC  CCTC
                                     CCG   CC
GAM70   SERPING1 3'  CTTCTCCATGGCCCTGCCATG  5348        A  A  TG
                                TATGGCA GG CC  ATGGAGAAG
                                ||||||| || ||  |||||||||
                                GTACCGT CC GG  TACCTCTTC
                                    C  _ __
GAM70   SLIT1    3'  TCTCCGGAAGTCCTTGC     13233        C GA
                                GCAAGGAC T  TGGAGA
                                |||||||| |  ||||||
                                CGTTCCTG A  GCCTCT
                                    _ AG
GAM70   ZDHHC8   3'  TCCCCACCAACTTCTCTGCC   64622     _   CC  A   A
                                GGCA AGGA  TG TGG GA
                                |||| ||||  || ||| ||
                                CCGT TCTT  AC ACC CT
                                  C   CA  C   C
GAM70   LOC112868 5'  CTCCCAGCCCTTGCCA     73268        AC   AT
                                TGGCAAGG  CTG  GGAG
                                ||||||||  |||  ||||
                                ACCGTTCC  GAC  CCTC
                                    C_  __
GAM70   LOC142946 3'  CCATGGTCCTTGCCATA     83783           TG
                                TATGGCAAGGACC  ATGG
                                ||||||||||||  ||||
                                ATACCGTTCCTGG  TACC
                                          __
GAM70   LOC150319 3'  CTTCTCCATCCTCCTGCCAT   80471       A   CCT
                                ATGGCA GGA   GATGGAGAAG
                                |||||| |||   ||||||||||
                                TACCGT CCT   CTACCTCTTC
                                   _   C__
GAM70   LOC159319 5'  TTCTCCACACCCCTGCC     83073     A  ACC  A
                                GGCA GG   TG TGGAGAA
                                |||| ||   || |||||||
                                CCGT CC   AC ACCTCTT
                                  C  C__  _
GAM70   LOC197423 5'  CTCCATCAGTGTCATTACCA   78424     CAAG  _
                                TGG    GAC CTGATGGAG
                                |||    ||| |||||||||
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                                ACC    CTG GACTACCTC
                                  ATTA   T
GAM70   LOC199923 5'  CTTCTCCACCTCCTGCCA    89871      A   CCTGA
                                TGGCA GGA    TGGAGAAG
                                ||||| |||    ||||||||
                                ACCGT CCT    ACCTCTTC
                                  _   CC___
GAM70   LOC206657 5'  CTTCTCAGTCTTGCCA      91105        AC    T
                                TGGCAAGG  CTGA GGAG
                                ||||||||  |||| ||||
                                ACCGTTCT  GACT CTTC
                                    __    _
GAM70   LOC220565 5'  CTCCATCAGTGTCATCACCA   92441     CAAG   _
                                TGG    GAC CTGATGGAG
                                |||    ||| |||||||||
                                ACC    CTG GACTACCTC
                                  ACTA   T
GAM70   LOC221975 5'  CTTCTCCATGGAGCCTGCC    94192      A  AC  G
                                GGCA GG  CT ATGGAGAAG
                                |||| ||  || |||||||||
                                CCGT CC  GG TACCTCTTC
                                  _  GA  _
GAM70   LOC222160 5'  TCCCATTAGGCCCCCA      95793     CAA  A       A
                                TGG   GG CCTGATGG GA
                                |||   || |||||||| ||
                                ACC   CC GGATTACC CT
                                  C__  _       _
GAM70   LOC257239 5'  CTTCTCCACCTCAACCACCA   98844     CAA  ACC   __
                                TGG   GG   TGA  TGGAGAAG
                                |||   ||   |||  ||||||||
                                ACC   CC   ACT  ACCTCTTC
                                  A__   A__   CC
GAM70   LOC90499  3'  CTTCTCCATGGCCCCCTCCA   63741     CAA  A  TG
                                TGG   GG CC  ATGGAGAAG
                                |||   || ||  |||||||||
                                ACC   CC GG  TACCTCTTC
                                  TCC  C  __
GAM71   AGRP      5'  CTTCATTAGGCCCTGCCATA   24616        A  A
                                TATGGCA GG CCTGATGGAG
                                ||||||| || ||||||||||
                                ATACCGT CC GGATTACTTC
                                    C  _
GAM71   CGTHBA    3'  CTTCCCTCCAGTCCTTGCCG   24890          C  AT  A
                                TGGCAAGGAC TG  GG GAAG
                                |||||||||| ||  || ||||
                                GCCGTTCCTG AC  CC CTTC
                                      _  CT  _
GAM71   COL5A3    3'  CTCCCCAGGCTCACCTTGCCAT 32318          A___    AT
              G                   TATGGCAAGG    CCTG  GGAG
                                  ||||||||||    ||||  ||||
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                                GTACCGTTCC   GGAC  CCTC
                                     ACTC   C_
GAM71   FGF23    3'  CTTCTCTGGGGTCCCTTCCA  40557    CAA    GA
                                TGG   GGACCT  TGGAGAAG
                                |||   ||||||  ||||||||
                                ACC   CCTGGG  GTCTCTTC
                                  TTC    __
GAM71   FUT3     3'  CTCCCAGAGACCTTGCCA    5621       AC_  AT
                                TGGCAAGG   CTG  GGAG
                                ||||||||   |||  ||||
                                ACCGTTCC   GAC  CCTC
                                     AGA   __
GAM71   FUT5     3'  CTCCCAGAGACCTTGCCA    10726      AC_  AT
                                TGGCAAGG   CTG  GGAG
                                ||||||||   |||  ||||
                                ACCGTTCC   GAC  CCTC
                                     AGA   __
GAM71   TCF12    3'  TCTCCTATCCTCTTGCCATA  13639       ACCT  _
                                TATGGCAAGG    GAT GGAGA
                                ||||||||||    ||| |||||
                                ATACCGTTCT    CTA CCTCT
                                      C___   T
GAM71   WSX1     3'  CTCCCCCACATCCTTTCCTTGC 17915       CCT  _____
           C                     GGCAAGGA   GAT    GGAG
                                ||||||||   |||    ||||
                                CCGTTCCT   CTA    CCTC
                                     TTC   CACCC
GAM71   ZAP70    3'  CTTCCCCACCCTCAGCCCCACC 71375    CAA  AC   ___  A
           CCA                    TGG   GG  CTGA   TGG GAAG
                                |||   ||  ||||   ||| ||||
                                ACC   CC  GACT   ACC CTTC
                                  CCA  CC    CCC   C
GAM71   C1orf34  3'  CCTCTGGCCATTGCCATA    61303       _  A  T  T
                                TATGGCAA GG CC GA GG
                                |||||||| || || || ||
                                ATACCGTT CC GG CT CC
                                     A  _  T  _
GAM71   CLSTN1   3'  CTCCCCAGAGCACCCCCTGCCA 30787      A  AC____  AT
           T                     ATGGCA GG     CTG  GGAG
                                ||||||  ||     |||  ||||
                                TACCGT CC     GAC  CCTC
                                   C  CCACGA   C_
GAM71   DKFZP434J193 3'  CTTCTCCACCACTCTCCTTGCC 71562          CC_  A
           ATG                     TATGGCAAGGA   TG TGGAGAAG
                                ||||||||||||   || ||||||||
                                GTACCGTTCCT   AC ACCTCTTC
                                      CTC  C
GAM71   DNAJC6   3'  CTCCAAAGTTCCCACCATA   29492      CAA   C  GA
                                TATGG   GGA CT  TGGAG
                                |||||   ||| ||  |||||
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                                ATACC   CCT GA  ACCTC
                                  AC_   T  A_
GAM71   FLJ12122  5'  CTGCCAGCTCAGGTCCCTGCCA 47092      A      __  _
                                TGGCA GGACCTGA  TGG AG
                                ||||| ||||||||  ||| ||
                                ACCGT CCTGGACT  ACC TC
                                   C       CG   G
GAM71   FLJ14642  3'  CTTCTCCGTAGTCCCCGCC   52575    AA   CTG
                                GGC  GGAC   ATGGAGAAG
                                |||  ||||   |||||||||
                                CCG  CCTG   TGCCTCTTC
                                  CC    A__
GAM71   FLJ20275  3'  CTGTCAGATCCTTGCCAT    35308         C
                                ATGGCAAGGA CTGATGG
                                |||||||||| |||||||
                                TACCGTTCCT GACTGTC
                                      A
GAM71   FLJ21369  3'  CTTCTCCATCAAGTTTCACCA  46051    CAA   C
                                TGG   GGAC TGATGGAGAAG
                                |||   |||| ||||||||||
                                ACC   TTTG ACTACCTCTTC
                                  AC_   A
GAM71   HSPC016   3'  TCTCTATTCCCTGCCATA    32503       A   CCTG
                                TATGGCA GGA    ATGGAGA
                                ||||||| |||    |||||||
                                ATACCGT CCT    TATCTCT
                                    C  _____
GAM71   HT014     3'  CTTCCTAATAAATCCTTGCCA  40153        CC  A   A
                                TGGCAAGGA  TG TGG GAAG
                                |||||||||  || ||| ||||
                                ACCGTTCCT  AT ATC CTTC
                                      AA  A   _
GAM71   KIAA0773  3'  CTTCTCCACGACCTCACC    28722    CA   ACC  A
                                GG  AGG   TG TGGAGAAG
                                ||  |||   || ||||||||
                                CC  TCC   GC ACCTCTTC
                                 AC   A__  _
GAM71   KIAA1493  3'  CTTCTCCACCTAGTCTGCC    64840     AG   CTGA
                                GGCA  GAC    TGGAGAAG
                                ||||  |||    ||||||||
                                CCGT  CTG    ACCTCTTC
                                   __   ATCC
GAM71   KIAA1819  5'  CTTCTCCACGGCTCCCCCA   70252    CAA   C   A
                                TGG   GGA CTG TGGAGAAG
                                |||   ||| ||| ||||||||
                                ACC   CCT GGC ACCTCTTC
                                  C__   C   _
GAM71   LAT1-3TM  3'  CTCCATCAGTGTCATCACCA  49143     CAAG  _
                                TGG    GAC CTGATGGAG
                                |||    ||| |||||||||
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                                ACC    CTG GACTACCTC
                                  ACTA   T
GAM71   LAT1-3TM  5'  CTCCATCAGTGTCATTACCA   49144     CAAG  _
                                TGG    GAC CTGATGGAG
                                |||    ||| |||||||||
                                ACC    CTG GACTACCTC
                                  ATTA   T
GAM71   OS4       3'  CTTCCCCATCATCCCTTCCATT 20389       _  CC___     A
           GCCA                    TGGCAA GGA     TGATGG GAAG
                                |||||| |||    |||||| ||||
                                ACCGTT CCT     ACTACC CTTC
                                   A   TCCCT     C
GAM71   RASSF2    3'  CTTCTCCACCTTCTCTCCA   29097     CA    CCTGA
                                TGG  AGGA    TGGAGAAG
                                |||  ||||    ||||||||
                                ACC  TCTT    ACCTCTTC
                                  TC    CC___
GAM71   SARM      3'  CTCCCCCAGGCCCTGCCAT   31285       A  A    AT
                                ATGGCA GG CCTG  GGAG
                                |||||| || ||||  ||||
                                TACCGT CC GGAC  CCTC
                                   C  _   CC
GAM71   SELB      3'  CTCCCCCAGGGCCTCCTTGCC  62591         ___    AT
                                GGCAAGGA   CCTG  GGAG
                                ||||||||   ||||  ||||
                                CCGTTCCT   GGAC  CCTC
                                     CCG    CC
GAM71   SERPING1  3'  CTTCTCCATGGCCCTGCCATG  5348         A  A  TG
                                TATGGCA GG CC  ATGGAGAAG
                                ||||||| || ||  |||||||||
                                GTACCGT CC GG  TACCTCTTC
                                    C  _  __
GAM71   ZDHHC8    3'  TCCCCACCAACTTCTCTGCC   64622      _   CC  A   A
                                GGCA AGGA  TG TGG GA
                                |||| ||||  || ||| ||
                                CCGT TCTT  AC ACC CT
                                  C    CA  C   C
GAM71   LOC150319 3'  CTTCTCCATCCTCCTGCCAT   80471       A   CCT
                                ATGGCA GGA   GATGGAGAAG
                                |||||| |||   ||||||||||
                                TACCGT CCT   CTACCTCTTC
                                   _   C__
GAM71   LOC197423 5'  CTCCATCAGTGTCATTACCA   78424     CAAG  _
                                TGG    GAC CTGATGGAG
                                |||    ||| |||||||||
                                ACC    CTG GACTACCTC
                                  ATTA   T
GAM71   LOC199923 5'  CTTCTCCACCTCCTGCCA    89871      A   CCTGA
                                TGGCA GGA    TGGAGAAG
                                ||||| |||    ||||||||
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                                ACCGT CCT    ACCTCTTC
                                  _  CC___
GAM71   LOC220565 5'  CTCCATCAGTGTCATCACCA  92441    CAAG  _
                                TGG   GAC CTGATGGAG
                                |||   ||| |||||||||
                                ACC   CTG GACTACCTC
                                  ACTA  T
GAM71   LOC221975 5'  CTTCTCCATGGAGCCTGCC   94192     A  AC  G
                                GGCA GG  CT ATGGAGAAG
                                |||| ||  || |||||||||
                                CCGT CC  GG TACCTCTTC
                                  _ GA  _
GAM71   LOC257239 5'  CTTCTCCACCTCAACCACCA  98844    CAA  ACC  __
                                TGG  GG  TGA  TGGAGAAG
                                |||  ||  |||  ||||||||
                                ACC  CC  ACT  ACCTCTTC
                                  A__  A__  CC
GAM71   LOC90499  3'  CTTCTCCATGGCCCCCTCCA  63741    CAA  A  TG
                                TGG  GG CC  ATGGAGAAG
                                |||  || ||  |||||||||
                                ACC  CC GG  TACCTCTTC
                                  TCC  C  __
GAM72   CA7     3'  CCAGTCACCAAAGCCACCT   60828    A_     TCGGA  A
                                AGG  GCTTTGGT    GAC GG
                                |||  ||||||||    ||| ||
                                TCC  CGAAACCA    CTG CC
                                  AC      _____  A
GAM72   E2F3    3'  CTGTCTCCATGAACCACTC   10467    CTT    __
                                GAG  TGGTTC  GGAGACAG
                                |||  ||||||  ||||||||
                                CTC  ACCAAG  CCTCTGTC
                                  ___     TA
GAM72   HD      3'  CCTATCCCCAGGACAGGTCCCT 10911    AG  TG  _  A  C
                                AGG  CTT  GTTC GG GA AGG
                                |||  |||  |||| || || |||
                                TCC  GGA  CAGG CC CT TCC
                                  CT  __   A  C  A
GAM72   LZTR1   3'  CTGTCACCCAAGGCTCCT   23170         TTCG A
                                AGGAGCTTTGG   G GACAG
                                ||||||||||   | |||||
                                TCCTCGGAACC   C CTGTC
                                      ____ A
GAM72   MECP2   3'  CCGTCTAACCACAGCTCCTT  18395       T   CGG   A
                                AAGGAGCT TGGTT  AGAC GG
                                |||||||| |||||  |||| ||
                                TTCCTCGA ACCAA  TCTG CC
                                    C    ___   C
GAM72   PLA2G2A  5'  CTGTCTCCAAACAGCCTT   6110     A  TTG  C
                                AGG GCT  GTT GGAGACAG
                                ||| |||  ||| ||||||||
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                                TTC CGA   CAA CCTCTGTC
                                  _  ___   A
GAM72   PLOD     3'  CCTGAAAAACCAAGGCCCC   6114     A       CGGAGA
                                GG GCTTTGGTT     CAGG
                                || |||||||||     ||||
                                CC CGGAACCAA     GTCC
                                 C        AAA___
GAM72   POLR2A   3'  CCTGTCCCCAAATTGAAGATCC 8128       G   TG   C  A
           TT                    AAGGA CTT  GTT GG GACAGG
                                ||||| |||  ||| || ||||||
                                TTCCT GAA  TAA CC CTGTCC
                                   A   GT   A  C
GAM72   RAB36    3'  CCTGTCTCCAACACCGCCTCCT 18163      CTT    TC_
                                AGGAG   TGGT   GGAGACAGG
                                |||||   ||||   |||||||||
                                TCCTC   GCCA   CCTCTGTCC
                                   C__    CAA
GAM72   RAP1     3'  CCTGTCCTTTGGCAGAAGCTCC 39111          G  T    _
           TT                    AAGGAGCTTT GT CGGAG ACAGG
                                |||||||||| || ||||| |||||
                                TTCCTCGAAG CG GTTTC TGTCC
                                     A  _    C
GAM72   SFRP5    3'  CCTGCCCCAAGGCCCAGAGCTC 13032          TT __  AGA
           C                     GGAGCTTTGG  C  GG   CAGG
                                |||||||||  |  ||   ||||
                                CCTCGAGACC  G  CC   GTCC
                                     CG AA  CC_
GAM72   SORCS2   3'  CCTGTCCCCCAGACCCAAAGCT 40800          T  _  A_
           CT                    GGAGCTTTGG TC GG  GACAGG
                                |||||||||| || ||  ||||||
                                TCTCGAAACC AG CC  CTGTCC
                                     C  A  CC
GAM72   TFR2     3'  CCCGTCCCCCAGTCAAGAGCTC 13698          _ GT C  A   A
           CT                    AGGAGCTTT G  T GG GAC GG
                                |||||||||  |  | || ||| ||
                                TCCTCGAGA C  A CC CTG CC
                                     A TG C  C   C
GAM72   C1orf35  3'  CTGCCTCGGAAGCTCCTT    44480        TTGGT  G   A
                                AAGGAGCT    TC GAG CAG
                                ||||||||    || ||| |||
                                TTCCTCGA    AG CTC GTC
                                     _____  G   C
GAM72   DKFZp434J1015 3'  CCGCCTCCACCTGAAAAGCTCC 94209          ___   TC    ACA
           TT                    AAGGAGCTTT   GGT  GGAG   GG
                                ||||||||||   |||  ||||   ||
                                TTCCTCGAAA   CCA  CCTC   CC
                                     AGT   __    CG_
GAM72   EFS2     3'  CTGCCTGCCAAAGCCCC     20773    A      TC  AGA
                                GG GCTTTGGT  GG   CAG
                                || ||||||||  ||   |||
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                                CC CGAAACCG  CC   GTC
                                 C       T_ ___
GAM72   FLJ10350 5' CCGCCTCCGAGTCGCTACTT  97248    G   TTT GT    ACA
                                AAG AGC   G  TCGGAG   GG
                                ||| |||   |  ||||||   ||
                                TTC TCG   C  AGCCTC   CC
                                  A  ___ TG     CG_
GAM72   HRI     3' CTGCCCCACAAGCTCCTT    27738         _  TT
                                AAGGAGCTT TGG  CGG
                                ||||||||| |||  |||
                                TTCCTCGAA ACC  GTC
                                     C   CC
GAM72   KIAA0057 3' CCTGTCTCTTGCAAGCTCC   25409       TG  TC
                                GGAGCTT  GT  GGAGACAGG
                                |||||||  ||  |||||||||
                                CCTCGAA  CG  TCTCTGTCC
                                   __  T_
GAM72   KIAA0189 3' CCTGTCCCCTTTCCTAAAGCTC 28941          TTC_  A
            CT                    AGGAGCTTTGG    GG GACAGG
                                ||||||||||    || ||||||
                                TCCTCGAAATC    CC CTGTCC
                                      CTTT  C
GAM72   KIAA1203 3' CCTGCCCTCCCACCAAAGCCTC 72087      _      TC    A_
            CT                    AGGAG CTTTGGT  GGAG  CAGG
                                ||||| |||||||  ||||  ||||
                                TCCTC GAAACCA  CCTC  GTCC
                                  C      C_   CC
GAM72   KIAA1533 5' CCTGCCCCCAAGCCGGCCCC   74140    A   TT    C  AGA
                                GG GCT  GGTT GG   CAGG
                                || |||  |||| ||   ||||
                                CC CGG  CCGA CC   GTCC
                                 C  __    A  CCC
GAM72   SAMHD1   3' CCTGCCCCCGTGAAGAGTTCC  61981        GGTT   AGA
                                GGAGCTTT    CGG   CAGG
                                ||||||||    |||   ||||
                                CCTTGAGA    GCC   GTCC
                                     AGT_   CCC
GAM72   SCGN     3' CCTGTCTCACTGAAAGCCCCT  23775     A    _  TCG
                                AGG GCTTT GGT   GAGACAGG
                                ||| ||||| |||   ||||||||
                                TCC CGAAA TCA   CTCTGTCC
                                  C    G  ___
GAM72   SYT6     3' CATCTCCGAAACCACCTC    79517     CTT    _     CA
                                GAG   TGGTT CGGAGA  G
                                |||   ||||| ||||||  |
                                CTC   ACCAA GCCTCT  C
                                  C__     A     AC
GAM72   UBXD2    3' CTGCCTCCATCAGCTTCTT   68892        TT   TC    A
                                AAGGAGCT  GGT  GGAG CAG
                                ||||||||  |||  |||| |||
```

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                                TTCTTCGA  CTA  CCTC GTC
                                   __  __    C
GAM72   LOC113146 3'  CCTAAAATGGAACCAAAGCTTC 73334          GGAGAC
                                GGAGCTTTGGTTC     AGG
                                ||||||||||||     |||
                                CTTCGAAACCAAG     TCC
                                     GTAAAA
GAM72   LOC113521 5'  CCCGTCTCCGAGCTGCTCC    73402      TTT        A
                                GGAGC   GGTTCGGAGAC GG
                                |||||   |||||||||||  ||
                                CCTCG   TCGAGCCTCTG CC
                                   ___         C
GAM72   LOC115704 3'  CCTGCAGCGGAAACCAAAGTCC 73906    AG     __  GAGA
          C                      GG  CTTTGGT  TCG    CAGG
                                ||  |||||||  |||    ||||
                                CC  GAAACCA  GGC    GTCC
                                 CT      AA   GAC_
GAM72   LOC136345 3'  CCTACCCCACCCAAAGCTGCCT 76712     _      TTC  AGAC
                                AGG AGCTTTGG   GG    AGG
                                ||| ||||||||   ||    |||
                                TCC TCGAAACC   CC    TCC
                                  G       CA_  CCA_
GAM72   LOC144231 5'  CCTGTCTTCCTTGACCAAAGCT 83938          C__
          CT                     GGAGCTTTGGTT   GGAGACAGG
                                ||||||||||||   |||||||||
                                TCTCGAAACCAG   CTTCTGTCC
                                     TTC
GAM72   LOC146856 5'  CTGTCTCCATGAACCACTC    83700     CTT     __
                                GAG   TGGTTC  GGAGACAG
                                |||   ||||||  |||||||||
                                CTC   ACCAAG  CCTCTGTC
                                  ___      TA
GAM72   LOC147669 5'  CCGCCTCCTGGGCAAGCTCC   85180        TG   _   ACA
                                GGAGCTT  GTTC GGAG   GG
                                |||||||  |||| ||||   ||
                                CCTCGAA  CGGG CCTC   CC
                                   __    T    CG_
GAM72   LOC148021 5'  CTACCTCCAGAGCTACTT     79316     G      TTC  _
                                AAG AGCTTTGG   GG AG
                                ||| ||||||||   || ||
                                TTC TCGAGACC   CC TC
                                  A       T__  A
GAM72   LOC153688 3'  CCTGCCCCCAAACCAAGGCCT  87307    A       C  AGA
                                GG GCTTTGGTT GG   CAGG
                                || |||||||| ||   ||||
                                TC CGGAACCAA CC   GTCC
                                 _       A  CCC
GAM72   LOC155032 5'  CCTACCCCACCCAAAGCTGCCT 87592     _      TTC  AGAC
                                AGG AGCTTTGG   GG    AGG
                                ||| ||||||||   ||    |||
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                                TCC TCGAAACC  CC   TCC
                                  G      CA_  CCA_
GAM72   LOC157349 5'  CCGTCTCCGGCAGCCCCT   82335    A  TTG  T    A
                                AGG GCT  GT CGGAGAC GG
                                ||| |||  || ||||||| ||
                                TCC CGA  CG GCCTCTG CC
                                  C  ___  _     C
GAM72   LOC157349 5'  CCGTCTCCGGCAGCCCCT   82336    A  TTG  T    A
                                AGG GCT  GT CGGAGAC GG
                                ||| |||  || ||||||| ||
                                TCC CGA  CG GCCTCTG CC
                                  C  ___  _     C
GAM72   LOC199991 3'  CCTGTCCACCCTCAAAGCCCT  91515    A     TTC  A_
                                AGG GCTTTGG  GG  GACAGG
                                ||| |||||||  ||  ||||||
                                TCC CGAAACT  CC  CTGTCC
                                  _     C__  AC
GAM73   ALEX1    3'  CACAGAAAGAATTTATTGATTT 33973      GAC  TT
           G                     CAAAT  AT  GTTCTTTCTGTG
                                ||||||  ||  ||||||||||||
                                GTTTA  TA  TAAGAAAGACAC
                                  GT_  TT
GAM73   CSN2     3'  CACAGAAGTTCAATACTCATTT 10310       CAT  TT  T
           G                     CAAATGA  TTG  CTT CTGTG
                                |||||||  |||  ||| |||||
                                GTTTACT  AAC  GAA GACAC
                                    CAT  TT  _
GAM73   IQGAP1   3'  CACAGAACTAAAATGTCAT   69600        GTTCT
                                ATGACATTT    TTCTGTG
                                |||||||||    |||||||
                                TACTGTAAA    AAGACAC
                                     ATC__
GAM73   MS4A7    3'  CACAGAAGGGAAAATGTGCA  41354   _    G
                                TG ACATTT TTCTTTCTGTG
                                || |||||| ||||||||||
                                AC TGTAAA AGGGAAGACAC
                                 G    _
GAM73   PPP3CA   3'  CACAGAAAAGAGTTGCATTTG  8133       A  TTTG    _
                                CAAATG CA   TTCTTT CTGTG
                                |||||| ||   |||||| |||||
                                GTTTAC GT   GAGAAA GACAC
                                   _ T___     A
GAM73   RARB     3'  CAGTTAATCAAATGTCATTTG  8258          TTCTTT
                                CAAATGACATTTG     CTG
                                ||||||||||||     |||
                                GTTTACTGTAAAC     GAC
                                      TAATT_
GAM73   RARB     3'  CAGTTAATCAAATGTCATTTG  32887          TTCTTT
                                CAAATGACATTTG     CTG
                                ||||||||||||     |||
```

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                                GTTTACTGTAAAC     GAC
                                      TAATT_
GAM73   RFC1     3'  CAGTGTGAAAAATGTCATTT   12827          G   TTT
                                AAATGACATTT TTC   CTG
                                |||||||||||| |||   |||
                                TTTACTGTAAA AAG   GAC
                                      _   TGT
GAM73   SCA2     3'  CACAGAAAACTAGAATTTCATT 12941       C    GTTC
           T                     AAATGA ATTT    TTTCTGTG
                                |||||| ||||    ||||||||
                                TTTACT TAAG    AAAGACAC
                                   T    ATCA
GAM73   SH3BP4   3'  AAGAACAATGCCATTTG     27997       A    T
                                CAAATG CATT GTTCTT
                                |||||| |||| ||||||
                                GTTTAC GTAA CAAGAA
                                   C    _
GAM73   GOLGA1   3'  ACAGAAAAACACGCATTTG    10846       ACATT    C
                                CAAATG     TGTT TTTCTGT
                                ||||||     |||| |||||||
                                GTTTAC     ACAA AAAGACA
                                   GC___    _
GAM73   KIAA0453 3'  CACCTTCTGGAACAAAGTCACT 69602     A    A       TTCT_
           TG                     CAA TGAC TTTGTTCT     GTG
                                ||| |||| ||||||||     |||
                                GTT ACTG AAACAAGG     CAC
                                  C    _       TCTTC
GAM73   PEG10    3'  CACAGAAAGTTTACATACATTT 31199      AC  T  TT
                                AAATG  AT TG  CTTTCTGTG
                                |||||  || ||  |||||||||
                                TTTAC  TA AT  GAAAGACAC
                                   A_  C  TT
GAM73   PLA2G12  3'  ACATGACAAATGTCAT      48777          CTTTC
                                ATGACATTTGTT     TGT
                                ||||||||||||     |||
                                TACTGTAAACAG     ACA
                                      T_____
GAM73   PPP2R3A  5'  CACAGAAAAATGAATCATTT   12239       CA  TG  C
                                AAATGA  TT  TT TTTCTGTG
                                ||||||  ||  || ||||||||
                                TTTACT  AA  AA AAAGACAC
                                   __  GT  _
GAM73   TLK1     3'  CACAGAAACAGGAATACCATGT 25433       T_     ___
           TA                     TGACAT  TGTTCT   TTCTGTG
                                ||||||  ||||||   |||||||
                                ATTGTA  ATAAGG   AAGACAC
                                   CC     ACA
GAM73   LOC144866 5' CACAGAAACACATGTTAT    84134       T    CTT
                                ATGACAT TGTT   TCTGTG
                                ||||||| ||||   ||||||
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                                TATTGTA ACAA   AGACAC
                                   C   ___
GAM73   LOC157556 5'  CACAGAAAGAATCTCAGTCATC 87779    A    ATTT
            TG                   CA ATGAC   GTTCTTTCTGTG
                                || |||||   ||||||||||||
                                GT TACTG   TAAGAAAGACAC
                                 C    ACTC
GAM73   LOC158046 3'  CACAGAAAGACAAACATCA   59902    CA    T
                                TGA  TTTGT CTTTCTGTG
                                |||  ||||| |||||||||
                                ACT  AAACA GAAAGACAC
                                  AC    _
GAM73   LOC158809 3'  ACAGAAAGCCATCATTT    88257      CATT  TT
                                AAATGA   TG  CTTTCTGT
                                ||||||   ||  ||||||||
                                TTTACT   AC  GAAAGACA
                                   _____  C_
GAM73   LOC159982 5'  CACAGAAAGAACTAGCTTTCA  88433    CATTT_
                                TGA     GTTCTTTCTGTG
                                |||     ||||||||||||
                                ACT     CAAGAAAGACAC
                                  TTCGAT
GAM73   LOC200132 3'  CACAGAAAGAATCTTGTT    89992     TTT
                                GACA   GTTCTTTCTGTG
                                ||||   ||||||||||||
                                TTGT   TAAGAAAGACAC
                                  TC_
GAM73   LOC200488 5'  CACAGAAAGCATTTCAATGTTA 91648         T__  T
            TTT                   AAATGACATT   GT CTTTCTGTG
                                ||||||||||   || |||||||||
                                TTTATTGTAA   TA GAAAGACAC
                                     CTT  C
GAM73   LOC51136  3'  CACAAAATACTAATGTCATTTG 32844          T  TCTTTC
                                CAAATGACATT GT     TGTG
                                |||||||||| ||     ||||
                                GTTTACTGTAA CA     ACAC
                                      T  TAAA__
GAM74   FLRT1    3'  CCCACGCAGCTCTCCCGCCACT 60365        ACCA__    CG_
            GGCCA                 TGGCCAGT     AGAGT   GTGGG
                                |||||||     |||||  |||||
                                ACCGGTCA     TCTCG   CACCC
                                    CCGCCC    ACG
GAM74   MYF6     3'  CCCACCGACCCTTCCTGGCC   11735       TACC   A
                                GGCCAG    AAG GTCGGTGGG
                                ||||||    ||| |||||||||
                                CCGGTC    TTC CAGCCACCC
                                   C___   C
GAM74   NFIC     3'  CCTGCCGACTCCCAGCCCGGCC 20012       A_  ACCAA      TG
            A                   TGGCC  GT    GAGTCGG  GG
                                |||||  ||    |||||||  ||
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                                ACCGG CG    CTCAGCC CC
                                  CC ACC__      GT
GAM74   PPY      3' CCCTCTGCACCCTTGGCTCTGG 12254        TA    A _  T
            CCA                   TGGCCAG  CCAAG GT CGG GGG
                                  ||||||| ||||| || ||| |||
                                  ACCGGTC  GGTTC CA GTC CCC
                                     TC    C C   T
GAM74   PTPN7    3' CCAGGTCTTCAACACTGGCCA  12593        ACC_   G  GG
                                  TGGCCAGT    AAGA TC  TGG
                                  ||||||||    |||| ||  |||
                                  ACCGGTCA    TTCT GG  ACC
                                     CAAC    _ __
GAM74   PTPN7    3' CCAGGTCTTCAACACTGGCCA  55459        ACC_   G  GG
                                  TGGCCAGT    AAGA TC  TGG
                                  ||||||||    |||| ||  |||
                                  ACCGGTCA    TTCT GG  ACC
                                     CAAC    _ __
GAM74   PTPN7    3' CCAGGTCTTCAACACTGGCCA  55466        ACC_   G  GG
                                  TGGCCAGT    AAGA TC  TGG
                                  ||||||||    |||| ||  |||
                                  ACCGGTCA    TTCT GG  ACC
                                     CAAC    _ __
GAM74   ARTN     3' GACTCTGGCACTGGCCA     15613        A  A
                                  TGGCCAGT CCA GAGTC
                                  |||||||| ||| |||||
                                  ACCGGTCA GGT CTCAG
                                     C  _
GAM74   ARTN     3' GACTCTGGCACTGGCCA     55109        A  A
                                  TGGCCAGT CCA GAGTC
                                  |||||||| ||| |||||
                                  ACCGGTCA GGT CTCAG
                                     C  _
GAM74   ARTN     3' GACTCTGGCACTGGCCA     55117        A  A
                                  TGGCCAGT CCA GAGTC
                                  |||||||| ||| |||||
                                  ACCGGTCA GGT CTCAG
                                     C  _
GAM74   ARTN     3' GACTCTGGCACTGGCCA     55137        A  A
                                  TGGCCAGT CCA GAGTC
                                  |||||||| ||| |||||
                                  ACCGGTCA GGT CTCAG
                                     C  _
GAM74   C1QTNF6  3' CCTGCCCTCAGTGACTGGCCA 49991        ACCAA  TC  TG
                                  TGGCCAGT    GAG  GG  GG
                                  ||||||||    |||  ||  ||
                                  ACCGGTCA    CTC  CC  CC
                                     GTGA_   __  GT
GAM74   DKFZP434G1415 3' CTGATACCCTTGGTATAACCA 49269     CCA      A__
                                  TGG  GTACCAAG  GTCGG
                                  |||  ||||||||  |||||
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                                ACC   TATGGTTC   TAGTC
                                  AA_       CCA
GAM74   DKFZP586F1524 3'  CTGGCTCTTAGCACTGACC    32106    C    ACC
                                GG CAGT   AAGAGTCGG
                                || ||||   |||||||||
                                CC GTCA   TTCTCGGTC
                                 A    CGA
GAM74   DKFZp761B1514 3'  CCCACCGACCCGCCACCTGCCA 51139      C  TACCAAGA
                                TGGC AG       GTCGGTGGG
                                |||| ||       |||||||||
                                ACCG TC       CAGCCACCC
                                  _ CACCGCC_
GAM74   KIAA0843  5'  CCTCTGGCTCCCGACACTGGCC 30798        ACCAA      T
                                GGCCAGT    GAGTCGG GG
                                |||||||    ||||||| ||
                                CCGGTCA    CTCGGTC CC
                                    CAGCC      T
GAM74   KIAA1755  3'  CCACCCTTCATACTGGCCA    62007         CC   AGTC
                                TGGCCAGTA  AAG   GGTGG
                                |||||||||  |||   |||||
                                ACCGGTCAT  TTC   CCACC
                                     AC  ____
GAM74   KREMEN    3'  ACCCTCAGGACTGGCCA     50222         A  AA   TC
                                TGGCCAGT CC  GAG  GGT
                                |||||||| ||  |||  |||
                                ACCGGTCA GG  CTC  CCA
                                    _ A_  __
GAM74   N4BP3     3'  CCCAGTCTGTCTTGGCACTGGC 66846         A     GT  __
           CA                     TGGCCAGT CCAAGA  CGG  TGGG
                                |||||||| ||||||  |||  ||||
                                ACCGGTCA GGTTCT  GTC  ACCC
                                     C     __   TG
GAM74   PRO1843   5'  CCCACTTCTTAGCTACTGGCCA 38141          CC_   GTC
                                TGGCCAGTA   AAGA   GGTGGG
                                |||||||||   ||||   ||||||
                                ACCGGTCAT   TTCT   TCACCC
                                     CGA   ___
GAM74   STI2      3'  CCCACCGACCCCGGGCTGGCTA 90406         A  AAGA
                                TGGCCAGT CC    GTCGGTGGG
                                |||||||| ||    |||||||||
                                ATCGGTCG GG    CAGCCACCC
                                    _ CCC_
GAM74   LOC118611 5'  CCCCCGGCTCTGGCCA      75995       GTACCAA      T
                                TGGCCA      GAGTCGG GGG
                                ||||||      ||||||| |||
                                ACCGGT      CTCGGCC CCC
                                  _______     _
GAM74   LOC149076 3'  CCCAGTCTACCTCGGTGCTGGC 79874           A  A  C  _
           CA                     TGGCCAGTACC AG GT GG TGGG
                                |||||||||| || || || ||||
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                                ACCGGTCGTGG TC CA CT ACCC
                                      C _ T G
GAM74   LOC256306 5'  TGACTCTTGATCTGGCCA    98521       TAC
                                TGGCCAG   CAAGAGTCG
                                |||||||   |||||||||
                                ACCGGTC   GTTCTCAGT
                                   TA_
GAM74   LOC90379  3'  CCCACCGACTGATGACCGGC   63202     A  AC  AG
                                GCC GT  CA  AGTCGGTGGG
                                ||| ||  ||  ||||||||||
                                CGG CA  GT  TCAGCCACCC
                                  C __  AG
GAM75   ARF4L     3'  AACCCCTCCCCACATTTGTAG  70385    _  TTT   A    AA
                                CT CG   TGT GGGA  GGTT
                                || ||   ||| ||||  ||||
                                GA GT   ACA CCCT  CCAA
                                 T  TT_   C    CC
GAM75   COL10A1   3'  AACCTTCCCCCTGAAAAGTGA  6681      CG    TA    A
                                TCACT  TTTTG  GGGAA GGTT
                                |||||  |||||  ||||| ||||
                                AGTGA  AAAGT  CCCTT CCAA
                                   __    CC    _
GAM75   GNAS      3'  AACCTTTCCCTTCCCCCGAGTG 33912       TTTTGT
          A                      TCACTCG     AGGGAAAGGTT
                                 |||||||     ||||||||||
                                 AGTGAGC     TCCCTTTCCAA
                                    CCCCT_
GAM75   GNAS      3'  AACCTTTCCCTTCCCCCGAGTG 55381       TTTTGT
          A                      TCACTCG     AGGGAAAGGTT
                                 |||||||     ||||||||||
                                 AGTGAGC     TCCCTTTCCAA
                                    CCCCT_
GAM75   GNAS      3'  AACCTTTCCCTTCCCCCGAGTG 55385       TTTTGT
          A                      TCACTCG     AGGGAAAGGTT
                                 |||||||     ||||||||||
                                 AGTGAGC     TCCCTTTCCAA
                                    CCCCT_
GAM75   GNAS      3'  AACCTTTCCCTTCCCCCGAGTG 6708        TTTTGT
          A                      TCACTCG     AGGGAAAGGTT
                                 |||||||     ||||||||||
                                 AGTGAGC     TCCCTTTCCAA
                                    CCCCT_
GAM75   GPM6A     3'  AACCTTTAAAAAACAAAACGA  19174        AGGG_
                                TCGTTTTGT    AAAGGTT
                                |||||||||    |||||||
                                AGCAAAACA    TTTCCAA
                                     AAAAA
GAM75   FLJ23033  3'  AACCTTTCTGGAAACG      45511       GTAG
                                CGTTTT    GGAAAGGTT
                                ||||||    |||||||||
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                                GCAAAG   TCTTTCCAA
                                   G___
GAM75   HBOA     3'  AACCCTTCCCCACATGTGGTAG 23928    _  CGTTT  A    A
              A                    TC ACT    TGT GGGAA GGTT
                                   || |||    ||| ||||| ||||
                                   AG TGG    ACA CCCTT CCAA
                                    A  TGT__  C    C
GAM75   KIAA1634  3'  AACCTTTAGTATAAAAC     64120        GGG
                                   GTTTTGTA  AAAGGTT
                                   ||||||||  |||||||
                                   CAAAATAT  TTTCCAA
                                        GA_
GAM75   MGC5466   3'  AACCTCTTTCTTACAAAAC    73436          _
                                   GTTTTGTAGGGAA AGGTT
                                   |||||||||||| |||||
                                   CAAAACATTCTTT TCCAA
                                            C
GAM75   PLA2G12   3'  AACCTCAAAGCAAAAAAAGTGA 48776      CG    AGG  AA
                                   TCACT  TTTTGT   GA  GGTT
                                   |||||  ||||||   ||  ||||
                                   AGTGA  AAAACG   CT  CCAA
                                      AA     AAA  __
GAM75   LOC119467 5'  AACCCTTCCTCAGGAAGAGTGA 74435       G    TA    A
                                   TCACTC TTTTG  GGGAA GGTT
                                   |||||| |||||  ||||| ||||
                                   AGTGAG AGGAC  TCCTT CCAA
                                      A    __    C
GAM75   LOC150605 5'  AACCCTCCCCTCCAGGGACGAG 86261    A      GT_   AAA
              AGA                     TC CTCGTTTT   AGGG   GGTT
                                   || ||||||||   ||||   ||||
                                   AG GAGCAGGG   TCCC   CCAA
                                    A       ACC    CTC
GAM75   LOC220883 3'  AACCCTTCCCCACATGTGGTAG 92888    _  CGTTT  A    A
              A                    TC ACT    TGT GGGAA GGTT
                                   || |||    ||| ||||| ||||
                                   AG TGG    ACA CCCTT CCAA
                                    A  TGT__  C    C
GAM75   LOC90639  3'  CCTGTCTCTACAAAACAAG   64410    C         A
                                   CT GTTTTGTAGGGA AGG
                                   || |||||||||||| |||
                                   GA CAAAACATCTCT TCC
                                    A          G
GAM76   GOCAP1    3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                   TACAC  CTCCCAAGAA AAT
                                   |||||  |||||||||| |||
                                   ATGTG  GAGGGTTCTT TTA
                                      AC         G
GAM76   DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090      T   AGAAG
                                   ACCAC CCCA    AATAAG
                                   ||||| ||||    ||||||
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                                TGGTG GGGT    TTATTC
                                  _   GTCA_
GAM76   DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
          A                      TACAC       AGAAGAATAAG
                                 |||||       ||||||||||
                                 ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM76   FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126        CCCAAGAA
                                 TACACCACT       GAATAAG
                                 |||||||||       |||||||
                                 ATGTGGTGA       TTTATTC
                                      AGACG___
GAM76   HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
          TA                     TACA   TCC   GAAGAATAAG
                                 ||||   |||   ||||||||||
                                 ATGT   AGG   TTTCTTATTC
                                   AAA_  ATTG
GAM76   KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA  68742              _
                                 TACACCACTCCCAAGA AGA
                                 |||||||||||||||| |||
                                 ATGTGGTGAGGGTTCT TCT
                                           G
GAM76   KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                 CAC  CT CCAAGAAGAA
                                 |||  || ||||||||||
                                 GTG  GA GGTTCTTTTT
                                   AC  A
GAM76   KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748     CCA__
                                 ACTC    AGAAGAATAAG
                                 ||||    ||||||||||
                                 TGAG    TCTTCTTATTC
                                   TACCG
GAM76   KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                                 CCA    CAAGAAGAATAAG
                                 |||    ||||||||||||
                                 GGT    GTTCTTCTTATTC
                                   TTTCA
GAM76   OSBPL11   3'  CTTAATTTCCCAAGAGTGGTG  43206        CCAA   AA
                                 CACCACTC   GAAG  TAAG
                                 ||||||||   ||||  ||||
                                 GTGGTGAG   CTTT  ATTC
                                      AACC   A_
GAM76   YME1L1    3'  TCATTCTTGATGTGGTGTA   58438        TCC    _
                                 TACACCAC   CAAGAA GA
                                 ||||||||   ||||||  ||
                                 ATGTGGTG   GTTCTT CT
                                      TA_     A
GAM76   ZNF262    3'  CTTATTTTGTTTGGGAGT    18723         A
                                 ACTCCCAAG AGAATAAG
                                 |||||||||  ||||||||
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                                TGAGGGTTT TTTTATTC
                                     G
GAM76   LOC91960 3'  TGTGGCTTGGAACGTGGTGTA  68294       TC_    AAGA
                                TACACCAC  CCAAG   ATA
                                ||||||||  |||||   |||
                                ATGTGGTG  GGTTC   TGT
                                     CAA    GG__
GAM77   CCR2     5'  CTGAGACAAGCCACAAGC    7219     C  AT   TC
                                GC TG  GTT  TGTCTCAG
                                || ||  |||  ||||||||
                                CG AC  CGA  ACAGAGTC
                                 A  AC  __
GAM77   CCR2     5'  CTGAGACAAGCCACAAGC    7221     C  AT   TC
                                GC TG  GTT  TGTCTCAG
                                || ||  |||  ||||||||
                                CG AC  CGA  ACAGAGTC
                                 A  AC  __
GAM77   DGAT2    5'  AGAAAGGGAATCAGGCAG    51773        G TT  G
                                CTGCCTGAT T  CT TCT
                                ||||||||| |  || |||
                                GACGGACTA A  GA AGA
                                     _ GG  A
GAM77   GARP     3'  TCTGAGACATTTCCAAGCAG   19787     C  ATGTTTC
                                CTGC TG      TGTCTCAGA
                                |||| ||      |||||||||
                                GACG AC      ACAGAGTCT
                                  A  CTTT___
GAM77   GAS7     3'  TCTGAAACAAACAGAGGCTGG  20860    T   GA   TC   C
                                CC GCCT  TGTT  TGT TCAGA
                                || ||||  ||||  ||| |||||
                                GG CGGA  ACAA  ACA AGTCT
                                 T   G_   __   A
GAM77   GAS7     3'  TCTGAAACAGACAGAGGCTGG  14670    T   GA  TT    C
                                CC GCCT  TG  TCTGT TCAGA
                                || ||||  ||  ||||| |||||
                                GG CGGA  AC  AGACA AGTCT
                                 T   G_ __    A
GAM77   GUCY2C   3'  CTGAGACCTCAATGAAGCAG   18300     CTGA   TCT
                                CTGC   TGTT   GTCTCAG
                                ||||   ||||  |||||||
                                GACG   GTAA   CAGAGTC
                                  AA__   CTC
GAM77   IL1RAP   5'  CTAAGAACTAGAACATCAGCAG 10986      C      CT  _  C
           G                     CCTGC TGATGTTT  GT CT AG
                                ||||| ||||||||  || || ||
                                GGACG ACTACAAG  CA GA TC
                                  _      AT  A  A
GAM77   MAPK14   3'  TCTGAGAGTTGGCTCAGGCAG  8982         T   TCTG
                                CTGCCTGA GTT    TCTCAGA
                                |||||||| |||   |||||||
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                              GACGGACT CGG   AGAGTCT
                                  _  TTG_
GAM77   MAPK14   3' TCTGAGAGTTGGCTCAGGCAG 58128       T  TCTG
                              CTGCCTGA GTT   TCTCAGA
                              |||||||| |||   |||||||
                              GACGGACT CGG   AGAGTCT
                                  _  TTG_
GAM77   MAPK14   3' TCTGAGAGTTGGCTCAGGCAG 58134       T  TCTG
                              CTGCCTGA GTT   TCTCAGA
                              |||||||| |||   |||||||
                              GACGGACT CGG   AGAGTCT
                                  _  TTG_
GAM77   PKD2L1   3' CTGAAGGGAATCAGGCA    32768       G TT  GTC
                              TGCCTGAT T  CT   TCAG
                              |||||||| |  ||   ||||
                              ACGGACTA A  GA   AGTC
                                  _ GG  ___
GAM77   RAB33A   5' GGGCGCACACAGGCAG     17741       A  TTC
                              CTGCCTG TGT   TGTCT
                              ||||||| |||   |||||
                              GACGGAC ACA   GCGGG
                                  _  C__
GAM77   TTC3     5' AGACAGAAACACACTGAG    13878    GCC  A
                              CT   TG TGTTTCTGTCT
                              ||   || ||||||||||
                              GA   AC ACAAAGACAGA
                               GTC  _
GAM77   VEGFB    3' CTGAGGCCATCATCAAACAGG  14048     CC    TTTCT
                              CCTG  TGATG    GTCTCAG
                              ||||  |||||    |||||||
                              GGAC  ACTAC    CGGAGTC
                                AA    TAC__
GAM77   XBP1     3' TCTGAGACAGAGAGCCAAGC   18678    C  ATG
                              GC TG   TTTCTGTCTCAGA
                              || ||   ||||||||||||
                              CG AC   AGAGACAGAGTCT
                               A  CG_
GAM77   C8orf6   3' TCTGGTTTCAGAAACATCAGAG 90785     GC         TC_
           AGG                  CCT  CTGATGTTTCTG   TCAGA
                              |||  ||||||||||||   |||||
                              GGA  GACTACAAAGAC   GGTCT
                                GA          TTT
GAM77   CGRP-RCP 3' CTGAGACAGCAGCCCAGGGCAG 27889       GAT   T
           G                   CCTGCCT   GTT CTGTCTCAG
                              |||||||   ||| |||||||||
                              GGACGGG   CGA GACAGAGTC
                                  ACC   C
GAM77   CREB-H   3' CTGAAAGAGACCCAGACAG   51872     C   AT     GTC
                              CTG CTG  GTTTCT   TCAG
                              ||| |||  ||||||   ||||
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                                GAC GAC  CAGAGA   AGTC
                                  A   C_     A__
GAM77   DKFZp434O0515 5'  CTGAAACAGTTCTTCAGACAGG 66510      C    TGTTT    C
                                CCTG CTGA     CTGT TCAG
                                |||| ||||     |||| ||||
                                GGAC GACT     GACA AGTC
                                  A    TCTT_    A
GAM77   FLJ11506  3'  CTGAAACAGATGGCAGAAGG   45434     GA    _     C
                                CCT  TGTT TCTGT TCAG
                                |||  |||| ||||| ||||
                                GGA  ACGG AGACA AGTC
                                  AG    T     A
GAM77   IL14     5'  TCTGAGCCTCAAATCAGACAG  97165     C     GTTTCT T
                                CTG CTGAT     G CTCAGA
                                ||| |||||     | ||||||
                                GAC GACTA     C GAGTCT
                                  A     AACTC_ _
GAM77   KIAA0683  3'  TCTGAGAGCCACCAAGCAGG   32766      C  A  TTTCTG
                                CCTGC TG TG      TCTCAGA
                                ||||| || ||      |||||||
                                GGACG AC AC      AGAGTCT
                                   A  C  CG_____
GAM77   KIAA1131  5'  CTGAGACAGAAACCAAG     62523     GAT
                                CT   GTTTCTGTCTCAG
                                ||   ||||||||||||||
                                GA   CAAAGACAGAGTC
                                 AC_
GAM77   KIAA1513  5'  TCTTGGTCAAGACACCAGGCAG 69099         A     C  T  C
            G                    CCTGCCTG TGTTT TG CT AGA
                                ||||||||| ||||| || || |||
                                GGACGGAC ACAGA AC GG TCT
                                     C     _  T  T
GAM77   MGC20470  5'  CTGAGACAAAGGCCAGCAG    59603      C  AT    C
                                CTGC TG  GTTT TGTCTCAG
                                ||||  ||  ||||  ||||||||
                                GACG AC  CGGA ACAGAGTC
                                  _  __    A
GAM77   ORF1-FL49 5'  CTGAGACAGGTGCGGCA     51566      TGAT  T
                                TGCC    GT TCTGTCTCAG
                                ||||    || ||||||||||
                                ACGG    CG GGACAGAGTC
                                  _____  T
GAM77   PDGFC     3'  TCTGAAAGAGGAGACATCAAAC 33023     CC         GTC_
            AG                    CTG  TGATGTTTCT    TCAGA
                                |||  ||||||||||    |||||
                                GAC  ACTACAGAGG    AGTCT
                                  AA         AGAA
GAM77   RGS17     3'  TCTAAGACAGAAAAAAAGCA   25773     CTGATG        C
                                TGC      TTTCTGTCT AGA
                                |||      ||||||||| |||
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                                ACG      AAAGACAGA TCT
                                  AAAA__         A
GAM77   RHOBTB2   3'  CTGAAACAAAGGTAGTAGGCAG 61597         A  TT C   C
              G                    CCTGCCTG TG  T TGT TCAG
                                   |||||||| ||  | ||| ||||
                                   GGACGGAT AT  A ACA AGTC
                                       G  GG A   A
GAM77   SNRK      3'  TCTGAGACAGAACCAAAGCA   35283     CTGA  T
                                   TGC    TG TTCTGTCTCAGA
                                   |||    || ||||||||||||
                                   ACG    AC AAGACAGAGTCT
                                     AA__  C
GAM77   ZDHHC9    3'  CTGAGACAGAGAGCAAGTA    62354     C  ATG
                                   TGC TG   TTTCTGTCTCAG
                                   ||| ||   ||||||||||||
                                   ATG AC   AGAGACAGAGTC
                                     A  G__
GAM77   LOC116113 3'  CTGAGACAGAACCAGGC     93837       ATGT
                                   GCCTG    TTCTGTCTCAG
                                   |||||    ||||||||||||
                                   CGGAC    AAGACAGAGTC
                                      C___
GAM77   LOC132228 3'  CTGAGACAGGACAGGAAGG    75545     G    ATGT
                                   CCT CCTG    TTCTGTCTCAG
                                   ||| ||||    ||||||||||||
                                   GGA GGAC    AGGACAGAGTC
                                     A   _____
GAM77   LOC148113 3'  TCCGATGGTAGAAACACCAGGA 79376    G    A      GT _  A
              AG                     CT CCTG TGTTTCT  C TC GA
                                     || |||| |||||||  | || ||
                                     GA GGAC ACAAAGA  G AG CT
                                      A    C       TG T  C
GAM77   LOC149072 5'  AGACAGAAACTCAAGCAGG    79885       C   T
                                   CCTGC TGA GTTTCTGTCT
                                   ||||| ||| ||||||||||
                                   GGACG ACT CAAAGACAGA
                                      A  _
GAM77   LOC151171 5'  ACAGAACATCAGGCAGG      80942            T
                                   CCTGCCTGATGTT CTGT
                                   |||||||||||| ||||
                                   GGACGGACTACAA GACA
                                                _
GAM77   LOC151446 3'  TCCAAGACAGAACAAAGCA    86574     CTGA   T     CA
                                   TGC    TGTT CTGTCT  GA
                                   |||    |||| ||||||  ||
                                   ACG    ACAA GACAGA  CT
                                     AA__    _      AC
GAM77   LOC152445 5'  CTGAGACAGAGGTCCCAGGAG  86946    G    AT TT
                                   CT CCTG  G  TCTGTCTCAG
                                   || ||||  |  ||||||||||
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                                GA GGAC  T  AGACAGAGTC
                                 _   CC GG
GAM77   LOC159065 3'  GACAGAACATCAAACAG     82956     CC      T
                                CTG  TGATGTT CTGTC
                                |||  ||||||| |||||
                                GAC  ACTACAA GACAG
                                  AA      _
GAM77   LOC164714 5'  GAGACAGGCAGCCCAGGCCGG  88582    T     AT   _
                                CC GCCTG  GTT TCTGTCTC
                                || |||||  ||| ||||||||
                                GG CGGAC  CGA GGACAGAG
                                 C     C_  C
GAM77   LOC165476 5'  GAGACAGAGAAGGGAG      88552    G   GATG
                                CT CCT    TTTCTGTCTC
                                || |||    ||||||||||
                                GA GGA    AGAGACAGAG
                                 G  _____
GAM77   LOC201549 5'  ACAGAAACCCAGACAGG     91820      C   AT
                                CCTG CTG  GTTTCTGT
                                |||| |||  ||||||||
                                GGAC GAC  CAAAGACA
                                  A  C_
GAM77   LOC254055 5'  CTGGAGAGAAACATCAGTCA   98107    C         G  T
                                TG CTGATGTTTCT TC CAG
                                || |||||||||| || |||
                                AC GACTACAAAGA AG GTC
                                 T          G  _
GAM78   ADRA1A    3'  CAATCAAAGAGGGGACCTG    7287      C    GG       C
                                CAG GTTC  CTCTTTGA TG
                                ||| ||||  |||||||| ||
                                GTC CAGG  GAGAAACT AC
                                  _   G_       A
GAM78   CPNE7     5'  CCAGCCGGGCCCCCGAACGC   27790         CTC    A
                                GCGTTCGG   TTTG CTGG
                                ||||||||   |||| ||||
                                CGCAAGCC   GGGC GACC
                                     CCC    C
GAM78   HOXD4     3'  CCAGGCTGAGCCGAAGCTG    28255      G       TTTGA
                                CAGC TTCGGCTC     CTGG
                                |||| ||||||||     ||||
                                GTCG AAGCCGAG     GACC
                                  _       TCG__
GAM78   SMURF1    3'  CCAGTCAGTCCCAAAGCTGTG  94045       GTTC  CTCT
                                CACAGC    GG    TTGACTGG
                                ||||||    ||    ||||||||
                                GTGTCG    CC    GACTGACC
                                   AAA_  CT__
GAM78   KIAA0997  5'  CCAGCCCGAGCGCCGAGCGC   30886         T   TGA
                                GCGTTCGGC CTT   CTGG
                                ||||||||| |||   ||||
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                                CGCGAGCCG GAG   GACC
                                     C   CCC
GAM78   KIAA1870  3'  CCAACCAAAGAGCCAGC     50581     C       AC
                                GTT GGCTCTTTG  TGG
                                ||| |||||||||  |||
                                CGA CCGAGAAAC  ACC
                                  _       CA
GAM78   LOC122792 3'  CAGTAAAAGCCAAACGTTGT   59821        C   C   A
                                ACAGCGTT GGCT TTTG CTG
                                |||||||| |||| |||| |||
                                TGTTGCAA CCGA AAAT GAC
                                     A   _   _
GAM79   ADAMTS13  3'  GTCCCCCAAAACGTGCATGGA  58156    G      CC   A
                                TC GTGTACGT  TGG GGAC
                                || ||||||||  ||| ||||
                                AG TACGTGCA  ACC CCTG
                                 G       AA   C
GAM79   ETS2      5'  CCTCGCCCGGCGCGCACCGAG  19117       TA   CTG_
                                CTCGGTG  CGTC   GAGG
                                |||||||  ||||   ||||
                                GAGCCAC  GCGG   CTCC
                                    GC   CCCG
GAM79   PAX5      3'  CCTCCAGGACCCCAGCAAGTG  34126     CG  GTAC
                                CACT  GT   GTCCTGGAGG
                                ||||  ||   ||||||||||
                                GTGA  CG   CAGGACCTCC
                                  A_  ACCC
GAM79   POLA      3'  GTCCAACAGACACACACTGAG  34199       AC   C  GA
                                CTCGGTGT  GTC TG  GGAC
                                ||||||||  ||| ||  ||||
                                GAGTCACA  CAG AC  CCTG
                                     CA   _  AA
GAM79   RBP3      3'  CCTCTGGGACACACACCAAG   12794    C    AC    TG
                                CT GGTGT  GTCC  GAGG
                                || |||||  ||||  ||||
                                GA CCACA  CAGG  CTCC
                                 A    CA    GT
GAM79   SCA1      3'  GTCCTCCAGAATACCAAGT    6184     C    ACGTC
                                ACT GGTGT    CTGGAGGAC
                                ||| |||||    |||||||||
                                TGA CCATA    GACCTCCTG
                                  A    A____
GAM79   SLC1A3    3'  GTCCTCCAAAACACAAGGGAG  16064    GG_  AC  CC
                                CTC   TGT  GT  TGGAGGAC
                                |||   |||  ||  ||||||||
                                GAG   ACA  CA  ACCTCCTG
                                  GGA   __  AA
GAM79   UBASH3A   3'  CCTGCAGCATGTACACCGAGTG 39048           C   G
                                CACTCGGTGTACGT CTG AGG
                                |||||||||||||| ||| |||
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                                GTGAGCCACATGTA GAC TCC
                                       C   G
GAM79   USH3A    3'  GTCCTCCAGAAAGCACCAAG   54843    C    ACG  C
                                CT GGTGT   TC TGGAGGAC
                                || |||||   || ||||||||
                                GA CCACG   AG ACCTCCTG
                                 A    AA_ _
GAM79   AGS3     5'  GTCCTCCAGGATCGATGACC   73512    GTA  _
                                GGT   CG TCCTGGAGGAC
                                |||   || ||||||||||
                                CCA   GC AGGACCTCCTG
                                  GTA  T
GAM79   C1orf34  3'  GTCCTCCACACCACACCCAGTG 61318     C    AC  CC
                                CACT GGTGT  GT  TGGAGGAC
                                |||| |||||  ||  ||||||||
                                GTGA CCACA  CA  ACCTCCTG
                                  C    C_  C_
GAM79   FLJ21034 3'  CCTCCCTGCAACACCGAGTG   46863         AC  CCT
                                CACTCGGTGT  GT   GGAGG
                                ||||||||||  ||   |||||
                                GTGAGCCACA  CG   CCTCC
                                     A_  TC_
GAM79   IDN3     3'  GTCTATTAAATGTACACCAAGT 56759     C       CC   A
                                ACT GGTGTACGT  TGG GGAC
                                ||| |||||||||  ||| ||||
                                TGA CCACATGTA  ATT TCTG
                                  A       A_   A
GAM79   KIAA1028 3'  TCCTCCAGGACATAGCCAG   93592    C   GTAC
                                CT GGT    GTCCTGGAGGA
                                || |||    ||||||||||
                                GA CCG    CAGGACCTCCT
                                 _   ATA_
GAM79   KIAA1750 3'  TCCTCCAGGACGACCAGTG   68811     C   GTA
                                CACT GGT   CGTCCTGGAGGA
                                |||| |||   ||||||||||||
                                GTGA CCA   GCAGGACCTCCT
                                  _   ___
GAM79   RDH-E2   3'  CCTGGATACGCAGACCGAGTG  58069        __  AC    T
                                CACTCGGT  GT  GTCC GG
                                ||||||||  ||  |||| ||
                                GTGAGCCA  CG  TAGG CC
                                     GA  CA    T
GAM79   LOC149076 3'  CCTCCAGGAACCACCAAG    79876    C    TACG
                                CT GGTG    TCCTGGAGG
                                || ||||    |||||||||
                                GA CCAC    AGGACCTCC
                                 A    CA__
GAM79   LOC255652 3'  CCTCCAGGACTGCCACAGAG   98529     G   _  C
                                CTC GTG TA GTCCTGGAGG
                                ||| ||| || ||||||||||
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                                GAG CAC GT CAGGACCTCC
                                  A   C  _
GAM80   GALNT2   3'  CTGGCCAGAGTCTGTCCTGGTG 16815        GGT   CC   A
                                CACCGGGA   GAC  CTG CCAG
                                ||||||||   |||  ||| ||||
                                GTGGTCCT   CTG  GAC GGTC
                                    GT_   A_   C
GAM80   IL6      3'  CTGGTCAGAAACCTGTCC    7007     _   GACCC
                                GGG AGGT    CTGACCAG
                                ||| ||||    ||||||||
                                CCT TCCA    GACTGGTC
                                  G   AA___
GAM80   MYO1D    3'  AGCTGGACCACCTCCCGCTG   72240    C       AC _____
                                CA CGGGAGGTG  CC    CT
                                || |||||||||  ||    ||
                                GT GCCCTCCAC  GG    GA
                                 C        CA  TC___
GAM80   OTX1     3'  GGCCAGAGCCTCCCGGCG    28056   A       GACCC   A
                                C CCGGGAGGT    CTG CC
                                | |||||||||    ||| ||
                                G GGCCCTCCG    GAC GG
                                 C        A____   C
GAM80   PNUTL1   3'  CTGGGCGGTGAGCCACCTCCTG 12190         ACCC_   A
           G                     CCGGGAGGTG    CTG CCAG
                                ||||||||||    ||| ||||
                                GGTCCTCCAC    GGC GGTC
                                      CGAGT   G
GAM80   PTPN14   3'  CTGGAGGAGAGTCACCTCC   19428        C__   GA
                                GGAGGTGAC   CCT  CCAG
                                |||||||||   |||  ||||
                                CCTCCACTG   GGA  GGTC
                                     AGA   __
GAM80   RASD1    3'  CTGGCGTCTCCCCTCCCGG   32727       T  CCCC  A
                                CCGGGAGG GA    TG CCAG
                                |||||||| ||    || ||||
                                GGCCCTCC CT    GC GGTC
                                    C  CT__  _
GAM80   SFTPA2   3'  TGGTCAGGCTCTCCAGGTG   23631     G    TGACC
                                CACC GGAGG    CCTGACCA
                                |||| |||||    ||||||||
                                GTGG CCTCT    GGACTGGT
                                  A    C____
GAM80   TAZ      5'  GTCAGGGGCCAGTGTCTCG   5485       G _  A
                                CGGGA G TG CCCCTGAC
                                ||||| | || ||||||||
                                GCTCT T AC GGGGACTG
                                   G G  C
GAM80   CST8     5'  CTGGTCAGGTCAGCTCCC    19713      G    CC
                                GGGAG TGACC  TGACCAG
                                ||||| |||||  |||||||
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                                CCCTC ACTGG  ACTGGTC
                                  G    __
GAM80   DKFZp434J0226 3' GTCACCGGCCACCTCCCAGG  72794   _      A  CC
                                CC GGGAGGTG CC  TGAC
                                || |||||||| ||  ||||
                                GG CCCTCCAC GG  ACTG
                                 A       C  CC
GAM80   FKSG28   3' CTGGCCAGTAGGACCTCC   48908      GA  C_  A
                                GGAGGT  CC  CTG CCAG
                                ||||||  ||  ||| ||||
                                CCTCCA  GG  GAC GGTC
                                   __ AT   C
GAM80   GAB3     3' GTCAGGGGTCGTCCAGTG   55522    CG   GG
                                CAC  GGA  TGACCCCTGAC
                                |||  |||  ||||||||||
                                GTG  CCT  GCTGGGGACTG
                                 A_  __
GAM80   KIAA0415 3' TCGGGATCACTTCCCAGTG   94170    C       CC
                                CAC GGGAGGTGA  CCTGA
                                ||| |||||||||  |||||
                                GTG CCCTTCACT  GGGCT
                                 A       A_
GAM80   KIAA0420 3' GTCAGGGGTCACCAACTTG   64093     A_
                                CGGG  GGTGACCCCTGAC
                                ||||  ||||||||||||
                                GTTC  CCACTGGGGACTG
                                  AA
GAM80   KIAA0495 5' CTGGCCTCGGTCACCTCCCGG  63265           CCTGA
                                CCGGGAGGTGACC    CCAG
                                ||||||||||||    ||||
                                GGCCCTCCACTGG    GGTC
                                       CTCC_
GAM80   KIAA0652 3' CGGGGGCAAAGTCACCTCCCAG 29122     C       _____
           TG                   CAC GGGAGGTGA    CCCCTG
                                ||| |||||||||    ||||||
                                GTG CCCTCCACT    GGGGGC
                                 A       GAAAC
GAM80   KIAA0876 3' CTGGCCAGGGGAAGCCCGG   65316      AGGTGA    A
                                CCGGG     CCCCTG CCAG
                                |||||     |||||| ||||
                                GGCCC     GGGGAC GGTC
                                  GAA___     C
GAM80   KIAA1396 3' CTGACGGGGAGACACCTCCC  63669        AC_    AC
                                GGGAGGTG   CCCTG  CAG
                                ||||||||   |||||  |||
                                CCCTCCAC   GGGGC  GTC
                                    AGA    A_
GAM80   KIAA1755 3' CTGGCCAGAGTGGCCCCTG   62013     A  G  CC   A
                                CGGG GGT AC  CTG CCAG
                                |||| ||| ||  ||| ||||
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                                GTCC CCG TG  GAC GGTC
                                  _  G A_  C
GAM80   KIAA1958  3'  CTGACCAGGTGTGACCTCCCGG 82782        G  C   AC
            T                    ACCGGGAGGT AC CCTG  CAG
                                 |||||||||| || ||||  |||
                                 TGGCCCTCCA TG GGAC  GTC
                                       G  T   CA
GAM80   KIF13B   3'  CTGACCAGCAGACTCACCTCCC 31560       CCC__  AC
                                 GGGAGGTGA    CTG  CAG
                                 |||||||||    |||  |||
                                 CCCTCCACT    GAC  GTC
                                       CAGAC   CA
GAM80   KIF13B   3'  CTGACCAGCAGACTCACCTCCC 31561       CCC__  AC
                                 GGGAGGTGA    CTG  CAG
                                 |||||||||    |||  |||
                                 CCCTCCACT    GAC  GTC
                                       CAGAC   CA
GAM80   KRT6     3'  GTCAGGAGCTCTCTCAGTG   83096    C   _ GACC
                                 CAC GGGAG GT   CCTGAC
                                 ||| ||||| ||   ||||||
                                 GTG CTCTC CG   GGACTG
                                   A    T A___
GAM80   MGC7036  3'  CTGGCAAAACCACCTCCCTGTG 59617    C      ACCCC  A
                                 CAC GGGAGGTG    TG CCAG
                                 ||| ||||||||    || ||||
                                 GTG CCCTCCAC    AC GGTC
                                   T      CAAA_ _
GAM80   PLSCR2   5'  TCAAATTCACCTCCCAGTG   40150    C      CCCC
                                 CAC GGGAGGTGA   TGA
                                 ||| |||||||||   |||
                                 GTG CCCTCCACT   ACT
                                   A       TAA_
GAM80   SYNGR4   5'  TGGCTCCCACCTCCCAGTG   25865    C      ACCCCT  _
                                 CAC GGGAGGTG    GA CCA
                                 ||| ||||||||    || |||
                                 GTG CCCTCCAC    CT GGT
                                   A      C_____  C
GAM80   LOC115399 3'  CTGGTCCCTTCACCTCCC    73814        CCCCT
                                 GGGAGGTGA    GACCAG
                                 |||||||||    ||||||
                                 CCCTCCACT    CTGGTC
                                       TCC__
GAM80   LOC129450 5'  CGGGCAGCACCTCCCGGT    75380         ACC
                                 ACCGGGAGGTG  CCTG
                                 ||||||||||  ||||
                                 TGGCCCTCCAC  GGGC
                                       GAC
GAM80   LOC146332 3'  CTGGGGAGGGGGGTCACCTCC  78356          GA__
                                 GGAGGTGACCCCT   CCAG
                                 ||||||||||||   ||||
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                                CCTCCACTGGGGG  GGTC
                                     GAGG
GAM80   LOC147160 5'  CTGGCCAGAAATCCCCACTTCC 85076       ACCC___  A
          C                    GGGAGGTG     CTG CCAG
                               ||||||||     ||| ||||
                               CCCTTCAC     GAC GGTC
                                    CCCTAAA  C
GAM80   LOC151009 3'  CTGGTCAACCTGCAACCTCCTG 86369       GACCCC_
                               CGGGAGGT     TGACCAG
                               ||||||||     |||||||
                               GTCCTCCA     ACTGGTC
                                    ACGTCCA
GAM80   LOC160646 3'  AGTGGTCACCTCCCCGTG   83105   C       C
                               CAC GGGAGGTGACC CT
                               ||| ||||||||||| ||
                               GTG CCCTCCACTGG GA
                                 C         T
GAM80   LOC257354 3'  GTCAGGGGTCACCAACTTG  96795    A_
                               CGGG  GGTGACCCCTGAC
                               ||||  ||||||||||||||
                               GTTC  CCACTGGGGACTG
                                 AA
GAM80   LOC57406  5'  CTGGTCAGGAGTCAGCCAGCC  40716   GA _   C
                               GG  GG TGAC CCTGACCAG
                               ||  || |||| |||||||||
                               CC  CC ACTG GGACTGGTC
                                GA  G   A
GAM81   SCAMP1    3'  GCTAAATAAATATTCTCC   54500    T    C
                               GGA AATATT ATTTAGC
                               ||| |||||| |||||||
                               CCT TTATAA TAAATCG
                                 C     A
GAM81   SCAMP1    3'  GCTAAATAAATATTCTCC   54501    T    C
                               GGA AATATT ATTTAGC
                               ||| |||||| |||||||
                               CCT TTATAA TAAATCG
                                 C     A
GAM81   NX-17     3'  TGAATATCAGCCCCTAATA   40706       ATA_
                               TATTAGGG   ATATTCA
                               ||||||||   |||||||
                               ATAATCCC   TATAAGT
                                    CGAC
GAM81   LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
          TA                    TATTAGGGATAATATTCATTTAGC
                               |||||||||||||||||||||||
                               ATAATCCCTATTATAAGTAAATCG

GAM82   ATP1B2    3'  CTCCTCTCCATCCCTATTCCCT 9832      TCCTTA_  A
          C                    GAGG     GAT GAGAGGAG
                               ||||      ||| ||||||||
```

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                                CTCC      CTA CTCTCCTC
                                  CTTATCC   C
GAM82   AXL     5'  TCTCCTCTCTTGAGTTAACCCC 41895    A  C__   GAT
              T                   AG GGT   CTTA   AGAGAGGAGA
                                  || |||   ||||  ||||||||||
                                  TC CCA   GAGT   TCTCTCCTCT
                                   C   ATT   ___
GAM82   CD1D    3'  TCTCTGGAACCCAGGACCTCT  80271         TAGA__
                                  AGAGGTCCT     TAGAGA
                                  |||||||||     ||||||
                                  TCTCCAGGA     GTCTCT
                                       CCCAAG
GAM82   CD5     3'  CCTCATCTAAAGACACCT    27220    AG   C     AGA
                                  AG  GTC TTAGAT   GAGG
                                  ||  ||| ||||||   ||||
                                  TC  CAG AATCTA   CTCC
                                   CA   A     ___
GAM82   COL2A1   5'  CTCCTCCTGCTCCAAGGGCCTC 10241         A  _   A
                                  GAGGTCCTT GA TAG GAGGAG
                                  ||||||||| || ||| ||||||
                                  CTCCGGGAA CT GTC CTCCTC
                                       C  C   _
GAM82   GPR56   3'  CTCCTCTCCCAGGGCCTC    20272         TAGATA
                                  GAGGTCCT     GAGAGGAG
                                  ||||||||     ||||||||
                                  CTCCGGGA     CTCTCCTC
                                       CC____
GAM82   GRAF    3'  CCTCCCAGGCTAGGAACCTCT  31232       C     ATAGA
                                  AGAGGT CTTAG     GAGG
                                  |||||| |||||     ||||
                                  TCTCCA GGATC     CTCC
                                     A     GGACC
GAM82   KRTHB6   5'  CTCCATCCTCAGAACCTC    11250      C  T  ATA  GA
                                  GAGGT CT AG   GA  GGAG
                                  ||||| || ||   ||  ||||
                                  CTCCA GA TC   CT  CCTC
                                     A  C  ___  A_
GAM82   LFG     3'  CTCCTCTCCTCCGGGCCCCT   77234    A    TT  ATA
                                  AG GGTCC  AG   GAGAGGAG
                                  || |||||  ||   ||||||||
                                  TC CCGGG  TC   CTCTCCTC
                                   C     CC  ___
GAM82   MEF2D    5'  CTCCCCTCCGTAGCACTGAGGA 20982          ____ TA   A
              CC                    GGTCCTTAG    A  GAG GGAG
                                  |||||||||    |  ||| ||||
                                  CCAGGAGTC    T  CTC CCTC
                                       ACGA GC   C
GAM82   NR1D1    3'  CTCCTCCCCTATTTAAACC   41668     CC       A_
                                  GGT  TTAGATAG  GAGGAG
                                  |||  ||||||||  ||||||
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                                CCA  AATTTATC  CTCCTC
                                  __       CC
GAM82   PBX2     3'  TCCCCTCCCTAACGAGACTCTC 11982      _   C  AGA   A    A
            T                    AGAG GTC TT   TAG GAGG GA
                                 |||| ||| ||   ||| |||| ||
                                 TCTC CAG AG   ATC CTCC CT
                                   T   _  CA_   C    C
GAM82   RTN3     3'  TCCCCTCCAAAGGACCTT    74331         AGATA   A
                                 GAGGTCCTT    GAG GGA
                                 |||||||||    ||| |||
                                 TTCCAGGAA    CTC CCT
                                      AC___   C
GAM82   SH2D1A   5'  TCCCCTCTCTGTATGAACCCT  11406    A   CC   G       A
                                 AG GGT  TTA ATAGAGAGG GA
                                 || |||  ||| |||||||||  ||
                                 TC CCA  AGT TGTCTCTCC CT
                                  _   __   A        C
GAM82   SOX9     5'  CTCCTCTCCAATTCGCCTC   6230       CCTTA  TA__
                                 GAGGT    GA    GAGAGGAG
                                 |||||    ||    ||||||||
                                 CTCCG    CT    CTCTCCTC
                                    _____  TAAC
GAM82   TACC1    3'  CTCCTCTCAAAGGATCTC    21870         AGATA
                                 GAGGTCCTT    GAGAGGAG
                                 |||||||||    ||||||||
                                 CTCTAGGAA    CTCTCCTC
                                      A____
GAM82   TFEB     3'  CTCCTCCCCGTTGGCCCCT   93751    A   CTTA   AGA
                                 AG GGTC    GAT   GAGGAG
                                 || ||||    |||   ||||||
                                 TC CCGG    TTG   CTCCTC
                                  C    _____   CCC
GAM82   CGB2     3'  CTCCTCTTCCTCAAAGGCCCCT 54131    A  T    A  TA
                                 AG GG CCTT GA  GAGAGGAG
                                 || || |||| ||  ||||||||
                                 TC CC GGAA CT  TTCTCCTC
                                  C  _    A  CC
GAM82   DKFZp434A1010 3'  CTCCTCTCCCTCCAGGAGCC   71855    TC   A  TA
                                 GG  CTT GA  GAGAGGAG
                                 ||  ||| ||  ||||||||
                                 CC  GGA CT  CTCTCCTC
                                  GA   C  CC
GAM82   DKFZp434G179 3'  CCTCCCCGTTAGGACCTC    80892         TA   AGA
                                 GAGGTCCT  GAT   GAGG
                                 ||||||||  |||   ||||
                                 CTCCAGGA  TTG   CTCC
                                      __   CCC
GAM82   DKFZp434I1930 3'  CTCCTCCCTTCGGCCTCT    51042       CTTA  T  A
                                 AGAGGTC    GA AG GAGGAG
                                 |||||||    || || ||||||
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                                TCTCCGG   CT TC CTCCTC
                                   _____ _  C
GAM82   DKFZP434M154 3'  CTCCTCCTTGAGAAGGGACCTC 72796         AGAT_  A
                                GAGGTCCTT    AG GAGGAG
                                |||||||||    || ||||||
                                CTCCAGGGA    TC CTCCTC
                                     AGAGT  _
GAM82   ERAF     3'  CTCCTCTCTGAGAAACTCT   34040     GTC   AGAT
                                AGAG   CTT   AGAGAGGAG
                                ||||   |||   |||||||||
                                TCTC   GAG   TCTCTCCTC
                                  AAA  _____
GAM82   FLJ21478  3'  CTCCTCTCAAAGAGCCTCT   45196      TC   AGATA
                                AGAGG  CTT    GAGAGGAG
                                |||||  |||    ||||||||
                                TCTCC  GAA    CTCTCCTC
                                   GA   A_____
GAM82   FREQ     3'  CTCCTCTCCCCAGGCCTCT   27371      T   TAGATA
                                AGAGG CCT     GAGAGGAG
                                ||||| |||     ||||||||
                                TCTCC GGA     CTCTCCTC
                                   _   CCC___
GAM82   HUMAGCGB  3'  TCCCTCTCTACCCTACC     26135     CCTT  A_      A
                                GGT    AG  TAGAGAGG GA
                                |||    ||  |||||||| ||
                                CCA    TC  ATCTCTCC CT
                                  _____ CC       C
GAM82   KIAA1649  5'  TCCCCTCCCCATCTAAGGA   51250         AGA    A
                                TCCTTAGAT   GAGG GA
                                |||||||||   |||| ||
                                AGGAATCTA   CTCC CT
                                     CCC    C
GAM82   MGC2705   3'  TCTCCTAGCTGCTACCCAGGAC 52083         ___   A   AG
          CTC                     GAGGTCCT   TAG TAG  AGGAGA
                                |||||||||   ||| |||  ||||||
                                CTCCAGGA   ATC GTC  TCCTCT
                                     CCC   _   GA
GAM82   PRO2325   3'  TCTCCTCTCCCTTAAAGCCCT  98041     TC   A  TA
                                AGG  CTT GA  GAGAGGAGA
                                |||  ||| ||  |||||||||
                                TCC  GAA TT  CTCTCCTCT
                                  C_   A  CC
GAM82   TADA3L    3'  CTCCCCTTCAAGGACTTCT    22039         A  TAG  A
                                AGAGGTCCTT GA   AG GGAG
                                |||||||||| ||   || ||||
                                TCTTCAGGAA CT   TC CCTC
                                     _  ___  C
GAM82   TUSP     3'  CTCCCCTCTACCCAGGGGCCT  40023         AGA    A
                                AGGTCCTT   TAGAG GGAG
                                ||||||||   ||||| ||||
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                                TCCGGGGA   ATCTC CCTC
                                     CCC     C
GAM82   LOC112616 3'  TCTCCTCTCCATCTCTGCCTTT 57298       CCTT    A
                                AGAGGT    AGAT GAGAGGAGA
                                ||||||    |||| |||||||||
                                TTTCCG    TCTA CTCTCCTCT
                                   TC__    C
GAM82   LOC124944 5'  CCTCCTCTATTTAAAGACT    74834      C        _
                                GGTC TTAGATAGAG AGG
                                |||| |||||||||| |||
                                TCAG AATTTATCTC TCC
                                  A         C
GAM82   LOC126917 3'  CTCCTCTCCTCTGACCCCT    75089    A    CTT   TA
                                AG GGTC   AGA  GAGAGGAG
                                || ||||   |||  ||||||||
                                TC CCAG   TCT  CTCTCCTC
                                 C   ____   C_
GAM82   LOC145719 5'  CTCCTCTTCTCAGAGACCTC   84463       _ T   TAG
                                GAGGTC CT AGA   AGAGGAG
                                |||||| || |||   |||||||
                                CTCCAG GA TCT   TCTCCTC
                                   A  C   ___
GAM82   LOC145720 5'  CTCCTCTTCTCAGAGACCTC   84449       _ T   TAG
                                GAGGTC CT AGA   AGAGGAG
                                |||||| || |||   |||||||
                                CTCCAG GA TCT   TCTCCTC
                                   A  C   ___
GAM82   LOC146243 3'  TCTCCTCTCTTCCAAACCTC   84622      CC  A  T
                                GAGGT  TT GA AGAGAGGAGA
                                |||||  || || ||||||||||
                                CTCCA  AA CT TCTCTCCTCT
                                   __  C  _
GAM82   LOC150606 3'  TCTCCTCTCCTGTGGGACTCTC 86275      _    _   ATA
          T                     AGAG GTCCT TAG   GAGAGGAGA
                                |||| ||||| |||   |||||||||
                                TCTC CAGGG GTC   CTCTCCTCT
                                  T    T   ___
GAM82   LOC152667 3'  TCCCCTCTCTATCCAACC    81527     CCTTA        A
                                GGT     GATAGAGAGG GA
                                |||     |||||||||| ||
                                CCA     CTATCTCTCC CT
                                  AC___         C
GAM82   LOC152905 3'  TCCCCTCCAAAGGACCTT     61095         AGATA   A
                                GAGGTCCTT     GAG GGA
                                |||||||||     ||| |||
                                TTCCAGGAA     CTC CCT
                                      AC___   C
GAM82   LOC197114 5'  CTCCTCTTCTCAGAGACCTC   91269       _ T   TAG
                                GAGGTC CT AGA   AGAGGAG
                                |||||| || |||   |||||||
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                                CTCCAG GA TCT   TCTCCTC
                                   A  C  ___
GAM82   LOC199786 3'  CTCCTCTCCATCCGAGCCCCT  89750     TC  TA   A
                                AGG  CT  GAT GAGAGGAG
                                |||  ||  ||| ||||||||
                                TCC  GA  CTA CTCTCCTC
                                  CC  GC   C
GAM82   LOC205011 5'  TCTCCTCTTCCAAAGAACTCT  92332      GTC   AGATA
                                AGAG   CTT    GAGAGGAGA
                                ||||   |||    |||||||||
                                TCTC   GAA    TTCTCCTCT
                                  AA_   ACC__
GAM82   LOC220020 5'  CTCCTCTCCCAGCACCCCT   95044    A   C  TAGATA
                                AG GGT CT     GAGAGGAG
                                || ||| ||     ||||||||
                                TC CCA GA     CTCTCCTC
                                 C   C  CC____
GAM83   ANKTM1    3'  TATTGTATGAGCCTTTGTTTGA 24702         C    AC   _
           G                     CTCGAGCAA GGTT  CAT CAATG
                                |||||||| ||||  ||| |||||
                                GAGTTTGTT CCGA  GTA GTTAT
                                     T    __   T
GAM83   CADPS     3'  CATTGGTGGTAAATGGATGTGA 65822      AGCAA  G
           G                     CTCG    CG TTACCATCAATG
                                ||||    || ||||||||||||
                                GAGT    GT AATGGTGGTTAC
                                  GTAG_  A
GAM83   CUL4B     3'  TGTTGATTGTTTGCTTGAG    14567          _     C
                                CTCGAGCAA CGGTTA CA
                                |||||||| |||||| ||
                                GAGTTCGTT GTTAGT GT
                                     T     T
GAM83   KERA      3'  TGTTGGTGGTACAAGTTTGA   23847       AACG  T
                                TCGAGC    GT ACCATCAATG
                                ||||||    || ||||||||||
                                AGTTTG    CA TGGTGGTTGT
                                   AA__  _
GAM83   MEN1      5'  TGTTGGTTAAGTTGTTGCTTGG 56363         GG  __   T  ATG
                                TCGAGCAAC  TT  ACCA CA
                                |||||||||  ||  |||| ||
                                GGTTCGTTG  GA  TGGT GT
                                     TT  AT    T
GAM83   MYEOV     3'  CATTGGTGGTAGCCCCTGGAG  57844     G  CAAC
                                CTC AG    GGTTACCATCAATG
                                |||  ||    ||||||||||||||
                                GAG TC    CCGATGGTGGTTAC
                                  G  C___
GAM83   RAD18     3'  TGATGGTTGTTGCCCGAG     39804      A     GTT
                                CTCG GCAACG   ACCATCA
                                |||| ||||||   |||||||
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                                GAGC CGTTGT   TGGTAGT
                                  C     ___
GAM83   RAD51L3  3' ATGACCTGTGCTGTTGTTTGGG 56882          TACCA  ATG
                                CTCGAGCAACGGT    TCA
                                ||||||||||||    |||
                                GGGTTTGTTGTCG    AGT
                                       TGTCC   AC
GAM83   RAD51L3  3' ATGACCTGTGCTGTTGTTTGGG 56883          TACCA  ATG
                                CTCGAGCAACGGT    TCA
                                ||||||||||||    |||
                                GGGTTTGTTGTCG    AGT
                                       TGTCC   AC
GAM83   RERE     5' TATTGATGGTGTAGCGCTTTAG 25020    C   AACGGT
                                CT GAGC     TACCATCAATG
                                || ||||     ||||||||||
                                GA TTCG     GTGGTAGTTAT
                                 T   CGAT__
GAM83   RFC1     3' GGAACTGGTAGTCTTGTTTGGG 12829        C GT    TCAATG
                                CTCGAGCAA G  TACCA
                                ||||||||| |  |||||
                                GGGTTTGTT C  ATGGT
                                     _ TG    CAAGGA
GAM83   SIX2     3' TGTTGGTTCTTGTTTGGG    34191        C  TT   T
                                CTCGAGCAA GG  ACCA CA
                                ||||||||| ||  |||| ||
                                GGGTTTGTT CT  TGGT GT
                                     _ __    T
GAM83   TCEB1L   3' CATTGCATGTGTAGTTGTAGCT 13607       A  GG   _  _
           CGAG                   CTCGAGC AC  TTAC CAT CAATG
                                ||||||| ||  |||| ||| |||||
                                GAGCTCG TG  GATG GTA GTTAC
                                    A  TT   T  C
GAM83   UGT2B4   3' TGTTGTTTTAACTGTTGTTGAG 72416     G        CCAT
                                CTC AGCAACGGTTA    CAATG
                                ||| ||||||||||    |||||
                                GAG TTGTTGTCAAT    GTTGT
                                  _         TTT_
GAM83   VIPR2    3' TGTTGATGGTCGGTGGTTGGG  14077      G  A  GTT
                                CTCGA CA CG   ACCATCAATG
                                ||||| || ||   ||||||||||
                                GGGTT GT GC   TGGTAGTTGT
                                   G  G  ___
GAM83   BCMP1    3' TGTTGGTTATTTGCTTGAG   49540        CGGTT   T
                                CTCGAGCAA    ACCA CA
                                |||||||||    |||| ||
                                GAGTTCGTT    TGGT GT
                                     TAT__    T
GAM83   C20orf35 5' TGCGTAGTCGTTGCGTGGG   38076     A     GT  _
                                CTCG GCAACG  TAC CA
                                |||| ||||||  ||| ||
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                                GGGT CGTTGC  ATG GT
                                  G     TG   C
GAM83   CDW92    3'  CATTGAAAATTCCGGTGCTTGG 42329        A   TTACCA
            G                    CTCGAGCA CGG     TCAATG
                                 |||||||| |||     ||||||
                                 GGGTTCGT GCC     AGTTAC
                                     G   TTAAA_
GAM83   CHODL    3'  CATTGATGAGGGTTTGCTTGAG 46884         CGG  AC
                                 CTCGAGCAA   TT  CATCAATG
                                 |||||||||   ||  ||||||||
                                 GAGTTCGTT   GG  GTAGTTAC
                                       T__  GA
GAM83   FEZ2     3'  TGTTGGTGGTGATGGATTTTGT 18781      CG___
                                 GCAA    GTTACCATCAATG
                                 ||||    ||||||||||||
                                 TGTT    TAGTGGTGGTTGT
                                   TTAGG
GAM83   FLJ10330 3'  TATTGATAATGGAGATTGCTGT 36510        A    A  ___
            TTGAG                  CTCGAGCA CGGTT CCA   TCAATG
                                 |||||||| ||||| |||   ||||||
                                 GAGTTTGT GTTAG GGT   AGTTAT
                                     C    A   AAT
GAM83   FLJ10656 3'  TGTTGCCAACTGTTGTTC    36912          AC  T
                                 GAGCAACGGTT  CA CA
                                 ||||||||||  || ||
                                 CTTGTTGTCAA  GT GT
                                       CC  T
GAM83   GOLGA3   3'  GTTGTGGCTGTTCTTGGG    20896       C       C
                                 CTCGAG AACGGTTAC AT
                                 |||||| ||||||||| ||
                                 GGGTTC TTGTCGGTG TG
                                    _       T
GAM83   KIAA0226 3'  TGTTGATGGTGAAGTCCTTTTG 64267      CA_  GG
            A                     TCGAG   AC  TTACCATCAATG
                                  |||||   ||  ||||||||||||
                                  AGTTT   TG  AGTGGTAGTTGT
                                     TCC  A_
GAM83   KIAA1155 3'  GTTCTGCTGACTTTTGTTTGGG 62919         C    C  TCAATG
                                 CTCGAGCAA GGTTA CA
                                 |||||||| ||||| ||
                                 GGGTTTGTT TCAGT GT
                                       T    C  CTTGT
GAM83   KIAA1493 3'  ATTGATGGTGATTTGGAG    64834     G  CAACG
                                 CTC AG    GTTACCATCAAT
                                 ||| ||    ||||||||||||
                                 GAG TT    TAGTGGTAGTTA
                                   G  _____
GAM83   KIAA1674 3'  CATTGACTAATCCTGTTGCTC  69333         TTACCA
                                 GAGCAACGG     TCAATG
                                 |||||||||     ||||||
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                                CTCGTTGTC     AGTTAC
                                     CTAATC
GAM83   M96     5'  TATTGAAGTGGGCTGTGTTTGA 24757        A   TA  __
            G                    CTCGAGCA CGGT  CCA  TCAATG
                                 |||||||| ||||  |||  ||||||
                                 GAGTTTGT GTCG  GGT  AGTTAT
                                      _   __  GA
GAM83   MEF-2   3'  TTTGAAAAATTGTTGTTAGAG  65035     G       ACCA   TG
                                 CTC AGCAACGGTT   TCAA
                                 ||| ||||||||||   ||||
                                 GAG TTGTTGTTAA   AGTT
                                   A        AA__   TT
GAM83   pcnp    3'  TATTGGTGGTAGCTGCTTGCTG 40143     G   _
            AG                   CTC AGCAA CGGTTACCATCAATG
                                 ||| ||||| ||||||||||||||
                                 GAG TCGTT GTCGATGGTGGTTAT
                                   _    C
GAM83   SSH2    3'  GTTGATGGTGGCTGTAGT    62893    A
                                 GC ACGGTTACCATCAAT
                                 || ||||||||||||||
                                 TG TGTCGGTGGTAGTTG
                                  A
GAM83   TREX2   5'  CATTGGGTGCTCCAGTTGCTCG 55641          _ T_   AT
            AG                   CTCGAGCAAC GG  TACC  CAATG
                                 |||||||||| ||  ||||  |||||
                                 GAGCTCGTTG CC  GTGG  GTTAC
                                      A  TC   __
GAM83   LOC118812 5'  CGTTGATGGTCACTGTTGCTTC 74364     _      T
            G                    CGA GCAACGGT ACCATCAATG
                                 ||| |||||||| ||||||||||
                                 GCT CGTTGTCA TGGTAGTTGC
                                   T       C
GAM83   LOC132617 3'  CGTTGATGGTCTCTGCTC    76413       ACG TT
                                 GAGCA   G  ACCATCAATG
                                 |||||   |  ||||||||||
                                 CTCGT   C  TGGTAGTTGC
                                    ____ TC
GAM83   LOC145676 5'  CATTGATTTTATGCTTGCTTGA 77845         AC   TACC_
            G                    CTCGAGCA  GGT    ATCAATG
                                 ||||||||  |||    |||||||
                                 GAGTTCGT  TCG    TAGTTAC
                                      __   TATTT
GAM83   LOC146957 3'  TGGGGAGGGCTGTTGCTTGAG  78820           A_  A
                                 CTCGAGCAACGGTT  CC TCA
                                 ||||||||||||||  || |||
                                 GAGTTCGTTGTCGG  GG GGT
                                          GA  _
GAM83   LOC151643 3'  CATTGATGGGCTATTTTTGAG  81138       C  CG  TA
                                 CTCGAG AA  GT  CCATCAATG
                                 |||||| ||  ||  |||||||||
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                                GAGTTT TT  CG  GGTAGTTAC
                                   _  AT  __
GAM83   LOC164684 3'  TGTTGAACACTTAGTTGTTTGA 83427          GGTTACCA
           G                    CTCGAGCAAC       TCAATG
                                ||||||||||       ||||||
                                GAGTTTGTTG       AGTTGT
                                     ATTCACA_
GAM83   LOC196424 3'  AATATGGTTGTTGCATGAG   89055     A     GTT    CAATG
                                CTCG GCAACG   ACCAT
                                |||| ||||||   |||||
                                GAGT CGTTGT   TGGTA
                                  A     ___     TAAA
GAM83   LOC196955 3'  TGGAGGTGGTCGTTTTTGAG   77877       C   GT   AT
                                CTCGAG AACG  TACC  CA
                                |||||| ||||  ||||  ||
                                GAGTTT TTGC  GTGG  GT
                                   _   TG    AG
GAM83   LOC222068 3'  TGTTGTAATAGCTGTGTTTGAG 94282         A     CCAT
                                CTCGAGCA CGGTTA    CAATG
                                |||||||| ||||||    |||||
                                GAGTTTGT GTCGAT    GTTGT
                                     _     AAT_
GAM83   LOC51036  5'  ATTTTCTGTGTGGCTGTGTGTT 32394          _      _  TCAATG
           TGGG                    CTCGAGCA ACGGTTAC CA
                                |||||||| |||||||| ||
                                GGGTTTGT TGTCGGTG GT
                                     G       T  CTTTTAC
GAM84   BLAME    3'  TTTCTTGGCACTTGGG      39661     GACAA    A
                                CCC    GAGT CCAAGAAA
                                |||    |||| ||||||||
                                GGG    TTCA GGTTCTTT
                                  ______    C
GAM84   COL2A1    3'  TTCCTGTAAGACCTTCGGGTCA 53680         CA  A  AC__  A
                                TGACCCGA  AG GT    CA GAA
                                ||||||||  || ||    || |||
                                ACTGGGCT  TC CA    GT CTT
                                     __  _  GAAT  C
GAM84   COL2A1    3'  TTCCTGTAAGACCTTCGGGTCA 10242         CA  A  AC__  A
                                TGACCCGA  AG GT    CA GAA
                                ||||||||  || ||    || |||
                                ACTGGGCT  TC CA    GT CTT
                                     __  _  GAAT  C
GAM84   FNTB     3'  TCTTGGTACTTTCTTGTC    10713        __
                                GACAAGA  GTACCAAGA
                                |||||||  |||||||||
                                CTGTTCT  CATGGTTCT
                                     TT
GAM84   PAX5     3'  CTTGCATAGTCTCTCTTGTCAA 34130      CC       T_  _____
           GTCA                     TGAC  GACAAGAG  AC    CAAG
                                ||||  ||||||||  ||    ||||
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                                ACTG  CTGTTCTC  TG   GTTC
                                  AA       TC  ATAC
GAM84   C20orf64  3'  CTTGGCACCCTGTTGGGT    54336        A A  A
                                ACCCGACA G GT CCAAG
                                |||||||| | || |||||
                                TGGGTTGT C CA GGTTC
                                    _ C  C
GAM84   FLJ10901  3'  TCTCACTGTGCTCTTACCGCAT 37373    CC  AC       CA__
          CA                      TGA  CG  AAGAGTAC   AGA
                                |||  ||  ||||||||   |||
                                ACT  GC  TTCTCGTG   TCT
                                  AC  CA       TCAC
GAM84   KIAA0140  3'  TTCCTGAGTGGTGTCGGGTC  28523         AGAG  _  A
                                GACCCGACA   TAC CA GAA
                                |||||||||   ||| || |||
                                CTGGGCTGT   GTG GT CTT
                                     G___   A  C
GAM84   KIAA0352  3'  TTTCTTGGTATGTACTCAGG  29832    C  CAAGA
                                CC GA    GTACCAAGAAA
                                || ||    ||||||||||
                                GG CT    TATGGTTCTTT
                                 A  CATG_
GAM84   KIAA1399  5'  TTCTTGGCTCATCTGGTCA   70797      C  CAA   TA
                                TGACC GA   GAG  CCAAGAA
                                ||||| ||   |||  |||||||
                                ACTGG CT   CTC  GGTTCTT
                                   T  A__   __
GAM84   MED8      3'  TTTCTTAGTACTCCTTTGTTGG 54628        __     C
                                CCGACAA  GAGTAC AAGAAA
                                |||||||  |||||| ||||||
                                GGTTGTT  CTCATG TTCTTT
                                    TC     A
GAM84   SDCCAG3   3'  TCTGGCTCCCGGGTCA     22805       ACAA   TA   A
                                TGACCCG    GAG  CCA GA
                                |||||||    |||  ||| ||
                                ACTGGGC    CTC  GGT CT
                                    C___   __   _
GAM84   STK38L    3'  TTTCTTGGCACTGGAAGGGT   69692     GACAAG   A
                                ACCC     AGT CCAAGAAA
                                ||||     ||| ||||||||
                                TGGG     TCA GGTTCTTT
                                  AAGG__   C
GAM84   UST       3'  TTTCTCTGCTCTTGTC      20357          CCA
                                GACAAGAGTA   AGAAA
                                ||||||||||   |||||
                                CTGTTCTCGT   TCTTT
                                      C__
GAM84   ZNF212    3'  TTTCTTGGCACCTTCAGGTC   25318     C  CA  A  A
                                GACC GA  AG GT CCAAGAAA
                                |||| ||  || || ||||||||
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                                CTGG CT  TC CA GGTTCTTT
                                  A __ _ C
GAM84   LOC158563 5'  TTTCTTGGATGGGACCTATCGG 82847        CA  A  A____
            GTCA                  TGACCCGA  AG GT    CCAAGAAA
                                  |||||||| || ||    ||||||||
                                  ACTGGGCT  TC CA    GGTTCTTT
                                    A_ _ GGGTA
GAM84   LOC221416 3'  TTTCTTGGTAAGGGTGCCCAGT 95410     CCGA  AGAG
            CA                    TGAC   CA   TACCAAGAAA
                                  ||||   ||   ||||||||||
                                  ACTG   GT   ATGGTTCTTT
                                    ACCC  GGGA
GAM84   LOC245771 3'  TCTCACTGTGCTCTTACCGCAT 94488     CC  AC       CA__
            CA                    TGA  CG  AAGAGTAC   AGA
                                  ||| || ||||||||   |||
                                  ACT  GC  TTCTCGTG   TCT
                                    AC  CA       TCAC
GAM84   LOC255177 3'  TTTCTTGGGTGAAATGTCTGAT 98404     CCC   AGAGTA
            CA                    TGA   GACA     CCAAGAAA
                                  |||   ||||     ||||||||
                                  ACT   CTGT     GGTTCTTT
                                    AGT    AAAGTG
GAM84   LOC91947  3'  TTTCTTGAAAAGCTTGTCGGTT 68229     C       AGTAC
            CA                    TGA CCGACAAG    CAAGAAA
                                  ||| ||||||||    |||||||
                                  ACT GGCTGTTC    GTTCTTT
                                    T       GAAAA
GAM84   LOC92710  3'  CTTCTGACTCCTTGTCCAGTCA 70864     CC     _   ACC
                                  TGAC  GACAAG AGT   AAG
                                  ||||  |||||| |||   |||
                                  ACTG  CTGTTC TCA   TTC
                                    AC     C   GTC
GAM85   ACVRL1    5'  TTTATTAGGAGGGAGTGGTG   5240          AAGAAG
                                  CACCACTCCC     AATAAG
                                  ||||||||||     ||||||
                                  GTGGTGAGGG     TTATTT
                                       AGGA__
GAM85   BCL11B    3'  TTTGTTTTTGGGGTGGGGGGTG 57582       A_ __       G  TAAG
            TG                    TACACC  CT  CCCAAGAA AA
                                  ||||||  ||  |||||||| ||
                                  GTGTGG  GG  GGGTTTTT TT
                                     GG  TG       G  T
GAM85   C18orf1   3'  CTTCGTGTGGGAGTGGTGTG   60865           A__
                                  TACACCACTCCCA   GAAG
                                  ||||||||||||   ||||
                                  GTGTGGTGAGGGT   CTTC
                                         GTG
GAM85   ITPR3     3'  CTTGTTTTTCTCCTTTTGGTGT 11085        CTCCCA
            A                      TACACCA     AGAAGAATAAG
                                  |||||||     ||||||||||
```

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                                ATGTGGT     TCTTTTTGTTC
                                    TTTCC_
GAM85   KCNAB1   3' GTTTGTTTTTTTTTGAAGGGGG 61585          ____
            TGGTGTG                 TACACCACTCCC   AAGAAGAATAAG  T
                                ||||||||||||   ||||||||||||  |
                                GTGTGGTGGGGG   TTTTTTTTGTTT  G
                                     AAGT
GAM85   KRAS2    3' CTTATTTTTCTTACCAAGTGTG 54123    C  CCC_
                                CAC ACT   AAGAAGAATAAG
                                ||| |||   ||||||||||||
                                GTG TGA   TTCTTTTTATTC
                                  _  ACCA
GAM85   KRAS2    3' CTTATTTTTCTTACCAAGTGTG 54124    C  CCC_
                                CAC ACT   AAGAAGAATAAG
                                ||| |||   ||||||||||||
                                GTG TGA   TTCTTTTTATTC
                                  _  ACCA
GAM85   LIFR     3' TTTGTTTTTTTTGGTTGGTTG  11315   C   CTC
                                A ACCA   CCAAGAAGAATAAG
                                | ||||   ||||||||||||||
                                G TGGT   GGTTTTTTTTGTTT
                                 T   T__
GAM85   MEN1     5' CTTGTTTTTTTCCTTTTGGTG  56348      CTCCCA
                                CACCA     AGAAGAATAAG
                                |||||     ||||||||||
                                GTGGT     TTTTTTTGTTC
                                   TTTCC_
GAM85   MLLT7    3' TTGTGCCTGGGAGTGTGTG   21043    _      AGAAGA
                                CAC CACTCCCA     ATAA
                                ||| ||||||||     ||||
                                GTG GTGAGGGT     TGTT
                                  T       CCG___
GAM85   SIAH1    3' TTTGTTTTTGCCGTGGGAGTGT 13128    _      AG__
            GTG                   CAC CACTCCCA    AAGAATAAG
                                ||| ||||||||   |||||||||
                                GTG GTGAGGGT    TTTTTGTTT
                                  T       GCCG
GAM85   SLC7A6   3' TTTGTTTTTGTGGTGGGTGCTG 15646     C    _  AG
            TG                    TACA CACTC CCA  AAGAATAAG
                                |||| ||||| |||  |||||||||
                                GTGT GTGGG GGT  TTTTTGTTT
                                  C    T  G_
GAM85   STAT6    5' TTTTTCTTTTTGGTGGTGGTG  13453       TC        TAAG
                                CACCAC  CCAAGAAGAA
                                ||||||  ||||||||||
                                GTGGTG  GGTTTTTCTT
                                   GT        TTTA
GAM85   TCF8     3' CTTGTTTTTTTAAGAGTGTGTG 48429    _    CCA
                                CAC CACTC   AGAAGAATAAG
                                ||| |||||   ||||||||||
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                                GTG GTGAG   TTTTTTTGTTC
                                  T    AA_
GAM85   B3GNT7   3'  TTGTTCTTGGCTGGTGGGTG   71685     A    C_     G
                                TAC CCACT  CCAAGAA AA
                                ||| |||||  ||||||| ||
                                GTG GGTGG  GGTTCTT TT
                                  _    TC      G
GAM85   BCDO     3'  TTATTCTTTCTGTGGGTG    34287      C  AG
                                CACTC CA  AAGAATAA
                                ||||| ||  ||||||||
                                GTGGG GT  TTCTTATT
                                   T  CT
GAM85   DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
            A                    TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM85   EPN2     3'  TTTATTTTTCTTTGACTCGTGT 31046       CAC  CC
            G                    TACAC   TC  AAGAAGAATAAG
                                |||||   ||  ||||||||||||
                                GTGTG   AG  TTCTTTTTATTT
                                   CTC  T_
GAM85   FLJ13855  3'  GGGTATTTTTCTTGGGGGTGGA 43853     A              AG
            GTA                   TAC CCACTCCCAAGAAGAATA
                                ||| ||||||||||||||||||
                                ATG GGTGGGGGTTCTTTTTAT
                                  A              GGGA
GAM85   FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM85   FLJ32865  3'  TTTGTTGGGGGTGGGGTG    58824     A        G
                                TAC CCACTCCCAA AAG
                                ||| |||||||||| |||
                                GTG GGTGGGGGTT TTT
                                  G        G
GAM85   HAND1    3'  TTTGTTCTTCGAATCGTGGTG  17880       TCCCAA
                                CACCAC     GAAGAATAAG
                                ||||||     ||||||||||
                                GTGGTG     CTTCTTGTTT
                                   CTAAG_
GAM85   KIAA0562  3'  TTTGTTTTGCGGGGGTGGTG   28834          AAGA
                                CACCACTCCC    AGAATAAG
                                ||||||||||    ||||||||
                                GTGGTGGGGG    TTTTGTTT
                                     CG__
GAM85   KIAA0871  5'  TTATTTTTTTGGTGTGTGTGTG 31022       _  TC        ATAAG
                                TACAC CAC  CCAAGAAGA
                                ||||| |||  |||||||||
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                                GTGTG GTG  GGTTTTTTT
                                  T  T_       ATTT
GAM85   KIAA0970 3'  TTTGTTTTTTTTGTTAGGGTG  30622      A  CC
                                CACC CT  CAAGAAGAATAAG
                                |||| ||  ||||||||||||
                                GTGG GA  GTTTTTTTTGTTT
                                  _  TT
GAM85   KIAA1240 3'  TTTATTTTTAGGGAGTGGGTA  67297     A       AAG
                                TAC CCACTCCC   AAGAATAAG
                                ||| ||||||||   |||||||||
                                ATG GGTGAGGG   TTTTTATTT
                                  _      A__
GAM85   KIAA1719 3'  TCTGTCTTGGGAGTGGTGTA   68742              _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                          G
GAM85   KIAA1750 3'  TTTATTTTTTTGTTCTAGGTGT 68815        ACTCCCA
            G                    TACACC      AGAAGAATAAG
                                ||||||      ||||||||||
                                GTGTGG      TTTTTTTATTT
                                   ATCTTG_
GAM85   MAP2K3   3'  CTTGTTTTTCTTGCATGGT   59686      CTCC
                                ACCA   CAAGAAGAATAAG
                                ||||   ||||||||||||
                                TGGT   GTTCTTTTTGTTC
                                  AC__
GAM85   MLN64    3'  CTTGTTGGGGAGTGGGTG    96062     A       _  G
                                TAC CCACTCCC AA AAG
                                ||| |||||||| || |||
                                GTG GGTGAGGG TT TTC
                                  _      G  G
GAM85   NY-REN-41 3'  TTTGTTTTTCTATCCTGGTGG  55564       CCCA_
                                CCACT    AGAAGAATAAG
                                |||||    ||||||||||
                                GGTGG    TCTTTTTGTTT
                                   TCCTA
GAM85   PRO1489   5'  TTTGTTTTTCGTGTGTGTGTG  38334       _   TCCCAA
                                TACAC CAC     GAAGAATAAG
                                ||||| |||     ||||||||||
                                GTGTG GTG     CTTTTTGTTT
                                   T  TG____
GAM85   SEC15L   3'  TTTGTTCTACTTGGGTGGT   72731      CT     A
                                ACCA  CCCAAG AGAATAAG
                                ||||  |||||| ||||||||
                                TGGT  GGGTTC TCTTGTTT
                                  __     A
GAM85   SHAPY    3'  TTTGTTCTTTTTGGAACTGTG  57915     TC__
                                CAC   CCAAGAAGAATAAG
                                |||   ||||||||||||||
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                                GTG   GGTTTTTCTTGTTT
                                  TCAA
GAM85   STAM2    3' GTTTTTCTTCCTGCAATGTGGT 20707       TCC_ A    TAAG
            GTG                   TACACCAC   CA GAAGAA
                                  |||||||||   || ||||||
                                  GTGTGGTG   GT CTTCTT
                                      TAAC  C     TTTGT
GAM85   TUBGCP3  3' TTTATTTTTTTTTTAGTGTTGTA 21982     C   CCC
                                  TACA CACT   AAGAAGAATAAG
                                  |||| ||||  ||||||||||||
                                  ATGT GTGA   TTTTTTTTATTT
                                    T   T__
GAM85   ZNF220   3' CTTGTTTTTTTTACCACCTGGTG 23157     CTCCCA
                                  CACCA     AGAAGAATAAG
                                  |||||     ||||||||||||
                                  GTGGT     TTTTTTTGTTC
                                     CCACCA
GAM85   LOC121219 5' TTGTTCTATGGGTGGGTG    74493     ACT   AGA
                                  CACC   CCCA   AGAATAA
                                  ||||   ||||   |||||||
                                  GTGG   GGGT   TCTTGTT
                                    GT_   A__
GAM85   LOC143146 3' TTTGTTGGAGGTGGTGTA    60767       TC   G
                                  TACACCAC  CCAA AAG
                                  ||||||||  |||| |||
                                  ATGTGGTG  GGTT TTT
                                       GA   G
GAM85   LOC146445 3' TTGTTCTTTGTGTGGTTG    84687   C   TCCCAA
                                  A ACCAC     GAAGAATAA
                                  | |||||     |||||||||
                                  G TGGTG     TTTCTTGTT
                                   T    TG_____
GAM85   LOC150174 3' TTTATTTTTTTTTTACAATGGTG 80444      CTCCC
                                  CACCA     AAGAAGAATAAG
                                  |||||     ||||||||||||
                                  GTGGT     TTTTTTTTATTT
                                     AACAT
GAM85   LOC150213 3' TTTATTTTTTTTTACAATGGTG  75363      CTCCC
                                  CACCA     AAGAAGAATAAG
                                  |||||     ||||||||||||
                                  GTGGT     TTTTTTTTATTT
                                     AACA_
GAM85   LOC150236 3' TTTATTTTTTTTTACAATGGTG  80505      CTCCC
                                  CACCA     AAGAAGAATAAG
                                  |||||     ||||||||||||
                                  GTGGT     TTTTTTTTATTT
                                     AACA_
GAM85   LOC154084 3' CTTGTTTTTTTTAGTAGGTGTG  87378       _   CCCA
                                  TACACC ACT    AGAAGAATAAG
                                  |||||| |||    ||||||||||
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                                GTGTGG TGA    TTTTTTTGTTC
                                   A  ____
GAM85   LOC170261 3'  TTTATTCTTTGTGAAAGTGGT  83472       CC  A
                                ACCACT  CA GAAGAATAAG
                                ||||||  || ||||||||||
                                TGGTGA  GT TTTCTTATTT
                                   AA  G
GAM85   LOC199692 3'  CTTGTTCTTCTGCTGTAGTGTG 59926       C  TCCCA
                                TACAC AC     AGAAGAATAAG
                                |||||| ||     ||||||||||
                                GTGTG TG     TCTTCTTGTTC
                                   A  TCG__
GAM85   LOC203414 3'  CTTGTCAACTGGGGGTGATGTG 90913      C       A AA  A
                                TACA CACTCCCA G  GA TAAG
                                |||| |||||||| |  || ||||
                                GTGT GTGGGGGT C  CT GTTC
                                   A       _ AA  _
GAM85   LOC257051 3'  TTTATTCTTTGTGAAAGTGGT  98054       CC  A
                                ACCACT  CA GAAGAATAAG
                                ||||||  || ||||||||||
                                TGGTGA  GT TTTCTTATTT
                                   AA  G
GAM85   LOC92303  3'  TTATTTTTTTTGAGGTGG    69400       CC
                                CCACT  CAAGAAGAATAA
                                |||||  ||||||||||||
                                GGTGG  GTTTTTTTTTATT
                                   A_
GAM86   ACP1      5'  GGCGTTGGTGCGGGACTGCGC  24015     TG CCA     TT
                                GCG  G   CTGCG  GATGTT
                                |||  |   |||||  ||||||
                                CGC  C   GGCGT  TTGCGG
                                  GT AG_     GG
GAM86   ACP2      3'  GATGTTTACCAAGTGCTGTGTT 9655        TG  C   _ C  T
           G                     TAGCG  GC ACT G GT GATGTT
                                |||||  || ||| | || ||||||
                                GTTGT  CG TGA C CA TTGTAG
                                   GT  _   A _  T
GAM86   ACVR1     5'  AGCATTGGTAAGCGTCACACTG 8473      C     CA  GC TT
                                TAG GTGGC  CT  G  GATGTT
                                ||| |||||  ||  |  ||||||
                                GTC CACTG  GA  T  TTACGA
                                  A    C_  A_ GG
GAM86   ACVR1B    3'  GGTCGGGGGGTGTGGTCGTCATG 40108         C  TG  ___     GTT
           CTG                     TAGCGTGGC AC  CG   TTGAT
                                |||||||||  ||  ||   |||||
                                GTCGTACTG TG  GT   GGCTG
                                     C  GT  GGG    G
GAM86   B4GALT2   5'  GGCCAGTGGCCGCCTG      48349     C         C
                                TAG GTGGCCACTG GTT
                                ||| ||||||||||  |||
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                                GTC CGCCGGTGAC CGG
                                  _       _
GAM86   B4GALT2  5'  GGCCAGTGGCCGCCTG     48350     C        C
                                TAG GTGGCCACTG GTT
                                ||| |||||||||| |||
                                GTC CGCCGGTGAC CGG
                                  _       _
GAM86   CABC1    5'  GGCGTCAGCGCGGTGGCCAGCG 40040     _
          C                      GCG TGGCCACTGCGTTGATGTT
                                ||| ||||||||||||||||||
                                CGC ACCGGTGGCGCGACTGCGG
                                  G
GAM86   CACNA1C  5'  AATGTCAATGCTTCTCATGT   7395       CCACT
                                GCGTGG    GCGTTGATGTT
                                ||||||    ||||||||||
                                TGTACT    CGTAACTGTAA
                                   CTT__
GAM86   CALCB    3'  AATGTCAATATTGTGCCAT    88959      C  TGC
                                GTGGC AC   GTTGATGTT
                                ||||| ||   ||||||||
                                TACCG TG   TAACTGTAA
                                  _ TTA
GAM86   CASP8    5'  TGACTGGTGGCTGCCTG     8769      C TG      C
                                TAG G  GCCACTG GTTG
                                ||| |  ||||||| ||||
                                GTC C  CGGTGGT CAGT
                                  _ GT      _
GAM86   CKAP1    5'  CAGGGCGGGGCCACGCTG    73899          A   G
                                TAGCGTGGCC CTGC TTG
                                |||||||||| |||| |||
                                GTCGCACCGG GGCG GAC
                                      _   G
GAM86   COL6A2   3'  CTCCCAGCTGGTGGCCGTGCTG 55202             C   ATGTT
                                TAGCGTGGCCACTG GTTG
                                |||||||||||||| ||||
                                GTCGTGCCGGTGGT CGAC
                                      _   CCTCA
GAM86   ECM1     5'  GGTCCAGTGGTCAGTTG     16657      G       CGTT  TG
                                TAGC TGGCCACTG   GA  T
                                |||| |||||||||   ||  |
                                GTTG ACTGGTGAC   CT  G
                                  _       _____ GT
GAM86   ENO2     3'  AGCGTCAGGGTTGGTGTGCT  10519    _    _ G
                                GGC CACTG C TTGATGTT
                                ||| ||||| | ||||||||
                                TCG GTGGT G GACTGCGA
                                  T    T G
GAM86   FASN     3'  GCATTGGCTCAGCCCGCTG   15912      T  CAC  C  TG
                                TAGCG GGC   TG GT  ATGT
                                ||||| |||   || ||  ||||
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                                GTCGC CCG   AC CG  TACG
                                  _  ____  T  GT
GAM86   FE65L2   5'  TAGCTCCAGAGGTCGCGCTG  21296         A  C_
                                TAGCGTGGCC CTG  GTTG
                                |||||||||| |||  ||||
                                GTCGCGCTGG GAC  CGAT
                                     A   CT
GAM86   FE65L2   5'  TAGCTCCAGAGGTCGCGCTG  56519         A  C_
                                TAGCGTGGCC CTG  GTTG
                                |||||||||| |||  ||||
                                GTCGCGCTGG GAC  CGAT
                                     A   CT
GAM86   FUS      5'  GGCGTCGGTGCTCAGCGGTGTT 18277       G  CACT   TT
           G                     TAGCGT GC    GCG  GATGTT
                                |||||| ||    |||  ||||||
                                GTTGTG CG    CGT  CTGCGG
                                   G  ACT_   GG
GAM86   GAK      3'  ACGTGGTGGGCCACGCTG    19140         _  TG
                                TAGCGTGGCC AC  CGT
                                |||||||||| ||  |||
                                GTCGCACCGG TG  GCA
                                     G  GT
GAM86   GRP58    5'  AGCGGGTTAGTGGTCGCGC    19206          ___
                                GCGTGGCCACTG   CGTT
                                ||||||||||||   ||||
                                CGCGCTGGTGAT   GCGA
                                     TGG
GAM86   HADHB    3'  AATATGGTGGTCAGCGTTA    5737       _      GC
                                TAGCG TGGCCACT  GTT
                                ||||| ||||||||  |||
                                ATTGC ACTGGTGG  TAA
                                   G       TA
GAM86   HPS3     3'  GATGTTAATGTTTTGCCATGGT 51484    G     CACT
           A                     TA CGTGGC    GCGTTGATGTT
                                || ||||||    ||||||||||
                                AT GTACCG    TGTAATTGTAG
                                 G     TTT_
GAM86   HR       5'  CGATCAGAGGTCGTGCTG    37909          A  C
                                TAGCGTGGCC CTG GTTG
                                |||||||||| ||| ||||
                                GTCGTGCTGG GAC TAGC
                                     A  _
GAM86   IDS      5'  CGGGCGGCGGCTGTGTTG    5776       TG  A   G
                                TAGCG  GCC CTGC TTG
                                |||||  ||| |||| |||
                                GTTGT  CGG GGCG GGC
                                   GT   C   _
GAM86   IGFBP1   5'  AGCATCGGCCCCTGTCTGCTG  6994       T  CACTGC
                                TAGCG GGC     GTTGATGTT
                                ||||| |||     |||||||||
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                                GTCGT CTG     CGGCTACGA
                                  _  TCCC__
GAM86   IL27    3'  AACATGGGGGCTATGCTG    65326         A  GC
                                TAGCGTGGCC CT  GTT
                                |||||||||| ||  |||
                                GTCGTATCGG GG  CAA
                                     G  TA
GAM86   IMMP2L  3'  GCATTGGGAGGCCAGTTA    51707     G    A TGCG TG
                                TAGC TGGCC C    T  ATGT
                                |||| ||||| |    |  ||||
                                ATTG ACCGG G    G  TACG
                                  _    A ____ GT
GAM86   JTV1    5'  AGCGTTGGCCTTTGGCACGCGC 21944       _   CTGC  TG
            TA                   TAGCGTG GCCA    GT  ATGTT
                                ||||||| ||||    ||  |||||
                                ATCGCGC CGGT    CG  TGCGA
                                    A    TTC_  GT
GAM86   LAMP2   3'  AACATCAACGTGCAATGTT   26564      G  CACT
                                AGCGT GC    GCGTTGATGTT
                                ||||| ||    ||||||||||
                                TTGTA CG    TGCAACTACAA
                                  A  ____
GAM86   LTA4H   5'  AGCGTTGGGCTGTAGGTCGCTG 7985       TG  CA_    __ TG
            TGCTG                TAGCG  GC   CTGCG  T  ATGTT
                                |||||  ||   |||||  |  |||||
                                GTCGT  CG   GATGT  G  TGCGA
                                  GT  CTG     CG GT
GAM86   LYPLA1  5'  TAGCGCGGGGCCGCGTTG    21998         A
                                TAGCGTGGCC CTGCGTTG
                                |||||||||| ||||||||
                                GTTGCGCCGG GGCGCGAT
                                      _
GAM86   MTA1L1  3'  GGCATCAACCCCAGGCCACGCT 17635         ACTGC
                                AGCGTGGCC    GTTGATGTT
                                |||||||||    |||||||||
                                TCGCACCGG    CAACTACGG
                                     ACCC_
GAM86   MYOG    3'  GATGCCAGTGGCTGGGCTG   60068     G       _
                                TAGC TGGCCACTG CGTT
                                |||| ||||||||| ||||
                                GTCG GTCGGTGAC GTAG
                                  G       C
GAM86   NUP214  5'  GGCGTGGGTGGCAGCGTTG   18682      G   _ TG
                                TAGCGT GCCA C  CGTT
                                |||||| |||| |  ||||
                                GTTGCG CGGT G  GCGG
                                   A   G GT
GAM86   NXF2    3'  AACGTTAACTTGCAGGCCACGT 35598        AC  __
                                GCGTGGCC  TGC  GTTGATGTT
                                ||||||||  |||  |||||||||
```

```
                                TGCACCGG  ACG  CAATTGCAA
                                   __   TT
GAM86   OGT     5'  AGCGTTAATGCGCATTGCGT   14592     TG CCAC
                                GCG  G    TGCGTTGATGTT
                                |||  |    ||||||||||||
                                TGC  T    GCGTAATTGCGA
                                  GT AC__
GAM86   PAWR    3'  AATGTTAATGGTCAATGCTA   11971       _    CT_
                                TAGCGT GGCCA   GCGTT
                                ||||||| |||||   |||||
                                ATCGTA CTGGT   TGTAA
                                   A    AAT
GAM86   PBP     3'  GCATCAGTATGTCACTCTG   11938     C    CAC   GT
                                TAG GTGGC   TGC  TGATGT
                                ||| |||||   |||  ||||||
                                GTC CACTG   ATG  ACTACG
                                  T    T__   __
GAM86   PCDH7   3'  GTATTAATGCAGAAATGTGCTA 11992       _ ___        GTT
            C                    GTGGC CA   CTGCGTTGAT
                                |||||| ||   ||||||||||
                                CATCG GT   GACGTAATTA
                                   T  AAA        TGA
GAM86   PDK1    5'  AACATTGGCGCGGGAAACCTG  12029     C  GG  AC    TG
                                TAG GT  CC  TGCGT  ATGTT
                                ||| ||  ||  |||||  |||||
                                GTC CA  GG  GCGCG  TACAA
                                  _ AA  __    GT
GAM86   PPP3CC  5'  GGCGTCGGAGGCCGGCGCTG   20029       _   A   _
                                TAGCGT GGCC CTG CGTT
                                |||||| |||| ||| ||||
                                GTCGCG CCGG GGC GCGG
                                   G   A   T
GAM86   PRDX3   3'  ACATCTTGGTGGCTGGCTA    73737     G      GCGTT
                                TAGC TGGCCACT    GATGT
                                |||| ||||||||    |||||
                                ATCG GTCGGTGG    CTACA
                                  _       TT___
GAM86   PSD     5'  GACATCGATGAGGTGCTGGCTG 12437     G   C   G
                                TAGC TGGC ACT CGTTGATGTT
                                |||| |||| ||| ||||||||||
                                GTCG GTCG TGG GTAGCTACAG
                                  _   _   A
GAM86   RPL37   3'  AATGTCAACGATTAGTCATGC  8274        CACTG
                                GCGTGGC    CGTTGATGTT
                                |||||||    ||||||||||
                                CGTACTG    GCAACTGTAA
                                    ATTA_
GAM86   SERPINI1 3' GTATTAAGCTAATGGTCCTGTT 18479      T    CT_  G    GTT
            A                    TAGCG GGCCA   GC TTGAT
                                ||||| |||||   || |||||
```

```
                                ATTGT CTGGT   CG AATTA
                                  C    AAT  _    TGA
GAM86   SH3GL3   5'  GATGTCGGTGGCCGGGCTG   13110     G       _
                                TAGC TGGCCACTG CGTT
                                |||| ||||||||| ||||
                                GTCG GCCGGTGGC GTAG
                                  G       T
GAM86   SPON2    3'  AGCGTCAGTGTTTCCATGTTA  25849       C__    _
                                TAGCGTGG   CACTG CGTT
                                ||||||||   ||||| ||||
                                ATTGTACC   GTGAC GCGA
                                     TTT    T
GAM86   SSX4     3'  ACATTAGCGTTTTCGCTG    20097      TGGCCACT
                                TAGCG       GCGTTGATGT
                                |||||       ||||||||||
                                GTCGC       TGCGATTACA
                                  TTT_____
GAM86   SSX4     3'  ACATTAGCGTTTTCGTTG    20098      TGGCCACT
                                TAGCG       GCGTTGATGT
                                |||||       ||||||||||
                                GTTGC       TGCGATTACA
                                  TTT_____
GAM86   TARDBP   5'  CGAAGCGGTGGCTGGGCTG   24787     G        G
                                TAGC TGGCCACTGC TTG
                                |||| |||||||||| |||
                                GTCG GTCGGTGGCG AGC
                                  G        A
GAM86   TNFSF10  3'  ACATTAATGCAATGGTTA    15085       C
                                TGGCCA TGCGTTGATGT
                                |||||| ||||||||||
                                ATTGGT ACGTAATTACA
                                   A
GAM86   TOP3B    5'  AGCATTGGTAATAGTGCTGTGC 15441      TG  C    CG_ TG
           TG                     TAGCG  GC ACTG   T  ATGTT
                                |||||  || ||||  |  |||||
                                GTCGT  CG TGAT   G  TACGA
                                  GT  _    AAT GT
GAM86   TRH      3'  GGCATACCCTGTGGTGTTGTGC 24053      TG  C  TG  TTG_
           TG                     TAGCG  GC AC  CG    ATGTT
                                |||||  || ||  ||   |||||
                                GTCGT  TG TG  GT    TACGG
                                  GT  _  GT  CCCA
GAM86   UTY      5'  AATGCAGTTGCCACGTTG    24060         C
                                TAGCGTGGC ACTGCGTT
                                ||||||||| ||||||||
                                GTTGCACCG TGACGTAA
                                     T
GAM86   XRCC4    3'  AACATTGATGTTTGAACATTTT 14146    C   GC  CT    TG
           A                     TAG GTG  CA  GCGT  ATGTT
                                ||| |||  ||  ||||  |||||
```

```
                                ATT TAC  GT  TGTA  TACAA
                                  T  AA  T_   GT
GAM86   ZNF198   3'  GCATTAGATAGTCATGCTG   14363        CACTGCG
                                TAGCGTGGC      TTGATGT
                                |||||||||      |||||||
                                GTCGTACTG      GATTACG
                                     ATA____
GAM86   ZNF239   3'  GTATCAAGCACTTTGTTATGCT 20243        CAC_  G    GTT
           G                     TAGCGTGGC   TGC TTGAT
                                |||||||||   ||| |||||
                                GTCGTATTG   ACG AACTA
                                     TTTC  _    TGA
GAM86   AHCYL1   3'  GATGTGGGTGGTGCATGTTA  22774       _   _ TG
                                TAGCGTG GCCA C  CGTT
                                ||||||| |||| |  ||||
                                ATTGTAC TGGT G  GTAG
                                    G   G GT
GAM86   ATE1     5'  GGCGGCGGCGGCCGCGCTA   73017        A   _
                                TAGCGTGGCC CTGC GTT
                                |||||||||| |||| |||
                                ATCGCGCCGG GGCG CGG
                                      C   G
GAM86   ATIC     3'  GTGAAGTGATGGTTATGTTA  15747         CT  G  G
                                TAGCGTGGCCA  GC TT AT
                                ||||||||||  || || ||
                                ATTGTATTGGT  TG AA TG
                                      AG  _  G
GAM86   C15orf15 3'  GACGTAAAATGGTTGTGCTA  33303      TG   C__
                                TAGCG  GCCA   TGCGTT
                                |||||  ||||   ||||||
                                ATCGT  TGGT   ATGCAG
                                   GT   AAA
GAM86   C20orf178 3'  AACATTGAGCTTCTGGACTACG 75291        _  CT_  G TG
           CTG                    TAGCGTGG CCA   GC T  ATGTT
                                |||||||| |||   || |  |||||
                                GTCGCATC GGT   CG A  TACAA
                                     A   CTT  _ GT
GAM86   C21orf55  5'  GTATCAGACCAGGTCATTGCTA 35675      _    AC  CG    GTT
                                TAGCG TGGCC  TG  TTGAT
                                ||||| |||||  ||  |||||
                                ATCGT ACTGG  AC  GACTA
                                   T    __  CA    TGA
GAM86   CCNA2    3'  ATTAATGATGCCAGCTG     8788      G   CACTG
                                TAGC TGGC    CGTTGAT
                                |||| ||||    |||||||
                                GTCG ACCG    GTAATTA
                                   _   TA___
GAM86   CDH22    5'  GACATCCCGGCGGCCGCGCTG  41440         A  CGTT
                                TAGCGTGGCC CTG   GATGTT
                                |||||||||| |||   ||||||
```

```
                                GTCGCGCCGG GGC    CTACAG
                                      C   C___
GAM86   CHM-I    3'  AGCATTAAGGCAGGTTGATGCT 60444       _    AC   G
            G                    TAGCGT GGCC  TGC TTGATGTT
                                 |||||| ||||  ||| ||||||||
                                 GTCGTA TTGG  ACG AATTACGA
                                    G   __  G
GAM86   CROC4    5'  GGTGTCATCGTAGGTGGCCACC 22066     C       _   T   TG
            TA                    TAG GTGGCCAC TGCG TGA  TT
                                 ||| |||||||| |||| |||  ||
                                 ATC CACCGGTG ATGC ACT  GG
                                   _      G   T   GT
GAM86   CTRP5    3'  ATGGGAACAGTGGCTGTCTG   32229     C TG      CG  G
                                 TAG G  GCCACTG  TT AT
                                 ||| |  |||||||  || ||
                                 GTC T  CGGTGAC  GG TA
                                   _ GT      AA  G
GAM86   DKFZp434A1520 3'  GACATCAGCGTCCACCCGCTA  61768       T  CCACT
                                 TAGCG GG     GCGTTGATGTT
                                 |||||| ||    ||||||||||
                                 ATCGC CC     TGCGACTACAG
                                    _ ACC__
GAM86   DKFZp547O146 3'  GATATTTGAGGAGGGTCGTGTT 39966          A  GCGTT
            G                    TAGCGTGGCC CT     GATGTT
                                 |||||||||| ||    ||||||
                                 GTTGTGCTGG GA     TTATAG
                                       _ GGAGT
GAM86   DKFZP761C169 3'  AATGTTTTGTTGGGCTGTGTTG 68416      TG   ACT   TT
                                 TAGCG  GCC   GCG  GATGTT
                                 |||||  |||   |||  ||||||
                                 GTTGT  CGG   TGT  TTGTAA
                                    GT   GT_   T_
GAM86   DKFZP761C169 5'  GATATTTTAAGTGGCCAT     68420         GCGTT
                                 GTGGCCACT     GATGTT
                                 |||||||||     ||||||
                                 TACCGGTGA     TTATAG
                                       ATT__
GAM86   Dlc2     3'  GATGTCCTCTCCAATGGCTGTG 55629       TG    C  CGTT_
            CTA                    TAGCG  GCCA TG     GATGTT
                                 |||||  |||| ||    ||||||
                                 ATCGT  CGGT AC     CTGTAG
                                    GT    A  CTCTC
GAM86   DMRTB1    5'  AGCTCCCAGAGGTGGTGGTTGT 66836       TG     TG G  GAT__
            GTTA                    TAGCG  GCCAC  C TT     GTT
                                 |||||  |||||  | ||    |||
                                 ATTGT  TGGTG  G AG     CGA
                                    GT    GT G  ACCCT
GAM86   DMWD     5'  GGCATCACACGCCAGTGGCCAC 61554     C        _  _
            CTG                    TAG GTGGCCACTG CGT TGATGTT
                                 ||| |||||||||| ||| |||||||
```

```
                                GTC CACCGGTGAC GCA ACTACGG
                                  _       C   C
GAM86   EIF2S2   5' ATCGGCAGGGGCAGCGCTG   15340      G   A   GT
                                TAGCGT GCC CTGC  TGAT
                                |||||| ||| ||||  ||||
                                GTCGCG CGG GACG  GCTA
                                   A   G   __
GAM86   FLJ10044 3' CGGCTCAGTGGCTCATGCTG   36240       _     C
                                TAGCGTG GCCACTG GTTG
                                ||||||| ||||||| ||||
                                GTCGTAC CGGTGAC CGGC
                                   T      T
GAM86   FLJ10081 5' GGCGTTAACGCGCACGCGCT   36291       _ CACT
                                AGCGTG GC    GCGTTGATGTT
                                |||||| ||    ||||||||||
                                TCGCGC CG    CGCAATTGCGG
                                   A _____
GAM86   FLJ10607 5' GGCGTTGGCGCTGCCACGTCTG 77640     _     CACT    TG
                                TAG CGTGGC    GCGT  ATGTT
                                ||| ||||||    ||||  |||||
                                GTC GCACCG    CGCG  TGCGG
                                  T     T___    GT
GAM86   FLJ10904 5' GTATTAGCGTCTCAGTTGCGCT 37386      TG  CACT      GTT
           G                     TAGCG  GC    GCGTTGAT
                                |||||  ||    ||||||||
                                GTCGC  TG    TGCGATTA
                                   GT  ACTC       TGA
GAM86   FLJ11191 3' ACATCAGAGTCCATGCTA    37740        CCACT  G
                                TAGCGTGG    GC TTGATGT
                                ||||||||    || |||||||
                                ATCGTACC    TG GACTACA
                                     _____  A
GAM86   FLJ11756 3' AATATTAACATATAGTTATGTT 45125         CAC  C
           G                     TAGCGTGGC   TG GTTGATGTT
                                |||||||||   || |||||||||
                                GTTGTATTG   AT CAATTATAA
                                      AT_  A
GAM86   FLJ13195 5' AGCGTTGGTGTTTGGCACGC   43548      G   CT   TT
                                GCGTG CCA  GCG  GATGTT
                                ||||| |||  |||  ||||||
                                CGCAC GGT  TGT  TTGCGA
                                   _  T_   GG
GAM86   FLJ13940 3' GATGTCAACGCTGCCATTGCTG 47307      _   CACT
                                TAGCG TGGC    GCGTTGATGTT
                                ||||| ||||    ||||||||||
                                GTCGT ACCG    CGCAACTGTAG
                                   T   T___
GAM86   FLJ20038 5' GGCATTAATTTATTGGGTGTGT 34865     GT G   C  C
           TA                     TAGC  G CCA TG GTTGATGTT
                                ||||  | ||| || |||||||||
```

```
                                ATTG  T GGT AT TAATTACGG
                                  TG G   T  T
GAM86   FLJ20280 5' AGGTTAGTCAGTGTTCTGCTG  35325      T GC    C    TG
                                TAGCG G  CACTG GTTGA  TT
                                ||||| |  ||||| |||||  ||
                                GTCGT C  GTGAC TGATT  GA
                                  _ TT    _    GT
GAM86   FLJ21613 3' GATGTCAACATTGAGTCGTGC  41926       _ CTGC
                                GCGTGGC CA    GTTGATGTT
                                ||||||| ||    |||||||||
                                CGTGCTG GT    CAACTGTAG
                                   A  TA__
GAM86   FLJ22242 5' AACGTGGCCACAGGGTTGTGCT 47554      TG  A  C_  G
          G                      TAGCG  GCC CTG  GTT ATGTT
                                ||||||  ||| |||  ||| |||||
                                GTCGT  TGG GAC  CGG TGCAA
                                  GT  _  AC  _
GAM86   FLJ22283 5' GTCATCGGCGCGGATGGCTATG 50904          _        TT
          CTG                     TAGCGTGGCCA CTGCGTTGATG
                                ||||||||||| ||||||||||
                                GTCGTATCGGT GGCGCGGCTAC
                                      A         TGA
GAM86   FLJ22940 5' CGAAGCGGTGGCAGCGTTG   44998       G      G
                                TAGCGT GCCACTGC TTG
                                |||||| |||||||| |||
                                GTTGCG CGGTGGCG AGC
                                   A       A
GAM86   FLJ23191 3' GATATCAACGTGTGTATATTG  45009   C   GC   T
                                G GTG  CAC GCGTTGATGTT
                                | |||  ||| ||||||||||
                                G TAT  GTG TGCAACTATAG
                                 T  AT  _
GAM86   FLJ23231 3' GACGTTGGCCTTGGCTGGCTA  47607     G     CTGC  TG
                                TAGC TGGCCA   GT  ATGTT
                                |||| ||||||   ||  |||||
                                ATCG GTCGGT   CG  TGCAG
                                  _     TC__  GT
GAM86   FLJ23375 5' AGCGCTGGTGGCCATGCT    46946          _
                                AGCGTGGCCACT GCGTT
                                |||||||||||| |||||
                                TCGTACCGGTGG CGCGA
                                      T
GAM86   FLJ23598 5' AGTGCGGTGGCCGCCTG     96503     C
                                TAG GTGGCCACTGCGTT
                                ||| ||||||||||||||
                                GTC CGCCGGTGGCGTGA
                                  _
GAM86   FLJ23816 3' GCATTGGCGGCCGCCCTG    58978     C     ACTGC  TG
                                TAG GTGGCC    GT  ATGT
                                ||| ||||||    ||  ||||
```

```
                                GTC CGCCGG    CG  TACG
                                  C     _____  GT
GAM86   FTS     3'  AGTGTCTTAGGGTGGTTATCTA 42757    C       GCGTT  TG
                                TAG GTGGCCACT    GA  TT
                                ||| |||||||||    ||  ||
                                ATC TATTGGTGG    CT  GA
                                  _       GATT_  GT
GAM86   GNB1L   3'  GACGTTGGCTTGGGCCTGCTG  54866      T   ACTGC  TG
                                TAGCG GGCC    GT  ATGTT
                                ||||| ||||    ||  |||||
                                GTCGT CCGG    CG  TGCAG
                                   _   GTT__  GT
GAM86   GPHN    5'  TCCTGTCAGTGCGGTGACTGCG 40820      TG C          TT
            CTG                    TAGCG  G CACTGCGTTGATG
                                |||||  | ||||||||||||
                                GTCGC  C GTGGCGTGACTGT
                                   GT A          CCTC
GAM86   GPR88   5'  AGGTCAGGATGGACCGCGCTG  42133        _  _  GCGT   TG
                                TAGCGTGG CCA CT    TGA  TT
                                |||||||| ||| ||    |||  ||
                                GTCGCGCC GGT GG    ACT  GA
                                     A   A  _____  GT
GAM86   HNRPC   5'  AGCGGTTGTGGCCGCGTTG   49379          TG_
                                TAGCGTGGCCAC   CGTT
                                ||||||||||||  ||||
                                GTTGCGCCGGTG   GCGA
                                      TTG
GAM86   HSPCA   5'  AGCGTCCCGGTGTGGCTGTGC  19292     TG    TG  TT
                                GCG  GCCAC  CG  GATGTT
                                |||  |||||  ||  ||||||
                                CGT  CGGTG  GC  CTGCGA
                                  GT    TG  C_
GAM86   HYPC    3'  AGCATCAGTGCCTGCTCCTGC  65215     T  CCACT
                                GCG GG    GCGTTGATGTT
                                ||| ||    ||||||||||
                                CGT CC    CGTGACTACGA
                                  _  TCGTC
GAM86   IL-17RC  3'  GGCGTCGGCCCTGTGCCAGCTG 52179      G    C  TGC
                                TAGC TGGC AC   GTTGATGTT
                                |||| |||| ||   |||||||||
                                GTCG ACCG TG   CGGCTGCGG
                                  _   _  TCC
GAM86   KCND1   5'  AGTGTCGACCAGGCTTTGTTG  18337      T   AC  C    TG
                                TAGCG GGCC  TG GTTGA  TT
                                ||||| ||||  || |||||  ||
                                GTTGT TCGG  AC CAGCT  GA
                                   T   __ _    GT
GAM86   KIAA0144 3'  AGCATCAATGCACACACCTGCT 29943      T  CCAC
            G                   TAGCG GG    TGCGTTGATGTT
                                ||||| ||   ||||||||||||
```

```
                                GTCGT CC   ACGTAACTACGA
                                  _ ACAC
GAM86   KIAA0179 5' GGCGGACGGTGGCTGGCTG   65456     G      __
                                TAGC TGGCCACTG  CGTT
                                |||| |||||||||  ||||
                                GTCG GTCGGTGGC  GCGG
                                  _       AG
GAM86   KIAA0350 5' AATGTCAGTGCTGGGCTG    61822     G   C   _
                                TAGC TGGC ACTG CGTT
                                |||| |||| |||| ||||
                                GTCG GTCG TGAC GTAA
                                  G   _   T
GAM86   KIAA0372 3' AACATTAATGGAAAATAATGCT 28379       GGCCACTG
            G                    TAGCGT       CGTTGATGTT
                                ||||||       ||||||||||
                                GTCGTA       GTAATTACAA
                                   ATAAAAG_
GAM86   KIAA0408 5' ATATCAATGAACGTGCTA    28793       GCCACTG
                                TAGCGTG      CGTTGATGT
                                |||||||      |||||||||
                                ATCGTGC      GTAACTATA
                                   AA_____
GAM86   KIAA0435 5' GGCATCTGTATAGGTGGTTAC  29662        GCGTT_
                                GTGGCCACT     GATGTT
                                |||||||||     ||||||
                                CATTGGTGG     CTACGG
                                     ATATGT
GAM86   KIAA0493 5' GGTGAATCGCGCTGGTCACGTT 64936          C   _ G  GTT
            G                    TAGCGTGGCCA TGCG TT AT
                                |||||||||||| |||| || ||
                                GTTGCACTGGT GCGC AA TG
                                     C   T  G  G
GAM86   KIAA0495 5' AATGTCAGTGCCAACGCTG   63254       _  C   _
                                TAGCGT GGC ACTG CGTT
                                |||||| ||| |||| ||||
                                GTCGCA CCG TGAC GTAA
                                   A  _   T
GAM86   KIAA0625 5' AATATCATTCTGGTTATGTT   31177        CTGCGT
                                AGCGTGGCCA     TGATGTT
                                ||||||||||     |||||||
                                TTGTATTGGT     ACTATAA
                                     CTT___
GAM86   KIAA1194 5' GGCGGCGGTGGCGGCGCTG   97637       G      _
                                TAGCGT GCCACTGC GTT
                                |||||| |||||||| |||
                                GTCGCG CGGTGGCG CGG
                                   G       G
GAM86   KIAA1297 5' AGTGTTGGTGCAGGACCGGCTG 72629     G  CCA    TT  TG
                                TAGC TGG   CTGCG  GA  TT
                                |||| |||   |||||  ||  ||
```

```
                                GTCG GCC   GACGT  TT  GA
                                  _  AG_    GG  GT
GAM86   KIAA1322  5'  GGCGTCGGAGCCGCGCTA    73113         CA  _
                                TAGCGTGGC  CTG CGTT
                                |||||||||  ||| ||||
                                ATCGCGCCG  GGC GCGG
                                     A_  T
GAM86   KIAA1359  5'  AGCAGCGGTGGCCGGCTA    91080      G        _
                                TAGC TGGCCACTGC GTT
                                |||| |||||||||| |||
                                ATCG GCCGGTGGCG CGA
                                  _       A
GAM86   KIAA1365  3'  GATGTTCATGTGGTTATGT    40814         T___
                                GCGTGGCCAC   GCGTT
                                ||||||||||   |||||
                                TGTATTGGTG   TGTAG
                                     TACT
GAM86   KIAA1372  5'  AGTGTCTGGCAGGTGGCTGTGC 93317      TG   _  GTT  TG
           TG                     TAGCG  GCCAC TGC   GA  TT
                                |||||  ||||| |||   ||  ||
                                GTCGT  CGGTG ACG   CT  GA
                                  GT    G   GT_  GT
GAM86   KIAA1432  5'  GACATCGGCATTGGCATGTTG  67302       G   C   GT
                                TAGCGTG CCA TGC  TGATGTT
                                ||||||| ||| |||  |||||||
                                GTTGTAC GGT ACG  GCTACAG
                                   _  T  __
GAM86   KIAA1466  5'  AGCATTAGCTGCCACTGCCATG 72404         CACT  _
           CTG                    TAGCGTGGC   GC GTTGATGTT
                                |||||||||   || |||||||||
                                GTCGTACCG   CG CGATTACGA
                                     TCAC  T
GAM86   KIAA1719  5'  AGTGTCGATGGAATCCCGCTG  68724      T  CCACTG     TG
                                TAGCG GG     CGTTGA  TT
                                ||||| ||     ||||||  ||
                                GTCGC CC     GTAGCT  GA
                                  _ TAAG__     GT
GAM86   KIAA1932  5'  ACAGCGGTGTCGTGGCCGTGTT 73819          T   TT A   T
           G                     TAGCGTGGCCAC GCG  G TGT
                                ||||||||||| |||  | |||
                                GTTGTGCCGGTG TGT  C ACA
                                     C   GG G   C
GAM86   KLF5     5'  GACGTTGGCGTTTACGT     9960        CCACT   TG
                                GCGTGG    GCGT  ATGTT
                                ||||||    ||||  |||||
                                TGCATT    TGCG  TGCAG
                                  _____   GT
GAM86   MANBAL   5'  GATGTGAAAAGTGGCCATCCTG 42218     C       ____
                                TAG GTGGCCACT   GCGTT
                                ||| |||||||||   |||||
```

```
                                GTC TACCGGTGA    TGTAG
                                  C        AAAG
GAM86   MANBAL   3'  TTAGCGTTAGTGATCCCACTAG 42223     __   C__    _   GATGTT
            CTG                    TAGC  GTGG   CACTG CGTT
                                |||| ||||  ||||| ||||
                                GTCG  CACC   GTGAT GCGA
                                  AT    CTA    T      TTG
GAM86   MCT-1    3'  AATGCCTGTGGTTATGCTG   26770          T_
                                TAGCGTGGCCAC  GCGTT
                                ||||||||||||  |||||
                                GTCGTATTGGTG  CGTAA
                                       TC
GAM86   MESDC1   3'  ATGTCATCTGCTGGTTGTGTTA 42897      TG   CT   T_    T
                                TAGCG  GCCA  GCG  TGATGT
                                |||||  ||||  |||  ||||||
                                ATTGT  TGGT  CGT  ACTGTA
                                   GT   __  CT     T
GAM86   MGC11296 5'  AGCGGCGGTGGCCGGGCTG   51355     G       _
                                TAGC TGGCCACTGC GTT
                                |||| ||||||||||| |||
                                GTCG GCCGGTGGCG CGA
                                  G        G
GAM86   MGC13102 3'  TGGTGCGGTGGTTGATGTTA   51294       _       TT
                                TAGCGT GGCCACTGCG  G
                                |||||| ||||||||||  |
                                ATTGTA TTGGTGGCGT  T
                                    G        GG
GAM86   MGC14386 5'  GGCGTCGACATCTGCCGCGT   54327       CACTGC
                                GCGTGGC     GTTGATGTT
                                |||||||     |||||||||
                                TGCGCCG     CAGCTGCGG
                                    TCTA__
GAM86   MGC14801 3'  ACATTGATGCGCTGGCTTG   52084   T    C    TG
                                G GGCCA TGCGT  ATGT
                                | |||||  |||||  ||||
                                G TCGGT GCGTA  TACA
                                 T    C    GT
GAM86   MGC26766 5'  GACGTTAGTGCATTAGTGATG  59469     G  CAC
                                CGT GC   TGCGTTGATGTT
                                |||  ||   ||||||||||||
                                GTA TG   ACGTGATTGCAG
                                  G  ATT
GAM86   MGC34869 5'  GGCGTTAGACGTGCTGTGTTG  58716      TG  CACT   _
                                TAGCG  GC    GCGT TGATGTT
                                |||||  ||    |||| |||||||
                                GTTGT  CG    TGCA ATTGCGG
                                   GT  ____   G
GAM86   MGC4308  3'  AATATCAGCAAATAGTTTATGT 66183        CC   C__
            TA                   TAGCGTGG  ACTG   GTTGATGTT
                                |||||||  ||||  |||||||||
```

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                                ATTGTATT  TGAT   CGACTATAA
                                    __    AAA
GAM86   MGC4368  5'  GGCATTGGCCCCAGGTCACCTG 44726     C     ACTGC  TG
                                TAG GTGGCC    GT  ATGTT
                                ||| ||||||    ||  |||||
                                GTC CACTGG    CG  TACGG
                                  _     ACCC_  GT
GAM86   MGC4796  5'  CGGCTCGGGTGGCTGCGCTG   62163      TG     _ C
                                TAGCG  GCCACT G GTTG
                                |||||  |||||| | ||||
                                GTCGC  CGGTGG C CGGC
                                   GT     G T
GAM86   MGC5139  5'  GACATCAGCGCAGGACGTT    74572      GGCCA
                                AGCGT    CTGCGTTGATGTT
                                |||||    ||||||||||||
                                TTGCA    GACGCGACTACAG
                                   G_____
GAM86   MGC5384  3'  GACATTCAAGTGTTTATGTTA  49090       GC   GCGTT
                                TAGCGTG  CACT    GATGTT
                                |||||||  ||||    ||||||
                                ATTGTAT  GTGA    TTACAG
                                    TT    AC___
GAM86   MGC9753  5'  GCGTGGTGGTGGTCTTGCTG   54193      T     TG GTTG    T
                                TAGCG GGCCAC  C    ATGT
                                ||||| ||||||  |    ||||
                                GTCGT CTGGTG  G    TGCG
                                   T     GT G___    T
GAM86   NFKBIE   3'  GTGAAGATGGTGCTGTGCTG   17055      TG  C    CG  G
                                TAGCG  GC ACTG  TT AT
                                |||||  || ||||  || ||
                                GTCGT  CG TGGT  AA TG
                                   GT  _    AG  G
GAM86   NKX2B    3'  GCGTTAATGTCGTCAC      11811       CACT
                                GTGGC    GCGTTGATGT
                                |||||    ||||||||||
                                CACTG    TGTAATTGCG
                                   C___
GAM86   NUP107   3'  GATATCAGCGTTTCTCTGTGT  40236     TG CCACT
                                GCG  G    GCGTTGATGTT
                                |||  |    ||||||||||
                                TGT  C    TGCGACTATAG
                                  GT TCTT_
GAM86   OAZIN    5'  GGTGTCAAGTGGGCTGTTGCTG 32439      _ TG   ACT  G    TG
                                TAGC G  GCC   GC TTGA  TT
                                |||| |  |||   || ||||  ||
                                GTCG T  CGG   TG AACT  GG
                                  T GT   G__  _    GT
GAM86   PASK     5'  AATGTCGTGCTTGCTGGTGGCC 31399           _   T___
            ACGTTG                  TAGCGTGGCCACT GCG    TGATGTT
                                ||||||||||||| |||    |||||||
```

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                                GTTGCACCGGTGG CGT   GCTGTAA
                                      T  TCGT
GAM86   PASK    5' GGTCGATGCTGGTCATGCTG  31418         CT      GTT
                                TAGCGTGGCCA GCGTTGAT
                                |||||||||||  ||||||||
                                GTCGTACTGGT CGTAGCTG
                                     __      GT
GAM86   PDZD2   5' ATGTCAGTGGGGCCAGTTA  81717     G    A TG GT
                                TAGC TGGCC C  C  TGATGT
                                |||| ||||| |  |  ||||||
                                ATTG ACCGG G  G  ACTGTA
                                  _    _ GT __
GAM86   PHF5A   3' AACATCAGTCTGCTGCAGCTG 52248     _ TG  CACT CG
                                TAGC G  GC   G  TTGATGTT
                                |||| |  ||   |  ||||||||
                                GTCG C  CG   T  GACTACAA
                                  A GT  _____ CT
GAM86   PP1628  3' GACATCAGTTGCCCAGTCATGT 48077       CACT   TT_
                                GCGTGGC   GCG   GATGTT
                                |||||||   |||   ||||||
                                TGTACTG   CGT   CTACAG
                                    ACC_   TGA
GAM86   PRO0149 3' GACGGCGGTGGCTGCGTT   26941     TG      _
                                AGCG  GCCACTGC GTT
                                ||||  |||||||| |||
                                TTGC  CGGTGGCG CAG
                                  GT       G
GAM86   PRO1575 5' AACATTTCACTGTGGTTACCTG 26870    C       TGCGTT
                                TAG GTGGCCAC     GATGTT
                                ||| ||||||||     ||||||
                                GTC CATTGGTG     TTACAA
                                  _       TCACT_
GAM86   PRO1598 5' GACGTTAGTGAGAGCTGTTCTA 38129    C TG ___    _
                                TAG G  GC   CACTG CGTT
                                ||| |  ||   ||||| ||||
                                ATC T  CG   GTGAT GCAG
                                  T GT  AGA    T
GAM86   PTR4    5' GCGCGGCGTGCGGGGCCGTGCT 74494         A   __   A  T
          G                     TAGCGTGGCC CTGC  GTTG TGT
                                |||||||||| ||||  |||| |||
                                GTCGTGCCGG GGCG  CGGC GCG
                                     _   TG   _  C
GAM86   RAN     3' AATATTAGTGCAGTTAAGCTA 21988     GTGGCC
                                TAGC     ACTGCGTTGATGTT
                                ||||     ||||||||||||||
                                ATCG     TGACGTGATTATAA
                                  AAT___
GAM86   RHO6    3' AGTGTGGGGGTGGTGGTGCTG 27872     GTG    TG G  G TG
                                TAGC   GCCAC  C TT A  TT
                                ||||   |||||  | || |  ||
```

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                                GTCG   TGGTG  G GG T  GA
                                  ___    GT G  G GT
GAM86   RHOBTB1   5'  CGAGGCAGTGCCATGCTG    93092         C    G
                                TAGCGTGGC ACTGC TTG
                                ||||||||| ||||| |||
                                GTCGTACCG TGACG AGC
                                     _    G
GAM86   RPS6KB1   3'  AGCATTAATGTATGACATGCTG 61636        GC  C
                                TAGCGTG  CA TGCGTTGATGTT
                                |||||||  || ||||||||||||
                                GTCGTAC  GT ATGTAATTACGA
                                   A_ _
GAM86   RRS1      5'  GGCACGAGGCACGTGGTTATGC 31471           _  G   A
            TG                    TAGCGTGGCCAC TGC TTG TGTT
                                ||||||||||| ||| ||| ||||
                                GTCGTATTGGTG ACG AGC ACGG
                                      C  G  _
GAM86   SCGN      3'  AGCCCCTGTGTAGTGTCTGTGT 23774      TG C      TTGAT
            TG                    TAGCG  G CACTGCG    GTT
                                |||||  | |||||||    |||
                                GTTGT  C GTGATGT    CGA
                                   GT T      GTCCC
GAM86   SENP2     3'  AACATAATGGGCAGTGGTCAT  76831          GTTG_
                                GTGGCCACTGC    ATGTT
                                ||||||||||    |||||
                                TACTGGTGACG    TACAA
                                      GGTAA
GAM86   SLC34A1   3'  AGTGTCGGTGTGTGTGCATGT  13205      GC   T   TT  TG
                                GCGTG  CAC GCG  GA  TT
                                |||||  ||| |||  ||  ||
                                TGTAC  GTG TGT  CT  GA
                                   GT  _  GG  GT
GAM86   SLC34A1   3'  GATGTTGGTGCCTGCGTTA   13206      TG C    _
                                TAGCG  G CACTG CGTT
                                |||||  | ||||| ||||
                                ATTGC  C GTGGT GTAG
                                   GT C    T
GAM86   SLC38A4   5'  GGTGTTGGGGTGAGGTGGTGGT 36346      TG    __  G TG TG
            GTTG                   TAGCG  GCCACT  GC T  A  TT
                                |||||  ||||||  || |  |  ||
                                GTTGT  TGGTGG  TG G  T  GG
                                   GG     AG  G GT GT
GAM86   SPUF      3'  GATGTCAGTATCAGCTGGCT   26245      _  CG_
                                GGCCA CTG   TTGATGTT
                                ||||| |||   ||||||||
                                TCGGT GAC   GACTGTAG
                                   C   TAT
GAM86   SSI-1     3'  AGCATTAACTGGGATGCCGTGT 14981         CA_  C
            TA                    TAGCGTGGC   CTG GTTGATGTT
                                |||||||||   ||| |||||||||
```

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                                ATTGTGCCG   GGT CAATTACGA
                                     TAG  _
GAM86   TAF13    3'  GATATTGGTGCATGTAATTGCC 20125     C TG CC  _    TT
           TG                    TAG G  G  AC TGCG  GATGTT
                                 ||| |  |  || ||||  ||||||
                                 GTC C  T  TG ACGT  TTATAG
                                  _ GT AA  T    GG
GAM86   TBCC     3'  CCCCAGCGTGGTGGCGCGCTG  13602        G    TG     ATGTT
                                 TAGCGTG CCAC  CGTTG
                                 |||||||| ||||  |||||
                                 GTCGCGC GGTG  GCGAC
                                     _   GT    CCCC
GAM86   TBL1Y    5'  GCATTGATGTCCTAGGTTG   53860      G   CCACT    TG
                                 TAGC TGG    GCGT  ATGT
                                 |||| |||    ||||  ||||
                                 GTTG ATC    TGTA  TACG
                                   G   C____    GT
GAM86   TBX21    3'  GATATTGTTTGTGGTGGTTGTG 26248     TG     TG  T_
           T                     GCG  GCCAC  CG  TGATGTT
                                 |||  |||||  ||  |||||||
                                 TGT  TGGTG  GT  GTTATAG
                                   GT    GT  TT
GAM86   TCL6     5'  GAAGGTTGGTGTGGGGCTGTGC 40474       TG   A TG  TT   G
           TG                    TAGCG  GCC C  CG  GAT TT
                                 |||||  ||| |  ||  ||| ||
                                 GTCGT  CGG G  GT  TTG AA
                                    GT   _ GT  GG   G  GT
GAM86   TGOLN2   3'  AACGTCACCAATGGATTGTGCT 64739       TG _   C  C  T
           G                     TAGCG  G CCA TG GT GATGTT
                                 |||||  | ||| || || ||||||
                                 GTCGT  T GGT AC CA CTGCAA
                                    GT A   A  _  _
GAM86   TRIP3    3'  GGCATTGATGTGGCTCATGTT  78825        _     TGC  TG
                                 AGCGTG GCCAC   GT  ATGTT
                                 ||||||  |||||   ||  |||||
                                 TTGTAC CGGTG   TA  TACGG
                                    T     ___  GT
GAM86   U5-100K  5'  GACGTTGAGGCCGCGTTG    60414          ACT
                                 TAGCGTGGCC   GCGTT
                                 ||||||||||   |||||
                                 GTTGCGCCGG   TGCAG
                                      AGT
GAM86   LOC112616 3'  ATATTGACTCGGCCAGTTA   57294      G    ACT C  TG
                                 TAGC TGGCC   G GT  ATGT
                                 |||| |||||   | ||  ||||
                                 ATTG ACCGG   C CA  TATA
                                   _    ___ T  GT
GAM86   LOC115131 3'  GGCGTCAGTGACGTATGCTG   59805        GC_    _
                                 TAGCGTG   CACTG CGTT
                                 |||||||   ||||| ||||
```

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                                GTCGTAT   GTGAC GCGG
                                    GCA    T
GAM86   LOC121133 3'  AACATGGAGGCCACGCTA    76507         A  GC
                                TAGCGTGGCC CT  GTT
                                |||||||||| ||  |||
                                ATCGCACCGG GG  CAA
                                      A  TA
GAM86   LOC121536 5'  CGAGGCGGTGGCGGCGCTG   74524       G      G
                                TAGCGT GCCACTGC TTG
                                |||||| |||||||| |||
                                GTCGCG CGGTGGCG AGC
                                   G       G
GAM86   LOC123624 3'  AACATTAATGTTGCTTTGTTG  76135      T   CACT
                                TAGCG GGC    GCGTTGATGTT
                                ||||| |||    ||||||||||
                                GTTGT TCG    TGTAATTACAA
                                   T   T___
GAM86   LOC124590 5'  AGCGTCTCCCGTGCCACGCTG  76152        CACT   TT_
                                TAGCGTGGC    GCG   GATGTT
                                |||||||||    |||   ||||||
                                GTCGCACCG    TGC   CTGCGA
                                      ____   CCT
GAM86   LOC125875 5'  GACATTGAACAGGCTGGGCTG  74886     G    ACTGCG TG
                                TAGC TGGCC     T  ATGTT
                                |||| |||||     |  |||||
                                GTCG GTCGG     A  TACAG
                                  G    ACA___ GT
GAM86   LOC126123 5'  GGCGCGCGCCGGGGCCGTGCTG 74905          A  _   T A
                                TAGCGTGGCC CTG CGT G TGTT
                                |||||||||| ||| ||| | ||||
                                GTCGTGCCGG GGC GCG C GCGG
                                      _   C   _ _
GAM86   LOC126549 5'  GACATCTGGGCCAGTGGTTGCG 76209    G  TG      C  __
           GTG                    TA CG  GCCACTG GTT  GATGTT
                                || ||  ||||||| |||  ||||||
                                GT GC  TGGTGAC CGG  CTACAG
                                 G  GT      _   GT
GAM86   LOC128259 5'  GGCGTCCATGGTGCTGTGCTG  75238      TG  C  TG   T
                                TAGCG  GC AC  CGT GATGTT
                                |||||  || ||  ||| ||||||
                                GTCGT  CG TG  GTA CTGCGG
                                   GT  _  __   C
GAM86   LOC129676 5'  AATGTCAGTGCGAGCAGCC    76229     CA  _
                                GGC  CT GCGTTGATGTT
                                |||  || ||||||||||
                                CCG  GA CGTGACTGTAA
                                  AC  G
GAM86   LOC138050 5'  GGCAGGGCGCTGGCCGCGCTG  75815          CT    GA
                                TAGCGTGGCCA  GCGTT  TGTT
                                ||||||||||  |||||  ||||
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                                GTCGCGCCGGT  CGCGG  ACGG
                                      __     G_
GAM86   LOC138130 5'  TGCTTTATGTGGTGGTCGTGTT 76483          TG   TGAT  T
                                AGCGTGGCCAC  CGT    GT
                                ||||||||||  |||    ||
                                TTGTGCTGGTG  GTA    CG
                                      GT   TTT_  TG
GAM86   LOC139420 3'  AATGTTAATGTAGTTTTGTTCT 76338     C TG CC
          A                      TAG G  G  ACTGCGTTGATGTT
                                ||| |  |  ||||||||||||||
                                ATC T  T  TGATGTAATTGTAA
                                  T GT T_
GAM86   LOC142893 5'  AACATTGGCTGTTGTGTGTT   83756     _   T  _  TG
                                GGC CAC GC GT  ATGTT
                                ||| ||| || ||  |||||
                                TTG GTG TG CG  TACAA
                                  T   T  T  GT
GAM86   LOC143914 5'  TCAATGTGGGGTTATGTTG    77112          A TG
                                TAGCGTGGCC C  CGTTGA
                                ||||||||||  |  ||||||
                                GTTGTATTGG G  GTAACT
                                      _ GT
GAM86   LOC145609 5'  AGCCCCAGCGTGGCTGTGTTA  84359      TG   ACT     AT
                                TAGCG  GCC   GCGTTG  GTT
                                |||||  |||   ||||||  |||
                                ATTGT  CGG   TGCGAC  CGA
                                   GT   ___     CC
GAM86   LOC145842 5'  GATATCAGTGAACCCCCATGTT 77993        CCACTG
                                AGCGTGG     CGTTGATGTT
                                |||||||     ||||||||||
                                TTGTACC     GTGACTATAG
                                    CCCAA_
GAM86   LOC145899 5'  GATGTTGATGTCTGCTGGGCTG 84557      G    CACT    TG
                                TAGC TGGC    GCGT  ATGTT
                                |||| ||||    ||||  |||||
                                GTCG GTCG    TGTA  TGTAG
                                  G    TC__    GT
GAM86   LOC146603 5'  ATATCTGTGGTCACGTTA    78589          TGCGTT
                                TAGCGTGGCCAC     GATGT
                                ||||||||||||     |||||
                                ATTGCACTGGTG     CTATA
                                      T_____
GAM86   LOC146669 5'  GACATTGATACCCAGCCACCTG 78662     C    CACTGC  TG
                                TAG GTGGC     GT  ATGTT
                                ||| |||||     ||  |||||
                                GTC CACCG     TA  TACAG
                                  _    ACCCA_  GT
GAM86   LOC146745 5'  GGCATCAACGTGGCAACTATG  78692      CCA TG
                                CGTGG   C  CGTTGATGTT
                                |||||   |  ||||||||||
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                                GTATC  G  GCAACTACGG
                                  AAC GT
GAM86   LOC147063 5' GGCATCAGTGAGCGATGGTTGT 85018    TG   C  GT__
          GC                    GCG  GCCA TGC   TGATGTT
                                ||| |||| |||   |||||||
                                CGT  TGGT GCG   ACTACGG
                                  GT   A  AGTG
GAM86   LOC147180 5' GCATCAGGAAGCTGTGTTA   85102     TG  CA  GCGT
                                TAGCG  GC  CT   TGATGT
                                |||||  ||  ||   ||||||
                                ATTGT  CG  GG   ACTACG
                                  GT  AA  ____
GAM86   LOC148145 3' GGGTCAGTGTTCCCACTGTTA  85259     _   CCACT     TG
                                TAGC GTGG   GCGTTGA  TT
                                |||| ||||   |||||||  ||
                                ATTG CACC   TGTGACT  GG
                                  T   CT___     GT
GAM86   LOC148371 5' GACATCTCAGGCTGGTTGTGCT 79552     TG   _  GCGTT
          G                     TAGCG  GCCA CT    GATGTT
                                |||||  |||| ||    ||||||
                                GTCGT  TGGT GG    CTACAG
                                  GT   C  ACT__
GAM86   LOC149372 5' AGTGTCAAGGAGGCTGCTGCTG 80099     _ TG   A  GCG   TG
                                TAGC G  GCC CT   TTGA  TT
                                |||| |  ||| ||   ||||  ||
                                GTCG C  CGG GG   AACT  GA
                                  T GT   A  ___   GT
GAM86   LOC149386 5' GATGTCGGTGGACTCTATG   85559     ___    _
                                CGTGG   CCACTG CGTT
                                |||||   |||||| ||||
                                GTATC   GGTGGC GTAG
                                  TCA     T
GAM86   LOC149706 3' GTTGGAGTGGGGTCGCGTTG   85809        A TG G TG
                                TAGCGTGGCC C  C T  AT
                                |||||||||| |  | |  ||
                                GTTGCGCTGG G  G G  TG
                                      _ GT A GT
GAM86   LOC150170 5' GGTGTTGAAGCAGGTCACTGCT 80415     _    AC   G TG TG
          G                     TAGC GTGGCC  TGC T  A  TT
                                |||| ||||||  ||| |  |  ||
                                GTCG CACTGG  ACG A  T  GG
                                  T     __   A GT GT
GAM86   LOC150175 5' GGTGTTGAAGCAGGTCACTGCT 80454     _    AC   G TG TG
          G                     TAGC GTGGCC  TGC T  A  TT
                                |||| ||||||  ||| |  |  ||
                                GTCG CACTGG  ACG A  T  GG
                                  T     __   A GT GT
GAM86   LOC150208 5' TGCAGTTGTGGTGTGCCATGCT 86079        _  TG  TTGA   T
          A                     TAGCGTGGC CAC  CG    TGT
                                |||||||| |||  ||    |||
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                                ATCGTACCG GTG  GT    ACG
                                     T   GT  TG__   TA
GAM86   LOC150215 5'  GGTGTTGAAGCAGGTCACTGCT 80457      _     AC   G TG TG
            G                    TAGC GTGGCC  TGC T  A  TT
                                 |||| ||||||  ||| |  |  ||
                                 GTCG CACTGG  ACG A  T  GG
                                   T     __   A GT GT
GAM86   LOC150218 5'  GGTGTTGAAGCAGGTCACTGCT 80526      _     AC   G TG TG
            G                    TAGC GTGGCC  TGC T  A  TT
                                 |||| ||||||  ||| |  |  ||
                                 GTCG CACTGG  ACG A  T  GG
                                   T     __   A GT GT
GAM86   LOC150445 3'  GCATCAGTATGTCGCTCTG    80678     C    CAC   GT
                                 TAG GTGGC   TGC  TGATGT
                                 ||| |||||   |||  ||||||
                                 GTC CGCTG   ATG  ACTACG
                                   T    T__   __
GAM86   LOC151904 5'  GGCATTGGCCCAGAGCCACCCT 81207     C    CA   C  TG
            G                    TAG GTGGC  CTG GT  ATGTT
                                 ||| |||||  ||| ||  |||||
                                 GTC CACCG  GAC CG  TACGG
                                   C    A_   C  GT
GAM86   LOC152373 5'  GATGTTGATGAAACCGCACTG  81450     C   CCACTG   TG
                                 TAG GTGG     CGT  ATGTT
                                 ||| ||||     |||  |||||
                                 GTC CGCC     GTA  TGTAG
                                   A   AAA___   GT
GAM86   LOC152426 5'  GGCATCAGTGTAAAGGGCTCTG 86899    T   AC_
                                 CG GGCC   TGCGTTGATGTT
                                 || ||||   ||||||||||||
                                 GT TCGG   ATGTGACTACGG
                                  C   GAA
GAM86   LOC152627 5'  AATATTGAAATTAGGCCAGTTA 81497      G    ACTGCG TG
                                 TAGC TGGCC     T  ATGTT
                                 |||| |||||     |  |||||
                                 ATTG ACCGG     A  TATAA
                                   _    ATTAA_ GT
GAM86   LOC152793 5'  CAGAACAGTGTCGTGCTA    81548        C   CG
                                 TAGCGTGGC ACTG  TTG
                                 |||||||| ||||  |||
                                 ATCGTGCTG TGAC  GAC
                                      _   AA
GAM86   LOC152897 5'  AGCATTAATGCCCCATCCTGGC 81602     GT  CCACT
            TG                   TAGC  GG    GCGTTGATGTT
                                 ||||  ||    ||||||||||
                                 GTCG  CC    CGTAATTACGA
                                   GT  TACCC
GAM86   LOC152992 3'  GGTGTCAGGCTTGCTATGTTG  81644        CACT  G   TG
                                 TAGCGTGGC   GC TTGA  TT
                                 |||||||||   || ||||  ||
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                                GTTGTATCG   CG GACT  GG
                                    TT__ _   GT
GAM86   LOC153139 5'  AGCATCAATGCAGCATCAATTA 87137       CCA___
          TGT                    GCGTGG     CTGCGTTGATGTT
                                 ||||||     ||||||||||||
                                 TGTATT     GACGTAACTACGA
                                   AACTAC
GAM86   LOC153811 5'  ACGTTAATGTCGGTGGTT    81822         _
                                 GGCCACTG CGTTGATGT
                                 |||||||| |||||||||
                                 TTGGTGGC GTAATTGCA
                                    T
GAM86   LOC158237 5'  GGCATTGATTTATTGGGTGTGT 61083     GT G   C  C  TG
          TA                     TAGC  G CCA TG GT  ATGTT
                                 ||||  | ||| || ||  |||||
                                 ATTG  T GGT AT TA  TACGG
                                   TG G   T  T  GT
GAM86   LOC158308 3'  AATGCCAGTGCCATGCTG    88063         C   _
                                 TAGCGTGGC ACTG CGTT
                                 ||||||||| |||| ||||
                                 GTCGTACCG TGAC GTAA
                                    _   C
GAM86   LOC158333 3'  AGAGCCCGGCGCAGTGAGTCGC 88120          _        ATGTT
          GTTG                   TAGCGTGGC CACTGCGTTG
                                 ||||||||| ||||||||||
                                 GTTGCGCTG GTGACGCGGC
                                    A         CCGAGAT
GAM86   LOC158856 5'  GGCGTCGGCGGCTCTGTCTG   88291    _ T   A  _
                                 TAG CG GGCC CTG CGTT
                                 ||| || |||| ||| ||||
                                 GTC GT TCGG GGC GCGG
                                   T  C   C  T
GAM86   LOC161580 5'  ACATCAATGCCCCAAGTTG   88456     G  CCACT
                                 TAGC TGG    GCGTTGATGT
                                 |||| |||    ||||||||||
                                 GTTG ACC    CGTAACTACA
                                   A  C_____
GAM86   LOC163115 5'  ATCCAGGTGGTCATGCTA    83314          GCGTT
                                 TAGCGTGGCCACT    GAT
                                 ||||||||||||    |||
                                 ATCGTACTGGTGG    CTA
                                    AC___
GAM86   LOC164397 5'  AACATTGGCAAATGCCTGTTG 83406      T  CACTGC  TG
                                 TAGCG GGC     GT  ATGTT
                                 ||||| |||     ||  |||||
                                 GTTGT CCG     CG  TACAA
                                   _  TAAA__  GT
GAM86   LOC169270 5'  ACATTTGGTGGCTGAGCTA   83610     GT      CGTT
                                 TAGC  GGCCACTG   GATGT
                                 ||||  ||||||||   |||||
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                                ATCG  TCGGTGGT    TTACA
                                  AG       ____
GAM86   LOC197336 3'  GGCATCACGCCTGGTCATGC   59923         CT    T
                                GCGTGGCCA  GCGT GATGTT
                                |||||||||  |||| ||||||
                                CGTACTGGT  CGCA CTACGG
                                    C_   _
GAM86   LOC197350 3'  AGCGTGGGGGTGGCCGTGC    89398          ___
                                GCGTGGCCACT   GCGTT
                                ||||||||||   |||||
                                CGTGCCGGTGG   TGCGA
                                      GGG
GAM86   LOC200107 5'  GATGTTGTTGCCTGGCTGTGCT 89988       TG    CT   TT
          G                      TAGCG  GCCA  GCG  GATGTT
                                |||||  ||||  |||  ||||||
                                GTCGT  CGGT  CGT  TTGTAG
                                   GT    C_   TG
GAM86   LOC200689 5'  TCTAGTAGTGGCCAGTTA    91675      G         GTT
                                TAGC TGGCCACTGC   GA
                                |||| ||||||||||   ||
                                ATTG ACCGGTGATG   CT
                                  _         AT_
GAM86   LOC200958 5'  AGCAGCGGTGGCCGGCTA    66504      G         _
                                TAGC TGGCCACTGC GTT
                                |||| |||||||||| |||
                                ATCG GCCGGTGGCG CGA
                                  _         A
GAM86   LOC201243 5'  GGCATCAACGTGGCAACTATG  89541       CCA TG
                                CGTGG   C  CGTTGATGTT
                                |||||   |  ||||||||||
                                GTATC   G  GCAACTACGG
                                   AAC GT
GAM86   LOC202460 5'  AATGTTAGCCTTTGCTATGT   90658        CACTGC
                                GCGTGGC     GTTGATGTT
                                |||||||     |||||||||
                                TGTATCG     CGATTGTAA
                                    TTTC__
GAM86   LOC219445 3'  GCGTCAGTAATGTACGCTG    93207        GC  C   GT
                                TAGCGTG  CA TGC  TGATGT
                                |||||||  || |||  ||||||
                                GTCGCAT  GT ATG  ACTGCG
                                    __ A   __
GAM86   LOC219690 3'  GGCATCTGCTGTGGCCATGTT  94665          T   TT
                                AGCGTGGCCAC GCG  GATGTT
                                ||||||||||| |||  ||||||
                                TTGTACCGGTG CGT  CTACGG
                                      T   __
GAM86   LOC219744 5'  AGCACAGTGTTTATGTTG    93002        GC    C
                                TAGCGTG  CACTG GTT
                                |||||||  ||||| |||
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                                GTTGTAT  GTGAC CGA
                                   TT    A
GAM86   LOC219940 5'  GATGTTAGTGCCTACCTG    95000    C   C    _
                                TAG GTGG CACTG CGTT
                                ||| |||| ||||| ||||
                                GTC CATC GTGAT GTAG
                                  _   C    T
GAM86   LOC220002 3'  AGCGTTCTGTGCCATGCTA   93269        _ CT
                                TAGCGTGGC CA  GCGTT
                                ||||||||| ||  |||||
                                ATCGTACCG GT  TGCGA
                                     T  CT
GAM86   LOC220038 5'  AGTATCAGTGCTACTCGGCTAT 93374        ACT__      GTT
           GCT                    AGCGTGGCC    GCGTTGAT
                                ||||||||    ||||||||
                                TCGTATCGG    CGTGACTA
                                     CTCAT      TGA
GAM86   LOC220064 3'  AATGTCCTAGTGGATTGTGTTG 95057      TG _    CGTT
                                TAGCG  G CCACTG   GATGTT
                                |||||  | ||||||   ||||||
                                GTTGT  T GGTGAT   CTGTAA
                                   GT A    C___
GAM86   LOC220081 5'  GACATTGATAATAAAGTGACGT 93404      G  CACTGC  TG
           TG                    TAGCGT GC    GT  ATGTT
                                |||||| ||    ||  |||||
                                GTTGCA TG    TA  TACAG
                                   G  AAATAA  GT
GAM86   LOC253219 3'  GCATCGGAGGCCGTGC      99348       A  GCGTT
                                GCGTGGCC CT    GATGT
                                |||||||| ||    |||||
                                CGTGCCGG GG    CTACG
                                     A  _____
GAM86   LOC254050 3'  AACGTTGGAGGGCATATGCTG  96559       _  A  GCG TG
                                TAGCGTG GCC CT   T  ATGTT
                                ||||||| ||| ||   |  |||||
                                GTCGTAT CGG GA   G  TGCAA
                                     A  _  ___ GT
GAM86   LOC254065 5'  AGCATTAATGTGGGAGGTACGC 99287       G  A_ TG
           TA                    TAGCGTG CC  C  CGTTGATGTT
                                ||||||| ||  |  ||||||||||
                                ATCGCAT GG  G  GTAATTACGA
                                   _  AG GT
GAM86   LOC254655 5'  AATATTAATGCCTATGTTGTGT 97206     TG  CACT
           T                     AGCG  GC    GCGTTGATGTT
                                ||||  ||   ||||||||||
                                TTGT  TG   CGTAATTATAA
                                  GT  TATC
GAM86   LOC255131 5'  AGTGTCAGTGTAGCTACTGT   97689    _    CAC      TG
                                GC GTGGC   TGCGTTGA  TT
                                || |||||  ||||||||  ||
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                                TG CATCG   ATGTGACT  GA
                                 T    ___       GT
GAM86   LOC255215 3' GGGTTAGCAAGAGCCGTGT   98668       CA  GC    TG
                                GCGTGGC  CT  GTTGA  TT
                                |||||||  ||  |||||  ||
                                TGTGCCG  GA  CGATT  GG
                                   A_  A_    GT
GAM86   LOC256948 3' GCGTCGGTGGCTGGGCTG    96117     G       _
                                TAGC TGGCCACTG CGT
                                |||| ||||||||| |||
                                GTCG GTCGGTGGC GCG
                                  G       T
GAM86   LOC257044 5' GATGATAATGGCTATGTTA   97263          C  _
                                TAGCGTGGCCA TG CGTT
                                |||||||||| || ||||
                                ATTGTATCGGT AT GTAG
                                      A  A
GAM86   LOC257478 5' GGCACGCTGGTGGTGGTGGTGC 73503      TG    ____   TGATGTT
           TG                     TAGCG  GCCACT   GCGT
                                |||||  ||||||   ||||
                                GTCGT  TGGTGG   CGCA
                                  GG     TGGT   CGG  T
GAM86   LOC51003  3' CAACTAGTGGTTAGTTA     32670     G       C
                                TAGC TGGCCACTG GTTG
                                |||| ||||||||| ||||
                                ATTG ATTGGTGAT CAAC
                                  _       _
GAM86   LOC51117  3' GTATCAGTCGTCTGGGCTCATG 32634       _  ACT  _    GTT
           CTG                    TAGCGTG GCC   GCG TTGAT
                                |||||||  |||   |||  |||||
                                GTCGTAC CGG   TGC GACTA
                                   T   GTC   T    TGA
GAM86   LOC51157  3' GTGAACCGGTGGTTGTCTG   33016     C TG      C   G
                                TAG G  GCCACTG GTT AT
                                |||  |  |||||||  |||  ||
                                GTC T  TGGTGGC CAA TG
                                 _ GT      _   G
GAM86   LOC54550  3' CAGAGCAGTGTCTGTGCTG   78183      TG C     G
                                TAGCG  G CACTGC TTG
                                |||||  |  ||||||  |||
                                GTCGT  C GTGACG GAC
                                  GT T     A
GAM86   LOC56899  5' ACATTAATCTGTCAAGCTG   39711     G   CACTGC
                                TAGC TGGC     GTTGATGT
                                ||||  ||||     ||||||||
                                GTCG ACTG     TAATTACA
                                  A   TC____
GAM86   LOC90019  5' GGCATTGATGCTGTGTGCGCGT 57532      GC   T   TG
                                GCGTG  CAC GCGT  ATGTT
                                |||||  |||  ||||  |||||
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                                TGCGC  GTG CGTA  TACGG
                                  GT   T    GT
GAM86   LOC90410  3'  AACATCAGTGCACAGCTGCTGC 63350     _ TG  CAC
            TG                   TAGC G  GC   TGCGTTGATGTT
                                 |||| |  ||   ||||||||||||
                                 GTCG C  CG   ACGTGACTACAA
                                   T GT  AC_
GAM86   LOC91266  5'  GGCATGGAGGTGGTCACGCT   66022          GCG  G
                                 AGCGTGGCCACT   TT ATGTT
                                 ||||||||||||   || |||||
                                 TCGCACTGGTGG   AG TACGG
                                        ___  G
GAM86   LOC91445  5'  GGCGTTAGTATTGGCCGTGT   61171         C   GT
                                 GCGTGGCCA TGC  TGATGTT
                                 |||||||||  |||  |||||||
                                 TGTGCCGGT ATG  ATTGCGG
                                      T  __
GAM86   LOC91862  3'  AGCGTTGGTGTGGTGGGCGGAG 54567    G_  G    TG  TT
            CT                   AGC  TG CCAC  CG  GATGTT
                                 |||  ||  ||||  ||  ||||||
                                 TCG  GC GGTG  GT  TTGCGA
                                   AG  G    GT  GG
GAM86   LOC92162  3'  AGCGTCAGTGGACCCAGTGCTG 68904      _  __     _
                                 TAGCG TGG  CCACTG CGTT
                                 |||||  |||  ||||||  ||||
                                 GTCGT ACC  GGTGAC GCGA
                                   G   CA     T
GAM86   LOC93017  3'  AACAGAGATAGTGGACTACGCT 71701        _    GC   GA
            G                    TAGCGTGG CCACT  GTT  TGTT
                                 ||||||||  |||||  |||  ||||
                                 GTCGCATC GGTGA  TAG  ACAA
                                      A    __  AG
GAM87   FLJ12903  3'  TTACTTTTTTATTTGAA     43080          C
                                 TTCAAATAA AAAAGTAG
                                 |||||||||  ||||||||
                                 AAGTTTATT TTTTCATT
                                          _
GAM87   FLJ12934  3'  CAGACTGGCTTTTGTTACCTGA 43487     AA        AGAT
                                 TCA  TAACAAAAGT    TCTG
                                 |||  ||||||||||    ||||
                                 AGT  ATTGTTTTCG    AGAC
                                   CC         GTC_
GAM87   KIAA0825  3'  TTACTTTTGTTTTCTGAA    61693      AAT
                                 TTCA   AACAAAAGTAG
                                 ||||   ||||||||||
                                 AAGT   TTGTTTTCATT
                                   CTT
GAM87   METAP1   3'  TTACTTTTATTATTTGAA    73038          C
                                 TTCAAATAA AAAAGTAG
                                 |||||||||  ||||||||
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                                AAGTTTATT TTTTCATT
                                     A
GAM87   POFUT1   3'  TCACTATTGTTATTTGAA    70983          A  A
                                TTCAAATAACAA AGT GA
                                |||||||||||| ||| ||
                                AAGTTTATTGTT TCA CT
                                      A  _
GAM87   SAC2     3'  CAGAGCACTTTGCTTATTTGAA 30722        CA   AGA
                                TTCAAATAA  AAAGT  TTCTG
                                |||||||||  |||||  |||||
                                AAGTTTATT  TTTCA  GAGAC
                                     CG   C__
GAM87   STK39    3'  CAGAATCTGAGTTTTACTTGAA 26010      A  CA  AG
                                TTCAA TAA  AA  TAGATTCTG
                                |||||  |||  ||  |||||||||
                                AAGTT ATT  TT  GTCTAAGAC
                                   C  __  GA
GAM87   LOC115294 3'  CTACTTTTGCTTTTGAA    73381       TAA
                                TTCAAA   CAAAAGTAG
                                ||||||   |||||||||
                                AAGTTT   GTTTTCATC
                                   TC_
GAM87   LOC122830 3'  CAGTGATGCTTTTGTTATTT   74629           GATT
                                AAATAACAAAAGTA   CTG
                                ||||||||||||||   |||
                                TTTATTGTTTTCGT   GAC
                                      AGT_
GAM87   LOC92344  3'  CTGCGTTTTGTTATTTGAA   69576           _
                                TTCAAATAACAAAA GTAG
                                |||||||||||||| ||||
                                AAGTTTATTGTTTT CGTC
                                      G
GAM88   KCNJ8    3'  CAGACTGAACCAGAGCTGG   18361       T   C  A
                                TCAGCT CTGG TCA TCTG
                                |||||| |||| ||| ||||
                                GGTCGA GACC AGT AGAC
                                   _   A  C
GAM88   MMP19    3'  CAGCATGGCCAGTAAACTGAGC 11619        C  _   T  AT
          AA                      TTGCTCAG TT CTGGC CA  CTG
                                |||||||| || ||||| ||  |||
                                AACGAGTC AA GACCG GT  GAC
                                   A  T    _  AC
GAM88   MMP19    3'  CAGCATGGCCAGTAAACTGAGC 43302        C  _   T  AT
          AA                      TTGCTCAG TT CTGGC CA  CTG
                                |||||||| || ||||| ||  |||
                                AACGAGTC AA GACCG GT  GAC
                                   A  T    _  AC
GAM88   MMP19    3'  CAGCATGGCCAGTAAACTGAGC 43310        C  _   T  AT
          AA                      TTGCTCAG TT CTGGC CA  CTG
                                |||||||| || ||||| ||  |||
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                                AACGAGTC AA GACCG GT  GAC
                                    A  T    _  AC
GAM88   MMP19    3'  CAGCATGGCCAGTAAACTGAGC 43313        C  _    T  AT
          AA                    TTGCTCAG TT CTGGC CA  CTG
                                |||||||| || ||||| ||  |||
                                AACGAGTC AA GACCG GT  GAC
                                    A  T    _  AC
GAM88   PRDM4    3'  CAGATTGGGAAAACTGAGCA   25740       CTTCTGG
                                TGCTCAG      CTCAATCTG
                                |||||||      |||||||||
                                ACGAGTC      GGGTTAGAC
                                   AAAA___
GAM88   DRIL2    3'  CAGATCACCCCCAAAGCCAAGC 22345      CA   C   CTCA_
          AA                    TTGCT  GCTT TGG    ATCTG
                                |||||  |||| |||    |||||
                                AACGA  CGAA ACC    TAGAC
                                  AC   _  CCCAC
GAM88   FLJ22405 3'  AGCCCCAAAGCTGAGCAA    42813         CT_
                                TTGCTCAGCTT   GGCT
                                ||||||||||   ||||
                                AACGAGTCGAA   CCGA
                                      ACC
GAM88   KIAA0472 3'  CAGATGTGTAAAAGCTGAGGAA 72342    G      CTG  TCA
                                TT CTCAGCTT   GC   ATCTG
                                || ||||||||   ||   |||||
                                AA GAGTCGAA   TG   TAGAC
                                 G       AA_  TG_
GAM88   KIAA1276 5'  GAACCAGCAGCTGAGCAA    67030         T   C
                                TTGCTCAGCT CTGG TC
                                |||||||||| |||| ||
                                AACGAGTCGA GACC AG
                                      C   A
GAM88   TMEM8    3'  CAGATTGATTTCCAGCTGA   41472       TCT  C__
                                TCAGCT   GG   TCAATCTG
                                ||||||   ||   ||||||||
                                AGTCGA   CC   AGTTAGAC
                                   ___  TTT
GAM88   LOC144603 3'  AGCCCCAAAGCTGAGCAA    61011         CT_
                                TTGCTCAGCTT   GGCT
                                ||||||||||   ||||
                                AACGAGTCGAA   CCGA
                                      ACC
GAM88   LOC149606 3'  AGATCTCAGAAGCTGAG     80255          CTCA
                                CTCAGCTTCTGG    ATCT
                                ||||||||||||    ||||
                                GAGTCGAAGACT    TAGA
                                      C___
GAM88   LOC150225 3'  GTCACAAAAGACTGAGCAA    86202        _   C__
                                TTGCTCAG CTT   TGGC
                                |||||||| |||   ||||
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                                AACGAGTC GAA   ACTG
                                    A   AAC
GAM88   LOC204084 5'  AGACAGAGAGCTGAGCAA    90989          _   G
                                TTGCTCAGCT TCTG CT
                                |||||||||| |||| ||
                                AACGAGTCGA AGAC GA
                                     G   A
GAM89   ALDH1A3   3'  AGAATCAATAGCCCAGAGA   7334       CA   _
                                TCTC  GGCT TTGATTTT
                                ||||  |||| ||||||||
                                AGAG  CCGA AACTAAGA
                                  AC   T
GAM89   EPB41L2   3'  ACAATGACCAGAAGCCTGAAGA 9290      C       GATTT_
                                TCT CAGGCTTT     TTGT
                                ||| ||||||||     ||||
                                AGA GTCCGAAG     AACA
                                  A       ACCAGT
GAM89   GDF2      3'  ACAACAGGAAAGCCTGGG    33018          GA  T
                                TCCAGGCTTT  TT TTGT
                                ||||||||||  || ||||
                                GGGTCCGAAA  GA AACA
                                     G_  C
GAM89   KCNA3     3'  ACAACTATCAAAGTCTAGA    11131    C        TT
                                TC AGGCTTTGAT  TTGT
                                || ||||||||||  ||||
                                AG TCTGAAACTA  AACA
                                 A         TC
GAM89   LNPEP     3'  GGTACAAAGTTAGCTCTGAAGA 19940     C   _   TTGAT
                                TCT CAG GCT     TTTTGTACC
                                ||| ||| |||     |||||||||
                                AGA GTC CGA     GAAACATGG
                                  A   T   TT____
GAM89   NQO1      3'  GGTACAATTGTAAACCTAGAG  8052      C   C    ATTT
                                CTC AGG TTTG    TTGTACC
                                ||| ||| ||||    |||||||
                                GAG TCC AAAT    AACATGG
                                  A   _    GTT_
GAM89   OPHN1     3'  ACACATTACAAGCCTGGA     11903          _    TTT
                                TCCAGGCTT TGAT   TGT
                                ||||||||| ||||   |||
                                AGGTCCGAA ATTA   ACA
                                     C    C__
GAM89   RPA3      5'  ACAAGTGGCAAAAGCCTGAAGA 12901      C       GATT_
                                TCT CAGGCTTT     TTTGT
                                ||| ||||||||     |||||
                                AGA GTCCGAAA     GAACA
                                  A       ACGGT
GAM89   TCF8      3'  GAAATCAAAACCTGGAGA     48430          C
                                TCTCCAGG TTTGATTTT
                                |||||||| |||||||||
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                                AGAGGTCC AAACTAAAG
                                    A
GAM89   TFRC     3'  ACATCTTCAAAGCTTGAAGA   13700     C        TTTT
                                TCT CAGGCTTTGA   TGT
                                ||| ||||||||||   |||
                                AGA GTTCGAAACT   ACA
                                  A        TCT_
GAM89   TNFRSF10A 3'  TACAAAAATTAACTGGA     15239      GCT
                                TCCAG   TTGATTTTTGTA
                                |||||   ||||||||||||
                                AGGTC   AATTAAAAACAT
                                  ___
GAM89   ASAHL    3'  TACAAAAATCAACCAGGCATG  64320    G  ___
                                CA GCT   TTGATTTTTGTA
                                || |||   ||||||||||||
                                GT CGG   AACTAAAAACAT
                                 A   ACC
GAM89   CASPR3   3'  ACACAGTTGAAGCCTGGA    54453        TG   TT
                                TCCAGGCTT  ATT  TGT
                                |||||||||  |||  |||
                                AGGTCCGAA  TGA  ACA
                                     GT   C_
GAM89   CNR2     3'  ACAAAAAGGCCTGGG      10232        TTGA
                                TCCAGGCT   TTTTTGT
                                ||||||||   |||||||
                                GGGTCCGG   AAAAACA
                                   _____
GAM89   DKFZP434D193 3'  TACAAGGTGAGCCCAGAGA   90293     CA    TGAT
                                TCTC  GGCTT   TTTTGTA
                                ||||  |||||   |||||||
                                AGAG  CCGAG   GGAACAT
                                  AC    T___
GAM89   FLJ14397  3'  GCAGCTGCCTCAATAGCCTGGA 52328          _   TTT__
            GA                    TCTCCAGGCT TTGA    TTGT
                                |||||||||| ||||    ||||
                                AGAGGTCCGA AACT    GACG
                                      T   CCGTC
GAM89   FLJ14675  5'  GGTACAAAACTAAACCTGAAGG 52590    C   C   AT
                                TCT CAGG TTTG  TTTTGTACC
                                ||| |||| ||||  |||||||||
                                GGA GTCC AAAT  AAAACATGG
                                  A   _   C_
GAM89   FLJ32954  3'  GCACAGTGAAGGCCTGGAGA   59189          G   TT
                                TCTCCAGGCTTT ATT  TGT
                                |||||||||||| |||  |||
                                AGAGGTCCGGAA TGA  ACG
                                       G   C_
GAM89   GAB3     3'  ACACAGGTCAAAACCAAGAGA  55517      CA  C      T
                                TCTC  GG TTTGATTT TGT
                                ||||  || ||||||||| |||
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                                AGAG  CC AAACTGGA ACA
                                  AA  A       C
GAM89   GBA2     3'  GGTACAAATAAAAGACCCAGA  71578    CA  _   GATT
                                TC  GG CTTT    TTTGTACC
                                ||  || ||||    ||||||||
                                AG  CC GAAA    AAACATGG
                                 AC  A    AT__
GAM89   GIOT-2   3'  GTACAAAAACCAGGGGAGA   33218      AGGC    A
                                TCTCC    TTTG TTTTTGTAC
                                |||||    |||| |||||||||
                                AGAGG    GGAC AAAAACATG
                                   _____    C
GAM89   HTEX4    5'  GGTACAAAATGTGAGAGCCCAG 99566    CA     G  _
          A                      TC  GGCTTT AT TTTTGTACC
                                ||  |||||| || |||||||||
                                AG  CCGAGA TG AAAACATGG
                                 AC      G  T
GAM89   HTEX4    5'  GGTACAAAATGTGAGAGCCCAG 99721    CA     G  _
          A                      TC  GGCTTT AT TTTTGTACC
                                ||  |||||| || |||||||||
                                AG  CCGAGA TG AAAACATGG
                                 AC      G  T
GAM89   HTEX4    5'  GGTACAAAATGTGAGAGCCCAG 93725    CA     G  _
          A                      TC  GGCTTT AT TTTTGTACC
                                ||  |||||| || |||||||||
                                AG  CCGAGA TG AAAACATGG
                                 AC      G  T
GAM89   KIAA0635 3'  TACAAAAATCAATCGTGAAGA  28419     C  GGCT
                                TCT CA    TTGATTTTTGTA
                                |||  ||    ||||||||||||
                                AGA GT    AACTAAAAACAT
                                  A  GCT_
GAM89   KIAA1505 5'  TACAAAAATTCTGGA       95849       GCTTT
                                TCCAG     GATTTTTGTA
                                |||||     ||||||||||
                                AGGTC     TTAAAAACAT
                                          _____
GAM89   KLHL4    3'  GAAATCAAAATCTGGAGA    39421        GC
                                TCTCCAG  TTTGATTTT
                                |||||||  |||||||||
                                AGAGGTC  AAACTAAAG
                                    TA
GAM89   MGC21675 3'  TACAAAAAGTGCCTGGGA    54597    T     TTTGA
                                TC CCAGGC     TTTTTGTA
                                || ||||||     ||||||||
                                AG GGTCCG     AAAAACAT
                                 _     TG___
GAM89   LOC124460 5'  GAAATCAAGGCCTGGAGA    76561
                                TCTCCAGGCTTTGATTTT
                                ||||||||||||||||||
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                                AGAGGTCCGGAACTAAAG

GAM89   LOC143916 3'  GGTACAGGGAGAAGACCTGGA  77143       _   GA
                                TCCAGG CTTT  TTTTTGTACC
                                |||||| ||||  ||||||||||
                                AGGTCC GAAG  AGGGACATGG
                                   A   __
GAM89   LOC150606 5'  TACAAAAATCACATTGTGAGA  86273     _  GCTT
                                TCTC CAG    TGATTTTTGTA
                                |||| |||    ||||||||||
                                AGAG GTT    ACTAAAAACAT
                                  T   AC__
GAM89   LOC152627 5'  TACAAAAACTAGCCTGG     81514        TTGA
                                CCAGGCT    TTTTTGTA
                                |||||||    ||||||||
                                GGTCCGA    AAAAACAT
                                    TC__
GAM89   LOC220279 5'  TACAAGGAAGTCTGGA      95979          GATT
                                TCCAGGCTTT    TTTGTA
                                ||||||||||    ||||||
                                AGGTCTGAAG    GAACAT
                                      ____
GAM89   LOC253298 5'  ACACCACAAACCTGGAGA    99011        C    ATTTT
                                TCTCCAGG TTTG     TGT
                                |||||||| ||||     |||
                                AGAGGTCC AAAC     ACA
                                    _    ACC__
GAM89   LOC256730 5'  ACATCCTAAAGCCTGAAGA   96938     C       ATTTT
                                TCT CAGGCTTTG     TGT
                                ||| |||||||||     |||
                                AGA GTCCGAAAT     ACA
                                  A        CCT__
GAM89   LOC257571 5'  ACACCACAAACCTGGAGA    99801        C    ATTTT
                                TCTCCAGG TTTG     TGT
                                |||||||| ||||     |||
                                AGAGGTCC AAAC     ACA
                                    _    ACC__
GAM89   LOC57086  3'  GGTAATTGTCAAAGCCTAGGA  40128     _        TTTTG
                                TCC AGGCTTTGAT     TACC
                                ||| ||||||||||     ||||
                                AGG TCCGAAACTG     ATGG
                                  A         TTA__
GAM89   LOC90589  5'  GTACAAAAATCCCAGGAGA   59776      A  CTTT
                                TCTCC GG    GATTTTTGTAC
                                ||||| ||    ||||||||||
                                AGAGG CC    CTAAAAACATG
                                   A  ____
GAM89   LOC90826  5'  TACTGGATAAAGCCTGGAGA  64787           A   TT
                                TCTCCAGGCTTTG TTT  GTA
                                |||||||||||| |||  |||
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                                AGAGGTCCGAAAT AGG  CAT
                                      _  T_
GAM90   NT5C2    5' GTAATACAAAATACAGTTA   25267   T         C
                                A ACTGTATTTTGTA TAT
                                | ||||||||||||| |||
                                A TGACATAAAACAT ATG
                                 T          A
GAM90   ARFGAP3  3' CATCACAAATCAATACGGTATA 28122          TT  TACTA
                                TATACTGTAT  TG    TGATG
                                ||||||||||  ||    |||||
                                ATATGGCATA  AC    ACTAC
                                      __  TAAAC
GAM90   KIAA0853 3' CATGTACAAAATACATATA   31212     C         T
                                TATA TGTATTTTGTAC ATG
                                |||| ||||||||||| |||
                                ATAT ACATAAAACATG TAC

                                  _         _
GAM90   SEC22A   3' CATCACAAGTATCGAAAATACA 25798          ___    A_
           GTA                    TACTGTATTTT  GTACT  TGATG
                                ||||||||||  |||||  |||||
                                ATGACATAAAA  TATGA  ACTAC
                                      GC    AC
GAM90   ZNF17    3' AGTAAAAATACAGTATA     83267           G
                                TATACTGTATTTT TACT
                                |||||||||||| ||||
                                ATATGACATAAAA ATGA

                                      _
GAM91   CASQ2    3' CAGCAGTCAATTAACTCTCCAG 8780          GA  _
           T                     ACTGGAGAG  AAT GACTGCTG
                                |||||||||  ||| ||||||||
                                TGACCTCTC  TTA CTGACGAC
                                     AA   A
GAM91   FCER2    3' CAACAGCACCCTCTCCAG    10600         AAA  A   C
                                CTGGAGAGG   TG CTG TG
                                |||||||||   || ||| ||
                                GACCTCTCC   AC GAC AC
                                     C__  _   A
GAM91   FCER2    3' CAACAGCACCCTCTCCAG    10601         AAA  A   C
                                CTGGAGAGG   TG CTG TG
                                |||||||||   || ||| ||
                                GACCTCTCC   AC GAC AC
                                     C__  _   A
GAM91   FCER2    3' CAACAGCACCCTCTCCAG    10602         AAA  A   C
                                CTGGAGAGG   TG CTG TG
                                |||||||||   || ||| ||
                                GACCTCTCC   AC GAC AC
                                     C__  _   A
GAM91   FCER2    3' CAACAGCACCCTCTCCAG    10603         AAA  A   C
                                CTGGAGAGG   TG CTG TG
                                |||||||||   || ||| ||
```

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                                GACCTCTCC   AC GAC AC
                                    C__  _   A
GAM91   FCER2    3'  CAACAGCACCCTCTCCAG    10604        AAA  A   C
                                CTGGAGAGG   TG CTG TG
                                |||||||||   || ||| ||
                                GACCTCTCC   AC GAC AC
                                    C__  _   A
GAM91   LFNG     3'  TCAGCATTTAATCTCCTCTCCA 94215        AA_   C
                                TGGAGAGGA   TGA TGCTGA
                                |||||||||   ||| ||||||
                                ACCTCTCCT   ATT ACGACT
                                    CTA   T
GAM91   MID2     3'  TCAGCAGTTCTTCCCCTCC    54483     A    AT
                                GGAG GGAA  GACTGCTGA
                                |||| ||||  |||||||||
                                CCTC CCTT  TTGACGACT
                                  C    C_
GAM91   NESH     5'  CAGTTTCCTCTCCAG       33568         AAT
                                CTGGAGAGGA   GACTG
                                ||||||||||   |||||
                                GACCTCTCCT   TTGAC
                                    ___
GAM91   PDE4A    5'  CGGCACCCCCTCCCCAGTG   21681       A    AAATGAC
                                TACTGG GAGG      TGCTG
                                |||||| ||||      |||||
                                GTGACC CTCC      ACGGC
                                   C    CCC____
GAM91   PTGIS    3'  TCAGCAGTCAGTCCCCCA    8228     AGA   AA
                                TGG   GGA  TGACTGCTGA
                                |||   |||  ||||||||||
                                ACC   CCT  ACTGACGACT
                                  C__   G_
GAM91   RSU1     3'  CAGCACCTTCTCTCTCCA    25781        _   ATGAC
                                TGGAGAG GAA    TGCTG
                                ||||||| |||    |||||
                                ACCTCTC CTT    ACGAC
                                    T   CC___
GAM91   FLJ14950 3'  TCAGCAGTCACCATCATCCAG  52798      _ _  AAA
                                CTGGA GA GG   TGACTGCTGA
                                ||||| || ||   ||||||||||
                                GACCT CT CC   ACTGACGACT
                                   A  A  ___
GAM91   FLJ23590 3'  CAGCAGTCACTTCCAGTTCA  45364     GA    A
                                TGGA  GGAA TGACTGCTG
                                ||||  |||| |||||||||
                                ACTT  CCTT ACTGACGAC
                                  GA    C
GAM91   HCA4     3'  CAGCAGTCACCACCAGT     57740      AGA  AAA
                                ACTGG   GG   TGACTGCTG
                                |||||   ||   |||||||||
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                                TGACC  CC  ACTGACGAC
                                  A__ ___
GAM91   INA     3' CAGCAGTCACTTCGGCCAG  52174    A_  AAA
                                CTGG GAGG  TGACTGCTG
                                |||| ||||  |||||||||
                                GACC CTTC  ACTGACGAC
                                  GG  ___
GAM91   KIAA0182 3' TCAACAAGCACCTTCCTCTCCA 72503       A_ AC C
                                TGGAGAGGAA TG TG TGA
                                |||||||||| || || |||
                                ACCTCTCCTT AC AC ACT
                                     CC GA A
GAM91   KIAA0218 3' CACAACCATCTCCTCTCCAG  29293       A  AC C
                                CTGGAGAGGA ATG TG TG
                                |||||||||| |||  || ||
                                GACCTCTCCT TAC AC AC
                                     C  CA _
GAM91   KIAA1634 3' CAGCAGTCATGGGCACAGTA  64122     GAGAGGAA
                                TACTG      ATGACTGCTG
                                |||||      ||||||||||
                                ATGAC      TACTGACGAC
                                  ACGGG___
GAM91   KLF12   3' AGCAATTTCCCTCCA     33275     A    GAC
                                TGGAG GGAAAT  TGCT
                                ||||| ||||||  ||||
                                ACCTC CCTTTA  ACGA
                                  _    ___
GAM91   MGC16063 3' CAGCAACACTCTTCAGTA   54927       GAAATGAC
                                TACTGGAGAG      TGCTG
                                ||||||||||      |||||
                                ATGACTTCTC      ACGAC
                                     ACA_____
GAM91   PPAN    3' CAGCCCTTCCACTCCAGTA   39981       A   ATGACT
                                TACTGGAG GGAA    GCTG
                                |||||||| ||||    ||||
                                ATGACCTC CCTT    CGAC
                                   A   CC____
GAM91   RNF20   3' CAGGCTCTCCTCTTCAGTA   39461         AATGA
                                TACTGGAGAGGA   CTG
                                ||||||||||||   |||
                                ATGACTTCTCCT   GAC
                                     CTCG_
GAM91   LOC144695 5' CAGCACTCCCTCCCTCCAG   84096      A  AAT  C
                                CTGGAG GGA  GA TGCTG
                                |||||| |||  || |||||
                                GACCTC CCT  CT ACGAC
                                  _  CC_  C
GAM91   LOC149301 3' CAGCCATTCCCTCTCCAG    80016       A   ACT
                                CTGGAGAGG AATG  GCTG
                                ||||||||| ||||  ||||
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                                GACCTCTCC TTAC   CGAC
                                    C   ___
GAM91   LOC196527 3'  GTCACTTCCTCTCTAGTA    89100          A
                                TACTGGAGAGGAA TGAC
                                |||||||||||| ||||
                                ATGATCTCTCCTT ACTG
                                      C
GAM91   LOC202052 3'  CGGTCATTTCCCCTCAGTA   91897      G  A
                                TACTG AG GGAAATGACTG
                                ||||| || ||||||||||
                                ATGAC TC CCTTTACTGGC
                                  _  C
GAM91   LOC221540 3'  CAGCAGTCATGGGTTTCAG   95475       AGGAA
                                CTGGAG    ATGACTGCTG
                                ||||||    ||||||||||
                                GACTTT    TACTGACGAC
                                   GGG__
GAM91   LOC221756 3'  CAGACTTCCTCTCCAGTG    93757           ATGA
                                TACTGGAGAGGAA   CTG
                                ||||||||||||   |||
                                GTGACCTCTCCTT   GAC
                                      CA__
GAM91   LOC257545 3'  CAGCAGTCATGGGTTTCAG   99639       AGGAA
                                CTGGAG    ATGACTGCTG
                                ||||||    ||||||||||
                                GACTTT    TACTGACGAC
                                   GGG__
GAM91   LOC257598 3'  CAGCAGTCATGGGTTTCAG   99747       AGGAA
                                CTGGAG    ATGACTGCTG
                                ||||||    ||||||||||
                                GACTTT    TACTGACGAC
                                   GGG__
GAM91   LOC92578  3'  TGGCCCTCCCTCTCCAG     70397        AAAT  CT
                                CTGGAGAGG   GA  GCTG
                                |||||||||   ||  ||||
                                GACCTCTCC   CT  CGGT
                                     ____  CC
GAM92   APXL2     5'  CTCTGCCACCTCTGATCCCA   75678       _  A   A  A
                                TGGGATC GA GTG CA AG
                                ||||||| || ||| || ||
                                ACCCTAG CT CAC GT TC
                                    T  C   C  C
GAM92   GAL3ST2   5'  ACGCTGCCACCTGATCCCA   53480        AA   ACAA
                                TGGGATCG  GTG   AGTGT
                                ||||||||  |||   |||||
                                ACCCTAGT  CAC   TCGCA
                                    C_   CG__
GAM93   ACCN1     3'  GGGGCTTCGGCGCCAAAGGTG 8461       CT__
                                CACC   GTGCTGGAGTCCC
                                ||||   ||||||||||||
```

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                                GTGG   CGCGGCTTCGGGG
                                  AAAC
GAM93   ADK     5'  GGGGCCGGCCGCGCGGGGTGTG 22990          T  A__
            TG                   CATGCACCCTGTGC GG   GTCCC
                                 |||||||||||||| ||   |||||
                                 GTGTGTGGGGCGCG CC   CGGGG
                                        _  GGC
GAM93   ANGPT2   5'  GGGACTCTGGACGTGTGTTTG  8560     T    CC   G TG
                                 CA GCAC  TGT C  GAGTCCC
                                 || ||||  ||| |  |||||||
                                 GT TGTG  GCA G  CTCAGGG
                                  T   T_  _ GT
GAM93   APXL    5'  GGGACTGCCCGGAGTGCATG   9715        C   T  TGG
                                 CATGCAC CTG GC   AGTCCC
                                 ||||||| ||| ||   ||||||
                                 GTACGTG GGC CG   TCAGGG
                                     A   C  ___
GAM93   ATP6IP1   3'  GGGCAGGAGCATGGGGTGC   8633          GGA   C
                                 GCACCCTGTGCT   GTCC
                                 ||||||||||||   ||||
                                 CGTGGGGTACGA   CGGG
                                        GGA
GAM93   B4GALT5   3'  GGGTGTGTGTAGGGGTGTGTG  17691         G   TGGAGT
                                 CATGCACCCT TGC     CCC
                                 |||||||||| |||     |||
                                 GTGTGTGGGG ATG     GGG
                                       _   TGTGT_
GAM93   BAK1     3'  GGGATTCTGGGCTTGGGGTGT  93632        T _ TG
                                 GCACCCTG G C  GAGTCCC
                                 |||||||| | |  |||||||
                                 TGTGGGGT C G  CTTAGGG
                                     T G GT
GAM93   BST2     3'  GGGGTGCGGTGTGGGGGGCATG 16341      A    TG   GA
                                 CATGC CCCTG  CTG  GTCCC
                                 ||||| |||||  |||  |||||
                                 GTACG GGGGT  GGC  TGGGG
                                    G    GT   G_
GAM93   CKTSF1B1  3'  GGGCCAAAGTGCAGGGTGGGTG 26295     G     TG  GGA   C
                                 CAT CACCCTG  CT   GTCC
                                 ||| |||||||  ||   ||||
                                 GTG GTGGGAC  GA   CGGG
                                   G      GT  AAC
GAM93   COL11A2   3'  GGAATAGTGTGGGGTGTGTG   55632          TG   GAG
                                 CATGCACCCTG  CTG   TCC
                                 ||||||||||||  |||   |||
                                 GTGTGTGGGGT  GAT   AGG
                                        GT   A__
GAM93   DHCR24    3'  GGGTGTGGCAGTGTATGGTGTG 29303        C  TG   GAGT_
            TG                   CATGCACC TG  CTG    CCC
                                 ||||||||  ||  |||    |||
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                                GTGTGTGG AT  GAC    GGG
                                    T  GT   GGTGT
GAM93   DLG4    5'  GGGAAGAGGGGGCCAGGGTGTG 9083          T   GGAG__
          TG                    CATGCACCCTG GCT     TCCC
                                |||||||||| |||     ||||
                                GTGTGTGGGAC CGG     AGGG
                                      _   GGGAGA
GAM93   EBF     3'  GGGATCTGCAAGTGCAGGGTGT 66637    T      TG  _ G  _
          TG                    A GCACCCTG  CT G AG TCCC
                                | ||||||||  || | || ||||
                                G TGTGGGAC  GA C TC AGGG
                                 T       GT  A G  T
GAM93   EGLN2   5'  GGGGCTCTGGCTGCTGTGTG   54919       CCCTGT  TG
                                CATGCA     GC  GAGTCCC
                                ||||||     ||  |||||||
                                GTGTGT     CG  CTCGGGG
                                    CGT___  GT
GAM93   EN2     3'  GGGGCTAAAGGCCTGGGGTGTG 9265          T   GG_
          TG                    CATGCACCCTG GCT   AGTCCC
                                |||||||||| |||   ||||||
                                GTGTGTGGGGT CGG   TCGGGG
                                      C   AAA
GAM93   GFRA2   3'  GGGACTCTGGGCTGTGCCTG   9465    T   CCT  G TG
                                CA GCAC   GT C  GAGTCCC
                                || ||||   || |  |||||||
                                GT CGTG   CG G  CTCAGGG
                                 C    T__  _ GT
GAM93   GM2A    3'  GGAGAGGTAGGGTGTGTG    68383         GT   GGAG
                                CATGCACCCT  GCT    TCC
                                ||||||||||  |||    |||
                                GTGTGTGGGA  TGG    AGG
                                      __   AG__
GAM93   GNA11   3'  GGTCCCGGGCATGTGGGGTGTG 10816          __    T____  AGTC
          TG                    CATGCACCCT  GTGC     GG    C
                                ||||||||||  ||||     ||    |
                                GTGTGTGGGG  TACG     CC    G
                                      TG    GG     CTGA
GAM93   GNAO1   3'  GGGGCTCCGGTGCGGTGCACTG 92617    _     CT TG
                                CA TGCACC  G  CTGGAGTCCC
                                || ||||||  |  ||||||||||
                                GT ACGTGG  C  GGCCTCGGGG
                                 C     __ GT
GAM93   GNAZ    3'  GGGAGGACCAGTGCAGGGTCTG 10829     C     TG    AG_
          TG                    CATG ACCCTG  CTGG   TCCC
                                ||||  ||||||  ||||   ||||
                                GTGT TGGGAC  GACC   AGGG
                                  C     GT    AGG
GAM93   GPC1    3'  GGGACTCTGGCACAGTGATGC  10862     CC_     TG
                                GCA   CTGTGC  GAGTCCC
                                |||   ||||||  |||||||
```

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                                CGT   GACACG  CTCAGGG
                                  AGT     GT
GAM93   GPR44    3'  GGGACTTTGGTCTATTGTCTG  17699    T   CCC  T  TG
                                CA GCA   TG GC  GAGTCCC
                                || |||   || ||  |||||||
                                GT TGT   AT TG  TTCAGGG
                                 C   T__  C  GT
GAM93   GZMM     3'  GGGGTGCAGTGGGGTGGGTG   19214     G     GT    GA
                                CAT CACCCT  GCTG  GTCCC
                                ||| ||||||  ||||  |||||
                                GTG GTGGGG  TGAC  TGGGG
                                  G     __    G_
GAM93   HLA-DMA  3'  GGGACATCCCTGGGGTGTGTG  21502          TGCT   _
                                CATGCACCCTG    GGA GTCCC
                                ||||||||||    ||| |||||
                                GTGTGTGGGGT    CCT CAGGG
                                       C___   A
GAM93   IRAK1    3'  GGGGCTGCTGTGCAGGGGTGTG 9616       A     TG T  _
                                CATGC CCCTG  C GG AGTCCC
                                ||||| |||||  | || ||||||
                                GTGTG GGGAC  G TC TCGGGG
                                   _    GT _  G
GAM93   KIF3B    3'  TTTGCCTGGTGTGGTGGTGCAT 17812         _   TG TG A  CCC
          G                      CATGCACC CTG  C  G GT
                                ||||||| |||  |  | ||
                                GTACGTGG GGT  G  C CG
                                     T   GT GT _  TTTG
GAM93   LRP4     3'  GGGGCTGGGACATGGGGGTGTG 65064      A      _  GG
                                CATGC CCCTGTG CT  AGTCCC
                                ||||| ||||||| ||  ||||||
                                GTGTG GGGGTAC GG  TCGGGG
                                   _      A  G_
GAM93   LSS      3'  GGGATGGGGACAGGGTGGGTG  11369     G       G  GGA
                                CAT CACCCTGT CT   GTCCC
                                ||| ||||||| ||   |||||
                                GTG GTGGGACA GG   TAGGG
                                  G       G  G__
GAM93   MAN2A2   3'  GGGATGGTGGCAGGGGTGT   21516       G    GA
                                GCACCCT TGCTG  GTCCC
                                ||||||| |||||  |||||
                                TGTGGGG ACGGT  TAGGG
                                   _    GG
GAM93   MBD4     3'  GGCTAGGCGTGGTGGTGCATG  15388        _ TG   GG
                                CATGCACC C  TGCT  AGTC
                                |||||||| |  ||||  ||||
                                GTACGTGG G  GCGG  TCGG
                                     T GT   A_
GAM93   MEN1     5'  GGGGCTCCTCATTGGGGTGC   56356        TGCT
                                GCACCCTG   GGAGTCCC
                                ||||||||   ||||||||
```

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                                CGTGGGGT   CCTCGGGG
                                    TACT
GAM93   MMP19    5'  GGGACTTCAGCATGAGCAATG  11636    _ ACCC
                                CAT GC   TGTGCTGGAGTCCC
                                ||| ||   ||||||||||||||
                                GTA CG   GTACGACTTCAGGG
                                  A  A___
GAM93   MTMR8    3'  GCCTGGTGTGGTGGTGTGTG  31912       _  TG TG A
                                CATGCACC CTG  C  G GT
                                |||||||| |||  |  | ||
                                GTGTGTGG GGT  G  C CG
                                    T   GT GT _
GAM93   MYO6     3'  GGTACTTAGGTAGGGTGTGTG  18442        GT   G   _
                                CATGCACCCT  GCT GAGT CC
                                ||||||||||  ||| |||| ||
                                GTGTGTGGGA  TGG TTCA GG
                                    __   A   T
GAM93   PLA2G10  5'  GGGGCGTGACAGCCGGGGTGTG 14533         T   GA__
           TG                    CATGCACCCTG GCTG   GTCCC
                                ||||||||||| ||||   |||||
                                GTGTGTGGGGC CGAC   CGGGG
                                    _   AGTG
GAM93   PPIC     3'  TATGCTTTGGCAGGGGTGTGTG 8132         G   TG   CCC
                                CATGCACCCT TGC  GAGT
                                |||||||||| |||  ||||
                                GTGTGTGGGG ACG  TTCG
                                    _  GT   TATA
GAM93   PTGIS    3'  GGGGCTCCATGCTGGTGT    8218      CT   C
                                GCACC  GTG TGGAGTCCC
                                |||||  ||| |||||||||
                                TGTGG  CGT ACCTCGGGG
                                  T_  _
GAM93   PTTG1IP  3'  GGGGCTCCAGTACACAGT    16350    CC
                                AC  TGTGCTGGAGTCCC
                                ||  ||||||||||||||
                                TG  ACATGACCTCGGGG
                                 AC
GAM93   PYGO2    3'  GGGAAGGCAGGCATGGGGTGT  64685         GGAG_
                                GCACCCTGTGCT    TCCC
                                ||||||||||||    ||||
                                TGTGGGGTACGG    AGGG
                                    ACGGA
GAM93   RAB5A    3'  GGGGCTTCAGTTGTTCCTCCAT 16042     CACCCTGT
           G                     CATG      GCTGGAGTCCC
                                ||||      ||||||||||
                                GTAC      TGACTTCGGGG
                                  CTCCTTGT
GAM93   RAG1     3'  GGGACTTCAGAAGTGCA     6546      CCTGTG
                                TGCAC     CTGGAGTCCC
                                |||||     ||||||||||
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                                ACGTG     GACTTCAGGG
                                  AA____
GAM93   RPA1     3'  GGGATTTTAGTAAGTGTGT   12897      C  G
                                GCAC CT TGCTGGAGTCCC
                                |||| || ||||||||||||
                                TGTG GA ATGATTTTAGGG
                                  T  _
GAM93   S100B    3'  GGGGCTCCAGCGTGGCCTCCGT 21852      CACC TG
           G                     CATG   C  TGCTGGAGTCCC
                                ||||   |  ||||||||||||
                                GTGC   G  GCGACCTCGGGG
                                  CTCC GT
GAM93   SCA1     3'  GGACGGGGCAGGTGTGT     6181       _    G  GGA
                                GCAC CCTGT CT   GTCC
                                |||| ||||| ||   ||||
                                TGTG GGACG GG   CAGG
                                  T    G  ___
GAM93   SFN      3'  GGGGCTGGAGATGGGTGTGTG  75071        TGTG  GG
                                CATGCACCC    CT  AGTCCC
                                |||||||||    ||  ||||||
                                GTGTGTGGG    GA  TCGGGG
                                     TA__  GG
GAM93   SLC8A2   3'  GGGACGCGGGAGGGTGCATG   66936         GTG   GA
                                CATGCACCCT   CTG  GTCCC
                                ||||||||||   |||  |||||
                                GTACGTGGGA   GGC  CAGGG
                                     G__   G_
GAM93   SOX11    3'  GGGGCTCCGGCGGCGGCGC    13321    A  CTG
                                GC CC   TGCTGGAGTCCC
                                || ||   ||||||||||||
                                CG GG   GCGGCCTCGGGG
                                 C  CG_
GAM93   SRD5A2   5'  GGGATTCTGAGTGGTGTCTG   60119    T    CTGT  _
                                CA GCACC    GCT GGAGTCCC
                                || |||||    ||| |||||||||
                                GT TGTGG    TGA TCTTAGGG
                                 C     _____   G
GAM93   TCF15    3'  TTGGTGACAGGGTGTGTG     17234           _  TG
                                CATGCACCCTGT GC  G
                                |||||||||||| ||  |
                                GTGTGTGGGACA TG  T
                                       G  GT
GAM93   TCF2     3'  GGACCTTCCACACAGGGTGCAT 6615            C   __   C
           G                     CATGCACCCTGTG TGGA  GTCC
                                ||||||||||||| ||||  ||||
                                GTACGTGGGACAC ACCT  CAGG
                                       _   TC
GAM93   TNFSF8   3'  GGGGCTTCAGTACCAGAGCA   8801      ACC  _
                                TGC   CTG TGCTGGAGTCCC
                                |||   ||| ||||||||||||
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                                ACG   GAC ATGACTTCGGGG
                                  A__   C
GAM93   UBE2V1   3'  GGGACTACTGCTAGGTGTGT   42065      _   T  TGG
                                GCAC CCTG GC   AGTCCC
                                |||| |||| ||   ||||||
                                TGTG GGAT CG   TCAGGG
                                  T   _  TCA
GAM93   VLGR1    5'  GGCAGAGCGAGGGTGTGTG   50411        G   GGA
                                CATGCACCCT TGCT   GTC
                                |||||||||| ||||   |||
                                GTGTGTGGGA GCGA   CGG
                                     _   GA_
GAM93   WHSC1    3'  GGGGTTCAGGGGTGTGTG    24680        TGTG    G
                                CATGCACCC    CTGGA TCC
                                |||||||||    ||||| |||
                                GTGTGTGGG    GACTT GGG
                                     ____    G
GAM93   WHSC1    3'  GGGGTTCAGGGGTGTGTG    24681        TGTG    G
                                CATGCACCC    CTGGA TCC
                                |||||||||    ||||| |||
                                GTGTGTGGG    GACTT GGG
                                     ____    G
GAM93   WHSC1    3'  GGGGTTCAGGGGTGTGTG    24682        TGTG    G
                                CATGCACCC    CTGGA TCC
                                |||||||||    ||||| |||
                                GTGTGTGGG    GACTT GGG
                                     ____    G
GAM93   ZNF175   5'  GGGGCTTGTTGGGGGTGGGGGT 24084        _ TG G  G___
          GCGTG                   CATGCACC C  T CT    GAGTCCC
                                |||||||| |  | ||    |||||||
                                GTGCGTGG G  G GG    TTCGGGG
                                    G GT G  GTTG
GAM93   AP1G2    5'  GGGGCGCCCGTGGGGTGCG    15352        TG  CT  A
                                TGCACCC  TG  GG GTCCC
                                |||||||  ||  || |||||
                                GCGTGGG  GC  CC CGGGG
                                    GT  __  G
GAM93   AP1M2    3'  GGGAGGGCAGGTGCGGGCTGTG 19725       C    TG  GGAG_
          TG                     CATGCA CCTG  CT     TCCC
                                |||||| ||||  ||     ||||
                                GTGTGT GGGC  GG     AGGG
                                   C    GT  ACGGG
GAM93   ATP6V1F  5'  GGGGTTTCAGTGGCTTCTGGTG 16166      CT__ _     GT
                                CACC    GT GCTGGA  CCC
                                ||||    || ||||||  |||
                                GTGG    CG TGACTT  GGG
                                  TCTT  G     TG
GAM93   BTN1A1   3'  GGGTCAGGTTAGCATGGGGTTG 9966       _         AGT__
          T                      GCA CCCTGTGCTGG     CCC
                                ||| ||||||||||     |||
```

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                                TGT GGGGTACGATT    GGG
                                  T         GGACT
GAM93   C1orf34   3'  GCCTGGCGTGGTGGTGCATG  61313        _ TG   TG A
                                CATGCACC C  TGC  G GT
                                |||||||| |  |||  | ||
                                GTACGTGG G  GCG  C CG
                                     T GT   GT _
GAM93   C21orf4   5'  GGGACGCCGGCAGGGTTGT   21540    _   GT    A
                                GCA CCCT  GCTGG GTCCC
                                ||| ||||  ||||| |||||
                                TGT GGGA  CGGCC CAGGG
                                  T   __    G
GAM93   C6orf33   5'  GGGCGCGGCACGGAGTGCATG  56718       C       GA
                                CATGCAC CTGTGCTG  GTCC
                                ||||||| ||||||||  ||||
                                GTACGTG GGCACGGC  CGGG
                                     A       G_
GAM93   CABP2     5'  GGGGTTCCAGGCCTGGCATG   49129      ACCCT  G    GT
                                CATGC    GT CTGGA  CCC
                                |||||    || |||||  |||
                                GTACG    CG GACCT  GGG
                                   GTC__ _    TG
GAM93   CAPN13    3'  GGGATAATTATGGGGTGT    58629         CTGGA
                                GCACCCTGTG    GTCCC
                                ||||||||||    |||||
                                TGTGGGGTAT    TAGGG
                                     TAA__
GAM93   CARHSP1   3'  GGGGCAGGTGTGGGGTGT    27481        TG  GGA
                                GCACCCTG  CT   GTCCC
                                ||||||||  ||   |||||
                                TGTGGGGT  GG   CGGGG
                                     GT  A__
GAM93   CCR1      3'  GGGGCTTCAGTCTTTTCCATG  8930      CACCCTGT
                                CATG       GCTGGAGTCCC
                                ||||       ||||||||||
                                GTAC       TGACTTCGGGG
                                  CTTTTC__
GAM93   CX46.6    3'  GGGGTGCGGGGGTGCGTG    40314         _ TG  GGAGT
                                CATGCACCCT G  CT    CC
                                |||||||||| |  ||    ||
                                GTGCGTGGGG C  GG    GG
                                     G GT  _____
GAM93   DKFZp434I1916 5'  GGGGCCACGCAAGTGTGGGTGT 50975         TG___   T GA
           GTG                    CATGCACCC    TGC G  GTCCC
                                |||||||||    ||| |  |||||
                                GTGTGTGGG    ACG C  CGGGG
                                     TGTGA  _ AC
GAM93   DKFZp434O0320 3'  GGGATTCCACTAGGTGCCATG  84700      _   CT  GCT
                                CATG CACC  GT   GGAGTCCC
                                |||| ||||  ||   ||||||||
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                                GTAC GTGG  CA   CCTTAGGG
                                  C    AT  ___
GAM93   DKFZp547M072 3'  GGGGTTTGGGTGCAGGGGCATG 61717      A    TG  G  GT
                                CATGC CCCTG  CT GA  CCC
                                ||||| |||||  || ||  |||
                                GTACG GGGAC  GG TT  GGG
                                  _    GT  G  TG
GAM93   DKFZp547M236 3'  GGGATTTTAGTTAAACGTGTCT 38661    T   CCTGT
           G                     CA GCAC    GCTGGAGTCCC
                                || ||||    ||||||||||
                                GT TGTG    TGATTTTAGGG
                                 C   CAAAT
GAM93   DKFZP564C186 5'  GGGGCCGGAAGTGGGGTGCA  72844       TG G_   AG
                                TGCACCC  T  CTGG  TCCC
                                |||||||  |  ||||  ||||
                                ACGTGGG  G  GGCC  GGGG
                                    GT AA   __
GAM93   DKFZp564I1922 3'  GGGGCTTCATTCAGGGTGTCTG 31851    T      TGC
                                CA GCACCCTG   TGGAGTCCC
                                || ||||||||   |||||||||
                                GT TGTGGGAC   ACTTCGGGG
                                 C       TT_
GAM93   DKFZP564O1863 3'  GGGTGAATGGGGTGGATG    69142    G      GCTGGA
                                CAT CACCCTGT     GTCC
                                ||| ||||||||     ||||
                                GTA GTGGGGTA     TGGG
                                  G       AG____
GAM93   DKFZP761D0211 3'  GGGATCCTCTAGCATGGGGGGT 50179      A         __
           GTG                    CATGC CCCTGTGCTGGAG  TCCC
                                ||||| ||||||||||||  ||||
                                GTGTG GGGGTACGATCTC  AGGG
                                   G          CT
GAM93   DRIL2    3'  GGTCCCGTGGCGTGGGTGTGTG 22353       _ TG   T_____  AGTC
           TG                     CATGCAC CC  TGC     GG   C
                                ||||||| ||  |||     ||   |
                                GTGTGTG GG  GCG     CC   G
                                    T  GT   GTG    CTGA
GAM93   EML4     3'  GGAAGGGTGTGGGTGTGTG   39323        T TG  GGAG
                                CATGCACCC G  CT   TCC
                                |||||||| |  ||   |||
                                GTGTGTGGG T  GG   AGG
                                     _ GT  GA__
GAM93   ETAA16   5'  GGCTGCCGTTGGTGCGGGGTGC 39169        TG  ___  _   CC
           G                     TGCACCCTG  CT   GG AGTC
                                |||||||||  ||   || ||||
                                GCGTGGGGC  GG   CC TCGG
                                     GT  TTG  G
GAM93   FADS2    3'  GGGGTGCAGGTGGGGTGATG   16217     G    TG G   GA
                                CAT CACCC  T CTG  GTCCC
                                ||| |||||  | |||  |||||
```

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                                GTA GTGGG  G GAC  TGGGG
                                  _    GT _   G_
GAM93   FAM8A1   3' GGGGTTTTATTATGTGTGTGTG 33199       CCT   C    GT
                                CATGCAC   GTG TGGA  CCC
                                |||||||   ||| ||||  |||
                                GTGTGTG   TAT ATTT  GGG
                                    TG_   T    TG
GAM93   FGF19    5' GGGGCCGGAGGCGGGGTGT   18856        G_   AG
                                GCACCCTGT  CTGG  TCCC
                                |||||||||  ||||  ||||
                                TGTGGGGCG  GGCC  GGGG
                                     GA   __
GAM93   FLJ10375 3' TTGGGGATGGGGTGTGTG    36563          G  G
                                CATGCACCCTGT CT GA
                                |||||||||||| || ||
                                GTGTGTGGGGTA GG TT
                                       G  G
GAM93   FLJ10579 3' CCGTGGTATGGGGTTTATG    36827     C       T_____
                                CATG ACCCTGTGC     GG
                                |||| |||||||||     ||
                                GTAT TGGGGTATG     CC
                                  T        GTG
GAM93   FLJ12122 5' GGGACTTTGGCGGAGTGTG    47093     C  G   TG
                                CAC CT TGC  GAGTCCC
                                ||| || |||  |||||||
                                GTG GA GCG  TTCAGGG
                                  T  G   GT
GAM93   FLJ12800 3' GGGGTACGGTGGGGTGGGTG   43531     G     GT    GAG
                                CAT CACCCT  GCTG   TCCC
                                ||| ||||||  ||||   ||||
                                GTG GTGGGG  TGGC   GGGG
                                  G     __    AT_
GAM93   FLJ13902 3' GGGCAGCCCGGCGCAGGGGCAT 45382       A         A__    C
           G                     CATGC CCCTGTGCTGG   GTCC
                                |||||  ||||||||||   ||||
                                GTACG GGGACGCGGCC   CGGG
                                  _          CGA
GAM93   FLJ13902 3' GGGTCACAAGGGCACAGGGTGT 45383             GGAGT__
           GTG                    CATGCACCCTGTGCT      CCC
                                |||||||||||||||      |||
                                GTGTGTGGGACACGG      GGG
                                       GAACACT
GAM93   FLJ14326 3' GGTACAGATGGCACAGGTGTGT 50780      _       GA_ _  C
                                GCAC CCTGTGCTG   GT CC
                                |||| |||||||||   || ||
                                TGTG GGACACGGT   CA GG
                                  T        AGA  T
GAM93   FLJ20294 3' GGGACTTCGGCATTTACTAATG 35357     GCACCCT
                                CAT      GTGCTGGAGTCCC
                                |||      ||||||||||||
```

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                                GTA      TACGGCTTCAGGG
                                  ATCATT_
GAM93   FLJ20979  3'  GATGGTTTCAGTATGTGGGTGT 44387         _       T  C
            GTG                   CATGCACCC TGTGCTGGAG CC
                                  ||||||||| |||||||||| ||
                                  GTGTGTGGG GTATGACTTT GG
                                       T        _  TAGA
GAM93   FLJ21276  3'  GGAGTCCCGCAATGGCATGGGG 45260           T_________  AGTC
            TGTGTG                CATGCACCCTGTGC       GG    CC
                                  ||||||||||||||       ||    ||
                                  GTGTGTGGGGTACG       CC    GG
                                        GTAACG    CTGA
GAM93   FLJ21432  3'  GGGGCTCTGCGTGGTACATG   44945     C   CTG   T
                                  CATG ACC   TGC GGAGTCCC
                                  |||| |||   ||| ||||||||
                                  GTAC TGG   GCG TCTCGGGG
                                    A  T__   _
GAM93   FLJ21977  3'  GGGGCTTTCAGGGGGTCATG   50874     C    G  CT
                                  CATG ACCCT TG  GGAGTCCC
                                  |||| ||||| ||  ||||||||
                                  GTAC TGGGG AC  TTTCGGGG
                                    _    G  __
GAM93   FLJ22659  5'  GGGGCTCCAGGTGGGTGC    46830       TGTG
                                  GCACCC    CTGGAGTCCC
                                  ||||||    ||||||||||
                                  CGTGGG    GACCTCGGGG
                                     TG__
GAM93   FLJ23323  3'  GGGGTTCTGCTGTGTGTGTGTG 45387        CCTGT  T   GT
                                  CATGCAC     GC GGA  CCC
                                  |||||||     || |||  |||
                                  GTGTGTG     CG TCT  GGG
                                      TGTGT  _   TG
GAM93   FLJ32865  3'  GGGGTGAGGGCACAGGGTGT   58815          GGA
                                  GCACCCTGTGCT   GTCCC
                                  ||||||||||||   |||||
                                  TGTGGGACACGG   TGGGG
                                        GAG
GAM93   G4        5'  GGACACCGTGGGGTGT      92637        GT  T  A
                                  GCACCCT  GC GG GTCC
                                  |||||||  || || ||||
                                  TGTGGGG  TG CC CAGG
                                     __  _  A
GAM93   GABARAPL1 3'  GGGGTAGGGGAGGGGTGTGTG  49420         GTG  GGAG
                                  CATGCACCCT   CT    TCCC
                                  ||||||||||   ||    ||||
                                  GTGTGTGGGG   GG    GGGG
                                        AGG  AT__
GAM93   GABARAPL3 3'  GGGGTAGGGGAGGGGTGTGTG  51784         GTG  GGAG
                                  CATGCACCCT   CT    TCCC
                                  ||||||||||   ||    ||||
```

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                                GTGTGTGGGG  GG   GGGG
                                     AGG  AT__
GAM93   GPR108   3'  GGGGCGCGGGCACAGGGTCCGT 69630     C       GGA
           G                  CATG ACCCTGTGCT  GTCCC
                              |||| ||||||||||  |||||
                              GTGC TGGGACACGG  CGGGG
                                C       GCG
GAM93   HAPIP    3'  GGGCTGGTGTGGGGTGCA    15468       TG  GG
                              TGCACCCTG  CT  AGTCC
                              |||||||||  ||  |||||
                              ACGTGGGGT  GG  TCGGG
                                   GT  __
GAM93   HT002    3'  GGGGCTCCAGCATCCGAGC   26795    ACCCT
                              GC    GTGCTGGAGTCCC
                              ||    ||||||||||||
                              CG    TACGACCTCGGGG
                               AGCC_
GAM93   IL-17RE  3'  GGGGTTGGGGGTGGGGTGGGTG 58941    G    TG G  G  G   C
                              CAT CACCC  T CT GA TCC
                              ||| |||||  | || || |||
                              GTG GTGGG  G GG TT GGG
                                G    GT G  G  G
GAM93   KBRAS2   3'  GGGGCTCTGGTAGATGTGTTG  34626   T   CCTG   TG
                              A GCAC    TGC  GAGTCCC
                              | ||||    |||  |||||||
                              G TGTG    ATG  CTCGGGG
                               T   TAG_  GT
GAM93   KCNQ5    3'  GCTAATGCTATGGGGTGTATG  39525          _  TGG
                              CATGCACCCTGT GC   AGT
                              ||||||||||| ||   |||
                              GTATGTGGGGTA CG   TCG
                                     T  TAA
GAM93   KIAA0140 3'  GGGTCTCCTGGTGCGGGGGCGT 28517      A    TG _   T
           G                  CATGC CCCTG  CT GGAG CCC
                              ||||| |||||  || |||| |||
                              GTGCG GGGGC  GG CCTC GGG
                                _    GT  T   T
GAM93   KIAA0152 3'  GGGGTGCCAGTGAGGGGTGCGT 28979         G    AG
           G                  CATGCACCCT TGCTGG  TCCC
                              |||||||||| ||||||  ||||
                              GTGCGTGGGG GTGACC  GGGG
                                   A     GT
GAM93   KIAA0237 3'  GGGGCTCCAGTTTTTGTGCAT  29229       CCTGT
                              ATGCAC    GCTGGAGTCCC
                              ||||||    ||||||||||
                              TACGTG    TGACCTCGGGG
                                 TTTT_
GAM93   KIAA0427 3'  GGGATGAGGGTGGGGGGTGT   29387       G   GGA
                              GCACCCT TGCT   GTCCC
                              ||||||| ||||   |||||
```

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                                TGTGGGG GTGG   TAGGG
                                    G   GAG
GAM93   KIAA0447 3' CCGGGGCGCGTGGTGTGTG   72115       C    T_____
                                CATGCACC TGTGC     GG
                                |||||||| |||||     ||
                                GTGTGTGG GCGCG     CC
                                    T    GGG
GAM93   KIAA0514 3' GGCTAGTGTGGGGTCATG    28751     C     TG   AGT
                                CATG ACCCTG  CTGG   CC
                                |||| ||||||  ||||   ||
                                GTAC TGGGGT  GATC   GG
                                  _     GT   ___
GAM93   KIAA0537 3' GGGGTGGGGGGTGTGGGTGCATG 29932        T TG  GGA
                                CATGCACCC G  CT   GTCCC
                                ||||||||| |  ||   |||||
                                GTACGTGGG T  GG   TGGGG
                                     _ GT  GGG
GAM93   KIAA0542 5' GGGATGCCCAGAGGGTGCATG  66664        GTG   A_
                                CATGCACCCT   CTGG  GTCCC
                                ||||||||||   ||||  |||||
                                GTACGTGGGA   GACC  TAGGG
                                     ___    CG
GAM93   KIAA0677 3' GGATAACATGGGTGTGTG    28532        TGTGC  GA
                                CATGCACCC    TG  GTCC
                                |||||||||    ||  ||||
                                GTGTGTGGG    AC  TAGG
                                     T____  AA
GAM93   KIAA0792 3' GGGCGGGATGGGGGTGTG    28767      A     G  GGA
                                CATGC CCCTGT CT   GTCC
                                ||||| |||||| ||   ||||
                                GTGTG GGGGTA GG   CGGG
                                  _     G  ___
GAM93   KIAA0819 3' GGAGCAGCACGGCGTGTATG   64333       C      GAG
                                CATGCAC CTGTGCTG   TCC
                                ||||||| ||||||||   |||
                                GTATGTG GGCACGAC   AGG
                                    C       G__
GAM93   KIAA1024 3' GGTGAAGTAACAGGGTGTGTG  69619          _   GGAGT
                                CATGCACCCTGT GCT     CC
                                |||||||||||| |||     ||
                                GTGTGTGGGACA TGA     GG
                                      A   AGT__
GAM93   KIAA1025 3' CCAGTGCGGTGGTGTGTG    64674        _  TG
                                CATGCACC CTG  CTGG
                                |||||||| |||  ||||
                                GTGTGTGG GGC  GACC
                                    T   GT
GAM93   KIAA1026 3' CCGTGCGTGGGGTGCGTG    71735        TG  _
                                CATGCACCC  TGC TGG
                                |||||||||  ||| |||
```

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                                GTGCGTGGG  GCG GCC
                                     GT   T
GAM93   KIAA1030  3' GGCTGTCTGGCATAGGGTGAGT 94983     G        TG __   CC
             G                    CAT CACCCTGTGC  GA  GTC
                                  ||| ||||||||||  ||  |||
                                  GTG GTGGGATACG  CT  CGG
                                    A         GT  GT
GAM93   KIAA1052  3' GGGGCTCCCAAGGAGGTTGTGT 30946       C   GTGCT
             G                    CATGCA CCT    GGAGTCCC
                                  |||||| |||    ||||||||
                                  GTGTGT GGA    CCTCGGGG
                                     T   GGAAC
GAM93   KIAA1164  3' GCCTGGCATGGTGGTGCGTG   70046        _     TG A
                                  CATGCACC CTGTGC  G GT
                                  |||||||| ||||||  | ||
                                  GTGCGTGG GGTACG  C CG
                                       T     GT _
GAM93   KIAA1271  3' GGGCAGGTATGTGGTGTGTG   70144        C     GGA
                                  CATGCACC TGTGCT   GTCC
                                  |||||||| ||||||   ||||
                                  GTGTGTGG GTATGG   CGGG
                                       T     A__
GAM93   KIAA1318  3' GGGACTACAAGAGTGTATGGTG 67877        C  TG  GG___
             TATG                   CATGCACC TG  CT    AGTCCC
                                  |||||||| ||  ||    ||||||
                                  GTATGTGG AT  GA    TCAGGG
                                       T  GT  GAACA
GAM93   KIAA1319  3' GGGACTTTGGTAGGGTCATG   40789     C    GT  TG
                                  CATG ACCCT  GC  GAGTCCC
                                  |||| |||||  ||  |||||||
                                  GTAC TGGGA  TG  TTCAGGG
                                    _    __  GT
GAM93   KIAA1822  3' GGGGCTTTGGGAGGGGGTGATG 68194     G     GTG TG
                                  CAT CACCCT   C  GAGTCCC
                                  ||| ||||||   |  |||||||
                                  GTA GTGGGG   G  TTCGGGG
                                    _     GAG GT
GAM93   KIAA1951  5' GGGCTGCCGTGGGGTGTGTG   74161         GT  T  _
                                  CATGCACCCT  GC GG AGTCC
                                  ||||||||||  || || |||||
                                  GTGTGTGGGG  TG CC TCGGG
                                       __  _  G
GAM93   KIF13B    3' GGGCTGGTGCAGGGAGTGTG   31572      A    TG  GG
                                  CATGC CCCTG  CT  AGTCC
                                  ||||| |||||  ||  |||||
                                  GTGTG GGGAC  GG  TCGGG
                                     A    GT  __
GAM93   KIF13B    3' GGGCTGGTGCAGGGAGTGTG   31573      A    TG  GG
                                  CATGC CCCTG  CT  AGTCC
                                  ||||| |||||  ||  |||||
```

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                                GTGTG GGGAC  GG  TCGGG
                                   A    GT __
GAM93   MAC30    5'  GGGGCTCCGGCAACCAGGCGC  63355    AC   __
                                GC  CCTG  TGCTGGAGTCCC
                                ||  ||||  ||||||||||||
                                CG  GGAC  ACGGCCTCGGGG
                                 C_   CA
GAM93   MGC2574  5'  GGGGCTGCACGTGCGCAGGGGT 44285      A      ___  G
           GTG                    CATGC CCCTGTGC   TG AGTCCC
                                ||||| ||||||||   || ||||||
                                GTGTG GGGACGCG   AC TCGGGG
                                   _       TGC  G
GAM93   MGC2628  3'  GGGGTTTCAGCGTGGCTGCGT  44200      CC TG      GT
                                ATGCA  C  TGCTGGA  CCC
                                |||||  |  |||||||  |||
                                TGCGT  G  GCGACTT  GGG
                                   C_ GT      TG
GAM93   MGC29654 5'  GGTGCGTGGTGCGTGGTGCGTG 67208        C  TG   GA TC
                                CATGCACC TG  CTG  G  CC
                                ||||||||  ||  |||  |  ||
                                GTGCGTGG GC  GGT  C  GG
                                     T  GT   G_ GT
GAM93   MIDORI   3'  GGGGTTGATGGGCTGGGTGCAT 74218         T  G   G_ GT
           G                     CATGCACCC GT CTG  A  CCC
                                |||||||||  ||  |||  |  |||
                                GTACGTGGG CG GGT  T  GGG
                                     T  _   AG TG
GAM93   MKRN4    3'  GGAGTCCCGGGGTGACATGGTG 48467        C  _  T_____  AGTC
           TGTG                    CATGCACC TGT GC     GG    CC
                                |||||||| ||| ||     ||    ||
                                GTGTGTGG ACA TG     CC    GG
                                     T   G  GGG    CTGA
GAM93   NCX      3'  GGGGCTCTAGCGGCGTTGCG   32946     _ _  TGT
                                TGCA C CC   GCTGGAGTCCC
                                |||| | ||   ||||||||||
                                GCGT G GG   CGATCTCGGGG
                                   T C  ___
GAM93   NUDT9    5'  GGGACTCGGAGCTGTGGGGTGT 44120       TG _   G_
                                GCACCC  T GCT  GAGTCCC
                                ||||||  | |||  |||||||
                                TGTGGG  G CGA  CTCAGGG
                                    GT T   GG
GAM93   OBTP     5'  GGGGCTTTGGCCCCAAGGCGTG 34668     _   GT__  TG
                                CAC CCT    GC  GAGTCCC
                                ||| |||    ||  |||||||
                                GTG GGA    CG  TTCGGGG
                                  C   ACCC  GT
GAM93   OSBPL5   3'  GGGGGGCGCAGGGGTGTG    73064      A       GGAG
                                CATGC CCCTGTGCT    TCCC
                                ||||| |||||||||    ||||
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                                GTGTG GGGACGCGG   GGGG
                                  _      ____   T
GAM93   P1P373C6 5'  GGGATTCAGAGTGGGGTGCA  39412      TG G  G
                                TGCACCC  T CTG AGTCCC
                                ||||||| | ||| ||||||
                                ACGTGGG  G GAC TTAGGG
                                   GT A  _
GAM93   PCDH17   3'  GGGATTCCAGTGAGATGGGTG  27838     TG__
                                CACCC   TGCTGGAGTCCC
                                |||||   ||||||||||||
                                GTGGG   GTGACCTTAGGG
                                  TAGA
GAM93   PDZD2    3'  GGAAGTCAGTGCAAGGTGCATG 81728      C  TG   AG  C
                                CATGCACC TG  CTGG  TCC
                                |||||||| ||  ||||  |||
                                GTACGTGG AC  GACT  AGG
                                    A  GT   GA
GAM93   PRDM7    3'  GGGTTTCAAGGGTGTAT    54847       GTGC   GT
                                ATGCACCCT   TGGA  CC
                                |||||||||   ||||  ||
                                TATGTGGGA   ACTT  GG
                                    ____   TG
GAM93   PRDM9    3'  GGGTTTCAAGGGTGTGT    39976       GTGC   GT
                                ATGCACCCT   TGGA  CC
                                |||||||||   ||||  ||
                                TGTGTGGGA   ACTT  GG
                                    ____   TG
GAM93   PTPRT    3'  GGGTAAGGCATGGGGTTGT   56506    _      GGAGT
                                GCA CCCTGTGCT    CCC
                                ||| |||||||||    |||
                                TGT GGGGTACGG    GGG
                                  T       AAT__
GAM93   RBAK     5'  GGCGGGCGCGGGGGTGTG    41273     A       GGA
                                CATGC CCCTGTGCT   GTC
                                ||||| |||||||||   |||
                                GTGTG GGGGCGCGG   CGG
                                  _       G__
GAM93   RCD-8    5'  GGTGAGCGAGGGTGCGTG    27524       G   GGAGT
                                CATGCACCCT TGCT    CC
                                |||||||||| ||||    ||
                                GTGCGTGGGA GCGA    GG
                                    _   GT___
GAM93   RI58     3'  GACTTAATTGGCATGGGGTGCA 25776         TG ___   CC
                                TGCACCCTGTGC  G   AGTC
                                |||||||||||| |   ||||
                                ACGTGGGGTACG  T   TCAG
                                    GT AAT
GAM93   RIL      3'  GGGGTGGTGGTGGGGTGC    14887      GT   GA
                                GCACCCT  GCTG  GTCCC
                                |||||||  ||||  |||||
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                                CGTGGGG  TGGT  TGGGG
                                   __    GG
GAM93   RoXaN    3'  GGGAAGGAGGTGCAGGGTGTTG 47296   T      TG  GGAG
                                A GCACCCTG  CT    TCCC
                                | ||||||||  ||    ||||
                                G TGTGGGAC  GG    AGGG
                                 T       GT  AGGA
GAM93   SCYA19   3'  GGACAGGGCCTGGGGTGTGTG  21856          T   GGA
                                CATGCACCCTG GCT   GTCC
                                |||||||||||| |||   ||||
                                GTGTGTGGGGT CGG   CAGG
                                      C   GA_
GAM93   SDC3     3'  GGGCAGGGCTTAGGGTGTGTG  28478          T   GGA
                                CATGCACCCTG GCT   GTCC
                                |||||||||||| |||   ||||
                                GTGTGTGGGAT CGG   CGGG
                                      T   GA_
GAM93   SDC3     3'  GGGGCTTTGGCATTTGCTG   28479    T   CCCT    TG
                                CA GCA    GTGC  GAGTCCC
                                || |||    ||||  |||||||
                                GT CGT    TACG  TTCGGGG
                                 _   T___    GT
GAM93   SEMA6B   3'  GGGCCACGCGTGCAGGGTGTGT 56661          TG _  GA    C
           G                     CATGCACCCTG  C TG  GTCC
                                ||||||||||  | ||  ||||
                                GTGTGTGGGAC  G GC  CGGG
                                      GT C  AC
GAM93   SRF      3'  GGGGTATGTGTGTGTGGGTGTG 13397          _  TG TGGAG
           TG                     CATGCACCC TG  C     TCCC
                                |||||||| ||  |     ||||
                                GTGTGTGGG GT  G     GGGG
                                     T  GT TGTAT
GAM93   STK25    3'  GGGGCTCCAGCCGCCGGCGTG  22095     _  T   _
                                CAC CC GTG CTGGAGTCCC
                                ||| || ||| ||||||||||
                                GTG GG CGC GACCTCGGGG
                                  C  C   C
GAM93   SV2      3'  GGGGCTCTGGTGTAGACCATG  29958      CACC   TG TG
                                CATG    CTG  C  GAGTCCC
                                ||||    |||  |  |||||||
                                GTAC    GAT  G  CTCGGGG
                                  CA__    GT GT
GAM93   TJP2     3'  GGGACTCCAGCTCGTGTGT    60329      CC  T
                                GCAC  TG GCTGGAGTCCC
                                ||||  || ||||||||||
                                TGTG  GC CGACCTCAGGG
                                  T_  T
GAM93   TOB2     3'  GGGATTTTAGAGTTAGTGTCTG 33241    T    CCTGTG
                                CA GCAC     CTGGAGTCCC
                                || ||||     ||||||||||
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                                GT TGTG     GATTTTAGGG
                                 C    ATTGA_
GAM93   USP20    3'  GGGCTGTGCAGGGTGCA     22902         TG TGG
                                TGCACCCTG  C   AGTCC
                                |||||||||  |   |||||
                                ACGTGGGAC  G   TCGGG
                                     GT ___
GAM93   VPS18    3'  GGGGCTCCAGTGTGAAGGGTGC 55401        __ TG
                                GCACCCT  G  CTGGAGTCCC
                                |||||||  |  ||||||||||
                                CGTGGGA  T  GACCTCGGGG
                                    AG GT
GAM93   YME1L1   3'  CCAGGTGTGGGGTGCATG    58429          TG _
                                CATGCACCCTG  C TGG
                                ||||||||||  | |||
                                GTACGTGGGGT  G ACC
                                      GT G
GAM93   ZFP106   3'  GGGACTTCACCAGGGGGTTTAT 42733      C    G  C
           G                     CATG ACCCT TG TGGAGTCCC
                                |||| ||||| || |||||||||
                                GTAT TGGGG AC ACTTCAGGG
                                  T    G  C
GAM93   LOC120856 3'  GGGATTTTAATCTGTGTGTG   74473       CCTGTGC
                                CATGCAC      TGGAGTCCC
                                |||||||      |||||||||
                                GTGTGTG      ATTTTAGGG
                                    TCTA___
GAM93   LOC126364 3'  GGCTGCTGGCTCAGGGTGCGTG 76195          T  TG _   CC
                                CATGCACCCTG GC  G AGTC
                                |||||||||||  ||  | ||||
                                GTGCGTGGGAC CG  C TCGG
                                      T  GT G
GAM93   LOC127262 3'  GGGACTCTAGCCTCTGTGT    76601     CCTGT
                                GCAC    GCTGGAGTCCC
                                ||||    ||||||||||
                                TGTG    CGATCTCAGGG
                                  TCTC_
GAM93   LOC128338 5'  GGGCTTCGGCGCCAGCGG    75253    _  _
                                CC CTG TGCTGGAGTCC
                                || ||| ||||||||||
                                GG GAC GCGGCTTCGGG
                                 C   C
GAM93   LOC129303 5'  GGGCCGAGCAGGGTGCG     75376         GC   AG
                                TGCACCCTGT  TGG  TCC
                                ||||||||||  |||  |||
                                GCGTGGGACG  GCC  GGG
                                      A_  __
GAM93   LOC130074 3'  GGGATTCCACAGCTGGTGC   76628      CT  GC
                                GCACC  GT  TGGAGTCCC
                                |||||  ||  |||||||||
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                                CGTGG  CG  ACCTTAGGG
                                  T_  AC
GAM93   LOC130612 3'  GGGGTTTAAATGCACGGTGCAT 75470       CT   TG__  GT
          G                    CATGCACC  GTGC   GA  CCC
                               ||||||||  ||||   ||  |||
                               GTACGTGG  CACG   TT  GGG
                                   __   TAAA  TG
GAM93   LOC143465 5'  GGGGCTTTGGTGGTGGTGTGCG 83877      _ TG  TG
          T                    ATGCAC CC  TGC  GAGTCCC
                               ||||||  ||  |||  |||||||
                               TGCGTG GG  GTG  TTCGGGG
                                  T  TG  GT
GAM93   LOC145725 3'  CCTCCTTCAGCGCGTGGTGCAT 77881       C       TCCC
          G                    CATGCACC TGTGCTGGAG
                               ||||||||  ||||||||||
                               GTACGTGG GCGCGACTTC
                                   T        CTCCG
GAM93   LOC145732 3'  CCTCCTTCAGCGCGTGGTGCAT 77893       C       TCCC
          G                    CATGCACC TGTGCTGGAG
                               ||||||||  ||||||||||
                               GTACGTGG GCGCGACTTC
                                   T        CTCCG
GAM93   LOC146667 5'  CTCCAGTGCAGTGTGTGTG   84710       C  TG
                               CATGCAC CTG  CTGGAG
                               |||||||  |||  ||||||
                               GTGTGTG GAC  GACCTC
                                   T  GT
GAM93   LOC146713 5'  GCACCCTGGTATGGGGTGAGTG 84732     G       TG A  CCC
                               CAT CACCCTGTGC  G GT
                               |||  ||||||||||  |  ||
                               GTG GTGGGGTATG  C CA
                                 A        GT C  CG
GAM93   LOC147040 3'  GACTCTTCTGGCACAGGGTGTG 78834          ___    CC
          T                    ATGCACCCTGTGCT   GGAGTC
                               ||||||||||||||   ||||||
                               TGTGTGGGACACGG   TCTCAG
                                       TCT
GAM93   LOC147165 3'  GGGACTCCTGGTGGGTGATG   85085    G    TGT  _
                               CAT CACCC   GCT GGAGTCCC
                               |||  |||||   |||  ||||||||
                               GTA GTGGG   TGG CCTCAGGG
                                 _    ___   T
GAM93   LOC147779 3'  GGGACTCCCTCCCCAGGGTGCA 79154        TGCT_
                               TGCACCCTG    GGAGTCCC
                               |||||||||    ||||||||
                               ACGTGGGAC    CCTCAGGG
                                    CCCTC
GAM93   LOC148014 3'  GGGATTACAACAGGTGCAGGGT 79311    _    TG  GG____
          TGT                    GCA CCCTG  CT     AGTCCC
                               |||  |||||  ||     ||||||
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                                TGT GGGAC  GG     TTAGGG
                                  T    GT  ACAACA
GAM93   LOC149111 5' GGGGCTTCTTGGCGTGTGTG  79931       _  TGTGCT
                                CATGCAC CC     GGAGTCCC
                                ||||||| ||     ||||||||
                                GTGTGTG GG     CTTCGGGG
                                   C  TT____
GAM93   LOC149603 3' GGAGCAGTATAGGGTCCATG  71174     C         GAG
                                CATG ACCCTGTGCTG   TCC
                                |||| ||||||||||   |||
                                GTAC TGGGATATGAC   AGG
                                  C         G__
GAM93   LOC149722 5' GGAGTGGCAAGGGGTGTGTG  85755         G    GAG
                                CATGCACCCT TGCTG   TCC
                                |||||||||| |||||   |||
                                GTGTGTGGGG ACGGT   AGG
                                     A    G__
GAM93   LOC150111 3' GGAGCGGGTGTGGGGCGCGTG  85999      A    TG  GGAG
                                CATGC CCCTG  CT    TCC
                                ||||| |||||  ||    |||
                                GTGCG GGGGT  GG    AGG
                                   C    GT  GCG_
GAM93   LOC150111 3' GGGGCGCGTGTGGGGCGCGTG  86000      A    TG TGGA
                                CATGC CCCTG  C    GTCCC
                                ||||| |||||  |    |||||
                                GTGCG GGGGT  G    CGGGG
                                   C    GT CG__
GAM93   LOC150111 3' GGGGCGCGTGTGGGGCGCGTG  86001      A    TG TGGA
                                CATGC CCCTG  C    GTCCC
                                ||||| |||||  |    |||||
                                GTGCG GGGGT  G    CGGGG
                                   C    GT CG__
GAM93   LOC150111 3' GGGGCGGGTGTGGGGCGCGTG  86002      A    TG  GGA
                                CATGC CCCTG  CT   GTCCC
                                ||||| |||||  ||   |||||
                                GTGCG GGGGT  GG   CGGGG
                                   C    GT  G__
GAM93   LOC150111 3' GGGGCGGGTGTGGGGCGCGTG  86003      A    TG  GGA
                                CATGC CCCTG  CT   GTCCC
                                ||||| |||||  ||   |||||
                                GTGCG GGGGT  GG   CGGGG
                                   C    GT  G__
GAM93   LOC150111 3' GGGGCGGGTGTGGGGCGCGTG  86004      A    TG  GGA
                                CATGC CCCTG  CT   GTCCC
                                ||||| |||||  ||   |||||
                                GTGCG GGGGT  GG   CGGGG
                                   C    GT  G__
GAM93   LOC150225 3' GGGGTTCCACAAATGTGTGTG  86197       CCTG  C   GT
                                CATGCAC    TG TGGA  CCC
                                |||||||    || ||||  |||
```

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                                GTGTGTG   AC ACCT  GGG
                                   TAA_ _   TG
GAM93   LOC150290 3' GCCTGGCACATGGTGTGTG   80589       C    TG A
                                CATGCACC TGTGC  G GT
                                |||||||| |||||  | ||
                                GTGTGTGG ACACG  C CG
                                   T    GT _
GAM93   LOC151979 3' GGGAGTCCAGCAGGGTGTGTG  81251         GT     G
                                CATGCACCCT  GCTGGA TCCC
                                ||||||||||  |||||| ||||
                                GTGTGTGGGA  CGACCT AGGG
                                    __     G
GAM93   LOC152925 3' GGAAACATAGGGTGTTTG    81621    T       CTGGAG
                                CA GCACCCTGTG     TCC
                                || ||||||||||     |||
                                GT TGTGGGATAC     AGG
                                 T        AA____
GAM93   LOC153346 3' CCGTGGTGGGGGGTGTGTG    87205         G  T_____
                                CATGCACCCT TGC     GG
                                |||||||||| |||     ||
                                GTGTGTGGGG GTG     CC
                                   _  GTG
GAM93   LOC153769 3' GGGGCTGCAGCAGGGGGTGT   81808       G    G
                                GCACCCT TGCTG AGTCCC
                                ||||||| ||||| ||||||
                                TGTGGGG ACGAC TCGGGG
                                   _    G
GAM93   LOC154877 3' GGGATTTCAGCTGTGTGCA   87563      CCTGT
                                TGCAC    GCTGGAGTCCC
                                |||||    ||||||||||
                                ACGTG    CGACTTTAGGG
                                   TGT__
GAM93   LOC196957 3' CCTCCTTCAGCGCGTGGTGCAT 89186       C        TCCC
          G                      CATGCACC TGTGCTGGAG
                                |||||||| ||||||||||
                                GTACGTGG GCGCGACTTC
                                     T        CTCCG
GAM93   LOC196961 3' CCTCCTTCAGCGCGTGGTGCAT 89200       C        TCCC
          G                      CATGCACC TGTGCTGGAG
                                |||||||| ||||||||||
                                GTACGTGG GCGCGACTTC
                                     T        CTCCG
GAM93   LOC197138 3' CTCCTTCAGCGCGTGGTGCATG 89249       C        TCCC
                                CATGCACC TGTGCTGGAG
                                |||||||| ||||||||||
                                GTACGTGG GCGCGACTTC
                                     T        CTCC
GAM93   LOC200860 3' GGGATGAGTTGAGGGTGCGTG  91753         GT   GGA
                                CATGCACCCT  GCT   GTCCC
                                ||||||||||  |||   |||||
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                                GTGCGTGGGA TGA  TAGGG
                                     GT  G__
GAM93   LOC200982 3' GGACTTGAATGGTGTGTG   91812       CT GCTG
                                CATGCACC GT   GAGTCC
                                |||||||| ||   ||||||
                                GTGTGTGG TA   TTCAGG
                                    __ AG__
GAM93   LOC202052 3' GGGGCTTTAGTGGCTTGTA   91902     CC GT
                                TGCA CT GCTGGAGTCCC
                                |||| || ||||||||||
                                ATGT GG TGATTTCGGGG
                                  TC __
GAM93   LOC202559 5' GGGAGTCGCAGGTGCTGGGTGC 90688        T TG _ _ G
           ATG                   CATGCACCC G C TG GA TCCC
                                |||||||| |  | || || ||||
                                GTACGTGGG C  G AC CT AGGG
                                     T GT G  G  G
GAM93   LOC219513 5' GGGATCTGTCGTGGGGTGC   95989      TG C   G
                                GCACCC TG TGGA TCCC
                                ||||||  || |||| ||||
                                CGTGGG  GC GTCT AGGG
                                   GT  T   _
GAM93   LOC219537 3' GGGGCTTAGGCAAGGGTGTGTG 93182        G   G
                                CATGCACCCT TGCT GAGTCCC
                                |||||||||| |||| |||||||
                                GTGTGTGGGA ACGG TTCGGGG
                                     _   A
GAM93   LOC219700 3' GGGTTCTCCTGAGGGTGCA   94654       GTGCT  T_
                                TGCACCCT   GGAG  CCC
                                ||||||||   ||||  |||
                                ACGTGGGA   CCTC  GGG
                                    GT___   TT
GAM93   LOC220001 3' CCGTGGCCCAGGGTGTGTG   93275        T  T_____
                                CATGCACCCTG GC    GG
                                |||||||||| ||    ||
                                GTGTGTGGGAC CG    CC
                                      C  GTG
GAM93   LOC220906 3' CCGGGCGTGGTGGTGCGTG   93035       _ TG   _
                                CATGCACC C  TGCT GG
                                |||||||| |  |||| ||
                                GTGCGTGG G  GCGG CC
                                    T GT   G
GAM93   LOC221463 3' GGTCCCGGGCAGGTAGGGTGTG 93710         __  T____  AGTC
           TG                   CATGCACCCTG  TGC   GG   C
                                |||||||||| |||   ||   |
                                GTGTGTGGGAT  ACG   CC   G
                                      GG  GG   CTGA
GAM93   LOC221922 5' GGGACTCCGGGGTCAGTGAGTG 94254    C__  _ G
                                CAC  CTG T CTGGAGTCCC
                                |||  ||| | ||||||||||
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                                GTG   GAC G GGCCTCAGGG
                                  AGT   T G
GAM93   LOC221931 3'  GGGATGAAATGAGGTGTGTG  95633       CT  GCTGGA
                                CATGCACC  GT     GTCCC
                                ||||||||  ||     |||||
                                GTGTGTGG  TA     TAGGG
                                    AG  AAG___
GAM93   LOC222166 3'  GGGGCTTTGGAAGTGGTGTATG 95742       _  GTG TG
                                CATGCACC CT   C  GAGTCCC
                                ||||||||  ||   |  |||||||
                                GTATGTGG GA   G  TTCGGGG
                                    T  A__ GT
GAM93   LOC222484 3'  GGGGCTTTAGTATCGTTGGTG  96002     CT__
                                CACC    GTGCTGGAGTCCC
                                ||||    ||||||||||||||
                                GTGG    TATGATTTCGGGG
                                  TTGC
GAM93   LOC222602 5'  GGGATTTTGGCTACACTTGTG  94434     CC_  _  TG
                                CAC   TGT GC  GAGTCCC
                                |||   ||| ||  |||||||
                                GTG   ACA CG  TTTAGGG
                                  TTC   T  GT
GAM93   LOC245727 3'  CCTCCTTCAGCGCGTGGTGCAT 92759       C        TCCC
          G                      CATGCACC TGTGCTGGAG
                                 ||||||||  ||||||||||
                                 GTACGTGG GCGCGACTTC
                                     T        CTCCG
GAM93   LOC253539 5'  GGGACTCTGGCAGTTCCTGCAT 97700       CCCTG   TG
          G                      CATGCA    TGC  GAGTCCC
                                 ||||||    |||  |||||||
                                 GTACGT    ACG  CTCAGGG
                                    CCTTG   GT
GAM93   LOC253681 3'  GACTCTTCTGGCACAGGGTGTG 96839           ___     CC
          T                      ATGCACCCTGTGCT   GGAGTC
                                 ||||||||||||||   ||||||
                                 TGTGTGGGACACGG   TCTCAG
                                        TCT
GAM93   LOC253805 5'  GGGGCCAGGGTGGGGTGAGTG  98180     G    TG G    AG
                                CAT CACCC  T CTGG  TCCC
                                ||| |||||  | ||||  ||||
                                GTG GTGGG  G GACC  GGGG
                                  A    GT G   __
GAM93   LOC255196 5'  GGGACTACCTGTAGGTGCGTG  98962       CTG   T  _
                                CATGCACC   TGC GG AGTCCC
                                ||||||||   ||| || ||||||
                                GTGCGTGG   ATG CC TCAGGG
                                    ___   T  A
GAM93   LOC255218 3'  GGGGCTTTGGCACAGGAGTGC  97469     _      TG
                                GCAC CCTGTGC  GAGTCCC
                                |||| |||||||  |||||||
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                                CGTG GGACACG  TTCGGGG
                                  A      GT
GAM93   LOC256537 3'  CCGTGGCACGGGGGCGTG    96936      A      T_____
                                CATGC CCCTGTGC     GG
                                ||||| ||||||||     ||
                                GTGCG GGGGCACG     CC
                                  _      GTG
GAM93   LOC256949 5'  GGAGCACCAGCGCGGGGTGAGT 96984     G          A TC
          G                      CAT CACCCTGTGCTGG G  CC
                                ||| |||||||||||| |  ||
                                GTG GTGGGGCGCGACC C  GG
                                  A           A GA
GAM93   LOC257017 5'  GGGATTTGTGTAGGGGTGTG   99220      A    TG TG
                                CATGC CCCTG  C  GAGTCCC
                                ||||| |||||  |  |||||||
                                GTGTG GGGAT  G  TTTAGGG
                                  _    GT __
GAM93   LOC257451 3'  GGGAAGGCAGGCATGGGGTGT  97297          GGAG_
                                GCACCCTGTGCT    TCCC
                                ||||||||||||    ||||
                                TGTGGGGTACGG    AGGG
                                      ACGGA
GAM93   LOC257481 3'  GGAGTCGCCGGTGCGGGGTGGG 61764     G      TG    AG__   C
          TG                    CAT CACCCTG  CTGG    TCC
                                ||| |||||||  ||||    |||
                                GTG GTGGGGC  GGCC    AGG
                                  G      GT    GCTG
GAM93   LOC84548  5'  GGCTGTGCAGCACGGGGTGCG  71764          G__    CC
                                TGCACCCTGTGCTG   AGTC
                                ||||||||||||||   ||||
                                GCGTGGGGCACGAC   TCGG
                                      GTG
GAM93   LOC90119  5'  GGGCAGGTGGGGTGCCTG    62210    T      GT   GGA
                                CA GCACCCT  GCT   GTCC
                                || |||||||  |||   ||||
                                GT CGTGGGG  TGG   CGGG
                                 C       __   A__
GAM93   LOC90190  3'  GACTTGGCATGGGGTGCAT    62424          TG A
                                ATGCACCCTGTGC  G GTC
                                ||||||||||||  | |||
                                TACGTGGGGTACG  T CAG
                                      GT _
GAM93   LOC90309  3'  GGTCCCGGGGTAAGGGGGTGTG 62875         G_   T_____  AGTC
          TG                    CATGCACCCT  TGC     GG   C
                                ||||||||||  |||     ||   |
                                GTGTGTGGGG  ATG     CC   G
                                      GA   GGG    CTGA
GAM93   LOC90835  5'  GGAGAGGCAGGGGTGTGTG   64815         G   GGAG
                                CATGCACCCT TGCT    TCC
                                ||||||||| ||||    |||
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                                GTGTGTGGGG ACGG   AGG
                                     _   AG__
GAM93   LOC90918  5'  GGGGTTCTAGCCAGTGCATG   65002      CC  T    GT
                                CATGCAC  TG GCTGGA  CCC
                                |||||||  || ||||||  |||
                                GTACGTG  AC CGATCT  GGG
                                   __ _     TG
GAM93   LOC91069  3'  GGGGTTGGAACAGGGGGTGTG  65402      A    G TG AG
                                CATGC CCCTGT C  G  TCCC
                                ||||| |||||| |  |  ||||
                                GTGTG GGGACA G  T  GGGG
                                   G     A GT __
GAM93   LOC91308  5'  GGGGCTTCACACATGGTG    66168     C   C
                                CACC TGTG TGGAGTCCC
                                |||| |||| |||||||||
                                GTGG ACAC ACTTCGGGG
                                  T   _
GAM93   LOC91517  3'  GGGGTTCCATGAGAGGTGTGTG 66913       _ GTGC   GT
                                CATGCACC CT   TGGA  CCC
                                |||||||| ||   ||||  |||
                                GTGTGTGG GA   ACCT  GGG
                                     A  GT__   TG
GAM93   LOC92249  3'  GGGGCTCTGGCACTAGCTG   69110   T  ACCCT   TG
                                CA GC    GTGC  GAGTCCC
                                || ||    ||||  |||||||
                                GT CG    CACG  CTCGGGG
                                 _ AT___   GT
GAM93   LOC93626  3'  GGTCCCGGGCATGTGGGGTGTG 73130         __   T____  AGTC
           TG                    CATGCACCCT  GTGC    GG   C
                                ||||||||||  ||||    ||   |
                                GTGTGTGGGG  TACG    CC   G
                                     TG   GG    CTGA
GAM94   DKFZP434J193 3'  ACAGAAAGTGACCACAAA    71555      A      AA
                                TTTGT GTCATTTT  GT
                                ||||| ||||||||  ||
                                AAACA CAGTGAAA  CA
                                   C       GA
GAM94   STIM2    3'  ACTTTGAATAACTGCAAA    40858        C   T
                                TTTGTAGT ATTT AAGT
                                |||||||| |||| ||||
                                AAACGTCA TAAG TTCA
                                     A   T
GAM94   LOC142973 5'  TACTGTGAATGACCACAA    60914     A     TA
                                TTGT GTCATTT  AGTA
                                |||| |||||||  ||||
                                AACA CAGTAAG  TCAT
                                  C      TG
GAM94   LOC221632 3'  CATGCTTAGGAACCACTACAAA 95446        CA   AAGT
                                TTTGTAGT  TTTT   AGCATG
                                ||||||||  ||||   ||||||
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                                AAACATCA  AAGG   TCGTAC
                                    CC   AT__
GAM95   GAK     3' GGAACAGCTGATTCATGCTCC 19141        A_ AC
                                GGAGCATGAG  AG  GTTCC
                                ||||||||||  ||  |||||
                                CCTCGTACTT  TC  CAAGG
                                     AG  GA
GAM95   TIMM23  3' GGGAGCGCCTCTGCCCCG   21989    A  T  AAGA
                                CGG GCA GAG   CGTTCCC
                                ||| ||| |||   |||||||
                                GCC CGT CTC   GCGAGGG
                                  C  _  C___
GAM95   TRPV1   3' GGGAACACCAGTGCTCTGT   55678       GAGAAGAC
                                ACGGAGCAT      GTTCCC
                                |||||||||      ||||||
                                TGTCTCGTG      CAAGGG
                                     ACCA____
GAM95   UBE2B   3' GAGTTTCTTCTCATATCC   13936    GC      CG
                                GGA  ATGAGAAGA  TTC
                                |||  |||||||||  |||
                                CCT  TACTCTTCT  GAG
                                  A_       TT
GAM95   C11orf25 3' GAGAGGTTCTCATGCTCC   49465         GACG
                                GGAGCATGAGAA   TTC
                                ||||||||||||   |||
                                CCTCGTACTCTT   GAG
                                     GGA_
GAM95   FLJ14735 3' GGAGAACGTTTAATACTTC   52668    C  GAGAA     _
                                GGAG AT    GACGTTC CC
                                |||| ||    ||||||| ||
                                CTTC TA    TTGCAAG GG
                                  A  AT___     A
GAM95   KIAA1036 3' AGCCTGGCTCCTCATGCTCAGT 30483   G       A  AC__
                                AC GAGCATGAG AG   GTT
                                || |||||||| ||   |||
                                TG CTCGTACTC TC   CGA
                                 A       C  GGTC
GAM95   KIAA1045 3' GGGGAACGTCCCCAAGCCCTGT 71606    A  A  AGAA
                                ACGG GC TG   GACGTTCCCC
                                |||| || ||   ||||||||||
                                TGTC CG AC   CTGCAAGGGG
                                  C  A  CC__
GAM95   KIAA1492 3' GGAATCGTGTCTTCCATGCTCC 65126       A    ___
                                GGAGCATG GAAGAC  GTTCC
                                |||||||| ||||||  |||||
                                CCTCGTAC CTTCTG  TAAGG
                                     _    TGC
GAM95   KIAA1674 3' GAGTTTCCTCTCACCTCCGT  69340      CA   A  CG
                                ACGGAG  TGAGA GA  TTC
                                ||||||  ||||| ||  |||
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                                TGCCTC  ACTCT CT  GAG
                                   C_    C  TT
GAM95   KIAA1674  3'  GAGTTTCCTCTCACCTCCGT   69341      CA    A  CG
                                ACGGAG  TGAGA GA  TTC
                                ||||||  ||||| ||  |||
                                TGCCTC  ACTCT CT  GAG
                                   C_    C  TT
GAM95   KIAA1674  3'  GAGTTTCCTCTCACCTCCGT   69342      CA    A  CG
                                ACGGAG  TGAGA GA  TTC
                                ||||||  ||||| ||  |||
                                TGCCTC  ACTCT CT  GAG
                                   C_    C  TT
GAM95   KIAA1751  3'  GGGCCACATTTCACATGCTCC  72163       A   ACGTT
                                GGAGCATG GAAG    CCC
                                |||||||| ||||    |||
                                CCTCGTAC CTTT    GGG
                                     A   ACACC
GAM95   KIAA1822  3'  GGACTCCTCATACTCTGT    68188      C    AA  C
                                ACGGAG ATGAG  GA GTTC
                                |||||| |||||  || ||||
                                TGTCTC TACTC  CT CAGG
                                   A    __ _
GAM95   LOC115207 3'  GGGAAATAAACCTCGTCATGCT 57398        GA  ACG___
          CC                     GGAGCATGA  AG     TTCCC
                                |||||||||  ||     |||||
                                CCTCGTACT  TC     AAGGG
                                     GC  CAAATA
GAM95   LOC154789 5'  GAACTCTCACTTCTCATCTCC  82028     C       AC___
                                GGAG ATGAGAAG    GTTC
                                |||| ||||||||    ||||
                                CCTC TACTCTTC    CAAG
                                  _       ACTCT
GAM95   LOC170395 5'  GAGTTTCCTCTCACCTCCGT   76869      CA    A  CG
                                ACGGAG  TGAGA GA  TTC
                                ||||||  ||||| ||  |||
                                TGCCTC  ACTCT CT  GAG
                                   C_    C  TT
GAM95   LOC170395 5'  GAGTTTCCTCTCACCTCCGT   76870      CA    A  CG
                                ACGGAG  TGAGA GA  TTC
                                ||||||  ||||| ||  |||
                                TGCCTC  ACTCT CT  GAG
                                   C_    C  TT
GAM95   LOC92973  5'  GAAGTTTTATTTCTCATGCT   71592        ____  G
                                AGCATGAGAA   GAC TTC
                                ||||||||||   ||| |||
                                TCGTACTCTT   TTG AAG
                                     TATT  _
GAM96   ADCY6    5'  GGTCTTGAACTCCTGACCTTGT 40961        C   A TG
          GA                     TCACAAGGTC GGAG T  AGACC
                                |||||||||| |||| |  |||||
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                                AGTGTTCCAG CCTC A  TCTGG
                                      T    A GT
GAM96   APM1     3'  GGTCTCGAACTCCTGACCTTGT 17788          C    A
            GA                   TCACAAGGTC GGAG TTGAGACC
                                ||||||||||  ||||  ||||||||
                                AGTGTTCCAG CCTC AGCTCTGG
                                      T    A
GAM96   APPL     3'  GATCTCCTGACCTCATGA    24949     CA    C
                                TCA  AGGTC GGAGATT
                                |||  |||||  |||||||
                                AGT  TCCAG CCTCTAG
                                  AC    T
GAM96   BAZ2B    5'  GATCTCCTGACCTTGTGA    26521          C
                                TCACAAGGTC GGAGATT
                                ||||||||||  |||||||
                                AGTGTTCCAG CCTCTAG
                                      T
GAM96   BLAME    3'  GGCTCAATCCAGTCTTGAT   39656     C  ___      A
                                GTC GGA   GATTGAG CC
                                |||  |||   |||||||  ||
                                TAG TCT   CTAACTC GG
                                  T  GAC      C
GAM96   CASP2    3'  GATCTCCTGACCTCATGA    53335     CA    C
                                TCA  AGGTC GGAGATT
                                |||  |||||  |||||||
                                AGT  TCCAG CCTCTAG
                                  AC    T
GAM96   CASP2    3'  GATCTCCTGACCTCATGA    53336     CA    C
                                TCA  AGGTC GGAGATT
                                |||  |||||  |||||||
                                AGT  TCCAG CCTCTAG
                                  AC    T
GAM96   CASP2    3'  GATCTCCTGACCTCATGA    8711      CA    C
                                TCA  AGGTC GGAGATT
                                |||  |||||  |||||||
                                AGT  TCCAG CCTCTAG
                                  AC    T
GAM96   CASP8    3'  GATCTCCTGACCTCGTGA    8754       A    C
                                TCAC AGGTC GGAGATT
                                ||||  |||||  |||||||
                                AGTG TCCAG CCTCTAG
                                   C    T
GAM96   CASP8    3'  GATCTCCTGACCTCGTGA    54078      A    C
                                TCAC AGGTC GGAGATT
                                ||||  |||||  |||||||
                                AGTG TCCAG CCTCTAG
                                   C    T
GAM96   CYP1B1   5'  GTCTCAATCTCAACGCTGTGA 5448       AG  CCG
                                TCACA  GT   GAGATTGAGAC
                                |||||  ||   ||||||||||
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                                AGTGT  CG   CTCTAACTCTG
                                  __  CAA
GAM96   DNAJB1   3'  GTCTTGATTCCCAGACCCTGT  21566     A    C  AG  TG
                                ACA GGTC GG  AT  AGAC
                                ||| |||| ||  ||  ||||
                                TGT CCAG CC  TA  TCTG
                                  C    A  CT  GT
GAM96   DSC3     3'  GATCTCCTGACCTCGTGA    44625     A    C
                                TCAC AGGTC GGAGATT
                                |||| ||||| |||||||
                                AGTG TCCAG CCTCTAG
                                  C    T
GAM96   DSC3     3'  GATCTCCTGACCTCGTGA    44626     A    C
                                TCAC AGGTC GGAGATT
                                |||| ||||| |||||||
                                AGTG TCCAG CCTCTAG
                                  C    T
GAM96   DSCR3    3'  GGTCTTGAACTCCTGACCTCGT 21321     A    C    A TG
           GA                     TCAC AGGTC GGAG T  AGACC
                                |||| ||||| |||| |  |||||
                                AGTG TCCAG CCTC A  TCTGG
                                  C    T   A GT
GAM96   EZH1     3'  GGTCTCAACCCCTCCCCACC   10554     CC   A__
                                GGT  GGAG   TTGAGACC
                                |||  ||||   ||||||||
                                CCA  CCTC   AACTCTGG
                                  CC   CCC
GAM96   FANCF    3'  GGTCTCAAACACCTGACCTTGT 42984          C  AGA
           GA                     TCACAAGGTC GG   TTGAGACC
                                |||||||||| ||   ||||||||
                                AGTGTTCCAG CC   AACTCTGG
                                     T  ACA
GAM96   FUT1     3'  GATCTCCTGACCTCGTGA    5597      A    C
                                TCAC AGGTC GGAGATT
                                |||| ||||| |||||||
                                AGTG TCCAG CCTCTAG
                                  C    T
GAM96   HCS      3'  GGTCTTGGACTCCTGACCTCGT 38989     A    C   A TG
           GA                     TCAC AGGTC GGAG T  AGACC
                                |||| ||||| |||| |  |||||
                                AGTG TCCAG CCTC G  TCTGG
                                  C    T   A GT
GAM96   IL10RA   3'  GGCCTCAATCTCCCATCTGTGA 60381      A  CC       A
                                TCACA GGT  GGAGATTGAG CC
                                ||||| |||  |||||||||| ||
                                AGTGT CTA  CCTCTAACTC GG
                                  _  C_       C
GAM96   LYZ      3'  GATCTCCTGACCTTGTGA    5896          C
                                TCACAAGGTC GGAGATT
                                |||||||||| |||||||
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                                AGTGTTCCAG CCTCTAG
                                      T
GAM96   MDM2    3' GATCTCCTGACCTCGTGA   11494     A   C
                                TCAC AGGTC GGAGATT
                                |||| ||||| |||||||
                                AGTG TCCAG CCTCTAG
                                  C    T
GAM96   MTR     3' GATCTCCCGACCTCGTGA   6019      A   C
                                TCAC AGGTC GGAGATT
                                |||| ||||| |||||||
                                AGTG TCCAG CCTCTAG
                                  C    C
GAM96   NFRKB   5' GATCACCCGGACCTTTTGA  21607     C       A_
                                TCA AAGGTCCGG  GATT
                                ||| |||||||||  ||||
                                AGT TTCCAGGCC  CTAG
                                  T       CA
GAM96   PCDHA9  3' GATCTCCTGACCTCATGA   49848     CA    C
                                TCA  AGGTC GGAGATT
                                |||  ||||| |||||||
                                AGT  TCCAG CCTCTAG
                                  AC    T
GAM96   PCDHA9  3' GGTCTCGAACTCCTGACCTTGT 49849         C   A
           GA                     TCACAAGGTC GGAG TTGAGACC
                                |||||||||| |||| ||||||||
                                AGTGTTCCAG CCTC AGCTCTGG
                                      T   A
GAM96   PIGR    3' GATCTCCTGACCTCGTGA   73002     A    C
                                TCAC AGGTC GGAGATT
                                |||| ||||| |||||||
                                AGTG TCCAG CCTCTAG
                                  C    T
GAM96   POU2AF1 3' GGTCTCGAACTCCTGACCTTGT 21748         C   A
           GA                     TCACAAGGTC GGAG TTGAGACC
                                |||||||||| |||| ||||||||
                                AGTGTTCCAG CCTC AGCTCTGG
                                      T   A
GAM96   PPID    3' GGTCTTGAACTCCTGACCTTGT 88826          C   A TG
           GA                     TCACAAGGTC GGAG T  AGACC
                                |||||||||| |||| |  |||||
                                AGTGTTCCAG CCTC A  TCTGG
                                      T   A GT
GAM96   PRKWNK3 3' GGTCTCAAACTCCTAACCTTGT 62235         CC   A
           GA                     TCACAAGGT  GGAG TTGAGACC
                                |||||||||  |||| ||||||||
                                AGTGTTCCA  CCTC AACTCTGG
                                     AT   A
GAM96   PTGIS   3' GGTCTCGAACTCCTGACCTCGT 8220      A   C   A
           GA                     TCAC AGGTC GGAG TTGAGACC
                                |||| ||||| |||| ||||||||
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                                AGTG TCCAG CCTC AGCTCTGG
                                  C    T   A
GAM96   RPP30    3'  GGTCTCAATCTCCTGACCT   22205      C
                                AGGTC GGAGATTGAGACC
                                ||||| |||||||||||||
                                TCCAG CCTCTAACTCTGG
                                  T
GAM96   SEDL     3'  GGTCTTGAACTCCTGACCTCGT 28105     A    C   A TG
            GA                    TCAC AGGTC GGAG T  AGACC
                                |||| ||||| |||| |  |||||
                                AGTG TCCAG CCTC A  TCTGG
                                  C    T   A GT
GAM96   SEDL     3'  GGTCTTGAACTCCTGACCTCGT 28106     A    C   A TG
            GA                    TCAC AGGTC GGAG T  AGACC
                                |||| ||||| |||| |  |||||
                                AGTG TCCAG CCTC A  TCTGG
                                  C    T   A GT
GAM96   SERPINB9 3'  GATCTCCTGACCTCGTGA    16022     A    C
                                TCAC AGGTC GGAGATT
                                |||| ||||| |||||||
                                AGTG TCCAG CCTCTAG
                                  C    T
GAM96   SH3GL3   5'  GATCTCCTGACCTCGTGA    13109     A    C
                                TCAC AGGTC GGAGATT
                                |||| ||||| |||||||
                                AGTG TCCAG CCTCTAG
                                  C    T
GAM96   SLC4A1AP 3'  AATCCCAAAAGAAAACCTTGTG 36867         CC_______ A
            G                    TCACAAGGT       GG GATT
                                |||||||||       || ||||
                                GGTGTTCCA       CC CTAA
                                     AAAGAAAA  _
GAM96   TAPBP    3'  GATCTCCTGACCTTGTGA    13567          C
                                TCACAAGGTC GGAGATT
                                |||||||||| |||||||
                                AGTGTTCCAG CCTCTAG
                                     T
GAM96   TERF2    3'  GATCTCCTGACCTCGTGA    20154     A    C
                                TCAC AGGTC GGAGATT
                                |||| ||||| |||||||
                                AGTG TCCAG CCTCTAG
                                  C    T
GAM96   TIM3     3'  GGTCTCAAACTCCTGACCTCAT 52359     CA   C   A
            GA                    TCA  AGGTC GGAG TTGAGACC
                                |||  ||||| |||| ||||||||
                                AGT  TCCAG CCTC AACTCTGG
                                  AC    T   A
GAM96   TP53BP2  5'  GATCTCCTGACCTTGTGA    19463          C
                                TCACAAGGTC GGAGATT
                                |||||||||| |||||||
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                                AGTGTTCCAG CCTCTAG
                                      T
GAM96   TYR     5' AGTTCCTGCAGACCTTGTGA  6324          __  AG
                                TCACAAGGTC  CGG  ATT
                                ||||||||||  |||  |||
                                AGTGTTCCAG  GTC  TGA
                                      AC   CT
GAM96   UGDH    3' GGTCTCAATCTCCTGACCTTGT 14001         C
           GA                   TCACAAGGTC GGAGATTGAGACC
                                |||||||||| ||||||||||||
                                AGTGTTCCAG CCTCTAACTCTGG
                                      T
GAM96   VENTX2  3' GGTCTCAAACTCCTGACCCTGT 27863      A   C   A
           GA                   TCACA GGTC GGAG TTGAGACC
                                ||||| |||| |||| ||||||||
                                AGTGT CCAG CCTC AACTCTGG
                                   C   T   A
GAM96   VHL     3' GATCTCCTGACCTTGTGA    6859          C
                                TCACAAGGTC GGAGATT
                                |||||||||| |||||||
                                AGTGTTCCAG CCTCTAG
                                      T
GAM96   VIPR2   3' GATCTCCTGACCTCGTGA    14065     A    C
                                TCAC AGGTC GGAGATT
                                |||| ||||| |||||||
                                AGTG TCCAG CCTCTAG
                                   C    T
GAM96   WHSC1   3' GGTCTTGAACTCCTGACCTCGT 24683     A    C   A TG
           GA                   TCAC AGGTC GGAG T  AGACC
                                |||| ||||| |||| |  |||||
                                AGTG TCCAG CCTC A  TCTGG
                                   C    T   A GT
GAM96   WHSC1   5' GGTCTTGAACTCCTGACCTTGT 24684         C   A TG
           GA                   TCACAAGGTC GGAG T  AGACC
                                |||||||||| |||| |  |||||
                                AGTGTTCCAG CCTC A  TCTGG
                                      T   A GT
GAM96   YES1    3' GATCTCCTGACCTTGTGA    19539         C
                                TCACAAGGTC GGAGATT
                                |||||||||| |||||||
                                AGTGTTCCAG CCTCTAG
                                      T
GAM96   ZNF264  3' GGTCTCAAACTCCTGACCTTGT 14221         C   A
           GA                   TCACAAGGTC GGAG TTGAGACC
                                |||||||||| |||| ||||||||
                                AGTGTTCCAG CCTC AACTCTGG
                                      T   A
GAM96   AKAP6   3' CTCAATCTCCCACCCCATGT  16249    A  TCC_
                                ACA GG   GGAGATTGAG
                                ||| ||   ||||||||||
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                                TGT CC    CCTCTAACTC
                                  A  CCAC
GAM96   ARHF     3'  GGTCTTGAACTCCTGACCTCGT 39275      A     C    A TG
              GA                  TCAC AGGTC GGAG T  AGACC
                                  |||| ||||| |||| |  |||||
                                  AGTG TCCAG CCTC A  TCTGG
                                    C     T    A GT
GAM96   ARHGAP11A 3'  GATCTCCTGACCTTGTGA    29450          C
                                  TCACAAGGTC GGAGATT
                                  |||||||||| |||||||
                                  AGTGTTCCAG CCTCTAG
                                        T
GAM96   ASE-1    3'  GGTCTCGAACTCCTGACCTCGT 24987      A     C    A
              GA                  TCAC AGGTC GGAG TTGAGACC
                                  |||| ||||| |||| ||||||||
                                  AGTG TCCAG CCTC AGCTCTGG
                                    C     T    A
GAM96   BAG5     3'  GGTCTCGAACTCCTGACCTCGT 18043      A     C    A
              GA                  TCAC AGGTC GGAG TTGAGACC
                                  |||| ||||| |||| ||||||||
                                  AGTG TCCAG CCTC AGCTCTGG
                                    C     T    A
GAM96   BAGE     3'  GATCTCCTGACCTCGTGA    8640       A     C
                                  TCAC AGGTC GGAGATT
                                  |||| ||||| |||||||
                                  AGTG TCCAG CCTCTAG
                                    C     T
GAM96   C13orf1  3'  GGTCTCAAACTCCTGACCTCAT 40366     CA    C    A
              GA                  TCA  AGGTC GGAG TTGAGACC
                                  |||  ||||| |||| ||||||||
                                  AGT  TCCAG CCTC AACTCTGG
                                    AC    T    A
GAM96   C6orf5   3'  GGTCTCGAACTCCTGACCTTGT 32000          C    A
              GA                  TCACAAGGTC GGAG TTGAGACC
                                  |||||||||| |||| ||||||||
                                  AGTGTTCCAG CCTC AGCTCTGG
                                        T    A
GAM96   C9orf9   3'  GGTCTCAATCTCCTGACCTCAT 39030     CA    C
              GA                  TCA  AGGTC GGAGATTGAGACC
                                  |||  ||||| ||||||||||||
                                  AGT  TCCAG CCTCTAACTCTGG
                                    AC    T
GAM96   CEACAM8  3'  GGTCTCAATCTCCTGACTTCAT 10184     CA    C
              GG                  TCA  AGGTC GGAGATTGAGACC
                                  |||  ||||| ||||||||||||
                                  GGT  TTCAG CCTCTAACTCTGG
                                    AC    T
GAM96   DKFZP434C212 3'  AATCTCCTGACCTCGTGA    69475      A     C
                                  TCAC AGGTC GGAGATT
                                  |||| ||||| |||||||
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                                AGTG TCCAG CCTCTAA
                                  C    T
GAM96   DKFZP564O0523 3'  GGTCTCGAACTCCTGACCTTGT 50422          C   A
            GA                    TCACAAGGTC GGAG TTGAGACC
                                  |||||||||| |||| ||||||||
                                  AGTGTTCCAG CCTC AGCTCTGG
                                       T   A
GAM96   DKFZp761J139 5'  GGTCTCGATATCCTGACCTTGT 51109          C   G
            GA                    TCACAAGGTC GGA ATTGAGACC
                                  |||||||||| ||| |||||||||
                                  AGTGTTCCAG CCT TAGCTCTGG
                                       T   A
GAM96   DKFZp761N1114 3'  GATCTCCTGACCTCATGA    79787     CA    C
                                  TCA  AGGTC GGAGATT
                                  |||  ||||| |||||||
                                  AGT  TCCAG CCTCTAG
                                    AC    T
GAM96   EREG    3'  GGTCTCAATCTCCTAACCTTGA 9312     A     CC
            GA                    TC CAAGGT  GGAGATTGAGACC
                                  || ||||||  ||||||||||||
                                  AG GTTCCA  CCTCTAACTCTGG
                                   A     AT
GAM96   FKBP9   3'  GGTCTCAATCTCGACCTCGTGA 95720      A    CG
                                  TCAC AGGTC  GAGATTGAGACC
                                  |||| |||||  ||||||||||||
                                  AGTG TCCAG  CTCTAACTCTGG
                                    C    __
GAM96   FLJ10560  3'  GATCTCCTGACCTCGTGA    36796     A    C
                                  TCAC AGGTC GGAGATT
                                  |||| ||||| |||||||
                                  AGTG TCCAG CCTCTAG
                                    C    T
GAM96   FLJ12581  3'  GATCTCCTGACCTTGTGA    46337          C
                                  TCACAAGGTC GGAGATT
                                  |||||||||| |||||||
                                  AGTGTTCCAG CCTCTAG
                                       T
GAM96   FLJ12876  3'  GATCTCCTGACCTCGTGA    43094     A    C
                                  TCAC AGGTC GGAGATT
                                  |||| ||||| |||||||
                                  AGTG TCCAG CCTCTAG
                                    C    T
GAM96   FLJ12960  3'  GATCTCCTGACCTCATGA    45301     CA    C
                                  TCA  AGGTC GGAGATT
                                  |||  ||||| |||||||
                                  AGT  TCCAG CCTCTAG
                                    AC    T
GAM96   FLJ14442  3'  GGTCTCAAACTTCTGACCTCGT 52388     A    C   A
            GA                    TCAC AGGTC GGAG TTGAGACC
                                  |||| ||||| |||| ||||||||
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                                AGTG TCCAG CTTC AACTCTGG
                                  C    T   A
GAM96   FLJ20136 3' GTCTCGAACTCCTGACCTTGTG 35101          C   A
          A                      TCACAAGGTC GGAG TTGAGAC
                                 |||||||||| |||| |||||||
                                 AGTGTTCCAG CCTC AGCTCTG
                                       T   A
GAM96   FLJ20511 3' GATCTCCTGACCTCGTGA    35775     A    C
                                 TCAC AGGTC GGAGATT
                                 |||| ||||| |||||||
                                 AGTG TCCAG CCTCTAG
                                   C    T
GAM96   FLJ20700 3' GGTCTCGAACTCCTGACCTCAT 36018    CA    C   A
          GA                     TCA  AGGTC GGAG TTGAGACC
                                 |||  ||||| |||| ||||||||
                                 AGT  TCCAG CCTC AGCTCTGG
                                   AC    T   A
GAM96   FLJ20813 3' GGTCTCAAACTCCTGACCTCAT 36133    CA    C   A
          GA                     TCA  AGGTC GGAG TTGAGACC
                                 |||  ||||| |||| ||||||||
                                 AGT  TCCAG CCTC AACTCTGG
                                   AC    T   A
GAM96   FLJ20897 5' GGTCTCAGTCTCCAGACCCTGT 51477      A   C
          GA                     TCACA GGTC GGAGATTGAGACC
                                 ||||| |||| ||||||||||||
                                 AGTGT CCAG CCTCTGACTCTGG
                                    C   A
GAM96   FLJ21302 3' GGTCTCGAACGCCTGACCTCAT 43512    CA    C AGA
          GA                     TCA  AGGTC GG   TTGAGACC
                                 |||  ||||| ||   ||||||||
                                 AGT  TCCAG CC   AGCTCTGG
                                   AC    T GCA
GAM96   FLJ21603 3' AATCTCCTGACCTCGTGA    45763     A    C
                                 TCAC AGGTC GGAGATT
                                 |||| ||||| |||||||
                                 AGTG TCCAG CCTCTAA
                                   C    T
GAM96   FLJ22167 5' GATCTCCTGACCTCGTGA    44875     A    C
                                 TCAC AGGTC GGAGATT
                                 |||| ||||| |||||||
                                 AGTG TCCAG CCTCTAG
                                   C    T
GAM96   FLJ22635 3' GTCTCAATCCCAGGCTCCTCTT 47675    CA  T_ _ A
          GA                     TCA  AGG  CC GG GATTGAGAC
                                 |||  |||  || || |||||||||
                                 AGT  TCC  GG CC CTAACTCTG
                                   TC   TC  A _
GAM96   FLJ22794 3' GGTCTCGAACTCCTGACCTCGT 93252     A    C   A
          GA                     TCAC AGGTC GGAG TTGAGACC
                                 |||| ||||| |||| ||||||||
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                                AGTG TCCAG CCTC AGCTCTGG
                                  C    T   A
GAM96   FLJ22969 3' GGTCTCAACCTCCTGGGCT   69215      _   A
                                GGTCC GGAG TTGAGACC
                                ||||| |||| ||||||||
                                TCGGG CCTC AACTCTGG
                                  T   C
GAM96   FLJ23392 3' GATCTCCTGACCTCGTGA    45895     A    C
                                TCAC AGGTC GGAGATT
                                |||| ||||| |||||||
                                AGTG TCCAG CCTCTAG
                                  C    T
GAM96   FLJ23519 3' GGTCTTGATATCCTGACCTCGT 50955     A    C  G  TG
           GA                   TCAC AGGTC GGA AT  AGACC
                                |||| ||||| ||| ||  |||||
                                AGTG TCCAG CCT TA  TCTGG
                                  C    T  A  GT
GAM96   FLJ23556 3' GATCTCCTGACCTTGTGA    46444          C
                                TCACAAGGTC GGAGATT
                                |||||||||| |||||||
                                AGTGTTCCAG CCTCTAG
                                      T
GAM96   FLJ31101 3' GGTCTTGAACTCCTGACCTCAT 36167     CA    C    A TG
           GA                   TCA  AGGTC GGAG T  AGACC
                                |||  ||||| |||| |  |||||
                                AGT  TCCAG CCTC A  TCTGG
                                  AC    T    A GT
GAM96   GNG4    3' GGTCTCAAACTCCTGACCTCGT 16851     A    C    A
           GA                   TCAC AGGTC GGAG TTGAGACC
                                |||| ||||| |||| ||||||||
                                AGTG TCCAG CCTC AACTCTGG
                                  C    T   A
GAM96   GREB1   3' GATCTCCTGACCTCGTGA    28570     A    C
                                TCAC AGGTC GGAGATT
                                |||| ||||| |||||||
                                AGTG TCCAG CCTCTAG
                                  C    T
GAM96   GTF2E1   3' GATCTCCTGACCTCATGA    19800     CA    C
                                TCA  AGGTC GGAGATT
                                |||  ||||| |||||||
                                AGT  TCCAG CCTCTAG
                                  AC    T
GAM96   HSPC065  3' GGTCTCGAACTCCTGACCTCAT 27157     CA    C    A
           GA                   TCA  AGGTC GGAG TTGAGACC
                                |||  ||||| |||| ||||||||
                                AGT  TCCAG CCTC AGCTCTGG
                                  AC    T   A
GAM96   HT002    3' GATCTCCTGACCTCGTGA    26789     A    C
                                TCAC AGGTC GGAGATT
                                |||| ||||| |||||||
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                                AGTG TCCAG CCTCTAG
                                  C    T
GAM96   ICK     3' GATCTCCTGACCTCGTGA   33689     A    C
                                TCAC AGGTC GGAGATT
                                |||| ||||| |||||||
                                AGTG TCCAG CCTCTAG
                                  C    T
GAM96   KIAA0303 5' TCAGTTTCCCGGACCTTTGA  69992    C      _
                                TCA AAGGTCCGG AGATTGA
                                ||| ||||||||| |||||||
                                AGT TTCCAGGCC TTTGACT
                                  _      C
GAM96   KIAA0426 3' GGTCTCGAACTCCTGACCTTGT 28930         C   A
            GA                    TCACAAGGTC GGAG TTGAGACC
                                ||||||||||| |||| ||||||||
                                AGTGTTCCAG CCTC AGCTCTGG
                                      T   A
GAM96   KIAA0459 3' GGTCTCAAACTCCTGACCTTGT 61657         C   A
            GA                    TCACAAGGTC GGAG TTGAGACC
                                ||||||||||| |||| ||||||||
                                AGTGTTCCAG CCTC AACTCTGG
                                      T   A
GAM96   KIAA0469 3' GATCTCCTGACCTTGTGA   29984         C
                                TCACAAGGTC GGAGATT
                                |||||||||| |||||||
                                AGTGTTCCAG CCTCTAG
                                      T
GAM96   KIAA0557 3' GGTCTTGAACTCCCGACCTTGT 78574         C   A TG
            GA                    TCACAAGGTC GGAG T  AGACC
                                |||||||||| |||| |  |||||
                                AGTGTTCCAG CCTC A  TCTGG
                                      C   A GT
GAM96   KIAA0561 3' GGTCTCGAACTCCTGACCTCAT 66485    CA   C   A
            GA                    TCA  AGGTC GGAG TTGAGACC
                                |||  ||||| |||| ||||||||
                                AGT  TCCAG CCTC AGCTCTGG
                                  AC    T   A
GAM96   KIAA0562 3' GGTCTCAAACTCCTGACCTTGT 28829         C   A
            GA                    TCACAAGGTC GGAG TTGAGACC
                                |||||||||| |||| ||||||||
                                AGTGTTCCAG CCTC AACTCTGG
                                      T   A
GAM96   KIAA0594 3' GGTCTCGAACTCCTGACCTTGT 65514         C   A
            GA                    TCACAAGGTC GGAG TTGAGACC
                                |||||||||| |||| ||||||||
                                AGTGTTCCAG CCTC AGCTCTGG
                                      T   A
GAM96   KIAA0737 3' GGTCTCGAACTCCTGACCTCAT 29815    CA   C   A
            GA                    TCA  AGGTC GGAG TTGAGACC
                                |||  ||||| |||| ||||||||
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                                AGT  TCCAG CCTC AGCTCTGG
                                  AC    T   A
GAM96   KIAA0861 3' GATCTCCTGACCTCGTGA    90351     A    C
                                TCAC AGGTC GGAGATT
                                |||| ||||| |||||||
                                AGTG TCCAG CCTCTAG
                                  C    T
GAM96   KIAA0924 3' GGTCTCAAACTCCTGACCTTGT 30368         C   A
            GA                    TCACAAGGTC GGAG TTGAGACC
                                |||||||||| |||| ||||||||
                                AGTGTTCCAG CCTC AACTCTGG
                                     T   A
GAM96   KIAA1143 3' GGTCTCAATCTCCTGACCTCAT 69246     CA    C
            GA                    TCA  AGGTC GGAGATTGAGACC
                                |||  ||||| ||||||||||||
                                AGT  TCCAG CCTCTAACTCTGG
                                  AC    T
GAM96   KIAA1198 3' GATCTCCTGACCTCGTGA    64042     A    C
                                TCAC AGGTC GGAGATT
                                |||| ||||| |||||||
                                AGTG TCCAG CCTCTAG
                                  C    T
GAM96   KIAA1198 3' GGTCTCAATCTCCTGACCTTGT 64052         C
            GA                    TCACAAGGTC GGAGATTGAGACC
                                |||||||||| ||||||||||||
                                AGTGTTCCAG CCTCTAACTCTGG
                                     T
GAM96   KIAA1198 3' GGTCTCGCCCTCCTGACCTTGT 64053         C   AT
            GA                    TCACAAGGTC GGAG  TGAGACC
                                |||||||||| ||||  |||||||
                                AGTGTTCCAG CCTC  GCTCTGG
                                     T   CC
GAM96   KIAA1210 3' GATCTCCTGACCTCGTGA    98073     A    C
                                TCAC AGGTC GGAGATT
                                |||| ||||| |||||||
                                AGTG TCCAG CCTCTAG
                                  C    T
GAM96   KIAA1257 3' GGTCTTGAACTCCTGACCTCGT 63407     A    C   A TG
            GA                    TCAC AGGTC GGAG T  AGACC
                                |||| ||||| |||| |  |||||
                                AGTG TCCAG CCTC A  TCTGG
                                  C    T   A GT
GAM96   KIAA1443 3' GATCTCCTGACCTCATGA    64572     CA    C
                                TCA  AGGTC GGAGATT
                                |||  ||||| |||||||
                                AGT  TCCAG CCTCTAG
                                  AC    T
GAM96   KIAA1497 5' GGTCTCGAACTCCTGACCTCAT 68126     CA    C   A
            GA                    TCA  AGGTC GGAG TTGAGACC
                                |||  ||||| |||| ||||||||
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                                AGT  TCCAG CCTC AGCTCTGG
                                  AC    T   A
GAM96   KIAA1615  3'  GTCTCGATTTCCTGACCTTGTG 69283         C
            A                    TCACAAGGTC GGAGATTGAGAC
                                ||||||||||  ||||||||||||
                                AGTGTTCCAG CCTTTAGCTCTG
                                      T
GAM96   KIAA1668  3'  GATCTCCTGACCTTGTGA    67072         C
                                TCACAAGGTC GGAGATT
                                ||||||||||  |||||||
                                AGTGTTCCAG CCTCTAG
                                      T
GAM96   KIAA1877  3'  GATCTCCTGACCTTGTGA    66751         C
                                TCACAAGGTC GGAGATT
                                ||||||||||  |||||||
                                AGTGTTCCAG CCTCTAG
                                      T
GAM96   KIAA1971  3'  GGTCTTGAACTCCTGACCTCGT 74686     A    C    A TG
            GA                    TCAC AGGTC GGAG T  AGACC
                                ||||  |||||  ||||  |  |||||
                                AGTG TCCAG CCTC A  TCTGG
                                  C    T   A GT
GAM96   KIAA1975  5'  GATCTCCTGACCTCGTGA    74423     A    C
                                TCAC AGGTC GGAGATT
                                ||||  |||||  |||||||
                                AGTG TCCAG CCTCTAG
                                  C    T
GAM96   MEF-2     3'  GGTCTCAAACTCCTGACCTCGT 65027     A    C    A
            GA                    TCAC AGGTC GGAG TTGAGACC
                                ||||  |||||  ||||  ||||||||
                                AGTG TCCAG CCTC AACTCTGG
                                  C    T   A
GAM96   MGC2477   5'  GGTCTCGAACTCCTGACCTCGT 44309     A    C    A
            GA                    TCAC AGGTC GGAG TTGAGACC
                                ||||  |||||  ||||  ||||||||
                                AGTG TCCAG CCTC AGCTCTGG
                                  C    T   A
GAM96   MGC4638   3'  GGTCTCAATCTCTTGACCTCTT 49739     CA    C
            GA                    TCA  AGGTC GGAGATTGAGACC
                                |||  |||||  ||||||||||||||
                                AGT  TCCAG TCTCTAACTCTGG
                                  TC    T
GAM96   MGC4766   5'  GATCTCCTGACCTCGTGA    49559     A    C
                                TCAC AGGTC GGAGATT
                                ||||  |||||  |||||||
                                AGTG TCCAG CCTCTAG
                                  C    T
GAM96   moblak    3'  GATCTCCTGACCTTGTGA    56402         C
                                TCACAAGGTC GGAGATT
                                ||||||||||  |||||||
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                                AGTGTTCCAG CCTCTAG
                                      T
GAM96   MOCS3    3' GGTCTCGAACTCCTGACCTCGT 27933      A    C    A
            GA                  TCAC AGGTC GGAG TTGAGACC
                                |||| ||||| |||| ||||||||
                                AGTG TCCAG CCTC AGCTCTGG
                                  C    T    A
GAM96   MRPS27   3' GGTCTCAACCTCCTGACCT   31331      C    A
                                AGGTC GGAG TTGAGACC
                                ||||| |||| ||||||||
                                TCCAG CCTC AACTCTGG
                                  T    C
GAM96   MtFMT    3' GGTCTCGAACTCCTGACCTTGT 58337          C    A
            GA                  TCACAAGGTC GGAG TTGAGACC
                                |||||||||| |||| ||||||||
                                AGTGTTCCAG CCTC AGCTCTGG
                                      T    A
GAM96   NDUFC2   3' GGTCTCAATCTCTTGACCTTGT 17034          C
            GA                  TCACAAGGTC GGAGATTGAGACC
                                |||||||||| ||||||||||||
                                AGTGTTCCAG TCTCTAACTCTGG
                                      T
GAM96   OR51E2   3' GATCTCCTGACCTTGTGA    48512          C
                                TCACAAGGTC GGAGATT
                                |||||||||| |||||||
                                AGTGTTCCAG CCTCTAG
                                      T
GAM96   PRO0365  5' GATCTCCTGACCTCATGA    26984     CA    C
                                TCA  AGGTC GGAGATT
                                |||  ||||| |||||||
                                AGT  TCCAG CCTCTAG
                                  AC    T
GAM96   PRO0899  5' GGTCTCAATCTCCTGGGCC   38313      _
                                GGTCC GGAGATTGAGACC
                                ||||| ||||||||||||
                                CCGGG CCTCTAACTCTGG
                                   T
GAM96   PSPH     3' GATCTCCTGACCTTGTGA    17135          C
                                TCACAAGGTC GGAGATT
                                |||||||||| |||||||
                                AGTGTTCCAG CCTCTAG
                                      T
GAM96   RAB21    3' GATCTCCTGACCTTGTGA    31091          C
                                TCACAAGGTC GGAGATT
                                |||||||||| |||||||
                                AGTGTTCCAG CCTCTAG
                                      T
GAM96   RAP140   3' GATCTCCTGACCTCATGA    31517     CA    C
                                TCA  AGGTC GGAGATT
                                |||  ||||| |||||||
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                                AGT  TCCAG CCTCTAG
                                  AC     T
GAM96   RASSF2   3'  GGTCTTGAACTCCTGACCTCGT 29106      A    C    A TG
              GA                  TCAC AGGTC GGAG T  AGACC
                                  |||| ||||| |||| |  |||||
                                  AGTG TCCAG CCTC A  TCTGG
                                    C     T    A GT
GAM96   SLC12A8  3'  GGTCTCGAACTCCTGACCTCGT 45243      A    C    A
              GA                  TCAC AGGTC GGAG TTGAGACC
                                  |||| ||||| |||| ||||||||
                                  AGTG TCCAG CCTC AGCTCTGG
                                    C     T    A
GAM96   SREC     3'  GATCTCCTGACCTCGTGA    14904      A    C
                                  TCAC AGGTC GGAGATT
                                  |||| ||||| |||||||
                                  AGTG TCCAG CCTCTAG
                                    C     T
GAM96   SS-56    3'  GATCTCCTGACCTCATGA    60353     CA    C
                                  TCA  AGGTC GGAGATT
                                  |||  ||||| |||||||
                                  AGT  TCCAG CCTCTAG
                                    AC     T
GAM96   TADA3L   3'  GATCTCCTGACCTCGTGA    22041      A    C
                                  TCAC AGGTC GGAGATT
                                  |||| ||||| |||||||
                                  AGTG TCCAG CCTCTAG
                                    C     T
GAM96   TUCAN    3'  GATCTCCTGACCTCATGA    30980     CA    C
                                  TCA  AGGTC GGAGATT
                                  |||  ||||| |||||||
                                  AGT  TCCAG CCTCTAG
                                    AC     T
GAM96   YWHAQ    3'  GTCCCAAAAAAGCCTTGTGA   23352          CCGGAGA   A
                                  TCACAAGGT      TTG GAC
                                  |||||||||      ||| |||
                                  AGTGTTCCG      AAC CTG
                                        AAAA___   C
GAM96   LOC113523 5'  GATCTCCTGACCTCGTGA    73425      A    C
                                  TCAC AGGTC GGAGATT
                                  |||| ||||| |||||||
                                  AGTG TCCAG CCTCTAG
                                    C     T
GAM96   LOC120114 3'  GGTCTCAAACTCCTGACCTCGT 76048    A    C    A
                                  AC AGGTC GGAG TTGAGACC
                                  || ||||| |||| ||||||||
                                  TG TCCAG CCTC AACTCTGG
                                    C     T    A
GAM96   LOC133686 3'  GGTCTCGAACTCCTGACCTTGT 75618          C    A
              GA                  TCACAAGGTC GGAG TTGAGACC
                                  |||||||||| |||| ||||||||
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                                AGTGTTCCAG CCTC AGCTCTGG
                                      T   A
GAM96   LOC144699 3' GGCTTCTGCTCCGGTACCTTGT 77437        _    ATT  GA
           GA                   TCACAAGGT CCGGAG   GA  CC
                                |||||||||  ||||||   ||  ||
                                AGTGTTCCA GGCCTC   CT  GG
                                      T     GT_  TC
GAM96   LOC144871 3' GATCTCCTGACCTTGTGA    84126         C
                                TCACAAGGTC GGAGATT
                                ||||||||||  |||||||
                                AGTGTTCCAG CCTCTAG
                                      T
GAM96   LOC145009 3' GGTCTTGAACTCCTGACCTCGT 60978     A    C    A TG
           GA                   TCAC AGGTC GGAG T  AGACC
                                ||||  |||||  ||||  |  |||||
                                AGTG TCCAG CCTC A  TCTGG
                                  C    T    A GT
GAM96   LOC146429 5' GATCTCCTGACCTCATGA    84667     CA    C
                                TCA  AGGTC GGAGATT
                                |||  |||||  |||||||
                                AGT  TCCAG CCTCTAG
                                  AC    T
GAM96   LOC146603 5' GATCTCCTGACCTCATGA    78597     CA    C
                                TCA  AGGTC GGAGATT
                                |||  |||||  |||||||
                                AGT  TCCAG CCTCTAG
                                  AC    T
GAM96   LOC146784 5' GGTCTTGAACCCCTGACCTCAT 78717     CA    C  AGA TG
           GA                   TCA  AGGTC GG   T  AGACC
                                |||  |||||  ||   |  |||||
                                AGT  TCCAG CC   A  TCTGG
                                  AC    T  CCA GT
GAM96   LOC146909 3' GGTCTCGATCTGACCTCATGA  78777     CA    CGG
                                TCA  AGGTC   AGATTGAGACC
                                |||  |||||   ||||||||||
                                AGT  TCCAG   TCTAGCTCTGG
                                  AC    ___
GAM96   LOC147080 5' GATCTCCTGACCTTGTGA    85040         C
                                TCACAAGGTC GGAGATT
                                ||||||||||  |||||||
                                AGTGTTCCAG CCTCTAG
                                      T
GAM96   LOC147429 3' GGTCTCGATTTCCTGACCTTGT 78997         C
           GA                   TCACAAGGTC GGAGATTGAGACC
                                ||||||||||  |||||||||||||
                                AGTGTTCCAG CCTTTAGCTCTGG
                                      T
GAM96   LOC147694 3' GATCTCCTGACCTTGTGA    79098         C
                                TCACAAGGTC GGAGATT
                                ||||||||||  |||||||
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                                AGTGTTCCAG CCTCTAG
                                      T
GAM96   LOC147817 3' GGTCTCAAACTCCTGACCTT  79187       C   A
                                AAGGTC GGAG TTGAGACC
                                |||||| |||| ||||||||
                                TTCCAG CCTC AACTCTGG
                                   T   A
GAM96   LOC147990 3' TCTCGAACTCCTGACCTTGTGA 85237          C   A
                                TCACAAGGTC GGAG TTGAGA
                                |||||||||| |||| ||||||
                                AGTGTTCCAG CCTC AGCTCT
                                      T   A
GAM96   LOC148137 3' GGTCTCCTGACCTCGTGA    59108     A    C
                                TCAC AGGTC GGAGATT
                                |||| ||||| |||||||
                                AGTG TCCAG CCTCTGG
                                  C    T
GAM96   LOC148189 5' GGTCTCAATCTCTTGACCTCGT 79453    A    C
                                AC AGGTC GGAGATTGAGACC
                                || ||||| ||||||||||||
                                TG TCCAG TCTCTAACTCTGG
                                 C    T
GAM96   LOC149421 3' GATCTCCTGACCTCGTGA    80145     A    C
                                TCAC AGGTC GGAGATT
                                |||| ||||| |||||||
                                AGTG TCCAG CCTCTAG
                                  C    T
GAM96   LOC149821 5' GATCTCCTGACCTCGTGA    85933     A    C
                                TCAC AGGTC GGAGATT
                                |||| ||||| |||||||
                                AGTG TCCAG CCTCTAG
                                  C    T
GAM96   LOC150630 5' GATCTCCTGACCTCGTGA    86302     A    C
                                TCAC AGGTC GGAGATT
                                |||| ||||| |||||||
                                AGTG TCCAG CCTCTAG
                                  C    T
GAM96   LOC151057 3' GGTCTCGAACTCCTGACCTTGT 86392          C   A
          GA                    TCACAAGGTC GGAG TTGAGACC
                                |||||||||| |||| ||||||||
                                AGTGTTCCAG CCTC AGCTCTGG
                                      T   A
GAM96   LOC151979 5' GATCTCCTGACCTCATGA    81250     CA    C
                                TCA  AGGTC GGAGATT
                                |||  ||||| |||||||
                                AGT  TCCAG CCTCTAG
                                  AC    T
GAM96   LOC152445 3' GATCTCCTGACCTCGTGA    86950     A    C
                                TCAC AGGTC GGAGATT
                                |||| ||||| |||||||
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                                AGTG TCCAG CCTCTAG
                                  C    T
GAM96   LOC152719 5'  GGTCTCAATCTCCTGACCTCGT 87039      A    C
                GA              TCAC AGGTC GGAGATTGAGACC
                                |||| ||||| ||||||||||||
                                AGTG TCCAG CCTCTAACTCTGG
                                  C    T
GAM96   LOC154282 5'  GGTCTCAATCTCTTGACCTTGT 87410          C
                GA              TCACAAGGTC GGAGATTGAGACC
                                |||||||||| ||||||||||||
                                AGTGTTCCAG TCTCTAACTCTGG
                                     T
GAM96   LOC170082 5'  GATCTCCTGACCTCGTGA    83444      A    C
                                TCAC AGGTC GGAGATT
                                |||| ||||| |||||||
                                AGTG TCCAG CCTCTAG
                                  C    T
GAM96   LOC196264 3'  GGTCTCAATCCCCTGACCTCGT 88990      A    C  A
                GA              TCAC AGGTC GG GATTGAGACC
                                |||| ||||| || ||||||||||
                                AGTG TCCAG CC CTAACTCTGG
                                  C    T  C
GAM96   LOC196411 3'  GGTCTCGAACTCCTGACCTCGT 89049      A    C    A
                GA              TCAC AGGTC GGAG TTGAGACC
                                |||| ||||| |||| ||||||||
                                AGTG TCCAG CCTC AGCTCTGG
                                  C    T    A
GAM96   LOC199725 5'  GGTCTCGAACTCCTGACCTCGT 91424      A    C    A
                GA              TCAC AGGTC GGAG TTGAGACC
                                |||| ||||| |||| ||||||||
                                AGTG TCCAG CCTC AGCTCTGG
                                  C    T    A
GAM96   LOC199786 3'  GGTCTTGAACTCCTGACCTCAT 89759     CA    C    A TG
                GA              TCA  AGGTC GGAG T  AGACC
                                |||  ||||| |||| |  |||||
                                AGT  TCCAG CCTC A  TCTGG
                                  AC    T    A GT
GAM96   LOC200014 3'  GGTCTCGAACTCCTGACCTCAT 89940     CA    C    A
                GA              TCA  AGGTC GGAG TTGAGACC
                                |||  ||||| |||| ||||||||
                                AGT  TCCAG CCTC AGCTCTGG
                                  AC    T    A
GAM96   LOC200310 3'  GGTCTCGAACTCCTGACCTCGT 66332      A    C    A
                GA              TCAC AGGTC GGAG TTGAGACC
                                |||| ||||| |||| ||||||||
                                AGTG TCCAG CCTC AGCTCTGG
                                  C    T    A
GAM96   LOC200316 5'  GGTCTCGAACTCCTGACCTCGT 90189      A    C    A
                GA              TCAC AGGTC GGAG TTGAGACC
                                |||| ||||| |||| ||||||||
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                                AGTG TCCAG CCTC AGCTCTGG
                                  C    T   A
GAM96   LOC201294 3' GGTCTCAATCTCTTGACCTCCT 89593     CA    C
           GA                   TCA  AGGTC GGAGATTGAGACC
                                |||  ||||| |||||||||||||
                                AGT  TCCAG TCTCTAACTCTGG
                                  CC    T
GAM96   LOC203350 3' GGTCTTGTACTCCTGACCTTGT 92245          C   AT
           GA                   TCACAAGGTC GGAG  TGAGACC
                                |||||||||| ||||  |||||||
                                AGTGTTCCAG CCTC  GTTCTGG
                                     T   AT
GAM96   LOC203369 3' GATCTCCTGACCTCGTGA    90888     A    C
                                TCAC AGGTC GGAGATT
                                |||| ||||| |||||||
                                AGTG TCCAG CCTCTAG
                                  C    T
GAM96   LOC219735 3' GATCTCCTGACCTCGTGA    94729     A    C
                                TCAC AGGTC GGAGATT
                                |||| ||||| |||||||
                                AGTG TCCAG CCTCTAG
                                  C    T
GAM96   LOC219894 3' GATCTCCTGACCTCATGA    94906     CA    C
                                TCA  AGGTC GGAGATT
                                |||  ||||| |||||||
                                AGT  TCCAG CCTCTAG
                                  AC    T
GAM96   LOC220074 3' GGTCTCCATCTCCTGACCTTGT 59988          C     T
           GA                   TCACAAGGTC GGAGAT GAGACC
                                |||||||||| |||||| ||||||
                                AGTGTTCCAG CCTCTA CTCTGG
                                     T    C
GAM96   LOC253981 3' GATCTCCTGACCTCGTGA    97537     A    C
                                TCAC AGGTC GGAGATT
                                |||| ||||| |||||||
                                AGTG TCCAG CCTCTAG
                                  C    T
GAM96   LOC254249 5' GATCTCCTGACCTCGTGA    97185     A    C
                                TCAC AGGTC GGAGATT
                                |||| ||||| |||||||
                                AGTG TCCAG CCTCTAG
                                  C    T
GAM96   LOC254295 5' GGTCTCGATTTCCTGACCTCGT 97894      A    C
           GA                   TCAC AGGTC GGAGATTGAGACC
                                |||| ||||| ||||||||||||
                                AGTG TCCAG CCTTTAGCTCTGG
                                  C    T
GAM96   LOC256221 3' GATCTCCTGACCTCGTGA    96912     A    C
                                TCAC AGGTC GGAGATT
                                |||| ||||| |||||||
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                                AGTG TCCAG CCTCTAG
                                  C    T
GAM96   LOC51696  3' GATCTCCTGACCTTGTGA    33084          C
                                TCACAAGGTC GGAGATT
                                |||||||||| |||||||
                                AGTGTTCCAG CCTCTAG
                                     T
GAM96   LOC81034  3' GGTCTCAATCTCCTGACCTTGT 48592          C
           GA                    TCACAAGGTC GGAGATTGAGACC
                                |||||||||| |||||||||||||
                                AGTGTTCCAG CCTCTAACTCTGG
                                     T
GAM96   LOC89919  3' GTCTCGATCTCCGGACCTCATG 61378     CA
           A                     TCA  AGGTCCGGAGATTGAGAC
                                |||  ||||||||||||||||||
                                AGT  TCCAGGCCTCTAGCTCTG
                                  AC
GAM96   LOC90591  3' GGTCTCAATCTCCTGACCTCGT 64179      A    C
           GA                    TCAC AGGTC GGAGATTGAGACC
                                |||| ||||| |||||||||||||
                                AGTG TCCAG CCTCTAACTCTGG
                                  C    T
GAM96   LOC91115  3' AATCTCCTGACCTTGTGA    65533          C
                                TCACAAGGTC GGAGATT
                                |||||||||| |||||||
                                AGTGTTCCAG CCTCTAA
                                     T
GAM96   LOC91373  3' GATCTCCTGACCTCGTGA    66415      A    C
                                TCAC AGGTC GGAGATT
                                |||| ||||| |||||||
                                AGTG TCCAG CCTCTAG
                                  C    T
GAM96   LOC91893  3' GGTCTCAATCTCCCGGCCTCGT 68076      A    C
           GA                    TCAC AGGTC GGAGATTGAGACC
                                |||| ||||| |||||||||||||
                                AGTG TCCGG CCTCTAACTCTGG
                                  C    C
GAM96   LOC92148  5' GATCTCCTGACCTTGTGA    68881          C
                                TCACAAGGTC GGAGATT
                                |||||||||| |||||||
                                AGTGTTCCAG CCTCTAG
                                     T
GAM96   LOC92689  3' GATCTCCTGACCTCGTGA    70776      A    C
                                TCAC AGGTC GGAGATT
                                |||| ||||| |||||||
                                AGTG TCCAG CCTCTAG
                                  C    T
GAM96   LOC93349  3' GGTCTCGAACTCCTGACCTCAT 57274     CA    C    A
           GA                    TCA  AGGTC GGAG TTGAGACC
                                |||  ||||| |||| ||||||||
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                                AGT  TCCAG CCTC AGCTCTGG
                                  AC    T   A
GAM96   LOC93356 3'  AATCTTCCTGACCTTGTGA   72546         C  _
                                TCACAAGGTC GGA GATT
                                |||||||||| ||| ||||
                                AGTGTTCCAG CCT CTAA
                                      T   T
GAM97   A1BG    3'  GTCACCCAGGCTGGAGTGCAGT 56295
            G                    CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCACTG

GAM97   A1BG    3'  GTTGCCCAGGCTGGAGTGCAAT 56296    C           TG
            G                    CA TGCACTCCAGCCTGGG  AC
                                || ||||||||||||||  ||
                                GT ACGTGAGGTCGGACCC  TG
                                 A            GT
GAM97   AASS    3'  GTCACCCAGGCTGGAGTGCAGT 20462
            G                    CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCACTG

GAM97   ACADSB   3'  GTCACCCAGGCTAGAGTGCAGT 9647          C
            G                    CACTGCACTC AGCCTGGGTGAC
                                |||||||||| ||||||||||
                                GTGACGTGAG TCGGACCCACTG
                                      A
GAM97   ADAMTS4  3'  GTCGCCCAGGCTGGAGTGCAAT 18770    C
            G                    CA TGCACTCCAGCCTGGGTGAC
                                || ||||||||||||||||||
                                GT ACGTGAGGTCGGACCCGCTG
                                 A
GAM97   ADCY2    3'  TCATCAGGCCGGGTGCAGTG   65654        T  A     G
                                CACTGCAC CC GCCTGG TGA
                                |||||||| || |||||| |||
                                GTGACGTG GG CGGACT ACT
                                     _  C     _
GAM97   ADCY6    5'  GTCACCCAGGCTGGAGTGCAAT 31592    C
            G                    CA TGCACTCCAGCCTGGGTGAC
                                || ||||||||||||||||||
                                GT ACGTGAGGTCGGACCCACTG
                                 A
GAM97   AHR     3'  CGCCCAAACTGGAGTGCAGTG  9675           CC
                                CACTGCACTCCAG  TGGGTG
                                ||||||||||||  ||||||
                                GTGACGTGAGGTC  ACCCGC
                                       AA
GAM97   AIM1    3'  CTCAGGCTGGAGTGCAGTG   93462
                                CACTGCACTCCAGCCTGGG
                                |||||||||||||||||
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                                GTGACGTGAGGTCGGACTC

GAM97   AIPL1    3'  CACCCAGGCAGGGAGCAAGTG  60533      GCA   A_
                                CACT  CTCC  GCCTGGGTG
                                ||||  ||||  |||||||||
                                GTGA  GAGG  CGGACCCAC
                                  AC_   GA
GAM97   ALDH1B1  3'  GTCGCCCAGGCTGGAGTGCAGT 7325
           G                     CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCGCTG

GAM97   ALOX15   3'  CACCCAGGCTGGAGTGCAGTG  8541
                                CACTGCACTCCAGCCTGGGTG
                                ||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCAC

GAM97   APAF1    3'  CCAGGCTGGAGTGCAGTG    8582
                                CACTGCACTCCAGCCTGG
                                ||||||||||||||||
                                GTGACGTGAGGTCGGACC

GAM97   APAF1    3'  TCACCCAGGCTGGAGTGCAGTG 8591
                                CACTGCACTCCAGCCTGGGTGA
                                |||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCACT

GAM97   APAF1    3'  CCAGGCTGGAGTGCAGTG    25964
                                CACTGCACTCCAGCCTGG
                                ||||||||||||||||
                                GTGACGTGAGGTCGGACC

GAM97   APAF1    3'  TCACCCAGGCTGGAGTGCAGTG 25982
                                CACTGCACTCCAGCCTGGGTGA
                                |||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCACT

GAM97   APM1     3'  CCAGGCTAGAGTGCAGTG    17768          C
                                CACTGCACTC AGCCTGG
                                |||||||||| |||||||
                                GTGACGTGAG TCGGACC
                                      A
GAM97   APM1     3'  GCCCTGGCTGGAGTTCAGTG  17783      C       T
                                CACTG ACTCCAGCC GGGT
                                ||||| ||||||||| ||||
                                GTGAC TGAGGTCGG CCCG
                                   T       T
GAM97   APM1     3'  GTCACCCAGGCTGGAGTACAGT 17789      C
           G                     CACTG ACTCCAGCCTGGGTGAC
                                 ||||| ||||||||||||||||
```

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                                GTGAC TGAGGTCGGACCCACTG
                                   A
GAM97   APOL1    3'  GTCGCCAAGTTGGAGTGCAATG 14742    C        CTG
                                CA TGCACTCCAGC   GGTGAC
                                || ||||||||||   ||||||
                                GT ACGTGAGGTTG   CCGCTG
                                 A         AA_
GAM97   APPL     3'  GTTGCCCAGGCTGGAGTGCAGT 24953              TG
           G                     CACTGCACTCCAGCCTGGG  AC
                                 ||||||||||||||||||  ||
                                 GTGACGTGAGGTCGGACCC  TG
                                              GT
GAM97   AQP6     3'  GTTACCCAGGCTGGAGTGCAGT 55010
           G                     CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCATTG

GAM97   AQP6     3'  GTTACCCAGGCTGGAGTGCAGT 9732
           G                     CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCATTG

GAM97   ARCN1    3'  ACCCAGGCTGGAATGCAATG   9741     C   C
                                CA TGCA TCCAGCCTGGGT
                                || |||| ||||||||||||
                                GT ACGT AGGTCGGACCCA
                                 A    A
GAM97   ATM      3'  GTCATTCGGGCTGGGCGCAG   57136      A T
                                CTGC C CCAGCCTGGGTGAC
                                |||| | ||||||||||||||
                                GACG G GGTCGGGCTTACTG
                                  C _
GAM97   ATM      3'  GTCATTCGGGCTGGGCGCAG   5300       A T
                                CTGC C CCAGCCTGGGTGAC
                                |||| | ||||||||||||||
                                GACG G GGTCGGGCTTACTG
                                  C _
GAM97   ATP1B2   3'  GTTGCCCAGGCTGGAGTGCAAT 9839     C            TG
           G                     CA TGCACTCCAGCCTGGG  AC
                                 || ||||||||||||||||  ||
                                 GT ACGTGAGGTCGGACCC  TG
                                  A              GT
GAM97   ATP6V1A1 3'  GTTGCCCAGGCTGGAGTGCAAT 9873     C             TG
           G                     CA TGCACTCCAGCCTGGG  AC
                                 || ||||||||||||||||  ||
                                 GT ACGTGAGGTCGGACCC  TG
                                  A              GT
GAM97   ATP7A    3'  GCCCAGGCTGGAGTGCAGTG   5326
                                CACTGCACTCCAGCCTGGGT
                                ||||||||||||||||||||
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                                GTGACGTGAGGTCGGACCCG

GAM97   ATP8B2   3'  GTCACCTAGGCAAGAGTGCAAT 65844    C      CA
            G                    CA TGCACTC  GCCTGGGTGAC
                                 || |||||||  ||||||||||
                                 GT ACGTGAG  CGGATCCACTG
                                  A      AA
GAM97   AXL      3'  GTCACCCAGGCTGGAGTGCAGT 41891
            G                    CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCACTG

GAM97   AXL      3'  GTCACCCAGGCTGGAGTGCAGT 9909
            G                    CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCACTG

GAM97   BAZ2A    5'  TTGCCCAGGCTTGAGTGCAATG 26517    C      C       TG
                                 CA TGCACTC AGCCTGGG  A
                                 || ||||||| ||||||||  |
                                 GT ACGTGAG TCGGACCC  T
                                  A      T       GT
GAM97   BCL10    3'  TCGCCCAGGCTGGAGTGCAGTG 15373
                                 CACTGCACTCCAGCCTGGGTGA
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCGCT

GAM97   BDKRB1   5'  GTCGGCCCAGACTGAAGTGCAG 7385          C  C    _
            TG                     CACTGCACT CAG CTGGGT GAC
                                   ||||||||| ||| |||||| |||
                                   GTGACGTGA GTC GACCCG CTG
                                        A  A     G
GAM97   BDKRB2   3'  GTCATTCAGCACCAGAGCACGT 7114     _  A  CCA  C
            G                      CAC TGC CT   GC TGGGTGAC
                                   ||| ||| ||   || ||||||||
                                   GTG ACG GA   CG ACTTACTG
                                     C   A  CCA  _
GAM97   BDP1     3'  GCCCAGGCAAGAGTGCAGTG   37968          CA
                                   CACTGCACTC  GCCTGGGT
                                   ||||||||||  ||||||||
                                   GTGACGTGAG  CGGACCCG
                                        AA
GAM97   BRIP1    3'  GTTGCCCAGGCTGGAATGCAGT 50211         C         TG
            G                      CACTGCA TCCAGCCTGGG  AC
                                   |||||||  ||||||||||  ||
                                   GTGACGT AGGTCGGACCC  TG
                                       A          GT
GAM97   C7       3'  GTTGCCCAGGCTGGAGCGCAGT 6987         A         TG
            G                      CACTGC CTCCAGCCTGGG  AC
                                   ||||||  ||||||||||||  ||
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                                GTGACG GAGGTCGGACCC  TG
                                   C           GT
GAM97   CAMLG    3'  GTTGCCCAGGCTAGAGTGCAAT 10005    C      C       TG
           G                    CA TGCACTC AGCCTGGG  AC
                                || ||||||| ||||||||  ||
                                GT ACGTGAG TCGGACCC  TG
                                 A      A       GT
GAM97   CASP10   3'  GTCACCCAGACTGGAGTGCAG  53223           C
                                CTGCACTCCAG CTGGGTGAC
                                |||||||||||| |||||||||
                                GACGTGAGGTC GACCCACTG
                                      A
GAM97   CASP10   3'  GTCACCCAGACTGGAGTGCAG  53260           C
                                CTGCACTCCAG CTGGGTGAC
                                |||||||||||| |||||||||
                                GACGTGAGGTC GACCCACTG
                                      A
GAM97   CASP2    3'  GTCGCCCAGGCTGGAGGGCAGT 53294        A
           G                    CACTGC CTCCAGCCTGGGTGAC
                                |||||| ||||||||||||||||
                                GTGACG GAGGTCGGACCCGCTG
                                   G
GAM97   CASP2    3'  GTCGCCCAGGCTGGAGGGCAGT 53310        A
           G                    CACTGC CTCCAGCCTGGGTGAC
                                |||||| ||||||||||||||||
                                GTGACG GAGGTCGGACCCGCTG
                                   G
GAM97   CASP2    3'  GTCGCCCAGGCTGGAGGGCAGT 53345        A
           G                    CACTGC CTCCAGCCTGGGTGAC
                                |||||| ||||||||||||||||
                                GTGACG GAGGTCGGACCCGCTG
                                   G
GAM97   CASP2    3'  GTCGCCCAGGCTGGAGGGCAGT 8718         A
           G                    CACTGC CTCCAGCCTGGGTGAC
                                |||||| ||||||||||||||||
                                GTGACG GAGGTCGGACCCGCTG
                                   G
GAM97   CASP8    3'  GTCGCCCAGGCTGGAGTGCAGT 8761
           G                    CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCGCTG

GAM97   CASP8    3'  GTCGCCCAGGCTGGAGTGCAGT 54082
           G                    CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCGCTG

GAM97   CASP8    3'  GTCGCCCAGGCTGGAGTGCAGT 54102
           G                    CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
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                                GTGACGTGAGGTCGGACCCGCTG

GAM97   CASP8    3'  GTCGCCCAGGCTGGAGTGCAGT 54118
                G                CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCGCTG

GAM97   CBFA2T2  3'  GTCTCCCAGGCTGGAGTGCA  18715            T
                                 TGCACTCCAGCCTGGG GAC
                                 |||||||||||||||| |||
                                 ACGTGAGGTCGGACCC CTG
                                           T
GAM97   CCNF     3'  GTCTCCCCGGCTGGAGTGCAGT 10085           T  T
                G                CACTGCACTCCAGCC GGG GAC
                                 ||||||||||||||| ||| |||
                                 GTGACGTGAGGTCGG CCC CTG
                                           C  T
GAM97   CDC6     3'  GTTGCCCAGGCTGGAGTGCAAT 8826     C          TG
                G                CA TGCACTCCAGCCTGGG  AC
                                 || ||||||||||||||||  ||
                                 GT ACGTGAGGTCGGACCC  TG
                                  A            GT
GAM97   CDH1     3'  TCGGCCAGGCTGGAGTGCAGTG 16408              G
                                 CACTGCACTCCAGCCTGG TGA
                                 |||||||||||||||| |||
                                 GTGACGTGAGGTCGGACC GCT
                                           G
GAM97   CDH17    3'  GTCGCCCAGGCTGGAGTACAGT 15787      C
                G                CACTG ACTCCAGCCTGGGTGAC
                                 ||||| ||||||||||||||||
                                 GTGAC TGAGGTCGGACCCGCTG
                                   A
GAM97   CELSR1   3'  TGCCCTTGAAGTGGAGTG    27280     G   C   CCT
                                 CACT CACT CAG   GGGTG
                                 |||| |||| |||   |||||
                                 GTGA GTGA GTT   CCCGT
                                   G   A  ___
GAM97   CIAS1    5'  GCCTAGGCTGGAGTGCAGTG  18098
                                 CACTGCACTCCAGCCTGGGT
                                 ||||||||||||||||||
                                 GTGACGTGAGGTCGGATCCG

GAM97   CLECSF12 3'  GTTACCCAGGCTGGAGTGCAGT 77217
                G                CACTGCACTCCAGCCTGGGTGAC
                                 |||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCATTG

GAM97   CLECSF12 3'  GTTGCCCAGGCTGGAGTGCA  77219            TG
                                 TGCACTCCAGCCTGGG  AC
                                 ||||||||||||||| ||
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                                ACGTGAGGTCGGACCC TG
                                      GT
GAM97  CMAR    5' GCCAAGGCTGGAGTGCAG   19032          G
                                CTGCACTCCAGCCT GGT
                                ||||||||||||| |||
                                GACGTGAGGTCGGA CCG
                                      A
GAM97  CMAR    5' GTCACCCAGGCTGGAGTGCAGT 19035
          G                      CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCACTG

GAM97  CNGA1   5' GCCCAGGCTGGAGTGCAGTG  60242
                                CACTGCACTCCAGCCTGGGT
                                ||||||||||||||||||
                                GTGACGTGAGGTCGGACCCG

GAM97  CNN2    3' GTTGCCCAGGCTGGAGTGCAGT 16462             TG
          G                     CACTGCACTCCAGCCTGGG AC
                                |||||||||||||||||  ||
                                GTGACGTGAGGTCGGACCC TG
                                      GT
GAM97  CNP     3' TTTCCCAAGCTGGAGTGCAGTG 53628          C  T
                                CACTGCACTCCAGC TGGG GA
                                |||||||||||| |||| ||
                                GTGACGTGAGGTCG ACCC TT
                                      A  T
GAM97  CORO2B  5' GTTGCCCAAGCTGGAGTGCAGT 65174          C  TG
          G                     CACTGCACTCCAGC TGGG AC
                                |||||||||||| |||| ||
                                GTGACGTGAGGTCG ACCC TG
                                      A  GT
GAM97  COX15   3' GTTGCCCAGGCTGGAGTACAAT 55288   C C       TG
          G                     CA TG ACTCCAGCCTGGG AC
                                || || ||||||||||||  ||
                                GT AC TGAGGTCGGACCC TG
                                 A A          GT
GAM97  CPS1    3' TCTCCAGGCTGGAGTGCAGTG  10289            T
                                CACTGCACTCCAGCCTGGG GA
                                |||||||||||||||||| ||
                                GTGACGTGAGGTCGGACCT CT
                                                 _
GAM97  CR1     3' GTCTCCCAGGCTGGAGTGCAGT 6949             T
          G                     CACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||| |||
                                GTGACGTGAGGTCGGACCC CTG
                                      T
GAM97  CRTAP   3' GCCCAGGCTGGAGTGCAATG  22082   C
                                CA TGCACTCCAGCCTGGGT
                                || ||||||||||||||||
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                              GT ACGTGAGGTCGGACCCG
                               A
GAM97   CSNK2A2   5'  GTCACCCAGGCTGGAGTGCAGT 10320
            G                  CACTGCACTCCAGCCTGGGTGAC
                               ||||||||||||||||||||||
                               GTGACGTGAGGTCGGACCCACTG

GAM97   CST      5'  ATCCAGAGCTGGAGTGCAG   17964          _
                               CTGCACTCCAGC CTGGGT
                               |||||||||||| ||||||
                               GACGTGAGGTCG GACCTA
                                      A
GAM97   CTF1     3'  GTCGCCCAGGCTGGGGTGCAGT 9019
            G                  CACTGCACTCCAGCCTGGGTGAC
                               ||||||||||||||||||||||
                               GTGACGTGGGGTCGGACCCGCTG

GAM97   CTSB     5'  CTGGGCTGGTGTGCAGTG   65361       T    TG
                               CACTGCAC CCAGCC  G
                               |||||||| ||||||  |
                               GTGACGTG GGTCGG  C
                                    T    GT
GAM97   CXCL16   3'  GTCATCCAGGCTGGAGTGCAGT 42176
            G                  CACTGCACTCCAGCCTGGGTGAC
                               ||||||||||||||||||||||
                               GTGACGTGAGGTCGGACCTACTG

GAM97   CYP1A2   3'  CCAGGCTGGAGTGCAGTG    7505
                               CACTGCACTCCAGCCTGG
                               ||||||||||||||||||
                               GTGACGTGAGGTCGGACC

GAM97   CYP1A2   3'  GTCACCCAGGTTGGAGTGCAGT 7523
            G                  CACTGCACTCCAGCCTGGGTGAC
                               ||||||||||||||||||||||
                               GTGACGTGAGGTTGGACCCACTG

GAM97   CYP1A2   3'  GTCTCCTAAGCTGGAGTGCAGT 7525           C   T
            G                  CACTGCACTCCAGC TGGG GAC
                               |||||||||||||| |||| |||
                               GTGACGTGAGGTCG ATCC CTG
                                       A   T
GAM97   CYP2B6   3'  GTCACCCAGGTTCGAGTTCAGT 7564      C   C
            G                  CACTG ACTC AGCCTGGGTGAC
                               ||||| |||| ||||||||||||
                               GTGAC TGAG TTGGACCCACTG
                                  T   C
GAM97   CYP2B6   3'  GTCTCCCAGGCTGGAGTGCTAT 7565    CT          T
            G                  CA  GCACTCCAGCCTGGG GAC
                               ||  |||||||||||||| |||
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                                GT  CGTGAGGTCGGACCC CTG
                                 AT            T
GAM97   CYP2B6   3'  GTTGCCCAGGCTGGAGTGCAGT 7567                TG
           G                     CACTGCACTCCAGCCTGGG  AC
                                 ||||||||||||||||||  ||
                                 GTGACGTGAGGTCGGACCC  TG
                                       GT
GAM97   CYP4F3   3'  GCCCAGGCTGGAGTGCGGTG  8011
                                 CACTGCACTCCAGCCTGGGT
                                 ||||||||||||||||||||
                                 GTGGCGTGAGGTCGGACCCG

GAM97   CYP51    3'  GTTGCCCAGGCTGGAGTGCAGT 7620                TG
           G                     CACTGCACTCCAGCCTGGG  AC
                                 ||||||||||||||||||  ||
                                 GTGACGTGAGGTCGGACCC  TG
                                       GT
GAM97   CYP8B1   3'  GCCCAGGCTGCAGTGCAGTG  16539         C
                                 CACTGCACT CAGCCTGGGT
                                 |||||||| ||||||||||
                                 GTGACGTGA GTCGGACCCG
                                      C
GAM97   DFFB     3'  GCTCAGGCTGGAGTGCAGTG  88772
                                 CACTGCACTCCAGCCTGGGT
                                 ||||||||||||||||||||
                                 GTGACGTGAGGTCGGACTCG

GAM97   DFFB     3'  GTTGCCCAGGCTGGAGTGTAGT 88782                TG
           G                     CACTGCACTCCAGCCTGGG  AC
                                 ||||||||||||||||||  ||
                                 GTGATGTGAGGTCGGACCC  TG
                                       GT
GAM97   DHFR     3'  GTTGCCCAGGCTAGCATGCAAT 7655     C   CTCC      TG
           G                     CA TGCA   AGCCTGGG  AC
                                 || ||||   ||||||||  ||
                                 GT ACGT   TCGGACCC  TG
                                  A   ACGA      GT
GAM97   DIAPH2   3'  GTCACCCAGGCTGCAGTGTAGT 23011          C
           G                     CACTGCACT CAGCCTGGGTGAC
                                 |||||||| ||||||||||||
                                 GTGATGTGA GTCGGACCCACTG
                                      C
GAM97   DISC1    3'  GTCACCCAAGTTGGAGTGCAGT 38513             C
           G                     CACTGCACTCCAGC TGGGTGAC
                                 |||||||||||||| ||||||||
                                 GTGACGTGAGGTTG ACCCACTG
                                       A
GAM97   DNAH11   3'  GCCTCTGCTGGAGTGCAGTG  15024             CT
                                 CACTGCACTCCAGC  GGGT
                                 ||||||||||||||  ||||
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                                GTGACGTGAGGTCG  TCCG
                                        TC
GAM97   DSCR3    3'  GTCACCCAGGCTGGAGTG    21322
                                CACTCCAGCCTGGGTGAC
                                ||||||||||||||||||
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GAM97   DYRK1A   5'  CCCGGCTGAAGTGCAGTG    56075         C    T
                                CACTGCACT CAGCC GGG
                                ||||||||| ||||| |||
                                GTGACGTGA GTCGG CCC
                                      A    _
GAM97   EDG8     3'  GTCACCCAGGCTGGAGTGCAAT 79149    C
           G                     CA TGCACTCCAGCCTGGGTGAC
                                || ||||||||||||||||||||
                                GT ACGTGAGGTCGGACCCACTG
                                 A
GAM97   EHD2     3'  GTCGCCCAGGCTGGAGTGCAGT 28227
           G                     CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCGCTG

GAM97   EIF2S3   3'  GTCACCCAGGCTGGAGTGCAGT 9212
           G                     CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||||
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GAM97   ENDOGL1  3'  ATCCAGGCTGGAGTGCGGTG   18820
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                                ||||||||||||||||||||
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GAM97   EPB72    3'  GTTGCCCAGGCTGGAGTGCA   15880              TG
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                                ||||||||||||||||  ||
                                ACGTGAGGTCGGACCC  TG
                                        GT
GAM97   F2RL2    3'  TCACCCAGACTGGCGTGCAGTG 15901         T   C
                                CACTGCAC CCAG CTGGGTGA
                                |||||||| |||| ||||||||
                                GTGACGTG GGTC GACCCACT
                                     C    A
GAM97   F2RL3    3'  GTTGCCCAGGCTGGAGTGCAGT 15525                TG
           G                     CACTGCACTCCAGCCTGGG  AC
                                ||||||||||||||||||  ||
                                GTGACGTGAGGTCGGACCC  TG
                                        GT
GAM97   F3       3'  GTTGCCCAGGCTGGAGTGCAGT 67680               TG
                                ACTGCACTCCAGCCTGGG  AC
                                ||||||||||||||||||  ||
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                                TGACGTGAGGTCGGACCC  TG
                                           GT
GAM97   FABP2    3' ACTCAGGCTGGAATGTAGTG  5531        C
                                CACTGCA TCCAGCCTGGGT
                                ||||||| ||||||||||||
                                GTGATGT AGGTCGGACTCA
                                   A
GAM97   FANCC    3' GCCTGGCTGGGTGCAGTG   71045       T    T
                                CACTGCAC CCAGCC GGGT
                                |||||||| |||||| ||||
                                GTGACGTG GGTCGG TCCG
                                   _    _
GAM97   FANCE    3' GTCATCCAGGCTGGAGTGCAGT 41901
           G                     CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
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GAM97   FANCF    3' GTCACCCAGTCTGGAGTGCAGT 42985          C
           G                     CACTGCACTCCAG CTGGGTGAC
                                 |||||||||||| |||||||||
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                                        T
GAM97   FCAR     3' GTCACCCAGGCTGAAGTGCAGT 56579        C
           G                     CACTGCACT CAGCCTGGGTGAC
                                 ||||||||| ||||||||||||
                                 GTGACGTGA GTCGGACCCACTG
                                    A
GAM97   FCAR     3' GTCACCCAGGCTGAAGTGCAGT 56595        C
           G                     CACTGCACT CAGCCTGGGTGAC
                                 ||||||||| ||||||||||||
                                 GTGACGTGA GTCGGACCCACTG
                                    A
GAM97   FCAR     3' GTCACCCAGGCTGAAGTGCAGT 56607        C
           G                     CACTGCACT CAGCCTGGGTGAC
                                 ||||||||| ||||||||||||
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                                    A
GAM97   FCAR     3' GTCACCCAGGCTGAAGTGCAGT 56619        C
           G                     CACTGCACT CAGCCTGGGTGAC
                                 ||||||||| ||||||||||||
                                 GTGACGTGA GTCGGACCCACTG
                                    A
GAM97   FCAR     3' GCCAAGGCTGGAGTGCAGTG  56636          G
                                CACTGCACTCCAGCCT GGT
                                |||||||||||||||| |||
                                GTGACGTGAGGTCGGA CCG
                                      A
GAM97   FCAR     3' GCCAAGGCTGGAGTGCAGTG  56647          G
                                CACTGCACTCCAGCCT GGT
                                |||||||||||||||| |||
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                                GTGACGTGAGGTCGGA CCG
                                        A
GAM97   FCAR     3'  GTCACCCAGGCTGGAGTGCAGT 10591
                G                CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCACTG

GAM97   FCGR2A   3'  GTTACCCAGGCTGGAGTGCAGT 80030
                G                CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCATTG

GAM97   FCRH1    3'  GTCACTCAATCTGGAATGCAGT 54729       C    CC
                G                CACTGCA TCCAG  TGGGTGAC
                                 ||||||| |||||  ||||||||
                                 GTGACGT AGGTC  ACTCACTG
                                     A    TA
GAM97   FEZ1     3'  TCGCCCAGGCTGGAGTGCAATG 42873    C
                                 CA TGCACTCCAGCCTGGGTGA
                                 || ||||||||||||||||||
                                 GT ACGTGAGGTCGGACCCGCT
                                  A
GAM97   FGF2     3'  ATCTAGGCCGGGTGCAGTG   10611       T  A
                                 CACTGCAC CC GCCTGGGT
                                 |||||||| || ||||||||
                                 GTGACGTG GG CGGATCTA
                                      _ C
GAM97   FGF5     3'  GTCACCAGGCTGGAGTGCAGTG 16763              G
                                 CACTGCACTCCAGCCTGG TGAC
                                 |||||||||||||||||| ||||
                                 GTGACGTGAGGTCGGACC ACTG
                                                _
GAM97   FGF5     3'  GTCACCAGGCTGGAGTGCAGTG 53667              G
                                 CACTGCACTCCAGCCTGG TGAC
                                 |||||||||||||||||| ||||
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                                                _
GAM97   FHL2     5'  GTCGCCCAGGCTGGAGTGCAGT 9369
                G                CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
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GAM97   FSHPRH1  5'  GTCACCCAGGCTGGAGTGCAGT 23068
                G                CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCACTG

GAM97   FUT1     3'  GCCCAGGCCAGAGTGCAGTG  5598          CA
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                                 |||||||||  ||||||||
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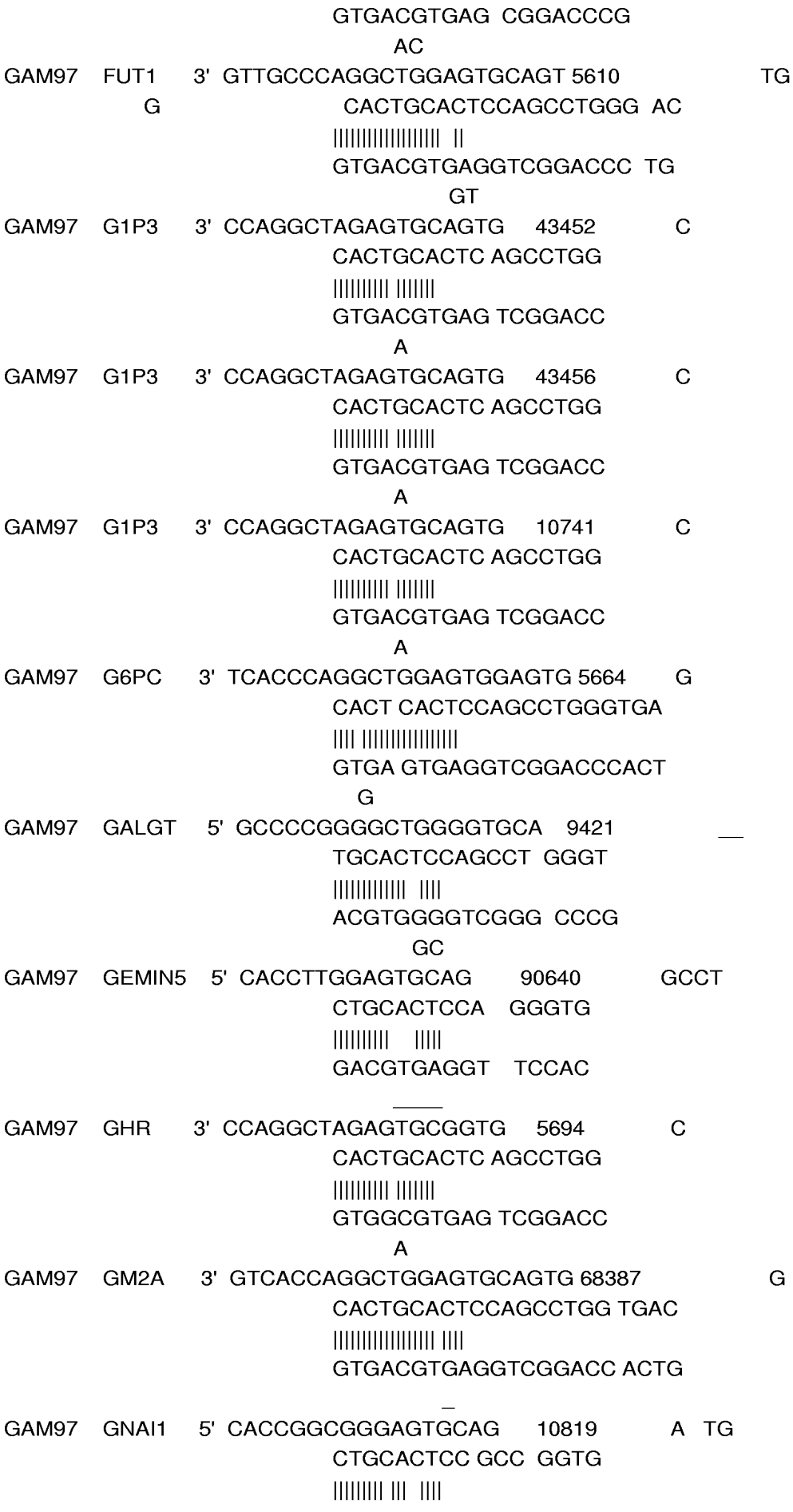
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GTGACGTGAG TCGGACC
A
GAM97 G1P3 3' CCAGGCTAGAGTGCAGTG 10741 C
CACTGCACTC AGCCTGG
GTGACGTGAG TCGGACC
A
GAM97 G6PC 3' TCACCCAGGCTGGAGTGGAGTG 5664 G
CACT CACTCCAGCCTGGGTGA
GTGA GTGAGGTCGGACCCACT
G
GAM97 GALGT 5' GCCCCGGGGCTGGGGTGCA 9421 __
TGCACTCCAGCCT GGGT
ACGTGGGGTCGGG CCCG
GC
GAM97 GEMIN5 5' CACCTTGGAGTGCAG 90640 GCCT
CTGCACTCCA GGGTG
GACGTGAGGT TCCAC
____
GAM97 GHR 3' CCAGGCTAGAGTGCGGTG 5694 C
CACTGCACTC AGCCTGG
GTGGCGTGAG TCGGACC
A
GAM97 GM2A 3' GTCACCAGGCTGGAGTGCAGTG 68387 G
CACTGCACTCCAGCCTGG TGAC
GTGACGTGAGGTCGGACC ACTG
_
GAM97 GNAI1 5' CACCGGCGGGAGTGCAG 10819 A TG
CTGCACTCC GCC GGTG

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                                GACGTGAGG CGG  CCAC
                                     G  __
GAM97   GNE     3'  CCCAGGCTGGAGTGCAGTG   19664
                                CACTGCACTCCAGCCTGGG
                                ||||||||||||||||||
                                GTGACGTGAGGTCGGACCC

GAM97   GNS     3'  GTCACCCAAGCTCTGTTCA   10844    C  TCC   C
                                TG AC   AGC TGGGTGAC
                                || ||   ||| ||||||||
                                AC TG   TCG ACCCACTG
                                 T  TC_   A
GAM97   GP6     3'  CACTGGGCCAAGTGCAGTG   33470         CCA   TG G
                                CACTGCACT   GCC  G TG
                                |||||||||   |||  | ||
                                GTGACGTGA   CGG  C AC
                                     AC_   GT _
GAM97   GPR4    3'  GCCCAGGCTGGAGTGCAGT   60579
                                ACTGCACTCCAGCCTGGGT
                                ||||||||||||||||||
                                TGACGTGAGGTCGGACCCG

GAM97   GPR4    3'  GTTGCCCAGGCTGGAGTGCAGT 60581              TG
                                ACTGCACTCCAGCCTGGG  AC
                                ||||||||||||||||  ||
                                TGACGTGAGGTCGGACCC  TG
                                       GT
GAM97   GPR56   5'  GTCACACAGGCTGGAGTGCAGT 20277              G
           G                    CACTGCACTCCAGCCTG GTGAC
                                |||||||||||||||| |||||
                                GTGACGTGAGGTCGGAC CACTG
                                       A
GAM97   GPR81   3'  CCCAGGCTGGAGTGCAGTG   51742
                                CACTGCACTCCAGCCTGGG
                                ||||||||||||||||||
                                GTGACGTGAGGTCGGACCC

GAM97   GRAF    3'  CCATGGCCGGGTGCAGTG    31226         T  A  _
                                CACTGCAC CC GCC TGG
                                |||||||| || ||| |||
                                GTGACGTG GG CGG ACC
                                     _  C   T
GAM97   GRAF    3'  GTGGCCCAGGCTGGAGTGCAGT 31243               G
           G                    CACTGCACTCCAGCCTGGGT AC
                                |||||||||||||||||||| ||
                                GTGACGTGAGGTCGGACCCG TG
                                       G
GAM97   GRINL1A 3'  GTCGCCCAGGCTGGAGTGCAGT 70066
           G                    CACTGCACTCCAGCCTGGGTGAC
                                |||||||||||||||||||||||
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                                GTGACGTGAGGTCGGACCCGCTG

GAM97   GRM6     3'  TTTCTTAGGCTGGAGTGCAGTG 7777                T
                                CACTGCACTCCAGCCTGGG GA
                                |||||||||||||||||| ||
                                GTGACGTGAGGTCGGATTC TT
                                      T
GAM97   HCS      3'  GCCAAGGCTGGAGTGCAGTG  38982             G
                                CACTGCACTCCAGCCT GGT
                                |||||||||||||||| |||
                                GTGACGTGAGGTCGGA CCG
                                      A
GAM97   HCS      3'  GCCCAGGCTGAGTACAGTG   38983      C   C
                                CACTG ACTC AGCCTGGGT
                                ||||| |||| |||||||||
                                GTGAC TGAG TCGGACCCG
                                   A  _
GAM97   HCS      3'  GTTGCCCAGGCTGGAGTGCAAT 38990    C           TG
          G                      CA TGCACTCCAGCCTGGG  AC
                                || ||||||||||||||||  ||
                                GT ACGTGAGGTCGGACCC  TG
                                 A            GT
GAM97   HEXA     3'  CCAGGCTGGAGTCAGTG     6717       C
                                CACTG ACTCCAGCCTGG
                                ||||| ||||||||||||
                                GTGAC TGAGGTCGGACC
                                     _
GAM97   HLCS     5'  CCAGGCTGGAGTGCAGTG    6408
                                CACTGCACTCCAGCCTGG
                                ||||||||||||||||||
                                GTGACGTGAGGTCGGACC

GAM97   HLCS     5'  GTCGTCCAGGCTGGAGTGCAGT 6416               GT
          G                      CACTGCACTCCAGCCTGG  GAC
                                ||||||||||||||||||  |||
                                GTGACGTGAGGTCGGACC  CTG
                                      TG
GAM97   HMG20A   3'  GCCCAGGCTGGAGTGCGGTG  37069
                                CACTGCACTCCAGCCTGGGT
                                ||||||||||||||||||||
                                GTGGCGTGAGGTCGGACCCG

GAM97   HTR1D    3'  CCAGGCTGGAGTGTAGTG    7841
                                CACTGCACTCCAGCCTGG
                                ||||||||||||||||||
                                GTGATGTGAGGTCGGACC

GAM97   HTR1E    5'  GTCGCCCAGGCTGGAGTGCAG  7865
                                CTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||
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                                GACGTGAGGTCGGACCCGCTG

GAM97   HUNK     3'  GTCACCCAGGCTGGAGTGCAGT 28189
                G                CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCACTG

GAM97   HUS1     3'  GTCACCCAGACTGGAGTGCAGT 92741           C
                G                CACTGCACTCCAG CTGGGTGAC
                                 |||||||||||| ||||||||
                                 GTGACGTGAGGTC GACCCACTG
                                        A
GAM97   HYAL4    5'  GTTGCCCAGGCTGGAGTGTAGT 25370              TG
                G                CACTGCACTCCAGCCTGGG  AC
                                 |||||||||||||||||  ||
                                 GTGATGTGAGGTCGGACCC  TG
                                       GT
GAM97   ICAM1    3'  GTCACCCAGGCTGGAGTGCAGT 72040
                G                CACTGCACTCCAGCCTGGGTGAC
                                 |||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCACTG

GAM97   IFNAR2   3'  GTCGCCCAAGCTGGAGCGCAAT 7904    C  A     C
                G                CA TGC CTCCAGC TGGGTGAC
                                 || ||| ||||||| ||||||||
                                 GT ACG GAGGTCG ACCCGCTG
                                  A  C     A
GAM97   IGF1     3'  GTCCCCCAGGCTGGAGTGCAGT 7079              T
                G                CACTGCACTCCAGCCTGGG GAC
                                 |||||||||||||||||| |||
                                 GTGACGTGAGGTCGGACCC CTG
                                       C
GAM97   IGLL1    5'  GCCACATGGACTGGGGTGCAAT 39639    C       _ _ _
                G                CA TGCACTCCAG CC TG GGT
                                 || |||||||||| || || |||
                                 GT ACGTGGGGTC GG AC CCG
                                  A        A T A
GAM97   IHPK2    3'  GCCTGGAGCTGATGTGCAGTG  62517        TC   _ TG
                                 CACTGCAC  CAGC C  GGT
                                 ||||||||  |||| |  |||
                                 GTGACGTG  GTCG G  CCG
                                     TA    A GT
GAM97   IL11     3'  GCCTAGGCTGGAGTGCAGTG  7187
                                 CACTGCACTCCAGCCTGGGT
                                 ||||||||||||||||||||
                                 GTGACGTGAGGTCGGATCCG

GAM97   INMT     3'  GTCACCCAGGCTAGAGTGCAAT 23222    C     C
                G                CA TGCACTC AGCCTGGGTGAC
                                 || ||||||| ||||||||||||
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                                GT ACGTGAG TCGGACCCACTG
                                 A      A
GAM97   INMT    3'  GTCGCCCAGGCTGGAGTGCAGT 23224
                G                CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCGCTG

GAM97   ITGAM   3'  GTCACCCAGGCTGGAGTGCAAT 72314    C
                G                CA TGCACTCCAGCCTGGGTGAC
                                 || ||||||||||||||||||
                                 GT ACGTGAGGTCGGACCCACTG
                                  A
GAM97   JAK3    3'  ACCCAGGGTGGAGTGCAGTG  5820           G
                                 CACTGCACTCCA CCTGGGT
                                 |||||||||||| |||||||
                                 GTGACGTGAGGT GGACCCA
                                        G
GAM97   JRK     3'  CCAGGCTGGAGTGAAGTG   87820     G
                                 CACT CACTCCAGCCTGG
                                 |||| ||||||||||||
                                 GTGA GTGAGGTCGGACC
                                   A
GAM97   JRK     3'  TCTTCAAGCTGGGTGCAGTG  87837       T   C   T
                                 CACTGCAC CCAGC TGGG GA
                                 |||||||| ||||| |||| ||
                                 GTGACGTG GGTCG ACTT CT
                                      _    A   _
GAM97   KLRD1   3'  TGCCCAGGCTGGAGCATAGTG  24711     CA
                                 CACTG  CTCCAGCCTGGGTG
                                 |||||  ||||||||||||||
                                 GTGAT  GAGGTCGGACCCGT
                                    AC
GAM97   KLRD1   3'  TGCCCAGGCTGGAGCATAGTG  11216     CA
                                 CACTG  CTCCAGCCTGGGTG
                                 |||||  ||||||||||||||
                                 GTGAT  GAGGTCGGACCCGT
                                    AC
GAM97   KMO     3'  CCAGGCTGGAGTGCAGTG    14839
                                 CACTGCACTCCAGCCTGG
                                 ||||||||||||||||||
                                 GTGACGTGAGGTCGGACC

GAM97   LAMC1   3'  GTCTTTAGGGCTGGAAGGCAG  11269     AC      GGGT
                                 CTGC  TCCAGCCT   GAC
                                 ||||  ||||||||   |||
                                 GACG  AGGTCGGG   CTG
                                   GA       ATTT
GAM97   LGR6    5'  ACTCTGGCCGCAGTGCAGTG  85353        CCA   T
                                 CACTGCACT   GCC GGGT
                                 |||||||||   ||| ||||
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                                GTGACGTGA  CGG CTCA
                                     CGC  T
GAM97   LILRA3   3'  GTCACCAGGCTGGAATGCAGTG 97020       C       G
                                CACTGCA TCCAGCCTGG TGAC
                                ||||||| |||||||||| ||||
                                GTGACGT AGGTCGGACC ACTG
                                   A       _
GAM97   LLGL1    3'  GTCGCCCAGGCTGGAGTGCAGT 67420
           G                     CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCGCTG

GAM97   LNK      3'  CCGGGCTGGAGTGCAGTG    19639
                                 CACTGCACTCCAGCCTGG
                                 ||||||||||||||||||
                                 GTGACGTGAGGTCGGGCC

GAM97   LTB4R    5'  GTCATTCAGGCTGGAGTGCAGT 7471
           G                     CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACTTACTG

GAM97   LYZ      3'  GTCGCCCAGGCTGGAGTGCAGT 5901
           G                     CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCGCTG

GAM97   LZTS1    3'  GTCCCCCAGGCTGGAGTGCAGT 41038              T
           G                     CACTGCACTCCAGCCTGGG GAC
                                 |||||||||||||||||| |||
                                 GTGACGTGAGGTCGGACCC CTG
                                              C
GAM97   MAK      3'  CCAGGCTGGAGTGCAGTG    20942
                                 CACTGCACTCCAGCCTGG
                                 ||||||||||||||||||
                                 GTGACGTGAGGTCGGACC

GAM97   MDM2     3'  GTTACCCAGGCTGGAGTGCAGT 23461
           G                     CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCATTG

GAM97   MDM2     3'  GTTACCCAGGCTGGAGTGCAGT 23474
           G                     CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCATTG

GAM97   MDM2     3'  GTTACCCAGGCTGGAGTGCAGT 23487
           G                     CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
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                                GTGACGTGAGGTCGGACCCATTG

GAM97   MDM2    3'  GTTACCCAGGCTGGAGTGCAGT 23500
            G                    CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCATTG

GAM97   MDM2    3'  GTTACCCAGGCTGGAGTGCAGT 11499
            G                    CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCATTG

GAM97   MDM4    3'  GTCTCCCAGGCTGAAGTGCAGT 11512        C       T
            G                    CACTGCACT CAGCCTGGG GAC
                                 ||||||||| ||||||||| |||
                                 GTGACGTGA GTCGGACCC CTG
                                       A        T
GAM97   MECP2   3'  CATTGCATGCCGGGTGCAG   18391       T  A  C  _
                                 CTGCAC CC GC TG GGTG
                                 |||||| || || || ||||
                                 GACGTG GG CG AC TTAC
                                    _  C  T  G
GAM97   MEF2A   5'  CCCAGGCTGAAGTGCAGTG   19996         C
                                 CACTGCACT CAGCCTGGG
                                 ||||||||| |||||||||
                                 GTGACGTGA GTCGGACCC
                                       A
GAM97   MEFV    3'  GTCACCCAGGCTGGAGTGCAGT 5945
            G                    CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCACTG

GAM97   MEFV    3'  GTGGCCCAGGCTGGAGTGCAGT 5947                  G
            G                    CACTGCACTCCAGCCTGGGT AC
                                 |||||||||||||||||| ||
                                 GTGACGTGAGGTCGGACCCG TG
                                              G
GAM97   MHC2TA  3'  GCCCACGCTGGAGTGCAGTG  5988             C
                                 CACTGCACTCCAGC TGGGT
                                 |||||||||||||| |||||
                                 GTGACGTGAGGTCG ACCCG
                                        C
GAM97   MHC2TA  3'  GTTGCCCAGGCTGGCGTGCAGT 5993         T       TG
            G                    CACTGCAC CCAGCCTGGG  AC
                                 |||||||| ||||||||||  ||
                                 GTGACGTG GGTCGGACCC  TG
                                      C         GT
GAM97   MICB    3'  GTCACCCAGGCTGCAGTTCACT 21024    C  C   C
            G                    CA TG ACT CAGCCTGGGTGAC
                                 || || ||| ||||||||||||
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                                GT AC TGA GTCGGACCCACTG
                                 C T   C
GAM97   MLANA    3'  GTTGCCCAGGCTGGAGTGCAAT 19768    C            TG
            G                    CA TGCACTCCAGCCTGGG  AC
                                 || ||||||||||||||||  ||
                                 GT ACGTGAGGTCGGACCC  TG
                                  A             GT
GAM97   MPL      3'  CCAGACTGGAGTGCAGTG    19344           C
                                 CACTGCACTCCAG CTGG
                                 |||||||||||||| ||||
                                 GTGACGTGAGGTC GACC
                                        A
GAM97   MPL      3'  GTCACCCAGGCTGCAGTGCAAT 19359    C     C
            G                    CA TGCACT CAGCCTGGGTGAC
                                 || |||||| ||||||||||||
                                 GT ACGTGA GTCGGACCCACTG
                                  A     C
GAM97   MRPL49   3'  GCCCAGGGTGGAGTGCAGTG   70170          G
                                 CACTGCACTCCA CCTGGGT
                                 ||||||||||||| |||||||
                                 GTGACGTGAGGT GGACCCG
                                        G
GAM97   MTR      3'  GCCCAGGCTGGAGTGCAG    6020
                                 CTGCACTCCAGCCTGGGT
                                 ||||||||||||||||||
                                 GACGTGAGGTCGGACCCG

GAM97   MUCDHL   3'  GCTTGGGTTGGAGCGCAG    35276      A       TG
                                 CTGC CTCCAGCC  GGT
                                 |||| ||||||||  |||
                                 GACG GAGGTTGG  TCG
                                   C       GT
GAM97   NCOA6    5'  GTCACCGAGGCTGGAGTGCAGT 26844              G
            G                    CACTGCACTCCAGCCT GGTGAC
                                 |||||||||||||||| ||||||
                                 GTGACGTGAGGTCGGA CCACTG
                                        G
GAM97   NCOA6    5'  GTCGCCCAGGCTGGAGTGCAGT 26845
                                 ACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 TGACGTGAGGTCGGACCCGCTG

GAM97   NCOA6IP  3'  CGCCCAGGCTGGAGTGCAGTG  46153
                                 CACTGCACTCCAGCCTGGGTG
                                 |||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCGC

GAM97   NDRG3    3'  GTTACCCAGGCTGGAGTGCAAT 50124    C
            G                    CA TGCACTCCAGCCTGGGTGAC
                                 || ||||||||||||||||||
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                                GT ACGTGAGGTCGGACCCATTG
                                 A
GAM97   NEU3    5'  GTCACCCAGGCTGGAGTGCAGT 22832
                G                CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCACTG

GAM97   NEURL   3'  GTCACCCAGAGCCATAGAGCA  16134     A  CCA  _
                                 TGC CT   GC CTGGGTGAC
                                 ||| ||   || |||||||||
                                 ACG GA   CG GACCCACTG
                                  A  TAC  A
GAM97   NONO    3'  GTCGCCCAGGCTGGAGTGTAGT 82891
                G                CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGATGTGAGGTCGGACCCGCTG

GAM97   NPR2L   3'  GTTACCCAGGCTGGAATACAGT 22597       CAC
                G                CACTG   TCCAGCCTGGGTGAC
                                 |||||   ||||||||||||||
                                 GTGAC   AGGTCGGACCCATTG
                                   ATA
GAM97   NQO1    3'  GTTACCCAGGCTGGAGTGCAGT 8053
                G                CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCATTG

GAM97   NT5C2   5'  TGCCCAGGCTGGAGTACAGTG  25272      C
                                 CACTG ACTCCAGCCTGGGTG
                                 ||||| ||||||||||||||
                                 GTGAC TGAGGTCGGACCCGT
                                   A
GAM97   ORC1L   3'  GTCGCCCAGGCTGGAGTGCAGT 15986
                G                CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCGCTG

GAM97   P2RY6   3'  CAGGGGGCGAAGTGCAGTG   15993         ___  AG
                                 CACTGCACT   CC  CCTG
                                 |||||||||   ||  ||||
                                 GTGACGTGA   GG  GGAC
                                      AGC  G_
GAM97   PAICS   3'  GTCGCCCAGGCTGGAGTGCAGT 22266
                G                CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCGCTG

GAM97   PART1   3'  GTCACCCAAATAGCTGAGTGCA 33902         C   C___
                GT                ACTGCACTC AGC    TGGGTGAC
                                 ||||||||| |||    ||||||||
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                                TGACGTGAG TCG    ACCCACTG
                                      _  ATAA
GAM97   PCDHA9   3'  CACCCAGGCTGGAGTACAGTG  26614      C
                                CACTG ACTCCAGCCTGGGTG
                                ||||| ||||||||||||||
                                GTGAC TGAGGTCGGACCCAC
                                   A
GAM97   PCDHA9   3'  GTTGCCCAGGCTGGAGTGCAGT 26624               TG
           G                     CACTGCACTCCAGCCTGGG  AC
                                ||||||||||||||||||  ||
                                GTGACGTGAGGTCGGACCC  TG
                                            GT
GAM97   PCDHB11  3'  GCCCTGGCTGGAGTGCAATG  38925    C         T
                                CA TGCACTCCAGCC GGGT
                                || |||||||||||| ||||
                                GT ACGTGAGGTCGG CCCG
                                 A          T
GAM97   PCDHB11  3'  GTCACCCAGACTAGAGGTCAGT 38929      CA   C  C
           G                     CACTG  CTC AG CTGGGTGAC
                                |||||  ||| || |||||||||
                                GTGAC  GAG TC GACCCACTG
                                   TG   A  A
GAM97   PCDHB16  3'  GTCACCCAGGCTGGAGTGCAGT 40908
           G                     CACTGCACTCCAGCCTGGGTGAC
                                |||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCACTG

GAM97   PCDHB9   3'  GTCGCCCAGGCTGGAGTGCAGT 39449
           G                     CACTGCACTCCAGCCTGGGTGAC
                                |||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCGCTG

GAM97   PDCL     3'  GTCACCCAGGCTGGAGTACA   19400    C
                                TG ACTCCAGCCTGGGTGAC
                                || ||||||||||||||||
                                AC TGAGGTCGGACCCACTG
                                 A
GAM97   PDE6B    3'  GTCACCCAGGCTGGAGTGCCGT 6078      T
           G                     CAC GCACTCCAGCCTGGGTGAC
                                ||| ||||||||||||||||||
                                GTG CGTGAGGTCGGACCCACTG
                                  C
GAM97   PDZK1    5'  GTTGCCCAGGCTGGAGTGCAGT 12034               TG
           G                     CACTGCACTCCAGCCTGGG  AC
                                ||||||||||||||||||  ||
                                GTGACGTGAGGTCGGACCC  TG
                                            GT
GAM97   PER2     3'  GCCCAGGCTGGAGTGCAGTG  43353
                                CACTGCACTCCAGCCTGGGT
                                ||||||||||||||||||||
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                                GTGACGTGAGGTCGGACCCG

GAM97   PIGR     3'  GTCACCCAGACTGGAATGCAGT 73007        C    C
                G                CACTGCA TCCAG CTGGGTGAC
                                 ||||||| ||||| |||||||||
                                 GTGACGT AGGTC GACCCACTG
                                    A    A
GAM97   PIGR     3'  GTCGCCCAGGCTGGAGTGCAGT 73008
                G                CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCGCTG

GAM97   PIK3C2B  3'  GTCGCCAGGCTGGAGTGTAGTG 12109              G
                                 CACTGCACTCCAGCCTGG TGAC
                                 |||||||||||||||| ||||
                                 GTGATGTGAGGTCGGACC GCTG
                                                  _
GAM97   PIK3CD   3'  GTTGCCCAGGCTGGAGTGCAGT 18498              TG
                G                CACTGCACTCCAGCCTGGG  AC
                                 |||||||||||||||||  ||
                                 GTGACGTGAGGTCGGACCC  TG
                                           GT
GAM97   PKNOX1   3'  GTTGCCCAGGCTGGAGGGCAAT 17101    C  A       TG
                G                CA TGC CTCCAGCCTGGG  AC
                                 || ||| ||||||||||||  ||
                                 GT ACG GAGGTCGGACCC  TG
                                  A  G          GT
GAM97   PMCHL1   3'  GTTGCCCAGGCTGGAGTGCAAT 49920    C          TG
                G                CA TGCACTCCAGCCTGGG  AC
                                 || ||||||||||||||||  ||
                                 GT ACGTGAGGTCGGACCC  TG
                                  A            GT
GAM97   PON1     3'  GTTGCCCAGGCTGGAGTGCAGT 6539               TG
                G                CACTGCACTCCAGCCTGGG  AC
                                 |||||||||||||||||  ||
                                 GTGACGTGAGGTCGGACCC  TG
                                           GT
GAM97   POU2AF1  3'  TTGCCCAGGCTGGAGTACAATG 21754    C  C       TG
                                 CA TG ACTCCAGCCTGGG  A
                                 || || ||||||||||||  |
                                 GT AC TGAGGTCGGACCC  T
                                  A  A          GT
GAM97   PPEF2    3'  GTTGCCCAGGCTGGAGTGCATT 21778    C          TG
                G                CA TGCACTCCAGCCTGGG  AC
                                 || ||||||||||||||||  ||
                                 GT ACGTGAGGTCGGACCC  TG
                                  T            GT
GAM97   PPID     3'  GTCACCCAGGCTGGAGTGCGGT 88827
                G                CACTGCACTCCAGCCTGGGTGAC
                                 |||||||||||||||||||||||
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                                GTGGCGTGAGGTCGGACCCACTG

GAM97   PPP1R12B 3'  GCCCAGGCTGGAGTGCAGTG   50391
                                CACTGCACTCCAGCCTGGGT
                                ||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCG

GAM97   PPP1R2   3'  CTGAACTGTGAGTGCAGT    21783        _  CC
                                ACTGCACTC CAG  TGG
                                ||||||||| |||  |||
                                TGACGTGAG GTC  GTC
                                      T  AA
GAM97   PRKR     3'  GTTGCCCAGGCTGGAGTGCAAT 12352    C           TG
           G                     CA TGCACTCCAGCCTGGG  AC
                                || ||||||||||||||  ||
                                GT ACGTGAGGTCGGACCC  TG
                                 A            GT
GAM97   PRKWNK3  3'  GTCACCCAGGTTGGAGTGCAGT 62237
           G                     CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||||
                                GTGACGTGAGGTTGGACCCACTG

GAM97   PRKY    3'  ATCTAGGCTAGGTGCAGTG   12362        CC
                                CACTGCACT  AGCCTGGGT
                                |||||||||  |||||||||
                                GTGACGTGG  TCGGATCTA
                                      A_
GAM97   PSMB2    3'  GCCCAGGCTGGAGTGCTGTG   12474     T
                                CAC GCACTCCAGCCTGGGT
                                ||| ||||||||||||||||
                                GTG CGTGAGGTCGGACCCG
                                  T
GAM97   PSMD9    3'  GTCACCCAGGCTGGAGTGCAGT 12528
           G                     CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCACTG

GAM97   PTGES    3'  GTTGCCCAAGCTGGAGTGAAGT 18071      G       C    TG
           G                     CACT CACTCCAGC TGGG  AC
                                |||| ||||||||| ||||  ||
                                GTGA GTGAGGTCG ACCC  TG
                                   A        A    GT
GAM97   PTGIS    3'  TGCCCAGGCTAGAGTGCAGTG  8232          C
                                CACTGCACTC AGCCTGGGTG
                                |||||||||| ||||||||||
                                GTGACGTGAG TCGGACCCGT
                                      A
GAM97   PTGIS    3'  TTGCCCAGGCTGGAGTGCAATG 8237     C           TG
                                CA TGCACTCCAGCCTGGG  A
                                || ||||||||||||||||  |
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                                GT ACGTGAGGTCGGACCC  T
                                 A             GT
GAM97   RAB36    3'  GTCACCCAGGCTGGAGTGCAAT 18177    C
                  G              CA TGCACTCCAGCCTGGGTGAC
                                 || ||||||||||||||||||||
                                GT ACGTGAGGTCGGACCCACTG
                                 A
GAM97   RAB36    3'  GTTGCCCAGGCTGGAGTGCAAT 18179    C            TG
                  G              CA TGCACTCCAGCCTGGG  AC
                                 || ||||||||||||||||  ||
                                GT ACGTGAGGTCGGACCC  TG
                                 A             GT
GAM97   RABL2A   3'  GTCGCCAGGCTGGAGTGCAGTG 26413              G
                                CACTGCACTCCAGCCTGG TGAC
                                |||||||||||||||||| ||||
                                GTGACGTGAGGTCGGACC GCTG
                                          _
GAM97   RABL2B   3'  GTCGCCAGGCTGGAGTGCAGTG 23984              G
                                CACTGCACTCCAGCCTGG TGAC
                                |||||||||||||||||| ||||
                                GTGACGTGAGGTCGGACC GCTG
                                          _
GAM97   RAI3     3'  GTCACCCAGGCTTGAGTGCAGT 15621          C
                  G              CACTGCACTC AGCCTGGGTGAC
                                 |||||||||| ||||||||||||
                                GTGACGTGAG TCGGACCCACTG
                                       T
GAM97   RBM10    5'  TCACCCAGGCTGGCAG     20248     ACTC
                                CTGC   CAGCCTGGGTGA
                                ||||   ||||||||||||
                                GACG   GTCGGACCCACT
                                  ____
GAM97   RET      3'  TCACTTATGAAGTCAGTG    40550      C   C  GCC
                                CACTG ACT CA   TGGGTGA
                                ||||| ||| ||   |||||||
                                GTGAC TGA GT   ATTCACT
                                   _  A  ___
GAM97   RHD      3'  GTCACCAGGCTGGAGTGCAGTG 32834              G
                                CACTGCACTCCAGCCTGG TGAC
                                |||||||||||||||||| ||||
                                GTGACGTGAGGTCGGACC ACTG
                                          _
GAM97   RHD      3'  GTCACCCAGGCTAGAGTGCAAT 32835    C      C
                  G              CA TGCACTC AGCCTGGGTGAC
                                 || ||||||| ||||||||||||
                                GT ACGTGAG TCGGACCCACTG
                                 A      A
GAM97   RHD      3'  GTCACCAGGCTGGAGTGCAGTG 33146              G
                                CACTGCACTCCAGCCTGG TGAC
                                |||||||||||||||||| ||||
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                                GTGACGTGAGGTCGGACC ACTG
                                                   _
GAM97   RHD     3'  GTCACCCAGGCTAGAGTGCAAT 33147    C     C
            G                    CA TGCACTC AGCCTGGGTGAC
                                 || ||||||| ||||||||||||
                                 GT ACGTGAG TCGGACCCACTG
                                  A      A
GAM97   RP2     3'  GTTGCCCAAGCTGGAGTGCAAT 23605    C        C   TG
            G                    CA TGCACTCCAGC TGGG  AC
                                 || |||||||||| ||||  ||
                                 GT ACGTGAGGTCG ACCC  TG
                                  A         A   GT
GAM97   RPH3AL  3'  GTTGCCCAGGCTGGGGTGCAGT 23740              TG
            G                    CACTGCACTCCAGCCTGGG  AC
                                 ||||||||||||||||||  ||
                                 GTGACGTGGGGTCGGACCC  TG
                                           GT
GAM97   RPP30   3'  GCTCAGGCTGGAGTACAGTG   22200      C
                                 CACTG ACTCCAGCCTGGGT
                                 ||||| ||||||||||||||
                                 GTGAC TGAGGTCGGACTCG
                                   A
GAM97   RPP30   3'  GTCCCCCAGGCTGGAGTGCAGT 22206              T
            G                    CACTGCACTCCAGCCTGGG GAC
                                 |||||||||||||||||| |||
                                 GTGACGTGAGGTCGGACCC CTG
                                           C
GAM97   SAS     3'  GTTGCCCAGGCTGGAGTGCAAT 21106    C          TG
            G                    CA TGCACTCCAGCCTGGG  AC
                                 || ||||||||||||||  ||
                                 GT ACGTGAGGTCGGACCC  TG
                                  A            GT
GAM97   SCML2   3'  TGCCCAGGCTGGAGTGCA    21432
                                 TGCACTCCAGCCTGGGTG
                                 ||||||||||||||||||
                                 ACGTGAGGTCGGACCCGT

GAM97   SEDL    3'  CCAGGCTGGAGTGCAATG    28083    C
                                 CA TGCACTCCAGCCTGG
                                 || ||||||||||||||
                                 GT ACGTGAGGTCGGACC
                                  A
GAM97   SEDL    3'  CCAGGCTGGAGTGCAGTG    28085
                                 CACTGCACTCCAGCCTGG
                                 ||||||||||||||||||
                                 GTGACGTGAGGTCGGACC

GAM97   SEPN1   3'  GTCACCCAGGCTGGAGTGCTAT 66979    CT
            G                    CA  GCACTCCAGCCTGGGTGAC
                                 ||  ||||||||||||||||||
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                                GT  CGTGAGGTCGGACCCACTG
                                 AT
GAM97   SERPINB9  3'  GTCACCCAGGCTGGAGTGTAGT 16028
            G                    CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGATGTGAGGTCGGACCCACTG

GAM97   SERPINB9  3'  GTCGCCCAGGCTGGAGTGCAGT 16030
            G                    CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCGCTG

GAM97   SH3BP2    3'  GCCGAGGCTGGAGCACAG    13074    CA       G
                                 CTG  CTCCAGCCT GGT
                                 |||  ||||||||| |||
                                 GAC  GAGGTCGGA CCG
                                   AC        G
GAM97   SH3BP2    3'  GTCGCCCAGGCTGGAGTGCAAT 13083    C
            G                    CA TGCACTCCAGCCTGGGTGAC
                                 || ||||||||||||||||||||
                                 GT ACGTGAGGTCGGACCCGCTG
                                  A
GAM97   SH3BP2    5'  GTTGCCCAGACTGGAGAGCAGT 13084       A     C     TG
            G                    CACTGC CTCCAG CTGGG  AC
                                 |||||| |||||| |||||  ||
                                 GTGACG GAGGTC GACCC  TG
                                     A     A    GT
GAM97   SHOX      3'  GTCACCCAGGCTGGAGCACACT 23521    C  CA
            G                    CA TG  CTCCAGCCTGGGTGAC
                                 || ||  ||||||||||||||||
                                 GT AC  GAGGTCGGACCCACTG
                                  C  AC
GAM97   SHOX      3'  GTCGCCCAGGCTGGAGCGCAGT 6582       A
                                 ACTGC CTCCAGCCTGGGTGAC
                                 ||||| ||||||||||||||||
                                 TGACG GAGGTCGGACCCGCTG
                                    C
GAM97   SIL       3'  GCCCAGGCTGGAGTGCAATG   13157    C
                                 CA TGCACTCCAGCCTGGGT
                                 || ||||||||||||||||
                                 GT ACGTGAGGTCGGACCCG
                                  A
GAM97   SLA2      3'  GCCCATGCTGGAGTGCAATG   50891    C        C
                                 CA TGCACTCCAGC TGGGT
                                 || |||||||||| |||||
                                 GT ACGTGAGGTCG ACCCG
                                  A         T
GAM97   SLC14A2   5'  GTCACCCAGGCTGGAGTACACT 24123    C  C
            G                    CA TG ACTCCAGCCTGGGTGAC
                                 || || ||||||||||||||||
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                                GT AC TGAGGTCGGACCCACTG
                                 C  A
GAM97   SLC15A1  3' CCAGGCTGGAGTGCAATG    18638    C
                                CA TGCACTCCAGCCTGG
                                || ||||||||||||||
                                GT ACGTGAGGTCGGACC
                                 A
GAM97   SLC19A2  3' GCCCAGGCTGCAGTGCAGTG  69552        C
                                CACTGCACT CAGCCTGGGT
                                ||||||||| ||||||||||
                                GTGACGTGA GTCGGACCCG
                                      C
GAM97   SLC24A1  3' GTTGCCCAGGCTGGTGTGCAAT 17566    C    T        TG
           G                     CA TGCAC CCAGCCTGGG  AC
                                || ||||| ||||||||||  ||
                                GT ACGTG GGTCGGACCC  TG
                                 A    T         GT
GAM97   SLC39A1  5' GCCCAGGCTGGAGTGCGGTG  27811
                                CACTGCACTCCAGCCTGGGT
                                ||||||||||||||||||||
                                GTGGCGTGAGGTCGGACCCG

GAM97   SLC7A6   3' ACTTGGTAAAGTGCAGTG    15635        CCA   T
                                CACTGCACT   GCC GGGT
                                |||||||||   ||| ||||
                                GTGACGTGA   TGG TTCA
                                      AA_  _
GAM97   SMAC     5' GTCGCCCAGGCTGGAGTGCAGT 58024
           G                     CACTGCACTCCAGCCTGGGTGAC
                                |||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCGCTG

GAM97   SMAC     5' GTTGCCCAGGCTGAAGTGCAGT 58026        C       TG
           G                     CACTGCACT CAGCCTGGG  AC
                                ||||||||| |||||||||  ||
                                GTGACGTGA GTCGGACCC  TG
                                      A        GT
GAM97   SNX15    3' GTCGCCCAGACTGGAGTGCAGT 74129           C
           G                     CACTGCACTCCAG CTGGGTGAC
                                |||||||||||| |||||||||
                                GTGACGTGAGGTC GACCCGCTG
                                        A
GAM97   SPN      3' GTCGCCCAGGCTGGAGTGCAAT 13379    C
           G                     CA TGCACTCCAGCCTGGGTGAC
                                || ||||||||||||||||||||
                                GT ACGTGAGGTCGGACCCGCTG
                                 A
GAM97   SRP46    3' GTCACCCAGGCCTTGCAG    50339      CTCCA
                                CTGCA    GCCTGGGTGAC
                                |||||    ||||||||||
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                                GACGT    CGGACCCACTG
                                  TC___
GAM97   SS18    3'  GTCGCCCAGGCTGGAGTGCAGT 20104
            G                    CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCGCTG

GAM97   STARD4  3'  GCCCATGCTGGAGGGCAGTG  58248       A     C
                                 CACTGC CTCCAGC TGGGT
                                 |||||| ||||||| |||||
                                 GTGACG GAGGTCG ACCCG
                                    G      T
GAM97   STAU    5'  GTCGCCCAGGCTGGAGTGCAGT 17201
            G                    CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCGCTG

GAM97   TAF11   3'  TCACCTAGGCTGGAGTGCAG  20122
                                 CTGCACTCCAGCCTGGGTGA
                                 ||||||||||||||||||
                                 GACGTGAGGTCGGATCCACT

GAM97   TAL1    3'  GTCACTCAGGCTGGAGTACAGT 13530      C
            G                    CACTG ACTCCAGCCTGGGTGAC
                                 ||||| ||||||||||||||||
                                 GTGAC TGAGGTCGGACTCACTG
                                    A
GAM97   TAPBP   3'  GCCCAGGCTGCAGTGCAGTG  13568        C
                                 CACTGCACT CAGCCTGGGT
                                 ||||||||| ||||||||||
                                 GTGACGTGA GTCGGACCCG
                                      C
GAM97   TAPBP   3'  GTCGCCCAGGCTGGAGTGCAGT 13582
            G                    CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCGCTG

GAM97   TAPBP   3'  GTTGCCCAGGCTGGAGTGCAGT 13584              TG
            G                    CACTGCACTCCAGCCTGGG  AC
                                 |||||||||||||||||  ||
                                 GTGACGTGAGGTCGGACCC  TG
                                           GT
GAM97   TAT     3'  GCCCATGCTGGAGTGCAGTG  6256            C
                                 CACTGCACTCCAGC TGGGT
                                 |||||||||||||| |||||
                                 GTGACGTGAGGTCG ACCCG
                                      T
GAM97   TBXA2R  3'  GTCCCCCAGGCTGGAGTGCAGT 8363              T
            G                    CACTGCACTCCAGCCTGGG GAC
                                 |||||||||||||||||| |||
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                                GTGACGTGAGGTCGGACCC CTG
                                                   C
GAM97   TCF2    3'  GTCACCCGAGCTGGAGTGCAGT 22410            C
                 G                  CACTGCACTCCAGC TGGGTGAC
                                    |||||||||||||| ||||||||
                                    GTGACGTGAGGTCG GCCCACTG
                                                 A
GAM97   TDGF1   3'  GTCACCCAGGCTGGACTGCAAT 13661    C   C
                 G                  CA TGCA TCCAGCCTGGGTGAC
                                    || |||| ||||||||||||||
                                    GT ACGT AGGTCGGACCCACTG
                                     A   C
GAM97   TEM7    3'  CCTTGGCCAGGTGCAGTG    40253         CCA   T
                                    CACTGCACT   GCC GGG
                                    |||||||||   ||| |||
                                    GTGACGTGG   CGG TCC
                                          AC_   T
GAM97   TERF1   3'  GTTGCCCAGGCTGGAGTGCAGT 34398               TG
                 G                  CACTGCACTCCAGCCTGGG  AC
                                    ||||||||||||||||||  ||
                                    GTGACGTGAGGTCGGACCC  TG
                                                 GT
GAM97   TERF2   3'  GTCACCCAGGCTGGAGTGCAGT 20161
                 G                  CACTGCACTCCAGCCTGGGTGAC
                                    |||||||||||||||||||||
                                    GTGACGTGAGGTCGGACCCACTG

GAM97   TIM3    3'  GTTGCCCAGGCTGGAGTGCAAT 52360    C           TG
                 G                  CA TGCACTCCAGCCTGGG  AC
                                    || ||||||||||||||  ||
                                    GT ACGTGAGGTCGGACCC  TG
                                     A            GT
GAM97   TIMM23  5'  CACCCAGGCTTGAGGCAGCG   60771   A   A  C
                                    C CTGC CTC AGCCTGGGTG
                                    | |||| ||| ||||||||||
                                    G GACG GAG TCGGACCCAC
                                     C   _   T
GAM97   TJP1    5'  CCAGGCAGGAGTGCAGTG    13761          A
                                    CACTGCACTCC GCCTGG
                                    |||||||||| ||||||
                                    GTGACGTGAGG CGGACC
                                           A
GAM97   TLR5    5'  GCCCAGGCTGGACTGCAGTG   13789       C
                                    CACTGCA TCCAGCCTGGGT
                                    ||||||| ||||||||||||
                                    GTGACGT AGGTCGGACCCG
                                        C
GAM97   TMC1    5'  GTTGCCCAGGCTGGAGTGCAGT 57710               TG
                 G                  CACTGCACTCCAGCCTGGG  AC
                                    ||||||||||||||||||  ||
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                                GTGACGTGAGGTCGGACCC  TG
                                          GT
GAM97   TMPRSS3   3'  GTTGCCCAGGCTGGAGTGCAGT 51521              TG
           G                    CACTGCACTCCAGCCTGGG  AC
                                ||||||||||||||||||  ||
                                GTGACGTGAGGTCGGACCC  TG
                                          GT
GAM97   TMPRSS3   3'  GTTGCCCAGGCTGGAGTGCAGT 51548              TG
           G                    CACTGCACTCCAGCCTGGG  AC
                                ||||||||||||||||||  ||
                                GTGACGTGAGGTCGGACCC  TG
                                          GT
GAM97   TMPRSS3   3'  GTTGCCCAGGCTGGAGTGCAGT 44031              TG
           G                    CACTGCACTCCAGCCTGGG  AC
                                ||||||||||||||||||  ||
                                GTGACGTGAGGTCGGACCC  TG
                                          GT
GAM97   TNFAIP2   3'  GTTGCCCAGGCTGGAGTGCAGT 21927              TG
           G                    CACTGCACTCCAGCCTGGG  AC
                                ||||||||||||||||||  ||
                                GTGACGTGAGGTCGGACCC  TG
                                          GT
GAM97   TNFRSF10B 3'  GTCTCCCAGGCTGGAGTGCAAT 15230    C          T
           G                    CA TGCACTCCAGCCTGGG GAC
                                || ||||||||||||||| |||
                                GT ACGTGAGGTCGGACCC CTG
                                 A           T
GAM97   TNFRSF11A 3'  GCCCAGGCTAGAGTGCAGTG   15195        C
                                CACTGCACTC AGCCTGGGT
                                |||||||||| |||||||||
                                GTGACGTGAG TCGGACCCG
                                      A
GAM97   TNFRSF1B  3'  TCACCTCAGGCCAGGTGCAGTG 8400         CCA   _
                                CACTGCACT   GCCTG GGTGA
                                |||||||||   ||||| |||||
                                GTGACGTGG   CGGAC CCACT
                                     AC_    T
GAM97   TNFRSF6B  3'  GCCCGGGCTGGAGCGG      53097      AC
                                CTGC  TCCAGCCTGGGT
                                ||||  ||||||||||||
                                GGCG  AGGTCGGGCCCG
                                  __
GAM97   TNFRSF9   3'  GTCACCCAGGCTGGAGTGCAGT 9584
           G                    CACTGCACTCCAGCCTGGGTGAC
                                |||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCACTG

GAM97   TP53      3'  GTTGCCCAGGCTGGAGTGGAGT 6804       G          TG
           G                    CACT CACTCCAGCCTGGG  AC
                                |||| ||||||||||||||  ||
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                                GTGA GTGAGGTCGGACCC  TG
                                  G           GT
GAM97   TPMT    3'  GCCCAACCTGGAGTGCAGTG  6314           CC
                                CACTGCACTCCAG  TGGGT
                                ||||||||||||  |||||
                                GTGACGTGAGGTC  ACCCG
                                      CA
GAM97   TRAF5   3'  GTCACCCAGGCTGGAGTACAGT 17280      C
          G                      CACTG ACTCCAGCCTGGGTGAC
                                 ||||| ||||||||||||||||
                                 GTGAC TGAGGTCGGACCCACTG
                                   A
GAM97   TRPM6   3'  ACCCAGGCTGGAGTGCAATG  35020   C
                                 CA TGCACTCCAGCCTGGGT
                                 || ||||||||||||||||
                                 GT ACGTGAGGTCGGACCCA
                                  A
GAM97   TRPS1   3'  GCTTGGTTAGAGTGCAG    26924       C   T
                                 CTGCACTC AGCC GGGT
                                 |||||||| |||| ||||
                                 GACGTGAG TTGG TTCG
                                     A   _
GAM97   TRPV1   3'  GTTGCCCAGGCTGGAGTGCAGT 38703              TG
          G                      CACTGCACTCCAGCCTGGG  AC
                                 ||||||||||||||||||  ||
                                 GTGACGTGAGGTCGGACCC  TG
                                       GT
GAM97   TRPV1   3'  TCACCCAGGCTGGAATGCAGTG 38705       C
                                 CACTGCA TCCAGCCTGGGTGA
                                 |||||||  ||||||||||||||
                                 GTGACGT AGGTCGGACCCACT
                                    A
GAM97   TRPV1   3'  GTTGCCCAGGCTGGAGTGCAGT 55684              TG
          G                      CACTGCACTCCAGCCTGGG  AC
                                 ||||||||||||||||||  ||
                                 GTGACGTGAGGTCGGACCC  TG
                                       GT
GAM97   TRPV1   3'  TCACCCAGGCTGGAATGCAGTG 55689       C
                                 CACTGCA TCCAGCCTGGGTGA
                                 |||||||  ||||||||||||||
                                 GTGACGT AGGTCGGACCCACT
                                    A
GAM97   TRPV1   3'  GTTGCCCAGGCTGGAGTGCAGT 55719              TG
          G                      CACTGCACTCCAGCCTGGG  AC
                                 ||||||||||||||||||  ||
                                 GTGACGTGAGGTCGGACCC  TG
                                       GT
GAM97   TRPV1   3'  TCACCCAGGCTGGAATGCAGTG 55721       C
                                 CACTGCA TCCAGCCTGGGTGA
                                 |||||||  ||||||||||||||
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                                GTGACGT AGGTCGGACCCACT
                                    A
GAM97   TRPV1    3'  GTTGCCCAGGCTGGAGTGCAGT 55750                TG
           G                    CACTGCACTCCAGCCTGGG  AC
                                |||||||||||||||||  ||
                                GTGACGTGAGGTCGGACCC  TG
                                          GT
GAM97   TRPV1    3'  TCACCCAGGCTGGAATGCAGTG 55752        C
                                CACTGCA TCCAGCCTGGGTGA
                                ||||||| |||||||||||||
                                GTGACGT AGGTCGGACCCACT
                                    A
GAM97   TUFT1    3'  GTCACCCAGGCTGGAGTGCAGT 39676
                                ACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
                                TGACGTGAGGTCGGACCCACTG

GAM97   UGDH     3'  GTTGCCCAGGCTGGAGTGCAGT 14002               TG
           G                    CACTGCACTCCAGCCTGGG  AC
                                |||||||||||||||||  ||
                                GTGACGTGAGGTCGGACCC  TG
                                          GT
GAM97   UMPS     3'  GCCCAGGATGGAGTGCAGTG  6332           G
                                CACTGCACTCCA CCTGGGT
                                |||||||||||| |||||||
                                GTGACGTGAGGT GGACCCG
                                       A
GAM97   VENTX2   3'  GTCACCCAGGCTGGAGTGCAAT 27864    C
           G                    CA TGCACTCCAGCCTGGGTGAC
                                || ||||||||||||||||||||
                                GT ACGTGAGGTCGGACCCACTG
                                 A
GAM97   VHL      3'  GCCCAGGCTGGAGTGCAG    6862
                                CTGCACTCCAGCCTGGGT
                                ||||||||||||||||||
                                GACGTGAGGTCGGACCCG

GAM97   VIPR2    3'  GTCGCCCAGGCTGGAGTGCAGT 14073
           G                    CACTGCACTCCAGCCTGGGTGAC
                                |||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCGCTG

GAM97   WNT7A    5'  GCGGGGGCTGGAGGCAG     17318     A       GG
                                CTGC CTCCAGCCT  GT
                                |||| |||||||||  ||
                                GACG GAGGTCGGG  CG
                                   _       GG
GAM97   XRCC2    3'  GCTGCTGGAGTGCAGTG     19504           CTG
                                CACTGCACTCCAGC   GGT
                                ||||||||||||||   |||
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                                GTGACGTGAGGTCG   TCG
                                      ____
GAM97   XRCC2    3'  GTCTCCCAGGCTGGAGTGCAGT 19509                T
            G                    CACTGCACTCCAGCCTGGG GAC
                                 |||||||||||||||||| |||
                                 GTGACGTGAGGTCGGACCC CTG
                                                    T
GAM97   YES1     3'  CGCCCAGGCTGGAGTGCAGTG  19535
                                 CACTGCACTCCAGCCTGGGTG
                                 ||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCGC

GAM97   ZNF133   5'  GTTGCCCAGGCTGGAGTGCAAT 14298    C            TG
            G                    CA TGCACTCCAGCCTGGG  AC
                                 || ||||||||||||||  ||
                                 GT ACGTGAGGTCGGACCC  TG
                                  A              GT
GAM97   ZNF157   3'  GTCACCCAGGCTGGAGTGCAAT 14336    C
            G                    CA TGCACTCCAGCCTGGGTGAC
                                 || ||||||||||||||||||
                                 GT ACGTGAGGTCGGACCCACTG
                                  A
GAM97   ZNF253   3'  GTCACCGAGGCTGGAGTGCAAT 41080    C          G
            G                    CA TGCACTCCAGCCT GGTGAC
                                 || ||||||||||||| ||||||
                                 GT ACGTGAGGTCGGA CCACTG
                                  A           G
GAM97   ZNF264   3'  GTCACCCACGCTGGAGTGCTGT 14224     T        C
            G                    CAC GCACTCCAGC TGGGTGAC
                                 ||| |||||||||| ||||||||
                                 GTG CGTGAGGTCG ACCCACTG
                                   T         C
GAM97   ZNF264   3'  GTCACCCAGGCTGGAGTGCAGT 14225
            G                    CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCACTG

GAM97   ZNF80    5'  ATTCGGGCCGGAGCCAG     24068     CA   A
                                 CTG  CTCC GCCTGGGT
                                 |||  |||| ||||||||
                                 GAC  GAGG CGGGCTTA
                                   C_    C
GAM97   20D7-FC4 5'  GTCACCCAGGCTGGAGTGCAGT 61566
            G                    CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCACTG

GAM97   AAK1     3'  GCCTGGGCTGGAGTGCAGTG   30525             TG
                                 CACTGCACTCCAGCC  GGT
                                 ||||||||||||||  |||
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                                GTGACGTGAGGTCGG  CCG
                                       GT
GAM97   AFAP    3'  CACCCAGGTGAGGTGCTGTG  41604    T   TC  G
                                CAC GCAC  CA CCTGGGTG
                                ||| ||||  || ||||||||
                                GTG CGTG  GT GGACCCAC
                                  T   GA  _
GAM97   AGMAT   3'  ATCTTGGCTGGAGTGAGTG   45734     G       T
                                CACT CACTCCAGCC GGGT
                                |||| |||||||||| ||||
                                GTGA GTGAGGTCGG TCTA
                                  _       T
GAM97   AGMAT   3'  GTCACCCAGGCTGGAGTGCAGT 45742
            G                    CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCACTG

GAM97   ANKRD6  3'  GTCACCCAGACTGGAGTGCAGT 30773          C
            G                    CACTGCACTCCAG CTGGGTGAC
                                |||||||||||| |||||||||
                                GTGACGTGAGGTC GACCCACTG
                                       A
GAM97   AP1S3   3'  GTCACCCAGGCTGGAGTGCAGT 75429
                                ACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||
                                TGACGTGAGGTCGGACCCACTG

GAM97   AP3D1   3'  CACCCCGCGGAGCACGT    15450   _  AC   A  CT
                                AC TGC  TCC GC  GGGTG
                                || |||  ||| ||  |||||
                                TG ACG  AGG CG  CCCAC
                                 C  __  _  C_
GAM97   AP3S2   3'  GTCACCCAGGCTGGAGTGCTGT 20656    T
            G                    CAC GCACTCCAGCCTGGGTGAC
                                ||| ||||||||||||||||||
                                GTG CGTGAGGTCGGACCCACTG
                                  T
GAM97   APOL2   3'  GCCCAGGATGGAGTGCAGTG  48791          G
                                CACTGCACTCCA CCTGGGT
                                |||||||||||| |||||||
                                GTGACGTGAGGT GGACCCG
                                       A
GAM97   APXL2   5'  GTCGCCAGGCTGGAGTGCAGTG 75683              G
                                CACTGCACTCCAGCCTGG TGAC
                                |||||||||||||||||| ||||
                                GTGACGTGAGGTCGGACC GCTG
                                                  _
GAM97   ARFRP1  3'  GTCACCCAGGGTGAGTGCA   13695       C G
                                TGCACTC A CCTGGGTGAC
                                ||||||| | ||||||||||
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                                ACGTGAG T GGACCCACTG
                                   _ G
GAM97   ARHF     3'  GTCACTCAGGCTAGAGTGCAGT 39276          C
           G                    CACTGCACTC AGCCTGGGTGAC
                                |||||||||| ||||||||||||
                                GTGACGTGAG TCGGACTCACTG
                                     A
GAM97   ARHGAP11A 3'  GTCGTCCAGGCTGGAGTGCAGT 29457                GT
           G                    CACTGCACTCCAGCCTGG  GAC
                                |||||||||||||||||  |||
                                GTGACGTGAGGTCGGACC  CTG
                                          TG
GAM97   ARHGAP5   5'  GTTGCCCAGGCTGGAGTGCAAT 77604    C            TG
           G                    CA TGCACTCCAGCCTGGG  AC
                                || ||||||||||||||  ||
                                GT ACGTGAGGTCGGACCC  TG
                                 A             GT
GAM97   ARPC5     3'  GTCACCCAGGGTTCAGAGCA   20358     A  CCAG
                                TGC CT    CCTGGGTGAC
                                ||| ||    ||||||||||
                                ACG GA    GGACCCACTG
                                  A  CTTG
GAM97   ASB16     5'  GTCGCCCAGGCTGGAGTGCAGT 70491
           G                    CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCGCTG

GAM97   ASB16     3'  GTGGCCCAGGCTGAAGTGCAGT 70493          C        G
           G                    CACTGCACT CAGCCTGGGT AC
                                ||||||||| |||||||||| ||
                                GTGACGTGA GTCGGACCCG TG
                                     A         G
GAM97   ASB16     3'  GTTGCCCAGGCTGGAGTGCAGT 55988                  TG
           G                    CACTGCACTCCAGCCTGGG  AC
                                |||||||||||||||||  ||
                                GTGACGTGAGGTCGGACCC  TG
                                          GT
GAM97   ASE-1     3'  GTCACCCAGGCTGGAGTGCAGT 24990
           G                    CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCACTG

GAM97   ASE-1     3'  GTCGCCCAGGTTGGAGTGCAGT 24992
           G                    CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
                                GTGACGTGAGGTTGGACCCGCTG

GAM97   ATP1B4    3'  GTCACCCAGGCTGGAGTGCAGT 24850
           G                    CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
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                                GTGACGTGAGGTCGGACCCACTG

GAM97   BA108L7.2 3'  GCCCAGGCTGGAGTGCGATG   49076    C
                                CA TGCACTCCAGCCTGGGT
                                || ||||||||||||||||
                                GT GCGTGAGGTCGGACCCG
                                 A
GAM97   BAG5    3'  GCCCAGGCTGCAGTGCAGTG   18041         C
                                CACTGCACT CAGCCTGGGT
                                ||||||||| ||||||||||
                                GTGACGTGA GTCGGACCCG
                                      C
GAM97   BC008967  5'  CACCCTGTACAGAGTGTAG    61415        CA_ CT
                                CTGCACTC   GC  GGGTG
                                ||||||||   ||  |||||
                                GATGTGAG   TG  CCCAC
                                     ACA  T_
GAM97   BIA2    3'  ACCTTAAGGCTGGGTGCAGTG  71788        T     __
                                CACTGCAC CCAGCCT  GGGT
                                |||||||| |||||||  ||||
                                GTGACGTG GGTCGGA  TCCA
                                     _      AT
GAM97   BNIP-S   3'  GTCGCCAGGCTGGAGTGCAGTG 57094              G
                                CACTGCACTCCAGCCTGG TGAC
                                |||||||||||||||| ||||
                                GTGACGTGAGGTCGGACC GCTG
                                                 _
GAM97   BRD2    5'  CATTTCGTGCTGGAGTGGAG   18792    G       C   _
                                CT CACTCCAGC TGGG TG
                                || |||||||| |||| ||
                                GA GTGAGGTCG GCTT AC
                                 G       T   T
GAM97   BTN3A1   3'  CTAGGCTGGAGTGCAGTG    23888
                                CACTGCACTCCAGCCTGG
                                ||||||||||||||||
                                GTGACGTGAGGTCGGATC

GAM97   BY55    5'  GTCAACCAGGCCAGAGTGCAGT 60063          CA     G
           G                     CACTGCACTC  GCCTGG TGAC
                                |||||||||  |||||| ||||
                                GTGACGTGAG  CGGACC ACTG
                                      AC     A
GAM97   C(27)-3BETA-HSD 3'  GTCACCCAGACTGGAGTGCAGT 48053            C
           G                     CACTGCACTCCAG CTGGGTGAC
                                |||||||||||| |||||||||
                                GTGACGTGAGGTC GACCCACTG
                                       A
GAM97   C11orf17  3'  GTTGCCCAGGCTGGAGTGCAGT 40587               TG
           G                     CACTGCACTCCAGCCTGGG  AC
                                |||||||||||||||||  ||
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                                GTGACGTGAGGTCGGACCC  TG
                                          GT
GAM97   C13orf1   3'  GTCACCCAGGCTAGAGTGCAGT 40368         C
            G                   CACTGCACTC AGCCTGGGTGAC
                                |||||||||| ||||||||||||
                                GTGACGTGAG TCGGACCCACTG
                                      A
GAM97   C1orf24   3'  GCCAAGGCTGGAGTGCAGTG  54793             G
                                CACTGCACTCCAGCCT GGT
                                |||||||||||||||| |||
                                GTGACGTGAGGTCGGA CCG
                                         A
GAM97   C1orf34   3'  GTCGTGTGGCTGGAGTGC    61319          TGGG
                                GCACTCCAGCC   TGAC
                                ||||||||||    ||||
                                CGTGAGGTCGG   GCTG
                                      TGT_
GAM97   C1QTNF6   3'  GTTGCCCAGGCTAGAGTGCAGT 49994         C      TG
            G                   CACTGCACTC AGCCTGGG  AC
                                |||||||||| ||||||||  ||
                                GTGACGTGAG TCGGACCC  TG
                                      A       GT
GAM97   C20orf172 3'  TTGAGGCTGGGCGCAATG    46769    C   A T     G
                                CA TGC C CCAGCCT GG
                                || ||| | ||||||| ||
                                GT ACG G GGTCGGA TT
                                 A   C _      G
GAM97   C20orf183 3'  CCCAACTGGGTGCAGTG     48530        T   CC
                                CACTGCAC CCAG  TGGG
                                |||||||| ||||  ||||
                                GTGACGTG GGTC  ACCC
                                     _   A_
GAM97   C21orf25  3'  GTTGCCCAGGCTGGAGTGCAAT 64299    C           TG
            G                   CA TGCACTCCAGCCTGGG  AC
                                || ||||||||||||||||  ||
                                GT ACGTGAGGTCGGACCC  TG
                                 A             GT
GAM97   C21orf25  3'  GCCTGACGCTGGAGTGCGGTG  64296           CT_
                                CACTGCACTCCAGC   GGGT
                                ||||||||||||||   ||||
                                GTGGCGTGAGGTCG   TCCG
                                      CAG
GAM97   C21orf67  5'  GTCGCCCAGGCTGGAGCGCAAT 55232    C   A
            G                   CA TGC CTCCAGCCTGGGTGAC
                                || ||| ||||||||||||||||
                                GT ACG GAGGTCGGACCCGCTG
                                 A   C
GAM97   C22orf19  3'  CCAGGCTGGAGTGCAGTG    14819
                                CACTGCACTCCAGCCTGG
                                ||||||||||||||||||
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                                GTGACGTGAGGTCGGACC

GAM97   C22orf19  3'  GTCACAAGGGGGCCTGAGTGCA 14826          CA   GG__
            GTG                   CACTGCACTC  GCCT   GTGAC
                                  ||||||||||  ||||   |||||
                                  GTGACGTGAG  CGGG   CACTG
                                        TC    GGAA
GAM97   C3F     3'  GTCACCCACGCTGGAATGCAGT 20481        C     C
            G                     CACTGCA TCCAGC TGGGTGAC
                                  |||||||  ||||||  ||||||||
                                  GTGACGT AGGTCG ACCCACTG
                                      A     C
GAM97   C6orf33   3'  GTCGCCCAGGCTGGAGTGCAGT 56719
            G                     CACTGCACTCCAGCCTGGGTGAC
                                  ||||||||||||||||||||||
                                  GTGACGTGAGGTCGGACCCGCTG

GAM97   C6orf5   3'  CCAGGCTGCAGTACAGTG    31979      C   C
                                  CACTG ACT CAGCCTGG
                                  |||||  |||  ||||||||
                                  GTGAC TGA GTCGGACC
                                     A   C
GAM97   C6orf5   3'  GTCGTCCAGGCTGGAGTGCAGT 32001              GT
            G                     CACTGCACTCCAGCCTGG  GAC
                                  ||||||||||||||||  |||
                                  GTGACGTGAGGTCGGACC  CTG
                                                TG
GAM97   C6orf5   3'  TTTAGGCTGGGCGCAGTG    32009       A T
                                  CACTGC C CCAGCCTGGG
                                  ||||||  |  ||||||||||
                                  GTGACG G GGTCGGATTT
                                     C _
GAM97   C9orf9   3'  GCCCAGGCTGGAGTGCGGTG   39024
                                  CACTGCACTCCAGCCTGGGT
                                  ||||||||||||||||||||
                                  GTGGCGTGAGGTCGGACCCG

GAM97   C9orf9   3'  GTCTCCCAGGCTGGAGTGCAGT 39031                T
            G                     CACTGCACTCCAGCCTGGG GAC
                                  ||||||||||||||||||  |||
                                  GTGACGTGAGGTCGGACCC CTG
                                                 T
GAM97   CAPN6    3'  ATCAAGAGCTGGAGTTCAATG  27390    C  C      _  G
                                  CA TG ACTCCAGC CT GGT
                                  ||  ||  ||||||||  ||  |||
                                  GT AC TGAGGTCG GA CTA
                                   A  T       A  A
GAM97   CARD6    3'  GTTGCCCAGGCTGGAGTGCAAT 51848    C            TG
            G                     CA TGCACTCCAGCCTGGG  AC
                                  ||  ||||||||||||||  ||
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                                GT ACGTGAGGTCGGACCC  TG
                                 A            GT
GAM97   CCRN4L   3'  GCCTAGGCGGAGTACAGTG   25070      C    A
                                CACTG ACTCC GCCTGGGT
                                ||||| ||||| ||||||||
                                GTGAC TGAGG CGGATCCG
                                   A    _
GAM97   CDC14B   3'  CCAGGCTGGAGTGCAGTG    54002
                                CACTGCACTCCAGCCTGG
                                ||||||||||||||||||
                                GTGACGTGAGGTCGGACC

GAM97   CEACAM8  3'  GTCGCCCAGGCTGGAGTGCAGT 10186
            G                    CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCGCTG

GAM97   CENPH    3'  GTTGCCCAGACTGGAGGGCAGT 43571       A     C     TG
            G                    CACTGC CTCCAG CTGGG  AC
                                |||||| |||||| |||||  ||
                                GTGACG GAGGTC GACCC  TG
                                   G     A    GT
GAM97   CHSY1    3'  GTTACCCAGGCTGGAATGCAGT 30571        C
            G                    CACTGCA TCCAGCCTGGGTGAC
                                ||||||| ||||||||||||||
                                GTGACGT AGGTCGGACCCATTG
                                    A
GAM97   CIP29    3'  GCCCAGCTGGAGTGCAGTG   51378            C
                                CACTGCACTCCAGC TGGGT
                                |||||||||||||| |||||
                                GTGACGTGAGGTCG ACCCG
                                          _
GAM97   CNNM4    3'  GTCCTTCCACTGGGTGCAG   39873       T   CC   T_
                                CTGCAC CCAG  TGGG  GAC
                                |||||| ||||  ||||  |||
                                GACGTG GGTC  ACCT  CTG
                                   _   ___   TC
GAM97   COLEC12  3'  GTCACCCAGGCTGGAATGACG  48616    _ C
                                TG CA TCCAGCCTGGGTGAC
                                || || ||||||||||||||
                                GC GT AGGTCGGACCCACTG
                                 A  A
GAM97   COLEC12  3'  GTTGCCCAGGCTGGAGTGCAGT 48618              TG
            G                    CACTGCACTCCAGCCTGGG  AC
                                |||||||||||||||||  ||
                                GTGACGTGAGGTCGGACCC  TG
                                             GT
GAM97   CPSF2    3'  GTCACCCAGGCTGGAGTGCAGT 62279
            G                    CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
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                                GTGACGTGAGGTCGGACCCACTG

GAM97   CPSF2    3'  GTTGCCCAGACTGGAGTGCAAT 62281    C       C    TG
            G                    CA TGCACTCCAG CTGGG  AC
                                 || |||||||||| |||||  ||
                                 GT ACGTGAGGTC GACCC  TG
                                  A        A    GT
GAM97   CSAD     3'  GCCTTTGAGGCCGGGTGCAGTG 32581        T  A   ___
                                 CACTGCAC CC GCCT   GGGT
                                 |||||||| || ||||   ||||
                                 GTGACGTG GG CGGA   TCCG
                                      _ C    GTT
GAM97   CYLC2    3'  GCCCTGGCTGGAGTTCAGTG   9033       C       T
                                 CACTG ACTCCAGCC GGGT
                                 ||||| ||||||||| ||||
                                 GTGAC TGAGGTCGG CCCG
                                    T       T
GAM97   CYorf14  3'  ACTCTGGCCAGGTGCAGT    38200        CCA   T
                                 ACTGCACT   GCC GGGT
                                 ||||||||   ||| ||||
                                 TGACGTGG   CGG CTCA
                                      AC_   T
GAM97   D15Wsu75e 3'  ATCCAGGCCAGTACGCAGT    67222      __   CCA
                                 ACTGC  ACT   GCCTGGGT
                                 |||||  |||   ||||||||
                                 TGACG  TGA   CGGACCTA
                                    CA   C__
GAM97   DBR1     3'  GTCACCTAGACTGGAGTGCAAT 33071    C       C
            G                    CA TGCACTCCAG CTGGGTGAC
                                 || |||||||||| |||||||||
                                 GT ACGTGAGGTC GATCCACTG
                                  A         A
GAM97   DCOHM    3'  GTCATGCAGACTGGAGTGCAGT 50533           C   G
            G                    CACTGCACTCCAG CTG GTGAC
                                 |||||||||||| ||| |||||
                                 GTGACGTGAGGTC GAC TACTG
                                         A   G
GAM97   DCOHM    3'  GTCGCCCAGGCTGGAGTGCAAT 50534    C
            G                    CA TGCACTCCAGCCTGGGTGAC
                                 || ||||||||||||||||||
                                 GT ACGTGAGGTCGGACCCGCTG
                                  A
GAM97   DKFZp434A2417 3'  GTTGCCCAGGCTGGAGGGCAAT 66684    C   A         TG
            G                    CA TGC CTCCAGCCTGGG  AC
                                 || ||| ||||||||||||  ||
                                 GT ACG GAGGTCGGACCC  TG
                                  A  G          GT
GAM97   DKFZP434B044 3'  GCCCAAGGTAGAGTGCAGTG   49719          CA   _
                                 CACTGCACTC  GCCT GGGT
                                 ||||||||||  |||| ||||
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                                GTGACGTGAG  TGGA CCCG
                                      A_    A
GAM97   DKFZP434B1727 3'  GTTACCCAGGCTGGAGTACAGT 50479       C
          G                    CACTG ACTCCAGCCTGGGTGAC
                               ||||| ||||||||||||||||
                               GTGAC TGAGGTCGGACCCATTG
                                 A
GAM97   DKFZp434C0923 3'  GTCACCCAGGCTGGAGTACAGT 34651       C
          G                    CACTG ACTCCAGCCTGGGTGAC
                               ||||| ||||||||||||||||
                               GTGAC TGAGGTCGGACCCACTG
                                 A
GAM97   DKFZP434C212 3'  GTTGCCCAGGCTGGAGTGCAAT 69498    C            TG
          G                    CA TGCACTCCAGCCTGGG  AC
                               || ||||||||||||||  ||
                               GT ACGTGAGGTCGGACCC  TG
                                A             GT
GAM97   DKFZP434D146 3'  GTCGCCCAGGCTAGAGTATAGT 32139       C   C
          G                    CACTG ACTC AGCCTGGGTGAC
                               ||||| |||| ||||||||||||
                               GTGAT TGAG TCGGACCCGCTG
                                 A   A
GAM97   DKFZp434E2220 5'  GTTGCCCAGGCTGGAGTGCAGT 34717              TG
          G                    CACTGCACTCCAGCCTGGG  AC
                               ||||||||||||||||||  ||
                               GTGACGTGAGGTCGGACCC  TG
                                          GT
GAM97   DKFZp434F1719 3'  GTTTCCCAGGCTGGAGTGCAAT 51016    C            T
          G                    CA TGCACTCCAGCCTGGG GAC
                               || |||||||||||||| |||
                               GT ACGTGAGGTCGGACCC TTG
                                A             T
GAM97   DKFZp434G0522 3'  GTTCAACTGAGTGCAGTG    34531          C  CC  GG
                               CACTGCACTC AG  TG  T
                               |||||||||| ||  ||  |
                               GTGACGTGAG TC  AC  G
                                     _  A_  TT
GAM97   DKFZP434G156 3'  GTCACCCAGGCTGAAAAGGC   70339    A  C__
                               GC CT   CAGCCTGGGTGAC
                               || ||   ||||||||||||
                               CG GA   GTCGGACCCACTG
                                _  AAA
GAM97   DKFZP434J037 3'  TGCCCAGGCTAGAGTGCAATG  48957    C      C
                               CA TGCACTC AGCCTGGGTG
                               || ||||||| ||||||||||
                               GT ACGTGAG TCGGACCCGT
                                A      A
GAM97   DKFZp547H025 3'  GCCCAGGCTGGACTGCAG    39775       C
                               CTGCA TCCAGCCTGGGT
                               ||||| ||||||||||||
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                                GACGT AGGTCGGACCCG
                                   C
GAM97   DKFZP564D166 3'  GCCTAGGCCAGAGTGCAGTG   48397          CA
                                CACTGCACTC  GCCTGGGT
                                ||||||||||  ||||||||
                                GTGACGTGAG  CGGATCCG
                                     AC
GAM97   DKFZP564G092 5'  GCCCAGGCTGTAGTGCAGTG   32162          C
                                CACTGCACT CAGCCTGGGT
                                ||||||||| ||||||||||
                                GTGACGTGA GTCGGACCCG
                                     T
GAM97   DKFZP564I122 3'  GTCACCTAGGCTGGAGTGCAGT 63880
           G                     CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
                                GTGACGTGAGGTCGGATCCACTG

GAM97   DKFZP564K0322 3'  GTTGCCCAGGCTGGAGTGCAGT 50189                TG
           G                     CACTGCACTCCAGCCTGGG  AC
                                ||||||||||||||||||  ||
                                GTGACGTGAGGTCGGACCC  TG
                                              GT
GAM97   DKFZP564O0523 3'  GTTGCCCAGGCTGGAATGCAGT 50423        C         TG
           G                     CACTGCA TCCAGCCTGGG  AC
                                |||||||  ||||||||||  ||
                                GTGACGT AGGTCGGACCC  TG
                                     A          GT
GAM97   DKFZP566I1024 3'  GTTGCCCAGGCTAGAGTGCACT 70651    C      C       TG
           G                     CA TGCACTC AGCCTGGG  AC
                                || |||||||  ||||||||  ||
                                GT ACGTGAG TCGGACCC  TG
                                 C      A       GT
GAM97   DKFZP761E2110 3'  GCCTAGGCTGGAATGCAGTG   48964        C
                                CACTGCA TCCAGCCTGGGT
                                |||||||  ||||||||||||
                                GTGACGT AGGTCGGATCCG
                                     A
GAM97   DKFZp761J139 5'  GTCACCCAGGCTGGAGTGCAGT 51111
           G                     CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCACTG

GAM97   DKFZp761N1114 3'  CCAGGCTGGAATGCAGTG    79776        C
                                CACTGCA TCCAGCCTGG
                                |||||||  ||||||||||
                                GTGACGT AGGTCGGACC
                                     A
GAM97   DKFZp761O0113 5'  GTTGCCCAGGCTTGAGTGCAGT 37899          C       TG
           G                     CACTGCACTC AGCCTGGG  AC
                                ||||||||||  ||||||||  ||
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                                GTGACGTGAG TCGGACCC  TG
                                      T       GT
GAM97   DKFZp762P2111 3'  GTTGCCCAGGCTGGAGTGCAAT 87639    C           TG
          G                    CA TGCACTCCAGCCTGGG  AC
                               || ||||||||||||||||  ||
                               GT ACGTGAGGTCGGACCC  TG
                                A             GT
GAM97   DMRTB1   3'  ATCCAGGTGGCTGGAGCCAG   66837     CA      ___
                               CTG  CTCCAGCC   TGGGT
                               |||  ||||||||   |||||
                               GAC  GAGGTCGG   ACCTA
                                 C_       TGG
GAM97   DORFIN   5'  GTCACCCAGGGTGGAATACAGT 31874      CAC   G
          G                    CACTG   TCCA CCTGGGTGAC
                               |||||   |||| ||||||||||
                               GTGAC   AGGT GGACCCACTG
                                  ATA   G
GAM97   DRIM     3'  GTCACCCAAGGCGGAGTGCAGT 27956          A   _
          G                    CACTGCACTCC GCCT GGGTGAC
                               |||||||||||| |||| |||||||
                               GTGACGTGAGG CGGA CCCACTG
                                     _   A
GAM97   DSCR6    3'  GTCTCCCAGGCTGGAGTGCAGT 39073              T
          G                    CACTGCACTCCAGCCTGGG GAC
                               |||||||||||||||||| |||
                               GTGACGTGAGGTCGGACCC CTG
                                                T
GAM97   ENDO180  3'  ACCCAGCTGAGTGCAG     21263        C   C
                               CTGCACTC AGC TGGGT
                               |||||||| ||| |||||
                               GACGTGAG TCG ACCCA
                                    _   _
GAM97   EREG     3'  GTTGCCCAGGTTGGAGTGCAGT 9314              TG
          G                    CACTGCACTCCAGCCTGGG  AC
                               |||||||||||||||||  ||
                               GTGACGTGAGGTTGGACCC  TG
                                           GT
GAM97   EVI5     3'  ACTCAGGCTGGAGTGCAGTG  20191
                               CACTGCACTCCAGCCTGGGT
                               ||||||||||||||||||
                               GTGACGTGAGGTCGGACTCA

GAM97   EVI5     3'  GTCACCCAGGCTGGAGTGCTGT 20214     T
          G                    CAC GCACTCCAGCCTGGGTGAC
                               ||| ||||||||||||||||||
                               GTG CGTGAGGTCGGACCCACTG
                                 T
GAM97   FBP17    3'  GTTCAGACTGGAGTGCAGTG  73157          C   GG
                               CACTGCACTCCAG CTG  T
                               |||||||||||| |||  |
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                                GTGACGTGAGGTC GAC  G
                                      A   TT
GAM97   FER1L4   3'  GTCTCCCAGGTTGGAGTGCAGT 48130              T
           G                   CACTGCACTCCAGCCTGGG GAC
                               |||||||||||||||||| |||
                               GTGACGTGAGGTTGGACCC CTG
                                      T
GAM97   FER1L4   3'  GTCTCCCAGGTTGGAGTGCAGT 48131              T
           G                   CACTGCACTCCAGCCTGGG GAC
                               |||||||||||||||||| |||
                               GTGACGTGAGGTTGGACCC CTG
                                      T
GAM97   FKBP9    3'  GTCGCCAGGCTGGAGTGCAGTG 95721             G
                               CACTGCACTCCAGCCTGG TGAC
                               |||||||||||||||| ||||
                               GTGACGTGAGGTCGGACC GCTG
                                      _
GAM97   FLJ00024 5'  GTCACCCAGGCTGGAGTGCAAT 64501    C
           G                   CA TGCACTCCAGCCTGGGTGAC
                               || ||||||||||||||||||
                               GT ACGTGAGGTCGGACCCACTG
                                A
GAM97   FLJ00060 5'  GTCACCCAGGCTGGAGTGCAGT 61752
           G                   CACTGCACTCCAGCCTGGGTGAC
                               ||||||||||||||||||||||
                               GTGACGTGAGGTCGGACCCACTG

GAM97   FLJ10101 3'  GTGGCCCAGGCTGGAGTGCAGT 45603               G
           G                   CACTGCACTCCAGCCTGGGT AC
                               |||||||||||||||||| ||
                               GTGACGTGAGGTCGGACCCG TG
                                      G
GAM97   FLJ10232 3'  GTCACCCAGGCTGGAGTGCGAT 36384    C
           G                   CA TGCACTCCAGCCTGGGTGAC
                               || ||||||||||||||||||
                               GT GCGTGAGGTCGGACCCACTG
                                A
GAM97   FLJ10297 3'  GTTGCCCAGGCTAGAGTGCAGT 36444         C      TG
           G                   CACTGCACTC AGCCTGGG  AC
                               |||||||||| ||||||||  ||
                               GTGACGTGAG TCGGACCC  TG
                                     A       GT
GAM97   FLJ10298 3'  GTTGCCCAGGCTGGAGTGCAGT 36462             TG
                               ACTGCACTCCAGCCTGGG  AC
                               |||||||||||||||||  ||
                               TGACGTGAGGTCGGACCC  TG
                                      GT
GAM97   FLJ10346 5'  GTCTCCCAGGCTGAAGTGCAGT 36528         C       T
           G                   CACTGCACT CAGCCTGGG GAC
                               |||||||| ||||||||| |||
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                                GTGACGTGA GTCGGACCC CTG
                                    A       T
GAM97   FLJ10535 3' GTCACCCAGGCTGGAGTGCAGT 36754
            G                    CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCACTG

GAM97   FLJ10560 3' GTCGCCCAGGCTGGCGTGCAGT 36800        T
            G                    CACTGCAC CCAGCCTGGGTGAC
                                 |||||||| ||||||||||||||
                                 GTGACGTG GGTCGGACCCGCTG
                                     C
GAM97   FLJ10607 3' GCCCAGGCTAGAGCGCAG    77636     A  C
                                 CTGC CTC AGCCTGGGT
                                 |||| ||| |||||||||
                                 GACG GAG TCGGACCCG
                                   C  A
GAM97   FLJ10607 3' TCACCCAGGCTGGAGTCCAGTG 77645      C
                                 CACTG ACTCCAGCCTGGGTGA
                                 ||||| ||||||||||||||||
                                 GTGAC TGAGGTCGGACCCACT
                                    C
GAM97   FLJ10640 5' GCCTAGGCTGAGTGCAGTG   39236         C
                                 CACTGCACTC AGCCTGGGT
                                 |||||||||| |||||||||
                                 GTGACGTGAG TCGGATCCG
                                          _
GAM97   FLJ10687 3' GCCCAGGCAGGAGTACAGT   36948     C    A
                                 ACTG ACTCC GCCTGGGT
                                 |||| ||||| ||||||||
                                 TGAC TGAGG CGGACCCG
                                   A    A
GAM97   FLJ10713 3' GTTGCCCAGGCTGGAGTGCAGT 37005               TG
            G                    CACTGCACTCCAGCCTGGG  AC
                                 |||||||||||||||||  ||
                                 GTGACGTGAGGTCGGACCC  TG
                                              GT
GAM97   FLJ10716 5' GCCCAGACTGGAATACAGTG  37019      CAC    C
                                 CACTG   TCCAG CTGGGT
                                 |||||   ||||| ||||||
                                 GTGAC   AGGTC GACCCG
                                    ATA    A
GAM97   FLJ10719 3' GTCACCTATAGAGTGCA     63207       CAGCC
                                 TGCACTC    TGGGTGAC
                                 |||||||    ||||||||
                                 ACGTGAG    ATCCACTG
                                     AT___
GAM97   FLJ10737 3' CACCCACCTCCAGAGTGCAGTG 37051          CAGCC_
                                 CACTGCACTC     TGGGTG
                                 ||||||||||     ||||||
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                              GTGACGTGAG     ACCCAC
                                   ACCTCC
GAM97   FLJ10846 3' GTCACCCAGGCTGGAGTGCAGT 37290
            G                   CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCACTG

GAM97   FLJ10847 3' GTCATGCAGGCTGGAGTGCGGT 37302              G
            G                   CACTGCACTCCAGCCTG GTGAC
                                |||||||||||||||| |||||
                                GTGGCGTGAGGTCGGAC TACTG
                                          G
GAM97   FLJ10900 3' ACCGGGGCTGGAGCGGAGTG  37343     GCA       G
                                CACT   CTCCAGCCT GGT
                                ||||   ||||||||| |||
                                GTGA   GAGGTCGGG CCA
                                  GGC        G
GAM97   FLJ10900 3' ACCGGGGCTGGAGCGGAGTG  66201     GCA       G
                                CACT   CTCCAGCCT GGT
                                ||||   ||||||||| |||
                                GTGA   GAGGTCGGG CCA
                                  GGC        G
GAM97   FLJ10901 3' GCCCAGGCTGGAATGCTGT   37365    T   C
                                AC GCA TCCAGCCTGGGT
                                || ||| ||||||||||||
                                TG CGT AGGTCGGACCCG
                                 T   A
GAM97   FLJ10922 3' GTTGCCCAGGCTGGAATGCAAT 37407    C    C         TG
            G                   CA TGCA TCCAGCCTGGG  AC
                                || |||| ||||||||||  ||
                                GT ACGT AGGTCGGACCC  TG
                                 A   A         GT
GAM97   FLJ10956 3' GCCCACATTGGAGTGCAGTG  37468           CC
                                CACTGCACTCCAG  TGGGT
                                ||||||||||||  |||||
                                GTGACGTGAGGTT  ACCCG
                                       AC
GAM97   FLJ10989 3' TTTAGGCTGGGTGCAGTG    37511         T
                                CACTGCAC CCAGCCTGGG
                                |||||||| ||||||||||
                                GTGACGTG GGTCGGATTT
                                       _
GAM97   FLJ10998 3' GTCACCCAAGCAGGATTGCAGT 37522        C   A  C
            G                   CACTGCA TCC GC TGGGTGAC
                                ||||||| ||| || ||||||||
                                GTGACGT AGG CG ACCCACTG
                                    T   A  A
GAM97   FLJ11004 5' GCCCAGACTGGAGTGCTGTG  37532     T       C
                                CAC GCACTCCAG CTGGGT
                                ||| ||||||||| ||||||
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                                GTG CGTGAGGTC GACCCG
                                  T       A
GAM97   FLJ11029 3' ACCCAGCTGGGTGCAGTG    61629        T    C
                                CACTGCAC CCAGC TGGGT
                                |||||||| ||||| |||||
                                GTGACGTG GGTCG ACCCA
                                      _    _
GAM97   FLJ11467 3' GTCACCCAGGCTGGAGTACAGT 46976      C
            G                    CACTG ACTCCAGCCTGGGTGAC
                                 ||||| ||||||||||||||||
                                 GTGAC TGAGGTCGGACCCACTG
                                   A
GAM97   FLJ11710 3' GTCTCCCAGGCTGGAGTGCAGT 46249              T
            G                    CACTGCACTCCAGCCTGGG GAC
                                 |||||||||||||||||| |||
                                 GTGACGTGAGGTCGGACCC CTG
                                        T
GAM97   FLJ11710 5' TTGAGGCTGGATGCAGTG    46254       C      G
                                CACTGCA TCCAGCCT GG
                                ||||||| |||||||| ||
                                GTGACGT AGGTCGGA TT
                                   _      G
GAM97   FLJ11715 3' GTTGCCCAGGCTGGAGGGCAGT 44982       A         TG
            G                    CACTGC CTCCAGCCTGGG  AC
                                 |||||| |||||||||||  ||
                                 GTGACG GAGGTCGGACCC  TG
                                    G          GT
GAM97   FLJ11800 3' GTCACCCAGGCCGGAGTGCAGT 47040          A
            G                    CACTGCACTCC GCCTGGGTGAC
                                 |||||||||| ||||||||||
                                 GTGACGTGAGG CGGACCCACTG
                                       C
GAM97   FLJ12363 3' GTCCCCCAGGCTGGAGTGCCGT 50639     T          T
            G                    CAC GCACTCCAGCCTGGG GAC
                                 ||| |||||||||||||| |||
                                 GTG CGTGAGGTCGGACCC CTG
                                   C           C
GAM97   FLJ12572 5' GTCACCCAGGCTGGAGTATAGT 43545      C
            G                    CACTG ACTCCAGCCTGGGTGAC
                                 ||||| ||||||||||||||||
                                 GTGAT TGAGGTCGGACCCACTG
                                   A
GAM97   FLJ12581 3' GTCGCCCAGGCTGGAGTGCAGT 46341
            G                    CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCGCTG

GAM97   FLJ12649 3' GCCCAGGCTGCAGTGCAGTG   45092         C
                                CACTGCACT CAGCCTGGGT
                                ||||||||| ||||||||||
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                                GTGACGTGA GTCGGACCCG
                                      C
GAM97   FLJ12666 3' ATTTGGGCTGGGCGCAGTG   45063       A T     TG
                                CACTGC C CCAGCC  GGT
                                |||||| | ||||||  |||
                                GTGACG G GGTCGG  TTA
                                   C _     GT
GAM97   FLJ12668 3' GTTGCCCAGGCTGGAGTACAGT 47160       C          TG
           G                     CACTG ACTCCAGCCTGGG  AC
                                ||||| ||||||||||||  ||
                                GTGAC TGAGGTCGGACCC  TG
                                   A           GT
GAM97   FLJ12747 3' GTCACCCAGGCTGGAGTGCAAT 50670    C
           G                     CA TGCACTCCAGCCTGGGTGAC
                                || ||||||||||||||||||
                                GT ACGTGAGGTCGGACCCACTG
                                 A
GAM97   FLJ12787 3' TCGCCCAGGCTGGAGTACAGTG 50696       C
                                CACTG ACTCCAGCCTGGGTGA
                                ||||| ||||||||||||||||
                                GTGAC TGAGGTCGGACCCGCT
                                   A
GAM97   FLJ12876 3' GTCACCCAGGCTGGAGTGCAGT 43098
           G                     CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCACTG

GAM97   FLJ12888 3' GTTGCCCAGGCTAGAGTGCAGT 46891          C       TG
           G                     CACTGCACTC AGCCTGGG  AC
                                |||||||||| ||||||||  ||
                                GTGACGTGAG TCGGACCC  TG
                                      A       GT
GAM97   FLJ12891 3' GTCACCCAGGTTAGAGTGTAGT 46931          C
           G                     CACTGCACTC AGCCTGGGTGAC
                                |||||||||| ||||||||||||
                                GTGATGTGAG TTGGACCCACTG
                                      A
GAM97   FLJ12903 3' GTTGCCCAGGCTGGAGTGCAAT 43076    C          TG
           G                     CA TGCACTCCAGCCTGGG  AC
                                || ||||||||||||||||  ||
                                GT ACGTGAGGTCGGACCC  TG
                                 A             GT
GAM97   FLJ12960 3' GTCGCCCAGGCTGGAGTGCAGT 45304
           G                     CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCGCTG

GAM97   FLJ12973 3' GTTGCCCAGGCTGGAGTGCA   46643             TG
                                TGCACTCCAGCCTGGG  AC
                                ||||||||||||||||  ||
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                                ACGTGAGGTCGGACCC  TG
                                      GT
GAM97   FLJ12975 3' GTCACCCAGGCTGGAGTGCAGT 70197
            G                  CACTGCACTCCAGCCTGGGTGAC
                               ||||||||||||||||||||||
                               GTGACGTGAGGTCGGACCCACTG

GAM97   FLJ13072 5' GTCGGCCAGGCTGGAGTGCAGT 91395              G
            G                  CACTGCACTCCAGCCTGG TGAC
                               |||||||||||||||| ||||
                               GTGACGTGAGGTCGGACC GCTG
                                     G
GAM97   FLJ13114 3' GTCGCCCAGGCTGGAATGCAGT 44907       C
            G                  CACTGCA TCCAGCCTGGGTGAC
                               ||||||| ||||||||||||||
                               GTGACGT AGGTCGGACCCGCTG
                                  A
GAM97   FLJ13188 3' GTCACCCAGGCTAGAGTGCAGT 42194        C
                               ACTGCACTC AGCCTGGGTGAC
                               ||||||||| ||||||||||||
                               TGACGTGAG TCGGACCCACTG
                                    A
GAM97   FLJ13193 3' CCCAGGCTGGAGTACAGTG   50717      C
                               CACTG ACTCCAGCCTGGG
                               ||||| ||||||||||||
                               GTGAC TGAGGTCGGACCC
                                  A
GAM97   FLJ13197 3' GTTGCCCAGGCTGGAGTGCAGT 45182              TG
            G                  CACTGCACTCCAGCCTGGG  AC
                               ||||||||||||||||||  ||
                               GTGACGTGAGGTCGGACCC  TG
                                     GT
GAM97   FLJ13456 3' GTCGCCCAAGCTGGAGTGCAGT 66559           C
            G                  CACTGCACTCCAGC TGGGTGAC
                               |||||||||||||| ||||||||
                               GTGACGTGAGGTCG ACCCGCTG
                                     A
GAM97   FLJ13590 5' TCAGGCTTGAGTGCAGTG    46207         C
                               CACTGCACTC AGCCTGG
                               |||||||||| |||||||
                               GTGACGTGAG TCGGACT
                                    T
GAM97   FLJ13952 3' GTTGCCCAGGCTGGAATGCAGT 46018       C       TG
            G                  CACTGCA TCCAGCCTGGG  AC
                               ||||||| ||||||||||  ||
                               GTGACGT AGGTCGGACCC  TG
                                  A        GT
GAM97   FLJ13984 5' GTCACCTAGGCTGGAGTGCAGT 45811
            G                  CACTGCACTCCAGCCTGGGTGAC
                               ||||||||||||||||||||||
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                                GTGACGTGAGGTCGGATCCACTG

GAM97   FLJ14326 3' GCTCAGGCTGGGTGCAGTG   50776        T
                                CACTGCAC CCAGCCTGGGT
                                |||||||| ||||||||||
                                GTGACGTG GGTCGGACTCG
                                    _
GAM97   FLJ14346 3' CCGGCCAGAGTGCGGTG     47361         CA  T
                                CACTGCACTC  GCC GG
                                ||||||||||  ||| ||
                                GTGGCGTGAG  CGG CC
                                      AC  _
GAM97   FLJ14351 3' GTCGCCCAGGCTGGAGTGCAGT 45649
            G                    CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCGCTG

GAM97   FLJ14442 3' GTTACCCAGGCTAGAGTGTAGT 52389          C
            G                    CACTGCACTC AGCCTGGGTGAC
                                |||||||||| ||||||||||||
                                GTGATGTGAG TCGGACCCATTG
                                      A
GAM97   FLJ14950 3' GTCACCCAGGCTGAACTGCAGT 52796        CTC
            G                    CACTGCA   CAGCCTGGGTGAC
                                |||||||   ||||||||||||
                                GTGACGT   GTCGGACCCACTG
                                    CAA
GAM97   FLJ14957 3' GCCGAGGCTGGAGTGCAATG   52822    C         G
                                CA TGCACTCCAGCCT GGT
                                || ||||||||||||| |||
                                GT ACGTGAGGTCGGA CCG
                                 A           G
GAM97   FLJ20034 3' GTTGCCCAGGCTGGAGTACAAT 34853    C  C          TG
            G                    CA TG ACTCCAGCCTGGG  AC
                                || || ||||||||||||  ||
                                GT AC TGAGGTCGGACCC  TG
                                 A  A           GT
GAM97   FLJ20045 3' GTTTCCCAGGCTGGAGTGCAGT 34890               T
            G                    CACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||| |||
                                GTGACGTGAGGTCGGACCC TTG
                                           T
GAM97   FLJ20079 3' GTTGCCCAGGCTGGAGTGCAAT 34974    C           TG
            G                    CA TGCACTCCAGCCTGGG  AC
                                || ||||||||||||||  ||
                                GT ACGTGAGGTCGGACCC  TG
                                 A             GT
GAM97   FLJ20136 3' GTCGCCCAGGCTGGAATGCAGT 35099        C
            G                    CACTGCA TCCAGCCTGGGTGAC
                                ||||||| ||||||||||||||
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                                GTGACGT AGGTCGGACCCGCTG
                                    A
GAM97   FLJ20147 3' GTTGCCCAGGCTAGAGTGCAG 35136       C      TG
                                CTGCACTC AGCCTGGG AC
                                ||||||| |||||||| ||
                                GACGTGAG TCGGACCC TG
                                    A      GT
GAM97   FLJ20344 3' GTCATCCAAACTGGAGTGCAGT 35486          CC
           G                     CACTGCACTCCAG TGGGTGAC
                                ||||||||||||| ||||||||
                                GTGACGTGAGGTC ACCTACTG
                                      AA
GAM97   FLJ20452 3' TCACTAAAGGCCAGGTGCAGTG 35651        CCA  G_
                                CACTGCACT  GCCT GGTGA
                                ||||||||| |||| |||||
                                GTGACGTGG  CGGA TCACT
                                     AC_   AA
GAM97   FLJ20507 3' GTCACCCGGGCTGGAGTGTA  35749
                                TGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||
                                ATGTGAGGTCGGGCCCACTG

GAM97   FLJ20507 3' GTCACCCGGGCTGGAGTGTA  60853
                                TGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||
                                ATGTGAGGTCGGGCCCACTG

GAM97   FLJ20511 3' GTCACCCAGGCTGGAGTGCAGT 35779
           G                     CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCACTG

GAM97   FLJ20671 3' GTTGCCCAGGCTGGAGTGCAGT 35943             TG
           G                     CACTGCACTCCAGCCTGGG AC
                                |||||||||||||||||| ||
                                GTGACGTGAGGTCGGACCC TG
                                      GT
GAM97   FLJ20700 3' GCCCAGGCTGGAGTGCAGTG  36010
                                CACTGCACTCCAGCCTGGGT
                                ||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCG

GAM97   FLJ20813 3' TCACCCAGGCTGGAGTGCAGTG 36135
                                CACTGCACTCCAGCCTGGGTGA
                                ||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCACT

GAM97   FLJ21162 3' CTTGGGCTGGGTGCAGTG   46372       T    TG
                                CACTGCAC CCAGCC  GG
                                |||||||| ||||||  ||
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                                GTGACGTG GGTCGG  TC
                                   _     GT
GAM97   FLJ21302 3' GTCTCCCAGGCTGGACTGCAG  43513      C        T
                                CTGCA TCCAGCCTGGG GAC
                                ||||| |||||||||| |||
                                GACGT AGGTCGGACCC CTG
                                   C         T
GAM97   FLJ21324 5' CACCCAGGCTGGCGTGCAGTG  92846        T
                                CACTGCAC CCAGCCTGGGTG
                                |||||||| ||||||||||||
                                GTGACGTG GGTCGGACCCAC
                                     C
GAM97   FLJ21459 3' GTCACCCAGGCTGGGGTGCAGT 44810
           G                     CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||||
                                 GTGACGTGGGGTCGGACCCACTG

GAM97   FLJ21603 3' GTCACCCAGGCTGGAGTACAGT 45775      C
           G                     CACTG ACTCCAGCCTGGGTGAC
                                 ||||| ||||||||||||||||
                                 GTGAC TGAGGTCGGACCCACTG
                                    A
GAM97   FLJ21736 5' ATCCAGGCTGCAGTGCAG    46778       C
                                CTGCACT CAGCCTGGGT
                                ||||||| |||||||||
                                GACGTGA GTCGGACCTA
                                     C
GAM97   FLJ21777 3' GTCACCCAGGCTGGAGTGCAAT 50847    C
           G                     CA TGCACTCCAGCCTGGGTGAC
                                 || ||||||||||||||||||
                                 GT ACGTGAGGTCGGACCCACTG
                                  A
GAM97   FLJ22167 5' ACTCAGGCTGCAGTGCAGTG   44856        C
                                CACTGCACT CAGCCTGGGT
                                ||||||||| |||||||||
                                GTGACGTGA GTCGGACTCA
                                     C
GAM97   FLJ22316 5' GTCTCCCAGGCTGGAGTGCAGT 47616              T
           G                     CACTGCACTCCAGCCTGGG GAC
                                 |||||||||||||||||| |||
                                 GTGACGTGAGGTCGGACCC CTG
                                              T
GAM97   FLJ22329 3' GTCACCCAGGCTGGAGTGCAGT 45406
           G                     CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCACTG

GAM97   FLJ22531 5' GTTACCCAGGCCGGAGTGCAGT 45373          A
           G                     CACTGCACTCC GCCTGGGTGAC
                                 |||||||||| ||||||||||
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                                GTGACGTGAGG CGGACCCATTG
                                      C
GAM97   FLJ22644 3' GCTCAGCCTGGAGTGCAGTG  47701          C
                                CACTGCACTCCAG CTGGGT
                                |||||||||||| ||||||
                                GTGACGTGAGGTC GACTCG
                                     C
GAM97   FLJ22794 3' GCCTGGGCTGGAGTACAGTG  93248      C       TG
                                CACTG ACTCCAGCC  GGT
                                ||||| |||||||||  |||
                                GTGAC TGAGGTCGG  CCG
                                   A        GT
GAM97   FLJ22795 3' GCTGGCTGGAGTGAG       47636    G       TG
                                CT CACTCCAGCC  GGT
                                || ||||||||||  |||
                                GA GTGAGGTCGG  TCG

                                _        __
GAM97   FLJ22965 3' GCCCAGGATGGAGTGCAGTG  42299          G
                                CACTGCACTCCA CCTGGGT
                                |||||||||||| |||||||
                                GTGACGTGAGGT GGACCCG
                                      A
GAM97   FLJ22969 3' GCCTAGGCTGGAGTGCAGTG  69209
                                CACTGCACTCCAGCCTGGGT
                                ||||||||||||||||||||
                                GTGACGTGAGGTCGGATCCG

GAM97   FLJ23024 3' GTCTCCCAGGCTAGAGTGCAAT 46845   C     C       T
           G                     CA TGCACTC AGCCTGGG GAC
                                || ||||||| |||||||| |||
                                GT ACGTGAG TCGGACCC CTG
                                 A      A       T
GAM97   FLJ23040 3' TCACCCAAGCCAGAGTGCAGTG 47990          CA  C
                                CACTGCACTC  GC TGGGTGA
                                ||||||||||  || |||||||
                                GTGACGTGAG  CG ACCCACT
                                      AC  A
GAM97   FLJ23040 3' TTGAGGCTGGGTGCAGTG    47995        T      G
                                CACTGCAC CCAGCCT GG
                                |||||||| ||||||| ||
                                GTGACGTG GGTCGGA TT
                                     _      G
GAM97   FLJ23053 3' TTGCCCAGGCTGGAGTGCAGTG 43558                TG
                                CACTGCACTCCAGCCTGGG  A
                                |||||||||||||||||||  |
                                GTGACGTGAGGTCGGACCC  T
                                        GT
GAM97   FLJ23186 3' GCTTAGCTGGAGTGCGGTG   61042          C
                                CACTGCACTCCAGC TGGGT
                                |||||||||||||| |||||
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                                GTGGCGTGAGGTCG ATTCG
                                               _
GAM97   FLJ23263  5' GTCGCCCAGGCTGGAGTGCAGT 47803
              G                 CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCGCTG

GAM97   FLJ23356  3' GCTGAGGCTGGAGTGCAGTG  50924            G
                                CACTGCACTCCAGCCT GGT
                                |||||||||||||||| |||
                                GTGACGTGAGGTCGGA TCG
                                          G
GAM97   FLJ23392  3' GTCACCCAGACTGGAGTGCAGT 45904          C
              G                 CACTGCACTCCAG CTGGGTGAC
                                |||||||||||| |||||||||
                                GTGACGTGAGGTC GACCCACTG
                                       A
GAM97   FLJ23392  3' GTCACTGAGGCTGGAGTGCAGT 45906            G
              G                 CACTGCACTCCAGCCT GGTGAC
                                |||||||||||||||| ||||||
                                GTGACGTGAGGTCGGA TCACTG
                                          G
GAM97   FLJ23392  3' GTCCCCCAGGCTGGAGTGCAGT 45907              T
              G                 CACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||| |||
                                GTGACGTGAGGTCGGACCC CTG
                                        C
GAM97   FLJ23416  3' GTTGCCCAGGCTGGAGTGCAGT 50935              TG
              G                 CACTGCACTCCAGCCTGGG  AC
                                |||||||||||||||||  ||
                                GTGACGTGAGGTCGGACCC  TG
                                        GT
GAM97   FLJ23510  3' GCTGGCTAATGTGCAGTG   45625       TCC   TG
                                CACTGCAC  AGCC  GGT
                                ||||||||  ||||  |||
                                GTGACGTG  TCGG  TCG
                                    TAA   __
GAM97   FLJ23519  3' GTCACCCAGGCTGGAGTGCAGT 50956
              G                 CACTGCACTCCAGCCTGGGTGAC
                                |||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCACTG

GAM97   FLJ23556  3' GTCACCCAGGCTGGAGTACCGG 46451     C_
              T                  ACTG  ACTCCAGCCTGGGTGAC
                                 ||||  ||||||||||||||||
                                 TGGC  TGAGGTCGGACCCACTG
                                   CA
GAM97   FLJ23556  3' GTCGCCCAGGCTGGAGTGCAGT 46452
              G                 CACTGCACTCCAGCCTGGGTGAC
                                |||||||||||||||||||||||
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                                GTGACGTGAGGTCGGACCCGCTG

GAM97   FLJ23563 3' GTTGCCCAGGCTAGAGTGCAAT 68217    C      C       TG
            G                    CA TGCACTC AGCCTGGG  AC
                                 || ||||||| ||||||||  ||
                                 GT ACGTGAG TCGGACCC  TG
                                  A      A       GT
GAM97   FLJ25416 5' GTCACCCAGGCTGGAGTGC   59456
                                 GCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||
                                 CGTGAGGTCGGACCCACTG

GAM97   FLJ30532 3' GTTGCCCAGGCTGGAGTACAGT 59225       C          TG
            G                    CACTG ACTCCAGCCTGGG  AC
                                 ||||| ||||||||||||  ||
                                 GTGAC TGAGGTCGGACCC  TG
                                    A           GT
GAM97   FLJ31101 3' GTCGCCCAGGCTGGAATGCAGT 36169        C
            G                    CACTGCA TCCAGCCTGGGTGAC
                                 ||||||| ||||||||||||||
                                 GTGACGT AGGTCGGACCCGCTG
                                     A
GAM97   FLJ31153 3' GTCACCCAGACTGGAGTGCAGT 58751           C
            G                    CACTGCACTCCAG CTGGGTGAC
                                 |||||||||||| |||||||||
                                 GTGACGTGAGGTC GACCCACTG
                                        A
GAM97   FLJ32499 3' GTCACCCAGTCTGGAGTGCAGT 58781           C
            G                    CACTGCACTCCAG CTGGGTGAC
                                 |||||||||||| |||||||||
                                 GTGACGTGAGGTC GACCCACTG
                                        T
GAM97   FLJ32865 3' GTCACCCAGGCTGGAGTACAAT 58819    C  C
            G                    CA TG ACTCCAGCCTGGGTGAC
                                 || || ||||||||||||||||
                                 GT AC TGAGGTCGGACCCACTG
                                  A  A
GAM97   FTSJ3    3' TCACAGCTGTCTGAAGAACAGT 34937      CA  C  _ CTGG
            G                    CACTG  CT CAG C    GTGA
                                 |||||  || ||| |    ||||
                                 GTGAC  GA GTC G    CACT
                                    AA  A   T TCGA
GAM97   GAL3ST-4  3' GTCCCCCAGGCTGGAGTGCAGT 45280              T
            G                    CACTGCACTCCAGCCTGGG GAC
                                 |||||||||||||||||| |||
                                 GTGACGTGAGGTCGGACCC CTG
                                           C
GAM97   GALNT6   3' TTCAGGCTGGGCACAGTG    24254       CA T
                                 CACTG  C CCAGCCTGGG
                                 |||||  | ||||||||||
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                                GTGAC  G GGTCGGACTT
                                  AC _
GAM97   GGA2     3'  GTCACTCAGGCTGGAGTGCGGT 31170
            G                    CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGGCGTGAGGTCGGACTCACTG

GAM97   GGA2     3'  GTCACTCAGGCTGGAGTGCGGT 57674
            G                    CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGGCGTGAGGTCGGACTCACTG

GAM97   GMPPB    5'  GCCCAGGCTGGAGTGCGATG  97452    C
                                 CA TGCACTCCAGCCTGGGT
                                 || ||||||||||||||||
                                 GT GCGTGAGGTCGGACCCG
                                  A
GAM97   GNG4     3'  GTCACCCAGGCTGGAGTGCAAT 16852    C
            G                    CA TGCACTCCAGCCTGGGTGAC
                                 || ||||||||||||||||||
                                 GT ACGTGAGGTCGGACCCACTG
                                  A
GAM97   GOLGA3   3'  GTTGCCCAGGCTGGAGTGCAGT 20894                TG
            G                    CACTGCACTCCAGCCTGGG  AC
                                 ||||||||||||||||||  ||
                                 GTGACGTGAGGTCGGACCC  TG
                                       GT
GAM97   GP5      3'  GTGGCCCAGGCTGGCGTGCAGT 16881        T        G
            G                    CACTGCAC CCAGCCTGGGT AC
                                 |||||||| |||||||||| ||
                                 GTGACGTG GGTCGGACCCG TG
                                     C         G
GAM97   GR6      5'  GTCACCCAGGCTGGAATGCAGT 24747        C
            G                    CACTGCA TCCAGCCTGGGTGAC
                                 ||||||| ||||||||||||||
                                 GTGACGT AGGTCGGACCCACTG
                                     A
GAM97   GREB1    3'  GTCACCCAGGCTGGAGTGCAGT 28577
            G                    CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCACTG

GAM97   GREB1    3'  TGCCCAGGCTGGAGTGCAATG  28581    C
                                 CA TGCACTCCAGCCTGGGTG
                                 || ||||||||||||||||
                                 GT ACGTGAGGTCGGACCCGT
                                  A
GAM97   GRWD     3'  GTCGCCCAGGCTGGAGTGCAGT 49787
                                 ACTGCACTCCAGCCTGGGTGAC
                                 |||||||||||||||||||||
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                                TGACGTGAGGTCGGACCCGCTG

GAM97   GTF2E1   3'  CCCAGGCTGGAGTGCAATG   19794    C
                                CA TGCACTCCAGCCTGGG
                                || ||||||||||||||||
                                GT ACGTGAGGTCGGACCC
                                 A
GAM97   GTPBG3   3'  GTCACCCAGGCTGGAGTTCAGT 51905      C
           G                     CACTG ACTCCAGCCTGGGTGAC
                                ||||| ||||||||||||||||||
                                GTGAC TGAGGTCGGACCCACTG
                                   T
GAM97   GTPBG3   3'  TTGCCCAGGCTGGAGTGCAGTG 51910              TG
                                CACTGCACTCCAGCCTGGG  A
                                |||||||||||||||||||  |
                                GTGACGTGAGGTCGGACCC  T
                                             GT
GAM97   H-plk    5'  GTCACCAGGATGGAGTGCAGTG 32387          G    G
                                CACTGCACTCCA CCTGG TGAC
                                |||||||||||| ||||| ||||
                                GTGACGTGAGGT GGACC ACTG
                                       A    _
GAM97   H2AV     3'  GTCACCCAGACTGGAGTGCGAT 57632    C       C
           G                     CA TGCACTCCAG CTGGGTGAC
                                || |||||||||| |||||||||
                                GT GCGTGAGGTC GACCCACTG
                                 A         A
GAM97   HCA4     3'  GTCGCCCAGGCTGGAGTGCATT 78043    C
           G                     CA TGCACTCCAGCCTGGGTGAC
                                || ||||||||||||||||||||
                                GT ACGTGAGGTCGGACCCGCTG
                                 T
GAM97   HEYL     3'  GCCAAGAGGCTGGAACATAGTG 28127      CAC      G__
                                CACTG   TCCAGCCT   GGT
                                |||||   ||||||||   |||
                                GTGAT   AGGTCGGA   CCG
                                   ACA       GAA
GAM97   HRH4     3'  GCCCACGCAGGAGTGCAGTG   41541          A  C
                                CACTGCACTCC GC TGGGT
                                |||||||||| || |||||
                                GTGACGTGAGG CG ACCCG
                                       A  C
GAM97   HRH4     3'  GTCACCCAGGCTGGAGTGCAGT 41546
                                ACTGCACTCCAGCCTGGGTGAC
                                |||||||||||||||||||||
                                TGACGTGAGGTCGGACCCACTG

GAM97   HRH4     3'  GTCTCCCAGGCTGGAGCGTAGT 41547      A         T
                                ACTGC CTCCAGCCTGGG GAC
                                ||||| |||||||||||| |||
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                                TGATG GAGGTCGGACCC CTG
                                  C          T
GAM97   HSC3     3'  ACTTAGCTGGGTGCAGTG    59728        T    C
                                CACTGCAC CCAGC TGGGT
                                |||||||| ||||| |||||
                                GTGACGTG GGTCG ATTCA
                                      _    _
GAM97   HSMPP8   3'  GTTGCCCAGGCTGGAGTGCAAT 95139    C            TG
           G                     CA TGCACTCCAGCCTGGG  AC
                                 || ||||||||||||||||  ||
                                 GT ACGTGAGGTCGGACCC  TG
                                  A             GT
GAM97   HSNOV1   3'  CAGAGTCTAGAGTGCAGTG   34430          C _ _
                                CACTGCACTC AG C CTG
                                |||||||||| || | |||
                                GTGACGTGAG TC G GAC
                                      A  T A
GAM97   ICK      3'  GTCACCCAGGCTGGAGTGCAGT 30599
           G                     CACTGCACTCCAGCCTGGGTGAC
                                 |||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCACTG

GAM97   IMPACT   3'  GTCACCTAGGCTGGAGTGCAGT 38009
           G                     CACTGCACTCCAGCCTGGGTGAC
                                 |||||||||||||||||||||||
                                 GTGACGTGAGGTCGGATCCACTG

GAM97   INPP5E   3'  GCCCAGCGCTGGAGTGCAG   73506          _
                                CTGCACTCCAGC CTGGGT
                                |||||||||||| ||||||
                                GACGTGAGGTCG GACCCG
                                      C
GAM97   JAM1     3'  GTCACCCAGGCTGGAGTGCAGT 58524
           G                     CACTGCACTCCAGCCTGGGTGAC
                                 |||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCACTG

GAM97   JAM1     3'  GTCACCCAGGCTGGAGTGCAGT 58551
           G                     CACTGCACTCCAGCCTGGGTGAC
                                 |||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCACTG

GAM97   JAM1     3'  GTCACCCAGGCTGGAGTGCAGT 58580
           G                     CACTGCACTCCAGCCTGGGTGAC
                                 |||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCACTG

GAM97   JAM1     3'  GTCACCCAGGCTGGAGTGCAGT 34242
           G                     CACTGCACTCCAGCCTGGGTGAC
                                 |||||||||||||||||||||||
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                                GTGACGTGAGGTCGGACCCACTG

GAM97   JM11     3' GTCACCAGGCTGGAGTGCAG  54370            G
                                CTGCACTCCAGCCTGG TGAC
                                |||||||||||||||| ||||
                                GACGTGAGGTCGGACC ACTG
                                                _
GAM97   JWA      3' CACCTGTTTGATGTGCAGTG  22158       _ C  CT
                                CACTGCAC TC AGC  GGGTG
                                |||||||| || |||  |||||
                                GTGACGTG AG TTG  TCCAC
                                     T  T  __
GAM97   KIAA0022 3' GCCCAGGCTACAGTGCAGTG  30282        CC
                                CACTGCACT  AGCCTGGGT
                                |||||||||  |||||||||
                                GTGACGTGA  TCGGACCCG
                                      CA
GAM97   KIAA0063 3' GTTGCCCAGGCTGGAGTGCAAT 30260    C          TG
           G                     CA TGCACTCCAGCCTGGG  AC
                                || ||||||||||||||||  ||
                                GT ACGTGAGGTCGGACCC  TG
                                 A            GT
GAM97   KIAA0087 3' GTCACCCAGGCTGGAGTGCAGT 29346
           G                     CACTGCACTCCAGCCTGGGTGAC
                                |||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCACTG

GAM97   KIAA0090 3' GTCACCCAGGCTGGAGAGCAGT 89817       A
           G                     CACTGC CTCCAGCCTGGGTGAC
                                ||||||| ||||||||||||||||
                                GTGACG GAGGTCGGACCCACTG
                                   A
GAM97   KIAA0161 3' GTCCCCCAAGCTGGAGTACAAT 29206    C C      C   T
           G                     CA TG ACTCCAGC TGGG GAC
                                || || |||||||| |||| |||
                                GT AC TGAGGTCG ACCC CTG
                                 A A       A   C
GAM97   KIAA0186 3' GTCACCCAGGCTGGGGTGCAGT 41112
           G                     CACTGCACTCCAGCCTGGGTGAC
                                |||||||||||||||||||||||
                                GTGACGTGGGGTCGGACCCACTG

GAM97   KIAA0205 3' GTCACCCAGGCTGTAGTGCAGT 30216        C
           G                     CACTGCACT CAGCCTGGGTGAC
                                |||||||||  ||||||||||||
                                GTGACGTGA GTCGGACCCACTG
                                      T
GAM97   KIAA0210 5' GCCCAGGCTGGAGTGCAGTG  29161
                                CACTGCACTCCAGCCTGGGT
                                ||||||||||||||||||||
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                                GTGACGTGAGGTCGGACCCG

GAM97   KIAA0210 5' GTCGCCCAGGCTGGAGTGCAGT 29171
                G                CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCGCTG

GAM97   KIAA0226 3' ATCCAGGCCAGGCACAGTG  64252      CACT  A_
                                 CACTG   CC  GCCTGGGT
                                 |||||   ||  ||||||||
                                 GTGAC   GG  CGGACCTA
                                    AC__  AC
GAM97   KIAA0391 3' ATCTAGGCTGGAGTGCAATG  28600    C
                                 CA TGCACTCCAGCCTGGGT
                                 || ||||||||||||||||
                                 GT ACGTGAGGTCGGATCTA
                                  A
GAM97   KIAA0418 5' GCTCAGGCTGGATTGCAGTG  28295       C
                                 CACTGCA TCCAGCCTGGGT
                                 ||||||| ||||||||||||
                                 GTGACGT AGGTCGGACTCG
                                      T
GAM97   KIAA0426 3' GTCGCCCAGGCTGGAGTGCAAT 28931    C
                G                CA TGCACTCCAGCCTGGGTGAC
                                 || ||||||||||||||||||||
                                 GT ACGTGAGGTCGGACCCGCTG
                                  A
GAM97   KIAA0427 3' TCTCTGGGGGCTGGAGCACA  29391    CA      _ G  T
                                 TG  CTCCAGCC T GG GA
                                 ||  |||||||| | || ||
                                 AC  GAGGTCGG G TC CT
                                  AC       G G  T
GAM97   KIAA0435 5' GTCACCCAGTTTGGAGTGCAGT 29663           C
                G                CACTGCACTCCAG CTGGGTGAC
                                 |||||||||||| |||||||||
                                 GTGACGTGAGGTT GACCCACTG
                                         T
GAM97   KIAA0441 3' TCACCCAGGCCAGAGTGTAGTG 29643         CA
                                 CACTGCACTC  GCCTGGGTGA
                                 ||||||||||  ||||||||||
                                 GTGATGTGAG  CGGACCCACT
                                       AC
GAM97   KIAA0446 5' GTCTCCTAGGCTGGAGTGCAGT 69456              T
                G                CACTGCACTCCAGCCTGGG GAC
                                 |||||||||||||||||| |||
                                 GTGACGTGAGGTCGGATCC CTG
                                             T
GAM97   KIAA0447 3' GTCACCCAGGCTGGAGTACAGT 72127      C
                G                CACTG ACTCCAGCCTGGGTGAC
                                 ||||| ||||||||||||||||
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                                GTGAC TGAGGTCGGACCCACTG
                                  A
GAM97   KIAA0469 3' GTCACCCAGGCTGGAGTGCAGT 29991
            G                    CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCACTG

GAM97   KIAA0469 3' GTCACCCAGGCTGGAGTGCAGT 29992
            G                    CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCACTG

GAM97   KIAA0472 5' GTCACCCATTCTGGAGTACAAT 72362    C  C      CC
            G                    CA TG ACTCCAG  TGGGTGAC
                                 || || |||||||  ||||||||
                                 GT AC TGAGGTC  ACCCACTG
                                  A  A      TT
GAM97   KIAA0475 3' GTTGCCCAGGCTGGAGTGCAGT 30127              TG
            G                    CACTGCACTCCAGCCTGGG  AC
                                 ||||||||||||||||||  ||
                                 GTGACGTGAGGTCGGACCC  TG
                                           GT
GAM97   KIAA0478 3' GTCACCCAGACTGGAACACAGT 30182      CAC    C
            G                    CACTG   TCCAG CTGGGTGAC
                                 |||||   ||||| |||||||||
                                 GTGAC   AGGTC GACCCACTG
                                   ACA    A
GAM97   KIAA0493 5' ACCCAAGCTGGAGTGCAGTG   64925           C
                                 CACTGCACTCCAGC TGGGT
                                 |||||||||||||| |||||
                                 GTGACGTGAGGTCG ACCCA
                                        A
GAM97   KIAA0495 3' GTCACCCAGGCTGGAGTGCAAT 63272    C
            G                    CA TGCACTCCAGCCTGGGTGAC
                                 || ||||||||||||||||||||
                                 GT ACGTGAGGTCGGACCCACTG
                                  A
GAM97   KIAA0513 3' GCCTGCAGAGTGCAGTG     29040         CA  CT
                                 CACTGCACTC  GC  GGGT
                                 |||||||||  ||  ||||
                                 GTGACGTGAG  CG  TCCG
                                       A_  __
GAM97   KIAA0513 3' GTTGCCCAGGCTGGAGTGCAGT 29048              TG
            G                    CACTGCACTCCAGCCTGGG  AC
                                 ||||||||||||||||||  ||
                                 GTGACGTGAGGTCGGACCC  TG
                                           GT
GAM97   KIAA0513 5' TTTCCCAGGCTGGAGTGCAG   29059             T
                                 CTGCACTCCAGCCTGGG GA
                                 |||||||||||||||| ||
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                                GACGTGAGGTCGGACCC TT
                                          T
GAM97   KIAA0527 3' GTTGCCCAGGCTGGAGTGCAGT 97500              TG
           G                 CACTGCACTCCAGCCTGGG  AC
                             ||||||||||||||||||  ||
                             GTGACGTGAGGTCGGACCC  TG
                                       GT
GAM97   KIAA0532 3' GTCACCCAGGCTAGAGTACAGT 71324      C   C
           G                 CACTG ACTC AGCCTGGGTGAC
                             ||||| |||| ||||||||||||
                             GTGAC TGAG TCGGACCCACTG
                               A   A
GAM97   KIAA0544 3' TGCCCAGGCTGGAGTGCAGTG  71477
                             CACTGCACTCCAGCCTGGGTG
                             |||||||||||||||||||||
                             GTGACGTGAGGTCGGACCCGT

GAM97   KIAA0555 3' GCCCATGCTGGAGTGCATTG   29551    C        C
                             CA TGCACTCCAGC TGGGT
                             || ||||||||||| |||||
                             GT ACGTGAGGTCG ACCCG
                              T         T
GAM97   KIAA0561 3' GCCCGGGCTGGAGTGCAG    66481
                             CTGCACTCCAGCCTGGGT
                             ||||||||||||||||||
                             GACGTGAGGTCGGGCCCG

GAM97   KIAA0562 3' GCCTAGGCTGGAGTGCAGTG   28825
                             CACTGCACTCCAGCCTGGGT
                             ||||||||||||||||||||
                             GTGACGTGAGGTCGGATCCG

GAM97   KIAA0563 5' GTTGCCCAGGCTGAAGTGCAGT 29887         C        TG
           G                 CACTGCACT CAGCCTGGG  AC
                             ||||||||| |||||||||  ||
                             GTGACGTGA GTCGGACCC  TG
                                   A        GT
GAM97   KIAA0594 3' GTTGCCCAGGCTGGAGTGCAGT 65516              TG
           G                 CACTGCACTCCAGCCTGGG  AC
                             ||||||||||||||||||  ||
                             GTGACGTGAGGTCGGACCC  TG
                                       GT
GAM97   KIAA0599 3' GTCACCCAGGCTGGAGTGCAAT 77697    C
           G                 CA TGCACTCCAGCCTGGGTGAC
                             || ||||||||||||||||||||
                             GT ACGTGAGGTCGGACCCACTG
                              A
GAM97   KIAA0599 3' GTCGCCCAGGCTGGAGCGCAGT 77699       A
           G                 CACTGC CTCCAGCCTGGGTGAC
                             ||||||  ||||||||||||||||
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                                GTGACG GAGGTCGGACCCGCTG
                                   C
GAM97   KIAA0682 3' ACCGAGAGGGCTGGAGTGCAGT 30007            G___
            G                   CACTGCACTCCAGCCT   GGT
                                |||||||||||||||   |||
                                GTGACGTGAGGTCGGG   CCA
                                      AGAG
GAM97   KIAA0720 3' GTCACCTAGGTTGGAGTGCAGT 62990
            G                   CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
                                GTGACGTGAGGTTGGATCCACTG

GAM97   KIAA0721 3' GCAAGGCTGGAACGCAGT   41654      AC      GG
                                ACTGC  TCCAGCCT  GT
                                |||||  ||||||||  ||
                                TGACG  AGGTCGGA  CG
                                   CA       A_
GAM97   KIAA0721 3' GCAAGGCTGGAACGCAGT   97657      AC      GG
                                ACTGC  TCCAGCCT  GT
                                |||||  ||||||||  ||
                                TGACG  AGGTCGGA  CG
                                   CA       A_
GAM97   KIAA0737 3' GTCACCCAGGCTGGAGTGCAGT 29816
            G                   CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCACTG

GAM97   KIAA0841 3' GTTGCCCAAGTTGGAGTGCAGT 71902            C   TG
            G                   CACTGCACTCCAGC TGGG  AC
                                |||||||||||||| ||||  ||
                                GTGACGTGAGGTTG ACCC  TG
                                      A   GT
GAM97   KIAA0841 3' GTTTCCCAGGCTGAAGTGCAGT 71904        C       T
            G                   CACTGCACT CAGCCTGGG GAC
                                ||||||||| ||||||||| |||
                                GTGACGTGA GTCGGACCC TTG
                                     A       T
GAM97   KIAA0861 3' GTCGCCCAGGCTGGAGTGCAGT 90358
            G                   CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCGCTG

GAM97   KIAA0889 3' GTCCCCCAGGCTTGAGTGCAAT 31783   C     C      T
            G                   CA TGCACTC AGCCTGGG GAC
                                || ||||||| |||||||| |||
                                GT ACGTGAG TCGGACCC CTG
                                 A      T      C
GAM97   KIAA0924 3' GCCTGGGCTGGAGTGCAGTG  30367            TG
                                CACTGCACTCCAGCC  GGT
                                |||||||||||||||  |||
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                                GTGACGTGAGGTCGG  CCG
                                      GT
GAM97   KIAA0924 3' GTTGCCCAGGCTAGAGTGCAGT 30372         C       TG
            G                    CACTGCACTC AGCCTGGG  AC
                                 |||||||||| ||||||||  ||
                                 GTGACGTGAG TCGGACCC  TG
                                       A       GT
GAM97   KIAA0924 3' GCCCAGGCTAGAGTGCAGTG  30366         C
                                 CACTGCACTC AGCCTGGGT
                                 |||||||||| |||||||||
                                 GTGACGTGAG TCGGACCCG
                                       A
GAM97   KIAA0930 3' ATTGGGGCTGGGCGCAGTG   71064       A T      G
                                 CACTGC C CCAGCCT GGT
                                 |||||| | ||||||| |||
                                 GTGACG G GGTCGGG TTA
                                     C _      G
GAM97   KIAA0931 3' GCTCAGGCTGGAGTGCAATG  68013    C
                                 CA TGCACTCCAGCCTGGGT
                                 || ||||||||||||||||
                                 GT ACGTGAGGTCGGACTCG
                                  A
GAM97   KIAA0939 3' ACCCTGGGCTAGAGCAAGCA  62706     A__  C    _
                                 TGC   CTC AGCCT GGGT
                                 |||   ||| ||||| ||||
                                 ACG   GAG TCGGG CCCA
                                   AAC   A    T
GAM97   KIAA0961 3' GCCCAGGCTGGCGTGCAGTG  30402        T
                                 CACTGCAC CCAGCCTGGGT
                                 |||||||| ||||||||||
                                 GTGACGTG GGTCGGACCCG
                                       C
GAM97   KIAA1001 3' GTCAGTTTAGGCTGGGCGCAGT 31011       A T        _
            G                    CACTGC C CCAGCCTGGG TGAC
                                 |||||| | |||||||||| ||||
                                 GTGACG G GGTCGGATTT ACTG
                                     C _         G
GAM97   KIAA1018 3' CACCCAGGCTGATCTGGGC   31055    A  C___
                                 GC CT    CAGCCTGGGTG
                                 || ||    ||||||||||
                                 CG GG    GTCGGACCCAC
                                  _  TCTA
GAM97   KIAA1026 3' GTCACCCAGGATGGAGTGCAGT 71742           G
            G                    CACTGCACTCCA CCTGGGTGAC
                                 |||||||||||| ||||||||||
                                 GTGACGTGAGGT GGACCCACTG
                                       A
GAM97   KIAA1028 3' GTCACCCAAGCTGGAGTGCAGT 93590            C
            G                    CACTGCACTCCAGC TGGGTGAC
                                 |||||||||||||| ||||||||
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                                GTGACGTGAGGTCG ACCCACTG
                                       A
GAM97   KIAA1037 3' GCTCTGAGGGCCAGGTGCAGTG 31135        CCA   ___
                                CACTGCACT   GCCT   GGGT
                                |||||||||  ||||  ||||
                                GTGACGTGG   CGGG   CTCG
                                     AC_    AGT
GAM97   KIAA1040 3' GTCACCCAGGCTGGAATGCAGT 72690        C
           G                     CACTGCA TCCAGCCTGGGTGAC
                                |||||||| ||||||||||||||||
                                GTGACGT AGGTCGGACCCACTG
                                    A
GAM97   KIAA1041 3' GTTGCCCAGGCTGGAGTGCAGT 30828              TG
           G                     CACTGCACTCCAGCCTGGG  AC
                                |||||||||||||||||||  ||
                                GTGACGTGAGGTCGGACCC  TG
                                          GT
GAM97   KIAA1045 3' GCCCTGAGGCTGGGCACAGTG  71605      CA T     __
                                CACTG  C CCAGCCT  GGGT
                                |||||  | |||||||  ||||
                                GTGAC  G GGTCGGA  CCCG
                                   AC _      GT
GAM97   KIAA1052 5' GTCACTCAGGCTGCAGTGCAGT 30947         C
           G                     CACTGCACT CAGCCTGGGTGAC
                                |||||||||  ||||||||||||
                                GTGACGTGA GTCGGACTCACTG
                                     C
GAM97   KIAA1054 3' GTTGCCCAGGCTGGAGTGCAGT 68968              TG
           G                     CACTGCACTCCAGCCTGGG  AC
                                |||||||||||||||||||  ||
                                GTGACGTGAGGTCGGACCC  TG
                                          GT
GAM97   KIAA1128 3' GCCCAGGCTGGATTACAGTG   69007      CAC
                                CACTG   TCCAGCCTGGGT
                                |||||   ||||||||||||
                                GTGAC   AGGTCGGACCCG
                                   ATT
GAM97   KIAA1143 3' GTCACCCAGGCTGGAGTGCAGT 69247
           G                     CACTGCACTCCAGCCTGGGTGAC
                                |||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCACTG

GAM97   KIAA1143 3' TCACCCAGGCCAGACACAATG  69250    C  CAC  CA
                                CA TG   TC  GCCTGGGTGA
                                || ||   ||  ||||||||||
                                GT AC   AG  CGGACCCACT
                                 A  AC_  AC
GAM97   KIAA1155 3' GTCACCCAGGCTGGAGTGCAGT 62915
           G                     CACTGCACTCCAGCCTGGGTGAC
                                |||||||||||||||||||||||
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                                GTGACGTGAGGTCGGACCCACTG

GAM97   KIAA1161  5' GTCACCCAGGTTGGAGTGCAGT 82649
             G                  CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
                                GTGACGTGAGGTTGGACCCACTG

GAM97   KIAA1169  5' GTCACCTGGGCTGGAGTCCAGT 35884      C       TG
             G                  CACTG ACTCCAGCC  GGTGAC
                                ||||| |||||||||  ||||||
                                GTGAC TGAGGTCGG  CCACTG
                                  C        GT
GAM97   KIAA1170  3' GTTGCCCAAGCTGGAGTGCAAT 70421    C        C    TG
             G                  CA TGCACTCCAGC TGGG  AC
                                || ||||||||||| ||||  ||
                                GT ACGTGAGGTCG ACCC  TG
                                 A         A    GT
GAM97   KIAA1185  3' GTCGCCAGGCTGGAGTGCAGTG 63293              G
                                CACTGCACTCCAGCCTGG TGAC
                                |||||||||||||||||| ||||
                                GTGACGTGAGGTCGGACC GCTG
                                          _
GAM97   KIAA1193  3' GTCGCCAGGCTGGAGTGCAGTG 68276              G
                                CACTGCACTCCAGCCTGG TGAC
                                |||||||||||||||||| ||||
                                GTGACGTGAGGTCGGACC GCTG
                                          _
GAM97   KIAA1198  3' CCAGGCTGGAGTGCAGTG    64012
                                CACTGCACTCCAGCCTGG
                                ||||||||||||||||||
                                GTGACGTGAGGTCGGACC

GAM97   KIAA1198  3' CCCAGGCTGGAGTGCAGTG   64019
                                CACTGCACTCCAGCCTGGG
                                |||||||||||||||||||
                                GTGACGTGAGGTCGGACCC

GAM97   KIAA1198  3' GCCCAGGCTGGAGTGCAGTG  64044
                                CACTGCACTCCAGCCTGGGT
                                ||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCG

GAM97   KIAA1198  3' GTTGCCCAGGCTGGAGTGCAGT 64056              TG
             G                  CACTGCACTCCAGCCTGGG  AC
                                |||||||||||||||||||  ||
                                GTGACGTGAGGTCGGACCC  TG
                                          GT
GAM97   KIAA1210  3' GTTACCCAGATTGGAGTGCAGT 98080          GC
             G                  CACTGCACTCCA  CTGGGTGAC
                                ||||||||||||  |||||||||
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                                GTGACGTGAGGT  GACCCATTG
                                      TA
GAM97   KIAA1254  3' GTCAGCCAGGCTGGAGTGCAGT 70564              G
             G                   CACTGCACTCCAGCCTGG TGAC
                                 |||||||||||||||||| ||||
                                 GTGACGTGAGGTCGGACC ACTG
                                       G
GAM97   KIAA1257  3' GTCGCCCAGGCTGGAGTGCAGT 63410
             G                   CACTGCACTCCAGCCTGGGTGAC
                                 |||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCGCTG

GAM97   KIAA1257  3' GTTGCCCAGGCTGGAGTACAAT 63413    C  C         TG
             G                   CA TG ACTCCAGCCTGGG  AC
                                 || || ||||||||||||  ||
                                 GT AC TGAGGTCGGACCC  TG
                                  A  A          GT
GAM97   KIAA1280  5' GTTGCCCAGGCTGGAGTGCAGT 70287              TG
             G                   CACTGCACTCCAGCCTGGG  AC
                                 ||||||||||||||||||  ||
                                 GTGACGTGAGGTCGGACCC  TG
                                       GT
GAM97   KIAA1287  3' GTTGCCCAGGCTGGAGTGCAGT 78940              TG
             G                   CACTGCACTCCAGCCTGGG  AC
                                 ||||||||||||||||||  ||
                                 GTGACGTGAGGTCGGACCC  TG
                                       GT
GAM97   KIAA1320  5' GTCACCCAGGCTGGAGTGCAGT 69846
             G                   CACTGCACTCCAGCCTGGGTGAC
                                 |||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCACTG

GAM97   KIAA1320  5' TCACCCAGGCTGGAGTATAGTG 69849      C
                                 CACTG ACTCCAGCCTGGGTGA
                                 ||||| ||||||||||||||||
                                 GTGAT TGAGGTCGGACCCACT
                                    A
GAM97   KIAA1323  5' ATCCAGGACTGGAGTGCA    63722          _
                                 TGCACTCCAG CCTGGGT
                                 |||||||||| |||||||
                                 ACGTGAGGTC GGACCTA
                                       A
GAM97   KIAA1373  3' GTCGCCCAGGCTGGAGTGCAGT 71510
             G                   CACTGCACTCCAGCCTGGGTGAC
                                 |||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCGCTG

GAM97   KIAA1404  3' TTTAGGCTGGGCGCAGTG    62696       A T
                                 CACTGC C CCAGCCTGGG
                                 |||||| | ||||||||||
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                                GTGACG G GGTCGGATTT
                                   C _
GAM97   KIAA1443 3' GCCCAGGCTGTAGTGCAATG  64573    C     C
                                CA TGCACT CAGCCTGGGT
                                || |||||| ||||||||||
                                GT ACGTGA GTCGGACCCG
                                 A     T
GAM97   KIAA1456 3' GTCGCCCAGGCTGGAGTGCACT 67566    C
           G                     CA TGCACTCCAGCCTGGGTGAC
                                || ||||||||||||||||||||
                                GT ACGTGAGGTCGGACCCGCTG
                                 C
GAM97   KIAA1465 3' GTCGCCAGGCTGGAGTGCAGTG 61507                G
                                CACTGCACTCCAGCCTGG TGAC
                                |||||||||||||||||| ||||
                                GTGACGTGAGGTCGGACC GCTG
                                                 _
GAM97   KIAA1467 3' GTCGCCCAGGCTGGAGTGCAGT 72075
           G                     CACTGCACTCCAGCCTGGGTGAC
                                |||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCGCTG

GAM97   KIAA1473 3' CCCAGGCTGGAGTACAGTG   71207      C
                                CACTG ACTCCAGCCTGGG
                                ||||| ||||||||||||
                                GTGAC TGAGGTCGGACCC
                                   A
GAM97   KIAA1497 5' GTTGCCCAGGCTGGAGTGCAGT 68129                TG
           G                     CACTGCACTCCAGCCTGGG  AC
                                |||||||||||||||||  ||
                                GTGACGTGAGGTCGGACCC  TG
                                             GT
GAM97   KIAA1508 3' ATCCGGCCGGGCGCAGTG    62542       A T  A   T
                                CACTGC C CC GCC GGGT
                                |||||| | || ||| ||||
                                GTGACG G GG CGG CCTA
                                   C _  C   _
GAM97   KIAA1508 3' GTCACCCAGGCTGGAGTGCA   62560
                                TGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||
                                ACGTGAGGTCGGACCCACTG

GAM97   KIAA1530 3' ACCCAGGCTGAGTGCAGTG   68541          C
                                CACTGCACTC AGCCTGGGT
                                |||||||||| |||||||||
                                GTGACGTGAG TCGGACCCA
                                                _
GAM97   KIAA1530 3' GTCGCCAGGCTGGAGTGCAATG 68568    C           G
                                CA TGCACTCCAGCCTGG TGAC
                                || |||||||||||||| ||||
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                                GT ACGTGAGGTCGGACC GCTG
                                 A           _
GAM97   KIAA1559 3' GTCCCCCAGGCTGGAGTGCAGT 73459              T
              G                  CACTGCACTCCAGCCTGGG GAC
                                 ||||||||||||||||||| |||
                                 GTGACGTGAGGTCGGACCC CTG
                                           C
GAM97   KIAA1571 3' GCCCAGGCTGGAGTGCAGTG  61618
                                 CACTGCACTCCAGCCTGGGT
                                 ||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCG

GAM97   KIAA1614 3' GCTTAGGCCGGGCGCAGTG   70666      A T  A
                                 CACTGC C CC GCCTGGGT
                                 |||||| | || ||||||||
                                 GTGACG G GG CGGATTCG
                                    C _  C
GAM97   KIAA1615 3' GCCTAGGCTGGAGTGCAGTG  69279
                                 CACTGCACTCCAGCCTGGGT
                                 ||||||||||||||||||||
                                 GTGACGTGAGGTCGGATCCG

GAM97   KIAA1615 3' GTCACCAGGCCGGAGTGCAGTG 69281          A     G
                                 CACTGCACTCC GCCTGG TGAC
                                 |||||||||| |||||| ||||
                                 GTGACGTGAGG CGGACC ACTG
                                       C     _
GAM97   KIAA1649 3' GCCAAGGCTGGAGTGCAGTG  51242             G
                                 CACTGCACTCCAGCCT GGT
                                 |||||||||||||||| |||
                                 GTGACGTGAGGTCGGA CCG
                                           A
GAM97   KIAA1655 3' GTTGCCCAGGCTGGAGTGCAGT 67200               TG
              G                  CACTGCACTCCAGCCTGGG  AC
                                 |||||||||||||||||||  ||
                                 GTGACGTGAGGTCGGACCC  TG
                                           GT
GAM97   KIAA1668 3' GTCGCCCAGGCTGGAGTGCAGT 67078
              G                  CACTGCACTCCAGCCTGGGTGAC
                                 |||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCGCTG

GAM97   KIAA1671 3' CCAGGCTGGAATGCAGTG    66271       C
                                 CACTGCA TCCAGCCTGG
                                 ||||||| ||||||||||
                                 GTGACGT AGGTCGGACC
                                    A
GAM97   KIAA1671 3' GCTCAAGCTGGAGTGGAGTG  66285     G       C
                                 CACT CACTCCAGC TGGGT
                                 |||| ||||||||| |||||
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                                GTGA GTGAGGTCG ACTCG
                                  G       A
GAM97   KIAA1712 3' GTTGCCCAGGCTGGAGTGCA  68164            TG
                                TGCACTCCAGCCTGGG  AC
                                ||||||||||||||||  ||
                                ACGTGAGGTCGGACCC  TG
                                      GT
GAM97   KIAA1712 3' TTGCCCAGGCTGGAGTGCACTG 68168    C           TG
                                CA TGCACTCCAGCCTGGG  A
                                || ||||||||||||||||  |
                                GT ACGTGAGGTCGGACCC  T
                                 C            GT
GAM97   KIAA1737 3' GCCCAGGCGGAGTACAATG   67944    C  C    A
                                CA TG ACTCC GCCTGGGT
                                || || ||||| ||||||||
                                GT AC TGAGG CGGACCCG
                                 A  A    _
GAM97   KIAA1751 3' GCCTAGGCTGGAGTGCAGTG  72160
                                CACTGCACTCCAGCCTGGGT
                                ||||||||||||||||||||
                                GTGACGTGAGGTCGGATCCG

GAM97   KIAA1755 3' CCAGGCTGGAGTGCAGTG    62008
                                CACTGCACTCCAGCCTGG
                                ||||||||||||||||||
                                GTGACGTGAGGTCGGACC

GAM97   KIAA1784 3' GTCACCTAGGCTGGAGTGCAGT 65754
                G                CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||||
                                 GTGACGTGAGGTCGGATCCACTG

GAM97   KIAA1821 3' GTTGCCCAGGCTGGAGTGTAGT 72273            TG
                G                CACTGCACTCCAGCCTGGG  AC
                                 ||||||||||||||||||  ||
                                 GTGATGTGAGGTCGGACCC  TG
                                       GT
GAM97   KIAA1829 3' ATCCAGGCTGGAATGCGGTG  62632       C
                                 CACTGCA TCCAGCCTGGGT
                                 |||||||  ||||||||||||
                                 GTGGCGT AGGTCGGACCTA
                                    A
GAM97   KIAA1829 3' GTTGCCCAGGCTGGAGTGCAGT 62653            TG
                G                CACTGCACTCCAGCCTGGG  AC
                                 ||||||||||||||||||  ||
                                 GTGACGTGAGGTCGGACCC  TG
                                       GT
GAM97   KIAA1877 3' GTCGCCCAGGCTAGAGTGCAGT 66758         C
                G                CACTGCACTC AGCCTGGGTGAC
                                 |||||||||  ||||||||||||
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                                GTGACGTGAG TCGGACCCGCTG
                                     A
GAM97   KIAA1922  5' GTTGCCCAGGCTGGAGTGCAAT 74003    C           TG
             G                   CA TGCACTCCAGCCTGGG  AC
                                 || ||||||||||||||||  ||
                                 GT ACGTGAGGTCGGACCC  TG
                                  A            GT
GAM97   KIAA1924  3' GCCCAGGATGGAGTGCAGTG  74049          G
                                 CACTGCACTCCA CCTGGGT
                                 |||||||||||| |||||||
                                 GTGACGTGAGGT GGACCCG
                                      A
GAM97   KIAA1924  3' GTCACCTAGGCTGGAATGCAGT 74057       C
             G                   CACTGCA TCCAGCCTGGGTGAC
                                 ||||||| ||||||||||||||
                                 GTGACGT AGGTCGGATCCACTG
                                    A
GAM97   KIAA1971  3' CCAGGCTGGGGTGCAGTG    74671
                                 CACTGCACTCCAGCCTGG
                                 ||||||||||||||||||
                                 GTGACGTGGGGTCGGACC

GAM97   KIAA1971  3' GTCATCCAGGCTAGAGTGCAGT 74690          C
             G                   CACTGCACTC AGCCTGGGTGAC
                                 |||||||||| ||||||||||||
                                 GTGACGTGAG TCGGACCTACTG
                                      A
GAM97   KIAA1971  3' GTCGCCCAGGCTGGGGTGCAGT 74692
             G                   CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGGGGTCGGACCCGCTG

GAM97   KIAA1987  5' GTTGCCCAGGTTAGAGTGCAGT 89388          C       TG
             G                   CACTGCACTC AGCCTGGG  AC
                                 |||||||||| ||||||||  ||
                                 GTGACGTGAG TTGGACCC  TG
                                      A       GT
GAM97   KLK7      3' GCTTGGGCTGCAATGCAGTG  18545       CTC    TG
                                 CACTGCA   CAGCC  GGT
                                 |||||||   |||||  |||
                                 GTGACGT   GTCGG  TCG
                                    AAC    GT
GAM97   KLK7      3' GCTTGGGCTGCAATGCAGTG  58391       CTC    TG
                                 CACTGCA   CAGCC  GGT
                                 |||||||   |||||  |||
                                 GTGACGT   GTCGG  TCG
                                    AAC    GT
GAM97   LAMP3     3' GTCACCCAGGCTGGAGTACAGT 60209      C
             G                   CACTG ACTCCAGCCTGGGTGAC
                                 ||||| ||||||||||||||||
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                                GTGAC TGAGGTCGGACCCACTG
                                  A
GAM97   LIECG3   3'  GTTGCCCAGGTTGGAGTGCAGT 88802                TG
            G                    CACTGCACTCCAGCCTGGG  AC
                                 ||||||||||||||||||  ||
                                 GTGACGTGAGGTTGGACCC  TG
                                       GT
GAM97   LY75     3'  GTTGCCCAGGCTGGAGTACAAT 11397    C  C        TG
            G                    CA TG ACTCCAGCCTGGG  AC
                                 || || ||||||||||||  ||
                                 GT AC TGAGGTCGGACCC  TG
                                  A  A          GT
GAM97   MAIL     3'  CGCCCAGGCTGGAGTACAGTG  49473      C
                                 CACTG ACTCCAGCCTGGGTG
                                 ||||| ||||||||||||||
                                 GTGAC TGAGGTCGGACCCGC
                                   A
GAM97   MAP-1    3'  GTCACCCAGGCTGGAGTGCAGT 42447
            G                    CACTGCACTCCAGCCTGGGTGAC
                                 |||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCACTG

GAM97   MAP2K3   5'  CACCCAGGCCTGCGAGGAGC   12321    A_  _  _
                                 GC  CTC CAG CCTGGGTG
                                 ||  ||| ||| ||||||||
                                 CG  GAG GTC GGACCCAC
                                  AG   C   C
GAM97   MCLC     3'  GTCACCCAGGCTGGAGTGAGGT 31385      G
            G                    CACT CACTCCAGCCTGGGTGAC
                                 |||| ||||||||||||||||
                                 GTGG GTGAGGTCGGACCCACTG
                                   A
GAM97   MCM10    3'  GTCACCCTGGCTGGAGTGCAGT 38178             T
                                 ACTGCACTCCAGCC GGGTGAC
                                 |||||||||||||| |||||||
                                 TGACGTGAGGTCGG CCCACTG
                                        T
GAM97   MDN1     3'  ACTTGGCCAGAAAGCAGTG   63356       AC  CA   T
                                 CACTGC  TC  GCC GGGT
                                 ||||||  ||  ||| ||||
                                 GTGACG  AG  CGG TTCA
                                    AA  AC  _
GAM97   MEF-2    3'  GCCCAGGCTGCTGGAGTGCCGT 65024     T      ___
            G                    CAC GCACTCCA   GCCTGGGT
                                 ||| ||||||||   ||||||||
                                 GTG CGTGAGGT   CGGACCCG
                                   C       CGT
GAM97   MESDC2   3'  GCCCTCACTAGAGTGCAGT   72917         C  CCT
                                 ACTGCACTC AG   GGGT
                                 |||||||||  ||   ||||
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                                TGACGTGAG TC   CCCG
                                     A  ACT
GAM97   MGC10200  3' ACCCAGGCCGGACTGCAG    59629      C   A
                                CTGCA TCC GCCTGGGT
                                ||||| ||| ||||||||
                                GACGT AGG CGGACCCA
                                   C   C
GAM97   MGC10200  3' GTCACGCAGGCTAGAGTGCAGT 59647          C     G
           G                     CACTGCACTC AGCCTG GTGAC
                                ||||||||||| |||||| |||||
                                GTGACGTGAG TCGGAC CACTG
                                     A     G
GAM97   MGC10818  3' GTCGCCCAGGCTGGAGTACAAT 48303    C  C
           G                     CA TG ACTCCAGCCTGGGTGAC
                                || || ||||||||||||||||
                                GT AC TGAGGTCGGACCCGCTG
                                 A  A
GAM97   MGC11324  5' CCGGTGTGCCAAAGTGCGGTG  52149         CCA__ _
                                CACTGCACT     GC CTGG
                                |||||||||     || ||||
                                GTGGCGTGA     TG GGCC
                                     AACCG  T
GAM97   MGC11386  3' GCCTAGGCTGAAGCACAGTG   53067      CA  C
                                CACTG  CT CAGCCTGGGT
                                |||||  || ||||||||||
                                GTGAC  GA GTCGGATCCG
                                   AC  A
GAM97   MGC12466  3' GTCAGCTAGGCTGAAGTGTAGT 79799         C       G
           G                     CACTGCACT CAGCCTGG TGAC
                                ||||||||| |||||||| ||||
                                GTGATGTGA GTCGGATC ACTG
                                     A       G
GAM97   MGC13017  3' GCCTTTTTGGGCTGGGCACAGT 55575       CA T      ____
           G                     CACTG  C CCAGCCT    GGGT
                                |||||  | |||||||    ||||
                                GTGAC  G GGTCGGG    TCCG
                                   AC _       TTTT
GAM97   MGC13138  3' GTCACCCAGGCTGGAGTGCAGT 54159
           G                     CACTGCACTCCAGCCTGGGTGAC
                                |||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCACTG

GAM97   MGC13138  3' GTTGCCCAGGCTGGAGTGCA   54162              TG
                                TGCACTCCAGCCTGGG  AC
                                ||||||||||||||||  ||
                                ACGTGAGGTCGGACCC  TG
                                          GT
GAM97   MGC13204  3' GTTGCCCAGGCTGGAGTGCAGT 49631                TG
           G                     CACTGCACTCCAGCCTGGG  AC
                                |||||||||||||||||  ||
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                                GTGACGTGAGGTCGGACCC  TG
                                      GT
GAM97   MGC14289  3'  GTTGCCCAGGCTGGAGTGCAGT 55593              TG
           G                   CACTGCACTCCAGCCTGGG  AC
                               ||||||||||||||||||  ||
                               GTGACGTGAGGTCGGACCC  TG
                                      GT
GAM97   MGC14436  5'  GTCACCCAGGCTGGGGTACGGT 52929      C
           G                   CACTG ACTCCAGCCTGGGTGAC
                               ||||| ||||||||||||||||
                               GTGGC TGGGGTCGGACCCACTG
                                 A
GAM97   MGC14836  3'  GTTGCCCAGGCTGGAGTGCAGT 54175              TG
           G                   CACTGCACTCCAGCCTGGG  AC
                               ||||||||||||||||||  ||
                               GTGACGTGAGGTCGGACCC  TG
                                      GT
GAM97   MGC15606  5'  GTTGCCCAGGCTGGAGTACATT 59524    C  C         TG
           G                   CA TG ACTCCAGCCTGGG  AC
                               || || ||||||||||||  ||
                               GT AC TGAGGTCGGACCC  TG
                                T  A          GT
GAM97   MGC1842   3'  GTTGCCCAGACTGGAGTGCAGT 66261          C    TG
           G                   CACTGCACTCCAG CTGGG  AC
                               ||||||||||||| |||||  ||
                               GTGACGTGAGGTC GACCC  TG
                                      A    GT
GAM97   MGC20235  3'  GTCTTACAGCTGGGTGCAGTG  59558       T    C  GGT
                               CACTGCAC CCAGC TG   GAC
                               |||||||| ||||| ||   |||
                               GTGACGTG GGTCG AC   CTG
                                  _    _  ATT
GAM97   MGC21675  3'  GTTGCCCAGGCTGGAGTGCAAT 54595    C           TG
           G                   CA TGCACTCCAGCCTGGG  AC
                               || ||||||||||||||||  ||
                               GT ACGTGAGGTCGGACCC  TG
                                A             GT
GAM97   MGC2452   5'  ATCCAGGGGCTGGAGCCCAATG 51964    C  CA       __
                               CA TG  CTCCAGCCT  GGGT
                               || ||  |||||||||  ||||
                               GT AC  GAGGTCGGG  CCTA
                                A  CC        GA
GAM97   MGC2474   3'  GTTGCCCAGGCTGGAGTGCAAT 43963    C           TG
           G                   CA TGCACTCCAGCCTGGG  AC
                               || ||||||||||||||||  ||
                               GT ACGTGAGGTCGGACCC  TG
                                A             GT
GAM97   MGC2474   3'  TCACCCAGGCTGGAATGCAGTG 43966       C
                               CACTGCA TCCAGCCTGGGTGA
                               ||||||| ||||||||||||||
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                                GTGACGT AGGTCGGACCCACT
                                    A
GAM97   MGC2477  5' GCCCAGCTGGAGTGCAGTG   44302          C
                                CACTGCACTCCAGC TGGGT
                                |||||||||||||| |||||
                                GTGACGTGAGGTCG ACCCG
                                                _
GAM97   MGC2477  5' GCCCAGGGCTGGAGTGCAGTG 44303          _
                                CACTGCACTCCAGCC TGGGT
                                |||||||||||||| |||||
                                GTGACGTGAGGTCGG ACCCG
                                      G
GAM97   MGC2603  3' GTCGCCAGGCTGGAGTGCAGTG 44081            G
                                CACTGCACTCCAGCCTGG TGAC
                                |||||||||||||||| ||||
                                GTGACGTGAGGTCGGACC GCTG
                                                 _
GAM97   MGC29891 3' GTCACCCAGGCTGGAGTGCGGT 58868
          G                      CACTGCACTCCAGCCTGGGTGAC
                                 |||||||||||||||||||||||
                                 GTGGCGTGAGGTCGGACCCACTG

GAM97   MGC29898 3' GTTGCCCAGACTGGAGTGCAGT 59587          C    TG
          G                      CACTGCACTCCAG CTGGG  AC
                                 |||||||||||| ||||| ||
                                 GTGACGTGAGGTC GACCC  TG
                                       A    GT
GAM97   MGC3113  3' GTTCCCCAGGCCGGAGTGCAGT 44062          A     TG
          G                      CACTGCACTCC GCCTGGG  AC
                                 |||||||||| ||||||| ||
                                 GTGACGTGAGG CGGACCC  TG
                                       C     CT
GAM97   MGC3329  3' CTAGGCTGGAGTGCCGTG   44244    T
                                CAC GCACTCCAGCCTGG
                                ||| ||||||||||||
                                GTG CGTGAGGTCGGATC
                                  C
GAM97   MGC4248  3' CCAGGCTGGGTGCAGTG    51311       T
                                CACTGCAC CCAGCCTGG
                                |||||||| |||||||||
                                GTGACGTG GGTCGGACC
                                                _
GAM97   MGC4638  3' GTCACCAGGCTGGAGTGCAGTG 49744            G
                                CACTGCACTCCAGCCTGG TGAC
                                |||||||||||||||| ||||
                                GTGACGTGAGGTCGGACC ACTG
                                                 _
GAM97   MGC5149  3' GTCACCAGGCTAGAGTGCAGTG 72761          C     G
                                CACTGCACTC AGCCTGG TGAC
                                |||||||||| ||||||| ||||
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                                GTGACGTGAG TCGGACC ACTG
                                     A     _
GAM97   MGC9912  3'  GTCGCCAGACTGGAGTGCAGTG 55608          C   G
                                CACTGCACTCCAG CTGG TGAC
                                |||||||||||| |||| ||||
                                GTGACGTGAGGTC GACC GCTG
                                     A   _
GAM97   MIDORI   3'  CACCCAGGAAGGAAGCACAG  74210    CA _ AG
                                CTG  CT CC  CCTGGGTG
                                |||  || ||  ||||||||
                                GAC  GA GG  GGACCCAC
                                  AC  A  AA
GAM97   MKRN4    3'  GTCACCCAGGCTGGAGTGCAGT 48472
           G                     CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCACTG

GAM97   MLZE     5'  GTTGCCCAGGCTGGAGTGCAG  49453            TG
                                CTGCACTCCAGCCTGGG  AC
                                ||||||||||||||||  ||
                                GACGTGAGGTCGGACCC  TG
                                          GT
GAM97   MMPL1    3'  GTCCTCCAGGCTGGAGTGCAAT 15966    C          T
           G                     CA TGCACTCCAGCCTGGG GAC
                                || |||||||||||||| |||
                                GT ACGTGAGGTCGGACCT CTG
                                 A            C
GAM97   moblak   3'  CCAGGCTGGAGTGCAGTG    56390
                                CACTGCACTCCAGCCTGG
                                ||||||||||||||||
                                GTGACGTGAGGTCGGACC

GAM97   moblak   3'  GCCCAGACTGGAGTCCAGTG  56404      C     C
                                CACTG ACTCCAG CTGGGT
                                ||||| ||||||| ||||||
                                GTGAC TGAGGTC GACCCG
                                   C      A
GAM97   MOCS3    3'  GTTGCCCAGGCTGGAGTGTAGT 27934             TG
           G                     CACTGCACTCCAGCCTGGG  AC
                                ||||||||||||||||||  ||
                                GTGATGTGAGGTCGGACCC  TG
                                          GT
GAM97   MRPL20   3'  GTCACCCAGGCTGGAGTGCAAT 36207    C
           G                     CA TGCACTCCAGCCTGGGTGAC
                                || ||||||||||||||||||
                                GT ACGTGAGGTCGGACCCACTG
                                 A
GAM97   MRPL35   3'  GTTGCCCAGGCTGGAGTGCAGT 34022             TG
           G                     CACTGCACTCCAGCCTGGG  AC
                                ||||||||||||||||||  ||
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                                GTGACGTGAGGTCGGACCC  TG
                                          GT
GAM97   MRPL44   3'  GCCCAGGCTGGACTGCAGTG   43599       C
                                CACTGCA TCCAGCCTGGGT
                                ||||||| ||||||||||||
                                GTGACGT AGGTCGGACCCG
                                    C
GAM97   MRPL56   3'  ATTCAGGGCCGGGTGCAGTG   52752       T  A  _
                                CACTGCAC CC GCC TGGGT
                                |||||||| || ||| |||||
                                GTGACGTG GG CGG ACTTA
                                    _  C   G
GAM97   MRPS27   3'  GTCACCCAGGCTGGAGTGCAGT 31332
           G                     CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCACTG

GAM97   MtFMT    3'  GTCACCCAGGCTGGAATCCAGT 58338      CAC
           G                     CACTG   TCCAGCCTGGGTGAC
                                |||||   ||||||||||||||||
                                GTGAC   AGGTCGGACCCACTG
                                   CTA
GAM97   MYO5C    3'  TCGCCAGGCTGGAGTGTAGTG  38726             G
                                CACTGCACTCCAGCCTGG TGA
                                |||||||||||||||| |||
                                GTGATGTGAGGTCGGACC GCT
                                          _
GAM97   NAPG     5'  GCCCAGGCTGGAGTGCAGTG   98538
                                CACTGCACTCCAGCCTGGGT
                                ||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCG

GAM97   NDP52    3'  GTCACCCAGGCTGGCGTGCAAT 20675    C    T
           G                     CA TGCAC CCAGCCTGGGTGAC
                                || ||||| ||||||||||||||
                                GT ACGTG GGTCGGACCCACTG
                                 A    C
GAM97   NDUFB1   5'  TCCCCCAGGCTGGAGTGTAGTG 17015              T
                                CACTGCACTCCAGCCTGGG GA
                                |||||||||||||||||| ||
                                GTGATGTGAGGTCGGACCC CT
                                          C
GAM97   NDUFC2   3'  GTCATCAGGCTGGAGTGCAGTG 17035             G
                                CACTGCACTCCAGCCTGG TGAC
                                |||||||||||||||| ||||
                                GTGACGTGAGGTCGGACT ACTG
                                          _
GAM97   NOSIP    5'  GCCTAGGCTGGAGTGCAATG  32544    C
                                CA TGCACTCCAGCCTGGGT
                                || ||||||||||||||||
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                                GT ACGTGAGGTCGGATCCG
                                 A
GAM97   NXN      3'  GTCGCCCAGGCTGGAGTGCAGT 42679
                G                CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCGCTG

GAM97   OCT11    3'  GCCCAGGCTGGAGTGCAGTG  27591
                                 CACTGCACTCCAGCCTGGGT
                                 ||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCG

GAM97   OR51E2   3'  GTCACCAGGCTGGAGTGCAGTG 48515              G
                                 CACTGCACTCCAGCCTGG TGAC
                                 |||||||||||||||||| ||||
                                 GTGACGTGAGGTCGGACC ACTG
                                                    _
GAM97   OSBPL2   3'  GTTGCCCAGGCTGGAGTGCAAT 29905    C           TG
                G                CA TGCACTCCAGCCTGGG  AC
                                 || ||||||||||||||||  ||
                                 GT ACGTGAGGTCGGACCC  TG
                                  A             GT
GAM97   OSBPL2   3'  GTTGCCCAGGCTGGAGTGCAAT 58491    C           TG
                G                CA TGCACTCCAGCCTGGG  AC
                                 || ||||||||||||||||  ||
                                 GT ACGTGAGGTCGGACCC  TG
                                  A             GT
GAM97   PASK     5'  GCTGAGGCTGGAGTGCAGTG  31416            G
                                 CACTGCACTCCAGCCT GGT
                                 |||||||||||||||| |||
                                 GTGACGTGAGGTCGGA TCG
                                           G
GAM97   PDZD2    3'  GTCACCCAGGCCGGGAGGGT  81730    A   A_
                                 GC CTCC  GCCTGGGTGAC
                                 || ||||  ||||||||||
                                 TG GAGG  CGGACCCACTG
                                  G   GC
GAM97   PDZD2    5'  TCACCCAGGACAATGCCGTG  81734    T   CTCCAG
                                 CAC GCA     CCTGGGTGA
                                 ||| |||     |||||||||
                                 GTG CGT     GGACCCACT
                                   C  AACA__
GAM97   PELI1    5'  GTCACCCAGGCTGGAGTGCAGT 40647
                G                CACTGCACTCCAGCCTGGGTGAC
                                 |||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCACTG

GAM97   PELI1    5'  GTCGCCCAGGCTGGAGTGCAGT 40649
                G                CACTGCACTCCAGCCTGGGTGAC
                                 |||||||||||||||||||||||
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                                GTGACGTGAGGTCGGACCCGCTG

GAM97   PELI1    5' GTTGCCCAGGTTGGAGTGCAGT 40651                TG
             G                  CACTGCACTCCAGCCTGGG  AC
                                ||||||||||||||||||  ||
                                GTGACGTGAGGTTGGACCC  TG
                                      GT
GAM97   PIP3-E   3' GTTGCCCAGGCTGGAGTGCAGT 67358                TG
             G                  CACTGCACTCCAGCCTGGG  AC
                                ||||||||||||||||||  ||
                                GTGACGTGAGGTCGGACCC  TG
                                      GT
GAM97   POFUT1   3' GTCTCCCAGGCTGGAGTGCAGT 70980                 T
             G                  CACTGCACTCCAGCCTGGG GAC
                                ||||||||||||||||||| |||
                                GTGACGTGAGGTCGGACCC CTG
                                      T
GAM97   POLE3    3' GTGGCCCAGGCTGGAGTGCAGT 34318                 G
             G                  CACTGCACTCCAGCCTGGGT AC
                                ||||||||||||||||||| ||
                                GTGACGTGAGGTCGGACCCG TG
                                       G
GAM97   PRO0365  5' GTCGCCAGGCTGAAGTGCAGTG 26992          C      G
                                CACTGCACT CAGCCTGG TGAC
                                ||||||||| |||||||| ||||
                                GTGACGTGA GTCGGACC GCTG
                                     A      _
GAM97   PRO0456  3' ATTTAGGCTGGGTGCAGTG   27004          T
                                CACTGCAC CCAGCCTGGGT
                                |||||||| ||||||||||
                                GTGACGTG GGTCGGATTTA
                                      _
GAM97   PRO0902  3' GTCACCCAGGCTGGAGTGTAGT 54968
             G                  CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
                                GTGATGTGAGGTCGGACCCACTG

GAM97   PRO1048  3' TGCCCAGGCTGGAGTACAGTG  38121       C
                                CACTG ACTCCAGCCTGGGTG
                                ||||| ||||||||||||||
                                GTGAC TGAGGTCGGACCCGT
                                   A
GAM97   PRO1386  3' ATCTGGCCAGGTGCAGTG    49211          CCA  T
                                CACTGCACT   GCC GGGT
                                |||||||||   ||| ||||
                                GTGACGTGG   CGG TCTA
                                     AC_  _
GAM97   PRO1992  5' GTCACCCAGACTGGAGTGCAGT 26909            C
             G                  CACTGCACTCCAG CTGGGTGAC
                                |||||||||||| |||||||||
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                                GTGACGTGAGGTC GACCCACTG
                                       A
GAM97   PRO1992   3'  GTCACCCAGGCTGGAGTGCAGT 26911
            G                   CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCACTG

GAM97   PRO2955   3'  GTCCCCCAGGCTGAAGTGCAG  38243        C        T
                                CTGCACT CAGCCTGGG GAC
                                ||||||| ||||||||| |||
                                GACGTGA GTCGGACCC CTG
                                    A        C
GAM97   PSPH      3'  GTTGCCCAGGCTGGAGTGCAGT 17138                 TG
            G                   CACTGCACTCCAGCCTGGG  AC
                                |||||||||||||||||  ||
                                GTGACGTGAGGTCGGACCC  TG
                                       GT
GAM97   PSR       3'  CACCAAGGCCAGGTGCAGTG   65775         CCA    G
                                CACTGCACT   GCCT GGTG
                                |||||||||   |||| ||||
                                GTGACGTGG   CGGA CCAC
                                     AC_    A
GAM97   PSTPIP2   3'  GTCCCCCAGGCTGAAGTGCAG  44660        C        T
                                CTGCACT CAGCCTGGG GAC
                                ||||||| ||||||||| |||
                                GACGTGA GTCGGACCC CTG
                                    A        C
GAM97   RAB21     3'  GTCACCCAGGCTGGAGTGCACT 31096    C
            G                    CA TGCACTCCAGCCTGGGTGAC
                                 || ||||||||||||||||||
                                 GT ACGTGAGGTCGGACCCACTG
                                  C
GAM97   RAB33B    3'  GTCTCCAGGCTGGAGTGCAGTG 49332                T
                                CACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||| |||
                                GTGACGTGAGGTCGGACCT CTG
                                                _
GAM97   RAB39     3'  GTCACCCAGGCTGGAGTGCAGT 77124
            G                   CACTGCACTCCAGCCTGGGTGAC
                                |||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCACTG

GAM97   RAI       5'  CTCGGCTGGAGTGCAGTG    22853             T
                                CACTGCACTCCAGCC GGG
                                |||||||||||||| |||
                                GTGACGTGAGGTCGG CTC
                                                _
GAM97   RAP140    3'  GTCGCCCAAGCTGGAGTACAGT 31522       C       C
            G                   CACTG ACTCCAGC TGGGTGAC
                                ||||| |||||||| ||||||||
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                                GTGAC TGAGGTCG ACCCGCTG
                                  A       A
GAM97   RASSF2   3'  GTTTCCCAGGCTGGAGTGCAGT 29110                T
            G                    CACTGCACTCCAGCCTGGG GAC
                                 |||||||||||||||||| |||
                                 GTGACGTGAGGTCGGACCC TTG
                                                  T
GAM97   RES4-25  3'  GTTGCCCAGGCTGGAGTGCAAT 65272    C            TG
            G                    CA TGCACTCCAGCCTGGG  AC
                                 || ||||||||||||||||  ||
                                 GT ACGTGAGGTCGGACCC  TG
                                  A             GT
GAM97   RHOBTB2  5'  GCCGGGAGGCTGGAGCCCAG  61604    CA       G__
                                 CTG  CTCCAGCCT   GGT
                                 |||  |||||||||   |||
                                 GAC  GAGGTCGGA   CCG
                                   CC        GGG
GAM97   RNF8     3'  GTTGCCCAAGCTGGAGTACAGT 15573     C       C    TG
                                 ACTG ACTCCAGC TGGG  AC
                                 |||| |||||||| ||||  ||
                                 TGAC TGAGGTCG ACCC  TG
                                   A       A    GT
GAM97   RNO2     5'  ACCAAGGCTGGAGTGCAG    53910            G
                                 CTGCACTCCAGCCT GGT
                                 |||||||||||||| |||
                                 GACGTGAGGTCGGA CCA
                                           A
GAM97   SARM     3'  CCAGGCTGGAGGGCAGTG    31282        A
                                 CACTGC CTCCAGCCTGG
                                 |||||| ||||||||||
                                 GTGACG GAGGTCGGACC
                                    G
GAM97   SCAMP-4  3'  GTCGCCCAGGCTGGAGTGCAGT 55353
            G                    CACTGCACTCCAGCCTGGGTGAC
                                 |||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCGCTG

GAM97   SCAND2   3'  TCACCCAGGCTGGAGTGGAGTG 42144      G
                                 CACT CACTCCAGCCTGGGTGA
                                 |||| ||||||||||||||||
                                 GTGA GTGAGGTCGGACCCACT
                                   G
GAM97   SCYA13   3'  TCAAGCTGGAGTACGTG     19431     T C       C
                                 CAC G ACTCCAGC TGG
                                 ||| | |||||||| |||
                                 GTG C TGAGGTCG ACT
                                   _ A       A
GAM97   SCYA16   3'  GTCACCCAGGCTGGAGTGCAGT 17176
            G                    CACTGCACTCCAGCCTGGGTGAC
                                 |||||||||||||||||||||||
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                                GTGACGTGAGGTCGGACCCACTG

GAM97   SCYA22   3' GTCACCCACGCTGGAGTGCAAT 92604    C        C
             G                  CA TGCACTCCAGC TGGGTGAC
                                || |||||||||| ||||||||
                                GT ACGTGAGGTCG ACCCACTG
                                 A          C
GAM97   SCYA22   3' GTCGCCCAGGCTGGAGTGCAGT 92605
             G                  CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCGCTG

GAM97   SCYA28   3' GTCACACAGGCTGGAGGGCAGT 39546       A        G
             G                  CACTGC CTCCAGCCTG GTGAC
                                |||||| |||||||||| |||||
                                GTGACG GAGGTCGGAC CACTG
                                   G         A
GAM97   SEMA5A   3' ACAAAGGCTGGGTGCAGTG   15585        T      GG
                                CACTGCAC CCAGCCT  GT
                                |||||||| |||||||  ||
                                GTGACGTG GGTCGGA  CA
                                   _      AA
GAM97   SERF1B   3' GCCCAGGCTGGACTGCAGTG  43698        C
                                CACTGCA TCCAGCCTGGGT
                                ||||||| ||||||||||||
                                GTGACGT AGGTCGGACCCG
                                    C
GAM97   SERF1B   3' GTCACCAGACTGGAGTGCAGTG 43701            C    G
                                CACTGCACTCCAG CTGG TGAC
                                |||||||||||| |||| ||||
                                GTGACGTGAGGTC GACC ACTG
                                       A   _
GAM97   SERF2    5' ACCCATGCTGGAGTACGGTG  20486       C       C
                                CACTG ACTCCAGC TGGGT
                                ||||| |||||||| |||||
                                GTGGC TGAGGTCG ACCCA
                                   A       T
GAM97   SFXN2    3' GTCGCCCAGGCTGGAATGCAGT 74383        C
             G                  CACTGCA TCCAGCCTGGGTGAC
                                ||||||| ||||||||||||||
                                GTGACGT AGGTCGGACCCGCTG
                                    A
GAM97   SIRPB1   3' CCCAGGCTGGAGTGCAATG   21361    C
                                CA TGCACTCCAGCCTGGG
                                || ||||||||||||||||
                                GT ACGTGAGGTCGGACCC
                                 A
GAM97   SLC11A1  3' GCCAAGGCTGGAGTGCAGTG  60158              G
                                CACTGCACTCCAGCCT GGT
                                |||||||||||||||| |||
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                                GTGACGTGAGGTCGGA CCG
                                        A
GAM97   SLC12A5  3' ATCTGGGACTGGGTACAGT   40768     C  T   _  TG
                                ACTG AC CCAG CC  GGT
                                |||| || |||| ||  |||
                                TGAC TG GGTC GG  CTA
                                  A  _   A  GT
GAM97   SLC12A8  3' GTCACCCAGGCTGGAGTCCAGT 45244      C
          G                      CACTG ACTCCAGCCTGGGTGAC
                                ||||| ||||||||||||||||
                                GTGAC TGAGGTCGGACCCACTG
                                  C
GAM97   SLC16A4  3' GCCCAGGCTGGAGTGCAGTG  17453
                                CACTGCACTCCAGCCTGGGT
                                ||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCG

GAM97   SLC16A6  5' GTCATTCAGGCAAGAGTGCAGT 17442         CA
                                ACTGCACTC  GCCTGGGTGAC
                                |||||||||  ||||||||||
                                TGACGTGAG  CGGACTTACTG
                                     AA
GAM97   SLC19A3  3' GTCAGAGGCTGGAGTGCAATG  48247    C          GGG
                                CA TGCACTCCAGCCT   TGAC
                                || ||||||||||||   ||||
                                GT ACGTGAGGTCGGA   ACTG
                                 A          G__
GAM97   SLC19A3  3' TCTATGGGCCAGGTGCAGTG   48252        CCA    GGT
                                CACTGCACT   GCCTG   GA
                                |||||||||   |||||   ||
                                GTGACGTGG   CGGGT   CT
                                     AC_    AT_
GAM97   SLC6A14  3' GCCTGGGCTGGAGTGCAGTG   24309            TG
                                CACTGCACTCCAGCC  GGT
                                ||||||||||||||  |||
                                GTGACGTGAGGTCGG  CCG
                                        GT
GAM97   SLI      3' GCCACATCCTGGAGTGCTGTG  79282     T       CC  _
                                CAC GCACTCCAG  TG GGT
                                ||| |||||||||  || |||
                                GTG CGTGAGGTC  AC CCG
                                  T        CT  A
GAM97   SMCR5    3' ACAGGGCCGGGTGCAGTG    59242        T  A    GG
                                CACTGCAC CC GCCT  GT
                                |||||||| || ||||  ||
                                GTGACGTG GG CGGG  CA
                                     _ C    A_
GAM97   SQV7L    5' GCCCAGGCAGGAGTACAGTG   71096      C     A
                                CACTG ACTCC GCCTGGGT
                                ||||| ||||| ||||||||
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                                GTGAC TGAGG CGGACCCG
                                  A    A
GAM97   SREC     3'  GTCCCCCAGGCTGGAGTGCAGT 14909                T
                G                 CACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||| |||
                                  GTGACGTGAGGTCGGACCC CTG
                                                    C
GAM97   SS-56    3'  GTTGCCCAGGCTGGAGTGCAGT 60358               TG
                G                 CACTGCACTCCAGCCTGGG  AC
                                  |||||||||||||||||| ||
                                  GTGACGTGAGGTCGGACCC  TG
                                                    GT
GAM97   SSR3     3'  CACTAGATGGAGTGCTGT    24029    T      GC   G
                                  AC GCACTCCA  CTGG TG
                                  || ||||||||  |||| ||
                                  TG CGTGAGGT  GATC AC
                                   T       A_   _
GAM97   STAF65(gamma) 3'  GTCACCCAGGCTGGAGTGCAAT 30072    C
                G                 CA TGCACTCCAGCCTGGGTGAC
                                  || ||||||||||||||||||
                                  GT ACGTGAGGTCGGACCCACTG
                                   A
GAM97   STAM2    3'  GTCACCCAGGCTGGAGTGCAGT 20706
                                  ACTGCACTCCAGCCTGGGTGAC
                                  ||||||||||||||||||||
                                  TGACGTGAGGTCGGACCCACTG

GAM97   SULT1C2  3'  GTCGCCCAGGCTGGAGTGCAGT 22719
                G                 CACTGCACTCCAGCCTGGGTGAC
                                  ||||||||||||||||||||
                                  GTGACGTGAGGTCGGACCCGCTG

GAM97   SUN1     3'  GTTGCCCAGGCTGGAGTGCAGT 47921               TG
                G                 CACTGCACTCCAGCCTGGG  AC
                                  |||||||||||||||||| ||
                                  GTGACGTGAGGTCGGACCC  TG
                                                    GT
GAM97   SYT12    5'  TCCTTCAGGCTGGAGTGCAGTG 96389               T
                                  CACTGCACTCCAGCCTGGG GA
                                  |||||||||||||||||| ||
                                  GTGACGTGAGGTCGGACTT CT
                                                    C
GAM97   SYT13    3'  GTTGCCCAGGCTGGAGTGCAGT 95104               TG
                G                 CACTGCACTCCAGCCTGGG  AC
                                  |||||||||||||||||| ||
                                  GTGACGTGAGGTCGGACCC  TG
                                                    GT
GAM97   TADA3L   3'  GTCACCCAGGCTGGAGTGCAGT 56813
                G                 CACTGCACTCCAGCCTGGGTGAC
                                  ||||||||||||||||||||
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                                GTGACGTGAGGTCGGACCCACTG

GAM97   TCL6    5' GTCACTCAGGCTGGAATGCAGT 40490       C
             G                  CACTGCA TCCAGCCTGGGTGAC
                                ||||||| ||||||||||||||
                                GTGACGT AGGTCGGACTCACTG
                                   A
GAM97   TCL6    5' GTCACTCAGGCTGGAATGCAGT 40517       C
             G                  CACTGCA TCCAGCCTGGGTGAC
                                ||||||| ||||||||||||||
                                GTGACGT AGGTCGGACTCACTG
                                   A
GAM97   TCL6    5' CCAGGCCAGAGTGCAGTG    40527       CA
                                CACTGCACTC  GCCTGG
                                ||||||||||  ||||||
                                GTGACGTGAG  CGGACC
                                     AC
GAM97   TCL6    5' CCAGGCCAGAGTGCAGTG    40535       CA
                                CACTGCACTC  GCCTGG
                                ||||||||||  ||||||
                                GTGACGTGAG  CGGACC
                                     AC
GAM97   TCL6    5' GTCACTCAGGCTGGAATGCAGT 25916       C
             G                  CACTGCA TCCAGCCTGGGTGAC
                                ||||||| ||||||||||||||
                                GTGACGT AGGTCGGACTCACTG
                                   A
GAM97   TCL6    5' GTCACTCAGGCTGGAATGCAGT 27768       C
             G                  CACTGCA TCCAGCCTGGGTGAC
                                ||||||| ||||||||||||||
                                GTGACGT AGGTCGGACTCACTG
                                   A
GAM97   TERA    3' GTTACCCAGGCTGGAGTGCAGT 41421
             G                  CACTGCACTCCAGCCTGGGTGAC
                                |||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCATTG

GAM97   TGIF2   3' GTCACCCGGGCTGGAGTGCAGT 41757
             G                  CACTGCACTCCAGCCTGGGTGAC
                                |||||||||||||||||||||||
                                GTGACGTGAGGTCGGGCCCACTG

GAM97   THEA    3' GTTGCCCAGGCTGGAGTGCAGT 66894              TG
             G                  CACTGCACTCCAGCCTGGG  AC
                                |||||||||||||||||  ||
                                GTGACGTGAGGTCGGACCC  TG
                                      GT
GAM97   TOR1B   3' GTCATCCAAGCTGGAGTGCAGT 27976          C
             G                  CACTGCACTCCAGC TGGGTGAC
                                |||||||||||||| ||||||||
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                                GTGACGTGAGGTCG ACCTACTG
                                       A
GAM97   TRIM16   3'  GTTGCCCAGGCTGGAGAGCAGT 22375       A          TG
            G                   CACTGC CTCCAGCCTGGG  AC
                                |||||| ||||||||||||  ||
                                GTGACG GAGGTCGGACCC  TG
                                   A          GT
GAM97   TRIM35   3'  TCACCCAGGCTGGAGTACAGTG 61519       C
                                CACTG ACTCCAGCCTGGGTGA
                                ||||| ||||||||||||||||
                                GTGAC TGAGGTCGGACCCACT
                                   A
GAM97   TRIM5    3'  GTTCCCCAGGCTGGAGTGCAAT 53474    C             TG
            G                   CA TGCACTCCAGCCTGGG  AC
                                || ||||||||||||||  ||
                                GT ACGTGAGGTCGGACCC  TG
                                 A             CT
GAM97   TRIM6    3'  GTCGCCCAGGCTGGAGTGCACT 55185    C
            G                   CA TGCACTCCAGCCTGGGTGAC
                                || ||||||||||||||||||||
                                GT ACGTGAGGTCGGACCCGCTG
                                 C
GAM97   TSGA2    3'  GTTAGCCGGGTGCAGTG     55954       ACTCCA     G
                                CACTGC     GCCTGG TGAC
                                ||||||     |||||| ||||
                                GTGACG     TGGGCC ATTG
                                   _____     G
GAM97   TU12B1-TY 3'  GCCCAGGCCGGAGTGCAATG   33853    C      A
                                CA TGCACTCC GCCTGGGT
                                || |||||||| ||||||||
                                GT ACGTGAGG CGGACCCG
                                 A       C
GAM97   TU12B1-TY 3'  TTGCCCAGGCTGGAGTGCAGTG 33867                TG
                                CACTGCACTCCAGCCTGGG  A
                                |||||||||||||||||||  |
                                GTGACGTGAGGTCGGACCC  T
                                      GT
GAM97   TUCAN    3'  ATCTAGGCTGGAGTGCAGTG   30965
                                CACTGCACTCCAGCCTGGGT
                                ||||||||||||||||||||
                                GTGACGTGAGGTCGGATCTA

GAM97   TUCAN    3'  GTTACCCAGGCTGGAGTGCAGT 30984
            G                   CACTGCACTCCAGCCTGGGTGAC
                                |||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCATTG

GAM97   TUSP     3'  GCCCAACTAGAGTGTAGTG   40029          C  CC
                                CACTGCACTC AG  TGGGT
                                |||||||||| ||  |||||
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                                GTGATGTGAG TC  ACCCG
                                     A  A_
GAM97   TXNL2    3'  GTCACCCAGGCTGGAGTGCAGT 22584
           G                  CACTGCACTCCAGCCTGGGTGAC
                              ||||||||||||||||||||||
                              GTGACGTGAGGTCGGACCCACTG

GAM97   UBF-fl   3'  GTCTCCCAGGCTAGAGTACCGT 52631     TGC   C      T
           G                  CAC   ACTC AGCCTGGG GAC
                              |||   |||| |||||||| |||
                              GTG   TGAG TCGGACCC CTG
                                CCA   A      T
GAM97   UHRF1    3'  TCATCTAAAGTCCAGTG     26126      C   CCAGCC
                              CACTG ACT     TGGGTGA
                              ||||| |||     |||||||
                              GTGAC TGA     ATCTACT
                                 C   A_____
GAM97   VDU1     3'  GTCACCCAGGCTGGAGTGCTGT 31127     T
           G                  CAC GCACTCCAGCCTGGGTGAC
                              ||| ||||||||||||||||||
                              GTG CGTGAGGTCGGACCCACTG
                                T
GAM97   VMP      3'  GCCTAGGTTGGAGTACAG     55764     C
                              CTG ACTCCAGCCTGGGT
                              ||| ||||||||||||
                              GAC TGAGGTTGGATCCG
                                A
GAM97   VPS33A   3'  GTCACCCAGACTAGAGTGCAGT 43614          C  C
           G                  CACTGCACTC AG CTGGGTGAC
                              |||||||||| || |||||||||
                              GTGACGTGAG TC GACCCACTG
                                   A  A
GAM97   WBSCR16  3'  GCTTAGCTTGAACACAGTG   96150      CAC  C   C
                              CACTG   TC AGC TGGGT
                              |||||   || ||| |||||
                              GTGAC   AG TCG ATTCG
                                 ACA  T  _
GAM97   ZNF17    3'  GTTGCCCAGACTAGAGTGCAGT 83275          C  C    TG
           G                  CACTGCACTC AG CTGGG  AC
                              |||||||||| || |||||  ||
                              GTGACGTGAG TC GACCC  TG
                                   A  A    GT
GAM97   ZNF338   3'  GTTTCCCAGGCTGGAGTGCAGT 42260               T
           G                  CACTGCACTCCAGCCTGGG GAC
                              |||||||||||||||||| |||
                              GTGACGTGAGGTCGGACCC TTG
                                              T
GAM97   ZNF339   3'  GTCACCCAGGCTGGAGTACAGT 41395      C
           G                  CACTG ACTCCAGCCTGGGTGAC
                              ||||| ||||||||||||||||
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                                GTGAC TGAGGTCGGACCCACTG
                                   A
GAM97   ZNF347   3' CTGGCTGGGTGCAGTG     51826        T    T
                                CACTGCAC CCAGCC GG
                                |||||||| |||||| ||
                                GTGACGTG GGTCGG TC

                                   _    _
GAM97   ZTL1     3' GCCCAGGCTGCAGTGCAGTG  44142         C
                                CACTGCACT CAGCCTGGGT
                                ||||||||| ||||||||||
                                GTGACGTGA GTCGGACCCG
                                     C
GAM97   LOC112687 3' GTCACCCAGGCTGGAGTGCAGT 73241
           G                     CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCACTG

GAM97   LOC112724 5' GTCGCCAGGCTGGAATGCAGT  57306       C        G
                                ACTGCA TCCAGCCTGG TGAC
                                |||||| |||||||||| ||||
                                TGACGT AGGTCGGACC GCTG
                                   A       _
GAM97   LOC112817 3' GTCACCCAGGCTGGAGTGCAAT 57331    C
           G                     CA TGCACTCCAGCCTGGGTGAC
                                 || ||||||||||||||||||
                                 GT ACGTGAGGTCGGACCCACTG
                                  A
GAM97   LOC113675 5' GTCACCCAGGCTGGAGTGCAGT 57381
           G                     CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCACTG

GAM97   LOC115196 3' CACCCAGGCTGGAGTCCAGTG  73649       C
                                CACTG ACTCCAGCCTGGGTG
                                ||||| ||||||||||||||
                                GTGAC TGAGGTCGGACCCAC
                                   C
GAM97   LOC115219 5' GTCCCCCAGGCTGGAGTGCGAT 73704    C            T
           G                     CA TGCACTCCAGCCTGGG GAC
                                 || |||||||||||||| |||
                                 GT GCGTGAGGTCGGACCC CTG
                                  A             C
GAM97   LOC115343 5' GCTGAGAGCTGGAGTACAG    72535    C      _  G
                                CTG ACTCCAGC CT GGT
                                ||| |||||||| || |||
                                GAC TGAGGTCG GA TCG
                                  A       A  G
GAM97   LOC115648 3' GCCTGGCTGGAGTGCAGTG    60024             T
                                CACTGCACTCCAGCC GGGT
                                |||||||||||||| ||||
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                                GTGACGTGAGGTCGG TCCG

                                          _
GAM97   LOC116411 5'  CCAGGCTGGAGTGCAGTG    74294
                                CACTGCACTCCAGCCTGG
                                ||||||||||||||||||
                                GTGACGTGAGGTCGGACC

GAM97   LOC118738 3'  ACCTGCTGGGTGCAG       75999       T    CT
                                CTGCAC CCAGC  GGGT
                                |||||| |||||  ||||
                                GACGTG GGTCG  TCCA

                                  _    __
GAM97   LOC119504 5'  GCCGCTGAGGTGCAGTG     74445        TC   CTG
                                CACTGCAC  CAGC   GGT
                                ||||||||  ||||   |||
                                GTGACGTG  GTCG   CCG
                                     GA   ___
GAM97   LOC120114 3'  GTCACCCAGGCTAGAGTGCAAT 76049    C      C
           G                     CA TGCACTC AGCCTGGGTGAC
                                || ||||||| ||||||||||||
                                GT ACGTGAG TCGGACCCACTG
                                 A      A
GAM97   LOC120224 5'  GTCACCCAGGCTGGAGTGCAAT 57892    C
           G                     CA TGCACTCCAGCCTGGGTGAC
                                || ||||||||||||||||||||
                                GT ACGTGAGGTCGGACCCACTG
                                 A
GAM97   LOC120526 3'  CCAGCTGGAGTGCAGTG     74463            C
                                CACTGCACTCCAGC TGG
                                |||||||||||||| |||
                                GTGACGTGAGGTCG ACC

                                          _
GAM97   LOC120939 3'  GCCCAGGCTGGGATGCAATG   76764    C    CT
                                CA TGCA  CCAGCCTGGGT
                                || ||||  ||||||||||
                                GT ACGT  GGTCGGACCCG
                                 A    AG
GAM97   LOC121504 3'  CACCGAGGCTGGAGTGCAGTG  74541              G
                                CACTGCACTCCAGCCT GGTG
                                |||||||||||||||| ||||
                                GTGACGTGAGGTCGGA CCAC
                                           G
GAM97   LOC124602 3'  GTTTTTCAGGCTGGGCACAGTG 74790       CA T        T
                                CACTG  C CCAGCCTGGG GAC
                                |||||  | ||||||||| |||
                                GTGAC  G GGTCGGACTT TTG
                                   AC _         T
GAM97   LOC124930 3'  CGCCTCGCGGGTGCAG      74824       T  A  CT
                                CTGCAC CC GC  GGGTG
                                |||||| || ||  |||||
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                                GACGTG GG CG  TCCGC
                                   _ _  C_
GAM97   LOC126133 3'  GTCACCCAGGCTGGAGCGCAGT 74914       A
            G                   CACTGC CTCCAGCCTGGGTGAC
                                |||||| ||||||||||||||||
                                GTGACG GAGGTCGGACCCACTG
                                   C
GAM97   LOC126364 3'  GTCACCCAGGCTGGAGTGCAAT 76197    C
            G                   CA TGCACTCCAGCCTGGGTGAC
                                || ||||||||||||||||||||
                                GT ACGTGAGGTCGGACCCACTG
                                 A
GAM97   LOC126661 3'  GTTGCCCAGGCTGGAGTGCAGT 75062              TG
            G                   CACTGCACTCCAGCCTGGG  AC
                                |||||||||||||||||  ||
                                GTGACGTGAGGTCGGACCC  TG
                                      GT
GAM97   LOC126669 3'  GTTGCCCAGGCTGGAGTGCAAT 75947    C          TG
            G                   CA TGCACTCCAGCCTGGG  AC
                                || ||||||||||||||  ||
                                GT ACGTGAGGTCGGACCC  TG
                                 A            GT
GAM97   LOC128077 3'  GCCCAGGCTGGAGTGCAGTG  75219
                                CACTGCACTCCAGCCTGGGT
                                ||||||||||||||||||
                                GTGACGTGAGGTCGGACCCG

GAM97   LOC128077 3'  GTCGCCCAGGCTAGAGTGCAGT 75228         C
            G                   CACTGCACTC AGCCTGGGTGAC
                                |||||||||| ||||||||||
                                GTGACGTGAG TCGGACCCGCTG
                                     A
GAM97   LOC128387 3'  GTTGCCCAGGCTGGAGTGCAAT 75258    C          TG
            G                   CA TGCACTCCAGCCTGGG  AC
                                || ||||||||||||||  ||
                                GT ACGTGAGGTCGGACCC  TG
                                 A            GT
GAM97   LOC128989 3'  GTCACCCAGGCTGGAGTGCAGT 75323
            G                   CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCACTG

GAM97   LOC130813 3'  GTCACCTAGGCTAGAGGGCAGT 76280       A  C
            G                   CACTGC CTC AGCCTGGGTGAC
                                |||||| ||| ||||||||||||
                                GTGACG GAG TCGGATCCACTG
                                   G  A
GAM97   LOC131308 3'  GTCACTCAGGCTGGAGTGCAGT 75496
            G                   CACTGCACTCCAGCCTGGGTGAC
                                |||||||||||||||||||||||
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                                GTGACGTGAGGTCGGACTCACTG

GAM97   LOC132241 5'  CCCAGGCTGGAGTGCAGTG    75558
                                CACTGCACTCCAGCCTGGG
                                ||||||||||||||||||
                                GTGACGTGAGGTCGGACCC

GAM97   LOC132338 5'  GTCACCCAACCTGCAGGCAGTG 76399       A  C   CC
                                CACTGC CT CAG  TGGGTGAC
                                |||||| || |||  ||||||||
                                GTGACG GA GTC  ACCCACTG
                                   _ C   CA
GAM97   LOC132625 3'  GTCACCCAGGCTGGAGTCTAGT 76443       C
           G                     CACTG ACTCCAGCCTGGGTGAC
                                |||||| ||||||||||||||||
                                GTGAT TGAGGTCGGACCCACTG
                                   C
GAM97   LOC133686 3'  GTCACCCAGGCTGGACTGCAGT 75619        C
           G                     CACTGCA TCCAGCCTGGGTGAC
                                |||||||| ||||||||||||||
                                GTGACGT AGGTCGGACCCACTG
                                    C
GAM97   LOC135154 3'  TCACCCAGGCTGGAGTGGAGTG 75735      G
                                CACT CACTCCAGCCTGGGTGA
                                |||| ||||||||||||||||
                                GTGA GTGAGGTCGGACCCACT
                                  G
GAM97   LOC135293 3'  CCAGGCTGGAGTGCAGTG     76680
                                CACTGCACTCCAGCCTGG
                                ||||||||||||||||||
                                GTGACGTGAGGTCGGACC

GAM97   LOC135293 3'  GTTGCCCAGGCTGAAGTGTAGT 76689          C        TG
           G                     CACTGCACT CAGCCTGGG  AC
                                |||||||| |||||||||  ||
                                GTGATGTGA GTCGGACCC  TG
                                      A        GT
GAM97   LOC135398 3'  GTCACCCAGCCTGGAATGTAGT 76469        C    C
           G                     CACTGCA TCCAG CTGGGTGAC
                                ||||||| ||||| |||||||||
                                GTGATGT AGGTC GACCCACTG
                                    A    C
GAM97   LOC135763 3'  GTCACCCAGGCTGGAGTGCAGT 57561
           G                     CACTGCACTCCAGCCTGGGTGAC
                                |||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCACTG

GAM97   LOC138050 5'  GTCACCCAGGCTGGAGTGCGGT 75817
           G                     CACTGCACTCCAGCCTGGGTGAC
                                |||||||||||||||||||||||
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                                GTGGCGTGAGGTCGGACCCACTG

GAM97   LOC138199 3'  GTCTCCCAGGCCGGAGTGCAGT 75826          A      T
            G                  CACTGCACTCC GCCTGGG GAC
                               |||||||||||| ||||||| |||
                               GTGACGTGAGG CGGACCC CTG
                                     C      T
GAM97   LOC138428 3'  GCTTGGAGGCCGGGTGCAGTG  75858        T  A   __
                               CACTGCAC CC GCCT  GGGT
                               |||||||| || ||||  ||||
                               GTGACGTG GG CGGA  TTCG
                                    _  C    GG
GAM97   LOC139422 5'  GTTGCCCAGACTGGAGTGCAGT 76354           C     TG
            G                  CACTGCACTCCAG CTGGG  AC
                               |||||||||||||| |||||  ||
                               GTGACGTGAGGTC GACCC  TG
                                       A     GT
GAM97   LOC142913 5'  TCACCCAGGCTGGAGTAGAGTG 76933      GC
                               CACT  ACTCCAGCCTGGGTGA
                               ||||  ||||||||||||||||
                               GTGA  TGAGGTCGGACCCACT
                                 GA
GAM97   LOC142927 5'  GCCCAGACTGTAGTACAGTG   76947      C   C   C
                               CACTG ACT CAG CTGGGT
                               ||||| ||| ||| ||||||
                               GTGAC TGA GTC GACCCG
                                  A   T   A
GAM97   LOC143153 3'  GTCACCCAGGCTGGAGTGCAG  76982
                               CTGCACTCCAGCCTGGGTGAC
                               |||||||||||||||||||||
                               GACGTGAGGTCGGACCCACTG

GAM97   LOC143154 3'  GTCACCCAGGCTGGAGTGCAG  76993
                               CTGCACTCCAGCCTGGGTGAC
                               |||||||||||||||||||||
                               GACGTGAGGTCGGACCCACTG

GAM97   LOC143187 3'  GCCTGGCTGGAGTGGAGTG    59760      G        T
                               CACT CACTCCAGCC GGGT
                               |||| |||||||||| ||||
                               GTGA GTGAGGTCGG TCCG
                                 G        _
GAM97   LOC143241 5'  GTTGCCCAGGCTGGAGTGCAAT 57974    C            TG
            G                  CA TGCACTCCAGCCTGGG  AC
                               || ||||||||||||||  ||
                               GT ACGTGAGGTCGGACCC  TG
                                A             GT
GAM97   LOC144248 5'  GCCCAGGCTGGAGTGCAATG   77254    C
                               CA TGCACTCCAGCCTGGGT
                               || |||||||||||||||
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                                GT ACGTGAGGTCGGACCCG
                                 A
GAM97   LOC144305 3'  GTTGCCCAGGCTGGAGTGCAGT 83974                TG
            G                    CACTGCACTCCAGCCTGGG  AC
                                 ||||||||||||||||||  ||
                                 GTGACGTGAGGTCGGACCC  TG
                                       GT
GAM97   LOC144317 5'  GCCCAGGCTGGAGTGCGATG  77296    C
                                 CA TGCACTCCAGCCTGGGT
                                 || ||||||||||||||||
                                 GT GCGTGAGGTCGGACCCG
                                  A
GAM97   LOC144519 5'  ACCTGGGCTGGAGTGCAGTG  77363            TG
                                 CACTGCACTCCAGCC  GGT
                                 ||||||||||||||  |||
                                 GTGACGTGAGGTCGG  CCA
                                       GT
GAM97   LOC144524 5'  GTTGCCCAAGCTGGAGTGCAAT 84060    C        C   TG
            G                    CA TGCACTCCAGC TGGG  AC
                                 || ||||||||||| ||||  ||
                                 GT ACGTGAGGTCG ACCC  TG
                                  A         A   GT
GAM97   LOC144742 5'  GCCTAGGCTGGAGTACAGTG  77461      C
                                 CACTG ACTCCAGCCTGGGT
                                 ||||| ||||||||||||||
                                 GTGAC TGAGGTCGGATCCG
                                    A
GAM97   LOC144776 5'  GTTGCCCAGGCTGGAGTGCAAT 77494    C            TG
            G                    CA TGCACTCCAGCCTGGG  AC
                                 || ||||||||||||||||  ||
                                 GT ACGTGAGGTCGGACCC  TG
                                  A             GT
GAM97   LOC144776 5'  TCACTCAGGCTGGAGTACAGTG 77496      C
                                 CACTG ACTCCAGCCTGGGTGA
                                 ||||| ||||||||||||||||
                                 GTGAC TGAGGTCGGACTCACT
                                    A
GAM97   LOC144817 5'  GTCGCCCAGGCTGGAGTGCAGT 77521
            G                    CACTGCACTCCAGCCTGGGTGAC
                                 |||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCGCTG

GAM97   LOC144871 3'  GCCCAGGCTGGAGTGCAG    84127
                                 CTGCACTCCAGCCTGGGT
                                 ||||||||||||||||||
                                 GACGTGAGGTCGGACCCG

GAM97   LOC145009 3'  GTCGCCCAGGCTGGAGTGCAGT 60979
            G                    CACTGCACTCCAGCCTGGGTGAC
                                 |||||||||||||||||||||||
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                                GTGACGTGAGGTCGGACCCGCTG

GAM97   LOC145268 5'  GCCCAGGCTGGAGCGAAGTG   77581      GCA
                                CACT   CTCCAGCCTGGGT
                                ||||   |||||||||||||
                                GTGA   GAGGTCGGACCCG
                                  AGC
GAM97   LOC145387 3'  GCCAAGGCCAGGTGCAGTG    84338         CCA    G
                                CACTGCACT   GCCT GGT
                                |||||||||   |||| |||
                                GTGACGTGG   CGGA CCG
                                     AC_    A
GAM97   LOC145622 3'  ACAGGGGTTGGAATGCAGTG   77800        C       GG
                                CACTGCA TCCAGCCT  GT
                                |||||||| ||||||||  ||
                                GTGACGT AGGTTGGG  CA
                                    A       GA
GAM97   LOC145676 5'  GTCATGGGAGACTGGAGTGCAG 77848           ___   GG
                                CTGCACTCCAG   CCT  GTGAC
                                ||||||||||   |||  |||||
                                GACGTGAGGTC   GGG  TACTG
                                      AGA   __
GAM97   LOC145725 3'  GTCACCAGGCTGGAGTACAGTG 77887       C          G
                                CACTG ACTCCAGCCTGG TGAC
                                ||||| |||||||||||| ||||
                                GTGAC TGAGGTCGGACC ACTG
                                  A          _
GAM97   LOC145732 3'  GTCACCAGGCTGGAGTACAGTG 77899       C          G
                                CACTG ACTCCAGCCTGG TGAC
                                ||||| |||||||||||| ||||
                                GTGAC TGAGGTCGGACC ACTG
                                  A          _
GAM97   LOC145757 5'  GCCCAGGCTGGAGTGCGGTG   77935
                                CACTGCACTCCAGCCTGGGT
                                ||||||||||||||||||||
                                GTGGCGTGAGGTCGGACCCG

GAM97   LOC145757 5'  GTCGCCCAGGCTGGAGTGCAGT 77940
          G                      CACTGCACTCCAGCCTGGGTGAC
                                 |||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCGCTG

GAM97   LOC145813 5'  GTCACCCAGGCTGGAGTGCAAT 84511    C
          G                      CA TGCACTCCAGCCTGGGTGAC
                                 || ||||||||||||||||||
                                 GT ACGTGAGGTCGGACCCACTG
                                  A
GAM97   LOC146050 3'  GTCGTCCAGGCTGGAGTGCAGT 78120              GT
          G                      CACTGCACTCCAGCCTGG  GAC
                                 ||||||||||||||||  |||
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                                GTGACGTGAGGTCGGACC CTG
                                      TG
GAM97   LOC146050 3' GTTGCCCAGGCTGGAGTGCAAT 78123    C          TG
           G                   CA TGCACTCCAGCCTGGG AC
                               || |||||||||||||||  ||
                               GT ACGTGAGGTCGGACCC TG
                                A            GT
GAM97   LOC146229 3' GCCTAGGCTGGAGTACAGTG  78288     C
                               CACTG ACTCCAGCCTGGGT
                               ||||| |||||||||||||
                               GTGAC TGAGGTCGGATCCG
                                  A
GAM97   LOC146229 3' GCCTAGGCTGGAGTGCAATG  78289    C
                               CA TGCACTCCAGCCTGGGT
                               || ||||||||||||||||
                               GT ACGTGAGGTCGGATCCG
                                A
GAM97   LOC146229 3' GTCGCCCAGGCTAGAGTGCAGT 78304         C
           G                   CACTGCACTC AGCCTGGGTGAC
                               |||||||||| ||||||||||||
                               GTGACGTGAG TCGGACCCGCTG
                                     A
GAM97   LOC146229 3' GTCGCCCAGGCTGGAGTGCAGT 78306
           G                   CACTGCACTCCAGCCTGGGTGAC
                               ||||||||||||||||||||||
                               GTGACGTGAGGTCGGACCCGCTG

GAM97   LOC146346 5' CCAGGCTGGAGTGCTGTG    78390    T
                               CAC GCACTCCAGCCTGG
                               ||| ||||||||||||||
                               GTG CGTGAGGTCGGACC
                                 T
GAM97   LOC146346 5' GTTGCCCAGGCTGGAGTGCAGT 78407              TG
           G                   CACTGCACTCCAGCCTGGG AC
                               |||||||||||||||||  ||
                               GTGACGTGAGGTCGGACCC TG
                                        GT
GAM97   LOC146429 5' GTCACCAGGCTGGAGTGCAGTG 84674              G
                               CACTGCACTCCAGCCTGG TGAC
                               |||||||||||||||| ||||
                               GTGACGTGAGGTCGGACC ACTG
                                        _
GAM97   LOC146443 5' CCCGGGCTGGAGTGCAGTG   78441
                               CACTGCACTCCAGCCTGGG
                               ||||||||||||||||||
                               GTGACGTGAGGTCGGGCCC

GAM97   LOC146455 3' GTCGCCCAGGCTGGAGTGTAGT 78464
           G                   CACTGCACTCCAGCCTGGGTGAC
                               |||||||||||||||||||||||
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                                GTGATGTGAGGTCGGACCCGCTG

GAM97   LOC146603 5'  GTCGCCCAGGCTGGAGTGCAGT 78604
                G                CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCGCTG

GAM97   LOC146784 5'  GCCCAGGCTGGAGTGCGGTG  78715
                                 CACTGCACTCCAGCCTGGGT
                                 ||||||||||||||||||||
                                 GTGGCGTGAGGTCGGACCCG

GAM97   LOC146839 3'  GTTGCCCAGGCTGGAGTGCAGT 84848              TG
                G                CACTGCACTCCAGCCTGGG  AC
                                 |||||||||||||||||  ||
                                 GTGACGTGAGGTCGGACCC  TG
                                       GT
GAM97   LOC146894 3'  TGCCCAGGCTGGAGTGCAGTG  59868
                                 CACTGCACTCCAGCCTGGGTG
                                 |||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCGT

GAM97   LOC146895 5'  GTCACCCAGGCTGGAGTGCAGT 84871
                G                CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCACTG

GAM97   LOC146901 3'  TCAGGCTGGAGTGCAGTG    84910
                                 CACTGCACTCCAGCCTGG
                                 ||||||||||||||||
                                 GTGACGTGAGGTCGGACT

GAM97   LOC146909 3'  GTCGCCCAGGCTGGAGTGCAGT 78778
                G                CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCGCTG

GAM97   LOC146909 3'  GTCGCCCAGGCTGGAGTGCAGT 78779
                G                CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCGCTG

GAM97   LOC146952 5'  GTTGCCCAGGCTGGAATGCAGT 84933       C        TG
                G                CACTGCA TCCAGCCTGGG  AC
                                 |||||||  ||||||||||  ||
                                 GTGACGT AGGTCGGACCC  TG
                                    A        GT
GAM97   LOC147071 5'  GTTGCCCAGGCTGAAGTGCAAT 73370    C    C       TG
                G                CA TGCACT CAGCCTGGG  AC
                                 ||  ||||||  |||||||||  ||
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                                GT ACGTGA GTCGGACCC  TG
                                 A     A        GT
GAM97   LOC147080 5' GTCCGCCAGGCTGGAGTGCAGT 85049              GT
           G                     CACTGCACTCCAGCCTGG  GAC
                                 |||||||||||||||||  |||
                                 GTGACGTGAGGTCGGACC  CTG
                                       GC
GAM97   LOC147166 3' GTTGCCCAGGCTGGAGTGCAGT 78892               TG
           G                     CACTGCACTCCAGCCTGGG  AC
                                 ||||||||||||||||||  ||
                                 GTGACGTGAGGTCGGACCC  TG
                                       GT
GAM97   LOC147276 3' GCCCACGCTGGAGTGCAATG   78964    C         C
                                 CA TGCACTCCAGC TGGGT
                                 || ||||||||||| |||||
                                 GT ACGTGAGGTCG ACCCG
                                  A          C
GAM97   LOC147343 5' GTCACCCAGGCTAGAGGGTGGT 85132     TG A   C
           G                     CAC  C CTC AGCCTGGGTGAC
                                 |||  | ||| ||||||||||||
                                 GTG  G GAG TCGGACCCACTG
                                   GT G   A
GAM97   LOC147429 5' GTTGCCCAGGCTGGAATACAGT 78998       CAC         TG
           G                     CACTG   TCCAGCCTGGG  AC
                                 |||||   ||||||||||  ||
                                 GTGAC   AGGTCGGACCC  TG
                                    ATA          GT
GAM97   LOC147622 3' GTCCCCTAGGCTGCAGTGCAGT 85170         C        T
           G                     CACTGCACT CAGCCTGGG GAC
                                 ||||||||| ||||||||| |||
                                 GTGACGTGA GTCGGATCC CTG
                                       C        C
GAM97   LOC147660 3' TGCCCAGGCTAGAGTGCAATG  79034    C      C
                                 CA TGCACTC AGCCTGGGTG
                                 || ||||||| ||||||||||
                                 GT ACGTGAG TCGGACCCGT
                                  A      A
GAM97   LOC147694 3' GTCACCCAGGCTGGAGTGCAGT 79105
           G                     CACTGCACTCCAGCCTGGGTGAC
                                 |||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCACTG

GAM97   LOC147817 3' GTCACCCAGGCTGTAGTGGAGT 79188      G    C
           G                     CACT CACT CAGCCTGGGTGAC
                                 |||| |||| ||||||||||||
                                 GTGA GTGA GTCGGACCCACTG
                                   G    T
GAM97   LOC147817 3' GTCGCCCAGGCTGGAGTGCAAT 79189    C
           G                     CA TGCACTCCAGCCTGGGTGAC
                                 || ||||||||||||||||||
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                                GT ACGTGAGGTCGGACCCGCTG
                                 A
GAM97   LOC147841 3'  CCAGTCTGGAGTGCAATG    79224    C        C
                                CA TGCACTCCAG CTGG
                                || |||||||||| ||||
                                GT ACGTGAGGTC GACC
                                 A         T
GAM97   LOC147895 5'  GCCTACGCTGGAGTGCAGTG   85200             C
                                CACTGCACTCCAGC TGGGT
                                |||||||||||||| |||||
                                GTGACGTGAGGTCG ATCCG
                                          C
GAM97   LOC147990 3'  GTCACCCAGGCTAGAATGCAGT 85229        C  C
           G                     CACTGCA TC AGCCTGGGTGAC
                                 ||||||| || ||||||||||||
                                 GTGACGT AG TCGGACCCACTG
                                     A  A
GAM97   LOC147990 3'  GTCACCCAGGCTGGAGTGCGGT 85231
           G                     CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||||
                                 GTGGCGTGAGGTCGGACCCACTG

GAM97   LOC148137 3'  GCCCAGGCTGTAGTACAATG   59101    C  C   C
                                CA TG ACT CAGCCTGGGT
                                || || ||| ||||||||||
                                GT AC TGA GTCGGACCCG
                                 A  A   T
GAM97   LOC148137 3'  GTCACCCAGGCTGGAGTGC    59111
                                GCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||
                                CGTGAGGTCGGACCCACTG

GAM97   LOC148147 3'  GTCACCAGGCTGGAGTGCAGTG 79404                 G
                                CACTGCACTCCAGCCTGG TGAC
                                |||||||||||||||| ||||
                                GTGACGTGAGGTCGGACC ACTG
                                          _
GAM97   LOC148195 3'  ATCCAGGCTGGTGTGCAGTG   85269         T
                                CACTGCAC CCAGCCTGGGT
                                |||||||| ||||||||||
                                GTGACGTG GGTCGGACCTA
                                     T
GAM97   LOC148195 5'  GTCACCTAGGCTGCAGTGCAGT 85288          C
           G                     CACTGCACT CAGCCTGGGTGAC
                                 ||||||||| ||||||||||||
                                 GTGACGTGA GTCGGATCCACTG
                                      C
GAM97   LOC148198 3'  CACCCAGGCTGGAGTACAGTG  71219       C
                                CACTG ACTCCAGCCTGGGTG
                                ||||| ||||||||||||||
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                                GTGAC TGAGGTCGGACCCAC
                                   A
GAM97   LOC148443 3'  GTCACCCAGGCTGGGATGCAGT 79605        CT
            G                    CACTGCA  CCAGCCTGGGTGAC
                                 |||||||  ||||||||||||||
                                 GTGACGT  GGTCGGACCCACTG
                                    AG
GAM97   LOC148645 5'  GCCAAGGCTGGAATGCAGTG   85336        C       G
                                 CACTGCA TCCAGCCT GGT
                                 ||||||| |||||||| |||
                                 GTGACGT AGGTCGGA CCG
                                    A       A
GAM97   LOC148709 5'  ACTCAGGCTGGAGTGCGGTG   79686
                                 CACTGCACTCCAGCCTGGGT
                                 ||||||||||||||||||||
                                 GTGGCGTGAGGTCGGACTCA

GAM97   LOC148709 3'  GCCCACACTAGAGTGCAATG   79694    C      C  CC
                                 CA TGCACTC AG  TGGGT
                                 || ||||||| ||  |||||
                                 GT ACGTGAG TC  ACCCG
                                  A      A  AC
GAM97   LOC148758 5'  GCTTAGGCCGGGCGCAGTG    79723       A T  A
                                 CACTGC C CC GCCTGGGT
                                 |||||| | || ||||||||
                                 GTGACG G GG CGGATTCG
                                    C _  C
GAM97   LOC148759 3'  TCACCCAGGCCCAGCGTA    85376     A  CCA
                                 TGC CT   GCCTGGGTGA
                                 ||| ||   ||||||||||
                                 ATG GA   CGGACCCACT
                                   C  CC_
GAM97   LOC148887 5'  GTCGCCCAGGCTGGAGTGCAGT 85409
            G                    CACTGCACTCCAGCCTGGGTGAC
                                 |||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCGCTG

GAM97   LOC149132 5'  CCAAGGCTGGAGTGTAGT    79924             G
                                 ACTGCACTCCAGCCT GG
                                 |||||||||||||| ||
                                 TGATGTGAGGTCGGA CC
                                           A
GAM97   LOC149296 5'  CACCCAGGCATATGGGCA    80019     ACT  ___
                                 TGC   CCA   GCCTGGGTG
                                 |||   |||   |||||||||
                                 ACG   GGT   CGGACCCAC
                                   ___   ATA
GAM97   LOC149421 3'  GTCGCCCAGGCTGGAGGGCAGT 80149        A
            G                    CACTGC CTCCAGCCTGGGTGAC
                                 ||||||| ||||||||||||||||
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                                GTGACG GAGGTCGGACCCGCTG
                                   G
GAM97   LOC149478 3'  CGAGGCTGGAGTGTAGTG    80166            G
                                CACTGCACTCCAGCCT G
                                |||||||||||||||| |
                                GTGATGTGAGGTCGGA C
                                      G
GAM97   LOC149506 3'  GCCCAGGCTGTAGTGCAGTG   85638         C
                                CACTGCACT CAGCCTGGGT
                                ||||||||| ||||||||||
                                GTGACGTGA GTCGGACCCG
                                     T
GAM97   LOC149506 3'  GTCGGCCAGGCTAGAGTGCAGT 85643         C      G
           G                     CACTGCACTC AGCCTGG TGAC
                                ||||||||| ||||||| ||||
                                GTGACGTGAG TCGGACC GCTG
                                     A      G
GAM97   LOC149577 3'  CACCCAAGCTGGAGTGCAGTG  85666            C
                                CACTGCACTCCAGC TGGGTG
                                |||||||||||||| ||||||
                                GTGACGTGAGGTCG ACCCAC
                                      A
GAM97   LOC149577 3'  GCCCAGGCTGGAGTGCGGTG   85679
                                CACTGCACTCCAGCCTGGGT
                                ||||||||||||||||||
                                GTGGCGTGAGGTCGGACCCG

GAM97   LOC149692 3'  GTCACCCAGGCTGGAGTGCAGT 85742
           G                     CACTGCACTCCAGCCTGGGTGAC
                                |||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCACTG

GAM97   LOC149705 3'  GCTCTTGGCCAGGTGCAGT    85783        CCA   T_
                                ACTGCACT   GCC  GGGT
                                ||||||||   |||  ||||
                                TGACGTGG   CGG  CTCG
                                     AC_   TT
GAM97   LOC149734 3'  CGTCACCCAGGCTGGAGTGCAG 85794                    ___
           TG                     CACTGCACTCCAGCCTGGGTGAC   G
                                |||||||||||||||||||||||   |
                                GTGACGTGAGGTCGGACCCACTG   C
                                                    ___
GAM97   LOC149734 3'  GTGACCCAGGCTGGAGTGTAGT 85798               G
                                ACTGCACTCCAGCCTGGGT AC
                                |||||||||||||||||| ||
                                TGATGTGAGGTCGGACCCA TG
                                      G
GAM97   LOC150054 5'  GTCGCCCAGGCTGGAGTGCAGT 85977
           G                     CACTGCACTCCAGCCTGGGTGAC
                                |||||||||||||||||||||||
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                                GTGACGTGAGGTCGGACCCGCTG

GAM97   LOC150225 3'  GCTCAGGCTGGAGTGCAGTG   86195
                                CACTGCACTCCAGCCTGGGT
                                ||||||||||||||||||||
                                GTGACGTGAGGTCGGACTCG

GAM97   LOC150290 3'  GTCACCCATCCTAGAGTGCAGT 80590          C  CC
                                ACTGCACTC AG  TGGGTGAC
                                ||||||||| ||  ||||||||
                                TGACGTGAG TC  ACCCACTG
                                      A  CT
GAM97   LOC150397 3'  GTCGTCCAGGTTAGAGTGCAAT 80665    C      C      GT
            G                    CA TGCACTC AGCCTGG  GAC
                                || ||||||| |||||||  |||
                                GT ACGTGAG TTGGACC  CTG
                                 A      A      TG
GAM97   LOC150407 3'  CCAGGCTAGAGTGCAGTG    80638          C
                                CACTGCACTC AGCCTGG
                                |||||||||| |||||||
                                GTGACGTGAG TCGGACC
                                      A
GAM97   LOC150696 3'  GTCACCCAGGCTGGAGTGTAGT 59165
            G                    CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||||
                                GTGATGTGAGGTCGGACCCACTG

GAM97   LOC150889 3'  ATCCAGGCCAGGTGCAGTG    80810         CCA
                                CACTGCACT   GCCTGGGT
                                |||||||||   ||||||||
                                GTGACGTGG   CGGACCTA
                                      AC_
GAM97   LOC150960 3'  GTCACCCAGGCTGGAGTGCAGT 80876
            G                    CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCACTG

GAM97   LOC151057 3'  GTCACCCAGGCTGGAGTGCAGT 86394
            G                    CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCACTG

GAM97   LOC151195 3'  CCAGGCTGGAGTGCAGTG    80968
                                CACTGCACTCCAGCCTGG
                                ||||||||||||||||||
                                GTGACGTGAGGTCGGACC

GAM97   LOC151201 3'  GTCACCAGGCTGGAGTGCAGTG 86481                G
                                CACTGCACTCCAGCCTGG TGAC
                                |||||||||||||||||| ||||
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                                GTGACGTGAGGTCGGACC ACTG
                                                   _
GAM97   LOC151201 3'  GTCACCCAGGCTGGAGTCCAAT 86483    C  C
            G                   CA TG ACTCCAGCCTGGGTGAC
                                || || ||||||||||||||||
                                GT AC TGAGGTCGGACCCACTG
                                 A  C
GAM97   LOC151429 3'  CAGTGTAGGCTGGGTGCAGTG  86528        T       G _
                                CACTGCAC CCAGCCTG G TG
                                |||||||| |||||||| | ||
                                GTGACGTG GGTCGGAT T AC
                                     _       G G
GAM97   LOC151475 5'  GTCATCCAGGCTGGAGTGCAGT 86600
            G                   CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCTACTG

GAM97   LOC151475 5'  GTGGCCCAGGCTGGAGTGTAGT 86602                 G
            G                   CACTGCACTCCAGCCTGGGT AC
                                |||||||||||||||||| ||
                                GTGATGTGAGGTCGGACCCG TG
                                              G
GAM97   LOC151701 3'  GTCGCCCAGGCTGGAGTGCAGT 86679
                                ACTGCACTCCAGCCTGGGTGAC
                                |||||||||||||||||||||
                                TGACGTGAGGTCGGACCCGCTG

GAM97   LOC151826 3'  GTCACCCAGGCTGGAGTGCAGT 81185
            G                   CACTGCACTCCAGCCTGGGTGAC
                                |||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCACTG

GAM97   LOC151877 3'  CCCAAGCTGGAGTCCAGTG    86695       C       C
                                CACTG ACTCCAGC TGGG
                                ||||| |||||||| ||||
                                GTGAC TGAGGTCG ACCC
                                   C       A
GAM97   LOC151979 5'  GTTGCCCAAGCTGGAATGCAGT 81253        C     C    TG
            G                   CACTGCA TCCAGC TGGG  AC
                                ||||||| |||||| ||||  ||
                                GTGACGT AGGTCG ACCC  TG
                                    A     A    GT
GAM97   LOC152137 3'  GTCACACAGGCTGGAGTGCAGT 81323                 G
            G                   CACTGCACTCCAGCCTG GTGAC
                                |||||||||||||||| |||||
                                GTGACGTGAGGTCGGAC CACTG
                                              A
GAM97   LOC152220 3'  GTCACTCAGGCTGGAGTGCAGT 86769
            G                   CACTGCACTCCAGCCTGGGTGAC
                                |||||||||||||||||||||||
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                                GTGACGTGAGGTCGGACTCACTG

GAM97   LOC152245 3'  GTCGCCCAGGCTGGAGTGAGTG 86783      G
                                CACT CACTCCAGCCTGGGTGAC
                                |||| ||||||||||||||||||
                                GTGA GTGAGGTCGGACCCGCTG
                                  _
GAM97   LOC152282 5'  GTTGCCCAGGCTGGAGTATAGT 81407      C          TG
                                ACTG ACTCCAGCCTGGG  AC
                                |||| ||||||||||||  ||
                                TGAT TGAGGTCGGACCC  TG
                                   A          GT
GAM97   LOC152300 3'  GTCACCCAGGCTGGAGTGCAGT 81388
            G                    CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCACTG

GAM97   LOC152343 3'  GTCACCCAGGCTGGAGTGCAGT 81431
            G                    CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCACTG

GAM97   LOC152445 3'  GTTGCCCAGGCTGGAGTGCAGT 86961              TG
            G                    CACTGCACTCCAGCCTGGG  AC
                                |||||||||||||||||  ||
                                GTGACGTGAGGTCGGACCC  TG
                                      GT
GAM97   LOC152620 3'  GTTGCCCAGGCTGGAGTGCAGT 60711              TG
            G                    CACTGCACTCCAGCCTGGG  AC
                                |||||||||||||||||  ||
                                GTGACGTGAGGTCGGACCC  TG
                                      GT
GAM97   LOC152719 5'  GCCCAGCCTGGAGTGCAGTG   87031          C
                                CACTGCACTCCAG CTGGGT
                                |||||||||||| ||||||
                                GTGACGTGAGGTC GACCCG
                                       C
GAM97   LOC152719 5'  GTCGCCCAGGCTGGAATGCAGT 87040       C
            G                    CACTGCA TCCAGCCTGGGTGAC
                                ||||||| ||||||||||||||
                                GTGACGT AGGTCGGACCCGCTG
                                   A
GAM97   LOC152794 5'  GTTACCCAGGCTGGAGTGCAGT 81561
            G                    CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCATTG

GAM97   LOC152804 3'  CAGGCTTGGAGTGCAGTG    87074          _
                                CACTGCACTCCA GCCTG
                                |||||||||||| |||||
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                                GTGACGTGAGGT CGGAC
                                       T
GAM97   LOC152851 3'  GCCTAGGCTGGAGTGCAGTG   81591
                                CACTGCACTCCAGCCTGGGT
                                ||||||||||||||||||||
                                GTGACGTGAGGTCGGATCCG

GAM97   LOC152925 3'  GCCCAGGCTGGAGTGCAG    81619
                                CTGCACTCCAGCCTGGGT
                                ||||||||||||||||||
                                GACGTGAGGTCGGACCCG

GAM97   LOC153077 3'  TCACCCAGGCTGGAGTGCAGTG 87131
                                CACTGCACTCCAGCCTGGGTGA
                                ||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCACT

GAM97   LOC153443 3'  GTTGCCCAGACTAGAGTACA   81690    C    C  C    TG
                                TG ACTC AG CTGGG  AC
                                || |||| || |||||  ||
                                AC TGAG TC GACCC  TG
                                 A    A  A    GT
GAM97   LOC153688 3'  GTCACCCAGGCTGGAGTGCAAT 87328    C
          G                      CA TGCACTCCAGCCTGGGTGAC
                                || ||||||||||||||||||||
                                GT ACGTGAGGTCGGACCCACTG
                                 A
GAM97   LOC153811 5'  GTCACCCAGGCAGGAGTGCAGT 81846          A
          G                      CACTGCACTCC GCCTGGGTGAC
                                ||||||||||| ||||||||||
                                GTGACGTGAGG CGGACCCACTG
                                       A
GAM97   LOC153811 3'  GTCGCCCAGACTGGAGTGCAGT 81847          C
                                ACTGCACTCCAG CTGGGTGAC
                                |||||||||||| |||||||||
                                TGACGTGAGGTC GACCCGCTG
                                       A
GAM97   LOC153811 3'  GTTGCCCAGACTGGAGTGCAGT 81848          C    TG
          G                      CACTGCACTCCAG CTGGG  AC
                                |||||||||||| |||||  ||
                                GTGACGTGAGGTC GACCC  TG
                                       A    GT
GAM97   LOC153883 5'  GCCCAGGCTGGAGTGCAGTG   81895
                                CACTGCACTCCAGCCTGGGT
                                ||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCG

GAM97   LOC153910 5'  GCCCAGTCTGGAGTGCAGTG   81908          C
                                CACTGCACTCCAG CTGGGT
                                |||||||||||| ||||||
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                                GTGACGTGAGGTC GACCCG
                                       T
GAM97   LOC154007 3'  CTGGCTGGAGTGCAGTG     81925            T
                                CACTGCACTCCAGCC GG
                                ||||||||||||||| ||
                                GTGACGTGAGGTCGG TC
                                        _
GAM97   LOC154282 5'  GTCGCCAGGTTGGAGTGCAGTG 87411              G
                                CACTGCACTCCAGCCTGG TGAC
                                |||||||||||||||||| ||||
                                GTGACGTGAGGTTGGACC GCTG
                                       _
GAM97   LOC154726 5'  GTTGCCCAGGCTGGAGTGCAGT 82012              TG
          G                      CACTGCACTCCAGCCTGGG  AC
                                |||||||||||||||||||  ||
                                GTGACGTGAGGTCGGACCC  TG
                                       GT
GAM97   LOC154822 3'  GTCAGCCAGGCTGGAGTGCAAT 87488    C          G
          G                      CA TGCACTCCAGCCTGG TGAC
                                || |||||||||||||| ||||
                                GT ACGTGAGGTCGGACC ACTG
                                 A           G
GAM97   LOC154877 3'  CCAGGCTGGAATGCCGTG    87536     T  C
                                CAC GCA TCCAGCCTGG
                                ||| ||| ||||||||||
                                GTG CGT AGGTCGGACC
                                  C  A
GAM97   LOC154877 3'  GCCCAGGGTGGAGTGCAGTG   87555          G
                                CACTGCACTCCA CCTGGGT
                                |||||||||||| |||||||
                                GTGACGTGAGGT GGACCCG
                                       G
GAM97   LOC154930 3'  CCAGGCTGGAGTGCACTG    82088    C
                                CA TGCACTCCAGCCTGG
                                || ||||||||||||||
                                GT ACGTGAGGTCGGACC
                                 C
GAM97   LOC155376 3'  ATTCAGGCTGGGTGCAGTG    82240        T
                                CACTGCAC CCAGCCTGGGT
                                |||||||| ||||||||||
                                GTGACGTG GGTCGGACTTA
                                       _
GAM97   LOC157247 5'  GCCCAGGGCTGGAGTGCAGTG  82299             _
                                CACTGCACTCCAGCC TGGGT
                                |||||||||||||| |||||
                                GTGACGTGAGGTCGG ACCCG
                                       G
GAM97   LOC157506 3'  GTCACCAGGCTGGAGTGCAGT  82372              G
                                ACTGCACTCCAGCCTGG TGAC
                                |||||||||||||||| ||||
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                                TGACGTGAGGTCGGACC ACTG
                                                  _
GAM97   LOC157562 5' CCAGGCCAGGTGCAGTG     87773         CCA
                                CACTGCACT   GCCTGG
                                |||||||||   ||||||
                                GTGACGTGG   CGGACC
                                     AC_
GAM97   LOC157858 5' GTCACCTGGTTGAAGTGCAG   87893       C    T
                                CTGCACT CAGCC GGGTGAC
                                ||||||| ||||| |||||||
                                GACGTGA GTTGG TCCACTG
                                    A    _
GAM97   LOC158014 5' GTCACCCAGGCTGGAGTGTAGT 82564
            G                    CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
                                GTGATGTGAGGTCGGACCCACTG

GAM97   LOC158310 5' GCCCAGGCTGGAGTGCAGTG   88083
                                CACTGCACTCCAGCCTGGGT
                                ||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCG

GAM97   LOC158310 5' GTCGCCCAGGCTGGAGTGCAGT 88087
            G                    CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCGCTG

GAM97   LOC158402 5' GTTGCCCAGGCTGGAGTGCAGT 88151               TG
            G                    CACTGCACTCCAGCCTGGG  AC
                                |||||||||||||||||  ||
                                GTGACGTGAGGTCGGACCC  TG
                                          GT
GAM97   LOC158476 3' GCCCCAGCTTGAGTGCAGTG   88195         C   CT
                                CACTGCACTC AGC  GGGT
                                |||||||||| |||  ||||
                                GTGACGTGAG TCG  CCCG
                                     T   AC
GAM97   LOC158476 3' GTCGCCCAGGCTGGAGTGCAGT 88202
            G                    CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCGCTG

GAM97   LOC158549 5' GTCTCCCAGGCTGGAGTGCAGT 88227               T
            G                    CACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||  |||
                                GTGACGTGAGGTCGGACCC CTG
                                          T
GAM97   LOC158668 3' GTTGCCCAGGCTGGAGTGCAAT 69904    C           TG
            G                    CA TGCACTCCAGCCTGGG  AC
                                ||  ||||||||||||||  ||
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                                GT ACGTGAGGTCGGACCC  TG
                                 A             GT
GAM97   LOC160646 3'  GTCACCCAGGCTGGAGTGCAGT 83119
                  G             CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCACTG

GAM97   LOC161829 3'  GTCACCCAGGCTGGAGTGTAGT 83192
                  G             CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
                                GTGATGTGAGGTCGGACCCACTG

GAM97   LOC162427 3'  GTTGCCCAGGCTGGAGTGCAGT 83228                TG
                  G             CACTGCACTCCAGCCTGGG  AC
                                |||||||||||||||||  ||
                                GTGACGTGAGGTCGGACCC  TG
                                              GT
GAM97   LOC162962 3'  CCAGGCTGGAATGCAGTG    83254        C
                                CACTGCA TCCAGCCTGG
                                ||||||| ||||||||||
                                GTGACGT AGGTCGGACC
                                   A
GAM97   LOC162962 3'  GTCGCCAGGCTGGAATGCAGTG 83259        C        G
                                CACTGCA TCCAGCCTGG TGAC
                                ||||||| |||||||||| ||||
                                GTGACGT AGGTCGGACC GCTG
                                   A        _
GAM97   LOC169611 3'  GCCCGGGCTGGAATGCAATG   83651    C    C
                                CA TGCA TCCAGCCTGGGT
                                || |||| ||||||||||||
                                GT ACGT AGGTCGGGCCCG
                                 A    A
GAM97   LOC170409 5'  ATAAGGGCTGGAGTGCTGTG   83741     T         GG
                                CAC GCACTCCAGCCT  GT
                                ||| ||||||||||||  ||
                                GTG CGTGAGGTCGGG  TA
                                  T          AA
GAM97   LOC196047 5'  GTCTCCCAGGCTGGAGTGCA   91162              T
                                TGCACTCCAGCCTGGG GAC
                                |||||||||||||||| |||
                                ACGTGAGGTCGGACCC CTG
                                          T
GAM97   LOC196264 3'  GTCGCCAGGCTGGAGTGCAGTG 88991                 G
                                CACTGCACTCCAGCCTGG TGAC
                                |||||||||||||||||| ||||
                                GTGACGTGAGGTCGGACC GCTG
                                                 _
GAM97   LOC196411 3'  GCCTGGGCTGGAATGCAGTG   89048        C      TG
                                CACTGCA TCCAGCC  GGT
                                ||||||| |||||||  |||
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                                GTGACGT AGGTCGG  CCG
                                   A      GT
GAM97   LOC196529 3'  GTTGCCCAGGCTGGAGTGCAAT 89138    C           TG
           G                    CA TGCACTCCAGCCTGGG  AC
                                || ||||||||||||||||  ||
                                GT ACGTGAGGTCGGACCC  TG
                                 A             GT
GAM97   LOC196529 3'  GTTGCCCAGGCTGGAGTGCAAT 89139    C           TG
           G                    CA TGCACTCCAGCCTGGG  AC
                                || ||||||||||||||||  ||
                                GT ACGTGAGGTCGGACCC  TG
                                 A             GT
GAM97   LOC196957 3'  GTCACCAGGCTGGAGTACAGTG 89193      C         G
                                CACTG ACTCCAGCCTGG TGAC
                                ||||| |||||||||||| ||||
                                GTGAC TGAGGTCGGACC ACTG
                                   A          _
GAM97   LOC196961 3'  GTCACCAGGCTGGAGTACAGTG 89206      C         G
                                CACTG ACTCCAGCCTGG TGAC
                                ||||| |||||||||||| ||||
                                GTGAC TGAGGTCGGACC ACTG
                                   A          _
GAM97   LOC197138 3'  GTCACCAGGCTGGAGTACAGTG 89255      C         G
                                CACTG ACTCCAGCCTGG TGAC
                                ||||| |||||||||||| ||||
                                GTGAC TGAGGTCGGACC ACTG
                                   A          _
GAM97   LOC197358 3'  GTCACCCAGGCTGGAGTGCAGT 89440
           G                    CACTGCACTCCAGCCTGGGTGAC
                                |||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCACTG

GAM97   LOC197358 3'  GTCGCCCAGGCTGGAGTGCAGT 89442
           G                    CACTGCACTCCAGCCTGGGTGAC
                                |||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCGCTG

GAM97   LOC199699 3'  GTCACCCAGGCTGGAGTGCAAT 89680    C
           G                    CA TGCACTCCAGCCTGGGTGAC
                                || |||||||||||||||||||
                                GT ACGTGAGGTCGGACCCACTG
                                 A
GAM97   LOC199699 3'  GTCGCCCAGGCTGGAGTGCAGT 89682
           G                    CACTGCACTCCAGCCTGGGTGAC
                                |||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCGCTG

GAM97   LOC199725 5'  GTCACCTAGGCTGGATTGCAAT 91425    C   C
           G                    CA TGCA TCCAGCCTGGGTGAC
                                || |||| ||||||||||||||||
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                                GT ACGT AGGTCGGATCCACTG
                                 A    T
GAM97   LOC199786 3'  GTCACCCGGGCTGGAGTGCAGT 89763
                  G                CACTGCACTCCAGCCTGGGTGAC
                                   ||||||||||||||||||||||
                                   GTGACGTGAGGTCGGGCCCACTG

GAM97   LOC199899 5'  CTCAGGCTGGAGTACAGTG   91466      C
                                   CACTG ACTCCAGCCTGGG
                                   ||||| ||||||||||||
                                   GTGAC TGAGGTCGGACTC
                                      A
GAM97   LOC199906 3'  CCAGGCTGGAGTGCAGTG    89848
                                   CACTGCACTCCAGCCTGG
                                   ||||||||||||||||||
                                   GTGACGTGAGGTCGGACC

GAM97   LOC199936 5'  GTCACCCAGGCTGGAGTGCA  91485
                                   TGCACTCCAGCCTGGGTGAC
                                   ||||||||||||||||||||
                                   ACGTGAGGTCGGACCCACTG

GAM97   LOC200014 3'  CAGCCAGGCTGGAGTGCAGTG 89923                G
                                   CACTGCACTCCAGCCTGG TG
                                   |||||||||||||||| ||
                                   GTGACGTGAGGTCGGACC AC
                                              G
GAM97   LOC200107 3'  CCAGGCTGGAGTGCAGTG    89982
                                   CACTGCACTCCAGCCTGG
                                   ||||||||||||||||||
                                   GTGACGTGAGGTCGGACC

GAM97   LOC200169 5'  GTCGTCCAGGCTGGAGTGCAGT 91560              GT
                                   ACTGCACTCCAGCCTGG  GAC
                                   ||||||||||||||||  |||
                                   TGACGTGAGGTCGGACC  CTG
                                              TG
GAM97   LOC200301 5'  TCGCCCAGGCTGGAGTACAGTG 90155       C
                                   CACTG ACTCCAGCCTGGGTGA
                                   ||||| ||||||||||||||||
                                   GTGAC TGAGGTCGGACCCGCT
                                      A
GAM97   LOC200310 3'  GTCACCTAGGCTGGAGTGCAGT 66333
                  G                CACTGCACTCCAGCCTGGGTGAC
                                   ||||||||||||||||||||||
                                   GTGACGTGAGGTCGGATCCACTG

GAM97   LOC200314 3'  CCAGGCTGGGGTGCAGTG    91593
                                   CACTGCACTCCAGCCTGG
                                   ||||||||||||||||||
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                                GTGACGTGGGGTCGGACC

GAM97   LOC200316 3'  GTCGCCCAGACTAGAGTGCAAT 90190    C      C  C
            G                    CA TGCACTC AG CTGGGTGAC
                                 || ||||||| || |||||||||
                                 GT ACGTGAG TC GACCCGCTG
                                  A      A  A
GAM97   LOC200845 5'  GCAGGGGCTGGTGTGCAGTG   90318         T      GG
                                 CACTGCAC CCAGCCT  GT
                                 |||||||| |||||||  ||
                                 GTGACGTG GGTCGGG  CG
                                       T      GA
GAM97   LOC200860 3'  CCAGGCTGGAGTGCAATG    91741    C
                                 CA TGCACTCCAGCCTGG
                                 || ||||||||||||||
                                 GT ACGTGAGGTCGGACC
                                  A
GAM97   LOC200860 3'  GTCACCCAGGCTGGAGTGCAGT 91755
            G                    CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCACTG

GAM97   LOC201164 3'  GTGGCCCAGGCTGGAGTGCAGT 89500                  G
            G                    CACTGCACTCCAGCCTGGGT AC
                                 |||||||||||||||||| ||
                                 GTGACGTGAGGTCGGACCCG TG
                                                   G
GAM97   LOC201173 5'  GTTGCCCAGGCTGAAGTGCAAT 88691    C     C       TG
            G                    CA TGCACT CAGCCTGGG  AC
                                 || |||||| |||||||||  ||
                                 GT ACGTGA GTCGGACCC  TG
                                  A     A        GT
GAM97   LOC201220 5'  GTTGCCCAGGCTGAAGTGCAAT 88724    C     C       TG
            G                    CA TGCACT CAGCCTGGG  AC
                                 || |||||| |||||||||  ||
                                 GT ACGTGA GTCGGACCC  TG
                                  A     A        GT
GAM97   LOC201294 3'  CCAGGCCAGAGTGCAGTG    89577          CA
                                 CACTGCACTC  GCCTGG
                                 ||||||||||  ||||||
                                 GTGACGTGAG  CGGACC
                                       AC
GAM97   LOC201294 3'  GTCGCCCAGGCTGGAGTGCAGT 89594
            G                    CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCGCTG

GAM97   LOC201411 3'  GCCCAACCTGGAGTGCAATG   63644    C        CC
                                 CA TGCACTCCAG  TGGGT
                                 || ||||||||||  |||||
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                                GT ACGTGAGGTC  ACCCG
                                 A         CA
GAM97   LOC201626 3'  GTTGCCCAGGCTGGAGTGCAAT 90437    C            TG
                G                CA TGCACTCCAGCCTGGG  AC
                                 || ||||||||||||||||  ||
                                GT ACGTGAGGTCGGACCC  TG
                                 A             GT
GAM97   LOC201627 3'  GTTGCCCAGGCTGGAGTGCAAT 90458    C            TG
                G                CA TGCACTCCAGCCTGGG  AC
                                 || ||||||||||||||||  ||
                                GT ACGTGAGGTCGGACCC  TG
                                 A             GT
GAM97   LOC201696 3'  GTTGCCCAGGCTGGAGTGCAAT 63826    C            TG
                G                CA TGCACTCCAGCCTGGG  AC
                                 || ||||||||||||||||  ||
                                GT ACGTGAGGTCGGACCC  TG
                                 A             GT
GAM97   LOC201702 5'  GTCACCCAGGCTGGAGTGCAAT 90472    C
                G                CA TGCACTCCAGCCTGGGTGAC
                                 || ||||||||||||||||||||
                                GT ACGTGAGGTCGGACCCACTG
                                 A
GAM97   LOC202460 5'  GTCACCAGGCTGGAGTGCAGTG 90675              G
                                CACTGCACTCCAGCCTGG TGAC
                                |||||||||||||||| ||||
                                GTGACGTGAGGTCGGACC ACTG
                                          _
GAM97   LOC202908 5'  ACCACAGGCTGGAGTACAGTG  90703      C       _
                                CACTG ACTCCAGCCTG GGT
                                ||||| |||||||||| |||
                                GTGAC TGAGGTCGGAC CCA
                                   A         A
GAM97   LOC202908 5'  CCAAGGCTGGAGTGTAGT    90716           G
                                ACTGCACTCCAGCCT GG
                                |||||||||||||| ||
                                TGATGTGAGGTCGGA CC
                                        A
GAM97   LOC202908 5'  GTCACCCAGGCTGGAGTACAGT 90730      C
                G                CACTG ACTCCAGCCTGGGTGAC
                                 ||||| ||||||||||||||||
                                GTGAC TGAGGTCGGACCCACTG
                                   A
GAM97   LOC202908 5'  GTCACCCAGGCTTGACTACAGT 90732      CAC  C
                                ACTG   TC AGCCTGGGTGAC
                                ||||   || ||||||||||||
                                TGAC   AG TCGGACCCACTG
                                  ATC  T
GAM97   LOC202934 3'  GTCACCAGGCTGGAGTGCAGTG 92047              G
                                CACTGCACTCCAGCCTGG TGAC
                                |||||||||||||||| ||||
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                                GTGACGTGAGGTCGGACC ACTG
                                                   _
GAM97   LOC202934 3'  GTCACCCAGGCTGGAGTACAGT 92049      C
            G                  CACTG ACTCCAGCCTGGGTGAC
                               ||||| ||||||||||||||||
                               GTGAC TGAGGTCGGACCCACTG
                                 A
GAM97   LOC203197 3'  GTCACCCAGGCTGGAGTGCAGT 90815
            G                  CACTGCACTCCAGCCTGGGTGAC
                               ||||||||||||||||||||||
                               GTGACGTGAGGTCGGACCCACTG

GAM97   LOC203260 3'  ACTCTGGCTGGAGCCCAG    90848    CA      T
                               CTG  CTCCAGCC GGGT
                               |||  |||||||| ||||
                               GAC  GAGGTCGG CTCA
                                 CC       T
GAM97   LOC203263 5'  TCATACTGGAGTGCGG     92412          CCTGG
                               CTGCACTCCAG    GTGA
                               ||||||||||     ||||
                               GGCGTGAGGTC    TACT
                                     A____
GAM97   LOC203272 5'  TCATACTGGAGTGCGG     92413          CCTGG
                               CTGCACTCCAG    GTGA
                               ||||||||||     ||||
                               GGCGTGAGGTC    TACT
                                     A____
GAM97   LOC203297 5'  GTCACCCAGGCTGGAGTGCAAT 75873    C
            G                  CA TGCACTCCAGCCTGGGTGAC
                               || ||||||||||||||||||
                               GT ACGTGAGGTCGGACCCACTG
                                A
GAM97   LOC203350 3'  GTTGCCCAGGCTGGAGTGCAGT 92246               TG
            G                  CACTGCACTCCAGCCTGGG  AC
                               |||||||||||||||||  ||
                               GTGACGTGAGGTCGGACCC  TG
                                          GT
GAM97   LOC203369 3'  GTCTCCCAGGCTGGAGTGCAGT 90891               T
            G                  CACTGCACTCCAGCCTGGG GAC
                               |||||||||||||||||| |||
                               GTGACGTGAGGTCGGACCC CTG
                                          T
GAM97   LOC203378 3'  GTCGCCCAGGCTGGAGAGCAGT 92296       A
            G                  CACTGC CTCCAGCCTGGGTGAC
                               ||||||| ||||||||||||||||
                               GTGACG GAGGTCGGACCCGCTG
                                  A
GAM97   LOC203397 3'  GTTTTTCAGGCTGGGCACAGTG 90903      CA T       T
                               CACTG  C CCAGCCTGGG GAC
                               |||||  | ||||||||| |||
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                                GTGAC  G GGTCGGACTT TTG
                                  AC _         T
GAM97   LOC203427 3'  GTCACCCAGACTGGAGTACAAT 90921    C  C      C
          G                     CA TG ACTCCAG CTGGGTGAC
                                || || ||||||| |||||||||
                                GT AC TGAGGTC GACCCACTG
                                 A  A      A
GAM97   LOC204804 3'  GTCACCCAGGCTAGAGTGCAGT 91047          C
          G                     CACTGCACTC AGCCTGGGTGAC
                                |||||||||| ||||||||||||
                                GTGACGTGAG TCGGACCCACTG
                                      A
GAM97   LOC204804 3'  GTCTCCCAGGCTGGAGTACAGT 91049       C          T
          G                     CACTG ACTCCAGCCTGGG GAC
                                ||||| |||||||||||| |||
                                GTGAC TGAGGTCGGACCC CTG
                                  A           T
GAM97   LOC206795 5'  CACCGAACACGTAGAGTGCAG  92410        CA  C  ___
                                CTGCACTC  GC TG   GGTG
                                |||||||  || ||   ||||
                                GACGTGAG  TG AC   CCAC
                                    A_  C  AAG
GAM97   LOC219294 3'  GTCACCCAGGCTGGAGTGCAG  94598
                                CTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||
                                GACGTGAGGTCGGACCCACTG

GAM97   LOC219295 3'  GTCACCCAGGCTGGAGTGCAG  94589
                                CTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||
                                GACGTGAGGTCGGACCCACTG

GAM97   LOC219406 3'  GCAAGGCTGGGTGCAGTG    95204         T      GG
                                CACTGCAC CCAGCCT  GT
                                ||||||| |||||||  ||
                                GTGACGTG GGTCGGA  CG
                                    _      A_
GAM97   LOC219529 5'  ACCCAGCCTGGAGTGCAGTG   94561           C
                                CACTGCACTCCAG CTGGGT
                                |||||||||||| ||||||
                                GTGACGTGAGGTC GACCCA
                                      C
GAM97   LOC219673 5'  CACCCAGTCTGGAGTGCAGTG  94613           C
                                CACTGCACTCCAG CTGGGTG
                                |||||||||||| |||||||
                                GTGACGTGAGGTC GACCCAC
                                      T
GAM97   LOC219673 5'  GTTGCCCAGGCTGGAGGGCAGT 94630       A          TG
          G                     CACTGC CTCCAGCCTGGG  AC
                                |||||| ||||||||||||  ||
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                                GTGACG GAGGTCGGACCC  TG
                                   G          GT
GAM97   LOC219731 5'  GTCATCCAGGCTGGAGTGCAGT 94712
                 G                 CACTGCACTCCAGCCTGGGTGAC
                                   ||||||||||||||||||||||
                                   GTGACGTGAGGTCGGACCTACTG

GAM97   LOC219735 3'  GTTGCCCAGGCTGGAGTGCAGT 94734                TG
                                   ACTGCACTCCAGCCTGGG  AC
                                   ||||||||||||||||||  ||
                                   TGACGTGAGGTCGGACCC  TG
                                             GT
GAM97   LOC219894 3'  CCCAGGCTGGAGTGCAGTG   94901
                                   CACTGCACTCCAGCCTGGG
                                   ||||||||||||||||||
                                   GTGACGTGAGGTCGGACCC

GAM97   LOC220074 3'  GTCACACAGGCTGGAGTGCAGT 59991                 G
                 G                 CACTGCACTCCAGCCTG GTGAC
                                   |||||||||||||||| |||||
                                   GTGACGTGAGGTCGGAC CACTG
                                             A
GAM97   LOC220074 3'  GTCACCCAGGCTGGAGTGCAGT 59992
                 G                 CACTGCACTCCAGCCTGGGTGAC
                                   |||||||||||||||||||||||
                                   GTGACGTGAGGTCGGACCCACTG

GAM97   LOC220074 3'  GTCACCCCAGCTGGAGTGCAGT 59994              CT
                 G                 CACTGCACTCCAGC  GGGTGAC
                                   ||||||||||||||  |||||||
                                   GTGACGTGAGGTCG  CCCACTG
                                             AC
GAM97   LOC220537 3'  GCTGGCTGGAGTGAG      92426    G       TG
                                   CT CACTCCAGCC  GGT
                                   || ||||||||||  |||
                                   GA GTGAGGTCGG  TCG
                                    _       __
GAM97   LOC220575 3'  GTCACCCAGGCCGGAGTGCAGT 76815           A
                 G                 CACTGCACTCC GCCTGGGTGAC
                                   |||||||||||| ||||||||||
                                   GTGACGTGAGG CGGACCCACTG
                                         C
GAM97   LOC220662 3'  GCCCAGGCTGGAGTGCGGTG   92823
                                   CACTGCACTCCAGCCTGGGT
                                   |||||||||||||||||||
                                   GTGGCGTGAGGTCGGACCCG

GAM97   LOC220739 3'  GTCAGGGGCCAGAGTGCAG   94525        CA   GGG
                                   CTGCACTC  GCCT   TGAC
                                   ||||||||  ||||   ||||
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                                GACGTGAG  CGGG   ACTG
                                    AC    G__
GAM97   LOC220827 3'  GTCACCTAAAAGCACAGTGC   92881      CCA  C__
                                GCACT   GC   TGGGTGAC
                                |||||   ||   ||||||||
                                CGTGA   CG   ATCCACTG
                                  CA_  AAA
GAM97   LOC220936 3'  GCTGGCTGGAGTGCAG      93043           TG
                                CTGCACTCCAGCC  GGT
                                ||||||||||||  |||
                                GACGTGAGGTCGG  TCG
                                      __
GAM97   LOC221035 3'  GTCACCAGGCTGGAGTGCAGTG 94781               G
                                CACTGCACTCCAGCCTGG TGAC
                                |||||||||||||||||| ||||
                                GTGACGTGAGGTCGGACC ACTG
                                      _
GAM97   LOC221060 3'  GTTGCCCAGGCTGGAGTGCAAT 94835    C            TG
          G                      CA TGCACTCCAGCCTGGG  AC
                                || ||||||||||||||||  ||
                                GT ACGTGAGGTCGGACCC  TG
                                 A             GT
GAM97   LOC221122 3'  GTCACCCCTGCTGCTGGAGTGC 95086          CT___
          A                      TGCACTCCAGC     GGGTGAC
                                ||||||||||     |||||||
                                ACGTGAGGTCG     CCCACTG
                                      TCGTC
GAM97   LOC221271 3'  GTCACTCAGGCTGGAGTGCAAT 93526    C
          G                      CA TGCACTCCAGCCTGGGTGAC
                                || ||||||||||||||||||
                                GT ACGTGAGGTCGGACTCACTG
                                 A
GAM97   LOC221296 3'  GTCGCCCAGGTTGGAGTGCAGT 93615
          G                      CACTGCACTCCAGCCTGGGTGAC
                                ||||||||||||||||||||||
                                GTGACGTGAGGTTGGACCCGCTG

GAM97   LOC221474 3'  GCTGGCCGGGTGCAGT      93996        T  A   TG
                                ACTGCAC CC GCC  GGT
                                ||||||| || |||  |||
                                TGACGTG GG CGG  TCG
                                   _  C   __
GAM97   LOC221663 5'  GCCAAGGCTGGAGTGCAGTG   95464              G
                                CACTGCACTCCAGCCT GGT
                                |||||||||||||||| |||
                                GTGACGTGAGGTCGGA CCG
                                      A
GAM97   LOC221760 5'  TCATGGCTGGCTGGAGTGCAGT 95430              TGG_
          G                      CACTGCACTCCAGCC    GTGA
                                ||||||||||||||    ||||
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                                GTGACGTGAGGTCGG    TACT
                                       TCGG
GAM97   LOC221773 3'  GTCTCCCAGGCTGGAGTGCAGT 92696              T
            G                   CACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||| |||
                                GTGACGTGAGGTCGGACCC CTG
                                          T
GAM97   LOC221814 5'  GTCGCCAAGCCAGAGTGCAGTG 95558         CA  CTG
                                CACTGCACTC  GC   GGTGAC
                                ||||||||||  ||   ||||||
                                GTGACGTGAG  CG   CCGCTG
                                      AC  AA_
GAM97   LOC221960 3'  GTGACCCAGGCTGGAATGCAAT 92727    C    C         G
            G                   CA TGCA TCCAGCCTGGGT AC
                                || |||| |||||||||||| ||
                                GT ACGT AGGTCGGACCCA TG
                                 A    A          G
GAM97   LOC221964 3'  GTCTCCCAGGCTGGACTGCAGT 95610       C        T
            G                   CACTGCA TCCAGCCTGGG GAC
                                ||||||| |||||||||| |||
                                GTGACGT AGGTCGGACCC CTG
                                    C         T
GAM97   LOC221979 3'  CCAAGCTGTACCAGAGTGCAG  94218        _____   C
                                CTGCACTC    CAGC TGG
                                ||||||||    |||| |||
                                GACGTGAG    GTCG ACC
                                     ACCAT    A
GAM97   LOC222057 5'  CCAAGGCTGGAGTGTAGT    94347             G
                                ACTGCACTCCAGCCT GG
                                |||||||||||||| ||
                                TGATGTGAGGTCGGA CC
                                          A
GAM97   LOC222066 3'  ACAGGGCCAGGTGCAGTG    94306         CCA    GG
                                CACTGCACT   GCCT  GT
                                |||||||||   ||||  ||
                                GTGACGTGG   CGGG  CA
                                      AC_    A_
GAM97   LOC222068 3'  GTCGCCCAGGCTGGAGTGCAAT 94278    C
            G                   CA TGCACTCCAGCCTGGGTGAC
                                || ||||||||||||||||||
                                GT ACGTGAGGTCGGACCCGCTG
                                 A
GAM97   LOC222070 5'  GTCTCCCAGGCTGGAGTGCAGT 95821              T
            G                   CACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||| |||
                                GTGACGTGAGGTCGGACCC CTG
                                          T
GAM97   LOC222189 5'  GCTGAGAGCTGGAGTACAG   95836     C      _  G
                                CTG ACTCCAGC CT GGT
                                ||| |||||||| || |||
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                                GAC TGAGGTCG GA TCG
                                  A       A  G
GAM97   LOC245727 3'  CACCCAGGCCGGGCTAG     92758    _  ACT  A
                                CT GC   CC GCCTGGGTG
                                || ||   || |||||||||
                                GA CG   GG CGGACCCAC
                                 T  ___  C
GAM97   LOC245771 5'  GTCGCCCAGGCTGGAATGCAGT 94486       C
                                ACTGCA TCCAGCCTGGGTGAC
                                |||||| ||||||||||||||
                                TGACGT AGGTCGGACCCGCTG
                                   A
GAM97   LOC253532 3'  ATTCAGGCTGGGTGCAGTG    97729        T
                                CACTGCAC CCAGCCTGGGT
                                |||||||| ||||||||||
                                GTGACGTG GGTCGGACTTA

                                  _
GAM97   LOC253612 5'  GTCTCCCAGGCTGGAGTGCGGT 98555              T
          G                      CACTGCACTCCAGCCTGGG GAC
                                 |||||||||||||||||| |||
                                 GTGGCGTGAGGTCGGACCC CTG
                                            T
GAM97   LOC253664 3'  GTTGCCCAGGCTGGAGTGCAGT 96473              TG
          G                      CACTGCACTCCAGCCTGGG  AC
                                 |||||||||||||||||  ||
                                 GTGACGTGAGGTCGGACCC  TG
                                            GT
GAM97   LOC253779 3'  GTCACCCAGGTTGGAGTGCAGT 98925
          G                      CACTGCACTCCAGCCTGGGTGAC
                                 |||||||||||||||||||||
                                 GTGACGTGAGGTTGGACCCACTG

GAM97   LOC253805 3'  GTTGCCCAGGCTGGAGTGCAGT 98183              TG
          G                      CACTGCACTCCAGCCTGGG  AC
                                 |||||||||||||||||  ||
                                 GTGACGTGAGGTCGGACCC  TG
                                            GT
GAM97   LOC254013 3'  CCCAGGCTGGAATGCAGTG    96532        C
                                CACTGCA TCCAGCCTGGG
                                ||||||| ||||||||||
                                GTGACGT AGGTCGGACCC
                                   A
GAM97   LOC254013 3'  GTCGTCCAGGCTGGAGTGCAGT 96535              GT
          G                      CACTGCACTCCAGCCTGG  GAC
                                 ||||||||||||||||  |||
                                 GTGACGTGAGGTCGGACC  CTG
                                            TG
GAM97   LOC254082 5'  GTCGCCCAAGCTAGAGTGCAGT 98996          C   C
          G                      CACTGCACTC AGC TGGGTGAC
                                 |||||||||| ||| ||||||||
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                                GTGACGTGAG TCG ACCCGCTG
                                     A   A
GAM97   LOC254351 3' CCAGGCTGGAGTGCAATG    96684    C
                                CA TGCACTCCAGCCTGG
                                || ||||||||||||||
                                GT ACGTGAGGTCGGACC
                                 A
GAM97   LOC254381 5' GCCCGGGGCTGGAGCGCAG   99329     A      _
                                CTGC CTCCAGCCT GGGT
                                |||| ||||||||| ||||
                                GACG GAGGTCGGG CCCG
                                  C       G
GAM97   LOC254655 3' GTCTCCCAGGCTGGAGTGCAGT 97224              T
          G                      CACTGCACTCCAGCCTGGG GAC
                                 |||||||||||||||||| |||
                                 GTGACGTGAGGTCGGACCC CTG
                                                T
GAM97   LOC254672 3' GTTGCCCAGGCTGGAGTGCAAT 96298    C           TG
          G                      CA TGCACTCCAGCCTGGG  AC
                                 || ||||||||||||||||  ||
                                 GT ACGTGAGGTCGGACCC  TG
                                  A             GT
GAM97   LOC254875 3' ATTCAGGCTGGGTGCAGTG    97773       T
                                 CACTGCAC CCAGCCTGGGT
                                 |||||||| ||||||||||
                                 GTGACGTG GGTCGGACTTA
                                          _
GAM97   LOC255027 5' CCGGCTGCTGCAGTGCAGT    96775       C   __
                                 ACTGCACT CAGC  CTGG
                                 |||||||| ||||  ||||
                                 TGACGTGA GTCG  GGCC
                                      C    TC
GAM97   LOC255031 3' GCCCAGGCTAGAGTGCAGTG   99036         C
                                 CACTGCACTC AGCCTGGGT
                                 |||||||||| |||||||||
                                 GTGACGTGAG TCGGACCCG
                                      A
GAM97   LOC255177 3' GTTGCCCAGGCTGGAGTGCAAT 98399    C           TG
          G                      CA TGCACTCCAGCCTGGG  AC
                                 || ||||||||||||||||  ||
                                 GT ACGTGAGGTCGGACCC  TG
                                  A             GT
GAM97   LOC255196 3' ATTCAGGGCTGGGCACAGTG   98949      CA T    _
                                 CACTG  C CCAGCC TGGGT
                                 |||||  | |||||| |||||
                                 GTGAC  G GGTCGG ACTTA
                                    AC _     G
GAM97   LOC255196 5' GCCCAGGCTGGAGTGCAG    98959
                                 CTGCACTCCAGCCTGGGT
                                 ||||||||||||||||||
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                                GACGTGAGGTCGGACCCG

GAM97   LOC255196 5'  GCTCAGGCTGGAGTGCAGTG   98960
                                CACTGCACTCCAGCCTGGGT
                                ||||||||||||||||||||
                                GTGACGTGAGGTCGGACTCG

GAM97   LOC255326 3'  TCTGGCCGGGTGCAGTG     98125        T  A   T
                                CACTGCAC CC GCC GG
                                |||||||| || ||| ||
                                GTGACGTG GG CGG CT
                                     _  C   T
GAM97   LOC255458 5'  CCAGGCTGGAGTATAGTG    98931      C
                                CACTG ACTCCAGCCTGG
                                ||||| ||||||||||||
                                GTGAT TGAGGTCGGACC
                                   A
GAM97   LOC255465 3'  GTCACCAGGCTGGAGTGCAGTG 99122                 G
                                CACTGCACTCCAGCCTGG TGAC
                                |||||||||||||||||| ||||
                                GTGACGTGAGGTCGGACC ACTG
                                                  _
GAM97   LOC255465 3'  GTCACCCAGGCTGGAGTACAGT 99124      C
           G                     CACTG ACTCCAGCCTGGGTGAC
                                |||||| ||||||||||||||||
                                GTGAC TGAGGTCGGACCCACTG
                                   A
GAM97   LOC255803 5'  TCATACTGGAGTGCGG      99474          CCTGG
                                CTGCACTCCAG    GTGA
                                ||||||||||     ||||
                                GGCGTGAGGTC    TACT
                                      A____
GAM97   LOC255919 3'  CCAGGCTGGAGGGCAGTG    96743       A
                                CACTGC CTCCAGCCTGG
                                |||||| ||||||||||
                                GTGACG GAGGTCGGACC
                                   G
GAM97   LOC255975 5'  CCAAGGCTGGAGTGTAGT    97573             G
                                ACTGCACTCCAGCCT GG
                                |||||||||||||| ||
                                TGATGTGAGGTCGGA CC
                                          A
GAM97   LOC256158 5'  GCCTGTGGCGCTGGAGTGCGTG 99498     T       _ __
                                CAC GCACTCCAGC CT  GGGT
                                ||| |||||||||| ||  ||||
                                GTG CGTGAGGTCG GG  TCCG
                                  _        C  TG
GAM97   LOC256158 5'  TCGCTACTGGAGTGAGT     99516     G       CCTG
                                ACT CACTCCAG    GGTGA
                                ||| ||||||||    |||||
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                                TGA GTGAGGTC    TCGCT
                                  _       A___
GAM97   LOC256221 3'  ACTCAGGCTGGAGTGCAGTG   96903
                                CACTGCACTCCAGCCTGGGT
                                ||||||||||||||||||||
                                GTGACGTGAGGTCGGACTCA

GAM97   LOC256273 3'  GCTCAGCTGGAGTCAG      98143     C       C
                                CTG ACTCCAGC TGGGT
                                ||| |||||||| |||||
                                GAC TGAGGTCG ACTCG
                                  _       _
GAM97   LOC256306 3'  GCCCAGGCTGGAGTGCAG    98516
                                CTGCACTCCAGCCTGGGT
                                ||||||||||||||||||
                                GACGTGAGGTCGGACCCG

GAM97   LOC256476 5'  GTCACCCAGGCTGGAGTGCATG 98625    C
                                CA TGCACTCCAGCCTGGGTGAC
                                || ||||||||||||||||||||
                                GT ACGTGAGGTCGGACCCACTG
                                  _
GAM97   LOC256878 5'  CCAAGGCTGGAGTGTAGT    98684             G
                                ACTGCACTCCAGCCT GG
                                |||||||||||||| ||
                                TGATGTGAGGTCGGA CC
                                          A
GAM97   LOC256923 5'  GCCTGGGCTGGAGTGCAGTG   96847             TG
                                CACTGCACTCCAGCC  GGT
                                |||||||||||||||  |||
                                GTGACGTGAGGTCGG  CCG
                                          GT
GAM97   LOC256940 5'  CCAGTGCTGAAGTGCAGT    98245         C   _
                                ACTGCACT CAGC CTGG
                                |||||||| |||| ||||
                                TGACGTGA GTCG GACC
                                     A   T
GAM97   LOC257054 5'  TCACCCAGGCTGGAGTGCAGTG 97377
                                CACTGCACTCCAGCCTGGGTGA
                                ||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCACT

GAM97   LOC257095 5'  CACCAGGCTGGGTGCAATG   98717    C    T       G
                                CA TGCAC CCAGCCTGG TG
                                || ||||| ||||||||| ||
                                GT ACGTG GGTCGGACC AC
                                  A   _       _
GAM97   LOC257463 3'  TCCCCAGGCTGGAGTGCAATG  71624    C            T
                                CA TGCACTCCAGCCTGGG GA
                                || ||||||||||||||| ||
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                                GT ACGTGAGGTCGGACCC CT
                                 A          _
GAM97   LOC257465 3'  GTCTTCCAGGCTGGAGTGCAGT 82498              T
            G                    CACTGCACTCCAGCCTGGG GAC
                                 |||||||||||||||||| |||
                                 GTGACGTGAGGTCGGACCT CTG
                                           T
GAM97   LOC257486 3'  GTTACCCAGATTGGAGTGCAGT 69780          GC
            G                    CACTGCACTCCA  CTGGGTGAC
                                 ||||||||||||  |||||||||
                                 GTGACGTGAGGT  GACCCATTG
                                       TA
GAM97   LOC51031  5'  GTCATCAGGCTGGAGTGCAGTG 32710             G
                                 CACTGCACTCCAGCCTGG TGAC
                                 |||||||||||||||||| ||||
                                 GTGACGTGAGGTCGGACT ACTG
                                           _
GAM97   LOC51122  3'  CTAAGCTGGGTGCAGTG     66196       T    C
                                 CACTGCAC CCAGC TGG
                                 |||||||| ||||| |||
                                 GTGACGTG GGTCG ATC
                                     _    A
GAM97   LOC51193  3'  CCAGGATGGAGTGCAGTG    33361          G
                                 CACTGCACTCCA CCTGG
                                 |||||||||||| |||||
                                 GTGACGTGAGGT GGACC
                                       A
GAM97   LOC51193  5'  GTTACCCAGGCTGGAGGACAGT 33369      CA
            G                    CACTG  CTCCAGCCTGGGTGAC
                                 |||||  ||||||||||||||||
                                 GTGAC  GAGGTCGGACCCATTG
                                    AG
GAM97   LOC51219  5'  GTCGCCCAGGCTGGAGTGCAAT 33549    C
            G                    CA TGCACTCCAGCCTGGGTGAC
                                 || ||||||||||||||||||||
                                 GT ACGTGAGGTCGGACCCGCTG
                                  A
GAM97   LOC51336  3'  GTTACCCAGGCTGGAGTGCAAT 34075    C
            G                    CA TGCACTCCAGCCTGGGTGAC
                                 || ||||||||||||||||||||
                                 GT ACGTGAGGTCGGACCCATTG
                                  A
GAM97   LOC51622  3'  GTGACCCAGGCTGGAATGCAAT 32210    C   C        G
            G                    CA TGCA TCCAGCCTGGGT AC
                                 || |||| |||||||||||| ||
                                 GT ACGT AGGTCGGACCCA TG
                                  A   A          G
GAM97   LOC51696  3'  GTCACCCAGGCTGGAGTGCAGT 33087
                                 ACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
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                                TGACGTGAGGTCGGACCCACTG

GAM97   LOC55954  5'  GTCACCCAGGCTGGAGTGTAGT 39398
                 G                CACTGCACTCCAGCCTGGGTGAC
                                  ||||||||||||||||||||||
                                  GTGATGTGAGGTCGGACCCACTG

GAM97   LOC56181  5'  GTCACCCAGGTTGGAGTGCAGT 97282
                 G                CACTGCACTCCAGCCTGGGTGAC
                                  ||||||||||||||||||||||
                                  GTGACGTGAGGTTGGACCCACTG

GAM97   LOC57107  3'  GCCCAGGCTGGAGTGCAATG  40190   C
                                  CA TGCACTCCAGCCTGGGT
                                  || ||||||||||||||||
                                  GT ACGTGAGGTCGGACCCG
                                   A
GAM97   LOC57107  3'  GTTGCCCAGGCTGGAGTGCAAT 40192   C          TG
                 G                CA TGCACTCCAGCCTGGG  AC
                                  || ||||||||||||||||  ||
                                  GT ACGTGAGGTCGGACCC  TG
                                   A            GT
GAM97   LOC57118  3'  TCACTGGGCTGGGTGCAGTG  40226       T    TG G
                                  CACTGCAC CCAGCC  G TGA
                                  |||||||| ||||||  | |||
                                  GTGACGTG GGTCGG  C ACT
                                       _     GT _
GAM97   LOC57146  3'  GTTGCCCAGGCTGGAGTGCA  40297           TG
                                  TGCACTCCAGCCTGGG  AC
                                  ||||||||||||||||  ||
                                  ACGTGAGGTCGGACCC  TG
                                            GT
GAM97   LOC81034  3'  GTCGCCCAGGCTGGAGTGCAGT 48593
                 G                CACTGCACTCCAGCCTGGGTGAC
                                  ||||||||||||||||||||||
                                  GTGACGTGAGGTCGGACCCGCTG

GAM97   LOC89231  3'  GTTGCCCAGGCTGGAGTGCAAT 94300   C          TG
                 G                CA TGCACTCCAGCCTGGG  AC
                                  || ||||||||||||||||  ||
                                  GT ACGTGAGGTCGGACCC  TG
                                   A            GT
GAM97   LOC89932  3'  GCCCAGGCTGGAGTACAATG  61466   C  C
                                  CA TG ACTCCAGCCTGGGT
                                  || || ||||||||||||||
                                  GT AC TGAGGTCGGACCCG
                                   A  A
GAM97   LOC89932  3'  GTTGCCCAGGCTGGAGGGCAAT 61472   C  A        TG
                 G                CA TGC CTCCAGCCTGGG  AC
                                  || ||| ||||||||||||  ||
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                                GT ACG GAGGTCGGACCC  TG
                                 A  G          GT
GAM97   LOC90141  3'  GTCACCTAAGCTGGAGTACAGT 62308      C       C
            G                    CACTG ACTCCAGC TGGGTGAC
                                 ||||| |||||||| ||||||||
                                 GTGAC TGAGGTCG ATCCACTG
                                   A       A
GAM97   LOC90155  3'  CCCAGGCTAGAGTGCAGTG   62365          C
                                 CACTGCACTC AGCCTGGG
                                 |||||||||| ||||||||
                                 GTGACGTGAG TCGGACCC
                                       A
GAM97   LOC90288  3'  GCCTAGGCTGGAGTGAAGTG  62791      G
                                 CACT CACTCCAGCCTGGGT
                                 |||| ||||||||||||||
                                 GTGA GTGAGGTCGGATCCG
                                   A
GAM97   LOC90288  3'  GTCACCCAGGCTGGAGTGCAGT 62796
            G                    CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCACTG

GAM97   LOC90333  3'  GTCGCCCAGGTTGGAGTGCAGT 62961
            G                    CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||||
                                 GTGACGTGAGGTTGGACCCGCTG

GAM97   LOC90371  5'  GTCACCCAGGCTGGAGTGCAGT 63164
            G                    CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCACTG

GAM97   LOC90408  5'  GTTACCCAGGCTGGAGTGCAGT 63345
            G                    CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCATTG

GAM97   LOC90459  3'  GTCTGCCAGGATGGAGTGCAGT 63560          G    GT
            G                    CACTGCACTCCA CCTGG  GAC
                                 |||||||||||| |||||  |||
                                 GTGACGTGAGGT GGACC  CTG
                                       A    GT
GAM97   LOC90485  3'  GTCACCCAGGCTAGAGTGCAGT 63706         C
            G                    CACTGCACTC AGCCTGGGTGAC
                                 |||||||||| ||||||||||||
                                 GTGACGTGAG TCGGACCCACTG
                                       A
GAM97   LOC90485  3'  GTCGCCCAGGCTGGAGTGCAGT 63708
            G                    CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||||
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                                GTGACGTGAGGTCGGACCCGCTG

GAM97   LOC90557  5' CACTGAGCCGGGGTGCAGTG   57854          A  C G
                                CACTGCACTCC GC T GGTG
                                |||||||||||  || | ||||
                                GTGACGTGGGG CG A TCAC
                                      C  _ G
GAM97   LOC90591  3' GTCACCCAGGCTGGAGTGCAGT 64183
           G                     CACTGCACTCCAGCCTGGGTGAC
                                 ||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCACTG

GAM97   LOC90591  3' GTTGCCCAGGCTGGAGTGCAGT 64186                TG
           G                     CACTGCACTCCAGCCTGGG  AC
                                 ||||||||||||||||||  ||
                                 GTGACGTGAGGTCGGACCC  TG
                                             GT
GAM97   LOC90999  3' GTTGCCCAGGCTGGAGTACAGT 65184       C          TG
           G                     CACTG ACTCCAGCCTGGG  AC
                                 |||||  ||||||||||||  ||
                                 GTGAC TGAGGTCGGACCC  TG
                                    A           GT
GAM97   LOC91115  3' ACCCAGGCTGGAGTGCTGTG   65538     T
                                 CAC GCACTCCAGCCTGGGT
                                 |||  ||||||||||||||
                                 GTG CGTGAGGTCGGACCCA
                                   T
GAM97   LOC91115  3' GTCACCCAGGCTGGAGTGCAAT 65574    C
           G                     CA TGCACTCCAGCCTGGGTGAC
                                 ||  ||||||||||||||||||
                                 GT ACGTGAGGTCGGACCCACTG
                                  A
GAM97   LOC91115  3' GTTGCCCAGGCTGGAGTGCAAT 65576    C            TG
           G                     CA TGCACTCCAGCCTGGG  AC
                                 ||  ||||||||||||||  ||
                                 GT ACGTGAGGTCGGACCC  TG
                                  A             GT
GAM97   LOC91250  5' GTCACCCAGGCTGGAGTTATAG 65920      C_
           T                      ACTG  ACTCCAGCCTGGGTGAC
                                  ||||  ||||||||||||||||
                                  TGAT  TGAGGTCGGACCCACTG
                                    AT
GAM97   LOC91291  5' GTCGCCCAGACTAGAATGCAGT 66092        C  C  C
           G                     CACTGCA TC AG CTGGGTGAC
                                 |||||||  ||  ||  |||||||||
                                 GTGACGT AG TC GACCCGCTG
                                     A  A  A
GAM97   LOC91373  3' GTTGCCCAGGCTGGAGTGAAGT 66418      G          TG
           G                     CACT CACTCCAGCCTGGG  AC
                                 ||||  ||||||||||||||  ||
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                                GTGA GTGAGGTCGGACCC  TG
                                  A           GT
GAM97   LOC91380  3'  CCAGGCTGGAGTTCAGTG    66442      C
                                CACTG ACTCCAGCCTGG
                                ||||| ||||||||||||
                                GTGAC TGAGGTCGGACC
                                   T
GAM97   LOC91661  3'  GTCGGCCAGGCTGGAATGCAAT 57218    C   C        G
           G                     CA TGCA TCCAGCCTGG TGAC
                                || |||| |||||||||| ||||
                                GT ACGT AGGTCGGACC GCTG
                                 A   A         G
GAM97   LOC91893  3'  GCCCAGGCGGGAGTGCAGTG   68075          A
                                CACTGCACTCC GCCTGGGT
                                |||||||||| ||||||||
                                GTGACGTGAGG CGGACCCG
                                       G
GAM97   LOC92148  5'  CGCCCAGGCTAGAGTGCAGTG  68876          C
                                CACTGCACTC AGCCTGGGTG
                                |||||||||| ||||||||||
                                GTGACGTGAG TCGGACCCGC
                                      A
GAM97   LOC92267  3'  GTCCCCCAGGCTGGAGTGCCGT 69174     T           T
           G                     CAC GCACTCCAGCCTGGG GAC
                                ||| |||||||||||||| |||
                                GTG CGTGAGGTCGGACCC CTG
                                  C           C
GAM97   LOC92283  3'  ACCCAGGCTGGAGTCCAGTG   69297      C
                                CACTG ACTCCAGCCTGGGT
                                ||||| ||||||||||||||
                                GTGAC TGAGGTCGGACCCA
                                   C
GAM97   LOC92299  3'  TTAGGCTGGGCGCAGTG     69375       A T
                                CACTGC C CCAGCCTGG
                                |||||| | |||||||||
                                GTGACG G GGTCGGATT
                                    C _
GAM97   LOC92303  3'  GCCCGGGCTGGAGTGCAATG   69393    C
                                CA TGCACTCCAGCCTGGGT
                                || ||||||||||||||||
                                GT ACGTGAGGTCGGGCCCG
                                 A
GAM97   LOC92609  3'  GTTGCCCAGGCTGGAGTGCATT 73210    C           TG
           G                     CA TGCACTCCAGCCTGGG  AC
                                || ||||||||||||||||  ||
                                GT ACGTGAGGTCGGACCC  TG
                                 T           GT
GAM97   LOC92661  5'  CGCCCAGGCTGGAGTGCAGTG  70627
                                CACTGCACTCCAGCCTGGGTG
                                ||||||||||||||||||||
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                                GTGACGTGAGGTCGGACCCGC

GAM97   LOC92697  5'  TGCCCAGGCTGGAGTGCAGTG  70818
                                CACTGCACTCCAGCCTGGGTG
                                ||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCGT

GAM97   LOC92841  3'  GTTGCCCAGGCTGGAGTGCAAT 71262    C           TG
            G                    CA TGCACTCCAGCCTGGG  AC
                                || ||||||||||||||||  ||
                                GT ACGTGAGGTCGGACCC  TG
                                 A            GT
GAM97   LOC93129  3'  CCAGGCTGGAGTGTAGTG    71954
                                CACTGCACTCCAGCCTGG
                                ||||||||||||||||||
                                GTGATGTGAGGTCGGACC

GAM97   LOC93132  5'  GTCACCAGGCTGGAGGGCAGTG 71997       A        G
                                CACTGC CTCCAGCCTGG TGAC
                                |||||| |||||||||| ||||
                                GTGACG GAGGTCGGACC ACTG
                                   G        _
GAM97   LOC93408  5'  GTCGCCCAGGCTGGAGCGCAAT 57288    C   A
            G                    CA TGC CTCCAGCCTGGGTGAC
                                || ||| ||||||||||||||||
                                GT ACG GAGGTCGGACCCGCTG
                                 A  C
GAM97   LOC93550  5'  GCCTAGAACTGGAATACAGT   72977     CAC    C_
                                ACTG   TCCAG  CTGGGT
                                ||||   |||||  ||||||
                                TGAC   AGGTC  GATCCG
                                  ATA    AA
GAM97   LOC93613  5'  TCACCCCCGGGAGTGCAG    73080         AGCCT
                                CTGCACTCC    GGGTGA
                                |||||||||    ||||||
                                GACGTGAGG    CCCACT
                                     GCC__
GAM98   ACADSB    3'  ACAGGTGTGCACCACCATGCCT 9641         CA   CGG
            GG                    CCGGGCA  GTGG   GCGCCTGT
                                |||||||  ||||   ||||||||
                                GGTCCGT  CACC   TGTGGACA
                                   AC    ACG
GAM98   ADAMTS4   3'  ACAGGCGTGAGCCACCGTGCCT 18739        A    GG
            GG                    CCGGGCAC GTGGC  GCGCCTGT
                                ||||||||| |||||  ||||||||
                                GGTCCGTG CACCG  TGCGGACA
                                   C    AG
GAM98   ADAMTS4   3'  ACAGGCTCCTGCCACCACGCCC 18740      ACA       C
                                GGGC   GTGGCGGG GCCTGT
                                ||||   |||||||| ||||||
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                                CCCG  CACCGTCC CGGACA
                                  CAC       T
GAM98   ADAMTS4  3' ACAGGTGTGAGCCACCACGCCC 18742       ACA    GG
           GG                   CCGGGC  GTGGC  GCGCCTGT
                                |||||| |||||  ||||||||
                                GGCCCG  CACCG  TGTGGACA
                                  CAC    AG
GAM98   ADCY6    5' ACAGGCGCCCGCCACCACGCCC 31581       ACA
           GG                   CCGGGC  GTGGCGGGCGCCTGT
                                ||||||  ||||||||||||||
                                GGCCCG  CACCGCCCGCGGACA
                                  CAC
GAM98   ADCY6    5' ACAGGTGTAAGCCACTGTGCCT 31582           GG
           GG                   CCGGGCACAGTGGC  GCGCCTGT
                                |||||||||||||  ||||||||
                                GGTCCGTGTCACCG  TGTGGACA
                                     AA
GAM98   ADRA1A   3' ACAGGCGTGAGCCACCGTGCCC 53948        A    GG
           GG                   CCGGGCAC GTGGC  GCGCCTGT
                                |||||||| |||||  ||||||||
                                GGCCCGTG CACCG  TGCGGACA
                                   C    AG
GAM98   APAF1    3' ACAGGCGTGAGCCACCGTGCCT 25953        A    GG
           GG                   CCGGGCAC GTGGC  GCGCCTGT
                                |||||||| |||||  ||||||||
                                GGTCCGTG CACCG  TGCGGACA
                                   C    AG
GAM98   APAF1    3' ACAGGCGTGAGCCACCGTGCCT 8574         A    GG
           GG                   CCGGGCAC GTGGC  GCGCCTGT
                                |||||||| |||||  ||||||||
                                GGTCCGTG CACCG  TGCGGACA
                                   C    AG
GAM98   APM1     3' ACAGGCTCATGCCACTGCGCCC 17751      A      GGC
                                GGGC CAGTGGCG   GCCTGT
                                |||| ||||||||   ||||||
                                CCCG GTCACCGT   CGGACA
                                  C       ACT
GAM98   APOL1    3' ACAGGCGCCTACCACCATGCCC 14718      CA   CG
                                GGGCA  GTGG  GGCGCCTGT
                                |||||  ||||  |||||||||
                                CCCGT  CACC  CCGCGGACA
                                  AC    AT
GAM98   APPBP2   3' ACAGGCTCCTGCCACCACGCCT 22113       ACA      C
           GG                   CCGGGC  GTGGCGGG GCCTGT
                                ||||||  |||||||| ||||||
                                GGTCCG  CACCGTCC CGGACA
                                  CAC       T
GAM98   APPL     3' ACAGGCGTGAGCCACCGTGCCC 24939        A    GG
           GG                   CCGGGCAC GTGGC  GCGCCTGT
                                |||||||| |||||  ||||||||
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                                GGCCCGTG CACCG  TGCGGACA
                                    C    AG
GAM98   AQP6    3'  ACAGGCGCCTGCCACCACGCCC 9720      ACA
                                GGGC  GTGGCGGGCGCCTGT
                                ||||  |||||||||||||||
                                CCCG  CACCGTCCGCGGACA
                                  CAC
GAM98   AQP6    3'  ACAGGCGTGAGCCACCGTGCCC 9721        A   GG
          GG                    CCGGGCAC GTGGC  GCGCCTGT
                                |||||||| |||||  ||||||||
                                GGCCCGTG CACCG  TGCGGACA
                                    C    AG
GAM98   AQP6    3'  ACAGGCGCCTGCCACCACGCCC 54978     ACA
                                GGGC  GTGGCGGGCGCCTGT
                                ||||  |||||||||||||||
                                CCCG  CACCGTCCGCGGACA
                                  CAC
GAM98   AQP6    3'  ACAGGCGTGAGCCACCGTGCCC 54979       A   GG
          GG                    CCGGGCAC GTGGC  GCGCCTGT
                                |||||||| |||||  ||||||||
                                GGCCCGTG CACCG  TGCGGACA
                                    C    AG
GAM98   ARCN1   3'  ACAGGTGCACGCCACCACGCCT 9740       ACA    G
          GG                    CCGGGC  GTGGCG GCGCCTGT
                                ||||||  |||||| ||||||||
                                GGTCCG  CACCGC CGTGGACA
                                  CAC    A
GAM98   ATP1B2  3'  ACAGGCGTGAGCCACCGCGCCT 9823       ACA   GG
          GG                    CCGGGC  GTGGC  GCGCCTGT
                                ||||||  |||||  ||||||||
                                GGTCCG  CACCG  TGCGGACA
                                  CGC    AG
GAM98   ATP6V1A1 3'  ACAGGCGTGAGCCACCGCGCCT 9861       ACA   GG
          GG                    CCGGGC  GTGGC  GCGCCTGT
                                ||||||  |||||  ||||||||
                                GGTCCG  CACCG  TGCGGACA
                                  CGC    AG
GAM98   ATP7A   3'  ACAGGTGCCTGCCACCACACCC 5309      CACA
          GG                    CCGGG   GTGGCGGGCGCCTGT
                                |||||   ||||||||||||||||
                                GGCCC   CACCGTCCGTGGACA
                                  ACAC
GAM98   ATP7A   3'  ACAGGTGTGAGCCTCCATGCCC 5310      CAGT  GG
                                GGGCA   GGC  GCGCCTGT
                                |||||   |||  ||||||||
                                CCCGT   CCG  TGTGGACA
                                  ACCT  AG
GAM98   ATP8B2  3'  ACAGGCGTGAGCCACCACACCC 65827    CACA   GG
                                GGG   GTGGC  GCGCCTGT
                                |||   |||||  ||||||||
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                                CCC   CACCG  TGCGGACA
                                  ACAC    AG
GAM98   AXL     3'  ACAGGTGTGTGCCACCACACCC 41870      CACA    G
            GG                    CCGGG   GTGGCG GCGCCTGT
                                  ||||||  |||||| ||||||||
                                  GGCCC   CACCGT TGTGGACA
                                    ACAC    G
GAM98   AXL     3'  ACAGGTGTGTGCCACCACACCC 9897       CACA    G
            GG                    CCGGG   GTGGCG GCGCCTGT
                                  ||||||  |||||| ||||||||
                                  GGCCC   CACCGT TGTGGACA
                                    ACAC    G
GAM98   B4GALT5  3'  ACAGGTGCACACCACCACACCT 17679      CACA   C ___
            GG                    CCGGG   GTGG GG   GCGCCTGT
                                  ||||||  |||| ||  ||||||||
                                  GGTCC   CACC CC   CGTGGACA
                                    A___    A  ACA
GAM98   BRIP1    3'  ACAGGTGTGCACCACCATGCCC 50201      CA   CGG
                                  GGGCA  GTGG   GCGCCTGT
                                  ||||||  ||||  ||||||||
                                  CCCGT  CACC   TGTGGACA
                                    AC    ACG
GAM98   C7      3'  ACAGGTGCCCGCCACCACGCCC 6974       ACA
                                  GGGC   GTGGCGGGCGCCTGT
                                  ||||  ||||||||||||||||
                                  CCCG   CACCGCCCGTGGACA
                                    CAC
GAM98   CAMLG    3'  ACAGGCGTGAGCCACTGCACCT 9989       CA     GG
            GG                    CCGGG  CAGTGGC  GCGCCTGT
                                  ||||||  |||||||  ||||||||
                                  GGTCC  GTCACCG  TGCGGACA
                                    AC      AG
GAM98   CASP2    3'  ACAGGCGTGAGCCACTGCGCCC 8699        A     GG
            GG                    CCGGGC CAGTGGC  GCGCCTGT
                                  ||||||| |||||||  ||||||||
                                  GGCCCG GTCACCG  TGCGGACA
                                     C      AG
GAM98   CASP2    3'  ACAGGTGCCCGCCACCGTGCCC 8701         A
            GG                    CCGGGCAC GTGGCGGGCGCCTGT
                                  ||||||||| ||||||||||||||
                                  GGCCCGTG CACCGCCCGTGGACA
                                       C
GAM98   CASP2    3'  ACAGGCGTGAGCCACTGCGCCC 53280       A     GG
            GG                    CCGGGC CAGTGGC  GCGCCTGT
                                  ||||||| |||||||  ||||||||
                                  GGCCCG GTCACCG  TGCGGACA
                                     C      AG
GAM98   CASP2    3'  ACAGGTGCCCGCCACCGTGCCC 53282         A
            GG                    CCGGGCAC GTGGCGGGCGCCTGT
                                  ||||||||| ||||||||||||||
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                                GGCCCGTG CACCGCCCGTGGACA
                                    C
GAM98   CASP2   3' ACAGGCGTGAGCCACTGCGCCC 53296       A     GG
           GG                   CCGGGC CAGTGGC  GCGCCTGT
                                |||||| |||||||  ||||||||
                                GGCCCG GTCACCG  TGCGGACA
                                   C      AG
GAM98   CASP2   3' ACAGGTGCCCGCCACCGTGCCC 53298         A
           GG                   CCGGGCAC GTGGCGGGCGCCTGT
                                |||||||| ||||||||||||||
                                GGCCCGTG CACCGCCCGTGGACA
                                    C
GAM98   CASP2   3' ACAGGCGTGAGCCACTGCGCCC 53312       A     GG
           GG                   CCGGGC CAGTGGC  GCGCCTGT
                                |||||| |||||||  ||||||||
                                GGCCCG GTCACCG  TGCGGACA
                                   C      AG
GAM98   CASP2   3' ACAGGTGCCCGCCACCGTGCCC 53314         A
           GG                   CCGGGCAC GTGGCGGGCGCCTGT
                                |||||||| ||||||||||||||
                                GGCCCGTG CACCGCCCGTGGACA
                                    C
GAM98   CASP8   3' ACAGGCGTGAGCCACCGCGCCT 54104       ACA    GG
           GG                   CCGGGC  GTGGC  GCGCCTGT
                                ||||||  |||||  ||||||||
                                GGTCCG  CACCG  TGCGGACA
                                   CGC    AG
GAM98   CASP8   3' ACAGGGGCCCGCCACCACACCT 54105      CACA       G
           GG                   CCGGG   GTGGCGGGC CCTGT
                                |||||   ||||||||| |||||
                                GGTCC   CACCGCCCG GGACA
                                  ACAC       G
GAM98   CASP8   3' ACAGGCGTGAGCCACCGCGCCT 54063       ACA    GG
           GG                   CCGGGC  GTGGC  GCGCCTGT
                                ||||||  |||||  ||||||||
                                GGTCCG  CACCG  TGCGGACA
                                   CGC    AG
GAM98   CASP8   3' ACAGGGGCCCGCCACCACACCT 54064      CACA       G
           GG                   CCGGG   GTGGCGGGC CCTGT
                                |||||   ||||||||| |||||
                                GGTCC   CACCGCCCG GGACA
                                  ACAC       G
GAM98   CASP8   3' ACAGGCGTGAGCCACCGCGCCT 54089       ACA    GG
           GG                   CCGGGC  GTGGC  GCGCCTGT
                                ||||||  |||||  ||||||||
                                GGTCCG  CACCG  TGCGGACA
                                   CGC    AG
GAM98   CASP8   3' ACAGGGGCCCGCCACCACACCT 54090      CACA       G
           GG                   CCGGG   GTGGCGGGC CCTGT
                                |||||   ||||||||| |||||
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                                GGTCC    CACCGCCCG GGACA
                                  ACAC        G
GAM98   CASP8    3'  ACAGGCGTGAGCCACCGCGCCT 8739        ACA     GG
           GG                     CCGGGC   GTGGC  GCGCCTGT
                                  ||||||   |||||  ||||||||
                                  GGTCCG   CACCG  TGCGGACA
                                    CGC     AG
GAM98   CASP8    3'  ACAGGGGCCCGCCACCACACCT 8740       CACA       G
           GG                     CCGGG    GTGGCGGGC CCTGT
                                  ||||||    |||||||||| |||||
                                  GGTCC    CACCGCCCG GGACA
                                    ACAC        G
GAM98   CBFA2T2  3'  ACAGGCATGAGCCACTGTGTCC 18697             GGGC
           GG                     CCGGGCACAGTGGC    GCCTGT
                                  ||||||||||||||    ||||||
                                  GGCCTGTGTCACCG    CGGACA
                                          AGTA
GAM98   CDC6     3'  ACAGGTGCCCACCACCGCGCCC 8813       ACA    C
                                  GGGC   GTGG GGGCGCCTGT
                                  ||||   |||| ||||||||||
                                  CCCG   CACC CCCGTGGACA
                                    CGC    A
GAM98   CHRNB4   3'  ACAGGTGTGAGCCACTATGCCT 7445         C      GG
           GG                     CCGGGCA AGTGGC  GCGCCTGT
                                  |||||||  ||||||  ||||||||
                                  GGTCCGT TCACCG  TGTGGACA
                                      A      AG
GAM98   CHST6    3'  ACAGGCATGAGCCACTGTACCT 41496       C       GGGC
           GG                     CCGGG ACAGTGGC    GCCTGT
                                  |||||  ||||||||    ||||||
                                  GGTCC TGTCACCG    CGGACA
                                    A       AGTA
GAM98   CIAS1    5'  ACAGGCGCCCGCCACCACACCC 18090       CACA
           GG                     CCGGG    GTGGCGGGCGCCTGT
                                  |||||    ||||||||||||||||
                                  GGCCC    CACCGCCCGCGGACA
                                    ACAC
GAM98   CIAS1    5'  ACAGGCGTGAGCCACTGTGCCC 18091             GG
           GG                     CCGGGCACAGTGGC  GCGCCTGT
                                  ||||||||||||||  ||||||||
                                  GGCCCGTGTCACCG  TGCGGACA
                                          AG
GAM98   CLECSF12 3'  ACAGGCGTGAGCCACTGCACCC 77200     CA      GG
                                  GGG  CAGTGGC  GCGCCTGT
                                  |||  |||||||  ||||||||
                                  CCC  GTCACCG  TGCGGACA
                                    AC       AG
GAM98   CLECSF12 3'  ACAGGTGCATGCCACCATGCCA 77201    G    CA     G
           GG                     CC GGCA  GTGGCG GCGCCTGT
                                  || ||||  |||||| ||||||||
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                                GG CCGT  CACCGT CGTGGACA
                                 A   AC     A
GAM98   CNN2    3'  ACAGGTGTGAGCCACCGTGCCC 16450       A    GG
                                GGGCAC GTGGC  GCGCCTGT
                                |||||| |||||  ||||||||
                                CCCGTG CACCG  TGTGGACA
                                   C    AG
GAM98   CRTAP   3'  ACAGGCGTGAGCCACCATGCCC 22072       CA    GG
           GG                     CCGGGCA  GTGGC  GCGCCTGT
                                |||||||  |||||  ||||||||
                                GGCCCGT  CACCG  TGCGGACA
                                   AC    AG
GAM98   CXCL16  3'  ACAGGTGCTCACCACCACACCC 42155      CACA   C
           GG                     CCGGG   GTGG GGGCGCCTGT
                                |||||   |||| ||||||||||
                                GGCCC   CACC CTCGTGGACA
                                   ACAC   A
GAM98   CYP1A2  3'  ACAGGTGTGAGCCACCACATCC 7493     CACA    GG
                                GGG   GTGGC  GCGCCTGT
                                |||   |||||  ||||||||
                                CCT   CACCG  TGTGGACA
                                  ACAC    AG
GAM98   CYP1A2  3'  ACAGGTGTGAGCCACGGTGCCC 7494        A    GG
           GG                     CCGGGCAC GTGGC  GCGCCTGT
                                |||||||| |||||  ||||||||
                                GGCCCGTG CACCG  TGTGGACA
                                    G    AG
GAM98   CYP2B6  3'  ACAGGCGTCCCCCACCACGCCT 7548       ACA   C
           GG                     CCGGGC   GTGG GGGCGCCTGT
                                ||||||   |||| ||||||||||
                                GGTCCG   CACC CCTGCGGACA
                                   CAC   C
GAM98   CYP2B6  3'  ACAGGCGTGAGTCACCGTGCCC 7549       A    GG
                                GGGCAC GTGGC  GCGCCTGT
                                |||||| |||||  ||||||||
                                CCCGTG CACTG  TGCGGACA
                                   C    AG
GAM98   CYP51   3'  ACAGGCACCTGCCACCATGCCT 7606       CA      C
           GG                     CCGGGCA  GTGGCGGG GCCTGT
                                |||||||  ||||||||  ||||||
                                GGTCCGT  CACCGTCC CGGACA
                                   AC       A
GAM98   CYP8B1  3'  ACAGGCATGAGCCACTGTGCCC 16528          GGGC
                                GGGCACAGTGGC   GCCTGT
                                ||||||||||||   ||||||
                                CCCGTGTCACCG   CGGACA
                                      AGTA
GAM98   CYP8B1  3'  GGTGCGCACCACCACACCCGG  16540     CACA   C _   _
                                CCGGG   GTGG GG GCGC CT
                                |||||   |||| || |||| ||
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                                GGCCC   CACC CC CGCG GG
                                  A___   A A   T
GAM98   DFFB    3'  ACAGGTGTGAGCCACTGCGCCC 88747     A     GG
                                GGGC CAGTGGC  GCGCCTGT
                                |||| |||||||  ||||||||
                                CCCG GTCACCG  TGTGGACA
                                  C      AG
GAM98   DIAPH2  3'  ACAGGTGCATACCACCATGCCT 22999       CA   CGG
          GG                      CCGGGCA  GTGG  GCGCCTGT
                                |||||||  ||||  ||||||||
                                GGTCCGT  CACC  CGTGGACA
                                   AC   ATA
GAM98   DIAPH2  3'  ACAGGTGTAAGCCACCATGCCC 23000      CA    GG
                                GGGCA  GTGGC  GCGCCTGT
                                |||||  |||||  ||||||||
                                CCCGT  CACCG  TGTGGACA
                                  AC    AA
GAM98   DISC1   3'  ACAGGTGTGAGCCACCGCACCC 38496      CACA    GG
          GG                      CCGGG   GTGGC  GCGCCTGT
                                ||||||   |||||  ||||||||
                                GGCCC   CACCG  TGTGGACA
                                  ACGC    AG
GAM98   DSC3    3'  ACAGGCGCCCACCACCACGCCC 10430       ACA   C
          GG                      CCGGGC   GTGG GGGCGCCTGT
                                ||||||   |||| ||||||||||
                                GGCCCG   CACC CCCGCGGACA
                                   CAC   A
GAM98   DSC3    3'  ACAGGCGCCCACCACCACGCCC 44610       ACA   C
          GG                      CCGGGC   GTGG GGGCGCCTGT
                                ||||||   |||| ||||||||||
                                GGCCCG   CACC CCCGCGGACA
                                   CAC   A
GAM98   DSCR3   3'  ACAGGTGACTGCCACCGTGCCC 21300        A     G
          GG                      CCGGGCAC GTGGCGG CGCCTGT
                                |||||||| ||||||| |||||||
                                GGCCCGTG CACCGTC GTGGACA
                                    C      A
GAM98   DSCR3   3'  ACAGGTGTGAGCCACCACACCC 21301    CACA    GG
                                GGG   GTGGC  GCGCCTGT
                                |||   |||||  ||||||||
                                CCC   CACCG  TGTGGACA
                                  ACAC    AG
GAM98   DSCR3   3'  ACAGGTGTGAGCCACTGTGCCC 21302          GG
                                GGGCACAGTGGC  GCGCCTGT
                                ||||||||||||  ||||||||
                                CCCGTGTCACCG  TGTGGACA
                                       AG
GAM98   EHD2    3'  ACAGGCATGAGCCACCGTGCCC 28208        A    GGGC
          GG                      CCGGGCAC GTGGC   GCCTGT
                                ||||||||  |||||   ||||||
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                                GGCCCGTG CACCG    CGGACA
                                    C     AGTA
GAM98   EIF2S3   3'  ACAGGCGTGAGCCACCTTGCCC 9202       CA    GG
                                GGGCA  GTGGC  GCGCCTGT
                                |||||  |||||  ||||||||
                                CCCGT  CACCG  TGCGGACA
                                   TC     AG
GAM98   F2RL3    3'  ACAGGCGCCCACCACCGCACCC 15482     CACA    C
                                GGG    GTGG GGGCGCCTGT
                                |||    |||| ||||||||||
                                CCC    CACC CCCGCGGACA
                                  ACGC    A
GAM98   FANCE    3'  ACAGGTGTGAGCCACCACACCA 41896    G  CACA    GG
           GG                     CC GG    GTGGC  GCGCCTGT
                                || ||    |||||  ||||||||
                                GG CC    CACCG  TGTGGACA
                                 A  ACAC     AG
GAM98   FANCF    3'  ACAGGCGTGAGCCACCGCGCCT 42966       ACA    GG
           GG                     CCGGGC   GTGGC  GCGCCTGT
                                ||||||   |||||  ||||||||
                                GGTCCG   CACCG  TGCGGACA
                                   CGC     AG
GAM98   FANCF    3'  ACAGGTGCAGGCCACCATGCCC 42967       CA    GG
           GG                     CCGGGCA  GTGGC  GCGCCTGT
                                |||||||  |||||  ||||||||
                                GGCCCGT  CACCG  CGTGGACA
                                    AC     GA
GAM98   FCAR     3'  ACAGGCGTGAGCCACCGCGCCT 56626       ACA    GG
           GG                     CCGGGC   GTGGC  GCGCCTGT
                                ||||||   |||||  ||||||||
                                GGTCCG   CACCG  TGCGGACA
                                   CGC     AG
GAM98   FEZ1     3'  ACAGGCGTGAGTCACCACACCT 42862      CACA    GG
           GG                     CCGGG    GTGGC  GCGCCTGT
                                |||||    |||||  ||||||||
                                GGTCC    CACTG  TGCGGACA
                                   ACAC     AG
GAM98   FEZ1     3'  ACAGGTGTGCGCCACCATGCCC 42863       CA     G
           G                       CGGGCA  GTGGCG GCGCCTGT
                                ||||||  |||||| ||||||||
                                GCCCGT  CACCGC TGTGGACA
                                   AC     G
GAM98   FUT1     3'  ACAGGCGCCCGCCACCACGCCC 5574        ACA
           GG                     CCGGGC   GTGGCGGGCGCCTGT
                                ||||||   ||||||||||||||||
                                GGCCCG   CACCGCCCGCGGACA
                                   CAC
GAM98   G6PC     3'  ACAGGTGCAAGCCACTATGTCC 5648       C     GG
                                GGGCA AGTGGC  GCGCCTGT
                                ||||| ||||||  ||||||||
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                                CCTGT TCACCG  CGTGGACA
                                   A     AA
GAM98   GCNT2    3'  CAGTCACCACTGTGCTC     9452          C  GCGC
                                GGGCACAGTGG GG    CTG
                                |||||||||||  ||    |||
                                CTCGTGTCACC CT    GAC
                                      A  ____
GAM98   GHR      3'  ACAGGTGTAAGCCACCGTGCCC 5686        A    GG
                                GGGCAC GTGGC  GCGCCTGT
                                ||||||  |||||  ||||||||
                                CCCGTG CACCG  TGTGGACA
                                   C     AA
GAM98   GM2A     3'  ACAGGCCCTGCCACCACGCCCG 68369       ACA       C
           G                     CCGGGC   GTGGCGGG GCCTGT
                                ||||||   ||||||||  ||||||
                                GGCCCG   CACCGTCC CGGACA
                                   CAC       _
GAM98   GPR81    3'  ACAGGCGTGAGCCACCGTGCCC 51729         A    GG
           GG                    CCGGGCAC GTGGC  GCGCCTGT
                                ||||||||  |||||  ||||||||
                                GGCCCGTG CACCG  TGCGGACA
                                    C     AG
GAM98   GPR81    3'  ACAGGTGTAAGCCACCGCACCC 51730      CACA_    GG
           CG                    CGGG    GTGGC  GCGCCTGT
                                ||||    |||||  ||||||||
                                GCCC    CACCG  TGTGGACA
                                  CACGC    AA
GAM98   HCS      3'  ACAAGCATGCGCCACCATGCCC 38957       CA     GGC  C
                                GGGCA  GTGGCG   GC TGT
                                |||||  ||||||   || |||
                                CCCGT  CACCGC   CG ACA
                                   AC     GTA  A
GAM98   HCS      3'  ACAGGCGTGAGCCACCACGCCT 38958        ACA    GG
           GG                    CCGGGC   GTGGC  GCGCCTGT
                                ||||||   |||||  ||||||||
                                GGTCCG   CACCG  TGCGGACA
                                   CAC    AG
GAM98   HCS      3'  ACAGGTGTGAGCCACCACGTCC 38959       ACA    GG
           GG                    CCGGGC   GTGGC  GCGCCTGT
                                ||||||   |||||  ||||||||
                                GGCCTG   CACCG  TGTGGACA
                                   CAC    AG
GAM98   HFE      3'  ACAGGTGTGAGCCACCCTGCCC 58122       CA    GG
                                GGGCA  GTGGC  GCGCCTGT
                                |||||  |||||  ||||||||
                                CCCGT  CACCG  TGTGGACA
                                   CC    AG
GAM98   HFE      3'  ACAGGTGTGAGCCACCCTGCCC 6396        CA    GG
                                GGGCA  GTGGC  GCGCCTGT
                                |||||  |||||  ||||||||
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                                CCCGT  CACCG  TGTGGACA
                                  CC    AG
GAM98   HLCS    5'  ACAGGTGCACGCTACCATGCCC 6402        CA    G
            GG                  CCGGGCA  GTGGCG GCGCCTGT
                                ||||||| ||||||| ||||||||
                                GGCCCGT  CATCGC CGTGGACA
                                   AC     A
GAM98   HLCS    5'  ACAGGTGTGAGCCACCGCGCCT 6403        ACA    GG
            GG                  CCGGGC  GTGGC  GCGCCTGT
                                ||||||  |||||  ||||||||
                                GGTCCG  CACCG  TGTGGACA
                                   CGC    AG
GAM98   HTR1D   3'  ACAGGCATGAGCCACTGTGCCT 7832            GGGC
            GG                  CCGGGCACAGTGGC   GCCTGT
                                ||||||||||||||   ||||||
                                GGTCCGTGTCACCG   CGGACA
                                      AGTA
GAM98   HUNK    3'  ACAGGCGTGAGCCACTGTGCCT 28170           GG
            GG                  CCGGGCACAGTGGC  GCGCCTGT
                                |||||||||||||  ||||||||
                                GGTCCGTGTCACCG  TGCGGACA
                                      AG
GAM98   IFNAR2  3'  ACAGGCGCCTGCCACCATGCCT 7892       CA
                                GGGCA  GTGGCGGGCGCCTGT
                                |||||  ||||||||||||||
                                TCCGT  CACCGTCCGCGGACA
                                  AC
GAM98   IL11    3'  ACAGGTGTGAGCCACCACACCT 7171      CACA    GG
            G                    CGGG   GTGGC  GCGCCTGT
                                ||||   |||||  ||||||||
                                GTCC   CACCG  TGTGGACA
                                  ACAC    AG
GAM98   IL11    3'  ACAGGTGTGCACCACCATGCCC 7172       CA   CGG
                                GGGCA  GTGG   GCGCCTGT
                                |||||  ||||   ||||||||
                                CCCGT  CACC   TGTGGACA
                                  AC   ACG
GAM98   INMT    3'  ACAGGAGCTCGCCACCACACCC 23202     CACA       G
                                GGG   GTGGCGGGC CCTGT
                                |||   ||||||||| |||||
                                CCC   CACCGCTCG GGACA
                                  ACAC        A
GAM98   INMT    3'  ACAGGCGTGAGCCACCGCACCC 23203     CACA    GG
                                GGG   GTGGC  GCGCCTGT
                                |||   |||||  ||||||||
                                CCC   CACCG  TGCGGACA
                                  ACGC    AG
GAM98   JAK3    3'  ACAGGTGTGCACCACCACACCC 5819       CACA   C ___
            GG                  CCGGG   GTGG GG   GCGCCTGT
                                |||||   |||| ||   ||||||||
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                                GGCCC   CACC CC  TGTGGACA
                                  A___   A  ACG
GAM98  LLGL1   3'  ACAGGCGCCCACCACCACGCCC 67408     ACA   C
                                GGGC  GTGG GGGCGCCTGT
                                ||||  |||| ||||||||||
                                CCCG  CACC CCCGCGGACA
                                  CAC   A
GAM98  LNK     3'  ACAGGCGCGAGCCACCGCGCCC 19625     ACA   GG
                                GGGC  GTGGC  GCGCCTGT
                                ||||  |||||  ||||||||
                                CCCG  CACCG  CGCGGACA
                                  CGC   AG
GAM98  LYZ     3'  ACAGGCGTGAGCCACTGCGCCC 5887       A     GG
           GG                   CCGGGC CAGTGGC  GCGCCTGT
                                |||||| |||||||  ||||||||
                                GGCCCG GTCACCG  TGCGGACA
                                   C      AG
GAM98  LYZ     3'  ACGGGCGCCCGCCACCACGCCC 5889       ACA
           GG                   CCGGGC  GTGGCGGGCGCCTGT
                                ||||||  ||||||||||||||||
                                GGCCCG  CACCGCCCGCGGGCA
                                   CAC
GAM98  LZTS1   3'  ACAGGTGCGCGCCACCGTGCCT 41020        A     G
           GG                   CCGGGCAC GTGGCG GCGCCTGT
                                |||||||| |||||| ||||||||
                                GGTCCGTG CACCGC CGTGGACA
                                    C     G
GAM98  MAK     3'  ACAGGTGTGAGCCACAGTGCCC 20935      A    GG
                                GGGCAC GTGGC  GCGCCTGT
                                |||||| |||||  ||||||||
                                CCCGTG CACCG  TGTGGACA
                                   A    AG
GAM98  MEF2A    5'  ACAGGCGCCTGCCACCATGCCT 19986       CA
           GG                   CCGGGCA  GTGGCGGGCGCCTGT
                                |||||||  ||||||||||||||||
                                GGTCCGT  CACCGTCCGCGGACA
                                   AC
GAM98  MEFV    3'  ACAGGCATGAGCCACTGTGCCC 5918            GGGC
           GG                   CCGGGCACAGTGGC   GCCTGT
                                ||||||||||||||   ||||||
                                GGCCCGTGTCACCG   CGGACA
                                      AGTA
GAM98  MEFV    3'  ACAGGCGCCCGCCACCATGCCC 5919       CA
           GG                   CCGGGCA  GTGGCGGGCGCCTGT
                                |||||||  ||||||||||||||||
                                GGCCCGT  CACCGCCCGCGGACA
                                   AC
GAM98  MEFV    3'  ACAGGTGCGTGCCACCACACCA 5920    G  CACA    G
           GG                   CC GG   GTGGCG GCGCCTGT
                                || ||   |||||| ||||||||
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                                GG CC    CACCGT CGTGGACA
                                 A  ACAC     G
GAM98   MHC2TA   3'  ACAGGTGTGAACCACCACACCC 5964      CACA    C ___
                                GGG    GTGG GG   GCGCCTGT
                                |||    |||| ||   ||||||||
                                CCC    CACC CC   TGTGGACA
                                  A___    A  AAG
GAM98   MICB     3'  ACAAGAATGAGCCACCGTGCCT 21017         A     GGGCGCC
            GG                    CCGGGCAC GTGGC      TGT
                                |||||||| |||||       |||
                                GGTCCGTG CACCG      ACA
                                     C     AGTAAGA
GAM98   MLANA    3'  ACAGGCGTGAGCCACCACGCCT 19753       ACA     GG
            GG                    CCGGGC   GTGGC  GCGCCTGT
                                ||||||   |||||  ||||||||
                                GGTCCG   CACCG  TGCGGACA
                                   CAC     AG
GAM98   MLANA    3'  ACAGGCGTGCGCCACTATGCCT 19754       C       G
            G                     CGGGCA AGTGGCG GCGCCTGT
                                ||||||| ||||||| ||||||||
                                GTCCGT TCACCGC TGCGGACA
                                   A       G
GAM98   MRPL49   3'  ACAGGCGCCCACCACCACAGCC 70155       ACA_    C
            TG                    CGGGC    GTGG GGGCGCCTGT
                                |||||    |||| ||||||||||
                                GTCCG    CACC CCCGCGGACA
                                   ACAC    A
GAM98   MTR      3'  ACAGGTGCCCACCACCACACCC 6009        CACA    C
            GG                    CCGGG    GTGG GGGCGCCTGT
                                |||||    |||| ||||||||||
                                GGCCC    CACC CCCGTGGACA
                                   ACAC    A
GAM98   MTR      3'  AGGTGCCCACCACCACACCCGG 6012        CACA    C
                                CCGGG    GTGG GGGCGCCT
                                |||||    |||| ||||||||
                                GGCCC    CACC CCCGTGGA
                                   ACAC    A
GAM98   NCOA6    5'  ACAGGCATGCGCCACCATGCCC 26819       CA     GGC
                                GGGCA  GTGGCG   GCCTGT
                                |||||  ||||||   ||||||
                                CCCGT  CACCGC   CGGACA
                                   AC     GTA
GAM98   NCOA6    5'  ACAGGTGTGAGCCACTGCGCCT 26820       A      GG
            GG                    CCGGGC CAGTGGC  GCGCCTGT
                                |||||| |||||||  ||||||||
                                GGTCCG GTCACCG  TGTGGACA
                                   C       AG
GAM98   NCOA6    5'  ACAGGTGTGAGCTACTGTGCCC 26821           GG
                                GGGCACAGTGGC  GCGCCTGT
                                ||||||||||||  ||||||||
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                                CCCGTGTCATCG  TGTGGACA
                                      AG
GAM98   NCOA6IP  3'  ACAGGCGTGAGCTACTGTGCCC 46148          GG
                                GGGCACAGTGGC  GCGCCTGT
                                ||||||||||||  ||||||||
                                CCCGTGTCATCG  TGCGGACA
                                      AG
GAM98   NDRG3    3'  ACAGGCACCTGCCACCATACCC 50113     CACA       C
                                GGG    GTGGCGGG GCCTGT
                                |||    |||||||| ||||||
                                CCC    CACCGTCC CGGACA
                                  ATAC       A
GAM98   NQO1     3'  ACAGGCGTGATCCACCACACCT 8038       CACA    C ___
            GG                    CCGGG    GTGG GG   GCGCCTGT
                                  |||||    |||| ||   ||||||||
                                  GGTCC    CACC CC   TGCGGACA
                                     A___    A  TAG
GAM98   PCDHA9   3'  ACAGGCGCCTGCCACCATGCCC 26604       CA
            G                      CGGGCA  GTGGCGGGCGCCTGT
                                   ||||||  ||||||||||||||||
                                   GCCCGT  CACCGTCCGCGGACA
                                      AC
GAM98   PCDHA9   3'  ACAGGCGTGAGCCACCGCGCCT 26605       ACA     GG
            GG                    CCGGGC   GTGGC  GCGCCTGT
                                  ||||||   |||||  ||||||||
                                  GGTCCG   CACCG  TGCGGACA
                                     CGC     AG
GAM98   PCDHB11  3'  ACAGGCGCCCACCACCACGCTC 38911       ACA    C
            GG                    CCGGGC   GTGG GGGCGCCTGT
                                  ||||||   |||| ||||||||||
                                  GGCTCG   CACC CCCGCGGACA
                                     CAC    A
GAM98   PCDHB11  3'  ACAGGCGTGCGCCACCATGCCC 38912        CA     G
            GG                    CCGGGCA  GTGGCG GCGCCTGT
                                  |||||||  |||||| ||||||||
                                  GGCCCGT  CACCGC TGCGGACA
                                      AC     G
GAM98   PER2     3'  ACAGGCGTGAGCCACCACGCCC 43337      ACA    GG
                                GGGC   GTGGC  GCGCCTGT
                                ||||   |||||  ||||||||
                                CCCG   CACCG  TGCGGACA
                                  CAC    AG
GAM98   PIGR     3'  ACAGGCGTGAGCCACCGCGTCC 72981       ACA    GG
            GG                    CCGGGC   GTGGC  GCGCCTGT
                                  ||||||   |||||  ||||||||
                                  GGCCTG   CACCG  TGCGGACA
                                     CGC    AG
GAM98   PIK3C2B  3'  ACAGGCGTGAGCCACCATGCCC 12084      CA    GG
                                GGGCA  GTGGC  GCGCCTGT
                                |||||  |||||  ||||||||
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                                CCCGT  CACCG  TGCGGACA
                                  AC     AG
GAM98   PLA2G10  5' ACAGGCGTGAGTCACCGCGCCC 14531       ACA    GG
           GG                   CCGGGC   GTGGC  GCGCCTGT
                                |||||||   |||||  ||||||||
                                GGCCCG   CACTG  TGCGGACA
                                   CGC     AG
GAM98   PMCHL1   3' ACAGGTGCCCACCACCATGCCT 49911        CA   C
           GG                   CCGGGCA  GTGG GGGCGCCTGT
                                |||||||  ||||  ||||||||||
                                GGTCCGT  CACC CCCGTGGACA
                                   AC    A
GAM98   POU2AF1  3' ACAGGCGTGAGCCACCGCACCC 21725     CACA    GG
                                GGG    GTGGC  GCGCCTGT
                                |||    |||||  ||||||||
                                CCC    CACCG  TGCGGACA
                                  ACGC    AG
GAM98   POU2AF1  3' ACAGGTGCATGCCACCATGCCT 21726        CA     G
           GG                   CCGGGCA  GTGGCG GCGCCTGT
                                |||||||  ||||||| ||||||||
                                GGTCCGT  CACCGT CGTGGACA
                                   AC     A
GAM98   PPID     3' ACAGGTGTGAGCCACCGTGCCC 88817         A    GG
           GG                   CCGGGCAC GTGGC  GCGCCTGT
                                |||||||| |||||  ||||||||
                                GGCCCGTG CACCG  TGTGGACA
                                    C     AG
GAM98   PRKAB1   3' ACAGATGTACCCACTAGCCC  21812     AC    CGG   C
                                GGGC  AGTGG   GCG CTGT
                                ||||  |||||   ||| ||||
                                CCCG  TCACC   TGT GACA
                                  A_    CA_   A
GAM98   PRKR     3' ACAGGCATGTGCCACCCACCC  12335     CACA     GGC
                                GGG   GTGGCG   GCCTGT
                                |||   ||||||   ||||||
                                CCC   CACCGT   CGGACA
                                  ACC_     GTA
GAM98   PRKWNK3  3' ACAGGCGCCAGCCACCATGCCT 62222        CA    G
           GG                   CCGGGCA  GTGGC GGCGCCTGT
                                |||||||  |||||  |||||||||
                                GGTCCGT  CACCG CCGCGGACA
                                   AC    A
GAM98   PSMD9    3' ACAGGCGTGAGCCACTGCGCCC 12521      A      GG
                                GGGC CAGTGGC  GCGCCTGT
                                ||||  |||||||  ||||||||
                                CCCG GTCACCG  TGCGGACA
                                  C      AG
GAM98   PTGES    3' ACAGGCATGAATCACTGTGCTC 18050          CGGGC
                                GGGCACAGTGG    GCCTGT
                                ||||||||||     ||||||
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                                CTCGTGTCACT    CGGACA
                                      AAGTA
GAM98   PTGES    3'  ACAGGCGCGTATCACCATACCC 18051    CACA   C ___
                                GGG   GTGG GG  GCGCCTGT
                                |||   |||| ||  ||||||||
                                CCC   TACC CT  CGCGGACA
                                  A___   A  ATG
GAM98   PTGIS    3'  ACAGGCACCCGCCACCACACCC 8182      CACA      C
          GG                      CCGGG   GTGGCGGG GCCTGT
                                |||||   |||||||| ||||||
                                GGCCC   CACCGCCC CGGACA
                                  ACAC      A
GAM98   PTGIS    3'  ACAGGCGCACACCACCACGCCC 8183      ACA   C ___
                                GGGC  GTGG GG  GCGCCTGT
                                ||||  |||| ||  ||||||||
                                CCCG  CACC CC  CGCGGACA
                                  ___   A  ACA
GAM98   PTGIS    3'  ACAGGTGTGAGCCACCGCGCCC 8184      ACA    GG
                                GGGC  GTGGC  GCGCCTGT
                                ||||  |||||  ||||||||
                                CCCG  CACCG  TGTGGACA
                                  CGC    AG
GAM98   RHD      3'  ACAGGCCTGAGCCACTGTGCCC 32801         G_  C
                                GGGCACAGTGGC  GG GCCTGT
                                ||||||||||||  || ||||||
                                CCCGTGTCACCG  TC CGGACA
                                      AG  _
GAM98   RHD      3'  ACAGGTGTGAGCCACCGTGCCC 32805      A    GG
                                GGGCAC GTGGC  GCGCCTGT
                                ||||||| |||||  ||||||||
                                CCCGTG CACCG  TGTGGACA
                                   C    AG
GAM98   RHD      3'  ACAGGCCTGAGCCACTGTGCCC 33128         G_  C
                                GGGCACAGTGGC  GG GCCTGT
                                ||||||||||||  || ||||||
                                CCCGTGTCACCG  TC CGGACA
                                      AG  _
GAM98   RHD      3'  ACAGGTGTGAGCCACCGTGCCC 33130      A    GG
                                GGGCAC GTGGC  GCGCCTGT
                                ||||||| |||||  ||||||||
                                CCCGTG CACCG  TGTGGACA
                                   C    AG
GAM98   RPH3AL   3'  ACAGATGCCCGCCACCACACCC 23724    CACA      C
                                GGG   GTGGCGGGCG CTGT
                                |||   |||||||||| ||||
                                CCC   CACCGCCCGT GACA
                                  ACAC       A
GAM98   RPH3AL   3'  ACAGGTGTGAGCCACCGCACCC 23725    CACA    GG
                                GGG   GTGGC  GCGCCTGT
                                |||   |||||  ||||||||
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                                CCC   CACCG  TGTGGACA
                                  ACGC    AG
GAM98   RPP30    3'  ACAGGCGTTAGCCACTGCGCCC 22186       A      GG
           GG                     CCGGGC CAGTGGC  GCGCCTGT
                                  ||||||| |||||||  ||||||||
                                  GGCCCG GTCACCG  TGCGGACA
                                     C      AT
GAM98   SAS      3'  ACAGGTGTGCACCACCACGCCT 21091      ACA   C ___
           G                      CGGGC   GTGG GG   GCGCCTGT
                                  |||||   |||| ||   ||||||||
                                  GTCCG   CACC CC   TGTGGACA
                                     ___   A  ACG
GAM98   SEDL     3'  ACAGGCATGAACCACCGTGCCC 28065        A   CGGGC
           GG                     CCGGGCAC GTGG    GCCTGT
                                  |||||||| ||||    ||||||
                                  GGCCCGTG CACC    CGGACA
                                      C    AAGTA
GAM98   SEDL     3'  ACAGGCGCGTGCCACCACGCCC 28066       ACA     G
           GG                     CCGGGC   GTGGCG GCGCCTGT
                                  ||||||   |||||| ||||||||
                                  GGCCCG   CACCGT CGCGGACA
                                     CAC     G
GAM98   SEDL     3'  ACAGGCGTGAGCCACCGTGCCC 28067       A    GG
                                  GGGCAC GTGGC  GCGCCTGT
                                  |||||| |||||  ||||||||
                                  CCCGTG CACCG  TGCGGACA
                                     C     AG
GAM98   SEDL     3'  ACAGGTGTGAGCCACCGTGCCC 28070        A    GG
           GG                     CCGGGCAC GTGGC  GCGCCTGT
                                  |||||||| |||||  ||||||||
                                  GGCCCGTG CACCG  TGTGGACA
                                      C     AG
GAM98   SERPINB9 3'  ACAGGCGCCCGCCACCACGCCC 16003       ACA
           GG                     CCGGGC   GTGGCGGGCGCCTGT
                                  ||||||   ||||||||||||||||
                                  GGCCCG   CACCGCCCGCGGACA
                                     CAC
GAM98   SH3BP2   3'  ACAGGCATGAGCCACTGTGCCT 13043            GGGC
           GG                     CCGGGCACAGTGGC    GCCTGT
                                  ||||||||||||||   ||||||
                                  GGTCCGTGTCACCG    CGGACA
                                         AGTA
GAM98   SH3BP2   3'  ACAGGCGCGAGCCACGGCGCCC 13044     ACA    GG
                                  GGGC   GTGGC  GCGCCTGT
                                  ||||   |||||  ||||||||
                                  CCCG   CACCG  CGCGGACA
                                     CGG    AG
GAM98   SH3BP2   3'  AGGCGCCCGCCACCACGCCTGG 13049       ACA
                                  CCGGGC   GTGGCGGGCGCCT
                                  ||||||   ||||||||||||
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                                GGTCCG  CACCGCCCGCGGA
                                   CAC
GAM98  SH3GL3  5' ACAGGTGTGAGCCACTGTGCCC 13100          GG
                                GGGCACAGTGGC GCGCCTGT
                                |||||||||||| ||||||||
                                CCCGTGTCACCG TGTGGACA
                                      AG
GAM98  SHOX    3' ACAGGCGTGAGCCCCTGCGCCC 23511      A  T  GG
          GG                    CCGGGC CAG GGC GCGCCTGT
                                |||||| ||| ||| ||||||||
                                GGCCCG GTC CCG TGCGGACA
                                   C  C  AG
GAM98  SLA2    3' ACAGGCGTACACCACCATGCCT 50877       CA   CGG
          GG                    CCGGGCA GTGG  GCGCCTGT
                                ||||||| ||||  ||||||||
                                GGTCCGT CACC  TGCGGACA
                                    AC   ACA
GAM98  SLA2    3' ACAGGTGTGAGCCACGGCACCC 50878    CACA   GG
                                GGG  GTGGC GCGCCTGT
                                |||  ||||| ||||||||
                                CCC  CACCG TGTGGACA
                                 ACGG   AG
GAM98  SLC14A2 5' ACAGGCGTGGGCCGCCGCACCC 24104     CACA    ___
          GG                    CCGGG  GTGGCGG  GCGCCTGT
                                ||||| ||||||| ||||||||
                                GGCCC  CGCCGCC  TGCGGACA
                                   A___     GGG
GAM98  SLC17A5 3' ACAGGCATGAGCCACTGTGCCC 25820          GGGC
                                GGGCACAGTGGC  GCCTGT
                                ||||||||||||  ||||||
                                CCCGTGTCACCG  CGGACA
                                      AGTA
GAM98  SLC24A1 3' ACAGGCGTCAGCCACCGCGCCT 17558      ACA   G
          GG                    CCGGGC  GTGGC GGCGCCTGT
                                |||||| ||||| |||||||||
                                GGTCCG  CACCG CTGCGGACA
                                   CGC   A
GAM98  SLC39A1 5' ACAGGCGCGAGCCACTGCGTCC 27805      A    GG
          GG                    CCGGGC CAGTGGC  GCGCCTGT
                                |||||| |||||||  ||||||||
                                GGCCTG GTCACCG  CGCGGACA
                                   C     AG
GAM98  SMAC    5' AGGCGCCCGCCACCACGCCCGG 58014      ACA
                                CCGGGC  GTGGCGGGCGCCT
                                ||||||  |||||||||||||
                                GGCCCG  CACCGCCCGCGGA
                                   CAC
GAM98  SNAP23  3' ACAGGCGTGAGCCACTGTGCCT 56329          GG
          GG                    CCGGGCACAGTGGC  GCGCCTGT
                                |||||||||||||  ||||||||
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                                GGTCCGTGTCACCG  TGCGGACA
                                      AG
GAM98   SNAP23   3'  ACAGGCGTGTGTCACCACGCTC 56330       ACA     G
           GG                   CCGGGC   GTGGCG GCGCCTGT
                                |||||||   |||||| ||||||||
                                GGCTCG   CACTGT TGCGGACA
                                   CAC     G
GAM98   SNAP23   3'  ACAGGCGTGAGCCACTGTGCCT 15129            GG
           GG                   CCGGGCACAGTGGC  GCGCCTGT
                                |||||||||||||  ||||||||
                                GGTCCGTGTCACCG  TGCGGACA
                                      AG
GAM98   SNAP23   3'  ACAGGCGTGTGTCACCACGCTC 15130       ACA     G
           GG                   CCGGGC   GTGGCG GCGCCTGT
                                ||||||   |||||| ||||||||
                                GGCTCG   CACTGT TGCGGACA
                                   CAC     G
GAM98   SULT2B1  5'  ACAGGAGTGTGCCACTGCGCCT 17219      A       G  G
           G                    CGGGC CAGTGGCG GC CCTGT
                                ||||| |||||||| || |||||
                                GTCCG GTCACCGT TG GGACA
                                   C       G  A
GAM98   TAF11    3'  ACAGGCACACACTACTGTGCCC 20115          CGGGC
                                GGGCACAGTGG    GCCTGT
                                ||||||||||    ||||||
                                CCCGTGTCATC    CGGACA
                                      ACACA
GAM98   TAL1     3'  ACAGGTGTCAGCCATTGCACCC 13521     CA      G
                                GGG  CAGTGGC GGCGCCTGT
                                |||  ||||||| |||||||||
                                CCC  GTTACCG CTGTGGACA
                                  AC      A
GAM98   TAL1     3'  ACAGGTGTGAGCCACCACACCT 13522       CACA    GG
           GG                   CCGGG    GTGGC  GCGCCTGT
                                |||||    |||||  ||||||||
                                GGTCC    CACCG  TGTGGACA
                                   ACAC     AG
GAM98   TAPBP    3'  ACAGGCGTGACGACCACACCAG 13536    G  CACA   _  G_
           G                    CC GG    GTGG CG  GCGCCTGT
                                || ||    |||| ||  ||||||||
                                GG CC    CACC GC  TGCGGACA
                                 A  A___    A  AG
GAM98   TAPBP    3'  ACAGGCGTGACGACCGCGCCCG 13537       ACA   _  G_
           G                    CCGGGC   GTGG CG  GCGCCTGT
                                ||||||   |||| ||  ||||||||
                                GGCCCG   CGCC GC  TGCGGACA
                                   ___    A  AG
GAM98   TAPBP    3'  ACAGGGGCCCGCCACCACGCCC 13538       ACA       G
           GG                   CCGGGC   GTGGCGGGC CCTGT
                                ||||||   ||||||||| |||||
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                                GGCCCG   CACCGCCCG GGACA
                                   CAC        G
GAM98   TAPBP    3'  AGGGGCCCGCCACCACGCCCGG 13551       ACA        G
                                CCGGGC   GTGGCGGGC CCT
                                ||||||   ||||||||| |||
                                GGCCCG   CACCGCCCG GGA
                                   CAC        G
GAM98   TAT      3'  ACAGGCGTGAGCCACCATGCCC 6244         CA    GG
           GG                     CCGGGCA  GTGGC  GCGCCTGT
                                ||||||| |||||  ||||||||
                                GGCCCGT  CACCG  TGCGGACA
                                   AC     AG
GAM98   TAT      3'  ACAGGCGTGAGCCACCTCGCCC 6245       ACA    GG
                                GGGC   GTGGC  GCGCCTGT
                                ||||   |||||  ||||||||
                                CCCG   CACCG  TGCGGACA
                                  CTC     AG
GAM98   TBXA2R   3'  ACAGGCGTAAGCCACTGCGCCC 8335        A      GG
           GG                     CCGGGC CAGTGGC  GCGCCTGT
                                |||||| |||||||  ||||||||
                                GGCCCG GTCACCG  TGCGGACA
                                   C       AA
GAM98   TBXA2R   3'  AGGCGCGCGCCACCACGCCCGG 8343        ACA     G
                                CCGGGC   GTGGCG GCGCCT
                                ||||||   |||||| ||||||
                                GGCCCG   CACCGC CGCGGA
                                   CAC     G
GAM98   TERF2    3'  ACAGGCGCCCGCCATCACGCCC 20141       ACA
           GG                     CCGGGC   GTGGCGGGCGCCTGT
                                ||||||   ||||||||||||||||
                                GGCCCG   TACCGCCCGCGGACA
                                   CAC
GAM98   TES      3'  ACAGGTGCATGCCACCACACCC 72455     CACA     G
                                GGG    GTGGCG GCGCCTGT
                                |||    |||||| ||||||||
                                CCC    CACCGT CGTGGACA
                                  ACAC     A
GAM98   TIM3     3'  ACAGGCGTGAGCCACCACATCC 52344     CACA    GG
                                GGG    GTGGC  GCGCCTGT
                                |||    |||||  ||||||||
                                CCT    CACCG  TGCGGACA
                                  ACAC     AG
GAM98   TIRAP    3'  ACAGGCGTGAAGCACCACGCCC 54663      ACA   G GG_
                                GGGC   GTG C   GCGCCTGT
                                ||||   ||| |   ||||||||
                                CCCG   CAC G   TGCGGACA
                                  CAC   _ AAG
GAM98   TMPRSS3  3'  ACAGGTGCCCGCCACCACACCC 51508     CACA
                                GGG    GTGGCGGGCGCCTGT
                                |||    ||||||||||||||
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                                CCC   CACCGCCCGTGGACA
                                  ACAC
GAM98   TMPRSS3   3'  ACAGGTGCCCGCCACCACACCC 51536    CACA
                                GGG   GTGGCGGGCGCCTGT
                                |||   ||||||||||||||
                                CCC   CACCGCCCGTGGACA
                                  ACAC
GAM98   TMPRSS3   3'  ACAGGTGCCCGCCACCACACCC 44010    CACA
                                GGG   GTGGCGGGCGCCTGT
                                |||   ||||||||||||||
                                CCC   CACCGCCCGTGGACA
                                  ACAC
GAM98   TNFRSF10B 3'  ACAGGTGTGCACCACCACGCCC 15208      ACA   C ___
            GG                    CCGGGC  GTGG GG  GCGCCTGT
                                |||||| ||||  ||  ||||||||
                                GGCCCG  CACC CC  TGTGGACA
                                   ___   A  ACG
GAM98   TPMT      3'  ACAGGCGTGAGCCACTGCACCT 6297      CA     GG
            GG                    CCGGG  CAGTGGC  GCGCCTGT
                                ||||| |||||||  ||||||||
                                GGTCC  GTCACCG  TGCGGACA
                                   AC      AG
GAM98   TRAF5     3'  ACAGGCGCCCGTCACCACACCC 17263    CACA
                                GGG   GTGGCGGGCGCCTGT
                                |||   ||||||||||||||
                                CCC   CACTGCCCGCGGACA
                                  ACAC
GAM98   TRPM6     3'  ACAGGCGTGAGCCACTGCGCCT 35018      A     GG
            GG                    CCGGGC CAGTGGC  GCGCCTGT
                                |||||| |||||||  ||||||||
                                GGTCCG GTCACCG  TGCGGACA
                                   C      AG
GAM98   TRPM6     3'  ACAGGTGTGCACCACTATGCCT 35019      C    CGG
            GG                    CCGGGCA AGTGG   GCGCCTGT
                                ||||||| |||||   ||||||||
                                GGTCCGT TCACC   TGTGGACA
                                   A    ACG
GAM98   TUFT1     3'  ACAGGTGTGCCACCACGCCTGG 39664      ACA   C _
                                CCGGGC   GTGG GG GCGCCTGT
                                ||||||   |||| || ||||||||
                                GGTCCG   CACC CC TGTGGACA
                                   ___   A  G
GAM98   UGDH      3'  ACAGGCACCCGCCACAGTGCCT 13985       A      C
            GG                    CCGGGCAC GTGGCGGG GCCTGT
                                |||||||| |||||||| ||||||
                                GGTCCGTG CACCGCCC CGGACA
                                   A       A
GAM98   UGDH      3'  ACAGGTGTGAGCCACCACGCCT 13987      ACA    GG
            GG                    CCGGGC  GTGGC  GCGCCTGT
                                ||||||  |||||  ||||||||
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                                GGTCCG  CACCG  TGTGGACA
                                   CAC    AG
GAM98  UMPS    3' ACAGGTGTGAGCCACTGTGCCC 6326          GG
                                GGGCACAGTGGC  GCGCCTGT
                                ||||||||||||  ||||||||
                                CCCGTGTCACCG  TGTGGACA
                                      AG
GAM98  VENTX2  3' ACAGACACCCGCCACCACGCCC 27850      ACA     CGC
          GG                    CCGGGC  GTGGCGGG  CTGT
                                ||||||  ||||||||  ||||
                                GGCCCG  CACCGCCC  GACA
                                   CAC     ACA
GAM98  VHL     3' ACAGGCGCCTGCCACCATGCCT 6814       CA
          GG                    CCGGGCA GTGGCGGGCGCCTGT
                                |||||||  ||||||||||||||
                                GGTCCGT  CACCGTCCGCGGACA
                                    AC
GAM98  VHL     3' ACAGGTGTGAGCCACCGCGTCC 6815      ACA   GG
                                GGGC  GTGGC  GCGCCTGT
                                ||||  |||||  ||||||||
                                CCTG  CACCG  TGTGGACA
                                   CGC    AG
GAM98  VIPR2   3' ACAGGCGCCCGCCAACACGCCT 14053      ACAG
          GG                    CCGGGC   TGGCGGGCGCCTGT
                                ||||||   ||||||||||||||
                                GGTCCG   ACCGCCCGCGGACA
                                   CACA
GAM98  WHSC1   3' ACAGGCGTAAGCCACTGCACCT 56686     CA     GG
          GG                    CCGGG  CAGTGGC  GCGCCTGT
                                |||||  |||||||  ||||||||
                                GGTCC  GTCACCG  TGCGGACA
                                   AC     AA
GAM98  YES1    3' ACAGGCGTGAGCCACCGCGCCC 19524     ACA   GG
                                GGGC  GTGGC  GCGCCTGT
                                ||||  |||||  ||||||||
                                CCCG  CACCG  TGCGGACA
                                   CGC    AG
GAM98  YES1    3' ACAGGTGCCCACCACCACGCCT 19525      ACA   C
          GG                    CCGGGC  GTGG GGGCGCCTGT
                                ||||||  |||| ||||||||||
                                GGTCCG  CACC CCCGTGGACA
                                   CAC   A
GAM98  ZNF133  5' ACAGGCGCCTCACCATGCCTGG 14290       CA  GC
                                CCGGGCA GTG  GGGCGCCTGT
                                |||||||  |||  ||||||||||
                                GGTCCGT  CAC  TCCGCGGACA
                                    AC  __
GAM98  ZNF137  3' ACAGGCGCGAGCACCGCGCCCG 14306      ACA  G GG
          G                     CCGGGC  GTG C  GCGCCTGT
                                ||||||  ||| |  ||||||||
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                                GGCCCG  CAC G  CGCGGACA
                                   CGC  _ AG
GAM98   ZNF157   3' ACAGGTGTGCACCACCATGCCT 14319       CA   CGG
           GG                    CCGGGCA  GTGG  GCGCCTGT
                                 ||||||| ||||  ||||||||
                                 GGTCCGT  CACC  TGTGGACA
                                    AC   ACG
GAM98   ZNF264   3' ACAGGCGCCCGCCACCACGCCT 14179       ACA
           GG                    CCGGGC  GTGGCGGGCGCCTGT
                                 ||||||  ||||||||||||||||
                                 GGTCCG  CACCGCCCGCGGACA
                                    CAC
GAM98   ZNF264   3' ACAGGTGTGAGCCACTGCACCC 14180      CA     GG
           GG                    CCGGG  CAGTGGC  GCGCCTGT
                                 |||||  |||||||  ||||||||
                                 GGCCC  GTCACCG  TGTGGACA
                                    AC     AG
GAM98   ZNF264   3' ACAGGTGTGCGCCGCCACACCC 14181    CACA    G
                                 GGG   GTGGCG GCGCCTGT
                                 |||   |||||| ||||||||
                                 CCC   CGCCGC TGTGGACA
                                   ACAC    G
GAM98   13CDNA73 5' CAGGCGCATCACGCCCGG   43786      ACA   CGG
                                 CCGGGC  GTGG  GCGCCTG
                                 ||||||  ||||  |||||||
                                 GGCCCG  CACT  CGCGGAC
                                    ___   A__
GAM98   AAK1     3' ACAGGCGTGCACCACCATGCCT 30510       CA   CGG
           GG                    CCGGGCA  GTGG  GCGCCTGT
                                 ||||||| ||||  ||||||||
                                 GGTCCGT  CACC  TGCGGACA
                                    AC   ACG
GAM98   AD7C-NTP 3' ACAGGCGTGAGCCACCTCACCC 27937    CACA    GG
                                 GGG   GTGGC  GCGCCTGT
                                 |||   |||||  ||||||||
                                 CCC   CACCG  TGCGGACA
                                   ACTC    AG
GAM98   AP3S2    3' ACAGGTGTGAGCCACCGTGCCC 20638       A    GG
           GG                    CCGGGCAC GTGGC  GCGCCTGT
                                 ||||||| |||||  ||||||||
                                 GGCCCGTG CACCG  TGTGGACA
                                    C    AG
GAM98   APOL2    3' ACAGGCACCTGCCACCACGCCC 48782      ACA      C
           GG                    CCGGGC  GTGGCGGG GCCTGT
                                 ||||||  |||||||| ||||||
                                 GGCCCG  CACCGTCC CGGACA
                                    CAC      A
GAM98   APOL2    3' ACAGGCGTGAGCCACCGCGCCT 48783      ACA    GG
           GG                    CCGGGC  GTGGC  GCGCCTGT
                                 ||||||  |||||  ||||||||
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                                GGTCCG  CACCG  TGCGGACA
                                   CGC    AG
GAM98  APXL2   5' ACAGGCGTGTGCCACCACGCCC 75666     ACA    G
                                GGGC  GTGGCG GCGCCTGT
                                ||||  |||||| ||||||||
                                CCCG  CACCGT TGCGGACA
                                  CAC    G
GAM98  ARHF    3' ACAGGCGTGAGCCACCGTGCCC 39255       A   GG
          GG                    CCGGGCAC GTGGC  GCGCCTGT
                                |||||||| |||||  ||||||||
                                GGCCCGTG CACCG  TGCGGACA
                                    C    AG
GAM98  ARHGAP11A 3' ACAGGTGCCCGCCACCACGCCC 29439     ACA
                                GGGC  GTGGCGGGCGCCTGT
                                ||||  ||||||||||||||
                                CCCG  CACCGCCCGTGGACA
                                  CAC
GAM98  ARHGAP5  5' ACAGGCGTGAGCCACTGCACCT 77592     CA     GG
          GG                    CCGGG  CAGTGGC  GCGCCTGT
                                |||||  |||||||  ||||||||
                                GGTCC  GTCACCG  TGCGGACA
                                  AC     AG
GAM98  ARHGAP5  5' ACAGGCTTTGTCACTACGCCTG 77593      AC      C
          G                     CCGGGC  AGTGGCGGG GCCTGT
                                ||||||  |||||||||| ||||||
                                GGTCCG  TCACTGTTT CGGACA
                                   CA      _
GAM98  ASB16   3' ACAGGTGTGAGCCACCACACCC 70483     CACA    GG
          GG                    CCGGG   GTGGC  GCGCCTGT
                                |||||   |||||  ||||||||
                                GGCCC   CACCG  TGTGGACA
                                  ACAC    AG
GAM98  ASE-1   3' ACAGGTGTGAGCCACCGCACCC 24964     CACA    GG
                                GGG   GTGGC  GCGCCTGT
                                |||   |||||  ||||||||
                                CCC   CACCG  TGTGGACA
                                  ACGC    AG
GAM98  ASE-1   3' AGGTGCCCACCACTATACCCGG 24969     CAC    C
                                CCGGG  AGTGG GGGCGCCT
                                |||||  ||||| ||||||||
                                GGCCC  TCACC CCCGTGGA
                                  ATA    A
GAM98  ATP1B4  3' ACAGGCGTGAGCCACCGCACCC 24828     CACA    GG
          GG                    CCGGG   GTGGC  GCGCCTGT
                                |||||   |||||  ||||||||
                                GGCCC   CACCG  TGCGGACA
                                  ACGC    AG
GAM98  BA108L7.2 3' ACAAGCATGAGCCACTGTGCCC 49059          GGGC  C
                                GGGCACAGTGGC   GC TGT
                                ||||||||||||   || |||
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                                CCCGTGTCACCG   CG ACA
                                      AGTA  A
GAM98   BNIP-S   3'  ACAGGTGTGAGCCACCGCGCTC 57082       ACA    GG
           GG                   CCGGGC  GTGGC  GCGCCTGT
                                |||||| |||||  ||||||||
                                GGCTCG  CACCG  TGTGGACA
                                   CGC    AG
GAM98   BPNT1    3'  ACAGGTGTGAGCCACCGCACCT 65381      CACA    GG
           GG                   CCGGG   GTGGC  GCGCCTGT
                                |||||   |||||  ||||||||
                                GGTCC   CACCG  TGTGGACA
                                   ACGC    AG
GAM98   BTN3A1   3'  AGGTGCACGCCACCACACCC  23886    CACA    G
                                GGG   GTGGCG GCGCCT
                                |||   |||||| ||||||
                                CCC   CACCGC CGTGGA
                                  ACAC    A
GAM98   C(27)-3BETA-HSD 3'  ACAGGTGCACGCCACCACACCT 48048      CACA    G
           GG                   CCGGG   GTGGCG GCGCCTGT
                                |||||   |||||| ||||||||
                                GGTCC   CACCGC CGTGGACA
                                   ACAC    A
GAM98   C11orf17  3'  ACAGGCACCCGCCACCATGCCC 40570       CA      C
           GG                   CCGGGCA  GTGGCGGG GCCTGT
                                |||||||  |||||||| ||||||
                                GGCCCGT  CACCGCCC CGGACA
                                   AC      A
GAM98   C11orf17  3'  ACAGGCGTGAGCCACCGCGCCC 40571       ACA    GG
           GG                   CCGGGC  GTGGC  GCGCCTGT
                                ||||||  |||||  ||||||||
                                GGCCCG  CACCG  TGCGGACA
                                   CGC    AG
GAM98   C13orf1   3'  ACAGGTGCCCGCCACCACGCCC 40344      ACA
           G                    CGGGC  GTGGCGGGCGCCTGT
                                |||||  ||||||||||||||||
                                GCCCG  CACCGCCCGTGGACA
                                   CAC
GAM98   C1QTNF6   3'  ACAGGCGCCTGCTACCATGCCT 49981       CA
           GG                   CCGGGCA  GTGGCGGGCGCCTGT
                                |||||||  ||||||||||||||||
                                GGTCCGT  CATCGTCCGCGGACA
                                   AC
GAM98   C1QTNF6   3'  ACAGGTGTGAGCCACCGTGCCT 49982        A    GG
           GG                   CCGGGCAC GTGGC  GCGCCTGT
                                |||||||| |||||  ||||||||
                                GGTCCGTG CACCG  TGTGGACA
                                   C    AG
GAM98   C3F      3'  ACAGGCGTGAGCCACCGTGCCC 20471        A    GG
           GG                   CCGGGCAC GTGGC  GCGCCTGT
                                |||||||| |||||  ||||||||
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                                GGCCCGTG CACCG  TGCGGACA
                                    C    AG
GAM98   C6orf33  3' ACAGGCGCGTGCCACCACACCT 56708      CACA    G
            GG                    CCGGG   GTGGCG GCGCCTGT
                                  |||||   |||||| ||||||||
                                  GGTCC   CACCGT CGCGGACA
                                    ACAC    G
GAM98   C6orf5   3' ACAGGTGTGAGCCACCACACCC 31958    CACA   GG
                                  GGG   GTGGC  GCGCCTGT
                                  |||   |||||  ||||||||
                                  CCC   CACCG  TGTGGACA
                                   ACAC   AG
GAM98   C6orf5   3' AGGCGCCTGCCACCATGCCC  31973      CA
                                  GGGCA  GTGGCGGGCGCCT
                                  |||||  ||||||||||||
                                  CCCGT  CACCGTCCGCGGA
                                    AC
GAM98   C9orf14  5' ACAGGCGTGAGCCACCGCGCCC 87951       ACA    GG
            GG                    CCGGGC  GTGGC  GCGCCTGT
                                  ||||||  |||||  ||||||||
                                  GGCCCG  CACCG  TGCGGACA
                                    CGC    AG
GAM98   C9orf9   3' ACAGGCGCCCACCACCCCACCT 39004      CACA   C
            GG                    CCGGG   GTGG GGGCGCCTGT
                                  |||||   |||| ||||||||||
                                  GGTCC   CACC CCCGCGGACA
                                    ACCC   A
GAM98   C9orf9   3' ACAGGCGCCCACCACCTCGCCT 39005       ACA   C
            GG                    CCGGGC  GTGG GGGCGCCTGT
                                  ||||||  |||| ||||||||||
                                  GGTCCG  CACC CCCGCGGACA
                                    CTC   A
GAM98   C9orf9   3' ACAGGCGTGAGCCACAGCGCCC 39006       ACA    GG
            GG                    CCGGGC  GTGGC  GCGCCTGT
                                  ||||||  |||||  ||||||||
                                  GGCCCG  CACCG  TGCGGACA
                                    CGA    AG
GAM98   CACNA1I  3' CAGGCGCCCGACAGCCGG    41182     G ACAG  G
                                  CCGG C   TG CGGGCGCCTG
                                  |||| |   || ||||||||||
                                  GGCC G   AC GCCCGCGGAC
                                    _ ____  A
GAM98   CCRN4L   3' ACAGGCGCCCGTCACCACGCCC 25063      ACA
                                  GGGC  GTGGCGGGCGCCTGT
                                  ||||  ||||||||||||||
                                  CCCG  CACTGCCCGCGGACA
                                    CAC
GAM98   CDC14B   3' ACAGGTGTCAGCCACCGCACCC 53995     CACA    G
                                  GGG   GTGGC GGCGCCTGT
                                  |||   ||||| |||||||||
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                                CCC    CACCG CTGTGGACA
                                  ACGC     A
GAM98   CEACAM8   3'  ACAGGCGCCTGCCACAACGCCC 10173        ACA
            GG                    CCGGGC   GTGGCGGGCGCCTGT
                                  ||||||   ||||||||||||||||
                                  GGCCCG   CACCGTCCGCGGACA
                                     CAA
GAM98   CEACAM8   3'  ACAGGTGTGAGCCACCGCGCCC 10174      ACA    GG
                                  GGGC   GTGGC  GCGCCTGT
                                  ||||   |||||  ||||||||
                                  CCCG   CACCG  TGTGGACA
                                    CGC    AG
GAM98   CHRAC1    3'  ACAGGCGTGAGCCACCATGCCT 34327        CA    GG
            GG                    CCGGGCA  GTGGC  GCGCCTGT
                                  |||||||  |||||  ||||||||
                                  GGTCCGT  CACCG  TGCGGACA
                                     AC    AG
GAM98   CHRAC1    3'  ACAGGCGTGTGCCACCATGCCC 34328       CA     G
                                  GGGCA  GTGGCG GCGCCTGT
                                  |||||  |||||| ||||||||
                                  CCCGT  CACCGT TGCGGACA
                                    AC     G
GAM98   CIP29     3'  ACAGGCATAGGCCACTGTGCCC 51365             GGGC
            GG                    CCGGGCACAGTGGC    GCCTGT
                                  ||||||||||||||    ||||||
                                  GGCCCGTGTCACCG    CGGACA
                                        GATA
GAM98   CPLX1     3'  ACAGGCGCCGCCTCGCCCCCGG 22819       CACAGT    G
                                  CCGGG     GGCGG CGCCTGT
                                  |||||     ||||| |||||||
                                  GGCCC     CCGCC GCGGACA
                                    CCGCT_    _
GAM98   DBR1      3'  ACAGGCGTGAGCCACTGTGCCT 33055             GG
            GG                    CCGGGCACAGTGGC  GCGCCTGT
                                  ||||||||||||||  ||||||||
                                  GGTCCGTGTCACCG  TGCGGACA
                                        AG
GAM98   DBR1      3'  ACAGGTGCCCGCCACCACACCC 33058       CACA
            GG                    CCGGG    GTGGCGGGCGCCTGT
                                  |||||    ||||||||||||||||
                                  GGCCC    CACCGCCCGTGGACA
                                    ACAC
GAM98   DCOHM     3'  ACAGGTGCATGCCACCACACCC 50504     CACA     G
                                  GGG    GTGGCG GCGCCTGT
                                  |||    |||||| ||||||||
                                  CCC    CACCGT CGTGGACA
                                    ACAC     A
GAM98   DDX34     3'  ACAGGCGTGAGCCACTGCACCC 28654       CA      GG
            GG                    CCGGG  CAGTGGC  GCGCCTGT
                                  |||||  |||||||  ||||||||
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                                GGCCC  GTCACCG  TGCGGACA
                                  AC       AG
GAM98   DKFZP434B044 3'  ACAGGCGTGAGCTACCATGCCC 49708        CA     GG
           GG                    CCGGGCA  GTGGC  GCGCCTGT
                                 |||||||  |||||  ||||||||
                                 GGCCCGT  CATCG  TGCGGACA
                                    AC     AG
GAM98   DKFZP434C212 3'  ACAGGCGCATGTCACCAAGCCC 69476       ACA      G
           GG                    CCGGGC   GTGGCG GCGCCTGT
                                 ||||||   |||||| ||||||||
                                 GGCCCG   CACTGT CGCGGACA
                                   AAC     A
GAM98   DKFZp434E2220 5'  ACAGGCGCCCGCCACGGCGCCC 34702      ACA
                                 GGGC   GTGGCGGGCGCCTGT
                                 ||||   ||||||||||||||
                                 CCCG   CACCGCCCGCGGACA
                                   CGG
GAM98   DKFZp434F1719 3'  ACAGGCATAAGCCATTGTGCCC 51007             GGGC
           GG                    CCGGGCACAGTGGC    GCCTGT
                                 ||||||||||||||    ||||||
                                 GGCCCGTGTTACCG    CGGACA
                                       AATA
GAM98   DKFZP434J037 3'  ACAGGCGCCCGCCACCATGCCC 48934        CA
           GG                    CCGGGCA  GTGGCGGGCGCCTGT
                                 |||||||  ||||||||||||||
                                 GGCCCGT  CACCGCCCGCGGACA
                                    AC
GAM98   DKFZP434J037 3'  ACAGGCGTGAGCCACCGCGCCC 48935      ACA    GG
                                 GGGC   GTGGC  GCGCCTGT
                                 ||||   |||||  ||||||||
                                 CCCG   CACCG  TGCGGACA
                                   CGC    AG
GAM98   DKFZp547H025 3'  ACAGGTGTGAGCCACCAGGCCC 39764      ACA    GG
                                 GGGC   GTGGC  GCGCCTGT
                                 ||||   |||||  ||||||||
                                 CCCG   CACCG  TGTGGACA
                                   GAC    AG
GAM98   DKFZP564G092 5'  ACAGGCGTGAGCCACTGCGCCC 32147      A      GG
                                 GGGC CAGTGGC  GCGCCTGT
                                 |||| |||||||  ||||||||
                                 CCCG GTCACCG  TGCGGACA
                                   C      AG
GAM98   DKFZP564O0423 3'  ACAGGTGTGAGCCACTGCGCCT 93336       A      GG
           GG                    CCGGGC CAGTGGC  GCGCCTGT
                                 ||||||| |||||||  ||||||||
                                 GGTCCG GTCACCG  TGTGGACA
                                   C      AG
GAM98   DKFZP564O0523 3'  ACAGGCGTGCACCACCATGCCT 50415        CA   CGG
           GG                    CCGGGCA  GTGG   GCGCCTGT
                                 |||||||  ||||   ||||||||
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                                GGTCCGT  CACC   TGCGGACA
                                   AC    ACG
GAM98   DKFZp761J139 5'  ACAGGCGTGAGCCACCATACCC 51094      CACA    GG
           GG                    CCGGG   GTGGC  GCGCCTGT
                                 |||||   |||||  ||||||||
                                 GGCCC   CACCG  TGCGGACA
                                   ATAC    AG
GAM98   DKFZp761N1114 3'  ACAGGCGTGAGCCACTGCACCC 79770     CA      GG
                                 GGG  CAGTGGC  GCGCCTGT
                                 |||  |||||||  ||||||||
                                 CCC  GTCACCG  TGCGGACA
                                   AC      AG
GAM98   DKFZp761O0113 5'  ACAGGCGTGAGCCACCGCGCCC 37885       ACA    GG
           GG                    CCGGGC   GTGGC  GCGCCTGT
                                 ||||||   |||||  ||||||||
                                 GGCCCG   CACCG  TGCGGACA
                                    CGC    AG
GAM98   DKFZp762P2111 3'  ACAGGCGCCCACCACCACTCCC 87620      CACA   C
           GG                    CCGGG   GTGG GGGCGCCTGT
                                 |||||   ||||  ||||||||||
                                 GGCCC   CACC CCCGCGGACA
                                   TCAC   A
GAM98   DSCR6    3'  ACAGGCGTGAGCCACTGAGCCC 39052       A      GG
           GG                    CCGGGC CAGTGGC  GCGCCTGT
                                 ||||||| |||||||  ||||||||
                                 GGCCCG GTCACCG  TGCGGACA
                                    A      AG
GAM98   EREG     3'  ACAGGCGCATGCCACCATGCCC 9298       CA     G
                                 GGGCA  GTGGCG GCGCCTGT
                                 |||||  |||||| ||||||||
                                 CCCGT  CACCGT CGCGGACA
                                   AC     A
GAM98   ERO1L    3'  ACAGGTGTCTGCCACCATACCC 28151     CACA
                                 GGG   GTGGCGGGCGCCTGT
                                 |||   ||||||||||||||||
                                 CCC   CACCGTCTGTGGACA
                                   ATAC
GAM98   EVI5     3'  ACAGGTGTGAGCCACTGCACCC 20188     CA      GG
                                 GGG  CAGTGGC  GCGCCTGT
                                 |||  |||||||  ||||||||
                                 CCC  GTCACCG  TGTGGACA
                                   AC      AG
GAM98   FBP17    3'  ACAGGCGTGCACCACCACGCCC 73138       ACA   C ___
           GG                    CCGGGC   GTGG GG   GCGCCTGT
                                 ||||||   ||||  ||   ||||||||
                                 GGCCCG   CACC CC   TGCGGACA
                                    ___    A  ACG
GAM98   FER1L4   3'  ACAGGTGTGAGCCACCATGCCA 48106    G   CA    GG
           GG                    CC GGCA  GTGGC  GCGCCTGT
                                 ||  ||||  |||||  ||||||||
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                                GG CCGT  CACCG  TGTGGACA
                                 A   AC    AG
GAM98   FKBP9    3' ACAGGTGTGCACCACCACGCCC 95708     ACA   C ___
                                GGGC  GTGG GG  GCGCCTGT
                                ||||  |||| ||  ||||||||
                                CCCG  CACC CC  TGTGGACA
                                  ___   A ACG
GAM98   FLB6421  3' ACAGGCATGAGCCACCGTGCCT 39641        A    GGGC
           GG                    CCGGGCAC GTGGC   GCCTGT
                                ||||||||| |||||   ||||||
                                GGTCCGTG CACCG   CGGACA
                                    C    AGTA
GAM98   FLJ00060 5' ACAGGCGCCCACCACCATGCCC 61728       CA   C
           GG                    CCGGGCA  GTGG GGGCGCCTGT
                                |||||||  |||| ||||||||||
                                GGCCCGT  CACC CCCGCGGACA
                                   AC   A
GAM98   FLJ00060 5' ACAGGCGTGAGCCAGTGTGCCC 61729         G   GG
           GG                    CCGGGCACA TGGC  GCGCCTGT
                                |||||||||| ||||  ||||||||
                                GGCCCGTGT ACCG  TGCGGACA
                                    G   AG
GAM98   FLJ10346 5' ACAGGCGCCCGCCACCACGCCT 36517       ACA
           GG                    CCGGGC  GTGGCGGGCGCCTGT
                                ||||||  ||||||||||||||||
                                GGTCCG  CACCGCCCGCGGACA
                                  CAC
GAM98   FLJ10346 5' ACAGGCGTGAGCCACCGCGCCC 36518       ACA    GG
           GG                    CCGGGC  GTGGC  GCGCCTGT
                                ||||||  |||||  ||||||||
                                GGCCCG  CACCG  TGCGGACA
                                  CGC    AG
GAM98   FLJ10560 3' ACAGGCGCCCGCCACCACGCCC 36786       ACA
           GG                    CCGGGC  GTGGCGGGCGCCTGT
                                ||||||  ||||||||||||||||
                                GGCCCG  CACCGCCCGCGGACA
                                  CAC
GAM98   FLJ10560 3' ACAGGCGTGAGCCACCGTGCCC 36787       A    GG
                                GGGCAC GTGGC  GCGCCTGT
                                ||||||| |||||  ||||||||
                                CCCGTG CACCG  TGCGGACA
                                   C    AG
GAM98   FLJ10607 3' ACAGGTGCGAGCCACTGCACCT 77619      CA     GG
           GG                    CCGGG  CAGTGGC  GCGCCTGT
                                |||||  |||||||  ||||||||
                                GGTCC  GTCACCG  CGTGGACA
                                  AC      AG
GAM98   FLJ10713 3' ACAGGCACCTGCCACCACACCC 36993     CACA      C
                                GGG   GTGGCGGG GCCTGT
                                |||   |||||||| ||||||
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                                CCC    CACCGTCC CGGACA
                                  ACAC       A
GAM98   FLJ10846 3' ACAGGCACCTGCCACCATGCCC 37279      CA       C
                                GGGCA  GTGGCGGG GCCTGT
                                |||||  |||||||| ||||||
                                CCCGT  CACCGTCC CGGACA
                                   AC       A
GAM98   FLJ10846 3' ACAGGCGTGAGCCACTGCGCCT 37280       A      GG
           GG                     CCGGGC CAGTGGC  GCGCCTGT
                                |||||| |||||||  ||||||||
                                GGTCCG GTCACCG  TGCGGACA
                                   C      AG
GAM98   FLJ10847 3' ACAGGCGTGTGCCACCACGCCT 37296     ACA     G
                                GGGC   GTGGCG GCGCCTGT
                                ||||   |||||| ||||||||
                                TCCG   CACCGT TGCGGACA
                                  CAC     G
GAM98   FLJ10936 3' ACAGGCGTGCACCATCACGCCC 37436       ACA    CGG
           GG                     CCGGGC   GTGG   GCGCCTGT
                                ||||||   ||||   ||||||||
                                GGCCCG   TACC   TGCGGACA
                                   CAC    ACG
GAM98   FLJ11186 3' ACAGGCATGAGCCACTGTGCCT 37721             GGGC
           GG                     CCGGGCACAGTGGC    GCCTGT
                                ||||||||||||||   ||||||
                                GGTCCGTGTCACCG    CGGACA
                                      AGTA
GAM98   FLJ12363 3' ACAGGCACCTGTCACCACACCC 50624     CACA       C
                                GGG    GTGGCGGG GCCTGT
                                |||    |||||||| ||||||
                                CCC    CACTGTCC CGGACA
                                  ACAC       A
GAM98   FLJ12581 3' ACAGGCGCCCGCCACCTCGCCC 46325       ACA
           GG                     CCGGGC   GTGGCGGGCGCCTGT
                                ||||||   ||||||||||||||||
                                GGCCCG   CACCGCCCGCGGACA
                                   CTC
GAM98   FLJ12581 3' ACAGGCGTGAGCCACCGCGCCC 46326     ACA    GG
                                GGGC   GTGGC  GCGCCTGT
                                ||||   |||||  ||||||||
                                CCCG   CACCG  TGCGGACA
                                   CGC    AG
GAM98   FLJ12649 3' ACAGGTGTGAGCCACTGCACCC 45083     CA      GG
                                GGG  CAGTGGC  GCGCCTGT
                                |||  |||||||  ||||||||
                                CCC  GTCACCG  TGTGGACA
                                  AC      AG
GAM98   FLJ12787 3' ACAGGTGTGAGCCACTGTGTCC 50686           GG
                                GGGCACAGTGGC  GCGCCTGT
                                ||||||||||||  ||||||||
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                                CCTGTGTCACCG TGTGGACA
                                      AG
GAM98   FLJ12876 3' ACAGGCGCCCGCCACCACGCCC 43082       ACA
            GG                  CCGGGC  GTGGCGGGCGCCTGT
                                |||||| ||||||||||||||||
                                GGCCCG  CACCGCCCGCGGACA
                                   CAC
GAM98   FLJ12960 3' ACAGGCGCCCGCCACCATGCCT 45287        CA
            GG                  CCGGGCA GTGGCGGGCGCCTGT
                                ||||||| ||||||||||||||||
                                GGTCCGT CACCGCCCGCGGACA
                                   AC
GAM98   FLJ12973 3' ACAGGCACCTGCCACCACGCCT 46634       ACA      C
            GG                  CCGGGC  GTGGCGGG GCCTGT
                                |||||| |||||||| ||||||
                                GGTCCG  CACCGTCC CGGACA
                                   CAC      A
GAM98   FLJ12973 3' ACAGGCGTGAGCCACCATGCCT 46635        CA    GG
            GG                  CCGGGCA GTGGC  GCGCCTGT
                                ||||||| ||||| ||||||||
                                GGTCCGT CACCG  TGCGGACA
                                   AC    AG
GAM98   FLJ13072 5' ACAGGTGTGAGCCACCACACCC 91380      CACA    GG
            GG                  CCGGG   GTGGC  GCGCCTGT
                                ||||| ||||| ||||||||
                                GGCCC   CACCG  TGTGGACA
                                  ACAC    AG
GAM98   FLJ13114 3' ACAGGCGTGAGCCACCACACCC 44890    CACA    GG
                                GGG   GTGGC  GCGCCTGT
                                |||   ||||| ||||||||
                                CCC   CACCG  TGCGGACA
                                 ACAC    AG
GAM98   FLJ13193 3' ACAGGTGTGTACCACCACGCCC 50701     ACA   C ___
                                GGGC  GTGG GG  GCGCCTGT
                                ||||  |||| ||  ||||||||
                                CCCG  CACC CC  TGTGGACA
                                  ___   A ATG
GAM98   FLJ13305 5' ACAGGCATGAACCACTGTGCCT 91701           CGGGC
            GG                  CCGGGCACAGTGG   GCCTGT
                                |||||||||||||   ||||||
                                GGTCCGTGTCACC   CGGACA
                                      AAGTA
GAM98   FLJ13952 3' ACAGGCATCCGCCACCATGCCC 45999       CA     GC
            GG                  CCGGGCA GTGGCGG  GCCTGT
                                ||||||| ||||||| ||||||
                                GGCCCGT CACCGCC  CGGACA
                                   AC      TA
GAM98   FLJ14351 3' ACAGGCGTGAGCCACTTACCCG 45644      CAC     GG
            G                   CCGGG  AGTGGC  GCGCCTGT
                                ||||| ||||||  ||||||||
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                                GGCCC   TCACCG  TGCGGACA
                                  AT_     AG
GAM98   FLJ14442 3' ACAGGTGTAAGCCACTGAGCCC 52371       A      GG
           GG                     CCGGGC CAGTGGC  GCGCCTGT
                                  |||||| |||||||  ||||||||
                                  GGCCCG GTCACCG  TGTGGACA
                                     A       AA
GAM98   FLJ14442 3' ACAGGTGTGCGCCACCATGTCC 52372        CA     G
           GG                     CCGGGCA  GTGGCG GCGCCTGT
                                  |||||||  |||||| ||||||||
                                  GGCCTGT  CACCGC TGTGGACA
                                     AC      G
GAM98   FLJ14824 3' ACAGGCGTGAGCCACCGTGCCT 52713         A    GG
           GG                     CCGGGCAC GTGGC  GCGCCTGT
                                  |||||||| |||||  ||||||||
                                  GGTCCGTG CACCG  TGCGGACA
                                      C     AG
GAM98   FLJ20034 3' ACAGAAGTGAGCCACTGTACCT 34829       C       GG  GC
           GG                     CCGGG ACAGTGGC  GC  CTGT
                                  ||||| ||||||||  ||  ||||
                                  GGTCC TGTCACCG  TG  GACA
                                     A       AG  AA
GAM98   FLJ20136 3' ACAGGTGTGTGCCACCACGCCT 35088        ACA     G
           GG                     CCGGGC   GTGGCG GCGCCTGT
                                  ||||||   |||||| ||||||||
                                  GGTCCG   CACCGT TGTGGACA
                                     CAC     G
GAM98   FLJ20147 3' ACAGGTGTGTGCCACCACACCT 35129       CACA     G
           GG                     CCGGG    GTGGCG GCGCCTGT
                                  |||||    |||||| ||||||||
                                  GGTCC    CACCGT TGTGGACA
                                     ACAC     G
GAM98   FLJ20320 3' ACAGGTGTGCCACCGCGCCCGG 35416        ACA    GG
                                  CCGGGC   GTGGC  GCGCCTGT
                                  ||||||   |||||  ||||||||
                                  GGCCCG   CACCG  TGTGGACA
                                     CGC    __
GAM98   FLJ20342 3' ACAGGCGTGAGCCACTCCACCC 35464     CAC     GG
                                  GGG   AGTGGC  GCGCCTGT
                                  |||   ||||||  ||||||||
                                  CCC   TCACCG  TGCGGACA
                                    ACC     AG
GAM98   FLJ20452 3' ACAGGCGTAAGCCACTGCGCCC 35641      A      GG
                                  GGGC CAGTGGC  GCGCCTGT
                                  |||| |||||||  ||||||||
                                  CCCG GTCACCG  TGCGGACA
                                     C       AA
GAM98   FLJ20485 3' ACAGGCGCGCACCACCACGCCT 39289      ACA    C ___
                                  GGGC   GTGG GG   GCGCCTGT
                                  ||||   |||| ||   ||||||||
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                                TCCG   CACC CC   CGCGGACA
                                  ___    A  ACG
GAM98   FLJ20511  3' ACAGGCGCCCGCCACCATGCCC 35762      CA
                                GGGCA  GTGGCGGGCGCCTGT
                                |||||  ||||||||||||||||
                                CCCGT  CACCGCCCGCGGACA
                                   AC
GAM98   FLJ20700  3' ACAGGTGTGAGCCACCACACCC 35992     CACA    GG
                                GGG    GTGGC  GCGCCTGT
                                |||    |||||  ||||||||
                                CCC    CACCG  TGTGGACA
                                  ACAC    AG
GAM98   FLJ20718  3' ACAGGCGTGAGCCACCGTGCCT 36040        A    GG
            GG                    CCGGGCAC GTGGC  GCGCCTGT
                                |||||||| |||||  ||||||||
                                GGTCCGTG CACCG  TGCGGACA
                                     C    AG
GAM98   FLJ20813  3' ACAGGCATCTGCCACCGCACTC 36124      CACA     GC
            GG                    CCGGG   GTGGCGG  GCCTGT
                                |||||   |||||||  ||||||
                                GGCTC   CACCGTC  CGGACA
                                   ACGC      TA
GAM98   FLJ20958  3' ACAGGCGTGAACCACTGTGTCC 42305          CGG
                                GGGCACAGTGG   GCGCCTGT
                                ||||||||||   ||||||||
                                CCTGTGTCACC   TGCGGACA
                                      AAG
GAM98   FLJ20958  3' ACAGGCGTGAGCCACCACACCC 42306     CACA    GG
                                GGG    GTGGC  GCGCCTGT
                                |||    |||||  ||||||||
                                CCC    CACCG  TGCGGACA
                                  ACAC    AG
GAM98   FLJ21135  3' ACAGGCGCCCCACCACCACCC  46346     CACA   C_
                                GGG    GTGG  GGGCGCCTGT
                                |||    ||||  ||||||||||
                                CCC    CACC  CCCGCGGACA
                                  AC__    AC
GAM98   FLJ21302  3' ACAGGCATGGAGCACCGTGCCT 43497        A   G GGGC_
            GG                    CCGGGCAC GTG C    GCCTGT
                                |||||||| ||| |    ||||||
                                GGTCCGTG CAC G    CGGACA
                                     C   _ AGGTA
GAM98   FLJ21302  3' ACAGGTGCACACCACCATGCCT 43499        CA    CGG
            GG                    CCGGGCA  GTGG   GCGCCTGT
                                |||||||  ||||   ||||||||
                                GGTCCGT  CACC   CGTGGACA
                                   AC    ACA
GAM98   FLJ22167  5' ACAGGCGCCCACCATCACGCCT 44853       ACA    C
            GG                    CCGGGC   GTGG GGGCGCCTGT
                                ||||||   |||| ||||||||||
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                                GGTCCG   TACC CCCGCGGACA
                                   CAC    A
GAM98   FLJ22329  3' ACAGGCATGAGCCACTGTGCCC 45388          GGGC
                                GGGCACAGTGGC    GCCTGT
                                ||||||||||||   ||||||
                                CCCGTGTCACCG    CGGACA
                                      AGTA
GAM98   FLJ22529  3' ACAGGCGTGAGCCACTGTGGCC 45932    G       GG
                                GG CACAGTGGC  GCGCCTGT
                                || |||||||||  ||||||||
                                CC GTGTCACCG  TGCGGACA
                                 G        AG
GAM98   FLJ22684  3' ACAGGCACCTGCCACCACATCC 47460     CACA       C
                                GGG    GTGGCGGG GCCTGT
                                |||    |||||||| ||||||
                                CCT    CACCGTCC CGGACA
                                  ACAC       A
GAM98   FLJ22800  3' ACAGGTGCGTGCCACTATGCC  45990     C      G
                                GGCA AGTGGCG GCGCCTGT
                                |||| ||||||| ||||||||
                                CCGT TCACCGT CGTGGACA
                                  A      G
GAM98   FLJ23323  3' ACAGGCGTGAGCCACCGCGCCC 45385       ACA    GG
           GG                     CCGGGC   GTGGC  GCGCCTGT
                                |||||   |||||  ||||||||
                                GGCCCG   CACCG  TGCGGACA
                                   CGC    AG
GAM98   FLJ23356  3' ACAGGCGTGAGCCACTGCGCCC 50921       A      GG
           GG                     CCGGGC CAGTGGC  GCGCCTGT
                                |||||| |||||||  ||||||||
                                GGCCCG GTCACCG  TGCGGACA
                                   C      AG
GAM98   FLJ23392  3' ACAGGCGCCTATCACCATGCCT 45867        CA   GC
           GG                     CCGGGCA  GTG  GGGCGCCTGT
                                |||||||  |||  ||||||||||
                                GGTCCGT  CAC  TCCGCGGACA
                                    AC   TA
GAM98   FLJ23392  3' ACAGGCTTGAGCCACCGTGCCT 45868         A    GGGC
           GG                     CCGGGCAC GTGGC    GCCTGT
                                |||||||| |||||    ||||||
                                GGTCCGTG CACCG    CGGACA
                                     C     AGTT
GAM98   FLJ23519  3' ACAGGCGCCCGTCACCACACCA 50940    G  CACA
           GG                     CC GG    GTGGCGGGCGCCTGT
                                || ||    ||||||||||||||||
                                GG CC    CACTGCCCGCGGACA
                                 A  ACAC
GAM98   FLJ23519  3' ACAGGCGTGAGCCACCACGCCT 50941       ACA    GG
           GG                     CCGGGC   GTGGC  GCGCCTGT
                                ||||||   |||||  ||||||||
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                                GGTCCG  CACCG  TGCGGACA
                                   CAC    AG
GAM98   FLJ23556 3' ACAGGCACCCGCCACCACGCCC 46418      ACA      C
           G                    CGGGC  GTGGCGGG GCCTGT
                                |||||  |||||||| ||||||
                                GCCCG  CACCGCCC CGGACA
                                   CAC      A
GAM98   FLJ23556 3' ACAGGCGTGAGCCACTACACCC 46419    CAC    GG
                                GGG  AGTGGC  GCGCCTGT
                                |||  ||||||  ||||||||
                                CCC  TCACCG  TGCGGACA
                                  ACA    AG
GAM98   FLJ23563 3' ACAGGGGTGAGCCACTGTGCCC 68207           GG  G
           GG                     CCGGGCACAGTGGC  GC CCTGT
                                |||||||||||||  || |||||
                                GGCCCGTGTCACCG  TG GGACA
                                       AG  G
GAM98   FLJ23563 3' ACAGGTGCCCGCCACCATGCTC 68208      CA
                                GGGCA  GTGGCGGGCGCCTGT
                                |||||  ||||||||||||||||
                                CTCGT  CACCGCCCGTGGACA
                                   AC
GAM98   FLJ30532 3' ACAGGCGTGAGTCACCGCGCCC 59212     ACA    GG
                                GGGC   GTGGC  GCGCCTGT
                                ||||   |||||  ||||||||
                                CCCG   CACTG  TGCGGACA
                                   CGC    AG
GAM98   FLJ31101 3' ACAGGCACCTGCCACCACGCCC 36155     ACA      C
                                GGGC   GTGGCGGG GCCTGT
                                ||||   |||||||| ||||||
                                CCCG   CACCGTCC CGGACA
                                   CAC      A
GAM98   FLJ31153 3' ACAGGTGTGAGCCACTGAGCCC 58737     A      GG
                                GGGC CAGTGGC  GCGCCTGT
                                |||| |||||||  ||||||||
                                CCCG GTCACCG  TGTGGACA
                                   A      AG
GAM98   FLJ32865 3' ACAGGCGTGAGCCACTGCACCC 58794     CA     GG
           GG                     CCGGG  CAGTGGC  GCGCCTGT
                                |||||  |||||||  ||||||||
                                GGCCC  GTCACCG  TGCGGACA
                                   AC     AG
GAM98   GGA2    3' ACAGGCGTGAGCCACCGCACCC 31152      CACA    GG
           GG                     CCGGG   GTGGC  GCGCCTGT
                                |||||   |||||  ||||||||
                                GGCCC   CACCG  TGCGGACA
                                   ACGC    AG
GAM98   GGA2    3' ACAGGCGTGAGCCAGCACGCCC 31153     ACAG   GG
                                GGGC   TGGC  GCGCCTGT
                                ||||   ||||  ||||||||
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                              CCCG   ACCG  TGCGGACA
                                CACG   AG
GAM98   GGA2    3'  ACAGGCGTGAGCCACCGCACCC 57646      CACA    GG
          GG                    CCGGG   GTGGC  GCGCCTGT
                                |||||   |||||  ||||||||
                              GGCCC   CACCG  TGCGGACA
                                 ACGC    AG
GAM98   GGA2    3'  ACAGGCGTGAGCCAGCACGCCC 57647     ACAG   GG
                              GGGC   TGGC  GCGCCTGT
                              ||||   ||||  ||||||||
                              CCCG   ACCG  TGCGGACA
                                CACG   AG
GAM98   GMPPB   5'  ACAGGCGTGAGCCACCGCGCCC 97428       ACA    GG
          GG                    CCGGGC  GTGGC  GCGCCTGT
                                ||||||  |||||  ||||||||
                              GGCCCG  CACCG  TGCGGACA
                                 CGC    AG
GAM98   GNG4    3'  ACAGGCGTGAGCCACCACACCC 16834      CACA    GG
          GG                    CCGGG   GTGGC  GCGCCTGT
                                |||||   |||||  ||||||||
                              GGCCC   CACCG  TGCGGACA
                                 ACAC    AG
GAM98   GOLGA3  3'  ACAGGCGTGCGCCACTATGCCA 20877    G   C     G
          GG                    CC GGCA AGTGGCG GCGCCTGT
                                || |||| ||||||| ||||||||
                              GG CCGT TCACCGC TGCGGACA
                               A   A     G
GAM98   GREB1   3'  ACAGGCGCCCACCACCACGCCC 28549       ACA   C
          GG                    CCGGGC  GTGG GGGCGCCTGT
                                ||||||  |||| ||||||||||
                              GGCCCG  CACC CCCGCGGACA
                                 CAC   A
GAM98   GREB1   3'  ATGGGCGCCCACCACCATGCCC 28557      CA   C
                              GGGCA  GTGG GGGCGCCTGT
                              |||||  |||| ||||||||||
                              CCCGT  CACC CCCGCGGGTA
                                 AC   A
GAM98   GRWD    3'  ACAGGCGTGAGCCACCGCGTCC 49769       ACA    GG
          GG                    CCGGGC  GTGGC  GCGCCTGT
                                ||||||  |||||  ||||||||
                              GGCCTG  CACCG  TGCGGACA
                                 CGC    AG
GAM98   GTF2H3  3'  ACAGGCGTGAGCCACCGCACCC 9500       CACA    GG
          GG                    CCGGG   GTGGC  GCGCCTGT
                                |||||   |||||  ||||||||
                              GGCCC   CACCG  TGCGGACA
                                 ACGC    AG
GAM98   GTPBG3  3'  ACAGGCGCACACCACCACGCCA 51885    G  ACA   C ___
          GG                    CC GGC  GTGG GG  GCGCCTGT
                                || |||  |||| ||  ||||||||
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                                GG CCG   CACC CC   CGCGGACA
                                 A  ___    A  ACA
GAM98   H2AV     3'  ACAGGCGCACGCCACCATGCCC 57625       CA     G
                                GGGCA  GTGGCG GCGCCTGT
                                |||||  |||||| ||||||||
                                CCCGT  CACCGC CGCGGACA
                                   AC     A
GAM98   HARS2    3'  ACAGGTGTGAACTACCGCGCCC 55859      ACA    CG ___
                                GGGC   GTGG  G   GCGCCTGT
                                ||||   ||||  |   ||||||||
                                CCCG   CGCC  C   TGTGGACA
                                   ___    AT AAG
GAM98   HCA4     3'  ACAGGTGCCCGCCACCACGTCC 78036       ACA
            GG                    CCGGGC   GTGGCGGGCGCCTGT
                                  ||||||   ||||||||||||||||
                                  GGCCTG   CACCGCCCGTGGACA
                                     CAC
GAM98   HRH4     3'  ACAGGTACTCGCCACCACACCT 41519       CACA       CG
            GG                    CCGGG    GTGGCGGG  CCTGT
                                  |||||    ||||||||  |||||
                                  GGTCC    CACCGCTC  GGACA
                                     ACAC       AT
GAM98   HSMPP8   3'  ACAGACACCCGCCATGGCACCC 95122     CACA       CGC
                                  GGG    GTGGCGGG   CTGT
                                  |||    ||||||||   ||||
                                  CCC    TACCGCCC   GACA
                                    ACGG       ACA
GAM98   HSNOV1   3'  ACAGATGTGAACCACTGTGCCT 34421            CGG   C
            GG                    CCGGGCACAGTGG   GCG CTGT
                                  ||||||||||||||   ||| ||||
                                  GGTCCGTGTCACC   TGT GACA
                                         AAG   A
GAM98   HSPC065  3'  ACAGGCGCCCACCACCACACCT 27130       CACA    C
            GG                    CCGGG    GTGG GGGCGCCTGT
                                  |||||    |||| ||||||||||
                                  GGTCC    CACC CCCGCGGACA
                                     ACAC    A
GAM98   HSPC065  3'  ACAGGCGTGAGCCACTGCACCC 27131       CA      GG
            GG                    CCGGG  CAGTGGC  GCGCCTGT
                                  |||||  |||||||  ||||||||
                                  GGCCC  GTCACCG  TGCGGACA
                                     AC      AG
GAM98   HUMGT198A 5'  GCCCGCTACCGCGCCCGG    26139       ACA
                                  CCGGGC   GTGGCGGGC
                                  ||||||   |||||||||
                                  GGCCCG   CATCGCCCG
                                     CGC
GAM98   ICK      3'  ACAGGCGCCCGCCACCACGCCC 30588      ACA
                                  GGGC   GTGGCGGGCGCCTGT
                                  ||||   ||||||||||||||||
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                                CCCG  CACCGCCCGCGGACA
                                  CAC
GAM98   IMPACT   3' ACAGGTGTGAGCCACCATGCCT 37998       CA    GG
           GG                   CCGGGCA  GTGGC  GCGCCTGT
                                ||||||| |||||  ||||||||
                                GGTCCGT  CACCG  TGTGGACA
                                   AC    AG
GAM98   KIAA0022 3' ACAGACATCTGTCACCACACCC 30274    CACA      CGC
                                GGG   GTGGCGGG  CTGT
                                |||   ||||||||  ||||
                                CCC   CACTGTCT  GACA
                                 ACAC      ACA
GAM98   KIAA0063 3' ACAGGCGCCTGCCACCACACCT 30246      CACA
           GG                   CCGGG   GTGGCGGGCGCCTGT
                                |||||   ||||||||||||||||
                                GGTCC   CACCGTCCGCGGACA
                                  ACAC
GAM98   KIAA0063 3' ACAGGCGTGAGCCACCGCACCC 30247      CACA    GG
           GG                   CCGGG   GTGGC  GCGCCTGT
                                |||||   |||||  ||||||||
                                GGCCC   CACCG  TGCGGACA
                                  ACGC    AG
GAM98   KIAA0186 3' ACAGGCGTGAGCCACTGCACCC 41090     CA      GG
           G                    CGGG  CAGTGGC  GCGCCTGT
                                ||||  |||||||  ||||||||
                                GCCC  GTCACCG  TGCGGACA
                                  AC      AG
GAM98   KIAA0210 5' ACAGGCGCCCACCGCCATGCCC 29143       CA    C
           GG                   CCGGGCA  GTGG GGGCGCCTGT
                                |||||||  |||| ||||||||||
                                GGCCCGT  CGCC CCCGCGGACA
                                   AC    A
GAM98   KIAA0210 5' ACAGGTGTGAGCCACTGTGCTC 29144            GG
           GG                   CCGGGCACAGTGGC  GCGCCTGT
                                ||||||||||||||  ||||||||
                                GGCTCGTGTCACCG  TGTGGACA
                                      AG
GAM98   KIAA0210 5' AGCCGCCCGCCACCACTCCCG  29148     CACA       C
                                CGGG   GTGGCGGGCG CT
                                ||||   |||||||||| ||
                                GCCC   CACCGCCCGC GA
                                  TCAC        C
GAM98   KIAA0426 3' ACAGGCACTTGCCACCATTCCC 28913     CACA      C
                                GGG   GTGGCGGG GCCTGT
                                |||   |||||||| ||||||
                                CCC   CACCGTTC CGGACA
                                 TTAC      A
GAM98   KIAA0435 5' ACAGGCGTGAGCCACCGTGCTC 29655       A    GG
                                GGGCAC GTGGC  GCGCCTGT
                                |||||| |||||  ||||||||
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                                CTCGTG CACCG  TGCGGACA
                                   C    AG
GAM98   KIAA0446 5' ACAGGTGCATGCCACCATGCCT 69435       CA     G
            GG                   CCGGGCA  GTGGCG GCGCCTGT
                                 ||||||| ||||||| ||||||||
                                 GGTCCGT  CACCGT CGTGGACA
                                    AC     A
GAM98   KIAA0469 3' ACAGGCATGAGCCACCATGCCC 29962      CA    GGGC
                                 GGGCA  GTGGC    GCCTGT
                                 |||||  |||||   ||||||
                                 CCCGT  CACCG    CGGACA
                                   AC    AGTA
GAM98   KIAA0469 3' ACAGGCGTGTGCCACCACACCC 29963     CACA     G
                                 GGG    GTGGCG GCGCCTGT
                                 |||    ||||||| ||||||||
                                 CCC    CACCGT TGCGGACA
                                  ACAC     G
GAM98   KIAA0475 3' ACAGGCGCCCGCCATCGTGCCC 30105       A
                                 GGGCAC GTGGCGGGCGCCTGT
                                 |||||| ||||||||||||||||
                                 CCCGTG TACCGCCCGCGGACA
                                    C
GAM98   KIAA0495 3' ACAGGCGTGAGCCACCATGCTC 63255       CA    GG
            GG                   CCGGGCA  GTGGC  GCGCCTGT
                                 ||||||| |||||  ||||||||
                                 GGCTCGT  CACCG  TGCGGACA
                                    AC    AG
GAM98   KIAA0513 5' ACAGGCACCTGCCACCACGCCC 29004       ACA      C
            GG                   CCGGGC   GTGGCGGG GCCTGT
                                 ||||||  |||||||| ||||||
                                 GGCCCG   CACCGTCC CGGACA
                                    CAC      A
GAM98   KIAA0513 5' ACAGGCGTGAGCCACTGCCCCC 29005     CA     GG
                                 GGG  CAGTGGC  GCGCCTGT
                                 |||  |||||||  ||||||||
                                 CCC  GTCACCG  TGCGGACA
                                   CC     AG
GAM98   KIAA0513 3' ACAGGTGCACGCCACCACGCCC 29006       ACA     G
            GG                   CCGGGC   GTGGCG GCGCCTGT
                                 ||||||  |||||| ||||||||
                                 GGCCCG   CACCGC CGTGGACA
                                    CAC     A
GAM98   KIAA0532 3' ACAGGTGTGAGCCACCATGCCC 71315      CA    GG
                                 GGGCA  GTGGC  GCGCCTGT
                                 |||||  |||||  ||||||||
                                 CCCGT  CACCG  TGTGGACA
                                   AC    AG
GAM98   KIAA0544 3' ACAGGCGTGAGCCTCCGCGCCC 71454       ACAGT   GG
            GG                   CCGGGC    GGC  GCGCCTGT
                                 ||||||    |||  ||||||||
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                              GGCCCG    CCG  TGCGGACA
                                 CGCCT   AG
GAM98   KIAA0555 3' ACAGGTGCACACCACCACACCT 29541      CACA   C ___
           GG                  CCGGG   GTGG GG   GCGCCTGT
                               |||||   |||| ||   ||||||||
                               GGTCC   CACC CC   CGTGGACA
                                 A___   A  ACA
GAM98   KIAA0555 3' ACAGGTGTAAGCCACTGTGCCC 29542           GG
           GG                  CCGGGCACAGTGGC  GCGCCTGT
                               ||||||||||||||  ||||||||
                               GGCCCGTGTCACCG  TGTGGACA
                                     AA
GAM98   KIAA0557 3' ACAGGCGTGAGCCACCGCGCCC 78537       ACA    GG
           GG                  CCGGGC   GTGGC  GCGCCTGT
                               ||||||   |||||  ||||||||
                               GGCCCG   CACCG  TGCGGACA
                                  CGC    AG
GAM98   KIAA0557 3' ACAGGTGCGCACCACTACGCCT 78538       AC    CGG
           GG                  CCGGGC  AGTGG   GCGCCTGT
                               ||||||  |||||   ||||||||
                               GGTCCG  TCACC   CGTGGACA
                                  CA    ACG
GAM98   KIAA0557 3' ACAGGTGTGTGCCGCCATGCCC 78539      CA     G
                               GGGCA  GTGGCG GCGCCTGT
                               |||||  |||||| ||||||||
                               CCCGT  CGCCGT TGTGGACA
                                  AC     G
GAM98   KIAA0561 3' ACAGGCGCCCACCACTATGCCC 66459      C    C
                               GGGCA AGTGG GGGCGCCTGT
                               ||||| ||||| ||||||||||
                               CCCGT TCACC CCCGCGGACA
                                  A    A
GAM98   KIAA0561 3' ACAGGCGTGAGCCACTGGGCCC 66460      A      GG
                               GGGC CAGTGGC  GCGCCTGT
                               |||| |||||||  ||||||||
                               CCCG GTCACCG  TGCGGACA
                                 G      AG
GAM98   KIAA0562 3' ACAGGCGTGTGTCACCACGCCT 28811       ACA     G
           GG                  CCGGGC   GTGGCG GCGCCTGT
                               ||||||   |||||| ||||||||
                               GGTCCG   CACTGT TGCGGACA
                                  CAC     G
GAM98   KIAA0594 3' ACAGGCGCGTCCCACCACACCC 65503     CACA   C ___
                               GGG    GTGG GG   GCGCCTGT
                               |||    |||| ||   ||||||||
                               CCC    CACC CC   CGCGGACA
                                 A___    A  CTG
GAM98   KIAA0682 3' ACAGGTGTGAGCCACCATGCCC 30006      CA     GG
                               GGGCA  GTGGC  GCGCCTGT
                               |||||  |||||  ||||||||
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                                CCCGT  CACCG  TGTGGACA
                                  AC    AG
GAM98   KIAA0737 3' ACAGGCGCCCGCCACTACGCCC 29791     AC
                                GGGC  AGTGGCGGGCGCCTGT
                                ||||  ||||||||||||||||
                                CCCG  TCACCGCCCGCGGACA
                                  CA
GAM98   KIAA0737 3' ACAGGTGTGAGCCACTGTGCCT 29793          GG
                                GGGCACAGTGGC  GCGCCTGT
                                ||||||||||||  ||||||||
                                TCCGTGTCACCG  TGTGGACA
                                      AG
GAM98   KIAA0861 3' ACAGGCGCCCGCCACCACGCCC 90337       ACA
           GG                     CCGGGC  GTGGCGGGCGCCTGT
                                  ||||||  ||||||||||||||||
                                  GGCCCG  CACCGCCCGCGGACA
                                     CAC
GAM98   KIAA0861 3' ACAGGCGTGAGCCACCGCGCCC 90338     ACA    GG
                                GGGC  GTGGC  GCGCCTGT
                                ||||  |||||  ||||||||
                                CCCG  CACCG  TGCGGACA
                                  CGC    AG
GAM98   KIAA0889 3' ACAGGCGTGAGCCACCGCGCCT 31745       ACA    GG
           GG                     CCGGGC  GTGGC  GCGCCTGT
                                  ||||||  |||||  ||||||||
                                  GGTCCG  CACCG  TGCGGACA
                                     CGC    AG
GAM98   KIAA0889 3' AGGCGCCTGCCACCATGCCCGG 31753       CA
                                CCGGGCA  GTGGCGGGCGCCT
                                |||||||  |||||||||||||
                                GGCCCGT  CACCGTCCGCGGA
                                   AC
GAM98   KIAA0924 3' ACAGGCGTGAGCCACCACGTCC 30346     ACA    GG
                                GGGC  GTGGC  GCGCCTGT
                                ||||  |||||  ||||||||
                                CCTG  CACCG  TGCGGACA
                                  CAC    AG
GAM98   KIAA0924 3' ACAGGTGCATGCTACCATGCCC 30347      CA     G
                                GGGCA  GTGGCG GCGCCTGT
                                |||||  |||||| ||||||||
                                CCCGT  CATCGT CGTGGACA
                                  AC     A
GAM98   KIAA0931 3' ACAGGCACCTGCCATTATGCCC 67998       C       C
           GG                     CCGGGCA AGTGGCGGG GCCTGT
                                  ||||||| ||||||||| ||||||
                                  GGCCCGT TTACCGTCC CGGACA
                                     A       A
GAM98   KIAA0961 3' ACAGGCGCCCGCCACCACACCA 30382    G  CACA
           GG                     CC GG   GTGGCGGGCGCCTGT
                                  || ||   ||||||||||||||
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                              GG CC    CACCGCCCGCGGACA
                               A  ACAC
GAM98   KIAA1143 3' ACAGTCGCCCGCCACCACGCCC 69224       ACA        C
            GG                  CCGGGC   GTGGCGGGCG CTGT
                                |||||| ||||||||||  ||||
                                GGCCCG   CACCGCCCGC GACA
                                   CAC         T
GAM98   KIAA1170 3' ACAGGTGTGAGCCACCATGCCC 70406      CA     GG
                                GGGCA  GTGGC  GCGCCTGT
                                |||||  |||||  ||||||||
                                CCCGT  CACCG  TGTGGACA
                                   AC     AG
GAM98   KIAA1193 3' ACAGGCGTGAGACATCGCGCCC 68260       ACA   GCGG
            GG                  CCGGGC   GTG    GCGCCTGT
                                |||||| |||    ||||||||
                                GGCCCG   TAC    TGCGGACA
                                   CGC   AGAG
GAM98   KIAA1193 3' ACGGGCGCCCCGCCACCATGCCC 68261      CA
                                GGGCA  GTGGCGGGCGCCTGT
                                |||||  ||||||||||||||
                                CCCGT  CACCGCCCGCGGGCA
                                   AC
GAM98   KIAA1198 3' ACAGGCGCCCGCCACCACGCCC 63974       ACA
            GG                  CCGGGC   GTGGCGGGCGCCTGT
                                |||||| ||||||||||||||
                                GGCCCG   CACCGCCCGCGGACA
                                   CAC
GAM98   KIAA1198 3' ACAGGCGCGTGCCACCATACCG 63975     GCACA     G
                                CGG     GTGGCG GCGCCTGT
                                |||     |||||| ||||||||
                                GCC     CACCGT CGCGGACA
                                  ATAC_     G
GAM98   KIAA1198 3' ACAGGCGTGAGCCACCACACCC 63976      CACA     GG
            GG                  CCGGG    GTGGC  GCGCCTGT
                                |||||    |||||  ||||||||
                                GGCCC    CACCG  TGCGGACA
                                   ACAC     AG
GAM98   KIAA1198 3' ACAGGTGTGAGCCACAGCACCC 63977     CACA    GG
                                GGG    GTGGC  GCGCCTGT
                                |||    |||||  ||||||||
                                CCC    CACCG  TGTGGACA
                                  ACGA     AG
GAM98   KIAA1200 3' ACAGGTGTGCGCCACCATGCCC 63024       CA     G
            GG                  CCGGGCA  GTGGCG GCGCCTGT
                                |||||||  |||||| ||||||||
                                GGCCCGT  CACCGC TGTGGACA
                                   AC     G
GAM98   KIAA1209 3' ACAGGCGCCCGCCACCACACCT 61397      CACA
            GG                  CCGGG    GTGGCGGGCGCCTGT
                                |||||    ||||||||||||||
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                              GGTCC   CACCGCCCGCGGACA
                                ACAC
GAM98   KIAA1210 3' ACAGGCGCCCGCCATCACGCCC 98056       ACA
           GG                 CCGGGC  GTGGCGGGCGCCTGT
                              ||||||  ||||||||||||||
                              GGCCCG  TACCGCCCGCGGACA
                                 CAC
GAM98   KIAA1210 3' ACAGGCGTGAGCCACCGCGCCC 98057       ACA   GG
           GG                 CCGGGC  GTGGC GCGCCTGT
                              ||||||  |||||  ||||||||
                              GGCCCG  CACCG  TGCGGACA
                                 CGC    AG
GAM98   KIAA1257 3' ACAGGCGCATGCCACCATGCCA 63384    G   CA    G
           GG                 CC GGCA  GTGGCG GCGCCTGT
                              || ||||  |||||| ||||||||
                              GG CCGT  CACCGT CGCGGACA
                               A   AC    A
GAM98   KIAA1257 3' ACAGGTGCACACCACCACACCT 63385      CACA   C ___
           GG                 CCGGG   GTGG GG  GCGCCTGT
                              |||||   |||| ||  ||||||||
                              GGTCC   CACC CC  CGTGGACA
                                A___   A  ACA
GAM98   KIAA1287 3' ACAGGTGTGAGCCACCGCACCT 78931      CACA   GG
           GG                 CCGGG   GTGGC  GCGCCTGT
                              |||||   |||||  ||||||||
                              GGTCC   CACCG  TGTGGACA
                                 ACGC    AG
GAM98   KIAA1373 3' ACAGACATGAGCCACTGTGCCC 71499          GGGCGC
                              GGGCACAGTGGC     CTGT
                              ||||||||||||     ||||
                              CCCGTGTCACCG     GACA
                                    AGTACA
GAM98   KIAA1373 3' ACAGGCGTGCACCACCACGCCC 71500     ACA   C ___
                              GGGC  GTGG GG  GCGCCTGT
                              ||||  |||| ||  ||||||||
                              CCCG  CACC CC  TGCGGACA
                                ___   A  ACG
GAM98   KIAA1443 3' ACAGGCACCTGCCACCACACCC 64563      CACA      C
           GG                 CCGGG   GTGGCGGG GCCTGT
                              |||||   |||||||| ||||||
                              GGCCC   CACCGTCC CGGACA
                                ACAC      A
GAM98   KIAA1456 3' ACAGGCGTGAGCCACCGCGCCC 67520      ACA   GG
           GG                 CCGGGC  GTGGC  GCGCCTGT
                              ||||||  |||||  ||||||||
                              GGCCCG  CACCG  TGCGGACA
                                 CGC    AG
GAM98   KIAA1465 3' ACAGGCGCGCGCCACCACGACC 61479    GCACA    G
                              GG    GTGGCG GCGCCTGT
                              ||    |||||| ||||||||
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                              CC    CACCGC CGCGGACA
                               AGCAC     G
GAM98   KIAA1467 3' ACAGGCGTGAGCCACCATGCCC 72054       CA    GG
          GG                  CCGGGCA  GTGGC  GCGCCTGT
                              |||||||  |||||  ||||||||
                              GGCCCGT  CACCG  TGCGGACA
                                 AC    AG
GAM98   KIAA1493 3' ACAGGCGCCTGCCACCACACCC 64828    CACA
                              GGG   GTGGCGGGCGCCTGT
                              |||   ||||||||||||||||
                              CCC   CACCGTCCGCGGACA
                               ACAC
GAM98   KIAA1493 3' ACAGGCGTAAGCCACCACACCC 64829    CACA    GG
                              GGG   GTGGC  GCGCCTGT
                              |||   |||||  ||||||||
                              CCC   CACCG  TGCGGACA
                               ACAC    AA
GAM98   KIAA1497 5' ACAGGCGTGAGCCACCGCGCCC 68104       ACA    GG
          GG                  CCGGGC   GTGGC  GCGCCTGT
                              ||||||   |||||  ||||||||
                              GGCCCG   CACCG  TGCGGACA
                                 CGC    AG
GAM98   KIAA1508 3' ACAGGCGTGAGCCACCATGTCC 62534       CA    GG
          GG                  CCGGGCA  GTGGC  GCGCCTGT
                              |||||||  |||||  ||||||||
                              GGCCTGT  CACCG  TGCGGACA
                                 AC    AG
GAM98   KIAA1530 3' ACAGGCGCGCACCACCACGCCC 68539     ACA   C ___
                              GGGC   GTGG GG   GCGCCTGT
                              ||||   |||| ||   ||||||||
                              CCCG   CACC CC   CGCGGACA
                                ___    A  ACG
GAM98   KIAA1530 3' ACAGGTGTGAGCCACCGCACTC 68540    CACA    GG
                              GGG   GTGGC  GCGCCTGT
                              |||   |||||  ||||||||
                              CTC   CACCG  TGTGGACA
                               ACGC    AG
GAM98   KIAA1571 3' ACAGGCGTGCGCCACCATGCCC 61610       CA     G
          GG                  CCGGGCA  GTGGCG GCGCCTGT
                              |||||||  ||||||| ||||||||
                              GGCCCGT  CACCGC TGCGGACA
                                 AC     G
GAM98   KIAA1617 3' ACAGGTGTGAGCCACTACGCCC 93066     AC     GG
                              GGGC  AGTGGC  GCGCCTGT
                              ||||  ||||||  ||||||||
                              CCCG  TCACCG  TGTGGACA
                                CA     AG
GAM98   KIAA1649 3' ACAGGCGTGAGCCACCACGCCC 51208     ACA    GG
                              GGGC   GTGGC  GCGCCTGT
                              ||||   |||||  ||||||||
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                              CCCG  CACCG TGCGGACA
                                CAC    AG
GAM98  KIAA1655 3' ACAGGCACCCGCCACCACGCCC 67168      ACA      C
          GG                  CCGGGC  GTGGCGGG GCCTGT
                              ||||||  |||||||| ||||||
                              GGCCCG  CACCGCCC CGGACA
                                 CAC      A
GAM98  KIAA1655 3' ACAGGCGTGAGCCACTGCACCC 67169    CA     GG
                              GGG CAGTGGC GCGCCTGT
                              |||  ||||||| ||||||||
                              CCC GTCACCG TGCGGACA
                                AC      AG
GAM98  KIAA1655 3' ATGGGCGCCCACCACCACGCCC 67174    ACA   C
                              GGGC  GTGG GGGCGCCTGT
                              ||||  |||| ||||||||||
                              CCCG  CACC CCCGCGGGTA
                                CAC   A
GAM98  KIAA1668 3' ACAGGCGTGAGCCACCACGCCC 67054      ACA    GG
          GG                  CCGGGC  GTGGC GCGCCTGT
                              ||||||  |||||  ||||||||
                              GGCCCG  CACCG TGCGGACA
                                 CAC    AG
GAM98  KIAA1671 3' ACAGGCGCACATCACCACGCCC 66267    ACA   C ___
                              GGGC  GTGG GG  GCGCCTGT
                              ||||  |||| ||  ||||||||
                              CCCG  CACC CT  CGCGGACA
                                ___   A ACA
GAM98  KIAA1727 3' ACAGGCGTGCACCACCACGCCT 64745      ACA   C ___
          GG                  CCGGGC  GTGG GG  GCGCCTGT
                              ||||||  |||| ||  ||||||||
                              GGTCCG  CACC CC  TGCGGACA
                                ___   A ACG
GAM98  KIAA1737 3' ACAGGTGCCTGCCACCATGCCC 67927      CA
                              GGGCA GTGGCGGGCGCCTGT
                              |||||  ||||||||||||||
                              CCCGT CACCGTCCGTGGACA
                                 AC
GAM98  KIAA1784 3' ACAGGCGCCAGCCACTGCGCCC 65737      A     G
          GG                  CCGGGC CAGTGGC GGCGCCTGT
                              |||||| ||||||| |||||||||
                              GGCCCG GTCACCG CCGCGGACA
                                 C      A
GAM98  KIAA1877 3' ACAGGCACCCGCCACCACGCCC 66735    ACA      C
                              GGGC  GTGGCGGG GCCTGT
                              ||||  |||||||| ||||||
                              CCCG  CACCGCCC CGGACA
                                CAC      A
GAM98  KIAA1924 3' ACAGGCATGAGCCACTGTGCCC 74036          GGGC
                              GGGCACAGTGGC   GCCTGT
                              ||||||||||||   ||||||
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                                CCCGTGTCACCG  CGGACA
                                      AGTA
GAM98  KIAA1924 3' ACAGGCGTGTGCCACCACACCT 74037     CACA    G
          GG                    CCGGG  GTGGCG GCGCCTGT
                                ||||||  |||||| ||||||||
                                GGTCC  CACCGT TGCGGACA
                                  ACAC    G
GAM98  KIAA1971 3' ACAGGCGCCACCACCTTGCCC 74663     CA  CG
                                GGGCA GTGG GGCGCCTGT
                                ||||| |||| |||||||||
                                CCCGT CACC CCGCGGACA
                                  TC  A_
GAM98  KIAA1971 3' ACAGGTGTGAGCCACCACGCCC 74664    ACA   GG
                                GGGC  GTGGC GCGCCTGT
                                ||||  |||||  ||||||||
                                CCCG  CACCG TGTGGACA
                                  CAC   AG
GAM98  KIAA1975 5' ACAGGTGTGAGCCACCACGCCC 74408     ACA   GG
          GG                    CCGGGC  GTGGC GCGCCTGT
                                ||||||  |||||  ||||||||
                                GGCCCG  CACCG TGTGGACA
                                   CAC   AG
GAM98  KLHL6   3' ACAGGTGTGAGCCACTGGGCCC 56166      A     GG
          GG                    CCGGGC CAGTGGC GCGCCTGT
                                |||||| |||||||  ||||||||
                                GGCCCG GTCACCG TGTGGACA
                                   G     AG
GAM98  KLK7    3' ACAGGTGTGCACCACCACACCA 58384   G CACA   C ___
          GG                    CC GG   GTGG GG  GCGCCTGT
                                || ||   |||| ||  ||||||||
                                GG CC   CACC CC  TGTGGACA
                                 A A___   A ACG
GAM98  KLK7    3' ACAGGTGTGCACCACCACACCA 18535   G CACA   C ___
          GG                    CC GG   GTGG GG  GCGCCTGT
                                || ||   |||| ||  ||||||||
                                GG CC   CACC CC  TGTGGACA
                                 A A___   A ACG
GAM98  LIECG3  3' ACAGGTGCACCACCACACCTGG 88794     CACA   C _
                                CCGGG   GTGG GG GCGCCTGT
                                |||||   |||| || ||||||||
                                GGTCC   CACC CC CGTGGACA
                                  A___   A A
GAM98  MAP-1   3' ACAGGCGTGAGACACTGCGCCC 42428     A   GCGG
                                GGGC CAGTG   GCGCCTGT
                                |||| |||||   ||||||||
                                CCCG GTCAC   TGCGGACA
                                  C    AGAG
GAM98  MCLC    3' ACAGGCATGAGCCATTGTGCCC 31373         GGGC
                                GGGCACAGTGGC   GCCTGT
                                ||||||||||||   ||||||
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                                CCCGTGTTACCG  CGGACA
                                      AGTA
GAM98   MEF-2    3' ACAGGCGCGAGCCACCACACCC 65013      CACA    GG
           GG                  CCGGG  GTGGC  GCGCCTGT
                               |||||  |||||  ||||||||
                               GGCCC  CACCG  CGCGGACA
                                 ACAC    AG
GAM98   MGC12518 3' ACAGGCATGAGCCACAGTGCCC 64771        A    GGGC
           GG                  CCGGGCAC GTGGC  GCCTGT
                               |||||||| |||||  ||||||
                               GGCCCGTG CACCG  CGGACA
                                  A    AGTA
GAM98   MGC13061 3' ACAGGTGTGAGCCACCACACCT 51286      CACA    GG
           GG                  CCGGG  GTGGC  GCGCCTGT
                               |||||  |||||  ||||||||
                               GGTCC  CACCG  TGTGGACA
                                 ACAC    AG
GAM98   MGC13159 3' ACAGGCCCACGCCACCGTGCCT 53033        A    _ C
           GG                  CCGGGCAC GTGGCG GG GCCTGT
                               |||||||| |||||| || ||||||
                               GGTCCGTG CACCGC CC CGGACA
                                  C    A _
GAM98   MGC15619 5' ACAGGTGTGAGCCACCATGCCC 51400       CA    GG
           GG                  CCGGGCA  GTGGC  GCGCCTGT
                               |||||||  |||||  ||||||||
                               GGCCCGT  CACCG  TGTGGACA
                                  AC    AG
GAM98   MGC21675 3' ACAGGCATGAACCACTGTGCCC 54577          CGGGC
                               GGGCACAGTGG    GCCTGT
                               ||||||||||    ||||||
                               CCCGTGTCACC    CGGACA
                                     AAGTA
GAM98   MGC2474  3' ACAGGCACCTGCCACTATGCCC 43943       C       C
           GG                  CCGGGCA AGTGGCGGG GCCTGT
                               |||||||  |||||||| ||||||
                               GGCCCGT TCACCGTCC CGGACA
                                  A       A
GAM98   MGC2477  5' ACAGGCGCCCGCCACCACGGCC 44288     G ACA_
           GG                  CCGG C   GTGGCGGGCGCCTGT
                               ||||  |   ||||||||||||||
                               GGCC G   CACCGCCCGCGGACA
                                 _ GCAC
GAM98   MGC2477  5' ACAGGCGTGCACCACCACGCCC 44289      ACA   C ___
           GG                  CCGGGC  GTGG GG  GCGCCTGT
                               ||||||  ||||  ||  ||||||||
                               GGCCCG  CACC CC  TGCGGACA
                                  ___   A  ACG
GAM98   MGC2477  5' ACAGGTGTGAGCCACCGCGCCC 44290      ACA    GG
           GG                  CCGGGC  GTGGC  GCGCCTGT
                               ||||||  |||||  ||||||||
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                                GGCCCG  CACCG  TGTGGACA
                                   CGC    AG
GAM98   MGC29898  3'  ACAGGTGTGAGCCACCATGCCT 59582       CA    GG
           GG                   CCGGGCA  GTGGC  GCGCCTGT
                                |||||||  |||||  ||||||||
                                GGTCCGT  CACCG  TGTGGACA
                                   AC    AG
GAM98   MGC3771   5'  ACAGGCATGTGCCACCACACCT 49049      CACA    GGC
           GG                   CCGGG   GTGGCG  GCCTGT
                                |||||   ||||||  ||||||
                                GGTCC   CACCGT  CGGACA
                                  ACAC    GTA
GAM98   MGC3771   3'  ACAGGCGTGAGCCACCGCGCCC 49050     ACA    GG
                                GGGC  GTGGC  GCGCCTGT
                                ||||  |||||  ||||||||
                                CCCG  CACCG  TGCGGACA
                                  CGC    AG
GAM98   MGC5149   3'  ACAGGCGTGAGCCACCGCGCC  72749    ACA    GG
                                GGC  GTGGC  GCGCCTGT
                                |||  |||||  ||||||||
                                CCG  CACCG  TGCGGACA
                                 CGC    AG
GAM98   MGC9912   3'  ACAGGCATGAGCCACCGTGCCC 55604        A    GGGC
           GG                   CCGGGCAC GTGGC   GCCTGT
                                |||||||| |||||   ||||||
                                GGCCCGTG CACCG   CGGACA
                                   C    AGTA
GAM98   MKRN4     3'  ACAGGCATAAGCCACTGTGCCT 48445           GGGC
           GG                   CCGGGCACAGTGGC   GCCTGT
                                ||||||||||||||   ||||||
                                GGTCCGTGTCACCG   CGGACA
                                      AATA
GAM98   MKRN4     3'  ACAGGCGTCAGCCACCATGCCC 48446      CA    G
                                GGGCA  GTGGC GGCGCCTGT
                                |||||  ||||| |||||||||
                                CCCGT  CACCG CTGCGGACA
                                   AC    A
GAM98   MLZE      5'  ACAGACGTGAGCCACCGTGCCC 49443        A    GG   C
           GG                   CCGGGCAC GTGGC  GCG CTGT
                                |||||||| |||||  ||| ||||
                                GGCCCGTG CACCG  TGC GACA
                                   C    AG   A
GAM98   moblak    3'  ACAGGCGTGAGCCACTGTGCCC 56379           GG
           GG                   CCGGGCACAGTGGC  GCGCCTGT
                                ||||||||||||||  ||||||||
                                GGCCCGTGTCACCG  TGCGGACA
                                      AG
GAM98   moblak    3'  ACAGGTGTGCGCCACCACGCCC 56381      ACA     G
                                GGGC  GTGGCG GCGCCTGT
                                ||||  |||||| ||||||||
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                                CCCG  CACCGC TGTGGACA
                                  CAC     G
GAM98  MOCS3   3' ACAGGCGCACGCCACCACGCCT 27923       ACA     G
          GG                    CCGGGC  GTGGCG GCGCCTGT
                                |||||| ||||||| ||||||||
                                GGTCCG  CACCGC CGCGGACA
                                   CAC     A
GAM98  MRPL20  3' ACAGGCGTGAGACACCGTGCCC 36197       A  GCGG
                                GGGCAC GTG   GCGCCTGT
                                |||||| |||   ||||||||
                                CCCGTG CAC   TGCGGACA
                                   C  AGAG
GAM98  MRPL44  3' ACAGGTGTGAGCCACTATACCC 43590     CAC     GG
          G                     CGGG  AGTGGC  GCGCCTGT
                                ||||  ||||||  ||||||||
                                GCCC  TCACCG  TGTGGACA
                                  ATA     AG
GAM98  MtFMT   3' ACAGACGTGAGCCACCGTGCCT 58325       A    GG  C
          GG                    CCGGGCAC GTGGC  GCG CTGT
                                |||||||| |||||  ||| ||||
                                GGTCCGTG CACCG  TGC GACA
                                    C    AG  A
GAM98  MYO5C   3' ACAGGCACCTGCCACCACGCCC 38709     ACA      C
                                GGGC  GTGGCGGG GCCTGT
                                ||||  |||||||| ||||||
                                CCCG  CACCGTCC CGGACA
                                  CAC       A
GAM98  MYO5C   3' ACAGGCGTGTGCCACCGCGCCT 38710       ACA     G
          GG                    CCGGGC  GTGGCG GCGCCTGT
                                ||||||  ||||||| ||||||||
                                GGTCCG  CACCGT TGCGGACA
                                   CGC     G
GAM98  NDUFC2  3' ACAGGCGTGAGCCACCGCGCCT 17018       ACA    GG
          GG                    CCGGGC  GTGGC  GCGCCTGT
                                ||||||  |||||  ||||||||
                                GGTCCG  CACCG  TGCGGACA
                                   CGC     AG
GAM98  NDUFC2  3' ACAGGTGCATGCCACGACGCCC 17019     ACA     G
                                GGGC  GTGGCG GCGCCTGT
                                ||||  |||||| ||||||||
                                CCCG  CACCGT CGTGGACA
                                  CAG     A
GAM98  Nup43   3' ACAGGTGTGAGCCACTGCACCC 45339      CA      GG
          GG                    CCGGG  CAGTGGC  GCGCCTGT
                                |||||  |||||||  ||||||||
                                GGCCC  GTCACCG  TGTGGACA
                                  AC      AG
GAM98  NXN     3' ACAGGCACCCGCCACCGTACCT 42659      C  A      C
          GG                    CCGGG AC GTGGCGGG GCCTGT
                                ||||| || |||||||| ||||||
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                                GGTCC TG CACCGCCC CGGACA
                                  A C       A
GAM98   NXN      3'  ACAGGCGTGAGCCGCCGTGCCC 42660         A     GG
            GG                    CCGGGCAC GTGGC  GCGCCTGT
                                  |||||||| |||||  ||||||||
                                  GGCCCGTG CGCCG  TGCGGACA
                                     C     AG
GAM98   OCT11    3'  ACAGGTGTGAGCCACCGCGCCT 27577       ACA     GG
            GG                    CCGGGC   GTGGC  GCGCCTGT
                                  ||||||   |||||  ||||||||
                                  GGTCCG   CACCG  TGTGGACA
                                     CGC     AG
GAM98   OR51E2   3'  ACAGGTGTGAACCACTGTGCCC 48498           CGG
            GG                    CCGGGCACAGTGG   GCGCCTGT
                                  ||||||||||||   ||||||||
                                  GGCCCGTGTCACC   TGTGGACA
                                        AAG
GAM98   OSBPL2   3'  ACAGGCGTGAGCCACTGCGCCT 58476       A      GG
            GG                    CCGGGC CAGTGGC  GCGCCTGT
                                  |||||| |||||||  ||||||||
                                  GGTCCG GTCACCG  TGCGGACA
                                     C       AG
GAM98   OSBPL2   3'  ACAGGCGTGAGCCACTGCGCCT 29894       A      GG
            GG                    CCGGGC CAGTGGC  GCGCCTGT
                                  |||||| |||||||  ||||||||
                                  GGTCCG GTCACCG  TGCGGACA
                                     C       AG
GAM98   PELI1    5'  ACAGGCGTGAACCACTGCACCC 40615     CA     CGG
                                  GGG  CAGTGG   GCGCCTGT
                                  |||  ||||||   ||||||||
                                  CCC  GTCACC   TGCGGACA
                                    AC     AAG
GAM98   PELI1    5'  ACAGGCGTGAGCCACTGCTCCC 40616     CA      GG
                                  GGG  CAGTGGC  GCGCCTGT
                                  |||  |||||||  ||||||||
                                  CCC  GTCACCG  TGCGGACA
                                    TC      AG
GAM98   PIP3-E   3'  ACAGGTGTGAGCCACCACACCT 67340       CACA    GG
            GG                    CCGGG    GTGGC  GCGCCTGT
                                  |||||    |||||  ||||||||
                                  GGTCC    CACCG  TGTGGACA
                                     ACAC     AG
GAM98   PNPASE   3'  ACAGGTCACCTCTGTGCCC    71434         T  C GGC
                                  GGGCACAG GG G   GCCTGT
                                  |||||||| || |   ||||||
                                  CCCGTGTC CC C   TGGACA
                                      T  A ___
GAM98   PP2447   5'  ACAGGCGTGCGCCACTGCACCC 48097       CA       G
            GG                    CCGGG  CAGTGGCG GCGCCTGT
                                  |||||  |||||||| ||||||||
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                                GGCCC  GTCACCGC TGCGGACA
                                  AC       G
GAM98   PP3501   5' ACAGGTGTGGGCCACCATGCCC 41678      CA    GG
                                GGGCA  GTGGC  GCGCCTGT
                                |||||  |||||  ||||||||
                                CCCGT  CACCG  TGTGGACA
                                  AC     GG
GAM98   PRO0365  5' ACAGGCACCTGCCACCACGCCC 26974      ACA       C
                                GGGC   GTGGCGGG GCCTGT
                                ||||   |||||||| ||||||
                                CCCG   CACCGTCC CGGACA
                                  CAC       A
GAM98   PRO0456  5' ACAGGCGTGTGCCACTGTGCCT 27001             G
          GG                    CCGGGCACAGTGGCG GCGCCTGT
                                |||||||||||||| ||||||||
                                GGTCCGTGTCACCGT TGCGGACA
                                        G
GAM98   PRO0899  5' ACAGGTGTGAGCCACCATGCCT 38304        CA    GG
          GG                    CCGGGCA  GTGGC  GCGCCTGT
                                |||||||  |||||  ||||||||
                                GGTCCGT  CACCG  TGTGGACA
                                   AC     AG
GAM98   PRO2955  3' ACAGGCGTGAGCCACTGCGCCC 38229       A      GG
          GG                    CCGGGC CAGTGGC  GCGCCTGT
                                ||||||| |||||||  ||||||||
                                GGCCCG GTCACCG  TGCGGACA
                                  C       AG
GAM98   PSPH     3' ACAGGCACCCGCCACCACATCC 17126       CACA       C
          GG                    CCGGG    GTGGCGGG GCCTGT
                                |||||    |||||||| ||||||
                                GGCCT    CACCGCCC CGGACA
                                  ACAC       A
GAM98   PSTPIP2  3' ACAGGCGTGAGCCACTGCGCCC 44645       A      GG
          GG                    CCGGGC CAGTGGC  GCGCCTGT
                                |||||| |||||||  ||||||||
                                GGCCCG GTCACCG  TGCGGACA
                                  C       AG
GAM98   RAB21    3' ACAGGCGTGAGCCACCGTGCCC 31077        A    GG
          GG                    CCGGGCAC GTGGC  GCGCCTGT
                                |||||||| |||||  ||||||||
                                GGCCCGTG CACCG  TGCGGACA
                                   C     AG
GAM98   RAB21    3' AGGCGCCCACCACGACGCCCGG 31082       ACA    C
                                CCGGGC   GTGG GGGCGCCT
                                ||||||   |||| ||||||||
                                GGCCCG   CACC CCCGCGGA
                                  CAG    A
GAM98   RAB33B   3' ACAGGCGTGCACTACCACACCC 49310     CACA    CG ___
                                GGG   GTGG  G   GCGCCTGT
                                |||   ||||  |   ||||||||
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                                CCC   CACC C  TGCGGACA
                                  A___   AT ACG
GAM98   RAB33B   3' ACAGGTGTGAGTCACTGCACCC 49311    CA     GG
                                GGG CAGTGGC GCGCCTGT
                                ||| ||||||| ||||||||
                                CCC GTCACTG TGTGGACA
                                  AC     AG
GAM98   RASSF2   3' ACAGGGACCCGCCACCACGCCC 29089      ACA     CG
           GG                    CCGGGC  GTGGCGGG CCTGT
                                ||||||  |||||||| |||||
                                GGCCCG  CACCGCCC GGACA
                                   CAC      AG
GAM98   RASSF2   3' ACAGGCGTGAGCCACTGTGCCC 29088         GG
                                GGGCACAGTGGC GCGCCTGT
                                |||||||||||| ||||||||
                                CCCGTGTCACCG TGCGGACA
                                       AG
GAM98   RIS1     5' CGCCCGCACTGCGCCCGG   81457      A   G
                                CCGGGC CAGTG CGGGCG
                                |||||| ||||| ||||||
                                GGCCCG GTCAC GCCCGC
                                   C    _
GAM98   RNF8     3' ACAGGCGTGAGCCACCACGCCC 15553     ACA   GG
                                GGGC  GTGGC GCGCCTGT
                                ||||  |||||  ||||||||
                                CCCG  CACCG TGCGGACA
                                  CAC    AG
GAM98   Rpo1-2   3' ACAGGTGTGAGCCACTGTGCCT 50864          GG
           GG                    CCGGGCACAGTGGC GCGCCTGT
                                |||||||||||||  ||||||||
                                GGTCCGTGTCACCG TGTGGACA
                                       AG
GAM98   Rpo1-2   3' ACAGGTGTGAGCCACTGTGCCT 39205          GG
           GG                    CCGGGCACAGTGGC GCGCCTGT
                                |||||||||||||  ||||||||
                                GGTCCGTGTCACCG TGTGGACA
                                       AG
GAM98   SC4MOL   3' ACAGGCACCCGCCACCACGCCC 23100     ACA      C
                                GGGC  GTGGCGGG GCCTGT
                                ||||  |||||||| ||||||
                                CCCG  CACCGCCC CGGACA
                                  CAC      A
GAM98   SC4MOL   3' ACAGGTGTAAGCCACTGCGCCC 23101      A     GG
           GG                    CCGGGC CAGTGGC GCGCCTGT
                                ||||||| |||||||  ||||||||
                                GGCCCG GTCACCG  TGTGGACA
                                   C      AA
GAM98   SCAMP-4  3' ACAGTTGCCTGCCACCACGCCC 55329     ACA       C
                                GGGC  GTGGCGGGCG CTGT
                                ||||  |||||||||| ||||
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                                CCCG  CACCGTCCGT GACA
                                  CAC        T
GAM98   SCYA16   3' ACAGGCGTGAGCCACCACATCC 17164      CACA    GG
             GG                   CCGGG   GTGGC  GCGCCTGT
                                  |||||   |||||  ||||||||
                                  GGCCT   CACCG  TGCGGACA
                                    ACAC    AG
GAM98   SCYA22   3' ACAGGCGTGAGTCACTGCGCCT 92566       A      GG
             GG                   CCGGGC CAGTGGC  GCGCCTGT
                                  ||||||| |||||||  ||||||||
                                  GGTCCG GTCACTG  TGCGGACA
                                    C      AG
GAM98   SERF1B   3' ACAGGCGCCTGCCACCACGCCC 43683     ACA
                                  GGGC  GTGGCGGGCGCCTGT
                                  ||||  ||||||||||||||||
                                  CCCG  CACCGTCCGCGGACA
                                    CAC
GAM98   SLC11A1  3' ACAGGCGTGAGCCACCAAACCC 60153      CACA    GG
             GG                   CCGGG   GTGGC  GCGCCTGT
                                  |||||   |||||  ||||||||
                                  GGCCC   CACCG  TGCGGACA
                                    AAAC    AG
GAM98   SLC12A8  3' ACAGGCGTGAGCCACCATGCCT 45228       CA    GG
             GG                   CCGGGCA  GTGGC  GCGCCTGT
                                  |||||||  |||||  ||||||||
                                  GGTCCGT  CACCG  TGCGGACA
                                     AC    AG
GAM98   SLC19A3  3' ACAGGCGTGAGCCACCATGCCT 48230       CA    GG
             GG                   CCGGGCA  GTGGC  GCGCCTGT
                                  |||||||  |||||  ||||||||
                                  GGTCCGT  CACCG  TGCGGACA
                                     AC    AG
GAM98   SLC2A10  3' ACAGGCGCGTGCCACCACACCC 48541     CACA     G
                                  GGG   GTGGCG GCGCCTGT
                                  |||   |||||| ||||||||
                                  CCC   CACCGT CGCGGACA
                                    ACAC     G
GAM98   SLC6A14  3' ACAGGTGCCCGCCACCACACC  24300    GCACA
                                  GG    GTGGCGGGCGCCTGT
                                  ||    |||||||||||||||
                                  CC    CACCGCCCGTGGACA
                                   ACAC_
GAM98   SLC6A14  3' ACAGGTGTGAGCCACCGTGCCC 24301        A    GG
             GG                   CCGGGCAC GTGGC  GCGCCTGT
                                  |||||||| |||||  ||||||||
                                  GGCCCGTG CACCG  TGTGGACA
                                     C    AG
GAM98   SPRY4    3' ACAGGTGTGAGCCACTGTGCCC 48987           GG
                                  GGGCACAGTGGC  GCGCCTGT
                                  ||||||||||||  ||||||||
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                                CCCGTGTCACCG  TGTGGACA
                                      AG
GAM98   SQV7L    5'  ACAGGTGTGAACCACCATGCCC 71091      CA    CGG
                                GGGCA  GTGG   GCGCCTGT
                                |||||  ||||   ||||||||
                                CCCGT  CACC   TGTGGACA
                                   AC    AAG
GAM98   SS-56    3'  ACAGGCGCCCACCACGACGCCT 60340       ACA    C
           GG                     CCGGGC   GTGG GGGCGCCTGT
                                  ||||||   |||| ||||||||||
                                  GGTCCG   CACC CCCGCGGACA
                                     CAG    A
GAM98   STAF65(gamma) 3'  ACAGGCGTGAGCCACTGCACCT 30057      CA      GG
           GG                     CCGGG  CAGTGGC  GCGCCTGT
                                  |||||  |||||||  ||||||||
                                  GGTCC  GTCACCG  TGCGGACA
                                     AC       AG
GAM98   STRBP    5'  ACAGGCACGAGCCACTGTGCCT 37814            GGGC
           GG                     CCGGGCACAGTGGC    GCCTGT
                                  ||||||||||||||    ||||||
                                  GGTCCGTGTCACCG    CGGACA
                                        AGCA
GAM98   SULT1C2  3'  ATGGGCGCCCACCACCACTCCC 22709      CACA    C
           GG                     CCGGG    GTGG GGGCGCCTGT
                                  |||||    |||| ||||||||||
                                  GGCCC    CACC CCCGCGGGTA
                                     TCAC    A
GAM98   SUN1     3'  ACAGGCGCACACCACCACACCC 47904     CACA    C ___
                                GGG    GTGG GG   GCGCCTGT
                                |||    |||| ||   ||||||||
                                CCC    CACC CC   CGCGGACA
                                  A___    A  ACA
GAM98   TADA3L   3'  ACAGGCGTGAGCCACTGCGCCT 56801       A      GG
           GG                     CCGGGC CAGTGGC  GCGCCTGT
                                  ||||||| |||||||  ||||||||
                                  GGTCCG GTCACCG  TGCGGACA
                                     C      AG
GAM98   TBCC     3'  ACAGGCGTGAGCCACCACGCCA 13597    G   ACA    GG
           GG                     CC GGC   GTGGC  GCGCCTGT
                                  || |||   |||||  ||||||||
                                  GG CCG   CACCG  TGCGGACA
                                   A  CAC    AG
GAM98   TCL6     3'  ACAGGCGTGAGCCACCACGCCC 25892       ACA    GG
           GG                     CCGGGC   GTGGC  GCGCCTGT
                                  ||||||   |||||  ||||||||
                                  GGCCCG   CACCG  TGCGGACA
                                     CAC    AG
GAM98   TCL6     5'  ACAGGTGCCCACCACCATGCCA 25894    G   CA   C
           GG                     CC GGCA  GTGG GGGCGCCTGT
                                  || ||||  |||| ||||||||||
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                                GG CCGT  CACC CCCGTGGACA
                                 A   AC   A
GAM98   TCL6    3' ACAGGCGTGAGCCACCACGCCC 27744       ACA    GG
             GG                  CCGGGC  GTGGC  GCGCCTGT
                                 ||||||  |||||  ||||||||
                                GGCCCG  CACCG  TGCGGACA
                                   CAC    AG
GAM98   TCL6    5' ACAGGTGCCCACCACCATGCCA 27746    G   CA   C
             GG                  CC GGCA  GTGG GGGCGCCTGT
                                 || ||||  |||| ||||||||||
                                GG CCGT  CACC CCCGTGGACA
                                 A   AC   A
GAM98   TCL6    5' ACAGGTGCCCACCACCATGCCA 40454    G   CA   C
             GG                  CC GGCA  GTGG GGGCGCCTGT
                                 || ||||  |||| ||||||||||
                                GG CCGT  CACC CCCGTGGACA
                                 A   AC   A
GAM98   TCL6    5' ACAGGTGCCCACCACCATGCCA 40501    G   CA   C
             GG                  CC GGCA  GTGG GGGCGCCTGT
                                 || ||||  |||| ||||||||||
                                GG CCGT  CACC CCCGTGGACA
                                 A   AC   A
GAM98   TCL6    3' ACAGGTGTGAGCCACCACTCCC 40502    CACA    GG
                                GGG   GTGGC  GCGCCTGT
                                |||   |||||  ||||||||
                                CCC   CACCG  TGTGGACA
                                  TCAC    AG
GAM98   TCL6    5' ACAGGCGTGAGCCGCTGCACCC 40525    CA     GG
                                GGG  CAGTGGC  GCGCCTGT
                                |||  |||||||  ||||||||
                                CCC  GTCGCCG  TGCGGACA
                                  AC      AG
GAM98   TCL6    3' ACAGGTGTGAGCCACCACTCCC 40526    CACA    GG
                                GGG   GTGGC  GCGCCTGT
                                |||   |||||  ||||||||
                                CCC   CACCG  TGTGGACA
                                  TCAC    AG
GAM98   TCL6    5' ACAGGCGTGAGCCGCTGCACCC 40534    CA     GG
                                GGG  CAGTGGC  GCGCCTGT
                                |||  |||||||  ||||||||
                                CCC  GTCGCCG  TGCGGACA
                                  AC      AG
GAM98   TERA    3' AGGTGCCCGCCACCAGACCCGG 41416      CACA
                                CCGGG   GTGGCGGGCGCCT
                                |||||   |||||||||||||
                                GGCCC   CACCGCCCGTGGA
                                   AGAC
GAM98   THEA    3' ACAGGTGTGAACCACTGTGCTC 66862          CGG
                                GGGCACAGTGG   GCGCCTGT
                                ||||||||||   ||||||||
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                                CTCGTGTCACC  TGTGGACA
                                     AAG
GAM98   TOR1B    3'  ACAGGCATGAGCCACTGTGCCC 27966          GGGC
                                GGGCACAGTGGC  GCCTGT
                                ||||||||||||  ||||||
                                CCCGTGTCACCG  CGGACA
                                     AGTA
GAM98   TRIM16   3'  ACAGGTGCCTGCCACCACACCC 22360    CACA
                                GGG  GTGGCGGGCGCCTGT
                                |||  ||||||||||||||
                                CCC  CACCGTCCGTGGACA
                                  ACAC
GAM98   TRIM5    3'  ACAGGCGTGAGCCACGGCGCCC 53457    ACA   GG
                                GGGC  GTGGC  GCGCCTGT
                                ||||  |||||  ||||||||
                                CCCG  CACCG  TGCGGACA
                                   CGG   AG
GAM98   TRIM5    3'  ACAGGCGTGAGCCACGGCGCCC 53535    ACA   GG
                                GGGC  GTGGC  GCGCCTGT
                                ||||  |||||  ||||||||
                                CCCG  CACCG  TGCGGACA
                                   CGG   AG
GAM98   TU12B1-TY 3'  ACAGGTGCCCACCACCACATCC 33816    CACA  C
                                GGG  GTGG GGGCGCCTGT
                                |||  |||| ||||||||||
                                CCT  CACC CCCGTGGACA
                                  ACAC  A
GAM98   TU12B1-TY 3'  ACAGGTGTGAGCCACCGCACCT 33817     CACA   GG
           GG                   CCGGG  GTGGC  GCGCCTGT
                                |||||  |||||  ||||||||
                                GGTCC  CACCG  TGTGGACA
                                   ACGC   AG
GAM98   TUCAN    3'  ACAGGCATGAGCCACCGTGCCT 30959       A   GGGC
           GG                   CCGGGCAC GTGGC  GCCTGT
                                ||||||||| |||||  ||||||
                                GGTCCGTG CACCG  CGGACA
                                     C   AGTA
GAM98   TUCAN    3'  ACAGGTGCATGCCAACACGCCC 30961      ACAG   G
           GG                   CCGGGC  TGGCG GCGCCTGT
                                ||||||  ||||| ||||||||
                                GGCCCG  ACCGT CGTGGACA
                                   CACA   A
GAM98   TXNL2    3'  ACAGGCGTGCACCACCATGCCC 22574     CA   CGG
                                GGGCA  GTGG  GCGCCTGT
                                |||||  ||||  ||||||||
                                CCCGT  CACC  TGCGGACA
                                   AC   ACG
GAM98   VDU1     3'  ACAGGCACCTGCCACCATGCCC 31112       CA     C
           GG                   CCGGGCA  GTGGCGGG GCCTGT
                                |||||||  |||||||| ||||||
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                                GGCCCGT  CACCGTCC CGGACA
                                   AC       A
GAM98   VMP      3'  ACAGGCACCTGCCACCACCCCC 55758     CACA       C
                                GGG    GTGGCGGG GCCTGT
                                |||    |||||||| ||||||
                                CCC    CACCGTCC CGGACA
                                  CCAC       A
GAM98   VPS33A   3'  ACAGGCCTGAGCCACCGTGCCT 43605         A    G_  C
           GG                     CCGGGCAC GTGGC  GG GCCTGT
                                |||||||| |||||  || ||||||
                                GGTCCGTG CACCG  TC CGGACA
                                   C     AG  _
GAM98   ZNF17    3'  ACAGGCATGAGCCACCGTGCCC 83265         A    GGGC
           GG                     CCGGGCAC GTGGC    GCCTGT
                                |||||||| |||||    ||||||
                                GGCCCGTG CACCG    CGGACA
                                   C     AGTA
GAM98   ZNF221   3'  ACAGGTGCCCGCCACCACACCC 26260     CACA
                                GGG    GTGGCGGGCGCCTGT
                                |||    |||||||||||||||
                                CCC    CACCGCCCGTGGACA
                                  ACAC
GAM98   ZNF338   3'  ACAGGTGTGAGCCACCATGCCT 42249        CA    GG
           GG                     CCGGGCA  GTGGC  GCGCCTGT
                                |||||||  |||||  ||||||||
                                GGTCCGT  CACCG  TGTGGACA
                                   AC     AG
GAM98   LOC112817 3'  ACAGGCGCCTGCCACCACGCCC 57310      ACA
                                GGGC   GTGGCGGGCGCCTGT
                                ||||   ||||||||||||||||
                                CCCG   CACCGTCCGCGGACA
                                  CAC
GAM98   LOC115648 3'  ACAGGCGTGAGCCACCATGCCC 60010       CA    GG
                                GGGCA  GTGGC  GCGCCTGT
                                |||||  |||||  ||||||||
                                CCCGT  CACCG  TGCGGACA
                                   AC     AG
GAM98   LOC115648 3'  ACAGGTGCCCACCAGCACGCCC 60011      ACAG   C
                                GGGC    TGG GGGCGCCTGT
                                ||||    ||| ||||||||||
                                CCCG    ACC CCCGTGGACA
                                  CACG   A
GAM98   LOC119392 3'  ACAGGCGCCCGCCACCATGCCC 59808         CA
           GG                     CCGGGCA  GTGGCGGGCGCCTGT
                                |||||||  |||||||||||||||
                                GGCCCGT  CACCGCCCGCGGACA
                                   AC
GAM98   LOC120114 3'  ACAGGTGTGTGCCACCACGCCT 76034        ACA     G
           GG                     CCGGGC   GTGGCG GCGCCTGT
                                ||||||   |||||| ||||||||
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                                GGTCCG   CACCGT TGTGGACA
                                   CAC     G
GAM98   LOC120224 5' ACAGGCGTGAGCCACCGCACCT 57876      CACA    GG
           GG                    CCGGG   GTGGC  GCGCCTGT
                                 |||||   |||||  ||||||||
                                 GGTCC   CACCG  TGCGGACA
                                   ACGC    AG
GAM98   LOC120224 5' ACAGGCTCCTGCCACCGCGCCC 57877       ACA       C
           GG                    CCGGGC   GTGGCGGG GCCTGT
                                 ||||||   |||||||| ||||||
                                 GGCCCG   CACCGTCC CGGACA
                                   CGC       T
GAM98   LOC120939 3' ACAGCTGCCTGCCACCGTGCCC 76753       A        C
                                 GGGCAC GTGGCGGGCG CTGT
                                 ||||||| |||||||||| ||||
                                 CCCGTG CACCGTCCGT GACA
                                   C         C
GAM98   LOC121506 5' ACAGGTATGAGCCACCACGCCC 74531       ACA    GGGC
           GG                    CCGGGC   GTGGC    GCCTGT
                                 ||||||   |||||    ||||||
                                 GGCCCG   CACCG    TGGACA
                                   CAC     AGTA
GAM98   LOC126272 3' ACAGGCGTGAGCCACCGCGCCC 76584       ACA    GG
           GG                    CCGGGC   GTGGC  GCGCCTGT
                                 ||||||   |||||  ||||||||
                                 GGCCCG   CACCG  TGCGGACA
                                   CGC     AG
GAM98   LOC126364 3' ACAGCACCCGCCACCATGCC   76178     CA       C  C
                                 GGCA  GTGGCGGG GC TGT
                                 ||||  |||||||| || |||
                                 CCGT  CACCGCCC CG ACA
                                   AC       A  _
GAM98   LOC126364 3' ACAGGCGTGGCCACTGCGCCC  76179      A      GG
                                 GGGC CAGTGGC  GCGCCTGT
                                 |||| |||||||  ||||||||
                                 CCCG GTCACCG  TGCGGACA
                                   C      G_
GAM98   LOC128077 3' ACAGGTGCCCACCACCACGCCC 75195      ACA    C
                                 GGGC   GTGG GGGCGCCTGT
                                 ||||   |||| ||||||||||
                                 CCCG   CACC CCCGTGGACA
                                   CAC    A
GAM98   LOC128989 3' ACAGGCGTGAGCCACCACGCCT 75303       ACA    GG
           GG                    CCGGGC   GTGGC  GCGCCTGT
                                 ||||||   |||||  ||||||||
                                 GGTCCG   CACCG  TGCGGACA
                                   CAC     AG
GAM98   LOC128989 3' ACAGGCGTGTGCCACCATGCCC 75304       CA     G
                                 GGGCA  GTGGCG GCGCCTGT
                                 |||||  |||||| ||||||||
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                                CCCGT  CACCGT TGCGGACA
                                  AC     G
GAM98   LOC130813 3'  ACAGGTGTGAGCCACTGCGCCC 76260       A      GG
          GG                    CCGGGC CAGTGGC  GCGCCTGT
                                |||||| |||||||  ||||||||
                                GGCCCG GTCACCG  TGTGGACA
                                  C      AG
GAM98   LOC131965 3'  ACAGGTGTAAGCCACCATGCCT 75513       CA    GG
          GG                    CCGGGCA  GTGGC  GCGCCTGT
                                |||||||  |||||  ||||||||
                                GGTCCGT  CACCG  TGTGGACA
                                  AC     AA
GAM98   LOC132241 5'  ACAGGCGTGAGCCACCGCGCCC 75551       ACA    GG
          GG                    CCGGGC   GTGGC  GCGCCTGT
                                ||||||   |||||  ||||||||
                                GGCCCG   CACCG  TGCGGACA
                                  CGC    AG
GAM98   LOC132625 3'  ACAGGTGTGAGCCACTGTGCCT 76426            GG
          GG                    CCGGGCACAGTGGC  GCGCCTGT
                                ||||||||||||||  ||||||||
                                GGTCCGTGTCACCG  TGTGGACA
                                      AG
GAM98   LOC132625 3'  ACAGGTGTGTGTCACCACGCCC 76427       ACA     G
          GG                    CCGGGC   GTGGCG GCGCCTGT
                                ||||||   |||||| ||||||||
                                GGCCCG   CACTGT TGTGGACA
                                  CAC    G
GAM98   LOC134266 3'  ACAGGCGTTCACCACTGCGCCC 75641      A     C
          G                     CGGGC CAGTGG GGGCGCCTGT
                                ||||| |||||| ||||||||||
                                GCCCG GTCACC CTTGCGGACA
                                  C     A
GAM98   LOC135293 3'  ACAGGTGTGTGGCACCATGCCC 76674      CA   G  G
                                GGGCA  GTG CG GCGCCTGT
                                |||||  ||| || ||||||||
                                CCCGT  CAC GT TGTGGACA
                                  AC   G  G
GAM98   LOC135818 3'  ACAGGCGTGAGCCACCACACCT 75741      CACA    GG
          GG                    CCGGG    GTGGC  GCGCCTGT
                                |||||    |||||  ||||||||
                                GGTCC    CACCG  TGCGGACA
                                  ACAC     AG
GAM98   LOC143916 3'  ACAGGCGTGAACCACTGCACCC 77132     CA     CGG
                                GGG  CAGTGG   GCGCCTGT
                                |||  ||||||   ||||||||
                                CCC  GTCACC   TGCGGACA
                                  AC     AAG
GAM98   LOC144305 3'  ACAGGCGTGCACCACCACGCCT 83967     ACA   C ___
                                GGGC   GTGG GG   GCGCCTGT
                                ||||   |||| ||   ||||||||
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                                TCCG  CACC CC  TGCGGACA
                                  ___   A  ACG
GAM98  LOC144317 5' ACAGGTGTGAGCCACCACGCCT 77285      ACA   GG
          GG                    CCGGGC  GTGGC  GCGCCTGT
                                |||||||  |||||  ||||||||
                                GGTCCG  CACCG  TGTGGACA
                                   CAC    AG
GAM98  LOC144519 5' ACAGGTGCGCACCACCATGCCC 77362     CA   CGG
                                GGGCA  GTGG  GCGCCTGT
                                |||||  ||||  ||||||||
                                CCCGT  CACC  CGTGGACA
                                  AC   ACG
GAM98  LOC144524 5' ACAGGCGCCCACCACCATACCT 84045     CACA   C
          GG                    CCGGG   GTGG GGGCGCCTGT
                                |||||   |||| ||||||||||
                                GGTCC   CACC CCCGCGGACA
                                  ATAC   A
GAM98  LOC144871 3' ACAGGCGTGAGCCACTGCGCCT 84114      A     GG
          GG                    CCGGGC CAGTGGC  GCGCCTGT
                                |||||| |||||||  ||||||||
                                GGTCCG GTCACCG  TGCGGACA
                                   C      AG
GAM98  LOC145009 3' ACAGGCACCTGCCACCACGCCT 60966      ACA      C
          GG                    CCGGGC  GTGGCGGG GCCTGT
                                ||||||  |||||||| ||||||
                                GGTCCG  CACCGTCC CGGACA
                                   CAC      A
GAM98  LOC145268 5' ACAGGTGCTCACCACCACGTCC 77566     ACA   C
                                GGGC  GTGG GGGCGCCTGT
                                ||||  |||| ||||||||||
                                CCTG  CACC CTCGTGGACA
                                  CAC   A
GAM98  LOC145622 3' ACAGGCGTGAGCCACTGTGCCT 77799           GG
          GG                    CCGGGCACAGTGGC  GCGCCTGT
                                ||||||||||||||  ||||||||
                                GGTCCGTGTCACCG  TGCGGACA
                                      AG
GAM98  LOC146050 3' ACAGGTGTGAGCCACTGCACCC 78095     CA     GG
          GG                    CCGGG  CAGTGGC  GCGCCTGT
                                |||||  |||||||  ||||||||
                                GGCCC  GTCACCG  TGTGGACA
                                  AC     AG
GAM98  LOC146229 3' ACAGGCGCCCACCTCCACACCC 78240     CACAGT  C
                                GGG     GG GGGCGCCTGT
                                |||     || ||||||||||
                                CCC     CC CCCGCGGACA
                                  ACACCT  A
GAM98  LOC146229 3' ACAGGCGTGAGCAACCGCACCC 78241      CACA  G  GG
          GG                    CCGGG   GT GC  GCGCCTGT
                                |||||   || ||  ||||||||
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                              GGCCC    CA CG  TGCGGACA
                                 ACGC  A  AG
GAM98   LOC146229 3'  ACAGGTGCCCACCAACACGCCC 78243       ACAG   C
           GG                    CCGGGC    TGG GGGCGCCTGT
                                 ||||||    ||| ||||||||||
                                 GGCCCG    ACC CCCGTGGACA
                                    CACA   A
GAM98   LOC146229 3'  ACAGGTGCCCGCTACCACACCC 78244      CACA
           GG                    CCGGG    GTGGCGGGCGCCTGT
                                 |||||    ||||||||||||||
                                 GGCCC    CATCGCCCGTGGACA
                                    ACAC
GAM98   LOC146337 5'  ACAGGCATGAGCCACCGTGCCC 84637        A    GGGC
           GG                    CCGGGCAC GTGGC    GCCTGT
                                 ||||||||| |||||    ||||||
                                 GGCCCGTG CACCG    CGGACA
                                      C     AGTA
GAM98   LOC146346 5'  ACAGGCGTGAGCCACCACGCCC 78381       ACA    GG
           GG                    CCGGGC   GTGGC  GCGCCTGT
                                 ||||||   |||||  ||||||||
                                 GGCCCG   CACCG  TGCGGACA
                                    CAC     AG
GAM98   LOC146438 3'  ACAGGCGTGAGCCACCGCGCCC 78451     ACA    GG
                              GGGC   GTGGC  GCGCCTGT
                              ||||   |||||  ||||||||
                              CCCG   CACCG  TGCGGACA
                                CGC     AG
GAM98   LOC146443 5'  ACAGGCGCACGCCACCACCC   78438    CACA     G
                              GGG    GTGGCG GCGCCTGT
                              |||    |||||| ||||||||
                              CCC    CACCGC CGCGGACA
                                AC__      A
GAM98   LOC146603 5'  ACAGGCGTGAGCCACCGCGCCG 78585     _  ACA    GG
           G                   CCGG GC   GTGGC  GCGCCTGT
                              |||| ||   |||||  ||||||||
                              GGCC CG   CACCG  TGCGGACA
                                G  C__     AG
GAM98   LOC146784 5'  ACAGGTGCGTGCCACCACACCC 78700     CACA     G
                              GGG    GTGGCG GCGCCTGT
                              |||    |||||| ||||||||
                              CCC    CACCGT CGTGGACA
                                ACAC     G
GAM98   LOC146839 3'  ACAGGCGCCCGCCACCACACCT 84831       CACA
           GG                    CCGGG    GTGGCGGGCGCCTGT
                                 |||||    |||||||||||||||
                                 GGTCC    CACCGCCCGCGGACA
                                    ACAC
GAM98   LOC146839 3'  ACAGGCGTGAACCACTGTGCCG 84832    G        CGG
           GG                    CC GGCACAGTGG   GCGCCTGT
                                 || ||||||||||   ||||||||
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                                GG CCGTGTCACC   TGCGGACA
                                 G         AAG
GAM98   LOC146901 3'  ACAGGTGTGCACCACCACGCCC 84878       ACA    C ___
                GG                 CCGGGC   GTGG GG   GCGCCTGT
                                   ||||||   |||| ||   ||||||||
                                   GGCCCG   CACC CC   TGTGGACA
                                      ___    A  ACG
GAM98   LOC146909 3'  ACAGGCGCCCACCACCACGCCT 78755       ACA    C
                GG                 CCGGGC   GTGG GGGCGCCTGT
                                   ||||||   |||| ||||||||||
                                   GGTCCG   CACC CCCGCGGACA
                                      CAC    A
GAM98   LOC146909 3'  ACAGGCGTGAGCCACTGCGCCC 78756       A      GG
                GG                 CCGGGC CAGTGGC  GCGCCTGT
                                   |||||| |||||||  ||||||||
                                   GGCCCG GTCACCG  TGCGGACA
                                      C       AG
GAM98   LOC146952 5'  ACAGGTGTGTGCCACCCTGCCC 84920      CA     G
                                   GGGCA  GTGGCG GCGCCTGT
                                   |||||  |||||| ||||||||
                                   CCCGT  CACCGT TGTGGACA
                                      CC     G
GAM98   LOC147054 3'  ACAGGCGTGAGTCACCGCGCCC 84998      ACA    GG
                                   GGGC   GTGGC  GCGCCTGT
                                   ||||   |||||  ||||||||
                                   CCCG   CACTG  TGCGGACA
                                      CGC    AG
GAM98   LOC147080 5'  ACAGGCGCCCGCTACCGTACCC 85020      C  A
                GG                 CCGGG AC GTGGCGGGCGCCTGT
                                   ||||| || ||||||||||||||||
                                   GGCCC TG CATCGCCCGCGGACA
                                      A  C
GAM98   LOC147080 5'  ACAGGCGTGAGCCACCGCGCCC 85021      ACA    GG
                G                   CGGGC   GTGGC  GCGCCTGT
                                    |||||   |||||  ||||||||
                                    GCCCG   CACCG  TGCGGACA
                                      CGC    AG
GAM98   LOC147093 5'  ACAGGCGTGGGTCACTGCACCT 85055      CA     GG
                GG                 CCGGG  CAGTGGC  GCGCCTGT
                                   |||||  |||||||  ||||||||
                                   GGTCC  GTCACTG  TGCGGACA
                                      AC      GG
GAM98   LOC147166 3'  ACAGGTGCCTGCCACCACACCC 78877     CACA
                                   GGG    GTGGCGGGCGCCTGT
                                   |||    ||||||||||||||||
                                   CCC    CACCGTCCGTGGACA
                                     ACAC
GAM98   LOC147166 3'  ACAGGCGTGAGCCACTGCGCCC 78876      A      GG
                                   GGGC CAGTGGC  GCGCCTGT
                                   |||| |||||||  ||||||||
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                                CCCG GTCACCG  TGCGGACA
                                  C      AG
GAM98   LOC147429 3'  ACAGGCGCCCGCAACCACGCCC 78985       ACA  G
           GG                   CCGGGC   GT GCGGGCGCCTGT
                                |||||||  || ||||||||||||
                                GGCCCG   CA CGCCCGCGGACA
                                   CAC  A
GAM98   LOC147429 3'  ACAGGCGTGAGCCACCGCGCCC 78986       ACA    GG
           GG                   CCGGGC   GTGGC  GCGCCTGT
                                |||||||  |||||  ||||||||
                                GGCCCG   CACCG  TGCGGACA
                                   CGC    AG
GAM98   LOC147990 3'  ACAGGCGTGAGCCACTGCGTCC 85205      A      GG
                                GGGC CAGTGGC  GCGCCTGT
                                |||| |||||||  ||||||||
                                CCTG GTCACCG  TGCGGACA
                                  C      AG
GAM98   LOC148114 5'  ACAAACACCCGCAGGTGCCGGG 79357    G    AGTG    CGCC
                                CC GGCAC    GCGGG    TGT
                                || |||||    |||||    |||
                                GG CCGTG    CGCCC    ACA
                                 G    GA__    ACAA
GAM98   LOC148147 3'  ACAGGCGTGAACCACTGCACGC 79380    A__     CGG
                                GC   CAGTGG   GCGCCTGT
                                ||   ||||||   ||||||||
                                CG   GTCACC   TGCGGACA
                                 CAC     AAG
GAM98   LOC148189 5'  ACAGGCGTGAGCCACCATGCCT 79440       CA    GG
           GG                   CCGGGCA  GTGGC  GCGCCTGT
                                |||||||  |||||  ||||||||
                                GGTCCGT  CACCG  TGCGGACA
                                   AC     AG
GAM98   LOC148645 5'  ACAGGCGTGCACCACTGCGCCT 85325      A     CGG
                                GGGC CAGTGG   GCGCCTGT
                                |||| ||||||   ||||||||
                                TCCG GTCACC   TGCGGACA
                                  C     ACG
GAM98   LOC148887 5'  ACAGGCGTGAGCCACCGCGCCC 85386       ACA    GG
           GG                   CCGGGC   GTGGC  GCGCCTGT
                                |||||||  |||||  ||||||||
                                GGCCCG   CACCG  TGCGGACA
                                   CGC    AG
GAM98   LOC148887 5'  CAGGCGTCACCACACCTGG    85395      CACA    CG
                                CCGGG    GTGG  GGCGCCTG
                                |||||    ||||  ||||||||
                                GGTCC    CACC  CTGCGGAC
                                  A___    A_
GAM98   LOC149132 5'  ACAGGTGCTTGCCACTATGCCC 79922       C
                                GGGCA AGTGGCGGGCGCCTGT
                                ||||| ||||||||||||||||
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                                CCCGT TCACCGTTCGTGGACA
                                  A
GAM98   LOC149171 5'  ACAGGTGTGAGCCACCGTGCCC 79959        A    GG
          GG                    CCGGGCAC GTGGC  GCGCCTGT
                                |||||||| |||||  ||||||||
                                GGCCCGTG CACCG  TGTGGACA
                                   C    AG
GAM98   LOC149421 3'  ACAGGCGCCCACCACCACGCCC 80136       ACA   C
          GG                    CCGGGC   GTGG GGGCGCCTGT
                                ||||||   |||| ||||||||||
                                GGCCCG   CACC CCCGCGGACA
                                  CAC   A
GAM98   LOC149478 3'  ACAGGTGTGCGCCACCATGCCC 80161        CA    G
          GG                    CCGGGCA  GTGGCG GCGCCTGT
                                |||||||  |||||| ||||||||
                                GGCCCGT  CACCGC TGTGGACA
                                   AC    G
GAM98   LOC149506 3'  ACAGGCATGAGCCACTGTGCCC 85620           GGGC
                                GGGCACAGTGGC   GCCTGT
                                ||||||||||||   ||||||
                                CCCGTGTCACCG   CGGACA
                                     AGTA
GAM98   LOC149506 3'  ACAGGCGCCTGCCACCATGCCT 85621        CA
          GG                    CCGGGCA  GTGGCGGGCGCCTGT
                                |||||||  ||||||||||||||||
                                GGTCCGT  CACCGTCCGCGGACA
                                   AC
GAM98   LOC149506 3'  AGGTGCCCACCACCACGCCC   85624     ACA   C
                                GGGC   GTGG GGGCGCCT
                                ||||   |||| ||||||||
                                CCCG   CACC CCCGTGGA
                                  CAC   A
GAM98   LOC149577 3'  ACAGGCGTGAGCCACCGCGCCT 85660        ACA    GG
          GG                    CCGGGC   GTGGC  GCGCCTGT
                                ||||||   |||||  ||||||||
                                GGTCCG   CACCG  TGCGGACA
                                   CGC    AG
GAM98   LOC149577 3'  ACAGGTGTGTGCCACCACACCC 85661       CACA    G
          GG                    CCGGG    GTGGCG GCGCCTGT
                                |||||    |||||| ||||||||
                                GGCCC    CACCGT TGTGGACA
                                   ACAC     G
GAM98   LOC149692 3'  ACAGGCGTGAGCCACTGCGCCC 85719        A     GG
          GG                    CCGGGC CAGTGGC  GCGCCTGT
                                |||||| |||||||  ||||||||
                                GGCCCG GTCACCG  TGCGGACA
                                   C      AG
GAM98   LOC149703 5'  ACAGGCGTGAGCCACTGCACCC 85812     CA     GG
                                GGG  CAGTGGC  GCGCCTGT
                                |||  |||||||  ||||||||
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                                CCC  GTCACCG  TGCGGACA
                                  AC       AG
GAM98   LOC149703 5' ACAGGCGTGTGCCATCATACCC 85813       CACA     G
           GG                    CCGGG    GTGGCG GCGCCTGT
                                 |||||    |||||| ||||||||
                                 GGCCC    TACCGT TGCGGACA
                                   ATAC     G
GAM98   LOC149711 3' ACAGGTGCCCACCATCATGCCC 85830       CA    C
                                 GGGCA  GTGG GGGCGCCTGT
                                 |||||  |||| ||||||||||
                                 CCCGT  TACC CCCGTGGACA
                                   AC    A
GAM98   LOC149711 3' ACAGGTGGGAGCCACTGTGCCT 85831             GGG
           GG                    CCGGGCACAGTGGC   CGCCTGT
                                 ||||||||||||||   |||||||
                                 GGTCCGTGTCACCG   GTGGACA
                                        AGG
GAM98   LOC149821 5' ACAGGCGTGAGCCACTGCGCCC 85924       A      GG
           GG                    CCGGGC CAGTGGC  GCGCCTGT
                                 ||||||| |||||||  ||||||||
                                 GGCCCG GTCACCG  TGCGGACA
                                   C       AG
GAM98   LOC149821 5' ACAGGTGCCCGCCACCACGCTC 85925       ACA
           GG                    CCGGGC   GTGGCGGGCGCCTGT
                                 ||||||   ||||||||||||||
                                 GGCTCG   CACCGCCCGTGGACA
                                   CAC
GAM98   LOC150166 5' ACAGGCGTGCACCACTGTGCCC 86028           CGG
           GG                    CCGGGCACAGTGG   GCGCCTGT
                                 ||||||||||||   ||||||||
                                 GGCCCGTGTCACC   TGCGGACA
                                       ACG
GAM98   LOC150225 3' ACAGGTGTGAGCCACTGCACCC 86175     CA      GG
                                 GGG  CAGTGGC  GCGCCTGT
                                 |||  |||||||  ||||||||
                                 CCC  GTCACCG  TGTGGACA
                                   AC       AG
GAM98   LOC150282 5' ACAGGCATGAGCCACCGTGCCC 80530        A    GGGC
           GG                    CCGGGCAC GTGGC    GCCTGT
                                 |||||||| |||||    ||||||
                                 GGCCCGTG CACCG    CGGACA
                                    C     AGTA
GAM98   LOC150282 5' ACAGGCGCCCGCCACCACGCCC 80531       ACA
           GG                    CCGGGC   GTGGCGGGCGCCTGT
                                 ||||||   ||||||||||||||
                                 GGCCCG   CACCGCCCGCGGACA
                                   CAC
GAM98   LOC150290 3' ACAGATGTTTGCCACCATGCCC 80582       CA        C
           G                     CGGGCA  GTGGCGGGCG CTGT
                                 ||||||  |||||||||| ||||
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                                GCCCGT  CACCGTTTGT GACA
                                   AC         A
GAM98   LOC150407 3'  ACAAACATAAGCCACTGTGCCC 80635           GGGCGCC
                                GGGCACAGTGGC      TGT
                                ||||||||||||      |||
                                CCCGTGTCACCG      ACA
                                      AATACAA
GAM98   LOC150630 5'  ACAGGCGCCCGCCACTGCGCCC 86279       A
           GG                    CCGGGC CAGTGGCGGGCGCCTGT
                                ||||||| ||||||||||||||||||
                                GGCCCG GTCACCGCCCGCGGACA
                                   C
GAM98   LOC150630 5'  ACAGGCGTGAGCCACCGCGCCC 86280       ACA    GG
           GG                    CCGGGC  GTGGC  GCGCCTGT
                                ||||||  |||||  ||||||||
                                GGCCCG  CACCG  TGCGGACA
                                   CGC    AG
GAM98   LOC150960 3'  ACAGGTGTGCACCACCATGCCC 80861      CA   CGG
                                GGGCA  GTGG   GCGCCTGT
                                |||||  ||||   ||||||||
                                CCCGT  CACC   TGTGGACA
                                  AC    ACG
GAM98   LOC151057 3'  ACAGGTGTGAGCCACCGCGCCC 86377       ACA    GG
           GG                    CCGGGC  GTGGC  GCGCCTGT
                                ||||||  |||||  ||||||||
                                GGCCCG  CACCG  TGTGGACA
                                   CGC    AG
GAM98   LOC151201 3'  ACAGACACCCGCCACCACACCT 86458      CACA      CGC
           GG                    CCGGG   GTGGCGGG  CTGT
                                |||||   ||||||||  ||||
                                GGTCC   CACCGCCC  GACA
                                  ACAC      ACA
GAM98   LOC151201 3'  ACAGGCGTGAGCCACCACGCCC 86459     ACA    GG
                                GGGC  GTGGC  GCGCCTGT
                                ||||  |||||  ||||||||
                                CCCG  CACCG  TGCGGACA
                                  CAC    AG
GAM98   LOC151201 3'  ACAGGTACATGCCACTGTGCCT 86460           GGC
           G                     CGGGCACAGTGGCG  GCCTGT
                                ||||||||||||||  ||||||
                                GTCCGTGTCACCGT  TGGACA
                                      ACA
GAM98   LOC151614 3'  ACAGGTGTGAGCCACTGCACCC 81116     CA     GG
                                GGG CAGTGGC  GCGCCTGT
                                ||| |||||||  ||||||||
                                CCC GTCACCG  TGTGGACA
                                  AC     AG
GAM98   LOC151701 3'  ACAGGTGTGAGCCACCACGTCC 86659     ACA    GG
                                GGGC  GTGGC  GCGCCTGT
                                ||||  |||||  ||||||||
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                                CCTG   CACCG  TGTGGACA
                                  CAC    AG
GAM98   LOC152220 3'  ACAGGCACCCGCCACCACACCC 86755    CACA      C
                                GGG    GTGGCGGG GCCTGT
                                |||    |||||||| ||||||
                                CCC    CACCGCCC CGGACA
                                  ACAC       A
GAM98   LOC152220 3'  ACAGGCGTGAGCCACTGCACCT 86756      CA      GG
           GG                     CCGGG  CAGTGGC  GCGCCTGT
                                  |||||  |||||||  ||||||||
                                  GGTCC  GTCACCG  TGCGGACA
                                    AC      AG
GAM98   LOC152343 3'  ACAGGTGTGAGCCACTGCGCCC 81413      A      GG
                                GGGC CAGTGGC  GCGCCTGT
                                |||| |||||||  ||||||||
                                CCCG GTCACCG  TGTGGACA
                                  C      AG
GAM98   LOC152343 3'  ACAGGTGTGCACCACCACACCC 81414     CACA    C ___
                                GGG    GTGG GG   GCGCCTGT
                                |||    |||| ||   ||||||||
                                CCC    CACC CC   TGTGGACA
                                  A___    A  ACG
GAM98   LOC152445 3'  ACAGGCGTGAGCCACTGCGCCC 86921       A      GG
           GG                     CCGGGC CAGTGGC  GCGCCTGT
                                  ||||||| |||||||  ||||||||
                                  GGCCCG GTCACCG  TGCGGACA
                                    C      AG
GAM98   LOC152719 5'  ACAGGCGCCCGCCGCCACGCCC 87008      ACA
           G                      CGGGC   GTGGCGGGCGCCTGT
                                  |||||   ||||||||||||||
                                  GCCCG   CGCCGCCCGCGGACA
                                    CAC
GAM98   LOC152719 5'  ACAGGCGTGAGACACCGCGCCC 87009      ACA   GCGG
                                GGGC   GTG    GCGCCTGT
                                ||||   |||    ||||||||
                                CCCG   CAC    TGCGGACA
                                  CGC   AGAG
GAM98   LOC152719 5'  ACAGGTGCGTGCCACCACGCAC 87010     G  ACA     G
           GG                     CCG GC   GTGGCG GCGCCTGT
                                  ||| ||   |||||| ||||||||
                                  GGC CG   CACCGT CGTGGACA
                                    A  CAC      G
GAM98   LOC152851 3'  ACAGGCATGCACCACCACGCCC 81586       ACA    C _ __
           GG                     CCGGGC   GTGG GG GC  GCCTGT
                                  ||||||   |||| || ||  ||||||
                                  GGCCCG   CACC CC CG  CGGACA
                                     ___    A  A  TA
GAM98   LOC152851 3'  ACAGGCGTGAGCCACCGCACCT 81587      CACA     GG
           GG                     CCGGG    GTGGC  GCGCCTGT
                                  |||||    |||||  ||||||||
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                                GGTCC    CACCG  TGCGGACA
                                  ACGC     AG
GAM98   LOC153077 3'  ACAGGCATGAGCCACCGTGCCT 87100        A     GGGC
          GG                    CCGGGCAC GTGGC    GCCTGT
                                |||||||| |||||    ||||||
                                GGTCCGTG CACCG    CGGACA
                                   C     AGTA
GAM98   LOC153077 3'  ACAGGCGCATGCCACCACACCC 87101       CACA     G
          GG                    CCGGG    GTGGCG GCGCCTGT
                                |||||    |||||| ||||||||
                                GGCCC    CACCGT CGCGGACA
                                  ACAC     A
GAM98   LOC153606 5'  ACAGGTGCGTGCCACCACACCT 87250       CACA     G
          GG                    CCGGG    GTGGCG GCGCCTGT
                                |||||    |||||| ||||||||
                                GGTCC    CACCGT CGTGGACA
                                  ACAC     G
GAM98   LOC153688 3'  ACAGGCGTGAGCCACTGTGCCC 87280           GG
                                GGGCACAGTGGC  GCGCCTGT
                                ||||||||||||  ||||||||
                                CCCGTGTCACCG  TGCGGACA
                                      AG
GAM98   LOC153688 3'  ACAGGCTCCCGCCACCACGCCT 87281       ACA       C
          GG                    CCGGGC   GTGGCGGG GCCTGT
                                ||||||   |||||||| ||||||
                                GGTCCG   CACCGCCC CGGACA
                                   CAC       T
GAM98   LOC153688 3'  ACAGGTGTAAGCCACTGCTCCC 87283     CA      GG
                                GGG  CAGTGGC  GCGCCTGT
                                |||  |||||||  ||||||||
                                CCC  GTCACCG  TGTGGACA
                                  TC      AA
GAM98   LOC154007 3'  ACAAGTGTGAGCCACTGTGCCT 81921           GG    C
                                GGGCACAGTGGC  GCGC TGT
                                ||||||||||||  |||| |||
                                TCCGTGTCACCG  TGTG ACA
                                      AG    A
GAM98   LOC154141 5'  ACAGGCGCCACCTGCTTGCCCG 87383       C  TG CG
          G                      CCGGGCA AG  G  GGCGCCTGT
                                 ||||||| ||  |  |||||||||
                                 GGCCCGT TC  C  CCGCGGACA
                                    _  GT CA
GAM98   LOC154141 5'  ACAGGCGTGAGCCACCGCGCCC 87384       ACA     GG
          GG                    CCGGGC   GTGGC  GCGCCTGT
                                ||||||   |||||  ||||||||
                                GGCCCG   CACCG  TGCGGACA
                                   CGC     AG
GAM98   LOC154726 5'  ACAGGCATGAGCCACCGTGCCT 82004        A     GGGC
          GG                    CCGGGCAC GTGGC    GCCTGT
                                |||||||| |||||    ||||||
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                                GGTCCGTG CACCG    CGGACA
                                    C     AGTA
GAM98   LOC154877 5'  ACAGGCGCCTGCCACCACATCC 87513      CACA
            GG                    CCGGG    GTGGCGGGCGCCTGT
                                  |||||    ||||||||||||||
                                  GGCCT    CACCGTCCGCGGACA
                                     ACAC
GAM98   LOC154877 3'  ACAGGCGTGAGCCACCACACCC 87514      CACA     GG
            GG                    CCGGG    GTGGC  GCGCCTGT
                                  |||||    |||||  ||||||||
                                  GGCCC    CACCG  TGCGGACA
                                     ACAC     AG
GAM98   LOC154877 3'  ACAGGTGCCCGCCACCACACCG 87516     GCACA
            G                     CCGG     GTGGCGGGCGCCTGT
                                  ||||     ||||||||||||||
                                  GGCC     CACCGCCCGTGGACA
                                     ACAC_
GAM98   LOC154930 3'  ACAGGTGTGAGCCACTGTTCCC 82084     C       GG
                                  GGG ACAGTGGC  GCGCCTGT
                                  |||  ||||||||  ||||||||
                                  CCC TGTCACCG  TGTGGACA
                                    T       AG
GAM98   LOC154992 3'  ACAGGCGTGCATCACCATGTCC 82122      CA    CGG
                                  GGGCA  GTGG   GCGCCTGT
                                  |||||  ||||   ||||||||
                                  CCTGT  CACT   TGCGGACA
                                     AC    ACG
GAM98   LOC157247 5'  ACAGGCATGAACCACCGTGCCC 82279        A    CGGGC
            GG                    CCGGGCAC GTGG     GCCTGT
                                  ||||||||  ||||     ||||||
                                  GGCCCGTG CACC     CGGACA
                                      C    AAGTA
GAM98   LOC157247 5'  ACAGGCGTGCGCCACCACGCCC 82280      ACA     G
                                  GGGC   GTGGCG GCGCCTGT
                                  ||||   ||||||  ||||||||
                                  CCCG   CACCGC TGCGGACA
                                     CAC     G
GAM98   LOC157623 3'  ACAAGCATGAGCCACTGTGCCT 82406           GGGC  C
            G                     CGGGCACAGTGGC    GC TGT
                                  ||||||||||||    ||  |||
                                  GTCCGTGTCACCG    CG ACA
                                         AGTA  A
GAM98   LOC158476 3'  ACAGGCATGAGCCACCACGCCC 88173      ACA     GGGC
            G                     CGGGC   GTGGC    GCCTGT
                                  |||||   |||||    ||||||
                                  GCCCG   CACCG    CGGACA
                                     CAC     AGTA
GAM98   LOC158476 3'  ACAGGCGCCCACCACCGCGCCT 88174       ACA    C
            GG                    CCGGGC   GTGG GGGCGCCTGT
                                  ||||||   |||| ||||||||||
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                              GGTCCG   CACC CCCGCGGACA
                                 CGC    A
GAM98   LOC158549 5'  ACAGGCGTGCACCACCACGCCT 88212       ACA    C ___
           GG                    CCGGGC   GTGG GG   GCGCCTGT
                                 ||||||   |||| ||   ||||||||
                                 GGTCCG   CACC CC   TGCGGACA
                                    ___    A  ACG
GAM98   LOC158709 3'  ACAGGCGTGAGCCACCGCACCC 82864     CACA    GG
                                 GGG    GTGGC  GCGCCTGT
                                 |||    |||||  ||||||||
                                 CCC    CACCG  TGCGGACA
                                   ACGC     AG
GAM98   LOC158865 5'  ACAGGCGCATGCCACCACACCT 88300      CACA     G
           GG                    CCGGG    GTGGCG GCGCCTGT
                                 |||||    |||||| ||||||||
                                 GGTCC    CACCGT CGCGGACA
                                    ACAC     A
GAM98   LOC158865 5'  ACAGGCGTGAGCCACCATGTCC 88301      CA    GG
                                 GGGCA  GTGGC  GCGCCTGT
                                 |||||  |||||  ||||||||
                                 CCTGT  CACCG  TGCGGACA
                                    AC     AG
GAM98   LOC160391 3'  ACAGGCACGAGCCACTGTGCCC 88438            GGGC
           GG                    CCGGGCACAGTGGC    GCCTGT
                                 ||||||||||||||    ||||||
                                 GGCCCGTGTCACCG    CGGACA
                                          AGCA
GAM98   LOC160646 3'  ACAGGCGTGAGCCACCGTGCCC 83098        A    GG
           GG                    CCGGGCAC GTGGC  GCGCCTGT
                                 ||||||||  |||||  ||||||||
                                 GGCCCGTG CACCG  TGCGGACA
                                      C     AG
GAM98   LOC160646 3'  ACAGGTGCCCACCACTGCGCCC 83099      A     C
                                 GGGC CAGTGG GGGCGCCTGT
                                 ||||  ||||||  ||||||||||
                                 CCCG GTCACC CCCGTGGACA
                                    C     A
GAM98   LOC161829 3'  ACAGGTGCGTGCCACCACGCCC 83178       ACA     G
           GG                    CCGGGC   GTGGCG GCGCCTGT
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                                 GGCCCG   CACCGT CGTGGACA
                                    CAC     G
GAM98   LOC162427 3'  ACAGGTGCCCGCTACTATGCCC 83218        C
           GG                    CCGGGCA AGTGGCGGGCGCCTGT
                                 |||||||  ||||||||||||||||
                                 GGCCCGT TCATCGCCCGTGGACA
                                    A
GAM98   LOC163590 5'  ACAGGCGTGAGCCACCACGCCT 59507       ACA    GG
           GG                    CCGGGC   GTGGC  GCGCCTGT
                                 ||||||   |||||  ||||||||
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                                GGTCCG  CACCG  TGCGGACA
                                   CAC    AG
GAM98   LOC170082 5' ACAGGTGCCCGCCACCACACCC 83435     CACA
           GG                    CCGGG   GTGGCGGGCGCCTGT
                                 |||||   ||||||||||||||
                                 GGCCC   CACCGCCCGTGGACA
                                   ACAC
GAM98   LOC196047 5' ACAGGTGCCTGCCACCACGCCC 91135     ACA
                                 GGGC  GTGGCGGGCGCCTGT
                                 ||||  ||||||||||||||
                                 CCCG  CACCGTCCGTGGACA
                                   CAC
GAM98   LOC196411 3' ACAGGCGCCCGCCACCACGCCC 89036     ACA
                                 GGGC  GTGGCGGGCGCCTGT
                                 ||||  ||||||||||||||
                                 CCCG  CACCGCCCGCGGACA
                                   CAC
GAM98   LOC196529 3' ACAGGCGTGAGCAACCGCACCC 89116     CACA  G  GG
                                 GGG   GT GC  GCGCCTGT
                                 |||   || ||  ||||||||
                                 CCC   CA CG  TGCGGACA
                                   ACGC  A  AG
GAM98   LOC196529 3' ACAGGTGCCCACCACCATGCCC 89117      CA   C
                                 GGGCA  GTGG GGGCGCCTGT
                                 |||||  |||| ||||||||||
                                 CCCGT  CACC CCCGTGGACA
                                   AC   A
GAM98   LOC197358 3' ACAGGCACCCGCCACCATGCCC 89406       CA      C
           GG                    CCGGGCA  GTGGCGGG GCCTGT
                                 |||||||  |||||||| ||||||
                                 GGCCCGT  CACCGCCC CGGACA
                                    AC       A
GAM98   LOC197358 3' ACAGGTGTGAGCCACTGCACCT 89407      CA     GG
           GG                    CCGGG  CAGTGGC  GCGCCTGT
                                 |||||  |||||||  ||||||||
                                 GGTCC  GTCACCG  TGTGGACA
                                   AC     AG
GAM98   LOC199699 3' ACAGGCACCCGCCACCATGCCC 89659      CA      C
                                 GGGCA  GTGGCGGG GCCTGT
                                 |||||  |||||||| ||||||
                                 CCCGT  CACCGCCC CGGACA
                                   AC       A
GAM98   LOC200014 3' ACAGGTGTGAGCCACCGCACCC 89910      CACA    GG
           GG                    CCGGG   GTGGC  GCGCCTGT
                                 |||||   |||||  ||||||||
                                 GGCCC   CACCG  TGTGGACA
                                   ACGC    AG
GAM98   LOC200107 3' ACAGGTGTGAGCCACTGTGCCC 89980          GG
                                 GGGCACAGTGGC  GCGCCTGT
                                 ||||||||||||  ||||||||
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                                CCCGTGTCACCG  TGTGGACA
                                      AG
GAM98   LOC200169 5'  AGGCGCCCGCCACCACACCCGG 91551      CACA
                                CCGGG   GTGGCGGGCGCCT
                                |||||   ||||||||||||
                                GGCCC   CACCGCCCGCGGA
                                  ACAC
GAM98   LOC200282 5'  ACAGGTGTGAGCCACCGTGCAC 90096    G   A    GG
          GG                      CCG GCAC GTGGC  GCGCCTGT
                                ||| |||| |||||  ||||||||
                                GGC CGTG CACCG  TGTGGACA
                                  A   C    AG
GAM98   LOC200301 5'  ACAGGCGCCCGCCACCACGCCC 90127     ACA
                                GGGC   GTGGCGGGCGCCTGT
                                ||||   ||||||||||||||
                                CCCG   CACCGCCCGCGGACA
                                  CAC
GAM98   LOC200301 5'  ACAGGCGTGAGCCACCGTGCCT 90128       A    GG
          GG                      CCGGGCAC GTGGC  GCGCCTGT
                                |||||||| |||||  ||||||||
                                GGTCCGTG CACCG  TGCGGACA
                                    C    AG
GAM98   LOC200310 3'  ACAGGCGTGAGCCACCGTGCCT 66314       A    GG
          GG                      CCGGGCAC GTGGC  GCGCCTGT
                                |||||||| |||||  ||||||||
                                GGTCCGTG CACCG  TGCGGACA
                                    C    AG
GAM98   LOC200316 3'  ACAGATGCCTGCCACCACGCCC 90162     ACA       C
                                GGGC   GTGGCGGGCG CTGT
                                ||||   |||||||||| ||||
                                CCCG   CACCGTCCGT GACA
                                  CAC        A
GAM98   LOC200316 5'  ACAGGCGCACGTCACCACACCT 90163     CACA    G
          GG                      CCGGG   GTGGCG GCGCCTGT
                                |||||   |||||| ||||||||
                                GGTCC   CACTGC CGCGGACA
                                  ACAC     A
GAM98   LOC200316 5'  ACAGGCGTGAGCCACCGTGCCC 90164       A    GG
          GG                      CCGGGCAC GTGGC  GCGCCTGT
                                |||||||| |||||  ||||||||
                                GGCCCGTG CACCG  TGCGGACA
                                    C    AG
GAM98   LOC200339 3'  ACAGGTGTGTGCCACCATGCCT 91612       CA    G
          GG                      CCGGGCA  GTGGCG GCGCCTGT
                                |||||||  |||||| ||||||||
                                GGTCCGT  CACCGT TGTGGACA
                                    AC     G
GAM98   LOC200407 3'  ACAGGTGTCCACCACCACGCCT 91622       ACA   C
          GG                      CCGGGC   GTGG GGGCGCCTGT
                                ||||||   |||| ||||||||||
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                                GGTCCG   CACC CCTGTGGACA
                                   CAC    A
GAM98   LOC200491 5' ACAGATGCCCGCCACCGCACCC 91646     CACA        C
                                GGG    GTGGCGGGCG CTGT
                                |||    |||||||||| ||||
                                CCC    CACCGCCCGT GACA
                                  ACGC         A
GAM98   LOC200845 5' ACAGGTGCCCACCACCACGCCC 90309      ACA    C
                                GGGC   GTGG GGGCGCCTGT
                                ||||   |||| ||||||||||
                                CCCG   CACC CCCGTGGACA
                                  CAC    A
GAM98   LOC200860 3' ACAGGCGTGAGCCACCACGCCC 91736      ACA     GG
           G                     CGGGC   GTGGC  GCGCCTGT
                                |||||   |||||  ||||||||
                                GCCCG   CACCG  TGCGGACA
                                   CAC     AG
GAM98   LOC201164 3' ACAGGTGTGAGCCGCCATGCCC 89482       CA     GG
           GG                     CCGGGCA  GTGGC  GCGCCTGT
                                |||||||  |||||  ||||||||
                                GGCCCGT  CGCCG  TGTGGACA
                                   AC     AG
GAM98   LOC201294 3' ACAGGCGTGAGCCACCACGCCC 89567       ACA     GG
           GG                     CCGGGC   GTGGC  GCGCCTGT
                                ||||||   |||||  ||||||||
                                GGCCCG   CACCG  TGCGGACA
                                   CAC     AG
GAM98   LOC201411 3' ACAGGCGTGAGCCACTGTGCCT 63628            GG
           GG                     CCGGGCACAGTGGC  GCGCCTGT
                                ||||||||||||||  ||||||||
                                GGTCCGTGTCACCG  TGCGGACA
                                        AG
GAM98   LOC201411 3' ACAGGTGTGCGCCACCATGCCC 63630      CA     G
                                GGGCA  GTGGCG GCGCCTGT
                                |||||  ||||||  ||||||||
                                CCCGT  CACCGC TGTGGACA
                                   AC     G
GAM98   LOC201510 3' ACAAGCATGAGCCACTGTACCC 89628     C       GGGC  C
                                GGG ACAGTGGC    GC TGT
                                ||| ||||||||    || |||
                                CCC TGTCACCG    CG ACA
                                  A       AGTA  A
GAM98   LOC201626 3' ACAGGCGTGAGCCACCGCACCC 90422      CACA     GG
           GG                     CCGGG    GTGGC  GCGCCTGT
                                |||||    |||||  ||||||||
                                GGCCC    CACCG  TGCGGACA
                                   ACGC     AG
GAM98   LOC201627 3' ACAGGTGTGAGCCACCGCACCT 90443      CACA     GG
           GG                     CCGGG    GTGGC  GCGCCTGT
                                |||||    |||||  ||||||||
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                                GGTCC    CACCG  TGTGGACA
                                   ACGC     AG
GAM98   LOC201696 3' ACAGGTGTGAGCCACCGTGACC 63808    G   A    GG
                                GG CAC GTGGC  GCGCCTGT
                                || ||| |||||  ||||||||
                                CC GTG CACCG  TGTGGACA
                                 A   C    AG
GAM98   LOC201705 5' ACAGGCGTGAGCCACCGCGTCC 91852     ACA    GG
                                GGGC   GTGGC  GCGCCTGT
                                ||||   |||||  ||||||||
                                CCTG   CACCG  TGCGGACA
                                   CGC    AG
GAM98   LOC201868 3' ACAGGCGTGCATCACCATGTCC 90509     CA   CGG
                                GGGCA  GTGG   GCGCCTGT
                                |||||  ||||   ||||||||
                                CCTGT  CACT   TGCGGACA
                                   AC    ACG
GAM98   LOC202459 5' ACAGGCGTGCACCATCACACCC 59930    CACA   GC ___
                                GGG    GTG  GG   GCGCCTGT
                                |||    |||  ||   ||||||||
                                CCC    CAC  CC   TGCGGACA
                                 A___   TA  ACG
GAM98   LOC202460 5' ACAGGTGCATGCCACGACACCC 90659    CACA     G
                                GGG    GTGGCG GCGCCTGT
                                |||    |||||| ||||||||
                                CCC    CACCGT CGTGGACA
                                  ACAG     A
GAM98   LOC202908 5' ACAGGCGCCTGCCACCATGCCC 90701      CA
                                GGGCA  GTGGCGGGCGCCTGT
                                |||||  ||||||||||||||
                                CCCGT  CACCGTCCGCGGACA
                                   AC
GAM98   LOC202908 5' ACAGGTGCTTGCCACTATGCCC 90702      C
                                GGGCA AGTGGCGGGCGCCTGT
                                ||||| ||||||||||||||||
                                CCCGT TCACCGTTCGTGGACA
                                   A
GAM98   LOC203369 3' ACAGGCGCCCGCCACCATGCCC 90876       CA
           GG                     CCGGGCA  GTGGCGGGCGCCTGT
                                  |||||||  ||||||||||||||
                                  GGCCCGT  CACCGCCCGCGGACA
                                     AC
GAM98   LOC203369 3' ACAGGCGTGAGCCACCACGCCC 90877       ACA    GG
           GG                     CCGGGC   GTGGC  GCGCCTGT
                                  ||||||   |||||  ||||||||
                                  GGCCCG   CACCG  TGCGGACA
                                     CAC    AG
GAM98   LOC203369 3' CGCCCGCCACCATGCCCGG   90885       CA
                                CCGGGCA  GTGGCGGGCG
                                |||||||  ||||||||||
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                                GGCCCGT  CACCGCCCGC
                                   AC
GAM98   LOC203378 3'  ACAGGCGCGCGCCACCATGCCT 92268      CA     G
                                GGGCA  GTGGCG GCGCCTGT
                                |||||  |||||| ||||||||
                                TCCGT  CACCGC CGCGGACA
                                   AC     G
GAM98   LOC204804 3'  ACAGGCGTGGGCCACTGCGCCT 91029      A      GG
                                GGGC CAGTGGC  GCGCCTGT
                                |||| |||||||  ||||||||
                                TCCG GTCACCG  TGCGGACA
                                  C      GG
GAM98   LOC219445 5'  AGGCTCCCGCCACCGTGCCGGG 93196    G    A      C
                                CC GGCAC GTGGCGGG GCCT
                                || ||||| |||||||| ||||
                                GG CCGTG CACCGCCC CGGA
                                 G    C       T
GAM98   LOC219735 3'  ACAGGCGCCTGCCACCACACCC 94720      CACA
           GG                     CCGGG   GTGGCGGGCGCCTGT
                                |||||   ||||||||||||||
                                GGCCC   CACCGTCCGCGGACA
                                   ACAC
GAM98   LOC220064 3'  AGGCGCCCCCCACCACGCCC   95060     ACA   C
                                GGGC   GTGG GGGCGCCT
                                ||||   |||| ||||||||
                                CCCG   CACC CCCGCGGA
                                  CAC   C
GAM98   LOC220074 3'  ACAGGCGCCTGCTACCACATCC 59950     CACA
                                GGG   GTGGCGGGCGCCTGT
                                |||   ||||||||||||||
                                CCT   CATCGTCCGCGGACA
                                  ACAC
GAM98   LOC221035 3'  ACAGGCGTGAGCCACCGCACCC 94778     CACA    GG
                                GGG   GTGGC  GCGCCTGT
                                |||   |||||  ||||||||
                                CCC   CACCG  TGCGGACA
                                  ACGC    AG
GAM98   LOC221060 3'  ACAGGCATGAGCTACTGTGCCC 94824          GGGC
                                GGGCACAGTGGC   GCCTGT
                                ||||||||||||   ||||||
                                CCCGTGTCATCG   CGGACA
                                       AGTA
GAM98   LOC221271 3'  ACAGGCATGAGCCACTGTGCCC 93485          GGGC
                                GGGCACAGTGGC   GCCTGT
                                ||||||||||||   ||||||
                                CCCGTGTCACCG   CGGACA
                                       AGTA
GAM98   LOC221296 3'  ACAGGCGCGCGCCGCCACGCCC 93598      ACA    G
           GG                     CCGGGC   GTGGCG GCGCCTGT
                                ||||||   |||||| ||||||||
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                                GGCCCG  CGCCGC CGCGGACA
                                   CAC     G
GAM98   LOC221773 3'  ACAGGTGTGAGCCACTGCACCC 92692     CA      GG
                                GGG  CAGTGGC  GCGCCTGT
                                |||  |||||||  ||||||||
                                CCC  GTCACCG  TGTGGACA
                                  AC      AG
GAM98   LOC222031 3'  ACAGGCGCCCGCCACCATGCCC 95663      CA
                                GGGCA  GTGGCGGGCGCCTGT
                                |||||  ||||||||||||||
                                CCCGT  CACCGCCCGCGGACA
                                   AC
GAM98   LOC222057 5'  ACAGGTGCTTGCCACTATGCCC 94342      C
                                GGGCA AGTGGCGGGCGCCTGT
                                |||||  ||||||||||||||
                                CCCGT TCACCGTTCGTGGACA
                                   A
GAM98   LOC222068 3'  ACAGGTGCCCGCCACCACGCTC 94264      ACA
                                GGGC   GTGGCGGGCGCCTGT
                                ||||   ||||||||||||||
                                CTCG   CACCGCCCGTGGACA
                                   CAC
GAM98   LOC222070 5'  ACAGGCGTGAGCCCCCGTGCCC 95804       AGT   GG
                                GGGCAC   GGC  GCGCCTGT
                                ||||||   |||  ||||||||
                                CCCGTG   CCG  TGCGGACA
                                   CCC   AG
GAM98   LOC253778 3'  ACAGGCGTGAGCCACCGCGCCC 96520      ACA    GG
                                GGGC   GTGGC  GCGCCTGT
                                ||||   |||||  ||||||||
                                CCCG   CACCG  TGCGGACA
                                   CGC    AG
GAM98   LOC253842 5'  ACAGGCGCCCGCCACCACACCC 99231      CACA
           GG                      CCGGG   GTGGCGGGCGCCTGT
                                |||||   ||||||||||||||
                                GGCCC   CACCGCCCGCGGACA
                                   ACAC
GAM98   LOC253842 5'  ACAGGCGTGAGCCACTGCACCC 99232     CA      GG
                                GGG  CAGTGGC  GCGCCTGT
                                |||  |||||||  ||||||||
                                CCC  GTCACCG  TGCGGACA
                                  AC      AG
GAM98   LOC253956 5'  ACAGGCGTGAGCCACTGTGCCC 97744            GG
           GG                      CCGGGCACAGTGGC  GCGCCTGT
                                |||||||||||||  ||||||||
                                GGCCCGTGTCACCG  TGCGGACA
                                        AG
GAM98   LOC254018 5'  ACAGGCGTGAGCCACTGTGCCC 98734           GG
                                GGGCACAGTGGC  GCGCCTGT
                                ||||||||||||  ||||||||
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                                CCCGTGTCACCG TGCGGACA
                                      AG
GAM98   LOC254295 5' ACAGGTGCCCGCCACCACGCCC 97884       ACA
            GG                  CCGGGC  GTGGCGGGCGCCTGT
                                |||||| ||||||||||||||||
                                GGCCCG  CACCGCCCGTGGACA
                                   CAC
GAM98   LOC254532 5' ACAGGCGTGAGCCACTCTGCCC 98442       C     GG
            GG                  CCGGGCA AGTGGC GCGCCTGT
                                ||||||| |||||| ||||||||
                                GGCCCGT TCACCG TGCGGACA
                                   C     AG
GAM98   LOC254655 3' ACAGGCGCCTGCCACCACGCCT 97207       ACA
            GG                  CCGGGC  GTGGCGGGCGCCTGT
                                |||||| ||||||||||||||||
                                GGTCCG  CACCGTCCGCGGACA
                                   CAC
GAM98   LOC254655 3' ACAGGCGTGAGTCACTGCACCC 97208     CA      GG
                                GGG CAGTGGC GCGCCTGT
                                ||| ||||||| ||||||||
                                CCC GTCACTG TGCGGACA
                                  AC      AG
GAM98   LOC254672 3' ACAGGTGCCCACCACCATGCCT 96289       CA    C
            GG                  CCGGGCA GTGG GGGCGCCTGT
                                ||||||| |||| ||||||||||
                                GGTCCGT CACC CCCGTGGACA
                                   AC    A
GAM98   LOC255037 5' ACAGGCGCCCACCACCATGCCC 98434      CA    C
                                GGGCA GTGG GGGCGCCTGT
                                ||||| |||| ||||||||||
                                CCCGT CACC CCCGCGGACA
                                  AC    A
GAM98   LOC255196 5' ACAGGTGTGAGTCACTGTGCCC 98942          GG
                                GGGCACAGTGGC GCGCCTGT
                                |||||||||||| ||||||||
                                CCCGTGTCACTG TGTGGACA
                                      AG
GAM98   LOC255707 3' ACAGGCGTGAGCCACCAAACCC 98731     CACA    GG
                                GGG   GTGGC GCGCCTGT
                                |||   ||||| ||||||||
                                CCC   CACCG TGCGGACA
                                  AAAC    AG
GAM98   LOC255919 3' ACAGGCGCATGCCACCATGCCC 96739      CA     G
                                GGGCA GTGGCG GCGCCTGT
                                ||||| |||||| ||||||||
                                CCCGT CACCGT CGCGGACA
                                   AC     A
GAM98   LOC255975 5' ACAGGTGCTTGCCACCATGCCC 97567      CA
                                GGGCA GTGGCGGGCGCCTGT
                                ||||| ||||||||||||||||
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                                CCCGT  CACCGTTCGTGGACA
                                  AC
GAM98   LOC256221 3'  ACAGGCGCCCACGACCACGCCC 96901       ACA   _ __
                GG                CCGGGC   GTGG C  GGGCGCCTGT
                                  ||||||   |||| |  ||||||||||
                                  GGCCCG   CACC G  CCCGCGGACA
                                    ___    A CA
GAM98   LOC256306 3'  ACAGGTGCCCACCACCATGCCT 98498       CA    C
                GG                CCGGGCA  GTGG GGGCGCCTGT
                                  |||||||  |||| ||||||||||
                                  GGTCCGT  CACC CCCGTGGACA
                                    AC    A
GAM98   LOC256878 5'  ACAGGTGCTTGCCACTATGCCC 98681      C
                                  GGGCA AGTGGCGGGCGCCTGT
                                  ||||| ||||||||||||||||
                                  CCCGT TCACCGTTCGTGGACA
                                    A
GAM98   LOC257127 5'  ACAGGTGTGAGCCACCGTGCCC 98493        A    GG
                GG                CCGGGCAC GTGGC  GCGCCTGT
                                  |||||||| |||||  ||||||||
                                  GGCCCGTG CACCG  TGTGGACA
                                     C    AG
GAM98   LOC257465 3'  ACAGGCGCGTGCCACCACGCCC 82486     ACA     G
                                  GGGC   GTGGCG GCGCCTGT
                                  ||||   |||||| ||||||||
                                  CCCG   CACCGT CGCGGACA
                                    CAC     G
GAM98   LOC257486 3'  ACAGGCGCCCGCCATCACGCCC 69757       ACA
                GG                CCGGGC   GTGGCGGGCGCCTGT
                                  ||||||   ||||||||||||||
                                  GGCCCG   TACCGCCCGCGGACA
                                     CAC
GAM98   LOC257486 3'  ACAGGCGTGAGCCACCGCGCCC 69758       ACA    GG
                GG                CCGGGC   GTGGC  GCGCCTGT
                                  ||||||   |||||  ||||||||
                                  GGCCCG   CACCG  TGCGGACA
                                     CGC    AG
GAM98   LOC51193  3'  ACAGGCATGTGGCACCATGCCC 33353       CA   G  GGC
                G                  CGGGCA  GTG CG   GCCTGT
                                   ||||||  ||| ||   ||||||
                                   GCCCGT  CAC GT   CGGACA
                                     AC   G  GTA
GAM98   LOC51193  5'  ACAGGCGTGAACCACTGCACCC 33354      CA     CGG
                GG                CCGGG  CAGTGG   GCGCCTGT
                                  |||||  ||||||   ||||||||
                                  GGCCC  GTCACC   TGCGGACA
                                    AC     AAG
GAM98   LOC51200  3'  ACAGGGGGAGCCACTGTGCCGG 33431     G       GGGCG
                                  CCGG CACAGTGGC    CCTGT
                                  |||| |||||||||    |||||
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                                GGCC GTGTCACCG    GGACA
                                  _       AGGG_
GAM98   LOC51275 5' ACAGGCGTGAGCCACCGTGCCT 33734        A    GG
          GG                    CCGGGCAC GTGGC  GCGCCTGT
                                |||||||| |||||  ||||||||
                                GGTCCGTG CACCG  TGCGGACA
                                   C     AG
GAM98   LOC51601 5' ACAGGCGCCCGCCACCACGCCC 32497     ACA
                                GGGC   GTGGCGGGCGCCTGT
                                ||||   ||||||||||||||
                                CCCG   CACCGCCCGCGGACA
                                  CAC
GAM98   LOC51696 3' ACAGGCGTGAGTCACTGCGCCT 33074       A      GG
          GG                    CCGGGC CAGTGGC  GCGCCTGT
                                ||||||| |||||||  ||||||||
                                GGTCCG GTCACTG  TGCGGACA
                                   C      AG
GAM98   LOC56181 5' ACAGGTGCCCGCCACCACACCT 97266      CACA
          GG                    CCGGG    GTGGCGGGCGCCTGT
                                |||||    ||||||||||||||
                                GGTCC    CACCGCCCGTGGACA
                                  ACAC
GAM98   LOC57107 3' ACAGGCACCTGCCACCACGCCT 40177       ACA       C
          GG                    CCGGGC   GTGGCGGG GCCTGT
                                ||||||   |||||||| ||||||
                                GGTCCG   CACCGTCC CGGACA
                                   CAC       A
GAM98   LOC57146 3' ACAGGCACCCGCCACCGTGCCC 40286        A       C
          GG                    CCGGGCAC GTGGCGGG GCCTGT
                                |||||||| |||||||| ||||||
                                GGCCCGTG CACCGCCC CGGACA
                                   C       A
GAM98   LOC57146 3' ACAGGCGTGAGCCACTGTGCCC 40287           GG
                                GGGCACAGTGGC  GCGCCTGT
                                ||||||||||||  ||||||||
                                CCCGTGTCACCG  TGCGGACA
                                      AG
GAM98   LOC81034 3' ACAGGCACCTGCCACCACGCCT 48578       ACA       C
          GG                    CCGGGC   GTGGCGGG GCCTGT
                                ||||||   |||||||| ||||||
                                GGTCCG   CACCGTCC CGGACA
                                   CAC       A
GAM98   LOC81034 3' ACAGGCGTGAGCCACTGCGCCT 48579       A      GG
          GG                    CCGGGC CAGTGGC  GCGCCTGT
                                ||||||| |||||||  ||||||||
                                GGTCCG GTCACCG  TGCGGACA
                                   C      AG
GAM98   LOC90072 3' ACAGGCGTGAGCCACCGCGCCT 61943       ACA    GG
          GG                    CCGGGC   GTGGC  GCGCCTGT
                                ||||||   |||||  ||||||||
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                              GGTCCG  CACCG  TGCGGACA
                                 CGC    AG
GAM98  LOC90110 5' ACAGGTGTAAGCCACCGCACCT 62175     CACA    GG
          GG                  CCGGG   GTGGC  GCGCCTGT
                              |||||   |||||  ||||||||
                              GGTCC   CACCG  TGTGGACA
                                 ACGC    AA
GAM98  LOC90288 3' ACAGGTGCACACCACTGCACCC 62763     CA    CGG
          GG                  CCGGG  CAGTGG  GCGCCTGT
                              |||||  ||||||  ||||||||
                              GGCCC  GTCACC  CGTGGACA
                                 AC     ACA
GAM98  LOC90333 3' ACAGGAGTGAGCCACTGTGCCT 62954          GG  G
          GG                  CCGGGCACAGTGGC  GC CCTGT
                              ||||||||||||||  || |||||
                              GGTCCGTGTCACCG  TG GGACA
                                     AG  A
GAM98  LOC90459 3' ACAGGCGCGTGCCACCACACCC 63545     CACA    G
          G                   CGGG   GTGGCG GCGCCTGT
                              ||||   |||||| ||||||||
                              GCCC   CACCGT CGCGGACA
                                 ACAC    G
GAM98  LOC90485 3' ACAGGCGCCCGGCCACCACACC 63683     CACA    _
          CG                  CGGG   GTGGC GGGCGCCTGT
                              ||||   ||||| ||||||||||
                              GCCC   CACCG CCCGCGGACA
                                 ACAC    G
GAM98  LOC90591 3' ACAGGCATGAGCCACTGCACCC 64130    CA     GGGC
                              GGG  CAGTGGC   GCCTGT
                              |||  |||||||   ||||||
                              CCC  GTCACCG   CGGACA
                                AC     AGTA
GAM98  LOC90591 3' ACAGGTATGAGCCACCGTGCCC 64131       A    GGGC
          GG                  CCGGGCAC GTGGC   GCCTGT
                              ||||||||| |||||   ||||||
                              GGCCCGTG CACCG   TGGACA
                                   C    AGTA
GAM98  LOC90591 3' ACAGGTGCCTGCCACCACACCC 64132     CACA
          GG                  CCGGG   GTGGCGGGCGCCTGT
                              |||||   ||||||||||||||||
                              GGCCC   CACCGTCCGTGGACA
                                 ACAC
GAM98  LOC91115 3' ACAGGCACCCGCCACCATGCCC 65534       CA      C
          GG                  CCGGGCA  GTGGCGGG GCCTGT
                              |||||||  |||||||| ||||||
                              GGCCCGT  CACCGCCC CGGACA
                                 AC       A
GAM98  LOC91115 3' ACAGGCGTGAGCCACCGCACCT 65535     CACA    GG
          GG                  CCGGG   GTGGC  GCGCCTGT
                              |||||   |||||  ||||||||
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                                GGTCC   CACCG  TGCGGACA
                                  ACGC    AG
GAM98   LOC91250  5' ACAGGCATCAGCCACCACACCC 65900    CACA    G GC
                                GGG   GTGGC G  GCCTGT
                                |||   ||||| |  ||||||
                                CCC   CACCG C  CGGACA
                                 ACAC    A TA
GAM98   LOC91308  3' ACAGGCGTGAGCCACCACCCCC 66159     CACA    GG
           GG                    CCGGG   GTGGC  GCGCCTGT
                                |||||   |||||  ||||||||
                                GGCCC   CACCG  TGCGGACA
                                  CCAC    AG
GAM98   LOC91308  3' ACAGGTGCGTGCCACCACACCC 66160     CACA     G
           GG                    CCGGG   GTGGCG GCGCCTGT
                                |||||   |||||| ||||||||
                                GGCCC   CACCGT CGTGGACA
                                  ACAC     G
GAM98   LOC91547  3' ACAGATGTGAGCCACTGTGCCT 66994          GG   C
           GG                    CCGGGCACAGTGGC  GCG CTGT
                                ||||||||||||||  ||| ||||
                                GGTCCGTGTCACCG  TGT GACA
                                      AG   A
GAM98   LOC91549  5' ACAGGTGTGAGCCACCACACCC 67021     CACA    GG
           GG                    CCGGG   GTGGC  GCGCCTGT
                                |||||   |||||  ||||||||
                                GGCCC   CACCG  TGTGGACA
                                  ACAC    AG
GAM98   LOC91561  5' ACAGGCGCTGGCCACCACACCT 67036     CACA    G
           GG                    CCGGG   GTGGC GGCGCCTGT
                                |||||   ||||| |||||||||
                                GGTCC   CACCG TCGCGGACA
                                  ACAC    G
GAM98   LOC91893  3' ACAGGCACCTGCCACCACGCCT 68064      ACA      C
           GG                    CCGGGC  GTGGCGGG GCCTGT
                                ||||||  |||||||| ||||||
                                GGTCCG  CACCGTCC CGGACA
                                   CAC      A
GAM98   LOC92148  5' ACAGGTGCCCACCACCATGCCC 68866     CA   C
                                GGGCA  GTGG GGGCGCCTGT
                                |||||  |||| ||||||||||
                                CCCGT  CACC CCCGTGGACA
                                  AC   A
GAM98   LOC92148  5' ACAGGTGTGAGCCACCGCACCC 68867    CACA    GG
                                GGG   GTGGC  GCGCCTGT
                                |||   |||||  ||||||||
                                CCC   CACCG  TGTGGACA
                                 ACGC    AG
GAM98   LOC92303  3' ACAGGTGCGAGCCACCGTGCCC 69380       A    GG
           GG                    CCGGGCAC GTGGC  GCGCCTGT
                                |||||||| |||||  ||||||||
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                                GGCCCGTG CACCG  CGTGGACA
                                    C    AG
GAM98   LOC92305  3'  ACAGCGTCTGCCCCCG     57229     CACAGT       C
                                CGGG     GGCGGGCGC TGT
                                ||||     ||||||||| |||
                                GCCC     CCGTCTGCG ACA
                                  _______       _
GAM98   LOC92609  3'  ACAGGTGCGTGCTACCATACCC 73202     CACA     G
                                GGG   GTGGCG GCGCCTGT
                                |||   |||||| ||||||||
                                CCC   CATCGT CGTGGACA
                                  ATAC     G
GAM98   LOC92689  3'  ACAGGTGTGTGCCACCACGCCC 70766     ACA     G
                                GGGC   GTGGCG GCGCCTGT
                                ||||   |||||| ||||||||
                                CCCG   CACCGT TGTGGACA
                                  CAC     G
GAM98   LOC92841  3'  ACGGGCGCCCGCCACCACACCC 71238     CACA
                                GGG   GTGGCGGGCGCCTGT
                                |||   ||||||||||||||
                                CCC   CACCGCCCGCGGGCA
                                  ACAC
GAM98   LOC93070  3'  ACAGGCGTGCACCATCACGCCC 71800       ACA   CGG
          GG                    CCGGGC   GTGG   GCGCCTGT
                                ||||||   ||||   ||||||||
                                GGCCCG   TACC   TGCGGACA
                                   CAC    ACG
GAM98   LOC93349  3'  ACAGTGCCTGCCACCATGCCC  57259      CA        C
                                GGGCA  GTGGCGGGCGC TGT
                                |||||  |||||||||| |||
                                CCCGT  CACCGTCCGTG ACA
                                  AC        _
GAM98   LOC93356  3'  ACAGGCGTGAGCCACTGCACCC 72547     CA      GG
                                GGG  CAGTGGC  GCGCCTGT
                                |||  |||||||  ||||||||
                                CCC  GTCACCG  TGCGGACA
                                  AC      AG
GAM98   LOC93496  3'  ACAGGCGTGAGCCACCACGCCC 72860       ACA    GG
          GG                    CCGGGC   GTGGC  GCGCCTGT
                                ||||||   |||||  ||||||||
                                GGCCCG   CACCG  TGCGGACA
                                   CAC    AG
GAM99   CERD4     3'  TTCTCCACACGTGTCACAGCCA 24886      A_ _   CAGTC
                                TGGC  TG CGC    TGTGGAGAA
                                ||||  || |||    |||||||||
                                ACCG  AC GTG    ACACCTCTT
                                  AC  T   C____
GAM99   MADH7     5'  CTCCGGGAGACTGGCGCATGCC 20925             G_
          A                      TGGCATGCGCCAGTCT  TGGAG
                                ||||||||||||||||  |||||
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                                ACCGTACGCGGTCAGA  GCCTC
                                        GG
GAM99   NKX2E    5'  CTGTGAGACTGGCGCTGCCA   16522      T       _ TG
                                TGGCA GCGCCAGTCT G  G
                                ||||| |||||||||| |  |
                                ACCGT CGCGGTCAGA T  C
                                   _        G GT
GAM99   KIAA0618 3'  CTCCACGACCCTGGCGCACGCC 29851     A      TC_
                                GGC TGCGCCAG   TGTGGAG
                                ||| ||||||||   |||||||
                                CCG ACGCGGTC   GCACCTC
                                  C       CCA
GAM99   KIAA1169 5'  TCTCCCTGCGGCCCATGCCA   35885       C   A  CTGT
                                TGGCATG GCC GT    GGAGA
                                ||||||| ||| ||    |||||
                                ACCGTAC CGG CG    CCTCT
                                    C   _  TC__
GAM99   KIAA1853 3'  CTCCGGTTGGCGCCTGCCA    69920      T     GT TGT
                                TGGCA GCGCCA  C   GGAG
                                ||||| ||||||  |   ||||
                                ACCGT CGCGGT  G   CCTC
                                   C     TG ____
GAM99   LOC137090 5'  CCACAGACTGAGTGCCTCCA   76473     CAT   _
                                TGG   GCGC CAGTCTGTGG
                                |||   |||| ||||||||||
                                ACC   CGTG GTCAGACACC
                                  TC_   A
GAM99   LOC147054 5'  CTACTGTGAACTGCGCATGCCA 85004          C   CT TG _
                                TGGCATGCGC AGT  G  G AG
                                |||||||||| |||  |  | ||
                                ACCGTACGCG TCA  T  C TC
                                      _  AG GT A
GAM99   LOC220980 3'  TCTCCACAATCTGCAGCCA    94773     A   GCC  TC
                                TGGC TGC   AG  TGTGGAGA
                                |||| |||   ||  ||||||||
                                ACCG ACG   TC  ACACCTCT
                                  _  ____  TA
GAM100  BBS4     3'  ATTTGCCCAAAGGGAATCCAGA 53447         G_ G_   A
             ACA                   TGTTCTGGA  CT  TTGG CAAAT
                                |||||||||  ||  |||| |||||
                                ACAAGACCT  GG  AACC GTTTA
                                     AA  GA   C
GAM100  CENTD2   3'  CCAACAAACTCCAGAACA    31539         C_
                                TGTTCTGGAG  TGTTGG
                                ||||||||||  ||||||
                                ACAAGACCTC  ACAACC
                                      AA
GAM100  HAMP     3'  TCCTGCTGCCCCAGAACA    41289         A  T  T
                                TGTTCTGG GC GT GGA
                                |||||||| || || |||
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                                ACAAGACC CG CG CCT
                                    C  T  T
GAM100  ITGA11   3'  TCTGCCGGCCCCCAGGACA   25213        A_   TT
                                TGTTCTGG  GCTG  GGA
                                ||||||||  ||||  |||
                                ACAGGACC  CGGC  TCT
                                    CC    CG
GAM100  KITLG    3'  ATTTGCATGGCTCCAGAA    8023          TGGA
                                TTCTGGAGCTGT   CAAAT
                                ||||||||||||   |||||
                                AAGACCTCGGTA   GTTTA
                                      C___
GAM100  MAPK4    5'  CCTGGGCAGCTCCAGATCA   12300    T        __
                                TG TCTGGAGCTGTT  GG
                                || ||||||||||||  ||
                                AC AGACCTCGACGG  CC
                                 T         GT
GAM100  MGAT2    3'  ATTTGTCCAAACAGGACA    11557       GAGCTG
                                TGTTCTG     TTGGACAAAT
                                |||||||     ||||||||||
                                ACAGGAC     AACCTGTTTA
                                    A_____
GAM100  PSPHL    5'  TTGTCATACAGCTCCAAACA   94499     C       TG
                                TGTT TGGAGCTGT  GACAA
                                |||| |||||||||  |||||
                                ACAA ACCTCGACA  CTGTT
                                  _       TA
GAM100  TTC3     3'  TATTTGTCCAACAACTGTCAGA 13885        _ C
            ATA                    TGTTCTGG AG TGTTGGACAAATA
                                |||||||| || ||||||||||||
                                ATAAGACT TC ACAACCTGTTTAT
                                    G  A
GAM100  H2BFQ    3'  TTTAAGAGAACTCCAGGACA   60079         __ G
                                TGTTCTGGAG  CT TTGGA
                                ||||||||||  || |||||
                                ACAGGACCTC  GA AATTT
                                     AA  G
GAM100  LRG      3'  TCCATCCATGCTTCCTAGAACA 54825       _  _ _ T_
                                TGTTCT GGA GC TG  TGGA
                                ||||||  ||| || ||  ||||
                                ACAAGA CCT CG AC  ACCT
                                   T   T  T  CT
GAM100  NMT2     3'  ATTTGTCCATGTAACAGAACA  17852       GA  TGT
                                TGTTCTG  GC   TGGACAAAT
                                |||||||  ||   |||||||||
                                ACAAGAC  TG   ACCTGTTTA
                                    AA  T__
GAM100  NYD-SP21 3'  TATTTGTCCAATCTAGATTCAG 51863         G  __
            AACA                   TGTTCTGGA CT  GTTGGACAAATA
                                |||||||||  ||  ||||||||||||
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                                ACAAGACTT GA  TAACCTGTTTAT
                                      A  TC
GAM100  PSPH     3'  TTGTCGTACAGCTCCAAACA   17143     C       TG
                                TGTT TGGAGCTGT  GACAA
                                |||| |||||||||  |||||
                                ACAA ACCTCGACA  CTGTT
                                  _       TG
GAM100  LOC122258 3'  CCACCAGCCTCCGGAACA    59820         _  T
                                TGTTCTGGAG CTG TGG
                                |||||||||| ||| |||
                                ACAAGGCCTC GAC ACC
                                      C   C
GAM100  LOC151826 3'  ATTTGTCCAACCTAGCACA   81176    T   AGCT
                                TGT CTGG   GTTGGACAAAT
                                ||| ||||   ||||||||||
                                ACA GATC   CAACCTGTTTA
                                  C   ____
GAM100  LOC169611 3'  TCCAGTGGCAGCTCCAGAA   83663          ___
                                TTCTGGAGCTGT   TGGA
                                ||||||||||||   ||||
                                AAGACCTCGACG   ACCT
                                       GTG
GAM100  LOC196746 3'  TCAGAGCAGCTCCAAGACA   88903    TC       G_
                                TGT  TGGAGCTGTT  GA
                                |||  ||||||||||  ||
                                ACA  ACCTCGACGA  CT
                                  GA        GA
GAM100  LOC253142 5'  TTGCTAGGATGCCCCAGAATA  99230       A  TG_   A
                                TGTTCTGG GC   TTGG CAA
                                |||||||| ||   |||| |||
                                ATAAGACC CG   GATC GTT
                                     C  TAG   _
GAM101  CDKN2C   5'  CCTCCGGAGCACGTCAG     8846    _   CACA
                                CT ACGT   CTCCGGAGG
                                || ||||   |||||||||
                                GA TGCA   GAGGCCTCC
                                 C   C___
GAM101  TNS      3'  CGAGGGGAAAGTGCAACGTGGG 42949         CA  T_______  GGAG
           GAG                    CTCCCTACGT  CAC      CC   G
                                |||||||||  |||      ||   |
                                GAGGGGTGCA  GTG     GG   C
                                      AC   AAAG___  GAGG
GAM101  CLPTM1   3'  CCAGCGTGTGACGTAGGG    8922           TCC
                                CCCTACGTCACAC   GG
                                ||||||||||||   ||
                                GGGATGCAGTGTG   CC
                                       CGA
GAM101  FLJ32334  3'  CTGGAGTCGACGCAGAGA    58607    C  A   AC
                                TC CT CGTC  ACTCCGG
                                || || ||||  |||||||
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                                AG GA GCAG  TGAGGTC
                                 A  C    C_
GAM101  KIAA0635  5'  CCATGCAGTGTGACACAGG   28413     AC       C  GA
                                CCT  GTCACACT CG  GG
                                |||  |||||||| ||  ||
                                GGA  CAGTGTGA GT  CC
                                  CA       C  A_
GAM101  LOC157503 3'  CCCCACGAGTGTGCGTAGGGA  87763         T      C GA
                                TCCCTACG CACACTC G  GGG
                                |||||||| ||||||| |  |||
                                AGGGATGC GTGTGAG C  CCC
                                     _      _ AC
GAM102  SCAMP1    3'  GCTAAATAAATATTCTCC    54500     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C      A
GAM102  SCAMP1    3'  GCTAAATAAATATTCTCC    54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C      A
GAM102  NX-17     3'  TGAATATCAGCCCCTAATA   40706         ATA_
                                TATTAGGG    ATATTCA
                                ||||||||    |||||||
                                ATAATCCC    TATAAGT
                                     CGAC
GAM102  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
              TA                  TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM103  SREBF1    3'  CGGCGGCCATGATGGTGCTGA  96076         C  CGAA  _
                                TTAGCACCA CA    GTC TCG
                                ||||||||| ||    ||| |||
                                AGTCGTGGT GT    CGG GGC
                                      A  AC__   C
GAM103  AKT3      3'  GTCGAGACTTCACGGGC     19609     A  ACCAC
                                GC CC     GAAGTCTCGAC
                                || ||     ||||||||||
                                CG GG     CTTCAGAGCTG
                                 _  CA___
GAM103  MGC10765  3'  CGGGCGTGGTGGTGCT      44559           AAGT
                                AGCACCACCACG    CTCG
                                ||||||||||||    ||||
                                TCGTGGTGGTGC    GGGC
                                                ____
GAM103  ZIN       3'  GAGCCTGGTGGTGCTAA     26393           CGAA T
                                TTAGCACCACCA    G CTC
                                ||||||||||||    | |||
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                                AATCGTGGTGGT   C GAG
                                      C___ _
GAM103  ZNF334   5' CGAGACTTGGACCTGGTGC   36638      ___  CGA
                                GCACCA  CCA  AGTCTCG
                                ||||||  |||  |||||||
                                CGTGGT  GGT  TCAGAGC
                                   CCA  ___
GAM103  LOC149837 3' CGAGTGTGGTGGGGGTGCTAA 85895       A   GAAGT
                                TTAGCACC CCAC    CTCG
                                |||||||| ||||    ||||
                                AATCGTGG GGTG    GAGC
                                     G   GTGT_
GAM104  SCAMP1   3' GCTAAATAAATATTCTCC   18013    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM104  SCAMP1   3' GCTAAATAAATATTCTCC   54501    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM104  NX-17    3' TGAATATCAGCCCCTAATA   40706       ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                     CGAC
GAM104  LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
            TA                   TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM105  ALDH1A3  3' TTTTCTTTTCCTCTTTGGGA  7338        AT   T
                                TTCCAAAGA  GGGA AGAAAA
                                |||||||||  |||| ||||||
                                AGGGTTTCT  CCTT TCTTTT
                                     __   T
GAM105  ATP6V0E  3' TTTCTGCCATCTTTTGGAA   15462      GA   GA
                                TTCCAAA  ATGG  TAGAAA
                                |||||||  ||||  ||||||
                                AAGGTTT  TACC  GTCTTT
                                   TC   __
GAM105  CHD2     3' CTCTCTTCTTCTTTGGAG    8866         TG   T
                                TTCCAAAGAA  GGA AG
                                ||||||||||  ||| ||
                                GAGGTTTCTT  TCT TC
                                      CT   C
GAM105  CLASP2   3' TTCTCAAACACATCCTTTGGAA 65205       A   GGAT__
                                TTCCAAAG ATG     AGAA
                                |||||||| |||     ||||
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                                AAGGTTTC TAC     TCTT
                                    C   ACAAAC
GAM105  DISC1    3'  TTTTCCATGTCATTCTTGGGAA 38522      A       G  A
                                TTCC AAGAATGG AT GAAAA
                                |||| |||||||| || |||||
                                AAGG TTCTTACT TA CTTTT
                                  G       G  C
GAM105  EIF4E    3'  TTTTGTGCATTCTTTGG     10507          GG
                                CCAAAGAATG  ATAGAA
                                ||||||||||  ||||||
                                GGTTTCTTAC  TGTTTT
                                      G_
GAM105  FLRT2    3'  CTGTTCCACTTTTGAA      25997     C    AA
                                TTC AAAG  TGGGATAG
                                ||| ||||  ||||||||
                                AAG TTTC  ACCTTGTC
                                  T   __
GAM105  GALNT7   3'  TTTTCTACTGTAGGCTGCTTTG 34282         AATG____  A
            GAA                    TTCCAAAG       GG TAGAAAA
                                ||||||||       || |||||||
                                AAGGTTTC       TC ATCTTTT
                                    GTCGGATG  _
GAM105  GRM7     3'  CTGTTCCATTCCATGGAA    7786       AA
                                TTCCA  GAATGGGATAG
                                |||||  ||||||||||
                                AAGGT  CTTACCTTGTC
                                   AC
GAM105  ICA1     3'  TTCTGTCCCCCTTGGAG     42513       A AAT
                                TTCCAA G   GGGATAGAA
                                |||||| |   |||||||||
                                GAGGTT C   CCCTGTCTT
                                   _ C__
GAM105  KIAA0857 3'  TCTGGATTCCCTTTGGAG    67257        AAT    __
                                TTCCAAAG   GGGAT  AGA
                                ||||||||   |||||  |||
                                GAGGTTTC   CCTTA  TCT
                                    ___    GG
GAM105  KPNA1    3'  TCTATTGGCGCCATTCTTCAGA 81133    CA      ____
                                TC  AAGAATGG   GATAGA
                                ||  ||||||||   ||||||
                                AG  TTCTTACC   TTATCT
                                  AC       GCGG
GAM105  LAMC1    3'  TTCTAGAGTTCTTTGGA     11274          GGGA
                                TCCAAAGAAT   TAGAA
                                ||||||||||   |||||
                                AGGTTTCTTG   ATCTT
                                      AG__
GAM105  MAP4     3'  TCTGTCCCATTCCCTGGGA   11451       AA
                                TTCCA  GAATGGGATAGA
                                |||||  ||||||||||||
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                                AGGGT CTTACCCTGTCT
                                   CC
GAM105  MAP4    3' TCTGTCCCATTCCCTGGGA  48800     AA
                                TTCCA GAATGGGATAGA
                                ||||| ||||||||||||
                                AGGGT CTTACCCTGTCT
                                   CC
GAM105  MLLT2   3' TTTTGTGTCATTCTATTGGAA 21035     _    G
                                TTCCAA AGAATGG ATAGAA
                                |||||| ||||||| ||||||
                                AAGGTT TCTTACT TGTTTT
                                   A     G
GAM105  PBX1    3' TCTTCTCTTCTTTGGGA    11976       T  T
                                TTCCAAAGAA GGGA AGA
                                |||||||||| |||| |||
                                AGGGTTTCTT CTCT TCT
                                      _  _
GAM105  PCDH11X 3' TTCCAACCATGCTTTGGAA  53139      A  GATA
                                TTCCAAAG ATGG   GAA
                                |||||||| ||||   |||
                                AAGGTTTC TACC   CTT
                                    G   AAC_
GAM105  PCDH11X 3' TTCTTTTATATTTTTTGGAA 53140       G  T
                                TTCCAAAGAATG GA AGAA
                                |||||||||||| || ||||
                                AAGGTTTTTTAT TT TCTT
                                      A  T
GAM105  PCDH11X 3' TTCCAACCATGCTTTGGAA  53146      A  GATA
                                TTCCAAAG ATGG   GAA
                                |||||||| ||||   |||
                                AAGGTTTC TACC   CTT
                                    G   AAC_
GAM105  PCDH11X 3' TTCTTTTATATTTTTTGGAA 53147       G  T
                                TTCCAAAGAATG GA AGAA
                                |||||||||||| || ||||
                                AAGGTTTTTTAT TT TCTT
                                      A  T
GAM105  PCDH11Y 3' TTCTTTTATATTTTTTGGAA 53191       G  T
                                TTCCAAAGAATG GA AGAA
                                |||||||||||| || ||||
                                AAGGTTTTTTAT TT TCTT
                                      A  T
GAM105  PLAC1   5' TTCTTCCCTTTGGAA     41721      GAAT  T
                                TTCCAAA   GGGA AGAA
                                |||||||   |||| ||||
                                AAGGTTT   CCCT TCTT
                                     ____  _
GAM105  PPP1R2  3' TTTTCTACAAACTATTTTTTG 21789       GA__
                                CAAAGAATGG   TAGAAAA
                                |||||||||   |||||||
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                                GTTTTTTATC   ATCTTTT
                                     AAAC
GAM105  PXF     3'  TCTGTCTCTCTAGGAA     12659     AA  AT
                                TTCC  AGA  GGGATAGA
                                ||||  |||  ||||||||
                                AAGG  TCT  CTCTGTCT
                                  A_  __
GAM105  REG1A   3'  CTACCCCAGTCTTTGGAA   90265       A   A
                                TTCCAAAGA TGGG TAG
                                ||||||||| |||| |||
                                AAGGTTTCT ACCC ATC
                                     G   C
GAM105  STARD5  3'  CTGTGTTCACTCTTTGGAA  48317       A   _
                                TTCCAAAGA TGGG ATAG
                                ||||||||| |||| ||||
                                AAGGTTTCT ACTT TGTC
                                     C   G
GAM105  SULT1C1  3'  TTCAATGCCACCCTTTTGGAA 8325       AA_  G  A
                                TTCCAAAG   TGG AT GAA
                                ||||||||   ||| || |||
                                AAGGTTTT   ACC TA CTT
                                     CCC   G  A
GAM105  TBXAS1   5'  CTGTCTCATCTGGAA      8374      AA  A
                                TTCCA  GA TGGGATAG
                                |||||  || ||||||||
                                AAGGT  CT ACTCTGTC
                                  __ _
GAM105  TBXAS1   5'  CTGTCTCATCTGGAA      49120     AA  A
                                TTCCA  GA TGGGATAG
                                |||||  || ||||||||
                                AAGGT  CT ACTCTGTC
                                  __ _
GAM105  THBS1    3'  TTTTCTAATTCTCTCTTTTGGA 13751       AAT   __
          A                      TTCCAAAG   GGGA  TAGAAAA
                                ||||||||   ||||  |||||||
                                AAGGTTTT   CTCT  ATCTTTT
                                     CT_   TA
GAM105  TNFSF8   3'  TTCTGTCTCTTGGAA      8803      AGAAT
                                TTCCAA    GGGATAGAA
                                ||||||    |||||||||
                                AAGGTT    CTCTGTCTT
                                  _____
GAM105  UMPK     3'  TTTTCTTTTTGTACTTTGGAA  25936       A  GG  T
                                TTCCAAAG AT  GA AGAAAA
                                |||||||| ||  || ||||||
                                AAGGTTTC TG  TT TCTTTT
                                     A  TT  _
GAM105  UNC5C    3'  TTCTGGTGCCCTTTGGGA    14950       AAT  G  _
                                TTCCAAAG   GG AT AGAA
                                ||||||||   || || ||||
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                                AGGGTTTC  CC TG TCTT
                                   ___  G  G
GAM105  WNT5A    3'  TTTTCTTAGTTCATTCTGCAGA 14125    CAA     AT_
            A                    TTC  AGAATGGG  AGAAAA
                                 |||  ||||||||  ||||||
                                 AAG  TCTTACTT  TCTTTT
                                   ACG      GAT
GAM105  XRCC4    3'  TTTTCTATTCATTTCTTT   14149     TG
                                 AAAGAA GGATAGAAAA
                                 ||||||  ||||||||||
                                 TTTCTT  CTTATCTTTT
                                    TA
GAM105  XRCC4    3'  TTTTCTATTCATTTCTTT   42600     TG
                                 AAAGAA GGATAGAAAA
                                 ||||||  ||||||||||
                                 TTTCTT  CTTATCTTTT
                                    TA
GAM105  XRCC4    3'  TTTTCTATTCATTTCTTT   42879     TG
                                 AAAGAA GGATAGAAAA
                                 ||||||  ||||||||||
                                 TTTCTT  CTTATCTTTT
                                    TA
GAM105  ZNF200   5'  TTTTCTATCTCTCCCGGAG   14368    AAA  AT
                                 TTCC   GA  GGGATAGAAAA
                                 ||||   ||  ||||||||||||
                                 GAGG   CT  CTCTATCTTTT
                                   CC_  __
GAM105  AQP10    3'  TCTATTCCCTTCTTCCGAA   55398    CA    T
                                 TTC  AAGAA GGGATAGA
                                 |||  ||||| ||||||||
                                 AAG  TTCTT CCTTATCT
                                   CC    C
GAM105  ATP5I    3'  CTGCGACCCACTCTTTGGA   24016      A   A__
                                 TCCAAAGA TGGG   TAG
                                 ||||||||  ||||   |||
                                 AGGTTTCT ACCC   GTC
                                      C    AGC
GAM105  BOP      5'  TTCTTCCCTTTGGAA      86232      GAAT   T
                                 TTCCAAA    GGGA AGAA
                                 |||||||    |||| ||||
                                 AAGGTTT    CCCT TCTT
                                      ____   _
GAM105  C11orf15 3'  TCTGTCCTCTTTGGAA     40596       ATG
                                 TTCCAAAGA   GGATAGA
                                 |||||||||   |||||||
                                 AAGGTTTCT   CCTGTCT
                                       ___
GAM105  C20orf108 3' TTCTATCTCAAACTTCAGA   55885    CA   AA
                                 TC  AAG  TGGGATAGAA
                                 ||  |||  ||||||||||
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                                AG  TTC  ACTCTATCTT
                                 AC   AA
GAM105  C20orf162 5'  CTGTGGGCCCATCTTTGGAA  55500        A   ___
                                TTCCAAAGA TGGG   ATAG
                                ||||||||| ||||   ||||
                                AAGGTTTCT ACCC   TGTC
                                      _   GGG
GAM105  C20orf46  5'  TTTTCTGTCTATTCACTGGAA 37738      AA     G
                                TTCCA  GAATGG ATAGAAAA
                                |||||  |||||| ||||||||
                                AAGGT  CTTATC TGTCTTTT
                                   CA     _
GAM105  CRNKL1    5'  CTTTCCGACACTCTTTGGGA  34096        A __   T
                                TTCCAAAGA TG  GGA AG
                                ||||||||| ||  ||| ||
                                AGGGTTTCT AC  CCT TC
                                      C  AG   T
GAM105  DDX36     3'  TCATGCCCACTCTTTGGGA   40866        A   ATA
                                TTCCAAAGA TGGG   GA
                                ||||||||| ||||   ||
                                AGGGTTTCT ACCC   CT
                                      C    GTA
GAM105  dJ383J4.3 3'  TTCCCCACCATGCCTTTGGAG  67500        A_   GATA
                                TTCCAAAG  ATGG   GAA
                                ||||||||  ||||   |||
                                GAGGTTTC  TACC   CTT
                                     CG    ACCC
GAM105  DKFZP761F241 3'  CTGGCCACATCTTTGGAA    49581        A _ A
                                TTCCAAAGA TG GG TAG
                                ||||||||| || || |||
                                AAGGTTTCT AC CC GTC
                                      _ A  G
GAM105  FLJ11506  3'  TCTGGGCATTCTTTTGAA    45436     C      GGA
                                TTC AAAGAATG   TAGA
                                ||| ||||||||   ||||
                                AAG TTTCTTAC   GTCT
                                  T      GG_
GAM105  FLJ12526  3'  TTTTCTGTTCCTCCCTGGAG   45931      AA  AT
                                TTCCA  GA  GGGATAGAAAA
                                |||||  ||  ||||||||||||
                                GAGGT  CT  CCTTGTCTTTT
                                   CC  __
GAM105  FLJ13166  5'  TTCAATATCCCTTTGGAA    47191       GAAT    __
                                TTCCAAA   GGGATA  GAA
                                |||||||   ||||||  |||
                                AAGGTTT   CCCTAT  CTT
                                     ____     AA
GAM105  FLJ13373  5'  TTCTGAAAACATCCTTTGGGA  47203        A  GGA_
                                TTCCAAAG ATG   TAGAA
                                |||||||| |||   |||||
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                                AGGGTTTC TAC    GTCTT
                                    C   AAAA
GAM105  FLJ20174  3'  TTCCATCTGCAGCTTTGGGA   35196        AATG    A
                                TTCCAAAG    GGAT GAA
                                ||||||||    |||| |||
                                AGGGTTTC    TCTA CTT
                                    GACG    C
GAM105  FLJ20273  3'  CTTTCCATCATTCTTTTGAA   39249     C      __   T
                                TTC AAAGAATG  GGA AG
                                ||| ||||||||  ||| ||
                                AAG TTTCTTAC  CCT TC
                                  T       TA   T
GAM105  FLJ21272  5'  TTTTCAATTTCATTCTTAGAA  47395     CA      GG  A
                                TTC  AAGAATG  AT GAAAA
                                |||  |||||||  || |||||
                                AAG  TTCTTAC  TA CTTTT
                                  A_      TT  A
GAM105  FLJ21865  3'  TTTCTGTCTCATTTGGAA    43116       AGA
                                TTCCAA   ATGGGATAGAAA
                                ||||||   ||||||||||||
                                AAGGTT   TACTCTGTCTTT
                                    ___
GAM105  FLJ22215  3'  CTACCCTGTTCTCCGGAG    98638      AA       A
                                TTCC  AGAATGGG TAG
                                ||||  |||||||| |||
                                GAGG  TCTTGTCC ATC
                                  CC       C
GAM105  FLJ22457  5'  TTCTATTCCCTCTCTGGAA   46612       A   AT
                                TTCCA AGA  GGGATAGAA
                                ||||| |||  |||||||||
                                AAGGT TCT  CCTTATCTT
                                  C   C_
GAM105  FLJ30567  3'  TTTTCTATATCCTTTGGAA   59480         AAT GG
                                TTCCAAAG   G  ATAGAAAA
                                ||||||||   |  ||||||||
                                AAGGTTTC   C  TATCTTTT
                                    ___ TA
GAM105  FPGT      3'  TTTTCTAAGCATACCTTTGGAA 15183        A_   GGA
                                TTCCAAAG  ATG   TAGAAAA
                                ||||||||  |||   |||||||
                                AAGGTTTC  TAC   ATCTTTT
                                    CA   GA_
GAM105  GP5       3'  TTCTATTCTTGGTTCTTTG    16885        __
                                CAAAGAAT  GGGATAGAA
                                ||||||||  |||||||||
                                GTTTCTTG  TCTTATCTT
                                    GT
GAM105  HARS2     3'  TTTCATGCCCATTTTTCAGAA  55871     CA       ATA
                                TTC  AAGAATGGG   GAAA
                                |||  |||||||||   ||||
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                                AAG  TTTTTACCC   CTTT
                                  AC        GTA
GAM105  HCA4     3'  CTTTCCAGTTCTTTGAGA    78040    _      G   T
                                TC CAAAGAAT GGA AG
                                || |||||||| ||| ||
                                AG GTTTCTTG CCT TC
                                 A       A   T
GAM105  HEY2     3'  TTGTCACCCTTTGGGA      25324         AAT  _
                                TTCCAAAG   GG GATAG
                                ||||||||   || |||||
                                AGGGTTTC   CC CTGTT
                                     ___  A
GAM105  ICK      3'  TTTATTCCATTTTTGAA     30601     CA
                                TTC  AAGAATGGGATAGA
                                |||  ||||||||||||||
                                AAG  TTTTTACCTTATTT
                                  __
GAM105  IMP-2    3'  TCCATCTCCATTCTTTTGAA  22611     C       _  A
                                TTC AAAGAATGG GAT GA
                                ||| ||||||||| ||| ||
                                AAG TTTCTTACC CTA CT
                                  T       T  C
GAM105  K6HF     3'  TCTGTTCCCTCCCTGGAA    17439      AA  AT
                                TTCCA  GA  GGGATAGA
                                |||||  ||  ||||||||
                                AAGGT  CT  CCTTGTCT
                                   CC  C_
GAM105  KIAA0256 3'  TCTATCTCCAGCTGTGGAA   65052      A  AAT
                                TTCCA AG   GGGATAGA
                                ||||| ||   ||||||||
                                AAGGT TC   CTCTATCT
                                   G  GAC
GAM105  KIAA0355 3'  TTTTCATATTTCATCTTTG   28713      A  GG  _
                                CAAAGA TG  ATA GAAAA
                                |||||| ||  ||| |||||
                                GTTTCT AC  TAT CTTTT
                                   _ TT   A
GAM105  KIAA0884 3'  TTTTCTAAGTCCTTTGGAA   70763       AAT  GA
                                TTCCAAAG   GG  TAGAAAA
                                ||||||||   ||  |||||||
                                AAGGTTTC   CT  ATCTTTT
                                     ___  GA
GAM105  KIAA0978 3'  TCTTCCCTCTGCTGGAA     70998      A_  AT   T
                                TTCCA  AGA  GGGA AGA
                                |||||  |||  |||| |||
                                AAGGT  TCT  CCCT TCT
                                   CG  __   _
GAM105  KIAA1136 3'  TTTCTATTGCACTTCAGGA   92962     AAA  _  G
                                TCC   GAA TG GATAGAAA
                                |||   ||| || ||||||||
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                                AGG   CTT AC TTATCTTT
                                  A__   C  G
GAM105  KIAA1456 3'  TCTAGAACGGTTCTTTGGAG   67570          _ GGA
                                TTCCAAAGAAT G   TAGA
                                ||||||||||| |   ||||
                                GAGGTTTCTTG C   ATCT
                                      G AAG
GAM105  KIAA1508 5'  TTTTCTTAGACTCATTCTTTG  62569          AT__
                                CAAAGAATGGG    AGAAAA
                                ||||||||||    ||||||
                                GTTTCTTACTC    TCTTTT
                                      AGAT
GAM105  KIAA1679 3'  TTCTCTTCCTGTTTGGAA    70719        GAAT    T
                                TTCCAAA    GGGA AGAA
                                |||||||    |||| ||||
                                AAGGTTT    CCTT TCTT
                                    GT__    C
GAM105  KIAA1906 3'  TTTTCCATTTCATTCTCTG    73578    A     GG  A
                                CA AGAATG  AT GAAAA
                                || ||||||  || |||||
                                GT TCTTAC  TA CTTTT
                                 C     TT  C
GAM105  KREMEN   3'  TTTGTCCTCTCGTGGAA     50241      AA  AT
                                TTCCA  GA  GGGATAGA
                                |||||  ||  ||||||||
                                AAGGT  CT  TCCTGTTT
                                   G_  C_
GAM105  LAP1B    3'  TTTTCTTTTGTTTTTTGGAA   65199          GG AT
                                TTCCAAAGAAT  G  AGAAAA
                                ||||||||||  |  ||||||
                                AAGGTTTTTTG  T  TCTTTT
                                      TT __
GAM105  LMOD1    3'  TTTCTGAATTTCATTCTCTTG  25110    _     GG  __
                                CAA AGAATG  AT  AGAAA
                                ||| ||||||  ||  |||||
                                GTT TCTTAC  TA  TCTTT
                                  C     TT  AG
GAM105  MGC14421 5'  TCTATCAGAGGTCTCTTTGGAA 52963         ATGG___
                                TTCCAAAGA      GATAGA
                                |||||||||      ||||||
                                AAGGTTTCT      CTATCT
                                     CTGGAGA
GAM105  MGC21688 3'  TCTTCTCTTCTCTGGGA     58918      A   T   T
                                TTCCA AGAA GGGA AGA
                                ||||| |||| |||| |||
                                AGGGT TCTT CTCT TCT
                                   C   _   _
GAM105  MGC4677  5'  TCTGTCTGTCTTTGGAA     54617         ATG
                                TTCCAAAGA   GGATAGA
                                |||||||||   |||||||
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                                AAGGTTTCT   TCTGTCT
                                    G__
GAM105  MOT8    3'  TCCCAGAGTTTTCTTTGGAG  38731        _____
                                TTCCAAAGAA    TGGGA
                                ||||||||||    |||||
                                GAGGTTTCTT    ACCCT
                                    TTGAG
GAM105  MRVI1   3'  TCCCATTCTTTCCTTTGGAA  56098      _____
                                TTCCAA    AGAATGGGA
                                ||||||    |||||||||
                                AAGGTT    TCTTACCCT
                                   TCCTT
GAM105  MRVI1   3'  TCCCATTCTTTCCTTTGGAA  21381      _____
                                TTCCAA    AGAATGGGA
                                ||||||    |||||||||
                                AAGGTT    TCTTACCCT
                                   TCCTT
GAM105  NXPH3   3'  TCCCAAACCTTAATTCTTTGGA 66347        _________
                A                TTCCAAAGAA       TGGGA
                                ||||||||||       |||||
                                AAGGTTTCTT       ACCCT
                                    AATTCCAA
GAM105  PCBP4   5'  TCTCATCACTCTTTGGAG   40281        ___
                                TTCCAAAGA   ATGGGA
                                |||||||||   ||||||
                                GAGGTTTCT   TACTCT
                                    CAC
GAM105  pcnp    3'  TCTTCAAACATTTTTTGGAA  40144          GGAT_
                                TTCCAAAGAATG    AGA
                                ||||||||||||    |||
                                AAGGTTTTTTAC    TCT
                                    AAACT
GAM105  PMAIP1  3'  TCCCAGATTATCATTCTTTGGG 41213        _________
                A                TTCCAAAGAA       TGGGA
                                ||||||||||       |||||
                                AGGGTTTCTT       ACCCT
                                    ACTATTAG
GAM105  RAB1B   3'  CTACACACCTTTCTTTGGAA  49116         T  GA__
                                TTCCAAAGAA GG   TAG
                                |||||||||| ||   |||
                                AAGGTTTCTT CC   ATC
                                    T  ACAC
GAM105  SEMA3E  5'  TCTGAAGACTCACTCTTTGGAA 25813        A   A___
                                TTCCAAAGA TGGG   TAGA
                                ||||||||| ||||   ||||
                                AAGGTTTCT ACTC   GTCT
                                    C   AGAA
GAM105  ShrmL   5'  TCTGTCTCTTCGGGA      40852     AAA  T
                                TTCC  GAA GGGATAGA
                                ||||  ||| ||||||||
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                                AGGG   CTT CTCTGTCT
                                  ___  _
GAM105  SLC38A4  3'  CTTTCTTTTTCTATTGGAA   36341      _   TG   T
                                TTCCAA AGAA  GGA AG
                                |||||| ||||  ||| ||
                                AAGGTT TCTT  TCT TC
                                   A   TT   T
GAM105  TOMM70A  3'  TTTCAAAGTCAATCTTTGGAA 29741        A   GATA
                                TTCCAAAGA TGG   GAAA
                                ||||||||| |||   ||||
                                AAGGTTTCT ACT   CTTT
                                     A  GAAA
GAM105  WNT8A    3'  TTCTATTACTCCCTTTGGAA  50034       AATGG
                                TTCCAAAG    GATAGAA
                                ||||||||    |||||||
                                AAGGTTTC    TTATCTT
                                     CCTCA
GAM105  WNT8A    3'  TTCTATTACTCCCTTTGGAA  55258       AATGG
                                TTCCAAAG    GATAGAA
                                ||||||||    |||||||
                                AAGGTTTC    TTATCTT
                                     CCTCA
GAM105  WSB1     3'  TCTGTGCTATTTTTTGGAA   56982         G
                                TTCCAAAGAATGG ATAGA
                                |||||||||||| |||||
                                AAGGTTTTTTATC TGTCT
                                       G
GAM105  LOC112885 3'  TTTCTTGTCTCCTTTGGAA   57344       AAT    _
                                TTCCAAAG  GGGATA GAAA
                                ||||||||  |||||| ||||
                                AAGGTTTC  CTCTGT CTTT
                                     ___     T
GAM105  LOC120103 3'  TTTTGTCCCATTTCTGAA    74460    CAAA
                                TTC   GAATGGGATAGAA
                                |||   ||||||||||||
                                AAG   TTTACCCTGTTTT
                                  TC__
GAM105  LOC122553 3'  TTCTGACATTCTTTGGA     74596         GGA
                                TCCAAAGAATG  TAGAA
                                ||||||||||  |||||
                                AGGTTTCTTAC  GTCTT
                                      A__
GAM105  LOC125488 5'  CTTTCCACACTGCTTTGGAA  74873       AA_ _  T
                                TTCCAAAG  TG GGA AG
                                ||||||||  || ||| ||
                                AAGGTTTC  AC CCT TC
                                     GTC  A   T
GAM105  LOC134957 3'  TTTTATTACATTCTTTAGGA  58343    _     GG
                                TCC AAAGAATG  ATAGAA
                                ||| ||||||||  ||||||
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                                AGG TTTCTTAC  TATTTT
                                  A       AT
GAM105  LOC138099 5'  TCTATAACCCTCTTTGGA    76477        AT  __
                                TCCAAAGA  GGG  ATAGA
                                ||||||||  |||  |||||
                                AGGTTTCT  CCC  TATCT
                                    __  AA
GAM105  LOC138617 5'  CTGTCCTATCTGGAA      76485      AA  A
                                TTCCA  GA TGGGATAG
                                |||||  || ||||||||
                                AAGGT  CT ATCCTGTC
                                  __ _
GAM105  LOC142820 3'  TCCTAAATGCAGTTCTTTGGAA 76918          _______
                                TTCCAAAGAAT      GGGA
                                ||||||||||       ||||
                                AAGGTTTCTTG      TCCT
                                     ACGTAAA
GAM105  LOC144317 3'  TCTGATGGCAATCTTTGGAA   77299         A  GGA_
                                TTCCAAAGA TG    TAGA
                                |||||||| ||    ||||
                                AAGGTTTCT AC    GTCT
                                    A  GGTA
GAM105  LOC145453 5'  TTCTTTTTTTTCTTTGGAG    77676         TG   T
                                TTCCAAAGAA  GGA AGAA
                                |||||||||  ||| ||||
                                GAGGTTTCTT  TTT TCTT
                                     TT  _
GAM105  LOC146243 3'  CTAGCCCCATTCTCTGGAG    84619      A      A_
                                TTCCA AGAATGGG  TAG
                                ||||| ||||||||  |||
                                GAGGT TCTTACCC  ATC
                                   C       CG
GAM105  LOC146506 3'  TCTTTTTTTTTCTTTGGAA    78495         TG   T
                                TTCCAAAGAA  GGA AGA
                                |||||||||  ||| |||
                                AAGGTTTCTT  TTT TCT
                                     TT   T
GAM105  LOC149372 5'  TCTGTTCTCCTTGGGAA     80106     A  AAT
                                TTCC AAG   GGGATAGA
                                |||| |||   ||||||||
                                AAGG TTC   TCTTGTCT
                                  G   C__
GAM105  LOC149372 3'  TTTCTGTATTACCTTTTGGAA  80109        AA   G
                                TTCCAAAG  TGG ATAGAAA
                                ||||||||  ||| |||||||
                                AAGGTTTT  ATT TGTCTTT
                                    CC   A
GAM105  LOC153910 3'  TCAATCCCATTCTTCAGAA    81912     CA         A
                                TTC  AAGAATGGGAT GA
                                |||  |||||||||| ||
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                                AAG  TTCTTACCCTA CT
                                  AC         A
GAM105  LOC154562 3'  TCTAAGCTCTACTCTTTGGAG  81998         AT_   A_
                                TTCCAAAGA   GGG  TAGA
                                |||||||||   |||  ||||
                                GAGGTTTCT   CTC  ATCT
                                     CAT   GA
GAM105  LOC155038 3'  CTGTCTCCTTTGGGA       82183         AAT
                                TTCCAAAG   GGGATAG
                                ||||||||   |||||||
                                AGGGTTTC   CTCTGTC
                                    ___
GAM105  LOC157638 3'  CTATCCTGGGCTTGGAA     82421        A AA
                                TTCCAA G  TGGGATAG
                                ||||||  |  ||||||||
                                AAGGTT C  GTCCTATC
                                   _ GG
GAM105  LOC157660 3'  TTTCTAGGTCTTTGGAG     87809         ATGGGA
                                TTCCAAAGA     TAGAAA
                                |||||||||     ||||||
                                GAGGTTTCT     ATCTTT
                                     GG____
GAM105  LOC203350 3'  CTGTGAGCCCATTCTCTGGAG  92238       A      ___
                                TTCCA AGAATGGG   ATAG
                                |||||  ||||||||   ||||
                                GAGGT TCTTACCC   TGTC
                                   C       GAG
GAM105  LOC205327 3'  TTTTCTATCATTTTGGAA    91075        GAATGG
                                TTCCAAA     GATAGAAAA
                                |||||||     |||||||||
                                AAGGTTT     CTATCTTTT
                                    TA____
GAM105  LOC207085 5'  TCTACACCATCTCTTTGGAA   92396         _   GA
                                TTCCAAAGA ATGG  TAGA
                                |||||||||  ||||  ||||
                                AAGGTTTCT TACC  ATCT
                                     C    AC
GAM105  LOC220549 5'  TTTTGGAACATCTTTGGAA    94514         A  GGA
                                TTCCAAAGA TG   TAGAA
                                |||||||||  ||   |||||
                                AAGGTTTCT AC   GTTTT
                                     _  AAG
GAM105  LOC221261 5'  TTCATACCCCATTCTTCTGAA  95250     CA        A  _
                                TTC  AAGAATGGG TA GAA
                                |||  |||||||||  ||  |||
                                AAG  TTCTTACCC AT CTT
                                  TC        C  A
GAM105  LOC253992 3'  CTTTCCCTCTTTGGGA      98424         AT    T
                                TTCCAAAGA  GGGA AG
                                |||||||||  ||||  ||
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                                AGGGTTTCT  CCCT TC
                                    __   T
GAM105  LOC90550  3'  TCTTCCTCCTTTGGGA      73482        AAT   T
                                TTCCAAAG   GGGA AGA
                                ||||||||   |||| |||
                                AGGGTTTC   TCCT TCT
                                    C__   _
GAM105  LOC91286  5'  TTTTAAACCATCTTTGGAA   66066        A   GA
                                TTCCAAAGA TGG  TAGAA
                                |||||||||  |||  |||||
                                AAGGTTTCT ACC  ATTTT
                                    _  AA
GAM105  LOC91445  3'  TTTTATCACCTTCTGGAA    61177      AA   T  _
                                TTCCA  GAA GG GATAGAA
                                |||||  |||  ||  |||||||
                                AAGGT  CTT CC CTATTTT
                                   __  _  A
GAM105  LOC91750  3'  CTTTCTCATTTCTGGAA     67652      AA       T
                                TTCCA  GAATGGGA AG
                                |||||  ||||||||  ||
                                AAGGT  TTTACTCT TC
                                   C_       T
GAM106  CMRF35    3'  CTTTGTGAGCCTCCTTCAG    22907        C  _  _
                                TTGAAGGAG GC CA AAAG
                                |||||||||  ||  ||  ||||
                                GACTTCCTC CG GT TTTC
                                    _  A  G
GAM106  GYG2      3'  CTTCTGGGCTTTCTTCAG     15362        _  G   A
                                TTGAAGGA GC CCA AAG
                                ||||||||  ||  |||  |||
                                GACTTCTT CG GGT TTC
                                    T  _   C
GAM106  HADHA     3'  AGCTTCTGGTTTAAACGCCTCC 5733         _  _______   A   ___
            TTCAA                 TTGAAGGAG CG     CCA AAG   CT
                                |||||||||  ||     |||  |||   ||
                                AACTTCCTC GC     GGT TTC   GA
                                    C  AAATTT   C   ___
GAM106  HTR4      3'  CTTTTGGCTTTGTTTCAA     7882        G  C
                                TTGAAG AG GCCAAAAG
                                ||||||  ||  ||||||||
                                AACTTT TT CGGTTTTC
                                   G  T
GAM106  ITGA1     3'  CTTTTGGAATTTCCTTCA     64273        CG_
                                TGAAGGAG   CCAAAAG
                                ||||||||   |||||||
                                ACTTCCTT   GGTTTTC
                                    TAA
GAM106  LDHC      5'  CTTCTGTGCCTTCCTTCAA    11295        C  _  A
                                TTGAAGGAG GC CA AAG
                                |||||||||  ||  ||  |||
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                                AACTTCCTT CG GT TTC
                                     C  T  C
GAM106  LDHC     5'  CTTCTGTGCCTTCCTTCAA   34341        C  _  A
                                TTGAAGGAG GC CA AAG
                                ||||||||| || || |||
                                AACTTCCTT CG GT TTC
                                     C  T  C
GAM106  MAGEC1   3'  CTTTTGGGTATTTTTCAA    19596        _  G
                                TTGAAGGA GC CCAAAAG
                                |||||||| || |||||||
                                AACTTTTT TG GGTTTTC
                                     A  _
GAM106  MCM5     3'  CTTTTGGCATCCGTTAA     60632      A   GC
                                TTGA GGA  GCCAAAAG
                                |||| |||  ||||||||
                                AATT CCT  CGGTTTTC
                                  G   A_
GAM106  MUC3B    3'  CTTTTGACCCCGTTCCTTCA  95923         C___
                                TGAAGGAGCG    CAAAAG
                                ||||||||||    ||||||
                                ACTTCCTTGC    GTTTTC
                                     CCCA
GAM106  P23      3'  CTTCTGGTGTTATCCTTCAG   22753         __     A
                                TTGAAGGA  GCGCCA AAG
                                ||||||||  |||||| |||
                                GACTTCCT  TGTGGT TTC
                                     AT     C
GAM106  PDGFRA   3'  CTTTTGGCCTCCTGCAA     21695     A    C
                                TTG AGGAG GCCAAAAG
                                ||| ||||| ||||||||
                                AAC TCCTC CGGTTTTC
                                  G    _
GAM106  RNF26    3'  CTTTTCCTGCCTCCTTCA     50136        C  C__
                                TGAAGGAG GC   AAAAG
                                |||||||| ||   |||||
                                ACTTCCTC CG   TTTTC
                                     _  TCC
GAM106  ROBO1    5'  TTTTTGGCCCTCCCTCAG    56902      A   C
                                TTGA GGAG GCCAAAAG
                                |||| |||| ||||||||
                                GACT CCTC CGGTTTTT
                                  C   C
GAM106  TRIM8    3'  CTTTTGGCACCTTCAG      48853        AGC
                                TTGAAGG   GCCAAAAG
                                |||||||   ||||||||
                                GACTTCC   CGGTTTTC
                                     A__
GAM106  TSG      3'  CTTTTCTGCTCTTTCAA     40604          CC
                                TTGAAGGAGCG  AAAAG
                                ||||||||||  |||||
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                                AACTTTCTCGT  TTTTC
                                      C_
GAM106  BS69     3'  CTTTTGTTAATGCTCCTCCGA  22779     A      C___
                                TTG AGGAGCG    CAAAAG
                                ||| |||||||    ||||||
                                AGC TCCTCGT    GTTTTC
                                  C      AATT
GAM106  C1orf25  3'  CTTTTTCTGTTCTTTCAA    72941          CC
                                TTGAAGGAGCG  AAAAG
                                ||||||||||  |||||
                                AACTTTCTTGT  TTTTC
                                      CT
GAM106  DUSP14   3'  CTTCTGGTTCTCCCTCAA    23818     A   C   A
                                TTGA GGAG GCCA AAG
                                |||| |||| |||| |||
                                AACT CCTC TGGT TTC
                                  C   T   C
GAM106  FLJ20060 3'  CTTTTAGCCTTCTTTAA     34931        C  C
                                TTGAAGGAG GC AAAAG
                                |||||||||  || |||||
                                AATTTCTTC CG TTTTC
                                     _  A
GAM106  FLJ20073 3'  TTTTTGGTTTCTTCAA      34965        GC
                                TTGAAGGA  GCCAAAAG
                                ||||||||  ||||||||
                                AACTTCTT  TGGTTTTT
                                     __
GAM106  FLJ20984 3'  CTTTTGGTGACCCTCCAG    45248     A  AG
                                TTG AGG  CGCCAAAAG
                                ||| |||  |||||||||
                                GAC TCC  GTGGTTTTC
                                  C  CA
GAM106  HSPF2    5'  CTTCTGGGTTCCTTCAG     19835        G  A
                                TTGAAGGAGC CCA AAG
                                |||||||||| ||| |||
                                GACTTCCTTG GGT TTC
                                     _  C
GAM106  KIAA0215 3'  CTTTTGGCTACATCTTCAA   29083       AGC_
                                TTGAAGG   GCCAAAAG
                                |||||||   ||||||||
                                AACTTCT   CGGTTTTC
                                    ACAT
GAM106  KIAA0349 3'  CTTTTGGCTTTTTTTCAG    93916        C
                                TTGAAGGAG GCCAAAAG
                                |||||||||  ||||||||
                                GACTTTTTT CGGTTTTC
                                      T
GAM106  KIAA1204 3'  CTTTTTAATGCTCTTTCAA   69739         CC_
                                TTGAAGGAGCG   AAAAG
                                ||||||||||   |||||
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                                AACTTTCTCGT   TTTTC
                                      AAT
GAM106  KIAA1724  3'  CTTTTGTGATCCTTTAA     67614        G   C
                                TTGAAGGA CGC AAAAG
                                |||||||| ||| |||||
                                AATTTCCT GTG TTTTC
                                    A   _
GAM106  KIAA1975  5'  CTTTATGTGTGCCTTCAG     74421        A    CA
                                TTGAAGG GCGC  AAAG
                                ||||||| ||||  ||||
                                GACTTCC TGTG  TTTC
                                   G    TA
GAM106  POFUT1    3'  CTTTTGGCTGCTTTTCAA     70977       G   _
                                TTGAAG AGC GCCAAAAG
                                |||||| ||| ||||||||
                                AACTTT TCG CGGTTTTC
                                   _   T
GAM106  SPTLC2    3'  TTTTTGGTGCTCCCTCAG     18008      A
                                TTGA GGAGCGCCAAAAG
                                |||| ||||||||||||
                                GACT CCTCGTGGTTTTT
                                  C
GAM106  LOC143888 3'  CTTTTGGCTTTCATTAA     77171      A    C
                                TTGA GGAG GCCAAAAG
                                |||| |||| ||||||||
                                AATT CTTT CGGTTTTC
                                  A   _
GAM106  LOC145197 3'  CTTCAGGCTCTCCTTTAA     84233         C   AA
                                TTGAAGGAG GCC  AAG
                                ||||||||| |||  |||
                                AATTTCCTC CGG  TTC
                                     T   AC
GAM106  LOC148530 5'  CTTTTGGCCTGATTCGA     85314       GG  C
                                TTGAA  AG GCCAAAAG
                                |||||  || ||||||||
                                AGCTT  TC CGGTTTTC
                                  AG  _
GAM106  LOC149674 3'  CTTTTGGTCCCTCTCAA     80332      _   AGC
                                TTGA AGG   GCCAAAAG
                                |||| |||   ||||||||
                                AACT TCC   TGGTTTTC
                                  C   C__
GAM106  LOC149705 3'  CTTTGAAGCCTCCTTTAA     85779         C  CA_
                                TTGAAGGAG GC   AAAG
                                ||||||||| ||   ||||
                                AATTTCCTC CG   TTTC
                                     _  AAG
GAM106  LOC152941 3'  CTTTAGGGTTTCTTCAA     81633         G  A
                                TTGAAGGAGC CC AAAG
                                |||||||||| || ||||
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                                AACTTCTTTG GG TTTC
                                      _  A
GAM106  LOC153733 3'  TTTTTGGTTTCCTTCAG     81804          C
                                TTGAAGGAG GCCAAAAG
                                ||||||||| ||||||||
                                GACTTCCTT TGGTTTTT
                                      _
GAM106  LOC154421 3'  CTTCTGACGTGTCCTTCAG    87420         _  C  A
                                TTGAAGGA GCG CA AAG
                                |||||||| ||| || |||
                                GACTTCCT TGC GT TTC
                                     G   A  C
GAM106  LOC158527 5'  CTTTTGGCAGTTCCTCCA    82839    A     _
                                TG AGGAGC GCCAAAAG
                                || |||||| ||||||||
                                AC TCCTTG CGGTTTTC
                                  C     A
GAM106  LOC165283 3'  CTTTCAGTGCTTCTCAA     88546     A      CA
                                TTGA GGAGCGC  AAAG
                                |||| |||||||  ||||
                                AACT CTTCGTG  TTTC
                                   _      AC
GAM106  LOC222001 3'  CTTTTAGCCTTCTTTAA     94497          C  C
                                TTGAAGGAG GC AAAAG
                                ||||||||| || |||||
                                AATTTCTTC CG TTTTC
                                      _  A
GAM106  LOC254734 3'  CTTTTGGTATATTCCTTTAA  96625          C__
                                TTGAAGGAG   GCCAAAAG
                                |||||||||   ||||||||
                                AATTTCCTT   TGGTTTTC
                                     ATA
GAM106  LOC257069 3'  CTTTTGGCGGCCTCTTCA    97304       GA  _
                                TGAAG  GC GCCAAAAG
                                |||||  || ||||||||
                                ACTTC  CG CGGTTTTC
                                   TC  G
GAM107  DDX9     3'  GATCTCTTAAAAATACC     89952       A   C
                                GGTAT TTT AAGAGATT
                                ||||| ||| ||||||||
                                CCATA AAA TTCTCTAG
                                   A  _
GAM107  NCOA3    3'  AATCTCTTAAATACACGTA   22558      GTA    C
                                TACG   TATTT AAGAGATT
                                ||||   ||||| ||||||||
                                ATGC   ATAAA TTCTCTAA
                                  AC_    _
GAM107  VNN1     3'  AGAATCTCTTGACATTAC    17421     TATT
                                GTA    TCAAGAGATTCT
                                |||    ||||||||||||
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                                CAT    AGTTCTCTAAGA
                                  TAC_
GAM107  C20orf21  3'  AATCTCTTGAAAATACTG    35567       A
                                CGGTAT TTTCAAGAGATT
                                |||||| ||||||||||||
                                GTCATA AAAGTTCTCTAA
                                   _
GAM107  FLJ13187  3'  AATCTGAATATACCG       45159         CAAG
                                CGGTATATTT    AGATT
                                ||||||||||    |||||
                                GCCATATAAG    TCTAA
                                     _____
GAM107  FLJ30294  3'  TAGAATCTCTCCAGACACC   58897     ATA   CA
                                GGT   TTT  AGAGATTCTA
                                |||   |||  ||||||||||
                                CCA   AGA  TCTCTAAGAT
                                  C__   CC
GAM107  KIAA0256  3'  AATTTCTAAATATACC      65046         CA
                                GGTATATTT  AGAGATT
                                |||||||||  |||||||
                                CCATATAAA  TCTTTAA
                                     __
GAM107  KIAA1243  3'  TAGGGTTTGAAACATGCC    74029       A     AGA
                                GGTAT TTTCA   GATTCTA
                                ||||| |||||   |||||||
                                CCGTA AAAGT   TTGGGAT
                                   C    ___
GAM107  KIAA1257  3'  AGAACCTCTTGAGAGGCAAC   63387    ATA_       A
                                GT    TTTCAAGAG TTCT
                                ||    |||||||||| ||||
                                CA    AGAGTTCTC AAGA
                                  ACGG        C
GAM108  CYP4F3    3'  CTGTTTTTGTCCTATGAACAAG 8005      C   AT_  TA
            CA                    TGC TTG   GT  GACAAAAACAG
                                |||| |||   ||  ||||||||||||
                                ACG AAC   TA  CTGTTTTTGTC
                                  _   AAG  TC
GAM108  HIP1      5'  CTGCCTCTGTCTAGCAACGCA  19254     CTT A       AAAA
                                TGC   G TGTTAGACA    CAG
                                |||   | |||||||||    |||
                                ACG   C ACGATCTGT    GTC
                                  ____ A        CTCC
GAM108  HLA-G     3'  CTGTTTTTGTTCTACTCTAGGC 10936       T  T  TA
            A                     TGCCT GA GT  GACAAAAACAG
                                ||||| || ||  ||||||||||||
                                ACGGA CT CA  TTGTTTTTGTC
                                   T  _  TC
GAM108  MEA       3'  GTCTCCCTTTCCACATCAAGGC 28276           T________
            A                     TGCCTTGATGT       AGAC
                                ||||||||||        ||||
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                                ACGGAACTACA       TCTG
                                      CCTTTCCC
GAM108  NR3C2    3'  TTTGTCTAAACAAGGTA     8025         ATG
                                TGCCTTG   TTAGACAAA
                                |||||||   |||||||||
                                ATGGAAC   AATCTGTTT
                                   A__
GAM108  RORB     3'  TGTCAATGACATCAAAGC    23593    C       __
                                GC TTGATGTTA  GACA
                                || |||||||||  ||||
                                CG AACTACAGT  CTGT
                                 A        AA
GAM108  VPS41    3'  CTGTTTTTGCAACAACAAAAGC 27692     C_   A    AGA
           A                     TGC  TTG TGTT   CAAAAACAG
                                |||  ||| ||||   |||||||||
                                ACG  AAC ACAA   GTTTTTGTC
                                  AA   A    C__
GAM108  VPS41    3'  CTGTTTTTGCAACAACAAAAGC 55529     C_   A    AGA
           A                     TGC  TTG TGTT   CAAAAACAG
                                |||  ||| ||||   |||||||||
                                ACG  AAC ACAA   GTTTTTGTC
                                  AA   A    C__
GAM108  EFA6R    3'  TGCTTTTGTCTCAAAGCA    31641     C    TGTTA      A
                                TGC TTGA     GACAAAA CA
                                ||| ||||     ||||||| ||
                                ACG AACT     CTGTTTT GT
                                  A   _____       C
GAM108  FLJ12903 3'  CTGTTTTTATCCAGTCAAGG   43069        GTTA  C
                                CCTTGAT    GA AAAAACAG
                                |||||||    || ||||||||
                                GGAACTG    CT TTTTTGTC
                                   AC__  A
GAM108  FLJ14721 3'  TGTCCCACACGATCAAGGCA   52644         ___   TA
                                TGCCTTGA   TGT  GACA
                                ||||||||   |||  ||||
                                ACGGAACT   ACA  CTGT
                                     AGC   CC
GAM108  FLJ21144 3'  TTTTTATCTTGATCAAGGC    43196        GTT   C
                                GCCTTGAT   AGA AAAAA
                                ||||||||   ||| |||||
                                CGGAACTA   TCT TTTTT
                                     GT_   A
GAM108  GIT2     3'  CTGTTTTTGTCCTCAATGGCA  55150      _    TGTTA
                                TGCC TTGA     GACAAAAACAG
                                ||||| ||||     ||||||||||
                                ACGG AACT     CTGTTTTTGTC
                                  T    C____
GAM108  GIT2     3'  CTGTTTTTGTCCTCAATGGCA  55153      _    TGTTA
                                TGCC TTGA     GACAAAAACAG
                                ||||| ||||     ||||||||||
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                                ACGG AACT    CTGTTTTTGTC
                                  T   C____
GAM108  GIT2     3'  CTGTTTTTGTCCTCAATGGCA  29410     _   TGTTA
                                TGCC TTGA    GACAAAAACAG
                                |||| ||||    ||||||||||
                                ACGG AACT    CTGTTTTTGTC
                                  T   C____
GAM108  KIAA0057 3'  CTGTTTCTGTCTGGTTTTAA  25415     TG     A
                                TTGA  TTAGACA AAACAG
                                ||||  ||||||| ||||||
                                AATT  GGTCTGT TTTGTC
                                  TT      C
GAM108  KIAA1075 3'  TTTTTGTCTAATAATAAAG   62388     GA_
                                CTT   TGTTAGACAAAAA
                                |||   ||||||||||||
                                GAA   ATAATCTGTTTTT
                                  ATA
GAM108  PDCD6IP  3'  TTTTGCATAATCAAGGCA    83166        GT  GA
                                TGCCTTGAT  TA  CAAAA
                                |||||||||  ||  |||||
                                ACGGAACTA  AT  GTTTT
                                     __ AC
GAM108  LOC147276 5'  CTGTTCCTGTTTGGCCAAGG   78959      AT      AA
                                CCTTG  GTTAGACA  AACAG
                                |||||  ||||||||  |||||
                                GGAAC  CGGTTTGT  TTGTC
                                   __       CC
GAM109  CNR1     3'  AGGTCTGACATCAGAGGTATCT 32718        TC    CA  TT
          TA                     TAAGATAC  CTGA  TC  GCTT
                                 ||||||||  ||||  ||  ||||
                                 ATTCTATG  GACT  AG  TGGA
                                      GA    AC  TC
GAM109  GYG2     3'  AAGCCTCATTGTCAGAAGTATC 15358        C     TCTT_
          TT                     AAGATACT CTGACA    GCTT
                                 ||||||||  ||||||    ||||
                                 TTCTATGA GACTGT    CGAA
                                      A     TACTC
GAM109  NT5E     3'  AAGCAAGAGCTAAAGAGCATTT 11847     A   CTGACA
                                 AGAT CTC     TCTTGCTT
                                 ||||  |||     ||||||||
                                 TTTA GAG     AGAACGAA
                                   C   AAATCG
GAM109  SPF30    3'  AAGCAAGATACCATTGTCGTC  20792     _  TCC  AC
                                 GAT AC   TG  ATCTTGCTT
                                 |||  ||   ||  |||||||||
                                 CTG TG   AC  TAGAACGAA
                                   C  TT_  CA
GAM109  TEM8     3'  AAGCAGGGGCCAGAATATCT   50819      CTC   ACA
                                 AGATA   CTG   TCTTGCTT
                                 |||||   |||   ||||||||
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                                TCTAT  GAC  GGGACGAA
                                  AA_  CG_
GAM109  C7orf11   3'  AAGCTTCATGTGTCAGGAACAT 57734      AC      CTT__
          CTTG                    TAAGAT  TCCTGACAT    GCTT
                                |||||| |||||||||   ||||
                                GTTCTA  AGGACTGTG    CGAA
                                   CA       TACTT
GAM109  FLJ10008  3'  CAAGATGTCAAGAGCATC    36179    A   C
                                GAT CTC TGACATCTTG
                                ||| ||| ||||||||||
                                CTA GAG ACTGTAGAAC
                                  C   A
GAM109  MGC11266  5'  AAGCAAGGACATTGGAGTCCCT 44486    AT    TGACA
                                AG  ACTCC    TCTTGCTT
                                ||  |||||    ||||||||
                                TC  TGAGG    GGAACGAA
                                 CC    TTACA
GAM109  UBP1      3'  GCATTATCAGGAGTACCTTG   27992     A       CATCT
                                TAAG TACTCCTGA    TGC
                                |||| |||||||||    |||
                                GTTC ATGAGGACT    ACG
                                  C       ATT__
GAM109  LOC115286 3'  CAAAATGTCAGGAATCT     73762     AC       C
                                AGAT  TCCTGACAT TTG
                                ||||  ||||||||| |||
                                TCTA  AGGACTGTA AAC
                                  __       A
GAM109  LOC129676 5'  AAGCAAGACCTGCAAGTACCTT 76228     A   CC  A  __
          G                      TAAG TACT  TG CA  TCTTGCTT
                                |||| ||||  || ||  ||||||||
                                GTTC ATGA  AC GT  AGAACGAA
                                  C   __  _  CC
GAM109  LOC138428 5'  AAGCAAGAGCTCCGAGCGTC   75850    TA   CT  CA
                                GA  CTC  GA  TCTTGCTT
                                ||  |||  ||  ||||||||
                                CT  GAG  CT  AGAACGAA
                                 GC   C_  CG
GAM109  LOC220763 5'  AGTTGATACCAGAGTATCT    73733        C  AC   TT
                                AGATACTC TG  ATC  GCT
                                |||||||| ||  |||  |||
                                TCTATGAG AC  TAG  TGA
                                     _  CA   T_
GAM109  LOC221927 3'  AAGCAAGGTCAAGAAATC    94220     AC  C    AT
                                GAT  TC TGAC  CTTGCTT
                                |||  || ||||  |||||||
                                CTA  AG ACTG  GAACGAA
                                  A_  A   __
GAM109  LOC222234 3'  AAGCAAGATGGGTAACATC    95898     ACT_  TGA
                                GAT   CC   CATCTTGCTT
                                |||   ||   ||||||||||
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                                CTA   GG   GTAGAACGAA
                                  CAAT  ___
GAM110  HRH1     3'  CTCAAACATGTTTAGAGTGGA  7819       A    TGG
                                TCCA TCTGA   GCATGTTTGAG
                                |||| |||||   ||||||||||
                                AGGT AGATT   TGTACAAACTC
                                  G    ___
GAM110  TRIM37   3'  CTCAAATTTGTCATCAG     31625        G  T
                                CTGATGG CA GTTTGAG
                                ||||||| || |||||||
                                GACTACT GT TAAACTC
                                    _ T
GAM110  HTMP10   3'  CTCAAAAAAGCCATCAGATCTG 53758    CA       G ATG
            A                    TC  ATCTGATGG C   TTTGAG
                                ||  |||||||||  |   ||||||
                                AG  TAGACTACC G   AAACTC
                                 TC       _ AAA
GAM110  PAK2     5'  CTCAAATATCACCAAACTAGA  67140     A__   GC
                                TCTG   TGG  ATGTTTGAG
                                ||||   |||  |||||||||
                                AGAT   ACC  TATAAACTC
                                  CAA   AC
GAM110  SEMA6A   3'  CTCGAGTACCCACCAGA     40818     A    CA
                                TCTG TGGG  TGTTTGAG
                                |||| ||||  ||||||||
                                AGAC ACCC  ATGAGCTC
                                  C   __
GAM110  TTY7     3'  TCAAACATGCAGGCTGGA    50019     AT  GATGG
                                TCCA  CT    GCATGTTTGA
                                ||||  ||    ||||||||||
                                AGGT  GA    CGTACAAACT
                                  CG  _____
GAM110  LOC144766 3'  CTCAAACATGAGAAGACTGGG  77481      A   GATGGG
                                TCCA TCT     CATGTTTGAG
                                |||| |||     ||||||||||
                                GGGT AGA     GTACAAACTC
                                  C   AGA___
GAM110  LOC201685 5'  TAAACACCCATCAGATGGA   91845     A       CA
                                TCCA TCTGATGGG  TGTTTG
                                |||| |||||||||  ||||||
                                AGGT AGACTACCC  ACAAAT
                                    _       __
GAM110  LOC221596 5'  CTCAAACAAAACTCAGATT   93623        TG GCA
                                AATCTGA  G   TGTTTGAG
                                |||||||  |   ||||||||
                                TTAGACT  C   ACAAACTC
                                    __ AAA
GAM110  LOC93622  3'  CTCTGCAGACCATCAGAT    57729         GCA   TT
                                ATCTGATGG   TGT  GAG
                                |||||||||   |||  |||
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                                TAGACTACC  ACG  CTC
                                     AG_  T_
GAM111  DAP3    3'  GATGAGGAAGTCGGGCAGT   17341      AAATTTG
                                ACTGCCC     TCCTCATC
                                |||||||     ||||||||
                                TGACGGG     AGGAGTAG
                                   CTGA___
GAM111  DAP3    3'  GATGAGGAAGTCGGGCAGT   54459      AAATTTG
                                ACTGCCC     TCCTCATC
                                |||||||     ||||||||
                                TGACGGG     AGGAGTAG
                                   CTGA___
GAM111  FMOD    3'  GACAAAGCCATCTGGGCAGTC  10673       AA____
                                GACTGCCCA    TTTGTC
                                |||||||||    ||||||
                                CTGACGGGT    AAACAG
                                     CTACCG
GAM111  PTK7    3'  GATGAGGAGGGTGGGCCATCC  12549    CT    AAT  G
                                GGA  GCCCA   TT TCCTCATC
                                |||  |||||   || ||||||||
                                CCT  CGGGT   GG AGGAGTAG
                                  AC    ___  G
GAM111  SH3BP2  3'  GACCCAAACTTGGGCAGTCT   13073        A   TCC
                                GGACTGCCCAA TTTG   TC
                                |||||||||| ||||   ||
                                TCTGACGGGTT AAAC   AG
                                      C   CC_
GAM111  TERF2   3'  GATGAGAATTTTGGGCAACC   20155   AC      TTT  C
                                GG  TGCCCAAA   GT CTCATC
                                ||  ||||||||   || ||||||
                                CC  ACGGGTTT   TA GAGTAG
                                 A_       ___  A
GAM111  UBE4A   3'  ATGAGGATTGGTAGGGCAATCC 17730    C    AA  TT
                                GGA TGCCC  AT  GTCCTCAT
                                ||| |||||  ||  ||||||||
                                CCT ACGGG  TG  TAGGAGTA
                                  A    A_  GT
GAM111  XPNPEP2 3'  GAGAACAAACTTGGGCAGCC   14144   A      A    C
                                GG CTGCCCAA TTTGT CTC
                                || |||||||| ||||| |||
                                CC GACGGGTT AAACA GAG
                                 _       C    A
GAM111  C20orf150 3'  GATGAGGACAAACCAAAGCC   66012   A  GCCCAAA
                                GG CT      TTTGTCCTCATC
                                || ||      ||||||||||||
                                CC GA      AAACAGGAGTAG
                                 _ AACC___
GAM111  CBARA1  3'  GATGAGGATGACCTAGGCACC  21395    AC   CAAAT TG
                                GG  TGCC    T  TCCTCATC
                                ||  ||||    |  ||||||||
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                                CC  ACGG    A  AGGAGTAG
                                 __   ATCC_ GT
GAM111  CXYorf1   3'  GAGGACGACTGGGAATCC    82914    CTG   AAT
                                GGA   CCCA   TTGTCCTC
                                |||   ||||   ||||||||
                                CCT   GGGT   AGCAGGAG
                                  AA_   C__
GAM111  KIAA1069  3'  ATGAGAATGAGCCGGGCAGTTC 68526        AAA  TG C
                                GGACTGCCC   TT  T CTCAT
                                |||||||||   ||  | |||||
                                CTTGACGGG   GA  A GAGTA
                                      CC_  GT A
GAM111  KIAA1155  3'  ATGAGGAATTGGAGAGCC    62907    A  GC    ATTTG
                                GG CT  CCAA    TCCTCAT
                                || ||  ||||    |||||||
                                CC GA  GGTT    AGGAGTA
                                 _  GA    A____
GAM111  SDC3      3'  GATGAGGAGTCTGACCAGCC   28476    A   CC  A  TTG
                                GG CTG  CA AT   TCCTCATC
                                || |||  || ||   ||||||||
                                CC GAC  GT TG   AGGAGTAG
                                 _   CA  C  ___
GAM111  LOC127534 5'  ATGAGGACAGGGGCAATCC    75964     C     AAAT
                                GGA TGCCC    TTGTCCTCAT
                                ||| |||||    ||||||||||
                                CCT ACGGG    GACAGGAGTA
                                  A    _____
GAM111  LOC130074 3'  GACATTCCTAATTTGGGAGTCC 76627       G       _____
                                GGACT CCCAAATT     TGTC
                                ||||| ||||||||     ||||
                                CCTGA GGGTTTAA     ACAG
                                   _       TCCTT
GAM111  LOC148697 3'  ATGAGGACAGGAAATAGCAGTC 79673       CCAAA
                                GACTGC     TTTGTCCTCAT
                                ||||||     ||||||||||||
                                CTGACG     GGACAGGAGTA
                                    ATAAA
GAM111  LOC151877 3'  ATGAGTGGATTTCAGCAGTCC  86692       CC     GTC
                                GGACTGC  AAATTT   CTCAT
                                |||||||  ||||||   |||||
                                CCTGACG  TTTAGG   GAGTA
                                    AC     T__
GAM111  LOC202108 5'  GACACGTAAATTCGGGCAAGTC 90630       _   A   ____
          C                      GGACT GCCC AATT    TGTC
                                |||||  |||| ||||    ||||
                                CCTGA CGGG TTAA    ACAG
                                   A    C    ATGC
GAM111  LOC219686 3'  GACCTAAATTTGTACAGTCC   92508       CC      __
                                GGACTG  CAAATTT  GTC
                                ||||||  |||||||  |||
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                                CCTGAC  GTTTAAA  CAG
                                   AT      TC
GAM112  ABCB10   3'  GTTTTGTATTTTCTTTTCTTGT 24905       CC        TG
            G                    CACGGG  GAGGAGGATG  GAGC
                                 ||||||  ||||||||||  ||||
                                 GTGTTC  TTTCTTTTAT  TTTG
                                    T_        GT
GAM112  ACAD8    3'  GTTTCATGTTAAGACGCCTGTG 27666        CGAGGAG
                                 CACGGGC      GATGTGGAGC
                                 |||||||      ||||||||||
                                 GTGTCCG      TTGTACTTTG
                                     CAGAA__
GAM112  ACK1     3'  GTTCCATGTTTTCCCACCAGCC 20517       CGA__
            TG                     CGGGC    GGAGGATGTGGAGC
                                   |||||    ||||||||||||||
                                   GTCCG    CCTTTTGTACCTTG
                                      ACCAC
GAM112  ADAT1    3'  CTTTGCATCTCTGTTGTG    24916      G CGA    G   TG
                                 CACGG C   GGAG ATG  GAG
                                 ||||| |   |||| |||  |||
                                 GTGTT G   TCTC TAC  TTC
                                    _ ___    _  GT
GAM112  ARF4L    3'  GTTTTTATTTTTGTGTCTGTG  70392        _     GGATGT
                                 CACGGGC CGAGGA     GGAGC
                                 ||||||| ||||||     |||||
                                 GTGTCTG GTTTTT     TTTTG
                                     T     AT____
GAM112  ARHGEF6  3'  CTCACTTCTTTGGCTTTTG   68756    CG        ATGTG
                                 CA  GGCCGAGGAGG    GAG
                                 ||  ||||||||||     |||
                                 GT  TCGGTTTCTTC    CTC
                                  TT         A____
GAM112  AXUD1    3'  GCTTTGGTTGCACTTCTTTGGC 53443     G         A  ____
            TGGTG                   CAC GGCCGAGGAGG TGT    GGAGC
                                 ||| ||||||||||| |||    |||||
                                 GTG TCGGTTTCTTC ACG    TTTCG
                                   G          _   TTGG
GAM112  B3GALT5  5'  GTTCTGAGGCTCTTGGTCTTG  53736   C       G  GATG
                                 A GGGCCGAG AG    TGGAGC
                                 | ||||||| ||    ||||||
                                 G TCTGGTTC TC    GTCTTG
                                  T       _  GGA_
GAM112  BACH2    3'  GTTTTTGTTTTTTCTTGTTTGT 41788        C       TGT
            G                    CACGGGC GAGGAGGA   GGAGC
                                 ||||||| ||||||||   |||||
                                 GTGTTTG TTCTTTTT   TTTTG
                                     _       TGT
GAM112  BCL11B   3'  GTTTTGTAATTTTTTTGGCATG 57579      G        A  TG
            TG                     CACG GCCGAGGAGG TG  GAGC
                                 |||| |||||||||| ||  ||||
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                                GTGT CGGTTTTTTT AT  TTTG
                                  A        A  GT
GAM112  BTG2    3'  CTAATTTTCTGGTTTGTG    23145        GA      G
                                CACGGGCC  GGAGGAT TGG
                                ||||||||  ||||||| |||
                                GTGTTTGG  TCTTTTA ATC
                                          __      _
GAM112  C1QBP   3'  GTTTCATGGCAGGCTTTGGCCA 60858     G       AGGA_
           GTG                    CAC GGCCGAGG     TGTGGAGC
                                ||| ||||||||     ||||||||
                                GTG CCGGTTTC     GTACTTTG
                                  A       GGACG
GAM112  CACNA1C 3'  GTTGCAGTTTCTTTTCGGTTTT 7401    C          TG  G
           G                     A GGGCCGAGGAGGA  TG AGC
                                | ||||||||||||  || |||
                                G TTTGGCTTTTCTT  AC TTG
                                 T          TG  G
GAM112  CEP2    3'  TTCCGGGCCTTTGGCTTTG   24199   C      GG   ATG
                                A GGGCCGA  AGG   TGGAG
                                | |||||||  |||   |||||
                                G TTCGGTT  TCC   GCCTT
                                 T      __   GG_
GAM112  CHAD    5'  GCTCCACGTAGGAGCTGGCTCG 8854         AGGAGG
                                CGGGCCG     ATGTGGAGC
                                |||||||     |||||||||
                                GCTCGGT     TGCACCTCG
                                    CGAGGA
GAM112  COL4A2  3'  GCTCCATGTTCTCCCAAATACC 10244      GCCGA_
           GT                    ACGG     GGAGGATGTGGAGC
                                ||||     ||||||||||||||
                                TGCC     CCTCTTGTACCTCG
                                  ATAAAC
GAM112  CRAT    3'  GTTCCACTCAGCTTGGTTC   15676        GAG  T
                                GGGCCGAG   GA GTGGAGC
                                ||||||||   || |||||||
                                CTTGGTTC   CT CACCTTG
                                    GA_  _
GAM112  CRSP6   5'  TACCTCGTTTTTTGGCTCGTG  16223            _  T
                                CACGGGCCGAGGAG GA GTG
                                |||||||||||||| || |||
                                GTGCTCGGTTTTTT CT CAT
                                         G  C
GAM112  CYP17   3'  CCTTCTTTTTCAGCTTGTG   5439        C       TGT
                                CACGGGC GAGGAGGA   GG
                                ||||||| ||||||||   ||
                                GTGTTCG CTTTTTCT   CC
                                    A       T__
GAM112  DIAPH2  3'  GCTGCCATCATTCCTTGGTTTG 23009            GAT   _
           TG                    CACGGGCCGAGGAG   GTGG AGC
                                ||||||||||||||   |||| |||
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                                GTGTTTGGTTCCTT   TACC TCG
                                      AC_   G
GAM112  DMD     3'  GTTTTGCATCCTTTTGGCGTG  5468     G     G     TG
                                CG GCCGAG AGGATG  GAGC
                                || |||||| ||||||  ||||
                                GT CGGTTT TCCTAC  TTTG
                                 G     _     GT
GAM112  DMD     3'  GTTTTGCATCCTTTTGGCGTG  15726    G     G     TG
                                CG GCCGAG AGGATG  GAGC
                                || |||||| ||||||  ||||
                                GT CGGTTT TCCTAC  TTTG
                                 G     _     GT
GAM112  DUSP4    5'  GCTCCAGGACCTCGGCCC    9153          AGGATG
                                GGGCCGAGG     TGGAGC
                                |||||||||     ||||||
                                CCCGGCTCC     ACCTCG
                                      AGG___
GAM112  DVL3    3'  GCTCTACTATTTTTGGTTGTG  16648       G      GGAT
                                CACGG CCGAGGA    GTGGAGC
                                ||||| |||||||    |||||||
                                GTGTT GGTTTTT    CATCTCG
                                   _      AT__
GAM112  ENC1    5'  GTTCGTCGCCTCCTTGCCCGTG 14651        C      A  TG
                                CACGGGC GAGGAGG TG  GAGC
                                ||||||| ||||||| ||  ||||
                                GTGCCCG TTCCTCC GC  CTTG
                                   _      _ TG
GAM112  EXT2    3'  CGTTCCATGAGCTATTCCTCTT 6380           _______
            TGGTTTG                 CGGGCCGAGGAGGA     TGTGGAGC   G
                                |||||||||||||     ||||||||  |
                                GTTTGGTTTCTCCT     GTACCTTG   C
                                      TATCGA
GAM112  FACL5    3'  CCTTCTTCTTTGTTTTGTG   64858      GC       TGT
                                CACGG  CGAGGAGGA   GG
                                |||||  |||||||||   ||
                                GTGTT  GTTTCTTCT   CC
                                   TT       T__
GAM112  FAT2    3'  CTCCACGTCAGGCACTGTG   9348       _  GAGGAG
                                CACGG GCC     GATGTGGAG
                                ||||| |||     |||||||||
                                GTGTC CGG     CTGCACCTC
                                   A  A_____
GAM112  FCER1G   3'  GTCATATTCTTCTTTGGCTTCT 15914    CG         _    AGC
            G                    CA  GGCCGAGGAGGA TGTGG
                                ||  ||||||||||| |||||
                                GT  TCGGTTTCTTCT ATACT
                                 CT          T    G
GAM112  FOSB    3'  TCTTTTCTCCTCCGCCTGTG  23060        C       TGT
                                CACGGGC GAGGAGGA   GGA
                                ||||||| ||||||||   |||
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                                GTGTCCG CTCCTCTT  TCT
                                    C      T__
GAM112  GARP    3'  GCTCTATATTTTATCCCCGT  19783     CC  GG
                                ACGGG  GA  AGGATGTGGAGC
                                |||||  ||  ||||||||||||
                                TGCCC  CT  TTTTATATCTCG
                                  __  A_
GAM112  GEMIN5  5'  GCTTCACATTTTCTCATCACCC 90644    CC  __
                                GGG  GA  GGAGGATGTGGAGC
                                |||  ||  ||||||||||||||
                                CCC  CT  TCTTTTACACTTCG
                                 A_  AC
GAM112  GPI     5'  GCTCCTTCCTCCTCGGCTCG  5726          TGT
                                CGGGCCGAGGAGGA  GGAGC
                                ||||||||||||||  |||||
                                GCTCGGCTCCTCCT  CCTCG
                                       T__
GAM112  GPM6A   3'  GTTCCGTGTCTTAACAGTTTGT 19176      CGAGG   TG
            G                   CACGGGC    AGGA  TGGAGC
                                |||||||    ||||  ||||||
                                GTGTTTG    TTCT  GCCTTG
                                    ACAA_   GT
GAM112  HGD     5'  GCTTTATATCCTCTGGGCCTG  5745      GA
                                CGGGCC  GGAGGATGTGGAGC
                                ||||||  ||||||||||||||
                                GTCCGG  TCTCCTATATTTCG
                                   G_
GAM112  HNRPH2  3'  GTTTTGCATTACAGGCTTGTG  39466       GAGGAG   TG
                                CACGGGCC    GATG  GAGC
                                ||||||||    ||||  ||||
                                GTGTTCGG    TTAC  TTTG
                                     ACA___   GT
GAM112  IDH3A   3'  TATTTTCTTCGGTTTTTG   19847   CG
                                CA  GGCCGAGGAGGATG
                                ||  ||||||||||||||
                                GT  TTGGCTTCTTTTAT
                                 TT
GAM112  IGHMBP2 3'  CACCTCTTTCTGGCCTGTG   10983       G     T
                                CACGGGCC AGGAGGA GTG
                                |||||||| ||||||| |||
                                GTGTCCGG TCTTTCT CAC
                                     _     C
GAM112  INPPL1  3'  GTTCTCACTGTCTCCTGGTCTG 9603        G    AT  _
            TG                    CACGGGCC AGGAGG  GTG GAGC
                                |||||||| ||||||  ||| ||||
                                GTGTCTGG TCCTCT  CAC CTTG
                                     _    GT  T
GAM112  ITPR3   3'  GTTTTACAAATCCTTTGGCCTG 11087       _  GGA
                                CGGGCCGA GGA  TGTGGAGC
                                |||||||| |||  ||||||||
```

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                                GTCCGGTT CCT   ACATTTTG
                                    T  AA_
GAM112  JAG1    3'  GTTCTGTATTTGAAAGTGCCTT 5813    C   CGAGGA    TG
            TG                   CA GGGC     GGATG  GAGC
                                || ||||     |||||  ||||
                                GT TCCG     TTTAT  CTTG
                                 T   TGAAAG    GT
GAM112  KCNF1   5'  GCTTTGTGTTTAGAAAAGGCTC 11146      GAGGA_    TG
            G                    CGGGCC     GGATG  GAGC
                                ||||||     |||||  ||||
                                GCTCGG     TTTGT  TTCG
                                   AAAAGA    GT
GAM112  LOR     3'  GTTTAGCCTCTTTGGTTTCTG  6465    CG        ATGTG
                                CA  GGCCGAGGAGG    GAGC
                                ||  ||||||||||     ||||
                                GT  TTGGTTTCTCC    TTTG
                                 CT         GA___
GAM112  MAGEL2  3'  GTTCTGTATTTTGGCATCTGTG 39330      __    GGAG   TG
                                CACGG  GCCGA   GATG  GAGC
                                |||||  |||||   ||||  ||||
                                GTGTC  CGGTT   TTAT  CTTG
                                   TA    _____   GT
GAM112  MAN2A2  3'  GCCTGAATTCTCTTTGGCTTCT 21514    CG         GT_  AGC
            G                    CA  GGCCGAGGAGGAT   GG
                                ||  ||||||||||||   ||
                                GT  TCGGTTTCTCTTA   CC
                                 CT          AGT  G
GAM112  MAX     3'  GTTTTGTATTGAGGGCCAGTG  11476    G   GAGGAG   TG
                                CAC GGCC     GATG  GAGC
                                ||| ||||     ||||  ||||
                                GTG CCGG     TTAT  TTTG
                                  A   GAG___   GT
GAM112  MBD3    3'  GCTCCTGGCTCCCTCCTCGGCC 15392           AT  __
            CGT                    ACGGGCCGAGGAGG  GT  GGAGC
                                ||||||||||||||  ||  |||||
                                TGCCCGGCTCCTCC  CG  CCTCG
                                        CT  GT
GAM112  MEIS2   3'  TTCTGAGCCTTGGTTGTG    39728      G    AGGATG
                                CACGG CCGAGG     TGGAG
                                ||||| ||||||     |||||
                                GTGTT GGTTCC     GTCTT
                                   _     GA_____
GAM112  MEN1    3'  GTTCCACATCTTTGCAATTGTG 56357      GCCGAG
                                CACGG     GAGGATGTGGAGC
                                |||||     ||||||||||||
                                GTGTT     TTTCTACACCTTG
                                   AACG__
GAM112  MEN1    3'  GTTCCATATCTTTGCAATTCTG 56358     CCGAG
                                CGGG    GAGGATGTGGAGC
                                ||||    ||||||||||||
```

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                                GTCT    TTTCTATACCTTG
                                  TAACG
GAM112  MEN1    3'  GTTTTTACTTTTGTGGTCTGTG 95014        AG   ATGT
                                CACGGGCCG  GAGG   GGAGC
                                |||||||||  ||||   |||||
                                GTGTCTGGT  TTTC   TTTTG
                                     GT   AT__
GAM112  MIC2    5'  GCTTCGCCCCACCCGGCCCGTG 11581         A  A  AT
                                CACGGGCCG GG GG  GTGGAGC
                                |||||||||  ||  ||  |||||||
                                GTGCCCGGC CC CC  CGCTTCG
                                     _  A  C_
GAM112  MLLT3   3'  GTTTTTTTTTTTTTTTGGTTGTG 16961       G        TGT
                                CACGG CCGAGGAGGA   GGAGC
                                |||||  ||||||||||   |||||
                                GTGTT GGTTTTTTTT   TTTTG
                                  _        TT_
GAM112  MNT     3'  GTTGCTGTTTTTCTTGTGTTTG 40088        _        _ TG AGC
            TG                    CACGGGC CGAGGAGGAT G  G
                                |||||||  ||||||||||  |  |
                                GTGTTTG GTTCTTTTTG C  T
                                     T         T GT G
GAM112  MVK     3'  GCTTCAGGCCCCCGCCTTGGCC 61279           A  AT  __
            TGTG                   CACGGGCCGAGG GG  GT  GGAGC
                                ||||||||||||  ||  ||  |||||
                                GTGTCCGGTTCC CC  CG  CTTCG
                                       G  CC  GA
GAM112  MYCL2   3'  GCTTTGTGTTTTCTGGCACC   19377    _  GA       TG
                                GG GCC  GGAGGATG  GAGC
                                ||  |||  ||||||||  ||||
                                CC CGG  TCTTTTGT  TTCG
                                 A   __       GT
GAM112  MYLK    3'  GTTCCATATTTTTCTTCTTAAA 98796      GGCC__
            TGTG                   CACG     GAGGAGGATGTGGAGC
                                ||||     ||||||||||||||||
                                GTGT     TTCTTTTTATACCTTG
                                  AAATTC
GAM112  MYO6    3'  GTGTCTTTTTTGGCCTTTG    18443    C          TG
                                CA GGGCCGAGGAGGA  T
                                ||  ||||||||||||  |
                                GT TCCGGTTTTTTCT  G
                                 T           GT
GAM112  NAPB    3'  GCTTTGCATTTTCTCTGTGCTT 70742    C   _  AG      TG
            TG                    A GGGC CG  GAGGATG  GAGC
                                |  ||||  ||  |||||||  ||||
                                G TTCG GT  CTTTTAC  TTCG
                                 T    T  CT      GT
GAM112  NKX3A   3'  GTTTAAAATTACTTGGTTTGTG 21615          GAG   GTG
                                CACGGGCCGAG   GAT   GAGC
                                ||||||||||   |||   ||||
```

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                                GTGTTTGGTTC  TTA  TTTG
                                     A__  AAA
GAM112  NRAS    5'  TCTCCAACATTTTTCCCGGTCT 11846        A      _   C
            GTG                   CACGGGCCG GGAGGATGT GGAG
                                  ||||||||| ||||||||| ||||
                                  GTGTCTGGC CTTTTTACA CCTC
                                      C       A   TG
GAM112  NUCB1   3'  CTCCGCATCCTGCTGTGTG   21640   G  CG  G
                                  CG GC  AG AGGATGTGGAG
                                  || ||  || ||||||||||
                                  GT TG  TC TCCTACGCCTC
                                   G  __  G
GAM112  PAICS   3'  GCTTTATGTTCGCTGTCC    22263     CGA  A
                                  GGGC   GG GGATGTGGAGC
                                  ||||   || ||||||||||
                                  CCTG   TC CTTGTATTTCG
                                     ___  G
GAM112  PART1   3'  GTTTACATTTATTTTCTTCAGC 33903       C     ____      GC
            CTGTG                  CACGGGC GAGGAG   GATGTGGA
                                   ||||||| ||||||   ||||||||
                                   GTGTCCG CTTCTT   TTACATTT
                                       A     TTAT      G
GAM112  PCBP1   3'  GTTTTGTTTTGGGTTTTTTGGC 21670          ___  T TG
            TC                    GGGCCGAGGAG   GA G  GAGC
                                  ||||||||||   || |  ||||
                                  CTCGGTTTTTT   TT T  TTTG
                                        GGG  T GT
GAM112  PDYN    3'  GCACTCTCTTTTGGTTTGTG   44587          _  GA
                                  CACGGGCCGAG GAG  TGT
                                  |||||||||| |||  |||
                                  GTGTTTGGTTT CTC  ACG
                                        T   TC
GAM112  PIK4CB  3'  GCTTCCCTGCCCCTCCTGGTCT 12131        G    AT  ___
            GTG                   CACGGGCC AGGAGG  GT   GGAGC
                                  |||||||| ||||||  ||   |||||
                                  GTGTCTGG TCCTCC  CG   CTTCG
                                       _     C_  TCC
GAM112  PPIA    3'  TTCCATGTTTTCCTTGTTC   41215   GC
                                  G  CGAGGAGGATGTGGAG
                                  |  ||||||||||||||||
                                  C  GTTCCTTTTGTACCTT
                                   TT
GAM112  PPIF    5'  GTTCTGTGTTCTCCCCGCCCGT 20376       C A      TG
            G                     CACGGGC G GGAGGATG  GAGC
                                  ||||||| | ||||||||  ||||
                                  GTGCCCG C CCTCTTGT  CTTG
                                      _ C       GT
GAM112  PPP1R12B 3'  GTTTTATATCCTTCATTCTG   50365     CCGA
                                  CGGG   GGAGGATGTGGAGC
                                  ||||   ||||||||||||||
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                                GTCT   CTTCCTATATTTTG
                                  TA__
GAM112  PPP2R2B  3'  CAAATTCTTCTTGTTTTGTG  17119      GC       G
                                CACGG  CGAGGAGGAT TG
                                |||||  |||||||||| ||
                                GTGTT  GTTCTTCTTA AC
                                   TT        A
GAM112  PRDM2    3'  CTCTGTATCTGCCATGTG    32417     _  CGAGGA    TG
                                CACG GGC     GGATG  GAG
                                |||| |||     |||||  |||
                                GTGT CCG     TCTAT  CTC
                                  A  _______    GT
GAM112  PRKAB1   3'  GCTCCTGCAGCGCCTCGGTCTG 21813          AGGA  _
          TG                     CACGGGCCGAGG    TGT GGAGC
                                ||||||||||||    ||| |||||
                                GTGTCTGGCTCC    ACG CCTCG
                                      GCG_   T
GAM112  RABIF    3'  GTTCCGCTGCCTTCTTGTCTGT 12729        C      AT
          G                      CACGGGC GAGGAGG  GTGGAGC
                                |||||||  |||||||  |||||||
                                GTGTCTG TTCTTCC  CGCCTTG
                                   _      GT
GAM112  RAD52    3'  AATACCTTTTCTTCGGCTTGTG 57015            T   GAGC
                                CACGGGCCGAGGAGGA GTG
                                |||||||||||||||| |||
                                GTGTTCGGCTTCTTTT CAT
                                      C   AAG
GAM112  RAD52    3'  GAATACCTTTTCTTCGGCTTGT 57029            T   GAGC
          G                      CACGGGCCGAGGAGGA GTG
                                |||||||||||||||| |||
                                GTGTTCGGCTTCTTTT CAT
                                      C   AAG
GAM112  RAD52    3'  GAATACCTTTTCTTCGGCTTGT 57030            T   GAGC
          G                      CACGGGCCGAGGAGGA GTG
                                |||||||||||||||| |||
                                GTGTTCGGCTTCTTTT CAT
                                      C   AAG
GAM112  RAD52    3'  GAATACCTTTTCTTCGGCTTGT 57031            T   GAGC
          G                      CACGGGCCGAGGAGGA GTG
                                |||||||||||||||| |||
                                GTGTTCGGCTTCTTTT CAT
                                      C   AAG
GAM112  RGS14    3'  GCTCTGCATGCCCTGTCTGTG  22399       CGA  A  _   TG
                                CACGGGC   GG GG ATG  GAGC
                                |||||||   || || |||  ||||
                                GTGTCTG   TC CC TAC  CTCG
                                   ___  _  G   GT
GAM112  RNASE4   3'  GCTCTGTATTTTTTGGC     12878        GG   TG
                                GCCGAGGA  ATG  GAGC
                                ||||||||  |||  ||||
```

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                                CGGTTTTT  TAT  CTCG
                                    __  GT
GAM112  RPH3AL   3'  GTTTAGTTTCTTTGGTTTTTG  23742   CG       ATGTG
                                CA  GGCCGAGGAGG   GAGC
                                ||  ||||||||||    ||||
                                GT  TTGGTTTCTTT   TTTG
                                 TT       GA___
GAM112  RPS6KA2  3'  CTTCGATTTTTCTGGTCTGTG  41223       G     G   C
                                CACGGGCC AGGAGGAT TGGAG
                                |||||||| |||||||| |||||
                                GTGTCTGG TCTTTTTA GCTTC
                                    _      _   A
GAM112  SCN4A    3'  GATTGGATATTCTCCTCGGACT 6202      G         GGAGC
           GTG                    CACGG CCGAGGAGGATGT
                                |||||  ||||||||||||
                                GTGTC GGCTCCTCTTATA
                                   A          GGTTAGT
GAM112  SEMG1    3'  GTTTCAGATTCTTGGTCC    13013     GAG    G
                                GGGCC   GAGGAT TGGAGC
                                ||||||  |||||| ||||||
                                CCTGG   TTCTTA ACTTTG
                                   ___     G
GAM112  SERPINB9  3'  GTTTTATATTTTCTCTCATTCT 16032     CC_  _
           TG                    CGGG   GAG GAGGATGTGGAGC
                                ||||   ||| ||||||||||||
                                GTTC   CTC CTTTTATATTTTG
                                  TTA   T
GAM112  SERPINE1  3'  GCTCCTAGTGTTTCTTTGTGGT 7011         AG    TGT___
           CTGTG                   CACGGGCCG  GAGGA     GGAGC
                                |||||||||  |||||     |||||
                                GTGTCTGGT  TTCTT     CCTCG
                                     GT    TGTGAT
GAM112  SGT      3'  TTTCACGTTCAGCCGTGTG   13042     _  CGAGGA
                                CACG GGC     GGATGTGGAG
                                |||| |||     ||||||||||
                                GTGT CCG     CTTGCACTTT
                                  G  A_____
GAM112  SHC1     3'  GTTCTGTGGGCTTGGCCTTGTG 13123     _     GAGGA  TG
                                CACG GGCCGAG    TG  GAGC
                                |||| |||||||    ||  ||||
                                GTGT CCGGTTC    GT  CTTG
                                  T      GG___  GT
GAM112  SHOC2    3'  GTTTTATATCTTGACTTGCCTT 24784   C    C   G_
           G                     A GGGC GAG  AGGATGTGGAGC
                                | |||| |||  ||||||||||||
                                G TCCG TTC  TTCTATATTTTG
                                 T   _  AG
GAM112  SIAT4C   5'  GCTTTGCGGGGTCCGCCTGTG  21858       CGA   GGA  TG
                                CACGGGC   GGA   TG  GAGC
                                |||||||   |||   ||  ||||
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                              GTGTCCG  CCT  GC  TTCG
                                 ___  GGG  GT
GAM112  SLC22A5  3'  GTTCCTTAGCCTCCTGGTTTGT 13229       G    ATGT
           G                  CACGGGCC AGGAGG   GGAGC
                              |||||||| ||||||   |||||
                              GTGTTTGG TCCTCC   CCTTG
                                 _    GATT
GAM112  SLC25A1  3'  CTCTGTAGCCTGGTCTGTG  21118       GAGG  A  TG
                              CACGGGCC   AGG TG  GAG
                              ||||||||   ||| ||  |||
                              GTGTCTGG   TCC AT  CTC
                                 _____  G  GT
GAM112  SLC25A1  3'  GTTTCATGTTCTGTGTCACGTG 21119    _  CGAGG
                              CACG GGC    AGGATGTGGAGC
                              |||| |||    ||||||||||||
                              GTGC CTG    TCTTGTACTTTG
                                A  TG___
GAM112  SMPX    5'  GCTTTGTATTCTTGCATCTG  27535    CCGAG    TG
                              CGGG   GAGGATG  GAGC
                              ||||   |||||||  ||||
                              GTCT   TTCTTAT  TTCG
                                ACG__     GT
GAM112  SNAI1   3'  GTTCTGTGTCCTCTGCCTG  21125     CGA     TG
                              CGGGC  GGAGGATG  GAGC
                              |||||  ||||||||  ||||
                              GTCCG  TCTCCTGT  CTTG
                                 ___      GT
GAM112  SUV39H1  3'  CTCTACGTTCAGGGCTGTG  13495     G  GAGGA
                              CACGG CC    GGATGTGGAG
                              ||||| ||    ||||||||||
                              GTGTC GG    CTTGCATCTC
                                G  A____
GAM112  SYBL1   3'  GCTTTTGTTTATTTCTTTGGTT 20110          ATGT__
           TGT                  ACGGGCCGAGGAGG    GGAGC
                              ||||||||||||||    |||||
                              TGTTTGGTTTCTTT    TTTCG
                                      ATTTGT
GAM112  SYK     3'  TGTTTTCTTGTCTGTG     13499      CG
                              CACGGGC  AGGAGGATG
                              |||||||  |||||||||
                              GTGTCTG  TTCTTTTGT
                                 __
GAM112  TAZ     5'  GTTCCGCAGCGCGCCCACGGCC 5486        A  AGGA__
           TGTG                  CACGGGCCG GG    TGTGGAGC
                              |||||||||  ||    ||||||||
                              GTGTCCGGC CC    ACGCCTTG
                                   A  CGCGCG
GAM112  TCTEL1   3'  CATTCTCTTTGTTTTGTG   22534     GC
                              CACGG  CGAGGAGGATG
                              |||||  ||||||||||
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                                GTGTT  GTTTCTCTTAC
                                   TT
GAM112  TEC     3'  CCTTCCTTTTTGCCTTGTG   13677       C       TGT
                                CACGGG CGAGGAGGA   GG
                                |||||| |||||||||   ||
                                GTGTTC GTTTTTCCT   CC
                                   C       T__
GAM112  TFCP2    5'  TTTGTAGTTTTCTTGGTTTG   20167           A  TG  GC
                                CGGGCCGAGGAGG TG  GA
                                |||||||||||| ||  ||
                                GTTTGGTTCTTTT AT  TT
                                       G  GT  G
GAM112  TMPO     5'  GCTTTGTGTCCGCGAGTTTTTG 13814    CG  _  AGGA    TG
                                CA  GGC CG   GGATG  GAGC
                                ||  ||| ||   |||||  ||||
                                GT  TTG GC   CCTGT  TTCG
                                 TT   A  G___    GT
GAM112  TPT1     5'  GCTCCGAGTTTCAGGCTCGTG  13840        GAG   ATG
                                CACGGGCC   GAGG   TGGAGC
                                ||||||||   ||||   ||||||
                                GTGCTCGG   CTTT   GCCTCG
                                    A__    GA_
GAM112  TRIM14   3'  TTCTGCGTCCTGTTTTGTC   29523     C  G     TG
                                GGC GAG AGGATG  GAG
                                ||| ||| ||||||  |||
                                CTG TTT TCCTGC  CTT
                                  T   G     GT
GAM112  TRPV1    5'  CGTTTTCCTTGTTCTGTG    55669      GC
                                CACGG  CGAGGAGGATG
                                |||||  ||||||||||
                                GTGTC  GTTCCTTTTGC
                                   TT
GAM112  UBE2G2   3'  GTTCTGTGTTTTCCCTGCCC   65493     CGA      TG
                                GGGC   GGAGGATG  GAGC
                                ||||   ||||||||  ||||
                                CCCG   CCTTTTGT  CTTG
                                  TC_       GT
GAM112  USP6     3'  GTTTCACCTTATTTTTGGTCTT 92782    C       G  T
            TG                    CA GGGCCGAGGA GA GTGGAGC
                                || ||||||||| || |||||||
                                GT TCTGGTTTTT TT CACTTTG
                                 T        A  C
GAM112  WASF3    3'  GCTTTCAGTTTCTTGGCTTG   22814          GA  T
                                CGGGCCGAGGAG  TG GGAGC
                                ||||||||||||  || |||||
                                GTTCGGTTCTTT  AC TTTCG
                                       G_  _
GAM112  YWHAH    3'  GTTTCAGTAGCTCCTTGGTTTT 14153   C        GA  _
            G                     A GGGCCGAGGAG  TG TGGAGC
                                | ||||||||||  || ||||||
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                                G TTTGGTTCCTC  AT ACTTTG
                                 T         G_  G
GAM112  ZNF255   5'  GTTCCATGTCTTTGAAATTGTG 20498       GCCGAG
                                CACGG     GAGGATGTGGAGC
                                |||||     ||||||||||||||
                                GTGTT     TTTCTGTACCTTG
                                   AAAG__
GAM112  ZNF74    5'  GCTCCGCGTCCGATGGCTC   14262       AGGA
                                GGGCCG   GGATGTGGAGC
                                ||||||   ||||||||||
                                CTCGGT   CCTGCGCCTCG
                                   AG__
GAM112  ZNF85    5'  GCTTTGTGTTTTCTGCTCGTG  14275       CGA      TG
                                CACGGGC   GGAGGATG  GAGC
                                |||||||   ||||||||  ||||
                                GTGCTCG   TCTTTTGT  TTCG
                                    ___       GT
GAM112  ALS2CR7  3'  CTTTATGTCCTCACCTATG   58229    CG  CCGAG
                                CA  GG    GAGGATGTGGAG
                                ||  ||    ||||||||||||
                                GT  CC    CTCCTGTATTTC
                                 AT  A____
GAM112  AP1S2    3'  GCTCTATATTTTTTAAAGCT   15349     CGA
                                GGC   GGAGGATGTGGAGC
                                |||   ||||||||||||||
                                TCG   TTTTTTATATCTCG
                                  AAA
GAM112  ATE1     3'  GTTGTGCATTTTTTTTGGTTC  73018             G
                                GGGCCGAGGAGGATGTG AGC
                                |||||||||||||||| |||
                                CTTGGTTTTTTTTACGT TTG
                                          G
GAM112  B3GNT7   3'  GTTCCTTGTTCTTGGCTGGTG  71682     G       G  TGT
                                CAC GGCCGAGGA GA   GGAGC
                                ||| ||||||||| ||   |||||
                                GTG TCGGTTCTT TT   CCTTG
                                  G       G ___
GAM112  BHLHB2   3'  GCTTCAAAGTCTTGGTCTGTG  14765          AGGATG
                                CACGGGCCGAGG     TGGAGC
                                ||||||||||||     ||||||
                                GTGTCTGGTTCT     ACTTCG
                                       GAA___
GAM112  BLCAP    3'  GCGCCTTTTTGGCCTGTG    22945            A
                                CACGGGCCGAGGAGG TGT
                                |||||||||||||| |||
                                GTGTCCGGTTTTTCC GCG
                                                _
GAM112  C20orf12 3'  TTCTGTATCTTGCTCTGTT   36854     C   G     TG
                                GGC GAG AGGATG  GAG
                                ||| ||| ||||||  |||
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                                TTG CTC TTCTAT  CTT
                                  T  G     GT
GAM112  C20orf129 3'  GTTTTGCATTTTTCTTAGGTT  62044     _       TG
                                GGCC GAGGAGGATG  GAGC
                                |||| ||||||||||  ||||
                                TTGG TTCTTTTTAC  TTTG
                                  A        GT
GAM112  CAP350    3'  CCTTTTCTTTTCAGTTTGTG   29704       C      TGT
                                CACGGGC GAGGAGGA   GG
                                |||||||| ||||||||   ||
                                GTGTTTG CTTTTCTT   CC
                                    A       TT_
GAM112  CAP350    3'  GCATTTCTTCTGGGCTTGTG   29706        G     _
                                CACGGGCC AGGAGGA TGT
                                |||||||| ||||||| |||
                                GTGTTCGG TCTTCTT ACG
                                     G      T
GAM112  CCNE1     3'  GCTCCACGTTCTCTTCTGTCTG 55165       C
              T                  ACGGGC GAGGAGGATGTGGAGC
                                 |||||| ||||||||||||||||
                                 TGTCTG CTTCTCTTGCACCTCG
                                    T
GAM112  CGI-01    3'  GCTTCGTATTTTTCTTGGTTT  32506
                                 GGGCCGAGGAGGATGTGGAGC
                                 ||||||||||||||||||||
                                 TTTGGTTCTTTTTATGCTTCG

GAM112  CLDN1     3'  GTTTTATATCTTCCTAATAAGG 41189     GGGCCG
              TG                   CAC     AGGAGGATGTGGAGC
                                   |||     ||||||||||||||||
                                   GTG     TCCTTCTATATTTTG
                                     GAATAA
GAM112  COLEC12   3'  TTTTACATCCTCACTCTGG   48622    _  _
                                 CC GAG GAGGATGTGGAG
                                 || ||| ||||||||||||
                                 GG CTC CTCCTACATTTT
                                  T  A
GAM112  CRMP5     3'  GTTTTGCACGTTTGGTTTG    39706         GAGGA  TG
                                 CGGGCCGAG     TG  GAGC
                                 |||||||||     ||  ||||
                                 GTTTGGTTT     AC  TTTG
                                       GC___  GT
GAM112  DDX17     5'  GTTCTATGTTCTGGTTTTGT   22126      _  GAGG
                                 ACGGG CC    AGGATGTGGAGC
                                 ||||| ||    ||||||||||||
                                 TGTTT GG    TCTTGTATCTTG
                                    T  _____
GAM112  DDX33     3'  TTGTATCTTTTTTGGTGTGTG  39791      G          TG
                                 CACG GCCGAGGAGGATG  G
                                 |||| ||||||||||||  |
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                                GTGT TGGTTTTTTCTAT  T
                                  G          GT
GAM112  DKFZp434E0519 5'  GCTTTGTATCTTTTAGGTGCTT 50995       CGA_       TG
          GT                    ACGGGC   GGAGGATG  GAGC
                                ||||||   ||||||||  ||||
                                TGTTCG   TTTTCTAT  TTCG
                                   TGGA       GT
GAM112  DKFZp434F1819 5'  GTTTCATGTCTTTCCTCAACTG 51024     GCC     _
                                CGG   GAGGAG GATGTGGAGC
                                |||   |||||| ||||||||||
                                GTC   CTCCTT CTGTACTTTG
                                  AA_     T
GAM112  DKFZP434G1411 5'  GCTTTGTGTCTTCCAGATGG   93732     A__       TG
                                CCG   GGAGGATG  GAGC
                                |||   ||||||||  ||||
                                GGT   CCTTCTGT  TTCG
                                  AGA       GT
GAM112  DKFZp434I1916 3'  GTTTTGTGTTTTGGGGGTTGGT 50976     G    GAGG     TG
          G                     CAC GGCC    AGGATG  GAGC
                                ||| ||||    ||||||  ||||
                                GTG TTGG    TTTTGT  TTTG
                                  G    GGG_     GT
GAM112  DKFZP434M154 3'  CTCTGTCCTCCTTGGCTTG    72797            GT    C
                                CGGGCCGAGGAGGAT  GGAG
                                ||||||||||||||  ||||
                                GTTCGGTTCCTCCTG  TCTC
                                      __    C
GAM112  DKFZP434P1750 5'  CTCCACGTCCAGCCTGGG    32024    G   A_
                                CC AGG  GGATGTGGAG
                                || |||  ||||||||||
                                GG TCC  CCTGCACCTC
                                 G   GA
GAM112  DKFZP434P1750 3'  GCTCTGTGTTCTCAGGCCC    32026      GAG      TG
                                GGGCC   GAGGATG  GAGC
                                |||||   |||||||  ||||
                                CCCGG   CTCTTGT  CTCG
                                   A__      GT
GAM112  DKFZP564F0522 3'  GTTTTACATTCTCCCTTACTG  69140     GCCGA
                                CGG     GGAGGATGTGGAGC
                                |||     ||||||||||||||
                                GTC     CCTCTTACATTTTG
                                  ATTC_
GAM112  DKFZP564O0423 5'  CATCTTCCTTGGCTGTG     93345      G
                                CACGG CCGAGGAGGATG
                                ||||| ||||||||||||
                                GTGTC GGTTCCTTCTAC
                                      _
GAM112  ESM1      3'  GCTTTTTTTTTTTTTTTTGGCTT 23849    C          TGT_
          TG                    A GGGCCGAGGAGGA    GGAGC
                                | ||||||||||||    |||||
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                                G TTCGGTTTTTTTT   TTTCG
                                 T          TTTT
GAM112  EZF-2    3' CTGTGGTCTTCTTGGTCTTG  37676   C       GA  TG
                                A GGGCCGAGGAG  TG  G
                                | ||||||||||  ||  |
                                G TCTGGTTCTTC  GT  C
                                 T         TG  GT
GAM112  FHOD2    3' GTTTCACATTCTACTACTTCTG 74264     CCG  G
                                CGGG   AG AGGATGTGGAGC
                                ||||   || ||||||||||||
                                GTCT   TC TCTTACACTTTG
                                  TCA  A
GAM112  FLJ10314 3' GCTCTGTGTCGGGCTTTGGCTG 36490    G      AG_   TG
           GTG                   CAC GGCCGAGG   GATG  GAGC
                                ||| ||||||||   ||||  ||||
                                GTG TCGGTTTC   CTGT  CTCG
                                  G       GGG    GT
GAM112  FLJ10375 3' GTTTCGCAGTGGCTTGGCTCG  36561         GAGGA
                                CGGGCCGAG    TGTGGAGC
                                |||||||||    ||||||||
                                GCTCGGTTC    ACGCTTTG
                                     GGTG_
GAM112  FLJ10468 3' TTTTGTGTTTTCTTCTGT    36636    C       TG
                                GC GAGGAGGATG  GAG
                                || ||||||||||  |||
                                TG CTTCTTTTGT  TTT
                                 T         GT
GAM112  FLJ10511 3' GCTTTACATTTTATTTTACGTG 36688     GGCC   G
                                CACG    GAG AGGATGTGGAGC
                                ||||    ||| ||||||||||||
                                GTGC    TTT TTTTACATTTCG
                                  AT__   A
GAM112  FLJ10607 3' GCTTTACATTTTTCTGTGG    77638     _
                                CCG AGGAGGATGTGGAGC
                                ||| ||||||||||||||
                                GGT TCTTTTTACATTTCG
                                  G
GAM112  FLJ10697 3' GTTTTGTGTTTTCTTTTGC    36958    C       TG
                                GC GAGGAGGATG  GAGC
                                || ||||||||||  ||||
                                CG TTTCTTTTGT  TTTG
                                 T         GT
GAM112  FLJ10824 5' GCTCTGCAGTCCTCGGCGTGTG 72957     G      GGA  TG
                                CACG GCCGAGGA   TG  GAGC
                                |||| ||||||||   ||  ||||
                                GTGT CGGCTCCT   AC  CTCG
                                  G       G__  GT
GAM112  FLJ10904 5' GGTCTGCATTCCTTCGGCCCGT 37385          A    TG  GC
           G                    CACGGGCCGAGG GGATG  GA
                                |||||||||||| |||||  ||
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                                GTGCCCGGCTTC CTTAC  CT
                                      _    GT  GGT
GAM112  FLJ11116 3' GCTTTATGTTTTGTTATGTTTG 83475       CG  G
           TG                  CACGGGC  AG AGGATGTGGAGC
                               ||||||| || ||||||||||||
                               GTGTTTG  TT TTTTGTATTTCG
                                  TA  G
GAM112  FLJ11342 3' GCTTTACAAGGTTGGCCC    37835       GGAGGA
                               GGGCCGA     TGTGGAGC
                               |||||||     ||||||||
                               CCCGGTT     ACATTTCG
                                  GGA___
GAM112  FLJ11342 3' GTTTTGTATCCTTTCACTGT   37837     GCCGA      TG
                               ACGG    GGAGGATG  GAGC
                               ||||    |||||||| ||||
                               TGTC    TTTCCTAT  TTTG
                                 AC___      GT
GAM112  FLJ11413 3' GTTCTGTGTTCTGGCCTGTG   44958       GAGG     TG
                               CACGGGCC    AGGATG  GAGC
                               ||||||||    ||||||  ||||
                               GTGTCCGG    TCTTGT  CTTG
                                    ____     GT
GAM112  FLJ12484 3' GCTTTGATCCCTTGGTCTG    43175        AG   G GG
                               CGGGCCGAGG  GAT T  AGC
                               |||||||||  ||| |  |||
                               GTCTGGTTCC  CTA G  TCG
                                    __  _ TT
GAM112  FLJ12547 3' CTCTGGGTCTGGGTCTGTG    47133       GAGGA    G
                               CACGGGCC    GGAT TGGAG
                               ||||||||    |||| |||||
                               GTGTCTGG    TCTG GTCTC
                                  G____    G
GAM112  FLJ12688 3' GCTCTATATTCTTTCAGGCT   73555     GA
                               GGCC  GGAGGATGTGGAGC
                               ||||  ||||||||||||||
                               TCGG  TTTCTTATATCTCG
                                 AC
GAM112  FLJ12783 3' GCTTTACATCCTCCCATGTT   49487     CGA
                               GGC   GGAGGATGTGGAGC
                               |||   ||||||||||||||
                               TTG   CCTCCTACATTTCG
                                 TAC
GAM112  FLJ13052 3' ACAAGACGTTCTCCTCTGCCCG 43752        C         GGAGC
           TG                  CACGGGC GAGGAGGATGT
                               ||||||| ||||||||||
                               GTGCCCG CTCCTCTTGCA
                                  T         GAACAC
GAM112  FLJ13102 3' GCTGGCATCTCTCTTTGGCCTG 46533          _    GG
                               CGGGCCGAGGAG GATGT  AGC
                               |||||||||||| |||||  |||
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                              GTCCGGTTTCTC CTACG  TCG
                                    T    G_
GAM112  FLJ13187  3'  GCTTTTATGATTTTTTTTGGTT 45165            GT__
            TGT                 ACGGGCCGAGGAGGAT   GGAGC
                              ||||||||||||||||   |||||
                              TGTTTGGTTTTTTTTA   TTTCG
                                    GTAT
GAM112  FLJ13340  3'  GTTTTACGTTTTTTATCCTG  55160     CCGA
                              CGGG   GGAGGATGTGGAGC
                              ||||   ||||||||||||||
                              GTCC   TTTTTTGCATTTTG
                                TA__
GAM112  FLJ13391  3'  GTTTCAGCAGACTTCCTTGCTC 50748      GC      A_ _
            TGTG                 CACGG  CGAGGAGG  TG TGGAGC
                              |||||  ||||||||  || ||||||
                              GTGTC  GTTCCTTC  AC ACTTTG
                                 TC       AG  G
GAM112  FLJ13491  3'  GCTCCGTTGCCTTGGTCTG   45220         AGGATG
                              CGGGCCGAGG     TGGAGC
                              ||||||||||     ||||||
                              GTCTGGTTCC     GCCTCG
                                    GTT___
GAM112  FLJ13576  5'  GCTCTCCTCCTTTTTGGTTTG  42809           TGT
                              CGGGCCGAGGAGGA   GGAGC
                              ||||||||||||||   |||||
                              GTTTGGTTTTTCCT   TCTCG
                                    CC_
GAM112  FLJ14001  5'  GCTGAGCTTTCCTCGGCCTG   45490          AT  GG
                              CGGGCCGAGGAGG  GT  AGC
                              ||||||||||||||  ||  |||
                              GTCCGGCTCCTTT  CG  TCG
                                    __  AG
GAM112  FLJ14007  3'  AGATTCATCTTTTTTGTTTGTG 45533        C        TGGAGC
                              CACGGGC GAGGAGGATG
                              |||||||  ||||||||||
                              GTGTTTG TTTTTTCTAC
                                 _        TTAGAG
GAM112  FLJ14642  3'  GCTTCATGTTCAGAAGCTC   52576     CGAGGA
                              GGGC     GGATGTGGAGC
                              ||||     ||||||||||||
                              CTCG     CTTGTACTTCG
                                AAGA__
GAM112  FLJ20033  3'  GTTTTATATTCACAGTTGGT   34821      GGA_
                              GCCGA    GGATGTGGAGC
                              |||||    ||||||||||||
                              TGGTT    CTTATATTTTG
                                 GACA
GAM112  FLJ20312  5'  GTTCGTGGGCTTTGTCGGTCCG 35411          G    ATGTG
            TG                   CACGGGCCGA GAGG     GAGC
                              |||||||||| ||||     ||||
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                                GTGCCTGGCT TTTC    CTTG
                                     G   GGGTG
GAM112  FLJ20811  3'  GCTTTGAGTAACTTCTTGGTTG 67709      G      GATG_ GG
          TG                   CACGG CCGAGGAG    T  AGC
                               ||||| ||||||||    |  |||
                               GTGTT GGTTCTTC    G  TCG
                                 _       AATGA TT
GAM112  FLJ21324  5'  CTCTGTGTGTGGCCTGTG    92854         AGGAGG   TG
                               CACGGGCCG     ATG  GAG
                               |||||||||     |||  |||
                               GTGTCCGGT     TGT  CTC
                                    G_____   GT
GAM112  FLJ22313  5'  GCTTCGTATCCTCCAGTGC   42580    CGA
                               GC   GGAGGATGTGGAGC
                               ||   ||||||||||||||
                               CG   CCTCCTATGCTTCG
                                TGA
GAM112  FLJ22357  3'  GCTCCATGTGGGGACTGGCCTG 42620       G  GAGG_
          T                    ACGGGCC AG    ATGTGGAGC
                               |||||||  ||    |||||||||
                               TGTCCGG TC    TGTACCTCG
                                  _  AGGGG
GAM112  FLJ22378  3'  CTTAGCTTTTTGGCCTGTG   47596           GATGTG
                               CACGGGCCGAGGAG     GAG
                               ||||||||||||||     |||
                               GTGTCCGGTTTTTC     TTC
                                     GA____
GAM112  FLJ23185  5'  GCTTTGTGTTTTTCTGTAGTT  47519    CG_      TG
                               GGC   AGGAGGATG  GAGC
                               |||   |||||||||  ||||
                               TTG   TCTTTTTGT  TTCG
                                 ATG       GT
GAM112  FLJ23360  3'  GCTCCGTCCTGCATTTCTGTGG 43833        A   G   _____
          TCCGTG               CACGGGCCG GGAG ATGT    GGAGC
                               |||||||||  |||| ||||    |||||
                               GTGCCTGGT TCTT TACG    CCTCG
                                    G   _   TCCTG
GAM112  FLJ32191  5'  GCTCTGCATTCTCCAGACTCTG 59079      CCGA      TG
          TG                   CACGGG   GGAGGATG  GAGC
                               ||||||   ||||||||  ||||
                               GTGTCT   CCTCTTAC  CTCG
                                  CAGA      GT
GAM112  GPR88    3'  GTTTCACATTTTCTATAGC   42139    CGA
                               GC   GGAGGATGTGGAGC
                               ||   ||||||||||||||
                               CG   TCTTTTACACTTTG
                                ATA
GAM112  GS3955   3'  GTTTTGTGTCAATTGGGTCCGT 41626       G  GAG   TG
          G                    CACGGGCC AG   GATG  GAGC
                               |||||||  ||   ||||  ||||
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                                GTGCCTGG TT   CTGT  TTTG
                                    G  AA_    GT
GAM112  HBP17    3'  GTTTTGTATTTTTTGCTTTTGT 18888       CCGA      TG
            G                    CACGGG   GGAGGATG  GAGC
                                 ||||||   ||||||||  ||||
                                 GTGTTT   TTTTTTAT  TTTG
                                    TCG_      GT
GAM112  HINT3    3'  CTCTGTATTTTTTTTAAGTT   57550     CG       TG
                                 GGC  AGGAGGATG  GAG
                                 |||  |||||||||  |||
                                 TTG  TTTTTTTAT  CTC
                                   AA       GT
GAM112  HNRPU    3'  TTCTACATTTTATCTGT     49817    C  GG
                                 GC GA  AGGATGTGGAG
                                 || ||  ||||||||||
                                 TG CT  TTTTACATCTT
                                  T  A_
GAM112  HRH3     3'  GCTCTGCATGCTCCTCTGCCTG 24319        C     G   TG
            TG                    CACGGGC GAGGAG ATG  GAGC
                                 |||||||  ||||||  |||  ||||
                                 GTGTCCG CTCCTC TAC  CTCG
                                     T     G   GT
GAM112  HSA011916 3'  GCTTTGTGTCTTTTTTCCT    60906     CC        TG
                                 GGG  GAGGAGGATG  GAGC
                                 |||  ||||||||||  ||||
                                 TCC  TTTTTTCTGT  TTCG
                                   __         GT
GAM112  HSU79274  5'  GCTCCGCATCCTTGCGCCACGT 26148      _  C AG
            G                     CACG GGC G  GAGGATGTGGAGC
                                 ||||  ||| |  ||||||||||||
                                 GTGC CCG C  TTCCTACGCCTCG
                                   A  _ G_
GAM112  HYPH     3'  TTACCATCTTCTTTGTTTGTG  96571        C        TG
                                 CACGGGC GAGGAGGATG  GA
                                 |||||||  ||||||||||  ||
                                 GTGTTTG TTTCTTCTAC  TT
                                     _         CA
GAM112  KIAA0061  3'  GCTTTGTATTATGATCTCTTGG 68837          _ G___    TG
            TCTGTG                 CACGGGCCGAG GA    GATG  GAGC
                                 ||||||||||| ||    ||||  ||||
                                 GTGTCTGGTTC CT    TTAT  TTCG
                                       T  AGTA    GT
GAM112  KIAA0418  3'  GTTTTGTTTCCTTTTGTTTTGT 28299      GC    G    T TG
            G                     CACGG  CGAG AGGA G  GAGC
                                 |||||  ||||  ||||  |  ||||
                                 GTGTT  GTTT TCCT T  TTTG
                                   TT    _    T GT
GAM112  KIAA0450  5'  GCTCCCCCTGTCTCTTTGGTCT 28360    C          ATGT_
            TG                     A GGGCCGAGGAGG     GGAGC
                                 |  ||||||||||||     |||||
```

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                                G TCTGGTTTCTCT    CCTCG
                                 T         GTCCC
GAM112  KIAA0562 3' GCTCGGGCTCCTTGGTCTCTG 28826   C        GATGTG
                                CA GGGCCGAGGAG     GAGC
                                || ||||||||||     ||||
                                GT TCTGGTTCCTC     CTCG
                                 C         GGG___
GAM112  KIAA0660 3' GTTAATTTTTTTTTTGGCTTTG 25471   C         T  GG
                                A GGGCCGAGGAGGA GT  AGC
                                | ||||||||||||| ||  |||
                                G TTCGGTTTTTTTT TA  TTG
                                 T         T  A_
GAM112  KIAA0720 5' GCTTTGGCAGTCTCGGCCCG  62985         AGGA  G  _
                                CGGGCCGAGG   TGT GA GC
                                ||||||||||   ||| || ||
                                GCCCGGCTCT   ACG TT CG
                                      G___   G  T
GAM112  KIAA0721 3' CTGCCTTCCTGGGCTTGTG   41652        G     AT TG
                                CACGGGCC AGGAGG  G  G
                                |||||||| ||||||  |  |
                                GTGTTCGG TCCTTC  C  C
                                     G     __ GT
GAM112  KIAA0826 3' GTTTTTTTGTTTTTTGGTCTGT 83529           GATGT
                                ACGGGCCGAGGAG    GGAGC
                                ||||||||||||    |||||
                                TGTCTGGTTTTTT    TTTTG
                                       GTTT_
GAM112  KIAA0869 3' TTTAGATTTTTTTTTGGTTTGT  71423            G   GC
                                ACGGGCCGAGGAGGAT TGGA
                                |||||||||||||||| ||||
                                TGTTTGGTTTTTTTTA ATTT
                                          G   G
GAM112  KIAA0953 3' GTTCTGTGTCTGCTGCTTTTG  67332   CG  CGA  A    TG
                                CA  GGC   GG GGATG  GAGC
                                ||  |||   || |||||  ||||
                                GT  TCG   TC TCTGT  CTTG
                                 TT   ___  G    GT
GAM112  KIAA0970 3' GTTTTATGTCAAATGATCTGTG 30619     GC  AGGAG
                                CACGG  CG    GATGTGGAGC
                                |||||  ||    ||||||||||
                                GTGTC  GT    CTGTATTTTG
                                   TA  AAA__
GAM112  KIAA0971 3' GCTTTGTTTTCATGGCCTGTG  30673        A   GAT TG
                                CACGGGCCG GGAG   G  GAGC
                                |||||||| ||||   |  ||||
                                GTGTCCGGT CTTT   T  TTCG
                                      A    ___ GT
GAM112  KIAA0998 5' TTCTGTGCTTGGTCTGT     31259         GAGGA  TG
                                ACGGGCCGAG    TG  GAG
                                ||||||||||    ||  |||
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                                TGTCTGGTTC    GT  CTT
                                      _____ GT
GAM112  KIAA1443 3' GCTTTGTGTTCTTCAGGGT   64574    GA      TG
                                GCC  GGAGGATG  GAGC
                                |||  ||||||||  ||||
                                TGG  CTTCTTGT  TTCG
                                  GA       GT
GAM112  KIAA1511 3' GTTTCATGTCTTAGTTCCTG  70729     CC  GG
                                CGGG  GA  AGGATGTGGAGC
                                ||||  ||  ||||||||||||
                                GTCC  TT  TTCTGTACTTTG
                                  __ GA
GAM112  KIAA1535 3' GTTCTGGGGTTCTTGGTGTGTG 80215     G       GGATGT
                                CACG GCCGAGGA     GGAGC
                                |||| ||||||||      |||||
                                GTGT TGGTTCTT     TCTTG
                                  G       GGGG__
GAM112  KIAA1557 3' GCTTCGTATTCTGATCTCTG  61785     CC  GG
                                CGGG  GA  AGGATGTGGAGC
                                ||||  ||  ||||||||||||
                                GTCT  CT  TCTTATGCTTCG
                                  __ AG
GAM112  KIAA1571 5' CGTGACTTTTTTGGTTC     61615          A  TG
                                GGGCCGAGGAGG TG  G
                                ||||||||||| ||  |
                                CTTGGTTTTTTC GT  C
                                      A  GT
GAM112  KIAA1598 3' GTTCTATATTACACAGGTTTGT 37640        GAGGAG
                                ACGGGCC     GATGTGGAGC
                                |||||||     ||||||||||
                                TGTTTGG     TTATATCTTG
                                   ACACA_
GAM112  KIAA1691 3' GTTCTGAGTTTTCGGTGCCGTG 94136       _       GGATG
                                CACGG GCCGAGGA     TGGAGC
                                ||||| ||||||||     ||||||
                                GTGCC TGGCTTTT     GTCTTG
                                  G       GA___
GAM112  KIAA1735 3' GTTCTGTATCTTCTCACATTCT 89008       CCGA_       TG
           GT                   ACGGG    GGAGGATG  GAGC
                                |||||    ||||||||  ||||
                                TGTCT    TCTTCTAT  CTTG
                                  TACAC       GT
GAM112  KIAA1751 3' GTTCTGCACTGCCCCTTGGCCT 72165           A  A__  TG
           GTG                    CACGGGCCGAGG GG   TG  GAGC
                                ||||||||||| ||   ||  ||||
                                GTGTCCGGTTCC CC   AC  CTTG
                                      _ GTC  GT
GAM112  KIAA1755 3' GTTTTACATTCTGCCTCTGCT  62020     C   _
                                GGC GAGG AGGATGTGGAGC
                                ||| |||| ||||||||||||
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                                TCG CTCC TCTTACATTTTG
                                  T   G
GAM112  KIAA1799 5' CTGCGCTTCCTTGTTTGTG   75128       C     A  TG
                                CACGGGC GAGGAGG TG  G
                                ||||||| ||||||| ||  |
                                GTGTTTG TTCCTTC GC  C
                                   _     _ GT
GAM112  KIAA1799 5' GCTCTGCATCTTATTTCCGGT  75129     AG __    TG
                                GCCG  GA  GGATG  GAGC
                                ||||  ||  |||||  ||||
                                TGGC  TT  TCTAC  CTCG
                                  CT  AT    GT
GAM112  KIAA1870 3' GCTTTATGACCTTGGCCATGTG 50584     _      AGGA
                                CACG GGCCGAGG    TGTGGAGC
                                |||| ||||||||    ||||||||
                                GTGT CCGGTTCC    GTATTTCG
                                  A       A___
GAM112  KIAA1878 3' GTTCCAGGAGCTCTTTGGTTTG 93371          GATG
                                CGGGCCGAGGAG    TGGAGC
                                ||||||||||||    ||||||
                                GTTTGGTTTCTC    ACCTTG
                                      GAGG
GAM112  KIAA1887 3' TTTTGTACTTGCCCTGTG    77282       C    GAGGA  TG
                                CACGGG CGAG    TG  GAG
                                |||||| ||||    ||  |||
                                GTGTCC GTTC    AT  TTT
                                   C   _____  GT
GAM112  KIAA1909 5' GTTCTTGCATCCTCAGCCTGTG 74284       CGAG       _
                                CACGGGC    GAGGATGTG GAGC
                                |||||||    ||||||||| ||||
                                GTGTCCG    CTCCTACGT CTTG
                                   A___        T
GAM112  KIAA1940 3' GCTCCTGTTTTCTTGGTTCTGT 80787       _       ATGT
          G                     CACGGG CCGAGGAGG    GGAGC
                                |||||| |||||||||    |||||
                                GTGTCT GGTTCTTTT    CCTCG
                                   T        GT__
GAM112  L3MBTL   3' TGTCTTTGTTCTCCTTGGCCTG 70090             T  GC
          TG                    CACGGGCCGAGGAGGATG GGA
                                ||||||||||||||||| |||
                                GTGTCCGGTTCCTCTTGT TCT
                                      T  GTC
GAM112  LRP1B    5' CTCTGTTCCTTGGCTTGT    38275          GGAT TG
                                ACGGGCCGAGGA   G  GAG
                                ||||||||||||   |  |||
                                TGTTCGGTTCCT    T  CTC
                                      _____ GT
GAM112  LSFR2    3' GTTCCAGAACCTCGGTCAGTG  61188    G      AGGATG
                                CAC GGCCGAGG     TGGAGC
                                ||| ||||||||     ||||||
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                                GTG CTGGCTCC     ACCTTG
                                  A       AAG___
GAM112  MAD4     3'  GCTCTGTCTGCCCCGGCCCGTG 22275         A  A   GT
                                CACGGGCCG GG GGAT  GGAGC
                                ||||||||| || ||||  |||||
                                GTGCCCGGC CC TCTG  TCTCG
                                    C  G   __
GAM112  MAGEF1   5'  GCTCCCACACCCCTCGGCCCGT 60699           A  A   _
            G                    CACGGGCCGAGG GG TGTGG AGC
                                ||||||||||| || ||||| |||
                                GTGCCCGGCTCC CC ACACC TCG
                                      _ _    C
GAM112  MAP2K3   3'  GCTTTATGGGTTTGGCTTGT   59688          GAGGA
                                ACGGGCCGAG    TGTGGAGC
                                ||||||||||    ||||||||
                                TGTTCGGTTT    GTATTTCG
                                    GG___
GAM112  MGC10067 3'  GTTTTGTGTTTTTGTCTCATTG 59591      GCC  G      TG
            TG                   CACGG   GA GAGGATG  GAGC
                                |||||   || |||||||  ||||
                                GTGTT   CT TTTTTGT  TTTG
                                  ACT  G      GT
GAM112  MGC14433 3'  CTTCATGTCCAGTGTGTG    52953      G  CGAGGA
                                CACG GC     GGATGTGGAG
                                |||| ||     ||||||||||
                                GTGT TG     CCTGTACTTC
                                  G  A_____
GAM112  MGC14859 3'  GCCGACATGTTTTCTTTGGCCT 62603              GA_
            G                    CGGGCCGAGGAGGATGTG   GC
                                |||||||||||||||||   ||
                                GTCCGGTTTCTTTTGTAC   CG
                                      AGC
GAM112  MGC16075 3'  GTTCAATTTCCTCTTCGGTCC  52253           TGTG
                                GGGCCGAGGAGGA    GAGC
                                ||||||||||||    ||||
                                CCTGGCTTCTCCT    CTTG
                                    TTAA
GAM112  MGC2550   3'  GCTTCATGTTTTAGAATTTGTG 44173       CCGAGG
                                CACGGG     AGGATGTGGAGC
                                ||||||     ||||||||||||
                                GTGTTT     TTTTGTACTTCG
                                  AAGA__
GAM112  MGC5139   5'  TTCTGTATCTGGGGCTGTG   74576      G  GAGGA    TG
                                CACGG CC    GGATG  GAG
                                ||||| ||    |||||  |||
                                GTGTC GG    TCTAT  CTT
                                  G  G____    GT
GAM112  MGC5149   3'  GCTTCGTGTCCTTTGGCATGT  72758     G    GG    TG
                                ACG GCCGA  AGGA  TGGAGC
                                ||| |||||  ||||  ||||||
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                                TGT CGGTT  TCCT  GCTTCG
                                  A    __   GT
GAM112  MGC5601   5' GTTCCAAACACTCGGCCTGTG  48259          GAGGATG
                                CACGGGCCGAG     TGGAGC
                                ||||||||||      ||||||
                                GTGTCCGGCTC     ACCTTG
                                      ACAA___
GAM112  MLZE     5' TTTCACCATCTTGGCCTG    49457        GA  ATG
                                CGGGCCGAG  GG   TGGAG
                                |||||||||  ||   |||||
                                GTCCGGTTC  CC   ACTTT
                                     TA  ___
GAM112  MYH10    3' GTTTTGTGTCCGAGGCTTGT   69674       GAGGA    TG
                                ACGGGCC    GGATG  GAGC
                                |||||||    |||||  ||||
                                TGTTCGG    CCTGT  TTTG
                                   AG___    GT
GAM112  NAP1L2   3' GTTCTGTATTTTTCTTGTAGTG 42014     GGGC        TG
                                CAC   CGAGGAGGATG  GAGC
                                |||   ||||||||||  ||||
                                GTG   GTTCTTTTTAT  CTTG
                                  AT__        GT
GAM112  NCBP2    3' GTTTTATATTCTTTTGTAGT   24768    GG  CG
                                AC  GC  AGGAGGATGTGGAGC
                                ||  ||  ||||||||||||||
                                TG  TG  TTTTCTTATATTTTG
                                 A_  __
GAM112  NR2F1    3' GTTTTGTATTTTTTTCTGGTTC 97643      _        TG
                                GGGCC GAGGAGGATG  GAGC
                                |||||  ||||||||||  ||||
                                CTTGG CTTTTTTTAT  TTTG
                                   T        GT
GAM112  NSG-X    3' TTTTATGTTTTCTCTGTC    27730     C   G
                                GGC GAG AGGATGTGGAG
                                ||| ||| ||||||||||
                                CTG CTC TTTTGTATTTT
                                  T  _
GAM112  NXN      3' GCAACACAGTCTTCCTCGGTCT 42676           _   GA
           G                     CGGGCCGAGGAGGA TGTG  GC
                                ||||||||||||| ||||  ||
                                GTCTGGCTCCTTCT ACAC  CG
                                       G   AA
GAM112  NY-REN-41 3' TCTTTCTTCTTTGGCTTGT   55563            TGT
                                ACGGGCCGAGGAGGA   GGA
                                ||||||||||||||   |||
                                TGTTCGGTTTCTTCT   TCT
                                      T__
GAM112  P37NB    3' GTTTTGTATTTTCTATACTGGT 20628     G  CCGA      TG
           G                     CAC GG   GGAGGATG  GAGC
                                ||| ||   ||||||||  ||||
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                                GTG TC   TCTTTTAT  TTTG
                                  G  ATA_      GT
GAM112  PARVA    5'  GCTCCGCGTCCCGACCGGCCCG 37182       AGGA
                                CGGGCCG   GGATGTGGAGC
                                |||||||   ||||||||||
                                GCCCGGC   CCTGCGCCTCG
                                    CAGC
GAM112  PAT2     3'  GTTCTGTATTTACAGTCTGT  81656      CGAGGA   TG
                                ACGGGC    GGATG  GAGC
                                ||||||    |||||  ||||
                                TGTCTG    TTTAT  CTTG
                                   ACA___    GT
GAM112  PB1      3'  GTTTTTGTTTTCTTGGTTTTG  36879   C        ATGT
                                A GGGCCGAGGAGG   GGAGC
                                | ||||||||||||   |||||
                                G TTTGGTTCTTTT   TTTTG
                                 T         GT__
GAM112  PC4      3'  TTTATAAACTTTTGGTTTGTG  22973         G  GA
                                CACGGGCCGAG AG  TGTGGA
                                |||||||||||| ||  ||||||
                                GTGTTTGGTTT TC  ATATTT
                                       _ AA
GAM112  PCDH20   3'  CTTCCTTTCTTTGGTTTTG   43421   C        ATGT
                                A GGGCCGAGGAGG   GGAG
                                | ||||||||||||   ||||
                                G TTTGGTTTCTTT   CTTC
                                 T         C___
GAM112  PIP5K1C  3'  CTCTGTGTTTTGTCTGT    71299      CGAGG    TG
                                ACGGGC    AGGATG  GAG
                                ||||||    ||||||  |||
                                TGTCTG    TTTTGT  CTC
                                   ______    GT
GAM112  PREI3    3'  GCTTGCCAGTCTTTTTGGCTTT 66926   C        GA  TG
            G                    A GGGCCGAGGAG  TG  GAGC
                                | ||||||||||  ||  ||||
                                G TTCGGTTTTTC  AC  TTCG
                                 T         TG  CG
GAM112  PRKAG3   3'  GCTTCTGGATCCTCGGTTTCTG 34289   CG       GGATGT
                                CA  GGCCGAGGA     GGAGC
                                ||  |||||||||     |||||
                                GT  TTGGCTCCT     CTTCG
                                 CT       AGGT__
GAM112  PRO0132  5'  TTCCCTTTCTTGGTTTATG   26939   CG       ATGT
                                CA  GGCCGAGGAGG   GGAG
                                ||  ||||||||||   ||||
                                GT  TTGGTTCTTTC   CCTT
                                 AT        _____
GAM112  PSTPIP1  5'  GCTCCTCTCTGGCTCGTG    15617        AG    T
                                CACGGGCCG  GAGGA GT
                                |||||||||  ||||| ||
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                                GTGCTCGGT  CTCCT CG
                                     CT    _
GAM112  PTPRT    3'  GCTCCTTCTTAGCCTGTG    56499       CG     T
                                CACGGGC  AGGAGGA GT
                                |||||||  ||||||| ||
                                GTGTCCG  TCTTCCT CG
                                    AT     _
GAM112  PURG     3'  TTCCTCTTTTTTGGCCCGT   26258           TGT   C
                                ACGGGCCGAGGAGGA  GGAG
                                ||||||||||||||  ||||
                                TGCCCGGTTTTTTCT  CCTT
                                         ___   T
GAM112  RAB33B   3'  CTTTATATTTTATTTTGG    49326       _
                                CCGAGG AGGATGTGGAG
                                ||||||| ||||||||||
                                GGTTTT TTTTATATTTC
                                   A
GAM112  RAD51    3'  TGTGTTTTCTTTGGTTTTG   56836   C         TG
                                A GGGCCGAGGAGGA  TG
                                | ||||||||||||  ||
                                G TTTGGTTTCTTTT  GT
                                 T          GT
GAM112  RANBP1   3'  GCCCCTCTTTTTCGGTTTGT   12764            TGT  A
                                ACGGGCCGAGGAGGA  GG GC
                                ||||||||||||||  || ||
                                TGTTTGGCTTTTTCT  CC CG
                                         C__  _
GAM112  RFX4     3'  GTTCCATGACTTTGCTTTGTG  12857       C    AGGA
                                CACGGG CGAGG   TGTGGAGC
                                |||||| |||||   ||||||||
                                GTGTTT GTTTC   GTACCTTG
                                   C    A___
GAM112  RNF9     3'  GCTCTATATCTGAAAGAGCTC  23238      CGAGGA
                                GGGC     GGATGTGGAGC
                                ||||     ||||||||||
                                CTCG     TCTATATCTCG
                                  AGAAAG
GAM112  RTN4IP1  5'  GTTCCGTATTCTTCTTTCAGTT 52176     C__
           T                     GGGC   GAGGAGGATGTGGAGC
                                ||||  ||||||||||||||||
                                TTTG   TTCTTCTTATGCCTTG
                                  ACT
GAM112  RTP801   3'  GTTTTGTATCTTGTTTTTCTG  39318     CC   G     TG
                                CGGG  GAG AGGATG  GAGC
                                ||||  ||| ||||||  ||||
                                GTCT  TTT TTCTAT  TTTG
                                  T_   G     GT
GAM112  SART3    3'  TTTCAGCCCTTTGGTTTTG   28839   C       A  ATG
                                A GGGCCGAGG GG   TGGAG
                                | |||||||| ||   |||||
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                                G TTTGGTTTC CC   ACTTT
                                 T       _ G__
GAM112  SDF1     3'  GTTTTGTATTCTCTGAGCTGTG 92519      G CGA      TG
                                CACGG C   GGAGGATG  GAGC
                                ||||| |   ||||||||  ||||
                                GTGTC G   TCTCTTAT  TTTG
                                   _ AG_      GT
GAM112  SFRS4    3'  GTTCCATATTCTGGTATTGTG  20061      _  GAGG
                                CACGG GCC    AGGATGTGGAGC
                                ||||| |||    ||||||||||||
                                GTGTT TGG    TCTTATACCTTG
                                   A  _____
GAM112  SLC34A1  3'  GCTCCGCAAAGCTCTGGGCTTG 13207        GA   GA_
           TG                     CACGGGCC  GGAG   TGTGGAGC
                                ||||||||  ||||   ||||||||
                                GTGTTCGG  TCTC   ACGCCTCG
                                     G_    GAA
GAM112  SNX11    3'  CTCTACTCTTAGGTTTGTG   26171        G   GGAT
                                CACGGGCC AGGA    GTGGAG
                                |||||||| ||||    ||||||
                                GTGTTTGG TTCT    CATCTC
                                     A   _____
GAM112  SSR3     3'  GCTTTGTGTCTATGGGTGGCCT 24037         AGGA_    TG
           GTG                    CACGGGCCG    GGATG  GAGC
                                |||||||||    |||||  ||||
                                GTGTCCGGT    TCTGT  TTCG
                                     GGGTA    GT
GAM112  SYNCOILIN 3'  GTTTTATGTCTTTCACTTTCCC 48630     CCGA_
                                GGG    GGAGGATGTGGAGC
                                |||    ||||||||||||||
                                CCC    CTTTCTGTATTTTG
                                  TTTCA
GAM112  TNFRSF21  3'  GTTCCATATTTTCTCC     27827    CCGA
                                GG   GGAGGATGTGGAGC
                                ||   ||||||||||||||
                                CC   TCTTTTATACCTTG
                                  ____
GAM112  TOMM70A  3'  GTTTCATGTCTAGGTGTTGTG  29738      _  GAGGA
                                CACGG GCC    GGATGTGGAGC
                                ||||| |||    ||||||||||
                                GTGTT TGG    TCTGTACTTTG
                                   G  A____
GAM112  TRIM22   3'  GTTCCATGCCTCTCTCCTTGGC 21387          _ __
           TTGT                   ACGGGCCGAGGAG GA  TGTGGAGC
                                |||||||||||| ||  ||||||||
                                TGTTCGGTTCCTC CT  GTACCTTG
                                       T  CC
GAM112  TRIP10   3'  GTTTTACATCTTTTCTTTCTGC 16182    C  ___
                                GC GAG   GAGGATGTGGAGC
                                || |||   ||||||||||||
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                                CG CTT   TTTCTACATTTTG
                                 T   TCT
GAM112  UBF-fl   3'  GTTTTGCATTTTTTTTTGTTTTG 52634     GC         TG
                                CGG  CGAGGAGGATG  GAGC
                                |||  ||||||||||  ||||
                                GTT  GTTTTTTTTAC  TTTG
                                  TT         GT
GAM112  UBXD2    3'  CTTTATATTTTCCAACTG    68893     GCCGA
                                CGG    GGAGGATGTGGAG
                                |||    ||||||||||||||
                                GTC    CCTTTTATATTTC
                                  AA___
GAM112  URG4     3'  GCTCTGTGTCCCCAGGGCCTG  35925       GA  A    TG
                                CGGGCC  GG GGATG  GAGC
                                ||||||  || |||||  ||||
                                GTCCGG  CC CCTGT  CTCG
                                    GA  _    GT
GAM112  X123     5'  CTGCTCTCTGTGGTTTGTG    70479          A    AT TG
                                CACGGGCCG GGAGG  G  G
                                |||||||||| |||||  |  |
                                GTGTTTGGT TCTCT  C  C
                                      G     __ GT
GAM112  YAP1     5'  GCTTCTCCACCTCGGCCCGTG  21461            A   TGT
                                CACGGGCCGAGG GGA   GGAGC
                                |||||||||||| |||   |||||
                                GTGCCCGGCTCC CCT   CTTCG
                                       A   ___
GAM112  ZER6     3'  GTTCTGTCTCTGTCTTTGGCTT 64116    CG       _   T TG
             CTG                    CA  GGCCGAGGA GGA G  GAGC
                                ||  |||||||||| ||| |  ||||
                                GT  TCGGTTTCT TCT T  CTTG
                                 CT        G   C GT
GAM112  ZNF238   3'  GTTTCACATTCTTCCTTTGTT  22029     C       _
                                GGC GAGGAGGA TGTGGAGC
                                ||| |||||||| ||||||||
                                TTG TTCCTTCT ACACTTTG
                                  T       T
GAM112  LOC112687 3'  CTCACCTCCTTGCCTGTG    73232        C      ATGTG
                                CACGGGC GAGGAGG     GAG
                                |||||||  |||||||     |||
                                GTGTCCG TTCCTCC     CTC
                                    _      A_____
GAM112  LOC115648 5'  GCTCTGTGTCCTCAGCGTGTGT 60026      G  C AG      TG
             G                   CACG GC G  GAGGATG  GAGC
                                ||||  || |  |||||||  ||||
                                GTGT TG C  CTCCTGT  CTCG
                                  G  _ GA      GT
GAM112  LOC115939 3'  CTCTGTGTCCTGCCTCGG    74032        _     TG
                                CCGAGG AGGATG  GAG
                                ||||||  ||||||  |||
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                                GGCTCC TCCTGT  CTC
                                   G     GT
GAM112  LOC116028 3'  GTTTCATTTTCCTTCCTGGTTT 74097         A     T_
                GTG                  CACGGGCCG GGAGGA  GTGGAGC
                                     ||||||||| ||||||  |||||||
                                     GTGTTTGGT CTTCCT  TACTTTG
                                        C     TT
GAM112  LOC116068 3'  CTTTACATGTGTGTCTGTG   74107       _ AGGAGG
                                     CACGGGC CG     ATGTGGAG
                                     ||||||| ||     ||||||||
                                     GTGTCTG GT     TACATTTC
                                        T  G_____
GAM112  LOC116143 3'  GTTCCATATTTTATCTTT    74192       __
                                     GAGGA  GGATGTGGAGC
                                     |||||  ||||||||||
                                     TTTCT  TTTATACCTTG
                                        AT
GAM112  LOC121273 5'  GCTCCAGAGTCCTTGGTTTCTG 74498    CG       GGATG
                                     CA  GGCCGAGGA    TGGAGC
                                     ||  |||||||||    ||||||
                                     GT  TTGGTTCCT    ACCTCG
                                      CT       GAG__
GAM112  LOC122830 3'  GCTTCACTTCAGGTTCTTGGTC 74632   C       G__  T
                TTG                    A GGGCCGAGGA   GA GTGGAGC
                                     | ||||||||||   || |||||||
                                     G TCTGGTTCTT   CT CACTTCG
                                      T        GGA  T
GAM112  LOC124916 5'  CTGCCTTCTTCTTGGCCC    76162           T TG
                                     GGGCCGAGGAGGA G  G
                                     |||||||||||||| |  |
                                     CCCGGTTCTTCTT C  C
                                             C GT
GAM112  LOC125434 3'  GTTCCACGTCTTTCTTTAGGC  74871     __
                                     GCC  GAGGAGGATGTGGAGC
                                     |||  ||||||||||||||||
                                     CGG  TTCTTTCTGCACCTTG
                                       AT
GAM112  LOC126661 3'  GCTTTAAGAATTTTTTGGCTGT 75059      G      GATG
                G                     CACGG CCGAGGAG    TGGAGC
                                     ||||| ||||||||    ||||||
                                     GTGTC GGTTTTTT    ATTTCG
                                        _       AAGA
GAM112  LOC126755 3'  GTTCCGTGTCTTGGCCCCTG   75075    C     AGGA   TG
                                     CA GGGCCG    GGA  TGGAGC
                                     || ||||||    |||  ||||||
                                     GT CCCGGT    TCT  GCCTTG
                                      C      _____  GT
GAM112  LOC126913 3'  TTTTGTATTTTCTCTCTGG    75103    _  _      TG
                                     CC GAG GAGGATG  GAG
                                     || ||| |||||||  |||
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                                GG CTC CTTTTAT  TTT
                                 T  T     GT
GAM112  LOC127696 5' GCTCTGTGTCCTCGCTTTTG  75980   CG  CGAG     TG
                                CA  GGC   GAGGATG  GAGC
                                ||  |||   |||||||  ||||
                                GT  TCG   CTCCTGT  CTCG
                                 TT  ____     GT
GAM112  LOC130612 3' GTTTTACATCTTTTATAAATGT 75473     GGCCGA
           G                     CACG     GGAGGATGTGGAGC
                                ||||     ||||||||||||||
                                GTGT     TTTTCTACATTTTG
                                  AAATA_
GAM112  LOC133022 3' CGTGCTCTTCGGTTTTTG    76450   CG       G
                                CA  GGCCGAGGAG ATG
                                ||  ||||||||||| |||
                                GT  TTGGCTTCTC TGC
                                 TT        G
GAM112  LOC133923 5' CTCTGAGTCACGGTCTGTG   76460        AGGAG  G
                                CACGGGCCG    GAT TGGAG
                                |||||||||    ||| |||||
                                GTGTCTGGC    CTG GTCTC
                                     A____  A
GAM112  LOC134187 3' GTTTTGTGTTTTCCCTTTGTT  76465    C  _    TG
                                GGC GAGG AGGATG  GAGC
                                ||| |||| ||||||  ||||
                                TTG TTCC TTTTGT  TTTG
                                  T   C     GT
GAM112  LOC134530 3' TTCCATGTTTTCCTTGTTC   75664   GC
                                G  CGAGGAGGATGTGGAG
                                |  ||||||||||||||||
                                C  GTTCCTTTTGTACCTT
                                 TT
GAM112  LOC138130 5' CTTTATGTGGTGGTCGTG    76480     G  AGGAGG
                                CACGG CCG     ATGTGGAG
                                ||||| |||     ||||||||
                                GTGCT GGT     TGTATTTC
                                   _  GG____
GAM112  LOC139422 3' TTCTATGTGATGGCTTG     76358       AGGAGG
                                CGGGCCG     ATGTGGAG
                                |||||||     ||||||||
                                GTTCGGT     TGTATCTT
                                    AG____
GAM112  LOC144231 3' GTTTTGTATCTTTAAGCTGTG  83942      G CGAG     TG
                                CACGG C   GAGGATG  GAGC
                                ||||| |   |||||||  ||||
                                GTGTC G   TTTCTAT  TTTG
                                   _ AA__      GT
GAM112  LOC144563 5' GCTTCATGTCTTCTTCCTGCTC 77399     C_
                                GGGC  GAGGAGGATGTGGAGC
                                ||||  ||||||||||||||||
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                                CTCG  CTTCTTCTGTACTTCG
                                  TC
GAM112  LOC144747 5'  TATTCCTATGTGTTTCTTTGGC 77474           _   _   C
          CTGTG                  CACGGGCCGAGGAGG ATGT GGAG
                                 ||||||||||||||| |||| ||||
                                 GTGTCCGGTTTCTTT TGTA CCTT
                                        G   T   ATG
GAM112  LOC145134 5'  CTTTGCATTCTTTGCCTG   84209     CGA      TG
                                 CGGGC  GGAGGATG  GAG
                                 |||||  ||||||||  |||
                                 GTCCG  TTTCTTAC  TTC
                                    ___     GT
GAM112  LOC145231 3'  GCTTTGCCAGTTCTTTGGCCTA 84251   CG       GAT TG
          TG                     CA  GGCCGAGGAG  G  GAGC
                                 ||  ||||||||||  |  ||||
                                 GT  CCGGTTTCTT  C  TTCG
                                  AT        GAC GT
GAM112  LOC145815 5'  GTTCTGTATCTTCAGTATCTTG 84521     CCGAG     TG
                                 CGGG   GAGGATG  GAGC
                                 ||||   |||||||  ||||
                                 GTTC   CTTCTAT  CTTG
                                   TATGA     GT
GAM112  LOC145824 3'  ATATTTTCTTTGGCTTTG   77981   C
                                 A GGGCCGAGGAGGATGT
                                 | ||||||||||||||||
                                 G TTCGGTTTCTTTTATA
                                  T
GAM112  LOC145844 3'  GTTTTGTGTTATTTTTGGTTTG 77998         G   TG
          T                      ACGGGCCGAGGA GATG  GAGC
                                 ||||||||||||| ||||  ||||
                                 TGTTTGGTTTTT TTGT  TTTG
                                        A   GT
GAM112  LOC146337 3'  GCTCCACTCCACCGGCCTGTG  84641       GA  A   T
                                 CACGGGCC  GG GGA GTGGAGC
                                 ||||||||  || ||| |||||||
                                 GTGTCCGG  CC CCT CACCTCG
                                    __  A  _
GAM112  LOC146723 3'  GTTTTATATTTTCCATATCTGT 78686      CCGA
          G                      CACGGG   GGAGGATGTGGAGC
                                 ||||||   ||||||||||||||
                                 GTGTCT   CCTTTTATATTTTG
                                    ATA_
GAM112  LOC146839 3'  GTTTTGTATCACTGAGTGCTTG 84850      CGA_  AG   TG
          TG                     CACGGGC   GG  GATG  GAGC
                                 |||||||   ||  ||||  ||||
                                 GTGTTCG   TC  CTAT  TTTG
                                     TGAG  A_   GT
GAM112  LOC146839 3'  GTTTTGTATTTTCTTGC    84851   CG      TG
                                 GC  AGGAGGATG  GAGC
                                 ||  |||||||||  ||||
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                                CG  TTCTTTTAT  TTTG
                                 __       GT
GAM112  LOC147694 5'  GTTTCACCAACTTCGGCCTATG 79107    CG       AGGAT
                                CA  GGCCGAGG    GTGGAGC
                                ||  ||||||||    |||||||
                                GT  CCGGCTTC    CACTTTG
                                 AT       AAC__
GAM112  LOC148734 5'  ATCTACCCTTGGTCTTTG    79708    C       AGGAT    GC
                                CA GGGCCGAGG    GTGGA
                                || |||||||||    |||||
                                GT TCTGGTTCC    CATCT
                                 T       _____    AT
GAM112  LOC148760 3'  TTCTGTTTCTGGTTTGTG    85367        G    GGAT TG
                                CACGGGCC AGGA    G  GAG
                                |||||||| ||||   |  |||
                                GTGTTTGG TCTT    T  CTT
                                     _   ____ GT
GAM112  LOC149351 5'  GTTTTGTGTCTTCATTCTGG   80088    _  _     TG
                                CC GAG GAGGATG  GAGC
                                || ||| |||||||  ||||
                                GG CTT CTTCTGT  TTTG
                                 T  A      GT
GAM112  LOC149650 3'  GCTCCGTGTTACAGGAGGCTTG 80286        GAGGAG  TG
          TG                     CACGGGCC     GA  TGGAGC
                                |||||||     ||  ||||||
                                GTGTTCGG     TT  GCCTCG
                                     AGGACA  GT
GAM112  LOC149668 5'  GCTCTGTATTTAGTGGGCCTTG 85701   C    GAGGA    TG
                                A GGGCC    GGATG  GAGC
                                | |||||    |||||  ||||
                                G TCCGG    TTTAT  CTCG
                                 T    GTGA_    GT
GAM112  LOC149832 5'  TGTCCTTCTGGGTTTGTG    85871        G
                                CACGGGCC AGGAGGATG
                                |||||||| |||||||||
                                GTGTTTGG TCTTCCTGT
                                     G
GAM112  LOC149992 5'  CTCTACACTGGGCCTGTG    80375        G  GAGGA
                                CACGGGCC AG    TGTGGAG
                                |||||||| ||    |||||||
                                GTGTCCGG TC    ACATCTC
                                     G _____
GAM112  LOC150577 3'  GCTCCACGTCCTCACCGCATTT 86256    _____  AG
          GCT                     GGC    CG  GAGGATGTGGAGC
                                |||    ||  ||||||||||||||
                                TCG    GC  CTCCTGCACCTCG
                                  TTTAC  CA
GAM112  LOC152271 3'  GCTCCGTGTCTTCTTCCTGCTC 81360     C_      TG
                                GGGC  GAGGAGGA  TGGAGC
                                ||||  ||||||||  ||||||
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                                CTCG  CTTCTTCT  GCCTCG
                                  TC       GT
GAM112  LOC152559 3'  CTCTGGTCCTCGGTTTCTG   81492    CG       GGATG
                                CA  GGCCGAGGA    TGGAG
                                ||  |||||||||    |||||
                                GT  TTGGCTCCT    GTCTC
                                 CT       G____
GAM112  LOC153205 3'  GCTTTACCAAAACTTGGTTTAT 87161    CG      GAGGAT
              G                  CA  GGCCGAG     GTGGAGC
                                ||  |||||||     |||||||
                                GT  TTGGTTC     CATTTCG
                                 AT      AAAAC_
GAM112  LOC157567 5'  GCTTCTTCGCGGTCTGTG    82392         A     T
                                CACGGGCCG GGAGGA GT
                                |||||||||| |||||| ||
                                GTGTCTGGC CTTCTT CG
                                      G     _
GAM112  LOC158187 3'  GCTGTCACTTCTTTTGGCTTGT 87994          G    T   _
              G                  CACGGGCCGAG AGGA GTGG AGC
                                |||||||||||| |||| |||| |||
                                GTGTTCGGTTT TCTT CACT TCG
                                      _   _    G
GAM112  LOC158279 5'  GCTCCAAAATGGTCTCCTGGTC 60331        G     ATG___
              CGTG                  CACGGGCC AGGAGG     TGGAGC
                                |||||||| ||||||     ||||||
                                GTGCCTGG TCCTCT     ACCTCG
                                   _     GGTAAA
GAM112  LOC158293 5'  CTTCGGGCTCTCGGTTGTG   82746      G    G  GATG
                                CACGG CCGAG AG    TGGAG
                                ||||| ||||| ||    |||||
                                GTGTT GGCTC TC    GCTTC
                                  _    _ GG__
GAM112  LOC158549 5'  GTTCTTCCCTTCCTCGGCCC   88229          ATGT
                                GGGCCGAGGAGG    GGAGC
                                ||||||||||||    |||||
                                CCCGGCTCCTTC    TCTTG
                                       CCT_
GAM112  LOC163682 3'  CCCGTTCTCCTGGTTTGTG    88401        G       T
                                CACGGGCC AGGAGGATG GG
                                |||||||| ||||||||| ||
                                GTGTTTGG TCCTCTTGC CC
                                   _       _
GAM112  LOC164382 5'  TTCCACTTTGGGTTTGTG     88562        G   AGGAT
                                CACGGGCC AGG     GTGGAG
                                |||||||| |||    ||||||
                                GTGTTTGG TTT     CACCTT
                                   G  ______
GAM112  LOC165104 5'  GTTCCGCCTCAGGCTTCGGTCT 83352          AG_  T
              G                  CGGGCCGAGG   GA GTGGAGC
                                ||||||||||   || |||||||
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                                GTCTGGCTTC   CT CGCCTTG
                                     GGA  C
GAM112   LOC170132 5'  GTTCTGGCCCTTGGCTGTG   83463      G     ___
                                CACGG CCGAGG   AGGAT
                                ||||| ||||||   |||||
                                GTGTC GGTTCC   TCTTG
                                   _     CGG
GAM112   LOC199858 5'  GTTCAACTTTCTCATTTGGCCT 89802          _    T  G
           GTG                    CACGGGCCGAG GAGGA GT GAGC
                                ||||||||||| ||||| || ||||
                                GTGTCCGGTTT CTCTT CA CTTG
                                     A    T  A
GAM112   LOC200734 3'  CGTATACTTTTTGGTTTGTG   90274            G
                                CACGGGCCGAGGAG ATGTG
                                |||||||||||||| |||||
                                GTGTTTGGTTTTTC TATGC
                                       A
GAM112   LOC200812 5'  GCTCCACATCCAGGATGCCC   90304     CGAGGA
                                GGGC     GGATGTGGAGC
                                ||||     ||||||||||
                                CCCG     CCTACACCTCG
                                  TAGGA_
GAM112   LOC200982 3'  GCTCCACATTCTCCTCCTCG   91811     CC
                                CGGG  GAGGAGGATGTGGAGC
                                ||||  ||||||||||||||||
                                GCTC  CTCCTCTTACACCTCG
                                   __
GAM112   LOC201283 3'  GTTTTATATTTTGTCCTGT    61054      C   GGAG
                                ACGGG CGA    GATGTGGAGC
                                ||||| |||    ||||||||||
                                TGTCC GTT    TTATATTTTG
                                   T  _____
GAM112   LOC201617 5'  CTCTGTGCTGGGCTTGTG    91825        G  GAGGA  TG
                                CACGGGCC AG     TG  GAG
                                |||||||| ||     ||  |||
                                GTGTTCGG TC     GT  CTC
                                     G  ______  GT
GAM112   LOC201780 3'  GCTTCATATTTATAGCCTGTG  90483        CGAGGA
                                CACGGGC     GGATGTGGAGC
                                |||||||     ||||||||||||
                                GTGTCCG     TTTATACTTCG
                                    ATA___
GAM112   LOC201799 3'  GCTTTGTGTTTTCCTTGCTC   90492     C        TG
                                GGGC GAGGAGGATG  GAGC
                                |||| ||||||||||  ||||
                                CTCG TTCCTTTTGT  TTCG
                                   _        GT
GAM112   LOC201824 3'  GTTTCATGTCACAGGCCC    90504      GAGGAG
                                GGGCC     GATGTGGAGC
                                |||||     ||||||||||
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                                CCCGG     CTGTACTTTG
                                  ACA___
GAM112  LOC202451 5'  TTTTACATCTTTCATTGG    91958      _
                                CCGA GGAGGATGTGGAG
                                |||| ||||||||||||
                                GGTT CTTTCTACATTTT
                                  A
GAM112  LOC203378 5'  GTTCTGTGTTCTAAGCAGGCTT 92300        GAGG_     TG
          GT                     ACGGGCC    AGGATG  GAGC
                                |||||||    ||||||  ||||
                                TGTTCGG    TCTTGT  CTTG
                                   ACGAA     GT
GAM112  LOC219672 5'  GTTCTGCTTGTGGCCTGTG   92971         __  G
                                CACGGGCC  GAG AGGAT
                                ||||||||  ||| |||||
                                GTGTCCGG  TTC TCTTG
                                    TG   G
GAM112  LOC219743 3'  GCTTCAATGGGGCCTTGGCTC  94747          AGGATG
                                GGGCCGAGG     TGGAGC
                                |||||||||     ||||||
                                CTCGGTTCC     ACTTCG
                                     GGGGTA
GAM112  LOC219988 3'  GTTTTGCATTTTCTTTGCCC   93265      C        TG
                                GGGC GAGGAGGATG  GAGC
                                |||| ||||||||||  ||||
                                CCCG TTTCTTTTAC  TTTG
                                  _        GT
GAM112  LOC220573 3'  GTTTCACCTTATTTTTGGTCTT 70206    C        G  T
          TG                     CA GGGCCGAGGA GA GTGGAGC
                                || ||||||||||  || |||||||
                                GT TCTGGTTTTT TT CACTTTG
                                 T         A  C
GAM112  LOC220864 5'  GCTCCAAAATGGTCTCCTGGTC 92488         G     ATG___
          CGTG                     CACGGGCC AGGAGG     TGGAGC
                                |||||||| ||||||     ||||||
                                GTGCCTGG TCCTCT     ACCTCG
                                   _     GGTAAA
GAM112  LOC221683 3'  GCTTCTCTGTGGCCTGTG    95330          A     T
                                CACGGGCCG GGAGGA GT
                                ||||||||| |||||| ||
                                GTGTCCGGT TCTCTT CG
                                    G     _
GAM112  LOC222057 3'  GCTTTGCATCTTCTCCAGGCCC 94359       GA_       TG
                                GGGCC   GGAGGATG  GAGC
                                |||||   ||||||||  ||||
                                CCCGG   TCTTCTAC  TTCG
                                  ACC       GT
GAM112  LOC222160 3'  TTCTGCATCCTGTTCCCTG   95797      CC   G     TG
                                CGGG  GAG AGGATG  GAG
                                ||||  ||| ||||||  |||
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                                GTCC  CTT TCCTAC  CTT
                                  __  G     GT
GAM112  LOC222225 5'  GCTTTGCGGCATCTCGGCCC  95959        AGGA  TG
                                GGGCCGAGG   TG  GAGC
                                |||||||||   ||  ||||
                                CCCGGCTCT   GC  TTCG
                                     ACG_  GT
GAM112  LOC253725 5'  GCTCTGCGGTCCTCGGCCTGTG 96357          GGA  TG
                                CACGGGCCGAGGA  TG  GAGC
                                ||||||||||||  ||  ||||
                                GTGTCCGGCTCCT  GC  CTCG
                                       G__  GT
GAM112  LOC254428 3'  CTCTGGATTTTTGGTTTTG   97196   C      GAG   G
                                A GGGCCGAG   GAT TGGAG
                                | ||||||||  ||| |||||
                                G TTTGGTTT   TTA GTCTC
                                 T       ___  G
GAM112  LOC254892 3'  ATGTTTTCTTCGGCCTTG    97262   C
                                A GGGCCGAGGAGGATGT
                                | ||||||||||||||||
                                G TCCGGCTTCTTTTGTA
                                 T
GAM112  LOC255031 5'  GCTCCATCCAAGCCTCCTTGGC 99037          AT___
          CC                      GGGCCGAGGAGG    GTGGAGC
                                ||||||||||||    |||||||
                                CCCGGTTCCTCC    TACCTCG
                                       GAACC
GAM112  LOC255826 3'  CTCTGGTCTTGGCTCCGTG   99369      _     AGGATGT
                                CACGG GCCGAGG      GGAG
                                ||||| |||||||      ||||
                                GTGCC CGGTTCT      TCTC
                                   T     GG_____
GAM112  LOC255975 3'  GCTTTGCATCCTCTCCAGGCCC 97588      GA_      TG
                                GGGCC   GGAGGATG  GAGC
                                |||||   ||||||||  ||||
                                CCCGG   TCTCCTAC  TTCG
                                   ACC       GT
GAM112  LOC256160 3'  GCTTCATATTTATAGCCTGTG  97563       CGAGGA
                                CACGGGC     GGATGTGGAGC
                                |||||||     ||||||||||||
                                GTGTCCG     TTTATACTTCG
                                    ATA___
GAM112  LOC256183 3'  TTTTGTACTTGCCCTGTG    98282       C   GAGGA  TG
                                CACGGG CGAG    TG  GAG
                                |||||| ||||    ||  |||
                                GTGTCC GTTC    AT  TTT
                                   C   _____  GT
GAM112  LOC256337 5'  GCTCTGCGGTCCTCGGCCTGTG 96345          GGA  TG
                                CACGGGCCGAGGA  TG  GAGC
                                ||||||||||||  ||  ||||
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                                GTGTCCGGCTCCT  GC  CTCG
                                       G__  GT
GAM112  LOC256374 3'  TTCCATGTTTTCCTTGTTC   96274   GC
                                G  CGAGGAGGATGTGGAG
                                |  ||||||||||||||||
                                C  GTTCCTTTTGTACCTT
                                 TT
GAM112  LOC51015  3'  GTTCTATATTTTCTTCACCT   32648    CC
                                GGG  GAGGAGGATGTGGAGC
                                |||  ||||||||||||||||
                                TCC  CTTCTTTTATATCTTG
                                  A_
GAM112  LOC51333  3'  CTACATTCCCTCGGCCCGTG   34051          A
                                CACGGGCCGAGG GGATGTGG
                                |||||||||||| ||||||||
                                GTGCCCGGCTCC CTTACATC
                                          _
GAM112  LOC51333  3'  GTTCCCGGCACCTCGGTTTGTG 34055          AGGA  T
                                CACGGGCCGAGG   TG GGAGC
                                ||||||||||||   || |||||
                                GTGTTTGGCTCC   GC CCTTG
                                       ACG_ _
GAM112  LOC51701  5'  GCTCTATGTTTTTTGAGGT   33171    GA
                                GCC  GGAGGATGTGGAGC
                                |||  ||||||||||||||
                                TGG  TTTTTTGTATCTCG
                                  AG
GAM112  LOC90233  3'  GCTTTGTGTTCCTGTATTGTG  57194     GCCGA  A    TG
                                CACGG    GG GGATG  GAGC
                                |||||    || |||||  ||||
                                GTGTT    TC CTTGT  TTCG
                                   ATG__  _    GT
GAM112  LOC90268  3'  GCTTTGTGTTCTTCACTGTG   62665     GCCGA      TG
                                CACGG    GGAGGATG  GAGC
                                |||||    ||||||||  ||||
                                GTGTC    CTTCTTGT  TTCG
                                   A____       GT
GAM112  LOC91133  3'  GCTTTACATTTTTTTTTCACTG 65636    GCC
                                CGG   GAGGAGGATGTGGAGC
                                |||   ||||||||||||||||
                                GTC   TTTTTTTTACATTTCG
                                  ACT
GAM112  LOC91133  3'  GTTCCATTAACCATTTCTTGGT 65637      G     __  AT_
          TGTG                    CACGG CCGAGGA  GG   GTGGAGC
                                |||||  |||||||  ||   |||||||
                                GTGTT GGTTCTT  CC   TACCTTG
                                   _     TA  AAT
GAM112  LOC92270  3'  GTTCTGTGCTATTTGACTTGTG 69189       C    G  G  GT
                                CACGGG CGAG AG AT  GGAGC
                                |||||| |||| || ||  |||||
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                                GTGTTC GTTT TC TG  TCTTG
                                   A   A  G  __
GAM113  CENPB    3'  CCCACCGTGGAAGTAACCAA  70111      AATC        A
                                TTGGT   TTTCCACGGT GG
                                |||||   |||||||||| ||
                                AACCA   GAAGGTGCCA CC
                                   AT__        C
GAM113  HIP12    3'  CTCTGGAAAGGCTACCAA    66816      AT      C
                                TTGGTA  CTTTCCA GG
                                ||||||  ||||||| ||
                                AACCAT  GAAAGGT TC
                                   CG      C
GAM113  DIO2     3'  CCTATGTGAAAAGATCCCAA  7665      TA     C   G
                                TTGG  ATCTTT CACG TAGG
                                ||||  |||||| |||| ||||
                                AACC  TAGAAA GTGT ATCC
                                  C_     A   _
GAM113  DIO2     3'  CCTATGTGAAAAGATCCCAA  26551     TA     C   G
                                TTGG  ATCTTT CACG TAGG
                                ||||  |||||| |||| ||||
                                AACC  TAGAAA GTGT ATCC
                                  C_     A   _
GAM113  KIAA0174 3'  CTGTGGGAAGACCACCAA    79294      AA
                                TTGGT  TCTTTCCACGG
                                |||||  ||||||||||
                                AACCA  AGAAGGGTGTC
                                   CC
GAM113  TTC4     3'  CCTAAAAAGATTGCCAA     66909          CCACGG
                                TTGGTAATCTTT     TAGG
                                ||||||||||||     ||||
                                AACCGTTAGAAA     ATCC
                                      A_____
GAM113  LOC90786 3'  CCAATAACAGAAAGATTACTAA 64728          CACG  A
                                TTGGTAATCTTTC   GT GG
                                ||||||||||||   || ||
                                AATCATTAGAAAG   TA CC
                                      ACAA  A
GAM114  ABCB4    5'  CCAGTTTAGCTCCAAAGGA   38757      _     CTCC
                                TCCTT GGAGCT   ATTGG
                                ||||| ||||||   |||||
                                AGGAA CCTCGA   TGACC
                                   A     TT__
GAM114  AK3      3'  CCAATGGAAGAACCAGGAA   26397      T  AG  C
                                TTCCT GG  CT TCCATTGG
                                ||||| ||  || ||||||||
                                AAGGA CC  GA AGGTAACC
                                   _  AA  _
GAM114  ARNT2    3'  CCACAGGAGCCCCAAGGGA   30084        A    CCAT
                                TTCCTTGG GCTCT   TGG
                                |||||||| |||||   |||
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                                AGGGAACC CGAGG   ACC
                                    C    AC__
GAM114  ATP2B2   3' CCAATGGAACCGAAGAA    9847     C   AGCTC
                                TTC TTGG    TCCATTGG
                                ||| ||||    ||||||||
                                AAG AGCC    AGGTAACC
                                  A   A____
GAM114  BLAME    3' CCAACTGGCACCAAGGAA    39652       A  CTCCA
                                TTCCTTGG GCT    TTGG
                                |||||||| |||    ||||
                                AAGGAACC CGG    AACC
                                    A  TC___
GAM114  DUSP4    5' CCAAAGCGCTCCAAGAGA    9151    _      T  CCA
                                TC CTTGGAGC CT   TTGG
                                || |||||||| ||   ||||
                                AG GAACCTCG GA   AACC
                                 A       C  ___
GAM114  G6PT1    3' CCAATACCTCAGACTCCAGGGA 9400         C  CC___
            A                    TTCCTTGGAG TCT    ATTGG
                                ||||||||||| |||    |||||
                                AAGGGACCTC AGA    TAACC
                                      _  CTCCA
GAM114  IL1RAP   3' CCAATAGAGAACATTCAAGGGA 57071       GC_   C
                                TTCCTTGGA   TCTC ATTGG
                                |||||||||   |||| |||||
                                AGGGAACTT   AGAG TAACC
                                     ACA   A
GAM114  MMP14    3' CCAGGGAACTTCCAAGGAA   18427        CTC   A
                                TTCCTTGGAG   TCC TTGG
                                ||||||||||   ||| ||||
                                AAGGAACCTT   AGG GACC
                                     CA_  _
GAM114  RLBP1    5' CCAGGTAGCCCCAAGGAG    6163       A  CT  AT
                                TTCCTTGG GCT  CC  TGG
                                |||||||| |||  ||  |||
                                GAGGAACC CGA  GG  ACC
                                    C   T_  __
GAM114  TBXA2R   5' CCAACAGCATCCTAGGAA    8347      T  _  CTCCA
                                TTCCT GGA GCT    TTGG
                                ||||| ||| |||    ||||
                                AAGGA CCT CGA    AACC
                                   T   A  C____
GAM114  TEC      3' CCTTGTGAGCGCCAAGGAA   13678       A   TC  TT
                                TTCCTTGG GCTC  CA  GG
                                |||||||| ||||  ||  ||
                                AAGGAACC CGAG  GT  CC
                                    G   T_  T_
GAM114  UBE3A    3' CCAACAGAACTACTCTCCCAAG 6624        _ CTC___  CA
            GAA                   TTCCTTGG AG     TC  TTGG
                                ||||||||  ||     ||  ||||
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                                AAGGAACC TC     AG  AACC
                                     C  TCATCA  AC
GAM114  USH3A    3'  CCAGAAAGCACCAAGGAA    54840        A   C  CAT
                                TTCCTTGG GCT TC   TGG
                                |||||||| ||| ||   |||
                                AAGGAACC CGA AG   ACC
                                     A   A  ___
GAM114  BRE      3'  CCAATGGAAAGCTCTAGGAA   18116      T     C
                                TTCCT GGAGCT TCCATTGG
                                ||||| |||||| ||||||||
                                AAGGA TCTCGA AGGTAACC
                                   _     A
GAM114  C20orf39  3'  CCAAAGGAAAGCTCCAAAGA   46572    C       C   A
                                TC TTGGAGCT TCC TTGG
                                || |||||||| ||| ||||
                                AG AACCTCGA AGG AACC
                                 A       A   A
GAM114  caspr5    5'  CCAGCTGCAGCTCCGAAGAA   58114    C       CTC  _
                                TTC TTGGAGCT   CA TTGG
                                ||| ||||||||   || ||||
                                AAG AGCCTCGA   GT GACC
                                  A       C__  C
GAM114  COVA1     3'  CCAATGGAGAGTATTTCA    73640      __
                                TGGA  GCTCTCCATTGG
                                ||||  ||||||||||||
                                ACTT  TGAGAGGTAACC
                                   TA
GAM114  DDX34     3'  CCAGTCAGCCCCAAGGAG    28666        A   CTCC
                                TTCCTTGG GCT    ATTGG
                                |||||||| |||    |||||
                                GAGGAACC CGA    TGACC
                                     C   C___
GAM114  DKFZp434J0226 5'  CCAATGGAGAAGACAGGGA    72791       GAGC
                                TCCTTG    TCTCCATTGG
                                ||||||    ||||||||||
                                AGGGAC    AGAGGTAACC
                                   AGA_
GAM114  DKFZp434N074 5'  CCAATGGAATTCGCAAAGA    63329    C   _   CTC
                                TC TTG GAG   TCCATTGG
                                || ||| |||   ||||||||
                                AG AAC CTT   AGGTAACC
                                 A   G   A__
GAM114  FLJ20330  5'  CCAACGGAGAGCTAGGGAG    39141       GG       A
                                TTCCTT  AGCTCTCC TTGG
                                ||||||  |||||||| ||||
                                GAGGGA  TCGAGAGG AACC
                                   __       C
GAM114  KIAA0981  3'  CCTGTGTAAAACTGCCAAGGAA 62085         _  CTCTC   T
                                TTCCTTGG AG     CAT GG
                                |||||||| ||     ||| ||
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                                AAGGAACC TC     GTG CC
                                     G  AAAAT   T
GAM114  KIAA1345  5'  CCAACTGCTGTCCCCAAGGAA  88617         A_  TCTC  _
                                TTCCTTGG  GC    CA TTGG
                                ||||||||  ||    || ||||
                                AAGGAACC  TG    GT AACC
                                     CC  TC__  C
GAM114  KIAA1453  3'  CCATGGAAGAGTCTCCAAGGAA 47661          _   _   T
                                TTCCTTGGAG CTCT CCAT GG
                                |||||||||| |||| |||| ||
                                AAGGAACCTC GAGA GGTA CC
                                      T    A   _
GAM114  L3MBTL2   5'  CCAATGGAGGAAGAGGAA    90159       GGAG T
                                TTCCTT    C CTCCATTGG
                                ||||||    | |||||||||
                                AAGGAG    G GAGGTAACC
                                    AA__ _
GAM114  MGC16309  3'  CCAGTGAAAGCTCCAGGAA    54180      T     CTC
                                TTCCT GGAGCT   CATTGG
                                ||||| ||||||   ||||||
                                AAGGA CCTCGA   GTGACC
                                   _     AA_
GAM114  MUC13     3'  CCAATGGAGAGATTCTGG    53507    TG  _
                                T  GAG CTCTCCATTGG
                                |  ||| ||||||||||
                                G  CTT GAGAGGTAACC
                                 GT   A
GAM114  RAB17     5'  CCATACAGCTCCAAGGAA    42616          CTCCAT
                                TTCCTTGGAGCT     TGG
                                ||||||||||||     |||
                                AAGGAACCTCGA     ACC
                                       CAT___
GAM114  SEMA4G    5'  CCAACAGGTCCCAGGGAA    96323        AG T  CCA
                                TTCCTTGG  C CT   TTGG
                                ||||||||  | ||   ||||
                                AAGGGACC  G GA   AACC
                                     CT _  C__
GAM114  SLC25A18  5'  CCAACAGCGGCTACCCCAAGGA 49750         ___   _  CCA
          G                      TTCCTTGG   AGCT CT   TTGG
                                ||||||||   |||| ||   ||||
                                GAGGAACC   TCGG GA   AACC
                                     CCA    C  C__
GAM114  TRIM4     3'  CCAATGGAGATGGGACAGGAA  53405      TGGAGC
                                TTCCT     TCTCCATTGG
                                |||||     ||||||||||
                                AAGGA     AGAGGTAACC
                                   CAGGGT
GAM114  LOC126917 3'  CCACTTTGAGCTCCAAAGAA   75084     C       TCCAT
                                TTC TTGGAGCTC     TGG
                                ||| |||||||||     |||
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                                AAG AACCTCGAG    ACC
                                  A       TTTC_
GAM114  LOC151162 5'  CCAGACTTCAGCCCCCAAGGAA 86427       A_  CTCCA
                                TTCCTTGG  GCT    TTGG
                                ||||||||  |||    ||||
                                AAGGAACC  CGA    GACC
                                    CC   CTTCA
GAM114  LOC151516 3'  TGGAAGAGCTCCCAAGGAA   81070       _    _
                                TTCCTTGG AGCTCT CCA
                                |||||||| |||||| |||
                                AAGGAACC TCGAGA GGT
                                    C     A
GAM114  LOC152245 3'  CCAATGGTGTCATCCAATGGAA 86776     _    GCTCT
                                TTCC TTGGA    CCATTGG
                                |||| |||||    |||||||
                                AAGG AACCT    GGTAACC
                                  T    ACTGT
GAM114  LOC152426 3'  CCAATGGAAGGAAAAAGGAA  86892      GGAG TC
                                TTCCTT   C  TCCATTGG
                                ||||||   |  ||||||||
                                AAGGAA   G  AGGTAACC
                                   AAA_ GA
GAM114  LOC162333 5'  CCAATGGAGGAGGGAAGGAA  88488      GGAG T
                                TTCCTT   C CTCCATTGG
                                ||||||   | |||||||||
                                AAGGAA   G GAGGTAACC
                                   GGGA _
GAM114  LOC201283 3'  TGTAGATGCCCCAAGGAA   61056       A _  C
                                TTCCTTGG GC TCT CA
                                |||||||| || ||| ||
                                AAGGAACC CG AGA GT
                                    C  T   T
GAM114  LOC203377 5'  CCAGACTTCAGCCCCCAAGGAA 92256       A_  CTCCA
                                TTCCTTGG  GCT    TTGG
                                |||||||  |||    ||||
                                AAGGAACC  CGA    GACC
                                    CC   CTTCA
GAM114  LOC220081 3'  CCTTGGGAGCTCCAGGGAA   93403         T  TT
                                TTCCTTGGAGCTC CCA  GG
                                |||||||||||| |||  ||
                                AAGGGACCTCGAG GGT  CC
                                      _  T_
GAM114  LOC221543 5'  CCATCAAGAGTCTCCAAGGAA  95369        _   CCAT
                                TTCCTTGGAG CTCT   TGG
                                |||||||||| ||||   |||
                                AAGGAACCTC GAGA   ACC
                                     T   ACT_
GAM114  LOC221543 5'  TGGGGAAAACTCCAAGGA    95390        C__
                                TCCTTGGAG  TCTCCA
                                |||||||||  ||||||
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                                AGGAACCTC   AGGGGT
                                     AAA
GAM114   LOC222031 3'  CCAGGGCTGGCTCCAAGGAA  95675          CT  A
                                TTCCTTGGAGCT  CC TTGG
                                ||||||||||||  || ||||
                                AAGGAACCTCGG  GG GACC
                                      TC  _
GAM114   LOC222159 5'  CCAATGCTTGTCCAAGGA    95728        G TCTC
                                TCCTTGGA C    CATTGG
                                |||||||| |    ||||||
                                AGGAACCT G    GTAACC
                                     _ TTC_
GAM114   LOC253574 5'  CCAACAGAGAGCTTGACAAG  99338      __       CA
                                CTTG  GAGCTCTC  TTGG
                                ||||  ||||||||  ||||
                                GAAC  TTCGAGAG  AACC
                                  AG       AC
GAM114   LOC255193 5'  CCAATTCATCTGCACCCCAAGG 97100        A__  TCTCC_
           AA                     TTCCTTGG   GC     ATTGG
                                |||||||   ||     |||||
                                AAGGAACC   CG     TAACC
                                     CCA  TCTACT
GAM114   LOC257596 5'  CCATCAAGAGTCTCCAAGGAA  99772          _    CCAT
                                TTCCTTGGAG CTCT    TGG
                                |||||||||| ||||    |||
                                AAGGAACCTC GAGA    ACC
                                      T    ACT_
GAM114   LOC257596 5'  TGGGGAAAACTCCAAGGA    99793         C__
                                TCCTTGGAG   TCTCCA
                                |||||||||   ||||||
                                AGGAACCTC   AGGGGT
                                     AAA
GAM114   LOC51236  3'  CCACTGCAAGCCCCAAGGAG  33620         A   CTC  T
                                TTCCTTGG GCT   CA TGG
                                |||||||| |||   || |||
                                GAGGAACC CGA   GT ACC
                                     C   AC_  C
GAM115   CDH12     3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM115   GOCAP1    3'  ATTGTTCTTGGGAGCAGTGTA  43007       CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                  AC         G
GAM115   DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090       T    AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||     ||||||
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                                TGGTG GGGT    TTATTC
                                  _   GTCA_
GAM115  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
            A                     TACAC       AGAAGAATAAG
                                  |||||       ||||||||||
                                  ATGTG       TCTTCTTATTC
                                    TACTCCC_
GAM115  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126        CCCAAGAA
                                  TACACCACT       GAATAAG
                                  |||||||||       |||||||
                                  ATGTGGTGA       TTTATTC
                                       AGACG___
GAM115  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
            TA                    TACA   TCC   GAAGAATAAG
                                  ||||   |||   ||||||||||
                                  ATGT   AGG   TTTCTTATTC
                                    AAA_  ATTG
GAM115  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA  68742             _
                                  TACACCACTCCCAAGA AGA
                                  |||||||||||||||| |||
                                  ATGTGGTGAGGGTTCT TCT
                                            G
GAM115  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                  CAC  CT CCAAGAAGAA
                                  |||  || ||||||||||
                                  GTG  GA GGTTCTTTTT
                                    AC  A
GAM115  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748     CCA__
                                  ACTC    AGAAGAATAAG
                                  ||||    ||||||||||
                                  TGAG    TCTTCTTATTC
                                    TACCG
GAM115  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                                  CCA    CAAGAAGAATAAG
                                  |||    ||||||||||||
                                  GGT    GTTCTTCTTATTC
                                    TTTCA
GAM115  OSBPL11   3'  CTTAATTTCCCAAGAGTGGTG  43206        CCAA    AA
                                  CACCACTC    GAAG  TAAG
                                  ||||||||    ||||  ||||
                                  GTGGTGAG    CTTT  ATTC
                                       AACC    A_
GAM115  YME1L1    3'  TCATTCTTGATGTGGTGTA    58438        TCC     _
                                  TACACCAC   CAAGAA GA
                                  ||||||||   |||||| ||
                                  ATGTGGTG   GTTCTT CT
                                       TA_     A
GAM115  ZNF262    3'  CTTATTTTGTTTGGGAGT     18723         A
                                  ACTCCCAAG AGAATAAG
                                  ||||||||| ||||||||
```

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                                TGAGGGTTT TTTTATTC
                                     G
GAM115  LOC91960  3'  TGTGGCTTGGAACGTGGTGTA  68294        TC_    AAGA
                                TACACCAC  CCAAG   ATA
                                ||||||||  |||||   |||
                                ATGTGGTG  GGTTC   TGT
                                     CAA    GG__
GAM116  AMACR     3'  CCAGAAATAAAGATCTCAGGA  69100     A      CCCACAG
                                TCC TGAGATCT      TTGG
                                ||| ||||||||      ||||
                                AGG ACTCTAGA      GACC
                                  _      AATAAA_
GAM116  FMR2      3'  CCAACTGTGATGTCACTGA   10684    CA   G   TCCC
                                TC  TGA ATC   ACAGTTGG
                                ||  ||| |||   ||||||||
                                AG  ACT TAG   TGTCAACC
                                 TC   G  ____
GAM116  IL15RA    3'  CAGCAGGATCTCACGGA     10996     A      CCCACA
                                TCC TGAGATCT     GTTG
                                ||| ||||||||     ||||
                                AGG ACTCTAGG     CGAC
                                  C       A_____
GAM116  APOA5     3'  CCAACTGTGGGAGCTC      54800     AT
                                GAG  CTCCCACAGTTGG
                                |||  ||||||||||||
                                CTC  GAGGGTGTCAACC
                                  __
GAM116  KCNJ14    5'  CCAACTGTGAAAGGGGGT    26241       ___
                                ATCTCC   CACAGTTGG
                                ||||||   |||||||||
                                TGGGGG   GTGTCAACC
                                   AAA
GAM116  LOC130074 3'  CACAGTTGGCCTAGAGAGCCTC 76623         A_   ________   CAGT
           ATGGAT                  ATCCATGAG  TCTC      CCA    TG
                                |||||||||  ||||      |||   ||
                                TAGGTACTC  AGAG      GGT    AC
                                     CG    ATCC___   TGAC
GAM116  LOC149483 5'  AAGTTGGCTTGAAGATCTCACA 80182    CA      _ _______   CAGT
           GA                    TC  TGAGATCT C     CCA    T
                                ||  |||||||| |     |||    |
                                AG  ACTCTAGA G     GGT    A
                                 AC       A TTC___   TGAC
GAM116  LOC158927 3'  CCAACTGTGGAACTGAATGGG  88313      GAGATCTC
                                TCCAT       CCACAGTTGG
                                |||||       ||||||||||
                                GGGTA       GGTGTCAACC
                                  AGTCAA__
GAM116  LOC220758 3'  CCATCTGTGGGAAATCCCAGGA 92462     A  A   C      T
                                TCC TG GAT TCCCACAG TGG
                                ||| || ||| |||||||| |||
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                                AGG AC CTA AGGGTGTC ACC
                                  _ C   A       T
GAM116  LOC256846 5'  AAGTTGGCTTGAAGATCTCACA 97153    CA      _ _______  CAGT
            GA                    TC  TGAGATCT C     CCA    T
                                ||  |||||||| |     |||    |
                                AG  ACTCTAGA G     GGT    A
                                 AC       A TTC___   TGAC
GAM116  LOC51131  3'  AAGTTGGCCAGAAAAACTCATG 32782         ATC_  _______  CAGT
            GAT                   ATCCATGAG    TC     CCA    T
                                |||||||||    ||     |||   |
                                TAGGTACTC    AG     GGT    A
                                     AAAA  ACC___   TGAC
GAM117  SCAMP1    3'  GCTAAATAAATATTCTCC    54500     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM117  SCAMP1    3'  GCTAAATAAATATTCTCC    54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM117  NX-17     3'  TGAATATCAGCCCCTAATA    40706         ATA_
                                TATTAGGG    ATATTCA
                                ||||||||    |||||||
                                ATAATCCC    TATAAGT
                                     CGAC
GAM117  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
            TA                    TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM118  BTEB1     5'  ATTATAGATTCACACTGC     8669       CA  _
                                GCAG  TGA TTTATAAT
                                ||||  ||| ||||||||
                                CGTC  ACT AGATATTA
                                  AC   T
GAM118  CLCN5     3'  ATTATAAGACAATGCTGCT    5384         GA_
                                AGCAGCAT   TTTATAAT
                                ||||||||   ||||||||
                                TCGTCGTA   GAATATTA
                                     ACA
GAM118  FGF2      3'  ATTAGAAATTATGCTGCTA    10612             A
                                TAGCAGCATGATTT TAAT
                                |||||||||||||| ||||
                                ATCGTCGTATTAAA ATTA
                                       G
GAM118  CNOT4     5'  ATTATAAACTTTTGCTGCTG   26165         T  _
                                TAGCAGCA GA TTTATAAT
                                |||||||| || ||||||||
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                                GTCGTCGT TT AAATATTA
                                     T  C
GAM118  DKFZP564K247 3'  ATTATATTTTTGCTGCTG    26765        T  TT
                                TAGCAGCA GA  TATAAT
                                |||||||| ||  ||||||
                                GTCGTCGT TT  ATATTA
                                     _  TT
GAM118  EIF4B    3'  ATTATTTTGCATGCTGCTG   76496         ATTT
                                TAGCAGCATG   ATAAT
                                ||||||||||   |||||
                                GTCGTCGTAC   TATTA
                                      GTTT
GAM118  FLJ14600  3'  ATTATAAATTGTGCCCTA   52524    CA   TG
                                TAG  GCA  ATTTATAAT
                                |||  |||  |||||||||
                                ATC  CGT  TAAATATTA
                                  C_  GT
GAM118  KIAA1336  3'  ATTATAAATTGTTTTGCTA   72784      C TG
                                TAGCAG A  ATTTATAAT
                                ||||||  |  |||||||||
                                ATCGTT T  TAAATATTA
                                    T GT
GAM118  SEMA5A   3'  ATTAGCAGGTCATGCTGT    15589          A_
                                GCAGCATGATTT  TAAT
                                ||||||||||||  ||||
                                TGTCGTACTGGA  ATTA
                                      CG
GAM118  LOC130813 3'  ATTATAAATCATTGTAGC    76265    A  _
                                GC GCA TGATTTATAAT
                                || ||| ||||||||||
                                CG TGT ACTAAATATTA
                                 A  T
GAM118  LOC144766 3'  ATTATAAATCATGCTGCTA   77479
                                TAGCAGCATGATTTATAAT
                                ||||||||||||||||||
                                ATCGTCGTACTAAATATTA

GAM118  LOC145384 3'  ATTATAAATCATGCTGCTA   77712
                                TAGCAGCATGATTTATAAT
                                ||||||||||||||||||
                                ATCGTCGTACTAAATATTA

GAM118  LOC150935 3'  ATTATAAATCTTGCTGCTG   80824        T
                                TAGCAGCA GATTTATAAT
                                ||||||||  ||||||||||
                                GTCGTCGT CTAAATATTA
                                     T
GAM118  LOC151040 3'  ATTATAAATCATGCTGCTA   80904
                                TAGCAGCATGATTTATAAT
                                ||||||||||||||||||
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                                ATCGTCGTACTAAATATTA

GAM118  LOC200609 5'  ATTGTGAATAATGCTGCTA   91659        G
                                TAGCAGCAT ATTTATAAT
                                ||||||||| |||||||||
                                ATCGTCGTA TAAGTGTTA
                                     A
GAM118  LOC222252 3'  ATTATAAATCATGCTGCTA   95964
                                TAGCAGCATGATTTATAAT
                                ||||||||||||||||||
                                ATCGTCGTACTAAATATTA

GAM118  LOC90520  3'  ATTATAAAGGTATGCTGCT   63834        A_
                                AGCAGCATG  TTTATAAT
                                |||||||||  ||||||||
                                TCGTCGTAT  AAATATTA
                                     GG
GAM118  LOC91923  5'  ATTGTGAATAATGCTGCTA   68170        G
                                TAGCAGCAT ATTTATAAT
                                ||||||||| |||||||||
                                ATCGTCGTA TAAGTGTTA
                                     A
GAM119  AKAP1     3'  ACTATGGGTTCTCTTCGCAAA  14472      A  CTT      C
                                TTTGT GA   GGAACCCA AGT
                                ||||| ||   |||||||| |||
                                AAACG CT   TCTTGGGT TCA
                                   _ TC_       A
GAM119  AKAP1     3'  ACTATGGGTTCTCTTCGCAAA  58373      A  CTT      C
                                TTTGT GA   GGAACCCA AGT
                                ||||| ||   |||||||| |||
                                AAACG CT   TCTTGGGT TCA
                                   _ TC_       A
GAM119  EGF       3'  ACTATAGGTTTTGGTTCCACAA 10488      A  C TG    CAC
                                TTGT GA T  GAACC   AGT
                                |||| || |  |||||   |||
                                AACA CT G  TTTGG   TCA
                                  C  T GT     ATA
GAM119  EZH1      3'  GACTGTGGGTTCCAAATTAC   10551      AC
                                GTAG  TTGGAACCCACAGTC
                                ||||  |||||||||||||||
                                CATT  AACCTTGGGTGTCAG
                                  A_
GAM119  STAC      3'  GACTGTGGAGTAATAGCCACAA 13427      AGA  TGGA  _
          A                      TTTGT   CT    AC CCACAGTC
                                |||||   ||    || ||||||||
                                AAACA   GA    TG GGTGTCAG
                                   CC_  TAA_  A
GAM119  CCR1      3'  GACTGTGGGCTCCATTC     8927     CT    A
                                GA  TGGA CCCACAGTC
                                ||  |||| |||||||||
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                                CT  ACCT GGGTGTCAG
                                 T_    C
GAM119  FLJ10483  3'  GACTGTGGAAGAGATTACAAA  36652        A   GGAAC
                                TTTGTAG CTT    CCACAGTC
                                ||||||| |||    ||||||||
                                AAACATT GAG    GGTGTCAG
                                    A   AA___
GAM119  KIAA1871  3'  ACTGTAAGAGTCTACAAA    61890          GGAACCC
                                TTTGTAGACTT      ACAGT
                                ||||||||||       |||||
                                AAACATCTGAG      TGTCA
                                      AA_____
GAM119  LOC150821 3'  GGGTTCCACATCCACAAA    60944      A  CT
                                TTTGT GA  TGGAACCC
                                ||||| ||  ||||||||
                                AAACA CT  ACCTTGGG
                                   C  AC
GAM119  LOC151057 3'  ACTGTGGGTACACCTATAAA  86379       ACT  GA
                                TTTGTAG   TG  ACCCACAGT
                                |||||||   ||  |||||||||
                                AAATATC   AC  TGGGTGTCA
                                    C__  A_
GAM119  LOC157507 5'  ACTGTAAAAGTCTGCAAA    82377          GGAACCC
                                TTTGTAGACTT      ACAGT
                                ||||||||||       |||||
                                AAACGTCTGAA      TGTCA
                                      AA_____
GAM119  LOC203339 5'  GGATTCCCAGTCTACAAA    92214          T    C
                                TTTGTAGACT GGAA CC
                                |||||||||| |||| ||
                                AAACATCTGA CCTT GG
                                      C    A
GAM119  LOC51030  3'  ACTGTAAATTAAACCAATCTAC 32695        C    AACCC___
           AAA                    TTTGTAGA TTGG       ACAGT
                                |||||||| ||||       |||||
                                AAACATCT AACC       TGTCA
                                    _   AAATTAAA
GAM119  LOC90906  3'  GACTGTGGATCCCAAACTTTGC 64951       C_    AAC
           A                     TGTAGA  TTGG   CCACAGTC
                                ||||||  ||||   ||||||||
                                ACGTTT  AACC   GGTGTCAG
                                   CA    CTA
GAM120  SCAMP1    3'  GCTAAATAAATATTCTCC    54500     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM120  SCAMP1    3'  GCTAAATAAATATTCTCC    54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
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                                CCT TTATAA TAAATCG
                                  C     A
GAM120  NX-17    3'  TGAATATCAGCCCCTAATA   40706        ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM120  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
            TA                    TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM121  EHF      3'  TCCAAAACCCAAGGTTGGCT   25127     AT   _   C
                                AGT  GCCT GGGT TTGGA
                                |||  |||| |||| |||||
                                TCG  TGGA CCCA AACCT
                                  GT   A   A
GAM121  EPHA2    3'  CCATCGGCCAAGAATACTTGAA 16675         GC  G   T_
            G                    CTTCAAGTAT  CT GGTC  TGG
                                ||||||||||  || ||||  |||
                                GAAGTTCATA  GA CCGG  ACC
                                     A_  A   CT
GAM121  ITGA5    3'  CCCAGAGACATACTTGAAG   61933          C__
                                CTTCAAGTATG   CTGGG
                                ||||||||||   |||||
                                GAAGTTCATAC   GACCC
                                     AGA
GAM121  TREM2    3'  TCCAAGACTGTCATATTT    39098       CCTG
                                AAGTATG   GGTCTTGGA
                                |||||||   |||||||||
                                TTTATAC   TCAGAACCT
                                   TG__
GAM121  UQCRB    3'  CCAACATAGGCATACTTAAG  21939    C        GGTC
                                CTT AAGTATGCCTG   TTGG
                                ||| ||||||||||   ||||
                                GAA TTCATACGGAT   AACC
                                  _        AC__
GAM121  ATP10D   3'  CAGAGACCACTTGAAG      73526        ATGCCTG   _
                                CTTCAAGT      GGTCT TG
                                ||||||||      ||||| ||
                                GAAGTTCA      CCAGA AC
                                    _______    G
GAM121  B3GNT7   3'  CCCTTCCAGGCAACCTGAA   71678     A  A      TCTT
                                TTCA GT TGCCTGGG   GG
                                |||| || ||||||||   ||
                                AAGT CA ACGGACCT   CC
                                  C  _       TC__
GAM121  DKFZp547I224 3'  TCCAAAATTGACCACATACTTG 39963         CCTG   ____
            GA                   TTCAAGTATG   GGTC   TTGGA
                                ||||||||||   ||||   |||||
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                                AGGTTCATAC   CCAG   AACCT
                                     A___   TTAA
GAM121  FLJ22341  3'  CCAAGCTCAGGCACACCCAAG  45114    CAA  A     T
                                CTT   GT TGCCTGGG CTTGG
                                |||   || |||||||| |||||
                                GAA   CA ACGGACTC GAACC
                                  CC_  C      _
GAM121  KIAA0779  3'  CCGAACAGCATACTTGAAG   86908         C  GGTC
                                CTTCAAGTATGC TG   TTGG
                                ||||||||||| ||   ||||
                                GAAGTTCATACG AC   AGCC
                                      _ A___
GAM121  LOC144233 3'  CCAAGGCACATAATTGAA    77246     G   CCTGG
                                TTCAA TATG    GTCTTGG
                                ||||| ||||    |||||||
                                AAGTT ATAC    CGGAACC
                                   A   A____
GAM121  LOC147341 3'  ACCCAGGCATAACTGAAG    85116     AG
                                CTTCA  TATGCCTGGGT
                                |||||  ||||||||||
                                GAAGT  ATACGGACCCA
                                   CA
GAM121  LOC221088 5'  TCCAAGGTGCTGGCCACTCGAA 94888     A   AT   TGGG
          G                     CTTC AGT  GCC   TCTTGGA
                                |||| |||  |||   |||||||
                                GAAG TCA  CGG   GGAACCT
                                  C   C_   TCGT
GAM122  FLJ14009  5'  GGTGAAGGACAAGACCCTGCA  45753       A  A  ATC
                                TGCAGGGT TT TC   TACC
                                |||||||| || ||   ||||
                                ACGTCCCA AA AG   GTGG
                                     G  C  GAA
GAM122  KIAA1155  3'  CGGTAGACAGAGCACCTCTGCA 62910     _   ATTA  A_
                                TGCAG GGT   TC  TCTACCG
                                ||||| |||   ||  |||||||
                                ACGTC CCA   AG  AGATGGC
                                   T   CG__  AC
GAM122  LCHN     3'  CTCAGCAGATGATACTGCCC   87467     T      ACC
                                GGGTA TATCATCT   GAG
                                ||||| ||||||||   |||
                                CCCGT ATAGTAGA   CTC
                                   C       CGA
GAM122  MGC4309   3'  CTCAATAAATGATAATACT    44368         C  CC
                                GGTATTATCAT TA  GAG
                                |||||||||| ||  |||
                                TCATAATAGTA AT  CTC
                                       A  AA
GAM122  LOC255265 5'  CTCAGTAGATGATGAAACTC   97092     A        C
                                GGGT TTATCATCTAC GAG
                                |||| |||||||||| |||
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                                CTCA AGTAGTAGATG CTC
                                  A         A
GAM123  BIN3     3'  AGCCCTGGCAGGCCCT      38571         TA  A
                                AGGGCCTG  CCA GGCT
                                ||||||||  ||| ||||
                                TCCCGGAC  GGT CCGA
                                    __   C
GAM123  COLQ     3'  AGCCTTGGCTGGCTCCCCATC  55418     TAA    TGTA
                                GAT   GGGCC    CCAAGGCT
                                |||   |||||    ||||||||
                                CTA   CTCGG    GGTTCCGA
                                  CCC    TC__
GAM123  OPCML    3'  CCTTTTCAGGCCCTCAGTC    11897      A       TACC
                                GATT AGGGCCTG    AAGG
                                |||| ||||||||    ||||
                                CTGA TCCCGGAC    TTCC
                                  C       TT__
GAM123  SOX9     3'  AGCCCACTGACAGACCTTAATC 6228          GC    ACCAA
                                GATTAAGG  CTGT    GGCT
                                ||||||||  ||||    ||||
                                CTAATTCC  GACA    CCGA
                                    A_    GTCAC
GAM123  DKFZp434E2220 5'  GTACACAAGCCCTTAATT    34716          C__
                                GATTAAGGGC   TGTAC
                                ||||||||||   |||||
                                TTAATTCCCG   ACATG
                                     AAC
GAM123  FLJ14600  3'  CCTCAGTACCCTTTAAT     52525         CCT    CA
                                ATTAAGGG   GTAC  AGG
                                ||||||||   ||||  |||
                                TAATTTCC   CATG  TCC
                                    ___    AC
GAM123  LOC145693 5'  AGCCTTGGACAAGACCCT    77851      C  _  A
                                AGGG CT GT CCAAGGCT
                                |||| || || ||||||||
                                TCCC GA CA GGTTCCGA
                                  A  A  _
GAM124  ADCY2    3'  ACCAGAATTAGTCCTC      65640        C       T
                                GAGGAC TAATTCTG GT
                                |||||| |||||||| ||
                                CTCCTG ATTAAGAC CA
                                    _       _
GAM124  CARD10   3'  GCACACACAGGACCGTGCCTC  28037      ACCTAA       A
                                GAGG     TTCTGTGT TGC
                                ||||     |||||||| |||
                                CTCC     AGGACACA ACG
                                  GTGCC_       C
GAM124  CSPG3    3'  CATACACAAGATCTTC      16516       C  AATTC
                                GAGGA CT    TGTGTATG
                                ||||| ||    ||||||||
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                                CTTCT GA    ACACATAC
                                  A _____
GAM124  ITGAL    3'  ACACTTGGTTGGGTCCTC    11037          CT
                                GAGGACCTAATT  GTGT
                                ||||||||||||  ||||
                                CTCCTGGGTTGG  CACA
                                      TT
GAM124  MEF2A    3'  CATACACAGAATCAGGCACTT  19993     GA   A
                                GAG  CCT ATTCTGTGTATG
                                |||  ||| ||||||||||||
                                TTC  GGA TAAGACACATAC
                                  AC   C
GAM124  PITPNB   3'  CATGCACAGGTTCTC       25701         AATTCT
                                GAGGACCT     GTGTATG
                                ||||||||     |||||||
                                CTCTTGGA     CACGTAC
                                     _______
GAM124  RECQL5   3'  GCAAGGGAACAGGTCCTC    16201         AA    G
                                GAGGACCT  TTCT TGT
                                ||||||||  |||| |||
                                CTCCTGGA  AGGG ACG
                                     CA    A
GAM124  RNGTT    3'  CATACACCACCAGGTCCTT    15063         AATTCT
                                GAGGACCT     GTGTATG
                                ||||||||     |||||||
                                TTCCTGGA     CACATAC
                                     CCAC__
GAM124  AMOT     3'  CATACACATTAGTCCTC     56537       C   TTC
                                GAGGAC TAA   TGTGTATG
                                ||||||| |||   ||||||||
                                CTCCTG ATT   ACACATAC
                                   _  ___
GAM124  C8orf17  5'  CATACACGTAATCCTC      39991       CCTAA  C
                                GAGGA    TT TGTGTATG
                                |||||    || ||||||||
                                CTCCT    AA GCACATAC
                                   _____ T
GAM124  DKFZP564G202 3'  ACATCAATCAGGTTCTC     65885         A   CT
                                GAGGACCT ATT  GTGT
                                |||||||| |||  ||||
                                CTCTTGGA TAA  TACA
                                     C   C_
GAM124  KIAA0077 3'  GCATACACAGGCGTAATCC    67580     CC  AT
                                GGA  TA  TCTGTGTATGC
                                |||  ||  ||||||||||||
                                CCT  AT  GGACACATACG
                                  A_  GC
GAM124  KIAA0444 3'  GCTGGTAGAATCAGGGTCCTC  63001         A_     TGTAT
                                GAGGACCT  ATTCTG    GC
                                ||||||||  ||||||    ||
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                                CTCCTGGG  TAAGAT    CG
                                    AC     GGT__
GAM124  KIAA0596  3'  CATACACAGGGTACTC     63485     G   TAATT
                                GAG ACC    CTGTGTATG
                                ||| |||    |||||||||
                                CTC TGG    GACACATAC
                                  A  _____
GAM124  KIAA0766  3'  GCACAATGAAGAATTAGCCCTC 29673      AC       _____
                                GAGG  CTAATTCT    GTGT
                                ||||  ||||||||    ||||
                                CTCC  GATTAAGA    CACG
                                  C_      AGTAA
GAM124  KLHL6     3'  GCATACACAGGGAGCCTC    56172     AC  AATT
                                GAGG  CT   CTGTGTATGC
                                ||||  ||   ||||||||||
                                CTCC  GG   GACACATACG
                                  GA  _____
GAM124  MGC34923  3'  CACACACAGAGTCTCTC     59194     _  CTAAT      A
                                GAG GAC    TCTGTGT TG
                                ||| |||    ||||||| ||
                                CTC CTG    AGACACA AC
                                  T  ______      C
GAM124  ST7L      3'  GCATTTCAGAACCAGGTTCTC  58280        AA    TGT
                                GAGGACCT  TTCTG   ATGC
                                ||||||||  |||||   ||||
                                CTCTTGGA  AAGAC   TACG
                                     CC    TT_
GAM124  ST7L      3'  GCATTTCAGAACCAGGTTCTC  58284        AA    TGT
                                GAGGACCT  TTCTG   ATGC
                                ||||||||  |||||   ||||
                                CTCTTGGA  AAGAC   TACG
                                     CC    TT_
GAM124  TTY7      3'  CACACACAGAAGGTCC      50017       AAT      A
                                GGACCT   TCTGTGT TG
                                ||||||   ||||||| ||
                                CCTGGA   AGACACA AC
                                   ___       C
GAM124  LOC118851 3'  CATACACAGATTGTCTTC    76013       CTAAT
                                GAGGAC    TCTGTGTATG
                                ||||||    ||||||||||
                                CTTCTG    AGACACATAC
                                   TT___
GAM124  LOC124460 5'  GCACACACAGAATAACCCT   76563     ACCTA       A
                                AGG    ATTCTGTGT TGC
                                |||    ||||||||| |||
                                TCC    TAAGACACA ACG
                                  CAA__       C
GAM124  LOC127703 5'  GCAGAGAATGAGGTCCTC    75177         A    G
                                GAGGACCT ATTCT TGT
                                |||||||| ||||| |||
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                                CTCCTGGA TAAGA ACG
                                    G    G
GAM124  LOC142820 3'  GCATACACAGAATCTGCACT   76915    GACCTA
                                AG     ATTCTGTGTATGC
                                ||     ||||||||||||
                                TC     TAAGACACATACG
                                 ACGTC_
GAM124  LOC146050 3'  GCACAAGGTCAACAGGTCCTC  78119        A___  TC
                                GAGGACCT    AT  TGTGT
                                ||||||||    ||  |||||
                                CTCCTGGA    TG  ACACG
                                    CAAC  GA
GAM124  LOC152317 5'  ACACAGAGCAGATCCTC     86818      C  AA
                                GAGGA CT  TTCTGTGT
                                ||||| ||  ||||||||
                                CTCCT GA  GAGACACA
                                   A  C_
GAM124  LOC152445 3'  CATGGCTGAGCTAGGTCCTC   86940        A   T  G
                                GAGGACCTA TTC GT TATG
                                ||||||||| ||| || ||||
                                CTCCTGGAT GAG CG GTAC
                                     C   T  _
GAM124  LOC219940 5'  GCCCAAGATTAGGTCCTC    95001          TC  T
                                GAGGACCTAAT  TG GT
                                ||||||||||  || ||
                                CTCCTGGATTA  AC CG
                                      GA  C
GAM124  LOC51301  5'  GCACACACACGGGATCTTC    33905      _  AATTC    A
                                GAGGA CCT     TGTGT TGC
                                ||||| |||     ||||| |||
                                CTTCT GGG     ACACA ACG
                                   A   C____     C
GAM124  LOC90786  5'  ACACAGTAGGTTCTC       64725         ATT
                                GAGGACCTA   CTGTGT
                                |||||||||   ||||||
                                CTCTTGGAT   GACACA
                                     ___
GAM125  IL12RB2   3'  AGCAGGCTGTACACAGCAG    9561         CGGAG
                                TTGCTGTG    GGCCTGCT
                                ||||||||    ||||||||
                                GACGACAC    TCGGACGA
                                    ATG__
GAM125  IVD       3'  AGCAGGCCCTCCTGCCCAG    11088     T  _
                                CTG GC GGAGGGCCTGCT
                                ||| || ||||||||||||
                                GAC CG CCTCCCGGACGA
                                  C  T
GAM125  DKFZP564P1916 5'  CAGTCTCAGCTCCCACAGCAAG 32238         C   ___  C
                                CTTGCTGTG GGAG   GG CTG
                                ||||||||| ||||   || |||
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                                GAACGACAC CCTC   TC GAC
                                     _   GAC  T
GAM125  KIAA0125  3'  ATAGCAGACCCTGCCCCAGCAG 29558       TGC _   C
            G                    CTTGCTG   GG AGGG CTGCTAT
                                 |||||||   || |||| |||||||
                                 GGACGAC   CC TCCC GACGATA
                                    C__  G   A
GAM125  KIAA0125  3'  ATAGCAGACCCTGCCCCAGCAG 29559       TGC _   C
            G                    CTTGCTG   GG AGGG CTGCTAT
                                 |||||||   || |||| |||||||
                                 GGACGAC   CC TCCC GACGATA
                                    C__  G   A
GAM125  LOC203248 3'  TAGCAGGCACCAAAGCAAG   90845      GTGCGGA _
                                 CTTGCT      GG GCCTGCTA
                                 ||||||      || ||||||||
                                 GAACGA      CC CGGACGAT
                                    AA_____  A
GAM126  CHRM1    3'  GCATCAGCAAGACAATGACA   96433        CCC   CTC_
                                 TGTTATTGTC   TGC   GC
                                 ||||||||||   |||   ||
                                 ACAGTAACAG   ACG   CG
                                      A__   ACTA
GAM126  COX15    3'  CAGGCTGATGGAGACAGTAACA 16488         C  TGCCTC
                                 TGTTATTGTC CC     GCCTG
                                 |||||||||| ||     |||||
                                 ACAATGACAG GG     CGGAC
                                      A  TAGT__
GAM126  FLJ22056  3'  AGGCCCTGGGGACAATACA   42830     T       TGCCTC
                                 TGT ATTGTCCCC     GCCT
                                 ||| |||||||||     ||||
                                 ACA TAACAGGGG     CGGA
                                   _       TCC___
GAM126  GDF11    3'  CAGACGAGGCAGAGACAAAACA 20558     A    CC      C
                                 TGTT TTGTC  CTGCCTCG CTG
                                 |||| |||||  |||||||| |||
                                 ACAA AACAG  GACGGAGC GAC
                                   _    A_      A
GAM126  SNX11    3'  CAGACGGGAACAGTAACA    26170         _  __
                                 TGTTATTGT CCC  CTG
                                 |||||||| |||  |||
                                 ACAATGACA GGG  GAC
                                      A  CA
GAM126  ZAK      3'  CAGACACAGAGCAAGACAATAA 34099         CCC  _ CGC_
            CA                    TGTTATTGTC   TGC CT    CTG
                                  ||||||||||   ||| ||    |||
                                  ACAATAACAG   ACG GA    GAC
                                       A__   A  CACA
GAM126  LOC145622 3'  CAGTAACGAACAGGGAACAGTA 77806        C    CC   C__
            ACA                    TGTTATTGT CCCTG  TCG   CTG
                                   ||||||||| |||||  |||   |||
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                                ACAATGACA GGGAC  AGC   GAC
                                     A    A_   AAT
GAM127  KIAA1416 3'  AAAACTGCTATCATGTAAGATA 87754        C    A   T
                                TATCTTAC ATGA GGT GTTTT
                                |||||||| |||| ||| |||||
                                ATAGAATG TACT TCG CAAAA
                                     _   A   T
GAM127  PIP3-E   3'  AAAACAACCTTAGCATTAAGA  67337      CCATG
                                TCTTA    AAGGTTGTTTT
                                |||||    ||||||||||
                                AGAAT    TTCCAACAAAA
                                   TACGA
GAM127  TTTY12   5'  AAAACAACTCAGGCAAGA    50027     A  A   AG
                                TCTT CC TGA  GTTGTTTT
                                |||| || |||  ||||||||
                                AGAA GG ACT  CAACAAAA
                                  C  _  __
GAM127  LOC116068 3'  AAAATTATTCATGGTAGGATA  74104           GGTT
                                TATCTTACCATGAA   GTTTT
                                ||||||||||||||   |||||
                                ATAGGATGGTACTT   TAAAA
                                        AT__
GAM127  LOC145623 3'  AAATACTCTTCATGACCAGATA 84387      TAC      GT
                                TATCT   CATGAAG  TGTTT
                                |||||   |||||||  |||||
                                ATAGA   GTACTTC  ATAAA
                                   CCA      TC
GAM128  CDC2     5'  TGGCTTCAAAGCTGGCTC    10130    T   ACC
                                GA GCCA   TTGAAGCCA
                                || ||||   |||||||||
                                CT CGGT   AACTTCGGT
                                 _   CGA
GAM128  COG7     3'  GGCCACTGACATCGACTA    68255        C  ACCT  AA
                                TAGTTGATG CA   TG  GCC
                                ||||||||| ||   ||  |||
                                ATCAGCTAC GT   AC  CGG
                                     A  C___  __
GAM128  HYAL1    5'  GCCCCAAGGTTGTCCTCGAC  53704      TGC      AA
                                GTTGA   CAACCTTG  GC
                                |||||   ||||||||  ||
                                CAGCT   GTTGGAAC  CG
                                   CCT      CC
GAM128  CARD6    3'  GGTGTGGTTAAATCAACTA   51847       GCC   TTGAA
                                TAGTTGAT   AACC    GCC
                                ||||||||   ||||    |||
                                ATCAACTA   TTGG    TGG
                                     AA_   TG___
GAM128  KIAA1712 3'  AAGAAGTTAGCATCAACTG   68143         C  __
                                TAGTTGATGC AAC  CTT
                                |||||||||| |||  |||
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                                GTCAACTACG TTG  GAA
                                     A   AA
GAM128  KIAA1751  3'  GCCTCACTGGCATCAGCTA   72161          ACCT   A
                                TAGTTGATGCCA   TGA GC
                                ||||||||||||   ||| ||
                                ATCGACTACGGT   ACT CG
                                      C___   C
GAM128  LSR7    5'  GGCTTCAAGGCCCGCGGAAC  38281    GA   CAA
                                GTT  TGC   CCTTGAAGCC
                                |||  |||   ||||||||||
                                CAA  GCG   GGAACTTCGG
                                  G_   CCC
GAM128  MEGF11   3'  GCTACTCATCAACATCAGCTA  51600        CCAACCT  __
                                TAGTTGATG     TGA  AGC
                                |||||||||     |||  |||
                                ATCGACTAC     ACT  TCG
                                      AACT___   CA
GAM128  SIAT8D   3'  GGCTGGGTTTCAGCATCCAC   20232    T    C__    TGA
                                GT GATGC   AACCT   AGCC
                                || |||||   |||||   ||||
                                CA CTACG   TTGGG   TCGG
                                 C    ACT    ___
GAM128  LOC150113 5'  GGCCCCCAGGCGGCATCAAT   88568        AA   TGAA
                                GTTGATGCC  CCT    GCC
                                |||||||||  |||    |||
                                TAACTACGG  GGA    CGG
                                     C_   CCCC
GAM128  LOC158014 5'  TAAGAATGGCATCAACTA    82567          AC
                                TAGTTGATGCCA  CTTG
                                ||||||||||||  ||||
                                ATCAACTACGGT  GAAT
                                      AA
GAM128  LOC221814 3'  GCTTCAAGGTCACTTCCAACT  95557      ATGCCA
                                AGTTG     ACCTTGAAGC
                                |||||     ||||||||||
                                TCAAC     TGGAACTTCG
                                   CTTCAC
GAM128  LOC221815 3'  GCTTCAAGGTCACTTCCAACT  95552      ATGCCA
                                AGTTG     ACCTTGAAGC
                                |||||     ||||||||||
                                TCAAC     TGGAACTTCG
                                   CTTCAC
GAM128  LOC254735 5'  TGGCCCATCACCACCATCAACT 97478        CCAACCT  AA
            A                    TAGTTGATG      TG  GCCA
                                 |||||||||      ||  ||||
                                 ATCAACTAC      AC  CGGT
                                       CACCACT  C_
GAM128  LOC92552  5'  GCCTCAATTGCACATCAGCTA  70242        C_   CC    A
                                TAGTTGATG  CAA  TTGA GC
                                |||||||||  |||  |||| ||
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                                ATCGACTAC  GTT  AACT CG
                                     AC   __   C
GAM129  ADCY8   5'  AAGGGGATGAGAACTGTGTGC  8496        C   TGTA
                                GCACACAG TCTC   CCTT
                                |||||||| ||||   ||||
                                CGTGTGTC AGAG   GGAA
                                    A   TAGG
GAM129  CNGA3   3'  AAGGAGGAGAGCTATGTACA  8938    C  C      GTA
                                TG ACA AGCTCTCT  CCTT
                                || ||| ||||||||  ||||
                                AC TGT TCGAGAGG  GGAA
                                 A  A      A__
GAM129  EDG6    3'  GGGTACAGGAAGCTGTGTGCA  15021         CT
                                TGCACACAGCT  CTGTACCT
                                ||||||||||  ||||||||
                                ACGTGTGTCGA  GACATGGG
                                      AG
GAM129  ERBB4   3'  AAGATACAGAGATGCAATG   19107   CA _     C
                                CA  GC TCTCTGTA CTT
                                ||  || |||||||| |||
                                GT  CG AGAGACAT GAA
                                 AA  T      A
GAM129  GOLGA4   5'  AAGGTACAGAAAGCCATTTGAG 60694    A ____  C
           TG                    CAC CA   GCT TCTGTACCTT
                                ||| ||   ||| ||||||||||
                                GTG GT   CGA AGACATGGAA
                                  A  TTAC  A
GAM129  OLIG2   3'  AGGTACCGCTGTGTGCAT   20546         TCTCT
                                ATGCACACAGC   GTACCT
                                ||||||||||    ||||||
                                TACGTGTGTCG   CATGGA
                                      C____
GAM129  PTEN    3'  AAGGTTGTGTAGCTGTGTCATG 6136     C      CTCTGT
                                CATG ACACAGCT    ACCTT
                                |||| ||||||||    |||||
                                GTAC TGTGTCGA    TGGAA
                                  _      TGTGT_
GAM129  RNF6    3'  AGGTATACAGTATGCATG   21085      CACA  CTC
                                CATGCA   GCT  TGTACCT
                                ||||||   |||  |||||||
                                GTACGT   TGA  ATATGGA
                                   A___  C__
GAM129  VDAC2   3'  GTGCAATTGTGTGCATG    14037         CTCTC
                                CATGCACACAG   TGTAC
                                ||||||||||    |||||
                                GTACGTGTGTT   ACGTG
                                      A____
GAM129  CAMTA1  3'  ACAGAGATATGTGCATG    68504       CAGC
                                CATGCACA   TCTCTGT
                                ||||||||   |||||||
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                                GTACGTGT   AGAGACA
                                    AT__
GAM129  FLJ14213  3'  AAGGTTAAGCATATGTGCATG  46211       CA_  CTCTGT
                                CATGCACA  GCT    ACCTT
                                ||||||||  |||    |||||
                                GTACGTGT  CGA    TGGAA
                                    ATA  AT____
GAM129  FLJ14596  5'  TGCAGAGAGCCTGTACATG   52523     C  CA
                                CATG ACA  GCTCTCTGTA
                                |||| |||  ||||||||||
                                GTAC TGT  CGAGAGACGT
                                  A  C_
GAM129  KIAA0493  3'  AAGGTAGAAACCATGTGTATG  64924       CAGCTC  GT
                                CATGCACA    TCT  ACCTT
                                ||||||||    |||  |||||
                                GTATGTGT    AGA  TGGAA
                                    ACCAA_  __
GAM129  KIAA0625  5'  AAGATACAGAGAGAAATGACAT 31176    _  CACAG       C
                                ATG CA    CTCTCTGTA CTT
                                ||| ||    ||||||||| |||
                                TAC GT    GAGAGACAT GAA
                                  A  AAA__       A
GAM129  KIAA0669  3'  AAGAAGCAAAGCTGTGTAATG  29429    GC      CTC  AC
                                CAT  ACACAGCT   TGT  CTT
                                |||  ||||||||  |||  |||
                                GTA  TGTGTCGA   ACG  GAA
                                  A_      A__  AA
GAM129  KIAA1643  3'  AGGCCAGAGAGCTGCATGC   65152    CA       TA
                                GCA  CAGCTCTCTG  CCT
                                |||  ||||||||||  |||
                                CGT  GTCGAGAGAC  GGA
                                  AC        C_
GAM129  LOC112868 3'  AAGGTACAGTGTGTATGTGTGT 73264         _  TCT
            ATG                   CATGCACACA GC   CTGTACCTT
                                ||||||||||  ||  |||||||||
                                GTATGTGTGT TG   GACATGGAA
                                     A  TGT
GAM129  LOC126964 3'  GCACTTGAGCGTGCATGCATG  75116       __  A   TC_
                                CATGCA  CAC GCTC   TGT
                                ||||||  ||| ||||   |||
                                GTACGT  GTG CGAG   ACG
                                   AC   _    TTC
GAM129  LOC144920 5'  GTACCCTTGGCTGTGTACAT   84112    C      CTCT
                                ATG ACACAGCT    GTAC
                                ||| ||||||||    ||||
                                TAC TGTGTCGG    CATG
                                  A       TTCC
GAM129  LOC153768 3'  CAGAGAGCTGTATCCATG    57499     CAC
                                CATG   ACAGCTCTCTG
                                ||||   ||||||||||
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                                GTAC   TGTCGAGAGAC
                                  CTA
GAM129  LOC170261 3'  AAGGTACAAAAAGTGAAGTACA 83470    C  ACA   CTC
                                TG AC   GCT   TGTACCTT
                                || ||   |||   ||||||||
                                AC TG   TGA   ACATGGAA
                                 A  AAG   AAA
GAM129  LOC196559 3'  AGGTACAATTGTGTGCA     91210         CTCTC
                                TGCACACAG    TGTACCT
                                |||||||||    |||||||
                                ACGTGTGTT    ACATGGA
                                     A____
GAM129  LOC202986 5'  TGGAGAGAGCCTGTGCATG   92071         CA      G
                                CATGCACA  GCTCTCT TA
                                ||||||||  ||||||| ||
                                GTACGTGT  CGAGAGA GT
                                     C_      G
GAM129  LOC257051 3'  AAGGTACAAAAAGTGAAGTACA 98052    C  ACA   CTC
                                TG AC   GCT   TGTACCTT
                                || ||   |||   ||||||||
                                AC TG   TGA   ACATGGAA
                                 A  AAG   AAA
GAM129  LOC90850  5'  AGGCGGGAGCTGCGTGC     64880      A       TGTA
                                GCAC CAGCTCTC    CCT
                                |||| ||||||||    |||
                                CGTG GTCGAGGG    GGA
                                  C       C___
GAM129  LOC91421  3'  AAGGTACAGAAAATGCCGGCA  66593     ACA  GCTC
                                TGC   CA    TCTGTACCTT
                                |||   ||    ||||||||||
                                ACG   GT    AGACATGGAA
                                  GCC  AAA_
GAM130  IRS1      3'  CCATAGATGGTTCTCAATTGTA 19874      C         TGAAC
                                TACA ATTGAGAACC     ATGG
                                |||| ||||||||||     ||||
                                ATGT TAACTCTTGG     TACC
                                  _         TAGA_
GAM130  SERPINF1  3'  CCTGTAAGGTTTCAATG     12038         A   GA   T
                                CATTGAGA CCT  ACA GG
                                |||||||| |||  ||| ||
                                GTAACTTT GGA  TGT CC
                                     _   A_   _
GAM130  HSA243396 3'  CCATGTTCAGCAATGTCAATG  37844        GAAC_
                                CATTGA    CTGAACATGG
                                ||||||    ||||||||||
                                GTAACT    GACTTGTACC
                                   GTAAC
GAM130  KIAA1387  3'  CAGGAATTTTCAATATGTA    71444      C       ___
                                TACA ATTGAGAA  CCTG
                                |||| ||||||||  ||||
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                                ATGT TAACTTTT  GGAC
                                  A       AA
GAM130  MGC16063  3'  TTCAAATTCCAATGTGTA    54930         A   CC
                                TACACATTG GAA  TGAA
                                ||||||||| |||  ||||
                                ATGTGTAAC CTT  ACTT
                                     _  AA
GAM130  SMCR8     3'  CCATGCTCAGGTTTGACTATGT 59253     TGA_      A
                                ACAT   GAACCTGA CATGG
                                ||||   |||||||| |||||
                                TGTA   TTTGGACT GTACC
                                  TCAG       C
GAM130  UPLC1     3'  CCATGCTAGGCCCCAATGT   35227      AGAA   AA
                                ACATTG   CCTG  CATGG
                                ||||||   ||||  |||||
                                TGTAAC   GGAT  GTACC
                                   CCC_   C_
GAM130  ZNF334    3'  CCATAAGTCAACCCTCAATGT  36637       AACC   AC_
                                ACATTGAG   TGA   ATGG
                                ||||||||   |||   ||||
                                TGTAACTC   ACT   TACC
                                    CCA_   GAA
GAM130  LOC145082 3'  TATGGAATGCCCTTAATGTGTA 84196          AACCTGAA
                                TACACATTGAG       CATG
                                ||||||||||        ||||
                                ATGTGTAATTC       GTAT
                                      CCGTAAG_
GAM130  LOC157723 3'  CCAAGTAAGGTTCTCAAATGT  82465      _      GA  A
                                ACATT GAGAACCT  AC TGG
                                ||||| ||||||||  || |||
                                TGTAA CTCTTGGA  TG ACC
                                  A       A_  A
GAM130  LOC219988 5'  CCATGTTCGGCCCCCAATG   93262      AGAAC
                                CATTG    CTGAACATGG
                                |||||    ||||||||||
                                GTAAC    GGCTTGTACC
                                  CCCC_
GAM131  ETV5      3'  TGATGACAATTTCCATTTC   16730     CG    C
                                GAA  GGAAG TTGTCATCA
                                |||  ||||| |||||||||
                                CTT  CCTTT AACAGTAGT
                                  TA    _
GAM131  HTRA3     3'  TGAGCCGGCTTCCCCTTCCCA  90585    A   C       T  CA
                                TG GAA GGGAAGCT GT  TCA
                                || ||| |||||||| ||  |||
                                AC CTT CCCTTCGG CG  AGT
                                 C  C       C __
GAM131  KCNK5     3'  TTGATGGCCTCTTCCCCCCTCA 14973     AAC     CTT
                                TGAG   GGGAAG   GTCATCAA
                                ||||   ||||||   ||||||||
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                                ACTC  CCCTTC  CGGTAGTT
                                  CC_    TC_
GAM131  MTM1    3'  TGGTGTTGGCTTCCCCTC   6007    AAC     TGT
                                GAG  GGGAAGCT  CATCA
                                |||  ||||||||  |||||
                                CTC  CCCTTCGG  GTGGT
                                 ____     TT_
GAM131  NFRKB   5'  TGGTCCAGCTTCCCTTCCTCA 21608    AAC     T TC
                                TGAG  GGGAAGCT G  ATCA
                                ||||  |||||||| |  ||||
                                ACTC  CCCTTCGA C  TGGT
                                  CTT      _ C_
GAM131  STX1A   3'  GGCCTCAGCTTCCCTTCCCA  17213   A  C     T__
                                TG GAA GGGAAGCT  GTC
                                || ||| ||||||||  |||
                                AC CTT CCCTTCGA  CGG
                                 C  _      CTC
GAM131  B3GNT7  3'  TTGGTGTGAAACTTCCTGTTCC 71684   A       C  GT
          CA                      TG GAACGGGAAG TT  CATCAA
                                || ||||||||| ||  ||||||
                                AC CTTGTCCTTC AA  GTGGTT
                                 C        A  GT
GAM131  BA108L7.2 3'  TGACATCTGGCTTCCCTTCTCA 49082      C      ___
                                TGAGAA GGGAAGCT  TGTCA
                                |||||| ||||||||  |||||
                                ACTCTT CCCTTCGG  ACAGT
                                   _      TCT
GAM131  BRPF3   3'  GGCAGCTTCCCCCTCTCA   93932     AC      T
                                TGAGA  GGGAAGCT GTC
                                |||||  |||||||| |||
                                ACTCT  CCCTTCGA CGG
                                  CC      _
GAM131  C3orf4  3'  TGATATTTTCCCCACCTCTCA  39597     AC__    CT
                                TGAGA   GGGAAG  TGTCA
                                |||||   ||||||  |||||
                                ACTCT   CCCTTT  ATAGT
                                  CCAC    T_
GAM131  EPB41L4 3'  ACAAGCTTCCCGCCTCA    42422     AA
                                TGAG  CGGGAAGCTTGT
                                ||||  ||||||||||||
                                ACTC  GCCCTTCGAACA
                                  C_
GAM131  FLJ14457 5'  GAGCCGGGGCTTCCCCTTCTCA 52407      C       GTCA
                                TGAGAA GGGAAGCTT   TC
                                |||||| |||||||||   ||
                                ACTCTT CCCTTCGGG   AG
                                   C       GCCG
GAM131  FLJ20254 3'  GCAGCCTCCTGTTCCCA    35297   A      A  T
                                TG GAACGGGA GCT GT
                                || |||||||| ||| ||
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                                AC CTTGTCCT CGA CG
                                 C       C  _
GAM131  HLA-DOA  3' ACTAGCTTCCCTTCCCA     10929    A  C       T
                                TG GAA GGGAAGCT GT
                                || ||| |||||||| ||
                                AC CTT CCCTTCGA CA
                                 C  _       T
GAM131  MGC29654 5' TGACCCTCCTGTTCCCA     67210    A       A CTT
                                TG GAACGGGA G   GTCA
                                || |||||||| |   ||||
                                AC CTTGTCCT C   CAGT
                                 C       _ C__
GAM131  RAB35    3' TTGATGACTGCTCCCCG     23421     A   TT
                                CGGG AGC  GTCATCAA
                                |||| |||  ||||||||
                                GCCC TCG  CAGTAGTT
                                  C  T_
GAM131  LOC149386 5' ATGACAAGCTTCCCGTTTTCA  85554
                                TGAGAACGGGAAGCTTGTCAT
                                |||||||||||||||||||||
                                ACTTTTGCCCTTCGAACAGTA

GAM131  LOC253974 3' TTGATGACAAATTTCCCGTTCT 99285           C
           CA                     TGAGAACGGGAAG TTGTCATCAA
                                |||||||||||| ||||||||||
                                ACTCTTGCCCTTT AACAGTAGTT
                                       A
GAM132  ADCY6    3' GGGAGCAGGGGAGGGGTCAG   31590    C      G   ATG
                                CTG CCCCTCT CTG   CCC
                                ||| ||||||| |||   |||
                                GAC GGGGAGG GAC   GGG
                                  T      G   GA_
GAM132  ADCY6    3' GGGAGCAGGGGAGGGGTCAG   40959    C      G   ATG
                                CTG CCCCTCT CTG   CCC
                                ||| ||||||| |||   |||
                                GAC GGGGAGG GAC   GGG
                                  T      G   GA_
GAM132  AGRN     3' GGGGCAGGTGCAGAGGTGGCAG 79588      C      TGA
                                CTGCC CCTCTGC   TGCCCC
                                ||||| |||||||   ||||||
                                GACGG GGAGACG   ACGGGG
                                   T      TGG
GAM132  AKAP2    3' TGGGGGCATTTTTAGAGCGGCA 24231     CC    CT
                                TGCC  CTCTG  GATGCCCCCA
                                ||||  |||||  ||||||||||
                                ACGG  GAGAT  TTACGGGGGT
                                  C_    TT
GAM132  AQP6     3' GGGACAGAGCAGAGGAAGGCAG 9731      C_      GA  _
                                CTGCC  CCTCTGCT  TG CCC
                                |||||  ||||||||  || |||
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                                GACGG  GGAGACGA  AC GGG
                                  AA       G_  A
GAM132  AQP6     3'  GGGACAGAGCAGAGGAAGGCAG 55009      C_       GA  _
                                CTGCC  CCTCTGCT  TG CCC
                                |||||  ||||||||  || |||
                                GACGG  GGAGACGA  AC GGG
                                  AA       G_  A
GAM132  AQP6     3'  TGGGGACAGGGGCAGGGGCAG  55018       CTC    GA  C
                                CTGCCCC   TGCT  TG CCCCA
                                |||||||   ||||  || |||||
                                GACGGGG   ACGG  AC GGGGT
                                    ___    GG  A
GAM132  ASIC4    5'  GCGGCAGCAGAGGCAGCAG   38537     CC        A
                                CTGC  CCTCTGCTG TGC
                                ||||  ||||||||| |||
                                GACG  GGAGACGAC GCG
                                  AC       G
GAM132  ATOX1    3'  GGATGGACCAAAGGGGGCAG   15749         C  CTGATG  C_
                                CTGCCCCCT TG     CC  CC
                                ||||||||| ||     ||  ||
                                GACGGGGGA AC     GG  GG
                                     A  CA____  TA
GAM132  ATP1A2   3'  GGGTAGCAGCAGAGGCAG    7367       CCC      A
                                CTGCC   TCTGCTG TGCCC
                                |||||   ||||||| |||||
                                GACGG   AGACGAC ATGGG
                                  ___       G
GAM132  ATRN     3'  TGAGGACACAGCCAGGACGGCA 58447      C_   CT    A  C  C
          G                      CTGCC  CCT  GCTG TG CC CA
                                |||||  |||  |||| || || ||
                                GACGG  GGA  CGAC AC GG GT
                                  CA   C_   _ A  A
GAM132  AVP      5'  GCCAGCAGAGGCAGCAG     6675       CC        AT
                                CTGC  CCTCTGCTG  GC
                                ||||  |||||||||  ||
                                GACG  GGAGACGAC  CG
                                  AC       __
GAM132  B3GNT3   3'  TGGAGGTGTGGGCAGAGGAGGG 27306     _      G    C
                                CCC CCTCTGCT ATGCC CCA
                                ||| |||||||| ||||| |||
                                GGG GGAGACGG TGTGG GGT
                                  A       G    A
GAM132  CBFA2T2  3'  GGAGTCGGCAGAGAAGCAG   18712      CCC        G
                                CTGC   CTCTGCTGAT CC
                                ||||   |||||||||| ||
                                GACG   GAGACGGCTG GG
                                  AA_        A
GAM132  CDS2     3'  GGAACAGAACTGAGCAGGGGCA 15108        __   TG__   ATG
          G                      CTGCCCC  CTC    CTG   CC
                                |||||||  |||   |||   ||
```

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                                GACGGGG GAG   GAC  GG
                                   AC  TCAA  AA_
GAM132  CEP2    3' TGGGGGCAGGGGAAGAGACAG 23250    CCCC   G  GA
                                CTG   CTCT CT  TGCCCCCA
                                |||   |||| ||  ||||||||
                                GAC   GAGA GG  ACGGGGGT
                                  A___   A  GG
GAM132  COPA    5' GGGGGGACAGAGGGGCAG   16479      C   CTGATG
                                CTGCCCC TCTG    CCCCC
                                ||||||| ||||    |||||
                                GACGGGG AGAC    GGGGG
                                   _   AG____
GAM132  DAG1    3' TGGGGGCACCTGGGAGGTCA  16557   T  _  TCTGCTGA
                                C GCC CCC      TGCCCCCA
                                | ||| |||      ||||||||
                                A TGG GGG      ACGGGGGT
                                 C  A  TCC_____
GAM132  DBCCR1  5' GGGAGGCAGAGGGAGTAG   28243    C      GATG
                                CTGC CCCTCTGCT   CCC
                                |||| |||||||||   |||
                                GATG GGGAGACGG   GGG
                                  A      A___
GAM132  DDB2    3' TGGGTGGTAGCAGAGGGATCA 5458    CC      GAT  _
                                TG  CCCTCTGCT  GCC CCCA
                                ||  |||||||||  ||| ||||
                                AC  GGGAGACGA  TGG GGGT
                                 TA       ___  T
GAM132  DTNA    3' GCCAGCAGGGGGGAGCAG    9146     C       AT
                                CTGC CCCTCTGCTG  GC
                                |||| ||||||||||  ||
                                GACG GGGGGACGAC  CG
                                  A       __
GAM132  DTNA    3' GCCAGCAGGGGGGAGCAG    53270    C       AT
                                CTGC CCCTCTGCTG  GC
                                |||| ||||||||||  ||
                                GACG GGGGGACGAC  CG
                                  A       __
GAM132  DTNA    3' GCCAGCAGGGGGGAGCAG    53272    C       AT
                                CTGC CCCTCTGCTG  GC
                                |||| ||||||||||  ||
                                GACG GGGGGACGAC  CG
                                  A       __
GAM132  DTNA    3' GCCAGCAGGGGGGAGCAG    53277    C       AT
                                CTGC CCCTCTGCTG  GC
                                |||| ||||||||||  ||
                                GACG GGGGGACGAC  CG
                                  A       __
GAM132  DTR     3' GGGGTCAGTGCAGCAGAGGACA 10457    CCC      AT___
           G                     CTG  CCTCTGCTG   GCCCC
                                |||  |||||||||   |||||
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                                GAC  GGAGACGAC    TGGGG
                                  A__       GTGAC
GAM132  DUSP3    3'  GGGGGCTCAGAGGGGG     15837        CTGAT
                                CCCCCTCTG    GCCCCC
                                |||||||||    ||||||
                                GGGGGAGAC    CGGGGG
                                     T_____
GAM132  EGFL4    3'  GGGGATCCAGGAGGAGCAG   62470     CC    GCT   G
                                CTGC  CCTCT   GAT CCCC
                                ||||  |||||   ||| ||||
                                GACG  GGAGG   CTA GGGG
                                  A_    AC_  _
GAM132  EHD2     3'  TGGAAGCATTTAGAGGGG    28231       CT    CC
                                CCCCTCTG  GATGC  CCA
                                ||||||||  |||||  |||
                                GGGGAGAT  TTACG  GGT
                                     __    AA
GAM132  EIF2B5   3'  GGGAACAGCAGAGAGCAG    62205     CCC      ATG
                                CTGC   CTCTGCTG   CCC
                                ||||   ||||||||   |||
                                GACG   GAGACGAC   GGG
                                  A__       AA_
GAM132  EPHA8    3'  TGGAGGCATCATGGCAGAG   40441       __     C
                                CTCTGCT  GATGCC CCA
                                |||||||  |||||| |||
                                GAGACGG  CTACGG GGT
                                    TA     A
GAM132  EZH1     3'  TGGGAGTGTTACAGTAGGGAGC 10558     C   _  C     C
          AG                      CTGC CCCT CTG TGATGC CCCA
                                |||| |||| ||| |||||| ||||
                                GACG GGGA GAC ATTGTG GGGT
                                  A   T  _     A
GAM132  FGFR4    5'  GGAGGAGCCAGGAAGGCAG   10637     C_  CT   GATG  C
                                CTGCC  CCT  GCT    CC CC
                                |||||  |||  |||    || ||
                                GACGG  GGA  CGA    GG GG
                                   AA   C_   ____  A
GAM132  FGFR4    5'  GGAGGAGCCAGGAAGGCAG   43630     C_  CT   GATG  C
                                CTGCC  CCT  GCT    CC CC
                                |||||  |||  |||    || ||
                                GACGG  GGA  CGA    GG GG
                                   AA   C_   ____  A
GAM132  GCNT2    5'  GGGGAGGCAGAGGGAGG     9455     _       GATG
                                CC CCCTCTGCT    CCCC
                                || |||||||||    ||||
                                GG GGGAGACGG    GGGG
                                 A        A___
GAM132  GDF5     3'  GGAATCACAGAGGGGTCAG   6896      C       C    G
                                CTG CCCCTCTG TGAT CC
                                ||| |||||||| |||| ||
```

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                                GAC GGGGAGAC ACTA GG
                                  T       _   A
GAM132  GRLF1    3'  TGGGGACAGAGGCAGGGGCA  79263       CTC    GA  C
                                TGCCCC  TGCT  TG CCCCA
                                ||||||  ||||  || |||||
                                ACGGGG  ACGG  AC GGGGT
                                   ___   AG  A
GAM132  H1F0     5'  GGCAGAGGCAGAGGCAG     19219      CCC     GA
                                CTGCC  TCTGCT  TGCC
                                |||||  ||||||  ||||
                                GACGG  AGACGG  ACGG
                                   ___    AG
GAM132  H1F0     5'  TGGGAAAAGGGAGGCAGAGGAG 19220      C       GATG  ____
            GCAG                   CTGCC CCTCTGCT    CC    CCCA
                                ||||| ||||||||   ||   ||||
                                GACGG GGAGACGG    GG    GGGT
                                   A       AG__  AAAA
GAM132  HMG20A   3'  TGGGGGCAGAGAAAGAGTGCAG 37072     CCC    GCTGA
                                CTGC   CTCT    TGCCCCCA
                                ||||   ||||    ||||||||
                                GACG   GAGA    ACGGGGGT
                                  T__    AAGAG
GAM132  HNRPD    5'  GGGAGGCGAAGGGGGCAG    49389        CTGCTGA   _
                                CTGCCCCCT      TGCC CCC
                                |||||||||      |||| |||
                                GACGGGGGA      GCGG GGG
                                    A_______    A
GAM132  HNRPD    5'  GGGAGGCGAAGGGGGCAG    10950        CTGCTGA   _
                                CTGCCCCCT      TGCC CCC
                                |||||||||      |||| |||
                                GACGGGGGA      GCGG GGG
                                    A_______    A
GAM132  HOXB3    5'  GGGGGGCAGAGAGGGG      10955     _     TGATG
                                CCCC CTCTGC    CCCCC
                                |||| ||||||    |||||
                                GGGG GAGACG    GGGGG
                                  A     ______
GAM132  ISG20    5'  GGCAGCAGAGAGGCAG      11022      CC      GAT
                                CTGCC  CTCTGCT   GCC
                                |||||  |||||||  |||
                                GACGG  GAGACGA   CGG
                                  A_      ___
GAM132  ITIH1    3'  GGGGCCAAGGCAGAGGAGG    11058    C       GAT
                                CC CCTCTGCT   GCCCC
                                || ||||||||   |||||
                                GG GGAGACGG   CGGGG
                                 A       AAC
GAM132  JRK      5'  GGATCAGCAGAGCAGGCAG    87829      CC        G
                                CTGCC  CTCTGCTGAT CC
                                |||||  |||||||||| ||
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                                GACGG  GAGACGACTA GG
                                  AC        _
GAM132  LEP     3'  GGGGTGATTTCAGAGAGGGCAG 5866        C    CT  _
                                CTGCCC CTCTG  GAT GCCCC
                                |||||| |||||  ||| |||||
                                GACGGG GAGAC  TTA TGGGG
                                   A    T_  G
GAM132  LMO2    5'  GGAGGCCGAGCAAGCGGAGGCA 19938      _ _ C   GAT  C
          G                      CTGCC CC CT TGCT   GCC CC
                                ||||| || || ||||   ||| ||
                                GACGG GG GA ACGA   CGG GG
                                  A  C  _   GC_  A
GAM132  LUZP1   5'  GGGGCCGCAGAGGGGACA   54404   C       TGAT
                                TG CCCCTCTGC   GCCCC
                                || |||||||||   |||||
                                AC GGGGAGACG   CGGGG
                                 A       C___
GAM132  MAP3K9  3'  GGGGCGGGCAAGGGGGACAG  61365   _    C   GA
                                CTG CCCCCT TGCT  TGCCCC
                                ||| ||||||  ||||  ||||||
                                GAC GGGGGA ACGG  GCGGGG
                                 A    _   __
GAM132  MGEA5   5'  GGAGGGCAGCAGAGGCAG   25220     CCC    GAT  _
                                CTGCC   TCTGCT   GCCC CC
                                |||||   ||||||   |||| ||
                                GACGG   AGACGA   CGGG GG
                                  ___     ___   A
GAM132  MMP14   3'  GGCAGAACAGCCAGAGGGGGCA 18430          _  A__
          G                      CTGCCCCCTCTG CTG   TGCC
                                |||||||||||| |||   ||||
                                GACGGGGGAGAC GAC   ACGG
                                      C   AAG
GAM132  MSL3L1  3'  GGAAGTCAGCAGCAGGGGAGGC 55322     _   __      GC
          AG                     CTGCC CCCT  CTGCTGAT  CC
                                ||||| ||||  ||||||||  ||
                                GACGG GGGG  GACGACTG  GG
                                  A   AC       AA
GAM132  NCOA6IP 5'  GGGGGCAGGGGCAGGGGCAG  46155      CTC   GA
                                CTGCCCC   TGCT  TGCCCCC
                                |||||||   ||||  |||||||
                                GACGGGG   ACGG  ACGGGGG
                                   ___    GG
GAM132  NCSTN   5'  GCTCAGCAGAGAGGCA     74136     CC       T
                                TGCC  CTCTGCTGA GC
                                ||||  |||||||| ||
                                ACGG  GAGACGACT CG
                                  A_       _
GAM132  NR4A2   3'  TGGAAACTGTCAAGAGGGGGCA 21647         GC   GCCC_
                                TGCCCCCTCT  TGAT    CCA
                                |||||||||  ||||    |||
```

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                                ACGGGGGAGA  ACTG    GGT
                                      __    TCAAA
GAM132  P2RY6    3'  GGAAGCTTCTTAGAAGAGGCAG 15999      CCC    CT  T  CC
                                CTGCC   TCTG  GA GC  CC
                                |||||   ||||  || ||  ||
                                GACGG   AGAT  CT CG  GG
                                   AGA    T_  T  AA
GAM132  PCSK5    5'  GGGCCAGCAGAGGGGGC     21676           AT
                                GCCCCCTCTGCTG  GCCC
                                ||||||||||||  ||||
                                CGGGGGAGACGAC  CGGG
                                      __
GAM132  PEX13    5'  GGGAGCCGAGAGGAGGCGG    12043      C    GCTGAT  C
                                CTGCC CCTCT     GC CCC
                                ||||| |||||     || |||
                                GGCGG GGAGA     CG GGG
                                   A    GC____  A
GAM132  PGF      3'  TGAAGGCAGTGGCAGGGGAGCA 12067     C   T    GA   CC
             G                   CTGC CCC CTGCT  TGCC  CA
                                ||||| ||| |||||  ||||  ||
                                GACG GGG GACGG  ACGG  GT
                                   A  _    TG   AA
GAM132  PHLDA3   5'  GGAGGCATCTGGCAGAGGCGG  25694    _      _     C
                                CC CCTCTGCT GATGCC CC
                                || |||||||| |||||| ||
                                GG GGAGACGG CTACGG GG
                                 C       T     A
GAM132  PLAB     5'  TGGGGGCACCCTGAGGGGGCA  66428         TGCTGA
                                TGCCCCCTC     TGCCCCCA
                                |||||||||     ||||||||
                                ACGGGGGAG     ACGGGGGT
                                     TCCC__
GAM132  PPP2R2B  5'  GGGCAGCGGAGGCAG      17122      CCC     GAT   C
                                CTGCC   TCTGCT   GCC C
                                |||||   ||||||   ||| |
                                GACGG   AGGCGA   CGG G
                                   ___     ___   A
GAM132  PROK1    3'  TGGGAGCAAGGGACAGGGAGCA 51571     C   CTG  GA   C
             G                   CTGC CCCT   CT  TGC CCCA
                                |||| ||||   ||  ||| ||||
                                GACG GGGA   GG  ACG GGGT
                                   A   CA_  GA   A
GAM132  PSCD3    3'  GGAAGGCGTGGCAGGGAGGCAG 16164      C  T    G    C_
                                CTGCC CC CTGCT ATGCC  CC
                                ||||| || ||||| |||||  ||
                                GACGG GG GACGG TGCGG  GG
                                   A  _    _    AA
GAM132  PTCRA    3'  GGGGCATTTAGGGAGCAG    57154      C   CTGCT
                                CTGC CCCT    GATGCCCC
                                |||| ||||    ||||||||
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                                GACG GGGA    TTACGGGG
                                  A   T____
GAM132  PTGS1    3'  GCATACAACAGAGGGGGCA   55474         C  _
                                TGCCCCCTCTG TG ATGC
                                |||||||||| || ||||
                                ACGGGGGAGAC AC TACG
                                      A  A
GAM132  PTGS1    3'  GCATACAACAGAGGGGGCA   8242          C  _
                                TGCCCCCTCTG TG ATGC
                                |||||||||| || ||||
                                ACGGGGGAGAC AC TACG
                                      A  A
GAM132  RAP1GA1  3'  GGGATTGCTCAGTGGAAGCAG  12774     CCCC  TG   T  C__
                                CTGC   TC  CTGA GC   CCC
                                ||||   ||  |||| ||   |||
                                GACG   AG  GACT CG   GGG
                                  A___  GT   _  TTA
GAM132  RIMS1    5'  GCGAGCAGAGGGGGCGG    73030          GA
                                CTGCCCCCTCTGCT  TGC
                                ||||||||||||||  |||
                                GGCGGGGGAGACGA  GCG
                                                __
GAM132  RPA2     5'  GGAGCATGGGCAGAGGAGACAG 12899    CCC      G   C
                                CTG   CCTCTGCT ATGC CC
                                |||   |||||||| |||| ||
                                GAC   GGAGACGG TACG GG
                                  AGA       G   A
GAM132  RPS6KA2  3'  GGCACAGGTGGGAGGGCAG   41225      C  TG  A
                                CTGCCC CTC  CTG TGCC
                                |||||| |||  ||| ||||
                                GACGGG GGG  GAC ACGG
                                   A  TG  _
GAM132  S100A10  5'  GGGGGCAGGAAGAGGGGG   60048       GCTGA
                                CCCCCTCT    TGCCCCC
                                ||||||||    |||||||
                                GGGGGAGA    ACGGGGG
                                     AGG__
GAM132  SIRT1    5'  GGGAGCAGAGGAGGCG     25289     C     GATG
                                TGCC CCTCTGCT   CCC
                                |||| ||||||||   |||
                                GCGG GGAGACGA   GGG
                                  A      _____
GAM132  SLC12A4  5'  GGGGACAGCGGCGGGGACAG  18629    C   T    ATG
                                CTG CCCC CTGCTG   CCCC
                                ||| |||| ||||||   ||||
                                GAC GGGG GGCGAC   GGGG
                                  A   C     A__
GAM132  SLC22A12 3'  GGAGAGCAGAGGGGTCAG    58690    C       GATG
                                CTG CCCCTCTGCT   CC
                                ||| ||||||||||   ||
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                                GAC GGGGAGACGA   GG
                                  T       GA__
GAM132  SLC5A5   5' GGGGCGGACGCAGAGACAG   6597     CCCC    TGA
                                CTG   CTCTGC  TGCCCC
                                |||   ||||||  ||||||
                                GAC   GAGACG  GCGGGG
                                  A___     CAG
GAM132  SOX11    3' CAAAGGCAGAGGGGGCGG    13310          GA
                                CTGCCCCCTCTGCT  TG
                                ||||||||||||||  ||
                                GGCGGGGGAGACGG  AC
                                       AA
GAM132  SPAG8    3' GGGGGCAGAGCGGGGCAG    25841       CTCT  GA
                                CTGCCCC   GCT  TGCCCCC
                                |||||||   |||  |||||||
                                GACGGGG   CGA  ACGGGGG
                                    _____  G_
GAM132  STK11    3' GGGCCGGGCAGGGGGACAG   6599     C   T    GAT
                                CTG CCCC CTGCT   GCCC
                                ||| |||| |||||   ||||
                                GAC GGGG GACGG   CGGG
                                  A   _    GC_
GAM132  STX1A    3' GGGAAGAGGCAGAGGGAGGCAG 17214      _       GATG
                                CTGCC CCCTCTGCT   CCC
                                ||||| |||||||||   |||
                                GACGG GGGAGACGG   GGG
                                   A       AGAA
GAM132  TTYH1    3' GGGAGTAGCTGAGGGGGCAG  40685         T   ATG
                                CTGCCCCCTC GCTG   CCC
                                |||||||||| ||||   |||
                                GACGGGGGAG CGAT   GGG
                                      T   GA_
GAM132  UBE2G2   3' GGGAGGCAGAGGTAGCAG   65490     CC      GATG
                                CTGC  CCTCTGCT   CCC
                                ||||  ||||||||   |||
                                GACG  GGAGACGG   GGG
                                  AT      A___
GAM132  USP5     3' GGGCAGAGCAGAGGGGCAG   14448       C     GA
                                CTGCCCC TCTGCT  TGCCC
                                |||||||  ||||||  |||||
                                GACGGGG AGACGA  ACGGG
                                   _     G_
GAM132  WHSC1    3' TGGGGACATTGGGAAGGTGGGC 56703       _  CTG TG   C
          AG                    CTGCCC CCT   C  ATG CCCCA
                                ||||||  |||   |  ||| |||||
                                GACGGG GGA   G  TAC GGGGT
                                   T  AG_ GT   A
GAM132  ZNF219   3' GCCAGCAGGGGGCAG      33555         CT    AT
                                CTGCCCCCT  GCTG  GC
                                |||||||||  ||||  ||
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                                GACGGGGGA  CGAC  CG
                                           __   __
GAM132  20D7-FC4  3'  GGACCCACCAGCAGGGAGCAG  61564     CC  T     A  CCC
                                CTGC  CC CTGCTG TG   CC
                                ||||  || ||||||  ||   ||
                                GACG  GG GACGAC AC   GG
                                  A_  _     C  CCA
GAM132  ABIN-2    3'  GGAACATCTGGCAGAGGG    44461          _   CC
                                CCCTCTGCT GATG  CC
                                |||||||||  ||||  ||
                                GGGAGACGG CTAC  GG
                                     T    AA
GAM132  AIP       5'  GGAAGTTGCCGAAAGGGAGCAG 15615      _  C_  T  T   GC
                                CTGC CCC  TC GC GAT  CC
                                ||||  |||  ||  ||  |||  ||
                                GACG GGG  AG CG TTG  GG
                                  A   AA  C  _   AA
GAM132  ASB13     3'  TGGGGAGCACAGAGGAGGC   45547     C     CTGA  _
                                GCC CCTCTG    TGC CCCCA
                                |||  ||||||    |||  |||||
                                CGG GGAGAC    ACG GGGGT
                                  A      _____   A
GAM132  BATF      5'  GGGCAGGCAGAGGAGGCA    22147      C       GA
                                TGCC CCTCTGCT  TGCCC
                                ||||  ||||||||  |||||
                                ACGG GGAGACGG  ACGGG
                                  A       __
GAM132  BCDO2     3'  TGAGGACTCCAAAAGGGGGGCA 50036        T  GC  ATGC  C
                                TGCCCCC CT  TG    CC CA
                                |||||||  ||  ||    ||  ||
                                ACGGGGG GA  AC    GG GT
                                     _  AA  CTCA  A
GAM132  BRP44I    5'  TGGGAAGCGGCAGCAGAGGCAG 32740       CCC      A   C_
                                CTGCC   TCTGCTG TGC  CCCA
                                |||||   |||||||  |||  ||||
                                GACGG   AGACGAC GCG  GGGT
                                  ____      G   AA
GAM132  C12orf22  3'  GGAGGCAGTAGGGAGCA     48708     C    CT   GAT   C
                                TGC CCCT  GCT   GCC CC
                                |||  ||||  |||   |||  ||
                                ACG GGGA  TGA   CGG GG
                                  A   __   ___   A
GAM132  C12orf3   3'  GGGGTCTTGAAGAGGGGGCAG  40166          GC   T
                                CTGCCCCCTCT  TGA GCCCC
                                ||||||||||  |||  |||||
                                GACGGGGGAGA  GTT TGGGG
                                      A_   C
GAM132  C17orf31  5'  TGAAGGTGGCAGAGGATGCAG  34545      CC       GAT   CC
                                CTGC  CCTCTGCT   GCC  CA
                                ||||  ||||||||   |||  ||
```

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                                GACG  GGAGACGG   TGG  GT
                                  TA       ___   AA
GAM132  C20orf110 3'  TGGGGGAGACAGAAGGGGCAG  80367       C   _  GATG
                                CTGCCCC TCTG CT    CCCCCA
                                ||||||| |||| ||    ||||||
                                GACGGGG AGAC GA    GGGGGT
                                   A   A ____
GAM132  C20orf39  5'  TGAGGGGAGGGCAGAGGAGG   46579    C      GATG   _
                                CC CCTCTGCT    CCCC CA
                                || ||||||||    |||| ||
                                GG GGAGACGG    GGGG GT
                                 A      GA__   A
GAM132  C8orf13   3'  GGGGTGTCAGAGGAAGC    82481    CC    GCT
                                GC  CCTCT   GATGCCCC
                                ||  |||||   ||||||||
                                CG  GGAGA   CTGTGGGG
                                 AA    ___
GAM132  CAMTA1    3'  GGAAATTTGCAGAGGGGCAG   68506       C    T   GC
                                CTGCCCC TCTGC GAT  CC
                                ||||||| ||||| |||  ||
                                GACGGGG AGACG TTA  GG
                                   _    T   AA
GAM132  CBLN1     5'  GGGAACACAGCGCGGAGGGG   16369        __    A  CC
                                CCCCTCT  GCTG TG  CCC
                                |||||||  |||| ||  |||
                                GGGGAGG  CGAC AC  GGG
                                    CG   _  AA
GAM132  CENTG3    3'  GGAAGAGGGCAGAGGGGCCAG  50047     C        GATG_
                                CTG CCCCTCTGCT     CC
                                ||| ||||||||||     ||
                                GAC GGGGAGACGG     GG
                                  C         GAGAA
GAM132  cerk      3'  TGGGGGCAGTCAGGAGGAAGC  43172    CC    TG   _
                                GC  CCTC  CTGA TGCCCCCA
                                ||  ||||  |||| ||||||||
                                CG  GGAG  GACT ACGGGGGT
                                 AA   __   G
GAM132  COASTER   3'  TGGGGGCAGGGCAAGAGGAGAC 32083     CCC    _  GA
          AG                    CTG   CCTCT GCT  TGCCCCCA
                                |||   ||||| |||  ||||||||
                                GAC   GGAGA CGG  ACGGGGGT
                                  AGA    A  G_
GAM132  CXYorf1   3'  TGGGGGCATCGGCAAGG     82925     C
                                CCT TGCTGATGCCCCCA
                                ||| ||||||||||||||
                                GGA ACGGCTACGGGGGT
                                  _
GAM132  DIO2      3'  TGGAGAAATGAAGCAGAGGAAG 26558    C_       G_  GCCC
          G                     CC  CCTCTGCT  AT    CCA
                                ||  ||||||||  ||    |||
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                                GG  GGAGACGA  TA    GGT
                                 AA       AG  AAGA
GAM132  DIO2     3'  TGGAGAAATGAAGCAGAGGAAG 7668     C_      G_  GCCC
             G                   CC  CCTCTGCT  AT    CCA
                                 ||  ||||||||  ||    |||
                                GG  GGAGACGA  TA    GGT
                                 AA       AG  AAGA
GAM132  DKFZP564B1162 5'  GGGGGTGCTATAAAAGAAGCAG 49350      CCCC   GC__  AT
                                CTGC    TCT    TG  GCCCCC
                                ||||    |||    ||  ||||||
                                GACG    AGA    AT  TGGGGG
                                  A___   AAAT  CG
GAM132  DKFZP564C103 3'  GGGGGCACTGAGGAAGCAG    32241      CC    TGCTGA
                                CTGC  CCTC     TGCCCCC
                                ||||  ||||     |||||||
                                GACG  GGAG     ACGGGGG
                                  AA   TC____
GAM132  DKFZP667O116 3'  CAGAAGCAGAGGAGGCAG     95939      C       GA
                                CTGCC CCTCTGCT  TG
                                |||||  ||||||||  ||
                                GACGG GGAGACGA  AC
                                   A       AG
GAM132  DKFZP761C169 5'  GGGGCACCTCTGGTGGGGCAG  68424        C  TGCTGA
                                CTGCCCC TC     TGCCCC
                                |||||||  ||     ||||||
                                GACGGGG GG     ACGGGG
                                    T  TCTCC_
GAM132  DKFZp762K222 5'  GGGGACTGCAGCGGAGGCAG   71671      CCC      ATG_
                                CTGCC   TCTGCTG   CCCC
                                |||||   |||||||   ||||
                                GACGG   AGGCGAC   GGGG
                                   ___      GTCA
GAM132  DKFZp762O076 5'  GGCAGCAGAGGCAGCAG     73957      CC       GAT
                                CTGC  CCTCTGCT   GCC
                                ||||  ||||||||   |||
                                GACG  GGAGACGA   CGG
                                  AC       ___
GAM132  DPCR1    3'  TGGGGGCACCAATGCAGA     56000       __  A
                                TCTGC  TG TGCCCCCA
                                |||||  ||  ||||||||
                                AGACG  AC ACGGGGGT
                                   TA  C
GAM132  DRF1     3'  TGGAGGAGGCAGTGGGGGCAG  47762         T    GATG  C
                                CTGCCCCC CTGCT    CC CCA
                                ||||||||  |||||    ||  |||
                                GACGGGGG GACGG    GG GGT
                                    T    A___  A
GAM132  FAM3D    3'  GGGGCTGAGGAGGAGGAGCAG  57947      _  _    GCTGAT
                                CTGC CC CCTCT     GCCCC
                                ||||  ||  |||||     |||||
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                                GACG GG GGAGG     CGGGG
                                  A A    AGT___
GAM132  FBP17    3'  TGGGAGCATCTGGCAGGCAGGG 73163        ___   _   C
             GGGCAG                  CTGCCCCCT  CTGCT GATGC CCCA
                                |||||||||  ||||| ||||| ||||
                                GACGGGGGG  GACGG CTACG GGGT
                                     ACG    T    A
GAM132  FBXO9    5'  GGGGGCGGTGCAGAGGGGGCA  54251          TGA
                                TGCCCCCTCTGC  TGCCCCC
                                ||||||||||||  |||||||
                                ACGGGGGAGACG  GCGGGGG
                                      TG_
GAM132  FLJ10415 3'  CAGCAGCAGAGGCAGCAG    36586     CC       A
                                CTGC  CCTCTGCTG TG
                                ||||  ||||||||| ||
                                GACG  GGAGACGAC AC
                                  AC       G
GAM132  FLJ10415 3'  GGGAGGAACAGCAGCAGAGGCA 36588      CC  _    ATG  _
             G                   CTGCC  CT CTGCTG   CC CCC
                                |||||  || ||||||   || |||
                                GACGG  GA GACGAC   GG GGG
                                  A_  C     AA_  A
GAM132  FLJ10468 3'  ATCAGCAGAGCAGGACAG    36631    _ CC
                                CTG CC  CTCTGCTGAT
                                ||| ||  ||||||||||
                                GAC GG  GAGACGACTA
                                  A  AC
GAM132  FLJ11126 3'  GGCAGCAGAGAGGCCAG     37652     C  C      GAT
                                CTG CC CTCTGCT   GCC
                                ||| || |||||||   |||
                                GAC GG GAGACGA   CGG
                                  C  A      ___
GAM132  FLJ12242 3'  GGGGAGAGGCAGCAGAAGGGGC 45504       C      ATG__
                                GCCCC TCTGCTG    CCCC
                                ||||| |||||||    ||||
                                CGGGG AGACGAC    GGGG
                                  A      GGAGA
GAM132  FLJ12547 3'  TGGAAGCACAGCGTGAGGGGGC 47136          _    A   CC
             A                   TGCCCCCTC TGCTG TGC  CCA
                                |||||||| ||||| |||  |||
                                ACGGGGGAG GCGAC ACG  GGT
                                     T    _   AA
GAM132  FLJ12577 3'  GGTGAGCAGGGGAGCA     48886     C   T    GA
                                TGC CCC CTGCT  TGCC
                                ||| ||| |||||  ||||
                                ACG GGG GACGA  GTGG
                                  A  _    __
GAM132  FLJ12700 5'  GGGGCAGTCAGGGAGCAG    46658     C   CTGCT  _
                                CTGC CCCT    GA TGCCCC
                                |||| ||||    || ||||||
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                                GACG GGGA    CT ACGGGG
                                  A  _____  G
GAM132  FLJ12770  3'  GGGGCAGTTGATGAGGCAG   50680      CCC  T   GAT
                                CTGCC   TC GCT   GCCCC
                                |||||   || |||   |||||
                                GACGG   AG TGA   CGGGG
                                  AGT  T  ___
GAM132  FLJ12998  3'  TGGAGGGACAGAGCAGAGGGGC 43152     C        GA  _  _
          CAG                     CTG CCCCTCTGCT  TG CCC CCA
                                |||  ||||||||||  || ||| |||
                                GAC GGGGAGACGA  AC GGG GGT
                                  C        G_  A   A
GAM132  FLJ13111  3'  TGAGGGACACACAGAGGTGACA 47629     CCC     C  A  _   C
          G                      CTG   CCTCTG TG TG CCC CA
                                |||   ||||||  || || ||| ||
                                GAC   GGAGAC AC AC GGG GT
                                  AGT     _  _  A   A
GAM132  FLJ13114  3'  GGAGCTTGGGCAGCAGGGGCAG 44905        CT    GAT  C
                                CTGCCCC  CTGCT   GC CC
                                |||||||  |||||   || ||
                                GACGGGG  GACGG   CG GG
                                   AC    GTT  A
GAM132  FLJ14249  3'  TGGGGACATCGGTGTGAAGGG  42647     C  _      C
                                CCC TC TGCTGATG CCCCA
                                ||| || |||||||| |||||
                                GGG AG GTGGCTAC GGGGT
                                  A  T       A
GAM132  FLJ14594  3'  GGAGCAGGCTAGGGGGCAG   52507         CT   GA   C
                                CTGCCCCCT  GCT  TGC CC
                                |||||||||  |||  ||| ||
                                GACGGGGGA  CGG  ACG GG
                                     T_   __   A
GAM132  FLJ14642  3'  GGGAAGCAGAGGTGGCAG    52577      C       GATG
                                CTGCC CCTCTGCT    CCC
                                |||||  ||||||||    |||
                                GACGG GGAGACGA    GGG
                                   T       A___
GAM132  FLJ14810  3'  TGGGGACAGAGAGCAGGGGGCA 52705         CT   GA_  C
          G                      CTGCCCCCT  GCT   TG CCCCA
                                |||||||||  |||   || |||||
                                GACGGGGGA  CGA   AC GGGGT
                                     __   GAG  A
GAM132  FLJ20296  3'  GGGCACAGCAGGGGACAG    35366     CC   T     A
                                CTG  CCC CTGCTG TGCCC
                                |||  ||| |||||| |||||
                                GAC  GGG GACGAC ACGGG
                                  A_  _     _
GAM132  FLJ20619  5'  GGGTGAGGCCAGGGGAGCAG   35894      _    CT   GAT
                                CTGC CCCCT  GCT   GCCC
                                ||||  |||||  |||   ||||
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                                GACG GGGGA  CGG   TGGG
                                  A    C_   AG_
GAM132  FLJ20700  3'  GGGAGGCCAAGGGGGCAG    36013        C  CTGAT  _
                                CTGCCCCCT TG    GCC CCC
                                ||||||||| ||    ||| |||
                                GACGGGGGA AC    CGG GGG
                                     _ _____  A
GAM132  FLJ22160  3'  GGGCATCAGGGACGCAG     45034     CCCC  G
                                CTGC   TCT CTGATGCCC
                                ||||   ||| |||||||||
                                GACG   AGG GACTACGGG
                                  C___  _
GAM132  FLJ23058  5'  GGCATCTCGGGGCAGGGGGCAG 45527         ___  CT
                                CTGCCCCCT  CTG  GATGCC
                                |||||||||  |||  ||||||
                                GACGGGGGA  GGC  CTACGG
                                     CGG  T_
GAM132  FLJ23403  3'  CAACAGCAATAGGGGGCAG   42204        C_   A
                                CTGCCCCCT  TGCTG TG
                                |||||||||  ||||| ||
                                GACGGGGGA  ACGAC AC
                                     TA    A
GAM132  FLJ32818  5'  GGGGGTGCCAGGGAAGCAG   59074     C_   CT  TGAT
                                CTGC  CCCT  GC   GCCCCC
                                ||||  ||||  ||   ||||||
                                GACG  GGGA  CG   TGGGGG
                                  AA   C_ _____
GAM132  FREQ    3'  TGGGAGCTGGAAGAAGGGGCA  27378      C   G  GAT  C
                                TGCCCC TCT CT   GC CCCA
                                |||||| ||| ||   || ||||
                                ACGGGG AGA GG   CG GGGT
                                   A   A  T__  A
GAM132  GMPPB   5'  GGGCATAGCAGATGGGGCAG  97455       C      A
                                CTGCCCC TCTGCTG TGCCC
                                ||||||| ||||||| |||||
                                GACGGGG AGACGAT ACGGG
                                     T      _
GAM132  HIC2    3'  GGTGATGCAGCAGCAGGGGCA  65873       CT     AT__
                                TGCCCC  CTGCTG   GCC
                                ||||||  ||||||   |||
                                ACGGGG  GACGAC   TGG
                                   AC     GTAG
GAM132  KBRAS2  3'  TGAGGGCAAAGTAGAGG     34631        GA    C
                                CCTCTGCT  TGCCC CA
                                ||||||||  ||||| ||
                                GGAGATGA  ACGGG GT
                                     A_    A
GAM132  KIAA0057 3'  TGGGGGCCGAGCAGGGGGCA  25426        CT   GAT
                                TGCCCCCT  GCT   GCCCCCA
                                ||||||||  |||   |||||||
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                                ACGGGGGA  CGA   CGGGGGT
                                    __   GC_
GAM132  KIAA0265 5' GGGCTGGGACAGTGGGGGCAG  70442        T  _  GAT
                                CTGCCCCC CTG CT   GCCC
                                |||||||| ||| ||   ||||
                                GACGGGGG GAC GG   CGGG
                                    T   A  GT_
GAM132  KIAA0280 3' GGGAATCCAGAGAGGGGCAG   93307        _    CT   G
                                CTGCCCC CTCTG  GAT CCC
                                ||||||| |||||  ||| |||
                                GACGGGG GAGAC  CTA GGG
                                    A    __   A
GAM132  KIAA0321 5' GGGTCTTTGCAGCAGGGGCAG  63059        CT    T  T
                                CTGCCCC  CTGC GA GCCC
                                |||||||  |||| || ||||
                                GACGGGG  GACG TT TGGG
                                    AC    T  C
GAM132  KIAA0329 3' GGTGGCAGCAGAGGCAG     29941       CCC      AT
                                CTGCC   TCTGCTG  GCC
                                |||||   |||||||  |||
                                GACGG   AGACGAC  TGG
                                   ___      GG
GAM132  KIAA0540 3' GGGAACACCCCGGGGGTGGGCAG 64616       C     CTGA  CC
                                CTGCCC CTCTG    TG  CCC
                                |||||| |||||    ||  |||
                                GACGGG GGGGC    AC  GGG
                                   T    CCC_  AA
GAM132  KIAA0557 3' GGGCAGCGTATGGGGGCAG   78572        TC   TGA
                                CTGCCCCC  TGC   TGCCC
                                ||||||||  |||   |||||
                                GACGGGGG  ATG   ACGGG
                                    T_   CG_
GAM132  KIAA0620 3' GGGGGCTGGAGGGGGGCAG   62813        T  G  GAT
                                CTGCCCCC CT CT   GCCCCC
                                |||||||| || ||   ||||||
                                GACGGGGG GA GG   CGGGGG
                                    _  _  T__
GAM132  KIAA0720 3' GGCCGAGCAGAGGGGGCA    62988           GAT
                                TGCCCCCTCTGCT   GCC
                                ||||||||||||   |||
                                ACGGGGGAGACGA   CGG
                                      GC_
GAM132  KIAA0769 3' GGAGCAAAGAGGGGGGCAG   29758        T  G  GA   C
                                CTGCCCCC CT CT  TGC CC
                                |||||||| || ||  ||| ||
                                GACGGGGG GA GA  ACG GG
                                    _  _  A_   A
GAM132  KIAA0836 3' GCATCAAAGGGGGCAG      65167         CTGC
                                CTGCCCCCT    TGATGC
                                |||||||||    ||||||
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                                GACGGGGGA   ACTACG
                                     A___
GAM132  KIAA0913 5' TGGGGGCGAGGAAGAGAAGGC 69535    CC   G  GA
                                GCC  CTCT CT  TGCCCCCA
                                |||  |||| ||  ||||||||
                                CGG  GAGA GG  GCGGGGGT
                                  AA   A  A_
GAM132  KIAA0945 3' TGGGGGCGGGAAGGAGGGGCA 30907      CT  GCTGA
                                TGCCCC  CT    TGCCCCCA
                                ||||||  ||    ||||||||
                                ACGGGG  GA    GCGGGGGT
                                   AG  AGG__
GAM132  KIAA0980 3' TGGGAGCTGTCAGCAAGGAGCA 47999     CC   C     _  C
           G                     CTGC  CCT TGCTGAT GC CCCA
                                ||||  ||| ||||||| || ||||
                                GACG  GGA ACGACTG CG GGGT
                                  A_  _     T  A
GAM132  KIAA1130 3' GGGAGGCAGAGGTAGCAG    63099     CC      GATG
                                CTGC  CCTCTGCT    CCC
                                ||||  ||||||||    |||
                                GACG  GGAGACGG    GGG
                                  AT       A___
GAM132  KIAA1136 3' GGCATGGGTAGAAGAGGACCAG 92959    CC  _  _    G
                                CTG  CC CT CTGCT ATGCC
                                |||  || || ||||| |||||
                                GAC  GG GA GATGG TACGG
                                  CA  A  A    G
GAM132  KIAA1193 3' GGGGCACAGAGGGCAG     68275      CC   CTGA    C
                                CTGCCC  TCTG    TGCCC C
                                ||||||  ||||    ||||| |
                                GACGGG  AGAC    ACGGG G
                                   __   _____    A
GAM132  KIAA1199 3' GGCCCAGCAGAGGGAGTAG   72931     C       AT
                                CTGC CCCTCTGCTG  GCC
                                |||| ||||||||||  |||
                                GATG GGGAGACGAC  CGG
                                  A        C_
GAM132  KIAA1259 3' GGGCGGAGAGAGGGGGCAG   50800          G  GA
                                CTGCCCCCTCT CT  TGCCC
                                ||||||||||| ||  |||||
                                GACGGGGGAGA GA  GCGGG
                                      _  G_
GAM132  KIAA1277 3' GCTGTCCTGCAGCGGGGACAG  65079    C   T   T_  _
                                CTG CCCC CTGC  GAT GC
                                ||| |||| ||||  ||| ||
                                GAC GGGG GACG  CTG CG
                                  A   C   TC   T
GAM132  KIAA1277 3' GGGACAGCGGGGAGGCAG    65080     C  T    ATG
                                CTGCC CC CTGCTG   CCC
                                ||||| || ||||||   |||
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                                GACGG GG GGCGAC   GGG
                                  A _     A__
GAM132  KIAA1277 3' GGGGACAGTGGGGACAG     65082     C   TCT   ATG
                                CTG CCCC   GCTG   CCCC
                                ||| ||||   ||||   ||||
                                GAC GGGG   TGAC   GGGG
                                  A   ____   A__
GAM132  KIAA1363 5' GGACACCGTAGAGGGGGCA   69791          T A _
                                TGCCCCCTCTGC G TG CC
                                |||||||||||| | || ||
                                ACGGGGGAGATG C AC GG
                                       _ C  A
GAM132  KIAA1399 3' GGAGCCAACAGAGGGAGCAG   70793      C      C  AT  C
                                CTGC CCCTCTG TG  GC CC
                                |||| ||||||| ||  || ||
                                GACG GGGAGAC AC  CG GG
                                  A      A __ A
GAM132  KIAA1610 5' GGGAGCGGCAGAGACGGCAG   67739      CC       ATG
                                CTGCC  CTCTGCTG   CCC
                                |||||  ||||||||   |||
                                GACGG  GAGACGGC   GGG
                                   CA       GA_
GAM132  KIAA1879 5' TGGAGGACGTGCAGAGGGTGCA 73949      C       TG  _  C
          G                      CTGC CCCTCTGC  ATG CC CCA
                                |||| ||||||||  ||| || |||
                                GACG GGGAGACG  TGC GG GGT
                                  T       __   A  A
GAM132  KIAA1957 3' GGTGGGCGCGGAGGGAGCAG   76217      C       TGAT   _
                                CTGC CCCTCTGC    GCCC CC
                                |||| ||||||||    |||| ||
                                GACG GGGAGGCG    CGGG GG
                                  A       _____   T
GAM132  KIF13B   3' CAGCAGCAGAGGGGACAG    83713     C         A
                                CTG CCCCTCTGCTG TG
                                ||| ||||||||||| ||
                                GAC GGGGAGACGAC AC
                                  A         G
GAM132  KIF13B   3' CAGCAGCAGAGGGGACAG    31557     C         A
                                CTG CCCCTCTGCTG TG
                                ||| ||||||||||| ||
                                GAC GGGGAGACGAC AC
                                  A         G
GAM132  KRTHB2   3' TGGGGACAGACGGCAGAG    53454         A_  C
                                CTCTGCTG  TG CCCCA
                                ||||||||  || |||||
                                GAGACGGC  AC GGGGT
                                     AG  A
GAM132  LIN-28   3' TGGGGGCAACCAGGAGGGGGG  45473        G   A_
                                CCCCTCT CTG  TGCCCCCA
                                ||||||| |||  ||||||||
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                                GGGGGGA GAC  ACGGGGGT
                                    G   CA
GAM132  MESDC2   3' GGCAGGCAGAGGAAACAG    72918     CCC       GA
                                CTG   CCTCTGCT  TGCC
                                |||   ||||||||  ||||
                                GAC   GGAGACGG  ACGG
                                  AAA       __
GAM132  MGC10334 5' GGGTGCGGTGCAGAGCAGAGCA 48321      CCC_     TGA   C
            G                    CTGC    CTCTGC   TGC CCC
                                ||||    ||||||   ||| |||
                                GACG    GAGACG   GCG GGG
                                  AGAC     TG_   T
GAM132  MGC10765 3' GGGAGGCAGAGGGTGCAG    44564      C        GATG
                                CTGC CCCTCTGCT    CCC
                                |||| |||||||||    |||
                                GACG GGGAGACGG    GGG
                                  T        A___
GAM132  MGC13010 5' TGGAGGCACGGCAGAGGAGGCA 52062       C        A    C
            G                    CTGCC CCTCTGCTG TGCC CCA
                                ||||| ||||||||| |||| |||
                                GACGG GGAGACGGC ACGG GGT
                                  A        _    A
GAM132  MGC15416 5' TGGGGGCAGCCAGGGAGAGGGC 57349       C    G   A_
            A                    TGCCC CTCT CTG  TGCCCCCA
                                ||||| |||| |||  ||||||||
                                ACGGG GAGG GAC  ACGGGGGT
                                  A    _  CG
GAM132  MGC16025 3' TGGAAGGTTTTAGCAGAAAAAG 53029    CCC_      T   C_
            G                    CC    TCTGCTGA GCC  CCA
                                ||    |||||||| |||  |||
                                GG    AGACGATT TGG  GGT
                                 AAAA       T   AA
GAM132  MGC21688 3' GTGTTTGGAGAGGAGGCAG    58917      C     GCT
                                CTGCC CCTCT   GATGC
                                ||||| |||||   |||||
                                GACGG GGAGA   TTGTG
                                  A     GGT
GAM132  MGC35558 3' TGAGGGCATCGTGGAAGGG    59422     C  TG T      C
                                CCC TC  C GATGCCC CA
                                ||| ||  | ||||||| ||
                                GGG AG  G CTACGGG GT
                                  A  GT _      A
GAM132  MGC5566  3' TGGAAGCATTGCCAGAGGGG   44125        CT    CC
                                CCCCTCTG  GATGC  CCA
                                ||||||||  |||||  |||
                                GGGGAGAC  TTACG  GGT
                                     CG    AA
GAM132  NOPAR    5' GGGGGGAGCAGAGGAGGCAG   54860      C       GATG
                                CTGCC CCTCTGCT    CCCCC
                                ||||| ||||||||    |||||
```

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                                GACGG GGAGACGA    GGGGG
                                  A       G___
GAM132  NOPAR     5'  TGGAGACAAGGTAGGGGGGAGC 54861     _       GA  CCC
                AG                  CTGC CCCCTCTGCT  TG   CCA
                                    |||| ||||||||||  ||   |||
                                    GACG GGGGGGATGG  AC   GGT
                                      A        A_  AGA
GAM132  OBTP      3'  GGAAGCCTCCAAGCAGAGGACA 34667     CCC      __ T  CC
                G                   CTG   CCTCTGCT  GA GC  CC
                                    |||   ||||||||  || ||  ||
                                    GAC   GGAGACGA  CT CG  GG
                                      A__       AC  C  AA
GAM132  P114-RHO-GEF 3'  GGGGGGCATGGGCAGAGAGGGC  31674     C      G
                                    GCCC CTCTGCT ATGCCCCC
                                    |||| ||||||| ||||||||
                                    CGGG GAGACGG TACGGGGG
                                      A      G
GAM132  p25       3'  TGGGGGGTGACAAGAGGAGACAG 23839     CCC    GC  A
                                    CTG   CCTCT  TG TGCCCCCA
                                    |||   |||||  || ||||||||
                                    GAC   GGAGA  AC GTGGGGGT
                                      AGA     __  A
GAM132  P2RXL1    3'  TGGAGGTCTGGGAGAGAGAGCA 19565     CCC    G  GAT   C
                G                   CTGC   CTCT CT   GCC CCA
                                    ||||   |||| ||   ||| |||
                                    GACG   GAGA GG   TGG GGT
                                      AGA    G  TC_   A
GAM132  P2RXL1    3'  TGGGAGAGAGAGCAGAGGGCGG 19566      _       GATGCC
                CAG                   CTGCC CCCTCTGCT     CCCA
                                    ||||| |||||||||     ||||
                                    GACGG GGGAGACGA     GGGT
                                      C        GAGAGA
GAM132  PP591     5'  TGGAGGGCCTTGCAGAGGGGCA 48152       C     TGAT   _
                G                   CTGCCCC TCTGC    GCCC CCA
                                    ||||||| |||||    |||| |||
                                    GACGGGG AGACG    CGGG GGT
                                       _    TTC_    A
GAM132  PRO1257   5'  TGAGGGCATGAGCAGAGG    38327        G     C
                                    CCTCTGCT ATGCCC CA
                                    |||||||| |||||| ||
                                    GGAGACGA TACGGG GT
                                         G     A
GAM132  REPRIMO   3'  TGGGGGCAGGTGGAGAGGGCGG 39532       C   TG  GA
                                    CTGCCC CTC  CT  TGCCCCCA
                                    |||||| |||  ||  ||||||||
                                    GGCGGG GAG  GG  ACGGGGGT
                                       A  GT  __
GAM132  RINZF     5'  GGGGGGCGAGACAGAGGGGG   43939         _  GA
                                    CCCCCTCTG CT  TGCCCCC
                                    |||||||| ||  |||||||
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                                GGGGGAGAC GA  GCGGGGG
                                     A __
GAM132  RP4-622L5 3'  GGATATACAGACGGGGGCAG  39428       _   CTG  G
                                CTGCCCCC TCTG   AT CC
                                |||||||| ||||   || ||
                                GACGGGGG AGAC   TA GG
                                     C    ATA  _
GAM132  SIAT8A   5'  GGAGCATCGCTCGGAGGGGACA 13144    C      C_     C
                                TG CCCCTCTG  TGATGC CC
                                || ||||||||  |||||| ||
                                AC GGGGAGGC  GCTACG GG
                                 A       TC     A
GAM132  SKIP     3'  TGGGGGCAGGCAGAAGGG    33713     C     GA
                                CCC TCTGCT  TGCCCCCA
                                ||| ||||||  ||||||||
                                GGG AGACGG  ACGGGGGT
                                  A     __
GAM132  SKIP     3'  TGGGGGCAGGCAGAAGGG    56248     C     GA
                                CCC TCTGCT  TGCCCCCA
                                ||| ||||||  ||||||||
                                GGG AGACGG  ACGGGGGT
                                  A     __
GAM132  SLC16A6  3'  GGGGACACAAGGAGGCAG    17441      C   CTGC  A  C
                                CTGCC CCT    TG TG CCCC
                                ||||| |||    || || ||||
                                GACGG GGA    AC AC GGGG
                                   A  _____  _  A
GAM132  SLC2A10  5'  GGAGGGCAGGGCAGGAGGGACA 48556     C   CT    GA    _
            G                    CTG CCC  CTGCT  TGCCC CC
                                ||| |||  |||||  ||||| ||
                                GAC GGG  GACGG  ACGGG GG
                                  A  AG    G_    A
GAM132  SLC37A1  3'  GGCCAGCAGAGAAGCAG     39092      CCC       AT
                                CTGC   CTCTGCTG  GCC
                                ||||   ||||||||  |||
                                GACG   GAGACGAC  CGG
                                   AA_       __
GAM132  SPRY4    3'  GGATAGCAGGGGAGGCAG    49021      C       ATG
                                CTGCC CCTCTGCTG   CC
                                ||||| |||||||||   ||
                                GACGG GGGGACGAT   GG
                                   A       A__
GAM132  SPRY4    3'  GGGCATCATCAGGCAG      49027      CCCTC  C
                                CTGCC    TG TGATGCCC
                                |||||    || ||||||||
                                GACGG    AC ACTACGGG
                                   _____  T
GAM132  SSH-3    3'  GGAGCAGGAGCAGGGGCAG   37418       CTC   GA   C
                                CTGCCCC   TGCT  TGC CC
                                |||||||   ||||  ||| ||
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                                GACGGGG  ACGA  ACG GG
                                   ___   GG   A
GAM132  SSH-3   3' GGAGCAGGGGCAGGGGCAG  37419      CTC   GA  C
                                CTGCCCC  TGCT  TGC CC
                                |||||||  ||||  ||| ||
                                GACGGGG  ACGG  ACG GG
                                   ___   GG   A
GAM132  SSH-3   3' GGGGCAGGGGCAGGGGCAG  37420      CTC   GA
                                CTGCCCC  TGCT  TGCCCC
                                |||||||  ||||  ||||||
                                GACGGGG  ACGG  ACGGGG
                                   ___   GG
GAM132  STAT2   3' GGGTACAGAGGGGACA     19454   C     CTGA
                                TG CCCCTCTG   TGCCC
                                || ||||||||   |||||
                                AC GGGGAGAC   ATGGG
                                 A      ____
GAM132  STC2    3' GGAGAAGGGTGGAGAGGAGGCA 14934     C   G  GAT  ____
          G                      CTGCC CCTCT CT  GCCC   CC
                                |||||  |||||  ||  ||||   ||
                                GACGG GGAGA GG  TGGG   GG
                                   A    _ ___   AAGA
GAM132  STX1B2  5' GGAGCAGCAGCAGAGGCAG  54619     CCC     A  C
                                CTGCC  TCTGCTG TGC CC
                                |||||  ||||||| ||| ||
                                GACGG  AGACGAC ACG GG
                                   ___     G  A
GAM132  SYT13   3' GGCTGGCAGAGTAGGCAG   95102     CC     GAT
                                CTGCC  CTCTGCT  GCC
                                |||||  |||||||  |||
                                GACGG  GAGACGG  CGG
                                   AT     T__
GAM132  TED     3' GGGGGCACAGAGGGG      32273       CTGA
                                CCCCTCTG   TGCCCCC
                                ||||||||   |||||||
                                GGGGAGAC   ACGGGGG
                                           ____
GAM132  TGIF2   3' GCCACAGCAGGGGGCAG    41751       CT   AT
                                CTGCCCCCT  GCTG  GC
                                |||||||||  ||||  ||
                                GACGGGGGA  CGAC  CG
                                   __   AC
GAM132  THTPA   5' TGAGGACATCAGCAGCAGTGG  44511   C  _      C  C
                                CC CT CTGCTGATG CC CA
                                || || ||||||||| || ||
                                GG GA GACGACTAC GG GT
                                 T  C       A  A
GAM132  TM4-B   5' GGACACAGAGGGGCAG     25889       C   C  ATG
                                CTGCCCC TCTG TG  CC
                                ||||||| |||| ||  ||
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                                GACGGGG AGAC AC   GG
                                   _   _ A__
GAM132  YKT6     3'  GGTAGCTGCAGAGGGGGGAG  22642    G        TGA
                                CT CCCCCTCTGC   TGCC
                                || ||||||||||   ||||
                                GA GGGGGAGACG   ATGG
                                 G         TCG
GAM132  ZIC5     5'  TGAAGGCGGGCAGAGGG     53615         GA    CC
                                CCCTCTGCT  TGCC  CA
                                |||||||||  ||||  ||
                                GGGAGACGG  GCGG  GT
                                      __    AA
GAM132  ZNF263   3'  GGAATTGGCAGAGGAAGTAG  20427     CC      TG  G
                                CTGC  CCTCTGC  AT CC
                                ||||  |||||||  || ||
                                GATG  GGAGACG  TA GG
                                   AA      GT  A
GAM132  ZNF263   3'  GGGAGGTGCAGAGGCAGCAG  20428     CC      TGAT  _
                                CTGC  CCTCTGC    GCC CCC
                                ||||  |||||||    ||| |||
                                GACG  GGAGACG    TGG GGG
                                   AC       _____   A
GAM132  LOC116173 3'  GCCAGCCAGAGAGGACAG    57427     C  C    _   AT
                                CTG CC CTCTG CTG  GC
                                ||| || ||||| |||  ||
                                GAC GG GAGAC GAC  CG
                                  A  A    C   __
GAM132  LOC124470 3'  TGGAAAGGCAGGCAGAGGG   76149         GA    C__
                                CCCTCTGCT  TGCC   CCA
                                |||||||||  ||||   |||
                                GGGAGACGG  ACGG   GGT
                                      __    AAA
GAM132  LOC124590 3'  TGGAGGCACCAGAGGGGCA   76153       C    CTGA    C
                                TGCCCC TCTG    TGCC CCA
                                ||||||  ||||    ||||  |||
                                ACGGGG AGAC    ACGG GGT
                                   _    C___    A
GAM132  LOC124997 3'  GCCTTCAGCTGAGGGGGCAG   74848          T     T_
                                CTGCCCCCTC GCTGA  GC
                                ||||||||||  |||||  ||
                                GACGGGGGAG CGACT  CG
                                      T     TC
GAM132  LOC127841 5'  GCCCAGGCAGAGAGGGCAG   75188       C      GAT
                                CTGCCC CTCTGCT   GC
                                ||||||  |||||||   ||
                                GACGGG GAGACGG   CG
                                   A       ACC
GAM132  LOC129181 5'  TGGGGGCTGCAGCAGGGAGGCA 76315      C  T     AT
                                TGCC CC CTGCTG  GCCCCCA
                                ||||  ||  ||||||  |||||||
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                                ACGG GG GACGAC  CGGGGGT
                                  A _     GT
GAM132  LOC129303 3'  GGGAACAGCAGAGGGGATAG   75375     C         ATG
                                CTG CCCCTCTGCTG   CCC
                                ||| ||||||||||   |||
                                GAT GGGGAGACGAC   GGG
                                  A         AA_
GAM132  LOC130940 5'  GGGGGTGGCGGAGAGGACAG   57939     C  C      GAT
                                CTG CC CTCTGCT   GCCCCC
                                ||| || |||||||   ||||||
                                GAC GG GAGGCGG   TGGGGG
                                  A  A      ___
GAM132  LOC143437 5'  TGGGGATACAGCAGGGAGCA   83861     CC  T     A  C
                                TGC  CC CTGCTG TG CCCCA
                                |||  || |||||| || |||||
                                ACG  GG GACGAC AT GGGGT
                                  A_ _     _ A
GAM132  LOC145241 5'  TGAAGGTGATCAGCAGGGGCAG 63529         CTC      _   CC
                                CTGCCCC   TGCTGAT GCC  CA
                                |||||||   ||||||| |||  ||
                                GACGGGG   ACGACTA TGG  GT
                                    ___      G   AA
GAM132  LOC146802 3'  GCAGCAGCAGAGAGCAG     78726      CCC       A
                                CTGC   CTCTGCTG TGC
                                ||||   |||||||| |||
                                GACG   GAGACGAC ACG
                                  A__       G
GAM132  LOC147043 5'  GGCATCAGAAGGGGAGC     88504    _    CTG
                                GC CCCCT   CTGATGCC
                                || |||||   ||||||||
                                CG GGGGA   GACTACGG
                                 A    A__
GAM132  LOC147645 5'  CACGGTTGGGGGGAGGCAG    79066       _    T    A
                                CTGCC CCCTC GCTG TG
                                ||||| ||||| |||| ||
                                GACGG GGGGG TGGC AC
                                   A    T   _
GAM132  LOC147912 5'  TGGGGGCGAAAAGGGGGGACAG 79266     C      GCTGA
                                CTG CCCCTCT     TGCCCCCA
                                ||| |||||||     ||||||||
                                GAC GGGGGGA     GCGGGGGT
                                  A      AAA__
GAM132  LOC148413 3'  GGGGCATCGGGGGGGCAG     79581          CTGCT
                                CTGCCCCCT     GATGCCCC
                                |||||||||     ||||||||
                                GACGGGGGG     CTACGGGG
                                              _____
GAM132  LOC149386 5'  TGGGGGCGTCAGCAGAGGGGCA 85565         C
             G                   CTGCCCC TCTGCTGATGCCCCCA
                                 |||||||| ||||||||||||||||
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                                GACGGGG AGACGACTGCGGGGGT
                                      _
GAM132  LOC150481 3'  TGAGGGGATGGGCAGAGGAGGC 80717     C       G  G   _
                                GCC CCTCTGCT AT CCCC CA
                                ||| |||||||| || |||| ||
                                CGG GGAGACGG TA GGGG GT
                                  A       G  _   A
GAM132  LOC152220 3'  TGGGACTAGCAGCAGAGGCAG  86771       CCC      ATGCC
                                CTGCC   TCTGCTG    CCCA
                                |||||   |||||||    ||||
                                GACGG   AGACGAC    GGGT
                                   ___      GATCA
GAM132  LOC152627 3'  GGGAGGCAGAGGGTGCAG    81512      C        GATG
                                CTGC CCCTCTGCT    CCC
                                |||| |||||||||    |||
                                GACG GGGAGACGG    GGG
                                  T        A___
GAM132  LOC155066 5'  GGACCCGGCCAGAGGGACAG   82210     CC      _  ATG
                                CTG  CCCTCTG CTG   CC
                                |||  ||||||| |||   ||
                                GAC  GGGAGAC GGC   GG
                                  A_      C   CCA
GAM132  LOC157860 3'  GGGGCATCTGGGCGCAG     87880      C   TCTGCT
                                CTGC CCC      GATGCCCC
                                |||| |||     ||||||||
                                GACG GGG     CTACGGGG
                                  C  T_____
GAM132  LOC158062 3'  GGGGAGAGCCACAGAGGAGCAG 87964      CC     C  AT  ___
                                CTGC  CCTCTG TG  GC   CCCC
                                ||||  |||||| ||  ||   ||||
                                GACG  GGAGAC AC  CG   GGGG
                                  A_     _ __  AGA
GAM132  LOC158191 3'  TGAGGGGATGGGCAGAGGAGGC 82686     C       G  G   _
                                GCC CCTCTGCT AT CCCC CA
                                ||| |||||||| || |||| ||
                                CGG GGAGACGG TA GGGG GT
                                  A       G  _   A
GAM132  LOC159121 3'  TGGGGGCAAGGGCAAGAGG    88389       _  GA
                                CCTCT GCT  TGCCCCCA
                                ||||| |||  ||||||||
                                GGAGA CGG  ACGGGGGT
                                   A  GA
GAM132  LOC159199 5'  GGGCAGCAGAGTGAGCAG    83066      CCC      GAT
                                CTGC   CTCTGCT   GCCC
                                ||||   |||||||   ||||
                                GACG   GAGACGA   CGGG
                                  AGT      ___
GAM132  LOC162083 3'  GGAAAGCTGAGGGGGCAG    83208          T   GATG
                                CTGCCCCCTC GCT    CC
                                |||||||||| |||    ||
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                                GACGGGGGAG CGA    GG
                                      T   AA__
GAM132   LOC163682 3'  GGGGGCACAGGGGGCAG     88412         CTGCT A
                                CTGCCCCCT    G TGCCCCC
                                |||||||||    | |||||||
                                GACGGGGGA    C ACGGGGG
                                      _____ _
GAM132   LOC164714 3'  GGCAGCAGGGGGGGGCAG     88586            GAT
                                CTGCCCCCTCTGCT   GCC
                                ||||||||||||||   |||
                                GACGGGGGGGGACGA   CGG
                                      ____
GAM132   LOC169693 5'  GGGAAGCAGAGGAGCAG     88630      CC       GATG
                                CTGC  CCTCTGCT    CCC
                                ||||  ||||||||    |||
                                GACG  GGAGACGA    GGG
                                  A_       A___
GAM132   LOC196214 5'  GTACAGCAAGGGGGGCAG     91183         C     A
                                CTGCCCCCT TGCTG TGC
                                ||||||||| ||||| |||
                                GACGGGGGA ACGAC ATG
                                      _    _
GAM132   LOC196410 3'  TGGGGGCACCAGGGAGAATCAG 89034     CCCC    G   A
                                CTG    CTCT CTG TGCCCCCA
                                |||    |||| ||| ||||||||
                                GAC    GAGG GAC ACGGGGGT
                                  TAA_    _   C
GAM132   LOC196955 5'  TGAGGGCATTGTAAAAGG    77876     C_   T      C
                                CCT  TGC GATGCCC CA
                                |||  ||| ||||||| ||
                                GGA  ATG TTACGGG GT
                                  AA   _      A
GAM132   LOC200093 3'  TGGGGGCATCGGCAAGG     63781     C
                                CCT TGCTGATGCCCCCA
                                ||| ||||||||||||||
                                GGA ACGGCTACGGGGGT
                                  _
GAM132   LOC200563 5'  GCATCAGTCAGTGGACAG     91656     CCC  T   _
                                CTG   CC CTG CTGATGC
                                |||   || ||| |||||||
                                GAC   GG GAC GACTACG
                                  A__  T   T
GAM132   LOC200734 3'  TGAAGGCATCGGTTAAGGGCA  90284       CCTCT       CC
                                TGCCC    GCTGATGCC  CA
                                |||||    |||||||||  ||
                                ACGGG    TGGCTACGG  GT
                                   AAT__       AA
GAM132   LOC201685 5'  GCCAGCAGACAGGGCAG     91842       CC      AT
                                CTGCCC  TCTGCTG  GC
                                ||||||  |||||||  ||
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                                GACGGG  AGACGAC  CG
                                   AC      __
GAM132  LOC203238 3'  GTTTCAGCAGAAGTGGCAG   90824      CCC       T
                                CTGCC   TCTGCTGA GC
                                |||||   |||||||| ||
                                GACGG   AGACGACT TG
                                   TGA       T
GAM132  LOC203554 5'  GGGAGGCAGCAGAGGGG     92328         GAT  _
                                CCCCTCTGCT   GCC CCC
                                ||||||||||   ||| |||
                                GGGGAGACGA   CGG GGG
                                      ___   A
GAM132  LOC220024 5'  GGGAGCTGAGCGCAGCAGAGAG 95032      CCC       AT____  C
          CAG                     CTGC   CTCTGCTG     GC CCC
                                ||||   ||||||||      || |||
                                GACG   GAGACGAC     CG GGG
                                  A__       GCGAGT  A
GAM132  LOC221184 5'  TGGGGGTGCCCCAGCAGCGGGG 93411         T     A__
          GCAG                     CTGCCCCC CTGCTG   TGCCCCCA
                                |||||||| ||||||   ||||||||
                                GACGGGGG GACGAC   GTGGGGGT
                                     C     CCC
GAM132  LOC221922 5'  GGGAGGGTCAGGAGGGCAG    94255       CCTC G     G  _
                                CTGCCC    T CTGAT CC CCC
                                ||||||    | ||||| || |||
                                GACGGG    A GACTG GG GGG
                                   ____ G     _  A
GAM132  LOC221922 5'  GGGGGAGCAGGAGGGCAG    94258       C T     GATG
                                CTGCCC C CTGCT    CCCCC
                                |||||| | |||||    |||||
                                GACGGG G GACGA    GGGGG
                                   A _    ____
GAM132  LOC221922 5'  GGGGGAGCAGGAGGGCAG    94259       C T     GATG
                                CTGCCC C CTGCT    CCCCC
                                |||||| | |||||    |||||
                                GACGGG G GACGA    GGGGG
                                   A _    ____
GAM132  LOC221964 3'  GGGGCAGGGGCAGGGGCAG    95607        CTC    GA
                                CTGCCCC   TGCT  TGCCCC
                                |||||||   ||||  ||||||
                                GACGGGG   ACGG  ACGGGG
                                     ___    GG
GAM132  LOC253367 3'  GGGGAGTTTCGAGGGGGCA    99438         TGCT  T  _
                                TGCCCCCTC    GA GC CCCC
                                |||||||||    || || ||||
                                ACGGGGGAG    CT TG GGGG
                                     _____  T  A
GAM132  LOC253531 5'  TGGGGATACAGCAGGGAGCA   98227     CC  T     A  C
                                TGC  CC CTGCTG TG CCCCA
                                |||  || |||||| || |||||
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                                ACG  GG GACGAC AT GGGGT
                                  A_ _     _ A
GAM132   LOC253974 3'  TGGGGGCATCAGCAGAGGGGGC 99284
                AG                CTGCCCCCTCTGCTGATGCCCCCA
                                  ||||||||||||||||||||||
                                  GACGGGGGAGACGACTACGGGGGT

GAM132   LOC254050 3'  GGAAGGCAGAGGTGGCAG    96562      C      GATG
                                  CTGCC CCTCTGCT    CC
                                  ||||| ||||||||    ||
                                  GACGG GGAGACGG    GG
                                     T       AA__
GAM132   LOC254181 5'  GGGCCCCAGCAGAGCAGGCAG  99442      CC      AT
                                  CTGCC  CTCTGCTG  GCCC
                                  |||||  ||||||||  ||||
                                  GACGG  GAGACGAC  CGGG
                                     AC       CC
GAM132   LOC254263 3'  GGCTCAGCAGGGGGGCAG    96369       T     T
                                  CTGCCCCC CTGCTGA GCC
                                  |||||||| ||||||| |||
                                  GACGGGGG GACGACT CGG
                                        _      _
GAM132   LOC255394 5'  TGAGGGCCCCAGAGGGGG    96544        CTGAT   C
                                  CCCCCTCTG    GCCC CA
                                  |||||||||    |||| ||
                                  GGGGGAGAC    CGGG GT
                                       CC___    A
GAM132   LOC256073 5'  GGAAGCTCCAAGAGGGCAG   98487      CC   GCT  T  CC
                                  CTGCCC  TCT   GA GC  CC
                                  ||||||  |||   || ||  ||
                                  GACGGG  AGA   CT CG  GG
                                     __   AC_  _  AA
GAM132   LOC256254 3'  GTTTCAGCAGAAGTGGCAG   97902      CCC      T
                                  CTGCC   TCTGCTGA GC
                                  |||||   |||||||| ||
                                  GACGG   AGACGACT TG
                                     TGA       T
GAM132   LOC256530 3'  GGGAGTTCAGTGGGGACAG   98622    C   TCT    T  C
                                  CTG CCCC   GCTGA GC CCC
                                  ||| ||||   ||||| || |||
                                  GAC GGGG   TGACT TG GGG
                                    A   ____    _ A
GAM132   LOC256949 5'  GGCTGCGGAGGAGGCAG    96985      C      TGAT
                                  CTGCC CCTCTGC    GCC
                                  ||||| |||||||    |||
                                  GACGG GGAGGCG    CGG
                                     A      T___
GAM132   LOC257095 5'  GGGCAGCGGGGGCAG       98721        TCT   GAT   C
                                  CTGCCCCC   GCT   GCC C
                                  ||||||||   |||   ||| |
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                                GACGGGGG  CGA  CGG G
                                   ___  ___  A
GAM132  LOC257450 3'  GGGGTCAAGCAGAGGAGG   91451   C      GAT
                                CC CCTCTGCT  GCCCC
                                || ||||||||  |||||
                                GG GGAGACGA  TGGGG
                                 A       AC_
GAM132  LOC51125  5'  GGAGGGCAGAGGAGGCGG   32743     C    GCTGAT  _
                                CTGCC CCTCT     GCCC CC
                                ||||| |||||     |||| ||
                                GGCGG GGAGA     CGGG GG
                                   A    _______  A
GAM132  LOC56832  3'  GGCTATCAGCAGAAGGATCAG  65447    CC  C       _
                                CTG  CC TCTGCTGAT GCC
                                |||  || |||||||| |||
                                GAC  GG AGACGACTA CGG
                                  TA  A       T
GAM132  LOC56964  5'  GGACAGTCAGTGGGAGCAG   63252    C  T  _  ATG
                                CTGC CCC CTG CTG  CC
                                |||| ||| ||| |||  ||
                                GACG GGG GAC GAC  GG
                                  A  T  T  A__
GAM132  LOC90119  5'  GGGGAGGGCAGAGGGGTCAG  62211    C       GATG
                                CTG CCCCTCTGCT   CCCC
                                ||| ||||||||||   ||||
                                GAC GGGGAGACGG   GGGG
                                  T       GA__
GAM132  LOC90462  3'  GGCCCAGCAGAGGGCAG    63572      CC     AT
                                CTGCCC  TCTGCTG  GCC
                                ||||||  |||||||  |||
                                GACGGG  AGACGAC  CGG
                                   __     C_
GAM132  LOC90494  5'  GGAGTAGGCAGAGGGATCAG  63734    CC      GA  C
                                CTG  CCCTCTGCT  TGC CC
                                |||  |||||||||  ||| ||
                                GAC  GGGAGACGG  ATG GG
                                  TA       __  A
GAM132  LOC91040  3'  TGGGGGCATCGGCAAGG    65356    C
                                CCT TGCTGATGCCCCCA
                                ||| ||||||||||||||
                                GGA ACGGCTACGGGGGT
                                  _
GAM132  LOC91974  5'  TGGGAGCAAACTTCAGAGAAGG 68365     CC    CTGA_  C
           CAG                    CTGCC  CTCTG    TGC CCCA
                                |||||  |||||    ||| ||||
                                GACGG  GAGAC    ACG GGGT
                                   AA    TTCAA  A
GAM132  LOC92230  5'  GGGGGCAAAAGGGGCAG    69087       CTCTGC GA
                                CTGCCCC     T  TGCCCCC
                                |||||||     |  |||||||
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                                GACGGGG     A  ACGGGGG
                                    _______ AA
GAM132  LOC92340  3'  TGGGGACCTCAGTGGGGGCAG  69570        TCT    TGC
                                CTGCCCCC   GCTGA   CCCCA
                                ||||||||   |||||   |||||
                                GACGGGGG   TGACT   GGGGT
                                    ___     CCA
GAM132  LOC92710  3'  GGGTGCAGAGAGGCAG      70866      CC     TGAT
                                CTGCC  CTCTGC    GCCC
                                |||||  ||||||    ||||
                                GACGG  GAGACG    TGGG
                                  A_     _____
GAM133  GRF2      5'  ACAGTTTCTAAGCTACCCA    19199     A    CCTCCG
                                TGG TGGC     GGAAACTGT
                                ||| ||||     |||||||||
                                ACC ATCG     TCTTTGACA
                                  C    AA_____
GAM133  FLJ10661  3'  CACAGCTTCCCGAGTCATTCA  36915        CCTC     A
                                TGGATGGC    CGGGAA CTGTG
                                ||||||||    |||||| |||||
                                ACTTACTG    GCCCTT GACAC
                                    A___      C
GAM133  HIF1AN    3'  ACAACTTGAAGGGCCATC     62666         C    AAAC
                                GATGGCCCT CGGG    TGT
                                ||||||||| ||||    |||
                                CTACCGGGA GTTC    ACA
                                     A    A___
GAM133  PRO1635   3'  CACAGTTTTTAAAACGATCC   38341      _ GCCCTCCG
                                GGAT G       GGAAACTGTG
                                |||| |       ||||||||||
                                CCTA C       TTTTTGACAC
                                  G AAAA_____
GAM133  LOC155438 3'  CACAGTTTCCCAGACCCCCG   87682     CCC  C
                                TGG   TC GGGAAACTGTG
                                |||   || ||||||||||
                                GCC   AG CCCTTTGACAC
                                  CCC  A
GAM133  LOC157280 3'  CAGATCCCCGAAAGCGCCATCC 74342         C  C_    AAA
          A                      TGGATGGC CT  CGGG   CTG
                                 ||||||| ||  ||||   |||
                                 ACCTACCG GA  GCCC   GAC
                                     C  AA    CTA
GAM133  LOC157450 3'  CACAGCTTCCCGGGTCATTCA  71529          TCC    A
                                TGGATGGCCC   GGGAA CTGTG
                                ||||||||||   ||||| |||||
                                ACTTACTGGG   CCCTT GACAC
                                    ___     C
GAM133  LOC157807 5'  CACAGTTTCAGCAGACCATC   82511       CC  CCGG
                                GATGG  CT    GAAACTGTG
                                |||||  ||    |||||||||
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                                CTACC  GA    CTTTGACAC
                                  A_  CGA_
GAM133  LOC255448 3'  CAGATCCCCGAAAGCGCCATCC 96302        C  C_    AAA
           A                     TGGATGGC CT  CGGG   CTG
                                 |||||||| ||  ||||   |||
                                 ACCTACCG GA  GCCC   GAC
                                     C  AA    CTA
GAM134  PMM2     3'  GGACACAGCCATCCAGCGG   72561    A       TCC
                                 TC CTGGATGGCT   GTGTCC
                                 || ||||||||||   ||||||
                                 GG GACCTACCGA   CACAGG
                                  C        ___
GAM134  SLC1A4   3'  TGGGACACAGAGTTGACCCAG  13176     AT_    CC
                                 CTGG   GGCTT  GTGTCCCA
                                 ||||   |||||  ||||||||
                                 GACC   TTGAG  CACAGGGT
                                   CAG    A_
GAM134  SLC4A4   3'  GGGCTAAAGTCATCCAGTGA   14996           CCGT
                                 TCACTGGATGGCTT    GTCC
                                 ||||||||||||||    ||||
                                 AGTGACCTACTGAA    CGGG
                                         AT__
GAM134  CG012    5'  GGACACGGAGATTGCAGTGA   84162       _  GGC
                                 TCACTG GAT   TTCCGTGTCC
                                 |||||| |||   ||||||||||
                                 AGTGAC TTA   GAGGCACAGG
                                    G   ___
GAM134  CNTN5    5'  TGAGACACAGAAGATTCTAGTG 27633        TGG    C    C
           A                     TCACTGGA   CTTC GTGTC CA
                                 ||||||||   |||| ||||| ||
                                 AGTGATCT   GAAG CACAG GT
                                      TA_    A    A
GAM134  DKFZP434P211 3'  GGACACGGATTGTCCAGGGA   28029    A    TG CT
                                 TC CTGGA  G  TCCGTGTCC
                                 || |||||  |  |||||||||
                                 AG GACCT  T  AGGCACAGG
                                  G    GT __
GAM134  DKFZP566G1424 3'  GGATCAAGCCATCCAGGA    85943    A        CCGT
                                 TC CTGGATGGCTT    GTCC
                                 || ||||||||||    ||||
                                 AG GACCTACCGAA    TAGG
                                  _         C___
GAM134  FLJ00026  3'  TGGGACATTTGCCACCCAGGA  65622    A   A    TTCC
                                 TC CTGG TGGC    GTGTCCCA
                                 || |||| ||||    ||||||||
                                 AG GACC ACCG    TACAGGGT
                                  _   C    TT__
GAM134  FLJ10057  3'  TGGGACGAAGCCTCCAGTGA   36253        T     CGT   _
                                 TCACTGGA GGCTTC   GTCC CA
                                 |||||||| ||||||   |||| ||
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                                AGTGACCT CCGAAG   CAGG GT
                                   _     ___    A
GAM134   FLJ32468  5'  TGAGACACGGGCCTTCCAGGA  59712    A    T   TT     C
                                TC CTGGA GGC  CCGTGTC CA
                                || ||||| |||  ||||||| ||
                                AG GACCT CCG  GGCACAG GT
                                 _    T   __      A
GAM134   HPCAL4    5'  GGCTCGGAGCCATCCAGCGA   33210    A        T   T
                                TC CTGGATGGCT CCG GTC
                                || |||||||||| ||| |||
                                AG GACCTACCGA GGC CGG
                                 C         _  T
GAM134   KIAA0350  3'  GGGACACGCCACACCCAG    61831     A__    TTCC
                                CTGG   TGGC    GTGTCCC
                                ||||   ||||    |||||||
                                GACC   ACCG    CACAGGG
                                  CAC    _____
GAM134   NIR3      3'  TGGGAGACCAGCCATCCAGAGA 66835    A        TCC  G
                                TC CTGGATGGCT   GT TCCCA
                                || ||||||||||   || |||||
                                AG GACCTACCGA   CA AGGGT
                                 A         C__  G
GAM134   TLE4      3'  TGGGACATCAGCCACCCAG    68518     A    TCC
                                CTGG TGGCT   GTGTCCCA
                                |||| |||||   ||||||||
                                GACC ACCGA   TACAGGGT
                                  C     C__
GAM134   UBN1      5'  CAAAGAAGCCATGCAGTGA    34194       G       CG
                                TCACTG ATGGCTTC  TG
                                |||||| ||||||||  ||
                                AGTGAC TACCGAAG  AC
                                   G       AA
GAM134   LOC150174 3'  GGACACGGATTGCCCAGGGA   80438    A   ATG  T_
                                TC CTGG   GC  TCCGTGTCC
                                || ||||   ||  |||||||||
                                AG GACC   CG  AGGCACAGG
                                 G    ___  TT
GAM134   LOC150213 3'  GGACACGGATTGTCCAGGGA   75357    A    TG CT
                                TC CTGGA  G  TCCGTGTCC
                                || |||||  |  |||||||||
                                AG GACCT  T  AGGCACAGG
                                 G    GT __
GAM134   LOC199964 3'  TGGGACACAGTAGGCACTCAG  91497     GA  G  TCC
                                CTG  TG CT   GTGTCCCA
                                |||  || ||   ||||||||
                                GAC  AC GA   CACAGGGT
                                  TC  G  TGA
GAM134   LOC91522  3'  TGGGACACACCCTATCCA    66919        CTTCC
                                TGGATGG    GTGTCCCA
                                |||||||    ||||||||
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                                ACCTATC    CACAGGGT
                                    CCA__
GAM135  BBS4    3'  ATTTGCCCAAAGGGAATCCAGA 53447        G_ G_   A
            ACA                   TGTTCTGGA  CT  TTGG CAAAT
                                  |||||||||  ||  |||| |||||
                                  ACAAGACCT  GG  AACC GTTTA
                                       AA  GA   C
GAM135  CENTD2  3'  CCAACAAACTCCAGAACA   31539        C_
                                  TGTTCTGGAG  TGTTGG
                                  ||||||||||  ||||||
                                  ACAAGACCTC  ACAACC
                                       AA
GAM135  HAMP    3'  TCCTGCTGCCCCAGAACA   41289        A  T  T
                                  TGTTCTGG GC GT GGA
                                  |||||||| || || |||
                                  ACAAGACC CG CG CCT
                                       C  T  T
GAM135  ITGA11  3'  TCTGCCGGCCCCCAGGACA  25213        A_   TT
                                  TGTTCTGG  GCTG  GGA
                                  |||||||  ||||  |||
                                  ACAGGACC  CGGC  TCT
                                       CC    CG
GAM135  KITLG   3'  ATTTGCATGGCTCCAGAA   8023           TGGA
                                  TTCTGGAGCTGT   CAAAT
                                  ||||||||||||   |||||
                                  AAGACCTCGGTA   GTTTA
                                        C___
GAM135  MAPK4   5'  CCTGGGCAGCTCCAGATCA  12300   T         __
                                  TG TCTGGAGCTGTT  GG
                                  || ||||||||||||  ||
                                  AC AGACCTCGACGG  CC
                                   T          GT
GAM135  MGAT2   3'  ATTTGTCCAAACAGGACA   11557        GAGCTG
                                  TGTTCTG     TTGGACAAAT
                                  |||||||     ||||||||||
                                  ACAGGAC     AACCTGTTTA
                                      A_____
GAM135  PSPHL   5'  TTGTCATACAGCTCCAAACA  94499     C       TG
                                  TGTT TGGAGCTGT  GACAA
                                  |||| |||||||||  |||||
                                  ACAA ACCTCGACA  CTGTT
                                    _        TA
GAM135  TTC3    3'  TATTTGTCCAACAACTGTCAGA 13885        _ C
            ATA                   TGTTCTGG AG TGTTGGACAAATA
                                  |||||||| || ||||||||||||
                                  ATAAGACT TC ACAACCTGTTTAT
                                       G  A
GAM135  H2BFQ   3'  TTTAAGAGAACTCCAGGACA  60079         __ G
                                  TGTTCTGGAG  CT TTGGA
                                  ||||||||||  || |||||
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                                ACAGGACCTC  GA AATTT
                                     AA  G
GAM135  LRG      3'  TCCATCCATGCTTCCTAGAACA 54825       _  _ _ T_
                                TGTTCT GGA GC TG  TGGA
                                |||||| ||| || ||  ||||
                                ACAAGA CCT CG AC  ACCT
                                   T   T  T  CT
GAM135  NMT2     3'  ATTTGTCCATGTAACAGAACA  17852       GA  TGT
                                TGTTCTG  GC   TGGACAAAT
                                |||||||  ||   |||||||||
                                ACAAGAC  TG   ACCTGTTTA
                                   AA  T__
GAM135  NYD-SP21  3'  TATTTGTCCAATCTAGATTCAG 51863         G  __
             AACA                  TGTTCTGGA CT  GTTGGACAAATA
                                |||||||||  ||  ||||||||||||
                                ACAAGACTT GA  TAACCTGTTTAT
                                     A  TC
GAM135  PSPH     3'  TTGTCGTACAGCTCCAAACA   17143     C       TG
                                TGTT TGGAGCTGT  GACAA
                                ||||  |||||||||  |||||
                                ACAA ACCTCGACA  CTGTT
                                  _       TG
GAM135  LOC122258 3'  CCACCAGCCTCCGGAACA    59820          _  T
                                TGTTCTGGAG CTG TGG
                                |||||||||| ||| |||
                                ACAAGGCCTC GAC ACC
                                     C   C
GAM135  LOC151826 3'  ATTTGTCCAACCTAGCACA   81176     T   AGCT
                                TGT CTGG   GTTGGACAAAT
                                |||  ||||   ||||||||||
                                ACA GATC   CAACCTGTTTA
                                  C   ____
GAM135  LOC169611 3'  TCCAGTGGCAGCTCCAGAA   83663          ___
                                TTCTGGAGCTGT   TGGA
                                ||||||||||||   ||||
                                AAGACCTCGACG   ACCT
                                       GTG
GAM135  LOC196746 3'  TCAGAGCAGCTCCAAGACA   88903     TC       G_
                                TGT  TGGAGCTGTT  GA
                                |||  ||||||||||  ||
                                ACA  ACCTCGACGA  CT
                                  GA        GA
GAM135  LOC253142 5'  TTGCTAGGATGCCCCAGAATA  99230        A  TG_   A
                                TGTTCTGG GC   TTGG CAA
                                |||||||| ||   |||| |||
                                ATAAGACC CG   GATC GTT
                                     C  TAG   _
GAM136  GALR1    5'  GAGAAGGTCCAGCTCCGGGCTC 9425          AA   GT_
             CCG                   CGGGAGCTC  AGT   GCCTTCTC
                                |||||||||  |||  ||||||||
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                                GCCCTCGGG TCG  TGGAAGAG
                                     CC  ACC
GAM136  GATA4   3' AGAAGGAGGCCCTGGGCTCCC 10771       AA GTG
                                GGGAGCTCA GT  CCTTCT
                                ||||||||| ||  ||||||
                                CCCTCGGGT CG  GGAAGA
                                     CC GA_
GAM136  INSRR   3' GAGAACAACCCTGGGCTCCC 68989       AA GTGCC
                                GGGAGCTCA GT   TTCTC
                                ||||||||| ||   |||||
                                CCCTCGGGT CA   AAGAG
                                     CC AC___
GAM136  MN1     3' GCTCCACTTTGAGCTCCC   11654         T_
                                GGGAGCTCAAAGTG GC
                                |||||||||||||| ||
                                CCCTCGAGTTTCAC CG
                                       CT
GAM136  NCOA3   3' AGAAAGGACCAGCTTTGAGCTC 22559         GTG_  _
           C                     GGAGCTCAAAGT   CCTT CT
                                ||||||||||||   |||| ||
                                CCTCGAGTTTCG   GGAA GA
                                       ACCA   A
GAM136  C14orf4 5' AGAAGGCGCCTGAGCTCCC  67894       AA T
                                GGGAGCTCA G GTGCCTTCT
                                ||||||||| | |||||||||
                                CCCTCGAGT C CGCGGAAGA
                                        __ _
GAM136  CLSTN3  5' AGAAGGCTATGACCTCCCG  28872     C  AAGTGT
                                CGGGAG TCA    GCCTTCT
                                |||||| |||    |||||||
                                GCCCTC AGT    CGGAAGA
                                   C  AT____
GAM136  FLJ10081 3' GAGAGGGTACCCTAAACCCC 36290   AGCTCAA  T
                                GGG     AG GTGCCTTCTC
                                |||     || ||||||||||
                                CCC     TC CATGGGAGAG
                                  CAAA___  C
GAM136  FLJ10120 3' GAGAAGTCGCTTGAGCTC   36308      AGT  C
                                GAGCTCAA  GTG CTTCTC
                                ||||||||  ||| ||||||
                                CTCGAGTT  CGC GAAGAG
                                     ___  T
GAM136  FLJ11710 5' AGAAAACATTTGAGCTCC   46238       G  GCC
                                GGAGCTCAAA TGT  TTCT
                                |||||||||| |||  ||||
                                CCTCGAGTTT ACA  AAGA
                                      _  A__
GAM136  FLJ13798 3' GAGAAGGCGGTGCCGAGCCCC 88474    A   AAA TG _
                                GGG GCTC  G  T GCCTTCTC
                                ||| ||||  |  | ||||||||
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                                CCC CGAG   C  G CGGAAGAG
                                  _    C__ GT G
GAM136  FLJ21709  3'  GCTGCCTCTGAGCTCCCG    78481          A  T  _
                                CGGGAGCTCA AG GT GC
                                |||||||||| || || ||
                                GCCCTCGAGT TC CG CG
                                      C  _  T
GAM136  FLJ21924  5'  AGAAGACAGTGAAGCTCCTG   45835        _  AA  GTGC
                                CGGGAGCT CA  GT   CTTCT
                                |||||||| ||  ||   |||||
                                GTCCTCGA GT  CA   GAAGA
                                     A  GA  ____
GAM136  KIAA0924  3'  AGAAGACTACCTTGAGCTC   30349        A   TGC
                                GAGCTCAA GTG   CTTCT
                                |||||||| |||   |||||
                                CTCGAGTT CAT   GAAGA
                                     C   CA_
GAM136  KIAA1297  3'  AGAAAGCCCGAGTTCCC     72624        AAAGT  T  C
                                GGGAGCTC    G GC TTCT
                                ||||||||    | || ||||
                                CCCTTGAG    C CG AAGA
                                     _____ C  A
GAM136  KIAA1932  5'  GAAAAAGCAGTCTGGCTCCCG  73823        CAA  TG   C__
                                CGGGAGCT   AG  TGC   TTC
                                ||||||||   ||  |||   |||
                                GCCCTCGG   TC  ACG   AAG
                                     ___  TG   AAA
GAM136  MGC21945  5'  GAGGGGCTGACACTTTAGCTCC 59612        C      __    T
           CG                    CGGGAGCT AAAGTGT  GCCT CTC
                                ||||||||| |||||||  |||| |||
                                GCCCTCGA TTTCACA  CGGG GAG
                                     _      GT   _
GAM136  MGC2865   5'  GAGAAAGCGGGCTGAGCCGCC  51459    GA    AA  G   C
                                GG  GCTCA  GT TGC TTCTC
                                ||  |||||  || ||| |||||
                                CC  CGAGT  CG GCG AAGAG
                                 GC    __  G   A
GAM136  RPH3A     3'  GAGCCTGCCTTTGAGCCCCCG  30933     A      T   CC
                                CGGG GCTCAAAG GTG  TTC
                                |||| |||||||| |||  |||
                                GCCC CGAGTTTC CGT  GAG
                                  C       _   CC
GAM136  LOC137991 5'  AGAAAAGCCCTGGCTCCCG   75806        CAA  T  GCC
                                CGGGAGCT   AG GT   TTCT
                                ||||||||   || ||   ||||
                                GCCCTCGG   TC CG   AAGA
                                     ___  C  AA_
GAM136  LOC150468 3'  GAGAAGGCAGTGCAAGCCCC   80686     A   CAAA   _
                                GGG GCT    GTG TGCCTTCTC
                                ||| |||    ||| |||||||||
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                                CCC CGA    CGT ACGGAAGAG
                                  _  A___   G
GAM136  LOC153146 5'  AGAAGGCAGGGGAAGCCCC   87138     A  _ AAAGTG
                                GGG GCT C     TGCCTTCT
                                ||| ||| |     ||||||||
                                CCC CGA G     ACGGAAGA
                                  _  A GGG___
GAM136  LOC158337 5'  GAGAACTTATCTTTAAGCTCCT 88110        C   T  CC
          G                      CGGGAGCT AAAG GTG  TTCTC
                                ||||||||| |||| |||  |||||
                                GTCCTCGA TTTC TAT  AAGAG
                                     A   _  TC
GAM136  LOC199990 3'  AAGGCATCAGAGGAGCTTCC  89904        AAAGT
                                GGGAGCTC    GTGCCTT
                                ||||||||    |||||||
                                CCTTCGAG    TACGGAA
                                     GAGAC
GAM136  LOC220954 3'  GAGGCAGCTTTAAACTCCC   94760      CTC    G
                                GGGAG   AAAGT TGCCTT
                                |||||   ||||| ||||||
                                CCCTC   TTTCG ACGGAG
                                   AAA    _
GAM136  LOC254170 5'  GAGAAGACAGAGGCTGGCTCCC 96598        CAA  G__  C
          G                      CGGGAGCT   AGT   TG CTTCTC
                                ||||||||   |||   || ||||||
                                GCCCTCGG   TCG   AC GAAGAG
                                     ___   GAG  A
GAM136  LOC256848 5'  GAGAAGGCCTACGCCAAGCTCC 99379       CAAA  T
                                GGAGCT    GTG GCCTTCTC
                                ||||||    ||| ||||||||
                                CCTCGA    CAT CGGAAGAG
                                   ACCG   C
GAM137  ASL     3'  GTTTGACACAGCCTGGGCAACA 72396     GA   A      C
                                TGT  CCCA GCTGTGTC AAT
                                |||  |||| |||||||| |||
                                ACA  GGGT CGACACAG TTG
                                  AC   C       T
GAM137  DHFR    3'  GACCAGCTTGGGCAACA     7647      GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM137  MMP19   3'  GACCAGCTTGGGCAACA     11630     GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM137  MMP19   3'  GACCAGCTTGGGCAACA     43304     GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
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                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM137  NR1I2    5'  AGATCAAAGTGGTGGGGTCACA 15294        AA  TG GTCCA
                                TGTGACCC  GC  T    ATCT
                                ||||||||  ||  |    ||||
                                ACACTGGG  TG  G    TAGA
                                    G_  GT AAAC_
GAM137  PRKY     3'  GACCAGCTTGGGCAACA     12375     GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM137  RAD54B   3'  AGATTGTCAGCTTGGTCCACA  57062      AC       TGTC
                                TGTG  CCAAGCTG    CAATCT
                                ||||  ||||||||    ||||||
                                ACAC  GGTTCGAC    GTTAGA
                                  CT       T___
GAM137  RCE1     3'  GATTTAACTTGGGTAACA    18890     G      C  T
                                TGT ACCCAAG TG GTC
                                ||| ||||||| || |||
                                ACA TGGGTTC AT TAG
                                  A      A  T
GAM137  SFRS2IP  5'  GACCAGCTTGGGCAACA     17540     GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM137  TEM7     3'  GACCAGCTTGGGCAACA     40259     GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM137  FLJ13263 3'  AGATTGCTCCTTCAGCTCAGGG 47809      A   A_    TGTC__
           CCACA                   TGTG CCC  AGCTG     CAATCT
                                ||||  |||  |||||     ||||||
                                ACAC GGG  TCGAC     GTTAGA
                                  C   AC    TTCCTC
GAM137  FLJ14327 3'  GACCAGCTTGGGCAACA     46679     GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM137  KIAA0172 3'  GACTGCTAGCCTGGGCACA   65596      A   A  _ _
                                TGTG CCCA GCT GT GTC
                                ||||  |||| ||| || |||
                                ACAC GGGT CGA CG CAG
                                  _   C   T  T
GAM137  KIAA1833 3'  GGACCACAGCCTGGGCACA   90753      A   A    _
                                TGTG CCCA GCTGTG TCC
                                ||||  |||| ||||||  |||
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                                ACAC GGGT CGACAC AGG
                                  _   C     C
GAM137  KIAA1870  3'  GACCAGCTTGGGCAACA     52901     GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM137  MEGF11    3'  ATTGGACAAATGTGGATACA   51599      AC   AGCTG
                                TGTG  CCA    TGTCCAAT
                                ||||  |||    ||||||||
                                ACAT  GGT    ACAGGTTA
                                  A_  GTAA_
GAM137  MGC15631  3'  GACCAGCCTGGGTGACA     52230     G    A   T
                                TGT ACCCA GCTG GTC
                                ||| ||||| |||| |||
                                ACA TGGGT CGAC CAG
                                  G    C   _
GAM137  MGC32043  3'  GACCAGGTCTTGGGCACA    58665     A    __   T
                                TGTG CCCAAG  CTG GTC
                                |||| ||||||  ||| |||
                                ACAC GGGTTC  GAC CAG
                                  _     TG  _
GAM137  PLP1      3'  ATTGGACATTAAGCATCACA   6755       CCCAA  __
                                TGTGA    GCT  GTGTCCAAT
                                |||||    |||  |||||||||
                                ACACT    CGA  TACAGGTTA
                                   A____   AT
GAM137  PTD012    3'  GACCAGCTTGGGCAACA     26738     GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM137  STAF42    3'  ATTGAATGTTTTTTGGGTCCA  54942    T      CT TG C
                                TG GACCCAAG  G  T CAAT
                                || ||||||||  |  | ||||
                                AC CTGGGTTT  T  A GTTA
                                 _       TT GT A
GAM137  TRIM31    3'  ACGCCAGCCTGGGTCACA     92649         A   _
                                TGTGACCCA GCTG TGT
                                ||||||||| |||| |||
                                ACACTGGGT CGAC GCA
                                     C   C
GAM137  LOC142893 5'  ATTGGAACATTTTTGGGTCCA  83757    T      CT   _
                                TG GACCCAAG  GTGT CCAAT
                                || ||||||||  |||| |||||
                                AC CTGGGTTT  TACA GGTTA
                                 _       T_   A
GAM137  LOC143503 5'  AGACTGGACAAAGGGGGTCACA 83882         AAGCTG     A
                                TGTGACCC     TGTCCA TCT
                                ||||||||     |||||| |||
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                                ACACTGGG     ACAGGT AGA
                                     GGAA__     C
GAM137  LOC145824 5'  GACTTGCAGCTTGGATACACA  77986      AC_       __
                                TGTG   CCAAGCTGT  GTC
                                ||||   |||||||||  |||
                                ACAC   GGTTCGACG  CAG
                                  ATA        TT
GAM137  LOC157603 3'  GACCAGCTTGGGCAACA     87786     GA        T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
                                ACA  GGGTTCGAC CAG
                                  AC        _
GAM137  LOC221300 3'  GACCAGCTTGGGTAACA     93576     G         T
                                TGT ACCCAAGCTG GTC
                                ||| |||||||||| |||
                                ACA TGGGTTCGAC CAG
                                  A         _
GAM137  LOC257608 3'  ACGCCAGCCTGGGTCACA    99664          A    _
                                TGTGACCCA GCTG TGT
                                ||||||||| |||| |||
                                ACACTGGGT CGAC GCA
                                     C    C
GAM137  LOC51337  3'  GACCAGAGCATCCTGGGTACA  34081      A    A___   G  _
                                TGTG CCCA    GCT TG TC
                                |||| ||||    ||| || ||
                                ACAT GGGT    CGA AC AG
                                  _    CCTA   G  C
GAM138  ABCD2     5'  ATGAGGGGCCTGGGAGGGA    18965         A__    G
                                TCCCTCCCA   CCCT GT
                                |||||||||   |||| ||
                                AGGGAGGGT   GGGA TA
                                     CCG    G
GAM138  ADSS      3'  TTTGGTGGGGCTGGGAGGGG   72235         A    G
                                TCCCTCCCA CCCTG TGAG
                                ||||||||| ||||| ||||
                                GGGGAGGGT GGGGT GTTT
                                     C     G
GAM138  AES       3'  CAGGGAGGTTGGGAGGGG     8522           ___
                                TCCCTCCCAA   CCCTG
                                ||||||||||   |||||
                                GGGGAGGGTT   GGGAC
                                      GGA
GAM138  ALDOB     3'  CAGTGGTAGGTTGGGAAGGA   68650     C       __   G
                                TCC TCCCAACC  CTG TG
                                ||| ||||||||  ||| ||
                                AGG AGGGTTGG  GGT AC
                                  A       AT   G
GAM138  AMH       5'  CTCTATCACTGGGGAGGGA    6652          AACCC    _
                                TCCCTCCC     TGGT GAG
                                ||||||||     |||| |||
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                                AGGGAGGG    ACTA CTC
                                    GTC__   T
GAM138  ANKRD3   3'  CTCACCAGTCTTGAGGGA   40562      CC  CC
                                TCCCTC  AA  CTGGTGAG
                                ||||||  ||  ||||||||
                                AGGGAG  TT  GACCACTC
                                   __  CT
GAM138  ARHGAP6  3'  CCATGGGAGTGGGAGGGA   8611        A_  _
                                TCCCTCCCA  CCC TGG
                                |||||||||  ||| |||
                                AGGGAGGGT  GGG ACC
                                     GA  T
GAM138  AVPR1A   5'  CAATAGGGCGGGAGGGA    7374        AA    G
                                TCCCTCCC  CCCTG TG
                                ||||||||  ||||| ||
                                AGGGAGGG  GGGAT AC
                                     C_    A
GAM138  B3GNT3   3'  CTCAGAAGGTTGGGGGGA   27303     T     C GG
                                TCCC CCCAACC T  TGAG
                                |||| ||||||| |  ||||
                                AGGG GGGTTGG A  ACTC
                                  _     _ AG
GAM138  BASP1    3'  CAATGGGAGTTGGGAGTGA   76493   C      _  GG
                                TC CTCCCAAC CCT  TG
                                || ||||||| |||  ||
                                AG GAGGGTTG GGG  AC
                                 T      A  TA
GAM138  BAZ2A    5'  CTCACAGTTTGGGAGG     26508       CC  G
                                CCTCCCAA  CTG TGAG
                                ||||||||  ||| ||||
                                GGAGGGTT  GAC ACTC
                                     T_  _
GAM138  BCL11B   3'  CTCATTAGGTTGGAAGG    43484    C    C
                                CCT CCAACC TGGTGAG
                                ||| |||||| |||||||
                                GGA GGTTGG ATTACTC
                                  A    _
GAM138  CACNG6   3'  CCGGGTGCGGTTGGGGGAGA  49946   C      _____
                                TC CTCCCAACC   CTGG
                                || |||||||||   ||||
                                AG GGGGGTTGG   GGCC
                                 A       CGTG
GAM138  CNTN2    3'  CTCACTCCTGCCTGGGAGGGG  18660       ACCCT_
                                TCCCTCCCA     GGTGAG
                                |||||||||     ||||||
                                GGGGAGGGT     TCACTC
                                     CCGTCC
GAM138  COL9A1   5'  CTCACCGGGGGCAGGAGGGA  10252       CAA
                                TCCCTCC   CCCTGGTGAG
                                |||||||   ||||||||||
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                                AGGGAGG  GGGGCCACTC
                                   ACG
GAM138  DHCR24   3' TTCATTAGTTGAAAGGGA   29305     CC   CC
                                TCCCT  CAAC  TGGTGAG
                                |||||  ||||  |||||||
                                AGGGA  GTTG  ATTACTT
                                  AA   __
GAM138  EPB49    3' CGGCGGGTTGGGAGGGG    10527          T G
                                TCCCTCCCAACCC G TG
                                |||||||||||| | ||
                                GGGGAGGGTTGGG C GC
                                       _ G
GAM138  FCMD     3' CTCACAGTAGGGTTGAAAGAG 23035    C__      __
                                CTC  CAACCCTG  GTGAG
                                |||  ||||||||  |||||
                                GAG  GTTGGGAT  CACTC
                                  AAA      GA
GAM138  FLRT2    3' CTCATCAGGGTAAGAGG    25996     CCA
                                CCTC  ACCCTGGTGAG
                                ||||  ||||||||||
                                GGAG  TGGGACTACTC
                                  AA_
GAM138  GGT1     3' CTCACCAGGACCAGGAAGGG  26420     _ CAAC
                                CCCT CC   CCTGGTGAG
                                |||| ||   |||||||||
                                GGGA GG   GGACCACTC
                                  A  ACCA
GAM138  GGT1     3' CTCACCAGGACCAGGAAGGG  26436     _ CAAC
                                CCCT CC   CCTGGTGAG
                                |||| ||   |||||||||
                                GGGA GG   GGACCACTC
                                  A  ACCA
GAM138  GGT1     3' CTCACCAGGACCAGGAAGGG  19158     _ CAAC
                                CCCT CC   CCTGGTGAG
                                |||| ||   |||||||||
                                GGGA GG   GGACCACTC
                                  A  ACCA
GAM138  GPR17    3' TGGTGGGGACGGGGAGGGA   19182        AA_   G
                                TCCCTCCC  CCCTG TG
                                ||||||||  ||||| ||
                                AGGGAGGG  GGGGT GT
                                    GCA   G
GAM138  GRIN2D   3' CGCGTGGGTTGGGAAGGA   7735     C       TG
                                TCC TCCCAACCC  GTG
                                ||| |||||||||  |||
                                AGG AGGGTTGGG  CGC
                                  A       TG
GAM138  KIAA0442 3' CTCACACAGACTGGGGGGGA  32094        ACC  _
                                TCCCTCCCA  CTG GTGAG
                                |||||||||  ||| |||||
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                                AGGGGGGGT  GAC CACTC
                                     CA_  A
GAM138  LAD1    5'  CACCTGGGCTGGAAGGGG   19900     C  A  T
                                TCCCT CCA CCC GGTG
                                ||||| ||| ||| ||||
                                GGGGA GGT GGG CCAC
                                   A  C  T
GAM138  LTF     5'  CGCGGGGAGTGGGGAGGGA   11374       A  _  G
                                TCCCTCCC AC CCT GTG
                                |||||||| || ||| |||
                                AGGGAGGG TG GGG CGC
                                     G  A  G
GAM138  LYL1    5'  CTCACTTTCCCTGGGGGGGA  19950       ACCCT
                                TCCCTCCCA   GGTGAG
                                |||||||||   ||||||
                                AGGGGGGGT   TCACTC
                                     CCCTT
GAM138  NDN     3'  CTCACCAGGGCTGTGGAAGG  11758   C  _  A
                                CC TCC CA CCCTGGTGAG
                                || ||| || ||||||||||
                                GG AGG GT GGGACCACTC
                                 A  T  C
GAM138  NEDD4L  3'  TTTATTAGAATTGGAAGG   31609    C   CC
                                CCT CCAA  CTGGTGAG
                                ||| ||||  ||||||||
                                GGA GGTT  GATTATTT
                                  A   AA
GAM138  OSCAR   5'  CTCATTTCCTGGGAGGGG   56249       ACCCT
                                TCCCTCCCA   GGTGAG
                                |||||||||   ||||||
                                GGGGAGGGT   TTACTC
                                     CCT__
GAM138  OSCAR   5'  CTCATTTCCTGGGAGGGG   56477       ACCCT
                                TCCCTCCCA   GGTGAG
                                |||||||||   ||||||
                                GGGGAGGGT   TTACTC
                                     CCT__
GAM138  OSCAR   5'  CTCATTTCCTGGGAGGGG   56480       ACCCT
                                TCCCTCCCA   GGTGAG
                                |||||||||   ||||||
                                GGGGAGGGT   TTACTC
                                     CCT__
GAM138  P53AIP1 3'  CTGTGGTGATGGGAGGGA   42336       __  C
                                TCCCTCCCA  ACC TGG
                                |||||||||  ||| |||
                                AGGGAGGGT  TGG GTC
                                     AG  T
GAM138  PIP5K1A 3'  TGTTAGGGGTGGGAGGGA   14523       A   GT
                                TCCCTCCCA CCCTG  G
                                ||||||||| |||||  |
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                                AGGGAGGGT GGGAT  T
                                     G    TG
GAM138  POV1     3'  CTCCTTGGGTTGGAGGAGA   14636   _    C    T  T
                                TC CCTCC AACCC GG GAG
                                || ||||| ||||| || |||
                                AG GGAGG TTGGG TC CTC
                                 A    _    T  _
GAM138  PPP2R5D  3'  CAAGTGGGGCCGGGGAGGGA  21803       AA_    G_
                                TCCCTCCC   CCCTG  TG
                                ||||||||   |||||  ||
                                AGGGAGGG   GGGGT  AC
                                     GCC    GA
GAM138  SERPINH2 3'  TATTGGGGTTGGGGGGGA    8787          TG
                                TCCCTCCCAACCC  GTG
                                ||||||||||||  |||
                                AGGGGGGGTTGGG  TAT
                                       GT
GAM138  SLC21A2  3'  CTCACCAGCCCTGGGGGGA   20083     T   ACC
                                TCCC CCCA   CTGGTGAG
                                |||| ||||   ||||||||
                                AGGG GGGT   GACCACTC
                                  _   CCC
GAM138  STK19    3'  CTCAGAGTGGGCCGGGAGGGG  16097       AA   TGG_
                                TCCCTCCC  CCC    TGAG
                                ||||||||  |||    ||||
                                GGGGAGGG  GGG    ACTC
                                     CC   TGAG
GAM138  STK19    3'  CTCAGAGTGGGCCGGGAGGGG  51613       AA   TGG_
                                TCCCTCCC  CCC    TGAG
                                ||||||||  |||    ||||
                                GGGGAGGG  GGG    ACTC
                                     CC   TGAG
GAM138  TSN      3'  TCAGCGGTTGCCAGGAAGGG   17305     _ ___    _
                                CCCT CC   CAACC CTGG
                                |||| ||   ||||| ||||
                                GGGA GG   GTTGG GACT
                                  A  ACC    C
GAM138  TUFT1    3'  TTCATCAGATTGGGAGAGG    39681    _     CC
                                CC CTCCCAA  CTGGTGAG
                                || |||||||  ||||||||
                                GG GAGGGTT  GACTACTT
                                 A      A_
GAM138  BHLHB2   3'  CTCACCAGACGTCGGGGAGAGA 14764    C    A_  C_
                                TC CTCCC  AC  CTGGTGAG
                                || |||||  ||  ||||||||
                                AG GAGGG  TG  GACCACTC
                                 A    GC  CA
GAM138  BPESC1   3'  CGATGGGGTTGAGAGGGG    41771       C      GG
                                TCCCTC CAACCCT  TG
                                ||||||| |||||||  ||
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                                GGGGAG GTTGGGG  GC
                                   A      TA
GAM138  BRPF3    5'  CAGCGCGGGCCGGGAGGGG   93927        AA  _  G
                                TCCCTCCC  CCC TG TG
                                ||||||||  ||| || ||
                                GGGGAGGG  GGG GC AC
                                    CC   C  G
GAM138  C20orf151 3'  CACCAGGGCCTGGAGAGG    90091     _  A_
                                CCTC CCA  CCCTGGTG
                                |||| |||  ||||||||
                                GGAG GGT  GGGACCAC
                                  A  CC
GAM138  C20orf180 5'  TGTCAGGGTTGGGGGGA     37974      T        GT
                                TCCC CCCAACCCTG  G
                                |||| ||||||||||  |
                                AGGG GGGTTGGGAC  T
                                  _        TG
GAM138  CCT5     5'  CGCCGGTTGGGGGGA      73033     T     CT
                                TCCC CCCAACC  GGTG
                                |||| |||||||  ||||
                                AGGG GGGTTGG  CCGC
                                  _     __
GAM138  CECR6    5'  CCGGGGTTGGCGGGGAGGGA  49931        ____
                                TCCCTCCC   AACCCTGG
                                ||||||||   ||||||||
                                AGGGAGGG   TTGGGGCC
                                    GCGG
GAM138  DGS-A    3'  CCAGGGCAGGCTGGGAGGGA  86051        A____
                                TCCCTCCCA    CCCTGG
                                |||||||||    ||||||
                                AGGGAGGGT    GGGACC
                                     CGGAC
GAM138  DKFZp761P1010 3'  CATGTGGGGTTGGAGGAGA   37942   _    C     _
                                TC CCTCC AACCCTG GTG
                                || ||||| ||||||| |||
                                AG GGAGG TTGGGGT TAC
                                 A   _     G
GAM138  ET(B)R-LP-2 3'  CAGTAGGGGTGGGGAGGGA   17672        AA_   G
                                TCCCTCCC   CCCTG TG
                                ||||||||   ||||| ||
                                AGGGAGGG   GGGAT AC
                                    GTG    G
GAM138  FLJ10057  3'  CTCATGGAAGATGTTGGGAGAG 36251    C      _____  TG
           A                     TC CTCCCAAC    CC  GTGAG
                                 || ||||||||    ||  |||||
                                 AG GAGGGTTG    GG  TACTC
                                  A       TAGAA __
GAM138  FLJ10853  3'  CTCACTGGGTCAAAGGGA    37315      CCCA   T
                                TCCCT    ACCC GGTGAG
                                |||||    |||| ||||||
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                                AGGGA   TGGG TCACTC
                                  AAC_   _
GAM138  FLJ11000  3'  CAGGAGGGTGGGGAGGGA   37525       A    GG
                                TCCCTCCC ACCCT  TG
                                |||||||| |||||  ||
                                AGGGAGGG TGGGA  AC
                                    G    GG
GAM138  FLJ12650  3'  CTCACCAGTTGGAAGG     44820    C    CC
                                CCT CCAAC  TGGTGAG
                                ||| |||||  |||||||
                                GGA GGTTG  ACCACTC
                                  A    __
GAM138  FLJ20489  3'  CTCACCTAACTTGGGAGGGA  35711        CCCT
                                TCCCTCCCAA   GGTGAG
                                ||||||||||   ||||||
                                AGGGAGGGTT   CCACTC
                                     CAAT
GAM138  FLJ20793  3'  CATTGTAGGTTGGGAAGGG   93448    _     CT_
                                CCCT CCCAACC   GGTG
                                |||| |||||||   ||||
                                GGGA GGGTTGG   TTAC
                                  A      ATG
GAM138  FLJ21313  3'  TCAGGAAAGTGGGGAGGGA   43934       A ___
                                TCCCTCCC AC   CCTGG
                                |||||||| ||   |||||
                                AGGGAGGG TG   GGACT
                                    G  AAA
GAM138  FLJ23231  3'  CTCAGAGGGTGGGGAGGGA   47605       A    GG
                                TCCCTCCC ACCCT  TGAG
                                |||||||| |||||  ||||
                                AGGGAGGG TGGGA  ACTC
                                    G    G_
GAM138  FLJ32915  5'  CTCACATTTTGGGAGGGA    59432        CCCTG
                                TCCCTCCCAA    GTGAG
                                ||||||||||    |||||
                                AGGGAGGGTT    CACTC
                                     TTA__
GAM138  FREQ     3'  CTCAAAGGCTGGGAGGGA    27370       AC   GG
                                TCCCTCCCA  CCT  TGAG
                                |||||||||  |||  ||||
                                AGGGAGGGT  GGA  ACTC
                                    C_   A_
GAM138  GGTL4    3'  CTCACCAGGACCAGGAAGGG   55944    _ CAAC
                                CCCT CC    CCTGGTGAG
                                |||| ||    |||||||||
                                GGGA GG    GGACCACTC
                                  A  ACCA
GAM138  GMPPB    3'  CCAAGGGGGTGGGAGGGA    97439       A_   _
                                TCCCTCCCA  CCCT GG
                                |||||||||  |||| ||
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                                AGGGAGGGT  GGGA CC
                                     GG    A
GAM138  GTPBP1    3' CTTCCAGGGTTAGGACAGA   16266    CC   C      T
                                TC  TCC AACCCTGG GAG
                                ||  ||| |||||||| |||
                                AG  AGG TTGGGACC TTC
                                 AC   A      _
GAM138  HGC6.1.1  3' CAGTGGGAGCTGGGAGGGA   27609        AC_   G
                                TCCCTCCCA   CCTG TG
                                |||||||||   |||| ||
                                AGGGAGGGT   GGGT AC
                                     CGA    G
GAM138  HOOK2     3' CCAGATTGGTGGGGAGGGA   26158        A  ____
                                TCCCTCCC ACC   CTGG
                                |||||||| |||   ||||
                                AGGGAGGG TGG   GACC
                                     G   TTA
GAM138  KIAA0140  3' CTCAGTCCTCTGGGAGGGA   28512        ACCCT  __
                                TCCCTCCCA    GG  TGAG
                                |||||||||    ||  ||||
                                AGGGAGGGT    CC  ACTC
                                     CT___  TG
GAM138  KIAA0182  3' TACGCAGGTGGGAGGGA     72502        AC   _
                                TCCCTCCCA  CCTG GTG
                                |||||||||  |||| |||
                                AGGGAGGGT  GGAC CAT
                                     __    G
GAM138  KIAA0252  3' TGGCAGGTGTGGGAGGGA    63461        AC    G
                                TCCCTCCCA  CCTG TG
                                |||||||||  |||| ||
                                AGGGAGGGT  GGAC GT
                                     GT    G
GAM138  KIAA0285  3' CTCAGAAGAAACTGGGAGGGG 29683        ACC_  GG
                                TCCCTCCCA    CT  TGAG
                                |||||||||    ||  ||||
                                GGGGAGGGT    GA  ACTC
                                     CAAA  AG
GAM138  KIAA0677  3' CACTGTAGGTGGGAGGGA    28529        A  CT_
                                TCCCTCCCA CC   GGTG
                                |||||||||  ||   ||||
                                AGGGAGGGT GG   TCAC
                                     _  ATG
GAM138  KIAA0789  5' CTCACCTTCAGTTTGGGAGGG 64429        CCCT__
                                CCCTCCCAA     GGTGAG
                                |||||||||     ||||||
                                GGGAGGGTT     CCACTC
                                     TGACTT
GAM138  KIAA0843  3' CTTTGTAGATTGGGGGGA    30802     T    CC   GT
                                TCCC CCCAA  CTG  GAG
                                ||||  |||||  |||  |||
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                                AGGG GGGTT  GAT  TTC
                                  _    A_  GT
GAM138  KIAA0853  3'  TTTATTAATGGGGAGGGA    31217        AACCC
                                TCCCTCCC    TGGTGAG
                                ||||||||    |||||||
                                AGGGAGGG    ATTATTT
                                    GTA__
GAM138  KIAA0864  3'  CAGTGGGGGCTGGGAGGG    63938        A_    G
                                CCCTCCCA  CCCTG TG
                                ||||||||  ||||| ||
                                GGGAGGGT  GGGGT AC
                                    CG    G
GAM138  KIAA1018  3'  TTCATCAGCCAGGAGGGA    31059        CAACC
                                TCCCTCC    CTGGTGAG
                                |||||||    ||||||||
                                AGGGAGG    GACTACTT
                                    ACC__
GAM138  KIAA1061  3'  CACACGGGTTGGGAGAGG    71716    _        TG
                                CC CTCCCAACCC  GTG
                                || ||||||||||  |||
                                GG GAGGGTTGGG  CAC
                                 A         CA
GAM138  KIAA1171  3'  GCTCACGGGGAGAGGTATGGGA 89344          _  ____  G    III
          GGGA                    TCCCTCCCA ACC    CT GTGAG   C
                                |||||||||  |||    || |||||   |
                                AGGGAGGGT TGG    GG CACTC   G
                                     A   AGAG  G    III
GAM138  KIAA1190  3'  CTCGGGGGATTGGGGGGA    71646      T    _    GG
                                TCCC CCCAA CCCT  TGAG
                                ||||  |||||  ||||  ||||
                                AGGG GGGTT GGGG  GCTC
                                  _    A   __
GAM138  KIAA1649  3'  TGCTGGTTGGGAGTGA      67518    C        CT
                                TC CTCCCAACC  GGTG
                                || |||||||||  ||||
                                AG GAGGGTTGG  TCGT
                                 T        __
GAM138  KIAA1649  3'  TGCTGGTTGGGAGTGA      51256    C        CT
                                TC CTCCCAACC  GGTG
                                || |||||||||  ||||
                                AG GAGGGTTGG  TCGT
                                 T        __
GAM138  KIAA1655  5'  CTCACCTCCAGTGGGAGGGA   67182          ACCCT
                                TCCCTCCCA    GGTGAG
                                |||||||||    ||||||
                                AGGGAGGGT    CCACTC
                                     GACCT
GAM138  KIAA1750  3'  CTCAGTGATAGAGTATGGGAGG 68809          _  C   G___
          GA                    TCCCTCCCA AC CTG    TGAG
                                |||||||||  || |||    ||||
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                                AGGGAGGGT TG GAT    ACTC
                                     A  A   AGTG
GAM138  KIAA1944  5'  CACCAGGTAGTCACTGGGCAGA 76077    C  _   ___  __
              GA                   TC CT CCCA   AC  CCTGGTG
                                || || ||||   ||  |||||||
                                AG GA GGGT   TG  GGACCAC
                                 A  C    CAC  AT
GAM138  KIAA1952  5'  CTCTGCCGGCTGGGAGGG    73544        ACC    _
                                CCCTCCCA   CTGGT GAG
                                ||||||||   ||||| |||
                                GGGAGGGT   GGCCG CTC
                                     C__     T
GAM138  LAGY     5'  CTCAGTCCAGGGAGGGA     51658        AACCC   __
                                TCCCTCCC    TGG  TGAG
                                ||||||||    |||  ||||
                                AGGGAGGG    ACC  ACTC
                                     _____   TG
GAM138  MGC10715  3'  CTTATCAGGCATGGGAGGGA   44498         AC
                                TCCCTCCCA  CCTGGTGAG
                                |||||||||  |||||||||
                                AGGGAGGGT  GGACTATTC
                                     AC
GAM138  MGC15429  3'  CTCACTGGCTGGGAAGG     52211    C    A  CT
                                CC TCCCA CC  GGTGAG
                                || ||||| ||  ||||||
                                GG AGGGT GG  TCACTC
                                 A    C  __
GAM138  MGC4737   5'  CTCACCAGCGGAGTGGA     49640    _   CAACC
                                TCC CTCC    CTGGTGAG
                                ||| ||||    ||||||||
                                AGG GAGG    GACCACTC
                                  T   C_____
GAM138  MGC5139   5'  CTTGAAAGGGTGGGGAGGGA   74571        A    GG
                                TCCCTCCC ACCCT  TGAG
                                |||||||| |||||  ||||
                                AGGGAGGG TGGGA  GTTC
                                     G    AA
GAM138  MLLT10    5'  CCGGGTGGAGGTGGGGAGGGA  17351        A   _____
                                TCCCTCCC ACC    CTGG
                                |||||||| |||    ||||
                                AGGGAGGG TGG    GGCC
                                     G   AGGTG
GAM138  MMP24     3'  CTCACCAGGGTCTGAGGGG    22918       CCA
                                TCCCTC   ACCCTGGTGAG
                                ||||||   ||||||||||||
                                GGGGAG   TGGGACCACTC
                                   TC_
GAM138  moblak    3'  CTCACCAGAATTGTCAGTGG   56396    _  CC   CC
                                CC CT  CAA  CTGGTGAG
                                || ||  |||  ||||||||
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                                GG GA  GTT  GACCACTC
                                 T  CT   AA
GAM138  NIP30    3'  CTCACTGATATTGGGAGG    46896        CCC
                                CCTCCCAA   TGGTGAG
                                ||||||||   |||||||
                                GGAGGGTT   GTCACTC
                                    ATA
GAM138  PRO0529  3'  CTCACCAGGGTGGGCAGAGA   26856    C  _   A
                                TC CT CCCA CCCTGGTGAG
                                || || |||| ||||||||||
                                AG GA GGGT GGGACCACTC
                                 A  C   _
GAM138  PTK6     5'  CTCTGAGGGTTGGGAAGG    21076    C       GGT
                                CC TCCCAACCCT   GAG
                                || ||||||||||   |||
                                GG AGGGTTGGGA   CTC
                                 A        GT_
GAM138  RAB3IL1  3'  CTCAGCCCTTGGGAGGGG    26365        CCCT  _
                                TCCCTCCCAA    GG TGAG
                                ||||||||||    || ||||
                                GGGGAGGGTT    CC ACTC
                                      C___  G
GAM138  RIN3     3'  TTCATTAGACGGAAAGGGA   46164      C_  AACC
                                TCCCT  CC    CTGGTGAG
                                |||||  ||    ||||||||
                                AGGGA  GG    GATTACTT
                                   AA  CA__
GAM138  RP4-622L5 3'  CTCATTTCTTGGGAGGG     39424        CCCT
                                CCCTCCCAA    GGTGAG
                                |||||||||    ||||||
                                GGGAGGGTT    TTACTC
                                     CT__
GAM138  SCMH1    3'  CTCACCAGGAGTTTAGG     25283     CCC  _
                                CCT   AAC CCTGGTGAG
                                |||   ||| |||||||||
                                GGA   TTG GGACCACTC
                                  T__   A
GAM138  SERPINH1  3'  TATTGGGGTTGGGGGGGA    16375           TG
                                TCCCTCCCAACCC  GTG
                                ||||||||||||  |||
                                AGGGGGGGTTGGG  TAT
                                       GT
GAM138  SIAT4B   5'  CTCACCAGGGTGGCAGGAGA   23634    _  C   A
                                TC CCT CCA CCCTGGTGAG
                                || ||| ||| ||||||||||
                                AG GGA GGT GGGACCACTC
                                 A   C   _
GAM138  SNPH     3'  CTCTGGGGGTTGGAGGGA    28902       C     GGT
                                TCCCTCC AACCCT   GAG
                                |||||||  ||||||   |||
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                                AGGGAGG TTGGGG  CTC
                                   _    GT_
GAM138  SSH-3    5' CGCGGGGTTGAGGGA      37417      CC     G
                                TCCCTC  AACCCTG TG
                                ||||||  ||||||| ||
                                AGGGAG  TTGGGGC GC
                                  __     _
GAM138  SSH-3    5' CGCGGGGTTGAGGGA      35790      CC     G
                                TCCCTC  AACCCTG TG
                                ||||||  ||||||| ||
                                AGGGAG  TTGGGGC GC
                                  __     _
GAM138  VIAAT    3' CGAGGGGGTTGGGAAGGGA  55450      _      GG
                                TCCCT CCCAACCCT  TG
                                |||||  |||||||||  ||
                                AGGGA GGGTTGGGG  GC
                                   A       GA
GAM138  LOC114987 3' CGGGAATGAGTTGGGAGGGG  59795        _____
                                TCCCTCCCAAC    CCTG
                                ||||||||||     ||||
                                GGGGAGGGTTG    GGGC
                                     AGTAA
GAM138  LOC121036 3' CAGTAGGATGGGAGGGA     74481        AC   G
                                TCCCTCCCA  CCTG TG
                                |||||||||  |||| ||
                                AGGGAGGGT  GGAT AC
                                     A_   G
GAM138  LOC123346 5' CTCTGAAAGAGTCGGGGAGGGA 76127       A_  C  GGT_
                                TCCCTCCC  AC CT   GAG
                                ||||||||  || ||   |||
                                AGGGAGGG  TG GA   CTC
                                    GC  A  AAGT
GAM138  LOC136306 3' CAAAGGGGTGTGAGAGGGA   75768      C  _   GG
                                TCCCTC CA ACCCT  TG
                                ||||||  || |||||  ||
                                AGGGAG GT TGGGG  AC
                                   A  G    AA
GAM138  LOC144596 3' CTCACCTGGAGGCAAGAGGGA  77427      ___  AAC  T
                                TCCCTC   CC   CC GGTGAG
                                ||||||   ||   || ||||||
                                AGGGAG   GG   GG CCACTC
                                   AAC  A__  T
GAM138  LOC145497 5' CCAGGGCTTGCTGGGAGGGA   77731       A____
                                TCCCTCCCA    CCCTGG
                                |||||||||    ||||||
                                AGGGAGGGT    GGGACC
                                     CGTTC
GAM138  LOC146439 5' CTCATTCCTGGGAGGGG     78449        ACCCT
                                TCCCTCCCA    GGTGAG
                                |||||||||    ||||||
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                                GGGGAGGGT    TTACTC
                                     CC___
GAM138  LOC147711 3'  CTCAGCCTTTGGGAGGG    79116       CCCT _
                                CCCTCCCAA   GG TGAG
                                |||||||||   || ||||
                                GGGAGGGTT   CC ACTC
                                     T___  G
GAM138  LOC150150 5'  CCAGTGTGGTGGGAGGGA    86009       A ___
                                TCCCTCCCA CC  CTGG
                                |||||||||  ||  ||||
                                AGGGAGGGT GG  GACC
                                     _ TGT
GAM138  LOC152667 3'  CTCACTGATATTGGGAGG    81523       CCC
                                CCTCCCAA  TGGTGAG
                                ||||||||  |||||||
                                GGAGGGTT  GTCACTC
                                     ATA
GAM138  LOC157931 3'  CTCACGGCCTGGGAGGG    87940       AC  TG
                                CCCTCCCA  CC  GTGAG
                                ||||||||  ||  |||||
                                GGGAGGGT  GG  CACTC
                                     CC  __
GAM138  LOC158055 3'  CCGGCGGCTGGTGAGGGA    82580      _  A  _
                                TCCCTC CCA CC CTGG
                                ||||||  ||| || ||||
                                AGGGAG GGT GG GGCC
                                   T   C  C
GAM138  LOC199927 3'  CCGGAGTGGCTGGGAGGGG   91479       A ___
                                TCCCTCCCA CC  CTGG
                                |||||||||  ||  ||||
                                GGGGAGGGT GG  GGCC
                                     C  TGA
GAM138  LOC201182 5'  CTCACTGGTTGAGATGGA    91336    C  C    CT
                                TCC TC CAACC  GGTGAG
                                |||  ||  |||||  ||||||
                                AGG AG GTTGG  TCACTC
                                  T  A    __
GAM138  LOC219920 5'  CTCATTAGACTGGGAGG     94947       ACC
                                CCTCCCA   CTGGTGAG
                                |||||||   ||||||||
                                GGAGGGT   GATTACTC
                                    CA_
GAM138  LOC220739 3'  TCAGGGCTTAGGGAGGGA    94529       _ _
                                TCCCTCCC AA CCCTGG
                                ||||||||  ||  ||||||
                                AGGGAGGG TT GGGACT
                                     A  C
GAM138  LOC221424 3'  CCTGGGACTTGGGAGGGA    95271        __  T
                                TCCCTCCCAA  CCC GG
                                ||||||||||  ||| ||
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                                AGGGAGGGTT  GGG CC
                                      CA   T
GAM138  LOC221718 5'  CTCACCAGCCTGAGGTAGGA   95280     CT  _  ACC
                                TCC  CC CA   CTGGTGAG
                                |||  || ||   ||||||||
                                AGG  GG GT   GACCACTC
                                  AT  A  CC_
GAM138  LOC253955 5'  CTCACCAGGTGCAGAGGGG    96072       CCAAC
                                TCCCTC    CCTGGTGAG
                                ||||||    |||||||||
                                GGGGAG    GGACCACTC
                                   ACGT_
GAM138  LOC255328 3'  CTCACCAGGTGAGGAGTGA    98338    C    _  AC
                                TC CTCC CA  CCTGGTGAG
                                || |||| ||  |||||||||
                                AG GAGG GT  GGACCACTC
                                 T    A  __
GAM138  LOC256973 3'  CTCACGGCCTCCGGGAGGGG   98198        AAC__  TG
                                TCCCTCCC    CC  GTGAG
                                ||||||||    ||  |||||
                                GGGGAGGG    GG  CACTC
                                     CCTCC  __
GAM138  LOC257456 3'  CTCACTAGGACCAGGAAGGG   80594     _  CAAC
                                CCCT CC    CCTGGTGAG
                                |||| ||    |||||||||
                                GGGA GG    GGATCACTC
                                  A  ACCA
GAM138  LOC51696  3'  CATTGGAGGTTGGGAAGGA    33079     C       _ TG
                                TCC TCCCAACC C  GTG
                                ||| ||||||| |  |||
                                AGG AGGGTTGG G  TAC
                                  A       A GT
GAM138  LOC91496  5'  CATTAGAGGTGGAAGGGA     66808      C   A  _
                                TCCCT CCA CC CTGGTG
                                ||||| ||| || ||||||
                                AGGGA GGT GG GATTAC
                                   A   _  A
GAM138  LOC92228  5'  CTCACCAGGGTGAGGG       69075      CCA
                                CCCTC   ACCCTGGTGAG
                                |||||   ||||||||||
                                GGGAG   TGGGACCACTC
                                   ___
GAM138  LOC92293  3'  CACACAGCTGGGGGGGA      69318        ACC  _
                                TCCCTCCCA   CTG GTG
                                |||||||||   ||| |||
                                AGGGGGGGT   GAC CAC
                                     C__   A
GAM139  KCNJ16    3'  AAACATTCTCAGACCCTTGG   38483        GT___
                                TCAAGGGTC    GTGTTT
                                |||||||||    ||||||
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                                GGTTCCCAG    TACAAA
                                     ACTCT
GAM139  RAD52    3'  AAATGCTTAGACTCTTGA    57013        GT_
                                TCAAGGGTC   GTGTTT
                                |||||||||   ||||||
                                AGTTCTCAG   CGTAAA
                                     ATT
GAM139  RAD52    3'  AAATGCTTAGACTCTTGA    57014        GT_
                                TCAAGGGTC   GTGTTT
                                |||||||||   ||||||
                                AGTTCTCAG   CGTAAA
                                     ATT
GAM139  ARF6     3'  AAACACAGCAGTTCTTGG    9787         TC _
                                TCAAGGG  G TGTGTTT
                                |||||||  | |||||||
                                GGTTCTT  C ACACAAA
                                    GA G
GAM139  C22orf19 3'  AAACTCAGTTGATCCTTGA   14806          __ T
                                TCAAGGGTCG  TG GTTT
                                ||||||||||  || ||||
                                AGTTCCTAGT  AC CAAA
                                      TG  T
GAM139  CEACAM7  3'  AAACTGCCCTGACTCTTGA   23541          T_ _
                                TCAAGGGTCG  GT GTTT
                                ||||||||||  || ||||
                                AGTTCTCAGT  CG CAAA
                                      CC  T
GAM139  CXYorf1  3'  AAACACAGTGGCCTTGGA    82901    A     _
                                TC AGGGTCG TGTGTTT
                                || ||||||| |||||||
                                AG TTCCGGT ACACAAA
                                  G      G
GAM139  FLJ10700 3'  AAATACAGTGACCTTTGA    36959          _
                                TCAAGGGTCG TGTGTTT
                                |||||||||| |||||||
                                AGTTTCCAGT ACATAAA
                                      G
GAM139  FLJ12547 3'  AAACACGAACGTCCTTGA    47123        T  __
                                TCAAGGG CGT  GTGTTT
                                ||||||| |||  ||||||
                                AGTTCCT GCA  CACAAA
                                    _  AG
GAM139  KIAA1233 3'  AAACACAGCAACCCATGA    63752     A   C _
                                TCA GGGT G TGTGTTT
                                ||| |||| | |||||||
                                AGT CCCA C ACACAAA
                                  A   A G
GAM139  KIAA1364 3'  TAAACACATTTATAAACCCTTG 64356         C_____       ___
            A                    TCAAGGGT     GTGTGTTT   A
                                 ||||||||     ||||||||   |
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                                AGTTCCCA     TACACAAA   T
                                     AATATT       ___
GAM139  MIC2L1   3'  AAACACAGGAACCCCATGA   49598     A   __  G
                                TCA GGG  TC TGTGTTT
                                ||| |||  || |||||||
                                AGT CCC  AG ACACAAA
                                  A   CA  G
GAM139  TRIM29   3'  AAAGGCAGTGTACCCTTGA   25002         _ _  G
                                TCAAGGGT CG TGT TTT
                                |||||||| || ||| |||
                                AGTTCCCA GT ACG AAA
                                     T  G   G
GAM139  ZNF333   3'  AAACACATGGGGCTATGA    51582     _ GG
                                TCA AG  TCGTGTGTTT
                                ||| ||  ||||||||||
                                AGT TC  GGTACACAAA
                                  A  GG
GAM139  LOC200093 3'  AAACACAGTGGCCTTGGA    63759    A      _
                                TC AGGGTCG TGTGTTT
                                || ||||||| |||||||
                                AG TTCCGGT ACACAAA
                                 G      G
GAM139  LOC222166 3'  AAACACATCCCTGACCCTT   95732        ____
                                AAGGGTC    GTGTGTTT
                                |||||||    ||||||||
                                TTCCCAG    TACACAAA
                                     TCCC
GAM139  LOC256433 5'  AAACCCAGTGACCCTGGA    99339    A      _ T
                                TC AGGGTCG TG GTTT
                                || ||||||| || ||||
                                AG TCCCAGT AC CAAA
                                 G      G  C
GAM139  LOC91040  3'  AAACACAGTGGCCTTGGA    65332    A      _
                                TC AGGGTCG TGTGTTT
                                || ||||||| |||||||
                                AG TTCCGGT ACACAAA
                                 G      G
GAM139  LOC92568  3'  AATGCCCCCGACCCTTGA    70320         T__
                                TCAAGGGTCG   GTGTT
                                ||||||||||   |||||
                                AGTTCCCAGC   CGTAA
                                     CCC
GAM140  BRPF3    3'  ATTGTAAAATACTGTTCTA    93925          GTTTC
                                TAGAACAGTATT    TATAAT
                                ||||||||||||    ||||||
                                ATCTTGTCATAA    ATGTTA
                                       A____
GAM140  FLJ13657  3'  AATTATAGCAGACACGCCATTC 46139      CA  AT    _
           TA                     TAGAA  GT  TGTTT CTATAATT
                                |||||  ||  ||||| ||||||||
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                                ATCTT  CG  ACAGA GATATTAA
                                  AC  C_    C
GAM140  LOC152220 3'  ATTATAGAAACTGGTTT    86758     AGTATT
                                GAAC     GTTTCTATAAT
                                ||||     ||||||||||
                                TTTG     CAAAGATATTA
                                  GT____
GAM140  LOC51336  3'  TATAGAATAACTGTTCT    34077       ATTGT
                                AGAACAGT    TTCTATA
                                ||||||||    |||||||
                                TCTTGTCA    AAGATAT
                                    AT___
GAM141  ADH7    3'  AAGATTAAGGGACGGGC    7268      ACA   G
                                GCCC   TCT TTTAATCTT
                                ||||   ||| |||||||||
                                CGGG   AGG GAATTAGAA
                                  C__   _
GAM141  ARAF1   5'  GGAAGGACTTCAGATGTGAGC  64644    C      TTTAA
                                GC CACATCTG    TCTTCC
                                || ||||||||    ||||||
                                CG GTGTAGAC    GGAAGG
                                 A       TTCA_
GAM141  CEACAM6  3'  GGAAGACTGGCAGATTGGACCA 11756    C   C      TAA
                                TGG CCA ATCTGTT   TCTTCC
                                ||| ||| |||||||   ||||||
                                ACC GGT TAGACGG   AGAAGG
                                  A  _      TC_
GAM141  CLECSF12  3'  GGATTACAGATGTGAGCCA   77214     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM141  CYP1A2   3'  GGATTAACAGGTATGAACCA   7518     CC  C      T
                                TGG  CA ATCTGTT AATCT
                                |||  || ||||||| |||||
                                ACC  GT TGGACAA TTAGG
                                  AA  A      _
GAM141  ENG     3'  GAACTTGAAACAGATTCAGGCC 5496       CAC       AATC
            A                    TGGCC   ATCTGTTT    TTC
                                |||||   ||||||||    |||
                                ACCGG   TAGACAAA    AAG
                                   ACT       GTTC
GAM141  ERCC3    3'  GAATAAACAGAATGGACCA   5506     C   CA       A
                                TGG CCA  TCTGTTTA TC
                                ||| |||  |||||||| ||
                                ACC GGT  AGACAAAT AG
                                  A  A_       A
GAM141  HTLF    5'  AAGATTGCAGGATTAAGCCA   10973     CCACA    TT
                                TGGC    TCTGT  AATCTT
                                ||||    |||||  ||||||
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                                ACCG    GGACG  TTAGAA
                                  AATTA    __
GAM141  MS4A8B   3'  GATTTTAAACAGATGTTAACCA 49588     CCC          TCT
                                TGG   ACATCTGTTTAA   TC
                                |||   ||||||||||||   ||
                                ACC   TGTAGACAAATT   AG
                                  AAT          TT_
GAM141  PRKAA2   3'  GAAGATTAAAAAGTAAAGAACC 21811     CCCACAT  G
          A                      TGG      CT TTTAATCTTC
                                |||      || ||||||||||
                                ACC      GA AAATTAGAAG
                                  AAGAAAT  A
GAM141  ASE-1    3'  GGATAACAGGTGTGAGCCA   24983     C        TA
                                TGGC CACATCTGTT  ATCT
                                |||| ||||||||||  ||||
                                ACCG GTGTGGACAA  TAGG
                                  A        __
GAM141  CITED2   3'  GGAAGATTAAACAGATGTGGGC 21403
          CA                     TGGCCCACATCTGTTTAATCTTCC
                                |||||||||||||||||||||||||
                                ACCGGGTGTAGACAAATTAGAAGG

GAM141  DKFZP564K0322 3'  GGATTACAGATGTGAGCCA   50188     C        TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A        __
GAM141  DZIP1    3'  GAAGATTATTCCAGAAGCCA   30703     CCACA    TT_
                                TGGC    TCTG   TAATCTTC
                                ||||    ||||   ||||||||
                                ACCG    AGAC   ATTAGAAG
                                  A____    CTT
GAM141  FLJ22969 3'  GGATTACAGATGTGAGCCA   69211     C        TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A        __
GAM141  HSNOV1   3'  GGATTACAGATGTGAACCA   34437     CC       TT
                                TGG  CACATCTGT  AATCT
                                |||  |||||||||  |||||
                                ACC  GTGTAGACA  TTAGG
                                  AA       __
GAM141  IMPACT   3'  GAATTACAGGTGTGAGCCA   38006     C        TTAATC
                                TGGC CACATCTGT     TTC
                                |||| |||||||||     |||
                                ACCG GTGTGGACA     AAG
                                  A        TT____
GAM141  JAM1     3'  GGATTACAGATGTGAGCCA   34234     C        TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
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                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM141  JAM1     3'  GGATTACAGATGTGAGCCA   58499     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM141  JAM1     3'  GGATTACAGATGTGAGCCA   58520     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM141  JAM1     3'  GGATTACAGATGTGAGCCA   58548     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM141  JAM1     3'  GGATTACAGATGTGAGCCA   58577     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM141  KIAA0210 5'  GAATTACAGGTGTGAGCCA   29159     C       TTAATC
                                TGGC CACATCTGT     TTC
                                |||| |||||||||     |||
                                ACCG GTGTGGACA     AAG
                                  A       TT_____
GAM141  KIAA0280 3'  GAGCATAAACAGATGTGGTCCA 93301     C          AT
                                TGG CCACATCTGTTTA  CTT
                                ||| ||||||||||||  |||
                                ACC GGTGTAGACAAAT  GAG
                                  T          AC
GAM141  KIAA0285 5'  GAAGATTGAGCTTGACCGGACC 29684     C  ACA  T_
           A                     TGG CC   TC  GTTTAATCTTC
                                ||| ||   ||  ||||||||||
                                ACC GG   AG  CGAGTTAGAAG
                                  A  CC_  TT
GAM141  KIAA0356 3'  GGAAGACCCTCAGATGTGGCCA 66778      C      TTTAA
                                TGGCC ACATCTG    TCTTCC
                                ||||| |||||||    ||||||
                                ACCGG TGTAGAC    AGAAGG
                                  _      TCCC_
GAM141  KIAA1354 3'  GGAAGATTGTCAGCATGT    61576     _  TT
                                ACAT CTG  TAATCTTCC
                                |||| |||  |||||||||
                                TGTA GAC  GTTAGAAGG
                                  C  T_
GAM141  KIAA1466 3'  ATTAAATAGTATGGGCCA    72406       CAT
                                TGGCCCA   CTGTTTAAT
                                |||||||   |||||||||
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                                ACCGGGT   GATAAATTA
                                   AT_
GAM141  KIAA1468  5'  AAGATCTTGTAGATGTGGCCA  93423      C      TTTA
                                TGGCC ACATCTG    ATCTT
                                ||||| |||||||    |||||
                                ACCGG TGTAGAT    TAGAA
                                   _      GTTC
GAM141  MRPS26    3'  GGAAGATTACAGTCTGAGGGCC 48723       A  T_    TT
           A                     TGGCCC CA  CTGT  AATCTTCC
                                ||||||  ||  ||||  ||||||||
                                ACCGGG GT  GACA  TTAGAAGG
                                   A  CT    __
GAM141  PANX3     3'  AAGATTAATAAAGATGTAAACC 54765    CCC     GT_
                                GG   ACATCT   TTAATCTT
                                ||   ||||||   ||||||||
                                CC   TGTAGA   AATTAGAA
                                 AAA     AAT
GAM141  PLCL1     3'  AAGATTAAACAGATGATG    21714    _
                                CA CATCTGTTTAATCTT
                                || ||||||||||||||
                                GT GTAGACAAATTAGAA
                                 A
GAM141  SPRY4     3'  GAAGACAGAACACAGATGTGGA 49013    GC        _  AA_
           CA                     TG  CCACATCTGT TT   TCTTC
                                ||  |||||||||| ||   |||||
                                AC  GGTGTAGACA AA   AGAAG
                                 A_        C  GAC
GAM141  WNT10A    3'  GAAGAGGAGATTGGACCA    48170     C   C    G TTAA
                                TGG CCA ATCT T    TCTTC
                                ||| ||| |||| |    |||||
                                ACC GGT TAGA G    AGAAG
                                  A   _    G _____
GAM141  LOC113523 5'  GGATTACAGATGTGAGCCA    73427      C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                   A        __
GAM141  LOC124216 3'  GGATTACAGATGTGAGCCA    74736      C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                   A        __
GAM141  LOC130639 5'  GGATTAAAGACGTGAGCCA    75480      C   A   GT
                                TGGC CAC TCT  TTAATCT
                                |||| ||| |||  |||||||
                                ACCG GTG AGA  AATTAGG
                                   A  C   __
GAM141  LOC144202 5'  GGAAGATTCGATGGACATGGAC 77226    GC   CA     T
           A                     TG  CCA  TCTGTT AATCTTCC
                                ||  |||  |||||| ||||||||
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                                AC  GGT  AGGTAG TTAGAAGG
                                 A_   AC     C
GAM141   LOC149171 5'  GAATTACAGGTGTGAGCCA   79967     C       TTAATC
                                TGGC CACATCTGT     TTC
                                |||| |||||||||      |||
                                ACCG GTGTGGACA     AAG
                                  A        TT____
GAM141   LOC150245 3'  GAAGCAAGACAGATGTGGGCC  86112             AAT
                                GGCCCACATCTGTTT   CTTC
                                ||||||||||||||   ||||
                                CCGGGTGTAGACAGA   GAAG
                                         AC_
GAM141   LOC152620 3'  AGATTACAGATGTGAGCCA   60703     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGA
                                  A        __
GAM141   LOC153577 3'  GAAGATTTTATGTGACCA    87239    CC    CTGTTT
                                TGG  CACAT     AATCTTC
                                |||  |||||     |||||||
                                ACC  GTGTA     TTAGAAG
                                 A_    TT____
GAM141   LOC154930 3'  GAATAACAGGTGTGAGCCA   82091     C       TAATC
                                TGGC CACATCTGTT    TTC
                                |||| ||||||||||    |||
                                ACCG GTGTGGACAA    AAG
                                  A        T____
GAM141   LOC157507 5'  AAGATTAAACCATGGATG    82376      ___
                                CATCT   GTTTAATCTT
                                |||||   ||||||||||
                                GTAGG   CAAATTAGAA
                                   TAC
GAM141   LOC158014 5'  AGAATTACAGGTGTGAGCCA  82549     C       TTAA
                                TGGC CACATCTGT    TCT
                                |||| |||||||||    |||
                                ACCG GTGTGGACA    AGA
                                  A        TTA_
GAM141   LOC158668 3'  AGATTACAGATGTGAGCCA   69892     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGA
                                  A        __
GAM141   LOC170409 5'  GGATTACAGATGTGAGCCA   83745     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A        __
GAM141   LOC200282 5'  GAAATTACAGGTGTGAGCCA  90099     C       TTAA
                                TGGC CACATCTGT    TC
                                |||| |||||||||    ||
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                                ACCG GTGTGGACA   AG
                                  A       TTAA
GAM141  LOC220595 3'  GGAAGACCTCAGATGTGACCA  92778    CC      TTTAA
                                TGG  CACATCTG    TCTTCC
                                |||  ||||||||    ||||||
                                ACC  GTGTAGAC    AGAAGG
                                  A_      TCC__
GAM141  LOC253805 3'  GGATTACAGATGTGAGCCA   98179     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM141  LOC56181  5'  GGATTACAGATGTGAGCCA   97278     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM141  LOC91547  3'  GGATTACAGATGTGAGCCA   67004     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM142  APOC3    3'  GGCTGCCCCTGTAGGTTGCTTA 5267       TGTGGG   AGA
          A                      TTAAGC     ACA   GCAGCC
                                 ||||||     |||   ||||||
                                 AATTCG     TGT   CGTCGG
                                    TTGGA_   CCC
GAM142  ATP8A2   3'  CTGCAGAGTCCCACACTTAA   95154      C      AAGA
                                TTAAG TGTGGGAC   GCAG
                                ||||| ||||||||   ||||
                                AATTC ACACCCTG   CGTC
                                  _       AGA_
GAM142  EN2      5'  GCTGCTCCTGTCACCCAG    9260      T _   A
                                CTG GG GACA GAGCAGC
                                ||| || |||| |||||||
                                GAC CC CTGT CTCGTCG
                                  _ A   C
GAM142  MAB21L1   5'  GCCGCATTGGATCCCACAGCTT 19969          __   GA  A
          A                      TAAGCTGTGGGA  CAA  GC GC
                                 ||||||||||||  |||  || ||
                                 ATTCGACACCCT  GTT  CG CG
                                        AG   A_  C
GAM142  PRX      3'  CTGTCCATCCCACAGCT     40895          CAA  G
                                AGCTGTGGGA   GA CAG
                                ||||||||||   || |||
                                TCGACACCCT   CT GTC
                                     AC_  _
GAM142  TMEPAI   3'  CTGCTCTCCTTTGCAGC     39828       __    CAA
                                GCTGT  GGGA   GAGCAG
                                |||||  ||||   ||||||
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                                CGACG  TCCT   CTCGTC
                                  TT   ___
GAM142  ZNF76    3'  GGCCACTCTTGCCCCCAAGGGC 14270    G_   A_    CA
                                GCT  TGGG  CAAGAG  GCC
                                |||  ||||  ||||||  |||
                                CGG  ACCC  GTTCTC  CGG
                                  GA   CC    AC
GAM142  CST8     5'  GGCCACCCCATCCTGCCCACAG 19714        A  A  GCA____
             CT                   AGCTGTGGG CA GA     GCC
                                |||||||||  || ||      |||
                                TCGACACCC GT CT     CGG
                                     _  C  ACCCCAC
GAM142  FLJ23392 3'  GGCTGCTCTTACCATCCTTAG  45896     CT   GAC
                                TTAAG  GTGG   AAGAGCAGCC
                                |||||  ||||   ||||||||||
                                GATTC  TACC   TTCTCGTCGG
                                   C_    A__
GAM142  FUT10    5'  GCTGCTCTGATGATAGCCTAA  51991    A    GGGACA
                                TTA GCTGT     AGAGCAGC
                                |||  |||||     ||||||||
                                AAT CGATA     TCTCGTCG
                                  C    GTAG__
GAM142  KIAA0379 3'  GCTGCCCCCCAGCTTAA     68716       T   ACAAGA   _
                                TTAAGCTG GGG     GCAG C
                                |||||||| |||     |||| |
                                AATTCGAC CCC     CGTC G
                                     C   _______   T
GAM142  KIAA0449 5'  GGCGCTCACCCCACAGC     34638       ACAA   A
                                GCTGTGGG    GAGC GCC
                                ||||||||    |||| |||
                                CGACACCC    CTCG CGG
                                     CA__    _
GAM142  KIAA0514 5'  GCTGTTATCCCACAGC      28750        CAAG
                                GCTGTGGGA   AGCAGC
                                |||||||||   ||||||
                                CGACACCCT   TTGTCG
                                     A___
GAM142  KIAA0514 3'  GGCTGCCCCTGCCCTGGCT   28752      T  A  AGA
                                AGCTG GGG CA   GCAGCC
                                |||||  ||| ||   ||||||
                                TCGGT CCC GT   CGTCGG
                                  _   _  CCC
GAM142  KIAA0676 3'  GGCTGCTCTTGCTTCTAC    31146      _
                                GTGGGA CAAGAGCAGCC
                                ||||||  ||||||||||
                                CATCTT GTTCTCGTCGG
                                   C
GAM142  KIAA1754 3'  GCTACCCCCAATCCCTCACAGC 63930    A    __   CAAG____
             CTGA                   TTA GCTGT  GGGA      AGC
                                |||  |||||  ||||       |||
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                                AGT CGACA  CCCT       TCG
                                  C    CT   AACCCCCA
GAM142  TUBB4    3'  GCTGCTCCTGTCTCTGTCTTA  71150      CTGT     A
                                TAAG   GGGACA GAGCAGC
                                ||||   ||||||| |||||||
                                ATTC   CTCTGT CTCGTCG
                                  TGT_     C
GAM142  LOC120114 3'  GGCTGCTCTTGAGGAAAGCT   76047      GTGGGA
                                AGCT     CAAGAGCAGCC
                                ||||     ||||||||||
                                TCGA     GTTCTCGTCGG
                                  AAGGA_
GAM142  LOC159199 5'  GGCTGCTCCTGTCGGAGGCTTA 83065       GTGG   A
                                TAAGCT   GACA GAGCAGCC
                                ||||||   |||| ||||||||
                                ATTCGG   CTGT CTCGTCGG
                                   AGG_   C
GAM142  LOC164295 3'  GCTGCTCTCTGGCAGT      83395      G   CAA
                                GCTGT GGA   GAGCAGC
                                ||||| |||   |||||||
                                TGACG TCT   CTCGTCG
                                  G   ___
GAM143  GGA1     3'  ACCCTTTGTTGCCCATGGCC   26276     _   A    C  TGAA
                                GGC ATGG CAACA AG    GGT
                                ||| |||| ||||| ||    |||
                                CCG TACC GTTGT TC    CCA
                                  G   C    T ____
GAM143  HNF4A    3'  ACCTTCACCTTCATCCATGTC  6606         CAACACA
                                GGCATGGA      GTGAAGGT
                                ||||||||      ||||||||
                                CTGTACCT      CACTTCCA
                                    ACTTC__
GAM143  ITPR3    3'  ACCTCACTGTCGTGTCCATGCC 11084          AC      A
                                GGCATGGACA  ACAGTGA GGT
                                ||||||||||  ||||||| |||
                                CCGTACCTGT  TGTCACT CCA
                                     GC      _
GAM143  MLLT2    3'  TCATGTTGTCCAGCC      21033     A       CAG
                                GGC TGGACAACA   TGA
                                ||| |||||||||   |||
                                CCG ACCTGTTGT   ACT
                                  _       ___
GAM143  TEM5     3'  ACCCCGCCTACTGTCCATGC   52293         ACACA   AA
                                GCATGGACA    GTG  GGT
                                |||||||||    |||  |||
                                CGTACCTGT    CGC  CCA
                                     CATC_   C_
GAM143  UNC13    3'  ACCTCTACCCATCTCCATGCC  22097         CAACACA   A
                                GGCATGGA      GTG AGGT
                                ||||||||      ||| ||||
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                                CCGTACCT      CAT TCCA
                                    CTACC__   C
GAM143  FLJ20958  3'  ACTATGTTGCCCATGCTG    42307        A    C
                                CGGCATGG CAACA AGT
                                |||||||| ||||| |||
                                GTCGTACC GTTGT TCA
                                    C    A
GAM143  FLJ31978  3'  ACCTCCACCGTACCTCCACATC 59006    CA   CAAC  A   A
                                GG  TGGA   AC GTG AGGT
                                ||  ||||   || ||| ||||
                                CT  ACCT   TG CAC TCCA
                                 AC   CCA_ C   C
GAM143  KIAA0534  3'  ACATTCCTGTCATCCATGCC   71928        CAAC   T   G
                                GGCATGGA   ACAG GAA GT
                                ||||||||   |||| ||| ||
                                CCGTACCT   TGTC CTT CA
                                    AC__   _   A
GAM143  KIAA1981  3'  ACCTCCCGCCAGCATTCCCATG 89707        ACAACACA  A_
            CCG                   CGGCATGG      GTG  AGGT
                                ||||||||       |||  ||||
                                GCCGTACC      CGC  TCCA
                                    CTTACGAC   CC
GAM143  MGC10818  3'  ACCTTCACTGCATTGAGGTGC  48296     GGA   CA
                                GCAT   CAA  CAGTGAAGGT
                                ||||   |||  ||||||||||
                                CGTG   GTT  GTCACTTCCA
                                  GA_   AC
GAM143  MGC3035   3'  ACCTTCACTGCATCCTTGCC   44393     T   CAACA
                                GGCA GGA    CAGTGAAGGT
                                |||| |||    ||||||||||
                                CCGT CCT    GTCACTTCCA
                                  T   AC___
GAM143  SFXN5     3'  ACCTTCACCCAGCACCCATGCC 58643       ACAACACA
                                GGCATGG       GTGAAGGT
                                |||||||       ||||||||
                                CCGTACC       CACTTCCA
                                    CACGACC_
GAM143  LOC124944 3'  CCTCTCACTGTTCATGCCG    74835        ACAAC      _
                                CGGCATGG    ACAGTGA AGG
                                ||||||||    ||||||| |||
                                GCCGTACT    TGTCACT TCC
                                    _____       C
GAM143  LOC145608 3'  CTTTTTTCTACATTGTCCATAC 84383    C       CAC  T_
            C                    GG ATGGACAA   AG  GAAGG
                                || ||||||||   ||  |||||
                                CC TACCTGTT   TC  TTTTC
                                 A       ACA  TT
GAM143  LOC146783 5'  CTTCCTGTGTTGCCCACGCTG  84823     A   A       T
                                CGGC TGG CAACACAG GAAG
                                |||| ||| |||||||| ||||
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                                GTCG ACC GTTGTGTC CTTC
                                  C  C      _
GAM143  LOC154559 3'  ACCCCCACTGTGTTGAGTGGC  81999    ATGGA        AA
                                GC    CAACACAGTG  GGT
                                ||    ||||||||||  |||
                                CG    GTTGTGTCAC  CCA
                                 GTGA_        CC
GAM143  LOC196047 5'  ACCCTCACTGTGTCCTGGATTC 91137    ____  T   AAC      A
          C                      GG   CA GGAC   ACAGTGA GGT
                                ||   || ||||   ||||||| |||
                                CC   GT CCTG   TGTCACT CCA
                                 TTAG  _   ___      C
GAM143  LOC203276 3'  CCTTAGTTCTCCATGCC     92121        C   ACAGTG
                                GGCATGGA AAC     AAGG
                                ||||||||  |||     ||||
                                CCGTACCT TTG     TTCC
                                    C   A_____
GAM143  LOC203305 3'  CCTTAGTTCTCCATGCC     92174        C   ACAGTG
                                GGCATGGA AAC     AAGG
                                ||||||||  |||     ||||
                                CCGTACCT TTG     TTCC
                                    C   A_____
GAM143  LOC254219 3'  ACCTCCCTGGGGCTGTCCATGC 98317         ACA_   T  A
          C                      GGCATGGACA    CAG GA GGT
                                ||||||||||    ||| || |||
                                CCGTACCTGT    GTC CT CCA
                                     CGGG   C  _
GAM143  LOC254243 3'  CCTTAGTTCTCCATGCC     99260        C   ACAGTG
                                GGCATGGA AAC     AAGG
                                ||||||||  |||     ||||
                                CCGTACCT TTG     TTCC
                                    C   A_____
GAM143  LOC51267  3'  ACCCCATCTGCCTTGTCCATGC 33673          CA   TGAA
          CG                     CGGCATGGACAA  CAG    GGT
                                ||||||||||||  |||    |||
                                GCCGTACCTGTT  GTC    CCA
                                      CC   TACC
GAM143  LOC90038  3'  CCTTAGTTCTCCATGCC     61803        C   ACAGTG
                                GGCATGGA AAC     AAGG
                                ||||||||  |||     ||||
                                CCGTACCT TTG     TTCC
                                    C   A_____
GAM143  LOC90625  5'  CAGTGTGTTGCTCCACACCG   64378     CA   _      G
                                CGG  TGGA CAACACA TG
                                |||  |||| ||||||| ||
                                GCC  ACCT GTTGTGT AC
                                  AC   C      G
GAM143  LOC93082  3'  CTTTCTGTCCATGCC       57255          ACACAGT
                                GGCATGGACA      GAAGG
                                ||||||||||      |||||
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                                CCGTACCTGT      CTTTC
                                          ________
GAM144  CANX     3'  CAGTTGAACACTAGTCTGTG   88866         TA_   CTTC
                                CACAGACTA   TTCG    ACTG
                                |||||||||   ||||    ||||
                                GTGTCTGAT   AAGT    TGAC
                                     CAC    ____
GAM144  CARPX    3'  TCAGTGAAATGCTACAACTGTG 39816       ACTATATT  C
                                CACAG       CG TTCACTGA
                                |||||       || ||||||||
                                GTGTC       GT AAGTGACT
                                   AACATC__  A
GAM144  DUT      3'  TCAGTGAAGTAGCAATAGGCTG 10462      A    ATTC
              T                  ACAG CTAT    GCTTCACTGA
                                |||| ||||    ||||||||||
                                TGTC GATA    TGAAGTGACT
                                  G    ACGA
GAM144  PGAM1    3'  CAGTGGAAGACGAATGTAACCT 76784      AC       _   _
              G                  CAG  TATATTCG CTTC ACTG
                                |||  |||||||| |||| ||||
                                GTC  ATGTAAGC GAAG TGAC
                                  CA       A    G
GAM144  SWAP70   3'  CAATGAAGAAATGGTCTGT    71861         ATTCG    C
                                ACAGACTAT    CTTCA TG
                                |||||||||    ||||| ||
                                TGTCTGGTA    GAAGT AC
                                     AA___     A
GAM144  SYBL1    3'  TCAATGAATGAACAAATTAGTC 20111         TA___    C    C
              TGT                  ACAGACTA    TTCG TTCA TGA
                                |||||||||    |||| |||| |||
                                TGTCTGAT    AAGT AAGT ACT
                                     TAAAC    _    A
GAM144  XBP1     3'  TCAGTGAAGGAAGAACCTGT   18677      ACTATA   G
                                ACAG     TTC CTTCACTGA
                                ||||     ||| |||||||||
                                TGTC     AAG GAAGTGACT
                                  CAAG__   _
GAM144  ARNTL2   3'  TCAGTGAAATGGCTTATAATC  39857    C    T_   C
                                GA TATA  TCG TTCACTGA
                                || ||||  ||| ||||||||
                                CT ATAT  GGT AAGTGACT
                                 A    TC   A
GAM144  BCL2L1   3'  CAGCTCTTTGAAATAGTCTGTG 57585          A    CTTCA
                                CACAGACTAT TTCG     CTG
                                |||||||||| ||||     |||
                                GTGTCTGATA AAGT     GAC
                                      _    TTCTC
GAM144  FLJ12505 3'  TCAGTGAAGTCTGGTAGTC    45718       ATTC
                                GACTAT    GCTTCACTGA
                                ||||||    ||||||||||
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                                CTGATG   TGAAGTGACT
                                   GTC_
GAM144  GT650    3' CAGTGAAGTTTAATCTAG    54548    T  C_
                                CTA ATT  GCTTCACTG
                                ||| |||  |||||||||
                                GAT TAA  TGAAGTGAC
                                  C   TT
GAM144  KIAA0237 3' CAGTGAAGCACGAGGTCTTG  29215   C    ATATTC
                                A AGACT     GCTTCACTG
                                | |||||     |||||||||
                                G TCTGG     CGAAGTGAC
                                 T    AGCA__
GAM144  KRTAP4-7 3' TCAGTGAGGTAGATATTATCTG 53518     CT    CG
                                CAGA  ATATT  CTTCACTGA
                                ||||  |||||  |||||||||
                                GTCT  TATAG  GGAGTGACT
                                   AT    AT
GAM144  SHARP    3' CAGTGAAGACAGGCTGTG    31100      A  ATATTCG
                                CACAG CT      CTTCACTG
                                ||||| ||      ||||||||
                                GTGTC GG      GAAGTGAC
                                   _ ACA____
GAM144  LOC144483 3' CAGTGGAAGACGAATGTAACCT 60812     AC       _   _
           G                     CAG  TATATTCG CTTC ACTG
                                ||| |||||||| |||| ||||
                                GTC  ATGTAAGC GAAG TGAC
                                  CA       A   G
GAM144  LOC150372 5' CAGATGGAGAACCAGCCTGTG  80606      A  ATATTCG    _
                                CACAG CT      CTTCA CTG
                                ||||| ||      ||||| |||
                                GTGTC GA      GAGGT GAC
                                   C  CCAA___    A
GAM144  LOC151201 3' CAGATCAAATATAGTCTGT    86468          CGCTTCA
                                ACAGACTATATT      CTG
                                ||||||||||||      |||
                                TGTCTGATATAA      GAC
                                       ACTA___
GAM144  LOC200942 5' CAGTGAGGCCTACAGTCTG    90376      A  TTC
                                CAGACT TA   GCTTCACTG
                                |||||| ||   |||||||||
                                GTCTGA AT   CGGAGTGAC
                                   C  C__
GAM145  ABCC11   5' AAGGGTGCGGTGTTGGGG    53681          TGTT
                                TCTCAATGCCGTG   CTCTT
                                ||||||||||||   |||||
                                GGGGTTGTGGCGT   GGGAA
                                                ____
GAM145  ABCC11   5' CAGGATCAAGGGTGCGGTGTTG 53682          TG G  C__   TG
           GGG                    TCTCAATGCCG  T TT   TCTT
                                ||||||||||  | ||   ||||
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                                GGGGTTGTGGC  G GA   AGGA
                                      GT G  ACT    C
GAM145  ABCC11   5'  GGGGAGGGTGGTTAGAGA    53685      AAT    TG G
                                TCTC   GCCG  T TTCTCT
                                ||||   ||||  | ||||||
                                AGAG   TGGT  G GAGGGG
                                  AT_   __ G
GAM145  ACK1     5'  GGGGGAGCGGCAGTGGGA    20516      A     GTG
                                TCTCA TGCCGT   TTCTCT
                                ||||| ||||||   ||||||
                                AGGGT ACGGCG   AGGGGG
                                  G     ____
GAM145  ACK1     5'  TGAAGGGGACGCAGGATGTAGG 20518      A  _  G
             GG                   TCTC ATG CC TGTGTTCTCTTTG
                                ||||| ||| || ||||||||||||
                                GGGG TGT GG ACGCAGGGGAAGT
                                  A  A  _
GAM145  ACTR1B   3'  CAAGGAGGGCGGGGCATGTTGG 71379      __     G   GT
             GA                   TCTCA  ATGCC TGT  TCTCTTTG
                                |||||  ||||| |||  ||||||||
                                AGGGT  TACGG GCG  GGAGGAAC
                                  TG    G  __
GAM145  ADAMTS13 3'  GGAGGACGATGGTGAGG     58155      AAT    G
                                TCTC   GCCGT TGTTCTCT
                                ||||   ||||| ||||||||
                                GGAG   TGGTA GCAGGAGG
                                  ___    _
GAM145  ADAMTS4   3'  TGGGAGGGGCTGTGGGCGTGAG 18777      A   GTGT   _  TT
             A                    TCTCA TGCC    GTTC TCT  G
                                ||||| ||||    |||| |||  |
                                AGAGT GCGG    CGGG AGG  T
                                  _   GTGT    G   GG
GAM145  ADAMTS8   3'  CTCCTGGACATGCGGTACTGAG 23852      A         TCTTTG
             G                    TCTCA TGCCGTGTGTTC
                                ||||| ||||||||||||
                                GGAGT ATGGCGTACAGG
                                  C          TCCTCG
GAM145  AKAP13   3'  AAAGAGGGTGGCTGTGAGG   91252      AT   GTGT TT
                                TCTCA  GCC    G  CTCTTT
                                |||||  |||    |  ||||||
                                GGAGT  CGG    T  GAGAAA
                                  GT   ____ GG
GAM145  AKT1     3'  GCGCAATGTGGCATTGGGG   18962          ___
                                TCTCAATGCCG   TGTGT
                                ||||||||||   |||||
                                GGGGTTACGGT   ACGCG
                                      GTA
GAM145  ALDH3B1  3'  TAGAGAATTAACCATTGA    93160       CC  GT     TT
                                TCAATG  GT  GTTCTCT  G
                                ||||||  ||  |||||||  |
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                                AGTTAC  CA  TAAGAGA  T
                                   __ AT      G
GAM145  ALK     5'  CGGGGAGAGCGAAGGGTGAGG  73771      ATG  GTG
                                TCTCA   CC   TGTTCTCTTTG
                                |||||   ||   ||||||||||
                                GGAGT   GG   GCGAGAGGGGC
                                   G__  AA_
GAM145  ANK1    5'  CAGAGAGAGTAAACAGTGAGA  40404      ATGCC  G
                                TCTCA    GT TGTTCTCTTTG
                                |||||    || ||||||||||
                                AGAGT    CA ATGAGAGAGAC
                                   GA___  A
GAM145  AP1S1   3'  TAAAGGGAAAAGGTGTTCAGG  55106    C     GTGTG
                                TCT AATGCC    TTCTCTTTG
                                ||| ||||||    |||||||||
                                GGA TTGTGG    AAGGGAAAT
                                  C     AA___
GAM145  ARF3    3'  GGGACCCAGGGCATTGGGG   9777         G  T
                                TCTCAATGCC TG GTTCT
                                |||||||||| || |||||
                                GGGGTTACGG AC CAGGG
                                      G  C
GAM145  ARG2    3'  AGAATTATGAGGCATTGAGG   8606         GTGT_
                                TCTCAATGCC    GTTCT
                                |||||||||    |||||
                                GGAGTTACGG    TAAGA
                                      AGTAT
GAM145  ASK     5'  CGGGGCACGGCGCGTGGCGTGA 22974      A        ___   TTG
           GA                     TCTCA TGCCGTGTGTT   CTCT
                                |||||| ||||||||||   ||||
                                AGAGT GCGGTGCGCGG   GGGG
                                   _        CAC   C
GAM145  ATF7    3'  TGGGGGAATTGTGTGTTGTGA  23405    T    _ TGT     TT
                                TC CAATGC CG   GTTCTCT  G
                                || |||||| ||   ||||||| |
                                AG GTTGTG GT   TAAGGGG  T
                                 T     T ___      GG
GAM145  ATP10C  3'  CAGAGAGGGCATAGGATCTGAG 44665      ATG  G
           G                     TCTCA   CC TGTGTTCTCTTTG
                                |||||   || ||||||||||||
                                GGAGT   GG ATACGGGAGAGAC
                                   CTA  _
GAM145  ATSV    3'  AGTCTGCGCGGCATGGAGG   16306     A       TT
                                TCTC ATGCCGTGTG  CT
                                |||| ||||||||||  ||
                                GGAG TACGGCGCGT  GA
                                  G        CT
GAM145  BAX     3'  GGGGAAGAGTGGTCTTGAGG   16317       T    GTG
                                TCTCAA GCCGT   TTCTCT
                                |||||| |||||   ||||||
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                                GGAGTT TGGTG   AAGGGG
                                   C    AG_
GAM145  BAX     3'  GGGGAAGAGTGGTCTTGAGG   16318       T    GTG
                                TCTCAA GCCGT   TTCTCT
                                |||||| |||||   ||||||
                                GGAGTT TGGTG   AAGGGG
                                   C    AG_
GAM145  BAZ2A   3'  GAGGGGGAGACGGCGTTGGGA  26510          GTG     TG
                                TCTCAATGCCGT   TTCTCTT
                                ||||||||||||   |||||||
                                AGGGTTGCGGCA   GGGGGAG
                                      GA_      T
GAM145  BCL7A   3'  GCAGGGCCCAAGGACGCGCAGG 40985         _       _____
           TGTTGGGG                 TCTCAATGCC GTGTGTTCT    CTTTG   C
                                |||||||||| |||||||||    |||||   |
                                GGGGTTGTGG CGCGCAGGA    GGGAC   G
                                      A        ACCC
GAM145  BLAME   3'  TAGAGAAAGGGTACTGAGG   39657      A   GTGTG     TT
                                TCTCA TGCC     TTCTCT  G
                                ||||| ||||    ||||||  |
                                GGAGT ATGG     AAGAGA  T
                                   C   GA___     G
GAM145  BMPR1B  5'  GGAGACCGCGGCGCTGAGG   8664       A      T  T
                                TCTCA TGCCGTG GT CTCT
                                ||||| ||||||| || ||||
                                GGAGT GCGGCGC CA GAGG
                                   C      _ _
GAM145  C11orf8 3'  AAAGAAAGCTGCATTGAGA   9622          C  GTGTTC
                                TCTCAATGC GT     TCTTT
                                |||||||| ||     |||||
                                AGAGTTACG CG     AGAAA
                                      T  AA____
GAM145  C21orf33 3'  GTAAGGAGGATGTGCTGCAGTG 17383      A____   C TG
           CATGGGG                  TCTCA    TGC G  TGTTCTCTTTG   T
                                |||||    ||| |  ||||||||||   |
                                GGGGT    ACG C  GTAGGAGGAAT   G
                                   ACGTG   T GT
GAM145  CALR    3'  GGGGGGCAGTGGTGTGGAGA   63657     A    GTG
                                TCTC ATGCC   TGTTCTCT
                                |||| |||||   ||||||||
                                AGAG TGTGG   ACGGGGGG
                                   G    TG_
GAM145  CALU    3'  CAGAGAGGGCTCTTTGGTTTGA 8694       T   TGT_
           GG                    TCTCAA GCCG    GTTCTCTTTG
                                ||||||| ||||    ||||||||||
                                GGAGTT TGGT    CGGGAGAGAC
                                   _   TTCT
GAM145  CAV3    3'  GATGGAGCACACGGTGTAGGGA 54027      A          CTTTG
                                TCTC ATGCCGTGTGTTCT
                                |||| ||||||||||||||
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                                AGGG TGTGGCACACGAGG
                                  A           TAGT
GAM145  CCBL1    3'  GGGGAAGATGCTATTGGGA   15770        CC   G
                                TCTCAATG  GTGT TTCTCT
                                ||||||||  |||| ||||||
                                AGGGTTAT  CGTA AAGGGG
                                    __    G
GAM145  CCKBR    3'  TAGAGGGGCCGTGGGGGTTGAG 7417        G  G GT TT
              G                  TCTCAAT CC T  G  CTCTTTG
                                 ||||||| || |  |  |||||||
                                 GGAGTTG GG G  C  GGGAGAT
                                     G  _ TG CG
GAM145  CCNG1    5'  CGGGGAGGGTGGTTACCGCTGA 15773      AT  C   __  TT
              GG                   TCTCA  GC GTG  TG  CTCTTTG
                                   |||||  || |||  ||  |||||||
                                   GGAGT  CG CAT  GT  GAGGGGC
                                     __  C   TG  GG
GAM145  CD164    3'  TAAAGCATCTTATGTCATTGAG 21198        C   ___    CTCTTTG
              A                    TCTCAATG CGT   GTGTT
                                   ||||||||| |||   |||||
                                   AGAGTTAC GTA   TACGA
                                       T   TTC    AAT
GAM145  CD83     3'  CAGAGAGGGTGACAAGATAGAG 16170     A  GCCG   _ TT
              A                    TCTC AT    TGT G  CTCTTTG
                                   |||| ||    ||| |  |||||||
                                   AGAG TA    ACA T  GAGAGAC
                                     A  GA__   G GG
GAM145  CD97     3'  TGAAGAGACTAGGCGCTGGGG  55307      A   GTGT  T
                                TCTCA TGCC    GT CTCTTTG
                                ||||| ||||    || |||||||
                                GGGGT GCGG    CA GAGAAGT
                                   C    AT__  _
GAM145  CDK5R2   3'  AGAGGCCGCGGTGTTTGGA    15443     C       T  T
                                TCT AATGCCGTG GT CTCT
                                ||| |||||||| || ||||
                                AGG TTGTGGCGC CG GAGA
                                  T       _ _
GAM145  CENTD2   5'  CAGGGGGAGGGGAGTGTGAGG  31538      ATG_  GTGTG
                                TCTCA   CC    TTCTCTTTG
                                |||||   ||    |||||||||
                                GGAGT   GG    GAGGGGGAC
                                   GTGA  G____
GAM145  CHRNA2   3'  CAGGGAGAACAGCCAGGTGAGG 7428      AAT   GTG_
                                TCTC   GCC   TGTTCTCTTTG
                                ||||   |||   ||||||||||
                                GGAG   TGG   ACAAGAGGGAC
                                   ___   ACCG
GAM145  CLCA1    5'  TAAGGGGAGCATGAAGAGGTGT 8899          GT___
              TGAGG                TCTCAATGCC    GTGTTCTCTTTG
                                   ||||||||||    ||||||||||||
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                                GGAGTTGTGG    TACGAGGGGAAT
                                      AGAAG
GAM145  CLCN3    5'  CAAGGAGGGTGTGGTGGGTTGA 10203      __   TG GT
                                TCAAT  GCCG  T  TCTCTTTG
                                |||||  ||||  |  ||||||||
                                AGTTG  TGGT  G  GGAGGAAC
                                   GG   GT __
GAM145  CMAR     3'  TAGTCACGCATGCAGTGTTGGG 19037        __     TCTCTTTG
             G                   TCTCAATGC  CGTGTGT
                                |||||||||  |||||||
                                GGGGTTGTG  GTACGCA
                                      AC      CTGAT
GAM145  CNGA3    3'  CAGGGAGAGCATTTTAGATTGA 8940       GCCGT
                                TCAAT    GTGTTCTCTTTG
                                |||||    ||||||||||||
                                AGTTA    TACGAGAGGGAC
                                   GATTT
GAM145  COX6C    5'  AGGAAGGACGTTGGTGTTGAGG 16484         TGT    _   TG
                                TCTCAATGCCG   GTTCT CTT
                                ||||||||||   ||||| |||
                                GGAGTTGTGGT   CAGGA GGA
                                      TG_    A   C
GAM145  CRH      3'  TAAAGAGAATGTAGACCTGTGA 7483       ATGCCG  TG
             GA                   TCTCA     TG  TTCTCTTTG
                                |||||     ||  ||||||||
                                AGAGT     AT  AAGAGAAAT
                                   GTCCAG  GT
GAM145  CRIM1    3'  GGGAGGGTGGTGTTGGGA    33604         GTGT TT
                                TCTCAATGCC    G  CTCTT
                                ||||||||||    |  |||||
                                AGGGTTGTGG    T  GAGGG
                                      _____ GG
GAM145  CTSB     3'  GAGGAGAGACGGTGTTGGGA   65364          GTG
                                TCTCAATGCCGT   TTCTCTTT
                                ||||||||||||   ||||||||
                                AGGGTTGTGGCA   GAGAGGAG
                                      ___
GAM145  CYBB     3'  GGAGCTCTATGGTTTTGAGA   76850       T     T_
                                TCTCAA GCCGTG  GTTCT
                                ||||||  ||||||  |||||
                                AGAGTT TGGTAT  CGAGG
                                   T     CT
GAM145  DBN1     3'  GGGGAGCTCTGGTGGGA     16559      AAT    TGT
                                TCTC   GCCG   GTTCTCT
                                ||||   ||||   |||||||
                                AGGG   TGGT   CGAGGGG
                                   ___    CT_
GAM145  DDB1     5'  TGGAGTTCGCTGCGCGCTGTTG 10401        _  _   _   TT    TTG
             GGG                   TCTCAAT GC CGT GTG  CTCT
                                |||||||  ||  |||  |||  ||||
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                                GGGGTTG CG GCG CGC  GAGG
                                    T C   T   TT    T
GAM145  DDX3     5'  AGGGAATTGCGGTGTGAGA   9053       A      T
                                TCTCA TGCCGTG GTTCTCT
                                ||||| ||||||| |||||||
                                AGAGT GTGGCGT TAAGGGA
                                  _      _
GAM145  DDX38    3'  CAGAGAGGATGGCAGCAGGTAT 26597         G  ____
           TGGG                   CTCAATGCC TGT    GTTCTCTTTG
                                |||||||||| |||    ||||||||||
                                GGGTTATGG ACG    TAGGAGAGAC
                                    _  ACGG
GAM145  DIAPH2   5'  AGAATCACGTGTGTTGAGG   23001         _   T
                                TCTCAATGC CGTG GTTCT
                                ||||||||| |||| |||||
                                GGAGTTGTG GCAC TAAGA
                                     T   _
GAM145  DNM2     3'  CGAGGGGGGCGTGCTCTCGGGG 18234      AATGCC TG
           GG                     TCTC     G  TGTTCTCTTTG
                                ||||     |  ||||||||||||
                                GGGG     C  GCGGGGGGAGC
                                  GGCTCT GT
GAM145  DNMT3B   3'  TAGGGAGAACGGGAATTCAGA  23550     C   G  GTG
                                TCT AAT CC   TGTTCTCTTTG
                                ||| ||| ||   ||||||||||
                                AGA TTA GG   GCAAGAGGGAT
                                  C   A  ___
GAM145  DPYSL3   3'  CAGAGGGAGCACATTTTGTGG  9122      ATGCC
                                TCA     GTGTGTTCTCTTTG
                                |||     ||||||||||||||
                                GGT     TACACGAGGGAGAC
                                  GTTT_
GAM145  DRP2     3'  CAGGGATCTGGTGGTATGTGAG 10424       _     TGTGT     TTG
           G                     TCTCA ATGCCG     TCTCT
                                ||||| ||||||     |||||
                                GGAGT TATGGT     AGGGA
                                   G     GGTCT     C
GAM145  DSCR1    3'  GAAAAGTATGGCAGTGGGA   16622       A      TG_
                                TCTCA TGCCGTG   TTC
                                ||||| |||||||   |||
                                AGGGT ACGGTAT   AAG
                                   G      GAA
GAM145  DVL1     3'  AGGGAGGGAGGTCTTGGGG   60057       T   GTGTGT
                                TCTCAA GCC      TCTCTTT
                                |||||| |||     |||||||
                                GGGGTT TGG      GGAGGGA
                                   C   AG____
GAM145  EFNA3    3'  AAGGGGTGGGCATTGGGG    18249          GTGTGTT
                                TCTCAATGCC      CTCTTT
                                ||||||||||      ||||||
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                                GGGGTTACGG      GGGGAA
                                      GT_____
GAM145  EGFL4    3'  AGAGGATGTGGCAGTGAGG   62450      A    TG G
                                TCTCA TGCCG  T TTCT
                                ||||| |||||  | ||||
                                GGAGT ACGGT  A GAGA
                                   G    GT G
GAM145  EIF4G1   3'  TGAAGAGGCAGGATGGCTTGGG 18257      T    G_  T
           G                     TCTCAA GCCGT  TGT CTCTTTG
                                ||||||| |||||  ||| |||||||
                                GGGGTT CGGTA  ACG GAGAAGT
                                   _    GG  _
GAM145  ENG      3'  AGAACAGTGGGCGTTGGGA   5490          GTG
                                TCTCAATGCC   TGTTCT
                                ||||||||||   ||||||
                                AGGGTTGCGG   ACAAGA
                                      GTG
GAM145  EYA2     3'  GGGGGGTGCCTGGTGATGAGG  19126      A    T TG
                                TCTCA TGCCG G  TTCTCT
                                ||||| ||||| |  ||||||
                                GGAGT GTGGT C  GGGGGG
                                   A    C GT
GAM145  FANCC    3'  CGAGGGGGCCTTGACGGCGTTG 71038         GT__      TG
           G                     TCAATGCCGT   GTTCTCTT
                                ||||||||||   ||||||||
                                GGTTGCGGCA   CGGGGGAG
                                      GTTC       C
GAM145  FKBP10   3'  CGAGGGGGACAGTGGCGGTGGG 41934      A   GTG
           A                     TCTCA TGCC   TGTTCTCTTTG
                                ||||| ||||   ||||||||||
                                AGGGT GCGG   ACAGGGGGAGC
                                   G   TG_
GAM145  FVT1     3'  TAGAGAGGTGAAGGTATGAGA  10736      A   GTGTGT
                                TCTCA TGCC     TCTCTTTG
                                ||||| ||||     ||||||||
                                AGAGT ATGG     GGAGAGAT
                                   _   AAGT__
GAM145  G22P1    5'  TGGGGAGGTTTTTGGGCGGTAT 9409          G GT___    TT
           TGAGG                   TCTCAATGCCGT T    TCTCT  G
                                ||||||||||| |    |||||  |
                                GGAGTTATGGCG G    GGAGG  T
                                      G TTTTT    GG
GAM145  GAS1     3'  TAAGGGGTTGCCATGGTGTTGA 10762         T  T_
                                TCAATGCCGTG GT  CTCTTTG
                                |||||||||| ||  |||||||
                                AGTTGTGGTAC CG  GGGGAAT
                                      _ TT
GAM145  GAS7     3'  CAAGGAGAATTTCTGCGGTGGG 20842     AAT    GT__
           A                     TCTC   GCCGT   GTTCTCTTTG
                                ||||   |||||   ||||||||||
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                                AGGG  TGGCG   TAAGAGGAAC
                                  ___   TCTT
GAM145  GAS7    3'  TGGAGATTGCGTGTGGTGTTCA 20864    C     TG  __    TTG
            GG                   TCT AATGCCG  TGT  TCTCT
                                ||| |||||||  |||  |||||
                                GGA TTGTGGT  GCG  AGAGG
                                  C     GT   TT    T
GAM145  GFAP    3'  TGAGAGGGATGAGGTGCTGGGA 10785     AT   GTGTG    TT
                                TCTCA  GCC    TTCTCT  G
                                |||||  |||    ||||||  |
                                AGGGT  TGG    GGGAGA  T
                                   CG   AGTA_     GG
GAM145  GFAP    3'  TGAGGGGACGCTGGTAGAGA   10786     AA    T       TT
                                TCTC  TGCCG GTGTTCTCT  G
                                ||||  ||||| |||||||||  |
                                AGAG  ATGGT CGCAGGGGA  T
                                  __    _       GG
GAM145  GGA1    3'  TGGGGAGGAAGCACAGCTGTTG 26279       _ C   G     TT
            GGG                   TCTCAAT GC GTGT TTCTCT  G
                                ||||||| || |||| ||||||  |
                                GGGGTTG CG CACG AGGAGG  T
                                    T  A    A     GG
GAM145  GLI3    5'  CGAAGAGAGCTGAAGTAATGAG 5718       A   CGTGT
            A                    TCTCA TGC    GTTCTCTTTG
                                ||||| |||    ||||||||||
                                AGAGT ATG    CGAGAGAAGC
                                   A   AAGT_
GAM145  GLP1R   3'  GGCTGTAGGTGGTGTTGAGA   10798          TG   TC
                                TCTCAATGCCG  TGT  TC
                                ||||||||||  |||  ||
                                AGAGTTGTGGT  ATG  GG
                                      GG   TC
GAM145  GM2A    3'  GGAGAGGTAGGGTGTGTGGGG  68384      _    G  TGT
                                TCTCA ATGCC TG   TCTCT
                                ||||| ||||| ||   |||||
                                GGGGT TGTGG AT   AGAGG
                                   G    G  GG_
GAM145  GNAI3   3'  TGAAGAGAATGCATTTTGAG   22445      TGCC
                                CTCAA   GTGTGTTCTCTTTG
                                |||||   ||||||||||||||
                                GAGTT   TACGTAAGAGAAGT
                                   T___
GAM145  GOT1    3'  TGAAGAGAACATCCCTTGAGA  10855       TGCCGT
                                TCTCAA     GTGTTCTCTTTG
                                ||||||     ||||||||||||
                                AGAGTT     TACAAGAGAAGT
                                   CCC___
GAM145  GPC1    3'  GGAGGGGTGGTGTGGTGTTGGG 10861          TG GT     G
            A                    TCTCAATGCCG  T  TCTCTTT
                                ||||||||||  |  |||||||
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                                AGGGTTGTGGT  G  GGGGAGG
                                      GT GT      G
GAM145  GPR48    5'  AGAGCCGCTGCATTGAGA    38091         C   T
                                TCTCAATGC GTG GTTCT
                                ||||||||| ||| |||||
                                AGAGTTACG CGC CGAGA
                                     T  _
GAM145  GPR81    3'  TGGAGTGGAGCATGTGTGTGTT 51759         _ TG     _ TT
           GGGA                    TCTCAATGC CG  TGTTCT CT  G
                                ||||||||| ||  |||||| ||  |
                                AGGGTTGTG GT  ACGAGG GA  T
                                     T  GT     T  GG
GAM145  GPRC5B   3'  TGGAGATGACCGTTGCGTTGAG 33179         __ T  GT    TTG
           G                     TCTCAATGC  CG GT  TCTCT
                                |||||||||  || ||  |||||
                                GGAGTTGCG  GC CA  AGAGG
                                     TT  _  GT    T
GAM145  HKE4     5'  TAAAGAGAACTAGTCTTGGGA  23714       T  CGTGT
                                TCTCAA GC    GTTCTCTTTG
                                |||||| ||    ||||||||||
                                AGGGTT TG    CAAGAGAAAT
                                   C  AT___
GAM145  HMGB3    3'  AAGGGGGGTCAGCTGGCATGAG 19270       A    TG _      G
           A                     TCTCA TGCCG  TG TTCTCTTT
                                ||||| |||||  || ||||||||
                                AGAGT ACGGT  AC GGGGGGAA
                                   _    CG  T       A
GAM145  HNF3B    3'  GGGGAGACGGTGTTGCAGA   41713     _       GTG
                                TCT CAATGCCGT   TTCTCT
                                ||| |||||||||   ||||||
                                AGA GTTGTGGCA   GAGGGG
                                  C       ___
GAM145  HOXC4    5'  GGGGAGGGTGGGGATGGGA   28249      ATG  G  TG
                                TCTCA   CC TG  TTCTCT
                                |||||   || ||  ||||||
                                AGGGT   GG GT  GAGGGG
                                   A__  G  GG
GAM145  HOXD4    5'  GAGGGGAATGGGGTGCTGGGG  28260      AT   G   G
                                TCTCA  GCC TGT TTCTCTT
                                |||||  ||| ||| |||||||
                                GGGGT  TGG GTA AGGGGAG
                                   CG   G  _
GAM145  HS3ST3A1 5'  CGGAGAGAACGCGCCCAGGCG  21273     ___
                                TGCC   GTGTGTTCTCTTTG
                                ||||   ||||||||||||||
                                GCGG   CGCGCAAGAGAGGC
                                  ACC
GAM145  IFNGR1   3'  TAAAGAGGATGTGTGGCATT   72468       TG
                                AATGCCG  TGTTCTCTTTG
                                |||||||  ||||||||||
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                                TTACGGT  GTAGGAGAAAT
                                   GT
GAM145  IGSF1    3'  TAAAGGGGATTCTGGGAGTTGA 9558        G_  TGT
             GA                   TCTCAAT  CCG   GTTCTCTTTG
                                  |||||||  |||   ||||||||||
                                  AGAGTTG  GGT   TAGGGGAAAT
                                     AG   CT_
GAM145  IL18R1   3'  CAAAGGGAGCCCAGCACTGGGA 15252      A   CG  T
                                  TCTCA TGC  TG GTTCTCTTTG
                                  |||||  |||  ||  ||||||||||
                                  AGGGT ACG  AC CGAGGGAAAC
                                    C   __  C
GAM145  IL18RAP  5'  AAGGACAACATATGGTGATGGG 15248      A         C    G
             G                    TCTCA TGCCGTGTGTT TCTTT
                                  |||||  ||||||||||| |||||
                                  GGGGT GTGGTATACAA AGGAA
                                     A         C    G
GAM145  IL22RA2  3'  TGAGAGGGCGATGAATTAAGA  54775    C   GC   G      TT
                                  TCT AAT  CGT TGTTCTCT  G
                                  |||  |||  ||| ||||||||  |
                                  AGA TTA  GTA GCGGGAGA  T
                                    A   A_  _      GG
GAM145  IMMP2L   3'  GAGTTGCTGGCATTGGGA    51706          T   TT
                                  TCTCAATGCCG GTG  CTC
                                  ||||||||||| |||  |||
                                  AGGGTTACGGT CGT  GAG
                                        _   T_
GAM145  INHBB    3'  AGGGGCACGGTGGTGGGG    11004      AT     GTT
                                  TCTCA  GCCGTGT   CTCT
                                  |||||  |||||||   ||||
                                  GGGGT  TGGCACG   GGGA
                                     GG     ____
GAM145  ITGA6    3'  CAAAGATGTTATGGTGTTTAGA 5784      C       TGTTC
                                  TCT AATGCCGTG    TCTTTG
                                  ||| |||||||||    ||||||
                                  AGA TTGTGGTAT    AGAAAC
                                    T       TGT__
GAM145  ITGB3    3'  CAGGGAGAGCTGAACTATTAGA 5802     C   CC  GT_
                                  TCT AATG  GT   GTTCTCTTTG
                                  ||| ||||  ||   ||||||||||
                                  AGA TTAT  CA   CGAGAGGGAC
                                    _   __  AGT
GAM145  ITPR1    3'  TAAAGGGAGTGCACTTCTTTGA 11074     TGCC   TG
                                  TCAA   GTG  TTCTCTTTG
                                  ||||   |||  |||||||||
                                  AGTT   CAC  GAGGGAAAT
                                    TCTT   GT
GAM145  JAM2     5'  CGAGGGGAAGAAAGGAGTTGGG 41384       G  GTGTG
             G                    TCTCAAT CC    TTCTCTTTG
                                  |||||||  ||    |||||||||
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                                GGGGTTG GG     AAGGGGAGC
                                    A  AAAG_
GAM145  KCNA3    3'  CAAGGAGGAAAATATGGTGTTT 11133     C        G_
             GGA                    TCT AATGCCGTGT  TTCTCTTTG
                                ||| ||||||||||  |||||||||
                                AGG TTGTGGTATA  AGGAGGAAC
                                  T         AA
GAM145  KCNA6    5'  GGAGAGTGTGTGTTGGGA    11139         CGT TG
                                TCTCAATGC   G  TTCTCT
                                |||||||||   |  ||||||
                                AGGGTTGTG   T  GAGAGG
                                     ___ GT
GAM145  KCNA6    5'  TAAAGAGGGCGCACGGGAGCTG 11143      ATG_
             GG                   CTCA   CCGTGTGTTCTCTTTG
                                ||||   ||||||||||||||||
                                GGGT   GGCACGCGGGAGAAAT
                                  CGAG
GAM145  KCNAB1   3'  GAAGGGGGTGGTGTGGGA    61584      A   GTGT TT
                                TCTCA TGCC    G  CTCTTT
                                ||||| ||||    |  ||||||
                                AGGGT GTGG    T  GGGAAG
                                   _   _____ GG
GAM145  KCNK1    3'  TAAGGGGAATAATAAACTTGAG 11165       TGCCGTG
             A                   TCTCAA      TGTTCTCTTTG
                                ||||||      ||||||||||
                                AGAGTT      ATAAGGGGAAT
                                   CAAATA_
GAM145  KCNK4    3'  CGAGGAGAGCGTGCATAGCG   33981     C__ TG
                                TGC   G  TGTTCTCTTTG
                                |||   |  ||||||||||
                                GCG   C  GCGAGAGGAGC
                                  ATA GT
GAM145  KIF3C    3'  AGAGTGCTGTCGTTGGGG    11202         C  T TG
                                TCTCAATG CG G  TTCT
                                |||||||| || |  ||||
                                GGGGTTGC GT C  GAGA
                                     T  _ GT
GAM145  KIFC3    3'  TGAGGAGGGCGGGAGTGTGGAG 19893      A   CGTG
             G                   TCTC ATGC    TGTTCTCTTTG
                                |||| ||||    ||||||||||
                                GGAG TGTG    GCGGGAGGAGT
                                  G    AGG_
GAM145  L1CAM    3'  CAGAGAGGCTGTGGTTTGGGG  43985       T    TGT  T
                                TCTCAA GCCG   GT CTCTTTG
                                |||||| ||||   || |||||||
                                GGGGTT TGGT   CG GAGAGAC
                                   _    GT_  _
GAM145  LAMC2    3'  TAGAGAGAAGGCAGGTTGAGA  38769      AT   G   G
                                TCTCA  GCC TGT TTCTCTTTG
                                |||||  ||| ||| |||||||||
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                                AGAGT  TGG ACG AAGAGAGAT
                                  __  _  G
GAM145  LIF     3'  GAGGATGTGGCTGTTGAGA   11304       _   TG G
                                TCTCAAT GCCG  T TTC
                                ||||||| ||||  | |||
                                AGAGTTG CGGT  A GAG
                                   T   GT G
GAM145  LOH11CR2A 5'  TAGATTCCCAGCATGGCATTGA 28274           GTTC__  TTG
            GA                    TCTCAATGCCGTGT     TCT
                                ||||||||||||||     |||
                                AGAGTTACGGTACG     AGA
                                       ACCCTT   T
GAM145  MAFK    5'  CGAGGGGAGCGCGACAGTGAG  11419     ATGCCG
                                CTCA     TGTGTTCTCTTTG
                                ||||     ||||||||||||||
                                GAGT     GCGCGAGGGGAGC
                                  GACA__
GAM145  MAML1   5'  TGGGAGAGGCCGAGGCTTGAGG 29281      T   G  TG     TT
                                TCTCAA GCC TG  TTCTCT  G
                                |||||| ||| ||  ||||||  |
                                GGAGTT CGG GC  GAGAGG  T
                                   _  A  CG     GG
GAM145  MAP2    3'  GAGGAAGTGGTGTTTAGA    49820     C      TGTG
                                TCT AATGCCG    TTCTC
                                ||| |||||||    |||||
                                AGA TTGTGGT    AGGAG
                                  T      GA__
GAM145  MAPRE3   3'  CGAGGGGGGCTTGGGGGCATGG 25598      A    GTGT_
            GG                    TCTCA TGCC     GTTCTCTTTG
                                ||||| ||||     ||||||||||
                                GGGGT ACGG     CGGGGGGAGC
                                   _    GGGTT
GAM145  MASP1   3'  TAAGGGGAAGGTGGCAATGGGA 58218      A     TG G
                                TCTCA TGCCG  T TTCTCTTTG
                                ||||| |||||  | |||||||||
                                AGGGT ACGGT  G AAGGGGAAT
                                   A     __ G
GAM145  MAT1A   3'  AGGGTACATGGTGCTGGGA   92493      AT      TT
                                TCTCA  GCCGTGTG  CT
                                |||||  ||||||||  ||
                                AGGGT  TGGTACAT  GA
                                   CG       GG
GAM145  MATK    3'  GGAGAGTGCGGCGTGGGGG   11465     A     TG GT
                                TCTC ATGCCG  T  TCTCT
                                |||| ||||||  |  |||||
                                GGGG TGCGGC  G  AGAGG
                                  G     GT __
GAM145  MATN4   3'  CAGGGGGATAGCGGGTGGTGAG 48357      AT   G   GT
            G                     TCTCA  GCC TGT  TCTCTTTG
                                |||||  ||| |||  ||||||||
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                                GGAGT  TGG GCG  AGGGGGAC
                                  GG   _  AT
GAM145  MBD3    3'  TGAGGGAGCCGTGGGCGTGGGG 15394     A    GTGT     TT
            A                    TCTC ATGCC   GTTCTCT  G
                                 |||| |||||   |||||||  |
                                 AGGG TGCGG   CGAGGGA  T
                                   G    GTGC     GG
GAM145  MDFI    3'  TGGGAGGGTGGGCCGGTGGGG  19983     AAT   _ G  TT   TT
                                 TCTC   GCCG T TG  CTCT  G
                                 ||||   |||| | ||  ||||  |
                                 GGGG   TGGC G GT  GAGG  T
                                   ___   C G  GG   GG
GAM145  MEF2B   5'  CAAGGCAGACATGCAGCGTTGG 20978        C     CT
            GA                     TCTCAATGC GTGTGTT  CTTTG
                                 |||||||||| |||||||  |||||
                                 AGGGTTGCG CGTACAG  GGAAC
                                      A      AC
GAM145  MEF2D   3'  CAGAGGGAGGGAGGTGGTGAGG 20980      AT   GTGTG
                                 TCTCA  GCC    TTCTCTTTG
                                 |||||  |||    |||||||||
                                 GGAGT  TGG    GAGGGAGAC
                                   GG   AGG__
GAM145  MEN1    5'  GAGAGGGGGCGGGGCGGCCATT 56349        _   G_       G
            GGGG                   TCTCAATG CCGT  TGTTCTCTTT
                                 |||||||| ||||  ||||||||||
                                 GGGGTTAC GGCG  GCGGGGGAGA
                                      C   GG        GA
GAM145  MGAT4A  3'  TGAAGGGGGTACTTTTGAGG   25214      TGCCGT   TT
                                 TCTCAA     GTG  CTCTTTG
                                 ||||||     |||  |||||||
                                 GGAGTT     CAT  GGGAAGT
                                    TT____   GG
GAM145  MJD     5'  GAGGGGGTGGTTCGGCGTGGGG 18423      A    TGTGT     G
                                 TCTCA TGCCG    TCTCTTT
                                 ||||| |||||    |||||||
                                 GGGGT GCGGC    GGGGGAG
                                   _    TTGGT
GAM145  MLF2    5'  CGAGGGGGGCGTACGGAGGTGG 19555     ATG
                                 TCA   CCGTGTGTTCTCTTTG
                                 |||   ||||||||||||||||
                                 GGT   GGCATGCGGGGGGAGC
                                   GGA
GAM145  MMP19   5'  TAGAGAGGGTGCACCTGGTTGG 11639    AAT  __   TG
            A                      TC   GCC  GTG  TTCTCTTTG
                                   ||   |||  |||  |||||||||
                                   AG   TGG  CAC  GGGAGAGAT
                                    GT_   TC   GT
GAM145  MSL3L1  3'  TAGAGGGAATCGATATTGA   23292       C  TGT
                                 TCAATG CG   GTTCTCTTTG
                                 ||||||  ||   ||||||||||
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                                AGTTAT GC   TAAGGGAGAT
                                   A ___
GAM145  MTM1    3'  CAAAGGGGATATATGTTTGTGG 6004     T  ATGC
                A                   TC CA    CGTGTGTTCTCTTTG
                                    || ||    ||||||||||||||
                                    AG GT    GTATATAGGGGAAAC
                                     _ GTTT
GAM145  MUC4    3'  CAAGGAGAATGAATACTGGGA  37871      ATGCC   __
                                    TCTCA    GTGT  GTTCTCTTTG
                                    |||||    ||||  ||||||||||
                                    AGGGT    CATA  TAAGAGGAAC
                                       _____   AG
GAM145  MUC4    3'  CAAGGAGAATGAATACTGGGA  37872      ATGCC   __
                                    TCTCA    GTGT  GTTCTCTTTG
                                    |||||    ||||  ||||||||||
                                    AGGGT    CATA  TAAGAGGAAC
                                       _____   AG
GAM145  MXI1    3'  CAAGGAGAACAAATATTCAGA  56122     C   CCGTG
                                    TCT AATG    TGTTCTCTTTG
                                    ||| ||||    ||||||||||
                                    AGA TTAT    ACAAGAGGAAC
                                      C   AA___
GAM145  MXI1    3'  CAAGGAGAACAAATATTCAGA  56123     C   CCGTG
                                    TCT AATG    TGTTCTCTTTG
                                    ||| ||||    ||||||||||
                                    AGA TTAT    ACAAGAGGAAC
                                      C   AA___
GAM145  NEF3    3'  AGGGGGGATGTCTTGAGA    19388       T  CGTGT
                                    TCTCAA GC    GTTCTCTTT
                                    |||||| ||    |||||||||
                                    AGAGTT TG    TAGGGGGGA
                                       C _____
GAM145  NKTR    5'  CGGGGTTTAGCGTGGCATTGGG 19391           GTT_   TTG
                A                    TCTCAATGCCGTGT   CTCT
                                     ||||||||||||||   ||||
                                     AGGGTTACGGTGCG   GGGG
                                              ATTT   C
GAM145  NONO    3'  CAGAGAGAGCAGGAGATTCGGA 82884    C   G_  GTG
                                    TCT AAT  CC   TGTTCTCTTTG
                                    ||| |||  ||   ||||||||||
                                    AGG TTA  GG   ACGAGAGAGAC
                                      C   GA ___
GAM145  NORE1   3'  AAAGGGAGCAGGTGGAGA    49522     AAT   GTG
                                    TCTC   GCC   TGTTCTCTTT
                                    ||||   |||   ||||||||||
                                    AGAG   TGG   ACGAGGGAAA
                                      G__   ___
GAM145  NR1I2   5'  AGGGAGAACATAATGAGA    15296      ATGCCG
                                    TCTCA     TGTGTTCTCTTT
                                    |||||     ||||||||||||
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                                AGAGT     ATACAAGAGGGA
                                  A_____
GAM145  NR2F6    5'  CGGAGGGAAGAGCGCGGTGGGG 19104      AAT      G_
                                TCTC   GCCGTGT  TTCTCTTTG
                                ||||   |||||||  |||||||||
                                GGGG   TGGCGCG  AAGGGAGGC
                                  ___      AG
GAM145  OTOR     3'  TGAGGAGGATGCAGGTTTTGTG 39757    T   T   G
          G                      TC CAA GCC TGTGTTCTCTTTG
                                || ||| ||| ||||||||||||
                                GG GTT TGG ACGTAGGAGGAGT
                                 T   T   _
GAM145  PABPN1   3'  TGAGGAGGGACCTGCTTTGGGG 17359       T  CGT  G
                                TCTCAA GC   GT TTCTCTTTG
                                |||||| ||   || |||||||||
                                GGGGTT CG   CA GGGAGGAGT
                                    T  TC_  _
GAM145  PCOLN3   3'  CAGGGAGGGGCTAGTGTTGG   12408       CGT  G
                                TCAATGC   GT TTCTCTTTG
                                |||||||   || |||||||||
                                GGTTGTG   CG GGGAGGGAC
                                    AT_  _
GAM145  PDK1     3'  GGAAGGTATGGTGTTCAGA    12030     C       TG
                                TCT AATGCCGTG  TTCT
                                ||| |||||||||  ||||
                                AGA TTGTGGTAT  AAGG
                                  C        GG
GAM145  PEX6     3'  CAGGGTGCAAAGTGGCATTGAG 6084          TG_   T    TTG
          A                      TCTCAATGCCG   TGT CTCT
                                ||||||||||   ||| ||||
                                AGAGTTACGGT   ACG GGGA
                                       GAA   T    C
GAM145  PHKB     3'  GAGGAGGCTGAGGCATGAGA   6099       A   GT_  G
                                TCTCA TGCC   GT TTCTC
                                ||||| ||||   || |||||
                                AGAGT ACGG   CG AGGAG
                                  _    AGT  G
GAM145  PHLDA3   3'  GGCCTCATATGGCATGAGG    25695      A       TT_
                                TCTCA TGCCGTGTG   CT
                                ||||| |||||||||   ||
                                GGAGT ACGGTATAC   GG
                                  _        TCC
GAM145  PIGN     3'  AGGAAAATGGTATTTGGA     25600     C      GTG
                                TCT AATGCCGT   TTCT
                                ||| ||||||||   ||||
                                AGG TTATGGTA   AGGA
                                  T       AA_
GAM145  PIK4CB   3'  AGGGGGAGATGGGTGATGAGG  12128      A   G   G
                                TCTCA TGCC TGT TTCTCTT
                                ||||| |||| ||| |||||||
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                                GGAGT GTGG GTA AGGGGGA
                                  A   _  G
GAM145  PIM1     3'  TAGGGGGGAAACAGGTTGGGA  92691      AT  G  G
                                TCTCA  GCC TGT TTCTCTTTG
                                |||||  ||| ||| |||||||||
                                AGGGT  TGG ACA AGGGGGGAT
                                  __  _  A
GAM145  PMM1     3'  TAAAGAGAGGTCCTGGTGTTGG 12183         TGTG
                                TCAATGCCG   TTCTCTTTG
                                |||||||||   |||||||||
                                GGTTGTGGT   GAGAGAAAT
                                     CCTG
GAM145  PNN      3'  TAAAGAGGATGCTGCCTTAAGA 71663     C  T  CGT
                                TCT AA GC   GTGTTCTCTTTG
                                ||| || ||   ||||||||||||
                                AGA TT CG   CGTAGGAGAAAT
                                  A  C  T__
GAM145  POLR2C   3'  GGGATGCAGTGGTGTTTAGG   12205     C     _
                                TCT AATGCCG TGTGTTCT
                                ||| ||||||| ||||||||
                                GGA TTGTGGT ACGTAGGG
                                  T      G
GAM145  POU2AF1  3'  GGAGAGAGGGGTGTGGGA    21745      A   GTGTG
                                TCTCA TGCC    TTCTCT
                                ||||| ||||    ||||||
                                AGGGT GTGG    GAGAGG
                                  _   GGA__
GAM145  PPFIA3   3'  GGGCGACGTGGCGTGGGGG   61672     A      _
                                TCTC ATGCCGTGT GTTC
                                |||| ||||||||| ||||
                                GGGG TGCGGTGCA CGGG
                                  G       G
GAM145  PRAME    3'  TAAAGGGAGATTCTGGCTTGGG 21488       T   TGTG
            A                    TCTCAA GCCG   TTCTCTTTG
                                ||||||| ||||   |||||||||
                                AGGGTT CGGT   GAGGGAAAT
                                  _   CTTA
GAM145  PRY      3'  AGGAGAGTACATGGCATTGAGA 60890                TG
                                TCTCAATGCCGTGTGTTCTCTT
                                ||||||||||||||||||||||
                                AGAGTTACGGTACATGAGAGGA
                                             C
GAM145  PSMB9    3'  CAAAACCTGGTATGGTCATTGG 12491       _   T___  CTCTTTG
            GA                   TCTCAATG CCGTG   GTT
                                |||||||| |||||   |||
                                AGGGTTAC GGTAT   CAA
                                     T   GGTC  AAC
GAM145  PTK7     3'  TGGAGGGCTAGGCTTGGGA   12552      T  GTGT     TT
                                TCTCAA GCC   GTTCTCT  G
                                |||||| |||   ||||||| |
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                                AGGGTT CGG   CGGGAGG  T
                                   _  AT__     G
GAM145  RAB27A   5'  TGAAGAGGACATGTGATTGGA  17152    T   GC  TG
                                TC CAAT  CG  TGTTCTCTTTG
                                || ||||  ||  ||||||||||
                                AG GTTA  GT  ACAGGAGAAGT
                                 _   __  GT
GAM145  RAB33A   5'  CAAGGAGGGTGCGCTGGAGGAG 17739     AATG  _   TG
           G                     TCTC   CC GTG  TTCTCTTTG
                                ||||   || |||  |||||||||
                                GGAG   GG CGC  GGGAGGAAC
                                  GA__  T  GT
GAM145  RAP1GA1  3'  AGAGGGAACAAGGTGGGA    12768     AAT   GTG
                                TCTC   GCC   TGTTCTCTTT
                                ||||   |||   ||||||||||
                                AGGG   TGG   ACAAGGGAGA
                                  ___   A__
GAM145  RAP1GA1  3'  CAAGGAGGATGTGATATGTGGG 12770      ATGCCG  TG
           G                     TCTCA     TG  TTCTCTTTG
                                |||||     ||  |||||||||
                                GGGGT     GT  AGGAGGAAC
                                   GTATA_  GT
GAM145  RB1      3'  AGAGATCGTGTATTGAGA    92553          _  TGTGT
                                TCTCAATGC CG    TCTCT
                                |||||||| ||    |||||
                                AGAGTTATG GC    AGAGA
                                      T  T____
GAM145  RBM3     5'  CAAGGGGAACATGGTGCATTCA 71004     C    CG
           GG                     TCT AATGC  TGTGTTCTCTTTG
                                ||| |||||  ||||||||||||||
                                GGA TTACG  GTACAAGGGGAAC
                                  C    TG
GAM145  RTN3     3'  CAGAGGGAATATGCACTGGCG  74329      _   __
                                TGCC GTGT  GTTCTCTTTG
                                |||| ||||  ||||||||||
                                GCGG CACG  TAAGGGAGAC
                                   T   TA
GAM145  SAR1     3'  AACCATGTCTGGCGTTGAGA   39730          ____  T
                                TCTCAATGCC   GTG GTT
                                ||||||||||   ||| |||
                                AGAGTTGCGG   TAC CAA
                                      TCTG  _
GAM145  SET      3'  AAAGGGGTGGGGTTTGAGA    13017       T  G  TGT
                                TCTCAA GCC TG   TCTCTTT
                                |||||| ||| ||   |||||||
                                AGAGTT TGG GT   GGGGAAA
                                   _  G  ___
GAM145  SF3B1    3'  TAAAGGGAATGTTTAATTGAGA 25818        GCCGT TG
                                TCTCAAT    G  TTCTCTTTG
                                |||||||    |  |||||||||
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                                AGAGTTA    T  AAGGGAAAT
                                    ATT__ GT
GAM145  SGCB    3'  GAAAACAACATGGCATTTGGA  5877     C       _   C
                                TCT AATGCCGTGT GTT TC
                                ||| |||||||||| ||| ||
                                AGG TTACGGTACA CAA AG
                                  T        A   A
GAM145  SHOC2   3'  AGGGGAAGGGTATTGAGA    24780         GTGTG
                                TCTCAATGCC    TTCTCT
                                ||||||||||    ||||||
                                AGAGTTATGG    AGGGGA
                                      GA___
GAM145  SIRT7   3'  TAGGGAGAACGAACTCTTTGGG 33738       TGCC  G
            G                    TCTCAA    GT TGTTCTCTTTG
                                ||||||    || ||||||||||
                                GGGGTT    CA GCAAGAGGGAT
                                    TCT_  A
GAM145  SLC20A2  3'  TAAAGGGATGGTCTGGTGTTGG 23119         TG GT
                                TCAATGCCG  T  TCTCTTTG
                                |||||||||  |  ||||||||
                                GGTTGTGGT  G  AGGGAAAT
                                     CT GT
GAM145  SMAC    5'  AGGAGGAGGGACACGGCATGGG 57995     A       G       G
            GG                    TCTC ATGCCGTGT TTCTCTTT
                                ||||| |||||||| ||||||||
                                GGGG TACGGCACA GGGAGGAG
                                  G        _       GAG
GAM145  SMCX    5'  GAAGGCCGCGGCGTTTGGG   16085      _      T  TC
                                CTCAA TGCCGTG GT  TC
                                ||||| ||||||| ||  ||
                                GGGTT GCGGCGC CG  AG
                                   T       _  GA
GAM145  SMCX    5'  GAAGGCTGCGGTAGTGGGG   16086      A     _  G
                                TCTCA TGCCGT GT TTC
                                ||||| |||||| || |||
                                GGGGT ATGGCG CG AAG
                                   G     T  G
GAM145  SMPX    3'  GGAGGGTGTGGTTTTGAGG   27536       T    TG G
                                TCTCAA GCCG  T TTCT
                                |||||| ||||  | ||||
                                GGAGTT TGGT  G GAGG
                                    T    GT G
GAM145  SORCS3   3'  CAGAGAGAATGTGATATAGAGA 31070     A   C  TG GT
                                TCTC ATG CG  T  TCTCTTTG
                                |||| ||| ||  |  ||||||||
                                AGAG TAT GT  A  AGAGAGAC
                                  A   A  GT __
GAM145  SPG7    3'  TAGTCACGCATGCAGTGTTGGG 13348         __      TCTCTTTG
            G                    TCTCAATGC  CGTGTGT
                                |||||||||  |||||||
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                                GGGGTTGTG  GTACGCA
                                     AC      CTGAT
GAM145  SPON2    3'  GGCCGGCACGGGCATTGGGA  25853         G     CT
                                TCTCAATGCC TGTGTT  CT
                                |||||||||| ||||||  ||
                                AGGGTTACGG GCACGG  GG
                                      _     CC
GAM145  SRD5A2   5'  CAAAGAGAATTAATGATGAGG  60117      ATGC   GT
                                TCTCA   CGT  GTTCTCTTTG
                                |||||   |||  ||||||||||
                                GGAGT   GTA  TAAGAGAAAC
                                   A___   AT
GAM145  STIM1    3'  TAAAGAGAGGCCAGGCTTGGGA 60785       T   G  TG
                                TCTCAA GCC TG  TTCTCTTTG
                                |||||| ||| ||  |||||||||
                                AGGGTT CGG AC  GAGAGAAAT
                                   _  _ CG
GAM145  TCF19    3'  AGGGAGAATGTGCTTGGCA   99577     __ TG
                                TGCC  G  TGTTCTCTTT
                                ||||  |  ||||||||||
                                ACGG  C  GTAAGAGGGA
                                  TT GT
GAM145  TEAD3    3'  GGGGGGGTCCAGGATTGAGG   13673       G  G  TG
                                TCTCAAT CC TG  TTCTCTT
                                ||||||| || ||  |||||||
                                GGAGTTA GG AC  GGGGGGG
                                   _ _ CT
GAM145  TERF2    5'  CGGGGAGGGCGCGCGGCGATCG 20151     CAA
           GA                     TCT   TGCCGTGTGTTCTCTTTG
                                |||   ||||||||||||||||||
                                AGG   GCGGCGCGCGGGAGGGGC
                                 CTA
GAM145  TGFB3    3'  CAGAGGGGATGGGGATAGAGG  13716     A  G  GTG
                                TCTC AT CC   TGTTCTCTTTG
                                |||| || ||   ||||||||||
                                GGAG TA GG   GTAGGGGAGAC
                                  A  G  ___
GAM145  TGFB3    3'  TGAGATGTTGTGTGGCAATGGG 13720      A    TG GT__   TTTG
           A                     TCTCA TGCCG  T    TCTC
                                ||||| |||||  |   ||||
                                AGGGT ACGGT  G    AGAG
                                   A    GT TTGT    T
GAM145  TGFBR2   3'  TAGAGAGGATTTGAATGTGGGA 13735      ATGCCGTGT
                                TCTCA       GTTCTCTTTG
                                |||||       ||||||||||
                                AGGGT       TAGGAGAGAT
                                  GTAAGTT__
GAM145  TM7SF3   3'  CGGAGGGAGTTTATTATTGAG  60393       CC   TG
                                CTCAATG  GTG  TTCTCTTTG
                                |||||||  |||  |||||||||
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                                GAGTTAT  TAT  GAGGGAGGC
                                   __  TT
GAM145  TMEM4    5' GGAGGGGCGGGTTTGGGG    27301      TG   GTG
                                TCTCAA  CCGT   TTCTCT
                                ||||||  ||||   ||||||
                                GGGGTT  GGCG   GGGAGG
                                   TG   ___
GAM145  TP53BP2  3' AGGCCATACTGTGTTGGGG   19459       C    TT
                                TCTCAATGC GTGTG  CT
                                |||||||||| |||||  ||
                                GGGGTTGTG CATAC  GA
                                     T    CG
GAM145  TSC      3' AGGGTATGGTATGTGGGA    35873     _      TGTT
                                TCTCA ATGCCGTG   CTCT
                                ||||| ||||||||   ||||
                                AGGGT TATGGTAT   GGGA
                                   G     _____
GAM145  USP18    3' TGGGAGAGCAGTGGCAGTGGGA 64385     A   GTG      TT
                                TCTCA TGCC   TGTTCTCT  G
                                ||||| ||||  ||||||||  |
                                AGGGT ACGG   ACGAGAGG  T
                                   G   TG_      GG
GAM145  VEGF     5' CAGAGAGAGCGCGCGGGCGTGC 14040    A_   _
           GAG                  CTC  ATGCC GTGTGTTCTCTTTG
                                |||  ||||| ||||||||||||||
                                GAG  TGCGG CGCGCGAGAGAGAC
                                  CG    G
GAM145  VENTX2   3' CGGGGAGGACTCCCGCGTTGA  27861       CGTGT
                                TCAATGC    GTTCTCTTTG
                                |||||||    ||||||||||
                                AGTTGCG    CAGGAGGGGC
                                    CCCT_
GAM145  VNN2     3' TGAAGAGAATAGTAATGATGGG 17419      ATGCCGTG
           A                     TCTCA      TGTTCTCTTTG
                                |||||       ||||||||||
                                AGGGT       ATAAGAGAAGT
                                   AGTAATG_
GAM145  VPS26    5' TAGGGGGGACGCGGCGGCGGCG 18107         _____
           TTGA                   TCAATGCCGT    GTGTTCTCTTTG
                                |||||||||   ||||||||||||
                                AGTTGCGGCG   CGCAGGGGGGAT
                                     GCGG
GAM145  WHSC1    3' GGGGAGATGGGCATTTGGA   24679     C     G  G
                                TCT AATGCC TGT TTCTC
                                ||| |||||| ||| |||||
                                AGG TTACGG GTA AGGGG
                                  T     _  G
GAM145  WNT14    3' AGGCATTGCACACGGTGTGAGG 14132      A       TCT_  TG
                                TCTCA TGCCGTGTGT    CTT
                                ||||| ||||||||||   |||
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                                GGAGT GTGGCACACG    GGA
                                  _        TTAC   C
GAM145  WNT14    3'  AGGCATTGCACATGGTGTGAGA 14133       A        TCT_   TG
                                TCTCA TGCCGTGTGT    CTT
                                ||||| ||||||||||    |||
                                AGAGT GTGGTACACG    GGA
                                  _        TTAC   C
GAM145  XRCC3    3'  CAAAGAGGATCCGAGGTTGAGA 19515      AT   G  TG
                                TCTCA  GCC TG  TTCTCTTTG
                                |||||  ||| ||  |||||||||
                                AGAGT  TGG GC  AGGAGAAAC
                                  __  A  CT
GAM145  ZNF2     5'  CAAGGAGAGCACACAGGAGAGA 41157      AATG  _
                                TCTC    CC GTGTGTTCTCTTTG
                                ||||    || ||||||||||||||
                                AGAG    GG CACACGAGAGGAAC
                                  A___  A
GAM145  ZNF205   3'  TGGGGTGAGGCATGGCGATGGG 14372      A      G  _   TTG
          G                      TCTCA TGCCGTGT TT CTCT
                                |||||| |||||||| || ||||
                                GGGGT GCGGTACG AG GGGG
                                  A       G  T    T
GAM145  ZNF217   3'  GAATTGCAGGTATTGGGG    22543          G   _
                                TCTCAATGCC TGTG TTC
                                |||||||||| |||| |||
                                GGGGTTATGG ACGT AAG
                                     _    T
GAM145  ZNF217   3'  TAAAGGGGGTATGTGATAATAG 22545     A  GC_  TG  TT
          AG                      CTC AT   CG  TG  CTCTTTG
                                ||| ||   ||  ||  |||||||
                                GAG TA   GT  AT  GGGAAAT
                                  A  ATA  GT  GG
GAM145  ZNF257   5'  GACCTGCAGGTATTGGGA    54234          _   T
                                TCTCAATGCC GTG GTT
                                |||||||||| ||| |||
                                AGGGTTATGG CGT CAG
                                     A   C
GAM145  ZNF278   3'  TAGGGGGTTTCAATGCTGTTGG 50276        _  CG  T_ TT   TTG
          GA                      TCTCAAT GC  TG  G  CTCT
                                ||||||| ||  ||  |  ||||
                                AGGGTTG CG  AC  T  GGGA
                                   T  TA  TT GG   T
GAM145  ZNF278   3'  TAGGGGGTTTCAATGCTGTTGG 27502        _  CG  T_ TT   TTG
          GA                      TCTCAAT GC  TG  G  CTCT
                                ||||||| ||  ||  |  ||||
                                AGGGTTG CG  AC  T  GGGA
                                   T  TA  TT GG   T
GAM145  ZNF85    5'  GGCCTGCAGGTATTGGGA    14276          G   TT
                                TCTCAATGCC TGTG  CT
                                |||||||||| ||||  ||
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                                AGGGTTATGG ACGT  GG
                                      _   CC
GAM145  ALG5     5'  CGAGGGCTGCCACGGCATGGAG 26233      A       T__     TTTG
              A                   TCTC ATGCCGTG   GTTCTC
                                  |||| ||||||||   ||||||
                                  AGAG TACGGCAC   CGGGAG
                                    G       CGT     C
GAM145  ALS2CR8  3'  AGTCAAAGCGTGGCATTGAGA  45696            GTTCT
                                  TCTCAATGCCGTGT     CT
                                  ||||||||||||||     ||
                                  AGAGTTACGGTGCG     GA
                                           AAACT
GAM145  APMCF1   3'  AGAGAGGATATGATGAGA    41356       ATGC     G
                                  TCTCA    CGTGT TTCTCT
                                  |||||    ||||| ||||||
                                  AGAGT    GTATA GAGAGA
                                     A___     G
GAM145  APOA5    3'  TGGGGAGAACATGTGATGGTGT 54802     _      ___        TT
              GTGA                   TCA ATGCCGT   GTGTTCTCT  G
                                  ||| |||||||   |||||||||  |
                                  AGT TGTGGTA   TACAAGAGG  T
                                    G       GTG        GG
GAM145  AQP9     3'  CAAGGGGAGGACATTGTGGCAT 40938     C     ___    G
              TCAGA                   TCT AATGCC   GTGT TTCTCTTTG
                                  ||| ||||||   |||| |||||||||
                                  AGA TTACGG   TACA GAGGGGAAC
                                    C      TGT    G
GAM145  ARAP3    3'  AGGGAGAGCGAGTTTGGGA   42788        TGCCGTG
                                  TCTCAA       TGTTCTCTTT
                                  ||||||       ||||||||||
                                  AGGGTT       GCGAGAGGGA
                                     TGA____
GAM145  ARHGAP9  5'  CAGAGGAGGTGGTGGTATTGGG 51660           TG_ G     TTG
              A                   TCTCAATGCCG   T TTCTCT
                                  ||||||||||   | ||||||
                                  AGGGTTATGGT   G AGGAGA
                                        GGT G     C
GAM145  ARHGEF16 3'  CAGGGAGATTTCGGTTTTGAGG 27818        T    TGTGT
                                  TCTCAA GCCG     TCTCTTTG
                                  |||||| ||||     ||||||||
                                  GGAGTT TGGC     AGAGGGAC
                                     T    TTT__
GAM145  ATP10D   3'  AAGGGGAGTCATTTGAGA    73524        TGCCGT   _
                                  TCTCAA     GTG TTCTCTTT
                                  ||||||     ||| ||||||||
                                  AGAGTT     TAC GAGGGGAA
                                     _______  T
GAM145  B3GNT6   3'  CAGAGGTAGCTGTGGTGTTGA  23451          TGT   CT
                                  TCAATGCCG   GTT  CTTTG
                                  |||||||||   |||  |||||
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                                AGTTGTGGT  CGA  GAGAC
                                     GT_  TG
GAM145  BAG5    3'  AGAGGGCAGTCGGTATTTAGG  18033    C     TG
                                TCT AATGCCG  TGTTCTCT
                                ||| |||||||  ||||||||
                                GGA TTATGGC  ACGGGAGA
                                  T      TG
GAM145  BHC80   3'  GGAGGGAGCAGGGGGTGGGA  34014     A G  G   G
                                TCTCA T CC TGT TTCTCT
                                ||||| | || ||| ||||||
                                AGGGT G GG ACG GGGAGG
                                   _ G  G   A
GAM145  BIRC4   3'  GGGGAGGGGGGGATTGGGG   8601       G  GTGTG
                                TCTCAAT CC    TTCTCTTT
                                ||||||| ||    ||||||||
                                GGGGTTA GG    GGGAGGGG
                                    G  G____
GAM145  BRAG    3'  GAAGAGAACGCTTGAGCA    30100    _  T
                                TGC CG GTGTTCTCTTT
                                ||| || ||||||||||
                                ACG GT CGCAAGAGAAG
                                  A  T
GAM145  BSMAP   3'  CGGGGGGGGGCGCTGAGGCTGAG 25044      AT   GT_
           G                     TCTCA  GCC   GTGTTCTCTTTG
                                |||||  |||   ||||||||||||
                                GGAGT  CGG   CGCGGGGGGGGC
                                   __   AGT
GAM145  BTN1A1  3'  TGGAGGGAATATTATGATGGAG 9967      AATGC   _      TT
           G                     TCTC    CGTG TGTTCTCT  G
                                ||||    |||| ||||||||  |
                                GGAG    GTAT ATAAGGGA  T
                                  GTA__   T      GG
GAM145  BUCS1   3'  GAGGGTGGGGCATTGAGA    54761         G GT TT
                                TCTCAATGCC T  G  CTC
                                |||||||||| |  |  |||
                                AGAGTTACGG G  T  GAG
                                     G __ GG
GAM145  C19orf7 3'  CAAAGGGAACAGTTGGTGTCTG 61777      _     TG
           GGA                    TCTCA ATGCCG  TGTTCTCTTTG
                                ||||| ||||||  ||||||||||
                                AGGGT TGTGGT  ACAAGGGAAAC
                                   C     TG
GAM145  C1QTNF2 3'  GACAGGCGTGGTGTTGGG    49975         __  G
                                CTCAATGCC  GT TGTT
                                |||||||||  || ||||
                                GGGTTGTGG  CG ACAG
                                     TG  G
GAM145  C20orf12 5' TAAAGAGAATTGGTTATGGGG  36849      AT    TGT
                                TCTCA  GCCG   GTTCTCTTTG
                                |||||  ||||   ||||||||||
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                                GGGGT  TGGT   TAAGAGAAAT
                                  AT   ___
GAM145  C20orf139 3'  AGGGGAAGAGGTGTTGGGG   85914          GTGTG
                                TCTCAATGCC    TTCTCT
                                ||||||||||    ||||||
                                GGGGTTGTGG    AGGGGA
                                     AGA__
GAM145  C20orf21  3'  GGGCTGGATGGTGTTGGGG   35571           G _
                                TCTCAATGCCGT T GTTC
                                |||||||||||| | ||||
                                GGGGTTGTGGTA G CGGG
                                      G T
GAM145  C20orf3   3'  GCAGAGGGAGCATGGCCCAGGG 68642          _____ _
           GTGTTGAGG                TCTCAATGCC    GT GTGTTCTCTTTG   C
                                ||||||||||    || ||||||||||||   |
                                GGAGTTGTGG    CG TACGAGGGAGAC   G
                                     GGACC  G
GAM145  C20orf36  3'  TGAGAGAATCTTCATAGAGA   37337     A   CCGTGT     TT
                                TCTC ATG     GTTCTCT  G
                                |||| |||     |||||||  |
                                AGAG TAC     TAAGAGA  T
                                  A   TTC___      GG
GAM145  C21orf42  5'  TAGAGAACACACTGGAGA    55228     AATGCC        TT
                                TCTC     GTGTGTTCTCT  G
                                ||||     ||||||||||  |
                                AGAG     CACACAAGAGA  T
                                  GT____         G
GAM145  C22orf3   3'  AAAGAGGGCCACAGTGGGG   25348     ATGCC   T
                                TCTCA    GTG GTTCTCTTT
                                |||||    ||| |||||||||
                                GGGGT    CAC CGGGAGAAA
                                  GA___  _
GAM145  C5orf3    3'  AGTAGATATTTGGCATTGAGG  38591          T    CT
                                TCTCAATGCCG GTGTT  CT
                                |||||||||| |||||  ||
                                GGAGTTACGGT TATAG  GA
                                      T    AT
GAM145  C5orf4    3'  AAAGAGGATGGAGTGAGA    33420      ATG  GTGT
                                TCTCA   CC    GTTCTCTTT
                                |||||   ||    |||||||||
                                AGAGT   GG    TAGGAGAAA
                                  GA_  _____
GAM145  C6orf9    5'  TAGAAGAATACATGGAATTGGG 42328        G        _  TTG
             G                   TCTCAAT CCGTGTGTTCT CT
                                |||||||  ||||||||||| ||
                                GGGGTTA GGTACATAAGA GA
                                    A         A  T
GAM145  C7orf14   5'  CAGAGGGAGTCGCCATTCAGG  74290     C    CCGT  _
                                TCT AATG    GTG TTCTCTTTG
                                ||| ||||    ||| |||||||||
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                                GGA TTAC    CGC GAGGGAGAC
                                  C    ____   T
GAM145  CCR6     3'  GGAGAGGATGGTATTCAGG   49406     C       GTG
                                TCT AATGCCGT   TTCTCT
                                ||| ||||||||   ||||||
                                GGA TTATGGTA   GAGAGG
                                  C       G__
GAM145  CCR6     3'  GGAGAGGATGGTATTCAGG   16445     C       GTG
                                TCT AATGCCGT   TTCTCT
                                ||| ||||||||   ||||||
                                GGA TTATGGTA   GAGAGG
                                  C       G__
GAM145  CDC26    5'  TAGGAAATGGCGTCGTGGCATT 58412           _   C__    TG
            GAGG                    TCTCAATGCCGTG TGTT   TCTT
                                ||||||||||||| ||||   ||||
                                GGAGTTACGGTGC GCGG   AGGA
                                        T    TAA    T
GAM145  CDH22    3'  TGAGGGAGCACGCCGCTGAGA  41441      AT  C         TT
                                TCTCA  GC GTGTGTTCTCT  G
                                |||||  || ||||||||||  |
                                AGAGT  CG CGCACGAGGGA  T
                                   __  C          GG
GAM145  CENTG1   3'  GGGGAGGGCGTTTTGGGG    29356       T  CGT  G
                                TCTCAA GC   GT TTCTCT
                                |||||| ||   || ||||||
                                GGGGTT TG   CG GAGGGG
                                    T  ___  G
GAM145  CGI-01   3'  TGAGGGAGTGTATGGACCTGG  32508     ATG    TG     TT
                                TCA   CCGTG  TTCTCT  G
                                |||   |||||  ||||||  |
                                GGT   GGTAT  GAGGGA  T
                                  CCA     GT     GG
GAM145  CHCR     3'  CGGAGAGATGGGGGCATGGAGA 37824      A    GTGTGT
                                TCTC ATGCC      TCTCTTTG
                                |||| |||||      ||||||||
                                AGAG TACGG      AGAGAGGC
                                  G     GGGT__
GAM145  CLDN6    3'  CAAAGAGGGGATGCTTTGAGA  41333       T  CGT  G
                                TCTCAA GC   GT TTCTCTTTG
                                |||||| ||   || |||||||||
                                AGAGTT CG   TA GGGAGAAAC
                                    T  ___  G
GAM145  CLSTN1   5'  AGGGACGCGGAGTTGAGG    30785       G    TGT
                                TCTCAAT CCGTG   TCTCT
                                ||||||| |||||   |||||
                                GGAGTTG GGCGC   AGGGA
                                    A    ___
GAM145  COVA1    3'  CAGAGAGGATGGAGGTTTGGGG 73638       T   GTG
                                TCTCAA GCC   TGTTCTCTTTG
                                |||||| |||   ||||||||||
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                                GGGGTT TGG   GTAGGAGAGAC
                                   _   AG_
GAM145  CRK7     3'  TGAGAGGATCATTACATTGA   33668       CC   T      TT
                                TCAATG  GTG GTTCTCT  G
                                ||||||  ||| |||||||  |
                                AGTTAC  TAC TAGGAGA  T
                                   AT   _      GG
GAM145  DDM36    3'  AGAGGATGTGGTTTGGGG    40913       T    TG G
                                TCTCAA GCCG  T TTCT
                                |||||| ||||  | ||||
                                GGGGTT TGGT  A GAGA
                                   _   GT G
GAM145  DDX33    3'  CAGAGGGGGTGGGGGTGGGGG  39782      A  G  GTG  TT
                                TCTC AT CC   TG  CTCTTTG
                                |||| || ||   ||  |||||||
                                GGGG TG GG   GT  GGGAGAC
                                  G  G  ___  GG
GAM145  dJ383J4.3 5'  GGAGAGGGACGGGTTGGGA    67495        G    GTG
                                TCTCAAT CCGT   TTCTCT
                                |||||||  ||||   ||||||
                                AGGGTTG GGCA   GAGAGG
                                   _   GG_
GAM145  DKFZp434O0320 3'  AAGGAATAGACGCTGCGTTGGG 84695          __  G    T   TG
          G                      TCTCAATGC  CGT TGTTC CTT
                                |||||||||  ||| ||||| |||
                                GGGGTTGCG  GCA ATAAG GAA
                                     TC   G    _  C
GAM145  DKFZp547D155 3'  AACAGTGTGTGTATTGGGA    70942          _  TG _
                                TCTCAATGC CG  T GTT
                                |||||||||  ||  | |||
                                AGGGTTATG GT  G CAA
                                     T  GT A
GAM145  DKFZP564A1164 3'  AGGGCAGTGGGTGTTGGGA    71534          GTG
                                TCTCAATGCC   TGTTCT
                                ||||||||||   ||||||
                                AGGGTTGTGG   ACGGGA
                                     GTG
GAM145  DKFZP564C196 3'  CAAAGAGAGCCACCTAGTGAGG 70601       ATGCC   T
                                TCTCA    GTG GTTCTCTTTG
                                |||||    ||| ||||||||||
                                GGAGT    CAC CGAGAGAAAC
                                   GATC_  _
GAM145  DKFZP564C196 5'  GGAGGGGATAAGGTGGGG    70604      AAT   G   G
                                TCTC   GCC TGT TTCTCT
                                ||||   ||| ||| ||||||
                                GGGG   TGG ATA GGGAGG
                                  ___   A   G
GAM145  DKFZP564L0862 5'  CAGGGGGAGCATGGAGTTTGGA 44252     C   G     GT
                                TCT AAT CCGTGT  TCTCTTTG
                                ||| ||| ||||||  ||||||||
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                                AGG TTG GGTACG  AGGGGGAC
                                  T  A    __
GAM145  DKFZP566G1424 5'  GGGGGGGGCACCAGTGAGG   85945      A  CC   G
                                TCTCA TG  GTGT TTCTCT
                                ||||| ||  |||| ||||||
                                GGAGT AC  CACG GGGGGG
                                   G  __   G
GAM145  DKFZp586H0623 3'  AAAGTTGGTGGTGTTGGGA   34495          TGTGT  T_
                                TCTCAATGCCG    TC  CTTT
                                ||||||||||    ||  ||||
                                AGGGTTGTGGT    GG  GAAA
                                      _____ TT
GAM145  DKFZp586I021 3'  CAAGGGGGCTGTGTGTGGCCTT 51081       T   TG ___      TG
           GAGG                  TCTCAA GCCG  T   GTTCTCTT
                                ||||||| ||||  |  ||||||||
                                GGAGTT CGGT  G   CGGGGGAA
                                   C   GT TGT       C
GAM145  DKFZp762K2015 3'  TGAAGGGAGTATGCCAGCA   72895     C_
                                TGC  GTGTGTTCTCTTTG
                                |||  ||||||||||||||
                                ACG  CGTATGAGGGAAGT
                                  AC
GAM145  DLX1     5'  CAGGGAGCGACAGCGGCGTTGG 81041          _  _     TTG
                                TCAATGCCG TGT GTTCTCT
                                ||||||||| ||| |||||||
                                GGTTGCGGC ACA CGAGGGA
                                     G  G      C
GAM145  DMRTA2   3'  CGGAGGGGGTGCGCGGCCTGGG 61290      AT     TG
                                CTCA  GCCGTG  TTCTCTTTG
                                ||||  ||||||  |||||||||
                                GGGT  CGGCGC  GGGGGAGGC
                                  C_     GT
GAM145  DPCR1    3'  CAAGGAGGGTGTAAGTTTAGGG 55996      AAT  CG  TG
           G                     TCTC   GC  TG  TTCTCTTTG
                                ||||   ||  ||  |||||||||
                                GGGG   TG  AT  GGGAGGAAC
                                  ATT  A_  GT
GAM145  DPP9     5'  CAAGGAGAACACCGGAAGTTGG 58230    T   G_  T
           A                     TC CAAT  CCG GTGTTCTCTTTG
                                || ||||  ||| ||||||||||||
                                AG GTTG  GGC CACAAGAGGAAC
                                 _   AA  _
GAM145  DRCTNNB1A 3'  CAAAGGGAGTCTGCATGTATGG 51808       A  C    __
           GA                    TCTCA TGC GTGTG  TTCTCTTTG
                                ||||| ||| |||||  |||||||||
                                AGGGT ATG TACGT  GAGGGAAAC
                                   _  _    CT
GAM145  E2-EPF   3'  CGGGGAGGGTACAGGGGGCACT 27948       A   G__   TT
           GGGA                   TCTCA TGCC   TGTG  CTCTTTG
                                ||||| ||||   ||||  |||||||
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                                AGGGT ACGG   ACAT  GAGGGGC
                                  C    GGG    GG
GAM145  EAT2     3'  AGGATATGGTGTTGGTGA    80046    _         G
                                TC TCAATGCCGTGT TT
                                || |||||||||||| ||
                                AG GGTTGTGGTATA GA
                                 T          G
GAM145  ELL2     5'  TGAAGGGAACAAGACCAATGAG 24898       A  CCGTG
              A                  TCTCA TG    TGTTCTCTTTG
                                ||||| ||    ||||||||||
                                AGAGT AC    ACAAGGGAAGT
                                  A  CAGA_
GAM145  EZFIT    3'  AGGAATGTGGTGTTGTGGA   41376    _      TG G
                                TCT CAATGCCG  T TTCT
                                ||| ||||||||  | ||||
                                AGG GTTGTGGT  A AGGA
                                  T       GT _
GAM145  EZFIT    5'  GGGGAGGGCGCGGCCTCGGGG  41380     AAT      G
                                TCTC   GCCGTGT TTCTCT
                                ||||   ||||||| ||||||
                                GGGG   CGGCGCG GAGGGG
                                  CTC      G
GAM145  FADS1    3'  CAAAGGTCAAGACTGTGGTATT 26372          GT_  G  C_
              GGGG                 TCTCAATGCC   GT TT  TCTTTG
                                ||||||||||   || ||  ||||||
                                GGGGTTATGG   CA AA  GGAAAC
                                     TGT  G  CT
GAM145  FADS1    3'  CAGAGGGGGTTGGGTTTGGGG  26375       T   GTGT TT
                                TCTCAA GCC    G  CTCTTTG
                                |||||| |||    |  |||||||
                                GGGGTT TGG    T  GGGAGAC
                                   _   GT__ GG
GAM145  FBXO26   3'  TGGGGAAATCTCTGGTGTTGGG 46632          TGTG_     TTG
              A                  TCTCAATGCCG     TTCTCT
                                ||||||||||     ||||||
                                AGGGTTGTGGT     AAGGGG
                                     CTCTA     T
GAM145  FBXO32   3'  TGGAGAGCTGGGAATATGGCAT 55244     C        _____      TTG
              TTGGA                TCT AATGCCGTGT    GTTCTCT
                                ||| ||||||||||     |||||||
                                AGG TTACGGTATA     CGAGAGG
                                  T         AGGGT      T   G
GAM145  FKBP14   3'  CAAGGAGGGTGGATCACTTGAG 36062       _  CC  G  TT
              A                  TCTCAA TG  GT TG  CTCTTTG
                                |||||| ||  || ||  |||||||
                                AGAGTT AC  TA GT  GAGGAAC
                                   C  __  G  GG
GAM145  FLJ00007 3'  GGAGAGGAACAGGCCTTGGGA  71779       T   G   G      G
                                TCTCAA GCC TGT TTCTCTTT
                                |||||| ||| ||| ||||||||
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                                AGGGTT CGG ACA AGGAGAGG
                                   C  _  _
GAM145  FLJ10035  3'  CAGGGAGAAATGATTGGATGTT 36211       _  TGTG_
          GAGG                   TCTCAATG CCG    TTCTCTTTG
                                 |||||||| |||    |||||||||
                                 GGAGTTGT GGT    AAGAGGGAC
                                    A   TAGTA
GAM145  FLJ10081  3'  CAGGGGGGATGTGTGTGATAGG 36287    AATGC_  TG
          AG                     CTC     CG  TGTTCTCTTTG
                                 |||     ||  ||||||||||
                                 GAG     GT  GTAGGGGGGAC
                                   GATAGT  GT
GAM145  FLJ10154  5'  CGAGGGGAACTGGCCGCGTGAG 36327      A   C  GT
          G                      TCTCA TGC GT  GTTCTCTTTG
                                 |||||| ||| ||  ||||||||||
                                 GGAGT GCG CG  CAAGGGGAGC
                                   _  C  GT
GAM145  FLJ10193  3'  TGAAGGGAACTACGCTTTGGGG 36351      T  C   T
                                 TCTCAA GC GTG GTTCTCTTTG
                                 |||||| || ||| ||||||||||
                                 GGGGTT CG CAT CAAGGGAAGT
                                    T  _  _
GAM145  FLJ10597  3'  AGGGAGGTGGGGGTTGGGG   36834      G  GTGTGT
                                 TCTCAAT CC     TCTCTTT
                                 ||||||| ||     |||||||
                                 GGGGTTG GG     GGAGGGA
                                    G  GT____
GAM145  FLJ10648  3'  GGAATCAGATGGTATTGAGA   36892         G  _
                                 TCTCAATGCCGT TG TTCT
                                 |||||||||||| || ||||
                                 AGAGTTATGGTA AC AAGG
                                       G  T
GAM145  FLJ10687  3'  TAAAGAGGATGTGCACTGAG   36949     A   CGT TG
                                 CTCA TGC   G  TTCTCTTTG
                                 |||| |||   |  |||||||||
                                 GAGT ACG   T  AGGAGAAAT
                                   C   ___ GT
GAM145  FLJ10751  3'  CGAGTTCATCTGTGGGTGTTGG 37109        GT___   TT   TTTG
          GG                     TCTCAATGCC    GTG  CTC
                                 ||||||||||    |||  |||
                                 GGGGTTGTGG    TAC  GAG
                                      GTGTC   TT   C
GAM145  FLJ10751  3'  CGAGTTCATCTGTGGGTGTTGG 37110        GT___   TT   TTTG
          GG                     TCTCAATGCC    GTG  CTC
                                 ||||||||||    |||  |||
                                 GGGGTTGTGG    TAC  GAG
                                      GTGTC   TT   C
GAM145  FLJ10826  5'  TAAAGGGGACATGCCGGGAG   37249     AATG  _
                                 CTC    CCG TGTGTTCTCTTTG
                                 |||    ||| ||||||||||||
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                                GAG    GGC GTACAGGGGAAAT
                                  _____  C
GAM145  FLJ10829  3'  CAGAGAGAATGTCACAGATGAG 37256      ATGCC  _
            G                    TCTCA    GTG TGTTCTCTTTG
                                 |||||    ||| ||||||||||
                                 GGAGT    CAC GTAAGAGAGAC
                                   AGA__   T
GAM145  FLJ10829  3'  CAGGGAGAGCATGGGCAATGGA 37257      AA_   G
            GA                   TCTC   TGCC TGTGTTCTCTTTG
                                 ||||   |||| ||||||||||||
                                 AGAG   ACGG GTACGAGAGGGAC
                                   GTA   _
GAM145  FLJ10898  3'  TGAAGGGAGTGCCTCTCTGGGA 60141      ATGCCGT TG
                                 TCTCA      G  TTCTCTTTG
                                 |||||      |  |||||||||
                                 AGGGT      C  GAGGGAAGT
                                   CTCTC__ GT
GAM145  FLJ11193  5'  CGGAGAGAGCTGGCCGGGTTGA 37747       G   T  __
            GG                   TCTCAAT CCG GT  GTTCTCTTTG
                                 ||||||| ||| ||  ||||||||||
                                 GGAGTTG GGC CG  CGAGAGAGGC
                                    _  _  GT
GAM145  FLJ11294  5'  GGAGGAGCGGGATTGAGA    37798       G   GTG
                                 TCTCAAT CCGT   TTCTCT
                                 ||||||| ||||   ||||||
                                 AGAGTTA GGCG   AGGAGG
                                    G   ____
GAM145  FLJ11320  3'  AGAATACGGTGGTTGAGA    37826       _     GT
                                 TCTCAAT GCCGTGT  TCT
                                 ||||||| |||||||  |||
                                 AGAGTTG TGGCATA  AGA
                                    G      __
GAM145  FLJ11526  5'  CGGGGGGAGCGAACTGTTGTG  45254    AT  C  G
                                 CA  GC GT TGTTCTCTTTG
                                 ||  || || ||||||||||
                                 GT  TG CA GCGAGGGGGGC
                                  GT  T  A
GAM145  FLJ11560  5'  GGAGACTGCTGTGTGTTGAGG  48011         _  T  GT
                                 TCTCAATGC CG GT  TCTCT
                                 |||||||| || ||  |||||
                                 GGAGTTGTG GT CG  AGAGG
                                      T  _  TC
GAM145  FLJ11598  3'  CGAGGGGGGTGAATGGTTGATG 46978    _  AT    G  TT
            A                    TC TCA  GCCGT TG  CTCTTTG
                                 || |||  ||||| ||  |||||||
                                 AG AGT  TGGTA GT  GGGGAGC
                                  T   __    A  GG
GAM145  FLJ11700  3'  CGAGGAGGGCAGATCACTTGAG 46561       _  CC  G
            A                    TCTCAA TG  GT TGTTCTCTTTG
                                 ||||||  ||  || ||||||||||
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                                AGAGTT AC  TA ACGGGAGGAGC
                                   C __  G
GAM145  FLJ11783  3'  GAGGGGGGAGGATGGCATGGGG 46549      A      GTG       G
            G                    TCTC ATGCCGT   TTCTCTTT
                                 |||| |||||||   ||||||||
                                 GGGG TACGGTA   GGGGGGAG
                                   G      GGA       A
GAM145  FLJ12089  5'  GGAGGAAGAGGCATTGAGG    44952          GTGTG
                                 TCTCAATGCC    TTCTCT
                                 ||||||||||    ||||||
                                 GGAGTTACGG    AGGAGG
                                       AGA__
GAM145  FLJ12242  3'  GGAGATTCAGGTATTGGGG    45500          G  TGT
                                 TCTCAATGCC TG   TCTCT
                                 |||||||||| ||   |||||
                                 GGGGTTATGG AC   AGAGG
                                       _  TT_
GAM145  FLJ12409  3'  GAAGGGACATGGTGTGGGGG   47770      A        G TC
                                 TCTC ATGCCGTGT T  TC
                                 |||| |||||||| |  ||
                                 GGGG TGTGGTACA G  AG
                                   G        G GA
GAM145  FLJ12529  3'  GAGACGTGGCATGTGAGA     46085      _        G
                                 TCTCA ATGCCGTGT TT
                                 ||||| |||||||| ||
                                 AGAGT TACGGTGCA AG
                                    G        G
GAM145  FLJ12547  3'  AGAGAGAGTGAACTGGGA     47126      ATGCC  G GT
                                 TCTCA    GT T  TCTCTTT
                                 |||||    || |  |||||||
                                 AGGGT    CA G  AGAGAGA
                                    _____  A TG
GAM145  FLJ12643  5'  GGGAGTGGGGCGTTGAGG     83673          G  TG
                                 TCTCAATGCC TG  TTCTC
                                 |||||||||| ||  |||||
                                 GGAGTTGCGG GT  GAGGG
                                       G  __
GAM145  FLJ12681  3'  AGAGGAGAGCGGTGGGA      43181      AAT    GTG
                                 TCTC   GCCGT   TTCTCT
                                 ||||   |||||   ||||||
                                 AGGG   TGGCG   AGGAGA
                                    ___     AG_
GAM145  FLJ12707  3'  CAGAGAGAGCTCTTCTTTGGGA 42201        TGCCGTGT
                                 TCTCAA       GTTCTCTTTG
                                 ||||||       ||||||||||
                                 AGGGTT       CGAGAGAGAC
                                    TCTTCT__
GAM145  FLJ12788  3'  TAGAGAGAAGGTATTGA      42849        GTGTG     TT
                                 TCAATGCC    TTCTCT  G
                                 ||||||||    ||||||  |
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                              AGTTATGG    GAGAGA  T
                                  AA___     G
GAM145  FLJ13153  3' GGGAGCACAGTATTGGGA    45923        CG
                              TCTCAATGC  TGTGTTCTC
                              |||||||||  |||||||||
                              AGGGTTATG  ACACGAGGG
                                  __
GAM145  FLJ13576  3' GGTATATATAAGGCGTTGGGA  42810         G    TCT
                              TCTCAATGCC TGTGT   CT
                              |||||||||| |||||   ||
                              AGGGTTGCGG ATATA   GG
                                    A    TAT
GAM145  FLJ13659  5' GACCTGCAGGTATTGGGA    48031         _  T
                              TCTCAATGCC GTG GTT
                              |||||||||| ||| |||
                              AGGGTTATGG CGT CAG
                                    A  C
GAM145  FLJ14009  3' AAGGGGGACATGGTGGAGG   45751     AAT  GT
                              TCTC   GCC  GTGTTCTCTTT
                              ||||   |||  ||||||||||||
                              GGAG   TGG  TACAGGGGGAA
                                G__   __
GAM145  FLJ14054  3' CGGAGAGAATGAGATGATGGTG 44966     C      _ ___
          TTCAGA                TCT AATGCCGT GT   GTTCTCTTTG
                              ||| ||||||||  ||   ||||||||||
                              AGA TTGTGGTA TA   TAAGAGAGGC
                                C       G  GAG
GAM145  FLJ14082  3' GGAGCGCCATGGTATGGGGA  47322      A      _
                              TCTC ATGCCGTG TGTTCT
                              |||| |||||||| ||||||
                              AGGG TATGGTAC GCGAGG
                                G       C
GAM145  FLJ14596  3' CAGAGGGGACATTTCCATGGAG 52511     A  CCGT
          A                    TCTC ATG    GTGTTCTCTTTG
                              |||| |||    ||||||||||||
                              AGAG TAC    TACAGGGGAGAC
                                G  CTT_
GAM145  FLJ14641  3' TAAAGGGAGGGGATGTTGGGA  52566        _ GTGTG
                              TCTCAATG CC    TTCTCTTTG
                              |||||||| ||    |||||||||
                              AGGGTTGT GG    GAGGGAAAT
                                   A  G____
GAM145  FLJ14681  3' AGAGAGAGATGTCTTGAGG   52592       T  CGTGTG
                              TCTCAA GC     TTCTCTTT
                              |||||| ||     ||||||||
                              GGAGTT TG     GAGAGAGA
                                 C  TA____
GAM145  FLJ20004  3' AGGGGAGAATGGCTTGGGG   34747       T    GTG
                              TCTCAA GCCGT   TTCTCT
                              |||||| |||||   ||||||
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                                GGGGTT CGGTA   AGGGGA
                                   _    AG_
GAM145  FLJ20038  3' AGAGAAGTATTGTATTGAGA  34861        C   G
                                TCTCAATGC GTGT TTCTCT
                                ||||||||| |||| ||||||
                                AGAGTTATG TATG AAGAGA
                                     T   _
GAM145  FLJ20174  5' GGGGGGATTCTCGGCGATGAGA 35193      A    TGT      TG
                                TCTCA TGCCG   GTTCTCTT
                                ||||| |||||   ||||||||
                                AGAGT GCGGC   TAGGGGGG
                                   A    TCT      T
GAM145  FLJ20288  5' GGAGGGGACGCGGCGCTGG   45446    A      G
                                TCA TGCCGTGT TTCTCT
                                ||| |||||||| ||||||
                                GGT GCGGCGCA GGGAGG
                                  C       G
GAM145  FLJ20320  3' CAAGGAGGATTCAAACTGTTGG 35417        CCG  T
           GG                     TCTCAATG   TG GTTCTCTTTG
                                ||||||||   || ||||||||||
                                GGGGTTGT   AC TAGGAGGAAC
                                     CAA  T
GAM145  FLJ20330  3' CAGAGGGATTACTGCGGTGTTA 39140    C      _  T
           AGG                    TCT AATGCCGT GTG TCTCTTTG
                                ||| |||||||| ||| ||||||||
                                GGA TTGTGGCG CAT AGGGAGAC
                                  A       T  T
GAM145  FLJ20507  3' AGAGGGAATCGCTGTTGGGA  35731       GCC  T      G
                                TCTCAAT   GTG GTTCTCTTT
                                |||||||   ||| |||||||||
                                AGGGTTG   CGC TAAGGGAGA
                                    T__  _       G
GAM145  FLJ20546  3' TGAAGGGGGAAGGTAGTGGGA  35815      A   GTGTG
                                TCTCA TGCC    TTCTCTTTG
                                ||||| ||||    |||||||||
                                AGGGT ATGG    GGGGGAAGT
                                   G   AA___
GAM145  FLJ20584  3' TGGGAGGACACAGCCTAGGA  35856    CAAT  CG       TT
                                TCT   GC  TGTGTTCTCT  G
                                |||   ||  |||||||||| |
                                AGG   CG  ACACAGGAGG  T
                                  ATC_ __        GG
GAM145  FLJ20986  5' CAGGGAGAGGGAGGGTGTTAGA 44835     _    GTGTG
           GA                     TCTC AATGCC    TTCTCTTTG
                                |||| ||||||    |||||||||
                                AGAG TTGTGG    GAGAGGGAC
                                  A     GAGG_
GAM145  FLJ21106  5' GGAGAGCGGCGGTGCTGGGA  47695      AT   G
                                TCTCA  GCCGT TGTTCTCT
                                |||||  ||||| ||||||||
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                                AGGGT  TGGCG GCGAGAGG
                                  CG    _
GAM145  FLJ21324  5' AAAGAGAGGAGGTTGAGA    92836      AT   GTGTG
                                TCTCA  GCC    TTCTCTTT
                                |||||  |||    ||||||||
                                AGAGT  TGG    GAGAGAAA
                                  __   AG___
GAM145  FLJ21324  5' GGGGAGGGTGGCTGTGGGA   92857      AT    TG G
                                TCTCA  GCCG  T TTCTCT
                                |||||  ||||  | ||||||
                                AGGGT  CGGT  G GAGGGG
                                  GT    __ G
GAM145  FLJ21709  3' AGGGAGAACTTTTTTGGGA   78477       TGCCGTGT
                                TCTCAA       GTTCTCTTT
                                ||||||       |||||||||
                                AGGGTT       CAAGAGGGA
                                   TTTT_____
GAM145  FLJ21777  5' TAAGGGGAATGAAATCGGTGAG 50850     AAT    TG__
          A                      TCTC   GCCG    TGTTCTCTTTG
                                 ||||   ||||    ||||||||||||
                                 AGAG   TGGC    GTAAGGGGAAT
                                   ___    TAAA
GAM145  FLJ21791  3' TAAAGAGAATATCTGGTGTTAG 62130    TC      T
          GA                     TC  AATGCCG GTGTTCTCTTTG
                                 ||  ||||||| ||||||||||||
                                 AG  TTGTGGT TATAAGAGAAAT
                                  GA      C
GAM145  FLJ21916  3' TGGGGAACACATGACATGA   43899     A  C         TT
                                 TCA TG CGTGTGTTCTCT  G
                                 ||| || ||||||||||||  |
                                 AGT AC GTACACAAGGGG  T
                                   _ A          G
GAM145  FLJ22029  3' CAAAGGGAAGAATGTGTGTGGG 46907       A  _   GTG
          G                      TCTCA TGC CGT   TTCTCTTTG
                                 ||||| ||| |||   |||||||||
                                 GGGGT GTG GTA   AAGGGAAAC
                                   _   T   AG_
GAM145  FLJ22329  3' GGAGGGGGCGCCAGTTGGAGA  45403      AAT  C_   G
                                 TCTC   GC  GTGT TTCTCT
                                 ||||   ||  |||| ||||||
                                 AGAG   TG  CGCG GGGAGG
                                   GT_  AC    G
GAM145  FLJ22378  3' CAGAGATGGGGCACGGGCATTG 47593          G      __
          GGG                      TCTCAATGCC TGTGTTC  TCTTTG
                                   |||||||||| |||||||  ||||||
                                   GGGGTTACGG GCACGGG  AGAGAC
                                          _      GT
GAM145  FLJ22378  3' GGGGAGGACGAGGATGTGGGA  47599       ATG  G   G
                                 TCTCA   CC TGT TTCTCT
                                 |||||   || ||| ||||||
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                                AGGGT   GG GCA GAGGGG
                                   GTA  A   G
GAM145  FLJ22386  3' GGAGGGCATGGTGTCGGGG   45042      A       G
                                TCTC ATGCCGTGT TTCT
                                |||| ||||||||| ||||
                                GGGG TGTGGTACG GAGG
                                  C       G
GAM145  FLJ22615  3' AGGGCTGCGTGCATTGAGG   69036        _   T
                                TCTCAATGC CGTG GTTCT
                                ||||||||| |||| |||||
                                GGAGTTACG GCGT CGGGA
                                      T   _
GAM145  FLJ22679  3' CAGGTCTCTGTGCACTGGTATT 35176         _   TG TCT__   TG
           GGGG                   TCTCAATGCC GTG  T    CTT
                                |||||||||| |||  |    |||
                                GGGGTTATGG CAC  G    GGA
                                      T   GT TCTCT   C
GAM145  FLJ22679  3' CAGGTCTCTGTGCACTGGTATT 50907         _   TG TCT__   TG
           GGGG                   TCTCAATGCC GTG  T    CTT
                                |||||||||| |||  |    |||
                                GGGGTTATGG CAC  G    GGA
                                      T   GT TCTCT   C
GAM145  FLJ22794  5' AGGGAGAGCAAGGTTGGAG   93238    AAT   GTG
                                CTC   GCC   TGTTCTCTTT
                                |||   |||   ||||||||||
                                GAG   TGG   ACGAGAGGGA
                                  GT_   A__
GAM145  FLJ23185  3' GGAGAGGATGAGGTTTGAGG   47520      T   GT  G
                                TCTCAA GCC  GT TTCTCT
                                |||||| |||  || ||||||
                                GGAGTT TGG  TA GAGAGG
                                   _   AG  G
GAM145  FLJ23277  3' TAAGGGGGGTGGTGGGTGGGA  50919      A_   GTGT TT
                                TCTCA  TGCC    G  CTCTTTG
                                |||||  ||||    |  |||||||
                                AGGGT  GTGG    T  GGGGAAT
                                   GG    ____ GG
GAM145  FLJ30058  3' AGACTGTATTGTATTGAGG    59301        C  GT T
                                TCTCAATGC GT  G TCT
                                |||||||| ||  | |||
                                GGAGTTATG TA  T AGA
                                      T  TG C
GAM145  FLJ31528  3' GTTTGGTGCATGTGGGTTGAGG 59035       G   TG   T  CTTTG
                                TCTCAAT CCG  TGT CT
                                ||||||| |||  ||| ||
                                GGAGTTG GGT  ACG GG
                                   _   GT   T  TTTGG
GAM145  FLJ32468  3' GGGGGTTGTGCGTTGGGG    59711        _  TGT TT
                                TCTCAATGC CG   G  CTC
                                |||||||| ||   |  |||
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                                GGGGTTGCG GT   T  GGG
                                      T ___ GG
GAM145  FTSJ3    3'  TAAAGGGAAGTTCGGTGTTGGA 34935    T      TGTG
                                TC CAATGCCG   TTCTCTTTG
                                || ||||||||   |||||||||
                                AG GTTGTGGC   AAGGGAAAT
                                 _      TTG_
GAM145  FXYD3    3'  TGGAGACTTCCTATGTGTGCAT 21061        _ TG  T____    TTG
           TGGGG                TCTCAATGC CG  TG    TCTCT
                                ||||||||| ||  ||    |||||
                                GGGGTTACG GT  AT    AGAGG
                                      T  GT  CCTTC    T
GAM145  G0S2     3'  CAGAGGGGGCGCGCGCACAGGA 32304     AA_  C
           G                    CTC   TGC GTGTGTTCTCTTTG
                                |||   ||| ||||||||||||||
                                GAG   ACG CGCGCGGGGGAGAC
                                 GAC  _
GAM145  G4       3'  TGAAGAGAGTGTGGGCTTTAGG 92643    TC  T   G  TG
           A                    TC  AA GCC TG  TTCTCTTTG
                                ||  || ||| ||  |||||||||
                                AG  TT CGG GT  GAGAGAAGT
                                 GA  T   _  GT
GAM145  GMPPB    5'  CGGGGCCGGGCACGGCGTTGGG 97444            ___    CTTTG
           A                    TCTCAATGCCGTGT   GTTCT
                                ||||||||||||||   |||||
                                AGGGTTGCGGCACG   CGGGG
                                       GGC    C
GAM145  GP3ST    3'  AGGGCTTCTGGGGCGTTGGGA  42407         G GT__
                                TCTCAATGCC T    GTTCT
                                ||||||||||| |    |||||
                                AGGGTTGCGG G    CGGGA
                                      G TCTT
GAM145  GPR64    3'  CAAGGGGAGTAGCTATTGGGA  20443        CC  GTG
                                TCTCAATG  GT   TTCTCTTTG
                                ||||||||  ||   |||||||||
                                AGGGTTAT  CG   GAGGGGAAC
                                     __  AT_
GAM145  GPR9     3'  CGGGGAGTACAAGGCATGGCGT 9486       A       G  ___
           AGAGG                    TCTC ATGCCGTGT TT   CTCTTTG
                                |||| |||||||| ||   |||||||
                                GGAG TGCGGTACG AA   GAGGGGC
                                  A        G  CAT
GAM145  GPS2     5'  CAAAGAGAGTGTGTGCTGGGG  88507      AT  CGT TG
                                TCTCA  GC   G  TTCTCTTTG
                                |||||  ||   |  |||||||||
                                GGGGT  TG   T  GAGAGAAAC
                                  CG  ___ GT
GAM145  GREB1    3'  AGAGCCCTCATGCTGTTGAGG  28555       GC    TGTT
                                TCTCAAT  CGTG    CTCT
                                |||||||  ||||    ||||
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                                GGAGTTG  GTAC    GAGA
                                    TC    TCCC
GAM145  GTPBP1    3'  GGAGGGGAATGGCGATGGGA   16268       A     GTG
                                TCTCA TGCCGT   TTCTCT
                                ||||| ||||||   ||||||
                                AGGGT GCGGTA   GGGAGG
                                   A     AG_
GAM145  GTSE1     3'  GGAGAGGGTGGGCTGAGG    33563       AT   GTG G
                                TCTCA  GCC   T TTCTCT
                                |||||  |||   | ||||||
                                GGAGT  CGG   G GAGAGG
                                   __  GT_ G
GAM145  HCRTR1    5'  GAAGGGAGTGGGCTGAGG    9512        AT   GTG GT
                                TCTCA  GCC   T  TCTCTTT
                                |||||  |||   |  |||||||
                                GGAGT  CGG   G  AGGGAAG
                                   __  ____ TG
GAM145  HEMGN     3'  CGGGGAGAGGATAGTGGTGGGA 37983      AAT   _   G
                                TCTC   GCCG TGT TTCTCTTTG
                                ||||   |||| ||| |||||||||
                                AGGG   TGGT ATA GAGAGGGGC
                                   ___   G   G
GAM145  HIC       3'  CAGGGAGAATGTGGCATTTGAG 68046        _    TG GT
              G                  TCTCAA TGCCG  T  TCTCTTTG
                                 |||||| |||||  |  ||||||||
                                 GGAGTT ACGGT  A  AGAGGGAC
                                    T    GT __
GAM145  HSPC055   3'  AGGATAATGTGCATTGAGA    27119         _  G
                                TCTCAATGC CGT TGTTCT
                                ||||||||| ||| ||||||
                                AGAGTTACG GTA ATAGGA
                                      T  _
GAM145  HSPF2     5'  CAAAGGGGGTGCTGATCTGGAG 19833      AATGC  T TG
              A                  TCTC    CG G  TTCTCTTTG
                                 ||||    || |  |||||||||
                                 AGAG    GT C  GGGGGAAAC
                                   GTCTA  _ GT
GAM145  HSU47926  3'  TGAAGAGGATGGTGGGGTTGGG 27311        G   TGT
              A                  TCTCAAT CCG   GTTCTCTTTG
                                 ||||||| |||   ||||||||||
                                 AGGGTTG GGT   TAGGAGAAGT
                                    G   GG_
GAM145  HSU79266  5'  TAAGGGGAGCGCGCGAAGCTGA 26145     AT  __
                                TCA  GC  CGTGTGTTCTCTTTG
                                |||  ||  ||||||||||||||
                                AGT  CG  GCGCGCGAGGGGAAT
                                  __  AA
GAM145  HUMNPIIY20 3'  AACTGCGCGGTGATGGGG    84321       A      _
                                TCTCA TGCCGTGT GTT
                                ||||| |||||||| |||
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                                GGGGT GTGGCGCG CAA
                                   A       T
GAM145  IL17D    3'  GAAGAGAGTGCACCGAGCA   57120     _ _ TG
                                TGC CG TG  TTCTCTTT
                                ||| || ||  ||||||||
                                ACG GC AC  GAGAGAAG
                                  A  C  GT
GAM145  IL18BP   5'  GGACTGGTATGGCATTGAG   20313          T__
                                CTCAATGCCGTG   GTTC
                                ||||||||||||   ||||
                                GAGTTACGGTAT   CAGG
                                       GGT
GAM145  ITGB8    3'  CAGAGAGAACAATGCTGTGAGA 11054      AT  CGTG
                                TCTCA  GC    TGTTCTCTTTG
                                |||||  ||    ||||||||||
                                AGAGT  CG    ACAAGAGAGAC
                                   GT  TA__
GAM145  KCNE4    3'  GGGGCCTGGGTGTTGGGG    55626         GTGT
                                TCTCAATGCC    GTTCT
                                |||||||||    |||||
                                GGGGTTGTGG    CGGGG
                                      GTC_
GAM145  KCNJ9    3'  ACCAGGGTGCATGGCTTGGGG  18362       T     TG    CTTTG
                                TCTCAA GCCGTG  TTCT
                                |||||| ||||||  ||||
                                GGGGTT CGGTAC  GGGA
                                   _     GT    CCAA
GAM145  KCNT1    3'  GACCACGTGGTGTGTGAGG    62490      _        T
                                TCTCA ATGCCGTGTG TC
                                ||||| |||||||||| ||
                                GGAGT TGTGGTGCAC AG
                                   G         C
GAM145  KCNV1    5'  TGGAGAGGGTGCGCCAAGGAGA 27658      AA  C  TG G     TTG
                                TCTC  TG CG  T TTCTCT
                                ||||  || ||  | ||||||
                                AGAG  AC GC  G GAGAGG
                                  GA  C  GT G     T
GAM145  KHDRBS1  3'  TGAAGAGGTTGATGGTGGTGGG 22664      AT    GTGT
           G                     TCTCA  GCCGT    TCTCTTTG
                                |||||  |||||   ||||||||
                                GGGGT  TGGTA    GGAGAAGT
                                   GG    GTT_
GAM145  KIAA0084 3'  AAAGAAAATGACATTGGGG   68702        C   GTGTTC
                                TCTCAATG CGT     TCTTT
                                |||||||| |||     |||||
                                GGGGTTAC GTA     AGAAA
                                    A   AA_____
GAM145  KIAA0144 3'  GGCCTGCGTGGCTTGGGG    29945       T       TT
                                TCTCAA GCCGTGTG  CT
                                |||||| ||||||||  ||
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                                GGGGTT CGGTGCGT  GG
                                   _       CC
GAM145  KIAA0252 3' TGGGGAGCGGGGATTGGG    63462       G  GTG       TT
                                CTCAAT CC   TGTTCTCT  G
                                |||||| ||   ||||||||  |
                                GGGTTA GG   GCGAGGGG  T
                                   G  ___       G
GAM145  KIAA0280 3' GGGGAGGGAGGGCATTGTGG   93308    T      GTGTG       G
                                TC CAATGCC     TTCTCTTT
                                || |||||||     ||||||||
                                GG GTTACGG     GGGAGGGG
                                 T      GA___
GAM145  KIAA0284 3' GGGGGAGCGGCACTGGGG     63805      A     GTG
                                TCTCA TGCCGT   TTCTCT
                                ||||| ||||||   ||||||
                                GGGGT ACGGCG   AGGGGG
                                   C     ___
GAM145  KIAA0318 5' CAGGGAGAGTATCTCCTGAGA  69527      ATGCCGT
                                TCTCA      GTGTTCTCTTTG
                                |||||      ||||||||||||
                                AGAGT      TATGAGAGGGAC
                                   CCTC___
GAM145  KIAA0321 5' GAGGAGCTGTTGTGTTGAGG   63052        CGTGT    T
                                TCTCAATGC     GTTC CTT
                                |||||||||     |||| |||
                                GGAGTTGTG     CGAG GAG
                                     TTGT_   _
GAM145  KIAA0451 5' GGGAGAGAAAATATAGTATTGA 29776        CG   G       G
           GA                     TCTCAATGC  TGT TTCTCTTT
                                |||||||||  |||  ||||||||
                                AGAGTTATG  ATA AAGAGAGG
                                     AT   A       GA
GAM145  KIAA0513 3' GGGAGAGAGTGGGTGCGGTGTA 29042      A     TG G__       G
           GAGG                    TCTC ATGCCG  T   TTCTCTTT
                                |||| ||||||  |   ||||||||
                                GGAG TGTGGC  G   GAGAGAGG
                                   A     GT GGT       GA
GAM145  KIAA0522 3' GGGGGAGGGTGGCAGTGGGA   72425      A     TG G
                                TCTCA TGCCG  T TTCTCTT
                                ||||| |||||  | |||||||
                                AGGGT ACGGT  G GAGGGGG
                                   G     __ G
GAM145  KIAA0556 3' CCTCTGGATGCAGGTGTTGGGG 69644          G      TCTTTG
                                TCTCAATGCC TGTGTTC
                                |||||||||| |||||||
                                GGGGTTGTGG ACGTAGG
                                     _      TCTCCC
GAM145  KIAA0556 3' GAGGGGAGCCCGCTGGGA    69650      ATGCC   T
                                TCTCA    GTG GTTCTCTTT
                                |||||    ||| |||||||||
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                                AGGGT    CGC CGAGGGGAG
                                  _____  C
GAM145  KIAA0574  3' GGGGGCTGCGGTGTGGGA    69821      A     T
                                TCTCA TGCCGTG GTTCTC
                                ||||| ||||||| ||||||
                                AGGGT GTGGCGT CGGGGG
                                  _     _
GAM145  KIAA0594  3' CAAGGGGAAAAAAGCACTGGGG 65508      A  CGTGTG
                                TCTCA TGC     TTCTCTTTG
                                ||||| |||     |||||||||
                                GGGGT ACG     AAGGGGAAC
                                   C  AAAA__
GAM145  KIAA0618  3' CAGAGGGAGCACATGGAGTAGA 29846    A  G
                                TC AT CCGTGTGTTCTCTTTG
                                || || ||||||||||||||||
                                AG TG GGTACACGAGGGAGAC
                                 A  A
GAM145  KIAA0637  3' AGAGACGTGGCATTTGGA    29920    C       TGT
                                TCT AATGCCGTG   TCTCT
                                ||| |||||||||   |||||
                                AGG TTACGGTGC   AGAGA
                                  T       ___
GAM145  KIAA0677  3' AAAGCTGCAGTATTGAGA    28526        CGTG   TCT
                                TCTCAATGC    TGT   CTTT
                                |||||||||    |||   ||||
                                AGAGTTATG    ACG   GAAA
                                     _____   TC_
GAM145  KIAA0685  3' TGGGGGGACATGGTGTGGCACT 28648      A    ___        TG
           GGGG                   TCTCA TGCCG   TGTGTTCTCTT
                                |||||  |||||   ||||||||||
                                GGGGT ACGGT   GTACAGGGGGG
                                   C    GTG         T
GAM145  KIAA0721  3' AGAGTTGGGGCATTGAGG    41648         G GTGTT
                                TCTCAATGCC T     CTCT
                                |||||||||| |     ||||
                                GGAGTTACGG G     GAGA
                                      G TT___
GAM145  KIAA0775  5' AGAGAGGATGGGGCTGAGG    28946      AT   G   G
                                TCTCA  GCC TGT TTCTCT
                                |||||  ||| ||| ||||||
                                GGAGT  CGG GTA GAGAGA
                                   __   G   G
GAM145  KIAA0794  3' CAGGGAGGGCACAGGGTA    81226      G
                                TGCC TGTGTTCTCTTTG
                                |||| ||||||||||||
                                ATGG ACACGGGAGGGAC
                                  G
GAM145  KIAA0830  3' TGAGAGAACACATGGTA     70272             TT
                                TGCCGTGTGTTCTCT  G
                                ||||||||||||||  |
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                                ATGGTACACAAGAGA  T
                                      GG
GAM145  KIAA0841 3' TGAGGGGGACAGTGTAGGTTGG 71907      AT   GTG__
            GG                  TCTCA  GCC    TGTTCTCTTTG
                                |||||  |||    ||||||||||
                                GGGGT  TGG    ACAGGGGGAGT
                                  __  ATGTG
GAM145  KIAA0888 3' CAGGGATTTAACTGTGGCATGT 63925      _    GT_  GT__    TTG
            GGGG                  TCTCA ATGCC   GT    TCTCT
                                |||||  |||||   ||    |||||
                                GGGGT TACGG   CA    AGGGA
                                  G    TGT  ATTT    C
GAM145  KIAA0984 3' CGGAGGGGATTGTGTCGTGTGA 66139      _  C  TGT
            GA                  TCTCA ATG CG   GTTCTCTTTG
                                |||||  ||| ||   ||||||||||
                                AGAGT TGC GT   TAGGGGAGGC
                                  G   T  GT_
GAM145  KIAA1032 3' GAGGAGCCTTGGGGTTGGGG   66726       G   TGT    T
                                TCTCAAT CCG   GTTC CTT
                                |||||||  |||   ||||  |||
                                GGGGTTG GGT   CGAG GAG
                                   G   TC_   _
GAM145  KIAA1061 3' CAGAGAGAACACATTTCGGCG  71717      ___
                                TGCCG   TGTGTTCTCTTTG
                                |||||   ||||||||||||||
                                GCGGC   ACACAAGAGAGAC
                                  TTT
GAM145  KIAA1091 3' CGGGGAGGCAGTCAATGGCATT 70260    T       GTGT__
            GTGA                  TC CAATGCCGT     TCTCTTTG
                                ||  |||||||||     ||||||||
                                AG GTTACGGTA     GGAGGGGC
                                 T        ACTGAC
GAM145  KIAA1136 3' CAAGGAGGACATGCTAGGGT   92956     ___
                                GCC   GTGTGTTCTCTTTG
                                |||   ||||||||||||||
                                TGG   CGTACAGGAGGAAC
                                  GAT
GAM145  KIAA1183 3' CGGAGGGGGTGTGTGTGTGGA  63190    A   _  TG G     TTG
                                TC ATGC CG  T TTCTCT
                                ||  ||||  ||  |  ||||||
                                AG TGTG GT  G GGGAGG
                                 G    T  GT G     C
GAM145  KIAA1271 3' ACTGGAACATGTGGTGCTTGGG 70125      _    TG     CTTTG
            A                   TCTCAA TGCCG  TGTTCT
                                ||||||  |||||  ||||||
                                AGGGTT GTGGT  ACAAGG
                                   C     GT     TCAC
GAM145  KIAA1274 3' TGAGAGACTGAGCGGAGTTGGG 93016       G   GTGT    TT
            A                   TCTCAAT CCGT    TCTCT  G
                                |||||||  ||||    |||||  |
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                                AGGGTTG GGCG   AGAGA  T
                                    A   AGTC    GG
GAM145  KIAA1285  3'  CAAGGAGAACAGAGTTGTAGAG 91979     AA   CG G_
            A                    TCTC  TGC  T  TGTTCTCTTTG
                                 ||||  |||  |  ||||||||||
                                 AGAG  ATG  G  ACAAGAGGAAC
                                   __   TT AG
GAM145  KIAA1297  5'  CGGGGAGGATGAGGACCATCGA 72636     A   __  GTGT
            GG                    TCTC ATG  CC   GTTCTCTTTG
                                  |||| |||  ||   ||||||||||
                                  GGAG TAC  GG   TAGGAGGGGC
                                    C   CA  AG__
GAM145  KIAA1303  3'  GGAGAGGCAGGCGCTGGGG   66607      A   G   G
                                  TCTCA TGCC TGT TTCTCT
                                  ||||| |||| ||| ||||||
                                  GGGGT GCGG ACG GAGAGG
                                     C   _  _
GAM145  KIAA1317  3'  AGATCATATGGTATTGTGA   87207   T        T
                                  TC CAATGCCGTGTG TCT
                                  || ||||||||||| |||
                                  AG GTTATGGTATAC AGA
                                   T         T
GAM145  KIAA1318  3'  ACTACAAGAGTGTATGGTGTAT 67873      _      TG   CTTTG
            GAGG                    TCTCA ATGCCGTG  TTCT
                                  ||||| ||||||||  ||||
                                  GGAGT TGTGGTAT  GAGA
                                     A       GT   ACATCAG
GAM145  KIAA1336  3'  TGAAGGGAGTAGGGAGTGGGG  72789      ATG  G  TG
                                  TCTCA   CC TG  TTCTCTTTG
                                  |||||   || ||  |||||||||
                                  GGGGT   GG AT  GAGGGAAGT
                                     GA_  G  __
GAM145  KIAA1340  3'  TAAAGAGGATATATTATTTAGA 69698     C   CC
                                  TCT AATG  GTGTGTTCTCTTTG
                                  ||| ||||  ||||||||||||||
                                  AGA TTAT  TATATAGGAGAAAT
                                    T   __
GAM145  KIAA1458  5'  GGGGGGACCCTGGCGGTGGGG  69572      A    TGT
                                  TCTCA TGCCG   GTTCTCTT
                                  ||||| |||||   ||||||||
                                  GGGGT GCGGT   CAGGGGGG
                                     G    CC_
GAM145  KIAA1465  5'  GAGGGGCCACCGCGGCTTGGGG 61497       T    _  TT    TG
                                  TCTCAA GCCGTG TG  CTCTT
                                  |||||| |||||| ||  |||||
                                  GGGGTT CGGCGC AC  GGGAG
                                     _     C  CG    T
GAM145  KIAA1522  3'  AGAGGGGATGTGGTGAGA    65603      AAT    TG G
                                  TCTC   GCCG  T TTCTCT
                                  ||||   ||||  | ||||||
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                                AGAG   TGGT  A GGGAGA
                                  ___    GT G
GAM145  KIAA1705  5'  TAGAGGGCGGCGGCGTTGA   72856          G       TT
                                TCAATGCCGT TGTTCTCT  G
                                |||||||||| ||||||||  |
                                AGTTGCGGCG GCGGGAGA  T
                                      _       G
GAM145  KIAA1737  5'  TGAGGAGGGGGGCTGCGTGTGGG 67949      _    CGT  G
          G                     TCTCA ATGC   GT TTCTCTTTG
                                ||||| ||||   || |||||||||
                                GGGGT TGCG   CG GGGAGGAGT
                                   G    T__  G
GAM145  KIAA1765  3'  TGAAGGGAATAAGCTCCTTGGG 71135       TGCC  G
          G                     TCTCAA    GT TGTTCTCTTTG
                                ||||||    || ||||||||||
                                GGGGTT    CG ATAAGGGAAGT
                                    CCT_  A
GAM145  KIAA1808  3'  CAGACAACCACACGCTGTTGGG 87047        GC     _  C   TTG
          G                     TCTCAAT  CGTGTG TT TCT
                                |||||||  |||||| || |||
                                GGGGTTG  GCACAC AA AGA
                                     TC     C  C   C
GAM145  KIAA1813  5'  AGAGAGGTTGGCAGTGGGG    70821       A     TGTGT
                                TCTCA TGCCG     TCTCTTT
                                ||||| |||||     |||||||
                                GGGGT ACGGT     GGAGAGA
                                   G    T_____
GAM145  KIAA1841  5'  TAAGGAGAATAAAGATTGTGA  80856    T    GCCGTG
                                TC CAAT      TGTTCTCTTTG
                                || ||||      ||||||||||
                                AG GTTA      ATAAGAGGAAT
                                 T   GAA___
GAM145  KIAA1879  5'  GGAGACACATGTGTTGAGG    73942         C     T
                                TCTCAATGC GTGTGT CTCT
                                ||||||||| |||||| ||||
                                GGAGTTGTG TACACA GAGG
                                      _     _
GAM145  KIAA1879  3'  TGAAGAGAGTGGACGATGAGG  73947       ATGC   G GT
                                TCTCA    CGT T  TCTCTTTG
                                |||||    ||| |  ||||||||
                                GGAGT    GCA G  AGAGAAGT
                                   A___   G TG
GAM145  KIAA1913  5'  GGGGCTTTATGGCGTGAGG    74319       A      T_
                                TCTCA TGCCGTG  GTTCT
                                ||||| |||||||  |||||
                                GGAGT GCGGTAT  CGGGG
                                   _      TT
GAM145  KIAA1932  3'  TAGGGAGACACCTGTGTTGAGG 73825         CGT    T
                                TCTCAATGC   GTGT CTCTTTG
                                |||||||||   |||| |||||||
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                                GGAGTTGTG  CACA GAGGGAT
                                    TC_  _
GAM145  KIAA1944  3'  ACGTGCAGGGCGTGTGGAGTTG 76075      G  TG    CTTTG
            GGG                   TCTCAAT CCG  TGTTCT
                                  ||||||| |||  ||||||
                                  GGGGTTG GGT  GCGGGA
                                     A  GT    CGTGCAA
GAM145  KIAA1969  5'  GACCTGCAGGTATTGGGA   79478        _  T
                                  TCTCAATGCC GTG GTT
                                  |||||||||| ||| |||
                                  AGGGTTATGG CGT CAG
                                     A  C
GAM145  KIAA1987  3'  TAGAGGGGATTGGCTTTGGGG  89390     T   TGT
                                  TCTCAA GCCG  GTTCTCTTTG
                                  |||||| ||||  ||||||||||
                                  GGGGTT CGGT  TAGGGGAGAT
                                     T  ____
GAM145  KIF13B   3'  GACACTAATGGTGTTGGGG   83717         __
                                  TCTCAATGCCGT  GTGTT
                                  ||||||||||||  |||||
                                  GGGGTTGTGGTA  CACAG
                                        AT
GAM145  KIF13B   3'  GACACTAATGGTGTTGGGG   31564         __
                                  TCTCAATGCCGT  GTGTT
                                  ||||||||||||  |||||
                                  GGGGTTGTGGTA  CACAG
                                        AT
GAM145  KPTN     5'  CGGAGAGGGTGCTTAACTGAGG 73805     ATGCCGT TG
                                  TCTCA      G  TTCTCTTTG
                                  |||||      |  |||||||||
                                  GGAGT      C  GGGAGAGGC
                                     CAATT__ GT
GAM145  KREMEN   3'  TGAGGAGGGTGGATCACTTGAG 50239      _  CC  G  TT
            G                     TCTCAA TG  GT TG  CTCTTTG
                                  |||||| ||  || ||  |||||||
                                  GGAGTT AC  TA GT  GAGGAGT
                                     C  __  G  GG
GAM145  LSM10    3'  CAGAATCCTATATGTGGCCTTG 52867      T   TG   TC___   TTG
            GGG                   TCTCAA GCCG  TGT    TCT
                                  |||||| ||||  |||    |||
                                  GGGGTT CGGT  ATA    AGA
                                     C   GT   TCCTA   C
GAM145  MAD4     3'  TGAGGGGGGCGTGCGCTAGAGG 22280     AA  C  TG
            GG                    TCTC  TG CG  TGTTCTCTTTG
                                  ||||  || ||  ||||||||||
                                  GGGG  AT GC  GCGGGGGGAGT
                                     AG  C  GT
GAM145  MADP-1   3'  AGGTGGGTATATGGTAATGGGA 53576      A       TT T   TG
                                  TCTCA TGCCGTGTG  C CTT
                                  ||||| |||||||||  | |||
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                                AGGGT ATGGTATAT  G GGA
                                   A       GG T   C
GAM145  MAGEB2   3' AGAAAATGTGGCATTAGA    11428     C      TG G
                                TCT AATGCCG  T TTCT
                                ||| |||||||  | ||||
                                AGA TTACGGT  A AAGA
                                  _      GT A
GAM145  MANBAL   3' AGGGAGAGGGTCTTGGGG    42214       T   GTGTG
                                TCTCAA GCC    TTCTCTTT
                                |||||| |||    ||||||||
                                GGGGTT TGG    GAGAGGGA
                                   C  _____
GAM145  MAP2K5   3' CAGAGAGGTAAAGGGTGGGGCA 12325          G GTGT____
           TTGAGA                  TCTCAATGCC T       TCTCTTTG
                                |||||||||| |       ||||||||
                                AGAGTTACGG G       GGAGAGAC
                                      G TGGGAAAT
GAM145  MDS024   3' CAAAGGGGATAGAAAAATGGGA 41818      ATGCCGTG
                                TCTCA       TGTTCTCTTTG
                                |||||       ||||||||||
                                AGGGT       ATAGGGGAAAC
                                   AAAAAG__
GAM145  MGC10715 3' CAGGGAGAATCTGCATGTGGGG 44496      ATGC    __
                                TCTCA   CGTGT  GTTCTCTTTG
                                |||||   |||||  ||||||||||
                                GGGGT   GTACG  TAAGAGGGAC
                                   _____    TC
GAM145  MGC14161 3' CAGAGGGGACACTAGTTGA   52907      GCCGT
                                TCAAT    GTGTTCTCTTTG
                                |||||    ||||||||||||
                                AGTTG    CACAGGGGAGAC
                                   AT___
GAM145  MGC14407 3' AAAGAGATAGGTAATGGGG   52964      A   GTGTGT
                                TCTCA TGCC     TCTCTTT
                                ||||| ||||     |||||||
                                GGGGT ATGG     AGAGAAA
                                   A   AT_____
GAM145  MGC14859 3' TGAAGAGGGTGCAGCCTGGGA 62605      AT  CG  TG
                                TCTCA  GC  TG  TTCTCTTTG
                                |||||  ||  ||  |||||||||
                                AGGGT  CG  AC  GGGAGAAGT
                                   C_  __  GT
GAM145  MGC21738 3' TAGAGAGGACTGGAATATAGAG 59579     A  __  T  G    TTG
           G                     TCTC ATG  CCG GT TTCTCT
                                |||| |||  ||| || ||||||
                                GGAG TAT  GGT CA GAGAGA
                                  A  AA  _ G    T
GAM145  MGC35521 3' CAGAGGGAGCTCTGCATGTGGG 59663      _   CGTGT
           A                     TCTCA ATGC    GTTCTCTTTG
                                ||||| ||||    ||||||||||
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                                AGGGT TACG    CGAGGGAGAC
                                  G   TCT__
GAM145  MGC4606  3'  TAGAGAGAGTGTGTGAGTGT  44794     _  TG GT
                                ATGC CG  T  TCTCTTTG
                                |||| ||  |  ||||||||
                                TGTG GT  G  AGAGAGAT
                                  A  GT TG
GAM145  MGC5149  3'  AGGGTCTCATCGTGTTGAGA  72753        C   TGTT
                                TCTCAATGC GTG   CTCT
                                |||||||||| |||   ||||
                                AGAGTTGTG TAC   GGGA
                                     C   TCT_
GAM145  MGC7036  3'  AGGAAAATGTGCTATTGAGA  59614       _ _  GTG
                                TCTCAAT GC CGT   TTCT
                                ||||||| || |||   ||||
                                AGAGTTA CG GTA   AGGA
                                    T  T   AA_
GAM145  MMPL1    3'  AAGGGATATGGCTTGAGG    15959      T     TGT
                                TCTCAA GCCGTG   TCTCTT
                                |||||| ||||||   ||||||
                                GGAGTT CGGTAT   AGGGAA
                                  _     ____
GAM145  MPZL1    5'  GGGGAGCGCGGCGTGGAGG   15538     A       GT
                                TCTC ATGCCGTGT  TCTCT
                                |||| |||||||||  |||||
                                GGAG TGCGGCGCG  AGGGG
                                  G       __
GAM145  NAP1L1   3'  AGGATGTATGTGGCCTTGAGG  58301      T   __  TG
                                TCTCAA GCC  GTG  TTCT
                                |||||| |||  |||  ||||
                                GGAGTT CGG  TAT  AGGA
                                   C   TG   GT
GAM145  NAP1L1   3'  TAAAGGGGATGTGGTTTGCAGA 58302    _  T   GT TG
                                TCT CAA GCC  G  TTCTCTTTG
                                ||| ||| |||  |  |||||||||
                                AGA GTT TGG  T  AGGGGAAAT
                                  C  _  __ GT
GAM145  NASP     3'  GAAGAGGAGGAGATTGGGA   68577      G_  GTGTG
                                TCTCAAT  CC    TTCTCTTT
                                |||||||  ||    ||||||||
                                AGGGTTA  GG    AGGAGAAG
                                    GA  _____
GAM145  NETO1    5'  GGCTGCGCGGCGCTGAGG    58050     A      _
                                TCTCA TGCCGTGT GTT
                                ||||| |||||||| |||
                                GGAGT GCGGCGCG CGG
                                  C       T
GAM145  NIBAN    3'  GGAGGGAATAGTATTGCAGG  42239     _     CGTG       G
                                TCT CAATGC    TGTTCTCTTT
                                ||| ||||||    ||||||||||
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                                GGA GTTATG    ATAAGGGAGG
                                  C     ____        A
GAM145  NUCKS    3'  TAGGGAGGGTGGGCAATGGGG  43004      A    GTG  TT
                                TCTCA TGCC   TG  CTCTTTG
                                ||||| ||||   ||  |||||||
                                GGGGT ACGG   GT  GAGGGAT
                                   A    ___  GG
GAM145  NUDT5    3'  GTGGAACACAGGGGTATTTGGT 27094          _________       CTTTG
            ATTGAGA                 TCTCAATGCCG       TGTGTTCT
                                ||||||||||        ||||||||
                                AGAGTTATGGT       ACACAAGG
                                      TTATGGGG       T   GT
GAM145  NXPH2    5'  GGAGGGGCTGGATTGGGA    73095       G   T  G
                                TCTCAAT CCG GT TTCTCT
                                ||||||| ||| || ||||||
                                AGGGTTA GGT CG GGGAGG
                                   _   _  _
GAM145  PADI1    3'  GAAGAGGGTGTGTGTGTTGGGA 62702         C TG  TT     G
                                TCTCAATGC G  TG  CTCTTT
                                ||||||||| |  ||  ||||||
                                AGGGTTGTG T  GT  GAGAAG
                                     _ GT  GG
GAM145  PAPOLB   5'  GAAGGTCGCGGTGGTGGGG   39719      AT     _ G
                                TCTCA  GCCGTG T TTC
                                |||||  |||||| | |||
                                GGGGT  TGGCGC G AAG
                                   GG     T G
GAM145  PCAF     5'  CGAAGGGGGCGGGAGGGCGTGG 15284     A    GTG_
            GGG                   TCTC ATGCC    TGTTCTCTTTG
                                |||| |||||    ||||||||||
                                GGGG TGCGG    GCGGGGGAAGC
                                  G    GAGG
GAM145  PCDH10   5'  TAGAGGGAAAGAGGCTTGGGA  53103       T   GTGTG
                                TCTCAA GCC     TTCTCTTTG
                                |||||| |||    |||||||||
                                AGGGTT CGG     AAGGGAGAT
                                   _   AGA__
GAM145  pcnp     3'  AGAGAGGGAGTATTGTATTGGG 40141         C   TG      G
            A                    TCTCAATGC GTG  TTCTCTTT
                                |||||||| |||  ||||||||
                                AGGGTTATG TAT  GGGAGAGA
                                     T   GA       G
GAM145  PCNT2    3'  AAGGAGGATACACAGAGA    21227      AATGCC
                                TCTC     GTGTGTTCTCTTT
                                ||||     ||||||||||||
                                AGAG     CACATAGGAGGAA
                                  A_____
GAM145  PDIP     3'  CAGAGGGAGCTGTGCATTGTGA 23393    T     CGTGT
                                TC CAATGC     GTTCTCTTTG
                                || ||||||     ||||||||||
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                                AG GTTACG    CGAGGGAGAC
                                 T     TGT__
GAM145  PIGQ    3'  GGAGGGGGCCGTGGCACTGAGG 16104      A      T       G
                                TCTCA TGCCGTG GTTCTCTTT
                                ||||| ||||||| |||||||||
                                GGAGT ACGGTGC CGGGGGAGG
                                   C      _       G
GAM145  PLCL2   3'  CGAGGAGAATGTGCAATTGG  68696      GCC TG
                                TCAAT  G  TGTTCTCTTTG
                                |||||  |  ||||||||||
                                GGTTA  C  GTAAGAGGAGC
                                   A__ GT
GAM145  PLEKHA3  5'  CCGGGAGGATGCGCGGTGTGGG 39380      A            TG
           G                     TCTCA TGCCGTGTGTTCTCTT
                                |||||| ||||||||||||||||
                                GGGGT GTGGCGCGTAGGAGGG
                                   _            CCG
GAM145  PNMA5   3'  GGGGGGGCCACACTGAGG   73976      ATGCC    TT
                                TCTCA    GTGTG  CTCTTT
                                |||||    |||||  ||||||
                                GGAGT    CACAC  GGGGGG
                                   _____    CG
GAM145  PP2447   5'  TGAAGGGAGCTACCTTTGAGA  48101       TGCC   T
                                TCTCAA    GTG GTTCTCTTTG
                                ||||||   ||| ||||||||||
                                AGAGTT    CAT CGAGGGAAGT
                                   TC__  _
GAM145  PPP1R13B  3'  CAAGGAGGGCGCTTCACTGAGG 31654      A  CCGT
                                TCTCA TG   GTGTTCTCTTTG
                                ||||| ||   ||||||||||||
                                GGAGT AC    CGCGGGAGGAAC
                                   C  TT__
GAM145  PPP1R13B  3'  GGAGGGTGGTTGGGGTTGGGG  31658       G   TG  TT
                                TCTCAAT CCG  TG  CTCT
                                ||||||| |||  ||  ||||
                                GGGGTTG GGT  GT  GAGG
                                    G   TG  GG
GAM145  PPP2R2A   3'  TAAAGGGGGTATATGTTGCA   12237     __     TT
                                TGC  CGTGTG  CTCTTTG
                                |||  ||||||  |||||||
                                ACG  GTATAT  GGGAAAT
                                  TT     GG
GAM145  PRAX-1   3'  TAGAGAGAGCAACATGACTGGG 17659      ATGC    _
           G                     TCTCA    CGTGT GTTCTCTTTG
                                |||||    ||||| ||||||||||
                                GGGGT    GTACA CGAGAGAGAT
                                   CA__     A
GAM145  PRO1843   5'  AGGGGGGACAAGGTAGGGG   38138     AA   G   G
                                TCTC  TGCC TGT TTCTCT
                                ||||  |||| ||| ||||||
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                                GGGG  ATGG ACA GGGGGA
                                  __   A  G
GAM145  PRO2015  3'  CAAAGGCAGGCGGTGCTGAGG  38156      AT    G   TCT
                                TCTCA  GCCGT TGT   CTTTG
                                |||||  ||||| |||   |||||
                                GGAGT  TGGCG ACG   GAAAC
                                   CG    G  ___
GAM145  PRO2714  3'  CAAGAGGTGTGGCATTGAGA   38191          TG GTT    T
                                TCTCAATGCCG  T   CTCT TG
                                ||||||||||  |  |||| ||
                                AGAGTTACGGT  G   GAGA AC
                                      GT ___    T
GAM145  PTPRN2   3'  TGAAGAGAAACCTCCGGTGTGA 56448      A    TGTG_
           GA                     TCTCA TGCCG    TTCTCTTTG
                                |||||  |||||    |||||||||
                                AGAGT GTGGC    AAGAGAAGT
                                  _    CTCCA
GAM145  PTPRT    3'  GGAGGGGGCACTATTAGGA   56504    TC   CC   G
                                TC  AATG  GTGT TTCTCT
                                ||  ||||  |||| ||||||
                                AG  TTAT  CACG GGGAGG
                                 GA   __   G
GAM145  RAB3-GAP150 5'  TGGAGGGGGCAGGGCGTGGTGA 25766      __    G  G    TTG
           GG                     TCTCA  ATGCC TGT TTCTCT
                                |||||  ||||| ||| ||||||
                                GGAGT  TGCGG ACG GGGAGG
                                   GG    G  G    T
GAM145  RAB3IL1  5'  GGGGACGCGGCGCTGGGA    26368      A      G
                                TCTCA TGCCGTGT TTC
                                ||||| |||||||| |||
                                AGGGT GCGGCGCA GGG
                                   C      G
GAM145  RASD2    3'  GGAGGGGACACGATGAGCA   27464    _  _
                                TGC CGT GTGTTCTCTTT
                                ||| ||| ||||||||||
                                ACG GTA CACAGGGGAGG
                                  A  G
GAM145  REC14    3'  CAAAGAGAATGTACGGATTGA  48217      G    TG
                                TCAAT CCGTG  TTCTCTTTG
                                |||||  |||||  |||||||||
                                AGTTA GGCAT  AAGAGAAAC
                                  _    GT
GAM145  RNAHP    3'  CGGGGAGAACAGACATGG    24778      __
                                CCGTGT  GTTCTCTTTG
                                ||||||  ||||||||||
                                GGTACA  CAAGAGGGGC
                                   GA
GAM145  RNF25    3'  GGGGGGAACAGGGAATTGGGG  42629       G  G  G
                                TCTCAAT CC TGT TTCTCTT
                                ||||||| || ||| |||||||
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                                GGGGTTA GG ACA AGGGGGG
                                   A  G  _
GAM145  RNF9     5'  AGAGAGAGTGGCCTTGAGG   23233       T   TGTG
                                TCTCAA GCCG   TTCTCTTT
                                ||||||| ||||   ||||||||
                                GGAGTT CGGT   GAGAGAGA
                                   C  _____
GAM145  RODH-4   3'  GTGAAGATCCCTGTACACGTGG 14925             TC_____
           TGTTGGGA                TCTCAATGCCGTGTGT     TCTTTG  T
                                ||||||||||||||||     ||||||  |
                                AGGGTTGTGGTGCACA     AGAAGT  G
                                          TGTCCCT
GAM145  SAMP14   5'  GAGGGACGCAGGGCGTTGGGA  56866         G     T
                                TCTCAATGCC TGTGTTC CTT
                                |||||||||| ||||||| |||
                                AGGGTTGCGG ACGCAGG GAG
                                      G     _
GAM145  SAS10    3'  TAAAGAGAATGCATCTTTGA  40155     TGCC
                                TCAA   GTGTGTTCTCTTTG
                                ||||   ||||||||||||||
                                AGTT   TACGTAAGAGAAAT
                                  TC__
GAM145  SDC3     5'  AAAGAGAGGGGGTTGGGA    28459       G  GTGTG
                                TCTCAAT CC    TTCTCTTT
                                ||||||| ||    ||||||||
                                AGGGTTG GG    GAGAGAAA
                                   G  _____
GAM145  SEC15B   5'  CGGAGGGGACGCGCTGCGGGG  67263     AA   C
                                CTC  TGC GTGTGTTCTCTTTG
                                |||  ||| ||||||||||||||
                                GGG  GCG CGCGCAGGGGAGGC
                                  __   T
GAM145  SELB     3'  TGAGGGGGATGGGTTGCTGGGG 62594      AT  CG G
                                TCTCA  GC  T TGTTCTCTTTG
                                |||||  ||  | ||||||||||
                                GGGGT  CG  G GTAGGGGGAGT
                                   __  TT G
GAM145  SEMA4C   3'  CAGAGGGAGTGCAGGGCTTGGG 35531       T   G  TG
           G                     TCTCAA GCC TG  TTCTCTTTG
                                ||||||| ||| ||  |||||||||
                                GGGGTT CGG AC  GAGGGAGAC
                                   _  G  GT
GAM145  SFXN5    3'  GGGGGTGCCATGGTGTTGGA  58655    T       T  T
                                TC CAATGCCGTG GT CTCTT
                                || ||||||||| || |||||
                                AG GTTGTGGTAC CG GGGGG
                                  _        _ T
GAM145  SIAT8C   3'  TAAAGGGAATGTTGCATTTGGG 32451       _  CGT TG
           A                     TCTCAA TGC   G  TTCTCTTTG
                                |||||| |||   |  |||||||||
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                                AGGGTT ACG   T  AAGGGAAAT
                                   T   T__ GT
GAM145  SLC2A10  5'  GGCGGCAGCGGCGTTGGGG   48557          G   TC
                                TCTCAATGCCGT TGT  TC
                                |||||||||||| |||  ||
                                GGGGTTGCGGCG ACG  GG
                                       _   GC
GAM145  SMOC1    3'  GGGGGAGGGTGTTGTTGGGG  42414        CC TG G
                                TCTCAATG  G  T TTCTCTT
                                ||||||||  |  | |||||||
                                GGGGTTGT  T  G GAGGGGG
                                     __ GT G
GAM145  SPBPBP   5'  AAGGGAGATAGGTATTGAGA  22926         G   G
                                TCTCAATGCC TGT TTCTCTT
                                |||||||||| ||| |||||||
                                AGAGTTATGG ATA GAGGGAA

                                       _  _
GAM145  SPINK4   3'  GGAGAGGATATGACATGA    27876     A  C     G
                                TCA TG CGTGT TTCTCT
                                ||| || ||||| ||||||
                                AGT AC GTATA GAGAGG
                                  _ A    G
GAM145  SPRY4    3'  AGGGGCAGGGTGTGGTTTGGGG 48994       T    TG G  _     TG
                                TCTCAA GCCG  T TT CTCTT
                                |||||| ||||  | || |||||
                                GGGGTT TGGT  G GA GGGGA
                                    _   GT G  C     C
GAM145  ST7L     3'  TGAGGAGAATACACAGGATTTG 35342      TG  _
           A                     TCAA  CC GTGTGTTCTCTTTG
                                 ||||  || ||||||||||||||
                                 AGTT  GG CACATAAGAGGAGT
                                   TA  A
GAM145  STX12    3'  TAAAGGGAACATAATTTGTTTA 66952     C    CCG
           GG                    TCT AATG   TGTGTTCTCTTTG
                                 ||| ||||   ||||||||||||
                                 GGA TTGT   ATACAAGGGAAAT
                                   T    TTA
GAM145  TCEB3L   3'  CAAAGTCAATGCGGGTTGGGG  33566        G     GTTCT
                                TCTCAAT CCGTGT     CTTTG
                                ||||||| ||||||     |||||
                                GGGGTTG GGCGTA     GAAAC
                                    _      ACT__
GAM145  TCL6     3'  GGAGGGACTGGGGTGTGGAGA  40483      A     G GTG
                                TCTC ATGCC T   TTCTCT
                                |||| ||||| |   ||||||
                                AGAG TGTGG G   GGGAGG
                                  G     G TCA
GAM145  TEX27    3'  GGGGGGGGTGGGGGGTGGGG   41954      A G  G  TG
                                TCTCA T CC TG  TTCTCT
                                ||||| | || ||  ||||||
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                                GGGGT G GG GT  GGGGGG
                                  _ G  G  GG
GAM145  TIX1     3'  GGTGGCACATGGGTGTTGGGG  62410          _     TC
                                TCTCAATGCC GTGTGT  TC
                                |||||||||| ||||||  ||
                                GGGGTTGTGG TACACG  GG
                                     G     GT
GAM145  TMG3     3'  TGGGAGGGTGGGGGTAGGGA  44224      A  G  GTG  TT    TT
                                TCTC AT CC   TG  CTCT  G
                                |||| || ||   ||  ||||  |
                                AGGG TG GG   GT  GAGG  T
                                  A  G  ___  GG   GG
GAM145  TNKS1BP1  5'  AAGAGTTGAGGATATGGCTGTT 54146        _     G  T_   G
            GGGA                  TCTCAAT GCCGTGT TTC  CTTT
                                |||||||  |||||||  |||  ||||
                                AGGGTTG CGGTATA GAG  GAGA
                                     T      G   TT    AG
GAM145  TOR2A    3'  TGAGGAGGACACAGGCCTGGGA 56190       AT   G
                                TCTCA  GCC TGTGTTCTCTTTG
                                |||||  |||  |||||||||||||
                                AGGGT  CGG ACACAGGAGGAGT
                                  C_  _
GAM145  TRAF4    3'  AAGGGGGTGGGAATTGGGG   63317        G  GTG  TT
                                TCTCAAT CC   TG  CTCTT
                                |||||||  ||   ||  |||||
                                GGGGTTA GG   GT  GGGAA
                                     A  ___  GG
GAM145  TREX1    5'  GGGGGGAACGGATGGTGGTGAG 50613       AT    G        G
            A                    TCTCA  GCCGT TGTTCTCTTT
                                |||||  |||||  ||||||||||
                                AGAGT  TGGTA GCAAGGGGGG
                                  GG    G        G
GAM145  TREX1    5'  GGGGGGAACGGATGGTGGTGAG 50614       AT    G        G
            A                    TCTCA  GCCGT TGTTCTCTTT
                                |||||  |||||  ||||||||||
                                AGAGT  TGGTA GCAAGGGGGG
                                  GG    G        G
GAM145  TREX1    5'  GGGGGGAACGGATGGTGGTGAG 50615       AT    G        G
            A                    TCTCA  GCCGT TGTTCTCTTT
                                |||||  |||||  ||||||||||
                                AGAGT  TGGTA GCAAGGGGGG
                                  GG    G        G
GAM145  TRIM26   3'  AGACATACACGGCTTTGGGG   14342        T       _
                                TCTCAA GCCGTGTGT TCT
                                ||||||  |||||||||  |||
                                GGGGTT CGGCACATA AGA
                                     T        C
GAM145  TRIM7    3'  CAGGGCTCGGTGTGTGTGGTGT 54041     T       TG  TT  ___
            TGGA                   TC CAATGCCG  TG  CT   CTTTG
                                ||  ||||||||  ||  ||   |||||
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                                AG GTTGTGGT  GT  GG   GGGAC
                                 _       GT  GT  CTC
GAM145  UBE2E1   3'  CAGGGAGGGTGGGAGTTGG   13947      G  GTG  TT
                                TCAAT CC   TG  CTCTTTG
                                ||||| ||   ||  |||||||
                                GGTTG GG   GT  GAGGGAC
                                  A ____ GG
GAM145  UHRF1    3'  AGAAACTACGTGGTGTGGAGG  26123      A       _  C
                                TCTC ATGCCGTGT GTT TCT
                                |||| ||||||||| ||| |||
                                GGAG TGTGGTGCA CAA AGA
                                  G       T  _
GAM145  UPB1     3'  CAGGGGGAGAGTGGCATGGGGA 33345      A     TGTG
                                TCTC ATGCCG    TTCTCTTTG
                                |||| ||||||    |||||||||
                                AGGG TACGGT    GAGGGGGAC
                                  G     GA__
GAM145  WNT8A    3'  CAGGGAGAGTTTGGTTTGGGG  50031       T   TGTG
                                TCTCAA GCCG    TTCTCTTTG
                                ||||||| ||||    |||||||||
                                GGGGTT TGGT    GAGAGGGAC
                                  _    TT__
GAM145  ZDHHC5   5'  GTGTGGGAGTGGTGGCATTGAG 93189          TGTG    TTTG
           A                     TCTCAATGCCG    TTCTC
                                ||||||||||    |||||
                                AGAGTTACGGT    GAGGG
                                      GGT_     TGTGG
GAM145  ZDHHC7   3'  CAGAAGCGTGTGCGCCGTTGGG 35318        _ _ TG   C   TTG
           G                     TCTCAATG C CG  TGTT TCT
                                |||||||| | ||  |||| |||
                                GGGGTTGC G GT  GCGA AGA
                                    C C  GT   _  C
GAM145  ZNF304   3'  TGAGGAGGGCATAGTTGGT   40684      __
                                GCCG  TGTGTTCTCTTTG
                                ||||  ||||||||||||
                                TGGT  ATACGGGAGGAGT
                                  TG
GAM145  ZNF313   3'  AAAATGAGCCATGGCATTGGGA 38562           T   TC  G
                                TCTCAATGCCGTG GTTC  TTT
                                |||||||||||| ||||  |||
                                AGGGTTACGGTAC CGAG  AAA
                                      _   TA
GAM145  ZNF333   5'  CAGGGAGAACACCGACTGAGA  51589      ATGC  T
                                TCTCA   CG GTGTTCTCTTTG
                                |||||   || ||||||||||||
                                AGAGT   GC CACAAGAGGGAC
                                  CA__  _
GAM145  ZNF384   3'  TGAAGGGGGCAAGGGCTGAGA  56797      AT  GTG
                                TCTCA  GCC   TGTTCTCTTTG
                                |||||  |||   ||||||||||
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                                AGAGT  CGG   ACGGGGGAAGT
                                  __   GA_
GAM145   LOC116437 5'  CAGGGAGGACGCGCGGTGCGGG 74324      AAT
                A                  TCTC   GCCGTGTGTTCTCTTTG
                                   ||||   ||||||||||||||||
                                   AGGG   TGGCGCGCAGGAGGGAC
                                     CG_
GAM145   LOC120114 3'  GATGACATATGGCATTGG     76046            C
                                   TCAATGCCGTGTGTT TC
                                   |||||||||||||| ||
                                   GGTTACGGTATACAG AG
                                              T
GAM145   LOC121504 3'  GAGGGGGGCGGGGTGGGGG    74546      A  G    GTG
                                   TCTC AT CCGT   TTCTCTT
                                   |||| || ||||   |||||||
                                   GGGG TG GGCG   GGGGGAG
                                     G  G   ___
GAM145   LOC122970 3'  CAAGGGGGGCATATTGCTTGAG 74638       T  C
                                   CTCAA GC GTGTGTTCTCTTTG
                                   ||||| || ||||||||||||||
                                   GAGTT CG TATACGGGGGGAAC
                                     _  T
GAM145   LOC123872 5'  TAAAGGTTTTGATCGCATTGAG 74711          C  GTGTT T
                A                  TCTCAATGC GT     C CTTTG
                                   |||||||||  ||     |  |||||
                                   AGAGTTACG TA     G GAAAT
                                        C  GTTTT _
GAM145   LOC124460 3'  GTCCCCAGCGTGTTGGTGTTGG 76567           _ TG    CTCTTTG
                GA                   TCTCAATGCC G  TGTT
                                   ||||||||||  |  ||||
                                   AGGGTTGTGG T  GCGA
                                         T GT    CCCCTGT
GAM145   LOC126402 5'  GCCAGGACACACGCGTTGGGG  76206          C        CTTTG
                                   TCTCAATGC GTGTGTTCT
                                   |||||||||  |||||||||
                                   GGGGTTGCG CACACAGGA
                                        _        CCGA
GAM145   LOC126823 5'  AGAGCGCGGTGTGTGGGA     75078       _        GT
                                   TCTCA ATGCCGTGT  TCT
                                   |||||  |||||||||  |||
                                   AGGGT TGTGGCGCG  AGA
                                     G        __
GAM145   LOC126964 3'  GGGGAGGGTTTTGGTGGGA    75118      AAT    TGT TT
                                   TCTC   GCCG   G  CTCTTT
                                   ||||   ||||   |  ||||||
                                   AGGG   TGGT   T  GAGGGG
                                     ___    TT_ GG
GAM145   LOC126964 3'  TAAAGGGAAGAGTGTGGTGAGA 75119      AAT    TG G_
                                   TCTC   GCCG  T  TTCTCTTTG
                                   ||||   ||||  |  |||||||||
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                                AGAG  TGGT  G  AAGGGAAAT
                                  ___   GT AG
GAM145  LOC127534 3'  TGAGGAGGGTGGCTGTGGGG  75972      AT  GTGT TT
                                TCTCA  GCC   G  CTCTTTG
                                |||||  |||   |  |||||||
                                GGGGT  CGG   T  GAGGAGT
                                  GT  ____ GG
GAM145  LOC127559 3'  CGAAGAAAACATGGCATTGAG  75170          GTTC
                                CTCAATGCCGTGT   TCTTTG
                                ||||||||||||   ||||||
                                GAGTTACGGTACA   AGAAGC
                                       AA__
GAM145  LOC127696 5'  GGAGCATTCCACGTATTGGGA  75981        C  ___
                                TCTCAATGC GTG  TGTTCT
                                |||||||| |||  ||||||
                                AGGGTTATG CAC  ACGAGG
                                     _  CTT
GAM145  LOC127841 5'  AGAGAGGGCAGTGTGGAGG   75183     A   CGTG
                                TCTC ATGC   TGTTCTCTTT
                                |||| ||||   ||||||||||
                                GGAG TGTG   ACGGGAGAGA
                                  G  ____
GAM145  LOC128954 5'  CAGGGAGGACATGAATGAG   76300     ATGCCG
                                CTCA    TGTGTTCTCTTTG
                                ||||    ||||||||||||
                                GAGT    GTACAGGAGGGAC
                                  AA____
GAM145  LOC130026 3'  TAGAGAGAGTAAGATTTGAGA  57440      TGCCGTG
                                TCTCAA     TGTTCTCTTTG
                                ||||||     ||||||||||
                                AGAGTT     ATGAGAGAGAT
                                   TAGA___
GAM145  LOC130470 5'  TGAGGGGGGTCCAAGGCTTGGG 75443      T  G  TG
          G                     TCTCAA GCC TG  TTCTCTTTG
                                |||||| ||| ||  |||||||||
                                GGGGTT CGG AC  GGGGGGAGT
                                   _  A  CT
GAM145  LOC130576 3'  AAAGAGAGCTACGTTTGGG   75457     TGC   T
                                CTCAA  CGTG GTTCTCTTT
                                |||||  |||| |||||||||
                                GGGTT  GCAT CGAGAGAAA
                                  T__   _
GAM145  LOC132112 3'  GAGGAGAGACGTGGGTTGAGA  75534      G    G     G
                                TCTCAAT CCGTGT TTCTCTTT
                                ||||||| |||||| ||||||||
                                AGAGTTG GGTGCA GAGAGGAG
                                     _    _
GAM145  LOC138649 5'  TGGGGGGATGGCGGATTTGGGG 75876      TG   G     TT
                                TCTCAA  CCGT TGTTCTCT  G
                                ||||||  |||| ||||||||  |
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                                GGGGTT  GGCG GTAGGGGG  T
                                   TA   _       GG
GAM145   LOC142779 3'  CAGAGAGAAATGTGCATGGGA  76901      A  _  GTG
                                TCTCA TGC CGT   TTCTCTTTG
                                ||||| ||| |||   |||||||||
                                AGGGT ACG GTA   AAGAGAGAC
                                  _  T  ___
GAM145   LOC143110 3'  TGAAGTTTACGTATGGCATGGG 76786      A        TCT
            A                    TCTCA TGCCGTGTGT   CTTTG
                                ||||| ||||||||||   |||||
                                AGGGT ACGGTATGCA   GAAGT
                                  _        TTT
GAM145   LOC143437 5'  TGGAGGGTCGCTGTTTGAGA   83859      T  C   T TT   TT
                                TCTCAA GC GTG G  CTCT  G
                                |||||| || ||| |  ||||  |
                                AGAGTT TG CGC T  GAGG  T
                                   _ T  _ GG   G
GAM145   LOC143524 3'  AGGGGGGAAATATGGTATGAGA 77093      A      G      G
                                TCTCA TGCCGTGT TTCTCTTT
                                ||||| |||||||| ||||||||
                                AGAGT ATGGTATA AGGGGGGA
                                  _       A       A
GAM145   LOC144110 3'  AAGGGGAGCAAGGATGGGA   77186      ATG  GTG
                                TCTCA   CC   TGTTCTCTTT
                                |||||   ||   ||||||||||
                                AGGGT   GG   ACGAGGGGAA
                                  A__  A__
GAM145   LOC144233 3'  GGAGAGGGCTGCTTTTGGGG   77247      T_  CGT  G
                                TCTCAA  GC   GT TTCTCT
                                ||||||  ||   || ||||||
                                GGGGTT  CG   CG GAGAGG
                                   TT  T__  G
GAM145   LOC144512 5'  AGCTGCATGGCATTAAGG    84036     C        _
                                TCT AATGCCGTGT GTT
                                ||| |||||||||| |||
                                GGA TTACGGTACG CGA
                                  A        T
GAM145   LOC145333 5'  AGAGGATGGTATCTGAGG    84286      _    GTGT
                                TCTCA ATGCC    GTTCTCT
                                ||||| |||||    |||||||
                                GGAGT TATGG    TAGGAGA
                                  C    _____
GAM145   LOC145601 3'  GGGGAGGGCTGTGCTGGGG   84354      AT  _  T  G
                                TCTCA  GC CG GT TTCTCT
                                |||||  || || || ||||||
                                GGGGT  CG GT CG GAGGGG
                                  __  T  _  G
GAM145   LOC145601 3'  TGGAGGGGGCTGGTTGGGA   84357      AT    T  G     TT
                                TCTCA  GCCG GT TTCTCT  G
                                |||||  |||| || ||||||  |
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                                AGGGT  TGGT CG GGGAGG  T
                                  __   _ G     G
GAM145  LOC145663 3'  CAGAACTTGATGCGTGGCATTA 84417     C        _____     CTTTG
                GA                  TCT AATGCCGTGT     GTTCT
                                |||  ||||||||||     |||||
                                AGA TTACGGTGCG     CAAGA
                                  _        TAGTT     C   G
GAM145  LOC145693 5'  TAGAGAGCACAGGACTGGGA   77857      ATG  G        TT
                                TCTCA   CC TGTGTTCTCT  G
                                |||||   ||  ||||||||||  |
                                AGGGT   GG ACACGAGAGA  T
                                   CA_  _         G
GAM145  LOC145989 3'  GGGGGGGTAGGGGTGTGGGGG  60295      A    GTG  TT
                                TCTC ATGCC   TG  CTCTT
                                ||||  |||||   ||  |||||
                                GGGG TGTGG   AT  GGGGG
                                   G    GG_  GG
GAM145  LOC145990 3'  GAGGAGAACTTCTTTGAGA    78057       TGCCGTGT
                                TCTCAA       GTTCTCTTT
                                ||||||       |||||||||
                                AGAGTT       CAAGAGGAG
                                    TCTT____
GAM145  LOC146138 3'  CAGGGAGGGAACTGGCTTTGAG 84589       T   T  G
                A                   TCTCAA GCCG GT TTCTCTTTG
                                ||||||  ||||  ||  |||||||||
                                AGAGTT CGGT CA GGGAGGGAC
                                    T   _  A
GAM145  LOC146268 3'  TGGAGAGGGCAGCTGGTGTTAA 78345     C      TG       TT
                GA                  TCT AATGCCG  TGTTCTCT  G
                                |||  |||||||  ||||||||  |
                                AGA TTGTGGT  ACGGGAGA  T
                                  A      CG       GG
GAM145  LOC146517 3'  GGAGAAGGATGGCACTGGGG   78508      A     GTG
                                TCTCA TGCCGT   TTCTCT
                                |||||  ||||||   ||||||
                                GGGGT ACGGTA   AAGAGG
                                   C     GG_
GAM145  LOC146667 5'  AGAGGGGCAGGGTTGGGA    84705      AT   G   G
                                TCTCA  GCC TGT TTCTCT
                                |||||  |||  |||  ||||||
                                AGGGT  TGG ACG GGGAGA
                                   __   G   _
GAM145  LOC146957 3'  TGGAGGGCTGTTGCTTGAGG   78819       T  CGTGT      TT
                                TCTCAA GC    GTTCTCT  G
                                ||||||  ||    |||||||  |
                                GGAGTT CG    CGGGAGG  T
                                   _  TTGT_      G
GAM145  LOC146990 5'  GAGGGGGGTGCGGCGCCTTGG  84955      __     TG G      TG
                                TCAA  TGCCG  T TTCTCTT
                                ||||  |||||  |  |||||||
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                                GGTT  GCGGC  G GGGGGAG
                                  CC    GT _     T
GAM145  LOC147341 5'  GAGGGGGAGTGGGTGTGTGAGG 85118     _    GTGTG     TG
                                TCTCA ATGCC    TTCTCTT
                                ||||| |||||    |||||||
                                GGAGT TGTGG    GGGGGAG
                                   G    GTGA_     T
GAM145  LOC147650 5'  AGGGACATGGTGTTGCGG    79015    T       TGT
                                TC CAATGCCGTG   TCTCT
                                || ||||||||||   |||||
                                GG GTTGTGGTAC   AGGGA
                                 C        ___
GAM145  LOC147650 5'  CAGGGAGGATAGAGACTTGGGA 79016       TGCCGTG
                                TCTCAA      TGTTCTCTTTG
                                ||||||      ||||||||||
                                AGGGTT      ATAGGAGGGAC
                                   CAGAG__
GAM145  LOC148066 3'  CAGGGAGGGGGGGTGCAATGAGG 79321      A   CGTGTG
                                TCTCA TGC     TTCTCTTTG
                                ||||| |||     |||||||||
                                GGAGT ACG     GGGAGGGAC
                                   A   TGGG__
GAM145  LOC148132 5'  GGAGAGGAAAGCACTGGGA    85256      A   CGTGTG
                                TCTCA TGC     TTCTCTTT
                                ||||| |||     ||||||||
                                AGGGT ACG     AGGAGAGG
                                   C   AA____
GAM145  LOC148148 5'  GACCTGCAGGTATTGGGA    79379          _   T
                                TCTCAATGCC GTG GTT
                                |||||||||| ||| |||
                                AGGGTTATGG CGT CAG
                                      A   C
GAM145  LOC148203 5'  GACCTGCAGGTATTGGGA    79460          _   T
                                TCTCAATGCC GTG GTT
                                |||||||||| ||| |||
                                AGGGTTATGG CGT CAG
                                      A   C
GAM145  LOC148206 5'  GACCTGCAGGTATTGAGA    79462          _   T
                                TCTCAATGCC GTG GTT
                                |||||||||| ||| |||
                                AGAGTTATGG CGT CAG
                                      A   C
GAM145  LOC148343 5'  CGAGGGGGGTGTGTGCGCCTGG 79543      AT  _  TG  TT
                  GG                TCTCA  GC CG  TG  CTCTTTG
                                ||||||  || ||  ||  |||||||
                                GGGGT  CG GT  GT  GGGGAGC
                                   C_  C  GT  GG
GAM145  LOC148397 3'  GGGGAGGCTGAGGTGTGAGG   79572      A    GT_  G
                                TCTCA TGCC   GT TTCTC
                                ||||| ||||   || |||||
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                                GGAGT GTGG   CG AGGGG
                                  _    AGT  G
GAM145   LOC148697 3'  AGAGAGAAAAGAATTGAGA   79672       GCCGTGTG
                                TCTCAAT       TTCTCTTT
                                |||||||       ||||||||
                                AGAGTTA       AAGAGAGA
                                   AGAA____
GAM145   LOC149506 5'  TAGAGAGCGTGGGTGGG     85648     AAT   G GT      TT
                                CTC   GCC T  GTTCTCT  G
                                |||   ||| |  ||||||| |
                                GGG   TGG G  CGAGAGA  T
                                  ____  _ TG      G
GAM145   LOC149603 3'  TGAGGAGGACTTTGATTGGGA  71177       GC  TGT
                                TCTCAAT  CG   GTTCTCTTTG
                                |||||||  ||   ||||||||||
                                AGGGTTA  GT   CAGGAGGAGT
                                   __ TT_
GAM145   LOC149650 3'  CAGAGGGAACTCCCTGTTGGA  80284    T   GCCGTGT
                                TC CAAT      GTTCTCTTTG
                                || ||||      ||||||||||
                                AG GTTG      CAAGGGAGAC
                                 _   TCCCT__
GAM145   LOC149668 5'  CAGGGAGAATGTGAAGCTGGGG 85696      AT  CG  TG
                                TCTCA  GC  TG  TTCTCTTTG
                                |||||  ||  ||  |||||||||
                                GGGGT  CG  GT  AAGAGGGAC
                                  __ AA  GT
GAM145   LOC149837 3'  GGTACCAATGGCATTGAGA   85903          GT  T
                                TCTCAATGCCGT  GT CT
                                ||||||||||||  || ||
                                AGAGTTACGGTA  CA GG
                                       AC  T
GAM145   LOC149995 5'  GGGGGGGGCAGGTTAGGGG   85987     AAT   G   G
                                CTC   GCC TGT TTCTCT
                                |||   ||| ||| ||||||
                                GGG   TGG ACG GGGGGG
                                  GAT   _   G
GAM145   LOC150157 5'  AGAAGATGTGGCAATGGGA   86018      A     TG G
                                TCTCA TGCCG  T TTCT
                                ||||| |||||  | ||||
                                AGGGT ACGGT  A AAGA
                                   A     GT G
GAM145   LOC150159 3'  CAAGAAAATGGATATGGTGTTG 58259            __  C    TG
            AGG                    TCTCAATGCCGTGT  GTT TCTT
                                ||||||||||||||  ||| ||||
                                GGAGTTGTGGTATA  TAA AGAA
                                       GG   A    C
GAM145   LOC150244 5'  TGAAGAGGGCGTCTGCTGGAGA 80553      AAT  C TG
                                TCTC   GC G  TGTTCTCTTTG
                                ||||   || |  ||||||||||
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                                AGAG   CG T  GCGGGAGAAGT
                                  GT_  _ CT
GAM145  LOC150481 5'  GGAGCTCCTGTGTGTTGAGG   80708         _  TGT
                                TCTCAATGC CG   GTTCT
                                |||||||||  ||   |||||
                                GGAGTTGTG GT   CGAGG
                                     T  CCT
GAM145  LOC150519 5'  TGGAGTCCCACACGCTGTTGAG 80733        GC     TT_   TTG
              G                  TCTCAAT  CGTGTG   CTCT
                                |||||||  ||||||   ||||
                                GGAGTTG  GCACAC   GAGG
                                    TC     CCT    T
GAM145  LOC150606 3'  CAAAGAGAGCAGATATTTGG   86266      TGCC  G
                                TCAA    GT TGTTCTCTTTG
                                ||||    || ||||||||||
                                GGTT    TA ACGAGAGAAAC
                                  TA__  G
GAM145  LOC151040 3'  TGAAGCATCCTATGGCATTCAG 80909     C       ___     CTCTTTG
              A                  TCT AATGCCGT   GTGTT
                                ||| ||||||||   |||||
                                AGA TTACGGTA   TACGA
                                  C       TCC     AGT   G
GAM145  LOC151056 3'  TGGAGGGAGGGTGTTGGA    80926    T      GTGTG     TT
                                TC CAATGCC     TTCTCT  G
                                || |||||||    ||||||  |
                                AG GTTGTGG     GGGAGG  T
                                  _      GA___      G
GAM145  LOC151124 5'  AGGGAGGGCGGGGGTTGTGG   86414    T   G  G   G
                                TC CAAT CC TGT TTCTCT
                                || |||| || ||| ||||||
                                GG GTTG GG GCG GAGGGA
                                 T   G  _   G
GAM145  LOC151154 5'  TAGGGAGGGCTGACCGCATTGT 86423    T     C  GT
              GG                   TC CAATGC GT  GTTCTCTTTG
                                || |||||| ||  ||||||||||
                                GG GTTACG CA  CGGGAGGGAT
                                 T     C  GT
GAM145  LOC151278 3'  TGAGGGAGCATGCGGCA     81013             TT
                                TGCCGTGTGTTCTCT  G
                                ||||||||||||||  |
                                ACGGCGTACGAGGGA  T
                                        GG
GAM145  LOC151304 3'  CAGGGAGAGCTGACCATTGAGG 86498        CC  GT
                                TCTCAATG  GT  GTTCTCTTTG
                                ||||||||  ||  ||||||||||
                                GGAGTTAC  CA  CGAGAGGGAC
                                    __  GT
GAM145  LOC151507 3'  TAGAGGGAATCCATATTGA   81062      GCC   TG
                                TCAAT   GTG  TTCTCTTTG
                                |||||   |||  |||||||||
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                                AGTTA  TAC  AAGGGAGAT
                                  ___  CT
GAM145  LOC151904 3'  TAAAGAGGATGTGCAGGCTGGG 81209     AT  _ TG
                                CTCA  GCC G  TGTTCTCTTTG
                                ||||  ||| |  ||||||||||
                                GGGT  CGG C  GTAGGAGAAAT
                                  __  A GT
GAM145  LOC152274 3'  GAGGGGAGCAGGTGTGGGGA  81342     A    GTG       G
                                TCTC ATGCC  TGTTCTCTTT
                                |||| |||||  ||||||||||
                                AGGG TGTGG  ACGAGGGGAG
                                  G   ___
GAM145  LOC152445 3'  AGCTCATGTGGTTGTTGGGA  86930       _  TG  TT
                                TCTCAATG CCG  TG  CT
                                |||||||| |||  ||  ||
                                AGGGTTGT GGT  AC  GA
                                     T  GT  TC
GAM145  LOC152453 5'  TGAAGTGTGTGTGTAGCATTGG 81482       CG  TG TCT
          GG                    TCTCAATGC  TG  T  CTTTG
                                |||||||||  ||  |  |||||
                                GGGGTTACG  GT  G  GAAGT
                                     AT  GT TGT
GAM145  LOC152633 5'  TAGAGGGGACGACGGGCTGGGG 86998     ATG   G
                                TCTCA  CCGT TGTTCTCTTTG
                                |||||  |||| ||||||||||
                                GGGGT  GGCA GCAGGGGAGAT
                                  CG_  _
GAM145  LOC152897 3'  GCCACACTGTATTGAGA    81606       C    TT
                                TCTCAATGC GTGTG  C
                                |||||||| |||||  |
                                AGAGTTATG CACAC  G
                                     T   CG
GAM145  LOC152905 3'  CAGAGGGAATATGCACTGGCG  61093     _  __
                                TGCC GTGT  GTTCTCTTTG
                                |||| ||||  ||||||||||
                                GCGG CACG  TAAGGGAGAC
                                  T   TA
GAM145  LOC153222 5'  CGAGGAGGATGTTGATGATGAG 81660     A GC  T TG
          G                     TCTCA T  CG G  TTCTCTTTG
                                ||||| |  || |  |||||||||
                                GGAGT G  GT T  AGGAGGAGC
                                  A TA  _ GT
GAM145  LOC153338 3'  TGGGAGGACAATCAGTAGAGG  87201     AA  CGTG     TT
                                TCTC  TGC   TGTTCTCT  G
                                ||||  |||   ||||||||  |
                                GGAG  ATG   ACAGGAGG  T
                                  __  ACTA      GG
GAM145  LOC153577 5'  GGAGAGGGCAGGGTGATGGGG  87242     A   G  G
                                TCTCA TGCC TGT TTCTCT
                                ||||| |||| ||| ||||||
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                                GGGGT GTGG ACG GAGAGG
                                   A   G  G
GAM145  LOC153987 5'  AGAGGCCATGACATTGGGG   81919       C   T  T
                                TCTCAATG CGTG GT CTCT
                                |||||||| |||| || ||||
                                GGGGTTAC GTAC CG GAGA
                                    A   _ _
GAM145  LOC154092 3'  TGGTCCTGCACGTGGGGTGTTG 87375        G__   TCT_  TTG
           GGG                   TCTCAATGCC  TGTGT   CT
                                |||||||||   |||||   ||
                                GGGGTTGTGG  GCACG   GG
                                      GGT   TCCT  T
GAM145  LOC154222 3'  CAGGGAGAATGTCTGGTTGTGA 87389    AT   T TG
                                TCA  GCCG G  TTCTCTTTG
                                |||  |||| |  |||||||||
                                AGT  TGGT T  AAGAGGGAC
                                  GT   C GT
GAM145  LOC155066 5'  TGAGGAGAACGCGTGCTGAGG  82212     AT  CGT
                                TCTCA  GC   GTGTTCTCTTTG
                                |||||  ||   ||||||||||||
                                GGAGT  TG   CGCAAGAGGAGT
                                   CG  ___
GAM145  LOC155435 3'  GGAGGGAGCATGGCGCTAGGG  82268    AA_      G
                                CTC   TGCCGTGT TTCTCT
                                |||   |||||||| ||||||
                                GGG   GCGGTACG GGGAGG
                                  ATC       A
GAM145  LOC157349 5'  CAGGGTCGTGCGTGGCGGTGGG 82329     A     TG T_   TTG
           G                   TCTCA TGCCGTG  T  CTCT
                                ||||| |||||||  |  ||||
                                GGGGT GCGGTGC  G  GGGA
                                   G      GT CT   C
GAM145  LOC157773 5'  AGAGCTGATGGCATTGAGA   82506         GT
                                TCTCAATGCCGT  GTTCT
                                ||||||||||||  |||||
                                AGAGTTACGGTA  CGAGA
                                       GT
GAM145  LOC158062 3'  GGGGGAAGTGGCATTTGGG   87965      _   TGTG
                                CTCAA TGCCG   TTCTCT
                                ||||| |||||   ||||||
                                GGGTT ACGGT   AGGGGG
                                   T    GA__
GAM145  LOC158078 3'  AGCCCATGTGTGTTGAGA    82599        _   T
                                TCTCAATGC CGTG GTT
                                ||||||||| |||| |||
                                AGAGTTGTG GTAC CGA
                                      T   C
GAM145  LOC158191 3'  CAGAGCAGGGTATGGTGGTGGG 82667     AT    ___     CTTTG
           G                   TCTCA  GCCGTG   TGTTCT
                                |||||  ||||||   ||||||
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                                GGGGT  TGGTAT   ACGAGA
                                  GG     GGG     C
GAM145   LOC158364 3'  TAAAGAGGGCGTAAGCAATAGA 82757      AA_   CG
           GG                     TCTC   TGC  TGTGTTCTCTTTG
                                  ||||   |||  ||||||||||||
                                  GGAG   ACG  ATGCGGGAGAAAT
                                    ATA   A_
GAM145   LOC158527 5'  TGAAGATCTCTGACATGGTGCT 82841       AT      GTTC__
           GAGA                    TCTCA  GCCGTGT     TCTTTG
                                  ||||||  |||||||      ||||||
                                  AGAGT  TGGTACA      AGAAGT
                                    CG      GTCTCT
GAM145   LOC159160 3'  AGGAGAGTACATGGCATTGAGA 61151                  TG
                                  TCTCAATGCCGTGTGTTCTCTT
                                  |||||||||||||||||||||
                                  AGAGTTACGGTACATGAGAGGA
                                                C
GAM145   LOC160484 5'  CAAGGTGTTGCCGCCGGTGTTG 83091           T   TTCT__
           GGG                     TCTCAATGCCG GTG     CTTTG
                                  ||||||||||| |||      |||||
                                  GGGGTTGTGGC CGC      GGAAC
                                        _   CGTTGT
GAM145   LOC160484 5'  TGGACAACTATGTGAGGCGTTG 83092          GTGT___   C   TTG
           GGA                     TCTCAATGCC       GTT TCT
                                  ||||||||||       ||| |||
                                  AGGGTTGCGG       CAA AGG
                                       AGTGTAT   C   T
GAM145   LOC160673 5'  GCTGGGGGTGGTGGCATTGGGG 88442           TGT TT   TTTG
                                  TCTCAATGCCG   G  CTC
                                  ||||||||||   |  |||
                                  GGGGTTACGGT   T  GGG
                                        GG_ GG   TCGA
GAM145   LOC162461 3'  GAGGGGTGCGGTGATGGGG    83239       A     TG G
                                  TCTCA TGCCG  T TTCTC
                                  ||||| |||||  | |||||
                                  GGGGT GTGGC  G GGGAG
                                    A     GT _
GAM145   LOC199678 3'  GGAGTGATGCGGTTTGGGG    91368       T      GTT
                                  TCTCAA GCCGTGT   CTCT
                                  ||||||  |||||||   ||||
                                  GGGGTT TGGCGTA   GAGG
                                     _      GT_
GAM145   LOC199796 3'  TGAGGAGGGTGCGCGGCA     74926        TG
                                  TGCCGTG  TTCTCTTTG
                                  |||||||  |||||||||
                                  ACGGCGC  GGGAGGAGT
                                      GT
GAM145   LOC199964 5'  CGGAGAGGGCGCGGCTGGTGAG 91496      AT_      G      TTG
                                  CTCA   GCCGTGT TTCTCT
                                  ||||   ||||||| ||||||
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                                GAGT   CGGCGCG GAGAGG
                                  GGT      G     C
GAM145   LOC199982 5'  TGAAGAATAATGCAGTATTGAG 89902         C   _    CTTTG
           A                     TCTCAATGC GTGT GTTCT
                                 ||||||||| |||| ||||||
                                 AGAGTTATG CGTA TAAGA
                                      A   A     AGT
GAM145   LOC200081 3'  CAAGCAGCTGTGTGAGTGTTGA 89971         _  TG _  _ CTTTG
           GA                    TCTCAATGC CG  T GTT CT
                                 ||||||||| ||  | ||| ||
                                 AGAGTTGTG GT  G CGA GA
                                      A  GT T   C  AC
GAM145   LOC200138 5'  TGGGGAACCCATGGTTGTTGGG 91544         _    T      TTG
           G                     TCTCAATG CCGTG GTTCTCT
                                 |||||||| ||||| |||||||
                                 GGGGTTGT GGTAC CAAGGGG
                                      T    C      T
GAM145   LOC200314 3'  CAGAGGGGGTCTGGGTGCTGGG 91591       AT   GTGT TT
           A                     TCTCA  GCC    G  CTCTTTG
                                 |||||  |||    |  |||||||
                                 AGGGT  TGG    T  GGGAGAC
                                   CG   GTC_ GG
GAM145   LOC200531 5'  CGAGGAGGGCAGAGTCCGTTGC 90248    T    CCGTG
           GG                     TC CAATG     TGTTCTCTTTG
                                  || |||||     ||||||||||
                                  GG GTTGC     ACGGGAGGAGC
                                   C    CTGAG
GAM145   LOC200982 3'  TGGGGACTTGAATGGTGTGTGG 91817       _      GT__     TTTG
           GG                     TCTCA ATGCCGT    GTTCTC
                                  ||||| |||||||    ||||||
                                  GGGGT TGTGGTA    CAGGGG
                                     G      AGTT     T
GAM145   LOC201245 5'  TGAGGACCTGGACGGCATTGG  88737         G __     TTTG
                                  TCAATGCCGT T  GTTCTC
                                  |||||||||| |  ||||||
                                  GGTTACGGCA G  CAGGAG
                                        G TC     T
GAM145   LOC201500 3'  GGAATCCAGTGGTGTTGGGG   91354          _  TG
                                  TCTCAATGCCG TG  TTCT
                                  |||||||||| ||  ||||
                                  GGGGTTGTGGT AC  AAGG
                                        G  CT
GAM145   LOC201514 3'  AAGGAGAGTGGCCGTGAGA    89632       AT    TGTG
                                  TCTCA  GCCG    TTCTCTTT
                                  |||||  ||||    ||||||||
                                  AGAGT  CGGT    GAGAGGAA
                                    GC    _____
GAM145   LOC201627 3'  TAGAGAGAATATGGCATTTGA  90460      _       G      TTG
                                  TCAA TGCCGTGT TTCTCT
                                  |||| |||||||| ||||||
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                                AGTT ACGGTATA GAGAGA
                                  T       A     T
GAM145  LOC201868 3'  CGAGGAGGGTGGATCATGAGG  90522      A  CC  G  TT
                                TCTCA TG  GT TG  CTCTTTG
                                ||||| ||  || ||  |||||||
                                GGAGT AC  TA GT  GAGGAGC
                                  _ __  G  GG
GAM145  LOC202802 3'  TAAAGAGGATGTGTGTGC    90691    _  TG
                                GC CG  TGTTCTCTTTG
                                || ||  ||||||||||||
                                CG GT  GTAGGAGAAAT
                                 T  GT
GAM145  LOC203197 5'  AGAGGCTGCGGCATTAGGG   90801    TC       T  T
                                TC  AATGCCGTG GT CTCT
                                ||  ||||||||| || ||||
                                GG  TTACGGCGT CG GAGA
                                 GA       _  _
GAM145  LOC203257 3'  TAAAGCCATACGGTATTGA   88881           TTCT
                                TCAATGCCGTGTG   CTTTG
                                ||||||||||||    |||||
                                AGTTATGGCATAC   GAAAT
                                       C___
GAM145  LOC204285 5'  AAGTGACTACTGGTGTTGGGA  91008          T   T  T
                                TCTCAATGCCG GTG TC CTT
                                |||||||||| ||| || |||
                                AGGGTTGTGGT CAT AG GAA
                                      _  C  T
GAM145  LOC205418 5'  AGAGGGAGTGGAATGGGG    92365      ATG   TGTG
                                TCTCA   CCG    TTCTCTTT
                                |||||   |||    ||||||||
                                GGGGT   GGT    GAGGGAGA
                                  AA_  ____
GAM145  LOC219700 5'  GTCACGTGGCTTTGAGG     94657       T       TT
                                TCTCAA GCCGTGTG  C
                                |||||| ||||||||  |
                                GGAGTT CGGTGCAC  G
                                   T       TG
GAM145  LOC219918 3'  AGGGGGGAAATATGGTATGAGA 93169       A       G       G
                                TCTCA TGCCGTGT TTCTCTTT
                                ||||| |||||||| ||||||||
                                AGAGT ATGGTATA AGGGGGGA
                                  _       A       A
GAM145  LOC219940 3'  CAGGGGGTTGCCTGTGGCATTG 94999    T      GT T  T_
          GA                    TC CAATGCC  G GT  CTCTTTG
                                || |||||||  | ||  |||||||
                                AG GTTACGG  T CG  GGGGGAC
                                 _      TG C  TT
GAM145  LOC220071 3'  AGGGGGGAAATATGGTATGAGA 95079       A       G       G
                                TCTCA TGCCGTGT TTCTCTTT
                                ||||| |||||||| ||||||||
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                                AGAGT ATGGTATA AGGGGGGA
                                  _      A      A
GAM145  LOC220110 5'  AAGTTTCTACACGTGTTGGGG  95114        C    TTCT
                                TCTCAATGC GTGTG   CTT
                                ||||||||| |||||   |||
                                GGGGTTGTG CACAT   GAA
                                    _    CTTT
GAM145  LOC220370 3'  GGAGAGGATGGGATGAGA    94400      A G   GTG
                                TCTCA T CCGT   TTCTCT
                                ||||| | ||||  ||||||
                                AGAGT A GGTA   GAGAGG
                                  _ G   G__
GAM145  LOC220753 5'  GGGAGACACTGCGTTGAGA   94535        C   G
                                TCTCAATGC GTGT TTCT
                                ||||||||| |||| ||||
                                AGAGTTGCG CACA AGGG
                                     T   G
GAM145  LOC220930 5'  TGAGGGGAAGGGCAGGTTTGGG 94753      T   G   G  _
          G                      TCTCAA GCC TGT TT CTCTTTG
                                ||||||| ||| ||| || |||||||
                                GGGGTT TGG ACG GA GGGGAGT
                                  _   _   G  A
GAM145  LOC220980 5'  AGAGAGAGTGCCTGTGGGG   94763      ATGC  T TG
                                TCTCA    CG G  TTCTCTTT
                                |||||    || |  ||||||||
                                GGGGT    GT C  GAGAGAGA
                                  _____  C GT
GAM145  LOC221017 5'  TGAGAGAACACAAGCTGAAGA  93114     _ AT  CG       TT
                                TCT CA  GC  TGTGTTCTCT  G
                                ||| ||  ||  ||||||||||  |
                                AGA GT  CG  ACACAAGAGA  T
                                  A  __  A_        GG
GAM145  LOC221495 5'  CAGAGAGGGGCCTGGGGGTTGA 95492       G  GT_  G
          GA                      TCTCAAT CC   GT TTCTCTTTG
                                ||||||| ||   || |||||||||
                                AGAGTTG GG   CG GGGAGAGAC
                                    G  GTC  _
GAM145  LOC221504 3'  CAGAGGGACTCAGGTTTGGGA  94019      T   G  T   T
                                TCTCAA GCC TG GTTC CTTTG
                                |||||| ||| || |||| |||||
                                AGGGTT TGG AC CAGG GAGAC
                                  _   _  T   _
GAM145  LOC221596 3'  TAGAGAGCATGATTCTGGG   93625     ATGCCG       TT
                                CTCA     TGTGTTCTCT  G
                                ||||     ||||||||||  |
                                GGGT     GTACGAGAGA  T
                                  CTTA__         G
GAM145  LOC221687 3'  TAAGGAGAATGAAAAGCACTGA 93872      A   CGTG
          GG                      TCTCA TGC    TGTTCTCTTTG
                                ||||| |||    ||||||||||
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                                GGAGT ACG   GTAAGAGGAAT
                                  C  AAAA
GAM145  LOC221755 3'  TGAAGGGGCTGGGCATTAAGA  94010    C    GTGT   T
                                TCT AATGCC   GTTC CTTTG
                                ||| ||||||   |||| |||||
                                AGA TTACGG   CGGG GAAGT
                                  A    GT__  _
GAM145  LOC221760 5'  TGGAGGGAGCGTGTGAGATGTG 95432     ATGC___ TG     TT
          TGGGG                   TCTCA     CG  TGTTCTCT  G
                                |||||      ||  ||||||||  |
                                GGGGT      GT  GCGAGGGA  T
                                  GTGTAGA  GT       GG
GAM145  LOC222070 5'  AAGGCCCAACTTGGTGTTGGGG 95803          T  GTTC   TG
                                TCTCAATGCCG GT   TCTT
                                |||||||||| ||   ||||
                                GGGGTTGTGGT CA   GGAA
                                       T  ACCC   T
GAM145  LOC222174 3'  TAGAGAGGACATAGGGTTTGGG 95766      T   G
          A                      TCTCAA GCC TGTGTTCTCTTTG
                                |||||| ||| ||||||||||||
                                AGGGTT TGG ATACAGGAGAGAT
                                   _  G
GAM145  LOC253291 5'  CAGAGGGAGCACATCCCCTGA  98756    ATGCC
                                TCA    GTGTGTTCTCTTTG
                                |||    ||||||||||||||
                                AGT    TACACGAGGGAGAC
                                  CCCC_
GAM145  LOC253531 5'  TGGAGGGTCGCTGTTTGAGA   98225      T  C   T TT   TT
                                TCTCAA GC GTG G  CTCT  G
                                |||||| || ||| |  ||||  |
                                AGAGTT TG CGC T  GAGG  T
                                   _ T  _ GG   G
GAM145  LOC253613 3'  TAAAGAGGGCGTAAGCAATAGA 97918     AA_   CG
          GG                      TCTC   TGC  TGTGTTCTCTTTG
                                ||||   |||  ||||||||||||
                                GGAG   ACG  ATGCGGGAGAAAT
                                  ATA   A_
GAM145  LOC254085 5'  CAGAGAAGCAACATGGCATTAG 97819    C       _  _   TTG
          G                       TCT AATGCCGTGT GTT CTCT
                                ||| |||||||||| ||| ||||
                                GGA TTACGGTACA CGA GAGA
                                  _       A  A   C
GAM145  LOC254110 3'  AGGGCTGATGTGGCACTGAGG  96810     A    TG __
                                TCTCA TGCCG  T  GTTCT
                                ||||| |||||  |  |||||
                                GGAGT ACGGT  A  CGGGA
                                  C    GT GT
GAM145  LOC254130 3'  TGAGGAGGAGCCTGTGCTGAGA 97381     AT  _  T  G
                                TCTCA  GC CG GT TTCTCTTTG
                                |||||  || || || |||||||||
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                                AGAGT  CG GT CG AGGAGGAGT
                                   __  T  C  _
GAM145  LOC254143 5'  AGCTGCATGGCATTAAGG    98250     C        _
                                TCT AATGCCGTGT GTT
                                ||| |||||||||| |||
                                GGA TTACGGTACG CGA
                                  A         T
GAM145  LOC254381 5'  CAGAGGGGACGCGCGGGTCTGG 99324     AATG_
                AG                CTC    CCGTGTGTTCTCTTTG
                                  |||    ||||||||||||||||
                                  GAG    GGCGCGCAGGGGAGAC
                                    GTCTG
GAM145  LOC254643 3'  CGGGGAGAGGGAGGGCAATGGG 97305       A    GTGTG
                A                  TCTCA TGCC    TTCTCTTTG
                                   ||||| ||||    |||||||||
                                   AGGGT ACGG    GAGAGGGGC
                                      A   GAGG_
GAM145  LOC254821 3'  CAGGGAGGGCATCACTTGGT   98409     __  _
                                   GCC  GTG TGTTCTCTTTG
                                   |||  ||| ||||||||||
                                   TGG  CAC ACGGGAGGGAC
                                     TT   T
GAM145  LOC254890 3'  AAAGGGAGAGTGGTTGAGA    96865      AT    TGTG
                                   TCTCA  GCCG    TTCTCTTT
                                   |||||  ||||    ||||||||
                                   AGAGT  TGGT    GAGGGAAA
                                      __    GA__
GAM145  LOC254944 3'  TGGAGGGGGCATGTCTGGAGG  99006     AATGC    G     TTG
                                   TCTC     CGTGT TTCTCT
                                   ||||     ||||| ||||||
                                   GGAG     GTACG GGGAGG
                                     GTCT_     G     T
GAM145  LOC255043 3'  CGGGGAGGGTCATCATTGTGA  97068    T    CC   T TT
                                   TC CAATG  GTG G  CTCTTTG
                                   || |||||  ||| |  |||||||
                                   AG GTTAC  TAC T  GAGGGGC
                                    T     __   _ GG
GAM145  LOC255314 5'  CAGGGAGGATTCTGTTTTGGGA 99471       T  CGTGT
                                   TCTCAA GC     GTTCTCTTTG
                                   |||||| ||     ||||||||||
                                   AGGGTT TG     TAGGAGGGAC
                                      T  TCT__
GAM145  LOC255394 5'  TGGGGGGACACTGGGGCTGGGG 96545       AT   G _       TT
                                   TCTCA  GCC T GTGTTCTCT  G
                                   |||||  ||| | |||||||||  |
                                   GGGGT  CGG G CACAGGGGG  T
                                      __  G T        GG
GAM145  LOC255461 5'  GGCACACATGCCGTTGGGG   99141         C      T
                                   TCTCAATG CGTGTGT CT
                                   |||||||| ||||||| ||
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                                GGGGTTGC GTACACA GG
                                    C      C
GAM145  LOC255515 3'  AGGGGGGAAATATGGTATGAGA 97810      A      G      G
                                TCTCA TGCCGTGT TTCTCTTT
                                ||||| |||||||| ||||||||
                                AGAGT ATGGTATA AGGGGGGA
                                  _       A      A
GAM145  LOC255516 5'  GGCACACATGCCGTTGGGG   99155       C      T
                                TCTCAATG CGTGTGT CT
                                |||||||| ||||||| ||
                                GGGGTTGC GTACACA GG
                                    C      C
GAM145  LOC256052 5'  GGAGAGCGTGGTGCTGGGA   99452      AT   TG
                                TCTCA  GCCG  TGTTCTCT
                                |||||  ||||  ||||||||
                                AGGGT  TGGT  GCGAGAGG
                                  CG   __
GAM145  LOC256158 5'  GGGGAGAGCACGGCTGTCGGA  99510     CAAT     G
                                TCT    GCCGTGT TTCTCT
                                |||    ||||||| ||||||
                                AGG    CGGCACG GAGGGG
                                 CTGT      A
GAM145  LOC256158 5'  TGGGGGAACCTACAGATTGAGA 99519       GCC   T     TT
                                TCTCAAT   GTG GTTCTCT  G
                                |||||||   ||| |||||||  |
                                AGAGTTA   CAT CAAGGGG  T
                                    GA_   C      GG
GAM145  LOC256221 5'  AGACATGCGTGGCGTCGGGG   96904     A        _
                                TCTC ATGCCGTGTGT TCT
                                |||| |||||||||| |||
                                GGGG TGCGGTGCGTA AGA
                                  C         C
GAM145  LOC256277 3'  TGAAGAGGATAATCTTTTTGGG 96355       TGCCGTG
          G                      TCTCAA      TGTTCTCTTTG
                                 ||||||      ||||||||||
                                 GGGGTT      ATAGGAGAAGT
                                    TTTCTA_
GAM145  LOC256337 3'  TGAAGAGGATAATCTTTTTGGG 96346       TGCCGTG
          G                      TCTCAA      TGTTCTCTTTG
                                 ||||||      ||||||||||
                                 GGGGTT      ATAGGAGAAGT
                                    TTTCTA_
GAM145  LOC256848 3'  TGAGGAGGATGACGAGGATGAG 99380      ATG  G  _
          G                      TCTCA   CC TGT GTTCTCTTTG
                                 |||||   || ||| ||||||||||
                                 GGAGT   GG GCA TAGGAGGAGT
                                   A__  A   G
GAM145  LOC256950 3'  CGAGGAGAACGTGAGCTGGGG  97154      AT  _  TG
                                TCTCA  GC CG  TGTTCTCTTTG
                                |||||  || ||  ||||||||||
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                                GGGGT  CG GT  GCAAGAGGAGC
                                  __  A  __
GAM145  LOC257407 5'  GAAATGTGTGTGTGTTGAGG   98759         _ TG    CT
                                TCTCAATGC CG  TGTT  C
                                |||||||||  ||  ||||  |
                                GGAGTTGTG GT  GTAA  G
                                    T  GT    AG
GAM145  LOC257469 5'  CGGGGAGGTACCAGGTATTTGA 97421        _   G  T  _
          GA                      TCTCAA TGCC TG GT TCTCTTTG
                                |||||| |||| || || ||||||||
                                AGAGTT ATGG AC CA GGAGGGGC
                                   T   _ _  T
GAM145  LOC257494 3'  AGACATACACGGCTTTGGGG   99627        T       _
                                TCTCAA GCCGTGTGT TCT
                                |||||| |||||||||  |||
                                GGGGTT CGGCACATA AGA
                                   T        C
GAM145  LOC257554 3'  TGAAGAGAGTGTGGGCTTTAGG 99538    TC  T   G  TG
          A                      TC  AA GCC TG  TTCTCTTTG
                                ||  ||  |||  ||  |||||||||
                                AG  TT CGG GT  GAGAGAAGT
                                 GA  T   _  GT
GAM145  LOC51094  5'  AGCTGCAGGGTATTGAGG    32595          G  _
                                TCTCAATGCC TGT GTT
                                ||||||||||  |||  |||
                                GGAGTTATGG ACG CGA
                                     G   T
GAM145  LOC51333  3'  GAGGGGGCTGAGGCATGAGA   34053       A   GTGT
                                TCTCA TGCC    GTTCTCTT
                                |||||  ||||    ||||||||
                                AGAGT ACGG    CGGGGGAG
                                   _    AGT_
GAM145  LOC55924  3'  GAAGGGAAGGTGGTTGGGA    39392       AT    TG G
                                TCTCA  GCCG  T TTCTCTTT
                                |||||  ||||  |  ||||||||
                                AGGGT  TGGT  G AAGGGAAG
                                   __    __ G
GAM145  LOC56920  3'  GGGAGGGAACACAGAGGTGTTG 39797          G_          G
          GGA                      TCTCAATGCC  TGTGTTCTCTTT
                                ||||||||||  ||||||||||||
                                AGGGTTGTGG  ACACAAGGGAGG
                                     AG          GG
GAM145  LOC56959  5'  AAGGAGAGCTTTTTGGGA    82809       TGCCGTGT
                                TCTCAA       GTTCTCTTT
                                ||||||       |||||||||
                                AGGGTT       CGAGAGGAA
                                   TTT_____
GAM145  LOC89919  3'  TAAAGGGAATGTATCATGTGA  61381     _   CC   TG
                                TCA ATG  GTG  TTCTCTTTG
                                |||  |||  |||  |||||||||
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                                AGT TAC  TAT  AAGGGAAAT
                                  G  __  GT
GAM145  LOC89944  3'  TGAGGAGGACATGTGAGTCCTG 93176    AT  _  TG
            G                    TCA  GC CG  TGTTCTCTTTG
                                 |||  || ||  ||||||||||
                                 GGT  TG GT  ACAGGAGGAGT
                                   CC  A  GT
GAM145  LOC90309  5'  GAGGTAATTATGGTACTGGGG  62872      A      TGT_
                                 TCTCA TGCCGTG    TCTC
                                 ||||| |||||||    ||||
                                 GGGGT ATGGTAT    GGAG
                                    C      TAAT
GAM145  LOC90342  5'  TAAAGAGGATGGCCATTGAGG  63017        _  GTGT
                                 TCTCAATG CC    GTTCTCTTTG
                                 |||||||| ||    ||||||||||
                                 GGAGTTAC GG    TAGGAGAAAT
                                      C  ____
GAM145  LOC90673  5'  CAAGGAGAATACACAGCAGCGA 64560    AA   C
                                 TC  TGC GTGTGTTCTCTTTG
                                 ||  ||| ||||||||||||||
                                 AG  ACG CACATAAGAGGAAC
                                  CG   A
GAM145  LOC90719  3'  TGGAGAGGGTGCGTTTCACTGT 64611    T  A  C__  TG G     TTG
            GG                    TC CA TG   CG  T TTCTCT
                                  || || ||   ||  | ||||||
                                  GG GT AC   GC  G GAGAGG
                                   T  C  TTT  GT G     T
GAM145  LOC90806  3'  AAAGAGGAAAAGATTGAGG    58610        GCCGTGTG
                                 TCTCAAT       TTCTCTTT
                                 |||||||       ||||||||
                                 GGAGTTA       AGGAGAAA
                                     GAAA____
GAM145  LOC90982  3'  CAGAGAGAATGCCACTAGAGA  65146      AATGCC  _
                                 TCTC      GTG TGTTCTCTTTG
                                 ||||      ||| ||||||||||
                                 AGAG      CAC GTAAGAGAGAC
                                   AT____   C
GAM145  LOC91035  5'  GCTGTGGGTACATTGTGTTGAG 65301         C     TT TCTTTG
            A                     TCTCAATGC GTGTG  C
                                  |||||||| |||||  |
                                  AGAGTTGTG TACAT  G
                                       T    GG TGTCGG
GAM145  LOC91319  3'  AAGGGGAGCAGGGTTAGGG    66190     AAT   G   GT
                                 CTC   GCC TGT  TCTCTTT
                                 |||   ||| |||  |||||||
                                 GGG   TGG ACG  AGGGGAA
                                   AT_   G   __
GAM145  LOC91355  5'  TGTGGGGGCATGGCCACATGAT 66311        _________      G   TCTTTG
            GTTGAGG                  TCTCAAT       GCCGTGT TTC
                                 |||||||       ||||||| |||
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                                GGAGTTG       CGGTACG GGG
                                   TAGTACAC      G  T  GTT
GAM145  LOC91565  5' CCCAGGGCACATGGCTTGGGG  67053       T         CTTTG
                                TCTCAA GCCGTGTGTTCT
                                |||||| ||||||||||||
                                GGGGTT CGGTACACGGGA
                                  _          CCCA
GAM145  LOC91807  5' CAAGGAGAGTCTGGGGCATGGG 67811     A    G  TG
          GG                      TCTC ATGCC TG  TTCTCTTTG
                                |||| ||||| ||  |||||||||
                                GGGG TACGG GT  GAGAGGAAC
                                  G    G  CT
GAM145  LOC91960  5' TGAGGGGAAGGCAGCGATGGGA 68293      A  CG  G
                                TCTCA TGC  TGT TTCTCTTTG
                                ||||| |||  ||| |||||||||
                                AGGGT GCG  ACG AAGGGGAGT
                                   A  __  G
GAM145  LOC92270  5' TGAGGAGTAGTGTGGCATTAGA 69192     C      TG GTT
                                TCT AATGCCG  T   CTCTTTG
                                ||| |||||||  |  |||||||
                                AGA TTACGGT  G   GAGGAGT
                                  _      GT AT_
GAM145  LOC92305  3' CAAAGAGGGGCAGTGGGTTGGG 57232       G  _  G
          G                      TCTCAAT CCG TGT TTCTCTTTG
                                ||||||| ||| ||| |||||||||
                                GGGGTTG GGT ACG GGGAGAAAC
                                   _  G  _
GAM145  LOC92344  3' GAGCTAATATGGTATTGAG   69577           GTT
                                CTCAATGCCGTGT   CTC
                                ||||||||||||   |||
                                GAGTTATGGTATA   GAG
                                       ATC
GAM145  LOC92997  3' GAAATGTGTGTGTGTTGAGG   71638        _ TG   CT
                                TCTCAATGC CG  TGTT  C
                                ||||||||| ||  ||||  |
                                GGAGTTGTG GT  GTAA  G
                                     T  GT   AG
GAM145  LOC93259  5' AGAGGGAGAGTGGTGAGA    72279     AAT   TGTG
                                TCTC   GCCG   TTCTCTTT
                                ||||   ||||   ||||||||
                                AGAG   TGGT   GAGGGAGA
                                  ___    GA__
GAM146  ANXA4    3' ACGCCTACAGCTGCCTCCT   63430      C
                                AGGAG CAGCTGTAGGTGT
                                ||||| ||||||||||||
                                TCCTC GTCGACATCCGCA
                                  C
GAM146  BACH2    3' AAGGACGGGGCCAACCAGCCAC 41773    GAGCCA   TA_  ___
          TG                     CAG    GCTG  GGT  GTCCTT
                                |||    ||||  |||  ||||||
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                                GTC     CGAC   CCG   CAGGAA
                                  AC_____    CAA   GGG
GAM146  BLAME    3'  AAGGATCAGCACAGCTGGCCTC 39649      _       AGGT
              C                    GGAG CCAGCTGT    GTCCTT
                                   |||| ||||||||    ||||||
                                   CCTC GGTCGACA    TAGGAA
                                     C       CGAC
GAM146  DLG5     5'  ACTCCACAGCCGGCTCCTG   83807        A    A  T
                                   CAGGAGCC GCTGT GG GT
                                   |||||||| ||||| || ||
                                   GTCCTCGG CGACA CC CA
                                        C     _ T
GAM146  HUNK     3'  AAGGACACCCCAGAGTCCC   28169    AG CAG   TA
                                   GG  C   CTG  GGTGTCCTT
                                   ||  |   |||  |||||||||
                                   CC  G   GAC  CCACAGGAA
                                    CT A__   C_
GAM146  IL5RA    3'  AGGGATGCTGGCTCTTG     6905          TGTAGGT
                                   CAGGAGCCAGC      GTCCTT
                                   ||||||||||       ||||||
                                   GTTCTCGGTCG      TAGGGA
                                                    _______
GAM146  KRT14    3'  GCACTTCACAGCTGGACCCTG  6720       AG       _
                                   CAGG  CCAGCTGT AGGTGT
                                   ||||  |||||||| ||||||
                                   GTCC  GGTCGACA TTCACG
                                     CA       C
GAM146  LNK      3'  AAGGACACATCTGACATCCTG  19624      GC_   CTGTAG
                                   CAGGA   CAG     GTGTCCTT
                                   |||||   |||     ||||||||
                                   GTCCT   GTC     CACAGGAA
                                      ACA   TA____
GAM146  MAPK14   3'  AGGACCAACTGGCTTCTG    8975          C  TAGGT
                                   CAGGAGCCAG TG    GTCCT
                                   ||||||||||| ||    |||||
                                   GTCTTCGGTC AC    CAGGA
                                        A _____
GAM146  MAPK14   3'  AGGACCAACTGGCTTCTG    58124         C  TAGGT
                                   CAGGAGCCAG TG    GTCCT
                                   ||||||||||| ||    |||||
                                   GTCTTCGGTC AC    CAGGA
                                        A _____
GAM146  MAPK14   3'  AGGACCAACTGGCTTCTG    58130         C  TAGGT
                                   CAGGAGCCAG TG    GTCCT
                                   ||||||||||| ||    |||||
                                   GTCTTCGGTC AC    CAGGA
                                        A _____
GAM146  OXCT     3'  AGGTGAGACAGCTGGCCTCTG  6484      GA       AGGTGT
                                   CAG  GCCAGCTGT     CCT
                                   |||  |||||||||     |||
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                                GTC  CGGTCGACA     GGA
                                  TC        GAGT__
GAM146  PRKCSH   3' AAGGCATGAAGCCAGCCCCTG 12291      A  CA   GTAG   T
                                CAGG GC  GCT    GTG CCTT
                                |||| ||  |||    ||| ||||
                                GTCC CG  CGA    TAC GGAA
                                  C  AC   AG__   _
GAM146  PTGES    3' AGGACAGGGCTGGCTCCT    18056          GTAGG
                                AGGAGCCAGCT    TGTCCT
                                ||||||||||     ||||||
                                TCCTCGGTCGG    ACAGGA
                                      G____
GAM146  CASKIN1  3' AAGGACACGAAGTCTAGCTCC  40779       C  _  GTAG
                                GGAGC AG CT    GTGTCCTT
                                ||||| || ||    ||||||||
                                CCTCG TC GA    CACAGGAA
                                   A  T  AG__
GAM146  DKFZp547I094 3'  AAGGACACCTCCAGCCTCC    50548      CCA    T
                                GGAG   GCTG AGGTGTCCTT
                                ||||   |||| ||||||||||
                                CCTC   CGAC TCCACAGGAA
                                  ___    C
GAM146  FLJ12587  3' AGGACACCCAGACCTCC     42773      CCAG   TA
                                GGAG    CTG  GGTGTCCT
                                ||||    |||  ||||||||
                                CCTC    GAC  CCACAGGA
                                  CA__   __
GAM146  FLJ14624  3' AGGATACACTGGCCCCT     71843     A    CTGTAG
                                AGG GCCAG     GTGTCCT
                                ||| |||||     |||||||
                                TCC CGGTC     CATAGGA
                                  C    A_____
GAM146  FLJ21918  3' GACAATGGCTGGACCCTG    46859      AG       AGG
                                CAGG  CCAGCTGT   TGTC
                                ||||  ||||||||   ||||
                                GTCC  GGTCGGTA   ACAG
                                  CA       ___
GAM146  FLJ32978  5' ACACCAGCAGCTGGTCCTG    58886      G       A
                                CAGGA CCAGCTGT GGTGT
                                ||||| |||||||| |||||
                                GTCCT GGTCGACG CCACA
                                  _       A
GAM146  HH114    3' AAGGACACAAACCTGGTCCC   51665    AG    CT  AG
                                GG  CCAG  GT  GTGTCCTT
                                ||  ||||  ||  ||||||||
                                CC  GGTC  CA  CACAGGAA
                                 CT    __  AA
GAM146  KIAA0748  3' AAGGACACCTCACTTTCTGGCT 29609         CT_  _
            CT                    GGAGCCAG   GT AGGTGTCCTT
                                ||||||||   || ||||||||||
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                                TCTCGGTC   CA TCCACAGGAA
                                     TTT  C
GAM146  KIAA1509  3'  GCCTCCAGCTGGCTCCTG    62296           T
                                CAGGAGCCAGCTG AGGT
                                |||||||||||| ||||
                                GTCCTCGGTCGAC TCCG
                                       C
GAM146  KIAA1822  3'  ACCTACAGCTGGCCGCTG    68177     GA
                                CAG  GCCAGCTGTAGGT
                                |||  ||||||||||||
                                GTC  CGGTCGACATCCA
                                  GC
GAM146  KIAA1904  3'  AAGGACACCAGTGACAGGTCCT 73862      G  AGCTGTA
                                AGGA CC      GGTGTCCTT
                                |||| ||      |||||||||
                                TCCT GG      CCACAGGAA
                                  _  ACAGTGA
GAM146  P5-1      3'  AAGGACACCCCTGGATGCCCCT 22887     A  CAG   TA
                                AGG GC   CTG  GGTGTCCTT
                                ||| ||   |||  |||||||||
                                TCC CG   GGT  CCACAGGAA
                                  C  TA_   CC
GAM146  PIG7      5'  AAGGACACCCGAGGCCCCTG   17966     A   AGCTGTA
                                CAGG GCC      GGTGTCCTT
                                |||| |||      |||||||||
                                GTCC CGG      CCACAGGAA
                                  C   AGC_____
GAM146  RNF8      3'  TATAGTACAGCTGAGCCCC    15575    A _      G_
                                GG GC CAGCTGTA  GTG
                                || || ||||||||  |||
                                CC CG GTCGACAT  TAT
                                 C  A       GA
GAM146  ZNF33A    3'  GAGGCCATCACAGCTAATCCT  92996     GCC     A    T
                                AGGA   AGCTGT GGTG CCTT
                                ||||   |||||| |||| ||||
                                TCCT   TCGACA CTAC GGAG
                                  AA_      _    C
GAM146  LOC122040 5'  GCCTAAGCTGGCTCCTG     76098           G
                                CAGGAGCCAGCT TAGGT
                                |||||||||||| |||||
                                GTCCTCGGTCGA ATCCG
                                          _
GAM146  LOC129073 5'  ACGCCACAGCTGGCTGCTG   76312     G        A
                                CAG AGCCAGCTGT GGTGT
                                ||| |||||||||| |||||
                                GTC TCGGTCGACA CCGCA
                                  G        _
GAM146  LOC155054 3'  GGGCACAGTGGCTCC       82205        G   AGGT
                                GGAGCCA CTGT    GTCC
                                ||||||| ||||    ||||
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                                CCTCGGT GACA    CGGG
                                    _   ____
GAM146  LOC155368 3'  GCCCCCAGCTGGCCCCTG    82264      A       TA
                                CAGG GCCAGCTG  GGT
                                |||| ||||||||  |||
                                GTCC CGGTCGAC  CCG
                                  C       CC
GAM146  LOC165476 5'  GCTGCCTACAGCCCGCCCC    88554    A  CA       _
                                GG GC  GCTGTAGGT GT
                                || ||  |||||||||  ||
                                CC CG  CGACATCCG CG
                                 C  CC        T
GAM146  LOC201242 3'  AGGACACCCAGAGCTGCC    88731    AGC    GTA
                                GG   CAGCT   GGTGTCCT
                                ||   |||||   ||||||||
                                CC   GTCGA   CCACAGGA
                                 ___     GAC
GAM146  LOC255388 5'  CACACAGCTGGCTCGTG     98976    G         AG
                                CA GAGCCAGCTGT  GTG
                                || ||||||||||  |||
                                GT CTCGGTCGACA  CAC
                                 G         __
GAM146  LOC256586 5'  AAGGTCTGTGCAAGCTGGCTCC 96616           _  GGTGT
          TG                     CAGGAGCCAGCT GTA     CCTT
                                ||||||||||| |||    ||||
                                GTCCTCGGTCGA CGT     GGAA
                                       A  GTCT_
GAM146  LOC51087  3'  AGGACACCCAGAGCTGCC    32565    AGC    GTA
                                GG   CAGCT   GGTGTCCT
                                ||   |||||   ||||||||
                                CC   GTCGA   CCACAGGA
                                 ___     GAC
GAM146  LOC90190  3'  AAGGATGACATAGAGCTGGCTC 62420          G  G  _
          C                      GGAGCCAGCT TA GT GTCCTT
                                |||||||||| || || ||||||
                                CCTCGGTCGA AT CA TAGGAA
                                      G  A  G
GAM146  LOC90268  3'  GATGCACAGGTGGCTCCTG    62664         G    AG
                                CAGGAGCCA CTGT  GTGTC
                                |||||||| ||||  |||||
                                GTCCTCGGT GACA  CGTAG
                                     G   __
GAM146  LOC91661  3'  GGTGTCCTTAAGCACGCTGGCT 57216          _  T_______   TGT
          CCTG                    CAGGAGCCAGC TG      AGG   CC
                                |||||||||| ||      |||   ||
                                GTCCTCGGTCG AC      TCC   GG
                                       C  GAA___T   TGT
GAM146  LOC91948  5'  ATGACTAAGCTGGCTCC     68233          G   GT
                                GGAGCCAGCT TAG  GT
                                |||||||||| |||  ||
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                                CCTCGGTCGA ATC  TA
                                      _  AG
GAM147  ABCD4   3'  ATGATGAGAGGATCTTGA   40102     AAC   C
                                TCAA  CCTC TCATCAT
                                ||||  |||| |||||||
                                AGTT  GGAG AGTAGTA
                                  CTA  _
GAM147  CTSL    3'  GTGATGAGGAAGGACTTGA   10345     AA  C
                                TCAA  CC TCCTCATCAT
                                ||||  || ||||||||||
                                AGTT  GG AGGAGTAGTG
                                  CA  A
GAM147  FUT8    3'  GTAGATGAAGAGGGCTCTGA  16813    AAA    CTCA
                                TCA  CCCTC   TCATCTAC
                                |||  |||||   ||||||||
                                AGT  GGGAG   AGTAGATG
                                  CTC   A___
GAM147  MAX     3'  AGATGCCAGTGAAGGGTTTTG 59701        CC   ___
                                CAAAACCCT  TCAT  CATCT
                                |||||||||  ||||  |||||
                                GTTTTGGGA  AGTG  GTAGA
                                     __   ACC
GAM147  MAX     3'  AGATGCCAGTGAAGGGTTTTG 11472        CC   ___
                                CAAAACCCT  TCAT  CATCT
                                |||||||||  ||||  |||||
                                GTTTTGGGA  AGTG  GTAGA
                                     __   ACC
GAM147  SCN4A   3'  AGAGTGAGGGAGGAGGGCTTTG 6194       A      A_  _
          A                      TCAAA CCCTCCTC  TCA TCT
                                |||||  ||||||||  ||| |||
                                AGTTT GGGAGGAG  AGT AGA
                                  C       GG  G
GAM147  SLC25A6 3'  GTAGATGGCCGGGGAAGG   90948   C    A_
                                CC TCCTC  TCATCTAC
                                || |||||  ||||||||
                                GG AGGGG  GGTAGATG
                                 A    CC
GAM147  BIRC4   3'  GTAGACCCCGAAGGGTTTT   8602        CC  ATCA
                                AAAACCCT  TC   TCTAC
                                ||||||||  ||   |||||
                                TTTTGGGA  AG   AGATG
                                     __ CCCC
GAM147  BTBD3   3'  TAGATGATGAAAAGCTGTT   31030    C_  CC
                                AAC  CT  TCATCATCTA
                                |||  ||  ||||||||||
                                TTG  GA  AGTAGTAGAT
                                  TC  AA
GAM147  FLJ10261 3' AGATGGTGTCAGGGTTT    36416       CCT
                                AAACCCT   CATCATCT
                                |||||||   ||||||||
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                                TTTGGGA  GTGGTAGA
                                    CT_
GAM147  FLJ11099  3'  GTGGGTGAGAACAGGTTCTGA  37609    A   CTCC  A
                                TCA AACC   TC TCATCTAC
                                ||| ||||   || ||||||||
                                AGT TTGG   AG AGTGGGTG
                                  C   ACA_  _
GAM147  FLJ11164  3'  ATGCCAGGTGGGTTTTGA   37698       T  CAT
                                TCAAAACCC CCT  CAT
                                ||||||||| |||  |||
                                AGTTTTGGG GGA  GTA
                                     T  CC_
GAM147  FLJ12899  3'  GTAGATGAGTCTGAATTTTGA  45061      CCC  CTCA
                                TCAAAA  TC   TCATCTAC
                                ||||||  ||   ||||||||
                                AGTTTT  AG   AGTAGATG
                                   A__  TCTG
GAM147  FLJ14753  3'  GTAGATATTTGTAAAGGGTTTT 51765       CCT  TC_
                                AAAACCCT  CA  ATCTAC
                                ||||||||  ||  ||||||
                                TTTTGGGA  GT  TAGATG
                                    AAT  TTA
GAM147  KIAA0063  3'  ATGAAGTGAGGAGGATACTGA  30251    AAAC     __
                                TCA   CCTCCTCA  TCAT
                                |||   ||||||||  ||||
                                AGT   GGAGGAGT  AGTA
                                  CATA      GA
GAM147  KIAA0157  5'  GTGAATGAGGAGAGTTTGGA  50750   A   C     _
                                TC AAAC CTCCTCAT CAT
                                || |||| |||||||| |||
                                AG TTTG GAGGAGTA GTG
                                 G   A      A
GAM147  KIAA0800  3'  GTAGATGATTCTTCCGGGTCCT 28807   AA   TCCTC_
          G                      CA  ACCC    ATCATCTAC
                                ||  ||||    |||||||||
                                GT  TGGG    TAGTAGATG
                                 CC   CCTTCT
GAM147  KIAA1384  5'  AGGTTGGAGGAGGGTTT    65178        ATC
                                AAACCCTCCTC  ATCT
                                ||||||||||  ||||
                                TTTGGGAGGAG  TGGA
                                      GT_
GAM147  KIAA1775  3'  TAGTGGTGATGAGGGCTTT   53546    A   C    T
                                AAA CCCTC TCATCA CTA
                                ||| ||||| |||||| |||
                                TTT GGGAG AGTGGT GAT
                                  C   T    _
GAM147  LAMP3   3'  GTAGATGAAAGGAGAGCTTTG  60208    ACC   CA
                                CAAA  CTCCT  TCATCTAC
                                ||||  |||||  ||||||||
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                                GTTT  GAGGA  AGTAGATG
                                  CGA    A_
GAM147  MGC2663  5' ATGAAAGGAGGGTTCTGA   44330    A      CA
                                TCA AACCCTCCT  TCAT
                                ||| |||||||||  ||||
                                AGT TTGGGAGGA  AGTA
                                  C       A_
GAM147  PCDH19   3' GGAGGGAGAAGGGTTTTGA   64445        C  ATCA
                                TCAAAACCCT CTC   TCT
                                |||||||||| |||   |||
                                AGTTTTGGGA GAG   AGG
                                      A  GG__
GAM147  PDZD2    5' GTGATGAGGAAGAGTTTGA   81733     ACCC
                                TCAAA   TCCTCATCAT
                                |||||   ||||||||||
                                AGTTT   AGGAGTAGTG
                                   GAGA
GAM147  RYBP     5' AGACGAAGGGTTTTGG     60174        CCTCA  A
                                TCAAAACCCT    TC TCT
                                ||||||||||    || |||
                                GGTTTTGGGA    AG AGA
                                      _____  C
GAM147  URG4     3' AGAAGACAGAGGGTTTGGA   35923    A     CTCA  A
                                TC AAACCCTC   TC TCT
                                || ||||||||   || |||
                                AG TTTGGGAG   AG AGA
                                 G      AC__  A
GAM147  LOC138130 5' GTAGTTCAGGATGGTTTTGA  76481       C   CATCAT
                                TCAAAACC TCCT     CTAC
                                |||||||| ||||     ||||
                                AGTTTTGG AGGA     GATG
                                     T   CTT___
GAM147  LOC145773 3' GTAGATGATGGGTGTTTT    77962     CCTC
                                AAAAC   CTCATCATCTAC
                                |||||   ||||||||||||
                                TTTTG   GGGTAGTAGATG
                                   T___
GAM147  LOC145921 3' ATGGGAGATAAAGGGTTTTGA  76523        C___  A
                                TCAAAACCCT   CTC TCAT
                                ||||||||||   ||| ||||
                                AGTTTTGGGA   GAG GGTA
                                      AATA  _
GAM147  LOC149603 3' ATGGTGAGGAGGACTTTGA   71173     AC
                                TCAAA  CCTCCTCATCAT
                                |||||  ||||||||||||
                                AGTTT  GGAGGAGTGGTA
                                   CA
GAM147  LOC150406 3' TAGATCAAAGAAGAAGGGTTTT 80675        _ C  ATC_
            G                    CAAAACCCT C TC   ATCTA
                                |||||||| | ||   |||||
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                                GTTTTGGGA G AG    TAGAT
                                     A A  AAAC
GAM147   LOC150519 3'  ATGATGAAGGAGGGTTTAGA   80729    A        _
                                TC AAACCCTCCT CATCAT
                                || |||||||||| ||||||
                                AG TTTGGGAGGA GTAGTA
                                 A         A
GAM147   LOC154562 3'  AGAAGAGGAGGAGGATTTTG   81995      C      A  A
                                CAAAA CCTCCTC TC TCT
                                ||||| ||||||| || |||
                                GTTTT GGAGGAG AG AGA
                                   A      G  A
GAM147   LOC158428 3'  AGATGCCCAGAGGTTTTGA    71080        C  CTCAT
                                TCAAAACC TC     CATCT
                                |||||||| ||     |||||
                                AGTTTTGG AG     GTAGA
                                     _  ACCC_
GAM147   LOC200000 3'  GTGGATGAAGAGGGCTTT    91522     A    CTCA
                                AAA CCCTC    TCATCTAC
                                ||| |||||    ||||||||
                                TTT GGGAG    AGTAGGTG
                                  C    A___
GAM147   LOC200058 3'  AGGTTGTGATGAGGGTTCTGA  89957     A      C    C
                                TCA AACCCTC TCAT ATCT
                                ||| ||||||| |||| ||||
                                AGT TTGGGAG AGTG TGGA
                                  C      T    T
GAM147   LOC253943 5'  GTAAATGATGATGATTTTGA   97848       CCC  C      C
                                TCAAAA   TC TCATCAT TAC
                                ||||||   || ||||||| |||
                                AGTTTT   AG AGTAGTA ATG
                                    ___  T      A
GAM147   LOC92710  3'  GTAGCATGGAGGAGGGCCCTGA 70867     AAA       AT  _
                                TCA   CCCTCCTC  CAT CTAC
                                |||   ||||||||  ||| ||||
                                AGT   GGGAGGAG  GTA GATG
                                  CCC        __   C
GAM148   ADAR     3'  GCAGAACACCAAAGCATC    8484        C  C   C
                                GATGCT TG TGT CTGT
                                |||||| || ||| ||||
                                CTACGA AC ACA GACG
                                    A  C   A
GAM148   ADAR     3'  GCAGAACACCAAAGCATC    32352       C  C   C
                                GATGCT TG TGT CTGT
                                |||||| || ||| ||||
                                CTACGA AC ACA GACG
                                    A  C   A
GAM148   ADAR     3'  GCAGAACACCAAAGCATC    32362       C  C   C
                                GATGCT TG TGT CTGT
                                |||||| || ||| ||||
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                                CTACGA AC ACA GACG
                                   A  C   A
GAM148  B3GAT1   3'  CCACACAGGACACCCAGC    38450     CTGC
                                GCT   TGTCCTGTGTGG
                                |||   ||||||||||||
                                CGA   ACAGGACACACC
                                  CCC_
GAM148  B3GAT1   3'  CCACACAGGACACCCAGC    55050     CTGC
                                GCT   TGTCCTGTGTGG
                                |||   ||||||||||||
                                CGA   ACAGGACACACC
                                  CCC_
GAM148  CLASP1   3'  ACACAAAAGAGCAGAGCACCT  65890     A       GTCC
                                AG TGCTCTGCT   TGTGT
                                || |||||||||   |||||
                                TC ACGAGACGA   ACACA
                                 C       GAAA
GAM148  CNTFR    3'  ACCCCATGAGGACATGCAGAGC 10237     A      _     _  T
           ACCT                    AG TGCTCTGC TGTCCT GTG GGT
                                || |||||||| |||||| ||| |||
                                TC ACGAGACG ACAGGA TAC CCA
                                 C       T     G   C
GAM148  DAZ      3'  CCACACAGCTAGAGCA      15825       CTGTC
                                TGCTCTG    CTGTGTGG
                                |||||||    ||||||||
                                ACGAGAT    GACACACC
                                    C____
GAM148  SLC25A11 3'  CACACAGGACAGCAGAAGATC  14534     GC
                                GAT  TCTGCTGTCCTGTGTG
                                |||  ||||||||||||||||
                                CTA  AGACGACAGGACACAC
                                  GA
GAM148  WBSCR1   3'  ACAGAGGGAACAGCAGAG    42478         __  G
                                CTCTGCTGT  CCT TGT
                                |||||||||  ||| |||
                                GAGACGACA  GGA ACA
                                      AG   G
GAM148  WBSCR1   3'  ACAGAGGGAACAGCAGAG    50083         __  G
                                CTCTGCTGT  CCT TGT
                                |||||||||  ||| |||
                                GAGACGACA  GGA ACA
                                      AG   G
GAM148  DORFIN   5'  GCTAGGACTACAGAACATC    31873     C   CT     T
                                GATG TCTG  GTCCTG GT
                                ||||  ||||  ||||||  ||
                                CTAC AGAC  CAGGAT CG
                                  A    AT     _
GAM148  FLJ14564 3'  ACGGAACAGCAGAGAATCT    77011     G       C
                                AGAT CTCTGCTGT CTGT
                                ||||  |||||||||  ||||
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                                TCTA GAGACGACA GGCA
                                  A       A
GAM148  MGC4767   3'  CGTGTGGTACAGCAGCAGAGCA 51259          T_______ TGTGT
            TCT                   AGATGCTCTGCTG       CC    G
                                  ||||||||||||       ||    |
                                  TCTACGAGACGAC       GG    C
                                        GACA___T  TGTGT
GAM148  LOC123242 5'  ACCACACAGAGCTGGCAGGCA  76108     T    _ TC
                                  TGC CTGCT G  CTGTGTGGT
                                  ||| ||||| |  |||||||||
                                  ACG GACGG C  GACACACCA
                                    _     T GA
GAM148  LOC131873 5'  ACAGGGAACAGCAGGCATC    76393      T      __
                                  GATGC CTGCTGT  CCTGT
                                  ||||| |||||||  |||||
                                  CTACG GACGACA  GGACA
                                     _      AG
GAM148  LOC196955 5'  ACCACACAGAGCTGGCAGGCA  77858     T    _ TC
                                  TGC CTGCT G  CTGTGTGGT
                                  ||| ||||| |  |||||||||
                                  ACG GACGG C  GACACACCA
                                    _     T GA
GAM148  LOC199729 3'  GCAGAACAGCAGAACTTCT    73394     TGC       C
                                  AGA   TCTGCTGT CTGT
                                  |||   |||||||| ||||
                                  TCT   AGACGACA GACG
                                    TCA       A
GAM148  LOC221100 5'  ACCAAGCCCACAGCAGAACA   94866    C       CCT  G
                                  TG TCTGCTGT   GT TGGT
                                  || ||||||||   || ||||
                                  AC AGACGACA   CG ACCA
                                   A       CC_  A
GAM148  LOC221191 5'  CCACACAGAACCAAGCACT    95220    A    C  CT  C
                                  AG TGCT TG  GT CTGTGTGG
                                  || |||| ||  || ||||||||
                                  TC ACGA AC  CA GACACACC
                                   _    _ ___  A
GAM148  LOC221535 5'  ACCACACCTTGCCATGCAGAGC 95441     A       _  TCCT_
            ACCT                    AG TGCTCTGC TG     GTGTGGT
                                  || |||||||| ||     |||||||
                                  TC ACGAGACG AC     CACACCA
                                   C       T  CGTTC
GAM148  LOC253018 5'  ACCACACCTTGCCATGCAGAGC 97704     A       _  TCCT_
            ACCT                    AG TGCTCTGC TG     GTGTGGT
                                  || |||||||| ||     |||||||
                                  TC ACGAGACG AC     CACACCA
                                   C       T  CGTTC
GAM148  LOC254057 3'  ACCACACAGATCGAAAAATCT  98775      GCTCTGC  TC
                                  AGAT      TG  CTGTGTGGT
                                  ||||      ||  |||||||||
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                                TCTA      GC  GACACACCA
                                  AAAA___  TA
GAM148  LOC257418 5'  GGGAGAACAGCAGAACATTT  99424      C     ___
                                AGATG TCTGCTG   TCCT
                                ||||| |||||||   ||||
                                TTTAC AGACGAC   AGGG
                                  A      AAG
GAM148  LOC257548 5'  ACCACACCTTGCCATGCAGAGC 99580    A     _ TCCT_
          ACCT                    AG TGCTCTGC TG    GTGTGGT
                                || ||||||||  ||    |||||||
                                TC ACGAGACG AC    CACACCA
                                 C       T  CGTTC
GAM148  LOC257549 5'  ACCACACCTTGCCATGCAGAGC 99587    A     _ TCCT_
          ACCT                    AG TGCTCTGC TG    GTGTGGT
                                || ||||||||  ||    |||||||
                                TC ACGAGACG AC    CACACCA
                                 C       T  CGTTC
GAM148  LOC257610 5'  ACCACACCTTGCCATGCAGAGC 99680    A     _ TCCT_
          ACCT                    AG TGCTCTGC TG    GTGTGGT
                                || ||||||||  ||    |||||||
                                TC ACGAGACG AC    CACACCA
                                 C       T  CGTTC
GAM148  LOC257611 5'  ACCACACCTTGCCATGCAGAGC 99689    A     _ TCCT_
          ACCT                    AG TGCTCTGC TG    GTGTGGT
                                || ||||||||  ||    |||||||
                                TC ACGAGACG AC    CACACCA
                                 C       T  CGTTC
GAM148  LOC90981  3'  CACAGCCAGCAGAACATC    65141     C     TC
                                GATG TCTGCTG  CTGTG
                                |||| |||||||  |||||
                                CTAC AGACGAC  GACAC
                                  A      C_
GAM149  ADCY8    5'  GGACATGCCTTTCTCCACGTCC 8502     A   A     __  CA
          GC                      GC GGAC TGGAGAA  GTA  TCC
                                || |||| |||||||  |||  |||
                                CG CCTG ACCTCTT  CGT  AGG
                                 _   C      TC   AC
GAM149  AKT2     5'  GTGCCTCCTGCATGTCCTGCT  9677          G  AA_
                                AGCAGGACATG AG   GTAC
                                ||||||||||| ||   ||||
                                TCGTCCTGTAC TC   CGTG
                                       G  CTC
GAM149  APOBEC2  3'  TACTTCTCATGCTGT      23280     GA   G
                                GCAG  CATG AGAAGTA
                                ||||  |||| |||||||
                                TGTC  GTAC TCTTCAT
                                  __   _
GAM149  GPD1     3'  GCTTTCTCCATATCCTCT    60397    C   C      _
                                AG AGGA ATGGAGAA GT
                                || |||| |||||||| ||
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                                TC TCCT TACCTCTT CG
                                 _   A       T
GAM149  HMGN2   3'  TGTCTGCCCATGTCCTGC    19810          AGA  T
                                GCAGGACATGG   AG ACA
                                ||||||||||   || |||
                                CGTCCTGTACC   TC TGT
                                      CG_  _
GAM149  MCM4    3'  GCTCCCTGCATGTCCTGCT   62579          G  A_
                                AGCAGGACATG AG  AGT
                                ||||||||||| ||  |||
                                TCGTCCTGTAC TC  TCG
                                      G  CC
GAM149  MEN1    3'  GGATGTACTAAAATGTATCCT  95013      C   GAGA
                                AGGA ATG    AGTACATCC
                                |||| |||    |||||||||
                                TCCT TGT    TCATGTAGG
                                  A   AAAA
GAM149  MTL5    3'  GATGTGGCAACCCATGCCCCCT 18199    CA  A    AGAAG
                                AG  GG CATGG    TACATC
                                ||  || |||||    ||||||
                                TC  CC GTACC    GTGTAG
                                 CC  _    CAACG
GAM149  MTMR3   5'  GCCTCGCCATGTCCTGCT    41164          A  A
                                AGCAGGACATGG GA GT
                                |||||||||||| || ||
                                TCGTCCTGTACC CT CG
                                      G  C
GAM149  PCDH9   3'  TGCTTCTCCACAGCCTGCT   83697       ACA
                                AGCAGG   TGGAGAAGTA
                                ||||||   ||||||||||
                                TCGTCC   ACCTCTTCGT
                                   GAC
GAM149  SLC39A1 3'  GCCTCTCCAGTCCTGCT     27813        A     A
                                AGCAGGAC TGGAGA GT
                                |||||||| |||||| ||
                                TCGTCCTG ACCTCT CG
                                   _     C
GAM149  SLC6A8  3'  GGATGCACTTCCCGCACCT   20073     ACA  A    A
                                AGG   TGG GAAGT CATCC
                                |||   ||| ||||| |||||
                                TCC   GCC CTTCA GTAGG
                                  AC_  _    C
GAM149  AD-020  3'  ACTTCTCCATTCCCTGCT    39713       AC
                                AGCAGG  ATGGAGAAGT
                                ||||||  ||||||||||
                                TCGTCC  TACCTCTTCA
                                   CT
GAM149  AD-020  3'  ACTTCTCCATTCCCTGCT    60090       AC
                                AGCAGG  ATGGAGAAGT
                                ||||||  ||||||||||
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                                TCGTCC  TACCTCTTCA
                                   CT
GAM149  ALDH9    3'  GTTCCTTCTCCATTCCCACT   7348     CA   C       T_
                                AG  GGA ATGGAGAAG  AC
                                ||  ||| |||||||||  ||
                                TC  CCT TACCTCTTC  TG
                                 AC   _        CT
GAM149  ARHGEF4  3'  GATGGCGCCCTGTCCTGC    53372        T  AGAA  A
                                GCAGGACA GG    GT CATC
                                |||||||| ||    || ||||
                                CGTCCTGT CC    CG GTAG
                                     _ CG__  _
GAM149  DDR1     3'  GGACACACTCTCATGTCC    10477        G   A  ACA
                                GGACATG AGA GT   TCC
                                ||||||| ||| ||   |||
                                CCTGTAC TCT CA   AGG
                                     _  _  CAC
GAM149  DDR1     3'  GGACACACTCTCATGTCC    26560        G   A  ACA
                                GGACATG AGA GT   TCC
                                ||||||| ||| ||   |||
                                CCTGTAC TCT CA   AGG
                                     _  _  CAC
GAM149  DDR1     3'  GGACACACTCTCATGTCC    26562        G   A  ACA
                                GGACATG AGA GT   TCC
                                ||||||| ||| ||   |||
                                CCTGTAC TCT CA   AGG
                                     _  _  CAC
GAM149  FLJ20150 3'  GTCCTCCCCCATGTCCTGC   35145          AGA  T
                                GCAGGACATGG   AG AC
                                ||||||||||   || ||
                                CGTCCTGTACC   TC TG
                                      CCC  C
GAM149  FLJ23259 3'  TGATTTCCCATGTCCTACT   45638    C       A    A
                                AG AGGACATGG GAAGT CA
                                || ||||||||| ||||| ||
                                TC TCCTGTACC CTTTA GT
                                 A       _    _
GAM149  GAL3ST2  3'  GCTGCCTCCATGTCCTGC    53484           A_
                                GCAGGACATGGAG  AGT
                                ||||||||||||  |||
                                CGTCCTGTACCTC  TCG
                                       CG
GAM149  GMEB2    3'  GCTCCTCCAGGTCCTGCT    25664        A    A
                                AGCAGGAC TGGAG AGT
                                |||||||| ||||| |||
                                TCGTCCTG ACCTC TCG
                                     G    C
GAM149  HMG17L1  3'  TGTCTGCCCATGTCCTGCT   41049          AGA  T
                                AGCAGGACATGG   AG ACA
                                ||||||||||||   || |||
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                                TCGTCCTGTACC   TC TGT
                                      CG_  _
GAM149  HNRPA3   3'  GGATATATACCCATGTCT    20453       AGAA   C
                                GGACATGG    GTA ATCC
                                ||||||||    ||| ||||
                                TCTGTACC    TAT TAGG
                                    CA__   A
GAM149  KIAA0441 3'  GGATGTACCACCACACCCAGCT 29636     A  ACA   AGAA
                                AGC GG   TGG    GTACATCC
                                ||| ||   |||    ||||||||
                                TCG CC   ACC    CATGTAGG
                                  A  CAC   AC__
GAM149  KIAA0522 3'  GTCCTCCTCCCCATGTCCT   72426        A  __  T
                                AGGACATGG GA  AG AC
                                ||||||||| ||  || ||
                                TCCTGTACC CT  TC TG
                                      C  CC  C
GAM149  KIAA1393 3'  TGTCTGCCCATGTCCTGC    72576         AGA  T
                                GCAGGACATGG   AG ACA
                                ||||||||||   || |||
                                CGTCCTGTACC   TC TGT
                                      CG_  _
GAM149  KIAA1922 3'  ATGTGGCATCATGTCCTGC   73987          AGAAG
                                GCAGGACATGG    TACAT
                                ||||||||||    |||||
                                CGTCCTGTACT    GTGTA
                                      ACG__
GAM149  LOC113220 5'  GGATGTACCATCTGCCCTTCT  57359    C   A  TG  GAA
                                AG AGG CA  GA   GTACATCC
                                || ||| ||  ||   ||||||||
                                TC TCC GT  CT   CATGTAGG
                                 T   C  __  AC_
GAM149  LOC143153 3'  GGCTGTTCTCCATCTCCCGCT  76980    A   C      AGT   T
                                AGC GGA ATGGAGA   ACA CC
                                ||| ||| |||||||   ||| ||
                                TCG CCT TACCTCT   TGT GG
                                  C   C      ____   C
GAM149  LOC145540 3'  TGTCTGCCCATGTCCTGC    77779         AGA  T
                                GCAGGACATGG   AG ACA
                                ||||||||||   || |||
                                CGTCCTGTACC   TC TGT
                                      CG_  _
GAM149  LOC148915 3'  TGTCTGCCCATGTCCTGC    79810         AGA  T
                                GCAGGACATGG   AG ACA
                                ||||||||||   || |||
                                CGTCCTGTACC   TC TGT
                                      CG_  _
GAM149  LOC150166 5'  GATATACTTCTTTCTTGCT   86038       CATG      C
                                AGCAGGA    GAGAAGTA ATC
                                |||||||    |||||||| |||
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                                TCGTTCT    TTCTTCAT TAG
                                   ____       A
GAM149   LOC150580 3'  TGTCTGCCCATGTCCTGC    61068          AGA  T
                                GCAGGACATGG   AG ACA
                                ||||||||||   || |||
                                CGTCCTGTACC   TC TGT
                                    CG_  _
GAM149   LOC152212 3'  TGTCTGCCCATGTCCTGC    83712          AGA  T
                                GCAGGACATGG   AG ACA
                                ||||||||||   || |||
                                CGTCCTGTACC   TC TGT
                                    CG_  _
GAM149   LOC152300 3'  ATGCACTTGTCCTGTT      81380         TGGAGA   A
                                AGCAGGACA     AGT CAT
                                |||||||||     ||| |||
                                TTGTCCTGT     TCA GTA
                                   _______  C
GAM149   LOC153346 5'  ATGCACTAGCTGTCCTGT    87203         TG AGA   A
                                GCAGGACA  G   AGT CAT
                                ||||||||  |   ||| |||
                                TGTCCTGT  C   TCA GTA
                                   __ GA_   C
GAM149   LOC153811 3'  GGACATACCATCTTGTCCTGCT 81839         T   GAA   CA
                                AGCAGGACA GGA   GTA  TCC
                                |||||||||  |||   |||  |||
                                TCGTCCTGT TCT   CAT  AGG
                                    _   AC_   AC
GAM149   LOC154807 5'  GATGGCGGCTCCCGTCCTGCT  87464         AT    AA  A
                                AGCAGGAC  GGAG  GT CATC
                                ||||||||  ||||  || ||||
                                TCGTCCTG  CCTC  CG GTAG
                                   C_    GG  _
GAM149   LOC196453 5'  ATGACATTTCATGTCCCACT   92341    CA         AA  A
                                AG  GGACATGGAG  GT CAT
                                ||  ||||||||||  || |||
                                TC  CCTGTACTTT  CA GTA
                                 AC         A_  _
GAM149   LOC221468 3'  ACTTCTCCATAGTCCTGCT    60003          _
                                AGCAGGAC ATGGAGAAGT
                                |||||||| ||||||||||
                                TCGTCCTG TACCTCTTCA
                                   A
GAM149   LOC254000 3'  TGTCTGCCCATGTCCTGC    96615          AGA  T
                                GCAGGACATGG   AG ACA
                                ||||||||||   || |||
                                CGTCCTGTACC   TC TGT
                                    CG_  _
GAM149   LOC257153 5'  GGCTGTTTCTCACATCCTGC   97467        CA  _    GT   T
                                GCAGGA  TG GAGAA  ACA CC
                                ||||||  || |||||  ||| ||
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                                CGTCCT  AC CTCTT  TGT GG
                                   __ A    __  C
GAM149  LOC88584  3'  GATTATCTGCCCATGTCCTGC  61102          AGA  TAC
                                GCAGGACATGG  AG  ATC
                                ||||||||||  ||  |||
                                CGTCCTGTACC  TC  TAG
                                     CG_  TAT
GAM150  BGN     3'  CCAGCCCCCCACCTCGGGTCCC 9923         C   CAGAGA
          T                      AGGGACCC AGGT    CTGG
                                ||||||||  ||||    ||||
                                TCCCTGGG TCCA    GACC
                                    C   CCCCCC
GAM150  BLMH    3'  TCCAGTCTCCACCAGGAACCT  6361     GA  CCA  CA
                                AGG  CC  GGT  GAGACTGGA
                                |||  ||  |||  |||||||||
                                TCC  GG  CCA  CTCTGACCT
                                  AA  A__  C_
GAM150  HSPA1B  5'  CCAGTCTCAGAGCGGAGCCC  19273    AC  CAGG  A
                                GGG  CC   TC GAGACTGG
                                |||  ||   || ||||||||
                                CCC  GG   AG CTCTGACC
                                  GA  CG__  A
GAM150  HTRA3   3'  CCACCTGACCTGAGGCCCC   90577    A  C      AGAC
                                GGG CC CAGGTCAG   TGG
                                ||| || ||||||||   |||
                                CCC GG GTCCAGTC   ACC
                                  C  A      C___
GAM150  HTRA3   3'  CTGCCAGCCTGGGGTCCCT   90580          ___
                                AGGGACCCCAGGT  CAG
                                ||||||||||||  |||
                                TCCCTGGGGTCCG  GTC
                                       ACC
GAM150  IL2RB   3'  CCAGCTAACTCTGACCTGGGAG 7935     AC        A___
          CCCT                  AGGG  CCCAGGTCAGAG   CTGG
                                ||||  ||||||||||||   ||||
                                TCCC  GGGTCCAGTCTC   GACC
                                  GA         AATC
GAM150  LENG4   3'  CCTATGACCTGGGTCCCT   44417       C    GAGACT
                                AGGGACCC AGGTCA    GG
                                |||||||| ||||||    ||
                                TCCCTGGG TCCAGT    CC
                                    _    AT_____
GAM150  LNK     3'  TCCTGCCCGGGGTCCCT    19652        A  T  A
                                AGGGACCCC GG CAG GA
                                ||||||||| || ||| ||
                                TCCCTGGGG CC GTC CT
                                     C  _  _
GAM150  LY95    5'  CCAGTCTTCTCCAGGTGTCCC  17896     C  A  TCA
                                GGGAC CC GG  GAGACTGG
                                ||||| || ||  ||||||||
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                                CCCTG GG CC   TTCTGACC
                                  T  A  TC_
GAM150  MOG     3'  TCCAGTCTTCCACCTGGAAGCC 11676     ACC     CA
            CT                   AGGG   CCAGGT  GAGACTGGA
                                ||||   ||||||  |||||||||
                                TCCC   GGTCCA  TTCTGACCT
                                  GAA     CC
GAM150  NESH    5'  CCAGTCTCCGACCCCATCCC   33570     CCCCA   A
                                GGGA    GGTC GAGACTGG
                                ||||    |||| ||||||||
                                CCCT    CCAG CTCTGACC
                                  ACC__   C
GAM150  NFATC1   3'  CCAGCCCTTCTGGCACCCCT   21596     ACCCCAG     A__
                                AGGG     GTCAGAG   CTGG
                                ||||     |||||||   ||||
                                TCCC     CGGTCTT   GACC
                                  CA_____     CCC
GAM150  RANBP3   3'  CCAACTATAGGCCTGGGACCCC 24641     AC      AG_  AC
                                GGG  CCCAGGTC   AG  TGG
                                |||  ||||||||   ||  |||
                                CCC  GGGTCCGG   TC  ACC
                                  CA       ATA  A_
GAM150  RANBP3   3'  CCAACTATAGGCCTGGGACCCC 14633     AC      AG_  AC
                                GGG  CCCAGGTC   AG  TGG
                                |||  ||||||||   ||  |||
                                CCC  GGGTCCGG   TC  ACC
                                  CA       ATA  A_
GAM150  RGS19IP1 3'  CCAGTCTGGCCGGGGTCCC    63169       A    GA
                                GGGACCCC GGTCA  GACTGG
                                |||||||| |||||  ||||||
                                CCCTGGGG CCGGT  CTGACC
                                    _    __
GAM150  SIRT2    3'  CCAATCTCTTACAGCTCCCT   25286      CCCCAG  C    C
                                AGGGA     GT AGAGA TGG
                                |||||     || ||||| |||
                                TCCCT     CA TCTCT ACC
                                  CGA___  T    A
GAM150  SIRT2    3'  CCAATCTCTTACAGCTCCCT   48360      CCCCAG  C    C
                                AGGGA     GT AGAGA TGG
                                |||||     || ||||| |||
                                TCCCT     CA TCTCT ACC
                                  CGA___  T    A
GAM150  SREBF1   3'  TCCTGACCTGAGGCTCCT    96078     GA  C      A
                                AGG  CC CAGGTCAG GA
                                |||  || |||||||| ||
                                TCC  GG GTCCAGTC CT
                                  TC  A      _
GAM150  TEM5     3'  CCAAGGTCTGACCTAGGGTTCC 52297       C      GA  _
                                GGGACCC AGGTCAGA  CT GG
                                ||||||| ||||||||  || ||
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                                CCTTGGG TCCAGTCT  GA CC
                                    A       G_  A
GAM150  TIMM17B  3'  CCAGTTAGCCCTGGGACCCT  20690     AC     TCAGA
                                AGGG  CCCAGG    GACTGG
                                ||||  ||||||    ||||||
                                TCCC  GGGTCC    TTGACC
                                  A_     CGA__
GAM150  ARHGDIG  3'  CCTGCTCTGTCCCGGGACCCC  8620     AC   A  T    ACT
                                GGG  CCC GG CAGAG   GG
                                |||  ||| || |||||   ||
                                CCC  GGG CC GTCTC   CC
                                  CA   C  T    GT_
GAM150  ATP5D    3'  CCAGCTCCTGGGGTCCC     9859          TCAG  A
                                GGGACCCCAGG    AG CTGG
                                ||||||||||    || ||||
                                CCCTGGGGTCC    TC GACC
                                      _____  _
GAM150  C17orf31  3'  CCTTATCAACCTGGGTCCCT  34538        C    CA  GACT
                                AGGGACCC AGGT  GA    GG
                                |||||||| ||||  ||    ||
                                TCCCTGGG TCCA  CT    CC
                                    _    A_  ATT_
GAM150  C2orf7   3'  TCCAGCCTCCCCTACCCAGGGT 51274        CA   CA__   A
           CTCT                   AGGGACCC  GGT    GAG CTGGA
                                |||||||  |||    ||| |||||
                                TCTCTGGG  CCA    CTC GACCT
                                     AC   TCCC   C
GAM150  CLIPR-59  5'  CCAGTCTCCACTTTGGTCCC   32015       CC    CA
                                GGGACC  AGGT  GAGACTGG
                                ||||||  ||||  ||||||||
                                CCCTGG  TTCA  CTCTGACC
                                   T_    C_
GAM150  CLIPR-59  3'  TCCAGGGCGGACCTGGGGCCCC 32021     A        AGAGA
                                GGG CCCCAGGTC     CTGGA
                                ||| |||||||||     |||||
                                CCC GGGGTCCAG     GACCT
                                  C        GCGG_
GAM150  COL12A1   3'  CCAGTCTCTGACCCTTCCC    16470     CCCCA
                                GGGA    GGTCAGAGACTGG
                                ||||    ||||||||||||
                                CCCT    CCAGTCTCTGACC
                                  TC___
GAM150  COL12A1   3'  CCAGTCTCTGACCCTTCCC    55534     CCCCA
                                GGGA    GGTCAGAGACTGG
                                ||||    ||||||||||||
                                CCCT    CCAGTCTCTGACC
                                  TC___
GAM150  CYP2A7    5'  TCAGCTGCCCTGGGGTCCC    7542           T   AGA
                                GGGACCCCAGG CAG   CTGG
                                |||||||||| |||   ||||
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                                CCCTGGGGTCC GTC   GACT
                                      C  ___
GAM150  CYP2A7   5'  TCAGCTGCCCTGGGGTCCC   48354          T  AGA
                                GGGACCCCAGG CAG   CTGG
                                |||||||||| |||   ||||
                                CCCTGGGGTCC GTC   GACT
                                      C  ___
GAM150  FASTK    3'  CCAGGATACCGGGGTCCC    47685        A  CAGAGA
                                GGGACCCC GGT     CTGG
                                |||||||| |||     ||||
                                CCCTGGGG CCA     GACC
                                   _  TAG___
GAM150  FBXL9    3'  CCAGTCTCCAACCCTGGCCTT  25139     ACC    TCA_
                                AGGG  CCAGG   GAGACTGG
                                ||||  |||||   ||||||||
                                TTCC  GGTCC   CTCTGACC
                                  ___    CAAC
GAM150  FLJ10874 3'  TCCAGAAAGAGTGACCTGGTGT 37330      C      GAGA__
            CCC                   GGGAC CCAGGTCA     CTGGA
                                |||||| ||||||||     |||||
                                CCCTG GGTCCAGT     GACCT
                                   T       GAGAAA
GAM150  FLJ13241 3'  CCAGTCTCTCAGGCCTCCC   47649     CCCCA   __
                                GGGA    GGTC  AGAGACTGG
                                ||||    ||||  |||||||||
                                CCCT    CCGG  TCTCTGACC
                                  ______   AC
GAM150  GIT1     3'  CCAACCTGTGTGCTGGGGTCCC 26720         GT  G  AC
                                GGGACCCCAG  CA AG  TGG
                                ||||||||||  || ||  |||
                                CCCTGGGGTC  GT TC  ACC
                                      GT  G  CA
GAM150  HYPC     5'  CCAGCCCCTGGAACAGGGGTTC 65216         AGG_   AGA
            CT                    AGGGACCCC   TCAG   CTGG
                                |||||||||   ||||  ||||
                                TCCTTGGGG   GGTC   GACC
                                     ACAA   CCC
GAM150  KIAA0258 3'  CCAGCCTCCTAGGATCCC    29466     C  C   TCAG  A
                                GGGA CC AGG    AG CTGG
                                |||| || |||    || ||||
                                CCCT GG TCC    TC GACC
                                  A  A  _____  C
GAM150  KIAA0397 3'  CCACGAGTGAACCTGGGGCCCC 62345     A      _  GAGAC
                                GGG CCCCAGGT CA    TGG
                                ||| |||||||| ||    |||
                                CCC GGGGTCCA GT    ACC
                                  C       A  GAGC_
GAM150  KIAA0447 3'  TCCAGTTTCCCTGCGGGCCCCT 72130     A  _   TCA
                                AGGG CCC CAGG   GAGACTGGA
                                |||| ||| ||||   |||||||||
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                                TCCC GGG GTCC   CTTTGACCT
                                  C   C   ___
GAM150  KIAA0449  5' CAGTTCCCTGGGGTCCCT    34634          TCAGA
                                AGGGACCCCAGG    GACTG
                                ||||||||||||    |||||
                                TCCCTGGGGTCC    TTGAC
                                      C____
GAM150  KIAA0493  5' CCAGCCCGAGACGCCTGGGGTC 64930          CAGAGA__
           CC                   GGGACCCCAGGT      CTGG
                                ||||||||||||      ||||
                                CCCTGGGGTCCG      GACC
                                      CAGAGCCC
GAM150  KIAA0674  3' TCAGACTGACCTGGGAGCCCT  61244     AC       AGA
                                AGGG  CCCAGGTCAG   CTGG
                                ||||  ||||||||||   ||||
                                TCCC  GGGTCCAGTC   GACT
                                  GA        A__
GAM150  KIAA1130  5' CCAGTCCCCCACCTGGGGCGCC 63082     A_      CAGA
           C                    GGG  CCCCAGGT    GACTGG
                                |||  ||||||||    ||||||
                                CCC  GGGGTCCA    CTGACC
                                  GC       CCCC
GAM150  KIAA1465  3' TCCAGCCCGGTGCCTGGGGCGC 61510     GA       CAGAGA
           CT                   AGG  CCCCAGGT     CTGGA
                                |||  ||||||||     |||||
                                TCC  GGGGTCCG     GACCT
                                  GC       TGGCCC
GAM150  KIAA1719  3' TCTGTCTCCAACCTGGGGTCCC 68740          CA     T
           T                    AGGGACCCCAGGT  GAGAC GGA
                                ||||||||||||  ||||| |||
                                TCCCTGGGGTCCA  CTCTG TCT
                                      AC    _
GAM150  KIAA1856  3' CCGGCCCAAGCCCAGGGTCCCT 94230        CA   CAGAGA
                                AGGGACCC  GGT     CTGG
                                ||||||||  |||     ||||
                                TCCCTGGG  CCG     GGCC
                                    AC   AACCC_
GAM150  KIAA1924  3' TCCAGCTTCATGTGACCCTGGG 74059        CA    _____   A
           TCCCT                  AGGGACCC  GGTCA    GAG CTGGA
                                ||||||||  |||||    ||| |||||
                                TCCCTGGG  CCAGT    TTC GACCT
                                    TC    GTAC  _
GAM150  KIAA1949  5' CCAGTCTCCGGATCTCCC    99590     CCCCA    A_
                                GGGA    GGTC  GAGACTGG
                                ||||    ||||  ||||||||
                                CCCT    CTAG  CTCTGACC
                                  _____   GC
GAM150  KIAA1949  5' CCAGTCTCCGGATCTCCC    99694     CCCCA    A_
                                GGGA    GGTC  GAGACTGG
                                ||||    ||||  ||||||||
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                                CCCT    CTAG  CTCTGACC
                                  _____   GC
GAM150  KIAA1949 5' CCAGTCTCCGGATCTCCC    93717     CCCCA   A_
                                GGGA    GGTC  GAGACTGG
                                ||||    ||||  ||||||||
                                CCCT    CTAG  CTCTGACC
                                  _____   GC
GAM150  KIAA1978 3' CCAGCCGTGGGGCCCGGGGTCC 74890         A   AGAGA_
          CT                      AGGGACCCC GGTC     CTGG
                                |||||||| ||||     ||||
                                TCCCTGGGG CCGG     GACC
                                    C   GGTGCC
GAM150  LASP1   3' CCAGTCTCCAGGGACCCT    21576     A   CAGGTCA
                                AGGG CCC      GAGACTGG
                                |||| |||      ||||||||
                                TCCC GGG      CTCTGACC
                                  A   AC_____
GAM150  MAPK11   3' TTCTGGCCTAGGACCCCT    12314     AC  C
                                AGGG  CC AGGTCAGAG
                                ||||  || |||||||||
                                TCCC  GG TCCGGTCTT
                                  CA  A
GAM150  MAPK11   3' TTCTGGCCTAGGACCCCT    58102     AC  C
                                AGGG  CC AGGTCAGAG
                                ||||  || |||||||||
                                TCCC  GG TCCGGTCTT
                                  CA  A
GAM150  MGC14859 3' TCTCTGACTGGGGCCCCT    62604     A     G
                                AGGG CCCCAG TCAGAGA
                                |||| |||||| |||||||
                                TCCC GGGGTC AGTCTCT
                                  C     _
GAM150  MGC15438 5' CCAGTCTCACAAAGGCCCC    52850     A  CCAG  CA
                                GGG CC    GT  GAGACTGG
                                ||| ||    ||  ||||||||
                                CCC GG    CA  CTCTGACC
                                  C  AAA_  __
GAM150  NLI-IF   3' TCCAACTGTTTCTGAAGCCCCT 41344      ACCCCAGG      ___
                                AGGG       TCAGAGAC   TGGA
                                ||||       ||||||||   ||||
                                TCCC       AGTCTTTG   ACCT
                                  CGA_____       TCA
GAM150  NOLC1    3' TCCAGTGGACCTGGGAACCCT  17637     AC       AGAG
                                AGGG  CCCAGGTC    ACTGGA
                                ||||  ||||||||    ||||||
                                TCCC  GGGTCCAG    TGACCT
                                  AA       G___
GAM150  PRO2389  3' CCAGTCAGCTTGGGTCCCT    64475        C    CAGA
                                AGGGACCC AGGT    GACTGG
                                |||||||| ||||    ||||||
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                                TCCCTGGG TTCG   CTGACC
                                    _   A___
GAM150  SHANK3   3'  CCAGCCTGAGCGGGGTTCC   66102       AGG   AGA
                                GGGACCCC  TCAG  CTGG
                                ||||||||  ||||  ||||
                                CCTTGGGG  AGTC  GACC
                                    CG_   C__
GAM150  SMARCA4  3'  TCCAGTCTCGACCCCGAGCCCC 13248     ACCCCA   A
           T                     AGGG     GGTC GAGACTGGA
                                ||||     |||| |||||||||
                                TCCC     CCAG CTCTGACCT
                                  CGAGCC   _
GAM150  SPIB     3'  CCACTTGTGCCTGGGGTCCCT  13355          CA   AC
                                AGGGACCCCAGGT  GAG  TGG
                                ||||||||||||  |||  |||
                                TCCCTGGGGTCCG  TTC  ACC
                                       TG  __
GAM150  SYNGR4   5'  CCAGGGCTGGCCTGAAGCCC  25864    ACCC      AGA
                                GGG   CAGGTCAG  CTGG
                                |||   ||||||||  ||||
                                CCC   GTCCGGTC  GACC
                                  GAA_      GG_
GAM150  T2BP     5'  CCAGTCTCCTCGATTCCC    70535     CCCCAG  A__
                                GGGA    GTC   GAGACTGG
                                ||||    |||  ||||||||
                                CCCT    TAG  CTCTGACC
                                  _______  CTC
GAM150  TACR3    5'  TCCAGTCTTATCTGAAGACCC  8331     ACCC    CA
                                GGG   CAGGT  GAGACTGGA
                                |||   |||||  |||||||||
                                CCC   GTCTA  TTCTGACCT
                                  AGAA    __
GAM150  TOMM40   3'  CCAGTGGGCCTGGGGTCCC   21482          AGAG
                                GGGACCCCAGGTC   ACTGG
                                ||||||||||||   |||||
                                CCCTGGGGTCCGG   TGACC
                                       G___
GAM150  TREX2    5'  TCCAACCTCTGACTGGCTGGTC 24233      __   G     AC
           CT                     GGGACC  CCAG TCAGAG  TGGA
                                ||||||  |||| ||||||  ||||
                                TCCTGG  GGTC AGTCTC  ACCT
                                   TC   _     CA
GAM150  VPS4A    3'  CCAGCCACTGCCCCTGGGTCCC 26020       CA  T   AGA
           T                     AGGGACCC  GG CAG   CTGG
                                ||||||||  || |||   ||||
                                TCCCTGGG  CC GTC   GACC
                                     TC  C   ACC
GAM150  LOC143287 3'  TCCGCTGTAACCCTAGGACCCC 83831     AC  C   T___   AGAC
                                GGG  CC AGG   CAG   TGGA
                                |||  || |||   |||   ||||
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                                CCC  GG TCC    GTC    GCCT
                                  CA  A   CAAT   ____
GAM150   LOC147136 3'  CCAGTGAGAACTGACCTGAGTC 78862      CC       AG___
                 CC                 GGGAC  CAGGTCAG     ACTGG
                                    |||||  ||||||||     |||||
                                    CCCTG  GTCCAGTC     TGACC
                                      A_       AAGAG
GAM150   LOC147929 5'  TCCAGCAGCCTTGGGGTCCC   79273         _   CAGAGA
                                    GGGACCCCA GGT      CTGGA
                                    |||||||||  |||      |||||
                                    CCCTGGGGT CCG      GACCT
                                          T   AC____
GAM150   LOC149566 3'  TCCAGCCTGGATGACCTGGGAC 85654     AC       G__  A
                 CCC                  GGG  CCCAGGTCA   AG CTGGA
                                    |||  |||||||||   || |||||
                                    CCC  GGGTCCAGT   TC GACCT
                                      CA        AGG  C
GAM150   LOC149773 5'  CCAGTCTTCTGAGGCCCT    80291      A  C   GTCA
                                    AGGG CC CAG    GAGACTGG
                                    |||| || |||    ||||||||
                                    TCCC GG GTC    TTCTGACC
                                      _ A   ____
GAM150   LOC152189 5'  TCCAGCCCCAGACCCGCCGGGG 81329          A___    AGAGA
                 TCCCT                AGGGACCCC    GGTC     CTGGA
                                    |||||||||    ||||     |||||
                                    TCCCTGGGG    CCAG     GACCT
                                         CCGC    ACCCC
GAM150   LOC153196 5'  CCAGTCTCAGGGGTCACC    87166    _     AGGTCA
                                    GG GACCCC      GAGACTGG
                                    || ||||||      ||||||||
                                    CC CTGGGG      CTCTGACC
                                     A     A_____
GAM150   LOC154807 5'  CTCTGCGACCTGGGGCCCT    87463      A        __
                                    AGGG CCCCAGGTC  AGAG
                                    |||| |||||||||  ||||
                                    TCCC GGGGTCCAG  TCTC
                                      _        CG
GAM150   LOC199958 3'  CCAGTCTCTGGCAACGCCCCT  91490      ACCCCAG
                                    AGGG       GTCAGAGACTGG
                                    ||||       ||||||||||||
                                    TCCC       CGGTCTCTGACC
                                      CGCAA__
GAM150   LOC201685 5'  CCAGTCTCATTGAATCCCT    91840      CCC   GTCA
                                    AGGGA   CAG    GAGACTGG
                                    |||||   |||    ||||||||
                                    TCCCT   GTT    CTCTGACC
                                      AA_   A___
GAM150   LOC204970 3'  CCAGCCGGAGCGTGGGGTCCC  90959          G  CAGAGA
                                    GGGACCCCA GT      CTGG
                                    ||||||||| ||      ||||
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                                CCCTGGGGT CG     GACC
                                     G  AGGCC_
GAM150  LOC221179 3'  CCAGTCTCTCCTCGGAGGCCCT 95193     A  _  _  TC
                                AGGG CC CC AGG  AGAGACTGG
                                |||| || || |||  |||||||||
                                TCCC GG GG TCC  TCTCTGACC
                                  _  A  C  __
GAM150  LOC254105 3'  CCAGTCCAGGGCCTGGGCTCCC 96419     C      AGA
                                GGGA CCCAGGTC   GACTGG
                                |||| ||||||||   ||||||
                                CCCT GGGTCCGG   CTGACC
                                  C       GAC
GAM150  LOC257185 5'  CCAGCATGCCAGGGGTCCC   98020       A  T  GAGA
                                GGGACCCC GG CA   CTGG
                                |||||||| || ||   ||||
                                CCCTGGGG CC GT   GACC
                                     A  _  AC__
GAM150  LOC51161  3'  TCCTGACCTGAGGGCCCT    33046     A  _      A
                                AGGG CCC CAGGTCAG GA
                                |||| ||| |||||||| ||
                                TCCC GGG GTCCAGTC CT
                                  _  A      _
GAM150  LOC91156  5'  CCAACTAAGGCCTGAGAGTCCC 65706      CC_    AG  AC
          T                      AGGGAC   CAGGTC  AG  TGG
                                ||||||  ||||||  ||  |||
                                TCCCTG   GTCCGG  TC  ACC
                                   AGA     AA  A_
GAM151  ITGA1    3'  CCAATGAGACAGTCCCTGA   64271      A   CAT  CA
                                TCAGG GAC   TG  TCATTGG
                                ||||| |||   ||  |||||||
                                AGTCC CTG   AC  AGTAACC
                                  _  ____  AG
GAM151  SH3GL3   5'  GCCAATATGGTCTCGATCTCCT 13111        CCATT  ATC
          GA                     TCAGGAGA    GC   ATTGGC
                                ||||||||    ||  ||||||
                                AGTCCTCT    TG   TAACCG
                                     AGCTC  GTA
GAM151  TRPM6    3'  CAATGATTGCCTCTGA     35028      G  ACCATT  _
                                TCAG AG     GCA TCATTG
                                |||| ||     ||| ||||||
                                AGTC TC     CGT AGTAAC
                                  _ _______  T
GAM151  ARHGEF15  3'  GCCAATGAAAACGGCCGCCTGA 30954      AGA  ATTGCA
                                TCAGG   CC     TCATTGGC
                                |||||   ||     ||||||||
                                AGTCC   GG     AGTAACCG
                                   GCC  CAAA__
GAM151  DKFZp434F2322 3'  CCACCGACGATCTCCTGA    70299        CCA   CA  AT
                                TCAGGAGA   TTG  TC  TGG
                                ||||||||   |||  ||  |||
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                                AGTCCTCT  AGC  AG  ACC
                                    ___   __  CC
GAM151  FLJ10716  3'  GCCACGTATCAACAATCTTCTG 37018        CCA   C  CAT
          A                      TCAGGAGA  TTG AT  TGGC
                                 ||||||||  ||| ||  ||||
                                 AGTCTTCT  AAC TA  ACCG
                                     AAC  _  TGC
GAM151  KIAA0527  3'  GCCACCTGCAATAGTCTCCTG  97499        C     TCAT
                                 CAGGAGAC ATTGCA   TGGC
                                 ||||||||  ||||||   ||||
                                 GTCCTCTG TAACGT   ACCG
                                     A    CC__
GAM151  KIAA1111  3'  GCCAATGACGCAGATAACCCTG 97946      AGACCA   A
          G                      TCAGG     TTGC TCATTGGC
                                 |||||     ||||  ||||||||
                                 GGTCC     GACG AGTAACCG
                                   CAATA_   C
GAM151  Kv6.3    3'  GCCAATGATGCAAAGGTCCCC  56855    A   A
                                 GG GACC TTGCATCATTGGC
                                 ||  ||||  ||||||||||||
                                 CC CTGG AACGTAGTAACCG
                                  C   A
GAM151  LOC145547 3'  GCCAATGGAGACAATTCCTGA  77782      GACC   CA_
                                 TCAGGA   ATTG   TCATTGGC
                                 ||||||   ||||   ||||||||
                                 AGTCCT   TAAC   GGTAACCG
                                     _____   AGA
GAM151  LOC162333 5'  GCCAATGACTGAGAACGCCCCT 88494      AGACCATTG  _
          GA                     TCAGG       CA TCATTGGC
                                 |||||       ||  ||||||||
                                 AGTCC       GT AGTAACCG
                                   CCGCAAGA_  C
GAM152  ATP12A   5'  GGCCCCCCACCGTGCGCT    9817         CAA   T
                                 AGCGCACG   GGGG GTC
                                 ||||||||   ||||  |||
                                 TCGCGTGC   CCCC CGG
                                     CAC   _
GAM152  AXIN1    5'  GGCTGGGCCCCTGCGGCGC   61539     A   A    GT  _
                                 GCGC CGCA GGGGT  CCA CC
                                 ||||  ||||  |||||  |||  ||
                                 CGCG GCGT CCCCG  GGT GG
                                   _   _    __   C
GAM152  BRF1     3'  GGCAGACACCCCCACCCCTGCC 9504     C   CGCAA_      CA
          T                      AG GCA     GGGGTGTC  CC
                                 ||  |||     ||||||||  ||
                                 TC CGT     CCCCACAG  GG
                                  _  CCCCAC       AC
GAM152  CDC20    5'  GACCCCTCCCCCTGCGGGCGCT 8832       A   A   T___
                                 AGCGC CGCA GGGG   GTC
                                 |||||  ||||  ||||   |||
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                                TCGCG GCGT CCCC   CAG
                                  G   C   TCCC
GAM152  CDKN2A   5' GGCGGACCGCGTGCGCT    55240        AA  GG
                                AGCGCACGC  GG  TGTC
                                |||||||||  ||  ||||
                                TCGCGTGCG  CC  GCGG
                                     __  AG
GAM152  CDKN2A   5' GGCGGACCGCGTGCGCT    5372         AA  GG
                                AGCGCACGC  GG  TGTC
                                |||||||||  ||  ||||
                                TCGCGTGCG  CC  GCGG
                                     __  AG
GAM152  CLCN7    3' GGCGCCTCCTTGCGCAGGC   8913    GCA     _
                                GC   CGCAAGG GGTGTC
                                ||   ||||||| ||||||
                                CG   GCGTTCC CCGCGG
                                 GAC      T
GAM152  HS3ST3A1 5' GGTGGACGGCTCTGCACGGGCC 21275   C  A  CA_   G
           T                     AG GC CG   AGGG TGTCCACC
                                 || || ||   |||| ||||||||
                                 TC CG GC   TCTC GCAGGTGG
                                  _ G  ACG   G
GAM152  INHBB    3' GGGAGGCTGCGTGTGC     11008        AGGG  G   A
                                GCGCACGCA   GT TCC C
                                |||||||||   || ||| |
                                CGTGTGCGT   CG AGG G
                                     ____  G   C
GAM152  NEURL    5' GGCGGGCACCCGCGCGCGC   16131     A   AAG      A
                                GCGC CGC   GGGTGTCC CC
                                |||| |||   |||||||| ||
                                CGCG GCG   CCCACGGG GG
                                  C  ___       C
GAM152  PITX1    5' GGCAGCCGCTTAGCGTGCGCT  12139        _  _  G
                                AGCGCACGC AAG GG TGTC
                                ||||||||| ||| || ||||
                                TCGCGTGCG TTC CC ACGG
                                     A  G  G
GAM152  PROS1    5' GGCGCCTCCGCGCGCTT     88815       A  CAA
                                AAGCGC CG   GGGGTGTC
                                ||||||  ||   ||||||||
                                TTCGCG GC   CTCCGCGG
                                   C  ___
GAM152  RPH3AL   5' GTGGACACTTGTACGTGCACTT 23739     C    CAAG
                                AAG GCACG   GGGTGTCCAC
                                ||| |||||   ||||||||||
                                TTC CGTGC   TTCACAGGTG
                                  A    ATG_
GAM152  SLC22A5  5' GGCGGGTGCCCCGCGCGCACGC 13228    CA  AA   TG  A
                                GCG  CGC  GGGG  TCC CC
                                |||  |||  ||||  ||| ||
```

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                                CGC  GCG  CCCC  GGG GG
                                  AC   CG   GT   C
GAM152  TNP1     3'  GGGCTCTGCCCTGGTGCGCTT  60162        G  A   GT__
                                AAGCGCAC CA GGG   GTCC
                                |||||||| || |||   ||||
                                TTCGCGTG GT CCC   CGGG
                                    _ _  GTCT
GAM152  TRAP100  3'  GTGGTCACCCCTGTGTGCGC  29724         A     T
                                GCGCACGCA GGGGTG CCAC
                                ||||||||| |||||| ||||
                                CGCGTGTGT CCCCAC GGTG
                                     _     T
GAM152  BIKE     5'  GGCGACCCCTCGCGGACGC   34607     CA   A     _
                                GCG  CGC AGGGGT GTC
                                |||  ||| |||||| |||
                                CGC  GCG TCCCCA CGG
                                  AG   C     G
GAM152  C20orf124 3'  GGCGCGGCTCCGCGTGCGC   45842        AA    _ _
                                GCGCACGC  GGGGT GT CC
                                ||||||||  ||||| || ||
                                CGCGTGCG  CCTCG CG GG
                                    __    G  C
GAM152  CAMK2G   3'  TGCACGCCCCTGCATGCAGC  69537    _  C   A     C
                                GC GCA GCA GGGGTGT CA
                                || ||| ||| ||||||| ||
                                CG CGT CGT CCCCGCA GT
                                 A   A   _      C
GAM152  CASKIN1  3'  GTGGAGTTCCCACGGACGCTT  40783      CA  CAA    TG
                                AAGCG  CG   GGGG  TCCAC
                                |||||  ||   ||||  |||||
                                TTCGC  GC   CCCT  AGGTG
                                   AG  A__   TG
GAM152  DGKD     3'  GAGACACCCCGTGGCT      60107     G   GCAA       CA
                                AGC CAC    GGGGTGTC  C
                                ||| |||    ||||||||  |
                                TCG GTG    CCCCACAG  G
                                  _  _____       AC
GAM152  ERP70    3'  GGCAGACGCCCTGCGTGGC   96145    G     AG      CA
                                GC CACGCA  GGGTGTC  CC
                                || ||||||  |||||||  ||
                                CG GTGCGT  CCCGCAG  GG
                                  _     __      AC
GAM152  FLJ00001 3'  GGTGCCCCCGCATGCCCT    82716    C   C  AA     T
                                AG GCA GC  GGGGTG CC
                                || ||| ||  |||||| ||
                                TC CGT CG  CCCCGT GG
                                 C   A  C_     _
GAM152  FLJ10159 3'  GGTAGATTCACTTGTGTGCACT 36336     C        GGGT   C
           T                     AAG GCACGCAAG    GTC ACC
                                ||| |||||||||    ||| |||
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                                TTC CGTGTGTTC    TAG TGG
                                  A        ACT_   A
GAM152   FLJ13241  3'  GATGCCGCCCTGCGTGCGCT   47654          A  _
                                AGCGCACGCA GG GGTGTC
                                |||||||||| || ||||||
                                TCGCGTGCGT CC CCGTAG
                                      C  G
GAM152   GPR       3'  GGTGGGTACCCCATGTGCACTT 24293     C     CAA     GT
                                AAG GCACG   GGGGT  CCACC
                                ||| |||||   |||||  |||||
                                TTC CGTGT   CCCCA  GGTGG
                                  A    A__     TG
GAM152   HSPC065   3'  GGTGAAGAGGCCCTTGTGTGC  27158          G G  __
                                GCACGCAAGGG T TC  CACC
                                |||||||||| | ||  ||||
                                CGTGTGTTCCC G AG  GTGG
                                      _ G  AA
GAM152   HUMAGCGB  5'  GGCGCCTCGCGCGTGCCT    26133    C     AA
                                AG GCACGC  GGGGTGTC
                                || ||||||  ||||||||
                                TC CGTGCG  CTCCGCGG
                                 _     CG
GAM152   KIAA0229  3'  GATGCTCCCCCGCGTGGC    94028    G     AA  _
                                GC CACGC  GGG GTGTC
                                || |||||  ||| |||||
                                CG GTGCG  CCC CGTAG
                                 _    CC   T
GAM152   KIAA0275  5'  GACAGCCGCGTGCGCTT     29327          AAG  G
                                AAGCGCACGC   GG TGTC
                                ||||||||||   || ||||
                                TTCGCGTGCG   CC ACAG
                                      ___  G
GAM152   KIAA0418  3'  GTGGATTTCCACACGTGCCT   28298    C     CAAG   T
                                AG GCACG    GGG GTCCAC
                                || |||||    ||| ||||||
                                TC CGTGC    CCT TAGGTG
                                 _    ACA_   T
GAM152   KIAA0794  3'  GTGGTCTCTTGCACGGCACTT  81236     C  AC_       TGT
                                AAG GC   GCAAGGGG   CCAC
                                ||| ||   ||||||||   ||||
                                TTC CG   CGTTCTCT   GGTG
                                  A  GCA       ___
GAM152   KIAA1635  3'  GGACATTTATTTGCATCGCT   68461      CAC    _
                                AGCG   GCAAG GGGTGTCC
                                ||||   ||||| ||||||||
                                TCGC   CGTTT TTTACAGG
                                  TA_    A
GAM152   KIAA1656  3'  TGAACACCCCCTTCCTTGCTGC 66387     C   _____      C
                                GCA GCAA    GGGGTGT CA
                                ||| ||||    ||||||| ||
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                                CGT CGTT    CCCCACA GT
                                  _   CCTTC      A
GAM152  KIAA1671  3'  TGGACACCCCTCAGCCCGC   66292    CAC  A_
                                GCG   GC  AGGGGTGTCCA
                                |||   ||  ||||||||||
                                CGC   CG  TCCCCACAGGT
                                  C__  AC
GAM152  KIAA1908  3'  GGCACCCCACAGTGCACTT   73791    C   GCAA
                                AAG GCAC   GGGGTGTC
                                ||| ||||   ||||||||
                                TTC CGTG   CCCCACGG
                                  A   ACA_
GAM152  KLF3      5'  GGCGGCGCCCTGCACCGCGC   33711    AC_  AG    T  A
                                GCGC   GCA  GGGTG CC CC
                                ||||   |||  ||||| || ||
                                CGCG   CGT  CCCGC GG GG
                                   CCA   __    _  C
GAM152  MGC3195   5'  GGCGGCTAGGCCCGCGTGCGCT 49964        AAG   GT__  A
                                AGCGCACGC   GGGT   CC CC
                                |||||||||   ||||   || ||
                                TCGCGTGCG   CCCG   GG GG
                                      ___   GATC  C
GAM152  MVD       3'  GTGGCTGCCCACGGCGCTT   11719      A  CAAG    T
                                AAGCGC CG   GGGTG CCAC
                                ||||||  ||   ||||| ||||
                                TTCGCG GC   CCCGT GGTG
                                   _  A___    C
GAM152  PCYT2     3'  GCACCGCTCCTGCGTGCGC   12683        __  G
                                GCGCACGCA  AG GGTGT
                                |||||||||  || |||||
                                CGCGTGCGT  TC CCACG
                                     CC  G
GAM152  Rab11-FIP3 5'  GGCGCCCCGCGCGCGC     28787     A   AA
                                GCGC CGC  GGGGTGTC
                                |||| |||  ||||||||
                                CGCG GCG  CCCCGCGG
                                  C   __
GAM152  RELB      5'  GGCCCAGCCCTTGCGCCGCT   22505     CA      G  T_
                                AGCG  CGCAAGGG TG  CC
                                ||||  |||||||| ||  ||
                                TCGC  GCGTTCCC AC  GG
                                  C_      G  CC
GAM152  SNPH      3'  GGCGGGGCACCTGCATGCACT  28905    C   C   AGG      A_
                                AG GCA GCA   GGTGTCC  CC
                                || ||| |||   |||||||  ||
                                TC CGT CGT   CCACGGG  GG
                                 A  A  ___      GC
GAM152  SPRY2     5'  ATACTCCGCGTGCGCTT     20700          AA
                                AAGCGCACGC  GGGGTGT
                                |||||||||  |||||||
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                                TTCGCGTGCG  CCTCATA
                                    __
GAM152  TNKS2    5'  GACGACGTCACGTGCGCT    48220       CAA  G  _
                                AGCGCACG   GG GT GTC
                                ||||||||   || || |||
                                TCGCGTGC   CT CA CAG
                                    A__  G  G
GAM152  VIAAT    3'  GGCGAGCCCCCGCCGCGCTT   55451      AC  AA    GT_
                                AAGCGC  GC  GGGGT   CC
                                ||||||  ||  |||||   ||
                                TTCGCG  CG  CCCCG   GG
                                   C_  C_    AGC
GAM152  WDF2     5'  GGCGGCGCCCCAGGCGCGC   54750     AC  AA     T  A
                                GCGC  GC  GGGGTG CC CC
                                ||||  ||  |||||| || ||
                                CGCG  CG  CCCCGC GG GG
                                  __  GA     _  C
GAM152  LOC115196 5'  GGCGCCTCAGCGCGCGC     73660     A   AA
                                GCGC CGC  GGGGTGTC
                                ||||  |||  ||||||||
                                CGCG GCG  CTCCGCGG
                                  C   A_
GAM152  LOC116349 5'  GGCGACCACCGCGTGCGC    74278        AA  _   _
                                GCGCACGC  GG GGT GTC
                                ||||||||  || ||| |||
                                CGCGTGCG  CC CCA CGG
                                    __  A   G
GAM152  LOC147040 3'  GGTGGGATACTCACGCACAGCT 78835     GCAC  AAG      _
          T                      AAGC    GC   GGGTGTCC ACC
                                ||||    ||   |||||||| |||
                                TTCG    CG   CTCATAGG TGG
                                  ACA_  CA_       G
GAM152  LOC147057 3'  GGCGGCGTCTTGGCGCGCGC   84988      A   _    G  GT
                                GCGC CGC AAGG GT  CC
                                |||| ||| |||| ||  ||
                                CGCG GCG TTCT CG  GG
                                  C   G   G  GC
GAM152  LOC151031 5'  GGCACCCCTGCACACCGCT    88542      CAC_   A
                                AGCG    GCA GGGGTGTC
                                ||||    ||| ||||||||
                                TCGC    CGT CCCCACGG
                                  CACA   _
GAM152  LOC165693 5'  GATGAACTGTTTTGCGTGAGC  83490    G      ___  GG
                                GC CACGCAA   GG  TGTC
                                || |||||||   ||  ||||
                                CG GTGCGTT   TC  GTAG
                                 A      TTG  AA
GAM152  LOC197044 3'  GGGGAGGCTCGCATGGCGCT   89219      AC_  AAG   G   A
                                AGCGC   GC   GGGT TCC CC
                                |||||   ||   |||| ||| ||
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                                TCGCG   CG   CTCG AGG GG
                                  GTA ____   G  _
GAM152  LOC205418 5'  GGCAGCCCCCTGCAGCGCT   92374      AC   A    GT
                                AGCGC  GCA GGGGT  CC
                                |||||  ||| |||||  ||
                                TCGCG  CGT CCCCG  GG
                                  A_   C    AC
GAM152  LOC220549 5'  GTGGACATCACTTACGCTT   94510      CACGC   G
                                AAGCG    AAG GGTGTCCAC
                                |||||    ||| |||||||||
                                TTCGC    TTC CTACAGGTG
                                  A_____  A
GAM152  LOC221061 3'  GAAACTTTTTGCATCGCTT   94841      CAC       G
                                AAGCG   GCAAGGGGT TC
                                |||||   ||||||||| ||
                                TTCGC   CGTTTTTCA AG
                                  TA_       A
GAM152  LOC253681 3'  GGTGGGATACTCACGCACAGCT 96840     GCAC  AAG      _
          T                      AAGC   GC   GGGTGTCC ACC
                                ||||   ||   |||||||| |||
                                TTCG   CG   CTCATAGG TGG
                                  ACA_  CA_      G
GAM152  LOC51117  5'  GGTAGACAGTTCGCGTGCGTTT 32633         AA   G   C
                                AAGCGCACGC  GGG TGTC ACC
                                ||||||||||  ||| |||| |||
                                TTTGCGTGCG  CTT ACAG TGG
                                     __  G   A
GAM152  LOC55829  3'  GTGTCCACCAATTGCCTTACGC 38034      CA  C   _________  GTCC
          ACGCTT                 AAGCG  CG AAGG      GGT   AC
                                |||||  || ||||       |||   ||
                                TTCGC  GC TTCC      CCA   TG
                                  AC  A   GTTAA___  CCTG
GAM152  LOC59346  5'  GGCACCTCCCCGCGGCGC   41573     A   AA  _
                                GCGC CGC  GG GGTGTC
                                |||| |||  || ||||||
                                CGCG GCG  CC CCACGG
                                  _  CC  T
GAM152  LOC92078  3'  GGTGGACACCCAGCTAGCGC  68609     AC  AAG
                                GCGC  GC   GGGTGTCCACC
                                ||||  ||   ||||||||||
                                CGCG  CG   CCCACAGGTGG
                                  AT  A__
GAM153  CALM3    3'  ACATCCCACTGGCTGCTG    18999         GA_
                                CAGCAGCCAG   GATGT
                                ||||||||||   |||||
                                GTCGTCGGTC   CTACA
                                     ACC
GAM153  CYP2B6   3'  TCAGGTGATTCTCCTAGCT   7569     C     T   C
                                AGC AGGAGA GTC TCTGA
                                ||| |||||| ||| |||||
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                                TCG TCCTCT TAG GGACT
                                  A     _  T
GAM153  DHCR7    3'  CAGAGAGGTCCCAGCACTG   9064     CA  CA  A   G  C
                                CAG  GC  GG GAT TC TCTG
                                |||  ||  || ||| || ||||
                                GTC  CG  CC CTG AG AGAC
                                  A_  A_  _   G  _
GAM153  EFNB2    3'  CAGAGGACACCTAATGTCC   15839   A   GCC   AGA
                                C GCA   AGG   TGTCCTCTG
                                | |||   |||   |||||||||
                                C TGT   TCC   ACAGGAGAC
                                 C   AA_   ___
GAM153  FAT2     3'  TCAGAGTCACACCACTGGCTGC 9352         GAGA   C_
                                GCAGCCAG    TGT  CTCTGA
                                ||||||||    |||  ||||||
                                CGTCGGTC    ACA  GAGACT
                                     ACC_   CT
GAM153  GRLF1    3'  CAGAGACTGATCCTGGCTCTG  79255     C       GAT   C
                                CAG AGCCAGGA   GTC TCTG
                                ||| ||||||||   ||| ||||
                                GTC TCGGTCCT   CAG AGAC
                                  _       AGT   _
GAM153  GTF2H1   3'  CAGAAGACAATGGCGCTG    19208      A   GGAGA   C
                                CAGC GCCA     TGTC TCTG
                                |||| ||||     |||| ||||
                                GTCG CGGT     ACAG AGAC
                                  _   A_____   A
GAM153  HDLBP    5'  TCAGGACGGACCTTCTGGCTAC 68509     C       AT   __
          TG                      CAG AGCCAGGAG  GTCC  TCTGA
                                ||| |||||||||  ||||  |||||
                                GTC TCGGTCTTC  CAGG  GGACT
                                  A        __    CA
GAM153  LOH11CR2A 5'  AGGTTTCCCTGGCTGCTG    28268          A  TGT
                                CAGCAGCCAGG GA   CCT
                                |||||||||||  ||   |||
                                GTCGTCGGTCC CT   GGA
                                       _  TT_
GAM153  MAT1A    3'  GACGCCTGGCTGCTG       92500          AGA
                                CAGCAGCCAGG   TGTC
                                ||||||||||   ||||
                                GTCGTCGGTCC   GCAG
                                        ___
GAM153  MFGE8    3'  CAGAGGACACAGGCAGCT    21004     A   AGGAGA
                                AGC GCC     TGTCCTCTG
                                ||| |||     |||||||||
                                TCG CGG     ACAGGAGAC
                                  A   AC_____
GAM153  NAT8     5'  CAGACGGTATCTCCTGGATGC  15582     G        T  _
                                GCA CCAGGAGATG CC TCTG
                                ||| ||||||||| || ||||
```

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                                CGT GGTCCTCTAT GG AGAC
                                  A        _ C
GAM153  PLA2G4B  3'  TCATTCATTCCCTGGCTGCTG  18694          AG   TCCTC
                                CAGCAGCCAGG  ATG    TGA
                                ||||||||||  |||    |||
                                GTCGTCGGTCC  TAC    ACT
                                      CT   TT___
GAM153  POLR2G   3'  CAGAGGTCCAGTCTGGCTGCTG 12209          AGATGT
                                CAGCAGCCAGG     CCTCTG
                                ||||||||||     ||||||
                                GTCGTCGGTCT     GGAGAC
                                      GACCT_
GAM153  RAB6A    5'  CAGAGGACACCCCTGGCTCCTG 12714     C      AGA
                                CAG AGCCAGG   TGTCCTCTG
                                ||| |||||||   |||||||||
                                GTC TCGGTCC   ACAGGAGAC
                                  C      CC_
GAM153  RAP1GA1  3'  CAAAGGCCAGCCTCCTGGC   12769        A_ T   C
                                GCCAGGAG  TG CCT TG
                                ||||||||  || ||| ||
                                CGGTCCTC  AC GGA AC
                                     CG  C   A
GAM153  RNF4     3'  TCAGAAGCTTCCTGGCCACTG  12886     CA       AT  CC
                                CAG  GCCAGGAG  GT  TCTGA
                                |||  ||||||||  ||  |||||
                                GTC  CGGTCCTT  CG  AGACT
                                  AC       __  A_
GAM153  RRM2     3'  CAGAAGGCCTGGCTGGCTG   8285      _      AGATGT  _
                                CAGC AGCCAGG     CCT CTG
                                |||| |||||||     ||| |||
                                GTCG TCGGTCC     GGA GAC
                                  G      _______  A
GAM153  RXRA     3'  TCAGGCCTTCTCTCTGGCTGC  12923        _   TGTCC
                                GCAGCCAG GAGA    TCTGA
                                |||||||| ||||    |||||
                                CGTCGGTC CTCT    GGACT
                                     T   TCC__
GAM153  SHMT2    3'  CAGAGGTCCAGTCTGGCTGCTG 19434          AGATGT
                                CAGCAGCCAGG     CCTCTG
                                ||||||||||     ||||||
                                GTCGTCGGTCT     GGAGAC
                                      GACCT_
GAM153  TARDBP   3'  TCAAAGGACATCCACATCTGTT 24789       CCAGGA       C
          G                     CAGCAG     GATGTCCT TGA
                                ||||||     |||||||| |||
                                GTTGTC     CTACAGGA ACT
                                   TACAC_       A
GAM153  TNFRSF6B 3'  CAGAACTTCCCTGGCTCCTG   53080     C      A  T  CC
                                CAG AGCCAGG GA GT  TCTG
                                ||| ||||||| || ||  ||||
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                                GTC TCGGTCC CT CA  AGAC
                                  C      _ T  __
GAM153  TNFRSF6B  3'  CAGAACTTCCCTGGCTCCTG   53081     C      A  T  CC
                                CAG AGCCAGG GA GT  TCTG
                                ||| ||||||| || ||  ||||
                                GTC TCGGTCC CT CA  AGAC
                                  C      _ T  __
GAM153  AOP2      3'  CAGAGGATGTCAGCTGC     18135       CAGGA
                                GCAGC    GATGTCCTCTG
                                ||||||    ||||||||||||
                                CGTCG    CTGTAGGAGAC
                                   A_____
GAM153  C20orf67  3'  TCAGAGGGACCCCGGCTGC   42323       A  AGATG
                                GCAGCC GG    TCCTCTGA
                                |||||| ||    ||||||||
                                CGTCGG CC    GGGAGACT
                                    C  CA___
GAM153  CIDEB     5'  TCAAAGGACATCCCCTGC     27798      CCA  A       C
                                GCAG   GG GATGTCCT TGA
                                ||||   || |||||||| |||
                                CGTC   CC CTACAGGA ACT
                                   ___ _       A
GAM153  DKFZP434F0318 3'  AGAGGACCCTGGTGCTG     48744       G     AGAT
                                CAGCA CCAGG    GTCCTCT
                                ||||| |||||    |||||||
                                GTCGT GGTCC    CAGGAGA
                                   _    _____
GAM153  DKFZP566M1046 5'  TCAGAGTGTAGGCCTCTGGCTG 50447          AGA_  TC
            C                    GCAGCCAGG    TG  CTCTGA
                                |||||||||    ||  ||||||
                                CGTCGGTCT    AT  GAGACT
                                     CCGG  GT
GAM153  DMRTB1    3'  CAGGCCCGCCCTCCTGGCCAGC 66838     A_       A_  TC T
                                GC  GCCAGGAG  TG  C CTG
                                ||  ||||||||  ||  | |||
                                CG  CGGTCCTC  GC  G GAC
                                 AC       CC  CC _
GAM153  FLJ00024  5'  CAGAAGCTTCCACTGACTGCTG 64489        C   GA  T  CC
                                CAGCAG CAG  GA GT  TCTG
                                |||||| |||  || ||  ||||
                                GTCGTC GTC  CT CG  AGAC
                                   A   AC  T  A_
GAM153  FLJ10300  5'  TCAGAAAACATCTCTGGGC    36474     A       CC
                                GCC GGAGATGT  TCTGA
                                ||| ||||||||  |||||
                                CGG TCTCTACA  AGACT
                                  G       AA
GAM153  FLJ12057  5'  TCAGAGGATTCCCAGCT     45796     CA   GAT
                                AGC  GGA   GTCCTCTGA
                                |||  |||   |||||||||
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                                TCG  CCT   TAGGAGACT
                                  AC  ___
GAM153  FLJ12960  3'  CAGAAGTTTGCCCAGCTGCT   45292      CA  _   GTCC
                                AGCAGC  GG AGAT   TCTG
                                ||||||  || ||||   ||||
                                TCGTCG  CC TTTG   AGAC
                                   AC  G   A___
GAM153  FLJ14596  5'  CAGAGGGTACCTGGCTCTG   52512    C     AGA GT
                                CAG AGCCAGG   T  CCTCTG
                                ||| |||||||  |  ||||||
                                GTC TCGGTCC   A  GGAGAC
                                  _     ___ TG
GAM153  FLJ14681  5'  AGGCATCTCCCAGCTGC    52593     CA     T
                                GCAGC  GGAGATG CCT
                                |||||  ||||||| |||
                                CGTCG  CCTCTAC GGA
                                   AC      _
GAM153  FLJ14810  5'  CAGCTGCCCCGGCTGCTG   52697       A  AGAT  CCT
                                CAGCAGCC GG   GT   CTG
                                |||||||| ||   ||   |||
                                GTCGTCGG CC   CG   GAC
                                     C  _____  TC_
GAM153  FLJ22393  3'  CAGCACCCATCCTGGCTGC   47776        GAT  CCT
                                GCAGCCAGGA   GT   CTG
                                ||||||||||   ||   |||
                                CGTCGGTCCT   CA   GAC
                                      ACC  C__
GAM153  HT002    3'  TCAGCTGCCTCCTGGCTGCTG  26802         AT  CCT
                                CAGCAGCCAGGAG  GT   CTGA
                                ||||||||||||  ||   ||||
                                GTCGTCGGTCCTC  CG   GACT
                                       __  TC_
GAM153  KIAA0247  3'  CAAAGGCACAAGCTCCTGGCCC 29063    CA      A_  _  C
           TG                    CAG  GCCAGGAG  TGT CCT TG
                                |||  ||||||||  ||| ||| ||
                                GTC  CGGTCCTC  ACA GGA AC
                                  C_      GA   C   A
GAM153  KIAA1856  3'  CAGGCCGGCCCTCCAGGCTGCT 94226       A   AT   C_
           G                     CAGCAGCC GGAG  GTC  TCTG
                                |||||||| ||||  |||  ||||
                                GTCGTCGG CCTC  CGG  GGAC
                                     A   C_  CC
GAM153  NEDD8    3'  CAGAGGGCCTTGCTGGCTACTG 21589    C     G  AT
                                CAG AGCCAG AG  GTCCTCTG
                                ||| |||||| ||  ||||||||
                                GTC TCGGTC TT  CGGGAGAC
                                  A     G  C_
GAM153  NT5C1B   5'  CAGAGCCCGATCCTGGCT    71749       GA  TC
                                AGCCAGGA  TG  CTCTG
                                ||||||||  ||  |||||
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                                TCGGTCCT  GC  GAGAC
                                    A_  CC
GAM153  OPN4     3'  CAGCCCCGCATCTCCCACTGC  53851     CCA      CCT_
                                GCAG  GGAGATGT   CTG
                                ||||  ||||||||   |||
                                CGTC  CCTCTACG   GAC
                                  AC_      CCCC
GAM153  PCDH19   3'  CAGAGAGGCCACTGGCTGC   64442       GAGAT  _
                                GCAGCCAG    GTC CTCTG
                                ||||||||    ||| |||||
                                CGTCGGTC    CGG GAGAC
                                    AC___   A
GAM153  PEMT     5'  TCAGCAGACCTCCTGGCCGT  24137    A      AT   CT
                                GC GCCAGGAG  GTC  CTGA
                                || ||||||||  |||  ||||
                                TG CGGTCCTC  CAG  GACT
                                 C       __  AC
GAM153  PRO0149  3'  CAGAGAGAAAGTCCTGGCTGCT 26940          GATG  _
            G                    CAGCAGCCAGGA   TC CTCTG
                                 ||||||||||||   || |||||
                                 GTCGTCGGTCCT   AG GAGAC
                                      GAA_  A
GAM153  RDH-E2   3'  CAGAGGACACACAGCTCTG   58068    C   CAGGAGA
                                CAG AGC      TGTCCTCTG
                                ||| |||      |||||||||
                                GTC TCG      ACAGGAGAC
                                  _  ACAC___
GAM153  USP20    3'  CAGAAGAGAGGCCGGGCTGCTG 22898        A  AGATG  C
                                CAGCAGCC GG    TC TCTG
                                |||||||| ||    || ||||
                                GTCGTCGG CC    AG AGAC
                                    G  GGAG_  A
GAM153  LOC127002 3' CAGATCCGGGCCCCAGGCTGCT 75123        A  AGAT   ___
            G                    CAGCAGCC GG   GTCC   TCTG
                                 |||||||| ||   ||||   ||||
                                 GTCGTCGG CC   CGGG   AGAC
                                    A  C___    CCT
GAM153  LOC131919 5' CAGAGGGACCTGGCCAGT    76398    A_     AGATG
                                GC  GCCAGG    TCCTCTG
                                ||  ||||||    |||||||
                                TG  CGGTCC    GGGAGAC
                                 AC     A____
GAM153  LOC146146 5' TCAATGAACCGCCTGGCTGCTG 78168          AGATG  CTC
                                CAGCAGCCAGG    TC   TGA
                                ||||||||||    ||   |||
                                GTCGTCGGTCC    AG   ACT
                                      GCCA_  TA_
GAM153  LOC147123 3' CAGAGGACCGCAGGCCTGGTTG 78854         AGAT__
            C                    GCAGCCAGG     GTCCTCTG
                                 |||||||||     ||||||||
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                                CGTTGGTCC     CAGGAGAC
                                      GGACGC
GAM153   LOC149464 5'  CAGCTGTCTCCTGGCCCTG   85586    CA        TCCT
                                CAG  GCCAGGAGATG   CTG
                                |||  ||||||||||   |||
                                GTC  CGGTCCTCTGT   GAC
                                  C_         C___
GAM153   LOC150685 5'  TCAAAGATTTCTCCTGGCTGTT 88537           T   CTC
             G                   CAGCAGCCAGGAGA GTC   TGA
                                ||||||||||||| |||   |||
                                GTTGTCGGTCCTCT TAG   ACT
                                        T   AA_
GAM153   LOC152274 5'  TCAGAGGAGAACCCGGCCGTT  81344    A   A  AGATG
                                AGC GCC GG    TCCTCTGA
                                ||| ||| ||    ||||||||
                                TTG CGG CC    AGGAGACT
                                  C   C  AAG__
GAM153   LOC153454 3'  TCAGATTTCTCCTGACTGGCTG 81696     _ C      TGTCC
                                CAGC AG CAGGAGA    TCTGA
                                |||| || |||||||    |||||
                                GTCG TC GTCCTCT    AGACT
                                  G  A      TT___
GAM153   LOC154881 3'  TCAGAACACCTCCTTGGCTGCT 82077        _   A   CC
                                AGCAGCCA GGAG TGT  TCTGA
                                |||||||| |||| |||  |||||
                                TCGTCGGT CCTC ACA  AGACT
                                     T   C  __
GAM153   LOC199986 5'  CAGCTGGTCTCCTGGCAACTG  91505    CA       TGT  T_
                                CAG  GCCAGGAGA   CC  CTG
                                |||  |||||||||   ||  |||
                                GTC  CGGTCCTCT   GG  GAC
                                  AA        ___  TC
GAM153   LOC200310 3'  TCAGAAGGTTCCTGGCTAGT   66335   _       ATGT   _
                                GC AGCCAGGAG    CCT CTGA
                                || |||||||||    ||| ||||
                                TG TCGGTCCTT    GGA GACT
                                 A        _____   A
GAM153   LOC203297 5'  CAGAAGCTTCCACTGACTGCTG 75868       C   GA  T  CC
                                CAGCAG CAG  GA GT  TCTG
                                ||||||  |||  || ||  ||||
                                GTCGTC GTC  CT CG  AGAC
                                    A   AC  T  A_
GAM153   LOC219917 3'  TCATTTCACCTTCTGGCCACTG 93167     CA       A  TCCTC
                                CAG  GCCAGGAG TG     TGA
                                |||  |||||||| ||     |||
                                GTC  CGGTCTTC AC     ACT
                                  AC       C  TTT__
GAM153   LOC254944 3'  CAGAAGACAGGGGGCTCTG   99001     C    AGGAGA    C
                                CAG AGCC      TGTC TCTG
                                ||| ||||      |||| ||||
```

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                                GTC TCGG     ACAG AGAC
                                  _   GGG___   A
GAM153  LOC51762  3' TCAGAATCACACCTCCCGGCTG 33709        A   A  CC_
            CTG                   CAGCAGCC GGAG TGT   TCTGA
                                |||||||| |||| |||   |||||
                                GTCGTCGG CCTC ACA   AGACT
                                    C   C  CTA
GAM153  LOC90917  3' TCAAGAACTCCTCCTGGC    64989        AT  C  C
                                GCCAGGAG  GT CT TGA
                                |||||||| || || |||
                                CGGTCCTC  CA GA ACT
                                    CT  A  _
GAM153  LOC91974  3' CAGAGGACATAAATGGTGCTG  68359      G  GGAG
                                CAGCA CCA   ATGTCCTCTG
                                ||||| |||   ||||||||||
                                GTCGT GGT   TACAGGAGAC
                                  _  AAA_
GAM153  LOC91974  5' CAGAGGACCTTCCTGGCT    68360        AT
                                AGCCAGGAG  GTCCTCTG
                                |||||||||  ||||||||
                                TCGGTCCTT  CAGGAGAC
                                    C_
GAM153  LOC92979  3' TCAGAGAAGAACTCTCATGGCT 57253        G   TG __
            GCTG                  CAGCAGCCA GAGA  TC  CTCTGA
                                |||||||| ||||  ||  ||||||
                                GTCGTCGGT CTCT  AG  GAGACT
                                    A   CA  AA
GAM154  DLEC1    3'  CATCTGGCCCTCCCTTG     24716      A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                  C    G  _
GAM154  DLEC1    3'  CATCTGGCCCTCCCTTG     24728      A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                  C    G  _
GAM154  PIP5K1A  3'  TATCCCACCCTGCCTTGATA  14520        A   CA  C
                                TATCAAGG AGGG  GG GTG
                                |||||||| ||||  || |||
                                ATAGTTCC TCCC  CC TAT
                                    G   A_  C
GAM154  SOX11    3'  ACCCACCCCCCCTTGGTA    13308        AA  CA  C
                                TATCAAGG  GGG  GG GT
                                ||||||||  |||  || ||
                                ATGGTTCC  CCC  CC CA
                                    CC  A_  _
GAM154  CHL1     3'  TGTTACCTTTCCTCAATA    22768     CA      CA
                                TAT  AGGAAGGG  GGCG
                                |||  ||||||||  ||||
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                                ATA  TCCTTTCC  TTGT
                                  AC       A_
GAM154  EPB41L1  3'  CATTCTGCCCTTCCCTGA    71104     A         C
                                TCA GGAAGGGCAGG GTG
                                ||| |||||||||| |||
                                AGT CCTTCCCGTCT TAC
                                  C         _
GAM154  FLJ00060 3'  CATACCCCCTGCCCTCCTCTGA 61741     _   A      CGTG
                                TCA AGGA GGGCAGG    ATG
                                ||| |||| |||||||    |||
                                AGT TCCT CCCGTCC    TAC
                                  C   _      CCCA
GAM154  FLJ10898 5'  CACCACAGCCCTTTCTCAATA  60126     CA        AGGC
                                TAT  AGGAAGGGC    GTG
                                |||  |||||||||    |||
                                ATA  TCTTTCCCG    CAC
                                  AC        ACAC
GAM154  FLJ22557 3'  ATCATCCCATCCTTAATA    45581     C    A   CAGGC
                                TAT AAGGA GGG     GTGAT
                                ||| ||||| |||     |||||
                                ATA TTCCT CCC     TACTA
                                  A    A  _____
GAM154  KIAA0574 3'  CATCCCCTGCCCTCCCCTGA   69808     A  A       CGT
                                TCA GG AGGGCAGG   GATG
                                ||| || ||||||||   ||||
                                AGT CC TCCCGTCC   CTAC
                                  C  C       C__
GAM154  KIAA0632 3'  CACCTCAGAAACCCTTCCTTGA 32071           CA___  C
                                TCAAGGAAGGG     GG GTG
                                ||||||||||     || |||
                                AGTTCCTTCCC     CT CAC
                                      AAAGA  C
GAM154  KIAA1045 3'  CATCACATGTCCTTCC      71599          GGC
                                GGAAGGGCA   GTGATG
                                |||||||||   ||||||
                                CCTTCCTGT   CACTAC
                                     A__
GAM154  KIAA1354 5'  CAGTGACTGCCTTCCCTTGATA 61572         A      G  _
                                TATCAAGG AGGGCAG CG TG
                                |||||||| ||||||| || ||
                                ATAGTTCC TTCCGTC GT AC
                                     C      A  G
GAM154  MGC20460 5'  CACCGCCTCCTACCCTTCTT   54901         C___    _
                                AGGAAGGG    AGGCG TG
                                ||||||||    ||||| ||
                                TTCTTCCC    TCCGC AC
                                     ATCC     C
GAM154  LOC158476 3'  CACGCCCGCCCCCCCCCATTGA  88186      _  AA_    A
                                TCAA GG   GGGC GGCGTG
                                ||||  ||   |||| ||||||
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                                AGTT CC   CCCG CCGCAC
                                  A  CCC    C
GAM154  LOC90459  3'  CACACCCGCCTAATTTTTG   63550       A_   A  C
                                CAAGGA  GGGC GG GTG
                                ||||||  |||| || |||
                                GTTTTT  TCCG CC CAC
                                   AA    C  A
GAM155  ABCD2     5'  ATGAGGGGCCTGGGAGGGA   18965        A__    G
                                TCCCTCCCA   CCCT GT
                                |||||||||   |||| ||
                                AGGGAGGGT   GGGA TA
                                     CCG    G
GAM155  ADSS      3'  TTTGGTGGGGCTGGGAGGGG  72235        A     G
                                TCCCTCCCA CCCTG TGAG
                                ||||||||| ||||| ||||
                                GGGGAGGGT GGGGT GTTT
                                     C     G
GAM155  AES       3'  CAGGGAGGTTGGGAGGGG    8522         ___
                                TCCCTCCCAA   CCCTG
                                ||||||||||   |||||
                                GGGGAGGGTT   GGGAC
                                     GGA
GAM155  ALDOB     3'  CAGTGGTAGGTTGGGAAGGA  68650     C      __   G
                                TCC TCCCAACC  CTG TG
                                ||| ||||||||  ||| ||
                                AGG AGGGTTGG  GGT AC
                                  A       AT   G
GAM155  AMH       5'  CTCTATCACTGGGGAGGGA   6652        AACCC   _
                                TCCCTCCC     TGGT GAG
                                ||||||||     |||| |||
                                AGGGAGGG     ACTA CTC
                                     GTC__    T
GAM155  ANKRD3    3'  CTCACCAGTCTTGAGGGA    40562       CC  CC
                                TCCCTC  AA  CTGGTGAG
                                ||||||  ||  ||||||||
                                AGGGAG  TT  GACCACTC
                                   __  CT
GAM155  ARHGAP6   3'  CCATGGGAGTGGGAGGGA    8611         A_   _
                                TCCCTCCCA  CCC TGG
                                |||||||||  ||| |||
                                AGGGAGGGT  GGG ACC
                                     GA   T
GAM155  AVPR1A    5'  CAATAGGGCGGGAGGGA     7374         AA     G
                                TCCCTCCC  CCCTG TG
                                ||||||||  ||||| ||
                                AGGGAGGG  GGGAT AC
                                     C_     A
GAM155  B3GNT3    3'  CTCAGAAGGTTGGGGGGA    27303      T      C GG
                                TCCC CCCAACC T  TGAG
                                |||| ||||||| |  ||||
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                                AGGG GGGTTGG A  ACTC
                                  _      _ AG
GAM155  BASP1    3'  CAATGGGAGTTGGGAGTGA   76493    C       _   GG
                                TC CTCCCAAC CCT  TG
                                || |||||||| |||  ||
                                AG GAGGGTTG GGG  AC
                                 T       A   TA
GAM155  BAZ2A    5'  CTCACAGTTTGGGAGG      26508        CC   G
                                CCTCCCAA  CTG TGAG
                                ||||||||  ||| ||||
                                GGAGGGTT  GAC ACTC
                                     T_  _
GAM155  BCL11B   3'  CTCATTAGGTTGGAAGG     43484     C     C
                                CCT CCAACC TGGTGAG
                                ||| |||||| |||||||
                                GGA GGTTGG ATTACTC
                                  A     _
GAM155  CACNG6   3'  CCGGGTGCGGTTGGGGGAGA  49946    C       _____
                                TC CTCCCAACC    CTGG
                                || |||||||||    ||||
                                AG GGGGGTTGG    GGCC
                                 A        CGTG
GAM155  CNTN2    3'  CTCACTCCTGCCTGGGAGGGG  18660         ACCCT_
                                TCCCTCCCA     GGTGAG
                                |||||||||     ||||||
                                GGGGAGGGT     TCACTC
                                     CCGTCC
GAM155  COL9A1   5'  CTCACCGGGGGCAGGAGGGA   10252        CAA
                                TCCCTCC   CCCTGGTGAG
                                |||||||   ||||||||||
                                AGGGAGG   GGGGCCACTC
                                    ACG
GAM155  DHCR24   3'  TTCATTAGTTGAAAGGGA    29305      CC    CC
                                TCCCT  CAAC  TGGTGAG
                                |||||  ||||  |||||||
                                AGGGA  GTTG  ATTACTT
                                   AA   __
GAM155  EPB49    3'  CGGCGGGTTGGGAGGGG     10527           T G
                                TCCCTCCCAACCC G TG
                                |||||||||||| | ||
                                GGGGAGGGTTGGG C GC
                                       _ G
GAM155  FCMD     3'  CTCACAGTAGGGTTGAAAGAG  23035     C__       __
                                CTC   CAACCCTG  GTGAG
                                |||   ||||||||  |||||
                                GAG   GTTGGGAT  CACTC
                                  AAA       GA
GAM155  FLRT2    3'  CTCATCAGGGTAAGAGG     25996      CCA
                                CCTC   ACCCTGGTGAG
                                ||||   ||||||||||
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                                GGAG  TGGGACTACTC
                                  AA_
GAM155  GGT1    3'  CTCACCAGGACCAGGAAGGG  26420    _  CAAC
                                CCCT CC   CCTGGTGAG
                                |||| ||   |||||||||
                                GGGA GG   GGACCACTC
                                  A  ACCA
GAM155  GGT1    3'  CTCACCAGGACCAGGAAGGG  26436    _  CAAC
                                CCCT CC   CCTGGTGAG
                                |||| ||   |||||||||
                                GGGA GG   GGACCACTC
                                  A  ACCA
GAM155  GGT1    3'  CTCACCAGGACCAGGAAGGG  19158    _  CAAC
                                CCCT CC   CCTGGTGAG
                                |||| ||   |||||||||
                                GGGA GG   GGACCACTC
                                  A  ACCA
GAM155  GPR17   3'  TGGTGGGGACGGGGAGGGA  19182       AA_   G
                                TCCCTCCC  CCCTG TG
                                ||||||||  ||||| ||
                                AGGGAGGG  GGGGT GT
                                    GCA   G
GAM155  GRIN2D  3'  CGCGTGGGTTGGGAAGGA   7735    C      TG
                                TCC TCCCAACCC  GTG
                                ||| |||||||||  |||
                                AGG AGGGTTGGG  CGC
                                  A       TG
GAM155  KIAA0442 3'  CTCACACAGACTGGGGGGGA  32094       ACC  _
                                TCCCTCCCA  CTG GTGAG
                                |||||||||  ||| |||||
                                AGGGGGGGT  GAC CACTC
                                    CA_  A
GAM155  LAD1    5'  CACCTGGGCTGGAAGGGG   19900     C  A  T
                                TCCCT CCA CCC GGTG
                                ||||| ||| ||| ||||
                                GGGGA GGT GGG CCAC
                                  A  C  T
GAM155  LTF     5'  CGCGGGGAGTGGGGAGGGA  11374       A  _  G
                                TCCCTCCC AC CCT GTG
                                |||||||| || ||| |||
                                AGGGAGGG TG GGG CGC
                                    G  A  G
GAM155  LYL1    5'  CTCACTTTCCCTGGGGGGGA  19950       ACCCT
                                TCCCTCCCA   GGTGAG
                                |||||||||   ||||||
                                AGGGGGGGT   TCACTC
                                    CCCTT
GAM155  NDN     3'  CTCACCAGGGCTGTGGAAGG  11758   C  _  A
                                CC TCC CA CCCTGGTGAG
                                || ||| || ||||||||||
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                                GG AGG GT GGGACCACTC
                                 A   T  C
GAM155  NEDD4L   3'  TTTATTAGAATTGGAAGG    31609     C    CC
                                CCT CCAA  CTGGTGAG
                                ||| ||||  ||||||||
                                GGA GGTT  GATTATTT
                                  A    AA
GAM155  OSCAR    5'  CTCATTTCCTGGGAGGGG    56249         ACCCT
                                TCCCTCCCA    GGTGAG
                                |||||||||    ||||||
                                GGGGAGGGT    TTACTC
                                     CCT__
GAM155  OSCAR    5'  CTCATTTCCTGGGAGGGG    56477         ACCCT
                                TCCCTCCCA    GGTGAG
                                |||||||||    ||||||
                                GGGGAGGGT    TTACTC
                                     CCT__
GAM155  OSCAR    5'  CTCATTTCCTGGGAGGGG    56480         ACCCT
                                TCCCTCCCA    GGTGAG
                                |||||||||    ||||||
                                GGGGAGGGT    TTACTC
                                     CCT__
GAM155  P53AIP1  3'  CTGTGGTGATGGGAGGGA    42336         __   C
                                TCCCTCCCA  ACC TGG
                                |||||||||  ||| |||
                                AGGGAGGGT  TGG GTC
                                     AG   T
GAM155  PIP5K1A  3'  TGTTAGGGGTGGGAGGGA    14523         A    GT
                                TCCCTCCCA CCCTG  G
                                ||||||||| |||||  |
                                AGGGAGGGT GGGAT  T
                                     G    TG
GAM155  POV1     3'  CTCCTTGGGTTGGAGGAGA    14636    _    C    T  T
                                TC CCTCC AACCC GG GAG
                                || ||||| ||||| || |||
                                AG GGAGG TTGGG TC CTC
                                 A    _    T  _
GAM155  PPP2R5D  3'  CAAGTGGGGCCGGGGAGGGA   21803        AA_    G_
                                TCCCTCCC   CCCTG  TG
                                ||||||||   |||||  ||
                                AGGGAGGG   GGGGT  AC
                                    GCC    GA
GAM155  SERPINH2 3'  TATTGGGGTTGGGGGGGA    8787            TG
                                TCCCTCCCAACCC  GTG
                                ||||||||||||  |||
                                AGGGGGGGTTGGG  TAT
                                       GT
GAM155  SLC21A2  3'  CTCACCAGCCCTGGGGGGA   20083     T   ACC
                                TCCC CCCA   CTGGTGAG
                                |||| ||||   ||||||||
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                                AGGG GGGT   GACCACTC
                                  _   CCC
GAM155  STK19    3'  CTCAGAGTGGGCCGGGAGGGG  16097       AA   TGG_
                                TCCCTCCC  CCC    TGAG
                                ||||||||  |||    ||||
                                GGGGAGGG  GGG    ACTC
                                    CC   TGAG
GAM155  STK19    3'  CTCAGAGTGGGCCGGGAGGGG  51613       AA   TGG_
                                TCCCTCCC  CCC    TGAG
                                ||||||||  |||    ||||
                                GGGGAGGG  GGG    ACTC
                                    CC   TGAG
GAM155  TSN      3'  TCAGCGGTTGCCAGGAAGGG   17305     _ ____    _
                                CCCT CC   CAACC CTGG
                                ||||  ||   ||||| ||||
                                GGGA GG   GTTGG GACT
                                  A  ACC    C
GAM155  TUFT1    3'  TTCATCAGATTGGGAGAGG    39681    _     CC
                                CC CTCCCAA  CTGGTGAG
                                ||  |||||||  ||||||||
                                GG GAGGGTT  GACTACTT
                                 A      A_
GAM155  BHLHB2   3'  CTCACCAGACGTCGGGGAGAGA 14764    C    A_  C_
                                TC CTCCC  AC  CTGGTGAG
                                ||  |||||  ||  ||||||||
                                AG GAGGG  TG  GACCACTC
                                 A    GC  CA
GAM155  BPESC1   3'  CGATGGGGTTGAGAGGGG    41771       C      GG
                                TCCCTC CAACCCT  TG
                                ||||||  |||||||  ||
                                GGGGAG GTTGGGG  GC
                                   A      TA
GAM155  BRPF3    5'  CAGCGCGGGCCGGGAGGGG    93927       AA   _  G
                                TCCCTCCC  CCC TG TG
                                ||||||||  ||| || ||
                                GGGGAGGG  GGG GC AC
                                    CC   C  G
GAM155  C20orf151 3'  CACCAGGGCCTGGAGAGG    90091     _   A_
                                CCTC CCA  CCCTGGTG
                                ||||  |||  ||||||||
                                GGAG GGT  GGGACCAC
                                  A   CC
GAM155  C20orf180 5'  TGTCAGGGTTGGGGGGA     37974      T        GT
                                TCCC CCCAACCCTG  G
                                ||||  ||||||||||  |
                                AGGG GGGTTGGGAC  T
                                  _        TG
GAM155  CCT5     5'  CGCCGGTTGGGGGGA       73033      T      CT
                                TCCC CCCAACC  GGTG
                                ||||  |||||||  ||||
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                                AGGG GGGTTGG  CCGC
                                  _     __
GAM155  CECR6    5'  CCGGGGTTGGCGGGGAGGGA  49931        ____
                                TCCCTCCC    AACCCTGG
                                ||||||||    ||||||||
                                AGGGAGGG    TTGGGGCC
                                    GCGG
GAM155  DGS-A    3'  CCAGGGCAGGCTGGGAGGGA  86051         A____
                                TCCCTCCCA    CCCTGG
                                |||||||||    ||||||
                                AGGGAGGGT    GGGACC
                                     CGGAC
GAM155  DKFZp761P1010 3'  CATGTGGGGTTGGAGGAGA   37942   _    C      _
                                TC CCTCC AACCCTG GTG
                                || ||||| ||||||| |||
                                AG GGAGG TTGGGGT TAC
                                 A    _      G
GAM155  ET(B)R-LP-2 3'  CAGTAGGGGTGGGGAGGGA   17672        AA_    G
                                TCCCTCCC   CCCTG TG
                                ||||||||   ||||| ||
                                AGGGAGGG   GGGAT AC
                                     GTG    G
GAM155  FLJ10057  3'  CTCATGGAAGATGTTGGGAGAG 36251    C       _____  TG
           A                     TC CTCCCAAC    CC  GTGAG
                                || ||||||||    ||  |||||
                                AG GAGGGTTG    GG  TACTC
                                 A       TAGAA __
GAM155  FLJ10853  3'  CTCACTGGGTCAAAGGGA    37315      CCCA    T
                                TCCCT    ACCC GGTGAG
                                |||||    |||| ||||||
                                AGGGA    TGGG TCACTC
                                   AAC_   _
GAM155  FLJ11000  3'  CAGGAGGGTGGGGAGGGA    37525        A    GG
                                TCCCTCCC ACCCT  TG
                                |||||||| |||||  ||
                                AGGGAGGG TGGGA  AC
                                     G    GG
GAM155  FLJ12650  3'  CTCACCAGTTGGAAGG      44820     C    CC
                                CCT CCAAC  TGGTGAG
                                ||| |||||  |||||||
                                GGA GGTTG  ACCACTC
                                  A    __
GAM155  FLJ20489  3'  CTCACCTAACTTGGGAGGGA   35711         CCCT
                                TCCCTCCCAA    GGTGAG
                                ||||||||||    ||||||
                                AGGGAGGGTT    CCACTC
                                      CAAT
GAM155  FLJ20793  3'  CATTGTAGGTTGGGAAGGG    93448      _      CT_
                                CCCT CCCAACC   GGTG
                                |||| |||||||   ||||
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                                GGGA GGGTTGG   TTAC
                                  A      ATG
GAM155   FLJ21313  3'  TCAGGAAAGTGGGGAGGGA   43934        A ___
                                TCCCTCCC AC   CCTGG
                                |||||||| ||   |||||
                                AGGGAGGG TG   GGACT
                                     G  AAA
GAM155   FLJ23231  3'  CTCAGAGGGTGGGGAGGGA   47605        A    GG
                                TCCCTCCC ACCCT  TGAG
                                |||||||| |||||  ||||
                                AGGGAGGG TGGGA  ACTC
                                     G    G_
GAM155   FLJ32915  5'  CTCACATTTTGGGAGGGA    59432         CCCTG
                                TCCCTCCCAA    GTGAG
                                ||||||||||    |||||
                                AGGGAGGGTT    CACTC
                                      TTA__
GAM155   FREQ     3'  CTCAAAGGCTGGGAGGGA    27370        AC   GG
                                TCCCTCCCA  CCT  TGAG
                                |||||||||  |||  ||||
                                AGGGAGGGT  GGA  ACTC
                                     C_   A_
GAM155   GGTL4    3'  CTCACCAGGACCAGGAAGGG   55944     _  CAAC
                                CCCT CC    CCTGGTGAG
                                |||| ||    |||||||||
                                GGGA GG    GGACCACTC
                                  A  ACCA
GAM155   GMPPB    3'  CCAAGGGGGTGGGAGGGA    97439        A_   _
                                TCCCTCCCA  CCCT GG
                                |||||||||  |||| ||
                                AGGGAGGGT  GGGA CC
                                     GG    A
GAM155   GTPBP1   3'  CTTCCAGGGTTAGGACAGA   16266    CC   C      T
                                TC  TCC AACCCTGG GAG
                                ||  ||| |||||||| |||
                                AG  AGG TTGGGACC TTC
                                 AC   A       _
GAM155   HGC6.1.1 3'  CAGTGGGAGCTGGGAGGGA   27609        AC_   G
                                TCCCTCCCA   CCTG TG
                                |||||||||   |||| ||
                                AGGGAGGGT   GGGT AC
                                     CGA    G
GAM155   HOOK2    3'  CCAGATTGGTGGGGAGGGA   26158        A  ____
                                TCCCTCCC ACC   CTGG
                                |||||||| |||   ||||
                                AGGGAGGG TGG   GACC
                                     G   TTA
GAM155   KIAA0140 3'  CTCAGTCCTCTGGGAGGGA   28512        ACCCT __
                                TCCCTCCCA    GG  TGAG
                                |||||||||    ||  ||||
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                                AGGGAGGGT    CC  ACTC
                                     CT___  TG
GAM155  KIAA0182  3'  TACGCAGGTGGGAGGGA    72502        AC   _
                                TCCCTCCCA  CCTG GTG
                                |||||||||  |||| |||
                                AGGGAGGGT  GGAC CAT
                                     __   G
GAM155  KIAA0252  3'  TGGCAGGTGTGGGAGGGA    63461        AC   G
                                TCCCTCCCA  CCTG TG
                                |||||||||  |||| ||
                                AGGGAGGGT  GGAC GT
                                     GT   G
GAM155  KIAA0285  3'  CTCAGAAGAAACTGGGAGGGG  29683        ACC_  GG
                                TCCCTCCCA   CT  TGAG
                                |||||||||   ||  ||||
                                GGGGAGGGT   GA  ACTC
                                     CAAA  AG
GAM155  KIAA0677  3'  CACTGTAGGTGGGAGGGA    28529        A  CT_
                                TCCCTCCCA CC   GGTG
                                |||||||||  ||   ||||
                                AGGGAGGGT GG   TCAC
                                     _  ATG
GAM155  KIAA0789  5'  CTCACCTTCAGTTTGGGAGGG  64429        CCCT__
                                CCCTCCCAA     GGTGAG
                                |||||||||     ||||||
                                GGGAGGGTT     CCACTC
                                     TGACTT
GAM155  KIAA0843  3'  CTTTGTAGATTGGGGGGA    30802     T    CC   GT
                                TCCC CCCAA  CTG  GAG
                                ||||  |||||  |||  |||
                                AGGG GGGTT  GAT  TTC
                                  _    A_  GT
GAM155  KIAA0853  3'  TTTATTAATGGGGAGGGA    31217        AACCC
                                TCCCTCCC    TGGTGAG
                                ||||||||    |||||||
                                AGGGAGGG    ATTATTT
                                     GTA__
GAM155  KIAA0864  3'  CAGTGGGGGCTGGGAGGG    63938        A_    G
                                CCCTCCCA  CCCTG TG
                                ||||||||  ||||| ||
                                GGGAGGGT  GGGGT AC
                                     CG    G
GAM155  KIAA1018  3'  TTCATCAGCCAGGAGGGA    31059       CAACC
                                TCCCTCC    CTGGTGAG
                                |||||||    ||||||||
                                AGGGAGG    GACTACTT
                                    ACC__
GAM155  KIAA1061  3'  CACACGGGTTGGGAGAGG    71716    _       TG
                                CC CTCCCAACCC  GTG
                                || ||||||||||  |||
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                                GG GAGGGTTGGG  CAC
                                 A         CA
GAM155  KIAA1171  3'  GCTCACGGGGAGAGGTATGGGA 89344         _  ____  G    ___
              GGGA                   TCCCTCCCA ACC    CT GTGAG   C
                                |||||||||  |||    || |||||   |
                                AGGGAGGGT TGG    GG CACTC   G
                                     A   AGAG  G    ___
GAM155  KIAA1190  3'  CTCGGGGGGATTGGGGGGGA    71646      T    _   GG
                                TCCC CCCAA CCCT  TGAG
                                |||| ||||| ||||  ||||
                                AGGG GGGTT GGGG  GCTC
                                  _    A   __
GAM155  KIAA1649  3'  TGCTGGTTGGGAGTGA      67518    C       CT
                                TC CTCCCAACC  GGTG
                                || |||||||||  ||||
                                AG GAGGGTTGG  TCGT
                                 T       __
GAM155  KIAA1649  3'  TGCTGGTTGGGAGTGA      51256    C       CT
                                TC CTCCCAACC  GGTG
                                || |||||||||  ||||
                                AG GAGGGTTGG  TCGT
                                 T       __
GAM155  KIAA1655  5'  CTCACCTCCAGTGGGAGGGA   67182         ACCCT
                                TCCCTCCCA    GGTGAG
                                |||||||||    ||||||
                                AGGGAGGGT    CCACTC
                                     GACCT
GAM155  KIAA1750  3'  CTCAGTGATAGAGTATGGGAGG 68809         _ C   G___
              GA                   TCCCTCCCA AC CTG    TGAG
                                |||||||||  || |||    ||||
                                AGGGAGGGT TG GAT    ACTC
                                     A  A   AGTG
GAM155  KIAA1944  5'  CACCAGGTAGTCACTGGGCAGA 76077    C  _   ___  __
              GA                   TC CT CCCA   AC  CCTGGTG
                                || || ||||   ||  |||||||
                                AG GA GGGT   TG  GGACCAC
                                 A  C    CAC  AT
GAM155  KIAA1952  5'  CTCTGCCGGCTGGGAGGG    73544        ACC    _
                                CCCTCCCA   CTGGT GAG
                                ||||||||   ||||| |||
                                GGGAGGGT   GGCCG CTC
                                     C__     T
GAM155  LAGY      5'  CTCAGTCCAGGGAGGGA     51658        AACCC  __
                                TCCCTCCC    TGG  TGAG
                                ||||||||    |||  ||||
                                AGGGAGGG    ACC  ACTC
                                     ______  TG
GAM155  MGC10715  3'  CTTATCAGGCATGGGAGGGA   44498         AC
                                TCCCTCCCA  CCTGGTGAG
                                |||||||||  |||||||||
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                                AGGGAGGGT GGACTATTC
                                     AC
GAM155  MGC15429 3' CTCACTGGCTGGGAAGG    52211   C    A CT
                                CC TCCCA CC  GGTGAG
                                || ||||| ||  ||||||
                                GG AGGGT GG  TCACTC
                                 A    C __
GAM155  MGC4737  5' CTCACCAGCGGAGTGGA    49640   _   CAACC
                                TCC CTCC    CTGGTGAG
                                ||| ||||    ||||||||
                                AGG GAGG    GACCACTC
                                  T   C____
GAM155  MGC5139  5' CTTGAAAGGGTGGGGAGGGA  74571       A    GG
                                TCCCTCCC ACCCT  TGAG
                                |||||||| |||||  ||||
                                AGGGAGGG TGGGA  GTTC
                                     G    AA
GAM155  MLLT10   5' CCGGGTGGAGGTGGGGAGGGA  17351       A _____
                                TCCCTCCC ACC    CTGG
                                |||||||| |||    ||||
                                AGGGAGGG TGG    GGCC
                                     G   AGGTG
GAM155  MMP24    3' CTCACCAGGGTCTGAGGGG   22918      CCA
                                TCCCTC   ACCCTGGTGAG
                                ||||||   ||||||||||||
                                GGGGAG   TGGGACCACTC
                                   TC_
GAM155  moblak   3' CTCACCAGAATTGTCAGTGG  56396   _ CC   CC
                                CC CT  CAA  CTGGTGAG
                                || ||  |||  ||||||||
                                GG GA  GTT  GACCACTC
                                 T  CT   AA
GAM155  NIP30    3' CTCACTGATATTGGGAGG    46896       CCC
                                CCTCCCAA   TGGTGAG
                                ||||||||   |||||||
                                GGAGGGTT   GTCACTC
                                     ATA
GAM155  PRO0529  3' CTCACCAGGGTGGGCAGAGA  26856   C _   A
                                TC CT CCCA CCCTGGTGAG
                                || || |||| ||||||||||
                                AG GA GGGT GGGACCACTC
                                 A  C   _
GAM155  PTK6     5' CTCTGAGGGTTGGGAAGG    21076   C       GGT
                                CC TCCCAACCCT   GAG
                                || ||||||||||   |||
                                GG AGGGTTGGGA   CTC
                                 A        GT_
GAM155  RAB3IL1  3' CTCAGCCCTTGGGAGGGG    26365         CCCT _
                                TCCCTCCCAA    GG TGAG
                                ||||||||||    || ||||
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                                GGGGAGGGTT   CC ACTC
                                     C___  G
GAM155  RIN3     3'  TTCATTAGACGGAAAGGGA   46164      C_  AACC
                                TCCCT  CC   CTGGTGAG
                                |||||  ||   ||||||||
                                AGGGA  GG   GATTACTT
                                   AA  CA__
GAM155  RP4-622L5 3'  CTCATTTCTTGGGAGGG    39424        CCCT
                                CCCTCCCAA   GGTGAG
                                |||||||||   ||||||
                                GGGAGGGTT   TTACTC
                                     CT__
GAM155  SCMH1    3'  CTCACCAGGAGTTTAGG     25283     CCC  _
                                CCT   AAC CCTGGTGAG
                                |||   ||| |||||||||
                                GGA   TTG GGACCACTC
                                  T__   A
GAM155  SERPINH1  3'  TATTGGGGTTGGGGGGGA    16375          TG
                                TCCCTCCCAACCC  GTG
                                ||||||||||||  |||
                                AGGGGGGGTTGGG  TAT
                                      GT
GAM155  SIAT4B   5'  CTCACCAGGGTGGCAGGAGA   23634    _  C   A
                                TC CCT CCA CCCTGGTGAG
                                || ||| ||| ||||||||||
                                AG GGA GGT GGGACCACTC
                                 A   C   _
GAM155  SNPH     3'  CTCTGGGGGTTGGAGGGA    28902       C     GGT
                                TCCCTCC AACCCT   GAG
                                ||||||| ||||||   |||
                                AGGGAGG TTGGGG   CTC
                                    _     GT_
GAM155  SSH-3    5'  CGCGGGGTTGAGGGA      35790       CC      G
                                TCCCTC  AACCCTG TG
                                ||||||  ||||||| ||
                                AGGGAG  TTGGGGC GC
                                    __     _
GAM155  SSH-3    5'  CGCGGGGTTGAGGGA      37417       CC      G
                                TCCCTC  AACCCTG TG
                                ||||||  ||||||| ||
                                AGGGAG  TTGGGGC GC
                                    __     _
GAM155  VIAAT    3'  CGAGGGGGTTGGGAAGGGA   55450      _       GG
                                TCCCT CCCAACCCT  TG
                                |||||  |||||||||  ||
                                AGGGA GGGTTGGGG  GC
                                   A        GA
GAM155  LOC114987 3'  CGGGAATGAGTTGGGAGGGG   59795          _____
                                TCCCTCCCAAC    CCTG
                                ||||||||||     ||||
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                                GGGGAGGGTTG    GGGC
                                      AGTAA
GAM155  LOC121036 3'  CAGTAGGATGGGAGGGA     74481        AC   G
                                TCCCTCCCA  CCTG TG
                                |||||||||  |||| ||
                                AGGGAGGGT  GGAT AC
                                     A_    G
GAM155  LOC123346 5'  CTCTGAAAGAGTCGGGGAGGGA 76127       A_  C  GGT_
                                TCCCTCCC  AC CT   GAG
                                ||||||||  || ||   |||
                                AGGGAGGG  TG GA   CTC
                                     GC  A  AAGT
GAM155  LOC136306 3'  CAAAGGGGTGTGAGAGGGA   75768      C  _    GG
                                TCCCTC CA ACCCT  TG
                                ||||||  || |||||  ||
                                AGGGAG GT TGGGG  AC
                                    A  G    AA
GAM155  LOC144596 3'  CTCACCTGGAGGCAAGAGGGA  77427      ___  AAC  T
                                TCCCTC   CC   CC GGTGAG
                                ||||||   ||   || ||||||
                                AGGGAG   GG   GG CCACTC
                                    AAC  A__  T
GAM155  LOC145497 5'  CCAGGGCTTGCTGGGAGGGA   77731       A____
                                TCCCTCCCA    CCCTGG
                                |||||||||    ||||||
                                AGGGAGGGT    GGGACC
                                     CGTTC
GAM155  LOC146439 5'  CTCATTCCTGGGAGGGG     78449        ACCCT
                                TCCCTCCCA    GGTGAG
                                |||||||||    ||||||
                                GGGGAGGGT    TTACTC
                                     CC___
GAM155  LOC147711 3'  CTCAGCCTTTGGGAGGG     79116        CCCT  _
                                CCCTCCCAA    GG TGAG
                                |||||||||    || ||||
                                GGGAGGGTT    CC ACTC
                                     T___  G
GAM155  LOC150150 5'  CCAGTGTGGTGGGAGGGA    86009        A  ___
                                TCCCTCCCA CC   CTGG
                                |||||||||  ||   ||||
                                AGGGAGGGT GG   GACC
                                     _  TGT
GAM155  LOC152667 3'  CTCACTGATATTGGGAGG    81523        CCC
                                CCTCCCAA   TGGTGAG
                                ||||||||   |||||||
                                GGAGGGTT   GTCACTC
                                     ATA
GAM155  LOC157931 3'  CTCACGGCCTGGGAGGG     87940        AC  TG
                                CCCTCCCA  CC  GTGAG
                                |||||||  ||  |||||
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                                GGGAGGGT  GG  CACTC
                                    CC  __
GAM155  LOC158055 3'  CCGGCGGCTGGTGAGGGA    82580       _  A  _
                                TCCCTC CCA CC CTGG
                                |||||| ||| || ||||
                                AGGGAG GGT GG GGCC
                                   T   C  C
GAM155  LOC199927 3'  CCGGAGTGGCTGGGAGGGG   91479         A  ___
                                TCCCTCCCA CC   CTGG
                                ||||||||| ||   ||||
                                GGGGAGGGT GG   GGCC
                                     C  TGA
GAM155  LOC201182 5'  CTCACTGGTTGAGATGGA    91336     C  C    CT
                                TCC TC CAACC  GGTGAG
                                ||| || |||||  ||||||
                                AGG AG GTTGG  TCACTC
                                  T  A    __
GAM155  LOC219920 5'  CTCATTAGACTGGGAGG     94947        ACC
                                CCTCCCA   CTGGTGAG
                                |||||||   ||||||||
                                GGAGGGT   GATTACTC
                                    CA_
GAM155  LOC220739 3'  TCAGGGCTTAGGGAGGGA    94529         _ _
                                TCCCTCCC AA CCCTGG
                                |||||||| || ||||||
                                AGGGAGGG TT GGGACT
                                     A  C
GAM155  LOC221424 3'  CCTGGGACTTGGGAGGGA    95271          __  T
                                TCCCTCCCAA  CCC GG
                                ||||||||||  ||| ||
                                AGGGAGGGTT  GGG CC
                                      CA   T
GAM155  LOC221718 5'  CTCACCAGCCTGAGGTAGGA  95280     CT  _  ACC
                                TCC  CC CA   CTGGTGAG
                                |||  || ||   ||||||||
                                AGG  GG GT   GACCACTC
                                  AT  A  CC_
GAM155  LOC253955 5'  CTCACCAGGTGCAGAGGGG   96072       CCAAC
                                TCCCTC    CCTGGTGAG
                                ||||||    |||||||||
                                GGGGAG    GGACCACTC
                                   ACGT_
GAM155  LOC255328 3'  CTCACCAGGTGAGGAGTGA   98338    C   _  AC
                                TC CTCC CA  CCTGGTGAG
                                || |||| ||  |||||||||
                                AG GAGG GT  GGACCACTC
                                 T   A  __
GAM155  LOC256973 3'  CTCACGGCCTCCGGGAGGGG  98198         AAC__  TG
                                TCCCTCCC    CC  GTGAG
                                ||||||||    ||  |||||
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                                GGGGAGGG    GG  CACTC
                                    CCTCC  __
GAM155  LOC257456 3'  CTCACTAGGACCAGGAAGGG   80594     _  CAAC
                                CCCT CC    CCTGGTGAG
                                |||| ||    |||||||||
                                GGGA GG    GGATCACTC
                                  A  ACCA
GAM155  LOC51696  3'  CATTGGAGGTTGGGAAGGA    33079     C       _ TG
                                TCC TCCCAACC C  GTG
                                ||| |||||||| |  |||
                                AGG AGGGTTGG G  TAC
                                  A       A GT
GAM155  LOC91496  5'  CATTAGAGGTGGAAGGGA     66808      C   A  _
                                TCCCT CCA CC CTGGTG
                                ||||| ||| || ||||||
                                AGGGA GGT GG GATTAC
                                   A   _  A
GAM155  LOC92228  5'  CTCACCAGGGTGAGGG      69075      CCA
                                CCCTC   ACCCTGGTGAG
                                |||||   ||||||||||
                                GGGAG   TGGGACCACTC
                                   ____
GAM155  LOC92293  3'  CACACAGCTGGGGGGGA     69318         ACC  _
                                TCCCTCCCA   CTG GTG
                                |||||||||   ||| |||
                                AGGGGGGGT   GAC CAC
                                     C__   A
GAM156  A1BG      3'  CTCAGGTGATCCACCCGCCTCA 56288
                                TGAGGTGGGTGGATCACCTGAG
                                |||||||||||||||||||||
                                ACTCCGCCCACCTAGTGGACTC

GAM156  AIM1      3'  CTCAGGTGATCCTCCCACCTCA 93463         T
                                TGAGGTGGG GGATCACCTGAG
                                ||||||||| ||||||||||
                                ACTCCACCC CCTAGTGGACTC
                                     T
GAM156  ALDH1B1   3'  ACCTCAGGTGATCCACCCGCCT 7312
              CA                  TGAGGTGGGTGGATCACCTGAGGT
                                ||||||||||||||||||||||||
                                ACTCCGCCCACCTAGTGGACTCCA

GAM156  ALOX15    3'  CTCAAATGATCCTCCCACCTCA 8545          T     CC
                                TGAGGTGGG GGATCA  TGAG
                                ||||||||| ||||||  ||||
                                ACTCCACCC CCTAGT  ACTC
                                     T     AA
GAM156  ARCN1     3'  CTCAGGCAATCCGCCCACCTCA 9750             CA
                                TGAGGTGGGTGGAT  CCTGAG
                                ||||||||||||||  ||||||
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                                ACTCCACCCGCCTA  GGACTC
                                      AC
GAM156  ATP1B2   3'  ACCTCAGGTGATCCACCTGCCT 9824      TG
           C                   GAGG  GGTGGATCACCTGAGGT
                               ||||  ||||||||||||||||
                               CTCC  CCACCTAGTGGACTCCA
                                 GT
GAM156  ATP6V1A1  3'  ACCTCAGGTGATCCGCCCACCT 9862
           C                   GAGGTGGGTGGATCACCTGAGGT
                               ||||||||||||||||||||||
                               CTCCACCCGCCTAGTGGACTCCA

GAM156  ATP7A    3'  ACCTCAGGTGATCCACCCGCCT 5311
                               AGGTGGGTGGATCACCTGAGGT
                               ||||||||||||||||||||||
                               TCCGCCCACCTAGTGGACTCCA

GAM156  AXL      3'  ACCTCAAGTGATCTGCCCACCT 41871         TG     C
           CA                    TGAGGTGGG  GATCAC TGAGGT
                               |||||||||  ||||||  ||||||
                               ACTCCACCC  CTAGTG ACTCCA
                                    GT     A
GAM156  CAMLG    3'  ACCTCAGGTGATCTGCCCACCT 9990         TG
           C                   GAGGTGGG  GATCACCTGAGGT
                               ||||||||  ||||||||||||
                               CTCCACCC  CTAGTGGACTCCA
                                    GT
GAM156  CASP10   3'  CTCAAGCGATCCTCCCACCTCA 53255         T    ACC
                               TGAGGTGGG GGATC   TGAG
                               |||||||||| |||||   ||||
                               ACTCCACCC CCTAG   ACTC
                                    T    CGA
GAM156  CASP10   3'  CTCAAGCGATCCTCCCACCTCA 53256         T    ACC
                               TGAGGTGGG GGATC   TGAG
                               |||||||||| |||||   ||||
                               ACTCCACCC CCTAG   ACTC
                                    T    CGA
GAM156  CBFA2T2  3'  CCTCAGGTGATCCCCCCAC   18708      T
                               GTGGG GGATCACCTGAGG
                               |||||  |||||||||||||
                               CACCC CCTAGTGGACTCC
                                  C
GAM156  CCNF     3'  CCTCAAGTGATCCGCCCAC   10072           C
                               GTGGGTGGATCAC TGAGG
                               |||||||||||||  |||||
                               CACCCGCCTAGTG ACTCC
                                       A
GAM156  CHRNB4   3'  ACCTCAGATGACCCACCTGCCT 7446      TG    A  C
           C                   GAGG  GGTGG TCA CTGAGGT
                               ||||  |||||  |||  |||||||
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                                CTCC  CCACC AGT GACTCA
                                  GT    C  A
GAM156  COX15    3'  CCTCAGGTAATCCGCCCAT   55282          C
                                GTGGGTGGAT ACCTGAGG
                                |||||||||| ||||||||
                                TACCCGCCTA TGGACTCC
                                     A
GAM156  CYP2B6   3'  CCTCAGGTGATCCACCCACCTC 7557
            A                    TGAGGTGGGTGGATCACCTGAGG
                                |||||||||||||||||||||||
                                ACTCCACCCACCTAGTGGACTCC

GAM156  CYP4F3   3'  ACCTCAGGTGATCCACCTGCCT 7989       TG
            C                    GAGG  GGTGGATCACCTGAGGT
                                ||||  ||||||||||||||||
                                CTCC  CCACCTAGTGGACTCCA
                                  GT
GAM156  DFFB     3'  ACCTCAGGTGATCCGCCCACCT 88748
            CA                    TGAGGTGGGTGGATCACCTGAGGT
                                |||||||||||||||||||||||||
                                ACTCCACCCGCCTAGTGGACTCCA

GAM156  DHFR     3'  ACCGCAAGCGATTCACCCACCT 7636              ACC  A
            CA                    TGAGGTGGGTGGATC   TG GGT
                                |||||||||||||||   || |||
                                ACTCCACCCACTTAG   AC CCA
                                      CGA  G
GAM156  DISC1    3'  ACCTCAGGCGATCCACCCCCAC 38497       __        A
            CTC                    GAGGT  GGGTGGATC CCTGAGGT
                                |||||  ||||||||| ||||||||
                                CTCCA  CCCACCTAG GGACTCCA
                                   CC        C
GAM156  EGR3     3'  ACCCCAAACTCTTCCCCACCTC 60299         T   TCACC  A
                                GAGGTGGG GGA    TG GGT
                                |||||||| |||    || |||
                                CTCCACCC CTT    AC CCA
                                     _  CTCAA  C
GAM156  EN2      3'  ACCTCAAGCCTGGACCAGCCAC 9251          G   A   CC__
            CTCA                    TGAGGTGG TGG TCA    TGAGGT
                                |||||||| ||| |||    ||||||
                                ACTCCACC ACC GGT    ACTCCA
                                     G   A   CCGA
GAM156  EPB72    3'  TACCTCAGGTGATCCACCCACC 15881                    ___
            TC                    GAGGTGGGTGGATCACCTGAGGT   A
                                |||||||||||||||||||||||   |
                                CTCCACCCACCTAGTGGACTCCA   T
                                                    ___
GAM156  FCAR     3'  ACCTCAGGTGATCCACCCACCT 56557
            T                    GAGGTGGGTGGATCACCTGAGGT
                                |||||||||||||||||||||||
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                                TTCCACCCACCTAGTGGACTCCA

GAM156  FCAR     3'  ACCTCAGGTGATCCACCTGCCT 56558      TG
                C                GAGG  GGTGGATCACCTGAGGT
                                 ||||  ||||||||||||||||
                                 CTCC  CCACCTAGTGGACTCCA
                                   GT
GAM156  FOXI1    3'  CCTAAATCCTCCCACCCCA   25168    A     T    CACCTG
                                 TG GGTGGG GGAT      AGG
                                 || |||||| ||||      |||
                                 AC CCACCC CCTA      TCC
                                  C     T    AA____
GAM156  FUT3     3'  CCCCAGGTTCTCACCTCA    5620           TGGATC     A
                                 TGAGGTGGG      ACCTG GG
                                 |||||||||      ||||| ||
                                 ACTCCACTC      TGGAC CC
                                       T_____     C
GAM156  G6PC     3'  ACCTCAAGTGATCCACCTGCCT 5649      TG         C
                                 AGG  GGTGGATCAC TGAGGT
                                 |||  ||||||||||| ||||||
                                 TCC  CCACCTAGTG ACTCCA
                                   GT         A
GAM156  GRAF     3'  CCTCAAGTGATCTGCCCA    31231      TG     C
                                 TGGG  GATCAC TGAGG
                                 ||||  |||||| |||||
                                 ACCC  CTAGTG ACTCC
                                   GT     A
GAM156  ICAM1    3'  CTCAAGTGATCCTCCCACCTCA 72037          T      C
                                 TGAGGTGGG GGATCAC TGAG
                                 ||||||||| ||||||| ||||
                                 ACTCCACCC CCTAGTG ACTC
                                       T      A
GAM156  IFNAR2   3'  ACCTCAAGTGATCTGCCCTCCT 7894        T   TG     C
                CA                 TGAGG GGG  GATCAC TGAGGT
                                   |||||  |||  |||||| ||||||
                                   ACTCC CCC  CTAGTG ACTCCA
                                     T  GT     A
GAM156  LNK      3'  ACCTCAGGTGATCCACCCGCCT 19627
                                   AGGTGGGTGGATCACCTGAGGT
                                   |||||||||||||||||||||
                                   TCCGCCCACCTAGTGGACTCCA

GAM156  MAK      3'  ACCTCAGGTGATCCACCTGCCT 20936      TG
                C                  GAGG  GGTGGATCACCTGAGGT
                                   ||||  ||||||||||||||||
                                   CTCC  CCACCTAGTGGACTCCA
                                     GT
GAM156  MEFV     3'  ACCTCAGGTGATCCACCCGCCT 5921
                CA                   TGAGGTGGGTGGATCACCTGAGGT
                                     |||||||||||||||||||||||
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                                ACTCCGCCCACCTAGTGGACTCCA

GAM156  MEFV     3'  ACCTCAGGTGATGCACCCACCT 5922            G
                CA                  TGAGGTGGGTG ATCACCTGAGGT
                                    |||||||||||  ||||||||||||
                                    ACTCCACCCAC TAGTGGACTCCA
                                          G
GAM156  MHC2TA   3'  ACCTCGGGTGATCCACCCACCT 5965
                CA                  TGAGGTGGGTGGATCACCTGAGGT
                                    |||||||||||||||||||||||
                                    ACTCCACCCACCTAGTGGGCTCCA

GAM156  MLANA    3'  ACCTCAGGTGATCTGCCCGCCT 19755         TG
                CA                  TGAGGTGGG  GATCACCTGAGGT
                                    |||||||||  ||||||||||||
                                    ACTCCGCCC  CTAGTGGACTCCA
                                         GT
GAM156  NCOA6    5'  ACCTCAAGTGATCCACCCGTC  26822   GT        C
                                    G  GGGTGGATCAC TGAGGT
                                    |  ||||||||||| ||||||
                                    C  CCCACCTAGTG ACTCCA
                                     TG         A
GAM156  NDRG3    3'  ACCTCAGGTGATCCACCTGCCT 42760       TG
                CA                  TGAGG  GGTGGATCACCTGAGGT
                                    |||||  ||||||||||||||||
                                    ACTCC  CCACCTAGTGGACTCCA
                                       GT
GAM156  NQO1     3'  ACCTCAGGTGATCCGCCTACCT 8039
                CA                  TGAGGTGGGTGGATCACCTGAGGT
                                    |||||||||||||||||||||||
                                    ACTCCATCCGCCTAGTGGACTCCA

GAM156  NUP62    3'  ACCTACTGCGACCACCCACCTC 25641            A  ACCTG
                A                    TGAGGTGGGTGG TC     AGGT
                                    ||||||||||| ||     ||||
                                    ACTCCACCCACC AG     TCCA
                                          _  CGTCA
GAM156  PER2     3'  ACCTCAAGCGATCCACCCACCT 43339             ACC
                C                    GAGGTGGGTGGATC   TGAGGT
                                    ||||||||||||||   ||||||
                                    CTCCACCCACCTAG   ACTCCA
                                          CGA
GAM156  PIK3CD   3'  ACCTCAGGTGATCCACCCGCCT 18482
                                    AGGTGGGTGGATCACCTGAGGT
                                    |||||||||||||||||||||
                                    TCCGCCCACCTAGTGGACTCCA

GAM156  PPEF2    3'  ACCTCAGGTGATCCACCCTCCT 21770       T
                CA                  TGAGG GGGTGGATCACCTGAGGT
                                    ||||| ||||||||||||||||||
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                                ACTCC CCCACCTAGTGGACTCCA
                                  T
GAM156  PRKR    3'  ACCTCAAGTAATCCACCTGCCT 12337     TG     C  C
           C                     GAGG  GGTGGAT AC TGAGGT
                                 ||||  ||||||| || ||||||
                                 CTCC  CCACCTA TG ACTCCA
                                   GT      A  A
GAM156  RBBP9   3'  CCTCAAGTGATCCACCCACCTC 70688              C
           A                     TGAGGTGGGTGGATCAC TGAGG
                                 |||||||||||||||| |||||
                                 ACTCCACCCACCTAGTG ACTCC
                                              A
GAM156  RP2     3'  ACCTCAGGTGATCCGTCCACCT 23597        GT
           CA                    TGAGGTGG  GGATCACCTGAGGT
                                 ||||||||  ||||||||||||||
                                 ACTCCACC  CCTAGTGGACTCCA
                                     TG
GAM156  SAS     3'  CCTCAGGTGATCCACCCGC   21099
                                 GTGGGTGGATCACCTGAGG
                                 |||||||||||||||||||
                                 CGCCCACCTAGTGGACTCC

GAM156  SCML2   3'  ACCTCAGGTGATCCGCCCACCT 21418
           C                     GAGGTGGGTGGATCACCTGAGGT
                                 ||||||||||||||||||||||
                                 CTCCACCCGCCTAGTGGACTCCA

GAM156  SEDL    3'  ACCTCAGTTGATCCACCCGCCT 28071            C
           CA                    TGAGGTGGGTGGATCA CTGAGGT
                                 |||||||||||||||| |||||||
                                 ACTCCGCCCACCTAGT GACTCCA
                                              T
GAM156  SEDL    3'  ACCTCGTGATCCACCCACCTCA 28072             CT
                                 TGAGGTGGGTGGATCAC  GAGGT
                                 ||||||||||||||||  |||||
                                 ACTCCACCCACCTAGTG  CTCCA
                                                —
GAM156  SEPN1   3'  ACCTCAGGTGATCCACCTGCCT 66957      TG
           CA                    TGAGG  GGTGGATCACCTGAGGT
                                 |||||  ||||||||||||||||
                                 ACTCC  CCACCTAGTGGACTCCA
                                   GT
GAM156  SH3BP2  3'  CCTCAGGTGATCTGCCCA    13060     TG
                                 TGGG  GATCACCTGAGG
                                 ||||  ||||||||||||
                                 ACCC  CTAGTGGACTCC
                                   GT
GAM156  SHOX    3'  ACCTCAGGTGATCCACCCGCCT 6557
           TA                    TGAGGTGGGTGGATCACCTGAGGT
                                 |||||||||||||||||||||||
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                                ATTCCGCCCACCTAGTGGACTCCA

GAM156  SHOX     3'  CTCAAGCAATCCTCCCACCTCA 6571          T    CACC
                                TGAGGTGGG GGAT    TGAG
                                |||||||| ||||    ||||
                                ACTCCACCC CCTA    ACTC
                                      T    ACGA
GAM156  SLA2     3'  ACCTCAGGTGATCCACCCACCT 50879
             T                   GAGGTGGGTGGATCACCTGAGGT
                                 |||||||||||||||||||||||
                                 TTCCACCCACCTAGTGGACTCCA

GAM156  SMAC     5'  ACCTCAAGTGATCCACCCGCCT 57991              C
             C                   GAGGTGGGTGGATCAC TGAGGT
                                 |||||||||||||||| ||||||
                                 CTCCGCCCACCTAGTG ACTCCA
                                          A
GAM156  SNX15    3'  ACCTCAAGTGATCCACCCGCCT 74112              C
             CA                    TGAGGTGGGTGGATCAC TGAGGT
                                   |||||||||||||||| ||||||
                                   ACTCCGCCCACCTAGTG ACTCCA
                                            A
GAM156  SULT2B1  5'  TACCTCAGGTGATCCACCCACC 17227                  ___
             TC                    GAGGTGGGTGGATCACCTGAGGT   A
                                   ||||||||||||||||||||||   |
                                   CTCCACCCACCTAGTGGACTCCA   T
                                                ___
GAM156  TAPBP    3'  ACCTCAGGTGATCTGCCCACCT 13539          TG
             CA                    TGAGGTGGG  GATCACCTGAGGT
                                   |||||||||  ||||||||||||
                                   ACTCCACCC  CTAGTGGACTCCA
                                        GT
GAM156  TBXA2R   3'  ACCTCAGGTGATTCACCAGCCT 8336         G
             CA                    TGAGGT GGTGGATCACCTGAGGT
                                   ||||||| ||||||||||||||||
                                   ACTCCG CCACTTAGTGGACTCCA
                                      A
GAM156  TCF2     3'  ACCTCAGACAATCCACTCTCA  6608       GTG      CAC
                                TGAG   GGTGGAT   CTGAGGT
                                ||||   |||||||   |||||||
                                ACTC   TCACCTA   GACTCCA
                                  ___       ACA
GAM156  TNFRSF10B 3'  ACCTCAGGTGATCCACCTTGGC 15209      __
             CT                    AGGT  GGGTGGATCACCTGAGGT
                                   ||||  ||||||||||||||||||
                                   TCCG  TCCACCTAGTGGACTCCA
                                     GT
GAM156  TNFRSF11A 3'  ATCCAAGTGATCCTCCCACCTC 15189          T      C  A
             A                     TGAGGTGGG GGATCAC TG GGT
                                   ||||||||| ||||||| || |||
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                                ACTCCACCC CCTAGTG AC CTA
                                      T      A  _
GAM156  TPMT     3'  ACCTCAGGTGATCTACCCACCT 6298
              C                  GAGGTGGGTGGATCACCTGAGGT
                                 ||||||||||||||||||||||
                                 CTCCACCCATCTAGTGGACTCCA

GAM156  TRPM6    3'  ACCTCAGATGATCCACCTGCCT 35021     TG       C
                                 AGG  GGTGGATCA CTGAGGT
                                 |||  ||||||||| |||||||
                                 TCC  CCACCTAGT GACTCCA
                                   GT        A
GAM156  TRPV1    3'  ACCTCAGGTGATCCGCCCACCT 55646
              C                  GAGGTGGGTGGATCACCTGAGGT
                                 ||||||||||||||||||||||
                                 CTCCACCCGCCTAGTGGACTCCA

GAM156  TUFT1    3'  ACCTCAGGTGATCCACCCACCT 39665
              C                  GAGGTGGGTGGATCACCTGAGGT
                                 ||||||||||||||||||||||
                                 CTCCACCCACCTAGTGGACTCCA

GAM156  UMPS     3'  ACCTCCCAGGTGATCCTCCCAC 6327          T       __
              CTCA                  TGAGGTGGG GGATCACCT  GAGGT
                                 |||||||| |||||||||  |||||
                                 ACTCCACCC CCTAGTGGA  CTCCA
                                      T        CC
GAM156  VDR      3'  ACCTCCCCTATCCACCCAGCCC 6336     A  _        CACCT
              A                  TG GG TGGGTGGAT     GAGGT
                                 || || |||||||||     |||||
                                 AC CC ACCCACCTA     CTCCA
                                  _  G        TCCC_
GAM156  VHL      3'  ACCTCAGGTGATCCGCCCACCT 6819
              CA                   TGAGGTGGGTGGATCACCTGAGGT
                                 ||||||||||||||||||||||
                                 ACTCCACCCGCCTAGTGGACTCCA

GAM156  XRCC2    3'  ACCTCAAGTGATCCACCCACCT 19483              C
              C                  GAGGTGGGTGGATCAC TGAGGT
                                 ||||||||||||||| ||||||
                                 CTCCACCCACCTAGTG ACTCCA
                                           A
GAM156  ZNF133   5'  ACCTCAGGTGATCCACCTGCCT 14291       TG
              CA                   TGAGG  GGTGGATCACCTGAGGT
                                 |||||  ||||||||||||||||
                                 ACTCC  CCACCTAGTGGACTCCA
                                    GT
GAM156  ZNF157   3'  ACCTCAGGTGATCCACCTGCCT 14320      TG
              C                  GAGG  GGTGGATCACCTGAGGT
                                 ||||  ||||||||||||||||
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                                CTCC  CCACCTAGTGGACTCCA
                                  GT
GAM156  ALTE     5'  ACCTCGACCCCTACCCACCCCA 60995    A       ATCACC
                                TG GGTGGGTGG      TGAGGT
                                || |||||||||      ||||||
                                AC CCACCCATC      GCTCCA
                                 C        CCCA__
GAM156  ANP32B   3'  ACCCCAGGACACCCACCCACCC 22150    A       ATCA    A
           A                     TG GGTGGGTGG    CCTG GGT
                                || |||||||||    |||| |||
                                AC CCACCCACC    GGAC CCA
                                 _       CACA    C
GAM156  ASB16    3'  ACCTCAGGTGATCCACCCGCCT 55967
                                AGGTGGGTGGATCACCTGAGGT
                                |||||||||||||||||||||
                                TCCGCCCACCTAGTGGACTCCA

GAM156  BA108L7.2 3'  ACCTCAGGTGATCCACCTGCCT 49060     TG
                                AGG  GGTGGATCACCTGAGGT
                                |||  ||||||||||||||||
                                TCC  CCACCTAGTGGACTCCA
                                  GT
GAM156  C21orf25  3'  ACCTCAGGTGATCCACCCACCT 64278
           T                     GAGGTGGGTGGATCACCTGAGGT
                                |||||||||||||||||||||||
                                TTCCACCCACCTAGTGGACTCCA

GAM156  C6orf33   3'  CTCAAGCAATCCTCCCACCTCA 56712          T    CACC
                                TGAGGTGGG GGAT    TGAG
                                ||||||||| ||||    ||||
                                ACTCCACCC CCTA    ACTC
                                      T    ACGA
GAM156  C6orf33   3'  CTCAAGTGATCCGCCCACCTCA 56713               C
                                TGAGGTGGGTGGATCAC TGAG
                                |||||||||||||||| ||||
                                ACTCCACCCGCCTAGTG ACTC
                                           A
GAM156  CARD6     3'  ACCTCAGGTGATCCGCCCACCT 51835
                                AGGTGGGTGGATCACCTGAGGT
                                |||||||||||||||||||||
                                TCCACCCGCCTAGTGGACTCCA

GAM156  COQ7      3'  CCTCAAGCAATCCACCCACCTC 32854             CACC
           A                     TGAGGTGGGTGGAT    TGAGG
                                ||||||||||||||    |||||
                                ACTCCACCCACCTA    ACTCC
                                           ACGA
GAM156  CPSF2     3'  ACCTCAAGCGATCCACCCACCT 62255             ACC
                                AGGTGGGTGGATC   TGAGGT
                                |||||||||||||   ||||||
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                                TCCACCCACCTAG   ACTCCA
                                        CGA
GAM156  DBR1     3'  ACCTCAGGCGATCCACCTGTCT 33059     TG       A
                                AGG  GGTGGATC CCTGAGGT
                                |||  |||||||| ||||||||
                                TCT  CCACCTAG GGACTCCA
                                  GT       C
GAM156  DKFZP434B044 3'  ACCTCAGGTGATCCACCCACCT 49709
           T                     GAGGTGGGTGGATCACCTGAGGT
                                 ||||||||||||||||||||||
                                 TTCCACCCACCTAGTGGACTCCA

GAM156  DKFZp434C0923 3'  CCTCAAGCGATCCTCCCACCTC 34647          T     ACC
           A                     TGAGGTGGG GGATC   TGAGG
                                 |||||||| |||||   |||||
                                 ACTCCACCC CCTAG   ACTCC
                                       T    CGA
GAM156  DKFZP434J037 3'  ACCTCAGGTGATCCACCCACCT 48936
           C                     GAGGTGGGTGGATCACCTGAGGT
                                 ||||||||||||||||||||||
                                 CTCCACCCACCTAGTGGACTCCA

GAM156  DKFZp547H025 3'  ACTTCAAGTGATCCACCCGCCT 39765              C
           CA                      TGAGGTGGGTGGATCAC TGAGGT
                                   |||||||||||||||| ||||||
                                   ACTCCGCCCACCTAGTG ACTTCA
                                                     A
GAM156  DKFZP564G092 5'  ACCTCAAGTAATCTGCCCTC   32148    T   TG   C  C
                                GG GGG  GAT AC TGAGGT
                                || |||  ||| || ||||||
                                CT CCC  CTA TG ACTCCA
                                  _   GT   A  A
GAM156  DKFZP564G202 3'  ACCCCAAATGACCCCACACCCA 65886    A   _  T  A   CC  A
                                TG GGTG GG GG TCA  TG GGT
                                || |||| || || |||  || |||
                                AC CCAC CC CC AGT  AC CCA
                                  _    A  _  _   AA  C
GAM156  DSCR6    3'  ACCTCAGGTGATCCACCCGCCT 39054
                                AGGTGGGTGGATCACCTGAGGT
                                |||||||||||||||||||||||
                                TCCGCCCACCTAGTGGACTCCA

GAM156  EVI5     3'  ACCTCAAGTGATCCACCCGCCT 20189              C
           CA                      TGAGGTGGGTGGATCAC TGAGGT
                                   |||||||||||||||| ||||||
                                   ACTCCGCCCACCTAGTG ACTCCA
                                                     A
GAM156  EVI5     3'  ACCTCAGGTGATCCACCCACTT 20190
           T                     GAGGTGGGTGGATCACCTGAGGT
                                 ||||||||||||||||||||||
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                                TTTCACCCACCTAGTGGACTCCA

GAM156  FBP17    3'  ACCTCAGGTGATCCGCCCGCCT 73140
            CA                   TGAGGTGGGTGGATCACCTGAGGT
                                 ||||||||||||||||||||||||
                                 ACTCCGCCCGCCTAGTGGACTCCA

GAM156  FER1L4   3'  TACCTCAAGTGATCCACCCACC 48136            C    ___
            TC                   GAGGTGGGTGGATCAC TGAGGT   A
                                 |||||||||||||||| ||||||   |
                                 CTCCACCCACCTAGTG ACTCCA   T
                                           A     ___
GAM156  FLJ10232 3'  ACCTCAGGTGATCCACCCGCCT 36370
            CA                   TGAGGTGGGTGGATCACCTGAGGT
                                 ||||||||||||||||||||||||
                                 ACTCCGCCCACCTAGTGGACTCCA

GAM156  FLJ10520 3'  CCTCAAGCAATCCTCCCACCTC 36704        T   CACC
            A                    TGAGGTGGG GGAT    TGAGG
                                 |||||||| ||||    |||||
                                 ACTCCACCC CCTA    ACTCC
                                       T    ACGA
GAM156  FLJ10607 3'  CTCAAGTGATCCTCCCACCTCA 77630        T     C
                                 TGAGGTGGG GGATCAC TGAG
                                 |||||||| ||||||| ||||
                                 ACTCCACCC CCTAGTG ACTC
                                       T      A
GAM156  FLJ10847 3'  CTCAAGTGATCCTCCCACCTCA 37301        T     C
                                 TGAGGTGGG GGATCAC TGAG
                                 |||||||| ||||||| ||||
                                 ACTCCACCC CCTAGTG ACTC
                                       T      A
GAM156  FLJ10901 3'  ACCTCAAGTGATCCACCTGCCT 37349     TG       C
                                 AGG  GGTGGATCAC TGAGGT
                                 |||  |||||||||| ||||||
                                 TCC  CCACCTAGTG ACTCCA
                                   GT         A
GAM156  FLJ11560 3'  CTCTGACCCACCTACCTCA    48007          A   CCT
                                 TGAGGTGGGTGG TCA   GAG
                                 |||||||||||| |||   |||
                                 ACTCCATCCACC AGT   CTC
                                        C  ___
GAM156  FLJ12687 3'  ACCTCAAGTGATCCACCCGCCT 46739            C
            C                    GAGGTGGGTGGATCAC TGAGGT
                                 ||||||||||||||| ||||||
                                 CTCCGCCCACCTAGTG ACTCCA
                                           A
GAM156  FLJ12747 3'  ACCTCAGGTGATCCGCCCACCT 50661
            C                    GAGGTGGGTGGATCACCTGAGGT
                                 ||||||||||||||||||||||||
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                                CTCCACCCGCCTAGTGGACTCCA

GAM156  FLJ12761  3'  CCTCTTCCACCCACCCCA    44922    A       TCACCT
                                TG GGTGGGTGGA     GAGG
                                || ||||||||||     ||||
                                AC CCACCCACCT     CTCC
                                 C        T_____
GAM156  FLJ12903  3'  ACCTCAGGTGATCTGCCCACCT 43060        TG
            C                    GAGGTGGG  GATCACCTGAGGT
                                ||||||||  ||||||||||||||
                                CTCCACCC  CTAGTGGACTCCA
                                     GT
GAM156  FLJ12975  3'  CCCAAGCAATCCTCCCACCTCA 70189         T   CAC  GA
                                TGAGGTGGG GGAT   CT  GG
                                ||||||||| ||||   ||  ||
                                ACTCCACCC CCTA   GA  CC
                                      T    AC_  AC
GAM156  FLJ13072  5'  ACCTCAGGTAATCCTCCCACCT 91381         T   C
            CA                   TGAGGTGGG GGAT ACCTGAGGT
                                ||||||||| |||| |||||||||
                                ACTCCACCC CCTA TGGACTCCA
                                      T    A
GAM156  FLJ13197  3'  ACCTCAAGTGATCCACTGCCTC 45170       TG G       C
            A                    TGAGG  G TGGATCAC TGAGGT
                                |||||  | |||||||| ||||||
                                ACTCC  C ACCTAGTG ACTCCA
                                   GT _       A
GAM156  FLJ14351  3'  CTCAAGCAATCCTCCCACCTCA 45647         T   CACC
                                TGAGGTGGG GGAT    TGAG
                                ||||||||| ||||    ||||
                                ACTCCACCC CCTA    ACTC
                                      T    ACGA
GAM156  FLJ14957  3'  ACCTCAGGTGATCCACCTGCCT 52803       TG
            CA                   TGAGG  GGTGGATCACCTGAGGT
                                |||||  ||||||||||||||||
                                ACTCC  CCACCTAGTGGACTCCA
                                   GT
GAM156  FLJ20452  3'  ACCTCAGGTGATCCACCCACCT 35642
            T                    GAGGTGGGTGGATCACCTGAGGT
                                ||||||||||||||||||||||
                                TTCCACCCACCTAGTGGACTCCA

GAM156  FLJ21777  3'  CTCAAGCGATCCACCCCCCTCA 50842       T       ACC
                                TGAGG GGGTGGATC   TGAG
                                ||||| |||||||||   ||||
                                ACTCC CCCACCTAG   ACTC
                                   C        CGA
GAM156  FLJ22002  3'  ACCTCAGGTGATCCATCCACCT 46190
            C                    GAGGTGGGTGGATCACCTGAGGT
                                ||||||||||||||||||||||
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                                CTCCACCTACCTAGTGGACTCCA

GAM156  FLJ22938  3'  ACCCCATCCCGTCCCCCACCCC 45478    A     T   CACC  A
              A                   TG GGTGGG GGAT    TG GGT
                                  || |||||| ||||    || |||
                                  AC CCACCC CCTG    AC CCA
                                   C     _    CCCT  C
GAM156  FLJ23392  3'  CCCCAGGTGATCTGCCCA    45887      TG       A
                                  TGGG  GATCACCTG GG
                                  ||||  |||||||||| ||
                                  ACCC  CTAGTGGAC CC
                                    GT        C
GAM156  FLJ23563  3'  ACCTCAGGTGATCCTCCCACCT 68209         T
              C                   GAGGTGGG GGATCACCTGAGGT
                                  |||||||| ||||||||||||||
                                  CTCCACCC CCTAGTGGACTCCA
                                       T
GAM156  FLJ31153  3'  ACCTCAGGTGATCTGTGTGCCC 58738    A    G TG
              CA                    TG GGTG G  GATCACCTGAGGT
                                  || |||| |  ||||||||||||
                                  AC CCGT T  CTAGTGGACTCCA
                                   C    G GT
GAM156  FLJ32865  3'  ACCTCAGGCAATCTGCCCACCT 58795          TG   CA
              CA                    TGAGGTGGG  GAT  CCTGAGGT
                                  |||||||||  |||  ||||||||
                                  ACTCCACCC  CTA  GGACTCCA
                                       GT   AC
GAM156  GAL3ST-4  3'  ACCTCAGGTGATCCACATGACT 45273     GTGG
              C                    GAG    GTGGATCACCTGAGGT
                                  |||    ||||||||||||||||
                                  CTC    CACCTAGTGGACTCCA
                                    AGTA
GAM156  GMPPB    5'  ACCTCAGGTGATCCACCTGCCT 26215     TG
                                  AGG  GGTGGATCACCTGAGGT
                                  |||  ||||||||||||||||
                                  TCC  CCACCTAGTGGACTCCA
                                    GT
GAM156  GOLGA3    3'  ACCTCAAGTGATCTGCCCATCT 20878         TG     C
              CA                    TGAGGTGGG  GATCAC TGAGGT
                                  |||||||||  ||||||  ||||||
                                  ACTCTACCC  CTAGTG ACTCCA
                                       GT     A
GAM156  GTPBG3    3'  CCTCAGGTAATCTGCCTA    51895      TG   C
                                  TGGG  GAT ACCTGAGG
                                  ||||  ||| ||||||||
                                  ATCC  CTA TGGACTCC
                                    GT   A
GAM156  KIAA0022  3'  ACCTCAAGTGATCCACCCACCT 30275              C
              T                    GAGGTGGGTGGATCAC TGAGGT
                                  |||||||||||||||| ||||||
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                                TTCCACCCACCTAGTG ACTCCA
                                       A
GAM156  KIAA0161  3'  ACCTCAGGTGATCTGCCCACCT 29184        TG
            C                   GAGGTGGG  GATCACCTGAGGT
                                ||||||||  ||||||||||||
                                CTCCACCC  CTAGTGGACTCCA
                                    GT
GAM156  KIAA0205  3'  ACCTCAGGTGATCTGCCCACCT 30197        TG
            C                   GAGGTGGG  GATCACCTGAGGT
                                ||||||||  ||||||||||||
                                CTCCACCC  CTAGTGGACTCCA
                                    GT
GAM156  KIAA0391  3'  ACCTCAGGTGATCCACCCGCCT 28595
            CA                    TGAGGTGGGTGGATCACCTGAGGT
                                  ||||||||||||||||||||||||
                                  ACTCCGCCCACCTAGTGGACTCCA

GAM156  KIAA0446  5'  CTCAGGTGATCCTCCCACCTCA 69450          T
                                TGAGGTGGG GGATCACCTGAG
                                ||||||||| ||||||||||||
                                ACTCCACCC CCTAGTGGACTC
                                      T
GAM156  KIAA0447  3'  CTCAAATGATCCTCCCACCTCA 72118          T     CC
                                TGAGGTGGG GGATCA  TGAG
                                ||||||||| ||||||  ||||
                                ACTCCACCC CCTAGT  ACTC
                                      T     AA
GAM156  KIAA0472  5'  ACCTCAAACGATCTGCCCACCC 72329    A     TG    ACC
            CA                    TG GGTGGG  GATC   TGAGGT
                                  || ||||||  ||||   ||||||
                                  AC CCACCC  CTAG   ACTCCA
                                   C     GT    CAA
GAM156  KIAA0475  3'  ACCCCAGGTGATCCACCTGCCT 30106       TG          A
            CA                    TGAGG  GGTGGATCACCTG GGT
                                  |||||  |||||||||||| |||
                                  ACTCC  CCACCTAGTGGAC CCA
                                     GT           C
GAM156  KIAA0513  3'  ACCTCAGGTGATCCCCCCCACC 29007          T_
            TCA                     TGAGGTGGG  GGATCACCTGAGGT
                                    |||||||||  ||||||||||||||
                                    ACTCCACCC  CCTAGTGGACTCCA
                                         CC
GAM156  KIAA0527  3'  ACCTCAAGTGATCTGCCCTCC  97484    T   TG     C
                                GG GGG  GATCAC TGAGGT
                                || |||  |||||| ||||||
                                CC CCC  CTAGTG ACTCCA
                                 T  GT     A
GAM156  KIAA0599  3'  ACCTCAGGTGATCCACCCACCT 77683
            C                   GAGGTGGGTGGATCACCTGAGGT
                                ||||||||||||||||||||||||
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                                CTCCACCCACCTAGTGGACTCCA

GAM156  KIAA0682  3'  ACCTCAAGTGATCCACCCACCT 30008              C
              T                  GAGGTGGGTGGATCAC TGAGGT
                                 |||||||||||||||| ||||||
                                 TTCCACCCACCTAGTG ACTCCA
                                          A
GAM156  KIAA0682  3'  ACCTCAAGTGATCCACCTACCT 30009              C
              C                  GAGGTGGGTGGATCAC TGAGGT
                                 |||||||||||||||| ||||||
                                 CTCCATCCACCTAGTG ACTCCA
                                          A
GAM156  KIAA0889  3'  CCTCAAGTGATCCGCCCAC   31772            C
                                 GTGGGTGGATCAC TGAGG
                                 |||||||||||| |||||
                                 CACCCGCCTAGTG ACTCC
                                          A
GAM156  KIAA0931  3'  ACCTCAGGTGATCCACCCTCCT 67999      T
              C                  GAGG GGGTGGATCACCTGAGGT
                                 |||| ||||||||||||||||||
                                 CTCC CCCACCTAGTGGACTCCA
                                   T
GAM156  KIAA0961  3'  ACCTCAGGTGATCCACCTGCCT 30384      TG
              C                  GAGG  GGTGGATCACCTGAGGT
                                 |||| ||||||||||||||||
                                 CTCC  CCACCTAGTGGACTCCA
                                   GT
GAM156  KIAA1026  3'  ACCTCAGGCGATCTGCCCACCT 71727         TG   A
              CA                   TGAGGTGGG  GATC CCTGAGGT
                                 |||||||||  |||| ||||||||
                                 ACTCCACCC  CTAG GGACTCCA
                                      GT   C
GAM156  KIAA1036  5'  TACCCCAGACAACCCACCCCCT 30496      T    ATCAC  A  ___
              CG                   TGAGG GGGTGG    CTG GGT  A
                                 ||||| ||||||    ||| |||  |
                                 GCTCC CCCACC    GAC CCA  T
                                   _     CAACA  C  ___
GAM156  KIAA1054  3'  ACCTCAAGTGATCGGCCCACCT 68957         G    C
              CA                   TGAGGTGGGT GATCAC TGAGGT
                                 |||||||||| |||||| ||||||
                                 ACTCCACCCG CTAGTG ACTCCA
                                      G    A
GAM156  KIAA1128  3'  TACCTCAAGTGATCCACCCACC 69010             C    ___
              TC                   GAGGTGGGTGGATCAC TGAGGT  A
                                 |||||||||||||||| ||||||  |
                                 CTCCACCCACCTAGTG ACTCCA  T
                                          A    __
GAM156  KIAA1198  3'  ACCTCAAATGATCCACCCACCT 63978            CC
              T                  GAGGTGGGTGGATCA  TGAGGT
                                 |||||||||||||| ||||||
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                                TTCCACCCACCTAGT  ACTCCA
                                      AA
GAM156  KIAA1198 3' ACCTCAGGTAATCCACCTGCCT 63979     TG      C
                                AGG  GGTGGAT ACCTGAGGT
                                |||  ||||||| |||||||||
                                TCC  CCACCTA TGGACTCCA
                                  GT      A
GAM156  KIAA1200 3' CCTCAGGTGATCTGCCCA    63035      TG
                                TGGG  GATCACCTGAGG
                                ||||  ||||||||||||
                                ACCC  CTAGTGGACTCC
                                  GT
GAM156  KIAA1254 3' ACCTCAAGTGATCCACACATGT 70549    G  G        C
              C                  GA GTG GTGGATCAC TGAGGT
                                || ||| ||||||||| ||||||
                                CT TAC CACCTAGTG ACTCCA
                                 G  A       A
GAM156  KIAA1320 5' ACCTCAAGTGATCTACCCACCT 69830              C
              C                  GAGGTGGGTGGATCAC TGAGGT
                                |||||||||||||||| ||||||
                                CTCCACCCATCTAGTG ACTCCA
                                      A
GAM156  KIAA1396 3' CTCAAGTGACCCTCCCACCTCA 63668         T  A    C
                                TGAGGTGGG GG TCAC TGAG
                                ||||||||| || |||| ||||
                                ACTCCACCC CC AGTG ACTC
                                     T  C    A
GAM156  KIAA1453 3' CCTCCGACCTCACCCACCCCA  47663    A       _ A  ACCT
                                TG GGTGGGTG G TC    GAGG
                                || |||||||| | ||    ||||
                                AC CCACCCAC C AG    CTCC
                                 C       T C  C___
GAM156  KIAA1465 3' ACCTCAGGTGATCCATCTGCCT 61480      TG
              C                  GAGG  GGTGGATCACCTGAGGT
                                ||||  ||||||||||||||||
                                CTCC  CTACCTAGTGGACTCCA
                                  GT
GAM156  KIAA1467 3' ACCTCAGATAATCCACCTGCTT 72055      TG      CAC
              C                  GAGG  GGTGGAT   CTGAGGT
                                ||||  |||||||   |||||||
                                CTTC  CCACCTA   GACTCCA
                                  GT      ATA
GAM156  KIAA1493 3' ACCTCAGGTGATCCACTCGCCT 64830
              C                  GAGGTGGGTGGATCACCTGAGGT
                                |||||||||||||||||||||||
                                CTCCGCTCACCTAGTGGACTCCA

GAM156  KIAA1508 3' ACCTCAGGTAATCCACCTGCTT 62535       TG      C
              CA                   TGAGG  GGTGGAT ACCTGAGGT
                                |||||  ||||||| |||||||||
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                                ACTTC  CCACCTA TGGACTCCA
                                  GT      A
GAM156  KIAA1615  3'  ACCTCAGGTGATCCACCCGCCT 69262
            CA                    TGAGGTGGGTGGATCACCTGAGGT
                                  ||||||||||||||||||||||||
                                  ACTCCGCCCACCTAGTGGACTCCA

GAM156  KIAA1649  3'  CTCAAGTGATCCTCCCACCTCA 51233          T     C
                                  TGAGGTGGG GGATCAC TGAG
                                  ||||||||| ||||||| ||||
                                  ACTCCACCC CCTAGTG ACTC
                                        T     A
GAM156  KIAA1727  3'  ACCCAAGTGATCCTCCCACCTC 64747          T     C  A
            A                     TGAGGTGGG GGATCAC TG GGT
                                  ||||||||| ||||||| || |||
                                  ACTCCACCC CCTAGTG AC CCA
                                        T     A _
GAM156  KIAA1727  3'  CTCAAGTGATCCTCCCACCTCA 64758          T     C
                                  TGAGGTGGG GGATCAC TGAG
                                  ||||||||| ||||||| ||||
                                  ACTCCACCC CCTAGTG ACTC
                                        T     A
GAM156  KIAA1821  3'  ACCTCAAGTGATCCTCCCACCT 72254          T     C
            CA                    TGAGGTGGG GGATCAC TGAGGT
                                  ||||||||| ||||||| ||||||
                                  ACTCCACCC CCTAGTG ACTCCA
                                        T     A
GAM156  KIAA1829  3'  CTCAAGCGACCCTCCCACCTCA 62641          T  A  ACC
                                  TGAGGTGGG GG TC   TGAG
                                  ||||||||| || ||   ||||
                                  ACTCCACCC CC AG   ACTC
                                        T  C  CGA
GAM156  KIAA1867  3'  ACCCCAGCCTCCCCACCCACCT 96478           ATCAC   A
            C                     GAGGTGGGTGG     CTG GGT
                                  ||||||||||     ||| |||
                                  CTCCACCCACC     GAC CCA
                                        CCTCC   C
GAM156  KIAA1987  5'  ACCTCAGGTGATCCACCCCCCG 89377       ___
            CCTC                    GAGGT   GGGTGGATCACCTGAGGT
                                  |||||   ||||||||||||||||||
                                  CTCCG   CCCACCTAGTGGACTCCA
                                     CCC
GAM156  KLK7      3'  ACCTCAGATGATCCACCCACCT 18536             C
            T                     GAGGTGGGTGGATCA CTGAGGT
                                  ||||||||||||||| |||||||
                                  TTCCACCCACCTAGT GACTCCA
                                           A
GAM156  LAMP3     3'  ACCTCAGGTGATCCACCCACCT 60190
            CA                    TGAGGTGGGTGGATCACCTGAGGT
                                  ||||||||||||||||||||||||
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                                ACTCCACCCACCTAGTGGACTCCA

GAM156  MAP-1    3'  ACCTCAAGTGATCCACCTGCTT 42429      TG        C
              C                   GAGG  GGTGGATCAC TGAGGT
                                  ||||  |||||||||| ||||||
                                  CTTC  CCACCTAGTG ACTCCA
                                    GT         A
GAM156  MCM10    3'  TAGCAATCCACCCACCTC    38179            CAC
                                  GAGGTGGGTGGAT   CTG
                                  ||||||||||||   |||
                                  CTCCACCCACCTA   GAT
                                           AC_
GAM156  MGC10200 3'  CTCAAACAATCCACCCTCCTCA 59641       T       CACC
                                  TGAGG GGGTGGAT    TGAG
                                  ||||| ||||||||    ||||
                                  ACTCC CCCACCTA    ACTC
                                     T       ACAA
GAM156  MGC10200 3'  CTCAAGTGATCCTCCCACCTCA 59642         T      C
                                  TGAGGTGGG GGATCAC TGAG
                                  ||||||||| ||||||| ||||
                                  ACTCCACCC CCTAGTG ACTC
                                        T      A
GAM156  MGC21675 3'  ACCTCAGGTGATCCACCCACGT 54578     G
              CA                    TGA GTGGGTGGATCACCTGAGGT
                                  ||| ||||||||||||||||||||
                                  ACT CACCCACCTAGTGGACTCCA
                                    G
GAM156  MGC2474  3'  AGGTGATCCACCCACCTC    43949
                                  GAGGTGGGTGGATCACCT
                                  ||||||||||||||||||
                                  CTCCACCCACCTAGTGGA

GAM156  MGC2603  3'  ACCTCCTGATCCGCCCACCTCA 44068              CCT
                                  TGAGGTGGGTGGATCA   GAGGT
                                  |||||||||||||||   |||||
                                  ACTCCACCCGCCTAGT   CTCCA
                                             C__
GAM156  MKRN4    3'  ACCTCAGGTGATCCACCTGCC  48447    TG
                                  GG  GGTGGATCACCTGAGGT
                                  ||  ||||||||||||||||
                                  CC  CCACCTAGTGGACTCCA
                                    GT
GAM156  MRPL44   3'  ACCTCAGGTGATCCACCCGCCT 43591
                                  AGGTGGGTGGATCACCTGAGGT
                                  ||||||||||||||||||||||
                                  TCCGCCCACCTAGTGGACTCCA

GAM156  MRPS27   3'  ACCTCAAGTGATCTGCCCGCCT 31315         TG     C
              CA                    TGAGGTGGG  GATCAC TGAGGT
                                  |||||||||  |||||| ||||||
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                                ACTCCGCCC  CTAGTG ACTCCA
                                     GT     A
GAM156  NXN      3'  ACCTCAGGTGATCCACCCGCCT 42661
              C                   GAGGTGGGTGGATCACCTGAGGT
                                  ||||||||||||||||||||||
                                  CTCCGCCCACCTAGTGGACTCCA

GAM156  OAZ2     5'  CCCCACACCCACCCACTCA   11873      G      ATCACC  A
                                  TGAG TGGGTGG     TG GG
                                  |||| |||||||     || ||
                                  ACTC ACCCACC     AC CC
                                    _      CAC___  C
GAM156  OCT11    3'  ACCTCCTGATCCACCCACCTCA 27578              CCT
                                  TGAGGTGGGTGGATCA   GAGGT
                                  ||||||||||||||||   |||||
                                  ACTCCACCCACCTAGT   CTCCA
                                             C__
GAM156  PELI1    5'  CCTCAAGTGATCTTCCCA    40636      T      C
                                  TGGG GGATCAC TGAGG
                                  |||| ||||||| |||||
                                  ACCC TCTAGTG ACTCC
                                    T      A
GAM156  PP1665   3'  CCTCAGGTTCCCACATCA    48637     G    TGGATC
                                  TGA GTGGG     ACCTGAGG
                                  ||| |||||     ||||||||
                                  ACT CACCC     TGGACTCC
                                    A    T_____
GAM156  PRO2955  3'  ACCTCAGGTGATCCACCTGCCT 38230      TG
              C                   GAGG  GGTGGATCACCTGAGGT
                                  ||||  ||||||||||||||||
                                  CTCC  CCACCTAGTGGACTCCA
                                    GT
GAM156  PSTPIP2  3'  ACCTCAGGTGATCCACCTGCCT 44646      TG
              C                   GAGG  GGTGGATCACCTGAGGT
                                  ||||  ||||||||||||||||
                                  CTCC  CCACCTAGTGGACTCCA
                                    GT
GAM156  RAB33B   3'  CTCAAGCAATCCTCCCACCTCA 49324          T   CACC
                                  TGAGGTGGG GGAT    TGAG
                                  ||||||||| ||||    ||||
                                  ACTCCACCC CCTA    ACTC
                                       T    ACGA
GAM156  RES4-25  3'  ACCTCAGGTAATCCACCTGCCT 65257     TG      C
                                  AGG  GGTGGAT ACCTGAGGT
                                  |||  ||||||| |||||||||
                                  TCC  CCACCTA TGGACTCCA
                                    GT      A
GAM156  Rpo1-2   3'  ACCTCAAGTGATCCACCCACCT 39207              C
              C                   GAGGTGGGTGGATCAC TGAGGT
                                  |||||||||||||||| ||||||
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                                  CTCCACCCACCTAGTG ACTCCA
                                           A
GAM156  Rpo1-2   3'  ACCTCAAGTGATCCACCCACCT 39206            C
              C                   GAGGTGGGTGGATCAC TGAGGT
                                  |||||||||||||||| ||||||
                                  CTCCACCCACCTAGTG ACTCCA
                                           A
GAM156  SC4MOL   3'  CCTCAAGTGATCTGCCCA   23104     TG    C
                                  TGGG  GATCAC TGAGG
                                  ||||  |||||| |||||
                                  ACCC  CTAGTG ACTCC
                                    GT     A
GAM156  SCAMP-4  3'  ACCTCAAGTGATCCACCCGCCT 55330           C
                                  AGGTGGGTGGATCAC TGAGGT
                                  |||||||||||||||| ||||||
                                  TCCGCCCACCTAGTG ACTCCA
                                           A
GAM156  SCYA22   3'  ACCTCAAGTGATCCACCTTCCT 92568    T      C
                                  AGG GGGTGGATCAC TGAGGT
                                  ||| |||||||||| ||||||
                                  TCC TCCACCTAGTG ACTCCA
                                    T         A
GAM156  SCYA22   3'  CCTCAGGTAATCCGCCCACCTC 92587           C
              A                    TGAGGTGGGTGGAT ACCTGAGG
                                  |||||||||||||| ||||||||
                                  ACTCCACCCGCCTA TGGACTCC
                                           A
GAM156  SFXN2    3'  ACCTCAGGTGATCCGCCCGCCT 74367
              CA                    TGAGGTGGGTGGATCACCTGAGGT
                                  ||||||||||||||||||||||||
                                  ACTCCGCCCGCCTAGTGGACTCCA

GAM156  SHANK3   5'  CCTTCATCCACCCACTCA    66104     G       CACCT
                                  TGAG TGGGTGGAT    GAGG
                                  |||| |||||||||    ||||
                                  ACTC ACCCACCTA    TTCC
                                    _       C_____
GAM156  SIRPB1   3'  ACCTCAGGTGATCCACCTGTCT 21351    TG
                                  AGG  GGTGGATCACCTGAGGT
                                  |||  ||||||||||||||||
                                  TCT  CCACCTAGTGGACTCCA
                                    GT
GAM156  SLC16A6  5'  CTCAAGCAATCCTCCCACCTCA 17440         T   CACC
                                  TGAGGTGGG GGAT   TGAG
                                  ||||||||| ||||   ||||
                                  ACTCCACCC CCTA   ACTC
                                        T   ACGA
GAM156  SLC2A10  3'  CTCAAGTGATCCACCCACCTCA 48550           C
                                  TGAGGTGGGTGGATCAC TGAG
                                  |||||||||||||||| ||||
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                                ACTCCACCCACCTAGTG ACTC
                                      A
GAM156  SLC6A14  3'  ACCTCAAGTGATCTGTCTACCT 24302        TG     C
            C                  GAGGTGGG  GATCAC TGAGGT
                               ||||||||  |||||| ||||||
                               CTCCATCT  CTAGTG ACTCCA
                                   GT     A
GAM156  SULT1C2  3'  ACCCCATGATCCACCCGCCTCA 22705             CC  A
                               TGAGGTGGGTGGATCA  TG GGT
                               ||||||||||||||||  || |||
                               ACTCCGCCCACCTAGT  AC CCA
                                      __ C
GAM156  TBCC     3'  ACCTCAGGTGATCCACCCGCTT 13598
            CA                   TGAGGTGGGTGGATCACCTGAGGT
                               ||||||||||||||||||||||||
                               ACTTCGCCCACCTAGTGGACTCCA

GAM156  TRIM5    3'  ACCTCAGGTGATCCACCCGCCT 53459
            C                  GAGGTGGGTGGATCACCTGAGGT
                               ||||||||||||||||||||||
                               CTCCGCCCACCTAGTGGACTCCA

GAM156  TRIM5    3'  ACCTCAGGTGATCCACCCGCCT 53460
            C                  GAGGTGGGTGGATCACCTGAGGT
                               ||||||||||||||||||||||
                               CTCCGCCCACCTAGTGGACTCCA

GAM156  TUCAN    3'  CCTCAAGTGATCCACCCACCTC 30970             C
            A                  TGAGGTGGGTGGATCAC TGAGG
                               |||||||||||||||| |||||
                               ACTCCACCCACCTAGTG ACTCC
                                      A
GAM156  UBF-fl   3'  ACCTCAAGTGATCCACCCGCCT 52614           C
                               AGGTGGGTGGATCAC TGAGGT
                               |||||||||||||| ||||||
                               TCCGCCCACCTAGTG ACTCCA
                                     A
GAM156  VDU1     3'  ACCTCAGGTGATCCACCCACCT 31113
            C                  GAGGTGGGTGGATCACCTGAGGT
                               ||||||||||||||||||||||
                               CTCCACCCACCTAGTGGACTCCA

GAM156  VMP      3'  CTCAAGCGATCCTCCCACCTCA 55761         T    ACC
                               TGAGGTGGG GGATC   TGAG
                               |||||||| |||||  ||||
                               ACTCCACCC CCTAG   ACTC
                                     T    CGA
GAM156  VPS33A   3'  ACCTCAGGTGATCCACCTGCCT 43606      TG
            C                  GAGG  GGTGGATCACCTGAGGT
                               ||||  ||||||||||||||||
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                                CTCC  CCACCTAGTGGACTCCA
                                  GT
GAM156  WBSCR23   3'  ACCTCAGGTGATCCACCTGCCT 47407     TG
                                AGG  GGTGGATCACCTGAGGT
                                |||  ||||||||||||||||
                                TCC  CCACCTAGTGGACTCCA
                                  GT
GAM156  ZNF338    3'  ACCTCAAGTGATCTGCCCACCT 42250         TG     C
           CA                     TGAGGTGGG  GATCAC TGAGGT
                                  |||||||||  ||||||  ||||||
                                  ACTCCACCC  CTAGTG ACTCCA
                                       GT     A
GAM156  LOC112687 3'  ACCTCATGTAATCCACCCACCT 73217            C  C
           CA                     TGAGGTGGGTGGAT AC TGAGGT
                                  ||||||||||||||  ||  ||||||
                                  ACTCCACCCACCTA TG ACTCCA
                                        A  T
GAM156  LOC112817 3'  ACCTCAGGTGATCCAACTGCCT 57311      TG G
           C                       GAGG  G TGGATCACCTGAGGT
                                  ||||  |  ||||||||||||||||
                                  CTCC  C ACCTAGTGGACTCCA
                                    GT A
GAM156  LOC115219 5'  ACTCGTGATCCGCCCACCTCA  73683              CT  G
                                  TGAGGTGGGTGGATCAC  GA GT
                                  ||||||||||||||||  ||  ||
                                  ACTCCACCCGCCTAGTG  CT CA
                                          __  G
GAM156  LOC115648 3'  ACCTCAGGTGATCCACCCGCCT 60012
                                  AGGTGGGTGGATCACCTGAGGT
                                  ||||||||||||||||||||||
                                  TCCGCCCACCTAGTGGACTCCA

GAM156  LOC119392 3'  ACCTCAGGTGATCCACCGCCT  59809       G
                                  AGGTGG TGGATCACCTGAGGT
                                  ||||||  ||||||||||||||
                                  TCCGCC ACCTAGTGGACTCCA
                                    _
GAM156  LOC126669 3'  ACCTCAAATGATCCACCCACCT 75918              CC
           CA                     TGAGGTGGGTGGATCA  TGAGGT
                                  ||||||||||||||||  ||||||
                                  ACTCCACCCACCTAGT  ACTCCA
                                        AA
GAM156  LOC128077 3'  AGGTAATCCACCCGCCTCA   75204             C
                                  TGAGGTGGGTGGAT ACCT
                                  ||||||||||||||| ||||
                                  ACTCCGCCCACCTA TGGA
                                        A
GAM156  LOC130639 5'  ACCTCAAGTGATCCTCCCACCT 75478         T      C
           CA                     TGAGGTGGG GGATCAC TGAGGT
                                  |||||||||  |||||||  ||||||
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                                ACTCCACCC CCTAGTG ACTCCA
                                     T      A
GAM156  LOC130813 3'  CTCAAGCAATCCTCCCACCTCA 76272         T   CACC
                                TGAGGTGGG GGAT    TGAG
                                ||||||||| ||||    ||||
                                ACTCCACCC CCTA    ACTC
                                     T    ACGA
GAM156  LOC134266 3'  CTCAAGTGATCCTCCCACCTCA 75643         T      C
                                TGAGGTGGG GGATCAC TGAG
                                ||||||||| ||||||| ||||
                                ACTCCACCC CCTAGTG ACTC
                                     T      A
GAM156  LOC135818 3'  ACCTCAGGTGATCTGCCCACCT 75742         TG
          C                      GAGGTGGG  GATCACCTGAGGT
                                ||||||||  |||||||||||||
                                CTCCACCC  CTAGTGGACTCCA
                                     GT
GAM156  LOC139422 5'  CTCAAGCAATCCTCCCACCTCA 76348         T   CACC
                                TGAGGTGGG GGAT    TGAG
                                ||||||||| ||||    ||||
                                ACTCCACCC CCTA    ACTC
                                     T    ACGA
GAM156  LOC143916 3'  ACCTCAGGTGATCCACCACCTC 77133         G
                                GAGGTGG TGGATCACCTGAGGT
                                ||||||| |||||||||||||||
                                CTCCACC ACCTAGTGGACTCCA
                                     _
GAM156  LOC144317 5'  ACCTCAGGTGATCCACCAGCCT 77286       G
          C                      GAGGT GGTGGATCACCTGAGGT
                                ||||| |||||||||||||||||
                                CTCCG CCACCTAGTGGACTCCA
                                   A
GAM156  LOC145268 5'  ACCTCGGGTGATCCACCCACCT 77567
          CA                     TGAGGTGGGTGGATCACCTGAGGT
                                ||||||||||||||||||||||||
                                ACTCCACCCACCTAGTGGGCTCCA

GAM156  LOC145801 3'  ACCCCAGGACACCCACCCACCC 77966    A       ATCA   A
          A                      TG GGTGGGTGG    CCTG GGT
                                || |||||||||    |||| |||
                                AC CCACCCACC    GGAC CCA
                                _       CACA    C
GAM156  LOC146229 3'  ACCTCAAGTGATCCACCCGCCT 78245             C
                                AGGTGGGTGGATCAC TGAGGT
                                |||||||||||||| ||||||
                                TCCGCCCACCTAGTG ACTCCA
                                        A
GAM156  LOC146229 3'  ACCTCAGGTGATCCACCCACCT 78246
          CA                     TGAGGTGGGTGGATCACCTGAGGT
                                ||||||||||||||||||||||||
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                                ACTCCACCCACCTAGTGGACTCCA

GAM156  LOC146336 3'  CTCAAGCGATCCTCCCACCTCA 78369         T    ACC
                                TGAGGTGGG GGATC   TGAG
                                ||||||||| |||||   ||||
                                ACTCCACCC CCTAG   ACTC
                                      T    CGA
GAM156  LOC146901 3'  ACCTCAGGTGATCCACCCGCCT 84880
              CA                  TGAGGTGGGTGGATCACCTGAGGT
                                ||||||||||||||||||||||||
                                ACTCCGCCCACCTAGTGGACTCCA

GAM156  LOC147276 3'  ACCTCAAGTGATCCACCTGCCT 78947      TG        C
              C                  GAGG  GGTGGATCAC TGAGGT
                                ||||  |||||||||| ||||||
                                CTCC  CCACCTAGTG ACTCCA
                                  GT         A
GAM156  LOC147817 3'  CCTCAAGTGATCTGCTCA    79172      TG     C
                                TGGG  GATCAC TGAGG
                                ||||  |||||| |||||
                                ACTC  CTAGTG ACTCC
                                  GT     A
GAM156  LOC147841 3'  ACCTCAGGTGATCCACCCGCCC 79218    A
                                G GGTGGGTGGATCACCTGAGGT
                                | ||||||||||||||||||||
                                C CCGCCCACCTAGTGGACTCCA
                                _
GAM156  LOC147990 3'  ACCCCAGGCATGCACCACCTCA 85207         G  G  CA    A
                                TGAGGTGG TG AT  CCTG GGT
                                |||||||| || ||  |||| |||
                                ACTCCACC AC TA  GGAC CCA
                                     _ G  C_    C
GAM156  LOC148443 3'  CTCAAGTGACCCTCCCACCTCA 79600         T  A    C
                                TGAGGTGGG GG TCAC TGAG
                                ||||||||| || |||| ||||
                                ACTCCACCC CC AGTG ACTC
                                      T  C    A
GAM156  LOC148918 5'  ACCTCAGGTGATCCACCCACCT 79813
              CA                  TGAGGTGGGTGGATCACCTGAGGT
                                ||||||||||||||||||||||||
                                ACTCCACCCACCTAGTGGACTCCA

GAM156  LOC148918 5'  CTCAAGCGATCCTCCCACCTCA 79825         T    ACC
                                TGAGGTGGG GGATC   TGAG
                                ||||||||| |||||   ||||
                                ACTCCACCC CCTAG   ACTC
                                      T    CGA
GAM156  LOC149171 5'  CCTCAGGTGATCTGCCCA    79965      TG
                                TGGG  GATCACCTGAGG
                                ||||  ||||||||||||
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                                ACCC  CTAGTGGACTCC
                                  GT
GAM156  LOC149577 3'  ACCTCAAGTGATCCACTGGCCT 85662      G        C
                                AGGT GGTGGATCAC TGAGGT
                                |||| |||||||||| ||||||
                                TCCG TCACCTAGTG ACTCCA
                                  G         A
GAM156  LOC149692 3'  ACCTCAGGTGATCCACCCCC   85721    T
                                GG GGGTGGATCACCTGAGGT
                                || ||||||||||||||||||
                                CC CCCACCTAGTGGACTCCA
                                 _
GAM156  LOC149711 3'  ACCTCAGGTGATCCACCCACCT 85833
             CA                   TGAGGTGGGTGGATCACCTGAGGT
                                ||||||||||||||||||||||||
                                ACTCCACCCACCTAGTGGACTCCA

GAM156  LOC150282 5'  ACCTCAGGTGATCCACCTGCCT 80532       TG
             CA                   TGAGG  GGTGGATCACCTGAGGT
                                |||||  ||||||||||||||||
                                ACTCC  CCACCTAGTGGACTCCA
                                  GT
GAM156  LOC150960 3'  ACCTCAGGTGATCCACCCACCT 80863
             C                    GAGGTGGGTGGATCACCTGAGGT
                                |||||||||||||||||||||||
                                CTCCACCCACCTAGTGGACTCCA

GAM156  LOC151701 3'  CCTCAGATGATCTGCCCA    86669      TG    C
                                TGGG  GATCA CTGAGG
                                ||||  ||||| ||||||
                                ACCC  CTAGT GACTCC
                                  GT    A
GAM156  LOC152137 3'  CCTCAAGTGATCCACCTGC    81312    TG        C
                                G  GGTGGATCAC TGAGG
                                |  |||||||||| |||||
                                C  CCACCTAGTG ACTCC
                                 GT         A
GAM156  LOC153077 3'  ACCTCAGGTGATCCACCTGCCT 87103      TG
             C                    GAGG  GGTGGATCACCTGAGGT
                                ||||  ||||||||||||||||
                                CTCC  CCACCTAGTGGACTCCA
                                  GT
GAM156  LOC153688 3'  CCTCAGGTGATCCGCCTA    87306
                                TGGGTGGATCACCTGAGG
                                ||||||||||||||||||
                                ATCCGCCTAGTGGACTCC

GAM156  LOC153811 3'  ACCTCAAATGATCCACCTGCCT 81819      TG        CC
             C                    GAGG  GGTGGATCA  TGAGGT
                                ||||  |||||||||  ||||||
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                                CTCC  CCACCTAGT  ACTCCA
                                  GT        AA
GAM156  LOC153883 5'  ACCTCAAGTGATCCACCCACTT 81884              C
                CA                TGAGGTGGGTGGATCAC TGAGGT
                                  |||||||||||||||| ||||||
                                  ACTTCACCCACCTAGTG ACTCCA
                                           A
GAM156  LOC154739 5'  ACCTCAGGTAATTTTTCACTCT 87426     _    T    C
                CA                TGAG GTGGG GGAT ACCTGAGGT
                                  |||| ||||| |||| |||||||||
                                  ACTC CACTT TTTA TGGACTCCA
                                    T    _    A
GAM156  LOC154877 3'  ACCTCAGGTGATCTACCCGCCT 87517
                CA                TGAGGTGGGTGGATCACCTGAGGT
                                  |||||||||||||||||||||||||
                                  ACTCCGCCCATCTAGTGGACTCCA

GAM156  LOC157247 5'  ACCTCAGGTGATCCACCCACCT 82281
                C                  GAGGTGGGTGGATCACCTGAGGT
                                   |||||||||||||||||||||||
                                   CTCCACCCACCTAGTGGACTCCA

GAM156  LOC158318 5'  AGGCAATCCACCCACCCA    88101    A        CA
                                  TG GGTGGGTGGAT  CCT
                                  || ||||||||||  |||
                                  AC CCACCCACCTA  GGA
                                    _         AC
GAM156  LOC158476 3'  CCCAGGTGATCCGCCCAT    88190             A
                                  GTGGGTGGATCACCTG GG
                                  |||||||||||||||| ||
                                  TACCCGCCTAGTGGAC CC
                                            C
GAM156  LOC169611 3'  ACCTCAGGTGATCCACCTGCCT 83630       TG
                CA                TGAGG  GGTGGATCACCTGAGGT
                                  |||||  ||||||||||||||||
                                  ACTCC  CCACCTAGTGGACTCCA
                                    GT
GAM156  LOC196047 5'  ACCTCAGGTGATCCACCTGCCT 91138      TG
                C                  GAGG  GGTGGATCACCTGAGGT
                                   ||||  ||||||||||||||||
                                   CTCC  CCACCTAGTGGACTCCA
                                     GT
GAM156  LOC196529 3'  ATCTCAGGCAATCCACCCACCT 89123            CA
                CA                TGAGGTGGGTGGAT  CCTGAGGT
                                  ||||||||||||||  ||||||||
                                  ACTCCACCCACCTA  GGACTCTA
                                            AC
GAM156  LOC197358 3'  ACCTCAAGTGATCCACCCACCT 89408              C
                CA                TGAGGTGGGTGGATCAC TGAGGT
                                  |||||||||||||||| ||||||
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                                ACTCCACCCACCTAGTG ACTCCA
                                        A
GAM156  LOC197358 3'  ACCTCAGGTGATCCATCAGCCT 89409     G
                                AGGT GGTGGATCACCTGAGGT
                                |||| ||||||||||||||||
                                TCCG CTACCTAGTGGACTCCA
                                  A
GAM156  LOC199906 3'  ACCTCAGGCGATCCGCCCGCCT 89840            A
          CA                      TGAGGTGGGTGGATC CCTGAGGT
                                |||||||||||||| ||||||||
                                ACTCCGCCCGCCTAG GGACTCCA
                                        C
GAM156  LOC200268 3'  CTCAAGTGATCCTCCCACCTCA 90083        T     C
                                TGAGGTGGG GGATCAC TGAG
                                ||||||||| ||||||| ||||
                                ACTCCACCC CCTAGTG ACTC
                                      T     A
GAM156  LOC200268 3'  TTCAAGTGATCCTCCCACCTCA 90089        T     C
                                TGAGGTGGG GGATCAC TGAG
                                ||||||||| ||||||| ||||
                                ACTCCACCC CCTAGTG ACTT
                                      T     A
GAM156  LOC200314 3'  ACCTCAGGTGATCCACCCGCCT 91584
                                AGGTGGGTGGATCACCTGAGGT
                                ||||||||||||||||||||||
                                TCCGCCCACCTAGTGGACTCCA

GAM156  LOC200316 3'  CCTCAGGTGATCTGCCCA    90174     TG
                                TGGG  GATCACCTGAGG
                                ||||  ||||||||||||
                                ACCC  CTAGTGGACTCC
                                  GT
GAM156  LOC200407 3'  ACCTCAGGTGATCCACCTGCCT 91623     TG
          C                      GAGG  GGTGGATCACCTGAGGT
                                ||||  ||||||||||||||||
                                CTCC  CCACCTAGTGGACTCCA
                                  GT
GAM156  LOC200860 3'  CCTCAGGTGATCCGCCTA    91745
                                TGGGTGGATCACCTGAGG
                                ||||||||||||||||||
                                ATCCGCCTAGTGGACTCC

GAM156  LOC201164 3'  ACCTCAAGTGATCCACCACTTC 89483       G     C
                                GAGGTGG TGGATCAC TGAGGT
                                ||||||| |||||||| ||||||
                                CTTCACC ACCTAGTG ACTCCA
                                    _     A
GAM156  LOC201294 3'  ACCTCCTGATCCACCCACCTC  89568            CCT
                                GAGGTGGGTGGATCA   GAGGT
                                ||||||||||||||   |||||
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                                CTCCACCCACCTAGT   CTCCA
                                        C__
GAM156   LOC201411 3'  ACCTCAGGTGATCTACCCACCT 63631
                CA                TGAGGTGGGTGGATCACCTGAGGT
                                  ||||||||||||||||||||||||
                                  ACTCCACCCATCTAGTGGACTCCA

GAM156   LOC201626 3'  ACCTCAGGTGATCCACCCACCT 90423
                C                 GAGGTGGGTGGATCACCTGAGGT
                                  ||||||||||||||||||||||||
                                  CTCCACCCACCTAGTGGACTCCA

GAM156   LOC203197 3'  ACCTCAGGTGATCCACCCGCCT 90798
                C                 GAGGTGGGTGGATCACCTGAGGT
                                  ||||||||||||||||||||||||
                                  CTCCGCCCACCTAGTGGACTCCA

GAM156   LOC203276 3'  ACCTCAGGTAACTTTCACTCTC 92106    T      TC__
                                  GG GGGTGGA    ACCTGAGGT
                                  || |||||||    |||||||||
                                  CT CTCACTT    TGGACTCCA
                                   _      TCAA
GAM156   LOC203305 3'  ACCTCAGGTAACTTTCACTCTC 92159    T      TC__
                                  GG GGGTGGA    ACCTGAGGT
                                  || |||||||    |||||||||
                                  CT CTCACTT    TGGACTCCA
                                   _      TCAA
GAM156   LOC204804 3'  CCTCAGGTGATCCACCCGCCTC 91040
                A                 TGAGGTGGGTGGATCACCTGAGG
                                  |||||||||||||||||||||||
                                  ACTCCGCCCACCTAGTGGACTCC

GAM156   LOC205251 5'  CCTCAAGTGATCTGCCTA    92355      TG     C
                                  TGGG  GATCAC TGAGG
                                  ||||  |||||| |||||
                                  ATCC  CTAGTG ACTCC
                                    GT     A
GAM156   LOC219673 5'  ACCTCAAGTAATCCACCTGCCT 94604       TG      C  C
                CA                TGAGG  GGTGGAT AC TGAGGT
                                  |||||  ||||||| || ||||||
                                  ACTCC  CCACCTA TG ACTCCA
                                    GT       A  A
GAM156   LOC220074 3'  ACCTCAGGTGATCTGCCCACCT 59951          TG
                CA                TGAGGTGGG  GATCACCTGAGGT
                                  |||||||||  ||||||||||||
                                  ACTCCACCC  CTAGTGGACTCCA
                                       GT
GAM156   LOC221060 3'  ACCTCAGGTGATCCGCCCACCT 94825
                C                 GAGGTGGGTGGATCACCTGAGGT
                                  ||||||||||||||||||||||||
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                                CTCCACCCGCCTAGTGGACTCCA

GAM156  LOC221416 3'  CCTCCACCCACCCACCTC    95404          ATCACCT
                      GAGGTGGGTGG      GAGG
                      ||||||||||       ||||
                      CTCCACCCACC      CTCC
                            CAC____
GAM156  LOC221960 3'  CTCAAGCAATCCTCCCACCTCA 92725         T   CACC
                      TGAGGTGGG GGAT   TGAG
                      ||||||||| ||||   ||||
                      ACTCCACCC CCTA   ACTC
                            T   ACGA
GAM156  LOC221964 3'  ACCTCAGGTGATCCACCCACCT 95597
          T                    GAGGTGGGTGGATCACCTGAGGT
                               ||||||||||||||||||||||
                               TTCCACCCACCTAGTGGACTCCA

GAM156  LOC222031 3'  ACCTCAGGTGATCCACCCTCCT 95665    T
                      AGG GGGTGGATCACCTGAGGT
                      ||| ||||||||||||||||
                      TCC CCCACCTAGTGGACTCCA
                        T
GAM156  LOC245771 5'  ACCTCAAGTGATCCACCTGCCT 94463    TG        C
                      AGG  GGTGGATCAC TGAGGT
                      |||  |||||||||| ||||||
                      TCC  CCACCTAGTG ACTCCA
                        GT         A
GAM156  LOC253805 3'  ACCTCAGATGATTCACCCGCCT 98164             C
          CA                   TGAGGTGGGTGGATCA CTGAGGT
                               |||||||||||||||| |||||||
                               ACTCCGCCCACTTAGT GACTCCA
                                        A
GAM156  LOC254243 3'  ACCTCAGGTAACTTTCACTCTC 99246    T     TC__
                      GG GGGTGGA    ACCTGAGGT
                      || |||||||    |||||||||
                      CT CTCACTT    TGGACTCCA
                       _      TCAA
GAM156  LOC254532 5'  ACCTCAAGTGATCCACCCACCT 98443             C
          T                    GAGGTGGGTGGATCAC TGAGGT
                               |||||||||||||||| ||||||
                               TTCCACCCACCTAGTG ACTCCA
                                        A
GAM156  LOC254655 3'  ACCTCAGGTGATCCACCTGCCT 97209    TG
                      AGG  GGTGGATCACCTGAGGT
                      |||  ||||||||||||||||
                      TCC  CCACCTAGTGGACTCCA
                        GT
GAM156  LOC255065 5'  ACCTCAAGTAATCCACCTGGCC 98368     _      C  C
          T                    AGGT GGGTGGAT AC TGAGGT
                               |||| |||||||| || ||||||
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                                TCCG TCCACCTA TG ACTCCA
                                  G       A  A
GAM156  LOC255196 5'  CTCAAGCAATCCTCCCACCTCA 98954         T    CACC
                                TGAGGTGGG GGAT    TGAG
                                ||||||||| ||||    ||||
                                ACTCCACCC CCTA    ACTC
                                     T    ACGA
GAM156  LOC255458 5'  CTCAAGCGATCCTCCCACCTCA 98933         T     ACC
                                TGAGGTGGG GGATC   TGAG
                                ||||||||| |||||   ||||
                                ACTCCACCC CCTAG   ACTC
                                     T    CGA
GAM156  LOC256306 3'  ACCTCAAATGATCCGCCCACCT 98499             CC
          C                      GAGGTGGGTGGATCA  TGAGGT
                                ||||||||||||||  ||||||
                                CTCCACCCGCCTAGT  ACTCCA
                                          AA
GAM156  LOC257095 5'  ACCTCATTCCTCCACCCACCTC 98715           TCACC
                                GAGGTGGGTGGA    TGAGGT
                                ||||||||||||    ||||||
                                CTCCACCCACCT    ACTCCA
                                      CCTT_
GAM156  LOC51008  5'  ACCTCAGGTGATCCACCTGCCT 32524     TG
                                AGG  GGTGGATCACCTGAGGT
                                |||  ||||||||||||||||
                                TCC  CCACCTAGTGGACTCCA
                                  GT
GAM156  LOC51200  3'  ACCTCAGGTGATCTGCCCTCC  33432    T   TG
                                GG GGG  GATCACCTGAGGT
                                || |||  ||||||||||||
                                CC CCC  CTAGTGGACTCCA
                                 T  GT
GAM156  LOC51219  5'  ACCTCAGGTGATCTGCCCACCT 33537         TG
          C                      GAGGTGGG  GATCACCTGAGGT
                                ||||||||  ||||||||||||
                                CTCCACCC  CTAGTGGACTCCA
                                     GT
GAM156  LOC51622  3'  CTCAAGCAATCCTCCCACCTCA 32207         T    CACC
                                TGAGGTGGG GGAT    TGAG
                                ||||||||| ||||    ||||
                                ACTCCACCC CCTA    ACTC
                                     T    ACGA
GAM156  LOC89932  3'  ACCTCAGATGATCTGCCCGCCT 61436         TG    C
          CA                     TGAGGTGGG  GATCA CTGAGGT
                                |||||||||  ||||| |||||||
                                ACTCCGCCC  CTAGT GACTCCA
                                     GT    A
GAM156  LOC90038  3'  ACCTCAGGTAACTTTCACTCTC 61790    T      TC__
                                GG GGGTGGA    ACCTGAGGT
                                || |||||||    |||||||||
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                                CT CTCACTT   TGGACTCCA
                                 _     TCAA
GAM156  LOC90072  3' CCTCAAGTGATCCGCCCAC   61957          C
                                GTGGGTGGATCAC TGAGG
                                |||||||||||| |||||
                                CACCCGCCTAGTG ACTCC
                                       A
GAM156  LOC90591  3' ACCTCAGGTGATCCACCTGCCT 64135      TG
           CA                    TGAGG  GGTGGATCACCTGAGGT
                                |||||  ||||||||||||||||
                                ACTCC  CCACCTAGTGGACTCCA
                                  GT
GAM156  LOC91115  3' ACCTCAGATGGTCCACCCACCT 65539           C
           C                     GAGGTGGGTGGATCA CTGAGGT
                                |||||||||||||| |||||||
                                CTCCACCCACCTGGT GACTCCA
                                       A
GAM156  LOC92303  3' ACCTCAGGTGATCCACCCGCCT 69381
           C                     GAGGTGGGTGGATCACCTGAGGT
                                |||||||||||||||||||||||
                                CTCCGCCCACCTAGTGGACTCCA

GAM156  LOC92697  5' ACCTCAGGTGATCCGCATGCCT 70802      GG
           CA                    TGAGGT  GTGGATCACCTGAGGT
                                ||||||  ||||||||||||||||
                                ACTCCG  CGCCTAGTGGACTCCA
                                   TA
GAM156  LOC92841  3' ACCTCAAGTGATCCCCCACCTC 71237       T     C
                                GAGGTGGG GGATCAC TGAGGT
                                |||||||| ||||||| ||||||
                                CTCCACCC CCTAGTG ACTCCA
                                     _     A
GAM156  LOC92876  5' ACCTCAGGTGATCCACCTACCT 71344
           C                     GAGGTGGGTGGATCACCTGAGGT
                                |||||||||||||||||||||||
                                CTCCATCCACCTAGTGGACTCCA

GAM157  ALPP    3' CCTCCAGCCCGAGTCGTCAT   69413      __     C
                                GTGGC  TTCGGGC GGAGG
                                |||||  ||||||| |||||
                                TACTG  GAGCCCG CCTCC
                                  CT      A
GAM157  BACE    5' CCTCTCCTGAGAAGCCACCAGC 58081    AACA      __  CC
                                GC   GTGGCTTC  GGG  GGAGG
                                ||   ||||||||  |||  |||||
                                CG   CACCGAAG  TCC  TCTCC
                                 AC__       AG  __
GAM157  BACE    5' CCTCTCCTGAGAAGCCACCAGC 25029    AACA      __  CC
                                GC   GTGGCTTC  GGG  GGAGG
                                ||   ||||||||  |||  |||||
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                              CG   CACCGAAG  TCC  TCTCC
                               AC__       AG  __
GAM157  CDK5R2   3'  CCCCGGGACCACAAAGCCACCG 15446    AACA      C__  G_   A
            CCGC                 GC   GTGGCTT   GG  CCGG GG
                              ||   |||||||  ||  |||| ||
                              CG   CACCGAA   CC  GGCC CC
                               CCGC      ACA  AG   _
GAM157  CLN5     5'  CCGGCTACCGAAGCCACCTTGC 22429      CA        __
                              GCAA  GTGGCTTCGG  GCCGG
                              ||||  ||||||||||  |||||
                              CGTT  CACCGAAGCC  CGGCC
                                C_        AT
GAM157  CNGB3    3'  CCCCCAAAGATGGTCACTGTT  39388          _  ___   CC
                              AACAGTGGCT TC   GGG  GG
                              |||||||||| ||   |||  ||
                              TTGTCACTGG AG   CCC  CC
                                    T  AAA   __
GAM157  FOXE1    5'  CCGGTCACGAGGCCACCGCCGC 16778    AACA       _
                              GC   GTGGCTTCG GGCCGG
                              ||   |||||||| ||||||
                              CG   CACCGGAGC CTGGCC
                               CCGC        A
GAM157  GATA6    5'  CCCCGGCCCGCTCGCTGCTGC  19144     A     CTT       A
                              GCA CAGTGG   CGGGCCGG GG
                              ||| ||||||   |||||||| ||
                              CGT GTCGCT   GCCCGGCC CC
                                C     C__       _
GAM157  HMGA2    5'  CCTCCGGCACCCACCCACCGCC 14451    AACA   CTTC  _
            GC                   GC   GTGG   GG GCCGGAGG
                              ||   ||||   || ||||||||
                              CG   CACC   CC CGGCCTCC
                               CCGC   CAC_  A
GAM157  JAM3     3'  CCCCCGCTCTAGCTCACTGTTG 52487         _  TC   C  A
            C                    GCAACAGTG GCT  GGGC GG GG
                              |||||||| |||  |||| || ||
                              CGTTGTCAC CGA  CTCG CC CC
                                    T  T_   C  _
GAM157  LMO7     3'  CCTCCATACGAAAGCACTGTTG 32367         GC   GGCC
            C                    GCAACAGTG  TTCG   GGAGG
                              |||||||||  ||||   |||||
                              CGTTGTCAC  AAGC   CCTCC
                                    GA   ATA_
GAM157  LMO7     3'  CCTCCATACGAAAGCACTGTTG 19304         GC   GGCC
            C                    GCAACAGTG  TTCG   GGAGG
                              |||||||||  ||||   |||||
                              CGTTGTCAC  AAGC   CCTCC
                                    GA   ATA_
GAM157  MRPL49   3'  CCTCCGAAGCTCACTGTTGC  70165         _      CC
                              GCAACAGTG GCTTCGGG  GG
                              |||||||| ||||||||  ||
```

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                                CGTTGTCAC CGAAGCCT  CC
                                     T       __
GAM157  POLR2E   3'  CCTCCAGCTGCTCCTCACTGCC 60594    AA     CTTCG   C
           GC                    GC  CAGTGG    GGC GGAGG
                                ||  ||||||    ||| |||||
                                CG  GTCACT    TCG CCTCC
                                 CC     CCTCG   A
GAM157  REPS2    5'  CCCCGGCACGGCCACTGCGGC  17554    AA      TCGG    A
                                GC  CAGTGGCT    GCCGG GG
                                ||  ||||||||    ||||| ||
                                CG  GTCACCGG    CGGCC CC
                                 GC       CA__    _
GAM157  STK11    3'  CCCCCAAGGCCACTGCGC    6598     AA       C   CC
                                GC  CAGTGGCTT GGG  GG
                                ||  |||||||||| |||  ||
                                CG  GTCACCGGA CCC  CC
                                 C_       A   __
GAM157  TBX1     3'  CCCCAGCCCCAGGGGCCACCGC 55543    AACA      __    C  A
           GGC                    GC    GTGGCTTC  GGGC GG GG
                                ||    ||||||||  |||| || ||
                                CG    CACCGGGG  CCCG CC CC
                                 GCGC       AC    A  _
GAM157  UBL1     5'  CCCCGGGTGAAGCCACCGT    13975    A       GG    A
                                AC GTGGCTTCG  CCGG GG
                                || |||||||||  |||| ||
                                TG CACCGAAGT  GGCC CC
                                 C        G_    _
GAM157  BCL2L12  5'  CCTCCAGCGTCGGCCACTGTAG 57642    A       TT   _  C
           C                     GC ACAGTGGC  CGG GC GGAGG
                                || ||||||||  ||| ||  |||||
                                CG TGTCACCG  GCT CG CCTCC
                                 A       __   G  A
GAM157  CRF      3'  CCCCGGCCCGTGCTCAACACCG 22912    AACAG  _  TT       A
           C                     GC    TG GC  CGGGCCGG GG
                                ||    || ||  |||||||| ||
                                CG    AC CG  GCCCGGCC CC
                                 CCACA  T  T_       _
GAM157  DKFZP434P211 5'  CCTCCAGCTCAGCCACTG    28027         TC    C
                                CAGTGGCT  GGGC GGAGG
                                ||||||||  |||| |||||
                                GTCACCGA  CTCG CCTCC
                                     __    A
GAM157  DKFZP564B147 5'  CCTCCGGCCCGCGGCGCGTCGC 82954    A  A   G  T
                                GC AC GTG CT CGGGCCGGAGG
                                || || ||| || ||||||||||
                                CG TG CGC GG GCCCGGCCTCC
                                 C  _   _  C
GAM157  DKFZP564D0478 3'  CCTCCAGCCCGTGCAGTCCGCT 50442       _  T__     C
                                AGTGG CT   CGGGC GGAGG
                                |||||  ||   ||||| |||||
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                                TCGCC GA   GCCCG CCTCC
                                  T  CGT    A
GAM157  FLJ10737  3'  CCTCCAGCCCACCCACAGCTGT 37053       GGCTTC_   C
             TGC                  GCAACAGT      GGGC GGAGG
                                  ||||||||      |||| |||||
                                  CGTTGTCG      CCCG CCTCC
                                     ACACCCA    A
GAM157  FLJ14146  3'  CCCCCAGTAGGCCACTGTT   45568         C__   CC
                                  AACAGTGGCTT   GGG  GG
                                  ||||||||||   |||  ||
                                  TTGTCACCGGA   CCC  CC
                                        TGA   __
GAM157  FLJ20320  3'  CCTCCAGCTTTGGGAGCCAC   35423        __    C
                                  GTGGCTTC  GGGC GGAGG
                                  ||||||||  |||| |||||
                                  CACCGAGG  TTCG CCTCC
                                     GT    A
GAM157  FLJ21919  3'  CCTCCAGCCCCTCACACTGCTG 43735     A    GCTTC    C
             T                    GCA CAGTG     GGGC GGAGG
                                  ||| |||||     |||| |||||
                                  TGT GTCAC     CCCG CCTCC
                                    C     ACTC_    A
GAM157  KIAA0329  5'  CCCCGGCGGAGCCAGCTGCTGC 29939     A  _      GG    A
                                  GCA CAG TGGCTTC  GCCGG GG
                                  ||| ||| |||||||  ||||| ||
                                  CGT GTC ACCGAGG  CGGCC CC
                                    C  G      __    _
GAM157  KIAA0914  5'  CCCCAACCCAGCTTAGCCACTG 30295        TC___   CC  A
             T                    ACAGTGGCT     GGG  GG GG
                                  |||||||||     |||  || ||
                                  TGTCACCGA     CCC  CC CC
                                        TTCGA   AA  _
GAM157  KIAA1018  3'  CTCCAGGGGGCCACTGCGC    31056    AA        GGGCC
                                  GC  CAGTGGCTTC     GGAG
                                  ||  ||||||||||     ||||
                                  CG  GTCACCGGGG     CCTC
                                   C_         GA___
GAM157  T1A-2     5'  CCTCCGGCCCCCCCACCGTCGC 22390    A  A   CTTC
                                  GC AC GTGG    GGGCCGGAGG
                                  || || ||||    ||||||||||
                                  CG TG CACC    CCCGGCCTCC
                                   C  C    CC__
GAM157  TCEA3     5'  CCCCCGAGGCCCTACTGC     89894     AC  T       CC
                                  GCA  AG GGCTTCGGG  GG
                                  |||  || |||||||||  ||
                                  CGT  TC CCGGAGCCC  CC
                                    CA  _        __
GAM157  ZNF317    3'  CCCCCAAACGTCACTGTTGC   72475          _  C   CC
                                  GCAACAGTGGC TT GGG  GG
                                  |||||||||| || |||  ||
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                                CGTTGTCACTG AA CCC  CC
                                      C  A  __
GAM157  LOC122970 5'  CCCCCAGGCCGCTGCTGC    74641    A       C   CC
                                GCA CAGTGGCTT GGG  GG
                                ||| ||||||||| |||  ||
                                CGT GTCGCCGGA CCC  CC
                                  C       _  __
GAM157  LOC127702 3'  CCTAGGTCAAAGCCACT     75985        CG   GG
                                AGTGGCTT  GGCC  AGG
                                ||||||||  ||||  |||
                                TCACCGAA  CTGG  TCC
                                     A_   A_
GAM157  LOC149668 5'  CCCCGACCTCCCAGCCACTGTC 85698   A       TC_   C   A
              C                  C ACAGTGGCT   GGG CGG GG
                                 | |||||||||   ||| ||| ||
                                 C TGTCACCGA   TCC GCC CC
                                  C       CCC   A  _
GAM157  LOC150174 5'  CCTCCAGCTCAGCCACTG    80435        TC    C
                                CAGTGGCT  GGGC GGAGG
                                ||||||||  |||| |||||
                                GTCACCGA  CTCG CCTCC
                                     __    A
GAM157  LOC150213 5'  CCTCCAGCTCAGCCACTG    75354        TC    C
                                CAGTGGCT  GGGC GGAGG
                                ||||||||  |||| |||||
                                GTCACCGA  CTCG CCTCC
                                     __    A
GAM157  LOC200093 3'  CCTCCGGTGGCTGGCCACTCTG 63768     AC      TCGG
              C                   GCA  AGTGGCT    GCCGGAGG
                                  |||  |||||||   ||||||||
                                  CGT  TCACCGG    TGGCCTCC
                                    C_      TCGG
GAM157  LOC203503 5'  CCTCCGGCCCGCGGCGCGTCGC 90935    A  A   G  T
                                GC AC GTG CT CGGGCCGGAGG
                                || || ||| || ||||||||||
                                CG TG CGC GG GCCCGGCCTCC
                                 C  _  _  C
GAM157  LOC221362 5'  CCCCCAAAAAGCCACTGT    95400         C__   CC
                                ACAGTGGCTT   GGG  GG
                                ||||||||||   |||  ||
                                TGTCACCGAA   CCC  CC
                                     AAA   __
GAM157  LOC221935 3'  GCCCAAAGCCACTTCTGC    94203     AC       C
                                GCA  AGTGGCTT GGGC
                                |||  |||||||| ||||
                                CGT  TCACCGAA CCCG
                                  CT       A
GAM157  LOC222488 3'  CTCCGGCCCACACTGATGC   96008     A    GCTTC
                                GCA CAGTG    GGGCCGGAG
                                ||| |||||    |||||||||
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                                CGT GTCAC    CCCGGCCTC
                                  A    A____
GAM157  LOC254048 3'  CCCCAGTCAACCACTGTT    99058        CTTCG   C  A
                                AACAGTGG    GGC GG GG
                                ||||||||    ||| || ||
                                TTGTCACC    CTG CC CC
                                    AA___   A  _
GAM157  LOC255941 5'  CCCCAGCCCGGAGCCACCACCG 99298    AACA         C  A
          C                      GC   GTGGCTTCGGGC GG GG
                                ||   ||||||||||||| || ||
                                CG   CACCGAGGCCCG CC CC
                                 CCAC          A  _
GAM158  SCAMP1   3'  GCTAAATAAATATTCTCC    54500     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM158  SCAMP1   3'  GCTAAATAAATATTCTCC    54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM158  NX-17    3'  TGAATATCAGCCCCTAATA    40706        ATA_
                                TATTAGGG    ATATTCA
                                ||||||||    |||||||
                                ATAATCCC    TATAAGT
                                    CGAC
GAM158  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
          TA                     TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM159  HAL      5'  GCCACTCCTGCATAAAGCTC   10903          TGAAAA
                                GAGCTTTATGC     GGTGGC
                                ||||||||||      ||||||
                                CTCGAAATACG     TCACCG
                                      TCC___
GAM159  HMGN2    3'  GGCCACCTTGGCACAAAAGC   19809      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _  GG
GAM159  NMI      5'  GGCCACCTCCTCAGGAAG    17436     ATG   AA
                                CTTT   CTGA  AGGTGGCC
                                ||||   ||||  ||||||||
                                GAAG   GACT  TCCACCGG
                                  ___    CC
GAM159  PACE     3'  GGCCACCTCTCCAAGGGCTT   11944        A  CT  AAA
                                GAGCTTT TG  GA   GGTGGCC
                                |||||||  ||  ||   |||||||
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                                TTCGGGA AC  CT   CCACCGG
                                   _ CT  ___
GAM159  PYCR1    3' CCACCTTCCTCTAGAGCTC   70639       TGCT  A_
                                GAGCTTTA   GA  AAGGTGG
                                ||||||||   ||  |||||||
                                CTCGAGAT   CT  TTCCACC
                                   _____ CC
GAM159  SDC1     3' GGCCACCTCCCCAGCATTCCAG 12991     TT_     AAA
           C                     GCT   ATGCTG   AGGTGGCC
                                 |||   ||||||   ||||||||
                                 CGA   TACGAC   TCCACCGG
                                   CCT     CCC
GAM159  FLJ11560 5' GCCCAGGCCCAGCATAAAG   48008         AAAA  ___
                                CTTTATGCTG   GGT   GGC
                                ||||||||||   |||   |||
                                GAAATACGAC   CCG   CCG
                                     _____  GAC
GAM159  KIAA0446 5' CCACCTTTTGAAGAGCTC    69446       ATGCTG
                                GAGCTTT     AAAAGGTGG
                                |||||||     |||||||||
                                CTCGAGA     TTTTCCACC
                                   AG_____
GAM159  KIAA0971 3' GTTGTTCTCAGCATAAAGT   30677          AAA  TG
                                GCTTTATGCTGA   GG  GC
                                ||||||||||||   ||  ||
                                TGAAATACGACT   TT  TG
                                     C__  GT
GAM159  KIAA1393 3' GGCCACCTTGGCACAAAAGC  72574      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                   _ _  GG
GAM159  KIAA1656 3' GGCCACCTCCTCCTAGAAGCC 66377   A    ATGCT  AA
                                G GCTTT     GA  AGGTGGCC
                                | |||||     ||  ||||||||
                                C CGAAG     CT  TCCACCGG
                                _    ATC__  CC
GAM159  KIAA1884 3' GCCACCTTCATCTACCAAGGCT 73728       ATGCT  A_
           C                     GAGCTTT    GA  AAGGTGGC
                                 |||||||    ||  ||||||||
                                 CTCGGAA    CT  TTCCACCG
                                    CCAT_  AC
GAM159  PP3501   3' GGCCACCGTTGACAGCATAAAG 41683         AAAA_
                                CTTTATGCTG    GGTGGCC
                                ||||||||||    |||||||
                                GAAATACGAC    CCACCGG
                                     AGTTG
GAM159  SDCCAG3  3' GGTGTTCTCAGCATGAAGCTC  22803           AAA  TG
                                GAGCTTTATGCTGA   GG  GCC
                                ||||||||||||||   ||  |||
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                                CTCGAAGTACGACT  CT  TGG
                                      ___  TG
GAM159  SP140    3'  GGCCACCTCCATGCAGAAGC  24327      A  TGAAA
                                GCTTT TGC    AGGTGGCC
                                ||||| |||    ||||||||
                                CGAAG ACG    TCCACCGG
                                  _  TACC_
GAM159  LOC148760 3'  GGCCACCTTCTCCAACAAGCTC 85364       TA  CT  A
                                GAGCTT  TG  GA AAGGTGGCC
                                ||||||  ||  || |||||||||
                                CTCGAA  AC  CT TTCCACCGG
                                   CA  __  C
GAM159  LOC150170 5'  ACCTGTTTCACATAAAGC    80414        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                    _    G
GAM159  LOC150175 5'  ACCTGTTTCACATAAAGC    80453        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                    _    G
GAM159  LOC150215 5'  ACCTGTTTCACATAAAGC    80456        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                    _    G
GAM159  LOC150218 5'  ACCTGTTTCACATAAAGC    80525        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                    _    G
GAM159  LOC152065 3'  GGCCACCTTCTCCTTGGCAGGC 86737       TTA   ___  A
           TC                     GAGCT   TGCT   GA AAGGTGGCC
                                |||||   ||||   || |||||||||
                                CTCGG   ACGG   CT TTCCACCGG
                                  ___    TTC  C
GAM159  LOC152267 3'  GGCCACCTTGGCACAAAAGC   61036      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _  GG
GAM159  LOC158292 5'  CCTCTGGACCCAGCATAAGGCT 88046            AAAA_  T
           C                     GAGCTTTATGCTG     GG GG
                                ||||||||||||     || ||
                                CTCGGAATACGAC     TC CC
                                      CCAGG  T
GAM159  LOC219997 3'  GCCACCTCTTCAGCCTC     93256     CTTTAT     A
                                GAG     GCTGAA AGGTGGC
                                |||     |||||| |||||||
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                                CTC     CGACTT TCCACCG
                                  _______     C
GAM159  LOC256269 3'  GGCCACCTTGGCACAAAAGC  96608      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _ GG
GAM159  LOC91963  5'  GGCCACCTCCTCTGAGAAGC  68321      ATGCT  AA
                                GCTTT    GA  AGGTGGCC
                                |||||    ||  ||||||||
                                CGAAG    CT  TCCACCGG
                                   AGT__  CC
GAM160  CCND2     3'  TCCCAGCAAATCATCGGGCCA  10055          CCACA  _  A
                                TGGCCTGATGAT    GC GG GA
                                ||||||||||||    || || ||
                                ACCGGGCTACTA    CG CC CT
                                       AA___  A  C
GAM160  GCN5L2    5'  CTCCGCTGCGGGGGAGGCC   60529      GATGA  A
                                GGCCT    TCC CAGCGGAG
                                |||||    ||| ||||||||
                                CCGGA    GGG GTCGCCTC
                                   GG___  C
GAM160  GJA5      3'  CTGACCAGATCATCAGCCA   19164      C      CACAG
                                TGGC TGATGATC    CGG
                                |||| ||||||||    |||
                                ACCG ACTACTAG    GTC
                                  _       ACCA_
GAM160  HIVEP3    3'  TCCCCGCTGTGGTTGGCAGCCA 44702      C  ATGAT       A
                                TGGC TG    CCACAGCGG GA
                                |||| ||    ||||||||| ||
                                ACCG AC    GGTGTCGCC CT
                                  _ GGTT_       C
GAM160  HOXD1     5'  CCGCCGGTATATTAGGCCA   44696         AT  ACA
                                TGGCCTGATG  CC   GCGG
                                ||||||||||  ||   ||||
                                ACCGGATTAT  GG   CGCC
                                      AT  C__
GAM160  SUFU      3'  CCTTGTGACCCATCAGGCCA  32934         ATC    C
                                TGGCCTGATG   CACAG GG
                                ||||||||||   ||||| ||
                                ACCGGACTAC   GTGTT CC
                                      CCA    _
GAM160  DKFZP586J1624 3'  CTCCGCCCAGTCACCATCAGGC 32043          ATCCACA_
          CA                    TGGCCTGATG       GCGGAG
                                ||||||||||       ||||||
                                ACCGGACTAC       CGCCTC
                                      CACTGACC
GAM160  KIAA1671  3'  CTTTGCTTATGAATCATCAGAC 66282    C       C  C_
          C                     GG CTGATGAT CA  AGCGGAG
                                || |||||||| ||  |||||||
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                                CC GACTACTA GT  TCGTTTC
                                 A       A  AT
GAM160  LOC159110 5'  TCTCCGCTGCCCCGGTCAACCA 82995     CCTGA    CA__
                                TGG    TGATC   CAGCGGAGA
                                |||    |||||   |||||||||
                                ACC    ACTGG   GTCGCCTCT
                                  A____    CCCC
GAM160  LOC159116 5'  TCTCCGCTGCCCCGGTCAACCA 82978     CCTGA    CA__
                                TGG    TGATC   CAGCGGAGA
                                |||    |||||   |||||||||
                                ACC    ACTGG   GTCGCCTCT
                                  A____    CCCC
GAM160  LOC165476 5'  CTCCGCTGCCTGCTCAGCCA   88550     C   TGATCCA
                                TGGC TGA      CAGCGGAG
                                |||| |||      ||||||||
                                ACCG ACT      GTCGCCTC
                                  _   CGTCC__
GAM160  LOC200032 5'  CTGACCAGATCATCAGCCA    85475     C       CACAG
                                TGGC TGATGATC    CGG
                                |||| ||||||||    |||
                                ACCG ACTACTAG    GTC
                                  _       ACCA_
GAM160  LOC219654 5'  CTCCGCTGCGGAGGGGGGCC   92932      GATGA   A
                                GGCCT    TCC CAGCGGAG
                                |||||    ||| ||||||||
                                CCGGG    AGG GTCGCCTC
                                   GGG__   C
GAM160  LOC255862 3'  TCAAATGTAGACTATCAGGCCA 96115          A  C   GCG
                                TGGCCTGATG TC ACA   GA
                                |||||||||| || |||   ||
                                ACCGGACTAT AG TGT   CT
                                      C  A   AAA
GAM161  APOB     3'  CAAGCTGGCACCAGGGC     6355       GGGTCT       C
                                GCCC     GTGCCAGCT TG
                                ||||     ||||||||| ||
                                CGGG     CACGGTCGA AC
                                  AC____        A
GAM161  BCL3     3'  CAGAGCTGGTGGACCCAGGG   18990     _     GT
                                CCC GGGTCT  GCCAGCTCTG
                                ||| ||||||  ||||||||||
                                GGG CCCAGG  TGGTCGAGAC
                                  A     __
GAM161  CHRNA2    5'  CAGAGCTGGACAGCCCCAGG   7427     C   T   G
                                CC GGG CTGT CCAGCTCTG
                                || ||| |||| |||||||||
                                GG CCC GACA GGTCGAGAC
                                 A  C   _
GAM161  DDX11    3'  CAGAGCGCTGCCAGGACCCAGG 16572      C     GT  CA_
            CA                    TGCC GGGTCT  GC   GCTCTG
                                |||| ||||||  ||   ||||||
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                                ACGG CCCAGG  CG   CGAGAC
                                  A     AC  TCG
GAM161  DDX11    3'  CAGAGTGCTGCCAGGACCCAGG 16573     C     GT  CA_
             CA                   TGCC GGGTCT  GC   GCTCTG
                                |||| ||||||  ||   ||||||
                                ACGG CCCAGG  CG   TGAGAC
                                  A     AC  TCG
GAM161  DUSP4    3'  CAGAGCTGGCTCCCAGCA    55127     CC   TCTGT
                                TGC  GGG    GCCAGCTCTG
                                |||  |||    ||||||||||
                                ACG  CCC    CGGTCGAGAC
                                  A_   T_____
GAM161  FANCG    5'  CAGAGCTTCGCAGACCCGGCCA 17334    C         CC
                                TG CCGGGTCTGTG  AGCTCTG
                                || ||||||||||  |||||||
                                AC GGCCCAGACGC  TCGAGAC
                                  C         T_
GAM161  HMGA2    5'  TCAGAAAACTTCCAGCCCGGGC 14457         T   TGCCAGC
             A                    TGCCCGGG CTG      TCTGA
                                |||||||| |||      |||||
                                ACGGGCCC GAC      AGACT
                                     _  CTTCAAA
GAM161  KCNS2    3'  CTGGCACAGCCCAGGCA     68846      C   T
                                TGCC GGG CTGTGCCAG
                                |||| ||| |||||||||
                                ACGG CCC GACACGGTC
                                  A  _
GAM161  LZTS1    3'  CTGGGACACAGACCCAGG    41031    C       __
                                CC GGGTCTGTG  CCAG
                                || |||||||||  ||||
                                GG CCCAGACAC  GGTC
                                  A        AG
GAM161  MAPRE3   3'  CAGAGCTGACAGCACGGGC   25595      G T   GC
                                GCCCG G CTGT  CAGCTCTG
                                ||||| | ||||  ||||||||
                                CGGGC C GACA  GTCGAGAC
                                   A _   __
GAM161  SLC1A5   5'  TCAGTGTCCAAGACCCAGGCA  79241     C     G  CCA  T
                                TGCC GGGTCT TG   GC CTGA
                                |||| |||||| ||   || ||||
                                ACGG CCCAGA AC   TG GACT
                                  A     _ C__  T
GAM161  SLC1A5   5'  TCAGTGTCCAAGACCCAGGCA  79242     C     G  CCA  T
                                TGCC GGGTCT TG   GC CTGA
                                |||| |||||| ||   || ||||
                                ACGG CCCAGA AC   TG GACT
                                  A     _ C__  T
GAM161  TGFA     3'  CAGAGCTGACCCCCTAGCA   13704     CC   TCT  GC
                                TGC  GGG   GT  CAGCTCTG
                                |||  |||   ||  ||||||||
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                                ACG  CCC   CA  GTCGAGAC
                                  AT   C__  __
GAM161  TMSB4Y   5' CAGTACAGAGACCCGGACA   16101    C      G  CCAGCT
                                TG CCGGGTCT TG     CTG
                                || |||||||| ||     |||
                                AC GGCCCAGA AC     GAC
                                 A       G  AT_____
GAM161  XPNPEP2  3' CAGAGCTGTTCGAACCCAGC  14140    CC    C  TGC
                                GC  GGGT TG   CAGCTCTG
                                ||  |||| ||   ||||||||
                                CG  CCCA GC   GTCGAGAC
                                 A_    A  TT_
GAM161  CPEB1    3' CAAAGCTGGCAGGTCAGGCA  48364     CG GT  GT     C
                                TGCC  G  CT  GCCAGCT TG
                                ||||  |  ||  ||||||| ||
                                ACGG  C  GA  CGGTCGA AC
                                  A_ TG  __      A
GAM161  CREB-H   3' CTGAAACAGACCCGGACA   51867    C       GC
                                TG CCGGGTCTGT  CAG
                                || ||||||||||  |||
                                AC GGCCCAGACA  GTC
                                 A         AA
GAM161  CREB-H   3' CTGAAACAGACCCGGACA   51868    C       GC
                                TG CCGGGTCTGT  CAG
                                || ||||||||||  |||
                                AC GGCCCAGACA  GTC
                                 A         AA
GAM161  CREB-H   3' CTGAAACAGACCCGGACA   51869    C       GC
                                TG CCGGGTCTGT  CAG
                                || ||||||||||  |||
                                AC GGCCCAGACA  GTC
                                 A         AA
GAM161  CREB-H   3' CTGAAACAGACCCGGACA   51870    C       GC
                                TG CCGGGTCTGT  CAG
                                || ||||||||||  |||
                                AC GGCCCAGACA  GTC
                                 A         AA
GAM161  CREB-H   3' CTGAAACAGACCCGGACA   51871    C       GC
                                TG CCGGGTCTGT  CAG
                                || ||||||||||  |||
                                AC GGCCCAGACA  GTC
                                 A         AA
GAM161  DKFZP727G051 3' CTGGCACAGCCCAGGCA    70007     C   T
                                TGCC GGG CTGTGCCAG
                                |||| ||| |||||||||
                                ACGG CCC GACACGGTC
                                  A  _
GAM161  FLJ25442 5' CTGAGCACAGACCCGGGC    59496           _
                                GCCCGGGTCTGTGC CAG
                                |||||||||||||| |||
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                                CGGGCCCAGACACG GTC
                                       A
GAM161  KIAA0227  3'  TCAGAGCTACTTACAGCCAGGC 61353     CG  T    CC_
          A                     TGCC  GG CTGTG   AGCTCTGA
                                ||||  || |||||   ||||||||
                                ACGG  CC GACAT   TCGAGACT
                                  A_  _    TCA
GAM161  KIAA0257  3'  TCTTTGCAAAACAGACCCAAGC 71373    CC      GCCA  TCT
          A                     TGC  GGGTCTGT   GC   GA
                                |||  ||||||||   ||   ||
                                ACG  CCCAGACA   CG   CT
                                  AA       AAA_  TTT
GAM161  KIAA0574  3'  CAGAGCTGACCTTTCCCCGGGC 69807        TCTGTGC
          A                     TGCCCGGG      CAGCTCTG
                                ||||||||      ||||||||
                                ACGGGCCC      GTCGAGAC
                                     CTTTCCA
GAM161  KIAA0907  3'  CAAAGCTGGCACCTTCAGGCA  30867     C   TCT       C
                                TGCC GGG   GTGCCAGCT TG
                                |||| |||   ||||||||| ||
                                ACGG CTT   CACGGTCGA AC
                                  A  C__       A
GAM161  KIAA1157  3'  AGCCCACACAGCCCAGGCA   72694     C   T    CCA
                                TGCC GGG CTGTG   GCT
                                |||| ||| |||||   |||
                                ACGG CCC GACAC   CGA
                                  A  _    ACC
GAM161  KIAA1404  3'  CAGAAGCCAGACCCAGGC    62682     C      T  CAGC
                                GCC GGGTCTG GC    TCTG
                                ||| ||||||| ||    ||||
                                CGG CCCAGAC CG    AGAC
                                  A      _ A___
GAM161  LOXL4     3'  TGGAAGCACAGACCTCGGGCA  50863       _       CAGC  TG
                                TGCCCG GGTCTGTGC    TC  A
                                |||||| |||||||||    ||  |
                                ACGGGC CCAGACACG    AG  T
                                   T       A___  GT
GAM161  MGC12760  3'  CAGAGCCGGCAGGAGCAGG   52155    GGG   G    A
                                CC   TCT TGCC GCTCTG
                                ||   ||| |||| ||||||
                                GG   AGG ACGG CGAGAC
                                 ACG   _    C
GAM161  RPH3A     3'  AGTTGTCAGCAGACCCGGACA  30929    C        GC_
                                TG CCGGGTCTGT   CAGCT
                                || ||||||||||   |||||
                                AC GGCCCAGACG   GTTGA
                                 A         ACT
GAM161  SEMA7A    3'  TCAGAGCCGGCTGGCCCGGG   14611        TGT   A
                                CCCGGGTC   GCC GCTCTGA
                                ||||||||   ||| |||||||
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                                GGGCCCGG   CGG CGAGACT
                                    T__   C
GAM161   UCHL3     5'  TCAGAGCTGGAGGGCCGGGCA  21163       G   GTG
                                TGCCCGG TCT   CCAGCTCTGA
                                ||||||| |||   ||||||||||
                                ACGGGCC GGA   GGTCGAGACT
                                   G   ___
GAM161   LOC115950 3'  CAGAGCTGGGCCCCCTGGGCA  57871        TCT  G
                                TGCCCGGG   GT CCAGCTCTG
                                ||||||||   || |||||||||
                                ACGGGTCC   CG GGTCGAGAC
                                    CC_  _
GAM161   LOC129563 3'  CAGAGCTGGCTGCCTGGCA   75392     C    CTGT
                                TGCC GGGT    GCCAGCTCTG
                                |||| ||||    ||||||||||
                                ACGG TCCG    CGGTCGAGAC
                                  _    T___
GAM161   LOC146315 5'  CAGAGTGTTGCCAGGACCCAGG 61557     C     GT  CA_
            CA                    TGCC GGGTCT  GC   GCTCTG
                                |||| ||||||  ||   ||||||
                                ACGG CCCAGG  CG   TGAGAC
                                  A     AC  TTG
GAM161   LOC149076 3'  CTGGCAGACACAGACCCAGGCA 79878     C       ____
                                TGCC GGGTCTGT    GCCAG
                                |||| ||||||||    |||||
                                ACGG CCCAGACA    CGGTC
                                  A       CAGA
GAM161   LOC154427 3'  CAGGCCCACAGACCAAGGCA   87421     CG      CCA  T
                                TGCC  GGTCTGTG   GC CTG
                                ||||  ||||||||   || |||
                                ACGG  CCAGACAC   CG GAC
                                  AA       C__  _
GAM161   LOC168448 3'  TCAGAGCTGAGAGCCCCGAACA 83584    CC    T  GTGC
                                TG  CGGG CT    CAGCTCTGA
                                ||  |||| ||    |||||||||
                                AC  GCCC GA    GTCGAGACT
                                 AA    C  GA__
GAM161   LOC204820 3'  CAGAACCCTGCCAACCAAGGCA 92348     CG   C  T  C  C__
                                TGCC  GGT TG GC AG   TCTG
                                ||||  ||| || || ||   ||||
                                ACGG  CCA AC CG TC   AGAC
                                  AA   _  _  _  CCA
GAM161   LOC222681 5'  TCAGGCAATTCACAGACCAAGC 94429     CCG       CCA_  T
            A                     TGC   GGTCTGTG    GC CTGA
                                |||   ||||||||    || ||||
                                ACG   CCAGACAC    CG GACT
                                  AA_       TTAA  _
GAM161   LOC256401 3'  TCAGAGCTGAGAGACCCGAACA 97720    CC      GTGC
                                TG  CGGGTCT    CAGCTCTGA
                                ||  |||||||    |||||||||
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                                AC  GCCCAGA    GTCGAGACT
                                 AA      GA__
GAM161   LOC257415 3'  CAGAGCTGGCTACCAGCA    97799     CC  GTCTGT
                                TGC  GG     GCCAGCTCTG
                                |||  ||     ||||||||||
                                ACG  CC     CGGTCGAGAC
                                  A_  AT____
GAM161   LOC257507 5'  TCAGGCAATTCACAGACCAAGC 99616     CCG       CCA_  T
           A                     TGC   GGTCTGTG    GC CTGA
                                |||   ||||||||    || ||||
                                ACG   CCAGACAC    CG GACT
                                  AA_       TTAA  _
GAM161   LOC257625 5'  TCAGGCAATTCACAGACCAAGC 99736     CCG       CCA_  T
           A                     TGC   GGTCTGTG    GC CTGA
                                |||   ||||||||    || ||||
                                ACG   CCAGACAC    CG GACT
                                  AA_       TTAA  _
GAM162   ABCD4    3'  TGGAAGTGTGAGATCTGT    40104       _ TG    C
                                ACAGAT T  TATT TCCA
                                ||||||  |  |||| ||||
                                TGTCTA A  GTGA AGGT
                                   G GT    _
GAM162   ABCD4    3'  TGGAAGTGTGAGATCTGT    40105       _ TG    C
                                ACAGAT T  TATT TCCA
                                ||||||  |  |||| ||||
                                TGTCTA A  GTGA AGGT
                                   G GT    _
GAM162   ABCD4    3'  TGGAAGTGTGAGATCTGT    40106       _ TG    C
                                ACAGAT T  TATT TCCA
                                ||||||  |  |||| ||||
                                TGTCTA A  GTGA AGGT
                                   G GT    _
GAM162   ACADL    3'  TGGAAGGACAAATCTTTGA   9639      C       A TC
                                TCA AGATTTGT T  TCCA
                                |||  ||||||||  |  ||||
                                AGT TCTAAACA G  AGGT
                                  T       _ GA
GAM162   CHD1     5'  TGAAGAAAATTCATCTGTGA   8864         TT  A    C
                                TCACAGAT  GT TTCT CA
                                ||||||||  ||  ||||  ||
                                AGTGTCTA  TA AAGA GT
                                     CT  A    A
GAM162   CRH      3'  GAGAATGTAGACCTGTGA    7481         A
                                TCACAG TTTGTATTCTC
                                ||||||  ||||||||||
                                AGTGTC AGATGTAAGAG
                                   C
GAM162   CRY2     3'  TGGAAGGGCAAATCTGAGA   72667    A       ATTC
                                TC CAGATTTGT    TCCA
                                ||  |||||||||    ||||
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                                AG GTCTAAACG    AGGT
                                 A        GGA_
GAM162  GLP1R    3'  TGGAAATACTTTATCTGTGA   10800        TT_    C
                                TCACAGAT   GTATT TCCA
                                ||||||||   ||||| ||||
                                AGTGTCTA   CATAA AGGT
                                     TTT    _
GAM162  KCNK4    3'  TGGAGAATGAAGCTCTGGA   33990    A    TTTG
                                TC CAGA    TATTCTCCA
                                || ||||    |||||||||
                                AG GTCT    GTAAGAGGT
                                 _    CGAA
GAM162  MN1      3'  TGGAGAATAGTAGTTCTGGA   11659    A    T   _
                                TC CAGA TTG TATTCTCCA
                                || |||| ||| |||||||||
                                AG GTCT GAT ATAAGAGGT
                                 _    T   G
GAM162  PKIB     3'  TGGAAAATGCAAAATTTGT    51641         _    C
                                ACAGATTT GTATT TCCA
                                |||||||| ||||| ||||
                                TGTTTAAA CGTAA AGGT
                                     A     A
GAM162  PML      3'  AGAAATGCAGACCTGTGG     53792        A       _
                                TCACAG TTTGTATT CT
                                |||||| |||||||| ||
                                GGTGTC AGACGTAA GA
                                    C       A
GAM162  PMX1     5'  TGGAGAAAGGGGGTCTGTGA   23576          GTA
                                TCACAGATTT   TTCTCCA
                                ||||||||||   |||||||
                                AGTGTCTGGG   AAGAGGT
                                      GGA
GAM162  PTGIS    3'  TGGAGAAACAGGCTCTGAGA   8233     A    _    A
                                TC CAGA TTTGT TTCTCCA
                                || |||| ||||| |||||||
                                AG GTCT GGACA AAGAGGT
                                 A    C    _
GAM162  PTP4A2   3'  TGGAAATGTGAATCTGGA    14443    A     TG    C
                                TC CAGATT  TATT TCCA
                                || ||||||  |||| ||||
                                AG GTCTAA  GTAA AGGT
                                 _     GT    _
GAM162  PTP4A2   3'  TGGAAATGTGAATCTGGA    14444    A     TG    C
                                TC CAGATT  TATT TCCA
                                || ||||||  |||| ||||
                                AG GTCTAA  GTAA AGGT
                                 _     GT    _
GAM162  SART2    3'  TGAAGAATACAATTCTGAGA   26252    A    T       C
                                TC CAGA TTGTATTCT CA
                                || |||| |||||||| ||
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                                AG GTCT AACATAAGA GT
                                 A   T       A
GAM162  SON     3'  TGGAGAATGGGTTCCTGTGG  57987      ATTTG
                                TCACAG    TATTCTCCA
                                ||||||    |||||||||
                                GGTGTC    GTAAGAGGT
                                   CTTGG
GAM162  ST14    3'  TGGAAAACAGACGGGTCTGAGA 42043    A       ATTC__
                                TC CAGATTTGT     TCCA
                                || |||||||||     ||||
                                AG GTCTGGGCA     AGGT
                                 A        GACAAA
GAM162  TCN2    5'  TGGAGGATTAATCAGTGA    6267      A   TGT
                                TCAC GATT   ATTCTCCA
                                |||| ||||   ||||||||
                                AGTG CTAA   TAGGAGGT
                                  A   T__
GAM162  TM7SF3  3'  TGGTTTACAAATCTATGA    60396     C       TTCT
                                TCA AGATTTGTA    CCA
                                ||| |||||||||    |||
                                AGT TCTAAACAT    GGT
                                  A        TT__
GAM162  TRIM14  3'  AGAGCCACAAATCTGGGA    29503    A       A_
                                TC CAGATTTGT  TTCT
                                || |||||||||  ||||
                                AG GTCTAAACA  GAGA
                                 G        CC
GAM162  TYR     5'  TGGAAAGAGAAATCTGTGA   6325          GTA  C
                                TCACAGATTT   TT TCCA
                                ||||||||||   || ||||
                                AGTGTCTAAA   AA AGGT
                                      GAG  _
GAM162  UFD1L   3'  TGGAGAAGCAAACATGTGA   73677      GA    A
                                TCACA  TTTGT TTCTCCA
                                |||||  ||||| |||||||
                                AGTGT  AAACG AAGAGGT
                                   AC    _
GAM162  CSTF1   3'  TGGAAACACAGATCTGTG    9000          A  C
                                CACAGATTTGT TT TCCA
                                |||||||||| || ||||
                                GTGTCTAGACA AA AGGT
                                       C  _
GAM162  DKFZp434C0923 3'  TGGAGAATGTTGGTCCTG    34654     _  TG
                                CAG ATT  TATTCTCCA
                                ||| |||  |||||||||
                                GTC TGG  GTAAGAGGT
                                  C   TT
GAM162  DKFZP434C171 3'  TGGAAAATCAGATCTGTGA   32200          T   C
                                TCACAGATTTG ATT TCCA
                                |||||||||| ||| ||||
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                                AGTGTCTAGAC TAA AGGT
                                      _  A
GAM162  DKFZP566B183 3'  GAGGGCACCAATCTGTGA   31944        T  A
                                TCACAGATT GT TTCTC
                                ||||||||| || |||||
                                AGTGTCTAA CA GGGAG
                                     C  C
GAM162  DLAD    5'  TGGAGTCCCTAAACCTGTGA  41410      A   TATT
                                TCACAG TTTG   CTCCA
                                |||||| ||||   |||||
                                AGTGTC AAAT   GAGGT
                                   C   CCCT
GAM162  DOCK3   3'  TGGAGAATAAGTCAGTCTG   67101      TG__
                                CAGATT   TATTCTCCA
                                ||||||   |||||||||
                                GTCTGA   ATAAGAGGT
                                   CTGA
GAM162  DRIM    5'  GGAGAGTATAGCCTGTGA    27951      AT
                                TCACAG  TTGTATTCTCC
                                ||||||  ||||||||||
                                AGTGTC  GATATGAGAGG
                                   C_
GAM162  FBXO30   3'  TGAGAATGTGTCTGTGG    50491       TTG    C
                                TCACAGAT   TATTCT CA
                                ||||||||   |||||| ||
                                GGTGTCTG   GTAAGA GT
                                     T__     A
GAM162  FLJ10199 3'  TGGAGCTGGTGAATCTGTGG  71756        TG ATT
                                TCACAGATT  T   CTCCA
                                |||||||||  |   |||||
                                GGTGTCTAA  G   GAGGT
                                     GT GTC
GAM162  FLJ10898 5'  TGGTTAATACAAATCTGCGA  60143   A        CT
                                TC CAGATTTGTATT  CCA
                                || ||||||||||||  |||
                                AG GTCTAAACATAA  GGT
                                 C          TT
GAM162  FLJ11068 3'  TGGATTTACAAAATCTGTG   37589        _  TTC
                                CACAGATTT GTA   TCCA
                                |||||||||  |||   ||||
                                GTGTCTAAA CAT   AGGT
                                     A   TT_
GAM162  FLJ13693 3'  TGGAGAATGCAGCCTGGA    46076   A   AT
                                TC CAG  TTGTATTCTCCA
                                || |||  ||||||||||||
                                AG GTC  GACGTAAGAGGT
                                 _  C_
GAM162  FLJ13964 3'  TGAAGACTTAGAATCTGTGG  50756        GTAT   C
                                TCACAGATTT    TCT CA
                                ||||||||||    ||| ||
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                                GGTGTCTAAG   AGA GT
                                     ATTC   A
GAM162  FLJ14547  3' GAATCTCCAGATCTGTGA   52496        T__
                                TCACAGATTTG  ATTC
                                ||||||||||  ||||
                                AGTGTCTAGAC  TAAG
                                     CTC
GAM162  GPT2      3' TGGAAGTTACATCTGTGA   56773      TT   TTC
                                TCACAGA TGTA  TCCA
                                |||||||  ||||  ||||
                                AGTGTCT  ACAT  AGGT
                                   __   TGA
GAM162  KIAA0077  3' TGGAGAATACCCATCTGT   67581      TT
                                ACAGAT  GTATTCTCCA
                                ||||||  ||||||||||
                                TGTCTA  CATAAGAGGT
                                   CC
GAM162  KIAA0217  3' AGAAATAATTGATCTGTGA   67594       TG_  _
                                TCACAGATT   TATT CT
                                |||||||||   |||| ||
                                AGTGTCTAG   ATAA GA
                                     TTA   A
GAM162  KIAA0247  3' TGGAGAATCATGTCCATG   29078   CA  T  T
                                CA  GAT TG ATTCTCCA
                                ||  ||| || ||||||||
                                GT  CTG AC TAAGAGGT
                                 AC   T  _
GAM162  KIAA0293  3' AGAGTAATCAAATCTGGA   61234   A     __
                                TC CAGATTTG  TATTCT
                                || ||||||||  ||||||
                                AG GTCTAAAC  ATGAGA
                                 _      TA
GAM162  KIAA0332  3' AGAATATATATTCTGTGA   63364      TT_
                                TCACAGA   TGTATTCT
                                |||||||   ||||||||
                                AGTGTCT   ATATAAGA
                                     TAT
GAM162  KIAA0443  5' TGAAGAAACAAACCTGTGA   28855     A   A   C
                                TCACAG TTTGT TTCT CA
                                |||||| ||||| |||| ||
                                AGTGTC AAACA AAGA GT
                                   C    _   A
GAM162  KIAA0935  3' AGAATAGGCAAATCTGTG   73096        __
                                CACAGATTTGT  ATTCT
                                ||||||||||  |||||
                                GTGTCTAAACG  TAAGA
                                     GA
GAM162  KIAA1045  3' TGGAGAATCCTGACTGGA   71614   A  A  TGT
                                TC CAG TT   ATTCTCCA
                                || ||| ||   ||||||||
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                                AG GTC AG   TAAGAGGT
                                 _  _  TCC
GAM162  KIAA1165 3'  TGGAAGTGTGAACCTGTGA   67996       A  TG   C
                                TCACAG TT  TATT TCCA
                                |||||| ||  |||| ||||
                                AGTGTC AA  GTGA AGGT
                                   C  GT   _
GAM162  KIAA1327 3'  GAGAAAACTTATCTGTGA    72727        TT  A
                                TCACAGAT  GT TTCTC
                                |||||||||  || |||||
                                AGTGTCTA  CA AAGAG
                                     TT  A
GAM162  KIAA1718 3'  GAGGTTTCAAATCTGTGA    64975          TAT
                                TCACAGATTTG   TCTC
                                ||||||||||   ||||
                                AGTGTCTAAAC   GGAG
                                      TTT
GAM162  KIAA1831 3'  TGGAAGCAGAAGCTGTGA    64527       A_    ATTC
                                TCACAG  TTTGT   TCCA
                                ||||||  |||||   ||||
                                AGTGTC  AGACG   AGGT
                                   GA    A___
GAM162  KIAA1939 3'  TGAAGAATACAAAAGTGTG   46185      GA        C
                                CACA  TTTGTATTCT CA
                                ||||  |||||||||| ||
                                GTGT  AAACATAAGA GT
                                  GA         A
GAM162  KIAA1958 3'  TGGAAAAGCCAATCTGTGA   82797         T  A  C
                                TCACAGATT GT TT TCCA
                                ||||||||| || || ||||
                                AGTGTCTAA CG AA AGGT
                                     C  A  _
GAM162  MO25     3'  GAATCTGCCAGATCTGTGA   33288          T___
                                TCACAGATTTG   ATTC
                                ||||||||||   ||||
                                AGTGTCTAGAC   TAAG
                                      CGTC
GAM162  NDUFB5   3'  TGGAGAAATAGGAATTTGTGA  11767          G   _
                                TCACAGATTT TATT CTCCA
                                |||||||||| |||| |||||
                                AGTGTTTAAG ATAA GAGGT
                                      G   A
GAM162  P37NB    3'  ATGAAGAATACAAAGGATGGTC 20627        _______       C ___
           TGTGG                TCACAGAT     TTGTATTCT CA   T
                                ||||||||     ||||||||| ||   |
                                GGTGTCTG     AACATAAGA GT   A
                                     GTAGGA        A __
GAM162  PEPP3    3'  GAGAACAGCAGGTCTGTG    30708          A_
                                CACAGATTTGT  TTCTC
                                ||||||||||  |||||
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                                GTGTCTGGACG  AAGAG
                                      AC
GAM162  PLP1     3'  TGGAGAATAATTCTTTGA    6760     C   TTTG
                                TCA AGA    TATTCTCCA
                                ||| |||    |||||||||
                                AGT TCT    ATAAGAGGT
                                  T   TA__
GAM162  PTPNS1   3'  AGAAAACTTGATCTGTGG    55830        T_  A
                                TCACAGATT  GT TTCT
                                |||||||||  || ||||
                                GGTGTCTAG  CA AAGA
                                      TT  A
GAM162  RBBP7    5'  TGAAGAATATAAAATCTGGA   60662    A     _     C
                                TC CAGATTT GTATTCT CA
                                || ||||||| ||||||| ||
                                AG GTCTAAA TATAAGA GT
                                 _      A      A
GAM162  SIMRP7   3'  TGGAAGAGTACACCTGTGA    93981      ATT      _
                                TCACAG   TGTATTCT CCA
                                ||||||   |||||||| |||
                                AGTGTC   ACATGAGA GGT
                                   C__       A
GAM162  SPEC1    3'  GAAAACAATCATCTGTGA     40004        __   A
                                TCACAGAT  TTGT TTC
                                ||||||||  |||| |||
                                AGTGTCTA  AACA AAG
                                     CT    A
GAM162  STAG1    3'  TGAAGAAAATTTACAAATCTGG 20765    A       _____   C
           A                     TC CAGATTTGTA    TTCT CA
                                || ||||||||||    |||| ||
                                AG GTCTAAACAT    AAGA GT
                                 _        TTAA    A
GAM162  TLE4     3'  TGGAGAACAGCAATGTGG     68517      GAT    AT
                                TCACA   TTGT  TCTCCA
                                |||||   ||||  ||||||
                                GGTGT   GACA  AGAGGT
                                   AAC   __
GAM162  LOC114928 5' TGAAGAAACAAACCTGTGA    57392       A    A   C
                                TCACAG TTTGT TTCT CA
                                |||||| ||||| |||| ||
                                AGTGTC AAACA AAGA GT
                                   C    _   A
GAM162  LOC126167 3' TGGAGAGAAATCCTGTGA     74928       _   GTA
                                TCACAG ATTT   TTCTCCA
                                |||||| ||||   |||||||
                                AGTGTC TAAA   GAGAGGT
                                   C   ____
GAM162  LOC132321 3' GAAAATATAGTATCTGTGG    75571        _     C
                                TCACAGAT TTGTATT TC
                                |||||||| ||||||| ||
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                                GGTGTCTA GATATAA AG
                                     T      A
GAM162   LOC143310 3'  TGGAGAATAGGGATGATG    77052    G_   G
                                CA  ATTT TATTCTCCA
                                ||  |||| |||||||||
                                GT  TAGG ATAAGAGGT
                                 AG    G
GAM162   LOC146802 3'  TGGAGAATGCTGCATGTGA   78729      GATTT
                                TCACA    GTATTCTCCA
                                ||||||    ||||||||||
                                AGTGT    CGTAAGAGGT
                                   ACGT_
GAM162   LOC148195 3'  TGGAGAATACCATCATGT    85295    _   TT
                                ACA GAT  GTATTCTCCA
                                ||| |||  ||||||||||
                                TGT CTA  CATAAGAGGT
                                  A   C_
GAM162   LOC149072 5'  TGGAGAATAGTGTTTCTGTG   79888      TT  _
                                CACAGA  TG TATTCTCCA
                                ||||||  || |||||||||
                                GTGTCT  GT ATAAGAGGT
                                    TT  G
GAM162   LOC151201 3'  TGGAGGAAACACAAAACTATGA 86491    C  A    A__
                                TCA AG TTTGT   TTCTCCA
                                ||| || |||||   |||||||
                                AGT TC AAACA   AGGAGGT
                                  A  A    CAA
GAM162   LOC158777 3'  AGAACATAACATCTGTGA    82872        _   A
                                TCACAGAT TTGT TTCT
                                |||||||| |||| ||||
                                AGTGTCTA AATA AAGA
                                     C    C
GAM162   LOC162461 3'  TGGAGGTATGCAAATCTTGA   83241    C        _
                                TCA AGATTTGTAT TCTCCA
                                ||| ||||||||| ||||||
                                AGT TCTAAACGTA GGAGGT
                                  _        T
GAM162   LOC201696 3'  TGGACATCAAATCTGTGG    63831          TATTC
                                TCACAGATTTG    TCCA
                                ||||||||||    ||||
                                GGTGTCTAAAC    AGGT
                                       TAC__
GAM162   LOC202754 3'  TGAAGAATACAGCTGTGG    83590       AT       C
                                TCACAG  TTGTATTCT CA
                                ||||||  ||||||||| ||
                                GGTGTC  GACATAAGA GT
                                   __        A
GAM162   LOC219401 3'  AGAAGGCAGAAATCCTGTGA   94382       A___    A
                                TCACAG    TTTGT TTCT
                                ||||||    ||||| ||||
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                                AGTGTC   AGACG AAGA
                                   CTAA    G
GAM162  LOC219401 3'  TGGAGAAAGGCCCTGTGA    94388      ATTT  A_
                                TCACAG   GT  TTCTCCA
                                ||||||   ||  |||||||
                                AGTGTC   CG  AAGAGGT
                                   C___  GA
GAM162  LOC221017 3'  GGAGAACAAATCTCCGA     93113    AC      AT
                                TC  AGATTTGT  TCTCC
                                ||  ||||||||  |||||
                                AG  TCTAAACA  AGAGG
                                 CC       __
GAM162  LOC255645 3'  TGGAGAATAACAATCTCTGA   98477     C    TG
                                TCA AGATT  TATTCTCCA
                                ||| |||||  |||||||||
                                AGT TCTAA  ATAAGAGGT
                                  C    CA
GAM162  LOC257017 5'  TGGAAAAACTAGATCTGTG    99221         TA  C
                                CACAGATTTG  TT TCCA
                                ||||||||||  || ||||
                                GTGTCTAGAT  AA AGGT
                                      CA  A
GAM162  LOC54505  5'  TGGTCCTGCAAATCTGGA    68448    A       TTCT
                                TC CAGATTTGTA    CCA
                                || ||||||||||    |||
                                AG GTCTAAACGT    GGT
                                 _        CCT_
GAM163  AGRP      5'  CTTCATTAGGCCCTGCCATA   8534        A  A
                                TATGGCA GG CCTGATGGAG
                                ||||||| || ||||||||||
                                ATACCGT CC GGATTACTTC
                                    C  _
GAM163  CGTHBA    3'  CTTCCCTCCAGTCCTTGCCG   24890         C  AT  A
                                TGGCAAGGAC TG  GG GAAG
                                |||||||||| ||  || ||||
                                GCCGTTCCTG AC  CC CTTC
                                      _  CT  _
GAM163  COL5A3    3'  CTCCCCAGGCTCACCTTGCCAT 32318         A___   AT
          G                    TATGGCAAGG    CCTG  GGAG
                               ||||||||||    ||||  ||||
                               GTACCGTTCC    GGAC  CCTC
                                     ACTC    C_
GAM163  FGF23     3'  CTTCTCTGGGGTCCCTTCCA  40557     CAA     GA
                                TGG   GGACCT  TGGAGAAG
                                |||   ||||||  ||||||||
                                ACC   CCTGGG  GTCTCTTC
                                  TTC     __
GAM163  FUT3      3'  CTCCCAGAGACCTTGCCA    5621         AC_   AT
                                TGGCAAGG   CTG  GGAG
                                ||||||||   |||  ||||
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                                ACCGTTCC  GAC  CCTC
                                   AGA  __
GAM163  FUT5    3'  CTCCCAGAGACCTTGCCA   10726       AC_  AT
                                TGGCAAGG  CTG  GGAG
                                ||||||||  |||  ||||
                                ACCGTTCC  GAC  CCTC
                                   AGA  __
GAM163  TCF12   3'  TCTCCTATCCTCTTGCCATA  13639        ACCT  _
                                TATGGCAAGG   GAT GGAGA
                                ||||||||||   ||| |||||
                                ATACCGTTCT   CTA CCTCT
                                     C___  T
GAM163  WSX1    3'  CTCCCCCACATCCTTTCCTTGC 17915       CCT  _____
          C                      GGCAAGGA  GAT   GGAG
                                ||||||||  |||   ||||
                                CCGTTCCT  CTA   CCTC
                                   TTC  CACCC
GAM163  ZAP70   3'  CTTCCCCACCCTCAGCCCCACC 71375    CAA  AC  ___  A
          CCA                    TGG  GG  CTGA  TGG GAAG
                                |||  ||  ||||  ||| ||||
                                ACC  CC  GACT  ACC CTTC
                                  CCA  CC   CCC  C
GAM163  AMOT    3'  CTCCAAGCCTTGCCATA    56541         ACCTGA
                                TATGGCAAGG    TGGAG
                                ||||||||||    |||||
                                ATACCGTTCC    ACCTC
                                   GA____
GAM163  C1orf34 3'  CCTCTGGCCATTGCCATA   61303       _  A  T  T
                                TATGGCAA GG CC GA GG
                                |||||||| || || || ||
                                ATACCGTT CC GG CT CC
                                   A  _  T  _
GAM163  CLSTN1  3'  CTCCCCAGAGCACCCCCTGCCA 30787      A  AC____  AT
          T                     ATGGCA GG    CTG  GGAG
                                ||||||  ||    |||  ||||
                                TACCGT CC    GAC  CCTC
                                   C  CCACGA  C_
GAM163  DKFZP434J193 3'  CTTCTCCACCACTCTCCTTGCC 71562         CC_  A
          ATG                    TATGGCAAGGA  TG TGGAGAAG
                                ||||||||||  || ||||||||
                                GTACCGTTCCT  AC ACCTCTTC
                                     CTC  C
GAM163  DNAJC6  3'  CTCCAAAGTTCCCACCATA   29492      CAA  C  GA
                                TATGG  GGA CT  TGGAG
                                |||||  ||| ||  |||||
                                ATACC  CCT GA  ACCTC
                                   AC_  T  A_
GAM163  FLJ12122 5'  CTGCCAGCTCAGGTCCCTGCCA 47092      A      __  _
                                TGGCA GGACCTGA  TGG AG
                                ||||| ||||||||  ||| ||
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                                ACCGT CCTGGACT  ACC TC
                                  C       CG   G
GAM163  FLJ14642  3'  CTTCTCCGTAGTCCCCGCC   52575    AA   CTG
                                GGC  GGAC   ATGGAGAAG
                                |||  ||||   |||||||||
                                CCG  CCTG   TGCCTCTTC
                                  CC    A__
GAM163  FLJ20275  3'  CTGTCAGATCCTTGCCAT    35308         C
                                ATGGCAAGGA CTGATGG
                                |||||||||| |||||||
                                TACCGTTCCT GACTGTC
                                      A
GAM163  FLJ21369  3'  CTTCTCCATCAAGTTTCACCA  46051    CAA   C
                                TGG   GGAC TGATGGAGAAG
                                |||   |||| ||||||||||
                                ACC   TTTG ACTACCTCTTC
                                  AC_   A
GAM163  HSPC016   3'  TCTCTATTCCCTGCCATA    32503       A   CCTG
                                TATGGCA GGA    ATGGAGA
                                |||||||  |||    |||||||
                                ATACCGT CCT    TATCTCT
                                    C  _____
GAM163  HT014     3'  CTTCCTAATAAATCCTTGCCA  40153        CC  A   A
                                TGGCAAGGA  TG TGG GAAG
                                |||||||||  ||  ||| ||||
                                ACCGTTCCT  AT ATC CTTC
                                      AA  A  _
GAM163  KIAA0773  3'  CTTCTCCACGACCTCACC    28722    CA   ACC  A
                                GG  AGG   TG TGGAGAAG
                                ||  |||   || ||||||||
                                CC  TCC   GC ACCTCTTC
                                 AC   A__  _
GAM163  KIAA1181  3'  CTCCATCAGCTGGTCA      68911      A  GAC
                                TGGC AG   CTGATGGAG
                                ||||  ||   |||||||||
                                ACTG TC   GACTACCTC
                                  G  ____
GAM163  KIAA1321  3'  CTCCTTAGGTCCTCACA     62899    GCA       T
                                TG   AGGACCTGA GGAG
                                ||   ||||||||| ||||
                                AC   TCCTGGATT CCTC
                                 AC_        _
GAM163  KIAA1348  3'  CTTCTTAGGTCTTGCCA     69122        G     T
                                TGGCAAG ACCTGA GGAG
                                ||||||| |||||| ||||
                                ACCGTTC TGGATT CTTC
                                      _     _
GAM163  KIAA1493  3'  CTTCTCCACCTAGTCTGCC   64840      AG   CTGA
                                GGCA  GAC    TGGAGAAG
                                ||||  |||    ||||||||
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                                CCGT  CTG   ACCTCTTC
                                  __  ATCC
GAM163  KIAA1535  3'  CTCTGTGGTCCTTGCC     80212        TG
                                GGCAAGGACC  ATGGAG
                                ||||||||||  ||||||
                                CCGTTCCTGG  TGTCTC
                                      __
GAM163  KIAA1819  5'  CTTCTCCACGGCTCCCCCA   70252    CAA  C  A
                                TGG   GGA CTG TGGAGAAG
                                |||   ||| ||| ||||||||
                                ACC   CCT GGC ACCTCTTC
                                  C__   C  _
GAM163  LAT1-3TM  5'  CTCCATCAGTGTCATTACCA  69156    CAAG  _
                                TGG   GAC CTGATGGAG
                                |||   ||| |||||||||
                                ACC   CTG GACTACCTC
                                  ATTA  T
GAM163  LAT1-3TM  3'  CTCCATCAGTGTCATCACCA  49143    CAAG  _
                                TGG   GAC CTGATGGAG
                                |||   ||| |||||||||
                                ACC   CTG GACTACCTC
                                  ACTA  T
GAM163  OS4     3'  CTTCCCCATCATCCCTTCCATT 20389      _  CC___    A
           GCCA                   TGGCAA GGA    TGATGG GAAG
                                ||||||| |||    |||||| ||||
                                ACCGTT CCT    ACTACC CTTC
                                   A  TCCCT    C
GAM163  RASSF2   3'  CTTCTCCACCTTCTCTCCA   29097    CA   CCTGA
                                TGG  AGGA    TGGAGAAG
                                |||  ||||    ||||||||
                                ACC  TCTT    ACCTCTTC
                                  TC   CC___
GAM163  SARM     3'  CTCCCCCAGGCCCTGCCAT   31285      A  A   AT
                                ATGGCA GG CCTG  GGAG
                                |||||| || ||||  ||||
                                TACCGT CC GGAC  CCTC
                                   C  _   CC
GAM163  SELB     3'  CTCCCCCAGGGCCTCCTTGCC  62591        ___   AT
                                GGCAAGGA   CCTG  GGAG
                                ||||||||   ||||  ||||
                                CCGTTCCT   GGAC  CCTC
                                     CCG   CC
GAM163  SERPING1  3'  CTTCTCCATGGCCCTGCCATG  5348       A  A  TG
                                TATGGCA GG CC  ATGGAGAAG
                                ||||||| || ||  |||||||||
                                GTACCGT CC GG  TACCTCTTC
                                   C  _  __
GAM163  SLIT1    3'  TCTCCGGAAGTCCTTGC     13233        C GA
                                GCAAGGAC T  TGGAGA
                                |||||||| |  ||||||
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                                CGTTCCTG A  GCCTCT
                                    _ AG
GAM163  ZDHHC8    3'  TCCCCACCAACTTCTCTGCC  64622     _   CC  A   A
                                GGCA AGGA  TG TGG GA
                                |||| ||||  || ||| ||
                                CCGT TCTT  AC ACC CT
                                  C   CA  C   C
GAM163  LOC112868 5'  CTCCCAGCCCTTGCCA     73268       AC   AT
                                TGGCAAGG  CTG  GGAG
                                ||||||||  |||  ||||
                                ACCGTTCC  GAC  CCTC
                                    C_  __
GAM163  LOC142946 3'  CCATGGTCCTTGCCATA     83783          TG
                                TATGGCAAGGACC  ATGG
                                ||||||||||||  ||||
                                ATACCGTTCCTGG  TACC

                                      __
GAM163  LOC150319 3'  CTTCTCCATCCTCCTGCCAT  80471      A   CCT
                                ATGGCA GGA   GATGGAGAAG
                                |||||| |||   ||||||||||
                                TACCGT CCT   CTACCTCTTC
                                   _  C__
GAM163  LOC159319 5'  TTCTCCACACCCCTGCC     83073     A  ACC  A
                                GGCA GG   TG TGGAGAA
                                |||| ||   || |||||||
                                CCGT CC   AC ACCTCTT
                                  C  C__  _
GAM163  LOC197423 5'  CTCCATCAGTGTCATTACCA  78424     CAAG  _
                                TGG    GAC CTGATGGAG
                                |||    ||| |||||||||
                                ACC    CTG GACTACCTC
                                  ATTA   T
GAM163  LOC199923 5'  CTTCTCCACCTCCTGCCA    89871      A   CCTGA
                                TGGCA GGA    TGGAGAAG
                                ||||| |||    ||||||||
                                ACCGT CCT    ACCTCTTC
                                   _  CC___
GAM163  LOC206657 5'  CTTCTCAGTCTTGCCA      91105       AC   T
                                TGGCAAGG  CTGA GGAG
                                ||||||||  |||| ||||
                                ACCGTTCT  GACT CTTC

                                    __   _
GAM163  LOC220565 5'  CTCCATCAGTGTCATCACCA  92441     CAAG  _
                                TGG    GAC CTGATGGAG
                                |||    ||| |||||||||
                                ACC    CTG GACTACCTC
                                  ACTA   T
GAM163  LOC221975 5'  CTTCTCCATGGAGCCTGCC   94192     A  AC  G
                                GGCA GG  CT ATGGAGAAG
                                |||| ||  || |||||||||
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                                CCGT CC  GG TACCTCTTC
                                  _ GA  _
GAM163  LOC222160 5'  TCCCATTAGGCCCCCA     95793     CAA  A      A
                                TGG   GG CCTGATGG GA
                                |||   || |||||||| ||
                                ACC   CC GGATTACC CT
                                  C__  _       _
GAM163  LOC257239 5'  CTTCTCCACCTCAACCACCA  98844     CAA  ACC   __
                                TGG   GG   TGA  TGGAGAAG
                                |||   ||   |||  ||||||||
                                ACC   CC   ACT  ACCTCTTC
                                  A__  A__   CC
GAM163  LOC90499  3'  CTTCTCCATGGCCCCCTCCA  63741     CAA  A  TG
                                TGG   GG CC  ATGGAGAAG
                                |||   || ||  |||||||||
                                ACC   CC GG  TACCTCTTC
                                  TCC  C  __
GAM164  APBA1     3'  TCTCTGGAAGGCCCCTT     70476      A   TGG
                                AAGG GCTT   TTCGGAGA
                                |||| ||||   ||||||||
                                TTCC CGGA   AGGTCTCT
                                  C   ___
GAM164  CA7       3'  CCAGTCACCAAAGCCACCT   60828     A_      TCGGA   A
                                AGG  GCTTTGGT    GAC GG
                                |||  ||||||||    ||| ||
                                TCC  CGAAACCA    CTG CC
                                  AC       _____  A
GAM164  E2F3      3'  CTGTCTCCATGAACCACTC   10467     CTT     __
                                GAG   TGGTTC  GGAGACAG
                                |||   ||||||  ||||||||
                                CTC   ACCAAG  CCTCTGTC
                                  ___     TA
GAM164  HD        3'  CCTATCCCCAGGACAGGTCCCT 10911     AG   TG   _  A  C
                                AGG  CTT  GTTC GG GA AGG
                                |||  |||  |||| || || |||
                                TCC  GGA  CAGG CC CT TCC
                                  CT   __    A  C  A
GAM164  LZTR1     3'  CTGTCACCCAAGGCTCCT    23170          TTCG A
                                AGGAGCTTTGG    G GACAG
                                ||||||||||    | |||||
                                TCCTCGGAACC    C CTGTC
                                      ____ A
GAM164  MECP2     3'  CCCGTCTAACCACAGCTCCTT  18394        T    CGG    A
                                AAGGAGCT TGGTT   AGAC GG
                                |||||||| |||||   |||| ||
                                TTCCTCGA ACCAA   TCTG CC
                                     C     ___    C
GAM164  PLA2G2A   5'  CTGTCTCCAAACAGCCTT    6110      A   TTG   C
                                AGG GCT   GTT GGAGACAG
                                ||| |||   ||| ||||||||
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                                TTC CGA   CAA CCTCTGTC
                                  _  ___   A
GAM164  PLOD     3'  CCTGAAAAACCAAGGCCCC   6114     A       CGGAGA
                                GG GCTTTGGTT     CAGG
                                || |||||||||     ||||
                                CC CGGAACCAA     GTCC
                                 C       AAA___
GAM164  POLR2A   3'  CCTGTCCCCAAATTGAAGATCC 8128       G   TG   C  A
           TT                    AAGGA CTT  GTT GG GACAGG
                                ||||| |||  ||| || ||||||
                                TTCCT GAA  TAA CC CTGTCC
                                   A   GT   A  C
GAM164  RAB36    3'  CCTGTCTCCAACACCGCCTCCT 18163      CTT    TC_
                                AGGAG   TGGT   GGAGACAGG
                                |||||   ||||   |||||||||
                                TCCTC   GCCA   CCTCTGTCC
                                   C__    CAA
GAM164  RAP1     3'  CCTGTCCTTTGGCAGAAGCTCC 39111          G  T    _
           TT                    AAGGAGCTTT GT CGGAG ACAGG
                                |||||||||| || ||||| |||||
                                TTCCTCGAAG CG GTTTC TGTCC
                                     A  _    C
GAM164  SFRP5    3'  CCTGCCCCAAGGCCCAGAGCTC 13032          TT __  AGA
           C                     GGAGCTTTGG  C  GG   CAGG
                                |||||||||  |  ||   ||||
                                CCTCGAGACC  G  CC   GTCC
                                     CG AA  CC_
GAM164  SORCS2   3'  CCTGTCCCCCAGACCCAAAGCT 40800          T  _  A_
           CT                    GGAGCTTTGG TC GG  GACAGG
                                |||||||||| || ||  ||||||
                                TCTCGAAACC AG CC  CTGTCC
                                     C  A  CC
GAM164  TFR2     3'  CCCGTCCCCCAGTCAAGAGCTC 13698          _ GT C  A   A
           CT                    AGGAGCTTT G  T GG GAC GG
                                |||||||||  |  | || ||| ||
                                TCCTCGAGA C  A CC CTG CC
                                     A TG C  C   C
GAM164  C1orf35  3'  CTGCCTCGGAAGCTCCTT    44480         TTGGT  G   A
                                AAGGAGCT     TC GAG CAG
                                ||||||||     || ||| |||
                                TTCCTCGA     AG CTC GTC
                                     ______  G   C
GAM164  DKFZp434J1015 3'  CCGCCTCCACCTGAAAAGCTCC 94209          ___  TC    ACA
           TT                    AAGGAGCTTT   GGT  GGAG   GG
                                ||||||||||   |||  ||||   ||
                                TTCCTCGAAA   CCA  CCTC   CC
                                     AGT   __    CG_
GAM164  EFS2     3'  CTGCCTGCCAAAGCCCC     20773     A       TC  AGA
                                GG GCTTTGGT  GG   CAG
                                || ||||||||  ||   |||
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                                CC CGAAACCG  CC   GTC
                                 C       T_ ___
GAM164  FLJ10350  5'  CCGCCTCCGAGTCGCTACTT  97248     G   TTT GT     ACA
                                AAG AGC   G  TCGGAG   GG
                                ||| |||   |  ||||||   ||
                                TTC TCG   C  AGCCTC   CC
                                  A  ___ TG     CG_
GAM164  FLJ30294  5'  TGTCTCCGTACCCCTT      58900      AGCTTT   T
                                AAGG     GGT CGGAGACA
                                ||||     ||| ||||||||
                                TTCC     CCA GCCTCTGT
                                  ______  T
GAM164  HRI       3'  CTGCCCCACAAGCTCCTT    27738          _   TT
                                AAGGAGCTT TGG  CGG
                                ||||||||| |||  |||
                                TTCCTCGAA ACC  GTC
                                      C   CC
GAM164  KIAA0057  3'  CCTGTCTCTTGCAAGCTCC   25409        TG  TC
                                GGAGCTT  GT  GGAGACAGG
                                |||||||  ||  |||||||||
                                CCTCGAA  CG  TCTCTGTCC
                                    __  T_
GAM164  KIAA0189  3'  CCTGTCCCCTTTCCTAAAGCTC 28941           TTC_  A
          CT                    AGGAGCTTTGG    GG GACAGG
                                ||||||||||    || ||||||
                                TCCTCGAAATC    CC CTGTCC
                                      CTTT  C
GAM164  KIAA0326  3'  CTCCCCAAGCTCCTT       64961          T  TTC
                                AAGGAGCTT GG   GGAG
                                |||||||| ||   ||||
                                TTCCTCGAA CC   CCTC
                                    _  ___
GAM164  KIAA1203  3'  CCTGCCCTCCCACCAAAGCCTC 72087       _      TC    A_
          CT                    AGGAG CTTTGGT  GGAG  CAGG
                                ||||| |||||||  ||||  ||||
                                TCCTC GAAACCA  CCTC  GTCC
                                  C      C_   CC
GAM164  KIAA1533  5'  CCTGCCCCCAAGCCGGCCCC   74140    A   TT   C  AGA
                                GG GCT  GGTT GG   CAGG
                                || |||  |||| ||   ||||
                                CC CGG  CCGA CC   GTCC
                                 C  __    A  CCC
GAM164  MSTP028   3'  CTACCTCCCAGGCTCCT     50063        T  TTCG   AC
                                AGGAGCTT GG    GAG  AG
                                |||||||| ||    |||  ||
                                TCCTCGGA CC    CTC  TC
                                    _ _____   CA
GAM164  SAMHD1    3'  CCTGCCCCCGTGAAGAGTTCC  61981         GGTT   AGA
                                GGAGCTTT    CGG   CAGG
                                ||||||||    |||   ||||
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                                CCTTGAGA   GCC   GTCC
                                    AGT_   CCC
GAM164  SCGN     3'  CCTGTCTCACTGAAAGCCCCT  23775     A    _  TCG
                                AGG GCTTT GGT   GAGACAGG
                                ||| ||||| |||   ||||||||
                                TCC CGAAA TCA   CTCTGTCC
                                  C    G  ___
GAM164  SYT6     3'  CATCTCCGAAACCACCTC    79517     CTT    _     CA
                                GAG   TGGTT CGGAGA  G
                                |||   ||||| ||||||  |
                                CTC   ACCAA GCCTCT  C
                                  C__    A     AC
GAM164  UBE3B    3'  GTCTCCACAGTCCTT      77447      G  TTG  TC
                                AAGGA CT   GT  GGAGAC
                                ||||| ||   ||  ||||||
                                TTCCT GA   CA  CCTCTG
                                  _ ___  __
GAM164  UBXD2    3'  CTGCCTCCATCAGCTTCTT    68892        TT   TC    A
                                AAGGAGCT  GGT  GGAG CAG
                                ||||||||  |||  |||| |||
                                TTCTTCGA  CTA  CCTC GTC
                                    __   __    C
GAM164  LOC113146 3'  CCTAAAATGGAACCAAAGCTTC 73334            GGAGAC
                                GGAGCTTTGGTTC     AGG
                                ||||||||||||     |||
                                CTTCGAAACCAAG     TCC
                                      GTAAAA
GAM164  LOC113521 5'  CCCGTCTCCGAGCTGCTCC   73402      TTT         A
                                GGAGC   GGTTCGGAGAC GG
                                |||||   |||||||||| ||
                                CCTCG   TCGAGCCTCTG CC
                                   ___         C
GAM164  LOC115704 3'  CCTGCAGCGGAAACCAAAGTCC 73906    AG      __  GAGA
            C                    GG  CTTTGGT  TCG    CAGG
                                ||  |||||||  |||    ||||
                                CC  GAAACCA  GGC    GTCC
                                 CT      AA   GAC_
GAM164  LOC136345 3'  CCTACCCCACCCAAAGCTGCCT 76712     _      TTC  AGAC
                                AGG AGCTTTGG   GG    AGG
                                ||| ||||||||   ||    |||
                                TCC TCGAAACC   CC    TCC
                                  G       CA_  CCA_
GAM164  LOC144231 5'  CCTGTCTTCCTTGACCAAAGCT 83938           C__
            CT                    GGAGCTTTGGTT   GGAGACAGG
                                ||||||||||||   |||||||||
                                TCTCGAAACCAG   CTTCTGTCC
                                      TTC
GAM164  LOC146856 5'  CTGTCTCCATGAACCACTC    83700     CTT     __
                                GAG   TGGTTC  GGAGACAG
                                |||   ||||||  ||||||||
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                                CTC   ACCAAG  CCTCTGTC
                                  ___     TA
GAM164  LOC147669 5' CCGCCTCCTGGGCAAGCTCC   85180       TG   _   ACA
                                GGAGCTT  GTTC GGAG   GG
                                |||||||  |||| ||||   ||
                                CCTCGAA  CGGG CCTC   CC
                                   __   T   CG_
GAM164  LOC148021 5' CTACCTCCAGAGCTACTT    79316    G      TTC  _
                                AAG AGCTTTGG   GG AG
                                ||| ||||||||   || ||
                                TTC TCGAGACC   CC TC
                                  A       T__  A
GAM164  LOC153688 3' CCTGCCCCCAAACCAAGGCCT  87307    A       C  AGA
                                GG GCTTTGGTT GG   CAGG
                                || |||||||| ||   ||||
                                TC CGGAACCAA CC   GTCC
                                 _       A  CCC
GAM164  LOC155032 5' CCTACCCCACCCAAAGCTGCCT 87592     _      TTC  AGAC
                                AGG AGCTTTGG   GG    AGG
                                ||| ||||||||   ||    |||
                                TCC TCGAAACC   CC    TCC
                                  G       CA_  CCA_
GAM164  LOC157349 5' CCCGTCTCCGGCAGCCCCT    82333    A   TTG  T      A
                                AGG GCT   GT CGGAGAC GG
                                ||| |||   || ||||||| ||
                                TCC CGA   CG GCCTCTG CC
                                  C  ___  _      C
GAM164  LOC157349 5' CCCGTCTCCGGCAGCCCCT    82334    A   TTG  T      A
                                AGG GCT   GT CGGAGAC GG
                                ||| |||   || ||||||| ||
                                TCC CGA   CG GCCTCTG CC
                                  C  ___  _      C
GAM164  LOC199991 3' CCTGTCCACCCTCAAAGCCCT  91515    A      TTC  A_
                                AGG GCTTTGG   GG  GACAGG
                                ||| |||||||   ||  ||||||
                                TCC CGAAACT   CC  CTGTCC
                                  _      C__  AC
GAM165  DLEC1    3' CATCTGGCCCTCCCTTG     24716      A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                   C    G  _
GAM165  DLEC1    3' CATCTGGCCCTCCCTTG     24728      A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                   C    G  _
GAM165  PIP5K1A  3' TATCCCACCCTGCCTTGATA  14520        A   CA  C
                                TATCAAGG AGGG  GG GTG
                                |||||||| ||||  || |||
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                                ATAGTTCC TCCC  CC TAT
                                    G   A_  C
GAM165  SOX11    3'  ACCCACCCCCCCTTGGTA    13308        AA   CA  C
                                TATCAAGG  GGG  GG GT
                                ||||||||  |||  || ||
                                ATGGTTCC  CCC  CC CA
                                    CC   A_  _
GAM165  CHL1     3'  TGTTACCTTTCCTCAATA    22768     CA      CA
                                TAT  AGGAAGGG  GGCG
                                |||  ||||||||  ||||
                                ATA  TCCTTTCC  TTGT
                                  AC       A_
GAM165  EPB41L1  3'  CATTCTGCCCTTCCCTGA    71104     A         C
                                TCA GGAAGGGCAGG GTG
                                ||| ||||||||||| |||
                                AGT CCTTCCCGTCT TAC
                                  C         _
GAM165  FLJ00060 3'  CATACCCCCTGCCCTCCTCTGA 61741     _    A      CGTG
                                TCA AGGA GGGCAGG    ATG
                                ||| |||| |||||||    |||
                                AGT TCCT CCCGTCC    TAC
                                  C    _      CCCA
GAM165  FLJ10898 5'  CACCACAGCCCTTTCTCAATA  60126     CA        AGGC
                                TAT  AGGAAGGGC    GTG
                                |||  |||||||||    |||
                                ATA  TCTTTCCCG    CAC
                                  AC        ACAC
GAM165  FLJ22557 3'  ATCATCCCATCCTTAATA    45581     C    A   CAGGC
                                TAT AAGGA GGG     GTGAT
                                ||| ||||| |||     |||||
                                ATA TTCCT CCC     TACTA
                                  A    A  ______
GAM165  KIAA0574 3'  CATCCCCTGCCCTCCCCTGA   69808     A  A      CGT
                                TCA GG AGGGCAGG   GATG
                                ||| ||  ||||||||   ||||
                                AGT CC TCCCGTCC   CTAC
                                  C  C       C__
GAM165  KIAA0632 3'  CACCTCAGAAACCCTTCCTTGA 32071           CA___  C
                                TCAAGGAAGGG     GG GTG
                                ||||||||||     || |||
                                AGTTCCTTCCC     CT CAC
                                      AAAGA  C
GAM165  KIAA1045 3'  CATCACATGTCCTTCC      71599         GGC
                                GGAAGGGCA   GTGATG
                                |||||||||   ||||||
                                CCTTCCTGT   CACTAC
                                     A__
GAM165  KIAA1354 5'  CAGTGACTGCCTTCCCTTGATA 61572         A      G  _
                                TATCAAGG AGGGCAG CG TG
                                |||||||| ||||||| || ||
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                                ATAGTTCC TTCCGTC GT AC
                                    C      A  G
GAM165  MGC20460  5'  CACCGCCTCCTACCCTTCTT   54901        C___    _
                                AGGAAGGG    AGGCG TG
                                ||||||||    ||||| ||
                                TTCTTCCC    TCCGC AC
                                    ATCC     C
GAM165  LOC158476 3'  CACGCCCGCCCCCCCCATTGA  88186     _ AA_   A
                                TCAA GG   GGGC GGCGTG
                                |||| ||   |||| ||||||
                                AGTT CC   CCCG CCGCAC
                                  A  CCC    C
GAM165  LOC90459  3'  CACACCCGCCTAATTTTTG    63550       A_   A  C
                                CAAGGA  GGGC GG GTG
                                ||||||  |||| || |||
                                GTTTTT  TCCG CC CAC
                                   AA    C  A
GAM166  ACVRL1    5'  TTTATTAGGAGGGAGTGGTG   5240          AAGAAG
                                CACCACTCCC     AATAAG
                                ||||||||||     ||||||
                                GTGGTGAGGG     TTATTT
                                     AGGA__
GAM166  BCL11B    3'  TTTGTTTTTGGGGTGGGGGGTG 57582       A_ __      G  TAAG
          TG                    TACACC  CT  CCCAAGAA AA
                                ||||||  ||  |||||||| ||
                                GTGTGG  GG  GGGTTTTT TT
                                   GG  TG       G  T
GAM166  C18orf1   3'  CTTCGTGTGGGAGTGGTGTG   60865          A__
                                TACACCACTCCCA   GAAG
                                ||||||||||||   ||||
                                GTGTGGTGAGGGT   CTTC
                                       GTG
GAM166  ITPR3     3'  CTTGTTTTTCTCCTTTTGGTGT 11085       CTCCCA
          A                     TACACCA     AGAAGAATAAG
                                |||||||     ||||||||||
                                ATGTGGT     TCTTTTTGTTC
                                    TTTCC_
GAM166  KCNAB1    3'  GTTTGTTTTTTTTTGAAGGGGG 61585          ____
          TGGTGTG                 TACACCACTCCC    AAGAAGAATAAG   T
                                ||||||||||||   ||||||||||||   |
                                GTGTGGTGGGGG    TTTTTTTTGTTT   G
                                       AAGT
GAM166  KRAS2     3'  CTTATTTTTCTTACCAAGTGTG 54123     C   CCC_
                                CAC ACT    AAGAAGAATAAG
                                ||| |||    ||||||||||||
                                GTG TGA    TTCTTTTTATTC
                                  _   ACCA
GAM166  KRAS2     3'  CTTATTTTTCTTACCAAGTGTG 54124     C   CCC_
                                CAC ACT    AAGAAGAATAAG
                                ||| |||    ||||||||||||
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                                GTG TGA    TTCTTTTTATTC
                                  _  ACCA
GAM166  LIFR     3'  TTTGTTTTTTTTGGTTGGTTG  11315    C    CTC
                                A ACCA   CCAAGAAGAATAAG
                                | ||||   ||||||||||||||
                                G TGGT   GGTTTTTTTTGTTT
                                 T   T__
GAM166  MEN1     5'  CTTGTTTTTTTCCTTTTGGTG  56348       CTCCCA
                                CACCA     AGAAGAATAAG
                                ||||||     ||||||||||
                                GTGGT     TTTTTTTGTTC
                                   TTTCC_
GAM166  MLLT7    3'  TTGTGCCTGGGAGTGTGTG    21043     _      AGAAGA
                                CAC CACTCCCA     ATAA
                                ||| ||||||||     ||||
                                GTG GTGAGGGT     TGTT
                                  T       CCG___
GAM166  SIAH1    3'  TTTGTTTTTGCCGTGGGAGTGT 13128     _      AG__
             GTG                  CAC CACTCCCA    AAGAATAAG
                                ||| ||||||||    |||||||||
                                GTG GTGAGGGT    TTTTTGTTT
                                  T       GCCG
GAM166  SLC7A6   3'  TTTGTTTTTGTGGTGGGTGCTG 15646      C    _  AG
             TG                   TACA CACTC CCA  AAGAATAAG
                                |||| ||||| |||  |||||||||
                                GTGT GTGGG GGT  TTTTTGTTT
                                  C    T  G_
GAM166  STAT6    5'  ATTTTTCTTTTTGGTGGTGGTG 13448       TC        TAAG
                                CACCAC  CCAAGAAGAA
                                ||||||  ||||||||||
                                GTGGTG  GGTTTTTCTT
                                   GT        TTTAT
GAM166  TCF8     3'  CTTGTTTTTTTAAGAGTGTGTG 48429     _    CCA
                                CAC CACTC   AGAAGAATAAG
                                ||| |||||   ||||||||||
                                GTG GTGAG   TTTTTTTGTTC
                                  T    AA_
GAM166  B3GNT7   3'  TTGTTCTTGGCTGGTGGGTG   71685     A    C_     G
                                TAC CCACT  CCAAGAA AA
                                ||| |||||  ||||||| ||
                                GTG GGTGG  GGTTCTT TT
                                  _    TC      G
GAM166  BCDO     3'  TTATTCTTTCTGTGGGTG    34287      C  AG
                                CACTC CA  AAGAATAA
                                ||||| ||  ||||||||
                                GTGGG GT  TTCTTATT
                                   T  CT
GAM166  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
             A                    TACAC       AGAAGAATAAG
                                |||||       ||||||||||
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                              ATGTG      TCTTCTTATTC
                                 TACTCCC_
GAM166  EPN2    3'  TTTATTTTTCTTTGACTCGTGT 31046      CAC  CC
            G                   TACAC   TC  AAGAAGAATAAG
                                |||||   ||  ||||||||||||
                                GTGTG   AG  TTCTTTTTATTT
                                   CTC  T_
GAM166  FLJ13855  3'  GGGTATTTTTCTTGGGGGTGGA 43853     A             AG
            GTA                   TAC CCACTCCCAAGAAGAATA
                                  ||| ||||||||||||||||||
                                  ATG GGTGGGGGGTTCTTTTTAT
                                    A              GGGA
GAM166  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                  TACACCACT       GAATAAG
                                  |||||||||       |||||||
                                  ATGTGGTGA       TTTATTC
                                       AGACG___
GAM166  FLJ32865  3'  TTTGTTGGGGGTGGGGTG    58824     A        G
                                  TAC CCACTCCCAA AAG
                                  ||| |||||||||| |||
                                  GTG GGTGGGGGTT TTT
                                    G         G
GAM166  GRP3    3'  TTGTTCTTCTTGGTGTG     31742     TC
                                  CAC  CCAAGAAGAATAA
                                  |||  ||||||||||||
                                  GTG  GGTTCTTCTTGTT
                                    T_
GAM166  HAND1    3'  TTTGTTCTTCGAATCGTGGTG  17880       TCCCAA
                                  CACCAC     GAAGAATAAG
                                  ||||||     ||||||||||
                                  GTGGTG     CTTCTTGTTT
                                     CTAAG_
GAM166  KIAA0562  3'  TTTGTTTTGCGGGGGTGGTG   28834          AAGA
                                  CACCACTCCC    AGAATAAG
                                  ||||||||||    ||||||||
                                  GTGGTGGGGG    TTTTGTTT
                                        CG__
GAM166  KIAA0871  5'  TTTATTTTTTTGGTGTGTGTGT 31023       _  TC        ATAAG
            G                   TACAC CAC  CCAAGAAGA
                                |||||  |||  |||||||||
                                GTGTG GTG  GGTTTTTTT
                                   T   T_       ATTT
GAM166  KIAA0970  3'  TTTGTTTTTTTTGTTAGGGTG  30622      A  CC
                                  CACC CT  CAAGAAGAATAAG
                                  ||||  ||  ||||||||||||
                                  GTGG GA  GTTTTTTTTGTTT
                                    _  TT
GAM166  KIAA1240  3'  TTTATTTTTAGGGAGTGGGTA  67297     A       AAG
                                  TAC CCACTCCC   AAGAATAAG
                                  ||| ||||||||   |||||||||
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                                ATG GGTGAGGG   TTTTTATTT
                                  _      A__
GAM166  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68742            _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                      G
GAM166  KIAA1750  3'  TTTATTTTTTTGTTCTAGGTGT 68815       ACTCCCA
          G                    TACACC      AGAAGAATAAG
                               ||||||      ||||||||||
                               GTGTGG      TTTTTTTATTT
                                  ATCTTG_
GAM166  MAP2K3    3'  CTTGTTTTTCTTGCATGGT    59686     CTCC
                               ACCA    CAAGAAGAATAAG
                               ||||    ||||||||||||
                               TGGT    GTTCTTTTTGTTC
                                 AC__
GAM166  MLN64     3'  CTTGTTGGGGAGTGGGTG     96062     A      _ G
                               TAC CCACTCCC AA AAG
                               ||| |||||||| || |||
                               GTG GGTGAGGG TT TTC
                                 _      G  G
GAM166  NY-REN-41 3'  TTTGTTTTTCTATCCTGGTGG  55564      CCCA_
                               CCACT     AGAAGAATAAG
                               |||||     ||||||||||
                               GGTGG     TCTTTTTGTTT
                                  TCCTA
GAM166  PRO1489   5'  TTTGTTTTTCGTGTGTGTGTG  38334      _  TCCCAA
                               TACAC CAC     GAAGAATAAG
                               ||||| |||     ||||||||||
                               GTGTG GTG     CTTTTTGTTT
                                  T   TG____
GAM166  SEC15L    3'  TTTGTTCTACTTGGGTGGT    72731     CT     A
                               ACCA  CCCAAG AGAATAAG
                               ||||  |||||| ||||||||
                               TGGT  GGGTTC TCTTGTTT
                                 __      A
GAM166  SHAPY     3'  TTTGTTCTTTTTGGAACTGTG  57915     TC__
                               CAC    CCAAGAAGAATAAG
                               |||    ||||||||||||||
                               GTG    GGTTTTTCTTGTTT
                                 TCAA
GAM166  STAM2     3'  TGTTTTTCTTCCTGCAATGTGG 20709        TCC_  A     TAAG
          TGTG                    TACACCAC    CA GAAGAA
                                  ||||||||    || ||||||
                                  GTGTGGTG    GT CTTCTT
                                       TAAC  C     TTTGTT
GAM166  TUBGCP3   3'  TTTATTTTTTTTTAGTGTTGTA 21982      C    CCC
                               TACA CACT   AAGAAGAATAAG
                               |||| ||||   ||||||||||||
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                                ATGT GTGA   TTTTTTTTATTT
                                  T   T__
GAM166  ZNF220    3'  CTTGTTTTTTTTACCACCTGGTG 23157      CTCCCA
                                CACCA     AGAAGAATAAG
                                |||||     ||||||||||
                                GTGGT     TTTTTTTGTTC
                                   CCACCA
GAM166  LOC121219 5'  TTGTTCTATGGGTGGGTG    74493     ACT   AGA
                                CACC   CCCA   AGAATAA
                                ||||   ||||   |||||||
                                GTGG   GGGT   TCTTGTT
                                  GT_   A__
GAM166  LOC143146 3'  TTTGTTGGAGGTGGTGTA    60767       TC   G
                                TACACCAC  CCAA AAG
                                ||||||||  |||| |||
                                ATGTGGTG  GGTT TTT
                                     GA   G
GAM166  LOC146445 3'  TTGTTCTTTGTGTGGTTG    84687   C    TCCCAA
                                A ACCAC     GAAGAATAA
                                | |||||     |||||||||
                                G TGGTG     TTTCTTGTT
                                 T    TG____
GAM166  LOC150174 3'  TTTATTTTTTTTTACAATGGTG 80444      CTCCC
                                CACCA    AAGAAGAATAAG
                                |||||    ||||||||||||
                                GTGGT    TTTTTTTTATTT
                                   AACAT
GAM166  LOC150213 3'  TTTATTTTTTTTACAATGGTG  75363      CTCCC
                                CACCA    AAGAAGAATAAG
                                |||||    ||||||||||||
                                GTGGT    TTTTTTTTATTT
                                   AACA_
GAM166  LOC150236 3'  TTTATTTTTTTTACAATGGTG  80505      CTCCC
                                CACCA    AAGAAGAATAAG
                                |||||    ||||||||||||
                                GTGGT    TTTTTTTTATTT
                                   AACA_
GAM166  LOC154084 3'  CTTGTTTTTTTTAGTAGGTGTG  87378      _  CCCA
                                TACACC ACT   AGAAGAATAAG
                                |||||| |||   ||||||||||
                                GTGTGG TGA   TTTTTTTGTTC
                                   A  ____
GAM166  LOC170261 3'  TTTATTCTTTGTGAAAGTGGT  83472      CC  A
                                ACCACT  CA GAAGAATAAG
                                ||||||  || ||||||||||
                                TGGTGA  GT TTTCTTATTT
                                   AA  G
GAM166  LOC199692 3'  CTTGTTCTTCTGCTGTAGTGTG 59926      C  TCCCA
                                TACAC AC    AGAAGAATAAG
                                ||||| ||    ||||||||||
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                                GTGTG TG    TCTTCTTGTTC
                                   A  TCG__
GAM166  LOC203414 3'  CTTGTCAACTGGGGGTGATGTG 90913     C      A AA  A
                                TACA CACTCCCA G  GA TAAG
                                |||| |||||||| |  || ||||
                                GTGT GTGGGGGT C  CT GTTC
                                   A       _ AA  _
GAM166  LOC222256 3'  TTTTTCTTGTGGTGT      95915       TCCC
                                ACACCAC    AAGAAGAA
                                |||||||    ||||||||
                                TGTGGTG    TTCTTTTT
                                      ____
GAM166  LOC257051 3'  TTTATTCTTTGTGAAAGTGGT  98054       CC  A
                                ACCACT  CA GAAGAATAAG
                                ||||||  || ||||||||||
                                TGGTGA  GT TTTCTTATTT
                                   AA  G
GAM166  LOC92303  3'  TTATTTTTTTTGAGGTGG    69400      CC
                                CCACT  CAAGAAGAATAA
                                |||||  ||||||||||||
                                GGTGG  GTTTTTTTTATT
                                   A_
GAM167  CDH12    3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                      AA___   AC
GAM167  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM167  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT    98090       T    AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT     TTATTC
                                   _    GTCA_
GAM167  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
           A                     TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM167  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                      AGACG___
GAM167  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
           TA                    TACA   TCC    GAAGAATAAG
                                ||||   |||   ||||||||||
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                              ATGT   AGG   TTTCTTATTC
                                AAA_  ATTG
GAM167  KIAA1719 3' TCTGTCTTGGGAGTGGTGTA  68742           _
                              TACACCACTCCCAAGA AGA
                              |||||||||||||||| |||
                              ATGTGGTGAGGGTTCT TCT
                                       G
GAM167  KIAA1853 3' TTTTTCTTGGAAGCAGTG    69929    CA  C
                              CAC  CT CCAAGAAGAA
                              |||  || ||||||||||
                              GTG  GA GGTTCTTTTT
                                AC  A
GAM167  KIAA1877 3' CTTATTCTTCTGCCATGAGT  66748     CCA__
                              ACTC    AGAAGAATAAG
                              ||||    ||||||||||
                              TGAG    TCTTCTTATTC
                                TACCG
GAM167  KIAA1906 3' CTTATTCTTCTTGACTTTTGG 73571    CTCC_
                              CCA    CAAGAAGAATAAG
                              |||    ||||||||||||
                              GGT    GTTCTTCTTATTC
                                TTTCA
GAM167  OSBPL11  3' CTTAATTTCCCAAGAGTGGTG 43206       CCAA   AA
                              CACCACTC   GAAG  TAAG
                              ||||||||   ||||  ||||
                              GTGGTGAG   CTTT  ATTC
                                   AACC   A_
GAM167  YME1L1   3' TCATTCTTGATGTGGTGTA   58438       TCC    _
                              TACACCAC   CAAGAA GA
                              ||||||||   ||||||  ||
                              ATGTGGTG   GTTCTT CT
                                   TA_    A
GAM167  ZNF262   3' CTTATTTTGTTTGGGAGT    18723        A
                              ACTCCCAAG AGAATAAG
                              ||||||||| ||||||||
                              TGAGGGTTT TTTTATTC
                                   G
GAM167  LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_   AAGA
                              TACACCAC   CCAAG   ATA
                              ||||||||   |||||   |||
                              ATGTGGTG   GGTTC   TGT
                                   CAA    GG__
GAM168  AIRE     3' TGGGAGCCTGAGGCATGAGAA  7248     C     AC
                              TTC CATGCC  CAGGCTCCTG
                              ||| ||||||  ||||||||||
                              AAG GTACGG  GTCCGAGGGT
                                A     A_
GAM168  MEF2A    3' GCAAGGGGTGCATGGGAA    20001       CACCAG    __
                              TTCCCATGC     GCTCCT  GC
                              |||||||||     ||||||  ||
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                                AAGGGTACG     TGGGGA  CG
                                       _______     AA
GAM168  SLC10A2  3'  TGCAGGAGTAAGTAGTATAAGA 6594      CC    C  CAG
              A                    TTC  ATGC AC   GCTCCTGCA
                                   |||  |||| ||   |||||||||
                                   AAG  TATG TG   TGAGGACGT
                                     AA    A  AA_
GAM168  ACY-3    5'  AGTCCTGGTGGCCCGGGAA   55585      AT       _
                                   TTCCC  GCCACCAGG CT
                                   |||||  ||||||||| ||
                                   AAGGG  CGGTGGTCC GA
                                      CC        T
GAM168  DKFZP434C1715 3'  AGCCTGGACAACATGGGAA   87347        CCA_
                                   TTCCCATG    CCAGGCT
                                   ||||||||    |||||||
                                   AAGGGTAC    GGTCCGA
                                        AACA
GAM168  FLJ10898  5'  TGCCAAACCTGCAACATGGGAA 60142        CCAC    CTCCT
                                   TTCCCATG    CAGG    GCA
                                   ||||||||    ||||    |||
                                   AAGGGTAC    GTCC    CGT
                                        AAC_   AAAC_
GAM168  FLJ23598  5'  TGCAGGAGCCTAGCAGGAA   45865     CA   CACC
                                   TTCC  TGC    AGGCTCCTGCA
                                   ||||  |||    ||||||||||
                                   AAGG  ACG    TCCGAGGACGT
                                     __   A___
GAM168  G0S2     3'  CAGGAGCCTGACTCCGCTGGGA 32305      T  CAC__
                                   TCCCA GC     CAGGCTCCTG
                                   |||||  ||    ||||||||||
                                   AGGGT CG     GTCCGAGGAC
                                      _  CCTCA
GAM168  KIAA1171  3'  TGCAGGAGGAAGGACCGGGAA  89347      ATG  ACCAGG
                                   TTCCC   CC     CTCCTGCA
                                   |||||   ||     ||||||||
                                   AAGGG   GG     GAGGACGT
                                      CCA  AAG___
GAM168  KIAA1393  3'  CAAAAGCCTTGTGGTATGG    72569         C    CC
                                   CCATGCCAC AGGCT  TG
                                   ||||||||| |||||  ||
                                   GGTATGGTG TCCGA  AC
                                        T     AA
GAM168  MGC10772  5'  GCCCGCCGGCGCCATGGGAA   48291        CCA  A   TCCT
                                   TTCCCATG   CC GGC    GC
                                   ||||||||   || |||    ||
                                   AAGGGTAC   GG CCG    CG
                                        CGC  _   CC__
GAM168  My015    3'  TGCAGTCCCAGCAACATGGGAG 67237        CCACCA  CTC
                                   TTCCCATG     GG   CTGCA
                                   ||||||||     ||   |||||
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                                GAGGGTAC     CC   GACGT
                                    AACGA_  CT_
GAM168  OS4      3'  GCTTTGTGCTAAAAGCATGGGA 20392         _______  C
              A                   TTCCCATGC     CAC AGGC
                                  |||||||||     ||| ||||
                                  AAGGGTACG     GTG TTCG
                                       AAAATC   T
GAM168  PRKWNK2  5'  GCAGGAGCCCGGCCCGGA    92197     CAT   ACCA
                                  TCC   GCC    GGCTCCTGC
                                  |||   |||    |||||||||
                                  AGG   CGG    CCGAGGACG
                                    CC_   C___
GAM168  RASSF2   3'  GGCCTGGTGGCCAGGAA     29104      CAT
                                  TTCC   GCCACCAGGCT
                                  ||||   ||||||||||
                                  AAGG   CGGTGGTCCGG
                                    AC_
GAM168  WFDC3    3'  GCTGACCAGAGCATGGGAA    98703         CACCA  C  CT
                                  TTCCCATGC     GG TC  GC
                                  |||||||||     || ||  ||
                                  AAGGGTACG     CC AG  CG
                                       AGA__  _  T_
GAM168  LOC123872 5'  GCAGGAGCCCGGCGTGGAGGA  74709     _      ACCA
                                  TTC CCATGCC    GGCTCCTGC
                                  ||| |||||||    |||||||||
                                  AGG GGTGCGG    CCGAGGACG
                                    A      C___
GAM168  LOC142779 3'  CAGAGAGAAATGTGCATGGGAA 76902         C  CAGG  _
                                  TTCCCATGC AC    CTC CTG
                                  ||||||||| ||    ||| |||
                                  AAGGGTACG TG    GAG GAC
                                       _ TAAA   A
GAM168  LOC144262 5'  TGCAGAAGTACCTACCACATGG 77261         CCACCAG_  C
              GAA                    TTCCCATG       GCT CTGCA
                                     ||||||||       ||| |||||
                                     AAGGGTAC       TGA GACGT
                                          ACCATCCA   A
GAM168  LOC145758 5'  GGAGCCTGATGGATAGGAA    84486      C  G   C
                                  TTCC AT CCA CAGGCTCC
                                  |||| || ||| ||||||||
                                  AAGG TA GGT GTCCGAGG
                                    A  _   A
GAM168  LOC148014 3'  TGCAGGAGGCCCGCAGCCGGGA 79315       AT  CACCA  _
              A                    TTCCC  GC     GGC TCCTGCA
                                   |||||  ||     ||| |||||||
                                   AAGGG  CG     CCG AGGACGT
                                     C_  ACGC_   G
GAM168  LOC149501 3'  TGCAAGAGCCTGGCTGGGAA   75802       T   CCA    C
                                  TTCCCA GCCA   GGCTC TGCA
                                  |||||| ||||   ||||| ||||
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                                AAGGGT CGGT   CCGAG ACGT
                                  _   ____     A
GAM168   LOC150343 5'  CAGGAGCCTGGGGCAGGG    80490     A    A
                                CCC TGCC CCAGGCTCCTG
                                ||| |||| ||||||||||
                                GGG ACGG GGTCCGAGGAC
                                  _   _
GAM168   LOC150397 3'  CAGGAGCCTGAGTGAAGGA    80656     CATGC  _
                                TCC    CAC CAGGCTCCTG
                                |||    ||| ||||||||||
                                AGG    GTG GTCCGAGGAC
                                  AA___   A
GAM168   LOC152267 3'  CAAAAGCCTTGTGGTATGG    61034         C    CC
                                CCATGCCAC AGGCT  TG
                                |||||||| |||||  ||
                                GGTATGGTG TCCGA  AC
                                      T    AA
GAM168   LOC197125 3'  CAGAGCTTGGCATCATGGGAA  89241         CCA       C
                                TTCCCATG   CCAGGCTC TG
                                ||||||||   |||||||| ||
                                AAGGGTAC   GGTTCGAG AC
                                     TAC       _
GAM168   LOC200010 3'  TGCAGGAGGTGGAGCGGCAGAG 91528     CCA    A__   GG
           AA                    TTC   TGCC   CCA  CTCCTGCA
                                |||   ||||   |||  ||||||||
                                AAG   ACGG   GGT  GAGGACGT
                                  AG_   CGA   G_
GAM168   LOC203276 3'  TGCAGGAACCCTGGCCATGGGA 92136         CCA    C_
           G                     TTCCCATG   CCAGG  TCCTGCA
                                ||||||||   |||||  |||||||
                                GAGGGTAC   GGTCC  AGGACGT
                                     C__     CA
GAM168   LOC203305 3'  TGCAGGAACCCTGGCCATGGGA 92189         CCA    C_
           G                     TTCCCATG   CCAGG  TCCTGCA
                                ||||||||   |||||  |||||||
                                GAGGGTAC   GGTCC  AGGACGT
                                     C__     CA
GAM168   LOC203595 5'  CAGGTGGTGACCATGGGAA    92394         C_    GGCT
                                TTCCCATG  CACCA    CCTG
                                ||||||||  |||||    ||||
                                AAGGGTAC  GTGGT    GGAC
                                     CA    _____
GAM168   LOC220370 3'  AGGAAGCCTGGTGACACAGG   94392     CA  C       _
                                CC  TG CACCAGGCT CCT
                                ||  || ||||||||| |||
                                GG  AC GTGGTCCGA GGA
                                 AC  A        A
GAM168   LOC254243 3'  TGCAGGAACCCTGGCCATGGGA 99275         CCA    C_
           G                     TTCCCATG   CCAGG  TCCTGCA
                                ||||||||   |||||  |||||||
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                                GAGGGTAC  GGTCC  AGGACGT
                                    C__    CA
GAM168  LOC51146  5'  TGCAGGAGCAGGCTGGCACAGA 32930    CCA   _ AG
          G                      TTC  TGCCA CC  GCTCCTGCA
                                 |||  ||||| ||  |||||||||
                                 GAG  ACGGT GG  CGAGGACGT
                                   AC_   C  A_
GAM168  LOC90038  3'  TGCAGGAACCCTGGCCATGGGA 61819       CCA   C_
          G                      TTCCCATG  CCAGG  TCCTGCA
                                 ||||||||  |||||  |||||||
                                 GAGGGTAC  GGTCC  AGGACGT
                                    C__    CA
GAM168  LOC90538  3'  AGGCCCTGGTGGCATAGG   63894   C       CT
                                 CC ATGCCACCAGG  CCT
                                 || ||||||||||  |||
                                 GG TACGGTGGTCC  GGA
                                   A        C_
GAM168  LOC91750  3'  TGGGGGCCTGAGGCACGAGAA  67660    CCA   AC
                                 TTC  TGCC  CAGGCTCCTG
                                 |||  ||||  ||||||||||
                                 AAG  ACGG  GTCCGGGGGT
                                   AGC   A_
GAM169  PROK1    3'  CACCAACCTGCTGGCTTTAGAA 51567     TCAC  G    AGC
                                 TTCT   GG CAGCA  TGGTG
                                 ||||   || |||||  |||||
                                 AAGA   TC GTCGT  ACCAC
                                   TT__  G   CCA
GAM169  HSA404617 5'  CACCAGCTCGCCCTTCTGAGAA 73089     CAC_   AGCA
                                 TTCTT   GGGC   AGCTGGTG
                                 |||||   ||||   ||||||||
                                 AAGAG   CCCG   TCGACCAC
                                    TCTT   C___
GAM169  KIAA0431  3'  CACCAGCTTGGGCAACATAAGA 31546     CACGG  AG
          A                      TTCTT    GC  CAAGCTGGTG
                                 |||||    ||  ||||||||||
                                 AAGAA    CG  GTTCGACCAC
                                    TACAA  G_
GAM169  PAK6     5'  ACCAGCCTGCAGTGGAGAA   39806       GG   CAA
                                 TTCTTCAC  GCAG   GCTGGT
                                 ||||||||  ||||   ||||||
                                 AAGAGGTG  CGTC   CGACCA
                                    A_    ___
GAM169  LOC90670  3'  TTTGCTGCCCTGAAGAA    64486       C
                                 TTCTTCA GGGCAGCAAG
                                 ||||||| ||||||||||
                                 AAGAAGT CCCGTCGTTT
                                    _
GAM170  ABCA1    3'  GAAAGGACCTCTTCTGAA    19735          TGG
                                 TTCAGAAGAGGTT   CTTTC
                                 ||||||||||||   |||||
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                                AAGTCTTCTCCAG   GAAAG
                                        ___
GAM170  ABCE1    3'  AAAGCCAGTTGGGTTCTAAATT 60260     C   GAGGT
                                AGTT AGAA    TTGGCTTT
                                |||| ||||    ||||||||
                                TTAA TCTT    GACCGAAA
                                  A   GGGTT
GAM170  ARHGDIA  3'  GGAAAGCCAAATTGCCAAAACT 16296     CAGAAGA
                                AGTT      GGTTTGGCTTTCC
                                ||||      ||||||||||||
                                TCAA      TTAAACCGAAAGG
                                  AACCG__
GAM170  ESR1     3'  GAAAGCCCTCCCTCCCTGAACT 5515        AA   TTT
                                AGTTCAG  GAGG   GGCTTTC
                                |||||||  ||||   |||||||
                                TCAAGTC  CTCC   CCGAAAG
                                    C_   CTC
GAM170  GJA5     3'  GGAAAGACGTGTCCCTTCTGAA 19165         A  TT_  G
            CT                    AGTTCAGAAG GG   TG CTTTCC
                                |||||||||| ||   || ||||||
                                TCAAGTCTTC CC   GC GAAAGG
                                      _  TGT  A
GAM170  HRH1     3'  GAAAACTTCTCTTCTGAGC    7820           TTT  C
                                GTTCAGAAGAGG   GG TTTC
                                ||||||||||||   || ||||
                                CGAGTCTTCTCT   TC AAAG
                                      ___  A
GAM170  NPEPPS   3'  AAAGCCAGCTCTTGAAC     21955      GA   GT
                                GTTCA  AGAG  TTGGCTTT
                                |||||  ||||  ||||||||
                                CAAGT  TCTC  GACCGAAA
                                  __   __
GAM170  PCDHA9   3'  GAAAGAAACTTCCCCTAAACT  26619     C  AA     GG
                                AGTT AG  GAGGTTT  CTTTC
                                |||| ||  |||||||  |||||
                                TCAA TC  CTTCAAA  GAAAG
                                  A  CC      __
GAM170  SIRT3    3'  AAAGCTTTCTTCTGACT     25291     T      GTTT
                                AGT CAGAAGAG    GGCTTT
                                ||| ||||||||    ||||||
                                TCA GTCTTCTT    TCGAAA
                                  _      _____
GAM170  SLC1A4   3'  GGAAAGCCCAGCTCTCTTTAAA 13174     CA     _   T
            C                     GTT  GAAGAG GTT GGCTTTCC
                                |||  |||||| ||| ||||||||
                                CAA  TTTCTC CGA CCGAAAGG
                                  A_     T   C
GAM170  SLC9A6   3'  GAAAAATACCCTTCTGAAC   22062         A   TTGGC
                                GTTCAGAAG GGT    TTTC
                                |||||||| |||    ||||
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                                CAAGTCTTC CCA     AAAG
                                     _   TAA__
GAM170  TM4SF6   3'  GAAAATTCACCCCTCTGAACT  13796         A A   TTGGC
                                AGTTCAGA G GGT     TTTC
                                |||||||| | |||     ||||
                                TCAAGTCT C CCA     AAAG
                                    _ C   CTTA_
GAM170  TTC1     3'  AGCAAAAGCCTCTCCTGAAC   13875       A       G_
                                GTTCAG AGAGGTTT  GCT
                                |||||| ||||||||  |||
                                CAAGTC TCTCCGAA  CGA
                                   C       AA
GAM170  Cyt19    3'  GAAAAACATCTTCCTTCTGATC 73312    T      AG TT  GC
           T                     AG TCAGAAG  G  TG  TTTC
                                || |||||||  |  ||  ||||
                                TC AGTCTTC  T  AC  AAAG
                                 T      CT CT  AA
GAM170  DDX21    5'  GAAAGCAGAGCCTTCTGAA   17571       AG     G
                                TTCAGA  AGGTTT GCTTTC
                                ||||||  |||||| ||||||
                                AAGTCT  TCCGAG CGAAAG
                                   __      A
GAM170  FLJ20309 3'  AAAACCAAGCCTCCTGCACT   35405     T   AA       C
                                AGT CAG  GAGGTTTGG TTT
                                ||| |||  |||||||||| |||
                                TCA GTC  CTCCGAACC AAA
                                  C  __        A
GAM170  FLJ21918 3'  GGAAAGCCAGTTGCCCTGAAC  46860       AAGA  __
                                GTTCAG   GGT  TTGGCTTTCC
                                ||||||   |||  ||||||||||
                                CAAGTC   CCG  GACCGAAAGG
                                   _____  TT
GAM170  KIAA0022 3'  AAAGTAATCCCTCTTCTGAAT  30272          TTTG
                                GTTCAGAAGAGG   GCTTT
                                ||||||||||||   |||||
                                TAAGTCTTCTCC   TGAAA
                                      CTAA
GAM170  KIAA0247 3'  AAAGCCTTCCTTCTCCTGAA   29062      A    TTT
                                TTCAG AGAGG   GGCTTT
                                ||||| |||||   ||||||
                                AAGTC TCTTC   CCGAAA
                                   C    CTT
GAM170  KIAA0515 3'  GAAAGCCAGCTCTCTTCTGAA  64549         GT
                                TTCAGAAGAG  TTGGCTTTC
                                ||||||||||  |||||||||
                                AAGTCTTCTC  GACCGAAAG
                                      TC
GAM170  LALP1    3'  AAGGTTAGAACCCCTTCTAAAT 40137     C    A  _
                                GTT AGAAG GGT TTGGCTTT
                                ||| ||||| ||| ||||||||
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                                TAA TCTTC CCA GATTGGAA
                                  A    C  A
GAM170  MGC4251   3'  GAAAAATTCCTCTTTGAAC   51467       A   TTTGGC
                                GTTCAGA GAGG     TTTC
                                ||||||| ||||     ||||
                                CAAGTTT CTCC     AAAG
                                   _   TTAA__
GAM170  PRRG1     3'  AAAGCCAAATGCTTAAACT   8146      CAG  AG
                                AGTT  AAG  GTTTGGCTTT
                                ||||  |||  ||||||||||
                                TCAA  TTC  TAAACCGAAA
                                  A__  G_
GAM170  SLAM      3'  GAAAAACCAAAATGAACACTGA 13169       AAGAGG_    C_
             ACT                  AGTTCAG      TTTGG  TTTC
                                |||||||      |||||  ||||
                                TCAAGTC      AAACC  AAAG
                                   ACAAGTA     AA
GAM170  SLC26A9   3'  GAAAAGAACACTCTTCTGGAC  54714          _   GGC
                                GTTCAGAAGAG GTTT   TTTC
                                |||||||||||| ||||   ||||
                                CAGGTCTTCTC CAAG   AAAG
                                      A    A__
GAM170  SLC26A9   3'  GAAAAGAACACTCTTCTGGAC  57007          _   GGC
                                GTTCAGAAGAG GTTT   TTTC
                                |||||||||||| ||||   ||||
                                CAGGTCTTCTC CAAG   AAAG
                                      A    A__
GAM170  ust3      5'  GAAAACATTTTCCCTCTTTGAA 94854       A    TT___  GC
             C                   GTTCAGA GAGG     TG  TTTC
                                ||||||| ||||     ||  ||||
                                CAAGTTT CTCC     AC  AAAG
                                   _   CTTTT  A_
GAM170  WDR5B     5'  GAAAGCCAAAGTACTGGACT   39346       AAGAGG
                                AGTTCAG      TTTGGCTTTC
                                |||||||      ||||||||||
                                TCAGGTC      AAACCGAAAG
                                   ATG___
GAM170  ZDHHC3    3'  GGAAAGCCAGGAGGGCCCTGAC 33932     T   AAGAGG
             CT                   AG TCAG     TTTGGCTTTCC
                                || ||||     ||||||||||
                                TC AGTC     GGACCGAAAGG
                                 C   CCGGGA
GAM170  LOC120103 3'  GAAAACCTAATCTTCTGACT   74459     T      GGTTT  C
                                AGT CAGAAGA     GG TTTC
                                ||| |||||||     || ||||
                                TCA GTCTTCT     CC AAAG
                                  _      AAT__  A
GAM170  LOC130612 3'  GAAAGCCCCCTCCCAAGCT   75467      CAGAA    TTT
                                AGTT    GAGG   GGCTTTC
                                ||||    ||||   |||||||
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                                TCGA    CTCC   CCGAAAG
                                  ACC__   C__
GAM170  LOC145608 5'  AAAGCAAACCTCCCACAAACT  84372     CAGAA      G
                                AGTT    GAGGTTTG CTTT
                                ||||    |||||||| ||||
                                TCAA    CTCCAAAC GAAA
                                  ACACC      _
GAM170  LOC148930 3'  GAAAAACCAAAGTTTTCTGAA  79844       GG    C_
                                TTCAGAAGA  TTTGG  TTTC
                                |||||||||  |||||  ||||
                                AAGTCTTTT  AAACC  AAAG
                                     G_    AA
GAM170  LOC152275 3'  GAAAAACCAGTTCTCTTCTGA  86798       GT    C_
                                TCAGAAGAG  TTGG  TTTC
                                |||||||||  ||||  ||||
                                AGTCTTCTC  GACC  AAAG
                                     TT    AA
GAM170  LOC153387 5'  AAAGCCAAAGAAATATGAACT  87221      GAAGAGG
                                AGTTCA      TTTGGCTTT
                                ||||||      |||||||||
                                TCAAGT      AAACCGAAA
                                   ATAAAG_
GAM170  LOC158364 5'  GGAAAACCAAACCTAGTGATAC 82755    _  GAAG      C
          T                      AGT TCA    AGGTTTGG TTTCC
                                ||| |||    |||||||| |||||
                                TCA AGT    TCCAAACC AAAGG
                                  T  GA__       A
GAM170  LOC221025 3'  GAAAATGCTTTCCTGAAC    94786      AA    TTGGC
                                GTTCAG  GAGGT    TTTC
                                ||||||  |||||    ||||
                                CAAGTC  TTTCG    AAAG
                                   C_    TA___
GAM170  LOC221405 3'  AAAGACACTTCTTCCAAAC   95504    CA      TTGG
                                GTT  GAAGAGGT    CTTT
                                |||  ||||||||   ||||
                                CAA  CTTCTTCA    GAAA
                                  AC       CA__
GAM170  LOC256880 5'  GAAAACCAGCTTCTGGAC    98887       AGGT    C
                                GTTCAGAAG    TTGG TTTC
                                |||||||||   |||| ||||
                                CAGGTCTTC    GACC AAAG
                                     ____    A
GAM171  HAL     5'  GCCACTCCTGCATAAAGCTC   10903         TGAAAA
                                GAGCTTTATGC     GGTGGC
                                ||||||||||      ||||||
                                CTCGAAATACG     TCACCG
                                      TCC___
GAM171  HMGN2    3'  GGCCACCTTGGCACAAAAGC   19809      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
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                                CGAAA AC AC  TTCCACCGG
                                  _ _ GG
GAM171  NMI     5' GGCCACCTCCTCAGGAAG    17436     ATG   AA
                                CTTT  CTGA  AGGTGGCC
                                ||||  ||||  ||||||||
                                GAAG  GACT  TCCACCGG
                                  ___   CC
GAM171  PACE    3' GGCCACCTCTCCAAGGGCTT  11944       A  CT  AAA
                                GAGCTTT TG  GA  GGTGGCC
                                ||||||| ||  ||  |||||||
                                TTCGGGA AC  CT  CCACCGG
                                    _ CT  ___
GAM171  PYCR1   3' CCACCTTCCTCTAGAGCTC   70639       TGCT  A_
                                GAGCTTTA   GA  AAGGTGG
                                ||||||||   ||  |||||||
                                CTCGAGAT   CT  TTCCACC
                                    _____ CC
GAM171  SDC1    3' GGCCACCTCCCCAGCATTCCAG 12991    TT_    AAA
          C                      GCT   ATGCTG   AGGTGGCC
                                |||   ||||||   ||||||||
                                CGA   TACGAC   TCCACCGG
                                  CCT     CCC
GAM171  FLJ11560 5' GCCCAGGCCCAGCATAAAG   48008        AAAA  ___
                                CTTTATGCTG   GGT   GGC
                                ||||||||||   |||   |||
                                GAAATACGAC   CCG   CCG
                                     _____  GAC
GAM171  KIAA0446 5' CCACCTTTTGAAGAGCTC    69446      ATGCTG
                                GAGCTTT     AAAAGGTGG
                                |||||||     |||||||||
                                CTCGAGA     TTTTCCACC
                                   AG_____
GAM171  KIAA0971 3' GTTGTTCTCAGCATAAAGT   30677         AAA  TG
                                GCTTTATGCTGA   GG  GC
                                ||||||||||||   ||  ||
                                TGAAATACGACT   TT  TG
                                      C__  GT
GAM171  KIAA1393 3' GGCCACCTTGGCACAAAAGC  72574      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _ GG
GAM171  KIAA1656 3' GGCCACCTCCTCCTAGAAGCC 66377   A    ATGCT  AA
                                G GCTTT    GA  AGGTGGCC
                                | |||||    ||  ||||||||
                                C CGAAG    CT  TCCACCGG
                                 _    ATC__  CC
GAM171  KIAA1884 3' GCCACCTTCATCTACCAAGGCT 73728       ATGCT  A_
          C                      GAGCTTT    GA  AAGGTGGC
                                |||||||    ||  ||||||||
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                                CTCGGAA    CT  TTCCACCG
                                    CCAT_  AC
GAM171  PP3501    3'  GGCCACCGTTGACAGCATAAAG 41683          AAAA_
                                CTTTATGCTG    GGTGGCC
                                ||||||||||    |||||||
                                GAAATACGAC    CCACCGG
                                     AGTTG
GAM171  SDCCAG3   3'  GGTGTTCTCAGCATGAAGCTC  22803            AAA  TG
                                GAGCTTTATGCTGA   GG  GCC
                                ||||||||||||||   ||  |||
                                CTCGAAGTACGACT   CT  TGG
                                       ___  TG
GAM171  SP140     3'  GGCCACCTCCATGCAGAAGC   24327      A   TGAAA
                                GCTTT TGC    AGGTGGCC
                                ||||| |||    ||||||||
                                CGAAG ACG    TCCACCGG
                                  _  TACC_
GAM171  LOC148760 3'  GGCCACCTTCTCCAACAAGCTC 85364       TA  CT  A
                                GAGCTT  TG  GA AAGGTGGCC
                                ||||||  ||  || |||||||||
                                CTCGAA  AC  CT TTCCACCGG
                                   CA  __  C
GAM171  LOC150170 5'  ACCTGTTTCACATAAAGC    80414        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                    _    G
GAM171  LOC150175 5'  ACCTGTTTCACATAAAGC    80453        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                    _    G
GAM171  LOC150215 5'  ACCTGTTTCACATAAAGC    80456        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                    _    G
GAM171  LOC150218 5'  ACCTGTTTCACATAAAGC    80525        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                    _    G
GAM171  LOC152065 3'  GGCCACCTTCTCCTTGGCAGGC 86737       TTA   ___  A
          TC                      GAGCT   TGCT   GA AAGGTGGCC
                                |||||   ||||   || |||||||||
                                CTCGG   ACGG   CT TTCCACCGG
                                   ___    TTC  C
GAM171  LOC152267 3'  GGCCACCTTGGCACAAAAGC   61036      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
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                                CGAAA AC AC  TTCCACCGG
                                  _ _ GG
GAM171  LOC158292 5'  CCTCTGGACCCAGCATAAGGCT 88046           AAAA_ T
          C                      GAGCTTTATGCTG    GG GG
                                 ||||||||||||    || ||
                                 CTCGGAATACGAC    TC CC
                                       CCAGG  T
GAM171  LOC219997 3'  GCCACCTCTTCAGCCTC    93256    CTTTAT    A
                                 GAG    GCTGAA AGGTGGC
                                 |||    |||||| |||||||
                                 CTC    CGACTT TCCACCG
                                  _______    C
GAM171  LOC256269 3'  GGCCACCTTGGCACAAAAGC  96608     A  C  AA
                                 GCTTT TG TG  AAGGTGGCC
                                 ||||| || ||  |||||||||
                                 CGAAA AC AC  TTCCACCGG
                                   _ _ GG
GAM171  LOC91963  5'  GGCCACCTCCTCTGAGAAGC  68321     ATGCT  AA
                                 GCTTT    GA  AGGTGGCC
                                 |||||    ||  ||||||||
                                 CGAAG    CT  TCCACCGG
                                    AGT__  CC
GAM172  APXL    3'  AGCAGACGCGTGCGCGTG    9710          ___
                                 CACGCGCACGC   TGCT
                                 ||||||||||   ||||
                                 GTGCGCGTGCG   ACGA
                                       CAG
GAM172  MAP3K1   5'  AAGGCGAGCAGCGCGCCCGCGG 68425    T A  C  A      A
          C                      GC C CG GC CGCTGCTC CCTT
                                 || | || || |||||||| ||||
                                 CG G GC CG GCGACGAG GGAA
                                  _ C  C  C       C
GAM172  MAPK4    3'  AAGGTGAGTTTGGTGCATGC   12298    __   GCT
                                 GC  GCAC   GCTCACCTT
                                 ||  ||||   |||||||||
                                 CG  CGTG   TGAGTGGAA
                                  TA    GTT
GAM172  PRKAR2A  5'  GAGCGGCGCGACGTGAGC    16038        _  AC
                                 GCTCACG CGC  GCTGCTC
                                 ||||||| |||  |||||||
                                 CGAGTGC GCG  CGGCGAG
                                     A  __
GAM172  ATP9A    3'  AGCATCCTGCAGCGTGAGC    62734        _  CGC
                                 GCTCACGC GCA   TGCT
                                 |||||||| |||   ||||
                                 CGAGTGCG CGT   ACGA
                                      A   CCT
GAM172  FBP17    3'  AGTAGGTGAGCGTGAGC     73146         G  G
                                 GCTCACGC CAC CTGCT
                                 |||||||| ||| |||||
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                                CGAGTGCG GTG GATGA
                                    A  _
GAM172  KIAA0607  5'  GTGGGCAACGCGGCGTGAGC  72954       GCA  __
                                GCTCACGC  CGC  TGCTCAC
                                ||||||||  |||  |||||||
                                CGAGTGCG  GCG  ACGGGTG
                                    ____  CA
GAM172  KIAA1075  3'  AAGATGACCTTGCATGTGAGC  62383      C  CGCTGC  C
                                GCTCACG GCA     TCA CTT
                                ||||||| |||     ||| |||
                                CGAGTGT CGT     AGT GAA
                                    A  TCC___  A
GAM172  MAFB      3'  AAGGCGAGAGTAGCGCACGCCA 19585    CAC  CA     A__
            GC                    GCT  GCG  CGCTGCTC  CCTT
                                |||  |||  ||||||||  ||||
                                CGA  CGC  GCGATGAG  GGAA
                                  C__  AC      AGC
GAM172  LOC149997 5'  TGAAGCTGAGGCGTGAGC    76826       G_  C  GC
                                GCTCACGC  CA GCT  TCA
                                ||||||||  || |||  |||
                                CGAGTGCG  GT CGA  AGT
                                    GA  _  __
GAM172  LOC203392 5'  AGTGAGTGCGCGTGAGT     90908         GC
                                GCTCACGCGCAC  TGCT
                                ||||||||||||  ||||
                                TGAGTGCGCGTG  GTGA
                                    A_
GAM172  LOC253634 5'  AAGGTTGAGGACGCGCGCGTGA 98414       A  CTG  _
                                TCACGCGC CG   CTCA CCTT
                                ||||||||  ||   |||| ||||
                                AGTGCGCG GC   GAGT GGAA
                                    C  AG_   T
GAM172  LOC90183  3'  AAGGCGAGAGTAGCGCACGCCA 62400    CAC  CA     A__
            GC                    GCT  GCG  CGCTGCTC  CCTT
                                |||  |||  ||||||||  ||||
                                CGA  CGC  GCGATGAG  GGAA
                                  C__  AC      AGC
GAM173  CDH12     3'  CTTATCATTTAAAGTGGTGTA  15777       CCCAA  GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                    AA___  AC
GAM173  GOCAP1    3'  ATTGTTCTTGGGAGCAGTGTA  43007     CA       G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC       G
GAM173  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090     T   AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
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                                TGGTG GGGT    TTATTC
                                  _   GTCA_
GAM173  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
          A                      TACAC       AGAAGAATAAG
                                 |||||       ||||||||||
                                 ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM173  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                 TACACCACT       GAATAAG
                                 |||||||||       |||||||
                                 ATGTGGTGA       TTTATTC
                                      AGACG___
GAM173  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
          TA                     TACA   TCC   GAAGAATAAG
                                 ||||   |||   ||||||||||
                                 ATGT   AGG   TTTCTTATTC
                                   AAA_  ATTG
GAM173  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA  68742              _
                                 TACACCACTCCCAAGA AGA
                                 |||||||||||||||| |||
                                 ATGTGGTGAGGGTTCT TCT
                                           G
GAM173  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                 CAC  CT CCAAGAAGAA
                                 |||  || ||||||||||
                                 GTG  GA GGTTCTTTTT
                                   AC  A
GAM173  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748     CCA__
                                 ACTC    AGAAGAATAAG
                                 ||||    ||||||||||
                                 TGAG    TCTTCTTATTC
                                   TACCG
GAM173  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                                 CCA    CAAGAAGAATAAG
                                 |||    ||||||||||||
                                 GGT    GTTCTTCTTATTC
                                   TTTCA
GAM173  OSBPL11   3'  CTTAATTTCCCAAGAGTGGTG  43206        CCAA    AA
                                 CACCACTC    GAAG  TAAG
                                 ||||||||    ||||  ||||
                                 GTGGTGAG    CTTT  ATTC
                                      AACC    A_
GAM173  YME1L1    3'  TCATTCTTGATGTGGTGTA    58438        TCC     _
                                 TACACCAC   CAAGAA GA
                                 ||||||||   |||||| ||
                                 ATGTGGTG   GTTCTT CT
                                      TA_     A
GAM173  ZNF262    3'  CTTATTTTGTTTGGGAGT     18723         A
                                 ACTCCCAAG AGAATAAG
                                 |||||||||  ||||||||
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                                TGAGGGTTT TTTTATTC
                                    G
GAM173  LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_   AAGA
                                TACACCAC  CCAAG   ATA
                                ||||||||  |||||   |||
                                ATGTGGTG  GGTTC   TGT
                                    CAA   GG__
GAM174  ACPP     3' GATTAGAAAAATACTGGATA  67387       CTCCG
                                TATCCAGTAT    TGATT
                                ||||||||||    |||||
                                ATAGGTCATA    ATTAG
                                    AAAAG
GAM174  CYP51    3' AGGTAATTGGCAGATTCT    7609    T   _ GT
                                AG ATCT CC  GATTACCT
                                || |||| ||  ||||||||
                                TC TAGA GG  TTAATGGA
                                 T   C __
GAM174  DCN      3' TAAAAGCTAGATACTGGA    10388       CC  GA
                                TCCAGTATCT  GT  TTA
                                ||||||||||  ||  |||
                                AGGTCATAGA  CG  AAT
                                    T_  AA
GAM174  DCN      3' TAAAAGCTAGATACTGGA    56869       CC  GA
                                TCCAGTATCT  GT  TTA
                                ||||||||||  ||  |||
                                AGGTCATAGA  CG  AAT
                                    T_  AA
GAM174  DCN      3' TAAAAGCTAGATACTGGA    56871       CC  GA
                                TCCAGTATCT  GT  TTA
                                ||||||||||  ||  |||
                                AGGTCATAGA  CG  AAT
                                    T_  AA
GAM174  DCN      3' TAAAAGCTAGATACTGGA    56872       CC  GA
                                TCCAGTATCT  GT  TTA
                                ||||||||||  ||  |||
                                AGGTCATAGA  CG  AAT
                                    T_  AA
GAM174  DCN      3' TAAAAGCTAGATACTGGA    56873       CC  GA
                                TCCAGTATCT  GT  TTA
                                ||||||||||  ||  |||
                                AGGTCATAGA  CG  AAT
                                    T_  AA
GAM174  DCN      3' TAAAAGCTAGATACTGGA    56875       CC  GA
                                TCCAGTATCT  GT  TTA
                                ||||||||||  ||  |||
                                AGGTCATAGA  CG  AAT
                                    T_  AA
GAM174  HIS1     3' GGTAAGAAATACTGGAT     22340       C  CGTGA
                                ATCCAGTAT TC    TTACC
                                |||||||| ||    |||||
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                                TAGGTCATA AG    AATGG
                                     A _____
GAM174  SMT3H1   3' AGTTGAAGGGAAAATACTGGA 60627       ___   CG
                                TCCAGTA  TCTC  TGATT
                                |||||||  ||||  |||||
                                AGGTCAT  AGGG  GTTGA
                                    AAA   AA
GAM174  KIAA0429 3' AGGTAATCACAATAGATA   29241     CC_
                                TATCT  GTGATTACCT
                                |||||  ||||||||||
                                ATAGA  CACTAATGGA
                                   TAA
GAM174  KIAA0993 3' GTAAATTGAAGATACTGG   64821       C  TGA
                                CCAGTATCT CG  TTAC
                                ||||||||| ||  ||||
                                GGTCATAGA GT  AATG
                                     A  TA_
GAM174  KIAA1432 5' GATGAGGAAAATACTGGAT  67304       C_  GTG
                                ATCCAGTAT  TCC  ATT
                                |||||||||  |||  |||
                                TAGGTCATA  AGG  TAG
                                     AA  AG_
GAM174  KIAA1600 3' AGGCATTAAGAGATATTAGATA 71939    C      CG   TA
                                TATC AGTATCTC  TGAT  CCT
                                |||| ||||||||  ||||  |||
                                ATAG TTATAGAG  ATTA  GGA
                                  A      A_   C_
GAM174  USP25    3' AGGTAATCATGTTACT     26345     TCTC
                                AGTA   CGTGATTACCT
                                ||||   ||||||||||
                                TCAT   GTACTAATGGA
                                  T___
GAM174  LOC143920 3' GGGTGAGAAACTGGATA    77115       A   CGTGATT
                                TATCCAGT TCTC     ACCT
                                |||||||| ||||     ||||
                                ATAGGTCA AGAG     TGGG
                                     A  _______
GAM174  LOC145009 3' AGGTAATTGGCAGATTCT   60967   T   _  GT
                                AG ATCT CC  GATTACCT
                                || |||| ||  ||||||||
                                TC TAGA GG  TTAATGGA
                                 T   C __
GAM174  LOC150481 3' AGGTGGTCAAGAGACACTGGA 80693      A   CG
                                TCCAGT TCTC  TGATTACCT
                                |||||| ||||  |||||||||
                                AGGTCA AGAG  ACTGGTGGA
                                   C   A_
GAM174  LOC158191 3' AGGTGGTCAAGAGACACTGGA 82664      A   CG
                                TCCAGT TCTC  TGATTACCT
                                |||||| ||||  |||||||||
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                                AGGTCA AGAG  ACTGGTGGA
                                   C   A_
GAM174  LOC196319 3'  AGGCTTATGAAGATGCTGGA  91189         C    TTA
                                TCCAGTATCT CGTGA  CCT
                                |||||||||| |||||  |||
                                AGGTCGTAGA GTATT  GGA
                                     A    C__
GAM174  LOC90141  3'  AGGTAATTCCAAAATACTGG  62298       CTCCGT
                                CCAGTAT    GATTACCT
                                |||||||    ||||||||
                                GGTCATA    TTAATGGA
                                   AAACC_
GAM174  LOC90786  5'  AGGTGGGGACCAGGGATACT  64726       C_ GA
                                AGTATCTC  GT  TTACCT
                                ||||||||  ||  ||||||
                                TCATAGGG  CA  GGTGGA
                                    AC  GG
GAM174  LOC91549  3'  AGGTTTAGGAGGAGATACTAAG 67023     C_       GTGATT
          ATA                     TATC  AGTATCTCC     ACCT
                                ||||  |||||||||     ||||
                                ATAG  TCATAGAGG     TGGA
                                  AA        AGGATT
GAM175  CCR9    3'  CTGACCACACCCACAAGGC   22795    __   AC
                                GTC  GTGG  GTGGTCAG
                                |||  ||||  ||||||||
                                CGG  CACC  CACCAGTC
                                  AA   CA
GAM175  CCR9    3'  CTGACCACACCCACAAGGC   49123    __   AC
                                GTC  GTGG  GTGGTCAG
                                |||  ||||  ||||||||
                                CGG  CACC  CACCAGTC
                                  AA   CA
GAM175  COL1A1   3'  TGACCAACCGAACATGACCAAA 5397         GA __
                                TTTGGTCGTG  CG  TGGTCA
                                ||||||||||  ||  ||||||
                                AAACCAGTAC  GC  ACCAGT
                                     AA  CA
GAM175  UBE2L3   3'  TGGCTGCTCCAAAACCAAA   13967      CG   C TG
                                TTTGGT  TGGA G  GTCA
                                ||||||  |||| |  ||||
                                AAACCA  ACCT C  CGGT
                                   AA   _ GT
GAM175  UBE2L3   3'  TGGCTGCTCCAAAACCAAA   13967      CG   C TG
                                TTTGGT  TGGA G  GTCA
                                ||||||  |||| |  ||||
                                AAACCA  ACCT C  CGGT
                                   AA   _ GT
GAM175  FLJ14640  5'  GCTGAGGCCTCGACCAAA   52549       T  ACGTGG
                                TTTGGTCG GG    TCAGC
                                ||||||||  ||    |||||
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                                AAACCAGC CC     AGTCG
                                    T  GG____
GAM175  KIAA1854  3'  GCTGACACCCACGTCCAAA   72210      T    AC   G
                                TTTGG CGTGG  GTG TCAGC
                                ||||| |||||  ||| |||||
                                AAACC GCACC  CAC AGTCG
                                   T    __  _
GAM175  PDZD2     5'  GCAGCCATGGACGTCCACAACC 81725      C     T________  TCAG
          AAG                     TTTGGT GTGGACG       GG   C
                                ||||||| |||||||       ||   |
                                GAACCA CACCTGC       CC   G
                                   A      AGGT___A  GACT
GAM175  PDZD2     5'  GCAGCCATGGACGTCCACAACC 81725      C     T________  TCAG
          AAG                     TTTGGT GTGGACG       GG   C
                                ||||||| |||||||       ||   |
                                GAACCA CACCTGC       CC   G
                                   A      AGGT___A  GACT
GAM175  TTYH2     3'  GCTGGGATTCCCGACCAAA   51978       T  CGTGG
                                TTTGGTCG GGA    TCAGC
                                |||||||| |||    |||||
                                AAACCAGC CCT    GGTCG
                                    _  TAG__
GAM175  TTYH2     3'  GCTGGGATTCCCGACCAAA   51978       T  CGTGG
                                TTTGGTCG GGA    TCAGC
                                |||||||| |||    |||||
                                AAACCAGC CCT    GGTCG
                                    _  TAG__
GAM175  LOC91759  5'  GGCTGACCAAGCGCCAAA    67694      T  GGACG
                                TTTGG CGT    TGGTCAGCC
                                ||||| |||    |||||||||
                                AAACC GCG    ACCAGTCGG
                                   _  A____
GAM176  CCR9      3'  CTGACCACACCCACAAGGC    49123     __   AC
                                GTC  GTGG  GTGGTCAG
                                |||  ||||  ||||||||
                                CGG  CACC  CACCAGTC
                                  AA   CA
GAM176  CCR9      3'  CTGACCACACCCACAAGGC    22795     __   AC
                                GTC  GTGG  GTGGTCAG
                                |||  ||||  ||||||||
                                CGG  CACC  CACCAGTC
                                  AA   CA
GAM176  COL1A1    3'  TGACCAACCGAACATGACCAAA 5397         GA  __
                                TTTGGTCGTG  CG  TGGTCA
                                ||||||||||  ||  ||||||
                                AAACCAGTAC  GC  ACCAGT
                                     AA  CA
GAM176  SLC20A2   5'  TGACTGAACACAACCAAA    23122       C  GACG
                                TTTGGT GTG    TGGTCA
                                ||||||  |||   ||||||
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                                AAACCA CAC    GTCAGT
                                   A   AA__
GAM176  SLC20A2   5'  TGACTGAACACAACCAAA    23122       C   GACG
                                TTTGGT GTG    TGGTCA
                                |||||| |||    ||||||
                                AAACCA CAC    GTCAGT
                                   A   AA__
GAM176  FLJ14640  5'  GCTGAGGCCTCGACCAAA    52549        T  ACGTGG
                                TTTGGTCG GG     TCAGC
                                |||||||| ||     |||||
                                AAACCAGC CC     AGTCG
                                    T  GG____
GAM176  KIAA1596  3'  TGGCTGTGTCCCCAACCAAA   71481       CGT    TG
                                TTTGGT   GGACG  GTCA
                                ||||||   |||||  ||||
                                AAACCA   CCTGT  CGGT
                                   ACC     GT
GAM176  KIAA1596  3'  TGGCTGTGTCCCCAACCAAA   71481       CGT    TG
                                TTTGGT   GGACG  GTCA
                                ||||||   |||||  ||||
                                AAACCA   CCTGT  CGGT
                                   ACC     GT
GAM176  KIAA1854  3'  GCTGACACCCACGTCCAAA    72210      T    AC   G
                                TTTGG CGTGG  GTG TCAGC
                                ||||| |||||  ||| |||||
                                AAACC GCACC  CAC AGTCG
                                  T    __   _
GAM176  LOC204084 3'  GGCCACCTCCACGACCAA     90999          C
                                TTGGTCGTGGA GTGGTC
                                |||||||||| ||||||
                                AACCAGCACCT CACCGG
                                      C
GAM176  LOC204084 3'  GGCCACCTCCACGACCAA     90999          C
                                TTGGTCGTGGA GTGGTC
                                |||||||||| ||||||
                                AACCAGCACCT CACCGG
                                      C
GAM176  LOC91759  5'  GGCTGACCAAGCGCCAAA     67694      T   GGACG
                                TTTGG CGT    TGGTCAGCC
                                ||||| |||    |||||||||
                                AAACC GCG    ACCAGTCGG
                                  _   A____
GAM177  APCS      3'  GATCTGGTCAAAGCAACTGGAT 9700          ATGGGCT
                                ATCCAGTTG      GCCAGATC
                                |||||||||      ||||||||
                                TAGGTCAAC      TGGTCTAG
                                     GAAAC__
GAM177  INSRR     3'  GATCTAGCAGCCCGCAACTG   68990       A       C
                                CAGTTG TGGGCTGC AGATC
                                |||||| |||||||| |||||
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                                GTCAAC GCCCGACG TCTAG
                                  _      A
GAM177  KNSL1    3'  GATCTGGCAACCATATTTCTGG 16947      TTG_   GC
            A                    TCCAG   ATGG  TGCCAGATC
                                 |||||   ||||  |||||||||
                                 AGGTC   TACC  ACGGTCTAG
                                   TTTA   A_
GAM177  JDD1     3'  ATCTGACCTCATCAAATAGAT  63912     CAG      CTGC
                                 ATC   TTGATGGG   CAGAT
                                 |||   ||||||||   |||||
                                 TAG   AACTACTC   GTCTA
                                   ATA      CA__
GAM177  KIAA0092 3'  ATCTGTACCTCATCAATCAGAT 28649     CA       C   C
                                 ATC  GTTGATGGG TGC AGAT
                                 |||  ||||||||| ||| ||||
                                 TAG  TAACTACTC ATG TCTA
                                   AC       C  _
GAM177  KIAA1026 3'  ATCTGACAGCCCCCAATT    71730      AT     C
                                 AGTTG  GGGCTG CAGAT
                                 |||||  |||||| |||||
                                 TTAAC  CCCGAC GTCTA
                                   C_     A
GAM177  MGC16279 5'  GGCAGCCTTCATTAACAGGA   52986     A      __
                                 TCC GTTGATG  GGCTGCC
                                 ||| |||||||  |||||||
                                 AGG CAATTAC  CCGACGG
                                   A      TT
GAM178  B3GAT1   3'  CTCGCTGGCAAGCCCCACC   38452        GCA   T_
                                 GGTGGGGC   GCT  CGAG
                                 ||||||||   |||  ||||
                                 CCACCCCG   CGG  GCTC
                                      AA_   TC
GAM178  B3GAT1   3'  CTCGCTGGCAAGCCCCACC   55053        GCA   T_
                                 GGTGGGGC   GCT  CGAG
                                 ||||||||   |||  ||||
                                 CCACCCCG   CGG  GCTC
                                      AA_   TC
GAM178  BIRC8    5'  CGAGGAGCCCCGCCATG    54039    C      GCAG
                                 CA GGTGGGGC    CTTCG
                                 || ||||||||    |||||
                                 GT CCGCCCCG    GGAGC
                                   A      A___
GAM178  FLJ13241 3'  CTTGGAGCGCCCCACC     47652        GCA
                                 GGTGGGGC   GCTTCGAG
                                 ||||||||   ||||||||
                                 CCACCCCG   CGAGGTTC
                                              ___
GAM178  KIAA0140 5'  CGGAGCGCCCCGCCG      28511         GCA
                                 CGGTGGGGC   GCTTCG
                                 |||||||||   ||||||
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                                GCCGCCCCG  CGAGGC
                                    ___
GAM178  KIAA0222 5' GCTGCGCCCCCCATGTA    28398    C  T
                                TACA GG GGGGCGCAGC
                                |||| || ||||||||||
                                ATGT CC CCCCGCGTCG
                                  A  _
GAM179  DUOX1    5' TGCAGAGTGCTGGGCCAA   34293        CTA
                                TTGGCCCAGTAC  TGCA
                                ||||||||||||  ||||
                                AACCGGGTCGTG  ACGT
                                      AG_
GAM179  FGF5     3' TGCATAAGTTGTATAGGCTAA 53671     CA  C___
                                TTGGCC GTAC   TATGCA
                                ||||||  ||||   ||||||
                                AATCGG TATG   ATACGT
                                   A_   TTGA
GAM179  FGF5     3' TGCATAAGTTGTATAGGCTAA 53672     CA  C___
                                TTGGCC GTAC   TATGCA
                                ||||||  ||||   ||||||
                                AATCGG TATG   ATACGT
                                   A_   TTGA
GAM179  NEURL    3' TGGGTTCCCTGGGCCAAG   16138       T__
                                CTTGGCCCAG  ACCTA
                                ||||||||||  |||||
                                GAACCGGGTC  TGGGT
                                     CCT
GAM179  P2RY6    3' TGCATATCCAGCTGGGCCA  16002      ACC_
                                TGGCCCAGT   TATGCA
                                |||||||||   ||||||
                                ACCGGGTCG   ATACGT
                                     ACCT
GAM179  PLXNA1   3' TGGGAGCCACTGGGCCAGG  72774       A___
                                CTTGGCCCAGT   CCTA
                                ||||||||||   ||||
                                GGACCGGGTCA   GGGT
                                      CCGA
GAM179  SLC2A3   3' TGCACTCTAGCCTGGGCCA  23649      TAC  ___
                                TGGCCCAG  CTA  TGCA
                                ||||||||  |||  ||||
                                ACCGGGTC  GAT  ACGT
                                    C__  CTC
GAM179  SLC9A1   3' TGCAGGGGACTGGGCCA    70932      A  A
                                TGGCCCAGT CCT TGCA
                                ||||||||| ||| ||||
                                ACCGGGTCA GGG ACGT
                                     _  G
GAM179  SNX13    5' GCGAGCGACCGGGCCGAG   31394      A  AC  A
                                CTTGGCCC GT  CT TGC
                                |||||||| ||  || |||
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                                GAGCCGGG CA  GA GCG
                                     C  GC  _
GAM179  SPON1    3'  TGCATAGGAATGGCCA      63125       CA  A
                                TGGCC  GT CCTATGCA
                                |||||  || ||||||||
                                ACCGG  TA GGATACGT
                                   __  A
GAM179  CDW92    3'  TGCATAAGTCCTAGTGGGTCAA 42332         G ___  C
           G                     CTTGGCCCA T   AC TATGCA
                                |||||||||  |   || ||||||
                                GAACTGGGT A   TG ATACGT
                                     G TCC  A
GAM179  DKFZP434A043 3'  TGCACGTACATGGGCCAG    31824         _   CTA
                                TTGGCCCA GTAC   TGCA
                                |||||||| ||||   ||||
                                GACCGGGT CATG   ACGT
                                     A   C__
GAM179  FAM3A    3'  TGCCAGGACCGGGCCGAG    41733         A  A   AT
                                CTTGGCCC GT CCT  GCA
                                |||||||| || |||  |||
                                GAGCCGGG CA GGA  CGT
                                     C  _  C_
GAM179  FLJ13902  3'  TGCACAAGGAGGCCCGGGCCAG 45384         A_  A_  A_
           G                     CTTGGCCC  GT  CCT  TGCA
                                |||||||  ||  |||  ||||
                                GGACCGGG  CG  GGA  ACGT
                                     CC  GA   AC
GAM179  KIAA0391  3'  TGCATTTCTCCTACTGGGCCA  28624         CCT___
                                TGGCCCAGTA     ATGCA
                                ||||||||||     |||||
                                ACCGGGTCAT     TACGT
                                     CCTCTT
GAM179  KIAA0630  3'  TGCATGGATCTGGGTCAAG   90953         TAC
                                CTTGGCCCAG   CTATGCA
                                ||||||||||   |||||||
                                GAACTGGGTC   GGTACGT
                                     TA_
GAM179  KIAA1924  3'  TGCACAGGGTGCCACGGGGCCA 74062         A___     A_
           AG                     CTTGGCCC   GTACCT  TGCA
                                |||||||   ||||||  ||||
                                GAACCGGG   CGTGGG  ACGT
                                     GCAC     AC
GAM179  MGC15396  3'  TGCATCACCTCTGGGCCAAG   54565         TACCT
                                CTTGGCCCAG    ATGCA
                                ||||||||||    |||||
                                GAACCGGGTC    TACGT
                                     TCCAC
GAM179  PASK     5'  TGCAGGTGTCCTGGGCCAAG   31424         __    AT
                                CTTGGCCCAG  TACCT  GCA
                                ||||||||||  |||||  |||
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                                GAACCGGGTC  GTGGA  CGT
                                      CT    __
GAM179  PPP1R14A  5'  GCACAGCGCGGGGCCAGG    53829        A  AC  A
                                CTTGGCCC GT  CT TGC
                                |||||||| ||  || |||
                                GGACCGGG CG  GA ACG
                                     G  C_  C
GAM179  RASGRP4   3'  TGCACAGGTGCTGGACAAG   54748     GC       A
                                CTTG  CCAGTACCT TGCA
                                ||||  ||||||||| ||||
                                GAAC  GGTCGTGGA ACGT
                                  A_        C
GAM179  TRIM16    5'  TGCACAGATCCTGGGCCAAG   22381         TAC  A
                                CTTGGCCCAG   CT TGCA
                                ||||||||||   || ||||
                                GAACCGGGTC   GA ACGT
                                      CTA  C
GAM179  WIT-1     5'  TGCAGCCTGCGGGGCCAAG   32400        A   CCTA
                                CTTGGCCC GTA    TGCA
                                |||||||| |||    ||||
                                GAACCGGG CGT    ACGT
                                     G   CCG_
GAM179  LOC126364 3'  TGCAGTCACTGGGCCAGG    76201          ACCTA
                                CTTGGCCCAGT    TGCA
                                ||||||||||     ||||
                                GGACCGGGTCA    ACGT
                                      CTG__
GAM179  LOC132299 5'  CACAGACACTGGGTCAAG    75569          AC  A
                                CTTGGCCCAGT  CT TG
                                ||||||||||  || ||
                                GAACTGGGTCA  GA AC
                                      CA  C
GAM179  LOC147645 3'  TGCACAGGGCGTTTTGGGCCAG 79073         TA___  A
                                TTGGCCCAG    CCT TGCA
                                |||||||||    ||| ||||
                                GACCGGGTT    GGA ACGT
                                     TTGCG   C
GAM179  LOC151996 5'  TGCATAGGCACAAGTGGGCCAG 86723         ___  A
          G                      CTTGGCCCA   GT CCTATGCA
                                |||||||||   || ||||||||
                                GGACCGGGT   CA GGATACGT
                                     GAA  C
GAM179  LOC153077 3'  CATGTACATGGGCCAGG     87115         _   CT
                                CTTGGCCCA GTAC  ATG
                                ||||||||| ||||  |||
                                GGACCGGGT CATG  TAC
                                     A   __
GAM179  LOC200940 5'  TGCATGCCAGGTGGGCCGAG  90399        AGT   ___
                                CTTGGCCC   ACCT   ATGCA
                                ||||||||   ||||   |||||
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                                GAGCCGGG  TGGA  TACGT
                                    ___   CCG
GAM179  LOC205418 5'  TGCACGGGGCTGGGCCA    92375       A  TA
                                TGGCCCAGT CC  TGCA
                                ||||||||| ||  ||||
                                ACCGGGTCG GG  ACGT
                                    _  GC
GAM179  LOC219653 3'  TGCACAGCCAGCTCAGCCAAG  92923      CC  AC_  A
                                CTTGGC  AGT  CT TGCA
                                ||||||  |||  || ||||
                                GAACCG  TCG  GA ACGT
                                   AC  ACC  C
GAM179  LOC51207  5'  TGCACAGCCTGGGCCAG    33475       TAC  A
                                TTGGCCCAG  CT TGCA
                                |||||||||  || ||||
                                GACCGGGTC  GA ACGT
                                    C__  C
GAM179  LOC51580  3'  CATAGGTGTGTTCCAGG    32429      CC  G
                                CTTGG  CA TACCTATG
                                |||||  || ||||||||
                                GGACC  GT GTGGATAC
                                   TT  _
GAM179  LOC64182  3'  TGCCAGATACCGGGCTAAG   42556       A  C  AT
                                CTTGGCCC GTA CT  GCA
                                |||||||| ||| ||  |||
                                GAATCGGG CAT GA  CGT
                                    C  A  C_
GAM180  FLJ22332  5'  GGAAAGAAAACTACATCACA  45637     G  A     _______
                                TGTG AT TAGTTTTC     CC
                                |||| || ||||||||     ||
                                ACAC TA ATCAAAAG     GG
                                   _  C       AAA___
GAM181  FLJ21438  5'  CAAAACGCTTCCCCCCATCCCA 62190      GAGATTATC
                                TGGGA       AAGCGTTTTG
                                |||||       ||||||||||
                                ACCCT       TTCGCAAAAC
                                   ACCCCCC__
GAM181  FLJ32334  3'  AAAACGCTATTCCTTCCCA   58605       A  TTATCA
                                TGGGAG GA     AGCGTTTT
                                |||||| ||     ||||||||
                                ACCCTT CT     TCGCAAAA
                                   C  TA____
GAM181  HHLA2    3'  CAATGTACTTTGTAATCTCCCC 23953     A      C   CG T
           CA                     TGGG GAGATTAT AAG  T TTG
                                |||| |||||||| |||  | |||
                                ACCC CTCTAATG TTC  G AAC
                                  C       T   AT T
GAM182  ADAT1    3'  CCAGCAAAGAATGAAGGC    24914     __        C
                                GTC  CATTCTTTGC GG
                                |||  |||||||||| ||
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                                CGG  GTAAGAAACG CC
                                  AA        A
GAM182  M17S2    5'  CCGGTAGCGGACGGTCCTT   20910          ATTCT
                                AAGGACCGTCC    TTGCCGG
                                ||||||||||    |||||||
                                TTCCTGGCAGG    GATGGCC
                                      C_____
GAM182  ST14     5'  CCGGCAGGGACGACGCCT    42042     AC    CAT
                                AGG  CGTC   TCTTTGCCGG
                                |||  ||||   ||||||||||
                                TCC  GCAG   AGGGACGGCC
                                  __    C__
GAM182  HTGN29   5'  GCCAACTGTGTGGCGGTCC    39885        _   TC  T
                                GGACCGTC CAT  TT GC
                                |||||||| |||  || ||
                                CCTGGCGG GTG  AA CG
                                     T   TC  C
GAM182  PMAIP1   3'  GCAAGAATGGAAGACCCTT    41211      ACCG       T
                                AAGG    TCCATTCTT GC
                                ||||    ||||||||| ||
                                TTCC    AGGTAAGAA CG
                                  CAGA       _
GAM182  LOC144278 3'  GCCAGCAAAGACTGCTCGATGG 77274          ___  T      C
           TCCT                    AGGACCGTC   CA TCTTTGC GGC
                                |||||||||   || ||||||| |||
                                TCCTGGTAG   GT AGAAACG CCG
                                     CTC  C      A
GAM182  LOC147976 3'  CCGGTGAATGAAGACCCT    79287     ACC   CA   _  TG
                                AGG   GTC  TTC TT  CCGG
                                |||   |||  ||| ||  ||||
                                TCC   CAG  AAG AA  GGCC
                                  ___   __   T  GT
GAM182  LOC254263 5'  GCCGGCAGCGGACGCGCC    96367    AC    ATTCT
                                GG  CGTCC    TTGCCGGC
                                ||  |||||    ||||||||
                                CC  GCAGG    GACGGCCG
                                 GC    C_____
GAM183  AQP6     5'  ACTTCAAGGCCACAGGGCAGC  54980          A  CAACT
                                GCTGCCCTGTG CC    GGT
                                ||||||||||| ||    |||
                                CGACGGGACAC GG    TCA
                                      C  AACT_
GAM183  CTSL2    3'  ACCAGTTGAATCATTGAGG    9023      __    CC
                                CCT  GTGA  CAACTGGT
                                |||  ||||  ||||||||
                                GGA  TACT  GTTGACCA
                                  GT    AA
GAM183  H1F0     3'  ACCAGTTGTGCAAGGACAGCA  19216      C   G  ACC
                                TGCTG CCT TG   CAACTGGT
                                ||||| ||| ||   ||||||||
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                                ACGAC GGA AC   GTTGACCA
                                  A   _ GT_
GAM183  MAT2A    3'  CAGAGAAGTCACAGGGCAGTA  20967          CCAA
                                TGCTGCCCTGTGAC    CTG
                                ||||||||||||||   |||
                                ATGACGGGACACTG    GAC
                                      AAGA
GAM183  PIK3C2B  3'  ACCGAAGCCACAGGGCAGCAT  12085          ACCCAAC
                                ATGCTGCCCTGTG      TGGT
                                ||||||||||||      ||||
                                TACGACGGGACAC      GCCA
                                      CGAA___
GAM183  APOARGC  3'  CCACCGTCACAGGAAGCA    44674     GC       CCAAC
                                TGCT  CCTGTGAC    TGG
                                ||||  ||||||||    |||
                                ACGA  GGACACTG    ACC
                                  A_      CC___
GAM183  BRPF3    3'  ACCAGTTAGAAGTAGAAACAGC 93923     CC_   GACCC
                                GCTG   CTGT    AACTGGT
                                ||||   ||||    |||||||
                                CGAC   GATG    TTGACCA
                                  AAA    AAGA_
GAM183  CCR6     3'  ACCAATTGGATAAAGCAGC   49393     CC   GAC   C
                                GCTGC  TGT   CCAA TGGT
                                |||||  |||   |||| ||||
                                CGACG  ATA   GGTT ACCA
                                  AA   ___    A
GAM183  FLJ10619 3'  ACCAGTTGGAATGGAGCA    36861     G  CTGTGAC
                                TGCT CC      CCAACTGGT
                                |||| ||      |||||||||
                                ACGA GG      GGTTGACCA
                                  _  TAA____
GAM183  FLJ11722 5'  ACCCCCTGCCAGAGGGCAGCAT 46987         G  ACC  ACT
                                ATGCTGCCCT TG   CA   GGT
                                |||||||||| ||   ||   |||
                                TACGACGGGA AC   GT   CCA
                                      G  C__  CCC
GAM183  FLJ12788 3'  ACCAGCTGGGTCACCTTGG   42843    CT_      A
                                CC   GTGACCCA CTGGT
                                ||   |||||||| |||||
                                GG   CACTGGGT GACCA
                                 TTC       C
GAM183  FLJ20154 5'  ACCAGTTGACCGAGCAGC    73300      CCT  GACC
                                GCTGC   GT    CAACTGGT
                                |||||   ||    ||||||||
                                CGACG   CA    GTTGACCA
                                  AGC  ____
GAM183  KIAA1068 3'  ACCAGCCACTGCAGGCAGCAT  31683        C   GACCCAA
                                ATGCTGCC TGT      CTGGT
                                |||||||| |||      |||||
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                                TACGACGG ACG      GACCA
                                    _  TCACC__
GAM183  KIAA1297  3'  CCAACGTACTGGGCAGCAT   72632        T  ACCCAAC
                                ATGCTGCCC GTG     TGG
                                ||||||||| |||     |||
                                TACGACGGG CAT     ACC
                                    T  GCA____
GAM183  LEC3      3'  ACCAGCTAGGTCGCGGCAGCA  31530       CT    CAA
                                TGCTGCC  GTGACC  CTGGT
                                |||||||  ||||||  |||||
                                ACGACGG  CGCTGG  GACCA
                                   __    ATC
GAM183  STOML1    3'  AGCTGGGGCCCAGGGCAGCAT  17862         TGA   A
                                ATGCTGCCCTG  CCCA CT
                                ||||||||||  |||| ||
                                TACGACGGGAC  GGGT GA
                                     CCG   C
GAM183  LOC145719 3'  ACCAGGTGTCACCAGGCAGCAT 84458       CT    CCAA
                                ATGCTGCC  GTGAC   CTGGT
                                ||||||||  |||||   |||||
                                TACGACGG  CACTG   GACCA
                                    AC    TG__
GAM183  LOC145720 3'  ACCAGGTGTCACCAGGCAGCAT 84444       CT    CCAA
                                ATGCTGCC  GTGAC   CTGGT
                                ||||||||  |||||   |||||
                                TACGACGG  CACTG   GACCA
                                    AC    TG__
GAM183  LOC197114 3'  ACCAGGTGTCACCAGGCAGCAT 91263       CT    CCAA
                                ATGCTGCC  GTGAC   CTGGT
                                ||||||||  |||||   |||||
                                TACGACGG  CACTG   GACCA
                                    AC    TG__
GAM183  LOC197117 3'  ACCAGGTGTCACCAGGCAGCAT 91277       CT    CCAA
                                ATGCTGCC  GTGAC   CTGGT
                                ||||||||  |||||   |||||
                                TACGACGG  CACTG   GACCA
                                    AC    TG__
GAM183  LOC219920 5'  CCAGGGCCACAGGACACAT   94941    C  C     A   AAC
                                ATG TG CCTGTG CCC   TGG
                                ||| || |||||| |||   |||
                                TAC AC GGACAC GGG   ACC
                                  _ A     C   ___
GAM183  LOC255631 5'  ACCAGTCAACTTGGGGCAGC   97965        TGACCCA
                                GCTGCCCTG      ACTGGT
                                |||||||||      ||||||
                                CGACGGGGT      TGACCA
                                     TCAAC__
GAM183  LOC257115 3'  CCAAAACGCAAGGCAGCAT   98291        C    ACCCAAC
                                ATGCTGCC TGTG      TGG
                                |||||||| ||||      |||
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                                TACGACGG ACGC      ACC
                                   A   AAA____
GAM184  DAAM2    3' ATGTTGGAAGGATGATGCAGG 93900   _      C_   TT
                                CC GCATCATCC  CCAG  CAT
                                || |||||||||  ||||  |||
                                GG CGTAGTAGG  GGTT  GTA
                                 A       AA   __
GAM184  GNL1     3' ATGAACTGAGGTGAGAGCGG  99714    A  A  _  C
                                CCGC TC TC CC CAGTTCAT
                                |||| || || || ||||||||
                                GGCG AG AG GG GTCAAGTA
                                  _  _  T  A
GAM184  GNL1     3' ATGAACTGAGGTGAGAGCGG  93670    A  A  _  C
                                CCGC TC TC CC CAGTTCAT
                                |||| || || || ||||||||
                                GGCG AG AG GG GTCAAGTA
                                  _  _  T  A
GAM184  GPR30    3' AGCTGGGGACAACTGCGGTG  9490       TCATC
                                CACCGCA    CCCCAGTT
                                |||||||    ||||||||
                                GTGGCGT    GGGGTCGA
                                    CAACA
GAM184  MGAM     3' TGAACTGGGTCCATGATG    72814      CC_
                                CATCAT   CCCAGTTCA
                                ||||||   |||||||||
                                GTAGTA   GGGTCAAGT
                                   CCT
GAM184  OPHN1    3' ATGAACTGAAAGTGATGAACTG 11906    CCG    CCCC
           G                     CCA   CATCAT   CAGTTCAT
                                |||   ||||||   ||||||||
                                GGT   GTAGTG   GTCAAGTA
                                 CAA     AAA_
GAM184  PIGC     3' ATGAACCAAAGGCTTGGGTGGT 12081      A   TC  CCA_
           G                     CACCGC TCA  CC    GTTCAT
                                |||||| |||  ||    ||||||
                                GTGGTG GGT  GG    CAAGTA
                                   _   TC  AAAC
GAM184  TRPM2    3' ATGAACTGGAAGGGGTCAAGGT 13861     GCATC    __
           G                     CACC    ATCCC  CCAGTTCAT
                                ||||    |||||  |||||||||
                                GTGG    TGGGG  GGTCAAGTA
                                  AAC__    AA
GAM184  BC008967 5' ATGAACTGGGAGAGGGGC    61413    AT A  C
                                GC  C TC CCCAGTTCAT
                                ||  | || ||||||||||
                                CG  G AG GGGTCAAGTA
                                 GG _  A
GAM184  BPESC1   3' ATGAACTGTGATAATGC     41768     C   CCC
                                GCAT ATC   CAGTTCAT
                                |||| |||   ||||||||
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                                CGTA TAG   GTCAAGTA
                                  A  T__
GAM184  DNAJA2   3'  ATGAACTGAGGGACATCTGTTG 60486    CC   TCA_   C
           G                     CCA  GCA   TCCC CAGTTCAT
                                 |||  |||   |||| ||||||||
                                 GGT  TGT   AGGG GTCAAGTA
                                  __  CTAC   A
GAM184  HIF1AN   3'  ATGAACTGAGAGGATGCGTGTG 62668    _    A  CCC
           G                     CCAC CGCATC TC   CAGTTCAT
                                 |||| |||||| ||   ||||||||
                                 GGTG GCGTAG AG   GTCAAGTA
                                   T     G  A__
GAM184  KIAA0675 3'  ATGAACTGAAAGAGCTTGAAGC 28435    A  ___  CCC
                                 GC TCA   TC   CAGTTCAT
                                 || |||   ||   ||||||||
                                 CG AGT   AG   GTCAAGTA
                                  A   TCG  AAA
GAM184  KIAA0978 3'  AGTTGGGAATGATGTGGTG   70989         CC   GT
                                 CACCGCATCAT  CCCA  T
                                 ||||||||||  ||||  |
                                 GTGGTGTAGTA  GGGT  A
                                       A_   TG
GAM184  KIAA1918 3'  ATGAACTGAAAAATGTGTG   73534     T   CCCC
                                 CGCA CAT    CAGTTCAT
                                 |||| |||    ||||||||
                                 GTGT GTA    GTCAAGTA
                                   _  AAAA
GAM184  KIAA1951 3'  AACTGGCCAGGTGCGGTGG   74141         ATCCC
                                 CCACCGCATC    CCAGTT
                                 ||||||||||    ||||||
                                 GGTGGCGTGG    GGTCAA
                                       ACC__
GAM184  MKRN4    3'  ATGAACTGAGAATGTGCCACTG 48451    CC_   T   CCCC
           G                     CCA   GCA CAT    CAGTTCAT
                                 |||   ||| |||    ||||||||
                                 GGT   CGT GTA    GTCAAGTA
                                   CAC   _   AGA_
GAM184  MYH7B    3'  GAGCTGGATGATGCGGAGG   71056    A        CCC
                                 CC CCGCATCATCC   AGTTC
                                 || ||||||||||   |||||
                                 GG GGCGTAGTAGG   TCGAG
                                  A         ___
GAM184  PRO0365  5'  GCTGGAGAGATAATGTGGTGG  26987         C   CC_
                                 CCACCGCAT ATC   CCAGT
                                 |||||||| |||   |||||
                                 GGTGGTGTA TAG   GGTCG
                                       A   AGA
GAM184  PTD015   5'  TTGAGGAGACAGTGCGGTGG   93312         CA  _  C
                                 CCACCGCAT  TC CC CAG
                                 ||||||||  || || |||
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                                GGTGGCGTG  AG GG GTT
                                     AC  A  A
GAM184  RNF9     3'  ATGAACCAAGCAGTGTGGTGG  23235        CATCCCCCA
                                CCACCGCAT       GTTCAT
                                |||||||||       ||||||
                                GGTGGTGTG       CAAGTA
                                     ACGAAC___
GAM184  RNF9     3'  ATGAACCAAGCAGTGTGGTGG  54505        CATCCCCCA
                                CCACCGCAT       GTTCAT
                                |||||||||       ||||||
                                GGTGGTGTG       CAAGTA
                                     ACGAAC___
GAM184  TOM1     3'  ATGAACTGGGGGGACAGGTCTGC 19696     __  A_
           G                     CGCA  TC  TCCCCCAGTTCAT
                                 ||||  ||  ||||||||||||
                                 GCGT  GG  AGGGGGTCAAGTA
                                   CT  AC
GAM184  LOC155032 3'  TGTGGGGATGATGCAGGGG   87601    A  _        _
                                 CC CC GCATCATCCCC CA
                                 || || |||||||||||  ||
                                 GG GG CGTAGTAGGGG GT
                                  _  A         T
GAM184  LOC205100 5'  ATTGGGTGGATGATGCGG    92389          _
                                 CCGCATCATCC CCCAGT
                                 ||||||||||| ||||||
                                 GGCGTAGTAGG GGGTTA
                                        T
GAM184  LOC220766 5'  ATGGTGAGGGGATGATGAGGTG 92473       G        _  GT
           G                     CCACC CATCATCCCC CA  TCAT
                                 ||||| ||||||||||  ||  ||||
                                 GGTGG GTAGTAGGGG GT  GGTA
                                    A         A  __
GAM184  LOC257541 3'  ATGAACTGAGGTGAGAGCGG   99595      A  A  _  C
                                 CCGC TC TC CC CAGTTCAT
                                 |||| || || || ||||||||
                                 GGCG AG AG GG GTCAAGTA
                                   _  _  T  A
GAM184  LOC92228  3'  AACTGGGGGCCGGGCGCGTGG  69064      _   A  AT
                                 CCAC CGC TC  CCCCCAGTT
                                 |||| ||| ||  |||||||||
                                 GGTG GCG GG  GGGGGTCAA
                                   C   _  CC
GAM185  SCAMP1   3'  GCTAAATAAATATTCTCC    54500     T     C
                                 GGA AATATT ATTTAGC
                                 ||| |||||| |||||||
                                 CCT TTATAA TAAATCG
                                   C     A
GAM185  SCAMP1   3'  GCTAAATAAATATTCTCC    54501     T     C
                                 GGA AATATT ATTTAGC
                                 ||| |||||| |||||||
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                                CCT TTATAA TAAATCG
                                  C     A
GAM185  NX-17    3'  TGAATATCAGCCCCTAATA   40706        ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM185  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
              TA                  TATTAGGGATAATATTCATTTAGC
                                  ||||||||||||||||||||||||
                                  ATAATCCCTATTATAAGTAAATCG

GAM186  ADCY8    5'  CACCGCTCCTCCACCTGC    8497      A      GC  A
                                GCAG TGGAGGAG  CG TG
                                |||| ||||||||  || ||
                                CGTC ACCTCCTC  GC AC
                                  C       __ C
GAM186  ADRBK1   3'  GGTCTCCTCCACCGCCA     9668      AGA
                                TGGC   TGGAGGAGGCC
                                ||||   ||||||||||
                                ACCG   ACCTCCTCTGG
                                  CC_
GAM186  ATP7B    5'  CACGCTCTCCTCCACCGACCA  5333      CAGA      GC  A
                                TGG    TGGAGGAG  CG TG
                                |||    ||||||||  || ||
                                ACC    ACCTCCTC  GC AC
                                  AGCC       TC  _
GAM186  CSTB     3'  GTCATCCTCCGTCTACCA    5438      C         _
                                TGG AGATGGAGGA GGC
                                ||| |||||||||| |||
                                ACC TCTGCCTCCT CTG
                                  A        A
GAM186  DAZ      3'  ATCCTCCTCCTCCACCA     83002     CAGA      CC
                                TGG    TGGAGGAGG  GAT
                                |||    |||||||||  |||
                                ACC    ACCTCCTCC  CTA
                                  ____       TC
GAM186  DAZ      3'  ATCCTCCTCCTCCACCA     83003     CAGA      CC
                                TGG    TGGAGGAGG  GAT
                                |||    |||||||||  |||
                                ACC    ACCTCCTCC  CTA
                                  ____       TC
GAM186  DAZ      3'  ATCCTCCTCCTCCACCA     83004     CAGA      CC
                                TGG    TGGAGGAGG  GAT
                                |||    |||||||||  |||
                                ACC    ACCTCCTCC  CTA
                                  ____       TC
GAM186  DHCR24   3'  CATCGCCTCCATCAGCCA    29297     A      AGGC
                                TGGC GATGGAGG   CGATG
                                |||| ||||||||   |||||
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                                ACCG CTACCTCC   GCTAC
                                  A     ____
GAM186  EHF     5' GCCTCCCCTCCATCAACCA  25125    CA    __
                                TGG  GATGGA  GGAGGC
                                |||  ||||||  ||||||
                                ACC  CTACCT  CCTCCG
                                  AA     CC
GAM186  FANCC   3' TCTTCCTCCTCCCCTGCCA  71050      AT     CC
                                TGGCAG  GGAGGAGG  GA
                                ||||||  ||||||||  ||
                                ACCGTC  CCTCCTCC  CT
                                   C_      TT
GAM186  SCA1    5' ATCTCCTCCTCCACTGCCA  6170       A      CC
                                TGGCAG TGGAGGAGG  GAT
                                ||||||  |||||||||  |||
                                ACCGTC ACCTCCTCC  CTA
                                   _       T_
GAM186  TNFRSF1B 3' CATCCAACCCCCCACCTGCCA 8389       A  A  A  CC_
                                TGGCAG TGG GG GG   GATG
                                ||||||  |||  ||  ||   ||||
                                ACCGTC ACC CC CC   CTAC
                                   C   _  _  AAC
GAM186  UVRAG   3' GCCTTCCCCTCCTCTGCCA   14025      T    ___
                                TGGCAGA GGAGG   AGGC
                                |||||||  |||||   ||||
                                ACCGTCT CCTCC   TCCG
                                   _    CCT
GAM186  ARHGDIG  3' GCCACTCCTCCAGCTGCCA   8623       A     __
                                TGGCAG TGGAGGA  GGC
                                ||||||  |||||||  |||
                                ACCGTC ACCTCCT  CCG
                                   G      CA
GAM186  CAPN13   5' CATGCTCTCCTCCTCTGCCA  58628       T     _ CG
                                TGGCAGA GGAGGAG GC  ATG
                                |||||||  |||||||  ||  |||
                                ACCGTCT CCTCCTC CG  TAC
                                   _      T  __
GAM186  DKFZP434P0111 3' CATCCCACTCCTCTGCCA   67952       T   GA  CC
                                TGGCAGA GGAG  GG  GATG
                                |||||||  ||||  ||  ||||
                                ACCGTCT CCTC  CC  CTAC
                                   _   A_  __
GAM186  FLJ10521  3' GTCACCAGCCTCCTGATCTGCC 36721        GG      CGA
          A                      TGGCAGAT  AGGAGGC   TGAC
                                |||||||||  |||||||   ||||
                                ACCGTCTA  TCCTCCG   ACTG
                                   G_      ACC
GAM186  FLJ10815 3' TCTCCTCCTCCATCCCCA   37236     CA        CC
                                TGG  GATGGAGGAGG  GA
                                |||  ||||||||||  ||
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                                ACC  CTACCTCCTCC  CT
                                  C_         T_
GAM186  FLJ14642  3'  GTCACCAACCTCCTCCTCGTC  52579     A  T       CCGA
                                GGC GA GGAGGAGG    TGAC
                                ||| || ||||||||    ||||
                                CTG CT CCTCCTCC    ACTG
                                  _ _       AACC
GAM186  FLJ20040  3'  CACCGGCCTCCCGCCTGC    39157     A   AG      A
                                GCAG TGG  GAGGCCG TG
                                |||| |||  ||||||| ||
                                CGTC GCC  CTCCGGC AC
                                  C  __      C
GAM186  FLJ23119  3'  CATCGGCCTCTAGTTCTCCA   45375     C   TGGA
                                TGG AGA    GGAGGCCGATG
                                ||| |||    ||||||||||
                                ACC TCT    TCTCCGGCTAC
                                  _  TGA_
GAM186  GMPPB     3'  ATGGGACTCCCTCCATCCACCA 97435     CA      AG _  G
                                TGG  GATGGAGG  G CC AT
                                |||  ||||||||  | || ||
                                ACC  CTACCTCC  C GG TA
                                  AC       CT A  G
GAM186  KIAA0406  3'  GTCAGTTCCCCTCCATCTGC   61999          A  CCGA
                                GCAGATGGAGG GG    TGAC
                                ||||||||||| ||    ||||
                                CGTCTACCTCC CC    ACTG
                                       _ TTG_
GAM186  KIAA0620  3'  GTCAGGCTCCCCCATCTGCC   62815         A  AG   GA
                                GGCAGATGG GG  GCC  TGAC
                                |||||||| ||  |||  ||||
                                CCGTCTACC CC  CGG  ACTG
                                      _ CT  __
GAM186  KIAA1453  3'  CATGTCTCCTCCACCAGCCA   47658      AGA        CG
                                TGGC   TGGAGGAGGC  ATG
                                ||||   ||||||||||  |||
                                ACCG   ACCTCCTCTG  TAC
                                  ACC         __
GAM186  KIAA1530  3'  CATCAGCACTTTCTCCCTCTGC 68550        T     _ _  C
          CA                      TGGCAGA GGAGGA G GC GATG
                                |||||||  ||||||  | || ||||
                                ACCGTCT CCTCTT C CG CTAC
                                    C     T A  A
GAM186  KIAA1908  5'  GTCTCCCTCCTCCACCGCCA   73796      AGA       CC
                                TGGC   TGGAGGAGG  GAT
                                ||||   |||||||||  |||
                                ACCG   ACCTCCTCC  CTG
                                  CC_        CT
GAM186  KIAA1937  3'  TCACAGGCCCCCATCTGC    74074         A  AG   GA
                                GCAGATGG GG  GCC  TGA
                                ||||||||  ||  |||  |||
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                                CGTCTACC CC  CGG  ACT
                                     _ __   AC
GAM186  PEG10    3'  GTCAGTAGCCCTCCTCCTACCA 31204     CAGAT      _ CGA
                                TGG    GGAGGAGG C   TGAC
                                |||    |||||||| |   ||||
                                ACC    CCTCCTCC G   ACTG
                                  AT___       C ATG
GAM186  PRO1617  5'  GTCAAGTTTTCCTCCCCCCACC 38338     CAGAT      CCGA
            A                    TGG    GGAGGAGG    TGAC
                                |||    ||||||||    ||||
                                ACC    CCTCCTTT    ACTG
                                  ACCCC       TGA_
GAM186  SIAT8C   5'  GTCCCCCTCCTCCGCCA     32450      AGAT       CC
                                TGGC   GGAGGAGG  GAT
                                ||||   ||||||||  |||
                                ACCG   CCTCCTCC  CTG
                                  _____       CC
GAM186  LOC138311 5'  TCTCGGGCTCCGTCTGCCA    76722        GGA    G    T
                                TGGCAGAT   GGAG CCGA GA
                                ||||||||   |||| |||| ||
                                ACCGTCTG   CCTC GGCT CT
                                     ___    G   _
GAM186  LOC146488 5'  TCACCGGCCTCCTCAACCTCC  71363    C  ATG        A
                                GG AG   GAGGAGGCCG TGA
                                || ||   ||||||||||| |||
                                CC TC   CTCCTCCGGC ACT
                                 _  CAA         C
GAM186  LOC147299 3'  TCACCGTCTACCCCCATCTGCC 78983          A  _    C A
            A                    TGGCAGATGG GG AGGC G TGA
                                ||||||||||| || |||| | |||
                                ACCGTCTACC CC TCTG C ACT
                                      C  A    _ C
GAM186  LOC163782 5'  CACCGGCCTCCTCCTCCTCCCC 83034      _____  AT         A
            GCCA                    TGGC    AG  GGAGGAGGCCG TG
                                ||||    ||  ||||||||||| ||
                                ACCG    TC  CCTCCTCCGGC AC
                                  CCCC  CT          C
GAM186  LOC197350 3'  CATTCTTGCCTCCATCCACC   89399    CA       _   CC
                                GG  GATGGAGG AGG  GATG
                                ||  |||||||| |||  ||||
                                CC  CTACCTCC TTC  TTAC
                                 AC       G   __
GAM186  LOC201191 3'  ATCAGCCCTCCCCCATCTGCC  91341          A    _ C
                                GGCAGATGG GGAGG C GAT
                                ||||||||| ||||| | |||
                                CCGTCTACC CCTCC G CTA
                                      C    C A
GAM186  LOC221773 3'  GCCCATCCCCCCACCTGCCA    92695       A   A   __
                                TGGCAG TGG GGA  GGC
                                |||||| ||| |||  |||
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                                ACCGTC ACC CCT  CCG
                                   C   C   AC
GAM186  LOC221833 3'  GTCCTCCCCTCCTCCACCCCCC 94116     CAGA       CC  T
          A                     TGG    TGGAGGAGG  GA GAC
                                |||    |||||||||  || |||
                                ACC    ACCTCCTCC  CT CTG
                                  CCCC        C_  C
GAM186  LOC91813  5'  GCCACCGTATATCATCTGCCA  67842          A____  A
                                TGGCAGATGG     GG GGC
                                ||||||||||     || |||
                                ACCGTCTACT     CC CCG
                                      ATATG  A
GAM187  HMG20A    3'  ACCCACATACCATCACTTGGCA 37059          G   ACACACA
                                TGCCAAGTGG TGG       GGT
                                |||||||||| |||       |||
                                ACGGTTCACT ACC       CCA
                                      _   ATACAC_
GAM187  PROML1    3'  ACCTGCGTAACTCCATCTGAC  21199    _      C__  A
                                GT GGGTGGA   AC CAGGT
                                || |||||||   || |||||
                                CA TCTACCT   TG GTCCA
                                 G      CAA  C
GAM187  SYN3      3'  ACCCACGTGCCTGCTTACCTGC 56903    C  A    TG A   ACA
          CA                      TG CA GTGGG  G CAC   GGT
                                || || |||||  | |||   |||
                                AC GT CATTC  C GTG   CCA
                                 C  C    GT C   CAC
GAM187  SYN3      3'  ACCCACGTGCCTGCTTACCTGC 56905    C  A    TG A   ACA
          CA                      TG CA GTGGG  G CAC   GGT
                                || || |||||  | |||   |||
                                AC GT CATTC  C GTG   CCA
                                 C  C    GT C   CAC
GAM187  SYN3      3'  ACCCACGTGCCTGCTTACCTGC 14475    C  A    TG A   ACA
          CA                      TG CA GTGGG  G CAC   GGT
                                || || |||||  | |||   |||
                                AC GT CATTC  C GTG   CCA
                                 C  C    GT C   CAC
GAM187  SYNGR1    3'  CCTGCTTACTCACTCAGCA    17500     CA       ACACA
                                TGC  AGTGGGTGG    CAGG
                                |||  |||||||||    ||||
                                ACG  TCACTCATT    GTCC
                                  AC        C____
GAM187  TXNRD1    3'  ACCCATGCATCTGCCTGGCA   13919      A TG    GACA  CA
                                TGCCA G  GGTG    CA  GGT
                                ||||| |  ||||    ||  |||
                                ACGGT C  CTAC    GT  CCA
                                   C GT    _____  AC
GAM187  C20orf151 3'  ACCCCGTCTCCACCCACCTGG  90090     A        C  ACA
                                CCA GTGGGTGGA AC   GGT
                                ||| |||||||| ||   |||
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                                GGT CACCCACCT TG   CCA
                                  C        C  CC_
GAM187  CSMD1    3'  ACCTGTAGACGAAACCCACTTG 73513          GGACAC_
            GCA                   TGCCAAGTGGGT      ACAGGT
                                  ||||||||||||      ||||||
                                  ACGGTTCACCCA      TGTCCA
                                        AAGCAGA
GAM187  CTXL     5'  ACCTTGACCGCCCACCTGGCA  27471      A       A  CAC
                                  TGCCA GTGGGTGG CA   AGGT
                                  ||||| |||||||| ||   ||||
                                  ACGGT CACCCGCC GT   TCCA
                                    C       A  ___
GAM187  DKFZP564O0423 5'  ACCTGTACAACTTCACCTAC   93338         CAC__
                                  GTGGGTGGA    ACAGGT
                                  |||||||||    ||||||
                                  CATCCACTT    TGTCCA
                                       CAACA
GAM187  FLJ20950  5'  ACCTGTGTACCCACCCAAGGC  46939     AAG      AC
                                  GCC   TGGGTGG  ACACAGGT
                                  |||   |||||||  ||||||||
                                  CGG   ACCCACC  TGTGTCCA
                                    A__      CA
GAM187  FLJ22056  5'  ACCTGTGTGAGGACGCCCAGCA 42829     CAAG     GA__
                                  TGC    TGGGTG    CACACAGGT
                                  |||    ||||||    |||||||||
                                  ACG    ACCCGC    GTGTGTCCA
                                    _____     AGGA
GAM187  GGA2     3'  ACCTACATGCTCTTACTTG   31154         T  A  CAC
                                  CAAGTGGG GG CA   AGGT
                                  |||||||| || ||   ||||
                                  GTTCATTC TC GT   TCCA
                                       _ _  ACA
GAM187  GGA2     3'  ACCTACATGCTCTTACTTG   57648         T  A  CAC
                                  CAAGTGGG GG CA   AGGT
                                  |||||||| || ||   ||||
                                  GTTCATTC TC GT   TCCA
                                       _ _  ACA
GAM187  GPA33    3'  ACCTGTGTGCCCAGCACCTGG  20566     A   GG   A
                                  CCA GTG  TGG CACACAGGT
                                  ||| |||  ||| |||||||||
                                  GGT CAC  ACC GTGTGTCCA
                                    C   G_   C
GAM187  H2BFQ    3'  ACCTACGTCATCCACTCAGG   60075    A_       ACACAC
                                  CC  AGTGGGTGG     AGGT
                                  ||  |||||||||     ||||
                                  GG  TCACCTACT     TCCA
                                   AC        GCA___
GAM187  KIAA1718  3'  CTGTGCCACACCCACTCAGCA  64974     CA       GACA
                                  TGC  AGTGGGTG    CACAG
                                  |||  ||||||||    |||||
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                                ACG  TCACCCAC    GTGTC
                                  AC       ACC_
GAM187  LOC147077 3'  CCTGCGTGTCCCATCTAC    78846         _    A
                                GTGGGTGG ACAC CAGG
                                |||||||| |||| ||||
                                CATCTACC TGTG GTCC
                                     C    C
GAM187  LOC147817 3'  ACCTGTGTATCCACCATGCA   79163     CAAGTG     C
                                TGC     GGTGGA ACACAGGT
                                |||     |||||| ||||||||
                                ACG     CCACCT TGTGTCCA
                                  TA____      A
GAM187  LOC153397 3'  CCTGTGCATGTACTTGG     87226        G   GACA
                                CCAAGTG GTG    CACAGG
                                ||||||| |||    ||||||
                                GGTTCAT TAC    GTGTCC
                                    G  ____
GAM187  LOC157376 3'  CCCGTACCTCCACTCGGTA    82353     A     T  ACAC  A
                                TGCC AGTGGG GG    AC GG
                                |||| |||||| ||    || ||
                                ATGG TCACCT CC    TG CC
                                  C      _ A___  C
GAM187  LOC159319 5'  CCTGCCCACCCCCTGGCA     83072       A T      ACACA
                                TGCCA G GGGTGG     CAGG
                                ||||| | ||||||     ||||
                                ACGGT C CCCACC     GTCC
                                   _ C     C____
GAM187  LOC93259  5'  CCTGTCACCCACCTGG      72282     A      GACAC
                                CCA GTGGGTG     ACAGG
                                ||| |||||||     |||||
                                GGT CACCCAC     TGTCC
                                  C      _____
GAM188  CDH12     3'  CTTATCATTTAAAGTGGTGTA  15777          CCCAA   GA
                                TACACCACT     GAA  ATAAG
                                |||||||||     |||  |||||
                                ATGTGGTGA     TTT  TATTC
                                      AA___   AC
GAM188  GOCAP1    3'  ATTGTTCTTGGGAGCAGTGTA  43007       CA         G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC         G
GAM188  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT    98090       T    AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||     ||||||
                                TGGTG GGGT     TTATTC
                                   _    GTCA_
GAM188  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
          A                      TACAC       AGAAGAATAAG
                                |||||       ||||||||||
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                              ATGTG      TCTTCTTATTC
                                 TACTCCC_
GAM188  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126        CCCAAGAA
                              TACACCACT      GAATAAG
                              |||||||||      |||||||
                              ATGTGGTGA      TTTATTC
                                   AGACG___
GAM188  HMP19     3'  CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
           TA                   TACA   TCC   GAAGAATAAG
                              ||||   |||   ||||||||||
                              ATGT   AGG   TTTCTTATTC
                                AAA_  ATTG
GAM188  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA  68742             _
                              TACACCACTCCCAAGA AGA
                              |||||||||||||||| |||
                              ATGTGGTGAGGGTTCT TCT
                                        G
GAM188  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                              CAC  CT CCAAGAAGAA
                              |||  || ||||||||||
                              GTG  GA GGTTCTTTTT
                                AC  A
GAM188  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748     CCA__
                              ACTC    AGAAGAATAAG
                              ||||    ||||||||||
                              TGAG    TCTTCTTATTC
                                TACCG
GAM188  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                              CCA    CAAGAAGAATAAG
                              |||    ||||||||||||
                              GGT    GTTCTTCTTATTC
                                TTTCA
GAM188  OSBPL11   3'  CTTAATTTCCCAAGAGTGGTG  43206        CCAA    AA
                              CACCACTC   GAAG  TAAG
                              ||||||||   ||||  ||||
                              GTGGTGAG   CTTT  ATTC
                                   AACC   A_
GAM188  YME1L1    3'  TCATTCTTGATGTGGTGTA   58438        TCC     _
                              TACACCAC   CAAGAA GA
                              ||||||||   |||||| ||
                              ATGTGGTG   GTTCTT CT
                                   TA_     A
GAM188  ZNF262    3'  CTTATTTTGTTTGGGAGT    18723         A
                              ACTCCCAAG AGAATAAG
                              ||||||||| ||||||||
                              TGAGGGTTT TTTTATTC
                                   G
GAM188  LOC91960  3'  TGTGGCTTGGAACGTGGTGTA  68294        TC_    AAGA
                              TACACCAC   CCAAG   ATA
                              ||||||||   |||||   |||
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                                ATGTGGTG  GGTTC   TGT
                                    CAA   GG__
GAM189  TEM8     3' ATGGAAGCATTTCCTATCCA  50823       TTAT  TA
                                TGGATAGG   TG  CTTCCAT
                                ||||||||   ||  |||||||
                                ACCTATCC   AC  GAAGGTA
                                    TTT_  __
GAM189  ZNF8     3' AGGTAATATAACCTACCCAC  64769     A      TG
                                GTGG TAGGTTAT  TACTT
                                |||| ||||||||  |||||
                                CACC ATCCAATA  ATGGA
                                  C       TA
GAM189  KIAA0469 3' AAGTATTTCCTATCCAT    29961        TTATT
                                GTGGATAGG    GTACTT
                                |||||||||    ||||||
                                TACCTATCC    TATGAA
                                     TT___
GAM189  ZNF11B   3' GTTCAATAACTATCCAC    74436        G     T
                                GTGGATAG TTATTG AC
                                |||||||| |||||| ||
                                CACCTATC AATAAC TG
                                    _     T
GAM189  LOC116437 3' TGGAAGTACCACTTTCCAC   74328      T   TATT
                                GTGGA AGGT   GTACTTCCA
                                ||||| ||||   |||||||||
                                CACCT TTCA   CATGAAGGT
                                  _   C___
GAM189  LOC148738 3' GAAGTATCATCCCTACCC    59889    A   TT  T
                                GG TAGG  AT GTACTTC
                                || ||||  || |||||||
                                CC ATCC  TA TATGAAG
                                 C   C_  C
GAM189  LOC203523 3' AGACAACATAATCTACCCAC  90940     A      __  A
                                GTGG TAGGTTAT  TGT CT
                                |||| ||||||||  ||| ||
                                CACC ATCTAATA  ACA GA
                                  C       CA  _
GAM190  CDH12    3' CTTATCATTTAAAGTGGTGTA  15777        CCCAA  GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM190  GOCAP1   3' ATTGTTCTTGGGAGCAGTGTA  43007      CA       G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM190  DKFZp434N2435 5' CTTATTACTGTGGGGTGGT   98090      T   AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
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                                TGGTG GGGT    TTATTC
                                  _   GTCA_
GAM190  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
          A                      TACAC       AGAAGAATAAG
                                 |||||       ||||||||||
                                 ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM190  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                 TACACCACT       GAATAAG
                                 |||||||||       |||||||
                                 ATGTGGTGA       TTTATTC
                                      AGACG___
GAM190  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
          TA                     TACA   TCC   GAAGAATAAG
                                 ||||   |||   ||||||||||
                                 ATGT   AGG   TTTCTTATTC
                                   AAA_  ATTG
GAM190  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA  68742              _
                                 TACACCACTCCCAAGA AGA
                                 |||||||||||||||| |||
                                 ATGTGGTGAGGGTTCT TCT
                                           G
GAM190  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                 CAC  CT CCAAGAAGAA
                                 |||  || ||||||||||
                                 GTG  GA GGTTCTTTTT
                                   AC  A
GAM190  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748     CCA__
                                 ACTC    AGAAGAATAAG
                                 ||||    ||||||||||
                                 TGAG    TCTTCTTATTC
                                   TACCG
GAM190  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                                 CCA    CAAGAAGAATAAG
                                 |||    ||||||||||||
                                 GGT    GTTCTTCTTATTC
                                   TTTCA
GAM190  OSBPL11   3'  CTTAATTTCCCAAGAGTGGTG  43206        CCAA    AA
                                 CACCACTC    GAAG  TAAG
                                 ||||||||    ||||  ||||
                                 GTGGTGAG    CTTT  ATTC
                                      AACC    A_
GAM190  YME1L1    3'  TCATTCTTGATGTGGTGTA    58438        TCC     _
                                 TACACCAC   CAAGAA GA
                                 ||||||||   |||||| ||
                                 ATGTGGTG   GTTCTT CT
                                      TA_     A
GAM190  ZNF262    3'  CTTATTTTGTTTGGGAGT     18723         A
                                 ACTCCCAAG AGAATAAG
                                 |||||||||  ||||||||
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                                TGAGGGTTT TTTTATTC
                                     G
GAM190  LOC91960  3'  TGTGGCTTGGAACGTGGTGTA  68294        TC_    AAGA
                                TACACCAC  CCAAG   ATA
                                ||||||||  |||||   |||
                                ATGTGGTG  GGTTC   TGT
                                     CAA    GG__
GAM191  BGN     3'  CCAGCCCCCCACCTCGGGTCCC 9923         C   CAGAGA
          T                      AGGGACCC AGGT     CTGG
                                ||||||||| ||||     ||||
                                TCCCTGGG TCCA     GACC
                                     C   CCCCCC
GAM191  BLMH    3'  TCCAGTCTCCACCAGGAACCT  6361     GA  CCA   CA
                                AGG  CC   GGT  GAGACTGGA
                                |||  ||   |||  |||||||||
                                TCC  GG   CCA  CTCTGACCT
                                  AA  A__   C_
GAM191  HSPA1B  5'  CCAGTCTCAGAGCGGAGCCC   19273    AC  CAGG  A
                                GGG  CC    TC GAGACTGG
                                |||  ||    || ||||||||
                                CCC  GG    AG CTCTGACC
                                  GA  CG__  A
GAM191  HTRA3   3'  CCACCTGACCTGAGGCCCC   90577    A  C       AGAC
                                GGG CC CAGGTCAG    TGG
                                ||| || ||||||||    |||
                                CCC GG GTCCAGTC    ACC
                                  C  A       C___
GAM191  HTRA3   3'  CTGCCAGCCTGGGGTCCCT   90580           ___
                                AGGGACCCCAGGT   CAG
                                ||||||||||||   |||
                                TCCCTGGGGTCCG   GTC
                                       ACC
GAM191  IL2RB   3'  CCAGCTAACTCTGACCTGGGAG 7935      AC         A___
            CCCT                  AGGG  CCCAGGTCAGAG    CTGG
                                ||||  ||||||||||||    ||||
                                TCCC  GGGTCCAGTCTC    GACC
                                  GA          AATC
GAM191  LENG4   3'  CCTATGACCTGGGTCCCT    44417        C     GAGACT
                                AGGGACCC AGGTCA     GG
                                |||||||| ||||||     ||
                                TCCCTGGG TCCAGT     CC
                                     _     AT_____
GAM191  LNK     3'  TCCTGCCCGGGGTCCCT     19652         A  T   A
                                AGGGACCCC GG CAG GA
                                ||||||||| || ||| ||
                                TCCCTGGGG CC GTC CT
                                     C  _   _
GAM191  LY95    5'  CCAGTCTTCTCCAGGTGTCCC  17896      C  A  TCA
                                GGGAC CC GG   GAGACTGG
                                ||||| || ||   ||||||||
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                                CCCTG GG CC   TTCTGACC
                                  T  A  TC_
GAM191  MOG     3'  TCCAGTCTTCCACCTGGAAGCC 11676     ACC     CA
            CT                   AGGG   CCAGGT  GAGACTGGA
                                ||||   ||||||  |||||||||
                                TCCC   GGTCCA  TTCTGACCT
                                  GAA     CC
GAM191  NESH    5'  CCAGTCTCCGACCCCATCCC  33570     CCCCA   A
                                GGGA    GGTC GAGACTGG
                                ||||    |||| ||||||||
                                CCCT    CCAG CTCTGACC
                                  ACC__   C
GAM191  NFATC1  3'  CCAGCCCTTCTGGCACCCCT  21596     ACCCCAG     A__
                                AGGG     GTCAGAG  CTGG
                                ||||     |||||||  ||||
                                TCCC     CGGTCTT  GACC
                                  CA_____     CCC
GAM191  RANBP3  3'  CCAACTATAGGCCTGGGACCCC 24641    AC      AG_  AC
                                GGG  CCCAGGTC   AG  TGG
                                |||  ||||||||   ||  |||
                                CCC  GGGTCCGG   TC  ACC
                                  CA       ATA  A_
GAM191  RANBP3  3'  CCAACTATAGGCCTGGGACCCC 14633    AC      AG_  AC
                                GGG  CCCAGGTC   AG  TGG
                                |||  ||||||||   ||  |||
                                CCC  GGGTCCGG   TC  ACC
                                  CA       ATA  A_
GAM191  RGS19IP1 3'  CCAGTCTGGCCGGGGTCCC   63169       A    GA
                                GGGACCCC GGTCA  GACTGG
                                |||||||| |||||  ||||||
                                CCCTGGGG CCGGT  CTGACC
                                    _    __
GAM191  SIRT2   3'  CCAATCTCTTACAGCTCCCT  25286     CCCCAG  C    C
                                AGGGA     GT AGAGA TGG
                                |||||     || ||||| |||
                                TCCCT     CA TCTCT ACC
                                  CGA___  T    A
GAM191  SIRT2   3'  CCAATCTCTTACAGCTCCCT  48360     CCCCAG  C    C
                                AGGGA     GT AGAGA TGG
                                |||||     || ||||| |||
                                TCCCT     CA TCTCT ACC
                                  CGA___  T    A
GAM191  SREBF1  3'  TCCTGACCTGAGGCTCCT    96078    GA  C      A
                                AGG  CC CAGGTCAG GA
                                |||  || |||||||| ||
                                TCC  GG GTCCAGTC CT
                                  TC  A      _
GAM191  TEM5    3'  CCAAGGTCTGACCTAGGGTTCC 52297       C      GA  _
                                GGGACCC AGGTCAGA  CT GG
                                ||||||| ||||||||  || ||
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                                CCTTGGG TCCAGTCT  GA CC
                                    A       G_  A
GAM191  TIMM17B  3'  CCAGTTAGCCCTGGGACCCT  20690     AC     TCAGA
                                AGGG  CCCAGG    GACTGG
                                ||||  ||||||    ||||||
                                TCCC  GGGTCC    TTGACC
                                  A_     CGA__
GAM191  ARHGDIG  3'  CCTGCTCTGTCCCGGGACCCC  8620     AC   A  T    ACT
                                GGG  CCC GG CAGAG   GG
                                |||  ||| || |||||   ||
                                CCC  GGG CC GTCTC   CC
                                  CA   C  T    GT_
GAM191  ATP5D    3'  CCAGCTCCTGGGGTCCC     9859          TCAG  A
                                GGGACCCCAGG    AG CTGG
                                ||||||||||    || ||||
                                CCCTGGGGTCC    TC GACC
                                      _____  _
GAM191  C17orf31  3'  CCTTATCAACCTGGGTCCCT  34538        C    CA  GACT
                                AGGGACCC AGGT  GA    GG
                                |||||||| ||||  ||    ||
                                TCCCTGGG TCCA  CT    CC
                                    _    A_  ATT_
GAM191  C2orf7   3'  TCCAGCCTCCCCTACCCAGGGT 51274        CA   CA__   A
           CTCT                   AGGGACCC  GGT    GAG CTGGA
                                |||||||  |||    ||| |||||
                                TCTCTGGG  CCA    CTC GACCT
                                     AC   TCCC   C
GAM191  CLIPR-59  3'  TCCAGGGCGGACCTGGGGCCCC 32021     A       AGAGA
                                GGG CCCCAGGTC     CTGGA
                                ||| |||||||||     |||||
                                CCC GGGGTCCAG     GACCT
                                  C        GCGG_
GAM191  CLIPR-59  5'  CCAGTCTCCACTTTGGTCCC   32015       CC    CA
                                GGGACC  AGGT  GAGACTGG
                                ||||||  ||||  ||||||||
                                CCCTGG  TTCA  CTCTGACC
                                    T_    C_
GAM191  COL12A1   3'  CCAGTCTCTGACCCTTCCC    16470     CCCCA
                                GGGA    GGTCAGAGACTGG
                                ||||    ||||||||||||
                                CCCT    CCAGTCTCTGACC
                                  TC____
GAM191  COL12A1   3'  CCAGTCTCTGACCCTTCCC    55534     CCCCA
                                GGGA    GGTCAGAGACTGG
                                ||||    ||||||||||||
                                CCCT    CCAGTCTCTGACC
                                  TC____
GAM191  CYP2A7   5'  TCAGCTGCCCTGGGGTCCC    48354          T   AGA
                                GGGACCCCAGG CAG   CTGG
                                |||||||||| |||   ||||
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                                CCCTGGGGTCC GTC   GACT
                                      C  ___
GAM191  CYP2A7   5'  TCAGCTGCCCTGGGGTCCC   7542          T  AGA
                                GGGACCCCAGG CAG   CTGG
                                |||||||||| |||   ||||
                                CCCTGGGGTCC GTC   GACT
                                      C  ___
GAM191  FASTK    3'  CCAGGATACCGGGGTCCC    47685        A  CAGAGA
                                GGGACCCC GGT     CTGG
                                |||||||| |||     ||||
                                CCCTGGGG CCA     GACC
                                   _  TAG___
GAM191  FBXL9    3'  CCAGTCTCCAACCCTGGCCTT  25139     ACC    TCA_
                                AGGG   CCAGG   GAGACTGG
                                ||||   |||||   ||||||||
                                TTCC   GGTCC   CTCTGACC
                                  ___    CAAC
GAM191  FLJ10874 3'  TCCAGAAAGAGTGACCTGGTGT 37330      C      GAGA__
           CCC                    GGGAC CCAGGTCA     CTGGA
                                |||||| ||||||||     |||||
                                CCCTG GGTCCAGT     GACCT
                                   T       GAGAAA
GAM191  FLJ13241 3'  CCAGTCTCTCAGGCCTCCC   47649     CCCCA   __
                                GGGA    GGTC  AGAGACTGG
                                ||||    ||||  |||||||||
                                CCCT    CCGG  TCTCTGACC
                                  ______   AC
GAM191  GIT1     3'  CCAACCTGTGTGCTGGGGTCCC 26720         GT  G  AC
                                GGGACCCCAG  CA AG  TGG
                                ||||||||||  || ||  |||
                                CCCTGGGGTC  GT TC  ACC
                                      GT  G  CA
GAM191  HYPC     5'  CCAGCCCCTGGAACAGGGGTTC 65216         AGG_   AGA
           CT                    AGGGACCCC   TCAG   CTGG
                                |||||||||   ||||  ||||
                                TCCTTGGGG   GGTC   GACC
                                     ACAA    CCC
GAM191  KIAA0258 3'  CCAGCCTCCTAGGATCCC    29466     C  C   TCAG  A
                                GGGA CC AGG    AG CTGG
                                |||| || |||    || ||||
                                CCCT GG TCC    TC GACC
                                  A  A  _____  C
GAM191  KIAA0397 3'  CCACGAGTGAACCTGGGGCCCC 62345     A      _  GAGAC
                                GGG CCCCAGGT CA    TGG
                                ||| ||||||| ||    |||
                                CCC GGGGTCCA GT    ACC
                                  C       A  GAGC_
GAM191  KIAA0447 3'  TCCAGTTTCCCTGCGGGCCCCT 72130     A  _   TCA
                                AGGG CCC CAGG   GAGACTGGA
                                |||| ||| ||||   |||||||||
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                                TCCC GGG GTCC   CTTTGACCT
                                  C   C   ___
GAM191  KIAA0449  5'  CAGTTCCCTGGGGTCCCT    34634          TCAGA
                                AGGGACCCCAGG    GACTG
                                ||||||||||||    |||||
                                TCCCTGGGGTCC    TTGAC
                                      C____
GAM191  KIAA0493  5'  CCAGCCCGAGACGCCTGGGGTC 64930          CAGAGA__
          CC                    GGGACCCCAGGT      CTGG
                                ||||||||||||      ||||
                                CCCTGGGGTCCG      GACC
                                      CAGAGCCC
GAM191  KIAA0674  3'  TCAGACTGACCTGGGAGCCCT  61244     AC       AGA
                                AGGG  CCCAGGTCAG   CTGG
                                ||||  ||||||||||   ||||
                                TCCC  GGGTCCAGTC   GACT
                                  GA        A__
GAM191  KIAA1130  5'  CCAGTCCCCCACCTGGGGCGCC 63082     A_      CAGA
          C                     GGG  CCCCAGGT    GACTGG
                                |||  ||||||||    ||||||
                                CCC  GGGGTCCA    CTGACC
                                  GC       CCCC
GAM191  KIAA1465  3'  TCCAGCCCGGTGCCTGGGGCGC 61510     GA       CAGAGA
          CT                    AGG  CCCCAGGT     CTGGA
                                |||  ||||||||     |||||
                                TCC  GGGGTCCG     GACCT
                                  GC       TGGCCC
GAM191  KIAA1719  3'  TCTGTCTCCAACCTGGGGTCCC 68740          CA     T
          T                     AGGGACCCCAGGT  GAGAC GGA
                                ||||||||||||  ||||| |||
                                TCCCTGGGGTCCA  CTCTG TCT
                                      AC    _
GAM191  KIAA1856  3'  CCGGCCCAAGCCCAGGGTCCCT 94230        CA   CAGAGA
                                AGGGACCC  GGT     CTGG
                                ||||||||  |||     ||||
                                TCCCTGGG  CCG     GGCC
                                    AC   AACCC_
GAM191  KIAA1924  3'  TCCAGCTTCATGTGACCCTGGG 74059        CA    ____   A
          TCCCT                   AGGGACCC  GGTCA    GAG CTGGA
                                ||||||||  |||||    ||| |||||
                                TCCCTGGG  CCAGT    TTC GACCT
                                    TC    GTAC  _
GAM191  KIAA1949  5'  CCAGTCTCCGGATCTCCC    99590     CCCCA   A_
                                GGGA    GGTC  GAGACTGG
                                ||||    ||||  ||||||||
                                CCCT    CTAG  CTCTGACC
                                  _____   GC
GAM191  KIAA1949  5'  CCAGTCTCCGGATCTCCC    99694     CCCCA   A_
                                GGGA    GGTC  GAGACTGG
                                ||||    ||||  ||||||||
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                              CCCT    CTAG  CTCTGACC
                                _____   GC
GAM191  KIAA1949 5' CCAGTCTCCGGATCTCCC    93717     CCCCA   A_
                              GGGA    GGTC  GAGACTGG
                              ||||    ||||  ||||||||
                              CCCT    CTAG  CTCTGACC
                                _____   GC
GAM191  KIAA1978 3' CCAGCCGTGGGGCCCGGGGTCC 74890         A   AGAGA_
          CT                   AGGGACCCC GGTC     CTGG
                              ||||||||| ||||     ||||
                              TCCCTGGGG CCGG     GACC
                                   C    GGTGCC
GAM191  LASP1    3' CCAGTCTCCAGGGACCCT    21576     A   CAGGTCA
                              AGGG CCC      GAGACTGG
                              |||| |||      ||||||||
                              TCCC GGG      CTCTGACC
                                A   AC_____
GAM191  MAPK11   3' TTCTGGCCTAGGACCCCT    12314     AC  C
                              AGGG  CC AGGTCAGAG
                              ||||  || |||||||||
                              TCCC  GG TCCGGTCTT
                                CA  A
GAM191  MAPK11   3' TTCTGGCCTAGGACCCCT    58102     AC  C
                              AGGG  CC AGGTCAGAG
                              ||||  || |||||||||
                              TCCC  GG TCCGGTCTT
                                CA  A
GAM191  MGC14859 3' TCTCTGACTGGGGCCCCT    62604     A     G
                              AGGG CCCCAG TCAGAGA
                              |||| |||||| |||||||
                              TCCC GGGGTC AGTCTCT
                                C     _
GAM191  MGC15438 5' CCAGTCTCACAAAGGCCCC    52850     A  CCAG  CA
                              GGG CC    GT  GAGACTGG
                              ||| ||    ||  ||||||||
                              CCC GG    CA  CTCTGACC
                                C  AAA_  __
GAM191  NLI-IF   3' TCCAACTGTTTCTGAAGCCCCT 41344      ACCCCAGG      ___
                              AGGG       TCAGAGAC   TGGA
                              ||||       ||||||||   ||||
                              TCCC       AGTCTTTG   ACCT
                                CGA_____       TCA
GAM191  NOLC1    3' TCCAGTGGACCTGGGAACCCT  17637     AC       AGAG
                              AGGG  CCCAGGTC    ACTGGA
                              ||||  ||||||||    ||||||
                              TCCC  GGGTCCAG    TGACCT
                                AA       G___
GAM191  PRO2389  3' CCAGTCAGCTTGGGTCCCT    64475       C    CAGA
                              AGGGACCC AGGT    GACTGG
                              |||||||| ||||    ||||||
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                                TCCCTGGG TTCG   CTGACC
                                    _   A___
GAM191  SHANK3   3'  CCAGCCTGAGCGGGGTTCC   66102       AGG   AGA
                                GGGACCCC  TCAG  CTGG
                                ||||||||  ||||  ||||
                                CCTTGGGG  AGTC  GACC
                                    CG_   C__
GAM191  SMARCA4  3'  TCCAGTCTCGACCCCGAGCCCC 13248     ACCCCA   A
           T                     AGGG     GGTC GAGACTGGA
                                ||||     |||| |||||||||
                                TCCC     CCAG CTCTGACCT
                                  CGAGCC   _
GAM191  SPIB     3'  CCACTTGTGCCTGGGGTCCCT  13355          CA   AC
                                AGGGACCCCAGGT  GAG  TGG
                                ||||||||||||  |||  |||
                                TCCCTGGGGTCCG  TTC  ACC
                                       TG  __
GAM191  SYNGR4   5'  CCAGGGCTGGCCTGAAGCCC  25864    ACCC      AGA
                                GGG   CAGGTCAG  CTGG
                                |||   ||||||||  ||||
                                CCC   GTCCGGTC  GACC
                                  GAA_      GG_
GAM191  T2BP     5'  CCAGTCTCCTCGATTCCC    70535     CCCCAG  A__
                                GGGA    GTC   GAGACTGG
                                ||||    |||  ||||||||
                                CCCT    TAG  CTCTGACC
                                  _______  CTC
GAM191  TACR3    5'  TCCAGTCTTATCTGAAGACCC  8331     ACCC    CA
                                GGG   CAGGT  GAGACTGGA
                                |||   |||||  |||||||||
                                CCC   GTCTA  TTCTGACCT
                                  AGAA    __
GAM191  TOMM40   3'  CCAGTGGGCCTGGGGTCCC   21482          AGAG
                                GGGACCCCAGGTC   ACTGG
                                ||||||||||||   |||||
                                CCCTGGGGTCCGG   TGACC
                                       G___
GAM191  TREX2    5'  TCCAACCTCTGACTGGCTGGTC 24233      __   G     AC
           CT                    GGGACC  CCAG TCAGAG  TGGA
                                ||||||  |||| ||||||  ||||
                                TCCTGG  GGTC AGTCTC  ACCT
                                   TC   _     CA
GAM191  VPS4A    3'  CCAGCCACTGCCCCTGGGTCCC 26020       CA  T   AGA
           T                     AGGGACCC  GG CAG   CTGG
                                ||||||||  || |||   ||||
                                TCCCTGGG  CC GTC   GACC
                                     TC  C   ACC
GAM191  LOC143287 3'  TCCGCTGTAACCCTAGGACCCC 83831     AC  C   T___   AGAC
                                GGG  CC AGG    CAG    TGGA
                                |||  || |||   |||   ||||
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                                CCC  GG TCC    GTC    GCCT
                                  CA  A   CAAT   ____
GAM191   LOC147136 3'  CCAGTGAGAACTGACCTGAGTC 78862      CC       AG___
              CC                  GGGAC  CAGGTCAG     ACTGG
                                  |||||  ||||||||    |||||
                                  CCCTG  GTCCAGTC     TGACC
                                    A_       AAGAG
GAM191   LOC147929 5'  TCCAGCAGCCTTGGGGTCCC   79273         _  CAGAGA
                                  GGGACCCCA GGT     CTGGA
                                  |||||||||| |||     |||||
                                  CCCTGGGGT CCG     GACCT
                                       T   AC____
GAM191   LOC149566 3'  TCCAGCCTGGATGACCTGGGAC 85654     AC       G__  A
              CCC                   GGG  CCCAGGTCA   AG CTGGA
                                  |||  |||||||||   || |||||
                                  CCC  GGGTCCAGT   TC GACCT
                                    CA        AGG  C
GAM191   LOC149773 5'  CCAGTCTTCTGAGGCCCT    80291      A  C   GTCA
                                  AGGG CC CAG    GAGACTGG
                                  |||| || |||    ||||||||
                                  TCCC GG GTC    TTCTGACC
                                    _ A   ____
GAM191   LOC152189 5'  TCCAGCCCCAGACCCGCCGGGG 81329         A___    AGAGA
              TCCCT                 AGGGACCCC    GGTC     CTGGA
                                  |||||||||   ||||    |||||
                                  TCCCTGGGG    CCAG    GACCT
                                       CCGC    ACCCC
GAM191   LOC153196 5'  CCAGTCTCAGGGGTCACC    87166    _     AGGTCA
                                  GG GACCCC     GAGACTGG
                                  || ||||||     ||||||||
                                  CC CTGGGG     CTCTGACC
                                   A     A_____
GAM191   LOC154807 5'  CTCTGCGACCTGGGGCCCT    87463      A       __
                                  AGGG CCCCAGGTC  AGAG
                                  |||| |||||||||  ||||
                                  TCCC GGGGTCCAG  TCTC
                                    _       CG
GAM191   LOC199958 3'  CCAGTCTCTGGCAACGCCCCT  91490      ACCCCAG
                                  AGGG      GTCAGAGACTGG
                                  ||||      ||||||||||||
                                  TCCC      CGGTCTCTGACC
                                    CGCAA__
GAM191   LOC201685 5'  CCAGTCTCATTGAATCCCT    91840      CCC   GTCA
                                  AGGGA   CAG    GAGACTGG
                                  |||||   |||    ||||||||
                                  TCCCT   GTT    CTCTGACC
                                    AA_   A___
GAM191   LOC204970 3'  CCAGCCGGAGCGTGGGGTCCC  90959         G  CAGAGA
                                  GGGACCCCA GT     CTGG
                                  ||||||||| ||     ||||
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                                CCCTGGGGT CG     GACC
                                     G  AGGCC_
GAM191  LOC221179 3'  CCAGTCTCTCCTCGGAGGCCCT 95193     A  _  _  TC
                                AGGG CC CC AGG  AGAGACTGG
                                |||| || || |||  |||||||||
                                TCCC GG GG TCC  TCTCTGACC
                                  _  A  C  __
GAM191  LOC254105 3'  CCAGTCCAGGGCCTGGGCTCCC 96419     C      AGA
                                GGGA CCCAGGTC   GACTGG
                                |||| ||||||||   ||||||
                                CCCT GGGTCCGG   CTGACC
                                  C       GAC
GAM191  LOC257185 5'  CCAGCATGCCAGGGGTCCC   98020       A  T  GAGA
                                GGGACCCC GG CA   CTGG
                                |||||||| || ||   ||||
                                CCCTGGGG CC GT   GACC
                                     A  _  AC__
GAM191  LOC51161  3'  TCCTGACCTGAGGGCCCT    33046     A  _      A
                                AGGG CCC CAGGTCAG GA
                                |||| ||| |||||||| ||
                                TCCC GGG GTCCAGTC CT
                                  _  A      _
GAM191  LOC91156  5'  CCAACTAAGGCCTGAGAGTCCC 65706      CC_    AG  AC
           T                     AGGGAC   CAGGTC  AG  TGG
                                ||||||  ||||||  ||  |||
                                TCCCTG   GTCCGG  TC  ACC
                                   AGA     AA  A_
GAM192  CDH5     3'  GGCTCCCCAAGGCTGCAAA   10151        A___   A
                                TTTGCAGCTT   GAG TC
                                ||||||||||   ||| ||
                                AAACGTCGGA   CTC GG
                                     ACCC  _
GAM192  DMD      5'  GGTGAGTAAAAGCTGCAGA   15691        AGAGA
                                TTTGCAGCTT    TCACC
                                ||||||||||    |||||
                                AGACGTCGAA    AGTGG
                                     AATG_
GAM192  GTF2H1   3'  TGAGCTAAGTTGCAAA     19211          AGA
                                TTTGCAGCTTAG   TCA
                                ||||||||||||  |||
                                AAACGTTGAATC   AGT
                                      G__
GAM192  JAG1     3'  GAGGTGATCTGCTGCAGA   5812        TTAG      CA
                                TTTGCAGC   AGATCACC  C
                                ||||||||   ||||||||  |
                                AGACGTCG   TCTAGTGG  G
                                     _____       AC
GAM192  LFG      3'  GGTGTCACAAGCTGTAAA   77240        AGA  T
                                TTTGCAGCTT   GA CACC
                                |||||||||   || ||||
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                                AAATGTCGAA   CT GTGG
                                     CA_  _
GAM192  MAPRE1   3'  GGCAGGTGATCATGCTGCAAG  25594        TTAGA      CA
                                TTTGCAGC    GATCACC  CC
                                ||||||||    |||||||  ||
                                GAACGTCG    CTAGTGG  GG
                                    TA___      AC
GAM192  REPS2    3'  GTGGGTGACCTTGTCTGC    17557      CTTA   A
                                GCAG    GAG TCACCCAC
                                ||||    ||| ||||||||
                                CGTC    TTC AGTGGGTG
                                  TG__   C
GAM192  TRAF5    3'  GTGGGTGATGTAGTTACAAA   17282      C    TAGAG
                                TTTG AGCT    ATCACCCAC
                                |||| ||||    |||||||||
                                AAAC TTGA    TAGTGGGTG
                                  A   TG___
GAM192  ARHU     3'  GGTGGGTGACCCAGAGCCACCA 41363      CA_   AGAGA
           AA                    TTTG   GCTT    TCACCCACC
                                ||||   ||||    |||||||||
                                AAAC   CGAG    AGTGGGTGG
                                  CAC    ACCC_
GAM192  C8orf13  3'  TGAATGATCTCTAGTAGACAGA 82483      CA_   T       CC
                                TTTG   GCT AGAGATCA  CA
                                ||||   ||| ||||||||  ||
                                AGAC   TGA TCTCTAGT  GT
                                  AGA   _       AA
GAM192  CECR6    3'  TGAGTGATCTCTAAGGTTG    49935      _         C
                                CAGC TTAGAGATCAC CA
                                |||| ||||||||||| ||
                                GTTG AATCTCTAGTG GT
                                  G          A
GAM192  DKFZP434P106 3'  GGTGAAGAACTGCCCTGAGCTG 68651           ___  A___
           CAAA                   TTTGCAGCTTAG   AG    TCACC
                                |||||||||||   ||    |||||
                                AAACGTCGAGTC   TC    AGTGG
                                      CCG  AAGA
GAM192  EMILIN-2 3'  GGCGGGCCTTCGCCCAGCTGCA 50256         TAGA  TCA   A
           AA                    TTTGCAGCT    GA   CCC CC
                                |||||||||    ||   ||| ||
                                AAACGTCGA    CT   GGG GG
                                     CCCG  TCC   C
GAM192  FLJ20417 5'  GGCACTCTGAGCTACAAA     35603      C       ATCAC
                                TTTG AGCTTAGAG     CC
                                |||| |||||||||     ||
                                AAAC TCGAGTCTC     GG
                                  A        AC___
GAM192  FLJ22938 5'  GGCGGACGAGCTGAAGCTGCAA 45488          AG  A  AC  A
           G                     TTTGCAGCTT  AG TC  CC CC
                                ||||||||||  || ||  || ||
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                                GAACGTCGAA  TC AG  GG GG
                                     G_  G  CA  C
GAM192  MACMARCKS 3'  GGTGGGTGATCTCTAAGCTGCA 43729
           AA                    TTTGCAGCTTAGAGATCACCCACC
                                 ||||||||||||||||||||||||
                                 AAACGTCGAATCTCTAGTGGGTGG

GAM192  PCDH10   3'  TGATGCTCTAAGCTACAAA   53104     C       _
                                 TTTG AGCTTAGAG ATCA
                                 |||| ||||||||| ||||
                                 AAAC TCGAATCTC TAGT
                                   A        G
GAM192  LOC115129 3'  GGTGGGTCCCAGGCCCATAGCT 73627         TAGAGATC___
           GCAAA                   TTTGCAGCT         ACCCACC
                                 |||||||||         |||||||
                                 AAACGTCGA         TGGGTGG
                                      TACCCGGACCC
GAM192  LOC145945 5'  TGACTTCTCAAAGCTGCAAA   84573          A   __
                                 TTTGCAGCTT GAGA  TCA
                                 |||||||||| ||||  |||
                                 AAACGTCGAA CTCT  AGT
                                      A   TC
GAM192  LOC148894 5'  TGGATGATCTCTAAGGGCA   85425     AG         C
                                 TGC  CTTAGAGATCA CCA
                                 |||  |||||||||||| |||
                                 ACG  GAATCTCTAGT GGT
                                   G_         A
GAM192  LOC204161 5'  GTGGGTGACCTGGTGCAAA   92344       G  TAG  A
                                 TTTGCA CT   AG TCACCCAC
                                 |||||| ||   || ||||||||
                                 AAACGT GG   TC AGTGGGTG
                                    _ ____  C
GAM192  LOC221751 5'  GGCTACTTTCTAAGCTACAAA  93681      C         TCAC
                                 TTTG AGCTTAGAGA    CC
                                 |||| ||||||||||    ||
                                 AAAC TCGAATCTTT    GG
                                   A         CATC
GAM192  LOC222976 5'  GTGATCTCTGATGACAAA    96031      _  GC
                                 TTTG CA  TTAGAGATCAC
                                 |||| ||  ||||||||||||
                                 AAAC GT  AGTCTCTAGTG
                                   A  __
GAM192  LOC90092  5'  GGTTCTCCAAGCTGCA      62072         A    TC
                                 TGCAGCTT GAGA  ACC
                                 |||||||| ||||  |||
                                 ACGTCGAA CTCT  TGG
                                      C    __
GAM193  ARNT2    3'  ACCAAGCAGCACCAGCAGGC   30081     GCAA   CC
                                 GCC    GTT  TGCTGCTTGGT
                                 |||    |||  ||||||||||
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                                CGG   CGA  ACGACGAACCA
                                  A___   CC
GAM193  CA12     3'  ACCAAGCAGCAGGAATTCAAAG 8685      CGCA
              CT                   AGC   AGTTCCTGCTGCTTGGT
                                |||   ||||||||||||||||
                                TCG   TTAAGGACGACGAACCA
                                  AAAC
GAM193  MSR1     3'  ACCAAGTGGTAGACTCACAGC  11701    CGCA  TC   TG
                                GC   AGT  CTGC  CTTGGT
                                ||   |||  ||||  ||||||
                                CG   TCA  GATG  GAACCA
                                 ACAC  __   GT
GAM193  ALTE     5'  ACCAAGCAGCCCCCGTGCAGC  60993    C   AGTTCCT
                                GC GCA     GCTGCTTGGT
                                || |||     ||||||||||
                                CG CGT     CGACGAACCA
                                 A  GCCCC__
GAM193  AMOT     5'  GCAGCCAGGAACTCGCAGC   56545    C  A     _  _
                                GC GC AGTTCCTG CTG C
                                || || |||||||| ||| |
                                CG CG TCAAGGAC GAC G
                                 A  C      C   T
GAM193  DKFZp434N035 3'  ACGAGCAGCAACTCGCAGC   51057    C  A   TCC     G
                                GC GC AGT   TGCTGCTT GT
                                || || |||   |||||||| ||
                                CG CG TCA   ACGACGAG CA
                                 A  C  ___      G
GAM193  FLJ22938 3'  ACCAAGCAGCTTGTGGCGGCT  45477      AAGTTCCT
                                AGCCGC      GCTGCTTGGT
                                ||||||      ||||||||||
                                TCGGCG      CGACGAACCA
                                   GTGTT___
GAM193  MGC3329  5'  CGTCTGGCAGGAACCTCGGC   44243     CAA       CT
                                GCCG   GTTCCTGCTG  TG
                                ||||   ||||||||||  ||
                                CGGC   CAAGGACGGT  GC
                                  TC_        CT
GAM193  SPTLC2   3'  CCAAGCAGCAGTGGCGGTT   17984      AAGTTC
                                AGCCGC     CTGCTGCTTGG
                                ||||||     ||||||||||
                                TTGGCG     GACGACGAACC
                                   GT____
GAM194  GUCY1B2  3'  TACATACATTAGTCTTCAA   15947       CTCCCTC
                                TTGAAGACT      GTATGTA
                                |||||||||      |||||||
                                AACTTCTGA      CATACAT
                                     TTA____
GAM194  MGEA5    3'  TATACAGGGAGAGAGTCTTCAA 25227          _  TC
                                TTGAAGACTCTC CC  GTATG
                                |||||||||||| ||  |||||
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                                AACTTCTGAGAG GG  CATAT
                                      A  GA
GAM194  TACC1    3'  TTACATGCTGAAAGTCTTCA  21880       C  CCTC
                                TGAAGACT TC   GTATGTAA
                                |||||||| ||   ||||||||
                                ACTTCTGA AG   CGTACATT
                                    A  T___
GAM194  FLJ23584 5'  TGTGAGGGACAGTCTCCAA   45040    A    C
                                TTG AGACT TCCCTCGTA
                                ||| ||||| |||||||||
                                AAC TCTGA AGGGAGTGT
                                  C    C
GAM194  KIAA0759 3'  TAGGAGGAGAAAGAGTCTTCAG 67891         __ _   G
                                TTGAAGACTC  TC CCTC TA
                                ||||||||||  || |||| ||
                                GACTTCTGAG  AG GGAG AT
                                      AA  A   G
GAM194  LOC221718 5'  TTACAAGAAGAGGGAGAGTCCT 95284     A        GTA_
           CAG                    TTGA GACTCTCCCTC   TGTAA
                                |||| ||||||||||   |||||
                                GACT CTGAGAGGGAG   ACATT
                                  C         AAGA
GAM195  AHCY     3'  AGAGCCTGGCTTAGTGCTGG   7302       CCACAC
                                CCAGCAC     TCAGGCTCT
                                |||||||     |||||||||
                                GGTCGTG     GGTCCGAGA
                                    ATTC__
GAM195  CDH15    3'  AGAACCTGAGTGTGGATGGGGC 18213   A  AG  C        C
                                G CC  CA CCACACTCAGG TCT
                                | ||  || ||||||||||| |||
                                C GG  GT GGTGTGAGTCC AGA
                                 _ G_  A         A
GAM195  DHCR24   3'  TCTGAGTTGAGCACTGGTC   29304      CACC  C
                                GACCAG   CA ACTCAGG
                                ||||||   || |||||||
                                CTGGTC   GT TGAGTCT
                                   ACGA  _
GAM195  GDF2     5'  GGGTGAGAGTGGGTGCTGG   33020          A  AG
                                CCAGCACCCAC CTC  GCTC
                                |||||||||| |||  ||||
                                GGTCGTGGGTG GAG  TGGG
                                      A  __
GAM195  GPX1     3'  CCTCGAGATGGGTGCTGGTC  6966           CA  _
                                GACCAGCACCCA  CTC AGG
                                ||||||||||||  ||| |||
                                CTGGTCGTGGGT  GAG TCC
                                      A_  C
GAM195  HMGE     3'  AGAAATGGGTGTGGGCACTG  73104     CA        GGC
                                CAG  CCCACACTCA   TCT
                                |||  ||||||||||   |||
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                                GTC  GGGTGTGGGT   AGA
                                  AC         AA_
GAM195  PITPNB   3'  AGATGCAGTGTGAGTCTGG   25699      C  C     CAG  _
                                CCAG AC CACACT   GC TCT
                                |||| || ||||||   || |||
                                GGTC TG GTGTGA   CG AGA
                                  _  A     ___  T
GAM195  TNNI2    3'  AGAGCCTGCCAGGGAGGGCTGG 13820       A__   ACACT
                                CCAGC   CCC    CAGGCTCT
                                |||||   |||    ||||||||
                                GGTCG   GGG    GTCCGAGA
                                   GGA   ACC__
GAM195  WASF3    3'  AGAGCCTGTCCATTGGGTGCAG 22809     CA      CACT_
           TC                     GAC  GCACCCA    CAGGCTCT
                                |||  |||||||    ||||||||
                                CTG  CGTGGGT    GTCCGAGA
                                  A_      TACCT
GAM195  C11orf21  3'  AGAACCCCAGCGGTGCTGGTC  27099         CACA  CA  C
                                GACCAGCACC    CT  GG TCT
                                ||||||||||    ||  || |||
                                CTGGTCGTGG    GA  CC AGA
                                      C___  CC  A
GAM195  C14orf4   5'  AGAGGTGGGCGTGGGTGCTGGT 67895          A   GG
                                ACCAGCACCCAC CTCA  CTCT
                                |||||||||||| ||||  ||||
                                TGGTCGTGGGTG GGGT  GAGA
                                      C    G_
GAM195  FLJ10307  3'  GAGCCTTGTGAGCCTGGTC   36477      CACC    CTC
                                GACCAG    CACA   AGGCTC
                                ||||||    ||||   ||||||
                                CTGGTC    GTGT   TCCGAG
                                   CGA_    ___
GAM195  FLJ12891  3'  AGAGCCTGAATGTCTCCCCTGG 46917     CACCC   C
                                CCAG     ACA TCAGGCTCT
                                ||||     ||| |||||||||
                                GGTC     TGT AGTCCGAGA
                                  CCCTC   A
GAM195  FLJ22479  3'  AGAGCAGGCAGTGGGTGCTG   46604         ACTCAG
                                CAGCACCCAC     GCTCT
                                ||||||||||     |||||
                                GTCGTGGGTG     CGAGA
                                      ACGGA_
GAM195  HAVCR-1   5'  AGAGCCTGGATCTGAACGCTG  60733     ACC  CAC
                                CAGC   CA   TCAGGCTCT
                                ||||   ||   |||||||||
                                GTCG   GT   GGTCCGAGA
                                  CAA  CTA
GAM195  JM11     3'  GAGCCTGAAAGTGCTGTC    54363     C    CCACAC
                                GAC AGCAC     TCAGGCTC
                                ||| |||||     ||||||||
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                                CTG TCGTG     AGTCCGAG
                                  _    AA____
GAM195  KIAA0226 3'  AGAAATGGGCGTGGGTGCTG  64251         A   GGC
                                CAGCACCCAC CTCA   TCT
                                |||||||||| ||||   |||
                                GTCGTGGGTG GGGT   AGA
                                     C    AA_
GAM195  KIAA0513 3'  AGAGCCTGAGTGCACTGC    29012     CCCA
                                GCA   CACTCAGGCTCT
                                |||   ||||||||||||
                                CGT   GTGAGTCCGAGA
                                  CAC_
GAM195  KIAA0603 3'  AGAGCCTGCATGTCGCTGG   29834      ACCC  CT
                                CCAGC   ACA  CAGGCTCT
                                |||||   |||  ||||||||
                                GGTCG   TGT  GTCCGAGA
                                   C___   AC
GAM195  KIAA0664 3'  AGAGCCGCTTATGGGTGTGGTC 64943      G     CACTCA
                                GACCA CACCCA     GGCTCT
                                ||||| ||||||     ||||||
                                CTGGT GTGGGT     CCGAGA
                                   _     ATTCG_
GAM195  KIAA0775 3'  AGAGCCTGCTCTGTGCACTG  28947    CACC   CT_
                                CAG   CACA   CAGGCTCT
                                |||   ||||   ||||||||
                                GTC   GTGT   GTCCGAGA
                                  AC__   CTC
GAM195  KIAA1171 3'  AGAGCCTGAAGCTTTTGCTGG  89336      CCCACAC
                                CCAGCA      TCAGGCTCT
                                ||||||      |||||||||
                                GGTCGT      AGTCCGAGA
                                   TTTCGA_
GAM195  LSM1     5'  AGCCGGGGCAGAAGTGCTGGTC 27839        CCACA  A
                                GACCAGCAC    CTC GGCT
                                |||||||||    ||| ||||
                                CTGGTCGTG    GGG CCGA
                                     AAGAC   G
GAM195  NXPH3    3'  AGGGTCCCAAGTGCTGGTC   66337        CCACACTCA
                                GACCAGCAC       GGCTCT
                                |||||||||       ||||||
                                CTGGTCGTG       CTGGGA
                                     AACC_____
GAM195  SLC21A11 5'  AGAGCGCTGACGTGGGTGT   65094        AC   _
                                GCACCCAC  TCAG GCTCT
                                ||||||||  |||| |||||
                                TGTGGGTG  AGTC CGAGA
                                     C_    G
GAM195  LOC132112 3'  AGAGCCTGTCGAGGGTGCCAGT 75530     CA     ACACT
            T                    GAC  GCACCC    CAGGCTCT
                                |||  ||||||    ||||||||
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                                TTG  CGTGGG    GTCCGAGA
                                  AC     AGCT_
GAM195  LOC132617 3'  AGAGCCCTGGGGGTGCTGTTC  76407    C       ACAC    _
                                GA CAGCACCC    TCAGG CTCT
                                || ||||||||    ||||| ||||
                                CT GTCGTGGG    GGTCC GAGA
                                 T       ____     C
GAM195  LOC135763 3'  AGAGCCTGAGTGCACCATGT   57553     CCCA_
                                GCA    CACTCAGGCTCT
                                |||    ||||||||||||
                                TGT    GTGAGTCCGAGA
                                  ACCAC
GAM195  LOC149668 5'  AGGGGATGGTGTGGGTGTGG   85692     G       T  GG
                                CCA CACCCACAC CA  CTCT
                                ||| |||||||| ||  ||||
                                GGT GTGGGTGTG GT  GGGA
                                  _       _ AG
GAM195  LOC150157 5'  AGAGCCTGAGCATGGACCTG   86019     CAC   CA
                                CAG   CCA  CTCAGGCTCT
                                |||   |||  ||||||||||
                                GTC   GGT  GAGTCCGAGA
                                  CA_   AC
GAM195  LOC152453 5'  AGAGCCTGTGGGCAAGAGCTGG 81464       A____     CTCA
                                CCAGC    CCCACA    GGCTCT
                                |||||    ||||||    ||||||
                                GGTCG    GGGTGT    CCGAGA
                                   AGAAC     ____
GAM195  LOC158191 3'  AGAACTGGTGGTGGGTGCCAGT 82662    CA       _  T   GC
                                AC  GCACCCAC AC CAG  TCT
                                ||  |||||||| || |||  |||
                                TG  CGTGGGTG TG GTC  AGA
                                 AC       G  _   A_
GAM195  LOC162137 3'  AGAACCTGTCCTGGTGCTGG   88476        CACACT    C
                                CCAGCACC     CAGG TCT
                                ||||||||     |||| |||
                                GGTCGTGG     GTCC AGA
                                     TCCT__    A
GAM195  LOC164121 5'  CCTGAGTGTGGATGTGGTC    83048      G  C
                                GACCA CA CCACACTCAGG
                                ||||| || ||||||||||
                                CTGGT GT GGTGTGAGTCC
                                   _  A
GAM195  LOC196890 5'  AGAGCCTGAGCATGGACCTG   91221     CAC   CA
                                CAG   CCA  CTCAGGCTCT
                                |||   |||  ||||||||||
                                GTC   GGT  GAGTCCGAGA
                                  CA_   AC
GAM195  LOC219392 5'  AGAGCCTGAGCTGAATGCTG   92765      CC  CA
                                CAGCA  CA  CTCAGGCTCT
                                |||||  ||  ||||||||||
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                                GTCGT  GT  GAGTCCGAGA
                                   AA  C_
GAM195  LOC255452 3'  AGAGCTTGGGAGAGTGCTGGTC 99385         CCACA
                                GACCAGCAC    CTCAGGCTCT
                                |||||||||    ||||||||||
                                CTGGTCGTG    GGGTTCGAGA
                                     AGA__
GAM195  LOC257438 3'  GAGCCTTGTGAGCCTGGTC   95594      CACC   CTC
                                GACCAG   CACA   AGGCTC
                                ||||||   ||||  ||||||
                                CTGGTC   GTGT   TCCGAG
                                   CGA_   ___
GAM195  LOC91585  5'  AGAACCTGGGAATGGGCCTG  67158    CA   CA    C
                                CAG  CCCA  CTCAGG TCT
                                |||  ||||  |||||| |||
                                GTC  GGGT  GGGTCC AGA
                                  C_   AA    A
GAM196  CAPNS1    3'  CCAGGCCCTGCACACACCC   10014       TCC    C
                                GGGTGTGT   GGGCC GG
                                ||||||||   ||||| ||
                                CCCACACA   CCCGG CC
                                     CGT    A
GAM196  CAPNS1    3'  GCCAGACCCAGGTGCCCCA   10015       TGTT _  CCC
                                TGGGGTG   CC GGG   GGC
                                |||||||   || |||   |||
                                ACCCCGT   GG CCC   CCG
                                    _____ A   AGA
GAM196  COL11A2   3'  CCAGGCCCACCTGGAATCCCA 55631      GTGT _____    C
                                TGGGGT   TCC   GGGCC GG
                                ||||||   |||   ||||| ||
                                ACCCTA   AGG   CCCGG CC
                                   _____  TCCA    A
GAM196  ELMO1     3'  GCCGGGCCCAGACATGCCCC  56155        CC
                                GGGGTGTGTT  GGGCCCGGC
                                ||||||||||  |||||||||
                                CCCCGTACAG  CCCGGGCCG
                                     A_
GAM196  EXTL3     3'  CCGGACCCGGCCGCCGCCA   9333     _   T TT    C
                                TGG GGTG G  CCGGG CCGG
                                ||| |||| |  ||||| ||||
                                ACC CCGC C  GGCCC GGCC
                                  G   _ __    A
GAM196  FSTL3     3'  GCCAGGCAGCCCACCCCA    20738       T  _  G
                                TGGGGTG GTT CC GGC
                                ||||||| ||| || |||
                                ACCCCAC CGA GG CCG
                                    C   C  A
GAM196  HSPB1     5'  GCCGAGCCCAGCGCCCC     9521        GTTCC   C
                                GGGGTGT    GGGC CGGC
                                |||||||    |||| ||||
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                                CCCCGCG    CCCG GCCG
                                   A____   A
GAM196  ITGB1   5'  CCGGGCCCGAACGGCCCC   54462     G   C
                                GGGGT TGTTC GGGCCCGG
                                ||||| ||||| ||||||||
                                CCCCG GCAAG CCCGGGCC
                                  _   _
GAM196  LMO4    5'  GCCGGGCCCGGCCGGCCGCA  23185   G  GTGTT
                                TG GGT   CCGGGCCCGGC
                                || |||   ||||||||||
                                AC CCG   GGCCCGGGCCG
                                 G  GCC__
GAM196  LTK     3'  GCCGCCTTACACACACCCCA  11376       TCC   CC
                                TGGGGTGTGT  GGGC  GGC
                                ||||||||||  ||||  |||
                                ACCCCACACA  TCCG  CCG
                                     CAT  __
GAM196  NPTX1   3'  GCCGGGCCCCAGCACCCC   11836     GTTCC
                                GGGGTGT   GGGCCCGGC
                                |||||||   |||||||||
                                CCCCACG   CCCGGGCCG
                                   AC___
GAM196  PKD2L1  5'  CCGGGCCCCCCCCACCTCA   32767     TGTTCC
                                TGGGGTG    GGGCCCGG
                                |||||||    ||||||||
                                ACTCCAC    CCCGGGCC
                                   CCC___
GAM196  RANBP3  3'  GCCGGGAACCACACACCCCA  24634       TCC  G_
                                TGGGGTGTGT  GG  CCCGGC
                                ||||||||||  ||  ||||||
                                ACCCCACACA  CC  GGGCCG
                                     ___  AA
GAM196  TLX1    3'  GCCAGGCCCCCACCACACATCC 19824       TCC__   C
          CA                      TGGGGTGTGT   GGGCC GGC
                                ||||||||||   ||||| |||
                                ACCCTACACA   CCCGG CCG
                                     CCACC   A
GAM196  TMEM1   3'  GCCAGGGTGAACACACGCCA  13801   G     CGG  _
                                TGG GTGTGTTC  GCCC GGC
                                ||| ||||||||  |||| |||
                                ACC CACACAAG  TGGG CCG
                                  G      ___   A
GAM196  TULP1   3'  GCCAGGCACCCACATCCCCA  13903    _  TTCC _  C
                                TGGGG TGTG   GG GCC GGC
                                ||||| ||||   || ||| |||
                                ACCCC ACAC   CC CGG CCG
                                  T   _____ A  A
GAM196  VASP    5'  GCCGAGCCCGGAGCCAGCCCC  14028     GT      C
                                GGGGT  GTTCCGGGC CGGC
                                |||||  ||||||||| ||||
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                                CCCCG  CGAGGCCCG GCCG
                                  AC       A
GAM196  WEE1    5'  GCCGGGCCCCCCCGCCGCCCCA  14110       T  TCC
                                TGGGGTG GT   GGGCCCGGC
                                ||||||| ||   |||||||||
                                ACCCCGC CG   CCCGGGCCG
                                   _ CCC
GAM196  ZFH4    5'  CCAAACCCGAAAAACACCCCA  45629        G  C    CCC
                                TGGGGTGT TT CGGG   GG
                                |||||||| || ||||   ||
                                ACCCCACA AA GCCC   CC
                                     A  A    AAA
GAM196  AKAP8   3'  GCCACTGGAAACACACCC    20735         _   GCCC
                                GGGTGTGTT CCGG    GGC
                                ||||||||| ||||    |||
                                CCCACACAA GGTC    CCG
                                      A    A___
GAM196  BLR1    3'  GCCCCTCCCAGAACACACTCCA 53116          C   CCC
                                TGGGGTGTGTTC GGG   GGC
                                |||||||||||| |||   |||
                                ACCTCACACAAG CCC   CCG
                                       A   TCC
GAM196  C16orf5  3'  GCCGGGCCCCTCACCCCA    26351       TGTTCC
                                TGGGGTG     GGGCCCGGC
                                |||||||     |||||||||
                                ACCCCAC     CCCGGGCCG
                                   TC_____
GAM196  CG018   3'  CCAAAACTTGAGAACACACCC  54485         _   CCC_
                                GGGTGTGTTC CGGG    GG
                                |||||||||| ||||    ||
                                CCCACACAAG GTTC    CC
                                      A    AAAA
GAM196  DKFZp434G0920 5'  GCCGGGCCCAGAGCTCCCT   51027     TGT   C
                                GGGG   GTTC GGGCCCGGC
                                ||||   |||| |||||||||
                                TCCC   CGAG CCCGGGCCG
                                  T__    A
GAM196  FLJ11588  5'  GCCGGGCCCGAGAGCCCCC   45122     TGT   _
                                GGGG   GTTC CGGGCCCGGC
                                ||||   |||| ||||||||||
                                CCCC   CGAG GCCCGGGCCG
                                  ___    A
GAM196  FLJ11608  3'  GCCAAGCCCAGAAGTACCT   44960      G   C   CC
                                GGGTGT TTC GGGC  GGC
                                |||||| ||| ||||  |||
                                TCCATG AAG CCCG  CCG
                                   _  A   AA
GAM196  JDD1    5'  GCCAGGCCCGGAGGCCCCCA  63916      T  G       C
                                TGGGG GT TTCCGGGCC GGC
                                ||||| || ||||||||| |||
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                                ACCCC CG GAGGCCCGG CCG
                                  _ _       A
GAM196  KIAA1941  3'  GCCCAGCGGAACACCCCCA   75340      T     ___
                                TGGGG GTGTTCC   GGGC
                                ||||| |||||||   ||||
                                ACCCC CACAAGG   CCCG
                                  _      CGA
GAM196  MGC13170  3'  GCCAAGCAGGGCAACCCCA   52131      G   T  GG  CC
                                TGGGGT TGT CC  GC  GGC
                                |||||| ||| ||  ||  |||
                                ACCCCA ACG GG  CG  CCG
                                  _  _ A_  AA
GAM196  NIN       5'  GCCAAGCCCGGAGTGCGCC   40885     TG      CC
                                GGTG  TTCCGGGC  GGC
                                ||||  ||||||||  |||
                                CCGC  GAGGCCCG  CCG
                                  GT       AA
GAM196  RCD-8     3'  GCCAGGCCCAGCAAGCCC    27520     G   CC    C
                                GGGT TGTT  GGGCC GGC
                                |||| ||||  ||||| |||
                                CCCG ACGA  CCCGG CCG
                                  A   __    A
GAM196  RES4-22   3'  GCCAGGCTGCACCACCCCA   14916       _  TCCG   C
                                TGGGGTG TGT   GGCC GGC
                                ||||||| |||   |||| |||
                                ACCCCAC ACG   TCGG CCG
                                    C  ____   A
GAM196  RNF40     3'  GCCAAGCCCATTTACCCCCA  29364     T  TTCC   CC
                                TGGGG GTG   GGGC  GGC
                                ||||| |||   ||||  |||
                                ACCCC CAT   CCCG  CCG
                                  _  TTA_   AA
GAM196  SPIB      3'  GCCGGGCCTGAGCACACCC   13357        C
                                GGGTGTGTTC GGGCCCGGC
                                |||||||||| |||||||||
                                CCCACACGAG TCCGGGCCG
                                          _
GAM196  ZNF17     5'  GCATGACGGAACACACCCCA  83271          GGCCCG
                                TGGGGTGTGTTCCG     GC
                                ||||||||||||||     ||
                                ACCCCACACAAGGC     CG
                                       AGTA__
GAM196  LOC123096 3'  CCAGGCCTGGAACACCTCCA  74650      T        C
                                TGGGG GTGTTCCGGGCC GG
                                ||||| |||||||||||| ||
                                ACCTC CACAAGGTCCGG CC
                                  _         A
GAM196  LOC126695 3'  GCCAGGCCCAGCTGCC     75958     T  CC    C
                                GGTG GTT  GGGCC GGC
                                |||| |||  ||||| |||
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                                CCGT CGA  CCCGG CCG
                                  _  __    A
GAM196  LOC147817 5'  GCCGAGCTGCGCACACCCCA  79182        TCCG  C
                                TGGGGTGTGT   GGC CGGC
                                ||||||||||   ||| ||||
                                ACCCCACACG   TCG GCCG
                                     CG__   A
GAM196  LOC148936 5'  GCCAGGCCCGGGGTCCTCA   85456     TGT TT     C
                                TGGGG  G  CCGGGCC GGC
                                |||||  |  ||||||| |||
                                ACTCC  T  GGCCCGG CCG
                                   ___ GG     A
GAM196  LOC148938 5'  GCCAGGCCCGGGGTCCTCA   85438     TGT TT     C
                                TGGGG  G  CCGGGCC GGC
                                |||||  |  ||||||| |||
                                ACTCC  T  GGCCCGG CCG
                                   ___ GG     A
GAM196  LOC149076 3'  GCCCCCACAGACACACCCCA  79879        CC_  CCC
                                TGGGGTGTGTT  GGG  GGC
                                ||||||||||   |||  |||
                                ACCCCACACAG  CCC  CCG
                                      ACA  ___
GAM196  LOC155179 3'  GCCAGGCAGACACACCCC    82232        CCGG  C
                                GGGGTGTGTT   GCC GGC
                                ||||||||||   ||| |||
                                CCCCACACAG   CGG CCG
                                     A___   A
GAM196  LOC163682 5'  GCCAAGCCCAAAATAACCC   88407     G   CC   CC
                                GGGT TGTT  GGGC  GGC
                                |||| ||||  ||||  |||
                                CCCA ATAA  CCCG  CCG
                                  _   AA   AA
GAM196  LOC222183 3'  GCCAGGCTCTCCTCACCCCA  95828       TGTTCC    C
                                TGGGGTG     GGGCC GGC
                                |||||||     ||||| |||
                                ACCCCAC     CTCGG CCG
                                    TCCT__    A
GAM196  LOC256369 3'  CCAGTGGCTCAGAAGACACCCC 96610        G  C    C__
          A                      TGGGGTGT TTC GGGCC   GG
                                 ||||||| ||| |||||   ||
                                 ACCCCACA AAG CTCGG   CC
                                    G  A    TGA
GAM196  LOC257458 5'  GCCGGGCCCCTGTGGCCCCCA 68401      T  GTTCC
                                TGGGG GT    GGGCCCGGC
                                ||||| ||    |||||||||
                                ACCCC CG    CCCGGGCCG
                                  _ GTGTC
GAM196  LOC56270  3'  GCCGAGCCGTCACACCTCA   39507        TTCCG  C
                                TGGGGTGTG    GGC CGGC
                                |||||||||    ||| ||||
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                                ACTCCACAC    CCG GCCG
                                     TG___   A
GAM196  LOC57106  3'  GCCGAGCAGAATACACCCCA  64816          CGG  C
                                TGGGGTGTGTTC  GC CGGC
                                ||||||||||||  || ||||
                                ACCCCACATAAG  CG GCCG
                                      A__  A
GAM196  LOC90170  5'  GCCAGACCCCTGACACGCCC  62378        CC  CCC
                                GGGTGTGTT  GGG  GGC
                                |||||||||  |||  |||
                                CCCGCACAG  CCC  CCG
                                     TC  AGA
GAM197  N33       3'  ATGAAGATAAACTGTTCCTGAC 23152      A  ACTTC
                                GTCA GAA    TTATCTTCAT
                                |||| |||    ||||||||||
                                CAGT CTT    AATAGAAGTA
                                  C  GTCA_
GAM197  RNF26     3'  ATGAATAAAGTTCTCTTGACA  50132        _    CTTATC
                                TGTCAAGA AACTT     TTCAT
                                |||||||| |||||     |||||
                                ACAGTTCT TTGAA     AAGTA
                                     C    AT____
GAM197  AOP2      3'  TATGAAAATGGCACTAAAAGTT 18137          C_____   C    ___
          TCTTGA                TCAAGAAACTT     TTAT TTCAT  A
                                ||||||||||     |||| |||||  |
                                AGTTCTTTGAA     GGTA AAGTA  T
                                      AATCAC    A    __
GAM197  FLJ22643  3'  AAGGTTAATAAATTTCTTGACA 45264         CTTCTT_
                                TGTCAAGAAA      ATCTT
                                ||||||||||      |||||
                                ACAGTTCTTT      TGGAA
                                      AAATAAT
GAM197  PRO0255   3'  ATGAAAAGTTTAAAGTTTCTTG 26965          CTTATC_
          A                     TCAAGAAACTT      TTCAT
                                ||||||||||      |||||
                                AGTTCTTTGAA      AAGTA
                                      ATTTGAA
GAM197  ZNF-U69274 3'  ATGAAGATAAAAAGAAGTGACA 27741      AGAAA  C
                                TGTCA    CTT TTATCTTCAT
                                |||||    ||| ||||||||||
                                ACAGT    GAA AATAGAAGTA
                                   GAA__  A
GAM197  LOC91181  3'  ATGAAGATTTCTAGTCCTCGAC 65769     A  AA  TCTT
          A                     TGTC AG  ACT   ATCTTCAT
                                |||| ||  |||   ||||||||
                                ACAG TC  TGA   TAGAAGTA
                                  C  C_  TCTT
GAM198  EIF2S3    3'  CGGTCTCTCCTGACCTCAG   9207      AGC  ACAA
                                CTGA  CAG   AGAGATCG
                                ||||  |||   ||||||||
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                                GACT  GTC   TCTCTGGC
                                  CCA  C___
GAM198  KIAA0857  3'  CACTCTCATTGTCTGGCCTCAG 67249     A       A   TC
                                CTGA GCCAGACAA GAGA  GTG
                                |||| ||||||||| ||||  |||
                                GACT CGGTCTGTT CTCT  CAC
                                  C       A   __
GAM198  TACR1    5'  CACCCTCCTGTCTGGCTTTAG  32330          AA   ATC
                                CTGAAGCCAGACA  GAG   GTG
                                ||||||||||||  |||   |||
                                GATTTCGGTCTGT  CTC   CAC
                                       C_  C__
GAM198  UBE2I    5'  CACTTTCTCCCTGTCTGGC   13958        AA   TC
                                GCCAGACA  GAGA  GTG
                                ||||||||  ||||  |||
                                CGGTCTGT  CTCT  CAC
                                    CC   TT
GAM198  VCAM1    5'  CGGGCCTCACTGGCTTCAG   8412         ACAAA  A_
                                CTGAAGCCAG    GAG  TCG
                                ||||||||||    |||  |||
                                GACTTCGGTC    CTC  GGC
                                      A____   CG
GAM198  VCAM1    5'  CGGGCCTCACTGGCTTCAG   55637         ACAAA  A_
                                CTGAAGCCAG    GAG  TCG
                                ||||||||||    |||  |||
                                GACTTCGGTC    CTC  GGC
                                      A____   CG
GAM198  XPC      3'  GGTCCCGTCTGGCTCCAG    17333    A      AAAGA
                                CTG AGCCAGAC    GATC
                                ||| ||||||||    ||||
                                GAC TCGGTCTG    CTGG
                                  C       CC___
GAM198  C22orf2  3'  TGGCCTCCTCTGGCTTCAG   96090         CAAA   AT
                                CTGAAGCCAGA   GAG  CG
                                ||||||||||   |||  ||
                                GACTTCGGTCT   CTC  GT
                                      C___   CG
GAM198  DKFZp564A176 3'  CTCCCTGTCTGGTTTCAG    50972          AA
                                CTGAAGCCAGACA  GAG
                                ||||||||||||  |||
                                GACTTTGGTCTGT  CTC
                                       CC
GAM198  DKFZP727G051 3'  CTTCCTGCCTGGCTTCAG    70009         A  AA
                                CTGAAGCCAG CA  GAG
                                ||||||||| ||  |||
                                GACTTCGGTC GT  TTC
                                      C  CC
GAM198  FER1L4   3'  CACGATCTCGGCTGACTGCA  48114    A  C   ACAAA
                                TG AG CAG    GAGATCGTG
                                || || |||    |||||||||
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                                AC TC GTC    CTCTAGCAC
                                 G  A  GG___
GAM198  FER1L4   3' CACGATCTCGGCTGACTGCA  48115    A  C   ACAAA
                                TG AG CAG    GAGATCGTG
                                || || |||    |||||||||
                                AC TC GTC    CTCTAGCAC
                                 G  A  GG___
GAM198  FLJ10520 3' GAACTCATCTGGCTTCAG    36708          CAAA   A
                                CTGAAGCCAGA    GAG TC
                                ||||||||||    ||| ||
                                GACTTCGGTCT    CTC AG
                                      A___   A
GAM198  FLJ22746 5' CACGCTGTCTTTGTCAGCCTCA 45917     A  CA      GAT
           G                     CTGA GC  GACAAAGA   CGTG
                                ||||  ||  ||||||||   ||||
                                GACT CG  CTGTTTCT   GCAC
                                  C  A_       GTC
GAM198  KIAA0514 3' CACGCATCCCTTGTCTGGCCCC 28740     AA       A A  _
           AG                     CTG  GCCAGACAA G GAT CGTG
                                |||  |||||||||  |  ||| ||||
                                GAC  CGGTCTGTT C CTA GCAC
                                  CC        _ C   C
GAM198  KIAA1402 3' TCCTTTGTCTGCCTCAG     66993     A  C       A
                                CTGA GC AGACAAAG GA
                                |||| || |||||||| ||
                                GACT CG TCTGTTTC CT
                                  C  _       _
GAM198  LATS1    3' TGGCCTCTGCACTGGCTTCAG  60912          ACAA    AT
                                CTGAAGCCAG    AGAG  CG
                                ||||||||||    ||||  ||
                                GACTTCGGTC    TCTC  GT
                                      ACG_    CG
GAM198  mPA-PLA1 5' CACGATCTCTCCAGTTTC    58357      CA  CAAA
                                GAAGC  GA    GAGATCGTG
                                |||||  ||    |||||||||
                                CTTTG  CT    CTCTAGCAC
                                  AC  _____
GAM198  NDP52    3' CACGTGATCTGTCCACTTCAG  20665      CCA    AA  GAT
                                CTGAAG   GACA  GA   CGTG
                                ||||||   ||||  ||   ||||
                                GACTTC   CTGT  CT   GCAC
                                   AC_    __  AGT
GAM198  PEF      3' ATGCTCTGCTCGGCTTCAG   25682        A  CAA    AT
                                CTGAAGCC GA   AGAG  CGT
                                |||||||| ||   ||||  |||
                                GACTTCGG CT   TCTC  GTA
                                     _ CG_    __
GAM198  LOC125704 3' CGGTCTCTTTCCAGCTTCAG  74877        CA  CA
                                CTGAAGC  GA  AAGAGATCG
                                |||||||  ||  |||||||||
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                                GACTTCG  CT  TTCTCTGGC
                                    AC  __
GAM198  LOC158527 5'  GATTTCTTCAGCTGGCTTCA  82840        ACA
                                TGAAGCCAG  AAGAGATC
                                |||||||||  ||||||||
                                ACTTCGGTC  TTCTTTAG
                                    GAC
GAM198  LOC196214 5'  TGTCCTCCTCCCGGCTTCAG  91187        A_  CAAA  AT
                                CTGAAGCC  GA   GAG  CG
                                ||||||||  ||   |||  ||
                                GACTTCGG  CT   CTC  GT
                                    CC  C___  CT
GAM198  LOC196485 5'  ATTTCTATGTGGCTTCAG   89070        AG  A
                                CTGAAGCC  ACA AGAGAT
                                ||||||||  ||| ||||||
                                GACTTCGG  TGT TCTTTA
                                    __  A
GAM198  LOC203378 3'  GACTCTGCACTAGCTTCAG   92289        C  ACAA   A
                                CTGAAGC AG   AGAG TC
                                |||||||  ||   ||||  ||
                                GACTTCG TC   TCTC AG
                                    A  ACG_  _
GAM198  LOC220739 3'  CACCGCTCCACCTGGCTTCA  94515        ACAAA  ATC
                                TGAAGCCAG   GAG  GTG
                                |||||||||   |||  |||
                                ACTTCGGTC   CTC  CAC
                                    CAC__  GC_
GAM198  LOC221663 3'  CACTCTCCTTTGTGTGGCTTCA 95456        G    A  TC
                                TGAAGCCA ACAAAG GA  GTG
                                ||||||||  ||||||  ||  |||
                                ACTTCGGT TGTTTC CT  CAC
                                    G    _  CT
GAM198  LOC90538  3'  CACTTGGCTCCCTGGCTTCAG  63896        ACAAA  ATC_
                                CTGAAGCCAG   GAG   GTG
                                ||||||||||   |||   |||
                                GACTTCGGTC   CTC   CAC
                                    C____  GGTT
GAM199  ABCD4    3'  TGGAAGTGTGAGATCTGT   40104      _ TG   C
                                ACAGAT T  TATT TCCA
                                ||||||  |  |||| ||||
                                TGTCTA A  GTGA AGGT
                                   G GT   _
GAM199  ABCD4    3'  TGGAAGTGTGAGATCTGT   40105      _ TG   C
                                ACAGAT T  TATT TCCA
                                ||||||  |  |||| ||||
                                TGTCTA A  GTGA AGGT
                                   G GT   _
GAM199  ABCD4    3'  TGGAAGTGTGAGATCTGT   40106      _ TG   C
                                ACAGAT T  TATT TCCA
                                ||||||  |  |||| ||||
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                                TGTCTA A  GTGA AGGT
                                   G GT   _
GAM199  ACADL   3'  TGGAAGGACAAATCTTTGA   9639     C      A TC
                                TCA AGATTTGT T  TCCA
                                ||| |||||||| |  ||||
                                AGT TCTAAACA G  AGGT
                                  T      _ GA
GAM199  CHD1    5'  TGAAGAAAATTCATCTGTGA  8864        TT  A   C
                                TCACAGAT  GT TTCT CA
                                ||||||||  || |||| ||
                                AGTGTCTA  TA AAGA GT
                                     CT  A   A
GAM199  CRH     3'  GAGAATGTAGACCTGTGA    7481       A
                                TCACAG TTTGTATTCTC
                                |||||| ||||||||||
                                AGTGTC AGATGTAAGAG
                                   C
GAM199  CRY2    3'  TGGAAGGGCAAATCTGAGA   72667    A      ATTC
                                TC CAGATTTGT   TCCA
                                || |||||||||   ||||
                                AG GTCTAAACG   AGGT
                                 A       GGA_
GAM199  GLP1R   3'  TGGAAATACTTTATCTGTGA  10800       TT_   C
                                TCACAGAT   GTATT TCCA
                                ||||||||   ||||| ||||
                                AGTGTCTA   CATAA AGGT
                                     TTT   _
GAM199  KCNK4   3'  TGGAGAATGAAGCTCTGGA   33990    A   TTTG
                                TC CAGA   TATTCTCCA
                                || ||||   |||||||||
                                AG GTCT   GTAAGAGGT
                                 _   CGAA
GAM199  MN1     3'  TGGAGAATAGTAGTTCTGGA  11659    A   T  _
                                TC CAGA TTG TATTCTCCA
                                || |||| ||| |||||||||
                                AG GTCT GAT ATAAGAGGT
                                 _   T  G
GAM199  PKIB    3'  TGGAAAATGCAAAATTTGT   51641       _   C
                                ACAGATTT GTATT TCCA
                                |||||||| ||||| ||||
                                TGTTTAAA CGTAA AGGT
                                     A    A
GAM199  PML     3'  AGAAATGCAGACCTGTGG    53792      A     _
                                TCACAG TTTGTATT CT
                                |||||| |||||||| ||
                                GGTGTC AGACGTAA GA
                                   C      A
GAM199  PMX1    5'  TGGAGAAAGGGGGTCTGTGA  23576        GTA
                                TCACAGATTT   TTCTCCA
                                ||||||||||   |||||||
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                                AGTGTCTGGG  AAGAGGT
                                      GGA
GAM199  PTGIS    3'  TGGAGAAACAGGCTCTGAGA  8233    A   _   A
                                TC CAGA TTTGT TTCTCCA
                                || |||| ||||| |||||||
                                AG GTCT GGACA AAGAGGT
                                 A   C   _
GAM199  PTP4A2   3'  TGGAAATGTGAATCTGGA   14443   A    TG   C
                                TC CAGATT  TATT TCCA
                                || ||||||  |||| ||||
                                AG GTCTAA  GTAA AGGT
                                 _     GT   _
GAM199  PTP4A2   3'  TGGAAATGTGAATCTGGA   14444   A    TG   C
                                TC CAGATT  TATT TCCA
                                || ||||||  |||| ||||
                                AG GTCTAA  GTAA AGGT
                                 _     GT   _
GAM199  SART2    3'  TGAAGAATACAATTCTGAGA  26252   A   T      C
                                TC CAGA TTGTATTCT CA
                                || |||| |||||||| ||
                                AG GTCT AACATAAGA GT
                                 A   T       A
GAM199  SON      3'  TGGAGAATGGGTTCCTGTGG  57987      ATTTG
                                TCACAG    TATTCTCCA
                                ||||||    |||||||||
                                GGTGTC    GTAAGAGGT
                                   CTTGG
GAM199  ST14     3'  TGGAAAACAGACGGGTCTGAGA 42043   A       ATTC__
                                TC CAGATTTGT     TCCA
                                || |||||||||     ||||
                                AG GTCTGGGCA     AGGT
                                 A        GACAAA
GAM199  TCN2     5'  TGGAGGATTAATCAGTGA   6267     A   TGT
                                TCAC GATT   ATTCTCCA
                                |||| ||||   ||||||||
                                AGTG CTAA   TAGGAGGT
                                  A   T__
GAM199  TM7SF3   3'  TGGTTTACAAATCTATGA   60396    C      TTCT
                                TCA AGATTTGTA   CCA
                                ||| |||||||||   |||
                                AGT TCTAAACAT   GGT
                                  A       TT__
GAM199  TRIM14   3'  AGAGCCACAAATCTGGGA   29503   A      A_
                                TC CAGATTTGT  TTCT
                                || |||||||||  ||||
                                AG GTCTAAACA  GAGA
                                 G       CC
GAM199  TYR      5'  TGGAAAGAGAAATCTGTGA   6325         GTA  C
                                TCACAGATTT   TT TCCA
                                ||||||||||   || ||||
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                                AGTGTCTAAA   AA AGGT
                                     GAG  _
GAM199  UFD1L    3'  TGGAGAAGCAAACATGTGA   73677      GA    A
                                TCACA  TTTGT TTCTCCA
                                |||||  ||||| |||||||
                                AGTGT  AAACG AAGAGGT
                                   AC    _
GAM199  CSTF1    3'  TGGAAACACAGATCTGTG    9000          A  C
                                CACAGATTTGT TT TCCA
                                |||||||||||| || ||||
                                GTGTCTAGACA AA AGGT
                                      C  _
GAM199  DKFZp434C0923 3'  TGGAGAATGTTGGTCCTG    34654     _  TG
                                CAG ATT  TATTCTCCA
                                ||| |||  |||||||||
                                GTC TGG  GTAAGAGGT
                                  C   TT
GAM199  DKFZP434C171 3'  TGGAAAATCAGATCTGTGA   32200          T   C
                                TCACAGATTTG ATT TCCA
                                |||||||||||| ||| ||||
                                AGTGTCTAGAC TAA AGGT
                                      _  A
GAM199  DKFZP566B183 3'  GAGGGCACCAATCTGTGA    31944         T  A
                                TCACAGATT GT TTCTC
                                ||||||||| || |||||
                                AGTGTCTAA CA GGGAG
                                     C  C
GAM199  DLAD     5'  TGGAGTCCCTAAACCTGTGA  55264       A    TATT
                                TCACAG TTTG    CTCCA
                                |||||| ||||    |||||
                                AGTGTC AAAT    GAGGT
                                   C    CCCT
GAM199  DOCK3    3'  TGGAGAATAAGTCAGTCTG   67101       TG__
                                CAGATT    TATTCTCCA
                                ||||||    |||||||||
                                GTCTGA    ATAAGAGGT
                                   CTGA
GAM199  DRIM     5'  GGAGAGTATAGCCTGTGA    27951       AT
                                TCACAG  TTGTATTCTCC
                                ||||||  ||||||||||
                                AGTGTC  GATATGAGAGG
                                   C_
GAM199  FBXO30   3'  TGAGAATGTGTCTGTGG     50491        TTG     C
                                TCACAGAT   TATTCT CA
                                ||||||||   |||||| ||
                                GGTGTCTG   GTAAGA GT
                                     T__     A
GAM199  FLJ10199 3'  TGGAGCTGGTGAATCTGTGG   71756         TG ATT
                                TCACAGATT  T   CTCCA
                                |||||||||  |   |||||
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                                GGTGTCTAA  G   GAGGT
                                     GT GTC
GAM199  FLJ10898  5'  TGGTTAATACAAATCTGCGA   60143    A         CT
                                TC CAGATTTGTATT  CCA
                                || ||||||||||||  |||
                                AG GTCTAAACATAA  GGT
                                 C           TT
GAM199  FLJ11068  3'  TGGATTTACAAAATCTGTG    37589         _   TTC
                                CACAGATTT GTA   TCCA
                                |||||||||  |||   ||||
                                GTGTCTAAA CAT   AGGT
                                     A   TT_
GAM199  FLJ13693  3'  TGGAGAATGCAGCCTGGA    46076    A   AT
                                TC CAG  TTGTATTCTCCA
                                || |||  ||||||||||||
                                AG GTC  GACGTAAGAGGT
                                 _   C_
GAM199  FLJ13964  3'  TGAAGACTTAGAATCTGTGG   50756         GTAT   C
                                TCACAGATTT    TCT CA
                                ||||||||||    ||| ||
                                GGTGTCTAAG    AGA GT
                                      ATTC   A
GAM199  FLJ14547  3'  GAATCTCCAGATCTGTGA    52496          T__
                                TCACAGATTTG   ATTC
                                ||||||||||   ||||
                                AGTGTCTAGAC   TAAG
                                      CTC
GAM199  GPT2      3'  TGGAAGTTACATCTGTGA    56773       TT   TTC
                                TCACAGA  TGTA   TCCA
                                |||||||  ||||   ||||
                                AGTGTCT  ACAT   AGGT
                                    __    TGA
GAM199  KIAA0077  3'  TGGAGAATACCCATCTGT    67581       TT
                                ACAGAT  GTATTCTCCA
                                ||||||  ||||||||||
                                TGTCTA  CATAAGAGGT
                                   CC
GAM199  KIAA0217  3'  AGAAATAATTGATCTGTGA   67594         TG_   _
                                TCACAGATT   TATT CT
                                |||||||||   ||||  ||
                                AGTGTCTAG   ATAA GA
                                     TTA    A
GAM199  KIAA0247  3'  TGGAGAATCATGTCCATG    29078    CA   T  T
                                CA  GAT TG ATTCTCCA
                                ||  |||  ||  ||||||||
                                GT  CTG AC TAAGAGGT
                                 AC   T  _
GAM199  KIAA0293  3'  AGAGTAATCAAATCTGGA    61234    A       __
                                TC CAGATTTG  TATTCT
                                || ||||||||  ||||||
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                                AG GTCTAAAC  ATGAGA
                                 _       TA
GAM199  KIAA0332 3' AGAATATATATTCTGTGA    63364       TT_
                                TCACAGA   TGTATTCT
                                |||||||   ||||||||
                                AGTGTCT   ATATAAGA
                                    TAT
GAM199  KIAA0443 5' TGAAGAAACAAACCTGTGA   28855      A    A   C
                                TCACAG TTTGT TTCT CA
                                |||||| ||||| |||| ||
                                AGTGTC AAACA AAGA GT
                                   C    _   A
GAM199  KIAA0935 3' AGAATAGGCAAATCTGTG    73096          __
                                CACAGATTTGT  ATTCT
                                ||||||||||  |||||
                                GTGTCTAAACG  TAAGA
                                      GA
GAM199  KIAA1045 3' TGGAGAATCCTGACTGGA    71614    A  A  TGT
                                TC CAG TT   ATTCTCCA
                                || ||| ||   ||||||||
                                AG GTC AG   TAAGAGGT
                                 _  _ TCC
GAM199  KIAA1165 3' TGGAAGTGTGAACCTGTGA   67996      A  TG   C
                                TCACAG TT  TATT TCCA
                                |||||| ||  |||| ||||
                                AGTGTC AA  GTGA AGGT
                                   C  GT   _
GAM199  KIAA1327 3' GAGAAAACTTATCTGTGA    72727       TT  A
                                TCACAGAT  GT TTCTC
                                ||||||||  || |||||
                                AGTGTCTA  CA AAGAG
                                     TT  A
GAM199  KIAA1718 3' GAGGTTTCAAATCTGTGA    64975         TAT
                                TCACAGATTTG   TCTC
                                ||||||||||   ||||
                                AGTGTCTAAAC   GGAG
                                      TTT
GAM199  KIAA1831 3' TGGAAGCAGAAGCTGTGA    64527      A_    ATTC
                                TCACAG  TTTGT    TCCA
                                ||||||  |||||    ||||
                                AGTGTC  AGACG    AGGT
                                   GA    A___
GAM199  KIAA1939 3' TGAAGAATACAAAAGTGTG   46185     GA       C
                                CACA  TTTGTATTCT CA
                                ||||  |||||||||| ||
                                GTGT  AAACATAAGA GT
                                  GA        A
GAM199  KIAA1958 3' TGGAAAAGCCAATCTGTGA   82797        T  A  C
                                TCACAGATT GT TT TCCA
                                |||||||| || || ||||
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                                AGTGTCTAA CG AA AGGT
                                     C  A  _
GAM199  MO25     3'  GAATCTGCCAGATCTGTGA   33288          T___
                                TCACAGATTTG   ATTC
                                ||||||||||    ||||
                                AGTGTCTAGAC   TAAG
                                     CGTC
GAM199  NDUFB5   3'  TGGAGAAATAGGAATTTGTGA  11767          G   _
                                TCACAGATTT TATT CTCCA
                                |||||||||| |||| |||||
                                AGTGTTTAAG ATAA GAGGT
                                     G   A
GAM199  P37NB    3'  ATGAAGAATACAAAGGATGGTC 20627        _______       C ___
           TGTGG                    TCACAGAT     TTGTATTCT CA   T
                                |||||||     |||||||| ||   |
                                GGTGTCTG     AACATAAGA GT   A
                                     GTAGGA        A __
GAM199  PEPP3    3'  GAGAACAGCAGGTCTGTG    30708          A_
                                CACAGATTTGT  TTCTC
                                ||||||||||  |||||
                                GTGTCTGGACG  AAGAG
                                     AC
GAM199  PLP1     3'  TGGAGAATAATTCTTTGA    6760      C   TTTG
                                TCA AGA    TATTCTCCA
                                ||| |||    |||||||||
                                AGT TCT    ATAAGAGGT
                                  T   TA__
GAM199  PTPNS1   3'  AGAAAACTTGATCTGTGG    55830         T_  A
                                TCACAGATT  GT TTCT
                                |||||||||  || ||||
                                GGTGTCTAG  CA AAGA
                                     TT  A
GAM199  RBBP7    5'  TGAAGAATATAAAATCTGGA   60662    A     _     C
                                TC CAGATTT GTATTCT CA
                                || ||||||| ||||||| ||
                                AG GTCTAAA TATAAGA GT
                                 _      A      A
GAM199  SIMRP7   3'  TGGAAGAGTACACCTGTGA    93981       ATT      _
                                TCACAG   TGTATTCT CCA
                                ||||||   |||||||| |||
                                AGTGTC   ACATGAGA GGT
                                   C__       A
GAM199  SPEC1    3'  GAAAACAATCATCTGTGA    40004         __   A
                                TCACAGAT  TTGT TTC
                                ||||||||  |||| |||
                                AGTGTCTA  AACA AAG
                                     CT    A
GAM199  STAG1    3'  TGAAGAAAATTTACAAATCTGG 20765    A       ____   C
             A                   TC CAGATTTGTA    TTCT CA
                                || ||||||||||    |||| ||
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                                AG GTCTAAACAT    AAGA GT
                                 _       TTAA    A
GAM199  TLE4     3'  TGGAGAACAGCAATGTGG    68517      GAT    AT
                                TCACA   TTGT  TCTCCA
                                |||||   ||||  ||||||
                                GGTGT   GACA  AGAGGT
                                  AAC   __
GAM199  LOC114928 5' TGAAGAAACAAACCTGTGA   57392       A    A    C
                                TCACAG TTTGT TTCT CA
                                |||||| ||||| |||| ||
                                AGTGTC AAACA AAGA GT
                                   C    _   A
GAM199  LOC126167 3' TGGAGAGAAATCCTGTGA    74928       _   GTA
                                TCACAG ATTT   TTCTCCA
                                |||||| ||||   |||||||
                                AGTGTC TAAA   GAGAGGT
                                   C   ___
GAM199  LOC132321 3' GAAAATATAGTATCTGTGG   75571        _     C
                                TCACAGAT TTGTATT TC
                                |||||||| ||||||| ||
                                GGTGTCTA GATATAA AG
                                     T      A
GAM199  LOC143310 3' TGGAGAATAGGGATGATG    77052    G_   G
                                CA  ATTT TATTCTCCA
                                ||  |||| |||||||||
                                GT  TAGG ATAAGAGGT
                                 AG    G
GAM199  LOC146802 3' TGGAGAATGCTGCATGTGA   78729      GATTT
                                TCACA     GTATTCTCCA
                                |||||     ||||||||||
                                AGTGT     CGTAAGAGGT
                                  ACGT_
GAM199  LOC148195 3' TGGAGAATACCATCATGT    85295     _   TT
                                ACA GAT  GTATTCTCCA
                                ||| |||  ||||||||||
                                TGT CTA  CATAAGAGGT
                                  A   C_
GAM199  LOC149072 5' TGGAGAATAGTGTTTCTGTG  79888       TT  _
                                CACAGA  TG TATTCTCCA
                                ||||||  || |||||||||
                                GTGTCT  GT ATAAGAGGT
                                   TT  G
GAM199  LOC151201 3' TGGAGGAAACACAAAACTATGA 86491     C  A    A__
                                TCA AG TTTGT   TTCTCCA
                                ||| || |||||   |||||||
                                AGT TC AAACA   AGGAGGT
                                  A  A    CAA
GAM199  LOC158777 3' AGAACATAACATCTGTGA    82872        _   A
                                TCACAGAT TTGT TTCT
                                |||||||| |||| ||||
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                                AGTGTCTA AATA AAGA
                                     C    C
GAM199   LOC162461 3'  TGGAGGTATGCAAATCTTGA   83241     C        _
                                TCA AGATTTGTAT TCTCCA
                                ||| |||||||||| ||||||
                                AGT TCTAAACGTA GGAGGT
                                  _        T
GAM199   LOC201696 3'  TGGACATCAAATCTGTGG    63831          TATTC
                                TCACAGATTTG    TCCA
                                ||||||||||    ||||
                                GGTGTCTAAAC    AGGT
                                       TAC__
GAM199   LOC202754 3'  TGAAGAATACAGCTGTGG    83590       AT       C
                                TCACAG  TTGTATTCT CA
                                ||||||  |||||||| ||
                                GGTGTC  GACATAAGA GT
                                   __       A
GAM199   LOC219401 3'  AGAAGGCAGAAATCCTGTGA   94382       A___    A
                                TCACAG    TTTGT TTCT
                                ||||||    ||||| ||||
                                AGTGTC    AGACG AAGA
                                    CTAA    G
GAM199   LOC219401 3'  TGGAGAAAGGCCCTGTGA    94388       ATTT  A_
                                TCACAG    GT  TTCTCCA
                                ||||||    ||  |||||||
                                AGTGTC    CG  AAGAGGT
                                    C___  GA
GAM199   LOC221017 3'  GGAGAACAAATCTCCGA     93113    AC       AT
                                TC  AGATTTGT  TCTCC
                                ||  ||||||||  |||||
                                AG  TCTAAACA  AGAGG
                                 CC       __
GAM199   LOC255645 3'  TGGAGAATAACAATCTCTGA   98477     C    TG
                                TCA AGATT  TATTCTCCA
                                ||| |||||  |||||||||
                                AGT TCTAA  ATAAGAGGT
                                  C    CA
GAM199   LOC257017 5'  TGGAAAAACTAGATCTGTG    99221          TA  C
                                CACAGATTTG  TT TCCA
                                ||||||||||  || ||||
                                GTGTCTAGAT  AA AGGT
                                      CA  A
GAM199   LOC54505  5'  TGGTCCTGCAAATCTGGA    68448    A        TTCT
                                TC CAGATTTGTA    CCA
                                || ||||||||||    |||
                                AG GTCTAAACGT    GGT
                                  _        CCT_
GAM200   HLA-C     3'  TTACTTCCCTAATGAAGTT    93730     G    CAC
                                AAC TTTA   GGGAAGTAA
                                ||| ||||   |||||||||
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                                TTG AAGT   CCCTTCATT
                                  _    AAT
GAM200  JUND     3'  CTACTCGGGGAACAAACGTTGG 19296         ACA___   A
                                TCAACGTTT     CGGG AG
                                |||||||||     |||| ||
                                GGTTGCAAA     GCTC TC
                                     CAAGGG    A
GAM200  SHANK2   3'  TTTAAACCTAAACGTTGA    25536         CAC  GAAG
                                TCAACGTTTA   GG    TAAA
                                ||||||||||   ||    ||||
                                AGTTGCAAAT   CC    ATTT
                                     ____ AA__
GAM200  TACC2    3'  CTTAAGGAGTGTAAACTTGA  23773      C       GGG__
                                TCAA GTTTACAC     AAG
                                |||| ||||||||     |||
                                AGTT CAAATGTG     TTC
                                  _       AGGAA
GAM200  ZNF80    3'  TTTTATGTGTGAACGTTGA   24071            G
                                TCAACGTTTACACG GAAG
                                |||||||||||||| ||||
                                AGTTGCAAGTGTGT TTTT
                                        A
GAM200  ARF4     3'  TTTTACTTCCCATAAGCGT   83710        CAC
                                ACGTTTA   GGGAAGTAAAA
                                |||||||   ||||||||||
                                TGCGAAT   CCCTTCATTTT
                                   A__
GAM200  C15orf5  3'  TTTTATTTAATGTGAACATTGA 48923      C      CGGG
                                TCAA GTTTACA    AAGTAAAA
                                |||| |||||||    ||||||||
                                AGTT CAAGTGT    TTTATTTT
                                  A      AA__
GAM200  ENPP4    3'  TTTTACTTCCTTGTTAAC    30721     T  C
                                GTT ACA GGGAAGTAAAA
                                ||| ||| ||||||||||
                                CAA TGT TCCTTCATTTT
                                  T  _
GAM200  FLJ11996 3'  CTTCCTGTGTAAACACTGA   47061     AC
                                TCA  GTTTACACGGGAAG
                                |||  ||||||||||||||
                                AGT  CAAATGTGTCCTTC
                                  CA
GAM200  KIAA1854 3'  TTTACTTCAGTTAAATATTGA  72218      CG   C  GG
                                TCAA  TTTA AC  GAAGTAAA
                                ||||  |||| ||  ||||||||
                                AGTT  AAAT TG  CTTCATTT
                                  AT   _ A_
GAM200  MAP2K6   5'  TTTTATTTGATGTAAACGTGA  50080     A      CGGG
                                TCA CGTTTACA    AAGTAAAA
                                ||| ||||||||    ||||||||
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                                AGT GCAAATGT    TTTATTTT
                                  _      AG__
GAM200  MGC23980 3'  TTTTACTTCTCATTAAAGC   59397     ACAC
                                GTTT   GGGAAGTAAAA
                                ||||   ||||||||||
                                CGAA   CTCTTCATTTT
                                  ATTA
GAM200  PRO2405  5'  TACTTCCCGTTGTTGG     38420      TTTAC
                                TCAACG    ACGGGAAGTA
                                ||||||    ||||||||||
                                GGTTGT    TGCCCTTCAT
                                   _____
GAM200  RASSF2   3'  TTTACACTGGAAACGTTGA   29116        ACA   GAA
                                TCAACGTTT   CGG   GTAAA
                                |||||||||   |||   |||||
                                AGTTGCAAA   GTC   CATTT
                                     G__   A__
GAM200  SNRK     3'  CTCATTGTGTAAACATTGA   35278     C       GA
                                TCAA GTTTACACGG  AG
                                |||| ||||||||||  ||
                                AGTT CAAATGTGTT  TC
                                  A        AC
GAM200  SRF      3'  TACTTCCCCTGGGATGCTGA   13398     A    A  C
                                TCA CGTTT CA GGGAAGTA
                                ||| ||||| || ||||||||
                                AGT GTAGG GT CCCTTCAT
                                  C    _  C
GAM200  LOC132949 3'  TTTTACTTCCCATAGGAACG   75583      ACAC
                                CGTTT   GGGAAGTAAAA
                                |||||   ||||||||||
                                GCAAG   CCCTTCATTTT
                                   GATA
GAM200  LOC221882 3'  ACTTCCCGAGCGCTGG      94100     A   TACA
                                TCA CGTT   CGGGAAGT
                                ||| ||||   ||||||||
                                GGT GCGA   GCCCTTCA
                                  C   ____
GAM200  LOC54516  3'  TTACTCTCTTGAAAAACGTTGA 39287         ACA    _
                                TCAACGTTT   CGGGA AGTAA
                                |||||||||   ||||| |||||
                                AGTTGCAAA   GTTCT TCATT
                                     AA_    C
GAM200  LOC92822  3'  TTTCCCGCAAACGCTGA     71183     A    ACA
                                TCA CGTTT   CGGGAAG
                                ||| |||||   |||||||
                                AGT GCAAA   GCCCTTT
                                  C    C__
GAM201  ELF3     3'  TGACCTTGACCTTGACCAA    16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
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                                AACCA GTTCC   TC   CAGT
                                  _    AGT  ___
GAM201  JAK2     3'  TGACCTTCATTCTGAGACCAA  18318       CAA       AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_       C_
GAM201  SLC10A2  5'  ACTCTCTGTCTTGACCAA    6590        CAA       A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM201  FLJ10803 3'  GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM201  KIAA1958 5'  GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM201  MARCKS   3'  ACTTTCCACCCTGCCCA     11411     TTCA    A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM201  TUB      5'  GTGGGACCATCCCTTAAACC   13898     C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A        AG__
GAM201  LOC80298 3'  ACTTTTACCTTGAACCA     48062         GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                     A___
GAM202  ADRBK1   3'  CATCCTGGCCCATCAGTGTA   9664        CAGA  T  CA
                                TACACTGG    GC CA  GATG
                                ||||||||    || ||  ||||
                                ATGTGACT    CG GT  CTAC
                                   ACC_  _  C_
GAM202  EGLN2    5'  CATCCACGTGCATCATCAGTGT 34517        CA  _  TCACA
           A                     TACACTGG  GA GC    GATG
                                ||||||||  || ||    ||||
                                ATGTGACT  CT CG    CTAC
                                   A_  A  TGCAC
GAM202  FCN2     3'  CACCTGTGATCTCTGCCA    15916        C     A
                                TGGCAGAG TCACAG TG
                                |||||||| |||||| ||
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                                ACCGTCTC AGTGTC AC
                                    T     C
GAM202  FCN2    3'  CACTGTGATCTCTGCCA     15917        C     A
                                TGGCAGAG TCACAG TG
                                |||||||| |||||| ||
                                ACCGTCTC AGTGTC AC
                                    T     C
GAM202  MAPK10  3'  CATCTGTAATATATTGCCAGT  58095        AGCTC_
                                ACTGGCAG     ACAGATG
                                ||||||||     |||||||
                                TGACCGTT     TGTCTAC
                                    ATATAA
GAM202  MAPK10  3'  CATCTGTAATATATTGCCAGT  58096        AGCTC_
                                ACTGGCAG     ACAGATG
                                ||||||||     |||||||
                                TGACCGTT     TGTCTAC
                                    ATATAA
GAM202  MASP2   3'  TCATCTTTGCCCACCCAGTGTA 58307        CAGA  TCAC
                                TACACTGG   GC   AGATGA
                                ||||||||   ||   ||||||
                                ATGTGACC   CG   TCTACT
                                    CACC  TT__
GAM202  NEURL   3'  TCATCTCATTACCTCTGTCAGT 16137         CTCAC_
          G                      CACTGGCAGAG     AGATGA
                                ||||||||||     ||||||
                                GTGACTGTCTC     TCTACT
                                     CATTAC
GAM202  NT5C2   3'  CATCCGTATGTCAGTGTA    25256        GA  TCACA
                                TACACTGGCA  GC    GATG
                                ||||||||||  ||    ||||
                                ATGTGACTGT  TG    CTAC
                                    A_  C____
GAM202  PRKG1   3'  TCATCTGTAAATGTCAGTGT   21820        GAGCTC
                                ACACTGGCA     ACAGATGA
                                |||||||||     ||||||||
                                TGTGACTGT     TGTCTACT
                                    AAA___
GAM202  SOX12   3'  TCATCTGTCAGATCCAGTGTA  23687        CAGAG  C
                                TACACTGG    CT ACAGATGA
                                ||||||||    || ||||||||
                                ATGTGACC    GA TGTCTACT
                                    TA___  C
GAM202  AGPAT1  3'  CACTTCCCTCCCAGTGTA    22169        CA  CTCAC  A
                                TACACTGG  GAG    AG TG
                                ||||||||  |||    || ||
                                ATGTGACC  CTC    TC AC
                                    __  CCT__  C
GAM202  AGPAT1  3'  CACTTCCCTCCCAGTGTA    22170        CA  CTCAC  A
                                TACACTGG  GAG    AG TG
                                ||||||||  |||    || ||
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                                ATGTGACC  CTC    TC AC
                                    __   CCT__  C
GAM202  C21orf69  3'  TCCGTCAGCTCTGCCAGTG   55236          C  A
                                CACTGGCAGAGCT AC GA
                                |||||||||||| || ||
                                GTGACCGTCTCGA TG CT
                                      C  C
GAM202  C9orf5   3'  TTATTTGGAACTCTGCCA    50110        C  A
                                TGGCAGAG TC CAGATGA
                                |||||||| || |||||||
                                ACCGTCTC AG GTTTATT
                                    A  _
GAM202  CENTA2   3'  CACTGTGAACTCTGTTGGGTGT 37866     _ TG     C     A
          A                      TACA C  GCAGAG TCACAG TG
                                |||| |  |||||| |||||| ||
                                ATGT G  TGTCTC AGTGTC AC
                                  G GT     A     C
GAM202  DJ328E19.C1.1 3'  TCACCCAGGACTCTGCCGGTG  31798          C  ACAGA
                                CACTGGCAGAG TC    TGA
                                |||||||||| ||    |||
                                GTGGCCGTCTC AG    ACT
                                      _ GACCC
GAM202  DKFZp434D177 3'  TCACCTGGGACTCTGCCAGTG  51071          CT A   A
                                CACTGGCAGAG  C CAG TGA
                                |||||||||| | ||| |||
                                GTGACCGTCTC  G GTC ACT
                                      AG _   C
GAM202  FLJ23375  5'  TCATCTGTGTAGATGCCACTGT 46954     C    GAGCT
          A                      TACA TGGCA    CACAGATGA
                                |||| |||||    |||||||||
                                ATGT ACCGT    GTGTCTACT
                                  C    AGAT_
GAM202  FUK      5'  TCATCCTGACCTGCCAGT    59628        AGC   CA
                                ACTGGCAG   TCA  GATGA
                                ||||||||   |||  |||||
                                TGACCGTC   AGT  CTACT
                                    C__   C_
GAM202  KIAA1211  3'  CATCCCTACTGCCAGTTA    69467   C      _ CTCACA
                                A ACTGGCAG AG     GATG
                                | |||||||| ||     ||||
                                A TGACCGTC TC     CTAC
                                 T       A  C_____
GAM202  KIAA1822  3'  CATCCCCATCCCTGCTCAGTGT 68181        _   AGCTCACA
          A                      TACACTG GCAG       GATG
                                ||||||| ||||       ||||
                                ATGTGAC CGTC       CTAC
                                    T   CCTACCC_
GAM202  MGC1314  3'  CATTTTAACTCTCCAGTG    50138       C   CTCAC
                                CACTGG AGAG    AGATG
                                |||||| ||||    |||||
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                                GTGACC TCTC    TTTAC
                                   _   AAT__
GAM202  OPN4     3'  TCACCTGTGGCTTCTTCCCCCA 53855       C___  _ T   A
            GTGTA                  TACACTGG   AGA GC CACAG TGA
                                |||||||||   ||| || ||||| |||
                                ATGTGACC   TCT CG GTGTC ACT
                                    CCCT  T _   C
GAM202  PLAGL2   3'  CACTCCAGCCTCTGCCAG    70953        _ CAC  A
                                CTGGCAGAG CT  AG TG
                                |||||||||| ||  || ||
                                GACCGTCTC GA  TC AC
                                     C  CC_  C
GAM202  RNF9     3'  TCATCTGTTTACTCTGCTCAGT 23241       _    CTC
            GTA                    TACACTG GCAGAG  ACAGATGA
                                |||||||| ||||||  ||||||||
                                ATGTGAC CGTCTC  TGTCTACT
                                    T    ATT
GAM202  SIAT4A   3'  TCACTAAGCTCTGCCAGCGTG  13142    A       CAC  A
                                TAC CTGGCAGAGCT  AG TGA
                                ||| ||||||||||  || |||
                                GTG GACCGTCTCGA  TC ACT
                                  C        A__ _
GAM202  SIMRP7   3'  CATCTGCAAACGCTTTGCCA  93967       TCA__
                                TGGCAGAGC    CAGATG
                                |||||||||    ||||||
                                ACCGTTTCG    GTCTAC
                                     CAAAC
GAM202  LOC126755 3'  CATCTGTGAACTGAACAG    75074    G_  AGC
                                CTG  CAG   TCACAGATG
                                |||  |||   |||||||||
                                GAC  GTC   AGTGTCTAC
                                  AA   A__
GAM202  LOC146901 5'  TCACCTGATGCTCTGCCAGTG  84909         TCA  A
                                CACTGGCAGAGC   CAG TGA
                                ||||||||||||  ||| |||
                                GTGACCGTCTCG   GTC ACT
                                       TA_   C
GAM202  LOC149010 3'  TCACCCAGGACTCTGCCGGTG  79854         C  ACAGA
                                CACTGGCAGAG TC    TGA
                                ||||||||||| ||    |||
                                GTGGCCGTCTC AG    ACT
                                      _ GACCC
GAM202  LOC149013 3'  TCACCCAGGACTCTGCCGGTG  79859         C  ACAGA
                                CACTGGCAGAG TC    TGA
                                ||||||||||| ||    |||
                                GTGGCCGTCTC AG    ACT
                                      _ GACCC
GAM202  LOC149317 3'  TCACCCAGGACTCTGCCGGTG  80061         C  ACAGA
                                CACTGGCAGAG TC    TGA
                                ||||||||||| ||    |||
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                                GTGGCCGTCTC AG     ACT
                                      _ GACCC
GAM202  LOC151643 3'  CACTATGAGTGCCAGTG     81137        AGA    C  A
                                CACTGGC   GCTCA AG TG
                                |||||||   ||||| || ||
                                GTGACCG   TGAGT TC AC
                                   ___     A  C
GAM202  LOC220638 3'  TCACCCAGGACTCTGCCGATG  74341    C       C  ACAGA
                                CA TGGCAGAG TC     TGA
                                || ||||||||  ||     |||
                                GT GCCGTCTC AG     ACT
                                 A       _ GACCC
GAM202  LOC257031 3'  TCACCCAGGACTCTGCCGGTG  96250          C  ACAGA
                                CACTGGCAGAG TC     TGA
                                ||||||||||| ||     |||
                                GTGGCCGTCTC AG     ACT
                                      _ GACCC
GAM202  LOC51141  3'  CATCTGTAAATCAGTTGTA    69145      _    CAGAGCTC
                                TACA CTGG       ACAGATG
                                |||| ||||       |||||||
                                ATGT GACT       TGTCTAC
                                  T    AAA_____
GAM202  LOC92230  5'  CACCTATGAGCTCTGGGGCC   69082     ___      C  A
                                GGC   AGAGCTCA AG TG
                                |||   |||||||| || ||
                                CCG   TCTCGAGT TC AC
                                  GGG       A  C
GAM203  APBA1     3'  TCTCTGGAAGGCCCCTT     70476      A    TGG
                                AAGG GCTT   TTCGGAGA
                                |||| ||||   ||||||||
                                TTCC CGGA   AGGTCTCT
                                  C   ___
GAM203  CA7       3'  CCAGTCACCAAAGCCACCT    60828     A_      TCGGA   A
                                AGG  GCTTTGGT     GAC GG
                                |||  ||||||||     ||| ||
                                TCC  CGAAACCA     CTG CC
                                  AC       _____   A
GAM203  E2F3      3'  CTGTCTCCATGAACCACTC    10467     CTT     __
                                GAG   TGGTTC  GGAGACAG
                                |||   ||||||  ||||||||
                                CTC   ACCAAG  CCTCTGTC
                                   ___      TA
GAM203  HD        3'  CCTATCCCCAGGACAGGTCCCT 10911     AG   TG   _  A  C
                                AGG  CTT  GTTC GG GA AGG
                                |||  |||  |||| || || |||
                                TCC  GGA  CAGG CC CT TCC
                                  CT   __    A  C  A
GAM203  LZTR1     3'  CTGTCACCCAAGGCTCCT     23170          TTCG A
                                AGGAGCTTTGG    G GACAG
                                ||||||||||    | |||||
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                                TCCTCGGAACC   C CTGTC
                                      ____ A
GAM203  MECP2   3'  CCCGTCTAACCACAGCTCCTT  18394       T   CGG   A
                                AAGGAGCT TGGTT  AGAC GG
                                |||||||| |||||  |||| ||
                                TTCCTCGA ACCAA  TCTG CC
                                    C    ___   C
GAM203  PLA2G2A  5'  CTGTCTCCAAACAGCCTT   6110     A  TTG  C
                                AGG GCT  GTT GGAGACAG
                                ||| |||  ||| ||||||||
                                TTC CGA  CAA CCTCTGTC
                                  _  ___  A
GAM203  PLOD    3'  CCTGAAAAACCAAGGCCCC   6114     A       CGGAGA
                                GG GCTTTGGTT     CAGG
                                || |||||||||     ||||
                                CC CGGAACCAA     GTCC
                                 C       AAA___
GAM203  POLR2A   3'  CCTGTCCCCAAATTGAAGATCC 8128       G  TG  C  A
            TT                   AAGGA CTT  GTT GG GACAGG
                                |||||| |||  ||| || ||||||
                                TTCCT GAA  TAA CC CTGTCC
                                   A  GT  A  C
GAM203  RAB36   3'  CCTGTCTCCAACACCGCCTCCT 18163      CTT   TC_
                                AGGAG  TGGT  GGAGACAGG
                                |||||  ||||  |||||||||
                                TCCTC  GCCA  CCTCTGTCC
                                   C__   CAA
GAM203  RAP1    3'  CCTGTCCTTTGGCAGAAGCTCC 39111         G  T   _
            TT                   AAGGAGCTTT GT CGGAG ACAGG
                                |||||||||| || ||||| |||||
                                TTCCTCGAAG CG GTTTC TGTCC
                                     A  _   C
GAM203  SFRP5   3'  CCTGCCCCAAGGCCCAGAGCTC 13032         TT __  AGA
            C                    GGAGCTTTGG  C  GG  CAGG
                                |||||||||| |  ||  ||||
                                CCTCGAGACC  G  CC  GTCC
                                     CG AA  CC_
GAM203  SORCS2   3'  CCTGTCCCCCAGACCCAAAGCT 40800         T  _  A_
            CT                   GGAGCTTTGG TC GG  GACAGG
                                |||||||||| || ||  ||||||
                                TCTCGAAACC AG CC  CTGTCC
                                     C  A  CC
GAM203  TFR2    3'  CCCGTCCCCCAGTCAAGAGCTC 13698        _ GT C  A  A
            CT                   AGGAGCTTT G  T GG GAC GG
                                |||||||||  |  | || ||| ||
                                TCCTCGAGA C  A CC CTG CC
                                     A TG C  C  C
GAM203  C1orf35  3'  CTGCCTCGGAAGCTCCTT   44480       TTGGT  G  A
                                AAGGAGCT    TC GAG CAG
                                ||||||||    || ||| |||
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                                TTCCTCGA    AG CTC GTC
                                    _____ G   C
GAM203  DKFZp434J1015 3'  CCGCCTCCACCTGAAAAGCTCC 94209         ___  TC   ACA
           TT                   AAGGAGCTTT  GGT  GGAG  GG
                                ||||||||||  |||  ||||  ||
                                TTCCTCGAAA  CCA  CCTC  CC
                                     AGT  __   CG_
GAM203  EFS2    3'  CTGCCTGCCAAAGCCCC    20773    A      TC  AGA
                                GG GCTTTGGT  GG  CAG
                                || ||||||||  ||  |||
                                CC CGAAACCG  CC  GTC
                                 C      T_ ___
GAM203  FLJ10350  5'  CCGCCTCCGAGTCGCTACTT  97248    G  TTT GT    ACA
                                AAG AGC  G  TCGGAG  GG
                                ||| |||  |  ||||||  ||
                                TTC TCG  C  AGCCTC  CC
                                 A  ___ TG    CG_
GAM203  HRI     3'  CTGCCCCACAAGCTCCTT    27738        _  TT
                                AAGGAGCTT TGG  CGG
                                ||||||||| |||  |||
                                TTCCTCGAA ACC  GTC
                                     C  CC
GAM203  KIAA0057  3'  CCTGTCTCTTGCAAGCTCC   25409      TG  TC
                                GGAGCTT  GT  GGAGACAGG
                                |||||||  ||  |||||||||
                                CCTCGAA  CG  TCTCTGTCC
                                    __ T_
GAM203  KIAA0189  3'  CCTGTCCCCTTTCCTAAAGCTC 28941         TTC_  A
           CT                   AGGAGCTTTGG   GG GACAGG
                                ||||||||||    || ||||||
                                TCCTCGAAATC   CC CTGTCC
                                      CTTT  C
GAM203  KIAA0326  3'  CTCCCCAAGCTCCTT      64961        T  TTC
                                AAGGAGCTT GG   GGAG
                                |||||||| ||   ||||
                                TTCCTCGAA CC   CCTC
                                    _  ___
GAM203  KIAA1203  3'  CCTGCCCTCCCACCAAAGCCTC 72087      _     TC   A_
           CT                   AGGAG CTTTGGT  GGAG  CAGG
                                ||||| |||||||  ||||  ||||
                                TCCTC GAAACCA  CCTC  GTCC
                                   C      C_   CC
GAM203  KIAA1533  5'  CCTGCCCCCAAGCCGGCCCC  74140   A  TT   C  AGA
                                GG GCT  GGTT GG   CAGG
                                || |||  |||| ||   ||||
                                CC CGG  CCGA CC   GTCC
                                 C  __   A  CCC
GAM203  MSTP028  3'  CTACCTCCCAGGCTCCT    50063       T  TTCG   AC
                                AGGAGCTT GG   GAG  AG
                                |||||||| ||   |||  ||
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                                TCCTCGGA CC   CTC  TC
                                   _ _____  CA
GAM203  SAMHD1   3'  CCTGCCCCCGTGAAGAGTTCC  61981       GGTT  AGA
                                GGAGCTTT   CGG  CAGG
                                ||||||||   |||  ||||
                                CCTTGAGA   GCC  GTCC
                                    AGT_  CCC
GAM203  SCGN     3'  CCTGTCTCACTGAAAGCCCCT  23775    A   _  TCG
                                AGG GCTTT GGT  GAGACAGG
                                ||| ||||| |||  ||||||||
                                TCC CGAAA TCA  CTCTGTCC
                                  C   G  ___
GAM203  SYT6     3'  CATCTCCGAAACCACCTC    79517    CTT   _    CA
                                GAG  TGGTT CGGAGA  G
                                |||  ||||| ||||||  |
                                CTC  ACCAA GCCTCT  C
                                  C__    A    AC
GAM203  UBXD2    3'  CTGCCTCCATCAGCTTCTT   68892       TT  TC   A
                                AAGGAGCT  GGT  GGAG CAG
                                ||||||||  |||  |||| |||
                                TTCTTCGA  CTA  CCTC GTC
                                    __  __   C
GAM203  LOC113146 3'  CCTAAAATGGAACCAAAGCTTC 73334          GGAGAC
                                GGAGCTTTGGTTC    AGG
                                ||||||||||||    |||
                                CTTCGAAACCAAG    TCC
                                     GTAAAA
GAM203  LOC113521 5'  CCCGTCTCCGAGCTGCTCC   73402     TTT       A
                                GGAGC  GGTTCGGAGAC GG
                                |||||  |||||||||| ||
                                CCTCG  TCGAGCCTCTG CC
                                   ___       C
GAM203  LOC115704 3'  CCTGCAGCGGAAACCAAAGTCC 73906   AG    __  GAGA
          C                      GG  CTTTGGT  TCG   CAGG
                                 ||  |||||||  |||   ||||
                                 CC  GAAACCA  GGC   GTCC
                                  CT     AA   GAC_
GAM203  LOC136345 3'  CCTACCCCACCCAAAGCTGCCT 76712    _     TTC  AGAC
                                AGG AGCTTTGG   GG   AGG
                                ||| ||||||||   ||   |||
                                TCC TCGAAACC   CC   TCC
                                  G      CA_  CCA_
GAM203  LOC144231 5'  CCTGTCTTCCTTGACCAAAGCT 83938          C__
          CT                     GGAGCTTTGGTT  GGAGACAGG
                                 ||||||||||||  ||||||||||
                                 TCTCGAAACCAG  CTTCTGTCC
                                       TTC
GAM203  LOC146856 5'  CTGTCTCCATGAACCACTC   83700    CTT    __
                                GAG  TGGTTC  GGAGACAG
                                |||  ||||||  ||||||||
```

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                                CTC   ACCAAG  CCTCTGTC
                                  ___     TA
GAM203   LOC147669 5'  CCGCCTCCTGGGCAAGCTCC   85180       TG   _   ACA
                                GGAGCTT  GTTC GGAG   GG
                                |||||||  |||| ||||   ||
                                CCTCGAA  CGGG CCTC   CC
                                   __    T    CG_
GAM203   LOC148021 5'  CTACCTCCAGAGCTACTT    79316     G      TTC  _
                                AAG AGCTTTGG   GG AG
                                ||| ||||||||   || ||
                                TTC TCGAGACC   CC TC
                                  A       T__  A
GAM203   LOC153688 3'  CCTGCCCCCAAACCAAGGCCT  87307    A       C  AGA
                                GG GCTTTGGTT GG   CAGG
                                || |||||||| ||   ||||
                                TC CGGAACCAA CC   GTCC
                                 _       A  CCC
GAM203   LOC155032 5'  CCTACCCCACCCAAAGCTGCCT 87592     _      TTC  AGAC
                                AGG AGCTTTGG   GG    AGG
                                ||| ||||||||   ||    |||
                                TCC TCGAAACC   CC    TCC
                                  G       CA_  CCA_
GAM203   LOC157349 5'  CCCGTCTCCGGCAGCCCCT    82334     A   TTG  T      A
                                AGG GCT   GT CGGAGAC GG
                                ||| |||   || ||||||| ||
                                TCC CGA   CG GCCTCTG CC
                                  C  ___  _      C
GAM203   LOC157349 5'  CCCGTCTCCGGCAGCCCCT    82333     A   TTG  T      A
                                AGG GCT   GT CGGAGAC GG
                                ||| |||   || ||||||| ||
                                TCC CGA   CG GCCTCTG CC
                                  C  ___  _      C
GAM203   LOC199991 3'  CCTGTCCACCCTCAAAGCCCT  91515     A      TTC  A_
                                AGG GCTTTGG   GG  GACAGG
                                ||| |||||||   ||  ||||||
                                TCC CGAAACT   CC  CTGTCC
                                  _      C__  AC
GAM204   AGRP     5'  CTTCATTAGGCCCTGCCATA   24616        A  A
                                TATGGCA GG CCTGATGGAG
                                ||||||| || ||||||||||
                                ATACCGT CC GGATTACTTC
                                    C  _
GAM204   CGTHBA    3'  CTTCCCTCCAGTCCTTGCCG   24890          C  AT  A
                                TGGCAAGGAC TG  GG GAAG
                                |||||||||| ||  || ||||
                                GCCGTTCCTG AC  CC CTTC
                                      _  CT  _
GAM204   COL5A3    3'  CTCCCCAGGCTCACCTTGCCAT 32318          A___    AT
              G                   TATGGCAAGG    CCTG  GGAG
                                ||||||||||    ||||  ||||
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                                GTACCGTTCC   GGAC  CCTC
                                     ACTC   C_
GAM204  FGF23    3'  CTTCTCTGGGGTCCCTTCCA  40557    CAA    GA
                                TGG  GGACCT  TGGAGAAG
                                |||  ||||||  ||||||||
                                ACC  CCTGGG  GTCTCTTC
                                  TTC    __
GAM204  FUT3     3'  CTCCCAGAGACCTTGCCA   5621       AC_  AT
                                TGGCAAGG  CTG  GGAG
                                ||||||||  |||  ||||
                                ACCGTTCC  GAC  CCTC
                                    AGA  __
GAM204  FUT5     3'  CTCCCAGAGACCTTGCCA   10726       AC_  AT
                                TGGCAAGG  CTG  GGAG
                                ||||||||  |||  ||||
                                ACCGTTCC  GAC  CCTC
                                    AGA  __
GAM204  TCF12    3'  TCTCCTATCCTCTTGCCATA  13639        ACCT  _
                                TATGGCAAGG   GAT GGAGA
                                ||||||||||   ||| |||||
                                ATACCGTTCT   CTA CCTCT
                                     C___   T
GAM204  WSX1     3'  CTCCCCCACATCCTTTCCTTGC 17915       CCT  _____
          C                      GGCAAGGA  GAT   GGAG
                                 ||||||||  |||   ||||
                                 CCGTTCCT  CTA   CCTC
                                     TTC  CACCC
GAM204  ZAP70    3'  CTTCCCCACCCTCAGCCCCACC 71375    CAA  AC   ___  A
          CCA                     TGG  GG  CTGA  TGG GAAG
                                  |||  ||  ||||  ||| ||||
                                  ACC  CC  GACT  ACC CTTC
                                    CCA  CC   CCC  C
GAM204  C1orf34  3'  CCTCTGGCCATTGCCATA   61303       _  A  T  T
                                TATGGCAA GG CC GA GG
                                |||||||| || || || ||
                                ATACCGTT CC GG CT CC
                                     A  _  T  _
GAM204  CLSTN1   3'  CTCCCCAGAGCACCCCCTGCCA 30787      A  AC____  AT
          T                      ATGGCA GG    CTG  GGAG
                                 ||||||  ||     |||  ||||
                                 TACCGT CC     GAC  CCTC
                                    C  CCACGA  C_
GAM204  DKFZP434J193 3'  CTTCTCCACCACTCTCCTTGCC 71562          CC_  A
          ATG                      TATGGCAAGGA  TG TGGAGAAG
                                   ||||||||||||  || ||||||||
                                   GTACCGTTCCT  AC ACCTCTTC
                                        CTC  C
GAM204  DNAJC6   3'  CTCCAAAGTTCCCACCATA   29492      CAA  C  GA
                                TATGG  GGA CT  TGGAG
                                |||||  ||| ||  |||||
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                                ATACC   CCT GA  ACCTC
                                  AC_   T  A_
GAM204  FLJ12122  5'  CTGCCAGCTCAGGTCCCTGCCA 47092       A      __  _
                                TGGCA GGACCTGA  TGG AG
                                ||||| ||||||||  ||| ||
                                ACCGT CCTGGACT  ACC TC
                                   C       CG   G
GAM204  FLJ14642  3'  CTTCTCCGTAGTCCCCGCC   52575    AA   CTG
                                GGC  GGAC   ATGGAGAAG
                                |||  ||||   |||||||||
                                CCG  CCTG   TGCCTCTTC
                                  CC   A__
GAM204  FLJ20275  3'  CTGTCAGATCCTTGCCAT    35308         C
                                ATGGCAAGGA CTGATGG
                                |||||||||| |||||||
                                TACCGTTCCT GACTGTC
                                      A
GAM204  FLJ21369  3'  CTTCTCCATCAAGTTTCACCA  46051    CAA   C
                                TGG   GGAC TGATGGAGAAG
                                |||   |||| ||||||||||
                                ACC   TTTG ACTACCTCTTC
                                  AC_   A
GAM204  HSPC016   3'  TCTCTATTCCCTGCCATA    32503       A   CCTG
                                TATGGCA GGA    ATGGAGA
                                ||||||| |||    |||||||
                                ATACCGT CCT    TATCTCT
                                    C  _____
GAM204  HT014     3'  CTTCCTAATAAATCCTTGCCA  40153        CC  A   A
                                TGGCAAGGA  TG TGG GAAG
                                |||||||||  || ||| ||||
                                ACCGTTCCT  AT ATC CTTC
                                     AA  A   _
GAM204  KIAA0773  3'  CTTCTCCACGACCTCACC    28722    CA   ACC  A
                                GG  AGG   TG TGGAGAAG
                                ||  |||   || ||||||||
                                CC  TCC   GC ACCTCTTC
                                 AC   A__  _
GAM204  KIAA1181  3'  CTCCATCAGCTGGTCA      68911      A  GAC
                                TGGC AG   CTGATGGAG
                                |||| ||   |||||||||
                                ACTG TC   GACTACCTC
                                  G  ___
GAM204  KIAA1348  3'  CTTCTTAGGTCTTGCCA     69122        G     T
                                TGGCAAG ACCTGA GGAG
                                ||||||| |||||| ||||
                                ACCGTTC TGGATT CTTC
                                     _     _
GAM204  KIAA1493  3'  CTTCTCCACCTAGTCTGCC   64840      AG   CTGA
                                GGCA  GAC    TGGAGAAG
                                ||||  |||    ||||||||
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                                CCGT  CTG   ACCTCTTC
                                  __  ATCC
GAM204  KIAA1535  3'  CTCTGTGGTCCTTGCC     80212        TG
                                GGCAAGGACC  ATGGAG
                                ||||||||||  ||||||
                                CCGTTCCTGG  TGTCTC
                                      __
GAM204  KIAA1819  5'  CTTCTCCACGGCTCCCCCA   70252    CAA  C  A
                                TGG   GGA CTG TGGAGAAG
                                |||   ||| ||| ||||||||
                                ACC   CCT GGC ACCTCTTC
                                  C__   C  _
GAM204  LAT1-3TM  3'  CTCCATCAGTGTCATCACCA   49143    CAAG  _
                                TGG   GAC CTGATGGAG
                                |||   ||| |||||||||
                                ACC   CTG GACTACCTC
                                  ACTA  T
GAM204  LAT1-3TM  5'  CTCCATCAGTGTCATTACCA   49144    CAAG  _
                                TGG   GAC CTGATGGAG
                                |||   ||| |||||||||
                                ACC   CTG GACTACCTC
                                  ATTA  T
GAM204  OS4       3'  CTTCCCCATCATCCCTTCCATT 20389      _  CC___    A
           GCCA                   TGGCAA GGA    TGATGG GAAG
                                |||||| |||    |||||| ||||
                                ACCGTT CCT    ACTACC CTTC
                                   A  TCCCT    C
GAM204  RASSF2    3'  CTTCTCCACCTTCTCTCCA   29097    CA   CCTGA
                                TGG  AGGA    TGGAGAAG
                                |||  ||||    ||||||||
                                ACC  TCTT    ACCTCTTC
                                  TC   CC___
GAM204  SARM      3'  CTCCCCCAGGCCCTGCCAT   31285      A  A   AT
                                ATGGCA GG CCTG  GGAG
                                |||||| || ||||  ||||
                                TACCGT CC GGAC  CCTC
                                   C  _   CC
GAM204  SELB      3'  CTCCCCCAGGGCCTCCTTGCC  62591        ___   AT
                                GGCAAGGA  CCTG  GGAG
                                ||||||||  ||||  ||||
                                CCGTTCCT  GGAC  CCTC
                                    CCG   CC
GAM204  SERPING1  3'  CTTCTCCATGGCCCTGCCATG  5348        A  A  TG
                                TATGGCA GG CC  ATGGAGAAG
                                ||||||| || ||  |||||||||
                                GTACCGT CC GG  TACCTCTTC
                                   C  _  __
GAM204  SLIT1     3'  TCTCCGGAAGTCCTTGC     13233        C GA
                                GCAAGGAC T  TGGAGA
                                |||||||| |  ||||||
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                                CGTTCCTG A  GCCTCT
                                    _ AG
GAM204  ZDHHC8   3'  TCCCCACCAACTTCTCTGCC  64622     _   CC  A   A
                                GGCA AGGA  TG TGG GA
                                |||| ||||  || ||| ||
                                CCGT TCTT  AC ACC CT
                                  C   CA  C   C
GAM204  LOC112868 5'  CTCCCAGCCCTTGCCA     73268       AC   AT
                                TGGCAAGG  CTG  GGAG
                                ||||||||  |||  ||||
                                ACCGTTCC  GAC  CCTC
                                    C_  __
GAM204  LOC150319 3'  CTTCTCCATCCTCCTGCCAT  80471      A   CCT
                                ATGGCA GGA   GATGGAGAAG
                                ||||||| |||   ||||||||||
                                TACCGT CCT   CTACCTCTTC
                                   _  C__
GAM204  LOC159319 5'  TTCTCCACACCCCTGCC     83073     A  ACC  A
                                GGCA GG   TG TGGAGAA
                                |||| ||   || |||||||
                                CCGT CC   AC ACCTCTT
                                  C  C__  _
GAM204  LOC197423 5'  CTCCATCAGTGTCATTACCA  78424     CAAG  _
                                TGG    GAC CTGATGGAG
                                |||    ||| |||||||||
                                ACC    CTG GACTACCTC
                                  ATTA   T
GAM204  LOC199923 5'  CTTCTCCACCTCCTGCCA    89871     A   CCTGA
                                TGGCA GGA    TGGAGAAG
                                ||||| |||    ||||||||
                                ACCGT CCT    ACCTCTTC
                                   _  CC___
GAM204  LOC206657 5'  CTTCTCAGTCTTGCCA      91105       AC    T
                                TGGCAAGG  CTGA GGAG
                                ||||||||  |||| ||||
                                ACCGTTCT  GACT CTTC
                                    __   _
GAM204  LOC220565 5'  CTCCATCAGTGTCATCACCA  92441     CAAG  _
                                TGG    GAC CTGATGGAG
                                |||    ||| |||||||||
                                ACC    CTG GACTACCTC
                                  ACTA   T
GAM204  LOC221975 5'  CTTCTCCATGGAGCCTGCC   94192     A  AC  G
                                GGCA GG  CT ATGGAGAAG
                                |||| ||  || |||||||||
                                CCGT CC  GG TACCTCTTC
                                  _ GA  _
GAM204  LOC222160 5'  TCCCATTAGGCCCCCA      95793     CAA  A      A
                                TGG   GG CCTGATGG GA
                                |||   || |||||||| ||
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                                ACC   CC GGATTACC CT
                                  C__ _      _
GAM204  LOC257239 5'  CTTCTCCACCTCAACCACCA  98844    CAA  ACC  __
                                TGG   GG   TGA  TGGAGAAG
                                |||   ||   |||  ||||||||
                                ACC   CC   ACT  ACCTCTTC
                                  A__  A__   CC
GAM204  LOC90499  3'  CTTCTCCATGGCCCCCTCCA  63741    CAA  A  TG
                                TGG   GG CC  ATGGAGAAG
                                |||   || ||  |||||||||
                                ACC   CC GG  TACCTCTTC
                                  TCC  C  __
GAM205  MDM4      3'  CCCAAAAGAAAAACTCTTGA  11508          AATA
                                TCAAGAGTTTTTCT   TGGG
                                ||||||||||||||   ||||
                                AGTTCTCAAAAAGA   ACCC
                                       AA__
GAM205  PAX6      5'  CCCAACCAAACAAAACTCTTGA 6065          TCTAATA
              CA                  TGTCAAGAGTTTT     TGGG
                                ||||||||||||      ||||
                                ACAGTTCTCAAAA     ACCC
                                       CAAACCA
GAM205  PROL2     3'  CCCATATCCCTGGACTCTTGA  23322        TTCTA
                                TCAAGAGTTT    ATATGGG
                                ||||||||||    |||||||
                                AGTTCTCAGG    TATACCC
                                     TCCC_
GAM206  MME       3'  AAGATTTAAGCACAAACTT   8027        C   GATGGC
                                AAGTTTGT GCT     ATCTT
                                |||||||| |||     |||||
                                TTCAAACA CGA     TAGAA
                                   _   ATT___
GAM206  SGNE1     3'  GAAGATGCTAGACGAAAAC   13038     G   CTGA
                                GTTT TCG   TGGCATCTTC
                                |||| |||   ||||||||||
                                CAAA AGC   ATCGTAGAAG
                                  _   AG__
GAM206  UTX       3'  AAGATGCCATGAAACAACTT  62732      T  CGCTG
                                AAGTT GT    ATGGCATCTT
                                |||||  ||   ||||||||||
                                TTCAA CA    TACCGTAGAA
                                  _  AAG__
GAM206  ARHE      3'  GAAGATGCCACTTACCCAAGCT 18975       TCGCTGA
              T                  AAGTTTG      TGGCATCTTC
                                |||||||      ||||||||||
                                TTCGAAC      ACCGTAGAAG
                                    CCATTC_
GAM206  DKFZP434P0721 5'  AAGATGCCACTTGTTTAAAACT 64449      GTC  TGA
                                AGTTT   GC   TGGCATCTT
                                |||||   ||   |||||||||
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                                TCAAA  TG  ACCGTAGAA
                                   ATT  TTC
GAM206  ELOVL2   3'  ATGCCAGTTTGGCAAACT   35435       CTGA
                                AGTTTGTCG   TGGCAT
                                |||||||||   ||||||
                                TCAAACGGT   ACCGTA
                                     TTG_
GAM206  FLJ13910 3'  GAAGAGAACAGAGACAAACT  43250       G  ATGGCA
                                AGTTTGTC CTG    TCTTC
                                |||||||| |||    |||||
                                TCAAACAG GAC    AGAAG
                                     A  AAG___
GAM206  KIAA0978 3'  GAAAATGCCATCTGTAGAC   70994    _ T      C
                                GTC GC GATGGCAT TTC
                                ||| || |||||||| |||
                                CAG TG CTACCGTA AAG
                                  A T      A
GAM206  USP10    3'  TGCACCAGCAACAACACTT   64650    _   C   ATG
                                AAGT TTGT GCTG  GCA
                                |||| |||| ||||  |||
                                TTCA AACA CGAC  CGT
                                  C   A   CA_
GAM206  ZAK      3'  GTCGGGTAGCAACAAACTT   34107      C   A_
                                AAGTTTGT GCTG  TGGC
                                |||||||| ||||  ||||
                                TTCAAACA CGAT  GCTG
                                     A   GG
GAM206  LOC149448 3'  AAGATGCCATCTCCAAAC   85576     TCGCT
                                GTTTG    GATGGCATCTT
                                |||||    ||||||||||
                                CAAAC    CTACCGTAGAA
                                   CT___
GAM207  BCL2L2   3'  AACTCGCAGTCCTCTAGA    15753      TT  GG
                                TCTGGAG  GA  TGCGAGTT
                                |||||||  ||  ||||||||
                                AGATCTC  CT  ACGCTCAA
                                     __ G_
GAM207  CA3      5'  AACTCGCACAAGTGTCCAGAG  18993      GTTGAG
                                CTCTGGA     GTGCGAGTT
                                |||||||     |||||||||
                                GAGACCT     CACGCTCAA
                                     GTGAA_
GAM207  KIT      3'  AACTTGCATCCAACTCCAGGAT 5846     CT       A
           A                     TA  CTGGAGTTG GGTGCGAGTT
                                ||  ||||||||| ||||||||||
                                AT  GACCTCAAC CTACGTTCAA
                                 AG       _
GAM207  UBE4A    3'  ACCAAAACCAACCCCAGAGTG  17727       A   A____
                                TACTCTGG GTTG    GGT
                                |||||||| ||||    |||
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                                GTGAGACC CAAC    CCA
                                    C   CAAAA
GAM207  ACTR2    3'  AACTCATTCAACTCCAGG    20368          GTGC
                                TCTGGAGTTGAG   GAGTT
                                ||||||||||||   |||||
                                GGACCTCAACTT   CTCAA
                                     A___
GAM207  LOC196746 3'  AACTCAACAAACTTCAGAGTA  88896          GAG  GC
                                TACTCTGGAGTT   GT  GAGTT
                                ||||||||||||  ||  |||||
                                ATGAGACTTCAA   CA  CTCAA
                                     A__  A_
GAM208  HAL      5'  GCCACTCCTGCATAAAGCTC   10903          TGAAAA
                                GAGCTTTATGC    GGTGGC
                                ||||||||||     ||||||
                                CTCGAAATACG    TCACCG
                                     TCC___
GAM208  HMGN2    3'  GGCCACCTTGGCACAAAAGC   19809      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _  GG
GAM208  NMI      5'  GGCCACCTCCTCAGGAAG    17436      ATG   AA
                                CTTT   CTGA  AGGTGGCC
                                ||||   ||||  ||||||||
                                GAAG   GACT  TCCACCGG
                                  ___    CC
GAM208  PACE     3'  GGCCACCTCTCCAAGGGCTT   11944       A  CT  AAA
                                GAGCTTT TG  GA   GGTGGCC
                                ||||||| ||  ||   |||||||
                                TTCGGGA AC  CT   CCACCGG
                                   _ CT  ___
GAM208  PYCR1    3'  CCACCTTCCTCTAGAGCTC   70639        TGCT  A_
                                GAGCTTTA   GA  AAGGTGG
                                ||||||||   ||  |||||||
                                CTCGAGAT   CT  TTCCACC
                                     _____  CC
GAM208  SDC1     3'  GGCCACCTCCCCAGCATTCCAG 12991     TT_     AAA
          C                      GCT   ATGCTG   AGGTGGCC
                                 |||   ||||||   ||||||||
                                 CGA   TACGAC   TCCACCGG
                                   CCT     CCC
GAM208  FLJ11560  5'  GCCCAGGCCCAGCATAAAG   48008         AAAA  ___
                                CTTTATGCTG   GGT   GGC
                                ||||||||||   |||   |||
                                GAAATACGAC   CCG   CCG
                                     _____  GAC
GAM208  KIAA0446  5'  CCACCTTTTGAAGAGCTC    69446        ATGCTG
                                GAGCTTT     AAAAGGTGG
                                |||||||     |||||||||
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                                CTCGAGA     TTTTCCACC
                                   AG____
GAM208  KIAA0971  3'  GTTGTTCTCAGCATAAAGT   30677          AAA  TG
                                GCTTTATGCTGA   GG  GC
                                ||||||||||||   ||  ||
                                TGAAATACGACT   TT  TG
                                      C__  GT
GAM208  KIAA1393  3'  GGCCACCTTGGCACAAAAGC   72574      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                   _ _  GG
GAM208  KIAA1656  3'  GGCCACCTCCTCCTAGAAGCC  66377   A    ATGCT  AA
                                G GCTTT    GA  AGGTGGCC
                                | |||||    ||  ||||||||
                                C CGAAG    CT  TCCACCGG
                                _    ATC__  CC
GAM208  KIAA1884  3'  GCCACCTTCATCTACCAAGGCT 73728       ATGCT  A_
             C                   GAGCTTT    GA  AAGGTGGC
                                |||||||    ||  ||||||||
                                CTCGGAA    CT  TTCCACCG
                                    CCAT_  AC
GAM208  PP3501    3'  GGCCACCGTTGACAGCATAAAG 41683         AAAA_
                                CTTTATGCTG    GGTGGCC
                                ||||||||||    |||||||
                                GAAATACGAC    CCACCGG
                                      AGTTG
GAM208  SDCCAG3   3'  GGTGTTCTCAGCATGAAGCTC  22803           AAA  TG
                                GAGCTTTATGCTGA   GG  GCC
                                ||||||||||||||   ||  |||
                                CTCGAAGTACGACT   CT  TGG
                                       ___  TG
GAM208  SP140     3'  GGCCACCTCCATGCAGAAGC   24327      A   TGAAA
                                GCTTT TGC    AGGTGGCC
                                ||||| |||    ||||||||
                                CGAAG ACG    TCCACCGG
                                   _  TACC_
GAM208  LOC148760 3'  GGCCACCTTCTCCAACAAGCTC 85364       TA  CT  A
                                GAGCTT  TG  GA AAGGTGGCC
                                ||||||  ||  || |||||||||
                                CTCGAA  AC  CT TTCCACCGG
                                    CA  __  C
GAM208  LOC150170 5'  ACCTGTTTCACATAAAGC    80414        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                     _    G
GAM208  LOC150175 5'  ACCTGTTTCACATAAAGC    80453        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
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                                CGAAATAC ACTTT TCCA
                                   _    G
GAM208  LOC150215 5'  ACCTGTTTCACATAAAGC    80456        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                   _    G
GAM208  LOC150218 5'  ACCTGTTTCACATAAAGC    80525        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                   _    G
GAM208  LOC152065 3'  GGCCACCTTCTCCTTGGCAGGC 86737      TTA   ___  A
          TC                     GAGCT   TGCT   GA AAGGTGGCC
                                |||||   ||||   || |||||||||
                                CTCGG   ACGG   CT TTCCACCGG
                                  ___   TTC  C
GAM208  LOC152267 3'  GGCCACCTTGGCACAAAAGC   61036      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _  GG
GAM208  LOC158292 5'  CCTCTGGACCCAGCATAAGGCT 88046           AAAA_  T
          C                     GAGCTTTATGCTG    GG GG
                                ||||||||||||    || ||
                                CTCGGAATACGAC    TC CC
                                      CCAGG  T
GAM208  LOC219997 3'  GCCACCTCTTCAGCCTC    93256    CTTTAT    A
                                GAG     GCTGAA AGGTGGC
                                |||     |||||| |||||||
                                CTC     CGACTT TCCACCG
                                  _______     C
GAM208  LOC256269 3'  GGCCACCTTGGCACAAAAGC   96608      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _  GG
GAM208  LOC91963  5'  GGCCACCTCCTCTGAGAAGC   68321      ATGCT  AA
                                GCTTT    GA  AGGTGGCC
                                |||||    ||  ||||||||
                                CGAAG    CT  TCCACCGG
                                   AGT__  CC
GAM209  CCND2     3'  TCCCAGCAAATCATCGGGCCA  10055          CCACA  _  A
                                TGGCCTGATGAT    GC GG GA
                                ||||||||||||    || || ||
                                ACCGGGCTACTA    CG CC CT
                                      AA___  A  C
GAM209  GCN5L2    5'  CTCCGCTGCGGGGGAGGCC   60529      GATGA  A
                                GGCCT    TCC CAGCGGAG
                                |||||    ||| ||||||||
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                                CCGGA    GGG GTCGCCTC
                                  GG___  C
GAM209  GJA5     3'  CTGACCAGATCATCAGCCA   19164     C      CACAG
                                TGGC TGATGATC    CGG
                                |||| ||||||||    |||
                                ACCG ACTACTAG    GTC
                                  _      ACCA_
GAM209  HIVEP3   3'  TCCCCGCTGTGGTTGGCAGCCA 44702     C  ATGAT       A
                                TGGC TG    CCACAGCGG GA
                                |||| ||    ||||||||| ||
                                ACCG AC    GGTGTCGCC CT
                                  _ GGTT_       C
GAM209  HOXD1    5'  CCGCCGGTATATTAGGCCA   44696         AT  ACA
                                TGGCCTGATG  CC   GCGG
                                ||||||||||  ||   ||||
                                ACCGGATTAT  GG   CGCC
                                      AT  C__
GAM209  SUFU     3'  CCTTGTGACCCATCAGGCCA   32934         ATC    C
                                TGGCCTGATG   CACAG GG
                                ||||||||||   ||||| ||
                                ACCGGACTAC   GTGTT CC
                                      CCA    _
GAM209  DKFZP586J1624 3'  CTCCGCCCAGTCACCATCAGGC 32043          ATCCACA_
           CA                    TGGCCTGATG       GCGGAG
                                ||||||||||       ||||||
                                ACCGGACTAC       CGCCTC
                                      CACTGACC
GAM209  KIAA1671  3'  CTTTGCTTATGAATCATCAGAC 66282    C       C  C_
           C                     GG CTGATGAT CA  AGCGGAG
                                || ||||||| ||  |||||||
                                CC GACTACTA GT  TCGTTTC
                                 A       A  AT
GAM209  LOC159110 5'  TCTCCGCTGCCCCGGTCAACCA 82995     CCTGA    CA__
                                TGG    TGATC    CAGCGGAGA
                                |||    |||||   |||||||||
                                ACC    ACTGG    GTCGCCTCT
                                  A____     CCCC
GAM209  LOC159116 5'  TCTCCGCTGCCCCGGTCAACCA 82978     CCTGA    CA__
                                TGG    TGATC    CAGCGGAGA
                                |||    |||||   |||||||||
                                ACC    ACTGG    GTCGCCTCT
                                  A____     CCCC
GAM209  LOC165476 5'  CTCCGCTGCCTGCTCAGCCA   88550     C   TGATCCA
                                TGGC TGA      CAGCGGAG
                                |||| |||      ||||||||
                                ACCG ACT      GTCGCCTC
                                  _  CGTCC__
GAM209  LOC200032 5'  CTGACCAGATCATCAGCCA   85475     C       CACAG
                                TGGC TGATGATC    CGG
                                |||| ||||||||    |||
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                                ACCG ACTACTAG    GTC
                                  _      ACCA_
GAM209  LOC219654 5'  CTCCGCTGCGGAGGGGGGCC  92932      GATGA  A
                                GGCCT    TCC CAGCGGAG
                                |||||    ||| ||||||||
                                CCGGG    AGG GTCGCCTC
                                   GGG__  C
GAM209  LOC255862 3'  TCAAATGTAGACTATCAGGCCA 96115         A  C  GCG
                                TGGCCTGATG TC ACA  GA
                                |||||||||| || |||  ||
                                ACCGGACTAT AG TGT  CT
                                      C  A  AAA
GAM210  FACL5    5'  CAGAGCAGGGCAGAACTGGGGA 64857    G         GG
                                TCC CCAGTTCTGCTC  GCTCTG
                                ||| ||||||||||||  ||||||
                                AGG GGTCAAGACGGG  CGAGAC
                                  _         A_
GAM210  TEAD3    5'  CAGAGCCCAGAGCAACCAGC  13667    CA  TC    _
                                GC  GT  TGCTC GGGCTCTG
                                ||  ||  ||||| ||||||||
                                CG  CA  ACGAG CCCGAGAC
                                 AC  __    A
GAM210  DKFZP434P211 3'  CAGAACCCACTCCTGAGAACAG 28025      CA    GCTC___  C
           CGGA                   TCCGC  GTTCT      GGG TCTG
                                |||||  |||||      ||| ||||
                                AGGCG  CAAGA      CCC AGAC
                                   A_    GTCCTCA  A
GAM210  ELOVL2   3'  CAGAACTAGCAGAAGTAGC   35436    CAG     C  GC
                                GC   TTCTGCT GG  TCTG
                                ||   ||||||| ||  ||||
                                CG   AAGACGA TC  AGAC
                                 ATG      _  A_
GAM210  KIAA0125  5'  CAGAGCCCCAGGAGGACCAGC  29561    CA    G  C
                                GC  GTTCT CT GGGCTCTG
                                ||  ||||| || ||||||||
                                CG  CAGGA GA CCCGAGAC
                                 AC    G  C
GAM210  KIAA0620  3'  CAGAGAGCGGGCAGACCTGGC  62809      T      GG
                                GCCAG TCTGCTCG  CTCTG
                                |||||| ||||||||  |||||
                                CGGTC AGACGGGC  GAGAC
                                   C       GA
GAM210  RAB40C   3'  CAGAGCCCAAGCAGCACTCAGG 41276    GCC   T    C
           A                    TCC   AGT CTGCT GGGCTCTG
                                |||   ||| ||||| ||||||||
                                AGG   TCA GACGA CCCGAGAC
                                 AC_   C    A
GAM210  LOC150174 3'  CAGAACCCACTCCTGAGAACAG 80431      CA    GCTC___  C
           CGGA                   TCCGC  GTTCT      GGG TCTG
                                |||||  |||||      ||| ||||
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                                AGGCG  CAAGA      CCC AGAC
                                  A_    GTCCTCA   A
GAM210  LOC150213 3'  CAGAACCCACTCCTGAGAACAG 75350      CA    GCTC___   C
          CGGA                   TCCGC  GTTCT      GGG TCTG
                                |||||  |||||      ||| ||||
                                AGGCG  CAAGA      CCC AGAC
                                  A_    GTCCTCA   A
GAM210  LOC160156 5'  AGCCGAACAGAACTGC     83080    C      C    G
                                GC AGTTCTG TCGG CT
                                || ||||||| |||| ||
                                CG TCAAGAC AGCC GA
                                 _      A    _
GAM210  LOC204285 3'  AGAGCCCGAGGCCAGGGGA   91013     G  A_  TCTG
                                TCC CC  GT    CTCGGGCTCT
                                ||| ||  ||    ||||||||||
                                AGG GG  CG    GAGCCCGAGA
                                 _  AC  _____
GAM210  LOC256682 5'  CAGAGCCCAAGTCCTGTGGC   99435     GTTCT   C
                                GCCA     GCT GGGCTCTG
                                ||||     ||| ||||||||
                                CGGT     TGA CCCGAGAC
                                  GTCC_   A
GAM210  LOC51716  3'  CAGAGCAGGCAGAACAGGCGGA 33258       A      T GG
                                TCCGCC GTTCTGC C  GCTCTG
                                |||||| ||||||| |  ||||||
                                AGGCGG CAAGACG G  CGAGAC
                                   A      _ A_
GAM211  HAL     5'  GCCACTCCTGCATAAAGCTC   10903          TGAAAA
                                GAGCTTTATGC     GGTGGC
                                ||||||||||      ||||||
                                CTCGAAATACG     TCACCG
                                       TCC___
GAM211  HMGN2    3'  GGCCACCTTGGCACAAAAGC   19809      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _  GG
GAM211  NMI     5'  GGCCACCTCCTCAGGAAG    17436     ATG    AA
                                CTTT   CTGA  AGGTGGCC
                                ||||   ||||  ||||||||
                                GAAG   GACT  TCCACCGG
                                  ___    CC
GAM211  PACE     3'  GGCCACCTCTCCAAGGGCTT   11944       A  CT  AAA
                                GAGCTTT TG  GA   GGTGGCC
                                |||||||  ||  ||   |||||||
                                TTCGGGA AC  CT   CCACCGG
                                   _  CT  ___
GAM211  PYCR1    3'  CCACCTTCCTCTAGAGCTC    70639        TGCT  A_
                                GAGCTTTA    GA  AAGGTGG
                                ||||||||    ||  |||||||
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                                CTCGAGAT   CT  TTCCACC
                                     ____  CC
GAM211  SDC1     3' GGCCACCTCCCCAGCATTCCAG 12991    TT_    AAA
          C                   GCT   ATGCTG  AGGTGGCC
                              |||   ||||||  ||||||||
                              CGA   TACGAC  TCCACCGG
                                CCT    CCC
GAM211  FLJ11560 5' GCCCAGGCCCAGCATAAAG   48008       AAAA  ___
                              CTTTATGCTG   GGT  GGC
                              ||||||||||   |||  |||
                              GAAATACGAC   CCG  CCG
                                     ____  GAC
GAM211  KIAA0446 5' CCACCTTTTGAAGAGCTC    69446      ATGCTG
                              GAGCTTT     AAAAGGTGG
                              |||||||     |||||||||
                              CTCGAGA     TTTTCCACC
                                  AG____
GAM211  KIAA0971 3' GTTGTTCTCAGCATAAAGT   30677        AAA  TG
                              GCTTTATGCTGA  GG  GC
                              ||||||||||||  ||  ||
                              TGAAATACGACT  TT  TG
                                    C__   GT
GAM211  KIAA1393 3' GGCCACCTTGGCACAAAAGC  72574     A  C  AA
                              GCTTT TG TG  AAGGTGGCC
                              ||||| || ||  |||||||||
                              CGAAA AC AC  TTCCACCGG
                                 _ _  GG
GAM211  KIAA1656 3' GGCCACCTCCTCCTAGAAGCC 66377   A    ATGCT  AA
                              G GCTTT    GA  AGGTGGCC
                              | |||||    ||  ||||||||
                              C CGAAG    CT  TCCACCGG
                               _    ATC__  CC
GAM211  KIAA1884 3' GCCACCTTCATCTACCAAGGCT 73728      ATGCT  A_
          C                   GAGCTTT    GA  AAGGTGGC
                              |||||||    ||  ||||||||
                              CTCGGAA    CT  TTCCACCG
                                  CCAT_  AC
GAM211  PP3501   3' GGCCACCGTTGACAGCATAAAG 41683       AAAA_
                              CTTTATGCTG    GGTGGCC
                              ||||||||||    |||||||
                              GAAATACGAC    CCACCGG
                                    AGTTG
GAM211  SDCCAG3  3' GGTGTTCTCAGCATGAAGCTC  22803         AAA  TG
                              GAGCTTTATGCTGA  GG  GCC
                              ||||||||||||||  ||  |||
                              CTCGAAGTACGACT  CT  TGG
                                     ___  TG
GAM211  SP140    3' GGCCACCTCCATGCAGAAGC  24327     A  TGAAA
                              GCTTT TGC    AGGTGGCC
                              ||||| |||    ||||||||
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                                CGAAG ACG    TCCACCGG
                                  _  TACC_
GAM211  LOC148760 3'  GGCCACCTTCTCCAACAAGCTC 85364      TA  CT  A
                                GAGCTT  TG  GA AAGGTGGCC
                                ||||||  ||  || |||||||||
                                CTCGAA  AC  CT TTCCACCGG
                                   CA  __  C
GAM211  LOC150170 5'  ACCTGTTTCACATAAAGC    80414       C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                     _    G
GAM211  LOC150175 5'  ACCTGTTTCACATAAAGC    80453       C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                     _    G
GAM211  LOC150215 5'  ACCTGTTTCACATAAAGC    80456       C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                     _    G
GAM211  LOC150218 5'  ACCTGTTTCACATAAAGC    80525       C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                     _    G
GAM211  LOC152065 3'  GGCCACCTTCTCCTTGGCAGGC 86737      TTA   ___  A
          TC                    GAGCT   TGCT   GA AAGGTGGCC
                                |||||   ||||   || |||||||||
                                CTCGG   ACGG   CT TTCCACCGG
                                   ___   TTC  C
GAM211  LOC152267 3'  GGCCACCTTGGCACAAAAGC   61036      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                   _ _  GG
GAM211  LOC158292 5'  CCTCTGGACCCAGCATAAGGCT 88046          AAAA_  T
          C                     GAGCTTTATGCTG    GG GG
                                ||||||||||||    || ||
                                CTCGGAATACGAC    TC CC
                                      CCAGG  T
GAM211  LOC219997 3'  GCCACCTCTTCAGCCTC    93256    CTTTAT    A
                                GAG     GCTGAA AGGTGGC
                                |||     ||||||| |||||||
                                CTC     CGACTT TCCACCG
                                  _______     C
GAM211  LOC256269 3'  GGCCACCTTGGCACAAAAGC   96608      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
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                                CGAAA AC AC  TTCCACCGG
                                  _ _  GG
GAM211  LOC91963  5'  GGCCACCTCCTCTGAGAAGC  68321      ATGCT  AA
                                GCTTT    GA  AGGTGGCC
                                |||||    ||  ||||||||
                                CGAAG    CT  TCCACCGG
                                  AGT__  CC
GAM212  CCND2     3'  TCCCCAGCAAATCATCGGGCCA 10056          CCACA  _  A
                                TGGCCTGATGAT    GC GG GA
                                ||||||||||||    || || ||
                                ACCGGGCTACTA    CG CC CT
                                      AA___  A  C
GAM212  GCN5L2    5'  CTCCGCTGCGGGGGAGGCC   60529      GATGA  A
                                GGCCT    TCC CAGCGGAG
                                |||||    ||| ||||||||
                                CCGGA    GGG GTCGCCTC
                                  GG___  C
GAM212  GJA5      3'  CTGACCAGATCATCAGCCA   19164      C      CACAG
                                TGGC TGATGATC    CGG
                                ||||| ||||||||    |||
                                ACCG ACTACTAG    GTC
                                  _      ACCA_
GAM212  HIVEP3    3'  TCCCCGCTGTGGTTGGCAGCCA 44702      C  ATGAT       A
                                TGGC TG    CCACAGCGG GA
                                |||| ||    ||||||||| ||
                                ACCG AC    GGTGTCGCC CT
                                  _ GGTT_       C
GAM212  HOXD1     5'  CCGCCGGTATATTAGGCCA   44696         AT  ACA
                                TGGCCTGATG  CC   GCGG
                                ||||||||||  ||   ||||
                                ACCGGATTAT  GG   CGCC
                                      AT  C__
GAM212  SUFU      3'  CCTTGTGACCCATCAGGCCA  32934         ATC    C
                                TGGCCTGATG   CACAG GG
                                ||||||||||   ||||| ||
                                ACCGGACTAC   GTGTT CC
                                      CCA    _
GAM212  ARHGEF15  3'  CTGTGGACCACAGGCCA     30953        A  A
                                TGGCCTG TG TCCACAG
                                ||||||| || |||||||
                                ACCGGAC AC AGGTGTC
                                   _ C
GAM212  DKFZP586J1624 3'  CTCCGCCCAGTCACCATCAGGC 32043          ATCCACA_
          CA                    TGGCCTGATG       GCGGAG
                                ||||||||||       ||||||
                                ACCGGACTAC       CGCCTC
                                      CACTGACC
GAM212  KIAA1671  3'  CTTTGCTTATGAATCATCAGAC 66282    C      C  C_
          C                     GG CTGATGAT CA  AGCGGAG
                                || |||||||| ||  |||||||
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                                CC GACTACTA GT  TCGTTTC
                                 A       A  AT
GAM212  MGC18079  3'  CCGCGGACCTCAGGCCA     59033        TGA   ACA
                                TGGCCTGA   TCC   GCGG
                                ||||||||   |||   ||||
                                ACCGGACT   AGG   CGCC
                                    CC_   ___
GAM212  LOC115110 3'  TGCAGACATCAGGCCA      72186         A  CACA
                                TGGCCTGATG TC    GCG
                                |||||||||| ||    |||
                                ACCGGACTAC AG    CGT
                                      _  A___
GAM212  LOC159110 5'  TCTCCGCTGCCCCGGTCAACCA 82995     CCTGA    CA__
                                TGG    TGATC    CAGCGGAGA
                                |||    |||||    |||||||||
                                ACC    ACTGG    GTCGCCTCT
                                  A____     CCCC
GAM212  LOC159116 5'  TCTCCGCTGCCCCGGTCAACCA 82978     CCTGA    CA__
                                TGG    TGATC    CAGCGGAGA
                                |||    |||||    |||||||||
                                ACC    ACTGG    GTCGCCTCT
                                  A____     CCCC
GAM212  LOC165476 5'  CTCCGCTGCCTGCTCAGCCA   88550     C   TGATCCA
                                TGGC TGA      CAGCGGAG
                                |||| |||      ||||||||
                                ACCG ACT      GTCGCCTC
                                  _  CGTCC__
GAM212  LOC200032 5'  CTGACCAGATCATCAGCCA    85475     C       CACAG
                                TGGC TGATGATC     CGG
                                |||| ||||||||     |||
                                ACCG ACTACTAG     GTC
                                  _       ACCA_
GAM212  LOC219654 5'  CTCCGCTGCGGAGGGGGGCC   92932      GATGA   A
                                GGCCT     TCC CAGCGGAG
                                |||||     ||| ||||||||
                                CCGGG     AGG GTCGCCTC
                                   GGG__   C
GAM212  LOC255862 3'  TCAAATGTAGACTATCAGGCCA 96115          A  C   GCG
                                TGGCCTGATG TC ACA   GA
                                |||||||||| || |||   ||
                                ACCGGACTAT AG TGT   CT
                                      C  A   AAA
GAM213  ACP2     3'  CCAACAGCCAGCCAGCCACA   9652       _      AG  _
                                TGTGG TGGCTGG  GT GG
                                ||||| |||||||  || ||
                                ACACC ACCGACC  CA CC
                                   G      GA  A
GAM213  ANKTM1    3'  CCACCCACCCACCACA      24696         C   AG
                                TGTGGTGG TGG  GTGG
                                ||||||||  |||  ||||
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                                ACACCACC ACC  CACC
                                    C  __
GAM213  ATF7     3'  CCAGCCCCAGCCACCCCA    23399    T       A _
                                TG GGTGGCTGG GG TGG
                                || ||||||||| || |||
                                AC CCACCGACC CC ACC
                                 C       _ G
GAM213  BDKRB2   3'  GGCCCCAACCGCCACA      7111         C  AGGT
                                TGTGGTGG TGG   GGCC
                                |||||||| |||   ||||
                                ACACCGCC ACC   CCGG
                                    A  _____
GAM213  EGFL4    3'  GCCACCCCCAGCCCCAC     62467     T    A
                                GTGG GGCTGG GGTGGC
                                |||| |||||| ||||||
                                CACC CCGACC CCACCG
                                  _    C
GAM213  ENIGMA   3'  CTCCCTCCACCACCACA     62868        C    TG
                                TGTGGTGG TGGAGG  G
                                |||||||| ||||||  |
                                ACACCACC ACCTCC  C
                                    _    CT
GAM213  MKI67    3'  GGCACCTCCAACCACCACA    11598        C      G
                                TGTGGTGG TGGAGGTG CC
                                |||||||| |||||||| ||
                                ACACCACC ACCTCCAC GG
                                    A      _
GAM213  TNNT3    3'  TCCACATCCTCCAGCCCCCACA 23134      T       _ GCC
                                TGTGG GGCTGGAGG TG  GA
                                ||||| ||||||||| ||  ||
                                ACACC CCGACCTCC AC  CT
                                   C       T  AC_
GAM213  WNT3A    3'  ATTCAGCCCACCAGCCACCTCA 53609    T       AGGT  C
                                TG GGTGGCTGG   GGC GAAT
                                || |||||||||   ||| ||||
                                AC CCACCGACC   CCG CTTA
                                 T       AC__  A
GAM213  BCAN     3'  CTGCGCTCCCGCCACCACA   41971        T   _ TG
                                TGTGGTGGC GGAG G  G
                                ||||||||| |||| |  |
                                ACACCACCG CCTC C  C
                                    C   G GT
GAM213  C20orf173 5'  GCTCCTCCTGCCACCACA    55917        T   T
                                TGTGGTGGC GGAGG GGC
                                ||||||||| ||||| |||
                                ACACCACCG CCTCC TCG
                                    T   _
GAM213  CAPN13   3'  TCGGCCACCTCCCACCA     58630       CTG
                                TGGTGG  GAGGTGGCCGA
                                ||||||  ||||||||||
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                                ACCACC   CTCCACCGGCT
                                   ___
GAM213  FLNC     3'  CCACCTCCAGCCACACA     9390      G
                                TGTG TGGCTGGAGGTGG
                                |||| ||||||||||||
                                ACAC ACCGACCTCCACC
                                  _
GAM213  KIAA1952 5'  CCCCTCCAGCCACCCA      73542    T         T
                                TG GGTGGCTGGAGG GG
                                || ||||||||||| ||
                                AC CCACCGACCTCC CC
                                 _         _
GAM213  LANCL2   3'  CCTCCCCACCCACCACA     38619        C   A  T
                                TGTGGTGG TGG GG GG
                                |||||||| ||| || ||
                                ACACCACC ACC CC CC
                                     C   _  T
GAM213  LOC127435 3'  CCAGCTCAGCCACACA      76606     G     G  G
                                TGTG TGGCTG AG TGG
                                |||| |||||| || |||
                                ACAC ACCGAC TC ACC
                                  _     _  G
GAM213  LOC127435 3'  CTACCCTCCAAACCACCACA   76607         C_     _
                                TGTGGTGG  TGGAGG TGG
                                ||||||||  |||||| |||
                                ACACCACC  ACCTCC ATC
                                     AA     C
GAM213  LOC139840 5'  TCTCCACAGCCACCACA     76777          GA  T
                                TGTGGTGGCTG  GG GG
                                ||||||||||  || ||
                                ACACCACCGAC  CC CT
                                       A_  T
GAM213  LOC150319 3'  GCCACCTCCTGCCACCACA    80473         T
                                TGTGGTGGC GGAGGTGGC
                                ||||||||| |||||||||
                                ACACCACCG CCTCCACCG
                                     T
GAM213  LOC204084 3'  ATTCGGCCACCTCCACGACCA  90990      GGC
                                TGGT   TGGAGGTGGCCGAAT
                                ||||   ||||||||||||||
                                ACCA   ACCTCCACCGGCTTA
                                  GC_
GAM213  LOC221477 3'  TCCCCACCTCCACCACCACA   93778         C        CC
                                TGTGGTGG TGGAGGTGG  GA
                                |||||||| |||||||||  ||
                                ACACCACC ACCTCCACC  CT
                                     _        C_
GAM213  LOC222031 3'  CCACCTCCAGCCACCCCA     95674    T
                                TG GGTGGCTGGAGGTGG
                                || ||||||||||||||
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                                AC CCACCGACCTCCACC
                                 C
GAM214  AGRN     3'  CCAGGCAGCCGTGCTGCA    79584        CA    _
                                TGCAGCAC  GCTGC TGG
                                ||||||||  ||||| |||
                                ACGTCGTG  CGACG ACC
                                     C_    G
GAM214  ALEX1    5'  CTGCCTCAGAGCCGGCCCGCA  33974    AGCA  A   G   GA
                                TGC    CC GCT CTG  GCAG
                                |||    || ||| |||  ||||
                                ACG    GG CGA GAC  CGTC
                                  CCC_  C   _   TC
GAM214  AP1B1    3'  CCACCGACTGGCAGCTGCA   8516       A_   C  C
                                TGCAGC  CCAG TG TGG
                                ||||||  |||| || |||
                                ACGTCG  GGTC GC ACC
                                    AC    A  C
GAM214  ATM      3'  CTGCCGGGTAGCTGGGGCTACA 57144    C   A       GGA
                                TG AGC CCAGCTGCT   GCAG
                                || ||| |||||||||   ||||
                                AC TCG GGTCGATGG   CGTC
                                 A   G        GC_
GAM214  BDP1     3'  CTGCCGGGTAGCTGGGACTACA 37966    C  CA       GGA
                                TG AG  CCAGCTGCT   GCAG
                                || ||  |||||||||   ||||
                                AC TC  GGTCGATGG   CGTC
                                 A  AG        GC_
GAM214  CAPON    5'  CTGCTCTGGGGCCGGCGCCGC  64659    A  A  A   G TG
                                GC GC CC GCT C  GAGCAG
                                || || || ||| |  ||||||
                                CG CG GG CGG G  CTCGTC
                                 C  C  C   _ GT
GAM214  CTF1     3'  CCAGCAGCTGGGACTACA    9009     C  CA
                                TG AG  CCAGCTGCTGG
                                || ||  ||||||||||
                                AC TC  GGTCGACGACC
                                 A  AG
GAM214  DDB2     3'  CTGCTCCAGAGTTGGTGACACA 5456     CAG       G
                                TG   CACCAGCT CTGGAGCAG
                                ||   |||||||| |||||||||
                                AC   GTGGTTGA GACCTCGTC
                                 ACA       _
GAM214  ENDOGL1  3'  CTGCCCCCTGAGCAGCTGGGAC 18823    C  CA       ___  A
           TACA                    TG AG  CCAGCTGCT   GG GCAG
                                || ||  |||||||||   || ||||
                                AC TC  GGTCGACGA   CC CGTC
                                 A  AG        GTC  C
GAM214  FCRH1    3'  CTGCTGAGTAGCTGGGACTACA 54726    C  CA       GG
                                TG AG  CCAGCTGCT  AGCAG
                                || ||  |||||||||  |||||
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                                AC TC  GGTCGATGA  TCGTC
                                 A  AG        G_
GAM214  FTH1    5'  GCTCCAGCGCCGCGCA     68713     A  ACCA  T
                                TGC GC    GC GCTGGAGC
                                ||| ||    || ||||||||
                                ACG CG    CG CGACCTCG
                                  _  C___  _
GAM214  GAB2    3'  CCACAGCTGGTGCTCA      55404    C         C
                                TG AGCACCAGCTG TGG
                                || ||||||||||| |||
                                AC TCGTGGTCGAC ACC
                                  _         _
GAM214  GAB2    3'  CCACAGCTGGTGCTCA      25457    C         C
                                TG AGCACCAGCTG TGG
                                || ||||||||||| |||
                                AC TCGTGGTCGAC ACC
                                  _         _
GAM214  HTR4    3'  GCCCTGGCTGTGCTGCA     7885          C    GCT  A
                                TGCAGCAC AGCT   GG GC
                                |||||||| ||||   || ||
                                ACGTCGTG TCGG   CC CG
                                     _    T__  _
GAM214  KLHL3   3'  TTCCAAGCAGGTGCTGCA    88855         A   GC
                                TGCAGCACC GCT  TGGAG
                                ||||||||| |||  |||||
                                ACGTCGTGG CGA  ACCTT
                                     A  __
GAM214  LPIN1   3'  CTGCTCCAGCAAGTAGCT    67987     ACCA  _
                                AGC    GCT GCTGGAGCAG
                                |||    ||| ||||||||||
                                TCG    TGA CGACCTCGTC
                                  A___   A
GAM214  MAD2L2  3'  GCCTAGGGCAGTGCTGCA    22018        CA   G    A
                                TGCAGCAC  GCT CTGG GC
                                ||||||||  ||| |||| ||
                                ACGTCGTG  CGG GATC CG
                                     A_  _   _
GAM214  MPST    3'  TGCCCACCTGGTGCTG      41210         CTGC   A
                                CAGCACCAG    TGG GCA
                                |||||||||    ||| |||
                                GTCGTGGTC    ACC CGT
                                     C___   _
GAM214  MSF     3'  GCCCCCACTGGGCTGCA     89466       A    C  CT  A
                                TGCAGC CCAG TG  GG GC
                                |||||| |||| ||  || ||
                                ACGTCG GGTC AC  CC CG
                                   _    _  C_  _
GAM214  OLFM1   3'  GTATTTGCAGCTGGAACTGCA  27345       CA       TG A
                                TGCAG  CCAGCTGC  G GC
                                |||||  ||||||||  | ||
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                                ACGTC  GGTCGACG  T TG
                                  AA       TT A
GAM214  PTPN18   3'  CTGCCGAGTAGCTGGGACTACA 27650    C  CA       GGA
                                TG AG  CCAGCTGCT   GCAG
                                || ||  |||||||||   ||||
                                AC TC  GGTCGATGA   CGTC
                                 A  AG       GC_
GAM214  RPS18    5'  CCGCCGCTTGTGCTGCA     42880        C   T  T
                                TGCAGCAC AGC GC GG
                                |||||||| ||| || ||
                                ACGTCGTG TCG CG CC
                                     T   C  _
GAM214  SBF1     3'  CTGGTCCAGCCAGCGGCTGCA  66069       ACCA   _    G
                                TGCAGC    GCTG CTGGA CAG
                                ||||||    |||| ||||| |||
                                ACGTCG    CGAC GACCT GTC
                                   G___    C    G
GAM214  SCGB1A1  3'  CTGCTCCAGCCTCTGCCGCT   13983     AC   CT
                                AGC  CAG  GCTGGAGCAG
                                |||  |||  ||||||||||
                                TCG  GTC  CGACCTCGTC
                                  CC   TC
GAM214  SLC8A2   5'  CTGCTCCAGGCTGTAGCCGCA  66934     A  AC    TG
                                TGC GC  CAGC  CTGGAGCAG
                                ||| ||  ||||  |||||||||
                                ACG CG  GTCG  GACCTCGTC
                                  C  AT   __
GAM214  STARD5   3'  GCTCCCTCAGTCCTGTGCTGCA 48318        CA_   CT
                                TGCAGCAC   GCTG  GGAGC
                                ||||||||   ||||  |||||
                                ACGTCGTG   TGAC  CCTCG
                                     TCC    TC
GAM214  TARBP2   3'  CTGCAGGAGCTGGTGGTGCA   57004     G      G  G
                                TGCA CACCAGCT CTG AG
                                |||| |||||||| ||| ||
                                ACGT GTGGTCGA GAC TC
                                  G       G  G
GAM214  ARHGAP8  3'  CTGCCCCAGCCCTCTGGTGT   35201       CT_    A
                                GCACCAG   GCTGG GCAG
                                |||||||   ||||| ||||
                                TGTGGTC   CGACC CGTC
                                    TCC    C
GAM214  BCKDK    3'  CTGCTCCACACACTGCTGCA   60494       CCAGC  C
                                TGCAGCA    TG TGGAGCAG
                                |||||||    || ||||||||
                                ACGTCGT    AC ACCTCGTC
                                    CAC__  _
GAM214  C11orf21 3'  CTGAGATGGCAACTGGCACCGG 27103     AGCA_   C    GAG
           CA                    TGC    CCAG TGCTG   CAG
                                |||    |||| |||||   |||
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                                ACG    GGTC ACGGT   GTC
                                  GCCAC   A    AGA
GAM214  C14orf3   5' CTGCCGGGCGGCTGGCACT   25049    CA       GGA
                                AG  CCAGCTGCT   GCAG
                                ||  |||||||||   ||||
                                TC  GGTCGGCGG   CGTC
                                 AC        GC_
GAM214  CDCA4     3' CTGCTCTGTTAGACTGGTGCTG 36086         _  CT
                                CAGCACCAG CTG  GGAGCAG
                                ||||||||| |||  |||||||
                                GTCGTGGTC GAT  TCTCGTC
                                      A  TG
GAM214  CITED2    5' CTGCCCCAGCGGCCGCTGCG  21401       ACCA      A
                                TGCAGC   GCTGCTGG GCAG
                                ||||||   |||||||| ||||
                                GCGTCG   CGGCGACC CGTC
                                   C___       C
GAM214  COPS7B    3' CTGGGGCAGCTGGCACTCA   42999    C  CA       GG
                                TG AG  CCAGCTGCT  AG
                                || ||  |||||||||  ||
                                AC TC  GGTCGACGG  TC
                                 _ AC        GG
GAM214  CXYorf1   3' CCATCGTACAGTGGTGCTGCA  82908         G   C____
                                TGCAGCACCA CTG    TGG
                                |||||||||| |||    |||
                                ACGTCGTGGT GAC    ACC
                                      _  ATGCT
GAM214  CXYorf1   5' TGCTCCAGAGCGCCTGCA    82922      CACCA   G
                                TGCAG    GCT CTGGAGCA
                                |||||    ||| ||||||||
                                ACGTC    CGA GACCTCGT
                                   CG___  _
GAM214  D2S448    3' CTGCTCCAACAGCCAAATGC   73890     GCACCA   C
                                GCA     GCTG TGGAGCAG
                                |||     |||| ||||||||
                                CGT     CGAC ACCTCGTC
                                  AAAC__   A
GAM214  FER1L4    3' CTGCTCTGTGCAGCTGGCCCGC 48119     AGCA      _
          A                      TGC    CCAGCTGC TGGAGCAG
                                |||    |||||||| ||||||||
                                ACG    GGTCGACG GTCTCGTC
                                  CCC_       T
GAM214  FLJ10604  3' CTCCAGCTTTCTGGTGTCACA  36858    CA     CT_
                                TG  GCACCAG   GCTGGAG
                                ||  |||||||   |||||||
                                AC  TGTGGTC   CGACCTC
                                 AC      TTT
GAM214  FLJ10640  5' CCGAGTAGCTGGGACTACA   39232    C  CA       _
                                TG AG  CCAGCTGCT GG
                                || ||  ||||||||| ||
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                                AC TC  GGTCGATGA CC
                                 A  AG        G
GAM214  FLJ11125  5' CCACGTAGCTGGGGCTACA   60322    C   A       _
                                TG AGC CCAGCTGC TGG
                                || ||| |||||||| |||
                                AC TCG GGTCGATG ACC
                                 A   G       C
GAM214  FLJ11280  5' CTGGAAGGCAGCTGGCACTGGC 37786     _ CA       GGAG
           A                     TGC AG  CCAGCTGCT    CAG
                                ||| ||  |||||||||    |||
                                ACG TC  GGTCGACGG    GTC
                                  G  AC        AAG_
GAM214  FLJ12581  3' CCGAGCAGCTGGGACTACA    46334    C  CA       _
                                TG AG  CCAGCTGCT GG
                                || ||  ||||||||| ||
                                AC TC  GGTCGACGA CC
                                 A  AG        G
GAM214  FLJ12697  3' GCCCCAGCAGCCCCCGCGCA   94158     A  ACCA       A
                                TGC GC    GCTGCTGG GC
                                ||| ||    |||||||| ||
                                ACG CG    CGACGACC CG
                                  _  CCCC       C
GAM214  FLJ13710  3' CTGCCCCATCCCTGGTGCT    46098         CTGC   A
                                AGCACCAG    TGG GCAG
                                ||||||||    ||| ||||
                                TCGTGGTC    ACC CGTC
                                     CCT_   C
GAM214  FLJ14681  5' CTGCCTGGGGCGGTGCTGCA   52595          A   G TG A
                                TGCAGCACC GCT C  G GCAG
                                ||||||||| ||| |  | ||||
                                ACGTCGTGG CGG G  C CGTC
                                     _   _ GT _
GAM214  FLJ14871  3' TCAGCAATGGTGCTGCA     52731          GC
                                TGCAGCACCA  TGCTGG
                                ||||||||||  ||||||
                                ACGTCGTGGT  ACGACT
                                     A_
GAM214  FLJ20150  3' CTGCTCCAGCTGTTCACATGCA 35140      GCACC   T
                                TGCA    AGC GCTGGAGCAG
                                ||||    ||| ||||||||||
                                ACGT    TTG CGACCTCGTC
                                  ACAC_   T
GAM214  FLJ30678  5' CTGCCCCAGCAGCGGCCTG    58981     CA  A       A
                                CAG  CC GCTGCTGG GCAG
                                |||  || |||||||| ||||
                                GTC  GG CGACGACC CGTC
                                  C_  _       C
GAM214  HCA112    3' CTGCTCCAGCAGCACTTGC    38082     CCA
                                GCA   GCTGCTGGAGCAG
                                |||   ||||||||||||
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                                CGT   CGACGACCTCGTC
                                  TCA
GAM214  HEMK     3'  CTGTCGGGGCAGCTGGGGCCAC 32956    CA  A       GGA
             A                    TG  GC CCAGCTGCT   GCAG
                                  ||  || |||||||||   ||||
                                  AC  CG GGTCGACGG   TGTC
                                   AC  G        GGC
GAM214  ITGB8    5'  CTGCTCCGCAGACGGGGCTGCA 11055       A  AG_   T
                                  TGCAGC CC   CTGC GGAGCAG
                                  |||||| ||   |||| |||||||
                                  ACGTCG GG   GACG CCTCGTC
                                     _ GCA   _
GAM214  KIAA0084 5'  GCTCCAGCGGCTGCTGT     68709       CCA
                                  GCAGCA   GCTGCTGGAGC
                                  ||||||   ||||||||||
                                  TGTCGT   CGGCGACCTCG
                                     ___
GAM214  KIAA0290 3'  CTGCCCCAGCTCTACACTGC   66716     CACC  CT    A
                                  GCAG    AG  GCTGG GCAG
                                  ||||    ||  ||||| ||||
                                  CGTC    TC  CGACC CGTC
                                    ACA_  T_    C
GAM214  KIAA0415 3'  GCCCAGGCCAGCTGGTGCT    94163          __    A
                                  AGCACCAGCTG  CTGG GC
                                  ||||||||||  |||| ||
                                  TCGTGGTCGAC  GACC CG
                                        CG   _
GAM214  KIAA0453 3'  CTGCCCTGTGGGCTGGTGCTTC 69605    C       _ TG T  A
             A                    TG AGCACCAG C  C GG GCAG
                                  || ||||||| |  | || ||||
                                  AC TCGTGGTC G  G CC CGTC
                                   T       G GT T  _
GAM214  KIAA0532 3'  CCAAGCAGCTGGGACTACA    71319    C  CA       _
                                  TG AG  CCAGCTGCT GG
                                  || ||  |||||||| ||
                                  AC TC  GGTCGACGA CC
                                   A  AG        A
GAM214  KIAA0720 3'  CTCTAGTAGCTGGAACTGCA   62981      CA
                                  TGCAG  CCAGCTGCTGGAG
                                  |||||  ||||||||||||
                                  ACGTC  GGTCGATGATCTC
                                    AA
GAM214  KIAA0934 3'  CTGCCCCAGTGTGACCCTGCA  64883      CACCA  T    A
                                  TGCAG    GC GCTGG GCAG
                                  |||||    || ||||| ||||
                                  ACGTC    TG TGACC CGTC
                                    CCAG_ _    C
GAM214  KIAA1160 3'  CTGCAGACACAGGCTGGTGCTG 40756          GC  GA_
             CA                     TGCAGCACCAGCT  TG   GCAG
                                  ||||||||||||  ||   ||||
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                                ACGTCGTGGTCGG AC  CGTC
                                      AC  AGA
GAM214  KIAA1169 5' CCAAGCAGCTGGAACTACA  35878   C  CA      _
                                TG AG  CCAGCTGCT GG
                                || ||  ||||||||| ||
                                AC TC  GGTCGACGA CC
                                 A  AA       A
GAM214  KIAA1464 3' CTCGGGACAGCTGTGTGCTGCA 68818       _    _ G
                                TGCAGCAC CAGCTG CT GAG
                                |||||||| |||||| || |||
                                ACGTCGTG GTCGAC GG CTC
                                     T    A  G
GAM214  KIAA1465 3' CTGCCTAGTAGCTGGGACTACA 61494   C  CA       A
                                TG AG  CCAGCTGCTGG GCAG
                                || ||  |||||||||||| ||||
                                AC TC  GGTCGATGATC CGTC
                                 A  AG        _
GAM214  KIAA1671 3' CTGCTCCAACCTGGTGCTG   66281       CTGC
                                CAGCACCAG   TGGAGCAG
                                |||||||||   ||||||||
                                GTCGTGGTC   ACCTCGTC
                                     CA__
GAM214  KIAA1821 3' CTGCCTGAGTAGCTGGGACTAC 72264   C  CA      _ A
          A                      TG AG  CCAGCTGCT GG GCAG
                                || ||  ||||||||| || ||||
                                AC TC  GGTCGATGA TC CGTC
                                 A  AG       G  _
GAM214  MGC1842  5' CTGCTCCAGGATGGTGCTGCA  66254       GCTG
                                TGCAGCACCA   CTGGAGCAG
                                ||||||||||   |||||||||
                                ACGTCGTGGT   GACCTCGTC
                                     AG__
GAM214  MGC3178  3' CTGCTCTGGCCCTGGTGTGCA  48718    G    CT  TG
                                TGCA CACCAG  GC  GAGCAG
                                |||| ||||||  ||  ||||||
                                ACGT GTGGTC  CG  CTCGTC
                                  _    C_  GT
GAM214  MGC34923 5' CCAGCAGCTGGTGCTCA    59195   C
                                TG AGCACCAGCTGCTGG
                                || ||||||||||||||
                                AC TCGTGGTCGACGACC
                                 _
GAM214  moblak   3' CCAGCAGCTGGGACTACA   56389   C  CA
                                TG AG  CCAGCTGCTGG
                                || ||  ||||||||||
                                AC TC  GGTCGACGACC
                                 A  AG
GAM214  NDRG4    3' CTGGGCCCAGCTGGTGCTGTA  40381          CT  AG
                                TGCAGCACCAGCTG  GG  CAG
                                ||||||||||||||  ||  |||
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                                ATGTCGTGGTCGAC  CC  GTC
                                      __ GG
GAM214  NDRG4    3'  CTGGGCCCAGCTGGTGCTGTA  43578          CT  AG
                                TGCAGCACCAGCTG  GG  CAG
                                |||||||||||||  ||  |||
                                ATGTCGTGGTCGAC  CC  GTC
                                      __ GG
GAM214  NR4A3    5'  CCGGTGCAGCGCGGCGCCGCA  23718    A  A  A_   __
                                TGC GC CC  GCTGC  TGG
                                ||| || ||  |||||  |||
                                ACG CG GG  CGACG  GCC
                                  C  C  CG    TG
GAM214  NSAP1    5'  CTGCCTCAGCCAGTAGCGCA   22086    A  ACCA   _  GA
                                TGC GC    GCTG CTG  GCAG
                                ||| ||    |||| |||  ||||
                                ACG CG    TGAC GAC  CGTC
                                  _ A___    C   TC
GAM214  PDCD5    5'  CTGCTCCAGCGCTGACGC    17483    AC    T
                                GC  CAGC GCTGGAGCAG
                                ||  |||| ||||||||||
                                CG  GTCG CGACCTCGTC
                                 CA   _
GAM214  PDZD2    5'  CTCCTCTACCAGTGGCTGCA   81720       ACCA   C    C
                                TGCAGC    GCTG TGGAG AG
                                ||||||    |||| ||||| ||
                                ACGTCG    TGAC ATCTC TC
                                   G___    C    C
GAM214  PPP1R16B 3'  TTCCAAAGCAGGTGCTGCA   62042         A   GC
                                TGCAGCACC GCT  TGGAG
                                |||||||||| |||  |||||
                                ACGTCGTGG CGA  ACCTT
                                     A  A_
GAM214  PSIP2    5'  CTGCGGCAGCTGGTGGCGCA   53781     AG         G
                                TGC  CACCAGCTGCTG AG
                                |||  ||||||||||| ||
                                ACG  GTGGTCGACGGC TC
                                  CG          G
GAM214  RAB40C   3'  CTGCCCACAGCACTGGTGCTCA 41279    C       C    GA_
                                TG AGCACCAG TGCTG   GCAG
                                || |||||||| |||||   ||||
                                AC TCGTGGTC ACGAC   CGTC
                                 _       _    ACC
GAM214  RAB40C   3'  CTGCCCCAGCAGCCCCTCTGCA 41280      CACCA      A
                                TGCAG    GCTGCTGG GCAG
                                |||||    |||||||| ||||
                                ACGTC    CGACGACC CGTC
                                   TCCC_       C
GAM214  SFXN5    3'  CTGCCAGCCGCTGGTGC     58652         T   GA
                                GCACCAGC GCTG  GCAG
                                |||||||| ||||  ||||
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                                CGTGGTCG CGAC  CGTC
                                     C   __
GAM214  SIMRP7   3' CTGCTCCAGCAGACCATCTGCA 93972      CACCAG
                                TGCAG     CTGCTGGAGCAG
                                |||||     ||||||||||||
                                ACGTC     GACGACCTCGTC
                                   TACCA_
GAM214  ZNF297B  5' CTGTTGCGGCAGCTGAGGCTAC 82704    C   AC       G
           A                     TG AGC  CAGCTGCTG AGCAG
                                || |||  ||||||||| |||||
                                AC TCG  GTCGACGGC TTGTC
                                 A  GA       G
GAM214  LOC123242 5' CTGAGGCCCAGCTGGTGCTG   76114          CT  AG_
                                CAGCACCAGCTG  GG   CAG
                                ||||||||||||  ||   |||
                                GTCGTGGTCGAC  CC   GTC
                                      __  GGA
GAM214  LOC126603 5' TGCTTCGCTGATCCTGCA    75914      CAC    TGCT
                                TGCAG   CAGC    GGAGCA
                                |||||   ||||    ||||||
                                ACGTC   GTCG    CTTCGT
                                   CTA   _____
GAM214  LOC127841 5' CTGCTCCCCAGCAGCTGGTGC  75186          __
                                GCACCAGCTGCT  GGAGCAG
                                ||||||||||||  |||||||
                                CGTGGTCGACGA  CCTCGTC
                                      CC
GAM214  LOC130074 3' CCACAGCTGGTGCTGCA     76624            C
                                TGCAGCACCAGCTG TGG
                                |||||||||||||| |||
                                ACGTCGTGGTCGAC ACC
                                      _
GAM214  LOC132166 3' CCAGCCGCTGGTGTGCA     75535      G      T
                                TGCA CACCAGC GCTGG
                                |||| ||||||| |||||
                                ACGT GTGGTCG CGACC
                                   _      C
GAM214  LOC132332 5' CTGCCCTTGACTGGTGCTCA   76666    C       CTGCT  A
                                TG AGCACCAG     GG GCAG
                                || ||||||||     || ||||
                                AC TCGTGGTC     CC CGTC
                                 _       AGTT_ _
GAM214  LOC142820 3' GCTCCAGCTGCACTGCA     76916       CACCA  T
                                TGCAG     GC GCTGGAGC
                                |||||     || ||||||||
                                ACGTC     CG CGACCTCG
                                   A_____  T
GAM214  LOC143785 5' CCAGACGCTGGTGTGCA     77102      G      TG
                                TGCA CACCAGC  CTGG
                                |||| |||||||  ||||
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                                ACGT GTGGTCG  GACC
                                  _      CA
GAM214  LOC146229 3'  CCAAGTAGCTGGGACTACA   78267    C  CA       _
                                TG AG  CCAGCTGCT GG
                                || ||  ||||||||| ||
                                AC TC  GGTCGATGA CC
                                 A  AG        A
GAM214  LOC146268 3'  CTCTGGCTGGTGCTGC      78338           GCT
                                GCAGCACCAGCT   GGAG
                                ||||||||||||   ||||
                                CGTCGTGGTCGG   TCTC
                                       ____
GAM214  LOC147080 5'  CCGAGCAGCTGGGACTACA   85031    C  CA       _
                                TG AG  CCAGCTGCT GG
                                || ||  ||||||||| ||
                                AC TC  GGTCGACGA CC
                                 A  AG        G
GAM214  LOC147160 5'  CTGCTCCAGCACGTGTGC    85075     CA  _
                                GCAC  GC TGCTGGAGCAG
                                ||||  || ||||||||||||
                                CGTG  TG ACGACCTCGTC
                                  __ C
GAM214  LOC148089 3'  CCGGCAGCTAGTGGCA      79329     AG   C
                                TGC  CAC AGCTGCTGG
                                |||  ||| |||||||||
                                ACG  GTG TCGACGGCC
                                  __  A
GAM214  LOC150166 5'  CTGCTCCAGCAGCCGGGCCTGC 86037      CA  A
          A                      TGCAG  CC GCTGCTGGAGCAG
                                |||||  || ||||||||||||
                                ACGTC  GG CGACGACCTCGTC
                                   CG  C
GAM214  LOC151178 5'  CTTGCAGCTGAAGCTGCA    80959       AC      T
                                TGCAGC  CAGCTGC GG
                                ||||||  ||||||| ||
                                ACGTCG  GTCGACG TC
                                    AA      T
GAM214  LOC151568 5'  CTGCTCCGGCATCCAGCGCTGC 57495      ACCAGC
                                GCAGC     TGCTGGAGCAG
                                |||||     ||||||||||
                                CGTCG     ACGGCCTCGTC
                                   CGACCT
GAM214  LOC153205 5'  CTGCTCCTGACACGTGCTGCA  87157        CAGCTGCT
                                TGCAGCAC       GGAGCAG
                                ||||||||       |||||||
                                ACGTCGTG       CCTCGTC
                                     CACAGT__
GAM214  LOC154084 3'  CTGCCCCAGTAGCATCTGCA   87377      CACCA       A
                                TGCAG    GCTGCTGG GCAG
                                |||||    |||||||| ||||
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                                ACGTC    CGATGACC CGTC
                                   TA___       C
GAM214  LOC154813 5'  CCACCAATGGTGCTGCA     82057          GC  C
                                TGCAGCACCA  TG TGG
                                ||||||||||  || |||
                                ACGTCGTGGT  AC ACC
                                      A_  C
GAM214  LOC155006 3'  CTGCTCTGCCCTGATGTGCA   82168     G  C   CT  T
                                TGCA CA CAG  GC GGAGCAG
                                |||| || |||  || |||||||
                                ACGT GT GTC  CG TCTCGTC
                                  _ A   C_ _
GAM214  LOC166129 5'  CTGCTCCAAGCAGCAGCGGCTG 88609        ACCA     _
           CA                     TGCAGC    GCTGCT GGAGCAG
                                ||||||    |||||| |||||||
                                ACGTCG    CGACGA CCTCGTC
                                    GCGA     A
GAM214  LOC196500 5'  GCTCCAGCGCCCTGCCGC    89084    A   CCA  T
                                GC GCA   GC GCTGGAGC
                                || |||   || ||||||||
                                CG CGT   CG CGACCTCG
                                 C   CC_ _
GAM214  LOC200093 3'  CCATTGTACAGTGGTGCTGCA  63765          G   C____
                                TGCAGCACCA CTG     TGG
                                |||||||||| |||     |||
                                ACGTCGTGGT GAC     ACC
                                      _   ATGTT
GAM214  LOC200093 5'  TGCTCCAGGGCGCCTGCA     63778       CACCA   G
                                TGCAG     GCT CTGGAGCA
                                |||||     ||| ||||||||
                                ACGTC     CGG GACCTCGT
                                   CG___   _
GAM214  LOC253001 5'  CTGAGGCCCAGCTGGTGCTG   97993           CT  AG_
                                CAGCACCAGCTG  GG   CAG
                                ||||||||||||  ||   |||
                                GTCGTGGTCGAC  CC   GTC
                                      __  GGA
GAM214  LOC254266 5'  CCACCGTGCTGGTGCTCA     99196    C       _ C
                                TG AGCACCAGC TG TGG
                                || |||||||| || |||
                                AC TCGTGGTCG GC ACC
                                  _       T  C
GAM214  LOC255189 5'  GCTCCCCCATTGTGCTGCA    98376        C  C  CT
                                TGCAGCAC AG TG  GGAGC
                                |||||||| || ||  |||||
                                ACGTCGTG TT AC  CCTCG
                                     _ _  CC
GAM214  LOC255738 5'  CTGCCCACGTGGCTGGCATTGC 98629       CA    TG _   A
           A                     TGCAG  CCAGC  C TGG GCAG
                                |||||  |||||  | ||| ||||
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                                ACGTT  GGTCG  G ACC CGTC
                                  AC     GT C  _
GAM214  LOC91040  3'  CCATCGTACAGTGGTGCTGCA  65339         G   C____
                                TGCAGCACCA CTG     TGG
                                |||||||||| |||     |||
                                ACGTCGTGGT GAC     ACC
                                     _  ATGCT
GAM214  LOC91040  5'  TGCTCCAGAGCGCCTGCA    65353      CACCA   G
                                TGCAG    GCT CTGGAGCA
                                |||||    ||| ||||||||
                                ACGTC    CGA GACCTCGT
                                  CG___  _
GAM215  AQP7      5'  GACAGTCACGGAGGAACAAGAT 8605         A_
           CAA                    TTGATCTT  TCCTCCGTGACTGTC
                                |||||||  ||||||||||||||||
                                AACTAGAA  AGGAGGCACTGACAG
                                     CA
GAM215  MMP14     5'  GACTAAGCAGAAGAAAGATCAA 18428        A  C  C  GACT
                                TTGATCTT TC TC GT   GTC
                                |||||||| || || ||   |||
                                AACTAGAA AG AG CG   CAG
                                     _ A  A  AAT_
GAM215  KIAA0433  5'  ACAGTCATCATAATATCAA   31498      C   CCTCC
                                TTGAT TTAT    GTGACTGT
                                ||||| ||||    ||||||||
                                AACTA AATA    TACTGACA
                                  T   C____
GAM215  KIAA1915  5'  GACAGTATTTTAAAAATAAGGT 73667         CCTCCGTG_
           CAA                    TTGATCTTAT       ACTGTC
                                ||||||||||       ||||||
                                AACTGGAATA       TGACAG
                                     AAAATTTTA
GAM215  MGC5370   3'  CAGTTGAAAAGATCAA     52193        A  CTCCGT
                                TTGATCTT TC     GACTG
                                |||||||| ||     |||||
                                AACTAGAA AG     TTGAC
                                     A _______
GAM215  TREX1     5'  GACAGCTGGAGACAGAGATCAA 54382        ATC    TGA
                                TTGATCTT   CTCCG   CTGTC
                                ||||||||   |||||   |||||
                                AACTAGAG   GAGGT   GACAG
                                     ACA    C__
GAM215  TREX1     5'  GACAGCTGGAGACAGAGATCAA 54388        ATC    TGA
                                TTGATCTT   CTCCG   CTGTC
                                ||||||||   |||||   |||||
                                AACTAGAG   GAGGT   GACAG
                                     ACA    C__
GAM215  LOC127534 3'  ACAGCAGATAAGATCAA     75963          CTCCG  A  _
                                TTGATCTTATC    TG CTG T
                                ||||||||||     || ||| |
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                                AACTAGAATAG     AC GAC A
                                      _____ _   T
GAM215  LOC150480 5'  GACAGTCACGGAGGAAGAAGAT 61025         A_
            CAA                     TTGATCTT  TCCTCCGTGACTGTC
                                    ||||||||  ||||||||||||||||
                                    AACTAGAA  AGGAGGCACTGACAG
                                        GA
GAM215  LOC158279 5'  GACAGTCACAGAGGAACAAGAT 60330         A_    C
            CAA                     TTGATCTT  TCCTC GTGACTGTC
                                    ||||||||  |||||  |||||||||
                                    AACTAGAA  AGGAG CACTGACAG
                                        CA    A
GAM215  LOC201522 3'  GACCTTCGGGAGAACGAGATCA 89637         ATC    G   CT
            A                        TTGATCTT   CTCC TGA  GTC
                                    ||||||||   ||||  |||  |||
                                    AACTAGAG   GAGG GCT  CAG
                                        CAA    _   TC
GAM215  LOC220864 5'  GACAGTCACAGAGGAACAAGAT 92487         A_    C
            CAA                     TTGATCTT  TCCTC GTGACTGTC
                                    ||||||||  |||||  |||||||||
                                    AACTAGAA  AGGAG CACTGACAG
                                        CA    A
GAM215  LOC254381 5'  GACAGTCACGACAGCAGACCAA 99328      A   TATCCTC
                                    TTG TCT      CGTGACTGTC
                                    ||| |||      ||||||||||
                                    AAC AGA      GCACTGACAG
                                      C   CGACA__
GAM216  ALPL     3'  CGCTTGTGGCCAGACCCAGAGG 6647          _  GC________  CTTG
            CCCTG                   CAGGGCCTC GGG       CG    TG
                                    |||||||||  |||       ||    ||
                                    GTCCCGGAG CCC       GT    GC
                                        A   AGACC___G  GTTC
GAM216  ATP2B2    5'  CCACAAGCAGCCATCACCCGG  9848     A   CCTCGG   C
                                    CC GGG     GGC GCTTGTGG
                                    || |||     ||| ||||||||
                                    GG CCC     CCG CGAACACC
                                     _   ACTA__   A
GAM216  COL1A1    3'  AGCACCCCCAGGCCCTGG     5389          C    CC
                                    CCAGGGCCT GGGG  GCT
                                    |||||||||  ||||  |||
                                    GGTCCCGGA CCCC  CGA
                                        C    A_
GAM216  DGCR2     3'  CCACAAGCACTCAGGCCACTGG 18897      _    C   GCC
                                    CCAG GGCCT GGG   GCTTGTGG
                                    ||||  |||||  |||   ||||||||
                                    GGTC CCGGA CTC   CGAACACC
                                      A     _   A__
GAM216  EDN3      5'  CCACAAGCGGCCGTCCTCCTGG 5480        CCTC  __
                                    CCAGGG    GG  GGCCGCTTGTGG
                                    ||||||    ||  ||||||||||||
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                                GGTCCT   CC  CCGGCGAACACC
                                   ____  TG
GAM216  FAAH    3'  CCACAGTCCACCCCAGACCCTG 44450       C  C   CC_  T
          G                     CCAGGG CT GGGG  GCT GTGG
                                |||||| || ||||  ||| ||||
                                GGTCCC GA CCCC  TGA CACC
                                   A  _   ACC  _
GAM216  GRB14   5'  AGTGGCCCCGAGCGCCCCGG  16892    A   _
                                CC GGGC CTCGGGGCCGCT
                                || |||| ||||||||||||
                                GG CCCG GAGCCCCGGTGA
                                 C   C
GAM216  LZTS1   3'  CCATAGACCCTGAGGCCCTGG  41027           CCGC
                                CCAGGGCCTCGGGG   TTGTGG
                                ||||||||||||||   ||||||
                                GGTCCCGGAGTCCC   GATACC
                                      A___
GAM216  WTAP    5'  CCATTGTGCCTCGAGGCCC   18138          C  TT
                                GGGCCTCGGGGC GC  GTGG
                                |||||||||||| ||  ||||
                                CCCGGAGCTCCG TG  TACC
                                      _  T_
GAM216  ABTB1   3'  AGCCCCCAAGACCCTGG     51697       C  C   CC
                                CCAGGG CT GGGG  GCT
                                |||||| || ||||  |||
                                GGTCCC GA CCCC  CGA
                                   A  A   __
GAM216  FLJ22169 3'  CACAAGCAGCAGGCCCAGG   44229    A    CGGG  C
                                CC GGGCCT   GC GCTTGTG
                                || ||||||   || |||||||
                                GG CCCGGA   CG CGAACAC
                                 A     ____  A
GAM216  HEMK    3'  CCACAAGCAGGAGCCGGCCTCG 32952    AG   TC  GG  _
          G                     CC  GGCC  GG  CC GCTTGTGG
                                ||  ||||  ||  || ||||||||
                                GG  CCGG  CC  GG CGAACACC
                                 CT   __  GA  A
GAM216  HS6ST   3'  CAATGCCCCGAGGCCTGG    62727      G       CGCTTG
                                CCAGG CCTCGGGGC     TG
                                ||||| |||||||||     ||
                                GGTCC GGAGCCCCG     AC
                                   _       TA____
GAM216  HS6ST1  3'  CAATGCCCCGAGGCCTGG    17847      G       CGCTTG
                                CCAGG CCTCGGGGC     TG
                                ||||| |||||||||     ||
                                GGTCC GGAGCCCCG     AC
                                   _       TA____
GAM216  HSA249128 5'  GGGGCCCCGAGGCCTTGG    34561             G
                                CCAGGGCCTCGGGGCC CT
                                |||||||||||||||| ||
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                                GGTTCCGGAGCCCCGG GG
                                                 _
GAM216  HSJ001348 5'  AGCGGCCGCGAGGCCCTG    62855          G
                                CAGGGCCTCG GGCCGCT
                                |||||||||| |||||||
                                GTCCCGGAGC CCGGCGA
                                     G
GAM216  KIAA0447  3'  CCATCGAAGGCCCTGAGGCCCT 72111              GC  _
          GG                     CCAGGGCCTCGGGGCC  TTG TGG
                                |||||||||||||||  ||| |||
                                GGTCCCGGAGTCCCGG  AGC ACC
                                      A_   T
GAM216  KIAA1030  3'  AGCAGCCCAGAGGCCCTGG   94971          G   C
                                CCAGGGCCTC GGGC GCT
                                |||||||||| |||| |||
                                GGTCCCGGAG CCCG CGA
                                     A   A
GAM216  KIAA1169  5'  AGCAGCCCCGTGGCCCCGG   35875    A    T    C
                                CC GGGCC CGGGGC GCT
                                || ||||| |||||| |||
                                GG CCCGG GCCCCG CGA
                                 C    T    A
GAM216  KIAA1862  3'  GGCGCCCCCAAGGCCCTGG   69513         C   C
                                CCAGGGCCT GGGG CGCT
                                ||||||||| |||| ||||
                                GGTCCCGGA CCCC GCGG
                                     A   C
GAM216  MAGE-E1   3'  CGATGGCCCCGAGGTCC    48674            C
                                GGGCCTCGGGGCCG TTG
                                |||||||||||||| |||
                                CCTGGAGCCCCGGT AGC
                                                 _
GAM216  MGC16332  5'  TGAGCAGCCCGGAGGCCCTGG  57546          G   C
                                CCAGGGCCTC GGGC GCTTG
                                |||||||||| |||| |||||
                                GGTCCCGGAG CCCG CGAGT
                                     G   A
GAM216  MYL9      3'  CCACAGTGACCCCAGAGCCCTG 60612       _ C   C   T
          G                      CCAGGGC CT GGGG CGCT GTGG
                                ||||||| || |||| |||| ||||
                                GGTCCCG GA CCCC GTGA CACC
                                   A _   A   _
GAM216  NDP52     3'  CCACTGTGCTGGGCCCGAGGCC 20666          G _  TT_
          CTG                     CAGGGCCTCGGG CC GC   GTGG
                                ||||||||||| || ||   ||||
                                GTCCCGGAGCCC GG CG   CACC
                                      G  T  TGT
GAM216  NET-6     5'  GCAGCCCCAGGCCCCGG    27702    A    C    C
                                CC GGGCCT GGGGC GC
                                || |||||| ||||| ||
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                                GG CCCGGA CCCCG CG
                                 C     _     A
GAM216  SEMA4F    5'  AGTAGCCCCGGGGCCCTG    16206            CG
                                CAGGGCCTCGGGGC  CT
                                ||||||||||||||  ||
                                GTCCCGGGGCCCCG  GA
                                       AT
GAM216  LOC112703 3'  CCAGACTTGACCCCAAGACCTC 73877     _  C  C    C  CTTG
              TG                  CAG GG CT GGGG CG    TGG
                                ||| || || |||| ||    |||
                                GTC CC GA CCCC GT    ACC
                                  T  A  A    A  TCAG
GAM216  LOC115051 3'  CAATGCCCCGAGGCCTGG    60676       G        CGCTTG
                                CCAGG CCTCGGGGC      TG
                                ||||| |||||||||      ||
                                GGTCC GGAGCCCCG      AC
                                  _       TA_____
GAM216  LOC143915 3'  CCACAGATACCAAAGCCCTGG  83903        CTCG  GCCG  T
                                CCAGGGC    GG    CT GTGG
                                |||||||    ||    || ||||
                                GGTCCCG    CC    GA CACC
                                    AAA_  ATA_  _
GAM216  LOC148046 3'  GGCGGCCCCAAAGCCTCTGG   85247      _   CTC
                                CCAG GGC   GGGGCCGCT
                                |||| |||   |||||||||
                                GGTC CCG   CCCCGGCGG
                                  T   AAA
GAM216  LOC152283 5'  CCACAAGCCCCCCGACAACCCT 86869       CC_     CC
              GG                  CCAGGG   TCGGGG  GCTTGTGG
                                ||||||   ||||||  ||||||||
                                GGTCCC   AGCCCC  CGAACACC
                                   AAC     C_
GAM216  LOC152441 5'  ACAGCCCTGAAGCCCTG     86913       C      CGCT
                                CAGGGC TCGGGGC    TGT
                                |||||| |||||||    |||
                                GTCCCG AGTCCCG    ACA
                                   A      _____
GAM216  LOC152793 3'  CACCTCCCCAGGGCCCTGG    81547         TC    CCGCTT
                                CCAGGGCC  GGGG     GTG
                                ||||||||  ||||     |||
                                GGTCCCGG  CCCC     CAC
                                    GA    TC_____
GAM216  LOC164582 5'  AGCACCCCAGGCCCTGG     83415         C    CC
                                CCAGGGCCT GGGG  GCT
                                ||||||||| ||||  |||
                                GGTCCCGGA CCCC  CGA
                                      _   A_
GAM216  LOC169611 3'  CAGGGGGCCTCGAGGCCCCGG  83638    A          G
                                CC GGGCCTCGGGGCC CTTG
                                || ||||||||||||| ||||
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                                GG CCCGGAGCTCCGG GGAC
                                 C          G
GAM216  LOC199733 3'  CCACTAAGCCCCGAGGGCCTGG 91437      G       CGCTT
                                CCAGG CCTCGGGGC    GTGG
                                ||||| |||||||||    ||||
                                GGTCC GGAGCCCCG    CACC
                                   G       AAT__
GAM216  LOC222962 3'  CAGGGGCCCCGAGGCCT    94453           G
                                GGGCCTCGGGGCC CTTG
                                |||||||||||| ||||
                                TCCGGAGCCCCGG GGAC
                                          _
GAM216  LOC254848 5'  CCACAAGCAAGCTACGCCC   98880     CTCGG  C_
                                GGGC    GGC  GCTTGTGG
                                ||||    |||  ||||||||
                                CCCG    TCG  CGAACACC
                                  CA___   AA
GAM216  LOC255452 3'  CCACGAGCCCCAAGCCCCTG   99390     C  C    CGC
                                CAGGG CT GGGGC   TTGTGG
                                ||||| || |||||   ||||||
                                GTCCC GA CCCCG   AGCACC
                                   C  A    ___
GAM216  LOC84643  5'  CGCTTGTGGCCAACCCCAAGGG 51768        CG  G_________  CTTG
          CCCTGG                 CCAGGGCCT  GG       CCG    TG
                                |||||||||  ||       |||    ||
                                GGTCCCGGG  CC       GGT    GC
                                     AA  CCAACC___   GTTC
GAM216  LOC90639  3'  CCAGGGTGTGCTCCGAGACCC  64409     C      _    G
                                GGG CTCGGGGC CGCTT TGG
                                ||| |||||||| ||||| |||
                                CCC GAGCCTCG GTGGG ACC
                                  A       T    _
GAM216  LOC92080  3'  CAGGCCTAGCCCCGAAGCCTT  68622      C      C__
                                AGGGC TCGGGGC   GCTTG
                                ||||| |||||||   |||||
                                TTCCG AGCCCCG   CGGAC
                                   A      ATC
GAM216  LOC92305  3'  GCGGCCCCAAAGCCCCTG    57234      C  C_
                                CAGGG CT  GGGGCCGC
                                ||||| ||  ||||||||
                                GTCCC GA  CCCCGGCG
                                   C  AA
GAM217  C18orf1   3'  GGAACCAATATTTCAGCATTCT 60867          CAACG
                                AGAATGCTGA    ATTGGTTCC
                                ||||||||||    |||||||||
                                TCTTACGACT    TAACCAAGG
                                      TTA__
GAM217  DNTT      3'  GAAAGTGTTGTCAACATTTT   73662       C       ATTGG
                                AGAATG TGACAACG    TTC
                                |||||| ||||||||    |||
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                                TTTTAC ACTGTTGT    AAG
                                   A      GA___
GAM217  FBXL11   3' AGCCAGTCACCAGCCCTCT  25512    AT   ACAAC
                                AGA  GCTG    GATTGGTT
                                |||  ||||    ||||||||
                                TCT  CGAC    CTGACCGA
                                  CC    CA___
GAM217  GOLGA4   5' GGATTTCTCATTGTCAGCA   60695        C  TT
                                TGCTGACAA GA  GGTTC
                                |||||||||  ||  |||||
                                ACGACTGTT CT  TTAGG
                                      A  CT
GAM217  HADHA    3' AACCAAACTCTGTGTCAGCATC 5731     A      AC  __
           T                     AGA TGCTGACA  GA  TTGGTT
                                |||  ||||||||  ||  ||||||
                                TCT ACGACTGT  CT  AACCAA
                                  _      GT  CA
GAM217  HS3ST4   3' GGAGCAGTCAGCATTCT    73857          AACGATTG
                                AGAATGCTGAC       GTTCC
                                ||||||||||        |||||
                                TCTTACGACTG       CGAGG
                                      A________
GAM217  MAB21L1  5' AACCAACGCTGCAGCACTTC  19952    _    A  A  A
                                GAA TGCTG CA CG TTGGTT
                                |||  |||||  ||  ||  ||||||
                                CTT ACGAC GT GC AACCAA
                                  C    _  C  _
GAM217  OSCAR    3' GGACCAATCAGCACTCT    56251    A    CAACGA
                                AGA TGCTGA     TTGGTTC
                                |||  ||||||     |||||||
                                TCT ACGACT     AACCAGG
                                  C     _______
GAM217  OSCAR    3' GGACCAATCAGCACTCT    56479    A    CAACGA
                                AGA TGCTGA     TTGGTTC
                                |||  ||||||     |||||||
                                TCT ACGACT     AACCAGG
                                  C     _______
GAM217  OSCAR    3' GGACCAATCAGCACTCT    56482    A    CAACGA
                                AGA TGCTGA     TTGGTTC
                                |||  ||||||     |||||||
                                TCT ACGACT     AACCAGG
                                  C     _______
GAM217  STAC     3' GAACCAACAACAGCATCT   13426    A   ACAACGA
                                AGA TGCTG      TTGGTTC
                                |||  |||||      |||||||
                                TCT ACGAC      AACCAAG
                                  _    AAC____
GAM217  BIVM     5' GAATGTCCTCAGCATTCT   35158        CAAC  TG
                                AGAATGCTGA   GAT  GTTC
                                ||||||||||   |||  ||||
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                                TCTTACGACT   CTG  TAAG
                                     C___  __
GAM217  C20orf126 3'  GGAGTGTCATTCCAGCATTC   48735       ACAAC  T  __
                                GAATGCTG    GA TGG  TTCC
                                ||||||||    || |||  ||||
                                CTTACGAC    CT ACT  GAGG
                                     _____  T   GT
GAM217  CNNM4    3'  GGAACTGTCAGTCATCAGCATC 39870    A     CA  GAT
          T                      AGA TGCTGA  AC   TGGTTCC
                                 ||| ||||||  ||   |||||||
                                 TCT ACGACT  TG   GTCAAGG
                                   _     AC  ACT
GAM217  DKFZp434O0320 3'  GGAACCAGCCCTGTCAACACCC 84698    AA  C    ACGA
          T                      AG  TG TGACA    TTGGTTCC
                                 ||  || |||||    ||||||||
                                 TC  AC ACTGT    GACCAAGG
                                  CC  A    CCC_
GAM217  DKFZP727G051 3'  GAACCAACATTCAAATTCT    70010      GC   CAACGA
                                 AGAAT  TGA     TTGGTTC
                                 |||||  |||     |||||||
                                 TCTTA  ACT     AACCAAG
                                    A_   TAC___
GAM217  DKFZP727M111 5'  GGAACCAGGGCTGCCAGCTTC  32062     T    A  ACGA
                                 GAA GCTG CA    TTGGTTCC
                                 ||| |||| ||    ||||||||
                                 CTT CGAC GT    GACCAAGG
                                   _    C  CGG_
GAM217  FLJ20337  3'  GGACCACTGTCAGTATTC     35443          ACGAT
                                 GAATGCTGACA     TGGTTC
                                 ||||||||||     ||||||
                                 CTTATGACTGT     ACCAGG
                                       C_____
GAM217  FLJ21144  5'  AGCCTTGTCATTTCAGCATTCT 43188          C  C   T_
                                 AGAATGCTGA AA GAT  GGTT
                                 |||||||||| || |||  ||||
                                 TCTTACGACT TT CTG  CCGA
                                       _  A   TT
GAM217  GPR88    3'  AATCATATGTCAGCATTCT    42132          AC_
                                 AGAATGCTGACA   GATT
                                 ||||||||||||   ||||
                                 TCTTACGACTGT   CTAA
                                        ATA
GAM217  HTMP10   3'  AGCTAATCACCAGCATTT     53756        ACAAC
                                 GAATGCTG    GATTGGTT
                                 ||||||||    ||||||||
                                 TTTACGAC    CTAATCGA
                                      CA___
GAM217  KIAA0319  3'  GACCAACCAGCATTCT      29699         ACAACGA
                                 AGAATGCTG      TTGGTT
                                 |||||||||      ||||||
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                                TCTTACGAC      AACCAG
                                    C_______
GAM217  KIAA0513  3'  AGCCGCCTCGTCGTCAGCGTTC 29017          A    T_
            T                    AGAATGCTGAC ACGA  TGGTT
                                 |||||||||||| ||||  |||||
                                 TCTTGCGACTG TGCT  GCCGA
                                      C    CC
GAM217  KIAA1495  3'  GAACCTCACTGTAGCATTCT   73565        A  AC  TT
                                 AGAATGCTG CA  GA  GGTTC
                                 ||||||||| ||  ||  |||||
                                 TCTTACGAT GT  CT  CCAAG
                                      _ CA  __
GAM217  KRTAP4-13 3'  GATTCTCATCAACCAGCATTCT 53751         ACAAC   T  T_
                                 AGAATGCTG    GAT GG  TC
                                 |||||||||    ||| ||  ||
                                 TCTTACGAC    CTA TC  AG
                                      CAA__   C  TT
GAM217  KRTAP4-4  3'  GATTCTCATCAACCAGCATTCT 51689         ACAAC   T  T_
                                 AGAATGCTG    GAT GG  TC
                                 |||||||||    ||| ||  ||
                                 TCTTACGAC    CTA TC  AG
                                      CAA__   C  TT
GAM217  MGC5590   5'  ACCACTGTCAGCACTCT     44147     A       ACGAT
                                 AGA TGCTGACA    TGGT
                                 ||| ||||||||    ||||
                                 TCT ACGACTGT    ACCA
                                   C       C____
GAM217  PLP1      3'  GAAACAGGGTGTTGTCAGCATC 6757      A         A_   G
            T                    AGA TGCTGACAACG  TTG TTC
                                 ||| ||||||||||  ||| |||
                                 TCT ACGACTGTTGT  GAC AAG
                                   _         GG   A
GAM217  SLC12A8   5'  GGAGCCTGCCGCCAGCATTC   45240        ACAA  ATT
                                 GAATGCTG   CG   GGTTCC
                                 ||||||||   ||   ||||||
                                 CTTACGAC   GC   CCGAGG
                                      C___  CGT
GAM217  SPTLC2    3'  AGTCACTGTCAGCATCT     17978     A       AC
                                 AGA TGCTGACA  GATT
                                 ||| ||||||||  ||||
                                 TCT ACGACTGT  CTGA
                                   _       CA
GAM217  XT2       3'  GGGCACCAGCAGCATTC     42476         ACAACGA    _
                                 GAATGCTG      TTGGT TCC
                                 ||||||||      ||||| |||
                                 CTTACGAC      GACCA GGG
                                      ________    C
GAM217  LOC112609 3'  ACCTATTGTCAGCATTCT    73198           CGATT
                                 AGAATGCTGACAA    GGT
                                 ||||||||||||     |||
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                                TCTTACGACTGTT    CCA
                                      AT___
GAM217  LOC142948 3'  GGACCAATCAGCACTCT    83779    A    CAACGA
                                AGA TGCTGA    TTGGTTC
                                ||| ||||||    |||||||
                                TCT ACGACT    AACCAGG
                                  C    _______
GAM217  LOC147791 5'  GGTACCCACTGTCAGCAGCCT  85191    AA      ACGATT   T
                                AG  TGCTGACA    GGT CC
                                ||  ||||||||    ||| ||
                                TC  ACGACTGT    CCA GG
                                 CG       CAC___   T
GAM217  LOC150837 3'  GACCACTGCAGCATTC     80804        A  ACGAT
                                GAATGCTG CA    TGGTT
                                |||||||| ||    |||||
                                CTTACGAC GT    ACCAG
                                     _  C____
GAM217  LOC150935 3'  ACCAATCAGCATTCT      80821          CAACGA
                                AGAATGCTGA    TTGGT
                                ||||||||||    |||||
                                TCTTACGACT    AACCA
                                      _______
GAM217  LOC150935 3'  GGACCAATCAGCACTCT    80831    A    CAACGA
                                AGA TGCTGA    TTGGTTC
                                ||| ||||||    |||||||
                                TCT ACGACT    AACCAGG
                                  C    _______
GAM217  LOC150935 3'  GGACCAATCAGCATTCT    80832          CAACGA
                                AGAATGCTGA    TTGGTTC
                                ||||||||||    |||||||
                                TCTTACGACT    AACCAGG
                                      _______
GAM217  LOC154092 3'  AACCAAATCCTGTTGTCAGCAA 87366    A        __   _
                TCT                  AGA TGCTGACAAC  GATT GGTT
                                ||| ||||||||||  |||| ||||
                                TCT ACGACTGTTG  CTAA CCAA
                                  A         TC    A
GAM217  LOC197414 3'  AACCTCCCCAGCATTCT    89454          ACAAC  TT
                                AGAATGCTG    GA  GGTT
                                |||||||||    ||  ||||
                                TCTTACGAC    CT  CCAA
                                     CC___  __
GAM217  LOC201305 3'  GGAATGGAGCTGTCAGCACTCT 89607    A      ACGA  G
                                AGA TGCTGACA    TT GTTCC
                                ||| ||||||||    || |||||
                                TCT ACGACTGT    AG TAAGG
                                  C       CG__  G
GAM217  LOC220001 3'  AGTCGTTTCCACTGTCAGCATC 93274    A       _______
                CT                   AG ATGCTGACA     ACGATT
                                || |||||||||     ||||||
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                                TC TACGACTGT     TGCTGA
                                 C       CACCTT
GAM217  LOC90410  3'  AACCTCTGTAGCATTC     63351        A  AC  TT
                                GAATGCTG CA  GA  GGTT
                                |||||||| ||  ||  ||||
                                CTTACGAT GT  CT  CCAA
                                     _  __  __
GAM218  GNRHR     5'  ATAACAGCAACTACAATA    6390      A   C
                                TATT TGG TGCTGTTGT
                                |||| ||| |||||||||
                                ATAA ATC ACGACAATA
                                  C   A
GAM218  JAM3      3'  TGGTCGTTCAGCAGCCACGA  52493   TA       T_  T
                                T  TGGCTGCTG  TG CCA
                                |  |||||||||  || |||
                                A  ACCGACGAC  GC GGT
                                 GC       TT  T
GAM218  MAN1A1    3'  GTTGCAAAAAGCCATAATA   93557         GCTG   TC
                                TATTATGGCT    TTG  CAAC
                                ||||||||||    |||  ||||
                                ATAATACCGA    AAC  GTTG
                                      AA__   __
GAM218  C7orf13   3'  TGTTAGGATAACAGCCATAA  51923        GCT     _
                                TTATGGCT   GTTGTCC AACA
                                ||||||||   ||||||| ||||
                                AATACCGA   CAATAGG TTGT
                                     ___       A
GAM218  CDW52     3'  TGGGGGCAACAGCCAAAATA  10163     A     C    G
                                TATT TGGCTG TGTT TCCA
                                |||| |||||| |||| ||||
                                ATAA ACCGAC ACGG GGGT
                                  A     A   _
GAM218  MGC5149   3'  TTGGACAACACTTCTATAA   72765      CTGC
                                TTATGG    TGTTGTCCAA
                                ||||||    ||||||||||
                                AATATC    ACAACAGGTT
                                    TTC_
GAM218  LOC151040 3'  TTGAATACTATGCAGCCATAA  80911         _  T   C
                                TTATGGCTGC TG TGT CAA
                                |||||||||| || ||| |||
                                AATACCGACG AT ATA GTT
                                      T  C   A
GAM218  LOC51026  3'  ATTTCAACAGCCATAGTA    32684         C  TT
                                TATTATGGCTG TG  GT
                                |||||||||||  ||  ||
                                ATGATACCGAC AC  TA
                                      A  TT
GAM219  ADAT1     3'  ACTTTGGGAAGCCCAGGCAGG  24908    CA   C   _
                                CC  CCT GGCT CCCAAAGT
                                ||  ||| |||| ||||||||
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                                GG  GGA CCGA GGGTTTCA
                                 AC   C    A
GAM219  ADORA2B  5'  ACTTTGGGCTCGGGCGAGTGGG 7279       C   G ___
                                CCCAC TCG CT   CCCAAAGT
                                ||||| ||| ||   ||||||||
                                GGGTG AGC GG   GGGTTTCA
                                  _  G  CTC
GAM219  AICDA    3'  ACTTTGGGAGGCCGAGCCGGGC 40687     A   AC     _
           GGA                    TCC CCC  CTCGGC TCCCAAAGT
                                ||| |||  |||||| |||||||||
                                AGG GGG  GAGCCG AGGGTTTCA
                                  C   CC     G
GAM219  AK1      3'  ACTTTGGGAAGCTGAGGCAGGA 6631      A  CA       _
           GGA                    TCC CC  CCTCGGCT CCCAAAGT
                                ||| ||  |||||||| ||||||||
                                AGG GG  GGAGTCGA GGGTTTCA
                                  A  AC       A
GAM219  ALDH3A2  3'  ACTTTGGGAGGCCGAGGTGGGA 69795     A         _
           GGA                    TCC CCCACCTCGGC TCCCAAAGT
                                ||| ||||||||||| |||||||||
                                AGG GGGTGGAGCCG AGGGTTTCA
                                  A          G
GAM219  ALDH3B1  3'  ACTTTGGGAGGCCGAGGCAGGC 93148     A  CA      _
           GGA                    TCC CC  CCTCGGC TCCCAAAGT
                                ||| ||  ||||||| |||||||||
                                AGG GG  GGAGCCG AGGGTTTCA
                                  C  AC      G
GAM219  ALDH8A1  3'  ACTTTGGGAGGCCAAGGTGGGT 42909           C   _
           GGA                    TCCACCCACCT GGC TCCCAAAGT
                                |||||||||||  ||| |||||||||
                                AGGTGGGTGGA CCG AGGGTTTCA
                                     A   G
GAM219  ALPP     3'  ACTTTGGGAGGCCGAGGTGGGC 69404     A         _
           GGA                    TCC CCCACCTCGGC TCCCAAAGT
                                ||| ||||||||||| |||||||||
                                AGG GGGTGGAGCCG AGGGTTTCA
                                  C          G
GAM219  APOL1    3'  ACTTTGGGAGGCCAAGGCGGGC 14722    A   A   C   _
           GG                     CC CCC CCT GGC TCCCAAAGT
                                || ||| ||| ||| |||||||||
                                GG GGG GGA CCG AGGGTTTCA
                                 C   C   A   G
GAM219  ATM      3'  ACTTTGGGAGGCCGAGGTGAGC 5285      ACC       _
           GGA                    TCC   CACCTCGGC TCCCAAAGT
                                |||   ||||||||| |||||||||
                                AGG   GTGGAGCCG AGGGTTTCA
                                  CGA        G
GAM219  ATM      3'  ACTTTGGGAGGCCGAGGTGAGC 57128     ACC       _
           GGA                    TCC   CACCTCGGC TCCCAAAGT
                                |||   ||||||||| |||||||||
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                                AGG   GTGGAGCCG AGGGTTTCA
                                  CGA        G
GAM219  ATM      3'  ACTCCGGAGGCTGAGGTGGGAG 57140     A         TC  AA
              GA                   TCC CCCACCTCGGC  CC  AGT
                                   ||| ||||||||||  ||  |||
                                   AGG GGGTGGAGTCG  GG  TCA
                                     A          GA  CC
GAM219  ATM      3'  ACTTTGGGAGGTTGAGGTAGGT 57141     C  C      _
              AGA                    TC ACC ACCTCGGC TCCCAAAGT
                                     || ||| |||||||| |||||||||
                                     AG TGG TGGAGTTG AGGGTTTCA
                                      A  A       G
GAM219  ATP1A2   3'  ACTTTGGGAGGCCGAGGCAGGT 7353         CA      _
              GGA                    TCCACC  CCTCGGC TCCCAAAGT
                                     ||||||  ||||||| |||||||||
                                     AGGTGG  GGAGCCG AGGGTTTCA
                                        AC      G
GAM219  BAX      3'  ACTTTGGGACGCCCACGTGG   57839      CTC  _
                                     CCAC   GGC TCCCAAAGT
                                     ||||   ||| |||||||||
                                     GGTG   CCG AGGGTTTCA
                                       CAC   C
GAM219  BCAS1    3'  ACTTTGGGAGGCCGAGGCAGGT 14705        CA      _
              GGA                    TCCACC  CCTCGGC TCCCAAAGT
                                     ||||||  ||||||| |||||||||
                                     AGGTGG  GGAGCCG AGGGTTTCA
                                        AC      G
GAM219  BHMT2    3'  ACTTTGGGAGGCCGAGGCGGGC 34726     A  A      _
              GGA                    TCC CCC CCTCGGC TCCCAAAGT
                                     ||| ||| ||||||| |||||||||
                                     AGG GGG GGAGCCG AGGGTTTCA
                                       C  C      G
GAM219  BPHL     3'  ACTTTGGGAGGCTGAGGTGGG  16332           _
                                     CCCACCTCGGC TCCCAAAGT
                                     |||||||||| |||||||||
                                     GGGTGGAGTCG AGGGTTTCA
                                           G
GAM219  BRCA1    3'  ACTTTGGGAGGCCAAGGTGGG  24443         C  _
                                     CCCACCT GGC TCCCAAAGT
                                     ||||||| ||| |||||||||
                                     GGGTGGA CCG AGGGTTTCA
                                        A  G
GAM219  BRCA1    3'  ACTTTGGGAGGCCAAGGTGGG  24453         C  _
                                     CCCACCT GGC TCCCAAAGT
                                     ||||||| ||| |||||||||
                                     GGGTGGA CCG AGGGTTTCA
                                        A  G
GAM219  BRCA1    3'  ACTTTGGGAGGCCAAGGTGGG  24466         C  _
                                     CCCACCT GGC TCCCAAAGT
                                     ||||||| ||| |||||||||
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                                GGGTGGA CCG AGGGTTTCA
                                   A   G
GAM219  BRCA1    3' ACTTTGGGAGGCCAAGGTGGG  24475      C  _
                                CCCACCT GGC TCCCAAAGT
                                ||||||| ||| |||||||||
                                GGGTGGA CCG AGGGTTTCA
                                   A   G
GAM219  BRCA1    3' ACTTTGGGAGGCCAAGGTGGG  24483      C  _
                                CCCACCT GGC TCCCAAAGT
                                ||||||| ||| |||||||||
                                GGGTGGA CCG AGGGTTTCA
                                   A   G
GAM219  BRCA1    3' ACTTTGGGAGGCCAAGGTGGG  24491      C  _
                                CCCACCT GGC TCCCAAAGT
                                ||||||| ||| |||||||||
                                GGGTGGA CCG AGGGTTTCA
                                   A   G
GAM219  BRCA1    3' ACTTTGGGAGGCCAAGGTGGG  24500      C  _
                                CCCACCT GGC TCCCAAAGT
                                ||||||| ||| |||||||||
                                GGGTGGA CCG AGGGTTTCA
                                   A   G
GAM219  BRCA1    3' ACTTTGGGAGGCCAAGGTGGG  24510      C  _
                                CCCACCT GGC TCCCAAAGT
                                ||||||| ||| |||||||||
                                GGGTGGA CCG AGGGTTTCA
                                   A   G
GAM219  BRCA1    3' ACTTTGGGAGGCCAAGGTGGG  24518      C  _
                                CCCACCT GGC TCCCAAAGT
                                ||||||| ||| |||||||||
                                GGGTGGA CCG AGGGTTTCA
                                   A   G
GAM219  BRCA1    3' ACTTTGGGAGGCCAAGGTGGG  24526      C  _
                                CCCACCT GGC TCCCAAAGT
                                ||||||| ||| |||||||||
                                GGGTGGA CCG AGGGTTTCA
                                   A   G
GAM219  BRCA1    3' ACTTTGGGAGGCCAAGGTGGG  24538      C  _
                                CCCACCT GGC TCCCAAAGT
                                ||||||| ||| |||||||||
                                GGGTGGA CCG AGGGTTTCA
                                   A   G
GAM219  BRCA2    3' ACTTTGAGAAGCTGAGGTGGGA 5343      A        _ C
              GGA                  TCC CCCACCTCGGCT C CAAAGT
                                ||| |||||||||||| | ||||||
                                AGG GGGTGGAGTCGA G GTTTCA
                                  A          A A
GAM219  C21orf5  3' ACTTTGGGAGGCCAAGGCAGG  18880    CA  C  _
                                CC  CCT GGC TCCCAAAGT
                                ||  ||| ||| |||||||||
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                                GG  GGA CCG AGGGTTTCA
                                 AC   A   G
GAM219  C5R1    3'  ACTTTGGGAGGCTAAGGTGGGT 9970          CG  _
          GGA                    TCCACCCACCT  GC TCCCAAAGT
                                 ||||||||||  || |||||||||
                                 AGGTGGGTGGA  CG AGGGTTTCA
                                       AT  G
GAM219  CARKL   3'  ACTTTGGGAAGCCCAAGTGGGT 26097       CTC   _
          G                     CACCCAC   GGCT CCCAAAGT
                                 |||||||   |||| |||||||||
                                 GTGGGTG   CCGA GGGTTTCA
                                     AAC    A
GAM219  CASP6   3'  ACTTTGGGAGTCCAAGGTGGGC 53359    A     C  _
          GG                     CC CCCACCT GG CTCCCAAAGT
                                 || ||||||| || ||||||||||
                                 GG GGGTGGA CC GAGGGTTTCA
                                  C      A  T
GAM219  CASP6   3'  ACTTTGGGAGTCCAAGGTGGGC 8728     A     C  _
          GG                     CC CCCACCT GG CTCCCAAAGT
                                 || ||||||| || ||||||||||
                                 GG GGGTGGA CC GAGGGTTTCA
                                  C      A  T
GAM219  CASP8   3'  ACTTTGGGAGGTTGAGGTGGGA 8742      A       _
          GGA                    TCC CCCACCTCGGC TCCCAAAGT
                                 ||| |||||||||| |||||||||
                                 AGG GGGTGGAGTTG AGGGTTTCA
                                   A         G
GAM219  CASP8   3'  ACTTTGGGAGGTTGAGGTGGGA 54066     A       _
          GGA                    TCC CCCACCTCGGC TCCCAAAGT
                                 ||| |||||||||| |||||||||
                                 AGG GGGTGGAGTTG AGGGTTTCA
                                   A         G
GAM219  CASP8   3'  ACTTTGGGAGGTTGAGGTGGGA 54092     A       _
          GGA                    TCC CCCACCTCGGC TCCCAAAGT
                                 ||| |||||||||| |||||||||
                                 AGG GGGTGGAGTTG AGGGTTTCA
                                   A         G
GAM219  CASP8   3'  ACTTTGGGAGGTTGAGGTGGGA 54107     A       _
          GGA                    TCC CCCACCTCGGC TCCCAAAGT
                                 ||| |||||||||| |||||||||
                                 AGG GGGTGGAGTTG AGGGTTTCA
                                   A         G
GAM219  CD28    3'  ACTTTGGGAGGCCGAGGTGGGC 21547    CA      _
          AGA                    TC  CCCACCTCGGC TCCCAAAGT
                                 ||  |||||||||| |||||||||
                                 AG  GGGTGGAGCCG AGGGTTTCA
                                  AC         G
GAM219  CD68    3'  ACTTTGGGAGGCTGAGGCAGGT 60498       CA     _
          GGA                    TCCACC  CCTCGGC TCCCAAAGT
                                 ||||||  ||||||| |||||||||
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                                AGGTGG  GGAGTCG AGGGTTTCA
                                   AC      G
GAM219  CDH13    3'  GGTTAAGCAAGGTGGGTGGA  8838          CG   C__
                                TCCACCCACCT  GCT   CC
                                ||||||||||  |||   ||
                                AGGTGGGTGGA  CGA   GG
                                      A_   ATT
GAM219  COPA     3'  ACTTTGGGAGGCTACGGTGGG  16475       TC  _
                                CCCACC  GGC TCCCAAAGT
                                ||||||  ||| |||||||||
                                GGGTGG  TCG AGGGTTTCA
                                   CA   G
GAM219  CORO2A   3'  ACTCTGGGAGGCTGAGGTGGGC 14098     A        _    A
           GGA                    TCC CCCACCTCGGC TCCCA AGT
                                ||| |||||||||| ||||| |||
                                AGG GGGTGGAGTCG AGGGT TCA
                                  C         G    C
GAM219  CORO2A   3'  ACTCTGGGAGGCTGAGGTGGGC 54490     A        _    A
           GGA                    TCC CCCACCTCGGC TCCCA AGT
                                ||| |||||||||| ||||| |||
                                AGG GGGTGGAGTCG AGGGT TCA
                                  C         G    C
GAM219  CPM      3'  ACTTTGGGAGGCCAAGGTGGGC 60401    A      C  _
           GG                     CC CCCACCT GGC TCCCAAAGT
                                || ||||||| ||| |||||||||
                                GG GGGTGGA CCG AGGGTTTCA
                                 C      A  G
GAM219  CRACC    3'  ACTTTGGGAGGCCAAGGTGGGT 41304          C  _
           GGG                    TCCACCCACCT GGC TCCCAAAGT
                                ||||||||||| ||| |||||||||
                                GGGTGGGTGGA CCG AGGGTTTCA
                                      A  G
GAM219  CTMP     3'  ACTTTAGGAGGCCGAGGCAGGC 54943     A  CA      TC  _
           GGA                    TCC CC  CCTCGGC  CC AAAGT
                                ||| ||  |||||||  || |||||
                                AGG GG  GGAGCCG  GG TTTCA
                                  C  AC      GA  A
GAM219  CUBN     3'  ACTTTGGGAGGCCGAGGCAGGT 8415     C   CA      _
           TGA                    TC ACC  CCTCGGC TCCCAAAGT
                                || |||  ||||||| |||||||||
                                AG TGG  GGAGCCG AGGGTTTCA
                                 T   AC      G
GAM219  DBT      3'  ACTTTGGGAGGCCCAGGTGGG  10360        C  _
                                CCCACCT GGC TCCCAAAGT
                                ||||||| ||| |||||||||
                                GGGTGGA CCG AGGGTTTCA
                                   C   G
GAM219  DBT      3'  ACTTTGGGAGGCCGAGGTGG   10361          _
                                CCACCTCGGC TCCCAAAGT
                                |||||||||| |||||||||
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                                GGTGGAGCCG AGGGTTTCA
                                    G
GAM219  DDOST    3'  ACTTTGGGAGGCCGAGGCAGGC 19058    A  CA     _
              GG                  CC CC  CCTCGGC TCCCAAAGT
                                  || ||  ||||||| |||||||||
                                  GG GG  GGAGCCG AGGGTTTCA
                                   C  AC      G
GAM219  DMC1     3'  ACTTTGGGAGGCCGAGGCAGGT 23936       CA     _
              GGA                   TCCACC  CCTCGGC TCCCAAAGT
                                    ||||||  ||||||| |||||||||
                                    AGGTGG  GGAGCCG AGGGTTTCA
                                      AC      G
GAM219  DNASE2   3'  ACTTTGGGAGGCTGAGATGGG  9096      C    _
                                    CCCA CTCGGC TCCCAAAGT
                                    |||| |||||| |||||||||
                                    GGGT GAGTCG AGGGTTTCA
                                      A     G
GAM219  DOC1     3'  ACTTTGGGAAGGTTTGTG    60177     CC   CGGC
                                    CAC  ACCT    TCCCAAAGT
                                    |||  ||||    |||||||||
                                    GTG  TGGA    AGGGTTTCA
                                     TT   ____
GAM219  DVL3     3'  ACTTTGGGAGGCTGAGACAGGT 16634       CAC    _
              GG                    CCACC   CTCGGC TCCCAAAGT
                                    |||||   |||||| |||||||||
                                    GGTGG   GAGTCG AGGGTTTCA
                                       ACA     G
GAM219  EGFL5    3'  ACTTTGGGAGGCCGAGGCGGGT 87902        A    _
              GGA                   TCCACCC CCTCGGC TCCCAAAGT
                                    ||||||| ||||||| |||||||||
                                    AGGTGGG GGAGCCG AGGGTTTCA
                                       C      G
GAM219  EGLN2    3'  ACTTTGAGAGCCCGAGGGGTGG 34516        AC   _  C
              G                     TCCACCC  CTCGG CTC CAAAGT
                                    |||||||  ||||| ||| ||||||
                                    GGGTGGG  GAGCC GAG GTTTCA
                                       __    C  A
GAM219  EHHADH   3'  ACTTTGGGAGGCTGAGGCAGGA 10497     A  CA     _
              GGA                   TCC CC  CCTCGGC TCCCAAAGT
                                    ||| ||  ||||||| |||||||||
                                    AGG GG  GGAGTCG AGGGTTTCA
                                     A  AC      G
GAM219  ERBB3    3'  ACTTTGGGAGGCTGAGGCAGAA 10535     ACCCA    _
              GGA                   TCC    CCTCGGC TCCCAAAGT
                                    |||    ||||||| |||||||||
                                    AGG    GGAGTCG AGGGTTTCA
                                     AAGAC      G
GAM219  F2R      3'  ACTTTGGGAGGCTGAGGCGGGT 10561        A    _
              GGA                   TCCACCC CCTCGGC TCCCAAAGT
                                    ||||||| ||||||| |||||||||
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                                AGGTGGG GGAGTCG AGGGTTTCA
                                   C      G
GAM219  F2RL3    3' ACTTTGGAAGGCCGAGGTGGGC 15486    CA         C_
             AGA                    TC  CCCACCTCGGCT  CCAAAGT
                                ||  ||||||||||||  |||||||
                                AG  GGGTGGAGCCGG  GGTTTCA
                                 AC           AA
GAM219  FGFR2    3' ACTCCGGGAGGCTGAGGCAGG  43647    CA     _   AA
                                CC  CCTCGGC TCCC  AGT
                                ||  |||||||  ||||  |||
                                GG  GGAGTCG AGGG  TCA
                                 AC      G    CC
GAM219  FGFR2    3' ACTTTGGGAGGCCGAGGCAGGC 43648     A  CA     _
             GGA                    TCC CC  CCTCGGC TCCCAAAGT
                                |||  ||  |||||||  |||||||||
                                AGG GG  GGAGCCG AGGGTTTCA
                                  C  AC      G
GAM219  FGFR2    3' ACTCCGGGAGGCTGAGGCAGG  43660    CA     _   AA
                                CC  CCTCGGC TCCC  AGT
                                ||  |||||||  ||||  |||
                                GG  GGAGTCG AGGG  TCA
                                 AC      G    CC
GAM219  FGFR2    3' ACTTTGGGAGGCCGAGGCAGGC 43661     A  CA     _
             GGA                    TCC CC  CCTCGGC TCCCAAAGT
                                |||  ||  |||||||  |||||||||
                                AGG GG  GGAGCCG AGGGTTTCA
                                  C  AC      G
GAM219  FKRP     3' ACTTTGGGAGGCCGAGGTGGGA 44433     A        _
             GGA                    TCC CCCACCTCGGC TCCCAAAGT
                                |||  ||||||||||  |||||||||
                                AGG GGGTGGAGCCG AGGGTTTCA
                                  A          G
GAM219  FOXD2    5' TGGGAGCCAGGAAGGTGGG   16795       CA   C
                                TCCACC  CCT GGCTCCCA
                                ||||||  |||  ||||||||
                                GGGTGG  GGA CCGAGGGT
                                   AA  _
GAM219  FUT3     3' ACTTTGGGAGGCTGAGGTAGGA 5618      A  C      _
             GGA                    TCC CC ACCTCGGC TCCCAAAGT
                                |||  ||  ||||||||  |||||||||
                                AGG GG TGGAGTCG AGGGTTTCA
                                  A  A       G
GAM219  FUT6     3' ACTTTGGGAGGCCGAGGCAGGC 5627      A  CA     _
             GGA                    TCC CC  CCTCGGC TCCCAAAGT
                                |||  ||  |||||||  |||||||||
                                AGG GG  GGAGCCG AGGGTTTCA
                                  C  AC      G
GAM219  GAS7     3' GGGAGGCCGAGGTGGGCAGA   20856    CA        _
                                TC  CCCACCTCGGC TCCC
                                ||  ||||||||||| ||||
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                                AG  GGGTGGAGCCG AGGG
                                 AC         G
GAM219  GNE     3'  ACTTTGGGAGGCCGAGGCGGGC 19660     A  A     _
             GGA                  TCC CCC CCTCGGC TCCCAAAGT
                                  ||| ||| ||||||| |||||||||
                                  AGG GGG GGAGCCG AGGGTTTCA
                                    C  C      G
GAM219  GPR81   3'  ACTTTGGGAGACTGAGGCGG   51733    A    _
                                  CC CCTCGG CTCCCAAAGT
                                  || |||||| ||||||||||
                                  GG GGAGTC GAGGGTTTCA
                                   C     A
GAM219  GPRK7   3'  ACTTTGGGAGGCCAAGGCAGAT 58308     CCCA   C  _
             GG                   CCA    CCT GGC TCCCAAAGT
                                  |||    ||| ||| |||||||||
                                  GGT    GGA CCG AGGGTTTCA
                                    AGAC   A   G
GAM219  GRAF    3'  ACTCTGGAGGCTGAGGCAGG   31219    CA      TC   A
                                  CC  CCTCGGC  CCA AGT
                                  ||  |||||||  ||| |||
                                  GG  GGAGTCG  GGT TCA
                                   AC      GA   C
GAM219  GRAF    3'  ACTTTGGGAGGCCGAGGCGGGC 31220     A  A     _
             GGA                  TCC CCC CCTCGGC TCCCAAAGT
                                  ||| ||| ||||||| |||||||||
                                  AGG GGG GGAGCCG AGGGTTTCA
                                    C  C      G
GAM219  GRM6    3'  ACTTTGGGAGGCCGAGGCAGGT 7756        CA     _
             GGA                  TCCACC  CCTCGGC TCCCAAAGT
                                  ||||||  ||||||| |||||||||
                                  AGGTGG  GGAGCCG AGGGTTTCA
                                     AC      G
GAM219  HCS     3'  ACTTTGGGAGGCCAAGGCAGG  38961    CA  C  _
                                  CC  CCT GGC TCCCAAAGT
                                  ||  ||| ||| |||||||||
                                  GG  GGA CCG AGGGTTTCA
                                   AC  A  G
GAM219  HIP1    3'  ACTTTGGGAGGCAGGGGCGGGT 19246       A   G  _
             GG                   CCACCC CCTC GC TCCCAAAGT
                                  |||||| |||| || |||||||||
                                  GGTGGG GGGG CG AGGGTTTCA
                                     C   A  G
GAM219  HSPA5   3'  ACTTTGGGAGGCCAAGGCGGGT 19276       A  C  _
             GG                   CCACCC CCT GGC TCCCAAAGT
                                  |||||| ||| ||| |||||||||
                                  GGTGGG GGA CCG AGGGTTTCA
                                     C  A  G
GAM219  HUNK    3'  ACTTCGGGGACTGAGGTGGGAG 28171     A       CT   A
             GA                   TCC CCCACCTCGG  CCC AAGT
                                  ||| ||||||||||  ||| ||||
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                                AGG GGGTGGAGTC  GGG TTCA
                                  A         AG   C
GAM219  HUNK     3'  ACTTTGGGAGGCCGAGGCAGGT 28172        CA      _
              GGA                   TCCACC  CCTCGGC TCCCAAAGT
                                    ||||||  ||||||| |||||||||
                                    AGGTGG  GGAGCCG AGGGTTTCA
                                       AC       G
GAM219  IAPP     3'  ACTTTGGGAGGCCGAGGCAGGC 6434     CA  CA      _
              AGA                   TC  CC  CCTCGGC TCCCAAAGT
                                    ||  ||  ||||||| |||||||||
                                    AG  GG  GGAGCCG AGGGTTTCA
                                     AC  AC      G
GAM219  IFIT4    3'  ACTTTGGGAGGCCGAGGTGGGC 71487     A         _
              GGA                   TCC CCCACCTCGGC TCCCAAAGT
                                    |||  |||||||||| |||||||||
                                    AGG GGGTGGAGCCG AGGGTTTCA
                                      C         G
GAM219  IFNAR1   3'  ACTTTGGGAGGCTGAGGCAGGC 7133     CA  CA      _
              AGA                   TC  CC  CCTCGGC TCCCAAAGT
                                    ||  ||  ||||||| |||||||||
                                    AG  GG  GGAGTCG AGGGTTTCA
                                     AC  AC      G
GAM219  IL10     3'  ACTTTGGGAGGCTGAGGCGGGT 6920         A      _
              GGA                   TCCACCC CCTCGGC TCCCAAAGT
                                    |||||||  ||||||| |||||||||
                                    AGGTGGG GGAGTCG AGGGTTTCA
                                       C       G
GAM219  IL11     3'  ACTTTGGGAGGACGAAGCGAGT 7173       CCACC   G_
              GG                    CCAC    TCG  CTCCCAAAGT
                                    ||||    |||  ||||||||||
                                    GGTG    AGC  GAGGGTTTCA
                                      AGCGA   AG
GAM219  IL13RA1  3'  GGGAAGCTGAGGCAGGTG    9573       CA      _
                                    CACC  CCTCGGCT CCC
                                    ||||  |||||||| |||
                                    GTGG  GGAGTCGA GGG
                                      AC       A
GAM219  IL17R    3'  GGGAGGCCGAGGCAGGTGGA   27557        CA      _
                                    TCCACC  CCTCGGC TCCC
                                    ||||||  ||||||| ||||
                                    AGGTGG  GGAGCCG AGGG
                                       AC       G
GAM219  IL1R1    3'  ACTTTGGGAGGCTGAAGTGGGT 7919          C    _
              GGA                   TCCACCCAC TCGGC TCCCAAAGT
                                    |||||||||  ||||| |||||||||
                                    AGGTGGGTG AGTCG AGGGTTTCA
                                         A    G
GAM219  IL6R     3'  ACTTCGGGAGGTCGAGGCAGGA 6907      A  CA     _   A
              GGA                   TCC CC  CCTCGGC TCCC AAGT
                                    |||  ||  ||||||| |||| ||||
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                                AGG GG  GGAGCTG AGGG TTCA
                                  A  AC      G    C
GAM219  IPP      3'  ACTTTGGAAGGCTGAGGCAGGG 20901     A   A_       C_
              GGA                   TCC CCC  CCTCGGCT  CCAAAGT
                                ||| |||  ||||||||  |||||||
                                AGG GGG  GGAGTCGG  GGTTTCA
                                  _  AC       AA
GAM219  IRAK4    3'  ACTTTGGGAGGCCGAGGCAGGC 61838    CA  CA      _
              AGA                   TC  CC  CCTCGGC TCCCAAAGT
                                ||  ||  |||||||  |||||||||
                                AG  GG  GGAGCCG AGGGTTTCA
                                 AC  AC      G
GAM219  ITCH     3'  ACTCTGGGAGGCCGAGGCAGGA 49753     A  CA      _    A
              GGA                   TCC CC  CCTCGGC TCCCA AGT
                                ||| ||  |||||||  |||||  |||
                                AGG GG  GGAGCCG AGGGT TCA
                                  A  AC      G    C
GAM219  KAI1     3'  ACTTTGGGAGGCCGAGGCGGGT 11117        A      _
              GGA                   TCCACCC CCTCGGC TCCCAAAGT
                                |||||||  |||||||  |||||||||
                                AGGTGGG GGAGCCG AGGGTTTCA
                                    C      G
GAM219  KCNA7    3'  ACTTTGGGAGGCCGAGGTGGG  49884           _
                                CCCACCTCGGC TCCCAAAGT
                                ||||||||||  |||||||||
                                GGGTGGAGCCG AGGGTTTCA
                                      G
GAM219  KCNJ5    3'  GGGAGGCCGAGGCGGGTGGA   7975         A      _
                                TCCACCC CCTCGGC TCCC
                                |||||||  |||||||  ||||
                                AGGTGGG GGAGCCG AGGG
                                    C      G
GAM219  KCNK6    3'  ACTTCAGAGGCTGAGGTGGAAG 17882     AC         CCCA
              GA                    TCC  CCACCTCGGCT    AAGT
                                |||  ||||||||||    ||||
                                AGG  GGTGGAGTCGG    TTCA
                                  AA          AGAC
GAM219  KIF1B    3'  ACTTGGGGAGGCCGAGGCGGGC 31261    CA  A      _   A
              AGA                   TC  CCC CCTCGGC TCCC AAGT
                                ||  |||  |||||||  ||||  ||||
                                AG  GGG GGAGCCG AGGG TTCA
                                 AC  C      G    G
GAM219  KIF3B    3'  ACTTTGGGAGGCCGAGGTGGGT 17799             _
              GGA                   TCCACCCACCTCGGC TCCCAAAGT
                                ||||||||||||||  |||||||||
                                AGGTGGGTGGAGCCG AGGGTTTCA
                                       G
GAM219  KLF8     5'  ACTTTGGGAGGCTGAGGCAGGA 24369     A  CA      _
              GGA                   TCC CC  CCTCGGC TCCCAAAGT
                                |||  ||  |||||||  |||||||||
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                                AGG GG  GGAGTCG AGGGTTTCA
                                  A AC      G
GAM219  KNSL1    3'  ACTTTGGGAGGCTGAGGCGGGT 16938        A     _
            GGA                    TCCACCC CCTCGGC TCCCAAAGT
                                   ||||||| ||||||| |||||||||
                                   AGGTGGG GGAGTCG AGGGTTTCA
                                      C      G
GAM219  LAMC2    3'  ACTTTGGGAGACTGAAGCGGGT 38765       ACC   _
            GG                     CCACCC   TCGG CTCCCAAAGT
                                   ||||||   |||| ||||||||||
                                   GGTGGG   AGTC GAGGGTTTCA
                                      CGA    A
GAM219  LAMP2    3'  ACTTTGGGAGGCCGAAGTGGGT 26567         C    _
            GGA                    TCCACCCAC TCGGC TCCCAAAGT
                                   ||||||||| ||||| |||||||||
                                   AGGTGGGTG AGCCG AGGGTTTCA
                                       A    G
GAM219  LDLR     3'  ACTTTGGGAGGCCGAGGCGGGT 6721         A     _
            GGA                    TCCACCC CCTCGGC TCCCAAAGT
                                   ||||||| ||||||| |||||||||
                                   AGGTGGG GGAGCCG AGGGTTTCA
                                      C      G
GAM219  LDLR     3'  ACTTTGGGAGGCTGAGCTGG   6722      C    _
                                   CCA CTCGGC TCCCAAAGT
                                   ||| |||||| |||||||||
                                   GGT GAGTCG AGGGTTTCA
                                     C     G
GAM219  LILRB1   3'  ACTTTGGGAGGCCGAGGCGGGC 22868    CA  A     _
            AGA                    TC  CCC CCTCGGC TCCCAAAGT
                                   ||  ||| ||||||| |||||||||
                                   AG  GGG GGAGCCG AGGGTTTCA
                                    AC  C      G
GAM219  LRRC2    3'  ACTTTGGGAGGCCGAAGTGGGT 44733         C    _
            GGA                    TCCACCCAC TCGGC TCCCAAAGT
                                   ||||||||| ||||| |||||||||
                                   AGGTGGGTG AGCCG AGGGTTTCA
                                       A    G
GAM219  LRRC2    3'  ACTTTGGGAGGCCGAGATGGGT 44734       C     _
            G                       CACCCA CTCGGC TCCCAAAGT
                                    |||||| |||||| |||||||||
                                    GTGGGT GAGCCG AGGGTTTCA
                                       A     G
GAM219  LUZP1    3'  ACTTTGGGAGGCCAAGGCAGGC 54395    A  CA   C  _
            GG                      CC CC  CCT GGC TCCCAAAGT
                                    || ||  ||| ||| |||||||||
                                    GG GG  GGA CCG AGGGTTTCA
                                     C AC   A   G
GAM219  MCM4     3'  ACTTTGGGAGGCCAATGTGGGT 62574          CTC   _
            GGA                    TCCACCCAC   GGC TCCCAAAGT
                                   |||||||||   ||| |||||||||
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                                AGGTGGGTG  CCG AGGGTTTCA
                                     TAA  G
GAM219  MOG     3'  ACTTTGGGAGGCCGAGGCGGG  11665    A    _
                                CCC CCTCGGC TCCCAAAGT
                                ||| ||||||| |||||||||
                                GGG GGAGCCG AGGGTTTCA
                                  C      G
GAM219  MS4A1   3'  GGGAGGCCGAGGTGGGCAGA  5550    CA       _
                                TC  CCCACCTCGGC TCCC
                                ||  |||||||||||| ||||
                                AG  GGGTGGAGCCG AGGG
                                 AC         G
GAM219  MSH3    3'  ACTTTGGGAGGCCAAGGTAGG  11686   C   C  _
                                CC ACCT GGC TCCCAAAGT
                                || |||| ||| |||||||||
                                GG TGGA CCG AGGGTTTCA
                                 A   A  G
GAM219  MTMR8   3'  ACTTTGGGAGGCCAAGGCGGGC 31901   A  A  C  _
           GG                     CC CCC CCT GGC TCCCAAAGT
                                || ||| ||| ||| |||||||||
                                GG GGG GGA CCG AGGGTTTCA
                                 C  C  A  G
GAM219  MTNR1A  3'  ACTTTGGGAGGCTGAGGTGGGC 21053   CA       _
           AGA                    TC  CCCACCTCGGC TCCCAAAGT
                                ||  |||||||||||| |||||||||
                                AG  GGGTGGAGTCG AGGGTTTCA
                                 AC         G
GAM219  MYO1C   3'  ACTTTGGGAGGCGGAGACGGG  61851    AC  G  _
                                CCC  CTC GC TCCCAAAGT
                                |||  ||| || |||||||||
                                GGG  GAG CG AGGGTTTCA
                                  CA  G  G
GAM219  NFKBIL2 3'  ACTTTGGGAGGCCCAGGCGGGC 26441   A  A  C  _
           GG                     CC CCC CCT GGC TCCCAAAGT
                                || ||| ||| ||| |||||||||
                                GG GGG GGA CCG AGGGTTTCA
                                 C  C  C  G
GAM219  NPHP1   3'  ACTTTGGGAGGCCGAGGTGGGT 63138          _
           GGA                    TCCACCCACCTCGGC TCCCAAAGT
                                |||||||||||||| |||||||||
                                AGGTGGGTGGAGCCG AGGGTTTCA
                                       G
GAM219  NPHS1   3'  ACTTTGGGAGGCTGAGGCGGGT 17364       A    _
           GGA                    TCCACCC CCTCGGC TCCCAAAGT
                                ||||||| ||||||| |||||||||
                                AGGTGGG GGAGTCG AGGGTTTCA
                                   C      G
GAM219  NT5C2   3'  ACTTTGGGAGGCCGAGACAGGC 25252   A  CAC    _
           GG                     CC CC   CTCGGC TCCCAAAGT
                                || ||   |||||| |||||||||
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                                GG GG   GAGCCG AGGGTTTCA
                                 C  ACA     G
GAM219  NUP62    3'  ACTTTGGGTGGCCAAGGCGGG  33778     A  C   _
                                CCC CCT GGCT CCCAAAGT
                                ||| ||| |||| ||||||||
                                GGG GGA CCGG GGGTTTCA
                                  C   A    T
GAM219  OASL     3'  ACTTTGGGAGGCCGAGGTGGGA 14954     A         _
           GGA                    TCC CCCACCTCGGC TCCCAAAGT
                                ||| |||||||||||| |||||||||
                                AGG GGGTGGAGCCG AGGGTTTCA
                                  A          G
GAM219  OPA3     3'  ACCTTGGGAGGCCGAGGCGGGC 47838     A  A     _     A
           GGA                    TCC CCC CCTCGGC TCCCAA GT
                                ||| ||| ||||||| |||||| ||
                                AGG GGG GGAGCCG AGGGTT CA
                                  C  C      G     C
GAM219  OPTN     3'  ACTTTGGGAGGTCGAGGTGGGT 42046             _
           GGA                    TCCACCCACCTCGGC TCCCAAAGT
                                |||||||||||||| |||||||||
                                AGGTGGGTGGAGCTG AGGGTTTCA
                                       G
GAM219  P2RX7    3'  GGGAGGCCGAGGCAGGCAGA   11927    CA  CA     _
                                TC  CC  CCTCGGC TCCC
                                ||  ||  ||||||| ||||
                                AG  GG  GGAGCCG AGGG
                                 AC  AC      G
GAM219  PA2G4    3'  ACTTTGGGAGGCTGAGGCGGGT 71821         A     _
           GGA                    TCCACCC CCTCGGC TCCCAAAGT
                                ||||||| ||||||| |||||||||
                                AGGTGGG GGAGTCG AGGGTTTCA
                                    C      G
GAM219  PCDH11X  3'  ACTTTGGGAGGCCGAGGCGGGT 53122         A     _
           GGA                    TCCACCC CCTCGGC TCCCAAAGT
                                ||||||| ||||||| |||||||||
                                AGGTGGG GGAGCCG AGGGTTTCA
                                    C      G
GAM219  PCDH11X  3'  ACTTTGGGAGGCCGAGGTGGGT 53123             _
           GGA                    TCCACCCACCTCGGC TCCCAAAGT
                                |||||||||||||| |||||||||
                                AGGTGGGTGGAGCCG AGGGTTTCA
                                       G
GAM219  PCDH11Y  3'  ACTTTGGGAGGCCGAGGCGGGT 53150         A     _
           GGA                    TCCACCC CCTCGGC TCCCAAAGT
                                ||||||| ||||||| |||||||||
                                AGGTGGG GGAGCCG AGGGTTTCA
                                    C      G
GAM219  PCDH11Y  3'  ACTTTGGGAGGCCGAGGCGGGT 53151         A     _
           GGA                    TCCACCC CCTCGGC TCCCAAAGT
                                ||||||| ||||||| |||||||||
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                                AGGTGGG GGAGCCG AGGGTTTCA
                                   C      G
GAM219  PCDH11Y  3' ACTTTGGGAGGCCGAGGCGGGT 53173        A     _
           GGA                   TCCACCC CCTCGGC TCCCAAAGT
                                 ||||||| ||||||| |||||||||
                                 AGGTGGG GGAGCCG AGGGTTTCA
                                    C      G
GAM219  PCDH11Y  3' ACTTTGGGAGGCCGAGGCGGGT 53174        A     _
           GGA                   TCCACCC CCTCGGC TCCCAAAGT
                                 ||||||| ||||||| |||||||||
                                 AGGTGGG GGAGCCG AGGGTTTCA
                                    C      G
GAM219  PCDHB9   3' ACTTTGGGAGGCCAAGGCGGG  39434     A  C  _
                                 CCC CCT GGC TCCCAAAGT
                                 ||| ||| ||| |||||||||
                                 GGG GGA CCG AGGGTTTCA
                                   C  A   G
GAM219  PDE4C    3' ACTTTGGGAGGCTGAGGCAGGT 8093        CA     _
           GGA                   TCCACC  CCTCGGC TCCCAAAGT
                                 ||||||  ||||||| |||||||||
                                 AGGTGG  GGAGTCG AGGGTTTCA
                                    AC      G
GAM219  PDE4C    3' ACTTTGGGAGGCTGAGGTGGGA 8094      A        _
           GGA                   TCC CCCACCTCGGC TCCCAAAGT
                                 ||| |||||||||| |||||||||
                                 AGG GGGTGGAGTCG AGGGTTTCA
                                   A         G
GAM219  PHKB     3' ACTTCGGGAGGCTGAGGCAGGT 6094        CA     _  A
           GGA                   TCCACC  CCTCGGC TCCC AAGT
                                 ||||||  ||||||| |||| ||||
                                 AGGTGG  GGAGTCG AGGG TTCA
                                    AC      G   C
GAM219  PIK3R2   3' ACTTTGGGAGGCCAAGACGGGC 18508    A  AC  C  _
           GG                     CC CCC  CT GGC TCCCAAAGT
                                  || |||  || ||| |||||||||
                                  GG GGG  GA CCG AGGGTTTCA
                                   C  CA A   G
GAM219  PKD2     3' ACTTTGGGAGGCCGAAACAGG  60714    CACC    _
                                 CC    TCGGC TCCCAAAGT
                                 ||    ||||| |||||||||
                                 GG    AGCCG AGGGTTTCA
                                  ACAA    G
GAM219  POLH     3' ACTTTGGGAGGCCAAGGCGGG  22468     A  C  _
                                 CCC CCT GGC TCCCAAAGT
                                 ||| ||| ||| |||||||||
                                 GGG GGA CCG AGGGTTTCA
                                   C  A   G
GAM219  PPP1R12B 3' ACTTCAGGAGGCCGAGGTGG  50375          _  CA
                                 CCACCTCGGC TCC  AAGT
                                 |||||||||| |||  ||||
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                                GGTGGAGCCG AGG  TTCA
                                     G   AC
GAM219  PRKY    3' ACTCTGGGAACCTGGGTTGGGA 12357     A   _  C C    A
           GGA                   TCC CCCA CCT GG TCCCA AGT
                                 ||| |||| ||| || ||||| |||
                                 AGG GGGT GGG CC AGGGT TCA
                                   A   T   T A    C
GAM219  PRKY    3' ACTTTGGGAGGCCAAGGCAGG  12358    CA  C  _
                                 CC  CCT GGC TCCCAAAGT
                                 ||  ||| ||| |||||||||
                                 GG  GGA CCG AGGGTTTCA
                                  AC  A  G
GAM219  PRKY    3' ACTTTGGGAGGCTGGGGCGAGA 12359     ACCCA     _
           GGA                   TCC    CCTCGGC TCCCAAAGT
                                 |||    ||||||| |||||||||
                                 AGG    GGGGTCG AGGGTTTCA
                                   AGAGC      G
GAM219  PSD     5' ACTTTGGGAGGCCAGGCGGGCG 12429     A  A  C  _
           GA                    TCC CCC CCT GGC TCCCAAAGT
                                 ||| ||| ||| ||| |||||||||
                                 AGG GGG GGA CCG AGGGTTTCA
                                   C  C  _  G
GAM219  PSMB2   3' ACTTTGGGAGGCCGAGGCGGGC 12457     A  A     _
           GGA                   TCC CCC CCTCGGC TCCCAAAGT
                                 ||| ||| ||||||| |||||||||
                                 AGG GGG GGAGCCG AGGGTTTCA
                                   C  C      G
GAM219  PSMB9   3' ACTTTGGGAGGCCAAGGCAGGC 12483    A CA  C  _
           GG                    CC CC  CCT GGC TCCCAAAGT
                                 || ||  ||| ||| |||||||||
                                 GG GG  GGA CCG AGGGTTTCA
                                  C AC  A  G
GAM219  PSMD5   3' ACTTTGGGAGGCCAAGATGGG  18553      C C  _
                                 CCCA CT GGC TCCCAAAGT
                                 |||| || ||| |||||||||
                                 GGGT GA CCG AGGGTTTCA
                                   A A  G
GAM219  PTAFR   3' ACTTTGGGAGGCCGAGGTGGGC 8161     CA        _
           AGA                   TC  CCCACCTCGGC TCCCAAAGT
                                 ||  |||||||||| |||||||||
                                 AG  GGGTGGAGCCG AGGGTTTCA
                                  AC         G
GAM219  PTGIS   3' ACTTTGGGAGGCCGAGGTGGGC 8186      A        _
           GGA                   TCC CCCACCTCGGC TCCCAAAGT
                                 ||| |||||||||| |||||||||
                                 AGG GGGTGGAGCCG AGGGTTTCA
                                   C         G
GAM219  RAB3B   3' ACTTTGGGAGGCCGAGGCGGGT 12699        A     _
           GGA                   TCCACCC CCTCGGC TCCCAAAGT
                                 ||||||| ||||||| |||||||||
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                                AGGTGGG GGAGCCG AGGGTTTCA
                                   C      G
GAM219  RAB7L1   3' ACTCTGGAGACTGAGGTGGG  15397          _   CAA
                                CCCACCTCGG CTCC   AGT
                                |||||||||| ||||   |||
                                GGGTGGAGTC GAGG   TCA
                                     A   TC_
GAM219  RAB7L1   3' ACTTTGGGAGGCTGAGGCAGGT 15398       CA     _
           GGA                    TCCACC  CCTCGGC TCCCAAAGT
                                  ||||||  ||||||| |||||||||
                                  AGGTGG  GGAGTCG AGGGTTTCA
                                     AC      G
GAM219  RAD1     3' ACTTTGGGAACCCGAGGTGGGC 12637     A       C_
           GGA                    TCC CCCACCTCGG  TCCCAAAGT
                                  ||| ||||||||||  |||||||||
                                  AGG GGGTGGAGCC  AGGGTTTCA
                                    C         CA
GAM219  RAD1     3' ACTTTGGGAACCCGAGGTGGGC 56651     A       C_
           GGA                    TCC CCCACCTCGG  TCCCAAAGT
                                  ||| ||||||||||  |||||||||
                                  AGG GGGTGGAGCC  AGGGTTTCA
                                    C         CA
GAM219  RAD1     3' ACTTTGGGAACCCGAGGTGGGC 56747     A       C_
           GGA                    TCC CCCACCTCGG  TCCCAAAGT
                                  ||| ||||||||||  |||||||||
                                  AGG GGGTGGAGCC  AGGGTTTCA
                                    C         CA
GAM219  RBBP5    3' ACTTTGGGAGGCCAAGGCGGGT 18573       A  C  _
           GG                     CCACCC CCT GGC TCCCAAAGT
                                  |||||| ||| ||| |||||||||
                                  GGTGGG GGA CCG AGGGTTTCA
                                     C  A  G
GAM219  RBL1     3' ACTTTGGGAGGCCAAGGCGGG  12780     A  C  _
                                CCC CCT GGC TCCCAAAGT
                                ||| ||| ||| |||||||||
                                GGG GGA CCG AGGGTTTCA
                                  C  A  G
GAM219  RFC2     3' ACTTTGGGAGGCCGAGGCAGGT 12834       CA     _
           GGA                    TCCACC  CCTCGGC TCCCAAAGT
                                  ||||||  ||||||| |||||||||
                                  AGGTGG  GGAGCCG AGGGTTTCA
                                     AC      G
GAM219  ROCK2    3' ACTTTGGGAGGCCAAGACGGGC 66611    A  AC  C  _
           GG                     CC CCC  CT GGC TCCCAAAGT
                                  || |||  || ||| |||||||||
                                  GG GGG  GA CCG AGGGTTTCA
                                   C  CA A  G
GAM219  ROCK2    3' GGGAGGCCAAGACGGGCGGA  66621     A  AC  C  _
                                TCC CCC  CT GGC TCCC
                                ||| |||  || ||| ||||
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                                AGG GGG  GA CCG AGGG
                                  C   CA A   G
GAM219  SFRS2IP  5' GGGAGGCCGAGGCAGGCAGA  17543    CA  CA      _
                                TC  CC  CCTCGGC TCCC
                                ||  ||  ||||||| ||||
                                AG  GG  GGAGCCG AGGG
                                 AC  AC      G
GAM219  SIGLEC11 3' ACTTTGGGAGGCTGAAGTGGGT 54645          C    _
           GGA                    TCCACCCAC TCGGC TCCCAAAGT
                                |||||||||| ||||| |||||||||
                                AGGTGGGTG AGTCG AGGGTTTCA
                                     A    G
GAM219  SIM2     3' ACTTTGGGAGGCCAAGGTGGGC 24795    A      C  _
           GG                     CC CCCACCT GGC TCCCAAAGT
                                || ||||||| ||| |||||||||
                                GG GGGTGGA CCG AGGGTTTCA
                                 C      A  G
GAM219  SLC14A2  3' ACTTTGGGAGGCCGAGGCGGGT 24106        A     _
           GGA                    TCCACCC CCTCGGC TCCCAAAGT
                                ||||||| ||||||| |||||||||
                                AGGTGGG GGAGCCG AGGGTTTCA
                                    C      G
GAM219  SLC17A5  3' ACTTTGGGGGGCTGAGGTGGG  25823             _
                                CCCACCTCGGCTCCC AAAGT
                                |||||||||||||| |||||
                                GGGTGGAGTCGGGGG TTTCA
                                       G
GAM219  SLC26A4  3' ACTTTGGGAGGCCGAGGCGGGT 6519         A     _
           GGA                    TCCACCC CCTCGGC TCCCAAAGT
                                ||||||| ||||||| |||||||||
                                AGGTGGG GGAGCCG AGGGTTTCA
                                    C      G
GAM219  SLC28A2  3' GGGAGGCCGAGGCGGGCGGA  16152    A  A     _
                                TCC CCC CCTCGGC TCCC
                                ||| ||| ||||||| ||||
                                AGG GGG GGAGCCG AGGG
                                  C  C      G
GAM219  SLC2A3   3' ACTTTGGGAGGCCTAGGCGGGC 23637    A  A  C  _
           GG                     CC CCC CCT GGC TCCCAAAGT
                                || ||| ||| ||| |||||||||
                                GG GGG GGA CCG AGGGTTTCA
                                 C  C  T  G
GAM219  SMG1     3' ACTTTGGGAGGCCGAGGCGGGC 31339    A  A     _
           GGA                    TCC CCC CCTCGGC TCCCAAAGT
                                ||| ||| ||||||| |||||||||
                                AGG GGG GGAGCCG AGGGTTTCA
                                  C  C      G
GAM219  STAT3    3' ACTTTGGGAGGCCGAGGCGG  58376    A     _
                                CC CCTCGGC TCCCAAAGT
                                || ||||||| |||||||||
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                                GG GGAGCCG AGGGTTTCA
                                 C      G
GAM219  STAT3    3' ACTTTGGGAGGCCGAGGCGG  13430    A     _
                                CC CCTCGGC TCCCAAAGT
                                || ||||||| |||||||||
                                GG GGAGCCG AGGGTTTCA
                                 C      G
GAM219  SUDD     3' ACTTTGGGAGACCAAGGCGGGT 15150       A  C  _
           GG                    CCACCC CCT GG CTCCCAAAGT
                                ||||||| ||| || ||||||||||
                                GGTGGG GGA CC GAGGGTTTCA
                                   C  A  A
GAM219  SUV39H2  3' ACTTTGGGAGGCTGAGGTAGGA 45449     A  C      _
           GGA                   TCC CC ACCTCGGC TCCCAAAGT
                                ||| || |||||||| |||||||||
                                AGG GG TGGAGTCG AGGGTTTCA
                                 A  A       G
GAM219  SWAP70   3' ACTTTGGGAGGCCGAGGCGGGT 71857        A     _
           GGA                   TCCACCC CCTCGGC TCCCAAAGT
                                ||||||| ||||||| |||||||||
                                AGGTGGG GGAGCCG AGGGTTTCA
                                   C      G
GAM219  TBX6     3' ACTCTGGGAGGCTGAGGCGGGC 55806    CA  A     _    A
           AGA                   TC  CCC CCTCGGC TCCCA AGT
                                ||  ||| ||||||| ||||| |||
                                AG  GGG GGAGTCG AGGGT TCA
                                 AC  C      G    C
GAM219  TCF7     3' ACTTTGGCAGGCCGAGGCAGGT 13612       CA      C_
           GGA                   TCCACC  CCTCGGCT  CCAAAGT
                                ||||||  ||||||||  |||||||
                                AGGTGG  GGAGCCGG  GGTTTCA
                                   AC       AC
GAM219  TCTA     3' ACTTTGGGAGGCTGAGGCAGGC 42487    CA  CA     _
           AGA                   TC  CC  CCTCGGC TCCCAAAGT
                                ||  ||  ||||||| |||||||||
                                AG  GG  GGAGTCG AGGGTTTCA
                                 AC  AC      G
GAM219  TEM7     3' ACTTTGGGAGGCTGAGGCAGGC 40240     A  CA     _
           GGA                   TCC CC  CCTCGGC TCCCAAAGT
                                ||| ||  ||||||| |||||||||
                                AGG GG  GGAGTCG AGGGTTTCA
                                  C  AC      G
GAM219  TEP1     3' ACTTTGGGAGGCCGAGGTGGGC 24043    CA        _
           AGA                   TC  CCCACCTCGGC TCCCAAAGT
                                ||  |||||||||||| |||||||||
                                AG  GGGTGGAGCCG AGGGTTTCA
                                 AC         G
GAM219  TNFAIP6  3' ACTTTGGAAGGCCGAGGCAGAG 60164     ACCCA      C_
           GA                    TCC    CCTCGGCT  CCAAAGT
                                |||    ||||||||  |||||||
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                                AGG    GGAGCCGG  GGTTTCA
                                  AGAC_       AA
GAM219  TNFRSF10A 3'  ACTTTGGGAGGCTGAGGCGGGT 15236        A     _
           GGA                    TCCACCC CCTCGGC TCCCAAAGT
                                  ||||||| ||||||| |||||||||
                                  AGGTGGG GGAGTCG AGGGTTTCA
                                     C      G
GAM219  TNFRSF10D 3'  ACTTTGATAGGCTGAGGCAGGT 15200       CA      CC_
           GGA                    TCCACC  CCTCGGCT   CAAAGT
                                  ||||||  ||||||||   ||||||
                                  AGGTGG  GGAGTCGG   GTTTCA
                                     AC       ATA
GAM219  TNFRSF1B  3'  ACTTTGGGAGGCTGAGGCGGGT 8381         A     _
           GGA                    TCCACCC CCTCGGC TCCCAAAGT
                                  ||||||| ||||||| |||||||||
                                  AGGTGGG GGAGTCG AGGGTTTCA
                                     C      G
GAM219  TNFSF10   3'  ATTTTGGGAACCCAAGGTGGGT 15087    C      C  C_
           AGA                    TC ACCCACCT GG  TCCCAAAGT
                                  || |||||||| ||  |||||||||
                                  AG TGGGTGGA CC  AGGGTTTTA
                                   A       A  CA
GAM219  TNFSF14   3'  ACTTTGGGAGGCCAAGGCAGGC 15074    A  CA   C  _
           GG                     CC CC  CCT GGC TCCCAAAGT
                                  || ||  ||| ||| |||||||||
                                  GG GG  GGA CCG AGGGTTTCA
                                   C  AC   A   G
GAM219  TNFSF15   3'  ACTTTGGGAGGCCAAGGTGGGT 18861          C  _
           GGA                    TCCACCCACCT GGC TCCCAAAGT
                                  |||||||||||| ||| |||||||||
                                  AGGTGGGTGGA CCG AGGGTTTCA
                                        A   G
GAM219  TRIM9    5'  ACTTTGGGAGGCTAAGGCAGGC 31437    A  CA   CG  _
           GG                     CC CC  CCT  GC TCCCAAAGT
                                  || ||  |||  || |||||||||
                                  GG GG  GGA  CG AGGGTTTCA
                                   C  AC   AT  G
GAM219  TSNAX    3'  ACTTTGGGAGGCCGAGGTAGGC 21149    CA  C      _
           AGA                    TC  CC ACCTCGGC TCCCAAAGT
                                  ||  || |||||||| |||||||||
                                  AG  GG TGGAGCCG AGGGTTTCA
                                   AC  A       G
GAM219  UBE2G2   3'  ACTTTGGGAGACTGAGGCGGGC 65475    A  A    _
           GG                     CC CCC CCTCGG CTCCCAAAGT
                                  || ||| |||||| ||||||||||
                                  GG GGG GGAGTC GAGGGTTTCA
                                   C  C     A
GAM219  UPK1B    3'  ACTTTGGGAGGCCGAGGTGGGC 23697    CA        _
           AGA                    TC  CCCACCTCGGC TCCCAAAGT
                                  ||  |||||||||| |||||||||
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                                AG  GGGTGGAGCCG AGGGTTTCA
                                 AC          G
GAM219  USP14    3'  ACTTTGGGAGGCTGAGGCAGGT 18926       CA      _
              GG                   CCACC  CCTCGGC TCCCAAAGT
                                   |||||  ||||||| |||||||||
                                   GGTGG  GGAGTCG AGGGTTTCA
                                     AC      G
GAM219  VHL      3'  ACTTTGGGAGGCCAGGGCAGG  6821     CA  TC  _
                                   CC  CC  GGC TCCCAAAGT
                                   ||  ||  ||| |||||||||
                                   GG  GG  CCG AGGGTTTCA
                                    AC  GA   G
GAM219  VHL      3'  ACTTTGGGAGGCCTAGGCGGGT 6822         A   C  _
              GG                   CCACCC CCT GGC TCCCAAAGT
                                   ||||||| ||| ||| |||||||||
                                   GGTGGG GGA CCG AGGGTTTCA
                                      C   T   G
GAM219  VHL      3'  ACTTTGGGGGGTCGAGGTGGGC 6823     CA           _
              AGA                   TC  CCCACCTCGGCTCCC AAAGT
                                   ||  |||||||||||||| |||||
                                   AG  GGGTGGAGCTGGGGG TTTCA
                                    AC             G
GAM219  WIG1     3'  ACTCTGGAGGCTGAGGCAGG   96092    CA      TC   A
                                   CC  CCTCGGC  CCA AGT
                                   ||  |||||||  ||| |||
                                   GG  GGAGTCG  GGT TCA
                                    AC       GA   C
GAM219  WIG1     3'  ACTTTGGGAGGCCGAAGCAGGC 96093    A  CACC    _
              GG                   CC CC    TCGGC TCCCAAAGT
                                   || ||    ||||| |||||||||
                                   GG GG    AGCCG AGGGTTTCA
                                    C  ACGA    G
GAM219  WW45     3'  GGGAGGCCGAGGTGGGTGGA   41814             _
                                   TCCACCCACCTCGGC TCCC
                                   |||||||||||||| ||||
                                   AGGTGGGTGGAGCCG AGGG
                                             G
GAM219  XRCC2    3'  ACTTTGCGAGGCCGAGGTGGGT 19486             _  C
              GGA                   TCCACCCACCTCGGC TC CAAAGT
                                   |||||||||||||| || ||||||
                                   AGGTGGGTGGAGCCG AG GTTTCA
                                             G  C
GAM219  XT3      3'  ACCTTGGGGGTCAAGGTGGGTG 39899           C        A
              GA                   TCCACCCACCT GGCTCCCAA GT
                                   |||||||||| ||||||||| ||
                                   AGGTGGGTGGA CTGGGGGTT CA
                                          A        C
GAM219  ZNF136   3'  ACTTTGGGAGGCTGAGGCAGGA 60567     A  CA      _
              GGA                   TCC CC  CCTCGGC TCCCAAAGT
                                   ||| ||  ||||||| |||||||||
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                                AGG GG  GGAGTCG AGGGTTTCA
                                  A  AC      G
GAM219  ZNF36    3'  ACTTTGGGAGGCCGAGGTGAGC 95574     ACC       _
           GGA                    TCC   CACCTCGGC TCCCAAAGT
                                  |||   ||||||||| |||||||||
                                AGG   GTGGAGCCG AGGGTTTCA
                                  CGA        G
GAM219  AF020591 3'  ACCTTGCGAGGCCGAGGCAGGT 27899       CA      _ C   A
           GGA                    TCCACC  CCTCGGC TC CAA GT
                                  ||||||  ||||||| || ||| ||
                                AGGTGG  GGAGCCG AG GTT CA
                                   AC      G  C   C
GAM219  AF020591 3'  ACTCTGGAAGGCTGAGGTGGGT 27900             C_   A
           GGA                    TCCACCCACCTCGGCT  CCA AGT
                                  ||||||||||||||||  ||| |||
                                AGGTGGGTGGAGTCGG  GGT TCA
                                        AA   C
GAM219  AF020591 3'  ACTTAGGTAGGCCAAGGTGGGT 27901          C    C_  A
           GGA                    TCCACCCACCT GGCT  CC AAGT
                                  ||||||||||| ||||  || ||||
                                AGGTGGGTGGA CCGG  GG TTCA
                                      A    AT  A
GAM219  AKR1D1   3'  ACTTTGGGAGGCCAAGGTGGG  21128       C   _
                                CCCACCT GGC TCCCAAAGT
                                ||||||| ||| |||||||||
                                GGGTGGA CCG AGGGTTTCA
                                   A   G
GAM219  ALOX15B  3'  ACTTTGGGAGATGGAGGCGGG  8552      A    GG_
                                CCC CCTC   CTCCCAAAGT
                                ||| ||||   ||||||||||
                                GGG GGAG   GAGGGTTTCA
                                  C    GTA
GAM219  ALTE     3'  ACTTTGGGAGGCCGAGGTGGGC 17575     CA        _
           AGA                    TC  CCCACCTCGGC TCCCAAAGT
                                  ||  |||||||||| |||||||||
                                AG  GGGTGGAGCCG AGGGTTTCA
                                  AC          G
GAM219  ALTE     3'  ACTTTGGGAGGCCGAGGTGGGC 60996     CA        _
           AGA                    TC  CCCACCTCGGC TCCCAAAGT
                                  ||  |||||||||| |||||||||
                                AG  GGGTGGAGCCG AGGGTTTCA
                                  AC          G
GAM219  APXL2    3'  ACTTTGGGAGGCCGAGGCGGGC 75668     A  A     _
           GGA                    TCC CCC CCTCGGC TCCCAAAGT
                                  ||| ||| ||||||| |||||||||
                                AGG GGG GGAGCCG AGGGTTTCA
                                  C  C      G
GAM219  ARNTL2   3'  ACTTTGGGAGGCCGAAGTGGGC 39836    A    C    _
           GG                     CC CCCAC TCGGC TCCCAAAGT
                                  || ||||| ||||| |||||||||
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                                GG GGGTG AGCCG AGGGTTTCA
                                 C    A    G
GAM219  ARNTL2   3' ACTTTGGGAGGCTGAGACGGG 39837     AC     _
                                CCC  CTCGGC TCCCAAAGT
                                |||  |||||| |||||||||
                                GGG  GAGTCG AGGGTTTCA
                                  CA     G
GAM219  BFAR     3' ACTTTGGGTGGGTGAGGCAGGC 61420    A  CA    G _
           GG                    CC CC  CCTCG CT CCCAAAGT
                                || ||  ||||| || ||||||||
                                GG GG  GGAGT GG GGGTTTCA
                                 C AC    G  T
GAM219  BIA2     3' ACTTTGGGAGGCTGAGGCGGGT 71789        A     _
           GGA                    TCCACCC CCTCGGC TCCCAAAGT
                                ||||||| ||||||| |||||||||
                                AGGTGGG GGAGTCG AGGGTTTCA
                                    C      G
GAM219  BIRC1    3' ACTTTGGGAGGCTGAGGCGGG  16984     A     _
                                CCC CCTCGGC TCCCAAAGT
                                ||| ||||||| |||||||||
                                GGG GGAGTCG AGGGTTTCA
                                  C      G
GAM219  BTN3A2   3' ACTTTGGAAGGCTGAGGAGGGC 23868     A  A      C_
           GGA                    TCC CCC CCTCGGCT  CCAAAGT
                                ||| ||| ||||||||  |||||||
                                AGG GGG GGAGTCGG  GGTTTCA
                                  C  A       AA
GAM219  C11orf9  3' ACTCTGACTCTGAGGTGGG   26114          CTCC  A
                                CCCACCTCGG    CA AGT
                                ||||||||||    || |||
                                GGGTGGAGTC    GT TCA
                                      TCA_  C
GAM219  C12orf2  3' ACTTTGGGAGGCCGAGGTGGG  83676          _
                                CCCACCTCGGC TCCCAAAGT
                                |||||||||| |||||||||
                                GGGTGGAGCCG AGGGTTTCA
                                      G
GAM219  C13orf1  3' ACTCTGGAGGCTGAGGCAGG   40346    CA     TC   A
                                CC  CCTCGGC  CCA AGT
                                ||  |||||||  ||| |||
                                GG  GGAGTCG  GGT TCA
                                 AC      GA   C
GAM219  C13orf1  3' ACTTTGGGAGGCTGAGGCGGGA 40347     A  A     _
           GGA                    TCC CCC CCTCGGC TCCCAAAGT
                                ||| ||| ||||||| |||||||||
                                AGG GGG GGAGTCG AGGGTTTCA
                                  A  C      G
GAM219  C1orf33  3' ACTTTGGGAAGCCGAGGTGGGC 32977    CA         _
           AGA                    TC  CCCACCTCGGCT CCCAAAGT
                                ||  |||||||||||| ||||||||
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                                AG  GGGTGGAGCCGA GGGTTTCA
                                 AC          A
GAM219  C1orf34   3'  ACTTTGGGAGGCTGAGGCGGGC 61293     A  A      _
            GGA                   TCC CCC CCTCGGC TCCCAAAGT
                                  ||| ||| ||||||| |||||||||
                                  AGG GGG GGAGTCG AGGGTTTCA
                                    C  C      G
GAM219  C1QTNF2   3'  ACTTTGGGAAGCTGAGGTGGAC 49967     AC          _
            GGA                   TCC  CCACCTCGGCT CCCAAAGT
                                  |||  |||||||||| ||||||||
                                  AGG  GGTGGAGTCGA GGGTTTCA
                                    CA          A
GAM219  C20orf106 3'  ACTTTGGGAGGCCAGGGCAGGT 55890       CA  TC   _
            GG                    CCACC  CC  GGC TCCCAAAGT
                                  |||||  ||  ||| |||||||||
                                  GGTGG  GG  CCG AGGGTTTCA
                                     AC  GA   G
GAM219  C20orf106 3'  ACTTTGGGAGGCCGAGACGGG  55891     AC     _
                                  CCC  CTCGGC TCCCAAAGT
                                  |||  |||||| |||||||||
                                  GGG  GAGCCG AGGGTTTCA
                                    CA     G
GAM219  C20orf106 3'  ACTTTGGGAGGCTGAGGCGGGT 55892       A      _
            G                      CACCC CCTCGGC TCCCAAAGT
                                  ||||| ||||||| |||||||||
                                  GTGGG GGAGTCG AGGGTTTCA
                                     C      G
GAM219  C20orf142 3'  ACTTTGGGAGGCTGAGGTGGGA 75268     A          _
            GGA                   TCC CCCACCTCGGC TCCCAAAGT
                                  ||| |||||||||| |||||||||
                                  AGG GGGTGGAGTCG AGGGTTTCA
                                    A          G
GAM219  C20orf175 3'  ACTTTGGGAGGCCGAGGCAGGC 55920     A  CA      _
            GGA                   TCC CC  CCTCGGC TCCCAAAGT
                                  ||| ||  ||||||| |||||||||
                                  AGG GG  GGAGCCG AGGGTTTCA
                                    C  AC      G
GAM219  C20orf177 3'  ACTTTGGGAGGCCGAGGCAGGC 62824     A  CA      _
            GGA                   TCC CC  CCTCGGC TCCCAAAGT
                                  ||| ||  ||||||| |||||||||
                                  AGG GG  GGAGCCG AGGGTTTCA
                                    C  AC      G
GAM219  C20orf183 3'  ACTTTGGGAGGCCGAGGCGGGC 48526     A  A      _
            GGA                   TCC CCC CCTCGGC TCCCAAAGT
                                  ||| ||| ||||||| |||||||||
                                  AGG GGG GGAGCCG AGGGTTTCA
                                    C  C      G
GAM219  C20orf46  5'  ACTCCAGGAGCTGAGTTGGGTG 37732          C        CAA
            GA                    TCCACCCA CTCGGCTCC   AGT
                                  |||||||| |||||||||   |||
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                                AGGTGGGT GAGTCGAGG   TCA
                                   T        ACC
GAM219  C21orf108 3'  ACTTTGGGAGGCCAAGGCGGGT 90107       A   C  _
          G                     CACCC CCT GGC TCCCAAAGT
                                |||||| ||| ||| |||||||||
                                GTGGG GGA CCG AGGGTTTCA
                                  C   A   G
GAM219  C22orf19  3'  ACTTTGGGAGGCCAAGGCGGGT 14810       A   C  _
          GG                    CCACCC CCT GGC TCCCAAAGT
                                |||||| ||| ||| |||||||||
                                GGTGGG GGA CCG AGGGTTTCA
                                  C   A   G
GAM219  C22orf19  3'  ACTTTGGGAGGCTGGTGGGCGG 14811     A     TC  _
          A                     TCC CCCACC  GGC TCCCAAAGT
                                ||| ||||||  ||| |||||||||
                                AGG GGGTGG  TCG AGGGTTTCA
                                  C     __  G
GAM219  C2F      3'  ACTTTGGGAGGCGGAGGCGGGT 22000       A   G  _
          GG                    CCACCC CCTC GC TCCCAAAGT
                                |||||| |||| || |||||||||
                                GGTGGG GGAG CG AGGGTTTCA
                                  C   G  G
GAM219  C6orf29   3'  ACTTTGAGAGGCTGAGGCGGGC 52452     A   A     _  C
          GGA                   TCC CCC CCTCGGC TC CAAAGT
                                ||| ||| ||||||| || ||||||
                                AGG GGG GGAGTCG AG GTTTCA
                                  C   C      G  A
GAM219  C6orf29   3'  ACTTTGAGAGGCTGAGGCGGGC 48262     A   A     _  C
          GGA                   TCC CCC CCTCGGC TC CAAAGT
                                ||| ||| ||||||| || ||||||
                                AGG GGG GGAGTCG AG GTTTCA
                                  C   C      G  A
GAM219  C6orf5   3'  ACTTTGGGAAGCTAAGGCAGG  31963    CA   CG  _
                                CC  CCT  GCT CCCAAAGT
                                ||  |||  ||| ||||||||
                                GG  GGA  CGA GGGTTTCA
                                 AC   AT   A
GAM219  C6orf5   3'  ACTTTGGGAGGCTGAGGCAGGC 31964     A  CA      _
          GGA                   TCC CC  CCTCGGC TCCCAAAGT
                                ||| ||  ||||||| |||||||||
                                AGG GG  GGAGTCG AGGGTTTCA
                                  C  AC      G
GAM219  C8orf2   3'  ACTTTGGGAGGCCAAGGCAGGC 24142    A  CA   C  _
          GG                    CC CC  CCT GGC TCCCAAAGT
                                || ||  ||| ||| |||||||||
                                GG GG  GGA CCG AGGGTTTCA
                                 C  AC   A   G
GAM219  C9orf5   3'  ACTTTGGAAGGCTGAGGTGGGT 50099              C_
          GGA                   TCCACCCACCTCGGCT  CCAAAGT
                                ||||||||||||||||  |||||||
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                                AGGTGGGTGGAGTCGG  GGTTTCA
                                      AA
GAM219  CALN1    3'  ACTTTGGGAGGCCAAGGCAGGT 49656      CA  C  _
            GG                  CCACC  CCT GGC TCCCAAAGT
                                ||||||  ||| ||| |||||||||
                                GGTGG  GGA CCG AGGGTTTCA
                                  AC  A  G
GAM219  CBCIP2   3'  ACTTTGGGAGGCCTAGGTGGGC 52647    A     C  _
            GG                  CC CCCACCT GGC TCCCAAAGT
                                || ||||||| ||| |||||||||
                                GG GGGTGGA CCG AGGGTTTCA
                                 C      T  G
GAM219  CCR6     3'  GGAAGCTAAGATGGGTGGA   16444       C  CG  C
                                TCCACCCA CT  GCT CC
                                |||||||| ||  ||| ||
                                AGGTGGGT GA  CGA GG
                                     A  AT  A
GAM219  CCR6     3'  GGAAGCTAAGATGGGTGGA   49405       C  CG  C
                                TCCACCCA CT  GCT CC
                                |||||||| ||  ||| ||
                                AGGTGGGT GA  CGA GG
                                     A  AT  A
GAM219  CDC14A   5'  ACTTTGGAAGCCGGGGGGG   14782    A      C
                                CCC CCTCGGCT CCAAAGT
                                ||| |||||||| |||||||
                                GGG GGGGCCGA GGTTTCA
                                  _      A
GAM219  CDT1     3'  ACTTTGGGAGGCCAAGGTGGG  78155       C  _
                                CCCACCT GGC TCCCAAAGT
                                ||||||| ||| |||||||||
                                GGGTGGA CCG AGGGTTTCA
                                    A  G
GAM219  cerk     3'  ACTTTGGGAGGCCGAGGCGGGT 43155       A    _
            GGA                 TCCACCC CCTCGGC TCCCAAAGT
                                ||||||| ||||||| |||||||||
                                AGGTGGG GGAGCCG AGGGTTTCA
                                    C      G
GAM219  CGRP-RCP 3'  ACTTTGGGAGGGCAAGGCAGGC 27883    A  CA  CGG_
            GG                  CC CC  CCT    CTCCCAAAGT
                                || ||  |||   ||||||||||
                                GG GG  GGA    GAGGGTTTCA
                                 C  AC   ACGG
GAM219  CLDN15   3'  ACTTTGGTAGGCTGAGGTGGGT 57367             C_
            GGA                 TCCACCCACCTCGGCT  CCAAAGT
                                |||||||||||||||  |||||||
                                AGGTGGGTGGAGTCGG  GGTTTCA
                                      AT
GAM219  CRTAM    3'  ACTTTGGGAGGCTGAGGTAGGC 39469    CA  C      _
            AGA                 TC  CC ACCTCGGC TCCCAAAGT
                                ||  || |||||||| |||||||||
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                                  AG  GG TGGAGTCG AGGGTTTCA
                                   AC  A       G
GAM219  CSAD     3'  ACTTTGGGAGGCCGAGGCGGGT 32575         A     _
              GGA                    TCCACCC CCTCGGC TCCCAAAGT
                                  ||||||| ||||||| |||||||||
                                  AGGTGGG GGAGCCG AGGGTTTCA
                                      C       G
GAM219  CX46.6   3'  TGGGGCCAAGGTGGGGTGGA  40316        _   C   T
                                  TCCACCC ACCT GGC CCCA
                                  ||||||| |||| ||| ||||
                                  AGGTGGG TGGA CCG GGGT
                                      G   A  _
GAM219  CYorf14  3'  ACTTTGGGAGGCTGAGGTAGGC 38202    CA  C       _
              AGA                    TC  CC ACCTCGGC TCCCAAAGT
                                  ||  || |||||||| |||||||||
                                  AG  GG TGGAGTCG AGGGTTTCA
                                   AC  A       G
GAM219  D21S2056E 3'  ACTTTGGGAGGCCGAGGTGG   14860          _
                                  CCACCTCGGC TCCCAAAGT
                                  |||||||||| |||||||||
                                  GGTGGAGCCG AGGGTTTCA
                                        G
GAM219  DCOHM    3'  ACTTTGAGAGGCTGGGGCGG   50505    A     _ C
                                  CC CCTCGGC TC CAAAGT
                                  || ||||||| || ||||||
                                  GG GGGGTCG AG GTTTCA
                                   C       G  A
GAM219  DDX34    3'  ACTTTGGGAGGCCTAGGCGGG  28656     A   C  _
                                  CCC CCT GGC TCCCAAAGT
                                  ||| ||| ||| |||||||||
                                  GGG GGA CCG AGGGTTTCA
                                    C   T   G
GAM219  DEGS     3'  ACTTTGGGAGGCCAAGGTGGGT 14799           C  _
              GGA                    TCCACCCACCT GGC TCCCAAAGT
                                  |||||||||||  ||| |||||||||
                                  AGGTGGGTGGA CCG AGGGTTTCA
                                        A   G
GAM219  DJ1042K10.2 3'  ACCTTGTGAGGAGGTGGGGGA  32298     A       GG   C   A
                                  TCC CCCACCTC  CTC CAA GT
                                  ||| ||||||||  ||| ||| ||
                                  AGG GGGTGGAG  GAG GTT CA
                                    _       __   T   C
GAM219  dJ383J4.3 3'  ACTTTGGGAGGCTGAGGTGGGT 67488             _
              GGA                    TCCACCCACCTCGGC TCCCAAAGT
                                  ||||||||||||||| |||||||||
                                  AGGTGGGTGGAGTCG AGGGTTTCA
                                           G
GAM219  DKFZP434B168 3'  ACTTTGGGAGGCTGAGGTGGGC 31863     A         _
              GG                     CC CCCACCTCGGC TCCCAAAGT
                                  || ||||||||||| |||||||||
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                                GG GGGTGGAGTCG AGGGTTTCA
                                 C         G
GAM219  DKFZP434C171 3'  ACTTTGGGAGGCCGAGGTGGGT 32180                _
           GGA                    TCCACCCACCTCGGC TCCCAAAGT
                                  ||||||||||||||| |||||||||
                                  AGGTGGGTGGAGCCG AGGGTTTCA
                                        G
GAM219  DKFZp434E0519 3'  ACTTTGGGAGGCCGAGACAGG  50981    CAC     _
                                  CC   CTCGGC TCCCAAAGT
                                  ||   |||||| |||||||||
                                  GG   GAGCCG AGGGTTTCA
                                   ACA     G
GAM219  DKFZp434E2220 5'  ACTTTGGGAGGCCGAGGCGGGT 34704        A      _
           GGA                    TCCACCC CCTCGGC TCCCAAAGT
                                  ||||||| ||||||| |||||||||
                                  AGGTGGG GGAGCCG AGGGTTTCA
                                      C      G
GAM219  DKFZp434G171 3'  ACTTTGGGAGGCCAAGGCAGG  80228    CA   C  _
                                  CC  CCT GGC TCCCAAAGT
                                  ||  ||| ||| |||||||||
                                  GG  GGA CCG AGGGTTTCA
                                   AC   A   G
GAM219  DKFZp434G171 3'  ACTTTGGGAGGCCAAGGTGGGT 80229           C  _
           GGA                    TCCACCCACCT GGC TCCCAAAGT
                                  |||||||||| ||| |||||||||
                                  AGGTGGGTGGA CCG AGGGTTTCA
                                        A   G
GAM219  DKFZP434N1511 3'  ACTTTGGGAGGCCGAGGCGGGA 93049     A   A      _
           GGA                    TCC CCC CCTCGGC TCCCAAAGT
                                  ||| ||| ||||||| |||||||||
                                  AGG GGG GGAGCCG AGGGTTTCA
                                    A   C      G
GAM219  DKFZp547C176 3'  ACTTTGGGGAGCTGAGGCGGGC 67795     A   A         _
           GGA                    TCC CCC CCTCGGCTCCC AAAGT
                                  ||| ||| |||||||||| |||||
                                  AGG GGG GGAGTCGAGGG TTTCA
                                    C   C          G
GAM219  DKFZp547G183 3'  ACTTTGGGAGGCCAAGGTGAGC 38637    ACC     C  _
           GG                     CC   CACCT GGC TCCCAAAGT
                                  ||   ||||| ||| |||||||||
                                  GG   GTGGA CCG AGGGTTTCA
                                   CGA    A   G
GAM219  DKFZp547I094 3'  ACTTTGGGAGGCCGAGGTGGGA 50551     A         _
           GGA                    TCC CCCACCTCGGC TCCCAAAGT
                                  ||| |||||||||| |||||||||
                                  AGG GGGTGGAGCCG AGGGTTTCA
                                    A          G
GAM219  DKFZP564A022 3'  ACTTTGGGAGGCTGAGGCGGGT 48968    C    A     _
           AGA                    TC ACCC CCTCGGC TCCCAAAGT
                                  || |||| ||||||| |||||||||
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                                AG TGGG GGAGTCG AGGGTTTCA
                                 A   C      G
GAM219  DKFZP564B1023 3'  ACTCTGGAGGCTGAGGTGAGGG 49356     A _       TC   A
           GA                    TCC CC CACCTCGGC  CCA AGT
                                 ||| || |||||||||  ||| |||
                                 AGG GG GTGGAGTCG  GGT TCA
                                  _ A        GA   C
GAM219  DKFZP564B1023 3'  ACTTTGGGAGGCCGAGGGGAGT 49357       _ A      _
           GGA                    TCCAC CC CCTCGGC TCCCAAAGT
                                 ||||| || ||||||| |||||||||
                                 AGGTG GG GGAGCCG AGGGTTTCA
                                   A _      G
GAM219  DKFZP564I052 3'  ACTTTGGGAGGCTGATATGGGT 67276         CC    _
           GGA                    TCCACCCA  TCGGC TCCCAAAGT
                                 ||||||||  ||||| |||||||||
                                 AGGTGGGT  AGTCG AGGGTTTCA
                                     AT    G
GAM219  DKFZp564K142 3'  ACTTTGGGAGGCCAAGGCAGG  50428    CA   C  _
                                 CC  CCT GGC TCCCAAAGT
                                 ||  ||| ||| |||||||||
                                 GG  GGA CCG AGGGTTTCA
                                  AC   A   G
GAM219  DKFZP564M182 3'  ACTTTGGGAGGCCGAGGCAGGC 78615     A  CA     _
           GGA                    TCC CC  CCTCGGC TCCCAAAGT
                                 ||| ||  ||||||| |||||||||
                                 AGG GG  GGAGCCG AGGGTTTCA
                                   C  AC      G
GAM219  DKFZP564M182 3'  CTTTGGAACGCTGGGTGG    78629      T    TC_
                                 CCACC CGGC   CCAAAG
                                 ||||| ||||   ||||||
                                 GGTGG GTCG   GGTTTC
                                    _   CAA
GAM219  DKFZP566J2046 3'  ACTCTGGAGGCTGAGGCAGG   49132    CA      TC   A
                                 CC  CCTCGGC  CCA AGT
                                 ||  |||||||  ||| |||
                                 GG  GGAGTCG  GGT TCA
                                  AC       GA   C
GAM219  DKFZP566J2046 3'  ACTTTGGGAGGCCGAGGCGGGC 49134    A   A     _
           GG                     CC CCC CCTCGGC TCCCAAAGT
                                 || ||| ||||||| |||||||||
                                 GG GGG GGAGCCG AGGGTTTCA
                                  C   C      G
GAM219  DKFZP586C1324 3'  ACTTTGGGAGGCCGAGGCAGGT 70352       CA     _
           GGA                    TCCACC  CCTCGGC TCCCAAAGT
                                 ||||||  ||||||| |||||||||
                                 AGGTGG  GGAGCCG AGGGTTTCA
                                    AC      G
GAM219  DKFZP586M1120 3'  ACTTTGAGAGGCTGAGGCGGGA 49273     A   A     _ C
           GGA                    TCC CCC CCTCGGC TC CAAAGT
                                 ||| ||| ||||||| || ||||||
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                                AGG GGG GGAGTCG AG GTTTCA
                                  A  C      G A
GAM219  DKFZP761G1913 3'  ACTTTGGGAGGCTGAGGTGGGT 49690                _
           GGA                    TCCACCCACCTCGGC TCCCAAAGT
                                  ||||||||||||||| |||||||||
                                  AGGTGGGTGGAGTCG AGGGTTTCA
                                         G
GAM219  DKFZp761J139 5'  ACTTTGGGAGGTCGAGGCGGGC 51095    CA  A     _
           AGA                    TC  CCC CCTCGGC TCCCAAAGT
                                  ||  ||| ||||||| |||||||||
                                  AG  GGG GGAGCTG AGGGTTTCA
                                   AC  C      G
GAM219  DRF1     3'  ACTTTGGGAGGCCAAGGCGGGT 47732       A  C  _
           GG                     CCACCC CCT GGC TCCCAAAGT
                                  |||||| ||| ||| |||||||||
                                  GGTGGG GGA CCG AGGGTTTCA
                                     C  A  G
GAM219  DRF1     3'  ACTTTGGGAGGCTGAGGTGGGT 47733                _
           GGA                    TCCACCCACCTCGGC TCCCAAAGT
                                  ||||||||||||||| |||||||||
                                  AGGTGGGTGGAGTCG AGGGTTTCA
                                         G
GAM219  ERAP140   3'  ACTTTGGGAGGCCGAGGCAGGT 75698       CA     _
           GGA                    TCCACC  CCTCGGC TCCCAAAGT
                                  ||||||  ||||||| |||||||||
                                  AGGTGG  GGAGCCG AGGGTTTCA
                                     AC      G
GAM219  ET       3'  ACTTTGGGAGGCTGAGGTGGGT 44463              _
           GGA                    TCCACCCACCTCGGC TCCCAAAGT
                                  ||||||||||||||| |||||||||
                                  AGGTGGGTGGAGTCG AGGGTTTCA
                                         G
GAM219  FBXO26   3'  ACTTCAGGAGGCCGAGGTGGGA 46621     A        _  CA
           GGA                    TCC CCCACCTCGGC TCC  AAGT
                                  ||| |||||||||| |||  ||||
                                  AGG GGGTGGAGCCG AGG  TTCA
                                    A         G  AC
GAM219  FBXO27   3'  ACTTTGGGAGGCTGAGGCAGGC 74999     A  CA     _
           GGA                    TCC CC  CCTCGGC TCCCAAAGT
                                  ||| ||  ||||||| |||||||||
                                  AGG GG  GGAGTCG AGGGTTTCA
                                    C  AC      G
GAM219  FBXO6    3'  ACTTTGGGAGACCGAGGCAGGT 37986       CA    _
           GG                     CCACC  CCTCGG CTCCCAAAGT
                                  |||||  |||||| ||||||||||
                                  GGTGG  GGAGCC GAGGGTTTCA
                                     AC     A
GAM219  FBXO9    3'  ACTTTGGGAGGCTAAGACAGG  54237    CAC  CG  _
                                  CC   CT  GC TCCCAAAGT
                                  ||   ||  || |||||||||
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                                GG   GA  CG AGGGTTTCA
                                 ACA  AT  G
GAM219  FKBP14   3' ACTTTGGGAGGCTGAGGCGGGC 36057     A   A      _
           GGA                    TCC CCC CCTCGGC TCCCAAAGT
                                  ||| ||| ||||||| |||||||||
                                  AGG GGG GGAGTCG AGGGTTTCA
                                    C   C       G
GAM219  FKBP14   3' ACTTTGGGGGCCAAGGAGGGTG 36058         A   C
           GA                     TCCACCC CCT GGCTCCCAAAGT
                                  ||||||| ||| ||||||||||||
                                  AGGTGGG GGA CCGGGGGTTTCA
                                     A   A
GAM219  FKSG17   3' ACTTTGGGAGGCCAAGGCAGG  50149    CA   C  _
                                  CC  CCT GGC TCCCAAAGT
                                  ||  ||| ||| |||||||||
                                  GG  GGA CCG AGGGTTTCA
                                   AC   A   G
GAM219  FLJ00060 3' ACTCTGGGGGGCCGAGGTGGGT 61731                AA_
           GGA                    TCCACCCACCTCGGCTCCC   AGT
                                  ||||||||||||||||||   |||
                                  AGGTGGGTGGAGCCGGGGG   TCA
                                              GTC
GAM219  FLJ10008 3' ACTTTGGGAGGCCGAGGCGGAC 36177     AC  A      _
           GGA                    TCC  CC CCTCGGC TCCCAAAGT
                                  |||  || ||||||| |||||||||
                                  AGG  GG GGAGCCG AGGGTTTCA
                                    CA  C       G
GAM219  FLJ10043 3' ACTTTGGGGGGCTGAGGCAGGT 36226        CA         _
           GGA                    TCCACC  CCTCGGCTCCC AAAGT
                                  ||||||  |||||||||||| |||||
                                  AGGTGG  GGAGTCGGGGG TTTCA
                                     AC          G
GAM219  FLJ10058 3' ACTTTGGGAGGCTGAGGCAAGT 36256       CCA      _
           GGA                    TCCAC   CCTCGGC TCCCAAAGT
                                  |||||   ||||||| |||||||||
                                  AGGTG   GGAGTCG AGGGTTTCA
                                     AAC      G
GAM219  FLJ10139 3' ACTTTGGGAGGCTGAGGCAGGC 36313    CA  CA      _
           AGA                    TC  CC  CCTCGGC TCCCAAAGT
                                  ||  ||  ||||||| |||||||||
                                  AG  GG  GGAGTCG AGGGTTTCA
                                   AC  AC      G
GAM219  FLJ10244 3' ACTTTGGGAGGCCGAGGCGGGT 36396        A      _
           GGA                    TCCACCC CCTCGGC TCCCAAAGT
                                  ||||||| ||||||| |||||||||
                                  AGGTGGG GGAGCCG AGGGTTTCA
                                     C       G
GAM219  FLJ10460 3' ACTTTGGGAGGCCTAGGTGGG  36607        C  _
                                  CCCACCT GGC TCCCAAAGT
                                  ||||||| ||| |||||||||
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                                GGGTGGA CCG AGGGTTTCA
                                   T  G
GAM219  FLJ10460  3'  TACTTTGGGAGGCCGACCCAGA 36622        C ____   _      ___
            TGGGTGGA                TCCACCCA C   TCGGC TCCCAAAGT  A
                                |||||||| |   ||||| |||||||||  |
                                AGGTGGGT G   AGCCG AGGGTTTCA  T
                                   A ACCC    G       ___
GAM219  FLJ10547  3'  ACTTTGGGAGGCCAAGGTGAGT 36771     C    C  _
            GG                    CCAC CACCT GGC TCCCAAAGT
                                |||| ||||| ||| |||||||||
                                GGTG GTGGA CCG AGGGTTTCA
                                  A   A  G
GAM219  FLJ10607  3'  ACTTTGGGAGGCTGAGGTGGGC 77621    CA        _
            AGA                   TC  CCCACCTCGGC TCCCAAAGT
                                ||  |||||||||| |||||||||
                                AG  GGGTGGAGTCG AGGGTTTCA
                                 AC         G
GAM219  FLJ10613  3'  ACTTTGGGAGGCCGAGGTGGGC 39332     A        _
            GGA                   TCC CCCACCTCGGC TCCCAAAGT
                                ||| |||||||||| |||||||||
                                AGG GGGTGGAGCCG AGGGTTTCA
                                  C         G
GAM219  FLJ10650  3'  ACTTTGGGAGGCCGAGGTGGGC 36896    CA        _
            AGA                   TC  CCCACCTCGGC TCCCAAAGT
                                ||  |||||||||| |||||||||
                                AG  GGGTGGAGCCG AGGGTTTCA
                                 AC         G
GAM219  FLJ10665  3'  ACTTTGGGAGGCTGAGGTGGGA 36920     A        _
            GGA                   TCC CCCACCTCGGC TCCCAAAGT
                                ||| |||||||||| |||||||||
                                AGG GGGTGGAGTCG AGGGTTTCA
                                  A         G
GAM219  FLJ10704  3'  GGGAGGCCGAGGCAGGTGGA   36982       CA     _
                                TCCACC  CCTCGGC TCCC
                                ||||||  ||||||| ||||
                                AGGTGG  GGAGCCG AGGG
                                   AC      G
GAM219  FLJ10781  3'  ACTTTGGGAGGCTGAGGCAGGT 37165    C   CA     _
            CGA                   TC ACC  CCTCGGC TCCCAAAGT
                                || |||  ||||||| |||||||||
                                AG TGG  GGAGTCG AGGGTTTCA
                                 C  AC      G
GAM219  FLJ10803  3'  ACTTTGGGAGACCAAGGTGGG  37194       C  _
                                CCCACCT GG CTCCCAAAGT
                                ||||||| || ||||||||||
                                GGGTGGA CC GAGGGTTTCA
                                   A  A
GAM219  FLJ10803  3'  ACTTTGGGAGGCTGGGGCGGGT 37195       A     _
            GGA                   TCCACCC CCTCGGC TCCCAAAGT
                                ||||||| ||||||| |||||||||
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                                AGGTGGG GGGGTCG AGGGTTTCA
                                   C      G
GAM219  FLJ10932  3' ACTTTGGGAGGCCAAGGTGGG  37422        C  _
                                CCCACCT GGC TCCCAAAGT
                                ||||||| ||| |||||||||
                                GGGTGGA CCG AGGGTTTCA
                                   A   G
GAM219  FLJ10989  3' ACTTTGGGAGGCCAAGGCGAGC 37493    ACCCA  C  _
           GG                    CC     CCT GGC TCCCAAAGT
                                ||     ||| ||| |||||||||
                                GG     GGA CCG AGGGTTTCA
                                 CGAGC   A   G
GAM219  FLJ11029  3' ACTTTGGGAGGCTGAGGCAGGT 61630        CA      _
           GGA                    TCCACC  CCTCGGC TCCCAAAGT
                                ||||||  ||||||| |||||||||
                                AGGTGG  GGAGTCG AGGGTTTCA
                                   AC      G
GAM219  FLJ11106  3' ACTTTGGGAGGCCAAGGCGGGC 37615    A   A   C  _
           GG                    CC CCC CCT GGC TCCCAAAGT
                                || ||| ||| ||| |||||||||
                                GG GGG GGA CCG AGGGTTTCA
                                 C   C   A   G
GAM219  FLJ11136  3' ACTTTGGGAGGCCGAGGCCAGT 37663       CCA      _
           GGA                    TCCAC   CCTCGGC TCCCAAAGT
                                |||||   ||||||| |||||||||
                                AGGTG   GGAGCCG AGGGTTTCA
                                   ACC      G
GAM219  FLJ11149  3' ACTTTGGGAGGCCGAGGTGGGA 37684     A         _
           GGA                    TCC CCCACCTCGGC TCCCAAAGT
                                ||| |||||||||| |||||||||
                                AGG GGGTGGAGCCG AGGGTTTCA
                                  A         G
GAM219  FLJ11151  3' ACTTTGGGAGGCTGAGACGGG  68464     AC     _
                                CCC  CTCGGC TCCCAAAGT
                                |||  |||||| |||||||||
                                GGG  GAGTCG AGGGTTTCA
                                  CA     G
GAM219  FLJ11259  3' ACTTTGGGAGGCCTAGGCAGG  37762    CA   C  _
                                CC  CCT GGC TCCCAAAGT
                                ||  ||| ||| |||||||||
                                GG  GGA CCG AGGGTTTCA
                                 AC   T   G
GAM219  FLJ11267  3' ACTTTGGGAGGCCAAGGTGGGT 39495        C  _
                                ACCCACCT GGC TCCCAAAGT
                                |||||||| ||| |||||||||
                                TGGGTGGA CCG AGGGTTTCA
                                   A   G
GAM219  FLJ11637  3' ACTTTGGGAGGCCGAGGCAGGC 46979     A  CA     _
           GGA                    TCC CC  CCTCGGC TCCCAAAGT
                                ||| ||  ||||||| |||||||||
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                                AGG GG  GGAGCCG AGGGTTTCA
                                  C  AC      G
GAM219  FLJ11700 3' ACTTTGGGAGGCCGAGGAGGGC 46554    CA   A     _
              AGA                 TC  CCC CCTCGGC TCCCAAAGT
                                ||  ||| ||||||| |||||||||
                                AG  GGG GGAGCCG AGGGTTTCA
                                 AC   A      G
GAM219  FLJ11710 5' ACTCTGGGAGGTAGAGGTGGGA 46237     A      GG_    A
              GGA                 TCC CCCACCTC   CTCCCA AGT
                                ||| ||||||||   |||||| |||
                                AGG GGGTGGAG   GAGGGT TCA
                                  A       ATG     C
GAM219  FLJ11722 3' ACTTTGGGAGGCCGAGGTGGGT 46988           _
              GGA                 TCCACCCACCTCGGC TCCCAAAGT
                                |||||||||||||| |||||||||
                                AGGTGGGTGGAGCCG AGGGTTTCA
                                       G
GAM219  FLJ11726 3' ACTTTGGGAGGCCGAGGCAGGT 47013       CA     _
              GGA                 TCCACC  CCTCGGC TCCCAAAGT
                                ||||||  ||||||| |||||||||
                                AGGTGG  GGAGCCG AGGGTTTCA
                                   AC      G
GAM219  FLJ11800 3' ACTTTCGGAAGCTGAGGTGGGC 47035    CA         _ C
              AGA                 TC  CCCACCTCGGCT CC AAAGT
                                ||  |||||||||||| || |||||
                                AG  GGGTGGAGTCGA GG TTTCA
                                 AC           A  C
GAM219  FLJ11996 3' ACTTTGGGAGACTGAGGCAGGC 47050    A  CA    _
              GG                  CC CC  CCTCGG CTCCCAAAGT
                                || ||  |||||| ||||||||||
                                GG GG  GGAGTC GAGGGTTTCA
                                 C  AC     A
GAM219  FLJ11996 3' ACTTTGTGAGGCTGAGGCGAGT 47051       CCA     _ C
              GGA                 TCCAC   CCTCGGC TC CAAAGT
                                ||||||  ||||||| || ||||||
                                AGGTG   GGAGTCG AG GTTTCA
                                   AGC      G  T
GAM219  FLJ12056 3' ACTTTGGAAGGCCGAGGCAGGC 46814    A  CA      C_
              GGA                 TCC CC  CCTCGGCT  CCAAAGT
                                ||| ||  ||||||||  |||||||
                                AGG GG  GGAGCCGG  GGTTTCA
                                  C  AC       AA
GAM219  FLJ12078 3' ACTTTGGGAGGCCGAGGCAGGC 47075    A  CA    _
              GGA                 TCC CC  CCTCGGC TCCCAAAGT
                                ||| ||  ||||||| |||||||||
                                AGG GG  GGAGCCG AGGGTTTCA
                                  C  AC      G
GAM219  FLJ12178 3' ACTTTGGGAGCCTGAGGCAGGC 47826    A  CA   _
              GG                  CC CC  CCTC GGCTCCCAAAGT
                                || ||  |||| ||||||||||||
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                                GG GG  GGAG CCGAGGGTTTCA
                                 C  AC    T
GAM219  FLJ12190 3' ACTCTGGAGGCTGAGGCAGG  47558    CA      TC   A
                                CC  CCTCGGC  CCA AGT
                                ||  |||||||  ||| |||
                                GG  GGAGTCG  GGT TCA
                                 AC       GA   C
GAM219  FLJ12190 3' ACTTTGGGAGGCCAAGGCGGGT 47559       A   C  _
          G                      CACCC CCT GGC TCCCAAAGT
                                |||||| ||| ||| |||||||||
                                GTGGG GGA CCG AGGGTTTCA
                                   C   A   G
GAM219  FLJ12294 3' ACTTTGGGAGCCCCAGGTGGG  47705        C_
                                CCCACCT  GGCTCCCAAAGT
                                |||||||  ||||||||||||
                                GGGTGGA  CCGAGGGTTTCA
                                    CC
GAM219  FLJ12298 3' ACTTTGGGAGGCCAAGGCAGG  50593    CA   C  _
                                CC  CCT GGC TCCCAAAGT
                                ||  ||| ||| |||||||||
                                GG  GGA CCG AGGGTTTCA
                                 AC   A   G
GAM219  FLJ12363 3' ACTTTGGGACACCAGGGTGGGT 50626          TC  C_
          GGA                     TCCACCCACC  GG  TCCCAAAGT
                                ||||||||||  ||  |||||||||
                                AGGTGGGTGG  CC  AGGGTTTCA
                                     GA  AC
GAM219  FLJ12606 3' ACTTTGGGAGGCCGAGGCGGGT 46060        A      _
          GGA                     TCCACCC CCTCGGC TCCCAAAGT
                                |||||||  |||||||  |||||||||
                                AGGTGGG GGAGCCG AGGGTTTCA
                                    C      G
GAM219  FLJ12618 3' ACTTTGGGAAGCCAAGGCAGGT 46501     CA   C   _
                                ACC  CCT GGCT CCCAAAGT
                                |||  |||  ||||  ||||||||
                                TGG  GGA CCGA GGGTTTCA
                                  AC   A    A
GAM219  FLJ12660 3' ACTTTGGGAGGTTGAGGTGGGT 47891              _
          GGA                     TCCACCCACCTCGGC TCCCAAAGT
                                |||||||||||||||  |||||||||
                                AGGTGGGTGGAGTTG AGGGTTTCA
                                        G
GAM219  FLJ12671 3' ACTTAGGGAGGCCGAGGCGGGC 49099     A  A      _   A
          GGA                     TCC CCC CCTCGGC TCCC AAGT
                                |||  |||  |||||||  ||||  ||||
                                AGG GGG GGAGCCG AGGG TTCA
                                  C  C      G   A
GAM219  FLJ12800 3' ACTTTGGGAGTCCAAGGCAGGT 43524        CA   C  _
          GGG                     TCCACC  CCT GG CTCCCAAAGT
                                ||||||  |||  ||  ||||||||||
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                                GGGTGG  GGA CC GAGGGTTTCA
                                   AC   A  T
GAM219  FLJ12921  3' ACTTTGGGAGGCCGAGGCGGGC 46390     A  A     _
           GGA                    TCC CCC CCTCGGC TCCCAAAGT
                                  ||| ||| ||||||| |||||||||
                                  AGG GGG GGAGCCG AGGGTTTCA
                                    C  C      G
GAM219  FLJ12949  3' ACTTTGGGAGGCCGAGGTGAAA 43722     ACC       _
           GGA                    TCC   CACCTCGGC TCCCAAAGT
                                  |||   ||||||||| |||||||||
                                  AGG   GTGGAGCCG AGGGTTTCA
                                    AAA        G
GAM219  FLJ12985  3' ACTTTGGGAGGCCAAGACAGGT 46793     CAC  C  _
                                  ACC   CT GGC TCCCAAAGT
                                  |||   || ||| |||||||||
                                  TGG   GA CCG AGGGTTTCA
                                    ACA  A   G
GAM219  FLJ13117  3' ACTTTGGGAGGCTGAGGCGGGT 43801         A     _
           GGA                    TCCACCC CCTCGGC TCCCAAAGT
                                  ||||||| ||||||| |||||||||
                                  AGGTGGG GGAGTCG AGGGTTTCA
                                     C      G
GAM219  FLJ13162  3' ACTTTGGGAGGCCGAGGTGGGT 47178              _
           GGA                    TCCACCCACCTCGGC TCCCAAAGT
                                  |||||||||||||| |||||||||
                                  AGGTGGGTGGAGCCG AGGGTTTCA
                                        G
GAM219  FLJ13193  3' ACTTTGGGAGGTGGAGGCGGGT 50705       A    G  _
           GG                     CCACCC CCTC GC TCCCAAAGT
                                  |||||| |||| || |||||||||
                                  GGTGGG GGAG TG AGGGTTTCA
                                     C   G  G
GAM219  FLJ13390  3' ACTTTGGGAGGCCGAGGCAGG  42838    CA     _
                                  CC  CCTCGGC TCCCAAAGT
                                  ||  ||||||| |||||||||
                                  GG  GGAGCCG AGGGTTTCA
                                    AC      G
GAM219  FLJ13448  3' ACTTGGGGAAGCTGAGGTGGGC 47877    CA         _  A
           AGA                    TC  CCCACCTCGGCT CCC AAGT
                                  ||  |||||||||||| ||| ||||
                                  AG  GGGTGGAGTCGA GGG TTCA
                                    AC          A   G
GAM219  FLJ13456  3' ACTTTGGGAGGCCGAGGTGGGT 66523              _
           GGA                    TCCACCCACCTCGGC TCCCAAAGT
                                  |||||||||||||| |||||||||
                                  AGGTGGGTGGAGCCG AGGGTTTCA
                                        G
GAM219  FLJ13456  3' GGGAGGCCGAGGCGGGCAGA  66554    CA   A     _
                                  TC  CCC CCTCGGC TCCC
                                  ||  ||| ||||||| ||||
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                                AG  GGG GGAGCCG AGGG
                                 AC   C      G
GAM219  FLJ13544  3' ACTTTGGGAGGCCAAGGCAGG  47204    CA   C  _
                                CC  CCT GGC TCCCAAAGT
                                ||  ||| ||| |||||||||
                                GG  GGA CCG AGGGTTTCA
                                 AC   A   G
GAM219  FLJ13621  3' ACTTTGGGAGGCCGAGGCGGGT 47214         A      _
           GGA                    TCCACCC CCTCGGC TCCCAAAGT
                                  ||||||| ||||||| |||||||||
                                  AGGTGGG GGAGCCG AGGGTTTCA
                                     C      G
GAM219  FLJ13659  3' ACTTTGGGAGGCTGAGACGGGT 48026       AC     _
           G                       CACCC  CTCGGC TCCCAAAGT
                                   |||||  |||||| |||||||||
                                   GTGGG  GAGTCG AGGGTTTCA
                                      CA     G
GAM219  FLJ13769  3' ACTTTGGGAGGCCAAGGTGGGT 47238    C       C  _
           AGA                     TC ACCCACCT GGC TCCCAAAGT
                                   || |||||||| ||| |||||||||
                                   AG TGGGTGGA CCG AGGGTTTCA
                                    A       A   G
GAM219  FLJ13848  3' ACTTTGGGAGGCTGAGGCAGGC 45814     A  CA      _
           GGG                      TCC CC  CCTCGGC TCCCAAAGT
                                    ||| ||  ||||||| |||||||||
                                    GGG GG  GGAGTCG AGGGTTTCA
                                     C  AC      G
GAM219  FLJ13952  3' ACTTTGGGAGGCCAAGATGGGT 46001         C  C  _
           GGA                      TCCACCCA CT GGC TCCCAAAGT
                                    |||||||| || ||| |||||||||
                                    AGGTGGGT GA CCG AGGGTTTCA
                                       A  A   G
GAM219  FLJ13984  3' ACTTTGGGGGGCTGAGGCAGGC 45799    CA  CA         _
           AGA                      TC  CC  CCTCGGCTCCC AAAGT
                                    ||  ||  |||||||||||| |||||
                                    AG  GG  GGAGTCGGGGG TTTCA
                                     AC  AC          G
GAM219  FLJ14011  3' ACTTTGGGAGGCTGAGACAGGC 42311    A  CAC     _
           GG                       CC CC   CTCGGC TCCCAAAGT
                                    || ||   ||||||| |||||||||
                                    GG GG   GAGTCG AGGGTTTCA
                                     C  ACA     G
GAM219  FLJ14100  3' ACTTTGGGAGGCTGAGGCGGGC 47326     A  A     _
           GGA                      TCC CCC CCTCGGC TCCCAAAGT
                                    ||| ||| ||||||| |||||||||
                                    AGG GGG GGAGTCG AGGGTTTCA
                                     C  C      G
GAM219  FLJ14107  3' ACTTTGGGAGGCCAAGGCAGG  47343    CA   C  _
                                CC  CCT GGC TCCCAAAGT
                                ||  ||| ||| |||||||||
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                                GG  GGA CCG AGGGTTTCA
                                 AC   A   G
GAM219  FLJ14117 3' ACTTTGGGAGGCCAAGGTGGGC 43213    A      C  _
            GG                    CC CCCACCT GGC TCCCAAAGT
                                || ||||||| ||| |||||||||
                                GG GGGTGGA CCG AGGGTTTCA
                                 C      A   G
GAM219  FLJ14117 3' ACTTTGGGAGGCCGAGGCAGGC 43214     A  CA      _
            GGA                    TCC CC  CCTCGGC TCCCAAAGT
                                ||| ||  ||||||| |||||||||
                                AGG GG  GGAGCCG AGGGTTTCA
                                 C  AC      G
GAM219  FLJ14117 3' ACTTTGGGATGCTGAGGCGGGC 43215    A   A     _
            GG                    CC CCC CCTCGGC TCCCAAAGT
                                || ||| ||||||| |||||||||
                                GG GGG GGAGTCG AGGGTTTCA
                                 C  C      T
GAM219  FLJ14129 3' ACTTTGGGAGGCCGAGGCGGGC 48804     A   A     _
            GGA                    TCC CCC CCTCGGC TCCCAAAGT
                                ||| ||| ||||||| |||||||||
                                AGG GGG GGAGCCG AGGGTTTCA
                                 C  C      G
GAM219  FLJ14225 3' ACTTTGGGAGGCCGAGGCGGGC 46381     A   A     _
            GGA                    TCC CCC CCTCGGC TCCCAAAGT
                                ||| ||| ||||||| |||||||||
                                AGG GGG GGAGCCG AGGGTTTCA
                                 C  C      G
GAM219  FLJ14251 3' ACTTTGGGAGGCCAAGATGGGC 46470    A   C  C  _
            GG                    CC CCCA CT GGC TCCCAAAGT
                                || |||| || ||| |||||||||
                                GG GGGT GA CCG AGGGTTTCA
                                 C   A  A   G
GAM219  FLJ14251 3' ACTTTGGGAGGCTGAGGTGGGT 46471              _
            GGA                    TCCACCCACCTCGGC TCCCAAAGT
                                |||||||||||||| |||||||||
                                AGGTGGGTGGAGTCG AGGGTTTCA
                                        G
GAM219  FLJ14280 3' ACTGTGGGAGGCCGAGGCGGGC 46518     A   A     _    A
            GGA                    TCC CCC CCTCGGC TCCCA AGT
                                ||| ||| ||||||| ||||| |||
                                AGG GGG GGAGCCG AGGGT TCA
                                 C  C      G    G
GAM219  FLJ14327 3' ACTTCGGGAGGCCGAGGCAGGT 46670        CA     _   A
            GGA                    TCCACC  CCTCGGC TCCC AAGT
                                ||||||  ||||||| |||| ||||
                                AGGTGG  GGAGCCG AGGG TTCA
                                   AC      G   C
GAM219  FLJ14345 3' ACTTTGGGAGGCCGAGGCAGGG 45653     A   A_     _
            GGA                    TCC CCC  CCTCGGC TCCCAAAGT
                                ||| |||  ||||||| |||||||||
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                                AGG GGG  GGAGCCG AGGGTTTCA
                                  _  AC      G
GAM219  FLJ14346 3' ACTTTGGGAAGTCAAGGCAGGT 47353      CA  C   _
            GG                    CCACC  CCT GGCT CCCAAAGT
                                  |||||  ||| |||| ||||||||
                                  GGTGG  GGA CTGA GGGTTTCA
                                    AC  A   A
GAM219  FLJ14346 3' ACTTTGGGAGGCCGAGGCGGGC 47354    A  A     _
            GGA                   TCC CCC CCTCGGC TCCCAAAGT
                                  ||| ||| ||||||| |||||||||
                                  AGG GGG GGAGCCG AGGGTTTCA
                                    C  C      G
GAM219  FLJ14397 3' ACTTTGGGAGACCGAGGCAGGC 52310    A  CA    _
            GG                    CC CC  CCTCGG CTCCCAAAGT
                                  || ||  |||||| ||||||||||
                                  GG GG  GGAGCC GAGGGTTTCA
                                   C  AC     A
GAM219  FLJ14397 3' ACTTTGGGAGGCTGAGGCAGGC 52311    A  CA     _
            GGA                   TCC CC  CCTCGGC TCCCAAAGT
                                  ||| ||  ||||||| |||||||||
                                  AGG GG  GGAGTCG AGGGTTTCA
                                    C  AC      G
GAM219  FLJ14457 3' ACTTTGGGAGGCCGAGGCGG   52399    A     _
                                  CC CCTCGGC TCCCAAAGT
                                  || ||||||| |||||||||
                                  GG GGAGCCG AGGGTTTCA
                                   C      G
GAM219  FLJ14600 3' CTTTGAATGGTGGGGTGGA   52526       _  TCGGCTCC
                                  TCCACCC ACC       CAAAG
                                  ||||||| |||       |||||
                                  AGGTGGG TGG       GTTTC
                                     G   TAA_____
GAM219  FLJ14621 3' ACTTTGGGAGGCTGAGGCGGGT 52531       A     _
            GGA                   TCCACCC CCTCGGC TCCCAAAGT
                                  ||||||| ||||||| |||||||||
                                  AGGTGGG GGAGTCG AGGGTTTCA
                                     C      G
GAM219  FLJ20004 3' ACTTTGGGAGGCCGAGGCGGGC 34744    CA  A     _
            AGA                   TC  CCC CCTCGGC TCCCAAAGT
                                  ||  ||| ||||||| |||||||||
                                  AG  GGG GGAGCCG AGGGTTTCA
                                   AC  C      G
GAM219  FLJ20004 3' ACTTTGGGAGGCCAAGATGGGC 96994    A   C  C  _
            GG                    CC CCCA CT GGC TCCCAAAGT
                                  || |||| || ||| |||||||||
                                  GG GGGT GA CCG AGGGTTTCA
                                   C   A  A  G
GAM219  FLJ20013 3' ACTTTGGGAGGCTGAGGTGGGC 34792     A       _
            GGA                   TCC CCCACCTCGGC TCCCAAAGT
                                  ||| |||||||||| |||||||||
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                                AGG GGGTGGAGTCG AGGGTTTCA
                                  C         G
GAM219  FLJ20019  3'  ACTTTGGGAGGCTGAGGATGG  34811    _     _
                                CCA CCTCGGC TCCCAAAGT
                                ||| ||||||| |||||||||
                                GGT GGAGTCG AGGGTTTCA
                                  A      G
GAM219  FLJ20045  3'  ACTTTGGGAGGCTGAGGTAGGT 34870       C      _
          GGA                     TCCACC ACCTCGGC TCCCAAAGT
                                ||||||| |||||||| |||||||||
                                AGGTGG TGGAGTCG AGGGTTTCA
                                   A       G
GAM219  FLJ20055  3'  ACTTTAGGAGGCCGAGGCTGG  34902    _      TC  _
                                CCA CCTCGGC  CC AAAGT
                                ||| |||||||  || |||||
                                GGT GGAGCCG  GG TTTCA
                                  C      GA  A
GAM219  FLJ20059  3'  ACTTTGGGAGGCCGAGGTGG   34918          _
                                CCACCTCGGC TCCCAAAGT
                                |||||||||| |||||||||
                                GGTGGAGCCG AGGGTTTCA
                                      G
GAM219  FLJ20059  3'  ACTTTGGGAGGCTGAGGCAGG  34919    CA     _
                                CC  CCTCGGC TCCCAAAGT
                                ||  ||||||| |||||||||
                                GG  GGAGTCG AGGGTTTCA
                                 AC      G
GAM219  FLJ20069  3'  ACCTTGGGAGGCTGAGGCAGGT 34944       CA     _    A
          GGA                     TCCACC  CCTCGGC TCCCAA GT
                                ||||||  ||||||| |||||| ||
                                AGGTGG  GGAGTCG AGGGTT CA
                                   AC      G     C
GAM219  FLJ20211  3'  ACTTTGGGAGGCCGAGGTGGGC 35253     A        _
          GGA                     TCC CCCACCTCGGC TCCCAAAGT
                                ||| |||||||||| |||||||||
                                AGG GGGTGGAGCCG AGGGTTTCA
                                  C         G
GAM219  FLJ20280  3'  ACTTTGGGAGGCTGAGGCGGGT 35324       A     _
          GGA                     TCCACCC CCTCGGC TCCCAAAGT
                                ||||||| ||||||| |||||||||
                                AGGTGGG GGAGTCG AGGGTTTCA
                                    C      G
GAM219  FLJ20340  3'  ACTTTGCGGGGCCGAGGCAGGG 35448    A  CA       _
          GA                      TCC CC  CCTCGGCTCC CAAAGT
                                ||| ||  |||||||||| ||||||
                                AGG GG  GGAGCCGGGG GTTTCA
                                  _ AC        C
GAM219  FLJ20359  3'  ACTTTGGGAGGCCGAGGCAGG  35511    CA     _
                                CC  CCTCGGC TCCCAAAGT
                                ||  ||||||| |||||||||
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                                GG  GGAGCCG AGGGTTTCA
                                 AC      G
GAM219  FLJ20413  3' ACTTCGGGAAGCTGAGGCGGGC 35588     A  A      _  A
             GGA                  TCC CCC CCTCGGCT CCC AAGT
                                  ||| ||| |||||||| ||| ||||
                                  AGG GGG GGAGTCGA GGG TTCA
                                    C  C       A  C
GAM219  FLJ20456  3' ACTTTGGGAGGCTGAGGCAGGC 35660     A  CA     _
             GGA                  TCC CC  CCTCGGC TCCCAAAGT
                                  ||| ||  ||||||| |||||||||
                                  AGG GG  GGAGTCG AGGGTTTCA
                                    C  AC      G
GAM219  FLJ20464  3' ACTTTGGGAGGCTGAGGCGGGC 35680     A  A     _
             GGA                  TCC CCC CCTCGGC TCCCAAAGT
                                  ||| ||| ||||||| |||||||||
                                  AGG GGG GGAGTCG AGGGTTTCA
                                    C  C      G
GAM219  FLJ20464  3' ACTTTGGGAGGTCGAGGCAGGC 35681     A  CA     _
             GGA                  TCC CC  CCTCGGC TCCCAAAGT
                                  ||| ||  ||||||| |||||||||
                                  AGG GG  GGAGCTG AGGGTTTCA
                                    C  AC      G
GAM219  FLJ20686  3' TACTTTGGGAGGCTGAGCAAGG 35956          ____   _      ___
             TGGGTGGA               TCCACCCACC   TCGGC TCCCAAAGT  A
                                  ||||||||||   ||||| |||||||||  |
                                  AGGTGGGTGG   AGTCG AGGGTTTCA  T
                                       AACG    G      ___
GAM219  FLJ20694  3' ACTTTGGGAAGCCAAGGTGGGC 35968    A     C   _
             GG                   CC CCCACCT GGCT CCCAAAGT
                                  || ||||||| |||| ||||||||
                                  GG GGGTGGA CCGA GGGTTTCA
                                    C      A   A
GAM219  FLJ20695  3' ACTTTGGGAGGCCAAGGTGGGT 35982         C  _
             G                    CACCCACCT GGC TCCCAAAGT
                                  ||||||||| ||| |||||||||
                                  GTGGGTGGA CCG AGGGTTTCA
                                       A  G
GAM219  FLJ20700  3' ACTTTGGGAGGCCGAGGCGGGC 35994    CA  A     _
             AGA                  TC  CCC CCTCGGC TCCCAAAGT
                                  ||  ||| ||||||| |||||||||
                                  AG  GGG GGAGCCG AGGGTTTCA
                                    AC  C      G
GAM219  FLJ20808  3' ACTTTGGGAGGCTGAGGTGGGC 36116    CA        _
             AGA                  TC  CCCACCTCGGC TCCCAAAGT
                                  ||  |||||||||| |||||||||
                                  AG  GGGTGGAGTCG AGGGTTTCA
                                    AC         G
GAM219  FLJ20825  3' ACTTTGGAAGGCTGAGGCGGGC 36139    CA  A      C_
             AGA                  TC  CCC CCTCGGCT  CCAAAGT
                                  ||  ||| ||||||||  |||||||
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                                AG  GGG GGAGTCGG  GGTTTCA
                                 AC  C       AA
GAM219  FLJ20972  3'  ACTTTGGGAGGCCAAGGTGGGC 47377    A     C  _
            GG                    CC CCCACCT GGC TCCCAAAGT
                                  || ||||||| ||| |||||||||
                                  GG GGGTGGA CCG AGGGTTTCA
                                   C      A  G
GAM219  FLJ21144  3'  ACTTTGGGAAGCTGAGATGGGT 43186         C     _
            GGA                     TCCACCCA CTCGGCT CCCAAAGT
                                  |||||||| ||||||| ||||||||
                                  AGGTGGGT GAGTCGA GGGTTTCA
                                      A      A
GAM219  FLJ21162  3'  ACTTTGGGAGGCTGAGGCAGGT 46364       CA     _
            GGA                     TCCACC  CCTCGGC TCCCAAAGT
                                  ||||||  ||||||| |||||||||
                                  AGGTGG  GGAGTCG AGGGTTTCA
                                     AC      G
GAM219  FLJ21240  3'  ACTTTGGGAGGCCGAGGCAGGC 46258     A  CA     _
            GGA                     TCC CC  CCTCGGC TCCCAAAGT
                                  ||| ||  ||||||| |||||||||
                                  AGG GG  GGAGCCG AGGGTTTCA
                                   C  AC      G
GAM219  FLJ21369  3'  ACTTTGGGAGGCTGAAGCGGGT 46046       ACC    _
            GG                      CCACCC   TCGGC TCCCAAAGT
                                  ||||||   ||||| |||||||||
                                  GGTGGG   AGTCG AGGGTTTCA
                                     CGA    G
GAM219  FLJ21551  3'  ACTTTGGGAGGCTGAGGCAGGT 46026       CA     _
            GGA                     TCCACC  CCTCGGC TCCCAAAGT
                                  ||||||  ||||||| |||||||||
                                  AGGTGG  GGAGTCG AGGGTTTCA
                                     AC      G
GAM219  FLJ21657  3'  ACTTTGGGAGGCCGAGGCAGGC 42793    A_  CA     _
            AGG                     CC  CC  CCTCGGC TCCCAAAGT
                                  ||  ||  ||||||| |||||||||
                                  GG  GG  GGAGCCG AGGGTTTCA
                                   AC  AC      G
GAM219  FLJ21687  3'  ACTTTGGGAGGCCGAGGCTGGT 46287       CA     _
            GGA                     TCCACC  CCTCGGC TCCCAAAGT
                                  ||||||  ||||||| |||||||||
                                  AGGTGG  GGAGCCG AGGGTTTCA
                                     TC      G
GAM219  FLJ21870  3'  ACTTTGGGAGGCCGAGGCAGGT 43740       CA     _
            GGA                     TCCACC  CCTCGGC TCCCAAAGT
                                  ||||||  ||||||| |||||||||
                                  AGGTGG  GGAGCCG AGGGTTTCA
                                     AC      G
GAM219  FLJ22009  3'  ACTTTGGGAGGCTGAGGCAGGA 60915     A  CA     _
            GGA                     TCC CC  CCTCGGC TCCCAAAGT
                                  ||| ||  ||||||| |||||||||
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                                AGG GG  GGAGTCG AGGGTTTCA
                                  A AC      G
GAM219  FLJ22313  3' ACTTTGGGAGGCCGAGGCGGGT 42574        A     _
             GGG                   TCCACCC CCTCGGC TCCCAAAGT
                                |||||||  |||||||  |||||||||
                                GGGTGGG GGAGCCG AGGGTTTCA
                                   C      G
GAM219  FLJ22692  3' ACTCTGGAGGCTGAGGCAGG   47475    CA      TC   A
                                CC  CCTCGGC  CCA AGT
                                ||  |||||||  |||  |||
                                GG  GGAGTCG  GGT TCA
                                 AC      GA   C
GAM219  FLJ22692  3' ACTTTGGGAGGCCGAGGCAGGC 47476     A  CA      _
             GGA                   TCC CC  CCTCGGC TCCCAAAGT
                                |||  ||  |||||||  |||||||||
                                AGG GG  GGAGCCG AGGGTTTCA
                                  C  AC      G
GAM219  FLJ22814  3' ACTTTGGAAGGCCGAGGCGGGG 46709     A   A      C_
             GGA                   TCC CCC CCTCGGCT  CCAAAGT
                                |||  |||  ||||||||  |||||||
                                AGG GGG GGAGCCGG  GGTTTCA
                                  G   C       AA
GAM219  FLJ23040  3' ACTTTGGGAGGCCACGGCAGGT 47980       CA  TC   _
             GG                    CCACC  CC  GGC TCCCAAAGT
                                |||||  ||  |||  |||||||||
                                GGTGG  GG  CCG AGGGTTTCA
                                   AC  CA   G
GAM219  FLJ23042  3' ACTTTGGGAGGCCGAGGCGGGC 47932     A   A      _
             GGA                   TCC CCC CCTCGGC TCCCAAAGT
                                |||  |||  |||||||  |||||||||
                                AGG GGG GGAGCCG AGGGTTTCA
                                  C   C      G
GAM219  FLJ23042  3' ACTTTGGGAGGCTGAGGCAAGA 47933     ACCCA      _
             GGA                   TCC     CCTCGGC TCCCAAAGT
                                |||     |||||||  |||||||||
                                AGG     GGAGTCG AGGGTTTCA
                                  AGAAC       G
GAM219  FLJ23112  3' ACTTTGGGAGGCCGAGGCGGGT 46807        A     _
             GGA                   TCCACCC CCTCGGC TCCCAAAGT
                                |||||||  |||||||  |||||||||
                                AGGTGGG GGAGCCG AGGGTTTCA
                                   C      G
GAM219  FLJ23120  3' ACTTTGGGAGGCTGAGGCGGGT 86323        A     _
             GGA                   TCCACCC CCTCGGC TCCCAAAGT
                                |||||||  |||||||  |||||||||
                                AGGTGGG GGAGTCG AGGGTTTCA
                                   C      G
GAM219  FLJ23235  3' ACTTTGGGATTCTGAGGTGGGA 46873     A        C_
             GGA                   TCC CCCACCTCGG  TCCCAAAGT
                                |||  ||||||||||  |||||||||
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                                AGG GGGTGGAGTC  AGGGTTTCA
                                  A         TT
GAM219  FLJ23360  3' CTTTGGGAGGCGGGTGG     43829       T  G
                                CCACC CG CTCCCAAAG
                                ||||| || |||||||||
                                GGTGG GC GAGGGTTTC
                                  _ G
GAM219  FLJ23447  3' ACTTTGGGGAGCCAAGGCAGG  46128    CA   C      _
                                CC  CCT GGCTCCC AAAGT
                                ||  ||| ||||||| |||||
                                GG  GGA CCGAGGG TTTCA
                                 AC   A      G
GAM219  FLJ23499  3' ACTTTGGGAGGCCGAGGCAGGT 43123        CA      _
           GGA                    TCCACC  CCTCGGC TCCCAAAGT
                                |||||| |||||||| |||||||||
                                AGGTGG  GGAGCCG AGGGTTTCA
                                   AC       G
GAM219  FLJ23499  3' ACTTTGGGAGGCTGAGGCAGGA 43124     A  CA      _
           GGA                    TCC CC  CCTCGGC TCCCAAAGT
                                ||| ||  |||||||| |||||||||
                                AGG GG  GGAGTCG AGGGTTTCA
                                  A  AC       G
GAM219  FLJ23499  3' ACTTTGGGAGGCTGAGGTGGGT 43125              _
           GGA                    TCCACCCACCTCGGC TCCCAAAGT
                                |||||||||||||| |||||||||
                                AGGTGGGTGGAGTCG AGGGTTTCA
                                       G
GAM219  FLJ23556  3' ACTTTGGGAGGCTGAGGCAGAA 46421     ACCCA      _
           GGA                    TCC     CCTCGGC TCCCAAAGT
                                |||     |||||||| |||||||||
                                AGG     GGAGTCG AGGGTTTCA
                                  AAGAC       G
GAM219  FLJ23878  3' ACTTTGGGAGGCTGAGGCGGGC 59365    CA   A      _
           AGA                    TC  CCC CCTCGGC TCCCAAAGT
                                ||  ||| ||||||| |||||||||
                                AG  GGG GGAGTCG AGGGTTTCA
                                 AC   C      G
GAM219  FLJ25012  3' ACTTTGGGAGGCCGAGGCAGGT 58706        CA      _
           GGA                    TCCACC  CCTCGGC TCCCAAAGT
                                |||||| |||||||| |||||||||
                                AGGTGG  GGAGCCG AGGGTTTCA
                                   AC       G
GAM219  FLJ30681  3' ACTTTGGGAGGCTGAGGCGGGG 93429    CA   A      _
           AGA                    TC  CCC CCTCGGC TCCCAAAGT
                                ||  ||| ||||||| |||||||||
                                AG  GGG GGAGTCG AGGGTTTCA
                                 AG   C      G
GAM219  FLJ31455  3' ACTTTGGGAGGCTGAGGTGAGT 59278       C       _
           GGA                    TCCAC CACCTCGGC TCCCAAAGT
                                ||||| ||||||||| |||||||||
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                                AGGTG GTGGAGTCG AGGGTTTCA
                                  A       G
GAM219  FLJ31737  3'  ACTTTGGGAGGCCGAGGTGGGT 59344            _
          GGA                   TCCACCCACCTCGGC TCCCAAAGT
                                |||||||||||||| |||||||||
                                AGGTGGGTGGAGCCG AGGGTTTCA
                                       G
GAM219  FRSB    3'  ACTTTGGGAGGCTGAGGTGGGC 20286    CA       _
          AGA                   TC  CCCACCTCGGC TCCCAAAGT
                                ||  |||||||||| |||||||||
                                AG  GGGTGGAGTCG AGGGTTTCA
                                 AC         G
GAM219  FUSIP1   3'  ACTTTGGGAGGCCGAGGCGGGC 55032    A  A     _
          GGA                   TCC CCC CCTCGGC TCCCAAAGT
                                ||| ||| ||||||| |||||||||
                                AGG GGG GGAGCCG AGGGTTTCA
                                  C  C      G
GAM219  GALNT6   3'  ACTTTGGGAGGCCAAGGCAGGT 24237      CA  C  _
          GG                    CCACC  CCT GGC TCCCAAAGT
                                |||||  ||| ||| |||||||||
                                GGTGG  GGA CCG AGGGTTTCA
                                  AC  A  G
GAM219  GAPCENA  3'  ACTTCAAAAGGCTGGGGTGGGT 25175            CCCA_
          G                     CACCCACCTCGGCT    AAGT
                                |||||||||||||    ||||
                                GTGGGTGGGGTCGG    TTCA
                                      AAAAC
GAM219  GLTP    3'  ACTTTGGGAGGCTGAGGCGGGT 33578       A     _
          GGA                   TCCACCC CCTCGGC TCCCAAAGT
                                ||||||| ||||||| |||||||||
                                AGGTGGG GGAGTCG AGGGTTTCA
                                   C      G
GAM219  GP5     3'  ACTTTGGGAGGCTGAGGTGGGT 16858           _
          GGA                   TCCACCCACCTCGGC TCCCAAAGT
                                |||||||||||||| |||||||||
                                AGGTGGGTGGAGTCG AGGGTTTCA
                                       G
GAM219  GTPBP5   3'  ACTTTGGGAGGCCGAGGCTGGT 65964       CA     _
          GGA                   TCCACC  CCTCGGC TCCCAAAGT
                                ||||||  ||||||| |||||||||
                                AGGTGG  GGAGCCG AGGGTTTCA
                                   TC      G
GAM219  HES2    3'  ACTTTGGGAGGCCGAGGCGGGC 39367    CA  A     _
          AGA                   TC  CCC CCTCGGC TCCCAAAGT
                                ||  ||| ||||||| |||||||||
                                AG  GGG GGAGCCG AGGGTTTCA
                                 AC  C      G
GAM219  HIG2    3'  ACTTTGGGAGGCTGAGGTGGGT 26194           _
          GGA                   TCCACCCACCTCGGC TCCCAAAGT
                                |||||||||||||| |||||||||
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                                AGGTGGGTGGAGTCG AGGGTTTCA
                                      G
GAM219  HRH4     3'  ACTTTGGGAGGCCAAGGTGGGC 41521    A      C  _
             GG                  CC CCCACCT GGC TCCCAAAGT
                                 || ||||||| ||| |||||||||
                                 GG GGGTGGA CCG AGGGTTTCA
                                  C      A  G
GAM219  HSA250303 3'  ACTTTGGGAGGCCGAGGTGGGC 38017     A         _
             GGG                   TCC CCCACCTCGGC TCCCAAAGT
                                   ||| |||||||||| |||||||||
                                   GGG GGGTGGAGCCG AGGGTTTCA
                                    C         G
GAM219  HSH2     3'  ACTCTGTGGGGCCGAGGCAGGC 52734    CA  CA        _ A
             AGA                   TC  CC  CCTCGGCTCC CA AGT
                                   ||  ||  |||||||||| || |||
                                   AG  GG  GGAGCCGGGG GT TCA
                                    AC  AC        T  C
GAM219  HSPC031  3'  ACTTTGGGAGGCCAAGGCGGAC 32745    AC  A   C  _
             GG                    CC  CC CCT GGC TCCCAAAGT
                                   ||  || ||| ||| |||||||||
                                   GG  GG GGA CCG AGGGTTTCA
                                    CA  C   A   G
GAM219  HSPC043  3'  ACTTTGGGAGGCCAAGGCGGG  68345     A   C  _
                                   CCC CCT GGC TCCCAAAGT
                                   ||| ||| ||| |||||||||
                                   GGG GGA CCG AGGGTTTCA
                                     C   A   G
GAM219  HYPK     3'  ACTTTGGGAGGTCGAGGCAGGT 33511    C   CA     _
             AGA                   TC ACC  CCTCGGC TCCCAAAGT
                                   || |||  ||||||| |||||||||
                                   AG TGG  GGAGCTG AGGGTTTCA
                                    A  AC      G
GAM219  ICAM4    3'  ACTTTGGGAGGCCGAGGCAGG  9531     CA     _
                                   CC  CCTCGGC TCCCAAAGT
                                   ||  ||||||| |||||||||
                                   GG  GGAGCCG AGGGTTTCA
                                    AC      G
GAM219  ICAM4    3'  ACTTTGGGAGGCCGAGGCAGG  42587    CA     _
                                   CC  CCTCGGC TCCCAAAGT
                                   ||  ||||||| |||||||||
                                   GG  GGAGCCG AGGGTTTCA
                                    AC      G
GAM219  IL-23R   3'  ACTTTGGTAGGCTGAGGTGGGT 59126              C_
             GGA                   TCCACCCACCTCGGCT  CCAAAGT
                                   ||||||||||||||||  |||||||
                                   AGGTGGGTGGAGTCGG  GGTTTCA
                                             AT
GAM219  KCNH6    3'  ACTTTGGGAGGCCGAGGCGGGC 48567    A  A     _
             GGA                   TCC CCC CCTCGGC TCCCAAAGT
                                   ||| ||| ||||||| |||||||||
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                                AGG GGG GGAGCCG AGGGTTTCA
                                  C  C     G
GAM219  KIAA0057 3' ACTTTGGGAGGTCGAGGTGGGC 25398    CA       _
            AGA                   TC  CCCACCTCGGC TCCCAAAGT
                                ||  |||||||||||| |||||||||
                                AG  GGGTGGAGCTG AGGGTTTCA
                                 AC         G
GAM219  KIAA0090 3' ACTTTGGGAGGCCAAGGCAGG  89808    CA  C  _
                                CC  CCT GGC TCCCAAAGT
                                ||  ||| ||| |||||||||
                                GG  GGA CCG AGGGTTTCA
                                 AC  A  G
GAM219  KIAA0186 3' ACTTTGGGAGGCCTAGATGGGT 41091        C  C  _
            GGA                   TCCACCCA CT GGC TCCCAAAGT
                                |||||||| || ||| |||||||||
                                AGGTGGGT GA CCG AGGGTTTCA
                                    A  T  G
GAM219  KIAA0252 3' ACTTTGGGAGGCCTAGGCGGGT 63449       A  C  _
            GG                    CCACCC CCT GGC TCCCAAAGT
                                |||||| ||| ||| |||||||||
                                GGTGGG GGA CCG AGGGTTTCA
                                   C  T  G
GAM219  KIAA0255 5' ACTCCGGGAGCGGGAGCTGG  29128    C  G_    AA
                                CCA CTC  GCTCCC  AGT
                                ||| |||  ||||||  |||
                                GGT GAG  CGAGGG  TCA
                                  C  GG    CC
GAM219  KIAA0266 3' ACTTTGGGAGGCCGAGATGGGT 41632        C    _
            GGA                   TCCACCCA CTCGGC TCCCAAAGT
                                |||||||| |||||| |||||||||
                                AGGTGGGT GAGCCG AGGGTTTCA
                                    A    G
GAM219  KIAA0266 3' ACTTTGGGAGGCCGAGATGGGT 41633        C    _
            GGA                   TCCACCCA CTCGGC TCCCAAAGT
                                |||||||| |||||| |||||||||
                                AGGTGGGT GAGCCG AGGGTTTCA
                                    A    G
GAM219  KIAA0355 3' ACTTTGGGAGGCCGAGGCAGGT 28697       CA     _
            GGA                   TCCACC  CCTCGGC TCCCAAAGT
                                ||||||  ||||||| |||||||||
                                AGGTGG  GGAGCCG AGGGTTTCA
                                   AC     G
GAM219  KIAA0391 3' ACTTTGGGAGGCCAAATGGG  28596     CCTC  _
                                CCCA   GGC TCCCAAAGT
                                ||||   ||| |||||||||
                                GGGT   CCG AGGGTTTCA
                                  AAA_  G
GAM219  KIAA0441 3' ACTTTGGGAGGCCAAGGTGGGC 29621    A     C  _
            GG                    CC CCCACCT GGC TCCCAAAGT
                                || ||||||| ||| |||||||||
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                                GG GGGTGGA CCG AGGGTTTCA
                                 C      A  G
GAM219  KIAA0446 5' ACTTTGGGAAGCCGAGGCGGGT 69438        A      _
              GGA                 TCCACCC CCTCGGCT CCCAAAGT
                                  ||||||| |||||||| ||||||||
                                  AGGTGGG GGAGCCGA GGGTTTCA
                                     C       A
GAM219  KIAA0472 3' ACTTTGGGAGGCTGAGGCGGGC 72331     A  A     _
              GGA                 TCC CCC CCTCGGC TCCCAAAGT
                                  ||| ||| ||||||| |||||||||
                                  AGG GGG GGAGTCG AGGGTTTCA
                                   C  C      G
GAM219  KIAA0514 3' ACTTTGGGAGGCTGAGGTGGGC 28736   _        _
              TG                  CA CCCACCTCGGC TCCCAAAGT
                                  || |||||||||| |||||||||
                                  GT GGGTGGAGTCG AGGGTTTCA
                                   C         G
GAM219  KIAA0544 3' ACTTTGGGAGACCGAGGGG   71455    A    _
                                  CC CCTCGG CTCCCAAAGT
                                  || |||||| ||||||||||
                                  GG GGAGCC GAGGGTTTCA
                                   _     A
GAM219  KIAA0557 3' ACTTTGGGAGGCCGAGGCAGGT 78541       CA     _
              GGA                 TCCACC  CCTCGGC TCCCAAAGT
                                  ||||||  ||||||| |||||||||
                                  AGGTGG  GGAGCCG AGGGTTTCA
                                     AC      G
GAM219  KIAA0563 3' ACTTTGGGAGGCCGAGGCGGGC 29865     A  A     _
              GGA                 TCC CCC CCTCGGC TCCCAAAGT
                                  ||| ||| ||||||| |||||||||
                                  AGG GGG GGAGCCG AGGGTTTCA
                                   C  C      G
GAM219  KIAA0565 3' ACTTTGGGAGGCCAAGGTGGGT 67429          C  _
              GGA                 TCCACCCACCT GGC TCCCAAAGT
                                  |||||||||| ||| |||||||||
                                  AGGTGGGTGGA CCG AGGGTTTCA
                                        A  G
GAM219  KIAA0570 3' ACTTTGAGTGGCTGAGGTGGGT 28847             CC_
              GGA                 TCCACCCACCTCGGCT   CAAAGT
                                  ||||||||||||||||   ||||||
                                  AGGTGGGTGGAGTCGG   GTTTCA
                                           TGA
GAM219  KIAA0596 3' ACTTTGGGAGGCCGAGGCGGGT 63478       A     _
              GGA                 TCCACCC CCTCGGC TCCCAAAGT
                                  ||||||| ||||||| |||||||||
                                  AGGTGGG GGAGCCG AGGGTTTCA
                                     C      G
GAM219  KIAA0628 3' ACTTTGGGAGGCCGAGGCGGGC 29525     A  A     _
              GGA                 TCC CCC CCTCGGC TCCCAAAGT
                                  ||| ||| ||||||| |||||||||
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                                AGG GGG GGAGCCG AGGGTTTCA
                                  C  C     G
GAM219  KIAA0635  3'  ACTTTGGGAGGCCGAGGCGAGT 28408      CCA     _
            GGA                   TCCAC  CCTCGGC TCCCAAAGT
                                |||||  ||||||| |||||||||
                                AGGTG  GGAGCCG AGGGTTTCA
                                   AGC     G
GAM219  KIAA0694  3'  ACTTTGGGAGGCCAAGACAGGC 72961    A  CAC  C  _
            GG                    CC CC  CT GGC TCCCAAAGT
                                || ||  || ||| |||||||||
                                GG GG  GA CCG AGGGTTTCA
                                 C ACA A  G
GAM219  KIAA0794  3'  ACTTTGGGAGGCGGAGGTGGGC 81221    CA      G  _
            AGA                   TC  CCCACCTC GC TCCCAAAGT
                                ||  |||||||| || |||||||||
                                AG  GGGTGGAG CG AGGGTTTCA
                                 AC       G  G
GAM219  KIAA0798  3'  ACTTTGGGAGGCCAAGGTGGGT 28438          C  _
            GGA                   TCCACCCACCT GGC TCCCAAAGT
                                ||||||||||| ||| |||||||||
                                AGGTGGGTGGA CCG AGGGTTTCA
                                      A  G
GAM219  KIAA0825  3'  ACTTTGGGAGGCCAAAGTGGG  61679      CTC  _
                                CCCAC  GGC TCCCAAAGT
                                |||||  ||| |||||||||
                                GGGTG  CCG AGGGTTTCA
                                   AAA  G
GAM219  KIAA0831  5'  ACTTTGGGAGGCCAAGACAGGT 30623      CAC  C  _
            GG                    CCACC  CT GGC TCCCAAAGT
                                |||||  || ||| |||||||||
                                GGTGG  GA CCG AGGGTTTCA
                                   ACA  A  G
GAM219  KIAA0831  3'  ACTTTGGGAGGCCGAGGCAGGC 30624    A  CA     _
            GGA                   TCC CC  CCTCGGC TCCCAAAGT
                                ||| ||  ||||||| |||||||||
                                AGG GG  GGAGCCG AGGGTTTCA
                                  C  AC     G
GAM219  KIAA0872  3'  ACTTTGGAAGGCCGAGGCGGGT 30735       A      C_
            GGG                   TCCACCC CCTCGGCT  CCAAAGT
                                |||||||  ||||||||  |||||||
                                GGGTGGG GGAGCCGG  GGTTTCA
                                    C       AA
GAM219  KIAA0872  3'  ACTTTGGGAGGCCGAGGCGGGC 30736    CA  A     _
            AGA                   TC  CCC CCTCGGC TCCCAAAGT
                                ||  ||| ||||||| |||||||||
                                AG  GGG GGAGCCG AGGGTTTCA
                                 AC  C     G
GAM219  KIAA0884  3'  ACTTTGGGAGGCAAAGGCAGGT 70744      CA  CG  _
            GG                    CCACC  CCT  GC TCCCAAAGT
                                |||||  |||  || |||||||||
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                                GGTGG  GGA  CG AGGGTTTCA
                                  AC   AA  G
GAM219  KIAA0889  3'  ACTTTGGGAGACTGAGGTGGGC 31749    CA       _
          AGA                     TC  CCCACCTCGG CTCCCAAAGT
                                ||  |||||||||| |||||||||
                                AG  GGGTGGAGTC GAGGGTTTCA
                                 AC         A
GAM219  KIAA0889  3'  ACTTTGGGAGGCCGAGGCGGGT 31750        A     _
          GGA                     TCCACCC CCTCGGC TCCCAAAGT
                                |||||||  |||||||  |||||||||
                                AGGTGGG GGAGCCG AGGGTTTCA
                                   C      G
GAM219  KIAA0894  3'  GGGAGGCCGAGGCAAGTGGA   30337      CCA     _
                                TCCAC   CCTCGGC TCCC
                                |||||   |||||||  ||||
                                AGGTG   GGAGCCG AGGG
                                   AAC      G
GAM219  KIAA0907  3'  ACTTTGGGAGGCCAAGGTGGGC 30860    A      C  _
          GG                      CC CCCACCT GGC TCCCAAAGT
                                ||  |||||||  |||  |||||||||
                                GG GGGTGGA CCG AGGGTTTCA
                                 C      A  G
GAM219  KIAA0907  3'  ACTTTGGGAGGCCGAGGTGGGC 30861    CA       _
          AGA                     TC  CCCACCTCGGC TCCCAAAGT
                                ||  ||||||||||| |||||||||
                                AG  GGGTGGAGCCG AGGGTTTCA
                                 AC          G
GAM219  KIAA0912  3'  ACTTTGGGAGGCTGAGGTGGGA 65039     A        _
          GGA                     TCC CCCACCTCGGC TCCCAAAGT
                                |||  |||||||||||  |||||||||
                                AGG GGGTGGAGTCG AGGGTTTCA
                                  A         G
GAM219  KIAA0930  3'  ACTTTGGGAGGCTGAGATGGGT 71060        C     _
          GGA                     TCCACCCA CTCGGC TCCCAAAGT
                                ||||||||  ||||||  |||||||||
                                AGGTGGGT GAGTCG AGGGTTTCA
                                    A     G
GAM219  KIAA0953  3'  ACTTTGGGAGGCCAAGGCAGGT 67319      CA   C  _
          GG                      CCACC  CCT GGC TCCCAAAGT
                                |||||  |||  |||  |||||||||
                                GGTGG  GGA CCG AGGGTTTCA
                                   AC   A   G
GAM219  KIAA0961  3'  ACTTTGGGAGGCCGGTGGGCAG 30385    CA     TC  _
          A                       TC  CCCACC  GGC TCCCAAAGT
                                ||  ||||||  |||  |||||||||
                                AG  GGGTGG  CCG AGGGTTTCA
                                 AC      __  G
GAM219  KIAA0981  3'  ACTTTGGGAGGCCTAGGCAGG  62081    CA   C  _
                                CC  CCT GGC TCCCAAAGT
                                ||  |||  |||  |||||||||
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                                GG  GGA CCG AGGGTTTCA
                                 AC   T   G
GAM219  KIAA1056 3' ACTTTGGGAAGCCAAGATGAGT 30307    C  C  C   _
                                AC CA CT GGCT CCCAAAGT
                                || || || |||| ||||||||
                                TG GT GA CCGA GGGTTTCA
                                 A  A  A    A
GAM219  KIAA1086 3' ACTTTGAGAGGCCGAGGTGGGC 71278    CA        _ C
           AGA                    TC  CCCACCTCGGC TC CAAAGT
                                || ||||||||||| || ||||||
                                AG  GGGTGGAGCCG AG GTTTCA
                                 AC          G  A
GAM219  KIAA1130 3' ACTTTGGGAGGCTGAGATGGGT 63074         C    _
           GGA                    TCCACCCA CTCGGC TCCCAAAGT
                                |||||||| |||||| |||||||||
                                AGGTGGGT GAGTCG AGGGTTTCA
                                    A     G
GAM219  KIAA1143 3' ACTTTGGGAAGCCAAGGTGGG  69226        C   _
                                CCCACCT GGCT CCCAAAGT
                                ||||||| |||| ||||||||
                                GGGTGGA CCGA GGGTTTCA
                                   A    A
GAM219  KIAA1160 3' ACTTTGGGAGGCCGAGGCGGGC 40749     A  A      _
           GGG                    TCC CCC CCTCGGC TCCCAAAGT
                                ||| ||| ||||||| |||||||||
                                GGG GGG GGAGCCG AGGGTTTCA
                                  C  C      G
GAM219  KIAA1164 3' ACTTTGGGAGGCCGAGGCAGGT 70030        CA      _
           GGA                    TCCACC  CCTCGGC TCCCAAAGT
                                ||||||  ||||||| |||||||||
                                AGGTGG  GGAGCCG AGGGTTTCA
                                   AC      G
GAM219  KIAA1191 3' ACTTTGGGAGGCCAAGGTAGGT 40328       C   C  _
           GG                     CCACC ACCT GGC TCCCAAAGT
                                ||||| |||| ||| |||||||||
                                GGTGG TGGA CCG AGGGTTTCA
                                   A   A  G
GAM219  KIAA1202 3' ACTTTGGGAGGCCGAGGCAGGT 72482        CA      _
           GGA                    TCCACC  CCTCGGC TCCCAAAGT
                                ||||||  ||||||| |||||||||
                                AGGTGG  GGAGCCG AGGGTTTCA
                                   AC      G
GAM219  KIAA1204 3' ACTTTGGGAGGCTGAGATGGGT 69735         C    _
           GGA                    TCCACCCA CTCGGC TCCCAAAGT
                                |||||||| |||||| |||||||||
                                AGGTGGGT GAGTCG AGGGTTTCA
                                    A     G
GAM219  KIAA1228 3' ACTTTGGGAGGCCGAGGCGGGC 65662     A  A      _
           GGA                    TCC CCC CCTCGGC TCCCAAAGT
                                ||| ||| ||||||| |||||||||
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                                AGG GGG GGAGCCG AGGGTTTCA
                                  C  C      G
GAM219  KIAA1244  3'  ACTTTGGGAGGCCAAGGTGGG  72438        C  _
                                CCCACCT GGC TCCCAAAGT
                                ||||||| ||| |||||||||
                                GGGTGGA CCG AGGGTTTCA
                                   A  G
GAM219  KIAA1253  3'  ACTTTGGGAGGCTGAGGTGGGT 93546    C         _
          AGA                     TC ACCCACCTCGGC TCCCAAAGT
                                || ||||||||||||| |||||||||
                                AG TGGGTGGAGTCG AGGGTTTCA
                                 A          G
GAM219  KIAA1257  3'  ACTTTGGGAGGCCGAGGCGGGT 63386        A     _
          GGA                     TCCACCC CCTCGGC TCCCAAAGT
                                ||||||| ||||||| |||||||||
                                AGGTGGG GGAGCCG AGGGTTTCA
                                   C      G
GAM219  KIAA1271  3'  ACTTTGGGAGGCCAAGGTGGG  70126        C  _
                                CCCACCT GGC TCCCAAAGT
                                ||||||| ||| |||||||||
                                GGGTGGA CCG AGGGTTTCA
                                   A  G
GAM219  KIAA1276  3'  ACTTTGGGAGGCTGAGGCAGAT 67027      CCCA     _
          GGA                     TCCA   CCTCGGC TCCCAAAGT
                                ||||   ||||||| |||||||||
                                AGGT   GGAGTCG AGGGTTTCA
                                  AGAC      G
GAM219  KIAA1348  3'  ACTGTGGGAGGCCGAGGCGGAT 69115     C A     _   A
          GGA                     TCCA CC CCTCGGC TCCCA AGT
                                |||| || ||||||| ||||| |||
                                AGGT GG GGAGCCG AGGGT TCA
                                  A C      G    G
GAM219  KIAA1404  3'  ACTTTGGGAGGCCGAGGCAGGC 62679     A  CA     _
          GGA                     TCC CC  CCTCGGC TCCCAAAGT
                                ||| ||  ||||||| |||||||||
                                AGG GG  GGAGCCG AGGGTTTCA
                                  C  AC      G
GAM219  KIAA1456  3'  ACTTCAGGAAGCTGAGGTGGGT 67524             _  CA
          GGA                     TCCACCCACCTCGGCT CC  AAGT
                                ||||||||||||||| ||  ||||
                                AGGTGGGTGGAGTCGA GG  TTCA
                                        A  AC
GAM219  KIAA1456  5'  ACTTTGGGAGGCCGAGGCAGGC 67525     A  CA     _
          GGA                     TCC CC  CCTCGGC TCCCAAAGT
                                ||| ||  ||||||| |||||||||
                                AGG GG  GGAGCCG AGGGTTTCA
                                  C  AC      G
GAM219  KIAA1473  3'  ACTTTGGGAGGCAAAGGTGGGT 71202    C       CG  _
          AGA                     TC ACCCACCT  GC TCCCAAAGT
                                || ||||||||  || |||||||||
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                                AG TGGGTGGA  CG AGGGTTTCA
                                 A       AA  G
GAM219  KIAA1486 3' ACTCTGGGAGGCAGAGGTGGGT 67967           G _    A
            GGA                   TCCACCCACCTC GC TCCCA AGT
                                  |||||||||||| || ||||| |||
                                  AGGTGGGTGGAG CG AGGGT TCA
                                        A G    C
GAM219  KIAA1508 3' ACTTTGGGAGGCTGAGGTGGGT 62536            _
            GGA                   TCCACCCACCTCGGC TCCCAAAGT
                                  |||||||||||||||| |||||||||
                                  AGGTGGGTGGAGTCG AGGGTTTCA
                                        G
GAM219  KIAA1559 3' ACTTTGGGAGGACAAGGTGGGT 73442          CGG_
            GGA                   TCCACCCACCT    CTCCCAAAGT
                                  ||||||||||    ||||||||||
                                  AGGTGGGTGGA    GAGGGTTTCA
                                        ACAG
GAM219  KIAA1559 3' ACTTTGGGAGGCCATGGCAGGT 73443      CA  TC  _
            GG                      CCACC  CC  GGC TCCCAAAGT
                                  |||||  ||  ||| |||||||||
                                  GGTGG  GG  CCG AGGGTTTCA
                                     AC  TA   G
GAM219  KIAA1602 3' ACTTCGGACATGGCCGAGGAAG 65234    CA  CA      C___  A
            GCAGA                   TC  CC  CCTCGGCT    CC AAGT
                                  ||  ||  ||||||||    || ||||
                                  AG  GG  GGAGCCGG    GG TTCA
                                   AC  AA       TACA  C
GAM219  KIAA1649 3' ACTTTGGAAGGCCGAGGCAGGC 51211    CA  CA      C_
            AGA                     TC  CC  CCTCGGCT  CCAAAGT
                                  ||  ||  ||||||||  |||||||
                                  AG  GG  GGAGCCGG  GGTTTCA
                                   AC  AC       AA
GAM219  KIAA1674 3' ACTTTGGGAGGCCGAGGCGAGT 69326       CCA     _
            GGA                     TCCAC   CCTCGGC TCCCAAAGT
                                  |||||   ||||||| |||||||||
                                  AGGTG   GGAGCCG AGGGTTTCA
                                     AGC      G
GAM219  KIAA1724 3' ACTTTGGGAAGCCAAGGCAGGT 67605       CA   C   _
            GG                      CCACC  CCT GGCT CCCAAAGT
                                  |||||  ||| |||| |||||||||
                                  GGTGG  GGA CCGA GGGTTTCA
                                     AC   A    A
GAM219  KIAA1727 3' ACTTTGGGAGGCTAAGATGAGT 64748      C  C  CG  _
            GG                      CCAC CA CT  GC TCCCAAAGT
                                  ||||  ||  ||  ||  |||||||||
                                  GGTG GT GA  CG AGGGTTTCA
                                    A  A  AT  G
GAM219  KIAA1735 3' ACTTTGGGAGGCCGAGGCAGG  88999    CA      _
                                  CC  CCTCGGC TCCCAAAGT
                                  ||  |||||||  |||||||||
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                                GG  GGAGCCG AGGGTTTCA
                                 AC      G
GAM219  KIAA1751  3'  ACTTTGGGAGGCCGAGGCAGGA 72148     A  CA     _
                GGA                TCC CC  CCTCGGC TCCCAAAGT
                                   ||| ||  ||||||| |||||||||
                                   AGG GG  GGAGCCG AGGGTTTCA
                                     A AC      G
GAM219  KIAA1811  5'  ACTTTGGGAAGCTGAGGTGGG  65415          _
                                   CCCACCTCGGCT CCCAAAGT
                                   ||||||||||||| ||||||||
                                   GGGTGGAGTCGA GGGTTTCA
                                          A
GAM219  KIAA1829  3'  ACTTTGGGAGGCCGAGGTGGGC 62627    CA        _
                AGA                TC  CCCACCTCGGC TCCCAAAGT
                                   ||  |||||||||||| |||||||||
                                   AG  GGGTGGAGCCG AGGGTTTCA
                                    AC          G
GAM219  KIAA1831  3'  ACTCTGGGAGTTGTGGTGGGAG 64519    A     T       A
                GA                 TCC CCCACC CGGCTCCCA AGT
                                   ||| |||||| ||||||||| |||
                                   AGG GGGTGG GTTGAGGGT TCA
                                     A     T        C
GAM219  KIAA1841  3'  ACTTTGGGAGGCCGAGGCGGGC 80843    CA   A     _
                AGA                TC  CCC CCTCGGC TCCCAAAGT
                                   ||  ||| ||||||| |||||||||
                                   AG  GGG GGAGCCG AGGGTTTCA
                                    AC  C      G
GAM219  KIAA1870  3'  ACTTTGGGAGGCCAAGGCAGG  52896    CA   C  _
                                   CC  CCT GGC TCCCAAAGT
                                   ||  ||| ||| |||||||||
                                   GG  GGA CCG AGGGTTTCA
                                    AC  A  G
GAM219  KIAA1871  3'  ACTTTGGGAAGCCAAGGTGGG  61891        C   _
                                   CCCACCT GGCT CCCAAAGT
                                   ||||||| |||| ||||||||
                                   GGGTGGA CCGA GGGTTTCA
                                       A   A
GAM219  KIAA1872  3'  ACTCTGGGAGGCTGAGGTGGGT 63587              _   A
                GGA                TCCACCCACCTCGGC TCCCA AGT
                                   |||||||||||||| ||||| |||
                                   AGGTGGGTGGAGTCG AGGGT TCA
                                           G    C
GAM219  KIAA1872  3'  ACTTTGGGAGACCGAGACAGGT 63588       CAC    _
                GG                   CCACC   CTCGG CTCCCAAAGT
                                     |||||   ||||| ||||||||||
                                     GGTGG   GAGCC GAGGGTTTCA
                                       ACA    A
GAM219  KIAA1872  3'  ACTTTGGGAGGCCGAGGCAGGC 63589    A  CA     _
                GGA                TCC CC  CCTCGGC TCCCAAAGT
                                   ||| ||  ||||||| |||||||||
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                                AGG GG  GGAGCCG AGGGTTTCA
                                  C AC      G
GAM219  KIAA1879 3' ACTCTGGAGGCTGAGGTGGGAG 73926     A        TC  A
            GA                    TCC CCCACCTCGGC  CCA AGT
                                  ||| ||||||||||  ||| |||
                                  AGG GGGTGGAGTCG  GGT TCA
                                    A         GA  C
GAM219  KIAA1879 3' ACTTTGGGAGGCTGAGGCGGGA 73927     A  A     _
            GGA                     TCC CCC CCTCGGC TCCCAAAGT
                                  ||| ||| ||||||| |||||||||
                                  AGG GGG GGAGTCG AGGGTTTCA
                                    A  C      G
GAM219  KIAA1941 3' ACTTTGGGAGGCTAAGGTGGGC 75332    A      CG  _
            GG                    CC CCCACCT  GC TCCCAAAGT
                                  || |||||||  || |||||||||
                                  GG GGGTGGA  CG AGGGTTTCA
                                   C      AT  G
GAM219  KIAA1948 3' ACTTTGGGAGGCCGAGGCAGGT 83290       CA     _
            GGA                     TCCACC  CCTCGGC TCCCAAAGT
                                  ||||||  ||||||| |||||||||
                                  AGGTGG  GGAGCCG AGGGTTTCA
                                     AC      G
GAM219  KIAA1951 3' ACTTTGGGAGGCCGAGGCGGGC 74144    CA  A     _
            AGA                     TC  CCC CCTCGGC TCCCAAAGT
                                  ||  ||| ||||||| |||||||||
                                  AG  GGG GGAGCCG AGGGTTTCA
                                   AC  C      G
GAM219  KIAA1958 3' ACTTTGGGAGGCCAAGGTGGG  82769       C  _
                                  CCCACCT GGC TCCCAAAGT
                                  ||||||| ||| |||||||||
                                  GGGTGGA CCG AGGGTTTCA
                                     A  G
GAM219  KIAA1979 3' ACTTTGGTAGGCCAAGGTGGGT 89644        C   C_
                                  ACCCACCT GGCT  CCAAAGT
                                  |||||||| ||||  |||||||
                                  TGGGTGGA CCGG  GGTTTCA
                                     A   AT
GAM219  KLHL8    3' ACTTTGGGAGGCCGAGGTGGGT 63503                _
            GGA                     TCCACCCACCTCGGC TCCCAAAGT
                                  |||||||||||||| |||||||||
                                  AGGTGGGTGGAGCCG AGGGTTTCA
                                        G
GAM219  KR18     3' ACTTTGGGAGGCTGAGGCAGGT 53877       CA     _
            GGA                     TCCACC  CCTCGGC TCCCAAAGT
                                  ||||||  ||||||| |||||||||
                                  AGGTGG  GGAGTCG AGGGTTTCA
                                     AC      G
GAM219  KREMEN   3' ACTTTGGGAGGCTGAGGAGGGT 50224       A     _
            GGA                     TCCACCC CCTCGGC TCCCAAAGT
                                  ||||||| ||||||| |||||||||
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                                AGGTGGG GGAGTCG AGGGTTTCA
                                   A      G
GAM219  LIM     3'  ACTTTGGGAGGCCAAGACGGGC 22311    A   AC  C   _
             GG                    CC CCC  CT GGC TCCCAAAGT
                                   || |||  || ||| |||||||||
                                   GG GGG  GA CCG AGGGTTTCA
                                    C   CA  A   G
GAM219  LIM     3'  ACTTTGGGAGGCCAAGGTGGGT 22312           C   _
             GGA                   TCCACCCACCT GGC TCCCAAAGT
                                   ||||||||||| ||| |||||||||
                                   AGGTGGGTGGA CCG AGGGTTTCA
                                         A   G
GAM219  LRG     3'  ACTTTGGGAGGCCCAGGTGGGC 54812    A      C   _
             GG                    CC CCCACCT GGC TCCCAAAGT
                                   || ||||||| ||| |||||||||
                                   GG GGGTGGA CCG AGGGTTTCA
                                    C      C   G
GAM219  LSR68   3'  ACTTTGGGAGGCCGAGGCGGGT 38547         A      _
             GGA                   TCCACCC CCTCGGC TCCCAAAGT
                                   ||||||| ||||||| |||||||||
                                   AGGTGGG GGAGCCG AGGGTTTCA
                                      C      G
GAM219  LYSAL1  3'  ACTTTGGGAGGCCGAGGCGGGC 18119     A   A      _
             GGA                   TCC CCC CCTCGGC TCCCAAAGT
                                   ||| ||| ||||||| |||||||||
                                   AGG GGG GGAGCCG AGGGTTTCA
                                     C   C      G
GAM219  MACF1   3'  ACTTTGGGAGGCCAAGGCAGGC 53491    A  CA   C   _
             GG                    CC CC  CCT GGC TCCCAAAGT
                                   || ||  ||| ||| |||||||||
                                   GG GG  GGA CCG AGGGTTTCA
                                    C  AC   A   G
GAM219  MAWBP   3'  ACTTTGAGAGGCCAAGGTGGGT 42374           C   _  C
             GGA                   TCCACCCACCT GGC TC CAAAGT
                                   |||||||||| ||| || ||||||
                                   AGGTGGGTGGA CCG AG GTTTCA
                                         A   G  A
GAM219  MCAM    3'  ACTTTGGGAGGCCGAGGCGGGC 22454     A   A      _
             GGA                   TCC CCC CCTCGGC TCCCAAAGT
                                   ||| ||| ||||||| |||||||||
                                   AGG GGG GGAGCCG AGGGTTTCA
                                     C   C      G
GAM219  MESDC2  3'  ACTTTGGGAGGCCGAGGTGGGT 72905              _
             GGA                   TCCACCCACCTCGGC TCCCAAAGT
                                   |||||||||||||| |||||||||
                                   AGGTGGGTGGAGCCG AGGGTTTCA
                                            G
GAM219  METAP1  3'  ACTTTGGGAGTATGTGTGTG  73035     C   CTCG
                                   CAC CAC    GCTCCCAAAGT
                                   ||| |||    ||||||||||
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                                GTG GTG    TGAGGGTTTCA
                                  T   TA__
GAM219  MGC10765  3' ACTTTGGGAGGCCGAGGTGGGT 44552                _
             GGA                    TCCACCCACCTCGGC TCCCAAAGT
                                    ||||||||||||||| |||||||||
                                    AGGTGGGTGGAGCCG AGGGTTTCA
                                           G
GAM219  MGC10771  3' ACTTTGGGAGGCTGAGACGGGT 44710        AC     _
             GG                     CCACCC  CTCGGC TCCCAAAGT
                                    ||||||  |||||| |||||||||
                                    GGTGGG  GAGTCG AGGGTTTCA
                                       CA     G
GAM219  MGC10814  3' ACTTCGGGAGGCCAAGGCGGGT 52009         A   C   _   A
             GGG                    TCCACCC CCT GGC TCCC AAGT
                                    ||||||| ||| ||| |||| ||||
                                    GGGTGGG GGA CCG AGGG TTCA
                                        C   A   G    C
GAM219  MGC10814  5' ACTTTGGGAGGCCGAGGTGGGT 52010                _
             GGA                    TCCACCCACCTCGGC TCCCAAAGT
                                    ||||||||||||||| |||||||||
                                    AGGTGGGTGGAGCCG AGGGTTTCA
                                           G
GAM219  MGC11287  5' ACTGTGGGAGGCCGAGGCAGAC 49609     ACCCA     _    A
             GGA                    TCC     CCTCGGC TCCCA AGT
                                    |||     ||||||| ||||| |||
                                    AGG     GGAGCCG AGGGT TCA
                                      CAGAC      G    G
GAM219  MGC11352  3' ACTCCGGAGGCTGAGGCAGGGG 65423     A  CA      TC  AA
             A                       TCC CC  CCTCGGC  CC  AGT
                                    ||| ||  |||||||  ||  |||
                                    AGG GG  GGAGTCG  GG  TCA
                                      _ AC      GA  CC
GAM219  MGC11386  3' ACTTTGGGAGGCCGAAGT     53052     C    _
                                    AC TCGGC TCCCAAAGT
                                    || ||||| |||||||||
                                    TG AGCCG AGGGTTTCA
                                     A    G
GAM219  MGC13017  3' ACTTTGGGAGGCCGAGGTG    55568          _
                                    CACCTCGGC TCCCAAAGT
                                    ||||||||| |||||||||
                                    GTGGAGCCG AGGGTTTCA
                                         G
GAM219  MGC13053  3' ACTTTGGGAGGCCGAGGCAGGC 52092     A  CA     _
             GGA                       TCC CC  CCTCGGC TCCCAAAGT
                                       ||| ||  ||||||| |||||||||
                                       AGG GG  GGAGCCG AGGGTTTCA
                                         C  AC      G
GAM219  MGC13053  3' ACTTTGGGAGGCTGAGCTGGGC 52093     CA    C     _
             AGA                       TC  CCCA CTCGGC TCCCAAAGT
                                       ||  |||| |||||| |||||||||
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                                AG  GGGT GAGTCG AGGGTTTCA
                                 AC    C     G
GAM219  MGC14126 3' ACTTTGGGAGGCTGAGGCGGGT 52935        A     _
            GGA                   TCCACCC CCTCGGC TCCCAAAGT
                                  ||||||| ||||||| |||||||||
                                  AGGTGGG GGAGTCG AGGGTTTCA
                                     C      G
GAM219  MGC14407 3' ACTTTGGGAAGTTGAGGTGGGT 52966              _
            GGA                   TCCACCCACCTCGGCT CCCAAAGT
                                  |||||||||||||||| ||||||||
                                  AGGTGGGTGGAGTTGA GGGTTTCA
                                           A
GAM219  MGC14799 3' ACTTTGGGAGGCCGAGGCGGGC 51322     A  A     _
            GGA                   TCC CCC CCTCGGC TCCCAAAGT
                                  ||| ||| ||||||| |||||||||
                                  AGG GGG GGAGCCG AGGGTTTCA
                                    C  C      G
GAM219  MGC14817 3' ACTTTGGGAGGCCGAGGCAGGT 51334        CA     _
            GGA                   TCCACC  CCTCGGC TCCCAAAGT
                                  ||||||  ||||||| |||||||||
                                  AGGTGG  GGAGCCG AGGGTTTCA
                                     AC      G
GAM219  MGC15606 3' ACTTTGGGAGGCCAGGCAGGAG 59518     A  CA   C  _
            GA                    TCC CC  CCT GGC TCCCAAAGT
                                  ||| ||  ||| ||| |||||||||
                                  AGG GG  GGA CCG AGGGTTTCA
                                    A  AC   _   G
GAM219  MGC16385 3' ACTTTGGGAGGCCGAGACGGGC 59532    A   AC     _
            GG                    CC CCC  CTCGGC TCCCAAAGT
                                  || |||  ||||||| |||||||||
                                  GG GGG  GAGCCG AGGGTTTCA
                                   C  CA     G
GAM219  MGC16703 3' ACTTTGGGAGGCCAAGGCAGG  73485    CA   C  _
                                  CC  CCT GGC TCCCAAAGT
                                  ||  ||| ||| |||||||||
                                  GG  GGA CCG AGGGTTTCA
                                   AC   A   G
GAM219  MGC17998 3' CTTTGGGGAGTGAAGTGG    59387      C   GC
                                  CCAC TCG  TCCCAAAG
                                  |||| |||  ||||||||
                                  GGTG AGT  GGGGTTTC
                                    A   GA
GAM219  MGC20235 3' ACTTTGGGAGGCCGAAGTGGGT 59547          C    _
            GGA                   TCCACCCAC TCGGC TCCCAAAGT
                                  ||||||||| ||||| |||||||||
                                  AGGTGGGTG AGCCG AGGGTTTCA
                                       A    G
GAM219  MGC20496 3' ACTTTGGGAGGCCGAGGCAGGC 54527    CA  CA     _
            AGA                   TC  CC  CCTCGGC TCCCAAAGT
                                  ||  ||  ||||||| |||||||||
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                                AG  GG  GGAGCCG AGGGTTTCA
                                 AC  AC      G
GAM219  MGC23244  3'  GGAAGCCGAGGCGGGTGGA   58834        A       C
                                TCCACCC CCTCGGCT CC
                                ||||||| |||||||| ||
                                AGGTGGG GGAGCCGA GG
                                    C       A
GAM219  MGC2562   3'  ACTTTGGGAGGCCGAGGCGGGT 51415        A      _
          GGA                     TCCACCC CCTCGGC TCCCAAAGT
                                ||||||| ||||||| |||||||||
                                AGGTGGG GGAGCCG AGGGTTTCA
                                    C      G
GAM219  MGC2562   3'  ACTTTGGGAGGCCGAGGTGGGC 51416    CA        _
          AGA                     TC  CCCACCTCGGC TCCCAAAGT
                                ||  |||||||||| |||||||||
                                AG  GGGTGGAGCCG AGGGTTTCA
                                 AC          G
GAM219  MGC2562   3'  ACTTTGGGTGGCCAAGGTGGGC 51417    A      C   _
          GG                      CC CCCACCT GGCT CCCAAAGT
                                || ||||||| |||| ||||||||
                                GG GGGTGGA CCGG GGGTTTCA
                                 C      A   T
GAM219  MGC2731   3'  ACTTTGGGAAGCCGAGGTGGGC 44157     A         _
          GGA                     TCC CCCACCTCGGCT CCCAAAGT
                                ||| |||||||||||| ||||||||
                                AGG GGGTGGAGCCGA GGGTTTCA
                                  C          A
GAM219  MGC29891  3'  ACTTTGGGACGTTGAAATGGG  58845      CC    _
                                CCCA  TCGGC TCCCAAAGT
                                ||||  ||||| |||||||||
                                GGGT  AGTTG AGGGTTTCA
                                   AA    C
GAM219  MGC29891  3'  ACTTTGGGAGGCCGAGGCGGGC 58846     A   A     _
          GGA                     TCC CCC CCTCGGC TCCCAAAGT
                                ||| ||| ||||||| |||||||||
                                AGG GGG GGAGCCG AGGGTTTCA
                                  C  C      G
GAM219  MGC29937  3'  ACTTTGGGAGGCCGTGGTGGGC 58725    A     T   _
          GG                      CC CCCACC CGGC TCCCAAAGT
                                || |||||| |||| |||||||||
                                GG GGGTGG GCCG AGGGTTTCA
                                 C     T   G
GAM219  MGC3079   3'  ACTTTGGGAGGCAGAGGTGGGA 51945     A       G  _
          GGA                     TCC CCCACCTC GC TCCCAAAGT
                                ||| |||||||| || |||||||||
                                AGG GGGTGGAG CG AGGGTTTCA
                                   A       A  G
GAM219  MGC3169   3'  ACTTTGGGAGGCCGAGGCGGGC 44178    CA   A     _
          AGA                     TC  CCC CCTCGGC TCCCAAAGT
                                ||  ||| ||||||| |||||||||
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                                AG  GGG GGAGCCG AGGGTTTCA
                                 AC  C      G
GAM219  MGC3207  3' ACTTTGGGAGGCCGAGGCAGGT 63230       CA     _
            GGA                   TCCACC  CCTCGGC TCCCAAAGT
                                  ||||||  ||||||| |||||||||
                                  AGGTGG  GGAGCCG AGGGTTTCA
                                    AC      G
GAM219  MGC39350 3' ACTTTGGGAGGCCAAGGCGGGC 59313    A   A   C  _
            GG                    CC CCC CCT GGC TCCCAAAGT
                                  || ||| ||| ||| |||||||||
                                  GG GGG GGA CCG AGGGTTTCA
                                   C  C   A   G
GAM219  MGC4248  3' ACTTTGGGAGGCCAAGGTG   51308      C  _
                                  CACCT GGC TCCCAAAGT
                                  ||||| ||| |||||||||
                                  GTGGA CCG AGGGTTTCA
                                    A   G
GAM219  MGC4562  3' ACTTTGGGAGGCTGAGGCGGGC 56731     A   A     _
            GGA                   TCC CCC CCTCGGC TCCCAAAGT
                                  ||| ||| ||||||| |||||||||
                                  AGG GGG GGAGTCG AGGGTTTCA
                                   C  C      G
GAM219  MGC4663  3' ACTTTAGGAGGCCGAGGCGGGC 44780     A   A     TC _
            GGA                   TCC CCC CCTCGGC  CC AAAGT
                                  ||| ||| |||||||  || |||||
                                  AGG GGG GGAGCCG  GG TTTCA
                                   C  C      GA  A
GAM219  MGC4771  3' ACTTTGGGAGGCTGAGGTGGGT 51998           _
            GGA                   TCCACCCACCTCGGC TCCCAAAGT
                                  |||||||||||||| |||||||||
                                  AGGTGGGTGGAGTCG AGGGTTTCA
                                         G
GAM219  MGC4771  3' TGGATGCCGAGGTGAGTGGA   52008      C       TC
                                  TCCAC CACCTCGGC  CCA
                                  ||||| |||||||||  |||
                                  AGGTG GTGGAGCCG  GGT
                                    A        TA
GAM219  MGC4840  3' ACTTTGGGAGGTCGAGGTAGGC 72014    CA  C      _
            AGA                   TC  CC ACCTCGGC TCCCAAAGT
                                  ||  || |||||||| |||||||||
                                  AG  GG TGGAGCTG AGGGTTTCA
                                   AC  A       G
GAM219  MGC5254  3' ACTTTGGGAGGCCGAGGTGGGT 51386           _
            GGA                   TCCACCCACCTCGGC TCCCAAAGT
                                  |||||||||||||| |||||||||
                                  AGGTGGGTGGAGCCG AGGGTTTCA
                                         G
GAM219  MGC5384  3' ACTTTGGGAGGCCGAGGCAGGC 49086    CA  CA     _
            AGA                   TC  CC  CCTCGGC TCCCAAAGT
                                  ||  ||  ||||||| |||||||||
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                                AG  GG  GGAGCCG AGGGTTTCA
                                 AC  AC      G
GAM219  MGC5457  3' ACTTTGGGAGGCTGAGGAAGG 51933    CA     _
                                CC  CCTCGGC TCCCAAAGT
                                ||  ||||||| |||||||||
                                GG  GGAGTCG AGGGTTTCA
                                 AA      G
GAM219  MGC9912  3' ACTTTGGGAGGCCGAGGTGGGA 55605     A        _
           GGA                    TCC CCCACCTCGGC TCCCAAAGT
                                ||| |||||||||| |||||||||
                                AGG GGGTGGAGCCG AGGGTTTCA
                                 A         G
GAM219  MKRN4    3' ACTCTGGAGGCTGAGGCGGG  48449     A      TC   A
                                CCC CCTCGGC  CCA AGT
                                ||| |||||||  ||| |||
                                GGG GGAGTCG  GGT TCA
                                 C      GA   C
GAM219  MKRN4    3' ACTTTGGGAGGCTGAGGCGGCC 48450     AC  A      _
           GGA                    TCC  CC CCTCGGC TCCCAAAGT
                                |||  || ||||||| |||||||||
                                AGG  GG GGAGTCG AGGGTTTCA
                                 CC  C      G
GAM219  MOST2    5' ACTTTGGGAGGCCAAGGCAGG  40049    CA   C  _
                                CC  CCT GGC TCCCAAAGT
                                ||  ||| ||| |||||||||
                                GG  GGA CCG AGGGTTTCA
                                 AC   A   G
GAM219  MRPL56   3' ACTTTGGAAGGCCGAGGTGGGT 52750              C_
           GGA                    TCCACCCACCTCGGCT  CCAAAGT
                                ||||||||||||||||  |||||||
                                AGGTGGGTGGAGCCGG  GGTTTCA
                                        AA
GAM219  MRPS10   3' ACTTTGGGAGGCCGAGGCAGGC 36810     A  CA     _
           GGA                    TCC CC  CCTCGGC TCCCAAAGT
                                ||| ||  ||||||| |||||||||
                                AGG GG  GGAGCCG AGGGTTTCA
                                 C  AC      G
GAM219  MYO3B    3' ACTTTGGGAGGCCAAGATGGGC 58105    A   C  C  _
           GG                     CC CCCA CT GGC TCCCAAAGT
                                || |||| || ||| |||||||||
                                GG GGGT GA CCG AGGGTTTCA
                                 C    A  A   G
GAM219  N4BP2    3' ACTTTGGGAGGCCGAGGTAGGT 36932        C      _
           GGA                    TCCACC ACCTCGGC TCCCAAAGT
                                ||||||| |||||||| |||||||||
                                AGGTGG TGGAGCCG AGGGTTTCA
                                   A       G
GAM219  NBR2     3' ACTTTGGGAGGCCGAGGCAGGT 20615       CA     _
           GG                     CCACC  CCTCGGC TCCCAAAGT
                                |||||  ||||||| |||||||||
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                                GGTGG  GGAGCCG AGGGTTTCA
                                  AC      G
GAM219  NMNAT    3'  ACTTTGGGAGGCCTAAGTGGGT 43276         CTC  _
            GGA                   TCCACCCAC   GGC TCCCAAAGT
                                  |||||||||   ||| |||||||||
                                  AGGTGGGTG   CCG AGGGTTTCA
                                    AAT   G
GAM219  NMT2     3'  ACTTTGGGAGGCCAAGGTGGG  17850        C  _
                                  CCCACCT GGC TCCCAAAGT
                                  ||||||| ||| |||||||||
                                  GGGTGGA CCG AGGGTTTCA
                                    A   G
GAM219  NPTXR    3'  ACTTTGGGAGGCTGAGACAGG  27423    CAC     _
                                  CC   CTCGGC TCCCAAAGT
                                  ||   |||||| |||||||||
                                  GG   GAGTCG AGGGTTTCA
                                   ACA     G
GAM219  NPTXR    3'  ACTTTGGGAGGCTGAGACAGG  55204    CAC     _
                                  CC   CTCGGC TCCCAAAGT
                                  ||   |||||| |||||||||
                                  GG   GAGTCG AGGGTTTCA
                                   ACA     G
GAM219  OCLM     5'  ACTTTGGGAGGCCGAGGTGGGT 42583             _
            GGA                   TCCACCCACCTCGGC TCCCAAAGT
                                  |||||||||||||| |||||||||
                                  AGGTGGGTGGAGCCG AGGGTTTCA
                                        G
GAM219  ORC6L    3'  ACTTTGGGAGGCCAAGGTGGGT 27486          C  _
            GGA                   TCCACCCACCT GGC TCCCAAAGT
                                  |||||||||||| ||| |||||||||
                                  AGGTGGGTGGA CCG AGGGTTTCA
                                    A   G
GAM219  P66      3'  TGGAAGCCTGAAATGGGTGGA  40745        CC  _   C
                                  TCCACCCA  TC GGCT CCA
                                  ||||||||  || |||| |||
                                  AGGTGGGT  AG CCGA GGT
                                    AA  T    A
GAM219  PAFAH2   3'  ACTTTGGGAGGCCAAGGCAGG  6492     CA   C  _
                                  CC  CCT GGC TCCCAAAGT
                                  ||  ||| ||| |||||||||
                                  GG  GGA CCG AGGGTTTCA
                                   AC   A   G
GAM219  PB1      3'  ACTTTGGGAGGCCAAGATGGGT 37571         C  C  _
            GGA                   TCCACCCA CT GGC TCCCAAAGT
                                  |||||||| || ||| |||||||||
                                  AGGTGGGT GA CCG AGGGTTTCA
                                    A  A   G
GAM219  PDCD7    3'  ACTTTGGGAGGCCGAGGCGGGC 72596    CA   A     _
            CGA                   TC  CCC CCTCGGC TCCCAAAGT
                                  ||  ||| ||||||| |||||||||
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                                AG  GGG GGAGCCG AGGGTTTCA
                                 CC  C      G
GAM219  phorbolin-1 3'  ACTCTGGAGGCTGAGGCAGG  90201    CA      TC   A
                                CC  CCTCGGC  CCA AGT
                                ||  |||||||  ||| |||
                                GG  GGAGTCG  GGT TCA
                                 AC       GA   C
GAM219  PIWIL2   3'  ACTTTGGGAGGCCGAGGCGGGT 36537         A      _
           GGA                    TCCACCC CCTCGGC TCCCAAAGT
                                |||||||  |||||||  |||||||||
                                AGGTGGG GGAGCCG AGGGTTTCA
                                    C      G
GAM219  POFUT1   3'  ACTTTGCGAGGCCGAGGTGGGC 70967    CA         _ C
           AGA                    TC  CCCACCTCGGC TC CAAAGT
                                ||  ||||||||||| ||  ||||||
                                AG  GGGTGGAGCCG AG GTTTCA
                                 AC          G  C
GAM219  POLYDOM  3'  ACTTTGGAAGGCTGAGGAGGGT 44682         A       C_
           GGA                    TCCACCC CCTCGGCT  CCAAAGT
                                |||||||  ||||||||  |||||||
                                AGGTGGG GGAGTCGG  GGTTTCA
                                    A       AA
GAM219  PP591    5'  ACTTTGGGAGGCTGAGGCAGGA 48145     A  CA      _
           GGA                    TCC CC  CCTCGGC TCCCAAAGT
                                |||  ||  |||||||  |||||||||
                                AGG GG  GGAGTCG AGGGTTTCA
                                 A  AC      G
GAM219  PPP1R3B  3'  ACTTTGGGAAGCCAAGGCGGG  45128     A  C   _
                                CCC CCT GGCT CCCAAAGT
                                |||  |||  ||||  ||||||||
                                GGG GGA CCGA GGGTTTCA
                                 C  A   A
GAM219  PPP1R3B  3'  ACTTTGGGAGGCCGAGGCAGGT 45129        CA      _
           GGA                    TCCACC  CCTCGGC TCCCAAAGT
                                ||||||  |||||||  |||||||||
                                AGGTGG  GGAGCCG AGGGTTTCA
                                    AC      G
GAM219  PRDM14   3'  ACTTTGGGAGGCAGAGGTGGGT 44704            G  _
           GGA                    TCCACCCACCTC GC TCCCAAAGT
                                ||||||||||||  ||  |||||||||
                                AGGTGGGTGGAG CG AGGGTTTCA
                                       A  G
GAM219  PRIC285  3'  ACTTTGGGAAGCCGAGGCGGGC 62106    CA   A      _
           AGA                    TC  CCC CCTCGGCT CCCAAAGT
                                ||  |||  ||||||||  ||||||||
                                AG  GGG GGAGCCGA GGGTTTCA
                                 AC  C       A
GAM219  PRO0255  3'  ACTTTAAGAGGCCGAGGCGGGC 26962    CA   A      _ CC
           AGA                    TC  CCC CCTCGGC TC  AAAGT
                                ||  |||  |||||||  ||  |||||
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                                AG  GGG GGAGCCG AG  TTTCA
                                 AC   C      G  AA
GAM219  PRO0456  3' ACTTTGGGAGGCCAGAGTAGGT 27002       C  _  C  _
                GG                 CCACC AC CT GGC TCCCAAAGT
                                   ||||| || || ||| |||||||||
                                   GGTGG TG GA CCG AGGGTTTCA
                                     A  A  _  G
GAM219  PRO0478  3' ACTTTGGGAGGCCGAGGCGGGC 27013     CA   A      _
                AGA                TC  CCC CCTCGGC TCCCAAAGT
                                   ||  ||| ||||||| |||||||||
                                   AG  GGG GGAGCCG AGGGTTTCA
                                    AC   C      G
GAM219  PRO0478  5' ACTTTGGGAGGCGGAGGTG   27014        G  _
                                   CACCTC GC TCCCAAAGT
                                   ||||||  || |||||||||
                                   GTGGAG CG AGGGTTTCA
                                      G  G
GAM219  PRO0628  3' ACTTTGGGAGGCCGAGGCTGGT 27059        CA      _
                GGA                TCCACC  CCTCGGC TCCCAAAGT
                                   ||||||  |||||||  |||||||||
                                   AGGTGG  GGAGCCG AGGGTTTCA
                                      TC       G
GAM219  PRO1048  3' ACTTTGGGAGGCCGAGGCGGGC 38102     A   A      _
                GGA                TCC CCC CCTCGGC TCCCAAAGT
                                   |||  ||| ||||||| |||||||||
                                   AGG GGG GGAGCCG AGGGTTTCA
                                     C   C      G
GAM219  PRO1853  3' ACTTTGGGAGGCTGAGGTGGG  38378           _
                                   CCCACCTCGGC TCCCAAAGT
                                   ||||||||||| |||||||||
                                   GGGTGGAGTCG AGGGTTTCA
                                         G
GAM219  PRO2198  5' ACTTTGGGAGGCCAAGGTGGGT 38403           C  _
                GGA                TCCACCCACCT GGC TCCCAAAGT
                                   ||||||||||| |||  |||||||||
                                   AGGTGGGTGGA CCG AGGGTTTCA
                                         A  G
GAM219  PRO2730  3' ACTTTGGGAGGCCGAGGCGGGC 48175     A   A      _
                GGA                TCC CCC CCTCGGC TCCCAAAGT
                                   |||  ||| ||||||| |||||||||
                                   AGG GGG GGAGCCG AGGGTTTCA
                                     C   C      G
GAM219  PRO2859  3' ACTTTGGGAGGCCGAGGTGGGC 38206     CA         _
                AGA                TC  CCCACCTCGGC TCCCAAAGT
                                   ||  |||||||||| |||||||||
                                   AG  GGGTGGAGCCG AGGGTTTCA
                                    AC          G
GAM219  PRO2949  3' ACTTTGGGAGGCCGAGACGGGC 38218     A   AC     _
                GG                 CC CCC  CTCGGC TCCCAAAGT
                                   ||  |||  |||||| |||||||||
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                                GG GGG  GAGCCG AGGGTTTCA
                                 C  CA     G
GAM219  PRPF4    3'  ACTTTGGGAGGCCGAGGTGGGT 17464    C        _
           AGA                    TC ACCCACCTCGGC TCCCAAAGT
                                  || |||||||||||| |||||||||
                                  AG TGGGTGGAGCCG AGGGTTTCA
                                   A          G
GAM219  PSR      3'  ACTTTGGGAAGCTGAGGCAGGG 65772     A  A_     _
           GGA                    TCC CCC  CCTCGGCT CCCAAAGT
                                  ||| |||  |||||||| |||||||||
                                  AGG GGG  GGAGTCGA GGGTTTCA
                                   _  AC       A
GAM219  PSR      3'  ACTTTGGGAGGCCATGGCAGGT 65773       CA  TC  _
           GG                     CCACC  CC  GGC TCCCAAAGT
                                  |||||  ||  ||| |||||||||
                                  GGTGG  GG  CCG AGGGTTTCA
                                     AC  TA   G
GAM219  PTK6     3'  ACTTTGGGAGGCTGAGGCAGGT 21066        CA      _
           GGA                    TCCACC  CCTCGGC TCCCAAAGT
                                  ||||||  ||||||| |||||||||
                                  AGGTGG  GGAGTCG AGGGTTTCA
                                     AC      G
GAM219  PTRF     3'  ACTTTGGAGGCTGAGGTGGGGA 64230    CA         TC
           GA                     TC  CCCACCTCGGC  CCAAAGT
                                  ||  ||||||||||  |||||||
                                  AG  GGGTGGAGTCG  GGTTTCA
                                   AG          GA
GAM219  PTRF     3'  ACTTTGGGAGGCCGAGGTGGGC 64231     A        _
           GGA                    TCC CCCACCTCGGC TCCCAAAGT
                                  ||| |||||||||| |||||||||
                                  AGG GGGTGGAGCCG AGGGTTTCA
                                    C          G
GAM219  PXMP4    3'  ACTTTGGGAGGCTGAGGCAGGT 24329        CA      _
           GGA                    TCCACC  CCTCGGC TCCCAAAGT
                                  ||||||  ||||||| |||||||||
                                  AGGTGG  GGAGTCG AGGGTTTCA
                                     AC      G
GAM219  RAB4B    5'  ACTTTGGGAGGCTGAGGCAGGC 32896     A  CA      _
           GGA                    TCC CC  CCTCGGC TCCCAAAGT
                                  ||| ||  ||||||| |||||||||
                                  AGG GG  GGAGTCG AGGGTTTCA
                                    C  AC      G
GAM219  RAD51    3'  ACTTTGGGAGGCCGAGGCAGGT 12742        CA      _
           GGA                    TCCACC  CCTCGGC TCCCAAAGT
                                  ||||||  ||||||| |||||||||
                                  AGGTGG  GGAGCCG AGGGTTTCA
                                     AC      G
GAM219  RAD51    3'  ACTTTGGGAGGCCGAGGCAGGT 56826        CA      _
           GGA                    TCCACC  CCTCGGC TCCCAAAGT
                                  ||||||  ||||||| |||||||||
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                                AGGTGG  GGAGCCG AGGGTTTCA
                                   AC      G
GAM219  RBPMS    3'  ACTTTGGGAGGCTGAGGCAGGC 23427     A  CA      _
             GGA                    TCC CC  CCTCGGC TCCCAAAGT
                                    ||| ||  ||||||| |||||||||
                                    AGG GG  GGAGTCG AGGGTTTCA
                                      C  AC      G
GAM219  RNO2     5'  ACTCTGGAGGCTGAGGCGGG   53912     A      TC   A
                                    CCC CCTCGGC  CCA AGT
                                    ||| |||||||  ||| |||
                                    GGG GGAGTCG  GGT TCA
                                      C      GA   C
GAM219  RNO2     3'  ACTTCGAGAGGCCGAGGCAGGT 53913        CA      _  CCA
             GGA                    TCCACC  CCTCGGC TC   AAGT
                                    ||||||  ||||||| ||   ||||
                                    AGGTGG  GGAGCCG AG   TTCA
                                       AC      G  AGC
GAM219  RNO2     5'  ACTTCGGGGGGTTGAGGCGGGC 53914    CA   A         A_
             AGA                    TC  CCC CCTCGGCTCCC  AAGT
                                    ||  ||| ||||||||||  ||||
                                    AG  GGG GGAGTTGGGGG  TTCA
                                     AC   C          GC
GAM219  RNO2     5'  ACTTTGGGAGGCCCAGATGGG  53915      C  C   _
                                    CCCA CT GGC TCCCAAAGT
                                    |||| || ||| |||||||||
                                    GGGT GA CCG AGGGTTTCA
                                      A  C   G
GAM219  RoXaN    3'  ACTCTGGGAGGCCGAGGCGGGT 47271         A      _    A
             GGA                    TCCACCC CCTCGGC TCCCA AGT
                                    |||||||| ||||||| ||||| |||
                                    AGGTGGG GGAGCCG AGGGT TCA
                                       C      G    C
GAM219  RPP14    3'  ACTTTGGGAGGCTGCGGCAGGC 60219    A  CA  T   _
             GG                     CC CC  CC CGGC TCCCAAAGT
                                    || ||  || |||| |||||||||
                                    GG GG  GG GTCG AGGGTTTCA
                                     C  AC  C   G
GAM219  SAMHD1   3'  ACTTTGGGAGGCCAAGGTGGGC 61973    A      C   _
             GG                     CC CCCACCT GGC TCCCAAAGT
                                    || |||||||  ||| |||||||||
                                    GG GGGTGGA CCG AGGGTTTCA
                                     C      A   G
GAM219  SC65     3'  GGGAGGCCAAGGTGGGTGGA   22297           C   _
                                    TCCACCCACCT GGC TCCC
                                    |||||||||||  ||| ||||
                                    AGGTGGGTGGA CCG AGGG
                                           A   G
GAM219  SCYA5    3'  ACTTTGGGAGGCCAAGGTGGGT 12955           C   _
             GGA                    TCCACCCACCT GGC TCCCAAAGT
                                    ||||||||||  ||| |||||||||
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                                AGGTGGGTGGA CCG AGGGTTTCA
                                    A   G
GAM219  SEMA3E   3'  ACTTTGGGAGGCCGAGGCGGGT 25802       A     _
          GGA                    TCCACCC CCTCGGC TCCCAAAGT
                                 ||||||| ||||||| |||||||||
                                 AGGTGGG GGAGCCG AGGGTTTCA
                                    C      G
GAM219  SEMA5A   3'  ACTTTGGGAGGCCAAGGTGGGC 15587    A     C  _
          GG                     CC CCCACCT GGC TCCCAAAGT
                                 || ||||||| ||| |||||||||
                                 GG GGGTGGA CCG AGGGTTTCA
                                  C      A  G
GAM219  SERF1B   3'  ACTTTGGGAGACCAAGGCGGGT 43685     A   C  _
                                 ACCC CCT GG CTCCCAAAGT
                                 |||| ||| || ||||||||||
                                 TGGG GGA CC GAGGGTTTCA
                                   C   A  A
GAM219  SGKL     3'  ACTTTGGGAGGCTGAGGCGGGC 26048    CA  A     _
          AGA                    TC  CCC CCTCGGC TCCCAAAGT
                                 ||  ||| ||||||| |||||||||
                                 AG  GGG GGAGTCG AGGGTTTCA
                                  AC  C      G
GAM219  SGKL     3'  TGGGAGGCCGAGGCAGGCAGA  26064    CA  CA     _
                                 TC  CC  CCTCGGC TCCCA
                                 ||  ||  ||||||| |||||
                                 AG  GG  GGAGCCG AGGGT
                                  AC  AC      G
GAM219  SH2D3A   3'  ACTTTGGGAGGCCGAGGCGGAA 19701     AC  A     _
          GGA                    TCC  CC CCTCGGC TCCCAAAGT
                                 |||  || ||||||| |||||||||
                                 AGG  GG GGAGCCG AGGGTTTCA
                                   AA  C      G
GAM219  SIAT4A   3'  ACTTTGGGAGGCCGAGGCGGGA 13132     A  A     _
          GGA                    TCC CCC CCTCGGC TCCCAAAGT
                                 ||| ||| ||||||| |||||||||
                                 AGG GGG GGAGCCG AGGGTTTCA
                                   A  C      G
GAM219  SLC7A11  3'  ACTTTGGGAGGCTGAGGGGGTG 27527       A     _
          GA                     TCCACCC CCTCGGC TCCCAAAGT
                                 ||||||| ||||||| |||||||||
                                 AGGTGGG GGAGTCG AGGGTTTCA
                                    _      G
GAM219  SMA3     3'  ACTTTGGGAGGCTGAGGCAGGC 23254     A  CA     _
          GGA                    TCC CC  CCTCGGC TCCCAAAGT
                                 ||| ||  ||||||| |||||||||
                                 AGG GG  GGAGTCG AGGGTTTCA
                                   C  AC      G
GAM219  SMAP-5   3'  ACTTTGGGAGGCCGAGGCGGGC 48654     A  A     _
          GGA                    TCC CCC CCTCGGC TCCCAAAGT
                                 ||| ||| ||||||| |||||||||
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                                AGG GGG GGAGCCG AGGGTTTCA
                                  C  C      G
GAM219  SNAPC1   3'  GGGAGGCCGAGGTGGGCGGA  13277     A        _
                                TCC CCCACCTCGGC TCCC
                                ||| |||||||||| ||||
                                AGG GGGTGGAGCCG AGGG
                                  C         G
GAM219  SNPH     3'  ACTTTGGGGAGGGGTGGG    28897        GG T
                                CCCACCTC  C CCCAAAGT
                                ||||||||  | ||||||||
                                GGGTGGGG  G GGGTTTCA
                                    A_ _
GAM219  SPRY4    3'  ACTTTGGGAGGCTGAGGCAGGT 48991       CA     _
           GGA                    TCCACC  CCTCGGC TCCCAAAGT
                                ||||||  ||||||| |||||||||
                                AGGTGG  GGAGTCG AGGGTTTCA
                                   AC      G
GAM219  SPRY4    3'  GGGAGGCCAAGGTGGGTGGA  49022          C  _
                                TCCACCCACCT GGC TCCC
                                |||||||||| ||| ||||
                                AGGTGGGTGGA CCG AGGG
                                      A  G
GAM219  SPTLC2   3'  ACTTTGGGAGGCTGAAGCAGG  17976    CACC    _
                                CC    TCGGC TCCCAAAGT
                                ||    ||||| |||||||||
                                GG    AGTCG AGGGTTTCA
                                 ACGA    G
GAM219  SPTLC2   3'  ACTTTGGGAGGCTGAGGCAGGT 17977      CA     _
           GG                     CCACC  CCTCGGC TCCCAAAGT
                                |||||  ||||||| |||||||||
                                GGTGG  GGAGTCG AGGGTTTCA
                                   AC      G
GAM219  SS18L1   3'  ACTTTGGGAGGCCGAAGCGGGC 65945    A  ACC    _
           GG                     CC CCC   TCGGC TCCCAAAGT
                                || |||   ||||| |||||||||
                                GG GGG   AGCCG AGGGTTTCA
                                 C  CGA    G
GAM219  STX12    3'  ACTTTGGAAGGCTGAGGCGGGA 66948    A  A      C_
           GGA                    TCC CCC CCTCGGCT  CCAAAGT
                                ||| ||| ||||||||  |||||||
                                AGG GGG GGAGTCGG  GGTTTCA
                                  A  C       AA
GAM219  SUN1     3'  ACTTTGGGAGGCTGAGGCGGGT 47905       A     _
           GGA                    TCCACCC CCTCGGC TCCCAAAGT
                                ||||||| ||||||| |||||||||
                                AGGTGGG GGAGTCG AGGGTTTCA
                                   C      G
GAM219  SYAP1    3'  ACTTTGGGAGGCCGAGGTGGGC 52465    CA       _
           AGA                    TC  CCCACCTCGGC TCCCAAAGT
                                ||  |||||||||| |||||||||
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                                AG  GGGTGGAGCCG AGGGTTTCA
                                 AC          G
GAM219  SYNPO2   3' ACTTTGGGAGGCTGAGGTAGGA 72382     A  C       _
           GGA                    TCC CC ACCTCGGC TCCCAAAGT
                                  ||| || |||||||| |||||||||
                                  AGG GG TGGAGTCG AGGGTTTCA
                                   A A       G
GAM219  TA-LRRP  3' ACTTTGGGAGGCCAAGATGGGC 31706    A    C  C  _
           GG                     CC CCCA CT GGC TCCCAAAGT
                                  || |||| || ||| |||||||||
                                  GG GGGT GA CCG AGGGTTTCA
                                   C   A A  G
GAM219  TACTILE  3' ACTTTGGGAGGCCGAGGTGGGT 20579              _
           GGA                    TCCACCCACCTCGGC TCCCAAAGT
                                  |||||||||||||| |||||||||
                                  AGGTGGGTGGAGCCG AGGGTTTCA
                                         G
GAM219  TCEA3    3' ACTCTGGGAGGCTGAGGTGGG  89893          _    A
                                  CCCACCTCGGC TCCCA AGT
                                  |||||||||| ||||| |||
                                  GGGTGGAGTCG AGGGT TCA
                                        G    C
GAM219  TDP1     5' ACTTTGGGAGGCCGAGGCGGCT 37598    C  A     _
           G                      CA CC CCTCGGC TCCCAAAGT
                                  || || ||||||| |||||||||
                                  GT GG GGAGCCG AGGGTTTCA
                                   C  C      G
GAM219  THEA     3' ACTTTGGGAGGCTGAGGTGGGC 66866    CA        _
           AGA                    TC  CCCACCTCGGC TCCCAAAGT
                                  ||  |||||||||| |||||||||
                                  AG  GGGTGGAGTCG AGGGTTTCA
                                   AC          G
GAM219  TIP47    3' ACTTTGGGAGGCTGAGGCGGGC 20598     A  A     _
           GGA                    TCC CCC CCTCGGC TCCCAAAGT
                                  ||| ||| ||||||| |||||||||
                                  AGG GGG GGAGTCG AGGGTTTCA
                                   C  C      G
GAM219  TRIAD3   3' ACTTTGGGAGGCCGAGGCGGGC 96128     A  A     _
           GGA                    TCC CCC CCTCGGC TCCCAAAGT
                                  ||| ||| ||||||| |||||||||
                                  AGG GGG GGAGCCG AGGGTTTCA
                                   C  C      G
GAM219  TXNL2    3' ACTTTGGGAGGCGGAGGCAGGC 22576    A  CA   G  _
           GG                     CC CC  CCTC GC TCCCAAAGT
                                  || ||  |||| || |||||||||
                                  GG GG  GGAG CG AGGGTTTCA
                                   C  AC   G  G
GAM219  Ubc6p    3' GGGGCCCAGGGGTGGA      55194        AC  C
                                  TCCACCC  CT GGCTCC
                                  |||||||  || ||||||
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                                AGGTGGG  GA CCGGGG
                                   __ C
GAM219  UBCE7IP5  3'  ACTTTGGGAGGCCAAGGTGGGT 30840          C  _
           GGA                    TCCACCCACCT GGC TCCCAAAGT
                                  |||||||||| ||| |||||||||
                                  AGGTGGGTGGA CCG AGGGTTTCA
                                        A  G
GAM219  UBF-fl   3'  ACTTTGGGAGGCCGAGGTGGGT 52615           _
           GGA                    TCCACCCACCTCGGC TCCCAAAGT
                                  |||||||||||||| |||||||||
                                  AGGTGGGTGGAGCCG AGGGTTTCA
                                        G
GAM219  ust3     3'  ACCTTGGGAGGCTGAGGCGGGC 94848    CA  A     _     A
           AGA                    TC  CCC CCTCGGC TCCCAA GT
                                  ||  ||| ||||||| |||||| ||
                                  AG  GGG GGAGTCG AGGGTT CA
                                   AC  C      G     C
GAM219  VIT1     5'  ACTTTGGGGGAGGCCCAGGTGG 38598          C  ___
           GTGGA                   TCCACCCACCT GGCT   CCCAAAGT
                                  |||||||||| ||||  ||||||||
                                  AGGTGGGTGGA CCGG   GGGTTTCA
                                        C   AGG
GAM219  VPS4B    3'  ACTTTGGGAGGCTACGATGGGT 18016        CCTC  _
           GGA                    TCCACCCA   GGC TCCCAAAGT
                                  ||||||||   ||| |||||||||
                                  AGGTGGGT   TCG AGGGTTTCA
                                       AGCA  G
GAM219  WBSCR21  3'  ACTCTGGAGGCTGAGGCAGG  49292    CA     TC  A
                                  CC  CCTCGGC  CCA AGT
                                  ||  |||||||  ||| |||
                                  GG  GGAGTCG  GGT TCA
                                   AC      GA  C
GAM219  WBSCR22  3'  ACCTTGGGAGGCTGAGGTGGGA 34465    A        _    A
           GGA                    TCC CCCACCTCGGC TCCCAA GT
                                  ||| |||||||||| |||||| ||
                                  AGG GGGTGGAGTCG AGGGTT CA
                                    A         G     C
GAM219  WBSCR23  3'  ACTTTGGGAGGCTGAGGCAGGT 47409       CA     _
           GGA                    TCCACC  CCTCGGC TCCCAAAGT
                                  ||||||  ||||||| |||||||||
                                  AGGTGG  GGAGTCG AGGGTTTCA
                                     AC      G
GAM219  YME1L1   3'  ACTCTGGGGGCCAAGGCAGG  27314    CA  C      A
                                  CC  CCT GGCTCCCA AGT
                                  ||  ||| |||||||| |||
                                  GG  GGA CCGGGGGT TCA
                                   AC  A       C
GAM219  YME1L1   3'  ACTCTGGGGGCCAAGGCAGG  58419    CA  C      A
                                  CC  CCT GGCTCCCA AGT
                                  ||  ||| |||||||| |||
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                                GG  GGA CCGGGGGT TCA
                                 AC   A       C
GAM219  ZAK      3'  ACTTTGGGAGGCCAAGGTGGGC 56937    A      C  _
             GG                   CC CCCACCT GGC TCCCAAAGT
                                  || ||||||| ||| |||||||||
                                  GG GGGTGGA CCG AGGGTTTCA
                                   C      A   G
GAM219  ZFD25    3'  ACTTTGGGAGGCCAAGGTGGGT 33104           C  _
             GGA                    TCCACCCACCT GGC TCCCAAAGT
                                    |||||||||||| ||| |||||||||
                                    AGGTGGGTGGA CCG AGGGTTTCA
                                          A   G
GAM219  ZFP106   3'  ACTTTGGGAGGCTGAGGCAGGC 42712    CA  CA     _
             AGA                    TC  CC  CCTCGGC TCCCAAAGT
                                    ||  ||  ||||||| |||||||||
                                    AG  GG  GGAGTCG AGGGTTTCA
                                     AC  AC      G
GAM219  ZFP106   3'  GGGAGGCCGAGGCGGGTGGA  42734        A     _
                                    TCCACCC CCTCGGC TCCC
                                    ||||||| ||||||| ||||
                                    AGGTGGG GGAGCCG AGGG
                                        C      G
GAM219  ZIM3     3'  ACTTTGGGAGGCTGAGGTGGG  54635          _
                                    CCCACCTCGGC TCCCAAAGT
                                    |||||||||| |||||||||
                                    GGGTGGAGTCG AGGGTTTCA
                                          G
GAM219  ZNF197   3'  ACTTTGGGAGGCCGAGGTGGG  23751          _
                                    CCCACCTCGGC TCCCAAAGT
                                    |||||||||| |||||||||
                                    GGGTGGAGCCG AGGGTTTCA
                                          G
GAM219  ZNF297B  5'  ACTTTAGGAGGCTGAGGCTGGT 26637       CA      TC  _
             GGA                    TCCACC  CCTCGGC  CC AAAGT
                                    ||||||  |||||||  || |||||
                                    AGGTGG  GGAGTCG  GG TTTCA
                                       TC      GA  A
GAM219  ZNF297B  3'  ACTTTGGGAGGCCGAGATGGGT 26638         C     _
             GGA                    TCCACCCA CTCGGC TCCCAAAGT
                                    |||||||| |||||| |||||||||
                                    AGGTGGGT GAGCCG AGGGTTTCA
                                       A     G
GAM219  ZNF297B  5'  ACTTTGGGAGGCTGAGGTGGGT 26639             _
             GGA                    TCCACCCACCTCGGC TCCCAAAGT
                                    |||||||||||||| |||||||||
                                    AGGTGGGTGGAGTCG AGGGTTTCA
                                          G
GAM219  ZNF33A   3'  ACTTTGGGAGGCTGAGGCGGGT 92990        A     _
             GGA                    TCCACCC CCTCGGC TCCCAAAGT
                                    ||||||| ||||||| |||||||||
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                                AGGTGGG GGAGTCG AGGGTTTCA
                                   C      G
GAM219  ZNF347   3' ACTTTGGGAGTCCGAGGCAGGT 51817      CA    _
           GG                   CCACC  CCTCGG CTCCCAAAGT
                                ||||| |||||| ||||||||||
                                GGTGG  GGAGCC GAGGGTTTCA
                                   AC     T
GAM219  LOC112687 3' ACTTTGGGAGGCTGAGGGAGGC 73219     A  CA     _
           GGA                  TCC CC  CCTCGGC TCCCAAAGT
                                ||| ||  ||||||| |||||||||
                                AGG GG  GGAGTCG AGGGTTTCA
                                 C  AG      G
GAM219  LOC115129 5' ACTTTGGGAGGCTGAGGCAGGT 73601       CA     _
           GGA                  TCCACC  CCTCGGC TCCCAAAGT
                                |||||| ||||||| |||||||||
                                AGGTGG  GGAGTCG AGGGTTTCA
                                   AC      G
GAM219  LOC115196 3' ACTTTAGGAGGCCGAGGCGGGT 73647       A      TC _
           GGA                  TCCACCC CCTCGGC  CC AAAGT
                                ||||||| ||||||| || |||||
                                AGGTGGG GGAGCCG  GG TTTCA
                                   C      GA  A
GAM219  LOC116143 3' ACTTTGGGAGGCCGAGGCGGGT 74173       A     _
           GGA                  TCCACCC CCTCGGC TCCCAAAGT
                                ||||||| ||||||| |||||||||
                                AGGTGGG GGAGCCG AGGGTTTCA
                                   C      G
GAM219  LOC116143 3' ACTTTGGGAGGCTGAGGCGGGT 74174      A     _
           G                     CACCC CCTCGGC TCCCAAAGT
                                ||||| ||||||| |||||||||
                                GTGGG GGAGTCG AGGGTTTCA
                                   C      G
GAM219  LOC116228 3' ACTTTGGGAGGCCGAGGCAGTT 74224      CCCA     _
           GGA                  TCCA    CCTCGGC TCCCAAAGT
                                ||||    ||||||| |||||||||
                                AGGT    GGAGCCG AGGGTTTCA
                                   TGAC      G
GAM219  LOC116236 3' ACTTTGGGAGGCCGAGGTGGGT 74236            _
           GGA                  TCCACCCACCTCGGC TCCCAAAGT
                                |||||||||||||| |||||||||
                                AGGTGGGTGGAGCCG AGGGTTTCA
                                      G
GAM219  LOC116349 3' ACTTTGGGAGGCGAGGCAGGTA 74269    C   CA    G
           GA                   TC ACC  CCTCG CTCCCAAAGT
                                || |||  ||||| ||||||||||
                                AG TGG  GGAGC GAGGGTTTCA
                                 A  AC    G
GAM219  LOC118471 3' ACTTTTAGAGGCCGAGGCAGGC 74349     A  CA     _ CC
           GGA                  TCC CC  CCTCGGC TC  AAAGT
                                ||| ||  ||||||| ||  |||||
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                                AGG GG  GGAGCCG AG  TTTCA
                                  C AC      G AT
GAM219  LOC119504 5' ACTTTGGGAGGCCAAGGCAGGT 74438      CA  C  _
           GG                     CCACC  CCT GGC TCCCAAAGT
                                |||||  ||| ||| |||||||||
                                GGTGG  GGA CCG AGGGTTTCA
                                   AC  A  G
GAM219  LOC121457 3' ACTTTGGGAGGCCGAGGTGGGC 74507    CA        _
           AGA                    TC  CCCACCTCGGC TCCCAAAGT
                                ||  ||||||||||| |||||||||
                                AG  GGGTGGAGCCG AGGGTTTCA
                                 AC          G
GAM219  LOC122704 3' ACTTTGGGAGGCTGAGGCGGGC 74598    CA  A     _
           AGA                    TC  CCC CCTCGGC TCCCAAAGT
                                ||  |||  ||||||| |||||||||
                                AG  GGG GGAGTCG AGGGTTTCA
                                 AC  C      G
GAM219  LOC126282 3' ACTTTGAGAGGCTGAGGCGGGC 74938     A  A     _ C
           GGA                    TCC CCC CCTCGGC TC CAAAGT
                                |||  ||| ||||||| ||  ||||||
                                AGG GGG GGAGTCG AG GTTTCA
                                  C  C      G A
GAM219  LOC126282 3' ACTTTGGGAGGCCGAGGCAGG  74939    CA     _
                                CC  CCTCGGC TCCCAAAGT
                                ||  ||||||| |||||||||
                                GG  GGAGCCG AGGGTTTCA
                                 AC      G
GAM219  LOC126282 3' ACTTTGGGAGGCTGAGGCGGGC 74940    CA  A     _
           AGA                    TC  CCC CCTCGGC TCCCAAAGT
                                ||  |||  ||||||| |||||||||
                                AG  GGG GGAGTCG AGGGTTTCA
                                 AC  C      G
GAM219  LOC126964 3' ACCTTGGGAGGGGTGGGAGGA  75111     A     CGG     A
                                TCC CCCACCT   CTCCCAA GT
                                |||  |||||||   |||||||  ||
                                AGG GGGTGGG   GAGGGTT CA
                                  A     ___      C
GAM219  LOC129880 3' ACTTTGGGAAGTAATGAGTTG  75402    C   __  _
                                CA CTCG  GCT CCCAAAGT
                                ||  ||||  |||  ||||||||
                                GT GAGT  TGA GGGTTTCA
                                 T   AA  A
GAM219  LOC130026 3' ACTTTGGGAGGCTGAGGCAGGC 57430     A  CA     _
           GGA                    TCC CC  CCTCGGC TCCCAAAGT
                                |||  ||  |||||||  |||||||||
                                AGG GG  GGAGTCG AGGGTTTCA
                                  C AC      G
GAM219  LOC130162 3' ACTTTGGGAGGTCGAGGCAGGA 75417     A  CA     _
           GGA                    TCC CC  CCTCGGC TCCCAAAGT
                                |||  ||  |||||||  |||||||||
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                                AGG GG  GGAGCTG AGGGTTTCA
                                  A  AC      G
GAM219  LOC130535 3'  ACCTTGAAGGCCGAGGCAGGTG 76636       CA       CC   A
            GA                    TCCACC  CCTCGGCT  CAA GT
                                  ||||||  ||||||||  ||| ||
                                  AGGTGG  GGAGCCGG  GTT CA
                                     AC       AA   C
GAM219  LOC130535 3'  ACTTTGGGAGGCCGAGGCAGGT 76638       CA     _
            GGA                   TCCACC  CCTCGGC TCCCAAAGT
                                  ||||||  |||||||  |||||||||
                                  AGGTGG  GGAGCCG AGGGTTTCA
                                     AC      G
GAM219  LOC130589 3'  ACTTTGGAAGGCCGAGGCAGGC 57926     A  CA       C_
            GGA                   TCC CC  CCTCGGCT  CCAAAGT
                                  ||| ||  ||||||||  |||||||
                                  AGG GG  GGAGCCGG  GGTTTCA
                                    C  AC       AA
GAM219  LOC134147 3'  ACTTTGGGAGGCCAAAGTGGGT 57952         CTC   _
            GGA                   TCCACCCAC   GGC TCCCAAAGT
                                  |||||||||   ||| |||||||||
                                  AGGTGGGTG   CCG AGGGTTTCA
                                       AAA   G
GAM219  LOC134147 3'  ACTTTGGGAGGCCGAGGTGGGT 57953              _
            GGA                   TCCACCCACCTCGGC TCCCAAAGT
                                  |||||||||||||||| |||||||||
                                  AGGTGGGTGGAGCCG AGGGTTTCA
                                             G
GAM219  LOC135154 3'  ACTCTGGAGGCTGAGGCAGG   75716    CA      TC   A
                                  CC  CCTCGGC  CCA AGT
                                  ||  |||||||  ||| |||
                                  GG  GGAGTCG  GGT TCA
                                    AC       GA   C
GAM219  LOC137362 3'  ACTTTGAGAGGCCGAGGCGGGT 75777        A      _  C
            GGG                   TCCACCC CCTCGGC TC CAAAGT
                                  |||||||  |||||||  ||  ||||||
                                  GGGTGGG GGAGCCG AG GTTTCA
                                      C       G  A
GAM219  LOC138150 5'  TGGGAGCCAGGGGCTG      75821     C  A   C
                                  CA CC CCT GGCTCCCA
                                  || || ||| ||||||||
                                  GT GG GGA CCGAGGGT
                                    C  _   _
GAM219  LOC139422 3'  ACTTTGGGAGGCCGAGGCAGGC 76340     A  CA      _
            GGA                   TCC CC  CCTCGGC TCCCAAAGT
                                  ||| ||  |||||||  |||||||||
                                  AGG GG  GGAGCCG AGGGTTTCA
                                    C  AC       G
GAM219  LOC142779 3'  ACTTTGGGAGGCCGAGGTGGGC 76899     CA         _
            AGA                   TC  CCCACCTCGGC TCCCAAAGT
                                  ||  ||||||||||| |||||||||
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                                AG  GGGTGGAGCCG AGGGTTTCA
                                 AC          G
GAM219   LOC142927 3'  ACTTTGGGAGCTGGAGGTGGG  76940         _
                                CCCACCTC GGCTCCCAAAGT
                                |||||||| ||||||||||||
                                GGGTGGAG TCGAGGGTTTCA
                                    G
GAM219   LOC143196 3'  ACTTTGGGAGGCCGAGGCGGGT 83798         A      _
           GGA                    TCCACCC CCTCGGC TCCCAAAGT
                                  ||||||| ||||||| |||||||||
                                  AGGTGGG GGAGCCG AGGGTTTCA
                                     C      G
GAM219   LOC143310 3'  ACTTTGGGAGGCCGAGGTGGGC 77032     CA          _
           CGA                      TC  CCCACCTCGGC TCCCAAAGT
                                  ||  |||||||||||| |||||||||
                                  AG  GGGTGGAGCCG AGGGTTTCA
                                   CC          G
GAM219   LOC143465 3'  ACTTTGGGAGGCTGAAGCAGG  83866    CACC     _
                                  CC    TCGGC TCCCAAAGT
                                  ||    ||||| |||||||||
                                  GG    AGTCG AGGGTTTCA
                                   ACGA     G
GAM219   LOC144289 3'  ACTTTGGGAGGGCGAGGTGGGT 83946             G _
           GGA                    TCCACCCACCTCG C TCCCAAAGT
                                  |||||||||||||| | |||||||||
                                  AGGTGGGTGGAGC G AGGGTTTCA
                                        G G
GAM219   LOC144465 3'  ACTTTGGGAGGCTGAGGCGGGT 77335    C    A      _
           TGA                      TC ACCC CCTCGGC TCCCAAAGT
                                  || |||| ||||||| |||||||||
                                  AG TGGG GGAGTCG AGGGTTTCA
                                   T   C      G
GAM219   LOC144465 3'  ACTTTGGGAGTCCCAGGCGGGC 77336    A   A   C _
           GG                       CC CCC CCT GG CTCCCAAAGT
                                  || ||| ||| || ||||||||||
                                  GG GGG GGA CC GAGGGTTTCA
                                   C   C   C  T
GAM219   LOC144481 3'  ACTTTGGGAGGCTGAGGCAAGT 84009     CCA      _
           G                        CAC   CCTCGGC TCCCAAAGT
                                  |||   ||||||| |||||||||
                                  GTG   GGAGTCG AGGGTTTCA
                                    AAC      G
GAM219   LOC144563 3'  GGGAGGCCGAGGCAGGCGGA   77402     A  CA      _
                                  TCC CC  CCTCGGC TCCC
                                  ||| ||  ||||||| ||||
                                  AGG GG  GGAGCCG AGGG
                                    C  AC      G
GAM219   LOC144583 3'  ACTTTGGGAGGCTGAGGTGGGC 77408    CA         _
           AGA                      TC  CCCACCTCGGC TCCCAAAGT
                                  ||  |||||||||||| |||||||||
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                                AG  GGGTGGAGTCG AGGGTTTCA
                                 AC          G
GAM219  LOC144817 3'  ACTTTGGGAGGCTGAGGCGGGC 77501     A  A     _
                GGA                TCC CCC CCTCGGC TCCCAAAGT
                                   ||| ||| ||||||| |||||||||
                                   AGG GGG GGAGTCG AGGGTTTCA
                                     C  C      G
GAM219  LOC144817 3'  ACTTTGGGAGGCTGAGGTGGGC 77502     A        _
                GGA                TCC CCCACCTCGGC TCCCAAAGT
                                   ||| |||||||||| |||||||||
                                   AGG GGGTGGAGTCG AGGGTTTCA
                                     C          G
GAM219  LOC144845 3'  ACTTTGGGAGGCCAAGGCGGG  57449     A  C  _
                                   CCC CCT GGC TCCCAAAGT
                                   ||| ||| ||| |||||||||
                                   GGG GGA CCG AGGGTTTCA
                                     C  A  G
GAM219  LOC145216 3'  ACTTTGGAAGGCTGAGGCGGGC 84213     A  A      C_
                GGA                TCC CCC CCTCGGCT  CCAAAGT
                                   ||| ||| ||||||||  |||||||
                                   AGG GGG GGAGTCGG  GGTTTCA
                                     C  C       AA
GAM219  LOC145231 3'  ACTTTGGCAGGCTGAGGTGGGC 84237     A         C_
                GGA                TCC CCCACCTCGGCT  CCAAAGT
                                   ||| ||||||||||||  |||||||
                                   AGG GGGTGGAGTCGG  GGTTTCA
                                     C          AC
GAM219  LOC145231 3'  ACTTTGGGAGGCTGAGGCGGGT 84238      A     _
                G                   CACCC CCTCGGC TCCCAAAGT
                                   ||||| ||||||| |||||||||
                                   GTGGG GGAGTCG AGGGTTTCA
                                      C      G
GAM219  LOC145299 3'  ACTTTGGGAGGCCGAGGCGGGT 84271        A     _
                GGA                TCCACCC CCTCGGC TCCCAAAGT
                                   ||||||| ||||||| |||||||||
                                   AGGTGGG GGAGCCG AGGGTTTCA
                                       C      G
GAM219  LOC145333 3'  ACTTTGGGAGGCCGAGGCGGGC 84285     A  A     _
                GGA                TCC CCC CCTCGGC TCCCAAAGT
                                   ||| ||| ||||||| |||||||||
                                   AGG GGG GGAGCCG AGGGTTTCA
                                     C  C      G
GAM219  LOC145438 3'  ACTTTGGGAGGCCGAGGCGGGC 84306     A  A     _
                GGA                TCC CCC CCTCGGC TCCCAAAGT
                                   ||| ||| ||||||| |||||||||
                                   AGG GGG GGAGCCG AGGGTTTCA
                                     C  C      G
GAM219  LOC145482 3'  ACTTTGGGAGGCAGAGGCGGG  77738     A   G  _
                                   CCC CCTC GC TCCCAAAGT
                                   ||| |||| || |||||||||
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                                GGG GGAG CG AGGGTTTCA
                                  C    A  G
GAM219   LOC145483 3'  ACTTTGGGAGGCTGAGGCAGGC 77749     CA  CA      _
            AGA                    TC  CC  CCTCGGC TCCCAAAGT
                                || ||  ||||||| |||||||||
                                AG  GG  GGAGTCG AGGGTTTCA
                                 AC  AC      G
GAM219   LOC145662 3'  ACTTTGGGAGGCTGAGGTGGGT 77831             _
            GGA                    TCCACCCACCTCGGC TCCCAAAGT
                                |||||||||||||| |||||||||
                                AGGTGGGTGGAGTCG AGGGTTTCA
                                         G
GAM219   LOC145663 3'  GGAAGGCCGAGGCAGGCGGA   84426     A  CA       C_
                                TCC CC  CCTCGGCT  CC
                                ||| ||  ||||||||  ||
                                AGG GG  GGAGCCGG  GG
                                  C  AC       AA
GAM219   LOC145663 3'  ACTTTGGGAGGCCGAGGCGGGC 84410     A   A      _
            GGA                    TCC CCC CCTCGGC TCCCAAAGT
                                ||| ||| ||||||| |||||||||
                                AGG GGG GGAGCCG AGGGTTTCA
                                  C  C      G
GAM219   LOC145757 3'  ACTTTGGGAGGCCAAGGCAGGT 77912       CA   C  _
            GG                     CCACC  CCT GGC TCCCAAAGT
                                |||||  ||| ||| |||||||||
                                GGTGG  GGA CCG AGGGTTTCA
                                   AC   A   G
GAM219   LOC145820 3'  ACTTTGGGAGGCCTAGGCGGGC 77969    A   A   C  _
            GG                     CC CCC CCT GGC TCCCAAAGT
                                || ||| ||| ||| |||||||||
                                GG GGG GGA CCG AGGGTTTCA
                                 C  C  T  G
GAM219   LOC146229 3'  ACTCTGGGAGGCTGAGGCGGGT 78250         A      _    A
            GGA                    TCCACCC CCTCGGC TCCCA AGT
                                ||||||| ||||||| ||||| |||
                                AGGTGGG GGAGTCG AGGGT TCA
                                    C      G    C
GAM219   LOC146272 5'  ACTTTGGGAGGCTGAGGTGGAA 78323     AC         _
            GGA                    TCC  CCACCTCGGC TCCCAAAGT
                                |||  |||||||||| |||||||||
                                AGG  GGTGGAGTCG AGGGTTTCA
                                  AA         G
GAM219   LOC146336 5'  ACTGTGGGAGGCCGAGGCGGGT 78362         A      _    A
            GGA                    TCCACCC CCTCGGC TCCCA AGT
                                ||||||| ||||||| ||||| |||
                                AGGTGGG GGAGCCG AGGGT TCA
                                    C      G    G
GAM219   LOC146336 3'  CTTTGGGATGTGGCTGGA    78371      C    CTCGGC
                                TCCA CCAC     TCCCAAAG
                                |||| ||||     ||||||||
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                                AGGT GGTG     AGGGTTTC
                                  C   T_____
GAM219  LOC146540 3'  ACTTTGGGAGGCTGAGGCAGGA 78523     A  CA     _
          GGA                     TCC CC  CCTCGGC TCCCAAAGT
                                  ||| ||  ||||||| |||||||||
                                  AGG GG  GGAGTCG AGGGTTTCA
                                    A  AC      G
GAM219  LOC146667 3'  ACTTTGGGAGGCCGAGGCGGTT 84704      C  A     _
          GGA                     TCCA CC CCTCGGC TCCCAAAGT
                                  |||| || ||||||| |||||||||
                                  AGGT GG GGAGCCG AGGGTTTCA
                                    T C      G
GAM219  LOC146723 3'  ACTTTGGGAGGCCAAGGCGG   78672    A   C  _
                                  CC CCT GGC TCCCAAAGT
                                  || ||| ||| |||||||||
                                  GG GGA CCG AGGGTTTCA
                                   C   A   G
GAM219  LOC146756 3'  ACTTTGGGAGGCCGAGGCGGGC 84792     A   A     _
          GGA                     TCC CCC CCTCGGC TCCCAAAGT
                                  ||| ||| ||||||| |||||||||
                                  AGG GGG GGAGCCG AGGGTTTCA
                                    C   C      G
GAM219  LOC146901 3'  ACTTTGGAAGGCCGAGGCAGGT 84882        CA       C_
          GGA                     TCCACC  CCTCGGCT  CCAAAGT
                                  |||||| ||||||||  |||||||
                                  AGGTGG  GGAGCCGG  GGTTTCA
                                     AC        AA
GAM219  LOC146923 3'  ACTTTGGGAGGCCGAGGCGGGC 78793     A   A     _
          GGA                     TCC CCC CCTCGGC TCCCAAAGT
                                  ||| ||| ||||||| |||||||||
                                  AGG GGG GGAGCCG AGGGTTTCA
                                    C   C      G
GAM219  LOC146975 5'  ACTTTGGGAGGCCGAGGCAGGT 78826        CA     _
          GGA                     TCCACC  CCTCGGC TCCCAAAGT
                                  |||||| ||||||| |||||||||
                                  AGGTGG  GGAGCCG AGGGTTTCA
                                     AC      G
GAM219  LOC147057 3'  ACTTTGGGAGGCCGAGGCAGGC 84974     A  CA     _
          GGA                     TCC CC  CCTCGGC TCCCAAAGT
                                  ||| ||  ||||||| |||||||||
                                  AGG GG  GGAGCCG AGGGTTTCA
                                    C  AC      G
GAM219  LOC147071 3'  ACTTTGGGAGGCCGAGGCGGGC 73345     A   A     _
          GGA                     TCC CCC CCTCGGC TCCCAAAGT
                                  ||| ||| ||||||| |||||||||
                                  AGG GGG GGAGCCG AGGGTTTCA
                                    C   C      G
GAM219  LOC147180 5'  GGGAGGCCGAGGCGGGCGGA   85103     A   A     _
                                  TCC CCC CCTCGGC TCCC
                                  ||| ||| ||||||| ||||
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                                AGG GGG GGAGCCG AGGG
                                  C  C      G
GAM219  LOC147599 3' TGGGAGGCCGAGGCAGGTGGA 85168       CA     _
                                TCCACC  CCTCGGC TCCCA
                                ||||||  ||||||| |||||
                                AGGTGG  GGAGCCG AGGGT
                                   AC      G
GAM219  LOC147660 3' ACTTTGGGAGGCCAAGGCAGG  79023    CA  C  _
                                CC  CCT GGC TCCCAAAGT
                                ||  ||| ||| |||||||||
                                GG  GGA CCG AGGGTTTCA
                                 AC  A  G
GAM219  LOC147664 3' ACTTTGGGAGGCTGAGGCAGGC 79037    CA  CA     _
           AGA                    TC  CC  CCTCGGC TCCCAAAGT
                                ||  ||  ||||||| |||||||||
                                AG  GG  GGAGTCG AGGGTTTCA
                                 AC  AC      G
GAM219  LOC147700 3' ACTCCGGAAGCTGAGGCAGG   59874    CA      C  AA
                                CC  CCTCGGCT CC  AGT
                                ||  |||||||| ||  |||
                                GG  GGAGTCGA GG  TCA
                                 AC       A  CC
GAM219  LOC147727 5' ACTTTGGGAAGCTGAGGTGGGC 79122     A         _
           GGA                    TCC CCCACCTCGGCT CCCAAAGT
                                ||| |||||||||||| ||||||||
                                AGG GGGTGGAGTCGA GGGTTTCA
                                  C          A
GAM219  LOC147727 5' ACTTTGGGAGGCCGAGGCGGGC 79123     A  A     _
           GGA                    TCC CCC CCTCGGC TCCCAAAGT
                                ||| ||| ||||||| |||||||||
                                AGG GGG GGAGCCG AGGGTTTCA
                                  C  C      G
GAM219  LOC147990 3' ACTTTGGGAGGTCGAGGCGGGC 85208    CA  A     _
           AGA                    TC  CCC CCTCGGC TCCCAAAGT
                                ||  ||| ||||||| |||||||||
                                AG  GGG GGAGCTG AGGGTTTCA
                                 AC  C      G
GAM219  LOC148147 3' ACTTTGGGAGGCTGAGGTGGGC 79383     A         _
           GGA                    TCC CCCACCTCGGC TCCCAAAGT
                                ||| |||||||||| |||||||||
                                AGG GGGTGGAGTCG AGGGTTTCA
                                  C          G
GAM219  LOC148198 3' ACTTTGGGAGGCAAAGGCGGGC 71217    A  A  CG _
           GG                     CC CCC CCT  GC TCCCAAAGT
                                || ||| |||  || |||||||||
                                GG GGG GGA  CG AGGGTTTCA
                                 C  C  AA  G
GAM219  LOC148267 3' ACTTTGGGAAGCCAAGGTGG   79511       C   _
                                CCACCT GGCT CCCAAAGT
                                |||||| |||| ||||||||
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                                GGTGGA CCGA GGGTTTCA
                                   A   A
GAM219  LOC148343 3'  ACTTTGGGATGCCAAGGCGGGT 79535       A  C  _
                GG                 CCACCC CCT GGC TCCCAAAGT
                                   |||||| ||| ||| |||||||||
                                   GGTGGG GGA CCG AGGGTTTCA
                                      C  A  T
GAM219  LOC148534 3'  ACTTTGGGAGGCCAAGGTGGGT 79626    C      C  _
                CGA                TC ACCCACCT GGC TCCCAAAGT
                                   || |||||||| ||| |||||||||
                                   AG TGGGTGGA CCG AGGGTTTCA
                                    C       A  G
GAM219  LOC148734 3'  ACTTTGGGAGGCCGAGGTGGGC 79706    A        _
                GGA                TCC CCCACCTCGGC TCCCAAAGT
                                   ||| ||||||||||| |||||||||
                                   AGG GGGTGGAGCCG AGGGTTTCA
                                     C         G
GAM219  LOC148809 5'  ACTTTGGGAGGCTGAGGCGGGT 79745        A     _
                GGA                TCCACCC CCTCGGC TCCCAAAGT
                                   ||||||| ||||||| |||||||||
                                   AGGTGGG GGAGTCG AGGGTTTCA
                                      C      G
GAM219  LOC148823 3'  ACTTTGGGAAGCCAAGACAGGT 59890      CAC  C   _
                GG                 CCACC   CT GGCT CCCAAAGT
                                   |||||   || |||| ||||||||
                                   GGTGG   GA CCGA GGGTTTCA
                                      ACA  A    A
GAM219  LOC148918 5'  ACTTTGGGAGACCAAGGTGGG  79814       C  _
                                   CCCACCT GG CTCCCAAAGT
                                   ||||||| || ||||||||||
                                   GGGTGGA CC GAGGGTTTCA
                                      A  A
GAM219  LOC148918 5'  ACTTTGGGAGGCCAAGGCAGG  79815    CA   C  _
                                   CC  CCT GGC TCCCAAAGT
                                   ||  ||| ||| |||||||||
                                   GG  GGA CCG AGGGTTTCA
                                    AC   A   G
GAM219  LOC148936 3'  ACTTTGGAAGGCCGAGGCAGGA 85446     A  CA       C_
                GGA                TCC CC  CCTCGGCT  CCAAAGT
                                   ||| ||  ||||||||  |||||||
                                   AGG GG  GGAGCCGG  GGTTTCA
                                     A  AC       AA
GAM219  LOC148938 3'  ACTTTGGGAGGCCGAGGCAGGA 85428     A  CA      _
                GGA                TCC CC  CCTCGGC TCCCAAAGT
                                   ||| ||  ||||||| |||||||||
                                   AGG GG  GGAGCCG AGGGTTTCA
                                     A  AC      G
GAM219  LOC149073 3'  ACTTTGGGAGGCCAAGGCAGAT 85479     CCCA   C  _
                GG                 CCA    CCT GGC TCCCAAAGT
                                   |||    ||| ||| |||||||||
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                                GGT    GGA CCG AGGGTTTCA
                                  AGAC   A   G
GAM219   LOC149113 3'  ACTTTAGGAGGCTGAGGTGGGA 79898     A         TC  _
             GGA                    TCC CCCACCTCGGC  CC AAAGT
                                    ||| ||||||||||  || |||||
                                    AGG GGGTGGAGTCG  GG TTTCA
                                      A          GA  A
GAM219   LOC149113 3'  ACTTTGGGAGGCCGAGGAGGGT 79899         A      _
             GGA                    TCCACCC CCTCGGC TCCCAAAGT
                                    ||||||| ||||||| |||||||||
                                    AGGTGGG GGAGCCG AGGGTTTCA
                                       A      G
GAM219   LOC149175 3'  ACTTTGGGAGGCCGAGATGGGC 79945    A    C     _
             GG                     CC CCCA CTCGGC TCCCAAAGT
                                    || |||| |||||| |||||||||
                                    GG GGGT GAGCCG AGGGTTTCA
                                     C    A     G
GAM219   LOC149194 5'  ACTTTGGGAGGCCAAGGCGGGT 79974        A   C   _
             GG                     CCACCC CCT GGC TCCCAAAGT
                                    |||||| ||| ||| |||||||||
                                    GGTGGG GGA CCG AGGGTTTCA
                                       C   A   G
GAM219   LOC149271 3'  ACTTTGGGACACCAAGGTGGGT 79993           C  C_
             GGA                    TCCACCCACCT GG  TCCCAAAGT
                                    |||||||||||  ||  |||||||||
                                    AGGTGGGTGGA CC  AGGGTTTCA
                                          A  AC
GAM219   LOC149319 3'  ACTTTGGGAGGCCGAGGTGGGT 80064              _
             GGA                    TCCACCCACCTCGGC TCCCAAAGT
                                    |||||||||||||||  |||||||||
                                    AGGTGGGTGGAGCCG AGGGTTTCA
                                          G
GAM219   LOC149460 3'  ACTTTGGGAGGCCGAGGTGGGT 85604     C         _
             AGA                    TC ACCCACCTCGGC TCCCAAAGT
                                    || ||||||||||| |||||||||
                                    AG TGGGTGGAGCCG AGGGTTTCA
                                     A          G
GAM219   LOC149464 5'  ACTTTGGGAGGCCAAAGTGGGT 85582          CTC  _
             GGA                    TCCACCCAC   GGC TCCCAAAGT
                                    |||||||||   ||| |||||||||
                                    AGGTGGGTG   CCG AGGGTTTCA
                                          AAA   G
GAM219   LOC149464 3'  ACTTTGGGAGGCCAAGGTGGGT 85583           C  _
             GGA                    TCCACCCACCT GGC TCCCAAAGT
                                    |||||||||||| ||| |||||||||
                                    AGGTGGGTGGA CCG AGGGTTTCA
                                          A  G
GAM219   LOC149628 3'  ACTTTGGGAGGCCGAGGCAGGT 80273        CA     _
             GGA                    TCCACC  CCTCGGC TCCCAAAGT
                                    ||||||  ||||||| |||||||||
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                                AGGTGG  GGAGCCG AGGGTTTCA
                                   AC      G
GAM219  LOC149668 3'  ACTTTGGGAGGCTAAGGTGGGC 85690    A     CG  _
           GG                    CC CCCACCT  GC TCCCAAAGT
                                 || |||||||  || |||||||||
                                 GG GGGTGGA  CG AGGGTTTCA
                                  C      AT  G
GAM219  LOC149705 3'  ACTTTGAGCGGCTGAGGTGGGT 85772            CC_
           G                     CACCCACCTCGGCT   CAAAGT
                                 ||||||||||||||   ||||||
                                 GTGGGTGGAGTCGG   GTTTCA
                                        CGA
GAM219  LOC149710 3'  ACTTTGGGAGGCCGAGGTGGGT 80327             _
           GGA                     TCCACCCACCTCGGC TCCCAAAGT
                                 ||||||||||||||| |||||||||
                                 AGGTGGGTGGAGCCG AGGGTTTCA
                                        G
GAM219  LOC150142 5'  ACTTTAGAGGCTGAGGCAGGAG 80398    A  CA      CCC
           GA                    TCC CC  CCTCGGCT   AAAGT
                                 ||| ||  ||||||||   |||||
                                 AGG GG  GGAGTCGG   TTTCA
                                   A  AC       AGA
GAM219  LOC150225 3'  ACTTTGGGAGGCTGAGGCAGGT 86177       CA     _
           GGA                     TCCACC  CCTCGGC TCCCAAAGT
                                 ||||||  ||||||| |||||||||
                                 AGGTGG  GGAGTCG AGGGTTTCA
                                    AC      G
GAM219  LOC150299 3'  ACTTTGGGAGGCTGAGGTGGGC 86159    CA        _
           AGA                     TC  CCCACCTCGGC TCCCAAAGT
                                 ||  |||||||||| |||||||||
                                 AG  GGGTGGAGTCG AGGGTTTCA
                                  AC         G
GAM219  LOC150319 3'  ACTTTGGGAGGCTGAGGCGGAC 80460    AC  A     _
           GGA                     TCC  CC CCTCGGC TCCCAAAGT
                                 |||  || ||||||| |||||||||
                                 AGG  GG GGAGTCG AGGGTTTCA
                                   CA  C      G
GAM219  LOC150343 3'  ACTTTGGGAGGCCGAGGCAGGT 80487       CA     _
           GGA                     TCCACC  CCTCGGC TCCCAAAGT
                                 ||||||  ||||||| |||||||||
                                 AGGTGG  GGAGCCG AGGGTTTCA
                                    AC      G
GAM219  LOC150358 3'  ACTTTGGGAGGCCGAGGTG    86084          _
                                 CACCTCGGC TCCCAAAGT
                                 ||||||||| |||||||||
                                 GTGGAGCCG AGGGTTTCA
                                       G
GAM219  LOC150358 3'  ACTTTGGGAGGCCGAGTTGGGC 86085    A   C     _
           GGA                     TCC CCCA CTCGGC TCCCAAAGT
                                 ||| |||| |||||| |||||||||
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                                AGG GGGT GAGCCG AGGGTTTCA
                                  C   T     G
GAM219  LOC150372 3' GGGAGGCCGAGGCGGGTGGA  80618        A     _
                                TCCACCC CCTCGGC TCCC
                                ||||||| ||||||| ||||
                                AGGTGGG GGAGCCG AGGG
                                    C      G
GAM219  LOC150465 3' ACTTTGGGAGGCCAAGACAGGT 80682     CAC  C  _
                                ACC   CT GGC TCCCAAAGT
                                |||   || ||| |||||||||
                                TGG   GA CCG AGGGTTTCA
                                  ACA  A   G
GAM219  LOC150481 3' ACTTTGGGAGGCCAAGGTGGGT 80690           C  _
            GGA                   TCCACCCACCT GGC TCCCAAAGT
                                ||||||||||| ||| |||||||||
                                AGGTGGGTGGA CCG AGGGTTTCA
                                      A   G
GAM219  LOC150622 3' ACTTTGGGAGGCCGAGGCAGGC 80752     A  CA     _
            GGA                   TCC CC  CCTCGGC TCCCAAAGT
                                ||| ||  ||||||| |||||||||
                                AGG GG  GGAGCCG AGGGTTTCA
                                  C  AC      G
GAM219  LOC150630 3' ACTTTGGGAGGCCGAGGCAGGC 86283    CA  CA     _
            AGA                   TC  CC  CCTCGGC TCCCAAAGT
                                ||  ||  ||||||| |||||||||
                                AG  GG  GGAGCCG AGGGTTTCA
                                 AC  AC      G
GAM219  LOC150889 3' ACTTTGGGAGGCTGAGGCCGGT 80808        CA     _
            GGA                   TCCACC  CCTCGGC TCCCAAAGT
                                ||||||  ||||||| |||||||||
                                AGGTGG  GGAGTCG AGGGTTTCA
                                   CC      G
GAM219  LOC150935 3' GGGAGGCCGAGGTGGGCGGA  80834     A        _
                                TCC CCCACCTCGGC TCCC
                                ||| |||||||||| ||||
                                AGG GGGTGGAGCCG AGGG
                                  C         G
GAM219  LOC151068 3' ACTTTAAAAGGCTGAGGCAGG  86403    CA      CCC_
                                CC  CCTCGGCT    AAAGT
                                ||  ||||||||    |||||
                                GG  GGAGTCGG    TTTCA
                                 AC       AAAA
GAM219  LOC151196 3' ACTTTGGGAGGCCGAGGCAGGT 86446        CA     _
            GGA                   TCCACC  CCTCGGC TCCCAAAGT
                                ||||||  ||||||| |||||||||
                                AGGTGG  GGAGCCG AGGGTTTCA
                                   AC      G
GAM219  LOC151248 3' ACTTTGGGAGGCCAAGGCAGG  80980    CA  C  _
                                CC  CCT GGC TCCCAAAGT
                                ||  ||| ||| |||||||||
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                                GG  GGA CCG AGGGTTTCA
                                 AC   A   G
GAM219   LOC151248 3'  ACTTTGGGAGGCTGAGGCGGGT 80981        A     _
              GGA                  TCCACCC CCTCGGC TCCCAAAGT
                                   ||||||| ||||||| |||||||||
                                   AGGTGGG GGAGTCG AGGGTTTCA
                                      C      G
GAM219   LOC151429 3'  GGGAGGCCGAGGCGGGCAGA   86541    CA   A     _
                                   TC  CCC CCTCGGC TCCC
                                   ||  ||| ||||||| ||||
                                   AG  GGG GGAGCCG AGGG
                                    AC   C      G
GAM219   LOC151446 3'  ACTTTGGGAGGCTAAGGGGTGG 86565     CA      __  _
              GCAGA                   TC  CCCACCTC  GGC TCCCAAAGT
                                   ||  ||||||||  ||| |||||||||
                                   AG  GGGTGGGG  TCG AGGGTTTCA
                                    AC       AA   G
GAM219   LOC151632 3'  ACCTTGGGAGGCCGGGGCAGGA 86637     A  CA     _     A
              GGA                  TCC CC  CCTCGGC TCCCAA GT
                                   ||| ||  ||||||| |||||| ||
                                   AGG GG  GGGGCCG AGGGTT CA
                                    A  AC      G     C
GAM219   LOC151904 3'  ACTTTGGGAGGCTGAGGCGGGT 81198        A     _
              GGA                  TCCACCC CCTCGGC TCCCAAAGT
                                   ||||||| ||||||| |||||||||
                                   AGGTGGG GGAGTCG AGGGTTTCA
                                      C      G
GAM219   LOC152271 3'  ACCTTGGGAGGCCGAGGCAGGC 81350     CA  CA     _     A
              AGA                  TC  CC  CCTCGGC TCCCAA GT
                                   ||  ||  ||||||| |||||| ||
                                   AG  GG  GGAGCCG AGGGTT CA
                                    AC  AC      G     C
GAM219   LOC152313 3'  ACTTTGGGAGGCTGAGGCGGGC 86842     CA   A     _
              AGA                  TC  CCC CCTCGGC TCCCAAAGT
                                   ||  ||| ||||||| |||||||||
                                   AG  GGG GGAGTCG AGGGTTTCA
                                    AC   C      G
GAM219   LOC152316 3'  ACTTTAGGAGGCTGAGGTGGGT 86788     C          TC  _
              AGA                  TC ACCCACCTCGGC  CC AAAGT
                                   ||  ||||||||||||  ||  |||||
                                   AG TGGGTGGAGTCG  GG TTTCA
                                    A           GA  A
GAM219   LOC152317 3'  ACTTTGGGAAGTTGAGGTGGGC 86821     CA          _
              AGA                  TC  CCCACCTCGGCT CCCAAAGT
                                   ||  ||||||||||||| ||||||||
                                   AG  GGGTGGAGTTGA GGGTTTCA
                                    AC           A
GAM219   LOC152345 3'  GGAAAGCCAGTGAGGTGGA    81447        _  CTC    C_
                                   TCCACC CAC   GGCT  CC
                                   |||||| |||   ||||  ||
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                                AGGTGG GTG   CCGA  GG
                                   A   A__    AA
GAM219   LOC152426 3'  ACTTTGGGAGGCCAAGGCAGGC 86887    A  CA   C  _
                GG                  CC CC  CCT GGC TCCCAAAGT
                                    || ||  ||| ||| |||||||||
                                    GG GG  GGA CCG AGGGTTTCA
                                     C  AC   A   G
GAM219   LOC152445 3'  ACTGTGGAAGGCCGAGGTGGGT 86925             C_  A
                GGA                 TCCACCCACCTCGGCT  CCA AGT
                                    ||||||||||||||||  ||| |||
                                    AGGTGGGTGGAGCCGG  GGT TCA
                                              AA   G
GAM219   LOC152453 3'  ACTTCGGGAGGCCGAGGCGGGA 81462    A  A     _   A
                GGA                 TCC CCC CCTCGGC TCCC AAGT
                                    ||| ||| ||||||| |||| ||||
                                    AGG GGG GGAGCCG AGGG TTCA
                                      A  C      G   C
GAM219   LOC152453 3'  ACTTTGGGAGGCTGAGGCAGGA 81463    A  CA     _
                GGA                 TCC CC  CCTCGGC TCCCAAAGT
                                    ||| ||  ||||||| |||||||||
                                    AGG GG  GGAGTCG AGGGTTTCA
                                      A  AC      G
GAM219   LOC152627 3'  ACTTTGGGAGACCGAGGCGGG  81499    A    _
                                    CCC CCTCGG CTCCCAAAGT
                                    ||| |||||| ||||||||||
                                    GGG GGAGCC GAGGGTTTCA
                                      C     A
GAM219   LOC152804 3'  ACTCTGGAGGCTGAGGCAGG   87065   CA     TC   A
                                    CC  CCTCGGC  CCA AGT
                                    ||  |||||||  ||| |||
                                    GG  GGAGTCG  GGT TCA
                                     AC      GA   C
GAM219   LOC152804 3'  ACTTTGGGAGGCCAACGTGG   87066     CTC  _
                                    CCAC   GGC TCCCAAAGT
                                    ||||   ||| |||||||||
                                    GGTG   CCG AGGGTTTCA
                                      CAA   G
GAM219   LOC152804 3'  ACTTTGGGAGGTGGAGGTGGGC 87067    A      G  _
                GGA                 TCC CCCACCTC GC TCCCAAAGT
                                    ||| |||||||| || |||||||||
                                    AGG GGGTGGAG TG AGGGTTTCA
                                      C       G  G
GAM219   LOC152860 3'  ACTTTGGGAGGCAGAGGCGGGC 81573    A   A   G  _
                GG                  CC CCC CCTC GC TCCCAAAGT
                                    || ||| |||| || |||||||||
                                    GG GGG GGAG CG AGGGTTTCA
                                     C   C    A  G
GAM219   LOC152925 3'  ACTTCGGGAGGCTGAGGTGGGA 81614    A        _   A
                GGA                 TCC CCCACCTCGGC TCCC AAGT
                                    ||| |||||||||| |||| ||||
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                                AGG GGGTGGAGTCG AGGG TTCA
                                  A         G   C
GAM219  LOC152926 3'  ACTTTGGGAGGCCAAGGTGGGT 81627    C       C  _
                AGA               TC ACCCACCT GGC TCCCAAAGT
                                  || |||||||| ||| |||||||||
                                  AG TGGGTGGA CCG AGGGTTTCA
                                   A       A   G
GAM219  LOC153260 3'  ACTTTGGCAGGCTGAGGCGGGC 81666    CA  A      C_
                AGA               TC  CCC CCTCGGCT  CCAAAGT
                                  ||  ||| ||||||||  |||||||
                                  AG  GGG GGAGTCGG  GGTTTCA
                                   AC  C       AC
GAM219  LOC153561 3'  ACTTTGGGAGGCCAAGGCAGG  81747    CA  C  _
                                  CC  CCT GGC TCCCAAAGT
                                  ||  ||| ||| |||||||||
                                  GG  GGA CCG AGGGTTTCA
                                   AC  A   G
GAM219  LOC153579 3'  ACTTTGGGAGGCCGAGGCGGGT 81761        A     _
                GGA               TCCACCC CCTCGGC TCCCAAAGT
                                  ||||||| ||||||| |||||||||
                                  AGGTGGG GGAGCCG AGGGTTTCA
                                     C      G
GAM219  LOC153682 3'  ACTCTGGAGGCTGAGGCAGGAG 87266     A  CA      TC   A
                GA                TCC CC  CCTCGGC  CCA AGT
                                  ||| ||  |||||||  ||| |||
                                  AGG GG  GGAGTCG  GGT TCA
                                   A  AC      GA   C
GAM219  LOC153688 3'  ACTTTGGGAGACCAAGGCGGGT 87285       A   C  _
                GG                CCACCC CCT GG CTCCCAAAGT
                                  |||||| ||| || ||||||||||
                                  GGTGGG GGA CC GAGGGTTTCA
                                     C   A  A
GAM219  LOC153727 3'  ACTTTGGGAGGCCGGGCGGGGG 87359     A   AC     _
                GA                TCC CCC  CTCGGC TCCCAAAGT
                                  ||| |||  |||||| |||||||||
                                  AGG GGG  GGGCCG AGGGTTTCA
                                   _  GC     G
GAM219  LOC154089 3'  ACTTTGGGAGGTCGAGGCAGGT 81939        CA      _
                GGA               TCCACC  CCTCGGC TCCCAAAGT
                                  ||||||  ||||||| |||||||||
                                  AGGTGG  GGAGCTG AGGGTTTCA
                                     AC      G
GAM219  LOC154403 3'  ACTTTAGGAGGCTGAGGTGGGA 81964     A         TC  _
                GGA               TCC CCCACCTCGGC  CC AAAGT
                                  ||| ||||||||||  || |||||
                                  AGG GGGTGGAGTCG  GG TTTCA
                                   A         GA  A
GAM219  LOC154403 3'  ACTTTGGGAGGCCGAGGAGGGT 81965        A      _
                GGA               TCCACCC CCTCGGC TCCCAAAGT
                                  ||||||| ||||||| |||||||||
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                                AGGTGGG GGAGCCG AGGGTTTCA
                                   A      G
GAM219  LOC154739 5' ACTCTGGAGGCTGAGGCAGG  87427    CA      TC   A
                                CC  CCTCGGC  CCA AGT
                                ||  |||||||  ||| |||
                                GG  GGAGTCG  GGT TCA
                                 AC       GA   C
GAM219  LOC154791 3' ACTTTGGGAGGCCAAGGCAGGC 82046    A  CA   C  _
           GG                    CC CC  CCT GGC TCCCAAAGT
                                || ||  ||| ||| |||||||||
                                GG GG  GGA CCG AGGGTTTCA
                                 C AC   A   G
GAM219  LOC154877 3' ACTTTGGGAGGCTGAGGCAGG  87519    CA      _
                                CC  CCTCGGC TCCCAAAGT
                                ||  ||||||| |||||||||
                                GG  GGAGTCG AGGGTTTCA
                                 AC       G
GAM219  LOC154881 3' ACTCTGGAGGCTGAGGCAGGAG 82066     A  CA      TC   A
           GA                    TCC CC  CCTCGGC  CCA AGT
                                |||  ||  |||||||  ||| |||
                                AGG GG  GGAGTCG  GGT TCA
                                  A  AC       GA   C
GAM219  LOC154992 3' ACTTTAGGAGGCTGAGGTAGGA 82126     A  C       TC  _
           GGA                     TCC CC ACCTCGGC  CC AAAGT
                                |||  ||  ||||||||  ||  |||||
                                AGG GG  TGGAGTCG  GG TTTCA
                                  A  A       GA  A
GAM219  LOC154992 3' ACTTTGGGAGGCCGAGGAGGGT 82127         A      _
           GGA                     TCCACCC CCTCGGC TCCCAAAGT
                                |||||||  |||||||  |||||||||
                                AGGTGGG GGAGCCG AGGGTTTCA
                                   A      G
GAM219  LOC155006 3' ACTTTGGGAGGCAGAGGTGGGC 82157    CA       G  _
           AGA                     TC  CCCACCTC GC TCCCAAAGT
                                ||  ||||||||  ||  |||||||||
                                AG  GGGTGGAG CG AGGGTTTCA
                                 AC       A  G
GAM219  LOC155054 3' ACTTTGGGAGGCCCAGGTGGG  82196        C  _
                                CCCACCT GGC TCCCAAAGT
                                |||||||  |||  |||||||||
                                GGGTGGA CCG AGGGTTTCA
                                   C   G
GAM219  LOC155054 3' ACTTTGGGAGGTTGAGGCAGGA 82197     A  CA      _
           GGA                     TCC CC  CCTCGGC TCCCAAAGT
                                |||  ||  |||||||  |||||||||
                                AGG GG  GGAGTTG AGGGTTTCA
                                  A  AC       G
GAM219  LOC155072 3' ACTTTGGGAGGCTGAGGCGGGT 87650         A      _
           GGA                     TCCACCC CCTCGGC TCCCAAAGT
                                |||||||  |||||||  |||||||||
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                                AGGTGGG GGAGTCG AGGGTTTCA
                                   C      G
GAM219  LOC155072 3'  ACTTTGGGAGGCTGAGGTAGGT 87651       C      _
                GGA                TCCACC ACCTCGGC TCCCAAAGT
                                   ||||||| |||||||| |||||||||
                                   AGGTGG TGGAGTCG AGGGTTTCA
                                      A       G
GAM219  LOC155376 3'  ACTTTGGGAAGCCAAGGCAGGC 82237    A  CA   C   _
                GG                   CC CC  CCT GGCT CCCAAAGT
                                     || ||  ||| |||| ||||||||
                                     GG GG  GGA CCGA GGGTTTCA
                                      C AC   A    A
GAM219  LOC157273 5'  ACTTCAGGGTTCCAGAGCTGAG 87714    C  C  C   _ CT   A_
                TAGA                 TC AC CA CTC GG  CCC  AAGT
                                     || || || ||| ||  |||  ||||
                                     AG TG GT GAG CC  GGG  TTCA
                                      A  A  C   A  TT   AC
GAM219  LOC157464 5'  ACTTTGGGAGGCTGAGGCGGGT 87742       A      _
                G                    CACCC CCTCGGC TCCCAAAGT
                                     ||||| ||||||| |||||||||
                                     GTGGG GGAGTCG AGGGTTTCA
                                        C      G
GAM219  LOC157657 3'  ACTTTGGGAGGCTGAGGCAGGC 82427    CA  CA      _
                AGA                  TC  CC  CCTCGGC TCCCAAAGT
                                     ||  ||  ||||||| |||||||||
                                     AG  GG  GGAGTCG AGGGTTTCA
                                      AC  AC      G
GAM219  LOC157660 3'  ACTTTGGGAGGCCGAGGCGG   87798    A      _
                                     CC CCTCGGC TCCCAAAGT
                                     || ||||||| |||||||||
                                     GG GGAGCCG AGGGTTTCA
                                      C      G
GAM219  LOC157983 3'  ACTTTGGGAGGCCGAGGCGGG  82534     A      _
                                     CCC CCTCGGC TCCCAAAGT
                                     ||| ||||||| |||||||||
                                     GGG GGAGCCG AGGGTTTCA
                                       C      G
GAM219  LOC158088 3'  TGGGAGGCCGAGGTGGGTGGA  87979              _
                                     TCCACCCACCTCGGC TCCCA
                                     ||||||||||||||| |||||
                                     AGGTGGGTGGAGCCG AGGGT
                                              G
GAM219  LOC158187 3'  ACTTTGGGAGGCCGAGGTGGGT 87983              _
                GGA                  TCCACCCACCTCGGC TCCCAAAGT
                                     ||||||||||||||| |||||||||
                                     AGGTGGGTGGAGCCG AGGGTTTCA
                                              G
GAM219  LOC158191 3'  ACTTTGGGAGGCCAAGGCGGGT 82661       A  C  _
                GG                   CCACCC CCT GGC TCCCAAAGT
                                     |||||| ||| ||| |||||||||
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                                GGTGGG GGA CCG AGGGTTTCA
                                   C   A   G
GAM219  LOC158287 3'  CTTTGGGGGCAAGTGGG     88031       CTCG
                                CCCAC    GCTCCCAAAG
                                |||||    ||||||||||
                                GGGTG    CGGGGGTTTC
                                  AA__
GAM219  LOC158288 3'  ACTTTGGGAGGCCAAGGTGGG  88016        C  _
                                CCCACCT GGC TCCCAAAGT
                                ||||||| ||| |||||||||
                                GGGTGGA CCG AGGGTTTCA
                                   A   G
GAM219  LOC158292 5'  ACTTTGGGAGGCCAAGGCGGGC 88035    A   A   C  _
          GG                      CC CCC CCT GGC TCCCAAAGT
                                || ||| ||| ||| |||||||||
                                GG GGG GGA CCG AGGGTTTCA
                                 C   C   A   G
GAM219  LOC158292 5'  ACTTTGGGAGGCCGAGACAGGT 88036       CAC     _
          GG                      CCACC   CTCGGC TCCCAAAGT
                                ||||||   |||||| |||||||||
                                GGTGG   GAGCCG AGGGTTTCA
                                  ACA     G
GAM219  LOC158337 3'  ACTTTGGGAGGCCGAGGCGGGC 88104    CA   A      _
          AGA                     TC  CCC CCTCGGC TCCCAAAGT
                                ||  ||| ||||||| |||||||||
                                AG  GGG GGAGCCG AGGGTTTCA
                                 AC   C      G
GAM219  LOC158382 5'  ACTTTGGGAGGCTGAGGTGGGA 88123     A         _
          GGA                     TCC CCCACCTCGGC TCCCAAAGT
                                |||  |||||||||||  |||||||||
                                AGG GGGTGGAGTCG AGGGTTTCA
                                  A          G
GAM219  LOC158434 3'  ACTTTGAGGGGTTGAGGTGGGA 88157     A           _
          GGA                     TCC CCCACCTCGGCTCC CAAAGT
                                |||  ||||||||||||| ||||||
                                AGG GGGTGGAGTTGGGG GTTTCA
                                  A            A
GAM219  LOC158677 5'  ACTTTGGGAAGCTGAGGTGGGT 88242    C          _
          AGA                     TC ACCCACCTCGGCT CCCAAAGT
                                ||  |||||||||||| ||||||||
                                AG TGGGTGGAGTCGA GGGTTTCA
                                 A           A
GAM219  LOC158819 5'  ACTTTGGGAGGCCCAGGCAGGC 88264    A  CA   C  _
          GG                      CC CC  CCT GGC TCCCAAAGT
                                || ||  ||| ||| |||||||||
                                GG GG  GGA CCG AGGGTTTCA
                                 C  AC   C   G
GAM219  LOC158819 3'  ACTTTGGGAGGCTGAGGCGGGT 88265        A      _
          GGA                     TCCACCC CCTCGGC TCCCAAAGT
                                |||||||  |||||||  |||||||||
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                                AGGTGGG GGAGTCG AGGGTTTCA
                                   C      G
GAM219  LOC158863 3'  ACTTTGGGATGCTGAGGTCGGC 88293     A  C       _
          GGA                    TCC CC ACCTCGGC TCCCAAAGT
                                 ||| || |||||||| |||||||||
                                 AGG GG TGGAGTCG AGGGTTTCA
                                   C C       T
GAM219  LOC159036 3'  ACTTTGGGAAGCCAAGGCGGGT 88340       A   C   _
          GG                     CCACCC CCT GGCT CCCAAAGT
                                 |||||| ||| |||| |||||||||
                                 GGTGGG GGA CCGA GGGTTTCA
                                    C   A    A
GAM219  LOC159053 3'  ACTTTGGGAGGCCAAGGCGGG  88357     A   C   _
                                 CCC CCT GGC TCCCAAAGT
                                 ||| ||| ||| |||||||||
                                 GGG GGA CCG AGGGTTTCA
                                   C   A   G
GAM219  LOC159053 3'  ACTTTGGGAGGCCCAGGCAGGC 88358    A  CA   C   _
          GG                     CC CC  CCT GGC TCCCAAAGT
                                 || ||  ||| ||| |||||||||
                                 GG GG  GGA CCG AGGGTTTCA
                                  C  AC   C   G
GAM219  LOC161823 3'  ACTTTGGGAAGCCAAAGTGGG  83173       CTC   _
                                 CCCAC   GGCT CCCAAAGT
                                 |||||   |||| ||||||||
                                 GGGTG   CCGA GGGTTTCA
                                    AAA    A
GAM219  LOC170395 3'  ACTTTGGGAGGCCGAGGTGGGC 76860     CA         _
          AGA                    TC  CCCACCTCGGC TCCCAAAGT
                                 ||  |||||||||||| |||||||||
                                 AG  GGGTGGAGCCG AGGGTTTCA
                                  AC          G
GAM219  LOC196027 3'  ACTTTGGGAGGCTAAGGCAGGT 88936       CA   CG  _
          GG                     CCACC  CCT  GC TCCCAAAGT
                                 |||||  |||  || |||||||||
                                 GGTGG  GGA  CG AGGGTTTCA
                                    AC   AT  G
GAM219  LOC196047 5'  ACTTTGGGAGGTTAAGGCAGGC 91141    A  CA   CG  _
          GG                     CC CC  CCT  GC TCCCAAAGT
                                 || ||  |||  || |||||||||
                                 GG GG  GGA  TG AGGGTTTCA
                                  C  AC   AT  G
GAM219  LOC196415 5'  ACTTTGGGAGGCTGAGGTGGGA 91192     A         _
          GGA                    TCC CCCACCTCGGC TCCCAAAGT
                                 ||| |||||||||| |||||||||
                                 AGG GGGTGGAGTCG AGGGTTTCA
                                   A          G
GAM219  LOC196528 3'  ACTTTGGGAGGCTGAGGCAGAA 89104     ACCCA      _
          GGA                    TCC     CCTCGGC TCCCAAAGT
                                 |||     ||||||| |||||||||
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                                AGG    GGAGTCG AGGGTTTCA
                                  AAGAC      G
GAM219  LOC196540 3'  ACTTTGGGAGGCCGAGGCAGGT 91195       CA     _
                GGA                TCCACC  CCTCGGC TCCCAAAGT
                                |||||| ||||||| |||||||||
                                AGGTGG  GGAGCCG AGGGTTTCA
                                   AC      G
GAM219  LOC196761 3'  ACTTTGGGAGGCCGCGGCGGGT 91114       A  T   _
                GG                 CCACCC CC CGGC TCCCAAAGT
                                |||||| || |||| |||||||||
                                GGTGGG GG GCCG AGGGTTTCA
                                   C  C    G
GAM219  LOC197196 3'  ACTTCGGGAGGCCGAGGTAGGC 91291     A  C      _   A
                GGA                TCC CC ACCTCGGC TCCC AAGT
                                ||| || |||||||| |||| ||||
                                AGG GG TGGAGCCG AGGG TTCA
                                  C  A       G    C
GAM219  LOC197196 3'  ACTTTGGGAGGCTGAGGTGGGT 91292             _
                GGA                TCCACCCACCTCGGC TCCCAAAGT
                                |||||||||||||| |||||||||
                                AGGTGGGTGGAGTCG AGGGTTTCA
                                         G
GAM219  LOC197201 3'  ACTTTGGGAGGCCGAGGTAGGC 89262     A  C      _
                GGA                TCC CC ACCTCGGC TCCCAAAGT
                                ||| || |||||||| |||||||||
                                AGG GG TGGAGCCG AGGGTTTCA
                                  C  A       G
GAM219  LOC197319 3'  ACTTTGGGAGGCCGAGGTGGGC 89310     A        _
                GGA                TCC CCCACCTCGGC TCCCAAAGT
                                ||| |||||||||| |||||||||
                                AGG GGGTGGAGCCG AGGGTTTCA
                                  C          G
GAM219  LOC197319 3'  ACTTTGGGAGGCCGAGGTGGGT 89311             _
                GGA                TCCACCCACCTCGGC TCCCAAAGT
                                |||||||||||||| |||||||||
                                AGGTGGGTGGAGCCG AGGGTTTCA
                                         G
GAM219  LOC199676 3'  TTTTGAGGCCGAGGTGGGCGGA 91364     A          CC
                                TCC CCCACCTCGGCT  CAAAG
                                ||| ||||||||||  |||||
                                AGG GGGTGGAGCCGG  GTTTT
                                  C          A_
GAM219  LOC199733 3'  ACTTTGGGAGGTCGAGGTGGGC 91431     A        _
                GGA                TCC CCCACCTCGGC TCCCAAAGT
                                ||| |||||||||| |||||||||
                                AGG GGGTGGAGCTG AGGGTTTCA
                                  C          G
GAM219  LOC199786 3'  ACTTTGGGAGGCTGAGACAGGT 89732       CAC     _
                GG                 CCACC   CTCGGC TCCCAAAGT
                                |||||   |||||| |||||||||
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                                GGTGG   GAGTCG AGGGTTTCA
                                  ACA     G
GAM219  LOC199786 3'  ACTTTGGGAGGCTGAGGCGGGC 89733    CA   A     _
          AGA                     TC  CCC CCTCGGC TCCCAAAGT
                                ||  ||| ||||||| |||||||||
                                AG  GGG GGAGTCG AGGGTTTCA
                                 AC   C      G
GAM219  LOC200014 3'  ACTTTGGAAAGCTGAGGCAGGT 89913       CA      C_
          GGA                     TCCACC  CCTCGGCT  CCAAAGT
                                ||||||  ||||||||  |||||||
                                AGGTGG  GGAGTCGA  GGTTTCA
                                   AC       AA
GAM219  LOC200317 3'  ACTTTGGGAGGCCGAAGCAGG  90218    CACC    _
                                CC    TCGGC TCCCAAAGT
                                ||    ||||| |||||||||
                                GG    AGCCG AGGGTTTCA
                                 ACGA    G
GAM219  LOC200470 3'  ACTTTGGGAGGCTGAGGCGGGA 91638     A   A     _
          GGA                     TCC CCC CCTCGGC TCCCAAAGT
                                ||| ||| ||||||| |||||||||
                                AGG GGG GGAGTCG AGGGTTTCA
                                  A   C      G
GAM219  LOC200728 3'  ACTTTGGGAGGCCGAGGTGGGC 91679    CA        _
          AGA                     TC  CCCACCTCGGC TCCCAAAGT
                                ||  |||||||||| |||||||||
                                AG  GGGTGGAGCCG AGGGTTTCA
                                  AC          G
GAM219  LOC200904 3'  ACCTTGGGAGGCCGAGGCAGGC 91770    CA  CA     _     A
          AGA                     TC  CC  CCTCGGC TCCCAA GT
                                ||  ||  ||||||| |||||| ||
                                AG  GG  GGAGCCG AGGGTT CA
                                 AC  AC      G     C
GAM219  LOC200904 3'  ACTCTGGAGGCTGAGGCAGG   91771    CA      TC   A
                                CC  CCTCGGC  CCA AGT
                                ||  |||||||  ||| |||
                                GG  GGAGTCG  GGT TCA
                                 AC      GA   C
GAM219  LOC200940 3'  ACTTTGGGAGGCTGAGGCAGGC 90383     A  CA     _
          GGA                     TCC CC  CCTCGGC TCCCAAAGT
                                ||| ||  ||||||| |||||||||
                                AGG GG  GGAGTCG AGGGTTTCA
                                  C  AC      G
GAM219  LOC201173 3'  ACTTTGGGAGGCCGAGGCGGGC 88664     A   A     _
          GGA                     TCC CCC CCTCGGC TCCCAAAGT
                                ||| ||| ||||||| |||||||||
                                AGG GGG GGAGCCG AGGGTTTCA
                                  C   C      G
GAM219  LOC201220 3'  ACTTTGGGAGGCCGAGGTGGGC 88699     A        _
          GGA                     TCC CCCACCTCGGC TCCCAAAGT
                                ||| |||||||||| |||||||||
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                                AGG GGGTGGAGCCG AGGGTTTCA
                                  C         G
GAM219  LOC201252 3'  ACTTTGGGAAGCCGAGGTGGGC 89544    CA        _
                AGA               TC  CCCACCTCGGCT CCCAAAGT
                                  ||  |||||||||||| ||||||||
                                  AG  GGGTGGAGCCGA GGGTTTCA
                                   AC          A
GAM219  LOC201564 3'  ACTTTGGGAGGCTGAGGTGGGC 81270    CA        _
                AGA               TC  CCCACCTCGGC TCCCAAAGT
                                  ||  |||||||||||| |||||||||
                                  AG  GGGTGGAGTCG AGGGTTTCA
                                   AC          G
GAM219  LOC201627 3'  ACTTTGGGAGGCCAAGGTGG   90445       C  _
                                  CCACCT GGC TCCCAAAGT
                                  |||||| ||| |||||||||
                                  GGTGGA CCG AGGGTTTCA
                                     A   G
GAM219  LOC201685 3'  ACTTTGGGAGGCCGAGGCAGGC 91833    A  CA     _
                GGA               TCC CC  CCTCGGC TCCCAAAGT
                                  ||| ||  ||||||| |||||||||
                                  AGG GG  GGAGCCG AGGGTTTCA
                                    C  AC       G
GAM219  LOC201810 3'  ACTTTGGGAGGCCGAGGCAGAT 90499      CCCA     _
                GGA               TCCA    CCTCGGC TCCCAAAGT
                                  ||||    ||||||| |||||||||
                                  AGGT    GGAGCCG AGGGTTTCA
                                    AGAC       G
GAM219  LOC201868 3'  ACTTTGGGAGGCCGAGGAGGGT 90512        A     _
                GGA               TCCACCC CCTCGGC TCCCAAAGT
                                  ||||||| ||||||| |||||||||
                                  AGGTGGG GGAGCCG AGGGTTTCA
                                     A      G
GAM219  LOC201895 3'  ACTTTGGGAGGCTGAGGTGGGT 90538              _
                GGA               TCCACCCACCTCGGC TCCCAAAGT
                                  |||||||||||||| |||||||||
                                  AGGTGGGTGGAGTCG AGGGTTTCA
                                           G
GAM219  LOC201911 3'  ACTTTGGGAGGCCGAGGCGGGC 91858    A  A     _
                GGA               TCC CCC CCTCGGC TCCCAAAGT
                                  ||| ||| ||||||| |||||||||
                                  AGG GGG GGAGCCG AGGGTTTCA
                                    C  C       G
GAM219  LOC201931 3'  ACTTTGGGAGGCTGAGGCAGGA 90559    A  CA     _
                GGA               TCC CC  CCTCGGC TCCCAAAGT
                                  ||| ||  ||||||| |||||||||
                                  AGG GG  GGAGTCG AGGGTTTCA
                                    A  AC       G
GAM219  LOC202038 3'  ACTTTGGAAGGCCGAGGCGGGC 90617    A  A      C_
                GGA               TCC CCC CCTCGGCT  CCAAAGT
                                  ||| ||| ||||||||  |||||||
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                                AGG GGG GGAGCCGG  GGTTTCA
                                  C  C       AA
GAM219  LOC202052 3'  ACTTTGGGAGGCTGTGGCAGGT 91895       CA  T   _
          GG                      CCACC  CC CGGC TCCCAAAGT
                                  ||||||  || |||| |||||||||
                                  GGTGG  GG GTCG AGGGTTTCA
                                    AC  T    G
GAM219  LOC202134 5'  ACTTTGGGAGTCCAAGGTGGGT 91914           C  _
          GGA                     TCCACCCACCT GG CTCCCAAAGT
                                  ||||||||||| || |||||||||
                                  AGGTGGGTGGA CC GAGGGTTTCA
                                        A  T
GAM219  LOC202781 3'  GGAGGCCGAGGTGGGCGGA   91974     A         TC
                                  TCC CCCACCTCGGC  CC
                                  ||| ||||||||||  ||
                                  AGG GGGTGGAGCCG  GG
                                    C          GA
GAM219  LOC202868 3'  ACTTTGGGAGGCTGAGGCGGGT 91983         A      _
          GGA                     TCCACCC CCTCGGC TCCCAAAGT
                                  ||||||| ||||||| |||||||||
                                  AGGTGGG GGAGTCG AGGGTTTCA
                                     C      G
GAM219  LOC202868 3'  ACTTTGGGAGGCTGAGGTAGGT 91984        C       _
          GGA                     TCCACC ACCTCGGC TCCCAAAGT
                                  |||||| |||||||| |||||||||
                                  AGGTGG TGGAGTCG AGGGTTTCA
                                     A       G
GAM219  LOC203025 3'  ACTTTGAGAGGCCGAGGCGGGT 90738         A      _ C
          GGG                     TCCACCC CCTCGGC TC CAAAGT
                                  ||||||| ||||||| || ||||||
                                  GGGTGGG GGAGCCG AG GTTTCA
                                     C      G  A
GAM219  LOC203083 3'  ACCTTGCGAGGCCGAGGCAGGT 92079        CA      _ C   A
          GGA                     TCCACC  CCTCGGC TC CAA GT
                                  ||||||  ||||||| || ||| ||
                                  AGGTGG  GGAGCCG AG GTT CA
                                     AC      G  C   C
GAM219  LOC203246 3'  ACTTTGGGAGGCCGAGGCGGGC 90826     A   A      _
          GGA                     TCC CCC CCTCGGC TCCCAAAGT
                                  ||| ||| ||||||| |||||||||
                                  AGG GGG GGAGCCG AGGGTTTCA
                                    C   C      G
GAM219  LOC203289 3'  ACTTTGGGAGGCCGAGGCGGG  90861     A      _
                                  CCC CCTCGGC TCCCAAAGT
                                  ||| ||||||| |||||||||
                                  GGG GGAGCCG AGGGTTTCA
                                    C      G
GAM219  LOC203350 3'  ACTTTGGGTGGCCGAGGCAGG  92224     CA       _
                                  CC  CCTCGGCT CCCAAAGT
                                  ||  |||||||| ||||||||
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                                GG  GGAGCCGG GGGTTTCA
                                 AC       T
GAM219   LOC203378 3'  ACTTTGGGAGGTTGAGGTGGGC 92270    CA        _
           AGA                   TC  CCCACCTCGGC TCCCAAAGT
                                 ||  |||||||||| |||||||||
                                 AG  GGGTGGAGTTG AGGGTTTCA
                                  AC         G
GAM219   LOC206338 5'  ACTTTTCGCAAAATGGGTGGA  91090        CCTCG  TCCC
                                 TCCACCCA    GC    AAAGT
                                 ||||||||    ||    |||||
                                 AGGTGGGT    CG    TTTCA
                                      AAAA_  CT__
GAM219   LOC219376 3'  ACTTTGGGAGGCTGGGGCAGGC 95512     A  CA     _
           GGA                   TCC CC  CCTCGGC TCCCAAAGT
                                 ||| ||  ||||||| |||||||||
                                 AGG GG  GGGGTCG AGGGTTTCA
                                   C  AC      G
GAM219   LOC219406 3'  ACTTTGGCAGGCCGAGGCGGGC 95201    CA   A      C_
           AGA                   TC  CCC CCTCGGCT  CCAAAGT
                                 ||  ||| ||||||||  |||||||
                                 AG  GGG GGAGCCGG  GGTTTCA
                                  AC   C       AC
GAM219   LOC219627 3'  ACTTTGGGAGGCCAAGGCGGG  93793     A   C   _
                                 CCC CCT GGC TCCCAAAGT
                                 ||| ||| ||| |||||||||
                                 GGG GGA CCG AGGGTTTCA
                                   C   A   G
GAM219   LOC219649 3'  ACTTTGGGAGGCTGAGGCGGGT 94541        A     _
           GGA                   TCCACCC CCTCGGC TCCCAAAGT
                                 ||||||| ||||||| |||||||||
                                 AGGTGGG GGAGTCG AGGGTTTCA
                                     C      G
GAM219   LOC219667 3'  ACTCTGGAAGCTGAGGTGAGAG 92946     ACC        C   A
           GA                    TCC   CACCTCGGCT CCA AGT
                                 |||   |||||||||| ||| |||
                                 AGG   GTGGAGTCGA GGT TCA
                                   AGA         A   C
GAM219   LOC219673 3'  ACTTTGGGAGGCCCAGGCGGGC 94605    A   A   C   _
           GG                    CC CCC CCT GGC TCCCAAAGT
                                 ||  ||| ||| ||| |||||||||
                                 GG GGG GGA CCG AGGGTTTCA
                                  C   C   C   G
GAM219   LOC219722 5'  ACTTTGGGAGGCCGAGGTAGGC 94673     A  C      _
           GGA                   TCC CC ACCTCGGC TCCCAAAGT
                                 ||| ||  |||||||| |||||||||
                                 AGG GG TGGAGCCG AGGGTTTCA
                                   C  A       G
GAM219   LOC219919 3'  GGGAGGCCGAGGCAGGCGGA   94929     A  CA     _
                                 TCC CC  CCTCGGC TCCC
                                 ||| ||  ||||||| ||||
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                                AGG GG  GGAGCCG AGGG
                                  C AC      G
GAM219  LOC220370 3'  ACTCTGGGAGGCCGAGGCGGG  94391     A     _    A
                                CCC CCTCGGC TCCCA AGT
                                ||| ||||||| ||||| |||
                                GGG GGAGCCG AGGGT TCA
                                  C      G    C
GAM219  LOC220506 3'  ACTTTAGGAGGCCGAGGCAGGC 74513     A  CA      TC  _
          GGA                     TCC CC  CCTCGGC  CC AAAGT
                                ||| ||  |||||||  || |||||
                                AGG GG  GGAGCCG  GG TTTCA
                                  C AC      GA A
GAM219  LOC220575 3'  ACTTTGGGAAGCTGAGGTGGGC 76811    CA          _
          AGA                     TC  CCCACCTCGGCT CCCAAAGT
                                ||  |||||||||||| ||||||||
                                AG  GGGTGGAGTCGA GGGTTTCA
                                 AC          A
GAM219  LOC220662 3'  ACTTTGGGAGGCTAGGTGGGCA 92801    CA      C  _
          GA                      TC  CCCACCT GGC TCCCAAAGT
                                ||  ||||||| ||| |||||||||
                                AG  GGGTGGA TCG AGGGTTTCA
                                 AC      _  G
GAM219  LOC220906 3'  ACTTTGGGAGGCTGAGGTGGGC 93027    CA          _
          AGA                     TC  CCCACCTCGGC TCCCAAAGT
                                ||  |||||||||| |||||||||
                                AG  GGGTGGAGTCG AGGGTTTCA
                                 AC          G
GAM219  LOC221178 3'  ACTTTGGGAGGCCAAGGCAGGT 95162       CA  C  _
          GG                      CCACC  CCT GGC TCCCAAAGT
                                |||||  ||| ||| |||||||||
                                GGTGG  GGA CCG AGGGTTTCA
                                   AC  A  G
GAM219  LOC221271 3'  ACTTTGGGAGGCCGAGACGGG  93491     AC    _
                                CCC  CTCGGC TCCCAAAGT
                                |||  |||||| |||||||||
                                GGG  GAGCCG AGGGTTTCA
                                  CA     G
GAM219  LOC221271 3'  ACTTTGGGAGGCCGAGGTGGGC 93492     A         _
          GGA                     TCC CCCACCTCGGC TCCCAAAGT
                                ||| ||||||||||| |||||||||
                                AGG GGGTGGAGCCG AGGGTTTCA
                                  C          G
GAM219  LOC221288 3'  ACTTTGGGAGGCCGAGGTGGGC 95253    CA          _
          AGA                     TC  CCCACCTCGGC TCCCAAAGT
                                ||  |||||||||| |||||||||
                                AG  GGGTGGAGCCG AGGGTTTCA
                                 AC          G
GAM219  LOC221410 3'  ACTTTGGGAGGCCGAGGCAGGT 93686    C  CA      _
          AGA                     TC ACC  CCTCGGC TCCCAAAGT
                                || |||  ||||||| |||||||||
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                                AG TGG  GGAGCCG AGGGTTTCA
                                 A  AC      G
GAM219  LOC221474 3'  ACTTTGGGAGGCCGAGGTGGGC 93986    CA        _
          AGA                    TC  CCCACCTCGGC TCCCAAAGT
                                ||  |||||||||||| |||||||||
                                AG  GGGTGGAGCCG AGGGTTTCA
                                 AC         G
GAM219  LOC221477 3'  ACTTTGGGAGGCTGAGGCAGGC 93763    CA  CA     _
          AGA                    TC  CC  CCTCGGC TCCCAAAGT
                                ||  ||  ||||||| |||||||||
                                AG  GG  GGAGTCG AGGGTTTCA
                                 AC  AC      G
GAM219  LOC221490 3'  ACTTTGGGAGGCCGAGGCGGGT 95296        A     _
          GGA                    TCCACCC CCTCGGC TCCCAAAGT
                                |||||||| ||||||| |||||||||
                                AGGTGGG GGAGCCG AGGGTTTCA
                                    C      G
GAM219  LOC221543 5'  ACTCTGGGAGGGCGAGGTGGGC 95356    A       G _    A
          GGA                    TCC CCCACCTCG C TCCCA AGT
                                ||| ||||||||| | ||||| |||
                                AGG GGGTGGAGC G AGGGT TCA
                                  C        G G    C
GAM219  LOC221543 3'  ACTTTGGGAGGCCGAGGCAGGT 95357       CA     _
          GGA                    TCCACC  CCTCGGC TCCCAAAGT
                                ||||||  ||||||| |||||||||
                                AGGTGG  GGAGCCG AGGGTTTCA
                                    AC      G
GAM219  LOC221543 3'  ACTTTGGGAGGCCGATGTGGGT 95358         C    _
          GGA                    TCCACCCAC TCGGC TCCCAAAGT
                                ||||||||| ||||| |||||||||
                                AGGTGGGTG AGCCG AGGGTTTCA
                                     T    G
GAM219  LOC221585 3'  ACTTTGGGAGGCCGAGACGGGC 95276    A   AC    _
          GG                     CC CCC  CTCGGC TCCCAAAGT
                                || |||  |||||| |||||||||
                                GG GGG  GAGCCG AGGGTTTCA
                                 C  CA     G
GAM219  LOC221585 3'  GGGAGGCCGAGACGGGCGGA  95277    A   AC    _
                                TCC CCC  CTCGGC TCCC
                                ||| |||  |||||| ||||
                                AGG GGG  GAGCCG AGGG
                                  C  CA     G
GAM219  LOC221641 5'  ACTTTGGGAGGCTGAGGTGGGT 95341             _
          GGA                    TCCACCCACCTCGGC TCCCAAAGT
                                |||||||||||||| |||||||||
                                AGGTGGGTGGAGTCG AGGGTTTCA
                                        G
GAM219  LOC221766 3'  ACTTTGGGAGGCCGAGGTGGGC 95417    CA        _
          AGA                    TC  CCCACCTCGGC TCCCAAAGT
                                ||  |||||||||| |||||||||
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                                AG  GGGTGGAGCCG AGGGTTTCA
                                 AC          G
GAM219  LOC221795 3'  ACCTTGGGAGGCCGAGGCAGGC 94065     A  CA      _     A
                GGA                TCC CC  CCTCGGC TCCCAA GT
                                   ||| ||  ||||||| |||||| ||
                                   AGG GG  GGAGCCG AGGGTT CA
                                     C  AC      G     C
GAM219  LOC221931 3'  ACTTTGGGAGGCCGAGGTGGG  95628          _
                                   CCCACCTCGGC TCCCAAAGT
                                   |||||||||||| |||||||||
                                   GGGTGGAGCCG AGGGTTTCA
                                         G
GAM219  LOC221943 5'  ACTTTGGGAGGCCAAGGCGGGT 95615        A   C   _
                GG                 CCACCC CCT GGC TCCCAAAGT
                                   |||||| ||| ||| |||||||||
                                   GGTGGG GGA CCG AGGGTTTCA
                                      C   A   G
GAM219  LOC221954 5'  ACTTTGGGAGGCTGAGGCAGGC 95637     A  CA      _
                GGA                TCC CC  CCTCGGC TCCCAAAGT
                                   ||| ||  ||||||| |||||||||
                                   AGG GG  GGAGTCG AGGGTTTCA
                                     C  AC      G
GAM219  LOC222060 5'  ACTTTGGGAGGCGGAGGCGGGT 95748        A    G  _
                GG                 CCACCC CCTC GC TCCCAAAGT
                                   |||||| |||| || |||||||||
                                   GGTGGG GGAG CG AGGGTTTCA
                                      C    G  G
GAM219  LOC222066 3'  ACTTTGGGAGGCCGAGGCAGGC 94309    CA  CA      _
                AGA                TC  CC  CCTCGGC TCCCAAAGT
                                   ||  ||  ||||||| |||||||||
                                   AG  GG  GGAGCCG AGGGTTTCA
                                    AC  AC      G
GAM219  LOC222160 5'  ACTTTGGGAGGCCGAGATGGGC 95769    A   C     _
                GG                 CC CCCA CTCGGC TCCCAAAGT
                                   || |||| |||||| |||||||||
                                   GG GGGT GAGCCG AGGGTTTCA
                                    C   A     G
GAM219  LOC222236 3'  ACTTTGGGAGGCCAAGGTGGGT 95960           C  _
                GGG                TCCACCCACCT GGC TCCCAAAGT
                                   |||||||||||| ||| |||||||||
                                   GGGTGGGTGGA CCG AGGGTTTCA
                                         A  G
GAM219  LOC222237 3'  ACTTTGGGAGGCTGAGGCAGGT 95946        CA      _
                GGA                TCCACC  CCTCGGC TCCCAAAGT
                                   ||||||  ||||||| |||||||||
                                   AGGTGG  GGAGTCG AGGGTTTCA
                                      AC      G
GAM219  LOC222865 3'  ACTTTGGGAGGCCGAGGCGGGT 94435        A      _
                GGA                TCCACCC CCTCGGC TCCCAAAGT
                                   ||||||| ||||||| |||||||||
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                                AGGTGGG GGAGCCG AGGGTTTCA
                                   C      G
GAM219  LOC253532 3'  ACTTTGGGAAGCCAAGGCAGGC 97726    A  CA   C   _
          GG                     CC CC  CCT GGCT CCCAAAGT
                                 || ||  ||| |||| ||||||||
                                 GG GG  GGA CCGA GGGTTTCA
                                  C  AC   A    A
GAM219  LOC253639 3'  ACTTTGGGAGGCTGAGGCGGGT 97508        A      _
          GGA                    TCCACCC CCTCGGC TCCCAAAGT
                                 ||||||| ||||||| |||||||||
                                 AGGTGGG GGAGTCG AGGGTTTCA
                                    C      G
GAM219  LOC253664 3'  GGGAGGCCGAGGCGGGTGGA   96470        A      _
                                 TCCACCC CCTCGGC TCCC
                                 ||||||| ||||||| ||||
                                 AGGTGGG GGAGCCG AGGG
                                    C      G
GAM219  LOC253786 3'  ACTTTGGGAGACTGAGTTGGGT 98826         C    _
          GGA                    TCCACCCA CTCGG CTCCCAAAGT
                                 |||||||| ||||| ||||||||||
                                 AGGTGGGT GAGTC GAGGGTTTCA
                                     T    A
GAM219  LOC253840 3'  ACTTTGGAAGGCCGAGGTGGGT 97908              C_
          GGA                    TCCACCCACCTCGGCT  CCAAAGT
                                 ||||||||||||||||  |||||||
                                 AGGTGGGTGGAGCCGG  GGTTTCA
                                        AA
GAM219  LOC253927 3'  ACTTTGGGAGGCTGAGGTGGGC 96725     A        _
          GGA                    TCC CCCACCTCGGC TCCCAAAGT
                                 ||| |||||||||| |||||||||
                                 AGG GGGTGGAGTCG AGGGTTTCA
                                   C         G
GAM219  LOC254041 5'  ACTTTGGGAGGCCGAGGCAGGC 96550    CA  CA     _
          AGA                    TC  CC  CCTCGGC TCCCAAAGT
                                 ||  ||  ||||||| |||||||||
                                 AG  GG  GGAGCCG AGGGTTTCA
                                  AC  AC      G
GAM219  LOC254045 3'  ACTTTGGGAGGCTGAGGCAAGT 98259     CCA     _
          G                       CAC   CCTCGGC TCCCAAAGT
                                  |||   ||||||| |||||||||
                                  GTG   GGAGTCG AGGGTTTCA
                                    AAC      G
GAM219  LOC254100 3'  GGGAGGCCGAGGCGGGCAGA   98159    CA  A     _
                                 TC  CCC CCTCGGC TCCC
                                 ||  ||| ||||||| ||||
                                 AG  GGG GGAGCCG AGGG
                                  AC  C      G
GAM219  LOC254176 3'  ACCTTGCGAGGCCGAGGCAGGT 99160        CA     _ C   A
          GGA                    TCCACC  CCTCGGC TC CAA GT
                                 ||||||  ||||||| || ||| ||
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                                AGGTGG  GGAGCCG AG GTT CA
                                   AC      G C   C
GAM219   LOC254266 3'  ACTTTGGGAGGCCGAGGCGGGC 99191    CA  A     _
           AGA                   TC  CCC CCTCGGC TCCCAAAGT
                                 ||  ||| ||||||| |||||||||
                                 AG  GGG GGAGCCG AGGGTTTCA
                                  AC  C      G
GAM219   LOC254531 5'  ACTTTGGGAGGCCAAGGCGGGT 96658       A  C  _
           GG                    CCACCC CCT GGC TCCCAAAGT
                                 |||||| ||| ||| |||||||||
                                 GGTGGG GGA CCG AGGGTTTCA
                                    C  A  G
GAM219   LOC254808 3'  ACTTTGGGAGGCCGAGGCGGGC 98799    A  A     _
           GGA                   TCC CCC CCTCGGC TCCCAAAGT
                                 ||| ||| ||||||| |||||||||
                                 AGG GGG GGAGCCG AGGGTTTCA
                                   C  C      G
GAM219   LOC254875 3'  ACTTTGGGAAGCCAAGGCAGGC 97770    A  CA  C  _
           GG                    CC CC  CCT GGCT CCCAAAGT
                                 ||  ||  ||| |||| ||||||||
                                 GG GG  GGA CCGA GGGTTTCA
                                  C  AC  A   A
GAM219   LOC255031 3'  ACTTTGGGAGGCCGAGGCAGGA 99027    A  CA     _
           GGA                   TCC CC  CCTCGGC TCCCAAAGT
                                 ||| ||  ||||||| |||||||||
                                 AGG GG  GGAGCCG AGGGTTTCA
                                   A  AC      G
GAM219   LOC255042 3'  ACTTTGGGAGGCCAAGGCAGG  97029    CA  C  _
                                 CC  CCT GGC TCCCAAAGT
                                 ||  ||| ||| |||||||||
                                 GG  GGA CCG AGGGTTTCA
                                  AC  A  G
GAM219   LOC255042 3'  ACTTTGGGAGGCTGAGGCGGGT 97030       A     _
           GGA                   TCCACCC CCTCGGC TCCCAAAGT
                                 ||||||| ||||||| |||||||||
                                 AGGTGGG GGAGTCG AGGGTTTCA
                                    C      G
GAM219   LOC255193 3'  ACTTTGGGAGGCCGAGGTGGG  97099          _
                                 CCCACCTCGGC TCCCAAAGT
                                 |||||||||| |||||||||
                                 GGGTGGAGCCG AGGGTTTCA
                                       G
GAM219   LOC255196 5'  ACTTTGGGAGGCCGAGATGGGC 98945    A  C    _
           GG                    CC CCCA CTCGGC TCCCAAAGT
                                 ||  |||| |||||| |||||||||
                                 GG GGGT GAGCCG AGGGTTTCA
                                  C   A     G
GAM219   LOC255196 3'  ACTTTGGGAGTCCGAGGCGAGT 98946     CCA    _
           G                     CAC   CCTCGG CTCCCAAAGT
                                 |||   |||||| ||||||||||
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                                GTG   GGAGCC GAGGGTTTCA
                                  AGC     T
GAM219  LOC255231 3'  ACTTTGGGAGGCCTAGGCAGG  97115    CA   C  _
                                CC  CCT GGC TCCCAAAGT
                                ||  ||| ||| |||||||||
                                GG  GGA CCG AGGGTTTCA
                                 AC   T   G
GAM219  LOC255252 3'  ACTTTGGGAGGCCAAGGCGGGT 96703       A   C  _
          GG                      CCACCC CCT GGC TCCCAAAGT
                                |||||| ||| ||| |||||||||
                                GGTGGG GGA CCG AGGGTTTCA
                                   C   A   G
GAM219  LOC255328 3'  ACTTTGTGAGGCTGAGGTGGGC 98331    CA         _ C
          AGA                     TC  CCCACCTCGGC TC CAAAGT
                                ||  |||||||||| || ||||||
                                AG  GGGTGGAGTCG AG GTTTCA
                                 AC          G  T
GAM219  LOC255463 3'  ACTTTGGGAGGCCAAGATGGG  96537      C  C  _
                                CCCA CT GGC TCCCAAAGT
                                ||||  ||  ||| |||||||||
                                GGGT GA CCG AGGGTTTCA
                                  A  A   G
GAM219  LOC255624 3'  ACTTTGGGAGGCCAAGACAGGT 96160     CAC  C  _
                                ACC   CT GGC TCCCAAAGT
                                |||   ||  ||| |||||||||
                                TGG   GA CCG AGGGTTTCA
                                  ACA  A   G
GAM219  LOC255671 3'  ACTTTGGGAGGCAGAGGTGGGC 99062     A       G  _
          GGA                     TCC CCCACCTC GC TCCCAAAGT
                                |||  ||||||||  ||  |||||||||
                                AGG GGGTGGAG CG AGGGTTTCA
                                  C       A  G
GAM219  LOC255937 3'  TGGAGGCCGAGGCAGGCGGA   97685     A  CA      TC
                                TCC CC  CCTCGGC  CCA
                                |||  ||  |||||||  |||
                                AGG GG  GGAGCCG  GGT
                                  C  AC       GA
GAM219  LOC255971 3'  ACTTTGGGAGGCCGAGGCGGGC 98305     A   A      _
          GGA                     TCC CCC CCTCGGC TCCCAAAGT
                                |||  ||| |||||||  |||||||||
                                AGG GGG GGAGCCG AGGGTTTCA
                                  C   C      G
GAM219  LOC256207 3'  ACCTTGGGAGGCCAAGGTGGGT 96868           C  _     A
          GGA                     TCCACCCACCT GGC TCCCAA GT
                                ||||||||||| ||| |||||| ||
                                AGGTGGGTGGA CCG AGGGTT CA
                                       A  G     C
GAM219  LOC256277 3'  ACTTTGGGAGGCTGAAGCGGGT 96348      ACC    _
                                ACCC   TCGGC TCCCAAAGT
                                ||||   ||||| |||||||||
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                                TGGG   AGTCG AGGGTTTCA
                                  CGA    G
GAM219   LOC256515 3'  ACCTTGGGAGGCCGAGGCAGGC 98202     A  CA     _     A
                GGA                TCC CC  CCTCGGC TCCCAA GT
                                   ||| ||  ||||||| |||||| ||
                                   AGG GG  GGAGCCG AGGGTT CA
                                     C  AC      G     C
GAM219   LOC256520 3'  ACTTTGGGAGGCAGAGGCGG   97662    A   G  _
                                   CC CCTC GC TCCCAAAGT
                                   || |||| || |||||||||
                                   GG GGAG CG AGGGTTTCA
                                    C    A  G
GAM219   LOC256544 3'  ACTTTGGGAGGCCGAGGCGGG  97925     A     _
                                   CCC CCTCGGC TCCCAAAGT
                                   ||| ||||||| |||||||||
                                   GGG GGAGCCG AGGGTTTCA
                                     C      G
GAM219   LOC256594 3'  ACCTTGGGAGGCCGAGGCAGGC 98852     A  CA     _     A
                GGA                TCC CC  CCTCGGC TCCCAA GT
                                   ||| ||  ||||||| |||||| ||
                                   AGG GG  GGAGCCG AGGGTT CA
                                     C  AC      G     C
GAM219   LOC257115 3'  GGGAGGCCGAGGCAGGTGGA   98294       CA     _
                                   TCCACC  CCTCGGC TCCC
                                   ||||||  ||||||| ||||
                                   AGGTGG  GGAGCCG AGGG
                                      AC      G
GAM219   LOC257180 3'  ACTTTGGGAGGCCGAGGCAGGT 97312       CA     _
                GGA                TCCACC  CCTCGGC TCCCAAAGT
                                   ||||||  ||||||| |||||||||
                                   AGGTGG  GGAGCCG AGGGTTTCA
                                      AC      G
GAM219   LOC257480 3'  ACTTTGGGAGGCTGAGGTGGGT 78430              _
                GGA                TCCACCCACCTCGGC TCCCAAAGT
                                   |||||||||||||| |||||||||
                                   AGGTGGGTGGAGTCG AGGGTTTCA
                                            G
GAM219   LOC257596 5'  ACTCTGGGAGGGCGAGGTGGGC 99759     A       G _    A
                GGA                TCC CCCACCTCG C TCCCA AGT
                                   ||| ||||||||| | ||||| |||
                                   AGG GGGTGGAGC G AGGGT TCA
                                     C        G G    C
GAM219   LOC257596 3'  ACTTTGGGAGGCCGAGGCAGGT 99760       CA     _
                GGA                TCCACC  CCTCGGC TCCCAAAGT
                                   ||||||  ||||||| |||||||||
                                   AGGTGG  GGAGCCG AGGGTTTCA
                                      AC      G
GAM219   LOC257596 3'  ACTTTGGGAGGCCGATGTGGGT 99761         C    _
                GGA                TCCACCCAC TCGGC TCCCAAAGT
                                   ||||||||| ||||| |||||||||
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                                AGGTGGGTG AGCCG AGGGTTTCA
                                     T    G
GAM219  LOC51122  3' ACTTTGGGAGGCCGAGGTGGG  66192          _
                                CCCACCTCGGC TCCCAAAGT
                                |||||||||| |||||||||
                                GGGTGGAGCCG AGGGTTTCA
                                      G
GAM219  LOC51145  3' ACTTTGGGAGGCCGAGGCAGGT 32918       CA     _
           GGA                    TCCACC  CCTCGGC TCCCAAAGT
                                  ||||||  ||||||| |||||||||
                                  AGGTGG  GGAGCCG AGGGTTTCA
                                     AC      G
GAM219  LOC51279  3' CTTAGGAGTCCGAGGTGGGTGG 33756            _  CA
           A                      TCCACCCACCTCGG CTCC  AAG
                                  ||||||||||||| ||||  |||
                                  AGGTGGGTGGAGCC GAGG  TTC
                                        T   A_
GAM219  LOC51336  3' ACCTTGGGAGGCCGAGGCAGGC 34065     A  CA     _    A
           GGA                    TCC CC  CCTCGGC TCCCAA GT
                                  ||| ||  ||||||| |||||| ||
                                  AGG GG  GGAGCCG AGGGTT CA
                                    C  AC      G     C
GAM219  LOC51759  3' ACTTTGGGAGGCCGAGGTGGGC 73166     A        _
           GGA                    TCC CCCACCTCGGC TCCCAAAGT
                                  ||| |||||||||| |||||||||
                                  AGG GGGTGGAGCCG AGGGTTTCA
                                    C          G
GAM219  LOC54518  3' ACTTTGGGAGGCTGAGGCAGGA 39297     A  CA     _
           GGA                    TCC CC  CCTCGGC TCCCAAAGT
                                  ||| ||  ||||||| |||||||||
                                  AGG GG  GGAGTCG AGGGTTTCA
                                    A  AC      G
GAM219  LOC55974  3' ACTTTGGGAGGCCAAGGTGGGC 38739    A      C  _
           GG                     CC CCCACCT GGC TCCCAAAGT
                                  || ||||||| ||| |||||||||
                                  GG GGGTGGA CCG AGGGTTTCA
                                   C      A  G
GAM219  LOC57118  3' ACTTTGGGAGGCTGAGGCAGGA 40213     A  CA     _
           GGA                    TCC CC  CCTCGGC TCCCAAAGT
                                  ||| ||  ||||||| |||||||||
                                  AGG GG  GGAGTCG AGGGTTTCA
                                    A  AC      G
GAM219  LOC63929  3' ACTTTGGGAGGTCCAGGCAGGT 42276       CA   C  _
           GG                     CCACC  CCT GGC TCCCAAAGT
                                  |||||  ||| ||| |||||||||
                                  GGTGG  GGA CTG AGGGTTTCA
                                     AC   C   G
GAM219  LOC85479  5' ACTTTGGGAGGCCGAGGCTGGC 53558     A  CA     _
           GGA                    TCC CC  CCTCGGC TCCCAAAGT
                                  ||| ||  ||||||| |||||||||
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                                AGG GG  GGAGCCG AGGGTTTCA
                                  C  TC      G
GAM219  LOC89890  3' ACTTTGGGAGGCCGAGGCAGGT 61200       CA      _
             GGA                    TCCACC  CCTCGGC TCCCAAAGT
                                    ||||||  ||||||| |||||||||
                                AGGTGG  GGAGCCG AGGGTTTCA
                                   AC      G
GAM219  LOC90072  3' ACTTTGGAAGGCCGAGGCGGGC 61945    CA   A      C_
             AGA                    TC  CCC CCTCGGCT  CCAAAGT
                                    ||  ||| ||||||||  |||||||
                                AG  GGG GGAGCCGG  GGTTTCA
                                 AC   C       AA
GAM219  LOC90092  3' ACTTTGGGAGGCTGAGGTGGG  62051          _
                                CCCACCTCGGC TCCCAAAGT
                                |||||||||||| |||||||||
                                GGGTGGAGTCG AGGGTTTCA
                                      G
GAM219  LOC90120  5' TGGGAGCCAGGGGCTG      62218    C  A   C
                                CA CC CCT GGCTCCCA
                                || || ||| ||||||||
                                GT GG GGA CCGAGGGT
                                 C  _  _
GAM219  LOC90148  3' ACTCTGGGAGCTCCTGGGATG  62339    _   CCTC       A
                                CA CCCA    GGCTCCCA AGT
                                || ||||    |||||||| |||
                                GT GGGT    TCGAGGGT TCA
                                 A    CC__       C
GAM219  LOC90155  5' ACTTTGGGAGGCCCAGGTGGGC 62359    A      C   _
             GG                     CC CCCACCT GGC TCCCAAAGT
                                    || ||||||| ||| |||||||||
                                GG GGGTGGA CCG AGGGTTTCA
                                 C      C   G
GAM219  LOC90233  3' ACTTTGGGAGGCCAAGGCGGGC 57188    A   A   C   _
             GG                     CC CCC CCT GGC TCCCAAAGT
                                    || ||| ||| ||| |||||||||
                                GG GGG GGA CCG AGGGTTTCA
                                 C   C   A   G
GAM219  LOC90321  3' ACTTTGGGAGGTTGAGGCAGGT 62927       CA      _
             GGA                    TCCACC  CCTCGGC TCCCAAAGT
                                    ||||||  ||||||| |||||||||
                                AGGTGG  GGAGTTG AGGGTTTCA
                                   AC      G
GAM219  LOC90342  5' ACTTTAAGAAGGACTGGGTGGT 63007       C   T   C   C____
             GGA                    TCCACC ACC CGG TCC     AAAGT
                                    |||||| ||| ||| |||     |||||
                                AGGTGG TGG GTC AGG     TTTCA
                                   _   _   _   AAGAA
GAM219  LOC90509  3' ACTTTGGGAGGCCGAGACAGGC 63789    A  CAC     _
             GG                     CC CC   CTCGGC TCCCAAAGT
                                    || ||   |||||| |||||||||
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                                GG GG   GAGCCG AGGGTTTCA
                                 C  ACA     G
GAM219  LOC90573  3' GGGAGGCCAAGGTGGGTG    63959         C  _
                                CACCCACCT GGC TCCC
                                ||||||||| ||| ||||
                                GTGGGTGGA CCG AGGG
                                    A   G
GAM219  LOC90589  3' GGGAGGCCGAGGCAGGCGGA  59774     A  CA     _
                                TCC CC  CCTCGGC TCCC
                                ||| ||  ||||||| ||||
                                AGG GG  GGAGCCG AGGG
                                  C  AC      G
GAM219  LOC90591  3' ACTTTGGGAGACCAAGGCAGG  64137    CA   C  _
                                CC  CCT GG CTCCCAAAGT
                                ||  ||| || ||||||||||
                                GG  GGA CC GAGGGTTTCA
                                 AC   A  A
GAM219  LOC90591  3' ACTTTGGGAGGCTGAGGTGGGC 64138     A         _
           GGA                    TCC CCCACCTCGGC TCCCAAAGT
                                ||| |||||||||| |||||||||
                                AGG GGGTGGAGTCG AGGGTTTCA
                                  C          G
GAM219  LOC90624  3' ACTTTGGGAGGCTGAGGCGGGC 64363    CA   A      _
           AGA                    TC  CCC CCTCGGC TCCCAAAGT
                                ||  ||| ||||||| |||||||||
                                AG  GGG GGAGTCG AGGGTTTCA
                                 AC   C      G
GAM219  LOC90979  3' ACTTTGGGAGGCTGAAGTGGG  65134       C    _
                                CCCAC TCGGC TCCCAAAGT
                                ||||| ||||| |||||||||
                                GGGTG AGTCG AGGGTTTCA
                                   A    G
GAM219  LOC91035  3' ACTTTGGGAGGCTGAGGTGGGC 65292     A         _
           GGA                    TCC CCCACCTCGGC TCCCAAAGT
                                ||| |||||||||| |||||||||
                                AGG GGGTGGAGTCG AGGGTTTCA
                                  C          G
GAM219  LOC91286  3' TGGGAGGCTGAGGTGGGTAGA  66065    C         _
                                TC ACCCACCTCGGC TCCCA
                                || ||||||||||| |||||
                                AG TGGGTGGAGTCG AGGGT
                                 A          G
GAM219  LOC91380  3' ACTTTGGGAGGCTGAGTTGGGT 66431         C     _
           GGA                    TCCACCCA CTCGGC TCCCAAAGT
                                |||||||| |||||| |||||||||
                                AGGTGGGT GAGTCG AGGGTTTCA
                                    T     G
GAM219  LOC91380  3' ACTTTGGGAGGTTGAGGCGGGT 66432        A     _
           GGA                    TCCACCC CCTCGGC TCCCAAAGT
                                ||||||| ||||||| |||||||||
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                                AGGTGGG GGAGTTG AGGGTTTCA
                                   C      G
GAM219  LOC91547  3' ACTTTGGGAGGCAGAGGTGGGC 66995     A      G _
             GGA                   TCC CCCACCTC GC TCCCAAAGT
                                   ||| |||||||| || |||||||||
                                   AGG GGGTGGAG CG AGGGTTTCA
                                     C       A  G
GAM219  LOC91574  3' ACTTTGGGAGGCCGAGGCGGGC 67107     A  A     _
             GGA                   TCC CCC CCTCGGC TCCCAAAGT
                                   ||| ||| ||||||| |||||||||
                                   AGG GGG GGAGCCG AGGGTTTCA
                                     C  C      G
GAM219  LOC91750  3' ACTTTGGGAGGCCGAGGCAGGT 67644       CA     _
             GGA                   TCCACC  CCTCGGC TCCCAAAGT
                                   ||||||  ||||||| |||||||||
                                   AGGTGG  GGAGCCG AGGGTTTCA
                                      AC      G
GAM219  LOC91796  5' ACTTTGGGAGGCTGAGGTGGGC 67783    CA        _
             AGA                   TC  CCCACCTCGGC TCCCAAAGT
                                   ||  |||||||||||| |||||||||
                                   AG  GGGTGGAGTCG AGGGTTTCA
                                    AC          G
GAM219  LOC91862  3' ACTTTGGGAGGCTGAGGTGGGT 54566             _
             GGA                   TCCACCCACCTCGGC TCCCAAAGT
                                   |||||||||||||| |||||||||
                                   AGGTGGGTGGAGTCG AGGGTTTCA
                                            G
GAM219  LOC91948  3' ACTTTGGGAGGCCAAGGTGGGT 68232          C  _
             GGA                   TCCACCCACCT GGC TCCCAAAGT
                                   |||||||||||| ||| |||||||||
                                   AGGTGGGTGGA CCG AGGGTTTCA
                                         A  G
GAM219  LOC91960  5' GGAGCCGAGGTTGGCGGA    68289     A  C
                                   TCC CC ACCTCGGCTCC
                                   ||| || ||||||||||
                                   AGG GG TGGAGCCGAGG
                                     C  T
GAM219  LOC91963  3' ACTTCGAGGCTACAGTGGGCTG 68310    _    CTC    CCCA
                                   CA CCCAC   GGCT    AAGT
                                   || |||||   ||||    ||||
                                   GT GGGTG   TCGG    TTCA
                                    C    ACA    AGC_
GAM219  LOC92078  3' ACTTTGGGAGGCCGAGGTGAGT 68587       C       _
             GGA                   TCCAC CACCTCGGC TCCCAAAGT
                                   ||||| ||||||||| |||||||||
                                   AGGTG GTGGAGCCG AGGGTTTCA
                                      A        G
GAM219  LOC92228  3' ACTTTGGGAGGCCGAGGCGGGG 69067    CA   A     _
             AGA                   TC  CCC CCTCGGC TCCCAAAGT
                                   ||  ||| ||||||| |||||||||
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                                AG  GGG GGAGCCG AGGGTTTCA
                                 AG   C      G
GAM219  LOC92283  3' ACTTTGGGAGGCCGAGGCGGGC 69298     A   A      _
             GGA                   TCC CCC CCTCGGC TCCCAAAGT
                                |||  ||| ||||||| |||||||||
                                AGG GGG GGAGCCG AGGGTTTCA
                                  C   C      G
GAM219  LOC92299  3' ACTTTGGGAGGCCGAGGCAGGT 69359       CA     _
             GGA                   TCCACC  CCTCGGC TCCCAAAGT
                                ||||||  ||||||| |||||||||
                                AGGTGG  GGAGCCG AGGGTTTCA
                                   AC      G
GAM219  LOC92405  3' ACTTTAGGAGGCCGAGGCAGGC 69708     A  CA      TC  _
             GGA                   TCC CC  CCTCGGC  CC AAAGT
                                |||  ||  |||||||  ||  |||||
                                AGG GG  GGAGCCG  GG TTTCA
                                  C  AC      GA  A
GAM219  LOC92465  5' ACTTTGGAAGGTTGAGGTGGGC 69935     CA         C_
             AGA                   TC  CCCACCTCGGCT  CCAAAGT
                                ||  ||||||||||||  |||||||
                                AG  GGGTGGAGTTGG  GGTTTCA
                                 AC           AA
GAM219  LOC92465  3' ACTTTGGGAGGCCAAGGTGGGT 69936    C       C  _
             AGA                   TC ACCCACCT GGC TCCCAAAGT
                                ||  |||||||| ||| |||||||||
                                AG TGGGTGGA CCG AGGGTTTCA
                                 A       A  G
GAM219  LOC92465  5' ACTTTGGGAGGCTGAGGCAGGC 69937     A  CA      _
             GGA                   TCC CC  CCTCGGC TCCCAAAGT
                                |||  ||  ||||||| |||||||||
                                AGG GG  GGAGTCG AGGGTTTCA
                                  C  AC      G
GAM219  LOC92499  5' ACTTTGGGAGGCCGAGGCAGGC 70101    CA  CA      _
             AGA                   TC  CC  CCTCGGC TCCCAAAGT
                                ||  ||  ||||||| |||||||||
                                AG  GG  GGAGCCG AGGGTTTCA
                                 AC  AC      G
GAM219  LOC92568  3' ACTTTGGGAGGCTGAGGTG    70323          _
                                CACCTCGGC TCCCAAAGT
                                |||||||| |||||||||
                                GTGGAGTCG AGGGTTTCA
                                     G
GAM219  LOC92573  5' ACTTTGGGAGGCCGAGGCAGGC 70366    CA  CA      _
             AGA                   TC  CC  CCTCGGC TCCCAAAGT
                                ||  ||  ||||||| |||||||||
                                AG  GG  GGAGCCG AGGGTTTCA
                                 AC  AC      G
GAM219  LOC92573  3' ACTTTGGGAGGCTGAGGGGGGT 70367        A      _
             GGA                   TCCACCC CCTCGGC TCCCAAAGT
                                |||||||  |||||||  |||||||||
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                                AGGTGGG GGAGTCG AGGGTTTCA
                                   G      G
GAM219  LOC92771  3'  ACTTTGGGAGACTGAGGTGGGT 54206                _
            GGA                  TCCACCCACCTCGG CTCCCAAAGT
                                 ||||||||||||| |||||||||
                                 AGGTGGGTGGAGTC GAGGGTTTCA
                                       A
GAM219  LOC93132  5'  ACTTTGGGAGGCCAAGGCGGGT 71973       A   C  _
            GG                   CCACCC CCT GGC TCCCAAAGT
                                 |||||| ||| ||| |||||||||
                                 GGTGGG GGA CCG AGGGTTTCA
                                   C   A   G
GAM219  LOC93132  5'  ACTTTGGGAGGCTGAGGCAGGT 71974       CA      _
            GGA                  TCCACC  CCTCGGC TCCCAAAGT
                                 ||||||  ||||||| |||||||||
                                 AGGTGG  GGAGTCG AGGGTTTCA
                                   AC      G
GAM219  LOC93613  3'  ACTTTGGGAGGCCGAGGCGGGC 73068    CA   A     _
            AGA                  TC  CCC CCTCGGC TCCCAAAGT
                                 ||  ||| ||||||| |||||||||
                                 AG  GGG GGAGCCG AGGGTTTCA
                                  AC   C      G
GAM219  LOC96597  5'  ACTTCGGGAGGCTGAGGTGGGC 67446     A        _   A
            GGA                  TCC CCCACCTCGGC TCCC AAGT
                                 ||| |||||||||| |||| ||||
                                 AGG GGGTGGAGTCG AGGG TTCA
                                   C         G   C
GAM220  DMPK     3'  CCGACTCGCTGACAGGCTACAG 16614     CAT       AATGCC
                                 CTG   CCTGTCAGC     CGG
                                 |||   |||||||||     |||
                                 GAC   GGACAGTCG     GCC
                                   ATC       CTCA__
GAM220  FES      3'  CACTGCCGGCAGGATGCAG   10608          A   A
                                 CTGCATCCTGTC GCA TG
                                 |||||||||||| ||| ||
                                 GACGTAGGACGG CGT AC
                                       C   C
GAM220  FMR2     3'  CCAGGCCCCTGACAGGATGC   10685          CAAT   C
                                 GCATCCTGTCAG    GCC GG
                                 ||||||||||||    ||| ||
                                 CGTAGGACAGTC    CGG CC
                                       CC__   A
GAM220  KDR      5'  CCGGGCATCACTTGCGCGCCGC 11199      ATCC   C  CA
            AG                   CTGC    TGT AG  ATGCCCGG
                                 ||||    ||| ||  ||||||||
                                 GACG    GCG TC  TACGGGCC
                                   CCGC   T  AC
GAM220  MAP4     3'  CCGAGTGGTGACAGGACGC    11445    A      G  ATGCC
                                 GC TCCTGTCA CA     CGG
                                 || |||||||| ||     |||
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                                CG AGGACAGT GT    GCC
                                 C      G  GA___
GAM220  MAP4     3'  CCGAGTGGTGACAGGACGC   48797    A      G  ATGCC
                                GC TCCTGTCA CA    CGG
                                || |||||||| ||    |||
                                CG AGGACAGT GT    GCC
                                 C      G  GA___
GAM220  AP1GBP1  3'  CCGGGCATTCAACTCAGAAACA 55437    CATC   TCAGC
           G                     CTG   CTG    AATGCCCGG
                                |||   |||    |||||||||
                                GAC   GAC    TTACGGGCC
                                  AAA_  TCAAC
GAM220  CGRP-RCP 5'  CCGGGCATTGCCGACAGGATGC 27888          A
           AG                    CTGCATCCTGTC GCAATGCCCGG
                                ||||||||||| ||||||||||
                                GACGTAGGACAG CGTTACGGGCC
                                       C
GAM220  DKFZP434C128 3'  CCGGGTGTCTGCAAAATGCAG  65468      CC  T   CA
                                CTGCAT  TG CAG  ATGCCCGG
                                ||||||  || |||  ||||||||
                                GACGTA  AC GTC  TGTGGGCC
                                   AA  _  __
GAM220  FLJ12121  3'  CCAGGCATTGCCCTAGAGGCAG 47090     ATC   TCA      C
                                CTGC   CTG   GCAATGCC GG
                                ||||   |||   |||||||| ||
                                GACG   GAT   CGTTACGG CC
                                  GA_   CC_       A
GAM220  FLJ14082  3'  CCAGGCCTGAAAAGGATGCA   47319       G_   CAAT   C
                                TGCATCCT  TCAG    GCC GG
                                ||||||||  ||||    ||| ||
                                ACGTAGGA  AGTC    CGG CC
                                    AA    _____   A
GAM220  KIAA0443  5'  GTATTCTGACAGGACACAG   28854     CA       C
                                CTG  TCCTGTCAG AATGC
                                |||  ||||||||| |||||
                                GAC  AGGACAGTC TTATG
                                  AC       _
GAM220  KIAA0763  3'  ATTGCTGACAGGAGCAG     30165     A
                                CTGC TCCTGTCAGCAAT
                                |||| ||||||||||||
                                GACG AGGACAGTCGTTA
                                   _
GAM220  KIAA1981  3'  CCGGGCATCACCGATGC     89712      CT  CAGCA
                                GCATC  GT    ATGCCCGG
                                |||||  ||    ||||||||
                                CGTAG  CA    TACGGGCC
                                  C_  C_____
GAM220  MGC2508   5'  CAGCGGCTGACAGGCGCAG   44505     AT       AA   CC
                                CTGC  CCTGTCAGC  TGC  G
                                ||||  |||||||||  |||  |
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                                GACG  GGACAGTCG  GCG  C
                                  C_        __   A_
GAM220  MGC26768  3'  CGGGGATGCAGGATGCAG    58911          CAGCA  G
                                CTGCATCCTGT     AT CCCG
                                ||||||||||     || ||||
                                GACGTAGGACG     TA GGGC
                                      _____  G
GAM220  MLL3      3'  CCAGGAGGAAGCTGACAGAAGC 41408      ATC       AATG_  C
            AG                    CTGC   CTGTCAGC     CC GG
                                ||||   ||||||||     || ||
                                GACG   GACAGTCG     GG CC
                                  AA_       AAGGA  A
GAM220  WBP4      3'  CCAGGCATTGTGTTAGGAATCC 24200     CA_    TCA       C
            AG                    CTG   TCCTG   GCAATGCC GG
                                |||   |||||   |||||||| ||
                                GAC   AGGAT   TGTTACGG CC
                                  CTA     TG_       A
GAM220  YWHAQ     3'  TGTTGCTGCCAGAATACA    23353    C  C   T
                                TG AT CTG CAGCAATG
                                || || ||| ||||||||
                                AC TA GAC GTCGTTGT
                                 A  A   C
GAM220  LOC143677 3'  CCGGGCACCCCTGGCAGGAAGC 83895      A        CAA
            AG                    CTGC TCCTGTCAG   TGCCCGG
                                |||| |||||||||   |||||||
                                GACG AGGACGGTC   ACGGGCC
                                  A        CCC
GAM220  LOC148936 5'  CATGACTGACAGGAGGCA    85449     A        CA
                                TGC TCCTGTCAG  ATG
                                ||| |||||||||  |||
                                ACG AGGACAGTC  TAC
                                  G        AG
GAM220  LOC162461 3'  CCAGGCACTGCTGAGGGGTGCG 83237          G     A    C
            G                     CTGCATCCT TCAGCA TGCC GG
                                |||||||||| |||||| |||| ||
                                GGCGTGGGG AGTCGT ACGG CC
                                      _     C    A
GAM220  LOC197342 3'  GCCGCTGACAGCATGCAG    89369        C        AAT
                                CTGCAT CTGTCAGC   GC
                                |||||| ||||||||   ||
                                GACGTA GACAGTCG   CG
                                   C       C__
GAM220  LOC221300 5'  TATTCTGACAGGACACAG    93578     CA        C
                                CTG  TCCTGTCAG AATG
                                |||  ||||||||| ||||
                                GAC  AGGACAGTC TTAT
                                  AC        _
GAM220  LOC256041 5'  CAGGGCTGAAGGATGCAG    99451          G     AA
                                CTGCATCCT TCAGC  TG
                                ||||||||| |||||  ||
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                                GACGTAGGA AGTCG  AC
                                      _    GG
GAM221  EP300    3'  ATGCAAGATGAACCTGA     9282         TT   _
                                TCAGGTTT  GTCT GCAT
                                ||||||||  |||| ||||
                                AGTCCAAG  TAGA CGTA
                                     __    A
GAM221  FBXW1B   3'  ATGCAGACAACCTTTGA     54445      TTT
                                TCAGG   TTGTCTGCAT
                                |||||   ||||||||||
                                AGTTT   AACAGACGTA
                                   CC_
GAM221  GUCY1B2  3'  ATGCAGACGCTCCTGAT     15945      TTTT
                                ATCAGG    TGTCTGCAT
                                ||||||    |||||||||
                                TAGTCC    GCAGACGTA
                                    TC__
GAM221  MADH6    3'  ATGCCCAGACAAAAAGCT    19973    G       __
                                AG TTTTTGTCT  GCAT
                                || |||||||||  ||||
                                TC AAAAACAGA  CGTA
                                 G        CC
GAM221  MAP2     3'  ATGCAGAAATTGACCTGAT   49818        TTTG
                                ATCAGGTT    TCTGCAT
                                ||||||||    |||||||
                                TAGTCCAG    AGACGTA
                                     TTAA
GAM221  MTMR8    3'  ATGTTTTTAAAAACCTGA    31903          TCT
                                TCAGGTTTTTG   GCAT
                                ||||||||||   ||||
                                AGTCCAAAAAT   TGTA
                                      TTT
GAM221  RORB     3'  ATGTAGCAAAAACTTGA     23585          T
                                TCAGGTTTTTG CTGCAT
                                |||||||||| ||||||
                                AGTTCAAAAAC GATGTA
                                     _
GAM221  SCML1    5'  ATGCTCTGCAAAACCTGG    23109        T  CT_
                                TCAGGTTTT GT   GCAT
                                ||||||||| ||   ||||
                                GGTCCAAAA CG   CGTA
                                     _ TCT
GAM221  AKL3L    3'  ATGGAGGAAAAACTTGAT    33268          G   G
                                ATCAGGTTTTT TCT CAT
                                |||||||||| ||| |||
                                TAGTTCAAAAA GGA GTA
                                      _  G
GAM221  C1orf9   3'  ATGCAGACAAATTTTTGA    33159      TT
                                TCAGG  TTTGTCTGCAT
                                |||||  ||||||||||
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                                AGTTT  AAACAGACGTA
                                   TT
GAM221  EREG     3'  ATGCAGTTTTTAAAAACCTG  9301          T___
                                CAGGTTTTTG   CTGCAT
                                ||||||||||   ||||||
                                GTCCAAAAAT   GACGTA
                                     TTTT
GAM221  FLJ20727 5'  ATGCAGACAATGCTCAGAT   36044    A_  TT
                                ATC  GGT  TTGTCTGCAT
                                |||  |||  ||||||||||
                                TAG  TCG  AACAGACGTA
                                  AC  T_
GAM221  FLJ21603 3'  ATGCAGACAACCATTGAT    45766     GTTT
                                ATCAG   TTGTCTGCAT
                                |||||   ||||||||||
                                TAGTT   AACAGACGTA
                                   ACC_
GAM221  HSPB7    3'  ATGCAGACAGGATCACCT    27781     __
                                AGGT  TTTTGTCTGCAT
                                ||||  ||||||||||||
                                TCCA  AGGACAGACGTA
                                  CT
GAM221  KIAA0217 3'  ATGTCTGAAAAAACCTGAT   67596         G  T_
                                ATCAGGTTTTT TC  GCAT
                                |||||||||| ||  ||||
                                TAGTCCAAAAA AG  TGTA
                                     _  TC
GAM221  KIAA0945 3'  ATGCTTGGGAAGCCTGAT    30899         GTCT
                                ATCAGGTTTTT   GCAT
                                ||||||||||   ||||
                                TAGTCCGAAGG   CGTA
                                     GTT_
GAM221  KIAA1922 5'  ATGCAACCTCAGACCTGAT   73986        TT_  C
                                ATCAGGTTT   GT TGCAT
                                |||||||||   || |||||
                                TAGTCCAGA   CA ACGTA
                                     CTC  _
GAM221  MGC27382 5'  ATGCAAGAGTAGAAGCTGAT   59124      G   TG  _
                                ATCAG TTTT  TCT GCAT
                                ||||| ||||  ||| ||||
                                TAGTC AAGA  AGA CGTA
                                   G   TG  A
GAM221  SLC26A10 5'  ATGCAGACAAGTATAGCT    56839     ___
                                GGTT   TTTGTCTGCAT
                                ||||   ||||||||||
                                TCGA   GAACAGACGTA
                                  TAT
GAM221  TOMM70A  3'  ATGCAAATAAAAACTGAT    29735      G      C
                                ATCAG TTTTTGT TGCAT
                                ||||| ||||||| |||||
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                                TAGTC AAAAATA ACGTA
                                  _      A
GAM221  ZFD25    3'  ATGCATGATGAAAACCTGA   33106        TG  _
                                TCAGGTTTT  TC TGCAT
                                |||||||||  || |||||
                                AGTCCAAAA  AG ACGTA
                                    GT  T
GAM221  LOC146287 5'  ATGCAGGAGTTAAAAACCTG  84630         ___
                                CAGGTTTTTG   TCTGCAT
                                ||||||||||   |||||||
                                GTCCAAAAAT   GGACGTA
                                     TGA
GAM221  LOC150940 3'  ATGCAGACAAGGCTGAT     80837      GT
                                ATCAG  TTTTGTCTGCAT
                                |||||  ||||||||||||
                                TAGTC  GGAACAGACGTA
                                  __
GAM221  LOC151174 5'  ATGCAGACAGAGCCCCGG    86434    A  T
                                TC GG TTTTGTCTGCAT
                                || || ||||||||||||
                                GG CC GAGACAGACGTA
                                 C  C
GAM221  LOC152756 3'  ATGCAGTTCTGAAAACCTGA  87054         GT__
                                TCAGGTTTTT    CTGCAT
                                ||||||||||    ||||||
                                AGTCCAAAAG    GACGTA
                                     TCTT
GAM221  LOC196892 3'  ATGCAGATTGACGCTGA     89179     _  TTT
                                TCAG GTT   GTCTGCAT
                                |||| |||   ||||||||
                                AGTC CAG   TAGACGTA
                                  G   T__
GAM221  LOC200314 3'  ATGTCTGTTCAAAAATCTGAT  91590          TCT__
                                ATCAGGTTTTTG    GCAT
                                ||||||||||||    ||||
                                TAGTCTAAAAAC    TGTA
                                      TTGTC
GAM221  LOC51246  3'  ATGCAGATGTGTCCTGGT    33637      TTTT
                                ATCAGG    TGTCTGCAT
                                ||||||    |||||||||
                                TGGTCC    GTAGACGTA
                                   TGT_
GAM221  LOC91549  5'  ATGAAGTAAAAACTTGAT    67024          T  G
                                ATCAGGTTTTTG CT CAT
                                |||||||||||| || |||
                                TAGTTCAAAAAT GA GTA
                                      _  A
GAM221  LOC91813  5'  GTGCAAAAGAACCTGA      67847         GTC
                                TCAGGTTTTT   TGCAT
                                ||||||||||   |||||
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                                AGTCCAAGAA   ACGTG
                                     A__
GAM221  LOC92912  3'  ATGCAGACAAAAGCTTTGA    71406      _
                                TCAG GTTTTTGTCTGCAT
                                |||| |||||||||||||
                                AGTT CGAAAACAGACGTA
                                  T
GAM222  IRTA1     3'  ACGAGACATGTCGACCAAAAGG 49237     CGAA_   __    C
            A                    TCC     GTTG  GTGTC CGT
                                |||     ||||  ||||| |||
                                AGG     CAGC  TACAG GCA
                                  AAAAC    TG    A
GAM222  KIAA0643  3'  ACGGGACAAAAACTCAAGAAGA 45968     G  CC  A   GG
            A                    TTC TC  GA GTT  TGTCCCGT
                                ||| ||  || |||  ||||||||
                                AAG AG  CT CAA  ACAGGGCA
                                  A  AA  _   AA
GAM223  KCNJ4     3'  GATCCACCACCCTTCCCCCACT 18357     C   TTTTCT
            G                    TAG GGG     GGTGGTGGATC
                                ||| |||     ||||||||||
                                GTC CCC     CCACCACCTAG
                                  A   CCTTC_
GAM223  LOC145453 3'  ATTTGTTCCAGAAAACTCC    77653    _       T  TG
                                GG GTTTTCTGG GG  GAT
                                || |||||||| ||  |||
                                CC CAAAAGACC TT  TTA
                                 T        _  GT
GAM223  LOC205095 3'  GATCCACGTGGAAAACACGC   92384     G       GTG
                                GCG GTTTTCTG   GTGGATC
                                ||| ||||||||   |||||||
                                CGC CAAAAGGT   CACCTAG
                                  A       G__
GAM224  ATP2B2    5'  CAGCCATCACCCGGCAGC     9846      A      __
                                GCT CTGGGTGA  GCTG
                                ||| ||||||||  ||||
                                CGA GGCCCACT  CGAC
                                  C       AC
GAM224  BSCL2     5'  GGACTACCGGCTTTACCCTCCC 51994          T_____    T___  ACTA
            AGTAGCT                AGCTACTGGG     GAGC    GG    CC
                                ||||||||||     ||||   ||    ||
                                TCGATGACCC     TTCG    CC    GG
                                      TCCCAT    G___  ATCA
GAM224  IMPA2     5'  AGTGTGTGCTCACCCACAGC   96944     AC       _  G
                                GCT  TGGGTGAGC TG ACT
                                |||  ||||||||| || |||
                                CGA  ACCCACTCG GT TGA
                                  C_        T  G
GAM224  KCNE1L    3'  AGTCCAGCTTCCAGTTGC     25388    T    GT
                                GC ACTGG  GAGCTGGACT
                                || |||||  ||||||||||
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                                CG TGACC  TTCGACCTGA
                                 T    __
GAM224  KRTHA1   3'  GGCAGCCAAGAAACTCACCCAA 11237     AC       C____   A  A
                AGC                   GCT  TGGGTGAG     TGG CT CC
                                ||| ||||||||    ||| || ||
                                CGA  ACCCACTC    ACC GA GG
                                  A_       AAAGA   _  C
GAM224  MADH7    3'  AGTATTGCTCACCCAGTGC   20922    T         TGG
                                GC ACTGGGTGAGC   ACT
                                || ||||||||||   |||
                                CG TGACCCACTCG   TGA
                                 _         TTA
GAM224  RXRA     3'  GTTGTTCACCCAGAGC      12922     A         TG
                                GCT CTGGGTGAGC  GAC
                                ||| ||||||||||  |||
                                CGA GACCCACTTG  TTG
                                  _        __
GAM224  SQSTM1   3'  GCTACCAGCAGCCCAGCACATA 15328       ____     GA  T___  ACTA
                GCT                   AGCTA    CTGGGT  GC    GG    C
                                |||||   ||||||  ||    ||    |
                                TCGAT    GACCCG  CG    CC    G
                                   ACAC     A_  A___  ATCA
GAM224  TPI1     3'  AGCCCAGAAGCCCAGTAACT   6294     C       GAG    A
                                AG TACTGGGT   CTGG CT
                                || ||||||||   |||| ||
                                TC ATGACCCG   GACC GA
                                 A       AA_   C
GAM224  TRHDE    3'  GGTATTCTCACCCAGTAG    26316           CTGG
                                CTACTGGGTGAG    ACT
                                ||||||||||||    |||
                                GATGACCCACTC    TGG
                                       TTA_
GAM224  C11orf21 3'  AGTCCAGCCCATGGAGC     27100     A  GG   A
                                GCT CT  GTG GCTGGACT
                                ||| ||  ||| ||||||||
                                CGA GG  TAC CGACCTGA
                                  _ __   C
GAM224  CAPN6    3'  CAGCATTTCACCCAGCAGC    27398     A       ___
                                GCT CTGGGTGA   GCTG
                                ||| ||||||||   ||||
                                CGA GACCCACT   CGAC
                                  C       TTA
GAM224  DT1P1A10 3'  AGTTTCTGGGCCCACCCTAGCA 62246     A _     A  ___
                GC                    GCT CT GGGTG GCT   GGACT
                                ||| || ||||| |||   |||||
                                CGA GA CCCAC CGG   TTTGA
                                  C  T    C   GTC
GAM224  FLJ12700 3'  GGCAGTCCACAGGCCTACAGCT 46657      AC     GAGC     A
                                AGCT  TGGGT    TGGACT CC
                                ||||  |||||    |||||| ||
```

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                                TCGA  ATCCG    ACCTGA GG
                                  C_     GAC_     C
GAM224  FLJ32780  3'  AGTCCTCTGGTCCCACAGCT   59297      AC    _ G  CT
                                AGCT  TGGG T AG  GGACT
                                ||||  |||| | ||  |||||
                                TCGA  ACCC G TC  CCTGA
                                  C_    T G  T_
GAM224  HRD1      3'  CCTGTCTCACCCAGCAGC    70148     A       _ T
                                GCT CTGGGTGAG C GG
                                ||| ||||||||| | ||
                                CGA GACCCACTC G CC
                                  C        T T
GAM224  KIAA0356  3'  GGTCTATGGGCCCACCCAGTGC 66779    T       A  ___
                                GC ACTGGGTG GCT   GGACT
                                || |||||||| |||   |||||
                                CG TGACCCAC CGG   TCTGG
                                 _       C   GTA
GAM224  KIAA0984  3'  AGCTCACTCACCCACCAGCT   66137     AC       C  GA
                                AGCT  TGGGTGAG TG  CT
                                ||||  |||||||| ||  ||
                                TCGA  ACCCACTC AC  GA
                                  CC        _  TC
GAM224  KIAA1598  5'  GTAGTCCAACTGGGATATTAGC 37639      _____ G   GAGC
                                GCTA    CT GGT    TGGACTAC
                                ||||    || |||    ||||||||
                                CGAT    GG TCA    ACCTGATG
                                  TATA  G   _____
GAM224  KIAA1681  3'  AGTCCAAGTCCAGTAACT    61714    C     GTGA  _
                                AG TACTGG    GCT GGACT
                                || ||||||    ||| |||||
                                TC ATGACC    TGA CCTGA
                                 A      _____   A
GAM224  MGC17303  3'  GGCAGTCAGATCCACCCAGTGC 58233     T       AG_   G   A
           T                     AGC ACTGGGTG   CTG ACT CC
                                ||| ||||||||   ||| ||| ||
                                TCG TGACCCAC   GAC TGA GG
                                  _       CTA   _   C
GAM224  PDE4DIP   5'  CCAGTGGTCACCCAGTAGC    97175           __  T___
                                GCTACTGGGTGA  GC    GG
                                ||||||||||||  ||    ||
                                CGATGACCCACT  TG    CC
                                       GG  A___
GAM224  SLC26A10  5'  CCGGTAACCCAACAGTGGCT   56842        ___    GA  T___
                                AGCTACT   GGGT  GC    GG
                                |||||||   ||||  ||    ||
                                TCGGTGA   CCCA  TG    CC
                                    CAA    A_  G___
GAM224  USP2      5'  AGCCGGGACTCACCCGCAGCT  16108      AC       __    A
                                AGCT  TGGGTGAG  CTGG CT
                                ||||  ||||||||  |||| ||
```

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                                TCGA  GCCCACTC  GGCC GA
                                  C_       AG   _
GAM224   LOC143425 3'  CTACTCACTCAGTAGCT     89013            C
                                AGCTACTGGGTGAG TGG
                                ||||||||||||| |||
                                TCGATGACTCACTC ATC
                                                _
GAM224   LOC145828 5'  AGTCCCTCCCAGTGGCT     84537          TGAGCT
                                AGCTACTGGG     GGACT
                                ||||||||||     |||||
                                TCGGTGACCC     CCTGA
                                      TC____
GAM224   LOC151174 5'  GGCCCGGCTCACCCCACAGCT  86438      ACT         A
                                AGCT   GGGTGAGCTGG CT
                                ||||   |||||||||||| ||
                                TCGA   CCCACTCGGCC GG
                                  CAC          C
GAM224   LOC158055 3'  AGGCCTCCACCCAGTGCT    82576     T       AGCT  A
                                AGC ACTGGGTG    GG CT
                                ||| ||||||||    || ||
                                TCG TGACCCAC    CC GA
                                  _       CT__  G
GAM224   LOC158696 3'  GTAGATCCACCAATAGCT    82861       C   GTGAGC   _
                                AGCTA TGG      TGGA CTAC
                                ||||| |||      |||| ||||
                                TCGAT ACC      ACCT GATG
                                  A  _______   A
GAM224   LOC196027 3'  GGTTTTCACCCAGTAGTT    88940            CTG
                                AGCTACTGGGTGAG   GACT
                                ||||||||||||||   ||||
                                TTGATGACCCACTT   TTGG
                                                 ___
GAM224   LOC200812 5'  CAGCCCATCCAGTATGCT    90301     _       A
                                AGC TACTGGGTG GCTG
                                ||| ||||||||| ||||
                                TCG ATGACCTAC CGAC
                                  T        C
GAM224   LOC253836 5'  CAGCGCTTCACCCAGTGC    99465    T       ___
                                GC ACTGGGTGA   GCTG
                                || |||||||||   ||||
                                CG TGACCCACT   CGAC
                                  _       TCG
GAM224   LOC256436 3'  AGCCCAGAAGCCCAGTAACT   96247    C       GAG    A
                                AG TACTGGGT   CTGG CT
                                || ||||||||   |||| ||
                                TC ATGACCCG   GACC GA
                                 A       AA_   C
GAM224   LOC256492 5'  TCCAGCTCAGTACAGCAGC    99434     A   GG_
                                GCT CTG   TGAGCTGGA
                                ||| |||   |||||||||
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                                CGA GAC   ACTCGACCT
                                  C   ATG
GAM224  LOC56181  3'  GTCACTCACTCAGCAGCT    97284      A       CTG
                                AGCT CTGGGTGAG   GAC
                                |||| |||||||||   |||
                                TCGA GACTCACTC   CTG
                                  C       A__
GAM224  LOC92148  5'  TCTACACACCCAGTACT     68888    C       AGC
                                AG TACTGGGTG   TGGA
                                || |||||||||   ||||
                                TC ATGACCCAC   ATCT
                                 _       AC_
GAM225  ACCN2     3'  GAACAGGACCTGTGAGCAGC   39626        TG __    C
                                GCTGCTCG  G  CCTG TC
                                ||||||||  |  |||| ||
                                CGACGAGT  C  GGAC AG
                                     GT CA    A
GAM225  ADAMTS1   5'  GAGCAGGCCAACGAGGC     23749    TG    _
                                GC  CTCGT GGCCTGCTC
                                ||  ||||| |||||||||
                                CG  GAGCA CCGGACGAG
                                 __     A
GAM225  ADCY1     3'  GAGCAGGCACAGCACAGCA   94340      __  C   G
                                TGCT  GCT GTG CCTGCTC
                                ||||  ||| ||| |||||||
                                ACGA  CGA CAC GGACGAG
                                  CA  _   _
GAM225  AQP6      5'  GAGCAGGCATATGAGCAACA   55004    C      _
                                TG TGCTCGTG GCCTGCTC
                                || |||||||| ||||||||
                                AC ACGAGTAT CGGACGAG
                                 A       A
GAM225  AQP6      5'  GAGCAGGTATATGAGCAACA   9730     C      _
                                TG TGCTCGTG GCCTGCTC
                                || |||||||| ||||||||
                                AC ACGAGTAT TGGACGAG
                                 A       A
GAM225  ARHGAP6   3'  AGCAGCCGAGCGAGAGCA    8609      G    __   C
                                TGCT CTCGT  GGC TGCT
                                |||| |||||  ||| ||||
                                ACGA GAGCG  CCG ACGA
                                  _     AG  _
GAM225  ARSB      5'  GAGCAGGCCCCGGCAGC     5279       T  T
                                GCTGC CG GGCCTGCTC
                                ||||| || |||||||||
                                CGACG GC CCGGACGAG
                                   _ C
GAM225  ATF5      3'  GAGCAGGCCAGTGGGAGG    24821    G    _
                                CT CTCG TGGCCTGCTC
                                || |||| ||||||||||
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                                GG GGGT ACCGGACGAG
                                 A   G
GAM225  ATP8B2   3'  GAGCAGGCCCAAGGGCAG    65836      GT_
                                CTGCTC   GGCCTGCTC
                                ||||||   |||||||||
                                GACGGG   CCGGACGAG
                                   AAC
GAM225  CACNG7   3'  GAGCAGGTTCGGGCAGC     49941       T
                                GCTGCTCG GGCCTGCTC
                                |||||||| |||||||||
                                CGACGGGC TTGGACGAG
                                      _
GAM225  CBFA2T3  3'  GAGCATGCGGAGCCAGCA    19016      _  GTG  C
                                TGCTG CTC   GC TGCTC
                                ||||| |||   || |||||
                                ACGAC GAG   CG ACGAG
                                   C   G__  T
GAM225  CCR9     3'  GAGCAGATATGGGCAGCA    49124        GC
                                TGCTGCTCGTG  CTGCTC
                                ||||||||||  ||||||
                                ACGACGGGTAT  GACGAG
                                      A_
GAM225  CCR9     3'  GAGCAGATATGGGCAGCA    22796        GC
                                TGCTGCTCGTG  CTGCTC
                                ||||||||||  ||||||
                                ACGACGGGTAT  GACGAG
                                      A_
GAM225  CD1A     5'  GAGCAGGGACATGGGAGCA   71726     G     G_
                                TGCT CTCGTG  CCTGCTC
                                ||||  ||||||  |||||||
                                ACGA GGGTAC  GGACGAG
                                  _     AG
GAM225  COCH     5'  GAGCAGGTGTGAGCAGC     15835       GTG
                                GCTGCTC   GCCTGCTC
                                |||||||   ||||||||
                                CGACGAG   TGGACGAG
                                    TG_
GAM225  CREBL2   3'  GAGCAGGGAAGAGCAGTA    8968        GTGG
                                TGCTGCTC    CCTGCTC
                                ||||||||    |||||||
                                ATGACGAG    GGACGAG
                                     AAG_
GAM225  CSNK1A1  3'  GAGCAGATGATCGGAGCAGCA  10312        G   C___
                                TGCTGCTC TGG    CTGCTC
                                |||||||| |||    ||||||
                                ACGACGAG GCT    GACGAG
                                    _  AGTA
GAM225  CYP1B1   3'  AGCAGGCTTGCCCAGTA     5444       CT  T
                                TGCTG  CG GGCCTGCT
                                |||||  || ||||||||
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                                ATGAC  GT TCGGACGA
                                   CC  _
GAM225  DXYS155E  3'  GAGCAGGCACCGCAGTA     18687       TC   G
                                TGCTGC  GTG CCTGCTC
                                ||||||  ||| |||||||
                                ATGACG  CAC GGACGAG
                                   C_   _
GAM225  EPAC      3'  GAGCAGGCACTTGCAGC     21453       TC   G
                                GCTGC  GTG CCTGCTC
                                |||||  ||| |||||||
                                CGACG  CAC GGACGAG
                                   TT   _
GAM225  F2R       3'  GAGCAGGCCAGGCGC       10566     T   CG
                                GC GCT  TGGCCTGCTC
                                || |||  ||||||||||
                                CG CGG  ACCGGACGAG
                                 _  ___
GAM225  FGF18     5'  GAGCGCCCCGGAGCAGCA    15259         G   CC
                                TGCTGCTC TGG  TGCTC
                                |||||||| |||  |||||
                                ACGACGAG GCC  GCGAG
                                     _  CC
GAM225  FGF18     5'  GAGCGCCCCGGAGCAGCA    54452         G   CC
                                TGCTGCTC TGG  TGCTC
                                |||||||| |||  |||||
                                ACGACGAG GCC  GCGAG
                                     _  CC
GAM225  FLG       3'  GAGCAGGCACGAGACAGC    71448      _     G
                                GCTG CTCGTG CCTGCTC
                                ||||  ||||||  |||||||
                                CGAC GAGCAC GGACGAG
                                  A     _
GAM225  FLG       5'  GAGCAGGCACGAGACAGC    71449      _     G
                                GCTG CTCGTG CCTGCTC
                                ||||  ||||||  |||||||
                                CGAC GAGCAC GGACGAG
                                  A     _
GAM225  FOXE1     3'  GAGCAGGCCACAGAGGC     16779     G  C
                                GCT CT GTGGCCTGCTC
                                |||  ||  ||||||||||
                                CGG GA CACCGGACGAG
                                  A  _
GAM225  GDF2      3'  GAGCAGGCCGCGTGTCACA   33019     CT  T
                                TG  GC CGTGGCCTGCTC
                                ||  ||  ||||||||||||
                                AC  TG GCGCCGGACGAG
                                 AC  T
GAM225  HADHSC    3'  AGCACTGCAGCGAGCAGCA   19225          G  C_
                                TGCTGCTCGT GC  TGCT
                                |||||||||  ||  ||||
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                                ACGACGAGCG CG  ACGA
                                      A  TC
GAM225  HCFC1    3'  GAGCAGGCCACCAGCAGCA   71548       C
                                TGCTGCT GTGGCCTGCTC
                                ||||||| ||||||||||
                                ACGACGA CACCGGACGAG
                                    C
GAM225  HOXA3    3'  GAGCAGGCCGGACGCAGCA   48400      _ G
                                TGCTGC TC TGGCCTGCTC
                                |||||| || ||||||||||
                                ACGACG AG GCCGGACGAG
                                   C  _
GAM225  HS3ST3B1 5'  GAGCAGCAGCAGCAGC     21272      C  G  C
                                GCTGCT GT GC TGCTC
                                |||||| || || |||||
                                CGACGA CG CG ACGAG
                                   _  A  _
GAM225  IL1RL1LG 5'  GAGCTCCGCCGAGTAGCA   23407        _  CCT
                                TGCTGCTCG TGG   GCTC
                                ||||||||| |||   ||||
                                ACGATGAGC GCC   CGAG
                                     C   T__
GAM225  LZTS1    3'  AGCAAGCCAGACCTAGCA   41024      C_  G   C
                                TGCTG  TC TGGC TGCT
                                |||||  || |||| ||||
                                ACGAT  AG ACCG ACGA
                                   CC  _    A
GAM225  MAP1A    3'  AGCAAGCCAGTGAGCAGC    11437       _   C
                                GCTGCTCG TGGC TGCT
                                |||||||| |||| ||||
                                CGACGAGT ACCG ACGA
                                     G    A
GAM225  MEIS2    3'  GAGCAGTGAGCCAAGGAGCA  39725      G_   ___
                                TGCTC  TGGC   CTGCTC
                                |||||  ||||   ||||||
                                ACGAG  ACCG   GACGAG
                                   GA    AGT
GAM225  MME      5'  GAGCAGGCTGGAGCAGC     8031       G
                                GCTGCTC TGGCCTGCTC
                                ||||||| ||||||||||
                                CGACGAG GTCGGACGAG
                                      _
GAM225  MMP16    3'  GAGCAGGCTTGTGGCAGC    21047      CGT
                                GCTGCT   GGCCTGCTC
                                ||||||   |||||||||
                                CGACGG   TCGGACGAG
                                   TGT
GAM225  MYO15A   5'  GAGCAGGCCACAGAACGCA   33183    TG_  C
                                TGC   CT GTGGCCTGCTC
                                |||   || ||||||||||
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                                ACG   GA CACCGGACGAG
                                  CAA  _
GAM225  MYO1D    3'  AGCAGGAAGCGGGGCAGCA   72239        _ GG
                                TGCTGCTC GT  CCTGCT
                                |||||||| ||  ||||||
                                ACGACGGG CG  GGACGA
                                     G  AA
GAM225  NFATC3   3'  GAGCAGGGGTGAGCAGGCA   17049    _    TGG
                                TGC TGCTCG   CCTGCTC
                                ||| ||||||   |||||||
                                ACG ACGAGT   GGACGAG
                                  G     GG_
GAM225  PAX5     5'  GAGCAGGCCCGGCCGC     34131    T  T  T
                                GC GC CG GGCCTGCTC
                                || || || |||||||||
                                CG CG GC CCGGACGAG
                                 C  _  _
GAM225  PML      3'  AGCAGGCCTCTGAGGCA     53793    TG   T_
                                TGC  CTCG  GGCCTGCT
                                |||  ||||  ||||||||
                                ACG  GAGT  CCGGACGA
                                  __   CT
GAM225  POU4F1   5'  GAGCGCCTGGCAGCAGCA    21762       C __  CT
                                TGCTGCT GT  GGC  GCTC
                                ||||||| ||  |||  ||||
                                ACGACGA CG  CCG  CGAG
                                     _ GT  __
GAM225  PSEN1    3'  GAGCAGGCACCAGCAGCA    24619       C  G
                                TGCTGCT GTG CCTGCTC
                                ||||||| ||| |||||||
                                ACGACGA CAC GGACGAG
                                     C  _
GAM225  PSEN1    3'  GAGCAGGCACCAGCAGCA    5242        C  G
                                TGCTGCT GTG CCTGCTC
                                ||||||| ||| |||||||
                                ACGACGA CAC GGACGAG
                                     C  _
GAM225  SLC11A3  5'  AGCACCTCAGCGAGAGCA    28165     G   _  CC
                                TGCT CTCG TGG  TGCT
                                |||| |||| |||  ||||
                                ACGA GAGC ACT  ACGA
                                  _   G  CC
GAM225  SLC12A7  3'  GAGCAGGCTAGAGGCACA    22740    C   CG
                                TG TGCT  TGGCCTGCTC
                                || ||||  ||||||||||
                                AC ACGG  ATCGGACGAG
                                 _   AG
GAM225  SORBS1   3'  GAGCAGATGGCCAAGCAG    31805      CG   ___
                                CTGCT  TGGCC   TGCTC
                                |||||  |||||   |||||
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                                GACGA  ACCGG   ACGAG
                                  __     TAG
GAM225  SOX11    3'  GAGCAGGCGGCTGCCGCA    13317     T  TC  G
                                TGC GC  GT GCCTGCTC
                                ||| ||  || ||||||||
                                ACG CG  CG CGGACGAG
                                  C  T_  G
GAM225  TCF1     3'  GAGCTCACAAGGCAGCA     6786        C_   CCT
                                TGCTGCT  GTGG   GCTC
                                |||||||  ||||   ||||
                                ACGACGG  CACT   CGAG
                                   AA   ___
GAM225  UVRAG    3'  GAGCAGGTCAACAGTA      14024       CTCG
                                TGCTG   TGGCCTGCTC
                                |||||   ||||||||||
                                ATGAC   ACTGGACGAG
                                   A___
GAM225  VTN      5'  GAGCAAACAGAGCAGCA     7163         G  GCC
                                TGCTGCTC TG   TGCTC
                                |||||||| ||   |||||
                                ACGACGAG AC   ACGAG
                                    _  AA_
GAM225  ARHGAP11A 3'  GAGCAGATTAGAGCAGCA    29449         G  GC
                                TGCTGCTC TG  CTGCTC
                                |||||||| ||  ||||||
                                ACGACGAG AT  GACGAG
                                    _  TA
GAM225  ATP6V1B1  5'  GAGCTGCCACCAGCAGCA    9879         C    CT
                                TGCTGCT GTGGC  GCTC
                                ||||||| |||||  ||||
                                ACGACGA CACCG  CGAG
                                   C    T_
GAM225  BPES     5'  AGCAAGCGCGGGCGGCA     43793          G C
                                TGCTGCTCGTG C TGCT
                                |||||||||||| | ||||
                                ACGGCGGGCGC G ACGA
                                     _ A
GAM225  C5orf6   3'  AGCAAAGGCTGTGAGAAGCA   33947     G   TG   __
                                TGCT CTCG  GCCT  GCT
                                |||| ||||  ||||  |||
                                ACGA GAGT  CGGA  CGA
                                  A   GT   AA
GAM225  C8orf6   5'  GAGCAGGTGCTTATAGCA    90779      CTC   G
                                TGCTG   GTG CCTGCTC
                                |||||   ||| |||||||
                                ACGAT   CGT GGACGAG
                                  ATT   _
GAM225  Cab45    3'  GAGTTCTTCACGGGCAGCA   33767          CCT
                                TGCTGCTCGTGG   GCTC
                                ||||||||||||   ||||
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                                ACGACGGGCACT  TGAG
                                      TCT
GAM225  CASKIN1  3'  AGCAGGGCATGTAGCA     40780      TC  G
                                TGCTGC  GTG CCTGCT
                                ||||||  ||| ||||||
                                ACGATG  TAC GGACGA
                                   __  G
GAM225  CDIPT    5'  GAGCAGGCCCGGGGCAGCA   21975       GT
                                TGCTGCTC  GGCCTGCTC
                                ||||||||  |||||||||
                                ACGACGGG  CCGGACGAG
                                     GC
GAM225  CIDEB    5'  GAGCAGGCCGGTGAGCAGCA  27796        _
                                TGCTGCTCGT GGCCTGCTC
                                |||||||||| |||||||||
                                ACGACGAGTG CCGGACGAG
                                      G
GAM225  CTSO     5'  CAGGCCGCGCGGGCGGCA    9027         __
                                TGCTGCTCGT  GGCCTG
                                ||||||||||  ||||||
                                ACGGCGGGCG  CCGGAC
                                      CG
GAM225  CXorf1   3'  GAACAGTCTGAGCAGC      17488       T  C  C
                                GCTGCTCG GGC TG TC
                                |||||||| ||| || ||
                                CGACGAGT CTG AC AG
                                   _  _ A
GAM225  DJ102H19.4 5'  AGCAGGCATAGGGTAGCA   42240       GTG
                                TGCTGCTC   GCCTGCT
                                ||||||||   |||||||
                                ACGATGGG   CGGACGA
                                     ATA
GAM225  DNAJC8   3'  GAGCACACAGAGCAGCA     27347       _  GCC
                                TGCTGCTC GTG   TGCTC
                                |||||||| |||   |||||
                                ACGACGAG CAC   ACGAG
                                     A  ___
GAM225  DOC-1R   5'  GAGCAGACGTCTGAAGCAGC   20721      _ T  __
                                GCTGCT CG GGC  CTGCTC
                                |||||| || |||  ||||||
                                CGACGA GT CTG  GACGAG
                                   A  _  CA
GAM225  EFS2     3'  GAGCATGGTGAGCAGC      20774       GTG  _
                                GCTGCTC   GCC TGCTC
                                |||||||   ||| |||||
                                CGACGAG   TGG ACGAG
                                   ___  T
GAM225  FLJ10563 5'  GAGCAGGACTTGAGCAGGCA  36804     _    TGG
                                TGC TGCTCG   CCTGCTC
                                ||| ||||||   |||||||
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                                ACG ACGAGT   GGACGAG
                                  G     TCA
GAM225  FLJ11807  3'  AGCAGGTTCGAGCCACA     46942    CT    T
                                TG  GCTCG GGCCTGCT
                                ||  ||||| ||||||||
                                AC  CGAGC TTGGACGA
                                 AC    _
GAM225  FLJ14213  3'  AGCACTTGGGGGCAGCA     46212        G   CC
                                TGCTGCTC TGG  TGCT
                                |||||||| |||  ||||
                                ACGACGGG GTT  ACGA
                                     G   C_
GAM225  FLJ14566  3'  GAGCAGGCCACAGCCTGGC    52500     __   C
                                GCT  GCT GTGGCCTGCTC
                                |||  ||| ||||||||||
                                CGG  CGA CACCGGACGAG
                                  TC  _
GAM225  FLJ20276  3'  GAGCAGGCTTGGTACA      35312    C    CGT
                                TG TGCT   GGCCTGCTC
                                || ||||   |||||||||
                                AC ATGG   TCGGACGAG
                                 _    T__
GAM225  FLJ20359  3'  GAGCAGGCCTGGTGCAGC    35515      _   T
                                GCTGC TCG GGCCTGCTC
                                ||||| ||| |||||||||
                                CGACG GGT CCGGACGAG
                                   T   _
GAM225  FLJ20546  3'  GAGCAGCACAGAGCAGCA    35808        G  GC
                                TGCTGCTC TG  CTGCTC
                                |||||||| ||  ||||||
                                ACGACGAG AC  GACGAG
                                     _  AC
GAM225  FLJ20583  5'  GAGCACAGGAGCAGCA      35852        G  GCC
                                TGCTGCTC TG   TGCTC
                                |||||||| ||   |||||
                                ACGACGAG AC   ACGAG
                                     G  ___
GAM225  FLJ20979  5'  GAGCAGGCCCGGGCAGGCA   44386     _     T
                                TGC TGCTCG GGCCTGCTC
                                ||| |||||| |||||||||
                                ACG ACGGGC CCGGACGAG
                                  G     _
GAM225  FLJ23588  5'  GAGCAGGCTCATCAGTA     43271       CTC  _
                                TGCTG   GTG GCCTGCTC
                                |||||   ||| ||||||||
                                ATGAC   TAC CGGACGAG
                                   ____  T
GAM225  H2AFY2    5'  GAGCAGGCGGCGCAGCA     38465       TC  G
                                TGCTGC  GT GCCTGCTC
                                ||||||  || ||||||||
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                                ACGACG  CG CGGACGAG
                                   __  G
GAM225  HSA404617 3'  GAGCCCAACAGAGCAGCA    73090        _ _  CCT
                                TGCTGCTC GT GG   GCTC
                                |||||||| || ||   ||||
                                ACGACGAG CA CC   CGAG
                                     A  A  ___
GAM225  KIAA0229  3'  GAGCAGGCAGAGCTGCA     94027     T   GTG
                                TGC GCTC   GCCTGCTC
                                ||| ||||   ||||||||
                                ACG CGAG   CGGACGAG
                                  T   A__
GAM225  KIAA0280  3'  GAACAGGCCCACAGTGAGCAGC 93299        ___   _   C
           A                     TGCTGCTC   GTGG CCTG TC
                                ||||||||   |||| |||| ||
                                ACGACGAG   CACC GGAC AG
                                     TGA   C   A
GAM225  KIAA0476  5'  GAGCCGGCCGAGCGAGCA    30039       __   T
                                TGCTCGT  GGCC GCTC
                                |||||||  |||| ||||
                                ACGAGCG  CCGG CGAG
                                    AG   C
GAM225  KIAA0481  3'  GAGCAGGCTCAGAGCAGC    72320       GT
                                GCTGCTC  GGCCTGCTC
                                |||||||  |||||||||
                                CGACGAG  TCGGACGAG
                                    AC
GAM225  KIAA0683  3'  GAGCAGCGGCCTGGAGCAGCA  32764       GT   __
                                TGCTGCTC  GGCC  TGCTC
                                ||||||||  ||||  |||||
                                ACGACGAG  CCGG  ACGAG
                                     GT   CG
GAM225  KIAA0781  3'  GAGCAAGCTCTCGAGGGCAGCA 68057       GT___  C
                                TGCTGCTC    GGC TGCTC
                                ||||||||    ||| |||||
                                ACGACGGG    TCG ACGAG
                                     AGCTC   A
GAM225  KIAA0820  5'  GAGCCCGGCGCAGCAGCA    69590       C   G  T_
                                TGCTGCT GTG CC  GCTC
                                ||||||| ||| ||  ||||
                                ACGACGA CGC GG  CGAG
                                   _  _  CC
GAM225  KIAA0939  3'  GAGCAGGCCAGCCAAGCAG   62716      CG__
                                CTGCT   TGGCCTGCTC
                                |||||   ||||||||||
                                GACGA   ACCGGACGAG
                                  ACCG
GAM225  KIAA1485  3'  GAGCAGGCTGTGGAGCAGC   90766       _ TG
                                GCTGCTC G  GCCTGCTC
                                ||||||| |  ||||||||
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                                CGACGAG T  CGGACGAG
                                    G GT
GAM225  KIAA1485  3'  GAGCTTGCCGAGCAGCA     90767        GT   CT
                                TGCTGCTC  GGC  GCTC
                                ||||||||  |||  ||||
                                ACGACGAG  CCG  CGAG
                                    __   TT
GAM225  KIAA1550  3'  AGCAGGCCGGGCAGCA      67151        GT
                                TGCTGCTC  GGCCTGCT
                                ||||||||  ||||||||
                                ACGACGGG  CCGGACGA
                                    __
GAM225  KIAA1577  5'  GAACAGGCCACATCGGACA    65100    _  CTC      C
                                TG CTG   GTGGCCTG TC
                                || |||   |||||||| ||
                                AC GGC   CACCGGAC AG
                                 A  TA_       A
GAM225  KIAA1817  3'  GAGCAGTGGCAGTAGCAGCA   68779       CGTG  __
                                TGCTGCT   GCC  TGCTC
                                |||||||   |||  |||||
                                ACGACGA   CGG  ACGAG
                                    TGA_   TG
GAM225  KIAA1937  3'  AGCAAGTCACACATGAGCAGCA 74067        ____    C
                                TGCTGCTC   GTGGC TGCT
                                ||||||||   ||||| ||||
                                ACGACGAG   CACTG ACGA
                                     TACA    A
GAM225  MEGF11    3'  AGCAAGGATGAGCAGCA     51598         GG  _
                                TGCTGCTCGT  CCT GCT
                                ||||||||||  ||| |||
                                ACGACGAGTA  GGA CGA
                                    __   A
GAM225  MGC14161  5'  GAGCAGGTTGATGAGCGGCA   52909         _
                                TGCTGCTCGT GGCCTGCTC
                                |||||||||| |||||||||
                                ACGGCGAGTA TTGGACGAG
                                     G
GAM225  MGC23937  5'  GAGCAACCGAGAGAGCA     59602     G   G   CC
                                TGCT CTC TGG  TGCTC
                                |||| ||| |||  |||||
                                ACGA GAG GCC  ACGAG
                                  _   A   A_
GAM225  MGC2668   3'  AGCAGGACGGGGCAGGCAGCA 61189        ___ G  G
                                TGCTGCT   C TG CCTGCT
                                |||||||   | || ||||||
                                ACGACGG   G GC GGACGA
                                    ACG G  A
GAM225  MGC2941   3'  AGCAAGGAGGTGGGCAGCA   44412         GG  _
                                TGCTGCTCGT  CCT GCT
                                ||||||||||  ||| |||
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                                ACGACGGGTG  GGA CGA
                                      GA   A
GAM225  MGC33182 3'  GAGCAGATGATTCGAGCAGCA  76094        TGGC__
                                TGCTGCTCG     CTGCTC
                                |||||||||     ||||||
                                ACGACGAGC     GACGAG
                                     TTAGTA
GAM225  NAV3     3'  AGCACTAGATGCAGCA      30450       _ G   CC
                                TGCTGC TC TGG  TGCT
                                |||||| || |||  ||||
                                ACGACG AG ATC  ACGA
                                   T  _  __
GAM225  NEDD8    5'  GAGCGGTAGGAGCAGCA     21590        G  G  T
                                TGCTGCTC TG CC GCTC
                                |||||||| || || ||||
                                ACGACGAG AT GG CGAG
                                     G  _  _
GAM225  PACSIN2  3'  GAGCAGGTGCTGCAGC      24298      TC   G
                                GCTGC  GTG CCTGCTC
                                |||||  ||| |||||||
                                CGACG  CGT GGACGAG
                                   T_   _
GAM225  PP1628   3'  GAGCAGAGGTGAGCAGCA    48078         TGGC
                                TGCTGCTCG    CTGCTC
                                |||||||||    ||||||
                                ACGACGAGT    GACGAG
                                     GGA_
GAM225  PRO1843  5'  AGCATCAGGAGCAGGCA     38137     _    G   CC
                                TGC TGCTC TGG  TGCT
                                ||| ||||| |||  ||||
                                ACG ACGAG ACT  ACGA
                                  G    G  __
GAM225  PRO2577  3'  AGCAGACTGTTAGGAGCAGTA  38424         G   ___
                                TGCTGCTC TGGC   CTGCT
                                |||||||| ||||   |||||
                                ATGACGAG ATTG   GACGA
                                     G    TCA
GAM225  PRSS25   5'  GAGCAGCAGCACGAGCAGTA   59674          GC_
                                TGCTGCTCGTG   CTGCTC
                                ||||||||||   ||||||
                                ATGACGAGCAC   GACGAG
                                      GAC
GAM225  PRSS25   5'  GAGCAGCAGCACGAGCAGTA   26031          GC_
                                TGCTGCTCGTG   CTGCTC
                                ||||||||||   ||||||
                                ATGACGAGCAC   GACGAG
                                      GAC
GAM225  PSTPIP2  3'  GGGCACCCAGAGCAGCA     44658        G   CC
                                TGCTGCTC TGG  TGCTC
                                |||||||| |||  |||||
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                                ACGACGAG ACC  ACGGG
                                     _  C_
GAM225  SRCAP    5'  GAGCAGGCCAAGCTGC     22845    T   CG
                                GC GCT  TGGCCTGCTC
                                || |||  ||||||||||
                                CG CGA  ACCGGACGAG
                                 T  __
GAM225  STK22D   3'  GAGCAGGAAGAGCAGCA     50144        GTGG
                                TGCTGCTC    CCTGCTC
                                ||||||||    |||||||
                                ACGACGAG    GGACGAG
                                    AA__
GAM225  TXI1     5'  GAGCAGGTGCTGGCAGGCA   37971     _   C   G
                                TGC TGCT GTG CCTGCTC
                                ||| |||| ||| |||||||
                                ACG ACGG CGT GGACGAG
                                  G   T  _
GAM225  UQCR     3'  GAGCAAGCCACAGTGC      23358    T   C    C
                                GC GCT GTGGC TGCTC
                                || ||| ||||| |||||
                                CG TGA CACCG ACGAG
                                 _  _    A
GAM225  VIT      3'  GAGCAGGCAGAGCACCA     54977    C    GTG
                                TG TGCTC   GCCTGCTC
                                || |||||   ||||||||
                                AC ACGAG   CGGACGAG
                                 C    A__
GAM225  ZNF31    3'  GAGCAGGCCACTGTGAGC    65613     ___
                                GCTC   GTGGCCTGCTC
                                ||||   ||||||||||
                                CGAG   CACCGGACGAG
                                  TGT
GAM225  LOC115264 3'  AGCAGCGGCTGGAGCAGCA   73738        G    __
                                TGCTGCTC TGGCC  TGCT
                                |||||||| |||||  ||||
                                ACGACGAG GTCGG  ACGA
                                    _    CG
GAM225  LOC127841 5'  GAGGGGAACAAGTAGCA     75187       C  GG   G
                                TGCTGCT GT  CCT CTC
                                ||||||| ||  ||| |||
                                ACGATGA CA  GGG GAG
                                    A  A_  _
GAM225  LOC133671 5'  GAGCTACCTGAGCAGCA     76457         T  CCT
                                TGCTGCTCG GG   GCTC
                                ||||||||| ||   ||||
                                ACGACGAGT CC   CGAG
                                     _ AT_
GAM225  LOC143153 3'  GAGCAGCCTAGAGCAGCA    76979        GT   C
                                TGCTGCTC  GGC TGCTC
                                ||||||||  ||| |||||
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                                ACGACGAG  CCG ACGAG
                                    AT  _
GAM225  LOC143154 3'  GAGCAGCCTAGAGCAGCA    76989       GT  C
                                TGCTGCTC  GGC TGCTC
                                ||||||||  ||| |||||
                                ACGACGAG  CCG ACGAG
                                    AT  _
GAM225  LOC145231 3'  GAGCAGGCATGTCGGCA    84249      CT   G
                                TGCTG  CGTG CCTGCTC
                                |||||  |||| |||||||
                                ACGGC  GTAC GGACGAG
                                  T_   _
GAM225  LOC146057 5'  GAGCAGGTGCTGGCACAAGAGC 78133     G  C  _____
          A                      TGCT CT GTG    GCCTGCTC
                                |||| || |||    ||||||||
                                ACGA GA CAC    TGGACGAG
                                  _ A  GGTCG
GAM225  LOC146445 3'  GAGCAGGTGACAGAAGCA    84681     G  C  G
                                TGCT CT GT GCCTGCTC
                                |||| || || ||||||||
                                ACGA GA CA TGGACGAG
                                  A  _  G
GAM225  LOC148229 5'  GAGCAGGACGTGAGCGCA    79488     T     G
                                TGC GCTCGTG CCTGCTC
                                ||| ||||||| |||||||
                                ACG CGAGTGC GGACGAG
                                  _     A
GAM225  LOC148490 5'  GAACAGCCACAAGCAGC     79621      C    C  C
                                GCTGCT GTGGC TG TC
                                |||||| ||||| || ||
                                CGACGA CACCG AC AG
                                   A    _  A
GAM225  LOC149296 5'  GAGCAGCAGCTACGGGCAGCA  80021           __
                                TGCTGCTCGTGGC  CTGCTC
                                ||||||||||||  ||||||
                                ACGACGGGCATCG  GACGAG
                                        AC
GAM225  LOC149318 3'  AGCAGCGGCTGGAGCAGCA   71233       G   __
                                TGCTGCTC TGGCC  TGCT
                                ||||||| |||||  ||||
                                ACGACGAG GTCGG  ACGA
                                    _    CG
GAM225  LOC149319 5'  GAGCTGGCACACCAGCAGCA  80073       C  _  T
                                TGCTGCT GTG GCC GCTC
                                ||||||| ||| ||| ||||
                                ACGACGA CAC CGG CGAG
                                   C  A  T
GAM225  LOC151438 5'  GAGCAGGTGCTTGAAAGCA   86557     GC  TG_
                                TGCT  TCG  GCCTGCTC
                                ||||  |||  ||||||||
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                                ACGA  AGT   TGGACGAG
                                  A_  TCG
GAM225  LOC151516 5'  GAACAGGCCACAGCACTGC   81066   __   C      C
                                GC  TGCT GTGGCCTG TC
                                ||  |||| |||||||| ||
                                CG  ACGA CACCGGAC AG
                                 TC   _      A
GAM225  LOC153218 5'  GAGCAGGCCCATATTCAGC   81657    CTC   _
                                GCTG   GTGG CCTGCTC
                                ||||   |||| |||||||
                                CGAC   TACC GGACGAG
                                  TTA   C
GAM225  LOC154860 5'  GAGCAGGTCGCTGCAGC    87503     TC
                                GCTGC  GTGGCCTGCTC
                                |||||  ||||||||||
                                CGACG  CGCTGGACGAG
                                   T_
GAM225  LOC155382 5'  GAGCGGGCCGAGCCAGCA    87677     _  GT
                                TGCTG CTC  GGCCTGCTC
                                ||||| |||  |||||||||
                                ACGAC GAG  CCGGGCGAG
                                   C  __
GAM225  LOC163911 5'  GAGCAAGCCAAGGAGCAGCA  88420       G_   C
                                TGCTGCTC  TGGC TGCTC
                                ||||||||  |||| |||||
                                ACGACGAG  ACCG ACGAG
                                     GA   A
GAM225  LOC164118 5'  GAGCAGGCCACAGTGC     83046    T   C
                                GC GCT GTGGCCTGCTC
                                || ||| ||||||||||
                                CG TGA CACCGGACGAG
                                 _  _
GAM225  LOC164714 5'  GAGCAGCGACCTGAGCAGCA  88583       T  C__
                                TGCTGCTCG GG   CTGCTC
                                ||||||||| ||   ||||||
                                ACGACGAGT CC   GACGAG
                                     _ AGC
GAM225  LOC164714 5'  GAGCTGCAGCAGGAGCAGCA  88584       G  __  CT
                                TGCTGCTC TG  GC  GCTC
                                |||||||| ||  ||  ||||
                                ACGACGAG AC  CG  CGAG
                                     G  GA  T_
GAM225  LOC196047 5'  AGCAGGCCAGGCACA      91143    C   CG
                                TG TGCT  TGGCCTGCT
                                || ||||  |||||||||
                                AC ACGG  ACCGGACGA
                                 _   __
GAM225  LOC200213 5'  AGCAGGCCACCAAGAGCA    90028     ___
                                TGCTC   GTGGCCTGCT
                                |||||   ||||||||||
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                                ACGAG   CACCGGACGA
                                   AAC
GAM225   LOC201181 5'  GAGCAGGCAGGGCACAGCA   89514     __   GTG
                                TGCT  GCTC   GCCTGCTC
                                ||||  ||||   ||||||||
                                ACGA  CGGG   CGGACGAG
                                  CA   A__
GAM225   LOC203696 5'  GAGCAGGTTCTGGCGGCA    92335      T  TG
                                TGCTGC CG  GCCTGCTC
                                ||||||  ||  ||||||||
                                ACGGCG GT  TGGACGAG
                                   _  CT
GAM225   LOC204970 3'  GAGCAGGGCTGGAACCAGCA  90963      C_  G    _
                                TGCTG  TC TGGCC TGCTC
                                |||||  ||  ||||| |||||
                                ACGAC  AG GTCGG ACGAG
                                   CA  _    G
GAM225   LOC219294 3'  GAGCAGCCTAGAGCAGCA    94594       GT   C
                                TGCTGCTC  GGC TGCTC
                                ||||||||  ||| |||||
                                ACGACGAG  CCG ACGAG
                                    AT  _
GAM225   LOC219295 3'  GAGCAGCCTAGAGCAGCA    94586       GT   C
                                TGCTGCTC  GGC TGCTC
                                ||||||||  ||| |||||
                                ACGACGAG  CCG ACGAG
                                    AT  _
GAM225   LOC219731 5'  GAGCAGGCGGGCCAGCA     94707      _  GTG
                                TGCTG CTC   GCCTGCTC
                                |||||  |||   ||||||||
                                ACGAC GGG   CGGACGAG
                                   C  ____
GAM225   LOC220514 3'  GAGCAGGTGCTGCAGC      61074      TC   G
                                GCTGC  GTG CCTGCTC
                                |||||  |||  |||||||
                                CGACG  CGT GGACGAG
                                   T_  _
GAM225   LOC220549 5'  GAGCAGGCGGTGGCGGCA    94507       T   G
                                TGCTGC CGT GCCTGCTC
                                ||||||  |||  ||||||||
                                ACGGCG GTG CGGACGAG
                                   _  G
GAM225   LOC253769 5'  GAGCAGGTTGAAGTAACA    99020    C   CG
                                TG TGCT  TGGCCTGCTC
                                ||  ||||  ||||||||||
                                AC ATGA  GTTGGACGAG
                                 A   A_
GAM225   LOC255057 3'  GAGCAGGCCCAGACCAGC    97095      C  GT
                                GCTG TC  GGCCTGCTC
                                ||||  ||  |||||||||
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                                CGAC AG  CCGGACGAG
                                  C  AC
GAM225  LOC255299 5'  AGCAGGTGCACGGGCAACA   99334    C      _
                                TG TGCTCGTG GCCTGCT
                                || |||||||| |||||||
                                AC ACGGGCAC TGGACGA
                                 A       G
GAM225  LOC256228 5'  AGCAGGACAGCAAGCA      97968     _  C  GG
                                TGCT GCT GT  CCTGCT
                                |||| ||| ||  ||||||
                                ACGA CGA CA  GGACGA
                                  A  _  __
GAM225  LOC256310 3'  GAGCTGGACGAGGAGCA     98099     G    GG  T
                                TGCT CTCGT  CC GCTC
                                |||| |||||  || ||||
                                ACGA GAGCA  GG CGAG
                                  G    __  T
GAM225  LOC256512 5'  GAGCAGGTAGAGGAGCA     97984     G   GTG
                                TGCT CTC   GCCTGCTC
                                |||| |||   ||||||||
                                ACGA GAG   TGGACGAG
                                  G   A__
GAM225  LOC257450 3'  GAGCAGGCACAAGACAGC    91450     C  G  _
                                GCTG TC TG GCCTGCTC
                                |||| || || ||||||||
                                CGAC AG AC CGGACGAG
                                  _  A  A
GAM225  LOC257479 5'  GAGCAGAACTGGGAGCAG    97987       G   C_
                                CTGCTC TGG  CTGCTC
                                |||||| |||  ||||||
                                GACGAG GTC  GACGAG
                                   G   AA
GAM225  LOC51219  5'  GAGCAGGCTGGGAACTGCA   33546     TGC  G
                                TGC   TC TGGCCTGCTC
                                |||   || ||||||||||
                                ACG   AG GTCGGACGAG
                                  TCA  G
GAM225  LOC57406  3'  GAGCGTCCGGAGCAGCA     40717       G   CC
                                TGCTGCTC TGG  TGCTC
                                |||||||| |||  |||||
                                ACGACGAG GCC  GCGAG
                                    _   T_
GAM225  LOC91517  3'  GAGCAGGCCTGCCAGC      66911     CT  T
                                GCTG  CG GGCCTGCTC
                                ||||  || |||||||||
                                CGAC  GT CCGGACGAG
                                  C_  _
GAM226  FLJ22332  5'  GGAAAGAAAACTACATCACA   45637     G  A      _______
                                TGTG AT TAGTTTTC     CC
                                |||| || ||||||||     ||
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                                ACAC TA ATCAAAAG     GG
                                  _ C       AAA___
GAM227  AMACR    3'  TTGTATGCATGGAAACATGGA  69103      ATC        G
                                TCCAT   TCCATGCATG CGG
                                |||||   |||||||||| |||
                                AGGTA   AGGTACGTAT GTT
                                   CAA        _
GAM227  BCL2L11  3'  TCGCCCAGAGATATGGA     57615        CA  CAT    G
                                TCCATATCTC  TG   GGCG A
                                ||||||||||  ||   |||| |
                                AGGTATAGAG  AC   CCGC T
                                     __ ___    G
GAM227  BCL2L11  3'  TCGCCCAGAGATATGGA     57616        CA  CAT    G
                                TCCATATCTC  TG   GGCG A
                                ||||||||||  ||   |||| |
                                AGGTATAGAG  AC   CCGC T
                                     __ ___    G
GAM227  FGFR2    5'  CGTCCACATGGAGATATGGA   43633           CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __   T
GAM227  FGFR2    5'  CGTCCACATGGAGATATGGA   43638           CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __   T
GAM227  FGFR2    5'  CGTCCACATGGAGATATGGA   43642           CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __   T
GAM227  FGFR2    5'  CGTCCACATGGAGATATGGA   43652           CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __   T
GAM227  FGFR2    5'  CGTCCACATGGAGATATGGA   43665           CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __   T
GAM227  FGFR2    5'  CGTCCACATGGAGATATGGA   43674           CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __   T
GAM227  FGFR2    5'  CGTCCACATGGAGATATGGA   43678           CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
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                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM227  FGFR2    5'  CGTCCACATGGAGATATGGA  43763          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM227  FGFR2    5'  CGTCCACATGGAGATATGGA  43767          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM227  FGFR2    5'  CGTCCACATGGAGATATGGA  43771          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM227  FGFR2    5'  CGTCCACATGGAGATATGGA  5559           CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM227  MAP3K14  3'  ATCCGCCACGTGAAGAGA   15541     CA  A
                                TCTC  TGC TGGCGGAT
                                ||||  ||| ||||||||
                                AGAG  GTG ACCGCCTA
                                  AA  C
GAM227  KIAA0819 3'  CCCCAGCATCACAGGAGACATG 64330      A   ____   A  C
           GA                     TCCAT TCTCC   ATGC TGG GG
                                |||||  |||||   ||||  ||| ||
                                AGGTA  AGAGG   TACG ACC CC
                                  C    ACAC   _  _
GAM227  PORIMIN  3'  CATACATGGAGTATGGA    54702       T    C
                                TCCATA CTCCATG ATG
                                ||||||  ||||||| |||
                                AGGTAT GAGGTAC TAC
                                   _     A
GAM227  RDC1     3'  CCGGCACGGGATATGGA     72832        T  A  A
                                TCCATATC CC TGC TGG
                                ||||||||  ||  ||| |||
                                AGGTATAG GG ACG GCC
                                    _ C  _
GAM227  VEZATIN  3'  ATCCGCCACAACAGACAATG  34656    A_  CCA  CA
                                CAT  TCT   TG  TGGCGGAT
                                |||  |||   ||  ||||||||
                                GTA  AGA   AC  ACCGCCTA
                                  AC   CA_  __
GAM227  LOC147645 5'  ATCCGCTGGTGGCAGAGACACG 79065    ATA   CA   AT__
           G                     CC   TCTC  TGC   GGCGGAT
                                ||   ||||  |||   |||||||
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                                GG  AGAG  ACG   TCGCCTA
                                 CAC   __  GTGG
GAM227  LOC199775 3'  TTGCTGCATCAGAGATATG   89726       C_   TG
                                CATATCTC  ATGCA  GCGG
                                ||||||||  |||||  ||||
                                GTATAGAG  TACGT  CGTT
                                    AC    __
GAM227  LOC51279  3'  CCGCTATTAGAGTATGGA    33752      T  CATGC
                                TCCATA CTC    ATGGCGG
                                ||||||| |||    |||||||
                                AGGTAT GAG    TATCGCC
                                   _  AT___
GAM228  AMFR      3'  ACCTCCAGCTGACACGCTCA   58040    A_  AC    _
                                TGA  GT  CAGCTG AGGT
                                |||  ||  |||||| ||||
                                ACT  CA  GTCGAC TCCA
                                  CG  CA     C
GAM228  ASH1      3'  ACCTACTGGTACTTTA      38084         CTG
                                TGAAGTACCAG   AGGT
                                ||||||||||   ||||
                                ATTTCATGGTC   TCCA
                                      A__
GAM228  ATP1B2    3'  AGCCACCGCGCCTGGCCTTCA  9826      TA   C  A
                                TGAAG  CCAG TG GGTGGCT
                                |||||  |||| || |||||||
                                ACTTC  GGTC GC CCACCGA
                                   C_   C  G
GAM228  C8orf1    3'  ACCTTGACAGGTACTTCA    16342        AGC
                                TGAAGTACC   TGAGGT
                                |||||||||   ||||||
                                ACTTCATGG   GTTCCA
                                      ACA
GAM228  CD8A      3'  GCCACTACATTACTTCA     10096       CCAGC  A
                                TGAAGTA    TG GGTGGC
                                |||||||    || ||||||
                                ACTTCAT    AC TCACCG
                                     T_____  A
GAM228  CDA       3'  AGCCACCTGGAGAACTTCA   10125      ACCAG  G
                                TGAAGT    CT AGGTGGCT
                                ||||||    || ||||||||
                                ACTTCA    GG TCCACCGA
                                   AGA__  _
GAM228  CYB5      3'  AGCCATTGCTAACTACTTCA   10349       CC_   TGA
                                TGAAGTA   AGC   GGTGGCT
                                |||||||   |||   |||||||
                                ACTTCAT   TCG   TTACCGA
                                     CAA   ___
GAM228  EPHB4     3'  AGCCACCTCGGGGAACTCCA   16705    A   A  AG
                                TG AGT CC  CTGAGGTGGCT
                                || ||| ||  ||||||||||
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                                AC TCA GG  GGCTCCACCGA
                                 C   A  __
GAM228  FAAH    3'  AGCCACCTCTCAGTGCCTCA  44448    A   CAGCT
                                TGA GTAC    GAGGTGGCT
                                ||| ||||    |||||||||
                                ACT CGTG    CTCCACCGA
                                  C   ACT__
GAM228  FOS     3'  GTTCCCAGTGACACTTCA    19136      ACCA   A  T
                                TGAAGT    GCTG GG GGC
                                ||||||    |||| || |||
                                ACTTCA    TGAC CC TTG
                                   CAG_   _ _
GAM228  GAS     3'  AGCCACCTCCCACCCCACTTCA 7688       ACCAGCT
                                TGAAGT      GAGGTGGCT
                                ||||||      |||||||||
                                ACTTCA      CTCCACCGA
                                   CCCCACC
GAM228  HEPH    5'  ACCTCAGCTGGCATCTCA    29647    AG A
                                TGA  T CCAGCTGAGGT
                                |||  | ||||||||||
                                ACT  A GGTCGACTCCA
                                  CT C
GAM228  HLA-DQA1 3'  AGCCACCCAGCTACCTAATTC  99723    GTACC_    A
                                GAA     AGCTG GGTGGCT
                                |||     ||||| |||||||
                                CTT     TCGAC CCACCGA
                                  AATCCA    _
GAM228  HSPB3   5'  AGCTGCTTCAACTGGTAATCCA 21950    AAG    C    TG
                                TG   TACCAG TGAGG  GCT
                                ||   |||||| |||||  |||
                                AC   ATGGTC ACTTC  CGA
                                 CTA     A    GT
GAM228  IDH3A   3'  AGCAGAGAGCTAGTACTTCA   19842       C   GAGGTG
                                TGAAGTAC AGCT     GCT
                                |||||||| ||||     |||
                                ACTTCATG TCGA     CGA
                                     A   GAGA__
GAM228  ITSN1   3'  CCACCATTTGGTATTCA     13092     G    CTGA
                                TGAA TACCAG    GGTGG
                                |||| ||||||    |||||
                                ACTT ATGGTT    CCACC
                                  _     TA__
GAM228  LAMA4   5'  AGCCACCTCGGGATACTGCA   11259    A   CCAG
                                TG AGTA    CTGAGGTGGCT
                                || ||||    ||||||||||
                                AC TCAT    GGCTCCACCGA
                                 G   AG__
GAM228  MOX2    5'  AGCCACCTCGCGCGCGCCTC   67475    A  ACCA  _
                                GA GT    GC TGAGGTGGCT
                                || ||    || ||||||||||
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                                CT CG   CG GCTCCACCGA
                                 C  CG__  C
GAM228  PET112L  3'  AGCCACCCCGCCTGCTTCA   17079       CCA  T A
                                TGAAGTA   GC G GGTGGCT
                                |||||||   || | |||||||
                                ACTTCGT   CG C CCACCGA
                                    C__  _ C
GAM228  UTY      3'  ATCCAGCTGTACTTCA     24062       C    A
                                TGAAGTAC AGCTG GGT
                                |||||||| ||||| |||
                                ACTTCATG TCGAC CTA
                                      _    _
GAM228  AP1GBP1  3'  AGCCACCTCAATTCTTCA   24341      TACCAGC
                                TGAAG     TGAGGTGGCT
                                |||||     ||||||||||
                                ACTTC     ACTCCACCGA
                                   TTA____
GAM228  AP1GBP1  3'  AGCCACCTCAATTCTTCA   55435      TACCAGC
                                TGAAG     TGAGGTGGCT
                                |||||     ||||||||||
                                ACTTC     ACTCCACCGA
                                   TTA____
GAM228  AP1GBP1  3'  AGCCACCTCAATTCTTCA   55443      TACCAGC
                                TGAAG     TGAGGTGGCT
                                |||||     ||||||||||
                                ACTTC     ACTCCACCGA
                                   TTA____
GAM228  ATP10B   3'  AGCCACCTTAAGCTAGTAC   64101     C   _
                                GTAC AGCT GAGGTGGCT
                                |||| |||| |||||||||
                                CATG TCGA TTCCACCGA
                                  A   A
GAM228  BLZF1    3'  AGCCAAGTTAACAAGTACTTCA 14753       CAGC   GG
                                TGAAGTAC   TGA  TGGCT
                                ||||||||   |||  |||||
                                ACTTCATG   ATT  ACCGA
                                     AACA   GA
GAM228  C14orf3  3'  GCCTGCTGGACACTTCA     25050      A_    TG
                                TGAAGT  CCAGC  AGGT
                                ||||||  |||||  ||||
                                ACTTCA  GGTCG  TCCG
                                   CA    __
GAM228  cerk     3'  AGCCACCTGCTGACATTCA   43156     GTAC    TG
                                TGAA   CAGC  AGGTGGCT
                                ||||   ||||  ||||||||
                                ACTT   GTCG  TCCACCGA
                                  ACA_   __
GAM228  CILP     3'  GCTTCAACTGTACTTCA     14615       C  C
                                TGAAGTAC AG TGAGGT
                                |||||||| || ||||||
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                                ACTTCATG TC ACTTCG
                                     _ A
GAM228  DKFZP564O0823 3'  ACCTGCACTGAGTACTTCA   60255       _  C _
                                TGAAGTAC CAG TG AGGT
                                |||||||| ||| || ||||
                                ACTTCATG GTC AC TCCA
                                     A  _ G
GAM228  DKFZp761B0514 3'  GTCTCAGCTGGAACCCCA   51148    AA  A
                                TG  GT CCAGCTGAGGT
                                ||  || ||||||||||
                                AC  CA GGTCGACTCTG
                                 CC  A
GAM228  EFA6R    3'  AGCCACCTCTCTTCATTTCA  31632      ACC  CT
                                TGAAGT   AG  GAGGTGGCT
                                ||||||   ||  |||||||||
                                ACTTTA   TC  CTCCACCGA
                                    CT_  T_
GAM228  FBXO21   3'  AGCCACCTGAGACCACTTCA  54347      ACCAG  G
                                TGAAGT    CT AGGTGGCT
                                ||||||    || ||||||||
                                ACTTCA    GA TCCACCGA
                                    CCA__  G
GAM228  FLJ12592  3'  ACCTCACTGTACTTCA     50648       C  C
                                TGAAGTAC AG TGAGGT
                                |||||||| || ||||||
                                ACTTCATG TC ACTCCA
                                     _ _
GAM228  FLJ20105  5'  CCACAGCCTCAGCCTTCA    35054     TACCA      ___
                                TGAAG    GCTGAGGT   GG
                                |||||    ||||||||   ||
                                ACTTC    CGACTCCG   CC
                                   _____       ACA
GAM228  FLJ20671  3'  AGCTCTGGAACTGGTATTCCA  35933    A      CTGA  T
                                TG AGTACCAG    GG GGCT
                                || |||||||    || ||||
                                AC TTATGGTC    TC TCGA
                                 C       AAGG  _
GAM228  FLJ20707  3'  AGCCACTTCCATGATCTCCA   36031    A  TAC  GCT
                                TG AG   CA   GAGGTGGCT
                                || ||   ||   |||||||||
                                AC TC   GT   CTTCACCGA
                                 C  TA_  AC_
GAM228  FLJ21148  3'  AGCTGTGTAACTGGTACTCG   46306     A      C  AG TG
                                TGA GTACCAG TG  G  GCT
                                ||| ||||||| ||  |  |||
                                GCT CATGGTC AT  T  CGA
                                  _      A  G_ GT
GAM228  HH114    3'  GCCACCTTTGTACTCA      51667     A   CAGCT
                                TGA GTAC    GAGGTGGC
                                ||| ||||    ||||||||
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                                ACT CATG    TTCCACCG
                                  _   T____
GAM228  ILF3    3' CATGTCAGCTGGCCCTCCA   25232   A  TA      G
                                TG AG  CCAGCTGA GTG
                                || ||  |||||||| |||
                                AC TC  GGTCGACT TAC
                                 C  CC       G
GAM228  KIAA0295 3' AGCTGGAGAGCTGGTACTT   68658         GAGGT
                                AAGTACCAGCT    GGCT
                                ||||||||||    ||||
                                TTCATGGTCGA    TCGA
                                      GAGG_
GAM228  KIAA0669 5' AGCCACCACCGCTACCTCA   29430    A  ACC   TGA
                                TGA GT   AGC   GGTGGCT
                                ||| ||   |||   |||||||
                                ACT CA   TCG   CCACCGA
                                  C  ___   CCA
GAM228  KIAA0953 3' AGCCATGATGGCAGCACGGCAC 67320       A  A_   AG___
           TTCA                   TGAAGT CC  GCTG    GTGGCT
                                ||||||| ||  ||||    ||||||
                                ACTTCA GG  CGAC    TACCGA
                                   C  CA   GGTAG
GAM228  KIAA1610 3' AGCCACTTTGCAACACTT    67737     ACCA  T
                                AAGT    GC GAGGTGGCT
                                ||||    || |||||||||
                                TTCA    CG TTTCACCGA
                                  CAA_  _
GAM228  KIAA1853 3' ACCCAGACTGGACTTCA     69917       A   _  A
                                TGAAGT CCAG CTG GGT
                                |||||| |||| ||| |||
                                ACTTCA GGTC GAC CCA
                                   _   A  _
GAM228  KIAA1958 3' AGCCAAGCTCTGATACCTCA   82773    A   C  GCT   G_
                                TGA GTA CA   GAG  TGGCT
                                ||| ||| ||   |||  |||||
                                ACT CAT GT   CTC  ACCGA
                                  C   A  ___   GA
GAM228  LMOD1    3' GGTTGCTTCAGCTGATCCTTCA 25105      TAC       TG
                                TGAAG   CAGCTGAGG  GCT
                                |||||   |||||||||  |||
                                ACTTC   GTCGACTTC  TGG
                                   CTA       GT
GAM228  METAP2   3' AGCCACCTCAACACCTTTA   60807     TACCAGC
                                TGAAG      TGAGGTGGCT
                                |||||      ||||||||||
                                ATTTC      ACTCCACCGA
                                   CACA___
GAM228  NXN     5' AGTCCTTCAAACAGTACTTCA  42666        CAGC    T
                                TGAAGTAC    TGAGG GGCT
                                ||||||||    ||||| ||||
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                                ACTTCATG    ACTTC CTGA
                                    ACAA    _
GAM228  SYT12    5'  AGCCACCTCTGTTGCTTCA   96374      TAC    T
                                TGAAG   CAGC GAGGTGGCT
                                |||||   |||| |||||||||
                                ACTTC   GTTG CTCCACCGA
                                   ___    T
GAM228  TSPAN-2  3'  AGCCACCTAGAGAATTCTTCA 20373      TACCAG  G
                                TGAAG     CT AGGTGGCT
                                |||||     || ||||||||
                                ACTTC     GA TCCACCGA
                                  TTAAGA  _
GAM228  TXN2     3'  AGCCACACCTTGGTCCTCA   25931     A T    CTGAG
                                TGA G ACCAG    GTGGCT
                                ||| | |||||    ||||||
                                ACT C TGGTT    CACCGA
                                  _ C    CCA__
GAM228  XRN2     3'  CTCTTGAGCTGGAACCTCA   25315     A  A     G   T
                                TGA GT CCAGCT AGG GG
                                ||| || |||||| ||| ||
                                ACT CA GGTCGA TTC TC
                                  C  A     G   _
GAM228  LOC115207 3'  CCACCCCTCCCCCAGATGGTAC 57396          G   A_____
           TTCA                    TGAAGTACCA CTG      GGTGG
                                |||||||||| |||      |||||
                                ACTTCATGGT GAC      CCACC
                                     A   CCCCTCC
GAM228  LOC129138 3'  AGCCTCTGCAGCTGCACTTCA  57919       AC     A  T
                                TGAAGT  CAGCTG GG GGCT
                                ||||||  |||||| || ||||
                                ACTTCA  GTCGAC TC CCGA
                                   C_     G  T
GAM228  LOC139221 5'  AGCCACCTCAACCTTTGGTA   76326       C___
                                TACCAG    TGAGGTGGCT
                                ||||||    ||||||||||
                                ATGGTT    ACTCCACCGA
                                    TCCA
GAM228  LOC143451 3'  AGCCACTCTTAGCCACACCTCA 77067     A  ACCA     _
                                TGA GT    GCTGAG GTGGCT
                                ||| ||    |||||| ||||||
                                ACT CA    CGATTC CACCGA
                                  C  CAC_     T
GAM228  LOC143677 3'  AGCCACCTCTGATACTTC    83891       C  GCT
                                GAAGTA CA   GAGGTGGCT
                                |||||| ||   |||||||||
                                CTTCAT GT   CTCCACCGA
                                   A  ___
GAM228  LOC145125 3'  AGCCACTCTTAGCCACACCTCA 77543     A  ACCA     _
                                TGA GT    GCTGAG GTGGCT
                                ||| ||    |||||| ||||||
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                                ACT CA    CGATTC CACCGA
                                  C  CAC_     T
GAM228   LOC147650 5'  AGCCACCTGCATGACACCTTCA 79014      TAC_ _  TG
                                TGAAG    CA GC  AGGTGGCT
                                |||||    || ||  ||||||||
                                ACTTC    GT CG  TCCACCGA
                                   CACA  A  __
GAM228   LOC148759 3'  CCACCCTGAGTGCTTCA     85375        _  CTGA
                                TGAAGTAC CAG    GGTGG
                                |||||||| |||    |||||
                                ACTTCGTG GTC    CCACC
                                     A  ____
GAM228   LOC150225 3'  ACTGTTCAGCATAGTACTTCA  86176       CA_    __
                                TGAAGTAC   GCTGA  GGT
                                ||||||||   |||||  |||
                                ACTTCATG   CGACT  TCA
                                     ATA    TG
GAM228   LOC162333 5'  AGCCACATCCTGGCATCTCA   88487    AG A    CT  G
                                TGA  T CCAG  GA GTGGCT
                                |||  | ||||  || ||||||
                                ACT  A GGTC  CT CACCGA
                                  CT C    __  A
GAM228   LOC165246 5'  AGCAGAGCTGGTACTTCA    83363          GAGGTG
                                TGAAGTACCAGCT     GCT
                                ||||||||||||      |||
                                ACTTCATGGTCGA     CGA
                                     GA____
GAM228   LOC169831 5'  ACTCCAGCAGGTACTTCA    83669         A    AG
                                TGAAGTACC GCTG  GT
                                |||||||| ||||  ||
                                ACTTCATGG CGAC  CA
                                     A    CT
GAM228   LOC196264 3'  ACCCAGCACTGGTGCTTCA   88976          __    A
                                TGAAGTACCA  GCTG GGT
                                ||||||||||  |||| |||
                                ACTTCGTGGT  CGAC CCA
                                     CA    _
GAM228   LOC200862 5'  AGTTCCTTCCAGCTGGTCCTCA 91765     A T       _   TG
                                TGA G ACCAGCTG AGG  GCT
                                ||| | |||||||| |||  |||
                                ACT C TGGTCGAC TTC  TGA
                                  _ C       C   CT
GAM228   LOC202908 5'  AGCCACCTCACCTGACCTGC   90708     C__   C
                                GTA   CAG TGAGGTGGCT
                                |||   ||| ||||||||||
                                CGT   GTC ACTCCACCGA
                                  CCA   C
GAM228   LOC220980 5'  AGCCACCTCAGCCACGTG    94764     CA_
                                TAC   GCTGAGGTGGCT
                                |||   ||||||||||||
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                                GTG   CGACTCCACCGA
                                  CAC
GAM228  LOC254440 3'  AGCCACTCTTAGCCACACCTCA 98846     A  ACCA     _
                                TGA GT    GCTGAG GTGGCT
                                ||| ||    |||||| ||||||
                                ACT CA    CGATTC CACCGA
                                  C  CAC_     T
GAM228  LOC255055 3'  CCACCTTGCATGTATTCA    96519      G   CA  T
                                TGAA TAC  GC GAGGTGG
                                |||| |||  || |||||||
                                ACTT ATG  CG TTCCACC
                                   _   TA  _
GAM228  LOC255251 3'  AGCCACCGGCGTTGAGTACTTC 97618         _    TGA
            A                    TGAAGTAC CAGC   GGTGGCT
                                |||||||| ||||   |||||||
                                ACTTCATG GTTG   CCACCGA
                                     A    CGG
GAM228  LOC256741 3'  GCACAGCTGGTACTGCA     98578    A         AG
                                TG AGTACCAGCTG  GT
                                || ||||||||||  ||
                                AC TCATGGTCGAC  CG
                                 G         A_
GAM228  LOC257429 3'  AGCCACCCAGCTACCTAATTC  97695     GTACC_    A
                                GAA      AGCTG GGTGGCT
                                |||      ||||| |||||||
                                CTT      TCGAC CCACCGA
                                  AATCCA    _
GAM228  LOC83693  3'  ACTTCAACTGGTATTTCA    49604          C
                                TGAAGTACCAG TGAGGT
                                |||||||||| ||||||
                                ACTTTATGGTC ACTTCA
                                       A
GAM229  KIAA0410  3'  CTCAAAGTGATCTCAAACTGGA 29425        C       C  C
                                TCCAGTT GAGATCAC TT GAG
                                ||||||| |||||||| || |||
                                AGGTCAA CTCTAGTG AA CTC
                                     A       _  A
GAM229  MGC4562   5'  CTCATTACGTGATCCCAGACTG 56740         CGA     CTTC_
            GAA                    TTCCAGTT   GATCAC    GAG
                                |||||||   ||||||    |||
                                AAGGTCAG   CTAGTG    CTC
                                     ACC     CATTA
GAM229  LOC92181  3'  CTCAAAGTTTGTCAACTGGAA  68945        CGA   CAC   C
                                TTCCAGTT   GAT   CTT GAG
                                ||||||||   |||   ||| |||
                                AAGGTCAA   CTG   GAA CTC
                                     ___   TTT   A
GAM230  ADAMTS4   3'  ACAGGGTTTCACCATGTTGGCC 18741          C        C
            AG                     TTGGCTAACA GGTGAAACCC GT
                                |||||||||| |||||||||| ||
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                                GACCGGTTGT CCACTTTGGG CA
                                     A         A
GAM230  ADAMTS4   3'  ACGGGGTTTCACCATGTTGGCC 18743          C
          AG                    TTGGCTAACA GGTGAAACCCCGT
                                |||||||||| ||||||||||||
                                GACCGGTTGT CCACTTTGGGGCA
                                     A
GAM230  ADCY6     5'  ACGAGGTTTCACCATCTTGGCC 31583         CAC        C
          AG                    TTGGCTAA   GGTGAAACC CGT
                                |||||||| ||||||||| |||
                                GACCGGTT   CCACTTTGG GCA
                                     CTA        A
GAM230  APAF1     3'  ACGGGGTTTCACCATGTTGGCC 25955         C
                                GGCTAACA GGTGAAACCCCGT
                                |||||||| ||||||||||||
                                CCGGTTGT CCACTTTGGGGCA
                                     A
GAM230  APAF1     3'  ACGGGGTTTCACCATGTTGGCC 8575          C
                                GGCTAACA GGTGAAACCCCGT
                                |||||||| ||||||||||||
                                CCGGTTGT CCACTTTGGGGCA
                                     A
GAM230  APM1      3'  ACAGGGTTTCACCATATTGGCC 17752         CAC        C
          AG                    TTGGCTAA   GGTGAAACCC GT
                                |||||||| ||||||||| ||
                                GACCGGTT   CCACTTTGGG CA
                                     ATA        A
GAM230  APM1      3'  ACGGGGTTTCACCACATTCGTC 17753       TAACAC
          AG                    TTGGC     GGTGAAACCCCGT
                                |||||     ||||||||||||
                                GACTG     CCACTTTGGGGCA
                                   CTTACA
GAM230  APPL      3'  ACGGGGTTTCACCGTGTTAGCC 24940
          AG                    TTGGCTAACACGGTGAAACCCCGT
                                ||||||||||||||||||||||||
                                GACCGATTGTGCCACTTTGGGGCA

GAM230  ARCN1     3'  ACGGGGTTTCACCGTGTTGCCC 9742       C
          AG                    TTGG TAACACGGTGAAACCCCGT
                                |||| ||||||||||||||||||
                                GACC GTTGTGCCACTTTGGGGCA
                                   C
GAM230  ATP6V1A1  3'  ACGGGGTTTCACCATATTGGTC 9863          CAC
          AG                    TTGGCTAA   GGTGAAACCCCGT
                                |||||||| ||||||||||||
                                GACTGGTT   CCACTTTGGGGCA
                                     ATA
GAM230  AXL       3'  ACAGGGTTTCACCATGTTGGCC 9896          C        C
          AG                    TTGGCTAACA GGTGAAACCC GT
                                |||||||||| ||||||||| ||
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                                GACCGGTTGT CCACTTTGGG CA
                                    A         A
GAM230  AXL     3'  ACAGGGTTTCACCATGTTGGCC 41869          C         C
                AG                  TTGGCTAACA GGTGAAACCC GT
                                    |||||||||| |||||||||| ||
                                GACCGGTTGT CCACTTTGGG CA
                                    A         A
GAM230  CASP2   3'  ACAGGGTTTCACCATGTTAGCC 53281          C         C
                G                   TGGCTAACA GGTGAAACCC GT
                                    ||||||||| |||||||||| ||
                                GCCGATTGT CCACTTTGGG CA
                                    A         A
GAM230  CASP2   3'  ACAGGGTTTCACCATGTTAGCC 53297          C         C
                G                   TGGCTAACA GGTGAAACCC GT
                                    ||||||||| |||||||||| ||
                                GCCGATTGT CCACTTTGGG CA
                                    A         A
GAM230  CASP2   3'  ACAGGGTTTCACCATGTTAGCC 53313          C         C
                G                   TGGCTAACA GGTGAAACCC GT
                                    ||||||||| |||||||||| ||
                                GCCGATTGT CCACTTTGGG CA
                                    A         A
GAM230  CASP2   3'  ACAGGGTTTCACCATGTTAGCC 8700           C         C
                G                   TGGCTAACA GGTGAAACCC GT
                                    ||||||||| |||||||||| ||
                                GCCGATTGT CCACTTTGGG CA
                                    A         A
GAM230  CASP8   3'  ACAGGGTTTCACTGTGTTAGCC 8741                    C
                AG                  TTGGCTAACACGGTGAAACCC GT
                                    |||||||||||||||||||| ||
                                GACCGATTGTGTCACTTTGGG CA
                                          A
GAM230  CASP8   3'  ACAGGGTTTCACTGTGTTAGCC 54065                   C
                AG                  TTGGCTAACACGGTGAAACCC GT
                                    |||||||||||||||||||| ||
                                GACCGATTGTGTCACTTTGGG CA
                                          A
GAM230  CASP8   3'  ACAGGGTTTCACTGTGTTAGCC 54091                   C
                AG                  TTGGCTAACACGGTGAAACCC GT
                                    |||||||||||||||||||| ||
                                GACCGATTGTGTCACTTTGGG CA
                                          A
GAM230  CASP8   3'  ACAGGGTTTCACTGTGTTAGCC 54106                   C
                AG                  TTGGCTAACACGGTGAAACCC GT
                                    |||||||||||||||||||| ||
                                GACCGATTGTGTCACTTTGGG CA
                                          A
GAM230  CCNF    3'  ACGGGATTTCACCATGTTGGCC 10063          C     C
                AG                  TTGGCTAACA GGTGAAA CCCGT
                                    |||||||||| ||||||| |||||
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                                GACCGGTTGT CCACTTT GGGCA
                                      A      A
GAM230  CDYL     3'  GGGGGTGTTAGCCAG       17888          GGTGAAA
                                TTGGCTAACAC      CCCC
                                ||||||||||       ||||
                                GACCGATTGTG      GGGG
                                          _______
GAM230  CMAR     5'  GTCTCGCTGTGTTGCCAA    19036      T        A
                                TTGGC AACACGGTGA AC
                                ||||| |||||||||| ||
                                AACCG TTGTGTCGCT TG
                                   _        C
GAM230  CNGA1    5'  ATGGGATTTCACCATGTTGGCC 60234          C      C
              AA                  TTGGCTAACA GGTGAAA CCCGT
                                ||||||||| ||||||| |||||
                                AACCGGTTGT CCACTTT GGGTA
                                      A      A
GAM230  CR1      3'  ACGGGGTTTCACCATGTTAGCC 6933           C
              AG                  TTGGCTAACA GGTGAAACCCCGT
                                ||||||||| ||||||||||||
                                GACCGATTGT CCACTTTGGGGCA
                                      A
GAM230  CXCL16   3'  ACGGGGTTTCACCATGTTGACC 42156      C    C
              AG                  TTGG TAACA GGTGAAACCCCGT
                                |||| ||||| ||||||||||||
                                GACC GTTGT CCACTTTGGGGCA
                                  A    A
GAM230  DFFB     3'  ACGGGGTTTCACCATGTTGGCC 88751          C
              AG                  TTGGCTAACA GGTGAAACCCCGT
                                ||||||||| ||||||||||||
                                GACCGGTTGT CCACTTTGGGGCA
                                      A
GAM230  DFFB     3'  ACGGGGTTTCACCATGTTGGTC 88752          C
              AG                  TTGGCTAACA GGTGAAACCCCGT
                                ||||||||| ||||||||||||
                                GACTGGTTGT CCACTTTGGGGCA
                                      A
GAM230  DISC1    3'  ACAGGGCTTCACCATGTTGGCT 38495          C    A  C
              AG                  TTGGCTAACA GGTGAA CCC GT
                                ||||||||| |||||| ||| ||
                                GATCGGTTGT CCACTT GGG CA
                                      A    C  A
GAM230  DSC3     3'  ACGGGGTTTCACTGTGTTAGCC 10431
              AG                  TTGGCTAACACGGTGAAACCCCGT
                                ||||||||||||||||||||||||
                                GACCGATTGTGTCACTTTGGGGCA

GAM230  DSC3     3'  ACGGGGTTTCACTGTGTTAGCC 44611
              AG                  TTGGCTAACACGGTGAAACCCCGT
                                ||||||||||||||||||||||||
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                                GACCGATTGTGTCACTTTGGGGCA

GAM230  DSCR3    3'  ACGGGGCTTCACCATCTTGGCC 21303         CAC      A
                AG                    TTGGCTAA   GGTGAA CCCCGT
                                      ||||||||   |||||| ||||||
                                      GACCGGTT   CCACTT GGGGCA
                                          CTA      C
GAM230  EHD2     3'  ACGGGGTTTCACCATGTTGGCC 28209           C
                AG                    TTGGCTAACA GGTGAAACCCCGT
                                      |||||||||| ||||||||||||
                                      GACCGGTTGT CCACTTTGGGGCA
                                            A
GAM230  EPB72    3'  ACGGGGTTTCACCATGTTGGCC 15864           C
                AG                    TTGGCTAACA GGTGAAACCCCGT
                                      |||||||||| ||||||||||||
                                      GACCGGTTGT CCACTTTGGGGCA
                                            A
GAM230  F2RL2    3'  ACGGGGTTTCACCATGTTGACC 15888      C    C
                AG                    TTGG TAACA GGTGAAACCCCGT
                                      |||| ||||| ||||||||||||
                                      GACC GTTGT CCACTTTGGGGCA
                                        A    A
GAM230  F2RL3    3'  ACGGAGTTTCACCATGTTGGCC 15485          C       C
                AG                    TTGGCTAACA GGTGAAAC CCGT
                                      |||||||||| |||||||| ||||
                                      GACCGGTTGT CCACTTTG GGCA
                                            A       A
GAM230  FANCF    3'  ACGGGGTTTCACCATGCTGGCC 42969        A  C
                AG                    TTGGCTA CA GGTGAAACCCCGT
                                      ||||||| || ||||||||||||
                                      GACCGGT GT CCACTTTGGGGCA
                                          C  A
GAM230  FCAR     3'  ACAGGGTTTCACCATGTTGGCC 56627          C        C
                AG                    TTGGCTAACA GGTGAAACCC GT
                                      |||||||||| |||||||||| ||
                                      GACCGGTTGT CCACTTTGGG CA
                                            A         A
GAM230  FGF5     3'  ACGGGGTTTCACCATGTTGGTC 53645          C
                AG                    TTGGCTAACA GGTGAAACCCCGT
                                      |||||||||| ||||||||||||
                                      GACTGGTTGT CCACTTTGGGGCA
                                            A
GAM230  FGF5     3'  ACGGGGTTTCACCATGTTGGTC 16754          C
                AG                    TTGGCTAACA GGTGAAACCCCGT
                                      |||||||||| ||||||||||||
                                      GACTGGTTGT CCACTTTGGGGCA
                                            A
GAM230  FUT1     3'  ACAGGGTTTCACCATGTTGGCC 5575          C        C
                                      GGCTAACA GGTGAAACCC GT
                                      |||||||| |||||||||| ||
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                                CCGGTTGT CCACTTTGGG CA
                                   A         A
GAM230  FUT1     3'  ACGGGGTTTCATCGTGTTAACC 5576       C
                AG                  TTGG TAACACGGTGAAACCCCGT
                                    |||| ||||||||||||||||||
                                    GACC ATTGTGCTACTTTGGGGCA
                                      A
GAM230  GHR      3'  ACGGGGTTTCACCATGTTGGCC 5687           C
                AG                  TTGGCTAACA GGTGAAACCCCGT
                                    |||||||||| ||||||||||||
                                    GACCGGTTGT CCACTTTGGGGCA
                                       A
GAM230  GNE      3'  ACAGGGTTTCACCATGTTGGCC 19658          C         C
                AG                  TTGGCTAACA GGTGAAACCC GT
                                    |||||||||| |||||||||| ||
                                    GACCGGTTGT CCACTTTGGG CA
                                       A         A
GAM230  HTR1E    5'  ACGGGATTTCACCATGTTGGCC 7853          C      C
                A                    TGGCTAACA GGTGAAA CCCGT
                                    ||||||||| ||||||| |||||
                                    ACCGGTTGT CCACTTT GGGCA
                                       A      A
GAM230  IL11     3'  ACAGGGTTTCACCATGTTGGCC 7170          C         C
                AG                  TTGGCTAACA GGTGAAACCC GT
                                    |||||||||| |||||||||| ||
                                    GACCGGTTGT CCACTTTGGG CA
                                       A         A
GAM230  INMT     3'  GTTTCACCGTGTTAGCCAG   23226
                                    TTGGCTAACACGGTGAAAC
                                    |||||||||||||||||||
                                    GACCGATTGTGCCACTTTG

GAM230  LLGL1    3'  GTTTCACCATGTTAGCCAG   67422          C
                                    TTGGCTAACA GGTGAAAC
                                    |||||||||| ||||||||
                                    GACCGATTGT CCACTTTG
                                       A
GAM230  LNK      3'  ACAGGGTTTCACCATGTTGGCC 19626          C         C
                AG                  TTGGCTAACA GGTGAAACCC GT
                                    |||||||||| |||||||||| ||
                                    GACCGGTTGT CCACTTTGGG CA
                                       A         A
GAM230  LTB4R    5'  ACGGGGTTTCACCATGTTGGCC 7455          C
                AG                  TTGGCTAACA GGTGAAACCCCGT
                                    |||||||||| ||||||||||||
                                    GACCGGTTGT CCACTTTGGGGCA
                                       A
GAM230  LYZ      3'  ACAGGGTTTCACCGTGTTAGCC 5888                C
                AG                  TTGGCTAACACGGTGAAACCC GT
                                    |||||||||||||||||||| ||
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                                GACCGATTGTGCCACTTTGGG CA
                                      A
GAM230  LZTS1   3' ACGGGGTCTCGTTTTGTTGCCA 41021      T   CG   A
          A                    TTGGC AACA  GTGA ACCCCGT
                               ||||| ||||  |||| |||||||
                               AACCG TTGT  TGCT TGGGGCA
                                 _   TT   C
GAM230  MAK     3' ACAGGGTTTCACCATGTTGGTC 20934          C       C
          AG                   TTGGCTAACA GGTGAAACCC GT
                               |||||||||| |||||||||| ||
                               GACTGGTTGT CCACTTTGGG CA
                                    A        A
GAM230  MDM2    3' ACAGGGTTTCACCGTGTTAGCC 23454                C
          AG                   TTGGCTAACACGGTGAAACCC GT
                               |||||||||||||||||||| ||
                               GACCGATTGTGCCACTTTGGG CA
                                      A
GAM230  MDM2    3' ACAGGGTTTCACCGTGTTAGCC 23467                C
          AG                   TTGGCTAACACGGTGAAACCC GT
                               |||||||||||||||||||| ||
                               GACCGATTGTGCCACTTTGGG CA
                                      A
GAM230  MDM2    3' ACAGGGTTTCACCGTGTTAGCC 23480                C
          AG                   TTGGCTAACACGGTGAAACCC GT
                               |||||||||||||||||||| ||
                               GACCGATTGTGCCACTTTGGG CA
                                      A
GAM230  MDM2    3' ACAGGGTTTCACCGTGTTAGCC 23493                C
          AG                   TTGGCTAACACGGTGAAACCC GT
                               |||||||||||||||||||| ||
                               GACCGATTGTGCCACTTTGGG CA
                                      A
GAM230  MDM2    3' ACAGGGTTTCACCGTGTTAGCC 11488                C
          AG                   TTGGCTAACACGGTGAAACCC GT
                               |||||||||||||||||||| ||
                               GACCGATTGTGCCACTTTGGG CA
                                      A
GAM230  MEFV    3' GGGGTTTCACCATGTTAGCCAG 5941          C
                               TTGGCTAACA GGTGAAACCCC
                               |||||||||| ||||||||||
                               GACCGATTGT CCACTTTGGGG
                                    A
GAM230  MTR     3' ACAGGATTTCACTGTGTTAGCC 6008               C  C
          AG                   TTGGCTAACACGGTGAAA CC GT
                               |||||||||||||||| || ||
                               GACCGATTGTGTCACTTT GG CA
                                        A  A
GAM230  PCDHB11 3' ACGGGGTTTCACCACGTTGGCC 38913        AC
                               GGCTAAC  GGTGAAACCCCGT
                               |||||||  ||||||||||||
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                                CCGGTTG  CCACTTTGGGGCA
                                   CA
GAM230  PER2    3'  ACAGGGTTTCACCATGTTGGCC 43338          C        C
           AG                    TTGGCTAACA GGTGAAACCC GT
                                 |||||||||| |||||||||| ||
                                 GACCGGTTGT CCACTTTGGG CA
                                      A         A
GAM230  PIGR    3'  ACAGGGTTTCACCGTGTTAGCC 72982                C
           AG                    TTGGCTAACACGGTGAAACCC GT
                                 |||||||||||||||||||| ||
                                 GACCGATTGTGCCACTTTGGG CA
                                           A
GAM230  PIK3C2B  3'  ACGGGGTTTCACCATGTTGGCC 12086          C
           AG                    TTGGCTAACA GGTGAAACCCCGT
                                 |||||||||| ||||||||||||
                                 GACCGGTTGT CCACTTTGGGGCA
                                      A
GAM230  POU2AF1  3'  ACGGGGTTTCACCATGTTGGCC 21727          C
           AG                    TTGGCTAACA GGTGAAACCCCGT
                                 |||||||||| ||||||||||||
                                 GACCGGTTGT CCACTTTGGGGCA
                                      A
GAM230  PRKR    3'  ACAGGGTTTCACCATGTTGGCC 12336          C        C
           AG                    TTGGCTAACA GGTGAAACCC GT
                                 |||||||||| |||||||||| ||
                                 GACCGGTTGT CCACTTTGGG CA
                                      A         A
GAM230  PTGIS   3'  TTTCACCGTATTAGCCAG    8238          C
                                 TTGGCTAA ACGGTGAAA
                                 |||||||| |||||||||
                                 GACCGATT TGCCACTTT
                                      A
GAM230  RAB36   3'  GTTTCACCATGTTAGCCAG   18181          C
                                 TTGGCTAACA GGTGAAAC
                                 |||||||||| ||||||||
                                 GACCGATTGT CCACTTTG
                                      A
GAM230  RABL2A  3'  ACGGGGTTTCACCATGTTGCCC 26401      C    C
           AG                    TTGG TAACA GGTGAAACCCCGT
                                 |||| ||||| ||||||||||||
                                 GACC GTTGT CCACTTTGGGGCA
                                   C    A
GAM230  RABL2B  3'  ACGGGGTTTCACCATGTTGCCC 23968      C    C
           AG                    TTGG TAACA GGTGAAACCCCGT
                                 |||| ||||| ||||||||||||
                                 GACC GTTGT CCACTTTGGGGCA
                                   C    A
GAM230  RBBP9   3'  ACAGGGTTTCACCATGTTGGCC 70675          C        C
           AG                    TTGGCTAACA GGTGAAACCC GT
                                 |||||||||| |||||||||| ||
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                                GACCGGTTGT CCACTTTGGG CA
                                     A         A
GAM230  RHD     3'  ACAGGGTTTCACCATGTTGGCT 32804          C         C
             AG                   TTGGCTAACA GGTGAAACCC GT
                                  |||||||||| |||||||||| ||
                                  GATCGGTTGT CCACTTTGGG CA
                                     A         A
GAM230  RHD     3'  ACAGGGTTTCACCATGTTGGCT 33129          C         C
             AG                   TTGGCTAACA GGTGAAACCC GT
                                  |||||||||| |||||||||| ||
                                  GATCGGTTGT CCACTTTGGG CA
                                     A         A
GAM230  RPP30   3'  ACGGGGTTTCACCGTGTTAGCC 22187
             AG                   TTGGCTAACACGGTGAAACCCCGT
                                  ||||||||||||||||||||||||
                                  GACCGATTGTGCCACTTTGGGGCA

GAM230  SAS     3'  ACAGGGTTTCACCATGTTAGTC 21090          C         C
             AG                   TTGGCTAACA GGTGAAACCC GT
                                  |||||||||| |||||||||| ||
                                  GACTGATTGT CCACTTTGGG CA
                                     A         A
GAM230  SEDL    3'  ACAGGGTTTCACCATATTGGTC 28068         CAC         C
             AG                   TTGGCTAA   GGTGAAACCC GT
                                  |||||||    |||||||||| ||
                                  GACTGGTT   CCACTTTGGG CA
                                     ATA         A
GAM230  SEDL    3'  ACAGGGTTTCACCATATTGGTC 28069         CAC         C
             AG                   TTGGCTAA   GGTGAAACCC GT
                                  |||||||    |||||||||| ||
                                  GACTGGTT   CCACTTTGGG CA
                                     ATA         A
GAM230  SERPINB9 3'  ACGGGGTTTCACCGTGTTAGCC 16006
             AG                   TTGGCTAACACGGTGAAACCCCGT
                                  ||||||||||||||||||||||||
                                  GACCGATTGTGCCACTTTGGGGCA

GAM230  SH3GL3  5'  GGGTTTCACCATGTTGGCCAA  13112          C
                                  TTGGCTAACA GGTGAAACCC
                                  |||||||||| ||||||||||
                                  AACCGGTTGT CCACTTTGGG
                                     A
GAM230  SIL     5'  ACGGGGTTTCACCATGTTGGTC 13148         C
                                  GGCTAACA GGTGAAACCCCGT
                                  |||||||| ||||||||||||
                                  CTGGTTGT CCACTTTGGGGCA
                                     A
GAM230  SLC14A2  5'  ACGGGGTTTCACCACATTGGCC 24105         CAC
             AG                   TTGGCTAA   GGTGAAACCCCGT
                                  ||||||||   ||||||||||||
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                                GACCGGTT   CCACTTTGGGGCA
                                     ACA
GAM230  SLC15A1  3'  GTTTCACCATGTTAACCAG   18645      C    C
                                TTGG TAACA GGTGAAAC
                                |||| ||||| ||||||||
                                GACC ATTGT CCACTTTG
                                  A    A
GAM230  SNAP23   3'  ACAGGGTTTCACCATGTCAAGC 15131      A_  C        C
           T                     GGCT  ACA GGTGAAACCC GT
                                ||||  ||| |||||||||| ||
                                TCGA  TGT CCACTTTGGG CA
                                  AC  A         A
GAM230  SNAP23   3'  ACAGGGTTTCACCATGTCAAGC 56331      A_  C        C
           T                     GGCT  ACA GGTGAAACCC GT
                                ||||  ||| |||||||||| ||
                                TCGA  TGT CCACTTTGGG CA
                                  AC  A         A
GAM230  TAPBP    3'  ACGGGGTTTCACCATGTTGGCC 13540          C
           AG                     TTGGCTAACA GGTGAAACCCCGT
                                |||||||||| ||||||||||||
                                GACCGGTTGT CCACTTTGGGGCA
                                     A
GAM230  TAPBP    3'  ACGGGGTTTCACCGTGTTAGCC 13541
           AG                     TTGGCTAACACGGTGAAACCCCGT
                                ||||||||||||||||||||||||
                                GACCGATTGTGCCACTTTGGGGCA

GAM230  TAPBP    3'  ACGGGGTTTCACCGTGTTAGCC 13542
           AG                     TTGGCTAACACGGTGAAACCCCGT
                                ||||||||||||||||||||||||
                                GACCGATTGTGCCACTTTGGGGCA

GAM230  TAT      3'  ACAGGGTTTCACCATGTTAGCC 6246           C        C
           AG                     TTGGCTAACA GGTGAAACCC GT
                                |||||||||| |||||||||| ||
                                GACCGATTGT CCACTTTGGG CA
                                     A         A
GAM230  TBXA2R   3'  ACGGGGTTTCACCGTGTTGGCC 8337
           AG                     TTGGCTAACACGGTGAAACCCCGT
                                ||||||||||||||||||||||||
                                GACCGGTTGTGCCACTTTGGGGCA

GAM230  TERF2    3'  ACGGGGTTTCACCGTGTTAGCC 20142
           AG                     TTGGCTAACACGGTGAAACCCCGT
                                ||||||||||||||||||||||||
                                GACCGATTGTGCCACTTTGGGGCA

GAM230  TES      3'  ACAGGTTTTCACCATGTTAGCC 72456          C      C  C
           AG                     TTGGCTAACA GGTGAAA CC GT
                                |||||||||| ||||||| || ||
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                                GACCGATTGT CCACTTT GG CA
                                     A      T  A
GAM230  TIM3     3'  ACAGGGTTTCACCATGTTGGCC 52345          C        C
              AG                   TTGGCTAACA GGTGAAACCC GT
                                   |||||||||| |||||||||| ||
                                   GACCGGTTGT CCACTTTGGG CA
                                     A         A
GAM230  TMPRSS3  3'  ACAGGGTTTCACCATGTTGGCC 51507          C        C
              AG                   TTGGCTAACA GGTGAAACCC GT
                                   |||||||||| |||||||||| ||
                                   GACCGGTTGT CCACTTTGGG CA
                                     A         A
GAM230  TMPRSS3  3'  ACAGGGTTTCACCATGTTGGCC 51535          C        C
              AG                   TTGGCTAACA GGTGAAACCC GT
                                   |||||||||| |||||||||| ||
                                   GACCGGTTGT CCACTTTGGG CA
                                     A         A
GAM230  TMPRSS3  3'  ACAGGGTTTCACCATGTTGGCC 44009          C        C
              AG                   TTGGCTAACA GGTGAAACCC GT
                                   |||||||||| |||||||||| ||
                                   GACCGGTTGT CCACTTTGGG CA
                                     A         A
GAM230  TNFRSF10B 3'  ACGGGGTTTCACCATGTTGGTC 15210          C
              AG                   TTGGCTAACA GGTGAAACCCCGT
                                   |||||||||| ||||||||||||
                                   GACTGGTTGT CCACTTTGGGGCA
                                     A
GAM230  TPMT     3'  ACGGGGTTTCACCATGTTGGTC 6300           C
              AG                   TTGGCTAACA GGTGAAACCCCGT
                                   |||||||||| ||||||||||||
                                   GACTGGTTGT CCACTTTGGGGCA
                                     A
GAM230  TRAF5    3'  ACGGAGTTTTGCCATGTTGGCC 17264          C  TG    C
              AA                   TTGGCTAACA GG  AAAC CCGT
                                   |||||||||| ||  |||| ||||
                                   AACCGGTTGT CC  TTTG GGCA
                                     A  GT    A
GAM230  TRIM9    5'  ACGGGGTTTCACCATACTGGCC 31436       ACAC
                                   GGCTA    GGTGAAACCCCGT
                                   |||||    ||||||||||||
                                   CCGGT    CCACTTTGGGGCA
                                      CATA
GAM230  TRPV1    3'  ACGGGGTTTCACCATGTTGGCC 38681          C
              AG                   TTGGCTAACA GGTGAAACCCCGT
                                   |||||||||| ||||||||||||
                                   GACCGGTTGT CCACTTTGGGGCA
                                     A
GAM230  TRPV1    3'  ACGGGGTTTCACCATGTTGGCC 55647          C
              AG                   TTGGCTAACA GGTGAAACCCCGT
                                   |||||||||| ||||||||||||
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                                GACCGGTTGT CCACTTTGGGGCA
                                      A
GAM230  TRPV1    3'  ACGGGGTTTCACCATGTTGGCC 55697          C
           AG                   TTGGCTAACA GGTGAAACCCCGT
                                |||||||||| ||||||||||||
                                GACCGGTTGT CCACTTTGGGGCA
                                      A
GAM230  TRPV1    3'  ACGGGGTTTCACCATGTTGGCC 55728          C
           AG                   TTGGCTAACA GGTGAAACCCCGT
                                |||||||||| ||||||||||||
                                GACCGGTTGT CCACTTTGGGGCA
                                      A
GAM230  UGDH     3'  ACAGGGTTTCACCATGTGAGCC 13986       A  C        C
           AG                   TTGGCT ACA GGTGAAACCC GT
                                |||||| ||| |||||||||| ||
                                GACCGA TGT CCACTTTGGG CA
                                   G  A        A
GAM230  VENTX2   3'  GTTTCACCATGTTAGCCAG   27865          C
                                TTGGCTAACA GGTGAAAC
                                |||||||||| ||||||||
                                GACCGATTGT CCACTTTG
                                      A
GAM230  VHL      3'  ACGGGGTTTCACCATGTTGTCC 6820       C    C
           AG                   TTGG TAACA GGTGAAACCCCGT
                                |||| ||||| ||||||||||||
                                GACC GTTGT CCACTTTGGGGCA
                                  T    A
GAM230  VIPR2    3'  ACAGGGTTTCACCATGTTAGCC 14054          C        C
           AG                   TTGGCTAACA GGTGAAACCC GT
                                |||||||||| |||||||||| ||
                                GACCGATTGT CCACTTTGGG CA
                                      A        A
GAM230  XRCC2    3'  ACGGGGTTTCACCATGTTGGCC 19484          C
           AG                   TTGGCTAACA GGTGAAACCCCGT
                                |||||||||| ||||||||||||
                                GACCGGTTGT CCACTTTGGGGCA
                                      A
GAM230  YES1     3'  GTTTCACCGTGTTAGCCAG   19544
                                TTGGCTAACACGGTGAAAC
                                ||||||||||||||||||
                                GACCGATTGTGCCACTTTG

GAM230  ZNF264   3'  ACGGGGTTTCACCATCTTGGCC 14184        CAC
           AG                   TTGGCTAA   GGTGAAACCCCGT
                                ||||||||   ||||||||||||
                                GACCGGTT   CCACTTTGGGGCA
                                   CTA
GAM230  ZNF264   3'  ACGGGGTTTCACCATGTTGCTC 14185     _  T    C
           AG                   TTG GC AACA GGTGAAACCCCGT
                                ||| || |||| ||||||||||||
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                                GAC CG TTGT CCACTTTGGGGCA
                                  T _   A
GAM230  AP3S2    3'  ACAGGGTTTCACCATGTTGGCC 20637          C        C
           AG                    TTGGCTAACA GGTGAAACCC GT
                                 |||||||||| |||||||||| ||
                                 GACCGGTTGT CCACTTTGGG CA
                                       A         A
GAM230  APOL2    3'  ACGGGGTTTCACTGTGTTAGCC 48784
           A                     TGGCTAACACGGTGAAACCCCGT
                                 ||||||||||||||||||||||
                                 ACCGATTGTGTCACTTTGGGGCA

GAM230  ARHF     3'  ACAGGGTTTCACCATGTTGGCC 39256          C        C
           AG                    TTGGCTAACA GGTGAAACCC GT
                                 |||||||||| |||||||||| ||
                                 GACCGGTTGT CCACTTTGGG CA
                                       A         A
GAM230  ARHGAP11A 3'  GGTTTCACCGTGTTAGCCAG   29454
                                 TTGGCTAACACGGTGAAACC
                                 ||||||||||||||||||||
                                 GACCGATTGTGCCACTTTGG

GAM230  ASE-1    3'  GTTTCACCACGTTAGCCAG    24994          AC
                                 TTGGCTAAC  GGTGAAAC
                                 |||||||||  ||||||||
                                 GACCGATTG  CCACTTTG
                                       CA
GAM230  ATP1B4   3'  ACAGGGTTTCACCATGTTGGCC 24829          C        C
           AG                    TTGGCTAACA GGTGAAACCC GT
                                 |||||||||| |||||||||| ||
                                 GACCGGTTGT CCACTTTGGG CA
                                       A         A
GAM230  BNIP-S   3'  ACGGGGTTTCACCATGTTGGCC 57083          C
           AG                    TTGGCTAACA GGTGAAACCCCGT
                                 |||||||||| ||||||||||||
                                 GACCGGTTGT CCACTTTGGGGCA
                                       A
GAM230  C3F      3'  ACGGGATTTCACCACGTTGGCC 20472          AC       C
           AG                    TTGGCTAAC  GGTGAAA CCCGT
                                 |||||||||  ||||||| |||||
                                 GACCGGTTG  CCACTTT GGGCA
                                       CA       A
GAM230  C9orf9   3'  ACGGGGCTTCACCACGTTGGCC 39007          AC       A
           AG                    TTGGCTAAC  GGTGAA CCCCGT
                                 |||||||||  ||||||  ||||||
                                 GACCGGTTG  CCACTT GGGGCA
                                       CA       C
GAM230  C9orf9   3'  GTTTCACCATGTTAGCCAG   39034          C
                                 TTGGCTAACA GGTGAAAC
                                 |||||||||| ||||||||
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                                GACCGATTGT CCACTTTG
                                      A
GAM230  CCRN4L   3'  ACGGGGTTTCACCGTGTTAGCC 25064
           AG                   TTGGCTAACACGGTGAAACCCCGT
                                ||||||||||||||||||||||||
                                GACCGATTGTGCCACTTTGGGGCA

GAM230  CDC14B   3'  ACAGGGTTTCACCATGTTGGCC 53994          C        C
           AG                   TTGGCTAACA GGTGAAACCC GT
                                |||||||||| |||||||||| ||
                                GACCGGTTGT CCACTTTGGG CA
                                      A         A
GAM230  CENPH    3'  ACGGGGTTTCACCGTGTTGCCC 43561      C
           AG                   TTGG TAACACGGTGAAACCCCGT
                                |||| ||||||||||||||||||
                                GACC GTTGTGCCACTTTGGGGCA
                                  C
GAM230  CHSY1    3'  ACGGGGTTTCACCATGCAAGCC 30558      AA  C
                                GGCT  CA GGTGAAACCCCGT
                                ||||  || ||||||||||||
                                CCGA  GT CCACTTTGGGGCA
                                  AC  A
GAM230  CIP29    3'  ACGGGGTTTCACCATGTTGCCC 51366      C    C
           AG                   TTGG TAACA GGTGAAACCCCGT
                                |||| ||||| ||||||||||||
                                GACC GTTGT CCACTTTGGGGCA
                                  C    A
GAM230  CPSF2    3'  ACAGGGTTTCACCATGTTGGCC 62254          C        C
           AG                   TTGGCTAACA GGTGAAACCC GT
                                |||||||||| |||||||||| ||
                                GACCGGTTGT CCACTTTGGG CA
                                      A         A
GAM230  DBR1     3'  ACAGGGTTTCACCGTGTTGGCC 33057                  C
           AG                   TTGGCTAACACGGTGAAACCC GT
                                |||||||||||||||||||| ||
                                GACCGGTTGTGCCACTTTGGG CA
                                           A
GAM230  DKFZP434C212 3'  ACGGGGTTTCACCATGTTGGCC 69479          C
           AG                   TTGGCTAACA GGTGAAACCCCGT
                                |||||||||| ||||||||||||
                                GACCGGTTGT CCACTTTGGGGCA
                                      A
GAM230  DKFZP564G092 5'  ACAGGATTTCACCATGTTGGCC 32146          C      C  C
           AG                   TTGGCTAACA GGTGAAA CC GT
                                |||||||||| ||||||| || ||
                                GACCGGTTGT CCACTTT GG CA
                                      A      A  A
GAM230  DKFZp761N1114 3'  ACGGGATTTCACCGTGTTAGCC 79771              C
           AG                   TTGGCTAACACGGTGAAA CCCGT
                                |||||||||||||||||| |||||
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                                GACCGATTGTGCCACTTT GGGCA
                                      A
GAM230  FBP17    3'  ACAGGGTTTCACCGTGTTGGTC 73139                C
           AG                   TTGGCTAACACGGTGAAACCC GT
                                |||||||||||||||||||| ||
                                GACTGGTTGTGCCACTTTGGG CA
                                      A
GAM230  FER1L4   3'  ACAGGGTTTCACCATGTTGTCC 48105     C    C       C
           AG                   TTGG TAACA GGTGAAACCC GT
                                |||| ||||| |||||||||| ||
                                GACC GTTGT CCACTTTGGG CA
                                  T    A        A
GAM230  FKBP9    3'  ACGGGGTTTCACCGTGTTGGCC 95709
           AG                   TTGGCTAACACGGTGAAACCCCGT
                                |||||||||||||||||||||||||
                                GACCGGTTGTGCCACTTTGGGGCA

GAM230  FLJ00060 5'  TTTCACCATGTTAGCCAG    61760          C
                                TTGGCTAACA GGTGAAA
                                |||||||||| |||||||
                                GACCGATTGT CCACTTT
                                      A
GAM230  FLJ10298 3'  ACGGGGTTTCACCATGTTGGTC 36449          C
           AG                   TTGGCTAACA GGTGAAACCCCGT
                                |||||||||| ||||||||||||
                                GACTGGTTGT CCACTTTGGGGCA
                                      A
GAM230  FLJ10560 3'  ACGGGGTTTCACCGTGTTAGTC 36788
           AG                   TTGGCTAACACGGTGAAACCCCGT
                                |||||||||||||||||||||||||
                                GACTGATTGTGCCACTTTGGGGCA

GAM230  FLJ10846 3'  ACAGGGTCTCACCATGTTAGCC 37281          C    A   C
           AG                   TTGGCTAACA GGTGA ACCC GT
                                |||||||||| ||||| |||| ||
                                GACCGATTGT CCACT TGGG CA
                                      A    C   A
GAM230  FLJ10956 3'  ACGGGGTTTCACCATGTTGGCC 37458          C
           AG                   TTGGCTAACA GGTGAAACCCCGT
                                |||||||||| ||||||||||||
                                GACCGGTTGT CCACTTTGGGGCA
                                      A
GAM230  FLJ12568 5'  GGATTCGCTCCATTAGCCAA  47141         CAC    A
                                TTGGCTAA   GGTGAA CC
                                ||||||||   |||||| ||
                                AACCGATT   TCGCTT GG
                                     ACC     A
GAM230  FLJ12581 3'  ACAGGGTTTCACTGTGTTAGCC 46327                C
           AG                   TTGGCTAACACGGTGAAACCC GT
                                |||||||||||||||||||| ||
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                                GACCGATTGTGTCACTTTGGG CA
                                      A
GAM230  FLJ12687  3'  ACAGGGTTTCACCATGTTGGCC 46738        C       C
          AG                  TTGGCTAACA GGTGAAACCC GT
                              |||||||||| |||||||||| ||
                              GACCGGTTGT CCACTTTGGG CA
                                   A        A
GAM230  FLJ12975  3'  ACAGGGTTCCACCGTATTGGCC 70178       C    A    C
          AG                  TTGGCTAA ACGGTG AACCC GT
                              |||||||| |||||| ||||| ||
                              GACCGGTT TGCCAC TTGGG CA
                                   A    C   A
GAM230  FLJ13072  5'  ACAGGGTTTCACCATGTTGGAC 91379    G    C       C
          AG                  TTG CTAACA GGTGAAACCC GT
                              ||| |||||| |||||||||| ||
                              GAC GGTTGT CCACTTTGGG CA
                                A    A        A
GAM230  FLJ14950  3'  ACAGGGTTTCACCATGTTGGCC 52776        C       C
          AG                  TTGGCTAACA GGTGAAACCC GT
                              |||||||||| |||||||||| ||
                              GACCGGTTGT CCACTTTGGG CA
                                   A        A
GAM230  FLJ14957  3'  ACGGGGTTTCACCATGTTGGTC 52804        C
          AG                  TTGGCTAACA GGTGAAACCCCGT
                              |||||||||| ||||||||||||
                              GACTGGTTGT CCACTTTGGGGCA
                                   A
GAM230  FLJ20344  3'  ACAGGGTTTCACCATGTTGGCC 35472        C       C
          AG                  TTGGCTAACA GGTGAAACCC GT
                              |||||||||| |||||||||| ||
                              GACCGGTTGT CCACTTTGGG CA
                                   A        A
GAM230  FLJ20507  3'  ACAGGGTTTCACCATGTTGGCC 35726        C       C
          AG                  TTGGCTAACA GGTGAAACCC GT
                              |||||||||| |||||||||| ||
                              GACCGGTTGT CCACTTTGGG CA
                                   A        A
GAM230  FLJ20507  3'  ACAGGGTTTCACCATGTTGGCC 60836        C       C
          AG                  TTGGCTAACA GGTGAAACCC GT
                              |||||||||| |||||||||| ||
                              GACCGGTTGT CCACTTTGGG CA
                                   A        A
GAM230  FLJ20511  3'  GTTTCACCGTGTTAGCCAA   35782
                              TTGGCTAACACGGTGAAAC
                              |||||||||||||||||||
                              AACCGATTGTGCCACTTTG

GAM230  FLJ21302  3'  ACAGGGTTTCACCATGTTGGCC 43498        C       C
          AG                  TTGGCTAACA GGTGAAACCC GT
                              |||||||||| |||||||||| ||
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                                GACCGGTTGT CCACTTTGGG CA
                                     A         A
GAM230  FLJ21324  5'  ATGGGGTTTCACCATGTTGGCC 92844          C
              AA                  TTGGCTAACA GGTGAAACCCCGT
                                  |||||||||| ||||||||||||
                                  AACCGGTTGT CCACTTTGGGGTA
                                     A
GAM230  FLJ22329  3'  ACGGGGTTTCACCATGTTGGCC 45389          C
              AG                  TTGGCTAACA GGTGAAACCCCGT
                                  |||||||||| ||||||||||||
                                  GACCGGTTGT CCACTTTGGGGCA
                                     A
GAM230  FLJ22529  3'  ACAGGGTTTCACCACATTGGCC 45933         CAC         C
              AG                  TTGGCTAA   GGTGAAACCC GT
                                  ||||||||   |||||||||| ||
                                  GACCGGTT   CCACTTTGGG CA
                                       ACA         A
GAM230  FLJ22684  3'  ACAGGGTTTCACCATGTTGGCC 47461          C         C
              A                    TGGCTAACA GGTGAAACCC GT
                                  ||||||||| |||||||||| ||
                                  ACCGGTTGT CCACTTTGGG CA
                                     A         A
GAM230  FLJ22794  3'  ACAGGGTTTCACCATGTTGGTC 93233          C         C
              AG                  TTGGCTAACA GGTGAAACCC GT
                                  |||||||||| |||||||||| ||
                                  GACTGGTTGT CCACTTTGGG CA
                                     A         A
GAM230  FLJ22969  3'  ACAGGGTTTCACCATGTTGCCC 69193      C    C         C
              AG                  TTGG TAACA GGTGAAACCC GT
                                  |||| ||||| |||||||||| ||
                                  GACC GTTGT CCACTTTGGG CA
                                    C    A         A
GAM230  FLJ23024  3'  ACGGGGTTTCACCATGTTGGCC 46833          C
              AG                  TTGGCTAACA GGTGAAACCCCGT
                                  |||||||||| ||||||||||||
                                  GACCGGTTGT CCACTTTGGGGCA
                                     A
GAM230  FLJ23392  3'  ACAGGGTTTCACCATGTTGGCC 45869          C         C
              AG                  TTGGCTAACA GGTGAAACCC GT
                                  |||||||||| |||||||||| ||
                                  GACCGGTTGT CCACTTTGGG CA
                                     A         A
GAM230  FLJ23392  3'  ACAGGGTTTCACCGTGTTAGCC 45870                   C
              AG                  TTGGCTAACACGGTGAAACCC GT
                                  |||||||||||||||||||| ||
                                  GACCGATTGTGCCACTTTGGG CA
                                           A
GAM230  FLJ23392  3'  ACGGGGTTTCACCGTGTTAGTC 45871
              AG                  TTGGCTAACACGGTGAAACCCCGT
                                  ||||||||||||||||||||||||
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                                GACTGATTGTGCCACTTTGGGGCA

GAM230  FLJ23519  3'  GTTTCACCGTGTTAGCCAG   50960
                                TTGGCTAACACGGTGAAAC
                                ||||||||||||||||||
                                GACCGATTGTGCCACTTTG

GAM230  FLJ23556  3'  ACGGGGTTTCACCGTGTTAGCC 46420
              AG                  TTGGCTAACACGGTGAAACCCCGT
                                  ||||||||||||||||||||||||
                                  GACCGATTGTGCCACTTTGGGGCA

GAM230  GGA2      3'  ACAGGATTTCACCATGTTGGCC 57645          C      C  C
              AG                  TTGGCTAACA GGTGAAA CC GT
                                  |||||||||| ||||||| || ||
                                  GACCGGTTGT CCACTTT GG CA
                                        A      A  A
GAM230  GGA2      3'  ACAGGATTTCACCATGTTGGCC 31151          C      C  C
              AG                  TTGGCTAACA GGTGAAA CC GT
                                  |||||||||| ||||||| || ||
                                  GACCGGTTGT CCACTTT GG CA
                                        A      A  A
GAM230  GNG4      3'  ACGGGGTTTCACCATGTTGGTC 16835          C
              AG                  TTGGCTAACA GGTGAAACCCCGT
                                  |||||||||| ||||||||||||
                                  GACTGGTTGT CCACTTTGGGGCA
                                        A
GAM230  GREB1     3'  ACGGGGTTTCACCATGTTAGCC 28550          C
              AG                  TTGGCTAACA GGTGAAACCCCGT
                                  |||||||||| ||||||||||||
                                  GACCGATTGT CCACTTTGGGGCA
                                        A
GAM230  GRWD      3'  ACGGGGTTTCACCATGTTGGCC 49770          C
              AG                  TTGGCTAACA GGTGAAACCCCGT
                                  |||||||||| ||||||||||||
                                  GACCGGTTGT CCACTTTGGGGCA
                                        A
GAM230  GTF2E1    3'  GTTTCACCATGTTAGCCAG   19804          C
                                TTGGCTAACA GGTGAAAC
                                |||||||||| ||||||||
                                GACCGATTGT CCACTTTG
                                      A
GAM230  GTPBG3    3'  GGTTTCACCATGTTGACCAG  51902     C    C
                                TTGG TAACA GGTGAAACC
                                |||| ||||| |||||||||
                                GACC GTTGT CCACTTTGG
                                  A    A
GAM230  HARS2     3'  ACGGGGTTTTACCATGTTAGCC 55860          C
              AG                  TTGGCTAACA GGTGAAACCCCGT
                                  |||||||||| ||||||||||||
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                                GACCGATTGT CCATTTTGGGGCA
                                     A
GAM230  HT002    3'  ACAGGGTTTCACCGTGTTGGCC 26785                C
              AG                   TTGGCTAACACGGTGAAACCC GT
                                   |||||||||||||||||||| ||
                                   GACCGGTTGTGCCACTTTGGG CA
                                        A
GAM230  ICK      3'  ACGGGGTTTCACTGTGTTAGCC 30589
              AG                   TTGGCTAACACGGTGAAACCCCGT
                                   ||||||||||||||||||||||||
                                   GACCGATTGTGTCACTTTGGGGCA

GAM230  JAM1     3'  ACAGGGTTTCACCATGTTGGTC 34207        C       C
                                   GGCTAACA GGTGAAACCC GT
                                   |||||||| |||||||||| ||
                                   CTGGTTGT CCACTTTGGG CA
                                        A        A
GAM230  JAM1     3'  ACAGGGTTTCACCATGTTGGTC 58502        C       C
                                   GGCTAACA GGTGAAACCC GT
                                   |||||||| |||||||||| ||
                                   CTGGTTGT CCACTTTGGG CA
                                        A        A
GAM230  JAM1     3'  ACAGGGTTTCACCATGTTGGTC 58530        C       C
                                   GGCTAACA GGTGAAACCC GT
                                   |||||||| |||||||||| ||
                                   CTGGTTGT CCACTTTGGG CA
                                        A        A
GAM230  JAM1     3'  ACAGGGTTTCACCATGTTGGTC 58557        C       C
                                   GGCTAACA GGTGAAACCC GT
                                   |||||||| |||||||||| ||
                                   CTGGTTGT CCACTTTGGG CA
                                        A        A
GAM230  JM11     3'  GGTTTCACCATATTGGCCAG  54368        CAC
                                   TTGGCTAA  GGTGAAACC
                                   ||||||||  |||||||||
                                   GACCGGTT  CCACTTTGG
                                        ATA
GAM230  KIAA0161 3'  ACGGGGTTTCACCATGTTGGCC 29185         C
              AG                   TTGGCTAACA GGTGAAACCCCGT
                                   |||||||||| ||||||||||||
                                   GACCGGTTGT CCACTTTGGGGCA
                                        A
GAM230  KIAA0426 3'  ACGGGGTTTCACCATGTTGGCC 28914         C
              AG                   TTGGCTAACA GGTGAAACCCCGT
                                   |||||||||| ||||||||||||
                                   GACCGGTTGT CCACTTTGGGGCA
                                        A
GAM230  KIAA0459 3'  ACGGGGTTTCACCATGTTAGCC 61640         C
              AG                   TTGGCTAACA GGTGAAACCCCGT
                                   |||||||||| ||||||||||||
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                                GACCGATTGT CCACTTTGGGGCA
                                    A
GAM230  KIAA0469 3' ACGGGATTTCACTGTGTTAGCC 29964              C
            AG                    TTGGCTAACACGGTGAAA CCCGT
                                  |||||||||||||||||| |||||
                                  GACCGATTGTGTCACTTT GGGCA
                                       A
GAM230  KIAA0561 3' ACGGGGTTTCACCATGTTGGTC 66461          C
            AG                    TTGGCTAACA GGTGAAACCCCGT
                                  |||||||||| ||||||||||||
                                  GACTGGTTGT CCACTTTGGGGCA
                                    A
GAM230  KIAA0562 3' ACGGGGTTTCACCATATTGGCC 28813         CAC
            AG                    TTGGCTAA   GGTGAAACCCCGT
                                  ||||||||   ||||||||||||
                                  GACCGGTT   CCACTTTGGGGCA
                                     ATA
GAM230  KIAA0682 3' ACGGGGTTTCACCATGTGGGCC 30010       A   C
            AG                    TTGGCT ACA GGTGAAACCCCGT
                                  |||||| ||| ||||||||||||
                                  GACCGG TGT CCACTTTGGGGCA
                                     G   A
GAM230  KIAA0737 3' ACAGGGTTTCACCATGTTGGCC 29792          C        C
            AG                    TTGGCTAACA GGTGAAACCC GT
                                  |||||||||| |||||||||| ||
                                  GACCGGTTGT CCACTTTGGG CA
                                       A         A
GAM230  KIAA0861 3' ACGGGGTTTCCCCGTGTTAGCC 90339            T
            AG                    TTGGCTAACACGG GAAACCCCGT
                                  |||||||||||| ||||||||||
                                  GACCGATTGTGCC CTTTGGGGCA
                                        C
GAM230  KIAA0889 3' ACGGGGTTTCACCGTGTTGGCC 31747
                                  GGCTAACACGGTGAAACCCCGT
                                  ||||||||||||||||||||||
                                  CCGGTTGTGCCACTTTGGGGCA

GAM230  KIAA0931 3' ACGGGGTTTCACCATGTTGGCC 68000          C
            AG                    TTGGCTAACA GGTGAAACCCCGT
                                  |||||||||| ||||||||||||
                                  GACCGGTTGT CCACTTTGGGGCA
                                       A
GAM230  KIAA1143 3' ACGGGGTTTCACTTTGTTAGCC 69225          C
            AG                    TTGGCTAACA GGTGAAACCCCGT
                                  |||||||||| ||||||||||||
                                  GACCGATTGT TCACTTTGGGGCA
                                       T
GAM230  KIAA1170 3' ACAGGGTTTCACCATGTTAGCC 70405          C        C
            AG                    TTGGCTAACA GGTGAAACCC GT
                                  |||||||||| |||||||||| ||
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                                GACCGATTGT CCACTTTGGG CA
                                    A         A
GAM230  KIAA1185 3' ACGGGGTTTCACCATTTTGACC 63281      C   CAC
          AG                  TTGG TAA   GGTGAAACCCCGT
                              |||| |||   ||||||||||||||
                              GACC GTT   CCACTTTGGGGCA
                                A   TTA
GAM230  KIAA1198 3' ACGGGGTTTCACCATGTTGGCC 63980          C
          AG                  TTGGCTAACA GGTGAAACCCCGT
                              |||||||||| ||||||||||||||
                              GACCGGTTGT CCACTTTGGGGCA
                                    A
GAM230  KIAA1198 3' ACGGGGTTTCACCATGTTGGCC 63981          C
          AG                  TTGGCTAACA GGTGAAACCCCGT
                              |||||||||| ||||||||||||||
                              GACCGGTTGT CCACTTTGGGGCA
                                    A
GAM230  KIAA1198 3' ACGGGGTTTCACCGTGTTAGCC 63982
          AG                  TTGGCTAACACGGTGAAACCCCGT
                              ||||||||||||||||||||||||||
                              GACCGATTGTGCCACTTTGGGGCA

GAM230  KIAA1200 3' ACGGGGTTTCACCATGTTGGCC 63025          C
          AG                  TTGGCTAACA GGTGAAACCCCGT
                              |||||||||| ||||||||||||||
                              GACCGGTTGT CCACTTTGGGGCA
                                    A
GAM230  KIAA1210 3' ACGGGGTTTCACCATGTTGGCC 98060          C
          AG                  TTGGCTAACA GGTGAAACCCCGT
                              |||||||||| ||||||||||||||
                              GACCGGTTGT CCACTTTGGGGCA
                                    A
GAM230  KIAA1328 5' GTTTCACCGTGTTAGCCAG    62332
                              TTGGCTAACACGGTGAAAC
                              |||||||||||||||||||
                              GACCGATTGTGCCACTTTG

GAM230  KIAA1456 3' ACGGGGTTTCACCGTGTTAGCC 67523
          AG                  TTGGCTAACACGGTGAAACCCCGT
                              ||||||||||||||||||||||||||
                              GACCGATTGTGCCACTTTGGGGCA

GAM230  KIAA1465 3' ACGGGGTTTCACCATGTTGGCC 61481          C
          AG                  TTGGCTAACA GGTGAAACCCCGT
                              |||||||||| ||||||||||||||
                              GACCGGTTGT CCACTTTGGGGCA
                                    A
GAM230  KIAA1467 3' ACGGGGTTTCACCATGTTGGCC 72056          C
          AG                  TTGGCTAACA GGTGAAACCCCGT
                              |||||||||| ||||||||||||||
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                                GACCGGTTGT CCACTTTGGGGCA
                                     A
GAM230  KIAA1497 5' ACAGGGTTTCACCATGTTGGTC 68105        C       C
            A                    TGGCTAACA GGTGAAACCC GT
                                 ||||||||| |||||||||| ||
                                 ACTGGTTGT CCACTTTGGG CA
                                     A        A
GAM230  KIAA1508 3' GGTTTCACCATGTTGGTCAG  62558          C
                                 TTGGCTAACA GGTGAAACC
                                 |||||||||| |||||||||
                                 GACTGGTTGT CCACTTTGG
                                     A
GAM230  KIAA1615 3' ATGGAGTTTCACCACGTTGGCC 69267         AC      C
            AA                   TTGGCTAAC  GGTGAAAC CCGT
                                 |||||||||  |||||||| ||||
                                 AACCGGTTG  CCACTTTG GGTA
                                     CA       A
GAM230  KIAA1617 3' ACAGGGTTTCACCATGTTGGTC 93065         C       C
            AG                   TTGGCTAACA GGTGAAACCC GT
                                 |||||||||| |||||||||| ||
                                 GACTGGTTGT CCACTTTGGG CA
                                     A        A
GAM230  KIAA1668 3' ACGGGGTTTCACCGTGTTAACC 67055     C
            AG                   TTGG TAACACGGTGAAACCCCGT
                                 |||| ||||||||||||||||||
                                 GACC ATTGTGCCACTTTGGGGCA
                                   A
GAM230  KIAA1712 3' ACAGGGTTTCACCATGTTGCCC 68145     C   C       C
            AG                   TTGG TAACA GGTGAAACCC GT
                                 |||| ||||| |||||||||| ||
                                 GACC GTTGT CCACTTTGGG CA
                                   C   A        A
GAM230  KIAA1784 3' ACGGGGTTTCACCATGTTGCTC 65740    _ T   C
            AG                   TTG GC AACA GGTGAAACCCCGT
                                 ||| || |||| ||||||||||||
                                 GAC CG TTGT CCACTTTGGGGCA
                                   T _   A
GAM230  KIAA1829 3' ACGGGGTTTCACCACATTGGTC 62626        CAC
            AG                   TTGGCTAA   GGTGAAACCCCGT
                                 ||||||||   ||||||||||||
                                 GACTGGTT   CCACTTTGGGGCA
                                     ACA
GAM230  KIAA1877 3' ACAGGGTTTCACCGTGTTAGCC 66736              C
            AG                   TTGGCTAACACGGTGAAACCC GT
                                 |||||||||||||||||||| ||
                                 GACCGATTGTGCCACTTTGGG CA
                                          A
GAM230  KIAA1971 3' ACGAGGTTTCACCGTGTTAGCC 74665              C
            AG                   TTGGCTAACACGGTGAAACC CGT
                                 |||||||||||||||||||| |||
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                                GACCGATTGTGCCACTTTGG GCA
                                          A
GAM230  KIAA1975  5'  GTTTCACCATGTTAACCAG   74428     C    C
                                TTGG TAACA GGTGAAAC
                                |||| ||||| ||||||||
                                GACC ATTGT CCACTTTG
                                  A    A
GAM230  KIAA1987  5'  ACGAGGTTTCACCATATTGGCC 89378        CAC       C
            AG                    TTGGCTAA   GGTGAAACC CGT
                                |||||||||   |||||||||| |||
                                GACCGGTT   CCACTTTGG GCA
                                    ATA       A
GAM230  KLK7      3'  ACAGGGTTTCACCATGTTGGCC 58383          C       C
            AG                    TTGGCTAACA GGTGAAACCC GT
                                |||||||||| |||||||||| ||
                                GACCGGTTGT CCACTTTGGG CA
                                    A         A
GAM230  KLK7      3'  ACAGGGTTTCACCATGTTGGCC 18534          C       C
            AG                    TTGGCTAACA GGTGAAACCC GT
                                |||||||||| |||||||||| ||
                                GACCGGTTGT CCACTTTGGG CA
                                    A         A
GAM230  LAMP3     3'  ACGGGGTTTCACCATGTTGGCC 60191          C
            AG                    TTGGCTAACA GGTGAAACCCCGT
                                |||||||||| ||||||||||||
                                GACCGGTTGT CCACTTTGGGGCA
                                    A
GAM230  MAP-1     3'  ACGGGGTTTCACCATGTTGGCC 42430          C
            AG                    TTGGCTAACA GGTGAAACCCCGT
                                |||||||||| ||||||||||||
                                GACCGGTTGT CCACTTTGGGGCA
                                    A
GAM230  MGC2603   3'  ACGAGGTTTCACCATATTAGCC 44069        CAC       C
            AG                    TTGGCTAA   GGTGAAACC CGT
                                |||||||||   |||||||| |||
                                GACCGATT   CCACTTTGG GCA
                                    ATA       A
GAM230  MGC4766   5'  ACGGGGTTTCACCGTGTTAGCC 49552
            AG                    TTGGCTAACACGGTGAAACCCCGT
                                |||||||||||||||||||||||||
                                GACCGATTGTGCCACTTTGGGGCA

GAM230  MKRN4     3'  ACGGGGTTTCACCATATTGGTC 48448        CAC
            AG                    TTGGCTAA   GGTGAAACCCCGT
                                |||||||||   ||||||||||||
                                GACTGGTT   CCACTTTGGGGCA
                                    ATA
GAM230  moblak    3'  ACAGGGTTTCACCGTGTTAGCC 56380              C
            AG                    TTGGCTAACACGGTGAAACCC GT
                                |||||||||||||||||||| ||
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                                GACCGATTGTGCCACTTTGGG CA
                                      A
GAM230  moblak   3' TTTCACCATGTTGGCCAG    56415          C
                                TTGGCTAACA GGTGAAA
                                |||||||||| |||||||
                                GACCGGTTGT CCACTTT
                                    A
GAM230  NDUFC2   3' ACGGGGTTTCACCATGTTGGCC 17021          C
          AA                      TTGGCTAACA GGTGAAACCCCGT
                                  |||||||||| ||||||||||||
                                  AACCGGTTGT CCACTTTGGGGCA
                                      A
GAM230  Nup43    3' ACAGGGTTTCACCATGTTGGCC 45338          C        C
          AG                      TTGGCTAACA GGTGAAACCC GT
                                  |||||||||| |||||||||| ||
                                  GACCGGTTGT CCACTTTGGG CA
                                      A         A
GAM230  OR51E2   3' GTTTCACCATGTTGGCCAG   48518          C
                                TTGGCTAACA GGTGAAAC
                                |||||||||| ||||||||
                                GACCGGTTGT CCACTTTG
                                    A
GAM230  PELI1    5' ACGGGGTTTCACCATGTTGCCC 40617      C    C
          AG                      TTGG TAACA GGTGAAACCCCGT
                                  |||| ||||| ||||||||||||
                                  GACC GTTGT CCACTTTGGGGCA
                                    C     A
GAM230  PSPH     3' ACGGGGTTTGACCGTGTTAGCC 17127            G
          AG                      TTGGCTAACACGGT AAACCCCGT
                                  |||||||||||||| |||||||||
                                  GACCGATTGTGCCA TTTGGGGCA
                                        G
GAM230  RAB21    3' ACGGGGTTTCACCAGGTTAGCC 31078          AC
          AG                      TTGGCTAAC  GGTGAAACCCCGT
                                  |||||||||  ||||||||||||
                                  GACCGATTG  CCACTTTGGGGCA
                                      GA
GAM230  RAP140   3' ACAGGGTTTCACTGTGTTAGCC 31503                C
          AG                      TTGGCTAACACGGTGAAACCC GT
                                  |||||||||||||||||||| ||
                                  GACCGATTGTGTCACTTTGGG CA
                                      A
GAM230  RNF8     3' ACAGGGTTTCACCATGTTGGCC 15554          C        C
          AG                      TTGGCTAACA GGTGAAACCC GT
                                  |||||||||| |||||||||| ||
                                  GACCGGTTGT CCACTTTGGG CA
                                      A         A
GAM230  SCYA22   3' ACGAGGCTTCACCATGTTGGCC 92569          C     A  C
          AG                      TTGGCTAACA GGTGAA CC CGT
                                  |||||||||| |||||| || |||
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                                GACCGGTTGT CCACTT GG GCA
                                      A     C  A
GAM230  SCYA28   3'  ACGGGGTTTCACCGTGTTGGCT 39535
                                GGCTAACACGGTGAAACCCCGT
                                ||||||||||||||||||||||
                                TCGGTTGTGCCACTTTGGGGCA

GAM230  SFXN2    3'  ACGGGGTTTCACCATGCTGGCC 74368        A  C
           AG                     TTGGCTA CA GGTGAAACCCCGT
                                ||||||| || ||||||||||||||
                                GACCGGT GT CCACTTTGGGGCA
                                   C  A
GAM230  SLC12A8  3'  ACAGGGTTTCACCATGTTGGCC 45229          C         C
           AG                     TTGGCTAACA GGTGAAACCC GT
                                |||||||||| |||||||||| ||
                                GACCGGTTGT CCACTTTGGG CA
                                      A         A
GAM230  SLC16A4  3'  GTTTCACCATGTTAGCCAG   17459          C
                                TTGGCTAACA GGTGAAAC
                                |||||||||| ||||||||
                                GACCGATTGT CCACTTTG
                                      A
GAM230  SREC     3'  ACAGGGTTTCACCATGTTAGCC 14894          C         C
           AG                     TTGGCTAACA GGTGAAACCC GT
                                |||||||||| |||||||||| ||
                                GACCGATTGT CCACTTTGGG CA
                                      A         A
GAM230  SS-56    3'  ACGGAGTTTCACCATGTTAGCT 60341          C       C
           AG                     TTGGCTAACA GGTGAAAC CCGT
                                |||||||||| |||||||| ||||
                                GATCGATTGT CCACTTTG GGCA
                                      A       A
GAM230  SULT1C2  3'  ACGAGGTTTCACCGTGTTAGCC 22706                  C
           AG                     TTGGCTAACACGGTGAAACC CGT
                                |||||||||||||||||| |||
                                GACCGATTGTGCCACTTTGG GCA
                                         A
GAM230  TADA3L   3'  ACGGGGTTTCACCGTGTTAGCC 56802
           AG                     TTGGCTAACACGGTGAAACCCCGT
                                ||||||||||||||||||||||||
                                GACCGATTGTGCCACTTTGGGGCA

GAM230  TCL6     3'  ACAGGGTTTCACCGTGTTAGCC 25893                  C
           AG                     TTGGCTAACACGGTGAAACCC GT
                                |||||||||||||||||| ||
                                GACCGATTGTGCCACTTTGGG CA
                                         A
GAM230  TCL6     5'  ACGAGGTTTCACCATGTTGGCC 25895          C       C
           AG                     TTGGCTAACA GGTGAAACC CGT
                                |||||||||| ||||||||| |||
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                                GACCGGTTGT CCACTTTGG GCA
                                     A       A
GAM230  TCL6     3'  ACAGGGTTTCACCGTGTTAGCC 27745                C
              AG                   TTGGCTAACACGGTGAAACCC GT
                                   |||||||||||||||||||| ||
                                   GACCGATTGTGCCACTTTGGG CA
                                        A
GAM230  TCL6     5'  ACGAGGTTTCACCATGTTGGCC 27747         C       C
              AG                   TTGGCTAACA GGTGAAACC CGT
                                   |||||||||| ||||||||| |||
                                   GACCGGTTGT CCACTTTGG GCA
                                     A       A
GAM230  TCL6     5'  ACGAGGTTTCACCATGTTGGCC 40455         C       C
              AG                   TTGGCTAACA GGTGAAACC CGT
                                   |||||||||| ||||||||| |||
                                   GACCGGTTGT CCACTTTGG GCA
                                     A       A
GAM230  TCL6     5'  ACGAGGTTTCACCATGTTGGCC 40503         C       C
              AG                   TTGGCTAACA GGTGAAACC CGT
                                   |||||||||| ||||||||| |||
                                   GACCGGTTGT CCACTTTGG GCA
                                     A       A
GAM230  TERA     3'  ACGGGGTTTCACCACGTTGGCC 41413          AC
              AG                   TTGGCTAAC  GGTGAAACCCCGT
                                   |||||||||  ||||||||||||
                                   GACCGGTTG  CCACTTTGGGGCA
                                       CA
GAM230  TGIF2    3'  ACGGGGTTTCACCATCTTGGCC 41739        CAC
              AG                   TTGGCTAA   GGTGAAACCCCGT
                                   ||||||||   ||||||||||||
                                   GACCGGTT   CCACTTTGGGGCA
                                      CTA
GAM230  TU12B1-TY 3'  ACGGGGTTTCACCATGTTGGCC 33818          C
              AG                   TTGGCTAACA GGTGAAACCCCGT
                                   |||||||||| ||||||||||||
                                   GACCGGTTGT CCACTTTGGGGCA
                                     A
GAM230  TUCAN    3'  ACAGGGTTTCACCATTTTGGCC 30960         CAC       C
              AG                   TTGGCTAA   GGTGAAACCC GT
                                   ||||||||   |||||||||| ||
                                   GACCGGTT   CCACTTTGGG CA
                                      TTA        A
GAM230  WBSCR23  3'  ACGGGGTTTCACCATGTTGGCC 47408          C
              AG                   TTGGCTAACA GGTGAAACCCCGT
                                   |||||||||| ||||||||||||
                                   GACCGGTTGT CCACTTTGGGGCA
                                     A
GAM230  ZNF221   3'  ACGGGGTTTCACCGTGTTAGCC 26265
              AG                   TTGGCTAACACGGTGAAACCCCGT
                                   ||||||||||||||||||||||||
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                                  GACCGATTGTGCCACTTTGGGGCA

GAM230  LOC113523 5'  ACAGGGTTTCACCATGTTAGCC 73406          C        C
                AG                    TTGGCTAACA GGTGAAACCC GT
                                      |||||||||| |||||||||| ||
                                      GACCGATTGT CCACTTTGGG CA
                                            A         A
GAM230  LOC115648 3'  ACGGGGTTTCACCATGTTGGCT 60013          C
                AA                    TTGGCTAACA GGTGAAACCCCGT
                                      |||||||||| ||||||||||||
                                      AATCGGTTGT CCACTTTGGGGCA
                                            A
GAM230  LOC120224 5'  ACAGGGTTTCACCATGTTTGTC 57878       T  C        C
                AG                    TTGGC AACA GGTGAAACCC GT
                                      ||||| |||| |||||||||| ||
                                      GACTG TTGT CCACTTTGGG CA
                                        T  A         A
GAM230  LOC121504 3'  ACGGGGTTTCACCATGTTGGCC 74538          C
                AG                    TTGGCTAACA GGTGAAACCCCGT
                                      |||||||||| ||||||||||||
                                      GACCGGTTGT CCACTTTGGGGCA
                                            A
GAM230  LOC128077 3'  ACAGGGTTTCACCATGTTGGCC 75194          C        C
                AG                    TTGGCTAACA GGTGAAACCC GT
                                      |||||||||| |||||||||| ||
                                      GACCGGTTGT CCACTTTGGG CA
                                            A         A
GAM230  LOC128077 3'  ACGGGGTTTCACCATGTTAGCC 75196          C
                AG                    TTGGCTAACA GGTGAAACCCCGT
                                      |||||||||| ||||||||||||
                                      GACCGATTGT CCACTTTGGGGCA
                                            A
GAM230  LOC128989 3'  ACGGGGTTTCACCATGTTGGTC 75305          C
                AG                    TTGGCTAACA GGTGAAACCCCGT
                                      |||||||||| ||||||||||||
                                      GACTGGTTGT CCACTTTGGGGCA
                                            A
GAM230  LOC135154 3'  GGTTTCACCATGTTAGCCAG   75733          C
                                      TTGGCTAACA GGTGAAACC
                                      |||||||||| |||||||||
                                      GACCGATTGT CCACTTTGG
                                            A
GAM230  LOC144524 5'  GTTTCACCGTGTTAGCCAG    84063
                                      TTGGCTAACACGGTGAAAC
                                      |||||||||||||||||||
                                      GACCGATTGTGCCACTTTG

GAM230  LOC145268 5'  GTTTCACCATGTTGGCCAG    77584          C
                                      TTGGCTAACA GGTGAAAC
                                      |||||||||| ||||||||
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                                GACCGGTTGT CCACTTTG
                                      A
GAM230  LOC146229 3'  ACAGGGTTTCACCATATTGGCC 78242        CAC       C
          AG                    TTGGCTAA   GGTGAAACCC GT
                                ||||||||   |||||||||| ||
                                GACCGGTT   CCACTTTGGG CA
                                    ATA         A
GAM230  LOC146229 3'  ACGGGGTTTCACCATGTTGGCC 78248         C
          AG                    TTGGCTAACA GGTGAAACCCCGT
                                |||||||||| ||||||||||||
                                GACCGGTTGT CCACTTTGGGGCA
                                      A
GAM230  LOC146229 3'  ACGGGGTTTCACCATGTTGGCC 78249         C
          AG                    TTGGCTAACA GGTGAAACCCCGT
                                |||||||||| ||||||||||||
                                GACCGGTTGT CCACTTTGGGGCA
                                      A
GAM230  LOC146346 5'  ACGGGGTTTCACCGTGTTGTCC 78382      C
          AG                    TTGG TAACACGGTGAAACCCCGT
                                |||| ||||||||||||||||||
                                GACC GTTGTGCCACTTTGGGGCA
                                  T
GAM230  LOC146429 5'  ACAGGGTTTCACCATGATAGCC 84654       A  C       C
          AG                    TTGGCTA CA GGTGAAACCC GT
                                ||||||| || |||||||||| ||
                                GACCGAT GT CCACTTTGGG CA
                                    A  A         A
GAM230  LOC146603 5'  ACGGGGTTTCACCGTGTTAGCC 78586
          AG                    TTGGCTAACACGGTGAAACCCCGT
                                ||||||||||||||||||||||||
                                GACCGATTGTGCCACTTTGGGGCA

GAM230  LOC146839 3'  ACGGGGTTTCACCGTGTTAGCC 84833
          AG                    TTGGCTAACACGGTGAAACCCCGT
                                ||||||||||||||||||||||||
                                GACCGATTGTGCCACTTTGGGGCA

GAM230  LOC146901 3'  ACGGGGTTTCACCATGTTGGCC 84881         C
          AG                    TTGGCTAACA GGTGAAACCCCGT
                                |||||||||| ||||||||||||
                                GACCGGTTGT CCACTTTGGGGCA
                                      A
GAM230  LOC146909 3'  GTTTCACCGTGTTAGCCAG    78782
                                TTGGCTAACACGGTGAAAC
                                |||||||||||||||||
                                GACCGATTGTGCCACTTTG

GAM230  LOC146952 5'  ACAGGGTTTCACCACATTGGCC 84919        CAC       C
          AG                    TTGGCTAA   GGTGAAACCC GT
                                ||||||||   |||||||||| ||
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                                GACCGGTT   CCACTTTGGG CA
                                    ACA         A
GAM230   LOC147071 5'  ACGGAGTTTCACCATGTTGGTT 73344          C       C
                AG                  TTGGCTAACA GGTGAAAC CCGT
                                    |||||||||| |||||||| ||||
                                    GATTGGTTGT CCACTTTG GGCA
                                       A       A
GAM230   LOC147080 5'  GGTTTCACCATGTTAGCCAG   85044          C
                                    TTGGCTAACA GGTGAAACC
                                    |||||||||| |||||||||
                                    GACCGATTGT CCACTTTGG
                                       A
GAM230   LOC147694 3'  ACGGGGTTTCACCGTGTTAGCC 79087
                AG                  TTGGCTAACACGGTGAAACCCCGT
                                    ||||||||||||||||||||||||
                                    GACCGATTGTGCCACTTTGGGGCA

GAM230   LOC147817 3'  ACGGAGTTTCACCATATTGGCT 79164        CAC       C
                                    GGCTAA   GGTGAAAC CCGT
                                    ||||||   |||||||| ||||
                                    TCGGTT   CCACTTTG GGCA
                                       ATA       A
GAM230   LOC148189 5'  ACGGGGTTTCACCATGTTGACC 79441      C     C
                AG                  TTGG TAACA GGTGAAACCCCGT
                                    |||| ||||| ||||||||||||
                                    GACC GTTGT CCACTTTGGGGCA
                                      A     A
GAM230   LOC148887 5'  ACAGGGTTTCACCATGTTGGTC 85387          C         C
                AG                  TTGGCTAACA GGTGAAACCC GT
                                    |||||||||| |||||||||| ||
                                    GACTGGTTGT CCACTTTGGG CA
                                       A         A
GAM230   LOC149421 3'  ACGGGGTTTCACCGCATTAGCC 80137         CA
                AA                  TTGGCTAA  CGGTGAAACCCCGT
                                    ||||||||  ||||||||||||||
                                    AACCGATT  GCCACTTTGGGGCA
                                       AC
GAM230   LOC149692 3'  ACAGGGTTTCACCATGTTGGCC 85720          C         C
                AG                  TTGGCTAACA GGTGAAACCC GT
                                    |||||||||| |||||||||| ||
                                    GACCGGTTGT CCACTTTGGG CA
                                       A         A
GAM230   LOC149821 5'  ACGGAGTTTCACCGTGTTAGCC 85926                C
                AG                  TTGGCTAACACGGTGAAAC CCGT
                                    |||||||||||||||||| ||||
                                    GACCGATTGTGCCACTTTG GGCA
                                                A
GAM230   LOC151050 5'  GTTTCACCATGTTGGCCA    80919          C
                                    TGGCTAACA GGTGAAAC
                                    ||||||||| ||||||||
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                                ACCGGTTGT CCACTTTG
                                    A
GAM230  LOC151057 3'  ACGGGGTTTCACCATGTTGGCC 86378         C
                AG                TTGGCTAACA GGTGAAACCCCGT
                                  |||||||||| ||||||||||||
                                  GACCGGTTGT CCACTTTGGGGCA
                                    A
GAM230  LOC151201 3'  ACGGGGTTTCACCATGTTGGCT 86461         C
                AG                TTGGCTAACA GGTGAAACCCCGT
                                  |||||||||| ||||||||||||
                                  GATCGGTTGT CCACTTTGGGGCA
                                    A
GAM230  LOC151475 5'  ACGAGGTTTCACCATGTTGGCC 86579         C       C
                AG                TTGGCTAACA GGTGAAACC CGT
                                  |||||||||| ||||||||| |||
                                  GACCGGTTGT CCACTTTGG GCA
                                    A       A
GAM230  LOC151701 3'  ACGGGGTTTCACCATGTTGGCC 86660         C
                AG                TTGGCTAACA GGTGAAACCCCGT
                                  |||||||||| ||||||||||||
                                  GACCGGTTGT CCACTTTGGGGCA
                                    A
GAM230  LOC151826 3'  ACAGGGTTTCACCGTGTTGGC  81173              C
                                  GCTAACACGGTGAAACCC GT
                                  |||||||||||||||| ||
                                  CGGTTGTGCCACTTTGGG CA
                                      A
GAM230  LOC151979 5'  ACGGGGTTTCACCATGTTACC  81241    C    C
                                  GG TAACA GGTGAAACCCCGT
                                  || ||||| ||||||||||||
                                  CC ATTGT CCACTTTGGGGCA
                                   _   A
GAM230  LOC152300 3'  ACAGGGTTTCACCATATTGGCC 81376         CAC       C
                AG                TTGGCTAA   GGTGAAACCC GT
                                  ||||||||   |||||||||| ||
                                  GACCGGTT   CCACTTTGGG CA
                                     ATA        A
GAM230  LOC152445 3'  ACAGGGTTTCACCATGTTAGCC 86922         C       C
                A                  TGGCTAACA GGTGAAACCC GT
                                  ||||||||| |||||||||| ||
                                  ACCGATTGT CCACTTTGGG CA
                                    A       A
GAM230  LOC152719 5'  ACGGGGTTTCACCATGTTGGTC 87011         C
                AG                TTGGCTAACA GGTGAAACCCCGT
                                  |||||||||| ||||||||||||
                                  GACTGGTTGT CCACTTTGGGGCA
                                    A
GAM230  LOC152719 5'  GGGTTTCACCATGTTAGCCAG  87037         C
                                  TTGGCTAACA GGTGAAACCC
                                  |||||||||| ||||||||||
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                                GACCGATTGT CCACTTTGGG
                                      A
GAM230  LOC153688 3'  ACAGGGTTTCACCATGTTGGCC 87282        C        C
                                GGCTAACA GGTGAAACCC GT
                                |||||||| |||||||||| ||
                                CCGGTTGT CCACTTTGGG CA
                                     A         A
GAM230  LOC153811 3'  ACGAGGTTTCACCACGTTGGCC 81820         AC        C
          AG                      TTGGCTAAC  GGTGAAACC CGT
                                |||||||||  ||||||||| |||
                                GACCGGTTG  CCACTTTGG GCA
                                     CA        A
GAM230  LOC154877 3'  ACAGGGTCTCACCATGTTGGCT 87515         C    A   C
          AG                      TTGGCTAACA GGTGA ACCC GT
                                |||||||||| ||||| |||| ||
                                GATCGGTTGT CCACT TGGG CA
                                     A    C   A
GAM230  LOC157506 3'  ACGGGGTTTCACCATGTTGGTC 82357         C
          AG                      TTGGCTAACA GGTGAAACCCCGT
                                |||||||||| ||||||||||||
                                GACTGGTTGT CCACTTTGGGGCA
                                     A
GAM230  LOC158014 5'  ACGGAGTTTCACCATGTTAGCC 82548         C       C
          AG                      TTGGCTAACA GGTGAAAC CCGT
                                |||||||||| |||||||| ||||
                                GACCGATTGT CCACTTTG GGCA
                                     A       A
GAM230  LOC158476 3'  ACAGGGTTTCACCATATTGGCC 88175        CAC        C
          AG                      TTGGCTAA   GGTGAAACCC GT
                                |||||||   |||||||||| ||
                                GACCGGTT   CCACTTTGGG CA
                                    ATA         A
GAM230  LOC158476 3'  ACAGGGTTTCACCATGTTGGTC 88176         C        C
          AG                      TTGGCTAACA GGTGAAACCC GT
                                |||||||||| |||||||||| ||
                                GACTGGTTGT CCACTTTGGG CA
                                     A         A
GAM230  LOC158549 5'  GTTTCACCGTGTTAGCCAG   88231
                                TTGGCTAACACGGTGAAAC
                                ||||||||||||||||||
                                GACCGATTGTGCCACTTTG

GAM230  LOC169611 3'  ACAGGATTTCACCATGTTGGCC 83629         C      C  C
          AG                      TTGGCTAACA GGTGAAA CC GT
                                |||||||||| ||||||| || ||
                                GACCGGTTGT CCACTTT GG CA
                                     A      A  A
GAM230  LOC170082 5'  GTTTCACCATGTTAGCCAG   83448          C
                                TTGGCTAACA GGTGAAAC
                                |||||||||| ||||||||
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                                GACCGATTGT CCACTTTG
                                      A
GAM230  LOC196264 3'  ACGGGGTTTCACCATTTTGGCC 88977        CAC
          AG                    TTGGCTAA   GGTGAAACCCCGT
                                ||||||||   ||||||||||||||
                                GACCGGTT   CCACTTTGGGGCA
                                   TTA
GAM230  LOC199699 3'  ACAGGGTTTCACCGTGTTAGCC 89660              C
          AG                    TTGGCTAACACGGTGAAACCC GT
                                |||||||||||||||||||| ||
                                GACCGATTGTGCCACTTTGGG CA
                                      A
GAM230  LOC199725 5'  ACGGGATTTCACCATGTTGGTC 91406        C     C
          AG                    TTGGCTAACA GGTGAAA CCCGT
                                |||||||||| ||||||| |||||
                                GACTGGTTGT CCACTTT GGGCA
                                      A     A
GAM230  LOC200169 5'  ACGGAGTTTCACCATGTTGGCC 91546        C     C
          A                     TGGCTAACA GGTGAAAC CCGT
                                ||||||||| |||||||| ||||
                                ACCGGTTGT CCACTTTG GGCA
                                      A     A
GAM230  LOC200301 5'  ACGGGGTTTCACCGTGTTAGCC 90130
          AG                    TTGGCTAACACGGTGAAACCCCGT
                                ||||||||||||||||||||||||
                                GACCGATTGTGCCACTTTGGGGCA

GAM230  LOC200310 3'  ACGGGGTTTCACCATGTTGGTC 66315        C
          AG                    TTGGCTAACA GGTGAAACCCCGT
                                |||||||||| ||||||||||||
                                GACTGGTTGT CCACTTTGGGGCA
                                      A
GAM230  LOC201164 3'  ACAGGGTTTCACCATGTTGGTT 89481        C     C
          AG                    TTGGCTAACA GGTGAAACCC GT
                                |||||||||| |||||||||| ||
                                GATTGGTTGT CCACTTTGGG CA
                                      A     A
GAM230  LOC201173 5'  ACGGAGTTTCACCATGTTGGTC 88663        C     C
          AG                    TTGGCTAACA GGTGAAAC CCGT
                                |||||||||| ||||||| ||||
                                GACTGGTTGT CCACTTTG GGCA
                                      A     A
GAM230  LOC201294 3'  ACGGGGTTTCACCATGTTGGCC 89569        C
          AG                    TTGGCTAACA GGTGAAACCCCGT
                                |||||||||| ||||||||||||
                                GACCGGTTGT CCACTTTGGGGCA
                                      A
GAM230  LOC201411 3'  ACAGGGTTTCACCATGTTGGTC 63629        C     C
          AG                    TTGGCTAACA GGTGAAACCC GT
                                |||||||||| |||||||||| ||
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                                GACTGGTTGT CCACTTTGGG CA
                                      A         A
GAM230  LOC202934 3'  ACAGGGTTTCACCACGTTGGCC 92022          AC         C
          AG                    TTGGCTAAC  GGTGAAACCC GT
                                |||||||||  |||||||||| ||
                                GACCGGTTG  CCACTTTGGG CA
                                    CA         A
GAM230  LOC203350 3'  ACGGGGTTTCACCGTGTTGGCC 92223
          AG                    TTGGCTAACACGGTGAAACCCCGT
                                ||||||||||||||||||||||||
                                GACCGGTTGTGCCACTTTGGGGCA

GAM230  LOC205251 5'  ACAGGGTTTCACCATGTTAACC 92353      C    C         C
          AG                    TTGG TAACA GGTGAAACCC GT
                                |||| ||||| |||||||||| ||
                                GACC ATTGT CCACTTTGGG CA
                                  A    A         A
GAM230  LOC219445 5'  ACGGGGTTTCACCGTGTTAGCC 93194
          AG                    TTGGCTAACACGGTGAAACCCCGT
                                ||||||||||||||||||||||||
                                GACCGATTGTGCCACTTTGGGGCA

GAM230  LOC219735 3'  ACGGGGTTTCACCGTGTTAGCC 94721
          AG                    TTGGCTAACACGGTGAAACCCCGT
                                ||||||||||||||||||||||||
                                GACCGATTGTGCCACTTTGGGGCA

GAM230  LOC219894 3'  GTTTCACCGTGTTAGCCAG    94908
                                TTGGCTAACACGGTGAAAC
                                |||||||||||||||||
                                GACCGATTGTGCCACTTTG

GAM230  LOC220074 3'  ACGGGGTTTCACCATGTTAGCC 59952          C
          AG                    TTGGCTAACA GGTGAAACCCCGT
                                |||||||||| ||||||||||||
                                GACCGATTGT CCACTTTGGGGCA
                                      A
GAM230  LOC221296 3'  ACGGGGTTTCACCATGCTGGCC 93599        A  C
          AG                    TTGGCTA CA GGTGAAACCCCGT
                                ||||||| || ||||||||||||
                                GACCGGT GT CCACTTTGGGGCA
                                   C  A
GAM230  LOC222224 5'  ACAGGGTTTCACCATGTTGGCC 95865          C         C
          AG                    TTGGCTAACA GGTGAAACCC GT
                                |||||||||| |||||||||| ||
                                GACCGGTTGT CCACTTTGGG CA
                                      A         A
GAM230  LOC253666 3'  ACGGGGTTTCACCATGTTCGCC 96756       T    C
          AG                    TTGGC AACA GGTGAAACCCCGT
                                ||||| |||| ||||||||||||
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                                GACCG TTGT CCACTTTGGGGCA
                                  C    A
GAM230   LOC253842 5'  GTTTCACCACGTTAGCCAG    99241          AC
                                TTGGCTAAC  GGTGAAAC
                                |||||||||  ||||||||
                                GACCGATTG  CCACTTTG
                                    CA
GAM230   LOC253981 3'  ACGGGGTTTCACCGCATTAGCG 97526    G     CA
           AA                    TT GCTAA  CGGTGAAACCCCGT
                                || |||||  ||||||||||||||
                                AA CGATT  GCCACTTTGGGGCA
                                 G    AC
GAM230   LOC254295 5'  ACGGGGTTTCACCGTGTTAGCC 97885
           AG                    TTGGCTAACACGGTGAAACCCCGT
                                ||||||||||||||||||||||||||
                                GACCGATTGTGCCACTTTGGGGCA

GAM230   LOC254655 3'  ACGGGGTTTCACCATGTTGGCC 97210          C
           AG                    TTGGCTAACA GGTGAAACCCCGT
                                ||||||||||  ||||||||||||||
                                GACCGGTTGT CCACTTTGGGGCA
                                    A
GAM230   LOC255497 3'  ACGGGGTTTCACCATGTTGGCC 98979          C
           AG                    TTGGCTAACA GGTGAAACCCCGT
                                ||||||||||  ||||||||||||||
                                GACCGGTTGT CCACTTTGGGGCA
                                    A
GAM230   LOC255927 5'  ACGGGGTTTCACCATCTTGGCC 97707         CAC
           AG                    TTGGCTAA   GGTGAAACCCCGT
                                ||||||||   ||||||||||||||
                                GACCGGTT   CCACTTTGGGGCA
                                   CTA
GAM230   LOC256221 3'  ACGGGGTTTCACCGTGTTAGCC 96902
           AG                    TTGGCTAACACGGTGAAACCCCGT
                                ||||||||||||||||||||||||||
                                GACCGATTGTGCCACTTTGGGGCA

GAM230   LOC256306 3'  ACGGGGTTTCACCATGTTGGCC 98500          C
           AG                    TTGGCTAACA GGTGAAACCCCGT
                                ||||||||||  ||||||||||||||
                                GACCGGTTGT CCACTTTGGGGCA
                                    A
GAM230   LOC257486 3'  ACGGGGTTTCACCATGTTGGCC 69761          C
           AG                    TTGGCTAACA GGTGAAACCCCGT
                                ||||||||||  ||||||||||||||
                                GACCGGTTGT CCACTTTGGGGCA
                                    A
GAM230   LOC51159  5'  ACGGGATTTCACCATGTTGGCC 33024          C      C
           AG                    TTGGCTAACA GGTGAAA CCCGT
                                ||||||||||  |||||||  |||||
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                                GACCGGTTGT CCACTTT GGGCA
                                     A      A
GAM230  LOC56181  5'  ACAGGGCTTCACTGTGTTAGCC 97265             A  C
              AG                  TTGGCTAACACGGTGAA CCC GT
                                  |||||||||||||||| ||| ||
                                  GACCGATTGTGTCACTT GGG CA
                                        C   A
GAM230  LOC81034  3'  GTTTCACCATGTTAGCCAG   48595         C
                                  TTGGCTAACA GGTGAAAC
                                  |||||||||| ||||||||
                                  GACCGATTGT CCACTTTG
                                     A
GAM230  LOC89919  3'  ACGGGGTTTCACCATGTTAG  61366       C
                                  CTAACA GGTGAAACCCCGT
                                  |||||| ||||||||||||
                                  GATTGT CCACTTTGGGGCA
                                    A
GAM230  LOC90288  3'  ACGGGGTTTCACAGTGTTAGCC 62765          G
              AG                  TTGGCTAACAC GTGAAACCCCGT
                                  |||||||||||| ||||||||||||
                                  GACCGATTGTG CACTTTGGGGCA
                                      A
GAM230  LOC90333  3'  GTTTCACCGTGTTAGCCAG   62964
                                  TTGGCTAACACGGTGAAAC
                                  |||||||||||||||||
                                  GACCGATTGTGCCACTTTG

GAM230  LOC90591  3'  ACGGAGTTTCATCGTGTTAGCC 64136              C
              AG                  TTGGCTAACACGGTGAAAC CCGT
                                  |||||||||||||||||| ||||
                                  GACCGATTGTGCTACTTTG GGCA
                                        A
GAM230  LOC91893  3'  ACGAGGTTTCACCGTGTTAGCC 68065              C
              AG                  TTGGCTAACACGGTGAAACC CGT
                                  |||||||||||||||||| |||
                                  GACCGATTGTGCCACTTTGG GCA
                                      A
GAM230  LOC92148  5'  ACGGGGTTTCACCGTGTTAGTC 68868
              AG                  TTGGCTAACACGGTGAAACCCCGT
                                  ||||||||||||||||||||||||
                                  GACTGATTGTGCCACTTTGGGGCA

GAM230  LOC92689  3'  ACAGGGTTTCACCATGTTGGCC 70765         C       C
              AG                  TTGGCTAACA GGTGAAACCC GT
                                  |||||||||| |||||||||| ||
                                  GACCGGTTGT CCACTTTGGG CA
                                     A        A
GAM230  LOC92841  3'  ACAGGGTTTCACCATGTTGGCC 71236        C       C
              A                    TGGCTAACA GGTGAAACCC GT
                                  |||||||| |||||||||| ||
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                                ACCGGTTGT CCACTTTGGG CA
                                    A         A
GAM230  LOC92841  3'  ACGGGGTTTCACCATGTTAGCC 71239          C
          AG                    TTGGCTAACA GGTGAAACCCCGT
                                |||||||||| ||||||||||||
                                GACCGATTGT CCACTTTGGGGCA
                                    A
GAM231  KIAA1712  3'  ACACACAGAGAAGGGACTTAA  68144       A   GG
                                TTAAGT TCT  CTCTGTGTGT
                                |||||| |||  ||||||||||
                                AATTCA GGG  GAGACACACA
                                   _   AA
GAM232  AF5Q31    3'  CCACAACACTGTGTCACATCAC 27777      CTA     __  AC
          G                     CGTG   TGACAT  TG  GTGG
                                ||||   ||||||  ||  ||||
                                GCAC   ACTGTG  AC  CACC
                                  TAC     TC  AA
GAM232  CLK2      3'  CCATGAGCACCATAGCAC    61020        ACAT  A_
                                GTGCTATG   TG  CGTGG
                                ||||||||   ||  |||||
                                CACGATAC   AC  GTACC
                                    C___  GA
GAM232  CYP8B1    3'  CCATTTGTATCATAGCAT    16535         C  TGAC
                                GTGCTATGA AT   GTGG
                                |||||||| ||   ||||
                                TACGATACT TG   TACC
                                    A  TT__
GAM232  HOXD1     3'  CATTTAATGTCATAGCATG   44695             C
                                CGTGCTATGACATTGA GTG
                                |||||||||||||||| |||
                                GTACGATACTGTAATT TAC
                                                _
GAM232  HRH1      3'  CCACAATATGTATAGCAC    7817          A   TGAC
                                GTGCTATG CAT   GTGG
                                |||||||| |||   ||||
                                CACGATAT GTA   CACC
                                    _  TAA_
GAM232  KCNK3     3'  CCACATTCTCATAGCAGG    11170   G       CATT  C
                                C TGCTATGA   GA GTGG
                                | ||||||||   || ||||
                                G ACGATACT   TT CACC
                                 G       C___  A
GAM232  MFAP3     3'  CCACACCAATGTCATAATGC  21001    GC        AC
                                GT  TATGACATTG  GTGG
                                ||  ||||||||||  ||||
                                CG  ATACTGTAAC  CACC
                                  TA        CA
GAM232  PIN1L     3'  CCACGTCATTGTCCGCACG   21708      TAT   T
                                CGTGC   GACA TGACGTGG
                                |||||   |||| ||||||||
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                                GCACG   CTGT ACTGCACC
                                  C__   T
GAM232  RANBP2L1  3'  CCACTTACGAATGTCATAACA  51049    C       _ AC_
                                TG TATGACATT G   GTGG
                                || ||||||||| |   ||||
                                AC ATACTGTAA C   CACC
                                 A        G ATT
GAM232  SLC4A4    3'  CCACGTCAATGTCCTATGCA   14991    _ T
                                TGC TA GACATTGACGTGG
                                ||| || ||||||||||||
                                ACG AT CTGTAACTGCACC
                                  T  C
GAM232  DKFZP434B205 3'  CCACGTCATAGACATACACG   75842     C   ACAT
                                CGTG TATG    TGACGTGG
                                |||| ||||    ||||||||
                                GCAC ATAC    ACTGCACC
                                  _    AGAT
GAM232  FKBP5     3'  CCACAGCAGTGTCACAGACG   15931     G  A      AC
                                CGT CT TGACATTG  GTGG
                                ||| || ||||||||  ||||
                                GCA GA ACTGTGAC  CACC
                                  _ C       GA
GAM232  FLJ10375  3'  CCACGTTCCCCTCATAGCA    36556        CATT
                                TGCTATGA    GACGTGG
                                ||||||||    |||||||
                                ACGATACT    TTGCACC
                                     CCCC
GAM232  FLJ20127  5'  CCAGCGCCACACATAGCAC    35079        ACAT  A  _
                                GTGCTATG    TG CG TGG
                                ||||||||    || || |||
                                CACGATAC    AC GC ACC
                                     AC__  C  G
GAM232  KIAA0212  3'  CCAGCCTCACATAGCACG     28625        ACAT   C _
                                CGTGCTATG    TGA G TGG
                                |||||||||    ||| | |||
                                GCACGATAC    ACT C ACC
                                     ____   C G
GAM232  KIAA1131  3'  CCAGCAAGTATATAGCAC     62522        _  A   ACG
                                GTGCTATG AC TTG   TGG
                                |||||||| || |||   |||
                                CACGATAT TG AAC   ACC
                                     A  _   G__
GAM232  LOC144776 3'  CATTTAAGTCATAGCACG     77487          A    C
                                CGTGCTATGAC TTGA GTG
                                |||||||||||| |||| |||
                                GCACGATACTG AATT TAC
                                          _   _
GAM232  LOC220692 3'  CCACTTACGAATGTCATAACA  92864    C       _ AC_
                                TG TATGACATT G   GTGG
                                || ||||||||| |   ||||
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                                AC ATACTGTAA C   CACC
                                 A        G ATT
GAM232  LOC90119  5'  CCACCATCGTGTCAGCAGCACG 62207       A_     T  C_
                                CGTGCT  TGACAT GA  GTGG
                                ||||||  |||||| ||  ||||
                                GCACGA  ACTGTG CT  CACC
                                   CG     _ AC
GAM233  AKAP2    3'  AGGAGGATCGTCTTTACC    24224    C  CC
                                GG AA  GCGATCCTCCT
                                || ||  ||||||||||
                                CC TT  TGCTAGGAGGA
                                 A  TC
GAM233  ASTN     3'  AGGAGGGTGAGGCTGCCG    69867      A  G G
                                TGGCA CC C ATCCTCCT
                                ||||| || | ||||||||
                                GCCGT GG G TGGGAGGA
                                   C  A _
GAM233  ATRN     3'  AGAAGGAATTGGTTGTCA    24855        CGA    C
                                TGGCAACCG   TCCT CT
                                |||||||||   |||| ||
                                ACTGTTGGT   AGGA GA
                                     TA_   A
GAM233  CNGB1    3'  AGGAGGATCACTGGAGGCC   8933     AA   C_
                                GGC  CCG  GATCCTCCT
                                |||  |||  |||||||||
                                CCG  GGT  CTAGGAGGA
                                  GA   CA
GAM233  CROT     3'  AGGAGGATCGGTTGAGCC    41256    __    GC
                                GGC  AACC  GATCCTCCT
                                |||  ||||  |||||||||
                                CCG  TTGG  CTAGGAGGA
                                  AG   __
GAM233  GORASP1  3'  AGGAAGGGGTTGCTGTCCA   49952     CA  C     __
                                TGG  AC GCGATCC  TCCT
                                |||  || |||||||  ||||
                                ACC  TG CGTTGGG  AGGA
                                  __ T      GA
GAM233  ICA1     3'  AGGAGGATCACTTGGAGCC   18309     AA   C__
                                GGC  CCG   GATCCTCCT
                                |||  |||   |||||||||
                                CCG  GGT   CTAGGAGGA
                                  A_   TCA
GAM233  IRAK1    3'  AGGAGGATCGCTGGAGCC    9608      AA  _
                                GGC  CC GCGATCCTCCT
                                |||  || ||||||||||
                                CCG  GG CGCTAGGAGGA
                                  A_  T
GAM233  AIF1     5'  AGGAGGGTTAGGATTTCCA   17923     C  _  GC
                                TGG AA CC  GATCCTCCT
                                ||| || ||  |||||||||
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                                ACC TT GG  TTGGGAGGA
                                  T  A  A_
GAM233  APOL4    3'  AGGAGGATGTATGTCA      48378      ACC  G
                                TGGCA   GC ATCCTCCT
                                |||||   || ||||||||
                                ACTGT   TG TAGGAGGA
                                  A__  _
GAM233  C20orf130 5'  AGGAGGGTCAGGCCGCCA    62412      AA  GC
                                TGGC  CC  GATCCTCCT
                                ||||  ||  |||||||||
                                ACCG  GG  CTGGGAGGA
                                  CC  A_
GAM233  C20orf59  5'  AGGAGGATGGGGCTGCC     42231      A  G G
                                GGCA CC C ATCCTCCT
                                |||| || | ||||||||
                                CCGT GG G TAGGAGGA
                                  C  G _
GAM233  FADS1    3'  AGGAGGATCACTTGGGCC    26371     AA   C__
                                GGC  CCG   GATCCTCCT
                                |||  |||   |||||||||
                                CCG  GGT   CTAGGAGGA
                                  __   TCA
GAM233  FLJ22195  3'  AGGATGGTAGGGTTGCCA    43106         __  G
                                TGGCAACC  GC ATCCT
                                ||||||||  || |||||
                                ACCGTTGG  TG TAGGA
                                     GA  G
GAM233  FLJ23185  3'  AGGAGGATGGCAGTACCA    47507     CA  C  G
                                TGG  AC GC ATCCTCCT
                                |||  || || ||||||||
                                ACC  TG CG TAGGAGGA
                                  A_  A  G
GAM233  KIAA0010  3'  AGGAGGAGGGTCTGCCA     28589      _   GCGA
                                TGGCA ACC    TCCTCCT
                                ||||| |||    |||||||
                                ACCGT TGG    AGGAGGA
                                   C   G___
GAM233  KIAA0042  3'  AGGGTTAACTGGTTGCCA    30232         C__
                                TGGCAACCG   GATCCT
                                |||||||||   ||||||
                                ACCGTTGGT   TTGGGA
                                     CAA
GAM233  KIAA0349  3'  AGGAGGATGACCGTCGCCA   93914      A  CG_ G
                                TGGC AC   C ATCCTCCT
                                |||| ||   | ||||||||
                                ACCG TG   G TAGGAGGA
                                  C  CCA _
GAM233  KIAA1184  3'  AGGAGGGTCCTGATTGCCA   42922       C  C
                                TGGCAA CG GATCCTCCT
                                |||||| || |||||||||
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                                ACCGTT GT CTGGGAGGA
                                   A  C
GAM233  KIAA1260  3'  AGGAGGATGTGATGTC      60666      AC   G
                                GGCA  CGC ATCCTCCT
                                ||||  ||| ||||||||
                                CTGT  GTG TAGGAGGA
                                  A_  _
GAM233  KIAA1374  3'  AGGAGAATAGTGGTTGCCA   61914          G  C
                                TGGCAACCGC AT CTCCT
                                |||||||||| || |||||
                                ACCGTTGGTG TA GAGGA
                                     A  A
GAM233  MGC3329   3'  AGGAGGAATTGTGGTCATCA  44238     CA       _
                                TGG  ACCGCGAT CCTCCT
                                |||  |||||||| ||||||
                                ACT  TGGTGTTA GGAGGA
                                  AC       A
GAM233  PRO0478   3'  AGGAGGATCGCTTGTGCC    27016      ACC
                                GGCA   GCGATCCTCCT
                                ||||   ||||||||||
                                CCGT   CGCTAGGAGGA
                                  GTT
GAM233  PSKH1     3'  AGGAGGGTTTGGTTCCCA    68789      C    C
                                TGG AACCG GATCCTCCT
                                ||| ||||| |||||||||
                                ACC TTGGT TTGGGAGGA
                                  C    _
GAM233  SNIP1     3'  AGAAGGATCCTGGTTGCTA   45536         C     C
                                TGGCAACCG GATCCT CT
                                ||||||||| |||||| ||
                                ATCGTTGGT CTAGGA GA
                                     C     A
GAM233  LOC127428 3'  AGGAAGCGCCATACGGTTGCTA 75153        _____  ATCC
                                TGGCAACC    GCG    TCCT
                                ||||||||    |||    ||||
                                ATCGTTGG    CGC    AGGA
                                     CATAC   GA__
GAM233  LOC147081 5'  AGGAGGATGCTGTGGCCA    78841      A  C  G
                                TGGC AC GC ATCCTCCT
                                |||| || || ||||||||
                                ACCG TG CG TAGGAGGA
                                  G  T  _
GAM233  LOC150082 5'  AGGAGATTGTGGACTGCC    80384      A_       C
                                GGCA  CCGCGATC TCCT
                                ||||  |||||||| ||||
                                CCGT  GGTGTTAG AGGA
                                  CA       _
GAM233  LOC150378 3'  AGGAGGATCCCGGGCCA     80555      AA   C
                                TGGC  CCG GATCCTCCT
                                ||||  ||| |||||||||
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                                ACCG  GGC CTAGGAGGA
                                  __  C
GAM233  LOC163682 5'  AGGAGGATGTGGGGCC     88396    AA   G
                                GGC  CCGC ATCCTCCT
                                |||  |||| ||||||||
                                CCG  GGTG TAGGAGGA
                                  G_   _
GAM233  LOC200197 3'  GAGGCATTCGCGGTTGCC    90017          T__
                                GGCAACCGCGA   CCTC
                                ||||||||||   ||||
                                CCGTTGGCGCT   GGAG
                                      TAC
GAM233  LOC220506 3'  AGGAGGATTCAGTTTCCA    74514    C   CGC
                                TGG AAC   GATCCTCCT
                                ||| |||   |||||||||
                                ACC TTG   TTAGGAGGA
                                  T   AC_
GAM233  LOC221477 3'  AGGAGTGGCTAGGGGTTGCCA  93766        ____  G TC
                                TGGCAACC    GC A  CTCCT
                                ||||||||    || |  |||||
                                ACCGTTGG    CG T  GAGGA
                                    GGAT  G __
GAM233  LOC255452 5'  AGGAGGGTGCTGGCGCCA    99387     AA  _  G
                                TGGC  CC GC ATCCTCCT
                                ||||  || || ||||||||
                                ACCG  GG CG TGGGAGGA
                                  C_  T  _
GAM233  LOC256529 5'  AGGAGGGTCATGCTAGCCA   99427     AAC  C
                                TGGC   CG GATCCTCCT
                                ||||   || |||||||||
                                ACCG   GT CTGGGAGGA
                                  ATC  A
GAM233  LOC90408  3'  AGGAGGATGTATGTCGCC    63337     A  C_  G
                                GGC AC  GC ATCCTCCT
                                ||| ||  || ||||||||
                                CCG TG  TG TAGGAGGA
                                  C  TA  _
GAM233  LOC92340  3'  AGGAGAAGTTGCGGTGGCCA  69556      A       C_
                                TGGC ACCGCGAT  CTCCT
                                |||| ||||||||  |||||
                                ACCG TGGCGTTG  GAGGA
                                  G       AA
GAM233  LOC92771  3'  AGGAGGCGGAGGTTGCC     54207       G_  AT
                                GGCAACC  CG  CCTCCT
                                |||||||  ||  ||||||
                                CCGTTGG  GC  GGAGGA
                                    AG  __
GAM233  LOC93349  3'  AGGAAATATGCTACTGGTTGCC 57263        ____   ATCC
          A                      TGGCAACC    GCG    TCCT
                                ||||||||    |||    ||||
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                                ACCGTTGG   CGT   AGGA
                                    TCAT  ATAA
GAM234  PCSK1    3'  GTCTCCAGTCACCTACAATG  6515        CT  G   A
                                CATTGTGGG  AC TGGA AC
                                |||||||||  || |||| ||
                                GTAACATCC  TG ACCT TG
                                    AC  _   C
GAM234  PPP1R8   5'  AGAGTTCAACACTGCCCACAA  57508       TAC  GA_  C
                                TTGTGGGC  GTG  AAC CT
                                ||||||||  |||  ||| ||
                                AACACCCG  CAC  TTG GA
                                    T__  AAC  A
GAM234  APELIN   3'  AGGGCCCCCCAAGTCCCACAAT 34262       CT  G  AAA_
                                ATTGTGGG  AC TGG   CCCT
                                ||||||||  || |||   ||||
                                TAACACCC  TG ACC   GGGA
                                    __  A  CCCC
GAM234  EMILIN-2 3'  AGAGTTTCCACATAGGCCCCAA 50253    T   AC_     C
                                TTG GGGCT  GTGGAAAC CT
                                ||| |||||  |||||||| ||
                                AAC CCCGG  CACCTTTG GA
                                  _   ATA      A
GAM234  LASP1    3'  AGAGTTTCCTCAGAACCCACAG 21571       CTACGT    C
           TG                    CATTGTGGG    GGAAAC CT
                                |||||||||    |||||| ||
                                GTGACACCC    CCTTTG GA
                                    AAGACT    A
GAM234  NY-REN-25 3'  GGTTTCCACGTAGACAC    61264    GG       C
                                GTG  CTACGTGGAAA CC
                                |||  |||||||||| ||
                                CAC  GATGCACCTTT GG
                                  A_        A
GAM234  OS4      3'  AGGGTTTCCACTCTGCACAT  20381    G  TAC
                                GTG GC  GTGGAAACCCT
                                ||| ||  ||||||||||
                                TAC CG  CACCTTTGGGA
                                  A  TCT
GAM234  PRO0899  3'  AGGGTCCCCAGCCCCACAGT  38305       CTACG  AA
                                ATTGTGGG   TGG  ACCCT
                                ||||||||   |||  |||||
                                TGACACCC   ACC  TGGGA
                                    CG___  CC
GAM234  SLC26A7  3'  TTCCACACACCAAGGCTACAAT 54514       G  AC____
           G                    CATTGTGG CT    GTGGAA
                                |||||||| ||    ||||||
                                GTAACATC GA    CACCTT
                                    G  ACCACA
GAM234  LOC118611 5'  GGTTCCCGAGGCCCACACTG  75996   T     A  T   A
                                CA TGTGGGCT CG GGAA CC
                                || |||||||| || |||| ||
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                                GT ACACCCGG GC CCTT GG
                                 C       A _   _
GAM234   LOC147136 3'  AGGGCAGCATCCATAGCCCACA 78857         AC     AA___
           A                     TTGTGGGCT  GTGGA     CCCT
                                 |||||||||  |||||     ||||
                                 AACACCCGA  TACCT     GGGA
                                      __     ACGAC
GAM234   LOC150759 3'  GGTAAGTGCAGCCCACAA     80795         A   GGAA
                                 TTGTGGGCT CGT    ACC
                                 |||||||||| |||    |||
                                 AACACCCGA GTG    TGG
                                      C   AA__
GAM234   LOC151323 3'  GGTAAGTGCAGCCCACAA     81026         A   GGAA
                                 TTGTGGGCT CGT    ACC
                                 |||||||||| |||    |||
                                 AACACCCGA GTG    TGG
                                      C   AA__
GAM234   LOC157349 5'  GTTGTTCACTAACTCACAATG  82349         C  C    _
                                 CATTGTGGG TA GTGGA AAC
                                 ||||||||| || ||||| |||
                                 GTAACACTC AT CACTT TTG
                                      A _    G
GAM234   LOC196485 5'  AGAGTTTCCACATAATCCCAA  89069     T  GC  C       C
                                 TTG GG  TA GTGGAAAC CT
                                 ||| ||  || |||||||| ||
                                 AAC CC  AT CACCTTTG GA
                                   _  TA  A       A
GAM234   LOC200399 3'  GGTAAGTGCAGCCCACAA     90240         A   GGAA
                                 TTGTGGGCT CGT    ACC
                                 |||||||||| |||    |||
                                 AACACCCGA GTG    TGG
                                      C   AA__
GAM234   LOC202986 5'  AGAGTTTCCACATAATCCCAA  92061     T  GC  C       C
                                 TTG GG  TA GTGGAAAC CT
                                 ||| ||  || |||||||| ||
                                 AAC CC  AT CACCTTTG GA
                                   _  TA  A       A
GAM234   LOC204593 5'  TTCACGTGAGCCCACAAT     92346          _
                                 ATTGTGGGCT ACGTGGA
                                 |||||||||| |||||||
                                 TAACACCCGA TGCACTT
                                      G
GAM234   LOC221431 3'  AGAGTTTCTCTAAGCCCACAAT 93727          ACGT     C
           G                      CATTGTGGGCT    GGAAAC CT
                                  ||||||||||    |||||| ||
                                  GTAACACCCGA    TCTTTG GA
                                       ATC_      A
GAM234   LOC221490 5'  GGATTTAATAGCCACAATG    95306         G   CGTG   A
                                 CATTGTGG CTA    GAA CC
                                 |||||||| |||    ||| ||
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                                GTAACACC GAT    TTT GG
                                     _  AA__   A
GAM234  LOC51285  3' AGGGCTCCAGGGAGCCCACAG  33800        ACG   AA
                                TTGTGGGCT   TGGA  CCCT
                                |||||||||   ||||  ||||
                                GACACCCGA   ACCT  GGGA
                                     GGG   C_
GAM234  LOC57862  3' AGGATGCCTTAGCCCACAA   41320        CGT  AAAC
                                TTGTGGGCTA   GG   CCT
                                ||||||||||   ||   |||
                                AACACCCGAT   CC   GGA
                                     T__  GTA_
GAM234  LOC90485  3' AGGGCCTCCTTTCCAACCTCAC 63688        CTACG    _____
           AATG                   CATTGTGGG    TGGAAA    CCCT
                                |||||||||    ||||||    ||||
                                GTAACACTC    ACCTTT    GGGA
                                     CA___     CCTCC
GAM235  LAMC3    3' CGGCACACACTCCCCCAC    21344    C   A   CGACA
                                GTG GGG AGT    TGTGCCG
                                ||| ||| |||    |||||||
                                CAC CCC TCA    ACACGGC
                                  _   C   C____
GAM235  C1orf21   5' CCGCGCGCCGCCGCCTCCCGCA 48689        A T  ACAT   _
           C                    GTGCGGGA G CG   GTGC CGG
                                |||||||| | ||   |||| |||
                                CACGCCCT C GC    CGCG GCC
                                     C _  CGC_   C
GAM235  FLJ20584  3' CCGTCGTGGCCGCCTCCCGCAC 35853        A T  A_   TGC
                                GTGCGGGA G CG  CATG   CGG
                                |||||||| | ||  ||||   |||
                                CACGCCCT C GC  GTGC   GCC
                                     C _  CG   T__
GAM235  FLJ22021  3' CCGGCACATGTCACCCCTGCAC 44884        AA  C
                                GTGCGGG  GT GACATGTGCCGG
                                |||||||  || ||||||||||||
                                CACGTCC  CA CTGTACACGGCC
                                    C_  _
GAM235  FLJ32762  5' CCAGTCACCCGACTTCCCACA  59483    C       ACAT   _ C
                                TG GGGAAGTCG    GTG C GG
                                || |||||||||    ||| | ||
                                AC CCCTTCAGC    CAC G CC
                                 A        C___   T A
GAM235  TRIM29    3' CCGGCCTCTCCGACTTCCCCAC 25008     C       ACATGT
                                GTG GGGAAGTCG     GCCGG
                                ||| |||||||||     |||||
                                CAC CCCTTCAGC     CGGCC
                                  _        CTCTC_
GAM235  LOC124460 5' CTGGCCCCGACCTCCCGCAC   76560        A    ACATGT
                                GTGCGGGA GTCG     GCCGG
                                |||||||| ||||     |||||
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                                CACGCCCT CAGC     CGGTC
                                     C   CC____
GAM235  LOC170221 5'  CGCCAACCTTCCCGCAC    83466         TCGACA  T  C
                                GTGCGGGAAG     TG GC G
                                ||||||||||     || || |
                                CACGCCCTTC     AC CG C
                                     CA____  _  C
GAM236  GPD1     3'  TCATGCCACCACATTTG     60398       C       C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A       _
GAM236  IL5RA    5'  TCGCATGGCCACCGCATTT   6906           AT__
                                AAATGCGGTGGC   CGA
                                ||||||||||||   |||
                                TTTACGCCACCG   GCT
                                       GTAC
GAM236  MYO1C    3'  TGCCGATGCCAAATATTTG   61873       CGG      A
                                TAAATG   TGGCATCG CA
                                ||||||   |||||||| ||
                                GTTTAT   ACCGTAGC GT
                                   AA_       C
GAM236  C6orf37  3'  TGTCACACTGCATTTA      68097          GCATC
                                TAAATGCGGTG    GACA
                                ||||||||||     ||||
                                ATTTACGTCAC    CTGT
                                      A____
GAM236  DNAJC6   3'  TTGCAGAACCACCGCATT    29498         CA  GA
                                AATGCGGTGG  TC  CAA
                                ||||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                      A_  AC
GAM236  FLJ11210 3'  GTCGATGTGCATGCTTTTA   60319     T   GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM236  FLJ12476 3'  TCGATCTTCTGCATTTA     43270         T  C
                                TAAATGCGG GG ATCGA
                                ||||||||| || |||||
                                ATTTACGTC TC TAGCT
                                      T  _
GAM236  KIAA1034 3'  TCGATGGCATCCGCATTTG   63134         _  G
                                TAAATGCGG TG CATCGA
                                ||||||||| || ||||||
                                GTTTACGCC AC GTAGCT
                                      T  G
GAM236  KIAA1987 3'  TCATGTAACTGCATTTA     89391          G   C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
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                                ATTTACGTCA TGTA CT
                                     A   _
GAM236  MGC16063  3'  TGTCCTGGCCACTGCATT    54929          ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                     GTC
GAM236  LOC147949 3'  TGTCAGATGTCCACATTGCA   79279     __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM236  LOC150577 3'  GTCCTCACCGCATTTG      86258          CATC
                                TAAATGCGGTGG    GAC
                                ||||||||||||    |||
                                GTTTACGCCACT    CTG
                                     C___
GAM236  LOC158219 3'  TGTGTGTCACCACATTT     82694      C       CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                   A       __
GAM236  LOC202020 3'  TGTCTCACCACATTTA      90605       C    CATC
                                TAAATG GGTGG    GACA
                                |||||| |||||    ||||
                                ATTTAC CCACT    CTGT
                                   A    _____
GAM236  LOC90826  5'  TGTCGATGCAGGTTTATTTG  64788       CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                   TTGGA
GAM236  LOC93587  3'  TTGTCTTTACCTGCATTTA   73042       _    CATC
                                TAAATGC GGTGG    GACAA
                                ||||||| |||||    |||||
                                ATTTACG CCATT    CTGTT
                                     T    T___
GAM237  ELF3      3'  TGACCTTGACCTTGACCAA   16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                   _    AGT  ___
GAM237  JAK2      3'  TGACCTTCATTCTGAGACCAA  18318       CAA      AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_       C_
GAM237  SLC10A2   5'  ACTCTCTGTCTTGACCAA    6590        CAA       A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
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                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM237  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM237  KIAA1958  5'  GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                GGTT   GGG   AAAGTCAC
                                ||||   |||   ||||||||
                                CCAA   CCC   TTTCAGTG
                                  A__   CAAG
GAM237  MARCKS    3'  ACTTTCCACCCTGCCCA     11411     TTCA   A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM237  TUB       5'  GTGGGACCATCCCTTAAACC   13898     C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A       AG__
GAM237  LOC80298  3'  ACTTTTACCTTGAACCA     48062         GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                     A___
GAM238  ALEX1     5'  TCCTAGTCTTCGTTTGG     33975        A  CCAC
                                TCAAACGAA AC    AGGA
                                ||||||||| ||    ||||
                                GGTTTGCTT TG    TCCT
                                     C  A___
GAM238  B4GALT3   3'  GGTCTCCTGTAGGGCTTATG   15029    A  A   _
                                CG AA CCC ACAGGAGACC
                                || || ||| ||||||||||
                                GT TT GGG TGTCCTCTGG
                                 A  C   A
GAM238  BACH1     3'  TTGTGGGTTTGCATTTGA    8635       CGA
                                TCAAA   AAACCCACAG
                                |||||   ||||||||||
                                AGTTT   TTTGGGTGTT
                                   ACG
GAM238  CBR1      3'  GGTCTTTTGTGATTTCCTCTGA 10043     AAC    ACC
                                TCA   GAAA   CACAGGAGACC
                                |||   ||||   ||||||||||
                                AGT   CTTT   GTGTTTTCTGG
                                  CTC    A__
GAM238  DACH      3'  TTGTGGGTTTTCTCCTGA    55827     AAC
                                TCA   GAAAACCCACAG
                                |||   ||||||||||
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                                AGT   CTTTTGGGTGTT
                                  CCT
GAM238  H3F3B    3'  TCCAGTTGGTTTTCTTCTGA   19222     AAC      C  A
                                TCA   GAAAACC AC GGA
                                |||   ||||||| || |||
                                AGT   CTTTTGG TG CCT
                                  CTT      T  A
GAM238  IMPA2    3'  TCTCCTGTGAAATACGTATTGA 96949      _   AAAACC
                                TCAA ACG     CACAGGAGA
                                |||| |||     |||||||||
                                AGTT TGC     GTGTCCTCT
                                  A  ATAAA_
GAM238  MCM2     3'  GTCTCCTGCAGGTTTCTGT   68522     A    CA
                                ACG AAACC  CAGGAGAC
                                ||| |||||  ||||||||
                                TGT TTTGG  GTCCTCTG
                                  C    AC
GAM238  MEF2D    3'  TTCTTATGAGTTTTGTTTGA   98697       G    C  C
                                TCAAAC AAAAC CA AGGAG
                                |||||| ||||| || |||||
                                AGTTTG TTTTG GT TTCTT
                                   _    A  A
GAM238  PML      3'  CTCTGGTTTTCTTTGA      53821       C      CACA
                                TCAAA GAAAACC    GGAG
                                ||||| |||||||    ||||
                                AGTTT CTTTTGG    TCTC
                                  _      _____
GAM238  PON1     3'  GTGCTGGTGGGTTTTTGTTT   6538             A  AG
                                AAACGAAAACCCAC GG  AC
                                |||||||||||||| ||  ||
                                TTTGTTTTTGGGTG TC  TG
                                       G  G_
GAM238  SERPINB13 3'  TCTCCCCTTTGGTTTCCTTTGA 25698       C    A  CACA_
                                TCAAA GAAA CC    GGAGA
                                ||||| |||| ||    |||||
                                AGTTT CTTT GG    CCTCT
                                  C    _  TTTCC
GAM238  TM4SF6   3'  GTCTTAGTTTTCGTTTG     13797          CCACAG
                                CAAACGAAAAC     GAGAC
                                ||||||||||      |||||
                                GTTTGCTTTTG     TTCTG
                                      A_____
GAM238  FLJ13204 3'  CCTAAATGAGTTTTCGTTGA   45758      A      C  C__
                                TCAA CGAAAAC CA   AGG
                                |||| ||||||| ||   |||
                                AGTT GCTTTTG GT   TCC
                                  _      A  AAA
GAM238  FLJ13213 3'  TCTCCTGTAAACTTTACTTGA  45731      ACG   ACCC
                                TCAA   AAA    ACAGGAGA
                                ||||   |||    ||||||||
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                                AGTT   TTT    TGTCCTCT
                                  CA_   CAAA
GAM238  FLJ20373  3'  GGTTATTTAGGTTTTCGT    35542         CAC   A
                                ACGAAAACC   AGG GACC
                                |||||||||   ||| ||||
                                TGCTTTTGG   TTT TTGG
                                     A__   A
GAM238  FLJ23093  5'  CCTGGGGTTTTCCCTGA     45324     AAC       A
                                TCA   GAAAACCC CAGG
                                |||   |||||||| ||||
                                AGT   CTTTTGGG GTCC
                                  CC_       _
GAM238  FUSIP1    3'  GCTCATTGTTTTGTTTGA     22782         AACCC   _  A
                                TCAAACGAA     ACAG GAG C
                                |||||||||     |||| ||| |
                                AGTTTGTTT     TGTT CTC G
                                     _____    A   C
GAM238  HELO1     3'  TCTTGTGGGTTTTCTGTTTGA  41798       _
                                TCAAAC GAAAACCCACAGGA
                                |||||| ||||||||||||||
                                AGTTTG CTTTTGGGTGTTCT
                                   T
GAM238  HERPUD1   3'  CTTTGCTGGGTTTTCTGTT    28694     _       CA
                                AAC GAAAACCCA  GGAG
                                ||| |||||||||  ||||
                                TTG CTTTTGGGT  TTTC
                                  T        CG
GAM238  KIAA0534  5'  GTCTTCTGTTTTCATTTGA    71935      C    ACCC
                                TCAAA GAAA    ACAGGAGAC
                                ||||| ||||    |||||||||
                                AGTTT CTTT    TGTCTTCTG
                                   A   ____
GAM238  KIAA0995  5'  GGTCTCCTCCTCCTCGTTTG   73253        AAACCCAC
                                CAAACGA       AGGAGACC
                                |||||||       ||||||||
                                GTTTGCT       TCCTCTGG
                                    CCTCC___
GAM238  KIAA1550  3'  GGTCTCCTTGCCCTCTCCTTGA 67154      AC  AAACC  C
                                TCAA  GA    CA AGGAGACC
                                ||||  ||    || ||||||||
                                AGTT  CT    GT TCCTCTGG
                                  C_  CTCCC  _
GAM238  KIAA1674  3'  TCTGTGGATTTTGTCTGA     69349     A     AC
                                TCA ACGAAA  CCACAGG
                                ||| ||||||  |||||||
                                AGT TGTTTT  GGTGTCT
                                  C     A_
GAM238  SEC15B    3'  CTCCTGTACTCTTTCGTTT    67264         ACCC
                                AAACGAAA    ACAGGAG
                                ||||||||    |||||||
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                                TTTGCTTT   TGTCCTC
                                    CTCA
GAM238  SYT13    3'  TCTCCTGTGAGTCATTGGCTGG 95108    AA  AA  C
                                TCA  CGA  AC CACAGGAGA
                                ||| |||  || |||||||||
                                GGT  GTT  TG GTGTCCTCT
                                  CG   AC  A
GAM238  TNKS1BP1 3'  CTCCCTTGGGTTTTCTTTTGA  54149      C       CA
                                TCAAA GAAAACCCA  GGAG
                                ||||| |||||||||  ||||
                                AGTTT CTTTTGGGT  CCTC
                                   T        TC
GAM238  LOC123342 3'  CCTGGAAGGTTTTCTTTGA   76125      C      CA_
                                TCAAA GAAAACC   CAGG
                                ||||| |||||||   ||||
                                AGTTT CTTTTGG   GTCC
                                   _      AAG
GAM238  LOC145622 3'  GGTCTCCTGTGAACTTTC    77822     ACC
                                GAAA   CACAGGAGACC
                                ||||   ||||||||||||
                                CTTT   GTGTCCTCTGG
                                  CAA
GAM238  LOC150166 5'  GTCTCCTGTCTCATGGTTTGA  86043       GAAAACCC
                                TCAAAC       ACAGGAGAC
                                ||||||       |||||||||
                                AGTTTG       TGTCCTCTG
                                    GTACTC__
GAM238  LOC150606 3'  CTTTACTGGGTTTTCTGTTTGA 86268       _       CA
                                TCAAAC GAAAACCCA  GGAG
                                |||||| |||||||||  ||||
                                AGTTTG CTTTTGGGT  TTTC
                                    T        CA
GAM238  LOC166042 5'  GGTTTTTTGTGGGTTCTCG   83507     A
                                CGA AACCCACAGGAGACC
                                ||| ||||||||||||||
                                GCT TTGGGTGTTTTTTGG
                                  C
GAM238  LOC256691 3'  GGTCTTGCAGGTTTCCTTTTGA 97923      CGA    CA  GG
                                TCAAA   AAACC  CA  AGACC
                                |||||   |||||  ||  |||||
                                AGTTT   TTTGG  GT  TCTGG
                                   TCC    AC  __
GAM238  LOC256946 3'  GCTCATTGTTTTGTTTGA    96184        AACCC   _   A
                                TCAAACGAA    ACAG GAG C
                                |||||||||    |||| ||| |
                                AGTTTGTTT    TGTT CTC G
                                     _____   A   C
GAM239  CASP2    3'  GATGTCTTGAGAGACCATCTCC 8712        CCAC_  CC
                                GGAGATGG    CG  GCATC
                                ||||||||    ||  |||||
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                                CCTCTACC    GT  TGTAG
                                    AGAGA  TC
GAM239  CD28    3'  AGGAAATGACCGCCATCTCC  21548        CACCGC  CA
                                GGAGATGGC     CG  TCCT
                                |||||||||     ||  ||||
                                CCTCTACCG     GT  AGGA
                                    CCA___  AA
GAM239  CDH23   5'  GACGCGGCGGTGGCCAGGGCC  42355    AGA          A
                                GG   TGGCCACCGCCGC TC
                                ||   |||||||||||||  ||
                                CC   ACCGGTGGCGGCG AG
                                 GGG          C
GAM239  CDH23   5'  GACGCGGCGGTGGCCAGGGCC  54516    AGA          A
                                GG   TGGCCACCGCCGC TC
                                ||   |||||||||||||  ||
                                CC   ACCGGTGGCGGCG AG
                                 GGG          C
GAM239  E2F3    3'  GTGGCAGCGGCCATCTCC    10470          ACC
                                GGAGATGGCC   GCCGC
                                ||||||||||   |||||
                                CCTCTACCGG   CGGTG
                                    CGA
GAM239  EPHA3   3'  AGAATGCTTACGGCCATCTCT  19101          ACCGCC    C
                                GGAGATGGCC     GCAT CT
                                ||||||||||     ||||  ||
                                TCTCTACCGG     CGTA GA
                                    CATT__    A
GAM239  IMMP2L  5'  AGGCGCGTGCGGCGGCCACCCC 51704    AGA    A   _   AT
                                GG   TGGCC CCGC CGC  CCT
                                ||   ||||| |||| |||  |||
                                CC   ACCGG GGCG GCG  GGA
                                 CC_    C    T   C_
GAM239  MS4A4A  3'  GATGCATGGCCATCTCC     44005          CCGCC
                                GGAGATGGCCA    GCATC
                                ||||||||||     |||||
                                CCTCTACCGGT    CGTAG
                                    A_____
GAM239  PTHLH   3'  GAAGCTAGTGACCATCTTC    12545        C   CGCC  A
                                GGAGATGG CAC    GC TC
                                |||||||| |||    || ||
                                CTTCTACC GTG    CG AG
                                    A   AT__  A
GAM239  TCF2    3'  AGGATGGCACTCCGGCCACCTC 22401     A    ACC__   GC
          C                      GGAG TGGCC    GCC  ATCCT
                                ||||  |||||    |||  |||||
                                CCTC ACCGG    CGG  TAGGA
                                  C    CCTCA   __
GAM239  TCOF1   3'  GCCGAGCAGTGGCCATCCC   6269     A       C  _  _
                                GG GATGGCCAC GC CG C
                                || |||||||| || || |
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                                CC CTACCGGTG CG GC G
                                 _       A  A  C
GAM239  BDG-29   3' AGGGGGCAGTGGCCATC     72802         C   GCA
                                GATGGCCAC GCC   TCCT
                                ||||||||| |||   ||||
                                CTACCGGTG CGG   GGGA
                                     A  ___
GAM239  FLJ14166 3' AGGATGGCTTGGTGGCCGTCCC 44985    A         CCG
                                GG GATGGCCACCG   CATCCT
                                || ||||||||||   ||||||
                                CC CTGCCGGTGGT   GTAGGA
                                 _         TCG
GAM239  FLJ23451 5' TGCGGCGGTGGCACCTCC    45790     ATG
                                GGAG   GCCACCGCCGCA
                                ||||   ||||||||||||
                                CCTC   CGGTGGCGGCGT
                                  CA_
GAM239  MGC33182 5' GCCTCGGTGGCCATTTCC    76095           CC
                                GGAGATGGCCACCG  GC
                                ||||||||||||||  ||
                                CCTTTACCGGTGGC  CG
                                       TC
GAM239  NYD-SP25 3' GTGAGGATGACCATCTCC    54304         C  _  GC
                                GGAGATGG CA CC  CGC
                                |||||||| || ||  |||
                                CCTCTACC GT GG  GTG
                                     A  A  A_
GAM239  PIGM     5' GATGCGGCGGCCACCTGC    59717    G  A    ACC
                                G AG TGGCC   GCCGCATC
                                | || |||||   ||||||||
                                C TC ACCGG   CGGCGTAG
                                 G  C    ___
GAM239  USP2     3' AGGAGCCGGCGCCCATCTCC   16109         CCAC    CA
                                GGAGATGG    CGCCG  TCCT
                                ||||||||    |||||  ||||
                                CCTCTACC    GCGGC  AGGA
                                     C___     CG
GAM239  ZNF340   5' AGGTGGGCGCGGTGGCCTCCTC 85710      AT       C  AT_
           C                     GGAG  GGCCACCGC GC   CCT
                                ||||  |||||||||  ||   |||
                                CCTC  CCGGTGGCG CG   GGA
                                  CT        _  GGT
GAM239  LOC146059 3' AGGAGCTGGACTGCCATCTCC  78084          CACCG  _  A
                                GGAGATGGC     CC GC TCCT
                                |||||||||     || || ||||
                                CCTCTACCG     GG CG AGGA
                                     TCA__  T  _
GAM239  LOC146856 3' GTGGCAGTGGTCATCTCC     83704           C
                                GGAGATGGCCAC GCCGC
                                |||||||||||| |||||
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                                CCTCTACTGGTG CGGTG
                                      A
GAM239  LOC148171 5'  AGGCCTCACGGTGGCCTCTCC  79427      T      CCGCAT
                                GGAGA GGCCACCG     CCT
                                ||||| ||||||||     |||
                                CCTCT CCGGTGGC     GGA
                                  _       ACTCC_
GAM239  LOC148181 3'  AGGCCTCGCGGTGGCCTCTCC  79429      T       CGCAT
                                GGAGA GGCCACCGC    CCT
                                ||||| |||||||||    |||
                                CCTCT CCGGTGGCG    GGA
                                  _       CTCC_
GAM239  LOC149124 5'  AGGCCTCACGGTGGCCTCTCC  79920      T      CCGCAT
                                GGAGA GGCCACCG     CCT
                                ||||| ||||||||     |||
                                CCTCT CCGGTGGC     GGA
                                  _       ACTCC_
GAM239  LOC150183 5'  AGGATGCGGGACTCCCCTCC   86073     AT  CCACCG
                                GGAG  GG     CCGCATCCT
                                ||||  ||     |||||||||
                                CCTC  CC     GGCGTAGGA
                                  C_  TCAG__
GAM239  LOC150184 5'  AGGATGCGGGACTCCCCTCC   86074     AT  CCACCG
                                GGAG  GG     CCGCATCCT
                                ||||  ||     |||||||||
                                CCTC  CC     GGCGTAGGA
                                  C_  TCAG__
GAM239  LOC150185 5'  AGGATGCGGGACTCCCCTCC   86060     AT  CCACCG
                                GGAG  GG     CCGCATCCT
                                ||||  ||     |||||||||
                                CCTC  CC     GGCGTAGGA
                                  C_  TCAG__
GAM239  LOC157247 5'  AGGATGTACCAGACAGTCATCT 82285         CACCGCC_
          CC                    GGAGATGGC       GCATCCT
                                |||||||||       |||||||
                                CCTCTACTG       TGTAGGA
                                     ACAGACCA
GAM239  LOC158515 5'  GGAGGGTCAGCCATCTCC    83430        CACC   GCA
                                GGAGATGGC    GCC   TCC
                                |||||||||    |||   |||
                                CCTCTACCG    TGG   AGG
                                     AC__    G__
GAM239  LOC202899 5'  AGGCGCGTGCGGCGGCCACCCC 92013     AGA    A   _   AT
                                GG   TGGCC CCGC CGC  CCT
                                ||   ||||| |||| |||  |||
                                CC   ACCGG GGCG GCG  GGA
                                 CC_     C    T   C_
GAM239  LOC255645 3'  AGGACGAGGGGGAGCCATCTCC 98472         CA  G  GCA
                                GGAGATGGC  CC CC   TCCT
                                |||||||||  || ||   ||||
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                                CCTCTACCG  GG GG   AGGA
                                     AG  _  AGC
GAM239  LOC255939 5'  GACGCGGCAACGGTGGTCCCTC 99297      AT      ___     A
          C                    GGAG  GGCCACC   GCCGC TC
                               ||||  |||||||   ||||| ||
                               CCTC  CTGGTGG   CGGCG AG
                                 C_      CAA     C
GAM239  LOC91828  5'  GCGGCCGGCGCCATCTCC     67860         CA  _
                               GGAGATGGC  CCG CCGC
                               |||||||||  ||| ||||
                               CCTCTACCG  GGC GGCG
                                     C_   C
GAM239  LOC92080  3'  GAGCACGGTGGCCACCCC     68630     AGA       CC  A
                               GG   TGGCCACCG  GC TC
                               ||   |||||||||  || ||
                               CC   ACCGGTGGC  CG AG
                                CC_       A_  _
GAM239  LOC92340  3'  GAAGTTGCGGTGGCCATCCTC  69561    GA         C  A
                               G  GATGGCCACCGC GC TC
                               |  ||||||||||||| || ||
                               C  CTACCGGTGGCG TG AG
                                TC          T  A
GAM239  LOC92405  5'  GGCCGGGGACGACACCATCTCC 69715         _______  A  _
                               GGAGATGG     CC CCG CC
                               ||||||||     || ||| ||
                               CCTCTACC     GG GGC GG
                                     ACAGCA  _   C
GAM239  LOC93349  3'  GGAACGGTGGCCATTTCC     57270            CCGCA
                               GGAGATGGCCACCG     TCC
                               ||||||||||||||     |||
                               CCTTTACCGGTGGC     AGG
                                        A____
GAM240  HSPC126   3'  TGACTTTCTTTTTAAAGCCAA  27177       CAAAG   T
                               TTGGTT     GGA GGAAAGTCA
                               ||||||     ||| |||||||||
                               AACCGA     TTT TCTTTCAGT
                                  AA___   T
GAM240  JAK2      3'  TGACCTTCATTCTGAGACCAA  18319       CAAA       AA
                               TTGGTT    GGGATGGA  GTCA
                               ||||||    ||||||||  ||||
                               AACCAG    TCTTACTT  CAGT
                                  AG__       C_
GAM240  SLC10A2   5'  ACTCTCTGTCTTGACCAA     6591        CAAA       A
                               TTGGTT    GGGATGGA AGT
                               ||||||    |||||||| |||
                               AACCAG    TTCTGTCT TCA
                                  ____       C
GAM240  FLJ23142  5'  ACTTTCCATAACAACCAA     45025       CAAAGGG
                               TTGGTT      ATGGAAAGT
                               ||||||      |||||||||
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                                AACCAA      TACCTTTCA
                                   CAA____
GAM240  KIAA0793  3'  TGACCTTCCATCTGGTGAACCA 29696        AAG       A
              A                    TTGGTTCA   GGATGGAA GTCA
                                   ||||||||   |||||||| ||||
                                   AACCAAGT   TCTACCTT CAGT
                                        GG_       C
GAM240  KIAA1228  3'  ACTTTTCTACCTTGAGCCAA   65664         A  GAT
                                   TTGGTTCAA GG   GGAAAGT
                                   |||||||||  ||   |||||||
                                   AACCGAGTT CC   CTTTTCA
                                         _  AT_
GAM240  MGC22014  3'  ACTTCAACATACCCTGGACCAA 65108        AA  _   GA_
                                   TTGGTTCA  GGG ATG   AAGT
                                   ||||||||  ||| |||   ||||
                                   AACCAGGT  CCC TAC   TTCA
                                        __   A   AAC
GAM240  LOC152313 3'  TGAAGGATCCATCCCCCTGATC 86854      T   AA       AAG_
              CAA                     TTGG TCA  GGGATGGA    TCA
                                   ||||  |||  ||||||||    |||
                                   AACC AGT  CCCTACCT    AGT
                                     T   CC       AGGA
GAM240  LOC163590 3'  TGACTTTTTTTCTTTGGACCAA 59510          GG TG
                                   TTGGTTCAAAG  A  GAAAGTCA
                                   ||||||||||  |  ||||||||
                                   AACCAGGTTTC  T  TTTTCAGT
                                         TT __
GAM240  LOC254065 3'  GACTCTGACTCTGAATCAA    99290        AA   A    AA
                                   TTGGTTCA  GGG TGGA  GTC
                                   ||||||||  ||| ||||  |||
                                   AACTAAGT  CTC GTCT  CAG
                                        __   A   __
GAM240  LOC80298  3'  ACTTTTACCTTGAACCA     48063         A  GATG
                                   TGGTTCAA GG    GAAAGT
                                   |||||||| ||    ||||||
                                   ACCAAGTT CC    TTTTCA
                                        _  A___
GAM241  ARHD     3'  GCCGAACTCCACTGCAACAGA  28147          CA_  C  T
                                   TCTGTTGCAG   GG TC GC
                                   ||||||||||   || || ||
                                   AGACAACGTC   TC AG CG
                                         ACC  A  C
GAM241  UBE3A    3'  GTCAAGCCTATTGCAACA    56441         C     CT
                                   TGTTGCAG AGGCT  GC
                                   |||||||| |||||  ||
                                   ACAACGTT TCCGA  TG
                                        A     AC
GAM241  UBE3A    3'  GTCAAGCCTATTGCAACA    56445         C     CT
                                   TGTTGCAG AGGCT  GC
                                   |||||||| |||||  ||
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                                ACAACGTT TCCGA  TG
                                    A     AC
GAM241  UBE3A    3'  GTCAAGCCTATTGCAACA    6627         C     CT
                                TGTTGCAG AGGCT  GC
                                |||||||| |||||  ||
                                ACAACGTT TCCGA  TG
                                    A     AC
GAM241  UBL1     3'  CATGCAGAAATGAATACAACAG 13973        CAG_  GGC
              A                  TCTGTTG   CA  TCTGCATG
                                 |||||||   ||  ||||||||
                                 AGACAAC   GT  AGACGTAC
                                    ATAA  AA_
GAM241  BIKE     3'  CATGCAACACAGCAGCAACAGA 34603         A  AGGCTC
                                TCTGTTGC GC     TGCATG
                                |||||||| ||     ||||||
                                AGACAACG CG     ACGTAC
                                    A  ACACA_
GAM241  FLJ12057 3'  GCATGCCTGCTGCAACGGA   45795             TC
                                TCTGTTGCAGCAGGC  TGC
                                |||||||||||||||  |||
                                AGGCAACGTCGTCCG  ACG
                                         T_
GAM241  KIAA0152 3'  GCTTTCCAGCCTGCAGCAACAG 28978         A      CT___
              A                  TCTGTTGC GCAGGCT    GC
                                 |||||||| |||||||    ||
                                 AGACAACG CGTCCGA    CG
                                    A      CCTTT
GAM241  KIAA0947 3'  CATGCAGAGCCCTTAGCAGA   62202        C  CA
                                TCTGTTG AG  GGCTCTGCATG
                                |||||||  ||  ||||||||||
                                AGACGAT TC  CCGAGACGTAC
                                   _  __
GAM241  KIAA1649 3'  GCACTCCAGCCTGTGCAACAGA 51240         G     C___
                                TCTGTTGCA CAGGCT    TGC
                                ||||||||| ||||||    |||
                                AGACAACGT GTCCGA    ACG
                                    _     CCTC
GAM241  MGC15631 3'  GCACTCCAGCCTGTGCAACAGA 52232         G     C___
                                TCTGTTGCA CAGGCT    TGC
                                ||||||||| ||||||    |||
                                AGACAACGT GTCCGA    ACG
                                    _     CCTC
GAM241  MRPL34   3'  GCATTTCGAACCTGCGCAACAG 43977         A    C  TGC
              A                  TCTGTTGC GCAGG TC   ATGC
                                 |||||||| ||||| ||   ||||
                                 AGACAACG CGTCC AG   TACG
                                    _    A  CTT
GAM241  PRO2949  5'  GCATACAGTTTCTGCAACG   38223         C    C__
                                TGTTGCAG AGGCT   TGC
                                |||||||| |||||   |||
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                                GCAACGTC TTTGA   ACG
                                   _    CAT
GAM241  RAB35    3'  GCCAGCCTGCTGCAACAGA   23415            CT
                                TCTGTTGCAGCAGGCT  GC
                                ||||||||||||||||  ||
                                AGACAACGTCGTCCGA  CG
                                     C_
GAM241  SLC39A3  3'  CACAGCCTTCTGCTGCAGCAGA 58599          ___   C
                                TCTGTTGCAGCA   GGCT TG
                                ||||||||||||   |||| ||
                                AGACGACGTCGT   CCGA AC
                                      CTT    C
GAM241  LOC148918 5'  GCATGTCTGCTGCACCAGA    79829      T        TC
                                TCTG TGCAGCAGGC  TGC
                                |||| ||||||||||  |||
                                AGAC ACGTCGTCTG  ACG
                                  C        T_
GAM241  LOC257480 3'  CAGATTGAGGGGCTGCAACAGA 78432          AGG   TGCA
                                TCTGTTGCAGC   CTC    TG
                                ||||||||||   |||    ||
                                AGACAACGTCG   GAG    AC
                                      GG_   TTAG
GAM242  SEMA3E   3'  GATAAGTCACCATGCTTCAAA  25809      TCATC    AC
                                TTTGA    TATG  GACTTATC
                                |||||    ||||  ||||||||
                                AAACT    GTAC  CTGAATAG
                                   TC___    CA
GAM242  LOC146515 3'  TGTCAGTAGATGACCAAA    78521      A      _
                                TTTG TCATCTA TGACG
                                |||| ||||||| |||||
                                AAAC AGTAGAT ACTGT
                                  C      G
GAM243  AF3P21   3'  ACACCCATGTGTACACTCAG   33613     C    A   TG   A
                                CTG AGTG TAT  ATG GTGT
                                ||| |||| |||  ||| ||||
                                GAC TCAC ATG  TAC CACA
                                  _   _  TG   C
GAM243  FOP      3'  CTACACTCAGTTTCATTACAG  23866     C    TATTGA
                                CTG AGTGA     TGAGTGTAG
                                ||| |||||     |||||||||
                                GAC TTACT     ACTCACATC
                                  A    TTG___
GAM243  ITGA6    3'  CTACACTCACCTGCACTAACAG 5788      C_   ATATTGA
                                CTG  AGTG     TGAGTGTAG
                                |||  ||||     |||||||||
                                GAC  TCAC     ACTCACATC
                                  AA   GTCC___
GAM243  C20orf39  3'  CTACACTCCACAGCTACCCCGC 46574      A__   ATA   AT
           AG                   CTGC   GTG   TTG  GAGTGTAG
                                ||||   |||   |||  ||||||||
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                                GACG  CAT  GAC CTCACATC
                                  CCC  C__  AC
GAM243  FLJ13089  5'  ACAGATGACAACTCACTGCAG 71426       TA  ATGAG
                                CTGCAGTGA TTG   TGT
                                |||||||||  |||   |||
                                GACGTCACT AAC   ACA
                                    C_  AGTAG
GAM243  FLJ13154  3'  ACACTCACCAGAATCTCCACTG 45100      ___  A  A
          TAG                    CTGCAGT  GAT TTG TGAGTGT
                                |||||||  ||| ||| |||||||
                                GATGTCA  CTA GAC ACTCACA
                                    CCT  A  C
GAM244  GRIA2    3'  GCGTGGTGGACATGCACAGCT  7708     CA       AG
                                AGC  TGCATGTCTA  TACGC
                                |||  ||||||||||  |||||
                                TCG  ACGTACAGGT  GTGCG
                                  AC       G_
GAM244  PSMA2    3'  GCATACTTATTTCTACATGGTT 12451       CATGTC    C
          TA                    TAAGCCATG    TAAGTA GC
                                |||||||||     |||||| ||
                                ATTTGGTAC    ATTCAT CG
                                    ATCTTT    A
GAM244  FLJ20150  3'  GCACACCTGGGGTGATGGCTTA 35143       G  G  TAA  AC
                                TAAGCCAT CAT TC  GT  GC
                                |||||||| ||| ||  ||  ||
                                ATTCGGTA GTG GG  CA  CG
                                    _  G  TC_  CA
GAM244  KIAA1881  3'  GCGCAGGCAGCACAGCTTA   97086     CA  A   AA
                                TAAGC  TGC TGTCT  GT
                                |||||  ||| |||||  ||
                                ATTCG  ACG ACGGA  CG
                                  AC  _    CG
GAM244  RIL      3'  GCGCAGGCCATGCATGGCT   14886         _  AA
                                AGCCATGCATG TCT  GT
                                ||||||||||| |||  ||
                                TCGGTACGTAC GGA  CG
                                    C  CG
GAM244  LOC144438 3'  GCATACTCCTCCACATACATGG 77326       C   CTA__   C
          CTT                    AAGCCATG ATGT    AGTA GC
                                |||||||| ||||    |||| ||
                                TTCGGTAC TACA    TCAT CG
                                    A   CCTCC   A
GAM244  LOC152317 5'  TTTAAACATCATGGCTTA   86840       C   C
                                TAAGCCATG ATGT TAAG
                                ||||||||| |||| ||||
                                ATTCGGTAC TACA ATTT
                                    _   A
GAM244  LOC154789 5'  GCGCACCTGGGGCGTGGCTTA  82030        ATG   A  A
                                TAAGCCATGC   TCTA GT CGC
                                ||||||||||   |||| || |||
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                                ATTCGGTGCG  GGGT CA GCG
                                    ___   C  C
GAM244  LOC257428 3'  ACCTGTACAGCATGGTT    95930       A  C  A
                                AGCCATGC TGT TA GT
                                |||||||| ||| || ||
                                TTGGTACG ACA GT CA
                                    _  T  C
GAM245  KCNJ10   3'  ATCTGATATCAACATATCC   11153     C  GCATT
                                GGATG GT    TATCAGAT
                                ||||| ||    ||||||||
                                CCTAT CA    ATAGTCTA
                                   A  ACT__
GAM245  AK5      3'  ATCTGATAAATTGTGTAACC  24929    A   GT C
                                GG TGC  G ATTTATCAGAT
                                || |||  | ||||||||||
                                CC ATG  T TAAATAGTCTA
                                 A   TG _
GAM245  CBLN1    3'  ATCTGATATATTACACACCC  16367    A  C   C  T
                                GG TG GTG AT TATCAGAT
                                || || ||| || ||||||||
                                CC AC CAT TA ATAGTCTA
                                 C  A   _  T
GAM245  FLJ10283  3'  ATCTGACTATACGCATCC    36429       CATTTA
                                GGATGCGTG     TCAGAT
                                |||||||||     ||||||
                                CCTACGCAT     AGTCTA
                                     ATC___
GAM245  KIAA1843  3'  ATCTGATAAACAGGTTTC    62881    T  G  CA
                                GA GC TG  TTTATCAGAT
                                || || ||  ||||||||||
                                CT TG AC  AAATAGTCTA
                                 T  G  __
GAM245  LOC205327 3'  GATCTAATAAATGTCAACC    91069    A  CGT      C
                                GG TG   GCATTTAT AGATC
                                || ||   |||||||| |||||
                                CC AC   TGTAAATA TCTAG
                                 A  ___       A
GAM246  ABR      3'  GGTAGTGACCGGCCCGG     8455        A   ACGC
                                TCGGGCCG TCGC    ACC
                                |||||||| ||||    |||
                                GGCCCGGC AGTG    TGG
                                     C    A___
GAM246  ABR      3'  GGTAGTGACCGGCCCGG     42007       A   ACGC
                                TCGGGCCG TCGC    ACC
                                |||||||| ||||    |||
                                GGCCCGGC AGTG    TGG
                                     C    A___
GAM246  ATP12A   5'  GGAGGTGCGTGCAGGGCCCG  9816       GATC      _
                                CGGGCC    GCACGCACC CC
                                ||||||    ||||||||| ||
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                                GCCCGG   CGTGCGTGG GG
                                   GA__       A
GAM246  BMP4    5'  GGAGCGCGGAGCCCGGCCCGG  56464       ATC  A_  ACC
                                TCGGGCCG  GC  CGC  CC
                                ||||||||  ||  |||  ||
                                GGCCCGGC  CG  GCG  GG
                                    C__  AG  CGA
GAM246  BMP4    5'  GGAGCGCGGAGCCCGGCCCGG  8662        ATC  A_  ACC
                                TCGGGCCG  GC  CGC  CC
                                ||||||||  ||  |||  ||
                                GGCCCGGC  CG  GCG  GG
                                    C__  AG  CGA
GAM246  CAMLG   5'  GGGGACGCGCGCCCTGCGGCCC 10003       ATC_ A  AC
           GG                    TCGGGCCG   GC CGC  CCCC
                                ||||||||   || |||  ||||
                                GGCCCGGC   CG GCG  GGGG
                                    GTCC  C   CA
GAM246  ID4     5'  GGGAGCGCGGCGGCCGCGA   9547     _    A   AC  A
                                TCG GGCCG TCGC  GC CCC
                                ||| ||||| ||||  || |||
                                AGC CCGGC GGCG  CG GGG
                                  G    _   __ A
GAM246  LFG     3'  GGGGGCAGGATCTGGCCCGA  77239       _   GCAC  A
                                TCGGGCC GATC   GC CCCC
                                ||||||| ||||   || ||||
                                AGCCCGG CTAG   CG GGGG
                                    T   GA__  _
GAM246  MMP2    3'  GGGCACTGGTGGCCCGA    16967       G   CAC  A
                                TCGGGCC ATCG   GC CC
                                ||||||| ||||   || ||
                                AGCCCGG TGGT   CG GG
                                    _   CA_  _
GAM246  PTGFRN  5'  GGAGGTGCACCGCGGCCCGG  67770       AT  CAC   _
                                TCGGGCCG  CG   GCACC CC
                                ||||||||  ||   ||||| ||
                                GGCCCGGC  GC   CGTGG GG
                                    __  CA_    A
GAM246  RAD23B  5'  GGAAGCACGGCGGCCCGA    12735       A  CAC  AC
                                TCGGGCCG TCG   GC  CC
                                ||||||| |||   ||  ||
                                AGCCCGGC GGC   CG  GG
                                    _   A__  AA
GAM246  RCN1    5'  GCGCGTGGTGCGGCCCGA    60374       _   A
                                TCGGGCCG ATCGC CGC
                                |||||||| ||||| |||
                                AGCCCGGC TGGTG GCG
                                    G    C
GAM246  SMARCC1 5'  GGGGGTGCGCGCGGGAACGA  13252    GG  GAT   A
                                TCG  CC   CGC CGCACCCCC
                                |||  ||   ||| |||||||||
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                                AGC  GG   GCG GCGTGGGGG
                                  AA ___  C
GAM246  SNL      5'  GGGTGCGTGCGGGCC      13291      GAT
                                GGCC  CGCACGCACCC
                                ||||  ||||||||||
                                CCGG  GCGTGCGTGGG
                                   ___
GAM246  SYNGR1   3'  GGGTGTGACTGGCCCGA     17509        A  GCAC
                                TCGGGCCG TC   GCACCC
                                |||||||| ||   ||||||
                                AGCCCGGT AG   TGTGGG
                                    C ____
GAM246  ETAA16   5'  GGAGGCGGCTGAGATCGGCCCG 39168         G  C  AC  _
                                CGGGCCGATC CA GC  CC CC
                                |||||||||| || ||  || ||
                                GCCCGGCTAG GT CG  GG GG
                                     A  _  GC  A
GAM246  FLJ10743 3'  GGAAGCCACAGGATCGGCCCGA 37086          GCAC_  AC
                                TCGGGCCGATC    GC  CC
                                ||||||||||    ||  ||
                                AGCCCGGCTAG    CG  GG
                                     GACAC  AA
GAM246  HSU79303 5'  GGGGCGCTAGCCTGGCCCGA   26153        ATC  AC  A
                                TCGGGCCG   GC  GC CCCC
                                ||||||||   ||  || ||||
                                AGCCCGGT   CG  CG GGGG
                                    C__  AT  C
GAM246  MGC15906 5'  GGACGCGCGCCGCCGGCCCGA  52886        ATC  A   AC
                                TCGGGCCG   GC CGC  CC
                                ||||||||   || |||  ||
                                AGCCCGGC   CG GCG  GG
                                    CGC  C   CA
GAM246  MGC29643 5'  GGAGGCGCGGTGCTCGGCCCGG 58694         T   A   A  _
                                TCGGGCCGA CGC CGC CC CC
                                ||||||||| ||| ||| || ||
                                GGCCCGGCT GTG GCG GG GG
                                     C   _   C  A
GAM246  PANX1    5'  GGGGGTGCGCGGGAGAGGCGCG 60806     G   GA  GCA
          A                      TCG GCC  TC   CGCACCCCC
                                 ||| |||  ||   |||||||||
                                 AGC CGG  AG   GCGTGGGGG
                                   G   AG  GGC
GAM246  RINZF    5'  GGGAGCGCGCGGGACGCGGCCC 43938        A___   A  A
          GA                     TCGGGCCG   TCGC CGC CCC
                                 ||||||||   |||| ||| |||
                                 AGCCCGGC   GGCG GCG GGG
                                     GCAG   C   A
GAM246  RIPK2    5'  GGGGGCACACCCGGAACCGGCC 15115        A__  CACGCA
          TGA                     TCGGGCCG  TCG    CCCCC
                                  ||||||||  |||    |||||
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                                AGTCCGGC  GGC    GGGGG
                                    CAA  CCACAC
GAM246  RPL13    5'  GGGGTGCGCGCGCCCGG    53825      CGATC  A
                                TCGGGC    GC CGCACCCC
                                ||||||    || ||||||||
                                GGCCCG    CG GCGTGGGG
                                   _____  C
GAM246  SLC37A1  3'  GGGGGTGCACAGGTAGCCCCGA 39094     CCG  GCAC
                                TCGGG  ATC   GCACCCCC
                                |||||  |||   ||||||||
                                AGCCC  TGG   CGTGGGGG
                                  CGA  ACA_
GAM246  TLE4     5'  GGGAATGCGGAGCGGCCCGG  68514      ATCGCA   CC
                                TCGGGCCG    CGCA  CCC
                                ||||||||    ||||  |||
                                GGCCCGGC    GCGT  GGG
                                    GAG___   AA
GAM246  LOC136120 5'  GGGCGCGCCCGGCCCGA    76708      ATC  A   A
                                TCGGGCCG   GC CGC CC
                                ||||||||   || ||| ||
                                AGCCCGGC   CG GCG GG
                                    C__  C  _
GAM246  LOC146656 3'  GGAAGTGCGTGTGTTGGACC  78667    G   T      CC
                                GG CCGA CGCACGCAC  CC
                                || |||| |||||||||  ||
                                CC GGTT GTGTGCGTG  GG
                                 A   _       AA
GAM246  LOC151009 5'  GGAGCGCGTGCGATAATCTG  86370    CCG      ACC
                                CGGG  ATCGCACGC   CC
                                ||||  |||||||||   ||
                                GTCT  TAGCGTGCG   GG
                                  AA_       CGA
GAM246  LOC165253 5'  GGAGGTGCGTGCCAGGCCC   88544     GATC      _
                                GGGCC   GCACGCACC CC
                                |||||   ||||||||| ||
                                CCCGG   CGTGCGTGG GG
                                  AC__       A
GAM246  LOC196214 5'  GGATGCAAAGACGGCCCGG   91181       A  GCAC   C
                                TCGGGCCG TC   GCA CC
                                |||||||| ||   ||| ||
                                GGCCCGGC AG   CGT GG
                                    _  AAA_   A
GAM246  LOC203636 3'  GGGGGCACACGGGCAGGCACGA 90979    G   GA_   CAC  A
                                TCG GCC   TCG   GC CCCC
                                ||| |||   |||   || ||||
                                AGC CGG   GGC   CG GGGG
                                 A   ACG   ACA  _
GAM246  LOC222962 5'  GGGCGCGCCCGGCCCGA    94456       ATC  A   A
                                TCGGGCCG   GC CGC CC
                                ||||||||   || ||| ||
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                                AGCCCGGC   CG GCG GG
                                    C__  C   _
GAM246  LOC255452 3'  GGGGACGCCAGCGCCTGGCCCG 99399        AT   AC  AC
          A                      TCGGGCCG  CGC  GC  CCCC
                                 ||||||||  |||  ||  ||||
                                 AGCCCGGT  GCG  CG  GGGG
                                     CC   AC  CA
GAM246  LOC255696 5'  GGGGTGGCGGCATCGGCCTGA  99368         C  A  _
                                 TCGGGCCGAT GC CGC ACCCC
                                 ||||||||||  || ||| |||||
                                 AGTCCGGCTA CG GCG TGGGG
                                      _  _  G
GAM246  LOC51295  3'  GGGCACGGGCTGTGGCCCGA  33890        ATC  A  CA
                                 TCGGGCCG   GC CG  CCC
                                 ||||||||   || ||  |||
                                 AGCCCGGT   CG GC  GGG
                                     GT_  G  AC
GAM246  LOC51690  3'  GGGGGTGCAGGGCAGGCCCGA  33011       GATC  AC_
                                 TCGGGCC   GC   GCACCCCC
                                 |||||||   ||   ||||||||
                                 AGCCCGG   CG   CGTGGGGG
                                     A___  GGA
GAM246  LOC91960  5'  GCCCGCGACTCGGCCCGA   68286         _   AC
                                 TCGGGCCGA TCGC  GC
                                 |||||||| ||||  ||
                                 AGCCCGGCT AGCG  CG
                                      C   CC
GAM246  LOC92223  3'  GGTGCGTGGATCACCTGA   69053      CC   G
                                 TCGGG  GATC CACGCACC
                                 |||||  |||| ||||||||
                                 AGTCC  CTAG GTGCGTGG
                                    A_   _
GAM247  MYLK     3'  TCTTTGCAGATGTCTAGC   98797   _      C
                                 G TGGACATC GCAAAGA
                                 | |||||||| |||||||
                                 C ATCTGTAG CGTTTCT
                                  G       A
GAM247  WHSC1    3'  TCTCCGAGTGAGTCACGTCA  56701        A_  TC  CAA
                                 TGACGTGG  CA  CG   AGA
                                 ||||||||  ||  ||   |||
                                 ACTGCACT  GT  GC   TCT
                                     GA  GA  C__
GAM247  Apg4B    3'  TCCTTGGGCTCCACGTC     26185        CAT  G   A
                                 GACGTGGA   CC CAA GA
                                 ||||||||   || ||| ||
                                 CTGCACCT   GG GTT CT
                                     C__  _   C
GAM247  FLJ10901  3'  TCTTTAGGGACCCAGTCA    37374     G   ACA   GC
                                 TGAC TGG   TCC  AAAGA
                                 |||| |||   |||  |||||
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                                ACTG ACC   AGG  TTTCT
                                  _  C__   GA
GAM247  FLJ23590  5'  TGCTGAGTGCCCACGTCA    45368        A  _  C
                                TGACGTGG CA TC GCA
                                |||||||| || || |||
                                ACTGCACC GT AG CGT
                                     C  G  T
GAM247  FOXO3A    5'  CTTCGCGGCGTCCACGTC    9381         AT   A
                                GACGTGGAC  CCGC AAG
                                |||||||||  |||| |||
                                CTGCACCTG  GGCG TTC
                                     C_   C
GAM247  HSA250839 3'  TCCTTGGGGCTGTCCATGTCA  37855          T  G   A
                                TGACGTGGACA CC CAA GA
                                |||||||||| || ||| ||
                                ACTGTACCTGT GG GTT CT
                                      C  G   C
GAM247  KIAA0276  3'  TCTTTGCAAACAGTGTTCAC   71524        CC___
                                GTGGACAT    GCAAAGA
                                ||||||||    |||||||
                                CACTTGTG    CGTTTCT
                                     ACAAA
GAM247  KIAA0493  3'  TCTCTGCGGATATGTCA     64938       GGAC      A
                                TGACGT   ATCCGCA AGA
                                ||||||   ||||||| |||
                                ACTGTA   TAGGCGT TCT
                                   ____      C
GAM247  KIAA0514  3'  TCTCAGTTTTGTTCACGCCA   28759    A      TCC  AA
                                TG CGTGGACA  GC  AGA
                                || ||||||||  ||  |||
                                AC GCACTTGT  TG  TCT
                                 C       TT_  AC
GAM247  KIAA0711  3'  TCTTTCAGTGGCCACATCA    30154    C   ACAT   __
                                TGA GTGG   CCGC  AAAGA
                                ||| ||||   ||||  |||||
                                ACT CACC   GGTG  TTTCT
                                  A   ____   AC
GAM247  KIAA1198  3'  TTTTGTGGCATCCAGTCA     64077     G   CAT
                                TGAC TGGA  CCGCAAAG
                                |||| ||||  ||||||||
                                ACTG ACCT  GGTGTTTT
                                   _   AC_
GAM247  KIAA1509  3'  TCTTTGGAACAAATAATCCACG 62297        CATCCG____
          TCA                     TGACGTGGA        CAAAGA
                                |||||||||        ||||||
                                ACTGCACCT        GTTTCT
                                     AATAAACAAG
GAM247  MDS006    3'  CTTTTGGTGTATACCACGTCA  39983        ___  T   C
                                TGACGTGG   ACA CCG AAAG
                                ||||||||   ||| ||| ||||
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                                ACTGCACC   TGT GGT TTTC
                                    ATA  _  _
GAM247  MGC11287  3'  TCTCTGTGGTCCACGTC     49622        CAT    A
                                GACGTGGA   CCGCA AGA
                                ||||||||   ||||| |||
                                CTGCACCT   GGTGT TCT
                                    ____    C
GAM247  MGC861    3'  TCTGTTGAGGATGTCCAGTCA  44133     G       G  _
                                TGAC TGGACATCC CAA AGA
                                |||| ||||||||| ||| |||
                                ACTG ACCTGTAGG GTT TCT
                                  _       A  G
GAM247  NETO2     3'  CTTTCAGTGTTCACATCA    36594     C      CCGC
                                TGA GTGGACAT    AAAG
                                ||| ||||||||    ||||
                                ACT CACTTGTG    TTTC
                                  A       AC__
GAM247  OCT11     3'  CTTCTGTCTGTCCACGTC    27588         TCC  _
                                GACGTGGACA   GCA AAG
                                ||||||||||   ||| |||
                                CTGCACCTGT   TGT TTC
                                     C__   C
GAM247  SEZ6      3'  CTTCATTGGGCCCATGTCA   74830        ACA   CA_
                                TGACGTGG   TCCG   AAG
                                ||||||||   ||||   |||
                                ACTGTACC   GGGT   TTC
                                    C__    TAC
GAM247  SRF       3'  TCCTTGCTGACCCCAGGTCA  13399     G  ACA  C   A
                                TGAC TGG   TC GCAA GA
                                |||| |||   || |||| ||
                                ACTG ACC   AG CGTT CT
                                  G  CC_  T   C
GAM247  TRAF3     5'  CTTCGGTCTCCATGTCA     60453        CAT   CA
                                TGACGTGGA   CCG  AAG
                                |||||||||   |||  |||
                                ACTGTACCT   GGC  TTC
                                     CT_   __
GAM247  LOC143884 3'  CTTCACGGAGGGTTTGCCCATG 77162        ____  A_   CA
          TCA                     TGACGTGG    AC  TCCG  AAG
                                ||||||||    ||  ||||  |||
                                ACTGTACC    TG  AGGC  TTC
                                    CGTT  GG    AC
GAM247  LOC144848 3'  CTCTGGAGGATGTCCACATCA  73958     C        G_  A
                                TGA GTGGACATCC  CA AG
                                ||| ||||||||||  || ||
                                ACT CACCTGTAGG  GT TC
                                  A         AG  C
GAM247  LOC148085 3'  TCTTTAAGGTGTCCACGCA    85253    A       T  GC
                                TG CGTGGACA CC  AAAGA
                                || ||||||| ||  |||||
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                                AC GCACCTGT GG  TTTCT
                                 _      _ AA
GAM247  LOC165257 5'  TTGTGTGCCCCACGTCA     83372        A_  TC
                                TGACGTGG  CA  CGCAA
                                ||||||||  ||  |||||
                                ACTGCACC  GT  GTGTT
                                     CC  __
GAM247  LOC220776 3'  CTTTGCTTTCTGTCCATGTCA  68930          TCC_
                                TGACGTGGACA    GCAAAG
                                ||||||||||    ||||||
                                ACTGTACCTGT    CGTTTC
                                      CTTT
GAM247  LOC221715 5'  TCTTTGCGGATGACCATG    95396      A
                                CGTGG CATCCGCAAAGA
                                ||||| ||||||||||||
                                GTACC GTAGGCGTTTCT
                                   A
GAM247  LOC245771 5'  TCTTTAGGGACCCAGTCA    94489     G   ACA   GC
                                TGAC TGG   TCC  AAAGA
                                |||| |||   |||  |||||
                                ACTG ACC   AGG  TTTCT
                                  _  C__   GA
GAM247  LOC254228 3'  CTCTGCTTTGTAGCCACGTCA  97650         __   TCC   A
                                TGACGTGG  ACA   GCA AG
                                ||||||||  |||   ||| ||
                                ACTGCACC  TGT   CGT TC
                                     GA   TT_   C
GAM247  LOC255838 5'  CTTTCCGGTTCACGTCA     97702         CAT   C
                                TGACGTGGA   CCG AAAG
                                |||||||||   ||| ||||
                                ACTGCACTT   GGC TTTC
                                     ___   C
GAM247  LOC92223  3'  CTTTTCCAGTGTCCACGCA   69049    A       CCGC
                                TG CGTGGACAT    AAAG
                                || |||||||||    ||||
                                AC GCACCTGTG    TTTC
                                 _       ACCT
GAM248  GPD1     3'  TCATGCCACCACATTTG     60398       C       C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A      _
GAM248  IL5RA    5'  TCGCATGGCCACCGCATTT    6906           AT__
                                AAATGCGGTGGC    CGA
                                ||||||||||||    |||
                                TTTACGCCACCG    GCT
                                      GTAC
GAM248  MYO1C    3'  TGCCGATGCCAAATATTTG    61873       CGG       A
                                TAAATG   TGGCATCG CA
                                ||||||   |||||||| ||
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                                GTTTAT   ACCGTAGC GT
                                   AA_       C
GAM248  C6orf37   3'  TGTCACACTGCATTTA      68097          GCATC
                                TAAATGCGGTG    GACA
                                ||||||||||    ||||
                                ATTTACGTCAC    CTGT
                                      A____
GAM248  DNAJC6    3'  TTGCAGAACCACCGCATT    29498          CA  GA
                                AATGCGGTGG  TC  CAA
                                |||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                      A_  AC
GAM248  FLJ11210  3'  GTCGATGTGCATGCTTTTA   60319      T   GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                   T   ACG
GAM248  FLJ12476  3'  TCGATCTTCTGCATTTA     43270         T  C
                                TAAATGCGG GG ATCGA
                                |||||||| || |||||
                                ATTTACGTC TC TAGCT
                                      T  _
GAM248  KIAA1034  3'  TCGATGGCATCCGCATTTG   63134          _  G
                                TAAATGCGG TG CATCGA
                                |||||||| || ||||||
                                GTTTACGCC AC GTAGCT
                                      T  G
GAM248  KIAA1987  3'  TCATGTAACTGCATTTA     89391          G   C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                      A   _
GAM248  MGC16063  3'  TGTCCTGGCCACTGCATT    54929           ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                      GTC
GAM248  LOC147949 3'  TGTCAGATGTCCACATTGCA  79279      __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                   TA   T   A
GAM248  LOC150577 3'  GTCCTCACCGCATTTG      86258          CATC
                                TAAATGCGGTGG    GAC
                                ||||||||||||    |||
                                GTTTACGCCACT    CTG
                                      C___
GAM248  LOC158219 3'  TGTGTGTCACCACATTT     82694       C       CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
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                                TTTAC CCACTGTG  TGT
                                   A       __
GAM248  LOC202020 3'  TGTCTCACCACATTTA      90605       C     CATC
                                TAAATG GGTGG    GACA
                                |||||| |||||    ||||
                                ATTTAC CCACT    CTGT
                                   A    _____
GAM248  LOC90826  5'  TGTCGATGCAGGTTTATTTG   64788       CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                   TTGGA
GAM248  LOC93587  3'  TTGTCTTTACCTGCATTTA    73042       _     CATC
                                TAAATGC GGTGG    GACAA
                                ||||||| |||||    |||||
                                ATTTACG CCATT    CTGTT
                                    T    T___
GAM249  ADCY8     5'  GAAGCACGGCGCCCAGGCGC   8500          AA  A_
                                GCGCCTGGGC  CG  CTTC
                                ||||||||||  ||  ||||
                                CGCGGACCCG  GC  GAAG
                                     CG  AC
GAM249  BUB1B     5'  GGAAGAAAGCCCAGGCGGT    8674     G       AACGA
                                AC CGCCTGGGC    CTTCC
                                || |||||||||    |||||
                                TG GCGGACCCG    GAAGG
                                 _       AAA__
GAM249  CENPB     3'  TGGAAGTAACCAAGGGCGC    70121       G_  CAACG
                                GCGCCT  GG    ACTTCCA
                                ||||||  ||    |||||||
                                CGCGGG  CC    TGAAGGT
                                   AA  AA___
GAM249  CLN5      5'  GTGGAAGCCGCCGCGGGCCGGG 22432          ___  AA  A
            CGCG                    CGCGCCTGG   GC  CG CTTCCAC
                                ||||||||||  ||  || |||||||
                                GCGCGGGCC   CG  GC GAAGGTG
                                     GGG  CC  C
GAM249  DLX2      3'  TGGAAGCCTCCCAGGCGCG    16607          CAACGA
                                CGCGCCTGGG     CTTCCA
                                ||||||||||     ||||||
                                GCGCGGACCC     GAAGGT
                                     TCC___
GAM249  EDARADD   5'  GGTTTGCTCCAGGCGCGT    55787          _   AC
                                ACGCGCCTGG GCA  GACT
                                |||||||||| |||  ||||
                                TGCGCGGACC CGT  TTGG
                                     T   __
GAM249  PLIN      3'  GAACCCGCACTGCCCAGGCG   12172          A__  AC
                                CGCCTGGGCA   CG  TTC
                                ||||||||||   ||  |||
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                                GCGGACCCGT  GC  AAG
                                     CAC  CC
GAM249  SLC19A1  5'  GAGCGCGCCCAGGCACGT    13216    C      AA  A
                                ACG GCCTGGGC  CG CTT
                                ||| ||||||||  || |||
                                TGC CGGACCCG  GC GAG
                                  A      C_  _
GAM249  SNRPN    5'  GTGGAAGTCCAAGTCAAACGC  43321    CCTG  AAC
                                GCG   GGC  GACTTCCAC
                                |||   |||  |||||||||
                                CGC   CTG  CTGAAGGTG
                                  AAA_  AAC
GAM249  SNRPN    5'  GTGGAAGTCCAAGTCAAACGC  43322    CCTG  AAC
                                GCG   GGC  GACTTCCAC
                                |||   |||  |||||||||
                                CGC   CTG  CTGAAGGTG
                                  AAA_  AAC
GAM249  SNRPN    5'  GTGGAAGTCCAAGTCAAACGC  43323    CCTG  AAC
                                GCG   GGC  GACTTCCAC
                                |||   |||  |||||||||
                                CGC   CTG  CTGAAGGTG
                                  AAA_  AAC
GAM249  SNRPN    5'  GTGGAAGTCCAAGTCAAACGC  43324    CCTG  AAC
                                GCG   GGC  GACTTCCAC
                                |||   |||  |||||||||
                                CGC   CTG  CTGAAGGTG
                                  AAA_  AAC
GAM249  ADMP     5'  GTAGAAGTCGTTGGGCTGC   59513   _  TGGG      C
                                GC GCC   CAACGACTTC AC
                                || |||   |||||||||| ||
                                CG CGG   GTTGCTGAAG TG
                                 T  ____       A
GAM249  C20orf106 3'  GAAATTAGGCCAGGCGCG    55904       G AAC  C
                                CGCGCCTGG C   GA TTC
                                ||||||||| |   || |||
                                GCGCGGACC G   TT AAG
                                     _ GA_  A
GAM249  DKFZP564F013 3'  GAAGCCATTGCTCAGCACCGT  95880    CGC     CGA
                                ACG  CTGGGCAA  CTTC
                                |||  ||||||||  ||||
                                TGC  GACTCGTT  GAAG
                                  CAC      ACC
GAM249  FLJ10702  5'  GTGGAAGTCGTCGACGCCGCCG 36971    CCTG  A___
          C                      GCG   GGC   ACGACTTCCAC
                                |||   |||   ||||||||||
                                CGC   CCG   TGCTGAAGGTG
                                  CG__  CAGC
GAM249  FLJ14957  3'  GAAGTCAGGCAGAGGCGTGT  52819      GG  AAC
                                ACGCGCCT  GC  GACTTC
                                ||||||||  ||  ||||||
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                                TGTGCGGA CG   CTGAAG
                                    GA  GA_
GAM249  HUMAGCGB 5' TGGACGCTGCCCAGGCCG    26136    C       A  ACT
                                CG GCCTGGGCA CG   TCCA
                                || ||||||||| ||   ||||
                                GC CGGACCCGT GC   AGGT
                                 _       C  ___
GAM249  KIAA0594 5' GGAAGTCGCTGTGGGACGC    65513    _  GG   A
                                GCG CCT  GCA CGACTTCC
                                ||| |||  ||| ||||||||
                                CGC GGG  TGT GCTGAAGG
                                  A  __  C
GAM249  NFAT5    5' GTGGAAGTCACTACCCTCGAGG 57776    ___  CAAC
                                CCT   GGG   GACTTCCAC
                                |||   |||   |||||||||
                                GGA   CCC   CTGAAGGTG
                                  GCT   ATCA
GAM249  NFAT5    5' GTGGAAGTCACTACCCTCGAGG 57777    ___  CAAC
                                CCT   GGG   GACTTCCAC
                                |||   |||   |||||||||
                                GGA   CCC   CTGAAGGTG
                                  GCT   ATCA
GAM249  PME-1    3' GTCCCTATTGCCCAGGCACG   32870    C       C___
                                CG GCCTGGGCAA   GAC
                                || ||||||||||   |||
                                GC CGGACCCGTT   CTG
                                 A        ATCC
GAM249  TOLLIP   5' GGAGGTCGCCCGGCGCGT    39196       T   AAC
                                ACGCGCC GGGC   GACTTCC
                                ||||||| ||||   |||||||
                                TGCGCGG CCCG   CTGGAGG
                                    _   ___
GAM249  LOC148166 5' GTGGAAGCCACCCCAGGCGC  79420        CAACGA
                                GCGCCTGGG     CTTCCAC
                                |||||||||     |||||||
                                CGCGGACCC     GAAGGTG
                                     CACC__
GAM249  LOC164584 5' GAGGACGCTGCCCAGGGC    83420    G      A  A
                                GC CCTGGGCA CG CTTC
                                || |||||||| || ||||
                                CG GGACCCGT GC GGAG
                                 _       C  A
GAM249  LOC164584 5' GAGGTCGCTGCCCAGGGC    83421    G      A
                                GC CCTGGGCA CGACTTC
                                || |||||||| |||||||
                                CG GGACCCGT GCTGGAG
                                 _       C
GAM249  LOC164584 5' GAGGTCGCTGCCCAGGGC    83422    G      A
                                GC CCTGGGCA CGACTTC
                                || |||||||| |||||||
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                                CG GGACCCGT GCTGGAG
                                 _       C
GAM249  LOC200197 3'  GTGGAAGTGGTGGTGCCCAGGA 90020     _      __  G
          CGC                     GCG CCTGGGCA  AC ACTTCCAC
                                ||| ||||||||  || ||||||||
                                CGC GGACCCGT  TG TGAAGGTG
                                  A       GG  G
GAM249  LOC253639 3'  TGAAAGCGGGGCCAGGCGCG   97518         G AA  A   C
                                CGCGCCTGG C  CG CTT CA
                                |||||||||| |  || ||| ||
                                GCGCGGACC G  GC GAA GT
                                      _ GG  _   A
GAM249  LOC92597  3'  TGGAAATCACTGTTGTTCAG   70515         ___  C
                                CTGGGCAAC   GA TTCCA
                                |||||||||   || |||||
                                GACTTGTTG   CT AAGGT
                                      TCA  A
GAM249  LOC96652  3'  GTGGAAGTCGCCCTGGC     66082     T    AAC
                                GCC GGGC   GACTTCCAC
                                ||| ||||   |||||||||
                                CGG CCCG   CTGAAGGTG
                                  T   ___
GAM250  GPD1      3'  TCATGCCACCACATTTG      60398       C       C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A      _
GAM250  IL5RA     5'  TCGCATGGCCACCGCATTT    6906           AT__
                                AAATGCGGTGGC    CGA
                                ||||||||||||    |||
                                TTTACGCCACCG    GCT
                                      GTAC
GAM250  MYO1C     3'  TGCCGATGCCAAATATTTG    61873       CGG       A
                                TAAATG   TGGCATCG CA
                                ||||||   |||||||| ||
                                GTTTAT   ACCGTAGC GT
                                   AA_       C
GAM250  C6orf37   3'  TGTCACACTGCATTTA      68097          GCATC
                                TAAATGCGGTG     GACA
                                ||||||||||     ||||
                                ATTTACGTCAC     CTGT
                                      A____
GAM250  DNAJC6    3'  TTGCAGAACCACCGCATT     29498         CA  GA
                                AATGCGGTGG  TC  CAA
                                ||||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                      A_  AC
GAM250  FLJ11210  3'  GTCGATGTGCATGCTTTTA    60319      T   GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
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                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM250   FLJ12476  3'  TCGATCTTCTGCATTTA     43270        T  C
                                TAAATGCGG GG ATCGA
                                ||||||||| || |||||
                                ATTTACGTC TC TAGCT
                                     T  _
GAM250   KIAA1034  3'  TCGATGGCATCCGCATTTG   63134        _  G
                                TAAATGCGG TG CATCGA
                                ||||||||| || ||||||
                                GTTTACGCC AC GTAGCT
                                     T  G
GAM250   KIAA1987  3'  TCATGTAACTGCATTTA     89391        G   C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                     A   _
GAM250   MGC16063  3'  TGTCCTGGCCACTGCATT    54929         ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                      GTC
GAM250   LOC147949 3'  TGTCAGATGTCCACATTGCA   79279     __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM250   LOC150577 3'  GTCCTCACCGCATTTG      86258         CATC
                                TAAATGCGGTGG   GAC
                                ||||||||||||   |||
                                GTTTACGCCACT   CTG
                                      C___
GAM250   LOC158219 3'  TGTGTGTCACCACATTT     82694      C      CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                   A       __
GAM250   LOC202020 3'  TGTCTCACCACATTTA      90605      C    CATC
                                TAAATG GGTGG   GACA
                                |||||| |||||   ||||
                                ATTTAC CCACT   CTGT
                                   A   ____
GAM250   LOC90826  5'  TGTCGATGCAGGTTTATTTG  64788      CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                    TTGGA
GAM250   LOC93587  3'  TTGTCTTTACCTGCATTTA   73042       _    CATC
                                TAAATGC GGTGG   GACAA
                                ||||||| |||||   |||||
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                                ATTTACG CCATT   CTGTT
                                   T    T___
GAM251  ADAMTS8  3' GGTGACTGGGTCCCTTGGCC  23855         GGAA
                                GGTCAAGGGAT   AGTCACC
                                ||||||||||   |||||||
                                CCGGTTCCCTG   TCAGTGG
                                     GG__
GAM251  AVP     5' GGTGACCCCCCAGTCTGTCC  6677    T  A  GA   AAA
                                GG CA GG  TGG   GTCACC
                                || || ||  |||   ||||||
                                CC GT CT  ACC   CAGTGG
                                 T  _  G_   CCC
GAM251  CLPS    3' GGCTGGCCACCTCCTTGACC  10215        _ A   AA
                                GGTCAAGG G TGG  AGTC
                                |||||||| | |||  ||||
                                CCAGTTCC C ACC  TCGG
                                     T C   GG
GAM251  COL7A1   3' GACCCGCCCCTTGACC     5411          A   AAA
                                GGTCAAGGG TGG   GTC
                                ||||||||| |||   |||
                                CCAGTTCCC GCC   CAG
                                     C   ___
GAM251  ELF3    3' GTGACCTTGACCTTGACC    16684        GAT  AAA
                                GGTCAAGG   GG   GTCAC
                                ||||||||   ||   |||||
                                CCAGTTCC   TC   CAGTG
                                     AGT  ___
GAM251  FOSB    3' ACTTCTCCCACCCCTTGGCC  23053         A   A__
                                GGTCAAGGG TGG   AAGT
                                ||||||||| |||   ||||
                                CCGGTTCCC ACC   TTCA
                                     C   CTC
GAM251  GDI1    3' GGTGACTTCTGCCCCCACC   60644    CAA   AT    A
                                GGT   GGG  GGAA GTCACC
                                |||   |||  |||| ||||||
                                CCA   CCC  TCTT CAGTGG
                                  C__   CG   _
GAM251  HTR2A    3' GGTGACTTTCCTATGAC     7105      AGGGAT
                                GTCA     GGAAAGTCACC
                                ||||     ||||||||||
                                CAGT     CCTTTCAGTGG
                                  AT____
GAM251  MADH7    5' GACTTTTCTCCTCGCC      20927     CAA    T
                                GGT   GGGA GGAAAGTC
                                |||   |||| ||||||||
                                CCG   TCCT CTTTTCAG
                                  C__    _
GAM251  NF1     3' GTGACCCCTTCCCTGTCC    6048     T  A    T  AAA
                                GG CA GGGA GG   GTCAC
                                || || |||| ||   |||||
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                                CC GT CCCT CC   CAGTG
                                 T _   T C__
GAM251  PXF     3'  GGTGAACCCAGCCCCTGACC  12656      A  A  AAAG
                                GGTCA GGG TGG   TCACC
                                ||||| ||| |||   |||||
                                CCAGT CCC ACC   AGTGG
                                   C  G  CA__
GAM251  SCD     3'  ACTCTCTTTCCTTGAGC    18588   G      T  A
                                G TCAAGGGA GGA AGT
                                | |||||||| ||| |||
                                C AGTTCCTT TCT TCA
                                 G       _  C
GAM251  SEL1L   3'  GTGACCCCAGATGACCTTGACT 18605        GA___  AAA
                                GGTCAAGG    TGG  GTCAC
                                ||||||||    |||  |||||
                                TCAGTTCC    ACC  CAGTG
                                     AGTAG  C__
GAM251  STIM1   3'  GACAACTCTCTCCCTTACC   60783    C     T  AA_
                                GGT AAGGGA GGA  GTC
                                ||| |||||| |||  |||
                                CCA TTCCCT TCT  CAG
                                  _     C  CAA
GAM251  UBL1    3'  TGACTTTCCAATTGGCC    13977       GGGA
                                GGTCAA   TGGAAAGTCA
                                ||||||   ||||||||||
                                CCGGTT   ACCTTTCAGT
                                   A___
GAM251  VSNL1   3'  ACTTTCCAACTTTTCATC    14080    C    A
                                GGT AAGGG TGGAAAGT
                                ||| ||||| ||||||||
                                CTA TTTTC ACCTTTCA
                                  C    A
GAM251  WHSC1L1 5'  GGCGACCCCCGTCCCTCGGCC 35503     A      AAA  A
                                GGTC AGGGATGG  GTC CC
                                |||| ||||||||  ||| ||
                                CCGG TCCCTGCC  CAG GG
                                  C       CC_  C
GAM251  WHSC1L1 5'  GGCGACCCCCGTCCCTCGGCC 43781     A      AAA  A
                                GGTC AGGGATGG  GTC CC
                                |||| ||||||||  ||| ||
                                CCGG TCCCTGCC  CAG GG
                                  C       CC_  C
GAM251  ALOX15B 3'  GATGACATCCCTTTGACC    8553       _    GAAA
                                GGTCAA GGGATG   GTC
                                |||||| ||||||   |||
                                CCAGTT CCCTAC   TAG
                                   T    AG__
GAM251  BAIAP1  3'  ACTTCTCCATCCCCCAACT   17638    CAA      _
                                GGT  GGGATGGA AAGT
                                |||  |||||||| ||||
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                                TCA   CCCTACCT TTCA
                                  ACC       C
GAM251  C16orf5   3' GGCGACCTCTGGCCCTGGCC  26354      A   AT   AA   A
                                GGTCA GGG  GGA  GTC CC
                                ||||| |||  |||  ||| ||
                                CCGGT CCC  TCT  CAG GG
                                   _  GG   C_   C
GAM251  DCLRE1B   5' GGTGACTTCCTTTTTCTGCC  43402    T  AG   T    A
                                GG CA  GGA GGAA GTCACC
                                || ||  ||| |||| ||||||
                                CC GT  TTT CCTT CAGTGG
                                 _ CT   T   _
GAM251  DKFZp434A1010 3' GGTCTGCCCATCCCCCCACC  71856     CAA      AA  TC
                                GGT   GGGATGG  AG  ACC
                                |||   |||||||  ||  |||
                                CCA   CCCTACC  TC  TGG
                                  CCC      CG  __
GAM251  DKFZP564B1162 5'  GGTAACTTATCCCTAAGCC   49351     CA      GAA   C
                                GGT  AGGGATG   AGT ACC
                                |||  |||||||   ||| |||
                                CCG  TCCCTAT   TCA TGG
                                  AA       ___   A
GAM251  DKFZP566J2046 3'  ACTTTCCGTTGTTTACC     49133     C   G
                                GGT AAG GATGGAAAGT
                                ||| ||| ||||||||||
                                CCA TTT TTGCCTTTCA
                                  _   G
GAM251  EDG2      3'  GACAACCCTCATCTTGATC   55131         _  T  AAA
                                GGTCAAGG GA GG   GTC
                                |||||||| || ||   |||
                                CTAGTTCT CT CC   CAG
                                     A  C  AA_
GAM251  EDG2      3'  GACAACCCTCATCTTGATC   9172          _  T  AAA
                                GGTCAAGG GA GG   GTC
                                |||||||| || ||   |||
                                CTAGTTCT CT CC   CAG
                                     A  C  AA_
GAM251  EFA6R     3'  GTGAGTCATCCCTTGACT    31640           AAAG
                                GGTCAAGGGATGG    TCAC
                                ||||||||||||    ||||
                                TCAGTTCCCTACT    AGTG
                                       G___
GAM251  FLJ10482  3'  ACTCCCATCCCTTACC      36647     C       AA
                                GGT AAGGGATGG  AGT
                                ||| |||||||||  |||
                                CCA TTCCCTACC  TCA
                                  _       C_
GAM251  FLJ10535  3'  GATTGTCTCCATCTCTTGACC  36750           A__
                                GGTCAAGGGATGGA   AGTC
                                ||||||||||||||   ||||
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                                CCAGTTCTCTACCT  TTAG
                                      CTG
GAM251  FLJ12704  3' ATTTTCCATCCCCCACC    47166    CAA
                                GGT  GGGATGGAAAGT
                                |||  ||||||||||||
                                CCA  CCCTACCTTTTA
                                  CC_
GAM251  FLJ14107  3' GTGACCCCATCTCTACC    47348    CA     AAA
                                GGT  AGGGATGG  GTCAC
                                |||  ||||||||  |||||
                                CCA  TCTCTACC  CAGTG
                                  __     C__
GAM251  FLJ14124  3' GACTCCATCCCTCAACT    46357    CA      AA
                                GGT  AGGGATGGA  GTC
                                |||  |||||||||  |||
                                TCA  TCCCTACCT  CAG
                                  AC       __
GAM251  FLJ20808  5' GTGACCTCATCTTGACT    36120     AG    AAA
                                GGTCA  GGATGG  GTCAC
                                |||||  ||||||  |||||
                                TCAGT  TCTACT  CAGTG
                                   __    C__
GAM251  FLJ22672  3' GGCCCCATCCCTGACC     46598     A     AAA
                                GGTCA GGGATGG  GTC
                                |||||  |||||||  |||
                                CCAGT  CCCTACC  CGG
                                   _     C__
GAM251  FLJ23598  5' ACTTTCCCAACCCCCTGACC  96502     A  AT__
                                GGTCA GGG   GGAAAGT
                                |||||  |||  |||||||
                                CCAGT  CCC   CCTTTCA
                                   C  CAAC
GAM251  FLJ31168  3' GTGCTCACTCCATCCCCTACC  59185    CAA     A__  T
                                GGT  GGGATGGA  AG CAC
                                |||  ||||||||  || |||
                                CCA  CCCTACCT  TC GTG
                                  TC_      CAC  _
GAM251  KIAA0417  3' GGTGACCCCATACCTTGCC   71761   T   G   AAA
                                GG CAAGG ATGG  GTCACC
                                ||  |||||  ||||  ||||||
                                CC  GTTCC  TACC  CAGTGG
                                 _    A   C__
GAM251  KIAA0453  3' GCTACCCAGTCCCTTGACC   69608        _  AA
                                GGTCAAGGGA TGG  AGT
                                ||||||||||  |||  |||
                                CCAGTTCCCT  ACC  TCG
                                      G  CA
GAM251  KIAA0547  3' GTGACTTTGAGGCCTTACC   29599    CA   ATGG
                                GGT  AGGG   AAAGTCAC
                                |||  ||||   ||||||||
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                                CCA  TTCC    TTTCAGTG
                                  __    GGAG
GAM251  KIAA0794  3'  GGTGACTTTCATTGTCCTAACC 81235     CA    ATG_
                                GGT  AGGG    GAAAGTCACC
                                |||  ||||    ||||||||||
                                CCA  TCCT    CTTTCAGTGG
                                  A_    GTTA
GAM251  KIAA0939  3'  GTGACCTTTTGTCCTTTACC  62721     C     TG   A
                                GGT AAGGGA  GAA GTCAC
                                ||| ||||||  ||| |||||
                                CCA TTTCCT  TTT CAGTG
                                  _     GT   C
GAM251  KIAA1163  3'  GATGACCGATCCCTTTAACC  79650     C_      _ AAA
                                GGT  AAGGGAT GG   GTC
                                |||  ||||||| ||   |||
                                CCA  TTCCCTA CC   TAG
                                  AT      G  AG_
GAM251  KIAA1193  3'  GACTCGACCATCCCTCACC   68271     CA       AA_
                                GGT  AGGGATGG   AGTC
                                |||  ||||||||   ||||
                                CCA  TCCCTACC   TCAG
                                  C_       AGC
GAM251  KIAA1500  3'  GACATCCATCCCTGACC     64809      A       AA
                                GGTCA GGGATGGA  GTC
                                |||||  ||||||||  |||
                                CCAGT CCCTACCT  CAG
                                   _       A_
GAM251  KIAA1671  3'  GGTGACCTTTGCCCCTTGGCC  66287          AT   AA
                                GGTCAAGGG  GGA  GTCACC
                                |||||||||  |||  ||||||
                                CCGGTTCCC  TTT  CAGTGG
                                     CG   C_
GAM251  KIAA1691  3'  ACTACTCCATCCCATGACC    94122      A       A_
                                GGTCA GGGATGGA  AGT
                                |||||  ||||||||  |||
                                CCAGT CCCTACCT  TCA
                                   A       CA
GAM251  KIAA1724  3'  GGTGACTTCATGCCCCAGCC   67620     CAA   ATG   A
                                GGT   GGG   GAA GTCACC
                                |||   |||   ||| ||||||
                                CCG   CCC   CTT CAGTGG
                                  AC_   GTA   _
GAM251  KIAA1755  5'  GGTACCCTCCATCCCTCGAC   62019     A       AA  C
                                GTC AGGGATGGA  GT ACC
                                |||  |||||||||  || |||
                                CAG TCCCTACCT  CA TGG
                                  C        CC  _
GAM251  KRTAP1-5  3'  ACTGTTCATCCCTTGACC     50072            A
                                GGTCAAGGGATGGA AGT
                                ||||||||||||| |||
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                                CCAGTTCCCTACTT TCA
                                       G
GAM251  MAFB    3' GGCTTAGCCATCCCTGACC   19593      A     A_
                                GGTCA GGGATGG  AAGTC
                                ||||| |||||||  |||||
                                CCAGT CCCTACC  TTCGG
                                   _      GA
GAM251  MAPK8IP2 3' GATCATCCCATCCTTGACC   25589        AT   AA
                                GGTCAAGGG  GGA  GTC
                                |||||||||  |||  |||
                                CCAGTTCCT  CCT  TAG
                                     AC   AC
GAM251  MAPK8IP2 3' GATCATCCCATCCTTGACC   33575        AT   AA
                                GGTCAAGGG  GGA  GTC
                                |||||||||  |||  |||
                                CCAGTTCCT  CCT  TAG
                                     AC   AC
GAM251  MAPK8IP2 3' GATCATCCCATCCTTGACC   58208        AT   AA
                                GGTCAAGGG  GGA  GTC
                                |||||||||  |||  |||
                                CCAGTTCCT  CCT  TAG
                                     AC   AC
GAM251  MG61    3' GACCCCCTCCATCCTTGACC  43381        G    AA__
                                GGTCAAGG ATGGA   GTC
                                |||||||| |||||   |||
                                CCAGTTCC TACCT   CAG
                                   _    CCCC
GAM251  MGC3207  3' GACCGTCCAGCCCCTGACC   63238      A  A   AA
                                GGTCA GGG TGGA  GTC
                                ||||| ||| ||||  |||
                                CCAGT CCC ACCT  CAG
                                   C   G   GC
GAM251  MGC4737  3' GACTTCCCTTTGGCC       49643        ATG  A
                                GGTCAAGGG   GAA GTC
                                |||||||||   ||| |||
                                CCGGTTTCC   CTT CAG
                                      ___  _
GAM251  MRPS11   5' TGACTTTCCCTTCTGTCC    43413    T  AG  AT
                                GG CA  GG  GGAAAGTCA
                                || ||  ||  |||||||||
                                CC GT  TC  CCTTTCAGT
                                 T  CT  __
GAM251  MRPS11   5' TGACTTTCCCTTCTGTCC    96198    T  AG  AT
                                GG CA  GG  GGAAAGTCA
                                || ||  ||  |||||||||
                                CC GT  TC  CCTTTCAGT
                                 T  CT  __
GAM251  RASD2    3' GTGACTCCCTCCTTGGCC    27466        AT   AA
                                GGTCAAGGG  GGA  GTCAC
                                |||||||||  |||  |||||
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                                CCGGTTCCT  CCT  CAGTG
                                     C_  __
GAM251  SARM     3'  GGTGACTCCTAGTTCTTGGCC  31301        AT_  AA
                                GGTCAAGGG  GGA  GTCACC
                                |||||||||  |||  ||||||
                                CCGGTTCTT  CCT  CAGTGG
                                     GAT  __
GAM251  SLC26A9  3'  GACAGTCCCCCTTGACC     54716        AT  AA
                                GGTCAAGGG  GGA  GTC
                                |||||||||  |||  |||
                                CCAGTTCCC  CCT  CAG
                                     __  GA
GAM251  SLC26A9  3'  GACAGTCCCCCTTGACC     57008        AT  AA
                                GGTCAAGGG  GGA  GTC
                                |||||||||  |||  |||
                                CCAGTTCCC  CCT  CAG
                                     __  GA
GAM251  STIP-1   3'  TGTCTACTCCATCCCCAACC  70241     CAA      A_  T
                                GGT  GGGATGGA  AG CA
                                |||  ||||||||  || ||
                                CCA  CCCTACCT  TC GT
                                  AC_      CA  T
GAM251  STRAIT11499 5'  GGCGGGCATCCCCTTGACC  41431         _  GAAA
                                GGTCAAGGG ATG   GTC
                                |||||||||  |||   |||
                                CCAGTTCCC TAC   CGG
                                     C  GGG_
GAM251  TBLR1    3'  TGACTGTCCCTGACC      45431      A    GGAA
                                GGTCA GGGAT   AGTCA
                                |||||  |||||   |||||
                                CCAGT CCCTG   TCAGT
                                  _   _____
GAM251  TCL6     3'  GACTCCATCTCCTGACC     27758      A      AA
                                GGTCA GGGATGGA  GTC
                                |||||  ||||||||  |||
                                CCAGT CTCTACCT  CAG
                                   C      __
GAM251  TCL6     3'  GACTCCATCTCCTGACC     25906      A      AA
                                GGTCA GGGATGGA  GTC
                                |||||  ||||||||  |||
                                CCAGT CTCTACCT  CAG
                                   C      __
GAM251  TUB      5'  GTGGGACCATCCCTTAAACC  13897     C_      AAAG
                                GGT  AAGGGATGG   TCAC
                                |||  |||||||||   ||||
                                CCA  TTCCCTACC   GGTG
                                  AA       AG__
GAM251  ZNF282   3'  TGACTTTCCCTGCCCTTGCC  90699    T     AT_
                                GG CAAGGG   GGAAAGTCA
                                ||  ||||||  |||||||||
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                                CC GTTCCC   CCTTTCAGT
                                 _     GTC
GAM251   LOC115297 3'  TGACTTAGAACCATCCTTGACC 73263        G    A___
                                GGTCAAGG ATGG    AAGTCA
                                |||||||| ||||    ||||||
                                CCAGTTCC TACC    TTCAGT
                                     _   AAGA
GAM251   LOC124753 5'  GGCTTCCATCTCCCAACC    74806     CAA       A
                                GGT   GGGATGGAA GTC
                                |||   ||||||||| |||
                                CCA   CTCTACCTT CGG
                                  ACC       _
GAM251   LOC131583 3'  GACAACCTCCCTGTCCCTTGCC 76380    T      __   AA__
                                GG CAAGGGAT  GGA    GTC
                                || ||||||||  |||    |||
                                CC GTTCCCTG  CCT    CAG
                                 _       TC   CCAA
GAM251   LOC145231 3'  GGCTTGTCCATCCCTTGAC    84254            _
                                GTCAAGGGATGGA AAGTC
                                |||||||||||| |||||
                                CAGTTCCCTACCT TTCGG
                                       G
GAM251   LOC145389 5'  ATGGTCCATCCCTTGTCC    77722    T        AA
                                GG CAAGGGATGGA  GT
                                || ||||||||||  ||
                                CC GTTCCCTACCT  TA
                                 T          GG
GAM251   LOC148137 3'  GGCCTGCCCATCCCTGACC    59106      A      AA  _
                                GGTCA GGGATGG  AG TC
                                ||||| |||||||  || ||
                                CCAGT CCCTACC  TC GG
                                   _      CG  C
GAM251   LOC162048 5'  GGTGAAGACGCCCTTGACC    83202         A  GAAAG
                                GGTCAAGGG TG     TCACC
                                ||||||||| ||     |||||
                                CCAGTTCCC GC     AGTGG
                                     _  AGA__
GAM251   LOC202018 3'  GACCTCCGGCCTTGACT     90608        GA    AA
                                GGTCAAGG  TGGA  GTC
                                ||||||||  ||||  |||
                                TCAGTTCC  GCCT  CAG
                                    G_    C_
GAM251   LOC202266 3'  GTAACTTCCATTTTTGTCC    91938    T    G     A  C
                                GG CAAGG ATGGAA GT AC
                                || ||||| |||||| || ||
                                CC GTTTT TACCTT CA TG
                                 T    _     _ A
GAM251   LOC221466 5'  GGCCCTTCCATCCCTTGTCC   95316    T         A_
                                GG CAAGGGATGGAA  GTC
                                || ||||||||||||  |||
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                                CC GTTCCCTACCTT  CGG
                                 T          CC
GAM251  LOC222865 3'  GGTTACCACCCCCTTGACC   94449         AT  AAA  C
                                GGTCAAGGG  GG   GT ACC
                                |||||||||  ||   || |||
                                CCAGTTCCC  CC   CA TGG
                                     __  AC_  T
GAM251  LOC254105 3'  GTGACCCAGACCTCTGACC   96421      _  GA   AAA
                                GGTCA AGG  TGG   GTCAC
                                |||||| |||  |||   |||||
                                CCAGT TCC  ACC   CAGTG
                                   C   AG  ___
GAM251  LOC54505  5'  GTGACCTTCATTCTGCC     68447     CAA       AA
                                GGT   GGGATGGA  GTCAC
                                |||   ||||||||  |||||
                                CCG   TCTTACTT  CAGTG
                                  ___       C_
GAM251  LOC56965  3'  GACTCCATCCCCTGACT     39924      A       AA
                                GGTCA GGGATGGA  GTC
                                |||||| ||||||||  |||
                                TCAGT CCCTACCT  CAG
                                   C       __
GAM251  LOC56965  3'  GACTCCATCCCCTGACT     39931      A       AA
                                GGTCA GGGATGGA  GTC
                                |||||| ||||||||  |||
                                TCAGT CCCTACCT  CAG
                                   C       __
GAM252  GPD1      3'  TCATGCCACCACATTTG     60398       C       C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A       _
GAM252  IL5RA     5'  TCGCATGGCCACCGCATTT   6906           AT__
                                AAATGCGGTGGC   CGA
                                ||||||||||||   |||
                                TTTACGCCACCG   GCT
                                      GTAC
GAM252  MYO1C     3'  TGCCGATGCCAAATATTTG   61873       CGG       A
                                TAAATG  TGGCATCG CA
                                ||||||  |||||||| ||
                                GTTTAT  ACCGTAGC GT
                                   AA_       C
GAM252  C6orf37   3'  TGTCACACTGCATTTA      68097          GCATC
                                TAAATGCGGTG    GACA
                                ||||||||||    ||||
                                ATTTACGTCAC    CTGT
                                      A____
GAM252  DNAJC6    3'  TTGCAGAACCACCGCATT    29498          CA  GA
                                AATGCGGTGG  TC  CAA
                                |||||||||  ||  |||
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                                TTACGCCACC  AG  GTT
                                     A_  AC
GAM252  FLJ11210  3'  GTCGATGTGCATGCTTTTA   60319     T  GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM252  FLJ12476  3'  TCGATCTTCTGCATTTA     43270        T  C
                                TAAATGCGG GG ATCGA
                                ||||||||| || |||||
                                ATTTACGTC TC TAGCT
                                     T  _
GAM252  KIAA1034  3'  TCGATGGCATCCGCATTTG   63134        _  G
                                TAAATGCGG TG CATCGA
                                ||||||||| || ||||||
                                GTTTACGCC AC GTAGCT
                                     T  G
GAM252  KIAA1987  3'  TCATGTAACTGCATTTA     89391        G   C
                                TAAATGCGGT GCAT GA
                                |||||||||| ||||| ||
                                ATTTACGTCA TGTA CT
                                     A   _
GAM252  MGC16063  3'  TGTCCTGGCCACTGCATT    54929         ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                      GTC
GAM252  LOC147949 3'  TGTCAGATGTCCACATTGCA  79279     __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM252  LOC150577 3'  GTCCTCACCGCATTTG      86258         CATC
                                TAAATGCGGTGG   GAC
                                ||||||||||||   |||
                                GTTTACGCCACT   CTG
                                      C___
GAM252  LOC158219 3'  TGTGTGTCACCACATTT     82694      C      CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                   A      __
GAM252  LOC202020 3'  TGTCTCACCACATTTA      90605      C    CATC
                                TAAATG GGTGG   GACA
                                |||||| |||||   ||||
                                ATTTAC CCACT   CTGT
                                   A    _____
GAM252  LOC90826  5'  TGTCGATGCAGGTTTATTTG  64788      CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
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                                GTTTAT    CGTAGCTGT
                                   TTGGA
GAM252  LOC93587  3'  TTGTCTTTACCTGCATTTA   73042       _    CATC
                                TAAATGC GGTGG   GACAA
                                ||||||| |||||   |||||
                                ATTTACG CCATT   CTGTT
                                    T    T___
GAM253  AIM1      3'  GTGCTAAACATTTCCTTGAA  93468          GAA  T
                                TTCAAGGGAATG   AG CAC
                                ||||||||||||   || |||
                                AAGTTCCTTTAC   TC GTG
                                       AAA  _
GAM253  BRCA1     3'  GTGACTCTTCTGCCCTTGAG  24572        AAT   A
                                TTCAAGGG   GGA AGTCAC
                                ||||||||   ||| ||||||
                                GAGTTCCC   CTT TCAGTG
                                     GT_   C
GAM253  CHRM1     5'  TGACTTTCCCCTGAG      96436      A   AATG
                                TTCA GGG    GAAAGTCA
                                |||| |||    ||||||||
                                GAGT CCC    CTTTCAGT
                                  _   ____
GAM253  D1S155E   5'  ACTTTCATCCTTTGAA     24100         ATG
                                TTCAAGGGA   GAAAGT
                                |||||||||   ||||||
                                AAGTTTCCT   CTTTCA
                                     A__
GAM253  DDEF2     3'  GACACACATTCCTTTGAA    15288          GAAA
                                TTCAAGGGAATG   GTC
                                ||||||||||||   |||
                                AAGTTTCCTTAC   CAG
                                       ACA_
GAM253  FBN2      3'  ACCGCCGTTCCCTTGAA     10576           AAA
                                TTCAAGGGAATGG   GT
                                ||||||||||||   ||
                                AAGTTCCCTTGCC   CA
                                       GC_
GAM253  FOXE1     3'  ACTCTCCCCCTTTCCCTTGAG  16775         T___   A
                                TTCAAGGGAA    GGA AGT
                                |||||||||    ||| |||
                                GAGTTCCCTT    CCT TCA
                                      TCCC   C
GAM253  GFAP      3'  GTGACTCATCCTCTTGAA     10783        A  GAA
                                TTCAAGGG ATG   AGTCAC
                                |||||||| |||   ||||||
                                AAGTTCTC TAC   TCAGTG
                                     C   ___
GAM253  GPC4      3'  GATATCATCCCCCTTGAA     9353         A_   AAA
                                TTCAAGGG  ATGG   GTC
                                ||||||||  ||||   |||
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                                AAGTTCCC  TACT   TAG
                                    CC    A__
GAM253  GRINL1A  3'  GGTGACTTTCATGTGCTTGAA  70064      GGAATG
                                TTCAAG     GAAAGTCACC
                                ||||||     ||||||||||
                                AAGTTC     CTTTCAGTGG
                                   GTGTA_
GAM253  LECT2    5'  GACTTGCTCCATCCTCTT    11296      A    __
                                AAGGG ATGGA  AAGTC
                                ||||| |||||  |||||
                                TTCTC TACCT  TTCAG
                                  C    CG
GAM253  NOTCH2   3'  GGTGACTCTCTGCCCTTGGA   44577       AAT   A
                                TTCAAGGG   GGA AGTCACC
                                ||||||||   ||| |||||||
                                AGGTTCCC   TCT TCAGTGG
                                    G__   C
GAM253  PCK1     3'  TGACCTACTAGTTTTCCTTGAA 60622         __   AAA
                                TTCAAGGGAA  TGG   GTCA
                                ||||||||||  |||   ||||
                                AAGTTCCTTT  ATC   CAGT
                                     TG   ATC
GAM253  PDL2     5'  ACTTTTCTTCTCTTGAA     48227         T
                                TTCAAGGGAA GGAAAGT
                                |||||||||| |||||||
                                AAGTTCTCTT CTTTTCA
                                          _
GAM253  PITX2    3'  GGCAACTCCGCCCTTGAA    6157        AA   AA_
                                TTCAAGGG  TGGA   GTC
                                ||||||||  ||||   |||
                                AAGTTCCC  GCCT   CGG
                                    __    CAA
GAM253  PPP1R12B 3'  GTGGTTCATTCCCTT      50393         AAG
                                AAGGGAATGGA   TCAC
                                ||||||||||   ||||
                                TTCCCTTACTT   GGTG
                                          ___
GAM253  PROS1    3'  GTGTGCCTTCCCTTGAA     88816         T  AAAGT
                                TTCAAGGGAA GG     CAC
                                |||||||||| ||     |||
                                AAGTTCCCTT CC     GTG
                                     _  GT___
GAM253  SCD      3'  GATAACTCTCTTTCCTTGAG  18593         T   AA_
                                TTCAAGGGAA GGA   GTC
                                |||||||||| |||   |||
                                GAGTTCCTTT TCT   TAG
                                     C   CAA
GAM253  SMARCD1  3'  ATTTTCCCTCCCTTGAA     13258         AT
                                TTCAAGGGA  GGAAAGT
                                |||||||||  |||||||
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                                AAGTTCCCT  CCTTTTA
                                     C_
GAM253  SMARCD1   3'  ATTTTCCCTCCCTTGAA     58184         AT
                                TTCAAGGGA  GGAAAGT
                                |||||||||  |||||||
                                AAGTTCCCT  CCTTTTA
                                     C_
GAM253  AKL3L     3'  TGACTTGTTTCCTTTGAA    33271         TGGA
                                TTCAAGGGAA   AAGTCA
                                ||||||||||   ||||||
                                AAGTTTCCTT   TTCAGT
                                      TG__
GAM253  ATP10D    3'  GGCATTCATTCCCTGAA     73527      A       AA
                                TTCA GGGAATGGA  GTC
                                |||| |||||||||  |||
                                AAGT CCCTTACTT  CGG
                                  _       A_
GAM253  C20orf72  3'  GGTGACTCTTGTACTCCCTTGA 54607         A  G  _
           G                     TTCAAGGGA TG AA AGTCACC
                                 |||||||||  ||  ||  |||||||
                                 GAGTTCCCT AT TT TCAGTGG
                                      C  G  C
GAM253  Cab45     3'  GCTCCTCCATTTCCTTGAA   32973           A_
                                TTCAAGGGAATGGA  AGT
                                |||||||||||||  |||
                                AAGTTCCTTTACCT  TCG
                                      CC
GAM253  COL21A1   3'  GATAACCAACAGTATCCCTTGA 48772         A_____   AAA
           A                     TTCAAGGGA     TGG   GTC
                                 |||||||||     |||   |||
                                 AAGTTCCCT     ACC   TAG
                                      ATGACA   AA_
GAM253  DKFZP434A0131 3'  GTGAAGTCATTTCCCCGAA   39153     AA       AAAG
                                TTC  GGGAATGG    TCAC
                                |||  ||||||||    ||||
                                AAG  CCTTTACT    AGTG
                                  CC       GA__
GAM253  DKFZp547D155 3'  GGCGACTTGCCTGCCCCTGAA  70950      A   AAT  A    A
                                TTCA GGG   GG AAGTC CC
                                |||| |||   ||  ||||| ||
                                AAGT CCC   CC TTCAG GG
                                  C   GT_  G    C
GAM253  FLJ13842  3'  GGCACCATTCCCTTGAG     45333           AAA
                                TTCAAGGGAATGG   GTC
                                ||||||||||||   |||
                                GAGTTCCCTTACC   CGG
                                      A__
GAM253  FLJ20498  3'  GACCCTCCACTCCTTGAA    39281         AA   AA
                                TTCAAGGG  TGGA  GTC
                                ||||||||  ||||  |||
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                                AAGTTCCT  ACCT  CAG
                                    C_   CC
GAM253  GREB1    5' GACTCCATCCTCTTGAA    72839       A    AA
                                TTCAAGGG ATGGA  GTC
                                |||||||| |||||  |||
                                AAGTTCTC TACCT  CAG
                                    C    __
GAM253  KIAA0040 3' GGCAACTGCTTGCTCCTTTGAA 28491        AT  AA   CA
                                TTCAAGGGA  GG  AGT  CC
                                |||||||||  ||  |||  ||
                                AAGTTTCCT  TT  TCA  GG
                                     CG  CG   AC
GAM253  KIAA0285 3' ACTGGTTATCCTTTGAA    29679        A   AA
                                TTCAAGGGA TGG  AGT
                                ||||||||| |||  |||
                                AAGTTTCCT ATT  TCA
                                    _  GG
GAM253  KIAA1354 5' GTGACTGCCTTCCCTTGA   61577        T  AA
                                TCAAGGGAA GG  AGTCAC
                                ||||||||| ||  ||||||
                                AGTTCCCTT CC  TCAGTG
                                    _ G_
GAM253  P2RXL1   3' CGGTGACCCCCCAGCCCAACCC 19559       AA_____  AAA    ___
          CTTGGA              TTCAAGGG     TGG   GTCACC   G
                                ||||||||     |||  ||||||  |
                                AGGTTCCC     ACC   CAGTGG   C
                                    CAACCCG   CCC    ___
GAM253  SLC5A7   3' ACTTCAGTCACTCCCTTGAA  41802       A  A__
                                TTCAAGGGA TGG   AAGT
                                ||||||||| |||   ||||
                                AAGTTCCCT ACT   TTCA
                                    C   GAC
GAM253  SRPK2    3' GGTGACTCTCATTCTTT    13412        AA
                                AGGGAATGG  AGTCACC
                                |||||||||  |||||||
                                TTTCTTACT  TCAGTGG
                                    C_
GAM253  STARD7   3' GGCTGGGCCACTCCCTTGGA  58371        A  AA_
                                TTCAAGGGA TGG   AGTC
                                ||||||||| |||   ||||
                                AGGTTCCCT ACC   TCGG
                                    C   GGG
GAM253  STARD7   3' GGCTGGGCCACTCCCTTGGA  39744        A  AA_
                                TTCAAGGGA TGG   AGTC
                                ||||||||| |||   ||||
                                AGGTTCCCT ACC   TCGG
                                    C   GGG
GAM253  WIRE     3' GGTCCCTTCCATTCCCCTGAA  78906     A       A TC
                                TTCA GGGAATGGAA G  ACC
                                |||| |||||||||| |  |||
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                                AAGT CCCTTACCTT C  TGG
                                  C        _ CC
GAM253  ZFP106    3'  GGTGTTTTCCACCCCCCTG   42737    A  AA      T
                                CA GGG  TGGAAAG CACC
                                || |||  ||||||| ||||
                                GT CCC  ACCTTTT GTGG
                                 C  CC      _
GAM253  ZNF262    3'  TGACCTTGTTGCCCTTGAA   18728         _ TG AAA
                                TTCAAGGG AA  G   GTCA
                                |||||||| ||  |   ||||
                                AAGTTCCC TT  T   CAGT
                                     G  GT C__
GAM253  LOC126964 3'  GATAAATTCTTCCCCTTGAA  75115         AAT   A__
                                TTCAAGGG   GGAA   GTC
                                ||||||||   ||||   |||
                                AAGTTCCC   TCTT   TAG
                                     CT_    AAA
GAM253  LOC145858 3'  GGCAACCTTCCTTTGGA     78002          T  AAA
                                TTCAAGGGAA GG   GTC
                                |||||||||| ||   |||
                                AGGTTTCCTT CC   CGG
                                      _  AA_
GAM253  LOC146177 3'  GTGCACACCATTTCCTTGAA  78190            AAA  _
                                TTCAAGGGAATGG   GT CAC
                                ||||||||||||   || |||
                                AAGTTCCTTTACC   CA GTG
                                       A__  C
GAM253  LOC146337 5'  GGCAACTCTAGCCTTTGAA   84643         AA   AA_
                                TTCAAGGG  TGGA   GTC
                                ||||||||  ||||   |||
                                AAGTTTCC  ATCT   CGG
                                     G_    CAA
GAM253  LOC147463 3'  TGACTTTGAGGTCCTTGGA   79005         AATGG
                                TTCAAGGG    AAAGTCA
                                ||||||||    |||||||
                                AGGTTCCT    TTTCAGT
                                     GGAG_
GAM253  LOC149072 5'  GGCCTGGCCATTCCCCTGGA  79886      A       AA  _
                                TTCA GGGAATGG  AG TC
                                |||| ||||||||  || ||
                                AGGT CCCTTACC  TC GG
                                  C       GG  C
GAM253  LOC149703 3'  GATAAAACATTCTCTTGAA   85821           GAAA
                                TTCAAGGGAATG    GTC
                                ||||||||||||    |||
                                AAGTTCTCTTAC    TAG
                                       AAAA
GAM253  LOC151057 3'  GTGACCCTACCCTTGAG     86396         AAT  AAA
                                TTCAAGGG   GG   GTCAC
                                ||||||||   ||   |||||
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                                GAGTTCCC  CC  CAGTG
                                    AT_ ___
GAM253  LOC151470 3' GGTGACTTTTCACCTT     81057     AA
                                AGGG TGGAAAGTCACC
                                |||| ||||||||||||
                                TTCC ACTTTTCAGTGG
                                  __
GAM253  LOC152018 3' GACCTCCACCCCCTTGAA    86728       AA   AA
                                TTCAAGGG TGGA GTC
                                |||||||| |||| |||
                                AAGTTCCC ACCT CAG
                                    CC   C_
GAM253  LOC155435 3' GGTGACTTTGGTAGCCCTTGAG 82270       AATGG
                                TTCAAGGG    AAAGTCACC
                                ||||||||    |||||||||
                                GAGTTCCC    TTTCAGTGG
                                    GATGG
GAM253  LOC219731 5' GGTCTTCCTGCCATTCCCCTGA 94711     A      AAAGTC_
          A                      TTCA GGGAATGG      ACC
                                |||| ||||||||      |||
                                AAGT CCCTTACC      TGG
                                  C      GTCCTTC
GAM253  LOC253336 3' GTAACTTTCTTCATCCCTTGAA 99181       AT_     C
                                TTCAAGGGA  GGAAAGT AC
                                |||||||||  ||||||| ||
                                AAGTTCCCT  TCTTTCA TG
                                     ACT     A
GAM253  LOC255743 3' GTGATACCCTCCTTGAA     97603       AAT  AAA
                                TTCAAGGG  GG  GTCAC
                                ||||||||  ||  |||||
                                AAGTTCCT  CC  TAGTG
                                    ___ CA_
GAM253  LOC58512  3' GGCTGTTCCCACATCCCCTTGA 65285       A ___  _
          A                      TTCAAGGG AT  GGAA AGTC
                                |||||||| ||  |||| ||||
                                AAGTTCCC TA  CCTT TCGG
                                    C  CAC   G
GAM253  LOC91960  3' GGCCAAAACCATTCCCTCGGA  68290    A      AAA__
                                TTC AGGGAATGG    GTC
                                ||| |||||||||    |||
                                AGG TCCCTTACC    CGG
                                  C        AAAAC
GAM254  BCAT1     3' GGCTACTTCCCATCACTCGAA  66788    A  G     __
                                TTC AG GATGGGAA  AGTC
                                ||| || ||||||||  ||||
                                AAG TC CTACCCTT  TCGG
                                  C  A       CA
GAM254  BRCA1     3' GTGACTCTTCTGCCCTTGAG  24572       A   A
                                TTCAAGGG TGGGA AGTCAC
                                |||||||| ||||| ||||||
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                                GAGTTCCC GTCTT TCAGTG
                                   _    C
GAM254  FHL1    3'  GTGACTAGTTGAATCCCTTG  9361        GG  A_
                                CAAGGGAT  GA  AGTCAC
                                ||||||||  ||  ||||||
                                GTTCCCTA  TT  TCAGTG
                                    AG  GA
GAM254  FOXE1   3'  ACTCTCCCCCTTTCCCTTGAG  16775        T___   A
                                TTCAAGGGA   GGGA AGT
                                |||||||||   |||| |||
                                GAGTTCCCT   CCCT TCA
                                     TTCC   C
GAM254  FOXE3   3'  GGTCTGCCCCATCCCCTGGA  25165     A      AA  TC
                                TTCA GGGATGGG  AG  ACC
                                |||| ||||||||  ||  |||
                                AGGT CCCTACCC  TC  TGG
                                  C       CG  __
GAM254  GARP    3'  TGACTTTCAGTCTCTCTGAA  19788     _     GG
                                TTCA AGGGAT  GAAAGTCA
                                |||| ||||||  ||||||||
                                AAGT TCTCTG  CTTTCAGT
                                  C     A_
GAM254  GFAP    3'  GTGACTCATCCTCTTGAA    10783       _    GGAA
                                TTCAAG GGATG   AGTCAC
                                |||||| |||||   ||||||
                                AAGTTC CCTAC   TCAGTG
                                   T    _____
GAM254  GRINL1A 3'  GGTGACTTTCATGTGCTTGAA  70064       GGATGG
                                TTCAAG     GAAAGTCACC
                                ||||||     ||||||||||
                                AAGTTC     CTTTCAGTGG
                                   GTGTA_
GAM254  HAP1    3'  GACCCTCCTTCCCATCCTCTGA 15476     AG       A_____
          A                     TTCA  GGATGGGAA    GTC
                                ||||  |||||||||    |||
                                AAGT  CCTACCCTT    CAG
                                  CT        CCTCC
GAM254  KCNMA1  3'  GTAACTTTCCCTGTTTTCCCCT 11180    A   T_____      C
          G                     CA GGGA    GGGAAAGT AC
                                || ||||    |||||||| ||
                                GT CCCT    CCCTTTCA TG
                                 C   TTTGT       A
GAM254  MLLT4   3'  TGACTTGCCTCTTGAA     72902       GGAT   A
                                TTCAAG   GGG AAGTCA
                                ||||||   ||| ||||||
                                AAGTTC   TCC TTCAGT
                                   _____  G
GAM254  NOTCH2  3'  GGTGACTCTCTGCCCTTGGA  44577        ATG   A
                                TTCAAGGG   GGA AGTCACC
                                ||||||||   ||| |||||||
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                                AGGTTCCC   TCT TCAGTGG
                                     G__   C
GAM254   PDL2     5'  ACTTTTCTTCTCTTGAA     48227         T
                                TTCAAGGGA GGGAAAGT
                                ||||||||| ||||||||
                                AAGTTCTCT TCTTTTCA
                                          _
GAM254   PITX2    3'  GGCAACTCCGCCCTTGAA     6157         A   AAA
                                TTCAAGGG TGGG   GTC
                                |||||||| ||||   |||
                                AAGTTCCC GCCT   CGG
                                     _   CAA
GAM254   PROS1    3'  GTGTGCCTTCCCTTGAA     88816         T   AAAGT
                                TTCAAGGGA GGG    CAC
                                ||||||||| |||    |||
                                AAGTTCCCT TCC    GTG
                                     _   GT___
GAM254   RAB36    3'  GGTAACTCACTCTGCAGCCCTT 18173         AT___   AA   C
            GAA                    TTCAAGGG    GGG  AGT ACC
                                |||||||     |||  ||| |||
                                AAGTTCCC    CTC  TCA TGG
                                     GACGT   AC   A
GAM254   SCD      3'  GATAACTCTCTTTCCTTGAG   18593         T   AA_
                                TTCAAGGGA GGGA   GTC
                                ||||||||| ||||   |||
                                GAGTTCCTT CTCT   TAG
                                     T   CAA
GAM254   SMARCD1  3'  ATTTTCCCTCCCTTGAA     58184         T
                                TTCAAGGGA GGGAAAGT
                                ||||||||| ||||||||
                                AAGTTCCCT CCCTTTTA
                                          _
GAM254   SMARCD1  3'  ATTTTCCCTCCCTTGAA     13258         T
                                TTCAAGGGA GGGAAAGT
                                ||||||||| ||||||||
                                AAGTTCCCT CCCTTTTA
                                          _
GAM254   TIMP4    3'  GTGACCATCACATCCCTT     13757         G  AA
                                AAGGGATG GA  GTCAC
                                |||||||| ||  |||||
                                TTCCCTAC CT  CAGTG
                                     A  AC
GAM254   AFAP     3'  GATGTCCATCCTTGAA      41607         G    AAA
                                TTCAAGG ATGGG   GTC
                                ||||||| |||||   |||
                                AAGTTCC TACCT   TAG
                                     _    G__
GAM254   AKL3L    3'  TGACTTGTTTCCTTTGAA    33271         TGGGA
                                TTCAAGGGA    AAGTCA
                                |||||||||    ||||||
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                                AAGTTTCCT    TTCAGT
                                     TTG__
GAM254  C20orf72  3'  GGTGACTCTTGTACTCCCTTGA 54607        _ G  A
          G                   TTCAAGGGA TG GA AGTCACC
                              ||||||||| || || |||||||
                              GAGTTCCCT AT TT TCAGTGG
                                   C  G  C
GAM254  COL21A1   3'  GATAACCAACAGTATCCCTTGA 48772         _____ AAA
          A                   TTCAAGGGATG    GG   GTC
                              ||||||||||     ||   |||
                              AAGTTCCCTAT    CC   TAG
                                    GACAA  AA_
GAM254  DKFZp547D155 3'  GGCGACTTGCCTGCCCCTGAA  70950     A  AT  A    A
                              TTCA GGG  GGG AAGTC CC
                              |||| |||  ||| ||||| ||
                              AAGT CCC  TCC TTCAG GG
                                _  CG  G    C
GAM254  EFA6R     3'  GTGAGTCATCCCTTGA     31639         GAAAG
                              TCAAGGGATGG    TCAC
                              ||||||||||     ||||
                              AGTTCCCTACT    AGTG
                                    G____
GAM254  EPB41L1   3'  GATGACTCTCCTTTGAA     71109         T   AAA
                              TTCAAGGGA GGG   GTC
                              ||||||||| |||   |||
                              AAGTTTCCT CTC   TAG
                                   _  AG_
GAM254  FLJ10008  3'  GGCAACCTGTCCCTTGAG    36190          AAA
                              TTCAAGGGATGGG   GTC
                              ||||||||||||   |||
                              GAGTTCCCTGTCC   CGG
                                    AA_
GAM254  FLJ20452  3'  ACCTTCCCTTCCCTTGAA    35643         T    A
                              TTCAAGGGA GGGAA GT
                              ||||||||| ||||| ||
                              AAGTTCCCT CCCTT CA
                                    T    C
GAM254  FLJ23420  3'  GGCCTTGCTCCCATCCCTAGAA 47542     A        AA___
                              TTC AGGGATGGGA    GTC
                              ||| ||||||||||    |||
                              AAG TCCCTACCCT    CGG
                                A         CGTTC
GAM254  FLJ23790  5'  GCAGTTCCACCTCTTGAA    59274         A    AA
                              TTCAAGGG TGGGA  GT
                              |||||||| |||||  ||
                              AAGTTCTC ACCTT  CG
                                   C    GA
GAM254  GFR       3'  TGACTTCTTATCCCTGGA    25451     A       A
                              TTC AGGGATGGG AAGTCA
                              ||| ||||||||| ||||||
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                                AGG TCCCTATTC TTCAGT
                                  _       _
GAM254  KIAA0082  3'  GGCCTCCTCTCCATCCCCTGAA 93784      A      _  AA__
                                TTCA GGGATGG GA    GTC
                                |||| ||||||| ||    |||
                                AAGT CCCTACC CT    CGG
                                  C      T  CCTC
GAM254  KIAA0285  3'  ACTGGTTATCCTTTGAA     29679           GAA
                                TTCAAGGGATGG   AGT
                                ||||||||||||   |||
                                AAGTTTCCTATT   TCA
                                       GG_
GAM254  KIAA0794  3'  GGTGACTTTCATTGTCCT    81234      TG _
                                GGGA  G GAAAGTCACC
                                ||||  | ||||||||||
                                TCCT  T CTTTCAGTGG
                                  GT A
GAM254  KIAA1798  3'  TGACTTTTCTTTGAA       61249      GGGAT
                                TTCAA    GGGAAAGTCA
                                |||||    ||||||||||
                                AAGTT    TCTTTTCAGT
                                  _____
GAM254  KIAA1956  3'  GTAACTCCCTCTTGGA      79080       GAT   AA  C
                                TTCAAGG   GGGA  GT AC
                                |||||||   ||||  || ||
                                AGGTTCT   CCCT  CA TG
                                   ___   __ A
GAM254  KLHL6     3'  GATACCCCATCCTCCTGAA   56171      A_      AAA
                                TTCA  GGGATGGG   GTC
                                ||||  ||||||||   |||
                                AAGT  TCCTACCC   TAG
                                  CC       CA_
GAM254  MGC4737   5'  TGACTTTCTGTGGCTTGGA   49652       GGATG
                                TTCAAG    GGAAAGTCA
                                ||||||    |||||||||
                                AGGTTC    TCTTTCAGT
                                   GGTG_
GAM254  MIDORI    3'  GGCAACCTAGGCCCTCCTTGAA 74217      ___    A_   AAA
                                TTCA   AGGG  TGGG   GTC
                                ||||   ||||  ||||   |||
                                AAGT   TCCC  ATCC   CGG
                                  TCC    GG    AA_
GAM254  P2RXL1    3'  CGGTGACCCCCCAGCCCAACCC 19559        A_   AAA____     ___
          CTTGGA                  TTCAAGGG  TGGG      GTCACC   G
                                ||||||||  ||||      ||||||  |
                                AGGTTCCC  ACCC      CAGTGG   C
                                    CA    GACCCCC     ___
GAM254  PRRDH     3'  GATCCCCATCCCTGAA      32323      A       AAA
                                TTCA GGGATGGG   GTC
                                |||| ||||||||   |||
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                                AAGT CCCTACCC   TAG
                                  _      C__
GAM254  SLC5A7    3'  ACTTCAGTCACTCCCTTGAA  41802        _  GA_
                                TTCAAGGGA TGG   AAGT
                                ||||||||| |||   ||||
                                AAGTTCCCT ACT   TTCA
                                     C   GAC
GAM254  SPRY4     3'  GATGACTGTCACCTTGAA    49015       _    GAAA
                                TTCAAGG GATGG    GTC
                                ||||||| |||||    |||
                                AAGTTCC CTGTC    TAG
                                   A    AG__
GAM254  ZNF262    3'  TGACCTTGTTGCCCTTGAA   18728        A  G  A
                                TTCAAGGG TGG AA GTCA
                                |||||||| ||| || ||||
                                AAGTTCCC GTT TT CAGT
                                     _  G  C
GAM254  LOC115265 3'  GGTGACTTCCTCACTCT     73741      A   A
                                AGGG TGGG AAGTCACC
                                |||| |||| ||||||||
                                TCTC ACTC TTCAGTGG
                                  _   C
GAM254  LOC121274 3'  GACCCCATCCCTAGAA      74496     A       AAA
                                TTC AGGGATGGG   GTC
                                ||| |||||||||   |||
                                AAG TCCCTACCC   CAG
                                  A       ____
GAM254  LOC143943 3'  GGCTACCCCCACCCCTTGGA  83919        A   AA_
                                TTCAAGGG TGGG   AGTC
                                |||||||| ||||   ||||
                                AGGTTCCC ACCC   TCGG
                                     C    CCA
GAM254  LOC146337 5'  GGCAACTCTAGCCTTTGAA   84643        A   AAA
                                TTCAAGGG TGGG   GTC
                                |||||||| ||||   |||
                                AAGTTTCC ATCT   CGG
                                     G    CAA
GAM254  LOC147463 3'  TGACTTTGAGGTCCTTGGA   79005        ATGGG
                                TTCAAGGG    AAAGTCA
                                ||||||||    |||||||
                                AGGTTCCT    TTTCAGT
                                     GGAG_
GAM254  LOC151470 3'  GGTGACTTTTCACCTT      81057      ATG
                                AGGG   GGAAAGTCACC
                                ||||   ||||||||||
                                TTCC   CTTTTCAGTGG
                                  A__
GAM254  LOC155435 3'  GGTGACTTTGGTAGCCCTTGAG 82270        A  GG
                                TTCAAGGG TG  AAAGTCACC
                                |||||||| ||  |||||||||
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                                GAGTTCCC AT  TTTCAGTGG
                                     G  GG
GAM254  LOC160717 5'  GGCCCCACCCTTGAA       83129         A    AAA
                                TTCAAGGG TGGG   GTC
                                |||||||| ||||   |||
                                AAGTTCCC ACCC   CGG
                                      _   ____
GAM254  LOC197342 3'  GACCTTCCTGTTACCTGAG    89366      A _       A
                                TTCA GG GATGGGAA GTC
                                |||| || |||||||| |||
                                GAGT CC TTGTCCTT CAG
                                   _ A       C
GAM254  LOC221584 3'  TGGAAGGTCCATCTCCTGAA   95473      A        AAAG
                                TTCA GGGATGGG    TCA
                                |||| ||||||||    |||
                                AAGT CTCTACCT    GGT
                                   C       GGAA
GAM254  LOC253336 3'  GTAACTTTCTTCATCCCTTGAA 99181            _     C
                                TTCAAGGGATGG GAAAGT AC
                                |||||||||||| |||||| ||
                                AAGTTCCCTACT CTTTCA TG
                                       T     A
GAM254  LOC92912  3'  GGTAACTTTCCTATATTGAG   71408      GGG        C
                                TTCAA   ATGGGAAAGT ACC
                                |||||   |||||||||| |||
                                GAGTT   TATCCTTTCA TGG
                                   A__         A
GAM255  GPD1      3'  TCATGCCACCACATTTG     60398       C       C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A       _
GAM255  IL5RA     5'  TCGCATGGCCACCGCATTT    6906           AT__
                                AAATGCGGTGGC    CGA
                                ||||||||||||    |||
                                TTTACGCCACCG    GCT
                                       GTAC
GAM255  MYO1C     3'  TGCCGATGCCAAATATTTG    61873       CGG       A
                                TAAATG   TGGCATCG CA
                                ||||||   |||||||| ||
                                GTTTAT   ACCGTAGC GT
                                   AA_       C
GAM255  C6orf37   3'  TGTCACACTGCATTTA      68097          GCATC
                                TAAATGCGGTG     GACA
                                ||||||||||     ||||
                                ATTTACGTCAC     CTGT
                                       A_____
GAM255  DNAJC6    3'  TTGCAGAACCACCGCATT     29498          CA  GA
                                AATGCGGTGG  TC  CAA
                                |||||||||  ||  |||
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                                TTACGCCACC  AG  GTT
                                     A_  AC
GAM255  FLJ11210  3'  GTCGATGTGCATGCTTTTA   60319     T  GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM255  FLJ12476  3'  TCGATCTTCTGCATTTA     43270        T  C
                                TAAATGCGG GG ATCGA
                                ||||||||| || |||||
                                ATTTACGTC TC TAGCT
                                     T  _
GAM255  KIAA1034  3'  TCGATGGCATCCGCATTTG   63134        _  G
                                TAAATGCGG TG CATCGA
                                ||||||||| || ||||||
                                GTTTACGCC AC GTAGCT
                                     T  G
GAM255  KIAA1987  3'  TCATGTAACTGCATTTA     89391        G   C
                                TAAATGCGGT GCAT GA
                                |||||||||| ||||| ||
                                ATTTACGTCA TGTA CT
                                     A   _
GAM255  MGC16063  3'  TGTCCTGGCCACTGCATT    54929         ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                      GTC
GAM255  LOC147949 3'  TGTCAGATGTCCACATTGCA  79279     __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM255  LOC150577 3'  GTCCTCACCGCATTTG      86258         CATC
                                TAAATGCGGTGG   GAC
                                ||||||||||||   |||
                                GTTTACGCCACT   CTG
                                      C___
GAM255  LOC158219 3'  TGTGTGTCACCACATTT     82694      C      CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                   A      __
GAM255  LOC202020 3'  TGTCTCACCACATTTA      90605      C    CATC
                                TAAATG GGTGG   GACA
                                |||||| |||||   ||||
                                ATTTAC CCACT   CTGT
                                   A    _____
GAM255  LOC90826  5'  TGTCGATGCAGGTTTATTTG  64788      CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
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                                GTTTAT    CGTAGCTGT
                                   TTGGA
GAM255  LOC93587  3'  TTGTCTTTACCTGCATTTA   73042       _    CATC
                                TAAATGC GGTGG   GACAA
                                ||||||| |||||   |||||
                                ATTTACG CCATT   CTGTT
                                    T    T___
GAM256  ACTR1B   3'  TGTGGCCAGGGCCCCACCTCCC 71381    A      GGAGAT
                                GG AGGTGGGG     GCCACA
                                || ||||||||     ||||||
                                CC TCCACCCC     CGGTGT
                                 C       GGGAC_
GAM256  ACVR1    5'  GCAGCCTCCACCTCCCA     8474      A       GAGA
                                TGG AGGTGGGGG   TGC
                                ||| |||||||||   |||
                                ACC TCCACCTCC   ACG
                                  C       G___
GAM256  ATP2B4   5'  GTGACACGGAGTCCACCTTCCA 70848          GGGAGA  C
                                TGGAAGGTGGG     TG CAC
                                ||||||||||      || |||
                                ACCTTCCACCT     AC GTG
                                       GAGGC_  A
GAM256  BAZ2A    3'  ATCTCCCCCCCACCTTCCA    26504
                                TGGAAGGTGGGGGGGAGAT
                                ||||||||||||||||||
                                ACCTTCCACCCCCCTCTA

GAM256  BAZ2A    3'  TGTGGCATCTCCCCCCCACCTTC 26516
            CA                    TGGAAGGTGGGGGGGAGATGCCACA
                                ||||||||||||||||||||||||
                                ACCTTCCACCCCCCTCTACGGTGT

GAM256  BHLHB3   3'  GCACCACCCCACCCTCCA    48487      A      _  AGA
                                TGGA GGTGGGG GG   TGC
                                |||| ||||||| ||   |||
                                ACCT CCACCCC CC   ACG
                                  C      A  ___
GAM256  BRPF1    3'  TAGATTCCCCCACCTTTCA   73477             GA
                                TGGAAGGTGGGGGGGA  TG
                                ||||||||||||||  ||
                                ACTTTCCACCCCCTT  AT
                                         AG
GAM256  C18orf2  3'  CATCCCGCCCACCCCCCA    49461     AA     G  A
                                TGG  GGTGGG GG GATG
                                |||  |||||| || ||||
                                ACC  CCACCC CC CTAC
                                  CC     G  _
GAM256  CD7      3'  CATGCCCCCCCACCCTGCCA   21541     AA_       AG
                                TGG   GGTGGGGGGG  ATG
                                |||   |||||||||  |||
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                                ACC   CCACCCCCC  TAC
                                  GTC       G_
GAM256  CLC      3'  TGTCTCCTCCCCACCTCCCA  26027    A      _
                                TGG AGGTGGGG GGAGATG
                                ||| |||||||| |||||||
                                ACC TCCACCCC CCTCTGT
                                  C       T
GAM256  CRABP1   3'  GTAGTGTCCCCCACCCCCA   60467    AA       AGA
                                TGG  GGTGGGGGGG   TGC
                                |||  |||||||||   |||
                                ACC  CCACCCCCT   ATG
                                  C_       GTG
GAM256  CXCL16   3'  GCAACCCCCATCTCCCA    42171    A       GAGA
                                TGG AGGTGGGGG    TGC
                                ||| |||||||||    |||
                                ACC TCTACCCCC    ACG
                                  C       A___
GAM256  CYP4A11  3'  ATCTCCACCCACCTCCCA   7585     A      G
                                TGG AGGTGGG GGAGAT
                                ||| ||||||| ||||||
                                ACC TCCACCC CCTCTA
                                  C      A
GAM256  DDX11    3'  TGTGGCATCTCCGTCCTGCC  48393    TG  _
                                GG  GGG GGAGATGCCACA
                                ||  ||| ||||||||||||
                                CC  CCT CCTCTACGGTGT
                                 GT   G
GAM256  DDX11    3'  TGTGGCATCTCCGTCCTGCC  48394    TG  _
                                GG  GGG GGAGATGCCACA
                                ||  ||| ||||||||||||
                                CC  CCT CCTCTACGGTGT
                                 GT   G
GAM256  DDX11    3'  TGGCACCTCCCTCCCTCTC   16582    AG T      A
                                GA  G GGGGGGAG TGCCA
                                ||  | |||||||| |||||
                                CT  C CCTCCCTC ACGGT
                                 CT _       C
GAM256  DDX11    3'  TGGCACCTCCCTCCCTCTC   16583    AG T      A
                                GA  G GGGGGGAG TGCCA
                                ||  | |||||||| |||||
                                CT  C CCTCCCTC ACGGT
                                 CT _       C
GAM256  DNMT2    3'  GTACTCCCCTCCCCCCA     16617    AA  T      A
                                TGG  GG GGGGGGAG TGC
                                |||  || |||||||| |||
                                ACC  CC CTCCCCTC ATG
                                  C_ _       _
GAM256  DSCR3    3'  GCAACCTCCACCTCCCA     21317    A       GAGA
                                TGG AGGTGGGGG    TGC
                                ||| |||||||||    |||
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                                ACC TCCACCTCC   ACG
                                  C       A___
GAM256  FEZ1    3'  GCAACCTCCACCTCCCA    18786    A      GAGA
                                TGG AGGTGGGGG   TGC
                                ||| |||||||||   |||
                                ACC TCCACCTCC   ACG
                                  C       A___
GAM256  FOXE3   3'  GTTTGCCCCCCACCTCCA    25166    A      _
                                TGGA GGTGGGGGGG AGAT
                                |||| ||||||||| ||||
                                ACCT CCACCCCCC TTTG
                                  _       G
GAM256  GABRE   3'  GTGACATCTCCCTCTCCT    42075    T      C
                                AGG GGGGGGAGATG CAC
                                ||| |||||||||| |||
                                TCC TCTCCCTCTAC GTG
                                  _        A
GAM256  HOXC10  3'  GTAGCACCCAGAGCCTCCA   61930    A  GGG  AGA  C
                                TGGA GGT  GGG  TGC AC
                                |||| |||  |||  ||| ||
                                ACCT CCG  CCC  ACG TG
                                  _  AGA  ___  A
GAM256  HSD17B1 5'  ATCATCTCCCACCTCCCA    6427     A      GA
                                TGG AGGTGGGGG  GAT
                                ||| |||||||||  |||
                                ACC TCCACCCTC  CTA
                                  C       TA
GAM256  KPNB1   5'  TGTGGTGACCCCCGCCCCCCA 11221    AA     GAGAT
                                TGG  GGTGGGGG   GCCACA
                                |||  ||||||||   ||||||
                                ACC  CCGCCCCC   TGGTGT
                                  CC      AG___
GAM256  MAP3K9  3'  CATGTCCCCCACCCTCCA    61360    A      AG
                                TGGA GGTGGGGGGG  ATG
                                |||| |||||||||  |||
                                ACCT CCACCCCCT  TAC
                                  C       G_
GAM256  MECP2   3'  CAGCTCCCCCCCACCTCCC    18389    A        A
                                GG AGGTGGGGGGGAG TG
                                || ||||||||||| ||
                                CC TCCACCCCCCTC AC
                                  C         G
GAM256  MECP2   3'  TGTGACATCTCTATTCCCCACC 18418    A    ___     C
          CTCC                    GGA GGTGGGG  GGAGATG CACA
                                ||| |||||||  ||||||| ||||
                                CCT CCACCCC  TCTCTAC GTGT
                                  C      TTA     A
GAM256  MEFV    3'  GCAACCTCCACCTCCCA    5939     A      GAGA
                                TGG AGGTGGGGG   TGC
                                ||| |||||||||   |||
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                                ACC TCCACCTCC    ACG
                                  C        A___
GAM256  MTMR3    3'  GTAGCACTTCCCACCCTC    41167    A       AGA   C
                                GA GGTGGGGGG   TGC AC
                                || |||||||||   ||| ||
                                CT CCACCCTTC   ACG TG
                                 C        ___   A
GAM256  NR1I2    3'  TGGGTGCCCCCCACCCCCA   15303    AA       AGATG
                                TGG  GGTGGGGGG    CCA
                                |||  |||||||||    |||
                                ACC  CCACCCCCC    GGT
                                  C_       GTG__
GAM256  NRCAM    3'  TGGGTTCCCCCCTCCCCCCA   18456    AA  T      ATG
                                TGG  GG GGGGGGAG   CCA
                                |||  || ||||||||   |||
                                ACC  CC CCCCCCTT   GGT
                                  CC  T       G__
GAM256  PARG     3'  GCATCTCCTCCCACCTCCCA   14640    A
                                TGG AGGTGGGGGGAGATGC
                                ||| ||||||||||||||||
                                ACC TCCACCCTCCTCTACG
                                  C
GAM256  PDE6B    3'  GCAACCTCCACCTCCCA     6077     A       GAGA
                                TGG AGGTGGGGG    TGC
                                ||| |||||||||    |||
                                ACC TCCACCTCC    ACG
                                  C        A___
GAM256  PFKFB3   3'  GTGGGGCCCCCACCTCCA    83754     A      GAGATG
                                TGGA GGTGGGGG     CCAC
                                |||| ||||||||     ||||
                                ACCT CCACCCCC     GGTG
                                   _       GG_____
GAM256  PIP5K1A  3'  GCATCCCCTCCACTCCA     14518     AG       A
                                TGGA  GTGGGGGG GATGC
                                ||||  |||||||| |||||
                                ACCT  CACCTCCC CTACG
                                   __       _
GAM256  PITX1    3'  GCAGCCCCCTCCTCCCA     12138    A  T     AGA
                                TGG AGG GGGGGG   TGC
                                ||| ||| ||||||   |||
                                ACC TCC TCCCCC   ACG
                                  C   _     G__
GAM256  PKM2     3'  TGCAGCAAACACTCCACCCTCC 12144      A      GGAGA   CA
            A                    TGGA GGTGGGG    TGC  CA
                                 ||||  |||||||    |||  ||
                                 ACCT CCACCTC     ACG  GT
                                   C      ACAA_   AC
GAM256  PLXNB2   3'  TGTGGCTGAGGCCCCCACCCTC 25728     A       GAGAT
            C                    GGA GGTGGGGG    GCCACA
                                 ||| ||||||||    ||||||
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                                CCT CCACCCCC    CGGTGT
                                  C       GGAGT
GAM256  PPP1R12B  3'  GCAACCTCCACCTCCCA    50358    A       GAGA
                                TGG AGGTGGGGG   TGC
                                ||| |||||||||   |||
                                ACC TCCACCTCC   ACG
                                  C       A___
GAM256  PSCD4   3'  GCAGCACCTGGAGACCCACCTC 26325    A     _____  AGA
            CCA                   TGG AGGTGGG    GGG   TGC
                                ||| |||||||    |||   |||
                                ACC TCCACCC    TCC   ACG
                                  C      AGAGG   ACG
GAM256  RAB2L   3'  TATAGCTTCCCACCTTCCA   17671            AG
                                TGGAAGGTGGGGGGG  ATG
                                ||||||||||||||  |||
                                ACCTTCCACCCTTC  TAT
                                        GA
GAM256  RAD23B   5'  TGTGACAAGCCCCCACCCCCA  12739    AA      GAGA  C
                                TGG  GGTGGGGGG   TG CACA
                                |||  |||||||||   || ||||
                                ACC  CCACCCCC    AC GTGT
                                  C_       GA__  A
GAM256  RGS19IP1  3'  GCAACCTCCTCCCCACCTCCCA 63170    A      _    A_
                                TGG AGGTGGGGG GGAG  TGC
                                ||| |||||||| ||||  |||
                                ACC TCCACCCC CCTC  ACG
                                  C       T    CA
GAM256  RTN1    3'  GTCTTTCCCCCCTCCCTCCA   41227     A  T       T
                                TGGA GG GGGGGGAGA GC
                                |||| || ||||||||| ||
                                ACCT CC CCCCCCTTT TG
                                  C  T       C
GAM256  RTN4    5'  TGCAGCATCATCTCCACCCTCC 67395     A      GA    CA
            A                    TGGA GGTGGGGGG  GATGC  CA
                                |||| ||||||||  |||||  ||
                                ACCT CCACCTCT  CTACG  GT
                                  C       A_    AC
GAM256  SECTM1   3'  GCAGACCCTTCCCCTCCACCCC 13008    AA    _    GA____
            CCA                   TGG  GGTGG GGGGA     TGC
                                |||  ||||| |||||     |||
                                ACC  CCACC CCCCT     ACG
                                  CC    T    TCCCAG
GAM256  SEPN1    3'  GCAACCTCCACCTCCCA    66973    A       GAGA
                                TGG AGGTGGGGG   TGC
                                ||| |||||||||   |||
                                ACC TCCACCTCC   ACG
                                  C       A___
GAM256  SLC14A2  5'  GCAACCTCCACCTCCCA    24118    A       GAGA
                                TGG AGGTGGGGG   TGC
                                ||| |||||||||   |||
```

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                                ACC TCCACCTCC    ACG
                                  C        A___
GAM256  SMP1     3'  GCATCCCCCCACCCTACA    27474    GAA        GA
                                TG   GGTGGGGGGGA  TGC
                                ||   ||||||||||  |||
                                AC   CCACCCCCCT  ACG
                                 ATC         __
GAM256  SNX15    3'  GCAACCTCCACCTCCCA     74123     A        GAGA
                                TGG AGGTGGGGGG    TGC
                                ||| |||||||||    |||
                                ACC TCCACCTCC    ACG
                                  C        A___
GAM256  STAU     5'  GCAACCTCCACCTCCCA     17200     A        GAGA
                                TGG AGGTGGGGGG    TGC
                                ||| |||||||||    |||
                                ACC TCCACCTCC    ACG
                                  C        A___
GAM256  TNFSF12  3'  CAACTCCCCCACCGCCCA    15083     AA       G  A
                                TGG  GGTGGGGGG AG TG
                                |||  |||||||| || ||
                                ACC  CCACCCCC TC AC
                                  CG       _  A
GAM256  UBE2H    3'  GCATATTCCCACATTCCA    13954      G     GGAG
                                TGGAA GTGGGG    ATGC
                                |||||| ||||||    ||||
                                ACCTT CACCCT    TACG
                                   A     TA__
GAM256  VENTX2   3'  GCAGGTCCCCACCCTCCA    27862      A       GAGA
                                TGGA GGTGGGGG    TGC
                                |||| ||||||||    |||
                                ACCT CCACCCCT    ACG
                                  C       GG__
GAM256  BAG5     3'  GCAACCTCCACCTCCCA     18040     A        GAGA
                                TGG AGGTGGGGGG    TGC
                                ||| |||||||||    |||
                                ACC TCCACCTCC    ACG
                                  C        A___
GAM256  BTN3A1   5'  TGTCTGCCCCCCCACCTTCCA   23896            _
                                TGGAAGGTGGGGGGG AGATG
                                |||||||||||||| |||||
                                ACCTTCCACCCCCC TCTGT
                                          G
GAM256  C20orf149 3'  GCCCCCCTCCCCACCTCCCA   44427     A         AGAT
                                TGG AGGTGGGGGGG    GC
                                ||| ||||||||||    ||
                                ACC TCCACCCCTC    CG
                                  C         CCCC
GAM256  CDCA7    3'  GCATCCCCCTCTATTTCCA    50042       GT     A
                                TGGAAG  GGGGGG GATGC
                                ||||||  |||||| |||||
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                                ACCTTT  CTCCCC CTACG
                                   AT     _
GAM256  CENTA1    3'  GCCCTCCCCCCACCTCCA    23445      A         AT
                                TGGA GGTGGGGGGAG  GC
                                |||| ||||||||||  ||
                                ACCT CCACCCCCCTC  CG
                                  _         C_
GAM256  CGRP-RCP  5'  TGCGGCATCCACGAGACCACCT 27895        GGGGA__     A
           TC                     GAAGGTGG      GATGCC CA
                                |||||||      ||||||  ||
                                CTTCCACC      CTACGG GT
                                     AGAGCAC     C
GAM256  DDX12     3'  TGGCACCTCCCTCCCTCTC    60425    AG T       A
                                GA  G GGGGGGAG TGCCA
                                ||  | ||||||| |||||
                                CT  C CCTCCCTC ACGGT
                                 CT _       C
GAM256  DDX12     3'  TGTGGCATCTCCGTCCTGCC   60427    TG  _
                                GG  GGG GGAGATGCCACA
                                ||  ||| ||||||||||||
                                CC  CCT CCTCTACGGTGT
                                 GT   G
GAM256  dJ309H15.1 3'  TGTGGGGAATGCCCCCCGCCTT 57573             AGATG_
           CCA                    TGGAAGGTGGGGGGG     CCACA
                                ||||||||||||||     |||||
                                ACCTTCCGCCCCCC     GGTGT
                                      GTAAGG
GAM256  DKFZp434A1010 3'  CATCCCCCCACCACCCTCCA   71853      A    _   A
                                TGGA GGTGG GGGG GATG
                                |||| ||||| |||| ||||
                                ACCT CCACC CCCC CTAC
                                  C    A   C
GAM256  DKFZP434C212 3'  GCAACCTCCACCTCCCA     69490     A       GAGA
                                TGG AGGTGGGGG    TGC
                                ||| |||||||||    |||
                                ACC TCCACCTCC    ACG
                                  C        A___
GAM256  DKFZP434G156 5'  GCAGCCAGCCCCCCACCCCCCA 70338     AA        AGA__
                                TGG  GGTGGGGGGG     TGC
                                |||  |||||||||     |||
                                ACC  CCACCCCCC     ACG
                                  CC        GACCG
GAM256  DKFZP434J037 3'  GCCTTCTCCCCCACCTCCCA   48950     A       GA  T
                                TGG AGGTGGGGG  GA GC
                                ||| |||||||||  || ||
                                ACC TCCACCCCC  TT CG
                                  C        TC  C
GAM256  DKFZp547I094 5'  GCATCTTCCCATCCTCCCA    50562     A   TGG
                                TGG AGG   GGGGAGATGC
                                ||| |||   ||||||||||
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                                ACC TCC   CCCTTCTACG
                                  C   TA_
GAM256  DKFZP547L112 5'  GCAGAACCCCCACCCTTCCA  67130        _     GAGA
                                TGGAAGG TGGGGG    TGC
                                ||||||| ||||||    |||
                                ACCTTCC ACCCCC    ACG
                                    C     AAG_
GAM256  DKFZP566J091 3'  CATCCCTCCCCACCTCCCA   48860     A        A
                                TGG AGGTGGGGGG GATG
                                ||| |||||||||| ||||
                                ACC TCCACCCCTC CTAC
                                  C         C
GAM256  DKFZP586G1122 3'  TGTGACACCTCTCCCCCACCCC 61941     AA       _  A  C
          CG                      TGG  GGTGGGGG GAG TG CACA
                                ||| ||||||| ||| || ||||
                                GCC  CCACCCCC CTC AC GTGT
                                  C_       T   C  A
GAM256  EPN2     3'  TGTCCTCCCCACCCCCCA    31045     AA       A
                                TGG  GGTGGGGGGG GATG
                                |||  ||||||||| ||||
                                ACC  CCACCCCTC CTGT
                                  CC        _
GAM256  FBXO29    3'  TGTGACACTTGCCACCACCACC 77263          _  _  AGA_  C
          TTCCA                    TGGAAGGTGG GG GG    TG CACA
                                |||||||||| || ||    || ||||
                                ACCTTCCACC CC CC    AC GTGT
                                     A  A  GTTC  A
GAM256  FLJ10468  3'  TGACACCTCCCCCTACCAGCC  36635    AA         A  C
                                GG  GGTGGGGGGAG TG CA
                                ||  |||||||||| || ||
                                CC  CCATCCCCCTC AC GT
                                 GA          C  A
GAM256  FLJ11939  3'  GGCCTCCTCCCCACCTCCCA   45496     A       _   AT
                                TGG AGGTGGGG GGAG  GCC
                                ||| |||||||| ||||  |||
                                ACC TCCACCCC CCTC  CGG
                                  C       T   __
GAM256  FLJ12484  3'  GTGGCCTTCCCCACCCCCCA   70229     AA       G  AT
                                TGG  GGTGGGGG AG  GCCAC
                                |||  |||||||| ||  |||||
                                ACC  CCACCCCT TC  CGGTG
                                  CC       _ __
GAM256  FLJ14642  3'  GTCCCCGCCCCACCTCCCA    52580     A       _  A
                                TGG AGGTGGGG GG GAT
                                ||| |||||||| || |||
                                ACC TCCACCCC CC CTG
                                  C       G  C
GAM256  FLJ14950  3'  GCAACCTCCACCTCCCA     52791     A        GAGA
                                TGG AGGTGGGGG    TGC
                                ||| |||||||||    |||
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                                ACC TCCACCTCC   ACG
                                  C       A___
GAM256  FLJ20254  3' CATGGCCCCCAGCCTCCA   35296     A  G   AG
                                TGGA GGT GGGGG  ATG
                                |||| ||| |||||  |||
                                ACCT CCG CCCCC  TAC
                                  _  A    GG
GAM256  FLJ20546  3' GCAAGCCCTCCCACCTCCCA  35809    A       AGA
                                TGG AGGTGGGGGG  TGC
                                ||| ||||||||||  |||
                                ACC TCCACCCTCC  ACG
                                  C       CGA
GAM256  FLJ21438  3' GGCCCTCCCCCCCCCCCCCA  62198    AA  T     AT
                                TGG  GG GGGGGGAG  GCC
                                |||  || ||||||||  |||
                                ACC  CC CCCCCCTC  CGG
                                  CC  C      C_
GAM256  FLJ22059  3' GGTGCCCCCCCCACCTTCCA  43057          AGA
                                TGGAAGGTGGGGGGG  TGCC
                                ||||||||||||||  ||||
                                ACCTTCCACCCCCC  GTGG
                                        C__
GAM256  FLJ22329  3' GCAGACAACATCCCCCCACCAC 45402    AA       GA_____
          CCA                     TGG  GGTGGGGGGA     TGC
                                |||  ||||||||||      |||
                                ACC  CCACCCCCCT     ACG
                                  CA        ACAACAG
GAM256  FLJ22531  5' GCAACCTCCACCTCCCA    45372    A      GAGA
                                TGG AGGTGGGGG   TGC
                                ||| |||||||||   |||
                                ACC TCCACCTCC   ACG
                                  C       A___
GAM256  FLJ23074  3' TGGCAACCCCCAACTCCCA  47504    A  G    GAGA
                                TGG AG TGGGGG   TGCCA
                                ||| || ||||||   |||||
                                ACC TC ACCCCC   ACGGT
                                  C  A    A___
GAM256  FUK     3' CAGTGTCCCCCACCTTCC    59624          AGA
                                GGAAGGTGGGGGG  TG
                                ||||||||||||  ||
                                CCTTCCACCCCCT  AC
                                        GTG
GAM256  GBTS1   3' TGTGGGTGCCCCCCACTCCCC  59727   AA     GAGATG
                                GG  GGTGGGGG    CCACA
                                ||  ||||||||    |||||
                                CC  TCACCCCC    GGTGT
                                 CC      GTG___
GAM256  H-plk   5' GCAACCTCCACCTCCCA    32386    A      GAGA
                                TGG AGGTGGGGG   TGC
                                ||| |||||||||   |||
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                                ACC TCCACCTCC   ACG
                                  C       A___
GAM256  HSRNAFEV  5'  CGTCCCCCCCCATCTCCCA   34448    A       A
                                TGG AGGTGGGGGG GATG
                                ||| |||||||||| ||||
                                ACC TCTACCCCCC CTGC
                                  C       _
GAM256  KIAA0435  3'  TGGCTCCCCCACACCTCCCA  29666    A   _    GAT
                                TGG AGGTG GGGGGA  GCCA
                                ||| ||||| ||||||  ||||
                                ACC TCCAC CCCCCT  CGGT
                                  C   A    ___
GAM256  KIAA0673  5'  TGGCACCCCCAGAGCCCTCC  62949    A  G__   AGA
                                GGA GGT  GGGGG  TGCCA
                                ||| |||  |||||  |||||
                                CCT CCG  CCCCC  ACGGT
                                  C  AGA   ___
GAM256  KIAA0678  3'  GTGGCCATCCTCCCCCCACCAT 67388     A       _  _
            CCA                   TGGA GGTGGGGGGAG ATG CCAC
                                ||||| |||||||||| ||| ||||
                                ACCT CCACCCCCCTC TAC GGTG
                                  A        C  C
GAM256  KIAA1030  3'  TGCAGCTTCTGCCCCCCACCCC 94987    AA      _  T  CA
            CC                    GG  GGTGGGGGG AGA GC  CA
                                ||  |||||||| ||| ||  ||
                                CC  CCACCCCCC TCT CG  GT
                                 CC       G  T  AC
GAM256  KIAA1373  3'  GCAACCTCCACCTCCCA    71508    A      GAGA
                                TGG AGGTGGGGG   TGC
                                ||| |||||||||   |||
                                ACC TCCACCTCC   ACG
                                  C       A___
GAM256  KIAA1615  3'  GCAACCTCCACCTCCCA    69278    A      GAGA
                                TGG AGGTGGGGG   TGC
                                ||| |||||||||   |||
                                ACC TCCACCTCC   ACG
                                  C       A___
GAM256  KIAA1909  5'  GCAGCCTGCCACACCTCCCA  74282    A   GG  G  A_
                                TGG AGGTG  GG AG  TGC
                                ||| |||||  || ||  |||
                                ACC TCCAC  CC TC  ACG
                                  C    A_  G  CG
GAM256  KIAA1971  3'  GCAACCTCCACCTCCCA    74683    A      GAGA
                                TGG AGGTGGGGG   TGC
                                ||| |||||||||   |||
                                ACC TCCACCTCC   ACG
                                  C       A___
GAM256  KIF13B   5'  GCAAGCCCCCCAGCCTCCCA  31565    A  _     AGA
                                TGG AGG TGGGGGG  TGC
                                ||| ||| |||||||  |||
```

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                                ACC TCC ACCCCCC   ACG
                                  C   G      GA_
GAM256  KLF12    3'  TGAGCATCTCCTGTCCCCC   33283    T  __       CA
                                GG GGG  GGGAGATGC  CA
                                || |||  |||||||||  ||
                                CC CCC  TCCTCTACG  GT
                                  _  TG        AC
GAM256  LRP1B    5'  GCATCCCTCCACCTTCCA    38277            GA
                                TGGAAGGTGGGGGGGA  TGC
                                ||||||||||||||  |||
                                ACCTTCCACCTCCCT  ACG
                                                 __
GAM256  MCLC     3'  GCAACCTCCACCTCCCA     31383     A       GAGA
                                TGG AGGTGGGGGG    TGC
                                ||| |||||||||    |||
                                ACC TCCACCTCC    ACG
                                  C        A___
GAM256  MEIS3    3'  TGTCCCCCCCACCTCCC     78874    A       A
                                GG AGGTGGGGGGG GATG
                                || ||||||||||  ||||
                                CC TCCACCCCCC CTGT
                                 C        _
GAM256  MGC2780  5'  TGTAGCAAGACCCCCCCCCCCC 48288     AA  T     AGA   C
          A                      TGG  GG GGGGGG   TGC ACA
                                |||  || ||||||   ||| |||
                                ACC  CC CCCCCC   ACG TGT
                                  CC  _     AGA   A
GAM256  MOST2    5'  GCACTCCTCCCCCCACCTCCC  40065    A         A__
                                GG AGGTGGGGGGGAG   TGC
                                || ||||||||||||   |||
                                CC TCCACCCCCCCTC   ACG
                                 C          CTC
GAM256  NFAT5    3'  GCAGCCTCCACCTCCCA     57772     A       GAGA
                                TGG AGGTGGGGGG    TGC
                                ||| |||||||||    |||
                                ACC TCCACCTCC    ACG
                                  C        G___
GAM256  phospho1 3'  GCATCCCCCCCACCCCCCA   83248     AA       A
                                TGG  GGTGGGGGGG GATGC
                                |||  ||||||||| |||||
                                ACC  CCACCCCCC CTACG
                                  CC        _
GAM256  PIP5K1C  3'  TGTGGGAATCCCCCACTTCCA  71313       G      AGATG
                                TGGAAG TGGGGGG    CCACA
                                |||||| |||||||    |||||
                                ACCTTC ACCCCCT    GGTGT
                                    _      AAG__
GAM256  PRO0365  5'  GCAACCTCCACCTCCCA     26985     A       GAGA
                                TGG AGGTGGGGG    TGC
                                ||| |||||||||    |||
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                                ACC TCCACCTCC   ACG
                                  C       A___
GAM256  PRRDH   3'  GCCCACCCCCCACCTCCA   32327     A       AGAT
                                TGGA GGTGGGGGGG   GC
                                |||| |||||||||   ||
                                ACCT CCACCCCCC   CG
                                  _       ACC_
GAM256  RAB25   5'  GCACCCCCACCTGCCA     73257     A       GAGA
                                TGG AGGTGGGGGG   TGC
                                ||| |||||||||   |||
                                ACC TCCACCCCC   ACG
                                  G       ____
GAM256  RRP4    3'  TGGCATCCCTGACCTCCA    27365     A  G   GAG
                                TGGA GGT GGGG  ATGCCA
                                |||| ||| ||||  ||||||
                                ACCT CCA TCCC  TACGGT
                                  _  G  ___
GAM256  SE70-2  5'  TGGACTCCCCCCACCTCCA   42348     A       ATG
                                TGGA GGTGGGGGGAG  CCA
                                |||| ||||||||||  |||
                                ACCT CCACCCCCCTC  GGT
                                  _       A__
GAM256  SELB    3'  TGCAGCAGCAGCCCCCACCCCC 62595    AA      GAGA  CA
          A                      TGG  GGTGGGGG   TGC  CA
                                |||  ||||||||   |||  ||
                                ACC  CCACCCCC   ACG  GT
                                  C_      GACG  AC
GAM256  STIM2   3'  TATTATCCCCCACCCTCCA   40863     A       A
                                TGGA GGTGGGGGG GATG
                                |||| ||||||||| ||||
                                ACCT CCACCCCCT TTAT
                                  C       A
GAM256  STMN3   3'  GCAGCATCCCCCACTTCTCCA 32467     _       AGA
                                TGGA AGGTGGGGGG  TGC
                                |||| ||||||||||  |||
                                ACCT TTCACCCCCT  ACG
                                  C       ACG
GAM256  TIX1    3'  GGTGCCCCTCACCTTCCA    62409           AGA
                                TGGAAGGTGGGGGG  TGCC
                                ||||||||||||||  ||||
                                ACCTTCCACTCCCC  GTGG
                                                ___
GAM256  WNT10A  5'  GTGAGCCCCCCACTCCCA    48171     AA      AGATGC
                                TGG  GGTGGGGGG    CAC
                                |||  |||||||||    |||
                                ACC  TCACCCCCC    GTG
                                  C_       GA____
GAM256  LOC123775 3'  CATTTCCCACCCACCCCCCA  76141     AA    _
                                TGG  GGTGGG GGGAGATG
                                |||  |||||| ||||||||
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                                ACC  CCACCC CCCTTTAC
                                  CC      A
GAM256   LOC143187 3'  GCAACCTCCACCTCCCA     59759     A        GAGA
                                TGG AGGTGGGGGG    TGC
                                ||| |||||||||    |||
                                ACC TCCACCTCC    ACG
                                  C        A___
GAM256   LOC144308 5'  TGGCACCCCCAGTCCCTGCCCA 83988     A_   TG__    AGA
                                TGG  AGG    GGGGG   TGCCA
                                |||  |||    |||||   |||||
                                ACC  TCC    CCCCC   ACGGT
                                  CG   CTGA    ___
GAM256   LOC144373 3'  TGGCACCTCCCTCCCTCTC    77315    AG T       A
                                GA  G GGGGGGAG TGCCA
                                ||  | ||||||||| |||||
                                CT  C CCTCCCTC ACGGT
                                 CT _       C
GAM256   LOC144373 3'  TGTGGCATCTCCGTCCTGCC   77316    TG  _
                                GG  GGG GGAGATGCCACA
                                ||  ||| ||||||||||||
                                CC  CCT CCTCTACGGTGT
                                 GT   G
GAM256   LOC145608 5'  CACCTCCCCCCACCCCCG    84375     AA         A
                                TGG  GGTGGGGGGGAG TG
                                |||  |||||||||| ||
                                GCC  CCACCCCCCTC AC
                                  C_          C
GAM256   LOC146784 5'  GCAACCTCCACCTCCCA     78714     A        GAGA
                                TGG AGGTGGGGGG    TGC
                                ||| |||||||||    |||
                                ACC TCCACCTCC    ACG
                                  C        A___
GAM256   LOC147700 3'  CAGTCCCCCAACCCTCCA     59879      A   G     GA
                                TGGA GGT GGGGGA  TG
                                |||| ||| ||||||  ||
                                ACCT CCA CCCCCT  AC
                                  C   A     G_
GAM256   LOC147817 3'  GCAACCTCCACCTCCCA     79181     A        GAGA
                                TGG AGGTGGGGGG    TGC
                                ||| |||||||||    |||
                                ACC TCCACCTCC    ACG
                                  C        A___
GAM256   LOC148147 3'  TGTGGCACCTCCCCCCACACTT 79407       _         A
            CC                    GGAAG GTGGGGGGAG TGCCACA
                                |||||| |||||||||| |||||||
                                CCTTC CACCCCCCTC ACGGTGT
                                   A         C
GAM256   LOC148887 3'  CAGCTTCCCCACCCCCA     85394     AA       G  A
                                TGG  GGTGGGGG AG TG
                                |||  |||||||| || ||
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                                ACC  CCACCCCT TC AC
                                  C_       _ G
GAM256  LOC148918 5'  GCAGCCTCCACCTCCCA     79828     A       GAGA
                                TGG AGGTGGGGGG    TGC
                                ||| |||||||||    |||
                                ACC TCCACCTCC    ACG
                                  C        G___
GAM256  LOC150319 3'  TGTGGCTGTGTCCCCACGCCCC 80480     AA   G    G _
          CA                      TGG  GGTG GGGGA AT GCCACA
                                ||| |||| ||||| || ||||||
                                ACC  CCGC CCCCT TG CGGTGT
                                  C_   A    G  T
GAM256  LOC150383 3'  GCAGCACCCCCCTACTCCA    80631      AG       AGA_
                                TGGA  GTGGGGGG    TGC
                                ||||  ||||||||    |||
                                ACCT  CATCCCCC    ACG
                                   __       CACG
GAM256  LOC151475 5'  GCAACCTCCACCTCCCA     86595     A       GAGA
                                TGG AGGTGGGGGG    TGC
                                ||| |||||||||    |||
                                ACC TCCACCTCC    ACG
                                  C        A___
GAM256  LOC153387 5'  CACTACCCCCACCCCCCA     87223     AA       G  A
                                TGG  GGTGGGGG AG TG
                                |||  |||||||| || ||
                                ACC  CCACCCCC TC AC
                                  CC       A  _
GAM256  LOC153480 5'  GCCTCCCCCCCACCCCCCG    73275     AA        AT
                                TGG  GGTGGGGGGAG  GC
                                |||  ||||||||||  ||
                                GCC  CCACCCCCCTC  CG
                                  CC          __
GAM256  LOC153910 3'  TGGCATCTCACATAACATCCCA 81913     AA    GGGG__
                                TGG  GGTG     GAGATGCCA
                                |||  ||||     |||||||||
                                ACC  CTAC     CTCTACGGT
                                  __    AATACA
GAM256  LOC154282 5'  GCAACCTCCACCTCCCA     87406     A       GAGA
                                TGG AGGTGGGGGG    TGC
                                ||| |||||||||    |||
                                ACC TCCACCTCC    ACG
                                  C        A___
GAM256  LOC164382 3'  TGTGACAATGCCCCCACTTCCA 88561       G     GAGA  C
                                TGGAAG TGGGGG    TG CACA
                                |||||| ||||||    || ||||
                                ACCTTC ACCCCC    AC GTGT
                                   _     GTA_  A
GAM256  LOC199678 3'  GTCCCTCCACCCCACCCTCCA  91371      A      _    AT
                                TGGA GGTGGGG GGAG  GC
                                |||| ||||||| ||||  ||
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                                ACCT CCACCCC CCTC  TG
                                  C      A    CC
GAM256  LOC200014 3'  GCAACCCCCACCTCCCA     89936     A        GAGA
                                TGG AGGTGGGGG    TGC
                                ||| |||||||||    |||
                                ACC TCCACCCCC    ACG
                                  C        A___
GAM256  LOC200860 3'  GCAACCTCCACCTCCCA     91750     A        GAGA
                                TGG AGGTGGGGG    TGC
                                ||| |||||||||    |||
                                ACC TCCACCTCC    ACG
                                  C        A___
GAM256  LOC206426 3'  GCATCCCCTCCACTCCA     91101      AG       A
                                TGGA  GTGGGGGG GATGC
                                ||||  |||||||| |||||
                                ACCT  CACCTCCC CTACG
                                   __       _
GAM256  LOC221037 5'  CATCTCTTTCAAAGCCTCCA   94776      A   G__ GG
                                TGGA GGT   G  GGAGATG
                                |||| |||   |  |||||||
                                ACCT CCG   C  TCTCTAC
                                  _  AAA TT
GAM256  LOC221738 3'  GCCCTTCCCCCACCCCCCA    95415     AA         AT
                                TGG  GGTGGGGGGGAG  GC
                                |||  ||||||||||  ||
                                ACC  CCACCCCCTTC  CG
                                  CC          C_
GAM256  LOC254946 5'  GCACCTGCCGCCCACCTTCCA  97758           _  G  A
                                TGGAAGGTGGG GG AG TGC
                                |||||||||| || || |||
                                ACCTTCCACCC CC TC ACG
                                       G  G  C
GAM256  LOC256980 3'  GCTCCCGCCCCCACCCTCCA   96930      A       GA_  T
                                TGGA GGTGGGGG   GA GC
                                |||| ||||||||   || ||
                                ACCT CCACCCCC   CT CG
                                  C       GCC  _
GAM256  LOC57406  3'  GCATCTGCTCCCATCCCCCA   40718     AA       G
                                TGG  GGTGGGGG AGATGC
                                |||  |||||||| ||||||
                                ACC  CTACCCTC TCTACG
                                  CC       G
GAM256  LOC89944  3'  TGGCCCCCGCCCCCCACCCCCC 93177     AA        AGAT_
           A                     TGG  GGTGGGGGG    GCCA
                                |||  |||||||||    ||||
                                ACC  CCACCCCCC    CGGT
                                  CC        GCCCC
GAM256  LOC90092  5'  GTGGCATCCCCAAACCCCA   62073     AA   GGG   A
                                TGG  GGT   GGG GATGCCAC
                                |||  |||   ||| ||||||||
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                                ACC  CCA   CCC CTACGGTG
                                  __   AA_  _
GAM256  LOC90371  5'  GCAACCTCCACCTCCCA     63163     A       GAGA
                                TGG AGGTGGGGG    TGC
                                ||| |||||||||    |||
                                ACC TCCACCTCC    ACG
                                  C        A___
GAM256  LOC91115  3'  GCAACCTCCACCTCCCA     65568     A       GAGA
                                TGG AGGTGGGGG    TGC
                                ||| |||||||||    |||
                                ACC TCCACCTCC    ACG
                                  C        A___
GAM256  LOC91397  5'  GCCCACCCCCACACCCTCCA   66498      A   _    AGAT
                                TGGA GGTG GGGGG    GC
                                |||| |||| |||||    ||
                                ACCT CCAC CCCCC    CG
                                  C    A     ACC_
GAM256  LOC92078  3'  GCTTCCTCCACCCCACCTTCCA 68604           _   AT_
                                TGGAAGGTGGGG GGAG   GC
                                |||||||||||| ||||   ||
                                ACCTTCCACCCC CCTC   CG
                                       A    CTT
GAM257  FLJ10307  3'  TGAAACAAATCTTTGCCAAG   36479          C   GTG
                                TTTGGCAAAGA TTG   CA
                                |||||||||| |||   ||
                                GAACCGTTTCT AAC   GT
                                       A   AAA
GAM257  KIAA0258  3'  CATTCAGCCTTTGCCAAA    29464          A  TG
                                TTTGGCAAAG CT  GTG
                                |||||||||| ||  |||
                                AAACCGTTTC GA  TAC
                                       C  CT
GAM257  KIAA1243  3'  TGCCAAGTATTTGCCAAA    74030          G
                                TTTGGCAAA ACTTGGTG
                                ||||||||| ||||||||
                                AAACCGTTT TGAACCGT
                                       A
GAM257  NET-5     3'  CATCTGCATATGCGTATTTGCC 22892         G  TTG_
              AAA                  TTTGGCAAA AC    GTGCAGATG
                                |||||||| ||    |||||||||
                                AAACCGTTT TG    TACGTCTAC
                                       A  CGTA
GAM257  PRO0902   5'  CATCAAGTGTCTGCCAAA    54963        AAG
                                TTTGGCA   ACTTGGTG
                                |||||||   ||||||||
                                AAACCGT   TGAACTAC
                                     CTG
GAM257  SIMRP7    3'  CATCTGCAAACGCTTTGCCAA  93968         ACTTGG
                                TTGGCAAAG     TGCAGATG
                                |||||||||     ||||||||
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                                AACCGTTTC     ACGTCTAC
                                     GCAA__
GAM257  LOC169026 3'  CATCTGTGCCATCTCTGC    83601     A   CT   TG
                                GCA AGA  TGG  CAGATG
                                ||| |||  |||  ||||||
                                CGT TCT  ACC  GTCTAC
                                  C   __   GT
GAM257  LOC200197 3'  CATCTGCACCTGCACTCCCAAA 90014      CAA  ACTT
                                TTTGG   AG    GGTGCAGATG
                                |||||   ||    ||||||||||
                                AAACC   TC    CCACGTCTAC
                                   C__  ACGT
GAM257  LOC222223 3'  GTCAAGTACCTTGCCAAA    95885       AGACTT    A_
                                TTTGGCAA     GGTGC  GAT
                                ||||||||     |||||  |||
                                AAACCGTT     CCATG  CTG
                                     _______    AA
GAM257  LOC90906  3'  CATTTGTCAGCCCTTGCCAAA  64948       A ACTT   __
                                TTTGGCAA G    GGT  GCAGATG
                                |||||||| |    |||  |||||||
                                AAACCGTT C    CCG  TGTTTAC
                                     _ _____  AC
GAM257  LOC91137  3'  CATCTGACTTCAATATTTGCCA 57859        GAC    TG_
          AA                    TTTGGCAAA   TTGG   CAGATG
                                |||||||||   ||||   ||||||
                                AAACCGTTT   AACT   GTCTAC
                                     AT_    TCA
GAM258  BRCA1    3'  CCAGAATTGACAGCTTCAACAG 24552      A       C___
          AA                    TTCT TTGAAGCTG    TTCTGG
                                |||| |||||||||    ||||||
                                AAGA AACTTCGAC    AAGACC
                                  C        AGTT
GAM258  CLCN6    3'  CCACCAGAAACATAAAGGA   41695     A   AAGC  C
                                TCT TTG    TG TTCTGGTGG
                                ||| |||    || |||||||||
                                AGG AAT    AC AAGACCACC
                                  A  _____  A
GAM258  CLCN6    3'  CCACCAGAAACATAAAGGA   41702     A   AAGC  C
                                TCT TTG    TG TTCTGGTGG
                                ||| |||    || |||||||||
                                AGG AAT    AC AAGACCACC
                                  A  _____  A
GAM258  CLCN6    3'  CCACCAGAAACATAAAGGA   8903      A   AAGC  C
                                TCT TTG    TG TTCTGGTGG
                                ||| |||    || |||||||||
                                AGG AAT    AC AAGACCACC
                                  A  _____  A
GAM258  CXCR6    3'  CACCAGGCACCTCACAGAA   22672      AT   A C   TT
                                TTCT  TGA G TGC  CTGGTG
                                ||||  ||| | |||  ||||||
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                                AAGA  ACT C ACG  GACCAC
                                  C_  _ C  __
GAM258  FLJ20371  3'  CCATTAGAACAACTCCATCAGA 35535     AT  A  C  C
            A                    TTCT  TG AG TG TTCTGGTGG
                                 |||| || || || |||||||||
                                 AAGA  AC TC AC AAGATTACC
                                   CT  C  A  _
GAM258  HDCMA18P  5'  CCACCAGAAGAAGCACCAAGAA 34091     AT  AA  G
                                 TTCT  TG  GCT CTTCTGGTGG
                                 ||||  ||  ||| ||||||||||
                                 AAGA  AC  CGA GAAGACCACC
                                   __ CA  A
GAM258  KIAA0843  3'  CACCAGAGCTCCAACTGAA   30796    TA  A  TGCT
                                 TTC  TTG AGC   TCTGGTG
                                 |||  ||| |||   |||||||
                                 AAG  AAC TCG   AGACCAC
                                   TC  C  ____
GAM258  KIAA1718  3'  CCACCAGACATCTTCAACAGA  64972    A    C  CT
                                 TCT TTGAAG TG  TCTGGTGG
                                 ||| ||||||  ||  ||||||||
                                 AGA AACTTC AC  AGACCACC
                                   C     T  __
GAM258  MCF2L   3'  CACCAAAAGCAGTTAGAA   61524      TTGAA     C
                                 TTCTA    GCTGCTT TGGTG
                                 |||||    ||||||| |||||
                                 AAGAT    TGACGAA ACCAC
                                   _____      A
GAM258  TED     3'  CCACCCCAAAAGCAGCTCCAAC 32264     A  A      CT__
            AGAA                   TTCT TTG AGCTGCTT   GGTGG
                                 |||| ||| ||||||||   |||||
                                 AAGA AAC TCGACGAA   CCACC
                                   C  C       AACC
GAM258  LOC197358 3'  CAAATGCAGCCTCAACAGAA  89423     A   A    TTC
                                 TTCT TTGA GCTGC   TG
                                 |||| |||| |||||   ||
                                 AAGA AACT CGACG   AC
                                   C   C    TAA
GAM258  LOC200597 3'  CCACCAGAATGTTCAATA    90255      AGCT  _
                                 TATTGA   GC TTCTGGTGG
                                 ||||||   || |||||||||
                                 ATAACT   TG AAGACCACC
                                    ____  T
GAM258  LOC90288  3'  CCACTTGTTCACAGCCTCAATA 62777        A   CTTCT_
            GAA                    TTCTATTGA GCTG     GGTGG
                                 |||||||||| ||||     |||||
                                 AAGATAACT CGAC     TCACC
                                      C   ACTTGT
GAM259  CDH12   3'  CTTATCATTTAAAGTGGTGTA  15777        CCCAA   GA
                                 TACACCACT    GAA  ATAAG
                                 |||||||||    |||  |||||
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                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM259  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM259  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090      T   AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                   _   GTCA_
GAM259  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
           A                     TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM259  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM259  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
           TA                    TACA   TCC   GAAGAATAAG
                                ||||   |||   ||||||||||
                                ATGT   AGG   TTTCTTATTC
                                  AAA_  ATTG
GAM259  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA  68742             _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                          G
GAM259  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM259  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748     CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM259  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM259  OSBPL11   3'  CTTAATTTCCCAAGAGTGGTG  43206        CCAA    AA
                                CACCACTC    GAAG  TAAG
                                ||||||||    ||||  ||||
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                                GTGGTGAG   CTTT  ATTC
                                    AACC   A_
GAM259  YME1L1   3'  TCATTCTTGATGTGGTGTA   58438       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   |||||| ||
                                ATGTGGTG   GTTCTT CT
                                    TA_    A
GAM259  ZNF262   3'  CTTATTTTGTTTGGGAGT    18723       A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                     G
GAM259  LOC91960 3'  TGTGGCTTGGAACGTGGTGTA 68294       TC_   AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
                                ATGTGGTG   GGTTC   TGT
                                    CAA    GG__
GAM260  CDH12    3'  CTTATCATTTAAAGTGGTGTA  15777       CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM260  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007     CA       G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM260  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090     T   AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||     ||||||
                                TGGTG GGGT     TTATTC
                                   _   GTCA_
GAM260  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
            A                    TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM260  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126       CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM260  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
            TA                    TACA   TCC   GAAGAATAAG
                                ||||   |||   ||||||||||
                                ATGT   AGG   TTTCTTATTC
                                  AAA_   ATTG
GAM260  KIAA1579 3'  TACTCTTAGTGGTGTA     37154        CCCAAG   A
                                TACACCACT     AAGA TA
                                |||||||||     |||| ||
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                                ATGTGGTGA     TTCT AT
                                      _______   C
GAM260  KIAA1719 3'  TCTGTCTTGGGAGTGGTGTA  68742            _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                       G
GAM260  KIAA1853 3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM260  KIAA1877 3'  CTTATTCTTCTGCCATGAGT   66748     CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM260  KIAA1906 3'  CTTATTCTTCTTGACTTTTGG  73571    CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM260  OSBPL11  3'  CTTAATTTCCCAAGAGTGGTG 43206       CCAA    AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                     AACC   A_
GAM260  YME1L1   3'  TCATTCTTGATGTGGTGTA   58438       TCC     _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                     TA_     A
GAM260  YME1L1   3'  TCATTCTTGATGTGGTGTA   27323       TCC     _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                     TA_     A
GAM260  ZNF262   3'  CTTATTTTGTTTGGGAGT    18723        A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                      G
GAM260  LOC91960 3'  TGTGGCTTGGAACGTGGTGTA 68294       TC_    AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
                                ATGTGGTG   GGTTC   TGT
                                     CAA    GG__
GAM261  FOXD2    5'  CCTATCCTGGGCCTCTGTAG   16787      AGATGA  AA
                                CTACAGA     AG  GATAGG
                                |||||||     ||  ||||||
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                                GATGTCT     TC  CTATCC
                                    CCGGG_ __
GAM261  KLK5     5'  CCTATCTTCTGAATTCTATAG  25784     C   GATGA
                                CTA AGAA    AGAAGATAGG
                                ||| ||||    ||||||||||
                                GAT TCTT    TCTTCTATCC
                                  A   AAG__
GAM261  SLC4A1   3'  CCTATATTTCCTCTTCTGTA   6222        T   GAAG
                                TACAGAAGA GAA   ATAGG
                                ||||||||| |||   |||||
                                ATGTCTTCT CTT   TATCC
                                     C   TA__
GAM261  ZNF35    3'  CTGTTTTCTTCCTCCTCT    14239     A  T
                                AGA GA GAAGAAGATAG
                                ||| || ||||||||||
                                TCT CT CTTCTTTTGTC
                                  C  C
GAM261  ZNF42    5'  CTTCTCTCCTCTGTAGA     14242        A  T  A
                                TCTACAGA GA GA GAAG
                                |||||||| || || ||||
                                AGATGTCT CT CT CTTC
                                     C  _  _
GAM261  C20orf16 3'  CCTGCCTTCCTGATCCTCTGTA 39240        A   GAA   A
           GA                     TCTACAGA GAT   GAAG TAGG
                                ||||||||| |||   |||| ||||
                                AGATGTCT CTA   CTTC GTCC
                                     C   GTC   C
GAM261  EPB41L1  3'  CATCCTTCTCTTTGTAGA    71103        A  T   AA   A
                                TCTACAGA GA GAAG  GAT G
                                |||||||| || ||||  ||| |
                                AGATGTTT CT CTTC  CTA C
                                     _  _   __   C
GAM261  FLJ10751 3'  CTTCTCCTCATCTGTGGA    37112        A  T  A
                                TCTACAGA GA GA GAAG
                                |||||||| || || ||||
                                AGGTGTCT CT CT CTTC
                                     A  C  _
GAM261  FLJ10751 3'  CTTCTCCTCATCTGTGGA    37275        A  T  A
                                TCTACAGA GA GA GAAG
                                |||||||| || || ||||
                                AGGTGTCT CT CT CTTC
                                     A  C  _
GAM261  KCNV1    3'  CCTATCTTCTTTTTCATGTA   27656     _  GAT
                                TACA GAA   GAAGAAGATAGG
                                |||| |||   ||||||||||||
                                ATGT CTT   TTTCTTCTATCC
                                  A  ___
GAM261  KIAA0295 3'  CCTGATTCTTCCCTTCTGTA   68663        AT    GA
                                TACAGAAG  GAAGAA  TAGG
                                ||||||||  ||||||  ||||
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                                ATGTCTTC  CTTCTT  GTCC
                                    C_     A_
GAM261  KIAA0553  3'  CCTCTGCTCTTCCCTTCTGTA  70446        AT    A AT_
                                TACAGAAG  GAAGA G   AGG
                                ||||||||  ||||| |   |||
                                ATGTCTTC  CTTCT C   TCC
                                    C_    _ GTC
GAM261  KIAA1950  3'  CCGATTTCCTTCATCTTCTG  94178          A   A
                                CAGAAGATGAAG AGAT GG
                                |||||||||||| |||| ||
                                GTCTTCTACTTC TTTA CC
                                      C   G
GAM261  MGC15437  3'  CCTATCCCCCCTCCTTGCTTCT 52843        AT__  AGAA_
          GTG                     TACAGAAG   GA    GATAGG
                                ||||||||   ||    ||||||
                                GTGTCTTC   CT    CTATCC
                                    GTTC  CCCCC
GAM261  SLC2A10   3'  CCTATCTTCTCCATTCTAGA  48547     CAGAA   A
                                TCTA    GATG AGAAGATAGG
                                ||||    |||| ||||||||||
                                AGAT    TTAC TCTTCTATCC
                                  C____   C
GAM261  LOC144438 3'  CCTGGAGCCTCAGCTTCTGTA  77325        A   AGAAGA
                                TACAGAAG TGA     TAGG
                                |||||||| |||     ||||
                                ATGTCTTC ACT     GTCC
                                    G   CCGAG_
GAM261  LOC146880 3'  CCTATCTTGCAGCATCCTGTA  78748      AA   AAG_
                                TACAG  GATG   AAGATAGG
                                |||||  ||||   ||||||||
                                ATGTC  CTAC   TTCTATCC
                                  __   GACG
GAM261  LOC150319 3'  CCAGTCTCCTCTTCTGTA    80466        T  AGAA   A
                                TACAGAAGA GA   GAT GG
                                |||||||||  ||   ||| ||
                                ATGTCTTCT CT   CTG CC
                                    C  ____   A
GAM261  LOC219700 5'  CCTTGGTTTCTCCTTCTGTA   94650        AT   AAGAT
                                TACAGAAG  GAAG    AGG
                                ||||||||  ||||    |||
                                ATGTCTTC  CTTT    TCC
                                    CT    GGT__
GAM261  LOC254848 3'  CCTGTGGGCTACCCTCTGTAGA 98882        AGATGA  AAG
                                TCTACAGA     AG   ATAGG
                                ||||||||     ||   |||||
                                AGATGTCT     TC   TGTCC
                                    CCCA__  GGG
GAM261  LOC51644  3'  CCTGGCTCTTCATCCTCTTC   32664      T  A    __
                                GAAGA GA GAAGA  TAGG
                                ||||| || |||||  ||||
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                                CTTCT CT CTTCT  GTCC
                                   C  A    CG
GAM261  LOC91445  3'  CCCCTCTTCTTCCTCTGTAGA  61167        AGAT      TA
                                TCTACAGA   GAAGAAGA  GG
                                ||||||||   ||||||||  ||
                                AGATGTCT   CTTCTTCT  CC
                                     C___      CC
GAM262  GK        3'  TCAAACACTTTTGGGC     5716         A  GCA
                                GCCCAAAA TG   TTTGA
                                |||||||| ||   |||||
                                CGGGTTTT AC   AAACT
                                     C ___
GAM262  H4F2      3'  CAAAGGCCCTTTTTGGGC    14516         T   A
                                GCCCAAAAA GGC TTTG
                                ||||||||| ||| ||||
                                CGGGTTTTT CCG AAAC
                                      C   G
GAM262  IL13RA1   3'  TCAAAGCCATTTTAGGCT    9575      CA      A
                                AGCC  AAAATGGC TTTGA
                                ||||  |||||||| |||||
                                TCGG  TTTTACCG AAACT
                                  A_      _
GAM262  LMAN1     3'  TAATCAAAGGCCTGGGC     19928      AAAAT   A
                                GCCCA    GGC TTTGATTA
                                |||||    ||| ||||||||
                                CGGGT    CCG AAACTAAT
                                   _____  G
GAM262  PKDREJ    3'  TAGATGCCACTTTAAGCT    21384     CCA   A
                                AGC   AAA TGGCATTTG
                                |||   ||| |||||||||
                                TCG   TTT ACCGTAGAT
                                  AA_   C
GAM262  PRX       3'  TCGAATGCCCACCTTTGGGCT  40903        AAT_
                                AGCCCAAA   GGCATTTGA
                                ||||||||   |||||||||
                                TCGGGTTT   CCGTAAGCT
                                     CCAC
GAM262  PSEN1     3'  CAATCTCCATCACCTTTGGGCT 24628        A___   CAT
                                AGCCCAAA   ATGG   TTG
                                ||||||||   ||||   |||
                                TCGGGTTT   TACC   AAC
                                     CCAC   TCT
GAM262  TXNIP     3'  TTAAAAGCCATTTTTGGAGC   22385    _        A
                                GC CCAAAAATGGC TTTGA
                                || ||||||||||| |||||
                                CG GGTTTTTACCG AAATT
                                 A         A
GAM262  TXNRD1    3'  TCAAAATACATTTCTGGGC    13922      A    GCA
                                GCCCA AAATG   TTTGA
                                ||||| |||||   |||||
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                                CGGGT TTTAC   AAACT
                                  C    ATA
GAM262  CCR7     3'  TCAAAGCCACACTCTGGGCT  10227      AAAA_   A
                                AGCCCA    TGGC TTTGA
                                ||||||    |||| |||||
                                TCGGGT    ACCG AAACT
                                   CTCAC   _
GAM262  DKFZP586F1524 3'  CATTGCCATTTCTGGCCT    32104    C   A      TT
                                AG CCA AAATGGCA  TG
                                || ||| ||||||||  ||
                                TC GGT TTTACCGT  AC
                                 C  C       T_
GAM262  FLJ11042  3'  TAAATGCCATTCTTATGCT   37565    CC  A
                                AGC  AA AATGGCATTTG
                                |||  || ||||||||||
                                TCG  TT TTACCGTAAAT
                                  TA  C
GAM262  FLJ21551  3'  TAATCAAATGTTCTCTGG    46040    AAAAT
                                CCA    GGCATTTGATTA
                                |||    ||||||||||||
                                GGT    TTGTAAACTAAT
                                  CTC__
GAM262  FLJ31951  3'  CAAATGCCACTTTTAAAGC   59229    CC_   A
                                GC   AAAA TGGCATTTG
                                ||   |||| |||||||||
                                CG   TTTT ACCGTAAAC
                                 AAA   C
GAM262  H2AFJ    3'  CATGTTGCCATTTTTGAGGT  37380    _       TT_
                                GCC CAAAAATGGCA   TG
                                ||| ||||||||||   ||
                                TGG GTTTTTACCGT   AC
                                  A         TGT
GAM262  KIAA0453  3'  TCAGATGCCCCCCTTGGGCT  69610      AAAT
                                AGCCCAA   GGCATTTGA
                                |||||||   |||||||||
                                TCGGGTT   CCGTAGACT
                                    CCCC
GAM262  KIAA0472  3'  TTAAAGCCCCCTTTGGGCT   72375      AAT   A
                                AGCCCAAA   GGC TTTGA
                                ||||||||   ||| |||||
                                TCGGGTTT   CCG AAATT
                                    CCC   _
GAM262  KIAA1922  3'  TAACCAAATGTCTGGGC    74005     AAAAT      A
                                GCCCA    GGCATTTG TTA
                                |||||    |||||||| |||
                                CGGGT    CTGTAAAC AAT
                                   _____       C
GAM262  MGC13017  3'  AAATGCCTTTTTGGGCT    55565         T
                                AGCCCAAAAA GGCATTT
                                |||||||||| |||||||
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                                TCGGGTTTTT CCGTAAA
                                          _
GAM262  MP1      5'  TCAGTCTACCAGCTTTGGGCT  31060        AA   CAT_
                                AGCCCAAA  TGG    TTGA
                                ||||||||  |||    ||||
                                TCGGGTTT  ACC    GACT
                                    CG    ATCT
GAM262  PC4      3'  AATCAAATGTCTAGGCT     22971      CAAAAAT
                                AGCC      GGCATTTGATT
                                ||||      ||||||||||
                                TCGG      CTGTAAACTAA
                                  AT_____
GAM262  SFXN5    3'  TCAAGTGCATTTCTGGGC     58658       A    G
                                GCCCA AAATG CATTTGA
                                ||||| ||||| |||||||
                                CGGGT TTTAC GTGAACT
                                   C    _
GAM262  TSP-NY   3'  TCAAGTTAACCATTTTTGTGCT 51793      C        C__
                                AGC CAAAAATGG   ATTTGA
                                ||| |||||||||   ||||||
                                TCG GTTTTTACC   TGAACT
                                  T        AAT
GAM262  WAC      3'  AATCTTAACATTTTTGAGCT   56069      C       GCATTT
                                AGC CAAAAATG     GATT
                                ||| ||||||||     ||||
                                TCG GTTTTTAC     CTAA
                                  A       AATT__
GAM262  WAC      3'  AATCTTAACATTTTTGAGCT   56071      C       GCATTT
                                AGC CAAAAATG     GATT
                                ||| ||||||||     ||||
                                TCG GTTTTTAC     CTAA
                                  A       AATT__
GAM262  WAC      3'  AATCTTAACATTTTTGAGCT   34031      C       GCATTT
                                AGC CAAAAATG     GATT
                                ||| ||||||||     ||||
                                TCG GTTTTTAC     CTAA
                                  A       AATT__
GAM262  LOC115330 3'  CAAATGCCACTCTTGGGC    57403        AAA
                                GCCCAA   TGGCATTTG
                                ||||||   |||||||||
                                CGGGTT   ACCGTAAAC
                                   CTC
GAM262  LOC143943 5'  CAAATGCCACTTTTGTGC    83913     C    A
                                GC CAAAA TGGCATTTG
                                || ||||| |||||||||
                                CG GTTTT ACCGTAAAC
                                 T    C
GAM262  LOC145693 3'  AATCAAATGGCCTTGAGC    77850     C   AAAT  _
                                GC CAA    GGC ATTTGATT
                                || |||    ||| ||||||||
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                                CG GTT    CCG TAAACTAA
                                 A  ____   G
GAM262  LOC151162 5'  TCAAGGAACATTTTTGAGCT   86431     C       GCA
                                AGC CAAAAATG   TTTGA
                                ||| ||||||||   |||||
                                TCG GTTTTTAC   GAACT
                                  A       AAG
GAM262  LOC157503 3'  AAATGCCATTCCTGTGCT    87760     C  AA
                                AGC CA  AATGGCATTT
                                ||| ||  ||||||||||
                                TCG GT  TTACCGTAAA
                                  T  CC
GAM262  LOC203377 5'  TCAAGGAACATTTTTGAGCT   92260     C       GCA
                                AGC CAAAAATG   TTTGA
                                ||| ||||||||   |||||
                                TCG GTTTTTAC   GAACT
                                  A       AAG
GAM262  LOC221975 3'  TTAACCAAGTGTTATTTGAGCT 94196     CCAA          A
                                AGC    AAATGGCATTTG TTAA
                                |||    |||||||||||| ||||
                                TCG    TTTATTGTGAAC AATT
                                  AG__           C
GAM263  NTSR1     3'  AGGCACAGACTCATTTGTCA   11851     G   T   AC
                                TGA CAG TGA  CTGTGCCT
                                ||| ||| |||  ||||||||
                                ACT GTT ACT  GACACGGA
                                  _   T   CA
GAM263  SNX9      3'  GCACAGGTTAGCTCCCCATTA  33121       AGC     A
                                TGATG   AGTTGA CCTGTGC
                                |||||   |||||| |||||||
                                ATTAC   TCGATT GGACACG
                                   CCC     _
GAM263  KLHL4     3'  CACAAATGTCCTCAACTGTCAT 55142       G      __  C__
                CA                TGATGA CAGTTGA  AC   TGTG
                                  |||||| |||||||  ||   ||||
                                  ACTACT GTCAACT  TG   ACAC
                                     _      CC  TAA
GAM263  LOC115811 5'  AGGCACAGAGGGCTGCTCACA  57408    A       GAAC
                                TG TGAGCAGTT    CTGTGCCT
                                || |||||||||    ||||||||
                                AC ACTCGTCGG    GACACGGA
                                  _       GA__
GAM263  LOC145384 3'  AGACACATGAAAAAATGCTCAT 77711          GTTGAACC    C
                CA                TGATGAGCA       TGTG CT
                                  |||||||||       |||| ||
                                  ACTACTCGT       ACAC GA
                                        AAAAAAGT    A
GAM263  LOC147229 3'  AGGCACAGATGCAGGCTCAGCA 78915    A    AG   AAC
                                TG TGAGC  TTG   CTGTGCCT
                                || |||||  |||   ||||||||
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                                AC ACTCG  GAC   GACACGGA
                                 G    __  GTA
GAM263  LOC201911 3'  GCACAGCGCTGCTCACA     91865    A      TGAAC    C
                                TG TGAGCAGT    CTGTG C
                                || ||||||||    ||||| |
                                AC ACTCGTCG    GACAC G
                                 _      C____    A
GAM263  LOC254827 5'  AGGTGATCAACCCAACACTCAT 98774       CA   AACCTG_
          CA                     TGATGAG  GTTG      TGCCT
                                |||||||  ||||     |||||
                                ACTACTC  CAAC      GTGGA
                                   A_   CCAACTA
GAM263  LOC92293  3'  AGGACAGCCTTCAACTGTCACC 69317    A  G      C_   G
          A                      TG TGA CAGTTGAA  CTGT CCT
                                || ||| ||||||||  |||| |||
                                AC ACT GTCAACTT  GACA GGA
                                 C  _      CC   _
GAM264  AMT      3'  TGTAAACTTGGGGATGGCT   6658          TTTGCT
                                AGCCATCCCC     TTTACA
                                ||||||||||     ||||||
                                TCGGTAGGGG     AAATGT
                                      TTC___
GAM264  CCNF     3'  GAGAGCAGAGAGGATGACTTG  10076     C    C
                                CAAG CATCC CTTTGCTTTT
                                |||| ||||| ||||||||||
                                GTTC GTAGG GAGACGAGAG
                                  A    A
GAM264  EGR2     3'  AAGGCAAAGGGGAGGCTCA   6373    A   A
                                C AGCC TCCCCTTTGCTTT
                                | |||| ||||||||||||
                                A TCGG AGGGGAAACGGAA
                                 C   _
GAM264  HSPA9B   3'  TGTAAAAGGAGGTAGGATGAAT 15954     GC    __   TG
          TG                     CAA  CATCC  CCTT  CTTTTACA
                                |||  |||||  ||||  ||||||||
                                GTT  GTAGG  GGAG  GAAAATGT
                                  AA    AT   __
GAM264  LOH11CR2A 3'  TAAAAGTAAAGGATGCTT    28273     C   CC
                                AAGC ATCC  TTTGCTTTTA
                                |||| ||||  ||||||||||
                                TTCG TAGG  AAATGAAAAT
                                   _   __
GAM264  PCMT1    3'  TGTAAAAGCAACATCAGCTTG  19406      CATCCCCT
                                CAAGC       TTGCTTTTACA
                                |||||       ||||||||||
                                GTTCG       AACGAAAATGT
                                  ACTAC___
GAM264  PDE4C    3'  GAGACAAAGGGGATCGCTTG   8103       C        _
                                CAAGC ATCCCCTTTG CTT
                                ||||| |||||||||| |||
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                                GTTCG TAGGGGAAAC GAG
                                   C         A
GAM264  PIK3R3   3' AGGGAGAGAAGATGGCTT    61703        CC    G
                                AAGCCATC  CTTT CTT
                                ||||||||  |||| |||
                                TTCGGTAG  GAGA GGA
                                    AA    G
GAM264  RAD51L1  5' TGTAAAGGGTGGGGAAACTTG 56881     CCA    TTTG
                                CAAG   TCCCC   CTTTTACA
                                ||||   |||||   ||||||||
                                GTTC   AGGGG   GGAAATGT
                                  AA_    TG__
GAM264  RAD51L1  5' TGTAAAGGGTGGGGAAACTTG 12752     CCA    TTTG
                                CAAG   TCCCC   CTTTTACA
                                ||||   |||||   ||||||||
                                GTTC   AGGGG   GGAAATGT
                                  AA_    TG__
GAM264  TACC1    3' TAAAGGTAACAAAGGGCAGCTC 21878   A   CATC     ___
           A                     C AGC   CCCTTTG   CTTTTA
                                | |||   |||||||  ||||||
                                A TCG   GGGAAAC   GGAAAT
                                 C   AC__      AAT
GAM264  CDC14A   3' TAATGGCATGGGATGGCTT   14787         CTT   T
                                AAGCCATCCC   TGCT TTA
                                ||||||||||   |||| |||
                                TTCGGTAGGG   ACGG AAT
                                     T__    T
GAM264  FADS1    3' TAGAAACAAAGGGGATGC    26385    C       C
                                GC ATCCCCTTTG TTTTA
                                || ||||||||||  |||||
                                CG TAGGGGAAAC AAGAT
                                 _         A
GAM264  FLJ10081 3' AGCAAAGGAAGTGGCTTG    36286       CC
                                CAAGCCAT  CCTTTGCT
                                ||||||||  ||||||||
                                GTTCGGTG  GGAAACGA
                                    AA
GAM264  FLJ10101 5' AAAAGCGAGGCGACGGCTT   45591     A  C    T
                                AAGCC TC CCTT GCTTTT
                                |||||  ||  ||||  ||||||
                                TTCGG AG GGAG CGAAAA
                                   C  C    _
GAM264  FLJ23058 3' TGTAAACTAAGGGGATGGTT  45529          TGCT
                                AGCCATCCCCTT   TTTACA
                                ||||||||||||   ||||||
                                TTGGTAGGGGAA   AAATGT
                                       TC__
GAM264  FLJ33069 3' AAAGCAAATATGGCCTG     58966    A    CCCC
                                CA GCCAT    TTTGCTTT
                                || |||||    ||||||||
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                                GT CGGTA    AAACGAAA
                                 C    T___
GAM264  HSA277841 3'  GGCTAAAGGGGAAGCTCA    38270   A   CA      _
                                C AGC  TCCCCTTT GCT
                                | |||  |||||||| |||
                                A TCG  AGGGGAAA CGG
                                 C   A_       T
GAM264  HTMP10   3'  AAAGTGAGGGATGACTTG    53754     C     CT TG
                                CAAG CATCCC  T  CTTT
                                |||| ||||||  |  ||||
                                GTTC GTAGGG  A  GAAA
                                  A     __ GT
GAM264  KIAA0222 3'  TGTAAAGGCAGGAAATGG    28400     CC   TT
                                CCAT  CCT  GCTTTTACA
                                ||||  |||  |||||||||
                                GGTA  GGA  CGGAAATGT
                                  AA  __
GAM264  KIAA0367 3'  TGAAATAAAAGAAATGGCTTG  67872       CCC    GC
                                CAAGCCAT   CTTT  TTTTA
                                ||||||||   ||||  |||||
                                GTTCGGTA   GAAA  AAAGT
                                     AA_   AT
GAM264  KIAA0459 3'  TATTAGAAAGGGGACAGTCA   61661   A  CA      G  TT
                                A GC  TCCCCTTT CT  TA
                                | ||  |||||||| ||  ||
                                A TG  AGGGGAAA GA  AT
                                 C  AC       _  TT
GAM264  KIAA0894 5'  GTAAAGGTGGGAATGCTCA   30340   A   CA   CTTT
                                C AGC  TCCC    GCTTTTAC
                                | |||  ||||   ||||||||
                                A TCG  AGGG    TGGAAATG
                                 C   TA   ____
GAM264  KIAA1750 3'  TGCAAAATCAGACAGAAATGGC 68813       CCCC_   C    A
           TTG                    CAAGCCAT     TTTG TTTT CA
                                ||||||||     |||| |||| ||
                                GTTCGGTA     AGAC AAAA GT
                                     AAGAC    T    C
GAM264  LIM      3'  AAAGTAAAGAGACGGTTTG   22309       A  CC
                                CAAGCC TC  CTTTGCTTT
                                |||||| ||  |||||||||
                                GTTTGG AG  GAAATGAAA
                                   C  A_
GAM264  MADCAM1  3'  GTGAAAGCAAAATAGCTTG   56239      C  CCCC
                                CAAGC AT    TTTGCTTTTAC
                                ||||| ||    ||||||||||
                                GTTCG TA    AAACGAAAGTG
                                  A  ____
GAM264  MADCAM1  3'  GTGAAAGCAAAATAGCTTG   56242      C  CCCC
                                CAAGC AT    TTTGCTTTTAC
                                ||||| ||    ||||||||||
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                                GTTCG TA   AAACGAAAGTG
                                  A ____
GAM264  MADCAM1   3' GTGAAAGCAAAATAGCTTG   56245     C  CCCC
                                CAAGC AT   TTTGCTTTTAC
                                ||||| ||   ||||||||||
                                GTTCG TA   AAACGAAAGTG
                                  A ____
GAM264  RP4-622L5 3' GAAAGCAGATGGCTT      39425       CCCTT
                                AAGCCATC    TGCTTTT
                                ||||||||    |||||||
                                TTCGGTAG    ACGAAAG
                                     _____
GAM264  SLC5A7    3' AAAAGCAAAGTGAAGTGATGAG 41800    _   CC____
           CT                     AGC CATC    CTTTGCTTTT
                                ||| ||||    ||||||||||
                                TCG GTAG    GAAACGAAAA
                                  A   TGAAGT
GAM264  SUCLG2    3' GTAAAAAGGGATGGTTCA   66224   A      C_
                                C AGCCATCCC  TTTGC
                                | |||||||||  |||||
                                A TTGGTAGGG  AAATG
                                 C       AA
GAM264  ZDHHC4    3' AAGCAAAAAAAAAATGGCTTG  36643       CCCC_
                                CAAGCCAT    TTTGCTT
                                ||||||||    |||||||
                                GTTCGGTA    AAACGAA
                                     AAAAA
GAM264  LOC113386 3' AAAACAAAAGGGGAGATGTT  57868    CA_     GC
                                AGC   TCCCCTTT  TTTT
                                |||   ||||||||  ||||
                                TTG   AGGGGAAA  AAAA
                                  TAG       AC
GAM264  LOC120227 5' AGTAAAGGAATGCCTTG    74461    C   CC
                                CAAG CAT  CCTTTGCT
                                |||| |||  ||||||||
                                GTTC GTA  GGAAATGA
                                  C   A_
GAM264  LOC143308 5' TAGAACAAAAGGATGGCT   83838       CC   C
                                AGCCATCC  TTTG TTTTA
                                ||||||||  |||| |||||
                                TCGGTAGG  AAAC AAGAT
                                     A_   _
GAM264  LOC143902 3' GGCAGAGGATGGCTCA     77120   A      CC
                                C AGCCATCC  TTTGCT
                                | ||||||||  ||||||
                                A TCGGTAGG  AGACGG
                                 C       __
GAM264  LOC145314 3' GTAATGCACTAGAAGGTGGC  77614      CC  T_   TT
                                GCCATC  CT  TGC  TTAC
                                ||||||  ||  |||  ||||
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                                CGGTGG  GA  ACG  AATG
                                    AA  TC   T_
GAM264   LOC146669 3'  AAAGGCAGGGGGTGGCCTG   78654    A        TT
                                CA GCCATCCCCT  GCTTTT
                                || ||||||||||  ||||||
                                GT CGGTGGGGGA  CGGAAA
                                 C        __
GAM264   LOC149606 3'  AAGGCAGAAGTGGCTCA     80254    A     CCCC
                                C AGCCAT    TTTGCTTT
                                | ||||||    ||||||||
                                A TCGGTG    AGACGGAA
                                 C     A___
GAM264   LOC153454 3'  GTAAAAGTTAGATGGTT     81694        CCCTTT
                                AGCCATC     GCTTTTAC
                                |||||||     ||||||||
                                TTGGTAG     TGAAAATG
                                    AT_____
GAM264   LOC158563 3'  AGGCCAGAAAGGAGGTGGC    82843       C    ___
                                GCCATC CCTTT   GCTT
                                |||||| |||||   ||||
                                CGGTGG GGAAA   CGGA
                                    A     GAC
GAM264   LOC202025 3'  TAAAATCAGGGATGGTT     91890         CTT  C
                                AGCCATCCC   TG TTTTA
                                |||||||||   || |||||
                                TTGGTAGGG   AC AAAAT
                                      ___  T
GAM264   LOC202754 3'  GCAGTAAGGGATGGCTTG    83588          CT_
                                CAAGCCATCCC   TTGC
                                ||||||||||   ||||
                                GTTCGGTAGGG   GACG
                                       AAT
GAM264   LOC203025 5'  AAGCTAGAGGGCAGCTTG    90735       CATC     _
                                CAAGC    CCCTTT GCTT
                                |||||    |||||| ||||
                                GTTCG    GGGAGA CGAA
                                   AC__      T
GAM264   LOC221296 3'  AGAGGCAAAGAAGTTGGCCTG  93604    A   TCCC
                                CA GCCA    CTTTGCTTTT
                                || ||||    ||||||||||
                                GT CGGT    GAAACGGAGA
                                 C    TGAA
GAM264   LOC221302 5'  GAGGCCCAAAGGGGAAGC    59662    CA       __
                                GC  TCCCCTTT  GCTTT
                                ||  ||||||||  |||||
                                CG  AGGGGAAA  CGGAG
                                 A_       CC
GAM264   LOC57116  3'  GTAACACAAAGGATGCTTG   40210      C   CC   CTT
                                CAAGC ATCC  TTTG   TTAC
                                ||||| ||||  ||||   ||||
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                                GTTCG TAGG  AAAC   AATG
                                  _   __    AC_
GAM264  LOC90750  3'  TAAAAGCAAGCAGTAATGGC   64632      CCCC_
                                GCCAT    TTTGCTTTTA
                                |||||    ||||||||||
                                CGGTA    GAACGAAAAT
                                   ATGAC
GAM264  LOC90750  3'  TGTAAAAGCAGCTGATG     64636     CCCT
                                CATC    TTGCTTTTACA
                                ||||    ||||||||||
                                GTAG    GACGAAAATGT
                                  TC__
GAM265  ADCY8     5'  GGACATGCCTTTCTCCACGTCC 8502     A   A     __   CA
           GC                     GC GGAC TGGAGAA  GTA  TCC
                                || |||| |||||||  |||  |||
                                CG CCTG ACCTCTT  CGT  AGG
                                 _   C      TC   AC
GAM265  AKT2      5'  GTGCCTCCTGCATGTCCTGCT  9677          G  AA_
                                AGCAGGACATG AG   GTAC
                                ||||||||||| ||   ||||
                                TCGTCCTGTAC TC   CGTG
                                      G  CTC
GAM265  APOBEC2   3'  TACTTCTCATGCTGT      23280      GA   G
                                GCAG  CATG AGAAGTA
                                ||||  |||| |||||||
                                TGTC  GTAC TCTTCAT
                                  __   _
GAM265  GPD1      3'  GCTTTCTCCATATCCTCT    60397    C   C      _
                                AG AGGA ATGGAGAA GT
                                || |||| |||||||| ||
                                TC TCCT TACCTCTT CG
                                 _   A       T
GAM265  HMGN2     3'  TGTCTGCCCATGTCCTGC    19810          AGA  T
                                GCAGGACATGG   AG ACA
                                ||||||||||   || |||
                                CGTCCTGTACC   TC TGT
                                      CG_  _
GAM265  MCM4      3'  GCTCCCTGCATGTCCTGCT   62579          G  A_
                                AGCAGGACATG AG  AGT
                                |||||||||| ||  |||
                                TCGTCCTGTAC TC  TCG
                                      G  CC
GAM265  MEN1      3'  GGATGTACTAAAATGTATCCT  95013      C   GAGA
                                AGGA ATG    AGTACATCC
                                ||||  |||   |||||||||
                                TCCT TGT    TCATGTAGG
                                  A   AAAA
GAM265  MTL5      3'  GATGTGGCAACCCATGCCCCCT 18199    CA  A    AGAAG
                                AG  GG CATGG    TACATC
                                ||  || |||||    ||||||
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                                TC  CC GTACC    GTGTAG
                                 CC  _    CAACG
GAM265  MTMR3    5'  GCCTCGCCATGTCCTGCT    41164          A  A
                                AGCAGGACATGG GA GT
                                |||||||||||| || ||
                                TCGTCCTGTACC CT CG
                                       G  C
GAM265  PCDH9    3'  TGCTTCTCCACAGCCTGCT    83697       ACA
                                AGCAGG   TGGAGAAGTA
                                ||||||   ||||||||||
                                TCGTCC   ACCTCTTCGT
                                   GAC
GAM265  SLC39A1  3'  GCCTCTCCAGTCCTGCT     27813        A     A
                                AGCAGGAC TGGAGA GT
                                |||||||| |||||| ||
                                TCGTCCTG ACCTCT CG
                                    _     C
GAM265  SLC6A8   3'  GGATGCACTTCCCGCACCT   20073     ACA   A    A
                                AGG   TGG GAAGT CATCC
                                |||   ||| ||||| |||||
                                TCC   GCC CTTCA GTAGG
                                  AC_  _    C
GAM265  AD-020   3'  ACTTCTCCATTCCCTGCT    39713       AC
                                AGCAGG  ATGGAGAAGT
                                ||||||  ||||||||||
                                TCGTCC  TACCTCTTCA
                                   CT
GAM265  AD-020   3'  ACTTCTCCATTCCCTGCT    60090       AC
                                AGCAGG  ATGGAGAAGT
                                ||||||  ||||||||||
                                TCGTCC  TACCTCTTCA
                                   CT
GAM265  ALDH9    3'  GTTCCTTCTCCATTCCCACT   7348     CA   C       T_
                                AG  GGA ATGGAGAAG  AC
                                ||  ||| |||||||||  ||
                                TC  CCT TACCTCTTC  TG
                                 AC   _        CT
GAM265  ARHGEF4  3'  GATGGCGCCCTGTCCTGC    53372        T  AGAA  A
                                GCAGGACA GG    GT CATC
                                |||||||| ||    || ||||
                                CGTCCTGT CC    CG GTAG
                                     _  CG__  _
GAM265  DDR1     3'  GGACACACTCTCATGTCC     10477        G   A  ACA
                                GGACATG AGA GT   TCC
                                ||||||| ||| ||   |||
                                CCTGTAC TCT CA   AGG
                                     _   _  CAC
GAM265  DDR1     3'  GGACACACTCTCATGTCC     26560        G   A  ACA
                                GGACATG AGA GT   TCC
                                ||||||| ||| ||   |||
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                                CCTGTAC TCT CA   AGG
                                   _  _  CAC
GAM265  DDR1     3'  GGACACACTCTCATGTCC    26562       G   A  ACA
                                GGACATG AGA GT   TCC
                                ||||||| ||| ||   |||
                                CCTGTAC TCT CA   AGG
                                   _  _  CAC
GAM265  FLJ20150 3'  GTCCTCCCCCATGTCCTGC   35145         AGA  T
                                GCAGGACATGG   AG AC
                                ||||||||||   || ||
                                CGTCCTGTACC   TC TG
                                      CCC  C
GAM265  FLJ23259 3'  TGATTTCCCATGTCCTACT   45638    C       A    A
                                AG AGGACATGG GAAGT CA
                                || ||||||||| ||||| ||
                                TC TCCTGTACC CTTTA GT
                                 A       _    _
GAM265  GAL3ST2  3'  GCTGCCTCCATGTCCTGC    53484          A_
                                GCAGGACATGGAG  AGT
                                ||||||||||||  |||
                                CGTCCTGTACCTC  TCG
                                      CG
GAM265  GMEB2    3'  GCTCCTCCAGGTCCTGCT    25664        A    A
                                AGCAGGAC TGGAG AGT
                                |||||||| ||||| |||
                                TCGTCCTG ACCTC TCG
                                     G    C
GAM265  HMG17L1  3'  TGTCTGCCCATGTCCTGCT   41049          AGA  T
                                AGCAGGACATGG   AG ACA
                                ||||||||||||   || |||
                                TCGTCCTGTACC   TC TGT
                                      CG_  _
GAM265  HNRPA3   3'  GGATATATACCCATGTCT    20453        AGAA   C
                                GGACATGG    GTA ATCC
                                ||||||||    ||| ||||
                                TCTGTACC    TAT TAGG
                                     CA__   A
GAM265  KIAA0441 3'  GGATGTACCACCACACCCAGCT 29636     A  ACA   AGAA
                                AGC GG   TGG    GTACATCC
                                ||| ||   |||    ||||||||
                                TCG CC   ACC    CATGTAGG
                                  A  CAC   AC__
GAM265  KIAA0522 3'  GTCCTCCTCCCCATGTCCT   72426         A  __  T
                                AGGACATGG GA  AG AC
                                ||||||||| ||  || ||
                                TCCTGTACC CT  TC TG
                                      C  CC  C
GAM265  KIAA1393 3'  TGTCTGCCCATGTCCTGC    72576          AGA  T
                                GCAGGACATGG   AG ACA
                                ||||||||||   || |||
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                                CGTCCTGTACC   TC TGT
                                      CG_  _
GAM265  KIAA1922  3'  ATGTGGCATCATGTCCTGC   73987         AGAAG
                                GCAGGACATGG    TACAT
                                ||||||||||    |||||
                                CGTCCTGTACT    GTGTA
                                      ACG__
GAM265  LOC113220 5'  GGATGTACCATCTGCCCTTCT  57359   C   A  TG  GAA
                                AG AGG CA  GA   GTACATCC
                                || ||| ||  ||   ||||||||
                                TC TCC GT  CT   CATGTAGG
                                 T   C  __  AC_
GAM265  LOC143153 3'  GGCTGTTCTCCATCTCCCGCT  76980    A   C      AGT   T
                                AGC GGA ATGGAGA   ACA CC
                                ||| ||| |||||||   ||| ||
                                TCG CCT TACCTCT   TGT GG
                                  C   C      ___   C
GAM265  LOC145540 3'  TGTCTGCCCATGTCCTGC    77779         AGA  T
                                GCAGGACATGG   AG ACA
                                ||||||||||   || |||
                                CGTCCTGTACC   TC TGT
                                      CG_  _
GAM265  LOC148915 3'  TGTCTGCCCATGTCCTGC    79810         AGA  T
                                GCAGGACATGG   AG ACA
                                ||||||||||   || |||
                                CGTCCTGTACC   TC TGT
                                      CG_  _
GAM265  LOC150166 5'  GATATACTTCTTTCTTGCT   86038       CATG      C
                                AGCAGGA    GAGAAGTA ATC
                                |||||||    |||||||| |||
                                TCGTTCT    TTCTTCAT TAG
                                    ____        A
GAM265  LOC150580 3'  TGTCTGCCCATGTCCTGC    61068         AGA  T
                                GCAGGACATGG   AG ACA
                                ||||||||||   || |||
                                CGTCCTGTACC   TC TGT
                                      CG_  _
GAM265  LOC152212 3'  TGTCTGCCCATGTCCTGC    83712         AGA  T
                                GCAGGACATGG   AG ACA
                                ||||||||||   || |||
                                CGTCCTGTACC   TC TGT
                                      CG_  _
GAM265  LOC152300 3'  ATGCACTTGTCCTGTT      81380        TGGAGA   A
                                AGCAGGACA     AGT CAT
                                |||||||||     ||| |||
                                TTGTCCTGT     TCA GTA
                                    _______  C
GAM265  LOC153346 5'  ATGCACTAGCTGTCCTGT    87203        TG AGA   A
                                GCAGGACA  G   AGT CAT
                                ||||||||  |   ||| |||
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                                TGTCCTGT  C   TCA GTA
                                    __ GA_   C
GAM265  LOC153811 3'  GGACATACCATCTTGTCCTGCT 81839        T   GAA   CA
                                AGCAGGACA GGA   GTA  TCC
                                ||||||||| |||   |||  |||
                                TCGTCCTGT TCT   CAT  AGG
                                     _  AC_   AC
GAM265  LOC154807 5'  GATGGCGGCTCCCGTCCTGCT  87464       AT   AA  A
                                AGCAGGAC  GGAG  GT CATC
                                ||||||||  ||||  || ||||
                                TCGTCCTG  CCTC  CG GTAG
                                    C_   GG  _
GAM265  LOC196453 5'  ATGACATTTCATGTCCCACT   92341    CA       AA  A
                                AG  GGACATGGAG  GT CAT
                                ||  ||||||||||  || |||
                                TC  CCTGTACTTT  CA GTA
                                 AC        A_ _
GAM265  LOC221468 3'  ACTTCTCCATAGTCCTGCT    60003       _
                                AGCAGGAC ATGGAGAAGT
                                |||||||| ||||||||||
                                TCGTCCTG TACCTCTTCA
                                    A
GAM265  LOC254000 3'  TGTCTGCCCATGTCCTGC    96615         AGA  T
                                GCAGGACATGG   AG ACA
                                ||||||||||   || |||
                                CGTCCTGTACC   TC TGT
                                      CG_  _
GAM265  LOC257153 5'  GGCTGTTTCTCACATCCTGC   97467      CA _    GT   T
                                GCAGGA  TG GAGAA  ACA CC
                                ||||||  || |||||  ||| ||
                                CGTCCT  AC CTCTT  TGT GG
                                   __  A    __   C
GAM265  LOC88584  3'  GATTATCTGCCCATGTCCTGC  61102         AGA  TAC
                                GCAGGACATGG   AG   ATC
                                ||||||||||   ||   |||
                                CGTCCTGTACC   TC   TAG
                                      CG_  TAT
GAM266  MYO1D    3'  CGGCAGAACCCACCAAGTGC   72243     A      C___
                                GCAC TGGTGGGT    CCG
                                |||| ||||||||    |||
                                CGTG ACCACCCA    GGC
                                  A       AGAC
GAM266  SH3BP4   3'  CGCCAATCATCCCACCAT    27999        TCCC
                                ATGGTGGG    GATTGGCG
                                ||||||||    ||||||||
                                TACCACCC    CTAACCGC
                                    TA__
GAM266  ABHD2    3'  CAGGGGGCACCCACCATG    23793         _  GA
                                CATGGTGGGT CCC  TTG
                                |||||||||| |||  |||
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                                GTACCACCCA GGG  GAC
                                      C   G_
GAM266  BCoR     3'  CAAGCTGGACCCACCATGT   35343           CGA
                                ACATGGTGGGTCC   TTG
                                ||||||||||||   |||
                                TGTACCACCCAGG   AAC
                                      TCG
GAM266  FLJ12488  3'  CCGATTGGCGCAAGGCCCACCA 49157     C        _________  GATT
           TATGC                   GCA ATGGTGGGTC       CC    GG
                                ||| ||||||||||       ||    ||
                                CGT TACCACCCGG       GG    CC
                                  A        AAC___GC  TTAG
GAM266  FLJ20856  5'  GTTAAGCACCCACCATGTGC   47865           CCCGA
                                GCACATGGTGGGT    TTGGC
                                ||||||||||||    |||||
                                CGTGTACCACCCA    AATTG
                                      CG___
GAM266  NXPH3    3'  CCAATGGACACCCACCGTGTGC 66340           C_  G
                                GCACATGGTGGGT  CC ATTGG
                                ||||||||||||  || |||||
                                CGTGTGCCACCCA  GG TAACC
                                      CA  _
GAM266  TSPEAR   3'  GCCAATCAGAACTGTG     59375       GGG  CC
                                CATGGT   TC  GATTGGC
                                ||||||   ||  |||||||
                                GTGTCA   AG  CTAACCG
                                   ___  A_
GAM266  LOC145453 3'  CCAACCAGGATGCTTCACCATG 77656         ___    CGA
                                CATGGTGG   GTCC   TTGG
                                ||||||||   ||||   ||||
                                GTACCACT   TAGG   AACC
                                     TCG    ACC
GAM266  LOC150935 5'  CGGACACCCACCACGTGC    80825      A       C_
                                GCAC TGGTGGGT  CCG
                                ||||  ||||||||  |||
                                CGTG ACCACCCA  GGC
                                  C       CA
GAM266  LOC56270  3'  CGCCACAGCACCCACCACCTGC 39504     CA       CCCGAT
                                GCA  TGGTGGGT     TGGCG
                                |||  |||||||      |||||
                                CGT  ACCACCCA     ACCGC
                                  CC       CGAC__
GAM267  ALOX15   3'  AAATAAAATATTGGCA      8538       TTGT
                                TGCC    GTATTTTATTT
                                ||||    ||||||||||
                                ACGG    TATAAAATAAA
                                  T___
GAM267  GABRA6   3'  TAAATAACATTACCACAAGGCA 7693          _  TT_
                                TGCCTTGTG TA   TTATTTA
                                |||||||| ||   |||||||
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                                ACGGAACAC AT   AATAAAT
                                     C  TAC
GAM267  GNAS    3'  TAAATAAAACAGCAGCAGCAA  33917       CT   GTA
                                TTGCTGC  TGT   TTTTATTTA
                                |||||||  |||   |||||||||
                                AACGACG  ACG   AAAATAAAT
                                   __   AC_
GAM267  GNAS    3'  TAAATAAAACAGCAGCAGCAA  55384       CT   GTA
                                TTGCTGC  TGT   TTTTATTTA
                                |||||||  |||   |||||||||
                                AACGACG  ACG   AAAATAAAT
                                   __   AC_
GAM267  GNAS    3'  TAAATAAAACAGCAGCAGCAA  55389       CT   GTA
                                TTGCTGC  TGT   TTTTATTTA
                                |||||||  |||   |||||||||
                                AACGACG  ACG   AAAATAAAT
                                   __   AC_
GAM267  GNAS    3'  TAAATAAAACAGCAGCAGCAA  6713        CT   GTA
                                TTGCTGC  TGT   TTTTATTTA
                                |||||||  |||   |||||||||
                                AACGACG  ACG   AAAATAAAT
                                   __   AC_
GAM267  SFRP4   3'  TAAATAAAAAGGAGAGGCAGAC 13030    _     GTGTA
          AA                    TTG CTGCCTT    TTTTATTTA
                                |||  |||||||    |||||||||
                                AAC  GACGGAG    AAAATAAAT
                                  A      AGGA_
GAM267  UBD     3'  TAAATAAATTTTTAAGGCA   22144       TGTAT
                                TGCCTTG    TTTATTTA
                                |||||||    ||||||||
                                ACGGAAT    AAATAAAT
                                   TTTT_
GAM267  FLJ22578 3'  AAATAAAACATCACTCAGCAA  46321      CCTT   TA_
                                TTGCTG   GTG   TTTTATTT
                                ||||||   |||   ||||||||
                                AACGAC   CAC   AAAATAAA
                                   T___   TAC
GAM267  MAPK6   3'  AAATAAAACATGGCCAGCAA   12305      _ T   GTAT
                                TTGCTG CC TGT   TTTATTT
                                |||||| || |||   |||||||
                                AACGAC GG ACA   AAATAAA
                                   C  T  _____
GAM268  AVPR1A  5'  CCAAGGAAACAAGCACCGCA   7376    A      __   A
                                TG GGTGCTTG  TCC TGG
                                || ||||||||  ||| |||
                                AC CCACGAAC  AGG ACC
                                 G       AA  A
GAM268  COL1A1  3'  CGGAAACAGACAAGCAACCCA  5394    A   _     CA  GCA
                                TG GGT GCTTGTC  TG   TCG
                                || ||| |||||||  ||   |||
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                                AC CCA CGAACAG  AC   GGC
                                 _  A      __ AAA
GAM268  GRM6     3'  ATGCCATGGGCTTTCCCCCA  7759     A  TGCTT
                                TG GG    GTCCATGGCAT
                                || ||    ||||||||||
                                AC CC    CGGGTACCGTA
                                 _ CCTTT
GAM268  MGC2574  3'  ATGTCAGACACAGCACCTCA  44282        _   CA
                                TGAGGTGCT TGTC  TGGCAT
                                ||||||||| ||||  ||||||
                                ACTCCACGA ACAG  ACTGTA
                                      C   __
GAM268  LOC162137 3'  GTCTGGACAACGCACCTCA   88482        _     T
                                TGAGGTGC TTGTCCA GGC
                                |||||||| ||||||| |||
                                ACTCCACG AACAGGT CTG
                                     C     _
GAM269  ELF3     3'  TGACCTTGACCTTGACCAA   16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                   _    AGT  ____
GAM269  JAK2     3'  TGACCTTCATTCTGAGACCAA  18318       CAA       AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_       C_
GAM269  SLC10A2  5'  ACTCTCTGTCTTGACCAA    6590        CAA       A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ____       C
GAM269  FLJ10803 3'  GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM269  KIAA1958 5'  GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM269  MARCKS   3'  ACTTTCCACCCTGCCCA     11411     TTCA    A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                 CG__   _
GAM269  TUB      5'  GTGGGACCATCCCTTAAACC   13898      C        AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
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                                CCAA TTCCCTACC   GGTG
                                  A       AG__
GAM269  LOC80298  3'  ACTTTTACCTTGAACCA    48062        GATG
                                TGGTTCAAGG   GAAAGT
                                ||||||||||   ||||||
                                ACCAAGTTCC   TTTTCA
                                     A___
GAM270  ELF3      3'  TGACCTTGACCTTGACCAA   16685     T   GAT  AAA
                                TTGGT CAAGG  GG  GTCA
                                ||||| |||||  ||  ||||
                                AACCA GTTCC  TC  CAGT
                                  _    AGT  ___
GAM270  JAK2      3'  TGACCTTCATTCTGAGACCAA 18318     CAA      AA
                                TTGGTT  GGGATGGA GTCA
                                ||||||  |||||||| ||||
                                AACCAG  TCTTACTT CAGT
                                   AG_      C_
GAM270  SLC10A2   5'  ACTCTCTGTCTTGACCAA   6590      CAA      A
                                TTGGTT  GGGATGGA AGT
                                ||||||  |||||||| |||
                                AACCAG  TTCTGTCT TCA
                                   ___      C
GAM270  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA 37205     CAAGG  G
                                TTGGTT   GAT GAAAGTCAC
                                ||||||   ||| |||||||||
                                AACCGA   TTG CTTTCAGTG
                                   AA___  A
GAM270  KIAA1958  5'  GTGACTTTGAACCCCAAACC  82788    CAA  ATGG
                                GGTT  GGG   AAAGTCAC
                                ||||  |||   ||||||||
                                CCAA  CCC   TTTCAGTG
                                  A__  CAAG
GAM270  MARCKS    3'  ACTTTCCACCCTGCCCA    11411    TTCA   A
                                TGG   AGGG TGGAAAGT
                                |||   |||| ||||||||
                                ACC   TCCC ACCTTTCA
                                  CG__  _
GAM270  TUB       5'  GTGGGACCATCCCTTAAACC  13898    C      AAAG
                                GGTT AAGGGATGG   TCAC
                                |||| |||||||||   ||||
                                CCAA TTCCCTACC   GGTG
                                  A       AG__
GAM270  LOC80298  3'  ACTTTTACCTTGAACCA    48062        GATG
                                TGGTTCAAGG   GAAAGT
                                ||||||||||   ||||||
                                ACCAAGTTCC   TTTTCA
                                     A___
GAM271  EPHA2     3'  GGCCAAGAATACTTGAA     16677        GC  G
                                TTCAAGTAT  CT GGTC
                                |||||||||  || ||||
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                                AAGTTCATA  GA CCGG
                                     A_  A
GAM271  TREM2    3'  ATCCAAGACTGTCATATTT   39096       CCTG
                                AAGTATG   GGTCTTGGAT
                                |||||||   ||||||||||
                                TTTATAC   TCAGAACCTA
                                   TG__
GAM271  B3GNT7   3'  ATCCCTTCCAGGCAACCTGAA  71677     A  A      TCTT
                                TTCA GT TGCCTGGG   GGAT
                                |||| || ||||||||   ||||
                                AAGT CA ACGGACCT   CCTA
                                  C  _      TC__
GAM271  CREB-H   3'  GACCCAGACACAGCCTGAA   51876     A  A_  C
                                TTCA GT  TG CTGGGTC
                                |||| ||  || |||||||
                                AAGT CG  AC GACCCAG
                                  C  AC  A
GAM271  CREB-H   3'  GACCCAGACACAGCCTGAA   51877     A  A_  C
                                TTCA GT  TG CTGGGTC
                                |||| ||  || |||||||
                                AAGT CG  AC GACCCAG
                                  C  AC  A
GAM271  FLJ25410 5'  GTCCACCAGGCATCTCGAA   58771     A  T      GTCT
                                TTC AG ATGCCTGG   TGGAT
                                ||| || ||||||||   |||||
                                AAG TC TACGGACC   ACCTG
                                 C  _      _____
GAM271  KIAA0779 3'  TCCGAACAGCATACTTGAA   86912          C  GGTC
                                TTCAAGTATGC TG   TTGGA
                                |||||||||||  ||   |||||
                                AAGTTCATACG AC   AGCCT
                                      _  A___
GAM272  ELF3     3'  TGACCTTGACCTTGACCAA   16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                  _    AGT  ____
GAM272  JAK2     3'  TGACCTTCATTCTGAGACCAA  18318       CAA       AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_       C_
GAM272  SLC10A2  5'  ACTCTCTGTCTTGACCAA    6590        CAA       A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ____       C
GAM272  FLJ10803 3'  GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
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                                AACCGA    TTG CTTTCAGTG
                                   AA___  A
GAM272  KIAA1958  5'  GTGACTTTGAACCCCAAACC  82788     CAA  ATGG
                                GGTT  GGG   AAAGTCAC
                                ||||  |||   ||||||||
                                CCAA  CCC   TTTCAGTG
                                  A__  CAAG
GAM272  MARCKS    3'  ACTTTCCACCCTGCCCA    11411     TTCA  A
                                TGG   AGGG TGGAAAGT
                                |||   |||| ||||||||
                                ACC   TCCC ACCTTTCA
                                 CG__  _
GAM272  TUB       5'  GTGGGACCATCCCTTAAACC  13898     C       AAAG
                                GGTT AAGGGATGG   TCAC
                                |||| |||||||||   ||||
                                CCAA TTCCCTACC   GGTG
                                  A       AG__
GAM272  LOC80298  3'  ACTTTTACCTTGAACCA    48062         GATG
                                TGGTTCAAGG   GAAAGT
                                ||||||||||   ||||||
                                ACCAAGTTCC   TTTTCA
                                     A___
GAM273  ELF3      3'  TGACCTTGACCTTGACCAA   16685     T   GAT  AAA
                                TTGGT CAAGG  GG  GTCA
                                ||||| |||||  ||  ||||
                                AACCA GTTCC  TC  CAGT
                                  _    AGT  ___
GAM273  JAK2      3'  TGACCTTCATTCTGAGACCAA  18318      CAA      AA
                                TTGGTT  GGGATGGA  GTCA
                                ||||||  ||||||||  ||||
                                AACCAG  TCTTACTT  CAGT
                                   AG_      C_
GAM273  SLC10A2   5'  ACTCTCTGTCTTGACCAA    6590       CAA      A
                                TTGGTT  GGGATGGA AGT
                                ||||||  |||||||| |||
                                AACCAG  TTCTGTCT TCA
                                  ___       C
GAM273  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA  37205      CAAGG  G
                                TTGGTT   GAT GAAAGTCAC
                                ||||||   ||| |||||||||
                                AACCGA   TTG CTTTCAGTG
                                   AA___  A
GAM273  KIAA1958  5'  GTGACTTTGAACCCCAAACC  82788     CAA  ATGG
                                GGTT  GGG   AAAGTCAC
                                ||||  |||   ||||||||
                                CCAA  CCC   TTTCAGTG
                                  A__  CAAG
GAM273  MARCKS    3'  ACTTTCCACCCTGCCCA    11411     TTCA  A
                                TGG   AGGG TGGAAAGT
                                |||   |||| ||||||||
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                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM273  TUB      5'  GTGGGACCATCCCTTAAACC   13898      C        AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A        AG__
GAM273  LOC80298 3'  ACTTTTACCTTGAACCA     48062          GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                      A___
GAM274  BIN3     3'  CACCCTCCAGCAGGCAGCCCAG 38573      AGGACA       A
                                CTGG     TGCTGGAG GTG
                                ||||     |||||||| |||
                                GACC     ACGACCTC CAC
                                  CGACGG       C
GAM274  CDH5     3'  CACTCCCCAACCCCTCTCCAG  10147       ACATGC   A
                                CTGGAGG     TGG GAGTG
                                |||||||     ||| |||||
                                GACCTCT     ACC CTCAC
                                    CCCCA_   C
GAM274  CDH5     3'  TCAGCACCCCTCCAGTT     10152         ACA
                                AACTGGAGG   TGCTGG
                                |||||||||   ||||||
                                TTGACCTCC   ACGACT
                                     CC_
GAM274  CISH     3'  CACTCTCTTCTGCCCCCAG   26178      A  A  TGCT
                                CTGG GG CA    GGAGAGTG
                                |||| || ||    ||||||||
                                GACC CC GT    TCTCTCAC
                                  C  _  CT__
GAM274  CISH     3'  CACTCTCTTCTGCCCCCAG   59668      A  A  TGCT
                                CTGG GG CA    GGAGAGTG
                                |||| || ||    ||||||||
                                GACC CC GT    TCTCTCAC
                                  C  _  CT__
GAM274  CSF1R    3'  CACTCTCCCCTCCTCCA     19052       CATGCT
                                TGGAGGA     GGAGAGTG
                                |||||||     ||||||||
                                ACCTCCT     CCTCTCAC
                                    CC____
GAM274  HDAC5    3'  CACTCTCCTCCCTTCTCCAG  58296        CATGCT
                                CTGGAGGA     GGAGAGTG
                                ||||||||     ||||||||
                                GACCTCTT     CCTCTCAC
                                     CCCT__
GAM274  HR       5'  CACTCCCCTGGGCGCCTCTCCA 18913       ACA   __  A
            G                    CTGGAGG   TGCT  GG GAGTG
                                |||||||   ||||  || |||||
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                                GACCTCT  GCGG  CC CTCAC
                                   CC_   GT  C
GAM274  ITGA6   3' CACTCAGGTGACATCCTCCAG 5786       CA_   GGA
                                CTGGAGGA  TGCT  GAGTG
                                ||||||||  ||||  |||||
                                GACCTCCT  GTGG  CTCAC
                                    ACA   A__
GAM274  MAX     3' CACCCTACCAGCTCCTCCAG  11473      CAT   _ A
                                CTGGAGGA  GCTGG AG GTG
                                ||||||||  ||||| || |||
                                GACCTCCT  CGACC TC CAC
                                   ___    A  C
GAM274  MAX     3' CACCCTACCAGCTCCTCCAG  59702      CAT   _ A
                                CTGGAGGA  GCTGG AG GTG
                                ||||||||  ||||| || |||
                                GACCTCCT  CGACC TC CAC
                                   ___    A  C
GAM274  MEN1    3' CACTTAGAATAATATCCTCCAG 95010       C  GCTGGA
                                CTGGAGGA AT    GAGTG
                                ||||||||  ||    |||||
                                GACCTCCT TA    TTCAC
                                    A  ATAAGA
GAM274  MKI67   3' CACCCCCATGCCTGTCCTCCAG 11590       T  _  AGA
                                CTGGAGGACA GC TGG  GTG
                                ||||||||||  ||  |||  |||
                                GACCTCCTGT CG ACC  CAC
                                    C  T  CC_
GAM274  MNT     3' ACTCTCTCACCCACCAG    40084    A  ACA  CT
                                CTGG GG  TG  GGAGAGT
                                ||||  ||  ||  |||||||
                                GACC CC  AC  TCTCTCA
                                  A  C__  __
GAM274  MYH11   3' CAGACACATCCTCCAGTT   43429       CA  _
                                AACTGGAGGA  TG CTG
                                ||||||||||  ||  |||
                                TTGACCTCCT  AC GAC
                                    AC  A
GAM274  MYH11   3' CAGACACATCCTCCAGTT   11738       CA  _
                                AACTGGAGGA  TG CTG
                                ||||||||||  ||  |||
                                TTGACCTCCT  AC GAC
                                    AC  A
GAM274  P2RY6   3' CTTCAGCTACCCTCCAGT   15997       ACAT
                                ACTGGAGG   GCTGGAG
                                ||||||||   |||||||
                                TGACCTCC   CGACTTC
                                    CAT_
GAM274  SLC24A1 3' CACCCTCCAGCATGTTCTC  17560           A
                                GAGGACATGCTGGAG GTG
                                ||||||||||||||| |||
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                                CTCTTGTACGACCTC CAC
                                        C
GAM274  SORCS3   3' CACTCTCCGCTTCCCCCAG   31069     A  CAT  T
                                CTGG GGA   GC GGAGAGTG
                                |||| |||   || ||||||||
                                GACC CCT   CG CCTCTCAC
                                  C  T__  _
GAM274  TCFL4    3' CACTCTTCTGACATCCTGCAGT 64207     G   CATGCT
                                ACTG AGGA     GGAGAGTG
                                |||| ||||     ||||||||
                                TGAC TCCT     CTTCTCAC
                                  G   ACAGT_
GAM274  TFAP4    3' CACTCTCCCACCCCCCAG    13688     A  ACA  CT
                                CTGG GG   TG  GGAGAGTG
                                |||| ||   ||  ||||||||
                                GACC CC   AC  CCTCTCAC
                                  _  CC_  __
GAM274  C20orf44 3' CACTCCCCAACCCCCTCCAG  37308       ACATGC   A
                                CTGGAGG     TGG GAGTG
                                |||||||     ||| |||||
                                GACCTCC     ACC CTCAC
                                    CCCA__   C
GAM274  CHERP    3' CACCCCAGCTCCTTCCTCCAG 22128       CAT_    AGA
                                CTGGAGGA   GCTGG   GTG
                                ||||||||   |||||  |||
                                GACCTCCT   CGACC   CAC
                                     TCCT    C__
GAM274  EREG     5' CACTCTCCGCAGCCGCCCTCC 9303      ACA__   T
                                GGAGG    TGC GGAGAGTG
                                |||||    ||| ||||||||
                                CCTCC    ACG CCTCTCAC
                                   CGCCG  _
GAM274  FLJ22215 3' CACTCTCCAGGGAGGCCCCAG 43396     A  ACATG
                                CTGG GG    CTGGAGAGTG
                                |||| ||    ||||||||||
                                GACC CC    GACCTCTCAC
                                  _  GGAGG
GAM274  FLJ22215 5' CACTCTCCAGGGAGGCCCCAG 98637     A  ACATG
                                CTGG GG    CTGGAGAGTG
                                |||| ||    ||||||||||
                                GACC CC    GACCTCTCAC
                                  _  GGAGG
GAM274  FLJ22635 3' ACCCTGGGTTCCTCCAG    47669       CAT   GG  A
                                CTGGAGGA   GCT  AG GT
                                ||||||||   |||  || ||
                                GACCTCCT   TGG  TC CA
                                     ___   G_  C
GAM274  FLJ30213 5' CCAGGGCATTGTCCTCCAG   59402         _   __
                                CTGGAGGACA TGCT  GG
                                |||||||||| ||||  ||
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                                GACCTCCTGT ACGG  CC
                                     T   GA
GAM274  HIC2     3'  CTCCTGCGCGTCCCCCGG    65866     A   A  T
                                CTGG GGAC TGC GGAG
                                |||| |||| ||| ||||
                                GGCC CCTG GCG CCTC
                                  C   C  T
GAM274  HSPB7    3'  CACCCCTCCCCACGTCTTCCAG 27782        A  CT   A_
                                CTGGAGGAC TG  GGAG  GTG
                                ||||||||| ||  ||||  |||
                                GACCTTCTG AC  CCTC  CAC
                                     C  C_   CC
GAM274  HSPC155  3'  CCTCCACCTCTAGTT      33520        ACATGC    A
                                AACTGGAGG     TGGAG G
                                |||||||||     ||||| |
                                TTGATCTCC     ACCTC C
                                     _______    C
GAM274  KIAA0097 3'  CACTCCCCCGGCACCCTGCAG  96499     G   ACA     A_
                                CTG AGG   TGCTGG  GAGTG
                                ||| |||   ||||||  |||||
                                GAC TCC   ACGGCC  CTCAC
                                  G   C__     CC
GAM274  KIAA0317 3'  ACTCTCCTGTCATCCAGTT   29742       G    TGCT
                                AACTGGA GACA    GGAGAGT
                                ||||||| ||||    |||||||
                                TTGACCT CTGT    CCTCTCA
                                    A   _____
GAM274  KIAA0637 3'  CACTCTCAGGGCCGCTCTCCAG 29921       ACAT   G_
                                CTGGAGG    GCT  GAGAGTG
                                |||||||    |||  |||||||
                                GACCTCT    CGG  CTCTCAC
                                    CGC_   GA
GAM274  KIAA0821 3'  CTCTCCAGGTGCCCCTCAG   30607     GA  A   G
                                CTG  GG CAT CTGGAGAG
                                |||  || ||| ||||||||
                                GAC  CC GTG GACCTCTC
                                  TC  C   _
GAM274  KIAA1202 3'  ACTCTCCTTCCCACAGTT    72481      GA   CATGCT
                                AACTG  GGA     GGAGAGT
                                |||||  |||     |||||||
                                TTGAC  CCT     CCTCTCA
                                   AC   T_____
GAM274  KIAA1522 3'  ACCCTCCTGCCTTCCAGTT   65602        ACAT  T   A
                                AACTGGAGG    GC GGAG GT
                                |||||||||    || |||| ||
                                TTGACCTTC    CG CCTC CA
                                     _____ T    C
GAM274  KIAA1855 3'  CACCCTCCCTGTCCTCC     93947        TGCT    A
                                GGAGGACA    GGAG GTG
                                ||||||||    |||| |||
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                                CCTCCTGT   CCTC CAC
                                    C___   C
GAM274  KIAA1879  5'  CACCCTCATGGAGCCTCCAGT  73929       ACATG  _  A
                                ACTGGAGG   CTG GAG GTG
                                ||||||||   ||| ||| |||
                                TGACCTCC   GGT CTC CAC
                                    GA___  A  C
GAM274  MGC15631  3'  ACTCTCCAGGCTCCCAGT   52224     AG ACATG
                                ACTGG  G   CTGGAGAGT
                                |||||  |   |||||||||
                                TGACC  C   GACCTCTCA
                                   CT G____
GAM274  MGC21675  5'  ACTCTCCATGGCCTCC     54579     A  TGC
                                GGAGG CA   TGGAGAGT
                                ||||| ||   ||||||||
                                CCTCC GT   ACCTCTCA
                                   G  ___
GAM274  MGC2477   3'  CACTCTCCAGATTTCCTCC   44292     C  G
                                GGAGGA AT CTGGAGAGTG
                                |||||| || ||||||||||
                                CCTCCT TA GACCTCTCAC
                                   T  _
GAM274  MGC2541   3'  CACTCTGACAGTCTCCTCCAGT 55621        CAT   G_
          T                     AACTGGAGGA  GCTG  AGAGTG
                                ||||||||||  ||||  ||||||
                                TTGACCTCCT  TGAC  TCTCAC
                                    C__   AG
GAM274  MGC4415   3'  CTCTCCCTGCCCTCCAG    49760      ACAT  T_
                                CTGGAGG   GC  GGAGAG
                                |||||||   ||  ||||||
                                GACCTCC   CG  CCTCTC
                                   _____  TC
GAM274  MYO3B     3'  CACTCTTCTCCATCCTCC    58107     CA  CT
                                GGAGGA  TG  GGAGAGTG
                                ||||||  ||  ||||||||
                                CCTCCT  AC  CTTCTCAC
                                   __  CT
GAM274  NAV1      5'  CACCCTCCATCAAGTCCTCCA  40320       A  C   A
                                TGGAGGAC TG TGGAG GTG
                                |||||||| || ||||| |||
                                ACCTCCTG AC ACCTC CAC
                                    A  T   C
GAM274  P11       5'  CACTCCCTTTTTGGCCTCCA   21216      A  TGCT  A
                                TGGAGG CA   GG GAGTG
                                |||||| ||   || |||||
                                ACCTCC GT   CC CTCAC
                                   G  TTTT  _
GAM274  PPFIA4    3'  CACTCTCTTGCTTGTCCCCA   70837    A   T  T
                                TGG GGACA GC GGAGAGTG
                                ||| ||||| || ||||||||
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                                ACC CCTGT CG TCTCTCAC
                                  _    T  T
GAM274  RPH3A    3'  CACTCAGAACCCCCTCCAGT  30931       ACATG  GGA
                                ACTGGAGG    CT   GAGTG
                                ||||||||    ||   |||||
                                TGACCTCC    GA   CTCAC
                                    CCCAA  ___
GAM274  SEMA4G   5'  CACTCTCCAGCTGCTCCC    96322    AG A  T
                                GG  G CA GCTGGAGAGTG
                                ||  | || ||||||||||
                                CC  C GT CGACCTCTCAC
                                 CT _  _
GAM274  LOC124460 3'  ACCCTCGGCATCCTCAGTT   76552      G   CA    G  A
                                AACTG AGGA  TGCTG AG GT
                                ||||| ||||  ||||| || ||
                                TTGAC TCCT  ACGGC TC CA
                                  _   __    _ C
GAM274  LOC145921 3'  CACAGGGACAGCATGTCTCCAG 76524       G      GAGA_
                                CTGGAG ACATGCTG    GTG
                                |||||| ||||||||    |||
                                GACCTC TGTACGAC    CAC
                                   _      AGGGA
GAM274  LOC147004 5'  CACTCCCCAGCATCATTCTTCA 84966       C_     A
                                TGGAGGA  ATGCTGG GAGTG
                                |||||||  ||||||| |||||
                                ACTTCTT  TACGACC CTCAC
                                    AC      C
GAM274  LOC147599 3'  ACCCCACTGTCCTCCAG     85157         TGC   AGA
                                CTGGAGGACA   TGG   GT
                                ||||||||||   |||   ||
                                GACCTCCTGT   ACC   CA
                                      C__   C__
GAM274  LOC148343 5'  ACTCCCCGTTCTCCCAG     79534     _    ATGCT  A
                                CTGG AGGAC    GG GAGT
                                |||| |||||    || ||||
                                GACC TCTTG    CC CTCA
                                  C    _____  C
GAM274  LOC150135 3'  CCGATCATGTGCTCCAGTT   80393       G    C_
                                AACTGGAG ACATG  TGG
                                |||||||| |||||  |||
                                TTGACCTC TGTAC  GCC
                                    G    TA
GAM274  LOC151304 3'  CACTCTCCCCTTCCTCCA    86497       CATGCT
                                TGGAGGA     GGAGAGTG
                                |||||||     ||||||||
                                ACCTCCT     CCTCTCAC
                                   TCC___
GAM274  LOC153480 5'  CACTCCCTCGCACACCCTCCAG 73273       ACA   T_  A
                                CTGGAGG   TGC  GG GAGTG
                                |||||||   |||  || |||||
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                                GACCTCC   ACG  CC CTCAC
                                    CAC   CT  _
GAM274   LOC200226 3'  TTTCAGCAGCCCTCCAG     90040        ACA
                                CTGGAGG   TGCTGGAG
                                |||||||   ||||||||
                                GACCTCC   ACGACTTT
                                    CG_
GAM274   LOC220021 3'  CACTCTCCAGCATCTGGCCCAG 95018      AGGAC
                                CTGG    ATGCTGGAGAGTG
                                ||||    ||||||||||||
                                GACC    TACGACCTCTCAC
                                  CGGTC
GAM274   LOC253566 3'  CACAGGGACAGCATGTCTCCAG 96634       G       GAGA_
                                CTGGAG ACATGCTG    GTG
                                |||||| ||||||||    |||
                                GACCTC TGTACGAC    CAC
                                   _       AGGGA
GAM274   LOC253955 3'  CACTCCCACACGCCCACCCAG  96070     A__  ACA  C   A
                                CTGG   GG   TG TGG GAGTG
                                ||||   ||   || ||| |||||
                                GACC   CC   AC ACC CTCAC
                                  CAC  GC_  _   _
GAM274   LOC254504 5'  CCCGCAGTCCTCCAGTT     99057          A   T
                                AACTGGAGGAC TGC GG
                                |||||||||||| ||| ||
                                TTGACCTCCTG ACG CC
                                      _  C
GAM274   LOC257185 5'  CACTCCCCAGCATGCCAG    98019     AGGA      A
                                CTGG    CATGCTGG GAGTG
                                ||||    |||||||| |||||
                                GACC    GTACGACC CTCAC
                                  _____       C
GAM274   LOC84549  3'  ACATACACACCTCCAGTT    51678        ACA  C  GAGA
                                AACTGGAGG   TG TG    GT
                                |||||||||   || ||    ||
                                TTGACCTCC   AC AC    CA
                                     ___  _  ATA_
GAM274   LOC92973  5'  CACCCTCCAGTGACCCGCAG   71584     GA  ACA      A
                                CTG  GG   TGCTGGAG GTG
                                |||  ||   |||||||| |||
                                GAC  CC   GTGACCTC CAC
                                  G_  CA_       C
GAM275   EN1       3'  TATTTAATTTCAGGTAA     9250          AC
                                TTACCTGGAA  TAAGTG
                                ||||||||||  ||||||
                                AATGGACTTT  ATTTAT
                                      A_
GAM275   MEN1      5'  GATTTGCTAGCTCCAAGTAA   95012      C    AA   A TG
                                TTAC TGGA  CTA G  GATT
                                |||| ||||  ||| |  ||||
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                                AATG ACCT  GAT C  TTAG
                                  A   C_  _ GT
GAM275  TEM8     3'  AATTCTTCCAGTTTCCAAGTGA 50821      C       AAGT
                                TTAC TGGAAACT   GGATT
                                |||| ||||||||   |||||
                                AGTG ACCTTTGA   CTTAA
                                  A       CCTT
GAM275  FLJ20150 3'  GATCATGTCTCCAGGTAA    35141         A  TAAGTG
                                TTACCTGGA AC    GATT
                                ||||||||| ||    ||||
                                AATGGACCT TG    CTAG
                                     C  TA____
GAM275  KIAA1040 3'  CACTAGTCCCAGGTAA      72683         AA   A
                                TTACCTGG  ACTA GTG
                                ||||||||  |||| |||
                                AATGGACC  TGAT CAC
                                     C_   _
GAM275  SEMA3C   3'  TTCATGCTTCCAGGTAA     22111         ACTAA
                                TTACCTGGAA    GTGGA
                                ||||||||||    |||||
                                AATGGACCTT    TACTT
                                     CG___
GAM275  SNX16    3'  ATTTGTTTAGTTTCCACGTAA  42406      C         TG
                                TTAC TGGAAACTAAG  GAT
                                |||| ||||||||||  |||
                                AATG ACCTTTGATTT  TTA
                                  C         GT
GAM275  LOC197342 3'  CACCAGCTTCCAGGTGA     89352         A  AA
                                TTACCTGGAA CT  GTG
                                |||||||||| ||  |||
                                AGTGGACCTT GA  CAC
                                     C  C_
GAM275  LOC199787 3'  TAATGCATCTAGTTTCCA    89778         AG  G
                                TGGAAACTA  TG ATTA
                                |||||||||  || ||||
                                ACCTTTGAT  AC TAAT
                                     CT  G
GAM275  LOC92935  3'  TAATACACAACTTTCAGGTAA  71517         ACTAA   G
                                TTACCTGGAA    GTG ATTA
                                ||||||||||    ||| ||||
                                AATGGACTTT    CAC TAAT
                                     CAA__   A
GAM276  ELF3     3'  TGACCTTGACCTTGACCAA    16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                  _    AGT  ____
GAM276  JAK2     3'  TGACCTTCATTCTGAGACCAA  18318       CAA       AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
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                                AACCAG   TCTTACTT  CAGT
                                   AG_      C_
GAM276  SLC10A2  5'  ACTCTCTGTCTTGACCAA    6590       CAA      A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___      C
GAM276  FLJ10803 3'  GTGACTTTCAGTTAAAGCCAA 37205      CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM276  KIAA1958 5'  GTGACTTTGAACCCCAAACC  82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM276  MARCKS   3'  ACTTTCCACCCTGCCCA     11411     TTCA    A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                 CG__   _
GAM276  TUB      5'  GTGGGACCATCCCTTAAACC   13898      C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A       AG__
GAM276  LOC80298 3'  ACTTTTACCTTGAACCA     48062         GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                     A___
GAM277  GPD1     3'  TCATGCCACCACATTTG     60398       C       C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A       _
GAM277  IL5RA    5'  TCGCATGGCCACCGCATTT    6906          AT__
                                AAATGCGGTGGC    CGA
                                ||||||||||||    |||
                                TTTACGCCACCG    GCT
                                      GTAC
GAM277  MYO1C    3'  TGCCGATGCCAAATATTTG    61873       CGG      A
                                TAAATG   TGGCATCG CA
                                ||||||   |||||||| ||
                                GTTTAT   ACCGTAGC GT
                                   AA_       C
GAM277  C6orf37  3'  TGTCACACTGCATTTA      68097          GCATC
                                TAAATGCGGTG    GACA
                                ||||||||||     ||||
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                                ATTTACGTCAC    CTGT
                                      A____
GAM277  DNAJC6   3' TTGCAGAACCACCGCATT   29498        CA  GA
                                AATGCGGTGG  TC  CAA
                                ||||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                      A_  AC
GAM277  FLJ11210 3' GTCGATGTGCATGCTTTTA  60319    T  GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM277  FLJ12476 3' TCGATCTTCTGCATTTA    43270       T  C
                                TAAATGCGG GG ATCGA
                                ||||||||| || |||||
                                ATTTACGTC TC TAGCT
                                      T  _
GAM277  KIAA1034 3' TCGATGGCATCCGCATTTG  63134       _  G
                                TAAATGCGG TG CATCGA
                                ||||||||| || ||||||
                                GTTTACGCC AC GTAGCT
                                      T  G
GAM277  KIAA1987 3' TCATGTAACTGCATTTA    89391       G   C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                      A   _
GAM277  MGC16063 3' TGTCCTGGCCACTGCATT   54929        ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                      GTC
GAM277  LOC147949 3' TGTCAGATGTCCACATTGCA  79279    __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM277  LOC150577 3' GTCCTCACCGCATTTG     86258         CATC
                                TAAATGCGGTGG   GAC
                                ||||||||||||   |||
                                GTTTACGCCACT   CTG
                                      C___
GAM277  LOC158219 3' TGTGTGTCACCACATTT    82694     C      CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                  A       __
GAM277  LOC202020 3' TGTCTCACCACATTTA     90605      C    CATC
                                TAAATG GGTGG   GACA
                                |||||| |||||   ||||
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                                ATTTAC CCACT    CTGT
                                   A    ____
GAM277  LOC90826  5'  TGTCGATGCAGGTTTATTTG  64788      CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                   TTGGA
GAM277  LOC93587  3'  TTGTCTTTACCTGCATTTA   73042      _    CATC
                                TAAATGC GGTGG    GACAA
                                ||||||| |||||    |||||
                                ATTTACG CCATT    CTGTT
                                   T    T___
GAM278  ELF3      3'  TGACCTTGACCTTGACCAA   16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                  _    AGT  ___
GAM278  JAK2      3'  TGACCTTCATTCTGAGACCAA 18318      CAA      AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_      C_
GAM278  SLC10A2   5'  ACTCTCTGTCTTGACCAA    6590       CAA      A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM278  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA 37205      CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM278  KIAA1958  5'  GTGACTTTGAACCCCAAACC  82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM278  MARCKS    3'  ACTTTCCACCCTGCCCA     11411     TTCA    A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM278  TUB       5'  GTGGGACCATCCCTTAAACC   13898     C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A       AG__
GAM278  LOC80298  3'  ACTTTTACCTTGAACCA     48062          GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
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                                ACCAAGTTCC    TTTTCA
                                     A___
GAM279  ESRRG    3'  GGTAGAGCAATATTAAACAAGC 66989            C
              TT                  AAGCTTGTTTAATAT GCTCTACC
                                  |||||||||||||| ||||||||
                                  TTCGAACAAATTATA CGAGATGG
                                        A
GAM279  SLC1A2   3'  GATGATATAAACAAGCTT    62614          A    C
                                  AAGCTTGTTTA TATCG TC
                                  |||||||||| ||||| ||
                                  TTCGAACAAAT ATAGT AG
                                     _    _
GAM279  DIO2     3'  TAGGTGCAAACAAACAAGCTT  7666          AATAT   T
                                  AAGCTTGTTT    CGC CTA
                                  |||||||||     ||| |||
                                  TTCGAACAAA    GTG GAT
                                       CAAAC  _
GAM279  DIO2     3'  TAGGTGCAAACAAACAAGCTT  26554         AATAT   T
                                  AAGCTTGTTT    CGC CTA
                                  |||||||||     ||| |||
                                  TTCGAACAAA    GTG GAT
                                       CAAAC  _
GAM279  MBLL39   5'  GAGAGCTAAACAAGGTT     20449    G      ATATC    A
                                  AA CTTGTTTA    GCTCT C
                                  || ||||||||    ||||| |
                                  TT GAACAAAT    CGAGA G
                                   G       _____    C
GAM279  MBLL39   5'  GAGAGCTAAACAAGGTT     59261    G      ATATC    A
                                  AA CTTGTTTA    GCTCT C
                                  || ||||||||    ||||| |
                                  TT GAACAAAT    CGAGA G
                                   G       _____    C
GAM279  SGK2     3'  AGAGATGTAACAAGCT      33249        TA    G
                                  AGCTTGTT  ATATC CT
                                  ||||||||  ||||| ||
                                  TCGAACAA  TGTAG GA
                                       __    A
GAM279  LOC146611 3'  AGAGCAATATTAGAAAGGCT   78611      G      C
                                  AGCTT TTTAATAT GCTCT
                                  ||||| |||||||| |||||
                                  TCGGA AGATTATA CGAGA
                                     A       A
GAM279  LOC147081 5'  AGTAGCTATTAGACAAGCT    78842           TC  _
                                  AGCTTGTTTAATA  GCT CT
                                  ||||||||||||  ||| ||
                                  TCGAACAGATTAT  CGA GA
                                          __  T
GAM279  LOC197201 3'  GACTGACTTTAAACAAGCT    89275          TA   C
                                  AGCTTGTTTAA  TCG TC
                                  ||||||||||  ||| ||
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                                TCGAACAAATT  AGT AG
                                      TC   C
GAM279  LOC90625  3'  TAGAGCGATTAGACTACAAGCT 64381       TTAAT_
                                AGCTTGT     ATCGCTCTA
                                |||||||     |||||||||
                                TCGAACA     TAGCGAGAT
                                    TCAGAT
GAM280  ELF3      3'  TGACCTTGACCTTGACCAA   16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                   _    AGT  ___
GAM280  JAK2      3'  TGACCTTCATTCTGAGACCAA  18318      CAA      AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                    AG_      C_
GAM280  SLC10A2   5'  ACTCTCTGTCTTGACCAA    6590       CAA      A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM280  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA  37205      CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                    AA___   A
GAM280  KIAA1958  5'  GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM280  MARCKS    3'  ACTTTCCACCCTGCCCA     11411     TTCA    A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM280  TUB       5'  GTGGGACCATCCCTTAAACC   13898     C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A        AG__
GAM280  LOC80298  3'  ACTTTTACCTTGAACCA     48062         GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                      A___
GAM281  ELF3      3'  TGACCTTGACCTTGACCAA   16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
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                                AACCA GTTCC   TC   CAGT
                                  _    AGT  ___
GAM281  JAK2     3'  TGACCTTCATTCTGAGACCAA  18318       CAA       AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_       C_
GAM281  SLC10A2  5'  ACTCTCTGTCTTGACCAA    6590        CAA       A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM281  FLJ10803 3'  GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM281  KIAA1958 5'  GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM281  MARCKS   3'  ACTTTCCACCCTGCCCA     11411     TTCA    A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                 CG__   _
GAM281  TUB      5'  GTGGGACCATCCCTTAAACC   13898     C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A        AG__
GAM281  LOC80298 3'  ACTTTTACCTTGAACCA     48062         GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                     A___
GAM282  GPD1     3'  TCATGCCACCACATTTG      60398       C       C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A      _
GAM282  IL5RA    5'  TCGCATGGCCACCGCATTT    6906          AT__
                                AAATGCGGTGGC    CGA
                                ||||||||||||    |||
                                TTTACGCCACCG    GCT
                                      GTAC
GAM282  MYO1C    3'  TGCCGATGCCAAATATTTG    61873       CGG       A
                                TAAATG   TGGCATCG CA
                                ||||||   |||||||| ||
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                                GTTTAT   ACCGTAGC GT
                                   AA_      C
GAM282  C6orf37   3'  TGTCACACTGCATTTA     68097         GCATC
                                TAAATGCGGTG    GACA
                                ||||||||||    ||||
                                ATTTACGTCAC    CTGT
                                      A____
GAM282  DNAJC6    3'  TTGCAGAACCACCGCATT    29498         CA  GA
                                AATGCGGTGG  TC  CAA
                                |||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                      A_  AC
GAM282  FLJ11210  3'  GTCGATGTGCATGCTTTTA   60319     T   GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM282  FLJ12476  3'  TCGATCTTCTGCATTTA     43270         T  C
                                TAAATGCGG GG ATCGA
                                |||||||| || |||||
                                ATTTACGTC TC TAGCT
                                      T  _
GAM282  KIAA1034  3'  TCGATGGCATCCGCATTTG   63134         _  G
                                TAAATGCGG TG CATCGA
                                |||||||| || ||||||
                                GTTTACGCC AC GTAGCT
                                      T  G
GAM282  KIAA1987  3'  TCATGTAACTGCATTTA     89391         G   C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                      A   _
GAM282  MGC16063  3'  TGTCCTGGCCACTGCATT    54929          ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                      GTC
GAM282  LOC147949 3'  TGTCAGATGTCCACATTGCA  79279     __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM282  LOC150577 3'  GTCCTCACCGCATTTG      86258          CATC
                                TAAATGCGGTGG   GAC
                                ||||||||||||   |||
                                GTTTACGCCACT   CTG
                                      C___
GAM282  LOC158219 3'  TGTGTGTCACCACATTT     82694      C      CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
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                                TTTAC CCACTGTG  TGT
                                   A       __
GAM282  LOC202020 3'  TGTCTCACCACATTTA      90605       C    CATC
                                TAAATG GGTGG    GACA
                                |||||| |||||    ||||
                                ATTTAC CCACT    CTGT
                                   A    ____
GAM282  LOC90826  5'  TGTCGATGCAGGTTTATTTG   64788       CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                   TTGGA
GAM282  LOC93587  3'  TTGTCTTTACCTGCATTTA    73042       _    CATC
                                TAAATGC GGTGG    GACAA
                                ||||||| |||||    |||||
                                ATTTACG CCATT    CTGTT
                                    T    T___
GAM283  ELF3      3'  GACCTTGACCTTGACCAA     16682      T    GATGG   A
                                TTGGT CAAGG     CAA GTC
                                ||||| |||||     ||| |||
                                AACCA GTTCC     GTT CAG
                                  _    A____   C
GAM283  IL6R      3'  ACTTTGTTTAGCCCAAAACCAA 6908       CAA   AT_
                                TTGGTT   GGG   GGCAAAGT
                                ||||||   |||   ||||||||
                                AACCAA   CCC   TTGTTTCA
                                   AA_   GAT
GAM283  FLJ13197  3'  TGACTTTGCCCATAGACCAA   45189      CAAGGGAT
                                TTGGTT       GGCAAAGTCA
                                ||||||       ||||||||||
                                AACCAG       CCGTTTCAGT
                                   ATAC____
GAM283  KIAA1322  5'  ACTCCGTTTCTCCTTGGACCAA 73106          AT   AA
                                TTGGTTCAAGGG  GGC  AGT
                                ||||||||||||  |||  |||
                                AACCAGGTTCCT  TTG  TCA
                                      CT   CC
GAM283  KIAA1958  5'  TGACTTTGAACCCCAAACC    82796      CAA   ATGG
                                GGTT   GGG    CAAAGTCA
                                ||||   |||    ||||||||
                                CCAA   CCC    GTTTCAGT
                                  AC_   AA__
GAM283  MGC22014  3'  ACTTCAACATACCCTGGACCAA 65108        A   _   GCA
                                TTGGTTCA GGG ATG   AAGT
                                |||||||| ||| |||   ||||
                                AACCAGGT CCC TAC   TTCA
                                    _   A   AAC
GAM283  MSTP032   5'  ACTTTGCTTTCAAATCAA     48203       CAAGG  T
                                TTGGTT    GA GGCAAAGT
                                ||||||    || ||||||||
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                                AACTAA    CT TCGTTTCA
                                   A____  T
GAM283  LOC149910 3'  TGACCCTGCCATCCTACC    80357     TCAA       AA
                                GGT   GGGATGGCA  GTCA
                                |||   |||||||||  ||||
                                CCA   TCCTACCGT  CAGT
                                 ____       CC
GAM283  LOC80298  3'  ACTTTTACCTTGAACCA     48063         GATGGC
                                TGGTTCAAGG     AAAGT
                                ||||||||||     |||||
                                ACCAAGTTCC     TTTCA
                                      AT____
GAM284  GPD1      3'  TCATGCCACCACATTTG     60398       C       C
                                TAAATG GGTGGCAT GA
                                |||||| ||||||||  ||
                                GTTTAC CCACCGTA CT
                                   A      _
GAM284  IL5RA     5'  TCGCATGGCCACCGCATTT   6906          AT__
                                AAATGCGGTGGC   CGA
                                ||||||||||||   |||
                                TTTACGCCACCG   GCT
                                      GTAC
GAM284  MYO1C     3'  TGCCGATGCCAAATATTTG   61873       CGG       A
                                TAAATG   TGGCATCG CA
                                ||||||   |||||||| ||
                                GTTTAT   ACCGTAGC GT
                                   AA_       C
GAM284  C6orf37   3'  TGTCACACTGCATTTA      68097         GCATC
                                TAAATGCGGTG    GACA
                                ||||||||||     ||||
                                ATTTACGTCAC    CTGT
                                      A____
GAM284  DNAJC6    3'  TTGCAGAACCACCGCATT    29498         CA  GA
                                AATGCGGTGG  TC  CAA
                                ||||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                      A_  AC
GAM284  FLJ11210  3'  GTCGATGTGCATGCTTTTA   60319     T   GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM284  FLJ12476  3'  TCGATCTTCTGCATTTA     43270         T  C
                                TAAATGCGG GG ATCGA
                                ||||||||| || |||||
                                ATTTACGTC TC TAGCT
                                      T  _
GAM284  KIAA1034  3'  TCGATGGCATCCGCATTTG   63134         _  G
                                TAAATGCGG TG CATCGA
                                ||||||||| || ||||||
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                                GTTTACGCC AC GTAGCT
                                     T  G
GAM284  KIAA1987  3'  TCATGTAACTGCATTTA     89391          G    C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                     A   _
GAM284  MGC16063  3'  TGTCCTGGCCACTGCATT    54929           ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                      GTC
GAM284  LOC147949 3'  TGTCAGATGTCCACATTGCA   79279      __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM284  LOC150577 3'  GTCCTCACCGCATTTG      86258           CATC
                                TAAATGCGGTGG    GAC
                                ||||||||||||    |||
                                GTTTACGCCACT    CTG
                                      C___
GAM284  LOC158219 3'  TGTGTGTCACCACATTT     82694       C       CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                   A       __
GAM284  LOC202020 3'  TGTCTCACCACATTTA      90605       C    CATC
                                TAAATG GGTGG    GACA
                                ||||||| |||||    ||||
                                ATTTAC CCACT    CTGT
                                   A    _____
GAM284  LOC90826  5'  TGTCGATGCAGGTTTATTTG   64788       CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                    TTGGA
GAM284  LOC93587  3'  TTGTCTTTACCTGCATTTA    73042        _    CATC
                                TAAATGC GGTGG    GACAA
                                ||||||| |||||    |||||
                                ATTTACG CCATT    CTGTT
                                     T    T___
GAM285  GPD1      3'  TCATGCCACCACATTTG      60398       C       C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A       _
GAM285  IL5RA     5'  TCGCATGGCCACCGCATTT    6906            AT__
                                AAATGCGGTGGC    CGA
                                ||||||||||||    |||
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                                TTTACGCCACCG   GCT
                                      GTAC
GAM285  MYO1C    3'  TGCCGATGCCAAATATTTG   61873      CGG      A
                                TAAATG  TGGCATCG CA
                                ||||||  |||||||| ||
                                GTTTAT  ACCGTAGC GT
                                   AA_      C
GAM285  C6orf37  3'  TGTCACACTGCATTTA     68097         GCATC
                                TAAATGCGGTG    GACA
                                ||||||||||    ||||
                                ATTTACGTCAC    CTGT
                                      A____
GAM285  DNAJC6   3'  TTGCAGAACCACCGCATT    29498        CA  GA
                                AATGCGGTGG  TC  CAA
                                |||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                      A_  AC
GAM285  FLJ11210 3'  GTCGATGTGCATGCTTTTA   60319     T  GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM285  FLJ12476 3'  TCGATCTTCTGCATTTA     43270        T  C
                                TAAATGCGG GG ATCGA
                                |||||||||  || |||||
                                ATTTACGTC TC TAGCT
                                      T  _
GAM285  KIAA1034 3'  TCGATGGCATCCGCATTTG   63134        _  G
                                TAAATGCGG TG CATCGA
                                |||||||||  || ||||||
                                GTTTACGCC AC GTAGCT
                                      T  G
GAM285  KIAA1987 3'  TCATGTAACTGCATTTA     89391        G   C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                      A   _
GAM285  MGC16063 3'  TGTCCTGGCCACTGCATT    54929         ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                      GTC
GAM285  LOC147949 3'  TGTCAGATGTCCACATTGCA  79279     __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM285  LOC150577 3'  GTCCTCACCGCATTTG     86258         CATC
                                TAAATGCGGTGG   GAC
                                ||||||||||||   |||
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                                GTTTACGCCACT   CTG
                                      C___
GAM285  LOC158219 3'  TGTGTGTCACCACATTT    82694      C      CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                   A      __
GAM285  LOC202020 3'  TGTCTCACCACATTTA     90605      C    CATC
                                TAAATG GGTGG   GACA
                                |||||| |||||   ||||
                                ATTTAC CCACT   CTGT
                                   A    _____
GAM285  LOC90826  5'  TGTCGATGCAGGTTTATTTG  64788      CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                    TTGGA
GAM285  LOC93587  3'  TTGTCTTTACCTGCATTTA   73042      _    CATC
                                TAAATGC GGTGG   GACAA
                                ||||||| |||||   |||||
                                ATTTACG CCATT   CTGTT
                                    T    T___
GAM286  GPD1      3'  TCATGCCACCACATTTG     60398      C      C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A      _
GAM286  IL5RA     5'  TCGCATGGCCACCGCATTT   6906         AT__
                                AAATGCGGTGGC   CGA
                                ||||||||||||   |||
                                TTTACGCCACCG   GCT
                                      GTAC
GAM286  MYO1C     3'  TGCCGATGCCAAATATTTG   61873      CGG      A
                                TAAATG   TGGCATCG CA
                                ||||||   |||||||| ||
                                GTTTAT   ACCGTAGC GT
                                   AA_      C
GAM286  C6orf37   3'  TGTCACACTGCATTTA     68097        GCATC
                                TAAATGCGGTG    GACA
                                ||||||||||     ||||
                                ATTTACGTCAC    CTGT
                                      A_____
GAM286  DNAJC6    3'  TTGCAGAACCACCGCATT    29498        CA  GA
                                AATGCGGTGG  TC  CAA
                                ||||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                      A_  AC
GAM286  FLJ11210  3'  GTCGATGTGCATGCTTTTA   60319     T  GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
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                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM286  FLJ12476  3'  TCGATCTTCTGCATTTA     43270        T  C
                                TAAATGCGG GG ATCGA
                                ||||||||| || |||||
                                ATTTACGTC TC TAGCT
                                     T  _
GAM286  KIAA1034  3'  TCGATGGCATCCGCATTTG   63134        _  G
                                TAAATGCGG TG CATCGA
                                ||||||||| || ||||||
                                GTTTACGCC AC GTAGCT
                                     T  G
GAM286  KIAA1987  3'  TCATGTAACTGCATTTA     89391        G   C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                     A   _
GAM286  MGC16063  3'  TGTCCTGGCCACTGCATT    54929         ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                      GTC
GAM286  LOC147949 3'  TGTCAGATGTCCACATTGCA   79279     __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM286  LOC150577 3'  GTCCTCACCGCATTTG      86258         CATC
                                TAAATGCGGTGG   GAC
                                ||||||||||||   |||
                                GTTTACGCCACT   CTG
                                      C___
GAM286  LOC158219 3'  TGTGTGTCACCACATTT     82694      C      CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                   A       __
GAM286  LOC202020 3'  TGTCTCACCACATTTA      90605      C    CATC
                                TAAATG GGTGG   GACA
                                |||||| |||||   ||||
                                ATTTAC CCACT   CTGT
                                   A   ____
GAM286  LOC90826  5'  TGTCGATGCAGGTTTATTTG  64788      CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                    TTGGA
GAM286  LOC93587  3'  TTGTCTTTACCTGCATTTA   73042       _    CATC
                                TAAATGC GGTGG   GACAA
                                ||||||| |||||   |||||
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                                ATTTACG CCATT   CTGTT
                                   T    T___
GAM287  ITGAL    3'  CTCAGGATGCCCAGGGCCAC  11043     GA       C
                                GTGGT  TGGGCATCC GAG
                                |||||  ||||||||| |||
                                CACCG  ACCCGTAGG CTC
                                  GG       A
GAM287  BIRC1    3'  GCTCAAGAAATAAATCATCACC 16993        GGGCA  CC
                                GGTGGTGAT    TC  GAGC
                                |||||||||    ||  ||||
                                CCACTACTA    AG  CTCG
                                     AATAA  AA
GAM287  MGC15476 3'  CTCCCCCACCACCACCGA    59610        A   CATCCC
                                TCGGTGGTG TGGG     GAG
                                ||||||||| ||||     |||
                                AGCCACCAC ACCC     CTC
                                     C   C_____
GAM287  THG-1    5'  CTCGGGACACCCACTCGC    48912     _   CA
                                GTGA TGGG  TCCCGAG
                                |||| ||||  |||||||
                                CGCT ACCC  AGGGCTC
                                  C   AC
GAM287  LOC245771 5' GCTGGTCGCCCACCACCCC   94483   T   A    AT  CG
                                GG GGTG TGGGC  CC  AGC
                                || |||| |||||  ||  |||
                                CC CCAC ACCCG  GG  TCG
                                 _   C    CT  __
GAM288  ALPI     3'  TGCCTCCTCAAGGTCTCCA   9681        CCAAG   A   T
                                TGGGGACC    GAG GAG CA
                                ||||||||    ||| ||| ||
                                ACCTCTGG    CTC CTC GT
                                     AA___   _   C
GAM288  CACNG3   5'  CTGACTCTCCCCCTCCAACCCC 22566      ACCCCAA  A
           CA                     TGGGG      GG GAGAGTCAG
                                |||||      || |||||||||
                                ACCCC      CC CTCTCAGTC
                                   CAACCTC  C
GAM288  CGTHBA   3'  CTGCTCCTTGGACCCCCCA   24889      ACC      _
                                TGGGG   CCAAGGAG AG
                                |||||   |||||||| ||
                                ACCCC   GGTTCCTC TC
                                   CCA       G
GAM288  CNTNAP2  3'  ACTCTCTCCTTGGATAGCCT   27088    ACC_
                                GGG    CCAAGGAGAGAGT
                                |||    ||||||||||||
                                TCC    GGTTCCTCTCTCA
                                  GATA
GAM288  DNMT3L   5'  CTCCCCACTGAGGTCCCCA   26286        C  A_  A
                                TGGGGACC CA  GG GAG
                                |||||||| ||  || |||
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                                ACCCCTGG GT  CC CTC
                                    A  CA  C
GAM288  HS3ST4   3' CTGTCCCCTAGGGTCCCTA   73856        CA   A  G
                                TGGGGACCC  AGG GA AG
                                |||||||||  ||| || ||
                                ATCCCTGGG  TCC CT TC
                                    A_   C  G
GAM288  LRP1     3' CTGCTCCTTGGCACCCCCA   11359      ACC      _
                                TGGGG   CCAAGGAG AG
                                |||||   |||||||| ||
                                ACCCC   GGTTCCTC TC
                                   CAC       G
GAM288  LRP1     3' CTGTCTCCAGGGCCCCCA    11360      A  CAA    G
                                TGGGG CCC   GGAGA AG
                                ||||| |||   ||||| ||
                                ACCCC GGG   CCTCT TC
                                   C  A__    G
GAM288  MEF2D    3' TGACTCTTTGGAATCCCC    20989      CC   AGGA
                                GGGGA  CCA   GAGAGTCA
                                |||||  |||   ||||||||
                                CCCCT  GGT   TTCTCAGT
                                   AA  ____
GAM288  RANBP3   3' CTGGAAGGGTCCCCAGGGTCCC 24631        CAA   GAGAG
            C                    GGGGACCC   GGA    TCAG
                                ||||||||   |||    ||||
                                CCCCTGGG   CCT    GGTC
                                    ACC   GGGAA
GAM288  SLC22A12 3' CTGCCCTCTGAGGTCCCCA   58689        C  _  AG
                                TGGGGACC CA AGG  AG
                                |||||||| || |||  ||
                                ACCCCTGG GT TCC  TC
                                    A  C   CG
GAM288  C22orf3  5' CTGACTCCCAGCCGGGGTCCCC 25349        AA  AGA_
                                GGGGACCCC  GG   GAGTCAG
                                |||||||||  ||   |||||||
                                CCCCTGGGG  CC   CTCAGTC
                                    __  GACC
GAM288  CD84-H1  3' CTGCTCCTTGGGAACCCCA   54224      AC       _
                                TGGGG  CCCAAGGAG AG
                                |||||  ||||||||| ||
                                ACCCC  GGGTTCCTC TC
                                   AA       G
GAM288  DKFZP564O1664 5' TGAGGCTCGGGGTCCCCA   48670         AAGGA   AG
                                TGGGGACCCC    GAG  TCA
                                ||||||||||    |||  |||
                                ACCCCTGGGG    CTC  AGT
                                    _____  GG
GAM288  FLJ00001 3' TGACATCTTTGGGTCCCCA   82719        CAA    GA
                                TGGGGACCC   GGAGA  GTCA
                                |||||||||   |||||  ||||
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                                ACCCCTGGG  TTTCT  CAGT
                                    ___    A_
GAM288  FLJ20584  3'  CTGGCCTTCGGGGTCCCCA   35854        _   AG
                                TGGGGACCCC AAGG  AG
                                |||||||||| ||||  ||
                                ACCCCTGGGG TTCC  TC
                                    C   GG
GAM288  FLJ22969  3'  CTACTCTCACTGGGGTCCCCA 69201        AG   _
                                TGGGGACCCCA  GAGAG AG
                                |||||||||||  ||||| ||
                                ACCCCTGGGGT  CTCTC TC
                                    CA    A
GAM288  GIT1      3'  TGGCTCCCCGGGGTCCCC    26724       AA  AGA
                                GGGGACCCC  GG   GAGTCA
                                |||||||||  ||   ||||||
                                CCCCTGGGG  CC   CTCGGT
                                    __ C__
GAM288  KIAA0285  3'  ACCTCCCTCAGGTCCCCA    29678       CCA  A  A
                                TGGGGACC   AGG GAG GT
                                ||||||||   ||| ||| ||
                                ACCCCTGG   TCC CTC CA
                                    AC_  _  _
GAM288  KIAA0545  3'  GACTCTCTCCTCCTCCTCCC  63843     CCCCA
                                GGGA    AGGAGAGAGTC
                                ||||    ||||||||||
                                CCCT    TCCTCTCTCAG
                                  CCTCC
GAM288  KIAA1190  3'  TGATGTCCTCAGGGTCCCC   71656       CA   GAGA
                                GGGGACCC  AGGA   GTCA
                                ||||||||  ||||   ||||
                                CCCCTGGG  TCCT   TAGT
                                    AC   G___
GAM288  KIAA1510  3'  TGAGCCCCTGGGGTCCCC    62025        A  AGAGAG
                                GGGGACCCCA GG     TCA
                                |||||||||| ||     |||
                                CCCCTGGGGT CC     AGT
                                    C  CG____
GAM288  MGC2941   3'  TGAGCCTCAGGGTCCTCA    44416       CAAGGA   AG
                                TGGGGACCC     GAG  TCA
                                |||||||||     |||  |||
                                ACTCCTGGG     CTC  AGT
                                    A_____   CG
GAM288  NFASC     3'  CTGTCCCTGGAGTTCCCA    70856       C   A   G
                                TGGGGAC CCA GGA AG
                                ||||||| ||| ||| ||
                                ACCCTTG GGT CCT TC
                                    A   C   G
GAM288  ZDHHC1    3'  CTGACTCTCTATGCAACACCCC 78211      ACCCCAAGG
          A                      TGGGG       AGAGAGTCAG
                                |||||       ||||||||||
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                                ACCCC       TCTCTCAGTC
                                  ACAACGTA_
GAM288  LOC128439 3'  GACTCCTGACTTTGGAAGCCCC 58136     ACC     __ A
                                GGGG  CCAAGG  AG GAGTC
                                ||||  ||||||  || |||||
                                CCCC  GGTTTC  TC CTCAG
                                  GAA     AG  _
GAM288  LOC132740 5'  TGGCTCTTAGGACCCCCA    75578      AC  CAAGGA
                                TGGGG  CC     GAGAGTCA
                                |||||  ||     ||||||||
                                ACCCC  GG     TTCTCGGT
                                  CA  A_____
GAM288  LOC145622 5'  TGGGATCCCAGGGTCCCCA   77826        CAA  A  GAG
                                TGGGGACCC   GG GA   TCA
                                |||||||||   || ||   |||
                                ACCCCTGGG   CC CT   GGT
                                     A__  _  AG_
GAM288  LOC148137 3'  GGGTCGCCCCCTAGGTCCCCA  59107       CCA   AGA_  G
                                TGGGGACC   AGG    GA TC
                                ||||||||   |||    || ||
                                ACCCCTGG   TCC    CT GG
                                     A__   CCCG  G
GAM288  LOC151816 5'  TGACTGTCCCAGGTCCCCA    86687       CCAA  A  G
                                TGGGGACC    GG GA AGTCA
                                ||||||||    || || |||||
                                ACCCCTGG    CC CT TCAGT
                                     A___  _  G
GAM288  LOC152286 5'  CTGCCCCTGCGGGTCCCCA    86808        _  A  AG
                                TGGGGACCC CA GG  AG
                                ||||||||| || ||  ||
                                ACCCCTGGG GT CC  TC
                                     C  C  CG
GAM288  LOC204285 3'  CTCTCCCTGGGGTCCCCA     91016         A
                                TGGGGACCCCA GGAGAG
                                |||||||||||| ||||||
                                ACCCCTGGGGT CCTCTC
                                       C
GAM288  LOC221399 5'  CTGACTCTCTCTAAGTAATCCC 95483     CCCCAA
                                GGGA     GGAGAGAGTCAG
                                ||||     ||||||||||||
                                CCCT     TCTCTCTCAGTC
                                  AATGAA
GAM288  LOC256032 5'  CTGACTCTCCGCAGGTACCCA  99359     G   CCAA    GA
                                TGGG ACC    GGAGA  GTCAG
                                |||| |||    |||||  |||||
                                ACCC TGG    CCTCT  CAGTC
                                  A  ACG_    __
GAM288  LOC257473 3'  CTGACTCTCTATGCAACACCCC 96807      ACCCCAAGG
          A                      TGGGG        AGAGAGTCAG
                                |||||        ||||||||||
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                                ACCCC       TCTCTCAGTC
                                  ACAACGTA_
GAM288  LOC51226  3'  TGACTCCTAAGGTCTCCA    33574       CCAAGG  A
                                TGGGGACC     AG GAGTCA
                                ||||||||     || ||||||
                                ACCTCTGG     TC CTCAGT
                                    AA____  _
GAM288  LOC92716  3'  TGACTTCCCCGGGGCCCCA   70901      A   AA  A  G
                                TGGGG CCCC  GG GA AGTCA
                                ||||| ||||  || || |||||
                                ACCCC GGGG  CC CT TCAGT
                                  _   C_  _  _
GAM289  ATP7B     3'  TGTCCTTGTGGTCTTTGCTGCT 5337          T  CTCGC
          G                      CAGCAGCAAAG CT    GACA
                                ||||||||||| ||    ||||
                                GTCGTCGTTTC GG    CTGT
                                      T  TGTTC
GAM289  CDS2      3'  TGCTGTAGACTTGCTGCTG   15109        A   CTC   A
                                CAGCAGCAA GTCT   GCG CA
                                ||||||||| ||||   ||| ||
                                GTCGTCGTT CAGA   TGT GT
                                    _   ____  C
GAM289  COL9A2    5'  CGCCGGGAGACTCTGCCGT   10254    A   A       _
                                GC GCA AGTCTCTCG CG
                                || ||| |||||||| ||
                                TG CGT TCAGAGGGC GC
                                 C   C        C
GAM289  DYSF      5'  GTGTCATTGGGAGACTCCGCAG 14491    A  AA       C_
          C                      GC GC  AGTCTCTCG  GACAC
                                || ||  |||||||||  |||||
                                CG CG  TCAGAGGGT  CTGTG
                                 A  CC        TA
GAM289  HOXA7     3'  GCGAGAAAATTTTGCTGCT   23557          C_
                                AGCAGCAAAGT  TCTCGC
                                ||||||||||  ||||||
                                TCGTCGTTTTA  AGAGCG
                                      AA
GAM289  HTR2A     3'  GTGGAAACCTTGCTGCT     7106         A  C  T
                                AGCAGCAA GT TC CGC
                                |||||||| || || |||
                                TCGTCGTT CA AG GTG
                                    C  A  _
GAM289  KCNK10    5'  TGCAGGGAGACTTTGCGC    41269    A         _
                                GC GCAAAGTCTCTC GCG
                                || ||||||||||| |||
                                CG CGTTTCAGAGGG CGT
                                 _          A
GAM289  LPHH1     3'  GTATTTTAAGATTCTGCTGCTG 25486        A    CTCGCG
                                CAGCAGCA AGTCT     AC
                                |||||||| |||||     ||
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                                GTCGTCGT TTAGA     TG
                                    C     ATTTTA
GAM289  LPIN2    3'  GCACTAGACTTTGTTGCTG   28431           CTC
                                CAGCAGCAAAGTCT   GC
                                |||||||||||||   ||
                                GTCGTTGTTTCAGA   CG
                                      TCA
GAM289  NTSR1    3'  GCGGAAGAGCTTTGCTGC    11857         _  CT
                                GCAGCAAAG TCT  CGC
                                |||||||| |||  |||
                                CGTCGTTTC AGA  GCG
                                    G   AG
GAM289  PSMD9    3'  GCACTGAGGCCTTGCTGCTG  12526         A    TC_
                                CAGCAGCAA GTCTC   GC
                                |||||||| |||||   ||
                                GTCGTCGTT CGGAG   CG
                                    C     TCA
GAM289  PTGS1    3'  GCATGAGACTTTCTGCTG    55475       C       TC
                                CAGCAG AAAGTCTC  GC
                                ||||||| ||||||||  ||
                                GTCGTC TTTCAGAG  CG
                                   _       TA
GAM289  PTGS1    3'  GCATGAGACTTTCTGCTG    8243        C       TC
                                CAGCAG AAAGTCTC  GC
                                ||||||| ||||||||  ||
                                GTCGTC TTTCAGAG  CG
                                   _       TA
GAM289  RET      3'  GCAGAGGCTTTGCTGCTG    40547           C
                                CAGCAGCAAAGTCTCT GC
                                |||||||||||||||| ||
                                GTCGTCGTTTCGGAGA CG
                                          _
GAM289  RET      3'  GCAGAGGCTTTGCTGCTG    40937           C
                                CAGCAGCAAAGTCTCT GC
                                |||||||||||||||| ||
                                GTCGTCGTTTCGGAGA CG
                                          _
GAM289  SLC22A2  3'  GAGAGACCGTTGCTGCTG    60279         A_
                                CAGCAGCAA  GTCTCTC
                                |||||||||  |||||||
                                GTCGTCGTT  CAGAGAG
                                    GC
GAM289  SOS2     3'  TGCCGGTATTTGCTGCTG    69063         GTCT  C
                                CAGCAGCAAA    CT GCG
                                ||||||||||    || |||
                                GTCGTCGTTT    GG CGT
                                     AT__  C
GAM289  TCF7L2   3'  GTCGTGAACCCCGCTGCT    48441       AAA  CTC
                                AGCAGC   GT   TCGCGAC
                                ||||||   ||   |||||||
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                                TCGTCG  CA  AGTGCTG
                                   CCC  ___
GAM289  TNNC2    3'  TGTGGGAGACTCCGCCCTG   13818    CA  AA
                                CAG  GC  AGTCTCTCGCG
                                |||  ||  ||||||||||
                                GTC  CG  TCAGAGGGTGT
                                  C_  CC
GAM289  BPESC1   3'  TGTCAAAGGACTCTGCATGCTG 41772     _  A   T  CGC
                                CAGCA GCA AGTC CT   GACA
                                ||||| ||| |||| ||   ||||
                                GTCGT CGT TCAG GA   CTGT
                                   A  C   _ AA_
GAM289  CDC10    5'  GTGCGAGATCCGCTGCTG    92754       AAA    T
                                CAGCAGC   GTCTC CGC
                                |||||||   ||||| |||
                                GTCGTCG   TAGAG GTG
                                    CC_    C
GAM289  DKFZp762P2111 5'  CGCAAGAGCCTGCTGCTG    87630        AA T   C
                                CAGCAGCA  G CTCT GCG
                                ||||||||  | |||| |||
                                GTCGTCGT  C GAGA CGC
                                    C_ _   A
GAM289  FEM-2    3'  GCAGAGGGACCTTGCTGCTG   28315        A     _
                                CAGCAGCAA GTCTCTC GC
                                ||||||||| ||||||| ||
                                GTCGTCGTT CAGGGAG CG
                                     C      A
GAM289  FLJ11274  5'  GTGTCAACTTTGCTGCTG    37781          CTCT
                                CAGCAGCAAAGT   CGC
                                ||||||||||||   |||
                                GTCGTCGTTTCA   GTG
                                       ACT_
GAM289  FLJ12171  3'  GTGACTCTGAGCCTCACTGCTG 45199       CAA  T  ____
                                CAGCAG   AG CTC   TCGC
                                ||||||   || |||   ||||
                                GTCGTC   TC GAG   AGTG
                                   AC_  C   TCTC
GAM289  FLJ20419  3'  GCATCAGGGACTTTGTGCT   35606     G       C__
                                AGCA CAAAGTCTCT   GC
                                |||| ||||||||||   ||
                                TCGT GTTTCAGGGA   CG
                                  _        CTA
GAM289  FLJ23306  3'  GCAAAGACTCTGCTGCTG    44848       A    CTC
                                CAGCAGCA AGTCT   GC
                                |||||||| |||||   ||
                                GTCGTCGT TCAGA   CG
                                    C    AA_
GAM289  FLJ32762  5'  GTGCCCGGCGGTCTTTGCTGC  59487        T  C   CGA
                                GCAGCAAAG CT TCG   CAC
                                ||||||||| || |||   |||
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                                CGTCGTTTC GG GGC   GTG
                                     T  C   CC_
GAM289  KIAA0322  3'  GCAAGAAAACACCTGCTGCTG  94331        AA_  C_   C
                                CAGCAGCA   GT  TCT GC
                                ||||||||   ||  ||| ||
                                GTCGTCGT   CA  AGA CG
                                     CCA  AA   A
GAM289  KIAA0700  3'  GTGCCCTGGGAGACCCCGCTCT 72523     C   AAA       CGA
          G                      CAG AGC   GTCTCTCG   CAC
                                ||| |||   ||||||||   |||
                                GTC TCG   CAGAGGGT   GTG
                                  _  CCC       CCC
GAM289  KIAA0731  5'  GTCGCGGGCGCTCTGCTAGC   67482    _   A   CT
                                GC AGCA AGT  CTCGCGAC
                                || |||| |||  ||||||||
                                CG TCGT TCG  GGGCGCTG
                                 A   C   C_
GAM289  KIAA1164  3'  TGAAAGACTATTGCTGCTG    70052         _    C
                                CAGCAGCAA AGTCT TCG
                                ||||||||| ||||| |||
                                GTCGTCGTT TCAGA AGT
                                     A    A
GAM289  KIAA1416  3'  GCGAAGAACCCTGCTGCTG    87756        AAG_   C
                                CAGCAGCA    TCT TCGC
                                ||||||||    ||| ||||
                                GTCGTCGT    AGA AGCG
                                     CCCA  _
GAM289  KIAA1951  3'  GCACCCAGGACTTTGCTCTG   74156     C        CTC__
                                CAG AGCAAAGTCT    GC
                                ||| ||||||||||    ||
                                GTC TCGTTTCAGG    CG
                                  _        ACCCA
GAM289  MARCKS    5'  GTGCCGCTGCCGCTGTTGCCGC 11414    A   _   CTCTC   A
                                GC GCAA AGT    GCG CAC
                                || |||| |||    ||| |||
                                CG CGTT TCG    CGC GTG
                                 C   G   CCGT_  C
GAM289  PCDH19    3'  TGCCGCTACTTTGCTGT     64448         CTCTC   A
                                GCAGCAAAGT    GCG CA
                                ||||||||||    ||| ||
                                TGTCGTTTCA    CGC GT
                                     T____   C
GAM289  PDCD6IP   3'  TGTGAGATTTGCTGCTG     83165         GTC
                                CAGCAGCAAA   TCTCGCG
                                ||||||||||   |||||||
                                GTCGTCGTTT   AGAGTGT
                                             ___
GAM289  PELI2     3'  GTGAAGATTTTGCCACT     41457    CA       C
                                AG  GCAAAGTCT TCGC
                                ||  ||||||||| ||||
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                                TC  CGTTTTAGA AGTG
                                 AC       _
GAM289  POLR3F   3'  CGTAGACTTGCTGCT      60618        A   CTC
                                AGCAGCAA GTCT   GCG
                                |||||||| ||||   |||
                                TCGTCGTT CAGA   TGC
                                    _   ____
GAM289  RAI15    3'  TGCCCTGGACACTGCTGCTG  67246        AA   CTC
                                CAGCAGCA  GTCT   GCG
                                ||||||||  ||||   |||
                                GTCGTCGT  CAGG   CGT
                                     CA    TCC
GAM289  SEC22C   3'  TGTCAAACTTCTGCTGCTG   16114        _   CTCTCGC
                                CAGCAGCA AAGT      GACA
                                |||||||| ||||      ||||
                                GTCGTCGT TTCA      CTGT
                                     C    AA_____
GAM289  SIAT9    3'  GTGCTCCGTAGCTCTGCTGCTG 15317        A  T  CT  C  _
                                CAGCAGCA AG CT  CG GA CAC
                                |||||||| || ||  || || |||
                                GTCGTCGT TC GA  GC CT GTG
                                     C  _  T_  _  C
GAM289  SYPL     3'  GTGGGTTTAAAACTTTGCTGCT 94502          CT____
                                AGCAGCAAAGT     CTCGC
                                ||||||||||      |||||
                                TCGTCGTTTCA     GGGTG
                                      AAATTT
GAM289  LOC151102 3'  AGAAGACTCTTGCTGCTG    86407         _    _
                                CAGCAGCAA AGTCT CT
                                ||||||||| ||||| ||
                                GTCGTCGTT TCAGA GA
                                     C    A
GAM289  LOC152137 5'  CGCGTCCGGCGCTGCTGCTG   81314        AA   TCT
                                CAGCAGCA  GTC   CGCG
                                ||||||||  |||   ||||
                                GTCGTCGT  CGG   GCGC
                                     CG   CCT
GAM289  LOC158677 5'  GTGAGCCAAGATTTTGCCACTG 88251     CA       ___
                                CAG  GCAAAGTCT   CTCGC
                                |||  |||||||||   |||||
                                GTC  CGTTTTAGA   GAGTG
                                  AC        ACC
GAM289  LOC160156 5'  TGCCTCCAGCCTTTGCTGCT   83081         T  CTC_
                                AGCAGCAAAG CT    GCG
                                |||||||||| ||    |||
                                TCGTCGTTTC GA    CGT
                                      C  CCTC
GAM289  LOC163682 3'  GTGCCCGGGGAGACTGCACTGC 88415       CAA      G  A_
           TG                   CAGCAG   AGTCTCTC CG  CAC
                                ||||||   |||||||| ||  |||
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                                GTCGTC   TCAGAGGG GC  GTG
                                   ACG       _ CC
GAM289  LOC203523 3'  TGTGGTCTAGACATTTGCTGCT 90942          _   CTC  G
          G                     CAGCAGCAAA GTCT   GC ACA
                                ||||||||||  ||||   || |||
                                GTCGTCGTTT CAGA   TG TGT
                                     A    TC_  G
GAM289  LOC222484 3'  GTGCCGCGTCCCCTGCTGTTG  96004        AAGTCTCT   A
                                CAGCAGCA       CGCG CAC
                                ||||||||       |||| |||
                                GTTGTCGT       GCGC GTG
                                     CCCCT___    C
GAM289  LOC256032 5'  CGCCACCCCTGAGCCTGCTGCT 99357         AA T   TC_____
          G                     CAGCAGCA  G CTC      GCG
                                ||||||||  | |||      |||
                                GTCGTCGT  C GAG      CGC
                                     C_ _   TCCCCAC
GAM289  LOC55829  3'  GTTAGAAATCCTTGCTGCT   38035        A_  C   C
                                AGCAGCAA  GT TCT GC
                                ||||||||  || ||| ||
                                TCGTCGTT  TA AGA TG
                                     CC  A   T
GAM289  LOC90110  5'  GTAAGTGAAACCTTTGCTGCTG 62180          ___  T  CG
                                CAGCAGCAAAG   TC CT  C
                                ||||||||||   || ||  |
                                GTCGTCGTTTC   AG GA  G
                                      CAA  T  AT
GAM289  LOC91461  3'  TGTAGCTAAAGCCCCTGCTGCT 66707        AAGT  CTC  G
          G                     CAGCAGCA    CT   GC ACA
                                ||||||||    ||   || |||
                                GTCGTCGT    GA   CG TGT
                                     CCCC  AAT  A
GAM290  ELF3     3'  TGACCTTGACCTTGACCAA    16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                   _    AGT  ___
GAM290  JAK2     3'  TGACCTTCATTCTGAGACCAA  18318       CAA       AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_       C_
GAM290  SLC10A2   5'  ACTCTCTGTCTTGACCAA    6590        CAA       A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___        C
GAM290  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
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                                AACCGA    TTG CTTTCAGTG
                                   AA___  A
GAM290  KIAA1958  5'  GTGACTTTGAACCCCAAACC  82788     CAA  ATGG
                                GGTT  GGG   AAAGTCAC
                                ||||  |||   ||||||||
                                CCAA  CCC   TTTCAGTG
                                  A__  CAAG
GAM290  MARCKS    3'  ACTTTCCACCCTGCCCA    11411     TTCA  A
                                TGG   AGGG TGGAAAGT
                                |||   |||| ||||||||
                                ACC   TCCC ACCTTTCA
                                 CG__  _
GAM290  TUB       5'  GTGGGACCATCCCTTAAACC  13898     C       AAAG
                                GGTT AAGGGATGG   TCAC
                                |||| |||||||||   ||||
                                CCAA TTCCCTACC   GGTG
                                  A       AG__
GAM290  LOC80298  3'  ACTTTTACCTTGAACCA    48062         GATG
                                TGGTTCAAGG   GAAAGT
                                ||||||||||   ||||||
                                ACCAAGTTCC   TTTTCA
                                     A___
GAM291  ELF3      3'  TGACCTTGACCTTGACCAA   16685     T   GAT  AAA
                                TTGGT CAAGG  GG  GTCA
                                ||||| |||||  ||  ||||
                                AACCA GTTCC  TC  CAGT
                                  _    AGT  ___
GAM291  JAK2      3'  TGACCTTCATTCTGAGACCAA  18318      CAA      AA
                                TTGGTT  GGGATGGA  GTCA
                                ||||||  ||||||||  ||||
                                AACCAG  TCTTACTT  CAGT
                                   AG_      C_
GAM291  SLC10A2   5'  ACTCTCTGTCTTGACCAA    6590       CAA      A
                                TTGGTT  GGGATGGA AGT
                                ||||||  |||||||| |||
                                AACCAG  TTCTGTCT TCA
                                  ___       C
GAM291  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA  37205      CAAGG  G
                                TTGGTT   GAT GAAAGTCAC
                                ||||||   ||| |||||||||
                                AACCGA   TTG CTTTCAGTG
                                   AA___  A
GAM291  KIAA1958  5'  GTGACTTTGAACCCCAAACC  82788     CAA  ATGG
                                GGTT  GGG   AAAGTCAC
                                ||||  |||   ||||||||
                                CCAA  CCC   TTTCAGTG
                                  A__  CAAG
GAM291  MARCKS    3'  ACTTTCCACCCTGCCCA    11411     TTCA  A
                                TGG   AGGG TGGAAAGT
                                |||   |||| ||||||||
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                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM291  TUB      5'  GTGGGACCATCCCTTAAACC   13898      C        AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A        AG__
GAM291  LOC80298 3'  ACTTTTACCTTGAACCA     48062          GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                      A___
GAM292  EHF      3'  TCCAAAACCCAAGGTTGGCT   25127     AT   _    C
                                AGT  GCCT GGGT TTGGA
                                |||  |||| |||| |||||
                                TCG  TGGA CCCA AACCT
                                  GT    A    A
GAM292  EPHA2    3'  CCATCGGCCAAGAATACTTGAA 16675          GC  G    T_
           G                     CTTCAAGTAT  CT GGTC  TGG
                                |||||||||  || ||||  |||
                                GAAGTTCATA  GA CCGG  ACC
                                      A_  A    CT
GAM292  ITGA5    3'  CCCAGAGACATACTTGAAG    61933          C__
                                CTTCAAGTATG   CTGGG
                                ||||||||||   |||||
                                GAAGTTCATAC   GACCC
                                      AGA
GAM292  TREM2    3'  TCCAAGACTGTCATATTT     39098        CCTG
                                AAGTATG    GGTCTTGGA
                                |||||||    |||||||||
                                TTTATAC    TCAGAACCT
                                    TG__
GAM292  UQCRB    3'  CCAACATAGGCATACTTAAG   21939     C         GGTC
                                CTT AAGTATGCCTG    TTGG
                                ||| ||||||||||    ||||
                                GAA TTCATACGGAT    AACC
                                  _         AC__
GAM292  ATP10D   3'  CAGAGACCACTTGAAG      73526         ATGCCTG    _
                                CTTCAAGT      GGTCT TG
                                ||||||||      ||||| ||
                                GAAGTTCA      CCAGA AC
                                    _______    G
GAM292  B3GNT7   3'  CCCTTCCAGGCAACCTGAA   71678      A  A       TCTT
                                TTCA GT TGCCTGGG    GG
                                |||| || ||||||||    ||
                                AAGT CA ACGGACCT    CC
                                  C  _       TC__
GAM292  DKFZp547I224 3'  TCCAAAATTGACCACATACTTG 39963          CCTG   _____
           GA                    TTCAAGTATG    GGTC    TTGGA
                                |||||||||    ||||    |||||
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                                AGGTTCATAC   CCAG   AACCT
                                     A___   TTAA
GAM292  FLJ22341  3'  CCAAGCTCAGGCACACCCAAG  45114    CAA  A     T
                                CTT   GT TGCCTGGG CTTGG
                                |||   || |||||||| |||||
                                GAA   CA ACGGACTC GAACC
                                  CC_  C      _
GAM292  KIAA0779  3'  CCGAACAGCATACTTGAAG   86908         C  GGTC
                                CTTCAAGTATGC TG   TTGG
                                ||||||||||| ||   ||||
                                GAAGTTCATACG AC   AGCC
                                       _  A___
GAM292  LOC144233 3'  CCAAGGCACATAATTGAA    77246     G   CCTGG
                                TTCAA TATG    GTCTTGG
                                ||||| ||||    |||||||
                                AAGTT ATAC    CGGAACC
                                   A   A____
GAM292  LOC147341 3'  ACCCAGGCATAACTGAAG    85116     AG
                                CTTCA  TATGCCTGGGT
                                |||||  ||||||||||
                                GAAGT  ATACGGACCCA
                                   CA
GAM292  LOC221088 5'  TCCAAGGTGCTGGCCACTCGAA 94888     A   AT   TGGG
          G                     CTTC AGT  GCC   TCTTGGA
                                |||| |||  |||   |||||||
                                GAAG TCA  CGG   GGAACCT
                                  C   C_   TCGT
GAM293  ELF3    3'  TGACCTTGACCTTGACCAA   16685     T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                   _    AGT  ___
GAM293  JAK2    3'  TGACCTTCATTCTGAGACCAA  18318      CAA      AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_       C_
GAM293  SLC10A2  5'  ACTCTCTGTCTTGACCAA    6590       CAA      A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM293  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM293  KIAA1958  5'  GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                GGTT   GGG   AAAGTCAC
                                ||||   |||   ||||||||
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                                CCAA  CCC   TTTCAGTG
                                  A__  CAAG
GAM293  MARCKS   3' ACTTTCCACCCTGCCCA    11411    TTCA   A
                                TGG   AGGG TGGAAAGT
                                |||   |||| ||||||||
                                ACC   TCCC ACCTTTCA
                                  CG__  _
GAM293  TUB      5' GTGGGACCATCCCTTAAACC  13898    C      AAAG
                                GGTT AAGGGATGG   TCAC
                                |||| |||||||||   ||||
                                CCAA TTCCCTACC   GGTG
                                  A       AG__
GAM293  LOC80298 3' ACTTTTACCTTGAACCA    48062        GATG
                                TGGTTCAAGG   GAAAGT
                                ||||||||||   ||||||
                                ACCAAGTTCC   TTTTCA
                                     A___
GAM294  GPD1     3' TCATGCCACCACATTTG    60398      C      C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A      _
GAM294  IL5RA    5' TCGCATGGCCACCGCATTT   6906         AT__
                                AAATGCGGTGGC   CGA
                                ||||||||||||   |||
                                TTTACGCCACCG   GCT
                                     GTAC
GAM294  MYO1C    3' TGCCGATGCCAAATATTTG   61873      CGG      A
                                TAAATG   TGGCATCG CA
                                ||||||   |||||||| ||
                                GTTTAT   ACCGTAGC GT
                                   AA_      C
GAM294  C6orf37  3' TGTCACACTGCATTTA     68097        GCATC
                                TAAATGCGGTG    GACA
                                ||||||||||    ||||
                                ATTTACGTCAC    CTGT
                                     A____
GAM294  DNAJC6   3' TTGCAGAACCACCGCATT   29498        CA  GA
                                AATGCGGTGG  TC  CAA
                                |||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                     A_  AC
GAM294  FLJ11210 3' GTCGATGTGCATGCTTTTA  60319    T  GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM294  FLJ12476 3' TCGATCTTCTGCATTTA    43270       T  C
                                TAAATGCGG GG ATCGA
                                ||||||||| || |||||
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                                ATTTACGTC TC TAGCT
                                     T  _
GAM294  KIAA1034  3'  TCGATGGCATCCGCATTTG   63134        _  G
                                TAAATGCGG TG CATCGA
                                ||||||||| || ||||||
                                GTTTACGCC AC GTAGCT
                                     T  G
GAM294  KIAA1987  3'  TCATGTAACTGCATTTA    89391         G   C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                     A   _
GAM294  MGC16063  3'  TGTCCTGGCCACTGCATT   54929          ATC
                                AATGCGGTGGC  GACA
                                ||||||||||  ||||
                                TTACGTCACCG  CTGT
                                      GTC
GAM294  LOC147949 3'  TGTCAGATGTCCACATTGCA  79279    __  _  _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM294  LOC150577 3'  GTCCTCACCGCATTTG     86258          CATC
                                TAAATGCGGTGG   GAC
                                ||||||||||||   |||
                                GTTTACGCCACT   CTG
                                      C___
GAM294  LOC158219 3'  TGTGTGTCACCACATTT    82694      C      CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                   A       __
GAM294  LOC202020 3'  TGTCTCACCACATTTA     90605       C    CATC
                                TAAATG GGTGG   GACA
                                |||||| |||||   ||||
                                ATTTAC CCACT   CTGT
                                    A   _____
GAM294  LOC90826  5'  TGTCGATGCAGGTTTATTTG  64788      CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                    TTGGA
GAM294  LOC93587  3'  TTGTCTTTACCTGCATTTA   73042       _   CATC
                                TAAATGC GGTGG   GACAA
                                ||||||| |||||   |||||
                                ATTTACG CCATT   CTGTT
                                    T   T___
GAM295  ELF3      3'  TGACCTTGACCTTGACCAA   16685      T   GAT  AAA
                                TTGGT CAAGG  GG  GTCA
                                ||||| |||||  ||  ||||
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                                AACCA GTTCC   TC   CAGT
                                  _    AGT ____
GAM295  JAK2     3'  TGACCTTCATTCTGAGACCAA  18318       CAA       AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_       C_
GAM295  SLC10A2  5'  ACTCTCTGTCTTGACCAA    6590        CAA       A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ____       C
GAM295  FLJ10803 3'  GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA____   A
GAM295  KIAA1958 5'  GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM295  MARCKS   3'  ACTTTCCACCCTGCCCA     11411     TTCA    A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM295  TUB      5'  GTGGGACCATCCCTTAAACC   13898     C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A        AG__
GAM295  LOC80298 3'  ACTTTTACCTTGAACCA     48062         GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                     A____
GAM296  HADHB    5'  CTCGCGGACGTCAGCCAAGATT 5738          _ _   A   A
           CCA                     TGGAATCTTG C GGC TCC CGAG
                                ||||||||||  | ||| ||| ||||
                                ACCTTAGAAC G CTG AGG GCTC
                                     C A   C   C
GAM296  BHLHB2   5'  CTCAAAGCCGAAGATTCCA    14763         G    ATCCAC
                                TGGAATCTT CGGC     GAG
                                |||||||||  ||||     |||
                                ACCTTAGAA GCCG     CTC
                                     _    AAA____
GAM296  CPSF1    3'  CGTGGATGCCGTCACCACCA   65160     AATCTT
                                TGG     GCGGCATCCACG
                                |||     ||||||||||||
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                                ACC     TGCCGTAGGTGC
                                  ACCAC_
GAM296  DKFZP434K0427 3'  TCTCACAGATGTGCTGTATCC  50500     ATCT      CCAC__
                                GGA   TGCGGCAT     GAGA
                                |||   ||||||||     ||||
                                CCT   ATGTCGTG     CTCT
                                  _____      TAGACA
GAM296  FLJ14166  3'  TCTCGGTTCCGGAAGATTCCA  44992         G   CATCCA
                                TGGAATCTT CGG     CGAGA
                                ||||||||| |||     |||||
                                ACCTTAGAA GCC     GCTCT
                                     G   TTG___
GAM296  FLJ20618  3'  TCTCACAAGGCTGCACCAGATT 35888         __     ATCCAC
           CCA                    TGGAATCT  TGCGGC     GAGA
                                ||||||||  ||||||     ||||
                                ACCTTAGA  ACGTCG     CTCT
                                     CC     GAACA_
GAM296  LOC125988 5'  TCTCAGAGCCGCAAGACACCA  74900     AA       A  CAC
                                TGG  TCTTGCGGC TC   GAGA
                                |||  |||||||||| ||   ||||
                                ACC  AGAACGCCG AG   CTCT
                                  AC        _ A__
GAM296  LOC148697 3'  TCTCGTGGACACCCACATCTCA 79681    GA  CT  C  CA
                                TG  AT  TG GG  TCCACGAGA
                                ||  ||  || ||  |||||||||
                                AC  TA  AC CC  AGGTGCTCT
                                 TC  C_  _  AC
GAM296  LOC150630 5'  CTCTGCCGCAGACCCCA     86300     AA   T     TCCAC
                                TGG  TCT GCGGCA     GAG
                                |||  ||| ||||||     |||
                                ACC  AGA CGCCGT     CTC
                                  CC  _     ______
GAM296  LOC195977 3'  GGATGCCGCCCAAGATTCC    88933         __
                                GGAATCTT  GCGGCATCC
                                ||||||||  |||||||||
                                CCTTAGAA  CGCCGTAGG
                                     CC
GAM297  CHAT     5'  GAGGAGAGCAGGTCCACACC   40969    CC  A       ATG
                                GG  TG ACCTGCTTT   CTC
                                ||  || |||||||||   |||
                                CC  AC TGGACGAGA   GAG
                                 AC  C        G__
GAM297  PNN      5'  TGTAAAGCAGTCTCAAGCC    71665     C   AC
                                GGC TGA  CTGCTTTATG
                                ||| |||  ||||||||||
                                CCG ACT  GACGAAATGT
                                  A   CT
GAM297  C16orf5   3'  GGTACAGGTTCAGTCC      26356    C       CTTTA
                                GG CTGAACCTG     TGCT
                                || |||||||||     ||||
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                                CC GACTTGGAC    ATGG
                                 T      _____
GAM297  C19orf7   3' GCGTGGAAGCAGGTCCAGGC  61781     A      _
                                GCCTG ACCTGCTTT ATGC
                                ||||| ||||||||| ||||
                                CGGAC TGGACGAAG TGCG
                                   C       G
GAM297  FLJ20085  5' CTGAGCCGGGAGCAGGTCCAAC 35006   CC  A      AT
          C                     GG  TG ACCTGCTTT  GCTCAG
                                ||  || |||||||||  ||||||
                                CC  AC TGGACGAGG  CGAGTC
                                 A_  C       GC
GAM297  FLJ23499  3' CTGAGCATGGTGGCTCACGCC  43135    C   A  T   TT
                                GGC TGA CC GCT  ATGCTCAG
                                ||| ||| || |||  ||||||||
                                CCG ACT GG TGG  TACGAGTC
                                  C   C  _  __
GAM297  KIAA0089  3' CTGAACTTTTACAGTTCAGGCC 70507       C   CTTTATGC
                                GGCCTGAA CTG       TCAG
                                |||||||| |||       ||||
                                CCGGACTT GAC       AGTC
                                     _  ATTTTCA_
GAM297  KIAA0257  3' AGCAGGGCAGGCTCAGACC   71370    C    A     TA
                                GG CTGA CCTGCTT  TGCT
                                || |||| |||||||  ||||
                                CC GACT GGACGGG  ACGA
                                 A   C      __
GAM297  KIAA1389  3' CTGAGCTTGCACAGATCAGACC 70318    C   ACC_   TTTAT
                                GG CTGA    TGC     GCTCAG
                                || ||||    |||     ||||||
                                CC GACT    ACG     CGAGTC
                                 A   AGAC   TT___
GAM297  KIAA1456  3' CTGAGCATGGTGGCTCATGCC  67552    C   A  T   TT
                                GGC TGA CC GCT  ATGCTCAG
                                ||| ||| || |||  ||||||||
                                CCG ACT GG TGG  TACGAGTC
                                  T   C  _  __
GAM297  LSM10     3' GAGAAGAAAGCAGGGCCAGGCC 52869       AA       ATG
                                GGCCTG  CCTGCTTT   CTC
                                ||||||  ||||||||   |||
                                CCGGAC  GGACGAAA   GAG
                                   CG       GAA
GAM297  MGC26954  3' AGACAGAGCAATTCAGGCC   59490       CC     ATG
                                GGCCTGAA  TGCTTT   CT
                                ||||||||  ||||||   ||
                                CCGGACTT  ACGAGA   GA
                                     A_     CA_
GAM297  OAZ2      3' GAGTAAGCAGGTCCGACC    11876    CC  A     TTA
                                GG  TG ACCTGCT   TGCTC
                                ||  || |||||||   |||||
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                                CC  GC TGGACGA   ATGAG
                                 A_  C      ___
GAM297  REM      3'  CTGAGCATCCCCCAGATCCAAG 26686     C  AAC   CTTT
              CC                   GGC TG   CTG    ATGCTCAG
                                ||| ||   |||   ||||||||
                                CCG AC   GAC    TACGAGTC
                                  A  CTA   CCCC
GAM297  TGOLN2   3'  GAGCATAAAACAGAACTTGGGC 64743     TG AC_   C
                                GCC  A   CTG TTTATGCTC
                                |||  |   ||| |||||||||
                                CGG  T   GAC AAATACGAG
                                  GT CAA   A
GAM297  TRIAD3   3'  TGAGCATCAGCTCAGCC     96141     C   ACCT   TT
                                GGC TGA    GCT  ATGCTCA
                                ||| |||    |||  |||||||
                                CCG ACT    CGA  TACGAGT
                                  _  _____   C_
GAM297  LOC123242 5'  CTGGAGGAGGCAGGCCCAAGCC 76115     C  AA       ATG T
                                GGC TG  CCTGCTTT   C CAG
                                ||| ||  ||||||||   | |||
                                CCG AC  GGACGGAG   G GTC
                                  A  CC       GA_ _
GAM297  LOC131405 5'  CTGAGCATCGAGCAGGCCCAG  76377     AA      T
                                CTG  CCTGCTT ATGCTCAG
                                |||  ||||||| ||||||||
                                GAC  GGACGAG TACGAGTC
                                  CC      C
GAM297  LOC146159 5'  GAGCGGGGCAGGTTCTGGCC   78176     T        TA
                                GGCC GAACCTGCTT  TGCTC
                                |||| ||||||||||  |||||
                                CCGG CTTGGACGGG  GCGAG
                                  T        __
GAM297  LOC158117 3'  CTGAGCATGTGCAGCCCTGGCC 82612      TGAAC    TT
                                GGCC    CTGC  TATGCTCAG
                                ||||    ||||  |||||||||
                                CCGG    GACG  GTACGAGTC
                                  TCCC_   T_
GAM297  LOC203275 3'  CTGAGCATGTGCAGCCCTGGCC 90854      TGAAC    TT
                                GGCC    CTGC  TATGCTCAG
                                ||||    ||||  |||||||||
                                CCGG    GACG  GTACGAGTC
                                  TCCC_   T_
GAM297  LOC253001 5'  CTGGAGGAGGCAGGCCCAAGCC 97994     C  AA       ATG T
                                GGC TG  CCTGCTTT   C CAG
                                ||| ||  ||||||||   | |||
                                CCG AC  GGACGGAG   G GTC
                                  A  CC       GA_ _
GAM297  LOC257464 3'  CTGAACATAAAGCAAGTTCAGC 91243     C    C        C
              T                    GGC TGAAC TGCTTTATG TCAG
                                ||| ||||| ||||||||| ||||
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                                TCG ACTTG ACGAAATAC AGTC
                                  _    A       A
GAM298  ADCY2    3'  AGCATTGGCCTTAATATA    65643     CC       A
                                TATG  AAGGCCAAT GCT
                                ||||  ||||||||| |||
                                ATAT  TTCCGGTTA CGA
                                  AA       _
GAM298  ANKH     3'  GTAAAGCTTAAACACTTGGCAT 39549        GCCAAT    C
              A                  TATGCCAAG     AGCTT AC
                                |||||||||     ||||| ||
                                ATACGGTTC     TCGAA TG
                                     ACAAAT    A
GAM298  ARAF1    5'  GTGAAGCTGAGACCTTGGCA   64645       CCAA
                                TGCCAAGG    TAGCTTCAC
                                ||||||||    |||||||||
                                ACGGTTCC    GTCGAAGTG
                                     AGA_
GAM298  CCND2    3'  GGTAATGTGGCCTTGGCAT    10052         ATA_
                                ATGCCAAGGCCA    GCT
                                ||||||||||||    |||
                                TACGGTTCCGGT    TGG
                                      GTAA
GAM298  KRT9     3'  TGAACTGACTTGGCATA     76806        GCCAA   C
                                TATGCCAAG     TAG TTCA
                                |||||||||     ||| ||||
                                ATACGGTTC     GTC AAGT
                                     A____   _
GAM298  MRC1     3'  TGAAGCTTCTTGGCATA     11682         CCAAT
                                TATGCCAAGG     AGCTTCA
                                ||||||||||     |||||||
                                ATACGGTTCT     TCGAAGT
                                      _____
GAM298  PVT1     3'  GGTGCGCGGGTGACCTTGGCA  66176        C  ATA  TT
                                TGCCAAGG CA   GC  CACC
                                |||||||| ||   ||  ||||
                                ACGGTTCC GT   CG  GTGG
                                     A  GGG  C_
GAM298  RARA     3'  AGGCTCCTGGCCTTGGCA    8250          AT
                                TGCCAAGGCCA  AGCTT
                                ||||||||||  |||||
                                ACGGTTCCGGT  TCGGA
                                      CC
GAM298  ARHGEF4  5'  GGCAAGGTTGGCCTTGGC    53375          A__
                                GCCAAGGCCAAT   GCT
                                ||||||||||||   |||
                                CGGTTCCGGTTG   CGG
                                      GAA
GAM298  C20orf162 5'  AGTATTTTGACCTTGGCAT   55497        C   TA_
                                ATGCCAAGG CAA   GCT
                                |||||||| |||   |||
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                                TACGGTTCC GTT   TGA
                                     A   TTA
GAM298  C21orf69  5'  GGTGGAGCCCAGCTCCTGACAT 55235     CCA   CCAATA
           A                    TATG   AGG     GCTTCACC
                                ||||   |||     ||||||||
                                ATAC   TCC     CGAGGTGG
                                  AG_   TCGACC
GAM298  CBX8     3'  GTGAGCGTGAGCTTGGCATA   40609        GC  ATA   T
                                TATGCCAAG  CA   GCT CAC
                                |||||||||  ||   ||| |||
                                ATACGGTTC  GT   CGA GTG
                                     GA  G__   _
GAM298  FLJ10829  3'  AGCATTGCCTTGGCATA     37253          C   A
                                TATGCCAAGGC AAT GCT
                                |||||||||| ||| |||
                                ATACGGTTCCG TTA CGA
                                          _   _
GAM298  FUK      3'  GACAGCCAGCCTTGGCATA   59627          CAATA   _
                                TATGCCAAGGC    GCT TC
                                ||||||||||     ||| ||
                                ATACGGTTCCG    CGA AG
                                      AC___   C
GAM298  KIAA1915  3'  GTGATTGTAGTTAACATTGGCA 73670       GGCC   A  T_
                                TGCCAA    AAT GC  TCAC
                                ||||||    ||| ||  ||||
                                ACGGTT    TTG TG  AGTG
                                   ACAA   A  TT
GAM298  LOC199883 3'  AAGCACTGGCCTTGAGATA   91462     GC       ATA
                                TAT  CAAGGCCA   GCTT
                                |||  ||||||||   ||||
                                ATA  GTTCCGGT   CGAA
                                  GA       CA_
GAM298  LOC200020 3'  AAGCACTGGCCTTGAGATA   91533     GC       ATA
                                TAT  CAAGGCCA   GCTT
                                |||  ||||||||   ||||
                                ATA  GTTCCGGT   CGAA
                                  GA       CA_
GAM298  LOC219700 5'  GGTGGGGCCAGCCCTGACA   94656    C  A   CAATA
                                TG CA GGC     GCTTCACC
                                || || |||     ||||||||
                                AC GT CCG     CGGGGTGG
                                 A  C   AC___
GAM298  LOC222484 5'  GTGAGGAGCCTGGCCTTGACA  96003    C       ATAG
                                TG CAAGGCCA    CTTCAC
                                || ||||||||    ||||||
                                AC GTTCCGGT    GGAGTG
                                 A       CCGA
GAM298  LOC255452 3'  GGCAAGGTTGGCCTTGGC     99397           A__
                                GCCAAGGCCAAT   GCT
                                ||||||||||||   |||
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                                CGGTTCCGGTTG  CGG
                                      GAA
GAM298  LOC51320  3'  TGATGCCCTTGGCATA     34029         CCAATA  T
                                TATGCCAAGG    GC TCA
                                ||||||||||    || |||
                                ATACGGTTCC    CG AGT
                                      _______ T
GAM299  FGFR1     3'  GACCTGTCCATGCCCCTGGAC  43886      A       AA_
                                GTTCA GGGCATGGA  GTC
                                ||||| |||||||||  |||
                                CAGGT CCCGTACCT  CAG
                                   C       GTC
GAM299  HNRPDL    3'  GATTTCTACCACACCTTTGAAC 19601        CA  A__
                                GTTCAAGGG  TGG  AAGTC
                                |||||||||  |||  |||||
                                CAAGTTTCC  ACC  TTTAG
                                      AC  ATC
GAM299  IL10      3'  TGATATCATGCCCCTGTAC   6932     T  A      AAA
                                GT CA GGGCATGG  GTCA
                                || || ||||||||  ||||
                                CA GT CCCGTACT  TAGT
                                 T  C       A__
GAM299  LANCL1    3'  TGACTTTCTAAACTTTAAC   21336     C   GCA
                                GTT AAGG  TGGAAAGTCA
                                ||| ||||  ||||||||||
                                CAA TTTC  ATCTTTCAGT
                                  _   AA_
GAM299  PODXL     3'  GGTTATTCATAACCTTGAAC  19418       GC    A GT
                                GTTCAAGG  ATGGA A  C
                                ||||||||  ||||| |  |
                                CAAGTTCC  TACTT T  G
                                     AA    A TG
GAM299  RAB30     5'  TGACTCCAGCCCTTGGAC    27941        A   AA
                                GTTCAAGGGC TGGA  GTCA
                                |||||||||| ||||  ||||
                                CAGGTTCCCG ACCT  CAGT
                                      _   __
GAM299  TMOD      3'  GGTGGAGTCCATGCCTTTGAAC 13811           AAG   A
                                GTTCAAGGGCATGGA  TCA CC
                                ||||||||||||||  ||| ||
                                CAAGTTTCCGTACCT  GGT GG
                                      GA_  _
GAM299  ARL8      3'  GTTGGAGCACACCCTTGAAC  94813       CA  GAAAG
                                GTTCAAGGG  TG   TCAAC
                                |||||||||  ||   |||||
                                CAAGTTCCC  AC   GGTTG
                                     __  ACGA_
GAM299  DKFZp434A2417 3'  GATTTACCCTGCCCTTGAAC  66680         T  A
                                GTTCAAGGGCA GG AAGTC
                                |||||||||| || |||||
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                                CAAGTTCCCGT CC TTTAG
                                      C  A
GAM299  DKFZp762E1312 3'  GGTTGACTTCTCTGCCCTT   37905       T GA
                                AAGGGCA G  AAGTCAACC
                                ||||||| |  |||||||||
                                TTCCCGT C  TTCAGTTGG
                                   _ TC
GAM299  FLJ14641  3'  GACTAACTGGGACCTTGAAC   52557       GCA   AA
                                GTTCAAGG   TGG  AGTC
                                ||||||||   |||  ||||
                                CAAGTTCC   GTC  TCAG
                                     AGG   AA
GAM299  FLJ21551  3'  GGTTAACCTTCCTCTTTCTTGG 46039        CAT   A  C
           AC                     GTTCAAGGG   GGAA GT AACC
                                ||||||||||   |||| || ||||
                                CAGGTTCTT   CCTT CA TTGG
                                     TCT   C  A
GAM299  HIG2     5'  GACTTTCCTCCGGAC      26201      AA   CAT
                                GTTC  GGG   GGAAAGTC
                                ||||  |||   ||||||||
                                CAGG  CCT   CCTTTCAG
                                  __  ___
GAM299  KIAA0265  3'  ACCATTCATGCCCTTAAAT   70436     C        AA
                                GTT AAGGGCATGGA  GT
                                ||| ||||||||||  ||
                                TAA TTCCCGTACTT  CA
                                  A         AC
GAM299  KIAA1016  5'  GGCTTCAACCTGCCCTTGAAC  93387          T  A__
                                GTTCAAGGGCA GG   AAGTC
                                ||||||||||| ||   |||||
                                CAAGTTCCCGT CC   TTCGG
                                      _  AAC
GAM299  KIAA1017  3'  ACTAAATCATGCTCCTGAAC   24265       A       AA_
                                GTTCA GGGCATGG   AGT
                                ||||| ||||||||   |||
                                CAAGT CTCGTACT   TCA
                                   C       AAA
GAM299  MGC22014  3'  ACTTCAACATACCCTGGAC    65105       A   C   GA_
                                GTTCA GGG ATG   AAGT
                                ||||| ||| |||   ||||
                                CAGGT CCC TAC   TTCA
                                   _   A   AAC
GAM299  TUBB5     3'  GGCTGACTCCCCGCTGACCCT  21415      _ _  AA    A
                                AGGG CA TGG  AGTCA CC
                                |||| || |||  ||||| ||
                                TCCC GT GCC  TCAGT GG
                                  A  C   CC    C
GAM299  LOC128344 3'  GGTTGACTTTCCCAGATTGA   75246      GGGCAT
                                TCAA     GGAAAGTCAACC
                                ||||     ||||||||||||
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                                AGTT     CCTTTCAGTTGG
                                  AGAC__
GAM299  LOC149684 5'  GGCTCCTGCCCTTGAAC     85767          T   AA
                                GTTCAAGGGCA GGA  GTC
                                |||||||||| |||  |||
                                CAAGTTCCCGT CCT  CGG
                                        _   __
GAM299  LOC150279 3'  GTTAACTCTAGCCCTGA     80482     A    A    AA  C
                                TCA GGGC TGGA  GT AAC
                                ||| |||| ||||  || |||
                                AGT CCCG ATCT  CA TTG
                                  _   _   __ A
GAM299  LOC152018 3'  GACCTCCACCCCCTTGAAC   86729         CA    AA
                                GTTCAAGGG  TGGA  GTC
                                |||||||||  ||||  |||
                                CAAGTTCCC  ACCT  CAG
                                     CC    C_
GAM299  LOC170395 3'  GATGCTTCCTGCCCTTGAAC   76871          T    A_
                                GTTCAAGGGCA GGAA  GTC
                                |||||||||| ||||  |||
                                CAAGTTCCCGT CCTT  TAG
                                      _   CG
GAM299  LOC257407 5'  GCTGAGGCATGGCCTTGAAC   98760        G    GAA_
                                GTTCAAGG CATG    AGT
                                |||||||| ||||    |||
                                CAAGTTCC GTAC    TCG
                                    G    GGAG
GAM299  LOC56965  3'  TGACTCCATCCCCTGA     39927     A   C    AA
                                TCA GGG ATGGA  GTCA
                                ||| ||| |||||  ||||
                                AGT CCC TACCT  CAGT
                                  C  _    __
GAM299  LOC56965  3'  TGACTCCATCCCCTGA     39933     A   C    AA
                                TCA GGG ATGGA  GTCA
                                ||| ||| |||||  ||||
                                AGT CCC TACCT  CAGT
                                  C  _    __
GAM299  LOC92578  3'  GCCATACATGCCCTTGAAT   70394           GAAA
                                GTTCAAGGGCATG    GT
                                ||||||||||||    ||
                                TAAGTTCCCGTAC    CG
                                       ATAC
GAM299  LOC92997  3'  GCTGAGGCATGGCCTTGAAC   71639        G    GAA_
                                GTTCAAGG CATG    AGT
                                |||||||| ||||    |||
                                CAAGTTCC GTAC    TCG
                                    G    GGAG
GAM300  GPD1      3'  TCATGCCACCACATTTG     60398        C       C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
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                                GTTTAC CCACCGTA CT
                                   A      _
GAM300  IL5RA    5'  TCGCATGGCCACCGCATTT   6906          AT__
                                AAATGCGGTGGC   CGA
                                ||||||||||||  |||
                                TTTACGCCACCG   GCT
                                      GTAC
GAM300  MYO1C    3'  TGCCGATGCCAAATATTTG   61873      CGG      A
                                TAAATG  TGGCATCG CA
                                ||||||  |||||||| ||
                                GTTTAT  ACCGTAGC GT
                                   AA_      C
GAM300  C6orf37  3'  TGTCACACTGCATTTA     68097         GCATC
                                TAAATGCGGTG    GACA
                                ||||||||||    ||||
                                ATTTACGTCAC    CTGT
                                      A____
GAM300  DNAJC6   3'  TTGCAGAACCACCGCATT   29498         CA  GA
                                AATGCGGTGG  TC  CAA
                                ||||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                      A_  AC
GAM300  FLJ11210 3'  GTCGATGTGCATGCTTTTA   60319     T   GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM300  FLJ12476 3'  TCGATCTTCTGCATTTA     43270        T  C
                                TAAATGCGG GG ATCGA
                                |||||||||  || |||||
                                ATTTACGTC TC TAGCT
                                      T  _
GAM300  KIAA1034 3'  TCGATGGCATCCGCATTTG   63134         _  G
                                TAAATGCGG TG CATCGA
                                |||||||||  || ||||||
                                GTTTACGCC AC GTAGCT
                                      T  G
GAM300  KIAA1987 3'  TCATGTAACTGCATTTA     89391         G   C
                                TAAATGCGGT GCAT GA
                                ||||||||||  ||||  ||
                                ATTTACGTCA TGTA CT
                                      A   _
GAM300  MGC16063 3'  TGTCCTGGCCACTGCATT    54929          ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                      GTC
GAM300  LOC147949 3'  TGTCAGATGTCCACATTGCA  79279      __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
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                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM300  LOC150577 3'  GTCCTCACCGCATTTG     86258          CATC
                                TAAATGCGGTGG   GAC
                                ||||||||||||  |||
                                GTTTACGCCACT   CTG
                                      C___
GAM300  LOC158219 3'  TGTGTGTCACCACATTT     82694      C      CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                  A       __
GAM300  LOC202020 3'  TGTCTCACCACATTTA      90605       C    CATC
                                TAAATG GGTGG   GACA
                                |||||| |||||   ||||
                                ATTTAC CCACT   CTGT
                                   A    _____
GAM300  LOC90826  5'  TGTCGATGCAGGTTTATTTG  64788       CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                   TTGGA
GAM300  LOC93587  3'  TTGTCTTTACCTGCATTTA   73042       _    CATC
                                TAAATGC GGTGG   GACAA
                                ||||||| |||||   |||||
                                ATTTACG CCATT   CTGTT
                                    T    T___
GAM301  VAT1      3'  TAACCAAGGCTGCCTCTT    22091     A  C   C
                                AAGA GC GCC TGGTTG
                                |||| || ||| ||||||
                                TTCT CG CGG ACCAAT
                                  C  T   A
GAM301  AP3M2     3'  CATGTGCAGAAGTAGCTTCT  23300       CG CCTGG
                                AGAAGC  C    TTGCACATG
                                ||||||  |    |||||||||
                                TCTTCG  G    GACGTGTAC
                                   AT AA___
GAM301  FLJ12505  5'  GTCAACAAGAGCGGCTTC    45717        C  G   C
                                GAAGCCGC CT GTTG AC
                                |||||||| || |||| ||
                                CTTCGGCG GA CAAC TG
                                    A  A   _
GAM301  KIAA0275  3'  CATGTGTTCAAAGAACGGTTTC 29324         CC  GGTT
          TT                    AAGAAGCCG  CT   GCACATG
                                |||||||||  ||   |||||||
                                TTCTTTGGC  GA   TGTGTAC
                                     AA  AACT
GAM301  KIAA0830  3'  GCATCCAAACGGCTTCTT    70268         CCC   T
                                AAGAAGCCG   TGG TGC
                                |||||||||   ||| |||
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                                TTCTTCGGC   ACC ACG
                                     AA_   T
GAM301  KIAA1399  3'  CATGTGCAATGCCAGCCCCTTC 70790     CC  CC   __
                                GAAG  GC  TGGT  TGCACATG
                                ||||  ||  ||||  ||||||||
                                CTTC  CG  ACCG  ACGTGTAC
                                  CC  __   TA
GAM301  KIAA1643  3'  CATATGCATAGAAACGGCTTCT 65154       CC_  GT   C
                                AGAAGCCG   CTG  TGCA ATG
                                ||||||||   |||  |||| |||
                                TCTTCGGC   GAT  ACGT TAC
                                     AAA   __   A
GAM301  MAGE-E1   3'  GCACCCTAGGCGGCTTCTT   48675         CT  T
                                AAGAAGCCGCC  GG TGC
                                ||||||||||  || |||
                                TTCTTCGGCGG  CC ACG
                                      AT  C
GAM301  MRPS2     3'  CATGTGCAGAACGGCCCCTT   32631     AA   CCCTGG
                                AAG  GCCG     TTGCACATG
                                |||  ||||     |||||||||
                                TTC  CGGC     GACGTGTAC
                                  CC   AA____
GAM301  SSTK      3'  CATGCGCATCCGCGATTC    50169     GC   CCT  T   A
                                GAA  CGC   GG TGC CATG
                                |||  |||   || ||| ||||
                                CTT  GCG   CC ACG GTAC
                                  A_   ___  T   C
GAM301  LOC148887 3'  CATGCGCATTAAAGCAGGGCGG 85396    A   _     G ____   A
           GCTCCT                  AG AGCC GCCCTG T    TGC CATG
                                || |||| |||||| |    ||| ||||
                                TC TCGG CGGGAC A    ACG GTAC
                                 C   G     G AATT   C
GAM301  LOC152402 5'  GTGCCCAGAGCCGGCTTCT   86884        _ C    TT
                                AGAAGCCG C CTGG  GCAC
                                |||||||| | ||||  ||||
                                TCTTCGGC G GACC  CGTG
                                     C A   __
GAM301  LOC158078 3'  CATGTGTGTTGAGAGCTTCT   82600       CGCC  GGT
                                AGAAGC   CT   TGCACATG
                                ||||||   ||   ||||||||
                                TCTTCG   GA   GTGTGTAC
                                   A___  GTT
GAM301  LOC163882 3'  CATAGGCAACCAGAGCCACTTC 83040      CC  C       AC
                                GAAG  GC CTGGTTGC  ATG
                                ||||  || ||||||||  |||
                                CTTC  CG GACCAACG  TAC
                                  AC  A       GA
GAM301  LOC200138 3'  CATGTGCTTCCAGGGTGGCTTC 91539            TT
                                GAAGCCGCCCTGG  GCACATG
                                ||||||||||||  |||||||
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                                CTTCGGTGGGACC  CGTGTAC
                                       TT
GAM301  LOC51099  3'  CAACCAGGCAGCCTTCTT    32600       _ C   C
                                AAGAAG C GCC TGGTTG
                                |||||| | ||| ||||||
                                TTCTTC G CGG ACCAAC
                                   C A   _
GAM302  ELF3      3'  TGACCTTGACCTTGACCAA   16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                   _    AGT  ___
GAM302  JAK2      3'  TGACCTTCATTCTGAGACCAA  18318       CAA       AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_       C_
GAM302  SLC10A2   5'  ACTCTCTGTCTTGACCAA    6590        CAA       A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM302  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM302  KIAA1958  5'  GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM302  MARCKS    3'  ACTTTCCACCCTGCCCA     11411     TTCA    A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM302  TUB       5'  GTGGGACCATCCCTTAAACC   13898     C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A       AG__
GAM302  LOC80298  3'  ACTTTTACCTTGAACCA     48062         GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                      A___
GAM303  ELF3      3'  TGACCTTGACCTTGACCAA   16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
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                                AACCA GTTCC   TC   CAGT
                                  _    AGT  ___
GAM303  JAK2     3'  TGACCTTCATTCTGAGACCAA  18318       CAA       AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_       C_
GAM303  SLC10A2  5'  ACTCTCTGTCTTGACCAA    6590        CAA       A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___        C
GAM303  FLJ10803 3'  GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM303  KIAA1958 5'  GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM303  MARCKS   3'  ACTTTCCACCCTGCCCA     11411     TTCA    A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM303  TUB      5'  GTGGGACCATCCCTTAAACC   13898     C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A        AG__
GAM303  LOC80298 3'  ACTTTTACCTTGAACCA     48062         GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                     A___
GAM304  GPD1     3'  TCATGCCACCACATTTG      60398       C       C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A       _
GAM304  IL5RA    5'  TCGCATGGCCACCGCATTT    6906          AT__
                                AAATGCGGTGGC    CGA
                                ||||||||||||    |||
                                TTTACGCCACCG    GCT
                                      GTAC
GAM304  MYO1C    3'  TGCCGATGCCAAATATTTG    61873       CGG       A
                                TAAATG   TGGCATCG CA
                                ||||||   |||||||| ||
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                                GTTTAT   ACCGTAGC GT
                                   AA_      C
GAM304  C6orf37   3'  TGTCACACTGCATTTA     68097         GCATC
                                TAAATGCGGTG    GACA
                                ||||||||||    ||||
                                ATTTACGTCAC    CTGT
                                      A____
GAM304  DNAJC6    3'  TTGCAGAACCACCGCATT    29498        CA  GA
                                AATGCGGTGG  TC  CAA
                                |||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                      A_  AC
GAM304  FLJ11210  3'  GTCGATGTGCATGCTTTTA   60319     T   GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM304  FLJ12476  3'  TCGATCTTCTGCATTTA     43270        T  C
                                TAAATGCGG GG ATCGA
                                |||||||| || |||||
                                ATTTACGTC TC TAGCT
                                      T  _
GAM304  KIAA1034  3'  TCGATGGCATCCGCATTTG   63134        _  G
                                TAAATGCGG TG CATCGA
                                |||||||| || ||||||
                                GTTTACGCC AC GTAGCT
                                      T  G
GAM304  KIAA1987  3'  TCATGTAACTGCATTTA     89391         G   C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                      A   _
GAM304  MGC16063  3'  TGTCCTGGCCACTGCATT    54929          ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                      GTC
GAM304  LOC147949 3'  TGTCAGATGTCCACATTGCA  79279     __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM304  LOC150577 3'  GTCCTCACCGCATTTG      86258          CATC
                                TAAATGCGGTGG   GAC
                                ||||||||||||   |||
                                GTTTACGCCACT   CTG
                                      C___
GAM304  LOC158219 3'  TGTGTGTCACCACATTT     82694      C      CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
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                                TTTAC CCACTGTG  TGT
                                   A      __
GAM304  LOC202020 3'  TGTCTCACCACATTTA      90605       C    CATC
                                TAAATG GGTGG    GACA
                                |||||| |||||    ||||
                                ATTTAC CCACT    CTGT
                                   A    ____
GAM304  LOC90826  5'  TGTCGATGCAGGTTTATTTG   64788       CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                   TTGGA
GAM304  LOC93587  3'  TTGTCTTTACCTGCATTTA    73042       _    CATC
                                TAAATGC GGTGG    GACAA
                                ||||||| |||||    |||||
                                ATTTACG CCATT    CTGTT
                                    T    T___
GAM305  GPD1      3'  TCATGCCACCACATTTG      60398       C       C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A      _
GAM305  IL5RA     5'  TCGCATGGCCACCGCATTT    6906          AT__
                                AAATGCGGTGGC    CGA
                                ||||||||||||    |||
                                TTTACGCCACCG    GCT
                                      GTAC
GAM305  MYO1C     3'  TGCCGATGCCAAATATTTG    61873       CGG      A
                                TAAATG   TGGCATCG CA
                                ||||||   |||||||| ||
                                GTTTAT   ACCGTAGC GT
                                   AA_      C
GAM305  C6orf37   3'  TGTCACACTGCATTTA       68097         GCATC
                                TAAATGCGGTG     GACA
                                ||||||||||     ||||
                                ATTTACGTCAC     CTGT
                                      A____
GAM305  DNAJC6    3'  TTGCAGAACCACCGCATT     29498         CA  GA
                                AATGCGGTGG  TC  CAA
                                ||||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                      A_  AC
GAM305  FLJ11210  3'  GTCGATGTGCATGCTTTTA    60319      T  GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM305  FLJ12476  3'  TCGATCTTCTGCATTTA      43270         T  C
                                TAAATGCGG GG ATCGA
                                ||||||||| || |||||
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                                ATTTACGTC TC TAGCT
                                     T  _
GAM305  KIAA1034  3'  TCGATGGCATCCGCATTTG   63134        _  G
                                TAAATGCGG TG CATCGA
                                ||||||||| || ||||||
                                GTTTACGCC AC GTAGCT
                                     T  G
GAM305  KIAA1987  3'  TCATGTAACTGCATTTA    89391         G   C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                     A   _
GAM305  MGC16063  3'  TGTCCTGGCCACTGCATT   54929          ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                      GTC
GAM305  LOC147949 3'  TGTCAGATGTCCACATTGCA  79279     __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM305  LOC150577 3'  GTCCTCACCGCATTTG      86258          CATC
                                TAAATGCGGTGG   GAC
                                ||||||||||||   |||
                                GTTTACGCCACT   CTG
                                      C___
GAM305  LOC158219 3'  TGTGTGTCACCACATTT     82694      C      CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                   A       __
GAM305  LOC202020 3'  TGTCTCACCACATTTA      90605       C    CATC
                                TAAATG GGTGG   GACA
                                |||||| |||||   ||||
                                ATTTAC CCACT   CTGT
                                    A    _____
GAM305  LOC90826  5'  TGTCGATGCAGGTTTATTTG  64788       CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                    TTGGA
GAM305  LOC93587  3'  TTGTCTTTACCTGCATTTA   73042       _    CATC
                                TAAATGC GGTGG   GACAA
                                ||||||| |||||   |||||
                                ATTTACG CCATT   CTGTT
                                    T    T___
GAM306  ELF3      3'  TGACCTTGACCTTGACCAA   16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
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                                AACCA GTTCC   TC   CAGT
                                  _    AGT  ___
GAM306  JAK2     3'  TGACCTTCATTCTGAGACCAA  18318       CAA       AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_       C_
GAM306  SLC10A2  5'  ACTCTCTGTCTTGACCAA    6590        CAA       A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM306  FLJ10803 3'  GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM306  KIAA1958 5'  GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM306  MARCKS   3'  ACTTTCCACCCTGCCCA     11411     TTCA    A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                 CG__   _
GAM306  TUB      5'  GTGGGACCATCCCTTAAACC   13898     C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A       AG__
GAM306  LOC80298 3'  ACTTTTACCTTGAACCA     48062         GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                     A___
GAM307  ANXA6    3'  TCCCCTCTGACCCTCAGGC    15742        TTG    AAA
                                GCCTGAGG   TGGA   GGA
                                ||||||||   ||||   |||
                                CGGACTCC   GTCT   CCT
                                   CA_    CC_
GAM307  ATP5J    5'  CCTCCCGCCTCCCAGGCA    9853        A  TT    AAA
                                TGCCTG GG  GTGG   AGG
                                ||||||  ||  ||||   |||
                                ACGGAC CC  CGCC   TCC
                                   _ TC    C__
GAM307  BCL2L2   3'  TCCTCTCCCACTCAGGCA    15761        GT  T   AA
                                TGCCTGAG  TG GGA  AGGA
                                ||||||||  ||  |||  ||||
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                                ACGGACTC  AC CCT  TCCT
                                   __ _  C_
GAM307  EBAG9   3'  TCAGCTCCACAACCCAAGCA  16157    C  A      AAAG
                                TGC TG GGTTGTGGA   GA
                                ||| || |||||||||   ||
                                ACG AC CCAACACCT   CT
                                  A _       CGA_
GAM307  FUT3    5'  TTCCTCCCGCCCCAGG     5625      A  TT   AAA
                                CCTG GG  GTGG   AGGAA
                                |||| ||  ||||  |||||
                                GGAC CC  CGCC   TCCTT
                                  _ __   C__
GAM307  GRB2    5'  TCCCTTCCCCCTGCTTCAGGC  10873        TGT_   AA
                                GCCTGAGGT   GGAA  GGA
                                |||||||||   ||||  |||
                                CGGACTTCG   CCTT  CCT
                                     TCCC   C_
GAM307  IFRD2   3'  CTTCCTTTCCTTTCTCAGGC  23150       TTGT    A
                                GCCTGAGG   GGAAA GGAAG
                                ||||||||   ||||| |||||
                                CGGACTCT   CCTTT CCTTC
                                    TT__   _
GAM307  ITGB3   3'  TCCTTTCCCCTCCCTCAGGC  5806        TTGT    A
                                GCCTGAGG   GGAAA GGA
                                ||||||||   ||||| |||
                                CGGACTCC   CCTTT CCT
                                    CTCC   _
GAM307  LIG3    3'  TTCCCTCTCCCTCAGGC    26530       TTGT   AAA
                                GCCTGAGG   GGA  GGAA
                                ||||||||   |||  ||||
                                CGGACTCC   TCT  CCTT
                                    C___   C__
GAM307  MADD    3'  CCTTCTCTGTGACCCGGCA   14855     T A  TG   A
                                TGCC G GGT  TGGA AAGG
                                |||| | |||  |||| ||||
                                ACGG C CCA  GTCT TTCC
                                  _ _  GT   C
GAM307  MADD    3'  CCTTCTCTGTGACCCGGCA   56206     T A  TG   A
                                TGCC G GGT  TGGA AAGG
                                |||| | |||  |||| ||||
                                ACGG C CCA  GTCT TTCC
                                  _ _  GT   C
GAM307  MADD    3'  CCTTCTCTGTGACCCGGCA   56220     T A  TG   A
                                TGCC G GGT  TGGA AAGG
                                |||| | |||  |||| ||||
                                ACGG C CCA  GTCT TTCC
                                  _ _  GT   C
GAM307  MADD    3'  CCTTCTCTGTGACCCGGCA   56224     T A  TG   A
                                TGCC G GGT  TGGA AAGG
                                |||| | |||  |||| ||||
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                                ACGG C CCA  GTCT TTCC
                                  _ _  GT   C
GAM307  MADD    3'  CCTTCTCTGTGACCCGGCA   56228     T A  TG   A
                                TGCC G GGT  TGGA AAGG
                                |||| | |||  |||| ||||
                                ACGG C CCA  GTCT TTCC
                                  _ _  GT   C
GAM307  MADD    3'  CCTTCTCTGTGACCCGGCA   56232     T A  TG   A
                                TGCC G GGT  TGGA AAGG
                                |||| | |||  |||| ||||
                                ACGG C CCA  GTCT TTCC
                                  _ _  GT   C
GAM307  MEN1    3'  TCCCTTCCCACAGAGGC    95015     GAGG    A A
                                GCCT   TTGTGG AA GGA
                                ||||   |||||| || |||
                                CGGA   GACACC TT CCT
                                  ____    C C
GAM307  MEOX1   3'  CTTCCTTCCCCAGCCAGGGCA  26580     GA    T  AA
                                TGCCT  GGTTG GGA  AGGAAG
                                |||||  ||||| |||  ||||||
                                ACGGG  CCGAC CCT  TCCTTC
                                  A_    C  __
GAM307  MEOX1   3'  CTTCCTTCCCCAGCCAGGGCA  16952     GA    T  AA
                                TGCCT  GGTTG GGA  AGGAAG
                                |||||  ||||| |||  ||||||
                                ACGGG  CCGAC CCT  TCCTTC
                                  A_    C  __
GAM307  MYH11   3'  TCCTGGTTTCCACACCTCAGAC 43434    C     T     __
          A                      TG CTGAGGT GTGGAAA  AGGA
                                || ||||||| |||||||  ||||
                                AC GACTCCA CACCTTT  TCCT
                                 A      _     GG
GAM307  MYH11   3'  TCCTGGTTTCCACACCTCAGAC 43449    C     T     __
          A                      TG CTGAGGT GTGGAAA  AGGA
                                || ||||||| |||||||  ||||
                                AC GACTCCA CACCTTT  TCCT
                                 A      _     GG
GAM307  MYH11   3'  TCCTGGTTTCCACACCTCAGAC 11750    C     T     __
          A                      TG CTGAGGT GTGGAAA  AGGA
                                || ||||||| |||||||  ||||
                                AC GACTCCA CACCTTT  TCCT
                                 A      _     GG
GAM307  NAGA    3'  TCCTTTTCCAAAGTGACC    6040      ___
                                GGTTG   TGGAAAAGGA
                                |||||   ||||||||||
                                CCAGT   ACCTTTTCCT
                                  GAA
GAM307  NF2     5'  TCCCCTTTCCGCTCAGGCA   6050       GGTT     A_
                                TGCCTGA   GTGGAAA  GGA
                                |||||||   |||||||  |||
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                                ACGGACT   CGCCTTT  CCT
                                   ____     CC
GAM307  NHLH1   3'  CTTCCTTTCTCTGACCCAGGCA 20017      A    T GA
                                TGCCTG GGTTG G  AAAGGAAG
                                |||||| ||||| |  ||||||||
                                ACGGAC CCAGT C  TTTCCTTC
                                   _    _ TC
GAM307  NIPSNAP1 3'  CTTCCCCTTCTCCCTCAGGCA  14658        TTGT   AA
                                TGCCTGAGG   GGAA  GGAAG
                                |||||||||   ||||  |||||
                                ACGGACTCC   TCTT  CCTTC
                                     C___   CC
GAM307  NTSR1   3'  CTTCCTCCCCCACAGAGCTC   11854    G_    AAA
                                GAG  TTGTGG   AGGAAG
                                |||  ||||||   ||||||
                                CTC  GACACC   TCCTTC
                                  GA     CCC
GAM307  PXF     3'  CTTCCTTTTCTGCTGCTCA   12654     GTT TG
                                TGAG   G  GAAAAGGAAG
                                ||||   |  ||||||||||
                                ACTC   C  CTTTTCCTTC
                                  GT_ GT
GAM307  RHAG    3'  CTTCCTTTCCCATTATCCAG   6154     A  T   A
                                CTG GGT GTGG AAAGGAAG
                                ||| ||| |||| ||||||||
                                GAC CTA TACC TTTCCTTC
                                  _  T   C
GAM307  SNTB1   5'  CCTTTTCCAATCACATGGCA   41047     _ A   TG
                                TGCC TG GGT  TGGAAAAGG
                                |||| || |||  |||||||||
                                ACGG AC CTA  ACCTTTTCC
                                  T  A  __
GAM307  TAGLN2  3'  CTTCCTTTCCCCTGGGACC   14537     G __  A
                                GGTT T  GG AAAGGAAG
                                |||| |  || ||||||||
                                CCAG G  CC TTTCCTTC
                                  G TC  C
GAM307  TBXA2R  3'  CTTCCTTTTGAACCTC      8354       GTGG
                                GAGGTT   AAAAGGAAG
                                ||||||   |||||||||
                                CTCCAA   TTTTCCTTC
                                   G___
GAM307  TEC     3'  CCCCTCCTCACTCAGGTA    13676       GT  T   AAA
                                TGCCTGAG  TG GGA   GG
                                ||||||||  || |||   ||
                                ATGGACTC  AC CCT   CC
                                    __  T   CC_
GAM307  TEM7    3'  CTTCCTTTCCCCCGACCT    40258       T  A
                                AGGTTG GG AAAGGAAG
                                |||||| || ||||||||
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                                TCCAGC CC TTTCCTTC
                                   C  C
GAM307  TMEM2    3'  CTTCCCTTTCCACAGGGT    26337      GAGGT      A
                                GCCT    TGTGGAAA GGAAG
                                ||||    |||||||| |||||
                                TGGG    ACACCTTT CCTTC
                                  _____       C
GAM307  VTN      5'  TCCCTCCCTTCCTCAGGCA   7165         TTGT   AAA
                                TGCCTGAGG   GGA   GGA
                                |||||||||   |||   |||
                                ACGGACTCC   CCT   CCT
                                     TTC_  C__
GAM307  WNT15    3'  CCTCCTCCCTTAACCCAAGCA  14138    C  A    T_   AA
                                TGC TG GGTTG  GGA  AGG
                                ||| || |||||  |||  |||
                                ACG AC CCAAT  CCT  TCC
                                  A _    TC   CC
GAM307  ZNF131   3'  CTTCCTTTTCTCTTTCCCAGGT 70723      A  TTGT
                                GCCTG GG    GGAAAAGGAAG
                                ||||| ||    ||||||||||
                                TGGAC CC    TCTTTTCCTTC
                                   _ TTTC
GAM307  ARHGEF15 3'  CCTCCCCTTCAGCTCAGGCA   30951        G   T_  AAA
                                TGCCTGAG TTG  GG   AGG
                                |||||||| |||  ||   |||
                                ACGGACTC GAC  CC   TCC
                                     _  TT  CC_
GAM307  C22orf5  3'  TCCCCTCCTGACCCAGGC    25346      A    T   AAA
                                GCCTG GGTTG GGA   GGA
                                ||||| ||||| |||   |||
                                CGGAC CCAGT CCT   CCT
                                   _    _  CC_
GAM307  CAMTA2   5'  CCTCCCCCCGGCCCCTCAGGC  61882       __    T  AAA
                                GCCTGA  GGTTG GG   AGG
                                ||||||  ||||| ||   |||
                                CGGACT  CCGGC CC   TCC
                                   CC    _ CCC
GAM307  CARD9    5'  TCCCTCCCTGCAGCCCCGGGCA 42550       A    TG AAAA
                                TGCCTG GGTTG  G    GGA
                                |||||| |||||  |    |||
                                ACGGGC CCGAC  C    CCT
                                   C    GT CCTC
GAM307  CARD9    5'  TCCCTCCCTGCAGCCCCGGGCA 54475       A    TG AAAA
                                TGCCTG GGTTG  G    GGA
                                |||||| |||||  |    |||
                                ACGGGC CCGAC  C    CCT
                                   C    GT CCTC
GAM307  CARD9    5'  TCCCTCCCTGCAGCCCCGGGCA 54479       A    TG AAAA
                                TGCCTG GGTTG  G    GGA
                                |||||| |||||  |    |||
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                                ACGGGC CCGAC  C    CCT
                                   C     GT CCTC
GAM307  CBARA1   3'  CTTCCTCCCGGGATGACCTCAG 21393        TG ___  AAA
            G                   CCTGAGGT  T   GG   AGGAAG
                                |||||||| |   ||   ||||||
                                GGACTCCA  A   CC   TCCTTC
                                    GT GGG  C__
GAM307  COP      3'  CTTCCTTCCCAGCTCTTCAGGC 54668        __    T   AA
            A                   TGCCTGA  GGTTG GGA  AGGAAG
                                |||||||  ||||| |||  ||||||
                                ACGGACT  TCGAC CCT  TCCTTC
                                   TC    _  __
GAM307  DC-TM4F2 3'  CCTAGCCACAACCCCAGGC   48899      A      AAA
                                GCCTG GGTTGTGG   AGG
                                ||||| ||||||||   |||
                                CGGAC CCAACACC   TCC
                                   C       GA_
GAM307  DDX31    5'  CCTTTTCCCTGCCCAGG    57612      A   TGT
                                CCTG GGT   GGAAAAGG
                                |||| |||   ||||||||
                                GGAC CCG   CCTTTTCC
                                  _   TC_
GAM307  DDX31    5'  CCTTTTCCCTGCCCAGG    43247      A   TGT
                                CCTG GGT   GGAAAAGG
                                |||| |||   ||||||||
                                GGAC CCG   CCTTTTCC
                                  _   TC_
GAM307  FLJ12389 3'  CTTCCCTTCCCATCTCAGGC   60899        T T    AA
                                GCCTGAGGT G GGAA  GGAAG
                                ||||||||| | ||||  |||||
                                CGGACTCTA C CCTT  CCTTC
                                     _ _    C_
GAM307  FLJ14100 3'  TCCCTTTCCTGCCGCCCAGGC  47341      A   T  _    A
                                GCCTG GGT GT GGAAA GGA
                                ||||| ||| || ||||| |||
                                CGGAC CCG CG CCTTT CCT
                                  _   C  T    C
GAM307  FLJ23436 3'  CCTCTTCTTCCTCAGGC     45463        TTGT    A
                                GCCTGAGG    GGAA AGG
                                ||||||||    |||| |||
                                CGGACTCC    TCTT TCC
                                     T___    C
GAM307  FOXP1    5'  CCTCCCAGTGACCCCAGGC   52044      A    _   AAA
                                GCCTG GGTTG TGG   AGG
                                ||||| ||||| |||   |||
                                CGGAC CCAGT ACC   TCC
                                   C    G   C__
GAM307  HARS2    3'  CTTCCCTTCCACCTCCTCAGCA 55864     C    TT     AA
                                TGC TGAGG  GTGGAA  GGAAG
                                ||| |||||  ||||||  |||||
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                                ACG ACTCC  CACCTT  CCTTC
                                  _    TC     C_
GAM307  HEMK     3'  TCCCTCCTGGCCTCAGGC    32964          T   AAA
                                GCCTGAGGTTG GGA   GGA
                                |||||||||| |||   |||
                                CGGACTCCGGT CCT   CCT
                                      _  C__
GAM307  KIAA0217 3'  TCCTTTACCCCCAGCA      67601     C  A  TTGT  A
                                TGC TG GG    GG AAAGGA
                                ||| || ||    || ||||||
                                ACG AC CC    CC TTTCCT
                                  _ _ ____ A
GAM307  KIAA0350 3'  CCTCCCACAACCCAGACA    61827    C   A       AAA
                                TG CTG GGTTGTGG   AGG
                                || ||| ||||||||   |||
                                AC GAC CCAACACC   TCC
                                 A  _       C__
GAM307  KIAA0451 3'  CCTTCTCTTCTCAGGCA     29771         TTGT   A
                                TGCCTGAGG    GGA AAGG
                                |||||||||    ||| ||||
                                ACGGACTCT    TCT TTCC
                                     ____  C
GAM307  KIAA0514 5'  TCCCTTTCTCTCTTCTGCAGGC 28758       _  TTGT    A
          A                      TGCCTG AGG    GGAAA GGA
                                ||||||| |||    ||||| |||
                                ACGGAC TCT    TCTTT CCT
                                   G   TCTC    C
GAM307  KIAA0721 3'  CTTCCCTTTCACTCTGAAGCA  97656     CTGA  TT     AA
                                TGC    GG  GTGGAA  GGAAG
                                |||    ||  ||||||  |||||
                                ACG    TC  CACTTT  CCTTC
                                  AAG_  T_     C_
GAM307  KIAA0721 3'  CTTCCCTTTCACTCTGAAGCA  41653     CTGA  TT     AA
                                TGC    GG  GTGGAA  GGAAG
                                |||    ||  ||||||  |||||
                                ACG    TC  CACTTT  CCTTC
                                  AAG_  T_     C_
GAM307  KIAA1280 5'  TCCCTTTTCAGAGCCCCCAGGC 70289      A_   G     A
                                GCCTG  GGTT TGGAAA GGA
                                |||||  |||| |||||| |||
                                CGGAC  CCGA ACTTTT CCT
                                   CC   G     C
GAM307  KIAA1332 3'  CTTCCCTTTCGCGACTCAGGC  71705       G       AA
                                GCCTGAG TTGTGGAA  GGAAG
                                ||||||| ||||||||  |||||
                                CGGACTC AGCGCTTT  CCTTC
                                     _       C_
GAM307  KIAA1975 5'  TTCCCTTCCCCTTCAGGTA   74434         TTGT   AA
                                TGCCTGAGG    GGAA  GGAA
                                |||||||||    ||||  ||||
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                                ATGGACTTC   CCTT  CCTT
                                    C___    C_
GAM307  MGC11352  5'  CCTAGCCACAACCCCAGGC   65431      A      AAA
                                GCCTG GGTTGTGG   AGG
                                ||||| ||||||||   |||
                                CGGAC CCAACACC   TCC
                                   C       GA_
GAM307  MGC15827  3'  TCCTCTCCTCCTCTCAGGCA  52876        TTGT   AA
                                TGCCTGAGG   GGA  AGGA
                                |||||||||   |||  ||||
                                ACGGACTCT   CCT  TCCT
                                    CCT_   C_
GAM307  RNF8      3'  CTTCCCTTCCTGCTCCCAGACA 15566    C   A  TTGT   AA
                                TG CTG GG   GGAA  GGAAG
                                || ||| ||   ||||  |||||
                                AC GAC CC   CCTT  CCTTC
                                 A  _  TCGT   C_
GAM307  SCAMP5    3'  CTTCCTCTCCCCTACCCCAG  58059    A   TGT   AA
                                CTG GGT   GGA  AGGAAG
                                ||| |||   |||  ||||||
                                GAC CCA   CCT  TCCTTC
                                  C   TCC   C_
GAM307  SUPT4H1   3'  CCTCTTCCATTCTCTTAGGCA  13485        TT     A
                                TGCCTGAGG  GTGGAA AGG
                                |||||||||  ||||||  |||
                                ACGGATTCT  TACCTT TCC
                                    CT     C
GAM307  SV2       5'  CTTCCTTTTCCTTCCTAGGCA  29957      G   TTGT
                                TGCCT AGG   GGAAAAGGAAG
                                ||||| |||   ||||||||||
                                ACGGA TCC   CCTTTTCCTTC
                                   _   TT__
GAM307  VI        3'  TCCTTTTCTGCCCTCTAGCA   26489     CT   TT TG
                                TGC  GAGG  G  GAAAAGGA
                                |||  ||||  |  ||||||||
                                ACG  CTCC  C  CTTTTCCT
                                  AT    __ GT
GAM307  ZDHHC1    3'  CCTCCCCCACGACTCAGCA   78209    C   G     AAA
                                TGC TGAG TTGTGG   AGG
                                ||| |||| ||||||   |||
                                ACG ACTC AGCACC   TCC
                                  _   _     CCC
GAM307  ZDHHC8    3'  CCCCTCCCCAGCCCTCAGGC   64619        _   T   AAA
                                GCCTGAGG TTG GGA   GG
                                |||||||| ||| |||   ||
                                CGGACTCC GAC CCT   CC
                                    C   C   CC_
GAM307  LOC121219 3'  TCCCCTCTCATGGCCCAGCCA  74489    C   A   TG  _  AAA
                                TG CTG GGT  TG GA   GGA
                                || ||| |||  || ||   |||
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                                AC GAC CCG  AC CT   CCT
                                 C   _   GT  T  CC_
GAM307   LOC129080 3'  CTTCCCTCTGAGCCCCCAGGC  56794      A_    G    AAA
                                GCCTG  GGTT TGGA   GGAAG
                                |||||  |||| ||||   |||||
                                CGGAC  CCGA GTCT   CCTTC
                                   CC    _    C__
GAM307   LOC142955 3'  CTTCCTTCCGCTCAATGCA    76959     C_   GGTT     AA
                                TGC  TGA    GTGGA  AGGAAG
                                |||  |||    |||||  ||||||
                                ACG  ACT    CGCCT  TCCTTC
                                  TA  _____    __
GAM307   LOC143162 5'  CCTCCTGCAGCCTCAAGCA    77003     C       TG AAA
                                TGC TGAGGTTG  G   AGG
                                ||| ||||||||  |   |||
                                ACG ACTCCGAC  C   TCC
                                  A       GT C__
GAM307   LOC143162 5'  CTTCCTTTCCCACTTCTCCAGG 77006      AG TT    A
            C                    GCCTG  G  GTGG AAAGGAAG
                                |||||  |  |||| ||||||||
                                CGGAC  C  CACC TTTCCTTC
                                   CT TT    C
GAM307   LOC145758 5'  TCCCTACAACCCCAGGC     84487      A       AAAA
                                GCCTG GGTTGTGG    GGA
                                ||||| ||||||||    |||
                                CGGAC CCAACATC    CCT
                                   C       _____
GAM307   LOC147042 3'  CCTTTTCTCCCAGGCA      84992       A  TTGT
                                TGCCTG GG    GGAAAAGG
                                |||||| ||    ||||||||
                                ACGGAC CC    TCTTTTCC
                                   _ _____
GAM307   LOC149113 3'  CTTCCTTTTTTTCCCCAGGC   79911      A  TTGT
                                GCCTG GG    GGAAAAGGAAG
                                ||||| ||    ||||||||||
                                CGGAC CC    TTTTTTCCTTC
                                   _  CT__
GAM307   LOC151178 3'  CTTCCTCTTCCCACCTTCATAC 80958    CC     T  T    A
            A                    TG  TGAGG TG GGAA AGGAAG
                                ||  ||||| || |||| ||||||
                                AC  ACTTC AC CCTT TCCTTC
                                  AT    C  _    C
GAM307   LOC153338 5'  CTTCCCCCTCCTTTTCTCAAGC 87197     C     TTGT   AAA
            A                    TGC TGAGG    GGA   GGAAG
                                ||| |||||    |||   |||||
                                ACG ACTCT    CCT   CCTTC
                                  A    TTT_   CCC
GAM307   LOC153811 3'  CTTCCTTTTCCACCCTAAGC   81834    CTG   TT
                                GC   AGG  GTGGAAAAGGAAG
                                ||   |||  ||||||||||||
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                                CG   TCC  CACCTTTTCCTTC
                                 AA_  __
GAM307  LOC155382 3'  CCTCCCCCTGGCCTCAGGCA  87676          T  AAA
                                TGCCTGAGGTTG GG   AGG
                                |||||||||||| ||   |||
                                ACGGACTCCGGT CC   TCC
                                       C  CC_
GAM307  LOC157349 3'  TCTACCCCACAGCCCCAGGCA  82350       A       AAAA
                                TGCCTG GGTTGTGG    GGA
                                |||||| ||||||||    |||
                                ACGGAC CCGACACC    TCT
                                   C       CCA_
GAM307  LOC196738 5'  CCTCCTGCAGCCTCAAGCA    88888     C       TG AAA
                                TGC TGAGGTTG  G   AGG
                                ||| ||||||||  |   |||
                                ACG ACTCCGAC  C   TCC
                                  A       GT C__
GAM307  LOC196738 5'  CTTCCTTTCCCACTTCTCCAGG 88891      AG TT    A
            C                    GCCTG  G  GTGG AAAGGAAG
                                ||||||  |  |||| ||||||||
                                CGGAC  C  CACC TTTCCTTC
                                   CT TT    C
GAM307  LOC200734 5'  CCCCCTCCCCAAATCAGGCG   90273       GG   T   AAA
                                TGCCTGA  TTG GGA   GG
                                |||||||  ||| |||   ||
                                GCGGACT  AAC CCT   CC
                                     A_   C   CCC
GAM307  LOC219700 5'  TCCCTCCCACAGCCCCAGG    94661      A       AAAA
                                CCTG GGTTGTGG    GGA
                                |||| ||||||||    |||
                                GGAC CCGACACC    CCT
                                  C       CTC_
GAM307  LOC219818 3'  TCCCCCTTCCTACTCAGGCA   92539        GTTGT    AA_
                                TGCCTGAG    GGAA   GGA
                                ||||||||    ||||   |||
                                ACGGACTC    CCTT   CCT
                                     AT___    CCC
GAM307  LOC222815 5'  CCTTCTCCACAGCTGGAGCCA  96022    C  GA       A
                                TG CT  GGTTGTGGA AAGG
                                || ||  |||||||| ||||
                                AC GA  TCGACACCT TTCC
                                 C  GG        C
GAM307  LOC255458 5'  CTTCCTCCTCTCTCTCAGGCA  98934         TTGT   AA
                                TGCCTGAGG    GGA  AGGAAG
                                |||||||||    |||  ||||||
                                ACGGACTCT    TCT  TCCTTC
                                     C___   CC
GAM307  LOC256895 3'  TCCCTTCCCTTCTCAGGC     98656         TTGT    AA
                                GCCTGAGG    GGAA  GGA
                                ||||||||    ||||  |||
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                                CGGACTCT   CCTT  CCT
                                    TC__   C_
GAM307  LOC257473 3'  CCTCCCCCACGACTCAGCA   96806    C   G    AAA
                                TGC TGAG TTGTGG   AGG
                                ||| |||| ||||||   |||
                                ACG ACTC AGCACC   TCC
                                  _   _    CCC
GAM307  LOC51055  5'  CTTCCTTCCCCAGGACAAAGCA 32475    CTGAG   G   AA
                                TGC    GTT TGG  AAGGAAG
                                |||    ||| |||  |||||||
                                ACG    CAG ACC  TTCCTTC
                                  AAA__   G   CC
GAM307  LOC90092  5'  CCTCCTATGCCTTCAGGCA   62059        TT   AAA
                                TGCCTGAGG  GTGG   AGG
                                |||||||||  ||||   |||
                                ACGGACTTC  TATC   TCC
                                     CG   C__
GAM307  LOC92568  3'  TCCTTGACCAAACCTCAGCCA  70332   C      G   AA
                                TG CTGAGGTT TGG  AAGGA
                                || ||||||||| |||  |||||
                                AC GACTCCAA ACC  TTCCT
                                 C       _  AG
GAM308  ELF3      3'  TGACCTTGACCTTGACCAA    16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                   _    AGT  ____
GAM308  JAK2      3'  TGACCTTCATTCTGAGACCAA  18318      CAA      AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_      C_
GAM308  SLC10A2   5'  ACTCTCTGTCTTGACCAA    6590       CAA      A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ____       C
GAM308  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA  37205      CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM308  KIAA1958  5'  GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                GGTT   GGG   AAAGTCAC
                                ||||   |||   ||||||||
                                CCAA   CCC   TTTCAGTG
                                  A__   CAAG
GAM308  MARCKS    3'  ACTTTCCACCCTGCCCA     11411     TTCA   A
                                TGG   AGGG TGGAAAGT
                                |||   |||| ||||||||
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                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM308  TUB      5'  GTGGGACCATCCCTTAAACC   13898      C        AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A        AG__
GAM308  LOC80298 3'  ACTTTTACCTTGAACCA     48062          GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                      A___
GAM309  ADAM11   3'  GGGGCTGGGCATCCCAGCT    41493       T       ACTA
                                AGCTGG GATGCCCA    CCC
                                |||||| ||||||||    |||
                                TCGACC CTACGGGT    GGG
                                   _       CG__
GAM309  ADAM11   3'  GGGGCTGGGCATCCCAGCT    41494       T       ACTA
                                AGCTGG GATGCCCA    CCC
                                |||||| ||||||||    |||
                                TCGACC CTACGGGT    GGG
                                   _       CG__
GAM309  EIF2C1   3'  ATGGGCAGCCAAGGGTGCACT  25183      A     AA__  A
                                GGTG TGCCC    CT CCCAT
                                |||| |||||    || |||||
                                TCAC GTGGG    GA GGGTA
                                  _     AACC  C
GAM309  MRC1     3'  TGGGTAGCTGATGTCAGCT    11683       GT ATGCC  A
                                AGCTG  G     CA CTACCCA
                                |||||  |     || |||||||
                                TCGAC  T     GT GATGGGT
                                   TG A_____  C
GAM309  NOLA1    3'  AGTTGACAGACATCACCAGTT  39124           CC___
                                AGCTGGTGATG     CAACT
                                ||||||||||     |||||
                                TTGACCACTAC     GTTGA
                                      AGACA
GAM309  TP53     3'  ATGGGGAGTAGGACATACCAGC 6795          A  C  A   A
          T                      AGCTGGTG TG CC ACT CCCAT
                                |||||||| || || ||| |||||
                                TCGACCAT AC GG TGA GGGTA
                                     _ A  A   G
GAM309  FLJ22055 3'  AGCTGGGCATCAGCAACT    45845    C  G       A
                                AG TG TGATGCCCA CT
                                || || ||||||||| ||
                                TC AC ACTACGGGT GA
                                 A  G        C
GAM309  FLJ22316 5'  ATGAGTAGCTGGGACTACAGGT 47610     G   ATG    A    C
                                GCT GTG   CCCA CTAC CAT
                                ||| |||   |||| |||| |||
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                                TGG CAT   GGGT GATG GTA
                                  A  CA_   C   A
GAM309  HCA4     3'  ATGGATAGCCTAGCACCAGTT  57739        ATGCCCAA  C
                                AGCTGGTG       CTA CCAT
                                ||||||||       ||| ||||
                                TTGACCAC       GAT GGTA
                                    GATCC___   A
GAM309  KIAA0222 3'  GGGTGGGGATCACCAGC     28399        G  AACT
                                GCTGGTGAT CCC    ACCC
                                ||||||||| |||    ||||
                                CGACCACTA GGG    TGGG
                                     G  ____
GAM309  KIAA0336 5'  TGGGGTGGCTTCACCAGCT   28325         T  CAACTA
                                AGCTGGTGA GCC     CCCA
                                ||||||||| |||     ||||
                                TCGACCACT CGG     GGGT
                                     T  TG____
GAM309  RASGRP4  3'  GTGGCACAGGCTCCACCAGCT  54746        AT  CAA_
                                AGCTGGTG  GCC    CTAC
                                ||||||||  |||    ||||
                                TCGACCAC  CGG    GGTG
                                    CT   ACAC
GAM309  RASSF2   3'  GGCAGCTGGGCATCAGTGC    29103    T G       A  A
                                GC G TGATGCCCA CT CC
                                || | ||||||||| || ||
                                CG T ACTACGGGT GA GG
                                 _ G        C  C
GAM309  LOC112724 3'  ATGGAGTGGGAACCCCACCAGC 57300        ATG__   A  AC
           T                     AGCTGGTG    CCCA CT  CCAT
                                 ||||||||    |||| ||  ||||
                                 TCGACCAC    GGGT GA  GGTA
                                     CCCAA   _  __
GAM309  LOC114987 3'  GGAGTTAGCACACCAGCT    59799        A  CC   A
                                AGCTGGTG TGC  AACT CC
                                ||||||| |||  |||| ||
                                TCGACCAC ACG  TTGA GG
                                    _   A_   _
GAM309  LOC150291 3'  ATGGCAGAGGAATCACCAGCT  86130         G  CAA  AC
                                AGCTGGTGAT CC   CT  CCAT
                                |||||||||| ||   ||  ||||
                                TCGACCACTA GG   GA  GGTA
                                     A  A__  C_
GAM309  LOC151996 5'  ATGGCACATGAGCATCACCCGC 86713     T       C  ACTAC
           T                     AGC GGTGATGC CA     CCAT
                                 ||| |||||||| ||     ||||
                                 TCG CCACTACG GT     GGTA
                                   C       A  ACAC_
GAM309  LOC158549 5'  GTTGTGCAAGCATCACCGCT   88230     T       C____
                                AGC GGTGATGC     CAAC
                                ||| ||||||||     ||||
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                                TCG CCACTACG    GTTG
                                  _      AACGT
GAM309  LOC205095 3'  GGGCCAAGGTCATCACCAGC  92387         C  AACTA
                                GCTGGTGATG CC    CCC
                                |||||||||| ||    |||
                                CGACCACTAC GG    GGG
                                      T  AACC_
GAM309  LOC254531 5'  AGTCTGGACACCACCAGCT   96661        A  C  _
                                AGCTGGTG TG CCA ACT
                                |||||||| || ||| |||
                                TCGACCAC AC GGT TGA
                                     C  A   C
GAM309  LOC90378  5'  GGTGCCCAGCACCACCAGCT  63187        A   CCAAC
                                AGCTGGTG TGC    TACC
                                |||||||| |||    ||||
                                TCGACCAC ACG    GTGG
                                     C   ACCC_
GAM309  LOC92565  5'  GTCATTGTGACATCACCAGC  70316         CC_  CT
                                GCTGGTGATG   CAA  AC
                                ||||||||||   |||  ||
                                CGACCACTAC   GTT  TG
                                      AGT   AC
GAM310  BNC     3'  TAGTCCATAGAAATGTTTC   9943    T    GACG
                                A AACATT    ATGGACTA
                                | ||||||    ||||||||
                                C TTGTAA    TACCTGAT
                                 T     AGA_
GAM310  EIF2C1   3'  AGTCCATTGTGAAATTATC   25182      CA  G
                                GATAA  TT ACGATGGACT
                                |||||  || ||||||||||
                                CTATT  AA TGTTACCTGA
                                   A_  G
GAM310  ITGA1    3'  AGCCAAGTCAATGTTTC    64269   T      GA   A
                                A AACATTGAC  TGG CT
                                | |||||||||  ||| ||
                                C TTGTAACTG  ACC GA
                                 T       A_  _
GAM310  PLA2G2A  5'  AGTCCATCTGCATTTGTC   6109      CAT  AC
                                GATAA   TG  GATGGACT
                                |||||   ||  ||||||||
                                CTGTT   AC  CTACCTGA
                                   T__  GT
GAM310  PLAG1    3'  AGTCCTACTCCGATGTTATC   12147        ACGAT
                                GATAACATTG    GGACT
                                ||||||||||    |||||
                                CTATTGTAGC    CCTGA
                                      CTCAT
GAM310  ROBO1    3'  TCCATGTGATTAATGTTTTC   12893    T      _  _
                                GA AACATTGA CG ATGGA
                                || |||||||| || |||||
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                                CT TTGTAATT GT TACCT
                                 T       A  G
GAM310  ROBO1    3'  TCCATGTGATTAATGTTTTC   56900    T      _ _
                                GA AACATTGA CG ATGGA
                                || |||||||| || |||||
                                CT TTGTAATT GT TACCT
                                 T       A  G
GAM310  SCML1    3'  TAGCTTCATCAATGTTATT    23111          C  T  A
                                GATAACATTGA GA GG CTA
                                |||||||||||| || || |||
                                TTATTGTAACT CT TC GAT
                                       A  _ _
GAM310  SF3B3    3'  AGTTTTGTACAATGTTATC    25782          _   TG
                                GATAACATTG ACGA  GACT
                                |||||||||| ||||  ||||
                                CTATTGTAAC TGTT  TTGA
                                      A   __
GAM310  B3GNT5   3'  TAGTCCATCAGAATGTTTC    50252   T    GAC
                                A AACATT   GATGGACTA
                                | ||||||   |||||||||
                                C TTGTAA   CTACCTGAT
                                 T     GA_
GAM310  C20orf3  3'  AGTGCACGTGTTAATGTCATC  68639    A       A_  G
                                GAT ACATTGACG  TG ACT
                                ||| |||||||||  || |||
                                CTA TGTAATTGT  AC TGA
                                  C        GC  G
GAM310  FLJ21168 3'  AGTTTTTCAATGTTATC     47582          CGAT
                                GATAACATTGA    GGACT
                                ||||||||||    |||||
                                CTATTGTAACT    TTTGA
                                       T___
GAM310  HSPC019  3'  AGGCATAGCAATGTTATC    26715          ACG   GA
                                GATAACATTG   ATG  CT
                                ||||||||||   |||  ||
                                CTATTGTAAC   TAC  GA
                                      GA_   G_
GAM310  KIAA0227 3'  TAGTATGTCAATGTTATT    61352          ATGG
                                GATAACATTGACG    ACTA
                                ||||||||||||    ||||
                                TTATTGTAACTGT    TGAT
                                       A___
GAM310  KIAA0594 3'  TAGTTTCTCCCAATGTTAT   65519         AC  TG
                                ATAACATTG  GA  GACTA
                                |||||||||  ||  |||||
                                TATTGTAAC  CT  TTGAT
                                     C_  CT
GAM310  MGC4161  3'  TTTTTCATCAATGTTATC    44447          C  TG
                                GATAACATTGA GA  GA
                                |||||||||| ||  ||
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                                CTATTGTAACT CT  TT
                                      A  TT
GAM310  PHIP     5'  TAGTCTGTTTCAATGCTA    36029    A     C
                                TA CATTGA GATGGACTA
                                || ||||||| |||||||||
                                AT GTAACT TTGTCTGAT
                                 C     _
GAM310  PRO2521  3'  AGTCTGTCCTCACTGCCATC  38190     AA  T   C
                                GAT  CA TGA GATGGACT
                                |||  || ||| ||||||||
                                CTA  GT ACT CTGTCTGA
                                  CC  C   C
GAM310  ZNF333   3'  GGTTCATCCATGTTATC     51594        TGAC
                                GATAACAT    GATGGACT
                                ||||||||    ||||||||
                                CTATTGTA    CTACTTGG
                                     C___
GAM310  LOC143188 5'  TAGTCCATCATGTGTGTTTC  83794   T    TGAC
                                A AACAT    GATGGACTA
                                | |||||    |||||||||
                                C TTGTG    CTACCTGAT
                                 T    TGTA
GAM310  LOC151094 3'  TAGTCCATACTGAGTGTCATC  65888     A    GACG
                                GAT ACATT    ATGGACTA
                                ||| |||||    ||||||||
                                CTA TGTGA    TACCTGAT
                                  C    GTCA
GAM310  LOC201696 3'  TCCATTCAGTAATGTTAT    63830        AC_
                                ATAACATTG   GATGGA
                                |||||||||   ||||||
                                TATTGTAAT   TTACCT
                                     GAC
GAM310  LOC202460 5'  AGTCTATCAATGTTA       90664        CGA
                                TAACATTGA   TGGACT
                                |||||||||   ||||||
                                ATTGTAACT   ATCTGA
                                            ___
GAM310  LOC219700 3'  GGTCAGTCAATGTATC      94655     A      GATG
                                GATA CATTGAC    GACT
                                |||| |||||||    ||||
                                CTAT GTAACTG    CTGG
                                  _      A___
GAM311  DLEC1    3'  CATCTGGCCCTCCCTTG     24716      A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                   C    G  _
GAM311  PIP5K1A  3'  TATCCCACCCTGCCTTGATA  14520        A   CA  C
                                TATCAAGG AGGG  GG GTG
                                |||||||| ||||  || |||
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                                ATAGTTCC TCCC  CC TAT
                                    G   A_ C
GAM311  SOX11    3' ACCCACCCCCCCTTGGTA    13308       AA   CA  C
                                TATCAAGG  GGG  GG GT
                                ||||||||  |||  || ||
                                ATGGTTCC  CCC  CC CA
                                    CC   A_ _
GAM311  CHL1     3' TGTTACCTTTCCTCAATA    22768     CA      CA
                                TAT  AGGAAGGG  GGCG
                                |||  ||||||||  ||||
                                ATA  TCCTTTCC  TTGT
                                  AC       A_
GAM311  EPB41L1  3' CATTCTGCCCTTCCCTGA    71104     A        C
                                TCA GGAAGGGCAGG GTG
                                ||| ||||||||||| |||
                                AGT CCTTCCCGTCT TAC
                                  C         _
GAM311  FLJ00060 3' CATACCCCCTGCCCTCCTCTGA 61741     _   A      CGTG
                                TCA AGGA GGGCAGG   ATG
                                ||| |||| |||||||   |||
                                AGT TCCT CCCGTCC   TAC
                                  C   _      CCCA
GAM311  FLJ10898 5' CACCACAGCCCTTTCTCAATA  60126     CA       AGGC
                                TAT  AGGAAGGGC   GTG
                                |||  |||||||||   |||
                                ATA  TCTTTCCCG   CAC
                                  AC        ACAC
GAM311  FLJ22557 3' ATCATCCCATCCTTAATA    45581     C    A  CAGGC
                                TAT AAGGA GGG    GTGAT
                                ||| ||||| |||    |||||
                                ATA TTCCT CCC    TACTA
                                  A    A  _____
GAM311  KIAA0574 3' CATCCCCTGCCCTCCCCTGA   69808     A  A      CGT
                                TCA GG AGGGCAGG   GATG
                                ||| ||  ||||||||  ||||
                                AGT CC TCCCGTCC   CTAC
                                  C  C       C__
GAM311  KIAA0632 3' CACCTCAGAAACCCTTCCTTGA 32071          CA___  C
                                TCAAGGAAGGG    GG GTG
                                ||||||||||    || |||
                                AGTTCCTTCCC    CT CAC
                                      AAAGA  C
GAM311  KIAA1354 5' CAGTGACTGCCTTCCCTTGATA 61572        A      G  _
                                TATCAAGG AGGGCAG CG TG
                                |||||||| ||||||| || ||
                                ATAGTTCC TTCCGTC GT AC
                                    C      A  G
GAM311  MGC20460 5' CACCGCCTCCTACCCTTCTT   54901        C___    _
                                AGGAAGGG   AGGCG TG
                                ||||||||   ||||| ||
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                                TTCTTCCC   TCCGC AC
                                    ATCC    C
GAM311  LOC158476 3'  CACGCCCGCCCCCCCCATTGA  88186     _ AA_   A
                                TCAA GG   GGGC GGCGTG
                                |||| ||   |||| ||||||
                                AGTT CC   CCCG CCGCAC
                                  A  CCC   C
GAM311  LOC90459  3'  CACACCCGCCTAATTTTTG   63550      A_   A  C
                                CAAGGA  GGGC GG GTG
                                ||||||  |||| || |||
                                GTTTTT  TCCG CC CAC
                                   AA   C  A
GAM312  HYAL2    3'  AAGCCCAGGAGGGCATCCATAC 53700               G
           CA                     TGGTATGGATGCCCTCCTGGG TT
                                ||||||||||||||||||| ||
                                ACCATACCTACGGGAGGACCC AA
                                          G
GAM312  ANP32B   3'  AACCCCAGGACACCCACCCACC 22149    TA   A  CCC_
           CA                     TGG  TGG TG   TCCTGGGGTT
                                |||  ||| ||   ||||||||||
                                ACC  ACC AC   AGGACCCCAA
                                  C_   C  CCAC
GAM312  BTN2A2   3'  AACCCCAGGATTTCCACAGC   23769    A_   TGCCC
                                GT  TGGA    TCCTGGGGTT
                                ||  ||||    ||||||||||
                                CG  ACCT    AGGACCCCAA
                                 AC    TT___
GAM312  C1orf17   3'  AACCCTCCCAGGCATCCCATAC 68762        _    CTCCT
           CA                     TGGTATGG ATGCC    GGGGTT
                                |||||||| |||||    ||||||
                                ACCATACC TACGG    TCCCAA
                                    C    ACCC_
GAM312  DKFZP434J193 3'  AACCCCAGGCCACCCCCACCA  71553     AT  A  CCCT
                                TGGT  GG TG   CCTGGGGTT
                                ||||  || ||   |||||||||
                                ACCA  CC AC   GGACCCCAA
                                  CC  C  C___
GAM312  DKFZp547I224 5'  CAGAAAGGACATCCACACCA   39952     A    C   C_
                                TGGT TGGATG CCT  CTG
                                |||| |||||| |||  |||
                                ACCA ACCTAC GGA  GAC
                                  C     A   AA
GAM312  FHX      5'  ACCCCAAACTCCAGTACCA   37916      _   TGCCCTCC
                                TGGTA TGGA      TGGGGT
                                ||||| ||||      ||||||
                                ACCAT ACCT      ACCCCA
                                  G   CAA_____
GAM312  FLJ32389  3'  ACCCCAGCCAGCCACACCA   58839     A  A  CCCTC
                                TGGT TGG TG    CTGGGGT
                                |||| ||| ||    |||||||
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                                ACCA ACC AC    GACCCCA
                                  C   G  C____
GAM312  MGC12466  3'  ACCCCAGATTCCAATACCA   79793      _  TGCCCTC
                                TGGTAT GGA     CTGGGGT
                                ||||||| |||     |||||||
                                ACCATA CCT     GACCCCA
                                   A   TA_____
GAM312  NYD-SP12  3'  AGGCAAGGGCATCCACTCCA  50070    TA       __
                                TGG  TGGATGCCCT  CCT
                                |||  ||||||||||  |||
                                ACC  ACCTACGGGA  GGA
                                  TC        AC
GAM312  LOC145801 3'  AACCCCAGGACACCCACCCACC 77965    TA   A  CCC_
          CA                    TGG  TGG TG   TCCTGGGGTT
                                |||  ||| ||   ||||||||||
                                ACC  ACC AC   AGGACCCCAA
                                  C_   C  CCAC
GAM312  LOC146713 3'  AACCCCAAGGTCCCCCACCCCA 84718    TA   ATGC   CC
                                TGG  TGG   CCT  TGGGGTT
                                |||  |||   |||  |||||||
                                ACC  ACC   GGA  ACCCCAA
                                  CC   CCCT   __
GAM312  LOC154007 3'  TTCAGAGGAATCCATACCA   81934        GC   C
                                TGGTATGGAT  CCTC TGGG
                                ||||||||||  |||| ||||
                                ACCATACCTA  GGAG ACTT
                                     A_   _
GAM312  LOC161734 3'  CAGAAAGGACATCCACACCA   88462     A    C   C_
                                TGGT TGGATG CCT  CTG
                                |||| |||||| |||  |||
                                ACCA ACCTAC GGA  GAC
                                  C     A   AA
GAM312  LOC169181 5'  GCCCCAAGAGGACCCCATACCA 83609       ATGC   C
                                TGGTATGG   CCTC TGGGGT
                                ||||||||   |||| ||||||
                                ACCATACC   GGAG ACCCCG
                                     CCA_   A
GAM312  LOC221069 5'  AACCCCAGAAGGCCGACACA   94814    _ A   ATGC   C
                                TG GT TGG   CCT CTGGGGTT
                                || || |||   ||| ||||||||
                                AC CA GCC   GGA GACCCCAA
                                 A  _  ____   A
GAM312  LOC255743 5'  AACCCCAGAAAGGCCAACCACC 97599    AT  A  C   C_
                                GGT  GG TG CCT  CTGGGGTT
                                |||  || || |||  ||||||||
                                CCA  CC AC GGA  GACCCCAA
                                  __  A  C   AA
GAM312  LOC90593  3'  CAGAAAGGACAACCACACCA   64203     A   A  C   C_
                                TGGT TGG TG CCT  CTG
                                |||| ||| || |||  |||
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                                ACCA ACC AC GGA  GAC
                                  C   A A   AA
GAM312  LOC92080  3'  GGGAGGGCACCCACCCA     68632     TA   A
                                TGG  TGG TGCCCTCCT
                                |||  ||| |||||||||
                                ACC  ACC ACGGGAGGG
                                  C_   C
GAM313  IGSF6     3'  CACTGAAAATCCAACTCCAGG  20718     C__    C
                                CTTG   TTGGA TTTCAGTG
                                ||||   ||||| ||||||||
                                GGAC   AACCT AAAGTCAC
                                  CTC    A
GAM313  ILF1      3'  CACTGAAAACCCAAAACCCAGC 16917     TGC__   AC
                                GCT    TTGG  TTTCAGTG
                                |||    ||||  ||||||||
                                CGA    AACC  AAAGTCAC
                                  CCCAA   CA
GAM313  NDUFV3    5'  CACTGAAAGCCTGGTGAGCAGA 41139     A   TG  T  A
                                TCT GCT  CT GG CTTTCAGTG
                                ||| |||  || || |||||||||
                                AGA CGA  GG CC GAAAGTCAC
                                  _  GT  T  _
GAM313  RENT1     3'  CACCGAAAGCCCAAATTGGGAG 12809     GC___   A    A
          C                      GCTT    TTGG CTTTC GTG
                                ||||    |||| ||||| |||
                                CGAG    AACC GAAAG CAC
                                  GGTTA   C    C
GAM313  YES1      3'  AGGGTCCAAACAAAATAGA   19528     GC   C
                                TCTA  TTG TTGGACTTT
                                ||||  ||| |||||||||
                                AGAT  AAC AACCTGGGA
                                  AA   A
GAM313  ERp44     3'  CACTGAGGACAAGGAAACTA  82603     C  G   GA TT
                                TAG TT CTTG  C  TCAGTG
                                ||| || ||||  |  ||||||
                                ATC AA GAAC  G  AGTCAC
                                  A  G   AG __
GAM313  MAP2K5    3'  CACTGAAAGCCCAGGACCAGT  12324     TG_    A
                                GCT   CTTGG CTTTCAGTG
                                |||   ||||| |||||||||
                                TGA   GGACC GAAAGTCAC
                                  CCA    C
GAM313  RAB40A    3'  CACCAAAAGGAAACAAGCTGGA 82943         C  GGA   CA
                                TCTAGCTTG TT   CTTT  GTG
                                ||||||||| ||   ||||  |||
                                AGGTCGAAC AA   GAAA  CAC
                                      _ AG_   AC
GAM313  LOC145439 5'  CACTGAAAGCAAGGAAAGCCTG 77724    TA   G_   GA
          A                     TC  GCTT  CTTG  CTTTCAGTG
                                ||  ||||  ||||  |||||||||
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                                AG  CGAA  GAAC  GAAAGTCAC
                                 TC    AG   __
GAM313  LOC63928  3'  CACTGAAAACCCAACTCAA   42267     C_   AC
                                TTG  TTGG  TTTCAGTG
                                |||  ||||  ||||||||
                                AAC  AACC  AAAGTCAC
                                  TC    CA
GAM313  LOC90231  3'  CACTGAAAGTCCCGCTGCCAGG 62528     A  TT  TT
                                TCT GC  GC  GGACTTTCAGTG
                                ||| ||  ||  ||||||||||||
                                GGA CG  CG  CCTGAAAGTCAC
                                  C  T_  C_
GAM314  MGA     3'  GGAAGAACTTCTGAAAATTGC  63467    TG__
                                GC    TTCAGAAGTTCTTCC
                                ||    ||||||||||||||||
                                CG    AAGTCTTCAAGAAGG
                                 TTAA
GAM314  MMP15    3'  ACTTCTGACAGCCTCAG     11610      A     T
                                CTGA GCTGT CAGAAGT
                                |||| ||||| |||||||
                                GACT CGACA GTCTTCA
                                  C     _
GAM314  NAGA     5'  GAAGAACTCAAGCTCCGG    6037      A    GTTCAGA
                                CTG AGCT      AGTTCTTC
                                ||| ||||      ||||||||
                                GGC TCGA      TCAAGAAG
                                  C    AC_____
GAM314  RBL2     3'  GAAGAACTGTGTTTCAAGTTCA 20040      GC  TT_  GA
                                TGAA  TG   CA  AGTTCTTC
                                ||||  ||   ||  ||||||||
                                ACTT  AC   GT  TCAAGAAG
                                  GA  TTT  G_
GAM314  SCN1A    5'  GGACCTGACAGCTTCA      90267         T   AA
                                TGAAGCTGT CAG  GTTC
                                ||||||||| |||  ||||
                                ACTTCGACA GTC  CAGG
                                          _  __
GAM314  SNRPN    5'  AGAACACTTAACAGCTTCAG   43318           C  AA
                                CTGAAGCTGTT AG  GTTCT
                                |||||||||| ||  |||||
                                GACTTCGACAA TC  CAAGA
                                       T  A_
GAM314  C20orf31  5'  GGAAGAACCCGCAGCAGCTCCC 37178     A_      CAGAA
           AG                    CTG  AGCTGTT    GTTCTTCC
                                |||  |||||||    ||||||||
                                GAC  TCGACGA    CAAGAAGG
                                  CC      CGCC_
GAM314  CNK2     3'  AAGAGAGGGATCAGCTTCA   76491         T  AGAAG
                                TGAAGCTG TC    TTCTT
                                |||||||| ||    |||||
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                                ACTTCGAC AG    GAGAA
                                    T  GGA__
GAM314  CRK7     3'  GGAAGAGAGAAAGAACAGTTTC 33666          AGAAG
            AG                   CTGAAGCTGTTC    TTCTTCC
                                 ||||||||||||    |||||||
                                 GACTTTGACAAG    GAGAAGG
                                       AAAGA
GAM314  FLJ10300 5'  GGAAGAACTTCCTCTAGCTCA 36473    A   TTCA
                                 TGA GCTG   GAAGTTCTTCC
                                 ||| ||||   ||||||||||
                                 ACT CGAT   CTTCAAGAAGG
                                   _   CTC_
GAM314  FLJ11259 3'  GAAGAACTTCTGGGTTCAG   37766     AGCT TT
                                 CTGA   G  CAGAAGTTCTTC
                                 ||||   |  ||||||||||||
                                 GACT   T  GTCTTCAAGAAG
                                   _____ GG
GAM314  FLJ14356 5'  AAGAACTTGGGCAACTCGAG  48779   GA  C    GA
                                 CT  AG TGTTCA  AGTTCTT
                                 ||  || ||||||  |||||||
                                 GA  TC ACGGGT  TCAAGAA
                                  GC  A     __
GAM314  FLJ21588 3'  AACCCCTCAACAGCCTCAG   50803     A     C  AA
                                 CTGA GCTGTT AG  GTT
                                 |||| |||||| ||  |||
                                 GACT CGACAA TC  CAA
                                   C     C  CC
GAM314  FLJ22477 3'  GAAGAGGCGAACAGCTCAG   45674     A     AGAAG
                                 CTGA GCTGTTC    TTCTTC
                                 |||| |||||||    ||||||
                                 GACT CGACAAG    GAGAAG
                                   _      CG___
GAM314  KIAA0061 3'  AAGAACTTCTGGAAACTTC   68834     CTG
                                 GAAG   TTCAGAAGTTCTT
                                 ||||   ||||||||||||||
                                 CTTC   AGGTCTTCAAGAA
                                   AA_
GAM314  KIAA0171 3'  AACTTCTGTTTGTTTTTAG   28547      CT TT
                                 CTGAAG  G  CAGAAGTT
                                 ||||||  |  ||||||||
                                 GATTTT  T  GTCTTCAA
                                    TG TT
GAM314  KIAA1219 3'  AGATCTGTCTGAAAGCCTCAG  62026     A  G    _  T
                                 CTGA GCT TTCAGA AG TCT
                                 |||| ||| |||||| || |||
                                 GACT CGA AAGTCT TC AGA
                                   C  _     G  T
GAM314  KIAA1600 3'  AAGATTATGAATAGCCTCAG   71937     A      GAAGT
                                 CTGA GCTGTTCA    TCTT
                                 |||| ||||||||    ||||
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                                GACT CGATAAGT     AGAA
                                  C       ATT__
GAM314  KIAA1918  3'  AAGAATTTTTAAACAATCTTCA 73533       C_    C
            G                    CTGAAG  TGTT AGAAGTTCTT
                                 ||||||  |||| ||||||||||
                                 GACTTC  ACAA TTTTTAAGAA
                                    TA    A
GAM314  MAP2K6    5'  AAGAAGCATTTGAACAACCTCA 50078      AGC       A  _
            G                    CTGA   TGTTCAGA GTT CTT
                                 ||||   |||||||| ||| |||
                                 GACT   ACAAGTTT CGA GAA
                                   CCA       A   A
GAM314  MAPK8IP3  3'  GGACTTGTTTCTGAACAGCCAC 54142    AA        _____
            A                    TG  GCTGTTCAGA    AGTTC
                                 ||  ||||||||||    |||||
                                 AC  CGACAAGTCT    TCAGG
                                  AC         TTGT
GAM314  MCM10     3'  AATTTCTGAACAGCCTTA     38173     A
                                 TGA GCTGTTCAGAAGTT
                                 ||| ||||||||||||||
                                 ATT CGACAAGTCTTTAA
                                   C
GAM314  MGC14436  5'  AGAATCGATACTGAACAGCTTC 52919             AA___
            AG                    CTGAAGCTGTTCAG     GTTCT
                                  ||||||||||||||     |||||
                                  GACTTCGACAAGTC     TAAGA
                                        ATAGC
GAM314  PASK      5'  GAAAAACTACAGCTTCA     31410          TCAGA    C
                                 TGAAGCTGT     AGTT TTC
                                 |||||||||     |||| |||
                                 ACTTCGACA     TCAA AAG
                                      _____    A
GAM314  PL6       3'  GGACCAGAACAGCTCCAG     23816     A       AGAA
                                 CTG AGCTGTTC    GTTC
                                 ||| ||||||||    ||||
                                 GAC TCGACAAG    CAGG
                                   C       AC__
GAM314  RRS1      3'  AGAAAACAAACAGTTTCAG    31470          CAGAAG
                                 CTGAAGCTGTT     TTCT
                                 ||||||||||      ||||
                                 GACTTTGACAA     AAGA
                                       ACAA__
GAM314  LOC118491 5'  GGCCTCCAAACAGCTTCAG    74357           CA  A
                                 CTGAAGCTGTT  GA GTT
                                 ||||||||||  ||  |||
                                 GACTTCGACAA  CT CGG
                                       AC  C
GAM314  LOC143173 5'  AACTTCTGTTTATTTCAG     61016       C  TT
                                 CTGAAG TG  CAGAAGTT
                                 ||||||  ||  ||||||||
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                                GACTTT AT  GTCTTCAA
                                   _ TT
GAM314   LOC145384 5'  AGAACCTCCTGAACAGCATC   77710    A       AA_
                                GA GCTGTTCAG   GTTCT
                                || |||||||||   |||||
                                CT CGACAAGTC   CAAGA
                                 A        CTC
GAM314   LOC145824 5'  GGAAATATTTCTGACCAACCCC 77987     AAGC  T       TC
           AG                     CTG    TG TCAGAAGT  TTCC
                                |||    || ||||||||  ||||
                                GAC    AC AGTCTTTA  AAGG
                                  CCCA  C       TA
GAM314   LOC146056 3'  GAAGAGAAGCAACAGCTTCA   78078          CAGAAG
                                TGAAGCTGTT     TTCTTC
                                ||||||||||     ||||||
                                ACTTCGACAA     GAGAAG
                                      CGAA__
GAM314   LOC147004 5'  AGAAAATGAACAGCTTCA    84964           GAAG
                                TGAAGCTGTTCA    TTCT
                                ||||||||||||    ||||
                                ACTTCGACAAGT    AAGA
                                      AA__
GAM314   LOC151996 3'  AAGAACTTCCAAACTCAG    86712      AGCT   CA
                                CTGA    GTT  GAAGTTCTT
                                ||||    |||  |||||||||
                                GACT    CAA  CTTCAAGAA
                                  _____  AC
GAM314   LOC152190 5'  GAAGAACTAAAGGATAACTTCA 70235       C     AGA
                                TGAAG TGTTC   AGTTCTTC
                                ||||| |||||   ||||||||
                                ACTTC ATAGG   TCAAGAAG
                                   A     AAA
GAM314   LOC154007 3'  GAAAGGCGATCAGCTTCAG    81926         T  AGAA  TC
                                CTGAAGCTG TC    GT  TTC
                                ||||||||| ||    ||  |||
                                GACTTCGAC AG    CG  AAG
                                      T _____  GA
GAM314   LOC154790 5'  AAGAACTTCCCAGCAGTTCAG  82036       G     CA
                                CTGAA CTGTT  GAAGTTCTT
                                ||||| |||||  |||||||||
                                GACTT GACGA  CTTCAAGAA
                                   _     CC
GAM314   LOC199907 3'  GGAAGAATATGAACAGCTTTA  89830           GAA
                                TGAAGCTGTTCA   GTTCTTCC
                                ||||||||||||   ||||||||
                                ATTTCGACAAGT   TAAGAAGG
                                      A__
GAM314   LOC200235 3'  GGATTCTGAACAAACTCAG    91570      AGC        G
                                CTGA   TGTTCAGAA TTC
                                ||||   ||||||||| |||
```

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                                GACT   ACAAGTCTT AGG
                                  CAA       _
GAM314  LOC200448 5'  AAGGTAACAGCTTCAG      90245          CAGAAGT
                                CTGAAGCTGTT      TCTT
                                ||||||||||       ||||
                                GACTTCGACAA      GGAA
                                      T_______
GAM314  LOC201164 3'  GGAAGAGGAGAGCAGCTTCAG  89498          AGAAG
                                CTGAAGCTGTTC    TTCTTCC
                                ||||||||||||    |||||||
                                GACTTCGACGAG    GAGAAGG
                                      AG___
GAM314  LOC56902  3'  AGAAACCATCTGAACAATTTCA 39716       C       AG__
          G                      CTGAAG TGTTCAGA    TTCT
                                ||||||| ||||||||    ||||
                                GACTTT ACAAGTCT    AAGA
                                   A       ACCA
GAM315  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT    98090      T    AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||     ||||||
                                TGGTG GGGT     TTATTC
                                  _    GTCA_
GAM316  ATF7     3'  TCCCAGCCCCGGAGCCTCATA  23404        _  TAGA   CC
                                TATGAGGC CC    GCT  GGGA
                                |||||||| ||    |||  ||||
                                ATACTCCG GG    CGA  CCCT
                                     A  CCC_  __
GAM316  CREBBP   5'  CCCGCCGGTCCCGGGCCCCA   16495    A    TA  G  C_
                                TG GGCCC  GA CT  CGGG
                                || |||||  || ||  ||||
                                AC CCGGG  CT GG  GCCC
                                 C     CC  _  CC
GAM316  EGLN2    5'  TTGGGGCTCCAGAACCTC    54926      CC  A
                                GAGG  CT GAGCTCCGG
                                ||||  || |||||||||
                                CTCC  GA CTCGGGGTT
                                  AA  C
GAM316  GNA11    5'  CCCAGTGACTCTGGGCCTCA   10810        T    C  C__
                                TGAGGCCC AGAG TC   GGG
                                |||||||| |||| ||   |||
                                ACTCCGGG TCTC AG   CCC
                                     _    _  TGA
GAM316  LATS2    3'  GTCCCGGAGCCGGTGCCCTCA  28135       _ _  TAGA
                                TGAGG C CC    GCTCCGGGAC
                                ||||| | ||    ||||||||||
                                ACTCC G GG    CGAGGCCCTG
                                  C T  C___
GAM316  NLGN3    3'  GTCTCTCTGGCTCTAGGACC   39121    C       CC_
                                GG CCTAGAGCT   GGGAC
                                || |||||||||   |||||
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                                CC GGATCTCGG  CTCTG
                                 A       TCT
GAM316  NOTCH1   5' GTCCCGGAGCCCCAAGTGCTT 92138     C  AGA_
                                AGGC CT   GCTCCGGGAC
                                |||| ||   ||||||||||
                                TTCG GA   CGAGGCCCTG
                                  T  ACCC
GAM316  RBBP9    3' TCCGGAGTCTAGAGCCCCA   70699    A  C    G
                                TG GGC CTAGA CTCCGGG
                                || ||| ||||| |||||||
                                AC CCG GATCT GAGGCCT
                                 C  A    _
GAM316  UBQLN1   5' CCGAGCTCCGGGGCCCCA    26473    A    TA    C
                                TG GGCCC  GAGCTC GG
                                || |||||  |||||| ||
                                AC CCGGG  CTCGAG CC
                                 C    GC    _
GAM316  ARTN     5' CCCGGGCCTGGAGCCCCA    15612    A  C   A  T
                                TG GGC CTAG GC CCGGG
                                || ||| |||| || |||||
                                AC CCG GGTC CG GGCCC
                                 C  A   _ _
GAM316  CNTNAP1  3' CCCAAAGGAGAAGCCTCATG  14641       CCTAGAG   ___
                                TATGAGGC     CTCC  GGG
                                ||||||||     ||||  |||
                                GTACTCCG     GAGG  CCC
                                    AA_____   AAA
GAM316  FLJ10898 5' CCCCAAGCCAGGCACAGCCTCA 60130       ____  AGA  CC
           TA                    TATGAGGC   CCT  GCT  GGG
                                ||||||||   |||  |||  |||
                                ATACTCCG   GGA  CGA  CCC
                                    ACAC  C__  AC
GAM316  KIAA1977 5' CGAAGGCTCAGGGCCTCA   74765       A    C_
                                TGAGGCCCT GAGCT  CG
                                ||||||||| |||||  ||
                                ACTCCGGGA CTCGG  GC
                                    _    AA
GAM316  P24B     3' TCCTGCTCTAGGGCCCCTCA  24774    __       TCC
                                TGA  GGCCCTAGAGC  GGGA
                                |||  ||||||||||  ||||
                                ACT  CCGGGATCTCG  TCCT
                                  CC        ___
GAM316  LOC146669 3' GTCTTTCTCCAGGGGCCTCA  78664       A_  CTCC
                                TGAGGCCCT  GAG   GGGAC
                                |||||||||  |||   |||||
                                ACTCCGGGG  CTC   TTCTG
                                    AC  T___
GAM316  LOC170127 5' CCCGGAGCCCCAGGGGCCCA  83456    A    AGA_
                                TG GGCCCT   GCTCCGGG
                                || ||||||   ||||||||
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                                AC CCGGGG   CGAGGCCC
                                 _    ACCC
GAM316  LOC256812 5'  CCCGGAGCCCCCTGGGCCCCA  99406   A    TAGA_
                                TG GGCCC    GCTCCGGG
                                || |||||    ||||||||
                                AC CCGGG    CGAGGCCC
                                 C    TCCCC
GAM316  LOC90408  5'  CCCCTCTCCGAGGCCTCATA  63342       CTA  CTCC
                                TATGAGGCC  GAG   GGG
                                |||||||||  |||   |||
                                ATACTCCGG  CTC   CCC
                                     AGC  TC__
GAM317  ADORA2A   3'  TGGAGCAGCATGAGGCCCAGCA 7278      C   TT    _
                                TGCTG GGCC  TCATGC GCTCCA
                                ||||| ||||  |||||| ||||||
                                ACGAC CCGG  AGTACG CGAGGT
                                  _   __     A
GAM317  BUB1B     5'  GAGGAAAGGCCTGCAGCA    8673       _     ATGCG
                                TGCTGC GGCCTTTC    CTC
                                |||||| ||||||||    |||
                                ACGACG CCGGAAAG    GAG
                                   T      _____
GAM317  H1F5      3'  GGCGTGTGAAAACCGCAACA   19221    C    CC
                                TG TGCGG  TTTCATGCGCT
                                || |||||  ||||||||||
                                AC ACGCC  AAAGTGTGCGG
                                 A    A_
GAM317  IRS2      5'  GGAGCGCGACGCGGCGGCAGCA 60441      G   TTTCA
                                TGCTGC GCC    TGCGCTCC
                                |||||| |||    ||||||||
                                ACGACG CGG    GCGCGAGG
                                   G   CGCA_
GAM317  ITGA6     5'  GGAGCGCAGGGCGGCCGCTGCA 5791     T    T   A
                                TGC GCGGCC TTC TGCGCTCC
                                ||| |||||| ||| ||||||||
                                ACG CGCCGG GGG ACGCGAGG
                                  T    C   _
GAM317  RLN1      5'  AGTCCTGAAAGGCTGCAACA   23580    C        TGC
                                TG TGCGGCCTTTCA   GCT
                                || ||||||||||||   |||
                                AC ACGTCGGAAAGT   TGA
                                 A          CC_
GAM317  UGCG      5'  GAGCCGGGAGACCGCAGCA    13984       C  TT AT C
                                TGCTGCGG CT  C  G GCTC
                                |||||||| ||  |  | ||||
                                ACGACGCC GA  G  C CGAG
                                     A  GG __ _
GAM317  FLJ22173  5'  GGGGCAAAAGGCCACAG     47400     C     CATGC
                                CTG GGCCTTT    GCTCC
                                ||| |||||||    |||||
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                                GAC CCGGAAA    CGGGG
                                  A      A____
GAM317  HSMPP8   3'  GAGCCGTGAAAGGCCACTGCA  95136    TGC        C
                                TGC   GGCCTTTCATG GCTC
                                |||   |||||||||||| ||||
                                ACG   CCGGAAAGTGC CGAG
                                  TCA         _
GAM317  KIAA1276 5'  TGGAGCACAGAGGCCGCA    67034        TCA  C
                                TGCGGCCTT   TG GCTCCA
                                |||||||||   || ||||||
                                ACGCCGGAG   AC CGAGGT
                                     ___ A
GAM317  KIAA1655 3'  GAGAGAGGAAAGGCCACACA   67188    C  C      ATGCG
                                TG TG GGCCTTTC    CTC
                                || || ||||||||    |||
                                AC AC CCGGAAAG    GAG
                                 _ A       GAGA_
GAM317  MGC11349 5'  GAGCATCTGAAAGGCCACAGCA 47790      C       TGC
                                TGCTG GGCCTTTCA   GCTC
                                ||||| |||||||||   ||||
                                ACGAC CCGGAAAGT   CGAG
                                   A        CTA
GAM317  My015    3'  GGATCTCTGAAAGGCCACAGC  67232     C       TGCGC
                                GCTG GGCCTTTCA    TCC
                                |||| |||||||||    |||
                                CGAC CCGGAAAGT    AGG
                                  A        CTCT_
GAM317  LOC255833 3'  GGCGTGTGAAAACCGCAACA   96284    C    CC
                                TG TGCGG  TTTCATGCGCT
                                || |||||  ||||||||||
                                AC ACGCC  AAAGTGTGCGG
                                 A    A_
GAM318  ABCA2    5'  CCCGGACGCCCGAGCGCCCCGC 97877     AT    CAA_
            CC                    GGGC  GGGT   GGGCGTCCGGG
                                ||||  ||||   ||||||||||
                                CCCG  CCCG   CCCGCAGGCCC
                                  C_   CGAG
GAM318  ADCY1    5'  CCAAGACTGACCATGCCC    94338        G  AGGGC  C_
                                GGGCATGG TCA    GTC  GG
                                |||||||| |||    |||  ||
                                CCCGTACC AGT    CAG  CC
                                     _  _____  AA
GAM318  ALPPL2   3'  CCGAGCCCTTGACACCACGCCC 69426     A  _      GTC
                                GGGC TGG GTCAAGGGC   CGG
                                |||| ||| |||||||||   |||
                                CCCG ACC CAGTTCCCG   GCC
                                  C  A       A__
GAM318  ATBF1    5'  CCCGGACGCCAGCGCCGCGCCC 23527     A  _  CAAG
                                GGGC TGG GT    GGCGTCCGGG
                                |||| ||| ||    ||||||||||
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                                CCCG GCC CG   CCGCAGGCCC
                                  C  G  A___
GAM318  ATP11A   3'  CCGGCCACCACCCATGCCC   77554          CAA  GC T
                                GGGCATGGGT  GG  G CCGG
                                ||||||||||  ||  | ||||
                                CCCGTACCCA  CC  C GGCC
                                    ____ AC _
GAM318  FZD1     3'  CCCGGGGCTCAGCCCATGCCC  14497          CAA   G
                                GGGCATGGGT  GGGC TCCGGG
                                ||||||||||  |||| ||||||
                                CCCGTACCCG  CTCG GGGCCC
                                    A__   _
GAM318  GAMT     3'  CCGGCCACACCCATGCCC    57983          CAAG  GTC
                                GGGCATGGGT   GGC  CGG
                                ||||||||||   |||  |||
                                CCCGTACCCA   CCG  GCC
                                    CA__  ___
GAM318  GPX4     3'  CCCGAGCCCCTGCCCACGCCC  10869     A    CA   C TC
                                GGGC TGGGT  AGGG G  CGGG
                                |||| |||||  |||| |  ||||
                                CCCG ACCCG  TCCC C  GCCC
                                  C    __   _ GA
GAM318  HOXC4    3'  CCCTGCCCCCACCCCATGCCC  28246        TCAA   TCC
                                GGGCATGGG   GGGCG  GGG
                                |||||||||   |||||  |||
                                CCCGTACCC   CCCGT  CCC
                                    CACC   ___
GAM318  KIP2     3'  TCCGCACCCCGCCCCATGCCC  22121        TCAA  C  C
                                GGGCATGGG   GGG GT CGGG
                                |||||||||   ||| || ||||
                                CCCGTACCC   CCC CA GCCT
                                    CG__  _  C
GAM318  LARGE    5'  CCGAGGCTGACCCAGGCCC   56926     A     AGG  G  C
                                GGGC TGGGTCA  GC TC GG
                                |||| |||||||  || || ||
                                CCCG ACCCAGT  CG AG CC
                                  G     ___  G  _
GAM318  LARGE    5'  CCGAGGCTGACCCAGGCCC   56927     A     AGG  G  C
                                GGGC TGGGTCA  GC TC GG
                                |||| |||||||  || || ||
                                CCCG ACCCAGT  CG AG CC
                                  G     ___  G  _
GAM318  LASS1    3'  CCCTCGCTGCCCCTGACCCGCG 41474     A     A   _ CC
            CCC                   GGGC TGGGTCA GGGC GT  GGG
                                |||| ||||||| |||| ||  |||
                                CCCG GCCCAGT CCCG CG  CCC
                                  C     C   T  CT
GAM318  MUCDHL   5'  CCCGGACACCCTCTCAGCTCCT 88638      T   CA__   C
            GCCC                   GGGCA GGGT   AGGG GTCCGGG
                                ||||| ||||   |||| |||||||
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                                CCCGT CTCG   TCCC CAGGCCC
                                  C   ACTC   A
GAM318  MYO1D    3'  TGCCTCCCAACCCATGCCC   72251        CAA_
                                GGGCATGGGT   GGGCG
                                ||||||||||   |||||
                                CCCGTACCCA   TCCGT
                                     ACCC
GAM318  SOST     3'  CCTCCCCCGACCCATAGCC   48224    _     AA  CGTCC
                                GGC ATGGGTC  GGG    GG
                                ||| |||||||  |||    ||
                                CCG TACCCAG  CCC    CC
                                 A     CC  T____
GAM318  FLJ20080 5'  CCCGGGCCCCTGAGCCATGCCC 34984       G  A  C
                                GGGCATGG TCA GGG GTCCGGG
                                |||||||| ||| ||| |||||||
                                CCCGTACC AGT CCC CGGGCCC
                                     G  _  _
GAM318  FLJ20308 3'  CCCAGGCGTCCTCCACCCACGC 67390     A   CA     C
           CC                    GGGC TGGGT  AGGGCGTC GGG
                                ||||| |||||  |||||||| |||
                                CCCG ACCCA  TCCTGCGG CCC
                                  C    CC      A
GAM318  FLJ20489 3'  CCCAAACCTGTGCCCATGCCC  35710        CA  GCGTCC
                                GGGCATGGGT  AGG    GGG
                                ||||||||||  |||    |||
                                CCCGTACCCG  TCC    CCC
                                     TG  AAA___
GAM318  IL-17RC  3'  CCGGACGCCGTACCCGCCC   52178    AT   CAAG
                                GGGC  GGGT   GGCGTCCGG
                                ||||  ||||   |||||||||
                                CCCG  CCCA   CCGCAGGCC
                                  __   TG__
GAM318  KIAA0450 5'  CCAGCCCCTTGTCCCATGCCC  28343       T    C  CC
                                GGGCATGGG CAAGGG GT  GG
                                ||||||||| |||||| ||  ||
                                CCCGTACCC GTTCCC CG  CC
                                     T    _  A_
GAM318  KIAA0964 3'  CCCATCTGCTCACCCATGCCC  30446        CAA   TCC
                                GGGCATGGGT  GGGCG  GGG
                                ||||||||||  |||||  |||
                                CCCGTACCCA  CTCGT  CCC
                                     ___    CTA
GAM318  KIS      5'  CCGTGCCCTTAACCCACACC  58884   CA   C     TC
                                GG  TGGGT AAGGGCG  CGG
                                ||  ||||| |||||||  |||
                                CC  ACCCA TTCCCGT  GCC
                                 AC   A     __
GAM318  PAPA-1   3'  CCCGGACTCTGCGCCCCGTCCC 49262        TCAA  _____
           ATGCCC                GGGCATGGG   GGGC   GTCCGGG
                                |||||||||   ||||   |||||||
```

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                                CCCGTACCC  CCCG   CAGGCCC
                                    TGC_  CGTCT
GAM318  TOLLIP   3'  CCCAGACGAAAACTCACGCCC  39193     A   CAAGGG   C
                                GGGC TGGGT    CGTC GGG
                                |||| |||||    |||| |||
                                CCCG ACTCA    GCAG CCC
                                  C    AAA___   A
GAM318  LOC148046 3'  CCCAGACGCGGGCGCCACATGC 85244       _  CAAGG   C
          CC                    GGGCATG GGT   GCGTC GGG
                                ||||||| |||    ||||| |||
                                CCCGTAC CCG    CGCAG CCC
                                   A  CGGG_   A
GAM319  ADAM17   3'  CACTCCAGCCTGGGTGACAGAG 41844       TG
          TG                    CACTTTGT  CCCAGGCTGGAGTG
                                ||||||||  ||||||||||||||
                                GTGAGACA  GGGTCCGACCTCAC
                                    GT
GAM319  ADAM17   3'  CACTCCAGCCTGGGTGACAGAG 13510       TG
          TG                    CACTTTGT  CCCAGGCTGGAGTG
                                ||||||||  ||||||||||||||
                                GTGAGACA  GGGTCCGACCTCAC
                                    GT
GAM319  ADAT1    3'  CACTCCAGCCTGGGTGATAGAG 24911      TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGATA  GGGTCCGACCTCAC
                                   GT
GAM319  ADCY2    3'  CACTCCAGCCTGGGTGACAGAG 65644      TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  AICDA    3'  CACTCCAGCCTGGGCGACAAG  40689
                                TTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||
                                GAACAGCGGGTCCGACCTCAC

GAM319  AK1      3'  CACTCCAGCCTGGGTGACAGAG 6632       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  ALDH3A2  3'  CAGCCTGGACAACACAGTG   69797     T   C
                                CACT TGTTG CCAGGCTG
                                |||| ||||| ||||||||
                                GTGA ACAAC GGTCCGAC
                                  C    A
GAM319  ANKH     3'  CACTCCAGCCTGGGTGACAAG  55064     TG
                                TTTGT  CCCAGGCTGGAGTG
                                |||||  ||||||||||||||
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                                GAACA  GGGTCCGACCTCAC
                                   GT
GAM319  APBA2    3'  ACCCCAGCCTGGCCACGCA   19737    _ C       A
                                TGT TG CCAGGCTGG GT
                                ||| || ||||||||| ||
                                ACG AC GGTCCGACC CA
                                  C C       C
GAM319  APOL1    3'  CACTCCAGCCTGGGTGACAGAG 14730       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  ARHGEF6  3'  ACTCCAACCTAGGTAACA    68750       C   C
                                TGTTGCC AGG TGGAGT
                                ||||||| ||| ||||||
                                ACAATGG TCC ACCTCA
                                     A   A
GAM319  ARSD     3'  CAGCCTGGGCAACATAGTG   24810     T
                                CACT TGTTGCCCAGGCTG
                                |||| ||||||||||||||
                                GTGA ACAACGGGTCCGAC
                                   T
GAM319  ATF5     3'  CAGCCTGGGCAACATAGT    24817     T
                                ACT TGTTGCCCAGGCTG
                                ||| ||||||||||||||
                                TGA ACAACGGGTCCGAC
                                  T
GAM319  ATM      3'  CACTCCAGCCTGGGTGACAAG  57131      TG
                                TTTGT  CCCAGGCTGGAGTG
                                |||||  ||||||||||||||
                                GAACA  GGGTCCGACCTCAC
                                   GT
GAM319  ATM      3'  CACTCCAGCCTGGGAGACAGAG 57142       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GA
GAM319  ATM      3'  CACTCCAGCCTGGGTGACAAG  5291       TG
                                TTTGT  CCCAGGCTGGAGTG
                                |||||  ||||||||||||||
                                GAACA  GGGTCCGACCTCAC
                                   GT
GAM319  ATP1A2   3'  CACTCCAGCCTGGGCGAAAGG  7358      G
                                CTTT TTGCCCAGGCTGGAGTG
                                |||| ||||||||||||||||
                                GGAA AGCGGGTCCGACCTCAC
                                  _
GAM319  BACH2    3'  CACTCCAGCCCGGCTGGGGAAG 41777     G _  CA
                                CTTT TT GCC  GGCTGGAGTG
                                |||| || |||  ||||||||||
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                                GAAG GG CGG  CCGACCTCAC
                                  G T  C_
GAM319  BPHL    3' CACTCCAACCTGGGCAACAGAG 16333          C
             T                  ACTTTGTTGCCCAGG TGGAGTG
                                ||||||||||||||| |||||||
                                TGAGACAACGGGTCC ACCTCAC
                                        A
GAM319  BRCA1   3' CACTCCAGCCTGGGTGACAGTG 24445    TT TG
                                CACT GT CCCAGGCTGGAGTG
                                |||| || ||||||||||||||
                                GTGA CA GGGTCCGACCTCAC
                                  __ GT
GAM319  BRCA1   5' CACTCCAGCCTGGGCGACAGAG 24455
                                CTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319  BRCA1   3' CACTCCAGCCTGGGTGACAGTG 24456    TT TG
                                CACT GT CCCAGGCTGGAGTG
                                |||| || ||||||||||||||
                                GTGA CA GGGTCCGACCTCAC
                                  __ GT
GAM319  BRCA1   3' CACTCCAGCCTGGGTGACAGTG 24468    TT TG
                                CACT GT CCCAGGCTGGAGTG
                                |||| || ||||||||||||||
                                GTGA CA GGGTCCGACCTCAC
                                  __ GT
GAM319  BRCA1   3' CACTCCAGCCTGGGTGACAGTG 24477    TT TG
                                CACT GT CCCAGGCTGGAGTG
                                |||| || ||||||||||||||
                                GTGA CA GGGTCCGACCTCAC
                                  __ GT
GAM319  BRCA1   3' CACTCCAGCCTGGGTGACAGTG 24485    TT TG
                                CACT GT CCCAGGCTGGAGTG
                                |||| || ||||||||||||||
                                GTGA CA GGGTCCGACCTCAC
                                  __ GT
GAM319  BRCA1   3' CACTCCAGCCTGGGTGACAGTG 24493    TT TG
                                CACT GT CCCAGGCTGGAGTG
                                |||| || ||||||||||||||
                                GTGA CA GGGTCCGACCTCAC
                                  __ GT
GAM319  BRCA1   3' CACTCCAGCCTGGGTGACAGTG 24502    TT TG
                                CACT GT CCCAGGCTGGAGTG
                                |||| || ||||||||||||||
                                GTGA CA GGGTCCGACCTCAC
                                  __ GT
GAM319  BRCA1   3' CACTCCAGCCTGGGTGACAGTG 24512    TT TG
                                CACT GT CCCAGGCTGGAGTG
                                |||| || ||||||||||||||
```

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                                GTGA  CA  GGGTCCGACCTCAC
                                  __  GT
GAM319  BRCA1    3'  CACTCCAGCCTGGGTGACAGTG 24520     TT  TG
                                CACT  GT  CCCAGGCTGGAGTG
                                ||||  ||  ||||||||||||||
                                GTGA  CA  GGGTCCGACCTCAC
                                  __  GT
GAM319  BRCA1    3'  CACTCCAGCCTGGGTGACAGTG 24528     TT  TG
                                CACT  GT  CCCAGGCTGGAGTG
                                ||||  ||  ||||||||||||||
                                GTGA  CA  GGGTCCGACCTCAC
                                  __  GT
GAM319  BRCA1    3'  CACTCCAGCCTGGGTGACAGTG 24543     TT  TG
                                CACT  GT  CCCAGGCTGGAGTG
                                ||||  ||  ||||||||||||||
                                GTGA  CA  GGGTCCGACCTCAC
                                  __  GT
GAM319  CARKL    3'  CACTCCAGCCTGGGTGACAGAG 26099       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  CASP6    3'  CACTCCAGCCTGGGCAACGAGT 8730       T
          G                      CACTT GTTGCCCAGGCTGGAGTG
                                 |||||  ||||||||||||||||||
                                 GTGAG CAACGGGTCCGACCTCAC
                                   _
GAM319  CASP6    3'  CACTCCAGCCTGGGCAACGAGT 53362      T
          G                      CACTT GTTGCCCAGGCTGGAGTG
                                 |||||  ||||||||||||||||||
                                 GTGAG CAACGGGTCCGACCTCAC
                                   _
GAM319  CBFA2T2  3'  CACAAAGCCTGGGCAACAGAG  18702            GGA
                                 CTTTGTTGCCCAGGCT  GTG
                                 ||||||||||||||||  |||
                                 GAGACAACGGGTCCGA  CAC
                                          AA_
GAM319  CD68     3'  CACTCCAGCCTGGGCGACAGAG 60502
                                 CTTTGTTGCCCAGGCTGGAGTG
                                 ||||||||||||||||||||||
                                 GAGACAGCGGGTCCGACCTCAC

GAM319  CDA      3'  CACTCCAGCCTGAGTCAGCA  10126      _ C
                                 TGTTG C CAGGCTGGAGTG
                                 |||||  |  ||||||||||||
                                 ACGAC G GTCCGACCTCAC
                                    T A
GAM319  CDH5     3'  CTTTAGCCTGGGCAACAAA   10150
                                 TTTGTTGCCCAGGCTGGAG
                                 |||||||||||||||||||
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                                AAACAACGGGTCCGATTTC

GAM319  CEACAM5  3'  CACTCCAGTCTGGCAACAGAG  16419          C
                                CTTTGTTGCC AGGCTGGAGTG
                                |||||||||| ||||||||||
                                GAGACAACGG TCTGACCTCAC
                                          _
GAM319  CRY2     3'  CTTGAGCCACAAAGTG      72662        TGCCCA   G
                                CACTTTGT     GGCT GAG
                                ||||||||     |||| |||
                                GTGAAACA     CCGA TTC
                                    _______   G
GAM319  CTMP     3'  CACTCCAACCTGGGCAACAGA  54946           C
                                TTTGTTGCCCAGG TGGAGTG
                                |||||||||||| |||||||
                                AGACAACGGGTCC ACCTCAC
                                       A
GAM319  CTNND2   3'  ACTCCTTGTCAACAAAGTG   9022          CC   GCT
                                CACTTTGTTG  CAG   GGAGT
                                ||||||||||  |||   |||||
                                GTGAAACAAC  GTT   CCTCA
                                     T_   ___
GAM319  CYP4F3   3'  CACTCCAGCCTGGGTGAAAGAG 7995       G TG
                                CTTT T  CCCAGGCTGGAGTG
                                |||| |  ||||||||||||||
                                GAGA A  GGGTCCGACCTCAC
                                  A GT
GAM319  DBT      3'  CACTCCAGCCTGGGCGACAGAG 10364
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319  DBT      3'  CACTCCAGCCTGGGTGGCAGAG 10365       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACG  GGGTCCGACCTCAC
                                    GT
GAM319  DBT      3'  CAGCCTGGGCAACATAGTG   10366      T
                                CACT TGTTGCCCAGGCTG
                                |||| ||||||||||||||
                                GTGA ACAACGGGTCCGAC
                                  T
GAM319  DCLRE1C  3'  CACTCCAGCCTGGGCAACAAG  42819
                                TTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||
                                GAACAACGGGTCCGACCTCAC

GAM319  DDOST    3'  CACTCCAGCCTGGGCAACAGTG 19060      TT
                                CACT  GTTGCCCAGGCTGGAGTG
                                ||||  ||||||||||||||||||
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                                GTGA  CAACGGGTCCGACCTCAC
                                  __
GAM319  DFFA    3'  CACTCCAGCCTGGGCAACAGAG 16588
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319  DMC1    3'  CACTCCAGCCTAGGTGACAGAG 23939         TG  C
          TG                      CACTTTGT  CC AGGCTGGAGTG
                                ||||||||  || ||||||||||
                                GTGAGACA  GG TCCGACCTCAC
                                    GT  A
GAM319  DNASE1  5'  CACTCCAGCCTTGGCAACACAG 19070      T      C
          TG                      CACT TGTTGCC AGGCTGGAGTG
                                |||| ||||||| ||||||||||
                                GTGA ACAACGG TCCGACCTCAC
                                  C      T
GAM319  DSC1    3'  CACTCCAGCCTGGGCAACAAG  44599
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAACAACGGGTCCGACCTCAC

GAM319  DSC1    3'  CACTCCAGCCTGGGCAACAAG  18240
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAACAACGGGTCCGACCTCAC

GAM319  DVL3    3'  CACTCCAGCCTGGGTGACAGAG 16639         TG
          TG                      CACTTTGT  CCCAGGCTGGAGTG
                                ||||||||  ||||||||||||||
                                GTGAGACA  GGGTCCGACCTCAC
                                    GT
GAM319  EGFL4   3'  CACTCCAACCTGGGTGACAGAG 62453        TG     C
                                CTTTGT  CCCAGG TGGAGTG
                                ||||||  |||||| |||||||
                                GAGACA  GGGTCC ACCTCAC
                                   GT     A
GAM319  EGFL5   3'  CACTCCAGCCTGGGCGACAGAG 87908
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319  F2RL3   3'  CACTCCAGCCTGGGCAACAGAG 15497
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319  F2RL3   3'  CACTCCAGCCTGGGCGAAAGAG 15498      G
                                CTTT TTGCCCAGGCTGGAGTG
                                |||| ||||||||||||||||
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                                GAGA AGCGGGTCCGACCTCAC
                                  A
GAM319  FANCC    3'  CACTCCAGCCTGGGCAACAGAG 71033
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319  FCAR     3'  CACTCCAGCCTGGGTGACAGA  56631      TG
                                TTTGT  CCCAGGCTGGAGTG
                                |||||  ||||||||||||||
                                AGACA  GGGTCCGACCTCAC
                                   GT
GAM319  FCAR     3'  CACTCCAGCCTGGGTGACAGA  56644      TG
                                TTTGT  CCCAGGCTGGAGTG
                                |||||  ||||||||||||||
                                AGACA  GGGTCCGACCTCAC
                                   GT
GAM319  FGF2     3'  CAGCCTAGGCAACAGAGTG    10614          C
                                CACTTTGTTGCC AGGCTG
                                |||||||||||| ||||||
                                GTGAGACAACGG TCCGAC
                                      A
GAM319  FGFR1    3'  CACTCCAGCCTGGGTGACAGAG 43874        TG
          TG                      CACTTTGT  CCCAGGCTGGAGTG
                                ||||||||  ||||||||||||||
                                GTGAGACA  GGGTCCGACCTCAC
                                     GT
GAM319  FGFR1    3'  CACTCCAGCCTGGGTGACAGAG 43879        TG
          TG                      CACTTTGT  CCCAGGCTGGAGTG
                                ||||||||  ||||||||||||||
                                GTGAGACA  GGGTCCGACCTCAC
                                     GT
GAM319  FLRT2    5'  CACTCCAGCCTAAGCAACAGAG 25992         CC
                                CTTTGTTGC  AGGCTGGAGTG
                                |||||||||  ||||||||||
                                GAGACAACG  TCCGACCTCAC
                                      AA
GAM319  FUT6     3'  CACTCCAACCTGGACGACAGAG 5630          C    C
                                CTTTGTTG CCAGG TGGAGTG
                                |||||||| ||||| |||||||
                                GAGACAGC GGTCC ACCTCAC
                                     A    A
GAM319  GALNT7   3'  CACTCCAACCTGGGTGACAGAG 55086        TG    C
          TG                      CACTTTGT  CCCAGG TGGAGTG
                                ||||||||  |||||| |||||||
                                GTGAGACA  GGGTCC ACCTCAC
                                     GT    A
GAM319  GP2      3'  CACTCCAGCCTGGGCAACAGAG 9480
                                CTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||||
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                                GAGACAACGGGTCCGACCTCAC

GAM319  GP6     3'  CAGCCTGGGCAACATAGTG   33471     T
                                CACT TGTTGCCCAGGCTG
                                |||| ||||||||||||||
                                GTGA ACAACGGGTCCGAC
                                  T
GAM319  GRAF    3'  CACTCCAGCCTGGGTGACAGAG 31222       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  GTF2F1  3'  CACTCCAGCCTGGGTGACAGTG 10888     TT  TG
                                CACT  GT  CCCAGGCTGGAGTG
                                ||||  ||  ||||||||||||||
                                GTGA  CA  GGGTCCGACCTCAC
                                  __  GT
GAM319  HIP1    3'  CACTCCAGCCTGAGTGACAGAG 19248       TG C
                                CTTTGT  C CAGGCTGGAGTG
                                ||||||  | ||||||||||||
                                GAGACA  G GTCCGACCTCAC
                                   GT A
GAM319  HLA-E   3'  CACTCCAGCCTGGGTGACAGGG 92670       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GGGACA  GGGTCCGACCTCAC
                                   GT
GAM319  HRH1    3'  CACTCCAGCCTGGGCAACAGAG 7815
                                CTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319  HSPA5   3'  CACTCCAGCCTGGCGACAAGAG 19279       _     C
          TG                      CACTTT GTTGCC AGGCTGGAGTG
                                ||||||| |||||| ||||||||||
                                GTGAGA CAGCGG TCCGACCTCAC
                                   A    _
GAM319  HTR2A   3'  CAACCTGGGTAACAAAGTG   7101              C
                                CACTTTGTTGCCCAGG TG
                                |||||||||||||||| ||
                                GTGAAACAATGGGTCC AC
                                        A
GAM319  IAPP    3'  CACTCCAGCCTGGGTGGCAGAG 6438         TG
          TG                      CACTTTGT  CCCAGGCTGGAGTG
                                ||||||||  ||||||||||||||
                                GTGAGACG  GGGTCCGACCTCAC
                                    GT
GAM319  ICA1    3'  CAGCCTGGGCAACAAAGTG   42516
                                CACTTTGTTGCCCAGGCTG
                                |||||||||||||||||||
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                                GTGAAACAACGGGTCCGAC

GAM319  IFIT4    3'  CACTCCAGCCTGGGCAACAGAG 71490
                                CTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319  IFNAR1   3'  CACTCCAGCCTGGTGACAG   7136      TG  C
                                TTGT  CC AGGCTGGAGTG
                                ||||  || ||||||||||
                                GACA  GG TCCGACCTCAC
                                  GT  _
GAM319  IL2RA    3'  CACTCCAGCCTGGGCAACAGAG 6447
                                CTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319  IL6R     3'  CACTCCAGCCTGGGGTGACAGA 6909       TG  _
              G                  CTTTGT  CCC AGGCTGGAGTG
                                ||||||  ||| ||||||||||
                                GAGACA  GGG TCCGACCTCAC
                                   GT   G
GAM319  IPP      3'  CACTCCACTCTGGGCAACAGAA 20903    C         GC
              TG                  CA TTTGTTGCCCAG  TGGAGTG
                                || ||||||||||  |||||||
                                GT AGACAACGGGTC  ACCTCAC
                                 A          TC
GAM319  IRAK1    3'  CACTCCAGCCTGGGTGACAGAG 9611        TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  IRAK4    3'  CACTCCAGCCTGGGTGACAGAG 61840        TG
              TG                  CACTTTGT  CCCAGGCTGGAGTG
                                ||||||||  ||||||||||||||
                                GTGAGACA  GGGTCCGACCTCAC
                                     GT
GAM319  ITGAL    3'  CACTCCAGCCTGGGCAACACAG 11041    T
                                CT TGTTGCCCAGGCTGGAGTG
                                || ||||||||||||||||||
                                GA ACAACGGGTCCGACCTCAC
                                 C
GAM319  KAI1     3'  CACTCCAGCCTGGGGGACAGA  11119       G
                                TTTGTT CCCAGGCTGGAGTG
                                |||||| ||||||||||||||
                                AGACAG GGGTCCGACCTCAC
                                   G
GAM319  KCNA7    3'  CACTCCAGCCTGGGCAACAGAG 49889
                                CTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||
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                                GAGACAACGGGTCCGACCTCAC

GAM319  KCNA7    3'  CACTCCAGCCTGGGCAGCAGAG 49890
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACGACGGGTCCGACCTCAC

GAM319  KCNJ5    3'  CACTCCAGCCTGGGCGACAGAG 7967
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319  KCNK6    3'  CACTCCAGCCTGCGGGACAGAG 17883          G  _
            TG                    CACTTTGTT CC CAGGCTGGAGTG
                                ||||||||| || ||||||||||||
                                GTGAGACAG GG GTCCGACCTCAC
                                     _  C
GAM319  KCNK6    3'  CTAGCCTAGGCAACACAGTG   17884      T      C
                                CACT TGTTGCC AGGCTGG
                                |||| ||||||| |||||||
                                GTGA ACAACGG TCCGATC
                                  C      A
GAM319  KIF1B    3'  CACTCCAGCCTGGGTGACAGAG 31263        TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  KNSL1    3'  CACTCCAGCCTGGGCAACAGAG 16940
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319  LDLR     3'  CACTCCAGCCTGGGCAACAGAT 6725     C
            G                     CA TTTGTTGCCCAGGCTGGAGTG
                                || ||||||||||||||||||||
                                GT AGACAACGGGTCCGACCTCAC
                                  _
GAM319  LDLR     3'  CAGCCTGGGCAACATAGT    6727      T
                                ACT TGTTGCCCAGGCTG
                                ||| ||||||||||||||
                                TGA ACAACGGGTCCGAC
                                  T
GAM319  LPIN1    3'  CACTCCAGCCTGGGTGACAGAG 67984         TG
            T                     ACTTTGT  CCCAGGCTGGAGTG
                                |||||||  ||||||||||||||
                                TGAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  LRRC2    3'  CACTCCAGCCTGGGCAACAGAG 44737
            TG                    CACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||||
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                                GTGAGACAACGGGTCCGACCTCAC

GAM319  LRRC2   3'  CACTCCAGCCTGGGTGACAGAG 44738       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  MAFF    3'  CACTCCAGCCTGGGCAACATAG 25574    T
                                CT TGTTGCCCAGGCTGGAGTG
                                || ||||||||||||||||||
                                GA ACAACGGGTCCGACCTCAC
                                 T
GAM319  MDM4    3'  CACTCCAGCCTGGGTGACAG   11505     TG
                                TTGT  CCCAGGCTGGAGTG
                                ||||  ||||||||||||||
                                GACA  GGGTCCGACCTCAC
                                  GT
GAM319  MSH3    3'  CACTCCAGCTTGGGCAACAGAG 11688
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAACGGGTTCGACCTCAC

GAM319  MSI1    3'  CCAGCTGAGAACAAAGTG    11697         GCCCA
                                CACTTTGTT    GGCTGG
                                |||||||||    ||||||
                                GTGAAACAA    TCGACC
                                     GAG__
GAM319  MTMR8   3'  CACTCCAGCCTGAGCAACAGAG 31904         C
                                CTTTGTTGC CAGGCTGGAGTG
                                ||||||||| ||||||||||||
                                GAGACAACG GTCCGACCTCAC
                                      A
GAM319  MTMR8   3'  CACTCCAGCCTGGGCGAAAGG  31905     G
                                CTTT TTGCCCAGGCTGGAGTG
                                |||| ||||||||||||||||
                                GGAA AGCGGGTCCGACCTCAC
                                   _
GAM319  MYH11   3'  CACTCCAGCCTGGGCAACAGAG 11737
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319  MYH11   3'  CACTCCAGCCTGGGCAACAGAG 43428
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319  MYO1B   3'  CACTCCAGCCCGGGTGACAA   25241     TG  A
                                TTGT  CCC GGCTGGAGTG
                                ||||  ||| ||||||||||
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                                AACA  GGG CCGACCTCAC
                                  GT   C
GAM319  MYO1C    3'  CACTCCAGCCTGGGCAACAGAG 61854
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319  NCOA6    5'  CTCCAGCCCAGGCAACAGAG   26834          CA
                                CTTTGTTGCC  GGCTGGAG
                                ||||||||||  ||||||||
                                GAGACAACGG  CCGACCTC
                                      AC
GAM319  NFKBIL2  3'  CACTCCAGCCTGGGCGACAGA  26443
                                TTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||
                                AGACAGCGGGTCCGACCTCAC

GAM319  NPHP1    3'  CACTCCAGCCTAGGCAACAAGA 63140       _     C
                  GT                  ACTTT GTTGCC AGGCTGGAGTG
                                |||||  ||||||  ||||||||||
                                TGAGA CAACGG TCCGACCTCAC
                                  A     A
GAM319  NPHS1    3'  CACTCCAGCCTGGGCGACAGAG 17366
                                CTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319  NT5C2    3'  CACTCCAGCCTGGGCAACAAG  25254
                                TTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||
                                GAACAACGGGTCCGACCTCAC

GAM319  NUP62    3'  CACTCCAGCCTAGGCAACAGAG 33782          C
                                CTTTGTTGCC AGGCTGGAGTG
                                ||||||||||  ||||||||||
                                GAGACAACGG TCCGACCTCAC
                                      A
GAM319  OGG1     5'  CACTCCAGCCTAGGCGACAGAG 34149          C
                  TG                  CACTTTGTTGCC AGGCTGGAGTG
                                ||||||||||||  ||||||||||
                                GTGAGACAGCGG TCCGACCTCAC
                                      A
GAM319  OGG1     5'  CACTCCAGCCTAGGCGACAGAG 34162          C
                  TG                  CACTTTGTTGCC AGGCTGGAGTG
                                ||||||||||||  ||||||||||
                                GTGAGACAGCGG TCCGACCTCAC
                                      A
GAM319  OGG1     5'  CACTCCAGCCTAGGCGACAGAG 11888          C
                  TG                  CACTTTGTTGCC AGGCTGGAGTG
                                ||||||||||||  ||||||||||
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                                GTGAGACAGCGG TCCGACCTCAC
                                      A
GAM319  OPA3    3'  CACCCTAGCCTGGGCAACAGAG 47840              A
                                CTTTGTTGCCCAGGCTGG GTG
                                |||||||||||||||||| |||
                                GAGACAACGGGTCCGATC CAC
                                        C
GAM319  OPTN    3'  CACTCCAGCCTGGGTGACAGAG 42049      TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  P2RY6   3'  CAGCCTGGGCAACACAGT    15992    T
                                ACT TGTTGCCCAGGCTG
                                ||| ||||||||||||||
                                TGA ACAACGGGTCCGAC
                                  C
GAM319  P53AIP1 3'  CACTCCAGCCTGGGCGACAGAG 42333
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319  PA2G4   3'  CACTCCAGCCTGGGTGACAGAA 71824    C    TG
          TG                      CA TTTGT  CCCAGGCTGGAGTG
                                || |||||  ||||||||||||||
                                GT AGACA  GGGTCCGACCTCAC
                                 A    GT
GAM319  PACE4   3'  CTAGCCTGGACAACACAG    57165    T    C
                                CT TGTTG CCAGGCTGG
                                || ||||| |||||||||
                                GA ACAAC GGTCCGATC
                                 C    A
GAM319  PAICS   3'  CACTCCAACCTGGGCAGCAGAG 22255            C
                                CTTTGTTGCCCAGG TGGAGTG
                                |||||||||||||| |||||||
                                GAGACGACGGGTCC ACCTCAC
                                        A
GAM319  PAX5    3'  CACCCCAGCCTGGGAAGGAGAG 34123     G  G       A
                                CTTT TT CCCAGGCTGG GTG
                                |||| || |||||||||| |||
                                GAGA GA GGGTCCGACC CAC
                                  G  A        C
GAM319  PCDH11X 3'  CACTCCAGCCTGGGTGACAGAG 53126      TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  PCDH11Y 3'  CACTCCAGCCTGGGTGACAGAG 53155      TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
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                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  PCDH11Y  3'  CACTCCAGCCTGGGTGACAGAG 53177       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  PDCL     3'  CACTCCAACCTGGGCGACAGAG 19394            C
                                CTTTGTTGCCCAGG TGGAGTG
                                |||||||||||||| |||||||
                                GAGACAGCGGGTCC ACCTCAC
                                         A
GAM319  PDE4C    3'  CACTCCAGCCTGGGCAACACAG 8097     T
                                CT TGTTGCCCAGGCTGGAGTG
                                || ||||||||||||||||||
                                GA ACAACGGGTCCGACCTCAC
                                 C
GAM319  PDE4C    3'  CACTCCAGCCTGGGGCTGACAG 8098        _   _
           AG                     CTTTGTT GCCC AGGCTGGAGTG
                                |||||||  ||||  ||||||||||
                                GAGACAG CGGG TCCGACCTCAC
                                   T   G
GAM319  PIK3CG   3'  CACTCCAGCCTGGATAACAGAG 12118         C
                                CTTTGTTG CCAGGCTGGAGTG
                                ||||||||  ||||||||||||
                                GAGACAAT GGTCCGACCTCAC
                                    A
GAM319  PIK3CG   3'  CAGCCTGGGCAACACAGTG   12119      T
                                CACT TGTTGCCCAGGCTG
                                ||||  ||||||||||||||
                                GTGA ACAACGGGTCCGAC
                                  C
GAM319  PLA2G2D  3'  CACTCCAGCCTGGGCAACAGAG 25708
           TG                     CACTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||||
                                GTGAGACAACGGGTCCGACCTCAC

GAM319  POLH     3'  CACTCCAGCCTGGGCAACAGAG 22474
                                CTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319  PPP1R12B 3'  CACTCCAGCCTGGGTGACAGAG 50379       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  PSMB2    3'  CACTCCAGCCTGGCTGACAGAG 12461        GC
                                CTTTGTT  CCAGGCTGGAGTG
                                |||||||  ||||||||||||
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                                GAGACAG  GGTCCGACCTCAC
                                    TC
GAM319   PSMB9    3'  CACTCCAGCCTGGGAAACAGAG 12493        G
                                CTTTGTT CCCAGGCTGGAGTG
                                ||||||| ||||||||||||||
                                GAGACAA GGGTCCGACCTCAC
                                    A
GAM319   PSMB9    3'  CACTCCAGCCTGGGCGACAAAG 12494
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAAACAGCGGGTCCGACCTCAC

GAM319   PSMD5    3'  CCAGCCTGGGCAACACAG    18556    T
                                CT TGTTGCCCAGGCTGG
                                || |||||||||||||||
                                GA ACAACGGGTCCGACC
                                 C
GAM319   PTGIS    3'  CACTCCAGCCTGGGCGACAGAG 8197
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319   RABIF    3'  CACTCCAGCCTGGGCAACAGAG 12722
           TG                     CACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||||
                                GTGAGACAACGGGTCCGACCTCAC

GAM319   RABIF    3'  CTAGCCTGGGCAACATAGTG   12726      T
                                CACT TGTTGCCCAGGCTGG
                                |||| |||||||||||||||
                                GTGA ACAACGGGTCCGATC
                                   T
GAM319   RAD1     3'  CACTCCAGCCTAGGCAATAAG  12639          C
                                TTTGTTGCC AGGCTGGAGTG
                                ||||||||| ||||||||||
                                GAATAACGG TCCGACCTCAC
                                     A
GAM319   RAD1     3'  CACTCCAGCCTAGGCAATAAG  56653          C
                                TTTGTTGCC AGGCTGGAGTG
                                ||||||||| ||||||||||
                                GAATAACGG TCCGACCTCAC
                                     A
GAM319   RAD1     3'  CACTCCAGCCTAGGCAATAAG  56749          C
                                TTTGTTGCC AGGCTGGAGTG
                                ||||||||| ||||||||||
                                GAATAACGG TCCGACCTCAC
                                     A
GAM319   RBL1     3'  CACTCCAGCCTGGGCAACAAGA 12784       _
           GT                     ACTTT GTTGCCCAGGCTGGAGTG
                                |||||| ||||||||||||||||||
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                                TGAGA CAACGGGTCCGACCTCAC
                                  A
GAM319  RFC2    3'  CACTCCAGCCTGGGCGACAGAG 12837
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319  ROCK2   3'  CACTCCAGCCTGGGCAGC    66613
                                GTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||
                                CGACGGGTCCGACCTCAC

GAM319  SCAP2   3'  CACTCCAGCCTGGGCGACAGAG 15423
                TG                CACTTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||||
                                  GTGAGACAGCGGGTCCGACCTCAC

GAM319  SFRS2IP 5'  CACTCCAGCCTGGGTGACAGAG 17537       TG
                TG                CACTTTGT  CCCAGGCTGGAGTG
                                  ||||||||  ||||||||||||||
                                  GTGAGACA  GGGTCCGACCTCAC
                                    GT
GAM319  SIAT1   3'  CACCCCAGCCTGGGAAGAACA  13129     G__       A
                                  TGTT   CCCAGGCTGG GTG
                                  ||||   |||||||||| |||
                                  ACAA   GGGTCCGACC CAC
                                    GAA         C
GAM319  SIGLEC11 3'  CACTCCAGCCTGGGCAACAGAG 54649
                TG                CACTTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||||
                                  GTGAGACAACGGGTCCGACCTCAC

GAM319  SIM2    3'  CACTCCAGCCTGGGTAACAGAG 24798
                TG                CACTTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||||
                                  GTGAGACAATGGGTCCGACCTCAC

GAM319  SLC14A1 3'  CACTCCAACCTGGGTGACAAG  32409      TG     C
                                  TTTGT  CCCAGG TGGAGTG
                                  |||||  |||||| |||||||
                                  GAACA  GGGTCC ACCTCAC
                                    GT     A
GAM319  SLC14A2 3'  CACTCCAGCCTGGGCAACGGAT 24111    C
                TG                CA TTTGTTGCCCAGGCTGGAGTG
                                  || ||||||||||||||||||||
                                  GT AGGCAACGGGTCCGACCTCAC
                                   T
GAM319  SLC17A5 3'  CACTCCAGCCTGGGCGATGGAG 25828     TG
                                  CTT  TTGCCCAGGCTGGAGTG
                                  |||  ||||||||||||||||
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                                GAG  AGCGGGTCCGACCTCAC
                                  GT
GAM319  SLC26A4  3'  CACTCCAGCCTGGGCGACAGAG 6521
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319  SLC2A6   3'  CACTCCAGCCTGGGCAACGAGA 34566      _
           GT                     ACTTT GTTGCCCAGGCTGGAGTG
                                ||||| ||||||||||||||||||
                                TGAGA CAACGGGTCCGACCTCAC
                                  G
GAM319  SLC31A1  3'  CACTCCAGCCTGGGTGACAAG  10273      TG
                                TTTGT  CCCAGGCTGGAGTG
                                |||||  ||||||||||||||
                                GAACA  GGGTCCGACCTCAC
                                   GT
GAM319  SMG1     3'  CACTCCAGCCTGGGCAACAGAG 31342
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319  SRGAP1   5'  CACTCCAGCCTGGGCAACAGAG 72711
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319  STK38    5'  CACTCCAGCCTGGGCAACAAG  24400
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAACAACGGGTCCGACCTCAC

GAM319  SULT2A1  3'  CACTCCAGCCTGGGTGACAGAG 72223       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  TADA2L   3'  CTCCAGCCTGGGCAACAAAGTG 9438
                                CACTTTGTTGCCCAGGCTGGAG
                                |||||||||||||||||||||
                                GTGAAACAACGGGTCCGACCTC

GAM319  TBX1     3'  CACTCCAGCCTGGGTGACAGAG 21137        TG
           TG                     CACTTTGT  CCCAGGCTGGAGTG
                                ||||||||  ||||||||||||||
                                GTGAGACA  GGGTCCGACCTCAC
                                     GT
GAM319  TEM7     3'  CACTCCAGCCTGGGTGACAGAG 40247       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
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                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  TNFRSF1B  3'  CACTCCAGCCTGAGCAACAGAG 8385          C
             TG                    CACTTTGTTGC CAGGCTGGAGTG
                                   |||||||||||  ||||||||||||
                                   GTGAGACAACG GTCCGACCTCAC
                                         A
GAM319  TNFRSF1B  3'  CACTCCAGCCTGGGCGACAGAG 8386
                                   CTTTGTTGCCCAGGCTGGAGTG
                                   ||||||||||||||||||||||
                                   GAGACAGCGGGTCCGACCTCAC

GAM319  TNFSF10   3'  CACTCCAGCCTGGCGACAGAG  15088         C
                                   CTTTGTTGCC AGGCTGGAGTG
                                   ||||||||||  ||||||||||
                                   GAGACAGCGG TCCGACCTCAC
                                            _
GAM319  TNFSF14   3'  CACTCCAACCTGGGAAAC    15077    G    C
                                   GTT CCCAGG TGGAGTG
                                   |||  ||||||  |||||||
                                   CAA GGGTCC ACCTCAC
                                     A     A
GAM319  TNFSF15   3'  CACTCCAGCCTGGGTAACAAG  18862
                                   TTTGTTGCCCAGGCTGGAGTG
                                   ||||||||||||||||||||||
                                   GAACAATGGGTCCGACCTCAC

GAM319  TRIM14    3'  CACTCCAGCCTGGGCAATAGAG 53772
             TG                    CACTTTGTTGCCCAGGCTGGAGTG
                                   ||||||||||||||||||||||||
                                   GTGAGATAACGGGTCCGACCTCAC

GAM319  TRIM14    3'  CACTCCAGCCTGGGGACAGAG  29504        G
                                   CTTTGTT CCCAGGCTGGAGTG
                                   |||||||  ||||||||||||||
                                   GAGACAG GGGTCCGACCTCAC
                                            _
GAM319  TRPM1     3'  CAGCCTGGGCAACATAGTG    11602      T
                                   CACT TGTTGCCCAGGCTG
                                   ||||  ||||||||||||||
                                   GTGA ACAACGGGTCCGAC
                                     T
GAM319  TSN       3'  CAGCCTGGGCAACAAAGTG    17295
                                   CACTTTGTTGCCCAGGCTG
                                   |||||||||||||||||||
                                   GTGAAACAACGGGTCCGAC

GAM319  TSNAX     3'  CACTCCAGCCTGGGTAACAGAG 21152
                                   CTTTGTTGCCCAGGCTGGAGTG
                                   |||||||||||||||||||||||
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                                GAGACAATGGGTCCGACCTCAC

GAM319  UBE2B    3'  CACTCCAGCCTGGGTGACAGAG 13934       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  UBE2G2   3'  CACTCCAGCCTGGGCAACAGAG 65478
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319  UBE2G2   3'  CACTCCAGCCTGGGCAACAGAG 65479
           TG                     CACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||||
                                GTGAGACAACGGGTCCGACCTCAC

GAM319  UC28     3'  CACTCCAGCCTGGGCAACAGGA 41584      _
           GT                     ACTT TGTTGCCCAGGCTGGAGTG
                                ||||| ||||||||||||||||||
                                TGAG ACAACGGGTCCGACCTCAC
                                  G
GAM319  USP14    3'  CACTCCAGCCTGGGTGACAGAG 18930       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  VHL      3'  CACTCCAGCCTGGGAAACAAG  6835        G
                                TTTGTT CCCAGGCTGGAGTG
                                ||||||| ||||||||||||||
                                GAACAA GGGTCCGACCTCAC
                                   A
GAM319  VHL      3'  CACTCCAGCCTGGGGGACAGAG 6836         G
                                CTTTGTT CCCAGGCTGGAGTG
                                ||||||| ||||||||||||||
                                GAGACAG GGGTCCGACCTCAC
                                    G
GAM319  VPS41    3'  CACTCCAGCCTGGGCAACAAG  27688
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAACAACGGGTCCGACCTCAC

GAM319  WIG1     3'  CACTCCAGCCTGGGTGACAGAG 96095       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  WNT5A    3'  CAGCCCAAGCAACAAGGT    14116         CCA
                                ACTTTGTTGC   GGCTG
                                ||||||||||   |||||
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                                TGGAACAACG   CCGAC
                                      AAC
GAM319   ZNF264    3'  CACTCCAGCCTGGGCAACAGAG 14200
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319   ZNF264    3'  CACTCCAGCCTGGGCAGCAGAG 14201
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACGACGGGTCCGACCTCAC

GAM319   ZNF36     3'  CACTCCAGCCTGGGTGAC    95576    TG
                                GT  CCCAGGCTGGAGTG
                                ||  ||||||||||||||
                                CA  GGGTCCGACCTCAC
                                 GT
GAM319   AF020591  3'  CACTCCAGCCTGGGCAACAGAG 27905
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319   AGMAT     3'  CACCCTGGGCAACACAGT    45735     T         C
                                ACT TGTTGCCCAGG TG
                                ||| ||||||||||| ||
                                TGA ACAACGGGTCC AC
                                  C          C
GAM319   ALTE      3'  CACTCCAGCCTGGGCGACAAG  60998
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAACAGCGGGTCCGACCTCAC

GAM319   ALTE      3'  CACTCCAGCCTGGAGGCCAGAG 17577        _  GC
            TG                    CACTTTG TT  CCAGGCTGGAGTG
                                ||||||| ||  ||||||||||||
                                GTGAGAC GG  GGTCCGACCTCAC
                                    C  A_
GAM319   ALTE      3'  CACTCCAGCCTGGGCGACAAG  17578
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAACAGCGGGTCCGACCTCAC

GAM319   AP4S1     3'  CACTCCAATCTGGCAACAGAG  23963          C  GC
                                CTTTGTTGCC AG  TGGAGTG
                                |||||||||| ||  |||||||
                                GAGACAACGG TC  ACCTCAC
                                      _  TA
GAM319   APXL2     3'  CACTCCAGCCTGGGCGACAGAG 75671
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
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                                GAGACAGCGGGTCCGACCTCAC

GAM319  ARNTL2   3'  CACCCCAGCCTGGGCGACAGAG 39838              A
                                CTTTGTTGCCCAGGCTGG GTG
                                |||||||||||||||||| |||
                                GAGACAGCGGGTCCGACC CAC
                                          C
GAM319  ARNTL2   3'  CACTCCAGTCTGGGCAACAGAG 39839
           TG                     CACTTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||||
                                  GTGAGACAACGGGTCTGACCTCAC

GAM319  ASAHL    3'  CTAGCCTGGGCAACAGAG    64316
                                CTTTGTTGCCCAGGCTGG
                                ||||||||||||||||||
                                GAGACAACGGGTCCGATC

GAM319  BIVM     3'  CACTCCAGCCTGGGCAACAGGG 35153
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GGGACAACGGGTCCGACCTCAC

GAM319  BLOV1    3'  CACTCCAGCCTGGGCAACAAG  76789
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||
                                GAACAACGGGTCCGACCTCAC

GAM319  BLOV1    3'  CACTCCAGCCTGGGCGACAGAG 76790
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319  BTN3A2   3'  CACTCCAGCCTGGGAGACAGAG 23871       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GA
GAM319  C12orf2  3'  CACTCCAGCCTGGGTAACAGAG 83680
           TG                     CACTTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||||
                                  GTGAGACAATGGGTCCGACCTCAC

GAM319  C13orf1  3'  CACTCCAGCCTAGGCAACAGAG 40356          C
           TG                     CACTTTGTTGCC AGGCTGGAGTG
                                  ||||||||||| ||||||||||
                                  GTGAGACAACGG TCCGACCTCAC
                                         A
GAM319  C1orf33  3'  CAGCCTGGGCAACAGAGT    32979
                                ACTTTGTTGCCCAGGCTG
                                ||||||||||||||||||
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                                TGAGACAACGGGTCCGAC

GAM319  C1QTNF2   3'  CACTCCAGCCTGGGCAACAGAG 49969
            TG                    CACTTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||||
                                  GTGAGACAACGGGTCCGACCTCAC

GAM319  C20orf106 3'  CACTCCAGCCCAGGTGACAGAG 55897        TG  CA
            TG                    CACTTTGT  CC  GGCTGGAGTG
                                  ||||||||  ||  ||||||||||
                                  GTGAGACA  GG  CCGACCTCAC
                                      GT  AC
GAM319  C20orf108 3'  CACTCCAGCCTGGGCGACAGAG 55875
                                  CTTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||
                                  GAGACAGCGGGTCCGACCTCAC

GAM319  C20orf12  3'  CACTCCAGCCTGGGCAACAAG  36844
                                  TTTGTTGCCCAGGCTGGAGTG
                                  |||||||||||||||||||||
                                  GAACAACGGGTCCGACCTCAC

GAM319  C20orf142 3'  CACTCCAGCCTGAGCGACAGAG 75273           C
            TG                    CACTTTGTTGC CAGGCTGGAGTG
                                  |||||||||||  ||||||||||||
                                  GTGAGACAGCG GTCCGACCTCAC
                                        A
GAM319  C20orf142 3'  CAGCCTGGGCAACATAGTG   75275      T
                                  CACT TGTTGCCCAGGCTG
                                  |||| ||||||||||||||
                                  GTGA ACAACGGGTCCGAC
                                    T
GAM319  C20orf172 3'  CACTCCAGCCTGAGCGACAGAG 46763           C
            TG                    CACTTTGTTGC CAGGCTGGAGTG
                                  |||||||||||  ||||||||||||
                                  GTGAGACAGCG GTCCGACCTCAC
                                        A
GAM319  C20orf177 3'  CACTCCAGCCTGGGCAACAAGA 62830      _
            G                     CTTT GTTGCCCAGGCTGGAGTG
                                  |||| ||||||||||||||||||
                                  GAGA CAACGGGTCCGACCTCAC
                                    A
GAM319  C20orf29  3'  CACTCCAGCCTGGGCAACAGAG 37707
            TG                    CACTTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||||
                                  GTGAGACAACGGGTCCGACCTCAC

GAM319  C22orf19  3'  CCATCTGGACAACAGAG     14821        C    C
                                  CTTTGTTG CCAGG TGG
                                  |||||||| ||||| |||
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                                GAGACAAC GGTCT ACC
                                   A    _
GAM319  C6.1A    3'  CACTCCAACCTGTGTAACAGAG 44527          C   C
             TG                   CACTTTGTTGC CAGG TGGAGTG
                                  |||||||||| |||| |||||||
                                  GTGAGACAATG GTCC ACCTCAC
                                        T   A
GAM319  C6.1A    3'  CAGCCTGGGCAACATAGTG   44528     T
                                  CACT TGTTGCCCAGGCTG
                                  |||| ||||||||||||||
                                  GTGA ACAACGGGTCCGAC
                                    T
GAM319  C6orf29  3'  CACTCCAACCTGGGTGACAGA  52454      TG    C
                                  TTTGT  CCCAGG TGGAGTG
                                  |||||  |||||| |||||||
                                  AGACA  GGGTCC ACCTCAC
                                     GT     A
GAM319  C6orf5   3'  CACTCCAGCCTGGGCAATAGAG 31975
             TG                   CACTTTGTTGCCCAGGCTGGAGTG
                                  |||||||||||||||||||||||
                                  GTGAGATAACGGGTCCGACCTCAC

GAM319  C8orf17  3'  CACTGCAGCCTGGGCAACAGAA 39988    C           G
             TG                   CA TTTGTTGCCCAGGCTG AGTG
                                  || |||||||||||||| ||||
                                  GT AGACAACGGGTCCGAC TCAC
                                   A             G
GAM319  C8orf2   3'  CACTTTTTGCAGGCAACAAAAT 24146    C       CAG  T_
             G                    CA TTTGTTGCC   GC  GGAGTG
                                  || |||||||||   ||  ||||||
                                  GT AAACAACGG   CG  TTTCAC
                                   A        A__  TT
GAM319  C9orf5   3'  CACTCCAGCCTGGGTGAGAGAG 50102        G TG
             TG                   CACTTT T  CCCAGGCTGGAGTG
                                  |||||| |  ||||||||||||||
                                  GTGAGA A  GGGTCCGACCTCAC
                                     G GT
GAM319  CAMKK2   5'  CACTCCAGCCTGGGCAACACAG 22618    T
                                  CT TGTTGCCCAGGCTGGAGTG
                                  || ||||||||||||||||||
                                  GA ACAACGGGTCCGACCTCAC
                                   C
GAM319  CBCIP2   3'  CACTCCAGCCTGGGCGACAGAG 52653
                                  CTTTGTTGCCCAGGCTGGAGTG
                                  |||||||||||||||||||||
                                  GAGACAGCGGGTCCGACCTCAC

GAM319  CCR6     3'  CACTCCAGCCTGGGTGACAGAG 16439        TG
                                  CTTTGT  CCCAGGCTGGAGTG
                                  ||||||  ||||||||||||||
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                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  CCR6    3'  CACTCCAGCCTGGGTGACAGAG 49398      TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  CDT1    3'  CACTCCAGCCTGGGTGACAGAG 78157      TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  CENTA2  3'  AGCCTGGGCAACATAGTG   37862     T
                                CACT TGTTGCCCAGGCT
                                ||||  ||||||||||||
                                GTGA ACAACGGGTCCGA
                                  T
GAM319  cerk    3'  CACTCCAGCCTGGGCAACAGAG 43159
                                CTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319  CG012   5'  CACTCCAGCCCAGGTGACAGAG 84144      TG  CA
                                CTTTGT  CC  GGCTGGAGTG
                                ||||||  ||  ||||||||||
                                GAGACA  GG  CCGACCTCAC
                                   GT  AC
GAM319  CG012   3'  CACTCCAGCCTCGCCGACAAAG 84145       CCC
                                CTTTGTTG   AGGCTGGAGTG
                                ||||||||   ||||||||||
                                GAAACAGC   TCCGACCTCAC
                                     CGC
GAM319  CG012   5'  CACTCCAGCCTGGGCAACAGA  84146
                                TTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||
                                AGACAACGGGTCCGACCTCAC

GAM319  CNNM1   3'  CACTTCATCCTAGGCAACAGAG 40114        C   C
                                CTTTGTTGCC AGG TGGAGTG
                                |||||||||| ||| |||||||
                                GAGACAACGG TCC ACTTCAC
                                      A   T
GAM319  COE2    3'  CACTCCAGCCTGGGTGACAGAG 64905      TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  CPR2    3'  CACTCCAGCCTGGGTAACAGAG 48826
                                CTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||
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                                GAGACAATGGGTCCGACCTCAC

GAM319  D21S2056E 3'  CACTCCAGCCTGGGCAACGAGA 14861      _
            G                  CTTT GTTGCCCAGGCTGGAGTG
                               |||| ||||||||||||||||||
                               GAGA CAACGGGTCCGACCTCAC
                                 G
GAM319  DCOHM    3'  CACTCCAGCCTGGGTGACGGA  50511      TG
                               TTTGT  CCCAGGCTGGAGTG
                               |||||  ||||||||||||||
                               AGGCA  GGGTCCGACCTCAC
                                  GT
GAM319  DDX34    3'  CACTCCAGCCTGGTTGACAGAG 28662       GC
                               CTTTGTT  CCAGGCTGGAGTG
                               |||||||  ||||||||||||
                               GAGACAG  GGTCCGACCTCAC
                                    TT
GAM319  DIS3     3'  CACTCCAGCCTGGGTGACAGA  30911      TG
                               TTTGT  CCCAGGCTGGAGTG
                               |||||  ||||||||||||||
                               AGACA  GGGTCCGACCTCAC
                                  GT
GAM319  dJ383J4.3 3'  CACTCCAGCCTGGGCAACAAAG 67489
            TG                   CACTTTGTTGCCCAGGCTGGAGTG
                                 ||||||||||||||||||||||||
                                 GTGAAACAACGGGTCCGACCTCAC

GAM319  DKFZP434C171 3'  CACTCCAGCCCGGGTGACAGAG 32184       TG   A
                               CTTTGT  CCC GGCTGGAGTG
                               ||||||  ||| ||||||||||
                               GAGACA  GGG CCGACCTCAC
                                  GT   C
GAM319  DKFZp434E2220 5'  CACTCCAGCCTGGGCGACAGGG 34707
                               CTTTGTTGCCCAGGCTGGAGTG
                               ||||||||||||||||||||||
                               GGGACAGCGGGTCCGACCTCAC

GAM319  DKFZp434G171 3'  CACTCCAGCCTGGGAGACACAG 80235    T   TG
                               CT TGT  CCCAGGCTGGAGTG
                               || |||  ||||||||||||||
                               GA ACA  GGGTCCGACCTCAC
                                C   GA
GAM319  DKFZP434I1735 3'  CACTCCAGCCTGGGCGACAGAG 89165
            TG                   CACTTTGTTGCCCAGGCTGGAGTG
                                 ||||||||||||||||||||||||
                                 GTGAGACAGCGGGTCCGACCTCAC

GAM319  DKFZP434K1421 3'  CACTCCAACCTGGGCAACAGAA 50464    C          C
            TG                   CA TTTGTTGCCCAGG TGGAGTG
                                 || |||||||||||| |||||||
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                                GT AGACAACGGGTCC ACCTCAC
                                 A          A
GAM319  DKFZP434N1511 3'  CACTCCAGCCTGGGCAACAGAG 93051
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319  DKFZP434P211 3'  CACTCCAGCCTGGTCGACAGAG 28024          C
          TG                    CACTTTGTTG CCAGGCTGGAGTG
                                |||||||||| ||||||||||||
                                GTGAGACAGC GGTCCGACCTCAC
                                      T
GAM319  DKFZp547C176 3'  CACTCCAGCCTGGCGACAGAG  67797          C
                                CTTTGTTGCC AGGCTGGAGTG
                                |||||||||| ||||||||||
                                GAGACAGCGG TCCGACCTCAC

                                _
GAM319  DKFZp547I094 3'  CACTCCAGCCTGGGCGGCAGAG 50553
          TG                    CACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||||
                                GTGAGACGGCGGGTCCGACCTCAC

GAM319  DKFZP564A022 3'  CACTCCAGCCTGGGCAACAGAG 48970
          TG                    CACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||||
                                GTGAGACAACGGGTCCGACCTCAC

GAM319  DKFZP564B1023 3'  CACTCCAGCCTGGGCAACAAGA 49361      _
          GT                    ACTTT GTTGCCCAGGCTGGAGTG
                                ||||| ||||||||||||||||||
                                TGAGA CAACGGGTCCGACCTCAC
                                  A
GAM319  DKFZP564I0422 3'  CACTCCAGCCTGGGCAATGGAG 49510      TG
          TG                    CACTT  TTGCCCAGGCTGGAGTG
                                |||||  ||||||||||||||||
                                GTGAG  AACGGGTCCGACCTCAC
                                  GT
GAM319  DKFZP564I052 3'  CACTCCAGGCTGGGCAACAGAG 67279            G
          TG                    CACTTTGTTGCCCAG CTGGAGTG
                                |||||||||||||| ||||||||
                                GTGAGACAACGGGTC GACCTCAC
                                      G
GAM319  DKFZp564K142 3'  CACTCCAGCCTGGCAACAGAG  50430          C
                                CTTTGTTGCC AGGCTGGAGTG
                                |||||||||| ||||||||||
                                GAGACAACGG TCCGACCTCAC

                                _
GAM319  DKFZP564M182 3'  CACTCCAGCCTGATGACAGAG  78617         CC
                                CTTTGTTG  CAGGCTGGAGTG
                                ||||||||  ||||||||||||
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                                GAGACAGT  GTCCGACCTCAC
                                    A_
GAM319   DKFZP564M182 3'  CACTCCAGCCTGGGCAACAGAG 78618
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319   DKFZP564M182 3'  CACTCCAGCCTGGGCGGCAGAG 78619
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACGGCGGGTCCGACCTCAC

GAM319   DKFZp566H0824 3'  CACTCCAGCCTGGGCAACAGAG 34477
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319   DKFZP586D2223 3'  CTAGCCTGGGCAACAGAGTG   38289
                                CACTTTGTTGCCCAGGCTGG
                                ||||||||||||||||||||
                                GTGAGACAACGGGTCCGATC

GAM319   DKFZP586D2223 3'  CTAGCCTGGGCAACATAG    38290    T
                                CT TGTTGCCCAGGCTGG
                                || ||||||||||||||
                                GA ACAACGGGTCCGATC
                                  T
GAM319   DKFZP586M1120 3'  CACTCCAGCCTGGGCAACAGAG 49277
            TG                    CACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||||
                                GTGAGACAACGGGTCCGACCTCAC

GAM319   DRF1     3'  CACTCCAGCCTGGGCGATAGAG 47738
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGATAGCGGGTCCGACCTCAC

GAM319   DRF1     3'  CACTCCAGCCTGGGTGACAGAG 47739       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                    GT
GAM319   ET       3'  CACTCCAGCCTGGATGACAAG  44465       GC
                                TTTGTT  CCAGGCTGGAGTG
                                ||||||  ||||||||||||
                                GAACAG  GGTCCGACCTCAC
                                    TA
GAM319   EVI5     3'  CACTCCAACCTGGGCAACATGG 20200    T         C
                                CT TGTTGCCCAGG TGGAGTG
                                || ||||||||||| |||||||
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                                GG ACAACGGGTCC ACCTCAC
                                 T          A
GAM319  FADS1    3'  CACTCCAGCCTGGGGTGATAGA 26374       TG  _
                                TTTGT  CCC AGGCTGGAGTG
                                |||||  ||| ||||||||||
                                AGATA  GGG TCCGACCTCAC
                                   GT   G
GAM319  FBXO26   3'  CACTCCAGCCTGGGTGAGAAAG 46622      G TG
                                CTTT T  CCCAGGCTGGAGTG
                                ||||  |  ||||||||||||||
                                GAAA A  GGGTCCGACCTCAC
                                  G GT
GAM319  FBXO26   3'  CAGCCTGGGCAACATAGTG   46623      T
                                CACT TGTTGCCCAGGCTG
                                |||| ||||||||||||||
                                GTGA ACAACGGGTCCGAC
                                  T
GAM319  FBXO27   3'  CACTCCAGCCTGGGCAACACAG 75004     T
                                CT TGTTGCCCAGGCTGGAGTG
                                || ||||||||||||||||||
                                GA ACAACGGGTCCGACCTCAC
                                 C
GAM319  FBXO27   3'  CACTCCAGCCTGGGTGACAGAG 75005       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  FBXO6    3'  CACTCCAGCCTGGGTGACAGAG 37988       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  FBXO9    3'  CACTCCAGCCTGAGCAACACAG 54241      T     C
           TG                     CACT TGTTGC CAGGCTGGAGTG
                                ||||  ||||||  ||||||||||||
                                GTGA ACAACG GTCCGACCTCAC
                                  C     A
GAM319  FKBP14   3'  CACTCCAGCCTGGGTGACAGAG 36063       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  FKSG17   3'  CACTCCAGCCTGGGTGACAGAG 50152        TG
           TG                     CACTTTGT  CCCAGGCTGGAGTG
                                ||||||||  ||||||||||||||
                                GTGAGACA  GGGTCCGACCTCAC
                                    GT
GAM319  FKSG43   5'  CACTCCAGCCTGGGTGACAGAG 50161       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
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                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  FKSG44   5' CACTCCAGCCTGGGCGACAGAG 49961
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319  FLJ00060 3' CACTCCAGCCTGGGCGATAGAG 61738
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||
                                GAGATAGCGGGTCCGACCTCAC

GAM319  FLJ10008 3' CACTCCAGCCTGGGCGACACAG 36180    T
                                CT TGTTGCCCAGGCTGGAGTG
                                || ||||||||||||||||||
                                GA ACAGCGGGTCCGACCTCAC
                                 C
GAM319  FLJ10043 3' CACTCCAGCCTGGGTGACAGAG 36228       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  FLJ10058 3' CACTCCAGCCTGGGCAACACAG 36259     T
          TG                      CACT TGTTGCCCAGGCTGGAGTG
                                ||||| ||||||||||||||||||
                                GTGA ACAACGGGTCCGACCTCAC
                                  C
GAM319  FLJ10244 3' CACTCCAGCCTGGGCAAAAAG  36398     G
                                CTTT TTGCCCAGGCTGGAGTG
                                ||||| ||||||||||||||||
                                GAAA AACGGGTCCGACCTCAC
                                  _
GAM319  FLJ10314 3' ACTCCAGCCTGCACAACA    36483      CC
                                TGTTG  CAGGCTGGAGT
                                |||||  ||||||||||
                                ACAAC  GTCCGACCTCA
                                   AC
GAM319  FLJ10460 3' CACTCCAACCTGGGTGATGGAG 36612    TG TG    C
                                CTT  T  CCCAGG TGGAGTG
                                |||  |  |||||| |||||||
                                GAG  A  GGGTCC ACCTCAC
                                  GT GT     A
GAM319  FLJ10547 3' CACTCCAGCCTGGGCTACAGAG 36773       T
                                CTTTGT GCCCAGGCTGGAGTG
                                |||||| ||||||||||||||
                                GAGACA CGGGTCCGACCTCAC
                                   T
GAM319  FLJ10613 3' CACTCTAGCCTGGGCAACAA   39335
                                TTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||
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                                AACAACGGGTCCGATCTCAC

GAM319  FLJ10640  3'  ACTCTTGAGCAATAAAGTG   39231          C  GGCT
                                CACTTTGTTGC CA   GGAGT
                                |||||||||||  ||   |||||
                                GTGAAATAACG GT   TCTCA
                                      A  ____
GAM319  FLJ10650  3'  CACTCCAGCCTGGGCGACAGAA 36899    C
          TG                      CA TTTGTTGCCCAGGCTGGAGTG
                                  || ||||||||||||||||||||
                                  GT AGACAGCGGGTCCGACCTCAC
                                   A
GAM319  FLJ10704  3'  CACTCCAGCCTGGACGACAGAG 36975          C
          TG                      CACTTTGTTG CCAGGCTGGAGTG
                                  |||||||||| ||||||||||||
                                  GTGAGACAGC GGTCCGACCTCAC
                                       A
GAM319  FLJ10781  3'  CACTCCAGCCTGGGCAGCAGAG 37169
          TG                      CACTTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||||
                                  GTGAGACGACGGGTCCGACCTCAC

GAM319  FLJ10803  3'  CACTCCAGCCTGGGCAACAGAG 37198
                                  CTTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||
                                  GAGACAACGGGTCCGACCTCAC

GAM319  FLJ10826  3'  CACTCCAGCCTGGGCAACAAGA 37243      _
          GT                      ACTTT GTTGCCCAGGCTGGAGTG
                                  ||||| ||||||||||||||||||
                                  TGAGA CAACGGGTCCGACCTCAC
                                     A
GAM319  FLJ10830  3'  CACTCCAGCCTGGGCGACAGA  37262
                                  TTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||
                                  AGACAGCGGGTCCGACCTCAC

GAM319  FLJ10932  3'  CACTCCAGCCCGGGTTACAGTG 37425     TT  T    A
                                  CACT  GT GCCC GGCTGGAGTG
                                  ||||  || |||| ||||||||||
                                  GTGA  CA TGGG CCGACCTCAC
                                     __ T   C
GAM319  FLJ10989  3'  CACTCCAGCCTGGGTGACAAAG 37497       TG
                                  CTTTGT  CCCAGGCTGGAGTG
                                  ||||||  ||||||||||||||
                                  GAAACA  GGGTCCGACCTCAC
                                     GT
GAM319  FLJ10998  3'  CACTCCAGCCTGGGTGACAGTG 37518     TT  TG
                                  CACT  GT  CCCAGGCTGGAGTG
                                  ||||  ||  ||||||||||||||
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                                GTGA  CA  GGGTCCGACCTCAC
                                  __  GT
GAM319  FLJ11036 3' CAACCTGGGCAACATAGTG   37550     T        C
                                CACT TGTTGCCCAGG TG
                                |||| |||||||||| ||
                                GTGA ACAACGGGTCC AC
                                  T         A
GAM319  FLJ11036 3' CACTCCAGCCTGGGCGACAGAG 37551
                                CTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319  FLJ11106 3' CACTCCAGCCTGGGTGACAGA  37618      TG
                                TTTGT  CCCAGGCTGGAGTG
                                |||||  ||||||||||||||
                                AGACA  GGGTCCGACCTCAC
                                   GT
GAM319  FLJ11126 3' CACTCCAGCCTGGGTAACAGAG 37647
                                CTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||
                                GAGACAATGGGTCCGACCTCAC

GAM319  FLJ11151 3' CACTCCAGCCTGGGCAACAGAG 68470
                                CTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319  FLJ11259 3' CACTCCAGTCTGGGCAACAGAG 37763
                TG                CACTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||||
                                GTGAGACAACGGGTCTGACCTCAC

GAM319  FLJ11301 3' CACTCCAGCCTGGGCGACAGAG 37802
                TG                CACTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||||
                                GTGAGACAGCGGGTCCGACCTCAC

GAM319  FLJ11577 3' CACTCCAGCCTGGGCAACAAGA 47954      _
                GT                ACTTT GTTGCCCAGGCTGGAGTG
                                |||||| ||||||||||||||||
                                TGAGA CAACGGGTCCGACCTCAC
                                  A
GAM319  FLJ11700 3' CACTCCAGCCTGGGCAACAGA  46557
                                TTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||
                                AGACAACGGGTCCGACCTCAC

GAM319  FLJ11710 5' CAGCCTGGGCAACACAGTG   46243     T
                                CACT TGTTGCCCAGGCTG
                                |||| ||||||||||||||
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                                GTGA ACAACGGGTCCGAC
                                  C
GAM319  FLJ11715  3'  CACTCCAGCCTGGGTGATAGAG 44975        TG
              TG                  CACTTTGT  CCCAGGCTGGAGTG
                                  ||||||||  ||||||||||||||
                                  GTGAGATA  GGGTCCGACCTCAC
                                     GT
GAM319  FLJ11722  3'  CACTCCAGCCTGGCAACAGAG  46993          C
                                  CTTTGTTGCC AGGCTGGAGTG
                                  |||||||||| ||||||||||
                                  GAGACAACGG TCCGACCTCAC
                                             _
GAM319  FLJ11722  3'  CACTCCAGCCTGGCCACAGAG  46994       T  C
                                  CTTTGT GCC AGGCTGGAGTG
                                  ||||||| ||| ||||||||||
                                  GAGACA CGG TCCGACCTCAC
                                     C  _
GAM319  FLJ11726  3'  CACTCCAGCCTGGGCGACAGAG 47015
                                  CTTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||
                                  GAGACAGCGGGTCCGACCTCAC

GAM319  FLJ11827  3'  CACTTCAGCCTGGGCAACATAG 47679    T
                                  CT TGTTGCCCAGGCTGGAGTG
                                  || ||||||||||||||||||
                                  GA ACAACGGGTCCGACTTCAC
                                   T
GAM319  FLJ11996  3'  CACTCCAACCTGGGCAACAGAG 47056             C
              T                    ACTTTGTTGCCCAGG TGGAGTG
                                  ||||||||||||||| |||||||
                                  TGAGACAACGGGTCC ACCTCAC
                                            A
GAM319  FLJ12190  3'  CACTCCAGCCTGGGCAACAGAG 47563
                                  CTTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||
                                  GAGACAACGGGTCCGACCTCAC

GAM319  FLJ12294  3'  CACTCCAGCCTGGGTGACAGAG 47709       TG
                                  CTTTGT  CCCAGGCTGGAGTG
                                  ||||||  ||||||||||||||
                                  GAGACA  GGGTCCGACCTCAC
                                     GT
GAM319  FLJ12298  3'  CACTCCAGCCTGGGCAACAGAG 50595
                                  CTTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||
                                  GAGACAACGGGTCCGACCTCAC

GAM319  FLJ12363  3'  CACTCCAGCCTGGGCAACAAG  50630
                                  TTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||
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                                GAACAACGGGTCCGACCTCAC

GAM319  FLJ12439 3' CTCCCTCCCAGGCAACAAACTG 43837    C       CA  CT
                                CA TTTGTTGCC  GG  GGAG
                                || |||||||||  ||  ||||
                                GT AAACAACGG  CC  CCTC
                                 C        AC  TC
GAM319  FLJ12586 3' CACTCCAGCCTGGGTGACAGAG 45205       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                    GT
GAM319  FLJ12618 3' CACTCCAGCCTGGGTGACAGAG 46503       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                    GT
GAM319  FLJ12666 3' CACTCCAGCCTGGGCAACAAA  45064
                                TTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||
                                AAACAACGGGTCCGACCTCAC

GAM319  FLJ12671 3' CACTCCAGCCTGGGTGACAAG  49103      TG
                                TTTGT  CCCAGGCTGGAGTG
                                |||||  ||||||||||||||
                                GAACA  GGGTCCGACCTCAC
                                   GT
GAM319  FLJ12687 3' CACTCCAGCCTGGGTGACAGAG 46747        TG
           TG                     CACTTTGT  CCCAGGCTGGAGTG
                                ||||||||  ||||||||||||||
                                GTGAGACA  GGGTCCGACCTCAC
                                     GT
GAM319  FLJ12847 3' CAGCCTGGGCAACAGAGT    45076
                                ACTTTGTTGCCCAGGCTG
                                ||||||||||||||||||
                                TGAGACAACGGGTCCGAC

GAM319  FLJ12921 3' CACTCCAGCCTGGGCGACGGAG 46393
                                CTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||
                                GAGGCAGCGGGTCCGACCTCAC

GAM319  FLJ12949 3' CACTCCAGCCTGGGCAACAAAG 43723
                                CTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||
                                GAAACAACGGGTCCGACCTCAC

GAM319  FLJ13117 3' CACTCCAGCCTGGGAGACAGAG 43803       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
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                                GAGACA  GGGTCCGACCTCAC
                                   GA
GAM319  FLJ13193  3'  CACTCCAGCCTGGCGACAGAG  50710          C
                                CTTTGTTGCC AGGCTGGAGTG
                                |||||||||| ||||||||||
                                GAGACAGCGG TCCGACCTCAC
                                          _
GAM319  FLJ13241  3'  CACTCCAGCCTGGGTGGCAGAG 47647        TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACG  GGGTCCGACCTCAC
                                   GT
GAM319  FLJ13352  3'  GCACTCCAGCCTGGCCTGGGCA 45054                 _____     ___
          ACAGAG                  CTTTGTTGCCCAGGCT    GGAGTG  C
                                ||||||||||||||||    ||||||  |
                                GAGACAACGGGTCCGG    CCTCAC  G
                                      TCCGA    ___
GAM319  FLJ13448  3'  CACTCCAGCCTGGGCAACAGAG 47880
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319  FLJ13456  3'  CACTCCAGCCTGGACAACGGAG 66530          C
          TG                    CACTTTGTTG CCAGGCTGGAGTG
                                |||||||||| ||||||||||||
                                GTGAGGCAAC GGTCCGACCTCAC
                                     A
GAM319  FLJ13456  3'  CACTCCAGCCTGGGTGACAGAG 66531        TG
          T                     ACTTTGT  CCCAGGCTGGAGTG
                                |||||||  ||||||||||||||
                                TGAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  FLJ13456  3'  CTAGCCTGGGCAACATAGTG  66543      T
                                CACT TGTTGCCCAGGCTGG
                                ||||  ||||||||||||||
                                GTGA ACAACGGGTCCGATC
                                  T
GAM319  FLJ13621  3'  CACTCCAGCCTGGGCGACAGAG 47217
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319  FLJ13659  3'  CACTCCAGCCTGGGCAACAAGA 48027       _
          GT                    ACTTT GTTGCCCAGGCTGGAGTG
                                |||||  ||||||||||||||||||
                                TGAGA CAACGGGTCCGACCTCAC
                                  A
GAM319  FLJ13769  3'  CACTCCAGCCTGGGTGACAGAG 47245        TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
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                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  FLJ13848  3'  CACTCCAGCCTAGGCGACAGAG 45816          C
              TG                  CACTTTGTTGCC AGGCTGGAGTG
                                  |||||||||||| ||||||||||
                                  GTGAGACAGCGG TCCGACCTCAC
                                         A
GAM319  FLJ13952  3'  CACTCCAGCCTGGGCAACAAGA 46006      _
              GT                  ACTTT GTTGCCCAGGCTGGAGTG
                                  ||||| ||||||||||||||||||
                                  TGAGA CAACGGGTCCGACCTCAC
                                    A
GAM319  FLJ14011  3'  CACTCCAGTCTGGGCAACAGAG 42312
                                  CTTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||
                                  GAGACAACGGGTCTGACCTCAC

GAM319  FLJ14100  3'  CACTCCAGCCTGGGCGACAAAG 47329
                                  CTTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||
                                  GAAACAGCGGGTCCGACCTCAC

GAM319  FLJ14251  3'  CACTCCAGCCTGGGTAACAGAG 46474
                                  CTTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||
                                  GAGACAATGGGTCCGACCTCAC

GAM319  FLJ14327  3'  CACTCCAGCCTGGACAACAGAG 46674          C
                                  CTTTGTTG CCAGGCTGGAGTG
                                  |||||||| ||||||||||||
                                  GAGACAAC GGTCCGACCTCAC
                                      A
GAM319  FLJ14345  3'  CACTCCAGCCTGGGCAACAAGA 45655      _
              GT                  ACTTT GTTGCCCAGGCTGGAGTG
                                  ||||| ||||||||||||||||||
                                  TGAGA CAACGGGTCCGACCTCAC
                                    A
GAM319  FLJ14346  3'  CACTCCAGCCTGGGGGACAGAG 47357          G
                                  CTTTGTT CCCAGGCTGGAGTG
                                  ||||||| ||||||||||||||
                                  GAGACAG GGGTCCGACCTCAC
                                      G
GAM319  FLJ14397  3'  CACTCCAGCCTGGGCAACAAGG 52316
                                  CTTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||
                                  GGAACAACGGGTCCGACCTCAC

GAM319  FLJ14397  3'  CACTCCAGCCTGGGTGACAGAG 52317          TG
                                  CTTTGT  CCCAGGCTGGAGTG
                                  ||||||  ||||||||||||||
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                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  FLJ14399  3'  CACTCCAGCCTGGGCATAGAGT 52339        T
                                ACTTTGT GCCCAGGCTGGAGTG
                                ||||||| ||||||||||||||||
                                TGAGATA CGGGTCCGACCTCAC
                                   _
GAM319  FLJ14457  3'  CACTCCAGCCTGGGAGACAGAG 52401         TG
          TG                      CACTTTGT  CCCAGGCTGGAGTG
                                ||||||||  ||||||||||||||||
                                GTGAGACA  GGGTCCGACCTCAC
                                   GA
GAM319  FLJ14466  3'  CACTCCAACCTGGGCAACAGAG 52420             C
                                CTTTGTTGCCCAGG TGGAGTG
                                |||||||||||||| |||||||
                                GAGACAACGGGTCC ACCTCAC
                                      A
GAM319  FLJ14466  3'  CACTCCAGCCTGGGCAACAACA 52421     _
          GT                      ACT TTGTTGCCCAGGCTGGAGTG
                                ||| ||||||||||||||||||||
                                TGA AACAACGGGTCCGACCTCAC
                                  C
GAM319  FLJ14490  3'  CACTCCAGCCTGGGCAACAGAG 52437
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319  FLJ14621  3'  CACTCCAGCCTGGGCAACAGAG 52533
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319  FLJ14642  3'  CAGCCTGGGCAACACAGTG   52573     T
                                CACT TGTTGCCCAGGCTG
                                |||| ||||||||||||||
                                GTGA ACAACGGGTCCGAC
                                  C
GAM319  FLJ20004  3'  CACTCCAGCCTAGGCAACAAGA 96999      _    C
          GT                      ACTTT GTTGCC AGGCTGGAGTG
                                ||||| |||||| ||||||||||
                                TGAGA CAACGG TCCGACCTCAC
                                   A     A
GAM319  FLJ20004  3'  CACTCCAGCCTGGGTGACAGAG 97000         TG
          TG                      CACTTTGT  CCCAGGCTGGAGTG
                                ||||||||  ||||||||||||||||
                                GTGAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  FLJ20004  3'  CACTCCAGCCTGGGCAACAGAG 34748
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
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                                GAGACAACGGGTCCGACCTCAC

GAM319  FLJ20013  3'  CAGCCTGGGCAACATAGTG   34795     T
                                CACT TGTTGCCCAGGCTG
                                |||| |||||||||||||
                                GTGA ACAACGGGTCCGAC
                                   T
GAM319  FLJ20019  3'  CACTCCAGCCTAGGTGACAGGG 34813       TG  C
                                CTTTGT  CC AGGCTGGAGTG
                                ||||||  || ||||||||||
                                GGGACA  GG TCCGACCTCAC
                                    GT  A
GAM319  FLJ20045  3'  CACTCCAGCCTGGGTGAGAAG  34875     G TG
                                CTTT T  CCCAGGCTGGAGTG
                                ||||  |  |||||||||||||
                                GAAG A  GGGTCCGACCTCAC
                                   _ GT
GAM319  FLJ20059  3'  CACTCCAGCCTGGACAGCAGG  34923       C
                                TTTGTTG CCAGGCTGGAGTG
                                ||||||| |||||||||||||
                                GGACGAC GGTCCGACCTCAC
                                    A
GAM319  FLJ20069  3'  CACTCCAGCCTGGGGGACAGAG 34946       G
                                CTTTGTT CCCAGGCTGGAGTG
                                ||||||| |||||||||||||
                                GAGACAG GGGTCCGACCTCAC
                                    G
GAM319  FLJ20084  3'  CACTCCAGCCTGGGCAACAGAG 34994
                                CTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319  FLJ20139  3'  CACTCCAGCCTGCGTGACAAAG 35113       TG C
           TG                     CACTTTGT  C CAGGCTGGAGTG
                                ||||||||  | ||||||||||||
                                GTGAAACA  G GTCCGACCTCAC
                                    GT C
GAM319  FLJ20139  3'  CACTCTAACTTGGGCAACAAAG 35114          C
                                CTTTGTTGCCCAGG TGGAGTG
                                |||||||||||||| |||||||
                                GAAACAACGGGTTC ATCTCAC
                                       A
GAM319  FLJ20200  3'  CAGCCTGGGCAACATAGTG   35233     T
                                CACT TGTTGCCCAGGCTG
                                |||| |||||||||||||
                                GTGA ACAACGGGTCCGAC
                                   T
GAM319  FLJ20211  3'  CACTCCAGCCTGGGCAACAGAG 35255
           TG                     CACTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||||
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                                GTGAGACAACGGGTCCGACCTCAC

GAM319  FLJ20211  3'  CACTCCAGCCTGGGCGACAGAG 35256
              TG                  CACTTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||||
                                  GTGAGACAGCGGGTCCGACCTCAC

GAM319  FLJ20241  3'  CACTCCAGCCTGGACAACAGAG 35288        C
                                  CTTTGTTG CCAGGCTGGAGTG
                                  |||||||| ||||||||||||
                                  GAGACAAC GGTCCGACCTCAC
                                       A
GAM319  FLJ20306  3'  CACTCCAGCCTGGCGACAGAG  35385        C
                                  CTTTGTTGCC AGGCTGGAGTG
                                  |||||||||| ||||||||||
                                  GAGACAGCGG TCCGACCTCAC
                                           _
GAM319  FLJ20456  3'  ACTCCAGCCTGGGTAACA    35659
                                  TGTTGCCCAGGCTGGAGT
                                  |||||||||||||||||
                                  ACAATGGGTCCGACCTCA

GAM319  FLJ20546  3'  CACTCCAGCCTGGGCAACGAG  35806
                                  TTTGTTGCCCAGGCTGGAGTG
                                  |||||||||||||||||||||
                                  GAGCAACGGGTCCGACCTCAC

GAM319  FLJ20694  3'  CACTCCAGCCTGGCGACAGAG  35972        C
                                  CTTTGTTGCC AGGCTGGAGTG
                                  |||||||||| ||||||||||
                                  GAGACAGCGG TCCGACCTCAC
                                           _
GAM319  FLJ20700  3'  CACTCCAGCCTGGGCGACACAG 35998    T
                                  CT TGTTGCCCAGGCTGGAGTG
                                  || ||||||||||||||||||
                                  GA ACAGCGGGTCCGACCTCAC
                                    C
GAM319  FLJ20802  3'  CACTCCAGCCTGGGCGACAGAG 36106
                                  CTTTGTTGCCCAGGCTGGAGTG
                                  |||||||||||||||||||||
                                  GAGACAGCGGGTCCGACCTCAC

GAM319  FLJ20972  3'  CACTCCAGCCTGGGCAACAAG  47381
                                  TTTGTTGCCCAGGCTGGAGTG
                                  |||||||||||||||||||||
                                  GAACAACGGGTCCGACCTCAC

GAM319  FLJ21144  3'  CACTCCAGCCTGGGCAACAGAG 43189
              TG                  CACTTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||||
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                                GTGAGACAACGGGTCCGACCTCAC

GAM319  FLJ21162  3'  CACTCCAGCCTGGGAAATAGAG 46367          G
              TG                  CACTTTGTT CCCAGGCTGGAGTG
                                  ||||||||| ||||||||||||||
                                  GTGAGATAA GGGTCCGACCTCAC
                                     A
GAM319  FLJ21240  3'  CACTCCAGCCTGGGCAAAAAG  46259      G
                                  CTTT TTGCCCAGGCTGGAGTG
                                  |||| ||||||||||||||||
                                  GAAA AACGGGTCCGACCTCAC
                                    _
GAM319  FLJ21272  3'  CAGCCTGGGCAACATAGTG   47392      T
                                  CACT TGTTGCCCAGGCTG
                                  |||| |||||||||||||
                                  GTGA ACAACGGGTCCGAC
                                    T
GAM319  FLJ21687  3'  CACTCCAGCCTGGGTGACAGAG 46291        TG
                                  CTTTGT  CCCAGGCTGGAGTG
                                  ||||||  ||||||||||||||
                                  GAGACA  GGGTCCGACCTCAC
                                     GT
GAM319  FLJ21870  3'  CACTCCAGCCTGGGCAACGGAG 43742
                                  CTTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||
                                  GAGGCAACGGGTCCGACCTCAC

GAM319  FLJ22054  3'  CACTCCAGCCTGGGCAACAGAG 96045
                                  CTTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||
                                  GAGACAACGGGTCCGACCTCAC

GAM319  FLJ22316  3'  CACTCCAGCCTGGGCAACAGAG 47611
                                  CTTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||
                                  GAGACAACGGGTCCGACCTCAC

GAM319  FLJ22415  3'  CACTCCAGCCTGGGTGACAAAG 93118        TG
                                  CTTTGT  CCCAGGCTGGAGTG
                                  ||||||  ||||||||||||||
                                  GAAACA  GGGTCCGACCTCAC
                                     GT
GAM319  FLJ22474  3'  CACTCCAGCCTGGGCAACAGAG 45610
              TG                  CACTTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||||
                                  GTGAGACAACGGGTCCGACCTCAC

GAM319  FLJ22644  3'  CACTCCAGCCTGGGCTACAGAG 47697        T
                                  CTTTGT GCCCAGGCTGGAGTG
                                  |||||| ||||||||||||||
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                                GAGACA CGGGTCCGACCTCAC
                                   T
GAM319  FLJ22814  3'  CACTCCAACCTGGGTGACGAGT 46716      T  TG     C
           G                    CACTT GT  CCCAGG TGGAGTG
                                |||||| ||  |||||| |||||||
                                GTGAG CA  GGGTCC ACCTCAC
                                  _ GT     A
GAM319  FLJ22814  3'  CACTCCAGCCTGGGTGACAGAG 46717       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  FLJ23022  3'  CACTCCAGCCTGGGCGACAAG  47491
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||
                                GAACAGCGGGTCCGACCTCAC

GAM319  FLJ23040  3'  CACTCCAGCCTGGGCAATAGAG 47981
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||
                                GAGATAACGGGTCCGACCTCAC

GAM319  FLJ23042  3'  CACTCCAGCCTGGGCAACAAGA 47937      _
           GT                     ACTTT GTTGCCCAGGCTGGAGTG
                                  ||||| ||||||||||||||||
                                  TGAGA CAACGGGTCCGACCTCAC
                                     A
GAM319  FLJ23185  3'  CACTCCAGCCTTGGCAACAAAG 47509          C
                                CTTTGTTGCC AGGCTGGAGTG
                                |||||||||| ||||||||||
                                GAAACAACGG TCCGACCTCAC
                                      T
GAM319  FLJ23185  3'  CACTCCAGCCTTGGCAACAGAG 47510           C
           TG                     CACTTTGTTGCC AGGCTGGAGTG
                                  |||||||||||| ||||||||||
                                  GTGAGACAACGG TCCGACCTCAC
                                        T
GAM319  FLJ23360  3'  CACTCCAGCCCGGGTGACAGAG 43823       TG   A
                                CTTTGT  CCC GGCTGGAGTG
                                ||||||  ||| ||||||||||
                                GAGACA  GGG CCGACCTCAC
                                   GT   C
GAM319  FLJ23420  3'  CACTCCCCCTCCCCATGCAACA 47537         CC____   CT
           AAG                    CTTTGTTGC     AGG  GGAGTG
                                  |||||||||     |||  ||||||
                                  GAAACAACG     TCC  CCTCAC
                                        TACCCC   C_
GAM319  FLJ23537  3'  CACTCCAGCCTGGGCAACAAGA 46540      _
           G                      CTTT GTTGCCCAGGCTGGAGTG
                                  |||| ||||||||||||||||||
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                                GAGA CAACGGGTCCGACCTCAC
                                  A
GAM319  FLJ23556  3'  CACTCCAGCCTGGGCGACTGTG 46431     TTT
                                CAC   GTTGCCCAGGCTGGAGTG
                                |||   ||||||||||||||||||
                                GTG   CAGCGGGTCCGACCTCAC
                                  T__
GAM319  FLJ23556  3'  CTAGGCTGGGCAACAAAG    46438          G
                                CTTTGTTGCCCAG CTGG
                                |||||||||||| ||||
                                GAAACAACGGGTC GATC
                                       G
GAM319  FLJ25006  3'  CAGCCTGAGCAACAGAGTG   58787          C
                                CACTTTGTTGC CAGGCTG
                                |||||||||| |||||||
                                GTGAGACAACG GTCCGAC
                                       A
GAM319  FLJ30092  3'  CAGCCTGGGCAACAGAGTG   59339
                                CACTTTGTTGCCCAGGCTG
                                |||||||||||||||||||
                                GTGAGACAACGGGTCCGAC

GAM319  FLJ30681  3'  CACTCCAGCCTAGGCAACAGAG 93432          C
                                CTTTGTTGCC AGGCTGGAGTG
                                |||||||||| ||||||||||
                                GAGACAACGG TCCGACCTCAC
                                       A
GAM319  FLJ30681  3'  CACTTTCTCACTGGACACACAA 93433        _ C    GCT_
          AGTG                     CACTTTGT TG CCAG    GGAGTG
                                |||||||| || ||||    ||||||
                                GTGAAACA AC GGTC    TTTCAC
                                     C  A    ACTC
GAM319  FLJ31168  3'  CACTCCAGCCTGGGCGACAGAG 59176
                                CTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319  FLJ31455  3'  CACTCCAGCCTGGGTGACAGAG 59280       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  FLJ31952  3'  CAGCCTGGGCAACAGAGTG   59043
                                CACTTTGTTGCCCAGGCTG
                                |||||||||||||||||||
                                GTGAGACAACGGGTCCGAC

GAM319  FLJ32915  5'  CACTCCAGCCTGGGCGACAAG  59427
                                TTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||
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                                GAACAGCGGGTCCGACCTCAC

GAM319  FUSIP1   3'  CACTCCAGCCTGGGCAACAGAG 55034
                TG                  CACTTTGTTGCCCAGGCTGGAGTG
                                    ||||||||||||||||||||||||
                                    GTGAGACAACGGGTCCGACCTCAC

GAM319  GALNT6   3'  CACCCCAGCCTGAGCAACAAG  24240        C       A
                                    TTTGTTGC CAGGCTGG GTG
                                    |||||||| |||||||| |||
                                    GAACAACG GTCCGACC CAC
                                         A       C
GAM319  GALNT6   3'  CACTCCAGCCTGGGCAACAGGT 24241      T
                                    ACTT GTTGCCCAGGCTGGAGTG
                                    |||| ||||||||||||||||||
                                    TGGA CAACGGGTCCGACCTCAC
                                     _
GAM319  GALNT6   3'  CGGCCTGAGCAACATAGTG   24246     T     C
                                    CACT TGTTGC CAGGCTG
                                    |||| |||||| |||||||
                                    GTGA ACAACG GTCCGGC
                                      T     A
GAM319  GCN2     3'  CACTCCAGTCTGGGACAACAGA 63435          _
                G                    CTTTGTTG CCCAGGCTGGAGTG
                                    |||||||| ||||||||||||||
                                    GAGACAAC GGGTCTGACCTCAC
                                         A
GAM319  GLTP     3'  CACTCCAGCCTGGGCAACAAG  33581
                                    TTTGTTGCCCAGGCTGGAGTG
                                    ||||||||||||||||||||||
                                    GAACAACGGGTCCGACCTCAC

GAM319  GNB4     3'  CACTCCAGCCTAGGCGACAGAG 41564            C
                TG                    CACTTTGTTGCC AGGCTGGAGTG
                                    |||||||||||| ||||||||||
                                    GTGAGACAGCGG TCCGACCTCAC
                                           A
GAM319  GTPBP5   3'  CACTCCAGCCTGAGCGACAGAG 65967          C
                                    CTTTGTTGC CAGGCTGGAGTG
                                    ||||||||| ||||||||||||
                                    GAGACAGCG GTCCGACCTCAC
                                         A
GAM319  GTPBP5   3'  CACTCCAGCCTGAGTGACAGAG 65968        TG C
                                    CTTTGT  C CAGGCTGGAGTG
                                    ||||||  | ||||||||||||
                                    GAGACA  G GTCCGACCTCAC
                                       GT A
GAM319  GTSE1    3'  CACTCCAGCCTGGGCACCAATG 33561     T   T
                TG                    CAC TTG TGCCCAGGCTGGAGTG
                                    ||| ||| ||||||||||||||||
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                                GTG AAC ACGGGTCCGACCTCAC
                                  T   C
GAM319  HCGIX    3'  CACTCCAGCCTGGGTGACAG   20713      TG
                                TTGT  CCCAGGCTGGAGTG
                                ||||  ||||||||||||||
                                GACA  GGGTCCGACCTCAC
                                  GT
GAM319  HEI10    3'  CACTCCAGCCTGGGCAACAGAG 41293
           TG                     CACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||||
                                GTGAGACAACGGGTCCGACCTCAC

GAM319  HIC      3'  CACTCCAGCCTGGGCAACAGAG 68043
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319  HSD17B7  3'  CACTCCAGCCTGGGTGACAG   33480      TG
                                TTGT  CCCAGGCTGGAGTG
                                ||||  ||||||||||||||
                                GACA  GGGTCCGACCTCAC
                                  GT
GAM319  HSMPP8   3'  CACTCCAGCCTGAGTGACAGAA 95127    C     TG C
           TG                     CA TTTGT  C CAGGCTGGAGTG
                                || |||||  | ||||||||||||
                                GT AGACA  G GTCCGACCTCAC
                                 A    GT A
GAM319  HSPC043  3'  CACTCCAGCCTGGGTGACAGTG 68348      TT  TG
                                CACT  GT  CCCAGGCTGGAGTG
                                ||||  ||  ||||||||||||||
                                GTGA  CA  GGGTCCGACCTCAC
                                  __  GT
GAM319  ICAM4    3'  CACTCCAGCCTGGGGGACAGAG 9533         G
                                CTTTGTT CCCAGGCTGGAGTG
                                ||||||| ||||||||||||||
                                GAGACAG GGGTCCGACCTCAC
                                    G
GAM319  ICAM4    3'  CAGCCTGGACAACATAGTG    9536       T    C
                                CACT TGTTG CCAGGCTG
                                |||| ||||| ||||||||
                                GTGA ACAAC GGTCCGAC
                                  T    A
GAM319  ICAM4    3'  CACTCCAGCCTGGGGGACAGAG 42589         G
                                CTTTGTT CCCAGGCTGGAGTG
                                ||||||| ||||||||||||||
                                GAGACAG GGGTCCGACCTCAC
                                    G
GAM319  ICAM4    3'  CAGCCTGGACAACATAGTG    42590      T    C
                                CACT TGTTG CCAGGCTG
                                |||| ||||| ||||||||
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                                GTGA ACAAC GGTCCGAC
                                  T    A
GAM319  IL-23R   3'  CACTCCAGCCTGGGCAACAAG  59128
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||
                                GAACAACGGGTCCGACCTCAC

GAM319  IL10RB   3'  CACTCCAGCCTGGGTGACAAAG 7124          TG
          TG                      CACTTTGT  CCCAGGCTGGAGTG
                                ||||||||  ||||||||||||||
                                GTGAAACA  GGGTCCGACCTCAC
                                    GT
GAM319  IMAGE:4907098 3'  CACTCCAGCCTGGGCGACAGAG 93323
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319  KBRAS2   3'  CACTCCAGCCTGGTCAACAGAG 34619         C
                                CTTTGTTG CCAGGCTGGAGTG
                                ||||||||| ||||||||||||
                                GAGACAAC GGTCCGACCTCAC
                                    T
GAM319  KCNH6    3'  CACTCCAGCCTGGGTGACAGAG 48568         TG
          TG                      CACTTTGT  CCCAGGCTGGAGTG
                                ||||||||  ||||||||||||||
                                GTGAGACA  GGGTCCGACCTCAC
                                    GT
GAM319  KIAA0057 3'  CACTCCAGCCTGGACAACAAG  25403        C
                                TTTGTTG CCAGGCTGGAGTG
                                ||||||| ||||||||||||
                                GAACAAC GGTCCGACCTCAC
                                    A
GAM319  KIAA0184 3'  CACTCCAGCCTGGGTGACAG   65805      TG
                                TTGT  CCCAGGCTGGAGTG
                                ||||  ||||||||||||||
                                GACA  GGGTCCGACCTCAC
                                  GT
GAM319  KIAA0226 3'  CACTCCAGCCTGGGTGACAGAG 64254         TG
          TG                      CACTTTGT  CCCAGGCTGGAGTG
                                ||||||||  ||||||||||||||
                                GTGAGACA  GGGTCCGACCTCAC
                                    GT
GAM319  KIAA0355 3'  CACTCCAGCCTGGGTGACAGAG 28699         TG
          TG                      CACTTTGT  CCCAGGCTGGAGTG
                                ||||||||  ||||||||||||||
                                GTGAGACA  GGGTCCGACCTCAC
                                    GT
GAM319  KIAA0391 3'  CACTCCAGCCTAGGTGACAGAG 28602         TG  C
          TG                      CACTTTGT  CC AGGCTGGAGTG
                                ||||||||  || ||||||||||
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                                GTGAGACA  GG TCCGACCTCAC
                                    GT  A
GAM319  KIAA0408  3'  CACTCCAGCCTGGGTGACAGAG 28794        TG
              TG                  CACTTTGT  CCCAGGCTGGAGTG
                                  ||||||||  ||||||||||||||
                                  GTGAGACA  GGGTCCGACCTCAC
                                      GT
GAM319  KIAA0420  3'  CAGCCTGGGCAACATAGTG   64083      T
                                  CACT TGTTGCCCAGGCTG
                                  ||||  ||||||||||||||
                                  GTGA ACAACGGGTCCGAC
                                    T
GAM319  KIAA0446  5'  CACTCCAGCCTGGGCGACAGAG 69442
                                  CTTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||
                                  GAGACAGCGGGTCCGACCTCAC

GAM319  KIAA0447  3'  CACTCCAGCCTGGGCAACAGGG 72103
                                  CTTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||
                                  GGGACAACGGGTCCGACCTCAC

GAM319  KIAA0451  5'  CACTTCAGCCTGGGCAACAGAG 29764
                                  CTTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||
                                  GAGACAACGGGTCCGACTTCAC

GAM319  KIAA0472  3'  CACTCCAGCCTGGGCAACAGAG 72337
                                  CTTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||
                                  GAGACAACGGGTCCGACCTCAC

GAM319  KIAA0472  3'  CACTCCAGCCTGGGCAGCAGAG 72338
                                  CTTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||
                                  GAGACGACGGGTCCGACCTCAC

GAM319  KIAA0472  3'  CACTCCAGCCTGGGCGACAGAG 72339
              TG                  CACTTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||||
                                  GTGAGACAGCGGGTCCGACCTCAC

GAM319  KIAA0475  3'  CACTCCAGCCTGGGAGACAGAG 30112       TG
                                  CTTTGT  CCCAGGCTGGAGTG
                                  ||||||  ||||||||||||||
                                  GAGACA  GGGTCCGACCTCAC
                                      GA
GAM319  KIAA0547  3'  CACTCCAGCCTGGCAACAGAG  29589         C
                                  CTTTGTTGCC AGGCTGGAGTG
                                  |||||||||| ||||||||||
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                                GAGACAACGG TCCGACCTCAC
                                      _
GAM319  KIAA0547 3' CAGCCCAGGCAACAAAGT    29590          CA
                                ACTTTGTTGCC  GGCTG
                                ||||||||||  |||||
                                TGAAACAACGG  CCGAC
                                      AC
GAM319  KIAA0563 3' CACTCCAGCCTGGGCGACAGAG 29870
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319  KIAA0565 3' CACTCCAACCTGGGCGACAGAG 67432              C
                                CTTTGTTGCCCAGG TGGAGTG
                                |||||||||||||| |||||||
                                GAGACAGCGGGTCC ACCTCAC
                                      A
GAM319  KIAA0596 3' CACTCCAACCTAGGTGACAAAG 63483       TG  C   C
                                CTTTGT  CC AGG TGGAGTG
                                ||||||  || ||| |||||||
                                GAAACA  GG TCC ACCTCAC
                                   GT  A   A
GAM319  KIAA0635 3' CACTCCAGCCTGGGTGACAGAG 28411        TG
           T                     ACTTTGT  CCCAGGCTGGAGTG
                                ||||||| ||||||||||||||
                                TGAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  KIAA0643 3' CACTCCAGCCTGGGTGACAGAG 45971         TG
           TG                      CACTTTGT  CCCAGGCTGGAGTG
                                ||||||||  ||||||||||||||
                                GTGAGACA  GGGTCCGACCTCAC
                                     GT
GAM319  KIAA0643 3' CTAGCCTGGACAACTAAGTG   45975      T   C
                                CACTT GTTG CCAGGCTGG
                                ||||| |||| |||||||||
                                GTGAA CAAC GGTCCGATC
                                   T   A
GAM319  KIAA0694 3' CACTCCAGCCTGGGCAACAGAG 72964
           TG                      CACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||||
                                GTGAGACAACGGGTCCGACCTCAC

GAM319  KIAA0694 3' CAGCCTGGGCAACATAGTG    72966      T
                                CACT TGTTGCCCAGGCTG
                                |||| ||||||||||||||
                                GTGA ACAACGGGTCCGAC
                                   T
GAM319  KIAA0738 3' CACTCCAGCCTGGGGGACAGAG 28883         G
           TG                      CACTTTGTT CCCAGGCTGGAGTG
                                |||||||| ||||||||||||||
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                                GTGAGACAG GGGTCCGACCTCAC
                                     G
GAM319  KIAA0752  3'  CACTCCAGCCTGGGCAACGAG  67631
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||
                                GAGCAACGGGTCCGACCTCAC

GAM319  KIAA0794  3'  CACTCCAGCCTGGGCGACAAAG 81225
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||
                                GAAACAGCGGGTCCGACCTCAC

GAM319  KIAA0825  3'  CACCCCAGCCTGGGCAATGAGT 61681     T TG          A
          G                      CAC T  TTGCCCAGGCTGG GTG
                                ||| |  |||||||||||| |||
                                GTG A  AACGGGTCCGACC CAC
                                  _ GT           C
GAM319  KIAA0831  3'  CACTCCAGCCTGGGCAACAAG  30629
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||
                                GAACAACGGGTCCGACCTCAC

GAM319  KIAA0853  3'  CACTCCAACCTAGGTGACAGAG 31211       TG  C   C
                                CTTTGT  CC AGG TGGAGTG
                                ||||||  || ||| |||||||
                                GAGACA  GG TCC ACCTCAC
                                    GT  A   A
GAM319  KIAA0872  3'  CACTCCAGCCTGGGTGACAGAG 30742        TG
          TG                      CACTTTGT  CCCAGGCTGGAGTG
                                ||||||||  ||||||||||||||
                                GTGAGACA  GGGTCCGACCTCAC
                                     GT
GAM319  KIAA0876  3'  CACTCCAGCCTGGGCAACAGAG 65314
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319  KIAA0889  3'  CACTCCAGCCTGGGTGACAGA  31759      TG
                                TTTGT  CCCAGGCTGGAGTG
                                |||||  |||||||||||||
                                AGACA  GGGTCCGACCTCAC
                                   GT
GAM319  KIAA0889  3'  CACTCCAGCCTGGGTGACAGAG 31760        TG
          TG                      CACTTTGT  CCCAGGCTGGAGTG
                                ||||||||  ||||||||||||||
                                GTGAGACA  GGGTCCGACCTCAC
                                     GT
GAM319  KIAA0894  3'  CACTCCAGCCTGGGTGACAGAG 30327       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
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                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  KIAA0961  3'  CACTCCAGCCTGGGCAACAAG  30393
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||
                                GAACAACGGGTCCGACCTCAC

GAM319  KIAA1001  3'  CACTCCAGCCTGGGTGATGGAG 31001     TG TG
                                CTT  T  CCCAGGCTGGAGTG
                                |||  |  ||||||||||||||
                                GAG  A  GGGTCCGACCTCAC
                                  GT GT
GAM319  KIAA1017  3'  CAGCCTGGGCAACATAGTG   24268      T
                                CACT TGTTGCCCAGGCTG
                                ||||| ||||||||||||||
                                GTGA ACAACGGGTCCGAC
                                   T
GAM319  KIAA1030  3'  CACTCCAGCCTGGGTGACAGAG 94972       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  KIAA1030  3'  CAGCCTGGGCAACATAGTG   94973      T
                                CACT TGTTGCCCAGGCTG
                                ||||| ||||||||||||||
                                GTGA ACAACGGGTCCGAC
                                   T
GAM319  KIAA1032  3'  CACTCCAGCCTGGGCAACAGA  66723
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||
                                AGACAACGGGTCCGACCTCAC

GAM319  KIAA1086  3'  CACTCCAGCCTGGGCAACAGA  71282
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||
                                AGACAACGGGTCCGACCTCAC

GAM319  KIAA1086  3'  CAGCCCAGACAACAGAGTG   71283          CCCA
                                CACTTTGTTG   GGCTG
                                |||||||||   |||||
                                GTGAGACAAC   CCGAC
                                      AGAC
GAM319  KIAA1143  3'  CACTCCAGCCTGGGCAACAGAG 69230
             T                   ACTTTGTTGCCCAGGCTGGAGTG
                                 ||||||||||||||||||||||
                                 TGAGACAACGGGTCCGACCTCAC

GAM319  KIAA1160  3'  CACTCCAGCCTGGCGACAGAGT 40752           C
             G                   CACTTTGTTGCC AGGCTGGAGTG
                                 |||||||||||| ||||||||||
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                                GTGAGACAGCGG TCCGACCTCAC
                                           _
GAM319  KIAA1164  3' CACTCCAGCCTGGGTGACAGAG 70035       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  KIAA1191  3' CACTCCAGCCTGGGCGACAGA  40331
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                AGACAGCGGGTCCGACCTCAC

GAM319  KIAA1202  3' CACTCCATCCTGGGCAACAGAG 72485              C
           TG                     CACTTTGTTGCCCAGG TGGAGTG
                                ||||||||||||||| |||||||
                                GTGAGACAACGGGTCC ACCTCAC
                                         T
GAM319  KIAA1228  3' CACTCCAGCCTGGGCAACAGAG 65668
           TG                     CACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||||
                                GTGAGACAACGGGTCCGACCTCAC

GAM319  KIAA1253  3' CACTCTAGCCTGGGCAACAGAG 93548
           T                      ACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                TGAGACAACGGGTCCGATCTCAC

GAM319  KIAA1257  3' CACTCCAGCCTGAAGCAA    63393     C_
                                TTGC  CAGGCTGGAGTG
                                ||||  ||||||||||||
                                AACG  GTCCGACCTCAC
                                  AA
GAM319  KIAA1271  3' CACTCCAACCTGGGTGAGAGAG 70128     G TG     C
                                CTTT T  CCCAGG TGGAGTG
                                |||| |  |||||| |||||||
                                GAGA A  GGGTCC ACCTCAC
                                  G GT     A
GAM319  KIAA1277  3' CACTCCAGCCTGGACAACAGAG 65071        C
                                CTTTGTTG CCAGGCTGGAGTG
                                |||||||| ||||||||||||
                                GAGACAAC GGTCCGACCTCAC
                                     A
GAM319  KIAA1328  3' CACTCCAGCCTGGGTGACAGAG 62317       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  KIAA1340  3' CACTCCAGCCTGGGCGACAGTG 69693     TT
                                CACT  GTTGCCCAGGCTGGAGTG
                                ||||  ||||||||||||||||||
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                                GTGA  CAGCGGGTCCGACCTCAC
                                  __
GAM319  KIAA1348  3'  CACTCCAGCCTGGGCAACAAGA 69119      _
              GT                  ACTTT GTTGCCCAGGCTGGAGTG
                                  |||||| ||||||||||||||||||
                                  TGAGA CAACGGGTCCGACCTCAC
                                    A
GAM319  KIAA1364  3'  CACTCCAGCCTGTGTGACAGAA 64343    C    TG C
              TG                  CA TTTGT  C CAGGCTGGAGTG
                                  || |||||  | ||||||||||||
                                  GT AGACA  G GTCCGACCTCAC
                                   A    GT T
GAM319  KIAA1399  3'  CCAACTCAACAACAAAGTG   70791          CCC  GC
                                  CACTTTGTTG   AG  TGG
                                  ||||||||||   ||  |||
                                  GTGAAACAAC   TC  ACC
                                        AAC  A_
GAM319  KIAA1423  3'  CACTCCAGCCTGGGTGTCAGAG 62390       T
                                  CTTTG TGCCCAGGCTGGAGTG
                                  |||||| ||||||||||||||||
                                  GAGAC GTGGGTCCGACCTCAC
                                     T
GAM319  KIAA1456  3'  CACTCCAACCTGGGCAACAAGA 67534       _        C
              GT                  ACTTT GTTGCCCAGG TGGAGTG
                                  |||||| |||||||||| |||||||
                                  TGAGA CAACGGGTCC ACCTCAC
                                     A         A
GAM319  KIAA1456  3'  CACTGCAGCCTGGGCAACATAG 67537    T           G
                                  CT TGTTGCCCAGGCTG AGTG
                                  || ||||||||||||| ||||
                                  GA ACAACGGGTCCGAC TCAC
                                   T           G
GAM319  KIAA1486  3'  CACTCCAGCCTGGGTGACAGAG 67969       TG
                                  CTTTGT  CCCAGGCTGGAGTG
                                  ||||||  ||||||||||||||
                                  GAGACA  GGGTCCGACCTCAC
                                     GT
GAM319  KIAA1494  3'  ACTTCACACAACAAAGT     68979          CCCAGGC
                                  ACTTTGTTG      TGGAGT
                                  |||||||||      ||||||
                                  TGAAACAAC      ACTTCA
                                        AC_____
GAM319  KIAA1497  5'  CACTCCAGCCTGGGCGACAGAG 68115
                                  CTTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||
                                  GAGACAGCGGGTCCGACCTCAC

GAM319  KIAA1503  3'  CACTCCAGCCTGGGCGACAGAG 68897
              TG                  CACTTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||||
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                                GTGAGACAGCGGGTCCGACCTCAC

GAM319  KIAA1508 3' CACTCCAGCCTGGGTGACAGAG 62543       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  KIAA1554 3' CACTCCAACCTGGGTGACAGAG 96853        TG     C
           TG                     CACTTTGT  CCCAGG TGGAGTG
                                ||||||||  ||||||| |||||||
                                GTGAGACA  GGGTCC ACCTCAC
                                     GT     A
GAM319  KIAA1559 3' CACTCCAGCCTGGGTAACAGAG 73446
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAATGGGTCCGACCTCAC

GAM319  KIAA1559 3' CACTCCAGCCTGGGTGACAGAG 73447        TG
           TG                     CACTTTGT  CCCAGGCTGGAGTG
                                ||||||||  ||||||||||||||
                                GTGAGACA  GGGTCCGACCTCAC
                                     GT
GAM319  KIAA1614 3' CACTCCAGCCTGGGCAACAAG  70662
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAACAACGGGTCCGACCTCAC

GAM319  KIAA1641 3' CACTCCAGCCTGAGCAACAGAG 81016          C
           TG                     CACTTTGTTGC CAGGCTGGAGTG
                                ||||||||||| ||||||||||||
                                GTGAGACAACG GTCCGACCTCAC
                                      A
GAM319  KIAA1644 3' CACTCCAGCCTGGGCAACAGAG 86217
           TG                     CACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||||
                                GTGAGACAACGGGTCCGACCTCAC

GAM319  KIAA1649 3' CACTCCAGCCTGTGCAACAGAG 51218         C
                                CTTTGTTGC CAGGCTGGAGTG
                                |||||||| ||||||||||||
                                GAGACAACG GTCCGACCTCAC
                                      T
GAM319  KIAA1649 3' CATCCTGGGCAACACAGTG   51222     T       C
                                CACT TGTTGCCCAGG TG
                                |||| |||||||||| ||
                                GTGA ACAACGGGTCC AC
                                  C         T
GAM319  KIAA1656 5' CACTCCAGCCTGGCAACAGAGT 66359          C
           G                      CACTTTGTTGCC AGGCTGGAGTG
                                ||||||||||| ||||||||||
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                                GTGAGACAACGG TCCGACCTCAC
                                           _
GAM319  KIAA1674  3' CACTCCAGCCTGGGCGACAGAG 69330
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319  KIAA1727  3' CACTCCAGCCTGGATGACAGAG 64750         GC
          TG                    CACTTTGTT  CCAGGCTGGAGTG
                                |||||||||  ||||||||||||
                                GTGAGACAG  GGTCCGACCTCAC
                                     TA
GAM319  KIAA1751  3' CACTCCAGCCTGGCCTATAAG  72150       TGC
                                TTTGT   CCAGGCTGGAGTG
                                |||||   ||||||||||||
                                GAATA   GGTCCGACCTCAC
                                   TCC
GAM319  KIAA1771  3' CACTCCAGCCTGGACAACAGAG 79864         C
          T                     ACTTTGTTG CCAGGCTGGAGTG
                                ||||||||| ||||||||||||
                                TGAGACAAC GGTCCGACCTCAC
                                     A
GAM319  KIAA1786  3' CACCCCAGCCCGGGTGACAGAG 66628       TG  A    A
                                CTTTGT  CCC GGCTGG GTG
                                ||||||  ||| |||||| |||
                                GAGACA  GGG CCGACC CAC
                                   GT  C    C
GAM319  KIAA1821  3' CAGCCTGGGCAACATAGTG   72260     T
                                CACT TGTTGCCCAGGCTG
                                |||| ||||||||||||||
                                GTGA ACAACGGGTCCGAC
                                  T
GAM319  KIAA1871  3' CACTCCAGCCTGGGCAACAAGT 61895       T
          G                     CACTT GTTGCCCAGGCTGGAGTG
                                ||||| ||||||||||||||||||
                                GTGAA CAACGGGTCCGACCTCAC
                                           _
GAM319  KIAA1872  3' CACTCCAGCCTGGGAGACAGAG 63596       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GA
GAM319  KIAA1872  3' CACTCCAGCCTGGGCAACAAG  63597
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAACAACGGGTCCGACCTCAC

GAM319  KIAA1879  3' CACTCCAGCCTGGGAGACAGAG 73930       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
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                                GAGACA  GGGTCCGACCTCAC
                                   GA
GAM319  KIAA1941  3'  CACTCCAGCCCGGGCGACAG  75334         A
                                TTGTTGCCC GGCTGGAGTG
                                ||||||||| ||||||||||
                                GACAGCGGG CCGACCTCAC
                                     C
GAM319  KIAA1948  3'  CACTCCAGCCTGGGTGACAGA  83293      TG
                                TTTGT  CCCAGGCTGGAGTG
                                |||||  ||||||||||||||
                                AGACA  GGGTCCGACCTCAC
                                   GT
GAM319  KIAA1948  5'  CACTCCAGCCTGGGTGACAGAG 83294        TG
            TG                    CACTTTGT  CCCAGGCTGGAGTG
                                ||||||||  ||||||||||||||
                                GTGAGACA  GGGTCCGACCTCAC
                                     GT
GAM319  KIAA1951  3'  CACTCCAGCCTGGGCGACAGAG 74146
            TG                    CACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||||
                                GTGAGACAGCGGGTCCGACCTCAC

GAM319  KIAA1958  3'  CACTCCAGCCTGGGCAACAAAG 82776
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAAACAACGGGTCCGACCTCAC

GAM319  KIAA1969  3'  CACTCCAGTTTGGCAACAGAGT 79474           C
            G                    CACTTTGTTGCC AGGCTGGAGTG
                                ||||||||||| ||||||||||
                                GTGAGACAACGG TTTGACCTCAC
                                          _
GAM319  KR18      3'  CACTCCAGCCTGGGCAACAAG  53881
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAACAACGGGTCCGACCTCAC

GAM319  KR18      3'  CACTCCAGCCTGGGCACCAGG  53882      T
                                TTTG TGCCCAGGCTGGAGTG
                                |||| ||||||||||||||||
                                GGAC ACGGGTCCGACCTCAC
                                   C
GAM319  KREMEN    3'  CACTCCAGCCTGAGCAGCAGAG 50227         C
                                CTTTGTTGC CAGGCTGGAGTG
                                ||||||||| ||||||||||||
                                GAGACGACG GTCCGACCTCAC
                                     A
GAM319  KREMEN    3'  CACTCCAGTGTAGGCAACAGAG 50228           CAG
            TG                    CACTTTGTTGCC   GCTGGAGTG
                                ||||||||||||   |||||||||
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                                GTGAGACAACGG  TGACCTCAC
                                      ATG
GAM319  LANO    3'  CACTCCAGCCCGGGTGACAGAG 47969       TG  A
                                CTTTGT  CCC GGCTGGAGTG
                                ||||||  ||| ||||||||||
                                GAGACA  GGG CCGACCTCAC
                                   GT   C
GAM319  LIM     3'  CACTCCAGCCTGGGTGACAGAG 22317        TG
           TG                     CACTTTGT  CCCAGGCTGGAGTG
                                ||||||||  ||||||||||||||
                                GTGAGACA  GGGTCCGACCTCAC
                                     GT
GAM319  LIM     3'  CACTCCAGCCTGGTGACAGAG  22318       TG  C
                                CTTTGT  CC AGGCTGGAGTG
                                ||||||  || ||||||||||
                                GAGACA  GG TCCGACCTCAC
                                   GT  _
GAM319  LIN-28  3'  CACTCCAGCCTGGTTACAGAG  45467       TGC
                                CTTTGT   CCAGGCTGGAGTG
                                ||||||   ||||||||||||
                                GAGACA   GGTCCGACCTCAC
                                   TT_
GAM319  LSR68   3'  CACTCCAGCCTGGGCGACAGAA 38550    C
           TG                     CA TTTGTTGCCCAGGCTGGAGTG
                                || ||||||||||||||||||||
                                GT AGACAGCGGGTCCGACCTCAC
                                 A
GAM319  MACF1   3'  CACTCCAGCCTGGGCAACAGAC 53493      ____
           AGAGTG                   CACTT   TGTTGCCCAGGCTGGAGTG
                                |||||   ||||||||||||||||||
                                GTGAG   ACAACGGGTCCGACCTCAC
                                   ACAG
GAM319  MAWBP   3'  CACTCCAGCCTGGGCAACAGAG 42377
           T                     ACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                TGAGACAACGGGTCCGACCTCAC

GAM319  MCAM    3'  CACTCCAGCCTGGGCAACACAG 22455    T
                                CT TGTTGCCCAGGCTGGAGTG
                                || ||||||||||||||||||
                                GA ACAACGGGTCCGACCTCAC
                                 C
GAM319  MED6    3'  CAGCCTGGGCAACATAGTG   19612     T
                                CACT TGTTGCCCAGGCTG
                                |||| ||||||||||||
                                GTGA ACAACGGGTCCGAC
                                   T
GAM319  MGC10200 3'  CACTCCAGTCTGGGCAACAGAG 59635
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
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                                GAGACAACGGGTCTGACCTCAC

GAM319  MGC10765  3' CACTCCAGCCTAGGCGACAGAG 44555          C
                                CTTTGTTGCC AGGCTGGAGTG
                                |||||||||| ||||||||||
                                GAGACAGCGG TCCGACCTCAC
                                      A
GAM319  MGC10771  3' CACTCCAGCCTGGCTGACAGTG 44711      TT   GC
                                CACT  GTT  CCAGGCTGGAGTG
                                ||||  |||  ||||||||||||
                                GTGA  CAG  GGTCCGACCTCAC
                                   __   TC
GAM319  MGC10814  5' CAGCCTGGGCAACAGAGTG   52014
                                CACTTTGTTGCCCAGGCTG
                                ||||||||||||||||||
                                GTGAGACAACGGGTCCGAC

GAM319  MGC10940  3' CAGCCTGGACAACATAGT    51184     T    C
                                ACT TGTTG CCAGGCTG
                                ||| ||||| ||||||||
                                TGA ACAAC GGTCCGAC
                                  T    A
GAM319  MGC11352  3' CACTCCAGCCTGGGCTCAAA   65427      TT
                                TTTG  GCCCAGGCTGGAGTG
                                ||||  ||||||||||||||
                                AAAC  CGGGTCCGACCTCAC
                                  T_
GAM319  MGC11386  3' CACTCCAGCCTGGGCAACAGAG 53057
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319  MGC12945  3' CACTCCAGCCTAGGCATGGTG  51264      TTGT    C
                                CACT    TGCC AGGCTGGAGTG
                                ||||    |||| ||||||||||
                                GTGG    ACGG TCCGACCTCAC
                                  T___    A
GAM319  MGC13008  3' CACTCCAGCCTGGGCAACAGAA 52056    C
           TG                     CA TTTGTTGCCCAGGCTGGAGTG
                                || ||||||||||||||||||
                                GT AGACAACGGGTCCGACCTCAC
                                 A
GAM319  MGC13017  3' CACTCCAGCCTAGGCAATAAG  55570          C
                                TTTGTTGCC AGGCTGGAGTG
                                ||||||||| ||||||||||
                                GAATAACGG TCCGACCTCAC
                                      A
GAM319  MGC13053  3' CACTCCAGCCTGGGCGACAG   52096
                                TTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||
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                              GACAGCGGGTCCGACCTCAC

GAM319  MGC13053  3' CACTCCAGCCTGGGCGACAGAG 52097
             TG                CACTTTGTTGCCCAGGCTGGAGTG
                               ||||||||||||||||||||||||
                               GTGAGACAGCGGGTCCGACCTCAC

GAM319  MGC14407  3' CACTCCAGCCTGGGTGACAGAG 52969       TG
                               CTTTGT  CCCAGGCTGGAGTG
                               ||||||  ||||||||||||||
                               GAGACA  GGGTCCGACCTCAC
                                  GT
GAM319  MGC14436  3' CACTCCAGCCTGGGTGACAGA  52921      TG
                               TTTGT  CCCAGGCTGGAGTG
                               |||||  ||||||||||||||
                               AGACA  GGGTCCGACCTCAC
                                  GT
GAM319  MGC14799  3' CACTCCAGCCTGGGTGACAGTG 51324     TT  TG
                               CACT  GT  CCCAGGCTGGAGTG
                               ||||  ||  ||||||||||||||
                               GTGA  CA  GGGTCCGACCTCAC
                                 __  GT
GAM319  MGC15397  3' CACTCCAGCCTGGGTGATAGAG 55550        TG
             TG                CACTTTGT  CCCAGGCTGGAGTG
                               ||||||||  ||||||||||||||
                               GTGAGATA  GGGTCCGACCTCAC
                                    GT
GAM319  MGC15606  3' CAGCCTGGGCAACATAGT    59520     T
                               ACT TGTTGCCCAGGCTG
                               ||| ||||||||||||||
                               TGA ACAACGGGTCCGAC
                                 T
GAM319  MGC16037  3' CACTCCAGCCTGGACAACAGAG 52889          C
             TG                CACTTTGTTG CCAGGCTGGAGTG
                               ||||||||||| ||||||||||||
                               GTGAGACAAC GGTCCGACCTCAC
                                     A
GAM319  MGC16175  3' CACTCCAGCCTGGGCAATAGAG 52273
                               CTTTGTTGCCCAGGCTGGAGTG
                               ||||||||||||||||||||||
                               GAGATAACGGGTCCGACCTCAC

GAM319  MGC16332  3' CACTCCAGCCTGGTCAACAAAG 57542         C
                               CTTTGTTG CCAGGCTGGAGTG
                               |||||||| ||||||||||||
                               GAAACAAC GGTCCGACCTCAC
                                    T
GAM319  MGC16332  3' CAGCCTGGGCAACATAGTG   57543      T
                               CACT TGTTGCCCAGGCTG
                               |||| ||||||||||||||
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                                GTGA ACAACGGGTCCGAC
                                  T
GAM319  MGC16703  3'  CACTCCAGCCTGGGCAACAGAG 73487
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319  MGC17998  3'  CACTCCAGCCTGGTGACAG   59386     TG  C
                                TTGT  CC AGGCTGGAGTG
                                ||||  || ||||||||||
                                GACA  GG TCCGACCTCAC
                                  GT  _
GAM319  MGC20235  3'  CACTCCAGCCTGGGCAAAAGAG 59549      G
                                CTTT TTGCCCAGGCTGGAGTG
                                ||||| ||||||||||||||||
                                GAGA AACGGGTCCGACCTCAC
                                  A
GAM319  MGC23244  3'  CACTCCAGCCTGGGCGACAGAG 58827
            TG                    CACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||||
                                GTGAGACAGCGGGTCCGACCTCAC

GAM319  MGC2396   3'  CACTCCAGCCTGGGCAATAAGA 54557       _
            GT                    ACTTT GTTGCCCAGGCTGGAGTG
                                ||||| ||||||||||||||||
                                TGAGA TAACGGGTCCGACCTCAC
                                  A
GAM319  MGC2562   3'  CACTCCAGCCTGACGACAAAGC 51426    A       CC
            G                     C CTTTGTTG  CAGGCTGGAGTG
                                | ||||||||  ||||||||||||
                                G GAAACAGC  GTCCGACCTCAC
                                 C       A_
GAM319  MGC2562   3'  CACTCCAGCCTGGAAGAC    51427     GC
                                GTT  CCAGGCTGGAGTG
                                |||  ||||||||||||
                                CAG  GGTCCGACCTCAC
                                  AA
GAM319  MGC2562   3'  CACTCCAGCCTGGGCGACAGAG 51428
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319  MGC2663   3'  CACTCCAGCCTGGGCGATGGAG 44331       TG
            TG                    CACTT  TTGCCCAGGCTGGAGTG
                                |||||  ||||||||||||||||
                                GTGAG  AGCGGGTCCGACCTCAC
                                  GT
GAM319  MGC26641  3'  CACTCCAGCCTGGGCAATAGGG 59321
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
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                                GGGATAACGGGTCCGACCTCAC

GAM319  MGC2731   3' CACTCCAGCCTGGGCAATAAG  44160
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||
                                GAATAACGGGTCCGACCTCAC

GAM319  MGC29891  3' CACTCCAGCCTGGCGACACAGT 58849     T      C
           G                     CACT TGTTGCC AGGCTGGAGTG
                                 |||| ||||||| ||||||||||
                                 GTGA ACAGCGG TCCGACCTCAC
                                   C      _
GAM319  MGC29891  3' CACTCCAGCCTGGGCAACAGAG 58850
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319  MGC29937  3' CACTCCAGCCTGGGCAACAAGA 58726       _
           GT                     ACTTT GTTGCCCAGGCTGGAGTG
                                  ||||| ||||||||||||||||||
                                  TGAGA CAACGGGTCCGACCTCAC
                                    A
GAM319  MGC3101   5' CACTCCAGCCTGGGTGACAGAG 44100       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  MGC3169   3' ACTCCAGCCTGGCCAATA    44177      C
                                TGTTG CCAGGCTGGAGT
                                ||||| ||||||||||||
                                ATAAC GGTCCGACCTCA
                                   C
GAM319  MGC3207   3' CACTCCAGCCTGGGCAACAGAG 63232
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319  MGC3329   3' CACTACAGCCTGGGCGACAAAG 44239                 G
           TG                     CACTTTGTTGCCCAGGCTG AGTG
                                  |||||||||||||||||| ||||
                                  GTGAAACAGCGGGTCCGAC TCAC
                                            A
GAM319  MGC4663   3' CACTCCAGCCTGGGCAACAGAG 44782
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319  MGC4771   3' CACTCCAGCCTGGGCAACAGAG 52000
           TG                     CACTTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||||
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                                GTGAGACAACGGGTCCGACCTCAC

GAM319  MGC4840  3' CACTCCAGCCTGGCTGACAGAG 72017       GC
                                CTTTGTT CCAGGCTGGAGTG
                                ||||||| ||||||||||||
                                GAGACAG GGTCCGACCTCAC
                                    TC
GAM319  MGC5457  3' CACTCCAGCCTGGGTGACAGAG 51936      TG
                                CTTTGT CCCAGGCTGGAGTG
                                |||||| ||||||||||||||
                                GAGACA GGGTCCGACCTCAC
                                   GT
GAM319  MOST2    5' CACTCCAGCCTGGGCACCACAG 40054    T T
                                CT TG TGCCCAGGCTGGAGTG
                                || || ||||||||||||||||
                                GA AC ACGGGTCCGACCTCAC
                                 C  C
GAM319  MRPL48   5' CACTCCAGCCTGCGCAACAGAG 32656       C
                                CTTTGTTGC CAGGCTGGAGTG
                                ||||||||| ||||||||||||
                                GAGACAACG GTCCGACCTCAC
                                     C
GAM319  MRPS10   3' CACTCCAGCCTGGCGACAGAG  36814       C
                                CTTTGTTGCC AGGCTGGAGTG
                                |||||||||| ||||||||||
                                GAGACAGCGG TCCGACCTCAC
                                          _
GAM319  MRPS18B  3' CACTCCAGCCTGGGTGACAG   26748     TG
                                TTGT CCCAGGCTGGAGTG
                                ||||  ||||||||||||||
                                GACA GGGTCCGACCTCAC
                                  GT
GAM319  My015    3' CACTCCAGCCTGGGAGACAGAG 67227      TG
                                CTTTGT CCCAGGCTGGAGTG
                                |||||| ||||||||||||||
                                GAGACA GGGTCCGACCTCAC
                                   GA
GAM319  NDUFC2   3' CACTCCAGCCTGGGTGACAAAG 17026      TG
                                CTTTGT CCCAGGCTGGAGTG
                                |||||| ||||||||||||||
                                GAAACA GGGTCCGACCTCAC
                                   GT
GAM319  NMNAT    3' CACTCCAGCCTGGCGACAGAG  43277       C
                                CTTTGTTGCC AGGCTGGAGTG
                                |||||||||| ||||||||||
                                GAGACAGCGG TCCGACCTCAC
                                          _
GAM319  NMNAT    3' CACTCCAGCCTGGGCAAAAAAG 43278     G
                                CTTT TTGCCCAGGCTGGAGTG
                                |||| ||||||||||||||||
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                                GAAA AACGGGTCCGACCTCAC
                                   A
GAM319  NMNAT    3'  CACTCCAGCCTGGGTGACAGAG 43279       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  NMT2     3'  CACTCCAGCCTGGGTGACAGAG 17853       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  NPTXR    3'  CACTCCAGCCTGGGCAACAGAG 27427
                                CTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319  NPTXR    3'  CACTCCAGCCTGGGCAACAGAG 55206
                                CTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319  Nup43    3'  CACTCCAGCCTGGGCAAAAGAG 45343      G
                                CTTT TTGCCCAGGCTGGAGTG
                                ||||  ||||||||||||||||
                                GAGA AACGGGTCCGACCTCAC
                                   A
GAM319  NY-BR-1  3'  CACTCCAGCCTAGGTGACAGAG 54850        TG  C
           TG                     CACTTTGT  CC AGGCTGGAGTG
                                ||||||||  ||  ||||||||||
                                GTGAGACA  GG TCCGACCTCAC
                                     GT  A
GAM319  OR51E2   3'  CACTCCAGCCTGGGCAACGGAG 48506
                                CTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||
                                GAGGCAACGGGTCCGACCTCAC

GAM319  ORC6L    3'  CACTCCAGCCTGGGTGACAGAG 27489       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  PAFAH2   3'  CACTCCAGCCTGGGTGACAGAG 6496        TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  PB1      3'  CAGCCTGGGCAACAGAGTG   37574
                                CACTTTGTTGCCCAGGCTG
                                |||||||||||||||||||
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                                GTGAGACAACGGGTCCGAC

GAM319  PDCD7    3'  CACTCCAGCCTGGGAGACAGAG 72598       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GA
GAM319  phorbolin-1 3'  CACTCCAGCCTGGGCGACAG  90205
                                TTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||
                                GACAGCGGGTCCGACCTCAC

GAM319  PIWIL2   3'  CACTCCAGCCTGTTGACAAAG  36540       GCC
                                CTTTGTT  CAGGCTGGAGTG
                                |||||||  ||||||||||||
                                GAAACAG  GTCCGACCTCAC
                                   TT_
GAM319  PLP1     3'  ACTGATGGAAACAAAGTG    6754         GC  GGCTGG
                                CACTTTGTT  CCA    AGT
                                |||||||||  |||    |||
                                GTGAAACAA  GGT    TCA
                                     A_  AG____
GAM319  POLYDOM  3'  CACTCCAGCCTGGGCAATGGAG 44684     TG
                                CTT  TTGCCCAGGCTGGAGTG
                                |||  ||||||||||||||||
                                GAG  AACGGGTCCGACCTCAC
                                  GT
GAM319  PRIC285  3'  CACTCCAGCCTGGGTGACAGAG 62109       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  PRO0038  3'  CACTCCAGCCTGGGTGACAGA  26928      TG
                                TTTGT  CCCAGGCTGGAGTG
                                |||||  |||||||||||||
                                AGACA  GGGTCCGACCTCAC
                                   GT
GAM319  PRO0038  3'  CAGCCTGGGTAACAAAGTG   26930
                                CACTTTGTTGCCCAGGCTG
                                |||||||||||||||||||
                                GTGAAACAATGGGTCCGAC

GAM319  PRO0478  5'  CACTCCAGCCTAGGCAACAAG  27020         C
                                TTTGTTGCC AGGCTGGAGTG
                                ||||||||| ||||||||||
                                GAACAACGG TCCGACCTCAC
                                     A
GAM319  PRO0478  5'  CACTCCAGCCTGGACAACAGAG 27021          C
           TG                     CACTTTGTTG CCAGGCTGGAGTG
                                ||||||||| ||||||||||||
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                                GTGAGACAAC GGTCCGACCTCAC
                                     A
GAM319   PRO0478   3'  CACTCCAGCCTGGGGGACAGAG 27022        G
                                CTTTGTT CCCAGGCTGGAGTG
                                ||||||| ||||||||||||||
                                GAGACAG GGGTCCGACCTCAC
                                    G
GAM319   PRO1386   3'  CAGCCTGGGCAACAGAGTG   49214
                                CACTTTGTTGCCCAGGCTG
                                ||||||||||||||||||
                                GTGAGACAACGGGTCCGAC

GAM319   PRO1942   5'  CACTCCAGCCTGGACAACAGA  38383        C
                                TTTGTTG CCAGGCTGGAGTG
                                ||||||| |||||||||||||
                                AGACAAC GGTCCGACCTCAC
                                    A
GAM319   PRO2015   3'  CACTCCAGCCTGGGCCACACAG 38157      T  T
           TG                     CACT TGT GCCCAGGCTGGAGTG
                                ||||| ||| ||||||||||||||
                                GTGA ACA CGGGTCCGACCTCAC
                                  C  C
GAM319   PRO2133   3'  CACTCCAGTCTGGGCAACAGAG 38398
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAACGGGTCTGACCTCAC

GAM319   PRO2893   3'  CACTCCAACCTGGGCAATAAG  38429           C
                                TTTGTTGCCCAGG TGGAGTG
                                |||||||||||| |||||||
                                GAATAACGGGTCC ACCTCAC
                                      A
GAM319   PRO2964   3'  CACTCCAGCCTGGGCAAAAAG  38253      G
                                CTTT TTGCCCAGGCTGGAGTG
                                |||| ||||||||||||||||
                                GAAA AACGGGTCCGACCTCAC
                                  _
GAM319   PROL2     3'  CACTCCAGCCTGGGTAACAGA  23320
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||
                                AGACAATGGGTCCGACCTCAC

GAM319   PSR       3'  CACTCCAGCCTGGGTGACAGA  65776       TG
                                TTTGT  CCCAGGCTGGAGTG
                                |||||  ||||||||||||||
                                AGACA  GGGTCCGACCTCAC
                                   GT
GAM319   PTK6      3'  CACTCCAGCCTGGGCGACAGAG 21068
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
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                                GAGACAGCGGGTCCGACCTCAC

GAM319  PTRF     3'  CACTCCAGCCTGGGTGACAGAG 64233         TG
                TG                  CACTTTGT  CCCAGGCTGGAGTG
                                    ||||||||  ||||||||||||||
                                    GTGAGACA  GGGTCCGACCTCAC
                                        GT
GAM319  PTRF     3'  CATCCTAGGCAACAGAGTG   64235           C   C
                                    CACTTTGTTGCC AGG TG
                                    |||||||||||| ||| ||
                                    GTGAGACAACGG TCC AC
                                          A   T
GAM319  RAB4B    5'  CACTCCAGCCTGGGCAACGAA  32900
                                    TTTGTTGCCCAGGCTGGAGTG
                                    |||||||||||||||||||||
                                    AAGCAACGGGTCCGACCTCAC

GAM319  Rabip4R  3'  CACTCCAACCTGGGTGACAGAG 36273       TG     C
                                    CTTTGT  CCCAGG TGGAGTG
                                    ||||||  |||||| |||||||
                                    GAGACA  GGGTCC ACCTCAC
                                       GT     A
GAM319  RES4-25  3'  CACTCCAGCCTCGGCCACAGTG 65262     TT  T   C
                                    CACT  GT GCC AGGCTGGAGTG
                                    ||||  || ||| ||||||||||
                                    GTGA  CA CGG TCCGACCTCAC
                                      __  C   C
GAM319  RFX4     3'  CAGCCTGGGCAACATAGTG   12854      T
                                    CACT TGTTGCCCAGGCTG
                                    |||| ||||||||||||||
                                    GTGA ACAACGGGTCCGAC
                                      T
GAM319  RHOBTB3  3'  CACTCCAGCCTGGGTGACAAG  30421      TG
                                    TTTGT  CCCAGGCTGGAGTG
                                    |||||  ||||||||||||||
                                    GAACA  GGGTCCGACCTCAC
                                       GT
GAM319  RNF8     3'  ACTCAGAGGCAACAAGT     15555      T     CAGG   G
                                    ACTT GTTGCC    CTG AGT
                                    |||| ||||||    ||| |||
                                    TGAA CAACGG    GAC TCA
                                      _      A___   _
GAM319  RNO2     5'  CACTCCAGCCTAGACAACAGGG 53925         CCC
                                    CTTTGTTG   AGGCTGGAGTG
                                    ||||||||   ||||||||||
                                    GGGACAAC   TCCGACCTCAC
                                         AGA
GAM319  RNO2     5'  CACTCCAGCCTGGGCAACAAG  53926
                                    TTTGTTGCCCAGGCTGGAGTG
                                    |||||||||||||||||||||
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                                GAACAACGGGTCCGACCTCAC

GAM319  RoXaN    3'  CACTCCAGCCTGAGAGACAGAA 47276    C     GCC
           TG                    CA TTTGTT   CAGGCTGGAGTG
                                 || ||||||   ||||||||||||
                                 GT AGACAG   GTCCGACCTCAC
                                  A     AGA
GAM319  RoXaN    3'  CACTCCAGCCTGGGCTACAGAG 47277         T
           TG                    CACTTTGT GCCCAGGCTGGAGTG
                                 |||||||| ||||||||||||||||
                                 GTGAGACA CGGGTCCGACCTCAC
                                      T
GAM319  Rpo1-2   3'  CACTCCAGCCTGGGCGACAGAA 39212    C
           TG                    CA TTTGTTGCCCAGGCTGGAGTG
                                 || ||||||||||||||||||||
                                 GT AGACAGCGGGTCCGACCTCAC
                                  A
GAM319  Rpo1-2   3'  CACTCCAGCCTGGGTGACAGAG 39213       TG
                                 CTTTGT  CCCAGGCTGGAGTG
                                 ||||||  ||||||||||||||
                                 GAGACA  GGGTCCGACCTCAC
                                    GT
GAM319  RRP4     3'  CACTCCAGCCTGGGTGACAGAG 27354       TG
                                 CTTTGT  CCCAGGCTGGAGTG
                                 ||||||  ||||||||||||||
                                 GAGACA  GGGTCCGACCTCAC
                                    GT
GAM319  SAMHD1   3'  CACTCCAGCCTGGGTGACAGAG 61977         TG
           TG                    CACTTTGT  CCCAGGCTGGAGTG
                                 ||||||||  ||||||||||||||
                                 GTGAGACA  GGGTCCGACCTCAC
                                      GT
GAM319  SC65     3'  CACTCCAGCCTGGGCGACAGAG 22287
                                 CTTTGTTGCCCAGGCTGGAGTG
                                 ||||||||||||||||||||||
                                 GAGACAGCGGGTCCGACCTCAC

GAM319  SC65     3'  CACTCCAGCCTGGGCGACAGAG 22288
           TG                    CACTTTGTTGCCCAGGCTGGAGTG
                                 ||||||||||||||||||||||||
                                 GTGAGACAGCGGGTCCGACCTCAC

GAM319  SCAND2   3'  CACTCCAGCCTGGGCGACAGAG 42141
           TG                    CACTTTGTTGCCCAGGCTGGAGTG
                                 ||||||||||||||||||||||||
                                 GTGAGACAGCGGGTCCGACCTCAC

GAM319  SCIN     3'  CACTCCAGCCTGGGCAACAGAG 53599
                                 CTTTGTTGCCCAGGCTGGAGTG
                                 ||||||||||||||||||||||
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                                GAGACAACGGGTCCGACCTCAC

GAM319  SCMH1    3'  CAGCCTAGACAACCAAGTG   25281      T   CCC
                                CACTT GTTG  AGGCTG
                                ||||| ||||  ||||||
                                GTGAA CAAC  TCCGAC
                                   C   AGA
GAM319  SCN12A   3'  CACTCCAGCCTGGTGACAGAGT 27078        TG  C
           G                     CACTTTGT  CC AGGCTGGAGTG
                                ||||||||  || ||||||||||
                                GTGAGACA  GG TCCGACCTCAC
                                     GT  _
GAM319  SCYA5    3'  CACTCCAGCCTGGGCGACAGAG 12959
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319  SCYA5    3'  CACTCCAGCCTGGGTGACAAAG 12960        TG
           TG                    CACTTTGT  CCCAGGCTGGAGTG
                                ||||||||  ||||||||||||||
                                GTGAAACA  GGGTCCGACCTCAC
                                     GT
GAM319  SIAT4A   3'  CAGCCTGGGCAACATAGTG   13136      T
                                CACT TGTTGCCCAGGCTG
                                |||| ||||||||||||||
                                GTGA ACAACGGGTCCGAC
                                  T
GAM319  SLC19A3  3'  CAGCCTGGGCAACACAGTG   48238      T
                                CACT TGTTGCCCAGGCTG
                                |||| ||||||||||||||
                                GTGA ACAACGGGTCCGAC
                                  C
GAM319  SMA3     3'  CACTCCAGCCTGGGTGACAGAG 23256       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                    GT
GAM319  SNAPC1   3'  CACTCCAGCCTGGGCAACAGAG 13273
           TG                    CACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||||
                                GTGAGACAACGGGTCCGACCTCAC

GAM319  SPRY4    3'  CACTCCAGCCTGGGTGACAGAG 48998       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                    GT
GAM319  SPRY4    3'  CACTCCAGCCTGGGTGACAGAG 48999        TG
           TG                    CACTTTGT  CCCAGGCTGGAGTG
                                ||||||||  ||||||||||||||
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                                GTGAGACA  GGGTCCGACCTCAC
                                    GT
GAM319  SPTLC2   3'  CACTCCAGCCTGGGTGACAGAG 17981        TG
           TG                    CACTTTGT  CCCAGGCTGGAGTG
                                 ||||||||  ||||||||||||||
                                 GTGAGACA  GGGTCCGACCTCAC
                                    GT
GAM319  SYAP1    3'  CACTCCAGCCTGGGTGATAGAG 52468        TG
           TG                    CACTTTGT  CCCAGGCTGGAGTG
                                 ||||||||  ||||||||||||||
                                 GTGAGATA  GGGTCCGACCTCAC
                                    GT
GAM319  SYNPO2   3'  CAGCCTGAGCAACATAGTG   72387     T     C
                                 CACT TGTTGC CAGGCTG
                                 ||||  ||||||  |||||||
                                 GTGA ACAACG GTCCGAC
                                   T     A
GAM319  TBX19    3'  CACTCCAGCCTGGGTGGTAGA  18921     TT
                                 TTTG  GCCCAGGCTGGAGTG
                                 ||||  ||||||||||||||||
                                 AGAT  TGGGTCCGACCTCAC
                                   GG
GAM319  TCL6     3'  ACTCCAGCATCAACAAGTG   27748      T   CCCAG
                                 CACTT GTTG    GCTGGAGT
                                 |||||  ||||    ||||||||
                                 GTGAA CAAC    CGACCTCA
                                    _   TA___
GAM319  TCL6     3'  ACTCCAGCATCAACAAGTG   25896      T   CCCAG
                                 CACTT GTTG    GCTGGAGT
                                 |||||  ||||    ||||||||
                                 GTGAA CAAC    CGACCTCA
                                    _   TA___
GAM319  THEA     3'  CACTCCAGCCCAGGCAATAGAG 66875          CA
           T                      ACTTTGTTGCC  GGCTGGAGTG
                                  ||||||||||  ||||||||||
                                  TGAGATAACGG  CCGACCTCAC
                                        AC
GAM319  THEA     3'  CACTCCAGCCTGGGTGACAGAG 66876        TG
           TG                    CACTTTGT  CCCAGGCTGGAGTG
                                 ||||||||  ||||||||||||||
                                 GTGAGACA  GGGTCCGACCTCAC
                                    GT
GAM319  TIP47    3'  CACTCCAGCCTGGGGGACAAG  20601       G
                                 TTTGTT CCCAGGCTGGAGTG
                                 ||||||  ||||||||||||||
                                 GAACAG GGGTCCGACCTCAC
                                    G
GAM319  TOMM70A  3'  CACTCCAGCCTGGGCAATATAG 29736    T
                                 CT TGTTGCCCAGGCTGGAGTG
                                 ||  ||||||||||||||||||
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                                GA ATAACGGGTCCGACCTCAC
                                 T
GAM319  TRIAD3   3'  CACTCCAGCCTGAGCAACAAA  96130        C
                                TTTGTTGC CAGGCTGGAGTG
                                |||||||| ||||||||||||
                                AAACAACG GTCCGACCTCAC
                                    A
GAM319  TUSP     3'  CACTGTGTTGGACCAACAAAGT 40017         C_   G T G
                                ACTTTGTTG  CCAG C G AGTG
                                |||||||||  |||| | | ||||
                                TGAAACAAC  GGTT G T TCAC
                                    CA   _ _ G
GAM319  UQCR     3'  CTAACCTGGGCAACAAAG    23357          C
                                CTTTGTTGCCCAGG TGG
                                |||||||||||||| |||
                                GAAACAACGGGTCC ATC
                                      A
GAM319  UST      3'  CACTCCAGCCTGGGTGACAGAG 20349        TG
           TG                     CACTTTGT  CCCAGGCTGGAGTG
                                ||||||||  ||||||||||||||
                                GTGAGACA  GGGTCCGACCTCAC
                                    GT
GAM319  VIT1     5'  CACTCCAGCCTGGGTGGCAGAG 38601        TG
           TG                     CACTTTGT  CCCAGGCTGGAGTG
                                ||||||||  ||||||||||||||
                                GTGAGACG  GGGTCCGACCTCAC
                                    GT
GAM319  VPS4B    3'  CACTCCAGCCTGGGCGAC    18019
                                GTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||
                                CAGCGGGTCCGACCTCAC

GAM319  WBSCR21  3'  CACTCCAGCCTAGGCAACAGAG 49297         C
                                CTTTGTTGCC AGGCTGGAGTG
                                |||||||||| ||||||||||
                                GAGACAACGG TCCGACCTCAC
                                    A
GAM319  WBSCR23  3'  CACTCCAGCCTGGGCGACAAAG 47418
           TG                     CACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||||
                                GTGAAACAGCGGGTCCGACCTCAC

GAM319  WBSCR23  5'  CACTCCAGCCTGGGCGACAGAG 47419
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319  WBSCR23  3'  CACTCCAGCCTGGGCGACAGAG 47420
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
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                                GAGACAGCGGGTCCGACCTCAC

GAM319  WBSCR23  3'  CACTCCAGCCTGGGTGATAGAG 47421       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGATA  GGGTCCGACCTCAC
                                   GT
GAM319  WIRE     3'  CACTCCAGCCTGGGCGACAGAG 78903
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319  WSB1     3'  CACTCCAACCTGGACAACAGAG 56964         C    C
                                CTTTGTTG CCAGG TGGAGTG
                                ||||||||| ||||| |||||||
                                GAGACAAC GGTCC ACCTCAC
                                     A    A
GAM319  WSB1     3'  CACTCCAACCTGGACAACAGAG 56989         C    C
                                CTTTGTTG CCAGG TGGAGTG
                                ||||||||| ||||| |||||||
                                GAGACAAC GGTCC ACCTCAC
                                     A    A
GAM319  YME1L1   3'  CACTCCAGCCTGGGCAACAGAG 58424
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319  YME1L1   3'  CACTCCAGCCTGGGTGACAGAG 58425         TG
           TG                     CACTTTGT  CCCAGGCTGGAGTG
                                ||||||||  ||||||||||||||
                                GTGAGACA  GGGTCCGACCTCAC
                                     GT
GAM319  YME1L1   3'  CACTCCAGCCTGGGCAACAGAG 27318
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319  YME1L1   3'  CACTCCAGCCTGGGTGACAGAG 27319         TG
           TG                     CACTTTGT  CCCAGGCTGGAGTG
                                ||||||||  ||||||||||||||
                                GTGAGACA  GGGTCCGACCTCAC
                                     GT
GAM319  ZAK      3'  CACTCCAGCCTGGATGACAGAG 56939        GC
           TG                     CACTTTGTT  CCAGGCTGGAGTG
                                ||||||||||  ||||||||||||
                                GTGAGACAG  GGTCCGACCTCAC
                                      TA
GAM319  ZFP106   3'  CACTCCAGCCTGGGCGACAAG  42716
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||
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                                GAACAGCGGGTCCGACCTCAC

GAM319  ZFP106   3'  CACTCCAGCCTGGTGACAGAGT 42717        TG  C
            G                    CACTTTGT  CC AGGCTGGAGTG
                                 ||||||||  || ||||||||||
                                 GTGAGACA  GG TCCGACCTCAC
                                     GT  _
GAM319  ZNF197   3'  CACTCCAGCCTGGGCAACAAG  23752
                                 TTTGTTGCCCAGGCTGGAGTG
                                 ||||||||||||||||||||
                                 GAACAACGGGTCCGACCTCAC

GAM319  ZNF271   3'  CACTCCAGTCTGGGCAACAGAG 96957
                                 CTTTGTTGCCCAGGCTGGAGTG
                                 ||||||||||||||||||||
                                 GAGACAACGGGTCTGACCTCAC

GAM319  ZNF271   3'  CAGCCTGGGCAACAGAGTG   96959
                                 CACTTTGTTGCCCAGGCTG
                                 ||||||||||||||||||
                                 GTGAGACAACGGGTCCGAC

GAM319  ZNF297B  5'  CACTCCAGCCTGGGCAACAAG  26645
                                 TTTGTTGCCCAGGCTGGAGTG
                                 ||||||||||||||||||||
                                 GAACAACGGGTCCGACCTCAC

GAM319  ZNF297B  5'  CACTCCAGCCTGGGCAACAGAG 26646
                                 CTTTGTTGCCCAGGCTGGAGTG
                                 ||||||||||||||||||||
                                 GAGACAACGGGTCCGACCTCAC

GAM319  ZNF297B  5'  CACTCCAGCCTGGGTAAAAGAG 26647       G
            TG                     CACTTT TTGCCCAGGCTGGAGTG
                                   |||||| ||||||||||||||||
                                   GTGAGA AATGGGTCCGACCTCAC
                                      A
GAM319  ZNF333   3'  CACTCCAGCCTGGGCAACAGAG 51586
            TG                     CACTTTGTTGCCCAGGCTGGAGTG
                                   ||||||||||||||||||||||
                                   GTGAGACAACGGGTCCGACCTCAC

GAM319  ZNF339   3'  CACTCCAGCCTGGGCAACAGAG 41387
            TG                     CACTTTGTTGCCCAGGCTGGAGTG
                                   ||||||||||||||||||||||
                                   GTGAGACAACGGGTCCGACCTCAC

GAM319  LOC112687 3'  CACTCCAGCCTGGGCAACAGAG 73222
            TG                     CACTTTGTTGCCCAGGCTGGAGTG
                                   ||||||||||||||||||||||
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                                GTGAGACAACGGGTCCGACCTCAC

GAM319   LOC113523 3'  CACTCCAGCCTGGGCGACAGGG 73415
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GGGACAGCGGGTCCGACCTCAC

GAM319   LOC114987 3'  CACTCCAGCCTGGGCAACAAG  59791
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAACAACGGGTCCGACCTCAC

GAM319   LOC115129 5'  CACTCCAGCCTGGGCATGAG   73605     TGT
                                CTT   TGCCCAGGCTGGAGTG
                                |||   ||||||||||||||||
                                GAG   ACGGGTCCGACCTCAC
                                  T__
GAM319   LOC115196 3'  CACTCCAGCCTGGGAGACAGAG 73650       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GA
GAM319   LOC115273 3'  CACTCCAGCCTGGGCAACAGAG 73747
            TG                    CACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||||
                                GTGAGACAACGGGTCCGACCTCAC

GAM319   LOC115761 3'  CACTCCAGTCTGGGCAACAGAG 93394
            TG                    CACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||||
                                GTGAGACAACGGGTCTGACCTCAC

GAM319   LOC116143 3'  CACTCCAGCCTGGGCAACTGAG 74177     T
                                CTT GTTGCCCAGGCTGGAGTG
                                ||| ||||||||||||||||
                                GAG CAACGGGTCCGACCTCAC
                                  T
GAM319   LOC116236 3'  CACTCCAGCCTGGGCGACAGAG 74238
            T                    ACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                TGAGACAGCGGGTCCGACCTCAC

GAM319   LOC120406 3'  CACTCCAGCCTGGGTGACAGAG 76064       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319   LOC122704 3'  CACTCCAACCTGGGCGACAGGG 74601             C
                                CTTTGTTGCCCAGG TGGAGTG
                                |||||||||||||| |||||||
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                                GGGACAGCGGGTCC ACCTCAC
                                       A
GAM319   LOC122970 3'  CACTCCAGCCCAGGTAACACAG 74639    T      CA
                                CT TGTTGCC  GGCTGGAGTG
                                || |||||||  ||||||||||
                                GA ACAATGG  CCGACCTCAC
                                 C       AC
GAM319   LOC126282 3'  CACTCCAGCCTGGGTGACAGAG 74944        TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                    GT
GAM319   LOC126297 5'  CACTCCAGCCTGGGCAAC    74977
                                GTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||
                                CAACGGGTCCGACCTCAC

GAM319   LOC126669 3'  CACTCCAGCCTGAGTGACAGAG 75926         TG C
            TG                    CACTTTGT  C CAGGCTGGAGTG
                                ||||||||  | ||||||||||||
                                GTGAGACA  G GTCCGACCTCAC
                                     GT A
GAM319   LOC127262 3'  CACTCCAGCCCGGGCGACAGAG 76592           A
                                CTTTGTTGCCC GGCTGGAGTG
                                |||||||||| ||||||||||
                                GAGACAGCGGG CCGACCTCAC
                                       C
GAM319   LOC127428 3'  CACTCCAGCCTGGGCAACAGAG 75155
            TG                    CACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||||
                                GTGAGACAACGGGTCCGACCTCAC

GAM319   LOC129880 3'  CACTCCAGCTTGGGCAACAGAG 75404
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAACGGGTTCGACCTCAC

GAM319   LOC130026 3'  CACTCCAGCCTAGGCAACAGAG 57432           C
                                CTTTGTTGCC AGGCTGGAGTG
                                |||||||||| ||||||||||
                                GAGACAACGG TCCGACCTCAC
                                       A
GAM319   LOC130535 3'  CACTCCAGCCTGGGCAACAAG  76643
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||
                                GAACAACGGGTCCGACCTCAC

GAM319   LOC130535 3'  CACTCCAGCCTGGGTGACAGAG 76644        TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
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                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319   LOC130589 3'  CACTGCACTGGGCAACAGAG   57928           GC  G
                                CTTTGTTGCCCAG  TG AGTG
                                ||||||||||||  || ||||
                                GAGACAACGGGTC  AC TCAC
                                       __  G
GAM319   LOC131965 3'  CACTCCAGCCTGGGCGACAGAG 75518
            TG                    CACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||||
                                GTGAGACAGCGGGTCCGACCTCAC

GAM319   LOC132625 3'  CAGCCTGGGCAACATAGTG   76436     T
                                CACT TGTTGCCCAGGCTG
                                ||||| ||||||||||||||
                                GTGA ACAACGGGTCCGAC
                                   T
GAM319   LOC133926 3'  CACTCCAGCCTGGGCGACAGAG 75628
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319   LOC134147 3'  CACTCCAGCCTGGACAACAGAG 57955        C
                                CTTTGTTG CCAGGCTGGAGTG
                                |||||||| ||||||||||||
                                GAGACAAC GGTCCGACCTCAC
                                     A
GAM319   LOC134265 3'  CACTCCAGCCTAAGCAAATAG  75654    TTG   CC
                                CT   TTGC  AGGCTGGAGTG
                                ||   ||||  ||||||||||
                                GA   AACG  TCCGACCTCAC
                                 TA_    AA
GAM319   LOC135154 3'  CACTCCAGCCTGGGCAACAAG  75723
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||
                                GAACAACGGGTCCGACCTCAC

GAM319   LOC142937 3'  CACTCCAGCCTGGGCCACAGA  57444      T
                                TTTGT GCCCAGGCTGGAGTG
                                ||||| ||||||||||||||
                                AGACA CGGGTCCGACCTCAC
                                   C
GAM319   LOC142948 3'  CACTCCAGCCTGGGTGACAGAG 83772       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319   LOC143196 3'  CACTCCAGCTTGGCAACAGAG  83800         C
                                CTTTGTTGCC AGGCTGGAGTG
                                |||||||||| ||||||||||
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                                GAGACAACGG TTCGACCTCAC
                                        _
GAM319  LOC143310 3'  CACCCCAGCCTGGGTGACAGAG 77035       TG        A
                                CTTTGT  CCCAGGCTGG GTG
                                ||||||  |||||||||| |||
                                GAGACA  GGGTCCGACC CAC
                                   GT        C
GAM319  LOC143465 3'  CACTCCAGCCTGGGTGACGGAG 83868        TG
           TG                     CACTTTGT  CCCAGGCTGGAGTG
                                ||||||||  ||||||||||||||
                                GTGAGGCA  GGGTCCGACCTCAC
                                    GT
GAM319  LOC143888 3'  CACTCCAGCCTGGGTGACAGAG 77166        TG
           TG                     CACTTTGT  CCCAGGCTGGAGTG
                                ||||||||  ||||||||||||||
                                GTGAGACA  GGGTCCGACCTCAC
                                    GT
GAM319  LOC143943 3'  CACTCCAGCCTGGGTGACAGAG 83914       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  LOC144289 3'  CACTCCAGCCTGGGTGACAGAG 83951        TG
           TG                     CACTTTGT  CCCAGGCTGGAGTG
                                ||||||||  ||||||||||||||
                                GTGAGACA  GGGTCCGACCTCAC
                                    GT
GAM319  LOC144308 5'  CACTCCAGCCTGGGTGACAGAG 83977       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  LOC144465 3'  CACTCCAGCCTGGGCAACAAG  77341
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||
                                GAACAACGGGTCCGACCTCAC

GAM319  LOC144465 3'  CACTCCAGCCTGGGCAACAAGA 77342       _
           GT                     ACTTT GTTGCCCAGGCTGGAGTG
                                |||||  ||||||||||||||||||
                                TGAGA CAACGGGTCCGACCTCAC
                                  A
GAM319  LOC144481 3'  CACCCATCTTGGGCAACAGAAT 84012     C          C   A
           G                      CA TTTGTTGCCCAGG TGG GTG
                                ||  ||||||||||||  ||| |||
                                GT AGACAACGGGTTC ACC CAC
                                 A          T  _
GAM319  LOC144519 5'  CACTCCAGCCTGGGCGACAGAG 77368
           TG                     CACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||||
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                                GTGAGACAGCGGGTCCGACCTCAC

GAM319   LOC144558 3'  CACTCCAGCCTGGGTTACAGA  84074       T
                                TTTGT GCCCAGGCTGGAGTG
                                ||||| ||||||||||||||||
                                AGACA TGGGTCCGACCTCAC
                                   T
GAM319   LOC144563 3'  CACTCCAGCTTGGGCAACAGAG 77392
            T                    ACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||||
                                TGAGACAACGGGTTCGACCTCAC

GAM319   LOC144583 3'  CACTCCAGCCCGAGTGACAGAA 77413    C     TG CCA
            TG                    CA TTTGT  C   GGCTGGAGTG
                                || |||||  |   ||||||||||
                                GT AGACA  G   CCGACCTCAC
                                 A     GT AGC
GAM319   LOC144817 3'  CACTCCAGCCCAGGGGACAATG 77508     T     G  CA
            TG                    CAC TTGTT CC  GGCTGGAGTG
                                ||| ||||| ||  ||||||||||
                                GTG AACAG GG  CCGACCTCAC
                                  T    G  AC
GAM319   LOC144845 3'  CACTCCAGCCCGGGCGACAGAG 57454           A
                                CTTTGTTGCCC GGCTGGAGTG
                                |||||||||||| ||||||||||
                                GAGACAGCGGG CCGACCTCAC
                                       C
GAM319   LOC145216 3'  CACCCCAGCCTAGCGACAGAG  84217          CC      A
                                CTTTGTTGC  AGGCTGG GTG
                                |||||||||  ||||||| |||
                                GAGACAGCG  TCCGACC CAC
                                     A_      C
GAM319   LOC145231 3'  CACTCCAGCCTGGGTGACAGTG 84243      TT  TG
                                CACT  GT  CCCAGGCTGGAGTG
                                ||||  ||  ||||||||||||||
                                GTGA  CA  GGGTCCGACCTCAC
                                  __  GT
GAM319   LOC145333 3'  CACTCCAGCCTGGGCGACAGAG 84290
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319   LOC145387 3'  CACTCCAGCCTGGGCGACAGAG 84329
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319   LOC145387 3'  CACTCCAGCCTGGGTGGCAGAG 84330         TG
            TG                    CACTTTGT  CCCAGGCTGGAGTG
                                ||||||||  ||||||||||||||
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                                GTGAGACG  GGGTCCGACCTCAC
                                    GT
GAM319   LOC145438 3'  CACTCCAGCCTGGGCGACAGAG 84308
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319   LOC145453 3'  CACTTCAGCCTGGGCAACAGAG 77655
           TG                     CACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||||
                                GTGAGACAACGGGTCCGACTTCAC

GAM319   LOC145482 3'  CACTCCAGCCTGGGCGACAAG  77740
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||
                                GAACAGCGGGTCCGACCTCAC

GAM319   LOC145483 3'  CACTCCAGCCTGGGCAGCAGAG 77752
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACGACGGGTCCGACCTCAC

GAM319   LOC145608 5'  CACTCCAGCCTGGGTGACAGAG 84376       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                    GT
GAM319   LOC145609 3'  CACTCCAGCCTGGGTGACAGAG 84361       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                    GT
GAM319   LOC145622 3'  CACTCTGAAGCAACAAAGT   77805          CCAGGCT
                                ACTTTGTTGC      GGAGTG
                                ||||||||||      ||||||
                                TGAAACAACG      TCTCAC
                                     AAG____
GAM319   LOC145663 3'  CACTCCAGCCTGGGCGACAGAG 84415
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319   LOC145820 3'  CACTCCAGCCTGGGCGACAGAG 77972
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319   LOC145988 5'  CACTCCAGCCTGGAAGGCAGAG 78060        GC
                                CTTTGTT  CCAGGCTGGAGTG
                                |||||||  ||||||||||||
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                                GAGACGG  GGTCCGACCTCAC
                                   AA
GAM319   LOC146229 3'  CACTCCAGCCTGGGCGACAGAG 78266
                                CTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319   LOC146540 3'  CACTCCAGCCTGGGCTACAAAG 78525       T
                                CTTTGT GCCCAGGCTGGAGTG
                                ||||||  ||||||||||||||||
                                GAAACA CGGGTCCGACCTCAC
                                   T
GAM319   LOC146713 3'  CACTCCAGCCTGGTCAACAGAG 84723         C
                                CTTTGTTG CCAGGCTGGAGTG
                                ||||||||  ||||||||||||
                                GAGACAAC GGTCCGACCTCAC
                                    T
GAM319   LOC146728 3'  CACTCCAGCCTGGGAAGCAGAG 84760          G
            TG                    CACTTTGTT CCCAGGCTGGAGTG
                                |||||||||  ||||||||||||||
                                GTGAGACGA GGGTCCGACCTCAC
                                    A
GAM319   LOC146756 3'  CACTCCAGCCTGGGCGACAGAG 84794
                                CTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319   LOC146839 5'  CACTCCAGCCTGGGCAACATAG 84836    T
                                CT TGTTGCCCAGGCTGGAGTG
                                ||  ||||||||||||||||||
                                GA ACAACGGGTCCGACCTCAC
                                 T
GAM319   LOC146895 3'  CACTCCAGCCTGGGTGACAAG  84860       TG
                                TTTGT  CCCAGGCTGGAGTG
                                |||||  ||||||||||||||
                                GAACA  GGGTCCGACCTCAC
                                   GT
GAM319   LOC146901 3'  CACTCCAGTTTGGGCAACAGAA 84892    C
            TG                    CA TTTGTTGCCCAGGCTGGAGTG
                                ||  ||||||||||||||||||||
                                GT AGACAACGGGTTTGACCTCAC
                                 A
GAM319   LOC146901 3'  CACTGCAGCCTAGACAACAGAG 84893         CCC     G
                                CTTTGTTG   AGGCTG AGTG
                                ||||||||   ||||||  ||||
                                GAGACAAC   TCCGAC TCAC
                                     AGA     G
GAM319   LOC146923 3'  CACTCCAGCCTGGGCGACAGAG 78795
            TG                    CACTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||||||
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                                GTGAGACAGCGGGTCCGACCTCAC

GAM319   LOC146958 3'  CACTCCAGCCTGGGTGACACAG 84940    T   TG
                                CT TGT  CCCAGGCTGGAGTG
                                || |||  ||||||||||||||
                                GA ACA  GGGTCCGACCTCAC
                                 C   GT
GAM319   LOC147063 5'  CAGCCTGGGCAACAGAGTG   85015
                                CACTTTGTTGCCCAGGCTG
                                ||||||||||||||||||
                                GTGAGACAACGGGTCCGAC

GAM319   LOC147071 3'  CACTCCAGCCTGGGCGACAGAG 73353
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319   LOC147118 5'  CACTCCAGCCCAGGACAA    85060    _  CA
                                TTG CC  GGCTGGAGTG
                                ||| ||  ||||||||||
                                AAC GG  CCGACCTCAC
                                  A  AC
GAM319   LOC147664 3'  CACTCCAGCCTGGGCAACGAGA 79043     _
           G                     CTTT GTTGCCCAGGCTGGAGTG
                                |||| ||||||||||||||||||
                                GAGA CAACGGGTCCGACCTCAC
                                  G
GAM319   LOC147669 3'  CACTCCAGCCTGGGTGACAAGG 85175       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GGAACA  GGGTCCGACCTCAC
                                    GT
GAM319   LOC147700 3'  CACTCCAGCCTGTGCAACAAG  59877        C
                                TTTGTTGC CAGGCTGGAGTG
                                |||||||| ||||||||||||
                                GAACAACG GTCCGACCTCAC
                                      T
GAM319   LOC147727 5'  CACTCCAGCCTGGGCGATAGAG 79129
           TG                     CACTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||||
                                GTGAGATAGCGGGTCCGACCTCAC

GAM319   LOC147837 3'  CACCCCAGCCTGGGCGACAGAG 79200              A
                                CTTTGTTGCCCAGGCTGG GTG
                                |||||||||||||||| |||
                                GAGACAGCGGGTCCGACC CAC
                                           C
GAM319   LOC147837 3'  CACTCCAGCCTGGGCAGCAAG  79201
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||
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                                GAACGACGGGTCCGACCTCAC

GAM319   LOC147990 3'  CACTCCAGCCTGGGCAACAGAG 85213
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319   LOC148166 3'  CACTCCAGCCTAGGCGACGGGG 79411          C
                                CTTTGTTGCC AGGCTGGAGTG
                                |||||||||| ||||||||||
                                GGGGCAGCGG TCCGACCTCAC
                                      A
GAM319   LOC148267 3'  CAGCCTGGGCAACATAGTG   79513     T
                                CACT TGTTGCCCAGGCTG
                                |||| ||||||||||||||
                                GTGA ACAACGGGTCCGAC
                                   T
GAM319   LOC148397 3'  CACCCCAGCCTGGGCAACAAGA 79560      _          A
           GT                     ACTTT GTTGCCCAGGCTGG GTG
                                |||||| |||||||||||||| |||
                                TGAGA CAACGGGTCCGACC CAC
                                   A           C
GAM319   LOC148534 3'  CACTCCAGCCTGGGCGACAGAG 79630
                                CTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319   LOC148758 5'  CACTCCAGCCTGGGCAACAAG  79719
                                TTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||
                                GAACAACGGGTCCGACCTCAC

GAM319   LOC148809 5'  CACTCCAGCCTGGGTGACAGAG 79747       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319   LOC148936 3'  CACTCCAGGTTGGGCAACAGAG 85447           G
                                CTTTGTTGCCCAG CTGGAGTG
                                |||||||||||| ||||||||
                                GAGACAACGGGTT GACCTCAC
                                      G
GAM319   LOC148938 3'  CACTCCAGGCTGGGCAACACAG 85430    T       G
                                CT TGTTGCCCAG CTGGAGTG
                                || |||||||||| ||||||||
                                GA ACAACGGGTC GACCTCAC
                                 C         G
GAM319   LOC149073 3'  CACTCCAGCCTGGGCAACAGTG 85482     T
           TG                     CAC TTGTTGCCCAGGCTGGAGTG
                                ||| ||||||||||||||||||||
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                                GTG GACAACGGGTCCGACCTCAC
                                  T
GAM319   LOC149113 5'  CACTCCAGCCTGGGCTACAAG  79902      T
                                TTTGT GCCCAGGCTGGAGTG
                                ||||| ||||||||||||||||
                                GAACA CGGGTCCGACCTCAC
                                   T
GAM319   LOC149175 3'  CACTCCAGCCTGGGCGACAGAG 79948
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319   LOC149194 5'  CACTCCAGCCTGGGCAACAAG  79981
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAACAACGGGTCCGACCTCAC

GAM319   LOC149271 3'  CACTCCAGCCTGGGCAACAAGA 79998      _
           GT                     ACTTT GTTGCCCAGGCTGGAGTG
                                ||||| ||||||||||||||||||
                                TGAGA CAACGGGTCCGACCTCAC
                                  A
GAM319   LOC149606 3'  CACTGCAGCCTGGGCAACATAG 80256    T          G
                                CT TGTTGCCCAGGCTG AGTG
                                || |||||||||||| ||||
                                GA ACAACGGGTCCGAC TCAC
                                 T           G
GAM319   LOC149628 3'  CACTCCAGCCTGGGTGACAGAG 80276       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319   LOC149672 5'  CACTCCAGCCTGGGCAACAGAG 80337
           TG                     CACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||||
                                GTGAGACAACGGGTCCGACCTCAC

GAM319   LOC149705 3'  CACTCCAGCCTGGGTGACGAGT 85773      T  TG
           G                      CACTT GT  CCCAGGCTGGAGTG
                                ||||| ||  ||||||||||||||
                                GTGAG CA  GGGTCCGACCTCAC
                                  _  GT
GAM319   LOC149711 3'  CACTCCAGCCTGGGTGACAGAG 85843        TG
           TG                     CACTTTGT  CCCAGGCTGGAGTG
                                ||||||||  ||||||||||||||
                                GTGAGACA  GGGTCCGACCTCAC
                                    GT
GAM319   LOC149912 3'  CACTCCAGCCTGGGCGACAGTG 85879     TT
                                CACT  GTTGCCCAGGCTGGAGTG
                                ||||  ||||||||||||||||||
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                                GTGA  CAGCGGGTCCGACCTCAC
                                  __
GAM319   LOC150095 3'  CACTCCAGCCTGGGCAACAGAG 85990
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319   LOC150142 5'  CAGCCTGGGCAACAAAGT    80402
                                ACTTTGTTGCCCAGGCTG
                                ||||||||||||||||||
                                TGAAACAACGGGTCCGAC

GAM319   LOC150174 3'  CACTCCAGCCTGGTCAACAGAG 80430          C
           TG                     CACTTTGTTG CCAGGCTGGAGTG
                                ||||||||||  ||||||||||||
                                GTGAGACAAC GGTCCGACCTCAC
                                      T
GAM319   LOC150185 3'  CACTCCAGCCTGGGTGACAGAG 86062        TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319   LOC150213 3'  CACTCCAGCCTGGTCAACAGAG 75349          C
           TG                     CACTTTGTTG CCAGGCTGGAGTG
                                ||||||||||  ||||||||||||
                                GTGAGACAAC GGTCCGACCTCAC
                                      T
GAM319   LOC150225 3'  CACTCCAGCCTGGGCGTCAGAG 86182         T
           TG                     CACTTTG TGCCCAGGCTGGAGTG
                                ||||||| ||||||||||||||||
                                GTGAGAC GCGGGTCCGACCTCAC
                                   T
GAM319   LOC150236 3'  CACTCCAGCCTGGTCAACAGAG 80498          C
           TG                     CACTTTGTTG CCAGGCTGGAGTG
                                ||||||||||  ||||||||||||
                                GTGAGACAAC GGTCCGACCTCAC
                                      T
GAM319   LOC150244 3'  CACTCCAGCCTGGGCGACAGAG 80548
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319   LOC150245 3'  CACTCCAGCCTGGGTGACAGA  86109       TG
                                TTTGT  CCCAGGCTGGAGTG
                                |||||  ||||||||||||||
                                AGACA  GGGTCCGACCTCAC
                                   GT
GAM319   LOC150299 3'  CACTCCAGCCTGGCGACAGAG  86161          C
                                CTTTGTTGCC AGGCTGGAGTG
                                ||||||||||  ||||||||||
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                                GAGACAGCGG TCCGACCTCAC
                                          _
GAM319   LOC150319 3'  CACTCCAGCCTGGGCAACAAG  80464
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||
                                GAACAACGGGTCCGACCTCAC

GAM319   LOC150577 3'  CACTCCAGCCTGGATGACAGAG 86250         GC
           TG                     CACTTTGTT  CCAGGCTGGAGTG
                                ||||||||| ||||||||||||
                                GTGAGACAG  GGTCCGACCTCAC
                                     TA
GAM319   LOC150622 3'  CACTCCAGCCTGGGCAACAAG  80755
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||
                                GAACAACGGGTCCGACCTCAC

GAM319   LOC150630 5'  CACTCCAGCCTGGGCAGCAGAG 86292
           TG                     CACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||||
                                GTGAGACGACGGGTCCGACCTCAC

GAM319   LOC150889 3'  CACTCCAGCCTGCGGGACAGAG 80811         G _
           TG                     CACTTTGTT CC CAGGCTGGAGTG
                                ||||||||| || ||||||||||||
                                GTGAGACAG GG GTCCGACCTCAC
                                     _ C
GAM319   LOC150960 3'  CACTCCAGCTTGGGCAACAAAG 80869
           TG                     CACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||||
                                GTGAAACAACGGGTTCGACCTCAC

GAM319   LOC151196 3'  CACTCCAGCCTGGGCAACACAG 86448     T
                                CT TGTTGCCCAGGCTGGAGTG
                                || ||||||||||||||||||
                                GA ACAACGGGTCCGACCTCAC
                                 C
GAM319   LOC151248 3'  CACTCCAGCCCAGGTAACAGAG 80985           CA
           TG                     CACTTTGTTGCC  GGCTGGAGTG
                                ||||||||||||  ||||||||||
                                GTGAGACAATGG  CCGACCTCAC
                                      AC
GAM319   LOC151248 3'  CACTCCAGCCTGGTGACAGAG  80986       TG  C
                                CTTTGT  CC AGGCTGGAGTG
                                ||||||  || ||||||||||||
                                GAGACA  GG TCCGACCTCAC
                                   GT  _
GAM319   LOC151429 3'  CACTCCAGCCTGGGCGACAGAG 86521
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
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                                GAGACAGCGGGTCCGACCTCAC

GAM319   LOC151429 3'  CACTCCAGCCTGGGTGACAGAG 86522       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                  GT
GAM319   LOC151556 3'  CACTCCAGCCTGAGCAACAGAG 81075         C
                                CTTTGTTGC CAGGCTGGAGTG
                                ||||||||| ||||||||||||
                                GAGACAACG GTCCGACCTCAC
                                    A
GAM319   LOC151623 3'  CACTCCAGCCTGGGCTACAGA  86631      T
                                TTTGT GCCCAGGCTGGAGTG
                                ||||| ||||||||||||||||
                                AGACA CGGGTCCGACCTCAC
                                  T
GAM319   LOC151632 3'  CACTCCAGCCTGGGCAACAGAG 86638
           T                     ACTTTGTTGCCCAGGCTGGAGTG
                                 ||||||||||||||||||||||
                                 TGAGACAACGGGTCCGACCTCAC

GAM319   LOC151720 3'  CACTCCAGCCTGGGCGACAGAG 81146
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319   LOC151871 5'  CAGCCTGGGCAACACAGTG   57977     T
                                CACT TGTTGCCCAGGCTG
                                |||| ||||||||||||||
                                GTGA ACAACGGGTCCGAC
                                  C
GAM319   LOC151904 3'  CACTCCAGCCTGGGCAACAGAG 81202
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319   LOC152002 3'  CACTCCAGCCTGGACGACAGAG 81263         C
           TG                     CACTTTGTTG CCAGGCTGGAGTG
                                  |||||||||| ||||||||||||
                                  GTGAGACAGC GGTCCGACCTCAC
                                      A
GAM319   LOC152106 3'  CACTCCAGCCTGGTCGACAGAG 70590         C
           TG                     CACTTTGTTG CCAGGCTGGAGTG
                                  |||||||||| ||||||||||||
                                  GTGAGACAGC GGTCCGACCTCAC
                                      T
GAM319   LOC152271 3'  CACTCCAGCCTGGGCAACAGAG 81353
           T                      ACTTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||
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                                TGAGACAACGGGTCCGACCTCAC

GAM319   LOC152283 3'  CACTCCAGCCTGGGCAACAAGA 86866       _
                GT                    ACTTT GTTGCCCAGGCTGGAGTG
                                      ||||| ||||||||||||||||||
                                      TGAGA CAACGGGTCCGACCTCAC
                                        A
GAM319   LOC152313 3'  CACTCCAGCCTGGGTGACAGAG 86846        TG
                                      CTTTGT  CCCAGGCTGGAGTG
                                      ||||||  ||||||||||||||
                                      GAGACA  GGGTCCGACCTCAC
                                         GT
GAM319   LOC152426 3'  CACTCCAGCCTGGGCGACAGAG 86890
                TG                    CACTTTGTTGCCCAGGCTGGAGTG
                                      ||||||||||||||||||||||||
                                      GTGAGACAGCGGGTCCGACCTCAC

GAM319   LOC152445 3'  CACTCCAGCCTGAGTGAGGAAG 86936      G TG C
                                      CTTT T  C CAGGCTGGAGTG
                                      |||| |  | ||||||||||||
                                      GAAG A  G GTCCGACCTCAC
                                        G GT A
GAM319   LOC152453 3'  CACTCCAGCCTGGGCAACAAG  81465
                                      TTTGTTGCCCAGGCTGGAGTG
                                      ||||||||||||||||||||
                                      GAACAACGGGTCCGACCTCAC

GAM319   LOC152627 5'  CACTCCAGCCTGGATAAAAGAG 81504      G   C
                                      CTTT TTG CCAGGCTGGAGTG
                                      |||| ||| ||||||||||||
                                      GAGA AAT GGTCCGACCTCAC
                                        A   A
GAM319   LOC152627 3'  CACTCCAGCCTGGGCCACAGAG 81505         T
                TG                    CACTTTGT GCCCAGGCTGGAGTG
                                      ||||||||| ||||||||||||||
                                      GTGAGACA CGGGTCCGACCTCAC
                                           C
GAM319   LOC152804 3'  CACTCCAGCCTGGGCAACAGAG 87070
                                      CTTTGTTGCCCAGGCTGGAGTG
                                      ||||||||||||||||||||||
                                      GAGACAACGGGTCCGACCTCAC

GAM319   LOC152829 5'  CACTCCAGCATGGGCAACACAG 81571      T        G
                TG                    CACT TGTTGCCCA GCTGGAGTG
                                      |||| ||||||||| |||||||||
                                      GTGA ACAACGGGT CGACCTCAC
                                        C        A
GAM319   LOC153077 3'  CACTCCAGCCTGGGCTACAGAG 87113        T
                                      CTTTGT GCCCAGGCTGGAGTG
                                      |||||| ||||||||||||||||
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                                GAGACA CGGGTCCGACCTCAC
                                   T
GAM319   LOC153146 3'  CACTCCAGCCTGGGTGACAGAG 87143       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319   LOC153338 3'  CACTCCAGCCTGGGTGACAGAG 87192       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319   LOC153561 3'  CACTTGAGCCTGGGCAACAGAG 81749              G
            TG                    CACTTTGTTGCCCAGGCT GAGTG
                                ||||||||||||||||| |||||
                                GTGAGACAACGGGTCCGA TTCAC
                                         G
GAM319   LOC153579 3'  CACTCCAGCCTGGGCGACAGAG 81764
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319   LOC153682 3'  CACTCCAGCCTGAGCGACAGAG 87270         C
                                CTTTGTTGC CAGGCTGGAGTG
                                |||||||| ||||||||||||
                                GAGACAGCG GTCCGACCTCAC
                                   A
GAM319   LOC153684 3'  CACCCTAAGCACAAAGTG    87263        T  CC   C
                                CACTTTGT GC  AGG TG
                                |||||||| ||  ||| ||
                                GTGAAACA CG  TCC AC
                                     _  AA   C
GAM319   LOC153688 3'  CACTCCAGCCTGGGCGACAGAG 87298
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319   LOC154403 5'  CACTCCAGCCTGGGCTACAAG  81968      T
                                TTTGT GCCCAGGCTGGAGTG
                                |||||  ||||||||||||||
                                GAACA CGGGTCCGACCTCAC
                                   T
GAM319   LOC154791 3'  CACTCCAGCCTGGGCAACAAG  82049
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAACAACGGGTCCGACCTCAC

GAM319   LOC154877 3'  CACTCCAGCCTAGGTGATAGAG 87531       TG  C
                                CTTTGT  CC AGGCTGGAGTG
                                ||||||  || ||||||||||
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                                GAGATA  GG TCCGACCTCAC
                                   GT  A
GAM319   LOC154992 5'  CACTCCAGCCTGGGCTATAAG  82130      T
                                TTTGT GCCCAGGCTGGAGTG
                                ||||| ||||||||||||||||
                                GAATA CGGGTCCGACCTCAC
                                   T
GAM319   LOC155006 3'  CACTCCAGCCTGGGCGGCAGAG 82164
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACGGCGGGTCCGACCTCAC

GAM319   LOC155054 3'  CACTCCAGCCTGGGTGACAGAG 82199       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319   LOC155072 3'  CACTCCAACCTGGGTGACAGAG 87656       TG     C
                                CTTTGT  CCCAGG TGGAGTG
                                ||||||  |||||| |||||||
                                GAGACA  GGGTCC ACCTCAC
                                   GT     A
GAM319   LOC155376 3'  CACTCCAGCCTGGGTGACAAAG 82242       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAAACA  GGGTCCGACCTCAC
                                   GT
GAM319   LOC157247 5'  CTAGCCTGGGCAACATAG    82295    T
                                CT TGTTGCCCAGGCTGG
                                || ||||||||||||||
                                GA ACAACGGGTCCGATC
                                  T
GAM319   LOC157278 3'  CACTCCAGCCTGGGCTACAGA  87705      T
                                TTTGT GCCCAGGCTGGAGTG
                                ||||| ||||||||||||||||
                                AGACA CGGGTCCGACCTCAC
                                   T
GAM319   LOC157464 5'  CACTCCAGCCTGGGCAACGGG  87743
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GGGCAACGGGTCCGACCTCAC

GAM319   LOC157562 5'  CACTCCAGCCTGGGCAACATAG 87771      T
            TG                    CACT TGTTGCCCAGGCTGGAGTG
                                ||||| ||||||||||||||||||||
                                GTGA ACAACGGGTCCGACCTCAC
                                  T
GAM319   LOC157657 3'  CAGCCTGGACAACACAGTG   82432      T    C
                                CACT TGTTG CCAGGCTG
                                |||| ||||| ||||||||
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                                GTGA ACAAC GGTCCGAC
                                  C    A
GAM319   LOC157660 3'  CACTCCAGCGTGGGCAACAGAG 87800           G
           TG                    CACTTTGTTGCCCA GCTGGAGTG
                                 |||||||||||||| |||||||||
                                 GTGAGACAACGGGT CGACCTCAC
                                       G
GAM319   LOC157737 3'  CACTCCAGCCTGGGCAACAGAG 87841
                                 CTTTGTTGCCCAGGCTGGAGTG
                                 ||||||||||||||||||||||
                                 GAGACAACGGGTCCGACCTCAC

GAM319   LOC157983 3'  CACTCCAGCCTGGCGACAGAG  82536         C
                                 CTTTGTTGCC AGGCTGGAGTG
                                 |||||||||| ||||||||||
                                 GAGACAGCGG TCCGACCTCAC
                                       _
GAM319   LOC158088 3'  CACTCCAGCCTGGCGACAGAG  87970         C
                                 CTTTGTTGCC AGGCTGGAGTG
                                 |||||||||| ||||||||||
                                 GAGACAGCGG TCCGACCTCAC
                                       _
GAM319   LOC158160 3'  CACTCCAGCCTGGGTGACAG   73470     TG
                                 TTGT  CCCAGGCTGGAGTG
                                 ||||  ||||||||||||||
                                 GACA  GGGTCCGACCTCAC
                                   GT
GAM319   LOC158187 3'  CACTCCAGCCTGGGTGACAGAG 87987       TG
                                 CTTTGT  CCCAGGCTGGAGTG
                                 ||||||  ||||||||||||||
                                 GAGACA  GGGTCCGACCTCAC
                                     GT
GAM319   LOC158288 5'  CAGCCTGGGCAACATAGTG   88018     T
                                 CACT TGTTGCCCAGGCTG
                                 |||| |||||||||||||
                                 GTGA ACAACGGGTCCGAC
                                   T
GAM319   LOC158292 5'  CACTCCAGCCTGGGCAACAGAG 88038
                                 CTTTGTTGCCCAGGCTGGAGTG
                                 ||||||||||||||||||||||
                                 GAGACAACGGGTCCGACCTCAC

GAM319   LOC158292 5'  CACTCCAGCCTGGGCGACAGAG 88039
                                 CTTTGTTGCCCAGGCTGGAGTG
                                 ||||||||||||||||||||||
                                 GAGACAGCGGGTCCGACCTCAC

GAM319   LOC158310 3'  CAGCCTGGGCAACATAGTG   88077     T
                                 CACT TGTTGCCCAGGCTG
                                 |||| |||||||||||||
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                                GTGA ACAACGGGTCCGAC
                                  T
GAM319   LOC158382 5'  CAGCCTGGGCAACATAGTG   88124     T
                                CACT TGTTGCCCAGGCTG
                                |||| |||||||||||||
                                GTGA ACAACGGGTCCGAC
                                  T
GAM319   LOC158677 5'  CACTCCAGCCTGGGTGACAGAG 88246       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  |||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319   LOC158819 3'  CACTCCAGCCTGGGTGACAGAG 88270       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  |||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319   LOC158987 3'  CACTCCAGCCTGGGCAACAGAG 88318
                                CTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319   LOC158987 3'  CAGCCTGGGCAACATAGTG   88320     T
                                CACT TGTTGCCCAGGCTG
                                |||| |||||||||||||
                                GTGA ACAACGGGTCCGAC
                                  T
GAM319   LOC159036 3'  CACTCCAGCCTGGGCGACAGAG 88344
            TG                    CACTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||
                                GTGAGACAGCGGGTCCGACCTCAC

GAM319   LOC159053 3'  CACTCCAGCCTGGGCAACAGTG 88364     TT
                                CACT  GTTGCCCAGGCTGGAGTG
                                ||||  |||||||||||||||||
                                GTGA  CAACGGGTCCGACCTCAC
                                  __
GAM319   LOC161823 3'  CACTCCAGCCTGGGCAACAGAG 83174
            TG                    CACTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||
                                GTGAGACAACGGGTCCGACCTCAC

GAM319   LOC162962 3'  CACTCCAGCCTGGGTGACAG   83253     TG
                                TTGT  CCCAGGCTGGAGTG
                                ||||  |||||||||||||
                                GACA  GGGTCCGACCTCAC
                                  GT
GAM319   LOC170395 3'  CACTCAAGCCTGGGCAACAGAG 76863               G
            TG                    CACTTTGTTGCCCAGGCT GAGTG
                                |||||||||||||||| |||||
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                                GTGAGACAACGGGTCCGA CTCAC
                                           A
GAM319   LOC170395 3'  CACTCCAGCCTGGGCAACAAG  76864
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||
                                GAACAACGGGTCCGACCTCAC

GAM319   LOC196047 5'  CACTCCAGCCTGGGTGACAGAG 91146       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319   LOC196761 3'  CACTCCAGCCTGGGCGATAGAG 91116
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGATAGCGGGTCCGACCTCAC

GAM319   LOC197196 3'  CACTCCAGCCTGGGCGACAAG  91297
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||
                                GAACAGCGGGTCCGACCTCAC

GAM319   LOC197201 3'  CACTCCAGCCTGGGCAACACAG 89266    T
                                CT TGTTGCCCAGGCTGGAGTG
                                || ||||||||||||||||||
                                GA ACAACGGGTCCGACCTCAC
                                 C
GAM319   LOC197319 3'  CACTCCAGCCTGGCAACAGAGT 89314          C
            G                    CACTTTGTTGCC AGGCTGGAGTG
                                ||||||||||| ||||||||||
                                GTGAGACAACGG TCCGACCTCAC
                                          _
GAM319   LOC199676 3'  CACTCCAGCCTGGGAGACAGAG 91357       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GA
GAM319   LOC199729 3'  CACTCCAGCCAGGGCAACAGAG 73392          A
            TG                    CACTTTGTTGCCC GGCTGGAGTG
                                ||||||||||||| ||||||||||
                                GTGAGACAACGGG CCGACCTCAC
                                        A
GAM319   LOC199733 3'  CACTCCAACCTGGGCAACAGAG 91434          C
                                CTTTGTTGCCCAGG TGGAGTG
                                ||||||||||||||| |||||||
                                GAGACAACGGGTCC ACCTCAC
                                        A
GAM319   LOC199858 3'  CACTCCAGCCTGGGCGACAGAG 89792
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
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                                GAGACAGCGGGTCCGACCTCAC

GAM319   LOC199923 3'  CACTCCAGCCTGGACGACAGAG 89862         C
                                CTTTGTTG CCAGGCTGGAGTG
                                |||||||| ||||||||||||
                                GAGACAGC GGTCCGACCTCAC
                                     A
GAM319   LOC199923 3'  CACTCCAGCCTGGGCAACTGAG 89863      T
                                CTT GTTGCCCAGGCTGGAGTG
                                ||| ||||||||||||||||||
                                GAG CAACGGGTCCGACCTCAC
                                  T
GAM319   LOC200014 3'  CACTCCAGCCTGGGCGACAGAG 89921
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319   LOC200251 3'  CACTCCAGCCTAGGCAACAAG  90058         C
                                TTTGTTGCC AGGCTGGAGTG
                                ||||||||| ||||||||||
                                GAACAACGG TCCGACCTCAC
                                     A
GAM319   LOC200317 3'  CACTCCAGCCTGGGCAACAAGA 90220       _
           GT                     ACTTT GTTGCCCAGGCTGGAGTG
                                ||||| ||||||||||||||||||
                                TGAGA CAACGGGTCCGACCTCAC
                                   A
GAM319   LOC200853 3'  CACTCCAGCCTGGGAGACAGAG 90324       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                    GA
GAM319   LOC200904 3'  CTAGCCTGGGCAACAGAGT    91779
                                ACTTTGTTGCCCAGGCTGG
                                ||||||||||||||||||
                                TGAGACAACGGGTCCGATC

GAM319   LOC200940 3'  CACTCCAGCCTGGGCGACAGAG 90386
           TG                     CACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||||
                                GTGAGACAGCGGGTCCGACCTCAC

GAM319   LOC201173 3'  CACTCCAGCCTGGGCGACAGAG 88672
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319   LOC201182 5'  CACTCCAGCCTGGTCAACAGAG 91333         C
                                CTTTGTTG CCAGGCTGGAGTG
                                |||||||| ||||||||||||
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                                GAGACAAC GGTCCGACCTCAC
                                     T
GAM319   LOC201220 3'  CACTCCAGCCTGGGTGACAGAG 88707       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319   LOC201564 3'  CACTCCAGCCTGGGCAACAAG  81272
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||
                                GAACAACGGGTCCGACCTCAC

GAM319   LOC201689 3'  CACTCCAGCCTGGGTGACAGGG 67731       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GGGACA  GGGTCCGACCTCAC
                                   GT
GAM319   LOC201689 3'  CAGCCTGGGCAACATAGTG    67733     T
                                CACT TGTTGCCCAGGCTG
                                ||||  ||||||||||||||
                                GTGA ACAACGGGTCCGAC
                                  T
GAM319   LOC201705 3'  CACTCCAGCCTGGGTGACAGAG 91854       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319   LOC201868 5'  CACTCCAGCCTGGGCTACAAG  90515      T
                                TTTGT GCCCAGGCTGGAGTG
                                |||||  ||||||||||||||
                                GAACA CGGGTCCGACCTCAC
                                   T
GAM319   LOC201931 3'  CACTCCAGCCTGGGCGACAGAG 90560
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319   LOC202781 3'  CACTCCAGCCTGGGCGACAGAG 91967
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319   LOC202868 3'  CACTCCAACCTGGGTGACAGAG 91990       TG     C
                                CTTTGT  CCCAGG TGGAGTG
                                ||||||  |||||| |||||||
                                GAGACA  GGGTCC ACCTCAC
                                   GT     A
GAM319   LOC203083 3'  CACTCCAGCCTGGGCAACAGAG 92081
              T                  ACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
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                                TGAGACAACGGGTCCGACCTCAC

GAM319   LOC203276 3'  CAGCCTGGGCAACAGAGTG   92111
                                CACTTTGTTGCCCAGGCTG
                                ||||||||||||||||||
                                GTGAGACAACGGGTCCGAC

GAM319   LOC203289 3'  CACTCCAGCCTGGCGACAGAG  90863          C
                                CTTTGTTGCC AGGCTGGAGTG
                                |||||||||| ||||||||||
                                GAGACAGCGG TCCGACCTCAC
                                          _
GAM319   LOC203305 3'  CAGCCTGGGCAACAGAGTG   92164
                                CACTTTGTTGCCCAGGCTG
                                ||||||||||||||||||
                                GTGAGACAACGGGTCCGAC

GAM319   LOC203350 3'  CACTCCAGCCTGGATGACAGAG 92230          GC
           TG                     CACTTTGTT  CCAGGCTGGAGTG
                                |||||||||  ||||||||||||
                                GTGAGACAG  GGTCCGACCTCAC
                                     TA
GAM319   LOC205327 3'  CACTCCAACCTGGGCAACATAG 91068      T         C
           TG                     CACT TGTTGCCCAGG TGGAGTG
                                |||| |||||||||| |||||||
                                GTGA ACAACGGGTCC ACCTCAC
                                  T         A
GAM319   LOC219347 3'  CACTCCAGCCTGGGCAACAGAG 94573
           TG                     CACTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||||
                                GTGAGACAACGGGTCCGACCTCAC

GAM319   LOC219540 3'  CACTCCAGCCTGGGCGACAGAG 95239
                                CTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319   LOC219627 3'  CACTCCAGCCTGGGCAACAAG  93801
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||
                                GAACAACGGGTCCGACCTCAC

GAM319   LOC219649 3'  CACTCCAGCCTAGGCAACAAG  94543          C
                                TTTGTTGCC AGGCTGGAGTG
                                ||||||||| ||||||||||
                                GAACAACGG TCCGACCTCAC
                                     A
GAM319   LOC219649 3'  CACTCCAGCCTGGGCGACAGAG 94544
           TG                     CACTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||||
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                                GTGAGACAGCGGGTCCGACCTCAC

GAM319   LOC219672 5'  CACTCCAGCCTGGGCAACAAGA 92964       _
                GT                  ACTTT GTTGCCCAGGCTGGAGTG
                                    ||||| ||||||||||||||||||
                                    TGAGA CAACGGGTCCGACCTCAC
                                      A
GAM319   LOC219722 5'  CACTTCAGCCTGGACAACAGAG 94675          C
                TG                  CACTTTGTTG CCAGGCTGGAGTG
                                    |||||||||| ||||||||||||
                                    GTGAGACAAC GGTCCGACTTCAC
                                         A
GAM319   LOC219919 3'  CACTCCAGCCTGGGCAACAGAG 94918
                T                   ACTTTGTTGCCCAGGCTGGAGTG
                                    ||||||||||||||||||||||||
                                    TGAGACAACGGGTCCGACCTCAC

GAM319   LOC220070 3'  ACTCCAGCCTGGAAAACG    59939     GC
                                    TGTT  CCAGGCTGGAGT
                                    ||||  ||||||||||||
                                    GCAA  GGTCCGACCTCA
                                      AA
GAM319   LOC220506 3'  CACTCCAGCCTGGGCAACAGA  74516
                                    TTTGTTGCCCAGGCTGGAGTG
                                    |||||||||||||||||||||
                                    AGACAACGGGTCCGACCTCAC

GAM319   LOC220549 3'  CACTCCAGCCTGGGTGACAGAA 94504    C    TG
                TG                    CA TTTGT  CCCAGGCTGGAGTG
                                    || |||||  ||||||||||||||
                                    GT AGACA  GGGTCCGACCTCAC
                                     A    GT
GAM319   LOC220906 3'  CACTCCAGCCTGGGCAACAAG  93030
                                    TTTGTTGCCCAGGCTGGAGTG
                                    |||||||||||||||||||||
                                    GAACAACGGGTCCGACCTCAC

GAM319   LOC220992 3'  CACTCCAGCCTGGGCAACATAG 93108    T
                                    CT TGTTGCCCAGGCTGGAGTG
                                    || ||||||||||||||||||
                                    GA ACAACGGGTCCGACCTCAC
                                     T
GAM319   LOC221042 3'  CACTCCAGCCTGGGTGACAGAG 94793       TG
                                    CTTTGT  CCCAGGCTGGAGTG
                                    ||||||  ||||||||||||||
                                    GAGACA  GGGTCCGACCTCAC
                                       GT
GAM319   LOC221069 3'  CACTCCAGCCTGGGCGACAGAG 94818
                                    CTTTGTTGCCCAGGCTGGAGTG
                                    |||||||||||||||||||||||
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                                GAGACAGCGGGTCCGACCTCAC

GAM319   LOC221178 3'  CACTCCAGCCTGGGAGATACAG 95166    T   TG
                                CT TGT  CCCAGGCTGGAGTG
                                || |||  ||||||||||||||
                                GA ATA  GGGTCCGACCTCAC
                                 C   GA
GAM319   LOC221271 3'  CACTCCAGCCTGGGCAACAGAG 93498
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319   LOC221271 3'  CACTCCAGCCTGGGTGACAGAG 93499       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                    GT
GAM319   LOC221288 3'  CACTCCAGCCTGGGCGACAGAG 95255
                   TG             CACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||||
                                GTGAGACAGCGGGTCCGACCTCAC

GAM319   LOC221337 3'  CACTCCAGCCTGGGCAACAAGA 93734      _
                   GT             ACTTT GTTGCCCAGGCTGGAGTG
                                ||||| ||||||||||||||||||
                                TGAGA CAACGGGTCCGACCTCAC
                                  A
GAM319   LOC221410 3'  CACTCCAGCCTGGGTGACAGAG 93689       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                    GT
GAM319   LOC221543 3'  CACTCCAGCCTGGGCAACAAGA 95363      _
                   GT             ACTTT GTTGCCCAGGCTGGAGTG
                                ||||| ||||||||||||||||||
                                TGAGA CAACGGGTCCGACCTCAC
                                  A
GAM319   LOC221543 5'  CACTCCAGCCTGGGCGACAGAG 95364
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319   LOC221641 5'  CACTCCAGCCTGGGTGGCAGAG 95343       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACG  GGGTCCGACCTCAC
                                    GT
GAM319   LOC221795 3'  CACTCCAGCCTGGGCAACAGAG 94068
                   T             ACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
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                                TGAGACAACGGGTCCGACCTCAC

GAM319   LOC221943 5'  CACTCCAGCCTGGGCGACAGAG 95617
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319   LOC221954 5'  CACTCCAGCCTGGGCAACAGAG 95638
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319   LOC221954 5'  CACTCCAGCCTGGGTGACAGAG 95639        TG
              T                  ACTTTGT  CCCAGGCTGGAGTG
                                |||||||  ||||||||||||||
                                TGAGACA  GGGTCCGACCTCAC
                                     GT
GAM319   LOC221962 3'  CACTCCAGCCTGGGCTACAGA  94237       T
                                TTTGT GCCCAGGCTGGAGTG
                                ||||| ||||||||||||||||
                                AGACA CGGGTCCGACCTCAC
                                   T
GAM319   LOC222060 5'  CACTCCAGCCTGGGCGACAGAG 95751
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319   LOC222160 3'  CACTCCAGCCTGGGCAGCAGAG 95771
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACGACGGGTCCGACCTCAC

GAM319   LOC222160 5'  CACTCCAGCCTGGGCGACAGAG 95772
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319   LOC222182 3'  CACTCCAGCCTGGGCAATAGAG 95852
              TG                   CACTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||||||
                                GTGAGATAACGGGTCCGACCTCAC

GAM319   LOC222865 3'  CACTCCAGCCTGAGTGACAGAG 94438        TG C
                                CTTTGT  C CAGGCTGGAGTG
                                ||||||  | ||||||||||||
                                GAGACA  G GTCCGACCTCAC
                                    GT A
GAM319   LOC253039 3'  CACTCCAGCCTGGGCGACAGAG 97863
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
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                                GAGACAGCGGGTCCGACCTCAC

GAM319   LOC253532 3'  CACTCCAGCCTGGGTGACAAAG 97731        TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAAACA  GGGTCCGACCTCAC
                                   GT
GAM319   LOC253612 5'  CAGCCTAGGCAACAGAGTG   98543            C
                                CACTTTGTTGCC AGGCTG
                                |||||||||||| ||||||
                                GTGAGACAACGG TCCGAC
                                      A
GAM319   LOC253639 3'  CACTCCAGCCTGGGCGACAGAG 97510
            TG                    CACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||||
                                GTGAGACAGCGGGTCCGACCTCAC

GAM319   LOC253664 3'  CAGCCTGGGCAACATAGTG   96460      T
                                CACT TGTTGCCCAGGCTG
                                |||| ||||||||||||||
                                GTGA ACAACGGGTCCGAC
                                  T
GAM319   LOC253786 3'  CACTCCAGCCTGGGCAATAGAG 98829
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGATAACGGGTCCGACCTCAC

GAM319   LOC253832 3'  CACTCCAGCCTGGGCGACGAGT 96589       T
            G                    CACTT GTTGCCCAGGCTGGAGTG
                                ||||| ||||||||||||||||||
                                GTGAG CAGCGGGTCCGACCTCAC
                                  _
GAM319   LOC253906 3'  CAGCCTGGGCAACAAAGTG   98298
                                CACTTTGTTGCCCAGGCTG
                                |||||||||||||||||||
                                GTGAAACAACGGGTCCGAC

GAM319   LOC254045 3'  CACCCATCTTGGGCAACAGAAT 98262    C          C   A
            G                    CA TTTGTTGCCCAGG TGG GTG
                                || |||||||||||| ||| |||
                                GT AGACAACGGGTTC ACC CAC
                                 A          T  _
GAM319   LOC254100 3'  CACTCCAGCCTGGGCAACAGAG 98148
            TG                    CACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||||
                                GTGAGACAACGGGTCCGACCTCAC

GAM319   LOC254176 3'  CACTCCAGCCTGGGCAACAGAG 99162
            T                    ACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||||
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                                TGAGACAACGGGTCCGACCTCAC

GAM319   LOC254243 3'  CAGCCTGGGCAACAGAGTG   99250
                                CACTTTGTTGCCCAGGCTG
                                ||||||||||||||||||
                                GTGAGACAACGGGTCCGAC

GAM319   LOC254531 5'  CACTCCAGCCTGGGTGACAGAG 96663       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319   LOC254756 3'  CACTCCAGCCTGGGCAATAGAG 99210
            T                    ACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||||
                                TGAGATAACGGGTCCGACCTCAC

GAM319   LOC254808 3'  CACTCCAGCCTGGGCAACAGAG 98801
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAACGGGTCCGACCTCAC

GAM319   LOC254875 3'  CACTCCAGCCTGGGTGACAAAG 97775       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAAACA  GGGTCCGACCTCAC
                                   GT
GAM319   LOC255030 5'  CACTCCAGCCTGGGTGACAGAG 99080       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319   LOC255031 3'  CACTCCAGCCTGGCTACAGAGT 99029        T  C
            G                    CACTTTGT GCC AGGCTGGAGTG
                                ||||||||| ||| ||||||||||
                                GTGAGACA CGG TCCGACCTCAC
                                     T  _
GAM319   LOC255031 3'  CAGCCTGGGCAACATAGTG   99030     T
                                CACT TGTTGCCCAGGCTG
                                ||||  ||||||||||||||
                                GTGA ACAACGGGTCCGAC
                                   T
GAM319   LOC255042 3'  CACTCCAGCCTGGGCAACAAG  97036
                                TTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAACAACGGGTCCGACCTCAC

GAM319   LOC255177 3'  CACTCCAGCCTAGGCAACAGAG 98387          C
            TG                    CACTTTGTTGCC AGGCTGGAGTG
                                ||||||||||| ||||||||||
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                                GTGAGACAACGG TCCGACCTCAC
                                      A
GAM319   LOC255231 3'  CACTCCAGCCTGGGTGACAGAG 97117        TG
           TG                    CACTTTGT  CCCAGGCTGGAGTG
                                 ||||||||  ||||||||||||||
                                 GTGAGACA  GGGTCCGACCTCAC
                                     GT
GAM319   LOC255326 3'  CACTCCAGCCTGGGTGACAGAG 98115       TG
                                 CTTTGT  CCCAGGCTGGAGTG
                                 ||||||  ||||||||||||||
                                 GAGACA  GGGTCCGACCTCAC
                                    GT
GAM319   LOC255328 3'  CACTCCAGCCTGGGTGATAAG  98333      TG
                                 TTTGT  CCCAGGCTGGAGTG
                                 |||||  ||||||||||||||
                                 GAATA  GGGTCCGACCTCAC
                                    GT
GAM319   LOC255461 3'  CACTCCAGCCTGGGCTACAGA  99137      T
                                 TTTGT GCCCAGGCTGGAGTG
                                 ||||| ||||||||||||||||
                                 AGACA CGGGTCCGACCTCAC
                                    T
GAM319   LOC255463 3'  CAGCCTGGACAACATAGTG    96538      T    C
                                 CACT TGTTG CCAGGCTG
                                 |||| ||||| ||||||||
                                 GTGA ACAAC GGTCCGAC
                                   T    A
GAM319   LOC255516 3'  CACTCCAGCCTGGGCTACAGA  99151      T
                                 TTTGT GCCCAGGCTGGAGTG
                                 ||||| ||||||||||||||||
                                 AGACA CGGGTCCGACCTCAC
                                    T
GAM319   LOC255671 5'  CACTCCAGCCTGGGCGACAGAG 99064
                                 CTTTGTTGCCCAGGCTGGAGTG
                                 ||||||||||||||||||||||
                                 GAGACAGCGGGTCCGACCTCAC

GAM319   LOC255671 3'  CACTCCAGCCTGGGTAACAGAG 99065
                                 CTTTGTTGCCCAGGCTGGAGTG
                                 ||||||||||||||||||||||
                                 GAGACAATGGGTCCGACCTCAC

GAM319   LOC255671 5'  CACTCCAGCCTGGGTGACAGAG 99066        TG
           TG                    CACTTTGT  CCCAGGCTGGAGTG
                                 ||||||||  ||||||||||||||
                                 GTGAGACA  GGGTCCGACCTCAC
                                     GT
GAM319   LOC255798 3'  CAGCCTGGGCAACACAGTG    98786      T
                                 CACT TGTTGCCCAGGCTG
                                 |||| ||||||||||||||
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                                GTGA ACAACGGGTCCGAC
                                  C
GAM319   LOC256207 3'  CACTCCAACCTGGGCGACAGAG 96871            C
                                CTTTGTTGCCCAGG TGGAGTG
                                ||||||||||||| |||||||
                                GAGACAGCGGGTCC ACCTCAC
                                       A
GAM319   LOC256267 3'  CACTCCAGCCTGGAAAACAAGT 98606      T   GC
           G                     CACTT GTT  CCAGGCTGGAGTG
                                ||||| |||  ||||||||||||
                                GTGAA CAA  GGTCCGACCTCAC
                                  _  AA
GAM319   LOC256515 3'  CACTCCAGCCTGGGCAACAGAG 98204
           T                     ACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                TGAGACAACGGGTCCGACCTCAC

GAM319   LOC256544 3'  CACTCCAGCCTGGCGACAGAG  97927          C
                                CTTTGTTGCC AGGCTGGAGTG
                                |||||||||| ||||||||||
                                GAGACAGCGG TCCGACCTCAC
                                       _
GAM319   LOC256594 3'  CACTCCAGCCTGGGCAACAGAG 98855
           T                     ACTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                TGAGACAACGGGTCCGACCTCAC

GAM319   LOC256980 3'  CACTCCAGCCTGGTCGACAAG  96925        C
                                TTTGTTG CCAGGCTGGAGTG
                                ||||||| ||||||||||||
                                GAACAGC GGTCCGACCTCAC
                                    T
GAM319   LOC257017 5'  CACTCCAGCCCTGGAACATAGT 99216      T   G  CA
           G                     CACT TGTT CC  GGCTGGAGTG
                                |||| |||| ||  ||||||||||
                                GTGA ACAA GG  CCGACCTCAC
                                  T   _  TC
GAM319   LOC257282 5'  CACTCAAGCCTGGGCAACAGAG 98132             G
                                CTTTGTTGCCCAGGCT GAGTG
                                |||||||||||||| |||||
                                GAGACAACGGGTCCGA CTCAC
                                       A
GAM319   LOC257354 3'  CAGCCTGGGCAACATAGTG   96785      T
                                CACT TGTTGCCCAGGCTG
                                |||| ||||||||||||
                                GTGA ACAACGGGTCCGAC
                                  T
GAM319   LOC257539 3'  CACTCCAGCCTGGGTGACAGGG 99544        TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
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                                GGGACA  GGGTCCGACCTCAC
                                   GT
GAM319   LOC257578 3'  CACTCCAGCCTGGGTGACAGGG 99656       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GGGACA  GGGTCCGACCTCAC
                                   GT
GAM319   LOC257596 3'  CACTCCAGCCTGGGCAACAAGA 99766       _
            GT                    ACTTT GTTGCCCAGGCTGGAGTG
                                ||||| ||||||||||||||||||
                                TGAGA CAACGGGTCCGACCTCAC
                                  A
GAM319   LOC257596 5'  CACTCCAGCCTGGGCGACAGAG 99767
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319   LOC51212  3'  CACTCCAGCCTGGGTGACAGAG 33497       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319   LOC51277  3'  CACCTGGGCAACATAGT     80839     T         C
                                ACT TGTTGCCCAGG TG
                                ||| |||||||||| ||
                                TGA ACAACGGGTCC AC
                                  T         _
GAM319   LOC51279  3'  CAGCCTAAGCAACATAGTG    33750      T     CC
                                CACT TGTTGC  AGGCTG
                                |||| ||||||  ||||||
                                GTGA ACAACG  TCCGAC
                                   T     AA
GAM319   LOC51333  3'  CAGCCTGGAGAACAAAGTG    34049          GC
                                CACTTTGTT  CCAGGCTG
                                |||||||||  ||||||||
                                GTGAAACAA  GGTCCGAC
                                      GA
GAM319   LOC51336  3'  CACTCCAGCCTGGGTGACAGCG 34067    T    TG
               T                   AC TTGT  CCCAGGCTGGAGTG
                                || ||||  ||||||||||||||
                                TG GACA  GGGTCCGACCTCAC
                                 C    GT
GAM319   LOC51716  3'  CAGCCAGGGCAACAAAGTG    33259            A
                                CACTTTGTTGCCC GGCTG
                                |||||||||||| |||||
                                GTGAAACAACGGG CCGAC
                                         A
GAM319   LOC57118  3'  CACTCCAGCCTGGGTGACAGA  40215       TG
                                TTTGT  CCCAGGCTGGAGTG
                                |||||  ||||||||||||||
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                                AGACA  GGGTCCGACCTCAC
                                   GT
GAM319  LOC63929  3' CACTCCAGCCTGGGTGACTGAG 42279    T  TG
                                CTT GT  CCCAGGCTGGAGTG
                                ||| ||  ||||||||||||||
                                GAG CA  GGGTCCGACCTCAC
                                  T  GT
GAM319  LOC85479  5' CACTCCAGCCTGGGCGACAGAG 53560
                                CTTTGTTGCCCAGGCTGGAGTG
                                ||||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319  LOC89890  3' CACTCCAGCCTGGATGACAGAG 61202         GC
           TG                     CACTTTGTT  CCAGGCTGGAGTG
                                ||||||||  ||||||||||||
                                GTGAGACAG  GGTCCGACCTCAC
                                     TA
GAM319  LOC90038  3' CAGCCTGGGCAACAGAGTG   61793
                                CACTTTGTTGCCCAGGCTG
                                |||||||||||||||||||
                                GTGAGACAACGGGTCCGAC

GAM319  LOC90072  3' CACTCCAGCCTGGGGAACAGAG 61949        G
                                CTTTGTT CCCAGGCTGGAGTG
                                |||||||  ||||||||||||
                                GAGACAA GGGTCCGACCTCAC
                                    G
GAM319  LOC90072  5' CACTCCAGCCTGGGTGACAGA  61950      TG
                                TTTGT  CCCAGGCTGGAGTG
                                |||||  ||||||||||||
                                AGACA  GGGTCCGACCTCAC
                                   GT
GAM319  LOC90072  3' CAGCCTGAGCAACATAGTG   61953     T     C
                                CACT TGTTGC CAGGCTG
                                |||| ||||||  |||||||
                                GTGA ACAACG GTCCGAC
                                  T     A
GAM319  LOC90092  3' CACTCCAGCCTGGCGACAAG   62055         C
                                TTTGTTGCC AGGCTGGAGTG
                                |||||||||  ||||||||||
                                GAACAGCGG TCCGACCTCAC
                                          _
GAM319  LOC90141  3' CACTCCAGCCTGGATGATAGAG 62299        GC
                                CTTTGTT  CCAGGCTGGAGTG
                                |||||||  ||||||||||||
                                GAGATAG  GGTCCGACCTCAC
                                    TA
GAM319  LOC90155  5' CACTCCAGCCTGGGCAACAAGA 62362       _
           GT                     ACTTT GTTGCCCAGGCTGGAGTG
                                |||||  ||||||||||||||||||
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                                TGAGA CAACGGGTCCGACCTCAC
                                  A
GAM319  LOC90233  3'  CACTCCAGCCCAGGCAACAGAG 57189          CA
            TG                    CACTTTGTTGCC  GGCTGGAGTG
                                  ||||||||||||  ||||||||||
                                  GTGAGACAACGG  CCGACCTCAC
                                     AC
GAM319  LOC90321  3'  CACTCCAACCTGGGTGACAGAG 62929       TG     C
                                  CTTTGT  CCCAGG TGGAGTG
                                  ||||||  |||||| |||||||
                                  GAGACA  GGGTCC ACCTCAC
                                     GT     A
GAM319  LOC90393  5'  CACTCCAGCCTGGGTGACAGAG 63303        TG
            TG                    CACTTTGT  CCCAGGCTGGAGTG
                                  ||||||||  ||||||||||||||
                                  GTGAGACA  GGGTCCGACCTCAC
                                       GT
GAM319  LOC90591  3'  CAGCCTGGGCAACATAGTG    64152      T
                                  CACT TGTTGCCCAGGCTG
                                  ||||  ||||||||||||||
                                  GTGA ACAACGGGTCCGAC
                                    T
GAM319  LOC90624  3'  CACTCCAGCCTGGGGGACAGAG 64365         G
            TG                    CACTTTGTT CCCAGGCTGGAGTG
                                  |||||||||  ||||||||||||||
                                  GTGAGACAG GGGTCCGACCTCAC
                                       G
GAM319  LOC90784  5'  CACTCCAGCCTGGGCAACAGAG 64692
            TG                    CACTTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||||
                                  GTGAGACAACGGGTCCGACCTCAC

GAM319  LOC90841  5'  CACTCCAGCCTGGGTGATAGAG 64863       TG
                                  CTTTGT  CCCAGGCTGGAGTG
                                  ||||||  ||||||||||||||
                                  GAGATA  GGGTCCGACCTCAC
                                     GT
GAM319  LOC90918  5'  CACTCCAGCCTAGGCAACAAGA 64995      _     C
            GT                    ACTTT GTTGCC AGGCTGGAGTG
                                  |||||  ||||||  ||||||||||
                                  TGAGA CAACGG TCCGACCTCAC
                                     A     A
GAM319  LOC91035  3'  CACTCCAGCCTGGACAACAAG  65295       C
                                  TTTGTTG CCAGGCTGGAGTG
                                  |||||||  |||||||||||||
                                  GAACAAC GGTCCGACCTCAC
                                       A
GAM319  LOC91056  3'  CACTCCAGCCTGGGCGACAGAG 96400
                                  CTTTGTTGCCCAGGCTGGAGTG
                                  ||||||||||||||||||||||
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                                GAGACAGCGGGTCCGACCTCAC

GAM319  LOC91250  5' CACTCCAGCCTGAGTGACAGAG 65909        TG C
             TG                  CACTTTGT  C CAGGCTGGAGTG
                                 |||||||| | ||||||||||||
                                 GTGAGACA  G GTCCGACCTCAC
                                     GT A
GAM319  LOC91250  5' CACTCCAGCCTGGGCAACAGAG 65910
             TG                  CACTTTGTTGCCCAGGCTGGAGTG
                                 ||||||||||||||||||||||||
                                 GTGAGACAACGGGTCCGACCTCAC

GAM319  LOC91286  3' TGCACTCCAGCCTGGACAACAG 66064        C          ___
             A                   TTTGTTG CCAGGCTGGAGTG   CA
                                 ||||||| |||||||||||||   ||
                                 AGACAAC GGTCCGACCTCAC   GT
                                     A          ___
GAM319  LOC91380  3' CACTCCAGCCTGGGTGACAGAG 66437         TG
             TG                  CACTTTGT  CCCAGGCTGGAGTG
                                 ||||||||  ||||||||||||||
                                 GTGAGACA  GGGTCCGACCTCAC
                                     GT
GAM319  LOC91442  3' CACTCCAGCCTGGGCACCAGAG 66640       T
                                 CTTTG TGCCCAGGCTGGAGTG
                                 |||||  ||||||||||||||||
                                 GAGAC ACGGGTCCGACCTCAC
                                    C
GAM319  LOC91547  3' CACTCCAGCCTGGGCGACAGAG 66997
                                 CTTTGTTGCCCAGGCTGGAGTG
                                 ||||||||||||||||||||||||
                                 GAGACAGCGGGTCCGACCTCAC

GAM319  LOC91750  3' CACTCCAGCCTGGGCAACAGAG 67648
             TG                  CACTTTGTTGCCCAGGCTGGAGTG
                                 ||||||||||||||||||||||||
                                 GTGAGACAACGGGTCCGACCTCAC

GAM319  LOC91812  3' CACTCCAGCCTGGGCAACAGA  67813
                                 TTTGTTGCCCAGGCTGGAGTG
                                 ||||||||||||||||||||||
                                 AGACAACGGGTCCGACCTCAC

GAM319  LOC91813  3' CACTCCAGCCTGGGCAACAGA  67837
                                 TTTGTTGCCCAGGCTGGAGTG
                                 ||||||||||||||||||||||
                                 AGACAACGGGTCCGACCTCAC

GAM319  LOC91862  3' CACTCCAGCCCAGGTGACAGAG 54569       TG  CA
                                 CTTTGT  CC  GGCTGGAGTG
                                 ||||||  ||  ||||||||||
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                                GAGACA  GG  CCGACCTCAC
                                   GT  AC
GAM319  LOC91963  5'  CACTCCAGCCTGGGCAACAGAG 68313
            TG                   CACTTTGTTGCCCAGGCTGGAGTG
                                 ||||||||||||||||||||||
                                 GTGAGACAACGGGTCCGACCTCAC

GAM319  LOC92078  3'  CACTCCAGCCTGGGTGACAGAG 68591        TG
            TG                   CACTTTGT  CCCAGGCTGGAGTG
                                 ||||||||  ||||||||||||||
                                 GTGAGACA  GGGTCCGACCTCAC
                                    GT
GAM319  LOC92223  3'  CACTCCAGCCTGGGCAACAAGA 69045      _
            GT                   ACTTT GTTGCCCAGGCTGGAGTG
                                 |||||  ||||||||||||||||||
                                 TGAGA CAACGGGTCCGACCTCAC
                                   A
GAM319  LOC92267  3'  CACTCCAGCCTGGGCAACAAG  69165
                                 TTTGTTGCCCAGGCTGGAGTG
                                 ||||||||||||||||||||
                                 GAACAACGGGTCCGACCTCAC

GAM319  LOC92299  3'  CACTCCAGCCTGGCGACAAAGC 69360   A       C
            G                    C CTTTGTTGCC AGGCTGGAGTG
                                 | ||||||||| ||||||||||
                                 G GAAACAGCGG TCCGACCTCAC
                                  C       _
GAM319  LOC92360  3'  CACTCCAGCCTGGGTGACAGAG 69622      TG
                                 CTTTGT  CCCAGGCTGGAGTG
                                 ||||||  ||||||||||||||
                                 GAGACA  GGGTCCGACCTCAC
                                    GT
GAM319  LOC92405  3'  CACTCTAGCCTGGGCAACAGAG 69710
                                 CTTTGTTGCCCAGGCTGGAGTG
                                 ||||||||||||||||||||||
                                 GAGACAACGGGTCCGATCTCAC

GAM319  LOC92465  5'  CACTCCAGCCTGGGCGACAGAG 69943
                                 CTTTGTTGCCCAGGCTGGAGTG
                                 ||||||||||||||||||||||
                                 GAGACAGCGGGTCCGACCTCAC

GAM319  LOC92466  3'  CACTCCAGCCTGGAAAACAAGT 69962      T  GC
            G                    CACTT GTT  CCAGGCTGGAGTG
                                 |||||  |||  ||||||||||||
                                 GTGAA CAA  GGTCCGACCTCAC
                                   _  AA
GAM319  LOC92482  3'  CACCCCAGCCTGGGCAACAGAG 70016            A
                                 CTTTGTTGCCCAGGCTGG GTG
                                 |||||||||||||||||  |||
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                                GAGACAACGGGTCCGACC CAC
                                           C
GAM319  LOC92492  3' CACTCCAGCCTGGATGACAG  70080      GC
                                TTGTT  CCAGGCTGGAGTG
                                |||||  ||||||||||||||
                                GACAG  GGTCCGACCTCAC
                                   TA
GAM319  LOC92521  3' CACTCCAGCCTGTGTGAAAGAG 70201     G TG C
                                CTTT T  C CAGGCTGGAGTG
                                |||| |  | ||||||||||||
                                GAGA A  G GTCCGACCTCAC
                                  A GT T
GAM319  LOC92568  3' CACTCCAGCCTGGGTGACAGAG 70325        TG
           TG                     CACTTTGT  CCCAGGCTGGAGTG
                                ||||||||  ||||||||||||||
                                GTGAGACA  GGGTCCGACCTCAC
                                     GT
GAM319  LOC92573  3' CACTCCAGCCTGGGTGACAGAG 70369       TG
                                CTTTGT  CCCAGGCTGGAGTG
                                ||||||  ||||||||||||||
                                GAGACA  GGGTCCGACCTCAC
                                   GT
GAM319  LOC92659  3' CACTCCAGCCTGGGCGACAGAG 70607
                                CTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||
                                GAGACAGCGGGTCCGACCTCAC

GAM319  LOC92771  3' CACTCCAGCCTGGGCCACAGAA 54208    C    T
           TG                     CA TTTGT GCCCAGGCTGGAGTG
                                || ||||| ||||||||||||||
                                GT AGACA CGGGTCCGACCTCAC
                                 A    C
GAM319  LOC92973  5' CACTCCAGCCTGGGCAACAGAG 71585
           TG                     CACTTTGTTGCCCAGGCTGGAGTG
                                |||||||||||||||||||||||
                                GTGAGACAACGGGTCCGACCTCAC

GAM319  LOC93132  3' CAGCTCGGGCAACAAAGTG   71980           AG
                                CACTTTGTTGCCC  GCTG
                                ||||||||||||  ||||
                                GTGAAACAACGGG  CGAC
                                      CT
GAM320  ADAT1    3'  ACCAGCCTGGCCAACCTGGTGA 24907        T
           AA                     TTTCACCA GTTGGCCAGGCTGGT
                                ||||||||  ||||||||||||||
                                AAAGTGGT CAACCGGTCCGACCA
                                     C
GAM320  AICDA    3'  ACCAGCCTGGCCAACATGG   40686
                                CCATGTTGGCCAGGCTGGT
                                |||||||||||||||||||
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                                GGTACAACCGGTCCGACCA

GAM320  ALDH3A2  3'  ACCAGCCTGGACAACACAGTGA 69794       CA    G
            GA                   TTTCAC  TGTTG CCAGGCTGGT
                                 ||||||  ||||| ||||||||||
                                 AGAGTG  ACAAC GGTCCGACCA
                                    AC    A
GAM320  ALDH3B1  3'  AGCCTGGCTAACATGGCGAAA  93149     A
                                 TTTC CCATGTTGGCCAGGCT
                                 |||| ||||||||||||||||
                                 AAAG GGTACAATCGGTCCGA
                                   C
GAM320  ALDH8A1  3'  ATCAGCCTAGGCAACATGGTGA 42912           G _
            AA                   TTTCACCATGTTG CC AGGCTGGT
                                 ||||||||||||| || ||||||||
                                 AAAGTGGTACAAC GG TCCGACTA
                                        _ A
GAM320  ALPP     3'  ACCATCCTGGCTAACACGGTGA 69402        A        C
            AA                   TTTCACC TGTTGGCCAGG TGGT
                                 ||||||| |||||||||| ||||
                                 AAAGTGG ACAATCGGTCC ACCA
                                    C         T
GAM320  ANKH     3'  ACCAGCCTGGCCAACATGGCGA 55062      A
            AA                   TTTC CCATGTTGGCCAGGCTGGT
                                 |||| ||||||||||||||||||
                                 AAAG GGTACAACCGGTCCGACCA
                                   C
GAM320  APOC4    3'  ACCAGCCTGGGCAACACAGCGA 9703       ACCA    G
            GA                   TTTC    TGTTG CCAGGCTGGT
                                 ||||    ||||| ||||||||||
                                 AGAG    ACAAC GGTCCGACCA
                                   CGAC    G
GAM320  APOL1    3'  ACCATCCTGGCTAACACAGTGA 14719       CA        C
            AA                   TTTCAC  TGTTGGCCAGG TGGT
                                 ||||||  |||||||||| ||||
                                 AAAGTG  ACAATCGGTCC ACCA
                                    AC         T
GAM320  ARSD     3'  ACCAGCCTGGGCAACATAGTGA 24809       C     G
            GA                   TTTCAC ATGTTG CCAGGCTGGT
                                 |||||| |||||| ||||||||||
                                 AGAGTG TACAAC GGTCCGACCA
                                    A     G
GAM320  ATF5     3'  ACCAGCCTGGGCAACATAGT   24814    C     G
                                 AC ATGTTG CCAGGCTGGT
                                 || |||||| ||||||||||
                                 TG TACAAC GGTCCGACCA
                                  A     G
GAM320  ATM      3'  ACCAGCCTGGCCAGTATGGTGA 5284
            AA                   TTTCACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||||||
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                                AAAGTGGTATGACCGGTCCGACCA

GAM320  ATM      3'  ACCAGCCTGGCCAGTATGGTGA 57127
            AA                    TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTATGACCGGTCCGACCA

GAM320  ATP1A2   3'  AGCCTGGCCAACATGGTGAAA  7354
                                  TTTCACCATGTTGGCCAGGCT
                                  |||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGA

GAM320  BCAS1    3'  AGCCTGGCCAACATCATGAAA  14706      CC
                                  TTTCA  ATGTTGGCCAGGCT
                                  |||||  |||||||||||||
                                  AAAGT  TACAACCGGTCCGA
                                     AC
GAM320  BHMT2    3'  ACCAGCCTGACCAACATGGTGA 34724            C
            AA                    TTTCACCATGTTGG CAGGCTGGT
                                  |||||||||||||| |||||||||
                                  AAAGTGGTACAACC GTCCGACCA
                                           A
GAM320  BRCA1    3'  ACCAGCCTGGCCAACATGGTGA 24537
            AA                    TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  BRCA1    3'  ACCAGCCTGGCCAACATGGTGA 24442
            AA                    TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  BRCA1    5'  ACCAGCCTGACCAACGTGGTGA 24451            C
            AA                    TTTCACCATGTTGG CAGGCTGGT
                                  |||||||||||||| |||||||||
                                  AAAGTGGTGCAACC GTCCGACCA
                                           A
GAM320  BRCA1    3'  ACCAGCCTGGCCAACATGGTGA 24452
            AA                    TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  BRCA1    3'  ACCAGCCTGGCCAACATGGTGA 24465
            AA                    TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  BRCA1    3'  ACCAGCCTGGCCAACATGGTGA 24474
            AA                    TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
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                                AAAGTGGTACAACCGGTCCGACCA

GAM320  BRCA1    3'  ACCAGCCTGGCCAACATGGTGA 24482
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  BRCA1    3'  ACCAGCCTGGCCAACATGGTGA 24490
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  BRCA1    3'  ACCAGCCTGGCCAACATGGTGA 24499
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  BRCA1    3'  ACCAGCCTGGCCAACATGGTGA 24509
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  BRCA1    3'  ACCAGCCTGGCCAACATGGTGA 24517
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  BRCA1    3'  ACCAGCCTGGCCAACATGGTGA 24525
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  C21orf5  3'  ACCAGCCTGACCAACATGGTGA 18879            C
                GA                TTTCACCATGTTGG CAGGCTGGT
                                  |||||||||||||| |||||||||
                                  AGAGTGGTACAACC GTCCGACCA
                                        A
GAM320  C5R1     3'  ACCAGGCTGGCCAGCATGGTGA 9969               G
                AA                TTTCACCATGTTGGCCAG CTGGT
                                  |||||||||||||||||| |||||
                                  AAAGTGGTACGACCGGTC GACCA
                                        G
GAM320  CARKL    3'  ACCAGCCTGACCAACATGGGGA 26096     A       C
                                  TTC CCATGTTGG CAGGCTGGT
                                  ||| ||||||||| |||||||||
                                  AGG GGTACAACC GTCCGACCA
                                    _       A
GAM320  CASP10   3'  ACCAGCCTGGCCAATACGG   53211    A
                                  CC TGTTGGCCAGGCTGGT
                                  || ||||||||||||||||
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                                GG ATAACCGGTCCGACCA
                                 C
GAM320  CASP10   3'  ACCAGCCTGGCCAATACGG   53235    A
                                CC TGTTGGCCAGGCTGGT
                                || ||||||||||||||||
                                GG ATAACCGGTCCGACCA
                                 C
GAM320  CASP6    3'  ACCAGCCTGACCAACATGGAGA 53358      A       C
            AG                    TTTC CCATGTTGG CAGGCTGGT
                                |||| ||||||||| |||||||||
                                GAAG GGTACAACC GTCCGACCA
                                  A       A
GAM320  CASP6    3'  ACCAGCCTGACCAACATGGAGA 8727       A       C
            AG                    TTTC CCATGTTGG CAGGCTGGT
                                |||| ||||||||| |||||||||
                                GAAG GGTACAACC GTCCGACCA
                                  A       A
GAM320  CD28     3'  ACCAGCCTGGTCAAGATGGTGA 21546          G
            AA                    TTTCACCAT TTGGCCAGGCTGGT
                                ||||||||| ||||||||||||||
                                AAAGTGGTA AACTGGTCCGACCA
                                    G
GAM320  CD68     3'  ACCAGCCTGGCCAACATGGTGA 60497
            AA                    TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGACCA

GAM320  CEACAM5  3'  ACCATCCTAGCCAACATCGTGA 16418       C       C  C
            AA                    TTTCAC ATGTTGGC AGG TGGT
                                |||||| |||||||| ||| ||||
                                AAAGTG TACAACCG TCC ACCA
                                   C       A  T
GAM320  CHST5    3'  ACCAGCCTGGCCAACATAGTGA 25083       C
            AA                    TTTCAC ATGTTGGCCAGGCTGGT
                                |||||| ||||||||||||||||
                                AAAGTG TACAACCGGTCCGACCA
                                   A
GAM320  COG7     3'  ACCAGCCTGACCAACATGGTGA 68249            C
            AA                    TTTCACCATGTTGG CAGGCTGGT
                                |||||||||||||| |||||||||
                                AAAGTGGTACAACC GTCCGACCA
                                        A
GAM320  COPA     3'  ACCTGCCTGGCCAACATGG   16473             T
                                CCATGTTGGCCAGGC GGT
                                |||||||||||||| |||
                                GGTACAACCGGTCCG CCA
                                         T
GAM320  CORO2A   3'  ACCAGCCTGACCAACATGGTGA 14097            C
            AA                    TTTCACCATGTTGG CAGGCTGGT
                                |||||||||||||| |||||||||
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                                AAAGTGGTACAACC GTCCGACCA
                                      A
GAM320  CORO2A   3'  ACCAGCCTGACCAACATGGTGA 54489          C
           AA                   TTTCACCATGTTGG CAGGCTGGT
                                |||||||||||||| |||||||||
                                AAAGTGGTACAACC GTCCGACCA
                                      A
GAM320  CPM      3'  ACCAGCCTGACCAACATGGTGA 60400          C
           AA                   TTTCACCATGTTGG CAGGCTGGT
                                |||||||||||||| |||||||||
                                AAAGTGGTACAACC GTCCGACCA
                                      A
GAM320  CPT2     3'  ACCAACCTGGCCAACATGGTGA 5417           C
           AA                   TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
                                AAAGTGGTACAACCGGTCC ACCA
                                       A
GAM320  CRACC    3'  ACCAGCCTGGCCAACATGGTGA 41302
           AA                   TTTCACCATGTTGGCCAGGCTGGT
                                |||||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGACCA

GAM320  CTMP     3'  AGTCTGGGCAACACGATGAAA  54944      CCA   G
                                TTTCA   TGTTG CCAGGCT
                                |||||   ||||| |||||||
                                AAAGT   ACAAC GGTCTGA
                                   AGC    G
GAM320  CTSS     3'  AGCCTGGCTAACATGGTGAAA  15817
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||||
                                AAAGTGGTACAATCGGTCCGA

GAM320  CUBN     3'  AGCCTGGCCAGCATGGTGAAA  8416
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||||
                                AAAGTGGTACGACCGGTCCGA

GAM320  CYP4F3   3'  ACCAGCCTGGCCAATATGGTGA 7988
           AA                   TTTCACCATGTTGGCCAGGCTGGT
                                |||||||||||||||||||||||||
                                AAAGTGGTATAACCGGTCCGACCA

GAM320  DAPP1    3'  ATCAGCCTGGCCAACATGATGA 27678       C
           AA                   TTTCA CATGTTGGCCAGGCTGGT
                                ||||| ||||||||||||||||||
                                AAAGT GTACAACCGGTCCGACTA
                                   A
GAM320  DBT      3'  ACCACCCTGGCCAACATGGTGA 10357          C
           AA                   TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
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                                AAAGTGGTACAACCGGTCC ACCA
                                           C
GAM320  DBT     3'  ACCAGCCTGGCCAACATGGTGA 10358
            AA                  TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGACCA

GAM320  DBT     3'  ACCAGCCTGGGCAACATAGTGA 10359      C     G
            GA                  TTTCAC ATGTTG CCAGGCTGGT
                                |||||| |||||| |||||||||
                                AGAGTG TACAAC GGTCCGACCA
                                  A     G
GAM320  DCLRE1C  3'  ACCAGCCTGGCCAACACAGTGA 42817       CA
            AA                  TTTCAC  TGTTGGCCAGGCTGGT
                                ||||||  ||||||||||||||||
                                AAAGTG  ACAACCGGTCCGACCA
                                  AC
GAM320  DFFA    3'  ACCATCCTGGCTAACATGGTGA 16585               C
            AA                  TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
                                AAAGTGGTACAATCGGTCC ACCA
                                           T
GAM320  DHFR    3'  ACCAGCCTGGCCACCTTAGTGA 7635        CATGT
            GA                  TTTCAC    TGGCCAGGCTGGT
                                ||||||    ||||||||||||
                                AGAGTG    ACCGGTCCGACCA
                                  ATTCC
GAM320  DMC1    3'  ACCAGCCTGGCCAACATGGAGA 23935     A
            AA                  TTTC CCATGTTGGCCAGGCTGGT
                                |||| ||||||||||||||||||
                                AAAG GGTACAACCGGTCCGACCA
                                  A
GAM320  DNASE2  3'  ACCAGCCTGGCCAACATGGTGA 9094
            AA                  TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGACCA

GAM320  DNASE2  3'  ACCAGCCTGGGCTACATAGTGA 9095       C   T   _
            GA                  TTTCAC ATGT GGCC AGGCTGGT
                                |||||| |||| |||| ||||||||
                                AGAGTG TACA TCGG TCCGACCA
                                  A   _   G
GAM320  EGFL4   3'  ACCAGCCTGGCCAATATGGTGA 62449
            AA                  TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTATAACCGGTCCGACCA

GAM320  EGFL5   3'  ACCAGCCTGGTCAACATGGCGA 87901     A
            AA                  TTTC CCATGTTGGCCAGGCTGGT
                                |||| ||||||||||||||||||
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                                AAAG GGTACAACTGGTCCGACCA
                                  C
GAM320  ERBB3   3'  ACCAGCTTAGCCAACATAGT  10534   C      C
                                AC ATGTTGGC AGGCTGGT
                                || |||||||| ||||||||
                                TG TACAACCG TTCGACCA
                                 A      A
GAM320  F2R     3'  ACCATCCTGGCTAACACGGTGA 10560       A        C
           AA                    TTTCACC TGTTGGCCAGG TGGT
                                 ||||||| |||||||||| ||||
                                 AAAGTGG ACAATCGGTCC ACCA
                                    C         T
GAM320  F2RL3   3'  ACCAGCCTGAGCAACATGGT  15483         GC
                                ACCATGTTG  CAGGCTGGT
                                |||||||||  |||||||||
                                TGGTACAAC  GTCCGACCA
                                     GA
GAM320  F2RL3   3'  ACCAGCCTGGCTAACATGGTGA 15484
           AA                    TTTCACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||||||
                                 AAAGTGGTACAATCGGTCCGACCA

GAM320  FANCD2  3'  ACCAGCCTGGCCAACATAGTGA 53528       C
           AA                    TTTCAC ATGTTGGCCAGGCTGGT
                                 |||||| ||||||||||||||||
                                 AAAGTG TACAACCGGTCCGACCA
                                    A
GAM320  FCMD    3'  ACCAGCCTGGCCAACATAGTGA 23022       C
           AA                    TTTCAC ATGTTGGCCAGGCTGGT
                                 |||||| ||||||||||||||||
                                 AAAGTG TACAACCGGTCCGACCA
                                    A
GAM320  FGFR1   3'  ACCAGCCCGGCCAACATGGTGA 43873             A
           AA                    TTTCACCATGTTGGCC GGCTGGT
                                 |||||||||||||| |||||||
                                 AAAGTGGTACAACCGG CCGACCA
                                           C
GAM320  FGFR1   3'  ACCAGCCCGGCCAACATGGTGA 43878             A
           AA                    TTTCACCATGTTGGCC GGCTGGT
                                 |||||||||||||| |||||||
                                 AAAGTGGTACAACCGG CCGACCA
                                           C
GAM320  FGFR2   3'  ACCAGCCTGGCCAACATGGTGA 43646
           AA                    TTTCACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||||||
                                 AAAGTGGTACAACCGGTCCGACCA

GAM320  FGFR2   3'  ACCAGCCTGGCCAACATGGTGA 43659
           AA                    TTTCACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||||||
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                                AAAGTGGTACAACCGGTCCGACCA

GAM320  FLI1    3'  ACCAGCCTAGCCAACGTGGTGA 77104            C
            AA                  TTTCACCATGTTGGC AGGCTGGT
                                |||||||||||||| ||||||||
                                AAAGTGGTGCAACCG TCCGACCA
                                        A
GAM320  FUT6    3'  ACCATCCTGGCCAATATGGTGA 5626              C
            AA                  TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
                                AAAGTGGTATAACCGGTCC ACCA
                                        T
GAM320  GAS7    3'  ACCATCCTGGCTAACATGGTGA 20838             C
            AA                  TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
                                AAAGTGGTACAATCGGTCC ACCA
                                        T
GAM320  GGCX    3'  ACCAGCCTGGCCAACATGG   7700
                                CCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||
                                GGTACAACCGGTCCGACCA

GAM320  GH1     3'  ACCAGCCTTGTCCTAATA    6705     _ _ C
                                TGTT GG C AGGCTGGT
                                |||| || | ||||||||
                                ATAA CC G TCCGACCA
                                  T  T T
GAM320  GH1     3'  ACCAGCCTTGTCCTAATA    42888    _ _ C
                                TGTT GG C AGGCTGGT
                                |||| || | ||||||||
                                ATAA CC G TCCGACCA
                                  T  T T
GAM320  GH1     3'  ACCAGCCTTGTCCTAATA    42891    _ _ C
                                TGTT GG C AGGCTGGT
                                |||| || | ||||||||
                                ATAA CC G TCCGACCA
                                  T  T T
GAM320  GH1     3'  ACCAGCCTTGTCCTAATA    42893    _ _ C
                                TGTT GG C AGGCTGGT
                                |||| || | ||||||||
                                ATAA CC G TCCGACCA
                                  T  T T
GAM320  GH1     3'  ACCAGCCTTGTCCTAATA    42895    _ _ C
                                TGTT GG C AGGCTGGT
                                |||| || | ||||||||
                                ATAA CC G TCCGACCA
                                  T  T T
GAM320  GH2     3'  ACCAGCCTTGTCCTAATA    42886    _ _ C
                                TGTT GG C AGGCTGGT
                                |||| || | ||||||||
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                                ATAA CC G TCCGACCA
                                  T  T T
GAM320  GH2     3'  ACCAGCCTTGTCCTAATA    42887      _ _ C
                                TGTT GG C AGGCTGGT
                                |||| || | ||||||||
                                ATAA CC G TCCGACCA
                                  T  T T
GAM320  GH2     3'  ACCAGCCTTGTCCTAATA    10789      _ _ C
                                TGTT GG C AGGCTGGT
                                |||| || | ||||||||
                                ATAA CC G TCCGACCA
                                  T  T T
GAM320  GNE     3'  ACCGCCCTGGCTAACATGGTGA 19659              C
            AA                    TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
                                AAAGTGGTACAATCGGTCC GCCA
                                              C
GAM320  GP6     3'  ACCAGCCTGGGCAACATAGTGA 33467       C     G
            GA                    TTTCAC ATGTTG CCAGGCTGGT
                                |||||| |||||| ||||||||||
                                AGAGTG TACAAC GGTCCGACCA
                                  A     G
GAM320  GPR81   3'  ACCAGCCTGACCGACATGGAGA 51731      A       C
            AA                    TTTC CCATGTTGG CAGGCTGGT
                                |||| ||||||||| |||||||||
                                AAAG GGTACAGCC GTCCGACCA
                                  A       A
GAM320  GRM6    3'  ACCAGCCTGGCCAATGTGGTGA 7755
            AA                    TTTCACCATGTTGGCCAGGCTGGT
                                |||||||||||||||||||||||
                                AAAGTGGTGTAACCGGTCCGACCA

GAM320  HCS     3'  ACCAGCCTGGTCAACATGGCGA 38960      A
            AA                    TTTC CCATGTTGGCCAGGCTGGT
                                |||| ||||||||||||||||||
                                AAAG GGTACAACTGGTCCGACCA
                                  C
GAM320  HIP1    3'  ACCAGCCTGTCCAACATGGTGA 19243             C
            AA                    TTTCACCATGTTGG CAGGCTGGT
                                |||||||||||||| |||||||||
                                AAAGTGGTACAACC GTCCGACCA
                                        T
GAM320  HIP1    3'  ACTAGCCTGGCCAACATGGTGA 19244
            AA                    TTTCACCATGTTGGCCAGGCTGGT
                                |||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGATCA

GAM320  HLA-E   3'  ACCATCCTGGCTAACACGGTGA 92667       A       C
            AA                    TTTCACC TGTTGGCCAGG TGGT
                                |||||||| |||||||||||| ||||
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                                AAAGTGG ACAATCGGTCC ACCA
                                   C         T
GAM320  HSPA5    3'  ACCATCTTTGCCAACATGGTGA 19275             C   C
                AA                  TTTCACCATGTTGGC AGG TGGT
                                    ||||||||||||||| ||| ||||
                                    AAAGTGGTACAACCG TTC ACCA
                                          T   T
GAM320  HUNK     3'  CAGCCTGGGCAACATGGTGAAA 28180            G
                                    TTTCACCATGTTG CCAGGCTG
                                    |||||||||||| ||||||||
                                    AAAGTGGTACAAC GGTCCGAC
                                          G
GAM320  IAPP     3'  ACCAGCCTGACCAACGTGGTGA 6432             C
                AA                  TTTCACCATGTTGG CAGGCTGGT
                                    |||||||||||||| |||||||||
                                    AAAGTGGTGCAACC GTCCGACCA
                                          A
GAM320  IFIT4    3'  ACCATCCTGGCTAACACAGTGA 71486        CA         C
                AA                  TTTCAC  TGTTGGCCAGG TGGT
                                    ||||||  |||||||||||| ||||
                                    AAAGTG  ACAATCGGTCC ACCA
                                       AC         T
GAM320  IFNAR1   3'  ACCAGCCTGGCCAACGTGGTGA 7132
                AA                  TTTCACCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||||||||
                                    AAAGTGGTGCAACCGGTCCGACCA

GAM320  IFRD1    3'  ACCAGCCTGGGCAACATAGCGA 60751      ACC      G
                GA                  TTTC   ATGTTG CCAGGCTGGT
                                    ||||   |||||| ||||||||||
                                    AGAG   TACAAC GGTCCGACCA
                                      CGA      G
GAM320  IL10     3'  ACCAGCCTGGTCAACATGGTGA 6919
                AA                  TTTCACCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||||||||
                                    AAAGTGGTACAACTGGTCCGACCA

GAM320  IL13RA1  3'  ACCAGCCTGACCAAAATGGTGA 9565          G    C
                AA                  TTTCACCAT TTGG CAGGCTGGT
                                    |||||||||  |||| |||||||||
                                    AAAGTGGTA AACC GTCCGACCA
                                         A    A
GAM320  IL17R    3'  CCAGCCTGGCCAACATGGTGAA 27551
                A                    TTTCACCATGTTGGCCAGGCTGG
                                    |||||||||||||||||||||||
                                    AAAGTGGTACAACCGGTCCGACC

GAM320  IL18     3'  ACCAGCCTGACCAACATGGTGA 9586             C
                AA                  TTTCACCATGTTGG CAGGCTGGT
                                    ||||||||||||| |||||||||
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                                AAAGTGGTACAACC GTCCGACCA
                                       A
GAM320  IL1R1    3'  ACCAGCCCAGCCAACATGG   7918          CA
                                CCATGTTGGC  GGCTGGT
                                ||||||||||  |||||||
                                GGTACAACCG  CCGACCA
                                      AC
GAM320  IRAK4    3'  ACCGGCCTGGCCAACATGGTGA 61835
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGGCCA

GAM320  JRK      3'  ACCAGCCTAGGCATGATA    87812       _  _
                                  TGTTG GCC AGGCTGGT
                                  |||||  |||  ||||||||
                                  ATAGT CGG TCCGACCA
                                     A   A
GAM320  KAI1     3'  ACCATCCTGGCTAACATGGTGA 11116               C
                AA                TTTCACCATGTTGGCCAGG TGGT
                                  |||||||||||||||||| ||||
                                  AAAGTGGTACAATCGGTCC ACCA
                                              T
GAM320  KCNA7    3'  ACCAGCCTGGGCAACATGGTGA 49882           G
                GA                TTTCACCATGTTG CCAGGCTGGT
                                  ||||||||||||  |||||||||
                                  AGAGTGGTACAAC GGTCCGACCA
                                        G
GAM320  KCNA7    3'  ACCATCCTGGCTAACACGGTGA 49883        A        C
                AA                TTTCACC TGTTGGCCAGG TGGT
                                  |||||||  ||||||||||| ||||
                                  AAAGTGG ACAATCGGTCC ACCA
                                     C         T
GAM320  KCNJ5    3'  ACCATCCTGGCTAACACGGTGA 7964         A        C
                AA                TTTCACC TGTTGGCCAGG TGGT
                                  |||||||  ||||||||||| ||||
                                  AAAGTGG ACAATCGGTCC ACCA
                                     C         T
GAM320  KCNK3    3'  ACCAGCCTAGGTGACATAGTGA 11168       C     G  _
                GA                TTTCAC ATGTTG CC AGGCTGGT
                                  ||||||  ||||||  ||  ||||||||
                                  AGAGTG TACAGT GG TCCGACCA
                                     A     _  A
GAM320  KIF1B    3'  ACCAGCCTGGCCAATGTGATGA 31260       C
                AA                TTTCA CATGTTGGCCAGGCTGGT
                                  |||||  |||||||||||||||||
                                  AAAGT GTGTAACCGGTCCGACCA
                                     A
GAM320  KIF3B    3'  ACCAGCCTGGCCAACATGGTGG 17798
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
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                                AAGGTGGTACAACCGGTCCGACCA

GAM320  KLF8     5'  ACCAGTCTGGGCAACATGG   24368        G
                                CCATGTTG CCAGGCTGGT
                                |||||||| ||||||||||
                                GGTACAAC GGTCTGACCA
                                     G
GAM320  KNSL1    3'  ACCAGCCTGGCCAACGTGG   16937
                                CCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||
                                GGTGCAACCGGTCCGACCA

GAM320  LAMC2    3'  ACCAGCCTGGCCAACATGGTGA 38764
              AA                  TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGACCA

GAM320  LAMP2    3'  ACCAGCCTGGCCAACATGGTGA 26565
              AA                  TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGACCA

GAM320  LEP      3'  CCTGGCCAACATGGTGAAA   5858
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||
                                AAAGTGGTACAACCGGTCC

GAM320  LILRB1   3'  ACCATCTTGGCCAACATGGTGA 22867              C
              AA                  TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
                                AAAGTGGTACAACCGGTTC ACCA
                                          T
GAM320  LRRC2    3'  ACCAGCCTAAACAACATAGTGA 44730       C     GCC
              AA                  TTTCAC ATGTTG   AGGCTGGT
                                |||||| ||||||   ||||||||
                                AAAGTG TACAAC   TCCGACCA
                                   A     AAA
GAM320  LUZP1    3'  ACCAGCCTGGACAATATAGTGA 54394       C     G
              AA                  TTTCAC ATGTTG CCAGGCTGGT
                                |||||| |||||| ||||||||||
                                AAAGTG TATAAC GGTCCGACCA
                                   A     A
GAM320  MAFF     3'  ACCAGCCTGGACAACATGGTGA 25570             G
              AA                  TTTCACCATGTTG CCAGGCTGGT
                                |||||||||||| ||||||||||
                                AAAGTGGTACAAC GGTCCGACCA
                                      A
GAM320  MCM4     3'  ACCAGCCTAGCCAAGATGGTGA 62573         G    C
              AA                  TTTCACCAT TTGGC AGGCTGGT
                                |||||||| ||||| ||||||||
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                                AAAGTGGTA AACCG TCCGACCA
                                    G    A
GAM320  MLLT4   3'  ACCATCCTGGCTAACACGGTGA 72896       A        C
          AA                    TTTCACC TGTTGGCCAGG TGGT
                                ||||||| |||||||||| ||||
                                AAAGTGG ACAATCGGTCC ACCA
                                   C         T
GAM320  MOG     3'  ACCAGCCTGGCCAACATGGTGA 11664
          AA                    TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGACCA

GAM320  MS4A1   3'  ACCAGCCTGGCCAACATAGTGA 5543        C
          AA                    TTTCAC ATGTTGGCCAGGCTGGT
                                |||||| ||||||||||||||||
                                AAAGTG TACAACCGGTCCGACCA
                                   A
GAM320  MSH3    3'  ACCAGCCTGGCCAACATGG   11685
                                CCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||
                                GGTACAACCGGTCCGACCA

GAM320  MTMR8   3'  ACCATCCTGGCTAACACGGTGA 31900       A        C
          AA                    TTTCACC TGTTGGCCAGG TGGT
                                ||||||| |||||||||| ||||
                                AAAGTGG ACAATCGGTCC ACCA
                                   C         T
GAM320  MYO1B   3'  ACTAGCCTGGCCAACATGG   25238
                                CCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||
                                GGTACAACCGGTCCGATCA

GAM320  NFKBIL2 3'  ACCATCCTGGCTAACATGGTGA 26440               C
          AA                    TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
                                AAAGTGGTACAATCGGTCC ACCA
                                        T
GAM320  NPHS1   3'  ACCAGCCTGGCCAACATGGT  17363
                                ACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||
                                TGGTACAACCGGTCCGACCA

GAM320  NT5C2   3'  ACCAGCCTTACCAACATGGAGA 25251     A       CC
          AA                    TTTC CCATGTTGG  AGGCTGGT
                                |||| |||||||||  ||||||||
                                AAAG GGTACAACC  TCCGACCA
                                  A       AT
GAM320  NUP62   3'  ACCAGCCTGGCCAACATGGTGA 33777
          AA                    TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
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                                AAAGTGGTACAACCGGTCCGACCA

GAM320  OAS3    3'  ACCAGCCCTCAGCATGAGGAAA 21648      AC       CCA
                                TTTC  CATGTTGG   GGCTGGT
                                ||||  ||||||||   |||||||
                                AAAG  GTACGACT   CCGACCA
                                  GA       C__
GAM320  OPA3    3'  ACCAGCCTGGCCAACATGGTGA 47836
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  OPTN    3'  ACCAGCCTGGCCAACATGGCGG 42045      A
                AA                TTTC CCATGTTGGCCAGGCTGGT
                                  |||| ||||||||||||||||||
                                  AAGG GGTACAACCGGTCCGACCA
                                    C
GAM320  P2RY6   3'  ACCAGCCTGGGCAACACAGT   15991    CA    G
                                  AC  TGTTG CCAGGCTGGT
                                  ||  |||||| ||||||||||
                                  TG  ACAAC GGTCCGACCA
                                   AC     G
GAM320  PA2G4   3'  ACCAGCCTAACCAACATGGCGA 71820      A       CC
                AA                TTTC CCATGTTGG  AGGCTGGT
                                  |||| |||||||||  ||||||||
                                  AAAG GGTACAACC  TCCGACCA
                                    C        AA
GAM320  PAICS   3'  ACCAGCCTGGCCAACATGGTGA 22253
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  PCDH11X 3'  ACCATCCTGGCTAACACGGTGA 53121        A         C
                AA                TTTCACC TGTTGGCCAGG TGGT
                                  ||||||| |||||||||| ||||
                                  AAAGTGG ACAATCGGTCC ACCA
                                     C         T
GAM320  PCDH11Y 3'  ACCATCCTGGCTAACATGGTGA 53149              C
                AA                TTTCACCATGTTGGCCAGG TGGT
                                  |||||||||||||||||| ||||
                                  AAAGTGGTACAATCGGTCC ACCA
                                              T
GAM320  PCDH11Y 3'  ACCATCCTGGCTAACATGGTGA 53172              C
                AA                TTTCACCATGTTGGCCAGG TGGT
                                  |||||||||||||||||| ||||
                                  AAAGTGGTACAATCGGTCC ACCA
                                              T
GAM320  PDE4C   3'  ACCAGCCTGGCCAACATGGTGA 8092
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
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                                AAAGTGGTACAACCGGTCCGACCA

GAM320  PHKB     3'  ACCAGCCCAGCCAACATGGTGA 6093              CA
                AA                  TTTCACCATGTTGGC  GGCTGGT
                                    ||||||||||||||  |||||||
                                    AAAGTGGTACAACCG  CCGACCA
                                          AC
GAM320  PIK3R2   3'  CCAGCCTGGCCAAAATGG    18511      G
                                    CCAT TTGGCCAGGCTGG
                                    |||| ||||||||||||
                                    GGTA AACCGGTCCGACC
                                      A
GAM320  PLA2G2D  3'  ACCAGCCTGCCCAACATGG   25704          C
                                    CCATGTTGG CAGGCTGGT
                                    |||||||| ||||||||
                                    GGTACAACC GTCCGACCA
                                         C
GAM320  POLH     3'  ACCAGCCTGGCCAACATGG   22467
                                    CCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||
                                    GGTACAACCGGTCCGACCA

GAM320  POLK     3'  ACCAGCCTCGCCAACATGGTGA 33096              C
                GA                  TTTCACCATGTTGGC AGGCTGGT
                                    |||||||||||||| ||||||||
                                    AGAGTGGTACAACCG TCCGACCA
                                          C
GAM320  PPP1R12B 3'  ACCATCCTGGCTAACACGGTGA 50374        A         C
                AA                  TTTCACC TGTTGGCCAGG TGGT
                                    |||||||| |||||||||| ||||
                                    AAAGTGG ACAATCGGTCC ACCA
                                       C         T
GAM320  PRKY     3'  ACCAGCCTGGCCAACATGATGA 12356       C
                AA                  TTTCA CATGTTGGCCAGGCTGGT
                                    ||||| ||||||||||||||||||
                                    AAAGT GTACAACCGGTCCGACCA
                                      A
GAM320  PSD      5'  ACCATCCTGGCCAACGTAGTGA 12428        C          C
                AA                  TTTCAC ATGTTGGCCAGG TGGT
                                    |||||| |||||||||||| ||||
                                    AAAGTG TGCAACCGGTCC ACCA
                                       A          T
GAM320  PSMB2    3'  ACCAGCCTGGCCAACATGGTGA 12455
                AA                  TTTCACCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||||||||
                                    AAAGTGGTACAACCGGTCCGACCA

GAM320  PSMB2    3'  ACCATCCTGACCAACATGGTGA 12456              C   C
                AA                  TTTCACCATGTTGG CAGG TGGT
                                    |||||||||||||| |||| ||||
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                                AAAGTGGTACAACC GTCC ACCA
                                       A    T
GAM320  PSMB9   3'  AGTCTGGCCAACATGGAGAAA  12488      A
                                TTTC CCATGTTGGCCAGGCT
                                |||| ||||||||||||||||
                                AAAG GGTACAACCGGTCTGA
                                  A
GAM320  PSMB9   3'  ATCAGCCTGACCAATATGGTGA 12489             C
              AA                  TTTCACCATGTTGG CAGGCTGGT
                                  |||||||||||||| |||||||||
                                  AAAGTGGTATAACC GTCCGACTA
                                         A
GAM320  PSMD5   3'  ACCAGCCTGGCCAATATGG   18552
                                  CCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||
                                  GGTATAACCGGTCCGACCA

GAM320  PTAFR   3'  ACCATCCTGGCCAACATTGT  8160     C          C
                                  AC ATGTTGGCCAGG TGGT
                                  || |||||||||||| ||||
                                  TG TACAACCGGTCC ACCA
                                   T          T
GAM320  PTGIS   3'  ACCAGCCTGGCCAACATGGCGA 8185       A
              AA                  TTTC CCATGTTGGCCAGGCTGGT
                                  |||| ||||||||||||||||||
                                  AAAG GGTACAACCGGTCCGACCA
                                    C
GAM320  RAB7L1  3'  ACCAACCTGGTCAGCATGG   15396             C
                                  CCATGTTGGCCAGG TGGT
                                  |||||||||||||| ||||
                                  GGTACGACTGGTCC ACCA
                                         A
GAM320  RAB7L1  3'  ATCAACCTGGCCAACATACTGA 15400       CC          C
              AA                  TTTCA  ATGTTGGCCAGG TGGT
                                  |||||  |||||||||||| ||||
                                  AAAGT  TACAACCGGTCC ACTA
                                     CA          A
GAM320  RAD1    3'  ACCAGCCTGACCAACGTGGAGA 12636      A       C
              AA                  TTTC CCATGTTGG CAGGCTGGT
                                  |||| ||||||||| |||||||||
                                  AAAG GGTGCAACC GTCCGACCA
                                    A       A
GAM320  RAD1    3'  ACCAGCCTGACCAACGTGGAGA 56650      A       C
              AA                  TTTC CCATGTTGG CAGGCTGGT
                                  |||| ||||||||| |||||||||
                                  AAAG GGTGCAACC GTCCGACCA
                                    A       A
GAM320  RAD1    3'  ACCAGCCTGACCAACGTGGAGA 56746      A       C
              AA                  TTTC CCATGTTGG CAGGCTGGT
                                  |||| ||||||||| |||||||||
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                                AAAG GGTGCAACC GTCCGACCA
                                  A       A
GAM320  RBBP5    3'  ACCAGCCTGGCCAACGTGGTGA 18572
                AA                  TTTCACCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||||||||
                                    AAAGTGGTGCAACCGGTCCGACCA

GAM320  RBL1     3'  ACCAGCCTGACCAACATGGAGA 12779      A       C
                AA                  TTTC CCATGTTGG CAGGCTGGT
                                    |||| ||||||||| |||||||||
                                    AAAG GGTACAACC GTCCGACCA
                                      A       A
GAM320  RBM3     3'  CCAGCCTGACCAACATGGTGAA 71007            C
                A                    TTTCACCATGTTGG CAGGCTGG
                                    |||||||||||||| ||||||||
                                    AAAGTGGTACAACC GTCCGACC
                                           A
GAM320  RECQL5   3'  ACCAGCCTGGGCAACATGGCAA 16197     CA      G
                GA                  TTT  CCATGTTG CCAGGCTGGT
                                    |||  |||||||| ||||||||||
                                    AGA  GGTACAAC GGTCCGACCA
                                      AC       G
GAM320  RFC2     3'  ACCAGCCTGGCCAACATGGGGA 12833      A
                AA                  TTTC CCATGTTGGCCAGGCTGGT
                                    |||| ||||||||||||||||||
                                    AAAG GGTACAACCGGTCCGACCA
                                      G
GAM320  ROCK2    3'  ACCAGCCTGCCCAACATAGTGA 66610       C      C
                AA                  TTTCAC ATGTTGG CAGGCTGGT
                                    ||||||| ||||||| |||||||||
                                    AAAGTG TACAACC GTCCGACCA
                                       A      C
GAM320  SCAP2    3'  AGCCAGGCCAACATGGTGAAA  15420             A
                                    TTTCACCATGTTGGCC GGCT
                                    |||||||||||||||| ||||
                                    AAAGTGGTACAACCGG CCGA
                                              A
GAM320  SFRS2IP  5'  ACCAGCTTGGGCAACATGG    17533         G
                                    CCATGTTG CCAGGCTGGT
                                    |||||||| ||||||||||
                                    GGTACAAC GGTTCGACCA
                                         G
GAM320  SIGLEC11 3'  ACCAGCCTGGGCAAGATGGTGA 54643          G   G
                AA                  TTTCACCAT TTG CCAGGCTGGT
                                    ||||||||| ||| ||||||||||
                                    AAAGTGGTA AAC GGTCCGACCA
                                         G   G
GAM320  SLC14A1  3'  ACCAGCCTGGGCAGCATGGTGA 32408            G
                AA                  TTTCACCATGTTG CCAGGCTGGT
                                    |||||||||||| ||||||||||
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                                AAAGTGGTACGAC GGTCCGACCA
                                      G
GAM320  SLC17A5  3'  ACCAGCCTGGCCAGCATGGTGA 25821
            AA                  TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTACGACCGGTCCGACCA

GAM320  SLC26A4  3'  ACCATCCTGGCTAACATGGT  6518            C
                                ACCATGTTGGCCAGG TGGT
                                |||||||||||||| ||||
                                TGGTACAATCGGTCC ACCA
                                      T
GAM320  SLC28A2  3'  ACCATCCTGGCTAACACGGTGA 16143       A       C
            AA                  TTTCACC TGTTGGCCAGG TGGT
                                ||||||| |||||||||| ||||
                                AAAGTGG ACAATCGGTCC ACCA
                                   C        T
GAM320  SLC2A3   3'  ACCAGTCTGGCCAACATCGTGA 23636      C
            AA                  TTTCAC ATGTTGGCCAGGCTGGT
                                |||||| ||||||||||||||||
                                AAAGTG TACAACCGGTCTGACCA
                                   C
GAM320  SLC2A6   3'  ACCAGCCTGGCCAACATGGTGA 34565
            AA                  TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGACCA

GAM320  SLC31A1  3'  ACCAGTCTGGCCAACATGGGGA 10270     A
            AA                  TTTC CCATGTTGGCCAGGCTGGT
                                |||| ||||||||||||||||||
                                AAAG GGTACAACCGGTCTGACCA
                                  G
GAM320  SMG1     3'  ACCATCCTGGCTAACACGGTGA 31338       A       C
            AA                  TTTCACC TGTTGGCCAGG TGGT
                                ||||||| |||||||||| ||||
                                AAAGTGG ACAATCGGTCC ACCA
                                   C        T
GAM320  STAT3    3'  ACCATCCTGGCTAACACGGTGA 13429       A       C
            AA                  TTTCACC TGTTGGCCAGG TGGT
                                ||||||| |||||||||| ||||
                                AAAGTGG ACAATCGGTCC ACCA
                                   C        T
GAM320  STAT3    3'  ACCATCCTGGCTAACACGGTGA 58375       A       C
            AA                  TTTCACC TGTTGGCCAGG TGGT
                                ||||||| |||||||||| ||||
                                AAAGTGG ACAATCGGTCC ACCA
                                   C        T
GAM320  SUDD     3'  ACCAGCCTGGGCAACATGGCGA 15149     A      G
            AA                  TTTC CCATGTTG CCAGGCTGGT
                                |||| |||||||| ||||||||||
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                                AAAG GGTACAAC GGTCCGACCA
                                  C       G
GAM320  SULT1A3  3'  ACCAGCCTGGTAAAATAGTGAG 13481       C  GTTG
           A                     TTTCAC AT    GCCAGGCTGGT
                                 |||||| ||    ||||||||||
                                 AGAGTG TA    TGGTCCGACCA
                                   A  AAA_
GAM320  SULT2A1  3'  ACCATCCTGGCCAACATGATGA 72219       C          C
           AA                     TTTCA CATGTTGGCCAGG TGGT
                                  ||||| |||||||||||| ||||
                                  AAAGT GTACAACCGGTCC ACCA
                                    A           T
GAM320  SULT2A1  3'  ACCATCCTGGCTAACACGGTGA 72220        A         C
           AA                     TTTCACC TGTTGGCCAGG TGGT
                                  ||||||| |||||||||| ||||
                                  AAAGTGG ACAATCGGTCC ACCA
                                     C         T
GAM320  SUV39H2  3'  ACCAGCCTGGCCATCATGGTGA 45448          T
           AA                     TTTCACCATG TGGCCAGGCTGGT
                                  |||||||||| ||||||||||||
                                  AAAGTGGTAC ACCGGTCCGACCA
                                        T
GAM320  SWAP70   3'  AGCCTGGCCAACCTGGTGAAA  71858         T
                                  TTTCACCA GTTGGCCAGGCT
                                  |||||||| ||||||||||
                                  AAAGTGGT CAACCGGTCCGA
                                     C
GAM320  TACC1    3'  CCTAGGCAACATGGTGAAA   21869           G  _
                                  TTTCACCATGTTG CC AGG
                                  |||||||||||| || |||
                                  AAAGTGGTACAAC GG TCC
                                        _  A
GAM320  TBX6     3'  ACCAGCCTGCCAACATGGTGAA 55805             C
           A                      TTTCACCATGTTGGC AGGCTGGT
                                  |||||||||||||| ||||||||
                                  AAAGTGGTACAACCG TCCGACCA
                                                _
GAM320  TCF7     3'  ACCAGCCTGGCCAACATGGTGA 13611
           AA                     TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  TCTA     3'  ACCAGCCTGACCAACATGGTGA 42486            C
           AA                     TTTCACCATGTTGG CAGGCTGGT
                                  |||||||||||||| |||||||||
                                  AAAGTGGTACAACC GTCCGACCA
                                        A
GAM320  TEP1     3'  ACCATCCTGGCTAACATAGTGA 24042       C          C
           AA                     TTTCAC ATGTTGGCCAGG TGGT
                                  |||||| |||||||||||| ||||
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                                AAAGTG TACAATCGGTCC ACCA
                                   A          T
GAM320  TGFB1    3'  ACCAGCCTGGGTAACATAGTGA 7249        C     G
                GA                  TTTCAC ATGTTG CCAGGCTGGT
                                    |||||| |||||| ||||||||||
                                    AGAGTG TACAAT GGTCCGACCA
                                       A     G
GAM320  TNFRSF10A 3'  ACCAGCCTGACCAACATCGTGA 15235       C      C
                AA                  TTTCAC ATGTTGG CAGGCTGGT
                                    |||||| ||||||| |||||||||
                                    AAAGTG TACAACC GTCCGACCA
                                       C      A
GAM320  TNFRSF10D 3'  ACCAGCCTCATCAACACAGTGA 15199       CA     CC
                AA                  TTTCAC  TGTTGG  AGGCTGGT
                                    ||||||  ||||||  ||||||||
                                    AAAGTG  ACAACT  TCCGACCA
                                       AC     AC
GAM320  TNFRSF1B  3'  ACCAGCCTGGCCAACATGGT   8379
                                    ACCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||||
                                    TGGTACAACCGGTCCGACCA

GAM320  TNFSF14   3'  ACCAGCCTGGCTAACATGG    15073
                                    CCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||
                                    GGTACAATCGGTCCGACCA

GAM320  TNFSF15   3'  ACCAGCCTGACCAACGTGGAGA 18860      A        C
                AA                  TTTC CCATGTTGG CAGGCTGGT
                                    |||| ||||||||| |||||||||
                                    AAAG GGTGCAACC GTCCGACCA
                                      A        A
GAM320  TPM4     3'  ACCAGCCCAGCCAACATGGCGA 13829      A         CA
                AA                  TTTC CCATGTTGGC  GGCTGGT
                                    |||| ||||||||||  |||||||
                                    AAAG GGTACAACCG  CCGACCA
                                      C         AC
GAM320  TRIM14    3'  ACTAGCCTGGCCAAGATGGTGA 53771          G
                AA                  TTTCACCAT TTGGCCAGGCTGGT
                                    |||||||||  ||||||||||||||
                                    AAAGTGGTA AACCGGTCCGATCA
                                        G
GAM320  TRIM9    5'  ACCAGCCTGACCAACATGG    31435          C
                                    CCATGTTGG CAGGCTGGT
                                    |||||||||  |||||||||
                                    GGTACAACC GTCCGACCA
                                        A
GAM320  TRPM1    3'  ACCAGCCTGGGCAACATAGTGA 11601      C     G
                                    TCAC ATGTTG CCAGGCTGGT
                                    ||||  ||||||  ||||||||||
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                                AGTG TACAAC GGTCCGACCA
                                  A     G
GAM320  TRPM8    3'  ACCAGCCTGGCCAACATGG   44203
                                CCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||
                                GGTACAACCGGTCCGACCA

GAM320  TSNAX    3'  ACCAGCCTGACCAACGTGGCGA 21148      A        C
            AA                   TTTC CCATGTTGG CAGGCTGGT
                                ||||| ||||||||| |||||||||
                                AAAG GGTGCAACC GTCCGACCA
                                  C        A
GAM320  UC28     3'  ACCAGCCTGACCAGCATGGTGG 41582             C
            AA                   TTTCACCATGTTGG CAGGCTGGT
                                |||||||||||||| |||||||||
                                AAGGTGGTACGACC GTCCGACCA
                                       A
GAM320  UPK1B    3'  ACCAGCCTGGCCAACATGGTGA 23696
            AA                   TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGACCA

GAM320  USP14    3'  ACCAGCCTGGCCACATGGTGAA 18925           T
            A                    TTTCACCATGT GGCCAGGCTGGT
                                ||||||||||| ||||||||||||
                                AAAGTGGTACA CCGGTCCGACCA
                                          _
GAM320  VDR      3'  ACCAACCTGACCAACATGGAGA 6334       A       C   C
            AA                   TTTC CCATGTTGG CAGG TGGT
                                ||||| ||||||||| |||| ||||
                                AAAG GGTACAACC GTCC ACCA
                                  A        A   A
GAM320  VHL      3'  ACCAGCCTGGCCAACATGGT   6816
                                ACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||
                                TGGTACAACCGGTCCGACCA

GAM320  VHL      3'  ACCAGCCTGGCCAACATGGTGA 6817
            AA                   TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGACCA

GAM320  VHL      3'  ACCAGCCTGGCTAACATGGTGA 6818
            AA                   TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTACAATCGGTCCGACCA

GAM320  VPS41    3'  ACCAGCCTGACCAACATGGAGA 27685      A       C
            AA                   TTTC CCATGTTGG CAGGCTGGT
                                ||||| ||||||||| |||||||||
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                                AAAG GGTACAACC GTCCGACCA
                                  A       A
GAM320  WIG1     3'  CCTGGCTAACACAGTGAAA   96099       CA
                                TTTCAC  TGTTGGCCAGG
                                ||||||  ||||||||||
                                AAAGTG  ACAATCGGTCC
                                   AC
GAM320  WW45     3'  ACCAGCCTGGGCAACATGGTGA 41811           G
                AG                TTTCACCATGTTG CCAGGCTGGT
                                  |||||||||||| |||||||||
                                  GAAGTGGTACAAC GGTCCGACCA
                                        G
GAM320  XRCC2    3'  ACCAGCCTGGGCAACACGGTGA 19482       A    G
                AA                TTTCACC TGTTG CCAGGCTGGT
                                  ||||||| ||||| ||||||||||
                                  AAAGTGG ACAAC GGTCCGACCA
                                     C    G
GAM320  XT3      3'  CCAGCCTGGCCAACATGGCGAA 39905      A
                A                  TTTC CCATGTTGGCCAGGCTGG
                                   |||| ||||||||||||||||||
                                   AAAG GGTACAACCGGTCCGACC
                                     C
GAM320  ZNF264   3'  ACCAGCCTGGCCAACATGG   14182
                                   CCATGTTGGCCAGGCTGGT
                                   ||||||||||||||||||
                                   GGTACAACCGGTCCGACCA

GAM320  ZNF36    3'  ACCAGCCTGGCCAACATGGT  95573
                                   ACCATGTTGGCCAGGCTGGT
                                   ||||||||||||||||||||
                                   TGGTACAACCGGTCCGACCA

GAM320  ZNF74    3'  ACCAGCCTGGACAACATGGTGA 14252           G
                GA                TTTCACCATGTTG CCAGGCTGGT
                                  |||||||||||| |||||||||
                                  AGAGTGGTACAAC GGTCCGACCA
                                        A
GAM320  AF020591 3'  ACCAGCCTGGCAAACATGG   27897       G
                                   CCATGTT GCCAGGCTGGT
                                   ||||||| ||||||||||
                                   GGTACAA CGGTCCGACCA
                                      A
GAM320  AF020591 3'  ACCAGCCTGGGTAACATGG   27898       G
                                   CCATGTTG CCAGGCTGGT
                                   |||||||| ||||||||||
                                   GGTACAAT GGTCCGACCA
                                       G
GAM320  AGMAT    3'  AGCCTGCCCAACATGGTGAAA  45733           C
                                   TTTCACCATGTTGG CAGGCT
                                   |||||||||||||| ||||||
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                                AAAGTGGTACAACC GTCCGA
                                       C
GAM320  AKAP11   3'  ACCAGCCTGGGCAACATGGTGA 58455           G
           AA                   TTTCACCATGTTG CCAGGCTGGT
                                |||||||||||| ||||||||||
                                AAAGTGGTACAAC GGTCCGACCA
                                       G
GAM320  ALTE     3'  ACCAGCCTGGCCAACATGGCGA 60994      A
           AA                   TTTC CCATGTTGGCCAGGCTGGT
                                |||| ||||||||||||||||||
                                AAAG GGTACAACCGGTCCGACCA
                                  C
GAM320  ALTE     3'  ACCAGCCTGGCCAACATGGCGA 17573      A
           AA                   TTTC CCATGTTGGCCAGGCTGGT
                                |||| ||||||||||||||||||
                                AAAG GGTACAACCGGTCCGACCA
                                  C
GAM320  ALTE     3'  ACCAGCCTGGCCAACCAACATG 17574          ____
           GTGAAA                  TTTCACCATGT   TGGCCAGGCTGGT
                                |||||||||||   ||||||||||||
                                AAAGTGGTACA   ACCGGTCCGACCA
                                      ACCA
GAM320  AP1GBP1  3'  ACCAGCCTGGCCAACACAATGA 55442       CCA
           AA                   TTTCA  TGTTGGCCAGGCTGGT
                                |||||  ||||||||||||||||
                                AAAGT  ACAACCGGTCCGACCA
                                  AAC
GAM320  APXL2    3'  ACCATCCTGGCTAACACGGTGA 75667        A        C
           AA                   TTTCACC TGTTGGCCAGG TGGT
                                ||||||| |||||||||| ||||
                                AAAGTGG ACAATCGGTCC ACCA
                                   C         T
GAM320  ARNTL2   3'  ACCAGCCTGGCCAATATGGTGA 39832
           AA                   TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTATAACCGGTCCGACCA

GAM320  ARNTL2   3'  ACCATCCTGGCCAACATGGTGA 39833               C
           AA                   TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
                                AAAGTGGTACAACCGGTCC ACCA
                                      T
GAM320  ARSDR1   3'  ACCAGCCTGGCCAACATGGTGA 32621
           AA                   TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGACCA

GAM320  ASAHL    3'  ACCAGCCTGGCCAACATGGTGA 64311
           AA                   TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
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                                AAAGTGGTACAACCGGTCCGACCA

GAM320  ASB13    3'  ACCAGCCTGGCCAACTTGATGA 45540      C  T
                AA                  TTTCA CA GTTGGCCAGGCTGGT
                                    ||||| || ||||||||||||||||
                                    AAAGT GT CAACCGGTCCGACCA
                                      A  T
GAM320  BANP     3'  ACCAGCCTGACCAATATGG   66798         C
                                    CCATGTTGG CAGGCTGGT
                                    |||||||||  |||||||||
                                    GGTATAACC GTCCGACCA
                                         A
GAM320  BFAR     3'  ACCAGCTTGGCCAACATGGTGA 61419
                AA                  TTTCACCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||||||||
                                    AAAGTGGTACAACCGGTTCGACCA

GAM320  BIA2     3'  ACCAGCCTGGCCAACATGGTGA 71787
                AA                  TTTCACCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||||||||
                                    AAAGTGGTACAACCGGTCCGACCA

GAM320  BIRC1    3'  ACCAGCCTGGCCAGCATGGTGA 16983
                AA                  TTTCACCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||||||||
                                    AAAGTGGTACGACCGGTCCGACCA

GAM320  BIVM     3'  ACCATCCTGGCTAACATGGTGA 35152               C
                AA                  TTTCACCATGTTGGCCAGG TGGT
                                    |||||||||||||||||| ||||
                                    AAAGTGGTACAATCGGTCC ACCA
                                                 T
GAM320  BLOV1    3'  ACCAGCCTGACCAACATGGAGA 76787      A       C
                AA                  TTTC CCATGTTGG CAGGCTGGT
                                    |||| |||||||| |||||||||
                                    AAAG GGTACAACC GTCCGACCA
                                      A       A
GAM320  BTN3A2   3'  ACCATCCTGGCTAACACGGTGA 23867        A         C
                AA                  TTTCACC TGTTGGCCAGG TGGT
                                    ||||||| |||||||||| ||||
                                    AAAGTGG ACAATCGGTCC ACCA
                                       C         T
GAM320  C13orf1  3'  ACCATCGTGGCTAACATGGTGA 40345              _  C
                AA                  TTTCACCATGTTGGCCA GG TGGT
                                    |||||||||||||||| || ||||
                                    AAAGTGGTACAATCGGT CT ACCA
                                                G  _
GAM320  C1orf27  3'  ACCAGCCTGGATGACATAATGA 35721      CC    GG
                GA                  TTTCA  ATGTT  CCAGGCTGGT
                                    |||||  |||||  ||||||||||
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                                AGAGT  TACAG  GGTCCGACCA
                                  AA     TA
GAM320  C1orf29   3'  ACTAGCCTGGGCAACATGATGA 23336       C      G
            AA                    TTTCA CATGTTG CCAGGCTGGT
                                  ||||| ||||||| ||||||||||
                                  AAAGT GTACAAC GGTCCGATCA
                                    A      G
GAM320  C1orf33   3'  ACCATCCTGGCTAACACGGTGA 32976         A          C
            AA                    TTTCACC TGTTGGCCAGG TGGT
                                  ||||||| |||||||||| ||||
                                  AAAGTGG ACAATCGGTCC ACCA
                                     C          T
GAM320  C1orf34   3'  ACCAGCCTGGCCAACATGGTGA 61292
            AA                    TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  C1QTNF2   3'  ACCAGCCTGACCAACATGG    49965          C
                                  CCATGTTGG CAGGCTGGT
                                  ||||||||| |||||||||
                                  GGTACAACC GTCCGACCA
                                       A
GAM320  C20orf106 3'  ACCAGCCTGGCCAACATGGTGA 55887
            GA                    TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AGAGTGGTACAACCGGTCCGACCA

GAM320  C20orf106 3'  ACCAGCTGGGCAACATGGTGAA 55888             G   G
            A                      TTTCACCATGTTG CCAG CTGGT
                                  |||||||||||| |||| |||||
                                  AAAGTGGTACAAC GGTC GACCA
                                        G   _
GAM320  C20orf106 3'  CAGCCTGGCCAACACGGTGAAA 55900          A
                                  TTTCACC TGTTGGCCAGGCTG
                                  ||||||| ||||||||||||||
                                  AAAGTGG ACAACCGGTCCGAC
                                       C
GAM320  C20orf108 3'  ACCAGCCTGGCCAACATGATGA 55873       C
            AA                    TTTCA CATGTTGGCCAGGCTGGT
                                  ||||| ||||||||||||||||||
                                  AAAGT GTACAACCGGTCCGACCA
                                    A
GAM320  C20orf12  3'  ACCAGCCTGACCAACATGGAGA 36841      A       C
            AA                    TTTC CCATGTTGG CAGGCTGGT
                                  |||| ||||||||| |||||||||
                                  AAAG GGTACAACC GTCCGACCA
                                    A        A
GAM320  C20orf142 3'  ACCAGCCTGGGCAACATAGTGA 75267        C      G
            GA                    TTTCAC ATGTTG CCAGGCTGGT
                                  |||||| |||||| ||||||||||
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                                AGAGTG TACAAC GGTCCGACCA
                                  A     G
GAM320   C20orf175 3'  ACCAGCCTGGCCAACATGATGA 55919       C
           AA                    TTTCA CATGTTGGCCAGGCTGGT
                                 ||||| ||||||||||||||||||
                                 AAAGT GTACAACCGGTCCGACCA
                                   A
GAM320   C20orf177 3'  ACCAGCCTGACCAACATGGAGA 62823      A        C
           AA                    TTTC CCATGTTGG CAGGCTGGT
                                 |||| ||||||||| |||||||||
                                 AAAG GGTACAACC GTCCGACCA
                                   A        A
GAM320   C20orf183 3'  ACCGTCCTGGCTAACATGGTGA 48525                C
           AA                    TTTCACCATGTTGGCCAGG TGGT
                                 |||||||||||||||||| ||||
                                 AAAGTGGTACAATCGGTCC GCCA
                                                T
GAM320   C20orf29  3'  ACCAGCCTGGCCAACATAGTGA 37703       C
           AA                    TTTCAC ATGTTGGCCAGGCTGGT
                                 |||||| ||||||||||||||||
                                 AAAGTG TACAACCGGTCCGACCA
                                   A
GAM320   C21orf108 3'  ACCAGCCTTCCCAACATGGTGA 90106            CC
           AA                    TTTCACCATGTTGG  AGGCTGGT
                                 |||||||||||||  ||||||||
                                 AAAGTGGTACAACC  TCCGACCA
                                        CT
GAM320   C22orf19  3'  ACCAGCCTGGCCGACATGGTGA 14808
           AA                    TTTCACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||||||
                                 AAAGTGGTACAGCCGGTCCGACCA

GAM320   C22orf19  3'  ACCGGCCTGGCCAACATGGTGA 14809
           AA                    TTTCACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||||||
                                 AAAGTGGTACAACCGGTCCGGCCA

GAM320   C2F       3'  ACCAGCCTGGCCAACGTGGTGA 21999
           AA                    TTTCACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||||||
                                 AAAGTGGTGCAACCGGTCCGACCA

GAM320   C4S-2     3'  CCTGGCCAACATGGTGAAA    38448
                                 TTTCACCATGTTGGCCAGG
                                 |||||||||||||||||||
                                 AAAGTGGTACAACCGGTCC

GAM320   C6.1A     3'  ACCAGCCTGGGCAACATAGTGA 44526       C     G
           GA                    TTTCAC ATGTTG CCAGGCTGGT
                                 |||||| |||||| ||||||||||
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                                AGAGTG TACAAC GGTCCGACCA
                                  A     G
GAM320  C6orf29  3'  ACCAGCCTGGCCAACATGGTGA 52451
            AA                    TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  C6orf29  3'  ACCAGCCTGGCCAACATGGTGA 48261
            AA                    TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  C6orf5   3'  ACCAGCCTGGCCAACATGGTGA 31959
            AA                    TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  C6orf5   3'  ACCATCCTGGCTAACACGGTGA 31960        A         C
            AA                    TTTCACC TGTTGGCCAGG TGGT
                                  ||||||| |||||||||| ||||
                                  AAAGTGG ACAATCGGTCC ACCA
                                     C         T
GAM320  C8orf2   3'  ACCACCCTGGCCAACATGCGAA 24140      AC          C
            A                     TTTC  CATGTTGGCCAGG TGGT
                                  ||||  |||||||||||| ||||
                                  AAAG  GTACAACCGGTCC ACCA
                                    C_          C
GAM320  C9orf5   3'  ATCAGCCTAGGCAACATGG    50100        G _
                                  CCATGTTG CC AGGCTGGT
                                  |||||||| || ||||||||
                                  GGTACAAC GG TCCGACTA
                                       _ A
GAM320  CALN1    3'  ACCAGCCTGGCCAACGTGGTGA 49655
            AA                    TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTGCAACCGGTCCGACCA

GAM320  CAMKK2   5'  ATTAGCCTGGACAACATGGTGA 22617           G
            AA                    TTTCACCATGTTG CCAGGCTGGT
                                  |||||||||||| ||||||||||
                                  AAAGTGGTACAAC GGTCCGATTA
                                        A
GAM320  CBCIP2   3'  ACCAGCCTGGCCAACATGGTGA 52646
            AA                    TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  CCR6     3'  ACCAGCCTGGCCAACATGGCGA 49394      A
            AA                    TTTC CCATGTTGGCCAGGCTGGT
                                  |||| ||||||||||||||||||
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                                AAAG GGTACAACCGGTCCGACCA
                                  C
GAM320  CCR6     3'  ACCAGCCTGGCCAACATGGCGA 16435      A
                AA                TTTC CCATGTTGGCCAGGCTGGT
                                  |||| ||||||||||||||||||
                                  AAAG GGTACAACCGGTCCGACCA
                                    C
GAM320  CDT1     3'  ACCATCCTGGCGAACATGGTGA 78154          G     C
                AA                TTTCACCATGTT GCCAGG TGGT
                                  |||||||||||| |||||| ||||
                                  AAAGTGGTACAA CGGTCC ACCA
                                        G     T
GAM320  cerk     3'  AGCCTGCCCAACATGGTGAAA  43157          C
                                  TTTCACCATGTTGG CAGGCT
                                  |||||||||||||| ||||||
                                  AAAGTGGTACAACC GTCCGA
                                      C
GAM320  CFLAR    3'  ACCAGCCTGGCCAACATGGT   15271
                                  ACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||
                                  TGGTACAACCGGTCCGACCA

GAM320  CG012    5'  AGCTTGGCCAACATAGTGAAA  84142       C
                                  TTTCAC ATGTTGGCCAGGCT
                                  |||||| ||||||||||||||
                                  AAAGTG TACAACCGGTTCGA
                                     A
GAM320  CGRP-RCP 3'  ACCAGCCTCACCAACATGG   27880        CC
                                  CCATGTTGG  AGGCTGGT
                                  |||||||||  ||||||||
                                  GGTACAACC  TCCGACCA
                                       AC
GAM320  CHRFAM7A 3'  ACCAGCCTGACCAATGTG    96713        C
                                  CATGTTGG CAGGCTGGT
                                  |||||||| |||||||||
                                  GTGTAACC GTCCGACCA
                                     A
GAM320  CHST3    3'  ACCAGCCTGGGCAACATGGTGA 16227          G
                GA                TTTCACCATGTTG CCAGGCTGGT
                                  |||||||||||| ||||||||||
                                  AGAGTGGTACAAC GGTCCGACCA
                                      G
GAM320  CLDN15   3'  ACCAGCCTGGCCAACATGGTGA 57366
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  CNNM1    3'  ACCAGCCTGGCCAACATGGTGA 40113
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
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                                AAAGTGGTACAACCGGTCCGACCA

GAM320  CPR2     3'  ACCAACCTGGCCAACATTGTGA 48824        C          C
                AA                  TTTCAC ATGTTGGCCAGG TGGT
                                    |||||| |||||||||||| ||||
                                    AAAGTG TACAACCGGTCC ACCA
                                       T          A
GAM320  CRTAM    3'  ACCAGCCTGGCCAACATAGTGA 39468        C
                AA                  TTTCAC ATGTTGGCCAGGCTGGT
                                    |||||| ||||||||||||||||
                                    AAAGTG TACAACCGGTCCGACCA
                                       A
GAM320  CSAD     3'  ACCAGCCTGGCCAATAAGGTGA 32574        A
                AA                  TTTCACC TGTTGGCCAGGCTGGT
                                    ||||||| ||||||||||||||||
                                    AAAGTGG ATAACCGGTCCGACCA
                                       A
GAM320  CYB5-M   3'  ACCAGCCTGGGCAACATAGCGA 48333      ACC      G
                GA                  TTTC   ATGTTG CCAGGCTGGT
                                    ||||   |||||| ||||||||||
                                    AGAG   TACAAC GGTCCGACCA
                                      CGA      G
GAM320  CYB5-M   3'  ACCAGCCTGGGCAACATAGCGA 96199      ACC      G
                GA                  TTTC   ATGTTG CCAGGCTGGT
                                    ||||   |||||| ||||||||||
                                    AGAG   TACAAC GGTCCGACCA
                                      CGA      G
GAM320  CYorf14  3'  ACCAGCCTGGGAAACATGG    38199        GG
                                    CCATGTT  CCAGGCTGGT
                                    |||||||  ||||||||||
                                    GGTACAA  GGTCCGACCA
                                       AG
GAM320  D21S2056E 3'  ACCAGACTGACCAACATGGAGA 14859      A        C   G
                AA                  TTTC CCATGTTGG CAG CTGGT
                                    |||| ||||||||| ||| |||||
                                    AAAG GGTACAACC GTC GACCA
                                      A        A   A
GAM320  DAPK2    3'  ACCAGCCTGGGCAACATGG    27509        G
                                    CCATGTTG CCAGGCTGGT
                                    |||||||| ||||||||||
                                    GGTACAAC GGTCCGACCA
                                        G
GAM320  DDX34    3'  ACCATCCTGGCTAACACGGTGA 28655        A         C
                AA                  TTTCACC TGTTGGCCAGG TGGT
                                    ||||||| |||||||||| ||||
                                    AAAGTGG ACAATCGGTCC ACCA
                                       C          T
GAM320  DDX34    3'  AGCCTGACCAACATGGAGAAA  28657      A        C
                                    TTTC CCATGTTGG CAGGCT
                                    |||| ||||||||| ||||||
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                                AAAG GGTACAACC GTCCGA
                                  A       A
GAM320  DEGS     3'  ACCAGCCTGGCCAACACGGTGA 14797       A
           AA                    TTTCACC TGTTGGCCAGGCTGGT
                                 ||||||| ||||||||||||||||
                                 AAAGTGG ACAACCGGTCCGACCA
                                    C
GAM320  DIS3     3'  ACCAGCCTGGCCAACATGGT  30909
                                 ACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||
                                 TGGTACAACCGGTCCGACCA

GAM320  DJ122O8.2 3'  ACCAGCCTGGCCAACATGGTGA 40390
           AA                    TTTCACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||||||
                                 AAAGTGGTACAACCGGTCCGACCA

GAM320  dJ383J4.3 3'  ACCAGCCTGGCCAACATGGTGA 67487
           AA                    TTTCACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||||||
                                 AAAGTGGTACAACCGGTCCGACCA

GAM320  DKFZP434B168 3'  ACCATCCTGGCTAACACAGTGA 31861       CA         C
           AA                    TTTCAC  TGTTGGCCAGG TGGT
                                 ||||||  |||||||||| ||||
                                 AAAGTG  ACAATCGGTCC ACCA
                                    AC         T
GAM320  DKFZP434C171 3'  ACCATCCTGGCTAACACAGTGA 32178       CA         C
           AA                    TTTCAC  TGTTGGCCAGG TGGT
                                 ||||||  |||||||||| ||||
                                 AAAGTG  ACAATCGGTCC ACCA
                                    AC         T
GAM320  DKFZP434C1715 3'  ACCAGCCTGGACAACATGGGAA 87346      A       G
           A                     TTTC CCATGTTG CCAGGCTGGT
                                 |||| |||||||| ||||||||||
                                 AAAG GGTACAAC GGTCCGACCA
                                   _       A
GAM320  DKFZp434E0519 3'  ACCAGCCTGGGCAACATGGTGA 50980           G
           AA                    TTTCACCATGTTG CCAGGCTGGT
                                 |||||||||||| ||||||||||
                                 AAAGTGGTACAAC GGTCCGACCA
                                       G
GAM320  DKFZp434E2220 5'  TCAGCCTGGCCAATATGGTGAA 34719
           A                     TTTCACCATGTTGGCCAGGCTGG
                                 |||||||||||||||||||||||
                                 AAAGTGGTATAACCGGTCCGACT

GAM320  DKFZP434F091 3'  ACCAGCCTGGCCAACATGGTGA 31891
           AA                    TTTCACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||||||
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                                AAAGTGGTACAACCGGTCCGACCA

GAM320  DKFZp434G171 3'  ACCAGCCTGGCCAACACGG    80226     A
                                CC TGTTGGCCAGGCTGGT
                                || ||||||||||||||||
                                GG ACAACCGGTCCGACCA
                                 C
GAM320  DKFZp434G171 3'  ACCAGCCTGGCCAACATGGTGA 80227
           AA                    TTTCACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||||||
                                 AAAGTGGTACAACCGGTCCGACCA

GAM320  DKFZP434I1735 3'  ACCAGCCTGACCAACATGGTGA 89161              C
           AA                    TTTCACCATGTTGG CAGGCTGGT
                                 |||||||||||||| |||||||||
                                 AAAGTGGTACAACC GTCCGACCA
                                           A
GAM320  DKFZP434K1421 3'  ACCAGCCTAGGCAGGATA     50462      G_  _
                                 TGTT  GCC AGGCTGGT
                                 ||||  ||| ||||||||
                                 ATAG  CGG TCCGACCA
                                   GA   A
GAM320  DKFZP434P0721 3'  AGCCTGGCCAACATGATGAAG  64453       C
                                 TTTCA CATGTTGGCCAGGCT
                                 ||||| ||||||||||||||
                                 GAAGT GTACAACCGGTCCGA
                                    A
GAM320  DKFZp547A023 3'  ACCAGCCTCATCAACATAGTGA 73020       C      CC
           GA                    TTTCAC ATGTTGG  AGGCTGGT
                                 |||||| |||||||  ||||||||
                                 AGAGTG TACAACT  TCCGACCA
                                    A       AC
GAM320  DKFZp547C176 3'  ACCATCCTGGCCAACATGGTGA 67794                C
           AA                    TTTCACCATGTTGGCCAGG TGGT
                                 |||||||||||||||||| ||||
                                 AAAGTGGTACAACCGGTCC ACCA
                                              T
GAM320  DKFZp547G183 3'  ACCAGCCTGGCCAACATGGCGA 38636      A
           AA                    TTTC CCATGTTGGCCAGGCTGGT
                                 |||| ||||||||||||||||||
                                 AAAG GGTACAACCGGTCCGACCA
                                   C
GAM320  DKFZp547I094 3'  ACCAGCCTGGGCAACATGGTGA 50549            G
           AA                    TTTCACCATGTTG CCAGGCTGGT
                                 |||||||||||| ||||||||||
                                 AAAGTGGTACAAC GGTCCGACCA
                                        G
GAM320  DKFZP564A022 3'  ACCATCCTGGCTAACATGGTGA 48966                C
           AA                    TTTCACCATGTTGGCCAGG TGGT
                                 |||||||||||||||||| ||||
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                                AAAGTGGTACAATCGGTCC ACCA
                                        T
GAM320  DKFZP564B1023 3'  ACCAGCCTAACCAACATGGAGA 49354      A        CC
          AA                    TTTC CCATGTTGG  AGGCTGGT
                                |||| |||||||||  ||||||||
                                AAAG GGTACAACC  TCCGACCA
                                  A        AA
GAM320  DKFZP564B1023 3'  ACCAGCCTGGGCAACATGGTGA 49355            G
          AA                    TTTCACCATGTTG CCAGGCTGGT
                                |||||||||||| ||||||||||
                                AAAGTGGTACAAC GGTCCGACCA
                                      G
GAM320  DKFZP564I052 3'  ACCAACCTGGCCAACATGGTGA 67274              C
          AA                    TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
                                AAAGTGGTACAACCGGTCC ACCA
                                        A
GAM320  DKFZp564K142 3'  ACCATCCTGGCCAACATGGTGA 50427              C
          AA                    TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
                                AAAGTGGTACAACCGGTCC ACCA
                                        T
GAM320  DKFZP564M182 3'  ACCAGCCTGGCTTACATGGTGA 78613          T
          AA                    TTTCACCATGT GGCCAGGCTGGT
                                |||||||||| ||||||||||
                                AAAGTGGTACA TCGGTCCGACCA
                                      T
GAM320  DKFZP564M182 3'  ACCATCCTGGCCAACATGGTGA 78614              C
          AA                    TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
                                AAAGTGGTACAACCGGTCC ACCA
                                        T
GAM320  DKFZP586C1324 3'  ACCAGCCTGGCCAACATGGTGA 70351
          AA                    TTTCACCATGTTGGCCAGGCTGGT
                                |||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGACCA

GAM320  DKFZP586D2223 3'  ACCAGCCTGGCCAACATGGTTA 38283     C
          AA                    TTT ACCATGTTGGCCAGGCTGGT
                                ||| ||||||||||||||||||
                                AAA TGGTACAACCGGTCCGACCA
                                  T
GAM320  DKFZP667O116 3'  ACCAGCCTGGGCAACATAGCGA 95937      ACC      G
          GA                    TTTC   ATGTTG CCAGGCTGGT
                                ||||   |||||| ||||||||||
                                AGAG   TACAAC GGTCCGACCA
                                  CGA      G
GAM320  DKFZp727G131 3'  ACCAGCCTGGCCAACATGGTGA 59690
          AA                    TTTCACCATGTTGGCCAGGCTGGT
                                |||||||||||||||||||||||
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                                AAAGTGGTACAACCGGTCCGACCA

GAM320  DKFZP761E2110 3'  ACCAGACTGGCCAACACAGCGA 48959      ACCA        G
            GA                  TTTC    TGTTGGCCAG CTGGT
                                ||||    |||||||||| |||||
                                AGAG    ACAACCGGTC GACCA
                                  CGAC          A
GAM320  DKFZP761G1913 3'  ACCAGCCTGGGTAATATGG    49689         G
                                CCATGTTG CCAGGCTGGT
                                |||||||| ||||||||||
                                GGTATAAT GGTCCGACCA
                                     G
GAM320  DKFZp761J139 5'  CCTGGGCAACATGGTGAAA    51104           G
                                TTTCACCATGTTG CCAGG
                                |||||||||||| |||||
                                AAAGTGGTACAAC GGTCC
                                       G
GAM320  DRF1     3'  ACCAGCCTGACCAACGTGGTGA 47729             C
            AA                  TTTCACCATGTTGG CAGGCTGGT
                                |||||||||||||| |||||||||
                                AAAGTGGTGCAACC GTCCGACCA
                                       A
GAM320  DRF1     3'  ACCAGCTTGGCCAACATGGCGA 47730      A
            AA                  TTTC CCATGTTGGCCAGGCTGGT
                                |||| ||||||||||||||||||
                                AAAG GGTACAACCGGTTCGACCA
                                  C
GAM320  DSCR6    3'  ACCAGCCTGACCAGCGTGGAGA 39053      A       C
            AA                  TTTC CCATGTTGG CAGGCTGGT
                                |||| ||||||||| |||||||||
                                AAAG GGTGCGACC GTCCGACCA
                                  A       A
GAM320  ERAP140  3'  ACCAGTCTGGCCAACATGGTGA 75697
            AA                  TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCTGACCA

GAM320  ERGL     3'  ACCATCCTGGCCAACATGGTGA 96729              C
            AA                  TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
                                AAAGTGGTACAACCGGTCC ACCA
                                          T
GAM320  FBXO26   3'  ACCAGCCTGGGCAACATAGTGA 46620       C     G
            AA                  TTTCAC ATGTTG CCAGGCTGGT
                                |||||| |||||| ||||||||||
                                AAAGTG TACAAC GGTCCGACCA
                                  A     G
GAM320  FBXO27   3'  ACCAGCCTGGCCAACATGGTGA 74995
            AA                  TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
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                                AAAGTGGTACAACCGGTCCGACCA

GAM320  FBXO6    3'  ACCATCCTGGCCAACACGGTGA 37984        A         C
                AA                  TTTCACC TGTTGGCCAGG TGGT
                                    ||||||| |||||||||||| ||||
                                    AAAGTGG ACAACCGGTCC ACCA
                                       C         T
GAM320  FBXO9    3'  ACCAGCCTGGGCAACATGG   54236        G
                                    CCATGTTG CCAGGCTGGT
                                    |||||||| ||||||||||
                                    GGTACAAC GGTCCGACCA
                                       G
GAM320  FKBP14   3'  ACCAGCCTGACCAACACGGAGA 36055     A  A     C
                AA                  TTTC CC TGTTGG CAGGCTGGT
                                    |||| || |||||| |||||||||
                                    AAAG GG ACAACC GTCCGACCA
                                      A  C     A
GAM320  FKBP14   3'  ACCAGCCTGGCCAACATGGTGA 36056
                AA                  TTTCACCATGTTGGCCAGGCTGGT
                                    |||||||||||||||||||||||||
                                    AAAGTGGTACAACCGGTCCGACCA

GAM320  FKSG17   3'  ACCAGCCTGGCCAACATGATGA 50148       C
                AA                  TTTCA CATGTTGGCCAGGCTGGT
                                    ||||| |||||||||||||||||
                                    AAAGT GTACAACCGGTCCGACCA
                                      A
GAM320  FLJ10008 3'  ACCATCCTGGCTAACATGGTGA 36175                C
                AA                  TTTCACCATGTTGGCCAGG TGGT
                                    |||||||||||||||||| ||||
                                    AAAGTGGTACAATCGGTCC ACCA
                                                 T
GAM320  FLJ10043 3'  ACCAGCCTGGCCAACAAGGCGA 36224      A  A
                AA                  TTTC CC TGTTGGCCAGGCTGGT
                                    |||| || ||||||||||||||||
                                    AAAG GG ACAACCGGTCCGACCA
                                      C  A
GAM320  FLJ10058 3'  ACCAGCCTGGCCAACATGGTG  36254
                                    CACCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||||
                                    GTGGTACAACCGGTCCGACCA

GAM320  FLJ10139 3'  ACCAGCCTGGGCAACATGGTGA 36312            G
                GA                  TTTCACCATGTTG CCAGGCTGGT
                                    |||||||||||| ||||||||||
                                    AGAGTGGTACAAC GGTCCGACCA
                                          G
GAM320  FLJ10244 3'  ACCAGCCTGACCAATATAGTGA 36395       C      C
                AA                  TTTCAC ATGTTGG CAGGCTGGT
                                    |||||| ||||||| |||||||||
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                                AAAGTG TATAACC GTCCGACCA
                                   A      A
GAM320  FLJ10460  3'  ACCAGCCTGGCCAACATGGCGA 36604      A
                AA                  TTTC CCATGTTGGCCAGGCTGGT
                                    |||| ||||||||||||||||||
                                    AAAG GGTACAACCGGTCCGACCA
                                      C
GAM320  FLJ10460  3'  ACCAGCCTGGGTAACATGGTGA 36605            G
                AA                  TTTCACCATGTTG CCAGGCTGGT
                                    |||||||||||| ||||||||||
                                    AAAGTGGTACAAT GGTCCGACCA
                                           G
GAM320  FLJ10460  3'  ACCAGCCTTGACAACATGGTGA 36606           GCC
                AA                  TTTCACCATGTTG   AGGCTGGT
                                    |||||||||||||   ||||||||
                                    AAAGTGGTACAAC   TCCGACCA
                                           AGT
GAM320  FLJ10520  3'  CCAGCCTGACCAACATGGTGAA 36702            C
                A                    TTTCACCATGTTGG CAGGCTGG
                                    |||||||||||||| ||||||||
                                    AAAGTGGTACAACC GTCCGACC
                                           A
GAM320  FLJ10547  3'  ACCAGCCTGACCAACATGGTGA 36770            C
                AA                  TTTCACCATGTTGG CAGGCTGGT
                                    |||||||||||||| |||||||||
                                    AAAGTGGTACAACC GTCCGACCA
                                           A
GAM320  FLJ10607  3'  ACCAGCCTGACCAAAATGGTGA 77620         G   C
                AA                  TTTCACCAT TTGG CAGGCTGGT
                                    ||||||||| |||| |||||||||
                                    AAAGTGGTA AACC GTCCGACCA
                                         A   A
GAM320  FLJ10613  3'  ACCAGCCTGGCCAACATGGTGA 39331
                G                    TTCACCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||||||||
                                    GAGTGGTACAACCGGTCCGACCA

GAM320  FLJ10650  3'  ACCAGCCTGGCCAACATGGTGA 36895
                GA                   TTTCACCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||||||||
                                    AGAGTGGTACAACCGGTCCGACCA

GAM320  FLJ10704  3'  ACCAGCCTGGCCAACATGGTGA 36972
                AA                  TTTCACCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||||||||
                                    AAAGTGGTACAACCGGTCCGACCA

GAM320  FLJ10781  3'  ACCAGCTTGACCAACATGGTGA 37164            C
                AA                  TTTCACCATGTTGG CAGGCTGGT
                                    |||||||||||||| |||||||||
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                                AAAGTGGTACAACC GTTCGACCA
                                      A
GAM320  FLJ10803  3'  ACCAGCCTGACCAACATGG   37191        C
                                CCATGTTGG CAGGCTGGT
                                ||||||||| |||||||||
                                GGTACAACC GTCCGACCA
                                   A
GAM320  FLJ10803  3'  ACCAGCCTGGGCAACATGGTGA 37192          G
          AA                      TTTCACCATGTTG CCAGGCTGGT
                                ||||||||||||| ||||||||||
                                AAAGTGGTACAAC GGTCCGACCA
                                      G
GAM320  FLJ10826  3'  ACCAGCCTGACAAACATGGAGA 37239     A     GGC
          AA                      TTTC CCATGTT   CAGGCTGGT
                                |||| |||||||   |||||||||
                                AAAG GGTACAA   GTCCGACCA
                                  A      ACA
GAM320  FLJ10936  3'  ACCGGCCTGGCCAACGTGGTGA 37437
          AA                      TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTGCAACCGGTCCGGCCA

GAM320  FLJ10989  3'  CAGCCTGGTCAACATGGTGAAA 37498
                                TTTCACCATGTTGGCCAGGCTG
                                |||||||||||||||||||||
                                AAAGTGGTACAACTGGTCCGAC

GAM320  FLJ11029  3'  ACCAGCCTGGCCAACATGGTGA 61628
          AA                      TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGACCA

GAM320  FLJ11042  3'  ACCATCTTGGGCAACATGGTGA 37560          G   C
          AA                      TTTCACCATGTTG CCAGG TGGT
                                |||||||||||| ||||| ||||
                                AAAGTGGTACAAC GGTTC ACCA
                                      G   T
GAM320  FLJ11126  3'  ACCAGCCTGGCCAACATGATGA 37645     C
          AA                      TTTCA CATGTTGGCCAGGCTGGT
                                ||||| ||||||||||||||||||
                                AAAGT GTACAACCGGTCCGACCA
                                  A
GAM320  FLJ11136  3'  ACCAGCTTGGCCAAGATGGTGA 37662        G
          AA                      TTTCACCAT TTGGCCAGGCTGGT
                                ||||||||| ||||||||||||||
                                AAAGTGGTA AACCGGTTCGACCA
                                      G
GAM320  FLJ11151  3'  CAGCCTGGCCAACATGGTGAAA 68473
                                TTTCACCATGTTGGCCAGGCTG
                                |||||||||||||||||||||
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                                AAAGTGGTACAACCGGTCCGAC

GAM320  FLJ11370  3'  ACCAGCCTGGCCAACATGGTGA 46959
              AA                 TTTCACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||||
                                 AAAGTGGTACAACCGGTCCGACCA

GAM320  FLJ11577  3'  ACCGGCCTGGCCAATATGGTGA 47953
              AA                 TTTCACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||||
                                 AAAGTGGTATAACCGGTCCGGCCA

GAM320  FLJ11700  3'  ACCAGCCTGGCCAACATGGTGA 46553
              AA                 TTTCACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||||
                                 AAAGTGGTACAACCGGTCCGACCA

GAM320  FLJ11710  5'  ACCAGCCTGGGCAACACAGTGA 46236       CA    G
              GA                 TTTCAC  TGTTG CCAGGCTGGT
                                 ||||||  ||||| ||||||||||
                                 AGAGTG  ACAAC GGTCCGACCA
                                    AC    G
GAM320  FLJ11722  3'  ACCATCCTGGCCAACACAGTGA 46985       CA         C
              AA                 TTTCAC  TGTTGGCCAGG TGGT
                                 ||||||  |||||||||| ||||
                                 AAAGTG  ACAACCGGTCC ACCA
                                    AC          T
GAM320  FLJ11722  3'  ACCATCCTGGCCAACATGGTGA 46986               C
              AA                 TTTCACCATGTTGGCCAGG TGGT
                                 |||||||||||||||||| ||||
                                 AAAGTGGTACAACCGGTCC ACCA
                                              T
GAM320  FLJ11726  3'  ACCAGCCTGGCCAACATGGTGA 47012
              AA                 TTTCACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||||
                                 AAAGTGGTACAACCGGTCCGACCA

GAM320  FLJ11800  3'  ACCAGCCTGGGCAACGTGGTGA 47034           G
              AA                 TTTCACCATGTTG CCAGGCTGGT
                                 |||||||||||| ||||||||||
                                 AAAGTGGTGCAAC GGTCCGACCA
                                       G
GAM320  FLJ11996  3'  ACCAGCCTGACCAACATGGTGA 47046           C
              AA                 TTTCACCATGTTGG CAGGCTGGT
                                 |||||||||||||| |||||||||
                                 AAAGTGGTACAACC GTCCGACCA
                                       A
GAM320  FLJ11996  3'  ACCAGCCTGGCCAACATGGTGA 47047
              AA                 TTTCACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||||
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                                AAAGTGGTACAACCGGTCCGACCA

GAM320  FLJ12190  3'  ACCAGGCTGGTCAACATGGCGA 47557      A          G
              AA                  TTTC CCATGTTGGCCAG CTGGT
                                  |||| |||||||||||| |||||
                                  AAAG GGTACAACTGGTC GACCA
                                    C           G
GAM320  FLJ12294  3'  ACCAGCCTGGCCAACATGGTGA 47704
              AA                  TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  FLJ12298  3'  ACCAGCCTGGCCAACATGGTGA 50591
              AA                  TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  FLJ12331  3'  ACCAGCCTGGCCAACATGG    47106
                                  CCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||
                                  GGTACAACCGGTCCGACCA

GAM320  FLJ12363  3'  ACCAGCCTGACCAACATGGTGA 50625              C
              AA                  TTTCACCATGTTGG CAGGCTGGT
                                  |||||||||||||| |||||||||
                                  AAAGTGGTACAACC GTCCGACCA
                                        A
GAM320  FLJ12409  3'  ACCAGCCTGGGCAACATGG    47765        G
                                  CCATGTTG CCAGGCTGGT
                                  |||||||| ||||||||||
                                  GGTACAAC GGTCCGACCA
                                      G
GAM320  FLJ12448  3'  ACCAGCCTGGCCAACATGGCGA 43473      A
              GA                  TTTC CCATGTTGGCCAGGCTGGT
                                  |||| ||||||||||||||||||
                                  AGAG GGTACAACCGGTCCGACCA
                                    C
GAM320  FLJ12547  3'  ACCGTCCTGGCCGACATGGTGA 47125               C
              AA                  TTTCACCATGTTGGCCAGG TGGT
                                  |||||||||||||||||| ||||
                                  AAAGTGGTACAGCCGGTCC GCCA
                                            T
GAM320  FLJ12586  3'  AGCCTGGCCAGCATGGTGAAA  45204
                                  TTTCACCATGTTGGCCAGGCT
                                  |||||||||||||||||||||
                                  AAAGTGGTACGACCGGTCCGA

GAM320  FLJ12592  3'  ACCAGCCTGGGCAACATAGCGA 50647      ACC      G
              GA                  TTTC   ATGTTG CCAGGCTGGT
                                  ||||   |||||| ||||||||||
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                                AGAG   TACAAC GGTCCGACCA
                                  CGA     G
GAM320  FLJ12606  3'  ACCATCCTGGCCAACACGGTGA 46058        A         C
            AA                    TTTCACC TGTTGGCCAGG TGGT
                                  ||||||| |||||||||| ||||
                                  AAAGTGG ACAACCGGTCC ACCA
                                     C         T
GAM320  FLJ12606  3'  CCTGGGCAACATGGTGAAA   46067           G
                                  TTTCACCATGTTG CCAGG
                                  |||||||||||| |||||
                                  AAAGTGGTACAAC GGTCC
                                        G
GAM320  FLJ12660  3'  ACCAGCCTGACCAACATGGTGA 47890            C
            AA                    TTTCACCATGTTGG CAGGCTGGT
                                  |||||||||||| |||||||||
                                  AAAGTGGTACAACC GTCCGACCA
                                        A
GAM320  FLJ12666  3'  ACCACCCTGGCCAATATGGTGA 45062               C
            AA                    TTTCACCATGTTGGCCAGG TGGT
                                  |||||||||||||||||| ||||
                                  AAAGTGGTATAACCGGTCC ACCA
                                           C
GAM320  FLJ12671  3'  ACCAGCCTGGCCAACATGGCGA 49098     A
            A                     TTC CCATGTTGGCCAGGCTGGT
                                  ||| ||||||||||||||||||
                                  AAG GGTACAACCGGTCCGACCA
                                    C
GAM320  FLJ12800  3'  ACCAGCCTGGCCAACATGGTGA 43523
            AA                    TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  FLJ12921  3'  ACCATCCTGGCTAACACGGTGA 46388        A         C
            AA                    TTTCACC TGTTGGCCAGG TGGT
                                  ||||||| |||||||||| ||||
                                  AAAGTGG ACAATCGGTCC ACCA
                                     C         T
GAM320  FLJ13117  3'  ACCAGCCTGGCCAACATGGTGA 43800
            AA                    TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  FLJ13162  3'  AGCCTGACCAACATGGAGAAA  47179      A       C
                                  TTTC CCATGTTGG CAGGCT
                                  |||| ||||||||| ||||||
                                  AAAG GGTACAACC GTCCGA
                                    A       A
GAM320  FLJ13193  3'  ACCAACCTGGTCTACATGGTGA 50702          T      C
            AA                    TTTCACCATGT GGCCAGG TGGT
                                  |||||||||| ||||||| ||||
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                                AAAGTGGTACA CTGGTCC ACCA
                                      T      A
GAM320  FLJ13193  3'  ACCAGCCAGGCCAACATGGTGA 50703              A
            AA                  TTTCACCATGTTGGCC GGCTGGT
                                |||||||||||||||| |||||||
                                AAAGTGGTACAACCGG CCGACCA
                                     A
GAM320  FLJ13193  3'  ACCATCCTGGCCAACATGGTGA 50704                C
            AA                  TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
                                AAAGTGGTACAACCGGTCC ACCA
                                      T
GAM320  FLJ13305  3'  ACCATCCTGGCTAACACGATGA 91702       CCA         C
            AA                  TTTCA   TGTTGGCCAGG TGGT
                                |||||   |||||||||||| ||||
                                AAAGT   ACAATCGGTCC ACCA
                                  AGC          T
GAM320  FLJ13352  3'  ACCAGCCTGGGCAACATGGTGA 45046            G
            AA                  TTTCACCATGTTG CCAGGCTGGT
                                |||||||||||| ||||||||||
                                AAAGTGGTACAAC GGTCCGACCA
                                      G
GAM320  FLJ13448  3'  ACCAGCCTGGTCAACATGGCGA 47876      A
            AA                  TTTC CCATGTTGGCCAGGCTGGT
                                |||| ||||||||||||||||||
                                AAAG GGTACAACTGGTCCGACCA
                                  C
GAM320  FLJ13456  3'  ACCAGCCTGGCCCAAATGGTGA 66522          GTT
            AA                  TTTCACCAT   GGCCAGGCTGGT
                                |||||||||   ||||||||||||
                                AAAGTGGTA   CCGGTCCGACCA
                                     AAC
GAM320  FLJ13456  3'  CCTGGCCAACGTGGTGAAA    66541
                                TTTCACCATGTTGGCCAGG
                                ||||||||||||||||||
                                AAAGTGGTGCAACCGGTCC

GAM320  FLJ13621  3'  ACCATCCTGGCCAACATGGTGA 47212                C
            AA                  TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
                                AAAGTGGTACAACCGGTCC ACCA
                                      T
GAM320  FLJ13659  3'  ACCAGCCTGACCAACATGGTGA 48025            C
            AA                  TTTCACCATGTTGG CAGGCTGGT
                                |||||||||||||| |||||||||
                                AAAGTGGTACAACC GTCCGACCA
                                     A
GAM320  FLJ13769  3'  ACCAGCCTGGCCAGCATGGTGA 47235
            AA                  TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
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                                AAAGTGGTACGACCGGTCCGACCA

GAM320  FLJ13769 3' AGCCTGGCCAACATAGCGAAA 47242      ACC
                                TTTC   ATGTTGGCCAGGCT
                                ||||   ||||||||||||||
                                AAAG   TACAACCGGTCCGA
                                  CGA
GAM320  FLJ13848 3' ACCAGCCTGGTCAACATGG    45813
                                CCATGTTGGCCAGGCTGGT
                                |||||||||||||||||||
                                GGTACAACTGGTCCGACCA

GAM320  FLJ13952 3' ACCAGCCTGACCACCATGGAGA 46000      A    T   C
             AA                   TTTC CCATG TGG CAGGCTGGT
                                ||||| ||||| ||| |||||||||
                                AAAG GGTAC ACC GTCCGACCA
                                  A    C   A
GAM320  FLJ13984 3' ACCAGCCTGGACAACATGG    45798         G
                                CCATGTTG CCAGGCTGGT
                                |||||||| ||||||||||
                                GGTACAAC GGTCCGACCA
                                    A
GAM320  FLJ14082 3' ACCAGCCTGGCCAACTTGGAGA 47317      A   T
             AA                   TTTC CCA GTTGGCCAGGCTGGT
                                |||| ||| ||||||||||||||||
                                AAAG GGT CAACCGGTCCGACCA
                                  A   T
GAM320  FLJ14100 3' ACCAACCTGGCTAACACGGTGA 47325         A         C
             AA                   TTTCACC TGTTGGCCAGG TGGT
                                ||||||| |||||||||| ||||
                                AAAGTGG ACAATCGGTCC ACCA
                                    C         A
GAM320  FLJ14117 3' ACCAGCCTGGCCAACATGG    43210
                                CCATGTTGGCCAGGCTGGT
                                |||||||||||||||||||
                                GGTACAACCGGTCCGACCA

GAM320  FLJ14117 3' ACCATCCTGGCCAACATGGTGA 43211                 C
             AA                   TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
                                AAAGTGGTACAACCGGTCC ACCA
                                          T
GAM320  FLJ14117 3' ACCATCCTGGCCAACGTGGTGA 43212                 C
             AA                   TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
                                AAAGTGGTGCAACCGGTCC ACCA
                                          T
GAM320  FLJ14129 3' ACCATCCTGGCCAACATGG    48803              C
                                CCATGTTGGCCAGG TGGT
                                |||||||||||||| ||||
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                                GGTACAACCGGTCC ACCA
                                       T
GAM320  FLJ14225  3'  CCTGGCTAACACGGTGAAA   46384       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                   C
GAM320  FLJ14251  3'  ACCACCCTGGCCAACATGGTGA 46468             C
          AA                     TTTCACCATGTTGGCCAGG TGGT
                                 |||||||||||||||||| ||||
                                 AAAGTGGTACAACCGGTCC ACCA
                                          C
GAM320  FLJ14251  3'  ACCAGCCTGGCCAACATAGTGA 46469       C
          AA                     TTTCAC ATGTTGGCCAGGCTGGT
                                 ||||||| ||||||||||||||||
                                 AAAGTG TACAACCGGTCCGACCA
                                    A
GAM320  FLJ14280  3'  ACCAGCCTAGGCAACATGGCGA 46517     A      G  _
          AA                     TTTC CCATGTTG CC AGGCTGGT
                                 |||| |||||||| || ||||||||
                                 AAAG GGTACAAC GG TCCGACCA
                                   C       _  A
GAM320  FLJ14326  3'  ACCAGCCTGGCCAACAGGTGAA 50757        A
          A                      TTTCACC TGTTGGCCAGGCTGGT
                                 ||||||| ||||||||||||||||
                                 AAAGTGG ACAACCGGTCCGACCA
                                         _
GAM320  FLJ14327  3'  ACCAGGCTGGCCAACACGGTGA 46668        A        G
          AA                     TTTCACC TGTTGGCCAG CTGGT
                                 ||||||| |||||||||| |||||
                                 AAAGTGG ACAACCGGTC GACCA
                                    C        G
GAM320  FLJ14345  3'  ACCAGGCTGGCCAACACGGTGA 45652        A        G
          AA                     TTTCACC TGTTGGCCAG CTGGT
                                 ||||||| |||||||||| |||||
                                 AAAGTGG ACAACCGGTC GACCA
                                    C        G
GAM320  FLJ14346  3'  ACCATCCCGGCTAACACGGTGA 47351        A      A  C
          AA                     TTTCACC TGTTGGCC GG TGGT
                                 ||||||| |||||||| || ||||
                                 AAAGTGG ACAATCGG CC ACCA
                                    C       C  T
GAM320  FLJ14397  3'  ACCAGCCTGACCAACATGGAGA 52308     A       C
          AA                     TTTC CCATGTTGG CAGGCTGGT
                                 |||| ||||||||| |||||||||
                                 AAAG GGTACAACC GTCCGACCA
                                   A       A
GAM320  FLJ14397  3'  ACCATCCTGGCTAACACGGTGA 52309        A        C
          AA                     TTTCACC TGTTGGCCAGG TGGT
                                 ||||||| |||||||||| ||||
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                                AAAGTGG ACAATCGGTCC ACCA
                                   C         T
GAM320  FLJ14399  3'  CCAGCCTGGGCAACATGGTGAA 52340           G
          A                     TTTCACCATGTTG CCAGGCTGG
                                |||||||||||| |||||||||
                                AAAGTGGTACAAC GGTCCGACC
                                     G
GAM320  FLJ14457  3'  ACCATCCTGGCTAACACAGTGA 52398       CA         C
          AA                    TTTCAC  TGTTGGCCAGG TGGT
                                ||||||  |||||||||| ||||
                                AAAGTG  ACAATCGGTCC ACCA
                                  AC          T
GAM320  FLJ14466  3'  ACCAGCCTGACCAACATGGAGA 52414      A       C
          AA                    TTTC CCATGTTGG CAGGCTGGT
                                |||| ||||||||| |||||||||
                                AAAG GGTACAACC GTCCGACCA
                                  A       A
GAM320  FLJ14490  3'  ACCATGCTGGCTAACATGGTGA 52436              G _
          AA                    TTTCACCATGTTGGCCAG C TGGT
                                |||||||||||||||||| | ||||
                                AAAGTGGTACAATCGGTC G ACCA
                                       _ T
GAM320  FLJ14641  3'  ACCATCCTGGCCAACATGGTGA 52550               C
          AA                    TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
                                AAAGTGGTACAACCGGTCC ACCA
                                      T
GAM320  FLJ20004  3'  ACCAGACTGACCAACATGGAGA 96992      A       C  G
          AA                    TTTC CCATGTTGG CAG CTGGT
                                |||| ||||||||| ||| |||||
                                AAAG GGTACAACC GTC GACCA
                                  A       A  A
GAM320  FLJ20004  3'  ACCAGCCTGGCCAACATGGTGA 96993
          AG                    TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                GAAGTGGTACAACCGGTCCGACCA

GAM320  FLJ20004  3'  ACCAGCCTGGCCAACATGGTGA 34742
          AA                    TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGACCA

GAM320  FLJ20006  3'  ACCAGCCTGACCAACATGG   34774         C
                                CCATGTTGG CAGGCTGGT
                                ||||||||| |||||||||
                                GGTACAACC GTCCGACCA
                                    A
GAM320  FLJ20006  3'  ACCAGCCTTGGCCAACATGGCG 34775      A        _
          AAA                   TTTC CCATGTTGGCCA GGCTGGT
                                |||| |||||||||||| |||||||
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                                AAAG GGTACAACCGGT CCGACCA
                                  C          T
GAM320  FLJ20013  3'  ACCAGCCTGGCCAACACGGTGA 34790        A
                AA                  TTTCACC TGTTGGCCAGGCTGGT
                                    ||||||| ||||||||||||||||
                                    AAAGTGG ACAACCGGTCCGACCA
                                       C
GAM320  FLJ20034  3'  ACCAACCTAGCCAACATGGTGA 34830             C  C
                AA                  TTTCACCATGTTGGC AGG TGGT
                                    ||||||||||||||| ||| ||||
                                    AAAGTGGTACAACCG TCC ACCA
                                           A  A
GAM320  FLJ20045  3'  ACCAGCCTGGCCAAATGGTGAA 34869         G
                A                   TTTCACCAT TTGGCCAGGCTGGT
                                    |||||||||  ||||||||||||||
                                    AAAGTGGTA AACCGGTCCGACCA

                                      _
GAM320  FLJ20055  3'  ACCATCCTGGCTAACACGGTGA 34901        A        C
                AA                  TTTCACC TGTTGGCCAGG TGGT
                                    ||||||| |||||||||| ||||
                                    AAAGTGG ACAATCGGTCC ACCA
                                       C         T
GAM320  FLJ20059  3'  ACCAGCCTGACCAACATGGAGA 34916     A       C
                AA                  TTTC CCATGTTGG CAGGCTGGT
                                    |||| ||||||||| |||||||||
                                    AAAG GGTACAACC GTCCGACCA
                                      A       A
GAM320  FLJ20059  3'  ACCAGCCTGGCTAATATGGTGA 34917
                AA                  TTTCACCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||||||||
                                    AAAGTGGTATAATCGGTCCGACCA

GAM320  FLJ20069  3'  ACCAGCCTGACCAACATGGTGA 34943             C
                AA                  TTTCACCATGTTGG CAGGCTGGT
                                    |||||||||||||| |||||||||
                                    AAAGTGGTACAACC GTCCGACCA
                                           A
GAM320  FLJ20139  3'  ACCAGCTGGGCAACATGGTGAA 35109            G  G
                A                   TTTCACCATGTTG CCAG CTGGT
                                    |||||||||||||  |||| |||||
                                    AAAGTGGTACAAC GGTC GACCA
                                           G  _
GAM320  FLJ20139  3'  AGCCTGGGCAACATGGTGAAA  35110           G
                                    TTTCACCATGTTG CCAGGCT
                                    |||||||||||||  |||||||
                                    AAAGTGGTACAAC GGTCCGA
                                           G
GAM320  FLJ20200  3'  ACCAGCCTGGGCAACATAGTGA 35230       C     G
                GA                  TTTCAC ATGTTG CCAGGCTGGT
                                    ||||||  ||||||  ||||||||||
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                                AGAGTG TACAAC GGTCCGACCA
                                   A     G
GAM320  FLJ20211  3'  ACCAGCCTGGCCAACATAGTGA 35250       C
                AA                  TTTCAC ATGTTGGCCAGGCTGGT
                                    |||||| ||||||||||||||||||
                                    AAAGTG TACAACCGGTCCGACCA
                                      A
GAM320  FLJ20280  3'  ACCAGCCTTGCCAACACAGTGA 35323       CA      C
                AA                  TTTCAC  TGTTGGC AGGCTGGT
                                    ||||||  ||||||| ||||||||
                                    AAAGTG  ACAACCG TCCGACCA
                                      AC      T
GAM320  FLJ20306  3'  CTGGCCAACGTGGTGAAA    35392
                                    TTTCACCATGTTGGCCAG
                                    ||||||||||||||||||
                                    AAAGTGGTGCAACCGGTC

GAM320  FLJ20340  3'  ACCAGCCTGGCCAACATG    35446
                                    CATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||
                                    GTACAACCGGTCCGACCA

GAM320  FLJ20340  3'  ACTGTCCTGGACAACATGGTGA 35447           G    C
                AA                  TTTCACCATGTTG CCAGG TGGT
                                    |||||||||||| ||||| ||||
                                    AAAGTGGTACAAC GGTCC GTCA
                                          A    T
GAM320  FLJ20359  3'  ACCAGCCTGCCCAACATGGTGA 35510           C
                AA                  TTTCACCATGTTGG CAGGCTGGT
                                    |||||||||||||| |||||||||
                                    AAAGTGGTACAACC GTCCGACCA
                                          C
GAM320  FLJ20413  3'  ACCATCCTGGCTAACACGGTGA 35587       A        C
                AA                  TTTCACC TGTTGGCCAGG TGGT
                                    ||||||| |||||||||| ||||
                                    AAAGTGG ACAATCGGTCC ACCA
                                       C         T
GAM320  FLJ20464  3'  ACCAGCCTGACCAACATGGAGA 35677     A       C
                AA                  TTTC CCATGTTGG CAGGCTGGT
                                    |||| ||||||||| |||||||||
                                    AAAG GGTACAACC GTCCGACCA
                                      A       A
GAM320  FLJ20464  3'  ACCAGTCTGACCAACACGGAGA 35679     A  A     C
                AA                  TTTC CC TGTTGG CAGGCTGGT
                                    |||| || |||||| |||||||||
                                    AAAG GG ACAACC GTCTGACCA
                                      A  C     A
GAM320  FLJ20627  3'  AGCCTGGCCAACATGGTGAAA  35906
                                    TTTCACCATGTTGGCCAGGCT
                                    |||||||||||||||||||||
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                                AAAGTGGTACAACCGGTCCGA

GAM320  FLJ20671  3'  AGCCTGGGCAACATGGTGAAA  35932            G
                                TTTCACCATGTTG CCAGGCT
                                ||||||||||||| |||||||
                                AAAGTGGTACAAC GGTCCGA
                                      G
GAM320  FLJ20686  3'  ACCAGCCTGGCCAACACGGTGA 35950        A
          GA                      TTTCACC TGTTGGCCAGGCTGGT
                                ||||||| ||||||||||||||||
                                AGAGTGG ACAACCGGTCCGACCA
                                   C
GAM320  FLJ20694  3'  ACCAGCCTGGCCAACATATAGT 35967      C__
          GA                      TCAC   ATGTTGGCCAGGCTGGT
                                ||||   ||||||||||||||||
                                AGTG   TACAACCGGTCCGACCA
                                  ATA
GAM320  FLJ20700  3'  ACCAGCCTGTTCAACATGGCGA 35993      A       GC
          AA                      TTTC CCATGTTG  CAGGCTGGT
                                |||| ||||||||  |||||||||
                                AAAG GGTACAAC  GTCCGACCA
                                  C       TT
GAM320  FLJ20700  3'  CTGGCCAACAGAATGAAA    36008       CCA
                                TTTCA   TGTTGGCCAG
                                |||||   ||||||||||
                                AAAGT   ACAACCGGTC
                                   AAG
GAM320  FLJ20783  3'  ACCATCCTGGCTAACACGGTGA 36091        A         C
          AA                      TTTCACC TGTTGGCCAGG TGGT
                                ||||||| |||||||||| ||||
                                AAAGTGG ACAATCGGTCC ACCA
                                   C         T
GAM320  FLJ20802  3'  ACCAGCCGGGCCAGCATGGTGA 36103              A
          AA                      TTTCACCATGTTGGCC GGCTGGT
                                |||||||||||||| |||||||
                                AAAGTGGTACGACCGG CCGACCA
                                      G
GAM320  FLJ20808  3'  ACCATCCTGGCTAACACGGTGA 36115        A         C
          AA                      TTTCACC TGTTGGCCAGG TGGT
                                ||||||| |||||||||| ||||
                                AAAGTGG ACAATCGGTCC ACCA
                                   C         T
GAM320  FLJ20825  3'  ACCAGCCTGACCAACATGGAGA 36138      A       C
          AA                      TTTC CCATGTTGG CAGGCTGGT
                                |||| ||||||||| |||||||||
                                AAAG GGTACAACC GTCCGACCA
                                  A       A
GAM320  FLJ20972  3'  ACCAGCCTGACCAACATGGAGA 47376      A       C
          AA                      TTTC CCATGTTGG CAGGCTGGT
                                |||| ||||||||| |||||||||
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                                AAAG GGTACAACC GTCCGACCA
                                  A       A
GAM320  FLJ21106  3'  CCTGGCTAACACGGTGAAA   47693       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| |||||||||||
                                AAAGTGG ACAATCGGTCC
                                    C
GAM320  FLJ21162  3'  ACCAGCCTGGCCAGCATGGTGA 46363
            AA                    TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACGACCGGTCCGACCA

GAM320  FLJ21240  3'  ACCAGCCTGACCAACGTGGAGA 46257     A       C
            AA                    TTTC CCATGTTGG CAGGCTGGT
                                  |||| ||||||||| |||||||||
                                  AAAG GGTGCAACC GTCCGACCA
                                    A       A
GAM320  FLJ21369  3'  ACCAGCCTGGCCAACATGGTGA 46045
            GA                    TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AGAGTGGTACAACCGGTCCGACCA

GAM320  FLJ21551  3'  CCTGGCCAACCTGGTGAAA   46035       T
                                TTTCACCA GTTGGCCAGG
                                |||||||| ||||||||||
                                AAAGTGGT CAACCGGTCC
                                    C
GAM320  FLJ21657  3'  ACCAGCCTGGCCAACATGGTGA 42792
            AA                    TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  FLJ21687  3'  CAGCCTGGCCAAGATGGTGAAA 46293         G
                                TTTCACCAT TTGGCCAGGCTG
                                ||||||||| ||||||||||||
                                AAAGTGGTA AACCGGTCCGAC
                                    G
GAM320  FLJ21777  3'  ACCAGCCTGGCCAACATGGTGA 50829
            AA                    TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  FLJ21870  3'  ACCAGCCTGGCCAACATGGTGA 43739
            AA                    TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  FLJ22054  3'  ATCAGCCTGGCCAACATGGTGA 96044
            AA                    TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
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                                AAAGTGGTACAACCGGTCCGACTA

GAM320  FLJ22167  3'  ACCAGCCTGGCCAACATAGTGA 44854       C
            AA                  TTTCAC ATGTTGGCCAGGCTGGT
                                |||||| ||||||||||||||||||
                                AAAGTG TACAACCGGTCCGACCA
                                  A
GAM320  FLJ22313  3'  ACCAGCCTGGCAAACATGGCGA 42573     A     G
            AA                  TTTC CCATGTT GCCAGGCTGGT
                                |||| ||||||| ||||||||||
                                AAAG GGTACAA CGGTCCGACCA
                                  C      A
GAM320  FLJ22474  3'  ACCAGCCTGGCCAACACGGTGA 45608       A
            AA                  TTTCACC TGTTGGCCAGGCTGGT
                                ||||||| ||||||||||||||||
                                AAAGTGG ACAACCGGTCCGACCA
                                   C
GAM320  FLJ22692  3'  ACCAGCCTGGCCAACACAGT   47474    CA
                                AC  TGTTGGCCAGGCTGGT
                                ||  ||||||||||||||||
                                TG  ACAACCGGTCCGACCA
                                 AC
GAM320  FLJ22814  3'  ACCAGCCTGGCCAGCATGGCGA 46707     A
            AA                  TTTC CCATGTTGGCCAGGCTGGT
                                |||| ||||||||||||||||||
                                AAAG GGTACGACCGGTCCGACCA
                                  C
GAM320  FLJ22814  3'  ACCATCCTGGCTAACATGGTGA 46708              C
            AA                  TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
                                AAAGTGGTACAATCGGTCC ACCA
                                           T
GAM320  FLJ22965  3'  GCCTGGGCAACATGGTGAAA   42300          G
                                TTTCACCATGTTG CCAGGC
                                |||||||||||| ||||||
                                AAAGTGGTACAAC GGTCCG
                                      G
GAM320  FLJ23022  3'  ACCAGCCTGGCCAACATGGTGA 47488
            AA                  TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGACCA

GAM320  FLJ23040  3'  ACCAGCCTGGCCAACATGATGA 47979       C
            AA                  TTTCA CATGTTGGCCAGGCTGGT
                                ||||| ||||||||||||||||||
                                AAAGT GTACAACCGGTCCGACCA
                                  A
GAM320  FLJ23042  3'  ACCAGCCTAGGCAACACAGTGA 47931       CA    G _
            AA                  TTTCAC  TGTTG CC AGGCTGGT
                                ||||||  ||||| || ||||||||
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                                AAAGTG  ACAAC GG TCCGACCA
                                  AC    _ A
GAM320  FLJ23042  3'  AGCCTGACCAACATGGAGAAA  47934      A       C
                                TTTC CCATGTTGG CAGGCT
                                |||| ||||||||| ||||||
                                AAAG GGTACAACC GTCCGA
                                  A       A
GAM320  FLJ23112  3'  ACCAACCTGGCCAACATGTTGA 46806      C          C
                AA                TTTCA CATGTTGGCCAGG TGGT
                                  ||||| |||||||||||| ||||
                                  AAAGT GTACAACCGGTCC ACCA
                                    T          A
GAM320  FLJ23235  3'  ACCATCCTGGCCAACATGGTGA 46872               C
                AA                TTTCACCATGTTGGCCAGG TGGT
                                  |||||||||||||||||| ||||
                                  AAAGTGGTACAACCGGTCC ACCA
                                             T
GAM320  FLJ23360  3'  ACCAGCCTGGCCACATGGTG   43820        T
                                  CACCATGT GGCCAGGCTGGT
                                  |||||||| ||||||||||||
                                  GTGGTACA CCGGTCCGACCA
                                  _
GAM320  FLJ23499  3'  ACCAGCCTGACCAACATGGTGA 43120            C
                AA                TTTCACCATGTTGG CAGGCTGGT
                                  |||||||||||||| |||||||||
                                  AAAGTGGTACAACC GTCCGACCA
                                        A
GAM320  FLJ23499  3'  ACCAGCCTGGCCAATGTGGTGA 43121
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTGTAACCGGTCCGACCA

GAM320  FLJ23537  3'  CCTGACCAACATGGAGAAA   46541      A       C
                                  TTTC CCATGTTGG CAGG
                                  |||| ||||||||| ||||
                                  AAAG GGTACAACC GTCC
                                    A       A
GAM320  FLJ25012  3'  ACCATGCTGGCTAACATGGTGA 58704               G _
                AA                TTTCACCATGTTGGCCAG C TGGT
                                  |||||||||||||||||| | ||||
                                  AAAGTGGTACAATCGGTC G ACCA
                                        _ T
GAM320  FLJ25012  3'  ACTAGCCTGGGCAACATGGTGA 58705            G
                AA                TTTCACCATGTTG CCAGGCTGGT
                                  |||||||||||| ||||||||||
                                  AAAGTGGTACAAC GGTCCGATCA
                                        G
GAM320  FLJ30092  3'  ACCAGCCTGGGCAACATGGCGA 59337      A       G
                GA                TTTC CCATGTTG CCAGGCTGGT
                                  |||| |||||||| ||||||||||
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                                AGAG GGTACAAC GGTCCGACCA
                                  C       G
GAM320  FLJ30681  3'  ACCAGCCTGACCAACATGGTGA 93428            C
           AA                     TTTCACCATGTTGG CAGGCTGGT
                                  ||||||||||||| |||||||||
                                  AAAGTGGTACAACC GTCCGACCA
                                         A
GAM320  FLJ31168  3'  ACCAGCCTGGCCAACATGGTGA 59173
           AA                     TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  FLJ31455  3'  ACCAGCCTGGCCAACATGGTGA 59276
           AA                     TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  FLJ31455  3'  ACCAGCCTGGCTAATATGGTGA 59277
           AA                     TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTATAATCGGTCCGACCA

GAM320  FLJ31737  3'  ACCAGCCTGGCCAACATGGTGA 59343
           AA                     TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  FLJ31952  3'  ACCAGCTTGGCCAACATGGAGA 59039      A
           AA                     TTTC CCATGTTGGCCAGGCTGGT
                                  |||| ||||||||||||||||||
                                  AAAG GGTACAACCGGTTCGACCA
                                    A
GAM320  FLJ32915  5'  ATCAGCCTGGCCAACATGGTGA 59426
           AA                     TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACTA

GAM320  FRSB      3'  ATCAGCCTGACCAACATGATGA 20288       C       C
           AA                     TTTCA CATGTTGG CAGGCTGGT
                                  ||||| |||||||| |||||||||
                                  AAAGT GTACAACC GTCCGACTA
                                    A       A
GAM320  FUSIP1    3'  ACCAGCCTGACCAACACGGTGA 55031        A     C
           AA                     TTTCACC TGTTGG CAGGCTGGT
                                  ||||||| |||||| |||||||||
                                  AAAGTGG ACAACC GTCCGACCA
                                     C     A
GAM320  GALNT6    3'  ACCAGCCTGGACTACATGGTGA 24236           TGG
           AA                     TTTCACCATGT   CCAGGCTGGT
                                  ||||||||||   ||||||||||
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                                AAAGTGGTACA  GGTCCGACCA
                                     TCA
GAM320  GLTP    3'  ACCAGCCTGGCCAACATGGTGA 33577
            AA                   TTTCACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||||||
                                 AAAGTGGTACAACCGGTCCGACCA

GAM320  GNB4    3'  ACCAGCCTACCCAACATGGTGA 41561          CC
            AA                   TTTCACCATGTTGG AGGCTGGT
                                 |||||||||||||| ||||||||
                                 AAAGTGGTACAACC TCCGACCA
                                       CA
GAM320  GP5     3'  CAGCTGGCCAAGATGGTGAAA 16864       G    G
                                 TTTCACCAT TTGGCCAG CTG
                                 ||||||||| |||||||| |||
                                 AAAGTGGTA AACCGGTC GAC
                                     G    _
GAM320  GTPBP5  3'  ACCATCCTGGCTAACACAGTGA 65963     CA     C
            AA                   TTTCAC TGTTGGCCAGG TGGT
                                 ||||||  |||||||||||| ||||
                                 AAAGTG ACAATCGGTCC ACCA
                                    AC       T
GAM320  GTSE1   3'  ACCAGCCTGGGAAATATAGTGA 33560     C   GG
            AA                   TTTCAC ATGTT CCAGGCTGGT
                                 |||||| |||||  ||||||||||
                                 AAAGTG TATAA GGTCCGACCA
                                    A   AG
GAM320  HES2    3'  ACCATCTTGGCTAACACGGTGA 39365     A      C
            AA                   TTTCACC TGTTGGCCAGG TGGT
                                 ||||||| |||||||||||| ||||
                                 AAAGTGG ACAATCGGTTC ACCA
                                    C       T
GAM320  HIC     3'  ACCAGCCAGGGCAACATGGTGA 68039         G  A
            AA                   TTTCACCATGTTG CC GGCTGGT
                                 |||||||||||| || |||||||
                                 AAAGTGGTACAAC GG CCGACCA
                                       G  A
GAM320  HIG2    3'  ACCAGCCTCGCCAACATGGCGA 26193    A      C
            AA                   TTTC CCATGTTGGC AGGCTGGT
                                 |||| |||||||||| ||||||||
                                 AAAG GGTACAACCG TCCGACCA
                                   C       C
GAM320  HRH4    3'  ACCATCCTGGCCAACATGGTGA 41520          C
            AA                   TTTCACCATGTTGGCCAGG TGGT
                                 |||||||||||||||||| ||||
                                 AAAGTGGTACAACCGGTCC ACCA
                                          T
GAM320  HSA250303 3'  ACCAGGCTGGCCAACATGGT  38016        G
                                 ACCATGTTGGCCAG CTGGT
                                 |||||||||||||| |||||
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                                TGGTACAACCGGTC GACCA
                                       G
GAM320  HSH2     3'  ACCAGCCTGGCCAACATGGTGA 52733
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  HSPC031  3'  ACCAGCCTGGCCAACATGGTGA 32744
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  HSPC043  3'  ACCAGCCTGGCCAACATGGTGA 68344
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  HYPK     3'  ACCAGCCTGGCCAACATGTGAA 33510       C
                A                  TTTCAC ATGTTGGCCAGGCTGGT
                                   |||||| ||||||||||||||||
                                   AAAGTG TACAACCGGTCCGACCA
                                          _
GAM320  ICAM4    3'  ACCAGCCTGGACAACATAGTGA 9530        C     G
                GA                 TTTCAC ATGTTG CCAGGCTGGT
                                   |||||| |||||| ||||||||||
                                   AGAGTG TACAAC GGTCCGACCA
                                      A     A
GAM320  ICAM4    3'  ACCAGCCTGGACAACATAGTGA 42586       C     G
                GA                 TTTCAC ATGTTG CCAGGCTGGT
                                   |||||| |||||| ||||||||||
                                   AGAGTG TACAAC GGTCCGACCA
                                      A     A
GAM320  IL10RB   3'  ACCAGCCTGGCCAATATGGTGA 7121
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTATAACCGGTCCGACCA

GAM320  IMAGE:4907098 3'  ACCAGCCTGGCCAATATGGTGA 93322
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTATAACCGGTCCGACCA

GAM320  INE1     3'  ACCAGCCTGGGCAGCATG    14755       G
                                  CATGTTG CCAGGCTGGT
                                  |||||||  ||||||||||
                                  GTACGAC GGTCCGACCA
                                     G
GAM320  JAM1     3'  AGCCTGACCAACATGGAGAAA  34217     A       C
                                  TTTC CCATGTTGG CAGGCT
                                  ||||  |||||||| ||||||
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                                AAAG GGTACAACC GTCCGA
                                  A       A
GAM320  JAM1    3' AGCCTGACCAACATGGAGAAA 58508     A       C
                                TTTC CCATGTTGG CAGGCT
                                |||| ||||||||| ||||||
                                AAAG GGTACAACC GTCCGA
                                  A       A
GAM320  JAM1    3' AGCCTGACCAACATGGAGAAA 58536     A       C
                                TTTC CCATGTTGG CAGGCT
                                |||| ||||||||| ||||||
                                AAAG GGTACAACC GTCCGA
                                  A       A
GAM320  JAM1    3' AGCCTGACCAACATGGAGAAA 58563     A       C
                                TTTC CCATGTTGG CAGGCT
                                |||| ||||||||| ||||||
                                AAAG GGTACAACC GTCCGA
                                  A       A
GAM320  KALI    3' ACCAGCCTGGCCAACTTGGTGA 54687         T
            AA                    TTTCACCA GTTGGCCAGGCTGGT
                                  |||||||| ||||||||||||||||
                                  AAAGTGGT CAACCGGTCCGACCA
                                     T
GAM320  KBRAS2  3' ACCAGCCTGGCCAACATTGTGA 34616       C
            AA                    TTTCAC ATGTTGGCCAGGCTGGT
                                  |||||| ||||||||||||||||
                                  AAAGTG TACAACCGGTCCGACCA
                                     T
GAM320  KCNH6   3' ACCATCCTGGCTAACACGGTGA 48565       A       C
            AA                    TTTCACC TGTTGGCCAGG TGGT
                                  ||||||| |||||||||| ||||
                                  AAAGTGG ACAATCGGTCC ACCA
                                     C        T
GAM320  KIAA0042 3' ACCGGCCTGGCCAACATGGTGA 30230
            AA                    TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGGCCA

GAM320  KIAA0057 3' ACCAGCCTGGCCAACATGGTGA 25396
            AA                    TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  KIAA0090 3' ACCAGCCTGGCCAACATGGTGA 89807
            AA                    TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  KIAA0159 3' ACCAGCCTGACCAACATGGAGA 30134     A       C
            AA                    TTTC CCATGTTGG CAGGCTGGT
                                  |||| ||||||||| |||||||||
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                                AAAG GGTACAACC GTCCGACCA
                                  A       A
GAM320  KIAA0184  3'  ACCATCCTGGCTAACATGGTGA 65802                C
                AA                TTTCACCATGTTGGCCAGG TGGT
                                  |||||||||||||||||| ||||
                                  AAAGTGGTACAATCGGTCC ACCA
                                             T
GAM320  KIAA0226  3'  ACCAGCCTGGCCAATGTGGTGA 64250
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTGTAACCGGTCCGACCA

GAM320  KIAA0266  3'  ACCAGCCTGAACAACATGGTGA 41631            GC
                AA                TTTCACCATGTTG  CAGGCTGGT
                                  ||||||||||||  |||||||||
                                  AAAGTGGTACAAC  GTCCGACCA
                                        AA
GAM320  KIAA0355  3'  ACCAGCCTGGCCAATATGGTGA 28695
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTATAACCGGTCCGACCA

GAM320  KIAA0419  3'  ACCAGCCTGACCAAACATGGCG 28856     A      _  C
                AA                TTC CCATGTT GG CAGGCTGGT
                                  ||| ||||||| || |||||||||
                                  AAG GGTACAA CC GTCCGACCA
                                    C      A  A
GAM320  KIAA0420  3'  ACCAGCCTGGGCAACATAGTGA 64080       C     G
                GA                TTTCAC ATGTTG CCAGGCTGGT
                                  |||||| |||||| ||||||||||
                                  AGAGTG TACAAC GGTCCGACCA
                                     A     G
GAM320  KIAA0445  5'  ACCAGCCTGACCAACGTGGAGA 28634      A       C
                AA                TTTC CCATGTTGG CAGGCTGGT
                                  |||| ||||||||| |||||||||
                                  AAAG GGTGCAACC GTCCGACCA
                                    A       A
GAM320  KIAA0446  5'  ACCATCCTGGCTAACATGGTGA 69436                C
                AA                TTTCACCATGTTGGCCAGG TGGT
                                  |||||||||||||||||| ||||
                                  AAAGTGGTACAATCGGTCC ACCA
                                             T
GAM320  KIAA0447  3'  ACCAGCCTGGCCAACATGATGA 72102       C
                AA                TTTCA CATGTTGGCCAGGCTGGT
                                  ||||| ||||||||||||||||||
                                  AAAGT GTACAACCGGTCCGACCA
                                    A
GAM320  KIAA0472  3'  ACCAGCCTGGTAACATGGTGAA 72328            G
                A                  TTTCACCATGTTG CCAGGCTGGT
                                   |||||||||||| ||||||||||
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                                AAAGTGGTACAAT GGTCCGACCA
                                      _
GAM320  KIAA0472  3'  CAGCCTGGCCAACATGGTGAAA 72343
                                TTTCACCATGTTGGCCAGGCTG
                                |||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGAC

GAM320  KIAA0547  3'  ACCAGCCTGGCCAATATGGTGA 29584
              AA                  TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTATAACCGGTCCGACCA

GAM320  KIAA0547  3'  ACCATCCTGGTCAACATGGTGA 29585                C
              AA                  TTTCACCATGTTGGCCAGG TGGT
                                  |||||||||||||||||| ||||
                                  AAAGTGGTACAACTGGTCC ACCA
                                        T
GAM320  KIAA0557  3'  ACCATCCTGGCCAACATGGTGA 78540                C
              AA                  TTTCACCATGTTGGCCAGG TGGT
                                  |||||||||||||||||| ||||
                                  AAAGTGGTACAACCGGTCC ACCA
                                        T
GAM320  KIAA0563  3'  ACCATCCTGGCTAACATGGTGA 29864                C
              AA                  TTTCACCATGTTGGCCAGG TGGT
                                  |||||||||||||||||| ||||
                                  AAAGTGGTACAATCGGTCC ACCA
                                        T
GAM320  KIAA0565  3'  ACCAACCTCCAACATGGTGAAA 67428             CC  C
                                TTTCACCATGTTGG  AGG TGGT
                                ||||||||||||||  ||| ||||
                                AAAGTGGTACAACC  TCC ACCA
                                      __  A
GAM320  KIAA0570  3'  ACCAGCCAAGGCAACATGGTGA 28846              G  A_
              AA                  TTTCACCATGTTG CC  GGCTGGT
                                  |||||||||||||  ||  |||||||
                                  AAAGTGGTACAAC GG  CCGACCA
                                      _  AA
GAM320  KIAA0596  3'  ATCAGCCTGGCCAACATGGTGA 63482
              AA                  TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACTA

GAM320  KIAA0618  3'  ACCAGCCTGGCCAACATGGAGA 29840      A
              AA                  TTTC CCATGTTGGCCAGGCTGGT
                                  |||| ||||||||||||||||||
                                  AAAG GGTACAACCGGTCCGACCA
                                    A
GAM320  KIAA0628  3'  ACCAGCCTGGCCGGGGTGGTGA 29524          G
              AA                  TTTCACCAT TTGGCCAGGCTGGT
                                  |||||||| ||||||||||||||
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                                AAAGTGGTG GGCCGGTCCGACCA
                                     G
GAM320  KIAA0694 3' ACCAGCCTGGGCAACATAGTGA 72958       C     G
              GA                  TTTCAC ATGTTG CCAGGCTGGT
                                  |||||| |||||| ||||||||||
                                  AGAGTG TACAAC GGTCCGACCA
                                     A     G
GAM320  KIAA0694 3' ACCAGCTTGGCCAACATGGTGA 72959
              AG                  TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  GAAGTGGTACAACCGGTTCGACCA

GAM320  KIAA0752 3' ACCAGCCTGACTGACATTGAGA 67628       CC    TG C
                                  TTTCA  ATGT  G CAGGCTGGT
                                  |||||  ||||  | |||||||||
                                  AGAGT  TACA  C GTCCGACCA
                                     __   GT A
GAM320  KIAA0794 3' CCAGCCTGAGCAACATGGTGAA 81228           GC
              A                    TTTCACCATGTTG  CAGGCTGG
                                  ||||||||||||  ||||||||
                                  AAAGTGGTACAAC  GTCCGACC
                                        GA
GAM320  KIAA0795 3' ACCAGCCTGGCCAACATGGTGA 47227
              AA                  TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  KIAA0798 3' ACCAGCCTGACCAACATGGTGA 28437           C
              G                    TTCACCATGTTGG CAGGCTGGT
                                  ||||||||||||| |||||||||
                                  GAGTGGTACAACC GTCCGACCA
                                        A
GAM320  KIAA0825 3' ACCAGCTTGACCAACATGGAGA 61678      A       C
              AA                  TTTC CCATGTTGG CAGGCTGGT
                                  |||| ||||||||| |||||||||
                                  AAAG GGTACAACC GTTCGACCA
                                     A       A
GAM320  KIAA0831 3' AGCCTGGCTAACATGGTGAAA  30627
                                  TTTCACCATGTTGGCCAGGCT
                                  |||||||||||||||||||||
                                  AAAGTGGTACAATCGGTCCGA

GAM320  KIAA0872 3' ACCAGCCTGGCCAGCATGGCGA 30733      A
              AA                  TTTC CCATGTTGGCCAGGCTGGT
                                  |||| ||||||||||||||||||
                                  AAAG GGTACGACCGGTCCGACCA
                                     C
GAM320  KIAA0872 3' CCAGCCTGACCAACATGGTGAA 30747           C
              A                    TTTCACCATGTTGG CAGGCTGG
                                  |||||||||||||| ||||||||
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                                AAAGTGGTACAACC GTCCGACC
                                      A
GAM320  KIAA0884  3'  ACCAGTCTGGTCAACATGGTGA 70743
            AA                  TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTACAACTGGTCTGACCA

GAM320  KIAA0889  3'  ACCGGTCTGGCCAACATGGTGA 31746
            AA                  TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCTGGCCA

GAM320  KIAA0889  3'  ATCAGCCTGGCCAATATGGTGA 31757
            AA                  TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTATAACCGGTCCGACTA

GAM320  KIAA0894  3'  ACCAGCGTGGCCAACATGATGA 30321      C         G
            AA                  TTTCA CATGTTGGCCA GCTGGT
                                ||||| |||||||||| ||||||
                                AAAGT GTACAACCGGT CGACCA
                                  A         G
GAM320  KIAA0907  3'  ACCAGCGTGGCTAACACGGTGA 30858       A       G
            AA                  TTTCACC TGTTGGCCA GCTGGT
                                ||||||| ||||||||| ||||||
                                AAAGTGG ACAATCGGT CGACCA
                                   C       G
GAM320  KIAA0907  3'  ACCAGCTTGGCCAACATAGTGA 30859       C
            AA                  TTTCAC ATGTTGGCCAGGCTGGT
                                ||||||| ||||||||||||||||
                                AAAGTG TACAACCGGTTCGACCA
                                   A
GAM320  KIAA0930  3'  ACCAGCCTGACTAACATGCTGA 71059      C       C
            AA                  TTTCA CATGTTGG CAGGCTGGT
                                ||||| |||||||| |||||||||
                                AAAGT GTACAATC GTCCGACCA
                                  C       A
GAM320  KIAA0953  3'  ACCAGCCTGATCAACATGGTGA 67318           GC
            AA                  TTTCACCATGTTG  CAGGCTGGT
                                ||||||||||||  |||||||||
                                AAAGTGGTACAAC  GTCCGACCA
                                      TA
GAM320  KIAA0961  3'  ACCAGCCTGACCATCATGGTGA 30383         T   C
            AA                  TTTCACCATG TGG CAGGCTGGT
                                |||||||||| ||| |||||||||
                                AAAGTGGTAC ACC GTCCGACCA
                                     T   A
GAM320  KIAA0981  3'  ACCAGCCTGGCCAACATGACGA 62080      AC
            AA                  TTTC  CATGTTGGCCAGGCTGGT
                                ||||  ||||||||||||||||||
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                                AAAG  GTACAACCGGTCCGACCA
                                  CA
GAM320  KIAA1001 3' ACCAGCCTGGCCAACATGGTGA 30996
                AA                  TTTCACCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||||||||
                                    AAAGTGGTACAACCGGTCCGACCA

GAM320  KIAA1001 3' ACCAGCCTGGCCAACATGGTGA 30997
                AA                  TTTCACCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||||||||
                                    AAAGTGGTACAACCGGTCCGACCA

GAM320  KIAA1017 3' ACCAGCCTGGGCAACATAGTGA 24264       C     G
                GA                  TTTCAC ATGTTG CCAGGCTGGT
                                    ||||||| |||||| ||||||||||
                                    AGAGTG TACAAC GGTCCGACCA
                                      A     G
GAM320  KIAA1032 3' ACCAGCCTGGCCAACATGGCGA 66718      A
                AA                  TTTC CCATGTTGGCCAGGCTGGT
                                    |||| ||||||||||||||||||
                                    AAAG GGTACAACCGGTCCGACCA
                                      C
GAM320  KIAA1056 3' ACCAACCTGGCCAATGTGG   30306             C
                                    CCATGTTGGCCAGG TGGT
                                    |||||||||||||| ||||
                                    GGTGTAACCGGTCC ACCA
                                          A
GAM320  KIAA1086 3' ACCGGCCTGGTCAACATGGTGA 71277
                AA                  TTTCACCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||||||||
                                    AAAGTGGTACAACTGGTCCGGCCA

GAM320  KIAA1117 3' ACCAGCCTAGGCAACATAGTGA 61770       C     G _
                GA                  TTTCAC ATGTTG CC AGGCTGGT
                                    |||||| |||||| || ||||||||
                                    AGAGTG TACAAC GG TCCGACCA
                                      A     _ A
GAM320  KIAA1130 3' ACCAGCCTGACCAAAATGGTGA 63073         G   C
                AA                  TTTCACCAT TTGG CAGGCTGGT
                                    |||||||| |||| |||||||||
                                    AAAGTGGTA AACC GTCCGACCA
                                        A   A
GAM320  KIAA1160 3' ACCATCCTGGCCAACATGGTGA 40748               C
                AA                  TTTCACCATGTTGGCCAGG TGGT
                                    |||||||||||||||||| ||||
                                    AAAGTGGTACAACCGGTCC ACCA
                                              T
GAM320  KIAA1164 3' ACCAGCCTGGCCAACATGG   70028
                                    CCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||
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                                GGTACAACCGGTCCGACCA

GAM320  KIAA1164  3' ACCAGCCTGGCCAGCATGGTGA 70029
             AA                 TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTACGACCGGTCCGACCA

GAM320  KIAA1191  3' ACCAGCCTGGCCAACATGGTGA 40327
             AA                 TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGACCA

GAM320  KIAA1202  3' ACCATCCTGGCTAACACGGTGA 72480       A       C
             AA                 TTTCACC TGTTGGCCAGG TGGT
                                ||||||| |||||||||| ||||
                                AAAGTGG ACAATCGGTCC ACCA
                                   C         T
GAM320  KIAA1204  3' ACCAGCCTGGGCAACACAGCGA 69734     ACCA    G
             GA                 TTTC   TGTTG CCAGGCTGGT
                                ||||   ||||| ||||||||||
                                AGAG   ACAAC GGTCCGACCA
                                  CGAC    G
GAM320  KIAA1228  3' ACCAGCCTGGCCAACATGGAGA 65660     A
             AA                 TTTC CCATGTTGGCCAGGCTGGT
                                |||| ||||||||||||||||||
                                AAAG GGTACAACCGGTCCGACCA
                                  A
GAM320  KIAA1244  3' ACCAGGCTGGACAACATGGTGA 72436          G   G
             AA                 TTTCACCATGTTG CCAG CTGGT
                                |||||||||||| |||| |||||
                                AAAGTGGTACAAC GGTC GACCA
                                       A   G
GAM320  KIAA1253  3' ACCAGCCTGGGCAACATGGTGA 93545          G
             AA                 TTTCACCATGTTG CCAGGCTGGT
                                |||||||||||| |||||||||
                                AAAGTGGTACAAC GGTCCGACCA
                                       G
GAM320  KIAA1257  3' CAGCCTGGCTAACACGGTGAAA 63394       A
                                TTTCACC TGTTGGCCAGGCTG
                                ||||||| |||||||||||||
                                AAAGTGG ACAATCGGTCCGAC
                                   C
GAM320  KIAA1271  3' ACCAGCCTGGCCAACAGGGTGA 70123       A
             AA                 TTTCACC TGTTGGCCAGGCTGGT
                                ||||||| ||||||||||||||||
                                AAAGTGG ACAACCGGTCCGACCA
                                   G
GAM320  KIAA1276  3' ACCAGCCTGGCCAATATGGTGA 67026
             AA                 TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
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                                AAAGTGGTATAACCGGTCCGACCA

GAM320  KIAA1277 3' ATCAGCCTGGCCAACATGG   65070
                                CCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||
                                GGTACAACCGGTCCGACTA

GAM320  KIAA1328 3' ACCATCCTGGCTAACACGGTGA 62312       A        C
           AA                    TTTCACC TGTTGGCCAGG TGGT
                                 ||||||| |||||||||| |||| |
                                 AAAGTGG ACAATCGGTCC ACCA
                                    C         T
GAM320  KIAA1348 3' ACCAGCCTGACCAACATGGAGA 69114     A       C
           AA                    TTTC CCATGTTGG CAGGCTGGT
                                 |||| ||||||||| |||||||||
                                 AAAG GGTACAACC GTCCGACCA
                                   A       A
GAM320  KIAA1364 3' ACCAGCCTGGCCAACATAATGA 64340      CC
           AA                    TTTCA  ATGTTGGCCAGGCTGGT
                                 |||||  ||||||||||||||||||
                                 AAAGT  TACAACCGGTCCGACCA
                                   AA
GAM320  KIAA1404 3' ACCAGCCTGACCAACATGGCGA 62678     A       C
           AA                    TTTC CCATGTTGG CAGGCTGGT
                                 |||| ||||||||| |||||||||
                                 AAAG GGTACAACC GTCCGACCA
                                   C       A
GAM320  KIAA1456 5' ACCAACCTGACCAACATGGAGA 67521     A       C   C
           AA                    TTTC CCATGTTGG CAGG TGGT
                                 |||| ||||||||| |||| ||||
                                 AAAG GGTACAACC GTCC ACCA
                                   A       A   A
GAM320  KIAA1456 3' ACCAGCCTGACCAACATGGTGA 67522           C
           AA                    TTTCACCATGTTGG CAGGCTGGT
                                 |||||||||||||| |||||||||
                                 AAAGTGGTACAACC GTCCGACCA
                                        A
GAM320  KIAA1473 3' ACCAGCCTGACCAACATGGAGA 71201     A       C
           AA                    TTTC CCATGTTGG CAGGCTGGT
                                 |||| ||||||||| |||||||||
                                 AAAG GGTACAACC GTCCGACCA
                                   A       A
GAM320  KIAA1559 3' ACCAACCTGGTTAACATGGTGA 73439             C
           AA                    TTTCACCATGTTGGCCAGG TGGT
                                 |||||||||||||||||| ||||
                                 AAAGTGGTACAATTGGTCC ACCA
                                        A
GAM320  KIAA1559 3' ACCAGCCTGACCAACACTGAGA 73440      CCA    C
                                 TTTCA   TGTTGG CAGGCTGGT
                                 |||||   |||||| |||||||||
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                                AGAGT   ACAACC GTCCGACCA
                                  C__     A
GAM320  KIAA1614  3'  ACCAGTCTGGCCCACATGGTGA 70660          T
            AA                    TTTCACCATGT GGCCAGGCTGGT
                                  |||||||||||| ||||||||||||
                                  AAAGTGGTACA CCGGTCTGACCA
                                        C
GAM320  KIAA1630  3'  ACCAGCCTGGCCAACACGGTGA 38652       A
            AA                    TTTCACC TGTTGGCCAGGCTGGT
                                  ||||||| ||||||||||||||||
                                  AAAGTGG ACAACCGGTCCGACCA
                                     C
GAM320  KIAA1641  3'  ACCAGCCTGGCCAATATGGTGA 81015
            AA                    TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTATAACCGGTCCGACCA

GAM320  KIAA1649  3'  ACCAGCCTAACCAACGTGGT   51209          CC
                                  ACCATGTTGG  AGGCTGGT
                                  ||||||||||  ||||||||
                                  TGGTGCAACC  TCCGACCA
                                        AA
GAM320  KIAA1656  5'  ACCATCCTGGCCAACATGGTGA 66355               C
            AA                    TTTCACCATGTTGGCCAGG TGGT
                                  |||||||||||||||||| ||||
                                  AAAGTGGTACAACCGGTCC ACCA
                                           T
GAM320  KIAA1674  3'  ACCATCCTGGCTAACACGGTGA 69324       A       C
            AA                    TTTCACC TGTTGGCCAGG TGGT
                                  ||||||| |||||||||| ||||
                                  AAAGTGG ACAATCGGTCC ACCA
                                     C         T
GAM320  KIAA1715  3'  ACCAGCCTGACCAACGTGGAGA 68680     A       C
            AA                    TTTC CCATGTTGG CAGGCTGGT
                                  |||| ||||||||| |||||||||
                                  AAAG GGTGCAACC GTCCGACCA
                                    A       A
GAM320  KIAA1724  3'  ACCAACCTGAGCAACATGGCGA 67604     A      GC   C
            AA                    TTTC CCATGTTG  CAGG TGGT
                                  |||| ||||||||  |||| ||||
                                  AAAG GGTACAAC  GTCC ACCA
                                    C       GA   A
GAM320  KIAA1727  3'  ACCAGCCTAGGCAACATGGAGA 64746     A      G _
            AA                    TTTC CCATGTTG CC AGGCTGGT
                                  |||| |||||||| || ||||||||
                                  AAAG GGTACAAC GG TCCGACCA
                                    A       _ A
GAM320  KIAA1751  3'  ACCAGCCTGGCCAACATGGTGA 72147
            AA                    TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
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                                AAAGTGGTACAACCGGTCCGACCA

GAM320  KIAA1811  5'  ACCAGCCTGACCAACATGGTGA 65414           C
              AA                  TTTCACCATGTTGG CAGGCTGGT
                                  |||||||||||||| |||||||||
                                  AAAGTGGTACAACC GTCCGACCA
                                        A
GAM320  KIAA1821  3'  ACCAGCCTGGGCAACATAGTGA 72253     C     G
                                  TCAC ATGTTG CCAGGCTGGT
                                  |||| |||||| ||||||||||
                                  AGTG TACAAC GGTCCGACCA
                                    A     G
GAM320  KIAA1829  3'  ACCAGCCTGACCAACATGGAGA 62624     A       C
              AA                  TTTC CCATGTTGG CAGGCTGGT
                                  |||| ||||||||| |||||||||
                                  AAAG GGTACAACC GTCCGACCA
                                    A       A
GAM320  KIAA1841  3'  ACCAGCCTGGCCAACGTGGTGA 80842
              AA                  TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTGCAACCGGTCCGACCA

GAM320  KIAA1872  3'  ACCAGCCTGGTGAACATGGCGA 63584     A     G
              AA                  TTTC CCATGTT GCCAGGCTGGT
                                  |||| ||||||| ||||||||||
                                  AAAG GGTACAA TGGTCCGACCA
                                    C     G
GAM320  KIAA1872  3'  ACCAGGCTGGCCAACATGGTGA 63586             G
              AA                  TTTCACCATGTTGGCCAG CTGGT
                                  |||||||||||||||| |||||
                                  AAAGTGGTACAACCGGTC GACCA
                                        G
GAM320  KIAA1872  3'  CAGCCTGGCCAACATGGTGAAA 63601
                                  TTTCACCATGTTGGCCAGGCTG
                                  |||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGAC

GAM320  KIAA1879  3'  ACCAGCCTGGCAACATGGCAAG 73924     CA      G
              A                    TTT  CCATGTTG CCAGGCTGGT
                                  |||  |||||||| ||||||||||
                                  AGA  GGTACAAC GGTCCGACCA
                                    AC      _
GAM320  KIAA1941  3'  ACCAGCCTGGCCAACATGGTGA 75331
              AA                  TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  KIAA1948  3'  ACCAGCCTGGGCAACATGGTGA 83286           G
              GA                  TTTCACCATGTTG CCAGGCTGGT
                                  |||||||||||| ||||||||||
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                                AGAGTGGTACAAC GGTCCGACCA
                                      G
GAM320  KIAA1948  3'  ACCATCCTGGCTAACACGGTGA 83287        A         C
           AA                   TTTCACC TGTTGGCCAGG TGGT
                                ||||||| |||||||||||| ||||
                                AAAGTGG ACAATCGGTCC ACCA
                                   C         T
GAM320  KIAA1951  3'  ACCATCCTGGCTAACACGGTGA 74143        A         C
           AA                   TTTCACC TGTTGGCCAGG TGGT
                                ||||||| |||||||||||| ||||
                                AAAGTGG ACAATCGGTCC ACCA
                                   C         T
GAM320  KIAA1954  3'  ACCAGCCTGGACAACATGGTGA 78221            G
           AA                   TTTCACCATGTTG CCAGGCTGGT
                                |||||||||||| ||||||||||
                                AAAGTGGTACAAC GGTCCGACCA
                                      A
GAM320  KIAA1969  3'  ACCATCCTGGCCAACATGGTGA 79469              C
           AA                   TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
                                AAAGTGGTACAACCGGTCC ACCA
                                         T
GAM320  KLHL8     3'  ACCAGCCTGACCAACATGGTGA 63502            C
           AA                   TTTCACCATGTTGG CAGGCTGGT
                                |||||||||||| |||||||||
                                AAAGTGGTACAACC GTCCGACCA
                                      A
GAM320  KR18      3'  ACCAGCCTGACCAACATGGAGA 53875      A       C
           AA                   TTTC CCATGTTGG CAGGCTGGT
                                |||| ||||||||| |||||||||
                                AAAG GGTACAACC GTCCGACCA
                                  A        A
GAM320  KR18      3'  ACCAGCCTGGCCAGCATAGTGA 53876       C
           AA                   TTTCAC ATGTTGGCCAGGCTGGT
                                |||||| ||||||||||||||||
                                AAAGTG TACGACCGGTCCGACCA
                                   A
GAM320  KREMEN    3'  ACCAGCCTGGCCAACATGGCGA 50221      A
           AA                   TTTC CCATGTTGGCCAGGCTGGT
                                |||| ||||||||||||||||||
                                AAAG GGTACAACCGGTCCGACCA
                                  C
GAM320  LAP1B     3'  ACCAGCCTGGCCAACATGGTGA 65186
           AA                   TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGACCA

GAM320  LIAS      3'  ACCAGCCTGGCCAACATGGTGA 71161
           AA                   TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
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                                AAAGTGGTACAACCGGTCCGACCA

GAM320  LIM      3'  ATCAGCCTGGCCAACATGGTGA 22315
              AA                  TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACTA

GAM320  LIM      3'  CCTGGCCAACATGGTGAAA   22323
                                  TTTCACCATGTTGGCCAGG
                                  |||||||||||||||||||
                                  AAAGTGGTACAACCGGTCC

GAM320  LRG      3'  ACCATCTTGGCTAACATGGTGA 54811              C
              AA                  TTTCACCATGTTGGCCAGG TGGT
                                  |||||||||||||||||| ||||
                                  AAAGTGGTACAATCGGTTC ACCA
                                                     T
GAM320  LRRFIP1  3'  CCAGCCTGGCCAACATGGTGAA 17610
              A                   TTTCACCATGTTGGCCAGGCTGG
                                  |||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACC

GAM320  LSR68    3'  ACCAGCCTGGCCGACATGGCGA 38546     A
              AA                  TTTC CCATGTTGGCCAGGCTGGT
                                  |||| ||||||||||||||||||
                                  AAAG GGTACAGCCGGTCCGACCA
                                    C
GAM320  LYSAL1   3'  ACCATCCTGGCTAACACGGTGA 18118       A       C
              AA                  TTTCACC TGTTGGCCAGG TGGT
                                  ||||||| |||||||||| ||||
                                  AAAGTGG ACAATCGGTCC ACCA
                                     C         T
GAM320  MACF1    3'  ACCAGCCTGGCCAACATGGTGA 53489
              AA                  TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  MACF1    3'  ACCATCCTGGCTAACACGGTGA 53490       A       C
              AA                  TTTCACC TGTTGGCCAGG TGGT
                                  ||||||| |||||||||| ||||
                                  AAAGTGG ACAATCGGTCC ACCA
                                     C         T
GAM320  MAWBP    3'  ACCAGCCTGGCCAACATGGTGA 42372
              AA                  TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  MAWBP    3'  ACCAGCCTGGGCAACACAGCGA 42373     ACCA    G
              GA                  TTTC   TGTTG CCAGGCTGGT
                                  ||||   ||||| ||||||||||
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                                AGAG   ACAAC GGTCCGACCA
                                  CGAC    G
GAM320  MCAM     3'  ACCATCCTGGCTAACACGGTGA 22453        A         C
                AA                  TTTCACC TGTTGGCCAGG TGGT
                                    ||||||| |||||||||||| ||||
                                    AAAGTGG ACAATCGGTCC ACCA
                                       C         T
GAM320  MED6     3'  ATCAGCCTGGGCAACATAGTGA 19611       C     G
                AA                  TTTCAC ATGTTG CCAGGCTGGT
                                    |||||| |||||| ||||||||||
                                    AAAGTG TACAAC GGTCCGACTA
                                      A     G
GAM320  MESDC2   3'  ACCAGCCTGGCCAACATGGTGA 72903
                AG                  TTTCACCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||||||||
                                    GAAGTGGTACAACCGGTCCGACCA

GAM320  MGC10765 3'  ACCAGCCTGACCAACATGGTGA 44551            C
                AA                  TTTCACCATGTTGG CAGGCTGGT
                                    |||||||||||||| |||||||||
                                    AAAGTGGTACAACC GTCCGACCA
                                           A
GAM320  MGC10771 3'  ACCAGCCTGGCCAACATGGTGA 44709
                AA                  TTTCACCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||||||||
                                    AAAGTGGTACAACCGGTCCGACCA

GAM320  MGC10814 5'  CAGCCTGGCCAACATGGTGAAA 52013
                                    TTTCACCATGTTGGCCAGGCTG
                                    |||||||||||||||||||||
                                    AAAGTGGTACAACCGGTCCGAC

GAM320  MGC10999 3'  ACCACCTGGCCAACATGGTGAA 51187              C
                A                    TTTCACCATGTTGGCCAGG TGGT
                                    |||||||||||||||||| ||||
                                    AAAGTGGTACAACCGGTCC ACCA
                                                 _
GAM320  MGC11287 5'  ACCAGCCTGGCCAACATGGT  49608
                                    ACCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||
                                    TGGTACAACCGGTCCGACCA

GAM320  MGC11386 3'  ACAAACCTGGCCAACATGGTGA 53050              CTG
                AA                  TTTCACCATGTTGGCCAGG  GT
                                    |||||||||||||||||  ||
                                    AAAGTGGTACAACCGGTCC  CA
                                           AAA
GAM320  MGC13017 3'  ACCAGCCTGGCCAACACGATGA 55567      CCA
                AA                  TTTCA  TGTTGGCCAGGCTGGT
                                    |||||  ||||||||||||||||
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                                AAAGT   ACAACCGGTCCGACCA
                                  AGC
GAM320  MGC13053  3'  CAGCCTAGCCAACATGGTGAAA 52100            C
                                TTTCACCATGTTGGC AGGCTG
                                ||||||||||||||| ||||||
                                AAAGTGGTACAACCG TCCGAC
                                      A
GAM320  MGC14126  3'  ACCAGCCTAGCCAACATGGTGA 52934            C
            AA                    TTTCACCATGTTGGC AGGCTGGT
                                ||||||||||||||| ||||||||
                                AAAGTGGTACAACCG TCCGACCA
                                      A
GAM320  MGC14407  3'  ACCAGCCTAGCCTACATGGTGA 52965          T  C
            AA                    TTTCACCATGT GGC AGGCTGGT
                                ||||||||||| ||| ||||||||
                                AAAGTGGTACA CCG TCCGACCA
                                      T  A
GAM320  MGC14799  3'  ACCAACCGACCAACATGGTGAA 51321            CCA  C
            A                     TTTCACCATGTTGG   GG TGGT
                                ||||||||||||||   || ||||
                                AAAGTGGTACAACC   CC ACCA
                                      AG_  A
GAM320  MGC15397  3'  ACCAGCCTGGCCAAGATGGTGA 55547         G
            AA                    TTTCACCAT TTGGCCAGGCTGGT
                                ||||||||| ||||||||||||||
                                AAAGTGGTA AACCGGTCCGACCA
                                     G
GAM320  MGC15606  3'  ACCAGCCTGGGCAACATAGT   59516    C     G
                                AC ATGTTG CCAGGCTGGT
                                || |||||| ||||||||||
                                TG TACAAC GGTCCGACCA
                                 A     G
GAM320  MGC16037  3'  ACCAGCCTGGCCAACTGCCTGA 52888       CCAT
            AA                    TTTCA    GTTGGCCAGGCTGGT
                                |||||    ||||||||||||||||
                                AAAGT    CAACCGGTCCGACCA
                                   CCGT
GAM320  MGC16142  3'  AGCCTGGCCAACGTGATGAAA  52259       C
                                TTTCA CATGTTGGCCAGGCT
                                ||||| ||||||||||||||||
                                AAAGT GTGCAACCGGTCCGA
                                   A
GAM320  MGC16332  3'  ACCAGCCTGGGCAACATAGTGA 57540       C     G
            GA                    TTTCAC ATGTTG CCAGGCTGGT
                                |||||| |||||| ||||||||||
                                AGAGTG TACAAC GGTCCGACCA
                                   A     G
GAM320  MGC16703  3'  ACCATCCTGGCTAACACGGTGA 73483        A         C
            AA                    TTTCACC TGTTGGCCAGG TGGT
                                ||||||| |||||||||| ||||
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                                AAAGTGG ACAATCGGTCC ACCA
                                   C         T
GAM320  MGC20235  3'  ACCAGCCTGGTCAACATGGTGA 59544
                AA                  TTTCACCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||||||||
                                    AAAGTGGTACAACTGGTCCGACCA

GAM320  MGC20496  3'  ACCAGCCTGGTCAACATGGT   54525
                                    ACCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||||
                                    TGGTACAACTGGTCCGACCA

GAM320  MGC2562   3'  ACCAGCCTGGCCAAACATGGTG 51412
                AAA                 TTTCACCATGTT GGCCAGGCTGGT
                                    |||||||||||| ||||||||||||
                                    AAAGTGGTACAA CCGGTCCGACCA
                                          A
GAM320  MGC2562   3'  ACCAGTTTGGGCAACATGGCGA 51413      A       G
                AA                  TTTC CCATGTTG CCAGGCTGGT
                                    |||| |||||||| ||||||||||
                                    AAAG GGTACAAC GGTTTGACCA
                                      C       G
GAM320  MGC2562   3'  ACCATCCTGCCCAACATGGTGA 51414             C    C
                AA                  TTTCACCATGTTGG CAGG TGGT
                                    |||||||||||||| |||| ||||
                                    AAAGTGGTACAACC GTCC ACCA
                                          C   T
GAM320  MGC2663   3'  ACCACCCTGGCCAACATGGTGA 44326                 C
                AA                  TTTCACCATGTTGGCCAGG TGGT
                                    |||||||||||||||||| ||||
                                    AAAGTGGTACAACCGGTCC ACCA
                                               C
GAM320  MGC26641  3'  ACCAGCCTGGTCAACATGGTGA 59319
                AA                  TTTCACCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||||||||
                                    AAAGTGGTACAACTGGTCCGACCA

GAM320  MGC2731   3'  ACCAGCCTGACCAACATGGAGA 44156      A       C
                AA                  TTTC CCATGTTGG CAGGCTGGT
                                    |||| |||||||| |||||||||
                                    AAAG GGTACAACC GTCCGACCA
                                      A       A
GAM320  MGC29762  3'  ACCAGCCTGGCCAATATGGTGA 59141
                GA                  TTTCACCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||||||||
                                    AGAGTGGTATAACCGGTCCGACCA

GAM320  MGC29891  3'  CATCCTGGCTAACACGGTGAAA 58853        A         C
                                    TTTCACC TGTTGGCCAGG TG
                                    ||||||| |||||||||| ||
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                                AAAGTGG ACAATCGGTCC AC
                                   C         T
GAM320  MGC29937  3'  ACCAGCCTGACCAACATGGTGA 58724            C
           AA                    TTTCACCATGTTGG CAGGCTGGT
                                 ||||||||||||| |||||||||
                                 AAAGTGGTACAACC GTCCGACCA
                                       A
GAM320  MGC3169   3'  ACCAGCTTGGCCAACATGGTGA 44176
           AA                    TTTCACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||||||
                                 AAAGTGGTACAACCGGTTCGACCA

GAM320  MGC3207   3'  ACCATCCTGGCTAACATGGTGA 63228              C
           AA                    TTTCACCATGTTGGCCAGG TGGT
                                 |||||||||||||||||| ||||
                                 AAAGTGGTACAATCGGTCC ACCA
                                       T
GAM320  MGC39350  3'  ACCAGCCTGGCCAACATGGCGA 59312     A
           AA                    TTTC CCATGTTGGCCAGGCTGGT
                                 |||| ||||||||||||||||||
                                 AAAG GGTACAACCGGTCCGACCA
                                   C
GAM320  MGC4248   3'  ACCAGCCTGAGCAACATGGCGA 51307     A      GC
           AA                    TTTC CCATGTTG  CAGGCTGGT
                                 |||| ||||||||  |||||||||
                                 AAAG GGTACAAC  GTCCGACCA
                                   C       GA
GAM320  MGC4562   3'  ACCATCCTGGCTAACACGGTGA 56730       A        C
           AA                    TTTCACC TGTTGGCCAGG TGGT
                                 |||||||| |||||||||| ||||
                                 AAAGTGG ACAATCGGTCC ACCA
                                    C         T
GAM320  MGC4663   3'  ACCGTCGTGGCTAACACGGTGA 44778       A       _  T
           AA                    TTTCACC TGTTGGCCA GGC GGT
                                 ||||||| ||||||||| ||| |||
                                 AAAGTGG ACAATCGGT CTG CCA
                                    C       G  _
GAM320  MGC4771   3'  ACCAGCCTGACCAACATAGTGA 51996      C      C
           AA                    TTTCAC ATGTTGG CAGGCTGGT
                                 |||||| ||||||| |||||||||
                                 AAAGTG TACAACC GTCCGACCA
                                    A      A
GAM320  MGC4840   3'  CCAGCCTGGGCAACATGG    72018        G
                                 CCATGTTG CCAGGCTGG
                                 |||||||| |||||||||
                                 GGTACAAC GGTCCGACC
                                      G
GAM320  MGC5457   3'  ACCAGCCTGGCCAGCATGGTGA 51931
           AA                    TTTCACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||||||
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                                AAAGTGGTACGACCGGTCCGACCA

GAM320  MOST2    5'  ACCAGCCTGGCCAACATGGT   40048
                                ACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||
                                TGGTACAACCGGTCCGACCA

GAM320  MRPL48   5'  ACCAGCCTGACAAACATGGAGA 32651      A      GGC
              AA                  TTTC CCATGTT   CAGGCTGGT
                                  |||| |||||||   |||||||||
                                  AAAG GGTACAA   GTCCGACCA
                                    A      ACA
GAM320  MRPL56   3'  ACCAGCCTGGCCAATGTGGTGA 52749
              AA                  TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTGTAACCGGTCCGACCA

GAM320  MRPS10   3'  ACCATCCTGGCTAACACGGTGA 36809        A         C
              AA                  TTTCACC TGTTGGCCAGG TGGT
                                  ||||||| |||||||||| ||||
                                  AAAGTGG ACAATCGGTCC ACCA
                                     C         T
GAM320  MRPS18B  3'  ACCAGCCTGGGCACCATGGTGA 26747          T  G
              AA                  TTTCACCATG TG CCAGGCTGGT
                                  |||||||||| || ||||||||||
                                  AAAGTGGTAC AC GGTCCGACCA
                                        C  G
GAM320  MT-ACT48 3'  ACCAGCCTGGGGAACATAGTGA 25608       C     GG
              GA                  TTTCAC ATGTT  CCAGGCTGGT
                                  |||||| |||||  ||||||||||
                                  AGAGTG TACAA  GGTCCGACCA
                                     A    GG
GAM320  My015    3'  ACCAGCCGGGCCAACATGGTG  67225            A
                                CACCATGTTGGCC GGCTGGT
                                |||||||||||| |||||||
                                GTGGTACAACCGG CCGACCA
                                        G
GAM320  MYO3B    3'  ACCAGCCTGACCAACATGGTGA 58104             C
              AA                  TTTCACCATGTTGG CAGGCTGGT
                                  |||||||||||||| |||||||||
                                  AAAGTGGTACAACC GTCCGACCA
                                        A
GAM320  N4BP2    3'  ACCAGCCTGGCCAACATGGTGA 36931
              A                   TTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAGTGGTACAACCGGTCCGACCA

GAM320  NBR2     3'  ACCAGCCTGGCCAACATAGCGA 20613      ACC
              GA                  TTTC   ATGTTGGCCAGGCTGGT
                                  ||||   ||||||||||||||||
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                                AGAG   TACAACCGGTCCGACCA
                                  CGA
GAM320  NDUFC2   3'  ACCAACTTGGGCAACATGGTGA 17020          G    C
           AA                    TTTCACCATGTTG CCAGG TGGT
                                 |||||||||||| ||||| ||||
                                 AAAGTGGTACAAC GGTTC ACCA
                                       G    A
GAM320  NMNAT    3'  ACCAGCCTGGCCAATATGGTGA 43274
           AA                    TTTCACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||||||
                                 AAAGTGGTATAACCGGTCCGACCA

GAM320  NMT2     3'  ACCATTCTGGCCAACATAGTGA 17849       C        GC
           AA                    TTTCAC ATGTTGGCCAG  TGGT
                                 |||||| |||||||||| ||||
                                 AAAGTG TACAACCGGTC  ACCA
                                    A         TT
GAM320  NPTXR    3'  AGCCTGGCCAACGTGGTGAAA  27425
                                 TTTCACCATGTTGGCCAGGCT
                                 ||||||||||||||||||||
                                 AAAGTGGTGCAACCGGTCCGA

GAM320  NPTXR    3'  AGCCTGGCCAACGTGGTGAAA  55205
                                 TTTCACCATGTTGGCCAGGCT
                                 ||||||||||||||||||||
                                 AAAGTGGTGCAACCGGTCCGA

GAM320  ORC6L    3'  ACCAGCCTGGCCAACATGGTGA 27485
           AA                    TTTCACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||||||
                                 AAAGTGGTACAACCGGTCCGACCA

GAM320  PAFAH2   3'  ACCACCTGGCCAACATGGTGAA 6491             C
           A                     TTTCACCATGTTGGCCAGG TGGT
                                 |||||||||||||||||| ||||
                                 AAAGTGGTACAACCGGTCC ACCA
                                                 _
GAM320  PB1      3'  ACCAGCCTGACCAACATGGTGA 37569          C
           AA                    TTTCACCATGTTGG CAGGCTGGT
                                 |||||||||||||| |||||||||
                                 AAAGTGGTACAACC GTCCGACCA
                                       A
GAM320  PB1      3'  ACCAGCCTGGCCAACGTGGTGA 37570
           AA                    TTTCACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||||||
                                 AAAGTGGTGCAACCGGTCCGACCA

GAM320  PDCD7    3'  CCTGGCTAACACGGTGAAA   72602       A
                                 TTTCACC TGTTGGCCAGG
                                 ||||||| ||||||||||
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                                AAAGTGG ACAATCGGTCC
                                    C
GAM320  phorbolin-1 3'  ACCATCCTGGCTAACACGGTGA 90200        A         C
          AA                    TTTCACC TGTTGGCCAGG TGGT
                                ||||||| |||||||||| ||||
                                AAAGTGG ACAATCGGTCC ACCA
                                    C         T
GAM320  PIWIL2   3'  ACCATCCTGGCCAACATGGTGA 36536              C
          AA                    TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
                                AAAGTGGTACAACCGGTCC ACCA
                                          T
GAM320  PNPASE   3'  ACCATCCTGGCTAACACGGTGA 71435        A         C
          AA                    TTTCACC TGTTGGCCAGG TGGT
                                ||||||| |||||||||| ||||
                                AAAGTGG ACAATCGGTCC ACCA
                                    C         T
GAM320  POFUT1   3'  ACCAGCCTGGCCAACATGGTGA 70966
          A                     TTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||
                                AAGTGGTACAACCGGTCCGACCA

GAM320  PP591    5'  ACCAGCCTGGGCAACATGGCAA 48144     CA       G
          GA                    TTT  CCATGTTG CCAGGCTGGT
                                |||  |||||||| ||||||||||
                                AGA  GGTACAAC GGTCCGACCA
                                  AC       G
GAM320  PPP1R3B  3'  ACCAGCCTGGCCAACATGGTGA 45126
          AA                    TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGACCA

GAM320  PPP1R3B  3'  ACCATCCTGGCTAACACGGTGA 45127        A         C
          AA                    TTTCACC TGTTGGCCAGG TGGT
                                ||||||| |||||||||| ||||
                                AAAGTGG ACAATCGGTCC ACCA
                                    C         T
GAM320  PRDM14   3'  ACCAGCCTGGGCAACATGGTGA 44703            G
          AA                    TTTCACCATGTTG CCAGGCTGGT
                                |||||||||||| ||||||||||
                                AAAGTGGTACAAC GGTCCGACCA
                                      G
GAM320  PRIC285  3'  ACCATCCTGGCCAACATGGTGA 62104              C
          AA                    TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
                                AAAGTGGTACAACCGGTCC ACCA
                                          T
GAM320  PRO0255  3'  ACCAGCCTGGCCAAGGCGG   26961    A  ATG
                                TC CC   TTGGCCAGGCTGGT
                                || ||   ||||||||||||||
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                                GG GG   AACCGGTCCGACCA
                                 C ___
GAM320  PRO0478  5' ACCAGCCTGACCAACATGG   27012         C
                                CCATGTTGG CAGGCTGGT
                                ||||||||| |||||||||
                                GGTACAACC GTCCGACCA
                                   A
GAM320  PRO0618  3' ACCATCCTGGCTAACATGGTGA 27043               C
          AA                      TTTCACCATGTTGGCCAGG TGGT
                                  |||||||||||||||||| ||||
                                  AAAGTGGTACAATCGGTCC ACCA
                                              T
GAM320  PRO0628  3' ACCATCCTGGCCAACACGGTGA 27058        A        C
          AA                      TTTCACC TGTTGGCCAGG TGGT
                                  ||||||| |||||||||| ||||
                                  AAAGTGG ACAACCGGTCC ACCA
                                     C         T
GAM320  PRO1048  3' ACCATCCTGGCTAACATGGTGA 38101               C
          AA                      TTTCACCATGTTGGCCAGG TGGT
                                  |||||||||||||||||| ||||
                                  AAAGTGGTACAATCGGTCC ACCA
                                              T
GAM320  PRO1853  3' ACCAGCCTGACCAAAATGGAGA 38377     A   G   C
          AA                      TTTC CCAT TTGG CAGGCTGGT
                                  |||| |||| |||| |||||||||
                                  AAAG GGTA AACC GTCCGACCA
                                    A   A   A
GAM320  PRO2015  3' ACCAGCCTGGCCAACATGGCGA 38152     A
          AA                      TTTC CCATGTTGGCCAGGCTGGT
                                  |||| ||||||||||||||||||
                                  AAAG GGTACAACCGGTCCGACCA
                                    C
GAM320  PRO2198  5' ACCAGCCTGGCCAAGATGGCGA 38402     A   G
          AA                      TTTC CCAT TTGGCCAGGCTGGT
                                  |||| |||| ||||||||||||||
                                  AAAG GGTA AACCGGTCCGACCA
                                    C   G
GAM320  PRO2730  3' ACCAGCCTGACCAACATGGAGA 48174     A       C
          AA                      TTTC CCATGTTGG CAGGCTGGT
                                  |||| ||||||||| |||||||||
                                  AAAG GGTACAACC GTCCGACCA
                                    A       A
GAM320  PRO2859  3' CCTGGCCAACATGGTGAAG   38209
                                  TTTCACCATGTTGGCCAGG
                                  ||||||||||||||||||
                                  GAAGTGGTACAACCGGTCC

GAM320  PRO2893  3' ACCAGCCTGACCAACATGGAGA 38426     A       C
          AA                      TTTC CCATGTTGG CAGGCTGGT
                                  |||| ||||||||| |||||||||
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                                AAAG GGTACAACC GTCCGACCA
                                  A       A
GAM320  PRO2949  3'  CCTGGCTAACACGGTGAAA   38221       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                   C
GAM320  PRO2964  3'  ACCATCCTGGCTAACACGGTGA 38251       A        C
          AA                    TTTCACC TGTTGGCCAGG TGGT
                                ||||||| |||||||||| ||||
                                AAAGTGG ACAATCGGTCC ACCA
                                   C         T
GAM320  PSR      3'  ACCAGCCTGGCCAACACGGTGA 65770       A
          AA                    TTTCACC TGTTGGCCAGGCTGGT
                                ||||||| ||||||||||||||||
                                AAAGTGG ACAACCGGTCCGACCA
                                   C
GAM320  PTD012   3'  ACCAGCCTGGGCACCATGGTGA 26734         T  G
          GA                    TTTCACCATG TG CCAGGCTGGT
                                |||||||||| || ||||||||||
                                AGAGTGGTAC AC GGTCCGACCA
                                     C  G
GAM320  PTK6     3'  ACCATCCTGGCTAACACGGTGA 21064       A        C
          AA                    TTTCACC TGTTGGCCAGG TGGT
                                ||||||| |||||||||| ||||
                                AAAGTGG ACAATCGGTCC ACCA
                                   C         T
GAM320  PXMP4    3'  ACCAGCCTGGGCAACATGGTGA 24328           G
          AA                    TTTCACCATGTTG CCAGGCTGGT
                                |||||||||||| ||||||||||
                                AAAGTGGTACAAC GGTCCGACCA
                                      G
GAM320  RAB4B    5'  ACCAGCCTGACCAACATGGAGA 32894      A       C
          AA                    TTTC CCATGTTGG CAGGCTGGT
                                |||| ||||||||| |||||||||
                                AAAG GGTACAACC GTCCGACCA
                                  A       A
GAM320  RAD51    3'  AGCTTGGCCAAGATGGTGAAA  12743         G
                                TTTCACCAT TTGGCCAGGCT
                                ||||||||| ||||||||||
                                AAAGTGGTA AACCGGTTCGA
                                     G
GAM320  RAD51    3'  AGCTTGGCCAAGATGGTGAAA  56827         G
                                TTTCACCAT TTGGCCAGGCT
                                ||||||||| ||||||||||
                                AAAGTGGTA AACCGGTTCGA
                                     G
GAM320  RBPMS    3'  ACCAGCCCAGCCAACATGGT  23426          CA
                                ACCATGTTGGC  GGCTGGT
                                ||||||||||  |||||||
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                                TGGTACAACCG  CCGACCA
                                      AC
GAM320  RHOBTB3  3'  ACCAGCCTGGCCAAAACAGTGA 30418       CATG
           AA                   TTTCAC    TTGGCCAGGCTGGT
                                ||||||    ||||||||||||||
                                AAAGTG    AACCGGTCCGACCA
                                   ACAA
GAM320  RNO2     5'  ACCAGCCTGGCCAACATGGTGA 53911
           AA                   TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGACCA

GAM320  RNO2     5'  AGCCTGGCCAGCACGGTGAAA  53919        A
                                TTTCACC TGTTGGCCAGGCT
                                ||||||| |||||||||||||
                                AAAGTGG ACGACCGGTCCGA
                                    C
GAM320  RNO2     3'  ATTAGCCTGGCCAAGATGGTGA 53924         G
           AA                   TTTCACCAT TTGGCCAGGCTGGT
                                |||||||||| ||||||||||||||
                                AAAGTGGTA AACCGGTCCGATTA
                                     G
GAM320  RoXaN    3'  ACCAGCCTGGCCAACATAATGA 47267       CC
           AA                   TTTCA  ATGTTGGCCAGGCTGGT
                                |||||  ||||||||||||||||
                                AAAGT  TACAACCGGTCCGACCA
                                   AA
GAM320  RoXaN    3'  ACCATCCTGGCTAACACGGTGA 47268        A         C
           AA                   TTTCACC TGTTGGCCAGG TGGT
                                ||||||| |||||||||| ||||
                                AAAGTGG ACAATCGGTCC ACCA
                                    C         T
GAM320  RoXaN    3'  CCTGGCTAACATGGTGAAA   47285
                                TTTCACCATGTTGGCCAGG
                                ||||||||||||||||||
                                AAAGTGGTACAATCGGTCC

GAM320  RPL13    3'  ACCAGCCTGGCCAACATG    53824
                                CATGTTGGCCAGGCTGGT
                                ||||||||||||||||||
                                GTACAACCGGTCCGACCA

GAM320  RPL13    3'  ACCAGCCTGGCCAACATG    8268
                                CATGTTGGCCAGGCTGGT
                                ||||||||||||||||||
                                GTACAACCGGTCCGACCA

GAM320  RPP14    3'  ACCAGCCTGGCCAACATGGTGA 60218
           AA                   TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
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                                AAAGTGGTACAACCGGTCCGACCA

GAM320  RRP4     3'  ACCAGCCTGGCCAACAAGGTGA 27351         A
                AA                    TTTCACC TGTTGGCCAGGCTGGT
                                      ||||||| ||||||||||||||||
                                      AAAGTGG ACAACCGGTCCGACCA
                                         A
GAM320  SAMHD1   3'  ACCAGCCTGGCTAGCATGGCGA 61971       A
                AA                    TTTC CCATGTTGGCCAGGCTGGT
                                      |||| ||||||||||||||||||
                                      AAAG GGTACGATCGGTCCGACCA
                                        C
GAM320  SC65     3'  ACCAGCCTGGCCAACATGATGA 22281       C
                GA                    TTTCA CATGTTGGCCAGGCTGGT
                                      ||||| ||||||||||||||||||
                                      AGAGT GTACAACCGGTCCGACCA
                                         A
GAM320  SC65     3'  ACCAGCCTGGGCAGCAGCAAGA 22282     ACCA    G
                A                     TTC    TGTTG CCAGGCTGGT
                                      |||    ||||| ||||||||||
                                      AAG    ACGAC GGTCCGACCA
                                        AACG     G
GAM320  SC65     3'  ACCTGCCTGGCCAACATGGTGA 22283                T
                AA                    TTTCACCATGTTGGCCAGGC GGT
                                      |||||||||||||||||| |||
                                      AAAGTGGTACAACCGGTCCG CCA
                                                        T
GAM320  SCIN     3'  ACCAGCCTGGCCAACATGGCGA 53596      A
                AA                    TTTC CCATGTTGGCCAGGCTGGT
                                      |||| ||||||||||||||||||
                                      AAAG GGTACAACCGGTCCGACCA
                                        C
GAM320  SCYA5    3'  CAGCCTGGCCAACATGATGAAA 12962       C
                                      TTTCA CATGTTGGCCAGGCTG
                                      ||||| ||||||||||||||||
                                      AAAGT GTACAACCGGTCCGAC
                                         A
GAM320  SEMA5A   3'  ACCAGCCTGGGCAACATGGGGA 15586      A       G
                AA                    TTTC CCATGTTG CCAGGCTGGT
                                      |||| |||||||| ||||||||||
                                      AAAG GGTACAAC GGTCCGACCA
                                        G       G
GAM320  SERF1B   3'  ACCAGCCTGGGCAACATGGCGA 43684      A       G
                AA                    TTTC CCATGTTG CCAGGCTGGT
                                      |||| |||||||| ||||||||||
                                      AAAG GGTACAAC GGTCCGACCA
                                        C       G
GAM320  SGKL     3'  ACCAGCCTGACCAACATGG    26046          C
                                      CCATGTTGG CAGGCTGGT
                                      ||||||||| |||||||||
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                                GGTACAACC GTCCGACCA
                                    A
GAM320  SGKL    3'  ACCATCCTGGGCAACATGGCGA 26047     A      G    C
            AA                   TTTC CCATGTTG CCAGG TGGT
                                 |||| |||||||| ||||| ||||
                                 AAAG GGTACAAC GGTCC ACCA
                                   C       G    T
GAM320  SH2D3A  3'  ACCAGCCAGGGCAACATGGTGA 19700           G  A
            GA                   TTTCACCATGTTG CC GGCTGGT
                                 |||||||||||||| || |||||||
                                 AGAGTGGTACAAC GG CCGACCA
                                       G  A
GAM320  SIAT4A  3'  ACCAGCCTGGGCAACATAGTGA 13131       C     G
            GA                   TTTCAC ATGTTG CCAGGCTGGT
                                 |||||| |||||| ||||||||||
                                 AGAGTG TACAAC GGTCCGACCA
                                    A     G
GAM320  SLC19A3  3'  ACCAGCCTGGGCAACACAGTGA 48231      CA    G
                                 TCAC  TGTTG CCAGGCTGGT
                                 ||||  ||||| ||||||||||
                                 AGTG  ACAAC GGTCCGACCA
                                   AC    G
GAM320  SLC2A11  3'  ACCAGCCTAGGTAACATAGTGA 48692       C     G  _
            GA                   TTTCAC ATGTTG CC AGGCTGGT
                                 |||||| |||||| || ||||||||
                                 AGAGTG TACAAT GG TCCGACCA
                                    A     _  A
GAM320  SLC7A11  3'  ACCAGCCTGACCAACATGGAGA 27526      A       C
            AA                   TTTC CCATGTTGG CAGGCTGGT
                                 |||| ||||||||| |||||||||
                                 AAAG GGTACAACC GTCCGACCA
                                   A        A
GAM320  Spir-2   3'  ACCAGCCTGGCCAACATGATGA 71154       C
            AA                   TTTCA CATGTTGGCCAGGCTGGT
                                 ||||| ||||||||||||||||||
                                 AAAGT GTACAACCGGTCCGACCA
                                   A
GAM320  SPRY4    3'  ACCAGCCTGGCCAACATAGTGA 48988       C
            AA                   TTTCAC ATGTTGGCCAGGCTGGT
                                 |||||| ||||||||||||||||||
                                 AAAGTG TACAACCGGTCCGACCA
                                    A
GAM320  SPRY4    3'  ACCAGCCTGGCCAATATGGT   48989
                                 ACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||
                                 TGGTATAACCGGTCCGACCA

GAM320  SPTLC2   3'  ACCAGCCTGGCCAACATGGTGA 17974
            AA                   TTTCACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||||||
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                                AAAGTGGTACAACCGGTCCGACCA

GAM320  SPTLC2   3'  AGTCTGGCCAACATGGCGAAA  17980      A
                                TTTC CCATGTTGGCCAGGCT
                                |||| ||||||||||||||||
                                AAAG GGTACAACCGGTCTGA
                                  C
GAM320  SS18L1   3'  ACCAGCCTGACCAACATGGAGA 65944      A        C
                AA                TTTC CCATGTTGG CAGGCTGGT
                                |||| ||||||||| |||||||||
                                AAAG GGTACAACC GTCCGACCA
                                  A        A
GAM320  SYAP1    3'  ACCAGCCTTGCCAACATAGTGA 52463       C       C
                AA                TTTCAC ATGTTGGC AGGCTGGT
                                |||||| |||||||| ||||||||
                                AAAGTG TACAACCG TCCGACCA
                                   A       T
GAM320  SYNPO2   3'  ACCAGCCTGAGCAACATAGTGA 72381        C     GC
                GA                TTTCAC ATGTTG  CAGGCTGGT
                                |||||| ||||||  |||||||||
                                AGAGTG TACAAC  GTCCGACCA
                                   A     GA
GAM320  TA-LRRP  3'  ACCAGTCTGGCCAACCTGGTGA 31705         T
                AA                TTTCACCA GTTGGCCAGGCTGGT
                                |||||||| ||||||||||||||||
                                AAAGTGGT CAACCGGTCTGACCA
                                   C
GAM320  TACTILE  3'  ACCATCCTGGCTAACACAGTGA 20578       CA         C
                AA                TTTCAC  TGTTGGCCAGG TGGT
                                ||||||  |||||||||||| ||||
                                AAAGTG  ACAATCGGTCC ACCA
                                   AC          T
GAM320  TDP1     5'  ATCAGCCCGGGCAACATGGTGA 37600            G  A
                AA                TTTCACCATGTTG CC GGCTGGT
                                |||||||||||||| || |||||||
                                AAAGTGGTACAAC GG CCGACTA
                                      G  C
GAM320  THEA     3'  ACCAGCCTGGGCAACATGGTGA 66863            G
                AA                TTTCACCATGTTG CCAGGCTGGT
                                |||||||||||||| ||||||||||
                                AAAGTGGTACAAC GGTCCGACCA
                                      G
GAM320  THEA     3'  ACCAGTCTGGCCAACATGGCGA 66864      A
                AA                TTTC CCATGTTGGCCAGGCTGGT
                                |||| ||||||||||||||||||
                                AAAG GGTACAACCGGTCTGACCA
                                  C
GAM320  THEA     3'  CAGCCTGGCCAACATGGTGAAA 66879
                                TTTCACCATGTTGGCCAGGCTG
                                |||||||||||||||||||||
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                                AAAGTGGTACAACCGGTCCGAC

GAM320  TIP47    3'  ACCAGCCAGGCCAACATGGTGA 20597              A
           AA                    TTTCACCATGTTGGCC GGCTGGT
                                 |||||||||||||||| |||||||
                                 AAAGTGGTACAACCGG CCGACCA
                                           A
GAM320  TMG4     3'  ACCAGCCTGGCCAACATGGTGA 44210
           AA                    TTTCACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||||||
                                 AAAGTGGTACAACCGGTCCGACCA

GAM320  TRIM38   3'  ACCAGCCTGGCCAACATGGTGA 22049
           AA                    TTTCACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||||||
                                 AAAGTGGTACAACCGGTCCGACCA

GAM320  TXNL2    3'  ACCAGCCTGAGCAACATGGCGA 22575     A      GC
           AA                    TTTC CCATGTTG  CAGGCTGGT
                                 |||| ||||||||  |||||||||
                                 AAAG GGTACAAC  GTCCGACCA
                                   C       GA
GAM320  UBCE7IP5 3'  ACCAGCCTGGCCAACATGGCAA 30839     CA
           GA                    TTT  CCATGTTGGCCAGGCTGGT
                                 |||  ||||||||||||||||||
                                 AGA  GGTACAACCGGTCCGACCA
                                   AC
GAM320  ust3     3'  ACCACCCTGGCCAACATGGTGA 94847              C
           AA                    TTTCACCATGTTGGCCAGG TGGT
                                 |||||||||||||||||| ||||
                                 AAAGTGGTACAACCGGTCC ACCA
                                           C
GAM320  VIT1     5'  ACCAGCCTGGCCAACATGGTGA 38596
           AA                    TTTCACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||||||
                                 AAAGTGGTACAACCGGTCCGACCA

GAM320  VPS4B    3'  ACCAGTCTGGCCAACATGGTGA 18015
           AA                    TTTCACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||||||
                                 AAAGTGGTACAACCGGTCTGACCA

GAM320  WBSCR21  3'  ACCAGCCTGGCCAACATGGTGA 49291
           AA                    TTTCACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||||||
                                 AAAGTGGTACAACCGGTCCGACCA

GAM320  WBSCR23  3'  ACCAGCCTGGCCAACATGGTGA 47406
           AA                    TTTCACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||||||
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                                AAAGTGGTACAACCGGTCCGACCA

GAM320  WSB1    3'  AGCCTGGCAAACATGATGAAA  56962      C     G
                                TTTCA CATGTT GCCAGGCT
                                ||||| |||||| ||||||||
                                AAAGT GTACAA CGGTCCGA
                                   A     A
GAM320  WSB1    3'  AGCCTGGCAAACATGATGAAA  56987      C     G
                                TTTCA CATGTT GCCAGGCT
                                ||||| |||||| ||||||||
                                AAAGT GTACAA CGGTCCGA
                                   A     A
GAM320  YME1L1  3'  ACCAGCCTGGCCAACATGGTGA 58416
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  YME1L1  3'  ACCAGCCTGGCCAACGTGGTGA 58417
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTGCAACCGGTCCGACCA

GAM320  YME1L1  3'  ACCAGCCTGGCCAACATGGTGA 27312
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  YME1L1  3'  ACCAGCCTGGCCAACGTGGTGA 27313
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTGCAACCGGTCCGACCA

GAM320  ZAK     3'  ACCAGCCTGGCCAACATGGTGA 56936
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  ZFP106  3'  ACCAGCCTGGCCAACATAGTGA 42710      C
                AA                TTTCAC ATGTTGGCCAGGCTGGT
                                  |||||| ||||||||||||||||
                                  AAAGTG TACAACCGGTCCGACCA
                                     A
GAM320  ZFP106  3'  ACCAGCCTGGCCAACATGG   42711
                                  CCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||
                                  GGTACAACCGGTCCGACCA

GAM320  ZIM3    3'  ACCAGCATGACCAACATGGTGA 54634          C  G
                AA                TTTCACCATGTTGG CA GCTGGT
                                  |||||||||||||| || ||||||
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                                AAAGTGGTACAACC GT CGACCA
                                      A  A
GAM320  ZNF197   3'  ACCAGCCTGACCAACATGGTGA 23750           C
           AA                   TTTCACCATGTTGG CAGGCTGGT
                                |||||||||||||| |||||||||
                                AAAGTGGTACAACC GTCCGACCA
                                      A
GAM320  ZNF271   3'  CCAGCCTGACCAACATGGTGAA 96961           C
           A                    TTTCACCATGTTGG CAGGCTGG
                                |||||||||||||| ||||||||
                                AAAGTGGTACAACC GTCCGACC
                                      A
GAM320  ZNF297B  3'  ACCAGCCTGACCAACATAGTGA 26635      C    C
           AA                   TTTCAC ATGTTGG CAGGCTGGT
                                |||||| ||||||| |||||||||
                                AAAGTG TACAACC GTCCGACCA
                                   A     A
GAM320  ZNF297B  5'  ACCAGCCTGGCCAACATAGTGA 26636      C
           AA                   TTTCAC ATGTTGGCCAGGCTGGT
                                |||||| ||||||||||||||||
                                AAAGTG TACAACCGGTCCGACCA
                                   A
GAM320  ZNF333   3'  ATCAGCCTGGCCAACATGGTGA 51585
           AA                   TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGACTA

GAM320  ZNF33A   3'  ACCAGCCTGGTCAACATGGTGA 92989
           AA                   TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTACAACTGGTCCGACCA

GAM320  ZNF347   3'  ACCAGCCTGACCAACATGGCGA 51816     A      C
           AA                   TTTC CCATGTTGG CAGGCTGGT
                                |||| ||||||||| |||||||||
                                AAAG GGTACAACC GTCCGACCA
                                   C      A
GAM320  LOC112687 3'  ACCAGCCTGGCCAACATGGTGA 73216
           AA                   TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC113523 3'  ACCAGCCCGGGCAACATGG   73407       G  A
                                CCATGTTG CC GGCTGGT
                                |||||||| || |||||||
                                GGTACAAC GG CCGACCA
                                     G  C
GAM320  LOC115129 5'  ACCAGCCTGGCCAACATGGTGA 73597
                                TCACCATGTTGGCCAGGCTGGT
                                |||||||||||||||||||||
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                                AGTGGTACAACCGGTCCGACCA

GAM320  LOC115129 5'  ACCAGCCTGGCCAACATGGTGA 73598
                AG                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  GAAGTGGTACAACCGGTCCGACCA

GAM320  LOC115129 3'  ACCAGCCTGGGCAACATAATGA 73599      CC     G
                GA                TTTCA  ATGTTG CCAGGCTGGT
                                  |||||  ||||||  ||||||||||
                                  AGAGT  TACAAC GGTCCGACCA
                                    AA     G
GAM320  LOC115196 3'  ACCATCCTGGCTAACACAGTGA 73646       CA         C
                AA                TTTCAC  TGTTGGCCAGG TGGT
                                  ||||||  |||||||||| ||||
                                  AAAGTG  ACAATCGGTCC ACCA
                                     AC         T
GAM320  LOC115273 3'  ACCAGCCTGGCCAACATGGTGA 73743
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC116143 3'  ACCAGCCTGGCCAACATGGTCA 74171     C
                AA                TTT ACCATGTTGGCCAGGCTGGT
                                  ||| ||||||||||||||||||
                                  AAA TGGTACAACCGGTCCGACCA
                                    C
GAM320  LOC116143 3'  ACCATCCTGGCTAACATGGTGA 74172               C
                AA                TTTCACCATGTTGGCCAGG TGGT
                                  |||||||||||||||||| ||||
                                  AAAGTGGTACAATCGGTCC ACCA
                                            T
GAM320  LOC116228 3'  ACCAGCCTGGCCAACAGGGTGA 74223        A
                AA                TTTCACC TGTTGGCCAGGCTGGT
                                  |||||||  ||||||||||||||||
                                  AAAGTGG ACAACCGGTCCGACCA
                                     G
GAM320  LOC116236 3'  ACCATCCTGGCTAACACAGTGA 74235       CA         C
                AA                TTTCAC  TGTTGGCCAGG TGGT
                                  ||||||  |||||||||| ||||
                                  AAAGTG  ACAATCGGTCC ACCA
                                     AC         T
GAM320  LOC116349 3'  ACCATCCTGGCTAACATGGTGA 74268               C
                AA                TTTCACCATGTTGGCCAGG TGGT
                                  |||||||||||||||||| ||||
                                  AAAGTGGTACAATCGGTCC ACCA
                                            T
GAM320  LOC118471 3'  ACCAGCCTGGGCAACATGGTGA 74348           G
                AA                TTTCACCATGTTG CCAGGCTGGT
                                  ||||||||||||| ||||||||||
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                                AAAGTGGTACAAC GGTCCGACCA
                                      G
GAM320  LOC119504 5'  ACCAGCCTGACCAACATGGAGA 74437      A       C
                AA                TTTC CCATGTTGG CAGGCTGGT
                                  |||| ||||||||| |||||||||
                                  AAAG GGTACAACC GTCCGACCA
                                    A       A
GAM320  LOC121504 3'  ACCAGCATGGCCAACATAGTGA 74536       C       G
                GA                TTTCAC ATGTTGGCCA GCTGGT
                                  |||||| |||||||||| ||||||
                                  AGAGTG TACAACCGGT CGACCA
                                    A       A
GAM320  LOC122704 3'  CCAGCCTGGTCAACATGGTGAA 74604
                A                 TTTCACCATGTTGGCCAGGCTGG
                                  |||||||||||||||||||||||
                                  AAAGTGGTACAACTGGTCCGACC

GAM320  LOC122970 3'  ACCAGCTTAGGCAACATGG   74636        G _
                                  CCATGTTG CC AGGCTGGT
                                  |||||||| || ||||||||
                                  GGTACAAC GG TTCGACCA
                                      _ A
GAM320  LOC124602 3'  ACCAGCCTGGCCAACATGGCGA 74782      A
                AA                TTTC CCATGTTGGCCAGGCTGGT
                                  |||| ||||||||||||||||||
                                  AAAG GGTACAACCGGTCCGACCA
                                    C
GAM320  LOC126282 3'  ACCATCCTGGCCAACATGGTGA 74935              C
                AA                TTTCACCATGTTGGCCAGG TGGT
                                  |||||||||||||||||| ||||
                                  AAAGTGGTACAACCGGTCC ACCA
                                           T
GAM320  LOC126282 3'  ACCATCCTGGCTAACACGGTGA 74936       A       C
                AA                TTTCACC TGTTGGCCAGG TGGT
                                  ||||||| |||||||||| ||||
                                  AAAGTGG ACAATCGGTCC ACCA
                                     C        T
GAM320  LOC126669 3'  ACCAGCCTGGCCAACATGGTGA 75917
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  |||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC127262 3'  CAGCCTGGGCAACATGGTGAAA 76593           G
                                  TTTCACCATGTTG CCAGGCTG
                                  |||||||||||| ||||||||
                                  AAAGTGGTACAAC GGTCCGAC
                                        G
GAM320  LOC127294 3'  ACCAGCCTGGCCAACATGACGA 75142      AC
                AA                TTTC  CATGTTGGCCAGGCTGGT
                                  ||||  ||||||||||||||||
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                                AAAG  GTACAACCGGTCCGACCA
                                  CA
GAM320   LOC127428 3'  ACCAGCCTGGCCAACATGGCGA 75151      A
                  AA                TTTC CCATGTTGGCCAGGCTGGT
                                    |||| ||||||||||||||||||
                                    AAAG GGTACAACCGGTCCGACCA
                                      C
GAM320   LOC130026 3'  ACCATCCTGGCTAACATGGTGA 57429                C
                  AA                TTTCACCATGTTGGCCAGG TGGT
                                    |||||||||||||||||| ||||
                                    AAAGTGGTACAATCGGTCC ACCA
                                                 T
GAM320   LOC130535 3'  ACCAGCATGACCAACATGGCGA 76634      A       C  G
                  AA                TTTC CCATGTTGG CA GCTGGT
                                    |||| ||||||||| || ||||||
                                    AAAG GGTACAACC GT CGACCA
                                      C       A  A
GAM320   LOC130535 3'  ACCATCCTGGCCAGCATGGTGA 76635                C
                  AA                TTTCACCATGTTGGCCAGG TGGT
                                    |||||||||||||||||| ||||
                                    AAAGTGGTACGACCGGTCC ACCA
                                                 T
GAM320   LOC130589 3'  ACCATCCTGGCTAACACGGTGA 57925        A       C
                  AA                TTTCACC TGTTGGCCAGG TGGT
                                    ||||||| |||||||||| ||||
                                    AAAGTGG ACAATCGGTCC ACCA
                                       C         T
GAM320   LOC131744 3'  ACCAGCCTGACCAACATGGTGA 76386            C
                  AA                TTTCACCATGTTGG CAGGCTGGT
                                    |||||||||||| |||||||||
                                    AAAGTGGTACAACC GTCCGACCA
                                             A
GAM320   LOC131965 3'  ACCAGCCTGGCCAACATGGTGA 75514
                  GA                TTTCACCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||||||||
                                    AGAGTGGTACAACCGGTCCGACCA

GAM320   LOC131965 3'  ACCAGTGTGGGCAACATGGTGA 75515           G  G
                  AA                TTTCACCATGTTG CCA GCTGGT
                                    |||||||||||| ||| ||||||
                                    AAAGTGGTACAAC GGT TGACCA
                                           G  G
GAM320   LOC132625 3'  ACCAGCCTGGGCAACATAGTGA 76428      C     G
                  GA                TTTCAC ATGTTG CCAGGCTGGT
                                    |||||| |||||| ||||||||||
                                    AGAGTG TACAAC GGTCCGACCA
                                       A     G
GAM320   LOC133926 3'  ACCATCCTGGCTAACACGGTGA 75626       A       C
                  AA                TTTCACC TGTTGGCCAGG TGGT
                                    ||||||| |||||||||| ||||
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                                AAAGTGG ACAATCGGTCC ACCA
                                   C         T
GAM320   LOC134147 3'  ACCAGCCTGGCCAACATGGTGA 57950
                 AA                TTTCACCATGTTGGCCAGGCTGGT
                                   ||||||||||||||||||||||||
                                   AAAGTGGTACAACCGGTCCGACCA

GAM320   LOC134147 3'  ACCAGCCTGGCCAACATGGTGA 57951
                 GA                TTTCACCATGTTGGCCAGGCTGGT
                                   ||||||||||||||||||||||||
                                   AGAGTGGTACAACCGGTCCGACCA

GAM320   LOC135154 3'  ACCAGCCTGACCAATATGGAGA 75714      A        C
                 AA                TTTC CCATGTTGG CAGGCTGGT
                                   |||| ||||||||| |||||||||
                                   AAAG GGTATAACC GTCCGACCA
                                     A        A
GAM320   LOC137362 3'  ACCAGCCTGGCCAACATGGTGA 75775
                 AA                TTTCACCATGTTGGCCAGGCTGGT
                                   ||||||||||||||||||||||||
                                   AAAGTGGTACAACCGGTCCGACCA

GAM320   LOC138241 3'  ACCAGCCTGGCCAACATGGCGG 75830      A
                 AA                TTTC CCATGTTGGCCAGGCTGGT
                                   |||| ||||||||||||||||||
                                   AAGG GGTACAACCGGTCCGACCA
                                     C
GAM320   LOC138389 3'  ACCAGCCTGGCCAAAATGATGA 76724      C   G
                 AA                TTTCA CAT TTGGCCAGGCTGGT
                                   ||||| ||| ||||||||||||||
                                   AAAGT GTA AACCGGTCCGACCA
                                     A   A
GAM320   LOC138428 3'  ACCAGCCTGGCCAACATGGTGA 75851
                 AA                TTTCACCATGTTGGCCAGGCTGGT
                                   ||||||||||||||||||||||||
                                   AAAGTGGTACAACCGGTCCGACCA

GAM320   LOC139422 3'  ACCATCTTGGCTAACACAGTGA 76339        CA          C
                 AA                TTTCAC  TGTTGGCCAGG TGGT
                                   ||||||  |||||||||| ||||
                                   AAAGTG  ACAATCGGTTC ACCA
                                      AC          T
GAM320   LOC142779 3'  ACCATCCTGGCCAACATGGTGA 76897                 C
                 AA                TTTCACCATGTTGGCCAGG TGGT
                                   |||||||||||||||||| ||||
                                   AAAGTGGTACAACCGGTCC ACCA
                                                T
GAM320   LOC142927 3'  ACCAGCCTGGGCAACATGGCGA 76939      A       G
                 AA                TTTC CCATGTTG CCAGGCTGGT
                                   |||| |||||||| ||||||||||
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                                AAAG GGTACAAC GGTCCGACCA
                                  C       G
GAM320  LOC142937 3'  ACCAGCCTGAGCAACATGATGA 57443       C       GC
                GA                TTTCA CATGTTG  CAGGCTGGT
                                  ||||| |||||||  |||||||||
                                  AGAGT GTACAAC  GTCCGACCA
                                    A      GA
GAM320  LOC142948 3'  ACCATCCTGGCCAACATGGTGA 83770                 C
                AA                TTTCACCATGTTGGCCAGG TGGT
                                  |||||||||||||||||| ||||
                                  AAAGTGGTACAACCGGTCC ACCA
                                             T
GAM320  LOC143196 3'  ACCATCCTGGCCAACATGGTGA 83797                 C
                AA                TTTCACCATGTTGGCCAGG TGGT
                                  |||||||||||||||||| ||||
                                  AAAGTGGTACAACCGGTCC ACCA
                                             T
GAM320  LOC143310 3'  ACCATCCTGGCTAACATGGTGA 77030                 C
                AA                TTTCACCATGTTGGCCAGG TGGT
                                  |||||||||||||||||| ||||
                                  AAAGTGGTACAATCGGTCC ACCA
                                             T
GAM320  LOC143465 3'  ACCAGCCTGGCCAACATGGTGA 83864
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC143888 3'  ACCAGCCTGGCCAACATGGTGA 77163
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC144289 3'  ACCAGCCTGGCCACCATGGTGA 83944           T
                AA                TTTCACCATG TGGCCAGGCTGGT
                                  |||||||||| ||||||||||||
                                  AAAGTGGTAC ACCGGTCCGACCA
                                       C
GAM320  LOC144465 3'  ACCAGCCTGACCAACATGGAGA 77333      A       C
                AA                TTTC CCATGTTGG CAGGCTGGT
                                  |||| ||||||||| |||||||||
                                  AAAG GGTACAACC GTCCGACCA
                                    A       A
GAM320  LOC144465 3'  ACCAGCCTGGCCAACATGGAGA 77334      A
                AA                TTTC CCATGTTGGCCAGGCTGGT
                                  |||| ||||||||||||||||||
                                  AAAG GGTACAACCGGTCCGACCA
                                    A
GAM320  LOC144481 3'  ACCAGCCTGGCCAACATGG    84008
                                  CCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||
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                                GGTACAACCGGTCCGACCA

GAM320  LOC144486 3'  CCTGGCCAACATGGTGAAA   84004
                                TTTCACCATGTTGGCCAGG
                                ||||||||||||||||||
                                AAAGTGGTACAACCGGTCC

GAM320  LOC144524 3'  ACTAGCCTGGCCAACACGGTGA 84047        A
              AA                  TTTCACC TGTTGGCCAGGCTGGT
                                  ||||||| ||||||||||||||||
                                  AAAGTGG ACAACCGGTCCGATCA
                                      C
GAM320  LOC144563 3'  ACCAGCCTGGCCAACATGGTGA 77388
              AA                  TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC144583 3'  CCAGCCTGGCCAACATGGTGAA 77415
              A                   TTTCACCATGTTGGCCAGGCTGG
                                  |||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACC

GAM320  LOC144817 3'  ACCATCCTGGCTAACACGGTGA 77500        A         C
              AA                  TTTCACC TGTTGGCCAGG TGGT
                                  ||||||| |||||||||| ||||
                                  AAAGTGG ACAATCGGTCC ACCA
                                      C         T
GAM320  LOC144817 3'  CCCGGCCAACATAGTGAAA   77513       C       A
                                TTTCAC ATGTTGGCC GG
                                ||||||| ||||||||| ||
                                AAAGTG TACAACCGG CC
                                    A       C
GAM320  LOC144845 3'  ACCAGCCTGGCCAACATGGT   57448
                                ACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||
                                TGGTACAACCGGTCCGACCA

GAM320  LOC145035 3'  ACCAGCCTGGGAAACATAGCGA 84173      ACC     GG
              AA                  TTTC   ATGTT  CCAGGCTGGT
                                  ||||   |||||  ||||||||||
                                  AAAG   TACAA  GGTCCGACCA
                                    CGA     AG
GAM320  LOC145082 5'  ACCAGACTGACCAACATGG   84177         C   G
                                CCATGTTGG CAG CTGGT
                                ||||||||| ||| |||||
                                GGTACAACC GTC GACCA
                                      A  A
GAM320  LOC145216 3'  ACCAGCCTGACCAACATG    84212         C
                                CATGTTGG CAGGCTGGT
                                |||||||| |||||||||
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                                GTACAACC GTCCGACCA
                                   A
GAM320  LOC145231 3'  ACCAGCCTGAGCAACATGATGA 84235      C      GC
                AA              TTTCA CATGTTG  CAGGCTGGT
                                ||||| |||||||  |||||||||
                                AAAGT GTACAAC  GTCCGACCA
                                  A      GA
GAM320  LOC145231 3'  ACTAGCCTGACCAACATGGTGA 84236            C
                AA              TTTCACCATGTTGG CAGGCTGGT
                                |||||||||||||| |||||||||
                                AAAGTGGTACAACC GTCCGATCA
                                      A
GAM320  LOC145387 3'  ACCAGCCTGGCCAATATGGTGA 84324
                AA              TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTATAACCGGTCCGACCA

GAM320  LOC145387 3'  ACCAGCCTGGGCAACATGG    84325        G
                                CCATGTTG CCAGGCTGGT
                                |||||||| ||||||||||
                                GGTACAAC GGTCCGACCA
                                   G
GAM320  LOC145482 3'  ACCAGCCTGGCCAACACGGTGA 77736       A
                AA              TTTCACC TGTTGGCCAGGCTGGT
                                ||||||| ||||||||||||||||
                                AAAGTGG ACAACCGGTCCGACCA
                                   C
GAM320  LOC145662 3'  ACCAGCCTGGCCAAGATGGTGA 77830        G
                AA              TTTCACCAT TTGGCCAGGCTGGT
                                ||||||||| ||||||||||||||
                                AAAGTGGTA AACCGGTCCGACCA
                                   G
GAM320  LOC145663 3'  ACCATCCTGGCTAACATGGTGA 84409              C
                AA              TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
                                AAAGTGGTACAATCGGTCC ACCA
                                            T
GAM320  LOC145663 3'  CCTGGTCAACATGATGAAA    84421       C
                                TTTCA CATGTTGGCCAGG
                                ||||| ||||||||||||
                                AAAGT GTACAACTGGTCC
                                   A
GAM320  LOC145757 3'  ACCAGCCTGGCCAACATGGTGA 77910
                AA              TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC145820 3'  ACCATCCTGGCTAACATGGTGA 77968              C
                AA              TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
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                                AAAGTGGTACAATCGGTCC ACCA
                                           T
GAM320  LOC146059 3'  ACCAGCCTGGCCAACATGG   78080
                                CCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||
                                GGTACAACCGGTCCGACCA

GAM320  LOC146332 3'  ACCATCCTGGCCAACATGGTGA 78351              C
          AA                    TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
                                AAAGTGGTACAACCGGTCC ACCA
                                           T
GAM320  LOC146667 3'  ACCATCCTGGCTAACATGGTGA 84703              C
          AA                    TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
                                AAAGTGGTACAATCGGTCC ACCA
                                           T
GAM320  LOC146669 3'  ACCAGCCTGGCCAACATGGCGA 78656     A
          AA                    TTTC CCATGTTGGCCAGGCTGGT
                                |||| ||||||||||||||||||
                                AAAG GGTACAACCGGTCCGACCA
                                  C
GAM320  LOC146713 3'  ACCAGCCTGGCCAACATGGCGA 84719     A
          AA                    TTTC CCATGTTGGCCAGGCTGGT
                                |||| ||||||||||||||||||
                                AAAG GGTACAACCGGTCCGACCA
                                  C
GAM320  LOC146713 3'  ACCAGCCTGGCCAATGTAGTGA 84720      C
          AA                    TTTCAC ATGTTGGCCAGGCTGGT
                                |||||| ||||||||||||||||
                                AAAGTG TGTAACCGGTCCGACCA
                                   A
GAM320  LOC146723 3'  ACCAGCCTGGCCAACATGGAGA 78671     A
          AA                    TTTC CCATGTTGGCCAGGCTGGT
                                |||| ||||||||||||||||||
                                AAAG GGTACAACCGGTCCGACCA
                                  A
GAM320  LOC146728 5'  ACCAGCCTGGCCAACATGGTGA 84756
          AA                    TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC146756 3'  ACCAGCCTGACCAACATGGTGA 84790           C
          AA                    TTTCACCATGTTGG CAGGCTGGT
                                |||||||||||||| |||||||||
                                AAAGTGGTACAACC GTCCGACCA
                                      A
GAM320  LOC146780 3'  ACCATCCTGGCTAACATGGTGA 84814              C
          AA                    TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
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                                AAAGTGGTACAATCGGTCC ACCA
                                           T
GAM320  LOC146895 3'  CAGCCTGGCCAACGTGATGAAA 84862      C
                                TTTCA CATGTTGGCCAGGCTG
                                ||||| ||||||||||||||||
                                AAAGT GTGCAACCGGTCCGAC
                                   A
GAM320  LOC146901 3'  ACCAGCCTGGCCAACATGGTGA 84879
           AA                     TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC147057 3'  ACCATCCTGGCCAACACGGTGA 84971       A        C
           AA                     TTTCACC TGTTGGCCAGG TGGT
                                  ||||||| |||||||||| ||||
                                  AAAGTGG ACAACCGGTCC ACCA
                                     C         T
GAM320  LOC147071 3'  ACCATCCTGGCTAACATGGTGA 73343              C
           AA                     TTTCACCATGTTGGCCAGG TGGT
                                  |||||||||||||||||| ||||
                                  AAAGTGGTACAATCGGTCC ACCA
                                             T
GAM320  LOC147180 5'  ACCAGCCTGTCCAACATGGTGA 85091           C
           AA                     TTTCACCATGTTGG CAGGCTGGT
                                  |||||||||||||| |||||||||
                                  AAAGTGGTACAACC GTCCGACCA
                                        T
GAM320  LOC147599 3'  ACCAGCCTAGCTAACATGGT  85156          C
                                  ACCATGTTGGC AGGCTGGT
                                  |||||||||||| ||||||||
                                  TGGTACAATCG TCCGACCA
                                        A
GAM320  LOC147649 3'  ACCATCCTGGCCAACACGGTGA 79053       A        C
           AA                     TTTCACC TGTTGGCCAGG TGGT
                                  ||||||| |||||||||| ||||
                                  AAAGTGG ACAACCGGTCC ACCA
                                     C         T
GAM320  LOC147660 3'  ACCGTCCTGGCTAACACGGTGA 79022       A        C
           AA                     TTTCACC TGTTGGCCAGG TGGT
                                  ||||||| |||||||||| ||||
                                  AAAGTGG ACAATCGGTCC GCCA
                                     C         T
GAM320  LOC147664 3'  ACCAGCCTGACCAACATGGAGA 79036     A       C
           AA                     TTTC CCATGTTGG CAGGCTGGT
                                  |||| ||||||||| |||||||||
                                  AAAG GGTACAACC GTCCGACCA
                                    A       A
GAM320  LOC147700 3'  ACCAGCATGACCAACATGGAGA 59873     A       C  G
           AA                     TTTC CCATGTTGG CA GCTGGT
                                  |||| ||||||||| || ||||||
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                                AAAG GGTACAACC GT CGACCA
                                  A       A  A
GAM320   LOC147727 5'  ACCAGCCTGGCCAACATGGTGA 79118
                 AA               TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320   LOC147727 5'  ACCAGCCTGGCCAGCATGGTGA 79119
                 AA               TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACGACCGGTCCGACCA

GAM320   LOC147990 3'  ACCAGCCTGGCCAACATGGTGG 85206
                 AA               TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAGGTGGTACAACCGGTCCGACCA

GAM320   LOC148147 3'  ACCATCGTGGCTAACACGGTGA 79381       A       _ C
                 AA               TTTCACC TGTTGGCCA GG TGGT
                                  ||||||| ||||||||| || ||||
                                  AAAGTGG ACAATCGGT CT ACCA
                                     C       G _
GAM320   LOC148198 3'  ACCAGCCTGACCCACATGGAGA 71216     A     T  C
                 AA               TTTC CCATGT GG CAGGCTGGT
                                  |||| |||||| || |||||||||
                                  AAAG GGTACA CC GTCCGACCA
                                    A     C  A
GAM320   LOC148254 3'  ACCAGCCTGGTTAACATGGTGA 79497
                 AA               TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAATTGGTCCGACCA

GAM320   LOC148267 3'  ACCAGCCTGGGCAACATAGTGA 79510       C     G
                 GA               TTTCAC ATGTTG CCAGGCTGGT
                                  |||||| |||||| ||||||||||
                                  AGAGTG TACAAC GGTCCGACCA
                                     A     G
GAM320   LOC148397 3'  ACCAGCCTGACCAACATGGAGA 79555     A       C
                 AA               TTTC CCATGTTGG CAGGCTGGT
                                  |||| ||||||||| |||||||||
                                  AAAG GGTACAACC GTCCGACCA
                                    A       A
GAM320   LOC148534 3'  AGCTTGGCCAACATGGTGAAA  79627
                                  TTTCACCATGTTGGCCAGGCT
                                  |||||||||||||||||||||
                                  AAAGTGGTACAACCGGTTCGA

GAM320   LOC148758 5'  ACCAGTCTGGCCCACATGGTGA 79717          T
                 AA               TTTCACCATGT GGCCAGGCTGGT
                                  |||||||||||| ||||||||||||
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                                AAAGTGGTACA CCGGTCTGACCA
                                      C
GAM320  LOC148809 5'  ACCAGCCTGGCCAACACAGTGA 79743       CA
                AA                TTTCAC  TGTTGGCCAGGCTGGT
                                  ||||||  ||||||||||||||||
                                  AAAGTG  ACAACCGGTCCGACCA
                                    AC
GAM320  LOC148809 3'  ACCAGCTGGCCAACATGGTGGA 79744              G
                A                  TTTCACCATGTTGGCCAG CTGGT
                                   |||||||||||||||||| |||||
                                   AAGGTGGTACAACCGGTC GACCA
                                                 _
GAM320  LOC148918 5'  ACCAGCCTGGCCAACATGGTGA 79812
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC148936 3'  ACCATCCTGGCCAACATGGTGA 85445              C
                AA                TTTCACCATGTTGGCCAGG TGGT
                                  |||||||||||||||||| ||||
                                  AAAGTGGTACAACCGGTCC ACCA
                                               T
GAM320  LOC148938 3'  ACCATCCTGGCCAACATGGTGA 85427              C
                AA                TTTCACCATGTTGGCCAGG TGGT
                                  |||||||||||||||||| ||||
                                  AAAGTGGTACAACCGGTCC ACCA
                                               T
GAM320  LOC149073 3'  ACCAGCCTGACCAACATGGCGA 85477     A       C
                AA                TTTC CCATGTTGG CAGGCTGGT
                                  |||| ||||||||| |||||||||
                                  AAAG GGTACAACC GTCCGACCA
                                    C       A
GAM320  LOC149113 3'  ACCAGCCTAGCCAAGATGGTGA 79895        G    C
                AA                TTTCACCAT TTGGC AGGCTGGT
                                  ||||||||| ||||| ||||||||
                                  AAAGTGGTA AACCG TCCGACCA
                                       G    A
GAM320  LOC149113 5'  ACCAGCCTGACCAACATGGTGA 79896             C
                AA                TTTCACCATGTTGG CAGGCTGGT
                                  |||||||||||||| |||||||||
                                  AAAGTGGTACAACC GTCCGACCA
                                        A
GAM320  LOC149113 3'  ACCAGCCTGGACAACATAATGA 79897      CC     G
                GA                TTTCA  ATGTTG CCAGGCTGGT
                                  |||||  |||||| ||||||||||
                                  AGAGT  TACAAC GGTCCGACCA
                                    AA     A
GAM320  LOC149194 5'  ACCAGCCTGGCTAACATGGTGA 79972
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
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                                AAAGTGGTACAATCGGTCCGACCA

GAM320   LOC149271 3'  ACTAGCCTGGTCAACATGGTGA 79992
                 AA                TTTCACCATGTTGGCCAGGCTGGT
                                   ||||||||||||||||||||||||
                                   AAAGTGGTACAACTGGTCCGATCA

GAM320   LOC149319 3'  ACCAGCCTGGCCAACATGGTGA 80063
                 AA                TTTCACCATGTTGGCCAGGCTGGT
                                   ||||||||||||||||||||||||
                                   AAAGTGGTACAACCGGTCCGACCA

GAM320   LOC149460 3'  ACTAGCCTGGCCAATATGGT  85603
                                   ACCATGTTGGCCAGGCTGGT
                                   ||||||||||||||||||||
                                   TGGTATAACCGGTCCGATCA

GAM320   LOC149464 5'  ACCAGCCTGGGCAACATGGT  85581        G
                                   ACCATGTTG CCAGGCTGGT
                                   ||||||||| ||||||||||
                                   TGGTACAAC GGTCCGACCA
                                        G
GAM320   LOC149579 5'  ACCAGCCTGACCAACGTGGAGA 71686     A       C
                 AA                TTTC CCATGTTGG CAGGCTGGT
                                   |||| ||||||||| |||||||||
                                   AAAG GGTGCAACC GTCCGACCA
                                     A       A
GAM320   LOC149628 3'  AGTCTGGCCAACATGGTGAAA  80275
                                   TTTCACCATGTTGGCCAGGCT
                                   |||||||||||||||||||||
                                   AAAGTGGTACAACCGGTCTGA

GAM320   LOC149668 3'  ACCAGCTTGGCCAATATAGTGA 85687       C
                 AA                TTTCAC ATGTTGGCCAGGCTGGT
                                   ||||||| ||||||||||||||||
                                   AAAGTG TATAACCGGTTCGACCA
                                      A
GAM320   LOC149705 3'  ACCAGCCTGGCCAACATGGTGA 85770
                 AA                TTTCACCATGTTGGCCAGGCTGGT
                                   ||||||||||||||||||||||||
                                   AAAGTGGTACAACCGGTCCGACCA

GAM320   LOC149705 3'  ACCAGCCTGGCCAACATGGTGA 85771
                 AA                TTTCACCATGTTGGCCAGGCTGGT
                                   ||||||||||||||||||||||||
                                   AAAGTGGTACAACCGGTCCGACCA

GAM320   LOC149710 3'  ACCAGCCTGACCAACATGGAGA 80326     A       C
                 AA                TTTC CCATGTTGG CAGGCTGGT
                                   |||| ||||||||| |||||||||
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                                AAAG GGTACAACC GTCCGACCA
                                  A       A
GAM320  LOC149711 5'  ACCAGCCTAGGCAGCATAGTGA 85832       C     G _
                GA              TTTCAC ATGTTG CC AGGCTGGT
                                |||||| |||||| || ||||||||
                                AGAGTG TACGAC GG TCCGACCA
                                  A     _ A
GAM320  LOC150139 3'  ACCAGCCTGAGCAACATAGCGA 80409      ACC     GC
                GA              TTTC   ATGTTG  CAGGCTGGT
                                ||||   ||||||  |||||||||
                                AGAG   TACAAC  GTCCGACCA
                                  CGA     GA
GAM320  LOC150185 3'  ACCAGCCTGACCAACATGGTAG 86057     _        C
                AA              TTC ACCATGTTGG CAGGCTGGT
                                ||| |||||||||| |||||||||
                                AAG TGGTACAACC GTCCGACCA
                                  A       A
GAM320  LOC150299 3'  ACCATCCTGGCCAACATGGTGA 86158               C
                AA              TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
                                AAAGTGGTACAACCGGTCC ACCA
                                          T
GAM320  LOC150319 3'  ACCAGCTTGACCAACATGGAGA 80459      A       C
                AA              TTTC CCATGTTGG CAGGCTGGT
                                |||| ||||||||| |||||||||
                                AAAG GGTACAACC GTTCGACCA
                                  A       A
GAM320  LOC150343 3'  ACCAGCCTGGCCAACATGGTGG 80486
                AA              TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAGGTGGTACAACCGGTCCGACCA

GAM320  LOC150358 3'  ACCAGCCTGGCCAACATGGTGA 86082
                                TCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||
                                AGTGGTACAACCGGTCCGACCA

GAM320  LOC150358 3'  ACCATCCTGGCTAACACAGTGA 86083       CA        C
                AA              TTTCAC  TGTTGGCCAGG TGGT
                                ||||||  |||||||||| ||||
                                AAAGTG  ACAATCGGTCC ACCA
                                  AC        T
GAM320  LOC150372 3'  ACCAGCCTGGCCAACGTGGTGA 80601
                AA              TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTGCAACCGGTCCGACCA

GAM320  LOC150465 3'  ACCAGCCTGGGCAGCCTGG   80681    T   G
                                CCA GTTG CCAGGCTGGT
                                ||| |||| ||||||||||
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                                GGT CGAC GGTCCGACCA
                                  C    G
GAM320   LOC150481 3'  ACCATCCTGGCCAACATGGTGA 80689                C
                AA                TTTCACCATGTTGGCCAGG TGGT
                                  |||||||||||||||||| ||||
                                  AAAGTGGTACAACCGGTCC ACCA
                                       T
GAM320   LOC150622 3'  ACCAGCCTGGCCACCATGGTGA 80751          T
                GA                TTTCACCATG TGGCCAGGCTGGT
                                  |||||||||| ||||||||||||
                                  AGAGTGGTAC ACCGGTCCGACCA
                                     C
GAM320   LOC150630 3'  ACCAGCCTGACCAACATGGAGA 86281      A       C
                AA                TTTC CCATGTTGG CAGGCTGGT
                                  |||| ||||||||| |||||||||
                                  AAAG GGTACAACC GTCCGACCA
                                    A       A
GAM320   LOC150935 3'  ACCAGCCTGGCCAACATGGTGA 80822
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320   LOC150960 3'  ACCAGCCTGGGCAACATGGTGA 80862           G
                AA                TTTCACCATGTTG CCAGGCTGGT
                                  |||||||||||| |||||||||
                                  AAAGTGGTACAAC GGTCCGACCA
                                       G
GAM320   LOC151068 3'  ACCAGCCTGGACAACATGGCAA 86402     CA      G
                GA                TTT  CCATGTTG CCAGGCTGGT
                                  |||  |||||||| ||||||||||
                                  AGA  GGTACAAC GGTCCGACCA
                                    AC       A
GAM320   LOC151196 3'  ACCAGCCTGGCCAACATGGTGA 86445
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320   LOC151248 3'  ACCAGCCTGATCAACGTGGTGA 80979           GC
                AA                TTTCACCATGTTG  CAGGCTGGT
                                  ||||||||||||  |||||||||
                                  AAAGTGGTGCAAC  GTCCGACCA
                                       TA
GAM320   LOC151429 3'  ACCAGCCTTGCCAACATGGTGA 86516           C
                AA                TTTCACCATGTTGGC AGGCTGGT
                                  |||||||||||||| ||||||||
                                  AAAGTGGTACAACCG TCCGACCA
                                       T
GAM320   LOC151429 3'  ACCATCCTGGCTAACACGGTGA 86517       A       C
                AA                TTTCACC TGTTGGCCAGG TGGT
                                  ||||||| |||||||||| ||||
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                                AAAGTGG ACAATCGGTCC ACCA
                                   C         T
GAM320  LOC151446 3'  ACCAGCCTAGGCAACATGGTGA 86564           G _
          AA                    TTTCACCATGTTG CC AGGCTGGT
                                |||||||||||| || ||||||||
                                AAAGTGGTACAAC GG TCCGACCA
                                      _ A
GAM320  LOC151556 3'  ACCAGCCTGGCCAACATGGCGA 81073     A
          AA                    TTTC CCATGTTGGCCAGGCTGGT
                                |||| ||||||||||||||||||
                                AAAG GGTACAACCGGTCCGACCA
                                  C
GAM320  LOC151602 3'  ATCAGCCTGGCCAACATGGTGA 81104
          AA                    TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGACTA

GAM320  LOC151614 3'  ACCCTCCTGGCTAACACAGTGA 81117       CA         CT
          AA                    TTTCAC  TGTTGGCCAGG  GGT
                                ||||||  ||||||||||  |||
                                AAAGTG  ACAATCGGTCC  CCA
                                   AC         TC
GAM320  LOC151632 3'  ACCAGCCTGGCCAAAATGGTGA 86636         G
          AA                    TTTCACCAT TTGGCCAGGCTGGT
                                |||||||| ||||||||||||||
                                AAAGTGGTA AACCGGTCCGACCA
                                    A
GAM320  LOC151720 3'  ACCATCCTGGCTAACATGGTGA 81143               C
          AA                    TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
                                AAAGTGGTACAATCGGTCC ACCA
                                          T
GAM320  LOC151904 3'  ACCAGCCTGGCCAACATGGTGA 81196
          AA                    TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC152106 3'  ACCAGCCCAGCCAACATGGCGA 70589     A        CA
          AA                    TTTC CCATGTTGGC  GGCTGGT
                                |||| ||||||||||  |||||||
                                AAAG GGTACAACCG  CCGACCA
                                  C         AC
GAM320  LOC152271 3'  ACCAGCCTGGCCAATGTGGTGA 81349
          AA                    TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTGTAACCGGTCCGACCA

GAM320  LOC152283 3'  CAGCCTGGTCAACATAGTGAAA 86867       C
                                TTTCAC ATGTTGGCCAGGCTG
                                ||||||  ||||||||||||||
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                                AAAGTG TACAACTGGTCCGAC
                                   A
GAM320  LOC152313 3'  ACCATCCTGGCTAACACGGTGA 86841        A         C
                AA              TTTCACC TGTTGGCCAGG TGGT
                                ||||||| |||||||||| ||||
                                AAAGTGG ACAATCGGTCC ACCA
                                   C         T
GAM320  LOC152316 3'  ACCAGCCTGGGAAACATGGT   86787        GG
                                ACCATGTT  CCAGGCTGGT
                                ||||||||  ||||||||||
                                TGGTACAA  GGTCCGACCA
                                   AG
GAM320  LOC152317 3'  ACCAGCCTGGGCAACATGGTGA 86820            G
                AA              TTTCACCATGTTG CCAGGCTGGT
                                |||||||||||| ||||||||||
                                AAAGTGGTACAAC GGTCCGACCA
                                      G
GAM320  LOC152426 3'  ACCATCCTGGCTAACATGGTGA 86885              C
                AA              TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
                                AAAGTGGTACAATCGGTCC ACCA
                                      T
GAM320  LOC152445 3'  ACCAGCCTGACCAACATGGAGA 86923      A       C
                AA              TTTC CCATGTTGG CAGGCTGGT
                                |||| ||||||||| |||||||||
                                AAAG GGTACAACC GTCCGACCA
                                   A       A
GAM320  LOC152445 3'  ACCAGCCTGGCCAACATGATGA 86924      C
                AA              TTTCA CATGTTGGCCAGGCTGGT
                                ||||| ||||||||||||||||||
                                AAAGT GTACAACCGGTCCGACCA
                                   A
GAM320  LOC152453 3'  ACCAGCCTGGGAAGCATGG    81460        GG
                                CCATGTT  CCAGGCTGGT
                                |||||||  ||||||||||
                                GGTACGA  GGTCCGACCA
                                   AG
GAM320  LOC152627 5'  ACTAGCCTGGCCAACATGGTGA 81498
                AA              TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGATCA

GAM320  LOC152804 3'  ACCAACCTAGTCAACATGGTGA 87062            C   C
                AA              TTTCACCATGTTGGC AGG TGGT
                                |||||||||||||| ||| ||||
                                AAAGTGGTACAACTG TCC ACCA
                                      A   A
GAM320  LOC152804 3'  ACCAGCCTGGCCAACATGGTGA 87063
                AA              TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
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                                AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC152926 3'  ACCAGCCTGGCCAACATGGTGA 81626
                AA              TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC153077 3'  ACCATCCTGGCTAACACAGTGA 87102      CA        C
                AA              TTTCAC  TGTTGGCCAGG TGGT
                                ||||||  |||||||||| ||||
                                AAAGTG  ACAATCGGTCC ACCA
                                  AC        T
GAM320  LOC153146 3'  ATCAGCCTGGGCAACATGGTGA 87141          G
                AA              TTTCACCATGTTG CCAGGCTGGT
                                ||||||||||||| ||||||||||
                                AAAGTGGTACAAC GGTCCGACTA
                                      G
GAM320  LOC153260 3'  ACCAGCCTGACCAACATGGTGA 81665          C
                AA              TTTCACCATGTTGG CAGGCTGGT
                                |||||||||||||| |||||||||
                                AAAGTGGTACAACC GTCCGACCA
                                       A
GAM320  LOC153338 3'  CCAGCCTGGCCAACATGGTGAA 87194
                A               TTTCACCATGTTGGCCAGGCTGG
                                |||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGACC

GAM320  LOC153579 3'  ACCAGCCTGGCTAACACAGTGA 81759      CA
                AA              TTTCAC  TGTTGGCCAGGCTGGT
                                ||||||  ||||||||||||||||
                                AAAGTG  ACAATCGGTCCGACCA
                                  AC
GAM320  LOC153642 3'  ACCATCCTGGCCAACATGGTGA 81781            C
                AA              TTTCACCATGTTGGCCAGG TGGT
                                ||||||||||||||||| ||||
                                AAAGTGGTACAACCGGTCC ACCA
                                         T
GAM320  LOC153682 3'  ACCATCCTGGCTAACACAGTGA 87265      CA        C
                AA              TTTCAC  TGTTGGCCAGG TGGT
                                ||||||  |||||||||| ||||
                                AAAGTG  ACAATCGGTCC ACCA
                                  AC        T
GAM320  LOC153688 3'  ACCAGCCTGGGCAACGTGGTGA 87284          G
                AA              TTTCACCATGTTG CCAGGCTGGT
                                |||||||||||| ||||||||||
                                AAAGTGGTGCAAC GGTCCGACCA
                                      G
GAM320  LOC153727 3'  ACCACCCTGGCCAACATGGTGA 87358            C
                AA              TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
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                                AAAGTGGTACAACCGGTCC ACCA
                                      C
GAM320  LOC154089 3'  ACCAGCCTAGGCAACATGGTGA 81938          G _
          AA                    TTTCACCATGTTG CC AGGCTGGT
                                |||||||||||||  || ||||||||
                                AAAGTGGTACAAC GG TCCGACCA
                                     _ A
GAM320  LOC154403 3'  ACCAGCCTAGCCAAGATGGTGA 81961        G    C
          AA                    TTTCACCAT TTGGC AGGCTGGT
                                |||||||||  |||||  ||||||||
                                AAAGTGGTA AACCG TCCGACCA
                                    G    A
GAM320  LOC154403 5'  ACCAGCCTGACCAACATGGTGA 81962          C
          AA                    TTTCACCATGTTGG CAGGCTGGT
                                ||||||||||||||  |||||||||
                                AAAGTGGTACAACC GTCCGACCA
                                      A
GAM320  LOC154403 3'  ACCAGCCTGGGCAACATAATGA 81963      CC     G
          GA                    TTTCA  ATGTTG CCAGGCTGGT
                                |||||  ||||||  ||||||||||
                                AGAGT  TACAAC GGTCCGACCA
                                  AA     G
GAM320  LOC154739 5'  ACCAGCCTGACCAACATGGTGA 87425          C
          AA                    TTTCACCATGTTGG CAGGCTGGT
                                ||||||||||||||  |||||||||
                                AAAGTGGTACAACC GTCCGACCA
                                      A
GAM320  LOC154791 3'  ACCAGCCTGACCAACATGG    82044        C
                                CCATGTTGG CAGGCTGGT
                                |||||||||  |||||||||
                                GGTACAACC GTCCGACCA
                                    A
GAM320  LOC154992 3'  ACCAGCCTAGCCAAGATGGTGA 82123        G    C
          AA                    TTTCACCAT TTGGC AGGCTGGT
                                |||||||||  |||||  ||||||||
                                AAAGTGGTA AACCG TCCGACCA
                                    G    A
GAM320  LOC154992 5'  ACCAGCCTGACCAACATGGTGA 82124          C
          AA                    TTTCACCATGTTGG CAGGCTGGT
                                ||||||||||||||  |||||||||
                                AAAGTGGTACAACC GTCCGACCA
                                      A
GAM320  LOC154992 3'  ACCAGCCTGGGCAACATAATGA 82125      CC     G
          GA                    TTTCA  ATGTTG CCAGGCTGGT
                                |||||  ||||||  ||||||||||
                                AGAGT  TACAAC GGTCCGACCA
                                  AA     G
GAM320  LOC155006 3'  ATCAGCCTGGCCAACATGGTGA 82161
          AA                    TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
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                                AAAGTGGTACAACCGGTCCGACTA

GAM320  LOC155072 3'  ACCATCCTGGCTAACATGGTGA 87648              C
                AA              TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
                                AAAGTGGTACAATCGGTCC ACCA
                                          T
GAM320  LOC155072 3'  ACCATCCTGGCTAACATGGTGA 87649              C
                AA              TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
                                AAAGTGGTACAATCGGTCC ACCA
                                          T
GAM320  LOC155376 3'  ACCAGCCTGGCCAACATGGTGA 82235
                AA              TTTCACCATGTTGGCCAGGCTGGT
                                |||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC157292 5'  ACCAGCCTGGCCAACTTGGTGA 87694       T
                AA              TTTCACCA GTTGGCCAGGCTGGT
                                |||||||| ||||||||||||||
                                AAAGTGGT CAACCGGTCCGACCA
                                    T
GAM320  LOC157464 5'  ACCAGCCTGGCCAACATGG  87741
                                CCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||
                                GGTACAACCGGTCCGACCA

GAM320  LOC157657 3'  ACCAGCCTGGCCAACATG   82426
                                CATGTTGGCCAGGCTGGT
                                ||||||||||||||||||
                                GTACAACCGGTCCGACCA

GAM320  LOC157660 3'  ACCAGCCTGACCAACATGGTGA 87797            C
                AA              TTTCACCATGTTGG CAGGCTGGT
                                |||||||||||||| |||||||||
                                AAAGTGGTACAACC GTCCGACCA
                                       A
GAM320  LOC157983 3'  ACCATCCTGGCCAACGTGGTGA 82533              C
                AA              TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
                                AAAGTGGTGCAACCGGTCC ACCA
                                          T
GAM320  LOC158187 3'  ACCACCCTGGCCAACATGGTGA 87982              C
                                TCACCATGTTGGCCAGG TGGT
                                |||||||||||||||| ||||
                                AGTGGTACAACCGGTCC ACCA
                                       C
GAM320  LOC158191 3'  ACCATCCTGGCCAACATGGTGA 82660              C
                AA              TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
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                                  AAAGTGGTACAACCGGTCC ACCA
                                                      T
GAM320  LOC158288 3'  ACCATCCTGGCTAACACAGTGA 88015       CA          C
                AA                  TTTCAC  TGTTGGCCAGG TGGT
                                    ||||||  |||||||||||| ||||
                                    AAAGTG  ACAATCGGTCC ACCA
                                       AC          T
GAM320  LOC158292 5'  ACCAGCCTAGCCAACATGCTGA 88032       C        C
                AA                  TTTCA CATGTTGGC AGGCTGGT
                                    ||||| ||||||||| ||||||||
                                    AAAGT GTACAACCG TCCGACCA
                                       C        A
GAM320  LOC158292 5'  ACCATCCTGGCTAACACGGTGA 88033        A          C
                AA                  TTTCACC TGTTGGCCAGG TGGT
                                    ||||||| |||||||||||| ||||
                                    AAAGTGG ACAATCGGTCC ACCA
                                       C          T
GAM320  LOC158310 3'  ACCAGCCTGGGCAACATAGTGA 88070       C     G
                GA                  TTTCAC ATGTTG CCAGGCTGGT
                                    |||||| |||||| ||||||||||
                                    AGAGTG TACAAC GGTCCGACCA
                                       A     G
GAM320  LOC158382 5'  ACCAGCCTGGGCAACATAGTGA 88122       C     G
                GA                  TTTCAC ATGTTG CCAGGCTGGT
                                    |||||| |||||| ||||||||||
                                    AGAGTG TACAAC GGTCCGACCA
                                       A     G
GAM320  LOC158677 5'  ACCAGCCTGGCCAACATGGCGA 88241      A
                AA                  TTTC CCATGTTGGCCAGGCTGGT
                                    |||| ||||||||||||||||||
                                    AAAG GGTACAACCGGTCCGACCA
                                      C
GAM320  LOC158819 5'  ACCAGCCTGGCCAACATGGTGA 88261
                AA                  TTTCACCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||||||||
                                    AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC158819 3'  ACCAGCCTGGCCAAGATGGTGA 88262          G
                AA                  TTTCACCAT TTGGCCAGGCTGGT
                                    ||||||||| ||||||||||||||
                                    AAAGTGGTA AACCGGTCCGACCA
                                       G
GAM320  LOC158863 3'  ACCAGCCTGGCCAGCATAGTGA 88292       C
                AA                  TTTCAC ATGTTGGCCAGGCTGGT
                                    |||||| ||||||||||||||||
                                    AAAGTG TACGACCGGTCCGACCA
                                       A
GAM320  LOC158987 3'  ACCAGCCTGGCCAACATGGTGA 88317
                AA                  TTTCACCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||||||||
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                                AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC159036 3'  ACCAGCCTGACCAATATGGTGA 88338           C
           AA                  TTTCACCATGTTGG CAGGCTGGT
                               |||||||||||||| |||||||||
                               AAAGTGGTATAACC GTCCGACCA
                                     A
GAM320  LOC159053 3'  ACCAGCCTGGCCAACATGGTGA 88355
           AA                  TTTCACCATGTTGGCCAGGCTGGT
                               ||||||||||||||||||||||||
                               AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC159053 3'  ACCATCCTGGCTAACACGGTGA 88356       A       C
           AA                  TTTCACC TGTTGGCCAGG TGGT
                               ||||||| |||||||||| ||||
                               AAAGTGG ACAATCGGTCC ACCA
                                  C        T
GAM320  LOC159110 3'  ACCAGCCTGGCCAACATGGTGA 82982
           AA                  TTTCACCATGTTGGCCAGGCTGGT
                               ||||||||||||||||||||||||
                               AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC159116 3'  ACCAGCCTGGCCAACATGGTGA 82965
           AA                  TTTCACCATGTTGGCCAGGCTGGT
                               ||||||||||||||||||||||||
                               AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC170395 3'  ACCAGCCTGGCCAACATGGAGA 76859     A
           AA                  TTTC CCATGTTGGCCAGGCTGGT
                               |||| ||||||||||||||||||
                               AAAG GGTACAACCGGTCCGACCA
                                 A
GAM320  LOC196027 3'  ACCAGCCTGGCCCGTATGGT  88935       TT
                               ACCATG  GGCCAGGCTGGT
                               ||||||  ||||||||||||
                               TGGTAT  CCGGTCCGACCA
                                  GC
GAM320  LOC196047 5'  ACCAGCCTGGCCAACATGGTGA 91136
           AA                  TTTCACCATGTTGGCCAGGCTGGT
                               ||||||||||||||||||||||||
                               AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC196528 3'  ACCAGCCTGGCAACATAGTGAG 89103       C     G
           A                    TTTCAC ATGTTG CCAGGCTGGT
                               |||||| |||||| ||||||||||
                               AGAGTG TACAAC GGTCCGACCA
                                  A    _
GAM320  LOC196540 3'  ACCAGCCTGGACAACATGGTGA 91194           G
           AA                  TTTCACCATGTTG CCAGGCTGGT
                               |||||||||||| ||||||||||
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                                AAAGTGGTACAAC GGTCCGACCA
                                      A
GAM320  LOC196761 3'  ACCAGCCTGGCCAACGTGGGGA 91112      A
                AA                TTTC CCATGTTGGCCAGGCTGGT
                                  |||| ||||||||||||||||||
                                  AAAG GGTGCAACCGGTCCGACCA
                                    G
GAM320  LOC197196 3'  ACCAGCCTGGCCAACATGATGA 91289      C
                AA                TTTCA CATGTTGGCCAGGCTGGT
                                  ||||| ||||||||||||||||||
                                  AAAGT GTACAACCGGTCCGACCA
                                    A
GAM320  LOC197196 3'  ACCAGCCTGGCCAACATGATGA 91290      C
                AA                TTTCA CATGTTGGCCAGGCTGGT
                                  ||||| ||||||||||||||||||
                                  AAAGT GTACAACCGGTCCGACCA
                                    A
GAM320  LOC197201 3'  ACCAGCCTGACCAACATGGAGA 89260      A       C
                AA                TTTC CCATGTTGG CAGGCTGGT
                                  |||| ||||||||| |||||||||
                                  AAAG GGTACAACC GTCCGACCA
                                    A       A
GAM320  LOC197201 3'  ACCAGCCTGGGCAACATGGCGA 89261      A       G
                AA                TTTC CCATGTTG CCAGGCTGGT
                                  |||| |||||||| ||||||||||
                                  AAAG GGTACAAC GGTCCGACCA
                                    C       G
GAM320  LOC197319 3'  ACCATCCTGGCCAACACAGTGA 89308       CA          C
                AA                TTTCAC  TGTTGGCCAGG TGGT
                                  ||||||  |||||||||||| ||||
                                  AAAGTG  ACAACCGGTCC ACCA
                                     AC          T
GAM320  LOC197319 3'  ACCATCCTGGCCAACATGGTGA 89309                C
                AA                TTTCACCATGTTGGCCAGG TGGT
                                  |||||||||||||||||| ||||
                                  AAAGTGGTACAACCGGTCC ACCA
                                              T
GAM320  LOC199733 3'  ACCAGCCCAGGCAACATGGTGA 91429            G  A_
                AA                TTTCACCATGTTG CC  GGCTGGT
                                  |||||||||||| ||  |||||||
                                  AAAGTGGTACAAC GG  CCGACCA
                                        _  AC
GAM320  LOC199733 3'  ACCATCCTGGCTAACATGGTGA 91430                C
                AA                TTTCACCATGTTGGCCAGG TGGT
                                  |||||||||||||||||| ||||
                                  AAAGTGGTACAATCGGTCC ACCA
                                              T
GAM320  LOC199786 3'  ACCAGCCTGGCGAACATAGTGA 89731       C    G
                GA                TTTCAC ATGTT GCCAGGCTGGT
                                  |||||| ||||| ||||||||||
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                                AGAGTG TACAA CGGTCCGACCA
                                  A    G
GAM320  LOC199858 3'  ACCATCCTGGCTAACACGGCGA 89789     A  A        C
          AA                    TTTC CC TGTTGGCCAGG TGGT
                                ||||  ||  |||||||||||  ||||
                                AAAG GG ACAATCGGTCC ACCA
                                  C  C         T
GAM320  LOC200014 3'  ACCAGCCTGGCCAACATGGTGA 89911
          AA                    TTTCACCATGTTGGCCAGGCTGGT
                                |||||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC200251 5'  ACCAGCCTGACCAACACGATGA 90055      CCA     C
          AA                    TTTCA   TGTTGG CAGGCTGGT
                                |||||   ||||||  |||||||||
                                AAAGT   ACAACC GTCCGACCA
                                  AGC     A
GAM320  LOC200251 3'  ACCAGCTTGACCAACATGGTGA 90056            C
          AA                    TTTCACCATGTTGG CAGGCTGGT
                                ||||||||||||||  |||||||||
                                AAAGTGGTACAACC GTTCGACCA
                                       A
GAM320  LOC200316 3'  ACCAGCCTGGGCCACACG    90165    _   _
                                TGT TGGCC AGGCTGGT
                                |||  |||||  ||||||||
                                GCA ACCGG TCCGACCA
                                  C    G
GAM320  LOC200317 3'  ACCAGCCTGACCAAGGTGGTGA 90217         G   C
          AA                    TTTCACCAT TTGG CAGGCTGGT
                                |||||||||  ||||  |||||||||
                                AAAGTGGTG AACC GTCCGACCA
                                     G   A
GAM320  LOC200728 3'  ACCATCCTGGCTAACACGGTGA 91678        A        C
          AA                    TTTCACC TGTTGGCCAGG TGGT
                                |||||||  ||||||||||  ||||
                                AAAGTGG ACAATCGGTCC ACCA
                                    C         T
GAM320  LOC200731 3'  CAGCCTTACCAACATGATGAAA 91692      C       CC
                                TTTCA CATGTTGG  AGGCTG
                                |||||  ||||||||  ||||||
                                AAAGT GTACAACC  TCCGAC
                                   A       AT
GAM320  LOC200803 3'  ACCAGCCTGGCCAACATGGTGA 90294
          AA                    TTTCACCATGTTGGCCAGGCTGGT
                                |||||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC200904 3'  ACCAGCCTGACCAACGTGGTGA 91769            C
          AA                    TTTCACCATGTTGG CAGGCTGGT
                                |||||||||||||  |||||||||
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                                AAAGTGGTGCAACC GTCCGACCA
                                       A
GAM320   LOC200918 3'  ACCAGCCTGGCCAACATGGTGA 90362
                 AA                TTTCACCATGTTGGCCAGGCTGGT
                                   ||||||||||||||||||||||||
                                   AAAGTGGTACAACCGGTCCGACCA

GAM320   LOC200940 3'  ACCAGCCTGGCCAACATAGCGA 90382      ACC
                 AA                TTTC   ATGTTGGCCAGGCTGGT
                                   ||||   ||||||||||||||||
                                   AAAG   TACAACCGGTCCGACCA
                                     CGA
GAM320   LOC201173 3'  ACCATCCTGGCTAACATGGTGA 88662                C
                 AA                TTTCACCATGTTGGCCAGG TGGT
                                   |||||||||||||||||| ||||
                                   AAAGTGGTACAATCGGTCC ACCA
                                              T
GAM320   LOC201182 5'  ACCAGCCTGGCCAACATTGTGA 91330       C
                 AA                TTTCAC ATGTTGGCCAGGCTGGT
                                   |||||| ||||||||||||||||
                                   AAAGTG TACAACCGGTCCGACCA
                                      T
GAM320   LOC201220 3'  ACCATCCTGGCTAACATGGTGA 88698                C
                 AA                TTTCACCATGTTGGCCAGG TGGT
                                   |||||||||||||||||| ||||
                                   AAAGTGGTACAATCGGTCC ACCA
                                              T
GAM320   LOC201252 3'  ACCAGCCTGGTCAACTTGGT   89543      T
                                   ACCA GTTGGCCAGGCTGGT
                                   |||| ||||||||||||||
                                   TGGT CAACTGGTCCGACCA
                                     T
GAM320   LOC201627 3'  ACCAGCCTGGCCAACATGGTGA 90444
                 AA                TTTCACCATGTTGGCCAGGCTGGT
                                   ||||||||||||||||||||||||
                                   AAAGTGGTACAACCGGTCCGACCA

GAM320   LOC201685 3'  ACCAGCATGGCCAACCTGGTGA 91831         T       G
                 AA                TTTCACCA GTTGGCCA GCTGGT
                                   |||||||| |||||||| ||||||
                                   AAAGTGGT CAACCGGT CGACCA
                                        C       A
GAM320   LOC201685 3'  ACCAGCCTGGGAAACATAGTGA 91832       C    GG
                 GA                TTTCAC ATGTT  CCAGGCTGGT
                                   |||||| |||||  ||||||||||
                                   AGAGTG TACAA  GGTCCGACCA
                                      A    AG
GAM320   LOC201689 3'  ACCAGCCTGGGCAACATAGTGA 67727       C     G
                 GA                TTTCAC ATGTTG CCAGGCTGGT
                                   |||||| |||||| ||||||||||
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                                AGAGTG TACAAC GGTCCGACCA
                                  A     G
GAM320  LOC201810 3'  ACCAGCCTGACCAACATGGTGA 90498           C
                AA              TTTCACCATGTTGG CAGGCTGGT
                                |||||||||||||| |||||||||
                                AAAGTGGTACAACC GTCCGACCA
                                      A
GAM320  LOC201868 3'  ACCAGCCTAGCCAAGATGGTGA 90510        G    C
                AA              TTTCACCAT TTGGC AGGCTGGT
                                ||||||||| ||||| ||||||||
                                AAAGTGGTA AACCG TCCGACCA
                                   G    A
GAM320  LOC201868 5'  ACCAGCCTGACCAACATGGTGA 90511           C
                AA              TTTCACCATGTTGG CAGGCTGGT
                                |||||||||||||| |||||||||
                                AAAGTGGTACAACC GTCCGACCA
                                      A
GAM320  LOC201895 3'  ACCAGCCTGGCCAACATGGTGA 90537
                AA              TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC201911 3'  ACCAGCCTGACCAACATGGAGA 91857     A       C
                AA              TTTC CCATGTTGG CAGGCTGGT
                                |||| ||||||||| |||||||||
                                AAAG GGTACAACC GTCCGACCA
                                  A       A
GAM320  LOC201931 3'  ACCAGCCTGGGCAACAATGAGA 90556      CCA    G
                                TTTCA   TGTTG CCAGGCTGGT
                                |||||   ||||| ||||||||||
                                AGAGT   ACAAC GGTCCGACCA
                                  A__    G
GAM320  LOC201931 3'  ACCATCCTGGCTAACACGGTGA 90557       A        C
                AA              TTTCACC TGTTGGCCAGG TGGT
                                ||||||| |||||||||| ||||
                                AAAGTGG ACAATCGGTCC ACCA
                                   C         T
GAM320  LOC202020 3'  ACCAGCCTGGCCAACATAGTGA 90594      C
                AA              TTTCAC ATGTTGGCCAGGCTGGT
                                ||||||| ||||||||||||||||
                                AAAGTG TACAACCGGTCCGACCA
                                  A
GAM320  LOC202038 3'  ACCATCCTGGCTAACACGGTGA 90615       A        C
                AA              TTTCACC TGTTGGCCAGG TGGT
                                ||||||| |||||||||| ||||
                                AAAGTGG ACAATCGGTCC ACCA
                                   C         T
GAM320  LOC202052 3'  ACCAGCCTGGCCAACACAGTGA 91894      CA
                AA              TTTCAC  TGTTGGCCAGGCTGGT
                                ||||||  ||||||||||||||||
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                                AAAGTG  ACAACCGGTCCGACCA
                                  AC
GAM320   LOC202134 5'  ACCGGCCTGGCCAACATGGTGA 91913
                 AA              TTTCACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||||||
                                 AAAGTGGTACAACCGGTCCGGCCA

GAM320   LOC202781 3'  ACCAGCCTGGGCGACACGGTGA 91965       A    G
                 AA              TTTCACC TGTTG CCAGGCTGGT
                                 |||||||  |||||  |||||||||
                                 AAAGTGG ACAGC GGTCCGACCA
                                   C    G
GAM320   LOC202868 3'  ACCATCCTGGCTAACATGGTGA 91981              C
                 AA              TTTCACCATGTTGGCCAGG TGGT
                                 ||||||||||||||||||  ||||
                                 AAAGTGGTACAATCGGTCC ACCA
                                             T
GAM320   LOC202868 3'  ACCATCCTGGCTAACATGGTGA 91982              C
                 AA              TTTCACCATGTTGGCCAGG TGGT
                                 ||||||||||||||||||  ||||
                                 AAAGTGGTACAATCGGTCC ACCA
                                             T
GAM320   LOC203025 3'  ACCAGCCTGGCCAACATGGTGA 90736
                 AA              TTTCACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||||||
                                 AAAGTGGTACAACCGGTCCGACCA

GAM320   LOC203083 3'  ACCAGCCTGGCCAACATGGTGA 92078
                 AA              TTTCACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||||||
                                 AAAGTGGTACAACCGGTCCGACCA

GAM320   LOC203276 3'  ACCAACCTGGCCAACATGGTGA 92105              C
                 AA              TTTCACCATGTTGGCCAGG TGGT
                                 ||||||||||||||||||  ||||
                                 AAAGTGGTACAACCGGTCC ACCA
                                             A
GAM320   LOC203289 3'  ACCATCCTGGCCAACGTGGTGA 90860              C
                 AA              TTTCACCATGTTGGCCAGG TGGT
                                 ||||||||||||||||||  ||||
                                 AAAGTGGTGCAACCGGTCC ACCA
                                             T
GAM320   LOC203305 3'  ACCAACCTGGCCAACATGGTGA 92158              C
                 AA              TTTCACCATGTTGGCCAGG TGGT
                                 ||||||||||||||||||  ||||
                                 AAAGTGGTACAACCGGTCC ACCA
                                             A
GAM320   LOC203378 3'  ACCAGCCTGGCCAACATGG    92269
                                 CCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||
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                                GGTACAACCGGTCCGACCA

GAM320  LOC203378 3'  AGCCTGGCAAACATGGCGAAA  92272      A      G
                                TTTC CCATGTT GCCAGGCT
                                |||| ||||||| ||||||||
                                AAAG GGTACAA CGGTCCGA
                                  C      A
GAM320  LOC203397 3'  ACCAGCCTGGCCAACATGGCGA 90895      A
              AA                  TTTC CCATGTTGGCCAGGCTGGT
                                  |||| ||||||||||||||||||
                                  AAAG GGTACAACCGGTCCGACCA
                                    C
GAM320  LOC219376 3'  ACCAGCCTGGCCAACATGGTGA 95511
              AA                  TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC219406 3'  ACCAGCCTGGGCAACGTGGCGA 95200      A      G
              AA                  TTTC CCATGTTG CCAGGCTGGT
                                  |||| |||||||| ||||||||||
                                  AAAG GGTGCAAC GGTCCGACCA
                                    C      G
GAM320  LOC219540 3'  ACCAGCTTGGCCAACATGGCGA 95236      A
              AA                  TTTC CCATGTTGGCCAGGCTGGT
                                  |||| ||||||||||||||||||
                                  AAAG GGTACAACCGGTTCGACCA
                                    C
GAM320  LOC219627 3'  ACCAGCCTGACCAACATGGAGA 93791      A      C
              AA                  TTTC CCATGTTGG CAGGCTGGT
                                  |||| ||||||||| |||||||||
                                  AAAG GGTACAACC GTCCGACCA
                                    A       A
GAM320  LOC219627 3'  ACCATCCTGGCCAACATGGTGA 93792                C
              AA                  TTTCACCATGTTGGCCAGG TGGT
                                  |||||||||||||||||| ||||
                                  AAAGTGGTACAACCGGTCC ACCA
                                                     T
GAM320  LOC219649 3'  ACCAGCCTGGCCAACATGGTGA 94537
              AA                  TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC219649 3'  ACCATCCTGGCTAACACGGTGA 94538        A         C
              AA                  TTTCACC TGTTGGCCAGG TGGT
                                  ||||||| |||||||||| ||||
                                  AAAGTGG ACAATCGGTCC ACCA
                                     C         T
GAM320  LOC219722 5'  ACTAGCCTGACCAACATGGTGA 94672             C
              AA                  TTTCACCATGTTGG CAGGCTGGT
                                  |||||||||||||| |||||||||
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                                AAAGTGGTACAACC GTCCGATCA
                                      A
GAM320   LOC219919 3'  ACCAGCCTGGCCAATGTGGTGA 94915
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTGTAACCGGTCCGACCA

GAM320   LOC220070 3'  ACCAGCCTGGGCAACATGGCAA 59938     CA       G
                GA                TTT  CCATGTTG CCAGGCTGGT
                                  |||  |||||||| ||||||||||
                                  AGA  GGTACAAC GGTCCGACCA
                                    AC       G
GAM320   LOC220370 3'  ACCAGCCTGGCCAACATGGTGA 94390
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320   LOC220506 3'  AGTCTGGGCAACACGATGAAA  74515       CCA     G
                                  TTTCA   TGTTG CCAGGCT
                                  |||||   ||||| |||||||
                                  AAAGT   ACAAC GGTCTGA
                                     AGC     G
GAM320   LOC220575 3'  ACCAGCCTGGGCAACATGGTGA 76810            G
                AA                TTTCACCATGTTG CCAGGCTGGT
                                  |||||||||||| ||||||||||
                                  AAAGTGGTACAAC GGTCCGACCA
                                        G
GAM320   LOC220662 3'  ACCAGCCTGGCCAACGTGGTGA 92799
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTGCAACCGGTCCGACCA

GAM320   LOC221042 3'  ACCATTCTGGCCAACATGGTGA 94790                GC
                AA                TTTCACCATGTTGGCCAG  TGGT
                                  ||||||||||||||||  ||||
                                  AAAGTGGTACAACCGGTC  ACCA
                                        TT
GAM320   LOC221069 3'  ACCAGCCTGGGCAACACGGTGA 94815        A    G
                AA                TTTCACC TGTTG CCAGGCTGGT
                                  |||||||  ||||| ||||||||||
                                  AAAGTGG ACAAC GGTCCGACCA
                                     C    G
GAM320   LOC221271 3'  ACCATCCTGGCTAACACAGTGA 93486       CA         C
                AA                TTTCAC  TGTTGGCCAGG TGGT
                                  ||||||  |||||||||| ||||
                                  AAAGTG  ACAATCGGTCC ACCA
                                     AC          T
GAM320   LOC221271 3'  ACCATCCTGGCTAACACGGTGA 93487        A         C
                AA                TTTCACC TGTTGGCCAGG TGGT
                                  |||||||  |||||||||| ||||
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                                AAAGTGG ACAATCGGTCC ACCA
                                   C         T
GAM320   LOC221410 3'  ACCATCCTGGCTAACATGGTGA 93684                C
                AA                  TTTCACCATGTTGGCCAGG TGGT
                                    |||||||||||||||||| ||||
                                    AAAGTGGTACAATCGGTCC ACCA
                                          T
GAM320   LOC221474 3'  ACCAGCCTGGCCAACATAGGGA 93984      A  _
                AA                  TTTC CC ATGTTGGCCAGGCTGGT
                                    |||| || |||||||||||||||||
                                    AAAG GG TACAACCGGTCCGACCA
                                     _  A
GAM320   LOC221477 3'  ACCAGCCTGGCCAACAGGGTGA 93761         A
                AA                  TTTCACC TGTTGGCCAGGCTGGT
                                    ||||||| |||||||||||||||
                                    AAAGTGG ACAACCGGTCCGACCA
                                       G
GAM320   LOC221490 3'  ACCAGCCTGACCAATATGGTGA 95295              C
                AA                  TTTCACCATGTTGG CAGGCTGGT
                                    |||||||||||||| |||||||||
                                    AAAGTGGTATAACC GTCCGACCA
                                          A
GAM320   LOC221543 3'  ACCAGCCTGGCCAACATGGTGA 95353
                AA                  TTTCACCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||||||||
                                    AAAGTGGTACAACCGGTCCGACCA

GAM320   LOC221543 3'  ACCAGCCTGGCCAACATGGTGA 95354
                AA                  TTTCACCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||||||||
                                    AAAGTGGTACAACCGGTCCGACCA

GAM320   LOC221543 5'  ACCATCCTGGCTAACACGGTGA 95355         A          C
                AA                  TTTCACC TGTTGGCCAGG TGGT
                                    ||||||| |||||||||| ||||
                                    AAAGTGG ACAATCGGTCC ACCA
                                       C         T
GAM320   LOC221550 3'  ACCAGCCTGGCCAACATGG    93741
                                    CCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||
                                    GGTACAACCGGTCCGACCA

GAM320   LOC221641 5'  ACCAGCCTGACCAACATGGTGA 95337              C
                AA                  TTTCACCATGTTGG CAGGCTGGT
                                    |||||||||||||| |||||||||
                                    AAAGTGGTACAACC GTCCGACCA
                                          A
GAM320   LOC221641 3'  ACCAGCCTGGACAACATAATGA 95338       CC     G
                GA                  TTTCA  ATGTTG CCAGGCTGGT
                                    |||||  |||||| ||||||||||
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                                AGAGT  TACAAC GGTCCGACCA
                                  AA     A
GAM320   LOC221795 3'  ACCAGCCTGGACAACATGGTGA 94064           G
                  AA                TTTCACCATGTTG CCAGGCTGGT
                                    |||||||||||| ||||||||||
                                    AAAGTGGTACAAC GGTCCGACCA
                                          A
GAM320   LOC221943 5'  ACCAGCCTGGCCAACATGGCGA 95614      A
                  AA                TTTC CCATGTTGGCCAGGCTGGT
                                    |||| ||||||||||||||||||
                                    AAAG GGTACAACCGGTCCGACCA
                                      C
GAM320   LOC221954 5'  ACCAGCCTGGCCAACATGGTGA 95636
                  AA                TTTCACCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||||||||
                                    AAAGTGGTACAACCGGTCCGACCA

GAM320   LOC222060 5'  ACCAGCCTGGTCAACATGGTGA 95747
                  AA                TTTCACCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||||||||
                                    AAAGTGGTACAACTGGTCCGACCA

GAM320   LOC222066 3'  ACCAACCTGGCCAAAGTGGTGA 94307         G        C
                  AA                TTTCACCAT TTGGCCAGG TGGT
                                    ||||||||| ||||||||| ||||
                                    AAAGTGGTG AACCGGTCC ACCA
                                         A        A
GAM320   LOC222160 3'  ACCAGCCTGGCCAGCATGG    95767
                                    CCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||
                                    GGTACGACCGGTCCGACCA

GAM320   LOC222160 5'  ACCATCCTGGCTAACACGGTGA 95768         A          C
                  AA                TTTCACC TGTTGGCCAGG TGGT
                                    ||||||| |||||||||| ||||
                                    AAAGTGG ACAATCGGTCC ACCA
                                       C          T
GAM320   LOC222182 3'  ACCAGCCTGGCCAACATGGTGA 95850
                  AA                TTTCACCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||||||||
                                    AAAGTGGTACAACCGGTCCGACCA

GAM320   LOC222865 3'  CCTGGCTAACACGGTGAAA    94444         A
                                    TTTCACC TGTTGGCCAGG
                                    ||||||| ||||||||||
                                    AAAGTGG ACAATCGGTCC
                                       C
GAM320   LOC253532 3'  ACCAGCCTGGCCAACATGGTGA 97725
                  AA                TTTCACCATGTTGGCCAGGCTGGT
                                    ||||||||||||||||||||||||
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                                AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC253612 5'  ACCAGCCTGACCAACATGGTGA 98541            C
                AA                TTTCACCATGTTGG CAGGCTGGT
                                  |||||||||||||| |||||||||
                                  AAAGTGGTACAACC GTCCGACCA
                                        A
GAM320  LOC253639 3'  ACCAGCCCGCCCAATATGGTGA 97506            CCA
                AA                TTTCACCATGTTGG   GGCTGGT
                                  ||||||||||||||   |||||||
                                  AAAGTGGTATAACC   CCGACCA
                                        CGC
GAM320  LOC253664 3'  ACCAGCCTGGGCAACATAGTGA 96452       C     G
                GA                TTTCAC ATGTTG CCAGGCTGGT
                                  |||||| |||||| ||||||||||
                                  AGAGTG TACAAC GGTCCGACCA
                                     A     G
GAM320  LOC253778 5'  ACCAGCCTGGCCAACATGGTGA 96521
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC253840 3'  ACCAGACTGGCCAACATGGAGA 97907      A          G
                AA                TTTC CCATGTTGGCCAG CTGGT
                                  |||| |||||||||||| |||||
                                  AAAG GGTACAACCGGTC GACCA
                                     A           A
GAM320  LOC253927 3'  ACCATCCTGGCAAACATGGTGA 96724           G     C
                AA                TTTCACCATGTT GCCAGG TGGT
                                  |||||||||||| |||||| ||||
                                  AAAGTGGTACAA CGGTCC ACCA
                                        A     T
GAM320  LOC254041 5'  ACCATCCTGGCCAACATGGGGA 96549      A          C
                AA                TTTC CCATGTTGGCCAGG TGGT
                                  |||| |||||||||||||| ||||
                                  AAAG GGTACAACCGGTCC ACCA
                                     G           T
GAM320  LOC254045 3'  ACCAGCCTGGCCAACATGG    98258
                                  CCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||
                                  GGTACAACCGGTCCGACCA

GAM320  LOC254100 3'  ACCAGCCTGGCCAACATAGTGA 98145       C
                AA                TTTCAC ATGTTGGCCAGGCTGGT
                                  |||||| ||||||||||||||||
                                  AAAGTG TACAACCGGTCCGACCA
                                     A
GAM320  LOC254176 3'  ACCAGCCTGGCCAACATGGTGA 99159
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
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                                AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC254243 3'  ACCAACCTGGCCAACATGGTGA 99245                C
                AA                TTTCACCATGTTGGCCAGG TGGT
                                  |||||||||||||||||| ||||
                                  AAAGTGGTACAACCGGTCC ACCA
                                             A
GAM320  LOC254249 5'  ACCAGCCTGGGCAACATGGTGA 97179            G
                AA                TTTCACCATGTTG CCAGGCTGGT
                                  |||||||||||| ||||||||||
                                  AAAGTGGTACAAC GGTCCGACCA
                                        G
GAM320  LOC254266 3'  ACCATCCTGGCTAACACAGTGA 99190       CA       C
                AA                TTTCAC  TGTTGGCCAGG TGGT
                                  ||||||  |||||||||||| ||||
                                  AAAGTG  ACAATCGGTCC ACCA
                                     AC         T
GAM320  LOC254351 3'  ACCGCCTGGGCAACATGGTGAA 96677            G     T
                A                 TTTCACCATGTTG CCAGGC GGT
                                  |||||||||||| |||||| |||
                                  AAAGTGGTACAAC GGTCCG CCA
                                        G     _
GAM320  LOC254531 5'  ACCAGCCTGACCAACATGG    96657         C
                                  CCATGTTGG CAGGCTGGT
                                  ||||||||| |||||||||
                                  GGTACAACC GTCCGACCA
                                       A
GAM320  LOC254808 3'  ACCATCCTGGCTAACACGGTGA 98798        A        C
                AA                TTTCACC TGTTGGCCAGG TGGT
                                  ||||||| |||||||||||| ||||
                                  AAAGTGG ACAATCGGTCC ACCA
                                     C         T
GAM320  LOC254875 3'  ACCAGCCTGGCCAACATGGTGA 97768
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC255031 3'  ACCAGCCTGGGCAACATAGTGA 99026       C     G
                GA                TTTCAC ATGTTG CCAGGCTGGT
                                  |||||| |||||| ||||||||||
                                  AGAGTG TACAAC GGTCCGACCA
                                     A     G
GAM320  LOC255042 3'  ACCAGCCTGACCAACAACATGG 97025      A    ___  C
                AGAAA               TTTC CCATGT   TGG CAGGCTGGT
                                    |||| ||||||   ||| |||||||||
                                    AAAG GGTACA   ACC GTCCGACCA
                                      A     ACA   A
GAM320  LOC255042 3'  ACCAGCCTGGACAACATGGTGA 97026            G
                AA                TTTCACCATGTTG CCAGGCTGGT
                                  |||||||||||| ||||||||||
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                                AAAGTGGTACAAC GGTCCGACCA
                                      A
GAM320  LOC255042 3'  ACCAGCCTGGCCAATACGATGA 97027      CCA
          AA                    TTTCA   TGTTGGCCAGGCTGGT
                                |||||   ||||||||||||||||
                                AAAGT   ATAACCGGTCCGACCA
                                  AGC
GAM320  LOC255177 3'  ACCAGCCAGACCAACATGATGA 98384      C       CCA
          AA                    TTTCA CATGTTGG   GGCTGGT
                                ||||| ||||||||   |||||||
                                AAAGT GTACAACC   CCGACCA
                                  A       AGA
GAM320  LOC255196 3'  ACCAGCCGGGCCAACATGGTGA 98943             A
          AA                    TTTCACCATGTTGGCC GGCTGGT
                                |||||||||||||||| |||||||
                                AAAGTGGTACAACCGG CCGACCA
                                      G
GAM320  LOC255196 3'  ACCAGCCTGGGGAACATAATGA 98944      CC    GG
          GA                    TTTCA  ATGTT  CCAGGCTGGT
                                |||||  |||||  ||||||||||
                                AGAGT  TACAA  GGTCCGACCA
                                  AA    GG
GAM320  LOC255231 3'  ACCAGCCTGGGCAACATGG   97113        G
                                CCATGTTG CCAGGCTGGT
                                |||||||| ||||||||||
                                GGTACAAC GGTCCGACCA
                                   G
GAM320  LOC255252 3'  AGCGTGGCCAACATGAGGAAA  96704      AC         G
                                TTTC  CATGTTGGCCA GCT
                                ||||  |||||||||| |||
                                AAAG  GTACAACCGGT CGA
                                  GA         G
GAM320  LOC255328 3'  ACCAGCCTGGCCAACATGGCGA 98330      A
          AA                    TTTC CCATGTTGGCCAGGCTGGT
                                |||| ||||||||||||||||||
                                AAAG GGTACAACCGGTCCGACCA
                                  C
GAM320  LOC255463 3'  ACCAGCTTGTGCAACATGGTGA 96536           GC
          AA                    TTTCACCATGTTG  CAGGCTGGT
                                ||||||||||||  |||||||||
                                AAAGTGGTACAAC  GTTCGACCA
                                      GT
GAM320  LOC255671 3'  ACCAGCCTGGCCCACATGGTGA 99060          T
          AA                    TTTCACCATGT GGCCAGGCTGGT
                                |||||||||| ||||||||||||
                                AAAGTGGTACA CCGGTCCGACCA
                                      C
GAM320  LOC255798 3'  ACCAGCCTGGGCAACACAGTGA 98785      CA    G
                                TCAC  TGTTG CCAGGCTGGT
                                ||||  ||||| ||||||||||
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                                AGTG  ACAAC GGTCCGACCA
                                  AC     G
GAM320   LOC255937 3'  ACCAGCCTGACCAACATGGTGA 97675            C
                 AA                TTTCACCATGTTGG CAGGCTGGT
                                   |||||||||||||| |||||||||
                                   AAAGTGGTACAACC GTCCGACCA
                                            A
GAM320   LOC255971 3'  ACCAGTCTGGCCAATATGGTGA 98303
                 AA                TTTCACCATGTTGGCCAGGCTGGT
                                   |||||||||||||||||||||||||
                                   AAAGTGGTATAACCGGTCTGACCA

GAM320   LOC256073 3'  ACCAGCCTGGGCAACATAGCGA 98482      ACC      G
                 GA                TTTC   ATGTTG CCAGGCTGGT
                                   ||||   |||||| ||||||||||
                                   AGAG   TACAAC GGTCCGACCA
                                     CGA      G
GAM320   LOC256207 3'  ACCAACCTCCAACATGGTGAAA 96867            CC   C
                                   TTTCACCATGTTGG  AGG TGGT
                                   ||||||||||||||  ||| ||||
                                   AAAGTGGTACAACC  TCC ACCA
                                            __   A
GAM320   LOC256267 3'  ACCAGCCTGGCCAACATGGTGA 98603
                 AA                TTTCACCATGTTGGCCAGGCTGGT
                                   |||||||||||||||||||||||||
                                   AAAGTGGTACAACCGGTCCGACCA

GAM320   LOC256277 3'  ACCAGCCTGGCCAACATGGTGA 96347
                 AA                TTTCACCATGTTGGCCAGGCTGGT
                                   |||||||||||||||||||||||||
                                   AAAGTGGTACAACCGGTCCGACCA

GAM320   LOC256515 3'  ACCAGCCTGGCCAACATGGTGA 98201
                 AA                TTTCACCATGTTGGCCAGGCTGGT
                                   |||||||||||||||||||||||||
                                   AAAGTGGTACAACCGGTCCGACCA

GAM320   LOC256520 3'  ACCAGCCTGGCCAACATGGTGA 97661
                 AA                TTTCACCATGTTGGCCAGGCTGGT
                                   |||||||||||||||||||||||||
                                   AAAGTGGTACAACCGGTCCGACCA

GAM320   LOC256544 3'  ACCATCCTGGCCAACGTGGTGA 97924              C
                 AA                TTTCACCATGTTGGCCAGG TGGT
                                   |||||||||||||||||| ||||
                                   AAAGTGGTGCAACCGGTCC ACCA
                                             T
GAM320   LOC257115 3'  ACCAGCCTGGATGACAGAGCGA 98289      ACCA    GG
                 AA                TTTC    TGTT  CCAGGCTGGT
                                   ||||    ||||  ||||||||||
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                                AAAG    ACAG  GGTCCGACCA
                                  CGAG    TA
GAM320   LOC257180 3'  ACTAGCCTGGCCAACATAGTGA 97311       C
           AA                     TTTCAC ATGTTGGCCAGGCTGGT
                                  |||||| ||||||||||||||||||
                                  AAAGTG TACAACCGGTCCGATCA
                                    A
GAM320   LOC257354 3'  ACCAGCCTGGGCAACATAGTGA 96782       C     G
           GA                     TTTCAC ATGTTG CCAGGCTGGT
                                  |||||| |||||| ||||||||||
                                  AGAGTG TACAAC GGTCCGACCA
                                    A     G
GAM320   LOC257495 3'  ACCAGCCTGGCCAACATGG    99568
                                  CCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||
                                  GGTACAACCGGTCCGACCA

GAM320   LOC257539 3'  ACCATCCTGGCTAACACGGTGA 99541        A         C
           AA                     TTTCACC TGTTGGCCAGG TGGT
                                  ||||||| |||||||||| ||||
                                  AAAGTGG ACAATCGGTCC ACCA
                                    C         T
GAM320   LOC257576 3'  ACCAGCCTGGCCAACATGG    99705
                                  CCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||
                                  GGTACAACCGGTCCGACCA

GAM320   LOC257578 3'  ACCATCCTGGCTAACACGGTGA 99653        A         C
           AA                     TTTCACC TGTTGGCCAGG TGGT
                                  ||||||| |||||||||| ||||
                                  AAAGTGG ACAATCGGTCC ACCA
                                    C         T
GAM320   LOC257596 3'  ACCAGCCTGGCCAACATGGTGA 99756
           AA                     TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320   LOC257596 3'  ACCAGCCTGGCCAACATGGTGA 99757
           AA                     TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320   LOC257596 5'  ACCATCCTGGCTAACACGGTGA 99758        A         C
           AA                     TTTCACC TGTTGGCCAGG TGGT
                                  ||||||| |||||||||| ||||
                                  AAAGTGG ACAATCGGTCC ACCA
                                    C         T
GAM320   LOC51122  3'  ACCTTCCTGGCTAACATGGTGA 66191              CT
           AA                     TTTCACCATGTTGGCCAGG  GGT
                                  |||||||||||||||||  |||
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                                AAAGTGGTACAATCGGTCC  CCA
                                      TT
GAM320  LOC51145  3'  ACCAGCCTGGCCAACATGGTGA 32916
              AA                  TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC51279  3'  CCTGGCCAACATGGTGAAA   33753
                                  TTTCACCATGTTGGCCAGG
                                  |||||||||||||||||||
                                  AAAGTGGTACAACCGGTCC

GAM320  LOC51333  3'  ACCAGCCTGGCCAACATGGTGA 34048
              AA                  TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC51336  3'  ACCAGCCTGGCCAAGATGGTGG 34063         G
              AA                  TTTCACCAT TTGGCCAGGCTGGT
                                  |||||||||  ||||||||||||||
                                  AAGGTGGTA AACCGGTCCGACCA
                                       G
GAM320  LOC51759  3'  ACCAGCCTGACCAACATGGAGA 73165      A       C
              AA                  TTTC CCATGTTGG CAGGCTGGT
                                  ||||  |||||||||  |||||||||
                                  AAAG GGTACAACC GTCCGACCA
                                    A        A
GAM320  LOC55974  3'  ACCAACCTGACTAACATGGTGA 38738            C   C
              AA                  TTTCACCATGTTGG CAGG TGGT
                                  ||||||||||||||  ||||  ||||
                                  AAAGTGGTACAATC GTCC ACCA
                                           A   A
GAM320  LOC57118  3'  ACCAGCCTGACCAACATGGTGA 40212            C
              AA                  TTTCACCATGTTGG CAGGCTGGT
                                  ||||||||||||||  |||||||||
                                  AAAGTGGTACAACC GTCCGACCA
                                           A
GAM320  LOC63929  3'  ACCAGCCTGGCCAACGTGGTGA 42274
              AA                  TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTGCAACCGGTCCGACCA

GAM320  LOC85479  5'  ACCATCCTGGCTAACACAGTGA 53557       CA         C
              AA                  TTTCAC  TGTTGGCCAGG TGGT
                                  ||||||  ||||||||||| ||||
                                  AAAGTG  ACAATCGGTCC ACCA
                                     AC          T
GAM320  LOC89890  3'  ACCAGCCTGGCCAACATGGTGA 61199
              AA                  TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
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                                AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC90038  3' ACCAACCTGGCCAACATGGTGA 61789                C
             AA                  TTTCACCATGTTGGCCAGG TGGT
                                 |||||||||||||||||| ||||
                                 AAAGTGGTACAACCGGTCC ACCA
                                           A
GAM320  LOC90072  3' ACCAGCCTGAGCAACATAGTGA 61944       C     GC
             GA                  TTTCAC ATGTTG  CAGGCTGGT
                                 |||||| ||||||  |||||||||
                                 AGAGTG TACAAC  GTCCGACCA
                                    A     GA
GAM320  LOC90092  3' ACCAGCCTGGCCAACATAATGA 62049      CC
             AA                  TTTCA  ATGTTGGCCAGGCTGGT
                                 |||||  ||||||||||||||||
                                 AAAGT  TACAACCGGTCCGACCA
                                    AA
GAM320  LOC90092  3' ACCAGCCTGGCCAACATGG    62050
                                 CCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||
                                 GGTACAACCGGTCCGACCA

GAM320  LOC90155  5' ACCAGCCTGGCCAACATGGTGA 62358
             A                    TTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||
                                  AAGTGGTACAACCGGTCCGACCA

GAM320  LOC90233  3' ACCAGCCTGGGCAACATGGTGA 57187            G
             AA                  TTTCACCATGTTG CCAGGCTGGT
                                 |||||||||||| ||||||||||
                                 AAAGTGGTACAAC GGTCCGACCA
                                       G
GAM320  LOC90321  3' ACCAGCCTGGCCAATATGGTGA 62926
             AA                  TTTCACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||||||
                                 AAAGTGGTATAACCGGTCCGACCA

GAM320  LOC90509  3' ACCATCCTGGCTAACACGGTGA 63788       A       C
             AA                  TTTCACC TGTTGGCCAGG TGGT
                                 ||||||| |||||||||| ||||
                                 AAAGTGG ACAATCGGTCC ACCA
                                    C         T
GAM320  LOC90573  3' ACCAGCCTGGCCAACATG    63952
                                 CATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||
                                 GTACAACCGGTCCGACCA

GAM320  LOC90589  3' ACCAGCCTGGTCAATATGGTGA 59771
             AA                  TTTCACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||||||
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                                AAAGTGGTATAACTGGTCCGACCA

GAM320  LOC90591  3' ACCAGCCTGGCTAACATGG   64133
                                CCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||
                                GGTACAATCGGTCCGACCA

GAM320  LOC90591  3' ACCAGCCTGGGCAACATAGTGA 64134       C     G
             AA                   TTTCAC ATGTTG CCAGGCTGGT
                                ||||||| ||||||| ||||||||||
                                AAAGTG TACAAC GGTCCGACCA
                                   A     G
GAM320  LOC90624  3' ACCAGCCTGGCCAATGTGGTGA 64362
             AA                   TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTGTAACCGGTCCGACCA

GAM320  LOC90785  3' ACCAGCCTGGCCAACGTGGTGA 64706
             AA                   TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTGCAACCGGTCCGACCA

GAM320  LOC90841  5' ACCAGCCTGGCCAACATGGTGA 64861
             AA                   TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC90918  5' ACCAGCCTGACCAACATGGTGA 64992             C
             AA                   TTTCACCATGTTGG CAGGCTGGT
                                |||||||||||||| |||||||||
                                AAAGTGGTACAACC GTCCGACCA
                                      A
GAM320  LOC90979  3' ACCATCCTGGCCAACATGGTGA 65133                 C
             AA                   TTTCACCATGTTGGCCAGG TGGT
                                |||||||||||||||||| ||||
                                AAAGTGGTACAACCGGTCC ACCA
                                         T
GAM320  LOC91035  3' ACCAGCCTGGGCAACATGGAGA 65291      A       G
             AA                   TTTC CCATGTTG CCAGGCTGGT
                                |||| |||||||| ||||||||||
                                AAAG GGTACAAC GGTCCGACCA
                                   A       G
GAM320  LOC91056  3' AGCCTGGCCAGCATGGCGAAA  96399      A
                                TTTC CCATGTTGGCCAGGCT
                                |||| ||||||||||||||||
                                AAAG GGTACGACCGGTCCGA
                                  C
GAM320  LOC91064  3' ACCAGCCTGGCCAACATGGTGA 65384
             AA                   TTTCACCATGTTGGCCAGGCTGGT
                                ||||||||||||||||||||||||
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                                AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC91115  3' ACCATCCTGGCCAACATAGTGA 65536       C          C
             AA                  TTTCAC ATGTTGGCCAGG TGGT
                                 |||||| |||||||||||| ||||
                                 AAAGTG TACAACCGGTCC ACCA
                                    A           T
GAM320  LOC91250  5' AGCCTGGCCAACTTAGTGAAA  65905       CAT
                                 TTTCAC   GTTGGCCAGGCT
                                 ||||||   ||||||||||||
                                 AAAGTG   CAACCGGTCCGA
                                    ATT
GAM320  LOC91286  3' ACCAGCCCGGCCAACATGGTGA 66055              A
             AA                  TTTCACCATGTTGGCC GGCTGGT
                                 |||||||||||||||| |||||||
                                 AAAGTGGTACAACCGG CCGACCA
                                           C
GAM320  LOC91380  3' CCAGCCTGGCCAACATGGCGAA 66441      A
             A                    TTTC CCATGTTGGCCAGGCTGG
                                  |||| ||||||||||||||||||
                                  AAAG GGTACAACCGGTCCGACC
                                    C
GAM320  LOC91397  3' ACCTGCCTGGGCAACATGG    66495        G     T
                                 CCATGTTG CCAGGC GGT
                                 |||||||| |||||| |||
                                 GGTACAAC GGTCCG CCA
                                       G     T
GAM320  LOC91442  3' ACCAGCCTGGCCAACATGGAGA 66638      A
             AA                  TTTC CCATGTTGGCCAGGCTGGT
                                 |||| ||||||||||||||||||
                                 AAAG GGTACAACCGGTCCGACCA
                                   A
GAM320  LOC91574  3' ACCAGCCTGGCCAACATGGTGA 67106
             AA                  TTTCACCATGTTGGCCAGGCTGGT
                                 ||||||||||||||||||||||||
                                 AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC91660  3' ACCAGCCTAGCCAACATGG    67400          C
                                 CCATGTTGGC AGGCTGGT
                                 |||||||||| ||||||||
                                 GGTACAACCG TCCGACCA
                                       A
GAM320  LOC91750  3' ACCATCCTGGCCAATATGGTGA 67642               C
             AA                  TTTCACCATGTTGGCCAGG TGGT
                                 |||||||||||||||||| ||||
                                 AAAGTGGTATAACCGGTCC ACCA
                                           T
GAM320  LOC91948  3' ACCAGCCTGGCCAACATGGCGA 68231      A
             AA                  TTTC CCATGTTGGCCAGGCTGGT
                                 |||| ||||||||||||||||||
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                                AAAG GGTACAACCGGTCCGACCA
                                  C
GAM320  LOC91963  5' ATCAGCCTGGCCAACATG    68311
                                CATGTTGGCCAGGCTGGT
                                ||||||||||||||||||
                                GTACAACCGGTCCGACTA

GAM320  LOC91974  5' ACCAGCCTGGTTTCATACCGAA 68358      ACC   TT
          A                      TTTC   ATG  GGCCAGGCTGGT
                                 ||||   |||  ||||||||||||
                                 AAAG   TAC  TTGGTCCGACCA
                                   CCA   T_
GAM320  LOC92078  3' ACCAGCCTGGCCAACATGGCGA 68585      A
          AA                     TTTC CCATGTTGGCCAGGCTGGT
                                 ||||| ||||||||||||||||||
                                 AAAG GGTACAACCGGTCCGACCA
                                   C
GAM320  LOC92223  3' ACCAGCCTGACCAATATGATGA 69043       C       C
          AA                     TTTCA CATGTTGG CAGGCTGGT
                                 ||||| |||||||| |||||||||
                                 AAAGT GTATAACC GTCCGACCA
                                    A       A
GAM320  LOC92228  3' ACCAGGTTGGCCAACATGGTGA 69066                 G
          GA                     TTTCACCATGTTGGCCAG CTGGT
                                 |||||||||||||||| |||||
                                 AGAGTGGTACAACCGGTT GACCA
                                          G
GAM320  LOC92267  3' ACCAGCCTGACCAATATGGTGA 69160              C
          AA                     TTTCACCATGTTGG CAGGCTGGT
                                 |||||||||||||| |||||||||
                                 AAAGTGGTATAACC GTCCGACCA
                                       A
GAM320  LOC92270  5' AGCCTGGCCAACATGGTGAAA  69183
                                 TTTCACCATGTTGGCCAGGCT
                                 |||||||||||||||||||||
                                 AAAGTGGTACAACCGGTCCGA

GAM320  LOC92283  3' ACCATCCTGGCTAACATGGTGA 69296                 C
          AA                     TTTCACCATGTTGGCCAGG TGGT
                                 |||||||||||||||||| ||||
                                 AAAGTGGTACAATCGGTCC ACCA
                                          T
GAM320  LOC92299  3' ACCAGCTTAGGCAACACGGTGA 69356        A    G  _
          AA                     TTTCACC TGTTG CC AGGCTGGT
                                 ||||||| ||||| || ||||||||
                                 AAAGTGG ACAAC GG TTCGACCA
                                    C    _  A
GAM320  LOC92299  3' CCTGGCCAACATGGTGAAA   69366
                                 TTTCACCATGTTGGCCAGG
                                 |||||||||||||||||||
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                                AAAGTGGTACAACCGGTCC

GAM320  LOC92360  3'  ACCAGCCTGGCCAACATGGCGA 69621      A
              AA                  TTTC CCATGTTGGCCAGGCTGGT
                                  |||| ||||||||||||||||||
                                  AAAG GGTACAACCGGTCCGACCA
                                    C
GAM320  LOC92405  3'  ACCAGCCTGGCCAACATGGTGA 69707
              AA                  TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC92421  3'  AGCCTGACCAACATGAAGAAA  69722      AC       C
                                  TTTC  CATGTTGG CAGGCT
                                  ||||  |||||||| ||||||
                                  AAAG  GTACAACC GTCCGA
                                    AA       A
GAM320  LOC92465  5'  ACCAGCCTGGCCAACATGG    69931
                                  CCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||
                                  GGTACAACCGGTCCGACCA

GAM320  LOC92465  5'  ACCAGCCTGGCCAACATGGTGA 69932
              AA                  TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC92465  3'  ACCAGCCTGGGCAACATGG    69933         G
                                  CCATGTTG CCAGGCTGGT
                                  |||||||| ||||||||||
                                  GGTACAAC GGTCCGACCA
                                       G
GAM320  LOC92466  3'  ACCAGCCTGGCCAACATGGTGA 69959
              AA                  TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC92482  3'  ACCAGCCTGGCCAACATGGTGA 70013
              AA                  TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC92499  5'  ACCATCCTGGCCAACATGGGGA 70100      A            C
              AA                  TTTC CCATGTTGGCCAGG TGGT
                                  |||| |||||||||||||| ||||
                                  AAAG GGTACAACCGGTCC ACCA
                                    G            T
GAM320  LOC92573  3'  ACCAGCCTGGCCAGCATGGTGA 70364
              AA                  TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
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                                AAAGTGGTACGACCGGTCCGACCA

GAM320  LOC92661  5'  ACCAGCTTGGCCAACATGGGAA 70615      A
                A                TTTC CCATGTTGGCCAGGCTGGT
                                 |||| ||||||||||||||||||
                                 AAAG GGTACAACCGGTTCGACCA
                                   _
GAM320  LOC92771  3'  ACCAGCCTGAGCAACATAGCGA 54204      ACC     GC
                GA                TTTC   ATGTTG  CAGGCTGGT
                                  ||||   ||||||  |||||||||
                                  AGAG   TACAAC  GTCCGACCA
                                    CGA     GA
GAM320  LOC92771  3'  ACCAGCCTGGCCAACATGGTGA 54205
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC93070  3'  ACCAGCCTGGCCAACATGGTGA 71801
                AA                TTTCACCATGTTGGCCAGGCTGGT
                                  ||||||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGACCA

GAM320  LOC93132  5'  ACCAGCCTGACCAACATGGTGA 71970             C
                AA                TTTCACCATGTTGG CAGGCTGGT
                                  |||||||||||||| |||||||||
                                  AAAGTGGTACAACC GTCCGACCA
                                         A
GAM320  LOC93132  5'  ACCAGCCTGGCCACATGG    71971       T
                                  CCATGT GGCCAGGCTGGT
                                  ||||||| ||||||||||||
                                  GGTACA CCGGTCCGACCA
                                    _
GAM320  LOC93613  3'  ACCAGCCTTGGCAACATGGTGA 73067            G  _
                AA                TTTCACCATGTTG CCA GGCTGGT
                                  |||||||||||||| ||| |||||||
                                  AAAGTGGTACAAC GGT CCGACCA
                                         _  T
GAM320  LOC96597  5'  ACCATCCTGGCCAACATGGCGA 67445      A           C
                AA                TTTC CCATGTTGGCCAGG TGGT
                                  |||| ||||||||||||| ||||
                                  AAAG GGTACAACCGGTCC ACCA
                                    C            T
GAM321  ACP1      5'  CAGCACCACAGCCCGCCAGC   24011     T  T T   CA
                                  GCT GC G GGC  TGGTGCTG
                                  ||| || | |||  ||||||||
                                  CGA CG C CCG  ACCACGAC
                                    C  _ _   AC
GAM321  CD97      3'  CAGCTCCTGTGGCCACAGCAGC 55302       T         _  T
                TT                  AAGCT GCTGTGGCCAT GG GCTG
                                    ||||| |||||||||||| || ||||
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                                TTCGA CGACACCGGTG CC CGAC
                                  _        T  T
GAM321  FXR2     3'  CACCATGGCCCTCACAGGC   17959      C  T_
                                GCTTG TG  GGCCATGGTG
                                ||||| ||  ||||||||||
                                CGGAC AC  CCGGTACCAC
                                  _ TC
GAM321  GLP1R    3'  CAGCACCATGGAGGCAGGCT  10792        GTGG
                                AGCTTGCT   CCATGGTGCTG
                                ||||||||   ||||||||||
                                TCGGACGG   GGTACCACGAC
                                    A___
GAM321  IL1RAP   3'  CATAACCACAGCAAGACT    57069    _       CC
                                AG CTTGCTGTGG  ATG
                                || ||||||||||  |||
                                TC GAACGACACC  TAC
                                 A         AA
GAM321  ARHGDIG  3'  CAGCACCATGAGCCGCCAGC  8617      _   _
                                GCTG TGGC CATGGTGCTG
                                |||| |||| ||||||||||
                                CGAC GCCG GTACCACGAC
                                  C    A
GAM321  FLJ12425 3'  AGTGTACTGGCACAGCAAGC  87093         G   TG TG
                                GCTTGCTGTG CCA  G  CT
                                |||||||||| |||  |  ||
                                CGAACGACAC GGT  T  GA
                                      _  CA GT
GAM321  FLJ13081 3'  CAGATGTTTGGCCACAGAAACT 46170     C  G       TGGTG
           T                     AAG TT CTGTGGCCA     CTG
                                ||| || |||||||||     |||
                                TTC AA GACACCGGT     GAC
                                 A  _        TTGTA
GAM321  HPIP     5'  GGTGGCAGCCACAGCAGC    40426     T      CA  G
                                GCT GCTGTGGC  TG TGCT
                                ||| ||||||||  || ||||
                                CGA CGACACCG  AC GTGG
                                  _       __  G
GAM321  KIAA0275 3'  GGACGCCCAGCCACAGCAAGC  29329          CAT   _
                                GCTTGCTGTGGC   GGTG CT
                                ||||||||||||   |||| ||
                                CGAACGACACCG   CCGC GG
                                      AC_    A
GAM321  KIAA1908 5'  CAGCTCTGTCCAACCACAGCGA 73781          CC__   T
           GC                     GCTTGCTGTGG    ATGG GCTG
                                ||||||||||||    |||| ||||
                                CGAGCGACACC    TGTC CGAC
                                      AACC    T
GAM321  KIAA1937 5'  CAGCACCATGGCCAGGGC    74068     G
                                GCT TGGCCATGGTGCTG
                                ||| ||||||||||||||
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                                CGG ACCGGTACCACGAC
                                  G
GAM321  MOST2    5'  CAGCCTGGGCACCACAGCAAGA 40056    _       __  A  T
              CT                  AG CTTGCTGTG  GCC TGG GCTG
                                  || |||||||||  ||| ||| ||||
                                  TC GAACGACAC  CGG GTC CGAC
                                   A       CA  _  _
GAM321  p25      3'  CAGGGCTGACCACAGCAGC   23824     T     C  TG  G
                                  GCT GCTGTGG CA  GT CTG
                                  ||| ||||||| ||  || |||
                                  CGA CGACACC GT  CG GAC
                                    _     A  __  G
GAM321  RAI17    3'  CAGCAAGCCTCCACCAGCAAGC 92901         _  CCATGG
              T                   AGCTTGCTG TGG     TGCTG
                                  |||||||||| |||     |||||
                                  TCGAACGAC ACC     ACGAC
                                       C   TCCGA_
GAM321  LOC113763 5'  AGACAGCCTCAGCAAGCT    57384         T  CATG  G
                                  AGCTTGCTG GGC    GT CT
                                  |||||||||| |||    || ||
                                  TCGAACGAC CCG    CA GA
                                       T   A___  _
GAM321  LOC124602 3'  ACTATCGCGACAGCAAGCT    74783          G  C
                                  AGCTTGCTGT GC ATGGT
                                  |||||||||| || |||||
                                  TCGAACGACA CG TATCA
                                       G  C
GAM321  LOC132235 5'  CAGCACCAACTGCCAACGAGCT 76663       CTG   CA_
                                  AGCTTG   TGGC   TGGTGCTG
                                  ||||||   ||||   ||||||||
                                  TCGAGC   ACCG   ACCACGAC
                                     A__    TCA
GAM321  LOC149464 5'  CAGCACGGAACCACGCAAACT  85585    C   T   __ ATG
                                  AG TTGC GTGG  CC   GTGCTG
                                  || |||| ||||  ||   ||||||
                                  TC AACG CACC  GG   CACGAC
                                   A   _   AA  ____
GAM321  LOC158314 3'  CAGCAAAGACCCACAGCAGC   88094     T     CCATGG
                                  GCT GCTGTGG     TGCTG
                                  ||| |||||||     |||||
                                  CGA CGACACC     ACGAC
                                    _      CAGAA_
GAM321  LOC170425 5'  AGCACCATGGCCAGAAGT    76883     G_
                                  GCT  TGGCCATGGTGCT
                                  |||  |||||||||||||
                                  TGA  ACCGGTACCACGA
                                    AG
GAM321  LOC203397 3'  ACTATCGCGACAGCAAGCT    90896          G  C
                                  AGCTTGCTGT GC ATGGT
                                  |||||||||| || |||||
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                                TCGAACGACA CG TATCA
                                      G  C
GAM322  CDH10    3'  TTCCTGCCAGTCAGCACA    22996        CA_
                                TGTGCTGAC   CAGGAA
                                |||||||||   ||||||
                                ACACGACTG   GTCCTT
                                      ACC
GAM322  SLC22A2  5'  ATCCAAGGACTGGTCAGCA   60277        CA GAA
                                TGCTGACCA  G   TTGGAT
                                |||||||||  |   ||||||
                                ACGACTGGT  C   AACCTA
                                      __ AGG
GAM322  FLJ10607 5'  GTTCCTGTAACCAGCACA    77643       ACC
                                TGTGCTG   ACAGGAAT
                                |||||||   ||||||||
                                ACACGAC   TGTCCTTG
                                     CAA
GAM322  PGGT1B   5'  ATCCATGAAAGTGTTCAGCACA 18476        C   AGGAAT
                                TGTGCTGA CAC     TGGAT
                                |||||||| |||     |||||
                                ACACGACT GTG     ACCTA
                                      T   AAAGT_
GAM322  LOC152024 5'  CCAGGTCTACTATCAGCACA   81269        CCACA   A
                                TGTGCTGA    GGA TTGG
                                ||||||||    ||| ||||
                                ACACGACT    TCT GACC
                                      ATCA_   G
GAM323  BBS4     3'  ATTTGCCCAAAGGGAATCCAGA 53447        G_ G_   A
           ACA                    TGTTCTGGA  CT  TTGG CAAAT
                                |||||||||  ||  |||| |||||
                                ACAAGACCT  GG  AACC GTTTA
                                      AA  GA   C
GAM323  CENTD2   3'  CCAACAAACTCCAGAACA    31539        C_
                                TGTTCTGGAG  TGTTGG
                                ||||||||||  ||||||
                                ACAAGACCTC  ACAACC
                                      AA
GAM323  HAMP     3'  TCCTGCTGCCCCAGAACA    41289        A  T  T
                                TGTTCTGG GC GT GGA
                                |||||||| || || |||
                                ACAAGACC CG CG CCT
                                      C  T  T
GAM323  ITGA11   3'  TCTGCCGGCCCCCAGGACA   25213        A_   TT
                                TGTTCTGG  GCTG  GGA
                                ||||||||  ||||  |||
                                ACAGGACC  CGGC  TCT
                                      CC    CG
GAM323  KITLG    3'  ATTTGCATGGCTCCAGAA    8023          TGGA
                                TTCTGGAGCTGT    CAAAT
                                ||||||||||||    |||||
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                                AAGACCTCGGTA   GTTTA
                                      C___
GAM323  MAPK4   5'  CCTGGGCAGCTCCAGATCA   12300   T        __
                                TG TCTGGAGCTGTT  GG
                                || ||||||||||||  ||
                                AC AGACCTCGACGG  CC
                                  T          GT
GAM323  MGAT2   3'  ATTTGTCCAAACAGGACA    11557       GAGCTG
                                TGTTCTG    TTGGACAAAT
                                |||||||    ||||||||||
                                ACAGGAC    AACCTGTTTA
                                    A_____
GAM323  PSPHL   5'  TTGTCATACAGCTCCAAACA  94499     C       TG
                                TGTT TGGAGCTGT  GACAA
                                |||| |||||||||  |||||
                                ACAA ACCTCGACA  CTGTT
                                  _       TA
GAM323  TTC3    3'  TATTTGTCCAACAACTGTCAGA 13885        _ C
            ATA                   TGTTCTGG AG TGTTGGACAAATA
                                |||||||| || ||||||||||||
                                ATAAGACT TC ACAACCTGTTTAT
                                     G  A
GAM323  FLJ14213 3'  TGATAACAGCTCCAGAA    46218           GA
                                TTCTGGAGCTGTTG  CA
                                ||||||||||||||  ||
                                AAGACCTCGACAAT  GT
                                      A_
GAM323  H2BFQ   3'  TTTAAGAGAACTCCAGGACA  60079         __ G
                                TGTTCTGGAG  CT TTGGA
                                ||||||||||  || |||||
                                ACAGGACCTC  GA AATTT
                                      AA  G
GAM323  LRG     3'  TCCATCCATGCTTCCTAGAACA 54825      _  _ _ T_
                                TGTTCT GGA GC TG  TGGA
                                |||||| ||| || ||  ||||
                                ACAAGA CCT CG AC  ACCT
                                   T   T  T  CT
GAM323  NMT2    3'  ATTTGTCCATGTAACAGAACA  17852       GA  TGT
                                TGTTCTG  GC   TGGACAAAT
                                |||||||  ||   |||||||||
                                ACAAGAC  TG   ACCTGTTTA
                                     AA  T__
GAM323  NYD-SP21 3'  TATTTGTCCAATCTAGATTCAG 51863        G __
            AACA                   TGTTCTGGA CT  GTTGGACAAATA
                                |||||||||  ||  ||||||||||||
                                ACAAGACTT GA  TAACCTGTTTAT
                                      A  TC
GAM323  PSPH    3'  TTGTCGTACAGCTCCAAACA  17143     C       TG
                                TGTT TGGAGCTGT  GACAA
                                |||| |||||||||  |||||
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                                ACAA ACCTCGACA  CTGTT
                                  _       TG
GAM323  LOC122258 3'  CCACCAGCCTCCGGAACA    59820         _  T
                                TGTTCTGGAG CTG TGG
                                |||||||||| ||| |||
                                ACAAGGCCTC GAC ACC
                                     C   C
GAM323  LOC151826 3'  ATTTGTCCAACCTAGCACA   81176    T   AGCT
                                TGT CTGG   GTTGGACAAAT
                                ||| ||||   ||||||||||
                                ACA GATC   CAACCTGTTTA
                                  C  ____
GAM323  LOC169611 3'  TCCAGTGGCAGCTCCAGAA   83663          ___
                                TTCTGGAGCTGT  TGGA
                                ||||||||||||  ||||
                                AAGACCTCGACG  ACCT
                                       GTG
GAM323  LOC196746 3'  TCAGAGCAGCTCCAAGACA   88903    TC       G_
                                TGT  TGGAGCTGTT  GA
                                |||  ||||||||||  ||
                                ACA  ACCTCGACGA  CT
                                  GA        GA
GAM323  LOC204119 5'  TGCCACAACTCAGAACA     92343       G  C   T  A
                                TGTTCTG AG TGT GG CA
                                ||||||| || ||| || ||
                                ACAAGAC TC ACA CC GT
                                    _ A  _ _
GAM323  LOC253142 5'  TTGCTAGGATGCCCCAGAATA  99230        A  TG_   A
                                TGTTCTGG GC   TTGG CAA
                                |||||||| ||   |||| |||
                                ATAAGACC CG   GATC GTT
                                     C  TAG   _
GAM324  CENTD2    5'  CTGGCCGGAGCTGTGGGA    31541        CAGA   A  A
                                TTCCACAGC    TTTG CCA G
                                |||||||||    |||| ||| |
                                AGGGTGTCG    AGGC GGT C
                                     ____   C   C
GAM324  E2F3      3'  GCCTGACGGATGGGCTGTAGAA 10468    C     AG    AC  A
                                TTC ACAGCC  ATTTG  CA GC
                                ||| ||||||  |||||  || ||
                                AAG TGTCGG  TAGGC  GT CG
                                  A     G_    A_  C
GAM324  HEM1      5'  GCCTGTGAGTATCTGTCTGTGG 19239        C    TTGAC  A
           AA                     TTCCACAG CAGAT    CA GC
                                ||||||||| |||||    || ||
                                AAGGTGTC GTCTA    GT CG
                                     T    TGAGT  C
GAM324  MGAT5     5'  GCCTGGTCAAGGGCTCTG    11569    C   AGA      A
                                CA AGCC   TTTGACCA GC
                                || ||||   |||||||| ||
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                                GT TCGG   GAACTGGT CG
                                 C   ___       C
GAM324  PCDH11X  3' CTGTAATCTGGCAATGGAA   28013      CA      TGACCA
                                TTCCA  GCCAGATT     AG
                                |||||  ||||||||     ||
                                AAGGT  CGGTCTAA     TC
                                   AA       TG____
GAM324  PCDH11Y  3' CTGTAATCTGGCAATGGAA   53161      CA      TGACCA
                                TTCCA  GCCAGATT     AG
                                |||||  ||||||||     ||
                                AAGGT  CGGTCTAA     TC
                                   AA       TG____
GAM324  PIK3R3   3' GCTTGACCCTGAGCCTGTGGAA 61707        _ _  ATTTGAC
                                TTCCACAG C CAG      CAAGC
                                |||||||| | |||      |||||
                                AAGGTGTC G GTC      GTTCG
                                     C A  CCA____
GAM324  PRKCABP  5' GCCTGGCCGGGACCCGGCTGTG 25748         AGA_   A  A
           GGA                    TTCCACAGCC    TTTG CCA GC
                                |||||||||    |||| ||| ||
                                AGGGTGTCGG    GGGC GGT CG
                                      CCCA    C   C
GAM324  T       3' GCTTACAGATGAACCCAACTGT 13507        CCAG____    ACC
           GGAG                  TTCCACAG      ATTTG   AAGC
                                |||||||      |||||  ||||
                                GAGGTGTC      TAGAC   TTCG
                                     AACCCAAG    A__
GAM324  VIPR1    3' CTTATCTCTCTGTGCTGTGGAA 17312         _   TTT  CC
                                TTCCACAGC CAGA   GA  AAG
                                |||||||| ||||   ||  |||
                                AAGGTGTCG GTCT   CT  TTC
                                     T    CT_  A_
GAM324  XRCC3    3' TTACATCTGGCTGGAA     19523      CA     T
                                TTCCA  GCCAGAT TGA
                                |||||  ||||||| |||
                                AAGGT  CGGTCTA ATT
                                   __       C
GAM324  YWHAG    3' GCTCGGCAGGTGGCTGTGGGA  25944          GA   A  A
                                TTCCACAGCCA  TTTG CC AGC
                                |||||||||||  |||| || |||
                                AGGGTGTCGGT  GGAC GG TCG
                                      __    _  C
GAM324  ZNF266   5' TTTGATGATCTGGCTGTGGA   89693            TGAC
                                TCCACAGCCAGATT    CAAG
                                ||||||||||||||    ||||
                                AGGTGTCGGTCTAG    GTTT
                                        TA__
GAM324  ARHU     3' GCCTGGCTTACCTATCTGTGGA 41361        CC  ATT  _   A
           A                     TTCCACAG  AG   TGA CCA GC
                                |||||||  ||   ||| ||| ||
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                                AAGGTGTC  TC   ATT GGT CG
                                    TA  C__   C   C
GAM324  C20orf28  3'  GCCTGGTCGAGGGCCCTGGAA  31845      CA   AGA      A
                                TTCCA  GCC   TTTGACCA GC
                                |||||  |||   |||||||| ||
                                AAGGT  CGG   GAGCTGGT CG
                                   CC  ___      C
GAM324  CNNM4     5'  GCTTGGTCAACGTGAGCCGCGG 39868     ACA  _  GAT
          GA                      TTCC   GC CA   TTGACCAAGC
                                ||||   || ||   ||||||||||
                                AGGG   CG GT   AACTGGTTCG
                                  CGC  A  GC_
GAM324  DKFZp761N1114 3'  CTGAGAATCTGGCTGGAA    79783      CA       GACCA
                                TTCCA  GCCAGATTT    AG
                                |||||  |||||||||    ||
                                AAGGT  CGGTCTAAG    TC
                                  __       AG___
GAM324  FLJ10204  3'  CTTGGTCTCAAGATGTGGAA  36357       GCCA  TTT
                                TTCCACA   GA   GACCAAG
                                |||||||   ||   |||||||
                                AAGGTGT   CT   CTGGTTC
                                    AGAA  ___
GAM324  FLJ11539  3'  TTAAATCTGCTGCAGAA    45710    CA   C
                                TTC  CAGC AGATTTGA
                                |||  |||| ||||||||
                                AAG  GTCG TCTAAATT
                                  AC   _
GAM324  FLJ12056  3'  TCATCTTCTGGCTGTGGAA   46824          TT_
                                TTCCACAGCCAGA   TGA
                                ||||||||||||   |||
                                AAGGTGTCGGTCT   ACT
                                       TCT
GAM324  FLJ13149  5'  GCCTGGTCAAATCTGTGAGGA  41831    A  GC         A
                                TCC CA  CAGATTTGACCA GC
                                ||| ||  ||||||||||||| ||
                                AGG GT  GTCTAAACTGGT CG
                                  A  __          C
GAM324  FLJ20084  3'  GCTTGGCCAATGACTGTGGAG  34997       C  GAT   A
                                TTCCACAG CA   TTG CCAAGC
                                |||||||| ||   ||| ||||||
                                GAGGTGTC GT   AAC GGTTCG
                                    A  ___   C
GAM324  FLJ20392  5'  GCCTGGCCAAATCTGAAATAGG 35576    ACAGC      A  A
          A                      TCC     CAGATTTG CCA GC
                                |||     |||||||| ||| ||
                                AGG     GTCTAAAC GGT CG
                                  ATAAA       C  C
GAM324  FLJ21940  3'  TCAGAACTCTTAGCTGTGGAA  43387        C_  __
                                TTCCACAGC  AGA  TTTGA
                                |||||||||  |||  |||||
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                                AAGGTGTCG  TCT  AGACT
                                     AT   CA
GAM324  KIAA0237  3'  CTGGTCTGGCTGGGAA     29221     A    GATTT    A
                                TTCC CAGCCA    GACCA G
                                |||| ||||||    ||||| |
                                AAGG GTCGGT    CTGGT C
                                  _    _____    C
GAM324  KIAA0596  3'  CTTGAGCCAGCTGTGGGA    63488        CAGATT  AC_
                                TTCCACAGC    TG   CAAG
                                |||||||||    ||  ||||
                                AGGGTGTCG    AC  GTTC
                                     _______ CGA
GAM324  KIAA0773  3'  CTTGGTGTGGCTGTGGAG    28723         GATTTG
                                TTCCACAGCCA    ACCAAG
                                ||||||||||    ||||||
                                GAGGTGTCGGT    TGGTTC
                                     G_____
GAM324  KIAA0789  5'  GCTTGGTCTTCAGCTGGGGAA  64433     A   CA  TTT
                                TTCC CAGC  GA   GACCAAGC
                                |||| ||||  ||   ||||||||
                                AAGG GTCG  CT   CTGGTTCG
                                  G   A_  T__
GAM324  L3MBTL    3'  CTTCACCTCACTGTGGAA    70084       CCA  TT   CCA
                                TTCCACAG   GA  TGA   AG
                                |||||||   ||  |||   ||
                                AAGGTGTC   CT  ACT   TC
                                     A__  CC   ___
GAM324  NUDEL     3'  CTTGGTCACTGGATGCAGAA  48697    CA  G   ATT
                                TTC  CA CCAG   TGACCAAG
                                |||  || ||||   ||||||||
                                AAG  GT GGTC   ACTGGTTC
                                  AC  A   ___
GAM324  SAST      5'  GCTCCCTTCATCTGGCTATGG  63662    C     TT   CCA_
                                CCA AGCCAGA  TGA    AGC
                                ||| |||||||  |||    |||
                                GGT TCGGTCT  ACT    TCG
                                  A      __   TCCC
GAM324  SLC26A8   5'  CTCAGTCAGTATCTGTGGAA   54769       CCAGAT    CA
                                TTCCACAG     TTGAC  AG
                                ||||||||     |||||  ||
                                AAGGTGTC     GACTG  TC
                                     TAT___     AC
GAM324  SNURF     3'  CTTGGTATCCATGACTGTGGAG 20261        C  GATTTG
                                TTCCACAG CA     ACCAAG
                                |||||||| ||     ||||||
                                GAGGTGTC GT     TGGTTC
                                     A  ACCTA_
GAM324  TMG3      3'  GCCTGGCCTGGGGGCTGTGGGA 44222          AGATTTGA   A
                                TTCCACAGCC       CCA GC
                                ||||||||||       ||| ||
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                                AGGGTGTCGG       GGT CG
                                      GGGTCC__   C
GAM324  LOC158956 3'  CTTGGTTACTGTGCTGTG    67213       _  ATT
                                CACAGC CAG   TGACCAAG
                                |||||| |||   ||||||||
                                GTGTCG GTC   ATTGGTTC
                                   T   ____
GAM324  LOC159199 5'  GCTTGGTCCAGAGGCCAGGAA  83063     ACA   AGA   _
                                TTCC   GCC   TTTG ACCAAGC
                                ||||   |||   |||| |||||||
                                AAGG   CGG   AGAC TGGTTCG
                                  AC_   ___    C
GAM324  LOC83693  3'  TCAAATCTGCTATGGAA     49607      C   C
                                TTCCA AGC AGATTTGA
                                ||||| ||| ||||||||
                                AAGGT TCG TCTAAACT
                                   A  _
GAM325  FANCC     3'  ATGCTAATAGATCCACTGA    71032     C      CTGCCC
                                TCA TGGATCTG     AGCAT
                                ||| ||||||||     |||||
                                AGT ACCTAGAT     TCGTA
                                  C       AA____
GAM325  FAP       5'  GGTTTTCACAGATCCAGTGA   16750          CT___
                                TCACTGGATCTG     GCC
                                ||||||||||||     |||
                                AGTGACCTAGAC     TGG
                                      ACTTT
GAM325  GABRP     3'  CTGAGCAACACTCTCCCAGTGG 27225       ATC__  C   C
                                TCACTGG     TG TGC CAG
                                |||||||     || ||| |||
                                GGTGACC     AC ACG GTC
                                    CTCTC  A   A
GAM325  KIAA1091  3'  CTGGGCAGATCCAGGA      70261    A      GCT
                                TC CTGGATCT   GCCCAG
                                || ||||||||   ||||||
                                AG GACCTAGA   CGGGTC
                                  _      ____
GAM325  KIAA1715  3'  TGTTGCCAAATCCAGTGA     68694         C  CTGCC
                                TCACTGGAT TG     CAGCA
                                ||||||||| ||     |||||
                                AGTGACCTA AC     GTTGT
                                     A  C_____
GAM325  LOC146350 5'  GCTGAGAGCAGCACCCAGTGG  84648        ATC     C__
                                TCACTGG   TGCTGC   CAGC
                                |||||||   ||||||   ||||
                                GGTGACC   ACGACG   GTCG
                                    C__      AGA
GAM326  IRS1      3'  CCATAGATGGTTCTCAATTGTA 19874      C        TGAAC
                                TACA ATTGAGAACC     ATGG
                                |||| ||||||||||     ||||
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                                ATGT TAACTCTTGG    TACC
                                  _        TAGA_
GAM326  SERPINF1  3'  CCTGTAAGGTTTCAATG     12038        A   GA   T
                                CATTGAGA CCT  ACA GG
                                |||||||| |||  ||| ||
                                GTAACTTT GGA  TGT CC
                                    _   A_   _
GAM326  HSA243396 3'  CCATGTTCAGCAATGTCAATG  37844       GAAC_
                                CATTGA    CTGAACATGG
                                ||||||    ||||||||||
                                GTAACT    GACTTGTACC
                                   GTAAC
GAM326  KIAA1387  3'  CAGGAATTTTCAATATGTA    71444      C       ___
                                TACA ATTGAGAA  CCTG
                                |||| ||||||||  ||||
                                ATGT TAACTTTT  GGAC
                                  A       AA
GAM326  MGC16063  3'  TTCAAATTCCAATGTGTA     54930         A   CC
                                TACACATTG GAA  TGAA
                                ||||||||| |||  ||||
                                ATGTGTAAC CTT  ACTT
                                     _  AA
GAM326  SMCR8     3'  CCATGCTCAGGTTTGACTATGT 59253      TGA_       A
                                ACAT    GAACCTGA CATGG
                                ||||    |||||||| |||||
                                TGTA    TTTGGACT GTACC
                                  TCAG       C
GAM326  UPLC1     3'  CCATGCTAGGCCCCAATGT    35227       AGAA    AA
                                ACATTG    CCTG  CATGG
                                ||||||    ||||  |||||
                                TGTAAC    GGAT  GTACC
                                   CCC_    C_
GAM326  ZNF334    3'  CCATAAGTCAACCCTCAATGT  36637        AACC   AC_
                                ACATTGAG    TGA   ATGG
                                ||||||||    |||   ||||
                                TGTAACTC    ACT   TACC
                                    CCA_   GAA
GAM326  LOC145082 3'  TATGGAATGCCCTTAATGTGTA 84196           AACCTGAA
                                TACACATTGAG       CATG
                                ||||||||||        ||||
                                ATGTGTAATTC       GTAT
                                      CCGTAAG_
GAM326  LOC157723 3'  CCAAGTAAGGTTCTCAAATGT  82465      _      GA  A
                                ACATT GAGAACCT  AC TGG
                                ||||| ||||||||  || |||
                                TGTAA CTCTTGGA  TG ACC
                                  A       A_  A
GAM326  LOC219988 5'  CCATGTTCGGCCCCCAATG    93262       AGAAC
                                CATTG    CTGAACATGG
                                |||||    ||||||||||
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                                GTAAC    GGCTTGTACC
                                   CCCC_
GAM327  FMR2     3'  GAAAGCACCTGGTTTGCACCAT 10693       _  _      C
             T                   GATGGT CAG CCAGGTGC TTC
                                 |||||| ||| |||||||| |||
                                 TTACCA GTT GGTCCACG AAG
                                    C  T       A
GAM327  ARHGEF4  5'  AAGTGAACCGACCATCAA    53368        AGCCA   GC_
                                 TTGATGGTC    GGT   CTT
                                 |||||||||    |||   |||
                                 AACTACCAG    CCA   GAA
                                       _____  AGT
GAM327  CABP4    3'  AAAACACCTGGCCTCAAT    59747      T GTCA      CC
                                 ATTGA G    GCCAGGTG  TT
                                 ||||| |    ||||||||  ||
                                 TAACT C    CGGTCCAC  AA
                                   _ ____       AA
GAM327  CDV-1    5'  ACTGTGGCTGACACCAAT    49688     ATG      _
                                 ATTG   GTCAGCCA GGT
                                 ||||   |||||||| |||
                                 TAAC   CAGTCGGT TCA
                                   CA_       G
GAM327  FLJ23598 3'  AAGACACCCCCCTGGACCCATC 96501        __   CCA    C
             AAT                   ATTGATGG  TCAG   GGTG CTT
                                 ||||||||  ||||   |||| |||
                                 TAACTACC  GGTC   CCAC GAA
                                      CA    CCC    A
GAM327  PTPRR    3'  GAAGACTTGTCAGACCATCAAT 56450         AGC    GC
                                 ATTGATGGTC   CAGGT  CTTC
                                 ||||||||||   |||||  ||||
                                 TAACTACCAG   GTTCA  GAAG
                                       ACT    __
GAM327  RHOBTB1  3'  GCACAAGCTCACCATCAAT   93093        C   CAG
                                 ATTGATGGT AGC   GTGC
                                 |||||||| |||   ||||
                                 TAACTACCA TCG   CACG
                                      C   AA_
GAM327  LOC146181 3'  TACTCTGGCTGACCATCA    69151          _
                                 TGATGGTCAGCCAG GTG
                                 |||||||||||||| |||
                                 ACTACCAGTCGGTC CAT
                                          T
GAM327  LOC255452 3'  AAGTGAACCGACCATCAA    99383        AGCCA   GC_
                                 TTGATGGTC    GGT   CTT
                                 |||||||||    |||   |||
                                 AACTACCAG    CCA   GAA
                                       _____  AGT
GAM327  LOC51026  3'  GCATTCTTGACCATGAAT    32686     G      CCA
                                 ATT ATGGTCAG   GGTGC
                                 ||| ||||||||   |||||
```

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                                TAA TACCAGTT   TTACG
                                  G       C__
GAM327  LOC85479  5'  AAGGCACCTGGCTCCTCAG   53555     T  TC
                                TTGA GG  AGCCAGGTGCCTT
                                |||| ||  ||||||||||||
                                GACT CC  TCGGTCCACGGAA
                                  _  __
GAM328  MRPL11    3'  ATCAGGCCTGAATAAACATCC  32649     CGG__
                                GGA    GTTCAGGCCTGAT
                                |||    ||||||||||||
                                CCT    TAAGTCCGGACTA
                                  ACAAA
GAM328  MYOZ2     5'  ATCAGGCCCAAGTGCCATCCAT 33938      CG   TCA__
                                ATGGA  GGT    GGCCTGAT
                                |||||  |||    ||||||||
                                TACCT  CCG    CCGGACTA
                                   A_   TGAAC
GAM328  LOC145226 3'  TCAGGCCCAATCCATGCCA   77561     AC_    CA
                                TGG   GGGTT  GGCCTGA
                                |||   |||||  |||||||
                                ACC   CCTAA  CCGGACT
                                  GTA    C_
GAM328  LOC146108 5'  ATCAGACCCAAGGGCCCGTTCA 78146          A__  C
                                TGGACGGGTTC   GG CTGAT
                                ||||||||||   || |||||
                                ACTTGCCCGGG   CC GACTA
                                      AAC  A
GAM329  ADCY7     3'  TGGGTGCATGCAGAGGCTCC   8495           CC  TG
                                GGAGCCTCTGTA  TG  CCCA
                                ||||||||||||  ||  ||||
                                CCTCGGAGACGT  AC  GGGT
                                      __  GT
GAM329  ALDH1B1   3'  TGGGCATGGGATTTGTTTTTG  7331    TG   CTCT  A
                                C  GAGC    GT CCTGTGCCCA
                                |  ||||    || ||||||||||
                                G  TTTG    TA GGGTACGGGT
                                 TT    TT__  _
GAM329  ANK1      3'  TGGGTGCAGGTGCCAGGCTCGA 40417    G     CT      TG
           G                     CT GAGCCT  GTACCTG  CCCA
                                || ||||||  |||||||  ||||
                                GA CTCGGA  CGTGGAC  GGGT
                                 G     C_      GT
GAM329  ANK1      3'  TGGGTGCAGGTGCCAGGCTCGA 40418    G     CT      TG
           G                     CT GAGCCT  GTACCTG  CCCA
                                || ||||||  |||||||  ||||
                                GA CTCGGA  CGTGGAC  GGGT
                                 G     C_      GT
GAM329  ANXA8     3'  TGGGTGTGAGGGGGGTCCCAG  73468     AG   TGTA  _ TG
                                CTGG  CCTC    CCT G  CCCA
                                ||||  ||||    ||| |  ||||
```

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                                GACC  GGGG   GGA T  GGGT
                                  CT   ____   G GT
GAM329  ASIP    3'  TGCAGGCGGGCGGAGGTTCCAG 9807          A__
                                CTGGAGCCTCTGT  CCTGTG
                                ||||||||||||  ||||||
                                GACCTTGGAGGCG  GGACGT
                                      GGC
GAM329  ATP5G1  5'  TGGGCCAAGCAGGGGTTGCAG  18981    G      ACC  T
                                CTG AGCCTCTGT  TG GCCCA
                                ||| |||||||||  || |||||
                                GAC TTGGGGACG  AC CGGGT
                                  G       A__  _
GAM329  AVPR2   3'  TGGGTGTAGGAGGGGCTGCAG  5340    G     GTA   TG
                                CTG AGCCTCT  CCTG  CCCA
                                ||| |||||||  ||||  ||||
                                GAC TCGGGGA  GGAT  GGGT
                                  G      ___   GT
GAM329  BAK1    3'  TGGGCACAGCCTAGGGTCTTGG 93635   TG AG  T  TAC
                                C  G  CC CTG  CTGTGCCCA
                                |  |  || |||  |||||||||
                                G  T  GG GAT  GACACGGGT
                                 GT CT  _  CC_
GAM329  BCL9    3'  GGGCATGGGTGGATTTAG   16321      G  TCTGT
                                CTGGA CC    ACCTGTGCCC
                                |||||  ||   ||||||||||
                                GATTT GG    TGGGTACGGG
                                   A  _____
GAM329  BMP1    3'  CGGAATGGGATGGGGGCTTCGG 21528          A    GC  A
                                CTGGAGCCTCTGT CCTGT  CC
                                |||||||||||||  |||||  ||
                                GGCTTCGGGGGTA GGGTA  GG
                                      _    A_  CA
GAM329  BMP1    3'  GGAATGGGATGGGGGCTTCGG  21533          A    GC  A
                                CTGGAGCCTCTGT CCTGT  CC
                                |||||||||||||  |||||  ||
                                GGCTTCGGGGGTA GGGTA  GG
                                      _    A_  C
GAM329  CD164   3'  GGACTAGTGCAGAGGCTTTA  21196          CT  G
                                TGGAGCCTCTGTAC  GT CC
                                ||||||||||||||  || ||
                                ATTTCGGAGACGTG  CA GG
                                      AT  _
GAM329  CD22    3'  TGGGCTGCAGCAGAGGCACTGG 10102   TG A     TAC   _
                                C  G GCCTCTG   CTGT GCCCA
                                |  | |||||||   |||| |||||
                                G  C CGGAGAC   GACG CGGGT
                                 GT A      ___   T
GAM329  CDK7    5'  GGGTGTTGGAGGCTTTA    10156          TACCT TG
                                TGGAGCCTCTG    G  CCC
                                ||||||||||    |  |||
```

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                                ATTTCGGAGGT    T  GGG
                                      _____ GT
GAM329  CHST6    3'  GGATGTGTAGAGGGTTTAG   41503      G       CTGTG
                                CTGGA CCTCTGTAC    CC
                                ||||| |||||||||    ||
                                GATTT GGAGATGTG    GG
                                   G       TA___
GAM329  CLCN6    3'  TGGGTGTGAGCAGAGGCTCTGG 41706   TG       ACC  TG
                                C  GAGCCTCTGT   TG  CCCA
                                |  ||||||||||   ||  ||||
                                G  CTCGGAGACG   GT  GGGT
                                 GT        A__  GT
GAM329  COG3     3'  TGGACATTGTCAGGGGTTCTGG 49500   TG       T  CT   C
                                C  GAGCCTCTG AC  GTG CCA
                                |  |||||||||  ||  ||| |||
                                G  CTTGGGGAC TG  TAC GGT
                                 GT        _  T_   A
GAM329  CPO      3'  GGCTGTGCAGGGGTTT      76254          CTGT
                                GAGCCTCTGTAC    GCC
                                ||||||||||||    |||
                                TTTGGGGACGTG    CGG
                                       T___
GAM329  DCTN1    5'  GGCTGTGTGGAGGCTCTAG    15829         TG   CTGT
                                CTGGAGCCTC  TAC    GCC
                                ||||||||||  |||    |||
                                GATCTCGGAG  GTG    CGG
                                      GT   T___
GAM329  DLEC1    3'  TGGGCATGAAAAGGATGCTCCG 96283       C   GTACCT
           G                     CTGGAGC TCT     GTGCCCA
                                |||||||  |||     |||||||
                                GGCCTCG AGG     TACGGGT
                                    T   AAAAG_
GAM329  E2F1     3'  CAGGTGGGGAGGCTTTGG    85948    TG      G
                                C  GAGCCTCT TACCTG
                                |  ||||||||  ||||||
                                G  TTCGGAGG GTGGAC
                                 GT       G
GAM329  EGFL4    3'  TGGGCCCCACATAGGGTTTTGG 62478    TG    T   ACCTGT
                                C  GAGCC CTGT     GCCCA
                                |  |||||  ||||     |||||
                                G  TTTGG GATA     CGGGT
                                 GT    _    CACCC_
GAM329  ESRRA    3'  TGGGACTGGTGGGGGTTCTGG  16726   TG      GT   T  G
                                C  GAGCCTCT  ACC GT CCCA
                                |  ||||||||  ||| || ||||
                                G  CTTGGGGG  TGG CA GGGT
                                 GT       __   T  _
GAM329  FLT1     3'  TGGGTGTGGGTGTATGTGTGTT 10666      CTC__       TG
           TT                     GGAGC    TGTACCTG  CCCA
                                |||||    ||||||||  ||||
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                                TTTTG    ATGTGGGT  GGGT
                                  TGTGT      GT
GAM329  FSTL3   3' TGGGTGAGTACGGAGGGTCTAG 20752      G       CTG
                   CTGGA CCTCTGTAC   TGCCCA
                   ||||| |||||||||   ||||||
                   GATCT GGAGGCATG   GTGGGT
                      G       A__
GAM329  FSTL3   3' TGGGTGAGTACGGAGGGTCTAG 20753      G       CTG
                   CTGGA CCTCTGTAC   TGCCCA
                   ||||| |||||||||   ||||||
                   GATCT GGAGGCATG   GTGGGT
                      G       A__
GAM329  FSTL3   3' TGGGTGAGTATGGAGGGTCTAG 20754      G       CTG
                   CTGGA CCTCTGTAC   TGCCCA
                   ||||| |||||||||   ||||||
                   GATCT GGAGGTATG   GTGGGT
                      G       A__
GAM329  FSTL3   3' TGGGTGAGTATGGAGGGTCTAG 20755      G       CTG
                   CTGGA CCTCTGTAC   TGCCCA
                   ||||| |||||||||   ||||||
                   GATCT GGAGGTATG   GTGGGT
                      G       A__
GAM329  FSTL3   3' TGGGTGAGTATGGAGGGTCTAG 20756      G       CTG
                   CTGGA CCTCTGTAC   TGCCCA
                   ||||| |||||||||   ||||||
                   GATCT GGAGGTATG   GTGGGT
                      G       A__
GAM329  FSTL3   3' TGGGTGAGTATGGAGGGTCTAG 20757      G       CTG
                   CTGGA CCTCTGTAC   TGCCCA
                   ||||| |||||||||   ||||||
                   GATCT GGAGGTATG   GTGGGT
                      G       A__
GAM329  FSTL3   3' TGGGTGTGTACGGAGGGTCTAG 20758      G       CT TG
                   CTGGA CCTCTGTAC  G  CCCA
                   ||||| |||||||||  |  ||||
                   GATCT GGAGGCATG  T  GGGT
                      G       __ GT
GAM329  FSTL3   3' TGGGTGTGTACGGAGGGTCTAG 20759      G       CT TG
                   CTGGA CCTCTGTAC  G  CCCA
                   ||||| |||||||||  |  ||||
                   GATCT GGAGGCATG  T  GGGT
                      G       __ GT
GAM329  FSTL3   3' TGGGTGTGTACGGAGGGTCTAG 20760      G       CT TG
                   CTGGA CCTCTGTAC  G  CCCA
                   ||||| |||||||||  |  ||||
                   GATCT GGAGGCATG  T  GGGT
                      G       __ GT
GAM329  FSTL3   3' TGGGTGTGTATGGAGGATCTAG 20761      G       CT TG
                   CTGGA CCTCTGTAC  G  CCCA
                   ||||| |||||||||  |  ||||
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                                GATCT GGAGGTATG  T  GGGT
                                   A       __ GT
GAM329  FSTL3    3'  TGGGTGTGTATGGAGGGTCTAG 20762      G       CT TG
                                CTGGA CCTCTGTAC  G  CCCA
                                ||||| |||||||||  |  ||||
                                GATCT GGAGGTATG  T  GGGT
                                   G       __ GT
GAM329  FSTL3    3'  TGGGTGTGTATGGAGGGTCTAG 20763      G       CT TG
                                CTGGA CCTCTGTAC  G  CCCA
                                ||||| |||||||||  |  ||||
                                GATCT GGAGGTATG  T  GGGT
                                   G       __ GT
GAM329  GALGT    3'  TGGGCACAAAAGAAGGGGCACC 9422      A     GTACC
           AG                     CTGG GCCTCT    TGTGCCCA
                                ||||| ||||||    ||||||||
                                GACC CGGGGA    ACACGGGT
                                   A     AGAAA
GAM329  GFRA2    3'  TGGGCTCTGGTGGGGGCTCC  9467         GT   TGT
                                GGAGCCTCT  ACC   GCCCA
                                |||||||||  |||   |||||
                                CCTCGGGGG  TGG   CGGGT
                                     __   TCT
GAM329  GNE      3'  TGGGTGTGGTGGCGGGTCCAG  19682      G  T  GT   T TG
                                CTGGA CC CT  ACC G  CCCA
                                ||||| || ||  ||| |  ||||
                                GACCT GG GG  TGG T  GGGT
                                   G  C  __   _ GT
GAM329  GYS1     3'  TGCGGTGGTGCCAGAGGTTTTA 89786          _   TG   CCA
           G                      CTGGAGCCTCTG TACC  TGC
                                ||||||||||| ||||  |||
                                GATTTTGGAGAC GTGG  GCG
                                      C   TG   T
GAM329  HDAC5    3'  GGTGAGAATGGAGGTTCTAG   19622           AC  G
                                CTGGAGCCTCTGT  CT TGCC
                                ||||||||||||  || ||||
                                GATCTTGGAGGTA  GA GTGG
                                      A_  _
GAM329  HMOX2    3'  TGGGTGTGGGTGGAAGCCTCAG 65760     GA  C   GT    TG
                                CTG  GC TCT  ACCTG  CCCA
                                |||  || |||  |||||  ||||
                                GAC  CG AGG  TGGGT  GGGT
                                  TC  A   __     GT
GAM329  HSD11B1  3'  TGGGCATGCTGAGGGATTTTGG 19829   TG   __    T  ACCT
                                C  GAG  CCTC GT    GTGCCCA
                                |  |||  |||| ||    |||||||
                                G  TTT  GGAG CG    TACGGGT
                                 GT   AG    T  ____
GAM329  IDH1     3'  GGGCACAGGGAAGTTCTGG   62097    TG   C  TGTA
                                C  GAGC TC    CCTGTGCCC
                                |  |||| ||    |||||||||
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                                G  CTTG AG    GGACACGGG
                                 GT    A  ____
GAM329  IFNGR2   5'  TGGGCGTCCCGCGGGGCTCCAG 19850         T    ACCTG
                                CTGGAGCC CTGT     TGCCCA
                                ||||||||  ||||     ||||||
                                GACCTCGG GGCG     GCGGGT
                                     _    CCCT_
GAM329  IHPK1    3'  TGGGTGCAGGTGCCCACATTCT 97466      CCTCT      TG
                                GGAG     GTACCTG  CCCA
                                ||||     |||||||  ||||
                                TCTT     CGTGGAC  GGGT
                                  ACACC      GT
GAM329  IL1F9    3'  GGGTATGAAGATGCTTCAG    39513        C   GTACCT
                                CTGGAGC TCT     GTGCCC
                                |||||||  |||     ||||||
                                GACTTCG AGA     TATGGG
                                    T   AG____
GAM329  IL6R     3'  TGGGCAGGTTGGTGGGGGCCTC 6917      GA     TG __    GT
            GG                    CTG  GCCTC  T  ACCT  GCCCA
                                |||  |||||  |  ||||  |||||
                                GGC  CGGGG  G  TGGA  CGGGT
                                  TC     GT GT    __
GAM329  KRT4     5'  TGGGCCCAGGCAGGGGCTTC   11229          TA    T
                                GGAGCCTCTG  CCTG GCCCA
                                ||||||||||  |||| |||||
                                CTTCGGGGAC  GGAC CGGGT
                                      __    C
GAM329  LDB3     3'  TGGGCAATTGCCAGGGCTCCAG 76928         T   TACCTG
                                CTGGAGCC CTG      TGCCCA
                                ||||||||  |||      ||||||
                                GACCTCGG GAC      ACGGGT
                                     _   CGTTA_
GAM329  LENG4    3'  TGGGCCGCTGCGTGGGCTTCGG 44422         C    CC  T
                                CTGGAGCCT TGTA  TG GCCCA
                                |||||||||  ||||  ||  |||||
                                GGCTTCGGG GCGT  GC CGGGT
                                     T    C_  _
GAM329  LIF      3'  TAAGTCAGGTGCAGAGGTTCT  11307              T  CCA
                                GGAGCCTCTGTACCTG GC
                                ||||||||||||||||  ||
                                TCTTGGAGACGTGGAC TG
                                          _  AATC
GAM329  MAP1B    3'  TGGGTGAGCGTGTGTGGGGGTA 20965      A     TG   C   __
            CTAG                    CTGG GCCTC  TAC TGT  GCCCA
                                ||||  |||||  |||  |||  |||||
                                GATC TGGGG  GTG GCG  TGGGT
                                  A    GT   T   AG
GAM329  MAX      3'  TGGGTGGCATAGAGGTTTT    11477           A  TGT
                                GGAGCCTCTGT CC   GCCCA
                                ||||||||||  ||   |||||
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                                TTTTGGAGATA GG   TGGGT
                                      C ___
GAM329  MYCL2    3'  GGATGTTGTTGGGGGCTCCAG  19378          T  CTGTG
                                CTGGAGCCTCTG AC    CC
                                |||||||||||| ||    ||
                                GACCTCGGGGGT TG    GG
                                      _ TTGTA
GAM329  NRG1     3'  ATAGGTGTGTGAGGCTCCGG   16902         TG_
                                CTGGAGCCTC   TACCTGT
                                ||||||||||   |||||||
                                GGCCTCGGAG   GTGGATA
                                      TGT
GAM329  NTF5     3'  TGGGTGAAACCACATGGGGTTT 21631    TG     _   ACCTG
           TGG                    C  GAGCCTC TGT    TGCCCA
                                |  ||||||| |||    ||||||
                                G  TTTGGGG ACA    GTGGGT
                                 GT      T   CCAAA
GAM329  OPRD1    3'  TGGGCATGGGGTGGGCCTCTGG 8071    TG   C   TGTA
                                C  GAG CTC    CCTGTGCCCA
                                |  ||| |||    ||||||||||
                                G  CTC GGG    GGGTACGGGT
                                 GT   C   TG__
GAM329  PACE     3'  TGGCCCTGAGGTGTGGGGGCTG 11945     G     TG    GT__   CA
           CAG                    CTG AGCCTC  TACCT    GCC
                                ||| ||||||  |||||    |||
                                GAC TCGGGG  GTGGA    CGG
                                  G     GT    GTCC   T
GAM329  PLA2G2D  3'  GGGAGGCAGAGGTTTCAG    25720           ACCTGTG
                                CTGGAGCCTCTGT      CCC
                                ||||||||||||      |||
                                GACTTTGGAGACG      GGG
                                      GA_____
GAM329  POMZP3   3'  TGGGCGTAGGCCTGGCTGTGG  25277     G   TCTGTA
                                CTG AGCC     CCTGTGCCCA
                                ||| ||||     ||||||||||
                                GGT TCGG     GGATGCGGGT
                                  G   TCC___
GAM329  PSD      5'  TGGGCTCAAGGCAGGGCTCTGG 12441    TG    T   ACC  T
                                C  GAGCC CTGT   TG GCCCA
                                |  ||||| ||||   || |||||
                                G  CTCGG GACG   AC CGGGT
                                 GT    _    GA_  T
GAM329  PTGER2   5'  TGGGTGCGGGAAGGGGGCTCTG 8174    TG      GTA   TG
           G                     C  GAGCCTCT   CCTG  CCCA
                                |  ||||||||   ||||  ||||
                                G  CTCGGGGG   GGGC  GGGT
                                 GT       AA_   GT
GAM329  RFNG     3'  TGGGTGTCAAGGAGCAGGCTCC 89564         CT  A   __ TG
           AG                     CTGGAGCCT  GT CCT  G  CCCA
                                |||||||||  || |||  |  ||||
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                                GACCTCGGA  CG GGA  T  GGGT
                                     __  A   AC GT
GAM329  RGS6    3'  TGGGCCCGGTGGAGGCTCC   16282        GT   T T
                                GGAGCCTCT  ACC G GCCCA
                                |||||||||  ||| | |||||
                                CCTCGGAGG  TGG C CGGGT
                                     __  _ C
GAM329  S100A11  5'  TGGGTTGAGGAGAGGCTCCAG  20056         GTA   GT
                                CTGGAGCCTCT   CCT  GCCCA
                                ||||||||||   |||  |||||
                                GACCTCGGAGA   GGA  TGGGT
                                      ___   GT
GAM329  SDHC    3'  GGGTTGGTGAGGCTTTGG    69913   TG     TGT   TGT
                                C  GAGCCTC   ACC   GCCC
                                |  |||||||   |||   ||||
                                G  TTCGGAG   TGG   TGGG
                                 GT      ___   T__
GAM329  SMURF1   3'  GGGCTGCTGAGGTTCTAG    94050         T   CCTGT
                                CTGGAGCCTC GTA    GCCC
                                ||||||||||  |||    ||||
                                GATCTTGGAG CGT    CGGG
                                      T  _____
GAM329  SYNGR3   3'  TGCCCAGGTGTGGGTGGTTCTG 16124   TG    _ TG     T  CCA
           G                     C  GAGCC TC  TACCTG GC
                                |  ||||| ||  |||||| ||
                                G  CTTGG GG  GTGGAC CG
                                 GT    T  GT     C  T
GAM329  TBXA2R   3'  TGGGCATCAGCAGCAGGGTTTT 8370    TG    T   AC   _
           GG                     C  GAGCC CTGT  CTG TGCCCA
                                |  ||||| ||||  ||| ||||||
                                G  TTTGG GACG  GAC ACGGGT
                                 GT    _    AC   T
GAM329  TEM6    3'  GGGCATGGGTGCACCCCA    43039     AGCCTC
                                TGG     TGTACCTGTGCCC
                                |||     ||||||||||||
                                ACC     ACGTGGGTACGGG
                                  CC____
GAM329  TGM2    3'  TGGGCAGCCTATGGGGGCTCT  17246          CCTG
                                GGAGCCTCTGTA   TGCCCA
                                ||||||||||||   ||||||
                                TCTCGGGGGTAT   ACGGGT
                                      CCG_
GAM329  TNFRSF7  3'  TGCAGGAGGGCGGGGGCTCTGG 8794    TG       A__
                                C  GAGCCTCTGT   CCTGTG
                                |  ||||||||||   ||||||
                                G  CTCGGGGGCG   GGACGT
                                 GT        GGA
GAM329  TRAF1    3'  TAGAGCTACAGGGGTTCTGG   20178   TG        C  G
                                C  GAGCCTCTGTA CT TG
                                |  |||||||||| || ||
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                                G  CTTGGGGACAT GA AT
                                 GT         C  G
GAM329  TRPC5    5'  TGGGTGCGCTTGAAGGGGCTCA 25928     G      GTACC  TG
            G                    CTG AGCCTCT     TG  CCCA
                                ||| |||||||     ||  ||||
                                GAC TCGGGGA     GC  GGGT
                                  _      AGTTC  GT
GAM329  ZP3A     3'  TGGGCGTAGGCCTGGCTGTGG  24099     G    TCTGTA
                                CTG AGCC     CCTGTGCCCA
                                ||| ||||     ||||||||||
                                GGT TCGG     GGATGCGGGT
                                  G   TCC___
GAM329  AD-003   3'  GGGTGGAAGGGGCTCCAG    26779          GTA  TGT
                                CTGGAGCCTCT   CC   GCCC
                                ||||||||||   ||   ||||
                                GACCTCGGGGA   GG   TGGG
                                      A__  ____
GAM329  APR-3    5'  TGGGCGTGGAAAGGGCTCTGG  55483   TG    T  GTAC TG
                                C  GAGCC CT    C  TGCCCA
                                |  ||||| ||    |  ||||||
                                G  CTCGG GA    G  GCGGGT
                                 GT     _  AA__ GT
GAM329  CBCIP2   3'  TGGGTGCAGGTGCACGCCAG   52662     AGCCTC      TG
                                CTGG     TGTACCTG  CCCA
                                ||||     ||||||||  ||||
                                GACC     ACGTGGAC  GGGT
                                   GC_____       GT
GAM329  CDC42BPB 3'  TGGGCACCTGGGGGGTTCTGG  21241   TG     TGTA  T_
                                C  GAGCCTC    CC  GTGCCCA
                                |  |||||||    ||  |||||||
                                G  CTTGGGG    GG  CACGGGT
                                 GT       _____  TC
GAM329  CECR6    3'  TGGGTGTGGGGCAGGGCCTGG  49938   TG A   T    A    TG
                                C  G GCC CTGT CCTG  CCCA
                                |  | ||| |||| ||||  ||||
                                G  C CGG GACG GGGT  GGGT
                                 GT _   _    _    GT
GAM329  CFLAR    3'  TGGGTGTGGGTGTGGGTACC   15276    A    CTG     TG
                                GG GCCT   TACCTG  CCCA
                                || ||||   ||||||  ||||
                                CC TGGG   GTGGGT  GGGT
                                  A    T__      GT
GAM329  CLL-1    3'  GTAGGGGGTGGGGGTTCTAG   57177          TG A   G
                                CTGGAGCCTC  T CCT TGC
                                ||||||||||  | ||| |||
                                GATCTTGGGG  G GGG ATG
                                      GT _   G
GAM329  DKFZP434P1750 5'  GGGACTTGTGAGGCTCCGG    32027          TGT  CT  G
                                CTGGAGCCTC   AC  GT CCC
                                ||||||||||   ||  || |||
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                                GGCCTCGGAG  TG  CA GGG
                                     ___  TT  _
GAM329  DKFZp547I094 3'  GCAGGGCAGGGGCTCCAG    50560           A
                                CTGGAGCCTCTGT CCTGT
                                |||||||||||| |||||
                                GACCTCGGGGACG GGACG
                                     _
GAM329  DKFZp586I021 3'  TGGGCATAGGTGGACAGGCTCT 51085   TG    CTG
          GG                    C  GAGCCT  TACCTGTGCCCA
                                |  ||||||  ||||||||||||
                                G  CTCGGA  GTGGATACGGGT
                                 GT    CAG
GAM329  DKFZp762A227 5'  TGGGCGGACGCGTGGGCTCTGG 26885   TG    C  A_  TGT
                                C  GAGCCT TGT  CC  GCCCA
                                |  |||||| |||  ||  |||||
                                G  CTCGGG GCG  GG  CGGGT
                                 GT    T  CA  ___
GAM329  E2IG4    3'  TGGGCCTAGGAGAGGCTTTGG  92548   TG     GTA   T
                                C  GAGCCTCT  CCTG GCCCA
                                |  ||||||||  |||| |||||
                                G  TTCGGAGA  GGAT CGGGT
                                 GT      ___   C
GAM329  EPB41L1  3'  TGGGTGTGGGTTGGCTCACAG  71121    _   TCTGT   TG
                                CTG GAGCC    ACCTG  CCCA
                                ||| |||||    |||||  ||||
                                GAC CTCGG    TGGGT  GGGT
                                  A    T____    GT
GAM329  FAM3A    3'  TGGGGGCTATGGGGGCTGCAG  41734    G       CCT  G
                                CTG AGCCTCTGTA  GT CCCA
                                ||| ||||||||||  || ||||
                                GAC TCGGGGGTAT  CG GGGT
                                  G       ___  G
GAM329  FLJ10520  5'  TGGGTATAGGTGCATTTCCA  36713     CCTC
                                TGGAG   TGTACCTGTGCCCA
                                |||||   ||||||||||||||
                                ACCTT   ACGTGGATATGGGT
                                   T___
GAM329  FLJ10904  5'  GGGTACGGGAGCGCTTTGG   37384   TG   CTCT  A
                                C  GAGC   GT CCTGTGCCC
                                |  ||||   || |||||||||
                                G  TTCG   CG GGGCATGGG
                                 GT   ____  A
GAM329  FLJ10936  3'  TGGGATGTGGAGGTTGCAG   37452    G    TG  _
                                CTG AGCCTC  TA CCTG
                                ||| ||||||  || ||||
                                GAC TTGGAG  GT GGGT
                                  G    GT  A
GAM329  FLJ11036  3'  TGGGTGTGGGGCCTGAGGCTTC 37558        TGTA   TG
          A                     TGGAGCCTC   CCTG  CCCA
                                |||||||||   ||||  ||||
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                                ACTTCGGAG   GGGT  GGGT
                                     TCCG   GT
GAM329  FLJ11362  3'  TGGGAATCTGCAGAGGGCTCTG 41966   TG   _    CCTGTG
          G                   C  GAGCC TCTGTA    CCCA
                              |  ||||| ||||||     ||||
                              G  CTCGG AGACGT    GGGT
                               GT    G    CTAA__
GAM329  FLJ12171  3'  TGGGTGCGGGGGAGGGTATCCG 45201     GC   GTA   TG
          G                   CTGGA  CTCT   CCTG  CCCA
                              |||||  ||||   ||||  ||||
                              GGCCT  GGGA   GGGC  GGGT
                                 AT   GG_   GT
GAM329  FLJ12221  5'  TGGGTGCGGTAGGGGTCCCGG  63226    AG    TAC   TG
                              CTGG  CCTCTG   CTG  CCCA
                              ||||  ||||||   |||  ||||
                              GGCC  GGGGAT   GGC  GGGT
                                CT    ___   GT
GAM329  FLJ12229  5'  TGGGGACCATGTGGAGGTTCT  46408      TG  CCT  G
                              GGAGCCTC  TA   GT CCCA
                              ||||||||  ||   || ||||
                              TCTTGGAG  GT   CA GGGT
                                   GT  AC_  G
GAM329  FLJ12750  3'  TGGGCAACGTTAGGGGTTT   45444       T  CTG
                              GAGCCTCTG AC   TGCCCA
                              |||||||||  ||   ||||||
                              TTTGGGGAT TG   ACGGGT
                                   _  CA_
GAM329  FLJ12788  3'  TGGGTCTGCAGAAGGCTTTAG  42850       _    CCTGT
                              CTGGAGCCT CTGTA    GCCCA
                              |||||||||  |||||    |||||
                              GATTTCGGA GACGT    TGGGT
                                   A    C____
GAM329  FLJ13848  3'  TGGGTGTAGAGGGCGGCTTCAG 45834       T  GTAC   TG
                              CTGGAGCC CT    CTG  CCCA
                              ||||||||  ||    |||  ||||
                              GACTTCGG GG    GAT  GGGT
                                   C  GA__   GT
GAM329  FLJ20036  5'  TGGGCGGTTCGGCGGCTCTGG  34860   TG    T   T   TGT
                              C  GAGCC CTG ACC   GCCCA
                              |  ||||| ||| |||   |||||
                              G  CTCGG GGC TGG   CGGGT
                               GT    C   T   ___
GAM329  FLJ20323  3'  GCCTCATCAGGGCAGAGGTTTT 39180          A   _  CCCA
          AG                    CTGGAGCCTCTGT CCTG TG
                              ||||||||||||| |||| ||
                              GATTTTGGAGACG GGAC AC
                                      _   T  TCCGT
GAM329  FLJ20533  5'  TGGAGTACGGGGCCTTCGG   35803       C      _
                              CTGGAG CTCTGTAC CTG
                              |||||| |||||||| |||
```

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                                GGCTTC GGGGCATG GGT
                                   C       A
GAM329  FLJ20584  3'  TGGGCACAGCCTCGGCTCTGG  35857   TG    TCTGTAC
                                C  GAGCC      CTGTGCCCA
                                |  |||||      |||||||||
                                G  CTCGG      GACACGGGT
                                 GT    CTCC___
GAM329  FLJ20825  5'  TGGGCACAGGTGCAGAAGGTGC 36151     GA   _
          AG                      CTG  GCCT CTGTACCTGTGCCCA
                                  |||  ||||  ||||||||||||||
                                  GAC  TGGA GACGTGGACACGGGT
                                    G_    A
GAM329  FLJ20825  5'  TGGGCATAGGTGCAGTGAGTGC 36152    _   __
                                  GC CTC  TGTACCTGTGCCCA
                                  || |||  ||||||||||||||
                                  CG GAG  ACGTGGATACGGGT
                                   T   TG
GAM329  FLJ20825  5'  TGGGCATAGGTGCAGTGAGTGC 36153    _   __
                                  GC CTC  TGTACCTGTGCCCA
                                  || |||  ||||||||||||||
                                  CG GAG  ACGTGGATACGGGT
                                   T   TG
GAM329  FLJ20825  5'  TGGGTGCAGGTGCAGTAGGTGC 36154     GA   _       TG
          AG                      CTG  GCCT CTGTACCTG  CCCA
                                  |||  ||||  |||||||||  ||||
                                  GAC  TGGA GACGTGGAC  GGGT
                                    G_    T        GT
GAM329  FLJ21019  3'  TGGGTGTGGGTAATTTTCTAG  46804       CCTCTG     TG
                                  CTGGAG     TACCTG  CCCA
                                  ||||||     ||||||  ||||
                                  GATCTT     ATGGGT  GGGT
                                     TTA___     GT
GAM329  FLJ21742  3'  CAGATGCAGGGGCTCTGG    50813   TG         C
                                  C  GAGCCTCTGTA CTG
                                  |  |||||||||| |||
                                  G  CTCGGGGACGT GAC
                                   GT         A
GAM329  FLJ22795  3'  TGGGCGTGGCAAGGTTCC    47637        C  TAC TG
                                  GGAGCCT TG   C  TGCCCA
                                  ||||||| ||   |  ||||||
                                  CCTTGGA AC   G  GCGGGT
                                      _  ___ GT
GAM329  FLJ22833  3'  GGGTACAGGTACATTTGG    43406    TC_
                                  CC   TGTACCTGTGCCC
                                  ||   ||||||||||||
                                  GG   ACATGGACATGGG
                                   TTT
GAM329  FLJ23022  5'  TGGGTACAGAAGAGGCTTCAG  47502          GTAC
                                  CTGGAGCCTCT    CTGTGCCCA
                                  ||||||||||    |||||||||
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                                GACTTCGGAGA   GACATGGGT
                                      A___
GAM329  FLJ23027  3'  TGGGTATAGGTATTTTCTTCC  50914     CCTCT
                                GGAG   GTACCTGTGCCCA
                                ||||   ||||||||||||
                                CCTT   TATGGATATGGGT
                                  CTTT_
GAM329  FLJ23251  5'  TGGGTGCACGTCCCCAGGGCTC 46101   TG   T  T__  C  TG
           TGG                   C  GAGCC CTG   AC TG  CCCA
                                |  ||||| |||  || ||  ||||
                                G  CTCGG GAC   TG AC  GGGT
                                 GT    _   CCC  C  GT
GAM329  FLJ23451  5'  TGGCACCTCCGGGTGTGGAAGG 45791        _ TG   ____    CA
           CTCCAG                 CTGGAGCCT C  TACCT   GTGCC
                                |||||||||  |  |||||   |||||
                                GACCTCGGA G  GTGGG   CACGG
                                      A GT    CCTC    T
GAM329  FLJ23506  5'  TGGGCCGCAGGTGGAGGTGTTG 46167   TG A    GT     _
           G                    C  G GCCTCT  ACCTGTG CCCA
                                |  | ||||||  ||||||| ||||
                                G  T TGGAGG  TGGACGC GGGT
                                 GT G     __      C
GAM329  FLJ32356  3'  TGGGTGTGGGTGGCACAGGATC 59029   TG  G   C   _    TG
           TGG                   C  GA CCT TGT ACCTG  CCCA
                                |  || ||| ||| |||||  ||||
                                G  CT GGA ACG TGGGT  GGGT
                                 GT  A   C   G    GT
GAM329  GMPPB    5'  GCCAGGTGCTGGGGGCTCTGG  26222   TG      _      T
                                C  GAGCCTCT GTACCTG GC
                                |  |||||||| ||||||| ||
                                G  CTCGGGGG CGTGGAC CG
                                 GT       T     _
GAM329  GMPPB    5'  TGGGTTCAAAGGTGGAGGTTCC 26226          GT   GT__
           AG                    CTGGAGCCTCT  ACCT   GCCCA
                                ||||||||||  ||||   |||||
                                GACCTTGGAGG  TGGA   TGGGT
                                      __   AACT
GAM329  GNB4     5'  TGGGTGTGGCCGGCGGCTCTGG 41571   TG    T   TAC   TG
                                C  GAGCC CTG   CTG  CCCA
                                |  ||||| |||   |||  ||||
                                G  CTCGG GGC   GGT  GGGT
                                 GT    C   C__   GT
GAM329  GNG4     3'  GGGCCCGCTGGGGTTTTAG   16848          T  ACCT T
                                CTGGAGCCTC GT    G GCCC
                                |||||||||| ||    | ||||
                                GATTTTGGGG CG    C CGGG
                                      T  ____ C
GAM329  GPS2     5'  TGGGCACAGGTGCACGCATTGG 88511   TG A  CTC
                                C  G GC   TGTACCTGTGCCCA
                                |  | ||   ||||||||||||||
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                              G  T CG   ACGTGGACACGGGT
                               GT A  C__
GAM329  HIC2     3'  TGGGTCCAGTGGAGGCTCCGG  65875          TAC   TG
                              CTGGAGCCTCTG   CTG  CCCA
                              ||||||||||||   |||  ||||
                              GGCCTCGGAGGT   GAC  GGGT
                                     ___   CT
GAM329  HSNOV1   3'  TGGGTACAGATGAGGCCTCGG  34444     GA    TGTAC
                              CTG  GCCTC    CTGTGCCCA
                              |||  |||||    |||||||||
                              GGC  CGGAG    GACATGGGT
                                TC    TA___
GAM329  HT001    5'  GGGTATTAGTGGCTTTAG    67243        T   TACCT
                              CTGGAGCC CTG    GTGCCC
                              ||||||||| |||    ||||||
                              GATTTCGG GAT    TATGGG
                                   T  _____
GAM329  HT002    3'  TGGGCTGCGGGGTCAGGGGCTC 26803          TA    _
           CAG                    CTGGAGCCTCTG  CCTGT GCCCA
                              ||||||||||||  ||||| |||||
                              GACCTCGGGGAC  GGGCG CGGGT
                                     TG    T
GAM329  KCND1    3'  TGGGATATGGAGCTTTGG    18350   TG   C     _
                              C  GAGC TCTGTA CCTG
                              |  |||| |||||| ||||
                              G  TTCG AGGTAT GGGT
                               GT   _     A
GAM329  KIAA0226 3'  TGGGCGTGGGTGCTGCCC    64266    A  CTCT    TG
                              GG GC    GTACC  TGCCCA
                              || ||    |||||  ||||||
                              CC CG    CGTGG  GCGGGT
                               _ T___     GT
GAM329  KIAA0329 3'  GCGGGCACAGGGGCTTCGG    29940           A
                              CTGGAGCCTCTGT CCTGT
                              |||||||||||| |||||
                              GGCTTCGGGGACA GGGCG
                                       C
GAM329  KIAA0450 3'  TGGGCGGCTCTGGAGGCCCAG  28376      A      TA_  TGT
                              CTGG GCCTCTG   CC   GCCCA
                              |||| |||||||   ||   |||||
                              GACC CGGAGGT   GG   CGGGT
                                 _      CTC  ___
GAM329  KIAA0513 3'  GGGTGTAGGAGAGCTCTGG   29043   TG   C   GTA   TG
                              C  GAGC TCT   CCTG  CCC
                              |  |||| |||   ||||  |||
                              G  CTCG AGA   GGAT  GGG
                               GT   _  ___    GT
GAM329  KIAA0514 5'  TGGGCACGCAGTAGGGGCTCAG 28761     G       TACC
                              CTG AGCCTCTG    TGTGCCCA
                              ||| ||||||||    ||||||||
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                                GAC TCGGGGAT    GCACGGGT
                                  _       GAC_
GAM329  KIAA0767  3'  TGGGCCATCCGAGAGGCTCTGG 61260    TG       GTACC  T
                                C  GAGCCTCT     TG GCCCA
                                |  ||||||||     || |||||
                                G  CTCGGAGA     AC CGGGT
                                 GT       GCCT_  _
GAM329  KIAA0798  3'  GGGAGGCAGAGGTTTCAG    28450            ACCTGTG
                                CTGGAGCCTCTGT      CCC
                                ||||||||||||       |||
                                GACTTTGGAGACG      GGG
                                       GA_____
GAM329  KIAA0884  3'  TGGGATGTGGAGGTTGCAG    70761     G     TG  _
                                CTG AGCCTC  TA CCTG
                                ||| ||||||  || ||||
                                GAC TTGGAG  GT GGGT
                                  G     GT  A
GAM329  KIAA1130  3'  TGGGCATTGCTGGAGGTTT    63102         _  CCT
                                GAGCCTCT GTA   GTGCCCA
                                |||||||| |||   |||||||
                                TTTGGAGG CGT   TACGGGT
                                     T  ____
GAM329  KIAA1545  3'  TGGGCGGCTCCTGTGGGCTTCA 61337          CTGTACCTG
          G                      CTGGAGCCT        TGCCCA
                                |||||||||        ||||||
                                GACTTCGGG        GCGGGT
                                     TGTCCTCG_
GAM329  KIAA1550  3'  TGGGCAGTGCTGGAGGCTCT   67155          _   CTG
                                GGAGCCTCT GTAC   TGCCCA
                                ||||||||| ||||   ||||||
                                TCTCGGAGG CGTG   ACGGGT
                                     T  ____
GAM329  KIAA1655  5'  TGGGAGCTTAGGGCAGGGGCTC 67205            A   TG__
          CGG                    CTGGAGCCTCTGT CCTG    CCCA
                                |||||||||||| ||||    ||||
                                GGCCTCGGGGACG GGAT    GGGT
                                       _   TCGA
GAM329  KIAA1904  3'  GGGCTTCGTGGGGGGCTTCAG  73875          G   CTGT   A
                                CTGGAGCCTCT TAC    GCCC
                                |||||||||| |||    ||||
                                GACTTCGGGGG GTG    CGGG
                                      _  CTT_    G
GAM329  KIAA1932  3'  TGGGCAATGTCAAGAGAGGTTT 73826    TG       GTACCTG_
          TGG                    C  GAGCCTCT       TGCCCA
                                |  ||||||||       ||||||
                                G  TTTGGAGA       ACGGGT
                                 GT       GAACTGTA
GAM329  KIAA1951  5'  GGGTGTGTGTAGGCTTCAG    74162         CTGT  C  TG
                                CTGGAGCCT    AC TG  CCC
                                |||||||||    || ||  |||
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                                GACTTCGGA   TG GT  GGG
                                     ____ T  GT
GAM329  KOC1    3'  TGGGTGTGGGTGGTCTCCA   92720     _ TCTGT   TG
                                TGGAG CC    ACCTG  CCCA
                                ||||| ||    |||||  ||||
                                ACCTC GG    TGGGT  GGGT
                                   T _____    GT
GAM329  LASP1   3'  TGGGCGATTTGGGGGCTCGGG  21581   G       TACCTG
                                CT GAGCCTCTG     TGCCCA
                                || |||||||||     ||||||
                                GG CTCGGGGGT     GCGGGT
                                 G       TTA___
GAM329  LRRFIP2  3'  GGGCACTCGGAGGCCTTGG   35294   TG A     TACCT
                                C  G GCCTCTG    GTGCCC
                                |  | |||||||    ||||||
                                G  T CGGAGGC    CACGGG
                                 GT C      T____
GAM329  MANBAL   3'  GCTCCATCAGGTGCAGGGGATT 42219   TG  G        _  CCCA
           TGG                    C  GA CCTCTGTACCTG TG
                                |  || ||||||||||||| ||
                                G  TT GGGGACGTGGAC AC
                                 GT  A          T  CTCGT
GAM329  MGC12921 3'  TGGGCATCGATGAGGCTTTGG  64516   TG     TGTACCT
                                C  GAGCCTC      GTGCCCA
                                |  |||||||      |||||||
                                G  TTCGGAG      TACGGGT
                                 GT      TAGC___
GAM329  MGC23284 5'  GGGCGCGGCGAGGTCTGG    59360   TG  G   TGTAC
                                C  GA CCTC    CTGTGCCC
                                |  || ||||    ||||||||
                                G  CT GGAG    GGCGCGGG
                                 GT  _   C____
GAM329  MGC2452  5'  TGGAGCGTTGTCTGGAGGTTCC 51970          GT  CTG  _
           AG                     CTGGAGCCTCT  AC   TGC CCA
                                ||||||||||  ||   ||| |||
                                GACCTTGGAGG  TG   GCG GGT
                                      TC  TT_   A
GAM329  MGC3178  3'  TGGGTATCCAGGGAGGCTCT   48721        TGTA   __
                                GGAGCCTC   CCTG  TGCCCA
                                ||||||||   ||||  ||||||
                                TCTCGGAG   GGAC  ATGGGT
                                     _____   CT
GAM329  MGC4293  3'  TGGGACTCTGCGGGAGGCTCTG 49346   TG      _  CCT  G
           G                     C  GAGCCTCT GTA   GT CCCA
                                |  |||||||| |||   || ||||
                                G  CTCGGAGG CGT   CA GGGT
                                 GT       G   CT_ _
GAM329  MGC4655  3'  TGGGGATATGCAAGGGGCTCTG 53962   TG      _  CC   G
           G                     C  GAGCCTCT GTA  TGT CCCA
                                |  |||||||| |||  ||| ||||
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                                G  CTCGGGGA CGT  ATA GGGT
                                 GT       A  __  G
GAM329  MGC5306  5'  GGTGTGTACAGAGCTCTAG   44372       C      CT TG
                                CTGGAGC TCTGTAC  G  CC
                                ||||||| |||||||  |  ||
                                GATCTCG AGACATG  T  GG
                                   _     __ GT
GAM329  MGLL     5'  TGGGTGCGGGAAGAGGGCTC   24419      _  GTA   TG
                                GAGCC TCT   CCTG  CCCA
                                ||||| |||   ||||  ||||
                                CTCGG AGA   GGGC  GGGT
                                   G   A__    GT
GAM329  MRPL41   5'  TGGAGCTCGTGTGGGGTCTCCG 51648      C   TG   CTGT  _
           G                     CTGGAG CTC  TAC    GC CCA
                                ||||||| |||  |||    || |||
                                GGCCTC GGG  GTG    CG GGT
                                   T   GT   CT__  A
GAM329  MRPL45   3'  TGGGCATGGACCAGCCTTCAG  51354      CCT   TA  T
                                CTGGAG   CTG  CC GTGCCCA
                                ||||||   |||  || |||||||
                                GACTTC   GAC  GG TACGGGT
                                   C__   CA  _
GAM329  NCX      3'  GGGCTCTGAGGGGCTCTAG   32945         GTACCTGT
                                CTGGAGCCTCT       GCCC
                                ||||||||||        ||||
                                GATCTCGGGGA       CGGG
                                      GTCT____
GAM329  NYD-SP25 3'  TGGGCAAGTCAGTGGCTCCAG  54306        T   T  CTG
                                CTGGAGCC CTG AC   TGCCCA
                                |||||||| ||| ||   ||||||
                                GACCTCGG GAC TG   ACGGGT
                                    T   _  A__
GAM329  P2RX1    3'  TGGGTGCAGCGTGAGGCTTCAG 67753         TGT  _  TG
                                CTGGAGCCTC   AC CTG  CCCA
                                ||||||||||   || |||  ||||
                                GACTTCGGAG   TG GAC  GGGT
                                      ___  C   GT
GAM329  P37NB    5'  TGGGTGCAGCCAGAGAGGTCCA 20629      G    GTAC   TG
           G                     CTGGA CCTCT    CTG  CCCA
                                ||||| |||||    |||  ||||
                                GACCT GGAGA    GAC  GGGT
                                   _    GACC   GT
GAM329  PDE2A    3'  TGGGGGATACAGGGGCCCCAG  12007     A       _  TGTG
                                CTGG GCCTCTGTA CC    CCCA
                                |||| ||||||||| ||    ||||
                                GACC CGGGGACAT GG    GGGT
                                  C       A  _____
GAM329  PGRMC2   3'  TGGGTGCATGGGGCTGTGG   21980     G    _
                                CTG AGCCTC TGTACCTG
                                ||| |||||| ||||||||
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                                GGT TCGGGG ACGTGGGT
                                  G     T
GAM329  PI4KII   3'  TGGGTCTCTGCAAGGGCTCTGG 37957    TG    TC    CCTGT
                                C  GAGCC  TGTA    GCCCA
                                |  |||||  ||||    |||||
                                G  CTCGG  ACGT    TGGGT
                                 GT    GA   CTC__
GAM329  PRIC285  5'  TGGGCACACAGTAGGTGCTTTA 62122       C    TACC
           G                     CTGGAGC TCTG    TGTGCCCA
                                |||||||  ||||   |||||||||
                                GATTTCG GGAT    ACACGGGT
                                    T   GAC_
GAM329  PRO1048  3'  TGGGCAATAATGGGGGCTTT   38122         ACCTG
                                GGAGCCTCTGT    TGCCCA
                                ||||||||||     ||||||
                                TTTCGGGGGTA    ACGGGT
                                      ATA__
GAM329  PRO1048  3'  TGGGCATGGTGGCAGGCGCCAG 38123     A    CTG    T
                                CTGG GCCT   TACC GTGCCCA
                                ||||  ||||   ||||  |||||||
                                GACC CGGA   GTGG TACGGGT
                                  G   CG_   _
GAM329  RAB24    3'  CAGGTATGAGGCTTTAG     56257          T
                                CTGGAGCCTC GTACCTG
                                ||||||||||  |||||||
                                GATTTCGGAG TATGGAC
                                          _
GAM329  SCAMP5   3'  GGCTGGTAGAGGCTCTAG    58061          GT   TGT
                                CTGGAGCCTCT  ACC   GCC
                                ||||||||||  |||   |||
                                GATCTCGGAGA  TGG   CGG
                                      __   T__
GAM329  SEMA4G   5'  TGGGCGTGGACGGGCTGCTGG  96335    TG _    CT  AC TG
                                C  G AGCCT  GT  C  TGCCCA
                                |  | |||||  ||  |  ||||||
                                G  C TCGGG  CA  G  GCGGGT
                                 GT G    __  __ GT
GAM329  SEPT3    3'  TGGGCATGGGAGGTGGGCGTTG 39407    TG A    _  GTA
           G                     C  G GCCT CT   CCTGTGCCCA
                                |  | |||| ||   ||||||||||
                                G  T CGGG GG   GGGTACGGGT
                                 GT G    T  A__
GAM329  SLC25A18 3'  TGGGCACAGCTACCAGGGGCTT 49752          _  C
           T                     GGAGCCTCTG TA CTGTGCCCA
                                ||||||||||  ||  |||||||||
                                TTTCGGGGAC AT GACACGGGT
                                      C  C
GAM329  SPINLW1  3'  TGGGTGCAGGTAGTTTGTTTGA 40233    G    CTCTG     TG
           G                     CT GAGC    TACCTG  CCCA
                                ||  ||||    ||||||  ||||
```

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                                GA TTTG    ATGGAC  GGGT
                                 G   TTTG_     GT
GAM329  SPRY4    3'  CAGCAAGGTCAGAGGTTTTAG  49001          T   G   CCA
                                CTGGAGCCTCTG ACCT TGC
                                |||||||||||| |||| |||
                                GATTTTGGAGAC TGGA ACG
                                       _   _  ACG
GAM329  TOLLIP   3'  TGGGTGCATGTGGGTTTTCGG  39201       _  CTGT  C  TG
                                CTGGAG CCT    AC TG  CCCA
                                |||||| |||    || ||  ||||
                                GGCTTT GGG    TG AC  GGGT
                                   T  ____  T  GT
GAM329  U5-100K  3'  TGGGATATGGGGGCTTAG    60416     G        _
                                CTG AGCCTCTGTA CCTG
                                ||| |||||||||| ||||
                                GAT TCGGGGGTAT GGGT
                                  _        A
GAM329  USP20    3'  TGGGTGGGGAAGGGGCTCTGG  22903   TG      GTA   GT
                                C  GAGCCTCT   CCT  GCCCA
                                |  ||||||||   |||  |||||
                                G  CTCGGGGA   GGG  TGGGT
                                 GT       AG_  __
GAM329  VI       3'  GGGTTGTGGAGGTTGTGG    26487     G     TG  CCTGT
                                CTG AGCCTC  TA    GCCC
                                ||| ||||||  ||    ||||
                                GGT TTGGAG  GT    TGGG
                                  G     GT  _____
GAM329  LOC118738 3'  TGGGTGCAGCAGCCAGCCTTTG 76007   TG   C  __   TAC   TG
           G                     C  GAG CT  CTG   CTG  CCCA
                                |  ||| ||  |||   |||  ||||
                                G  TTC GA  GAC   GAC  GGGT
                                 GT   C  CC   ___   GT
GAM329  LOC118987 5'  TGGGCGCGGGAGTAGGGGCCCG 74397      A      TA
           G                     CTGG GCCTCTG  CCTGTGCCCA
                                |||| |||||||  ||||||||||
                                GGCC CGGGGAT  GGGCGCGGGT
                                  _      GA
GAM329  LOC126374 3'  ATGGGTGTGGGTGTGGAGGGAG 74992    AG___    TG     TG
           GGCC                    GG    CCTC  TACCTG  CCCA   T
                                ||    ||||  ||||||  ||||   |
                                CC    GGAG  GTGGGT  GGGT   A
                                 GGGAG   GT     GT
GAM329  LOC128933 5'  TGGGCCTTGTGCAGGGGCTCC  76775           CTGT
                                GGAGCCTCTGTAC    GCCCA
                                ||||||||||||    |||||
                                CCTCGGGGACGTG    CGGGT
                                       TTC_
GAM329  LOC129566 3'  GGGTGCGGGCAGGCTTGGG   76226    G     CTGTA   TG
                                CT GAGCCT    CCTG  CCC
                                || ||||||    ||||  |||
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                                GG TTCGGA    GGGC  GGG
                                 G     C____    GT
GAM329  LOC138307 5'  GGGCGTGGGTGTCACCAG    75840      AGCCTC  _    TG
                                CTGG     TG TACC  TGCCC
                                ||||     || ||||  |||||
                                GACC     AC GTGG  GCGGG
                                  _______  T    GT
GAM329  LOC142972 3'  TGGGTGTGAGGGGGGTCCCAG  65723      AG    TGTA  _ TG
                                CTGG  CCTC    CCT G  CCCA
                                ||||  ||||    ||| |  ||||
                                GACC  GGGG    GGA T  GGGT
                                  CT    _____   G GT
GAM329  LOC144519 3'  GGGCGTGGACCAGGCCCGG    77377      A    CT  AC TG
                                CTGG GCCT  GT  C  TGCCC
                                |||| ||||  ||  |  |||||
                                GGCC CGGA  CA  G  GCGGG
                                  _    C_  __ GT
GAM329  LOC145717 3'  TGGGCGTGGCAAGGTTCC     67378        C  TAC TG
                                GGAGCCT TG   C  TGCCCA
                                ||||||| ||   |  ||||||
                                CCTTGGA AC   G  GCGGGT
                                   _  ___ GT
GAM329  LOC145831 3'  TGGGCACAATCAGGGCTCTGG  77990    TG    T   TACC
                                C  GAGCC CTG    TGTGCCCA
                                |  ||||| |||   ||||||||
                                G  CTCGG GAC    ACACGGGT
                                 GT    _   TA__
GAM329  LOC145873 3'  TGGGTGTAGGAGGCAGGCCCCA 78015      A   _  GTA    TG
           G                     CTGG GCCT CT   CCTG  CCCA
                                ||||| |||| ||   ||||  ||||
                                GACC CGGA GG   GGAT  GGGT
                                  C    C  A__    GT
GAM329  LOC146723 5'  GGGGAAAGATGGGTATAGGGGC 78685                G___   A
           TTCA                   TGGAGCCTCTGTACCTGT    CCC
                                |||||||||||||||||    |||
                                ACTTCGGGGATATGGGTA    GGG
                                          GAAA   GT
GAM329  LOC148132 3'  GGCTCAGGTGGAGGCTCCAG   85257          GT    T
                                CTGGAGCCTCT  ACCTG GCC
                                ||||||||||  ||||| |||
                                GACCTCGGAGG  TGGAC CGG
                                      __     T
GAM329  LOC149302 5'  TGGGTGTGGGTGAGGGCTTCGG 80045        T  G     TG
                                CTGGAGCC CT TACCTG  CCCA
                                ||||||||  || ||||||  ||||
                                GGCTTCGG GA GTGGGT  GGGT
                                     _ _     GT
GAM329  LOC149465 3'  TTTCATAGGTATAGAGTTTTGG 80195    TG   C          CCCA
                                C  GAGC TCTGTACCTGTG
                                |  |||| ||||||||||||
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                                G  TTTG AGATATGGATAC
                                 GT   _        TTTG
GAM329  LOC149506 5'  GGTGAGTGCGAAGGCTCTGG  85642   TG    C    CTG
                                C  GAGCCT TGTAC   TGCC
                                |  |||||| |||||   ||||
                                G  CTCGGA GCGTG   GTGG
                                 GT     A    A__
GAM329  LOC150378 5'  TGGGCCCACGGTGGAGGCCTCA 80561    GA    GT  _  T
          G                      CTG  GCCTCT  ACC TG GCCCA
                                 |||  ||||||  ||| || |||||
                                 GAC  CGGAGG  TGG AC CGGGT
                                   TC     __   C  C
GAM329  LOC150418 5'  TGGGTGTGGTACCGAGGCTTCA 66117         T    T TG
          G                      CTGGAGCCTC GTACC G  CCCA
                                 ||||||||||| ||||| |  ||||
                                 GACTTCGGAG CATGG T  GGGT
                                       C    _ GT
GAM329  LOC150946 3'  TGGAATGCTGGTATGGGGGCCC 86350     A        T  GC_
          CAG                      CTGG GCCTCTGTACC GT   CCA
                                 |||| ||||||||||| ||   |||
                                 GACC CGGGGGTATGG CG   GGT
                                   C         T  TAA
GAM329  LOC151516 5'  TGGGTTGCTGCTGAGGTTCCAG 81071         T   CCTGT
                                 CTGGAGCCTC GTA    GCCCA
                                 |||||||||| |||    |||||
                                 GACCTTGGAG CGT    TGGGT
                                       T   CGT__
GAM329  LOC152762 3'  TGGGTAGAGAACAGAGGTCCAG 81539     G     AC  G
                                 CTGGA CCTCTGT  CT TGCCCA
                                 ||||| |||||||  || ||||||
                                 GACCT GGAGACA  GA ATGGGT
                                   _     A_  G
GAM329  LOC153811 3'  GGGCTGGCAGGGGCTCTGG   81840   TG       ACCTGT
                                 C  GAGCCTCTGT     GCCC
                                 |  ||||||||||     ||||
                                 G  CTCGGGGACG     CGGG
                                  GT        GT____
GAM329  LOC154386 3'  TGTTTACTGGGTACAGAGTTTC 81991       C       _  CC
          AG                      CTGGAGC TCTGTACCT GTG  CA
                                 |||||||  ||||||||| |||  ||
                                 GACTTTG AGACATGGG CAT  GT
                                    _       T   TT
GAM329  LOC155032 3'  TGGGGATGATGCAGGGGTTTTG 87600   TG       CC   G
          G                       C  GAGCCTCTGTA  TGT CCCA
                                 |  ||||||||||  ||| ||||
                                 G  TTTGGGGACGT  GTA GGGT
                                  GT         A_  G
GAM329  LOC157773 5'  TGGATTGGATGTAGAGGCTTCA 82509           _  TGTG  CA
          G                       CTGGAGCCTCTGTA CC    CC
                                 |||||||||||||| ||    ||
```

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                                GACTTCGGAGATGT GG    GG
                                       A  TTA_  T
GAM329   LOC196955 3'  GGGTGCAGGTGCAGAGC     77869    C        TG
                                GC TCTGTACCTG  CCC
                                || ||||||||||  |||
                                CG AGACGTGGAC  GGG
                                  _        GT
GAM329   LOC197119 3'  TGGGTGGACGTGGAGGCTTCAG 91276          TG A_  TGT
                                CTGGAGCCTC  T  CC   GCCCA
                                ||||||||||  |  ||   |||||
                                GACTTCGGAG  G  GG   TGGGT
                                      GT CA  ___
GAM329   LOC197414 3'  TGGGCAGCTCTGTGGGGGCTCT 89459         TG  CCTG
                                GGAGCCTC  TA    TGCCCA
                                ||||||||  ||    ||||||
                                TCTCGGGG  GT    ACGGGT
                                     GT  CTCG
GAM329   LOC199953 3'  TGGGCAGCGCCCACACAGGCTC 89886    TG     C   ACC  _
            TGG                    C  GAGCCT TGT   TG TGCCCA
                                |  ||||||  |||   ||  ||||||
                                G  CTCGGA ACA   GC ACGGGT
                                 GT     C   CCC  G
GAM329   LOC203069 3'  GGGTGTGGTGGGCTTTAG     90762          _ TG
                                CTGGAGCCT C  TACCT
                                |||||||||  |  |||||
                                GATTTCGGG G  GTGGG
                                      T GT
GAM329   LOC203078 3'  GCATGGGGGCGGGGGCTCTGG  90790    TG       TA
                                C  GAGCCTCTG  CCTGTGC
                                |  |||||||||  |||||||
                                G  CTCGGGGGC  GGGTACG
                                 GT        GG
GAM329   LOC203080 5'  TGGGTGTAGGGACTGGCCC    90775    A   TCT  A    TG
                                GG GCC   GT CCTG  CCCA
                                || |||   || ||||  ||||
                                CC CGG   CA GGAT  GGGT
                                  _   T__  G    GT
GAM329   LOC204285 5'  GCAGGTGCAGAGCTCTGG     91020    TG    C
                                C  GAGC TCTGTACCTGT
                                |  |||| ||||||||||
                                G  CTCG AGACGTGGACG
                                 GT   _
GAM329   LOC219653 3'  GGGTTCACAGCGGCTTTAG    92919         T    ACCTGT
                                CTGGAGCC CTGT      GCCC
                                |||||||| ||||      ||||
                                GATTTCGG GACA      TGGG
                                     C    CT_____
GAM329   LOC219722 5'  TGGGCATGGTGGCTCAGAGGTT 94690     G        ___    T
            TGGG                    CT GAGCCTCTG   TACC GTGCCCA
                                || |||||||||   |||| |||||||
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                                GG TTTGGAGAC   GTGG TACGGGT
                                 G       TCG   _
GAM329  LOC219920 5'  GGGTGCCCACAGGCTCCGG   94958        C  TACCT TG
                                CTGGAGCCT TG    G  CCC
                                ||||||||| ||    |  |||
                                GGCCTCGGA AC    C  GGG
                                     C  C____ GT
GAM329  LOC220537 3'  TGGGCGTGGCAAGGTTCC    92427       C  TAC TG
                                GGAGCCT TG   C  TGCCCA
                                ||||||| ||   |  ||||||
                                CCTTGGA AC   G  GCGGGT
                                    _ ___ GT
GAM329  LOC221463 3'  GGGCTGGTGGGGGTGCTGG   93709   TG A    GT   TGT
                                C  G GCCTCT  ACC   GCCC
                                |  | ||||||  |||   ||||
                                G  C TGGGGG  TGG   CGGG
                                 GT G     __   T__
GAM329  LOC253219 3'  TGGGCGCGGAATCCGGGCTGCC 99349     _    CT  A  T
           GG                    CTGG AGCCT  GT CC GTGCCCA
                                ||||| |||||  || || |||||||
                                GGCC TCGGG  TA GG CGCGGGT
                                  G    CC  A  _
GAM329  LOC253219 5'  TGGGCGCGGAATCCGGGCTGCC 99350     _    CT  A  T
           GG                    CTGG AGCCT  GT CC GTGCCCA
                                ||||| |||||  || || |||||||
                                GGCC TCGGG  TA GG CGCGGGT
                                  G    CC  A  _
GAM329  LOC253451 5'  GGCGAGCAGGGGCTTCGG    97723          ACCTG
                                CTGGAGCCTCTGT    TGCC
                                ||||||||||||    ||||
                                GGCTTCGGGGACG    GCGG
                                       A____
GAM329  LOC254719 3'  TGGGCACAGTGCTGGTTCTGG  97766   TG    TCT   C
                                C  GAGCC   GTAC TGTGCCCA
                                |  |||||   |||| ||||||||
                                G  CTTGG   CGTG ACACGGGT
                                 GT    T__   _
GAM329  LOC254808 3'  TGGGTGTGGGCCGTGAGGTTTA 98812    G    TGTA   TG
           G                     CTG AGCCTC   CCTG  CCCA
                                ||| ||||||   ||||  ||||
                                GAT TTGGAG   GGGT  GGGT
                                  _     TGCC   GT
GAM329  LOC255031 3'  GGGAGGCAGAGGTTTCAG    99040          ACCTGTG
                                CTGGAGCCTCTGT     CCC
                                ||||||||||||      |||
                                GACTTTGGAGACG     GGG
                                       GA_____
GAM329  LOC256451 3'  TGGGCGCCCTGAGGAGGCTCC  97805        GTACCT
                                GGAGCCTCT     GTGCCCA
                                |||||||||     |||||||
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                                CCTCGGAGG     CGCGGGT
                                      AGTCC_
GAM329  LOC257476 3'  TGGGTGCAGGTGCCCACATTCT 61925      CCTCT      TG
                                GGAG    GTACCTG  CCCA
                                ||||    |||||||  ||||
                                TCTT    CGTGGAC  GGGT
                                  ACACC      GT
GAM329  LOC51157  5'  GGGTTAGTGGGGCTCTGG    33015    TG      TGTAC   T
                                C  GAGCCTC    CTG GCCC
                                |  |||||||    ||| ||||
                                G  CTCGGGG    GAT TGGG
                                 GT      T____  _
GAM329  LOC90346  3'  TGGGTATGGTGCTGGGCTGTTG 57201    TG _    CT    T
            G                    C  G AGCCT  GTACC GTGCCCA
                                |  | |||||  ||||| |||||||
                                G  T TCGGG  CGTGG TATGGGT
                                 GT G    T_    _
GAM329  LOC90637  5'  TGGGTGTGGGTGTGCCTCCG   64404      CCTCTG     TG
                                TGGAG     TACCTG  CCCA
                                |||||     ||||||  ||||
                                GCCTC     GTGGGT  GGGT
                                   CGT___     GT
GAM329  LOC90750  3'  TGGGCTTCGCATAGGCTTTAG  64635         C   ACCTGT
                                CTGGAGCCT TGT     GCCCA
                                |||||||| |||     |||||
                                GATTTCGGA ACG     CGGGT
                                      T   CTT___
GAM329  LOC90982  5'  TGGGCATAGCCAAGGGGGTTCC 65148           GTAC
            AG                    CTGGAGCCTCT    CTGTGCCCA
                                ||||||||||    |||||||||
                                GACCTTGGGGG    GATACGGGT
                                       AACC
GAM329  LOC92305  3'  TGGGTAGGGGTGGGGGTTTGAG 57239    G       GT    G
                                CT GAGCCTCT  ACCT TGCCCA
                                || ||||||||  |||| ||||||
                                GA TTTGGGGG  TGGG ATGGGT
                                 G       __    G
GAM329  LOC93070  3'  TGGGATGTGGAGGTTGCAG   71817     G     TG  _
                                CTG AGCCTC  TA CCTG
                                ||| ||||||  || ||||
                                GAC TTGGAG  GT GGGT
                                  G     GT  A
GAM329  LOC93259  5'  TGGGTGCAGGGGCTCAG     72298     G
                                CTG AGCCTCTGTACCTG
                                ||| ||||||||||||||
                                GAC TCGGGGACGTGGGT
                                  _
GAM330  BAP1      3'  ATGCCAAGGGGTAATGGG    17395      C    GG
                                CCCAT ATCT  TTTGGCAT
                                ||||| ||||  ||||||||
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                                GGGTA TGGG  GAACCGTA
                                  A   __
GAM330  FMR2     3'  CAGTATCAAATGAATGGGTCAA 10683         _  C   _
                                TTGACCCAT CAT TGGT TTG
                                ||||||||| ||| |||| |||
                                AACTGGGTA GTA ACTA GAC
                                    A  A   T
GAM330  FLJ11939 3'  ATGCCAAACCAATTTTGGGTCG 45494        TC  C
          A                      TTGACCCA  AT TGGTTTGGCAT
                                ||||||||  || ||||||||||
                                AGCTGGGT  TA ACCAAACCGTA
                                    TT  _
GAM330  MGC15606 3'  CCCTTAGAAGAATGGGTCAA   59522        _ A    TTT
                                TTGACCCAT C TCTGG   GG
                                ||||||||| | |||||   ||
                                AACTGGGTA G AGATT   CC
                                    A A    C__
GAM330  LOC126669 5'  ATGCCAAACGGACAAAGGGTCA 75924       ATCA   G
          A                      TTGACCC    TCTG TTTGGCAT
                                |||||||    |||| ||||||||
                                AACTGGG    AGGC AAACCGTA
                                    AAAC   _
GAM330  LOC145813 3'  CAAACTACAGACCACGGGCCAA 84503     A  ATCA   __
                                TTG CCC    TCTG  GTTTG
                                ||| |||    ||||  |||||
                                AAC GGG    AGAC  CAAAC
                                  C   CACC    AT
GAM330  LOC148293 3'  GGGCAGATGATAGTCAA     79530      CC      G
                                TTGAC  ATCATCTG TT
                                |||||  |||||||| ||
                                AACTG  TAGTAGAC GG
                                   A_      G
GAM331  BPAG1    3'  ACTACATCAATCCCTGAC    32074      A      A__
                                GTCA GGGATTGG   AGT
                                |||| ||||||||   |||
                                CAGT CCCTAACT   TCA
                                   _       ACA
GAM331  CHRNA5   3'  ACAGTAAAGTTCATCCTTTGAC 60465         T   AGTC  C
                                GTCAAGGGAT GGA    AC GT
                                |||||||||| |||    || ||
                                CAGTTTCCTA CTT    TG CA
                                    _  GAAA  A
GAM331  IL2RB    3'  ACAGTGACCCCAGTCCC     7931         AA    C
                                GGGATTGG  GTCAC GT
                                ||||||||  ||||| ||
                                CCCTGACC  CAGTG CA
                                    C_     A
GAM331  LTB      3'  ACGGTGACTCCAGTGCTGGAC  24807     AA  G     A
                                GTC  GG ATTGGA GTCACCGT
                                |||  || |||||| ||||||||
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                                CAG  TC TGACCT CAGTGGCA
                                  G_  G     _
GAM331  SLC8A2    3'  ACCGTTCCTTCCAATCCCTCCA 66930    CA         TC  C
              C                    GT  AGGGATTGGAAG  AC GT
                                ||  ||||||||||||  || ||
                                CA  TCCCTAACCTTC  TG CA
                                  CC           CT  C
GAM331  ARHGEF9   3'  ACAGTGACTTTGATTACCCTTG 31479       ATTG_      C
                                CAAGGG     GAAGTCAC GT
                                ||||||     |||||||| ||
                                GTTCCC     TTTCAGTG CA
                                   ATTAG       A
GAM331  MGC2477   5'  CGGTGACCTCCCGCTGGC    44299     A_    TTGGAA
                                GTCA  GGGA     GTCACCG
                                ||||  ||||     |||||||
                                CGGT  CCCT     CAGTGGC
                                  CG    C_____
GAM331  MGC3262   3'  ACGATGACTGAAGGCTCCTTTG 44050         _  GGA    C
              AC                   GTCAAGGGA TT   AGTCA CGT
                                |||||||||  ||   |||||  |||
                                CAGTTTCCT GG   TCAGT GCA
                                     C  AAG    A
GAM331  T1A-2     3'  ACGGTGACCTCTCCGCTTG    22389      _   TTG  A
                                CAAG GGA   GA GTCACCGT
                                ||||  |||   ||  ||||||||
                                GTTC CCT   CT CAGTGGCA
                                  G   ___  C
GAM331  LOC115761 3'  ACGGTGGGGGAATCCCTTGA   93391          GGAAG
                                TCAAGGGATT     TCACCGT
                                ||||||||||     |||||||
                                AGTTCCCTAA     GGTGGCA
                                     GGG__
GAM331  LOC145761 5'  ACGGTGACCTTCACCCC     84478     AT    A
                                GGG  TGGA GTCACCGT
                                |||  ||||  ||||||||
                                CCC  ACTT CAGTGGCA
                                  C_    C
GAM331  LOC197285 3'  ACGGTGCTTCCCCCCAATCCC  89150        ____     T
                                GGGATT    GGAAG CACCGT
                                ||||||    |||||  ||||||
                                CCCTAA    CCTTC GTGGCA
                                   CCCC     _
GAM331  LOC254600 3'  ACGGTGCTTCCCCCCAATCCC  97937        ____     T
                                GGGATT    GGAAG CACCGT
                                ||||||    |||||  ||||||
                                CCCTAA    CCTTC GTGGCA
                                   CCCC     _
GAM331  LOC56965  3'  TGACTCCATCCCCTGAC     39928      A    T   A
                                GTCA GGGAT GGA GTCA
                                ||||  |||||  |||  ||||
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                                CAGT CCCTA CCT CAGT
                                  C    _  _
GAM331  LOC56965  3'  TGACTCCATCCCCTGAC    39934     A    T  A
                                GTCA GGGAT GGA GTCA
                                |||| ||||| ||| ||||
                                CAGT CCCTA CCT CAGT
                                  C    _  _
GAM332  KRT16    5'  GTCATTGCGGCCACC      96891     TCAAG        C
                                GGT    GGCCGCAATGA C
                                |||    |||||||||||| |
                                CCA    CCGGCGTTACT G
                                  ______         A
GAM332  CKAP2    3'  GTCATGTCCCTTGAA      37106        CC   A
                                TTCAAGGG  GCA TGAC
                                ||||||||  ||| ||||
                                AAGTTCCC  TGT ACTG

                                   __  _
GAM332  FLJ13089  5'  GGTGGCAGCCCTTGAACC    71428          C  AATG
                                GGTTCAAGGGC GC    ACC
                                |||||||||||  ||    |||
                                CCAAGTTCCCG CG    TGG
                                      A  G___
GAM332  FLJ22031  3'  GGTTGAGCCCTTGACC      47588     T      _ GCAAT
                                GGT CAAGGGC C     GACC
                                ||| |||||||  |     ||||
                                CCA GTTCCCG G     TTGG
                                  _       A _____
GAM332  HNRPA0    3'  TCATTGTGTTTGACCGT     23306      T    GGC
                                ACGGT CAAG   CGCAATGA
                                |||||  ||||   ||||||||
                                TGCCA GTTT   GTGTTACT

                                   _    ____
GAM332  KLHL8    3'  GTCATTGCTGGATCTGAACC   63516       A GG  _
                                GGTTCA G  CC GCAATGAC
                                ||||||  |  ||  ||||||||
                                CCAAGT C  GG CGTTACTG
                                    _ TA  T
GAM332  LOC145919 3'  CACAGTGGACCCTTGAAC    78024          _    AA
                                GTTCAAGGG CCGC  TG
                                |||||||||  ||||  ||
                                CAAGTTCCC GGTG  AC
                                      A    AC
GAM332  LOC157273 3'  AGATCATTGTGTGCCTAAACC  87716      CAA   _      C
                                GGTT   GGGC CGCAATGA CT
                                ||||   |||| ||||||||  ||
                                CCAA   TCCG GTGTTACT GA
                                  A__    T       A
GAM332  LOC169505 3'  TCATTGTGCCATCCCAAACC   83623      CAA   C___
                                GGTT   GGG    CGCAATGA
                                ||||   |||    ||||||||
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                                CCAA   CCC    GTGTTACT
                                  A__   TACC
GAM332  LOC201139 3'  GTCATTGCGGCCACC      89509     TCAAG         C
                                GGT    GGCCGCAATGA C
                                |||    |||||||||||| |
                                CCA    CCGGCGTTACT G
                                 _____         A
GAM333  GYG2     3'  AGAAACACCTCGGCTGTGGTC  15360          AC    ACA
                                GATCACAGCT  GGTG   TTTCT
                                ||||||||||  ||||   |||||
                                CTGGTGTCGG  CCAC   AAAGA
                                      CT   ___
GAM333  HPRT1    3'  AGAAATGTCAGTTGCTG     5758       T  GG
                                CAGC AC  TGACATTTCT
                                |||| ||  ||||||||||
                                GTCG TG  ACTGTAAAGA
                                  T __
GAM333  PLAG1    3'  AGAAATGTATGTGTAGCTGTG  12145          GTG
                                CACAGCTACG   ACATTTCT
                                ||||||||||   ||||||||
                                GTGTCGATGT   TGTAAAGA
                                      GTA
GAM333  C20orf50  5'  AGAAATGTCACCACACAGGTAT 70611     C  AGCTAC
           C                     GAT AC      GGTGACATTTCT
                                ||| ||     ||||||||||||
                                CTA TG     CCACTGTAAAGA
                                  _ GACACA
GAM333  DKFZP564O0423 5'  AAATGATGCCAACTGTGATT   93334         CTAC    A
                                GATCACAG    GGTG CATTT
                                ||||||||    |||| |||||
                                TTAGTGTC    CCGT GTAAA
                                     AA__    A
GAM333  FLJ14735  3'  AAATGTCACCATGGCTTTCATC 52664     CAC     C
                                GAT   AGCTA GGTGACATTT
                                |||   ||||| ||||||||||
                                CTA   TCGGT CCACTGTAAA
                                  CTT    A
GAM333  LCE      3'  AGAAATGCCAGCTGCTGTAGA  44256    _    TAC   GA_
                                TC ACAGC   GGT   CATTTCT
                                || |||||   |||   |||||||
                                AG TGTCG   TCG   GTAAAGA
                                 A    ___   ACC
GAM333  SPARCL1   3'  AGAAATATATGCAGCTGTGAT  17431         A  GTGAC
                                ATCACAGCT CG     ATTTCT
                                |||||||||  ||    ||||||
                                TAGTGTCGA GT     TAAAGA
                                      C  ATA__
GAM333  STK33    5'  AGAAATACATTTCATACTGTGA 63568         CTAC_   AC
           TC                     GATCACAG    GGTG  ATTTCT
                                ||||||||    ||||  ||||||
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                                CTAGTGTC    TTAC  TAAAGA
                                    ATACT   A_
GAM333  TOM1L1   3'  AGAAATCGTCACACAGCTGTGA 19694        ACG    _
          T                  ATCACAGCT   GTGAC ATTTCT
                             |||||||||   ||||| ||||||
                             TAGTGTCGA   CACTG TAAAGA
                                 CA_     C
GAM333  LOC147660 3'  AGAAATGTCACAAGTGTGAT   79024      G  ACG
                             ATCACA CT   GTGACATTTCT
                             |||||| ||   ||||||||||
                             TAGTGT GA   CACTGTAAAGA
                                _ A__
GAM333  LOC148085 3'  AAATGTCAGGCCTGTGA     85252      _  ACGG
                             TCACAG CT    TGACATTT
                             |||||| ||    ||||||||
                             AGTGTC GG    ACTGTAAA
                                C _____
GAM333  LOC221756 3'  AGAAACAAAGGCAGCTGTGG   93756       ACGG_  ACA
                             TCACAGCT    TG   TTTCT
                             ||||||||    ||   |||||
                             GGTGTCGA    AC   AAAGA
                                 CGGAA  ___
GAM333  LOC256021 3'  AGCAGTGAACATAGCTGTGA   98276       CG  GA    T
                             TCACAGCTA  GT  CATT CT
                             |||||||||  ||  |||| ||
                             AGTGTCGAT  CA  GTGA GA
                                 A_  A_   C
GAM333  LOC56899  5'  GAAATGTGGAGCTAGGATC    39712     AC    ACGGTG
                             GATC  AGCT     ACATTTC
                             ||||  ||||     |||||||
                             CTAG  TCGA     TGTAAAG
                               GA   GG____
GAM334  ANKRD3    3'  ACCAAGCAGAGGTGACATGGTG 40561        T  AGGCGC  C
                             CACCATGT CG     GC TGGT
                             |||||||| ||     || ||||
                             GTGGTACA GT     CG ACCA
                                 _  GGAGA_  A
GAM334  PTPN7     3'  ACCAGGCACGCCGCCCCTGACA 55457     CGA___    C
                             TGTT     GGCG GCCTGGT
                             ||||     |||| |||||||
                             ACAG     CCGC CGGACCA
                               TCCCCG   A
GAM334  PTPN7     3'  ACCAGGCACGCCGCCCCTGACA 55465     CGA___    C
                             TGTT     GGCG GCCTGGT
                             ||||     |||| |||||||
                             ACAG     CCGC CGGACCA
                               TCCCCG   A
GAM334  PTPN7     3'  ACCAGGCACGCCGCCCCTGACA 12591     CGA___    C
                             TGTT     GGCG GCCTGGT
                             ||||     |||| |||||||
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                                ACAG     CCGC CGGACCA
                                  TCCCCG   A
GAM334  C21orf108 3'  ACCAGAGCCTCGAGCA      90105          GCGC
                                TGTTCGAGGC   CTGGT
                                ||||||||||  |||||
                                ACGAGCTCCG   GACCA
                                     A___
GAM334  DKFZP434B0335 3'  ACCAGACGGGCCAACATGGTG  94058         CGA  G  C
                                CACCATGTT  GGC CG CTGGT
                                |||||||||  ||| || |||||
                                GTGGTACAA  CCG GC GACCA
                                     ___  G  A
GAM334  FLJ10350  5'  ACCCCCCCCGCCTCGAACTTGGT 97245     T        CGCCT
                                ACCA GTTCGAGGCG    GGT
                                |||| ||||||||||    |||
                                TGGT CAAGCTCCGC    CCA
                                  T        CCCC_
GAM334  FLJ11267  3'  ACCTGTTACCTCGGACATG   39494          CGC  CT
                                CATGTTCGAGG  GC  GGT
                                ||||||||||  ||  |||
                                GTACAGGCTCC  TG  CCA
                                     AT_  T_
GAM334  FLJ20359  3'  ACCAGCCTGCCCAACATGGTG  35509         CGA   C  C
                                CACCATGTT  GGCG GC TGGT
                                |||||||||  |||| || ||||
                                GTGGTACAA  CCGT CG ACCA
                                     C__   C  _
GAM334  HSA250303 3'  ACCAGGCTGGCCAACATGGT  38016        CGA  GC
                                ACCATGTT  GGC  GCCTGGT
                                ||||||||  |||  |||||||
                                TGGTACAA  CCG  CGGACCA
                                     ___  GT
GAM334  KIAA0565  3'  CCAACCTCCAACATGGTG    67436         C   CGCGCC
                                CACCATGTT GAGG     TGG
                                ||||||||| ||||     |||
                                GTGGTACAA CTCC     ACC
                                     C   A_____
GAM334  KIAA1244  3'  ACCAGGCTGGACAACATGGTG  72435         CGAGG  C
                                CACCATGTT    CG GCCTGGT
                                |||||||||    || |||||||
                                GTGGTACAA    GT CGGACCA
                                     CAG__  _
GAM334  KIAA1872  3'  ACCAGGCTGGCCAACATGGTG  63585         CGA  GC
                                CACCATGTT  GGC  GCCTGGT
                                |||||||||  |||  |||||||
                                GTGGTACAA  CCG  CGGACCA
                                     ___  GT
GAM334  KIAA1950  3'  ACCAGACTGGGCAACATGGTG  94174         CGAG  G  C_
                                CACCATGTT   GC CG  CTGGT
                                |||||||||   || ||  |||||
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                                GTGGTACAA   CG GT  GACCA
                                     ____  G  CA
GAM334  PRO0899  3'  CCAGGTGACAAACATGGTG   38306       CGAGGCG
                                CACCATGTT     CGCCTGG
                                |||||||||     |||||||
                                GTGGTACAA     GTGGACC
                                     ACA____
GAM334  Rab11-FIP3 3'  ACCCTCACCTCGGACATGGTG  28781          CGCGCCT
                                CACCATGTTCGAGG     GGT
                                ||||||||||||||     |||
                                GTGGTACAGGCTCC     CCA
                                       ACTC___
GAM334  VCY2IP1  3'  ACCAGGCGCTGGGCATCACGGT 36922     ___     AGGC
          G                      CACC  ATGTTCG   GCGCCTGGT
                                ||||  |||||||  |||||||||
                                GTGG  TACGGGT   CGCGGACCA
                                  CAC     ____
GAM334  LOC256207 3'  CCAACCTCCAACATGGTG   96875       C   CGCGCC
                                CACCATGTT GAGG    TGG
                                ||||||||| ||||    |||
                                GTGGTACAA CTCC    ACC
                                     C   A_____
GAM334  LOC92228  3'  ACCAGGTTGGCCAACATGGTG  69065       CGA  GC
                                CACCATGTT  GGC  GCCTGGT
                                |||||||||  |||  |||||||
                                GTGGTACAA  CCG  TGGACCA
                                     ___  GT
GAM334  LOC92568  3'  ACCAGGCGAGGCAACATGG   70321      CGAG  G_
                                CCATGTT   GC  CGCCTGGT
                                |||||||   ||  ||||||||
                                GGTACAA   CG  GCGGACCA
                                     ____  GA
GAM335  B4GALT1  5'  GGCGGGTCGCCTCCCCTCCTG  9471       AA  T   GT  _
                                CAGGAG  GA GGCG  CT CC
                                ||||||  || ||||  || ||
                                GTCCTC  CT CCGC  GG GG
                                   CC  _   TG  C
GAM335  BCRP2    3'  TGTACTTTTTGCCATCTCACCC 63072     AGA      TCTCC
          TG                     CAGG  AGATGGCGG    ACA
                                ||||  |||||||||    |||
                                GTCC  TCTACCGTT    TGT
                                  CAC       TTTCA
GAM335  CFL1     3'  TGTGGAGATGACCCCTCCCTG  19749     A  AGAT  CG
                                CAGG GA   GG  GTCTCCACA
                                |||| ||   ||  |||||||||
                                GTCC CT   CC  TAGAGGTGT
                                  _  CC__  AG
GAM335  EDAR     5'  AGACCCATCTTCTGCTG     42520     G       CG
                                CAG AGAAGATGG  GTCT
                                ||| |||||||||  ||||
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                                GTC TCTTCTACC  CAGA
                                  G       __
GAM335  EP300    5'  GCCCCGGCCGTCTTCTCC    9285          ___
                                GGAGAAGATGGC  GGT
                                ||||||||||||  |||
                                CCTCTTCTGCCG  CCG
                                      GCC
GAM335  GCN1L1   3'  GTGGGTTCCTCTTCTCCTG   70313         TGGC  TC
                                CAGGAGAAGA   GG  TCCAC
                                ||||||||||   ||  |||||
                                GTCCTCTTCT   CC  GGGTG
                                     _____  TT
GAM335  GLP1R    3'  GGACACATTTTCTCCT      10797          GCG
                                AGGAGAAGATG   GTCT
                                ||||||||||   ||||
                                TCCTCTTTTAC   CAGG
                                      A__
GAM335  HTRA3    3'  TGGAGGTCCCCTCCTCTCCT   90586       A  T  C GT
                                AGGAGA GA GG G  CTCCA
                                |||||| || || |  |||||
                                TCCTCT CT CC C  GAGGT
                                   C  C  _ TG
GAM335  KCNC4    5'  GGGGGCCGCCACCGCCTCCTG  18334       AAGA
                                CAGGAG   TGGCGGTCTCC
                                ||||||   ||||||||||||
                                GTCCTC   ACCGCCGGGGG
                                   CGCC
GAM335  MAD1L1   3'  TGTGAAATAAAATCTTCTCC   88873        GGCG  CTC
                                GGAGAAGAT   GT   CACA
                                |||||||||   ||   ||||
                                CCTCTTCTA   TA   GTGT
                                     AAA_  AA_
GAM335  MRPL49   3'  TGGAAACCCTCACTCCTG    70175       AAGA  C   C
                                CAGGAG   TGG GGT TCCA
                                ||||||   ||| ||| ||||
                                GTCCTC   ACT CCA AGGT
                                   _____  C   A
GAM335  NLGN1    5'  GTAGAGACCGTCTCCT      30700       AAGATG       C
                                AGGAG     GCGGTCTC AC
                                |||||     |||||||| ||
                                TCCTC     TGCCAGAG TG
                                   _______       A
GAM335  OLIG2    5'  GACGACTATCTTCCCCTG    20547      A       CG
                                CAGG GAAGATGG  GTC
                                |||| ||||||||  |||
                                GTCC CTTCTATC  CAG
                                  C       AG
GAM335  PAFAH1B1 5'  TGTGAAAGAATCATTTTCCCCT 6481       A       CGG   C_
          G                      CAGG GAAGATGG   TCT  CACA
                                |||| ||||||||   |||  ||||
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                                GTCC CTTTTACT   AGA  GTGT
                                  C       A__   AA
GAM335  PYGB     3'  TGTGGAGGAGGCCATACTCCCC 12693     A  AG    GG
              T                   AGG GA  ATGGC  TCTCCACA
                                  ||| ||  |||||  ||||||||
                                  TCC CT  TACCG  GGAGGTGT
                                    C  CA    GA
GAM335  SLC1A3   3'  TGTGGGGAGCCCATCCTCTC   16065     A    CGG
                                  GAGA GATGG   TCTCCACA
                                  |||| |||||   ||||||||
                                  CTCT CTACC   AGGGGTGT
                                    C    CG_
GAM335  SLC24A1  5'  TGGAGAAATCTTCTCT      17570         GGCGG
                                  GGAGAAGAT    TCTCCA
                                  |||||||||    ||||||
                                  TCTCTTCTA    AGAGGT
                                       A____
GAM335  SMARCD2  3'  GGCCGCCATCATCTCCTG    13263        A
                                  CAGGAGA GATGGCGGTC
                                  ||||||| ||||||||||
                                  GTCCTCT CTACCGCCGG
                                      A
GAM335  STK11    3'  GTGGAGACCAGGCTCCTG    6601        AAGATGGC
                                  CAGGAG       GGTCTCCAC
                                  ||||||       |||||||||
                                  GTCCTC       CCAGAGGTG
                                     GGA_____
GAM335  SUV39H2  5'  TGCGGACGCCTATCCTCC    45460     AA  _   GTC  A
                                  GGAG  GAT GGCG   TCC CA
                                  ||||  ||| ||||   ||| ||
                                  CCTC  CTA CCGC   AGG GT
                                    __   T    ___   C
GAM335  TAL1     3'  GTGAGCCCCATCTTCACC    13531    A      C  T   C
                                  GG GAAGATGG GG CTC AC
                                  || |||||||| || ||| ||
                                  CC CTTCTACC CC GAG TG
                                   A       _  _   _
GAM335  UBE2H    3'  TGCAGATTTCATCTTCACCT   13955    A      C    C
                                  AGG GAAGATGG GGTCT CA
                                  ||| |||||||| ||||| ||
                                  TCC CTTCTACT TTAGA GT
                                    A       _    C
GAM335  ACYP2    5'  TGTGGAGACAGCATCCTCCCC  57407    A  A   G  G
                                  GG GA GATG C GTCTCCACA
                                  || || |||| | |||||||||
                                  CC CT CTAC G CAGAGGTGT
                                   C  C    _ A
GAM335  AP1GBP1  5'  TGTGATTTCGCCATCTTCTCC  55449            TCTC
                                  GGAGAAGATGGCGG    CACA
                                  ||||||||||||||    ||||
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                                CCTCTTCTACCGCT   GTGT
                                       TTA_
GAM335  B3GNT7   3'  GAGACCACCACTTCTCCTG   71679        A  C
                                CAGGAGAAG TGG GGTCTC
                                ||||||||| ||| ||||||
                                GTCCTCTTC ACC CCAGAG
                                     _  A
GAM335  CGI-127  3'  GAGAAATCCATCTTTTCC    32674         CGG
                                GGAGAAGATGG  TCTC
                                ||||||||||  ||||
                                CCTTTTCTACC  AGAG
                                       TAA
GAM335  DKFZP434B205 3'  GGCCTCGCACCTTCTTCTCCTG 75845         TG__ __
                                CAGGAGAAGA   GC  GGTC
                                ||||||||||   ||  ||||
                                GTCCTCTTCT   CG  CCGG
                                      TCCA  CT
GAM335  DKFZP434H0820 3'  TGGGTGCTGCCATCCTTCCTG  64587      AA       CT
                                CAGGAG  GATGGCGGT  CCA
                                ||||||  |||||||||  |||
                                GTCCTT  CTACCGTCG  GGT
                                   C_       TG
GAM335  DKFZP564G202 3'  TGTGGAGACTTTTCTTCCCC   65887    A    TGGC
                                GG GAAGA   GGTCTCCACA
                                || |||||   ||||||||||
                                CC CTTCT   TCAGAGGTGT
                                 C    TT__
GAM335  DKFZP564O043 5'  GGGAGACCGTCCGCCTG    94093     AGAAGAT       A
                                CAGG      GGCGGTCTCC C
                                ||||      |||||||||| |
                                GTCC      CTGCCAGAGG G
                                  GC_____        C
GAM335  DKFZP566H073 5'  GAGCTCCGCCACCCTTCCC   32031    A   A_    T_
                                GG GAAG  TGGCGG  CTC
                                || ||||  ||||||  |||
                                CC CTTC  ACCGCC  GAG
                                 _   CC     TC
GAM335  E46L     3'  TGGATTTTTCATCTTCTACC   26014    _       CG TC
                                GG AGAAGATGG  G  TCCA
                                || |||||||||  |  ||||
                                CC TCTTCTACT  T  AGGT
                                 A        TT T_
GAM335  FIGN     3'  AGAACCTCTCCATCTCCTCC   97362     A     C__  _
                                GGAG AGATGG   GGT CT
                                |||| ||||||   ||| ||
                                CCTC TCTACC   CCA GA
                                  C     TCT   A
GAM335  FLJ12517  3'  TGTGGAGACTGGCACTCTCC   43721      A A  G
                                GGAGA G TG CGGTCTCCACA
                                ||||| | || ||||||||||
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                                CCTCT C AC GTCAGAGGTGT
                                  _ _  G
GAM335  FLJ14437  5'  GTGAAGAATTTCCCTCTTCTCC 51798          T  CGG_  C
          TG                    CAGGAGAAGA GG    TCT CAC
                                |||||||||| ||    ||| |||
                                GTCCTCTTCT CC    AGA GTG
                                     C  TTTA   A
GAM335  FLJ14936  3'  GTGAAGACCAGCTGCCCTG   52773      AGAAGAT  _    C
                                CAGG      GGC GGTCT CAC
                                ||||      ||| ||||| |||
                                GTCC      TCG CCAGA GTG
                                  CG_____  A    A
GAM335  GENX-3414 3'  TGTAGGACCATCTCTCTCC   15458      _     CGGTC  _
                                GGAGA AGATGG    TCC ACA
                                ||||| ||||||    ||| |||
                                CCTCT TCTACC    AGG TGT
                                   C     _____  A
GAM335  HGC6.1.1  3'  GTGGAAAGTCCTCTTCTCC   27615        T   GGTC
                                GGAGAAGA GGC   TCCAC
                                |||||||| |||   |||||
                                CCTCTTCT CTG   AGGTG
                                     C  AA__
GAM335  HGC6.1.1  3'  TGGGGACCACCCTCCT     27616       AAGAT  C
                                AGGAG    GG GGTCTCCA
                                |||||    || ||||||||
                                TCCTC    CC CCAGGGGT
                                  _____  A
GAM335  KIAA0293  3'  TGTGGCCACCATCTTCCCCT  61240     A       C  TCT
                                AGG GAAGATGG GG   CCACA
                                ||| |||||||| ||   |||||
                                TCC CTTCTACC CC   GGTGT
                                  C       A  ___
GAM335  KIAA0322  3'  TGAAGAACTGCCTTCTTCT   94333       T     _  C
                                AGAAGA GGCGGT CT CA
                                |||||| |||||| || ||
                                TCTTCT CCGTCA GA GT
                                    T     A  A
GAM335  KIAA0545  3'  GTGATGCCATCTTCTCC     63847           GTCTC
                                GGAGAAGATGGCG    CAC
                                ||||||||||||    |||
                                CCTCTTCTACCGT    GTG
                                       A____
GAM335  KIAA1045  3'  GTGGCAGCATCCTCTCCTG   71609        A    G GGTCT
                                CAGGAGA GATG C    CCAC
                                ||||||| |||| |    ||||
                                GTCCTCT CTAC G    GGTG
                                    C   _ AC___
GAM335  KIAA1196  3'  TGTGGAGACCCGGACTCC    62156     AAGA   CG
                                GGAG   TGG  GTCTCCACA
                                ||||   |||  |||||||||
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                                CCTC   GCC  CAGAGGTGT
                                  AG__  __
GAM335  KIAA1679  3'  TGCAGAAAACCTTTCTCCT   70717       AT  CGG   C
                                AGGAGAAG  GG   TCT CA
                                ||||||||  ||   ||| ||
                                TCCTCTTT  CC   AGA GT
                                    __  AAA   C
GAM335  KIAA1853  3'  TGTGGAGACAGTTCTTCTCCT  69928        TG  G
                                AGGAGAAGA  GC GTCTCCACA
                                |||||||||  || |||||||||
                                TCCTCTTCT  TG CAGAGGTGT
                                    __  A
GAM335  KLF12     3'  TGTGAATTATTGCATCTTCTTC 24365         G   CTC_
                                GGAGAAGATG CGGT   CACA
                                |||||||||| ||||   ||||
                                CTTCTTCTAC GTTA   GTGT
                                    _   TTAA
GAM335  L3MBTL    3'  GAGAGCCATCTTCCCC     70085    A      GG
                                GG GAAGATGGC  TCTC
                                || |||||||||  ||||
                                CC CTTCTACCG  AGAG
                                 C       __
GAM335  LASP1     3'  TGAAGAGCTGTCTTCCCCTG   21579     A       GG   C
                                CAGG GAAGATGGC  TCT CA
                                |||| |||||||||  ||| ||
                                GTCC CTTCTGTCG  AGA GT
                                  C       __  A
GAM335  MGC14376  5'  TGTGCCTCTGCCATCTTCACC  52918    A        TCTC
                                GG GAAGATGGCGG   CACA
                                || ||||||||||   ||||
                                CC CTTCTACCGTC   GTGT
                                 A        TCC_
GAM335  MGC2605   5'  TGTGGAGAGCGGGCCCCGCCCT 51186     AGAAGAT  __ G
          G                     CAGG      GGC  G TCTCCACA
                                ||||      |||  | ||||||||
                                GTCC      CCG  C AGAGGTGT
                                  CGCC___   GG G
GAM335  MGC33901  3'  TGGAGACCTTCTTCTACC    59362   _     TGGC
                                GG AGAAGA   GGTCTCCA
                                || ||||||   ||||||||
                                CC TCTTCT   CCAGAGGT
                                 A     T___
GAM335  NY-REN-60 3'  ACATGCCATCTCTTCCTG    67707      GA      _
                                CAGGA  AGATGGCG GT
                                |||||  |||||||| ||
                                GTCCT  TCTACCGT CA
                                   TC       A
GAM335  PP1665    3'  TGTGGAGACACGTCCTCCTCCC 48642    A  A  T   _
          C                     GG GA GA GGCG GTCTCCACA
                                || || || |||| |||||||||
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                                CC CT CT CTGC CAGAGGTGT
                                 C  C  C    A
GAM335  PRRG1    3'  TGGAGAATTTTCCCCT      8154      A     GGCGG
                                AGG GAAGAT     TCTCCA
                                ||| ||||||     ||||||
                                TCC CTTTTA     AGAGGT
                                  C     _____
GAM335  SDCBP    3'  TGTGAAAACCAGTCACCTTTCT 20059         A_   _   CTC
             CCT                   AGGAGAAG  TGGC GGT   CACA
                                ||||||||  |||| |||   ||||
                                TCCTCTTT  ACTG CCA   GTGT
                                    CC    A   AAA
GAM335  SP140    3'  AGGCTCTTACCTCTTCTCCTG  24325          T  C___
                                CAGGAGAAGA GG    GGTCT
                                |||||||||| ||    |||||
                                GTCCTCTTCT CC    TCGGA
                                      _  ATTC
GAM335  SV2B     3'  GAGATCTACTTTTCTCCT     29950         TGGC
                                AGGAGAAGA    GGTCTC
                                |||||||||    ||||||
                                TCCTCTTTT    CTAGAG
                                     CAT_
GAM335  TUSP     3'  TGTAGAGAAATATTTCTTTTCC 40036          TGGCGG    C
             TG                   CAGGAGAAGA     TCTC ACA
                                ||||||||||     |||| |||
                                GTCCTTTTCT     AGAG TGT
                                      TTATAA    A
GAM335  ZFP91    3'  TGGGGACCACCTCCCCCT    54880     AGAA  T  C
                                AGG    GA GG GGTCTCCA
                                |||    || || ||||||||
                                TCC    CT CC CCAGGGGT
                                  CC__  _  A
GAM335  ZNF263   3'  TGTGGAGAATGAGATTCCCC   20429    A   GATGG  G
                                GG GAA     CG TCTCCACA
                                || |||     || ||||||||
                                CC CTT     GT AGAGGTGT
                                 C   AGA__  A
GAM335  LOC123591 3'  GGAGACCACCATCTGAGCCT   76131     AGA     C
                                AGG   AGATGG GGTCTCC
                                |||   |||||| |||||||
                                TCC   TCTACC CCAGAGG
                                  GAG     A
GAM335  LOC143524 3'  GAGACCACCACTTCTCCTG    77095         A   C
                                CAGGAGAAG TGG GGTCTC
                                ||||||||| ||| ||||||
                                GTCCTCTTC ACC CCAGAG
                                      _  A
GAM335  LOC144559 3'  TGTGAGGCCACCACTTCTCCTG 77386          A   C     C
                                CAGGAGAAG TGG GGTCTC ACA
                                ||||||||| ||| |||||| |||
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                                GTCCTCTTC ACC CCGGAG TGT
                                      _  A    _
GAM335  LOC145968 3'  TGAAGACGGCTTCTTCTCC   84578       T  G   C
                                GGAGAAGA GGC GTCT CA
                                |||||||| ||| |||| ||
                                CCTCTTCT TCG CAGA GT
                                     _  G   A
GAM335  LOC146268 3'  GAAACCCCTCTTCTCC     78340       T  C  C
                                GGAGAAGA GG GGT TC
                                |||||||| || ||| ||
                                CCTCTTCT CC CCA AG
                                     _ _  A
GAM335  LOC147976 3'  TGCGAAGCCTCATCTTCTCT  79292         C  TC  _
                                GGAGAAGATGG GG  TC CA
                                |||||||||||| ||  || ||
                                TCTCTTCTACT CC  AG GT
                                      _ GA  C
GAM335  LOC150935 3'  GAAAGTCACATCCTTCTCCTG 80827        A___   GG
                                CAGGAGAAG   TGGC  TC
                                |||||||||   ||||  ||
                                GTCCTCTTC   ACTG  AG
                                     CTAC   AA
GAM335  LOC158777 3'  TGTGAAAACCAGTCACCTTTCT 82873       A_   _  CTC
          CCT                   AGGAGAAG  TGGC GGT   CACA
                                |||||||  |||| |||   ||||
                                TCCTCTTT  ACTG CCA   GTGT
                                     CC   A   AAA
GAM335  LOC199678 3'  TGGGTTCCGCCACCTTCTCCTG 91373        A     TC
                                CAGGAGAAG TGGCGG  TCCA
                                |||||||| ||||||  ||||
                                GTCCTCTTC ACCGCC  GGGT
                                     C     TT
GAM335  LOC219918 3'  GAGACCACCACTTCTCCTG   93172        A  C
                                CAGGAGAAG TGG GGTCTC
                                |||||||| ||| ||||||
                                GTCCTCTTC ACC CCAGAG
                                     _  A
GAM335  LOC220071 3'  GAGACCACCACTTCTCCTG   95081        A  C
                                CAGGAGAAG TGG GGTCTC
                                |||||||| ||| ||||||
                                GTCCTCTTC ACC CCAGAG
                                     _  A
GAM335  LOC221927 5'  TGCGGTCGACACCATCTTCTCC 94222         CG  T_ A
                                GGAGAAGATGG  GTC  CC CA
                                |||||||||||  |||  || ||
                                CCTCTTCTACC  CAG  GG GT
                                      A_  CT  C
GAM335  LOC255146 3'  TGTGAAATAAAATCTTCTCC  97347        GGCG  CTC
                                GGAGAAGAT   GT   CACA
                                |||||||||   ||  ||||
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                                CCTCTTCTA   TA  GTGT
                                     AAA_  AA_
GAM335  LOC255338 5'  GACTCATGCCATCTTCCCCT  97631    A      ___
                                AGG GAAGATGGC  GGTC
                                ||| |||||||||  ||||
                                TCC CTTCTACCG  TCAG
                                  C       TAC
GAM335  LOC255360 3'  TGTGGACACCTCCTCCTCCTG  98765      AA  T  C  C
                                CAGGAG  GA GG GGT TCCACA
                                ||||||  || || ||| ||||||
                                GTCCTC  CT CC CCA AGGTGT
                                   __ _  T  C
GAM335  LOC255515 3'  GAGACCACCACTTCTCCTG   97812        A  C
                                CAGGAGAAG TGG GGTCTC
                                ||||||||| ||| ||||||
                                GTCCTCTTC ACC CCAGAG
                                     _  A
GAM335  LOC257289 5'  TGGAGACCGGCTCCTG     99356      AAGATGG
                                CAGGAG     CGGTCTCCA
                                ||||||     |||||||||
                                GTCCTC     GCCAGAGGT
                                   G_____
GAM335  LOC51279  3'  TGCAGAGACTGTGCTCTTCCC  33766   A    TG      CA
                                GG GAAGA  GCGGTCTC  CA
                                || |||||  ||||||||  ||
                                CC CTTCT  TGTCAGAG  GT
                                 _    CG       AC
GAM335  LOC81558  3'  TGTAGAGACTCTATTTTCTCC  48680        C    C
                                GGAGAAGATGG GGTCTC ACA
                                |||||||||||| |||||| |||
                                CCTCTTTTATC TCAGAG TGT
                                      _     A
GAM335  LOC90520  5'  GTGGGGTTGCCTCCCCCTCCTG 63839      AA_  T    T
                                CAGGAG   GA GGCGG CTCCAC
                                ||||||   || ||||| ||||||
                                GTCCTC   CT CCGTT GGGGTG
                                   CCC  _    _
GAM335  LOC90906  3'  GAGGTCGCCACTTCTCCTG   64952        A    GT
                                CAGGAGAAG TGGCG  CTC
                                |||||||| |||||  |||
                                GTCCTCTTC ACCGC  GAG
                                     _    TG
GAM335  LOC91263  3'  TGGAGACCAGCCCCCATCCTG  66003     GAAGAT  _
                                CAGGA     GGC GGTCTCCA
                                |||||     ||| ||||||||
                                GTCCT     CCG CCAGAGGT
                                  ACCC__   A
GAM335  LOC92335  3'  GGACCGCCACCTCTTCCC    69545    A    __
                                GG GAAGA  TGGCGGTCT
                                || |||||  |||||||||
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                                CC CTTCT  ACCGCCAGG
                                 _    CC
GAM336  BLAME    3'  TTGGACAAAGGATCAGCACAG  39660        CC    CACA
                                CTGTGCTG  CCTTT   TCAA
                                ||||||||  |||||   ||||
                                GACACGAC  GGAAA   GGTT
                                     TA    CA__
GAM336  CNR1     3'  TGATGCCTCCCTGGCAGCACAG 10231         CCTTTCA
                                CTGTGCTGCC      CATCA
                                ||||||||||      |||||
                                GACACGACGG      GTAGT
                                      TCCCTCC
GAM336  FMOD     3'  TGATGTGGGAGGAGACAGCCA  10675    T   CC_  TT
                                TG GCTG   CCT  CACATCA
                                || ||||   |||  |||||||
                                AC CGAC   GGA  GTGTAGT
                                 _   AGA   GG
GAM336  ITPR2    3'  TTTGATATGTCTGCATGCAGCA 11083        CCCTTT_ C
            CAG                    CTGTGCTGC      CA ATCAAA
                                |||||||||      || ||||||
                                GACACGACG      GT TAGTTT
                                      TACGTCT  A
GAM336  TBXA2R   5'  ATGTGAAGGTCAACACAG    8344       C  CCC
                                CTGTG TG   CTTTCACAT
                                |||||  ||   |||||||||
                                GACAC AC   GGAAGTGTA
                                   A  T__
GAM336  DKFZp434A171 3'  TGCTGTGAAAGGAGCAGTACA  51026        C       T
                                TGTGCTGC CCTTTCACA CA
                                |||||||| ||||||||| ||
                                ACATGACG GGAAAGTGT GT
                                     A        C
GAM336  ESDN     3'  TTGATCTTAGGAAACAGCACAG 56066        CC_   TTCAC
                                CTGTGCTG   CCT    ATCAA
                                |||||||   |||    |||||
                                GACACGAC   GGA    TAGTT
                                     AAA   TTC__
GAM336  FLJ11186 3'  TGATAGTGAGAGGACAACAG   37730     GC  CC      _
                                CTGT  TG  CCTTTCAC ATCA
                                ||||  ||  |||||||| ||||
                                GACA  AC  GGAGAGTG TAGT
                                  __ A_       A
GAM336  FLJ20986 5'  GTAAAGGAGGCAGCACAG    44840          _    C
                                CTGTGCTGCC CCTTT AC
                                |||||||||| ||||| ||
                                GACACGACGG GGAAA TG
                                      A    _
GAM336  KIAA0125 3'  TGATGCTGAAAACAGCACAG   29579        CCCC    _
                                CTGTGCTG    TTTCA CATCA
                                ||||||||    ||||| |||||
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                                GACACGAC   AAAGT GTAGT
                                    A___    C
GAM336  KIAA0186 3' TTTGATGTGAAATTTGGGAACA 41131     GCTG  C__
           G                     CTGT   CCC  TTTCACATCAAA
                                 ||||   |||  ||||||||||||
                                 GACA   GGG  AAAGTGTAGTTT
                                   A___  TTT
GAM336  KIAA0923 3' GTGTGAAAGAAACAGCAGAG  26708   G   CCC
                                 CT TGCTG  CTTTCACAT
                                 || |||||  |||||||||
                                 GA ACGAC  GAAAGTGTG
                                  G   AAA
GAM336  KIAA1719 3' TTTGAGGGTGAGGGACAGCACA 68743       C  TT   A_
           G                     CTGTGCTG CCC  TCAC  TCAAA
                                 |||||||| |||  ||||  |||||
                                 GACACGAC GGG  AGTG  AGTTT
                                    A  __   GG
GAM336  MGC14425 3' TTTGATGTTCAGAGCACACAG  52952     C  CC  TTC
                                 CTGTG TGC  CT   ACATCAAA
                                 ||||| |||  ||   ||||||||
                                 GACAC ACG  GA   TGTAGTTT
                                   _  A_  CT_
GAM336  MGC20235 3' TTTGACAATGTGGAGCAGCACA 59565       CCCT    ___
                                 TGTGCTGC   TTCACA  TCAAA
                                 ||||||||   ||||||  |||||
                                 ACACGACG   AGGTGT  AGTTT
                                    _____     AAC
GAM336  MGC22014 3' TTGATGTGAAAGAAAGGGCG  65122     ___
                                 TGCCC  CTTTCACATCAA
                                 |||||  ||||||||||||
                                 GCGGG  GAAAGTGTAGTT
                                   AAA
GAM336  MGC26651 3' TTTGATGTGAAAGATGTTATA  58953    CT  CC
                                 TGTG  GC  CTTTCACATCAAA
                                 ||||  ||  ||||||||||||
                                 ATAT  TG  GAAAGTGTAGTTT
                                   __  TA
GAM336  PIK3C2G  3' TTTGTTGTCAAAGACAGCACAG 17095       CCC   C   T
                                 CTGTGCTG  CTTT ACA CAAA
                                 ||||||||  |||| ||| ||||
                                 GACACGAC  GAAA TGT GTTT
                                    A__   C   T
GAM336  PP1628   5' TGACTTCTGAATACAGCACAG  48082       CCCCT   CA__
                                 CTGTGCTG   TTCA   TCA
                                 ||||||||   ||||   |||
                                 GACACGAC   AAGT   AGT
                                    AT___   CTTC
GAM336  SCAMP5   3' TGATGTAGGAGGGGCACACAG  58065     C      TC
                                 CTGTG TGCCCCTT  ACATCA
                                 ||||| ||||||||  ||||||
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                                GACAC ACGGGGAG  TGTAGT
                                  _      GA
GAM336  LOC144184 5'  GTGAGAAGAGGCAGCACGG   77196        C  _
                                CTGTGCTGCC CT TTCAC
                                |||||||||| || |||||
                                GGCACGACGG GA GAGTG
                                     A  A
GAM336  LOC157653 5'  TGTAACAAGGGACACACAG   82448     C  C    TC_
                                CTGTG TG CCCTT   ACA
                                ||||| || |||||   |||
                                GACAC AC GGGAA   TGT
                                  _ A    CAA
GAM336  LOC201910 3'  TTGAAAGCAAGGGGCAACAG  90553     GC      TCACA
                                CTGT  TGCCCCTT    TCAA
                                ||||  ||||||||    ||||
                                GACA  ACGGGGAA    AGTT
                                  __      CGAA_
GAM336  LOC221576 3'  TTGATGTGATAACGCACAG   95325     TGCCCCTT
                                CTGTGC      TCACATCAA
                                ||||||      |||||||||
                                GACACG      AGTGTAGTT
                                   CAAT____
GAM336  LOC221882 5'  TGATACTAAGAGCAGCACGG  94101       CC   TCAC
                                CTGTGCTGC  CTT   ATCA
                                |||||||||  |||   ||||
                                GGCACGACG  GAA   TAGT
                                     A_   TCA_
GAM336  LOC222234 5'  TTGACTTGAGGCGGCACAG   95903       CCTT   CA
                                CTGTGCTGCC   TCA  TCAA
                                ||||||||||   |||  ||||
                                GACACGGCGG   AGT  AGTT
                                     ____   TC
GAM336  LOC254266 5'  TTGACCTTGAGGACAGCATAG 99204       CC   TCACA
                                CTGTGCTG  CCTT    TCAA
                                ||||||||  ||||    ||||
                                GATACGAC  GGAG    AGTT
                                    A_   TTCC_
GAM336  LOC256158 5'  ATGTGGCAGGTAGCACAG    99479       CCTT
                                CTGTGCTGCC   TCACAT
                                ||||||||||   ||||||
                                GACACGATGG   GGTGTA
                                     AC__
GAM336  LOC257515 3'  TTGATGTGATAACGCACAG   99625     TGCCCCTT
                                CTGTGC      TCACATCAA
                                ||||||      |||||||||
                                GACACG      AGTGTAGTT
                                   CAAT____
GAM336  LOC257572 3'  TTGATGTGATAACGCACAG   99745     TGCCCCTT
                                CTGTGC      TCACATCAA
                                ||||||      |||||||||
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                                GACACG      AGTGTAGTT
                                   CAAT____
GAM336  LOC56965  3'  ATGGGAAAAGGACAGCACAG  39923       C  C   A
                                CTGTGCTG CC TTTC CAT
                                |||||||| || |||| |||
                                GACACGAC GG AAAG GTA
                                     A  A   G
GAM337  DSCR3     3'  TGGAAATGCATGACTTCC    21326       _  C  A
                                GGAAGTCA GCA TT CA
                                |||||||| ||| || ||
                                CCTTCAGT CGT AA GT
                                     A  A  G
GAM337  FIGF      3'  TCGTATGATCAGTACTGACTTT 16772        C  TACAT
             CT                   AGGAAGTCAG ACT    TACGA
                                ||||||||||| |||    |||||
                                TCTTTCAGTC TGA    ATGCT
                                      A  CTAGT
GAM337  IL7       5'  CGTAGTGTGTGCCGCCCCC   7948    AA  CA   TT
                                GG  GT  GCAC  ACATTACG
                                ||  ||  ||||  ||||||||
                                CC  CG  CGTG  TGTGATGC
                                 CC  C_   __
GAM337  NF1       3'  TGTAATGCTGCACTTCCT    6049        _    C
                                AGGAAGT CAGCA TTACA
                                ||||||| ||||| |||||
                                TCCTTCA GTCGT AATGT
                                    C    _
GAM337  PSCD4     5'  CGTGGGCCAGGACTGACTTCCT 26323         CA  TACA
                                AGGAAGTCAG  CT   TTACG
                                ||||||||||  ||   |||||
                                TCCTTCAGTC  GA   GGTGC
                                      AG  CCG_
GAM337  FLJ20079  3'  TGTAAGTGCCCACTTCCT    34982       CA
                                AGGAAGT  GCACTTACA
                                |||||||  |||||||||
                                TCCTTCA  CGTGAATGT
                                    CC
GAM337  IGSF9     3'  TGTATGTGCTGACCCCCT    40813    AA      T
                                AGG  GTCAGCAC TACA
                                |||  |||||||| ||||
                                TCC  CAGTCGTG ATGT
                                  CC       T
GAM337  KIAA0515  5'  ATGCCAGTGCTGACCTTCC   64542      _      TA
                                GGAAG TCAGCACT  CAT
                                ||||| ||||||||  |||
                                CCTTC AGTCGTGA  GTA
                                   C       CC
GAM337  LOC145828 3'  TAATGTAAATGCCTGGCCC   84540    AA    _  C
                                GG  GTCAG CA TTACATTA
                                ||  ||||| || ||||||||
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                                CC  CGGTC GT AATGTAAT
                                 __    C  A
GAM337  LOC253223 3'  TCGTGATAATGCAGACTTCCT  96127       A   CTTAC
                                AGGAAGTC GCA    ATTACGA
                                |||||||| |||    |||||||
                                TCCTTCAG CGT    TAGTGCT
                                    A   AA___
GAM337  LOC257513 3'  TCGTGATAATGCAGACTTCCT  99528       A   CTTAC
                                AGGAAGTC GCA    ATTACGA
                                |||||||| |||    |||||||
                                TCCTTCAG CGT    TAGTGCT
                                    A   AA___
GAM337  LOC257567 3'  TCGTGATAATGCAGACTTCCT  99670       A   CTTAC
                                AGGAAGTC GCA    ATTACGA
                                |||||||| |||    |||||||
                                TCCTTCAG CGT    TAGTGCT
                                    A   AA___
GAM338  CIAS1    3'  GCCTCAGTTAGAGGATGTTCCT 18099        G___   CA
              C                  GAGGAACATC   AGC  AGGC
                                 ||||||||||   |||  ||||
                                 CTCCTTGTAG   TTG  TCCG
                                      GAGA   AC
GAM338  DLEU2    3'  GTTTTACACTAAATGTTCCTC  21209       CG  CC_
                                GAGGAACAT  AG   AAGGC
                                |||||||||  ||   |||||
                                CTCCTTGTA  TC   TTTTG
                                     AA  ACA
GAM338  DRD2     3'  CTTGGCTCCATGCTCCTC    7676      A   C
                                GAGGA CAT GAGCCAAG
                                ||||| ||| ||||||||
                                CTCCT GTA CTCGGTTC
                                   C   C
GAM338  LIFR     3'  CCTTCTGGTGGATGTTCCTC  11311        GA   __
                                GAGGAACATC  GCCA  AGG
                                ||||||||||  ||||  |||
                                CTCCTTGTAG  TGGT  TCC
                                     G_    CT
GAM338  PPP3CC   5'  GGTGCCGAAGCGGTGTTCCCCG 20030    A       AGCCAA
                                CG GGAACATCG     GGCACC
                                || |||||||||     ||||||
                                GC CCTTGTGGC     CCGTGG
                                 C       GAAG__
GAM338  SCNN1A   3'  GTGCCTTGGCTCCAGCCCT   8296     AACATC
                                AGG     GAGCCAAGGCAC
                                |||     ||||||||||||
                                TCC     CTCGGTTCCGTG
                                  CGAC__
GAM338  SERPIND1 3'  GTGCCTTGGGGGCACCCTC   5744      AACA  GAG
                                GAGG   TC   CCAAGGCAC
                                ||||   ||   |||||||||
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                                CTCC   GG  GGTTCCGTG
                                  CACG  ___
GAM338  CX46.6   3'  GTGCCCTGGCTTGGTCACC   40315   AAC      A
                                GG  ATCGAGCCA GGCAC
                                ||  ||||||||| |||||
                                CC  TGGTTCGGT CCGTG
                                 AC_       C
GAM338  FLJ10607  5'  GGGCCTTGGCCTCCGCCTC   77641    AACATC  _     A
                                GAGG     GAG CCAAGGC CC
                                ||||     ||| ||||||| ||
                                CTCC     CTC GGTTCCG GG
                                  GC____  C      C
GAM338  KIAA0481  5'  TGCCTTGGAAATTGATGCCTC  72326    AA    G__
                                GAGG  CATCGA  CCAAGGCA
                                ||||  ||||||  ||||||||
                                CTCC  GTAGTT  GGTTCCGT
                                  __     AAA
GAM338  KIAA0918  3'  GTGCCTTGGCACGGGATTTCTC 73521      CA   A
                                GAGGAA  TCG GCCAAGGCAC
                                ||||||  ||| ||||||||||
                                CTCTTT  GGC CGGTTCCGTG
                                   AG   A
GAM338  MGC26914  3'  GTGCCTTGATATTGGACTTCC  59331    CA   GC_
                                GGAA  TCGA  CAAGGCAC
                                ||||  ||||  ||||||||
                                CCTT  GGTT  GTTCCGTG
                                  CA   ATA
GAM338  OLIG1    3'  GGGCTTTCCGCTGTTCCTC   97336      T  AGCC    A
                                GAGGAACA CG   AAGGC CC
                                ||||||||  ||   ||||| ||
                                CTCCTTGT GC   TTTCG GG
                                    C  C___    C
GAM338  SEMA5A   3'  TGGTTCCCCAATTGTTCCTCG  15601       TC____
                                CGAGGAACA     GAGCCA
                                |||||||||     ||||||
                                GCTCCTTGT     CTTGGT
                                     TAACCC
GAM338  SLC5A6   5'  CCTCAGCCCGGTGTTCCCCG   41178   A       A  CA
                                CG GGAACATCG GC  AGG
                                || |||||||||  ||  |||
                                GC CCTTGTGGC CG  TCC
                                 C       C  AC
GAM338  LOC147042 3'  GCCTTGGCTGGCACCCTC    84993     AACA  G
                                GAGG   TC AGCCAAGGC
                                ||||   || |||||||||
                                CTCC   GG TCGGTTCCG
                                  CAC_  _
GAM338  LOC149302 5'  GTGCCTTGGCTGTTTATCC   80043    ACAT G
                                GGA   C AGCCAAGGCAC
                                |||   | ||||||||||
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                                CCT   G TCGGTTCCGTG
                                  ATTT _
GAM338  LOC90750  3'  TGCCTTAACTGACGTAGCTCCT 64634     ___  A  G  CC
                                AGGA   AC TC AG  AAGGCA
                                ||||   || || ||  ||||||
                                TCCT   TG AG TC  TTCCGT
                                  CGA  C  _  AA
GAM339  E2F3     3'  TTCTCTAGCTGTGATCTTA   10473        _   ACCCC
                                TAAGATCA AGT    GAGAA
                                |||||||| |||    |||||
                                ATTCTAGT TCG    CTCTT
                                    G   AT___
GAM339  FEN1     3'  CTTTTTTACTTGATCTTA    15922          CCCC
                                TAAGATCAAGTA    GAG
                                ||||||||||||    |||
                                ATTCTAGTTCAT    TTC
                                      TTT_
GAM339  IL1R1    3'  TTCTGAGTACTTGATTT     7930          CC G
                                AGATCAAGTAC  C AGAA
                                ||||||||||  | ||||
                                TTTAGTTCATG  G TCTT
                                      A_ _
GAM339  ATP6V0A1 3'  TCTCGGGGTTGGCTTCTTC   18989    TC   __
                                GA  AAGT  ACCCCGAGA
                                ||  ||||  |||||||||
                                CT  TTCG  TGGGGCTCT
                                 TC   GT
GAM339  DKFZP434L0117 3'  TTCTCATGCCTGGTCTTA    43246        A   CCCC
                                TAAGATCA GTA    GAGAA
                                |||||||| |||    |||||
                                ATTCTGGT CGT    CTCTT
                                    C   A___
GAM339  FLJ12688  3'  CTCGGGGTGGTTTTA      73553        AAGT
                                TAAGATC    ACCCCGAG
                                |||||||    ||||||||
                                ATTTTGG    TGGGGCTC
                                     ____
GAM339  FLJ12998  3'  TTCTCGGGACACTCGGTCTT   43153       A   AC
                                AAGATC AGT  CCCGAGAA
                                ||||||  |||  ||||||||
                                TTCTGG TCA  GGGCTCTT
                                   C   CA
GAM339  FLJ22055  3'  CTCCCAAGTGCCTTGATCTT   45849        _   CCC_
                                AAGATCAAG TAC    GAG
                                |||||||||  |||   |||
                                TTCTAGTTC GTG    CTC
                                     C   AACC
GAM339  MGC10960  3'  TTCTCGGGACACATTCTTA   51984      TCAA  AC
                                TAAGA    GT  CCCGAGAA
                                |||||    ||  ||||||||
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                                ATTCT   CA  GGGCTCTT
                                   TA__  CA
GAM339  MGC3101   3'  TCTCGGGGTGGGGTTCA    44106   A   AAG
                                A GATC   TACCCCGAGA
                                | ||||   ||||||||||
                                A TTGG   GTGGGGCTCT
                                 C   G__
GAM339  ORMDL3    5'  TTCCCGGGCCGTTGATCTT   74799       GTAC   A
                                AAGATCAA   CCCG GAA
                                ||||||||   |||| |||
                                TTCTAGTT   GGGC CTT
                                     GCC_   C
GAM339  POLR3K    3'  CTCGGGGTAGATGCTTA    33313     _  AAG
                                TAAG ATC   TACCCCGAG
                                |||| |||   |||||||||
                                ATTC TAG   ATGGGGCTC
                                  G  ___
GAM339  POMT2     5'  TTCCCGGGGTACCCCGAGCT   26321    A  AA_     A
                                AG TC   GTACCCCG GAA
                                || ||   |||||||| |||
                                TC AG   CATGGGGC CTT
                                 G  CCC       C
GAM339  SERF1B    3'  CTCTGGTAACTGATCTTA    43696       AG   CC
                                TAAGATCA  TACC  GAG
                                ||||||||  ||||  |||
                                ATTCTAGT  ATGG  CTC
                                     CA   T_
GAM339  SPTLC2    3'  CTCCCAAGGGTTTGGTCTTA   17990       GT   C___
                                TAAGATCAA  ACCC   GAG
                                |||||||||  ||||   |||
                                ATTCTGGTT  TGGG   CTC
                                     __   AACC
GAM339  VDAC3     5'  CTCGGGGTGGAGGTCTT    20181      AAG
                                AAGATC   TACCCCGAG
                                ||||||   |||||||||
                                TTCTGG   GTGGGGCTC
                                   AG_
GAM339  LOC143524 3'  CTCAGGCTTACTTGATCT    77094        CC  _
                                AGATCAAGTA  CC GAG
                                ||||||||||  || |||
                                TCTAGTTCAT  GG CTC
                                      TC  A
GAM339  LOC147669 5'  TTCTCAGGACTTGACTC     85187    _    A  CC
                                GA TCAAGT CC  GAGAA
                                || ||||||  ||  |||||
                                CT AGTTCA GG  CTCTT
                                 C     _  A_
GAM339  LOC150051 3'  TCCCGGGGTGATCTTG      85955       AAGT    A
                                TAAGATC    ACCCCG GA
                                |||||||    |||||| ||
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                                GTTCTAG    TGGGGC CT
                                    ____     C
GAM339  LOC202865 5'  TCCGTGCGACTTGATCTTA    59934          ACCC  A
                                TAAGATCAAGT    CG GA
                                ||||||||||    || ||
                                ATTCTAGTTCA    GC CT
                                     GCGT  _
GAM339  LOC219918 3'  CTCAGGCTTACTTGATCT     93171          CC  _
                                AGATCAAGTA  CC GAG
                                ||||||||||  || |||
                                TCTAGTTCAT  GG CTC
                                     TC  A
GAM339  LOC221683 5'  TGAGGGTACTTAGTCTTA     95333       C       _
                                TAAGAT AAGTACCC CG
                                ||||||| |||||||| ||
                                ATTCTG TTCATGGG GT
                                   A       A
GAM339  LOC254808 3'  TCTCAGGAGTGAAATGATCTTA 98811         AG_  _ C
                                TAAGATCA   TAC CC GAGA
                                ||||||||   ||| || ||||
                                ATTCTAGT   GTG GG CTCT
                                    AAA   A  A
GAM339  LOC90906  3'  TTCTCACGCTTACTTGATCT   64958          CCCC_
                                AGATCAAGTA    GAGAA
                                ||||||||||    |||||
                                TCTAGTTCAT    CTCTT
                                     TCGCA
GAM340  RAD54B    3'  TATACACAAACCTTGA      57064          CTTT
                                TCAAGGTTT    TGTATA
                                |||||||||    ||||||
                                AGTTCCAAA    ACATAT
                                    C___
GAM340  DKFZp434I1930 3'  GTGGGAAAAAACCTTGA     51043          C    G
                                TCAAGGTTT TTTT TAT
                                ||||||||| |||| |||
                                AGTTCCAAA AAAG GTG
                                     _   G
GAM340  GHITM     3'  ATACAGAGAATCCTTGA     27674        T     T
                                TCAAGG TTCTTT GTAT
                                |||||| |||||| ||||
                                AGTTCC AAGAGA CATA
                                   T     _
GAM340  LOC169966 3'  AATTATATATCACAGAACCCTG 83433     A    T  TTT
          A                      TCA GGTT CT   GTATATAATT
                                 ||| |||| ||   ||||||||||
                                 AGT CCAA GA   TATATATTAA
                                   C    _ CAC
GAM341  ELF3      3'  TGACCTTGACCTTGACCAA    16685       T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
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                                AACCA GTTCC   TC   CAGT
                                  _    AGT  ___
GAM341  JAK2     3'  TGACCTTCATTCTGAGACCAA  18318       CAA       AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_       C_
GAM341  SLC10A2  5'  ACTCTCTGTCTTGACCAA    6590        CAA       A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM341  FLJ10803 3'  GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM341  KIAA1958 5'  GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM341  MARCKS   3'  ACTTTCCACCCTGCCCA     11411     TTCA    A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                 CG__   _
GAM341  TUB      5'  GTGGGACCATCCCTTAAACC   13898     C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A        AG__
GAM341  LOC80298 3'  ACTTTTACCTTGAACCA     48062         GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                     A___
GAM342  ABL1     3'  GGTCACTGTCACTGCCGA    24609      TG       C
                                TCGG  GTGATGGTG ATC
                                ||||  ||||||||| |||
                                AGCC  CACTGTCAC TGG
                                  GT       _
GAM342  ACADL    3'  CTTGGTTCTGTCAATTGCTGA  9638       TG  _    TGCATC
                                TCGG  GT GATGG     CCGAG
                                ||||  || |||||     |||||
                                AGTC  TA CTGTC     GGTTC
                                  GT  A    TT_____
GAM342  ADAM19   3'  TCGGGGCATGGCCATTGG    53847        G   GTGCA
                                TCGGTGGT ATG    TCCCGA
                                |||||||| |||    ||||||
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                                GGTTACCG TAC    GGGGCT
                                    G  _____
GAM342  ADD1    3'  CTCGACATCACCGTCATTGATG 27205    GT       C  CC
            G                    TCG  GGTGATGGTG AT  CGAG
                                 |||  |||||||||| ||  ||||
                                 GGT  TTACTGCCAC TA  GCTC
                                   AG        _  CA
GAM342  ADD1    3'  CTCGACATCACCGTCATTGATG 27206    GT       C  CC
            G                    TCG  GGTGATGGTG AT  CGAG
                                 |||  |||||||||| ||  ||||
                                 GGT  TTACTGCCAC TA  GCTC
                                   AG        _  CA
GAM342  ADD1    3'  CTCGGCAGATGCTGTTGTTGTT 27207    TG TG  GGT    __
                                 GG  G  AT   GCATC  CCGAG
                                 ||  |  ||   |||||  |||||
                                 TT  T  TG   CGTAG  GGCTC
                                  GT GT  T__    AC
GAM342  ADD1    3'  CTCGGCAGATGCTGTTGTTGTT 27208    TG TG  GGT    __
                                 GG  G  AT   GCATC  CCGAG
                                 ||  |  ||   |||||  |||||
                                 TT  T  TG   CGTAG  GGCTC
                                  GT GT  T__    AC
GAM342  ADH5    3'  CTTGTTTTATGCTGTCATCATT 7266           GCATCC
            G                    CGGTGGTGATGGT     CGAG
                                 ||||||||||||      ||||
                                 GTTACTACTGTCG     GTTC
                                        TATTTT
GAM342  ADM     5'  TTCGGAGTTTTGCCATTGCCAG 8513     G   TG    GC_ TC
            TGG                   TCG TGG  ATGGT   A  CCGAG
                                 |||  |||  |||||   |  |||||
                                 GGT ACC  TACCG   T  GGCTT
                                   G   GT    TTT GA
GAM342  ADORA3  3'  CTTGGGGACAACGTATTATTGA 7283         G   G  CA
                                 TCGGTGGT ATG TG  TCCCGAG
                                 ||||||||  |||  ||  |||||||
                                 AGTTATTA TGC AC  GGGGTTC
                                     _   A  A_
GAM342  ADRB3   3'  TTGGGGTTTTATCTCTGG    5251       T    TGGTGC
                                 TCGG GGTGA     ATCCCGA
                                 ||||  |||||     |||||||
                                 GGTC CTATT     TGGGGTT
                                   T    T_____
GAM342  ALDH1B1 3'  CTTGCCCTTCATTTTGCTACTG 7323         _____  T  T   TCCCGAG
            A                     TCGGTGGT    GA GG GCA
                                 ||||||||    || || |||
                                 AGTCATCG    CT CC CGT
                                      TTTTA  T  _   TC   G
GAM342  ANKRA2  5'  CTCGCTGTCTGCTGTCGTCGGT 43791     G  GT      C  CC
            GG                    TCG TG  GATGGTG AT  CGAG
                                 |||  ||  |||||||  ||  ||||
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                                GGT GC  CTGTCGT TG  GCTC
                                  G  TG      C  TC
GAM342  AOX1     5'  CTCGGCGGGTCGGTGCCGCCGG 8572         GA  GT  A  _
                                TCGGTGGT  TG  GC TC CCGAG
                                |||||||  ||  || || |||||
                                GGCCGCCG  GC  TG GG GGCTC
                                     TG  __  _  C
GAM342  APOBEC1  3'  GAGTATTATCACTGCTGG    20836      TG        A
                                TCGG  GTGATGGTGC TC
                                ||||  |||||||||| ||
                                GGTC  CACTATTATG AG
                                  GT        _
GAM342  AQP6     3'  TTCGGCCCTGCCATCATCATTG 55021             GCATC
              G                  TCGGTGGTGATGGT    CCGAG
                                ||||||||||||||    |||||
                                GGTTACTACTACCG    GGCTT
                                       TCCC_
GAM342  ARAF1    5'  GTTTGCTTCTAGACTATCATTA 64646           _______  TCCCGAG
              TTGG                 TCGGTGGTGATGGT     GCA
                                ||||||||||||||     |||
                                GGTTATTACTATCA     CGT
                                       GATCTT   TT   GA
GAM342  ARHGEF12 3'  TGACACTAACACCATCGA    31650         A    _
                                TCGGTGGTG TGGTG CA
                                ||||||||| ||||| ||
                                AGCTACCAC ATCAC GT
                                     A    A
GAM342  ASB1     3'  TTGGGTCATTGTCAGCTGA   32772      GG   TG   CAT
                                TCGGT  TGA  GTG   CCCGA
                                |||||  |||  |||   |||||
                                AGTCG  ACT  TAC   GGGTT
                                   __   GT   T__
GAM342  BBS4     3'  TTTGGGGAAAATTGTTATTCA  53449   T    TG  GCA
                                G GGTGA  GT   TCCCGAG
                                | |||||  ||   |||||||
                                A TTATT  TA   GGGGTTT
                                 C    GT  AAA
GAM342  BCL7A    3'  TTTGGAATGTTCATTATCGCC  41000          T   C
                                GGTGGTGATGG GCAT CCGAG
                                |||||||||| |||| |||||
                                CCGCTATTACT TGTA GGTTT
                                      _    A
GAM342  BMP1     3'  ACACGCTGTATTGTGTATCACC 21524         _ TG    TCCCGAG
              GG                   TCGGTGGTG A  GTGCA
                                |||||||| |  |||||
                                GGCCACTAT T  TATGT
                                     G GT    CGCACAT
GAM342  BRCA1    3'  TAGGCATAGCACCGTTGCTACC 24575        TG      _  C  GAG
              GA                   TCGGTGG  ATGGTGC AT CC
                                |||||||  ||||||| || ||
```

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                                AGCCATC  TGCCACG TA GG
                                   GT      A  C  ATC
GAM342  CDKN2A   3'  CTCGGGAACTTAGATCATCAGT 5371        _      GCA___
           CACCGA                 TCGGTGG TGATGGT     TCCCGAG
                                |||||||  |||||||      |||||||
                                AGCCACT ACTACTA     AGGGCTC
                                   G      GATTCA
GAM342  CHN1     3'  TTGGGGTCTATGTCATTGG    10197       GT A   TGC
                                TCGGTG  G TGG   ATCCCGA
                                ||||||  | |||   |||||||
                                GGTTAC  T ATC   TGGGGTT
                                   TG _   ___
GAM342  CHN2     3'  ATGCAGTATTATCATTGA     15794           G
                                TCGGTGGTGATG TGCAT
                                ||||||||||| |||||
                                AGTTACTATTAT ACGTA
                                      G
GAM342  CHRNA3   3'  TAACGTGATCATCACCACTGA  7434             G   CCCGAG
                                TCGGTGGTGATGGT CAT
                                ||||||||||||| |||
                                AGTCACCACTACTA GTG
                                      _   CAATT
GAM342  CHRNA7   3'  CTTGGCACATCCGTACCATCGG 7441          AT    CATC
                                TCGGTGGTG  GGTG    CCGAG
                                |||||||||  ||||    |||||
                                GGCTACCAT  CTAC    GGTTC
                                   GC    AC__
GAM342  CKAP1    5'  GCTTGGGGTACAGCATGTTGTT 73902       TG   G   ___
           ACTG                   CGGTGG  ATG TGC   ATCCCGAG   C
                                ||||||  ||| |||   |||||||||   |
                                GTCATT  TGT ACG   TGGGGTTC   G
                                   GT   _   ACA
GAM342  CLASP1   3'  CTTGGGAACACTGTTGTCATGG 65893    G    TG     CA
           G                    TC GTGG  ATGGTG  TCCCGAG
                                ||  ||||  ||||||  |||||||
                                GG TACT  TGTCAC  AGGGTTC
                                 G   GT     A_
GAM342  CLCN4    5'  TCGCAGCCGTCGCGCTGA    10211       G      GCATCC
                                TCGGTG TGATGGT     CGA
                                ||||||| |||||||     |||
                                AGTCGC GCTGCCG     GCT
                                   _      AC_____
GAM342  CLCN5    3'  TTTGGGATCTAACTGTTGTTAC 5387         TG    GC_
           TGG                    TCGGTGG  ATGGT   ATCCCGAG
                                |||||||  |||||   ||||||||
                                GGTCATT  TGTCA   TAGGGTTT
                                   GT    ATC
GAM342  CNGA1    3'  CTTGGGATTTTTCACAACTGA  60239      G    TGGTGC
                                TCGGT GTGA     ATCCCGAG
                                ||||| ||||     ||||||||
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                                AGTCA CACT     TAGGGTTC
                                  A   TTT___
GAM342  CNP     5'  CTCGGGTTGTGCCACCGCTGG  53618        GAT  TG  T
                                TCGGTGGT   GG  CA CCCGAG
                                ||||||||   ||  || ||||||
                                GGTCGCCA   CC  GT GGGCTC
                                     ___  GT  T
GAM342  CREBBP  3'  TTTGGATTCTTTTTGTCGTCAT 16496     TG     GT C_____   CGAG
          TGCTGG                  TCGG  GTGATG  G     ATCC
                                ||||  ||||||  |     ||||
                                GGTC  TACTGC  T     TAGG
                                  GT     TG TTTTCT    TTT
GAM342  CRKL    5'  TGTTGCTGTGGCTATTGG    19047        G     _
                                TCGGTGGT ATGGTG CA
                                |||||||| |||||| ||
                                GGTTATCG TGTCGT GT
                                     G     T
GAM342  CRYM    3'  CTTGAGGAATATTGCTGCTGG  10307     TG TG   GTGCA  _
                                TCGG  G  ATG    TCC CGAG
                                ||||  |  |||    ||| ||||
                                GGTC  C  TAT    AGG GTTC
                                  GT GT   A____   A
GAM342  CSDA    3'  CTCAGGCACCTTCACCATCGG  14689         T    ATCCC
                                TCGGTGGTGA GGTGC    GAG
                                |||||||||| |||||    |||
                                GGCTACCACT CCACG    CTC
                                     T    GA___
GAM342  CSE1L   5'  CTCGCTGTCGCGCCATTTTGCC 62512     TG T      _  CC
          GG                    TCGG  G GATGGTGC AT  CGAG
                                ||||  | |||||||| ||  ||||
                                GGCC  T TTACCGCG TG  GCTC
                                  GT _       C  TC
GAM342  CUL3    3'  TTCGTTGACTATCAGTACTG   14575      G     G  TCC
                                CGGTG TGATGGT CA   CGAG
                                ||||| ||||||| ||   ||||
                                GTCAT ACTATCA GT   GCTT
                                  G      _ T__
GAM342  CYP3A4  3'  TTTGGTCATTGTAATCACTGTT 34369     TG    GG    TC__
          GG                    TCGG  GTGAT  TGCA    CCGAG
                                ||||  |||||  ||||    |||||
                                GGTT  CACTA  ATGT    GGTTT
                                  GT    __    TACT
GAM342  CYP8B1  3'  CTTGGTTTCCATGATCATTGCT 16538     TG    G   CATC
          GA                    TCGG  GTGAT GTG    CCGAG
                                ||||  ||||| |||    |||||
                                AGTC  TACTA TAC    GGTTC
                                  GT    G   CTTT
GAM342  DDX11   3'  TTTGGCCCCGCCATTGCTGCTG 16584     TG TG     CATC
                                CGG  G  ATGGTG    CCGAG
                                |||  |  ||||||    |||||
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                              GTC  C  TACCGC   GGTTT
                                GT GT     CCC_
GAM342  DSCR3    3'  TTGGGATGTATATTGCTA    21328     TG   G
                              TGG  ATG TGCATCCCGA
                              |||  ||| ||||||||||
                              ATC  TAT ATGTAGGGTT
                                GT   _
GAM342  DYRK1A   3'  TTTGGGGTGTGACACTTTTGA  56088     T    ATGG
                              TCGG GGTG   TGCATCCCGAG
                              |||| ||||   ||||||||||
                              AGTT TCAC   GTGTGGGGTTT
                                T   A___
GAM342  DYRK1A   3'  TTTGGGGTGTGACACTTTTGA  56089     T    ATGG
                              TCGG GGTG   TGCATCCCGAG
                              |||| ||||   ||||||||||
                              AGTT TCAC   GTGTGGGGTTT
                                T   A___
GAM342  EEF2     3'  CTCCAGCTGTACTAGTGCCATT 96231        GA      TCCC
           GG                   TCGGTGGT  TGGTGCA   GAG
                              ||||||||  |||||||   |||
                              GGTTACCG  ATCATGT   CTC
                                  TG     CGAC
GAM342  EFNB1    3'  CTTGTCCGCTATCATCACTG   16669           CATCC
                              CGGTGGTGATGGTG    CGAG
                              ||||||||||||||    ||||
                              GTCACTACTATCGC    GTTC
                                     CT___
GAM342  EGFL5    5'  GTTTGACAGTCATCATCATTG  87919          _ _  TCCCGAG
                              CGGTGGTGATGG TG CA
                              |||||||||||| || ||
                              GTTACTACTACT AC GT
                                    G  A  TT   GA
GAM342  EGFR     3'  CTTGGAGTTTTTCATTGTCGCT 19086         TG   C___ TC
           ATTGA                TCGGTGGTGA  GTG    A  CCGAG
                              ||||||||||  |||   |  |||||
                              AGTTATCGCT  TAC    T  GGTTC
                                   GT   TTTT GA
GAM342  EHHADH   3'  CTCAAATGCTTTTATCATTGG  10499         TGGT    CCC
                              TCGGTGGTGA   GCAT   GAG
                              ||||||||||   ||||   |||
                              GGTTACTATT   CGTA   CTC
                                   TT__    AA_
GAM342  EIF4EBP2 3'  CTCCCTGCTTGCATCTCGTTGC 15855      GG   T     TCCC__
           TGG                  TCGGT  TGA GGTGCA     GAG
                              |||||  ||| ||||||     |||
                              GGTCG  GCT CTACGT     CTC
                                TT   _     TCGTCC
GAM342  EIF4G1   3'  CTCGGACTGCCGTCCTCGCTGC 18254     TG    T  T__   TC
           TGG                  TCGG  GTGA GG   GCA  CCGAG
                              ||||  |||| ||   |||  |||||
```

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                                GGTC  CGCT CC   CGT  GGCTC
                                  GT   _ TGC   CA
GAM342  EVA1     3'  TTCGGGGTTATATTTATTACTA 20534          TGC__
           CT                    GGTGGTGATGG    ATCCCGAG
                                ||||||||||    ||||||||
                                TCATCATTATT    TGGGGCTT
                                     TATAT
GAM342  EXTL2    3'  TTCGGGTAGTGCATTTTGTCAC 9329         TG T     __
           TGA                   TCGGTGG  A GGTGCAT  CCCGAG
                                ||||||| | ||||||| ||||||
                                AGTCACT  T TTACGTG  GGGCTT
                                   GT _     AT
GAM342  FBXO7    3'  TTGGGGTGCTGATCTCGA    25157     TGGT   GGT
                                TCGG   GAT   GCATCCCGA
                                ||||   |||  |||||||||
                                AGCT   CTA   CGTGGGGTT
                                  ____  GT_
GAM342  FKBP10   5'  CTCGCTCGCCCTCACTGCCGG  41936     TG   T   CATCC
                                TCGG  GTGA GGTG    CGAG
                                ||||  |||| ||||    ||||
                                GGCC  CACT CCGC    GCTC
                                  GT   C   TC___
GAM342  FMR1     3'  ACAAAATGTAACTGTTACCATT 10676           _   CCCGAG
           GG                    TCGGTGGTGATGGT GCAT
                                |||||||||||||| ||||
                                GGTTACCATTGTCA TGTA
                                      A   AAACAT
GAM342  FUT8     3'  ATGGTGGTATTGTGACCACTGA 16811        G TG   ATC   AG
                                TCGGTGGT A  GTGC   CCG
                                |||||||| |  ||||   |||
                                AGTCACCA T  TATG   GGT
                                    G GT   GT_   AG
GAM342  GAL      3'  CTTGATGTTGTGTTGTTATCAT 93147        TG TG  TCC_
           T                     GGTGGTGA  G  CA   CGAG
                                |||||||  |  ||   ||||
                                TTACTATT  T  GT   GTTC
                                    GT GT  TGTA
GAM342  GALR1    3'  TTTGGGGTTAAAACCATCACCA 9426           GC__
           TT                    GGTGGTGATGGT   ATCCCGAG
                                ||||||||||||   ||||||||
                                TTACCACTACCA   TGGGGTTT
                                      AAAT
GAM342  GAN      3'  TTTGGGAGAACACGTAACTGTT 42125     TG  G  _  GCA
           GA                    TCGG  GT ATG GT   TCCCGAG
                                ||||  || ||| ||   |||||||
                                AGTT  CA TGC CA   AGGGTTT
                                  GT  A   A  AG_
GAM342  GFRA2    5'  CTTGGCTATTATTATTGTTG   9464     TG       CATC
                                CGG  GTGATGGTG   CCGAG
                                |||  |||||||||   |||||
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                                GTT  TATTATTAT   GGTTC
                                  GT       C___
GAM342  GFRA2    5'  TTTGGGGCTGATTACCACTG  9468          GGT  AT
                                CGGTGGTGAT   GC  CCCGAG
                                ||||||||||   ||  ||||||
                                GTCACCATTA   CG  GGGTTT
                                     GT_  __
GAM342  GGA3     3'  TTTGAGTGTTACTCGTTACTGT 26592      TG    _  _  CC
           TGA                   TCGG  GTGATG GTG CAT  CGAG
                                ||||  |||||| ||| |||  ||||
                                AGTT  CATTGC CAT GTG  GTTT
                                  GT    T  T  A_
GAM342  GGT1     5'  CTTGGGGCCCCCGTCTGCTGCT 26422      TG _    T_ AT
           GG                    TCGG  GT GATGG  GC  CCCGAG
                                ||||  || |||||  ||  ||||||
                                GGTC  CG CTGCC  CG  GGGTTC
                                  GT  T    CC  __
GAM342  GGT1     5'  CTTGGGGCCCCCGTCTGCTGCT 26423      TG _    T_ AT
           GG                    TCGG  GT GATGG  GC  CCCGAG
                                ||||  || |||||  ||  ||||||
                                GGTC  CG CTGCC  CG  GGGTTC
                                  GT  T    CC  __
GAM342  GGT1     5'  CTTGGGGCCCCTGTCTGCTGCT 26424      TG _  _  T  AT
           GG                    TCGG  GT GAT GG GC  CCCGAG
                                ||||  || ||| || ||  ||||||
                                GGTC  CG CTG CC CG  GGGTTC
                                  GT  T   T  C  __
GAM342  GGT2     5'  CTTGGGGCCCCCGTCTGCTGCT 74087      TG _    T_ AT
           GG                    TCGG  GT GATGG  GC  CCCGAG
                                ||||  || |||||  ||  ||||||
                                GGTC  CG CTGCC  CG  GGGTTC
                                  GT  T    CC  __
GAM342  GJA1     3'  CTTGCACAATATCATTACCATC 5713          _____    TCCCGAG
                                GGTGGTGATG    GTGCA
                                ||||||||||    |||||
                                CTACCATTAC    CACGT
                                     TATAA    TC   G
GAM342  GK       3'  TCGGATCCTTACCATTGG    5717          T  TGCATC
                                TCGGTGGTGA GG     CCGA
                                |||||||||| ||     ||||
                                GGTTACCATT CC     GGCT
                                     _  TA____
GAM342  GMPS     5'  CTCGTACTGTCGCCGTCACCGC 15265           _  TCC
           CG                    CGGTGGTGATGGTG CA   CGAG
                                ||||||||||||||| ||   ||||
                                GCCGCCACTGCCGC GT   GCTC
                                       T  CAT
GAM342  GNE      3'  TACTAATGTATTAATACCACTG 19679         A       CCCGAG
           A                     TCGGTGGTG TGGTGCAT
                                |||||||| ||||||||
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                                AGTCACCAT ATTATGTA
                                     A       ATCATT
GAM342  GPRC5B   3'  CTTGGAGATGACCGTTGC    33176   TG    G   _
                                G  ATGGT CATC CCGAG
                                |  ||||| |||| |||||
                                C  TGCCA GTAG GGTTC
                                 GT    _   A
GAM342  GPRK7    3'  CTTGCACTACCATATGCCATCG 58314         _   ___  TCCCGAG
           G                     TCGGTGGTG ATGGT   GCA
                                |||||||||| |||||  |||
                                GGCTACCGT TACCA   CGT
                                     A    TCA  TC   G
GAM342  GPX3     5'  ATGTCACTGTCGCCCCGG    10866     T       _
                                TCGG GGTGATGGTG CAT
                                |||| |||||||||| |||
                                GGCC CCGCTGTCAC GTA
                                  _        T
GAM342  GRM1     5'  CTTGGACGACCATTGTTGGCGA 7736     G   TG    GCATC
                                TCG TGG  ATGGT    CCGAG
                                ||| |||  |||||    |||||
                                AGC GTT  TACCA    GGTTC
                                  G   GT    GCA__
GAM342  GUCY2D   3'  GTGACACTGCATTGCTGG    5730      TG   A    _
                                TCGG  GTG TGGTG CAT
                                ||||  ||| ||||| |||
                                GGTC  TAC GTCAC GTG
                                  GT   _    A
GAM342  HIC1     5'  CTCGCCCTGCCGTCGCTGCCG  88659    TG      GCATCC
                                CGG  GTGATGGT     CGAG
                                |||  ||||||||     ||||
                                GCC  CGCTGCCG     GCTC
                                  GT       TCCC__
GAM342  HLCS     3'  TTTGGGAAAAAATGTTATCATT 6424          GTGCA
                                GGTGGTGATG    TCCCGAG
                                ||||||||||    |||||||
                                TTACTATTGT    AGGGTTT
                                     AAAAA
GAM342  HMGA2    3'  CTCTAGTGTATTATCACTGTC  14454    TG         CCC
                                GG  GTGATGGTGCAT   GAG
                                ||  ||||||||||||   |||
                                CT  CACTATTATGTG   CTC
                                 GT          AT_
GAM342  HMGB3    3'  CTCTGTGCACTTTGCTGTTGG  19271     TG TG T      CCC
                                TCGG  G  A GGTGCAT   GAG
                                ||||  |  | |||||||  |||
                                GGTT  C  T TCACGTG   CTC
                                  GT GT _      T__
GAM342  HPRT1    3'  CTTGTTCAAATTATTACCAGTG 5759      G        GCATCC
           A                     TCG TGGTGATGGT     CGAG
                                ||| ||||||||||     ||||
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```
                                AGT ACCATTATTA     GTTC
                                  G        AACTT_
GAM342  HPS1    3'  TTGGTCATTGTTATCACTGA  5767          TG   CATC
                                TCGGTGGTGA  GTG    CCGA
                                ||||||||||  |||    ||||
                                AGTCACTATT  TAC    GGTT
                                     GT   T___
GAM342  HS2ST1  3'  TTTGCTTTGTACTTCATTGCTG 25333     TG    T     TCC
              G                  TCGG  GTGA GGTGCA   CGAG
                                ||||  |||| ||||||   ||||
                                GGTC  TACT TCATGT   GTTT
                                  GT    _     TTC
GAM342  HYOU1   3'  TTTGGGAAAAATCACTATT   60388         GGTGCA
                                GGTGGTGAT     TCCCGAG
                                |||||||||     |||||||
                                TTATCACTA     AGGGTTT
                                     AAA___
GAM342  IGFBP2  5'  CTCGCCCGCCGCGCCGCGCTGC 6998      TG   A     ATCC__
              CGA                  TCGG  GTG TGGTGC     CGAG
                                ||||  ||| ||||||     ||||
                                AGCC  CGC GCCGCG     GCTC
                                  GT   _     CCGCCC
GAM342  IK      5'  GTCGCTGCGGTGTTGCTGTTGG 76835     TG TG   G    TCC   G
                                TCGG  G  ATG TGCA   CGA
                                ||||  |  ||| ||||   |||
                                GGTT  C  TGT GCGT   GCT
                                  GT GT   G    C__   GT
GAM342  IKBKAP  5'  CTTGGAGGCCTAGTGCCGTCGG 71151     GT   GA   T  ATC
                                TCG  GGT  TGG GC   CCGAG
                                |||  |||  ||| ||   |||||
                                GGC  CCG  ATC CG   GGTTC
                                  TG   TG   _  GA_
GAM342  IL1RL1  3'  TTCGGGATGTTGTTTGCTGTCT 15255      _   TG TGGT
              GA                   TCGG TGG  A    GCATCCCGAG
                                |||| |||  |    ||||||||||
                                AGTC GTC  T    TGTAGGGCTT
                                  T   GT TGT_
GAM342  INPP5B  3'  TTTGGCAGCTTATTGCTTCGA  97261     T  TG    T  ATC
                                TCGG GG  ATGG GC   CCGAG
                                |||| ||  |||| ||   |||||
                                AGCT TC  TATT CG   GGTTT
                                  _  GT    _  AC_
GAM342  ITGA1   5'  CTCCTGGGCGCCGCTGCCACTG 64272         GA     A  CC
              G                   TCGGTGGT  TGGTGC TC  GAG
                                ||||||||  |||||| ||  |||
                                GGTCACCG  GCCGCG GG  CTC
                                     TC     _  TC
GAM342  ITGA3   3'  TCGGGACCAATACTACTGA   11034         A   TGCA
                                TCGGTGGTG TGG    TCCCGA
                                |||||||||  |||    ||||||
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                                AGTCATCAT ACC    AGGGCT
                                     A  _____
GAM342  ITGB1    5'  TGGGCGCTGTCACGTCGG    54464     GT G       ATC
                                TCG  G TGATGGTGC   CCG
                                |||  | |||||||||   |||
                                GGC  C ACTGTCGCG   GGT
                                  TG _       ___
GAM342  IVD      5'  CTCGGCCTGCGGCCGTTGCACT 11091      G TG    _   TC
             GG                   TCGGT G  ATGGT GCA  CCGAG
                                |||||  |  ||||| |||  |||||
                                GGTCA C  TGCCG CGT  GGCTC
                                   _ GT    G   CC
GAM342  JUP      3'  TTTGGGGGGATCCTTTGCTGCT 11115      TG TG T  TGCA
             GA                   TCGG  G  A GG    TCCCGAG
                                ||||  |  | ||    |||||||
                                AGTC  C  T CC    GGGGTTT
                                  GT GT T  TAGG
GAM342  KIF2     3'  GCAGGATGTGCCATATCATTGA 16930         A   TG    CGAG
                                TCGGTGGTG TGG  CATCC
                                |||||||||  |||  |||||
                                AGTTACTAT ACC  GTAGG
                                     _  GT    ACGT
GAM342  KIF5C    3'  GAGAACCATTACCACCGA    16934            GCA
                                TCGGTGGTGATGGT   TC
                                ||||||||||||||   ||
                                AGCCACCATTACCA   AG
                                      AG_
GAM342  KIT      3'  TTTGGGGTTGTGTTGTCACC   5851       TG TG  _
                                GGTGA  G  CA TCCCGAG
                                |||||  |  || |||||||
                                CCACT  T  GT GGGGTTT
                                   GT GT  T
GAM342  KMO      3'  TGTCGCTGTCGTCAACTGA    14850      _ GT      _
                                TCGGT G  GATGGTG CA
                                |||||  |  ||||||| ||
                                AGTCA C  CTGTCGC GT
                                   A TG      T
GAM342  LAF4     3'  TTGGACACTGTGCTACTGA    11251        G     CATC
                                TCGGTGGT ATGGTG    CCGA
                                |||||||| ||||||    ||||
                                AGTCATCG TGTCAC    GGTT
                                     _     A___
GAM342  LAMA5    3'  TGTCACCAATCATCACTGG    19903          _   _
                                TCGGTGGTGAT GGTG CA
                                |||||||||||  |||| ||
                                GGTCACTACTA CCAC GT
                                      A   T
GAM342  LENG4    3'  CTCGGTCCCGGGCCGCCGCCGC 44419          A    GCATC_
             TGG                   TCGGTGGTG TGGT     CCGAG
                                |||||||||  ||||     |||||
```

```
                                GGTCGCCGC GCCG     GGCTC
                                     C   GGCCCT
GAM342  LETM1    3'  CTCCTGCTGTGCCGTCACCCTG 25553     T      TG  TCCC
           G                    TCGG GGTGATGG  CA   GAG
                                |||| ||||||||  ||   |||
                                GGTC CCACTGCC  GT   CTC
                                  _      GT  CGTC
GAM342  LHX4     5'  CTTGGGGTTTTAATTATTATTT 54043     T      GC__
           TGA                   TCGG GGTGATGGT   ATCCCGAG
                                 |||| |||||||||   ||||||||
                                 AGTT TTATTATTA   TGGGGTTC
                                   _      ATTT
GAM342  LIMD1    3'  GCCAGGGTGTGCATCATCATTG 27262         G TG    CGAG
           G                     TCGGTGGTGAT G  CATCC
                                 |||||||||||  |  |||||
                                 GGTTACTACTA C  GTGGG
                                       _ GT    ACCGA
GAM342  LIPA     3'  CTTGGAGCCCGCTACTGTCGTT 5880      GG     _ ATC__
           ATTGA                   TCGGT  TGATGGT GC    CCGAG
                                   |||||  ||||||| ||    |||||
                                   AGTTA  GCTGTCA CG    GGTTC
                                     TT      T  CCCGA
GAM342  LOH11CR2A 3'  CTTGGGTTGAACTATAACTGTT 28270     TG  G    G  T
           GG                    TCGG  GT ATGGT CA CCCGAG
                                 ||||  || ||||| || ||||||
                                 GGTT  CA TATCA GT GGGTTC
                                   GT  A    A  T
GAM342  MAFF     3'  TGGGTGTCCTCACTGCTGA   25586     TG   T  T   T
                                 TCGG  GTGA GG GCA CCCG
                                 ||||  |||| || ||| ||||
                                 AGTC  CACT CC TGT GGGT
                                   GT   _ _  _
GAM342  MAP3K1   3'  CTCATTGTGCATTTTACTGTTG 68426     TG   T     CCC
           G                     TCGG  GTGA GGTGCAT   GAG
                                 ||||  |||| |||||||   |||
                                 GGTT  CATT TTACGTG   CTC
                                   GT   _      TTA
GAM342  MAP3K8   5'  TGCCGCTGCCGCCGCCGG    19044        AT   _
                                 TCGGTGGTG  GGTG CA
                                 |||||||||  |||| ||
                                 GGCCGCCGC  TCGC GT
                                      CG   C
GAM342  MAPK8IP1 3'  TTGGTCCTGTCACCCTGG    19584     T      TGCATC
                                 TCGG GGTGATGG     CCGA
                                 |||| ||||||||     ||||
                                 GGTC CCACTGTC     GGTT
                                   _      CT_____
GAM342  MAX      5'  CTCGGCTTGTTGTTGTCGGTGA 11474     G  TG  GT  TC
                                 TCG TGG  ATG  GCA  CCGAG
                                 ||| |||  |||  |||  |||||
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                                AGT GCT  TGT  TGT  GGCTC
                                  G  GT   __   TC
GAM342  MBTPS1   3'  CTTGATTTCACCATTGTCGGTG 15041    G  TG    CATCC
            A                    TCG TGG  ATGGTG    CGAG
                                ||| |||  ||||||    ||||
                                AGT GCT  TACCAC    GTTC
                                  G  GT    TTTA_
GAM342  MCM6     3'  AAGGTATGTGCTGTCCTATTGA 20973       T    TG   C  GAG
                                TCGGTGG GATGG  CAT CC
                                ||||||| |||||  ||| ||
                                AGTTATC CTGTC  GTA GG
                                    _    GT   T  AAT
GAM342  MECP2    3'  CTTGGCGGTTTATCGCCCTGG  18402     T      TGC  _
                                TCGG GGTGATGG   ATC CCGAG
                                |||| ||||||||   ||| |||||
                                GGTC CCGCTATT   TGG GGTTC
                                  _      ____  C
GAM342  MEL      3'  CTTGATTTTCAGCCGTCATCAT 19328           GCATCC_
            TGG                   TCGGTGGTGATGGT      CGAG
                                |||||||||||||      ||||
                                GGTTACTACTGCCG      GTTC
                                       ACTTTTA
GAM342  MEN1     5'  TTTGGGGTGTGGGTGTTATCA  56365        GT_
                                TGGTGATG   GCATCCCGAG
                                ||||||||   ||||||||||
                                ACTATTGT   TGTGGGGTTT
                                     GGG
GAM342  MEST     3'  AGAGATGTACTGTTATTAGCTG 70457      _          CCGAG
            G                    TCGG TGGTGATGGTGCATC
                                ||||| ||||||||||||||
                                GGTC ATTATTGTCATGTAG
                                  G            AGAC
GAM342  MFAP1    5'  TTCGGGAATCACCGTCGCTGCC 20999    TG       CA
                                GG  GTGATGGTG  TCCCGAG
                                ||  |||||||||  |||||||
                                CC  CGCTGCCAC  AGGGCTT
                                  GT        TA
GAM342  MGAT5    3'  CTCAGCCCTGCACCATGCTGCT 11568     TG  G      TCCC_
            GG                    TCGG  GT ATGGTGCA    GAG
                                ||||  || ||||||||    |||
                                GGTC  CG TACCACGT    CTC
                                  GT  _       CCCGA
GAM342  MHC2TA   3'  CTCAATGCACTGACATTGTTGG 5978      TG   A      CCC
                                TCGG  GTG TGGTGCAT   GAG
                                ||||  ||| ||||||||   |||
                                GGTT  TAC GTCACGTA   CTC
                                  GT   A       A__
GAM342  MME      5'  CTTGGGGAGTTATGTTTTGTTA 8030        TG TGGT__  AT
            CCGA                   TCGGTGG  A     GC  CCCGAG
                                |||||||  |     ||  ||||||
```

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                                AGCCATT  T     TG  GGGTTC
                                    GT TTGTAT  AG
GAM342  MMP19    3'  GGATGCACTGTCGTCCCCGG   11634      T  _
                                TCGG GG TGATGGTGCATCC
                                |||| || ||||||||||||
                                GGCC CC GCTGTCACGTAGG
                                  _  T
GAM342  MMP19    3'  GGATGCACTGTCGTCCCCGG   11635      T  _
                                TCGG GG TGATGGTGCATCC
                                |||| || ||||||||||||
                                GGCC CC GCTGTCACGTAGG
                                  _  T
GAM342  MOCS2    3'  TTTGTTAAACTATTATTATTGA 16971            ___   TCCCGAG
                                TCGGTGGTGATGGT   GCA
                                ||||||||||||||   |||
                                AGTTATTATTATCA   TGT
                                        AAT   TT   G
GAM342  MTCP1    5'  TTTGGGGCAGGCGTGGCCGTCG 27245     GT   G   G_   AT
            G                    TCG  GGT ATG  TGC  CCCGAG
                                |||  ||| |||  |||  ||||||
                                GGC  CCG TGC  ACG  GGGTTT
                                  TG   G   GG   __
GAM342  MUCDHL   3'  TGGGTGCGCTGCTGCTGCTGG  88652      TG  GA      T
                                TCGG  GT  TGGTGCA CCCG
                                ||||  ||  ||||||| ||||
                                GGTC  CG  GTCGCGT GGGT
                                  GT  TC     _
GAM342  MYC      5'  TCGCGGCCGCCACCGCCGG   11730         A   TGCAT  _
                                TCGGTGGTG TGG    CC CGA
                                ||||||||| |||    || |||
                                GGCCGCCAC GCC    GG GCT
                                     C   _____  C
GAM342  MYO6     3'  GTGTGCTGTTAGTATTGA    18444       G     TG
                                TCGGTG TGATGG  CAT
                                |||||| ||||||  |||
                                AGTTAT ATTGTC  GTG
                                    G     GT
GAM342  NAV2     3'  CTCGGGAAAGGATCATCGCCGT 60794    GG        GCA_
            TGA                   TC  TGGTGATGGT    TCCCGAG
                                ||  ||||||||||   |||||||
                                AG  GCCGCTACTA   AGGGCTC
                                  TT        GGAA
GAM342  NFATC2   5'  CTCGCGCCGCCGTCGCCGCCG  25626           CATCC
                                CGGTGGTGATGGTG    CGAG
                                ||||||||||||||    ||||
                                GCCGCCGCTGCCGC    GCTC
                                        CGC__
GAM342  NIF3L1   3'  TTCGAGGGTATCATCATTTCCG 61700      TG        AT  _
            G                    TCGG  GTGATGGTGC  CC CGAG
                                ||||  ||||||||||  || ||||
```

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                                GGCC  TACTACTATG  GG GCTT
                                  TT         __  A
GAM342  NLGN3    3'  TTGGAACTGCACCACCGA    39123          A    GCATC
                                TCGGTGGTG TGGT     CCGA
                                ||||||||| ||||     ||||
                                AGCCACCAC GTCA     GGTT
                                      _    A____
GAM342  NOL3     3'  CTCGGTCCAGCCCAGTACCGCT 15463          A   T  ATC_
            GG                    TCGGTGGTG TGG GC    CCGAG
                                ||||||||| ||| ||    |||||
                                GGTCGCCAT ACC CG    GGCTC
                                     G   _  ACCT
GAM342  NRG1     3'  CTTGGGATTGTGCTTACTGTTG 16903     TG   AT  TG  _
                                CGG  GTG  GG  CA TCCCGAG
                                |||  |||  ||  || |||||||
                                GTT  CAT  TC  GT AGGGTTC
                                  GT   __  GT  T
GAM342  NSF      3'  CTCTACTAGCACCATCACCCTT 63749      T         ATCCC
            GA                    TCGG GGTGATGGTGC     GAG
                                |||| ||||||||||     |||
                                AGTT CCACTACCACG     CTC
                                  C          ATCAT
GAM342  OSM      3'  TTGGGTCCTCGCTGCTGG    40451      TG    T  TGCAT
                                TCGG  GTGA GG     CCCGA
                                ||||  |||| ||     |||||
                                GGTC  CGCT CC     GGGTT
                                  GT    _  T____
GAM342  OSR1     3'  CTTGGGATATCTCTTTACCACT 18835          T  TGC
            GA                    TCGGTGGTGA GG   ATCCCGAG
                                |||||||||| ||   ||||||||
                                AGTCACCATT CT   TAGGGTTC
                                     T  CTA
GAM342  PAX9     5'  TGCGCTGTCGCTCACCGA    21666       _
                                TCGGTG GTGATGGTGCA
                                |||||| ||||||||||
                                AGCCAC CGCTGTCGCGT
                                    T
GAM342  PCDH9    5'  GATTGCCATCATCGCCGG     83694             C
                                TCGGTGGTGATGGTG ATC
                                ||||||||||||||| |||
                                GGCCGCTACTACCGT TAG
                                                _
GAM342  PCDHA1   3'  CTTGGGAGTTTGTGGCCACTGG 49413         G TG T  A
                                TCGGTGGT A  G GC TCCCGAG
                                |||||||| |  | || |||||||
                                GGTCACCG T  T TG AGGGTTC
                                     G GT _  _
GAM342  PCDHA10  3'  CTTGGGAGTTTGTGGCCACTGG 38790         G TG T  A
                                TCGGTGGT A  G GC TCCCGAG
                                |||||||| |  | || |||||||
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                                GGTCACCG T  T TG AGGGTTC
                                    G GT _  _
GAM342  PCDHA11  3'  CTTGGGAGTTTGTGGCCACTGG 49861       G TG T  A
                                TCGGTGGT A  G GC TCCCGAG
                                |||||||| |  | || |||||||
                                GGTCACCG T  T TG AGGGTTC
                                    G GT _  _
GAM342  PCDHA12  3'  CTTGGGAGTTTGTGGCCACTGG 38798       G TG T  A
                                TCGGTGGT A  G GC TCCCGAG
                                |||||||| |  | || |||||||
                                GGTCACCG T  T TG AGGGTTC
                                    G GT _  _
GAM342  PCDHA13  3'  CTTGGGAGTTTGTGGCCACTGG 49869       G TG T  A
                                TCGGTGGT A  G GC TCCCGAG
                                |||||||| |  | || |||||||
                                GGTCACCG T  T TG AGGGTTC
                                    G GT _  _
GAM342  PCDHA2   3'  CTTGGGAGTTTGTGGCCACTGG 38805       G TG T  A
                                TCGGTGGT A  G GC TCCCGAG
                                |||||||| |  | || |||||||
                                GGTCACCG T  T TG AGGGTTC
                                    G GT _  _
GAM342  PCDHA3   3'  CTTGGGAGTTTGTGGCCACTGG 49806       G TG T  A
                                TCGGTGGT A  G GC TCCCGAG
                                |||||||| |  | || |||||||
                                GGTCACCG T  T TG AGGGTTC
                                    G GT _  _
GAM342  PCDHA4   3'  CTTGGGAGTTTGTGGCCACTGG 38813       G TG T  A
                                TCGGTGGT A  G GC TCCCGAG
                                |||||||| |  | || |||||||
                                GGTCACCG T  T TG AGGGTTC
                                    G GT _  _
GAM342  PCDHA5   3'  CTTGGGAGTTTGTGGCCACTGG 49813       G TG T  A
                                TCGGTGGT A  G GC TCCCGAG
                                |||||||| |  | || |||||||
                                GGTCACCG T  T TG AGGGTTC
                                    G GT _  _
GAM342  PCDHA6   3'  CTTGGGAGTTTGTGGCCACTGG 38821       G TG T  A
                                TCGGTGGT A  G GC TCCCGAG
                                |||||||| |  | || |||||||
                                GGTCACCG T  T TG AGGGTTC
                                    G GT _  _
GAM342  PCDHA7   3'  CTTGGGAGTTTGTGGCCACTGG 49826       G TG T  A
                                TCGGTGGT A  G GC TCCCGAG
                                |||||||| |  | || |||||||
                                GGTCACCG T  T TG AGGGTTC
                                    G GT _  _
GAM342  PCDHA8   3'  CTTGGGAGTTTGTGGCCACTGG 38829       G TG T  A
                                TCGGTGGT A  G GC TCCCGAG
                                |||||||| |  | || |||||||
```

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                                GGTCACCG T  T TG AGGGTTC
                                    G GT _  _
GAM342  PCDHA9   3'  CTTGGGAGTTTGTGGCCACTGG 49842       G TG T  A
                                TCGGTGGT A  G GC TCCCGAG
                                |||||||| |  | || |||||||
                                GGTCACCG T  T TG AGGGTTC
                                    G GT _  _
GAM342  PCDHAC1  3'  CTTGGGAGTTTGTGGCCACTGG 38780       G TG T  A
                                TCGGTGGT A  G GC TCCCGAG
                                |||||||| |  | || |||||||
                                GGTCACCG T  T TG AGGGTTC
                                    G GT _  _
GAM342  PCDHAC2  3'  CTTGGGAGTTTGTGGCCACTGG 49877       G TG T  A
                                TCGGTGGT A  G GC TCCCGAG
                                |||||||| |  | || |||||||
                                GGTCACCG T  T TG AGGGTTC
                                    G GT _  _
GAM342  PCDHB11  3'  CTCCCAAAGTGCTGTGATTACC 38922       G   TG ATCCC
          GG                    TCGGTGGT ATGG  C    GAG
                                |||||||| ||||  |    |||
                                GGCCATTA TGTC  G    CTC
                                    G   GT AAACC
GAM342  PIK3CG   3'  TGACTATCTTACTATTGA    12126       __    G
                                TCGGTGGT  GATGGT CA
                                ||||||||  |||||| ||
                                AGTTATCA  CTATCA GT
                                    TT    _
GAM342  PLXNA1   3'  TGGGCCCGTTGCCACCGA    72775      TG   T  ATC
                                TCGGTGG  ATGG GC   CCG
                                |||||||  |||| ||   |||
                                AGCCACC  TGCC CG   GGT
                                   GT   _ ___
GAM342  PPP1R12A 3'  CTTGGAGACTGTCATTTTCGG  11752     TG      GCATC
                                TCGG  GTGATGGT    CCGAG
                                ||||  ||||||||    |||||
                                GGCT  TACTGTCA    GGTTC
                                  TT      GA___
GAM342  PPP1R14B 3'  TTTGGGGTTTTTTATTGTTATT 57703     TG   TGC
                                GGTGG  ATGG   ATCCCGAG
                                |||||  ||||   ||||||||
                                TTATT  TATT   TGGGGTTT
                                   GT   TTT
GAM342  PPP1R8   5'  GTGTGACTTTACCATTGA    57511        T  _
                                TCGGTGGTGA GGT GCAT
                                |||||||||| ||| ||||
                                AGTTACCATT TCA TGTG
                                      _  G
GAM342  PPP1R8   5'  GTGTGACTTTACCATTGA    57512        T  _
                                TCGGTGGTGA GGT GCAT
                                |||||||||| ||| ||||
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                                AGTTACCATT TCA TGTG
                                      _  G
GAM342  PRKY    3'  TTTGGGATGTGTTGTTCGCCA  12392      _ TG TG
                                TGGTG A  G  CATCCCGAG
                                |||||| |  |  |||||||||
                                ACCGC T  T  GTAGGGTTT
                                   T GT GT
GAM342  PTPRG   5'  CTCGGGCTGTGCTGCGCTGCCG 12612     TG   A   TG  T
          A                      TCGG  GTG TGG  CA CCCGAG
                                |||| |||  |||  || ||||||
                                AGCC  CGC GTC  GT GGGCTC
                                  GT   _  GT  C
GAM342  PTPRM   3'  TCGTTATTGTTACAGCTGA   12622      G   TG   CATCC
                                TCGGT GTGA  GTG    CGA
                                ||||| ||||  |||    |||
                                AGTCG CATT  TAT    GCT
                                   A   GT   T____
GAM342  RAB1A   3'  TTGGGATATGGCTGCTGG    70783     TG  G  GGTGC
                                TCGG  GT AT    ATCCCGA
                                ||||  || ||    |||||||
                                GGTC  CG TA    TAGGGTT
                                  GT  G  _____
GAM342  RAP1    3'  TTTGTTGTGTTGTTTTCATTGT 39112     TG   TGGT_   CC
          TGA                     TCGG  GTGA    GCAT  CGAG
                                ||||  ||||    ||||  ||||
                                AGTT  TACT    TGTG  GTTT
                                  GT    TTTGT    TT
GAM342  RARA    3'  GGGTGCACCTGTTACTGTTGG  8257      TG    _
                                TCGG  GTGAT GGTGCATCC
                                ||||  ||||| |||||||||
                                GGTT  CATTG CCACGTGGG
                                  GT    T
GAM342  RPIP8   5'  TGCTCTGGCATCGCCGCCGG   22930          G ___
                                TCGGTGGTGATG T   GCA
                                |||||||||||| |   |||
                                GGCCGCCGCTAC G   CGT
                                       G TCT
GAM342  RUNX3   3'  TTTGTGACATATTGTCATGCTG 16366      G   TG   CA  C
          A                      TCGGT GTGA  GTG  TC CGAG
                                ||||| ||||  |||  || ||||
                                AGTCG TACT  TAT  AG GTTT
                                   _   GT   AC  T
GAM342  RXRA    3'  CTTGGGAACTTTGTCGTTTCCG 12919     TG    TG TGCA
          G                      TCGG  GTGA  G   TCCCGAG
                                ||||  ||||  |   |||||||
                                GGCC  TGCT  T    AGGGTTC
                                  TT    GT TCA_
GAM342  SCAP1   3'  CTTGGGAGGAGGACATTACTGG 14947         ATGGTGCA
                                TCGGTGGTG       TCCCGAG
                                |||||||||       |||||||
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                                GGTCATTAC       AGGGTTC
                                     AGGAGG__
GAM342  SCD      3'  CTCCAACCACTGTGCCACTGA  18591         G     CATCCC
                                TCGGTGGT ATGGTG      GAG
                                |||||||| ||||||      |||
                                AGTCACCG TGTCAC      CTC
                                     _      CAAC__
GAM342  SCN1B    5'  CTCGCCCCGCTATTAATACCGG 8294         G       CATCC
                                TCGGTG TGATGGTG    CGAG
                                |||||| ||||||||    ||||
                                GGCCAT ATTATCGC    GCTC
                                   A       CCC__
GAM342  SDC1     3'  TTGGGGGGGGTGGCCGCTGA   12993         G  GGTGCA
                                TCGGTGGT AT     TCCCGA
                                |||||||| ||     ||||||
                                AGTCGCCG TG     GGGGTT
                                     G  GG____
GAM342  SERPINE2 3'  GTGCAGTGTGCCTGTCACTACT 75432          _ TG   CC  AG
           GG                     TCGGTGGTGAT GG  CAT  CG
                                |||||||||||  ||  |||  ||
                                GGTCATCACTG CC  GTG  GT
                                      T  GT   AC  GT
GAM342  SLC11A3  3'  CTCATGTTATCATCATTAGTGA 28167     G         _  CCC
                                TCG TGGTGATGGTG CAT   GAG
                                ||| |||||||||| |||   |||
                                AGT ATTACTACTAT GTA   CTC
                                  G         T  ___
GAM342  SLC20A2  5'  TGGAATGTGTTTTACCGCTGA  23123          T  TG   C
                                TCGGTGGTGA GG  CAT CCG
                                |||||||||| ||  ||| |||
                                AGTCGCCATT TT  GTA GGT
                                      _ GT   A
GAM342  SMURF1   3'  CACTGTTTTTATCACTGA    94043         ___
                                TCGGTGGT   GATGGTG
                                ||||||||   |||||||
                                AGTCACTA   TTGTCAC
                                     TTT
GAM342  SORCS3   3'  TTTGATGATTACTATTACTATT 31075           __   CCGAG
                                GGTGGTGATGGTG  CATC
                                ||||||||||||  ||||
                                TTATCATTATCAT  GTAG
                                       TA    TTT
GAM342  STAM     5'  CTCGGCTCCTTGCTGTTGCCGC 14419       TG    GCATC_
           CG                     CGGTGG  ATGGT     CCGAG
                                ||||||  |||||     |||||
                                GCCGCC  TGTCG     GGCTC
                                   GT    TTCCTC
GAM342  STARD5   3'  AGAGAATCATCATCGCCACTGA 48315            CA  CCGAG
                                TCGGTGGTGATGGTG  TC
                                ||||||||||||||  ||
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                                AGTCACCGCTACTAC  AG
                                      TA  AGAT
GAM342  STIM1    3'  CTTGGGTCCTTCATTATTATT  60782          TGCAT
                                GGTGGTGATGG    CCCGAG
                                ||||||||||    ||||||
                                TTATTATTACT    GGGTTC
                                      TCCT_
GAM342  SVIL     5'  TTTGGGATGTAGCCTTTACC  41710      T  _
                                GGTGA GG TGCATCCCGAG
                                ||||| || ||||||||||
                                CCATT CC ATGTAGGGTTT
                                   T  G
GAM342  TAF7L    3'  TTTGGGAATTATTATTATTA  46516          CA
                                TGGTGATGGTG  TCCCGAG
                                ||||||||||  |||||||
                                ATTATTATTAT  AGGGTTT
                                      TA
GAM342  TAP2     3'  TTTGAGACGTCAATCACCACTG 6780           GGT  A  C
           A                    TCGGTGGTGAT   GC TC CGAG
                                ||||||||||   || || ||||
                                AGTCACCACTA   TG AG GTTT
                                      AC_  C  A
GAM342  THBD     3'  TTTGTCCCAGGTCCTCACTACC 6279          _____  TG  TCCCGAG
           GG                     TCGGTGGTGA    TGG  CA
                                |||||||||    |||  ||
                                GGCCATCACT    ACC  GT
                                     CCTGG   CT  TT   G
GAM342  TLR5     5'  CATTGTATGCACTGTCACTCTG 13780      T          CCCGAG
           A                    TCGG GGTGATGGTGCAT
                                ||||  ||||||||||||
                                AGTC TCACTGTCACGTA
                                  _          TGTTACT
GAM342  TNFSF4   3'  TTCAAGATGCATTGTTTCTATT 13916       T  TG      CC
           GG                     TCGGTGG GA  GTGCATC  GAG
                                |||||||  ||  |||||||  |||
                                GGTTATC TT  TACGTAG  CTT
                                    T  GT      AA
GAM342  TNS      5'  GGTGCCCATCACCACTGA    42952           T
                                TCGGTGGTGATGG GCATC
                                |||||||||||| |||||
                                AGTCACCACTACC CGTGG
                                                _
GAM342  TRIM9    3'  TTTGGGAGAATGAATCTATCAC 31466        _  GGTGCA
           TGA                    TCGGTGGT GAT     TCCCGAG
                                ||||||||  |||     |||||||
                                AGTCACTA CTA     AGGGTTT
                                    T   AGTAAG
GAM342  UBQLN1   5'  TGCGCCCGTTGCTACTGA    26479        TG   _
                                TCGGTGG  ATGG TGCA
                                |||||||  ||||  ||||
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                                AGTCATC  TGCC GCGT
                                    GT    C
GAM342  UBQLN3   3'  TGTACCACTATACCACTGG   34373         A__
                                TCGGTGGTG   TGGTGCA
                                |||||||||   |||||||
                                GGTCACCAT   ACCATGT
                                     ATC
GAM342  VCP      5'  TTCGCCCGACGCCTCGCTGCCG 75891      TG    T    CATCC
            G                    TCGG  GTGA GGTG     CGAG
                                ||||  |||| ||||     ||||
                                GGCC  CGCT CCGC     GCTT
                                  GT    _    AGCCC
GAM342  WBSCR1   3'  TTTGGTCACCAGCCGTCATCCT 42485      T       GCATC_
            GG                    TCGG GGTGATGGT      CCGAG
                                |||| |||||||||      |||||
                                GGTC CTACTGCCG      GGTTT
                                  _        ACCACT
GAM342  WHSC1L1  3'  TTCGCCAATCATCATTATTGG  35507           GCATCC
                                TCGGTGGTGATGGT     CGAG
                                ||||||||||||||     ||||
                                GGTTATTACTACTA     GCTT
                                       ACC___
GAM342  WNT11    3'  TTTGGGATGTGGAAGCTACAGA 17328    G    GATGGT
                                TC GTGGT     GCATCCCGAG
                                || |||||     ||||||||||
                                AG CATCG     TGTAGGGTTT
                                 A    AAGG__
GAM342  YWHAE    3'  TTTGGAAACTCCCCATTGTCAC 23139       TG    TGCATC_
            TGA                   TCGGTGG  ATGG      CCGAG
                                |||||||  ||||      |||||
                                AGTCACT  TACC      GGTTT
                                    GT    CCTCAAA
GAM342  ZNF274   5'  GACGCACTTCGCCGCCGG    33340         T    A
                                TCGGTGGTGA GGTGC TC
                                |||||||||| ||||| ||
                                GGCCGCCGCT TCACG AG
                                      _     C
GAM342  ABCA8    3'  GTGTGCCATTTTCACTGG    24136        T    TG
                                TCGGTGG GATGG  CAT
                                ||||||| |||||  |||
                                GGTCACT TTACC  GTG
                                    T    GT
GAM342  AHCYL1   5'  CTTGTGGCCACCGTCGCTGTCC 22773     _        CAT  _
            G                    CGG TGGTGATGGTG   CC CGAG
                                ||| ||||||||||   || ||||
                                GCC GTCGCTGCCAC   GG GTTC
                                  T         C__  T
GAM342  AK5      3'  CTTGGAATACTGTCATTATGG  24930   G         CATC
                                C GTGGTGATGGTG    CCGAG
                                | ||||||||||||    |||||
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                                G TATTACTGTCAT    GGTTC
                                 G          AA__
GAM342  AKAP12    3'  ATGTTCTATTGTCATTGG    58473        TG    T
                                TCGGTGG  ATGG GCAT
                                |||||||  |||| ||||
                                GGTTACT  TATC TGTA
                                    GT    T
GAM342  ALY       3'  TTGGGATAAATTTTACTGG   20519        TGAT   GC
                                TCGGTGG   GGT  ATCCCGA
                                |||||||   |||  |||||||
                                GGTCATT   TTA  TAGGGTT
                                    ____  AA
GAM342  AMOT      3'  TTTGGGGTGCAGAAGGGTACTG 56550       GTGATGG
              G                  TCGGTG      TGCATCCCGAG
                                |||||||      ||||||||||||
                                GGTCAT      ACGTGGGGTTT
                                   GGGAAG_
GAM342  AP1S2     5'  TTCGCCGCCGCCGCCGCCGCCG 15351         A    CATCC
              G                  TCGGTGGTG TGGTG    CGAG
                                |||||||| |||||    ||||
                                GGCCGCCGC GCCGC    GCTT
                                    C    CGCC_
GAM342  ASE-1     3'  TTTAAAATGTACCATTATTATT 25000              CCCGAG
              GA                   TCGGTGGTGATGGTGCAT
                                |||||||||||||||||
                                AGTTATTATTACCATGTA
                                          AAATTT
GAM342  bA430M15.1 3'  TGCATGTGTGATGTTATCATTG 77529           GT   CCCGAG
              G                  TCGGTGGTGATG  GCAT
                                ||||||||||||  ||||
                                GGTTACTATTGT  TGTG
                                      AG   TACGTT
GAM342  BRP44I    5'  TTCGGGCTGGCTCGCCGTCGGC 32741      TG _     ___ T
              TGCCGG                TCGG  GT GATGGTG   CA CCCGAG
                                ||||  || |||||||   || ||||||
                                GGCC  CG CTGCCGC   GT GGGCTT
                                  GT  G      TCG  C
GAM342  BTN3A1    3'  CTCATTATCATCATTATTATTG 23890            C  CCC
                                CGGTGGTGATGGTG AT   GAG
                                |||||||||||||| ||   |||
                                GTTATTATTACTAC TA   CTC
                                      _  TTA
GAM342  C12orf3   3'  CTTGTACTTCACCATCATTTCT 40164      TG       CATCC
              GA                   TCGG  GTGATGGTG    CGAG
                                ||||  |||||||||    ||||
                                AGTC  TACTACCAC    GTTC
                                  TT        TTCAT
GAM342  C20orf163 5'  CTTGCGGTCACCATCATTGCC  55803    TG       C   C
                                GG  GTGATGGTG ATC CGAG
                                ||  ||||||||| ||| ||||
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                                CC  TACTACCAC TGG GTTC
                                 GT       _  C
GAM342  C20orf18  5'  CTCGGCGTCCGCCGCCGCCGG  49178       GAT   C  C
                                TCGGTGGT   GGTG AT CCGAG
                                ||||||||   |||| || |||||
                                GGCCGCCG   CCGC TG GGCTC
                                    ___    C  C
GAM342  C20orf72  3'  TTTGGGAACATATATTGCTG   54610    TG   ATG   CA
                                CGG  GTG   GTG  TCCCGAG
                                |||  |||   |||  |||||||
                                GTC  TAT   TAC  AGGGTTT
                                  GT   A__   A_
GAM342  C22orf4   5'  CTCGGGGTGTCTGGGCCGCGGG 61272    G    GA   T
                                TC GTGGT  TGG GCATCCCGAG
                                || |||||  ||| ||||||||||
                                GG CGCCG  GTC TGTGGGGCTC
                                 G    G_  _
GAM342  C5orf3    5'  CACATATCGCGTCACTGA    38592       __     _
                                TCGGTG  GTGATG GTG
                                ||||||  ||||||  |||
                                AGTCAC  CGCTAT CAC
                                   TG     A
GAM342  C5orf4    5'  CTTGGCCCTCATCATCACCACC 51490           CATC
                                GGTGGTGATGGTG   CCGAG
                                ||||||||||||   |||||
                                CCACCACTACTAC   GGTTC
                                       TCCC
GAM342  C5orf4    3'  CTTGGCCCTCATCATCACCACC 51491           CATC
                                GGTGGTGATGGTG   CCGAG
                                ||||||||||||   |||||
                                CCACCACTACTAC   GGTTC
                                       TCCC
GAM342  C5orf5    5'  CTCGCCCTCTTGCCGTCGCCGC 33943    G        GCATCC_
            GGG                   TC GTGGTGATGGT      CGAG
                                || ||||||||||      ||||
                                GG CGCCGCTGCCG      GCTC
                                 G         TTCTCCC
GAM342  CAMKK1    3'  TTTGGTTGGCATCGTTGTTTTT 51156     TG TG      ATC
            GA                   TCGG  G  ATGGTGC   CCGAG
                                ||||  |  |||||||   |||||
                                AGTT  T  TGCTACG   GGTTT
                                  TT GT      GTT
GAM342  CDC14A    3'  TTTGGGTATGAGGTTGTTGTTG 14788    TG TG  GG G_  _
            CC                   GG  G  AT  T  CAT CCCGAG
                                ||  |  ||  |  ||| ||||||
                                CC  T  TG  G  GTA GGGTTT
                                 GT GT  TT GA   T
GAM342  CHK       3'  CTCCATCCACCTCATCACTGG  8886          T   C  CCC
                                TCGGTGGTGA GGTG AT   GAG
                                |||||||||| |||| ||   |||
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                                GGTCACTACT CCAC TA   CTC
                                      _   C  C__
GAM342  CHK     3'  TTGGGTGGCTCACTACTGA   8888         TGGT  AT
                                TCGGTGGTGA   GC  CCCGA
                                ||||||||||   ||  |||||
                                AGTCATCACT   CG  GGGTT
                                     _____  GT
GAM342  CHODL   3'  TTCGGGGTTTGGGATTGACACT 46887      GT   GG  C
           GG                    TCGGTG  GAT  TG ATCCCGAG
                                ||||||  |||  || ||||||||
                                GGTCAC  TTA  GT TGGGGCTT
                                   AG   GG  T
GAM342  CLGN    3'  ATGCATACATTGCTATTGA   16414       TG  _
                                TCGGTGG  ATG GTGCAT
                                |||||||  ||| ||||||
                                AGTTATC  TAC TACGTA
                                    GT   A
GAM342  CLGN    5'  CTTGGACATCTGAGCTGTCACT 16415     TG      G  TC___
           GCCGA                  TCGG  GTGATGGT CA    CCGAG
                                ||||  |||||||| ||    |||||
                                AGCC  CACTGTCG GT    GGTTC
                                  GT       A  CTACA
GAM342  CMRF-35H 3'  TGTCCTGCCTCGCCATCGG   70936         T  ___
                                TCGGTGGTGA GGT   GCA
                                |||||||||| |||   |||
                                GGCTACCGCT CCG   TGT
                                      _  TCC
GAM342  CNNM3   3'  TGCCAACCTATCGCTGCTGG   34810     TG   _  __
                                TCGG  GTGAT GGT  GCA
                                ||||  ||||| |||  |||
                                GGTC  CGCTA CCA  CGT
                                  GT    T   AC
GAM342  CXorf2  5'  TTCTGGATTGCATTGATGCTAT 9627         A     _  C
           TGA                   TCGGTGGTG TGGTGCA TCC GAG
                                ||||||||| ||||||| ||| |||
                                AGTTATCGT GTTACGT AGG CTT
                                     A      T  T
GAM342  DDM36   3'  CTCGGGTGTCACTCACTGTTGA 40920     TG   TG  _ T
                                TCGG  GTGA  GTG CA CCCGAG
                                ||||  ||||  ||| || ||||||
                                AGTT  CACT  CAC GT GGGCTC
                                  GT   __   T _
GAM342  DDX12   3'  TTTGGCCCCGCCATTGCTGCTG 60428    TG TG    CATC
                                CGG  G  ATGGTG   CCGAG
                                |||  |  ||||||   |||||
                                GTC  C  TACCGC   GGTTT
                                  GT GT    CCC_
GAM342  DEGS    3'  GCTTGTGACTTGTGTATTATCG 14802      GT      _____  C
           TCATTGA                TCGGTG  GATGGTGCA   TC CGAG   C
                                ||||||  |||||||||   || ||||   |
```

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                                AGTTAC  CTATTATGT   AG GTTC   G
                                   TG       GTTC  T
GAM342  DKFZp434G179 3'  TTTGATGCTGCTATTGCTATAG 80895    G   TG    _    CCGAG
           A                    TC GTGG  ATGGT GCATC
                                || ||||  ||||| |||||
                                AG TATC  TATCG CGTAG
                                 A   GT    T    TTT
GAM342  DKFZp434L0850 3'  TTCGGGGTGCAGCTCTGCT   34525    TG TGAT  _
                                GG  G   GG TGCATCCCGAG
                                ||  |   || ||||||||||
                                TC  C   TC ACGTGGGGCTT
                                 GT _____  G
GAM342  DKFZP564B1162 3'  TTTGGCATTGTGTTATCATCG  49353        TG  TC_
                                TGGTGATGG  CA   CCGAG
                                |||||||||  ||   |||||
                                GCTACTATT  GT   GGTTT
                                      GT  TAC
GAM342  DKFZP564D172 3'  TGGATTGCATTATTATTGTT   50199    TG        TC   AG
                                GG  GTGATGGTGCA  CCG
                                ||  ||||||||||  |||
                                TT  TATTATTACGT  GGT
                                 GT         TA   C
GAM342  DKFZp761H2121 5'  TGGATGTGCATTATTAATGCTG 57181      GG        C_   AG
           G                    TCGGT  TGATGGTGCAT  CCG
                                |||||  ||||||||||  |||
                                GGTCG  ATTATTACGTG  GGT
                                   TA         TA   C
GAM342  DRIL2    3'  CTCGCCTGGCCACACCGTTGG  22349    GG    A    G  TCC
                                TC  TGGTG TGGT CA   CGAG
                                ||  ||||| |||| ||   ||||
                                GG  GCCAC ACCG GT   GCTC
                                 TT    _    _ CC_
GAM342  EIF3S1   3'  ATGTTGTCACCATAGA     63864    G       GT
                                TC GTGGTGATG  GCAT
                                || |||||||||  ||||
                                AG TACCACTGT  TGTA
                                 A       __
GAM342  EMILIN-2  3'  CTTGGCTCACCATTGCCGCC   50254      TG     CATC
                                GGTGG  ATGGTG    CCGAG
                                |||||  ||||||    |||||
                                CCGCC  TACCAC    GGTTC
                                   GT     TC__
GAM342  EML2     3'  TTCGGGAGATGTCTATTGCCGA 25129     TG  _   GTGCA
                                TCGG  GT GATG    TCCCGAG
                                ||||  || ||||    |||||||
                                AGCC  TA CTGT    AGGGCTT
                                  GT  T    AG___
GAM342  EVI5     3'  TGCCAAATCTTTACCACTGA   20220          T   ___
                                TCGGTGGTGA GGT   GCA
                                |||||||||| |||   |||
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                                AGTCACCATT CTA   CGT
                                     T   AAC
GAM342  FASTK    5'  CTTGTCCAAGGTCACGCCGCTG 22967         A   TGCATCC
            G                    TCGGTGGTG TGG      CGAG
                                 ||||||||| |||      ||||
                                 GGTCGCCGC ACT      GTTC
                                      _  GGAACCT
GAM342  FEZ2     3'  CTTGCTGCTTGTTTCACCACTG 18779          TGGT_  TCC
            G                    TCGGTGGTGA    GCA   CGAG
                                 ||||||||||    |||   ||||
                                 GGTCACCACT    CGT   GTTC
                                      TTGTT   C__
GAM342  FHR-4    5'  TGCATTACTATACTACTGA   22910         A__
                                 TCGGTGGTG   TGGTGCA
                                 |||||||||   |||||||
                                 AGTCATCAT   ATTACGT
                                      ATC
GAM342  FLJ10101  3'  CTTGTCCTGTGCCGGCACTGCT 45598     TG   A   TG  TCC
            GG                     TCGG  GTG TGG  CA   CGAG
                                   ||||  ||| |||  ||   ||||
                                   GGTC  CAC GCC  GT   GTTC
                                     GT   G   GT  CCT
GAM342  FLJ10154  3'  CTTGTGATACTGTCGCTCTTGA 36328      T       GC   C
                                 TCGG GGTGATGGT  ATC CGAG
                                 |||| |||||||||  ||| ||||
                                 AGTT TCGCTGTCA  TAG GTTC
                                   C        __   T
GAM342  FLJ10379  3'  TTTGAATTGTACCGTCTTTGTT 36571      TG T       TCC
            GA                     TCGG  G GATGGTGCA   CGAG
                                   ||||  | |||||||||   ||||
                                   AGTT  T CTGCCATGT   GTTT
                                     GT T        TAA
GAM342  FLJ10514  3'  CGGGCTGTTATTGCTGG     36694      TG      TGCAT
                                 TCGG  GTGATGG    CCCG
                                 ||||  |||||||    ||||
                                 GGTC  TATTGTC    GGGC
                                   GT     _____
GAM342  FLJ10525  3'  TTTGGGGTCACCTAGCCATTGA 36727         GAT    C
                                 TCGGTGGT   GGTG ATCCCGAG
                                 ||||||||   |||| ||||||||
                                 AGTTACCG   CCAC TGGGGTTT
                                      AT_   _
GAM342  FLJ10546  3'  TGTGTATTGTACTTATTGCCAC 60185        TG  _    TCCCGAG
            TGG                    TCGGTGG  ATG GTGCA
                                   |||||||  ||| |||||
                                   GGTCACC  TAT CATGT
                                       GT   T    TATGTGTT
GAM342  FLJ10656  3'  CTTGGGGTGCATTTTCTCACAG 36908    G    T  TG
            A                      TC GTGG GA  GTGCATCCCGAG
                                   || |||| ||  ||||||||||||
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                                AG CACT CT  TACGTGGGGTTC
                                 A   _ TT
GAM342  FLJ10922  3' CTCGATCAGCCATCACTAACGG 37400    G       GCATCC
                                TCG TGGTGATGGT     CGAG
                                ||| ||||||||||     ||||
                                GGC ATCACTACCG     GCTC
                                  A        ACTA__
GAM342  FLJ10922  3' TTTGGGCAGCCGGTTGTCGCTG 37410       TG _  GCAT
                                CGGTGG  AT GGT    CCCGAG
                                ||||||  || |||    ||||||
                                GTCGCT  TG CCG    GGGTTT
                                   GT  G   AC__
GAM342  FLJ10925  5' TCGGGTTCGTTGCCCCGG    37414     T  TG    TGCAT
                                TCGG GG  ATGG    CCCGA
                                |||| ||  ||||    |||||
                                GGCC CC  TGCT    GGGCT
                                  _ GT   T____
GAM342  FLJ11078  3' TTTGGGTCAACATTGCTACGGA 37597    G   TG   G  CAT
                                TC GTGG  ATG TG   CCCGAG
                                || ||||  ||| ||   ||||||
                                AG CATC  TAC AC   GGGTTT
                                 G   GT   A  T__
GAM342  FLJ11210  3' TGTTTGTATTATTACTGA    60321          GT_
                                TCGGTGGTGATG   GCA
                                ||||||||||||   |||
                                AGTCATTATTAT   TGT
                                       GTT
GAM342  FLJ11996  3' TTGAAAGTGTATTATTACTAAT 47073     G          CCCGAG
           GA                    TCG TGGTGATGGTGCAT
                                ||| ||||||||||||||
                                AGT ATCATTATTATGTG
                                  A           AAAGTTT
GAM342  FLJ12409  3' CTGGATGTGACTGTCATTGCTG 47768      TG      _     CGAG
           G                     TCGG  GTGATGGT GCATCC
                                ||||  |||||||| ||||||
                                GGTC  TACTGTCA TGTAGG
                                  GT       G     TC
GAM342  FLJ12484  3' TTTGACAATCACTGTGGCTGTT 70233     TG  G     CATCC
           GG                    TCGG  GT ATGGTG    CGAG
                                ||||  || ||||||    ||||
                                GGTT  CG TGTCAC    GTTT
                                  GT  G     TAACA
GAM342  FLJ12700  3' CTCAAATCCATCATCATCAACT 46655      _        C  CCC
           GA                    TCGGT GGTGATGGTG AT   GAG
                                ||||| |||||||||| ||   |||
                                AGTCA CTACTACTAC TA   CTC
                                  A         C  AA_
GAM342  FLJ12934  3' AAATAATGCAGCTATTACCACT 43486           _    CCCGAG
           GG                    TCGGTGGTGATGG TGCAT
                                |||||||||||| |||||
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                                GGTCACCATTATC ACGTA
                                      G    ATAAAT
GAM342  FLJ13187  5'  TTCGCCTTCGCTGTCGCCGCCG 45167           CATCC
                                CGGTGGTGATGGTG    CGAG
                                |||||||||||||    ||||
                                GCCGCCGCTGTCGC    GCTT
                                      TTCC_
GAM342  FLJ13189  3'  CTTGGGAATGATTTCATATTGT 46497     TG   A   TG_  _
          TGA                   TCGG  GTG TGG   CAT CCCGAG
                                ||||  ||| |||   ||| ||||||
                                AGTT  TAT ACT   GTA GGGTTC
                                  GT   _   TTA   A
GAM342  FLJ13241  3'  CTCGCTGGCTGTCGTCATGGG  47651    G   GT     G  TCC
                                TC GTG  GATGGT CA   CGAG
                                || |||  |||||| ||   ||||
                                GG TAC  CTGTCG GT   GCTC
                                 G   TG     _  C__
GAM342  FLJ14427  3'  CTTGGAGCCACGTGTTTTTATT 52343     TG    TG TG ATC___
          GCTGA                 TCGG  GTGA  G  C     CCGAG
                                ||||  ||||  |  |     |||||
                                AGTC  TATT  T  G     GGTTC
                                  GT    TT GT CACCGA
GAM342  FLJ14641  3'  ATGTGTCATGATCACTGA    52551        G    TG
                                TCGGTGGT ATGG  CAT
                                ||||||||  ||||  |||
                                AGTCACTA TACT  GTA
                                     G    GT
GAM342  FLJ20073  3'  CTTGGTTTGGTTAACATCATTG 34964         A GG G  TC
          A                     TCGGTGGTG T  T CA  CCGAG
                                |||||||||  |  | ||  |||||
                                AGTTACTAC A  G GT  GGTTC
                                      A TT _  TT
GAM342  FLJ20232  3'  TGCTGATCATCACCCTGG    39189      T       __
                                TCGG GGTGATGGT  GCA
                                ||||  |||||||||  |||
                                GGTC CCACTACTA  CGT
                                  _        GT
GAM342  FLJ20371  5'  CTTGGGACAGCGATCGCCGCGG 35536    G       G  GCA
          G                     TC GTGGTGAT GT   TCCCGAG
                                || ||||||| ||   |||||||
                                GG CGCCGCTA CG   AGGGTTC
                                 G       G  AC_
GAM342  FLJ20401  5'  CTCGGGCCCGCCACGCTGCTGG 35582     TG   A    CAT
                                TCGG  GTG TGGTG   CCCGAG
                                ||||  ||| |||||   ||||||
                                GGTC  CGC ACCGC   GGGCTC
                                  GT   _    CC_
GAM342  FLJ20507  3'  TGCTCAGCCATCACTCTGG   35753      T       ___
                                TCGG GGTGATGGT   GCA
                                ||||  |||||||||   |||
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                                GGTC TCACTACCG   CGT
                                  _       ACT
GAM342  FLJ20604  5' CTTGAGAGCGTCATCGCCCCCG 35867     T     GT  A  C
          A                     TCGG GGTGATG  GC TC CGAG
                                |||| |||||||  || || ||||
                                AGCC CCGCTAC  CG AG GTTC
                                  C      TG  _  A
GAM342  FLJ20625  3' TTGGTTTGTCACCCTCGA    35900     T   ATGGT   TC
                                TCGG GGTG    GCA  CCGA
                                |||| ||||    |||  ||||
                                AGCT CCAC    TGT  GGTT
                                  C   _____  TT
GAM342  FLJ20695  3' CTTGGCTCGCACTGTTCCTACT 35984       TG     ATC
          GA                    TCGGTGG  ATGGTGC   CCGAG
                                |||||||  |||||||   |||||
                                AGTCATC  TGTCACG   GGTTC
                                   CT      CTC
GAM342  FLJ20730  3' GATGTCATTACTCCTGA     36050     TG     GT
                                TCGG  GTGATG  GCATC
                                ||||  ||||||  |||||
                                AGTC  CATTAC  TGTAG
                                  CT     __
GAM342  FLJ22035  3' TTTGGGGTGCAGAAAACTTTGA 44832     T   GATGG
                                TCGG GGT    TGCATCCCGAG
                                |||| |||    ||||||||||
                                AGTT TCA    ACGTGGGGTTT
                                  _  AAAG_
GAM342  FLJ22056  3' TTGGGGTGTTGTGGCTGG    42837      G TG TGGTG
                                TCGGT G  A    CATCCCGA
                                ||||| |  |    ||||||||
                                GGTCG T  T    GTGGGGTT
                                   G GT _____
GAM342  FLJ22104  3' CTTGAATATCATTGTCACCATT 43626       TG   CATCC
                                GGTGGTGA  GTG    CGAG
                                ||||||||  |||    ||||
                                TTACCACT  TAC    GTTC
                                     GT   TATAA
GAM342  FLJ22479  3' TTTGGAGTCATCACTGTCGCTG 46609      GT A    C TC
                                CGGTG  G TGGTG A  CCGAG
                                |||||  | ||||| |  |||||
                                GTCGC  T ACTAC T  GGTTT
                                   TG C    _ GA
GAM342  FLJ22582  5' CCGGCTGTGCCATCGCCACC   47456         TG  TC   AG
                                GGTGGTGATGG  CA  CCG
                                ||||||||||  ||  |||
                                CCACCGCTACC  GT  GGC
                                       GT  C_   CC
GAM342  FLJ22644  3' CTTGGGGTGAGGCATCCTTGA  47700     T   ATGGTG
                                TCGG GGTG     CATCCCGAG
                                |||| ||||     |||||||||
```

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                                AGTT CTAC     GTGGGGTTC
                                  C   GGA___
GAM342  FLJ22800  3'  CTTGTGGTGTTACGTTACT   45992       GT    C
                                GGTGATG  GCATC CGAG
                                ||||||| ||||| ||||
                                TCATTGC  TGTGG GTTC
                                   AT    T
GAM342  FLJ22938  3'  CTCGTCCTCGTCGTCGTCCTCG 45482     T _    GT CATCC
          G                     TCGG GG TGATG  G    CGAG
                                |||| || ||||| |    ||||
                                GGCT CC GCTGC  C    GCTC
                                  _ T    TG TCCT_
GAM342  FLJ22944  3'  CTTGTAGGTGCTATCATTATT  47870          TG ATCC
                                GGTGGTGATGG  C   CGAG
                                |||||||||| |   ||||
                                TTATTACTATC  G   GTTC
                                      GT GAT_
GAM342  FLJ31890  3'  ATGTATCTTACTGTTGA    92984     TG   T
                                TCGG  GTGA GGTGCAT
                                ||||  |||| |||||||
                                AGTT  CATT CTATGTA
                                  GT   _
GAM342  FLJ32421  5'  CTCGGTAGCTGTCATGGCCGCC 59118       G  GT_  ATC
          GG                    TCGGTGGT ATG   GC   CCGAG
                                |||||||| |||   ||   |||||
                                GGCCGCCG TAC   CG   GGCTC
                                    G   TGT  AT_
GAM342  FLJ32783  3'  CTTGAGAAATCGTTGTTGCTG  59306    TG TG    GCA  C
                                CGG  G  ATGGT   TC CGAG
                                |||  |  |||||   || ||||
                                GTC  T  TGCTA   AG GTTC
                                  GT GT    A__  A
GAM342  FLNC    5'  CTCGGGGACCTTGTCTGTCACC 70341          T  _____
          ATTGA                   TCGGTGGTGATGG GCA    TCCCGAG
                                |||||||||||| |||   |||||||
                                AGTTACCACTGTC TGT    GGGGCTC
                                      _  TCCA
GAM342  G4      5'  TTGGGGTGCTGCCTGCTGG   92644       GTGAT  _
                                TCGGTG    GGT GCATCCCGA
                                ||||||    ||| |||||||||
                                GGTCGT    CCG CGTGGGGTT
                                   _____  T
GAM342  GABARAPL1 5'  CTCGGCCCAGCGCTGTTGCCCC 49417     T  TG      ATC_
          CGG                    TCGG GG  ATGGTGC    CCGAG
                                |||| ||  |||||||   |||||
                                GGCC CC  TGTCGCG    GGCTC
                                  C  GT      ACCC
GAM342  GFR     3'  CTCATTCATCCTCATTACTGA  25446         T   C  CCC
                                TCGGTGGTGA GGTG AT   GAG
                                |||||||||| |||| ||   |||
```

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                                AGTCATTACT CTAC TA   CTC
                                      C   T ___
GAM342  GMEB2    3'  CTTGGGGTGCAGATCCTGA   25662     T   GATGG
                                TCGG GGT    TGCATCCCGAG
                                |||| |||    ||||||||||
                                AGTC CTA    ACGTGGGGTTC
                                  _  G____
GAM342  GP5      3'  GTGCGCTGACACTGCCGG    16880     TG   A
                                TCGG  GTG TGGTGCAT
                                ||||  ||| ||||||||
                                GGCC  CAC GTCGCGTG
                                  GT   A
GAM342  GRSF1    5'  GAGCACCATCGCTGCTGG    10879     TG       A
                                TCGG  GTGATGGTGC TC
                                ||||  |||||||||| ||
                                GGTC  CGCTACCACG AG
                                  GT        _
GAM342  GSA7     3'  CTTGGCCTTGGCCTTGCTATTG 22143       TG T   G  TC_
            A                    TCGGTGG  A GGT CA   CCGAG
                                |||||||  | ||| ||   |||||
                                AGTTATC  T CCG GT   GGTTC
                                    GT _  _  TCC
GAM342  H11      3'  GTGTGTCATTATTATTTGA   27638     _      TG
                                TCGG TGGTGATGG  CAT
                                |||| |||||||||  |||
                                AGTT ATTATTACT  GTG
                                  T       GT
GAM342  H2AV     3'  ATGTATTGTTATCCCTGA    25756     T    TG
                                TCGG GGTGA  GTGCAT
                                |||| |||||  ||||||
                                AGTC CTATT  TATGTA
                                  C    GT
GAM342  HEMK     3'  TTTGGGGAGCCTATATTGCTGG 32970     TG   A   T  AT
                                TCGG  GTG TGG GC  CCCGAG
                                ||||  ||| ||| ||  ||||||
                                GGTC  TAT ATC CG  GGGTTT
                                  GT  _  _  AG
GAM342  HEYL     3'  CTTGGGCCACACCATCACACTG 28126       G      CAT
            A                    TCGGTG TGATGGTG   CCCGAG
                                ||||||| ||||||||   ||||||
                                AGTCAC ACTACCAC   GGGTTC
                                   _       ACC
GAM342  HIRIP5   5'  TGCGGCTGTTGCCGCCGG    32284       TG    _
                                TCGGTGG  ATGGT GCA
                                |||||||  ||||| |||
                                GGCCGCC  TGTCG CGT
                                    GT    G
GAM342  HNT      5'  TTCGGGGAAGTTGTGGCTGTCG 33700     TG  G  GG GCA
            A                    TCGG  GT AT  T   TCCCGAG
                                ||||  || ||  |   |||||||
```

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                                AGCT  CG TG  G   GGGGCTT
                                  GT  G  TT AA_
GAM342  HSRNAFEV  5'  TTCGGGCGGGGATCGGTGCCAC 34456        GA   GCAT_
            CGA                   TCGGTGGT  TGGT    CCCGAG
                                |||||||| ||||    ||||||
                                AGCCACCG  GCTA    GGGCTT
                                    TG    GGGGC
GAM342  humNRDR   3'  CTCGGGATTCCTGCTGTTGTTG 41012   G TG TG     C__
            TGG                   C G  G  ATGGTG   ATCCCGAG
                                | | | ||||||  ||||||||
                                G T  T  TGTCGT   TAGGGCTC
                                 G GT GT     CCT
GAM342  ICB-1    3'  CTTGGGATGCAGAGCAGCTGG  17932      G  GATGG
                                TCGGT GT    TGCATCCCGAG
                                ||||| ||    ||||||||||
                                GGTCG CG    ACGTAGGGTTC
                                   A  AG___
GAM342  ICK      3'  CTTGGTAAATTATTGCCTTGG  33687      T  TG    GCATC
                                TCGG GG  ATGGT    CCGAG
                                |||| ||  |||||    |||||
                                GGTT CC  TATTA    GGTTC
                                  _ GT    AAT__
GAM342  INE1     3'  GCCACATGCATCATCATCCTGG 14758      T          CCCGAG
                                TCGG GGTGATGGTGCAT
                                |||| ||||||||||||
                                GGTC CTACTACTACGTA
                                  _          CACCGT
GAM342  ITGA8    5'  CTTGGATACTCAGTTGCTGCTG 94844      TG TG __    CATC
            G                   TCGG  G  AT  GGTG   CCGAG
                                ||||  |  ||  ||||   |||||
                                GGTC  C  TG  TCAT   GGTTC
                                  GT GT  AC   A___
GAM342  KHDRBS1  5'  CTCGGGCCTCCGTCGCTGCCG  22660     TG      TGCAT
                                CGG  GTGATGG    CCCGAG
                                |||  |||||||    ||||||
                                GCC  CGCTGCC    GGGCTC
                                  GT      TCC__
GAM342  KIAA0033 3'  TTCCAGATTCATCATCATTGA  77084           TGC   CC
                                TCGGTGGTGATGG   ATC  GAG
                                ||||||||||||   |||  |||
                                AGTTACTACTACT   TAG  CTT
                                       ___   AC
GAM342  KIAA0193 3'  TTTGGCCTGGGCTTTCACTGTT 29320      TG    T   G  TC
            GG                    TCGG  GTGA GGT CA  CCGAG
                                ||||  |||| ||| ||  |||||
                                GGTT  CACT TCG GT  GGTTT
                                  GT    T   G  CC
GAM342  KIAA0194  5'  CTTGTTGCTGCTGTCACGACTG 66590       G      _   TCC
            G                   TCGGT GTGATGGT GCA   CGAG
                                |||||  |||||||| |||   ||||
```

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                                GGTCA CACTGTCG CGT   GTTC
                                  G       T   T__
GAM342  KIAA0210  5'  CTTGCTCAGCTATGCGTCATTG 29157       GT _    ___   TCCCGAG
            G                    TCGGTG  G ATGGT   GCA
                                 ||||||  | |||||   |||
                                 GGTTAC  C TATCG   CGT
                                    TG G    ACT   TC   G
GAM342  KIAA0337  3'  TTTGGGGTGGGTGGGTCATTGC 29486   TG    GG_ G
                                 G  GTGAT   T CATCCCGAG
                                 |  |||||   | |||||||||
                                 C  TACTG   G GTGGGGTTT
                                  GT    GGT G
GAM342  KIAA0427  3'  TGATACTGTCACCACTGG    29393            _
                                 TCGGTGGTGATGGTG CA
                                 |||||||||||||| ||
                                 GGTCACCACTGTCAT GT
                                           A
GAM342  KIAA0447  3'  CCTGGGCGCCGTCCTTGCTGA  72116     TG T      ATC   AG
                                 TCGG  G GATGGTGC   CCG
                                 ||||  | ||||||||   |||
                                 AGTC  T CTGCCGCG   GGT
                                   GT C       ___   CCA
GAM342  KIAA0469  3'  TGTGGATGTCATTGCTGTCGG  30000     TG TG   GT    _
                                 TCGG  G  ATG  GCATCC CG
                                 ||||  |  |||  |||||| ||
                                 GGCT  C  TAC  TGTAGG GT
                                   GT GT  __     T
GAM342  KIAA0537  3'  TTTGGGCTCTCCCCTTGCCACC 29936       TG T  TGCAT
            GG                     TCGGTGG  A GG    CCCGAG
                                 |||||||  | ||    ||||||
                                 GGCCACC  T CC    GGGTTT
                                     GT C  CTCTC
GAM342  KIAA0544  3'  CTTGGGGTGCATGGGTGCCGC  71465       ATG
                                 GTGGTG   GTGCATCCCGAG
                                 ||||||   ||||||||||||
                                 CGCCGT   TACGTGGGGTTC
                                    GGG
GAM342  KIAA0557  3'  TTTGGGATGCCCAGGCCGCAGA 78580    G    GA   T
                                 TC GTGGT  TGG GCATCCCGAG
                                 || |||||  ||| ||||||||||
                                 AG CGCCG  ACC CGTAGGGTTT
                                  A    G_  _
GAM342  KIAA0596  3'  CTTGGGTCTTTGTCATCTTGG  63489     T    TG TGCAT
                                 TCGG GGTGA  G    CCCGAG
                                 |||| |||||  |    ||||||
                                 GGTT CTACT  T    GGGTTC
                                   _    GT TCT__
GAM342  KIAA0599  5'  CTCCACTGCTGGCACTATCGG  77690        ATGGT   TCCC
                                 TCGGTGGTG    GCA   GAG
                                 |||||||||    |||   |||
```

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                              GGCTATCAC    CGT   CTC
                                   GGT__   CAC_
GAM342  KIAA0711  3' CTCATATGCTGTTATCACTG  30148          GC  CCC
                              CGGTGGTGATGGT  AT   GAG
                              ||||||||||||  ||   |||
                              GTCACTATTGTCG  TA   CTC
                                    TA  ___
GAM342  KIAA0802  3' CTTGTACTGTACTTTTATTGTT 63249     TG   T     TCC
          GG                    TCGG  GTGA GGTGCA   CGAG
                              ||||  |||| ||||||   ||||
                              GGTT  TATT TCATGT   GTTC
                                GT   T     CAT
GAM342  KIAA0869  3' TTTGGGTCCTACTGTTGTTATT 71424      TG     CAT
                              GGTGG  ATGGTG   CCCGAG
                              |||||  ||||||   ||||||
                              TTATT  TGTCAT   GGGTTT
                                 GT     CCT
GAM342  KIAA0947  3' TTTGGTTCCTGAGCTGTTGTTG 62203     TG TG    G  TC__
          TTGG                  TCGG  G  ATGGT CA    CCGAG
                              ||||  |  |||||  ||    |||||
                              GGTT  T  TGTCG GT    GGTTT
                                GT GT    A  CCTT
GAM342  KIAA0984  3' CTTGGGATTGTACCATTGCTGT 66140    _  TG       _
          CC                    GG TGG  ATGGTGCA TCCCGAG
                              ||  |||  |||||||| |||||||
                              CC GTC  TACCATGT AGGGTTC
                               T  GT       T
GAM342  KIAA1130  3' CTCACCCACACTGTCACCACT  63088           CATCCC
                              GGTGGTGATGGTG     GAG
                              ||||||||||||      |||
                              TCACCACTGTCAC     CTC
                                    ACCCA_
GAM342  KIAA1145  3' CTTGTTCAACCATCACCACT   66239          GCATCC
                              GGTGGTGATGGT     CGAG
                              ||||||||||||     ||||
                              TCACCACTACCA     GTTC
                                    ACTT__
GAM342  KIAA1169  3' TTTGGGAAAGCAACACATTATT 35887         A  G   A_
          GA                    TCGGTGGTG TG TGC  TCCCGAG
                              |||||||| || |||  |||||||
                              AGTTATTAC AC ACG  AGGGTTT
                                   _  A   AA
GAM342  KIAA1228  3' TTTGGCCAATATTATCATTGA  65680          G  CATC
                              TCGGTGGTGATG TG    CCGAG
                              ||||||||||||  ||    |||||
                              AGTTACTATTAT AC    GGTTT
                                    A  C___
GAM342  KIAA1229  3' TTTGGAATGAATGCTATTATTG 62761    TG       G__   C
          CT                    GG  GTGATGGT   CAT CCGAG
                              ||  ||||||||   ||| |||||
```

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                                TC  TATTATCG   GTA GGTTT
                                 GT       TAA   A
GAM342  KIAA1260  5'  TTGGAGCCACATCACTGG    60673         A    GCATC
                                TCGGTGGTG TGGT    CCGA
                                ||||||||| ||||    ||||
                                GGTCACTAC ACCG    GGTT
                                     _   A____
GAM342  KIAA1266  3'  CTTGCTGCACTGTCCTGCTGA  66696     TG T       TCC
                                TCGG  G GATGGTGCA   CGAG
                                ||||  | |||||||||   ||||
                                AGTC  C CTGTCACGT   GTTC
                                  GT _       C__
GAM342  KIAA1354  3'  TTGGGGTGCTTGCCCTGG    61578     T  TG TGGT
                                TCGG GG  A    GCATCCCGA
                                |||| ||  |   |||||||||
                                GGTC CC  T    CGTGGGGTT
                                  _  GT ____
GAM342  KIAA1484  5'  TCGCCGCCGTGCGCCGCCGA   70525         _     CATCC   G
                                TCGGTGGTG ATGGTG    CGA
                                ||||||||| ||||||    |||
                                AGCCGCCGC TGCCGC    GCT
                                     G     C____
GAM342  KIAA1509  3'  CTCGGGGTGTTGATTTATTTCT 62295     TG    TGGT
           GA                   TCGG  GTGA    GCATCCCGAG
                                ||||  ||||    ||||||||||
                                AGTC  TATT    TGTGGGGCTC
                                  TT    TAGT
GAM342  KIAA1514  3'  CTCCATGCACCATCACTGTGG  39326   G TG         CCC
                                C G  GTGATGGTGCAT   GAG
                                | |  ||||||||||||   |||
                                G T  CACTACCACGTA   CTC
                                 G GT          C__
GAM342  KIAA1545  3'  TTGGGATTCGGCTGTTGG    61339     TG  GATGG  C
                                TCGG  GT    TG ATCCCGA
                                ||||  ||    || |||||||
                                GGTT  CG    GC TAGGGTT
                                  GT  _____  T
GAM342  KIAA1586  5'  TTCGGAAAGATGTTGATGTCAT 93943       GT ATGGT    ___
           TGA                   TCGGTG  G    GCATC   CCGAG
                                ||||||  |    |||||   |||||
                                AGTTAC  T    TGTAG   GGCTT
                                   TG AGT__     AAA
GAM342  KIAA1613  3'  TTTGGTTAACACCATTGCTGTT 65444     TG TG     CATC
           GA                    TCGG  G  ATGGTG    CCGAG
                                ||||  |  ||||||    |||||
                                AGTT  C  TACCAC    GGTTT
                                  GT GT     AATT
GAM342  KIAA1617  3'  CTCGGGAGGTGGCCCATTATTG 93074     TG      T  A___
           CTGG                   TCGG  GTGATGG GC    TCCCGAG
                                ||||  ||||||| ||    |||||||
```

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                              GGTC  TATTACC CG    AGGGCTC
                                GT      _ GTGG
GAM342  KIAA1671  3'  CTCGGTGCAGGGTATTACCGCT 66277          G__    TC
             GG                  TCGGTGGTGATG   TGCA  CCGAG
                              ||||||||||||  ||||  |||||
                              GGTCGCCATTAT   ACGT  GGCTC
                                    GGG   __
GAM342  KIAA1673  3'  CTTGGGGTGTGCTATCGTGCTG 71327     GGT    TG
                              CGGT   GATGG  CATCCCGAG
                              ||||   |||||  |||||||||
                              GTCG   CTATC  GTGGGGTTC
                                TG_    GT
GAM342  KIAA1677  3'  TGCTGCTGCCACCATTGA    67666         AT  _
                              TCGGTGGTG  GGT GCA
                              |||||||||  ||| |||
                              AGTTACCAC  TCG CGT
                                    CG   T
GAM342  KIAA1728  3'  TTTGGGGTGGATCTGATGCCAT 68955         AT_  G
             TGA                  TCGGTGGTG   GGT CATCCCGAG
                              |||||||||   ||| |||||||||
                              AGTTACCGT   CTA GTGGGGTTT
                                    AGT   G
GAM342  KIAA1765  3'  TTGGGGGGTAAGCATTGTCATC 71137     G     TG   __    GAG
             AGTGA                TCG TGGTGA  GTGC  ATCCC
                              |||  ||||||  ||||  |||||
                              AGT ACTACT  TACG  TGGGG
                                G     GT    AA    GGTTT
GAM342  KIAA1866  3'  TTCGGTCTCATTTGTCACCGA  61592       TG TG   CATC
                              TCGGTGG  A  GTG    CCGAG
                              |||||||  |  |||    |||||
                              AGCCACT  T  TAC    GGCTT
                                  GT __   TCT_
GAM342  KIAA1908  5'  TCGGGTTCCGCGCTGCCGG    73801     TG   A   TGCAT
                              TCGG  GTG TGG    CCCGA
                              ||||  ||| |||    |||||
                              GGCC  CGC GCC    GGGCT
                                GT   _   TT____
GAM342  KIAA1915  5'  TTTGGGGCTCCCATCATCCTGA 73673      T       T_  AT
                              TCGG GGTGATGG  GC  CCCGAG
                              |||| ||||||||  ||  ||||||
                              AGTC CTACTACC  CG  GGGTTT
                                _       CT  __
GAM342  KLK14    3'  CTTGCTGTGTCACCATCACTAC 42129           _  CC
             T                   GGTGGTGATGGTG CAT  CGAG
                              ||||||||||||| |||  ||||
                              TCATCACTACCAC GTG  GTTC
                                      T   TC
GAM342  KLK6     3'  CTTGGGATGTACCTTTCTTCAC 12424       T  T_
             TG                    CGGTGG GA  GGTGCATCCCGAG
                              ||||||  ||  |||||||||||||
```

```
                                GTCACT CT  CCATGTAGGGTTC
                                   T  TT
GAM342  KPNA6    3'  CTCCTATTATCTATTATCACTG 25541          TGCATCCC
            A                   TCGGTGGTGATGG       GAG
                                ||||||||||||       |||
                                AGTCACTATTATC       CTC
                                       TATTATC_
GAM342  LCHN     3'  CTTGGGATACTGGGTTGTTGGT 87470     G   TG __  GC
            GA                    TCG TGG  AT  GGT  ATCCCGAG
                                ||| |||  ||  |||  ||||||||
                                AGT GTT  TG  TCA  TAGGGTTC
                                  G   GT  GG  __
GAM342  LGI3     3'  TTGGGATGTGGCCCTTGA    58400      T   GATGG
                                TCGG GGT    TGCATCCCGA
                                |||| |||    ||||||||||
                                AGTT CCG    GTGTAGGGTT
                                  C  _____
GAM342  LNX      3'  TGTTACCATCACCGATGA    51913     G        _
                                TCG TGGTGATGGTG CA
                                ||| |||||||||| ||
                                AGT GCCACTACCAT GT
                                  A         T
GAM342  MAGEF1   5'  CTTGTACTCCCGCCGTCACTGC 60698     TG       CATCC_
            CG                    CGG  GTGATGGTG     CGAG
                                |||  |||||||||     ||||
                                GCC  CACTGCCGC     GTTC
                                  GT       CCTCAT
GAM342  MEGF11   3'  TTTGGTTGCTGTTACCATC   51601           CATC
                                GGTGGTGATGGTG   CCGAG
                                ||||||||||||   |||||
                                CTACCATTGTCGT   GGTTT
                                       T___
GAM342  MFN1     3'  ATGGGCATCATTATTGTTGG   54320      TG       ATC   AG
                                TCGG  GTGATGGTGC   CCG
                                ||||  ||||||||||   |||
                                GGTT  TATTACTACG   GGT
                                  GT        ___   AT
GAM342  MGC10485 5'  CTCGGTGCGTTGCACCGCCGG  54623         A GG    TC
                                TCGGTGGTG T  TGCA  CCGAG
                                |||||||| |  ||||  |||||
                                GGCCGCCAC G  GCGT  GGCTC
                                     _ TT   __
GAM342  MGC11115 3'  CTCGGTTTCTCGCCTGTCATCA 51205          _   CATC_
            TCGA                   TCGGTGGTGAT GGTG    CCGAG
                                |||||||||| ||||    |||||
                                AGCTACTACTG CCGC    GGCTC
                                       T   TCTTT
GAM342  MGC13061 3'  CTTGGGATGTTTGAACCCTGG  51288      T   GATGGT
                                TCGG GGT     GCATCCCGAG
                                |||| |||     ||||||||||
```

```
                                GGTC CCA     TGTAGGGTTC
                                  _  AGTT__
GAM342  MGC13071  3'  GTGCGCCAGTCATCACTGG   52066          _
                                TCGGTGGTGA TGGTGCAT
                                |||||||||| ||||||||
                                GGTCACTACT ACCGCGTG
                                     G
GAM342  MGC13090  3'  CTCGGGGTGGCACTGGTGTTGC 52120      GG  AT    _
          TGG                    TCGGT  TG  GGTGC ATCCCGAG
                                |||||  ||  ||||| ||||||||
                                GGTCG  GT  TCACG TGGGGCTC
                                   TT  GG    G
GAM342  MGC13170  5'  CTCGAGAGCTGCTGCTGCCGG  52130     TG  GAT  _  A  C
                                TCGG  GT   GGT GC TC CGAG
                                ||||  ||   ||| || || ||||
                                GGCC  CG   TCG CG AG GCTC
                                  GT  ___   T  _  A
GAM342  MGC13269  5'  CTCGGGCCGCCTGTTGCTGGTG 52162    G   TG    T  AT
            G                    TCG TGG  ATGG GC  CCCGAG
                                ||| |||  |||| ||  ||||||
                                GGT GTC  TGTC CG  GGGCTC
                                  G  GT   _  CC
GAM342  MGC15631  3'  TGCTGGGTGTGTCGTCATCGTC 52239   GT      TG  T   AG
                                G  GGTGATGG  CA CCCG
                                |  ||||||||  || ||||
                                C  CTACTGCT  GT GGGT
                                 TG      GT  _   CGTA
GAM342  MGC15906  3'  CTTGGGGGAACTGTGGCTGCTG 52885     TG  G    GCA
            G                    TCGG  GT ATGGT   TCCCGAG
                                ||||  || |||||   |||||||
                                GGTC  CG TGTCA   GGGGTTC
                                  GT  G    AG_
GAM342  MGC17330  3'  TTTGGGATGGAACTCCCTACTG 54633       T  TG  G_
            A                    TCGGTGG GA  GT  CATCCCGAG
                                ||||||| ||  ||  |||||||||
                                AGTCATC CT  CA  GTAGGGTTT
                                    C  __  AG
GAM342  MGC3062   3'  TTTGGAAATAATCATTGCTGG  44155     TG    G  GCATC
                                TCGG  GTGAT GT    CCGAG
                                ||||  ||||| ||    |||||
                                GGTC  TACTA TA    GGTTT
                                  GT    A  AA___
GAM342  MGC3265   5'  TCGCCGCCGCCGCTGCTGG   44049     TG   A    CATCC
                                TCGG  GTG TGGTG    CGA
                                ||||  ||| |||||    |||
                                GGTC  CGC GCCGC    GCT
                                  GT   C    C____
GAM342  MGC34923  5'  GTGTACTATTCTGTCGA     59199      TG T
                                TCGG  G GATGGTGCAT
                                ||||  | ||||||||||
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```
                                AGCT  C TTATCATGTG
                                  GT _
GAM342  MGC4054  5' CCCGGCTGCCCTGTTGCTGTCG 44549     TG TG   T  TC  AG
           G                    TCGG  G  ATGG GCA  CCG
                                |||| |  |||| |||  |||
                                GGCT  C  TGTC CGT  GGC
                                  GT GT   C  C_  CCT
GAM342  MGC4415  3' CTTGGGGTGGGGCCCATCCGCC 49762       TGAT  G_
           GA                   TCGGTGG   GGT  CATCCCGAG
                                |||||||   |||  |||||||||
                                AGCCGCC   CCG  GTGGGGTTC
                                   TAC_  GG
GAM342  MGC4643  3' GTGTATTTCACTGCTGA    52144     TG   T
                                TCGG  GTGA GGTGCAT
                                |||| |||| |||||||
                                AGTC  CACT TTATGTG
                                  GT   _
GAM342  MGC4734  3' TTGAATGTCTTGCCACTGG   59597       TG TGGT   CC
                                TCGGTGG  A   GCAT  CGA
                                |||||||  |   ||||  |||
                                GGTCACC  T   TGTA  GTT
                                   GT C___   A_
GAM342  MGC4796  3' TTTGGCTAAAATCATCATCACT 62171          GCATC
                                GGTGGTGATGGT    CCGAG
                                ||||||||||||    |||||
                                TCACTACTACTA    GGTTT
                                      AAATC
GAM342  MGEA6    3' GATGTGTCATCATTTTGA    21012     T      TG
                                TCGG GGTGATGG  CATC
                                |||| ||||||||  ||||
                                AGTT TTACTACT  GTAG
                                  _      GT
GAM342  MKRN1    3' CTTGAGGCATTTTGTTGTCGG  26495     TG TG T    ATCC
                                TCGG  G  A GGTGC   CGAG
                                ||||  |  | |||||   ||||
                                GGCT  T  T TTACG   GTTC
                                  GT GT _    GA__
GAM342  MRPS26   3' TTTGCCCTCTGCTGTCACCACT 48726          _____  TCCCGAG
                                GGTGGTGATGGT    GCA
                                ||||||||||||    |||
                                TCACCACTGTCG    CGT
                                      TCTCC   TT   G
GAM342  NAV1     3' TTCGGCAATCACTGTCACCCCC 40326     T       CATC
           GG                   TCGG GGTGATGGTG   CCGAG
                                |||| ||||||||||   |||||
                                GGCC CCACTGTCAC   GGCTT
                                  C        TAAC
GAM342  NFASC    3' CTCGGCCTTGTCAGTTGCTGA  70854     TG _  TG T  ATCC
                                TCGG  G TGA  G GC   CGAG
                                ||||  | |||  | ||   ||||
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                                AGTC  T ACT  T CG   GCTC
                                  GT G   GT C  ____
GAM342  NIP30    5'  TTTGGGGTGGGCGCCGCCGA  46902        GATG  G
                                TCGGTGGT   GT CATCCCGAG
                                ||||||||   || |||||||||
                                AGCCGCCG   CG GTGGGGTTT
                                     ____  G
GAM342  NRBF-2   3'  CTTGGGAAACAGTCACTGT   48481   TG    G  GCA
                                G  GTGAT GT   TCCCGAG
                                |  ||||| ||   |||||||
                                T  CACTG CA   AGGGTTC
                                 GT    A  A__
GAM342  NS1-BP   5'  TTATGATGCATCATTATCACAG 72943    G            CCGAG
            A                    TC GTGGTGATGGTGCATC
                                || ||||||||||||||||
                                AG CACTATTACTACGTAG
                                 A             TATT
GAM342  NSE1     3'  TTCGGGATTCCGGGTTATCCTG 59680     T     __ TGC
            A                    TCGG GGTGAT  GG   ATCCCGAG
                                |||| ||||||  ||   ||||||||
                                AGTC CTATTG  CC   TAGGGCTT
                                  _     GG  T__
GAM342  NTF2     3'  GTGCGCTGCTGCCACTGA    20531        GA
                                TCGGTGGT  TGGTGCAT
                                ||||||||  ||||||||
                                AGTCACCG  GTCGCGTG
                                     TC
GAM342  OPRL1    3'  TTTGGGGTGGGACTTGCCCTGA 8074      T  TG TGGTG
                                TCGG GG  A    CATCCCGAG
                                |||| ||  |    |||||||||
                                AGTC CC  T    GTGGGGTTT
                                  _  GT CAGG_
GAM342  PDCD7    5'  GAGGCGCCGCCGCCGCCGG   72605        A     A
                                TCGGTGGTG TGGTGC TC
                                ||||||||| |||||| ||
                                GGCCGCCGC GCCGCG AG
                                     C     G
GAM342  PDE8B    5'  TTCGTCCAGACCGACGCCGCCG 68205         A   GCATCC
            A                    TCGGTGGTG TGGT     CGAG
                                ||||||||| ||||     ||||
                                AGCCGCCGC GCCA     GCTT
                                     A   GACCT_
GAM342  PDZD2    5'  TTCGGCCATCCGTCATCTCGA  81737     T      _ CATC
                                TCGG GGTGATGG TG    CCGAG
                                |||| |||||||| ||    |||||
                                AGCT CTACTGCC AC    GGCTT
                                  _       T  C___
GAM342  PECI     3'  AGGAAGGATGTGCTGTTACCTC 21495     T      TG    CGAG
            TGA                    TCGG GGTGATGG  CATCC
                                |||| ||||||||  |||||
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                                AGTC CCATTGTC  GTAGG
                                  T       GT     AAGGAA
GAM342  PEMT     5'  TTGGGGTGTTAACAGCTGA   24138       G  GATGGT
                                TCGGT GT      GCATCCCGA
                                |||||  ||     |||||||||
                                AGTCG CA      TGTGGGGTT
                                   A  AT____
GAM342  PLU-1    3'  TCTAACTGTAGCTATCATTACT 88807            _    TCCCGAG
             GG                   TCGGTGGTGATGG TGCA
                                |||||||||||| ||||
                                GGTCATTACTATC ATGT
                                       G    CAATCTT
GAM342  PPFIA4   3'  CTCGGCACCCCATTACCCCGA  70840      T       TGCATC
                                TCGG GGTGATGG      CCGAG
                                ||||  ||||||||      |||||
                                AGCC CCATTACC      GGCTC
                                  _       CCAC__
GAM342  PPP2R3A  3'  CTCAGGTATTGTAACCACTGG  12242         G TG    ATCCC
                                TCGGTGGT A  GTGC     GAG
                                ||||||||  |  ||||     |||
                                GGTCACCA T  TATG     CTC
                                    A GT    GA___
GAM342  PRC1     3'  TGCACATGTCACTACTGG     15631            _
                                TCGGTGGTGATG GTGCA
                                |||||||||||| |||||
                                GGTCATCACTGT CACGT
                                       A
GAM342  PRO0097  5'  ACTGCATGTATCATGCTATTGA 26932         G        CCCGAG
                                TCGGTGGT ATGGTGCAT
                                |||||||| |||||||||
                                AGTTATCG TACTATGTA
                                    _        CGTCAT
GAM342  PRO2086  5'  GTGTATTATTTTTATTGA     26920         T
                                TCGGTGG GATGGTGCAT
                                ||||||| ||||||||||
                                AGTTATT TTATTATGTG
                                     T
GAM342  PRRG1    3'  TTCGTAATGTTATTATTATTGT 8156     TG       _   CC
                                G  GTGATGGTG CAT  CGAG
                                |  |||||||| |||  ||||
                                T  TATTATTAT GTA  GCTT
                                 GT        T   AT
GAM342  PSK      5'  TTCGGCAGCTGTCGCCCTCGA  32884      T       GCATC
                                TCGG GGTGATGGT     CCGAG
                                ||||  |||||||||     |||||
                                AGCT CCGCTGTCG     GGCTT
                                  C        AC___
GAM342  PSR      5'  TTTGGGTACTGCCGTCGCCGCC 65798             CAT
             G                    CGGTGGTGATGGTG   CCCGAG
                                |||||||||||||   ||||||
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                                GCCGCCGCTGCCGT  GGGTTT
                                       CAT
GAM342  PTP4A1   3' ATGCATTTATCATCATTGA   14404          _
                                TCGGTGGTGATGG TGCAT
                                |||||||||||| |||||
                                AGTTACTACTATT ACGTA
                                       T
GAM342  PTPNS1   3' CTTGGCTGTCTGTCATGTGTTG 55840    GT _     T  TC
          A                     TCG  G GTGATGG GCA  CCGAG
                                |||  | ||||||| |||  |||||
                                AGT  T TACTGTC TGT  GGTTC
                                  TG G      _  C_
GAM342  RAB22A   3' CTTGGTTTCTGTTACCACTG  60609          TGCATC
                                CGGTGGTGATGG     CCGAG
                                ||||||||||||     |||||
                                GTCACCATTGTC     GGTTC
                                       TTT___
GAM342  Rabip4R  3' TTTGGTTATACCTGTAGTTACT 36282     GG GAT_   CATC
          GA                    TCGGT  T   GGTG   CCGAG
                                |||||  |   ||||   |||||
                                AGTCA  G   CCAT   GGTTT
                                   TT ATGT   ATT_
GAM342  RAGA     5' CTCCCGAGCCGTTGCCACTGA  22693       TG    GCA  CC
                                TCGGTGG  ATGGT   TC  GAG
                                |||||||  |||||  ||  |||
                                AGTCACC  TGCCG   AG  CTC
                                    GT    ____  CC
GAM342  RINZF    3' TTTGGGTATCTGTTACTTTGG  43940     T      TGCAT
                                TCGG GGTGATGG    CCCGAG
                                |||| ||||||||    ||||||
                                GGTT TCATTGTC    GGGTTT
                                  _      TAT__
GAM342  RIS1     3' ACACCGATATATTGTTACCGCT 81456         TG   C   CCGAG
          GA                    TCGGTGGTGA  GTG ATC
                                ||||||||||  ||| |||
                                AGTCGCCATT  TAT TAG
                                      GT   A   CCACAA
GAM342  RNF10    5' CTCCGACTGCCGTCGCCGCCGA 30160           GCA  CC
                                TCGGTGGTGATGGT   TC  GAG
                                ||||||||||||||   ||  |||
                                AGCCGCCGCTGCCG   AG  CTC
                                       TC_  C_
GAM342  RNF10    5' CTCGGTCGCCGCTGCCGCCGG  30161       GA    CATC
                                TCGGTGGT  TGGTG   CCGAG
                                ||||||||  |||||   |||||
                                GGCCGCCG  GCCGC   GGCTC
                                    TC    T____
GAM342  RNF11    3' TAAATAGTGTATTATTATCGTT 27653    GG          CCCGAG
          GG                    TC  TGGTGATGGTGCAT
                                ||  ||||||||||||||
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                                GG  GCTATTATTATGTG
                                 TT           ATAAATT
GAM342  RNF38    3'  CTTGTGTTTGCTGTTGCACACT 43259       _ TG    __    CCCGAG
           GA                    TCGGTG G  ATGGT  GCAT
                                 |||||| |  |||||  ||||
                                 AGTCAC C  TGTCG  TGTG
                                    A GT    TT    TTC
GAM342  RNF38    3'  TTTGGCATGAATTGTCATCTTT 43264      T    TG  G   C
           GG                    TCGG GGTGA  GT CAT CCGAG
                                 |||| |||||  || ||| |||||
                                 GGTT CTACT  TA GTA GGTTT
                                   T    GT  A   C
GAM342  RODH-4   3'  CTCCTGGGTGCATTGTCACCGT 14923    G      TG      C_
           GGG                    TC GTGGTGA  GTGCATCC  GAG
                                 || |||||||  ||||||||  |||
                                 GG TGCCACT  TACGTGGG  CTC
                                  G      GT       TC
GAM342  RPL13    5'  TTTGGGCATCATCCAGCGCCAT 78670         A  _  C  _
           CGG                    TCGGTGGTG TGG TG AT CCCGAG
                                 |||||||||| ||| || || ||||||
                                 GGCTACCGC ACC AC TA GGGTTT
                                      G   T  _  C
GAM342  SB52     3'  TGTGCTATATATCATTGG    57176          _    TG
                                 TCGGTGGTG ATGG  CA
                                 |||||||||| ||||  ||
                                 GGTTACTAT TATC  GT
                                      A    GT
GAM342  SEC61A1  3'  TTCGGGGTGCATGGGCTGTGG  26232   G TG  GATG
                                 C G  GT    GTGCATCCCGAG
                                 | |  ||    ||||||||||||
                                 G T  CG    TACGTGGGGCTT
                                  G GT  GG__
GAM342  SEMA3C   5'  CTCGGGGTGGGGCCTCGCGGCT 22107      G    T   G_
           GG                    TCGGT GTGA GGT  CATCCCGAG
                                 ||||| |||| |||  |||||||||
                                 GGTCG CGCT CCG  GTGGGGCTC
                                    G    _  GG
GAM342  SENP2    3'  CTTGGGGTGCAGAGGGCTGCT  76833    TG  GATGG
                                 GG  GT    TGCATCCCGAG
                                 ||  ||    ||||||||||||
                                 TC  CG    ACGTGGGGTTC
                                  GT  GGAG_
GAM342  SERP1    3'  TTTGGGTTTTCTAGTACTGTTG 27816     TG   A   TGCAT
           A                      TCGG  GTG TGG    CCCGAG
                                 ||||  ||| |||    ||||||
                                 AGTT  CAT ATC    GGGTTT
                                   GT   G   TTTT_
GAM342  SH3GLB2  3'  CTCGGGGTTTTAATTTTTGCTG 39721      TG T   GGTGC
           G                      TCGG  G GAT    ATCCCGAG
                                 ||||  | |||    ||||||||
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                                GGTC  T TTA    TGGGGCTC
                                  GT T   ATTT_
GAM342  SKRP1    5'  TTCGCCTTACATTGCATCGCTG 56013         A    CATCC
              G                    TCGGTGGTG TGGTG    CGAG
                                |||||||||| |||||    ||||
                                GGTCGCTAC GTTAC    GCTT
                                      _    ATTCC
GAM342  SSH2     3'  AAAATGTGCATCATCTTGTCGG 62888      TG T        CCCGAG
                                TCGG  G GATGGTGCAT
                                ||||  | ||||||||||
                                GGCT  T CTACTACGTG
                                  GT _        TAAAAT
GAM342  ST13     3'  TTCCACCGGCATCATCACTGCT 15436    TG        ATCCC
                                GG  GTGATGGTGC    GAG
                                ||  ||||||||||    |||
                                TC  CACTACTACG    CTT
                                 GT        GCCAC
GAM342  T2BP     3'  TTTGGAATTCAGTATTATCATT 70541          G  C  C
                                GGTGGTGATG TG AT CCGAG
                                |||||||||| || || |||||
                                TTACTATTAT AC TA GGTTT
                                      G  T  A
GAM342  TAO1     5'  TTCGGCAGCTGTCGCCCTCGA  17721      T       GCATC
                                TCGG GGTGATGGT    CCGAG
                                |||| |||||||||    |||||
                                AGCT CCGCTGTCG    GGCTT
                                  C        AC___
GAM342  TIGD1    5'  TTTGATGTTGCTATTGTCATTG 90288       TG    _   CCGAG
                                CGGTGG  ATGGTG CATC
                                ||||||  |||||| ||||
                                GTTACT  TATCGT GTAG
                                   GT     T    TTT
GAM342  TPC2     3'  CCGTGGTGCCTTTGCTGCCGG  58194      TG TG T  T    C  AG
                                TCGG  G  A GG GCATC CG
                                ||||  |  | || ||||| ||
                                GGCC  C  T TC CGTGG GC
                                  GT GT _  _    T  CT
GAM342  TRIM11   3'  TTCGTGGGCATGTTGCCATTGG 73193        TG   G   AT  _
                                TCGGTGG  ATG TGC  CC CGAG
                                |||||||  ||| |||  || ||||
                                GGTTACC  TGT ACG  GG GCTT
                                    GT   _  __  T
GAM342  TRIM2    3'  TTGGGGTCTTCTTCACTGA   31602        T  T  TGC
                                TCGGTGG GA GG   ATCCCGA
                                ||||||| || ||   |||||||
                                AGTCACT CT TC   TGGGGTT
                                    T  _  ____
GAM342  TRIM26   3'  TTTGGGGTACAAGCTGTGATCA 14351         G    GC__
              CTGA                  TCGGTGGT ATGGT    ATCCCGAG
                                |||||||| |||||    ||||||||
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                                AGTCACTA TGTCG    TGGGGTTT
                                    G     AACA
GAM342  TUBB5    3'  CTCTGAGCTGCACTTCACCGCT 21414          T     __  CC
            GA                    TCGGTGGTGA GGTGCA  TC  GAG
                                  |||||||||| ||||||  ||  |||
                                  AGTCGCCACT TCACGT  AG  CTC
                                       _     CG  T_
GAM342  TUSP     3'  TGAGTTTATTACTACTGG    40032           TG_
                                  TCGGTGGTGATGG   CA
                                  ||||||||||||   ||
                                  GGTCATCATTATT   GT
                                        TGA
GAM342  UBE2G1   3'  CTTGATCCCAGTCATTACCCCT 13952      T      _  CATCC
            GA                    TCGG GGTGATGG TG     CGAG
                                  |||| |||||||| ||     ||||
                                  AGTC CCATTACT AC     GTTC
                                    C       G  CCTA_
GAM342  UBE3B    3'  AGGAATGTATTAATATTATTGA 77440         A       C  GAG
                                  TCGGTGGTG TGGTGCAT CC
                                  ||||||||| |||||||| ||
                                  AGTTATTAT ATTATGTA GG
                                       A       A  AC
GAM342  YAP      5'  TTGGGCTCGCGCCGCTGA    58203          A   TGCAT
                                  TCGGTGGTG TGG     CCCGA
                                  ||||||||| |||     |||||
                                  AGTCGCCGC GCT     GGGTT
                                       _   C____
GAM342  ZFP      3'  TTTGAAATCCATCTCATCACTG 38473          T    C  CC
            A                      TCGGTGGTGA GGTG AT  CGAG
                                  |||||||||| |||| ||  ||||
                                  AGTCACTACT CTAC TA  GTTT
                                       _    C  AA
GAM342  ZNF302   5'  TTTGGGGCAGTGTCGTTCCCGG 38028      TG     G   AT
                                  TCGG  GTGATG TGC  CCCGAG
                                  ||||  |||||| |||  ||||||
                                  GGCC  TGCTGT ACG  GGGTTT
                                    CT     G  __
GAM342  ZNF84    5'  TCGGGGTGCAGTCCCCGA    14273      T  TGATGG
                                  TCGG GG     TGCATCCCGA
                                  |||| ||     ||||||||||
                                  AGCC CC     ACGTGGGGCT
                                    _  TG____
GAM342  LOC112609 3'  TGCCATGCTATTACCTTGG    73201      T       ___
                                  TCGG GGTGATGGT   GCA
                                  |||| |||||||||   |||
                                  GGTT CCATTATCG   CGT
                                    _        TAC
GAM342  LOC115129 3'  CTTGACATACATCATCATACTG 73617       G       C  CC
            A                      TCGGTG TGATGGTG AT  CGAG
                                  |||||| |||||||| ||  ||||
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                                AGTCAT ACTACTAC TA  GTTC
                                   _       A  CA
GAM342   LOC118987 3'  TGGGCACGTCATCATTGA    74396          G   ATC
                                TCGGTGGTGATG TGC   CCG
                                |||||||||||| |||   |||
                                AGTTACTACTGC ACG   GGT
                                      _  ___
GAM342   LOC120105 3'  CTTGCTCAGCACTATTGCTACC 76026      TG      ATCC
                                GGTGG  ATGGTGC    CGAG
                                |||||  |||||||    ||||
                                CCATC  TATCACG    GTTC
                                   GT      ACTC
GAM342   LOC122769 5'  CTTGACGTGGTTGTGGCCGTTG 74617    GG    G  GG G   CC
           G                     TC  TGGT AT  T CAT  CGAG
                                ||  |||| ||  | |||  ||||
                                GG  GCCG TG  G GTG  GTTC
                                 TT    G  TT _   CA
GAM342   LOC124753 5'  CTCGGATCGAGATCTCGTTGCT 74802      GG   T   GCATC_
           GG                     TCGGT  TGA GGT     CCGAG
                                |||||  ||| |||     |||||
                                GGTCG  GCT CTA     GGCTC
                                   TT   _   GAGCTA
GAM342   LOC126248 3'  TCGTCATCATCATCATCGG    74933            CATCC   G
                                TCGGTGGTGATGGTG    CGA
                                ||||||||||||||    |||
                                GGCTACTACTACTAC    GCT
                                      T_____
GAM342   LOC130436 5'  GTGGGATGTATTATTGTTACC  75438      TG          AG
                                GGTGG  ATGGTGCATCCCG
                                |||||  |||||||||||||
                                CCATT  TATTATGTAGGGT
                                   GT          GT
GAM342   LOC130536 5'  TGCTGCCATCACCCCTGG    76248      T       _
                                TCGG GGTGATGGT GCA
                                |||| ||||||||| |||
                                GGTC CCACTACCG CGT
                                  C       T
GAM342   LOC130612 3'  CTCGGGGTGTGAACCCCATTGG 75466        TGAT   __
                                TCGGTGG   GGT  GCATCCCGAG
                                |||||||   |||  ||||||||||
                                GGTTACC   CCA  TGTGGGGCTC
                                    _____  AG
GAM342   LOC130814 5'  TTCGGCAGAGCTGCGCCGCCGA 75485         A   GCATC
                                TCGGTGGTG TGGT    CCGAG
                                |||||||| ||||    |||||
                                AGCCGCCGC GTCG    GGCTT
                                      _   AGAC_
GAM342   LOC137886 3'  ATGTGGCATTACTGCTGG    75798      TG     G
                                TCGG  GTGATG TGCAT
                                ||||  |||||| |||||
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                                GGTC  CATTAC GTGTA
                                  GT     G
GAM342   LOC142927 3'  TTTGGGGTCATGGTTATCATC  76956         G   C
                                GGTGGTGAT GTG ATCCCGAG
                                ||||||||| ||| ||||||||
                                CTACTATTG TAC TGGGGTTT
                                    G   _
GAM342   LOC143437 5'  TGCCTCAGCTGTACCACTGA   83858         G    ____
                                TCGGTGGT ATGGT    GCA
                                |||||||| |||||    |||
                                AGTCACCA TGTCG    CGT
                                    _    ACTC
GAM342   LOC143465 3'  TTTGAGATATTTCATTGCTGA  83881      TG   TGGTGC   C
                                TCGG  GTGA     ATC CGAG
                                ||||  ||||     ||| ||||
                                AGTC  TACT     TAG GTTT
                                  GT    TTA___   A
GAM342   LOC144108 3'  GTGCACTGTTGTCTCCGA    77190      T  TG
                                TCGG GG  ATGGTGCAT
                                |||| ||  |||||||||
                                AGCC CT  TGTCACGTG
                                  T  GT
GAM342   LOC144698 5'  CTCCCCTGTGCTGCACTGCTGG 77434      TG   A   TG  TCCC
                                TCGG  GTG TGG  CA    GAG
                                ||||  ||| |||  ||    |||
                                GGTC  CAC GTC  GT    CTC
                                  GT   _   GT  CCC_
GAM342   LOC145195 3'  TGGAGAATGCATCATGGTCACT 84232        TG       _ _   AG
            GA                    TCGGTGG  ATGGTGCAT C CCG
                                |||||||  ||||||||| | |||
                                AGTCACT  TACTACGTA G GGT
                                    GG        A A
GAM342   LOC145384 3'  AAAAATGCTCATCATCACTGG  77707           T    CCCGAG
                                TCGGTGGTGATGG GCAT
                                |||||||||||| ||||
                                GGTCACTACTACT CGTA
                                        _    AAAAA
GAM342   LOC145608 5'  CTTGGGAAATTCATGTTGTTGA 84382      TG  G    TGCA
                                TCGG  GT ATGG    TCCCGAG
                                ||||  || ||||    |||||||
                                AGTT  TG TACT    AGGGTTC
                                  GT  _    TAA_
GAM342   LOC145926 3'  CTTGGCACATCCGTACCATCGG 78032         AT    CATC
                                TCGGTGGTG  GGTG    CCGAG
                                |||||||||  ||||    |||||
                                GGCTACCAT  CTAC    GGTTC
                                    GC    AC__
GAM342   LOC146159 5'  CTCGGGAGCAGCGGCACCGCTG 78175         A  G   A
            G                     TCGGTGGTG TG TGC TCCCGAG
                                |||||||||  || ||| |||||||
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                                GGTCGCCAC GC ACG AGGGCTC
                                     G  G  _
GAM342  LOC146728 5'  CTCCCCTGGTGTCACCACCGG  84765          GGT  ATCCC
                                TCGGTGGTGAT   GC    GAG
                                ||||||||||   ||    |||
                                GGCCACCACTG   TG    CTC
                                      ___  GTCCC
GAM342  LOC147353 3'  TTTGGGATGGTATGTGTTTCTG 85138      TGGTGATG   _
          G                      TCGG       GTGC ATCCCGAG
                                ||||       |||| ||||||||
                                GGTC       TATG TAGGGTTT
                                  TTTGTG__    G
GAM342  LOC147429 3'  ATGCATTAATCATCACTGA   78991          _
                                TCGGTGGTGAT GGTGCAT
                                |||||||||| |||||||
                                AGTCACTACTA TTACGTA
                                       A
GAM342  LOC147958 3'  CTCGGTCGCCCCACCGTTGTTT 88522      TG TG     CATC__
          CCGG                    TCGG  G  ATGGTG     CCGAG
                                ||||  |  ||||||     |||||
                                GGCC  T  TGCCAC     GGCTC
                                  TT GT     CCCGCT
GAM342  LOC148014 3'  TCGGGATGTAATTGGCTGA   79314       GGTGATGG
                                TCGGT       TGCATCCCGA
                                |||||       ||||||||||
                                AGTCG       ATGTAGGGCT
                                   GTTA____
GAM342  LOC148894 3'  CTTGGGTGCATGTGTATCATTG 85421          ATG    T
          G                      TCGGTGGTG   GTGCA CCCGAG
                                |||||||||   ||||| ||||||
                                GGTTACTAT   TACGT GGGTTC
                                      GTG    _
GAM342  LOC149319 5'  CTTGGGGCCCCCGTCTGCTGCT 80072      TG  _    T_  AT
          GG                      TCGG  GT GATGG  GC  CCCGAG
                                ||||  || |||||  ||  ||||||
                                GGTC  CG CTGCC  CG  GGGTTC
                                  GT  T    CC  __
GAM342  LOC149386 5'  GATGTCATCATTTTTGG     85558      TG     GT
                                TCGG  GTGATG  GCATC
                                ||||  ||||||  |||||
                                GGTT  TACTAC  TGTAG
                                  TT     __
GAM342  LOC149668 3'  TTGGGGTGTCCTGCCCTGG    85706      T   GAT  T
                                TCGG GGT   GG GCATCCCGA
                                |||| |||   || |||||||||
                                GGTC CCG   CC TGTGGGGTT
                                  _   T__  _
GAM342  LOC149685 5'  TGTGGGTTTGCTGTTGTTATTG 80297        TG     CAT    AG
          A                      TCGGTGG  ATGGTG   CCCG
                                |||||||  ||||||   ||||
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                                AGTTATT  TGTCGT   GGGT
                                    GT     TT_   GTC
GAM342   LOC150208 5'  TTTGGGAAAACTATCGCCATGG 86080    G         GCA
                                C GTGGTGATGGT   TCCCGAG
                                | ||||||||||   |||||||
                                G TACCGCTATCA   AGGGTTT
                                 G         AA_
GAM342   LOC150333 5'  CTCCATCATCACCATCACCATT 86212            CATCCC
                                GGTGGTGATGGTG     GAG
                                ||||||||||||     |||
                                TTACCACTACCAC     CTC
                                       TACTAC
GAM342   LOC150445 5'  CTCCATGTCGCTGTTGCCGCC  80676      TG     _   CCC
                                GGTGG  ATGGTG CAT   GAG
                                |||||  |||||| |||   |||
                                CCGCC  TGTCGC GTA   CTC
                                   GT     T   C__
GAM342   LOC150498 3'  CTTGGAAACTCCCCATTGTCAC 80720       TG    TGCATC_
            TGA                    TCGGTGG  ATGG      CCGAG
                                |||||||  ||||      |||||
                                AGTCACT  TACC      GGTTC
                                    GT    CCTCAAA
GAM342   LOC151009 5'  CGCCGTCCTCGCCATCGG    86365         ___
                                TCGGTGGT   GATGGTG
                                ||||||||   |||||||
                                GGCTACCG   CTGCCGC
                                     CTC
GAM342   LOC151009 5'  CTCGTCATCGTTGTCACC    86368      TG     CATCC
                                GGTGG  ATGGTG    CGAG
                                |||||  ||||||    ||||
                                CCACT  TGCTAC    GCTC
                                   GT     T____
GAM342   LOC151277 5'  ATGCCATTATCACATCGA    81005       G      _
                                TCGGTG TGATGGTG CAT
                                |||||| |||||||| |||
                                AGCTAC ACTATTAC GTA
                                   _       C
GAM342   LOC151477 3'  TTCGGGATGGGCCTCATTGATG 81059     GT    T   G
            G                     TCG  GGTGA GGT CATCCCGAG
                                |||  ||||| ||| |||||||||
                                GGT  TTACT CCG GTAGGGCTT
                                  AG    _  G
GAM342   LOC151516 5'  CTTGGGATGTGGGCTGGCTGG  81064      GGTGA   __
                                TCGGT    TGGT  GCATCCCGAG
                                |||||    ||||  ||||||||||
                                GGTCG    GTCG  TGTAGGGTTC
                                   ______   GG
GAM342   LOC151877 3'  GACACACTGTTACTGTCC    86697    _        CA
                                GG TGGTGATGGTG  TC
                                || ||||||||||  ||
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                                CC GTCATTGTCAC  AG
                                 T         AC
GAM342  LOC152185 3'  CTTGGGAAGTCATTGCTG    59202     TG    GGTGCA
                                CGG  GTGAT     TCCCGAG
                                |||  |||||     |||||||
                                GTC  TACTG     AGGGTTC
                                  GT    A_____
GAM342  LOC152633 5'  CTCGGGATGCCCCACACTGCC  86995    TG   A   T
                                GG  GTG TGG GCATCCCGAG
                                ||  ||| ||| ||||||||||
                                CC  CAC ACC CGTAGGGCTC
                                 GT   _   C
GAM342  LOC153505 3'  TTCGGGATGCTGTTCACCTTGG 81709      T    TGGT
                                TCGG GGTGA    GCATCCCGAG
                                |||| |||||    ||||||||||
                                GGTT CCACT    CGTAGGGCTT
                                  _     TGT_
GAM342  LOC154849 3'  CTTGGCAACTCCCCATTGTCAC 60942       TG    TGCATC_
           TGA                    TCGGTGG  ATGG      CCGAG
                                |||||||  ||||      |||||
                                AGTCACT  TACC      GGTTC
                                    GT    CCTCAAC
GAM342  LOC154860 5'  CTCGGGGACAATCACTACT    87501        G  GCA
                                GGTGGTGAT GT   TCCCGAG
                                |||||||| ||   |||||||
                                TCATCACTA CA   GGGGCTC
                                     A  ___
GAM342  LOC155072 5'  GCATGGTGCTTCGTCACCACCG 87667           T    CCGAG
           G                     TCGGTGGTGATGG GCATC
                                ||||||||||||| |||||
                                GGCCACCACTGCT CGTGG
                                       T    TACGT
GAM342  LOC155340 5'  TTTGGGGTGTGGGCAGCGCCCT 73770     T    ATG  __
           GA                    TCGG GGTG   GT  GCATCCCGAG
                                |||| ||||   ||  ||||||||||
                                AGTC CCGC   CG  TGTGGGGTTT
                                  _   GA_  GG
GAM342  LOC157349 5'  CTCGAGTGCTGTCTTCATTGA  82338       T    TG ATCC
                                TCGGTGG GATGG  C    CGAG
                                |||||||  |||||  |    ||||
                                AGTTACT CTGTC  G    GCTC
                                    T    GT A___
GAM342  LOC158364 5'  TTTGGATGGAAATCATTATTAT 82759          G__    CGAG
           TG                    CGGTGGTGATGGT   CATCC
                                ||||||||||||   |||||
                                GTTATTATTACTA   GTAGG
                                       AAG    TTT
GAM342  LOC158656 5'  CTCGTGCCATTGTTGCCATTGA 73399       TG TG   _  TCC
                                TCGGTGG  A  GTG CA   CGAG
                                |||||||  |  ||| ||   ||||
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                                AGTTACC  T  TAC GT   GCTC
                                   GT GT   C  ___
GAM342  LOC158863 3'  TTTGGGATGCTGAGGTCGGCG  88299    G   GGT_
                                TG TGAT    GCATCCCGAG
                                || ||||    ||||||||||
                                GC GCTG    CGTAGGGTTT
                                 G   GAGT
GAM342  LOC158969 3'  CTTGGCTTGCTGTCACTATAGA 82935    G      GGT   TC
                                TC GTGGTGAT   GCA  CCGAG
                                || ||||||||   |||  |||||
                                AG TATCACTG   CGT  GGTTC
                                 A       T__   TC
GAM342  LOC160335 5'  TTCGCCTGAACCATGCCATTGG 83085        G    G  TCC
                                TCGGTGGT ATGGT CA   CGAG
                                |||||||| ||||| ||   ||||
                                GGTTACCG TACCA GT   GCTT
                                     _    A  CC_
GAM342  LOC161589 5'  TTCGGGCAAGTCCACCACTGCT 83163     TG   A   TGCAT
           GG                    TCGG  GTG TGG    CCCGAG
                                ||||  ||| |||    ||||||
                                GGTC  CAC ACC    GGGCTT
                                  GT   C   TGAAC
GAM342  LOC161742 3'  TTTGCAGAGCATTATATTACTG 83170         A     A  C_
           G                     TCGGTGGTG TGGTGC TC  CGAG
                                |||||||| |||||| ||  ||||
                                GGTCATTAT ATTACG AG  GTTT
                                     _     _  AC
GAM342  LOC164584 5'  CTCCACGGCGTCGTCGCTAACG 83419     G       GT  ATCCC
           A                     TCG TGGTGATG  GC     GAG
                                ||| ||||||||  ||     |||
                                AGC ATCGCTGC  CG     CTC
                                  A       TG  GCAC_
GAM342  LOC170409 3'  TTTGGGATGCGCGGAGGCTCTG 83749     T   GATG
           A                     TCGG GGT    GTGCATCCCGAG
                                |||| |||    ||||||||||||
                                AGTC TCG    CGCGTAGGGTTT
                                  _   GAGG
GAM342  LOC196264 3'  TTTGAATGTTTGCCACACCGCT 88996         A   __   CC
           GA                    TCGGTGGTG TGGT  GCAT  CGAG
                                |||||||| ||||  ||||  ||||
                                AGTCGCCAC ACCG  TGTA  GTTT
                                     _   TT    A_
GAM342  LOC197201 3'  CCGCTGGCATTAGCATTGCTGG 89272     TG   A     ATCC  AG
                                TCGG  GTG TGGTGC    CG
                                ||||  ||| ||||||    ||
                                GGTC  TAC ATTACG    GC
                                  GT   G     GTC_  CT
GAM342  LOC199787 3'  CTCGGTGAGGACCATGTCGCTG 89776       GT A   GCA  _
           G                     TCGGTG  G TGGT   TC CCGAG
                                ||||||  | ||||   || |||||
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                                GGTCGC  T ACCA   AG GGCTC
                                   TG _    GG_  T
GAM342  LOC200138 5'  TTTGGGGAACCCATGGTTGTTG 91545     TG TG    TGCA
           G                    TCGG  G  ATGG    TCCCGAG
                                ||||  |  ||||    |||||||
                                GGTT  T  TACC    GGGGTTT
                                  GT GG    CAA_
GAM342  LOC200213 5'  CTCGGCTGCCGGCGCCACCGA  90030         A     CATC
                                TCGGTGGTG TGGTG    CCGAG
                                |||||||||| |||||    |||||
                                AGCCACCGC GCCGT    GGCTC
                                     G    C___
GAM342  LOC200227 3'  CTTGGGCTTCTGTTATTGCTTG 90042     _ TG      TGCAT
           A                    TCG G  GTGATGG    CCCGAG
                                ||| |  |||||||    ||||||
                                AGT C  TATTGTC    GGGTTC
                                  T GT      TTC__
GAM342  LOC200471 3'  CTCATTCGCTTTTACTATTGA  91635         T    C  CCC
                                TCGGTGGTGA GGTG AT   GAG
                                ||||||||||| |||| ||   |||
                                AGTTATCATT TCGC TA   CTC
                                     T    T  ___
GAM342  LOC200830 3'  CTTGTCCTTCTACCATCATCAC 91727             CATCC_
           TGG                    TCGGTGGTGATGGTG     CGAG
                                  ||||||||||||||     ||||
                                  GGTCACTACTACCAT     GTTC
                                        CTTCCT
GAM342  LOC201475 5'  CTTGTGTGGCATTGTTGCTCTT 89619     T  TG TG    ATCC
           GG                     TCGG GG  A  GTGC    CGAG
                                  |||| ||  |  ||||    ||||
                                  GGTT TC  T  TACG    GTTC
                                    C  GT GT    GTGT
GAM342  LOC202108 5'  TTCGGGCAAGTCCACCACTACT 90632         A   TGCAT
           GG                     TCGGTGGTG TGG     CCCGAG
                                  |||||||||| |||     ||||||
                                  GGTCATCAC ACC     GGGCTT
                                       C   TGAAC
GAM342  LOC202754 3'  CTCGTTCTATCACATTATTGA  83587         A     CATCC
                                  TCGGTGGTG TGGTG     CGAG
                                  |||||||||| |||||     ||||
                                  AGTTATTAC ACTAT     GCTC
                                       _    CTT__
GAM342  LOC202868 5'  GCATGGTGCTTTGTCATCACCG 92004          TG T     CCGAG
           G                      TCGGTGGTGA  G GCATC
                                  ||||||||||  | |||||
                                  GGCCACTACT  T CGTGG
                                        GT T     TACGT
GAM342  LOC202934 5'  TTTGGGAGACTTTTTGTTACTG 92060         TG T_   GCA
           A                      TCGGTGG  A  GGT   TCCCGAG
                                  |||||||  |  |||   |||||||
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                                AGTCATT  T  TCA   AGGGTTT
                                   GT TT   G__
GAM342  LOC203369 3'  ATGACTGTCATTGCTGG     90880      TG       G
                                TCGG  GTGATGGT CAT
                                ||||  |||||||| |||
                                GGTC  TACTGTCA GTA
                                  GT       _
GAM342  LOC203411 3'  CTTGAAGGTATCGTAATTGCCG 92313      TG  G      ATCC
           G                     TCGG  GT ATGGTGC    CGAG
                                ||||  || |||||||    ||||
                                GGCC  TA TGCTATG    GTTC
                                  GT  A      GAA_
GAM342  LOC219513 5'  TTGGGGTGTTACATTCTGG    95992      TGGT    GT
                                TCGG    GATG  GCATCCCGA
                                ||||    ||||  |||||||||
                                GGTC    TTAC  TGTGGGGTT
                                  _____   AT
GAM342  LOC219848 3'  TTTGGATATCAGCTGTCATCAC 93128            GC__    CGAG
           CGA                    TCGGTGGTGATGGT    ATCC
                                ||||||||||||||    ||||
                                AGCCACTACTGTCG    TAGG
                                       ACTA    TTT
GAM342  LOC219899 3'  CTTGGTTATCATTACTGTTGG  93132      TG       CATC
                                TCGG  GTGATGGTG    CCGAG
                                ||||  |||||||||    |||||
                                GGTT  CATTACTAT    GGTTC
                                  GT       T___
GAM342  LOC219994 3'  TCGGAAATCTCACTGTCGG    95008      TG    T   GCATC
                                TCGG  GTGA GGT     CCGA
                                ||||  |||| |||     ||||
                                GGCT  CACT CTA     GGCT
                                  GT    _   AA___
GAM342  LOC220135 5'  CTCATAGATGCCGTCATCTTGG 96016      T      GT     CC_
                                TCGG GGTGATG  GCATC   GAG
                                |||| |||||||  |||||   |||
                                GGTT CTACTGC  CGTAG   CTC
                                  _      __     ATA
GAM342  LOC220522 5'  CTTGGGGCCCCCGTCTGCTGCT 61140      TG  _    T_  AT
           GG                     TCGG  GT GATGG  GC  CCCGAG
                                ||||  || |||||  ||  ||||||
                                GGTC  CG CTGCC  CG  GGGTTC
                                  GT  T    CC  __
GAM342  LOC220558 3'  CTCCCCAGGCACCTTCACCATC 92773          T    ATCCC
           GG                     TCGGTGGTGA GGTGC    GAG
                                ||||||||||| |||||    |||
                                GGCTACCACT CCACG    CTC
                                     T    GACCC
GAM342  LOC220846 3'  TTGGGGTTTTATCTCTGG    92486      T    TGGTGC
                                TCGG GGTGA     ATCCCGA
                                |||| |||||     |||||||
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                                GGTC CTATT     TGGGGTT
                                  T    T_____
GAM342  LOC221288 3'  TTTGGCTGATTATTGCTGCC  95265    TG TG    G  TC
                                GG  G  ATGGT CA  CCGAG
                                ||  |  ||||| ||  |||||
                                CC  C  TATTA GT  GGTTT
                                 GT GT    _  C_
GAM342  LOC221543 5'  CTCGGAGGGTGCCATTTTGTCG 95373     TG T    TG A  _
          G                      TCGG  G GATGG  C TC CCGAG
                                ||||  | |||||  | || |||||
                                GGCT  T TTACC  G GG GGCTC
                                  GT _    GT _  A
GAM342  LOC221839 5'  TTCGGGCAAGTCCACCACTACT 94099         A   TGCAT
          GG                     TCGGTGGTG TGG    CCCGAG
                                |||||||||| |||    ||||||
                                GGTCATCAC ACC    GGGCTT
                                     C   TGAAC
GAM342  LOC221929 5'  TTTGGGATGTGTCCTAGCATT  94234     G  AT  TG
                                GGTG TG  GG  CATCCCGAG
                                |||| ||  ||  |||||||||
                                TTAC AT  CT  GTAGGGTTT
                                  G  C_  GT
GAM342  LOC222256 3'  TTTGGGGTGTGGAATTGTTGT  95914   TG TG  GG
                                G  G  AT  TGCATCCCGAG
                                |  |  ||  ||||||||||
                                T  T  TA  GTGTGGGGTTT
                                 GT GT  AG
GAM342  LOC222776 5'  TTGGGCTCTGCGCCGCCGA   96021         A   T  ATC
                                TCGGTGGTG TGG GC   CCGA
                                |||||||| ||| ||   ||||
                                AGCCGCCGC GTC CG   GGTT
                                     _   T  ___
GAM342  LOC253167 3'  TTCAGGGTCTGTTACCATTGA  97633           TGC    C
                                TCGGTGGTGATGG   ATCC GAG
                                ||||||||||||   |||| |||
                                AGTTACCATTGTC   TGGG CTT
                                      ___    A
GAM342  LOC253443 5'  TTCGTTTTTCATTGTTATTATT 97558         TG   CATCC
          G                      CGGTGGTGA  GTG    CGAG
                                |||||||||  |||    ||||
                                GTTATTATT  TAC    GCTT
                                     GT   TTTTT
GAM342  LOC253531 5'  TGCCTCAGCTGTACCACTGA   98224         G    ____
                                TCGGTGGT ATGGT    GCA
                                |||||||| |||||    |||
                                AGTCACCA TGTCG    CGT
                                     _    ACTC
GAM342  LOC253805 3'  CTCCACCCATCACACTACTGA  98172          A    CATCCC
                                TCGGTGGTG TGGTG     GAG
                                |||||||||  |||||     |||
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                                AGTCATCAC ACTAC     CTC
                                      _    CCAC__
GAM342  LOC254128 3'  GCCCAGTGCGTTGTTTTTACTG 97359       T  GG    CCCGAG
            G                  TCGGTGG GAT  TGCAT
                               ||||||| |||  |||||
                               GGTCATT TTG  GCGTG
                                   T  TT    ACCCGT
GAM342  LOC254147 5'  CTCGGGACGCTTTTGTTGCCGG 97975     TG TG T   CA
                               TCGG  G  A GGTG  TCCCGAG
                               ||||  |  | ||||  |||||||
                               GGCC  T  T TCGC  AGGGCTC
                                 GT GT T   __
GAM342  LOC254173 3'  CTCGGATGACACTAACGCCGCC 98643         A   _   C
            GG                   TCGGTGGTG TGGTG CATCC GAG
                               ||||||||| ||||| ||||| |||
                               GGCCGCCGC ATCAC GTAGG CTC
                                    A   A   _
GAM342  LOC254381 5'  CTCTAACCACCGTCACCCTGG  99327     T       CATCCC
                               TCGG GGTGATGGTG     GAG
                               |||| ||||||||||     |||
                               GGTC CCACTGCCAC     CTC
                                 _        CAAT__
GAM342  LOC254820 3'  TTTGGGATGTGTATATTCTTTT 99183     T  TGATG TG
            GA                   TCGG GG    G  CATCCCGAG
                               |||| ||    |  |||||||||
                               AGTT TC    T  GTAGGGTTT
                                 T  TTATA GT
GAM342  LOC255043 3'  CTCGGGGAGGGTCATCATTGT  97069   TG     TGCA
                               G  GTGATGG   TCCCGAG
                               |  |||||||   |||||||
                               T  TACTACT   GGGGCTC
                                GT     GGGA
GAM342  LOC255242 5'  CTTGGGATGCAGGAGCTGTTCC 97615     T__  GATGG
            GG                   TCGG   GGT    TGCATCCCGAG
                               ||||   |||    ||||||||||
                               GGCC   TCG    ACGTAGGGTTC
                                 TTG   AGG__
GAM342  LOC255458 3'  CTTGGACTTCCATGCCACCGG  98935       G   TGCATC
                               TCGGTGGT ATGG     CCGAG
                               |||||||| ||||     |||||
                               GGCCACCG TACC     GGTTC
                                    _   TTCA__
GAM342  LOC255465 3'  CTTGGCCAGACTGCAGTTGTTA 99113       TG  GG   _ ___
            TTGG                  TCGGTGG  AT  TGCA TC   CCGAG
                               |||||||  ||  |||| ||   |||||
                               GGTTATT  TG  ACGT AG   GGTTC
                                   GT  __    C  ACC
GAM342  LOC255465 5'  TTTGGGAGACATTTTGTTACTG 99133       TG T    CA
            A                    TCGGTGG  A GGTG  TCCCGAG
                               |||||||  | ||||  |||||||
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                                AGTCATT  T TTAC  AGGGTTT
                                   GT _    AG
GAM342   LOC255520 3'  TTTGGGTTTCTGTGATTATTGA 97556        G    TGCAT
                                TCGGTGGT ATGG     CCCGAG
                                |||||||| ||||     ||||||
                                AGTTATTA TGTC     GGGTTT
                                     G    TTT__
GAM342   LOC255620 5'  TTTGGGGTGTGGGCAGCACCCT 98876      T    ATG __
           GA                     TCGG GGTG   GT  GCATCCCGAG
                                |||| ||||   ||  ||||||||||
                                AGTC CCAC   CG  TGTGGGGTTT
                                  _    GA_  GG
GAM342   LOC255621 5'  TGGGCACTGTTACCACTGG    98886             ATC
                                TCGGTGGTGATGGTGC   CCG
                                ||||||||||||||||   |||
                                GGTCACCATTGTCACG   GGT
                                                ___
GAM342   LOC255761 5'  TGTCGCCATCACCCTCGA     98016      T        _
                                TCGG GGTGATGGTG CA
                                |||| |||||||||| ||
                                AGCT CCACTACCGC GT
                                  C         T
GAM342   LOC255762 3'  TGCAACATATCACTATTGG    96734           _ _
                                TCGGTGGTGATG GT GCA
                                |||||||||||| || |||
                                GGTTATCACTAT CA CGT
                                      A  A
GAM342   LOC256087 5'  CTCGCGCGGCTGTTGCCGCTG  96824       TG    _ ATCC
                                CGGTGG  ATGGT GC    CGAG
                                ||||||  ||||| ||    ||||
                                GTCGCC  TGTCG CG    GCTC
                                   GT     G  C___
GAM342   LOC256158 5'  TTTGGGGTGACCCTGGCCACTG 99521         GAT   G
           G                     TCGGTGGT   GGT CATCCCGAG
                                ||||||||   ||| |||||||||
                                GGTCACCG   CCA GTGGGGTTT
                                     GTC   _
GAM342   LOC256586 5'  TGGGCGCCGGCGTCATCGA    96621       GT A     ATC
                                TCGGTG  G TGGTGC   CCG
                                ||||||  | ||||||   |||
                                AGCTAC  C GCCGCG   GGT
                                   TG G     ___
GAM342   LOC256714 3'  TGTCACCCTTACCGCTGG     98049          T   _
                                TCGGTGGTGA GGTG CA
                                |||||||||| |||| ||
                                GGTCGCCATT CCAC GT
                                      C    T
GAM342   LOC257249 5'  GTGCATTTGTTACTACTGA    97613          TG _
                                TCGGTGGTGA  G TGCAT
                                ||||||||||  | |||||
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                                AGTCATCATT  T ACGTG
                                      GT T
GAM342  LOC257319 3'  CTTGTTTAACTTGTTGCTACTG 97471       TG  _  GCATCC
            G                   TCGGTGG  ATG GT     CGAG
                                |||||||  ||| ||     ||||
                                GGTCATC  TGT CA     GTTC
                                   GT   T  ATTT__
GAM342  LOC257494 3'  TTTGGGGTACAAGCTGTGATCA 99636        G    GC__
            CTGA                  TCGGTGGT ATGGT    ATCCCGAG
                                |||||||| |||||   ||||||||
                                AGTCACTA TGTCG    TGGGGTTT
                                     G    AACA
GAM342  LOC257554 5'  TTGGGGTGCTGCCTGCTGG   99539      GTGAT  _
                                TCGGTG    GGT GCATCCCGA
                                ||||||    ||| |||||||||
                                GGTCGT    CCG CGTGGGGTT
                                  _____  T
GAM342  LOC257596 5'  CTCGGAGGGTGCCATTTTGTCG 99776     TG T    TG A  _
            G                   TCGG  G GATGG  C TC CCGAG
                                ||||  | |||||  | || |||||
                                GGCT  T TTACC  G GG GGCTC
                                  GT _    GT _  A
GAM342  LOC50999  3'  CTTGGATAATTCATTATTACC  32637         TGC   C
                                GGTGGTGATGG   ATCC GAG
                                ||||||||||   |||| |||
                                CCATTATTACT   TAGG TTC
                                      TAA   _
GAM342  LOC51003  3'  TTGGGAAAGCTACCATTGA   32672       GAT   GCA
                                TCGGTGGT   GGT   TCCCGA
                                ||||||||   |||   ||||||
                                AGTTACCA   TCG   AGGGTT
                                     ___   AA_
GAM342  LOC51014  3'  AGAATTGATGCACCATTGCCAC 66423      TG       CCGAG
            TG                    CGGTGG  ATGGTGCATC
                                ||||||  ||||||||||
                                GTCACC  TACCACGTAG
                                   GT        TTAAGAG
GAM342  LOC51107  3'  TTTGGGAACTGGCATTACTGG  32611        AT   GCA
                                TCGGTGGTG  GGT   TCCCGAG
                                |||||||||  |||   |||||||
                                GGTCATTAC  TCA   AGGGTTT
                                     GG  ___
GAM342  LOC51161  3'  CTCCACTGCATTGTTTCACTGG 33040       T  TG    TCCC
                                TCGGTGG GA  GTGCA    GAG
                                |||||||  ||  |||||   |||
                                GGTCACT TT  TACGT    CTC
                                   _  GT    CAC_
GAM342  LOC51185  3'  TTTGGAAATTATTGCCTCTGA  33300     T  TG    GCATC
                                TCGG GG  ATGGT    CCGAG
                                ||||  ||  |||||    |||||
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                                AGTC CC  TATTA    GGTTT
                                  T  GT    AA___
GAM342  LOC51193  3' TTTGAGCCACTATCTATTGTTG 33375     TG _     CA  CCGAG
             A                   TCGG  GT GATGGTG  TC
                                 ||||  || |||||||  ||
                                 AGTT  TA CTATCAC  AG
                                   GT  T     CG  TTT
GAM342  LOC51339  3' CTCACTGAGCGCTATGCCACCG 34092        G     A  CC_
             A                   TCGGTGGT ATGGTGC TC   GAG
                                 ||||||||| ||||||| ||   |||
                                 AGCCACCG TATCGCG AG   CTC
                                     _     _  TCA
GAM342  LOC89919  3' GGGTGCCATTACCATTGG    61376          GT
                                 TCGGTGGTGATG  GCATCC
                                 ||||||||||||  ||||||
                                 GGTTACCATTAC  CGTGGG
                                               __
GAM342  LOC89941  3' TGGGTGTGCCTCGCTGCTGG   57853     TG    T  TG  T
                                 TCGG  GTGA GG  CA CCCG
                                 ||||  |||| ||  || ||||
                                 GGTC  CGCT CC  GT GGGT
                                   GT    _  GT  _
GAM342  LOC90835  5' CTTGGCAACCGTCGCCGTTGA  64814    GG        GCATC
                                 TC  TGGTGATGGT    CCGAG
                                 ||  ||||||||||    |||||
                                 AG  GCCGCTGCCA    GGTTC
                                  TT         AC___
GAM342  LOC91035  5' TTTGGGACAGGCTGTTGCTGTC 65310    TG TG    GCA
                                 GG  G  ATGGT   TCCCGAG
                                 ||  |  |||||   |||||||
                                 CT  C  TGTCG   AGGGTTT
                                  GT GT    GAC
GAM342  LOC91064  5' TTTGGGGCAAAGTGGTTGCTAT 65394        TG  G ___   AT
             TGG                   TCGGTGG  AT G   TGC  CCCGAG
                                 |||||||  || |   |||  ||||||
                                 GGTTATC  TG T   ACG  GGGTTT
                                     GT  G GAA  __
GAM342  LOC91308  5' TTTGGGGTGTAAAGTGCCAT   66170      G  GG
                                 GTGGT AT  TGCATCCCGAG
                                 |||||  ||  ||||||||||
                                 TACCG TG  ATGTGGGGTTT
                                   _  AA
GAM342  LOC91355  5' CTTGAGTGTTGCTGTGGCTGCC 66307     TG  G     _   CC
             GA                    TCGG  GT ATGGTG CAT  CGAG
                                 ||||  || |||||| |||  ||||
                                 AGCC  CG TGTCGT GTG  GTTC
                                   GT  G     T   A_
GAM342  LOC91355  5' TTTGGGTTTACATGCTGCTGG  66312     TG  G   GTGCAT
                                 TCGG  GT ATG     CCCGAG
                                 ||||  || |||     ||||||
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                                GGTC  CG TAC     GGGTTT
                                  GT  _   ATTT__
GAM342  LOC91408  3'  CTTGAGGTATTTTGCCACTGG  66516       TG T    ATCC
                                TCGGTGG  A GGTGC   CGAG
                                |||||||  | |||||   ||||
                                GGTCACC  T TTATG   GTTC
                                    GT _    GA__
GAM342  LOC91875  3'  TTGGGATCTTGCCATGGG    68037    G   TG T GTGC
                                TC GTGG  A G   ATCCCGA
                                || ||||  | |   |||||||
                                GG TACC  T C   TAGGGTT
                                 G   GT _ _____
GAM342  LOC91974  5'  CTTAGGAATATGCTATCATTGT 68362     TG      GC  _  CG
          TGA                     TCGG  GTGATGGT  AT CC  AG
                                ||||  ||||||||  || ||  ||
                                AGTT  TACTATCG  TA GG  TC
                                  GT       TA  A  AT
GAM342  LOC92710  5'  TTCGGGAAGTACACTGCCATCG 70873         ATG   A
          G                      TCGGTGGTG   GTGC TCCCGAG
                                |||||||||   |||| |||||||
                                GGCTACCGT   CATG AGGGCTT
                                     CA_   A
GAM343  ADAR    3'  TGAAAACTTTGGGTTCCCA   32365         C   GAGAGAG
                                TGGGGACCC AAG      TCA
                                ||||||||| |||      |||
                                ACCCTTGGG TTC      AGT
                                     T   AAA_____
GAM343  ADCY6   5'  CTGACTGTGTCTTGGGTTCTCA 40952         C    AGAG
                                TGGGGACCC AAGG    AGTCAG
                                ||||||||| ||||    ||||||
                                ACTCTTGGG TTCT    TCAGTC
                                     _   GTG_
GAM343  AGA     3'  TTGATTTTCTTTGCTTTTTTCC 5252       CCCCAA_
          TC                      GGGGA      GGAGAGAGTCAG
                                |||||      ||||||||||||
                                CTCCT      TTTCTTTTAGTT
                                   TTTTTCG
GAM343  AICDA   3'  TGGCTCTCGTGGGTCTCT    40701         CAAGGA
                                GGGGACCC     GAGAGTCA
                                ||||||||     ||||||||
                                TCTCTGGG     CTCTCGGT
                                     TG_____
GAM343  AMD1    3'  CTTTTTTTGGTGTTTCTA    9684      GG  C
                                TGG  AC CCAAGGAGAG
                                |||  || ||||||||||
                                ATC  TG GGTTTTTTTC
                                  TT  T
GAM343  APOBEC1  3'  CTGGTTCTTGTCCTGGAGTCCC 20835       C   A   _   GT
          T                      GGGGAC CCA GGA GAGA  CAG
                                ||||||| ||| ||| ||||  |||
```

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                                TCCCTG GGT CCT TTCT  GTC
                                   A  _  G   TG
GAM343  AQP6     3'  CTGGCCGCGCCTTGGGTTCCT  55002     C      AGAGA
                                GGGA CCCAAGG    GTCAG
                                |||| |||||||    |||||
                                TCCT GGGTTCC    CGGTC
                                  T      GCGC_
GAM343  ARF3     3'  TTGTTTTTTTGGGGGCTCCA  9783       A        G
                                TGGGG CCCCAAGGAGA AG
                                ||||| |||||||||| ||
                                ACCTC GGGGTTTTTTT TT
                                   G         G
GAM343  ARHGEF12 3'  TTGACTTTCTTTGGTTTTCCT  31652      CC   AG
                                GGGGA  CCA  GAGAGAGTCAG
                                |||||  |||  ||||||||||
                                TCCTT  GGT  TTCTTTCAGTT
                                   TT  __
GAM343  ASTN     3'  CTGGTTTTCTTCCTAGGCCTT  69871     A  CCA   _   GT
                                GGGG CC   AGGA GAGA  CAG
                                |||| ||   |||| ||||  |||
                                TTCC GG   TCCT CTTT  GTC
                                  _ A__    T    TG
GAM343  B3GNT3   3'  GAGTTTCTGGGGTCCTCA    27304          AGGA   G
                                TGGGGACCCCA   GAGA TC
                                ||||||||||    |||| ||
                                ACTCCTGGGGT    CTTT AG
                                      ____   G
GAM343  BAIAP3   3'  CTGCCCGCTTCCTTGGGCTCCC 15439      C      G  AGT_
           C                     GGGGA CCCAAGGA AG    CAG
                                |||||  |||||||| ||    |||
                                CCCCT GGGTTCCT TC    GTC
                                   C       _ GCCC
GAM343  BAT4     5'  CTGATTTTTTTTTCCTACTGGT 53742        CCA      ___
           CTCT                   GGGGACC   AGGAGAGA   GTCAG
                                |||||||   ||||||||   |||||
                                TCTCTGG   TCCTTTTT   TAGTC
                                    TCA       TTT
GAM343  BCL6     5'  TTGATTCTTAGAACTGGGGTTC 9919           A GA__
           TTA                    TGGGGACCCCA G    GAGAGTCAG
                                ||||||||||| |    |||||||||
                                ATTCTTGGGGT C    TTCTTAGTT
                                      _ AAGA
GAM343  BHLHB3   3'  CTGGCTCTTTTTTTTAATCCCC 48485      ACCCC
           CA                     TGGGG    AAGGAGAGAGTCAG
                                |||||    ||||||||||||||
                                ACCCC    TTTTTTTCTCGGTC
                                   CTAAT
GAM343  BRCA1    3'  CTGGTTCTTTTACTAAGTGTTC 24560     G  CCCAAG     GT
           A                      TGGG AC     GAGAGA  CAG
                                ||||  ||     ||||||  |||
```

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                                ACTT TG     TTTTCT  GTC
                                  G  AATCA_     TG
GAM343  BST2     3'  GCTTTTTTCTGGGGTCTTTG  16340   GG       A
                                T  GGACCCCA GGAGAGAGT
                                |  |||||||| |||||||||
                                G  TCTGGGGT CTTTTTTCG
                                 TT       _
GAM343  CALB2    3'  CCTTTTCTCTTTGGGTTTCTT  9980       C          TCAG
                                GGGGA CCCAAGGAGAGAG
                                ||||| ||||||||||||
                                TTCTT GGGTTTCTCTTTT
                                   T          CCT
GAM343  CALM3    3'  CTGGTTCTCTTTTTTTTTCTTT 19004      CCCC___       GT
            CCCC                   GGGGA      AAGGAGAGA  CAG
                                |||||      |||||||||  |||
                                CCCCT      TTTTTCTCT  GTC
                                   TTCTTTT       TG
GAM343  CALU     3'  TTGATTTTCTTCTTTTTCCCC  8698       CCCC
                                GGGGA    AAGGAGAGAGTCAG
                                |||||    ||||||||||||||
                                CCCCT    TTCTTCTTTTAGTT
                                   TT__
GAM343  CAPZA1   3'  TTGATTCTTTTGTGTTCTCT   73027      CCC  AG
                                GGGGA   CA  GAGAGAGTCAG
                                |||||   ||  ||||||||||
                                TCTCT   GT  TTTTCTTAGTT
                                   T__  G_
GAM343  CARD10   3'  CCACCTTTCCTGGGGTCTCCA  28035          A     A  CAG
                                TGGGGACCCCA GGAGAG GT
                                |||||||||| |||||| ||
                                ACCTCTGGGGT CCTTTC CA
                                      _     _ CCC
GAM343  CCNH     5'  TGATGCGTTTGGGTTCTC    8792         CAAG   AGA
                                GGGGACCC    GAG   GTCA
                                ||||||||    |||   ||||
                                CTCTTGGG    TTT   TAGT
                                     _____  GCG
GAM343  CD28     3'  TTGATTTTTAAGTGGGCTTCC  21562      C    AGGA
                                GGGA CCCA    GAGAGTCAG
                                |||| ||||    |||||||||
                                CCTT GGGT    TTTTTAGTT
                                   C    GAA_
GAM343  CDC34    3'  TTGGCTTTTTCTCCCTCCCCA  16392       CCCCAA
                                TGGGGA     GGAGAGAGTCAG
                                ||||||     ||||||||||||
                                ACCCCT     TCTTTTTCGGTT
                                   CCC___
GAM343  CDK9     3'  CTGGTTTTCTGGATGGTTCCCA 8844         __   AGGA   GT
                                TGGGGACC  CCA   GAGA  CAG
                                ||||||||  |||   ||||  |||
```

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                                ACCCTTGG GGT   CTTT GTC
                                    TA  ____   TG
GAM343 CENPB   3' TTGGTTTTCTTTCCAGATTGGA 70122    GG  _  ___     TCAG
          GGTTTCCA               TGG ACC CCAA  GGAGAGAG
                                |||  ||| ||||  ||||||||
                                ACC TGG GGTT  CCTTTCTT
                                  TT  A   AGA     TTGGTT
GAM343 CLCN3   5' TGACTCTAGGGATCTCCA   10206      C  AAGGAG
                                TGGGGA CCC    AGAGTCA
                                |||||| |||    |||||||
                                ACCTCT GGG    TCTCAGT
                                   A  A_____
GAM343 COL11A1  5' TTGACTTTTTCCCCCTCTCCCT 55528     CCCCAA
                                GGGGA    GGAGAGAGTCAG
                                |||||    ||||||||||||
                                TCCCT    CCTTTTTCAGTT
                                   CTCCC_
GAM343 COL19A1  3' TTGATTTTTTTTTTTTCGTTTT 10268   GG  CCC
          C                     G  GAC   AAGGAGAGAGTCAG
                                |  |||   ||||||||||||||
                                C  TTG   TTTTTTTTTTAGTT
                                 TT  CTT
GAM343 COPA    3' TTGACTTTTTTGAGGTCTTC  16483      C  GGA
                                GGGGACC CAA   GAGAGTCAG
                                ||||||| |||   |||||||||
                                CTTCTGG GTT   TTTTCAGTT
                                    A  ___
GAM343 DISC1   3' CTGACTTTCTTGAAGATCCTCA 38507      CCCCAAG
                                TGGGGA     GAGAGAGTCAG
                                ||||||     ||||||||||||
                                ACTCCT     TTCTTTCAGTC
                                   AGAAG__
GAM343 DLST    3' AGGTCTTTTCTTGGCGTTCCT  10413      C        GTCAG
                                GGGGAC CCAAGGAGAGA
                                |||||| ||||||||||||
                                TCCTTG GGTTCTTTTCT
                                   C         GGAC
GAM343 DNASE1L1 5' CTGTCCCTCTCTTTGGGTCTCC 23017        C      AGT
          A                     TGGGGACCC AAGGAGAG   CAG
                                |||||||| ||||||||   |||
                                ACCTCTGGG TTTCTCTC   GTC
                                    _       CCT
GAM343 EDNRA   3' TTCTTCACTTCTTGGGGTTTTC 64802    GG        A  TCAG
          A                     TG  GACCCCAAGGAG GAG
                                ||  |||||||||||| |||
                                AC  TTGGGGTTCTTC CTT
                                 TT         A  CTT
GAM343 EMP3    5' CTGACTTTTTTCGCGGCTCTC  9244      C  CAA
                                GGGA CC   GGAGAGAGTCAG
                                ||||  ||   ||||||||||||
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                                CTCT GG   CTTTTTTCAGTC
                                  C  CG_
GAM343  EMS1    3'  CTGGTTTTTTTCCTGTGCCCA  57518     G  CCCA     _ GT
                                TGGG AC    AGGAGAG A  CAG
                                |||| ||    ||||||| |  |||
                                ACCC TG    TCCTTTT T  GTC
                                  G _____      T TG
GAM343  EMS1    3'  CTGGTTTTTTTCCTGTGCCCA  19093     G  CCCA     _ GT
                                TGGG AC    AGGAGAG A  CAG
                                |||| ||    ||||||| |  |||
                                ACCC TG    TCCTTTT T  GTC
                                  G _____      T TG
GAM343  ENG     3'  CTGGCTTGGAACACCTTGGGGT 5495            AGA___
          CCCT                    GGGGACCCCAAGG     GAGTCAG
                                |||||||||||||     |||||||
                                TCCCTGGGGTTCC     TTCGGTC
                                      ACAAGG
GAM343  ETV5    3'  TTGATTCTGATGAGGTTTCT   16731    GG   C  AGGAG
                                GG  ACC CA    AGAGTCAG
                                ||  ||| ||    ||||||||
                                TC  TGG GT    TCTTAGTT
                                 TT   A  AG___
GAM343  FBXL3A  3'  TGACATTTTAGGGTCTTCA   25133         CAAG   GA
                                TGGGGACCC   GAGA  GTCA
                                |||||||||   ||||  ||||
                                ACTTCTGGG   TTTT  CAGT
                                     A___   A_
GAM343  FE65L2  3'  CTGGCTCCCCTTTCCTTGGGTC 21291         C     ___
          CTT                     GGGGACCC AAGGAGA   GAGTCAG
                                |||||||| |||||||   |||||||
                                TTCCTGGG TTCCTTT   CTCGGTC
                                     _      CCC
GAM343  FE65L2  3'  CTGGCTCCCCTTTCCTTGGGTC 21292         C     ___
          CTT                     GGGGACCC AAGGAGA   GAGTCAG
                                |||||||| |||||||   |||||||
                                TTCCTGGG TTCCTTT   CTCGGTC
                                     _      CCC
GAM343  FE65L2  3'  CTGGCTCCCCTTTCCTTGGGTC 21293         C     ___
          CTT                     GGGGACCC AAGGAGA   GAGTCAG
                                |||||||| |||||||   |||||||
                                TTCCTGGG TTCCTTT   CTCGGTC
                                     _      CCC
GAM343  FLRT2   3'  TTGACTTTTGAGGGTTTTTA   26008         CAAGGA
                                TGGGGACCC     GAGAGTCAG
                                |||||||||     |||||||||
                                ATTTTTGGG     TTTTCAGTT
                                     AG_____
GAM343  FOSB    3'  CTTTTTTTGGGGTGCCCA    23056      G
                                TGGG ACCCCAAGGAGAG
                                |||| ||||||||||||
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```
                                ACCC TGGGGTTTTTTTC
                                  G
GAM343  GAS7    3'  TGGAACTTTGTGGTCCTT    20863       C    AGAGAG
                                GGGGACC CAAGG     TCA
                                ||||||| |||||     |||
                                TTCCTGG GTTTC     GGT
                                   T    AA____
GAM343  GHRHR   3'  CTGACTCTCTTTTGAGGTCCCT 7705        C   G
                                GGGGACC CAAG AGAGAGTCAG
                                ||||||| |||| ||||||||||
                                TCCCTGG GTTT TCTCTCAGTC
                                   A   _
GAM343  GLP1R   3'  CTGCCCTCCCTGGGGTCCTT   10795         A  A   A T
                                GGGGACCCCA GG GAG G CAG
                                |||||||||| || ||| | |||
                                TTCCTGGGGT CC CTC C GTC
                                     _ _   C _
GAM343  GLRX    3'  TTGGTTTTCTTCTGGATGAGCT 10804     ACC__   A     GT
            CT                    GGGG    CCA GGAGAGA  CAG
                                ||||    ||| |||||||  |||
                                TCTC    GGT CTTCTTT  GTT
                                  GAGTA  _      TG
GAM343  GNB2    3'  CTGGCTTTTTTAAAACTGGTTT 19172       CCAAG_
            T                   GGGACC     GAGAGAGTCAG
                                ||||||     ||||||||||
                                TTTTGG     TTTTTTCGGTC
                                   TCAAAA
GAM343  GRIA3   3'  CTGATTTTTTTTTTCCTTCAGT 24644     G  CCC       ____
            GCCT                   GGG AC   AAGGAGAGA    GTCAG
                                ||| ||   |||||||||    |||||
                                TCC TG   TTCCTTTTT    TAGTC
                                  G  AC_       TTTT
GAM343  GRIN2A  3'  TTGGCTCTTTTGCACACGGCTT 7727       A  CCAAG_
            CA                    TGGGG CC     GAGAGAGTCAG
                                ||||| ||     ||||||||||
                                ACTTC GG     TTTTCTCGGTT
                                   _  CACACG
GAM343  HAO1    3'  TTGACTTTTCAATGGGTGTCCT 34511      _   AG   G
                                GGGAC CCCA  GAGA AGTCAG
                                ||||| ||||  |||| ||||||
                                TCCTG GGGT  CTTT TCAGTT
                                   T   AA   _
GAM343  HDAC7A  3'  CTGGTTCTCTTCTAACCCC   31832     ACCCCA      GT
                                GGGG     AGGAGAGA  CAG
                                ||||     ||||||||  |||
                                CCCC     TCTTCTCT  GTC
                                  AA____       TG
GAM343  HMGA2   3'  TTGACTTTCTCCCTGTTCCT   14460       CCCAA
                                GGGGAC    GGAGAGAGTCAG
                                ||||||    ||||||||||||
```

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                                TCCTTG    CCTCTTTCAGTT
                                   TC___
GAM343  HMGCR    3'  TTGGCTCTTTCAGAGAGGTCTC 7807       CCAAG
                                GGGACC    GAGAGAGTCAG
                                ||||||    ||||||||||
                                CTCTGG    CTTTCTCGGTT
                                   AGAGA
GAM343  HPSE     3'  CTGATTTTCTTCTTTCGGTTTT 22861   GG   CC
             C                   G  GACC  AAGGAGAGAGTCAG
                                |  ||||  ||||||||||||||
                                C  TTGG  TTCTTCTTTTAGTC
                                 TT   CT
GAM343  ICAM1    3'  TTGATTTTTTTTTTTTTTCCA  72042     GG CCCC
                                TGG  A   AAGGAGAGAGTCAG
                                |||  |   ||||||||||||||
                                ACC  T   TTTTTTTTTTAGTT
                                  TT T___
GAM343  ICMT     3'  CTGGCTTTCCCCCGGGGGTCTC 25734        AA  A
                                GGGACCCC  GG GAGAGTCAG
                                ||||||||  || |||||||||
                                CTCTGGGG  CC CTTTCGGTC
                                     GC  C
GAM343  JMJ      5'  TTGGCTCTTTTTTTTTCCTTCC 18326       CCCC
             CA                   TGGGGA   AAGGAGAGAGTCAG
                                ||||||   ||||||||||||||
                                ACCCTT   TTTTTTTCTCGGTT
                                   CCTT
GAM343  KCNA5    3'  CTGACTTTTTCTGTGCGCCTTA 60434      ACCC  A
                                TGGGG   CA GGAGAGAGTCAG
                                |||||   || ||||||||||||
                                ATTCC   GT TCTTTTTCAGTC
                                   GC__  G
GAM343  KCNK1    3'  CTGGAAACTTTGGGGTTTGCA  11163    G        AGAGAG
                                TG GGACCCCAAGG     TCAG
                                || ||||||||||     ||||
                                AC TTTGGGGTTTC     GGTC
                                 G         AAA___
GAM343  KCNK5    3'  TGGGGCCTGGGGTCCTCA    14972          A  AGAGAG
                                TGGGGACCCCA GG     TCA
                                |||||||||| ||     |||
                                ACTCCTGGGGT CC     GGT
                                      _ GG____
GAM343  KRAS2    3'  AAGATTTCTGTCTTGGGGTTTT 54120   GG        _    G  AG
             TG                   T  GGACCCCAAGG AGAGA TC
                                |  |||||||||| ||||| ||
                                G  TTTGGGGTTCT TCTTT AG
                                 TT         G    _ AAT
GAM343  KRAS2    3'  AAGATTTCTGTCTTGGGGTTTT 18374   GG        _    G  AG
             TG                   T  GGACCCCAAGG AGAGA TC
                                |  |||||||||| ||||| ||
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                                G  TTTGGGGTTCT TCTTT AG
                                TT         G    _ AAT
GAM343  LFG     3'  CTGACTTTCTCACCCGGTTCCC 77236         CCAAG
              A                  TGGGGACC    GAGAGAGTCAG
                                 ||||||||    ||||||||||
                                 ACCCTTGG    CTCTTTCAGTC
                                     CCCA_
GAM343  LGS     3'  TTGACTTTTTTTTTTGTCC   33810     CCC
                                 GGAC   AAGGAGAGAGTCAG
                                 ||||   ||||||||||||||
                                 CCTG   TTTTTTTTTCAGTT
                                   T__
GAM343  LILRB4   3'  TGGCTATTTGGGGTCCTT    23389          GGAGAG
                                 GGGGACCCCAA     AGTCA
                                 ||||||||||      |||||
                                 TTCCTGGGGTT     TCGGT
                                       TA____
GAM343  LNK     3'  CTGGCTTTCTCCTTATTGTTTA 19642    GG   CCC
              CA                   TG  GAC   AAGGAGAGAGTCAG
                                   ||  |||   ||||||||||||||
                                   AC  TTG   TTCCTCTTTCGGTC
                                    AT   TTA
GAM343  MADH7    3'  TTGGTTTTCTTCTTCTCGTCCT 20930       CCC       GT
              C                    GGGGAC   AAGGAGAGA  CAG
                                   ||||||   |||||||||  |||
                                   CTCCTG   TTCTTCTTT  GTT
                                      CTC       TG
GAM343  MAPT     3'  TTGATTCTTTTTTCTTCCCC   34180      CCCCA
                                 GGGGA    AGGAGAGAGTCAG
                                 |||||    ||||||||||||||
                                 CCCCT    TTTTTTCTTAGTT
                                    TC___
GAM343  MCL1     3'  TGTTTTTAGGGGCCCCA     41990      A    AAGGA    GT
                                 TGGGG CCCC    GAGA  CA
                                 ||||| ||||    ||||  ||
                                 ACCCC GGGG    TTTT  GT
                                    _   A____    TG
GAM343  MGAT4B   3'  TTGATTTTTTCACGTAAGTCC  27341     CCCAAG
                                 GGAC     GAGAGAGTCAG
                                 ||||     ||||||||||
                                 CCTG     CTTTTTTAGTT
                                   AATGCA
GAM343  MLLT3    3'  TTGATTTTCTTCTTTGTGGTCT 16964        C     _
              TT                   GGGGACC CAAGGA GAGAGTCAG
                                   |||||||  ||||||  |||||||||
                                   TTTCTGG GTTTCT CTTTTAGTT
                                      T     T
GAM343  NFIA     5'  TTGATTTTTTTTTCTCCCC    70890      CCCCA
                                 GGGGA    AGGAGAGAGTCAG
                                 |||||    ||||||||||||||
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                                CCCCT    TTTTTTTTTAGTT
                                  C____
GAM343  NFKBIA   3'  CTCACCTTTGTGGGGTTTTTG  40446   GG      ___  A
                                T  GGACCCCA   AGG GAG
                                |  ||||||||   ||| |||
                                G  TTTGGGGT   TCC CTC
                                 TT       GTT   A
GAM343  NR0B2    3'  CTGGGAGGCTTTTGGTGGTCCC 42019        _    G  AGAG
          CA                      TGGGGACC CCAAG AG    TCAG
                                ||||||||| ||||| ||    ||||
                                ACCCCTGG GGTTT TC    GGTC
                                     T    _  GGAG
GAM343  NR3C2    3'  CTGGCTCTTTGTGTGTCTCCA  8024        CC  AGGA
                                TGGGGAC  CA    GAGAGTCAG
                                |||||||  ||    |||||||||
                                ACCTCTG  GT    TTCTCGGTC
                                     T_  GT__
GAM343  NR4A1    3'  CTGGCTCTCTCTTCCTACCCTC 10945     ACCCCA
          C                       GGGG     AGGAGAGAGTCAG
                                ||||     ||||||||||||
                                CCTC     TTCTCTCTCGGTC
                                  CCATCC
GAM343  NRIP1    3'  TTGGAAGAGGTTTTGTGGTTCC 60626        C    AGAGAG
          CA                      TGGGGACC CAAGG     TCAG
                                |||||||| |||||     ||||
                                ACCCTTGG GTTTT     GGTT
                                     T    GGAGAA
GAM343  OAS2     3'  TTGGTTCTCTCCACCAGGTTCT 11871        CCAA      GT
          T                       GGGGACC    GGAGAGA  CAG
                                |||||||    |||||||  |||
                                TTCTTGG    CCTCTCT  GTT
                                     ACCA      TG
GAM343  OXCT     3'  CTGACTTTTCTTTTGGGGCTTC 6487       A       AG
          A                       TGGGG CCCCAAGG  AGAGTCAG
                                ||||| ||||||||  ||||||||
                                ACTTC GGGGTTTT  TTTCAGTC
                                  _       CT
GAM343  OXTR     3'  TTGATTTTTGACAAGGTTCCCA 8085          CCAAGGA
                                TGGGGACC       GAGAGTCAG
                                ||||||||       |||||||||
                                ACCCTTGG       TTTTTAGTT
                                     AACAG__
GAM343  PACSIN3  3'  CTGACCTCTGCTTTGGGGTTCC 33119           _   A
          T                       GGGGACCCCAAGG AGAG GTCAG
                                |||||||||||| |||| |||||
                                TCCTTGGGGTTTC TCTC CAGTC
                                       G   _
GAM343  PCDH11Y  3'  TTGATTTTTGTTTGTGGTTTTC 53171    GG   C   GA
          A                       TG  GACC CAAG  GAGAGTCAG
                                ||  |||| ||||  |||||||||
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                                AC  TTGG GTTT  TTTTTAGTT
                                 TT   T   G_
GAM343  PCDHB13  3'  TTGATTCTCTTTTTTTTAGTCTT 38937      CCC
                                GGGAC   AAGGAGAGAGTCAG
                                |||||   ||||||||||||||
                                TTCTG   TTTTTCTCTTAGTT
                                   ATT
GAM343  PDCL     3'  TGATTTTCCTGGCTTTTCA   19402    GG  C  CAA  A
                                TG  GA CC   GG GAGAGTCA
                                ||  || ||   || ||||||||
                                AC  TT GG   TC CTTTTAGT
                                 TT  C  ___  _
GAM343  PIK3R2   3'  CTGGCTCTTGTTTGGGGTTCTC 18513           GA
                                GGGGACCCCAAG  GAGAGTCAG
                                ||||||||||||  |||||||||
                                CTCTTGGGGTTT  TTCTCGGTC
                                       G_
GAM343  PIK3R3   3'  CTGTTTCATTGGGGTTTTTG   61705   GG       G   G
                                T  GGACCCCAA GAGA AG
                                |  |||||||||  ||||  ||
                                G  TTTGGGGTT CTTT TC
                                 TT       A   G
GAM343  POLB     5'  CTGGTTCTGAACACTCTGGGGT 12197          AG  _____  GT
           TCTC                   GGGGACCCCA  GAG    AGA  CAG
                                ||||||||||  |||    |||  |||
                                CTCTTGGGGT  CTC    TCT  GTC
                                      __  ACAAG   TG
GAM343  PPBP     3'  TGATTTTCTAGAGTTCTCA   12221       CCCAAGG
                                TGGGGAC      AGAGAGTCA
                                |||||||      |||||||||
                                ACTCTTG      TCTTTTAGT
                                    AGA____
GAM343  PPP1R3C  5'  TGGCTTTTAGGGTCCGCC    19427   _     CAAGGA
                                GG GGACCC     GAGAGTCA
                                || ||||||     ||||||||
                                CC CCTGGG     TTTTCGGT
                                 G     A_____
GAM343  PPP2R4   3'  TTGGCTCTGCTGGGTTTCC   61185   GG   CAA  AG
                                GG  ACCC   GG  AGAGTCAG
                                ||  ||||   ||  ||||||||
                                CC  TGGG   TC  TCTCGGTT
                                 TT   ___  G_
GAM343  PPP3R1   3'  CTGGTTTTTTTTTCTTGATTTG 76828     ACCC_        __
           CCC                    GGG    CAAGGAGAGAG  TCAG
                                |||    ||||||||||  ||||
                                CCC    GTTCTTTTTTT  GGTC
                                  GTTTA         TT
GAM343  PRKWNK3  3'  TGGCTTTACAGGGTTCTCA   62242         CAAGGAG
                                TGGGGACCC      AGAGTCA
                                |||||||||      |||||||
```

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                                ACTCTTGGG      TTTCGGT
                                     ACA____
GAM343  PRX      3'  CTGGGGCTCTGGGGGTCCCC  40894        AAGG   AG
                                GGGGACCCC   AGAG  TCAG
                                |||||||||   ||||  ||||
                                CCCCTGGGG   TCTC  GGTC
                                     G___   GG
GAM343  PTP4A2   5'  TTGATTTTTTTTTTTCACTTTC 14445       CCCC__
            CCCA                  TGGGGA     AAGGAGAGAGTCAG
                                |||||||     ||||||||||||||
                                ACCCCT     TTTTTTTTTTAGTT
                                   TTCACT
GAM343  PUM2     3'  AAACCCTCTTCTTGGGGTCCT  31663             A  CAG
                                GGGACCCCAAGGAGAG GT
                                |||||||||||||||| ||
                                TCCTGGGGTTCTTCTC CA
                                          C  AAT
GAM343  RAB1A    3'  CTGACTTTTTTTTTTATTCCCT  70781      CCCC
                                GGGGA   AAGGAGAGAGTCAG
                                |||||   ||||||||||||||
                                TCCCT   TTTTTTTTTCAGTC
                                  TA__
GAM343  RAB30    3'  TGGTTTTCTTGTCTACCA    27942    _   CCCAAG     GT
                                TGG GGAC     GAGAGA  CA
                                ||| ||||     ||||||  ||
                                ACC TCTG     TTCTTT  GT
                                  A   _______     TG
GAM343  RAB7     3'  CTGATTTTTTTTTATTGGTCTT  17347       CCAA
                                GGGACC   GGAGAGAGTCAG
                                ||||||   ||||||||||||
                                TTCTGG   TTTTTTTTAGTC
                                   TTA_
GAM343  RAP1GA1  3'  CTGCTTCTTGAGGTCCCT    12771        C     _
                                GGGGACC CAAGGAG AG
                                ||||||| ||||||| ||
                                TCCCTGG GTTCTTC TC
                                     A      G
GAM343  RASAL1   3'  TTGACTGAGACTGGGGTCTCTA 17404          A GAGAG
                                TGGGGACCCCA G    AGTCAG
                                |||||||||||  |    ||||||
                                ATCTCTGGGGT C    TCAGTT
                                      _ AGAG_
GAM343  RBBP9    3'  TGATTCTTTGTGGTCATCA   70704    GG   C  AGGA
                                TG  GACC CA   GAGAGTCA
                                ||  ||||  ||   ||||||||
                                AC  CTGG GT   TTCTTAGT
                                 TA   T  ____
GAM343  RECQL5   3'  CTGATTTTCAGTGGCGTCCTCA 16199        C   AGGA
                                TGGGGAC CCA   GAGAGTCAG
                                |||||||  |||   |||||||||
```

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                                ACTCCTG GGT   CTTTTAGTC
                                   C  GA__
GAM343  RORB    5'  CTGAGCGGGATTTTTGGGCTCT 23589      C      GAGA _
            CC                   GGGGA CCCAAGGA   G TCAG
                                |||||| ||||||||   | ||||
                                CCTCT GGGTTTTT   C AGTC
                                   C       AGGG G
GAM343  RRM2    3'  CTGATTTTTTTTTTCCATCTC  8286      CCCC
                                GGGA   AAGGAGAGAGTCAG
                                ||||   ||||||||||||||
                                CTCT   TTTTTTTTTTAGTC
                                  ACC_
GAM343  SCA1    3'  TTGGCTTTTTCCTTGTTTGGTT 6189      C__
                                GACC   CAAGGAGAGAGTCAG
                                ||||   ||||||||||||||
                                TTGG   GTTCCTTTTTCGGTT
                                  TTT
GAM343  SEDL    3'  TTGATCTTTGGGGTTTTT    28116           GA
                                GGGGACCCCAAGGA  GA
                                |||||||||||||  ||
                                TTTTTGGGGTTTCT  TT
                                       AG
GAM343  SHMT2   3'  CTGGTTTTCTCTTATCCCC   19436      CCCCA      GT
                                GGGGA    AGGAGAGA  CAG
                                |||||    ||||||||  |||
                                CCCCT    TTCTCTTT  GTC
                                   A_____       TG
GAM343  SLC18A1  3'  CTGATTTTCTCTGGCATAGTCC 13211      CCCAA_
            C                    GGGAC     GGAGAGAGTCAG
                                |||||     ||||||||||||
                                CCCTG     TCTCTTTTAGTC
                                   ATACGG
GAM343  SLC22A2  3'  TTGGTTTTCTGGAGGGTTTTT  60282       CAAGG    GT
                                GGGGACCC    AGAGA  CAG
                                ||||||||    |||||  |||
                                TTTTTGGG    TCTTT  GTT
                                     AGG__    TG
GAM343  SLC7A5   3'  CTGGCTTTTTTGTGGGGTTTTT 14465          AG
            A                    TGGGGACCCCA  GAGAGAGTCAG
                                ||||||||||  ||||||||||
                                ATTTTTGGGGT  TTTTTTCGGTC
                                       G_
GAM343  SMP1    3'  CTGGCTTTTGAGGGTCTCCCA  27472     _    CAAGGA
                                TGGG GACCC     GAGAGTCAG
                                |||| |||||     |||||||||
                                ACCC CTGGG     TTTTCGGTC
                                  T    AG_____
GAM343  SNX15   3'  CTGTCTTTTTGGGGTTTTT   74118            G
                                GGGGACCCCAAGGAGA AG
                                |||||||||||||||| ||
```

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                                TTTTTGGGGTTTTTCT TC
                                      G
GAM343  SOX11    3'  CTGGCTTTTTTTTTTTTTTTTT 13316    GG CCCC__
           TCC                   GG  A     AAGGAGAGAGTCAG
                                 ||  |     ||||||||||||||
                                 CC  T     TTTTTTTTTCGGTC
                                  TT TTTTTT
GAM343  SOX11    3'  TTGATTTTTTTTTGTTGGTCTC 13323        CCA
           T                     GGGGACC   AGGAGAGAGTCAG
                                 |||||||   ||||||||||||||
                                 TCTCTGG   TTTTTTTTTAGTT
                                     TTG
GAM343  SREBF2   3'  TTGATTCTCTCCCTGGGTCTGC 17192    G     CAA
           G                      TG GGACCC   GGAGAGAGTCAG
                                 || ||||||   ||||||||||||
                                 GC TCTGGG   CCTCTCTTAGTT
                                  G     TC_
GAM343  SSX2     5'  CTGATTTTCTCTTTGGATTCTT 97963      _ CC
           CCA                     TGGG GA  CCAAGGAGAGAGTCAG
                                 ||||  ||  ||||||||||||||||
                                 ACCT CT  GGTTTCTCTTTTAGTC
                                   T  TA
GAM343  SSX3     5'  CTGATTTTCTCTTTGGATTCTT 41014      _ CC
           CCA                     TGGG GA  CCAAGGAGAGAGTCAG
                                 ||||  ||  ||||||||||||||||
                                 ACCT CT  GGTTTCTCTTTTAGTC
                                   T  TA
GAM343  STAM     3'  CTGACTTTTTAGAGGTTCTT   14420        CCAAGG
                                 GGGGACC     AGAGAGTCAG
                                 |||||||     ||||||||||
                                 TTCTTGG     TTTTTCAGTC
                                     AGA___
GAM343  STC1     3'  TTGATTTTTTTAAAGTAGTTCC 13466        CCCAAG
           TA                      TGGGGAC     GAGAGAGTCAG
                                 |||||||     ||||||||||
                                 ATCCTTG     TTTTTTTAGTT
                                     ATGAAA
GAM343  STMN1    3'  CTGACTTTCTCCCCATCCCC   19913      CCCCAA
                                 GGGGA     GGAGAGAGTCAG
                                 |||||     ||||||||||||
                                 CCCCT     CCTCTTTCAGTC
                                   ACC___
GAM343  SYNGR1   3'  CTGGGAGGCCTTGGGGCCCTCA 17502       A       AGAGAG
                                 TGGGG CCCCAAGG     TCAG
                                 ||||| ||||||||     ||||
                                 ACTCC GGGGTTCC     GGTC
                                   C       GGAG__
GAM343  TACR1    3'  CTGATTTTCTTTTTTTCTTTTC 8327      GG CCCC
           CA                      TGG  A    AAGGAGAGAGTCAG
                                 |||  |   ||||||||||||||
```

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                                ACC  T    TTTTTCTTTTAGTC
                                  TT TCTT
GAM343  TEC      3'  CTGGTTGGACTTGGGTTCCT   13679      C     GAGA  G
                                GGGA CCCAAG    GA TCAG
                                |||| ||||||    || ||||
                                TCCT GGGTTC    TT GGTC
                                  T     AGG_  _
GAM343  TFE3     3'  TGATTTTTTTATTGCTCC    22539      ACCC   G
                                GGGG    CAA GAGAGAGTCA
                                ||||    ||| ||||||||||
                                CCTC    GTT TTTTTTTAGT
                                  ____  A
GAM343  TGFBR2   5'  CTGGTTCTACTTGCTTGGGTCC 13730         C  _  _  GT
           TTA                    TGGGGACCC AAG GAG AGA  CAG
                                |||||||| ||| ||| |||  |||
                                ATTCCTGGG TTC TTC TCT  GTC
                                     _  G  A  TG
GAM343  TMPRSS3  3'  CTGGTTTTCTCTCCAGGGGTCT 44023         AA      __
           T                     GGGACCCC  GGAGAGAG  TCAG
                                |||||||  ||||||||  ||||
                                TTCTGGGG  CCTCTCTT  GGTC
                                    A_       TT
GAM343  TNFRSF1B 3'  CTGGAGCCCTTGGGTTTTTTG  8395    GG   C      AGAGAG
                                T  GGA CCCAAGG     TCAG
                                |  ||| |||||||     ||||
                                G  TTT GGGTTCC     GGTC
                                 TT   T      CGA___
GAM343  UBE2V1   3'  CTGATTACACGGCCTGGGGTCT 42063          A  AGAG__
           CT                     GGGGACCCCA GG     AGTCAG
                                |||||||||| ||     ||||||
                                TCTCTGGGGT CC     TTAGTC
                                     _  GGCACA
GAM343  UNC13    3'  TGATTTTCTGTGGCTCCA    22102      A  C  AGGA
                                TGGGG CC CA    GAGAGTCA
                                ||||| || ||    ||||||||
                                ACCTC GG GT    CTTTTAGT
                                   _  T  _____
GAM343  UNG      3'  TTGGCTCTCTTTATCTCCCT   56026      CCCCAA
                                GGGGA     GGAGAGAGTCAG
                                |||||     ||||||||||||
                                TCCCT     TTTCTCTCGGTT
                                   CTA___
GAM343  VAMP8    3'  TGATTTCTTGGGTCCTTA    15003        CAAG     GT
                                TGGGGACCC   GAGAGA  CA
                                |||||||||   ||||||  ||
                                ATTCCTGGG   TTCTTT  GT
                                     _____     AC
GAM343  VCP      3'  CTGACTCTGGACAGGGGGTTTC 75888    GG    AAGGAG
           T                     GG  ACCCC     AGAGTCAG
                                ||  |||||     ||||||||
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                                TC  TGGGG     TCTCAGTC
                                 TT    GACAGG
GAM343  WHSC1    3'  TTGGTTCTTTTTTTGAGGGATC 24691      _  _       GT
              CTT                  GGGGA CCC CAAGGAGAGA  CAG
                                |||||| ||| ||||||||||  |||
                                TTCCT GGG GTTTTTTTCT  GTT
                                  A  A        TG
GAM343  WHSC1    3'  TTGGTTCTTTTTTTGAGGGATC 24692      _  _       GT
              CTT                  GGGGA CCC CAAGGAGAGA  CAG
                                |||||| ||| ||||||||||  |||
                                TTCCT GGG GTTTTTTTCT  GTT
                                  A  A        TG
GAM343  WHSC1    3'  TTGGTTCTTTTTTTGAGGGATC 24693      _  _       GT
              CTT                  GGGGA CCC CAAGGAGAGA  CAG
                                |||||| ||| ||||||||||  |||
                                TTCCT GGG GTTTTTTTCT  GTT
                                  A  A        TG
GAM343  Z39IG    3'  CTGACTCTCTCCTGGTGCTCA  24398     G   CCA
                                TGGG ACC   AGGAGAGAGTCAG
                                |||| |||   ||||||||||||
                                ACTC TGG   TCCTCTCTCAGTC
                                  G  ___
GAM343  ZIC1     5'  TTGGCTTTTTCTTTCTTTCTTC 14169       CCCC
              A                   TGGGGA    AAGGAGAGAGTCAG
                                ||||||   ||||||||||||||
                                ACTTCT    TTTCTTTTTCGGTT
                                   TTC_
GAM343  ZNF32    3'  CTGATTTTTTTCCTTTCCCC   93103      CCCC       _
                                GGGGA    AAGGAGAGAG TCAG
                                |||||   |||||||||| ||||
                                CCCCT    TTCCTTTTTT AGTC
                                   _____        T
GAM343  ZNF42    5'  TTGACTCCGATGTGGTTTTTG  14246   GG    C  AGGAGA
                                T  GGACC CA     GAGTCAG
                                |  ||||| ||     |||||||
                                G  TTTGG GT     CTCAGTT
                                 TT    T  AGC___
GAM343  AKAP11   3'  CTTTTTTTGGGGACTTTG    58460   GG  A
                                T  GG CCCCAAGGAGAG
                                |  || ||||||||||||
                                G  TC GGGGTTTTTTTC
                                 TT  A
GAM343  AKAP11   3'  TGACAATTTTGGGTTCCCA   58467        CAAG   GA
                                TGGGGACCC   GAGA  GTCA
                                |||||||||   ||||  ||||
                                ACCCTTGGG   TTTT  CAGT
                                     _____   AA
GAM343  AKAP7    5'  CTGCAATTTCTATTTGGGGTCC 57620           G    GT_
              TCA                  TGGGGACCCCAAG AGAGA   CAG
                                |||||||||||| |||||   |||
```

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                                ACTCCTGGGGTTT TCTTT   GTC
                                      A    AAC
GAM343  ARHGEF9  3' CTCCCTCCTTGGGGCTTC    31485     A       A
                                GGGG CCCCAAGGAG GAG
                                |||| |||||||||| |||
                                CTTC GGGGTTCCTC CTC
                                  _       C
GAM343  B3GNT6   3' TGTTCTCTCAGGGCTTC     23453     A  CAAG    GT
                                GGGG CCC   GAGAGA  CA
                                |||| |||   ||||||  ||
                                CTTC GGG   CTCTCT  GT
                                  _  A___     TG
GAM343  BDG-29   3' GTATTCTGTTTTTGGGGTTTTT 72806           G    CAG
           A                     TGGGGACCCCAAGGA AGAGT
                                |||||||||||||| |||||
                                ATTTTTGGGGTTTTT TCTTA
                                        G    TGA
GAM343  BRD4     3' CTGGTTCTCTGGGGTCCTC   55251         AGGA   GT
                                GGGGACCCCA   GAGA  CAG
                                ||||||||||   ||||  |||
                                CTCCTGGGGT   CTCT  GTC
                                     ____   TG
GAM343  BZW1     5' CTGGCTCTTTCCTCTTCGCCTT 28587      ACCCCA
           A                     TGGGG     AGGAGAGAGTCAG
                                |||||     ||||||||||||
                                ATTCC     TCCTTTCTCGGTC
                                   GCTTC_
GAM343  C11orf15 3' CTGGCTTTTTTCTTCCTCTGTC 40593      CCC__
           CTC                    GGGGAC    AAGGAGAGAGTCAG
                                ||||||    ||||||||||||||
                                CTCCTG    TTCTTTTTTCGGTC
                                   TCTCC
GAM343  C20orf13 3' CTGAGCTTTTGGGGGTTTTTA 35272         AAG    AG
                                TGGGGACCCC   GAGAG  TCAG
                                ||||||||||   |||||  ||||
                                ATTTTTGGGG   TTTTC  AGTC
                                      G__    G_
GAM343  C20orf55 3' TGACTCTCGAAGGGTTTT    49479       CAAGGA
                                GGGACCC     GAGAGTCA
                                |||||||     ||||||||
                                TTTTGGG     CTCTCAGT
                                   AAG___
GAM343  C20orf98 3' CTGGTTCCCTGAGGGTCCTCA 72006        CA   AGA  GT
                                TGGGGACCC  AGG   GA  CAG
                                |||||||||  |||   ||  |||
                                ACTCCTGGG  TCC   CT  GTC
                                     AG   ___  TG
GAM343  C22orf4  3' CTGGTTCCTTGGGGCTCTA   61273      A        AG
                                TGGGG CCCCAAGGAG  AG
                                ||||| ||||||||||  ||
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                                ATCTC GGGGTTCCTT  TC
                                  _       GG
GAM343  C2F     3'  CTGGTTGTTTTGGGGTTCCTA  22006          GGA  G GT
                                TGGGGACCCCAA   GA A  CAG
                                ||||||||||||  || |  |||
                                ATCCTTGGGGTT   TT T  GTC
                                      ____  G TG
GAM343  C6orf5  3'  CTGGTTTTTTTCTGTTCCTCCC 31990       CCCCA       GT
          CG                    TGGGGA    AGGAGAGA  CAG
                                ||||||    ||||||||  |||
                                GCCCCT    TCTTTTTT  GTC
                                   CCTTG       TG
GAM343  C9orf7  3'  CTGTGCAGTCCTGGGGTCCCT  34582          A   GAGAGT
                                GGGGACCCCA GGA     CAG
                                ||||||||||| |||     |||
                                TCCCTGGGGT CCT     GTC
                                      _  GACGT_
GAM343  CBX6    3'  CTGGCTCTTTCCTAACCCCC   27413      ACCCCA
                                GGGG     AGGAGAGAGTCAG
                                ||||     ||||||||||||||
                                CCCC     TCCTTTCTCGGTC
                                  CAA___
GAM343  CD200   3'  CTGATTTTCTTACAGTTCT    57948       CCCAAG
                                GGGAC     GAGAGAGTCAG
                                |||||     ||||||||||
                                TCTTG     TTCTTTTAGTC
                                   ACA___
GAM343  CEACAM7  3'  TTGGTTTGGTTCATGGGGTCTC 23544          A   GA  GT
          T                     GGGGACCCCA GGA  GA  CAG
                                |||||||||| |||  ||  |||
                                TCTCTGGGGT CTT  TT  GTT
                                      A   GG  TG
GAM343  CGBP    5'  CTGAGGGGTCTTGGGGGCTCTA 28200       A       AGAGAG
                                TGGGG CCCCAAGG     TCAG
                                ||||| ||||||||     ||||
                                ATCTC GGGGTTCT     AGTC
                                   G       GGGG__
GAM343  CLDN4   3'  TTCCTTCTTTGTGGTTTCT   8958     GG   C      A
                                GG  ACC CAAGGAG GAG
                                ||  ||| ||||||| |||
                                TC  TGG GTTTCTT CTT
                                 TT   T      C
GAM343  COE2    3'  TTGCTTCTTTCTTTGGGTTTTC 64913    GG    C        T
          A                     TG  GACCC AAGGAGAGAG CAG
                                ||  ||||| ||||||||||| |||
                                AC  TTGGG TTTCTTTCTT GTT
                                 TT    _        C
GAM343  CSRP2BP  3'  TTGGTTTGGGATTGGGGTTGTT 70659    G       GGAGA  GT
                                GG GACCCCAA     GA  CAG
                                || ||||||||     ||  |||
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                                TT TTGGGGTT    TT  GTT
                                 G       AGGG_  TG
GAM343  DATF1    3'  CTGGCTTTCTTGCCCTCGTCTC 55849       CCCAAG
             T                   GGGGAC     GAGAGAGTCAG
                                 ||||||     ||||||||||
                                 TCTCTG     TTCTTTCGGTC
                                    CTCCCG
GAM343  DATF1    3'  CTGGCTTTCTTGCCCTCGTCTC 42325       CCCAAG
             T                   GGGGAC     GAGAGAGTCAG
                                 ||||||     ||||||||||
                                 TCTCTG     TTCTTTCGGTC
                                    CTCCCG
GAM343  DKFZp434E0519 3'  GTTTTCTTTCTTTTGTCTTC   50998       CCC        TCAG
                                 GGGGAC   AAGGAGAGAG
                                 ||||||   ||||||||||
                                 CTTCTG   TTTCTTTCTT
                                    T__         TTGG
GAM343  DKFZp434H2226 5'  TCCCTCTTTGCGGTCTTCA    69132         C      A
                                 TGGGGACC CAAGGAG GA
                                 |||||||| ||||||| ||
                                 ACTTCTGG GTTTCTC CT
                                      C      C
GAM343  DKFZP434K2235 3'  TTGATTTTTTTTTTCTGGTCAC 84501     _    CC
             TC                    GGG GACC  AAGGAGAGAGTCAG
                                 ||| ||||  ||||||||||||||
                                 CTC CTGG  TTTTTTTTTTAGTT
                                   A   TC
GAM343  DKFZP564D0764 5'  CTGATGGCTTTGGGGGCCTT   89613      A       AGAGA
                                 GGGG CCCCAAGG     GTCAG
                                 |||| ||||||||     |||||
                                 TTCC GGGGTTTC     TAGTC
                                   G       GG___
GAM343  DKFZP564L0862 3'  TTGACATCCCTTGGGGCTCTA  44253       A       A  GA
                                 TGGGG CCCCAAGG GA  GTCAG
                                 ||||| |||||||| ||  |||||
                                 ATCTC GGGGTTCC CT  CAGTT
                                    _       _  A_
GAM343  DKFZP564O0423 3'  CTTTCCCTTGGGGTCCTT     93349             A
                                 GGGGACCCCAAGG GAGAG
                                 |||||||||||| |||||
                                 TTCCTGGGGTTCC CTTTC
                                                _
GAM343  DKFZP761L0424 3'  TTGGTTTTCTTTTTACCTAGTT 92980     G   CCC__       GT
             GCTA                   TGG GAC     AAGGAGAGA  CAG
                                 ||| |||     |||||||||  |||
                                 ATC TTG     TTTTTCTTT  GTT
                                   G   ATCCA        TG
GAM343  DRCTNNB1A 3'  TTGATTTTCTTTTAGCTCCA   51812       ACCCCA
                                 TGGGG     AGGAGAGAGTCAG
                                 |||||     ||||||||||||
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                                ACCTC     TTTTCTTTTAGTT
                                  GA____
GAM343  ESAM     3'  TTGGCTAAAGGATTTGGGGTCT 58047          GAGAG_
            CT                   GGGGACCCCAAG     AGTCAG
                                ||||||||||||     ||||||
                                TCTCTGGGGTTT     TCGGTT
                                      AGGAAA
GAM343  FLJ00001 3'  TGACATCTTTGGGTCCCCA   82719        CAA    GA
                                TGGGGACCC   GGAGA  GTCA
                                |||||||||   |||||  ||||
                                ACCCCTGGG   TTTCT  CAGT
                                     ___    A_
GAM343  FLJ10008 3'  CTGGCTTTTTTTGTTTTGTTTT 36187   GG   CCCAA
            C                    G  GAC    GGAGAGAGTCAG
                                |  |||    ||||||||||||
                                C  TTG    TTTTTTTCGGTC
                                 TT   TTTTG
GAM343  FLJ10210 5'  TGTTTTCTTTCTTCCCA     36360       CCCCAA      GT
                                TGGGGA     GGAGAGA  CA
                                ||||||     |||||||  ||
                                ACCCTT     TTTCTTT  GT
                                   C_____      TG
GAM343  FLJ10420 3'  TGGGTTTTCTCTTTGGTGGTTT 36592     GG  _        GT AG
            CTA                   TGG  ACC CCAAGGAGAGA  C
                                |||  ||| ||||||||||  |
                                ATC  TGG GGTTTCTCTTT  G
                                  TT   T         TG GTT
GAM343  FLJ10525 5'  TGGCTCTTTAGGGCTTCA    36725      A   CAAGG
                                TGGGG CCC    AGAGAGTCA
                                |||||  |||    |||||||||
                                ACTTC GGG    TTTCTCGGT
                                   _   A____
GAM343  FLJ10607 3'  CTGATTTTTTTCTTTTCATGGG 77633    GG    C____
            TATCT                  GG  ACCC    AAGGAGAGAGTCAG
                                ||  ||||    ||||||||||||||
                                TC  TGGG    TTCTTTTTTTAGTC
                                 TA    TACTT
GAM343  FLJ10971 3'  CTGTGTATTTCTTTTTCGGGGT 37483    GG    _       GT__
            TTCT                   GG  ACCCC AAGGAGAGA    CAG
                                ||  ||||| |||||||||    |||
                                TC  TGGGG TTTTTCTTT    GTC
                                 TT    C        ATGT
GAM343  FLJ11274 3'  TTGATTTTTAACATGGTTCCCA 37782         CCAAGGA
                                TGGGGACC      GAGAGTCAG
                                ||||||||      |||||||||
                                ACCCTTGG      TTTTTAGTT
                                     TACAA__
GAM343  FLJ12078 3'  TTGACTCTCTCTCTTCCC    47088      CCCCA  _
                                GGGA    AG GAGAGAGTCAG
                                ||||    ||  ||||||||||
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                                CCCT    TC CTCTCTCAGTT
                                  _____ T
GAM343  FLJ12960  3' TTGGTTTTTTGGTTTTTTGGGG 45310          ____   GT
             TTTTT                GGGGACCCCAAGGA   GAGA  CAG
                                  ||||||||||||||   ||||  |||
                                  TTTTTGGGGTTTTT   TTTT  GTT
                                        TGGT   TG
GAM343  FLJ13158  3' CTGGTGTTGCTTTGGGGTCTCT 46649          AG  AG
               A                   TGGGGACCCCAAGG  AG  TCAG
                                   ||||||||||||||  ||  ||||
                                   ATCTCTGGGGTTTC  TT  GGTC
                                         G_  GT
GAM343  FLJ13194  3' CTGGTTTTTTGGGGGTATTC  47872    GA_       AG
                                   GGG   CCCCAAGGAG  AG
                                   |||   ||||||||||  ||
                                   CTT   GGGGTTTTTT  TC
                                     ATG        GG
GAM343  FLJ13456  3' CTGATGTTTTGGGGGTTTCTA  66545    GG    AAG   GA
                                   TGG  ACCCC   GAGA  GTCAG
                                   |||  |||||   ||||  |||||
                                   ATC  TGGGG   TTTT  TAGTC
                                     TT    G__   G_
GAM343  FLJ13612  3' CTGTCTTTTTGGGTCCTCA   48088        C      G
                                   TGGGGACCC AAGGAGA AG
                                   |||||||||  |||||||  ||
                                   ACTCCTGGG TTTTTCT TC
                                         _      G
GAM343  FLJ13840  5' CTGGCTCTCTTCTGGCATTCTC 45698      CC   A
                                   GGGGA  CCA GGAGAGAGTCAG
                                   |||||  |||  ||||||||||||
                                   CTCTT  GGT CTTCTCTCGGTC
                                      AC   _
GAM343  FLJ20073  3' CTGGTTTTCTTTTTTGGTTTCT 34963       CC      _   GT
               TCA                   TGGGGA  CCAAGGA GAGA  CAG
                                     ||||||  |||||||  ||||  |||
                                     ACTTCT  GGTTTTT CTTT  GTC
                                        TT      T    TG
GAM343  FLJ20136  3' TTGTTTTTTTGGGGTTTTT   35107             G
                                   GGGGACCCCAAGGAGA AG
                                   ||||||||||||||||  ||
                                   TTTTTGGGGTTTTTTT TT
                                         G
GAM343  FLJ20189  3' TTGATTTTCTAAGGTCCTCA   35206        CCAAGG
                                   TGGGGACC     AGAGAGTCAG
                                   ||||||||     ||||||||||
                                   ACTCCTGG     TCTTTTAGTT
                                      AA_____
GAM343  FLJ20308  3' CTGGCTTTTTCCTTTCCCTTCC 67391       CCCC
               C                    GGGGA    AAGGAGAGAGTCAG
                                    |||||    ||||||||||||||
```

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                                CCCTT   TTCCTTTTTCGGTC
                                   CCCT
GAM343  FLJ20584  3'  CTGGCCTTCGGGGTCCCCA   35854         _   AG
                                TGGGGACCCC AAGG  AG
                                |||||||||| ||||  ||
                                ACCCCTGGGG TTCC  TC
                                     C   GG
GAM343  FLJ20729  3'  TTCTTCTTTGGAGTTTTTA   36084       C     G
                                TGGGGAC CCAAGGA AGAG
                                ||||||| ||||||| ||||
                                ATTTTTG GGTTTCT TCTT
                                    A     _
GAM343  FLJ21144  3'  TTGGTTCTTTTTTTTATTTCCA 43195    GG CCCC       GT
                                TGG  A   AAGGAGAGA  CAG
                                |||  |   |||||||||  |||
                                ACC  T   TTTTTTTCT  GTT
                                  TT AT__       TG
GAM343  FLJ21168  3'  TTGGCTTTCTTTTTTTTTGTTT 47586   GG   CCC_
          ACA                     TG  GAC   AAGGAGAGAGTCAG
                                ||  |||   ||||||||||||||
                                AC  TTG   TTTTTCTTTCGGTT
                                 AT   TTTT
GAM343  FLJ22529  3'  TTGGTTTTTTTTTTAAGGATTT 45958   GG A  CC       GT
          CA                      TG  G CC  AAGGAGAGA  CAG
                                ||  | ||  |||||||||  |||
                                AC  T GG  TTTTTTTTT  GTT
                                 TT A  AA       TG
GAM343  FLJ22969  3'  CTGATTCTCTAGGTCGGTTC   69202      CCAAGG
                                GGACC     AGAGAGTCAG
                                |||||     ||||||||||
                                CTTGG     TCTCTTAGTC
                                   CTGGA_
GAM343  FLJ22969  3'  CTGGCTCTTTTCTTTAAAGCCC 69203     ACCCC
                                GGG    AAGGAGAGAGTCAG
                                |||    ||||||||||||||
                                CCC    TTCTTTTCTCGGTC
                                  GAAAT
GAM343  FLJ23560  3'  TTGATTTTCTCCTGACCCCA   45510      ACCCCA
                                TGGGG     AGGAGAGAGTCAG
                                |||||     ||||||||||||
                                ACCCC     TCCTCTTTTAGTT
                                   AG____
GAM343  FLJ32926  3'  CTGGCTCTCTGTGGGGTCTTT  58635         AGG
                                GGGGACCCCA   AGAGAGTCAG
                                ||||||||||   ||||||||||
                                TTTCTGGGGT   TCTCTCGGTC
                                     G__
GAM343  GAB3      3'  CTGGCTTTTTCCTCAGTCCCT  55519       CCCA
                                GGGGAC   AGGAGAGAGTCAG
                                ||||||   ||||||||||||
```

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                                TCCCTG   TCCTTTTTCGGTC
                                   AC__
GAM343  GREB1    3'  CTGATTTTTTTCTCTTAGTTCT 28566      CCCA
                                GGGAC   AGGAGAGAGTCAG
                                |||||   ||||||||||||||
                                TCTTG   TCTTTTTTTAGTC
                                   ATTC
GAM343  HAND1    3'  CTGGCTCTTTCTCTCTTGTCCC 17879      CCCAA
           T                     GGGGAC   GGAGAGAGTCAG
                                |||||||   ||||||||||||
                                TCCCTG   TCTTTCTCGGTC
                                   TTCTC
GAM343  HBOA     3'  CTGGTTCTCTCCTCATGTCCTC 23931      CCCA      GT
                                GGGGAC   AGGAGAGA  CAG
                                ||||||   ||||||||  |||
                                CTCCTG   TCCTCTCT  GTC
                                   TAC_      TG
GAM343  HBXAP    3'  TTGATTTTCTTTTTCCAGGTTC 33883      CC_
                                GGACC   AAGGAGAGAGTCAG
                                |||||   ||||||||||||||
                                CTTGG   TTTTTCTTTTAGTT
                                   ACC
GAM343  HE3-ALPHA 3'  TTGACTCTCTTTATACCTACCC 60818     GACCCCAA
           A                     TGGG      GGAGAGAGTCAG
                                ||||      ||||||||||||
                                ACCC      TTTCTCTCAGTT
                                  ATCCATA_
GAM343  HSA250839 3'  TTCTTCCTGGGGTCTTTG    37857   GG      A
                                T  GGACCCCA GGAGAG
                                |  |||||||| ||||||
                                G  TCTGGGGT CTTCTT
                                 TT       C
GAM343  IL1RAPL1  3'  AACATTTCCTTGGGGTGCTT   27337    G         GA  CAG
                                GGG ACCCCAAGGAGA  GT
                                ||| ||||||||||||  ||
                                TTC TGGGGTTCCTTT  CA
                                  G          A_  AT
GAM343  KIAA0057  3'  CTGGTAGGCCCTTGGTGGTCCT 25414        _     AGAGAG
           CA                     TGGGGACC CCAAGG     TCAG
                                ||||||||  ||||||     ||||
                                ACTCCTGG GGTTCC     GGTC
                                     T     CGGAT_
GAM343  KIAA0143  3'  TTGATTTGGGTTTTGTTGGGGT 65412   GG      G   ___
           TTTTG                    T  GGACCCCAA GAGA   GAGTCAG
                                |  |||||||||  ||||   |||||||
                                G  TTTGGGGTT TTTT   TTTAGTT
                                 TT       G   GGG
GAM343  KIAA0164  3'  CTGATTCTCTTCCTTCCCT   29118      CCCCA   _
                                GGGGA    AGGA GAGAGTCAG
                                |||||    |||| |||||||||
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                              TCCCT    TCCT CTCTTAGTC
                                 _____   T
GAM343  KIAA0232 3' CTGATTTTTTTTTGTTTGTTTT 73120   GG  CCCA
            C                   G  GAC   AGGAGAGAGTCAG
                              |  |||   ||||||||||||
                              C  TTG   TTTTTTTTTAGTC
                               TT   TTTG
GAM343  KIAA0247 3' CTGGCTCTTTGCCTGGCCCC  29069     A  CCA  _
                              GGGG CC   AGG AGAGAGTCAG
                              |||| ||   ||| ||||||||||
                              CCCC GG   TCC TTTCTCGGTC
                                 _ ___   G
GAM343  KIAA0275 5' CTGATTCTCTCTCCCTCTCC  29325      CCCCAA
                              GGGGA     GGAGAGAGTCAG
                              |||||     ||||||||||||
                              CCTCT     TCTCTCTTAGTC
                                 CCC___
GAM343  KIAA0280 3' GATTCTTTTGGGTTTTTG    93302   GG    CAAG
                              T  GGACCC    GAGAGAGTC
                              |  ||||||    |||||||||
                              G  TTTGGG    TTTTCTTAG
                               TT    _____
GAM343  KIAA0286 3' TTGGTTCTTTTTCTTTGTGGTC 68864        C        __
            TTCA                TGGGGACC CAAGGAGAGAG  TCAG
                              |||||||| ||||||||||  ||||
                              ACTTCTGG GTTTCTTTTTC  GGTT
                                   T         TT
GAM343  KIAA0349 3' TTGGCTTTTTTTCAGATGTTCA 93920     _   CCCAA
            CCA                   TGG GGAC    GGAGAGAGTCAG
                              |||  ||||    ||||||||||||
                              ACC CTTG    TTTTTTTCGGTT
                                A   TAGAC
GAM343  KIAA0349 3' TTGGCTTTTTTTCATATGTTCA 93921     _   CCCAA
            CCA                   TGG GGAC    GGAGAGAGTCAG
                              |||  ||||    ||||||||||||
                              ACC CTTG    TTTTTTTCGGTT
                                A   TATAC
GAM343  KIAA0352 3' TTGGTTTTCTAAGGGGCTTTG  29831   GG  A   AAGG    GT
                              T  GG CCCC   AGAGA  CAG
                              |  || ||||   |||||  |||
                              G  TC GGGG   TCTTT  GTT
                               TT  _   AA__    TG
GAM343  KIAA0365 3' CTGACTCTCTTTTTCACTCCCT 79368       CCCC
            A                   TGGGGA   AAGGAGAGAGTCAG
                              ||||||   ||||||||||||||
                              ATCCCT   TTTTTCTCTCAGTC
                                 CAC_
GAM343  KIAA0450 3' CTGGCTCTCTCTCACTCCCC  28354      CCCCAA
                              GGGGA     GGAGAGAGTCAG
                              |||||     ||||||||||||
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                                CCCCT     TCTCTCTCGGTC
                                  CAC___
GAM343  KIAA0494  5' TGGCTTTTTTTTCGCCCT    29405     ACCCCA
                                GGGG     AGGAGAGAGTCA
                                ||||     ||||||||||||
                                TCCC     TTTTTTTTCGGT
                                  GC_____
GAM343  KIAA0514  5' TGGCTCTCTCCCTTCCCC    28760      CCCCAA
                                GGGGA     GGAGAGAGTCA
                                |||||     ||||||||||||
                                CCCCT     CCTCTCTCGGT
                                  TC____
GAM343  KIAA0633  3' TTGATTTTCGGTGTGTTCCT   95704       CC  AGGA
                                GGGGAC  CA   GAGAGTCAG
                                ||||||  ||   |||||||||
                                TCCTTG  GT   CTTTTAGTT
                                   T_  GG__
GAM343  KIAA0643  3' TTGGTTTTTTTCTTTTTTCTTC 45982      CCCC       GT
                                GGGGA   AAGGAGAGA  CAG
                                |||||   |||||||||  |||
                                CTTCT   TTCTTTTTT  GTT
                                   TTT_       TG
GAM343  KIAA0650  3' TTGGTTTTTTGTGGGGTTTTTA 89611          AGGA   GT
                                TGGGGACCCCA   GAGA  CAG
                                ||||||||||   ||||  |||
                                ATTTTTGGGGT   TTTT  GTT
                                      GT__   TG
GAM343  KIAA0721  3' CTGATGTCCCTTGGGTCTCCA  41651        C   A  GA
                                TGGGGACCC AAGG GA  GTCAG
                                ||||||||| |||| ||  |||||
                                ACCTCTGGG TTCC CT  TAGTC
                                     _   _  G_
GAM343  KIAA0721  3' TGGCTTTCTTGGCCCTCA    41658      A  CCAAG
                                TGGGG CC    GAGAGAGTCA
                                ||||| ||    ||||||||||
                                ACTCC GG    TTCTTTCGGT
                                  C  _____
GAM343  KIAA0748  3' CTGACTCTCTTTTTGGACTCAG 29614    G_  CC
          CC                      GG  GA  CCAAGGAGAGAGTCAG
                                ||  ||  ||||||||||||||||
                                CC  CT  GGTTTTTCTCTCAGTC
                                 GA  CA
GAM343  KIAA0757  3' TTGGTTCTTTTTTTGGGGTTTT 21260              GT
                                GGGACCCCAAGGAGAGA  CAG
                                ||||||||||||||||  |||
                                TTTTGGGGTTTTTTTCT  GTT
                                         TG
GAM343  KIAA0759  3' CTGATTCTCTTTCCTCTCCA  67887       CCCCAA
                                TGGGGA     GGAGAGAGTCAG
                                ||||||     ||||||||||||
```

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                                ACCTCT     TTTCTCTTAGTC
                                   CC____
GAM343  KIAA0773 3' TTCCTTCCATGGGGTCCCT   28731         A   A
                                GGGGACCCCA GGAG GAG
                                |||||||||| |||| |||
                                TCCCTGGGGT CCTT CTT
                                     A   C
GAM343  KIAA0828 3' CTGATTCTCTTCTTCTACCTC  82114     ACCCC
                                GGGG    AAGGAGAGAGTCAG
                                ||||    ||||||||||||||
                                CTCC    TTCTTCTCTTAGTC
                                  ATC__
GAM343  KIAA0854 3' CTGGCTGCCTTTTTGGGGGTCC 30778         _     AG
           CT                     GGGGACCCC AAGGAG  AGTCAG
                                |||||||| ||||||  ||||||
                                TCCCTGGGG TTTTTC  TCGGTC
                                     G     CG
GAM343  KIAA0924 3' TTGACTTGAGACTTGTGGTCTT 30379        C   GAGA
           CA                     TGGGGACC CAAG   GAGTCAG
                                |||||||| ||||   |||||||
                                ACTTCTGG GTTC   TTCAGTT
                                     T   AGAG
GAM343  KIAA1211 3' TTGACTTTTTCTTTCATCCT  69472     CCCC
                                GGGA   AAGGAGAGAGTCAG
                                ||||   ||||||||||||||
                                TCCT   TTTCTTTTTCAGTT
                                  AC__
GAM343  KIAA1272 3' TTGGCTTTCCCCGGGGTCTTT  70736        AA  A
                                GGGGACCCC  GG GAGAGTCAG
                                |||||||||  || |||||||||
                                TTTCTGGGG  CC CTTTCGGTT
                                     C_  _
GAM343  KIAA1277 3' CTGTTCTAGGGGTCTTCA    65076         A   G
                                TGGGGACCCC AGGA AG
                                |||||||||| |||| ||
                                ACTTCTGGGG TCTT TC
                                     A   G
GAM343  KIAA1322 3' CTGACTTTCCCAGGGTCGTT  73110    G    CAA  A
                                GG GACCC   GG GAGAGTCAG
                                || |||||   || |||||||||
                                TT CTGGG   CC CTTTCAGTC
                                 G    A__  _
GAM343  KIAA1677 3' TTGGTTTTTGGGGGTTTTT   67667        AAGGA   GT
                                GGGGACCCC    GAGA  CAG
                                |||||||||    ||||  |||
                                TTTTTGGGG    TTTT  GTT
                                     G____    TG
GAM343  KIAA1813 5' TTGTCTCTTTTGGGTCCCT   70835        C      G
                                GGGGACCC AAGGAGA AG
                                |||||||| ||||||| ||
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                                TCCCTGGG TTTCTCT TT
                                    T      G
GAM343  KIAA1866  3'  CTGGTACGAGTGTGGGGTCTCC 61587          AGGAGAGAG
            A                    TGGGGACCCCA       TCAG
                                 ||||||||||        ||||
                                 ACCTCTGGGGT       GGTC
                                       GTGAGCAT_
GAM343  KIAA1877  3'  TTGATTTTTTCTTTAATCTC   66767     CCCC
                                 GGGA   AAGGAGAGAGTCAG
                                 ||||   ||||||||||||||
                                 CTCT   TTTCTTTTTTAGTT
                                   AA__
GAM343  KIAA1879  5'  CTGACTTTCTCCTCCCTCCCC  73938      CCCCA
                                 GGGGA    AGGAGAGAGTCAG
                                 |||||    ||||||||||||
                                 CCCCT    TCCTCTTTCAGTC
                                    CCC__
GAM343  KIAA1948  5'  TTGGCTTTTTTTTTCTTTCCA  83309     GG CCCC
                                 TGG  A   AAGGAGAGAGTCAG
                                 |||  |   ||||||||||||||
                                 ACC  T   TTTTTTTTTCGGTT
                                   TT C___
GAM343  KIAA1958  3'  TTGATTGGAACATTTTTTGAGG 82798    GG   C      AG____
            TTTCT                  GG  ACC CAAGGAG     AGTCAG
                                 ||  ||| |||||||     ||||||
                                 TC  TGG GTTTTTT     TTAGTT
                                  TT   A      ACAAGG
GAM343  KLF3     3'  TGGCTCTCTCTCTGTCCT    33712      CCCAA
                                 GGGAC    GGAGAGAGTCA
                                 |||||    ||||||||||
                                 TCCTG    TCTCTCTCGGT
                                    TC___
GAM343  KOC1     3'  CTGGCTTTCTGGTTGGATTTC  92716     CC    GG
                                 GGA  CCAA  AGAGAGTCAG
                                 |||  ||||  ||||||||||
                                 CTT  GGTT  TCTTTCGGTC
                                   TA    GG
GAM343  LHFP     5'  CTGAACACTTACTTGGGGTCCT 20510           GA   AG_
            CA                   TGGGGACCCCAAG  GAG   TCAG
                                 ||||||||||||  |||   ||||
                                 ACTCCTGGGGTTC  TTC   AGTC
                                        A_   ACA
GAM343  LRRFIP2  3'  TGATGCTCCTTGGGGCCCTA   21953      A        AGA    G
                                 TGGGG CCCCAAGGAG   GTCA
                                 ||||| ||||||||||   ||||
                                 ATCCC GGGGTTCCTC   TAGT
                                    _        G__    G
GAM343  LZIC     3'  CTTTCTTCTGGGGTTTTCA   51398    GG      A
                                 TG  GACCCCA GGAGAGAG
                                 ||  ||||||| ||||||||
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                                AC  TTGGGGT CTTCTTTC
                                 TT      _
GAM343  MGC16075 3'  TTGATTTTTTTGGTGTTTTTG  52254   GG   C   GGA
                                T  GGAC CCAA   GAGAGTCAG
                                |  |||| ||||   |||||||||
                                G  TTTG GGTT   TTTTTAGTT
                                 TT   T   ___
GAM343  MGC22014 3'  TTGGCTTTTTTTTTTCCCTCCC 65123      CCCC
           C                     GGGGA   AAGGAGAGAGTCAG
                                |||||   ||||||||||||||
                                CCCCT   TTTTTTTTTCGGTT
                                   CCCT
GAM343  MGC2477  5'  TGGTTCTTTCAGTTCACCA   44314    _   CCCAAG    GT
                                TGG GGAC     GAGAGA  CA
                                ||| ||||     ||||||  ||
                                ACC CTTG     CTTTCT  GT
                                  A   A_____     TG
GAM343  MGC2668  3'  TGGAAGTCTTGGGGCCTCA   61198      A      AGAGAG
                                TGGGG CCCCAAGG     TCA
                                ||||| ||||||||     |||
                                ACTCC GGGGTTCT     GGT
                                   _       GAA___
GAM343  MGC2803  3'  CTGGCTCTTTCTGTCTTCCTC  44086      CCCCAA
                                GGGGA     GGAGAGAGTCAG
                                |||||     ||||||||||||
                                CTCCT     TCTTTCTCGGTC
                                   TCTG__
GAM343  MGC4796  3'  CTGGCTCTTTCTCTCCCGTCTC 62164      CCCAA
                                GGGAC     GGAGAGAGTCAG
                                |||||     ||||||||||||
                                CTCTG     TCTTTCTCGGTC
                                   CCCTC
GAM343  MGC4840  5'  CTGGCTCTTTTTGACAGCCCCC 72022      ACCCCAA
           A                     TGGGG      GGAGAGAGTCAG
                                |||||      ||||||||||||
                                ACCCC      TTTTTCTCGGTC
                                   CGACAG_
GAM343  MIG      3'  CTGGCTCTTTCCTGGCTACTCC 11586      ACC   A
           A                     TGGGG   CCA GGAGAGAGTCAG
                                |||||   ||| ||||||||||||
                                ACCTC   GGT CCTTTCTCGGTC
                                   ATC   _
GAM343  MTX2     5'  CTGGCGGTAACCTTGGGGGCCT 22636      A      AGAGA
           CA                     TGGGG CCCCAAGG     GTCAG
                                ||||| ||||||||     |||||
                                ACTCC GGGGTTCC     CGGTC
                                   G       AATGG
GAM343  NISCH    3'  CTGACTTTCTCTTCTACACGTC 24189       CCCA__
           CTT                     GGGGAC     AGGAGAGAGTCAG
                                ||||||     ||||||||||||
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                                TTCCTG     TTCTCTTTCAGTC
                                   CACATC
GAM343  NSG-X    5'  TGATTTTTGTGGGCCTTA    27729      A   CAAGGA
                                TGGGG CCC     GAGAGTCA
                                ||||| |||     ||||||||
                                ATTCC GGG     TTTTTAGT
                                   _   TG____
GAM343  P24B     3'  CTGGCTCTTCTTTCTTTGGGGT 24771           ___
           TCTC                    GGGGACCCCAAGGA   GAGAGTCAG
                                ||||||||||||||   |||||||||
                                CTCTTGGGGTTTCT   TTCTCGGTC
                                       TTC
GAM343  P66      3'  CTGGCTTTTTTCTTTCCTCCCT 40741      CCCC
                                GGGGA    AAGGAGAGAGTCAG
                                |||||    ||||||||||||||
                                TCCCT    TTCTTTTTTCGGTC
                                   CCT_
GAM343  PAFAH2   3'  CTGGATGTCTTTGGGGGTTTT  6501         AAG    GAG
                                GGGACCCC   GAGA   TCAG
                                ||||||||   ||||   ||||
                                TTTTGGGG   TTCT   GGTC
                                     GT_    GTA
GAM343  PI4KII   3'  CTTTCTTTTGGGTTTTTG    37951    GG     C
                                T  GGACCC AAGGAGAG
                                |  |||||| ||||||||
                                G  TTTGGG TTTCTTTC
                                 TT     T
GAM343  PLU-1    3'  TTGGCTTTCTCCCTGTCCCT   88808       CCCAA
                                GGGGAC    GGAGAGAGTCAG
                                ||||||    ||||||||||||
                                TCCCTG    CCTCTTTCGGTT
                                   TC___
GAM343  PP1044   3'  CTGTCCTTGGGGACTCTA    41675      A       G
                                TGGGG CCCCAAGGA AG
                                ||||| ||||||||| ||
                                ATCTC GGGGTTCCT TC
                                   A       G
GAM343  PRDM10   3'  CTGATTTTTTTTAACTTCCCTA 39978       CCCCAA
                                TGGGGA     GGAGAGAGTCAG
                                ||||||     ||||||||||||
                                ATCCCT     TTTTTTTTAGTC
                                   TCAA__
GAM343  PTBP2    3'  TTGTTTTTTTGGGGTTTCT   41330    GG         G
                                GG  ACCCCAAGGAGA AG
                                ||  |||||||||||| ||
                                TC  TGGGGTTTTTTT TT
                                 TT          G
GAM343  PTPN9    3'  TTGATTTTTGCTAGGGTCCCC  12599        CAA  AG
                                GGGGACCC   GG  AGAGTCAG
                                ||||||||   ||  ||||||||
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                                CCCCTGGG  TC  TTTTAGTT
                                    A__  GT
GAM343  RAB14    3'  CTGATTTTCTTAACTGTTCTT  33335      CCCAAG
                                GGGGAC    GAGAGAGTCAG
                                ||||||    ||||||||||
                                TTCTTG    TTCTTTTAGTC
                                   TCAA__
GAM343  RAB40C   3'  CTGGTTCTCTCCGAACCGTTCT 41281      CCCAA     GT
          T                     GGGGAC    GGAGAGA  CAG
                                ||||||    |||||||  |||
                                TTCTTG    CCTCTCT  GTC
                                   CCAAG     TG
GAM343  RGS19    3'  TGGCCGGCTGGGGTCCCCA   20803         AGGA AGA
                                TGGGGACCCCA   G   GTCA
                                ||||||||||   |  ||||
                                ACCCCTGGGGT   C   CGGT
                                      ____ GGC
GAM343  RNF38    3'  CTGTGGGTTTTTTGTGGGTTCT 43258       _     AGAGT
          T                     GGGGACCC CAAGGAG    CAG
                                ||||||||| |||||||    |||
                                TTCTTGGG GTTTTTT    GTC
                                     T     GGGT_
GAM343  SE57-1   3'  CTGACTTTTTTATAGTGGTTTT 48167       CCAAG
          TA                     TGGGGACC    GAGAGAGTCAG
                                ||||||||    ||||||||||
                                ATTTTTGG    TTTTTTCAGTC
                                     TGATA
GAM343  SEC24A   3'  TTGATTCTTTTTTTTTCCCC   83569     CCCC
                                GGGGA   AAGGAGAGAGTCAG
                                |||||   ||||||||||||||
                                CCCCT   TTTTTTTCTTAGTT
                                   T___
GAM343  SEMA4G   5'  CTGGCTCCCTTTGGGGGTCTT  96328       AAG  A
                                GGGACCCC  GAG GAGTCAG
                                ||||||||  ||| |||||||
                                TTCTGGGG  TTC CTCGGTC
                                     GT_  C
GAM343  SEMA6A   5'  TTGGTTTTCTTTTTCTTTTTCT 40819     CCCC_      GT
          TC                     GGGGA   AAGGAGAGA  CAG
                                |||||    |||||||||  |||
                                CTTCT    TTTTTCTTT  GTT
                                   TTTTC       TG
GAM343  SLC2A9   5'  TTGGCAGAGTCTGGGGTCCCT  39633        A  AGAGA
                                GGGGACCCCA GG    GTCAG
                                |||||||||| ||    |||||
                                TCCCTGGGGT CT    CGGTT
                                     _  GAGA_
GAM343  SNAPC2   3'  CTGGCTCTTTCTGAGGATCCC  13282     C  CAA
                                GGGA CC   GGAGAGAGTCAG
                                ||||  ||   ||||||||||||
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                                CCCT GG   TCTTTCTCGGTC
                                  A  AG_
GAM343  SRPK1    3'  CTGATTCTTTTCCAAACAGTCC 13406       CCCAA_
             CC                   GGGGAC     GGAGAGAGTCAG
                                  ||||||     ||||||||||||
                                  CCCCTG     CTTTTCTTAGTC
                                     ACAAAC
GAM343  TEB4     3'  CTGATTTTTTTCATGTGTCT   61283      CC  A
                                  GGAC  CA GGAGAGAGTCAG
                                  ||||  || ||||||||||||
                                  TCTG  GT CTTTTTTTAGTC
                                    T_  A
GAM343  TOR2A    3'  CTGACTCTCTGAGTGGTGTCCT 56187       C   AGG
             C                    GGGGAC CCA   AGAGAGTCAG
                                  |||||| |||   ||||||||||
                                  CTCCTG GGT   TCTCTCAGTC
                                     T   GAG
GAM343  TRIM16   3'  GCTGGCTTTTGAAATCCTATGG 22374         _   _____
             GGTCTCT                 GGGGACCCCA AGGA    GAGAGTCAG   C
                                  ||||||||||| ||||    |||||||||   |
                                  TCTCTGGGGT TCCT    TTTTCGGTC   G
                                       A    AAAG
GAM343  TRIM2    3'  TTGATAGTGACTTTGGGGTCTT 31601            AGAGA
             C                    GGGGACCCCAAGG    GTCAG
                                  ||||||||||||     |||||
                                  CTTCTGGGGTTTC    TAGTT
                                        AGTGA
GAM343  TRIM22   3'  TTGGTTCTTTCTGAGGTCTGCA 21390    G    CCAA      GT
                                  TG GGACC    GGAGAGA  CAG
                                  || |||||    |||||||  |||
                                  AC TCTGG    TCTTTCT  GTT
                                   G    AG__      TG
GAM343  UXS1     5'  TTGATTTTCATAGGGTTTTCA  47592    GG    CAAGGA
                                  TG  GACCC     GAGAGTCAG
                                  ||  |||||     |||||||||
                                  AC  TTGGG     CTTTTAGTT
                                   TT    ATA___
GAM343  VPS29    3'  TTGGTTTTTTTTCATTGTCCT  33155      CCCAA      GT
                                  GGGAC    GGAGAGA  CAG
                                  |||||    |||||||  |||
                                  TCCTG    TTTTTTT  GTT
                                     TTAC_      TG
GAM343  VRP      3'  TTGGCTTTTTTTTGCACTGTTT 23918   GG  CCCA_
             C                    G  AC    AGGAGAGAGTCAG
                                  |  ||    ||||||||||||
                                  C  TG    TTTTTTTTCGGTT
                                   TT  TCACG
GAM343  ZDHHC5   5'  CTGGTTTTCTTTTGTACTCCTC 93185       CCCCA       GT
                                  GGGGA    AGGAGAGA  CAG
                                  |||||    ||||||||  |||
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                                CTCCT    TTTTCTTT  GTC
                                   CATG_      TG
GAM343  ZDHHC7   3'  CTGATTTTTTTTTTTTTGTTCC  35320      CCC
                                GGGAC   AAGGAGAGAGTCAG
                                |||||   ||||||||||||||
                                CCTTG   TTTTTTTTTTAGTC
                                   TT_
GAM343  ZFP100   3'  CTGGTTTTTTTCTTAAGCCCCA 70586      ACCCC       GT
                                TGGGG    AAGGAGAGA  CAG
                                |||||    |||||||||  |||
                                ACCCC    TTCTTTTTT  GTC
                                   GAA__       TG
GAM343  ZFP91    3'  CTGATTTTTTTTTTTTTGGAGTC 54874   GG   C    __
           TTTG                    T  GGAC CCAAG  GAGAGAGTCAG
                                |  |||| |||||  ||||||||||
                                G  TCTG GGTTT  TTTTTTTAGTC
                                 TT   A    TT
GAM343  ZNF238   3'  CTGGTTTTCTGACAGTTCCCA  22028       CCCAAGG    GT
                                TGGGGAC      AGAGA  CAG
                                |||||||      |||||  |||
                                ACCCTTG      TCTTT  GTC
                                    ACAG___    TG
GAM343  ZNF340   3'  CTGACCGTTTTGGGGTTCCC   85713           AGAGA
                                GGGGACCCCAAGG    GTCAG
                                ||||||||||||    |||||
                                CCCTTGGGGTTTT    CAGTC
                                       GC___
GAM343  LOC112885 3'  CTGCTCCGTCTTTGGGGTCCTC 57339            GA   T
           A                     TGGGGACCCCAAGGA  GAG CAG
                                ||||||||||||||  ||| |||
                                ACTCCTGGGGTTTCT  CTC GTC
                                         GC  _
GAM343  LOC112970 3'  CTGACTTTTTGCTAGTTTCTA  57346    GG  CCCA  G
                                TGG  AC    AG AGAGAGTCAG
                                |||  ||    || ||||||||||
                                ATC  TG    TC TTTTTCAGTC
                                  TT  A___  G
GAM343  LOC116113 3'  TTGGCTTTTTCCTTTGTCGCC  93842    G   CCC
                                GG GAC   AAGGAGAGAGTCAG
                                || |||   ||||||||||||||
                                CC CTG   TTCCTTTTTCGGTT
                                 G   T__
GAM343  LOC118812 5'  TTTTCTTTGGGGTTGCCA    74365     G
                                TGG GACCCCAAGGAGAG
                                ||| ||||||||||||||
                                ACC TTGGGGTTTCTTTT
                                  G
GAM343  LOC118851 3'  TTGGTTCTCTCCAGGTGCTCA  76021      G   CCAA      GT
                                TGGG ACC    GGAGAGA  CAG
                                |||| |||    |||||||  |||
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                                ACTC TGG    CCTCTCT  GTT
                                  G  A___      TG
GAM343  LOC119559 3'  CTGGCGTCTCTGGGGTTTTTA  74454          AG    GA
                                TGGGGACCCCA  GAGA  GTCAG
                                ||||||||||  ||||  |||||
                                ATTTTTGGGGT  CTCT  CGGTC
                                      __   G_
GAM343  LOC124145 3'  TTGATTTTTTTTCTTGGCCTT  74726      ACC          _
                                GGGG   CCAAGGAGAGAG TCAG
                                ||||   |||||||||||| ||||
                                TTCC   GGTTCTTTTTTT AGTT
                                  ___          T
GAM343  LOC124753 5'  CTGGCTTTCTTCTTCCTGCCTC 74805      ACCCC
                                GGGG    AAGGAGAGAGTCAG
                                ||||    ||||||||||||||
                                CTCC    TTCTTCTTTCGGTC
                                  GTCC_
GAM343  LOC126917 3'  TTGACTGGGATTGTGGTCCCCA 75102         C   GGAGAG
                                TGGGGACC CAA     AGTCAG
                                |||||||| |||     ||||||
                                ACCCCTGG GTT     TCAGTT
                                     T   AGGG__
GAM343  LOC133634 3'  TTGATTCTCTCCTTGGGG    75602
                                CCCCAAGGAGAGAGTCAG
                                ||||||||||||||||||
                                GGGGTTCCTCTCTTAGTT

GAM343  LOC134266 3'  TTGGTTTTTTTTTTTTGGTT   75647     CC       GT
                                GACC  AAGGAGAGA  CAG
                                ||||  |||||||||  |||
                                TTGG  TTTTTTTTT  GTT
                                  TT        TG
GAM343  LOC138389 5'  CTGGCTTTTTCCTCCCTTTCTC 76738      CCCCA
          C                      GGGGA    AGGAGAGAGTCAG
                                |||||    ||||||||||||||
                                CCTCT    TCCTTTTTCGGTC
                                   TTCCC
GAM343  LOC143381 3'  CTGATTTTCTTCTCTTCCTC   77060      CCCCA
                                GGGGA    AGGAGAGAGTCAG
                                |||||    ||||||||||||||
                                CTCCT    TCTTCTTTTAGTC
                                   TC___
GAM343  LOC144501 3'  GTTGGCTTTCCCGTGCTCTTTG 84033       C      _______
          GGCTCCCCA                TGGGGA CCCAAGGA     GAGAGTCAG   T
                                |||||| ||||||||     |||||||||   |
                                ACCCCT GGGTTTCT     CTTTCGGTT   G
                                   C       CGTGCC
GAM343  LOC144571 5'  CTCCCTCTTTGGGGCCCT    84079      A        A
                                GGGG CCCCAAGGAG GAG
                                |||| |||||||||| |||
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                                TCCC GGGGTTTCTC CTC
                                  _       C
GAM343  LOC144742 5'  GATTCTTTGAGGTCCCT    77460       C  AGGA     AG
                                GGGGACC CA   GAGAGTC
                                ||||||| ||   |||||||
                                TCCCTGG GT   TTCTTAG
                                   A ____     G
GAM343  LOC144817 3'  TGTTTTCTTCAGTCCCT    77524       CCCAA     GT
                                GGGGAC    GGAGAGA  CA
                                ||||||    |||||||  ||
                                TCCCTG    CTTCTTT  GT
                                   A____      TG
GAM343  LOC145098 5'  TGACTTTATGGGTTCTCA    77539        CAAGGAG
                                TGGGGACCC      AGAGTCA
                                |||||||||      |||||||
                                ACTCTTGGG      TTTCAGT
                                     TA_____
GAM343  LOC145566 5'  CTGATTCTCTTGCCAGGTGTCC 77787     _  CAAG
                                GGAC CC   GAGAGAGTCAG
                                |||| ||   ||||||||||
                                CCTG GG   TTCTCTTAGTC
                                  T  ACCG
GAM343  LOC145608 5'  CTGCACTTTCTTGGGGTTCT   84381        AGG     _
                                GGGACCCCA   AGAGAGT CAG
                                |||||||||   ||||||| |||
                                TCTTGGGGT   TCTTTCA GTC
                                    ___      C
GAM343  LOC145826 5'  CTGGCTGAGCCTGGGGTTTTTA 84529          A  AGAG
                                TGGGGACCCCA GG   AGTCAG
                                |||||||||||  ||   ||||||
                                ATTTTTGGGGT CC   TCGGTC
                                     _  GAG_
GAM343  LOC146667 5'  CTGGCCGAATGTGGGGTCTCCA 84711          AGGAGAGA
                                TGGGGACCCCA      GTCAG
                                ||||||||||       |||||
                                ACCTCTGGGGT      CGGTC
                                     GTAAGC__
GAM343  LOC146988 3'  CTGGTTCTCTCCATTCCTCCTC 84958      CCCCAA     GT
                                GGGGA     GGAGAGA  CAG
                                |||||     |||||||  |||
                                CTCCT     CCTCTCT  GTC
                                   CCTTA_      TG
GAM343  LOC146988 5'  TGATTCTTTTACAGTCTC    84962      CCCAAG
                                GGGAC     GAGAGAGTCA
                                |||||     ||||||||||
                                CTCTG     TTTTCTTAGT
                                   ACA___
GAM343  LOC147166 3'  GCTGGCTTTTGAAATCCTATGG 78891         _   _____
            GGTCTCT                GGGGACCCCA AGGA   GAGAGTCAG   C
                                |||||||||| ||||   |||||||||   |
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                                TCTCTGGGGT TCCT    TTTTCGGTC   G
                                      A    AAAG
GAM343   LOC148343 5'  GGGCCCTCTCTTTGGGGTTCT  79546              A   AG
                                GGGACCCCAAGGAGAG GTC
                                |||||||||||||||| |||
                                TCTTGGGGTTTCTCTC CGG
                                          C   GT
GAM343   LOC149182 5'  CTGGCTGCTTGGGGTTCC     85533           G  AG
                                GGGACCCCAAG AG  AG
                                |||||||||| ||  ||
                                CCTTGGGGTTC TC  TC
                                       G  GG
GAM343   LOC149570 3'  CTGAGGGCTCCTTGGGGCCTT  85656      A         AGAG
                                GGGG CCCCAAGGAG    TCAG
                                |||| ||||||||||    ||||
                                TTCC GGGGTTCCTC    AGTC
                                  _         GGG_
GAM343   LOC150225 3'  CTGGCTTTCTTATCTGCTCCA  86190       ACCCCAAG
                                TGGGG       GAGAGAGTCAG
                                |||||       ||||||||||
                                ACCTC       TTCTTTCGGTC
                                   GTCTA___
GAM343   LOC151162 5'  TCGTTTTTCTTTGGGGTTTTTG 86432    GG             GTCAG
                                T  GGACCCCAAGGAGAGA
                                |  ||||||||||||||||
                                G  TTTGGGGTTTCTTTTT
                                 TT             GCTT
GAM343   LOC151283 3'  TTGATTCACCCCTTTTTGGGGA 81004       A         A___
            CCTTA                    TGGGG CCCCAAGGAG    GAGTCAG
                                |||||| ||||||||||    |||||||
                                ATTCC GGGGTTTTTC    CTTAGTT
                                   A         CCCA
GAM343   LOC151477 3'  CTGATTCTTCGGGATGGGCCTC 81058       A   CAAGGA
            A                     TGGGG CCC      GAGAGTCAG
                                ||||| |||      |||||||||
                                ACTCC GGG      TTCTTAGTC
                                   _   TAGGGC
GAM343   LOC151836 5'  TTGACTCTCTCAAAAGTCCTT  86689        CCCAAG
                                GGGGAC      GAGAGAGTCAG
                                ||||||      ||||||||||
                                TTCCTG      CTCTCTCAGTT
                                   AAAA__
GAM343   LOC151996 5'  TGGTGCCTGGGGGTCCCT     86725          A   AGAGAG
                                GGGGACCCC AGG      TCA
                                ||||||||| |||      |||
                                TCCCTGGGG TCC      GGT
                                      G   GT_____
GAM343   LOC152048 3'  CTGACTCTCACCTGGGCTTTG  86732    GG  A   CA   A
                                T  GG CCC  AGG GAGAGTCAG
                                |  || |||  ||| |||||||||
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                                G  TC GGG  TCC CTCTCAGTC
                                 TT  _  __   A
GAM343   LOC152185 3'  TTGACTTTCTCAAATAAGTTTT 59204    GG   CCCAAG
              CA                  TG  GAC     GAGAGAGTCAG
                                || |||     ||||||||||
                                AC  TTG     CTCTTTCAGTT
                                 TT   AATAAA
GAM343   LOC152765 5'  TGGCATTTGGGGTCTGCA    81546    G        GAGAGA
                                TG GGACCCCAAG     GTCA
                                || ||||||||||     ||||
                                AC TCTGGGGTTT     CGGT
                                 G        A_____
GAM343   LOC152804 3'  TTGATTTTTTTTTTCTATTGTT 87091    GG   CCC__
              TTC                 G  GAC     AAGGAGAGAGTCAG
                                |  |||    ||||||||||||||
                                C  TTG    TTTTTTTTTTAGTT
                                 TT   TTATC
GAM343   LOC157254 3'  CTGTCCCGTCTTGGGGTTCTT  82311            A__  G
                                GGGGACCCCAAGG   GA AG
                                ||||||||||||   || ||
                                TTCTTGGGGTTCT   CT TC
                                       GCC  G
GAM343   LOC157909 5'  TTGAGTTGCTTTCTTGGGTCTC 82521          C     A_  G
              TA                  TGGGGACCC AAGGAG  GA TCAG
                                |||||||| ||||||  || ||||
                                ATCTCTGGG TTCTTT  TT AGTT
                                      _     CG  G
GAM343   LOC157923 5'  CTGGCTCTTTCCACTCCCCG   82525       CCCCAA
                                TGGGGA     GGAGAGAGTCAG
                                ||||||     ||||||||||||
                                GCCCCT     CCTTTCTCGGTC
                                   CA____
GAM343   LOC159121 3'  CTGACTCTTTCTGATTTCCT   88386      CCCCAA
                                GGGA     GGAGAGAGTCAG
                                ||||     ||||||||||||
                                TCCT     TCTTTCTCAGTC
                                  TTAG__
GAM343   LOC166929 3'  CTGGTTTTCTTCTTCATCCT   83555      CCCC        GT
                                GGGA    AAGGAGAGA  CAG
                                ||||   |||||||||  |||
                                TCCT    TTCTTCTTT  GTC
                                  AC__        TG
GAM343   LOC199998 3'  CTGTGCAATTCCTGGGGTCTTC 91518           A    AGAGT
              A                   TGGGGACCCCA GGAG     CAG
                                ||||||||||| ||||    |||
                                ACTTCTGGGGT CCTT     GTC
                                       _   AACGT
GAM343   LOC200058 3'  TTGGTTTTCTCTTTGACATCTT 89966        CCC         GT
              CA                  TGGGGA   CAAGGAGAGA  CAG
                                ||||||   ||||||||||  |||
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                                ACTTCT   GTTTCTCTTT  GTT
                                   ACA        TG
GAM343   LOC200081 3'  CTGTCCTTGGGGATTCTA    89975      A       G
                                TGGGG CCCCAAGGA AG
                                ||||| ||||||||| ||
                                ATCTT GGGGTTCCT TC
                                   A       G
GAM343   LOC200471 5'  TGATTTTCTGGTGTTTTCA   91637    GG   C   AGGA
                                TG  GAC CCA    GAGAGTCA
                                ||  ||| |||    ||||||||
                                AC  TTG GGT    CTTTTAGT
                                 TT   T  ____
GAM343   LOC200734 3'  CTGATTTTCGGTGGGTTTTGTA 90279    G   C    AGGA
                                TG GGA CCCA    GAGAGTCAG
                                || ||| ||||    |||||||||
                                AT TTT GGGT    CTTTTAGTC
                                 G   T    GG__
GAM343   LOC200853 5'  CTGACTCGTGTGTTTGGGTTCC 90327         CAAGGAGA
            C                    GGGGACCC       GAGTCAG
                                ||||||||       |||||||
                                CCCTTGGG       CTCAGTC
                                     TTTGTGTG
GAM343   LOC201164 3'  CTGATTTTTTTTTTGGTATTTT 89493       CC
            TA                    TGGGGA  CCAAGGAGAGAGTCAG
                                ||||||  ||||||||||||||||
                                ATTTTT  GGTTTTTTTTTTAGTC
                                   AT
GAM343   LOC202347 5'  TTGGTTCTTTCCATTCTCCGCC 91952     _   CCCCAA      GT
            A                    TGG GGA     GGAGAGA  CAG
                                ||| |||     |||||||  |||
                                ACC CCT     CCTTTCT  GTT
                                  G   CTTA__      TG
GAM343   LOC203377 5'  TTGTTTTTCTTTGGGGTTTTTG 92263    GG            GTCAG
                                T  GGACCCCAAGGAGAGA
                                |  ||||||||||||||||
                                G  TTTGGGGTTTCTTTTT
                                 TT             GTT
GAM343   LOC204285 3'  CACCTCTCCCTGGGGTCCCCA  91015          A     A  CAG
                                TGGGGACCCCA GGAGAG GT
                                |||||||||| |||||| ||
                                ACCCCTGGGGT CCTCTC CA
                                      C     _  CT
GAM343   LOC204970 3'  CTGTCCATGGGGTTCTCA    90962          A   G
                                TGGGGACCCCA GGA AG
                                |||||||||| ||| ||
                                ACTCTTGGGGT CCT TC
                                      A   G
GAM343   LOC220883 3'  CTGGTTCTCTCCTCATGTCCTC 92892       CCCA       GT
                                GGGGAC    AGGAGAGA  CAG
                                ||||||    ||||||||  |||
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                                CTCCTG   TCCTCTCT  GTC
                                   TAC_      TG
GAM343  LOC220954 3'  CTGATATATTTTAGGGTCTTTG 94759   GG     CAAG   GA_
                                T  GGACCC   GAGA   GTCAG
                                |  ||||||   ||||   |||||
                                G  TCTGGG   TTTT   TAGTC
                                 TT     A___    ATA
GAM343  LOC221466 5'  GTGCTCCCTCTTTGGGGTTCCC 95317              A   CAG
           A                     TGGGGACCCCAAGGAG GAGT
                                 ||||||||||||||| ||||
                                 ACCCTTGGGGTTTCTC CTCG
                                           C   TGA
GAM343  LOC221584 5'  CTGACTTTTTTCAGGGTTCCTA 95470         CAA
                                 TGGGGACCC   GGAGAGAGTCAG
                                 |||||||||   ||||||||||||
                                 ATCCTTGGG   CTTTTTTCAGTC
                                       A__
GAM343  LOC221833 3'  TTGATTTTTTTTTTTTGTC    94117     CCC
                                 GAC   AAGGAGAGAGTCAG
                                 |||   ||||||||||||||
                                 CTG   TTTTTTTTTTAGTT
                                   TT_
GAM343  LOC222160 3'  CTGGCTCTTTCTTTGTTCAGAC 95785      ACCC__
           CTC                     GGGG     CAAGGAGAGAGTCAG
                                   ||||     ||||||||||||||||
                                   CTCC     GTTTCTTTCTCGGTC
                                     AGACTT
GAM343  LOC222161 3'  TGACTCTTTTGGCTCCTCA    94376       C  CAAG
                                 TGGGGA CC    GAGAGAGTCA
                                 ||||||  ||    ||||||||||
                                 ACTCCT GG    TTTTCTCAGT
                                    C  _____
GAM343  LOC253011 3'  GTTGGCTATGTCTTCTCCATGG 97634           A     ______
           GGTTTTTA                  TGGGGACCCCA GGAGAG     AGTCAG   T
                                 ||||||||||| ||||||    ||||||  |
                                 ATTTTTGGGGT CCTCTT     TCGGTT   G
                                       A     CTGTA
GAM343  LOC253187 5'  TTGGCTTTTTCCCCTTCCCT   98905       CCCCAA
                                 GGGGA     GGAGAGAGTCAG
                                 |||||     ||||||||||||
                                 TCCCT     CCTTTTTCGGTT
                                   TCC___
GAM343  LOC255057 3'  TTGACTTTTCCTGGGGGCTTCC 97098      GA   A     G
           A                      TGGG  CCCC AGGAGA AGTCAG
                                  ||||  |||| |||||| ||||||
                                  ACCT  GGGG TCCTTT TCAGTT
                                    TC   G     _
GAM343  LOC255975 5'  CTGACTCTTTCTTGAAGCCC   97580     ACCCCA
                                 GGG     AGGAGAGAGTCAG
                                 |||     ||||||||||||
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                                CCC     TTCTTTCTCAGTC
                                  GAAG__
GAM343  LOC256167 3'  CTGCTCTTCGGGGTCTTC    99522         A    _
                                GGGGACCCC AGGAG AG
                                ||||||||| ||||| ||
                                CTTCTGGGG TTCTC TC
                                     C    G
GAM343  LOC256542 3'  AGGTCTTTTCTGGGGTTCCT  97288         A     GTCAG
                                GGGGACCCCA GGAGAGA
                                |||||||||| |||||||
                                TCCTTGGGGT CTTTTCT
                                      _      GGAA
GAM343  LOC257152 3'  CTGGCTAAGTTTGGGTTCCCA 99184         CAAG  AG_
                                TGGGGACCC   GAG  AGTCAG
                                |||||||||   |||  ||||||
                                ACCCTTGGG   TTT  TCGGTC
                                     _____  GAA
GAM343  LOC257453 5'  CTGATTTTCTCTTTGGATTCTT 82928     _ CC
          CCA                    TGGG GA  CCAAGGAGAGAGTCAG
                                |||| ||  ||||||||||||||||
                                ACCT CT  GGTTTCTCTTTTAGTC
                                  T  TA
GAM343  LOC257464 5'  TTGGTTTTTTTTTTTACTTTCC 91248     CCCC_      GT
          TC                     GGGGA    AAGGAGAGA  CAG
                                |||||    |||||||||  |||
                                CTCCT    TTTTTTTTT  GTT
                                   TTCAT       TG
GAM343  LOC257466 3'  CTATTTCTTGGGCTCCTTA   97566      C       _
                                TGGGGA CCCAAGGAG AG
                                |||||| ||||||||| ||
                                ATTCCT GGGTTCTTT TC
                                   C       A
GAM343  LOC51313  3'  TTGGCTCTTTTGAGTCTCCA   33998       CC   GGA
                                TGGGGAC  CAA   GAGAGTCAG
                                |||||||  |||   |||||||||
                                ACCTCTG  GTT   TTCTCGGTT
                                     A_  ____
GAM343  LOC51652  3'  TTGAAAGACTTCTTGGTGGTTT 32704     GG  _      AGAG
          CCA                    TGG  ACC CCAAGGAG    TCAG
                                |||  ||| ||||||||    ||||
                                ACC  TGG GGTTCTTC    AGTT
                                  TT   T       AGAA
GAM343  LOC51696  3'  TTGATTCTCTCCTGTACCCA   33094     G  CCCA
                                TGGG AC    AGGAGAGAGTCAG
                                |||| ||    ||||||||||||
                                ACCC TG    TCCTCTCTTAGTT
                                  A  _____
GAM343  LOC63928  3'  TGACCCGTTTGGGGTCTC    42273          GAGAGA
                                GGGACCCCAAG     GTCA
                                ||||||||||      ||||
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                                CTCTGGGGTTT     CAGT
                                      GCC___
GAM343  LOC90639  5' TTGATTCTTTCTGGTTTTGCC  64419    G  CC   AG
                                GG GA  CCA  GAGAGAGTCAG
                                || ||  |||  ||||||||||
                                CC TT  GGT  CTTTCTTAGTT
                                 G  TT  __
GAM343  LOC91431  5' CTGATTCTTGTTGGGGATCCC  57725     _     G   GA
                                GGGA CCCCAA GAGA  GTCAG
                                |||| |||||| ||||  |||||
                                CCCT GGGGTT TTCT  TAGTC
                                  A     G   __
GAM343  LOC91431  5' TTGACAGAGTACTTCTTGGGCT 57728       C       AGA___
            TCTCA                   TGGGGA CCCAAGGAG     GTCAG
                                |||||| |||||||||     |||||
                                ACTCTT GGGTTCTTC     CAGTT
                                    C        ATGAGA
GAM343  LOC91907  3' CTGATTTTCTTTTGTAGTATCC 68101     GG  CC    G
            A                    TGG  AC  CAAG AGAGAGTCAG
                                |||  ||  |||| ||||||||||
                                ACC  TG  GTTT TCTTTTAGTC
                                  TA  AT   _
GAM343  LOC91947  3' TTGGTTTTCTTCATGTCCT   68228      CCCAA      GT
                                GGGAC    GGAGAGA  CAG
                                |||||    |||||||  |||
                                TCCTG    CTTCTTT  GTT
                                   TA___      TG
GAM343  LOC96597  5' TGATTCTCTAGAGGTCTT    67471       CCAAGG
                                GGGACC     AGAGAGTCA
                                ||||||     |||||||||
                                TTCTGG     TCTCTTAGT
                                   AGA___
GAM344  GPD1     3'  TCATGCCACCACATTTG     60398       C       C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A       _
GAM344  IL5RA    5'  TCGCATGGCCACCGCATTT   6906           AT__
                                AAATGCGGTGGC   CGA
                                ||||||||||||   |||
                                TTTACGCCACCG   GCT
                                      GTAC
GAM344  MYO1C    3'  TGCCGATGCCAAATATTTG   61873       CGG       A
                                TAAATG   TGGCATCG CA
                                ||||||   |||||||| ||
                                GTTTAT   ACCGTAGC GT
                                   AA_       C
GAM344  C6orf37  3'  TGTCACACTGCATTTA      68097          GCATC
                                TAAATGCGGTG    GACA
                                ||||||||||     ||||
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                                ATTTACGTCAC    CTGT
                                      A____
GAM344  DNAJC6   3' TTGCAGAACCACCGCATT   29498        CA  GA
                                AATGCGGTGG  TC  CAA
                                ||||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                      A_  AC
GAM344  FLJ11210 3' GTCGATGTGCATGCTTTTA  60319    T  GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM344  FLJ12476 3' TCGATCTTCTGCATTTA    43270       T  C
                                TAAATGCGG GG ATCGA
                                ||||||||| || |||||
                                ATTTACGTC TC TAGCT
                                      T  _
GAM344  KIAA1034 3' TCGATGGCATCCGCATTTG  63134       _  G
                                TAAATGCGG TG CATCGA
                                ||||||||| || ||||||
                                GTTTACGCC AC GTAGCT
                                      T  G
GAM344  KIAA1987 3' TCATGTAACTGCATTTA    89391       G   C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                      A   _
GAM344  MGC16063 3' TGTCCTGGCCACTGCATT   54929        ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                      GTC
GAM344  LOC147949 3' TGTCAGATGTCCACATTGCA  79279    __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM344  LOC150577 3' GTCCTCACCGCATTTG     86258        CATC
                                TAAATGCGGTGG   GAC
                                ||||||||||||   |||
                                GTTTACGCCACT   CTG
                                      C___
GAM344  LOC158219 3' TGTGTGTCACCACATTT    82694     C      CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                  A       __
GAM344  LOC202020 3' TGTCTCACCACATTTA     90605     C    CATC
                                TAAATG GGTGG   GACA
                                |||||| |||||   ||||
```

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                                ATTTAC CCACT    CTGT
                                   A    ____
GAM344  LOC90826  5'  TGTCGATGCAGGTTTATTTG  64788       CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                   TTGGA
GAM344  LOC93587  3'  TTGTCTTTACCTGCATTTA   73042       _    CATC
                                TAAATGC GGTGG    GACAA
                                ||||||| |||||    |||||
                                ATTTACG CCATT    CTGTT
                                   T    T___
GAM345  AARS      5'  AGGTGCAGCGGGCCCTTG    9633        _  AA  _
                                CAAGGGCC GC  TG ACCT
                                |||||||| ||  || ||||
                                GTTCCCGG CG  AC TGGA
                                   G  __  G
GAM345  BCL11A    3'  TAGGTCATTACAACCTGGCTTT 43468       C_____      ___
          T                      AAGGGCCG     AATGACCT   A
                                ||||||||     ||||||||   |
                                TTTTCGGT     TTACTGGA   T
                                   CCAACA       ___
GAM345  FOXE3     5'  GGGTCGGCGGCCCCTG     25164    A      AA
                                CA GGGCCGC  TGACCT
                                || |||||||  ||||||
                                GT CCCGGCG  GCTGGG
                                 C      __
GAM345  GAS7      3'  AGTGTCACACGGTCCTTG    20841        CAA   _
                                CAAGGGCCG   TGAC CT
                                |||||||||   |||| ||
                                GTTCCTGGC   ACTG GA
                                   AC_    T
GAM345  LIF       3'  AGGCCCACCTTGCGGCCCT   11302        __  A_
                                AGGGCCGCAA  TG  CCT
                                ||||||||||  ||  |||
                                TCCCGGCGTT  AC  GGA
                                   CC  CC
GAM345  MAPK7     5'  AGGTGGTGGCTGCGGCCTTTG  12308         ___  G
                                CAAGGGCCGCA   AT ACCT
                                ||||||||||   || ||||
                                GTTTCCGGCGT   TG TGGA
                                   CGG  G
GAM345  MGST2     5'  AGGTCATTCAGCCGCTTG    11577     _  CGC
                                CAAG GGC   AATGACCT
                                ||||  |||   ||||||||
                                GTTC CCG   TTACTGGA
                                  G   AC_
GAM345  PER2      3'  AGGTCATTTGGACACTTG    43343     GG_  C
                                CAAG   CCG AATGACCT
                                ||||   ||| ||||||||
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                                GTTC   GGT TTACTGGA
                                  ACA  _
GAM345  PYGO2    3'  AGGCATGGGGTGTGGCCCT   64683         ____  A
                                AGGGCCGCA   ATG CCT
                                |||||||||   ||| |||
                                TCCCGGTGT   TAC GGA
                                    GGGG  _
GAM345  RAD21    3'  AGGTCATTAGTTTCTTG    21834       CC  _
                                CAAGGG  GC AATGACCT
                                ||||||  || ||||||||
                                GTTCTT  TG TTACTGGA
                                   __ A
GAM345  SLC29A1  3'  AGGCCAGTGGAGGCTCTTG   18259        G_  A  A
                                CAAGGGCC  CA TG CCT
                                ||||||||  || || |||
                                GTTCTCGG  GT AC GGA
                                     AG  G  C
GAM345  WEE1     5'  AGGCCATTCGGTCCCTG    14106    A     C    A
                                CA GGGCCG AATG CCT
                                || |||||| |||| |||
                                GT CCTGGC TTAC GGA
                                 C     _   C
GAM345  BRAG     5'  AGGTTGCAGCGGCTCTTG    30097          AA
                                CAAGGGCCGC  TGACCT
                                ||||||||||  ||||||
                                GTTCTCGGCG  GTTGGA
                                     AC
GAM345  C6orf5   3'  AGGCCATGTTTGGGGCCCTTG  31972        G  ___  A
                                CAAGGGCC CA   ATG CCT
                                |||||||| ||   ||| |||
                                GTTCCCGG GT   TAC GGA
                                     G  TTG   C
GAM345  CBCIP2   3'  AGGTCATTGGCCGGGCCT    52649     G  __
                                AGG CCG  CAATGACCT
                                ||| |||  |||||||||
                                TCC GGC  GTTACTGGA
                                  G   CG
GAM345  DJ328E19.C1.1 3'  AGGTCATTGTCATCTTTG    31795       CC
                                CAAGGG  GCAATGACCT
                                ||||||  ||||||||||
                                GTTTCT  TGTTACTGGA
                                   AC
GAM345  FBP17    5'  AGATCATTGTGGACTTG     73144      GG       C
                                CAAG  CCGCAATGA CT
                                ||||  ||||||||| ||
                                GTTC  GGTGTTACT GA
                                  A_        A
GAM345  FLJ10743 3'  AGGTCAAGCTTGGCCTTTG   37077         __ AA
                                CAAGGGCC  GC  TGACCT
                                ||||||||  ||  ||||||
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                                GTTTCCGG  CG  ACTGGA
                                     TT  A_
GAM345  FLJ12687  5'  AGGCCATCCGCTGGCCTTT   46744       _  A_  A
                                AAGGGCC GC  ATG CCT
                                ||||||| ||  ||| |||
                                TTTCCGG CG  TAC GGA
                                     T  CC   C
GAM345  FLJ20446  3'  AGGTCACACCTGGCTCTTG   35635        CAA_
                                CAAGGGCCG   TGACCT
                                |||||||||   ||||||
                                GTTCTCGGT   ACTGGA
                                     CCAC
GAM345  FLJ22679  3'  GGGTCTCCTGCAGGCCCTTG  35184        _  AT_
                                CAAGGGCC GCA   GACCT
                                |||||||| |||   |||||
                                GTTCCCGG CGT   CTGGG
                                     A   CCT
GAM345  FLJ22679  3'  GGGTCTCCTGCAGGCCCTTG  35185        _  AT_
                                CAAGGGCC GCA   GACCT
                                |||||||| |||   |||||
                                GTTCCCGG CGT   CTGGG
                                     A   CCT
GAM345  KIAA1387  5'  AGGCCTCAGTGGCTCTTG    71443        AA  __
                                CAAGGGCCGC  TGA  CCT
                                ||||||||||  |||  |||
                                GTTCTCGGTG  ACT  GGA
                                      __  CC
GAM345  MGC11271  3'  AGGTCATTTGCCACCCTT    44493      CC   _
                                AAGGG  GCAA TGACCT
                                |||||  |||| ||||||
                                TTCCC  CGTT ACTGGA
                                   AC   T
GAM345  NEU4      5'  AGGTCAACTGCGGCCTCA    55790   A      A_
                                A GGGCCGCA  TGACCT
                                | ||||||||  ||||||
                                A TCCGGCGT  ACTGGA
                                 C       CA
GAM345  NXN       5'  GTCATTGCAGGGCCCTTG    42678        __
                                CAAGGGCC  GCAATGAC
                                ||||||||  ||||||||
                                GTTCCCGG  CGTTACTG
                                     GA
GAM345  PTDSS1    3'  TAGATCATCGCCTGGGGGGCCT 29253        _______ A   C  ___
          TTG                     CAAGGGCC     GC ATGA CT   A
                                ||||||||     || |||| ||   |
                                GTTTCCGG     CG TACT GA   T
                                     GGGGTC  C   A  ___
GAM345  RNF24     3'  AGGCCATGCAGGCCTTTG    24277        _  A  A
                                CAAGGGCC GCA TG CCT
                                |||||||| ||| || |||
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                                GTTTCCGG CGT AC GGA
                                     A  _  C
GAM345  SEMA5A   5'  AGGCCAGCCGCGGCCCTTG   15588          AA_  A
                                CAAGGGCCGC  TG CCT
                                ||||||||||  || |||
                                GTTCCCGGCG  AC GGA
                                     CCG  C
GAM345  STK17B   5'  AGGTCACAACCGTCGGCCCTTG 16163         _ AA___
                                CAAGGGCCG C    TGACCT
                                |||||||||  |    ||||||
                                GTTCCCGGC G    ACTGGA
                                     T CCAAC
GAM345  THEA     3'  AGGTCCCTGCGGCCTTTG    66871          AT
                                CAAGGGCCGCA  GACCT
                                ||||||||||  |||||
                                GTTTCCGGCGT  CTGGA
                                     CC
GAM345  USP19    3'  AGGCCATGCCTGCCTTTG    90400        C_  A  A
                                CAAGGGC  GCA TG CCT
                                |||||||  ||| || |||
                                GTTTCCG  CGT AC GGA
                                    TC  _  C
GAM345  LOC126823 5'  AGGTCACTGTGCGGCCCT    75080         A__
                                AGGGCCGCA  TGACCT
                                |||||||||  ||||||
                                TCCCGGCGT  ACTGGA
                                     GTC
GAM345  LOC148114 5'  AGGGCGGGCGCGGCCTTTG   79360          AA_  A
                                CAAGGGCCGC  TG CCT
                                ||||||||||  || |||
                                GTTTCCGGCG  GC GGA
                                     CGG  G
GAM345  LOC149317 3'  AGGTCATTGTCATCTTTG    80058       CC
                                CAAGGG  GCAATGACCT
                                ||||||  ||||||||||
                                GTTTCT  TGTTACTGGA
                                    AC
GAM345  LOC149706 3'  GGGTTTCTGGGGCCCTTG    85807        G  AT
                                CAAGGGCC CA  GACCT
                                ||||||||  ||  |||||
                                GTTCCCGG GT  TTGGG
                                     G  CT
GAM345  LOC150351 5'  AGGCCGTGCGCCGGCCTTTG  60877         _ A_  A
                                CAAGGGCCG C  ATG CCT
                                |||||||||  |  ||| |||
                                GTTTCCGGC G  TGC GGA
                                     C CG  C
GAM345  LOC202986 3'  AGGCCGGTGCAGGTCCTTG   92062         _  A  A
                                CAAGGGCC GCA TG CCT
                                ||||||||  ||| || |||
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                                GTTCCTGG CGT GC GGA
                                     A   G  C
GAM345  LOC220638 3'  AGGTCATTGTCATCTTTG    74338       CC
                                CAAGGG  GCAATGACCT
                                ||||||  ||||||||||
                                GTTTCT  TGTTACTGGA
                                   AC
GAM345  LOC257451 3'  AGGCATGGGGTGTGGCCCT   97295         ____  A
                                AGGGCCGCA   ATG CCT
                                |||||||||   ||| |||
                                TCCCGGTGT   TAC GGA
                                     GGGG  _
GAM346  GPD1     3'  TCATGCCACCACATTTG     60398       C       C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A      _
GAM346  IL5RA    5'  TCGCATGGCCACCGCATTT   6906          AT__
                                AAATGCGGTGGC   CGA
                                ||||||||||||   |||
                                TTTACGCCACCG   GCT
                                      GTAC
GAM346  MYO1C    3'  TGCCGATGCCAAATATTTG   61873       CGG      A
                                TAAATG  TGGCATCG CA
                                ||||||  |||||||| ||
                                GTTTAT  ACCGTAGC GT
                                   AA_      C
GAM346  C6orf37  3'  TGTCACACTGCATTTA     68097         GCATC
                                TAAATGCGGTG    GACA
                                ||||||||||     ||||
                                ATTTACGTCAC    CTGT
                                      A____
GAM346  DNAJC6   3'  TTGCAGAACCACCGCATT    29498         CA  GA
                                AATGCGGTGG  TC  CAA
                                ||||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                      A_  AC
GAM346  FLJ11210 3'  GTCGATGTGCATGCTTTTA   60319     T  GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM346  FLJ12476 3'  TCGATCTTCTGCATTTA     43270        T  C
                                TAAATGCGG GG ATCGA
                                ||||||||| || |||||
                                ATTTACGTC TC TAGCT
                                      T  _
GAM346  KIAA1034 3'  TCGATGGCATCCGCATTTG   63134         _  G
                                TAAATGCGG TG CATCGA
                                ||||||||| || ||||||
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                                GTTTACGCC AC GTAGCT
                                     T  G
GAM346  KIAA1987  3'  TCATGTAACTGCATTTA     89391          G    C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                     A   _
GAM346  MGC16063  3'  TGTCCTGGCCACTGCATT    54929           ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                      GTC
GAM346  LOC147949 3'  TGTCAGATGTCCACATTGCA  79279      __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM346  LOC150577 3'  GTCCTCACCGCATTTG      86258           CATC
                                TAAATGCGGTGG    GAC
                                ||||||||||||    |||
                                GTTTACGCCACT    CTG
                                      C___
GAM346  LOC158219 3'  TGTGTGTCACCACATTT     82694       C       CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                   A       __
GAM346  LOC202020 3'  TGTCTCACCACATTTA      90605       C    CATC
                                TAAATG GGTGG    GACA
                                ||||||| |||||    ||||
                                ATTTAC CCACT    CTGT
                                   A    _____
GAM346  LOC90826  5'  TGTCGATGCAGGTTTATTTG  64788       CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                    TTGGA
GAM346  LOC93587  3'  TTGTCTTTACCTGCATTTA   73042        _    CATC
                                TAAATGC GGTGG    GACAA
                                ||||||| |||||    |||||
                                ATTTACG CCATT    CTGTT
                                     T    T___
GAM347  ELF3      3'  TGACCTTGACCTTGACCAA   16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                   _    AGT  ___
GAM347  JAK2      3'  TGACCTTCATTCTGAGACCAA 18318       CAA       AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
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                                AACCAG   TCTTACTT  CAGT
                                   AG_      C_
GAM347  SLC10A2  5'  ACTCTCTGTCTTGACCAA    6590       CAA      A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM347  FLJ10803 3'  GTGACTTTCAGTTAAAGCCAA  37205      CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM347  KIAA1958 5'  GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||   ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM347  MARCKS   3'  ACTTTCCACCCTGCCCA     11411     TTCA    A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                 CG__   _
GAM347  TUB      5'  GTGGGACCATCCCTTAAACC   13898      C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A       AG__
GAM347  LOC80298 3'  ACTTTTACCTTGAACCA     48062         GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                     A___
GAM348  CYP7B1   3'  GTCACAAAGCCCATATAA    17875      GA    C
                                TTATG  GGCT TGTGAC
                                |||||  |||| ||||||
                                AATAT  CCGA ACACTG
                                   AC    A
GAM348  F8       3'  TCACAATCCACAAATGATG    5529         A    GGCTC
                                TATCATTT TGGA     TGTGA
                                |||||||| ||||     |||||
                                GTAGTAAA ACCT     ACACT
                                     C    A____
GAM348  DCTN4    3'  GTCACAGATGAAACTTAAATGA 68396         TGGAGGC
           TA                    TATCATTTA      TCTGTGAC
                                ||||||||||      ||||||||
                                ATAGTAAAT      AGACACTG
                                     TCAAAGT
GAM348  DIS3     3'  CACATTTGCCCCATAGAT    30910         A   TC_
                                ATTTATGG GGC   TGTG
                                |||||||| |||   ||||
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                                TAGATACC CCG   ACAC
                                    _  TTT
GAM348  FLJ10261  3'  ACCAAGTCTCATAAATGATA  36415          G    CT
                                TATCATTTATG AGGCT  GT
                                |||||||||| |||||  ||
                                ATAGTAAATAC TCTGA  CA
                                    _    AC
GAM348  FLJ20344  3'  GTCACAGAACATAAATGCATA  35485    _      GAGGC
                                TAT CATTTATG    TCTGTGAC
                                ||| ||||||||    ||||||||
                                ATA GTAAATAC    AGACACTG
                                  C       A____
GAM348  PRO2714   5'  TCACAGAGAAGGTCAAATGA   38195      TA   AGG_
                                TCATT  TGG    CTCTGTGA
                                |||||  |||    ||||||||
                                AGTAA  ACT    GAGACACT
                                   __  GGAA
GAM348  LOC115265 3'  TCACAGAATCATACTAAATGAT 73742         TGGA GC
          A                     TATCATTTA    G  TCTGTGA
                                |||||||||    |  |||||||
                                ATAGTAAAT    C  AGACACT
                                     CATA TA
GAM348  LOC159053 3'  CACAGAGCTAGTAAGT      88363       GGA
                                ATTTAT   GGCTCTGTG
                                ||||||   |||||||||
                                TGAATG   TCGAGACAC
                                   A__
GAM348  LOC221718 3'  GTCACAGAGACTGGAATAAAT  95283       GGA  _
                                ATTTAT   GG CTCTGTGAC
                                ||||||   || |||||||||
                                TAAATA   TC GAGACACTG
                                   AGG  A
GAM348  LOC51141  3'  GTCACAAAAGTGCAAAGTGATA 69149         A  GAG   C_
                                TATCATTT TG   GCT  TGTGAC
                                |||||||| ||   |||  ||||||
                                ATAGTGAA AC   TGA  ACACTG
                                     _ G__   AA
GAM348  LOC90139  3'  GCAACCCCATAAATGA      56270          A  CTC
                                TCATTTATGG GG   TGT
                                |||||||||| ||   |||
                                AGTAAATACC CC   ACG
                                     _ A__
GAM349  BECN1     3'  AATCCACAAAAGCCACTT    15004      _  C
                                GGGTG CTT TGTGGATT
                                ||||| ||| ||||||||
                                TTCAC GAA ACACCTAA
                                   C  A
GAM349  HD        3'  AATCTGTGGCAAGCACCCA   10904          _  TG
                                TGGGTGCTT CTG  GATT
                                ||||||||| |||  ||||
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                                ACCCACGAA GGT  CTAA
                                     C   GT
GAM349  RP2      3'  AATCCACATTCTTGGACCCAAT 23595        G  TC___
            C                    GATTGGGT CT    TGTGGATT
                                 |||||||| ||    ||||||||
                                 CTAACCCA GG    ACACCTAA
                                     _ TTCTT
GAM349  SLC22A3  3'  GAGACAAGAGAAGCCCCCAA  42039      T    G_ GAT
                                 TTGGG GCTTCT  TG   TCTC
                                 ||||| ||||||  ||   ||||
                                 AACCC CGAAGA  AC   AGAG
                                    C     GA ___
GAM349  HSPC133  3'  AATTTCAGCAAGCATCCAATC  27182          _  T
                                 GATTGGGTGCTT CTG GGATT
                                 |||||||||||| ||| |||||
                                 CTAACCTACGAA GAC TTTAA
                                       C  _
GAM349  TRF4-2   3'  GAAAATGCAAAGCACCCAA   42612         C   GA
                                 TTGGGTGCTT TGTG  TTC
                                 |||||||||| ||||  |||
                                 AACCCACGAA ACGT  AAG
                                     _   AA
GAM349  LOC154386 3'  AGAAAGAAAGCACCCAA    81986         _ GTGGA
                                 TTGGGTGCTT CT    TTCT
                                 |||||||||| ||    ||||
                                 AACCCACGAA GA    AAGA
                                       A _____
GAM349  LOC220980 3'  AATCCACAGCAGACCTA    94761      G  T
                                 TGGGT CT CTGTGGATT
                                 ||||| || |||||||||
                                 ATCCA GA GACACCTAA
                                    _ C
GAM349  LOC90829  5'  AGAAAAAAACAACCCAATC   64791        GCTTC  GGA_
                                 GATTGGGT    TGT   TTCT
                                 ||||||||    |||   ||||
                                 CTAACCCA    ACA   AAGA
                                     _____  AAAA
GAM350  BAZ1B    3'  CCCCACCACCGCCAGCTTC   51559         ATC  T
                                 GAAGCTGGTG  GT GGGG
                                 |||||||||  || ||||
                                 CTTCGACCGC  CA CCCC
                                       CAC  _
GAM350  CD34     3'  CCCTTATCACCAGCTGCCT   10105    A_       CGTT
                                 AG  AGCTGGTGAT   GGG
                                 ||  ||||||||||   |||
                                 TC  TCGACCACTA   CCC
                                  CG        TT__
GAM350  DGKE     3'  ATCCCCAAACCAGCCAGCCTTC 14679      _    GATCG
                                 GAAG CTGGT    TTGGGGAT
                                 |||| |||||    ||||||||
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                                CTTC GACCG    AACCCCTA
                                  C    ACCA_
GAM350  ITGAL    3'  CCAGACGGTTCACCAGCCTCT  11042     A      _    G
                                AGA GCTGGTGA TCGTT GG
                                ||| |||||||| ||||| ||
                                TCT CGACCACT GGCAG CC
                                  C       T    A
GAM350  MFAP4    3'  ATTCCCGAGCACCAACTCCTT  69788     A  C    ATCG
                                AAG AG TGGTG   TTGGGGAT
                                ||| || |||||   ||||||||
                                TTC TC ACCAC   AGCCCTTA
                                  C A    G___
GAM350  SCGB1A1  3'  ATCCCCAACTGCTCCAGCCTCT 13982     A    TGATC
                                AGA GCTGG    GTTGGGGAT
                                ||| |||||    |||||||||
                                TCT CGACC    CAACCCCTA
                                  C    TCGT_
GAM350  SORCS1   3'  ATCCCCAACCTGCCAGGCTTC  54678      _    ATC
                                GAAGC TGGTG   GTTGGGGAT
                                ||||| |||||   |||||||||
                                CTTCG ACCGT   CAACCCCTA
                                   G    C__
GAM350  VIPR1    3'  CCCCAGTGGCCACTCAGCTTC  17310       _  AT
                                GAAGCTG GTG  CGTTGGGG
                                ||||||| |||  ||||||||
                                CTTCGAC CAC  GTGACCCC
                                     T   CG
GAM350  C17orf31  5'  ATCCCCAAGGAAACCAATTTC  34536     C   GA  G
                                GAAG TGGT  TC TTGGGGAT
                                |||| ||||  || ||||||||
                                CTTT ACCA  AG AACCCCTA
                                  A   A_  G
GAM350  DKFZP434C131 3'  TCCCAGAGTCCCCAGCCTC   69642    A    T   CG
                                GA GCTGG GAT  TTGGGG
                                || ||||| |||  ||||||
                                CT CGACC CTG  GACCCT
                                 C    C   A_
GAM350  DKFZp434J0226 5'  TCGGCTGATCACCAGCTC    72795    A       _
                                GA GCTGGTGATC GTTGG
                                || |||||||||| |||||
                                CT CGACCACTAG CGGCT
                                  _        T
GAM350  FLJ13782  3'  CCCCTCTCTCTCCAGCCTCTT  46699     A    T  TCGTT
                                AAGA GCTGG GA    GGGG
                                |||| ||||| ||    ||||
                                TTCT CGACC CT    CCCC
                                  C    T  CTCT_
GAM350  FLJ14126  5'  CCCGGGATACCCCAGCTTCTT  46275         TG_  G
                                AAGAAGCTGG   ATC TTGGG
                                ||||||||||   ||| |||||
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                                TTCTTCGACC   TAG GGCCC
                                     CCA  _
GAM350  FLJ20340  5'  CCAGATCACCAACATCTT    35456     AGC      GT
                                AAGA   TGGTGATC  TGG
                                ||||   ||||||||  |||
                                TTCT   ACCACTAG  ACC
                                  ACA      __
GAM350  HIC2      3'  CCCCACCCATCACTAGCTTC   65863          CGT
                                GAAGCTGGTGAT   TGGGG
                                ||||||||||||   |||||
                                CTTCGATCACTA   ACCCC
                                       CCC
GAM350  KCND1     5'  CCCCTCAAGATGCACCAGCT   18339        _   GTT_
                                AGCTGGTG ATC    GGGG
                                ||||||||  |||    ||||
                                TCGACCAC TAG    CCCC
                                     G   AACT
GAM350  KIAA0494  5'  ATCCTTTGGGGTCACCAGCTCC 29398     A        GTT
           TT                     AAG AGCTGGTGATC   GGGGAT
                                ||| ||||||||||   ||||||
                                TTC TCGACCACTGG   TTCCTA
                                  C         GGT
GAM350  KIAA0836  3'  ATCATTCTTGATCATCAGCTTC 65165            TTGGG
                                GAAGCTGGTGATCG    GAT
                                ||||||||||||||    |||
                                CTTCGACTACTAGT    CTA
                                       TCTTA
GAM350  KIAA1190  3'  CCCCAGTTCCTCACCAGCTACT 71645    A       TCG_
                                AG AGCTGGTGA    TTGGGG
                                || |||||||||    ||||||
                                TC TCGACCACT    GACCCC
                                 A        CCTT
GAM350  KIAA1870  5'  CTCCTACCACCAGCTCCT    50582    A       ATC  T
                                AG AGCTGGTG   GT GGGG
                                || ||||||||   || ||||
                                TC TCGACCAC   CA CCTC
                                 C       ___  T
GAM350  MGC12837  3'  ATCCCCTCCATCCCCAACTTC  52169     C   T   CGTT
                                GAAG TGG GAT    GGGGAT
                                |||| ||| |||    ||||||
                                CTTC ACC CTA    CCCCTA
                                  A   C   CCT_
GAM350  SSH2      3'  TTCCAATCACCAGCTCCT    62895    A       CGT
                                AG AGCTGGTGAT   TGGGG
                                || ||||||||||   |||||
                                TC TCGACCACTA   ACCTT
                                 C         ___
GAM350  TNRC4     3'  CCCTCACCCCAGCCTCTT    24191     A    TGATC  T
                                AAGA GCTGG    GT GGGG
                                |||| |||||    || ||||
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                                TTCT CGACC     CA TCCC
                                  C     C____  C
GAM350   LOC126526 3'  CCCCAGCTCATCAGCCTC     75037    A       TC
                                GA GCTGGTGA  GTTGGGG
                                || ||||||||  |||||||
                                CT CGACTACT  CGACCCC
                                 C       __
GAM350   LOC144501 3'  TCCCAGCGGCACCAGCCTC    84034    A      A
                                GA GCTGGTG TCGTTGGGG
                                || ||||||| |||||||||
                                CT CGACCAC GGCGACCCT
                                 C      _
GAM350   LOC146940 3'  ATCCCCAACAGTGACGGCT    78805       G G  C
                                AGCTG T AT GTTGGGGAT
                                ||||| | || |||||||||
                                TCGGC A TG CAACCCCTA
                                   _ G  A
GAM350   LOC148760 3'  CCTATTTGCCCACCAGCTTCT  85362           AT  T_
                                AGAAGCTGGTG  CG  TGGG
                                ||||||||||  ||  ||||
                                TCTTCGACCAC  GT  ATCC
                                      CC  TT
GAM350   LOC148918 5'  CCCCACTGTCTCTCCAGCTCCT 79821     A     T  T_  T
           T                     AAG AGCTGG GA  CG TGGGG
                                ||| |||||| ||  || |||||
                                TTC TCGACC CT  GT ACCCC
                                  C     T  CT  C
GAM350   LOC151443 5'  ATCTCTCCGATGACCAGCTTCT 81042           G    TT
           T                     AAGAAGCTGGT ATCG  GGGGAT
                                ||||||||||| ||||  ||||||
                                TTCTTCGACCA TAGC  TCTCTA
                                      G    C_
GAM350   LOC157531 5'  CCCAGCCTCATCACTCAGCTTC 87766          _    C__
           TT                     AAGAAGCTG GTGAT   GTTGGG
                                |||||||| |||||   ||||||
                                TTCTTCGAC CACTA   CGACCC
                                     T     CTC
GAM350   LOC158427 3'  CCTTTTCATCACCAGCCTCT   58354     A       CGTT
                                AGA GCTGGTGAT    GGG
                                ||| |||||||||    |||
                                TCT CGACCACTA    TCC
                                  C        CTTT
GAM350   LOC219333 3'  TCAGAGATACCAGCTCCT     95188    A       A  G
                                AG AGCTGGTG TC TTGG
                                || |||||||| || ||||
                                TC TCGACCAT AG GACT
                                 C       _  A
GAM350   LOC85414  3'  CCCCAACTTTCCCCACCAGCT  53550         ATC___
                                AGCTGGTG     GTTGGGG
                                ||||||||     |||||||
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                                TCGACCAC     CAACCCC
                                     CCCTTT
GAM350  LOC92573  5'  TCTGTAATCCCAGCTTCTT   70380         T   CGT  G
                                AAGAAGCTGG GAT   TG GGA
                                |||||||||| |||   || |||
                                TTCTTCGACC CTA   AT TCT
                                     _  ___  G
GAM351  ADCY7     3'  TGAGTTGCCCCGGGCTG     8494         AACACT   __
                                CAGCCCGG     GGCA  TCA
                                ||||||||     ||||  |||
                                GTCGGGCC     CCGT  AGT
                                     _______   TG
GAM351  ADRBK1    3'  ATGATGCCACACCAAGCTGTG  9663        CC  AACAC
                                CACAGC  GG    TGGCATCAT
                                ||||||  ||    |||||||||
                                GTGTCG  CC    ACCGTAGTA
                                   AA  AC___
GAM351  BTEB1     5'  ATGTCAGTGTTCGAGGCTGT   8668        CG
                                ACAGCC  GAACACTGGCAT
                                ||||||  ||||||||||||
                                TGTCGG  CTTGTGACTGTA
                                   AG
GAM351  LAIR1     3'  GAGGACAGCCCGGGCTGTG    41662         AACA   GCA
                                CACAGCCCGG    CTG   TC
                                ||||||||||    |||   ||
                                GTGTCGGGCC    GAC   AG
                                     C___    AGG
GAM351  LILRB4    3'  TGATGTCTTCCTGGCTGT     23388       C    CACT
                                ACAGCC GGAA    GGCATCA
                                |||||| ||||    |||||||
                                TGTCGG CCTT    CTGTAGT
                                   T   _____
GAM351  P23       3'  ATGACTTGTCAGTGTTCCAGGT 22752     G  C         __
              GT                    ACA CC GGAACACTGGCA  TCAT
                                ||| || ||||||||||||  ||||
                                TGT GG CCTTGTGACTGT  AGTA
                                  _ A          TC
GAM351  PRV1      3'  TGAGCATTCAGGGCTGTG     73896         G   CACTG  A
                                CACAGCCC GAA    GC TCA
                                |||||||| |||    || |||
                                GTGTCGGG CTT    CG AGT
                                     A   A_____ _
GAM351  SOLH      5'  GGCGCCGCCGGGCTGTG      20094         AACAC    AT
                                CACAGCCCGG    TGGC  C
                                ||||||||||    ||||  |
                                GTGTCGGGCC    GCCG  G
                                     ______   CG
GAM351  SOX5      3'  ATGCCAGTAATTCAGCTG     23665      CC   AC
                                CAGC  GGA  ACTGGCAT
                                ||||  |||  ||||||||
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                                GTCG  CTT  TGACCGTA
                                  A_   AA
GAM351  ATP10B   3'  ATGATGCCAGCACTAGCCAGCT 64103     CC  AACA__
           G                     CAGC  GG     CTGGCATCAT
                                 ||||  ||     ||||||||||
                                 GTCG  CC     GACCGTAGTA
                                   A_  GATCAC
GAM351  C19orf7  3'  ATGCAGGTGTTCCAAGGTGTG  61776     G  C_      G
                                 CACA CC  GGAACACT GCAT
                                 |||| ||  |||||||| ||||
                                 GTGT GG  CCTTGTGG CGTA
                                   _  AA       A
GAM351  C1QR1    3'  ATGCCAGTGCTCCGAGCTCA  24867   C   C    A
                                 A AGC CGGA CACTGGCAT
                                 | ||| |||| |||||||||
                                 A TCG GCCT GTGACCGTA
                                  C   A   C
GAM351  CYP2A13  3'  ATGATGTCCTTCAGAGCTGTG  7546       CCG   CACT
                                 CACAGC   GAA   GGCATCAT
                                 ||||||   |||   ||||||||
                                 GTGTCG   CTT   CTGTAGTA
                                    AGA   C___
GAM351  KIAA0316 3'  ATGATGCCAATGAGCTGCTCTG 70243     CC   AA  C
                                 CAG  CGG  CA TGGCATCAT
                                 |||  |||  || |||||||||
                                 GTC  GTC  GT ACCGTAGTA
                                   TC   GA  A
GAM351  MGC4368  5'  ATGATGCCAGTGGCGCTGG   44723     AA_
                                 CCGG   CACTGGCATCAT
                                 ||||   ||||||||||||
                                 GGTC   GTGACCGTAGTA
                                   GCG
GAM351  NBL1     3'  ATGTTAGTGCCCCGCACTGTG  60045      CC   AA
                                 CACAG  CGG  CACTGGCAT
                                 |||||  |||  |||||||||
                                 GTGTC  GCC  GTGATTGTA
                                    AC   CC
GAM351  RNF13    5'  GCTAGTACTCCGGGCTGTG   24417          AC
                                 CACAGCCCGGA  ACTGGC
                                 ||||||||||  ||||||
                                 GTGTCGGGCCT  TGATCG
                                        CA
GAM351  RNPC1    3'  TGGGGCATCCAGGGCTGTG   34414        _  ACACTG  AT
                                 CACAGCCC GGA     GC  CA
                                 |||||||| |||     ||  ||
                                 GTGTCGGG CCT     CG  GT
                                     A  A_____  GG
GAM351  TIMM22   3'  ATGATGCCAGCCCCGGATCCGG 78911         ACA____
           GCTG                    CAGCCCGGA      CTGGCATCAT
                                 |||||||||      ||||||||||
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                                GTCGGGCCT      GACCGTAGTA
                                     AGGCCCC
GAM351  LOC143879 5'  ATGATGCCACTGATCAAACCTG 77157     CCCG  A  C
                                CAG    GA CA TGGCATCAT
                                |||    || || |||||||||
                                GTC    CT GT ACCGTAGTA
                                  CAAA  A  C
GAM351  LOC147858 5'  ATGCTGCACTCCGGAGCCGTG  79267     A  _    ACACT
                                CAC GC CCGGA    GGCAT
                                ||| || |||||    |||||
                                GTG CG GGCCT    TCGTA
                                  C  A    CACG_
GAM351  LOC149086 3'  ATGGGTTGGTGTCCGGGC    85491       A   TG  A
                                GCCCGGA CAC  GC TCAT
                                ||||||| |||  || ||||
                                CGGGCCT GTG  TG GGTA
                                    _  GT  _
GAM351  LOC200058 3'  TGTCGCAGCAGCCCGGGCTG   89965       AACA  __  AT
                                CAGCCCGG   CTG  GC  CA
                                ||||||||   |||  ||  ||
                                GTCGGGCC   GAC  CG  GT
                                     C___   GA  CT
GAM351  LOC257364 3'  ATGCTGGGCACCCAGGGCTGTG 96641        _  AACA TG
                                CACAGCCC GG    C  GCAT
                                |||||||| ||    |  ||||
                                GTGTCGGG CC    G  CGTA
                                     A  CACG GT
GAM351  LOC55893  5'  ATGATGCCAGGCTACCAGGC   38489     C  AACA
                                GCC GG    CTGGCATCAT
                                ||| ||    ||||||||||
                                CGG CC    GACCGTAGTA
                                  A  ATCG
GAM352  ELF3      3'  TGACCTTGACCTTGACCAA    16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                   _    AGT  ____
GAM352  JAK2      3'  TGACCTTCATTCTGAGACCAA  18318       CAA       AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                    AG_       C_
GAM352  SLC10A2   5'  ACTCTCTGTCTTGACCAA    6590        CAA       A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                    ___        C
GAM352  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
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                                AACCGA    TTG CTTTCAGTG
                                   AA___  A
GAM352  KIAA1958 5' GTGACTTTGAACCCCAAACC  82788     CAA  ATGG
                                GGTT  GGG   AAAGTCAC
                                ||||  |||   ||||||||
                                CCAA  CCC   TTTCAGTG
                                  A__  CAAG
GAM352  MARCKS   3' ACTTTCCACCCTGCCCA    11411     TTCA   A
                                TGG   AGGG TGGAAAGT
                                |||   |||| ||||||||
                                ACC   TCCC ACCTTTCA
                                 CG__  _
GAM352  TUB      5' GTGGGACCATCCCTTAAACC  13898     C       AAAG
                                GGTT AAGGGATGG   TCAC
                                |||| |||||||||   ||||
                                CCAA TTCCCTACC   GGTG
                                  A       AG__
GAM352  LOC80298 3' ACTTTTACCTTGAACCA    48062        GATG
                                TGGTTCAAGG   GAAAGT
                                ||||||||||   ||||||
                                ACCAAGTTCC   TTTTCA
                                     A___
GAM353  GPD1     3' TCATGCCACCACATTTG     60398      C      C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A      _
GAM353  IL5RA    5' TCGCATGGCCACCGCATTT   6906         AT__
                                AAATGCGGTGGC   CGA
                                ||||||||||||   |||
                                TTTACGCCACCG   GCT
                                       GTAC
GAM353  MYO1C    3' TGCCGATGCCAAATATTTG   61873      CGG      A
                                TAAATG   TGGCATCG CA
                                ||||||   |||||||| ||
                                GTTTAT   ACCGTAGC GT
                                   AA_      C
GAM353  C6orf37  3' TGTCACACTGCATTTA     68097        GCATC
                                TAAATGCGGTG    GACA
                                ||||||||||     ||||
                                ATTTACGTCAC    CTGT
                                     A____
GAM353  DNAJC6   3' TTGCAGAACCACCGCATT    29498        CA  GA
                                AATGCGGTGG  TC  CAA
                                ||||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                     A_  AC
GAM353  FLJ11210 3' GTCGATGTGCATGCTTTTA   60319     T   GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
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                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM353  FLJ12476  3'  TCGATCTTCTGCATTTA     43270        T  C
                                TAAATGCGG GG ATCGA
                                ||||||||| || |||||
                                ATTTACGTC TC TAGCT
                                     T  _
GAM353  KIAA1034  3'  TCGATGGCATCCGCATTTG   63134        _  G
                                TAAATGCGG TG CATCGA
                                ||||||||| || ||||||
                                GTTTACGCC AC GTAGCT
                                     T  G
GAM353  KIAA1987  3'  TCATGTAACTGCATTTA     89391        G   C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                     A   _
GAM353  MGC16063  3'  TGTCCTGGCCACTGCATT    54929         ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                     GTC
GAM353  LOC147949 3'  TGTCAGATGTCCACATTGCA   79279     __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM353  LOC150577 3'  GTCCTCACCGCATTTG      86258         CATC
                                TAAATGCGGTGG   GAC
                                ||||||||||||   |||
                                GTTTACGCCACT   CTG
                                     C___
GAM353  LOC158219 3'  TGTGTGTCACCACATTT     82694       C      CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                   A       __
GAM353  LOC202020 3'  TGTCTCACCACATTTA      90605       C    CATC
                                TAAATG GGTGG   GACA
                                |||||| |||||   ||||
                                ATTTAC CCACT   CTGT
                                   A   ____
GAM353  LOC90826  5'  TGTCGATGCAGGTTTATTTG  64788       CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                    TTGGA
GAM353  LOC93587  3'  TTGTCTTTACCTGCATTTA   73042       _    CATC
                                TAAATGC GGTGG   GACAA
                                ||||||| |||||   |||||
```

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                                ATTTACG CCATT    CTGTT
                                   T    T___
GAM354  ARF3     3'  AATCTGGGGCTGGAAATG    9767            A
                                TATTTTCAGCCCCA ATT
                                |||||||||||||| |||
                                GTAAAGGTCGGGGT TAA
                                       C
GAM354  EIF3S10  3'  TAATTTGGAATGAAGTAAGGTT 72169         T  GCC
                                AACCTTATTT CA   CCAAATTA
                                |||||||||| ||   ||||||||
                                TTGGAATGAA GT   GGTTTAAT
                                      _  AA_
GAM354  SPANXA1  3'  TTGGGCAATGAAAATAAAGTT  74267     C       GC_
                                AAC TTATTTTCA   CCCAA
                                ||| |||||||||   |||||
                                TTG AATAAAAGT   GGGTT
                                  A        AAC
GAM354  SPANXA1  3'  TTGGGCAATGAAAATAAAGTT  26525     C       GC_
                                AAC TTATTTTCA   CCCAA
                                ||| |||||||||   |||||
                                TTG AATAAAAGT   GGGTT
                                  A        AAC
GAM354  SPANXC   3'  TTGGGCAATGAAAATAAAGTT  42958     C       GC_
                                AAC TTATTTTCA   CCCAA
                                ||| |||||||||   |||||
                                TTG AATAAAAGT   GGGTT
                                  A        AAC
GAM354  ZNF265   3'  TAATTTGGGGCAAAAAAGAAAG 19577     A_    CA
                                CTT  TTTT  GCCCCAAATTA
                                |||  ||||  ||||||||||||
                                GAA  AAAA  CGGGGTTTAAT
                                  AG    AA
GAM354  ESM1     3'  AATTTAAGGTATGAAAATAAG  23848          _  CC
                                CTTATTTTCA GCC  AAATT
                                |||||||||| |||  |||||
                                GAATAAAAGT TGG  TTTAA
                                      A   AA
GAM354  FLJ20079 3'  TAATTTGGGGAACTAATAA    34976       TTCAG
                                TTATT    CCCCAAATTA
                                |||||    ||||||||||
                                AATAA    GGGGTTTAAT
                                   TCAA_
GAM354  FLJ22833 3'  TAATTTGGGGGAGTTATAAAGT 43408     C    T_   AG
           T                     AAC TTAT  TTC  CCCCAAATTA
                                |||  ||||  |||  ||||||||||
                                TTG AATA  GAG  GGGGTTTAAT
                                  A    TT   __
GAM354  KCNH8    3'  AATTTGGGGCTCAAAGTG    58902       C
                                TATTTT AGCCCCAAATT
                                ||||||  ||||||||||
```

```
                                GTGAAA TCGGGGTTTAA
                                   C
GAM354  KIAA0478  3'  AATTTGGGGCTGAAGGGAGTGT 30169    _  A
                                AC CTT TTTTCAGCCCCAAATT
                                || ||| ||||||||||||||||
                                TG GAG GGAAGTCGGGGTTTAA
                                 T  _
GAM354  KIAA1229  3'  TAATTTGGGGCTAAATGA    62758       TC
                                TTATTT  AGCCCCAAATTA
                                ||||||  ||||||||||||
                                AGTAAA  TCGGGGTTTAAT
                                   __
GAM354  KIAA1912  3'  TAATTTGGATGCAAGATAAG   73761        CA  C_
                                CTTATTTT  GC  CCAAATTA
                                ||||||||  ||  ||||||||
                                GAATAGAA  CG  GGTTTAAT
                                    __  TA
GAM354  LOC151201 3'  TAATTTGGAACTGATAATAGGT 86484     T   T    CC
                                ACCT ATT TCAG  CCAAATTA
                                |||| ||| ||||  ||||||||
                                TGGA TAA AGTC  GGTTTAAT
                                  _  T   AA
GAM354  LOC152315 5'  TGGAGCTGACATGATAAGGT   81410        T__    C
                                ACCTTATT   TCAGC CCA
                                ||||||||   ||||| |||
                                TGGAATAG   AGTCG GGT
                                    TAC    A
GAM354  LOC169166 3'  TAATTTGGAAAGCAATAAGG   83606       TTCA  C__
                                CCTTATT    GC   CCAAATTA
                                |||||||    ||   ||||||||
                                GGAATAA    CG   GGTTTAAT
                                   _____  AAA
GAM354  LOC257017 5'  AATTTGGGGCTGTAGAGT    99215      _
                                ATTTT CAGCCCCAAATT
                                ||||| ||||||||||||
                                TGAGA GTCGGGGTTTAA
                                  T
GAM355  ADAR    3'  AAAGAGGTGAACATAAAGG    8479        ATG   AC
                                CCTTTATG   TCAC  CTTT
                                ||||||||   ||||  ||||
                                GGAAATAC   AGTG  GAAA
                                    A__    GA
GAM355  ADAR    3'  AAAGAGGTGAACATAAAGG    32347       ATG   AC
                                CCTTTATG   TCAC  CTTT
                                ||||||||   ||||  ||||
                                GGAAATAC   AGTG  GAAA
                                    A__    GA
GAM355  ADAR    3'  AAAGAGGTGAACATAAAGG    32353       ATG   AC
                                CCTTTATG   TCAC  CTTT
                                ||||||||   ||||  ||||
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                              GGAAATAC  AGTG  GAAA
                                  A__   GA
GAM355  ERBB2IP  3'  TAAAGGTGTTCAAATAAAGGG  38615       GA  TC
                              CCCTTTAT  TG  ACACCTTTA
                              |||||||| ||  |||||||||
                              GGGAAATA  AC  TGTGGAAAT
                                  A_  T_
GAM355  KMO      3'  TGTGACATCACAATGGGT    14851     T  A
                              ACCC TT TGATGTCACA
                              |||| || ||||||||||
                              TGGG AA ACTACAGTGT
                                T  C
GAM355  MTR      3'  TAAAGTAGTAATCATAAAGG  6026         GTC  AC
                              CCTTTATGAT   AC  CTTTA
                              ||||||||||   ||  |||||
                              GGAAATACTA   TG  GAAAT
                                   A__  AT
GAM355  PTBP1    3'  AAAGCGTGTAACAAGGGT    12537     TTATGA  C   _
                              ACCCT     TGT ACAC CTTT
                              |||||     ||| |||| ||||
                              TGGGA     ACA TGTG GAAA
                                _______  A   C
GAM355  PTBP1    3'  AAAGCGTGTAACAAGGGT    50081     TTATGA  C   _
                              ACCCT     TGT ACAC CTTT
                              |||||     ||| |||| ||||
                              TGGGA     ACA TGTG GAAA
                                _______  A   C
GAM355  SLC13A4  5'  AAAGGTGTGGCTTAAAGG    25856      TGAT
                              CCTTTA   GTCACACCTTT
                              ||||||   ||||||||||
                              GGAAAT   CGGTGTGGAAA
                                 T___
GAM355  SLC16A2  3'  AAAGGTGCCATGAAAGGT    22519    C     ATGTCA
                              ACC TTTATG     CACCTTT
                              ||| ||||||     |||||||
                              TGG AAGTAC     GTGGAAA
                                A     C_____
GAM355  ARHGEF3  5'  AGCGGTGACATCCCAAAGGG   39457      AT      AC
                              CCCTTT  GATGTCAC  CT
                              ||||||  ||||||||  ||
                              GGGAAA  CTACAGTG  GA
                                 CC       GC
GAM355  CCR8     3'  AAAGGTGTGGGTGTGAAAGG   19040     ATGATG
                              CCTTT     TCACACCTTT
                              |||||     ||||||||||
                              GGAAA     GGTGTGGAAA
                                GTGTG_
GAM355  DKK2     5'  AAAGTTTGACACATAAAGG   27774        A    CAC
                              CCTTTATG TGTCA   CTTT
                              |||||||| |||||   ||||
```

```
                                GGAAATAC ACAGT   GAAA
                                   _    TT_
GAM355  MGC10848  3'  TAAAGATGCAAGTGCATGAAGG 48306        ATGTCA  C
                                CCTTTATG     CA CTTTA
                                ||||||||     || |||||
                                GGAAGTAC     GT GAAAT
                                    GTGAAC  A
GAM355  STRBP    5'  TAAAGGTGTGTTCCAGAG    37821      AT  TGT
                                CTTT  GA   CACACCTTTA
                                ||||  ||   ||||||||||
                                GAGA  CT   GTGTGGAAAT
                                  C_  T__
GAM355  LOC125476 3'  TAAAGGTGTTTGACAAGAAG   74872      ATGA   __
                                CTTT    TGTC  ACACCTTTA
                                ||||    ||||  |||||||||
                                GAAG    ACAG  TGTGGAAAT
                                  A___    TT
GAM355  LOC221495 3'  AAAGCAGACTCCCTAAAGGGT  95489        T_  T   ACAC
                                ACCCTTTA  GA GTC    CTTT
                                ||||||||  || |||    ||||
                                TGGGAAAT  CT CAG    GAAA
                                    CC  _   AC__
GAM355  LOC254055 3'  TAAAGGTGTAGTATAAAG    98108        ATGTC
                                CTTTATG     ACACCTTTA
                                |||||||     |||||||||
                                GAAATAT     TGTGGAAAT
                                    GA___
GAM356  ELF3     3'  TGACCTTGACCTTGACCAA    16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                  _    AGT  ____
GAM356  JAK2     3'  TGACCTTCATTCTGAGACCAA  18318       CAA       AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_       C_
GAM356  SLC10A2   5'  ACTCTCTGTCTTGACCAA    6590        CAA       A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM356  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM356  KIAA1958  5'  GTGACTTTGAACCCCAAACC   82788      CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
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                                CCAA  CCC   TTTCAGTG
                                  A__  CAAG
GAM356  MARCKS   3'  ACTTTCCACCCTGCCCA    11411    TTCA   A
                                TGG   AGGG TGGAAAGT
                                |||   |||| ||||||||
                                ACC   TCCC ACCTTTCA
                                  CG__  _
GAM356  TUB      5'  GTGGGACCATCCCTTAAACC  13898    C      AAAG
                                GGTT AAGGGATGG   TCAC
                                |||| |||||||||   ||||
                                CCAA TTCCCTACC   GGTG
                                  A       AG__
GAM356  LOC80298 3'  ACTTTTACCTTGAACCA    48062        GATG
                                TGGTTCAAGG   GAAAGT
                                ||||||||||   ||||||
                                ACCAAGTTCC   TTTTCA
                                     A___
GAM357  HRH1     3'  CTCAAACATGTTTAGAGTGGA  7819     A    TGG
                                TCCA TCTGA  GCATGTTTGAG
                                |||| |||||  ||||||||||
                                AGGT AGATT  TGTACAAACTC
                                  G   ___
GAM357  TRIM37   3'  CTCAAATTTGTCATCAG    31625      G  T
                                CTGATGG CA GTTTGAG
                                ||||||| || |||||||
                                GACTACT GT TAAACTC
                                    _ T
GAM357  HTMP10   3'  CTCAAAAAAGCCATCAGATCTG 53758   CA      G ATG
           A                     TC  ATCTGATGG C   TTTGAG
                                ||  |||||||||  |   ||||||
                                AG  TAGACTACC G   AAACTC
                                 TC       _ AAA
GAM357  PAK2     5'  CTCAAATATCACCAAACTAGA  67140    A__  GC
                                TCTG   TGG  ATGTTTGAG
                                ||||   |||  |||||||||
                                AGAT   ACC  TATAAACTC
                                  CAA   AC
GAM357  SEMA6A   3'  CTCGAGTACCCACCAGA    40818    A   CA
                                TCTG TGGG  TGTTTGAG
                                |||| ||||  ||||||||
                                AGAC ACCC  ATGAGCTC
                                  C   __
GAM357  TTY7     3'  TCAAACATGCAGGCTGGA    50019    AT  GATGG
                                TCCA  CT    GCATGTTTGA
                                ||||  ||    ||||||||||
                                AGGT  GA    CGTACAAACT
                                  CG  _____
GAM357  LOC144766 3'  CTCAAACATGAGAAGACTGGG  77481    A   GATGGG
                                TCCA TCT     CATGTTTGAG
                                |||| |||     ||||||||||
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                                GGGT AGA     GTACAAACTC
                                  C   AGA___
GAM357  LOC201685 5'  TAAACACCCATCAGATGGA   91845     A       CA
                                TCCA TCTGATGGG  TGTTTG
                                |||| |||||||||  ||||||
                                AGGT AGACTACCC  ACAAAT
                                  _       __
GAM357  LOC221596 5'  CTCAAACAAAACTCAGATT   93623       TG GCA
                                AATCTGA  G   TGTTTGAG
                                |||||||  |  ||||||||
                                TTAGACT  C   ACAAACTC
                                   __ AAA
GAM357  LOC93622  3'  CTCTGCAGACCATCAGAT    57729        GCA   TT
                                ATCTGATGG   TGT  GAG
                                |||||||||   |||  |||
                                TAGACTACC   ACG  CTC
                                     AG_   T_
GAM358  CTNS      5'  CCGGGGGACTGAGCAGCACGAG 18217     ATC        ACAG
            A                    TCTC   GCTGCTCAGT   CGG
                                ||||   ||||||||||   |||
                                AGAG   CGACGAGTCA   GCC
                                  CA_        GGGG
GAM358  ELSPBP1   3'  CCGCCATACTGAGGCTGAG   42424     TC  TG      CA
                                CTCA  GC  CTCAGTA  GCGG
                                ||||  ||  |||||||  ||||
                                GAGT  CG  GAGTCAT  CGCC
                                  __  __      AC
GAM358  SIMRP7    3'  CCGCACTGAGTACCTGGAGA   93969     ATCGC      ACA
                                TCTC    TGCTCAGT   GCGG
                                ||||    ||||||||  ||||
                                AGAG    ATGAGTCA   CGCC
                                  GTCC_      ___
GAM358  LOC200933 5'  CCGCTGCCTGCACGGCGATGAG 91791          CT   TA
            A                    TCTCATCGCTG  CAG  CAGCGG
                                ||||||||||  |||  ||||||
                                AGAGTAGCGGC  GTC  GTCGCC
                                     AC   C_
GAM359  APM1      3'  GTGAATGTCTAAGGTCA     17790      CCA   CTT
                                TGACC   TGG   ATATTCAC
                                |||||   |||   ||||||||
                                ACTGG   ATC   TGTAAGTG
                                  A__   ___
GAM359  EDNRA     3'  AATATAAGCCATAGGTTCA    64797     C  C
                                TGA CC ATGGCTTATATT
                                ||| || ||||||||||||
                                ACT GG TACCGAATATAA
                                  T  A
GAM359  MSN       3'  AATGTAGCCATGGGACCA    60879    AC       T
                                TG  CCCATGGCT ATATT
                                ||  ||||||||| |||||
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                                AC  GGGTACCGA TGTAA
                                 CA       _
GAM359  C20orf21  3'  ATAAGAAACCATGAGTCAT   35568      CC    ___
                                ATGAC  CATGG   CTTAT
                                |||||  |||||   |||||
                                TACTG  GTACC   GAATA
                                  A_    AAA
GAM359  DKFZP586M1120 3'  AGTGAATGTGTCCGTGAGGCCA 49275     A  C    CT
          T                      ATG CC CATGG  TATATTCACT
                                 ||| || |||||  ||||||||||
                                 TAC GG GTGCC  GTGTAAGTGA
                                   C  A    T_
GAM359  MRPS27    3'  AGTGAACTCAAGGCCATGAACT 31321     CCC       ATA_
          CA                     TGA   CATGGCTT    TTCACT
                                 |||   ||||||||    ||||||
                                 ACT   GTACCGGA    AAGTGA
                                   CAA       ACTC
GAM359  SCYB5     3'  AGTGTGAGCCAGGAATCA    12983     CC  A
                                 TGA  CC TGGCTTATATT
                                 |||  || ||||||||||
                                 ACT  GG ACCGAGTGTGA
                                   AA  _
GAM359  SPRY4     3'  TGGCTGGAGCCTGAAGTCAT   49037      CC  T    ATAT
                                 ATGAC  CA GGCTT    TCA
                                 |||||  || |||||    |||
                                 TACTG  GT CCGAG    GGT
                                    AA  _    GTC_
GAM359  LOC144481 3'  AGTGTTAAGCCATGGATTCA   84011     CC        TATT
                                 TGA  CCATGGCTTA    CACT
                                 |||  ||||||||||    ||||
                                 ACT  GGTACCGAAT    GTGA
                                   TA        T___
GAM359  LOC148938 5'  AGTGAATAAGTCTAACAGGATC 85429    C  CAT__      AT
                                 GA CC    GGCTTAT  TCACT
                                 || ||    |||||||  |||||
                                 CT GG    CTGAATA  AGTGA
                                  A  ACAAT      __
GAM359  LOC202934 3'  AGTGAATACGTCTCACAAGGTC 92026      CCAT__   TTA
                                 GACC     GGC   TATTCACT
                                 ||||     |||   ||||||||
                                 CTGG     CTG   ATAAGTGA
                                    AACACT   C__
GAM359  LOC254045 3'  AGTGTTAAGCCATGGATTCA   98261     CC        TATT
                                 TGA  CCATGGCTTA    CACT
                                 |||  ||||||||||    ||||
                                 ACT  GGTACCGAAT    GTGA
                                   TA        T___
GAM359  LOC255465 3'  AGTGAATACGTCTCACAAGGTC 99102      CCAT__   TTA
                                 GACC     GGC   TATTCACT
                                 ||||     |||   ||||||||
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                                CTGG     CTG   ATAAGTGA
                                  AACACT   C__
GAM360  ERBB2IP  5'  CCCTGAGACGGTGTCCCGC   38613    ATCTT
                                GC     TACCGTCTCAGGG
                                ||     |||||||||||||
                                CG     GTGGCAGAGTCCC
                                 CCCT_
GAM360  FRAP1    3'  CCTAGACTGTAAAGACACAG  18270    CA      C    C
                                CTG  TCTTTAC GTCT AGG
                                |||  ||||||| |||| |||
                                GAC  AGAAATG CAGA TCC
                                  AC      T    _
GAM360  JUN      5'  CCACGGCGGTAAAGACCAG   11100    CA         TCA
                                CTG  TCTTTACCGTC   GG
                                |||  ||||||||||   ||
                                GAC  AGAAATGGCGG   CC
                                  C_         CA_
GAM360  MRPL49   3'  CCCTGAGACAGGGGATACAG  70164    C    TTA  _
                                CTG ATCT   CC GTCTCAGGG
                                ||| ||||   || |||||||||
                                GAC TAGG   GG CAGAGTCCC
                                  A    ___  A
GAM360  OCA2     3'  CCCAAGGACAAAATGTAG    60825      C   ACC    CA
                                CTGCAT TTT   GTCT  GGG
                                ||||||| |||   ||||  |||
                                GATGTA AAA   CAGG  CCC
                                   _   ___    AA
GAM360  PDAP1    3'  AGACAGAAAGATGCAGGA    94056          ACC
                                TCCTGCATCTTT   GTCT
                                ||||||||||||   ||||
                                AGGACGTAGAAA   CAGA
                                       GA_
GAM360  ATP10B   3'  CCTCAGCAAAGATGCCAG    64105    _      ACC T  C
                                CTG CATCTTT   G CT AGG
                                ||| |||||||   | || |||
                                GAC GTAGAAA   C GA TCC
                                  C      ___ _  C
GAM360  CGRP-RCP 3'  CCCTGAGACAGCAGCCCAGGG  27887      CAT  TTACC
                                TCCTG   CT    GTCTCAGGG
                                |||||   ||    |||||||||
                                GGGAC   GA    CAGAGTCCC
                                   CC_  CGA__
GAM360  CST8     5'  CCTGAGACGACGAGGAGGA   19711    TGCA    AC
                                TCC    TCTTT  CGTCTCAGG
                                |||    |||||  |||||||||
                                AGG    AGGAG  GCAGAGTCC
                                  _____     CA
GAM360  FLJ13782 3'  CCTGAGATGCAGAGCAGGA   46701       A   TTAC
                                TCCTGC TCT    CGTCTCAGG
                                |||||| |||    |||||||||
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                                AGGACG AGA   GTAGAGTCC
                                   _  C___
GAM360  FLJ21324  5'  CCCTGAAGCGAAAAGATGCAGG 92852          AC  TC
                                CCTGCATCTTT  CG  TCAGGG
                                ||||||||||  ||  ||||||
                                GGACGTAGAAA  GC  AGTCCC
                                      A_  GA
GAM360  MGC16025  5'  CCCCACAATGAGTGAAAATGCA 53021        C   _  CTCA
          GGA                     TCCTGCAT TTTAC CGT   GGG
                                ||||||||| ||||| |||   |||
                                AGGACGTA AAGTG GTA   CCC
                                     A    A  ACAC
GAM360  REPRIMO  3'  CCCTGGGACAAAGACCCAG   39530    CA   ACC
                                CTG  TCTTT   GTCTCAGGG
                                |||  |||||   |||||||||
                                GAC  AGAAA   CAGGGTCCC
                                  CC    ___
GAM360  SEC63L   3'  CCCAGTAAAAGTAAAGATGCAG 24262           CGTCTCA
          GA                      TCCTGCATCTTTAC      GGG
                                ||||||||||||||      |||
                                AGGACGTAGAAATG      CCC
                                       AAAATGA
GAM360  LOC162137 3'  CCCTGGGGTGCAAAGAGCGCA  88477    A_    AC GT
                                TGC  TCTTT  C  CTCAGGG
                                |||  |||||  |  |||||||
                                ACG  AGAAA  G  GGGTCCC
                                  CG    C_ TG
GAM360  LOC219654 3'  CCCTGAGACAAGCCACAG    92928    CAT   TACC
                                CTG   CTT   GTCTCAGGG
                                |||   |||   |||||||||
                                GAC   GAA   CAGAGTCCC
                                  ACC   ____
GAM360  LOC255811 5'  CCAGGCAGTAAAGATCCAG   96307    C      C   CA
                                CTG ATCTTTAC GTCT  GG
                                ||| |||||||| ||||  ||
                                GAC TAGAAATG CGGA  CC
                                  C       A   __
GAM361  BBS4     3'  ATTTGCCCAAAGGGAATCCAGA 53447         G_ G_   A
          ACA                     TGTTCTGGA  CT  TTGG CAAAT
                                |||||||||  ||  |||| |||||
                                ACAAGACCT  GG  AACC GTTTA
                                      AA  GA   C
GAM361  CENTD2   3'  CCAACAAACTCCAGAACA    31539         C_
                                TGTTCTGGAG  TGTTGG
                                ||||||||||  ||||||
                                ACAAGACCTC  ACAACC
                                      AA
GAM361  HAMP     3'  TCCTGCTGCCCCAGAACA    41289         A  T  T
                                TGTTCTGG GC GT GGA
                                ||||||||| || || |||
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                                ACAAGACC CG CG CCT
                                    C  T  T
GAM361  ITGA11   3'  TCTGCCGGCCCCCAGGACA   25213        A_   TT
                                TGTTCTGG  GCTG  GGA
                                ||||||||  ||||  |||
                                ACAGGACC  CGGC  TCT
                                    CC    CG
GAM361  KITLG    3'  ATTTGCATGGCTCCAGAA    8023          TGGA
                                TTCTGGAGCTGT   CAAAT
                                ||||||||||||   |||||
                                AAGACCTCGGTA   GTTTA
                                      C___
GAM361  MAPK4    5'  CCTGGGCAGCTCCAGATCA   12300    T        __
                                TG TCTGGAGCTGTT  GG
                                || ||||||||||||  ||
                                AC AGACCTCGACGG  CC
                                 T         GT
GAM361  MGAT2    3'  ATTTGTCCAAACAGGACA    11557       GAGCTG
                                TGTTCTG     TTGGACAAAT
                                |||||||     ||||||||||
                                ACAGGAC     AACCTGTTTA
                                    A_____
GAM361  PSPHL    5'  TTGTCATACAGCTCCAAACA   94499     C       TG
                                TGTT TGGAGCTGT  GACAA
                                |||| |||||||||  |||||
                                ACAA ACCTCGACA  CTGTT
                                  _       TA
GAM361  TTC3     3'  TATTTGTCCAACAACTGTCAGA 13885        _ C
           ATA                    TGTTCTGG AG TGTTGGACAAATA
                                |||||||| || ||||||||||||
                                ATAAGACT TC ACAACCTGTTTAT
                                    G  A
GAM361  FLJ14213 3'  TGATAACAGCTCCAGAA     46218          GA
                                TTCTGGAGCTGTTG  CA
                                ||||||||||||||  ||
                                AAGACCTCGACAAT  GT
                                      A_
GAM361  H2BFQ    3'  TTTAAGAGAACTCCAGGACA   60079         __ G
                                TGTTCTGGAG  CT TTGGA
                                ||||||||||  || |||||
                                ACAGGACCTC  GA AATTT
                                     AA  G
GAM361  LRG      3'  TCCATCCATGCTTCCTAGAACA 54825       _  _ _ T_
                                TGTTCT GGA GC TG  TGGA
                                ||||||  ||| || ||  ||||
                                ACAAGA CCT CG AC  ACCT
                                   T  T  T  CT
GAM361  NMT2     3'  ATTTGTCCATGTAACAGAACA  17852       GA  TGT
                                TGTTCTG  GC   TGGACAAAT
                                |||||||  ||   |||||||||
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                                ACAAGAC  TG   ACCTGTTTA
                                    AA  T__
GAM361  NYD-SP21  3'  TATTTGTCCAATCTAGATTCAG 51863         G  __
          AACA                    TGTTCTGGA CT  GTTGGACAAATA
                                |||||||||  ||  ||||||||||||
                                ACAAGACTT GA  TAACCTGTTTAT
                                    A  TC
GAM361  PSPH     3'  TTGTCGTACAGCTCCAAACA   17143      C        TG
                                TGTT TGGAGCTGT  GACAA
                                ||||  |||||||||  |||||
                                ACAA ACCTCGACA  CTGTT
                                  _       TG
GAM361  LOC122258 3'  CCACCAGCCTCCGGAACA    59820          _  T
                                TGTTCTGGAG CTG TGG
                                ||||||||||  |||  |||
                                ACAAGGCCTC GAC ACC
                                    C   C
GAM361  LOC151826 3'  ATTTGTCCAACCTAGCACA   81176     T    AGCT
                                TGT CTGG    GTTGGACAAAT
                                |||  ||||    ||||||||||||
                                ACA GATC    CAACCTGTTTA
                                  C   ____
GAM361  LOC169611 3'  TCCAGTGGCAGCTCCAGAA   83663           ___
                                TTCTGGAGCTGT   TGGA
                                ||||||||||||   ||||
                                AAGACCTCGACG   ACCT
                                    GTG
GAM361  LOC196746 3'  TCAGAGCAGCTCCAAGACA   88903     TC        G_
                                TGT  TGGAGCTGTT  GA
                                |||  ||||||||||  ||
                                ACA  ACCTCGACGA  CT
                                  GA        GA
GAM361  LOC204119 5'  TGCCACAACTCAGAACA     92343        G  C   T  A
                                TGTTCTG AG TGT GG CA
                                |||||||  ||  |||  ||  ||
                                ACAAGAC TC ACA CC GT
                                    _  A   _  _
GAM361  LOC253142 5'  TTGCTAGGATGCCCCAGAATA  99230         A  TG_   A
                                TGTTCTGG GC   TTGG CAA
                                ||||||||  ||   ||||  |||
                                ATAAGACC CG   GATC GTT
                                    C  TAG   _
GAM362  CDH12    3'  CTTATCATTTAAAGTGGTGTA  15777          CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                    AA___   AC
GAM362  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007       CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  ||||||||||  |||
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                                ATGTG  GAGGGTTCTT TTA
                                  AC        G
GAM362  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090      T   AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                  _   GTCA_
GAM362  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
          A                      TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                  TACTCCC_
GAM362  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126        CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                    AGACG___
GAM362  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
          TA                     TACA   TCC   GAAGAATAAG
                                ||||   |||   ||||||||||
                                ATGT   AGG   TTTCTTATTC
                                  AAA_  ATTG
GAM362  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68742            _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                        G
GAM362  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM362  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748     CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM362  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM362  OSBPL11   3'  CTTAATTTCCCAAGAGTGGTG  43206        CCAA   AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                    AACC   A_
GAM362  YME1L1    3'  TCATTCTTGATGTGGTGTA   58438        TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
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                                ATGTGGTG  GTTCTT CT
                                    TA_    A
GAM362  ZNF262   3' CTTATTTTGTTTGGGAGT   18723       A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                   G
GAM362  LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_   AAGA
                                TACACCAC  CCAAG   ATA
                                ||||||||  |||||   |||
                                ATGTGGTG  GGTTC   TGT
                                    CAA   GG__
GAM363  ELF3     3' TGACCTTGACCTTGACCAA   16685     T   GAT  AAA
                                TTGGT CAAGG  GG  GTCA
                                ||||| |||||  ||  ||||
                                AACCA GTTCC  TC  CAGT
                                  _   AGT  ___
GAM363  JAK2     3' TGACCTTCATTCTGAGACCAA 18318     CAA     AA
                                TTGGTT  GGGATGGA GTCA
                                ||||||  |||||||| ||||
                                AACCAG  TCTTACTT CAGT
                                   AG_     C_
GAM363  SLC10A2  5' ACTCTCTGTCTTGACCAA   6590      CAA     A
                                TTGGTT  GGGATGGA AGT
                                ||||||  |||||||| |||
                                AACCAG  TTCTGTCT TCA
                                   ___      C
GAM363  FLJ10803 3' GTGACTTTCAGTTAAAGCCAA 37205     CAAGG  G
                                TTGGTT   GAT GAAAGTCAC
                                ||||||   ||| |||||||||
                                AACCGA   TTG CTTTCAGTG
                                   AA___  A
GAM363  KIAA1958 5' GTGACTTTGAACCCCAAACC  82788    CAA  ATGG
                                GGTT  GGG   AAAGTCAC
                                ||||  |||   ||||||||
                                CCAA  CCC   TTTCAGTG
                                  A__  CAAG
GAM363  MARCKS   3' ACTTTCCACCCTGCCCA    11411    TTCA  A
                                TGG   AGGG TGGAAAGT
                                |||   |||| ||||||||
                                ACC   TCCC ACCTTTCA
                                  CG__  _
GAM363  TUB      5' GTGGGACCATCCCTTAAACC  13898    C      AAAG
                                GGTT AAGGGATGG   TCAC
                                |||| |||||||||   ||||
                                CCAA TTCCCTACC   GGTG
                                  A       AG__
GAM363  LOC80298 3' ACTTTTACCTTGAACCA    48062        GATG
                                TGGTTCAAGG   GAAAGT
                                ||||||||||   ||||||
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                                ACCAAGTTCC    TTTTCA
                                     A___
GAM364  ELF3     3'  TGACCTTGACCTTGACCAA   16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                   _    AGT  ___
GAM364  JAK2     3'  TGACCTTCATTCTGAGACCAA  18318      CAA      AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_      C_
GAM364  SLC10A2  5'  ACTCTCTGTCTTGACCAA    6590       CAA      A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM364  FLJ10803 3'  GTGACTTTCAGTTAAAGCCAA  37205      CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM364  KIAA1958 5'  GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM364  MARCKS   3'  ACTTTCCACCCTGCCCA     11411     TTCA   A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                 CG__    _
GAM364  TUB      5'  GTGGGACCATCCCTTAAACC   13898     C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A       AG__
GAM364  LOC80298 3'  ACTTTTACCTTGAACCA     48062         GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                     A___
GAM365  AP3B2    5'  CCCGCGCCGCAACCTCCTCCT  17362    A  C  A  _
                                AG AG AG TT CGGCGCGGG
                                || || || || |||||||||
                                TC TC TC AA GCCGCGCCC
                                 C  C  C  C
GAM365  BCR      5'  CCGCGCGCCGAGCGCCCCGCT  16327     AGAA  AGA       _
                                AGC    GC   TTCGGCGCG GG
                                |||    ||   ||||||||| ||
```

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                                TCG   CG  GAGCCGCGC CC
                                  CCC_ C__       G
GAM365  BCR     5' CCGCGCGCCGAGCGCCCCGCT 41483    AGAA  AGA      _
                                AGC   GC  TTCGGCGCG GG
                                |||   ||  ||||||||| ||
                                TCG   CG  GAGCCGCGC CC
                                  CCC_ C__       G
GAM365  CENPB    3' CTGAGCCTGCTTCTGC     70113        GATTC  G
                                GCAGAAGCA    GGC CGG
                                |||||||||    ||| |||
                                CGTCTTCGT    CCG GTC
                                     _____  A
GAM365  EGLN3    5' CCCGCGCCTCGGCTTCGCGCT 42210    A_    A  TTC
                                AGC  GAAGC GA   GGCGCGGG
                                |||  ||||| ||   ||||||||
                                TCG  CTTCG CT   CCGCGCCC
                                  CG    G  ___
GAM365  EGLN3    5' CCCGCGCCTCGGCTTCGCGCT 54048    A_    A  TTC
                                AGC  GAAGC GA   GGCGCGGG
                                |||  ||||| ||   ||||||||
                                TCG  CTTCG CT   CCGCGCCC
                                  CG    G  ___
GAM365  FGF8     5' CCCGCACCCTCTCCGCTCGC  53711    A  A  A  TTC  C
                                GC GA GC GA   GG GCGGG
                                || || || ||   || |||||
                                CG CT CG CT   CC CGCCC
                                 _ _  C  CTC  A
GAM365  FGF8     5' CCCGCACCCTCTCCGCTCGC  53713    A  A  A  TTC  C
                                GC GA GC GA   GG GCGGG
                                || || || ||   || |||||
                                CG CT CG CT   CC CGCCC
                                 _ _  C  CTC  A
GAM365  FGF8     5' CCCGCACCCTCTCCGCTCGC  53715    A  A  A  TTC  C
                                GC GA GC GA   GG GCGGG
                                || || || ||   || |||||
                                CG CT CG CT   CC CGCCC
                                 _ _  C  CTC  A
GAM365  FGF8     5' CCCGCACCCTCTCCGCTCGC  21496    A  A  A  TTC  C
                                GC GA GC GA   GG GCGGG
                                || || || ||   || |||||
                                CG CT CG CT   CC CGCCC
                                 _ _  C  CTC  A
GAM365  FHIT     5' CCCGCGCTCCCTCCCTCTGC  10639      AGCA  TTC
                                GCAGA   GA   GGCGCGGG
                                |||||   ||   ||||||||
                                CGTCT   CT   TCGCGCCC
                                  CC__  CCC
GAM365  GAL      5' CCCGCGCCTTCTGCCCCTGCT 93146      AA    TTC
                                AGCAG  GCAGA   GGCGCGGG
                                |||||  |||||   ||||||||
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                                TCGTC  CGTCT   CCGCGCCC
                                  CC    T__
GAM365  GRM6     5'  CCCGCGCTCTCCTTCCCCCGC  7763     A___   C  TTCG
                                GC   GAAG AGA   GCGCGGG
                                ||   |||| |||   |||||||
                                CG   CTTC TCT   CGCGCCC
                                 CCCC   C  ____
GAM365  GTF2IRD1 5'  CCCGCGCTCCCGCTCTCCGCT  33347     A  _  AGATTC
                                AGC GA AGC     GGCGCGGG
                                ||| || |||     ||||||||
                                TCG CT TCG     TCGCGCCC
                                 C  C   CCC___
GAM365  HHIP     5'  CCCGCGCCCAGCCCCTGCT   42751      AA  AGATTC
                                AGCAG  GC     GGCGCGGG
                                |||||  ||     ||||||||
                                TCGTC  CG     CCGCGCCC
                                  CC  AC____
GAM365  ITPR2    5'  CCCGCGATCCGATCCGCTTCTG 11079        A   T  __
              C                  GCAGAAGC GAT CGG  CGCGGG
                                 |||||||| ||| |||  ||||||
                                 CGTCTTCG CTA GCC  GCGCCC
                                     C   _   TA
GAM365  KCNQ2    5'  CCCGCGCCGCCCCCCGCGCTCC 62046    A  A_  AGATT_
              GC                   GC GA  GC     CGGCGCGGG
                                   || ||  ||     |||||||||
                                   CG CT  CG     GCCGCGCCC
                                    C  CG  CCCCCC
GAM365  LBX1     5'  CCCGCGCCGGCCCGCGCCCTGC 22666     AA_  AGAT
                                GCAG   GC   TCGGCGCGGG
                                ||||   ||   ||||||||||
                                CGTC   CG   GGCCGCGCCC
                                  CCG  CCC_
GAM365  LEF1     5'  CCCGCGCTCGCCCGCCCCGCTT 33223      AGAA  AGATT  _
                                AAGC   GC    CG GCGCGGG
                                ||||   ||    || |||||||
                                TTCG   CG    GC CGCGCCC
                                  CCC_  CCC__  T
GAM365  MUC5B    3'  CCCGCGCTCCGTGCTCCTGCT  67397      A   GATTC
                                AGCAG AGCA    GGCGCGGG
                                ||||| ||||    ||||||||
                                TCGTC TCGT    TCGCGCCC
                                  C   GCC__
GAM365  NPDC1    5'  CCCGCGCCGAGCCCCTG    31812     AA  AGAT
                                CAG  GC   TCGGCGCGGG
                                |||  ||   ||||||||||
                                GTC  CG   AGCCGCGCCC
                                  CC  _____
GAM365  NT5M     5'  CCCGCACCCTGCGCTCCCCGC  39891    A__  A_   ATTC  C
                                GC   GA  GCAG   GG GCGGG
                                ||   ||  ||||   || |||||
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                                CG  CT  CGTC   CC CGCCC
                                 CCC  CG   ____  A
GAM365  PTK7    5'  CCCGCGCTCCGGTGCGCTCCGC 12548   A  A_  GATTC
                                GC GA  GCA    GGCGCGGG
                                || ||  |||    ||||||||
                                CG CT  CGT    TCGCGCCC
                                 C  CG   GGCC_
GAM365  RAB3B   3'  CCCACACCCAGTCTGCTTCT   12701         C  CGC
                                AGAAGCAGATT GG   GGG
                                |||||||||| ||   |||
                                TCTTCGTCTGA CC   CCC
                                      C  ACA
GAM365  SCAP1   5'  CCCGCGCCCCGTCCCGCCTCTC 14945   C   A  A_  TC
           T                     AG AGA GC  GAT  GGCGCGGG
                                || ||| ||  |||  ||||||||
                                TC TCT CG  CTG  CCGCGCCC
                                 _   C  CC   CC
GAM365  SERPINE1  3'  CCCGCGCCCCCCCGCGCCCCTCT 7010     C  AA  AGATTC
           T                     AAG AG  GC     GGCGCGGG
                                ||| ||  ||     ||||||||
                                TTC TC  CG     CCGCGCCC
                                 _  CC  CGCCCC
GAM365  SLBP    5'  CCCGCGCCGCCGCCGCCTCAGC 22553   A  A  AGATT
                                GC GA GC    CGGCGCGGG
                                || || ||    |||||||||
                                CG CT CG    GCCGCGCCC
                                 A  C  CCGCC
GAM365  SLC16A1   3'  CCCATTTATATCTGCTTCTAGC 13203    _       TCGGCGC
           T                     AGC AGAAGCAGAT      GGG
                                ||| ||||||||||      |||
                                TCG TCTTCGTCTA      CCC
                                 A        TATTTA_
GAM365  SLC1A4   5'  CCCGCACTCTGCGCCTCT    13170   C  AA    TTCG C
                                AG AG  GCAGA   G GCGGG
                                || ||  |||||   | |||||
                                TC TC  CGTCT   C CGCCC
                                 _  CG    ____ A
GAM365  SRGAP2   3'  CCCACTGCCCTCTGCTTC    75107       TTC   C_
                                GAAGCAGA   GGCG  GGG
                                ||||||||   ||||  |||
                                CTTCGTCT   CCGT  CCC
                                     C__    CA
GAM365  SYK     5'  CCCGCGCTGCGCCCGCCCTCGC 13497   A  A_  AGATT
                                GC GA  GC    CGGCGCGGG
                                || ||  ||    |||||||||
                                CG CT  CG    GTCGCGCCC
                                 _  CC  CCCGC
GAM365  TG737   5'  CCCGCGCCCGCGCTTCCGGC   22555   A_    AGATTC
                                GC  GAAGC     GGCGCGGG
                                ||  |||||     ||||||||
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                                CG  CTTCG     CCGCGCCC
                                 GC    CGC___
GAM365  TNFAIP1  3'  CCCGACGGAGCTGCTTCTGCT  41228          A   GCG
                                AGCAGAAGCAG TTCG   CGGG
                                |||||||||||  ||||   ||||
                                TCGTCTTCGTC AGGC   GCCC
                                      G   A__
GAM365  TNS      3'  CCCTGGGGAACCTACTTTCTGC 42948      _  C  A   GG  C
          T                     AGCAG AAG AG TTC  CG GGG
                                |||||  ||| ||  |||  ||  |||
                                TCGTC TTC TC AAG  GT CCC
                                  T   A  C   GG  _
GAM365  BRAP     5'  CCCGCGCCGGCCAGCGCCTGC  23176     AA  AGAT
                                GCAG  GC   TCGGCGCGGG
                                ||||  ||   ||||||||||
                                CGTC  CG   GGCCGCGCCC
                                  CG  ACC_
GAM365  BSMAP    5'  CCCGCGCCCCCCGCGTTCCGC  25043    A   _  AGATTC
                                GC GAA GC     GGCGCGGG
                                || ||| ||     ||||||||
                                CG CTT CG     CCGCGCCC
                                 C   G  CCCC__
GAM365  CASKIN1  3'  CCACGGACGCTTCTGCT     40782         AGA   GCGC
                                AGCAGAAGC   TTCG   GG
                                |||||||||   ||||   ||
                                TCGTCTTCG   AGGC   CC
                                     C__    A___
GAM365  DOC2A    3'  CCCGCGCTCCTCACTCCTGC   14561     A  CA  TTC
                                GCAG AG  GA   GGCGCGGG
                                ||||  ||  ||   ||||||||
                                CGTC TC  CT   TCGCGCCC
                                  C  A_  CC_
GAM365  DSCR6    5'  CCCGCGCCGCCCCGCCCCCGTT 39062     AGAA  AGATT
          T                     AAGC    GC    CGGCGCGGG
                                ||||    ||    |||||||||
                                TTTG    CG    GCCGCGCCC
                                  CCCC  CCCC_
GAM365  FBXO32   5'  CCCGCGCCGTTCCCGCCGC    55242    AGAA  A_  TT
                                GC    GC  GA  CGGCGCGGG
                                ||    ||  ||  |||||||||
                                CG    CG  CT  GCCGCGCCC
                                 C___  CC  T_
GAM365  FLJ00001 3'  CCCACAGCACTTCCCACTACTG 82711       A  CA_  TTCG  GC_
          CTT                     AAGCAG AG   GA   GC   GGG
                                ||||||  ||   ||   ||   |||
                                TTCGTC TC   CT   CG   CCC
                                   A  ACC  TCA_  ACA
GAM365  FLJ10901 3'  CCCACCAGCTATGCTTCTGCT  37356          GATTC  CGC
                                AGCAGAAGCA    GG   GGG
                                ||||||||||    ||   |||
```

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                                TCGTCTTCGT    CC   CCC
                                     ATCGA  A__
GAM365  FLJ22938  3'  CCCAAGGCTAAACCTGCCTGTG 45481     GAA   A  CG  GC_
          CT                   AGCA   GCAG TT  GC   GGG
                               ||||   |||| ||  ||   |||
                               TCGT   CGTC AA  CG   CCC
                                 GTC    C  AT  GAA
GAM365  FLJ32430  3'  CCCACACAGAATACTCTGCCTC 58970       A   ___  GGCGC
          TGCTT                 AAGCAGA GCAGA   TTC    GGG
                               |||||||  |||||   |||    |||
                               TTCGTCT CGTCT   AAG    CCC
                                  C    CAT   ACACA
GAM365  GIOT-3   5'  CCCAGGAGGATCTGCCTCCGCT 33219     A  A      GGCGC
          T                    AAGC GA GCAGATTC    GGG
                               ||||  ||  ||||||||    |||
                               TTCG CT CGTCTAGG    CCC
                                 C  C       AGGA_
GAM365  GMPPB    3'  CCCAACCTGCCTTCTGCT    97441       _  A  C
                               AGCAGAAG CAG TT GG
                               ||||||||  ||| || ||
                               TCGTCTTC GTC AA CC
                                    C   C  C
GAM365  GPR74    5'  CCCACCTCTTCTCTTCTGCTT  54895       C   TTC  CGC
                               AAGCAGAAG AGA   GG   GGG
                               |||||||||  |||   ||   |||
                               TTCGTCTTC TCT   CC   CCC
                                     _   TCT  A__
GAM365  HU-K4    3'  CCCGCACCCCCGCTTCTGT   25359       AGATTC  C
                               GCAGAAGC     GG GCGGG
                               ||||||||     || |||||
                               TGTCTTCG     CC CGCCC
                                    CCC___  A
GAM365  IL-17RE  3'  CCCGCGCCCGCTGCTGCTGCT  58937      A    ATTC
                               AGCAG AGCAG   GGCGCGGG
                               |||||  |||||   ||||||||
                               TCGTC TCGTC   CCGCGCCC
                                  G    GC__
GAM365  IL-17RE  3'  CCCGCGCCGCGCCCCTGCT   58938      AA  AGATT
                               AGCAG  GC    CGGCGCGGG
                               |||||  ||    |||||||||
                               TCGTC  CG    GCCGCGCCC
                                  CC  C____
GAM365  IMAGE:4907098 5'  CCCGCACGCGCGCTTTCTGCT  93324       _  AGATT  GC
                               AGCAGAA GC    CG  GCGGG
                               |||||||  ||    ||  |||||
                               TCGTCTT CG    GC  CGCCC
                                   T  CGC__  A_
GAM365  KIAA0240  3'  CCAGAATCTGCTTCTGGCT   94036     _         _
                               AGC AGAAGCAGATTC GG
                               |||  ||||||||||| ||
```

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                                TCG TCTTCGTCTAAG CC
                                  G         A
GAM365  KIAA0676  3'  CCCACATGGGGCTGCTCTTGCT 31143     GA    A   GCGC
            T                    AAGCA  AGCAG TTCG   GGG
                                 |||||  ||||| ||||   |||
                                 TTCGT  TCGTC GGGT   CCC
                                   TC    G   ACA_
GAM365  KIAA1145  3'  CCCGTGTGATCCACCCTGCTT  66235     AAGCA   CG
                                 AAGCAG    GATT  GCGCGGG
                                 ||||||    ||||  |||||||
                                 TTCGTC    CTAG  TGTGCCC
                                   CCAC_   __
GAM365  KIAA1737  5'  CCAATGAATCTGCCTCCAGCT  67937    A_ A      GCGC
                                 AGC  GA GCAGATTCG   GG
                                 |||  || |||||||||   ||
                                 TCG  CT CGTCTAAGT   CC
                                   AC  C       AA__
GAM365  MGC2749  3'  CCCGCACCCACTAATTCTGCTT 44168       GC  ATTC  C
                                 AAGCAGAA  AG   GG GCGGG
                                 ||||||||  ||   || |||||
                                 TTCGTCTT  TC   CC CGCCC
                                     AA  AC__  A
GAM365  MOT8    3'  CCCGCACCTACCACTTCTGTTT 38729        CAGATTC  C
                                 AAGCAGAAG      GG GCGGG
                                 |||||||||      || |||||
                                 TTTGTCTTC      CC CGCCC
                                      ACCAT__  A
GAM365  NECL1   3'  CTGAACTGCCTCTGCTT    41326       A   A
                                 AAGCAGA GCAG TTCGG
                                 |||||||  |||| |||||
                                 TTCGTCT CGTC AAGTC
                                     C   _
GAM365  NPTXR   3'  CCGCGCCCAGATCCTGCTT   27431      AT  __
                                 AAGCAG  TC  GGCGCGG
                                 ||||||  ||  |||||||
                                 TTCGTC  AG  CCGCGCC
                                    CT  AC
GAM365  NPTXR   3'  CCGCGCCCAGATCCTGCTT   55208      AT  __
                                 AAGCAG  TC  GGCGCGG
                                 ||||||  ||  |||||||
                                 TTCGTC  AG  CCGCGCC
                                    CT  AC
GAM365  ORCTL3  3'  CCCGCCTCCTCCTGCTCATGCT 16191     GA    ATTC  C
                                 AGCA  AGCAG   GG GCGGG
                                 ||||  |||||   || |||||
                                 TCGT  TCGTC   TC CGCCC
                                   AC    CTCC  _
GAM365  PDE4DIP  5'  CCCGCGCCAGTAGTGCTTTCTG 28405       _  G_  C
            CT                    AGCAGAA GCA  ATT GGCGCGGG
                                 |||||||  |||  ||| ||||||||
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                                TCGTCTT CGT  TGA CCGCGCCC
                                    T  GA  _
GAM365  PPIL3    5'  CCGCGCCCAACTTCCGCT    56475    A   CAGA  C
                                AGC GAAG   TT GGCGCGG
                                ||| ||||   || |||||||
                                TCG CTTC   AA CCGCGCC
                                  C   ____  C
GAM365  PPIL3    5'  CCGCGCCCAACTTCCGCT    51643    A   CAGA  C
                                AGC GAAG   TT GGCGCGG
                                ||| ||||   || |||||||
                                TCG CTTC   AA CCGCGCC
                                  C   ____  C
GAM365  PRSS25   5'  CCCGCGTCCTACTGTCCGC   59673   A AA   ATTC
                                GC G  GCAG   GGCGCGGG
                                || |  ||||   ||||||||
                                CG C  TGTC   CTGCGCCC
                                 C __   ATC_
GAM365  PRSS25   5'  CCCGCGTCCTACTGTCCGC   26030   A AA   ATTC
                                GC G  GCAG   GGCGCGGG
                                || |  ||||   ||||||||
                                CG C  TGTC   CTGCGCCC
                                 C __   ATC_
GAM365  RBPMS    5'  CCCGCGCTCCTCCGCCCCGCT  23428    AGAA  A  TTC
                                AGC   GC GA  GGCGCGGG
                                |||   || ||  ||||||||
                                TCG   CG CT  TCGCGCCC
                                  CCC_  C  CC_
GAM365  SLC21A14 5'  CCTAATCTCCTCTGCTT    34295       A C    C
                                AAGCAGA G AGATT GG
                                ||||||| | ||||| ||
                                TTCGTCT C TCTAA CC
                                    _ C    T
GAM365  SLC26A10 5'  CCCGCGCCAGATCGGCTGCTTC 56841    C      AT__  _
           TCT                    AG AGAAGCAG   TC GGCGCGGG
                                || ||||||||   || ||||||||
                                TC TCTTCGTC   AG CCGCGCCC
                                 _      GGCT  A
GAM365  TNK1     3'  CCCATACCAACTGCTTCT    15648       A  C  CGC
                                AGAAGCAG TT GG   GGG
                                |||||||| || ||   |||
                                TCTTCGTC AA CC   CCC
                                    _ _  ATA
GAM365  LOC147650 3'  CCCAGCAATCTGTTCCTGCTT  79017      A      CG  GC
                                AAGCAG AGCAGATT  GC  GGG
                                |||||| ||||||||  ||  |||
                                TTCGTC TTGTCTAA  CG  CCC
                                   C       __  A_
GAM365  LOC151176 5'  CCCGGGACCACCTGCGCCTGCT 86439      AA   ATTC  CG_
                                AGCAG  GCAG   GG   CGGG
                                |||||  ||||   ||   ||||
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                                TCGTC  CGTC   CC  GCCC
                                  CG   CA__  AGG
GAM365  LOC152915 5'  CCCGGCACACCTGCTCCTACTT 67582    C  A   ATTCG  G
                                AAG AG AGCAG    GC CGGG
                                ||| || |||||    || ||||
                                TTC TC TCGTC    CG GCCC
                                  A  C   CACA_  _
GAM365  LOC196985 5'  CCCGCGCCCCTGCCCCTGC   91236    AA   ATTC
                                GCAG  GCAG   GGCGCGGG
                                ||||  ||||   ||||||||
                                CGTC  CGTC   CCGCGCCC
                                  CC   C___
GAM365  LOC200718 5'  CCCGTCCACCTCCTCCTGCTT  91677      A  C  ATTC  C
                                AAGCAG AG AG   GG GCGGG
                                |||||| || ||   || |||||
                                TTCGTC TC TC   CC TGCCC
                                   C  C  CA__  _
GAM365  LOC201245 3'  CCCATACCAACTGCTTCT    88733       A  C  CGC
                                AGAAGCAG TT GG   GGG
                                |||||||| || ||   |||
                                TCTTCGTC AA CC   CCC
                                    _  _  ATA
GAM365  LOC201702 5'  CCCGCGCTCCCTCCCTCTGC   90470     AGCA  TTC
                                GCAGA   GA   GGCGCGGG
                                |||||   ||   ||||||||
                                CGTCT   CT   TCGCGCCC
                                  CC__  CCC
GAM365  LOC51145  5'  CCCGCACCCCGACTCCTGCTCC 32922     GA_   AT_   C__
          ATGCTT                AAGCA  AGCAG  TCGG  GCGGG
                                |||||  |||||  ||||  |||||
                                TTCGT  TCGTC  AGCC  CGCCC
                                  ACC    CTC   CCA
GAM365  LOC90019  3'  CCCGCCTTCGCCTGCGCCTGC  57523     AA   ATTC  C
                                GCAG  GCAG   GG GCGGG
                                ||||  ||||   || |||||
                                CGTC  CGTC   TC CGCCC
                                  CG   CGCT  _
GAM365  LOC92579  3'  CCCTAAATCTGCTTCCGC    70399    A       CG CGC
                                GC GAAGCAGATT  G   GG
                                || ||||||||||  |   ||
                                CG CTTCGTCTAA  C   CC
                                 C        AT ___
GAM366  LMNB1    3'  CTCTGGATGATGGATTCCA   19932     TC   CT
                                TGGA  TTA  GTCCAGAG
                                ||||  |||  ||||||||
                                ACCT  GGT  TAGGTCTC
                                  TA   AG
GAM366  C3orf1   3'  AGTGCTCTGAACTTGAAACTC  63105    TC  ACT  C
                                GA  TT   GT CAGAGCACT
                                ||  ||   || |||||||||
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                                CT  AA   CA GTCTCGTGA
                                 CA  GTT  A
GAM366  RNF34    3'  GTGGGGACAGAAAGATCCAT   47817         A     AGA
                                ATGGATCTT CTGTCC   GC
                                |||||||||  ||||||   ||
                                TACCTAGAA GACAGG   TG
                                     A     GG_
GAM366  SMUG1    3'  AGTGCCCTAGACAGTAACTTCT 27467      TC       C  A
           A                     TGGA  TTACTGTC AG GCACT
                                ||||  |||||||| || |||||
                                ATCT  AATGACAG TC CGTGA
                                  TC       A  C
GAM366  SPRY4    3'  GTGCTCTCTAAGAGTCCA    49029     _    CTGTCC
                                TGGA TCTTA     AGAGCAC
                                |||| |||||     |||||||
                                ACCT AGAAT     TCTCGTG
                                  G    C_____
GAM366  LOC145622 3'  AGTGCTCTGGAGTTTGGACCC  77802    A   TACTG
                                GG TCT    TCCAGAGCACT
                                || |||    ||||||||||
                                CC AGG    AGGTCTCGTGA
                                 C   TTTG_
GAM366  LOC145676 5'  AGTGCTCTGAAGGTGTAAGCCA 77842     ATCT    GTC
           T                     ATGG    TACT   CAGAGCACT
                                ||||    ||||   |||||||||
                                TACC    GTGG   GTCTCGTGA
                                  GAAT    AA_
GAM366  LOC152283 5'  AGTGCTCTGAGTCAGAGACCG  86864    A   TA   TC_
                                TGG TCT  CTG   CAGAGCACT
                                ||| |||  |||   |||||||||
                                GCC AGA  GAC   GTCTCGTGA
                                  _  __   TGA
GAM366  LOC89231  3'  CTGCTGAACAGCAAGGTCCA   94297        A   C   _
                                TGGATCTT CTGT CAG AG
                                |||||||| |||| ||| ||
                                ACCTGGAA GACA GTC TC
                                     C   A   G
GAM367  ELF3     3'  TGACCTTGACCTTGACCAA    16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                  _    AGT  ___
GAM367  JAK2     3'  TGACCTTCATTCTGAGACCAA  18318       CAA      AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_       C_
GAM367  SLC10A2  5'  ACTCTCTGTCTTGACCAA    6590        CAA      A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
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                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM367  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM367  KIAA1958  5'  GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM367  MARCKS    3'  ACTTTCCACCCTGCCCA     11411     TTCA    A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM367  TUB       5'  GTGGGACCATCCCTTAAACC   13898     C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A        AG__
GAM367  LOC80298  3'  ACTTTTACCTTGAACCA     48062          GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                     A___
GAM368  ARHGDIA   3'  CCCTCCCCCACCCACAGG    16295           ACAAGCT
                                CCTGTGGGTGGG      GGG
                                ||||||||||||      |||
                                GGACACCCACCC      CCC
                                     CCT_____
GAM368  FXYD6     3'  GCCCAGCTCATCCAGATGCAG  42093       GG    ACA
                                CTGTG  TGGG   AGCTGGGC
                                |||||  ||||   ||||||||
                                GACGT  ACCT   TCGACCCG
                                   AG    AC_
GAM368  LOXL1     3'  GCCCAGCCCCCAACCCACAGG  60820         _   ACAA
                                CCTGTGGGT GGG    GCTGGGC
                                ||||||||| |||    |||||||
                                GGACACCCA CCC    CGACCCG
                                     A   C___
GAM368  PPP2R5B   3'  GCCCAGCTCACCCTCTACACAG 21800       _  T   ACA
                                CTGTG GG GGG   AGCTGGGC
                                ||||| || |||   ||||||||
                                GACAC TC CCC   TCGACCCG
                                   A  T   AC_
GAM368  PTPN1     3'  GCCCAGCCTGTCCTGGTACAG  12578       GGT     A
                                CTGTG   GGGACA GCTGGGC
                                |||||   |||||| |||||||
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                                GACAT   TCCTGT CGACCCG
                                  GG_     C
GAM368  S100A10   5'  CCAGCGTGCCCCACCCGCAGGA 60047           A  A
                                TCCTGTGGGTGGG CA GCTGG
                                |||||||||||| || |||||
                                AGGACGCCCACCC GT CGACC
                                      C  G
GAM368  SLA2      3'  CCAGGCCCCACCCACAAGG   50883    _       ACAAG
                                CCT GTGGGTGGG    CTGG
                                ||| |||||||||    ||||
                                GGA CACCCACCC    GACC
                                  A       CG___
GAM368  SLC1A5    5'  GCCCCACGTCCCACCCAGAG   79239    G       AAGCT
                                CT TGGGTGGGAC    GGGC
                                || ||||||||||    ||||
                                GA ACCCACCCTG    CCCG
                                 G        CAC__
GAM368  SLC1A5    5'  GCCCCACGTCCCACCCAGAG   79240    G       AAGCT
                                CT TGGGTGGGAC    GGGC
                                || ||||||||||    ||||
                                GA ACCCACCCTG    CCCG
                                 G        CAC__
GAM368  DNAJB5    3'  CCCAGCTTGATGTCCACTGGA  25354     T   GT GGA
                                TCC GTGG  G   CAAGCTGGG
                                ||| ||||  |   |||||||||
                                AGG CACC  T   GTTCGACCC
                                  T    TG A__
GAM368  FLJ10743  3'  CCCAGCCTGAGGGGAAGCCACA 37078       GTGGGA__  A
          GGA                     TCCTGTGG       CA GCTGGG
                                ||||||||       || ||||||
                                AGGACACC       GT CGACCC
                                     GAAGGGGA  C
GAM368  FLJ20234  5'  GCCCAGCTGGGGCACCCACTGG 35286     T      GGACA
          A                      TCC GTGGGTG     AGCTGGGC
                                ||| |||||||     ||||||||
                                AGG CACCCAC     TCGACCCG
                                  T      GGGG_
GAM368  FLJ21156  3'  GCCCAGCCCCGCAGACCCACA  45120       _____   ACAA
                                TGTGGGT    GGG    GCTGGGC
                                |||||||    |||    |||||||
                                ACACCCA    CCC    CGACCCG
                                    GACG   _____
GAM368  FLJ21687  3'  CCCCATCCCCCCACAGGA    46295         T    CAAGCT
                                TCCTGTGGG GGGA     GGG
                                ||||||||| ||||     |||
                                AGGACACCC CCCT     CCC
                                      _   AC_____
GAM368  KIAA0321  5'  CCCAGCTTGTCATGGAAGGA   63048     GTGGGTGG
                                TCCT       GACAAGCTGGG
                                ||||       ||||||||||
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                                AGGA       CTGTTCGACCC
                                  AGGTA___
GAM368  PIPPIN   3'  GCCCAGCCTGTCCCATGAGGA  80510     GTGG       A
                                TCCT    GTGGGACA GCTGGGC
                                ||||    |||||||| |||||||
                                AGGA    TACCCTGT CGACCCG
                                  G___       C
GAM368  PKNOX2   3'  CCCATGGCCCCCACCCACGG   92527          ACAA  __
                                CTGTGGGTGGG    GCT  GGG
                                ||||||||||    |||  |||
                                GGCACCCACCC    CGG  CCC
                                      C___   TA
GAM368  ROBO4    3'  TCCTGTCCACCCACAAGA    39312    C       G   AGCT
                                TC TGTGGGTGG ACA    GGG
                                || |||||||| |||    |||
                                AG ACACCCACC TGT    CCT
                                 A       _  _____
GAM368  SEMA4G   5'  CCCAGCCCGTGGCTTCACAGG  96324       _  GGG  AA
                                CCTGTGG GT   AC  GCTGGG
                                ||||||| ||   ||  ||||||
                                GGACACT CG   TG  CGACCC
                                    T  G__  CC
GAM368  SHANK3   3'  GCCCAGCCTGTCCTTCCAGAG  66108    G    T     A
                                CT TGGG GGGACA GCTGGGC
                                || |||| |||||| |||||||
                                GA ACCT TCCTGT CGACCCG
                                 G   _     C
GAM368  LOC147180 5'  TCCCTTGTCCCCCCACAG    85107        T       CT
                                CTGTGGG GGGACAAG  GGG
                                ||||||| ||||||||  |||
                                GACACCC CCCTGTTC  CCT
                                      _      __
GAM368  LOC158056 5'  GCCCAGCTCGCGGCTCCAGGA  82592       TG G  G  CAA
                                TCCTG  G TG GA   GCTGGGC
                                |||||  | || ||   |||||||
                                AGGAC  C GC CT   CGACCCG
                                   CT G  G  ___
GAM368  LOC159765 5'  CCCACCCCACCCAGAGGA    83074      G       ACAAGC
                                TCCT TGGGTGGG     TGGG
                                |||| ||||||||     ||||
                                AGGA ACCCACCC     ACCC
                                  G       C_____
GAM368  LOC170127 3'  GCCCAACTTCCCACCCACAGG  83459           CA  C
                                CCTGTGGGTGGGA  AG TGGGC
                                ||||||||||||  || |||||
                                GGACACCCACCCT  TC ACCCG
                                       __  A
GAM368  LOC220766 5'  CCCAGCCCAAACATACCCATAG 92474         GGACAA_
                                CTGTGGGTG      GCTGGG
                                |||||||||      ||||||
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                                GATACCCAT      CGACCC
                                     ACAAACC
GAM368  LOC257277 5'  GCCCAGCTGCGTCACCCCAGGA 96972      T     GA  A
                                TCCTG GGGTGG  CA GCTGGGC
                                ||||| ||||||  || |||||||
                                AGGAC CCCACT  GT CGACCCG
                                   _     GC  _
GAM368  LOC91316  3'  GCCCCCACCCCACCCACAGGG  66185           ACAAGCT
                                TCCTGTGGGTGGG      GGGC
                                ||||||||||||       ||||
                                GGGACACCCACCC      CCCG
                                      CACC___
GAM368  LOC91353  3'  GCCCCCACCCCACCCACAGGG  61159           ACAAGCT
                                TCCTGTGGGTGGG      GGGC
                                ||||||||||||       ||||
                                GGGACACCCACCC      CCCG
                                      CACC___
GAM369  FGF23     3'  AGATCCCAGAAGCTTCTCCA   40554     ACCCTGC  C
                                TGGA      GC TCTGGGATCT
                                ||||      || ||||||||||
                                ACCT      CG AGACCCTAGA
                                  CTT_____  A
GAM369  HTR1D     5'  AGATGCCAAAGGCAAGAATCC  7838      ACC  GC   C   G
                                GGA   CT  GCCT TGG ATCT
                                |||   ||  |||| ||| ||||
                                CCT   GA  CGGA ACC TAGA
                                  AA_  A_   A   G
GAM369  KCNK5     3'  GGTTAAAGAGCAGGGTCCCA   14970     A      GCC   GG
                                TGG ACCCTGC   TCT  GATC
                                ||| |||||||   |||  ||||
                                ACC TGGGACG   AGA  TTGG
                                  C      ____   AA
GAM369  LIMD1     3'  AGATCCCAAAGCCAGCCTCCA  27258      ACC   C  CTC
                                TGGA   CTG GC   TGGGATCT
                                ||||   ||| ||   ||||||||
                                ACCT   GAC CG   ACCCTAGA
                                  CC_   _  AA_
GAM369  MTMR3     3'  TCCAGACTCAGGGTTCCA     41169          CGCC
                                TGGAACCCTG    TCTGGG
                                ||||||||||    ||||||
                                ACCTTGGGAC    AGACCT
                                      TC__
GAM369  SEZ6L     5'  CCAAAGGGCAGGGTCCCA     41203     A      G   C
                                TGG ACCCTGC CCT TGG
                                ||| ||||||| ||| |||
                                ACC TGGGACG GGA ACC
                                  C      _  A
GAM369  UBL1      3'  GATCCCAGAAAAGTTCTA     13976       CCTGCGCC
                                TGGAAC       TCTGGGATC
                                ||||||       |||||||||
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                                ATCTTG      AGACCCTAG
                                   AAA_____
GAM369  ABTB1    3'  GACCCCAGGGGAGGATCCA   51700     AC  GCG      A
                                TGGA  CCT   CCTCTGGG TC
                                ||||  |||   |||||||| ||
                                ACCT  GGA   GGGGACCC AG
                                  A_  ___       C
GAM369  C21orf57 5'  AGACCCCAGAGGACCCGGCCCC 75297    AAC  TGCG      A
           CA                     TGG   CC    CCTCTGGG TCT
                                ||| ||   |||||||| |||
                                ACC  GG   GGAGACCC AGA
                                  CCC  CCCA       C
GAM369  CLSTN1   3'  AGACCCCAGAGGGAGAGGCCCA 30782    AAC   GCG      A
                                TGG   CCT   CCTCTGGG TCT
                                |||   |||   |||||||| |||
                                ACC   GGA   GGAGACCC AGA
                                  C__   GAG       C
GAM369  FLJ10508 5'  AGACCCCAGAAAGAGTACCCA  36679    AACCC   GCC_    A
                                TGG    TGC    TCTGGG TCT
                                |||    |||    |||||| |||
                                ACC    ATG    AGACCC AGA
                                  C____   AGAA     C
GAM369  FLJ10512 3'  GATCTGGACAAGGTTCCA    36693       C  CG  TCTG
                                TGGAACC TG  CC    GGATC
                                ||||||| ||  ||    |||||
                                ACCTTGG AC  GG    TCTAG
                                    A  A_  _____
GAM369  FLJ20257 5'  AGGGGTGGAGGCCAGGGTTCCA 39479          C      GGA
                                TGGAACCCTG GCCTCTG   TCT
                                |||||||||| |||||||   |||
                                ACCTTGGGAC CGGAGGT   GGA
                                      _      GG_
GAM369  FLJ21777 5'  TAGGGCGCAGGGCTCCA     50852      A        T
                                TGGA CCCTGCGCC CTG
                                |||| ||||||||| |||
                                ACCT GGGACGCGG GAT
                                  C        _
GAM369  HEYL     3'  AGATCCTGTTCACCAGGACTCC 28123     AC    CGCCTCT
           A                     TGGA  CCTG      GGGATCT
                                ||||  ||||      |||||||
                                ACCT  GGAC      TCCTAGA
                                  CA    CACTTG_
GAM369  IGF2AS   3'  AGATCCCAGTTCGAAGACTCC  33526    ACC  G  CCT
                                GGA   CT CG   CTGGGATCT
                                |||   || ||   |||||||||
                                CCT   GA GC   GACCCTAGA
                                  CA_  A  TT_
GAM369  KCNH7    5'  GATCCCGGGAGAACTCCA    53838     ACC  GCGCC
                                TGGA   CT    TCTGGGATC
                                ||||   ||    |||||||||
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                                ACCT  GA    GGGCCCTAG
                                  CAA _____
GAM369  KIAA0645  3' CCCGGGGCGGAGGATTCCA   28524      C  G   T
                                TGGAA CCT CGCC CTGGG
                                ||||| ||| |||| |||||
                                ACCTT GGA GCGG GGCCC
                                  A  G   _
GAM369  KIAA0763  3' AGATCCCACCTGTCAGAGCCA 30164    AACC  C  CTC
                                TGG   CTG GC  TGGGATCT
                                |||   ||| ||  ||||||||
                                ACC   GAC TG  ACCCTAGA
                                 GA__  _ TCC
GAM369  KIAA0876  3' AGAGAAACGCAGGTGTTCCA  65312       _    C__
                                TGGAAC CCTGCG  CTCT
                                |||||| ||||||  ||||
                                ACCTTG GGACGC  GAGA
                                   T    AAA
GAM369  KIAA1975  5' ATCCCAGAGCACAGGCTC    74412    AC   C  C
                                GA  CCTG GC TCTGGGAT
                                ||  |||| || ||||||||
                                CT  GGAC CG AGACCCTA
                                 C_   A  _
GAM369  MGC13102  5' AGATCCCAGAACTGAGGCCCCA 51290     AAC  G  CC
                                TGG  CCT CG  TCTGGGATCT
                                |||  ||| ||  ||||||||||
                                ACC  GGA GT  AGACCCTAGA
                                 CC_  _  CA
GAM369  MGC14436  5' CCCAGAGGCTTGGAAATCCA  52924     AC_  TGC
                                TGGA  CC  GCCTCTGGG
                                ||||  ||  |||||||||
                                ACCT  GG  CGGAGACCC
                                  AAA  TT_
GAM369  NXPH3    3' AGACCCCAAAGGGCCAGGTCC  66336    AC   C   C_   A
                                GGA  CCTG GCCT  TGGG TCT
                                |||  |||| ||||  |||| |||
                                CCT  GGAC CGGG  ACCC AGA
                                  __   _   AA   C
GAM369  PME-1    3' AGACCCAGAGAGGCCAAGATCC 32867    ACCCT  GC     A
                                GGA    GC  CTCTGGG TCT
                                |||    ||  ||||||| |||
                                CCT    CG  GAGACCC AGA
                                  AGAAC  GA     _
GAM369  LOC147054 5' ATCCCAGAGGGCCCAGCCCCA  84999    AACC  C  _
                                TGG   CTG GCC TCTGGGAT
                                |||   ||| ||| ||||||||
                                ACC   GAC CGG AGACCCTA
                                  CC__  C  G
GAM369  LOC200205 3' AGATGGCGCCGGGTCCCA    90024    A   T   _
                                TGG ACCC GCGCC TCT
                                ||| |||| ||||| |||
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                                ACC TGGG CGCGG AGA
                                  C   C    T
GAM369  LOC201252 3'  AGATCCCGGACAAGACCGCCA  89545    AACC  GCGCC
                                TGG   CT    TCTGGGATCT
                                |||   ||    ||||||||||
                                ACC   GA    AGGCCCTAGA
                                  GCCA  AC___
GAM369  LOC201799 3'  ATTTCAAAGGCAGAGTTCCA  90489      C  GC   C  GG
                                TGGAAC CT  GCCT TG  AT
                                ||||||  ||  ||||  ||  ||
                                ACCTTG GA  CGGA AC  TA
                                   A  __   A  TT
GAM369  LOC254826 3'  AGATCCCAAAAGGATGTCCCA  99046    A  CCTGCG   C_
                                TGG AC     CCT  TGGGATCT
                                ||| ||     |||  ||||||||
                                ACC TG     GGA  ACCCTAGA
                                  C  TA_____   AA
GAM369  LOC51596  5'  ATCCCAGAGGTTGGCCCC    32486    AA  CTGC
                                GG  CC   GCCTCTGGGAT
                                ||  ||   ||||||||||
                                CC  GG   TGGAGACCCTA
                                 CC  T___
GAM369  LOC56832  3'  ATTCCAAGCGCAGGGCCCA   65445    AA      CTC
                                TGG  CCCTGCGC   TGGGAT
                                |||  ||||||||   ||||||
                                ACC  GGGACGCG   ACCTTA
                                  C_       A__
GAM369  LOC89919  3'  ATCCCAGGAAAGGTTCTA    61370       CTGCGCC
                                TGGAACC      TCTGGGAT
                                |||||||      ||||||||
                                ATCTTGG      GGACCCTA
                                   AAA_____
GAM370  CELSR3    3'  CAAGTTGATCTGAGTATCGTCA 9184      A    TG  __   C
                                TGAC ATACT  GG  AAC TG
                                |||| |||||  ||  ||| ||
                                ACTG TATGA  CT  TTG AC
                                  C    GT  AG   A
GAM370  FY        5'  TCTTCAGGCTCCCTGCTTTGTC 10740      TACTT   A
                                GACAA    GGGA CCTGAAGA
                                |||||    |||| ||||||||
                                CTGTT    CCCT GGACTTCT
                                   TCGT_   C
GAM370  KMO       3'  CTTCAAATATAAGTATTATCA  14845    C      GGAACC
                                TGA AATACTTG     TGAAG
                                ||| ||||||||     |||||
                                ACT TTATGAAT     ACTTC
                                  A       ATAA__
GAM370  RTN3      3'  CTTCAGGTTCTCACTCATAGTC 74330     A  ACT
            A                    TGAC AT   TGGGAACCTGAAG
                                ||||  ||   ||||||||||||
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                                ACTG TA   ACTCTTGGACTTC
                                  A  CTC
GAM370  ZNF266   5'  TCAGACTCTGTAGGTATTGCA  89692    A       _  AC
                                TG CAATACTTG GGA  CTGA
                                || ||||||||| |||  ||||
                                AC GTTATGGAT TCT  GACT
                                 _       G   CA
GAM370  C1orf24  3'  TCTCCAGTCCCAAGTATT    54796          AC   A
                                AATACTTGGGA  CTG AGA
                                ||||||||||  ||| |||
                                TTATGAACCCT  GAC TCT
                                       __  C
GAM370  IGF2AS   3'  CTTCAGGTCACCTTGTCA    33527       TACTT  GA
                                TGACAA    GG  ACCTGAAG
                                ||||||    ||  ||||||||
                                ACTGTT    CC  TGGACTTC
                                   ______ AC
GAM370  LOC138046 3'  TCTCCATTCCCAAGCATTGCCA 75811    A   A      CC  A
                                TG CAAT CTTGGGAA  TG AGA
                                || |||| ||||||||  || |||
                                AC GTTA GAACCCTT  AC TCT
                                 C   C       __ C
GAM370  LOC149132 5'  TCTCCAGGCCCTGAACATTCTC 79929     C   AC TG  AA   A
           A                     TGA AAT  T  GG  CCTG AGA
                                ||| |||  |  ||  |||| |||
                                ACT TTA  A  CC  GGAC TCT
                                  C   CA GT  C_   C
GAM370  LOC152905 3'  CTTCAGGTTCTCACTCATAGTC 61094     A  ACT
           A                     TGAC AT   TGGGAACCTGAAG
                                |||| ||   ||||||||||||
                                ACTG TA   ACTCTTGGACTTC
                                  A  CTC
GAM370  LOC158056 5'  TCTCCAGGCCCCAGGTG     82596        AA   A
                                TACTTGGG  CCTG AGA
                                ||||||||  |||| |||
                                GTGGACCC  GGAC TCT
                                     C_   C
GAM370  LOC91069  3'  CTTCCAGCCAGATATTGTCA   65401        C   GAAC  _
                                TGACAATA TTGG    CTG AAG
                                ||||||| ||||    ||| |||
                                ACTGTTAT GACC    GAC TTC
                                     A   ____   C
GAM370  LOC96597  5'  CTTTGTCCCAAGTATTCCCA   67459    AC        ACC
                                TG  AATACTTGGGA   TGAAG
                                ||  ||||||||||   |||||
                                AC  TTATGAACCCT   GTTTC
                                 CC         ___
GAM371  CTNS     5'  CCGGGGGACTGAGCAGCACGAG 18217      ATC        ACAG
           A                     TCTC   GCTGCTCAGT    CGG
                                ||||   ||||||||||    |||
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                                AGAG  CGACGAGTCA  GCC
                                  CA_       GGGG
GAM371  ELSPBP1  3' CCGCCATACTGAGGCTGAG  42424    TC  TG     CA
                                CTCA  GC  CTCAGTA  GCGG
                                ||||  ||  |||||||  ||||
                                GAGT  CG  GAGTCAT  CGCC
                                  __  __      AC
GAM371  SIMRP7   3' CCGCACTGAGTACCTGGAGA  93969    ATCGC      ACA
                                TCTC   TGCTCAGT  GCGG
                                ||||   ||||||||  ||||
                                AGAG   ATGAGTCA  CGCC
                                  GTCC_      ___
GAM371  LOC200933 5'  CCGCTGCCTGCACGGCGATGAG 91791          CT   TA
            A                    TCTCATCGCTG  CAG  CAGCGG
                                ||||||||||  |||  ||||||
                                AGAGTAGCGGC  GTC  GTCGCC
                                      AC   C_
GAM372  FLJ21438  5'  CAAAACGCTTCCCCCCATCCCA 62190      GAGATTATC
                                TGGGA       AAGCGTTTTG
                                |||||       ||||||||||
                                ACCCT       TTCGCAAAAC
                                  ACCCCCC__
GAM372  FLJ32334  3'  AAAACGCTATTCCTTCCCA   58605       A  TTATCA
                                TGGGAG GA     AGCGTTTT
                                |||||| ||     ||||||||
                                ACCCTT CT     TCGCAAAA
                                   C  TA____
GAM372  HHLA2    3'  CAATGTACTTTGTAATCTCCCC 23953     A      C   CG T
            CA                    TGGG GAGATTAT AAG  T TTG
                                |||| |||||||| |||  | |||
                                ACCC CTCTAATG TTC  G AAC
                                  C       T   AT T
GAM373  ADAT1    3'  CCAGCAAAGAATGAAGGC    24914    __        C
                                GTC  CATTCTTTGC GG
                                |||  |||||||||| ||
                                CGG  GTAAGAAACG CC
                                  AA        A
GAM373  M17S2    5'  CCGGTAGCGGACGGTCCTT   20910          ATTCT
                                AAGGACCGTCC    TTGCCGG
                                ||||||||||    |||||||
                                TTCCTGGCAGG    GATGGCC
                                      C____
GAM373  ST14     5'  CCGGCAGGGACGACGCCT    42042     AC    CAT
                                AGG  CGTC   TCTTTGCCGG
                                |||  ||||   ||||||||||
                                TCC  GCAG   AGGGACGGCC
                                  __    C__
GAM373  HTGN29   5'  GCCAACTGTGTGGCGGTCC   39885        _  TC  T
                                GGACCGTC CAT  TT GC
                                ||||||| |||  || ||
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                                CCTGGCGG GTG  AA CG
                                     T   TC  C
GAM373  PMAIP1    3'  GCAAGAATGGAAGACCCTT   41211      ACCG        T
                                AAGG    TCCATTCTT GC
                                ||||    ||||||||| ||
                                TTCC    AGGTAAGAA CG
                                  CAGA        _
GAM373  LOC144278 3'  GCCAGCAAAGACTGCTCGATGG 77274          ___ T      C
           TCCT                    AGGACCGTC   CA TCTTTGC GGC
                                |||||||||   || ||||||| |||
                                TCCTGGTAG   GT AGAAACG CCG
                                     CTC  C      A
GAM373  LOC147976 3'  CCGGTGAATGAAGACCCT    79287     ACC   CA   _  TG
                                AGG   GTC  TTC TT  CCGG
                                |||   |||  ||| ||  ||||
                                TCC   CAG  AAG AA  GGCC
                                  ___   __   T  GT
GAM373  LOC254263 5'  GCCGGCAGCGGACGCGCC    96367    AC     ATTCT
                                GG  CGTCC     TTGCCGGC
                                ||  |||||     ||||||||
                                CC  GCAGG     GACGGCCG
                                 GC    C____
GAM374  ARHGEF12  3'  AGGCCAGCTTTTATGACG    31644    C          _
                                CG CATGAAAGCTG CCT
                                || ||||||||||| |||
                                GC GTATTTTCGAC GGA
                                 A          C
GAM374  EGLN2     5'  GGACCAGCAAGCAACCCCCAGG 54915     A  AAA___   _  CT   _
           GC                     GCC TG     GCT GC  TGG CC
                                ||| ||     ||| ||  ||| ||
                                CGG AC     CGA CG  ACC GG
                                  G  CCCCAA   A  __   A
GAM374  EGLN2     5'  GGACCAGCAAGCAACCCCCAGG 54916     A  AAA___   _  CT   _
           GC                     GCC TG     GCT GC  TGG CC
                                ||| ||     ||| ||  ||| ||
                                CGG AC     CGA CG  ACC GG
                                  G  CCCCAA   A  __   A
GAM374  EMP1      3'  GCCAAGGCAGCTCTTCTGGAGT 9239     G   T   _
                                AC CCA GAA AGCTGCCTTGGC
                                || ||| ||| ||||||||||||
                                TG GGT CTT TCGACGGAACCG
                                 A   _   C
GAM374  EPAC      3'  GGCCAAGATACTCACAGGC    21455     A  AA  C  C
                                GCC TG  AG TG CTTGGCC
                                ||| ||  || || |||||||
                                CGG AC  TC AT GAACCGG
                                  _  AC  _  A
GAM374  EPHA1     3'  GGGCCAAGGTCGCTCATGGTCA 19100    C      AA  T
                                A GCCATGA  GC GCCTTGGCCC
                                | |||||||  || ||||||||||
```

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                                A TGGTACT  CG TGGAACCGGG
                                 C      __ C
GAM374  ICMT    3'  GGCCAAGGGGACCATGGC    25736       AAAG  G
                                GCCATG    CT CCTTGGCC
                                ||||||    || ||||||||
                                CGGTAC    GG GGAACCGG
                                   CA__  _
GAM374  MXI1    3'  GGCCAAGGTCTGAGCCACAGC  56128    CA  AAA  ___
                                GC  TG   GCT   GCCTTGGCC
                                ||  ||   |||   |||||||||
                                CG  AC   CGA   TGGAACCGG
                                 AC  ___   GTC
GAM374  MXI1    3'  GGCCAAGGTCTGAGCCACAGC  56129    CA  AAA  ___
                                GC  TG   GCT   GCCTTGGCC
                                ||  ||   |||   |||||||||
                                CG  AC   CGA   TGGAACCGG
                                 AC  ___   GTC
GAM374  PACE    3'  GGCCAAGGCAAGGCAGGT    11943     A  AAAGC      _
                                GCC TG    TGCCTTGG CC
                                |||  ||    |||||||| ||
                                TGG AC    ACGGAACC GG
                                  _  GGA__       A
GAM374  PCDHGA1  3'  GGCCAAGAGCCACAGGGC    50087     A  AAA  GC
                                GCC TG   GCT  CTTGGCC
                                |||  ||   |||  |||||||
                                CGG AC   CGA  GAACCGG
                                  G  AC_  __
GAM374  PCDHGA10 3'  GGCCAAGAGCCACAGGGC    50314     A  AAA  GC
                                GCC TG   GCT  CTTGGCC
                                |||  ||   |||  |||||||
                                CGG AC   CGA  GAACCGG
                                  G  AC_  __
GAM374  PCDHGA11 3'  GGCCAAGAGCCACAGGGC    38846     A  AAA  GC
                                GCC TG   GCT  CTTGGCC
                                |||  ||   |||  |||||||
                                CGG AC   CGA  GAACCGG
                                  G  AC_  __
GAM374  PCDHGA12 3'  GGCCAAGAGCCACAGGGC    50321     A  AAA  GC
                                GCC TG   GCT  CTTGGCC
                                |||  ||   |||  |||||||
                                CGG AC   CGA  GAACCGG
                                  G  AC_  __
GAM374  PCDHGA2  3'  GGCCAAGAGCCACAGGGC    38853     A  AAA  GC
                                GCC TG   GCT  CTTGGCC
                                |||  ||   |||  |||||||
                                CGG AC   CGA  GAACCGG
                                  G  AC_  __
GAM374  PCDHGA3  3'  GGCCAAGAGCCACAGGGC    50097     A  AAA  GC
                                GCC TG   GCT  CTTGGCC
                                |||  ||   |||  |||||||
```

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                                CGG AC  CGA  GAACCGG
                                  G  AC_  __
GAM374  PCDHGA4  3' GGCCAAGAGCCACAGGGC   38861   A  AAA  GC
                                GCC TG  GCT  CTTGGCC
                                ||| ||  |||  |||||||
                                CGG AC  CGA  GAACCGG
                                  G  AC_  __
GAM374  PCDHGA5  3' GGCCAAGAGCCACAGGGC   50295   A  AAA  GC
                                GCC TG  GCT  CTTGGCC
                                ||| ||  |||  |||||||
                                CGG AC  CGA  GAACCGG
                                  G  AC_  __
GAM374  PCDHGA6  3' GGCCAAGAGCCACAGGGC   38868   A  AAA  GC
                                GCC TG  GCT  CTTGGCC
                                ||| ||  |||  |||||||
                                CGG AC  CGA  GAACCGG
                                  G  AC_  __
GAM374  PCDHGA7  3' GGCCAAGAGCCACAGGGC   50302   A  AAA  GC
                                GCC TG  GCT  CTTGGCC
                                ||| ||  |||  |||||||
                                CGG AC  CGA  GAACCGG
                                  G  AC_  __
GAM374  PCDHGA8  3' GGCCAAGAGCCACAGGGC   26603   A  AAA  GC
                                GCC TG  GCT  CTTGGCC
                                ||| ||  |||  |||||||
                                CGG AC  CGA  GAACCGG
                                  G  AC_  __
GAM374  PCDHGA9  3' GGCCAAGAGCCACAGGGC   38871   A  AAA  GC
                                GCC TG  GCT  CTTGGCC
                                ||| ||  |||  |||||||
                                CGG AC  CGA  GAACCGG
                                  G  AC_  __
GAM374  PCDHGB1  3' GGCCAAGAGCCACAGGGC   38878   A  AAA  GC
                                GCC TG  GCT  CTTGGCC
                                ||| ||  |||  |||||||
                                CGG AC  CGA  GAACCGG
                                  G  AC_  __
GAM374  PCDHGB2  3' GGCCAAGAGCCACAGGGC   50327   A  AAA  GC
                                GCC TG  GCT  CTTGGCC
                                ||| ||  |||  |||||||
                                CGG AC  CGA  GAACCGG
                                  G  AC_  __
GAM374  PCDHGB3  3' GGCCAAGAGCCACAGGGC   38886   A  AAA  GC
                                GCC TG  GCT  CTTGGCC
                                ||| ||  |||  |||||||
                                CGG AC  CGA  GAACCGG
                                  G  AC_  __
GAM374  PCDHGB4  3' GGCCAAGAGCCACAGGGC   50332   A  AAA  GC
                                GCC TG  GCT  CTTGGCC
                                ||| ||  |||  |||||||
```

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                              CGG AC   CGA  GAACCGG
                                G  AC_  __
GAM374  PCDHGB5  3' GGCCAAGAGCCACAGGGC   38893    A  AAA  GC
                              GCC TG   GCT  CTTGGCC
                              ||| ||   |||  |||||||
                              CGG AC   CGA  GAACCGG
                                G  AC_  __
GAM374  PCDHGB6  3' GGCCAAGAGCCACAGGGC   50337    A  AAA  GC
                              GCC TG   GCT  CTTGGCC
                              ||| ||   |||  |||||||
                              CGG AC   CGA  GAACCGG
                                G  AC_  __
GAM374  PCDHGB7  3' GGCCAAGAGCCACAGGGC   50338    A  AAA  GC
                              GCC TG   GCT  CTTGGCC
                              ||| ||   |||  |||||||
                              CGG AC   CGA  GAACCGG
                                G  AC_  __
GAM374  PCDHGC3  3' GGCCAAGAGCCACAGGGC   51531    A  AAA  GC
                              GCC TG   GCT  CTTGGCC
                              ||| ||   |||  |||||||
                              CGG AC   CGA  GAACCGG
                                G  AC_  __
GAM374  PCDHGC4  3' GGCCAAGAGCCACAGGGC   38908    A  AAA  GC
                              GCC TG   GCT  CTTGGCC
                              ||| ||   |||  |||||||
                              CGG AC   CGA  GAACCGG
                                G  AC_  __
GAM374  PCDHGC5  3' GGCCAAGAGCCACAGGGC   51558    A  AAA  GC
                              GCC TG   GCT  CTTGGCC
                              ||| ||   |||  |||||||
                              CGG AC   CGA  GAACCGG
                                G  AC_  __
GAM374  TBX3     3' CCACGGGCCCGCCATGGCGT  21146       AAA  T_   _
                              ACGCCATG   GC  GCCT TGG
                              ||||||||   ||  |||| |||
                              TGCGGTAC   CG  CGGG ACC
                                   ___  CC    C
GAM374  CDC14B   3' GGACGACAGCCCTCATCGGCGT 53991      _   AA   CC   G
                              ACGCC ATGA  GCTG  TTG CC
                              ||||| ||||  ||||  ||| ||
                              TGCGG TACT  CGAC  AGC GG
                                 C    CC    __   A
GAM374  EDR2     3' GGCCAAGGGCTACTCTCTGGC  61114     T  A  CT  _
                              GCCA GA AG  GCC TTGGCC
                              |||| || ||  ||| ||||||
                              CGGT CT TC  CGG AACCGG
                                _  C  AT   G
GAM374  FLJ11026 3' GCGCAGGCAGCTCCCACG    37548    CCA  AA      T _
                              CG   TG  AGCTGCCT G GC
                              ||   ||  |||||||| | ||
```

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                                GC   AC  TCGACGGA C CG
                                 ___ CC       _ G
GAM374  FLJ12816  3'  GGCCAAGGCAGGACATGGC   42185       AAAG
                                GCCATG   CTGCCTTGGCC
                                ||||||   ||||||||||
                                CGGTAC   GACGGAACCGG
                                   AG__
GAM374  FLJ22558  5'  GGGCCAAGGCCCCTCAAGC   43034    CA   AAGCT
                                GC  TGA    GCCTTGGCCC
                                ||  |||    ||||||||||
                                CG  ACT    CGGAACCGGG
                                 A_   CCC__
GAM374  KCNV1     5'  GGCCAAAGCTTCCGGCGT    27657      AT   A   GCC   _
                                ACGCC  GAA GCT   TTGG CC
                                |||||  ||| |||   |||| ||
                                TGCGG  CTT CGA   AACC GG
                                   C_   _   ___    A
GAM374  KIAA0172  3'  GGCTGAAGCTTTCACAGTG   65598    CA      GCC TG
                                CGC  TGAAAGCT   T  GCC
                                |||  ||||||||   |  |||
                                GTG  ACTTTCGA   A  CGG
                                  AC       ___ GT
GAM374  KIAA1754  3'  GGGCCAAGGATGTCATAGC   63932    C    AAGCTG
                                GC ATGA     CCTTGGCCC
                                || ||||     |||||||||
                                CG TACT     GGAACCGGG
                                 A   GTA___
GAM374  KIAA1922  5'  GGGCCAAGGCAGCCCTGG    74000     TGAAA
                                CCA    GCTGCCTTGGCCC
                                |||    ||||||||||||
                                GGT    CGACGGAACCGGG
                                  CC___
GAM374  MGC23280  3'  GGCCAGGATGCTTGCCATGGC  59054       A_   TGC
                                GCCATG  AAGC   CTTGGCC
                                ||||||  ||||   |||||||
                                CGGTAC  TTCG   GGACCGG
                                   CG    TA_
GAM374  MGC4281   3'  GGGCCGGGGCTCTCATGG    55602       AAGCT
                                CCATGA    GCCTTGGCCC
                                ||||||    ||||||||||
                                GGTACT    CGGGGCCGGG
                                   CT___
GAM374  MGC4399   5'  GCCAAAGAGCAATTTAATGGC  89881      G   GC   _   _
                                GCCAT AAA  TGC CTT GGC
                                ||||| |||  ||| ||| |||
                                CGGTA TTT  ACG GAA CCG
                                   A   A_   A   A
GAM374  PANX1     5'  GGCGCCGCGCAGCTTTCCCGAC 60804    CCAT       CT   _
          G                     CG    GAAAGCTGC  TGGC CC
                                ||    |||||||||  |||| ||
                                ||    |||||||||  |||| ||
```

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                                GC   CTTTCGACG  GCCG GG
                                 AGCC       C_   C
GAM374  PV1     3'  GGGCCAAGGTACCCACAGG   49376    A  AAAGC
                                CC TG    TGCCTTGGCCC
                                || ||    ||||||||||
                                GG AC    ATGGAACCGGG
                                 _  ACCC_
GAM374  LOC114926 5'  GCCGGCAGCCCCCATGGC    57388       AAA     TT
                                GCCATG   GCTGCC  GGC
                                ||||||   ||||||  |||
                                CGGTAC   CGACGG  CCG
                                   CCC     __
GAM374  LOC120973 5'  GCCAAGTTATCTTCATGGTGT  76070          A C  C
                                ACGCCATGAA G TG CTTGGC
                                |||||||||| | || ||||||
                                TGTGGTACTT C AT GAACCG
                                      _ T  T
GAM374  LOC144512 5'  GGGTCAGCTTTCATGCCGT   84039     C         _
                                ACG CATGAAAGCTG CCT
                                ||| ||||||||||| |||
                                TGC GTACTTTCGAC GGG
                                  C          T
GAM374  LOC150421 3'  GGGCCAAGATGCCCCAGGC   86226     A  AAA  TGC
                                GCC TG   GC   CTTGGCCC
                                ||| ||   ||   ||||||||
                                CGG AC   CG   GAACCGGG
                                  _  CC_  TA_
GAM374  LOC199733 3'  GGCCAAGGCAGGAGGATGGC  91442       GAAAG
                                GCCAT    CTGCCTTGGCC
                                |||||    ||||||||||
                                CGGTA    GACGGAACCGG
                                   GGAG_
GAM374  LOC200953 5'  GCCGACCCACCATGGCGT    91803        AAAGC  CC
                                ACGCCATG    TG  TTGGC
                                ||||||||    ||  |||||
                                TGCGGTAC    AC  AGCCG
                                     C____  CC
GAM374  LOC254143 5'  GGGTCAGCTTTCATGCCGT   98253     C         _
                                ACG CATGAAAGCTG CCT
                                ||| ||||||||||| |||
                                TGC GTACTTTCGAC GGG
                                  C          T
GAM374  LOC257319 3'  GCCTGTTACTTTCATGACGT  97473     C       CT  CTT
                                ACG CATGAAAG  GC   GGC
                                ||| ||||||||  ||   |||
                                TGC GTACTTTC  TG   CCG
                                  A       AT  T__
GAM374  LOC90092  3'  GGCCAAGGCAGGAAGATGGC  62067       GAAAG
                                GCCAT    CTGCCTTGGCC
                                |||||    ||||||||||
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                                CGGTA    GACGGAACCGG
                                   GAAG_
GAM375  CDH12    3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM375  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM375  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT    98090      T    AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT     TTATTC
                                   _   GTCA_
GAM375  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
             A                   TACAC       AGAAGAATAAG
                                 |||||       ||||||||||
                                 ATGTG       TCTTCTTATTC
                                    TACTCCC_
GAM375  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM375  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
             TA                   TACA   TCC    GAAGAATAAG
                                  ||||   |||    ||||||||||
                                  ATGT   AGG    TTTCTTATTC
                                    AAA_   ATTG
GAM375  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68742             _
                                TACACCACTCCCAAGA AGA
                                ||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                          G
GAM375  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM375  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748      CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM375  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
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                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM375  OSBPL11  3' CTTAATTTCCCAAGAGTGGTG 43206       CCAA   AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                    AACC   A_
GAM375  YME1L1   3' TCATTCTTGATGTGGTGTA   58438       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                    TA_    A
GAM375  ZNF262   3' CTTATTTTGTTTGGGAGT    18723       A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                    G
GAM375  LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_    AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
                                ATGTGGTG   GGTTC   TGT
                                    CAA    GG__
GAM376  ANXA8    3' TGGGCACAGGTTATACAGACCC 73466     AGCC   ___
          CA                      TGG   TCTGT   ACCTGTGCCCA
                                |||   |||||  ||||||||||
                                ACC   AGACA   TGGACACGGGT
                                  CC__    TAT
GAM376  ANXA8    3' TGGGCACAGGTTATACAGACCC 73467     AGCC   ___
          CA                      TGG   TCTGT   ACCTGTGCCCA
                                |||   |||||  ||||||||||
                                ACC   AGACA   TGGACACGGGT
                                  CC__    TAT
GAM376  BHLHB3   5' TATTGTACAGAGCCCCA    48490     A  C     CT
                                TGG GC TCTGTAC  GTG
                                ||| || |||||||  |||
                                ACC CG AGACATG  TAT
                                  C  _     T_
GAM376  CASP3    3' TGGGCATGGTCAAAGGCTC   16355       C  T   T
                                GAGCCT TG ACC GTGCCCA
                                |||||| || ||| |||||||
                                CTCGGA AC TGG TACGGGT
                                   A  _  _
GAM376  CCND2    3' TGGACACAGGTGATTGGCTCC  10057       TCTG      C
                                GGAGCC   TACCTGTG CCA
                                ||||||   |||||||| |||
                                CCTCGG   GTGGACAC GGT
                                   TTA_      A
GAM376  DPEP1    5' GGCCAGCACAGAGGCACCAG   16620     A      AC   T
                                CTGG GCCTCTGT  CTG GCC
                                |||| ||||||||  ||| |||
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                                GACC CGGAGACA  GAC CGG
                                  A       C_  _
GAM376  EPHB4    3'  TGGGGACTCACAGAGGCCCC   16710    A       ACCT  G
                                GG GCCTCTGT    GT CCCA
                                || ||||||||    || ||||
                                CC CGGAGACA    CA GGGT
                                 C       CT__  G
GAM376  EVA1     5'  GGCACAGGTGAGGAACTC    59235     __    TGT
                                GAG  CCTC   ACCTGTGCC
                                |||  ||||   |||||||||
                                CTC  GGAG   TGGACACGG
                                 AA   ___
GAM376  FANCC    3'  TGGGCACAGGGGCAGCCGC   71053    CT   TA
                                GC  CTG  CCTGTGCCCA
                                ||  |||  ||||||||||
                                CG  GAC  GGACACGGGT
                                 CC   GG
GAM376  GRLF1    3'  GCAGGCAATGGCTCCAG     79260        TC  TA
                                CTGGAGCC  TG  CCTGT
                                ||||||||  ||  |||||
                                GACCTCGG  AC  GGACG
                                     TA  __
GAM376  ITGA5    3'  CAGGGACAGAGGCCCCAG    61932      A       A
                                CTGG GCCTCTGT CCTG
                                |||| |||||||| ||||
                                GACC CGGAGACA GGAC
                                  C       G
GAM376  LDB3     3'  TGGGCAATTGCCAGGGCTCCAG 76928         T   TACCTG
                                CTGGAGCC CTG     TGCCCA
                                |||||||| |||     ||||||
                                GACCTCGG GAC     ACGGGT
                                     _  CGTTA_
GAM376  LZTS1    3'  TGGGCACAGTCCAGACCCA   41042    AGCC   TAC
                                TGG   TCTG   CTGTGCCCA
                                |||   ||||   |||||||||
                                ACC   AGAC   GACACGGGT
                                  C___    CT_
GAM376  MDM1     3'  TGAGCACATAAGCAGAGGCTGC 39684     G       ACC    C
             AG                   CTG AGCCTCTGT   TGTGC CA
                                ||| |||||||||   ||||| ||
                                GAC TCGGAGACG   ACACG GT
                                  G        AAT    A
GAM376  MHC2TA   3'  CACAGGCCCGGCTCCAG     5969         TCT TA
                                CTGGAGCC   G  CCTGTG
                                ||||||||   |  ||||||
                                GACCTCGG   C  GGACAC
                                     ___ CC
GAM376  NEURL    3'  GGACAGGCTGCAGAGGGCTCCA 16130         _     _    G
             G                    CTGGAGCC TCTGTA CCTGT CC
                                |||||||| |||||| ||||| ||
```

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                                GACCTCGG AGACGT GGACA GG
                                    G     C    _
GAM376  ONECUT2  3'  GGGCACAAGTCACCTCCA    17943      CCTC  T  C
                                TGGAG   TG AC TGTGCCC
                                |||||   || || |||||||
                                ACCTC   AC TG ACACGGG
                                  C___  _  A
GAM376  PLCG1    3'  GGCACAGGAGACTCCA     12159      CC   GTA
                                TGGAG  TCT   CCTGTGCC
                                |||||  |||   ||||||||
                                ACCTC  AGA   GGACACGG
                                  __   ___
GAM376  PLOD     3'  GGCACAGGTGTTGCACCAG   6116      A  CTCTG
                                CTGG GC    TACCTGTGCC
                                |||| ||    ||||||||||
                                GACC CG    GTGGACACGG
                                  A  TT___
GAM376  SCN4A    3'  TGAGCACCACCAGGGCTCCAG  6209        T   TACCT   C
                                CTGGAGCC CTG    GTGC CA
                                |||||||| |||    |||| ||
                                GACCTCGG GAC    CACG GT
                                    _  CAC__   A
GAM376  SYNGR3   3'  GGAGAGAGGCCCAGAGGCTCCA 16120          TA   GTG_
           G                    CTGGAGCCTCTG  CCT   CC
                                ||||||||||||  |||   ||
                                GACCTCGGAGAC  GGA   GG
                                      CC   GAGA
GAM376  SYNGR3   3'  GGCACAGACCAGGGCTCCA   16121       T   TAC
                                TGGAGCC CTG   CTGTGCC
                                ||||||| |||   |||||||
                                ACCTCGG GAC   GACACGG
                                    _  CA_
GAM376  BG1      3'  TGGGCACAGGCATTTCTGCCA  88655     AGCCTCT  A
                                TGG      GT CCTGTGCCCA
                                |||      || ||||||||||
                                ACC      TA GGACACGGGT
                                  GTCTT__  C
GAM376  CALN1    3'  TGAGCACAAGTAAAACTAAGGC 49671        CT  ___  C    C
           TTCAG                  CTGGAGCCT  GT   AC TGTGC CA
                                |||||||||  ||   || ||||| ||
                                GACTTCGGA  CA   TG ACACG GT
                                     AT  AAA  A    A
GAM376  DGKD     3'  GGGCACAGACACTGACCAG   60111     AGCC  T  AC
                                CTGG   TC GT  CTGTGCCC
                                ||||   || ||  ||||||||
                                GACC   AG CA  GACACGGG
                                  ____  T  CA
GAM376  DKFZP566G1424 3'  GGGAGGGGCACAGGGCTCCAG  85944        T   A   GTG
                                CTGGAGCC CTGT CCT   CCC
                                |||||||| |||| |||   |||
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                                GACCTCGG GACA GGG   GGG
                                    _   C   GA_
GAM376  EMILIN-2  3'  TGAGCTTGCCACAGAGGCTCC  50258          ACCTGT  C
                                GGAGCCTCTGT     GC CA
                                ||||||||||      || ||
                                CCTCGGAGACA     CG GT
                                     CCGTT_  A
GAM376  FKSG28    3'  CAGAGGTGCAGGCACCAG    48906      A   CT     G
                                CTGG GCCT  GTACCT TG
                                |||| ||||  |||||| ||
                                GACC CGGA  CGTGGA AC
                                  A   __     G
GAM376  FLJ11286  3'  TGGGCACAGGCATGGTACCACC 37796     AGCCT   A
          AG                      CTGG    CTGT CCTGTGCCCA
                                ||||    |||| ||||||||||
                                GACC    GGTA GGACACGGGT
                                  ACCAT   C
GAM376  FLJ12056  3'  GGGCACAGGCACGGGCACAG   46822     GA   CT  A
                                CTG  GCCT  GT CCTGTGCCC
                                |||  ||||  || |||||||||
                                GAC  CGGG  CA GGACACGGG
                                 A_   __ C
GAM376  FLJ13052  3'  GGGCACAGGGGAAGCCCAG   43756      A  C   GTA
                                CTGG GC TCT   CCTGTGCCC
                                |||| || |||   |||||||||
                                GACC CG AGG   GGACACGGG
                                  _ A   ___
GAM376  FLJ14103  5'  GGACAGCCAGAGGCTGCAG   97938     G      TAC   G
                                CTG AGCCTCTG   CTGT CC
                                ||| ||||||||   |||| ||
                                GAC TCGGAGAC   GACA GG
                                  G       C__   _
GAM376  KIAA0321  5'  GCAGCCCAGAAAGCTCCAG   63054       C_   TAC
                                CTGGAGC  TCTG   CTGT
                                |||||||  ||||   ||||
                                GACCTCG  AGAC   GACG
                                    AA   CC_
GAM376  KIAA0352  3'  ACAGCAGAGGCTCCA      29822          TAC
                                TGGAGCCTCTG   CTGT
                                ||||||||||   ||||
                                ACCTCGGAGAC   GACA
                                     ___
GAM376  KIAA0476  3'  GCCCAGTCAAAGGCTCCA    30040        C  TAC   T
                                TGGAGCCT TG   CTG GC
                                ||||||||  ||   ||| ||
                                ACCTCGGA AC   GAC CG
                                    A  T__   C
GAM376  KIAA0819  5'  GGGAACCAGAGGCTCCAG    64334          TACCT  G
                                CTGGAGCCTCTG    GT CCC
                                ||||||||||||    || |||
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                                GACCTCGGAGAC    CA GGG
                                      _____ A
GAM376  KIAA1001  3'  GGCACAGGTGCCAGCTCCAG  31010       CTCT
                                CTGGAGC   GTACCTGTGCC
                                |||||||   ||||||||||
                                GACCTCG   CGTGGACACGG
                                   AC__
GAM376  KIAA1076  3'  TGGGCACAGTGAGGAGACCCCA 66129    AGC   G  C
                                TGG  CTCT TAC TGTGCCCA
                                |||  |||| ||| ||||||||
                                ACC  GAGG GTG ACACGGGT
                                  CCA   A  _
GAM376  MYH7B    3'  CAGGCCACAGAGGCCCAG   71055     A      A_
                                CTGG GCCTCTGT  CCTG
                                |||| ||||||||  ||||
                                GACC CGGAGACA  GGAC
                                  _      CC
GAM376  NYD-SP25  3'  TGGGCAAGTCAGTGGCTCCAG  54306       T  T  CTG
                                CTGGAGCC CTG AC   TGCCCA
                                |||||||| ||| ||   ||||||
                                GACCTCGG GAC TG   ACGGGT
                                     T  _  A__
GAM376  PDE2A    3'  TGGGGGATACAGGGGCCCCAG  12007     A      _  TGTG
                                CTGG GCCTCTGTA CC   CCCA
                                |||| |||||||| ||   ||||
                                GACC CGGGGACAT GG   GGGT
                                  C       A _____
GAM376  RoXaN    3'  CACAAGTAAATGCAGGCTGCAG 47275    G    CTG__  C
                                CTG AGCCT    TAC TGTG
                                ||| |||||    ||| ||||
                                GAC TCGGA    ATG ACAC
                                  G    CGTAA  A
GAM376  SPIB     3'  TGAGCACACCCGAGGCTCC   13358       TGTACC   C
                                GGAGCCTC     TGTGC CA
                                ||||||||     ||||| ||
                                CCTCGGAG     ACACG GT
                                     CCC___    A
GAM376  TIX1     3'  GGGCACAGACACCTCC     62408     CCTC  AC
                                GGAG   TGT  CTGTGCCC
                                ||||   |||  ||||||||
                                CCTC   ACA  GACACGGG
                                  C___   __
GAM376  TREX1    5'  GGAGACACAATGGCTCCAG   50609       TC  ACCT  GC
                                CTGGAGCC  TGT   GT  CC
                                ||||||||  |||   ||  ||
                                GACCTCGG  ACA   CA  GG
                                     TA  _____  GA
GAM376  TREX1    5'  GGAGACACAATGGCTCCAG   50610       TC  ACCT  GC
                                CTGGAGCC  TGT   GT  CC
                                ||||||||  |||   ||  ||
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                                GACCTCGG  ACA   CA  GG
                                    TA  ____  GA
GAM376  YKT6     3'  TGAGCCCACCACAGAGGCCACA 22645    GA      ACC  T  C
            G                    CTG  GCCTCTGT   TG GC CA
                                 |||  ||||||||   || || ||
                                 GAC  CGGAGACA   AC CG GT
                                   AC       CC_  C  A
GAM376  LOC121629 5' GGGTCACAAGAGGCTCCAG   76085         GTACC  _
                                 CTGGAGCCTCT    TGTG CCC
                                 ||||||||||     |||| |||
                                 GACCTCGGAGA    ACAC GGG
                                       _____   T
GAM376  LOC126006 5' GGGCACAGCGAGGTCCA     74897     G   TGTAC
                                 TGGA CCTC    CTGTGCCC
                                 |||| ||||    ||||||||
                                 ACCT GGAG    GACACGGG
                                   _   C____
GAM376  LOC127702 3' GGGCAGCACAGAGGCCCC    75986    A      ACCTG
                                 GG GCCTCTGT    TGCCC
                                 || ||||||||    |||||
                                 CC CGGAGACA    ACGGG
                                  C       CG___
GAM376  LOC142972 3' TGGGCACAGGTTATACAGACCC 65722    AGCC   ___
            CA                     TGG   TCTGT   ACCTGTGCCCA
                                 |||   |||||  ||||||||||
                                 ACC   AGACA   TGGACACGGGT
                                   CC__    TAT
GAM376  LOC145317 3' GCACAGACACAGAGGCCCAG  84280     A      AC
                                 CTGG GCCTCTGT  CTGTGC
                                 |||| ||||||||  ||||||
                                 GACC CGGAGACA  GACACG
                                   _       CA
GAM376  LOC147160 5' GGCACAGGGTCAGGCCCAG   85079     A   CTGTA
                                 CTGG GCCT    CCTGTGCC
                                 |||| ||||    ||||||||
                                 GACC CGGA    GGACACGG
                                   _   CTG__
GAM376  LOC148114 5' GGGCACAGACCAGCCCCA    79362    A  CTC  TAC
                                 TGG GC   TG   CTGTGCCC
                                 ||| ||   ||   ||||||||
                                 ACC CG   AC   GACACGGG
                                   C  ___  CA_
GAM376  LOC151438 5' GGACACCAGAGGCTCC      86559         TACCT   C
                                 GGAGCCTCTG    GTG CC
                                 ||||||||||    ||| ||
                                 CCTCGGAGAC    CAC GG
                                       _____  A
GAM376  LOC153205 3' ATATATACTAGAAGCTCCA   87152       C   _   CC
                                 TGGAGC TCT GTA  TGT
                                 |||||| ||| |||  |||
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                                ACCTCG AGA CAT  ATA
                                   A   T   AT
GAM376  LOC153561 3'  TGAGCACAGGAGTTGGAGGCTG 81753     G       TA_      C
           CAG                    CTG AGCCTCTG   CCTGTGC CA
                                  ||| ||||||||   ||||||| ||
                                  GAC TCGGAGGT   GGACACG GT
                                    G       TGA      A
GAM376  LOC158263 5'  GGGCACCACTCAGAGGCTCCAG 82730           TACCT
                                  CTGGAGCCTCTG    GTGCCC
                                  ||||||||||||    ||||||
                                  GACCTCGGAGAC    CACGGG
                                         TCAC_
GAM376  LOC167410 3'  CAGAGGTCCTCAGAGGCTCCAG 83563           T__   G
                                  CTGGAGCCTCTG   ACCT TG
                                  ||||||||||||   |||| ||
                                  GACCTCGGAGAC   TGGA AC
                                         TCC    G
GAM376  LOC170127 3'  TGGGCACAGATTCCGATTCCAG 83462       CC  TGTAC
                                  CTGGAG  TC    CTGTGCCCA
                                  ||||||  ||    |||||||||
                                  GACCTT  AG    GACACGGGT
                                     __  CCTTA
GAM376  LOC197336 3'  TGGACACAGGCTTGGCAGAGGC 59925      A       A___      C
           GCCAG                    CTGG GCCTCTGT    CCTGTG CCA
                                  |||| ||||||||    |||||| |||
                                  GACC CGGAGACG    GGACAC GGT
                                    G       GTTC      A
GAM376  LOC200282 3'  TGCTGGAACAGAGGCTCCA    90102           A  T
                                  TGGAGCCTCTGT CC GTG
                                  |||||||||||| || |||
                                  ACCTCGGAGACA GG CGT
                                         A  T
GAM376  LOC201100 3'  GCCCAGCACAGAGGCTCCA    91324           AC   T
                                  TGGAGCCTCTGT  CTG GC
                                  ||||||||||||  ||| ||
                                  ACCTCGGAGACA  GAC CG
                                         C_   C
GAM376  LOC203286 5'  ACAGGACAGCAGAGGCTCCAG  92139           A__
                                  CTGGAGCCTCTGT   CCTGT
                                  ||||||||||||   |||||
                                  GACCTCGGAGACG   GGACA
                                          ACA
GAM376  LOC203636 3'  CAGGTCTTCACAGAGGCCCCGG 90975      A       ____
                                  CTGG GCCTCTGT    ACCTG
                                  |||| ||||||||    |||||
                                  GGCC CGGAGACA    TGGAC
                                    C       CTTC
GAM376  LOC219513 3'  GGACACAGAGTGCAGAGACCCC 95987      AGC       _    C
           GG                     CTGG   CTCTGTAC CTGTG CC
                                  ||||   |||||||| ||||| ||
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                                GGCC   GAGACGTG GACAC GG
                                  CCA       A     A
GAM376  LOC221822 5'  GGACTGGACAGAGGCACCAG   94451      A       A  T  G
                                CTGG GCCTCTGT CC GT CC
                                |||| |||||||| || || ||
                                GACC CGGAGACA GG CA GG
                                  A       _  T  _
GAM376  LOC253027 3'  GGCACAGGTGCCCTGCCCA    98770     A  CTCT
                                TGG GC    GTACCTGTGCC
                                ||| ||    ||||||||||
                                ACC CG    CGTGGACACGG
                                  _  TCC_
GAM376  LOC255104 3'  GCACAGGTTAGAGTCCCAG    97128      AG C    T
                                CTGG  C TCTG ACCTGTGC
                                ||||  | |||| ||||||||
                                GACC  G AGAT TGGACACG
                                  CT _   _
GAM376  LOC90092  5'  TGGGCACAGACACTCACAGCCC 62078     A  CTCT_  AC
          CA                      TGG GC     GT  CTGTGCCCA
                                ||| ||     ||  |||||||||
                                ACC CG     CA  GACACGGGT
                                  C  ACACT  CA
GAM376  LOC90917  3'  GGCACAGGCCTCAGAGCCCAG  64987      A  C    TA_
                                CTGG GC TCTG   CCTGTGCC
                                |||| || ||||   ||||||||
                                GACC CG AGAC   GGACACGG
                                  _  _    TCC
GAM376  LOC91516  5'  GCAGCTCAGAGGCTCCAG     66908           TAC
                                CTGGAGCCTCTG   CTGT
                                ||||||||||||   ||||
                                GACCTCGGAGAC   GACG
                                       TC_
GAM376  LOC91661  3'  GGTGCACAGAGGCCCCGG     57215      A       ACCT TG
                                CTGG GCCTCTGT    G  CC
                                |||| ||||||||    |  ||
                                GGCC CGGAGACA    C  GG
                                  C       _____ GT
GAM376  LOC92340  3'  TGGGCACAGGGCTAAGTCCAG  69569       GC  CT  A
                                CTGGA  CT  GT CCTGTGCCCA
                                |||||  ||  || ||||||||||
                                GACCT  GA  CG GGACACGGGT
                                  ___  AT  _
GAM377  DKFZP434J193 3'  ACAGAAAGTGACCACAAA    71555       A       AA
                                TTTGT GTCATTTT  GT
                                |||||  ||||||||  ||
                                AAACA CAGTGAAA  CA
                                  C       GA
GAM377  STIM2     3'  ACTTTGAATAACTGCAAA     40858         C    T
                                TTTGTAGT ATTT AAGT
                                ||||||||  ||||  ||||
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                                AAACGTCA TAAG TTCA
                                    A   T
GAM377  LOC142973 5'  TACTGTGAATGACCACAA    60914     A     TA
                                TTGT GTCATTT  AGTA
                                |||| |||||||  ||||
                                AACA CAGTAAG  TCAT
                                  C      TG
GAM377  LOC221632 3'  CATGCTTAGGAACCACTACAAA 95446       CA   AAGT
                                TTTGTAGT  TTTT   AGCATG
                                ||||||||  ||||   ||||||
                                AAACATCA  AAGG   TCGTAC
                                    CC   AT__
GAM378  CDH12    3'  CTTATCATTTAAAGTGGTGTA  15777        CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM378  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007     CA       G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM378  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090      T   AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                   _   GTCA_
GAM378  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
            A                    TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM378  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126        CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM378  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
            TA                    TACA   TCC   GAAGAATAAG
                                ||||   |||   ||||||||||
                                ATGT   AGG   TTTCTTATTC
                                  AAA_   ATTG
GAM378  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68742           _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                          G
GAM378  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
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                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM378  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748     CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM378  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571    CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM378  OSBPL11   3'  CTTAATTTCCCAAGAGTGGTG  43206       CCAA   AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                     AACC   A_
GAM378  YME1L1    3'  TCATTCTTGATGTGGTGTA   58438       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                     TA_    A
GAM378  ZNF262    3'  CTTATTTTGTTTGGGAGT    18723       A
                                ACTCCCAAG AGAATAAG
                                |||||||||  ||||||||
                                TGAGGGTTT TTTTATTC
                                     G
GAM378  LOC91960  3'  TGTGGCTTGGAACGTGGTGTA  68294       TC_    AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
                                ATGTGGTG   GGTTC   TGT
                                     CAA    GG__
GAM379  ALEX3     5'  ACTAGGGAAAAGAAGAAGGGG  33971          _  ATCC
                                CCCTTTCTTCTTT CC   AGT
                                ||||||||||||| ||   |||
                                GGGGAAGAAGAAA GG   TCA
                                       A  GA__
GAM379  C18orf1   3'  CTGAATAAAGAAGGAAG     60864         CC  C
                                CTTTCTTCTTT  AT CAG
                                ||||||||||  || |||
                                GAAGGAAGAAA  TA GTC
                                      __  A
GAM379  CDH17     5'  CTGAATGGAAGAAAAGG     15784      CT   T   C
                                CCTTT  TCTT CCAT CAG
                                |||||  |||| |||| |||
                                GGAAA  AGAA GGTA GTC
                                  __   _   A
GAM379  CNTNAP2   3'  ACTAGAATGAAAGAAGGAA   27087         CA  C
                                TTTCTTCTTTC  TC AGT
                                ||||||||||  || |||
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                                AAGGAAGAAAG  AG TCA
                                      TA  A
GAM379  DDX6    3'  CTGGTGAAGAGAAAAAGG    16564      C     C  T
                                CCTTT TTCTTT CA CCAG
                                ||||| |||||| || ||||
                                GGAAA AAGAGA GT GGTC
                                  _     A  _
GAM379  DMD     5'  GGAGTGGAAGAAACAGGT    15685     CC      _
                                ACC  TTTCTTCT TTCC
                                |||  |||||||| ||||
                                TGG  AAAGAAGG GAGG
                                  AC       T
GAM379  DMD     5'  GGAGTGGAAGAAACAGGT    15689     CC      _
                                ACC  TTTCTTCT TTCC
                                |||  |||||||| ||||
                                TGG  AAAGAAGG GAGG
                                  AC       T
GAM379  ENC1    3'  ACTGGACATGAAGGAAAGGGG  14646        TCT   CA_
                                CCCCTTTCT   TTC   TCCAGT
                                |||||||||   |||   ||||||
                                GGGGAAAGG   AAG   AGGTCA
                                     ___   TAC
GAM379  FBXW7   3'  ACTAAGAAGGAAAAGAAGAAG  54408         _  A  C_
                                TTTCTTCTTT CC TC  AGT
                                |||||||||| || ||  |||
                                GAAGAAGAAA GG AG  TCA
                                      A  A  AA
GAM379  FBXW7   3'  ACTAAGAAGGAAAAGAAGAAG  37590         _  A  C_
                                TTTCTTCTTT CC TC  AGT
                                |||||||||| || ||  |||
                                GAAGAAGAAA GG AG  TCA
                                      A  A  AA
GAM379  HDAC8   3'  ACTGGACCTAGGGGAAGAAGGA 38079           A____
          G                      TTTCTTCTTTCC    TCCAGT
                                ||||||||||||    ||||||
                                GAGGAAGAAGGG    AGGTCA
                                       GATCC
GAM379  IL18R1  3'  ACTGGATGACTAAAAAGAG   15250      C  TC_
                                TTCTT TT   CATCCAGT
                                ||||| ||   ||||||||
                                GAGAA AA   GTAGGTCA
                                   A  TCA
GAM379  IL2RA   5'  ACTGGATGGACCCACAAGGG  6445       TCTTCTT
                                CCCTT      TCCATCCAGT
                                |||||      ||||||||||
                                GGGAA      AGGTAGGTCA
                                  CACCC__
GAM379  KCND3   5'  TGCAAGAAAAAGGGGT      18355        C    TCCATC
                                ACCCCTTT TTCTT     CA
                                |||||||| |||||     ||
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                                TGGGGAAA AAGAA     GT
                                   _    C_____
GAM379  MMP1    5'  ACTGAGAAAGAAGACAAAGG  11604     __      CATC
                                CCTT  TCTTCTTTC   CAGT
                                ||||  |||||||||   ||||
                                GGAA  AGAAGAAAG   GTCA
                                  AC       A___
GAM379  OAS3    3'  ACTGGATATGGAAAAAAGAAGG 21649       C     __
                                CTTTCTT TTTCCA  TCCAGT
                                |||||||  ||||||  ||||||
                                GGAAGAA AAAGGT  AGGTCA
                                    A     AT
GAM379  OCA2    3'  ACTGTTTGAAGAAGAAAAGG  60824    C       TC  TC
                                CC TTTCTTCTT  CA  CAGT
                                || |||||||||  ||  ||||
                                GG AAAGAAGAA  GT  GTCA
                                 A        __  TT
GAM379  PMX1    5'  CTGAGAAGGAAAAAGGAG    42961      C    A  _
                                TTCTT TTTCC TC CAG
                                ||||| ||||| || |||
                                GAGGA AAAGG AG GTC
                                   A    A  A
GAM379  PMX1    5'  CTGAGAAGGAAAAAGGAG    23567      C    A  _
                                TTCTT TTTCC TC CAG
                                ||||| ||||| || |||
                                GAGGA AAAGG AG GTC
                                   A    A  A
GAM379  SLC1A3  5'  ACTGAAGTGCAAAGAAGAGA  16058         C  C_
                                TTTCTTCTTT CAT  CAGT
                                |||||||||| |||  ||||
                                AGAGAAGAAA GTG  GTCA
                                      C  AA
GAM379  SMP1    3'  GAAGGAAAGGAAAAAAGGG   27473       C_      A
                                CCCTTT  TTCTTTCC TC
                                ||||||  |||||||| ||
                                GGGAAA  AGGAAAGG AG
                                   AA       A
GAM379  TES     3'  ACTGAATGGAAAGATGAG    72457     T       C
                                TTC TCTTTCCAT CAGT
                                ||| ||||||||| ||||
                                GAG AGAAAGGTA GTCA
                                  T       A
GAM379  TNFAIP2 3'  ACTGGAAGAGAAAGAAGGAA  21915         CA_
                                TTTCTTCTTTC   TCCAGT
                                ||||||||||   ||||||
                                AAGGAAGAAAG   AGGTCA
                                      AGA
GAM379  ZNF38   5'  GGAGAAAGAAGAGAAAGG   96030    CC        CA
                                CC  TTTCTTCTTTC  TCC
                                ||  ||||||||||  |||
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                                GG  AGAGAAGAAAG  AGG
                                 AA         __
GAM379  ABCA10   5'  ACTGGACAAGGAGAAA      55360         TCCA
                                TTTCTTCTT    TCCAGT
                                |||||||||    ||||||
                                AAAGAGGAA    AGGTCA
                                     C___
GAM379  ADAM9    3'  GCTGGAGAAAGAAGGAAG    15106          CA
                                CTTTCTTCTTTC  TCCAGT
                                ||||||||||||  ||||||
                                GAAGGAAGAAAG  AGGTCG
                                       __
GAM379  AP3M2    3'  GGAAAAAGAAGTAAAGGAGT   23301    C    _      CCA
                                AC CCTTT CTTCTTT   TCC
                                || ||||| |||||||   |||
                                TG GGAAA GAAGAAA   AGG
                                 A    T      A__
GAM379  C11orf11  5'  ATGACAAGAAGAAAGTGGT    94873     C        TC
                                ACC CTTTCTTCTT  CAT
                                ||| ||||||||||  |||
                                TGG GAAAGAAGAA  GTA
                                  T         CA
GAM379  C20orf60  3'  ACTGAACGGGTAAGAGAAGAGG 54803       CT    T  ATC_
                                CCTTT  TCTT CC    CAGT
                                |||||  |||| ||    ||||
                                GGAGA  AGAA GG    GTCA
                                   AG    T  GCAA
GAM379  C7orf13   3'  ACTGGATCTAGAAGAAAAGG   51920    C       TTCC
                                CC TTTCTTCT    ATCCAGT
                                || ||||||||    |||||||
                                GG AAAGAAGA    TAGGTCA
                                 A       TC__
GAM379  C8orf2    3'  ACTGTGGTGAAAAAGAAGAAA  24141          C_   _
                                TTTCTTCTTT  CATC CAGT
                                ||||||||||  |||| ||||
                                AAAGAAGAAA  GTGG GTCA
                                      AA    T
GAM379  CREG     3'  ACTGGATTGCAAAAGAAAGAGG 15245    C      CTTTCC
                                CC CTTTCTT      ATCCAGT
                                || |||||||      |||||||
                                GG GAAAGAA      TAGGTCA
                                 A       AACGT_
GAM379  DKFZP434C171 5'  ACTGGATGAGCAGCAAAGGG   32179       _  T  TTC
                                CCCTTT CT CT   CATCCAGT
                                |||||| || ||   ||||||||
                                GGGAAA GA GA   GTAGGTCA
                                   C  C  ___
GAM379  DKFZP434F0318 3'  ACTGGGAGAAAAAAGAGAGGAG 48740    C       C    CA
           T                     AC CCTTTCTT TTTC  TCCAGT
                                || |||||||| ||||  ||||||
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                                TG GGAGAGAA AAAG  GGGTCA
                                 A       A    A_
GAM379  DKFZP564I052 5'  ACTGGATGATTGTGAGAAAAGG 67275     C      CTTTC
          G                      CCC TTTCTT     CATCCAGT
                                 ||| ||||||     ||||||||
                                 GGG AAAGAG     GTAGGTCA
                                   A      TGTTA
GAM379  DKFZP566D193 3'  ACTGGAATAAAAAGGAAGAAA  86750          CCA__
                                 TTTCTTCTTT     TCCAGT
                                 ||||||||||     ||||||
                                 AAAGAAGGAA     AGGTCA
                                       AAATA
GAM379  EIF4G3   3'  GGGGAAAGAGAAAAAAAGGT   15001     CC__    T     AT
                                 ACC    TTTCT CTTTCC  CC
                                 |||    ||||| ||||||  ||
                                 TGG    AAAGA GAAAGG  GG
                                   AAAA    _     __
GAM379  ETAA16   5'  GTGAAAAGAAGAAAGCGG    39170    C         C
                                 CC CTTTCTTCTTT CAT
                                 || ||||||||||| |||
                                 GG GAAAGAAGAAA GTG
                                  C          A
GAM379  FLJ11996  3'  ACTGAAGTGTTGAAGAAGGAA  47048          C_   C_
                                 TTTCTTCTTT  CAT  CAGT
                                 ||||||||||  |||  ||||
                                 AAGGAAGAAG  GTG  GTCA
                                       TT   AA
GAM379  FLJ13782  3'  CAGATGGAAAGGGGGT      46698       TTTCTT       CA
                                 ACCCC     CTTTCCATC  G
                                 |||||     |||||||||  |
                                 TGGGG     GAAAGGTAG  C
                                    _______        AC
GAM379  FLJ13955  3'  GTGGAGAGAAGAAAGAGGT    45749     C
                                 ACC CTTTCTTCTTTCCAT
                                 ||| ||||||||||||||
                                 TGG GAAAGAAGAGAGGTG
                                   A
GAM379  FLJ21438  5'  GGCTGAAAGAGAAGAAAAAGG  62199    CC        C_  T
                                 CC  TTTCTTCTTT  CA CC
                                 ||  ||||||||||  || ||
                                 GG  AAAGAAGAGA  GT GG
                                  AA         AA  C
GAM379  KIAA0694  3'  ACTGAATGAACTAAGAAAGG   72960         CT   C  C
                                 CCTTTCTT  TTC AT CAGT
                                 ||||||||  ||| || ||||
                                 GGAAAGAA  AAG TA GTCA
                                       TC   _  A
GAM379  KIAA0794  3'  TTGGGAAAAGAAGAAA      81240          CCA
                                 TTTCTTCTTT   TCCAG
                                 ||||||||||   |||||
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                                AAAGAAGAAA  GGGTT
                                     A__
GAM379  KIAA0998 3' ACTGAATGAATTTGAAAGGG  31255      TTCT  C  C
                                CCCTTTC   TTC AT CAGT
                                |||||||   ||| || ||||
                                GGGAAAG   AAG TA GTCA
                                   TTT_  _ A
GAM379  KIAA1391 3' GGAGAAAGAAGAAAATGG   67852   CC       CA
                                CC  TTTCTTCTTTC  TCC
                                ||  ||||||||||  |||
                                GG  AAAGAAGAAAG  AGG
                                 TA        __
GAM379  KIAA1656 3' ACTGAATGGAAAGCAGGAAG  66356     T      C
                                CTTTCT CTTTCCAT CAGT
                                |||||| |||||||| ||||
                                GAAGGA GAAAGGTA GTCA
                                   C      A
GAM379  LSM5    3' CTGGAAAAAGAAGAAA     25569        CCA
                                TTTCTTCTTT  TCCAG
                                ||||||||||  |||||
                                AAAGAAGAAA  AGGTC
                                     A__
GAM379  MCJ     3' ACTGAAGGAAAAAAAAAGAGGG 26017    _   C  C    ATC
                                CCC CTTT TT TTTCC  CAGT
                                ||| |||| || |||||  ||||
                                GGG GAAA AA AAAGG  GTCA
                                 A   _ A    AA_
GAM379  MGC15606 3' ACTGGCTATCTAAGAAGAATGG 59517   T      TCCAT_
                                CC TTCTTCTT     CCAGT
                                || ||||||||     |||||
                                GG AAGAAGAA     GGTCA
                                 T      TCTATC
GAM379  MGC20460 5' CTGAAAGGAAAGAAGGAA   54907         ATC
                                TTTCTTCTTTCC  CAG
                                ||||||||||||  |||
                                AAGGAAGAAAGG  GTC
                                      AAA
GAM379  ORMDL3   3' ACTGAAGACAGAAAGAAGAAG 74796        CA __
                                TTTCTTCTTTC  TC  CAGT
                                ||||||||||  ||  ||||
                                GAAGAAGAAAG  AG  GTCA
                                      AC  AA
GAM379  PCDH10   5' CTGGAAGGAAAAAGAGA    53101      C    A
                                TTTCTT TTTCC TCCAG
                                |||||| ||||| |||||
                                AGAGAA AAAGG AGGTC
                                   _    A
GAM379  PCDH10   5' CTGGAAGGAAAAAGAGA    40822      C    A
                                TTTCTT TTTCC TCCAG
                                |||||| ||||| |||||
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                                AGAGAA AAAGG AGGTC
                                  _    A
GAM379  PDCD10   5' CTGGAAGAAGGAAGAGA    24274          CA
                                TTTCTTCTTTC  TCCAG
                                ||||||||||  |||||
                                AGAGAAGGAAG  AGGTC
                                     A_
GAM379  S164     5' CTGGAAGAAGAGAAAGG    61431       T   CCA
                                CCTTTCT CTTT   TCCAG
                                |||||||  ||||  |||||
                                GGAAAGA GAAG   AGGTC
                                  _   A__
GAM379  SERHL    3' ACTGGATGGAAAATAAAAGG  97348     CTTC
                                CCTTT   TTTCCATCCAGT
                                |||||   ||||||||||||
                                GGAAA   AAAGGTAGGTCA
                                   ATA_
GAM379  SRCRB4D  5' GCTGTGGAAAGAAAAGAAG   55797    C_      TC
                                CTTT  TTCTTTCCA  CAGT
                                ||||  |||||||||  ||||
                                GAAG  AAGAAAGGT  GTCG
                                  AA       __
GAM379  TED      3' CTGGACAAGAGAAGAGG    32267        CCA
                                TTTCTTCTTT   TCCAG
                                ||||||||||   |||||
                                GGAGAAGAGA   AGGTC
                                     AC_
GAM379  LOC120105 5' ACTGAATACTGTTAAGAAGGAG 76025         TC  TC___
           G                    CTTTCTTCTT  CA    CAGT
                                ||||||||||  ||    ||||
                                GGAGGAAGAA  GT    GTCA
                                     TT  CATAA
GAM379  LOC125270 3' ACTGGATGAATTAAAAAGAAA  74865       C  TC__
                                TTTCTT TT    CATCCAGT
                                ||||||  ||    ||||||||
                                AAAGAA AA    GTAGGTCA
                                   A  TTAA
GAM379  LOC131870 3' ACCAGATGAAAAGAAGGAG   75506         C    CA
                                TTTCTTCTTT CATC  GT
                                |||||||||| ||||  ||
                                GAGGAAGAAA GTAG  CA
                                     A    AC
GAM379  LOC135293 3' ACTGGGTGTAAGAAGAAA    76675         TC
                                TTTCTTCTT  CATCCAGT
                                |||||||||  ||||||||
                                AAAGAAGAA  GTGGGTCA
                                     T_
GAM379  LOC135932 5' CGGAGGAAAGGAAAAG      76697      C       A   A
                                CTTT TTCTTTCC TCC G
                                |||| |||||||| ||| |
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                                GAAA AGGAAAGG AGG C
                                  _      _  C
GAM379  LOC143392 5'  ACCGGATGGAAATGGGGAGA  83851       _       A
                                TTTCTTC TTTCCATCC GT
                                ||||||| ||||||||| ||
                                AGAGGGG AAAGGTAGG CA
                                    T       C
GAM379  LOC144811 3'  ACTAGATAATGGAAGTAAGAGG 84106    C  T    TTCC  C
          T                      ACC CTT CTTCT   ATC AGT
                                 ||| ||| |||||   ||| |||
                                 TGG GAA GAAGG   TAG TCA
                                   A  T    TAA_  A
GAM379  LOC146774 5'  GGAAAAGGAAGAAAGGGG   78697           CCA
                                 CCCCTTTCTTCTTT  TCC
                                 ||||||||||||||  |||
                                 GGGGAAAGAAGGAA  AGG
                                          A__
GAM379  LOC153077 3'  ACTGAGGTCAGAAAAAAGG   87104     C   TT  ATC
                                 CCTTT TTCT  CC  CAGT
                                 ||||| ||||  ||  ||||
                                 GGAAA AAGA  GG  GTCA
                                    A   CT  A__
GAM379  LOC154760 5'  CGGAGGAAAGGAAAAG     87453     C      A  A
                                 CTTT TTCTTTCC TCC G
                                 |||| |||||||| ||| |
                                 GAAA AGGAAAGG AGG C
                                   _      _  C
GAM379  LOC157381 3'  ACTGGATGACAGAGAAAG   87730      T  TTC
                                 CTTTCT CT   CATCCAGT
                                 |||||| ||  ||||||||
                                 GAAAGA GA   GTAGGTCA
                                    _ CA_
GAM379  LOC166042 5'  ACTGGATGTCCAGAAAAAGAGG 83503   C   C   TTC
                                 CC CTTT TTCT   CATCCAGT
                                 || |||| ||||   ||||||||
                                 GG GAAA AAGA   GTAGGTCA
                                  A   _   CCT
GAM379  LOC170372 5'  ACTGGCTGGAAAAGAAAGGG  76857        CT    T
                                 CCCTTTCTT  TTCCA CCAGT
                                 |||||||||  ||||| |||||
                                 GGGAAAGAA  AAGGT GGTCA
                                       __    C
GAM379  LOC197358 3'  ACTGGTGGAGAAAACAAAG   89410     C  C     T
                                 CTTT TT TTTCCA CCAGT
                                 |||| || |||||| |||||
                                 GAAA AA AGAGGT GGTCA
                                   C  A     _
GAM379  LOC200138 3'  ACTGGATGGCGTTGAAATGAAA 91538     __   TTT_
                                 TTTC  TTC   CCATCCAGT
                                 ||||  |||   |||||||||
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                                AAAG  AAG    GGTAGGTCA
                                  TA   TTGC
GAM379  LOC200314 3'  ACTGGATGAGAGCAAAAGGG   91585       CTT    C
                                CCCTTT   CTTTC ATCCAGT
                                ||||||   ||||| |||||||
                                GGGAAA   GAGAG TAGGTCA
                                   AC_    _
GAM379  LOC219287 3'  ACCGGATAACACCAGAAAGAGG 95216     _     TCTTTCC    A
          G                      CCC CTTTCT      ATCC GT
                                ||| ||||||      |||| ||
                                GGG GAAAGA      TAGG CA
                                  A     CCACAA_   C
GAM379  LOC221814 5'  ACTGGATGTTGTTAGAAAAAG  95553     C    TTC__
                                CTTT TTCT    CATCCAGT
                                |||| ||||    ||||||||
                                GAAA AAGA    GTAGGTCA
                                  _   TTGTT
GAM379  LOC222414 3'  CTAGATAGGAGGAAGGAGT    95974    C        TTCC   C
                                AC CCTTTCTTCT    ATC AG
                                || ||||||||||    ||| ||
                                TG GGAAGGAGGA    TAG TC
                                 A        _____  A
GAM379  LOC51075  3'  ACTGGAGCAAAGAAAGAGA    32553       _   CCA
                                TTTCTT CTTT   TCCAGT
                                |||||| ||||   ||||||
                                AGAGAA GAAA   AGGTCA
                                   A   CG_
GAM379  LOC90917  3'  CTGGACAGGAGGAAAAGG    64985      CT     CA
                                CCTTT  TCTTTC  TCCAG
                                |||||  ||||||  |||||
                                GGAAA  AGGAGG  AGGTC
                                   __     AC
GAM379  LOC92979  3'  ATGCCAGAAGAAAGGGG     57251           TTC
                                CCCCTTTCTTCT   CAT
                                ||||||||||||   |||
                                GGGGAAAGAAGA   GTA
                                       CC_
GAM380  A1BG     3'  CCCAAGTAGCTGGGAGCCTGGG 56283       TAG        CA
          CA                    TGCCTG   TCCCAGCTACT  GG
                                ||||||   ||||||||||| ||
                                ACGGGT   AGGGTCGATGA  CC
                                   CCG         AC
GAM380  A1BG     3'  CCTGAGTAGCTGGGACTACAGG 56286
          CA                    TGCCTGTAGTCCCAGCTACTCAGG
                                |||||||||||||||||||||||
                                ACGGACATCAGGGTCGATGAGTCC

GAM380  A1BG     3'  CCTGAGTAGCTGGGCTGACAGG 56287       _ T
          CA                    TGCCTGT AG CCCAGCTACTCAGG
                                |||||||  || ||||||||||||||
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                                ACGGACA TC GGGTCGATGAGTCC
                                    G  _
GAM380  ACADSB   3'  CCCAAGTAGCTGGAACTACAGG 9645          C       CA
           T                     GCCTGTAGT CCAGCTACT  GG
                                 ||||||||| |||||||||  ||
                                 TGGACATCA GGTCGATGA  CC
                                     A        AC
GAM380  ADAMTS4  3'  CCCGAGTAGCTGAGATTATAGG 18755          C       A
           CA                     TGCCTGTAGTC CAGCTACTC GG
                                  |||||||||||| ||||||||| ||
                                  ACGGATATTAG GTCGATGAG CC
                                      A        C
GAM380  ADAMTS4  3'  CCTGAGTAGCTGGGATTACAGG 18757
           C                      GCCTGTAGTCCCAGCTACTCAGG
                                  ||||||||||||||||||||||
                                  CGGACATTAGGGTCGATGAGTCC

GAM380  ADCY6    5'  CCTGAGTAGCTGGGATTACAGG 40948
           C                      GCCTGTAGTCCCAGCTACTCAGG
                                  ||||||||||||||||||||||
                                  CGGACATTAGGGTCGATGAGTCC

GAM380  AIM1     3'  CCCAAGTAGCTGGGACTATAGG 93460               CA
           CA                     TGCCTGTAGTCCCAGCTACT  GG
                                  |||||||||||||||||  ||
                                  ACGGATATCAGGGTCGATGA  CC
                                        AC
GAM380  ALDH1B1  3'  CCTGAGTAGCTGGGATTATAGG 7321
           TA                     TGCCTGTAGTCCCAGCTACTCAGG
                                  ||||||||||||||||||||||
                                  ATGGATATTAGGGTCGATGAGTCC

GAM380  ALOX15   3'  CCTGAGTAGCTGGGACTACAGG 8544
           C                      GCCTGTAGTCCCAGCTACTCAGG
                                  ||||||||||||||||||||||
                                  CGGACATCAGGGTCGATGAGTCC

GAM380  APAF1    3'  CCCAAGTAGCTGAGACTGCAGG 25968          C       CA
           CA                     TGCCTGTAGTC CAGCTACT  GG
                                  |||||||||| ||||||||  ||
                                  ACGGACGTCAG GTCGATGA  CC
                                      A        AC
GAM380  APAF1    3'  CCCGAGTAGCTGGGACTACAGG 25969               A
           T                      GCCTGTAGTCCCAGCTACTC GG
                                  |||||||||||||||||| ||
                                  TGGACATCAGGGTCGATGAG CC
                                        C
GAM380  APM1     3'  CCAAAGTGCTGGGATTACAGGC 17766             T  CA
           A                      TGCCTGTAGTCCCAGC ACT  GG
                                  |||||||||||||| |||  ||
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                                ACGGACATTAGGGTCG TGA  CC
                                      _  AA
GAM380  APM1    3'  CCAAAGTGCTGGGATTACAGGC 17767            T   CA
          A                    TGCCTGTAGTCCCAGC ACT  GG
                               ||||||||||||||| |||  ||
                               ACGGACATTAGGGTCG TGA  CC
                                      _  AA
GAM380  APM1    3'  CCCAAGTAGCTGGAACTACAGG 17772         C       CA
          C                    GCCTGTAGT CCAGCTACT  GG
                               |||||||| ||||||||  ||
                               CGGACATCA GGTCGATGA  CC
                                     A       AC
GAM380  APM1    3'  CCCGAGTAGCTGAGACTTCAG  17773    T   C       A
                               CTG AGTC CAGCTACTC GG
                               ||| |||| ||||||||| ||
                               GAC TCAG GTCGATGAG CC
                                 T   A       C
GAM380  APM1    3'  CCCGAGTAGCTGGGACCACAGG 17774       A          A
          T                    GCCTGT GTCCCAGCTACTC GG
                               |||||| |||||||||||| ||
                               TGGACA CAGGGTCGATGAG CC
                                  C          C
GAM380  APOL1   3'  CCCAAGTAGCTGGGACTACAGG 14733              CA
          C                    GCCTGTAGTCCCAGCTACT  GG
                               |||||||||||||||||  ||
                               CGGACATCAGGGTCGATGA  CC
                                     AC
GAM380  APPL    3'  CCCGAGTAGCTGGGACCACAGG 24945       A          A
                               CCTGT GTCCCAGCTACTC GG
                               ||||| |||||||||||| ||
                               GGACA CAGGGTCGATGAG CC
                                  C          C
GAM380  AQP6    3'  CCCAAGTAGCTGGGATTACAGG 54993              CA
          C                    GCCTGTAGTCCCAGCTACT  GG
                               |||||||||||||||||  ||
                               CGGACATTAGGGTCGATGA  CC
                                     AC
GAM380  AQP6    3'  CCCAAGTAGCTGGGATTACAGG 54994              CA
          C                    GCCTGTAGTCCCAGCTACT  GG
                               |||||||||||||||||  ||
                               CGGACATTAGGGTCGATGA  CC
                                     AC
GAM380  ARCN1   3'  CCAAAGTGTTGGGATTACAGGC 9746             T   CA
          A                    TGCCTGTAGTCCCAGC ACT  GG
                               |||||||||||||| |||  ||
                               ACGGACATTAGGGTTG TGA  CC
                                      _  AA
GAM380  ATM     3'  AGTGTGCTGGGATTACAGGCA  5288              _
                               TGCCTGTAGTCCCAGC TACT
                               |||||||||||||| ||||
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                                ACGGACATTAGGGTCG GTGA
                                        T
GAM380  ATP1B2   3'  CCCGAGTAGCTGGGACTACAGG 9831                A
          CA                    TGCCTGTAGTCCCAGCTACTC GG
                                |||||||||||||||||||| ||
                                ACGGACATCAGGGTCGATGAG CC
                                        C
GAM380  ATP6V1A1 3'  CCCGAGTAGCTGGGATTACAGG 9867                A
          CA                    TGCCTGTAGTCCCAGCTACTC GG
                                |||||||||||||||||||| ||
                                ACGGACATTAGGGTCGATGAG CC
                                        C
GAM380  ATP7A    3'  CCTGAGTAGCTAGGATTACAG  5319          C
                                CTGTAGTCC AGCTACTCAGG
                                ||||||||| ||||||||||
                                GACATTAGG TCGATGAGTCC
                                    A
GAM380  ATP8B2   3'  CCTGAGTAGCTGGGATTACAGG 65832
          CA                    TGCCTGTAGTCCCAGCTACTCAGG
                                |||||||||||||||||||||||
                                ACGGACATTAGGGTCGATGAGTCC

GAM380  AXL      3'  CCAAAGTGCTGAGATTACAGGC 41879          C   T   CA
          A                     TGCCTGTAGTC CAGC ACT  GG
                                |||||||||| |||| |||  ||
                                ACGGACATTAG GTCG TGA  CC
                                      A   _   AA
GAM380  AXL      3'  CCCAAGTAGCTGGGATTACAG  41881              CA
                                CTGTAGTCCCAGCTACT  GG
                                ||||||||||||||||  ||
                                GACATTAGGGTCGATGA  CC
                                        AC
GAM380  B4GALT5  3'  CCCGAGTAGCTGGGACTACAGG 17685                A
          T                     GCCTGTAGTCCCAGCTACTC GG
                                |||||||||||||||||||| ||
                                TGGACATCAGGGTCGATGAG CC
                                        C
GAM380  BAZ2B    5'  CCAAAGTGCTGGGATTACAGGC 26519            T   CA
          A                     TGCCTGTAGTCCCAGC ACT  GG
                                |||||||||||||||| |||  ||
                                ACGGACATTAGGGTCG TGA  CC
                                        _   AA
GAM380  BCL10    3'  CCAAAGTGCTGGGATTACAGAC 15367    C          T   CA
          A                     TG CTGTAGTCCCAGC ACT  GG
                                || |||||||||||| |||  ||
                                AC GACATTAGGGTCG TGA  CC
                                 A          _   AA
GAM380  BDP1     3'  CCGGGTAGCTGGGACTACAGGC 37965                A
          A                     TGCCTGTAGTCCCAGCTACTC GG
                                |||||||||||||||||||| ||
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                                ACGGACATCAGGGTCGATGGG CC
                                                    _
GAM380  BRCA1    3'  CCCAAGTAGCTGGGACTATTTT 24553    CT_          CA
                GC                   GC   GTAGTCCCAGCTACT  GG
                                     ||   ||||||||||||||  ||
                                     CG   TATCAGGGTCGATGA  CC
                                      TTT            AC
GAM380  C14orf1  3'  CCCAAGTAGCTGGGACTGCA  24165             CA
                                     TGTAGTCCCAGCTACT  GG
                                     ||||||||||||||||  ||
                                     ACGTCAGGGTCGATGA  CC
                                               AC
GAM380  C7       3'  CCCAAGCAGCTGGGATTACAG  6983            A  CA
                                     CTGTAGTCCCAGCT CT  GG
                                     ||||||||||||| ||  ||
                                     GACATTAGGGTCGA GA  CC
                                               C  AC
GAM380  CAMLG    3'  CCCAAGTAGCTGGGATTACAGG 9997                CA
                CA                   TGCCTGTAGTCCCAGCTACT  GG
                                     ||||||||||||||||||  ||
                                     ACGGACATTAGGGTCGATGA  CC
                                               AC
GAM380  CASP10   3'  CCCAAGTAGCTGAGACTACAGG 53251         C       CA
                T                    GCCTGTAGTC CAGCTACT  GG
                                     |||||||||| ||||||||  ||
                                     TGGACATCAG GTCGATGA  CC
                                           A       AC
GAM380  CASP10   3'  CCCAAGTAGCTGAGACTACAGG 53252         C       CA
                T                    GCCTGTAGTC CAGCTACT  GG
                                     |||||||||| ||||||||  ||
                                     TGGACATCAG GTCGATGA  CC
                                           A       AC
GAM380  CASP8    3'  CCCGAGTAGCTGGGACTACAGG 54073               A
                                     CCTGTAGTCCCAGCTACTC GG
                                     ||||||||||||||||||  ||
                                     GGACATCAGGGTCGATGAG CC
                                               C
GAM380  CASP8    3'  CCCGAGTAGCTGGGACTACAGG 8749                A
                                     CCTGTAGTCCCAGCTACTC GG
                                     ||||||||||||||||||  ||
                                     GGACATCAGGGTCGATGAG CC
                                               C
GAM380  CBFA2T2  3'  CCAAAGTGCCAGGATTACAGGC 18704          CA  T   CA
                A                    TGCCTGTAGTCC  GC ACT  GG
                                     ||||||||||||  || |||  ||
                                     ACGGACATTAGG  CG TGA  CC
                                           AC  _   AA
GAM380  CCNF     3'  CCAAAGTGCTGGGATTACAGGC 10068             T   CA
                A                    TGCCTGTAGTCCCAGC ACT  GG
                                     ||||||||||||||| |||  ||
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                                ACGGACATTAGGGTCG TGA  CC
                                        _  AA
GAM380  CCNF    3'  CCTGGGTAGCTGGGATTACAAG 10073    C
            CA                   TGC TGTAGTCCCAGCTACTCAGG
                                 ||| ||||||||||||||||||||
                                 ACG ACATTAGGGTCGATGGGTCC
                                   A
GAM380  CDC6    3'  CCCGAGTAGCTGGGATTACAG  8819              A
                                 CTGTAGTCCCAGCTACTC GG
                                 |||||||||||||||||  ||
                                 GACATTAGGGTCGATGAG CC
                                          C
GAM380  CDH1    3'  CCCAAGTAGCTGGGACCACAGG 16402       A         CA
            CA                   TGCCTGT GTCCCAGCTACT  GG
                                 |||||||  ||||||||||||  ||
                                 ACGGACA CAGGGTCGATGA  CC
                                     C          AC
GAM380  CDH17   3'  CCTAAGTAGCTGGGTTTACAGG 15783         T       C
            CA                   TGCCTGTAG CCCAGCTACT AGG
                                 |||||||||  ||||||||| |||
                                 ACGGACATT GGGTCGATGA TCC
                                       T        A
GAM380  CHRNB4  3'  CCCAAGTAGCTGGGATTACAG  7447              CA
                                 CTGTAGTCCCAGCTACT  GG
                                 ||||||||||||||||  ||
                                 GACATTAGGGTCGATGA  CC
                                          AC
GAM380  CIAS1   5'  CCTGAGTAGCTGGGATTACAGG 18095
            C                     GCCTGTAGTCCCAGCTACTCAGG
                                  ||||||||||||||||||||||
                                  CGGACATTAGGGTCGATGAGTCC

GAM380  CLECSF11 5'  CCTGAGTAGCCGAAATTACAG  56148       CCCA
                                 CTGTAGT   GCTACTCAGG
                                 |||||||   ||||||||||
                                 GACATTA   CGATGAGTCC
                                     AAGC
GAM380  CLECSF12 3'  CCCAAGTAGCTGGGATTACAGT 77207    C            CA
            CA                   TG CTGTAGTCCCAGCTACT  GG
                                 || ||||||||||||||||  ||
                                 AC GACATTAGGGTCGATGA  CC
                                  T             AC
GAM380  CNN2    3'  CCTGAGTAGCTAGGACTGCAG  16460         C
                                 CTGTAGTCC AGCTACTCAGG
                                 |||||||||  ||||||||||
                                 GACGTCAGG TCGATGAGTCC
                                       A
GAM380  COX15   3'  CCAAAGTGCTGAGATTACAGGC 16489          C   T  CA
            A                     TGCCTGTAGTC CAGC ACT  GG
                                  |||||||||||  ||||  |||  ||
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                                ACGGACATTAG GTCG TGA  CC
                                      A   _   AA
GAM380  COX15    3'  CCCGAGTAGCTGGGACTACAGG 55281                 A
            CA                    TGCCTGTAGTCCCAGCTACTC GG
                                  |||||||||||||||||||| ||
                                  ACGGACATCAGGGTCGATGAG CC
                                                C
GAM380  CR1      3'  AGTAGATGGGACTACAGGCA   6938              G
                                  TGCCTGTAGTCCCA CTACT
                                  |||||||||||||| |||||
                                  ACGGACATCAGGGT GATGA
                                        A
GAM380  CRTAP    3'  CCCGAGTACCTGGGATTACAGG 22077             C    A
            CA                    TGCCTGTAGTCCCAG TACTC GG
                                  |||||||||||||||| ||||| ||
                                  ACGGACATTAGGGTC ATGAG CC
                                        C    C
GAM380  CST      5'  AGTAACTAGGACTACAGGCA   17963           C  C
                                  TGCCTGTAGTCC AG TACT
                                  |||||||||||| || ||||
                                  ACGGACATCAGG TC ATGA
                                        A  A
GAM380  CTF1     3'  AGCAGCTGGGACTACAGGCA   9008              A
                                  TGCCTGTAGTCCCAGCT CT
                                  |||||||||||||||| ||
                                  ACGGACATCAGGGTCGA GA
                                           C
GAM380  CXCL16   3'  CCTAAGTAGCTGGGACTACAGG 42165               C
            T                      GCCTGTAGTCCCAGCTACT AGG
                                   |||||||||||||||||| |||
                                   TGGACATCAGGGTCGATGA TCC
                                           A
GAM380  CYP1A2   3'  CCCAAGCACCTGGGATTACAAG 69656     C         CTA  CA
            CA                    TGC TGTAGTCCCAG   CT  GG
                                  ||| |||||||||||   ||  ||
                                  ACG ACATTAGGGTC   GA  CC
                                    A          CAC  AC
GAM380  CYP1A2   3'  CCCAAGTAGCTGAGACTACAGG 7509          C       CA
            CA                    TGCCTGTAGTC CAGCTACT  GG
                                  |||||||||||| ||||||||  ||
                                  ACGGACATCAG GTCGATGA  CC
                                        A       AC
GAM380  CYP1A2   3'  CCCGAGTAGCTGGGACTATAG  7510               A
                                  CTGTAGTCCCAGCTACTC GG
                                  |||||||||||||||||| ||
                                  GATATCAGGGTCGATGAG CC
                                           C
GAM380  CYP2B6   3'  CCCAAGTAGCTGGGATTACAGG 7555                 CA
            CA                    TGCCTGTAGTCCCAGCTACT  GG
                                  |||||||||||||||||||  ||
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                                ACGGACATTAGGGTCGATGA  CC
                                      AC
GAM380  CYP2B6   3'  CCTAGTAGCTGGGATTACAGGC 7556              C
           A                   TGCCTGTAGTCCCAGCTACT AGG
                               |||||||||||||||||||| |||
                               ACGGACATTAGGGTCGATGA TCC
                                      _
GAM380  CYP51    3'  CCAAAGTGCTGGGATTACAGGC 7612            T  CA
           A                   TGCCTGTAGTCCCAGC ACT  GG
                               |||||||||||||||| |||  ||
                               ACGGACATTAGGGTCG TGA  CC
                                      _  AA
GAM380  CYP51    3'  CCCAAGTAGTTGGGATTACAGG 7614              CA
           CA                   TGCCTGTAGTCCCAGCTACT  GG
                               |||||||||||||||||||  ||
                               ACGGACATTAGGGTTGATGA  CC
                                      AC
GAM380  CYP8B1   3'  AGTAGCTGGGATTACAGGCA   16529
                               TGCCTGTAGTCCCAGCTACT
                               ||||||||||||||||||
                               ACGGACATTAGGGTCGATGA

GAM380  CYP8B1   3'  CCAAAGTTCTGGGATTACAGGC 16533           CT  CA
           A                   TGCCTGTAGTCCCAG  ACT  GG
                               |||||||||||||  |||  ||
                               ACGGACATTAGGGTC  TGA  CC
                                      T_  AA
GAM380  DFFB     3'  CCAAAGTGCTGGGATTACAGGC 88762           T  CA
           A                   TGCCTGTAGTCCCAGC ACT  GG
                               |||||||||||||||| |||  ||
                               ACGGACATTAGGGTCG TGA  CC
                                      _  AA
GAM380  DFFB     3'  CCCAAGTAGCTGGGATTACAGG 88764              CA
           CA                   TGCCTGTAGTCCCAGCTACT  GG
                               |||||||||||||||||||  ||
                               ACGGACATTAGGGTCGATGA  CC
                                      AC
GAM380  DFFB     3'  CCCGAGTAGCTGGGATTACAGG 88765               A
           CA                   TGCCTGTAGTCCCAGCTACTC GG
                               |||||||||||||||||||| ||
                               ACGGACATTAGGGTCGATGAG CC
                                      C
GAM380  DISC1    3'  CCCAAGTAGCTGGGGTTACAGG 38504        GT       CA
           CA                   TGCCTGTA  CCCAGCTACT  GG
                               ||||||||  ||||||||||  ||
                               ACGGACAT  GGGTCGATGA  CC
                                     TG        AC
GAM380  DNASE1L1 5'  CCAAAGTGCTGGGATTACAGGC 23015           T  CA
           A                   TGCCTGTAGTCCCAGC ACT  GG
                               |||||||||||||||| |||  ||
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                                ACGGACATTAGGGTCG TGA  CC
                                        _  AA
GAM380  DSC3    3'  CCAAAGTGCTGGGATTACAGGC 44616          T   CA
          A                      TGCCTGTAGTCCCAGC ACT  GG
                                 |||||||||||||||| |||  ||
                                 ACGGACATTAGGGTCG TGA  CC
                                        _  AA
GAM380  DSC3    3'  CCAAAGTGCTGGGATTACAGGC 44617          T   CA
          A                      TGCCTGTAGTCCCAGC ACT  GG
                                 |||||||||||||||| |||  ||
                                 ACGGACATTAGGGTCG TGA  CC
                                        _  AA
GAM380  DSC3    3'  CCTGAGTAGCTGGGACTACAGG 44619
          C                      GCCTGTAGTCCCAGCTACTCAGG
                                 |||||||||||||||||||||||
                                 CGGACATCAGGGTCGATGAGTCC

GAM380  DSC3    3'  CCTGAGTAGCTGGGACTACAGG 10437
          C                      GCCTGTAGTCCCAGCTACTCAGG
                                 |||||||||||||||||||||||
                                 CGGACATCAGGGTCGATGAGTCC

GAM380  DSCR3   3'  CCTGAGTAGCTGAGACTACAGG 21309        C
          T                      GCCTGTAGTC CAGCTACTCAGG
                                 |||||||||| ||||||||||
                                 TGGACATCAG GTCGATGAGTCC
                                       A
GAM380  EDG8    3'  CCTAGTAGCTGGGACTACAGGC 79148            C
          A                      TGCCTGTAGTCCCAGCTACT AGG
                                 |||||||||||||||||| |||
                                 ACGGACATCAGGGTCGATGA TCC
                                        _
GAM380  EHD2    3'  CCAAAGTGATGGGATTACAGGC 28218          GC   CA
          A                      TGCCTGTAGTCCCA  TACT  GG
                                 ||||||||||||  ||||  ||
                                 ACGGACATTAGGGT  GTGA  CC
                                       A_   AA
GAM380  EHD2    3'  CCTGAGTAGCTGGGACTGCAGG 28221
          CA                       TGCCTGTAGTCCCAGCTACTCAGG
                                   |||||||||||||||||||||||
                                   ACGGACGTCAGGGTCGATGAGTCC

GAM380  EIF2S3  3'  CCGAGTAGCTGAGATTACAG  9206       C      A
                                 CTGTAGTC CAGCTACTC GG
                                 ||||||||  |||||||| ||
                                 GACATTAG GTCGATGAG CC
                                      A       C
GAM380  ENDOGL1 3'  CCTGAGCAGCTGGGACTACAGG 18822            A
          CA                       TGCCTGTAGTCCCAGCT CTCAGG
                                   ||||||||||||||||| ||||||
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                                ACGGACATCAGGGTCGA GAGTCC
                                        C
GAM380  F2RL2    3'  CCCAAGTAGCTGGGATTACA  15895            CA
                                TGTAGTCCCAGCTACT  GG
                                ||||||||||||||||  ||
                                ACATTAGGGTCGATGA  CC
                                        AC
GAM380  F2RL3    3'  CCCAAGTAGCTGGGATAACAGG 15509       A         CA
          C                      GCCTGT GTCCCAGCTACT  GG
                                ||||||| ||||||||||||  ||
                                CGGACA TAGGGTCGATGA  CC
                                   A          AC
GAM380  F3       3'  CCCGAGTAGCTGGGATTACAG  67676             A
                                CTGTAGTCCCAGCTACTC GG
                                |||||||||||||||||| ||
                                GACATTAGGGTCGATGAG CC
                                        C
GAM380  FANCE    3'  CCCAAGTAGCTGGGACTACATG 41898     C            CA
          CA                      TGC TGTAGTCCCAGCTACT  GG
                                ||| ||||||||||||||  ||
                                ACG ACATCAGGGTCGATGA  CC
                                  T            AC
GAM380  FANCF    3'  CCCAAGTAGCTGGGATTACAG  42977              CA
                                CTGTAGTCCCAGCTACT  GG
                                ||||||||||||||||  ||
                                GACATTAGGGTCGATGA  CC
                                        AC
GAM380  FCAR     3'  CCCAAGTAGCTGGAATTACAGG 56568         C       CA
          CA                      TGCCTGTAGT CCAGCTACT  GG
                                |||||||||| |||||||||  ||
                                ACGGACATTA GGTCGATGA  CC
                                     A        AC
GAM380  FCRH1    3'  CTGAGTAGCTGGGACTACAGGC 54725
          A                       TGCCTGTAGTCCCAGCTACTCAG
                                |||||||||||||||||||||||
                                ACGGACATCAGGGTCGATGAGTC

GAM380  FEZ1     3'  CCTGAGTAGCTGGGACTACAGG 18784
          T                       GCCTGTAGTCCCAGCTACTCAGG
                                |||||||||||||||||||||||
                                TGGACATCAGGGTCGATGAGTCC

GAM380  FGF5     3'  CCCAAGTAGCTGGGATTACAG  53655              CA
                                CTGTAGTCCCAGCTACT  GG
                                ||||||||||||||||  ||
                                GACATTAGGGTCGATGA  CC
                                        AC
GAM380  FGF5     3'  CCCAAGTAGCTGGGATTACAG  53656              CA
                                CTGTAGTCCCAGCTACT  GG
                                ||||||||||||||||  ||
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                                GACATTAGGGTCGATGA  CC
                                      AC
GAM380  FHL2    5'  CCCAAGTAGCTGGGACTACAGG 9366                CA
          T                    GCCTGTAGTCCCAGCTACT  GG
                               ||||||||||||||||||  ||
                               TGGACATCAGGGTCGATGA  CC
                                     AC
GAM380  FSHPRH1  5'  CCTGAGTAGATGGGACTACAGG 23066            G
          TA                   TGCCTGTAGTCCCA CTACTCAGG
                               |||||||||||||| |||||||||
                               ATGGACATCAGGGT GATGAGTCC
                                     A
GAM380  FUT1    3'  CCTGAGTAGATGGGACTACAGG 5590              G
          CA                   TGCCTGTAGTCCCA CTACTCAGG
                               |||||||||||||| |||||||||
                               ACGGACATCAGGGT GATGAGTCC
                                     A
GAM380  FUT1    3'  CCTGAGTAGCTGGGACTACAGG 5591
          C                    GCCTGTAGTCCCAGCTACTCAGG
                               ||||||||||||||||||||||
                               CGGACATCAGGGTCGATGAGTCC

GAM380  G6PC    3'  CCAAGGTGCTAGGATTACAGGC 5655          C   T   CA
          A                    TGCCTGTAGTCC AGC ACT  GG
                               |||||||||||| ||| |||  ||
                               ACGGACATTAGG TCG TGG  CC
                                     A   _   AA
GAM380  GABRE   5'  CCTGAGTAATTATGACCACA  18280    A   CC  C
                               TGT GTC  AG TACTCAGG
                               ||| |||  || ||||||||
                               ACA CAG  TT ATGAGTCC
                                 C   TA  A
GAM380  GABRE   5'  CCTGAGTAATTATGACCACA  42071    A   CC  C
                               TGT GTC  AG TACTCAGG
                               ||| |||  || ||||||||
                               ACA CAG  TT ATGAGTCC
                                 C   TA  A
GAM380  GHR     3'  CCTGAGTAGCTGGGACTACAGG 5698
          CA                   TGCCTGTAGTCCCAGCTACTCAGG
                               ||||||||||||||||||||||
                               ACGGACATCAGGGTCGATGAGTCC

GAM380  GM2A    3'  CCCAAGTAGCTTGGACTACAGG 68378          C      CA
          C                    GCCTGTAGTCC AGCTACT  GG
                               |||||||||| |||||||  ||
                               CGGACATCAGG TCGATGA  CC
                                     T      AC
GAM380  GPR4    3'  CCCGAGTAGCTGGGACCACA  60575    A          A
                               TGT GTCCCAGCTACTC GG
                               ||| ||||||||||||| ||
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                                ACA CAGGGTCGATGAG CC
                                  C           C
GAM380  GPR56    5'  CCGAGTAGCTGGGATTACAG  20270                A
                                CTGTAGTCCCAGCTACTC GG
                                |||||||||||||||||| ||
                                GACATTAGGGTCGATGAG CC
                                        C
GAM380  GPR81    3'  CCCGAGTAGCTGGGATTAGAGG 51743      G           A
              C                  GCCT TAGTCCCAGCTACTC GG
                                 |||| |||||||||||||| ||
                                 CGGA ATTAGGGTCGATGAG CC
                                   G            C
GAM380  GRAF     3'  CCCAAGTAGCTGGGACTGCAGG 31228                CA
              CA                   TGCCTGTAGTCCCAGCTACT  GG
                                   |||||||||||||||||||  ||
                                   ACGGACGTCAGGGTCGATGA  CC
                                          AC
GAM380  HCS      3'  AGTAGCTGGGATTACAAGCA  38967     C
                                 TGC TGTAGTCCCAGCTACT
                                 ||| ||||||||||||||
                                 ACG ACATTAGGGTCGATGA
                                   A
GAM380  HCS      3'  CCTGAGTAGCTGGGATTGCAGG 38976
              CA                   TGCCTGTAGTCCCAGCTACTCAGG
                                   ||||||||||||||||||||||||
                                   ACGGACGTTAGGGTCGATGAGTCC

GAM380  HLCS     5'  CCCGAGTAGCTGGGACTACAGG 6410                 A
              T                    GCCTGTAGTCCCAGCTACTC GG
                                   |||||||||||||||||| ||
                                   TGGACATCAGGGTCGATGAG CC
                                          C
GAM380  HTR1D    3'  CCAAAGTGCTGGGATTACAGGC 7840              T   CA
              A                    TGCCTGTAGTCCCAGC ACT  GG
                                   |||||||||||||| |||  ||
                                   ACGGACATTAGGGTCG TGA  CC
                                         _   AA
GAM380  HTR2C    3'  CTGGTTAACCGGGACTACAG   7870          AGCT_  T
                                 CTGTAGTCCC     AC CAG
                                 |||||||||      || |||
                                 GACATCAGGG     TG GTC
                                      CCAAT  _
GAM380  HUNK     3'  CCCAAGTAGCTGGGACTACAG  28182              CA
                                 CTGTAGTCCCAGCTACT  GG
                                 ||||||||||||||||  ||
                                 GACATCAGGGTCGATGA  CC
                                        AC
GAM380  ICAM1    3'  CCTGAGTAGCTGGGACCATAGG 72035       A
              C                    GCCTGT GTCCCAGCTACTCAGG
                                   |||||| ||||||||||||||||
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                                CGGATA CAGGGTCGATGAGTCC
                                   C
GAM380  IGF1    3'  CCCAAATTGCTGGGATTACAGG 7068              TACTCA
            CA                   TGCCTGTAGTCCCAGC     GG
                                 ||||||||||||||||     ||
                                 ACGGACATTAGGGTCG     CC
                                          TTAAAC
GAM380  IGF1    3'  CCTGAGTAGCTGGGATTACAGG 7070
            CA                   TGCCTGTAGTCCCAGCTACTCAGG
                                 ||||||||||||||||||||||||
                                 ACGGACATTAGGGTCGATGAGTCC

GAM380  INMT    3'  CCGTGTAGCTGGGACTACAGGC 23212               TCA
            A                    TGCCTGTAGTCCCAGCTAC   GG
                                 ||||||||||||||||||   ||
                                 ACGGACATCAGGGTCGATG   CC
                                          TG_
GAM380  INMT    3'  CCTGAGTAGCTGGGACTACAGG 23214
                                 CCTGTAGTCCCAGCTACTCAGG
                                 ||||||||||||||||||||
                                 GGACATCAGGGTCGATGAGTCC

GAM380  ITGAM   3'  CCTGAGTAGCTGGGACTACAGG 72309
            CA                   TGCCTGTAGTCCCAGCTACTCAGG
                                 ||||||||||||||||||||||||
                                 ACGGACATCAGGGTCGATGAGTCC

GAM380  JAK3    3'  CCCGAGTAGCTGGGATTACAG  5829                A
                                 CTGTAGTCCCAGCTACTC GG
                                 |||||||||||||||||  ||
                                 GACATTAGGGTCGATGAG CC
                                          C
GAM380  JRK     3'  CCTGAGTAGCTGGGACTAGAGG 87823       G
            CA                   TGCCT TAGTCCCAGCTACTCAGG
                                 |||||  ||||||||||||||||||
                                 ACGGA ATCAGGGTCGATGAGTCC
                                    G
GAM380  KLRD1   3'  CCCAAGTAGCTAGGACTGCAGG 24707           C       CA
            CA                   TGCCTGTAGTCC AGCTACT  GG
                                 ||||||||||| |||||||  ||
                                 ACGGACGTCAGG TCGATGA  CC
                                        A      AC
GAM380  LLGL1   3'  CCCAAGTAGCTGGGACTACAGG 67417                CA
            C                    GCCTGTAGTCCCAGCTACT  GG
                                 ||||||||||||||||||  ||
                                 CGGACATCAGGGTCGATGA  CC
                                          AC
GAM380  LNK     3'  AGTAGCTGGGATTACAAGCA  19632     C
                                 TGC TGTAGTCCCAGCTACT
                                 ||| ||||||||||||||
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                                ACG ACATTAGGGTCGATGA
                                  A
GAM380  LTB4R    5'  CCCAAGTAGCTGAGACTACAGG 7461          C       CA
                CA                TGCCTGTAGTC CAGCTACT  GG
                                  |||||||||| ||||||||  ||
                                  ACGGACATCAG GTCGATGA  CC
                                        A       AC
GAM380  LYZ      3'  CCCGAGTAGCTGGGATTACGGG 5894                A
                C                 GCCTGTAGTCCCAGCTACTC GG
                                  |||||||||||||||||||| ||
                                  CGGGCATTAGGGTCGATGAG CC
                                              C
GAM380  MAK      3'  CCCGAGTAGCTGGGATTAGAGG 20944      G          A
                C                 GCCT TAGTCCCAGCTACTC GG
                                  |||| |||||||||||||| ||
                                  CGGA ATTAGGGTCGATGAG CC
                                    G             C
GAM380  MDM2     3'  CCAAAGTGCTGGGATTACAGGC 11491             T   CA
                A                 TGCCTGTAGTCCCAGC ACT  GG
                                  |||||||||||||||| |||  ||
                                  ACGGACATTAGGGTCG TGA  CC
                                              _  AA
GAM380  MEF2A    5'  CCCGAGTAGCTGGGATTACAGG 19998               A
                C                 GCCTGTAGTCCCAGCTACTC GG
                                  |||||||||||||||||||| ||
                                  CGGACATTAGGGTCGATGAG CC
                                              C
GAM380  MEFV     3'  CCAAAGTGCAGGGATTACAGGC 5931           A  T   CA
                A                 TGCCTGTAGTCCC GC ACT  GG
                                  |||||||||||| || |||  ||
                                  ACGGACATTAGGG CG TGA  CC
                                            A  _  AA
GAM380  MEFV     3'  CCAAAGTGCTGGGATTACAGGC 5932              T   CA
                A                 TGCCTGTAGTCCCAGC ACT  GG
                                  |||||||||||||||| |||  ||
                                  ACGGACATTAGGGTCG TGA  CC
                                              _  AA
GAM380  MEFV     3'  CCTGAGCAGCTGGGATTACAG  5935            A
                                  CTGTAGTCCCAGCT CTCAGG
                                  |||||||||||||| ||||||
                                  GACATTAGGGTCGA GAGTCC
                                            C
GAM380  MFI2     3'  CCTGAGTAGCTGGGATGACAGG 53970       A
                C                 GCCTGT GTCCCAGCTACTCAGG
                                  |||||| ||||||||||||||||
                                  CGGACA TAGGGTCGATGAGTCC
                                     G
GAM380  MHC2TA   3'  CCCGAATAGCTGGGACTACAGG 5975              C  A
                T                 GCCTGTAGTCCCAGCTA TC GG
                                  |||||||||||||||| || ||
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                                TGGACATCAGGGTCGAT AG CC
                                      A  C
GAM380  MHC2TA   3'  CCCGAGTAGCTGGGACTACAGG 5976                A
           CA                  TGCCTGTAGTCCCAGCTACTC GG
                               |||||||||||||||||||| ||
                               ACGGACATCAGGGTCGATGAG CC
                                        C
GAM380  MICB     3'  CCCGAATAGCTGGGATTACAGA 21020    C          C  A
           CA                  TG CTGTAGTCCCAGCTA TC GG
                               || ||||||||||||||| || ||
                               AC GACATTAGGGTCGAT AG CC
                                A           A  C
GAM380  MLANA    3'  CCTGAGTAGCTGGGATTACAGG 19761
           C                   GCCTGTAGTCCCAGCTACTCAGG
                               |||||||||||||||||||||||
                               CGGACATTAGGGTCGATGAGTCC

GAM380  MPL      3'  CCAAAGTGTTAGGATTACAGGC 19343          C   T   CA
           A                   TGCCTGTAGTCC AGC ACT  GG
                               ||||||||||| ||| |||  ||
                               ACGGACATTAGG TTG TGA  CC
                                      A  _  AA
GAM380  MPL      3'  CCCAAGTAGCTGGGAGTACAGC 19349    C   G        CA
                               GC TGTA TCCCAGCTACT  GG
                               || |||| ||||||||||  ||
                               CG ACAT AGGGTCGATGA  CC
                                _   G         AC
GAM380  NCOA6    5'  CCCAAGTGGCTGGGACTGCAGG 26832               CA
           CA                  TGCCTGTAGTCCCAGCTACT  GG
                               |||||||||||||||||||  ||
                               ACGGACGTCAGGGTCGGTGA  CC
                                        AC
GAM380  NDRG3    3'  CCAAAGTGCTGGGATTACAGGC 42762             T  CA
           A                   TGCCTGTAGTCCCAGC ACT  GG
                               |||||||||||||| |||  ||
                               ACGGACATTAGGGTCG TGA  CC
                                      _  AA
GAM380  NDRG3    3'  CCCGAGTAGCTGAGACTACAGG 42763          C       A
           CA                  TGCCTGTAGTC CAGCTACTC GG
                               |||||||||| |||||||| ||
                               ACGGACATCAG GTCGATGAG CC
                                      A       C
GAM380  NPR2L    3'  CCAGAGTGCTGGGATTACAGGC 22592             T   A
           A                   TGCCTGTAGTCCCAGC ACTC GG
                               |||||||||||||| |||| ||
                               ACGGACATTAGGGTCG TGAG CC
                                        _   A
GAM380  ORC1L    3'  CCCAGGTGGCTGAAACTACAGG 15982          CC      CA
           CA                  TGCCTGTAGT  CAGCTACT  GG
                               |||||||||  ||||||||  ||
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                                ACGGACATCA  GTCGGTGG  CC
                                     AA       AC
GAM380  PCDHA9   3'  CCCGAGTAGCTGGGACTACAGG 49837                A
          C                      GCCTGTAGTCCCAGCTACTC GG
                                 |||||||||||||||||||| ||
                                 CGGACATCAGGGTCGATGAG CC
                                                C
GAM380  PCDHA9   3'  CCTGAGTAGCTGGGATTATAGG 49840
          CA                     TGCCTGTAGTCCCAGCTACTCAGG
                                 |||||||||||||||||||||||||
                                 ACGGATATTAGGGTCGATGAGTCC

GAM380  PCDHB11  3'  AGTAGCTGGGACTACAGGC   38916
                                 GCCTGTAGTCCCAGCTACT
                                 ||||||||||||||||||
                                 CGGACATCAGGGTCGATGA

GAM380  PCDHB11  3'  CCCGAGTAGCTGGCATTACAGG 38918          C        A
          C                      GCCTGTAGT CCAGCTACTC GG
                                 ||||||||| |||||||||| ||
                                 CGGACATTA GGTCGATGAG CC
                                      C         C
GAM380  PDE6B    3'  CCTGAAGTGCTGGGATTACAGG 6074              T  _
          CA                     TGCCTGTAGTCCCAGC ACT CAGG
                                 |||||||||||||||| ||| ||||
                                 ACGGACATTAGGGTCG TGA GTCC
                                                _  A
GAM380  PDE6B    3'  CCTGAGTAGCTGGGACTACAGG 6075
          C                      GCCTGTAGTCCCAGCTACTCAGG
                                 |||||||||||||||||||||||||
                                 CGGACATCAGGGTCGATGAGTCC

GAM380  PER2     3'  CCTGAGTAGCTGGGACCACAGG 43349        A
          C                      GCCTGT GTCCCAGCTACTCAGG
                                 |||||| ||||||||||||||||
                                 CGGACA CAGGGTCGATGAGTCC
                                    C
GAM380  PIGR     3'  CCCAAGTAGCTGGGACTACAGG 72992               CA
          C                      GCCTGTAGTCCCAGCTACT  GG
                                 |||||||||||||||||  ||
                                 CGGACATCAGGGTCGATGA  CC
                                                AC
GAM380  PIK3C2B  3'  CCCGAGTAGCTGGGATTACAGG 12094                A
          CA                     TGCCTGTAGTCCCAGCTACTC GG
                                 |||||||||||||||||||| ||
                                 ACGGACATTAGGGTCGATGAG CC
                                                C
GAM380  PIK3CD   3'  CCAAAGTGCTGGGATTACAGGC 18486             T  CA
          A                      TGCCTGTAGTCCCAGC ACT  GG
                                 |||||||||||||||| |||  ||
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                                ACGGACATTAGGGTCG TGA  CC
                                        _  AA
GAM380  PIK3CD   3'  CCTGAGTAGCTGGGATTACAG  18489
                                CTGTAGTCCCAGCTACTCAGG
                                ||||||||||||||||||||
                                GACATTAGGGTCGATGAGTCC

GAM380  POU2AF1  3'  CCCGAGTAGCTGGGATTACAG  21736              A
                                CTGTAGTCCCAGCTACTC GG
                                |||||||||||||||||  ||
                                GACATTAGGGTCGATGAG CC
                                        C
GAM380  PPEF2    3'  CCAAAGTGCTGGGATTACAGGC 21772            T  CA
           A                     TGCCTGTAGTCCCAGC ACT  GG
                                |||||||||||||||  |||  ||
                                ACGGACATTAGGGTCG TGA  CC
                                        _  AA
GAM380  PPEF2    3'  CCTGAGTAGCTGGGATTACAGG 21774
           CA                     TGCCTGTAGTCCCAGCTACTCAGG
                                |||||||||||||||||||||||
                                ACGGACATTAGGGTCGATGAGTCC

GAM380  PPID     3'  CCCAAGTAGCTGGGATTACAGG 88823              CA
           CA                     TGCCTGTAGTCCCAGCTACT  GG
                                |||||||||||||||||  ||
                                ACGGACATTAGGGTCGATGA  CC
                                        AC
GAM380  PPP1R12B 3'  CCCGAGCAGCTAGGACTGCAG  50350        C   A  A
                                CTGTAGTCC AGCT CTC GG
                                |||||||| |||| ||| ||
                                GACGTCAGG TCGA GAG CC
                                     A   C  C
GAM380  PRKR     3'  CCTGAGTAGCTGGATTACAGGC 12345          C
           A                     TGCCTGTAGTCC AGCTACTCAGG
                                |||||||||||| ||||||||||
                                ACGGACATTAGG TCGATGAGTCC
                                        _
GAM380  PRKWNK3  3'  CCTGAGTAGCTGGGACTACAGG 62231
           C                      GCCTGTAGTCCCAGCTACTCAGG
                                |||||||||||||||||||||||
                                CGGACATCAGGGTCGATGAGTCC

GAM380  PSMB2    3'  CCTGAGTAGCTGGGATTACAGG 12467
           C                      GCCTGTAGTCCCAGCTACTCAGG
                                |||||||||||||||||||||||
                                CGGACATTAGGGTCGATGAGTCC

GAM380  PTGES    3'  CCTGAGTAGCTGGGATTACAGG 18059
           C                      GCCTGTAGTCCCAGCTACTCAGG
                                |||||||||||||||||||||||
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                                CGGACATTAGGGTCGATGAGTCC

GAM380  PTGIS    3'  CCAAAGTGCTAGGATTACAGGC 8198          C  T  CA
            A                 TGCCTGTAGTCC AGC ACT  GG
                              |||||||||||| ||| |||  ||
                              ACGGACATTAGG TCG TGA  CC
                                    A  _  AA
GAM380  PTGIS    3'  CCCAAGTAGCTGAGATTACAGG 8201         C      CA
            C                 GCCTGTAGTC CAGCTACT  GG
                              |||||||||| ||||||||  ||
                              CGGACATTAG GTCGATGA  CC
                                    A      AC
GAM380  PTGIS    3'  CCTGAGTAGCTGGGACTACAGG 8206
            CA                  TGCCTGTAGTCCCAGCTACTCAGG
                              |||||||||||||||||||||||
                              ACGGACATCAGGGTCGATGAGTCC

GAM380  PVR      3'  CCTGAGTAGCTATGACTACAGG 22491         CC
            TA                  TGCCTGTAGTC  AGCTACTCAGG
                              ||||||||||  ||||||||||
                              ATGGACATCAG  TCGATGAGTCC
                                    TA
GAM380  RAB36    3'  CCCAAGTAGCTGGGATTACAGG 18160           CA
            CA                  TGCCTGTAGTCCCAGCTACT  GG
                              ||||||||||||||||||  ||
                              ACGGACATTAGGGTCGATGA  CC
                                    AC
GAM380  RAB36    3'  CCCGAGTAGCTGGGACTACAGG 18161            A
            CA                  TGCCTGTAGTCCCAGCTACTC GG
                              |||||||||||||||||||| ||
                              ACGGACATCAGGGTCGATGAG CC
                                    C
GAM380  RABL2A   3'  CCAAAGTGCTGGGATTACAGGC 23993          T  CA
            A                 TGCCTGTAGTCCCAGC ACT  GG
                              |||||||||||||| |||  ||
                              ACGGACATTAGGGTCG TGA  CC
                                    _  AA
GAM380  RABL2B   3'  CCAAAGTGCTGGGATTACAGGC 23975          T  CA
            A                 TGCCTGTAGTCCCAGC ACT  GG
                              |||||||||||||| |||  ||
                              ACGGACATTAGGGTCG TGA  CC
                                    _  AA
GAM380  RBBP9    3'  CCAAAGTGTTGGGATTACAGGC 70686          T  CA
            A                 TGCCTGTAGTCCCAGC ACT  GG
                              |||||||||||||| |||  ||
                              ACGGACATTAGGGTTG TGA  CC
                                    _  AA
GAM380  RBM8A    3'  CCTAGTAGTTGGGATTACAGGC 18805            C
            A                 TGCCTGTAGTCCCAGCTACT AGG
                              |||||||||||||||||| |||
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                                ACGGACATTAGGGTTGATGA TCC
                                                 _
GAM380  RGS9     5'  CCCAAGTAGCTGGGACTACAGG 15173                CA
           T                    GCCTGTAGTCCCAGCTACT  GG
                                ||||||||||||||||||  ||
                                TGGACATCAGGGTCGATGA  CC
                                      AC
GAM380  RHD      3'  CCGAGTAGCTGGGATTACA   32821              A
                                TGTAGTCCCAGCTACTC GG
                                |||||||||||||||| ||
                                ACATTAGGGTCGATGAG CC
                                      C
GAM380  RHD      3'  GTAGCTGGGATTACAGGCA   32832
                                TGCCTGTAGTCCCAGCTAC
                                |||||||||||||||||
                                ACGGACATTAGGGTCGATG

GAM380  RHD      3'  GTAGCTGGGATTACAGGCA   32833
                                TGCCTGTAGTCCCAGCTAC
                                |||||||||||||||||
                                ACGGACATTAGGGTCGATG

GAM380  RHD      3'  CCCGAGTAGCTGGGATTACA  33140              A
                                TGTAGTCCCAGCTACTC GG
                                |||||||||||||||| ||
                                ACATTAGGGTCGATGAG CC
                                      C
GAM380  RP2      3'  CCTGAGTAGCTGGGAATACAGC 23599     C    G
           A                     TGC TGTA TCCCAGCTACTCAGG
                                ||| |||| ||||||||||||||
                                ACG ACAT AGGGTCGATGAGTCC
                                  _   A
GAM380  RPP30    3'  CCTGAGTAGCTGGGACTACAGG 22196
           C                     GCCTGTAGTCCCAGCTACTCAGG
                                |||||||||||||||||||||||
                                CGGACATCAGGGTCGATGAGTCC

GAM380  SAS      3'  CCAAGTAGCTGGGATTACAG  21097              CA
                                CTGTAGTCCCAGCTACT  GG
                                ||||||||||||||||  ||
                                GACATTAGGGTCGATGA  CC
                                      AC
GAM380  SCNN1G   3'  CCAAAGTGCAGGGATTACAGGC 8298           A  T   CA
           A                     TGCCTGTAGTCCC GC ACT  GG
                                |||||||||||| || |||  ||
                                ACGGACATTAGGG CG TGA  CC
                                      A  _   AA
GAM380  SEDL     3'  AGTAGCTGGGACTACAGGC   28077
                                GCCTGTAGTCCCAGCTACT
                                ||||||||||||||||||
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                                CGGACATCAGGGTCGATGA

GAM380  SEDL     3'  CCAAAGTGCTAGGATTACAGGC 28082          C   T   CA
              A                  TGCCTGTAGTCC AGC ACT  GG
                                 |||||||||||| ||| |||  ||
                                 ACGGACATTAGG TCG TGA  CC
                                        A   _   AA
GAM380  SEDL     3'  CCCGAGTAGCTGAGATTATAGG 28088        C       A
              C                  GCCTGTAGTC CAGCTACTC GG
                                 |||||||||| ||||||||| ||
                                 CGGATATTAG GTCGATGAG CC
                                       A        C
GAM380  SEDL     3'  CCCGAGTAGCTGGGATTACAGG 28089              A
              CA                   TGCCTGTAGTCCCAGCTACTC GG
                                   |||||||||||||||||||| ||
                                   ACGGACATTAGGGTCGATGAG CC
                                                C
GAM380  SEPN1    3'  CCCGAGTAGCTGGGATTACAG  66968              A
                                   CTGTAGTCCCAGCTACTC GG
                                   |||||||||||||||||| ||
                                   GACATTAGGGTCGATGAG CC
                                              C
GAM380  SERPINB9 3'  CCAAAGTGCTAGGATTACAGGC 16011          C   T   CA
              A                  TGCCTGTAGTCC AGC ACT  GG
                                 |||||||||||| ||| |||  ||
                                 ACGGACATTAGG TCG TGA  CC
                                        A   _   AA
GAM380  SERPINB9 3'  CCCAAGTAGCTGAGACTACAAG 16014    C      C       CA
              CA                   TGC TGTAGTC CAGCTACT  GG
                                   ||| ||||||| ||||||||  ||
                                   ACG ACATCAG GTCGATGA  CC
                                     A      A       AC
GAM380  SERPINB9 3'  CCCGAGTAGCTGGGACTACAGG 16015              A
              C                    GCCTGTAGTCCCAGCTACTC GG
                                   |||||||||||||||||| ||
                                   CGGACATCAGGGTCGATGAG CC
                                                C
GAM380  SH3BP2   3'  CCAAAGTGCTGGGATTACAGGC 13054            T   CA
              A                    TGCCTGTAGTCCCAGC ACT  GG
                                   |||||||||||||| |||  ||
                                   ACGGACATTAGGGTCG TGA  CC
                                              _   AA
GAM380  SH3BP2   3'  CCCGAGTAGCTGGGATTCCAGG 13057      T          A
              C                    GCCTG AGTCCCAGCTACTC GG
                                   ||||| |||||||||||||| ||
                                   CGGAC TTAGGGTCGATGAG CC
                                     C           C
GAM380  SHOX     3'  CCCGAGTAGCTGGGACTACAGG 6566               A
              CA                   TGCCTGTAGTCCCAGCTACTC GG
                                   |||||||||||||||||||| ||
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                                ACGGACATCAGGGTCGATGAG CC
                                                    C
GAM380  SHOX    3'  CCCGAGTAGCTGGGATTACAG  6567                A
                                CTGTAGTCCCAGCTACTC GG
                                |||||||||||||||||| ||
                                GACATTAGGGTCGATGAG CC
                                                    C
GAM380  SHOX    3'  CCTGAGTAGCTGGGACTACAGG 6570
            CA                    TGCCTGTAGTCCCAGCTACTCAGG
                                |||||||||||||||||||||||
                                ACGGACATCAGGGTCGATGAGTCC

GAM380  SIL     3'  CCCAGGTAGCTGGGATTACAGG 13154               CA
            CA                    TGCCTGTAGTCCCAGCTACT  GG
                                |||||||||||||||||||  ||
                                ACGGACATTAGGGTCGATGG  CC
                                                    AC
GAM380  SMAC    5'  CCCGAGTAGCTGGGATTACAGG 39580                 A
                                CCTGTAGTCCCAGCTACTC GG
                                |||||||||||||||||| ||
                                GGACATTAGGGTCGATGAG CC
                                                    C
GAM380  SMAC    5'  CCCGAGTAGCTGGGATTGCAGG 57996                 A
            C                    GCCTGTAGTCCCAGCTACTC GG
                                |||||||||||||||||| ||
                                CGGACGTTAGGGTCGATGAG CC
                                                    C
GAM380  SNAP23  3'  CCTGAGTAGCTGGGATTACAGG 15138
            C                    GCCTGTAGTCCCAGCTACTCAGG
                                |||||||||||||||||||||||
                                CGGACATTAGGGTCGATGAGTCC

GAM380  SNX15   3'  CCAAAGTGCTGAGATTACAGGC 74116          C   T   CA
            A                    TGCCTGTAGTC CAGC ACT  GG
                                |||||||||| |||| |||  ||
                                ACGGACATTAG GTCG TGA  CC
                                        A   _   AA
GAM380  SPN     3'  CCAAAGTGCTGAGATTACAGAC 13371    C      C   T   CA
            A                    TG CTGTAGTC CAGC ACT  GG
                                || ||||||| |||| |||  ||
                                AC GACATTAG GTCG TGA  CC
                                 A      A   _   AA
GAM380  SPN     3'  CCCGAGTAACTGAGATTACAGG 13374          C   C    A
            CA                    TGCCTGTAGTC CAG TACTC GG
                                |||||||||| ||| ||||| ||
                                ACGGACATTAG GTC ATGAG CC
                                        A  A    C
GAM380  STARD4  3'  CCTGAATAGCTGGGAATACAG  58246      G       C
                                CTGTA TCCCAGCTA TCAGG
                                ||||| ||||||||| |||||
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                                GACAT AGGGTCGAT AGTCC
                                  A       A
GAM380  SULT2B1  5' GTAACTGGGAGTACAGGCA  17225       G    C
                                TGCCTGTA TCCCAG TAC
                                |||||||| ||||||| |||
                                ACGGACAT AGGGTC ATG
                                    G    A
GAM380  TAF11    3' CCTGAGTAGCTAGGACTACAGG 20118          C
          CA                     TGCCTGTAGTCC AGCTACTCAGG
                                 |||||||||||| ||||||||||
                                 ACGGACATCAGG TCGATGAGTCC
                                       A
GAM380  TAF7L    3' CCTGAGTAGCTGGGACTACAG  46514
                                 CTGTAGTCCCAGCTACTCAGG
                                 ||||||||||||||||||||
                                 GACATCAGGGTCGATGAGTCC

GAM380  TAPBP    3' CCCGAGTAGCTGGGACTACAGG 13557              A
                                 CCTGTAGTCCCAGCTACTC GG
                                 |||||||||||||||||| ||
                                 GGACATCAGGGTCGATGAG CC
                                           C
GAM380  TAPBP    3' GTAGCTGGGATTACAGGCA   13581
                                 TGCCTGTAGTCCCAGCTAC
                                 |||||||||||||||||
                                 ACGGACATTAGGGTCGATG

GAM380  TAT      3' CCCAAGCAGTTGGGACTACAGG 6252            A  CA
          C                     GCCTGTAGTCCCAGCT CT  GG
                                |||||||||||||| ||  ||
                                CGGACATCAGGGTTGA GA  CC
                                      C  AC
GAM380  TBXA2R   3' CCAAAGTGCTGGGATCACAGGC 8346       A      T   CA
          A                     TGCCTGT GTCCCAGC ACT  GG
                                ||||||| |||||||| |||  ||
                                ACGGACA TAGGGTCG TGA  CC
                                    C       _  AA
GAM380  TBXA2R   3' CCCGAGCAGCTGGGATTACAGG 8351            A  A
          C                     GCCTGTAGTCCCAGCT CTC GG
                                |||||||||||||| ||| ||
                                CGGACATTAGGGTCGA GAG CC
                                      C  C
GAM380  TBXA2R   3' CCTGAGTAGCTGGGACTATAGG 8352
          C                     GCCTGTAGTCCCAGCTACTCAGG
                                ||||||||||||||||||||
                                CGGATATCAGGGTCGATGAGTCC

GAM380  TDGF1    3' CCCAAGTAACTGGGATTACAGG 13653           C   CA
          CA                     TGCCTGTAGTCCCAG TACT  GG
                                 |||||||||||||| ||||  ||
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                                ACGGACATTAGGGTC ATGA  CC
                                        A    AC
GAM380  TEM7     3'  CCTGAGTGGTTGGGACACAGGC 40252        A
                A                TGCCTGT GTCCCAGCTACTCAGG
                                 ||||||| ||||||||||||||||
                                 ACGGACA CAGGGTTGGTGAGTCC
                                        _
GAM380  TERF1    3'  GTAGCTGGGATTACAGGCA   34397
                                 TGCCTGTAGTCCCAGCTAC
                                 ||||||||||||||||||
                                 ACGGACATTAGGGTCGATG

GAM380  TERF2    3'  CCAAAGTGCTGGGATTACAGGC 20146             T  CA
                A                TGCCTGTAGTCCCAGC ACT  GG
                                 |||||||||||||||| |||  ||
                                 ACGGACATTAGGGTCG TGA  CC
                                        _  AA
GAM380  TERF2    3'  CCCGAGTAGCTGGGACTACAGG 20148               A
                C                GCCTGTAGTCCCAGCTACTC GG
                                 |||||||||||||||||||| ||
                                 CGGACATCAGGGTCGATGAG CC
                                          C
GAM380  TIM3     3'  CCTGAGTGGCTGGGATTACAGG 52355
                CA                TGCCTGTAGTCCCAGCTACTCAGG
                                  ||||||||||||||||||||||||
                                  ACGGACATTAGGGTCGGTGAGTCC

GAM380  TLR5     5'  CCCAAGTAGCTGGGATTACAG  13783             CA
                                 CTGTAGTCCCAGCTACT  GG
                                 ||||||||||||||||  ||
                                 GACATTAGGGTCGATGA  CC
                                          AC
GAM380  TMC1     5'  CCTGAGTAGCTGGGATTTCAGG 57708       T
                C                GCCTG AGTCCCAGCTACTCAGG
                                 ||||| ||||||||||||||||
                                 CGGAC TTAGGGTCGATGAGTCC
                                    T
GAM380  TMPRSS3  3'  CCACAGTGCTGGGATTACAGGC 44020             T  CA
                A                TGCCTGTAGTCCCAGC ACT  GG
                                 |||||||||||||||| |||  ||
                                 ACGGACATTAGGGTCG TGA  CC
                                        _  CA
GAM380  TNFRSF9  3'  CCAAAGTGCTGGGATTACAGAC 9579     C         T  CA
                A                TG CTGTAGTCCCAGC ACT  GG
                                 || |||||||||||| |||  ||
                                 AC GACATTAGGGTCG TGA  CC
                                  A          _  AA
GAM380  TNFRSF9  3'  CCTGAGTAGCTGGAACTACAAG 9581     _    C
                G                CCT GTAGT CCAGCTACTCAGG
                                 ||| ||||| ||||||||||||
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                                  GGA CATCA GGTCGATGAGTCC
                                    A   A
GAM380  TRAF5   3'  CCAAAGTGCTGAGATTACAGGC 17269          C   T  CA
          A                        TGCCTGTAGTC CAGC ACT  GG
                                   |||||||||| |||| |||  ||
                                   ACGGACATTAG GTCG TGA  CC
                                         A   _  AA
GAM380  TRAF5   3'  CCTGAGTAGCTGGGATTACAGG 17272
          C                        GCCTGTAGTCCCAGCTACTCAGG
                                   ||||||||||||||||||||||
                                   CGGACATTAGGGTCGATGAGTCC

GAM380  TRIM9   5'  CCCGAGTAGCTGGGATTACAGA 31447   C          A
          CA                       TG CTGTAGTCCCAGCTACTC GG
                                   || ||||||||||||||||| ||
                                   AC GACATTAGGGTCGATGAG CC
                                    A              C
GAM380  TRPV1   3'  CCCAAGTAGCTGGGATTACAGG 55664              CA
          CA                       TGCCTGTAGTCCCAGCTACT  GG
                                   |||||||||||||||||||  ||
                                   ACGGACATTAGGGTCGATGA  CC
                                              AC
GAM380  TUFT1   3'  CCCGAGTAGCTGGGACTACAGG 39671               A
          T                        GCCTGTAGTCCCAGCTACTC GG
                                   |||||||||||||||||| ||
                                   TGGACATCAGGGTCGATGAG CC
                                              C
GAM380  UGDH    3'  CCCAAGTAGCTGGGACTACAGG 13994              CA
          CA                       TGCCTGTAGTCCCAGCTACT  GG
                                   |||||||||||||||||||  ||
                                   ACGGACATCAGGGTCGATGA  CC
                                              AC
GAM380  VENTX2  3'  CCCAAGTAGCTAGGATTACAGA 27860   C      C      CA
          CA                       TG CTGTAGTCC AGCTACT  GG
                                   || |||||||| |||||||  ||
                                   AC GACATTAGG TCGATGA  CC
                                    A       A      AC
GAM380  VHL     3'  CCTGAGTAGCTGGGATTACAG  6849
                                   CTGTAGTCCCAGCTACTCAGG
                                   ||||||||||||||||||||
                                   GACATTAGGGTCGATGAGTCC

GAM380  WHSC1   5'  CCAAAGTGCTGGGATTACAGGC 24655             T  CA
          A                        TGCCTGTAGTCCCAGC ACT  GG
                                   |||||||||||||||| |||  ||
                                   ACGGACATTAGGGTCG TGA  CC
                                              _  AA
GAM380  WHSC1   3'  CCCGAGTAGCTGGGACTACAAG 24660   C          A
          C                        GC TGTAGTCCCAGCTACTC GG
                                   || ||||||||||||||||| ||
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                                CG ACATCAGGGTCGATGAG CC
                                 A             C
GAM380  XRCC2    3'  CCCAGGTAGCTGGGATTACAGG 19497                CA
                CA                TGCCTGTAGTCCCAGCTACT  GG
                                  ||||||||||||||||||  ||
                                  ACGGACATTAGGGTCGATGG  CC
                                              AC
GAM380  YES1     3'  CCCGAGTAGCTGGGACTACAGG 19533                A
                T                 GCCTGTAGTCCCAGCTACTC GG
                                  |||||||||||||||||| ||
                                  TGGACATCAGGGTCGATGAG CC
                                              C
GAM380  ZNF133   5'  CCCAAAATGCTGGGATTACAGG 14294              TACTCA
                CA                TGCCTGTAGTCCCAGC     GG
                                  ||||||||||||||||     ||
                                  ACGGACATTAGGGTCG     CC
                                          TAAAAC
GAM380  ZNF133   5'  CCCGAGTAGCTGGGATTACAGG 14295                A
                C                 GCCTGTAGTCCCAGCTACTC GG
                                  |||||||||||||||||| ||
                                  CGGACATTAGGGTCGATGAG CC
                                              C
GAM380  ZNF137   3'  CCCGAGTAGCTGGGATTACAGG 14308                A
                TA                TGCCTGTAGTCCCAGCTACTC GG
                                  |||||||||||||||||| ||
                                  ATGGACATTAGGGTCGATGAG CC
                                              C
GAM380  ZNF157   3'  CCCAAGTAGCTGGGATTACAG  14330              CA
                                  CTGTAGTCCCAGCTACT  GG
                                  ||||||||||||||||  ||
                                  GACATTAGGGTCGATGA  CC
                                              AC
GAM380  ZNF253   3'  CCCAAGTAGCTGGGATTACAG  41076              CA
                                  CTGTAGTCCCAGCTACT  GG
                                  ||||||||||||||||  ||
                                  GACATTAGGGTCGATGA  CC
                                              AC
GAM380  ZNF264   3'  CCTGAGTAGCTGGGATTACAG  14208
                                  CTGTAGTCCCAGCTACTCAGG
                                  ||||||||||||||||||||
                                  GACATTAGGGTCGATGAGTCC

GAM380  AAK1     3'  CCCGAGTAGCTGGGGTTACAGG 30518        GT        A
                C                 GCCTGTA  CCCAGCTACTC GG
                                  |||||||  |||||||||| ||
                                  CGGACAT  GGGTCGATGAG CC
                                      TG          C
GAM380  AP1S3    3'  CTGAGTAGCTGGGGCTACA   75427
                                  TGTAGTCCCAGCTACTCAG
                                  |||||||||||||||||
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                                ACATCGGGGTCGATGAGTC

GAM380  AP3S2    3'  AGTAGCTGGGATTACAGGCA   20646
                                TGCCTGTAGTCCCAGCTACT
                                ||||||||||||||||||||
                                ACGGACATTAGGGTCGATGA

GAM380  APOL2    3'  CCCGAGTAGCTGGGACTACAGG 48787                  A
              CA                  TGCCTGTAGTCCCAGCTACTC GG
                                  |||||||||||||||||||| ||
                                  ACGGACATCAGGGTCGATGAG CC
                                                       C
GAM380  APXL2    5'  CCCGAGTAGCTGGGACTACAGG 75674                  A
              C                   GCCTGTAGTCCCAGCTACTC GG
                                  |||||||||||||||||||| ||
                                  CGGACATCAGGGTCGATGAG CC
                                                       C
GAM380  ARHF     3'  CCTGAGTAGCTGGGACTACATG 39265    C
              C                   GC TGTAGTCCCAGCTACTCAGG
                                  || ||||||||||||||||||||
                                  CG ACATCAGGGTCGATGAGTCC
                                   T
GAM380  ARHGAP11A 3'  CCAAAGTGCTGGGATTACAGGC 29444              T   CA
              A                   TGCCTGTAGTCCCAGC ACT  GG
                                  |||||||||||||||| |||  ||
                                  ACGGACATTAGGGTCG TGA  CC
                                                _  AA
GAM380  ARHGAP11A 3'  CCCGAGTAGCTGGGACTACAGG 29446                A
              T                   GCCTGTAGTCCCAGCTACTC GG
                                  |||||||||||||||||||| ||
                                  TGGACATCAGGGTCGATGAG CC
                                                       C
GAM380  ARHGAP5   5'  CCCAAGTAGCTGGAATTACAGG 77599          C       CA
              C                   GCCTGTAGT CCAGCTACT  GG
                                  |||||||||  |||||||||  ||
                                  CGGACATTA GGTCGATGA  CC
                                        A        AC
GAM380  ARHGAP9   5'  CCCAAGTAGCTGGGACTACAGT 51661    __            CA
              AGC                   GC  CTGTAGTCCCAGCTACT  GG
                                    ||  ||||||||||||||||  ||
                                    CG  GACATCAGGGTCGATGA  CC
                                     AT              AC
GAM380  ASB16    3'  CCCAAGTAGCTGGGACCACAGG 55978        A         CA
              T                   GCCTGT GTCCCAGCTACT  GG
                                  ||||||  ||||||||||||  ||
                                  TGGACA CAGGGTCGATGA  CC
                                     C          AC
GAM380  ASB16    3'  CCGAGTAGCTGGGACTACAGGC 55979                  A
              A                   TGCCTGTAGTCCCAGCTACTC GG
                                  ||||||||||||||||||||| ||
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                                ACGGACATCAGGGTCGATGAG CC
                                                    _
GAM380  ASB16    5'  CCTAAGTAGCTGGGACTACAGG 55980              C
                                CCTGTAGTCCCAGCTACT AGG
                                |||||||||||||||||| |||
                                GGACATCAGGGTCGATGA TCC
                                           A
GAM380  ASE-1    3'  CCTGAGTAGCTGGGACTACAGG 24976
           C                     GCCTGTAGTCCCAGCTACTCAGG
                                |||||||||||||||||||||||
                                CGGACATCAGGGTCGATGAGTCC

GAM380  ATP1B4   3'  CCTGAGTAGCTGGGATTACAGG 24842
           CA                      TGCCTGTAGTCCCAGCTACTCAGG
                                |||||||||||||||||||||||
                                ACGGACATTAGGGTCGATGAGTCC

GAM380  BA108L7.2 3'  CCAAAGCACTGGGATTACAAGC 49067     C         CTA  CA
           A                     TGC TGTAGTCCCAG   CT  GG
                                ||| ||||||||||   ||  ||
                                ACG ACATTAGGGTC   GA  CC
                                  A          AC_  AA
GAM380  BAG5     3'  CCTGAGTAGCTGGGAGTACAGG 18037         G
           CA                      TGCCTGTA TCCCAGCTACTCAGG
                                |||||||| ||||||||||||||
                                ACGGACAT AGGGTCGATGAGTCC
                                     G
GAM380  BM-002   3'  GAGTAGCTGGGACTACAGGCA  34008
                                TGCCTGTAGTCCCAGCTACTC
                                ||||||||||||||||||||
                                ACGGACATCAGGGTCGATGAG

GAM380  C(27)-3BETA-HSD 3'  CCTGAACAGCTGGGACCACAGG 48052        A        AC
           T                     GCCTGT GTCCCAGCT  TCAGG
                                |||||| |||||||||  |||||
                                TGGACA CAGGGTCGA  AGTCC
                                   C         CA
GAM380  C11orf17  3'  CCCGAGTAGCTGGCACTACAGG 40579           C         A
           CA                      TGCCTGTAGT CCAGCTACTC GG
                                |||||||||| |||||||||| ||
                                ACGGACATCA GGTCGATGAG CC
                                      C         C
GAM380  C1orf24   3'  CCCAAGTAGCTGGAATTACAGC 54787     C      C        CA
           CA                      TG CTGTAGT CCAGCTACT  GG
                                || ||||||| |||||||||  ||
                                AC GACATTA GGTCGATGA  CC
                                  C       A         AC
GAM380  C20orf142 3'  CCAAAGTGCTGGGATTACAGGC 75278              T   CA
           A                     TGCCTGTAGTCCCAGC ACT  GG
                                |||||||||||||||| |||  ||
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                                ACGGACATTAGGGTCG TGA  CC
                                        _   AA
GAM380  C20orf142 3'  CCCGAGTAGCTGGGATTACAGG 75280                A
          CA                    TGCCTGTAGTCCCAGCTACTC GG
                                |||||||||||||||||||| ||
                                ACGGACATTAGGGTCGATGAG CC
                                        C
GAM380  C21orf25  3'  CCCAAGTAGCTGGGATTACAGG 64287                CA
          CA                    TGCCTGTAGTCCCAGCTACT  GG
                                |||||||||||||||||||  ||
                                ACGGACATTAGGGTCGATGA  CC
                                        AC
GAM380  C2F       3'  CCAAAGTGCTGGGATTACAGGC 22003              T   CA
          A                     TGCCTGTAGTCCCAGC ACT  GG
                                |||||||||||||||| |||  ||
                                ACGGACATTAGGGTCG TGA  CC
                                        _   AA
GAM380  C3F       3'  CCCAAGTAGCTGGGAATACAGG 20474          G         CA
          CA                    TGCCTGTA TCCCAGCTACT  GG
                                ||||||||| ||||||||||  ||
                                ACGGACAT AGGGTCGATGA  CC
                                     A          AC
GAM380  C6orf33   3'  CCAAAGTGTTGGGATTACAGAC 56709     C          T   CA
          A                     TG CTGTAGTCCCAGC ACT  GG
                                || ||||||||||||| |||  ||
                                AC GACATTAGGGTTG TGA  CC
                                 A           _   AA
GAM380  C6orf5    3'  CCCAAGTAGCTAGACCTATAGG 31981          _ CC      CA
          C                     GCCTGTAG TC  AGCTACT  GG
                                |||||||| ||  |||||||  ||
                                CGGATATC AG  TCGATGA  CC
                                     C  A_       AC
GAM380  C9orf9    3'  CCCAAGTAGCTGGGACTACAGG 39013                 CA
          C                     GCCTGTAGTCCCAGCTACT  GG
                                ||||||||||||||||||  ||
                                CGGACATCAGGGTCGATGA  CC
                                        AC
GAM380  C9orf9    3'  CCTGAGTAGCTGGAATTACAGG 39017          C
          C                     GCCTGTAGT CCAGCTACTCAGG
                                |||||||||  ||||||||||||
                                CGGACATTA GGTCGATGAGTCC
                                     A
GAM380  CARD6     3'  GAGTAGCTGGGATTACAGGCA  51843
                                TGCCTGTAGTCCCAGCTACTC
                                ||||||||||||||||||||
                                ACGGACATTAGGGTCGATGAG

GAM380  CDC14B    3'  CCTGAGTAGCTGGGATTATAGG 53988
          C                     GCCTGTAGTCCCAGCTACTCAGG
                                ||||||||||||||||||||||
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                                CGGATATTAGGGTCGATGAGTCC

GAM380  CEACAM8  3'  CCTGAGTAGCTGGGACTACAGG 10179
            C                    GCCTGTAGTCCCAGCTACTCAGG
                                 ||||||||||||||||||||||
                                 CGGACATCAGGGTCGATGAGTCC

GAM380  CHRAC1   3'  CCTGAGTAGCTGGGATTACAGG 34332
            C                    GCCTGTAGTCCCAGCTACTCAGG
                                 ||||||||||||||||||||||
                                 CGGACATTAGGGTCGATGAGTCC

GAM380  CHSY1    3'  CCCGAGTAGCTGGGATTACAGG 30566                A
            CA                    TGCCTGTAGTCCCAGCTACTC GG
                                 |||||||||||||||||||| ||
                                 ACGGACATTAGGGTCGATGAG CC
                                               C
GAM380  CIP29    3'  CCTGAGTAGCTGGGATTACAGG 51375
            CA                    TGCCTGTAGTCCCAGCTACTCAGG
                                 ||||||||||||||||||||||
                                 ACGGACATTAGGGTCGATGAGTCC

GAM380  CPSF2    3'  CCAAAGTGCTGGGATTACAGGC 62267             T  CA
            A                     TGCCTGTAGTCCCAGC ACT  GG
                                 |||||||||||||| |||  ||
                                 ACGGACATTAGGGTCG TGA  CC
                                              _  AA
GAM380  CPSF2    3'  CCCAAGTAGCTGGGACTACGGG 62269               CA
            CA                    TGCCTGTAGTCCCAGCTACT  GG
                                 ||||||||||||||||||  ||
                                 ACGGGCATCAGGGTCGATGA  CC
                                               AC
GAM380  CPSF2    3'  GAGTAGCTGGGATTACAGGCA  62272
                                 TGCCTGTAGTCCCAGCTACTC
                                 |||||||||||||||||||
                                 ACGGACATTAGGGTCGATGAG

GAM380  DCOHM    3'  CCAAAGTGCTGGGATTACAGGC 50515             T  CA
            A                     TGCCTGTAGTCCCAGC ACT  GG
                                 |||||||||||||| |||  ||
                                 ACGGACATTAGGGTCG TGA  CC
                                              _  AA
GAM380  DCOHM    3'  CTGAGTAGCTGAGATTACAGGC 50518          C
            A                     TGCCTGTAGTC CAGCTACTCAG
                                 |||||||||| ||||||||||
                                 ACGGACATTAG GTCGATGAGTC
                                        A
GAM380  DKFZp434A2417 3'  CCCAAGTAGCTGGGATTACAGG 66677                CA
            CA                    TGCCTGTAGTCCCAGCTACT  GG
                                 ||||||||||||||||||  ||
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                                ACGGACATTAGGGTCGATGA  CC
                                      AC
GAM380  DKFZP434B044 3'  CCCAAGTACCTGGGACTACAGG 49713          C    CA
          C                  GCCTGTAGTCCCAG TACT  GG
                             |||||||||||||| ||||  ||
                             CGGACATCAGGGTC ATGA  CC
                                   C    AC
GAM380  DKFZP434B044 3'  CCGAAGTGCTGGGATTACAGGC 49714            T   CA
          A                  TGCCTGTAGTCCCAGC ACT  GG
                             |||||||||||||||| |||  ||
                             ACGGACATTAGGGTCG TGA  CC
                                   _  AG
GAM380  DKFZP434B1727 3'  CCTGAGTAGCTGCAACTACAGA 50477    C      CC
          CA                  TG CTGTAGT  CAGCTACTCAGG
                              || |||||||  ||||||||||||
                              AC GACATCA  GTCGATGAGTCC
                               A       AC
GAM380  DKFZp434C0923 3'  CCTGAGTAGCTGGGATTATAGG 34648
          C                  GCCTGTAGTCCCAGCTACTCAGG
                             ||||||||||||||||||||||||
                             CGGATATTAGGGTCGATGAGTCC

GAM380  DKFZP434C212 3'  GAGTAGCTAGGACTACAGGC  69489          C
                             GCCTGTAGTCC AGCTACTC
                             |||||||||||  ||||||||
                             CGGACATCAGG TCGATGAG
                                    A
GAM380  DKFZP434D146 3'  CCCAAGTAGCTGGGATTG    32133          CA
                             TAGTCCCAGCTACT  GG
                             ||||||||||||||  ||
                             GTTAGGGTCGATGA  CC
                                   AC
GAM380  DKFZp434E2220 5'  CCCGAATAGCTGGGATTACAGG 34711            C  A
          C                  GCCTGTAGTCCCAGCTA TC GG
                             |||||||||||||||| || ||
                             CGGACATTAGGGTCGAT AG CC
                                   A  C
GAM380  DKFZP434F0318 3'  CCAAAGTGCTGGGATTACAGGC 48747            T   CA
          A                  TGCCTGTAGTCCCAGC ACT  GG
                             |||||||||||||||| |||  ||
                             ACGGACATTAGGGTCG TGA  CC
                                   _  AA
GAM380  DKFZP434F0318 3'  CCTGAGTAGCTGGGATTACAG  48750
                             CTGTAGTCCCAGCTACTCAGG
                             ||||||||||||||||||||
                             GACATTAGGGTCGATGAGTCC

GAM380  DKFZp547H025 3'  CCCAAGTAGCTGGGATTAAAGG 39772      G          CA
          CA                  TGCCT TAGTCCCAGCTACT  GG
                              ||||| ||||||||||||||  ||
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                                ACGGA ATTAGGGTCGATGA  CC
                                  A            AC
GAM380  DKFZP564D166 3'  CCAAAGCGCTAGGATTACAAGC 48016     C       C   TA  CA
          A                      TGC TGTAGTCC AGC  CT  GG
                                 ||| |||||||| |||  ||  ||
                                 ACG ACATTAGG TCG  GA  CC
                                   A       A   C_  AA
GAM380  DKFZP564G092 5'  CCTGAGTAGCTGGGATTACAGG 32158
          CA                     TGCCTGTAGTCCCAGCTACTCAGG
                                 ||||||||||||||||||||||||
                                 ACGGACATTAGGGTCGATGAGTCC

GAM380  DKFZP566I1024 3'  CCTGAGTAGCTGGGACTACAAG 70647    C
          T                      GC TGTAGTCCCAGCTACTCAGG
                                 || ||||||||||||||||||
                                 TG ACATCAGGGTCGATGAGTCC
                                  A
GAM380  DKFZp761N1114 3'  CCCAAGTAGCTGTGACTACAGG 79779          C       CA
          C                      GCCTGTAGTC CAGCTACT  GG
                                 |||||||||| ||||||||  ||
                                 CGGACATCAG GTCGATGA  CC
                                       T       AC
GAM380  DKFZp762L0311 3'  CCTGAGTAACTGGGATTACAG  38671           C
                                 CTGTAGTCCCAG TACTCAGG
                                 |||||||||||| ||||||||
                                 GACATTAGGGTC ATGAGTCC
                                        A
GAM380  DKFZp762P2111 3'  CCTGAGTAGCTGGGATTACAGG 87629
          C                      GCCTGTAGTCCCAGCTACTCAGG
                                 ||||||||||||||||||||||||
                                 CGGACATTAGGGTCGATGAGTCC

GAM380  EREG     3'  CCTGAGCAGCTGGGACTACAGG 9306              A
          C                      GCCTGTAGTCCCAGCT CTCAGG
                                 |||||||||||||| ||||||
                                 CGGACATCAGGGTCGA GAGTCC
                                          C
GAM380  ERO1L    3'  CCCAAGTAGCTGGGAATACAG  28158       G         CA
                                 CTGTA TCCCAGCTACT  GG
                                 ||||| ||||||||||  ||
                                 GACAT AGGGTCGATGA  CC
                                    A          AC
GAM380  EVI5     3'  CCCAAGTAGCTGGGACTACAGG 20203               CA
          T                      GCCTGTAGTCCCAGCTACT  GG
                                 ||||||||||||||||||  ||
                                 TGGACATCAGGGTCGATGA  CC
                                          AC
GAM380  FKBP9    3'  CCAAAGTGTTGGGATTACAGGC 95714              T   CA
          A                      TGCCTGTAGTCCCAGC ACT  GG
                                 |||||||||||||| |||  ||
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                                ACGGACATTAGGGTTG TGA  CC
                                      _  AA
GAM380  FKBP9    3' CCTGAGTAGCTAGGACTACAGG 95715          C
           T                   GCCTGTAGTCC AGCTACTCAGG
                               |||||||||||  ||||||||||
                               TGGACATCAGG TCGATGAGTCC
                                     A
GAM380  FLB6421  3' CCAAAGTGCTGGGATTACAGGC 39642            T  CA
           A                   TGCCTGTAGTCCCAGC ACT  GG
                               ||||||||||||||| |||  ||
                               ACGGACATTAGGGTCG TGA  CC
                                      _  AA
GAM380  FLJ00024 5' CCCGAGTAGCTGGGATTACAG  64492             A
                               CTGTAGTCCCAGCTACTC GG
                               ||||||||||||||||| ||
                               GACATTAGGGTCGATGAG CC
                                     C
GAM380  FLJ00060 5' CCCGATTAGCTGGGACTACAGG 61744             C  A
           C                   GCCTGTAGTCCCAGCTA TC GG
                               |||||||||||||||| || ||
                               CGGACATCAGGGTCGAT AG CC
                                     T  C
GAM380  FLJ10298 3' CCAAAGTGCTGGGATTACAGGC 36455            T  CA
           A                   TGCCTGTAGTCCCAGC ACT  GG
                               ||||||||||||||| |||  ||
                               ACGGACATTAGGGTCG TGA  CC
                                      _  AA
GAM380  FLJ10298 3' CCTAAGTATCTGGGATTACAGG 36456           C   C
           CA                    TGCCTGTAGTCCCAG TACT AGG
                               |||||||||||||| |||| |||
                               ACGGACATTAGGGTC ATGA TCC
                                     T   A
GAM380  FLJ10346 5' CCTGAGTAGCCGGGACTACAGG 36523           A
           CA                    TGCCTGTAGTCCC GCTACTCAGG
                               ||||||||||||  ||||||||||
                               ACGGACATCAGGG CGATGAGTCC
                                     C
GAM380  FLJ10535 3' CCAAAGTGCTGGGATTACAGAC 36740    C       T  CA
           A                   TG CTGTAGTCCCAGC ACT  GG
                               ||  ||||||||||||| |||  ||
                               AC GACATTAGGGTCG TGA  CC
                                A          _  AA
GAM380  FLJ10535 3' CCAAAGTGCTGGGATTACAGGC 36741            T  CA
           A                   TGCCTGTAGTCCCAGC ACT  GG
                               ||||||||||||||| |||  ||
                               ACGGACATTAGGGTCG TGA  CC
                                      _  AA
GAM380  FLJ10535 3' CCCAAGTAGCTGGGACTACAGG 36743              CA
           CA                    TGCCTGTAGTCCCAGCTACT  GG
                               ||||||||||||||||||  ||
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                                ACGGACATCAGGGTCGATGA  CC
                                      AC
GAM380  FLJ10560  3'  CCTGAGTAGCTGGGACTACAGG 36794
            C                  GCCTGTAGTCCCAGCTACTCAGG
                               ||||||||||||||||||||||
                               CGGACATCAGGGTCGATGAGTCC

GAM380  FLJ10640  5'  CCGAGTAGCTGGGACTACAGGC 39233                A
            A                  TGCCTGTAGTCCCAGCTACTC GG
                               |||||||||||||||||||| ||
                               ACGGACATCAGGGTCGATGAG CC
                                        _
GAM380  FLJ10718  3'  CCGGGGAGCTGGGACCACAGGC 37027       A       A  A
            A                  TGCCTGT GTCCCAGCT CTC GG
                               ||||||| ||||||||| ||| ||
                               ACGGACA CAGGGTCGA GGG CC
                                  C       _  G
GAM380  FLJ10829  5'  GTAGCTGGGATTACAGGCA   37261
                               TGCCTGTAGTCCCAGCTAC
                               |||||||||||||||||
                               ACGGACATTAGGGTCGATG

GAM380  FLJ10846  3'  CCCAAGTAGCTGGGACTACAGG 37286               CA
            CA                  TGCCTGTAGTCCCAGCTACT  GG
                               ||||||||||||||||||  ||
                               ACGGACATCAGGGTCGATGA  CC
                                      AC
GAM380  FLJ10847  3'  CCTGAGTAGCTGAGACCACAGG 37300       A  C
            C                  GCCTGT GTC CAGCTACTCAGG
                               ||||||  ||| ||||||||||||
                               CGGACA CAG GTCGATGAGTCC
                                  C  A
GAM380  FLJ10901  3'  GTAGCTGGGATTACAGGCA   37371
                               TGCCTGTAGTCCCAGCTAC
                               |||||||||||||||||
                               ACGGACATTAGGGTCGATG

GAM380  FLJ10956  3'  CCCGAGTAGCTGGGATTATAGG 37464                A
            CA                  TGCCTGTAGTCCCAGCTACTC GG
                               |||||||||||||||||||| ||
                               ACGGATATTAGGGTCGATGAG CC
                                        C
GAM380  FLJ11125  5'  GTAGCTGGGGCTACAGGCA   60325
                               TGCCTGTAGTCCCAGCTAC
                               |||||||||||||||||
                               ACGGACATCGGGGTCGATG

GAM380  FLJ11186  3'  CCAAAGTGTTGGGATTACAGGC 37724              T  CA
            A                  TGCCTGTAGTCCCAGC ACT  GG
                               |||||||||||||| |||  ||
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                                ACGGACATTAGGGTTG TGA  CC
                                        _  AA
GAM380  FLJ11467  3'  CCTGAGTAGCTGGGACTGCAG  46974
                                CTGTAGTCCCAGCTACTCAGG
                                ||||||||||||||||||||
                                GACGTCAGGGTCGATGAGTCC

GAM380  FLJ11710  3'  CCAAAGTATTGGGACTACAGGC 46244          C   CA
                                GCCTGTAGTCCCAG TACT  GG
                                |||||||||||||| ||||  ||
                                CGGACATCAGGGTT ATGA  CC
                                        _  AA
GAM380  FLJ11710  3'  CCCAAGTAGCTGGGACCGCAGG 46246      TA        CA
          CA                    TGCCTG  GTCCCAGCTACT  GG
                                ||||||  ||||||||||||  ||
                                ACGGAC  CAGGGTCGATGA  CC
                                   GC         AC
GAM380  FLJ12363  3'  CCCGAGTAGCTGGGATTACAGG 50634              A
          CA                    TGCCTGTAGTCCCAGCTACTC GG
                                |||||||||||||||||||||  ||
                                ACGGACATTAGGGTCGATGAG CC
                                        C
GAM380  FLJ12581  3'  CCCGAGCAGCTGGGACTACAGG 46333           A  A
          C                     GCCTGTAGTCCCAGCT CTC GG
                                |||||||||||||||  |||  ||
                                CGGACATCAGGGTCGA GAG CC
                                        C  C
GAM380  FLJ12610  3'  CCAAAGTGCTGGGATTACAGGC 45856           T  CA
          A                     TGCCTGTAGTCCCAGC ACT  GG
                                |||||||||||||||  |||  ||
                                ACGGACATTAGGGTCG TGA  CC
                                        _  AA
GAM380  FLJ12649  3'  AGTAGCTGGGATTACAGGCA  45085
                                TGCCTGTAGTCCCAGCTACT
                                ||||||||||||||||||||
                                ACGGACATTAGGGTCGATGA

GAM380  FLJ12668  3'  CCCAAGTAGCTGGGACTATAGT 47157    C          CA
          CA                    TG CTGTAGTCCCAGCTACT  GG
                                ||  ||||||||||||||||  ||
                                AC GATATCAGGGTCGATGA  CC
                                 T            AC
GAM380  FLJ12747  3'  CCCAAGTAGCTGGGATTACAGG 50663             CA
          CA                    TGCCTGTAGTCCCAGCTACT  GG
                                ||||||||||||||||||||  ||
                                ACGGACATTAGGGTCGATGA  CC
                                        AC
GAM380  FLJ12787  3'  CCTGAGTAGCTGGGATTACAG  50692
                                CTGTAGTCCCAGCTACTCAGG
                                ||||||||||||||||||||
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                                GACATTAGGGTCGATGAGTCC

GAM380  FLJ12891  3'  CCCAAGTAGCTGGGACCACAGG 46921        A          CA
              CA                  TGCCTGT GTCCCAGCTACT  GG
                                  ||||||| ||||||||||||  ||
                                  ACGGACA CAGGGTCGATGA  CC
                                      C           AC
GAM380  FLJ12903  3'  CCTAAAGTGCTGGGATTACAGG 43066             T   C_
              CA                  TGCCTGTAGTCCCAGC ACT  AGG
                                  |||||||||||||||| |||  |||
                                  ACGGACATTAGGGTCG TGA  TCC
                                              _  AA
GAM380  FLJ12903  3'  CCTGAGTAGCTGTGATTACAGG 43068          C
              CA                  TGCCTGTAGTC CAGCTACTCAGG
                                  |||||||||||| ||||||||||||
                                  ACGGACATTAG GTCGATGAGTCC
                                        T
GAM380  FLJ12960  3'  CCCGAGTAGCTGGGACTACAGG 45294               A
              C                   GCCTGTAGTCCCAGCTACTC GG
                                  |||||||||||||||||||| ||
                                  CGGACATCAGGGTCGATGAG CC
                                              C
GAM380  FLJ12973  3'  CCTAAGTAGCTGGGATTACAGG 46641               C
              CA                  TGCCTGTAGTCCCAGCTACT AGG
                                  |||||||||||||||||||| |||
                                  ACGGACATTAGGGTCGATGA TCC
                                              A
GAM380  FLJ12975  3'  CCAAAGTGCTGAGATTACAGGC 70187          C   T   CA
              A                   TGCCTGTAGTC CAGC ACT  GG
                                  |||||||||||| |||| |||  ||
                                  ACGGACATTAG GTCG TGA  CC
                                        A   _  AA
GAM380  FLJ12975  3'  CCGGAGAACTGGGATTACAGGC 70191             CTA   A
              A                   TGCCTGTAGTCCCAG   CTC GG
                                  ||||||||||||||   ||| ||
                                  ACGGACATTAGGGTC   GAG CC
                                        AA_   G
GAM380  FLJ13072  5'  CCCGAGTAGCTGGGATTACAGG 91389               A
              CA                  TGCCTGTAGTCCCAGCTACTC GG
                                  |||||||||||||||||||| ||
                                  ACGGACATTAGGGTCGATGAG CC
                                              C
GAM380  FLJ13102  3'  CCAAAGTGCTGGGATTACAGGC 46528             T   CA
              A                   TGCCTGTAGTCCCAGC ACT  GG
                                  |||||||||||||||| |||  ||
                                  ACGGACATTAGGGTCG TGA  CC
                                              _  AA
GAM380  FLJ13114  3'  CCCGAGTAGCTGGGACTACAGG 44899               A
                                  CCTGTAGTCCCAGCTACTC GG
                                  |||||||||||||||||| ||
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                                GGACATCAGGGTCGATGAG CC
                                      C
GAM380  FLJ13188  3'  CCTGAGTAGCTGGGATTATGGA 42189    C
          CA                   TG CTGTAGTCCCAGCTACTCAGG
                               || ||||||||||||||||||||
                               AC GGTATTAGGGTCGATGAGTCC
                                A
GAM380  FLJ13193  3'  CCAAAGTGCTGGGATCACAGGC 50713       A      T   CA
          A                    TGCCTGT GTCCCAGC ACT  GG
                               ||||||| |||||||| |||  ||
                               ACGGACA TAGGGTCG TGA  CC
                                  C       _   AA
GAM380  FLJ13193  3'  CCTGAGTAGCTGGGATCACAG  50720     A
                               CTGT GTCCCAGCTACTCAGG
                               |||| ||||||||||||||||
                               GACA TAGGGTCGATGAGTCC
                                 C
GAM380  FLJ13305  5'  CCAAAGTGCTGGGATTACAGGC 91707            T   CA
          A                    TGCCTGTAGTCCCAGC ACT  GG
                               |||||||||||||||| |||  ||
                               ACGGACATTAGGGTCG TGA  CC
                                        _   AA
GAM380  FLJ13456  3'  GTAGCTGGAACTACAGGC    66558         C
                               GCCTGTAGT CCAGCTAC
                               ||||||||| ||||||||
                               CGGACATCA GGTCGATG
                                    A
GAM380  FLJ13590  5'  CCCGAGTAGCTGGGACTACAG  46204              A
                               CTGTAGTCCCAGCTACTC GG
                               |||||||||||||||||| ||
                               GACATCAGGGTCGATGAG CC
                                        C
GAM380  FLJ13984  5'  CCCAAGAAGCTGGGACCACAGG 45803       A       A  CA
                               CCTGT GTCCCAGCT CT  GG
                               ||||| ||||||||| ||  ||
                               GGACA CAGGGTCGA GA  CC
                                  C        A  AC
GAM380  FLJ14442  3'  CCTGAGTAGCTGGGATTACAG  52381
                               CTGTAGTCCCAGCTACTCAGG
                               ||||||||||||||||||||
                               GACATTAGGGTCGATGAGTCC

GAM380  FLJ14803  3'  CTGAGTAGCTGGGATTATA   52694
                               TGTAGTCCCAGCTACTCAG
                               |||||||||||||||||
                               ATATTAGGGTCGATGAGTC

GAM380  FLJ14950  3'  CCCAAGTAGCTGGGATTACAGG 52786               CA
          CA                   TGCCTGTAGTCCCAGCTACT  GG
                               |||||||||||||||||| ||
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                                ACGGACATTAGGGTCGATGA  CC
                                      AC
GAM380  FLJ14957  3'  CCAAAGTGCTGAGATTACAGGC 52811          C   T  CA
          A                    TGCCTGTAGTC CAGC ACT  GG
                               |||||||||||  |||| |||  ||
                               ACGGACATTAG GTCG TGA  CC
                                     A   _  AA
GAM380  FLJ20004  3'  CCTGAGTAGCTGGGATAACAG  34756      A
                               CTGT GTCCCAGCTACTCAGG
                               ||||  ||||||||||||||||
                               GACA TAGGGTCGATGAGTCC
                                 A
GAM380  FLJ20034  3'  CCCGAGTAGCTGGCATTACAGG 34841          C        A
          CA                   TGCCTGTAGT CCAGCTACTC GG
                               ||||||||||  ||||||||||  ||
                               ACGGACATTA GGTCGATGAG CC
                                     C         C
GAM380  FLJ20045  3'  CCAAAGTGCTGGGATTACAGGC 34876             T  CA
          A                    TGCCTGTAGTCCCAGC ACT  GG
                               ||||||||||||||||  |||  ||
                               ACGGACATTAGGGTCG TGA  CC
                                         _  AA
GAM380  FLJ20045  3'  CCTGAGTAGCTGGGATTACAGG 34882
          CA                   TGCCTGTAGTCCCAGCTACTCAGG
                               ||||||||||||||||||||||||
                               ACGGACATTAGGGTCGATGAGTCC

GAM380  FLJ20097  3'  CCAAAGTGCTGGGATTACAGGC 35046             T  CA
          A                    TGCCTGTAGTCCCAGC ACT  GG
                               ||||||||||||||||  |||  ||
                               ACGGACATTAGGGTCG TGA  CC
                                         _  AA
GAM380  FLJ20136  3'  CCAAAGTGCTGGGATTACAGGC 35093             T  CA
          A                    TGCCTGTAGTCCCAGC ACT  GG
                               ||||||||||||||||  |||  ||
                               ACGGACATTAGGGTCG TGA  CC
                                         _  AA
GAM380  FLJ20136  3'  CCTGAGTAGCTAGGATTACAG  35096         C
                               CTGTAGTCC AGCTACTCAGG
                               |||||||||  ||||||||||
                               GACATTAGG TCGATGAGTCC
                                     A
GAM380  FLJ20147  3'  CCTGAGTAGCTAAGACCACAGG 35133       A  CC
          T                     GCCTGT GTC  AGCTACTCAGG
                                ||||||  |||  ||||||||||
                                TGGACA CAG  TCGATGAGTCC
                                   C  AA
GAM380  FLJ20344  3'  CCAAAGTGCTGGGATTACAGGC 35479             T  CA
          A                    TGCCTGTAGTCCCAGC ACT  GG
                               ||||||||||||||||  |||  ||
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                                ACGGACATTAGGGTCG TGA  CC
                                        _  AA
GAM380  FLJ20344  3'  TAGTTGGGATTACAGGCA    35489
                                TGCCTGTAGTCCCAGCTA
                                ||||||||||||||||||
                                ACGGACATTAGGGTTGAT

GAM380  FLJ20485  3'  CCTAAGTAGCTGGGAGTACAGG 39290        G         C
          C                      GCCTGTA TCCCAGCTACT AGG
                                 ||||||| |||||||||| |||
                                 CGGACAT AGGGTCGATGA TCC
                                    G         A
GAM380  FLJ20507  3'  CCTGAGTAGCTGGGATTACAGG 35735
          CA                      TGCCTGTAGTCCCAGCTACTCAGG
                                  ||||||||||||||||||||||||
                                  ACGGACATTAGGGTCGATGAGTCC

GAM380  FLJ20511  3'  CCTGAGTAGCTGGGACTACAGG 35770
          C                       GCCTGTAGTCCCAGCTACTCAGG
                                  ||||||||||||||||||||||||
                                  CGGACATCAGGGTCGATGAGTCC

GAM380  FLJ20671  3'  CCAAAGTGCTGGGATTACAGGC 35935              T   CA
          A                       TGCCTGTAGTCCCAGC ACT  GG
                                  |||||||||||||||| |||  ||
                                  ACGGACATTAGGGTCG TGA  CC
                                        _  AA
GAM380  FLJ20671  3'  CCTGAGTATCTAGGACTACAGG 35937          C  C
          C                       GCCTGTAGTCC AG TACTCAGG
                                  |||||||||||| || ||||||||
                                  CGGACATCAGG TC ATGAGTCC
                                       A  T
GAM380  FLJ20700  3'  CCCAAGTAGCTGGGACTACAGT 36003    C            CA
          CA                      TG CTGTAGTCCCAGCTACT  GG
                                  || ||||||||||||||||  ||
                                  AC GACATCAGGGTCGATGA  CC
                                   T             AC
GAM380  FLJ20813  3'  CCTAAAGTGCTGGGATTACAGG 36130              T  C_
          CA                      TGCCTGTAGTCCCAGC ACT  AGG
                                  |||||||||||||||| |||  |||
                                  ACGGACATTAGGGTCG TGA  TCC
                                        _  AA
GAM380  FLJ21302  3'  CCAAAGTGCTGGGATTACAGGC 43506              T  CA
          A                       TGCCTGTAGTCCCAGC ACT  GG
                                  |||||||||||||||| |||  ||
                                  ACGGACATTAGGGTCG TGA  CC
                                        _  AA
GAM380  FLJ21302  3'  CCCGAGTAGCTGGGAGTACAG  43507      G         A
                                CTGTA TCCCAGCTACTC GG
                                ||||| |||||||||||| ||
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                                GACAT AGGGTCGATGAG CC
                                  G         C
GAM380  FLJ21324  5'  CCAGAGTGCTGGGATTACAGGC 92848            T   A
          A                    TGCCTGTAGTCCCAGC ACTC GG
                               |||||||||||||||| |||| ||
                               ACGGACATTAGGGTCG TGAG CC
                                        _   A
GAM380  FLJ21324  5'  CCCAAGTAGCTGGGATTACAGG 92850              CA
          CA                   TGCCTGTAGTCCCAGCTACT  GG
                               ||||||||||||||||||  ||
                               ACGGACATTAGGGTCGATGA  CC
                                        AC
GAM380  FLJ21459  3'  CCTGAGTAACTGGGATTACAGG 44801            C
          CA                   TGCCTGTAGTCCCAG TACTCAGG
                               |||||||||||||| ||||||||
                               ACGGACATTAGGGTC ATGAGTCC
                                        A
GAM380  FLJ21603  3'  CCTAATAGCTGGGACTACAGGC 45771             CTC
          A                    TGCCTGTAGTCCCAGCTA   AGG
                               |||||||||||||||||   |||
                               ACGGACATCAGGGTCGAT   TCC
                                        AA_
GAM380  FLJ22002  3'  CCCAGGTAGCTGGGATTACAGG 46194              CA
          CA                   TGCCTGTAGTCCCAGCTACT  GG
                               ||||||||||||||||||  ||
                               ACGGACATTAGGGTCGATGG  CC
                                        AC
GAM380  FLJ22167  5'  CCCGAGTAGCTGGGACTACAGG 44865              A
          C                     GCCTGTAGTCCCAGCTACTC GG
                               |||||||||||||||||| ||
                               CGGACATCAGGGTCGATGAG CC
                                        C
GAM380  FLJ22316  5'  CCAAAGTGCTGGGATTACAGGC 47613            T   CA
          A                    TGCCTGTAGTCCCAGC ACT  GG
                               |||||||||||||| |||  ||
                               ACGGACATTAGGGTCG TGA  CC
                                        _   AA
GAM380  FLJ22329  3'  CCCAAGTAGCTGGGACTATAG  45397             CA
                               CTGTAGTCCCAGCTACT  GG
                               ||||||||||||||||  ||
                               GATATCAGGGTCGATGA  CC
                                        AC
GAM380  FLJ22529  3'  CCAAAGTGCTGGGAATACAGGC 45941         G     T   CA
          A                    TGCCTGTA TCCCAGC ACT  GG
                               |||||||| ||||||| |||  ||
                               ACGGACAT AGGGTCG TGA  CC
                                     A      _   AA
GAM380  FLJ22531  5'  CCCGAGTAGCTGGGATTACAG  45371              A
                               CTGTAGTCCCAGCTACTC GG
                               |||||||||||||||||| ||
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                                GACATTAGGGTCGATGAG CC
                                      C
GAM380  FLJ22684  3'  CCAAAGTGCTGGGATTACAGGC 47467            T  CA
          A                    TGCCTGTAGTCCCAGC ACT  GG
                               |||||||||||||||| |||  ||
                               ACGGACATTAGGGTCG TGA  CC
                                     _  AA
GAM380  FLJ22684  3'  CCCAAGTAGCTGGAATTACAGG 47468         C      CA
          CA                   TGCCTGTAGT CCAGCTACT  GG
                               |||||||||| |||||||||  ||
                               ACGGACATTA GGTCGATGA  CC
                                    A       AC
GAM380  FLJ22794  3'  CCTGAGCAGCTGGGATTACAGG 93242             A
          CA                   TGCCTGTAGTCCCAGCT CTCAGG
                               |||||||||||||||| ||||||
                               ACGGACATTAGGGTCGA GAGTCC
                                      C
GAM380  FLJ22965  3'  CCTGAGTAGCTGGGATTACGGG 42296
          CA                   TGCCTGTAGTCCCAGCTACTCAGG
                               |||||||||||||||||||||||||
                               ACGGGCATTAGGGTCGATGAGTCC

GAM380  FLJ22969  3'  TAGCTGGGATCACTGGCA    69217     T  A
                               TGCC GT GTCCCAGCTA
                               |||| || ||||||||||
                               ACGG CA TAGGGTCGAT
                                 T  C
GAM380  FLJ23024  3'  CCAAAGTGCTGGGATTACAGGC 46839            T  CA
          A                    TGCCTGTAGTCCCAGC ACT  GG
                               |||||||||||||||| |||  ||
                               ACGGACATTAGGGTCG TGA  CC
                                     _  AA
GAM380  FLJ23024  3'  CCTGAGTAGCTGGAATTATAGG 46841         C
          CA                   TGCCTGTAGT CCAGCTACTCAGG
                               |||||||||| ||||||||||||
                               ACGGATATTA GGTCGATGAGTCC
                                    A
GAM380  FLJ23040  3'  CCTGAGTAGCTGGGACATAC   47985    _
                               GTA GTCCCAGCTACTCAGG
                               ||| ||||||||||||||||
                               CAT CAGGGTCGATGAGTCC
                                 A
GAM380  FLJ23392  3'  CCCGAGTAGCTGGGACTACAGG 45888             A
          C                     GCCTGTAGTCCCAGCTACTC GG
                               |||||||||||||||||||| ||
                               CGGACATCAGGGTCGATGAG CC
                                      C
GAM380  FLJ23392  3'  CCGCAGTGCTGGGATTACAGGC 45889            T  CA
          A                    TGCCTGTAGTCCCAGC ACT  GG
                               |||||||||||||||| |||  ||
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                                ACGGACATTAGGGTCG TGA  CC
                                       _  CG
GAM380  FLJ23519  3'  CCCGAGTAGCTGGGACCACAGG 50946       A          A
          C                     GCCTGT GTCCCAGCTACTC GG
                                |||||| |||||||||||||| ||
                                CGGACA CAGGGTCGATGAG CC
                                   C           C
GAM380  FLJ23556  3'  CCAGAGTAGCTGGGACTACAGG 46434                  A
          CA                      TGCCTGTAGTCCCAGCTACTC GG
                                  |||||||||||||||||||| ||
                                  ACGGACATCAGGGTCGATGAG CC
                                             A
GAM380  FLJ23556  3'  CCTGAGTAGCTGGGATTACAGG 46437
          C                     GCCTGTAGTCCCAGCTACTCAGG
                                |||||||||||||||||||||||
                                CGGACATTAGGGTCGATGAGTCC

GAM380  FLJ23563  3'  CCCAAGTAGCTGGGATTACAG  68213              CA
                                CTGTAGTCCCAGCTACT  GG
                                |||||||||||||||  ||
                                GACATTAGGGTCGATGA  CC
                                         AC
GAM380  FLJ25416  5'  CCTGAGTAGCTGGGATTACAGG 59454
          CA                      TGCCTGTAGTCCCAGCTACTCAGG
                                  |||||||||||||||||||||||
                                  ACGGACATTAGGGTCGATGAGTCC

GAM380  FLJ30532  3'  CCCAAGTAGCTGGGATTACAGG 59218                CA
          CA                      TGCCTGTAGTCCCAGCTACT  GG
                                  |||||||||||||||||  ||
                                  ACGGACATTAGGGTCGATGA  CC
                                           AC
GAM380  FLJ31101  3'  CCCGAGTAGCTGGGATTACAGG 36159                  A
          CA                      TGCCTGTAGTCCCAGCTACTC GG
                                  |||||||||||||||||||| ||
                                  ACGGACATTAGGGTCGATGAG CC
                                             C
GAM380  FLJ31153  3'  CCCAAGTAGCTGGGAAAACAGG 58746       AG         CA
          C                       GCCTGT  TCCCAGCTACT  GG
                                  ||||||  ||||||||||  ||
                                  CGGACA  AGGGTCGATGA  CC
                                     AA          AC
GAM380  FLJ32865  3'  CCCGAGTAGCTGGGATTACAGG 58805                  A
          CA                      TGCCTGTAGTCCCAGCTACTC GG
                                  |||||||||||||||||||| ||
                                  ACGGACATTAGGGTCGATGAG CC
                                             C
GAM380  GGA2      3'  GAGTAGCTGGGACTACAGGC  57669
                                GCCTGTAGTCCCAGCTACTC
                                ||||||||||||||||||||
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                                CGGACATCAGGGTCGATGAG

GAM380  GGA2     3'  GAGTAGCTGGGACTACAGGC  57670
                                GCCTGTAGTCCCAGCTACTC
                                ||||||||||||||||||||
                                CGGACATCAGGGTCGATGAG

GAM380  GMPPB    5'  CCCGAGTAGCTGGAATTGCAG  26217        C        A
                                CTGTAGT CCAGCTACTC GG
                                ||||||| |||||||||| ||
                                GACGTTA GGTCGATGAG CC
                                    A        C
GAM380  GNG4     3'  CCTGAGTAGCTGGGATCATAGG 16845        A
            CA                    TGCCTGT GTCCCAGCTACTCAGG
                                ||||||| ||||||||||||||||
                                ACGGATA TAGGGTCGATGAGTCC
                                    C
GAM380  GOLPH2   3'  CCCGAGTAGCTGGGACTACAGG 33769                A
            CA                    TGCCTGTAGTCCCAGCTACTC GG
                                ||||||||||||||||||||| ||
                                ACGGACATCAGGGTCGATGAG CC
                                              C
GAM380  GR6      5'  CCTGAGTAGCTGGGATTACAG  24744
                                CTGTAGTCCCAGCTACTCAGG
                                ||||||||||||||||||||
                                GACATTAGGGTCGATGAGTCC

GAM380  GREB1    3'  CCCGAGTAGCTGGGATTATGGG 72838                A
            C                     GCCTGTAGTCCCAGCTACTC GG
                                ||||||||||||||||||||| ||
                                CGGGTATTAGGGTCGATGAG CC
                                              C
GAM380  GREB1    3'  CCCGAGTAGCTGGGACTACAGG 28560                A
            C                     GCCTGTAGTCCCAGCTACTC GG
                                ||||||||||||||||||||| ||
                                CGGACATCAGGGTCGATGAG CC
                                              C
GAM380  GRWD     3'  CCCAGGTAGCTGGGATTACAGG 49779                CA
            CA                    TGCCTGTAGTCCCAGCTACT  GG
                                ||||||||||||||||||||  ||
                                ACGGACATTAGGGTCGATGG  CC
                                              AC
GAM380  GTF2E1   3'  CCCGAGTAGCTGGGATTACAG  19796              A
                                CTGTAGTCCCAGCTACTC GG
                                |||||||||||||||||| ||
                                GACATTAGGGTCGATGAG CC
                                              C
GAM380  GTPBG3   3'  CCTGAGTAGCTGGGATTACAGG 51896
            CA                    TGCCTGTAGTCCCAGCTACTCAGG
                                ||||||||||||||||||||||||
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                                ACGGACATTAGGGTCGATGAGTCC

GAM380  GTPBG3   3'  GTAGCTGGGACTACAGGC    51904
                                GCCTGTAGTCCCAGCTAC
                                ||||||||||||||||||
                                CGGACATCAGGGTCGATG

GAM380  H-plk    5'  CCTGAGTAGCTGGGATCACAGG 32379      A
                                CCTGT GTCCCAGCTACTCAGG
                                ||||| ||||||||||||||||
                                GGACA TAGGGTCGATGAGTCC
                                   C
GAM380  H2AV     3'  CCCAAGTAGCTGGGATTACAGG 25757              CA
            C                    GCCTGTAGTCCCAGCTACT  GG
                                ||||||||||||||||||  ||
                                CGGACATTAGGGTCGATGA  CC
                                      AC
GAM380  HCA4     3'  CCTAAAGTGCTAGGATTACAGG 57741          C  T  C_
            CA                    TGCCTGTAGTCC AGC ACT  AGG
                                ||||||||||| ||| |||  |||
                                ACGGACATTAGG TCG TGA  TCC
                                      A  _  AA
GAM380  HCA4     3'  CCTGAGTAGCTGGGATTACAG  57742
                                CTGTAGTCCCAGCTACTCAGG
                                ||||||||||||||||||||
                                GACATTAGGGTCGATGAGTCC

GAM380  HRH4     3'  CCCAAGTATGTGGGACTACAGG 41531           GC   CA
            TA                    TGCCTGTAGTCCCA  TACT  GG
                                ||||||||||||||  ||||  ||
                                ATGGACATCAGGGT  ATGA  CC
                                      GT   AC
GAM380  HRH4     3'  CCTGAGCAGCTGGGATTGCAG  41535           A
                                CTGTAGTCCCAGCT CTCAGG
                                |||||||||||||| ||||||
                                GACGTTAGGGTCGA GAGTCC
                                      C
GAM380  HRH4     3'  GTAGCTGGGACCGCAGGCA   41545      TA
                                TGCCTG  GTCCCAGCTAC
                                ||||||  ||||||||||
                                ACGGAC  CAGGGTCGATG
                                   GC
GAM380  HSMPP8   3'  CCTGAGTAGCTGGGATTACAGA 95131    C
            CA                    TG CTGTAGTCCCAGCTACTCAGG
                                || ||||||||||||||||||||
                                AC GACATTAGGGTCGATGAGTCC
                                 A
GAM380  ICK      3'  CCAAAGTACTGGGATTACAGGC 33680           C   CA
            A                     TGCCTGTAGTCCCAG TACT  GG
                                ||||||||||||||| ||||  ||
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                                ACGGACATTAGGGTC ATGA  CC
                                        _    AA
GAM380  ICK     3'  CCTGAGTAACTGGGACTACAGG 33685           C
            C                    GCCTGTAGTCCCAG TACTCAGG
                                 ||||||||||||| ||||||||
                                 CGGACATCAGGGTC ATGAGTCC
                                         A
GAM380  IMPACT  3'  AGTAGCTGGGATTACAGACA  38002    C
                                 TG CTGTAGTCCCAGCTACT
                                 || ||||||||||||||||
                                 AC GACATTAGGGTCGATGA
                                  A
GAM380  JAM1    3'  CTGAGTAGCTGGGATTAC    34227
                                 GTAGTCCCAGCTACTCAG
                                 ||||||||||||||||||
                                 CATTAGGGTCGATGAGTC

GAM380  JAM1    3'  CTGAGTAGCTGGGATTAC    58571
                                 GTAGTCCCAGCTACTCAG
                                 ||||||||||||||||||
                                 CATTAGGGTCGATGAGTC

GAM380  JM11    3'  CCCGAGTAGCTGGGATTACAGG 54355                A
            CA                     TGCCTGTAGTCCCAGCTACTC GG
                                   |||||||||||||||||||| ||
                                   ACGGACATTAGGGTCGATGAG CC
                                             C
GAM380  KIAA0022 3' CCTTAGTAGCTGGGACCACAGA 30280    C   A        C
            CA                     TG CTGT GTCCCAGCTACT AGG
                                   || |||| |||||||||||| |||
                                   AC GACA CAGGGTCGATGA TCC
                                    A   C          T
GAM380  KIAA0087 3' CCTGAGTAGCTGGGATTACAG  29343
                                   CTGTAGTCCCAGCTACTCAGG
                                   ||||||||||||||||||||
                                   GACATTAGGGTCGATGAGTCC

GAM380  KIAA0090 3' CCAAAGTGCCGGGATTACAGGC 89812           A  T   CA
            A                      TGCCTGTAGTCCC GC ACT  GG
                                   |||||||||||| || |||  ||
                                   ACGGACATTAGGG CG TGA  CC
                                           C  _   AA
GAM380  KIAA0090 3' CCCGAGTAGCTGGGGCTCAGGC 89814       T          A
                                   GCCTG AGTCCCAGCTACTC GG
                                   ||||| |||||||||||||| ||
                                   CGGAC TCGGGGTCGATGAG CC
                                      _           C
GAM380  KIAA0161 3' CCCAAGTAGCTGGGATTACAGG 29195                CA
            CA                     TGCCTGTAGTCCCAGCTACT  GG
                                   |||||||||||||||||||  ||
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                                ACGGACATTAGGGTCGATGA  CC
                                      AC
GAM380  KIAA0186 3' CCCAAGTAGCTGGGATTACAGG 41102              CA
            CA                  TGCCTGTAGTCCCAGCTACT  GG
                                ||||||||||||||||||  ||
                                ACGGACATTAGGGTCGATGA  CC
                                      AC
GAM380  KIAA0205 3' CCCGAGTAGCTGGGACTACAGG 30207               A
            CA                  TGCCTGTAGTCCCAGCTACTC GG
                                |||||||||||||||||||| ||
                                ACGGACATCAGGGTCGATGAG CC
                                      C
GAM380  KIAA0212 3' CCGAGTAGCTGGGATTACAG  28626              A
                                CTGTAGTCCCAGCTACTC GG
                                |||||||||||||||||| ||
                                GACATTAGGGTCGATGAG CC
                                      C
GAM380  KIAA0426 3' CCAAAGTTCAGGGATTACAGGC 28921          AGCT  CA
            A                   TGCCTGTAGTCCC   ACT  GG
                                ||||||||||||   |||  ||
                                ACGGACATTAGGG   TGA  CC
                                      ACT_  AA
GAM380  KIAA0426 3' CCCGAGTAGCTGGGATTACAGG 28923               A
            CA                  TGCCTGTAGTCCCAGCTACTC GG
                                |||||||||||||||||||| ||
                                ACGGACATTAGGGTCGATGAG CC
                                      C
GAM380  KIAA0441 3' CCTAGTAGCTGGGACTACAGG  29631              C
                                CCTGTAGTCCCAGCTACT AGG
                                |||||||||||||||||| |||
                                GGACATCAGGGTCGATGA TCC
                                      _
GAM380  KIAA0446 5' CCCAAGTAGCTGGGACCACAGG 69447       A        CA
            T                   GCCTGT GTCCCAGCTACT  GG
                                ||||||  ||||||||||||  ||
                                TGGACA CAGGGTCGATGA  CC
                                   C          AC
GAM380  KIAA0447 3' CCATGTGGCTGGAACCACAGGC 72112       A  C      TCA
            A                   TGCCTGT GT CCAGCTAC   GG
                                |||||||  ||  ||||||||   ||
                                ACGGACA CA GGTCGGTG   CC
                                   C  A       TA_
GAM380  KIAA0459 3' CCTGAGTAGCTGGGATTACAG  61649
                                CTGTAGTCCCAGCTACTCAGG
                                ||||||||||||||||||||
                                GACATTAGGGTCGATGAGTCC

GAM380  KIAA0469 3' CCAAAGTGCTGGGATTACAGGC 29972              T  CA
            A                   TGCCTGTAGTCCCAGC ACT  GG
                                ||||||||||||||| |||  ||
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                                ACGGACATTAGGGTCG TGA  CC
                                      _  AA
GAM380  KIAA0469 3' CCCGAGTAGCTGGGACTACAGG 29975                A
            TA                   TGCCTGTAGTCCCAGCTACTC GG
                                 |||||||||||||||||||| ||
                                 ATGGACATCAGGGTCGATGAG CC
                                       C
GAM380  KIAA0469 3' CCTGAATAGCTGAGACTACAGG 29977          C     C
            C                    GCCTGTAGTC CAGCTA TCAGG
                                 |||||||||| |||||| |||||
                                 CGGACATCAG GTCGAT AGTCC
                                      A     A
GAM380  KIAA0472 5' CCTGAGTAGCTGGGACTACAGG 72348
            C                    GCCTGTAGTCCCAGCTACTCAGG
                                 |||||||||||||||||||||||
                                 CGGACATCAGGGTCGATGAGTCC

GAM380  KIAA0478 3' CCAAAGTGCTAGGATTACAGAC 30172    C       C  T  CA
            A                    TG CTGTAGTCC AGC ACT  GG
                                 || ||||||||| ||| |||  ||
                                 AC GACATTAGG TCG TGA  CC
                                  A       A  _  AA
GAM380  KIAA0478 3' CCCAAGTAGCTGGGACCACAGG 30174       A         CA
            C                    GCCTGT GTCCCAGCTACT  GG
                                 |||||| ||||||||||||  ||
                                 CGGACA CAGGGTCGATGA  CC
                                    C          AC
GAM380  KIAA0493 5' CCCAAGTAGCTGGGACTACAG  64932              CA
                                 CTGTAGTCCCAGCTACT  GG
                                 ||||||||||||||||  ||
                                 GACATCAGGGTCGATGA  CC
                                           AC
GAM380  KIAA0513 5' CCGAGTAGCTGGGATTACAGGC 29025                A
            A                    TGCCTGTAGTCCCAGCTACTC GG
                                 |||||||||||||||||||| ||
                                 ACGGACATTAGGGTCGATGAG CC
                                       _
GAM380  KIAA0513 3' CCTGAGTAGCTGGGATGACAG  29027     A
                                 CTGT GTCCCAGCTACTCAGG
                                 |||| ||||||||||||||||
                                 GACA TAGGGTCGATGAGTCC
                                   G
GAM380  KIAA0527 3' CCCAAGTAGGTGGGATTACAGG 97492           G    CA
            CA                     TGCCTGTAGTCCCA CTACT  GG
                                 |||||||||||||| |||||  ||
                                 ACGGACATTAGGGT GATGA  CC
                                          G    AC
GAM380  KIAA0532 3' CCCAAGCAGCTGGGACTACA   71321           A  CA
                                 TGTAGTCCCAGCT CT  GG
                                 |||||||||||| ||  ||
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                                ACATCAGGGTCGA GA  CC
                                      C  AC
GAM380  KIAA0544  3'  CCTGAGTAGCTGGGGATTACA  71463          _
                                TGTAGTCCC AGCTACTCAGG
                                ||||||||| ||||||||||
                                ACATTAGGG TCGATGAGTCC
                                     G
GAM380  KIAA0557  3'  CCTGAGTAGCTGGGATTACAG  78551
                                CTGTAGTCCCAGCTACTCAGG
                                ||||||||||||||||||||
                                GACATTAGGGTCGATGAGTCC

GAM380  KIAA0557  3'  CTGAGTAGCTGGGGTTACA   78556     GT
                                TGTA  CCCAGCTACTCAG
                                ||||  ||||||||||||
                                ACAT  GGGTCGATGAGTC
                                  TG
GAM380  KIAA0562  3'  CCAAAGTGCTGGAATTACAGGC 28817         C    T   CA
          A                      TGCCTGTAGT CCAGC ACT  GG
                                ||||||||| ||||| |||  ||
                                ACGGACATTA GGTCG TGA  CC
                                      A    _  AA
GAM380  KIAA0562  3'  CCCGAGTAGCTGGGATTACAGG 28818              A
          C                      GCCTGTAGTCCCAGCTACTC GG
                                |||||||||||||||||| ||
                                CGGACATTAGGGTCGATGAG CC
                                           C
GAM380  KIAA0563  5'  CTGAGTAGCTGGGGTTGCA   29881     GT
                                TGTA  CCCAGCTACTCAG
                                ||||  ||||||||||||
                                ACGT  GGGTCGATGAGTC
                                  TG
GAM380  KIAA0599  3'  CCCAGGTCGCTGGGACTACAGG 77689            T   CA
          CA                     TGCCTGTAGTCCCAGC ACT  GG
                                |||||||||||||| |||  ||
                                ACGGACATCAGGGTCG TGG  CC
                                      C   AC
GAM380  KIAA0643  5'  CCTAAGTAGCTGGGATTACAGG 45974              C
                                CCTGTAGTCCCAGCTACT AGG
                                |||||||||||||||||| |||
                                GGACATTAGGGTCGATGA TCC
                                           A
GAM380  KIAA0650  3'  CCTAAGTAGCAGGGATTACAGG 89610          A     C
          CA                     TGCCTGTAGTCCC GCTACT AGG
                                |||||||||||| |||||| |||
                                ACGGACATTAGGG CGATGA TCC
                                      A     A
GAM380  KIAA0663  5'  CCTGAGTAGCTGGGACTACAGG 29788
                                CCTGTAGTCCCAGCTACTCAGG
                                |||||||||||||||||||||
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                                GGACATCAGGGTCGATGAGTCC

GAM380  KIAA0737 3' CCAAAGTGCTGGGATTACAGGC 29803            T  CA
            A                TGCCTGTAGTCCCAGC ACT  GG
                             |||||||||||||||| |||  ||
                             ACGGACATTAGGGTCG TGA  CC
                                      _  AA
GAM380  KIAA0737 3' CCCGAGTAGCTAGGATTACAGG 29805         C      A
            C                 GCCTGTAGTCC AGCTACTC GG
                              |||||||||| |||||||| ||
                              CGGACATTAGG TCGATGAG CC
                                    A      C
GAM380  KIAA0798 3' CCAAAGTGCTGGGATTACAGGC 28443            T  CA
            A                TGCCTGTAGTCCCAGC ACT  GG
                             |||||||||||||||| |||  ||
                             ACGGACATTAGGGTCG TGA  CC
                                      _  AA
GAM380  KIAA0798 3' CCTAAGTAGCTGGGATTACAGG 28445              C
            CA                 TGCCTGTAGTCCCAGCTACT AGG
                               |||||||||||||||||| |||
                               ACGGACATTAGGGTCGATGA TCC
                                         A
GAM380  KIAA0828 3' CCTGAGTAGCTGGAACCACAGG 82113       A  C
            T                GCCTGT GT CCAGCTACTCAGG
                             |||||| || ||||||||||||
                             TGGACA CA GGTCGATGAGTCC
                                C  A
GAM380  KIAA0831 3' CCCGAGTAGCTGGGATTATAGG 30630              A
            CA                 TGCCTGTAGTCCCAGCTACTC GG
                               |||||||||||||||||||| ||
                               ACGGATATTAGGGTCGATGAG CC
                                         C
GAM380  KIAA0841 3' CCAAAGTGCTGGGATTACAGGC 71889            T  CA
            A                TGCCTGTAGTCCCAGC ACT  GG
                             |||||||||||||||| |||  ||
                             ACGGACATTAGGGTCG TGA  CC
                                      _  AA
GAM380  KIAA0841 3' CCTGAATAGCTGGGATTACAGG 71893              C
            CA                 TGCCTGTAGTCCCAGCTA TCAGG
                               |||||||||||||||||| |||||
                               ACGGACATTAGGGTCGAT AGTCC
                                         A
GAM380  KIAA0861 3' CCTGAGTAGCTGGGACTACAGG 90346
            C                GCCTGTAGTCCCAGCTACTCAGG
                             |||||||||||||||||||||||
                             CGGACATCAGGGTCGATGAGTCC

GAM380  KIAA0889 3' CCCAAGTAGCTGGGATTAAGGC 31767      G         CA
                             GCCT TAGTCCCAGCTACT  GG
                             |||| ||||||||||||||  ||
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                                CGGA ATTAGGGTCGATGA  CC
                                  _           AC
GAM380  KIAA0924 3' CCCGAGTAGCTGGAATTACAGG 30359         C        A
            CA                    TGCCTGTAGT CCAGCTACTC GG
                                  |||||||||| |||||||||| ||
                                  ACGGACATTA GGTCGATGAG CC
                                        A         C
GAM380  KIAA0931 3' CCCGAGTAGCTGGGATTACAGG 68007                  A
            CA                    TGCCTGTAGTCCCAGCTACTC GG
                                  |||||||||||||||||||| ||
                                  ACGGACATTAGGGTCGATGAG CC
                                              C
GAM380  KIAA1028 3' CCCGAGTAGCTGGGACTACGGG 93588                  A
            CA                    TGCCTGTAGTCCCAGCTACTC GG
                                  |||||||||||||||||||| ||
                                  ACGGGCATCAGGGTCGATGAG CC
                                              C
GAM380  KIAA1040 3' AGTAGCTGGGATTACAGACA   72680    C
                                  TG CTGTAGTCCCAGCTACT
                                  || ||||||||||||||||
                                  AC GACATTAGGGTCGATGA
                                   A
GAM380  KIAA1041 3' CCGAGTAGCTGGGAGTGCAG   30821       G          A
                                  CTGTA TCCCAGCTACTC GG
                                  ||||| |||||||||||| ||
                                  GACGT AGGGTCGATGAG CC
                                     G          C
GAM380  KIAA1041 3' CCTAGAGTGCTGGGATTACAGA 30822     C          T   _
            CA                    TG CTGTAGTCCCAGC ACTC AGG
                                  || |||||||||||| |||| |||
                                  AC GACATTAGGGTCG TGAG TCC
                                   A          _   A
GAM380  KIAA1054 3' CCCAAGTAGCTGGGACCACACG 68962     C   A          CA
            CA                    TGC TGT GTCCCAGCTACT  GG
                                  ||| ||| ||||||||||||  ||
                                  ACG ACA CAGGGTCGATGA  CC
                                   C   C          AC
GAM380  KIAA1128 3' CCTGAGTAGCTGGGACTACAGG 69001
            CA                    TGCCTGTAGTCCCAGCTACTCAGG
                                  |||||||||||||||||||||||||
                                  ACGGACATCAGGGTCGATGAGTCC

GAM380  KIAA1143 3' CCAAAGTGCTGGGATTACAGGC 69232              T   CA
            A                      TGCCTGTAGTCCCAGC ACT  GG
                                  |||||||||||||||| |||  ||
                                  ACGGACATTAGGGTCG TGA  CC
                                            _  AA
GAM380  KIAA1145 3' CCCAAGCAGCCGGGACTGCAGG 66234           A   A  CA
            CA                    TGCCTGTAGTCCC GCT CT  GG
                                  |||||||||||| ||| ||  ||
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                                ACGGACGTCAGGG CGA GA  CC
                                      C   C  AC
GAM380  KIAA1155 3' CCCGAGTAGCTGGGACAACAGG 62909       A          A
          TA                  TGCCTGT GTCCCAGCTACTC GG
                              ||||||| |||||||||||||| ||
                              ATGGACA CAGGGTCGATGAG CC
                                 A           C
GAM380  KIAA1161 5' CCAAAGTGTTGGGATTACAGGC 82642             T   CA
          A                   TGCCTGTAGTCCCAGC ACT  GG
                              |||||||||||||||| |||  ||
                              ACGGACATTAGGGTTG TGA  CC
                                    _  AA
GAM380  KIAA1161 5' GTAGCTGAGATTACAGGCA   82648          C
                              TGCCTGTAGTC CAGCTAC
                              |||||||||| |||||||
                              ACGGACATTAG GTCGATG
                                    A
GAM380  KIAA1169 5' CCCAAGCAGCTGGAACTACAGG 35880        C     A  CA
                              CCTGTAGT CCAGCT CT  GG
                              |||||||| |||||| ||  ||
                              GGACATCA GGTCGA GA  CC
                                 A     C  AC
GAM380  KIAA1170 3' CCCAAGGAGCTGGGATTACAGG 70413              A  CA
          CA                  TGCCTGTAGTCCCAGCT CT  GG
                              |||||||||||||||| ||  ||
                              ACGGACATTAGGGTCGA GA  CC
                                    G  AC
GAM380  KIAA1185 3' CCCAAGTAGCTGGGACTACAGG 63285               CA
          T                   GCCTGTAGTCCCAGCTACT  GG
                              |||||||||||||||||  ||
                              TGGACATCAGGGTCGATGA  CC
                                    AC
GAM380  KIAA1193 3' CCCGAGTAGCTGGGATTACAGG 68264               A
          C                   GCCTGTAGTCCCAGCTACTC GG
                              |||||||||||||||||| ||
                              CGGACATTAGGGTCGATGAG CC
                                    C
GAM380  KIAA1198 3' CCCAAGAAGCTGGGATTACAGG 64018              A  CA
          CA                  TGCCTGTAGTCCCAGCT CT  GG
                              |||||||||||||||| ||  ||
                              ACGGACATTAGGGTCGA GA  CC
                                    A  AC
GAM380  KIAA1198 3' CCCGAGTAGCTGGGACTACAGG 64022               A
          C                   GCCTGTAGTCCCAGCTACTC GG
                              |||||||||||||||||| ||
                              CGGACATCAGGGTCGATGAG CC
                                    C
GAM380  KIAA1198 3' CCTGAGTAGCTGGGACTATAGG 64028
          C                   GCCTGTAGTCCCAGCTACTCAGG
                              |||||||||||||||||||||
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                                CGGATATCAGGGTCGATGAGTCC

GAM380  KIAA1198  3'  CCTGAGTAGCTGGGATTACAGG 64029
              C                  GCCTGTAGTCCCAGCTACTCAGG
                                 |||||||||||||||||||||||
                                 CGGACATTAGGGTCGATGAGTCC

GAM380  KIAA1200  3'  CCAAAGTGCTGGGATTACAGGC 63033            T  CA
              A                  TGCCTGTAGTCCCAGC ACT  GG
                                 |||||||||||||||| |||  ||
                                 ACGGACATTAGGGTCG TGA  CC
                                           _  AA
GAM380  KIAA1209  3'  CCAGAGTGCTGGGATTACAGGC 61402            T   A
              A                  TGCCTGTAGTCCCAGC ACTC GG
                                 |||||||||||||||| |||| ||
                                 ACGGACATTAGGGTCG TGAG CC
                                           _   A
GAM380  KIAA1210  3'  CCCGACTAGCTGGGACTACAGG 98068             C  A
              C                  GCCTGTAGTCCCAGCTA TC GG
                                 |||||||||||||||| || ||
                                 CGGACATCAGGGTCGAT AG CC
                                           C  C
GAM380  KIAA1254  3'  CCCAAGTAGCTGGGACTATAGG 70557               CA
              CA                   TGCCTGTAGTCCCAGCTACT  GG
                                   |||||||||||||||||||  ||
                                   ACGGATATCAGGGTCGATGA  CC
                                             AC
GAM380  KIAA1257  3'  CCTGAGTAGTTGGGAATACAGG 63401        G
              CA                   TGCCTGTA TCCCAGCTACTCAGG
                                   |||||||| ||||||||||||||
                                   ACGGACAT AGGGTTGATGAGTCC
                                       A
GAM380  KIAA1287  3'  CCTGAGTAGCTGGGACTGCAGG 78936
              CA                   TGCCTGTAGTCCCAGCTACTCAGG
                                   |||||||||||||||||||||||
                                   ACGGACGTCAGGGTCGATGAGTCC

GAM380  KIAA1320  5'  CGAGTAGCTGGAATTATA    69838       C        A
                                 TGTAGT CCAGCTACTC G
                                 ||||||  |||||||||| |
                                 ATATTA GGTCGATGAG C
                                    A         C
GAM380  KIAA1373  3'  CCCGAGTAGCGAGGACTACAGG 71504           CA      A
              C                   GCCTGTAGTCC  GCTACTC GG
                                  ||||||||||  ||||||| ||
                                  CGGACATCAGG  CGATGAG CC
                                        AG      C
GAM380  KIAA1443  3'  CCCGAGTAGCTGGGACTACAGG 64569                A
              CA                   TGCCTGTAGTCCCAGCTACTC GG
                                   |||||||||||||||||||| ||
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                                ACGGACATCAGGGTCGATGAG CC
                                          C
GAM380  KIAA1456 3' CCCAAGTAGCTGGGACTACTGG 67542      T          CA
            CA                   TGCC GTAGTCCCAGCTACT  GG
                                 |||| ||||||||||||||  ||
                                 ACGG CATCAGGGTCGATGA  CC
                                   T           AC
GAM380  KIAA1465 3' CCTAGTAGCTGGGACTACAGGC 61489               C
                                 GCCTGTAGTCCCAGCTACT AGG
                                 |||||||||||||||||| |||
                                 CGGACATCAGGGTCGATGA TCC
                                          _
GAM380  KIAA1467 3' CCCAAGTAGCTGGGACTACAGG 72063               CA
            T                    GCCTGTAGTCCCAGCTACT  GG
                                 ||||||||||||||||||  ||
                                 TGGACATCAGGGTCGATGA  CC
                                          AC
GAM380  KIAA1493 3' CCTGAGTAGCTGGGACTACAGG 64837
            C                    GCCTGTAGTCCCAGCTACTCAGG
                                 |||||||||||||||||||||||
                                 CGGACATCAGGGTCGATGAGTCC

GAM380  KIAA1497 5' CCTGAGTAGCTGGGATTACAGG 68119
            CA                   TGCCTGTAGTCCCAGCTACTCAGG
                                 |||||||||||||||||||||||
                                 ACGGACATTAGGGTCGATGAGTCC

GAM380  KIAA1508 3' CCTGAGTACCTGAGATTACAGG 62547          C  C
            CA                   TGCCTGTAGTC CAG TACTCAGG
                                 |||||||||||  ||| ||||||||
                                 ACGGACATTAG GTC ATGAGTCC
                                       A  C
GAM380  KIAA1530 3' CCAAAGTGTTGGGATTACAGGC 68551            T  CA
            A                    TGCCTGTAGTCCCAGC ACT  GG
                                 ||||||||||||||| |||  ||
                                 ACGGACATTAGGGTTG TGA  CC
                                       _  AA
GAM380  KIAA1530 3' CCCAGGTAGCTGGGACTACAGG 68554               CA
            CA                   TGCCTGTAGTCCCAGCTACT  GG
                                 ||||||||||||||||||  ||
                                 ACGGACATCAGGGTCGATGG  CC
                                          AC
GAM380  KIAA1530 3' CCTGAGTAGCTGGGACTACAGG 68556
            C                    GCCTGTAGTCCCAGCTACTCAGG
                                 |||||||||||||||||||||||
                                 CGGACATCAGGGTCGATGAGTCC

GAM380  KIAA1571 3' GAGTAGCTGGGACTACAGGC  61617
                                 GCCTGTAGTCCCAGCTACTC
                                 ||||||||||||||||||||
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                                CGGACATCAGGGTCGATGAG

GAM380  KIAA1615 3' AGTAGCTGGGATTACAGGCA   69264
                                TGCCTGTAGTCCCAGCTACT
                                ||||||||||||||||||||
                                ACGGACATTAGGGTCGATGA

GAM380  KIAA1615 3' CCAAAGTGCTGGGATTACAGGC 69270              T   CA
            A                    TGCCTGTAGTCCCAGC ACT  GG
                                 |||||||||||||||| |||  ||
                                 ACGGACATTAGGGTCG TGA  CC
                                           _  AA
GAM380  KIAA1615 3' CCAAAGTGCTGGGATTACAGGC 69271              T   CA
            A                    TGCCTGTAGTCCCAGC ACT  GG
                                 |||||||||||||||| |||  ||
                                 ACGGACATTAGGGTCG TGA  CC
                                           _  AA
GAM380  KIAA1615 3' CCTGATTAGCTGGGATTACAGG 69275               C
            CA                     TGCCTGTAGTCCCAGCTA TCAGG
                                   |||||||||||||||||| |||||
                                   ACGGACATTAGGGTCGAT AGTCC
                                             T
GAM380  KIAA1617 3' CCCAAGTAGCTGGGATTACAGG 93073                 CA
            CA                     TGCCTGTAGTCCCAGCTACT  GG
                                   ||||||||||||||||||||  ||
                                   ACGGACATTAGGGTCGATGA  CC
                                             AC
GAM380  KIAA1655 3' CCTGAGTAGCTAGGATTACAGG 67180           C
            CA                     TGCCTGTAGTCC AGCTACTCAGG
                                   |||||||||||| ||||||||||
                                   ACGGACATTAGG TCGATGAGTCC
                                          A
GAM380  KIAA1655 3' CCTGAGTAGCTGGGATTATGGG 67181
            C                      GCCTGTAGTCCCAGCTACTCAGG
                                   |||||||||||||||||||||||
                                   CGGGTATTAGGGTCGATGAGTCC

GAM380  KIAA1668 3' CCTGAGCAGCTGGGACTACAGG 67065               A
            C                      GCCTGTAGTCCCAGCT CTCAGG
                                   |||||||||||||||| ||||||
                                   CGGACATCAGGGTCGA GAGTCC
                                             C
GAM380  KIAA1671 3' CCCAAGTAGCTGGGACTACAGG 66274                 CA
            T                      GCCTGTAGTCCCAGCTACT  GG
                                   ||||||||||||||||||  ||
                                   TGGACATCAGGGTCGATGA  CC
                                             AC
GAM380  KIAA1712 3' CCTGAGTAGCTGGGACTATAGG 68154
            C                      GCCTGTAGTCCCAGCTACTCAGG
                                   |||||||||||||||||||||||
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                                CGGATATCAGGGTCGATGAGTCC

GAM380  KIAA1712  3'  CCTGAGTAGCTGGGATTATAGG 68155
                CA                TGCCTGTAGTCCCAGCTACTCAGG
                                  |||||||||||||||||||||||
                                  ACGGATATTAGGGTCGATGAGTCC

GAM380  KIAA1727  3'  CCTCAGAGCTGGGACTACAGGC 64755              A  C
                                  GCCTGTAGTCCCAGCT CT AGG
                                  ||||||||||||||| || |||
                                  CGGACATCAGGGTCGA GA TCC
                                            _ C
GAM380  KIAA1737  3'  CCCAAGTAGCTGGGATTACAG  67938              CA
                                  CTGTAGTCCCAGCTACT  GG
                                  ||||||||||||||||  ||
                                  GACATTAGGGTCGATGA  CC
                                        AC
GAM380  KIAA1751  3'  CCTGAGTAGCTGGAACTACAGG 72154          C
                CA                TGCCTGTAGT CCAGCTACTCAGG
                                  |||||||||| ||||||||||||
                                  ACGGACATCA GGTCGATGAGTCC
                                       A
GAM380  KIAA1755  3'  CCTAAGTAGCTGGGACTACAG  62010              C
                                  CTGTAGTCCCAGCTACT AGG
                                  ||||||||||||||| |||
                                  GACATCAGGGTCGATGA TCC
                                        A
GAM380  KIAA1784  3'  CCAGATAGCTGGGACTACAGGC 65744               C  A
                A                 TGCCTGTAGTCCCAGCTA TC GG
                                  |||||||||||||||| || ||
                                  ACGGACATCAGGGTCGAT AG CC
                                            _ A
GAM380  KIAA1821  3'  CCTGAGTAGCTGGGACTACAGG 72263
                CA                TGCCTGTAGTCCCAGCTACTCAGG
                                  |||||||||||||||||||||||
                                  ACGGACATCAGGGTCGATGAGTCC

GAM380  KIAA1829  3'  CCTGAGTAGCTGGGACTACAGG 62639
                T                 GCCTGTAGTCCCAGCTACTCAGG
                                  |||||||||||||||||||||||
                                  TGGACATCAGGGTCGATGAGTCC

GAM380  KIAA1829  3'  CCTGAGTAGCTGGGATTACAG  62640
                                  CTGTAGTCCCAGCTACTCAGG
                                  |||||||||||||||||||||
                                  GACATTAGGGTCGATGAGTCC

GAM380  KIAA1877  3'  CCTGAGTAGCTGGGGACTACAG 66746          _
                GCA                 TGCCTGTAGTCCC AGCTACTCAGG
                                    |||||||||||| ||||||||||
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                                ACGGACATCAGGG TCGATGAGTCC
                                      G
GAM380  KIAA1922  5'  CCCAAGTAGCTGGGATTACAGG 73991                CA
            CA                   TGCCTGTAGTCCCAGCTACT  GG
                                 ||||||||||||||||||  ||
                                 ACGGACATTAGGGTCGATGA  CC
                                       AC
GAM380  KIAA1924  3'  AGTAGCTGGGACTACAGGC   74040
                                 GCCTGTAGTCCCAGCTACT
                                 ||||||||||||||||||
                                 CGGACATCAGGGTCGATGA

GAM380  KIAA1924  3'  CCAAAGTGCTGGGATCACAGGC 74042       A      T   CA
            A                    TGCCTGT GTCCCAGC ACT  GG
                                 |||||||  ||||||||  ||||  ||
                                 ACGGACA TAGGGTCG TGA  CC
                                     C       _   AA
GAM380  KIAA1971  3'  CCCGAGTAGCTGGGACTACAGG 74674                A
            C                    GCCTGTAGTCCCAGCTACTC GG
                                 ||||||||||||||||||| ||
                                 CGGACATCAGGGTCGATGAG CC
                                       C
GAM380  KIAA1971  3'  CCCGAGTAGCTGGGATTACAGG 74675                A
            CA                   TGCCTGTAGTCCCAGCTACTC GG
                                 ||||||||||||||||||| ||
                                 ACGGACATTAGGGTCGATGAG CC
                                       C
GAM380  KIAA1975  5'  CCCGAGTAACTGGGACTACAGG 74418           C    A
                                 CCTGTAGTCCCAG TACTC GG
                                 ||||||||||||  ||||| ||
                                 GGACATCAGGGTC ATGAG CC
                                      A    C
GAM380  KIAA1987  5'  CCCGAGTAGCTGGGATTACAGG 89381                A
            CA                   TGCCTGTAGTCCCAGCTACTC GG
                                 ||||||||||||||||||| ||
                                 ACGGACATTAGGGTCGATGAG CC
                                       C
GAM380  KLK7      3'  CCAAAGTGCTGGGATTACAGGC 18542             T   CA
            A                    TGCCTGTAGTCCCAGC ACT  GG
                                 ||||||||||||||| |||  ||
                                 ACGGACATTAGGGTCG TGA  CC
                                       _   AA
GAM380  Kv6.3     3'  CCGAGTCTGTGACTACAGGCA  56852          C   CT    A
                                 TGCCTGTAGTC CAG  ACTC GG
                                 ||||||||||| |||  |||| ||
                                 ACGGACATCAG GTC  TGAG CC
                                      T   __    C
GAM380  LAMP3     3'  CCAAAGTGCTGGGATTACAGGC 60199             T   CA
            A                    TGCCTGTAGTCCCAGC ACT  GG
                                 ||||||||||||||| |||  ||
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                                ACGGACATTAGGGTCG TGA  CC
                                        _  AA
GAM380  LAMP3    3'  CCCGAGTAGCTGGGATTACAGG 60201                A
            CA                   TGCCTGTAGTCCCAGCTACTC GG
                                 |||||||||||||||||||| ||
                                 ACGGACATTAGGGTCGATGAG CC
                                        C
GAM380  LY75     3'  CCAAAGTGCTGGGATTACAGGC 11390            T  CA
            A                    TGCCTGTAGTCCCAGC ACT  GG
                                 |||||||||||||||| |||  ||
                                 ACGGACATTAGGGTCG TGA  CC
                                        _  AA
GAM380  LY75     3'  CCTGAGTAGCTGGGATTACAGG 11392
            CA                   TGCCTGTAGTCCCAGCTACTCAGG
                                 |||||||||||||||||||||||
                                 ACGGACATTAGGGTCGATGAGTCC

GAM380  MAP-1    3'  CCCGAGTAGCTGGGACTACAGG 42439                A
            CA                   TGCCTGTAGTCCCAGCTACTC GG
                                 |||||||||||||||||||| ||
                                 ACGGACATCAGGGTCGATGAG CC
                                        C
GAM380  MCLC     3'  CCAAAGTGCTGGGATTACAGGC 31379            T  CA
            A                    TGCCTGTAGTCCCAGC ACT  GG
                                 |||||||||||||||| |||  ||
                                 ACGGACATTAGGGTCG TGA  CC
                                        _  AA
GAM380  MCLC     3'  CCGAGTAGCTAGGATTACAG  31380         C      A
                                 CTGTAGTCC AGCTACTC GG
                                 ||||||||| |||||||| ||
                                 GACATTAGG TCGATGAG CC
                                       A      C
GAM380  MEF-2    3'  CCTGAGTAGCTGGGATTACAGG 65021
            CA                   TGCCTGTAGTCCCAGCTACTCAGG
                                 |||||||||||||||||||||||
                                 ACGGACATTAGGGTCGATGAGTCC

GAM380  MGC10200 3'  CCTGAATGGCTGGGACTACAAG 59639    C          C
            C                    GC TGTAGTCCCAGCTA TCAGG
                                 || |||||||||||||| |||||
                                 CG ACATCAGGGTCGGT AGTCC
                                  A           A
GAM380  MGC10818 3'  CCTGAGTAACTGGAATTGCAG  48300       C   C
                                 CTGTAGT CCAG TACTCAGG
                                 ||||||| |||| ||||||||
                                 GACGTTA GGTC ATGAGTCC
                                     A   A
GAM380  MGC11386 5'  CCCGAGTAGCTGGAAGTACAG  53060      GTC       A
                                 CTGTA   CCAGCTACTC GG
                                 |||||   |||||||||| ||
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                                GACAT   GGTCGATGAG CC
                                   GAA         C
GAM380  MGC12466 3' CCTATGTAGCTGGAGCTACAGA 79795    C     TC       TC
            CA                   TG CTGTAG  CCAGCTAC  AGG
                                || ||||||  ||||||||  |||
                                AC GACATC  GGTCGATG  TCC
                                 A     GA       TA
GAM380  MGC12518 3' CCAAAGTGCTGGGATTACAGGC 64775              T   CA
            A                    TGCCTGTAGTCCCAGC ACT  GG
                                |||||||||||||||| |||  ||
                                ACGGACATTAGGGTCG TGA  CC
                                          _  AA
GAM380  MGC12518 3' CCCGAGTAGCTGGGATTATAGG 64776                 A
            C                    GCCTGTAGTCCCAGCTACTC GG
                                |||||||||||||||||||| ||
                                CGGATATTAGGGTCGATGAG CC
                                           C
GAM380  MGC12981 3' CTGAGTAGCTGGGCAGC     51360    A T
                                GT G CCCAGCTACTCAG
                                || | ||||||||||||
                                CG C GGGTCGATGAGTC
                                 A _
GAM380  MGC13138 3' CCCAAGTAGCTGGGACTACAGG 54157                  CA
            CA                   TGCCTGTAGTCCCAGCTACT  GG
                                |||||||||||||||||||  ||
                                ACGGACATCAGGGTCGATGA  CC
                                           AC
GAM380  MGC13204 3' AGTAGCTGGGATTACAGGCA   49624
                                TGCCTGTAGTCCCAGCTACT
                                ||||||||||||||||||||
                                ACGGACATTAGGGTCGATGA

GAM380  MGC14289 3' CCAGAGTGCTAGGATTACAGGC 55589           C  T   A
            A                    TGCCTGTAGTCC AGC ACTC GG
                                |||||||||||| ||| |||| ||
                                ACGGACATTAGG TCG TGAG CC
                                       A  _   A
GAM380  MGC14289 3' CCTGAGTAGCTGGGACTACAGG 55591
            TA                   TGCCTGTAGTCCCAGCTACTCAGG
                                |||||||||||||||||||||||||
                                ATGGACATCAGGGTCGATGAGTCC

GAM380  MGC15606 5' CCTGAGTAACTGGGACTATAGG 59523           C
                                CCTGTAGTCCCAG TACTCAGG
                                |||||||||||| ||||||||
                                GGATATCAGGGTC ATGAGTCC
                                       A
GAM380  MGC1842  3' TAGCTGGGACTACAGGCA    66263
                                TGCCTGTAGTCCCAGCTA
                                ||||||||||||||||||
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                                ACGGACATCAGGGTCGAT

GAM380  MGC21675  3'  CCAAAGTGCTGAGATTACAGGC 54588          C   T  CA
            A                    TGCCTGTAGTC CAGC ACT  GG
                                 |||||||||||  |||| |||  ||
                                 ACGGACATTAG GTCG TGA  CC
                                       A   _  AA
GAM380  MGC21675  3'  CCCGAGTAGCTGGAATTGCAGA 54590   C     C       A
            CA                    TG CTGTAGT CCAGCTACTC GG
                                  || |||||||  |||||||||| ||
                                  AC GACGTTA GGTCGATGAG CC
                                   A      A        C
GAM380  MGC2474   3'  CCCAAGTAGCTGGAATTACAGG 43955         C       CA
            CA                    TGCCTGTAGT CCAGCTACT  GG
                                  ||||||||||  |||||||||  ||
                                  ACGGACATTA GGTCGATGA  CC
                                        A        AC
GAM380  MGC2477   5'  CCCGAGTAGCTGGGACTACAGG 44297               A
            C                     GCCTGTAGTCCCAGCTACTC GG
                                  ||||||||||||||||||| ||
                                  CGGACATCAGGGTCGATGAG CC
                                              C
GAM380  MGC2603   3'  CCAAAGTGCTGAGATTACAGGC 44072          C   T  CA
            A                    TGCCTGTAGTC CAGC ACT  GG
                                 |||||||||||  |||| |||  ||
                                 ACGGACATTAG GTCG TGA  CC
                                       A   _  AA
GAM380  MGC2603   3'  CCCGAATAGCAGGGACTACAGG 44073           A   C  A
            CA                    TGCCTGTAGTCCC GCTA TC GG
                                  ||||||||||||  |||| || ||
                                  ACGGACATCAGGG CGAT AG CC
                                        A   A  C
GAM380  MGC2668   3'  CCTGAGTAGCTGAAGGAAGGC  61191     GTAG  __
                                  GCCT   TCC  CAGCTACTCAGG
                                  ||||   |||  ||||||||||||
                                  CGGA   AGG  GTCGATGAGTCC
                                    ____  AA
GAM380  MGC29891  3'  CCTGAGTAGCTGGGAGGACAGG 58859       AG
            CA                    TGCCTGT  TCCCAGCTACTCAGG
                                  |||||||  ||||||||||||||||
                                  ACGGACA  AGGGTCGATGAGTCC
                                     GG
GAM380  MGC3113   3'  CCTGAATAGCTGGGACTACAGG 44060              C
            C                     GCCTGTAGTCCCAGCTA TCAGG
                                  |||||||||||||||| |||||
                                  CGGACATCAGGGTCGAT AGTCC
                                              A
GAM380  MGC3771   5'  CCTGATTACCTGGGATTACAGG 49053            C  C
            CA                    TGCCTGTAGTCCCAG TA TCAGG
                                  |||||||||||||| || |||||
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                                ACGGACATTAGGGTC AT AGTCC
                                      C  T
GAM380  MGC4638  3'  CCCGAGCAGCTGGGATTACAGG 49735            A  A
          C                    GCCTGTAGTCCCAGCT CTC GG
                               |||||||||||||||| ||| ||
                               CGGACATTAGGGTCGA GAG CC
                                     C  C
GAM380  MGC5149  3'  CCCAAGTAGCTGGGACTACAGG 72756              CA
          CA                   TGCCTGTAGTCCCAGCTACT  GG
                               |||||||||||||||||||  ||
                               ACGGACATCAGGGTCGATGA  CC
                                      AC
GAM380  MGC9912  3'  CCCAAGTAGCTGGGACTACAGG 55606              CA
          CA                   TGCCTGTAGTCCCAGCTACT  GG
                               |||||||||||||||||||  ||
                               ACGGACATCAGGGTCGATGA  CC
                                      AC
GAM380  MLZE     5'  CCCAAGTAGCTGGGATTACAG  49449            CA
                               CTGTAGTCCCAGCTACT  GG
                               ||||||||||||||||  ||
                               GACATTAGGGTCGATGA  CC
                                      AC
GAM380  MMPL1    3'  CCTGAGTAGCTGGGACCACAGG 15962       A
          CA                   TGCCTGT GTCCCAGCTACTCAGG
                               |||||||  ||||||||||||||||
                               ACGGACA CAGGGTCGATGAGTCC
                                  C
GAM380  moblak   3'  AGCAGCTGGGACTACAGGCA  56385            A
                               TGCCTGTAGTCCCAGCT CT
                               ||||||||||||||||  ||
                               ACGGACATCAGGGTCGA GA
                                      C
GAM380  moblak   3'  CCCAAGTAGCTGGGATTACAG  56393            CA
                               CTGTAGTCCCAGCTACT  GG
                               ||||||||||||||||  ||
                               GACATTAGGGTCGATGA  CC
                                      AC
GAM380  MOCS3    3'  CCTGAGTAGCTGGGATTACAGG 27930
          C                    GCCTGTAGTCCCAGCTACTCAGG
                               ||||||||||||||||||||||
                               CGGACATTAGGGTCGATGAGTCC

GAM380  MRPL44   3'  CCTAGTAGCTGGGATTACAGGC 43595              C
          A                    TGCCTGTAGTCCCAGCTACT AGG
                               ||||||||||||||||||  |||
                               ACGGACATTAGGGTCGATGA TCC
                                                   _
GAM380  MtFMT    3'  CCTGAGTAGCTGGGATTACAGG 58334
          CA                   TGCCTGTAGTCCCAGCTACTCAGG
                               ||||||||||||||||||||||
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                                ACGGACATTAGGGTCGATGAGTCC

GAM380  MYO5C    3'  CCTGAGTAGCTGGGACTACAGG 38716
                CA                TGCCTGTAGTCCCAGCTACTCAGG
                                  ||||||||||||||||||||||||
                                  ACGGACATCAGGGTCGATGAGTCC

GAM380  NDP52    3'  CCCAAGTAGCTGGGATTACAG  20668              CA
                                  CTGTAGTCCCAGCTACT  GG
                                  ||||||||||||||||  ||
                                  GACATTAGGGTCGATGA  CC
                                        AC
GAM380  NDUFC2   3'  CCCGAGTAGCTGGGACTACAGG 17027                A
                T                  GCCTGTAGTCCCAGCTACTC GG
                                   ||||||||||||||||||| ||
                                   TGGACATCAGGGTCGATGAG CC
                                         C
GAM380  NEIL2    3'  CCAGAGTAGCTGGGACTACAGG 59567                A
                CA                 TGCCTGTAGTCCCAGCTACTC GG
                                   ||||||||||||||||||| ||
                                   ACGGACATCAGGGTCGATGAG CC
                                         A
GAM380  NFAT5    3'  CCAAAGTGCTAGGATTACAGGC 57762          C  T  CA
                A                  TGCCTGTAGTCC AGC ACT  GG
                                   |||||||||||| ||| |||  ||
                                   ACGGACATTAGG TCG TGA  CC
                                         A  _  AA
GAM380  NFAT5    3'  CCCAAGTAGCCAGGATTACAGG 57765          CA    CA
                CA                 TGCCTGTAGTCC  GCTACT  GG
                                   ||||||||||||  ||||||  ||
                                   ACGGACATTAGG  CGATGA  CC
                                         AC     AC
GAM380  NINJ2    3'  CCCGAGTAGCTGGGGTTACAGG 33719        GT        A
                CA                 TGCCTGTA  CCCAGCTACTC GG
                                   ||||||||  ||||||||||| ||
                                   ACGGACAT  GGGTCGATGAG CC
                                       TG         C
GAM380  NOSIP    5'  CCCGAGTAGCTGGGATTACAG  32541                A
                                   CTGTAGTCCCAGCTACTC GG
                                   ||||||||||||||||| ||
                                   GACATTAGGGTCGATGAG CC
                                         C
GAM380  NXN      3'  CCCGAGTAGCTGGGATTACAGG 42671                A
                CA                 TGCCTGTAGTCCCAGCTACTC GG
                                   ||||||||||||||||||| ||
                                   ACGGACATTAGGGTCGATGAG CC
                                         C
GAM380  OR51E2   3'  CCCGAGTAGCTGGGACTAGAGG 48507     G          A
                                   CCT TAGTCCCAGCTACTC GG
                                   ||| |||||||||||||| ||
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                                GGA ATCAGGGTCGATGAG CC
                                  G           C
GAM380  OSBPL2   3'  CCCAAGTAGCTGGGATTACAGG 58481                CA
            CA                    TGCCTGTAGTCCCAGCTACT  GG
                                  ||||||||||||||||||  ||
                                  ACGGACATTAGGGTCGATGA  CC
                                        AC
GAM380  PELI1    5'  CCCAAGTAGCTAGGACTACAAG 40634     _     C     CA
            GC                    GCCT GTAGTCC AGCTACT  GG
                                  |||| ||||||| |||||||  ||
                                  CGGA CATCAGG TCGATGA  CC
                                    A     A      AC
GAM380  PELI1    5'  CCCGAGTAGCTAGGACTACAGG 40635          C      A
            CA                    TGCCTGTAGTCC AGCTACTC GG
                                  |||||||||||| ||||||| ||
                                  ACGGACATCAGG TCGATGAG CC
                                        A      C
GAM380  PELI1    5'  CCTTAGTAGCTGGGATTACAGG 40637               C
            CA                    TGCCTGTAGTCCCAGCTACT AGG
                                  |||||||||||||||||| |||
                                  ACGGACATTAGGGTCGATGA TCC
                                        T
GAM380  PIP3-E   3'  CCCGAGTAGCTGGGACTAC   67349            A
                                  GTAGTCCCAGCTACTC GG
                                  |||||||||||||| ||
                                  CATCAGGGTCGATGAG CC
                                       C
GAM380  POLR2D   3'  CTGGTGAGATTACAGGCA    17841          ___
                                  TGCCTGTAGTC  CCAG
                                  ||||||||||  ||||
                                  ACGGACATTAG  GGTC
                                      AGT
GAM380  PRO0365  5'  CCCGAGTAGCTGGGACTACAGG 26979               A
            CA                    TGCCTGTAGTCCCAGCTACTC GG
                                  |||||||||||||||||| ||
                                  ACGGACATCAGGGTCGATGAG CC
                                        C
GAM380  PRO0456  5'  CCCAAGTAGCTAGGACTACAGG 27006          C     CA
            C                      GCCTGTAGTCC AGCTACT  GG
                                  |||||||||| |||||||  ||
                                  CGGACATCAGG TCGATGA  CC
                                      A      AC
GAM380  PRO1048  3'  CCAAGGTGTTGGGACCACAGGC 38105       A      T  CA
                                  GCCTGT GTCCCAGC ACT  GG
                                  |||||| ||||||| |||  ||
                                  CGGACA CAGGGTTG TGG  CC
                                     C       _  AA
GAM380  PRO1992  3'  CCAAAGTGCTGGGATTACAGGC 26897             T  CA
            A                      TGCCTGTAGTCCCAGC ACT  GG
                                  |||||||||||||| |||  ||
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                                ACGGACATTAGGGTCG TGA  CC
                                        _  AA
GAM380  PRO1992  3'  CCCAAGCAGCTGGGATTGTAGG 26900            A  CA
          TA                    TGCCTGTAGTCCCAGCT CT  GG
                                |||||||||||||||| ||  ||
                                ATGGATGTTAGGGTCGA GA  CC
                                      C  AC
GAM380  PRO1992  5'  CCCGAGTAGCTGGGCTTACGGG 26902       T       A
          CA                    TGCCTGTAG CCCAGCTACTC GG
                                ||||||||| |||||||||| ||
                                ACGGGCATT GGGTCGATGAG CC
                                     C         C
GAM380  PRO2955  3'  CCTGAGTAGCTGGGATTACAGG 38237
          CA                    TGCCTGTAGTCCCAGCTACTCAGG
                                ||||||||||||||||||||||||
                                ACGGACATTAGGGTCGATGAGTCC

GAM380  PSPH     3'  CCCGAGTAGCTGGGACTACAGG 17132             A
          CA                    TGCCTGTAGTCCCAGCTACTC GG
                                |||||||||||||||||| ||
                                ACGGACATCAGGGTCGATGAG CC
                                      C
GAM380  PSTPIP2  3'  CCTGAGTAGCTGGGATTACAGG 44653
          CA                    TGCCTGTAGTCCCAGCTACTCAGG
                                ||||||||||||||||||||||||
                                ACGGACATTAGGGTCGATGAGTCC

GAM380  RAB21    3'  CCCGAGTAGCTGGGACTATAGG 31086             A
          C                     GCCTGTAGTCCCAGCTACTC GG
                                |||||||||||||||||| ||
                                CGGATATCAGGGTCGATGAG CC
                                      C
GAM380  RAB33B   3'  CCCGAGTAGCTGGGATTACAGG 49322             A
          C                     GCCTGTAGTCCCAGCTACTC GG
                                |||||||||||||||||| ||
                                CGGACATTAGGGTCGATGAG CC
                                      C
GAM380  RAB39    3'  CCTGAGTAGCTGGAACTGCAG  77122       C
                                CTGTAGT CCAGCTACTCAGG
                                ||||||| ||||||||||||
                                GACGTCA GGTCGATGAGTCC
                                   A
GAM380  RAP140   3'  CCCGAATGGCTGGGACTACAGG 31512            C  A
          CA                    TGCCTGTAGTCCCAGCTA TC GG
                                |||||||||||||||| || ||
                                ACGGACATCAGGGTCGGT AG CC
                                      A  C
GAM380  RASSF2   3'  CCCAAGTAGCTGGAATTACAGG 29093       C       CA
                                CCTGTAGT CCAGCTACT  GG
                                |||||||| |||||||||  ||
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                                GGACATTA GGTCGATGA  CC
                                    A        AC
GAM380  RES4-25  3'  CCCGAGTAGCTGGGATTACAGA 65264    C             A
          CA                    TG CTGTAGTCCCAGCTACTC GG
                                || |||||||||||||||||| ||
                                AC GACATTAGGGTCGATGAG CC
                                 A              C
GAM380  RNF8     3'  CCAAAGTGCTGAGATTACAGGC 15562          C   T  CA
          A                     TGCCTGTAGTC CAGC ACT  GG
                                |||||||||| |||| |||  ||
                                ACGGACATTAG GTCG TGA  CC
                                      A   _  AA
GAM380  RNF8     3'  CCCAAGTAGCTGGGACTACAGG 15563               CA
          CA                    TGCCTGTAGTCCCAGCTACT  GG
                                |||||||||||||||||||  ||
                                ACGGACATCAGGGTCGATGA  CC
                                      AC
GAM380  RNO2     5'  CCTGAGCAGCTGGGACCGCGGG 53931      TA       A
                                CCTG  GTCCCAGCT CTCAGG
                                ||||  ||||||||| ||||||
                                GGGC  CAGGGTCGA GAGTCC
                                  GC        C
GAM380  SAMHD1   3'  CCCAAGTAGCTGGGACTAAAGT 61980    C  G          CA
          CA                    TG CT TAGTCCCAGCTACT  GG
                                || || ||||||||||||  ||
                                AC GA ATCAGGGTCGATGA  CC
                                 T  A            AC
GAM380  SC4MOL   3'  CCCAAGTAGCTGGGATTACAGG 23103               CA
          CA                    TGCCTGTAGTCCCAGCTACT  GG
                                |||||||||||||||||||  ||
                                ACGGACATTAGGGTCGATGA  CC
                                      AC
GAM380  SCYA16   3'  CCTGAGTAGCTGGGACTACAGG 17169
          C                     GCCTGTAGTCCCAGCTACTCAGG
                                |||||||||||||||||||||||
                                CGGACATCAGGGTCGATGAGTCC

GAM380  SCYA22   3'  CCAAGTAGCTGGGATTACAG  92582            CA
                                CTGTAGTCCCAGCTACT  GG
                                ||||||||||||||||  ||
                                GACATTAGGGTCGATGA  CC
                                     AC
GAM380  SCYA22   3'  CCTGAGTAGCTGGGATTACAG  92589
                                CTGTAGTCCCAGCTACTCAGG
                                |||||||||||||||||||||
                                GACATTAGGGTCGATGAGTCC

GAM380  SCYA28   3'  CCAGGGTGCTGGGATTACAGGC 39539            T   A
          A                     TGCCTGTAGTCCCAGC ACTC GG
                                |||||||||||||||| ||||| ||
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                                ACGGACATTAGGGTCG TGGG CC
                                        _   A
GAM380  SERF1B   3'  CCTGGGTAGCTGGGATTACAGG 43695
            CA                   TGCCTGTAGTCCCAGCTACTCAGG
                                 ||||||||||||||||||||||
                                 ACGGACATTAGGGTCGATGGGTCC

GAM380  SERF2    5'  CCTGAGTAGCTAAGGACTACA  20490        C_
                                 TGTAGTCC  AGCTACTCAGG
                                 ||||||||  ||||||||||
                                 ACATCAGG  TCGATGAGTCC
                                     AA
GAM380  SIRPB1   3'  CCAAAGTGCTGGGATTACAGGC 21358            T   CA
            A                    TGCCTGTAGTCCCAGC ACT  GG
                                 ||||||||||||||| |||  ||
                                 ACGGACATTAGGGTCG TGA  CC
                                        _  AA
GAM380  SIRPB1   3'  CCTGAGTAGCTGGGATTACAGG 21363
            CA                   TGCCTGTAGTCCCAGCTACTCAGG
                                 ||||||||||||||||||||||
                                 ACGGACATTAGGGTCGATGAGTCC

GAM380  SLC16A4  3'  CCCAAGTAGCTGGGACTACAGG 17449               CA
            CA                   TGCCTGTAGTCCCAGCTACT  GG
                                 ||||||||||||||||||  ||
                                 ACGGACATCAGGGTCGATGA  CC
                                        AC
GAM380  SLC2A10  3'  CCTAAGTAGCTGGGATTACAGG 48546              C
            C                     GCCTGTAGTCCCAGCTACT AGG
                                  |||||||||||||||||| |||
                                  CGGACATTAGGGTCGATGA TCC
                                        A
GAM380  SQV7L    5'  CCTAAGTAGCTGAGACCACAGG 71094      A  C      C
                                 CCTGT GTC CAGCTACT AGG
                                 |||||  |||  ||||||||  |||
                                 GGACA CAG GTCGATGA TCC
                                    C  A       A
GAM380  SREC     3'  CCCGAGTAGCTGGGACTACAGG 14901              A
            T                     GCCTGTAGTCCCAGCTACTC GG
                                  |||||||||||||||||||  ||
                                  TGGACATCAGGGTCGATGAG CC
                                        C
GAM380  SRF      3'  CCTGAGTAGCTGGGCCTGTGCA 13394     CTG   T
                                 TGC   TAG CCCAGCTACTCAGG
                                 |||   ||| ||||||||||||||
                                 ACG   GTC GGGTCGATGAGTCC
                                   T__   C
GAM380  SS-56    3'  CCCGAGTAGCTGGGACTACAGG 60347              A
            C                     GCCTGTAGTCCCAGCTACTC GG
                                  |||||||||||||||||||  ||
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                                  CGGACATCAGGGTCGATGAG CC
                                                    C
GAM380  STAF65(gamma) 3'  CCTGAGTAGCTGGGATTACACG 30067     C
            CA                     TGC TGTAGTCCCAGCTACTCAGG
                                   ||| ||||||||||||||||||||
                                   ACG ACATTAGGGTCGATGAGTCC
                                     C
GAM380  STRBP    5'  CCAAGGTGCTGGGATTACAGGC 37816             T   CA
            A                      TGCCTGTAGTCCCAGC ACT  GG
                                   |||||||||||||||| |||  ||
                                   ACGGACATTAGGGTCG TGG  CC
                                              _  AA
GAM380  SULT1C2  3'  CCCGAGTAGCTGGGACTATGGG 22711                A
            C                      GCCTGTAGTCCCAGCTACTC GG
                                   |||||||||||||||||||| ||
                                   CGGGTATCAGGGTCGATGAG CC
                                                    C
GAM380  SUN1     3'  CCTGAGTAGCTGGGACTACAGG 47912
            C                      GCCTGTAGTCCCAGCTACTCAGG
                                   ||||||||||||||||||||||
                                   CGGACATCAGGGTCGATGAGTCC

GAM380  SYTL4    5'  CCAAAGTGCTGGGATTACAGGC 55783             T   CA
            A                      TGCCTGTAGTCCCAGC ACT  GG
                                   |||||||||||||||| |||  ||
                                   ACGGACATTAGGGTCG TGA  CC
                                              _  AA
GAM380  TADA3L   3'  CCTGAGTAGCTGATACTACAGG 22037          CC
            CA                      TGCCTGTAGT  CAGCTACTCAGG
                                    ||||||||||  ||||||||||||
                                    ACGGACATCA  GTCGATGAGTCC
                                          TA
GAM380  TCL6     5'  CCAAAGTGCTGGGATTACAGGC 40464             T   CA
            A                      TGCCTGTAGTCCCAGC ACT  GG
                                   |||||||||||||||| |||  ||
                                   ACGGACATTAGGGTCG TGA  CC
                                              _  AA
GAM380  TCL6     5'  CCCAAGCAGCTAAGACTACAG  40466         CC    A  CA
                                   CTGTAGTC  AGCT CT  GG
                                   ||||||||  |||| ||  ||
                                   GACATCAG  TCGA GA  CC
                                        AA    C  AC
GAM380  TCL6     5'  CCCAAGCAGCTAAGACTACAGA 40467    C       CC    A  CA
            CA                      TG CTGTAGTC  AGCT CT  GG
                                    || ||||||||  |||| ||  ||
                                    AC GACATCAG  TCGA GA  CC
                                     A       AA    C  AC
GAM380  TCL6     5'  CCCAAGTAGCTGGGATTACAG  40468              CA
                                   CTGTAGTCCCAGCTACT  GG
                                   ||||||||||||||||  ||
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                                GACATTAGGGTCGATGA  CC
                                      AC
GAM380  TGIF2    3'  CCCGAGTAGCTGGGATTATAGG 41742                A
           CA                  TGCCTGTAGTCCCAGCTACTC GG
                               |||||||||||||||||||| ||
                               ACGGATATTAGGGTCGATGAG CC
                                      C
GAM380  TOR1B    3'  CCCGAGTAGCTGGGATTACAGG 27969                A
           CA                  TGCCTGTAGTCCCAGCTACTC GG
                               |||||||||||||||||||| ||
                               ACGGACATTAGGGTCGATGAG CC
                                      C
GAM380  TPSG1    5'  CCTGAGTAGCTGGGACTACAGG 25890
           T                   GCCTGTAGTCCCAGCTACTCAGG
                               |||||||||||||||||||||||
                               TGGACATCAGGGTCGATGAGTCC

GAM380  TRIM16   3'  CCCGAGTAGCTGGGATTACAG  22369               A
                               CTGTAGTCCCAGCTACTC GG
                               |||||||||||||||| ||
                               GACATTAGGGTCGATGAG CC
                                      C
GAM380  TRIM35   3'  CCTGAGTAGCTGGGACTACAGG 61515
           CA                  TGCCTGTAGTCCCAGCTACTCAGG
                               |||||||||||||||||||||||
                               ACGGACATCAGGGTCGATGAGTCC

GAM380  TRIM5    3'  CCCAAGTAGCTGGGATTACAG  53467              CA
                               CTGTAGTCCCAGCTACT  GG
                               |||||||||||||||  ||
                               GACATTAGGGTCGATGA  CC
                                      AC
GAM380  TRIM6    3'  CCCAAGTAGCTGGGATTACAGG 55176               CA
           CA                  TGCCTGTAGTCCCAGCTACT  GG
                               |||||||||||||||||  ||
                               ACGGACATTAGGGTCGATGA  CC
                                      AC
GAM380  TU12B1-TY 3'  CCAAGGTGCTGGGATTACAGGC 33832             T  CA
           A                   TGCCTGTAGTCCCAGC ACT  GG
                               |||||||||||||| |||  ||
                               ACGGACATTAGGGTCG TGG  CC
                                      _  AA
GAM380  TU12B1-TY 3'  CCCAAGTAGCTGGGATTACAGG 33836               CA
           CA                  TGCCTGTAGTCCCAGCTACT  GG
                               |||||||||||||||||  ||
                               ACGGACATTAGGGTCGATGA  CC
                                      AC
GAM380  TU12B1-TY 3'  CCCGAGTAGCTGGGACTACTGG 33840     T          A
           TA                  TGCC GTAGTCCCAGCTACTC GG
                               |||| ||||||||||||||| ||
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                                ATGG CATCAGGGTCGATGAG CC
                                  T            C
GAM380  TU12B1-TY 3'  CCCGAGTAGCTGGGATTACAG  33841              A
                                CTGTAGTCCCAGCTACTC GG
                                |||||||||||||||||| ||
                                GACATTAGGGTCGATGAG CC
                                             C
GAM380  TUCAN    3'  CCTGAGTAGCTAGGACTACAGG 30972          C
          T                      GCCTGTAGTCC AGCTACTCAGG
                                |||||||||||| ||||||||||
                                TGGACATCAGG TCGATGAGTCC
                                      A
GAM380  TUCAN    3'  CCTGAGTAGCTGGGATTACAGG 30973
          CA                      TGCCTGTAGTCCCAGCTACTCAGG
                                |||||||||||||||||||||||
                                ACGGACATTAGGGTCGATGAGTCC

GAM380  TUSP     3'  CCCAAGCAGCTGGGATTATAGA 40019    C          A  CA
          CA                      TG CTGTAGTCCCAGCT CT  GG
                                || ||||||||||||| ||  ||
                                AC GATATTAGGGTCGA GA  CC
                                 A           C  AC
GAM380  TXNL2    3'  GTAGCTGGGACCACAGGC    22583       A
                                GCCTGT GTCCCAGCTAC
                                |||||| ||||||||||
                                CGGACA CAGGGTCGATG
                                   C
GAM380  UBF-fl   3'  CCAAAGTGCTGAAATTACAGGC 52620          CC   T  CA
          A                      TGCCTGTAGT  CAGC ACT  GG
                                ||||||||||  |||| |||  ||
                                ACGGACATTA  GTCG TGA  CC
                                      AA   _   AA
GAM380  USP3     5'  CCCAAGTAGCTGGGACTACAG  91251              CA
                                CTGTAGTCCCAGCTACT  GG
                                ||||||||||||||||  ||
                                GACATCAGGGTCGATGA  CC
                                           AC
GAM380  VDU1     3'  GAGTAGCTGGGATTACAGGCA  31126
                                TGCCTGTAGTCCCAGCTACTC
                                |||||||||||||||||||||
                                ACGGACATTAGGGTCGATGAG

GAM380  VMP      3'  CCCAAGTAGCTGGGACTACAGG 55760               CA
          CA                      TGCCTGTAGTCCCAGCTACT  GG
                                ||||||||||||||||||  ||
                                ACGGACATCAGGGTCGATGA  CC
                                           AC
GAM380  VPS33A   3'  CCTGAGTAGCTGGGACTACAGG 43612
          CA                      TGCCTGTAGTCCCAGCTACTCAGG
                                |||||||||||||||||||||||
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                                ACGGACATCAGGGTCGATGAGTCC

GAM380  WBSCR23  3'  CCCAAGTAGCTGGGATTACAGG 47427                CA
            CA                  TGCCTGTAGTCCCAGCTACT  GG
                                ||||||||||||||||||  ||
                                ACGGACATTAGGGTCGATGA  CC
                                      AC
GAM380  ZNF17    3'  CCAAAGTGCTGGGATTACAGGC 83268             T   CA
            A                   TGCCTGTAGTCCCAGC ACT  GG
                                |||||||||||||||| |||  ||
                                ACGGACATTAGGGTCG TGA  CC
                                      _  AA
GAM380  ZNF17    3'  CCCAAGTGTCTGGGATTACAGG 83270             C   CA
            CA                  TGCCTGTAGTCCCAG TACT  GG
                                ||||||||||||||| ||||  ||
                                ACGGACATTAGGGTC GTGA  CC
                                      T   AC
GAM380  ZNF221   3'  CCCGAGTAACTGGGACTACAGG 26267           C    A
            T                   GCCTGTAGTCCCAG TACTC GG
                                |||||||||||||| |||||  ||
                                TGGACATCAGGGTC ATGAG CC
                                      A   C
GAM380  ZNF339   3'  CCCGAGTAGCTGGGACTATAG  41389             A
                                CTGTAGTCCCAGCTACTC GG
                                |||||||||||||||||  ||
                                GATATCAGGGTCGATGAG CC
                                      C
GAM380  ZTL1     3'  CCTGAGTAGCTGGAATTACAGG 43518          C
            CA                  TGCCTGTAGT CCAGCTACTCAGG
                                ||||||||||  ||||||||||||
                                ACGGACATTA GGTCGATGAGTCC
                                     A
GAM380  LOC112687 3'  GTAGCTGGGATTACAGGCA   73240
                                TGCCTGTAGTCCCAGCTAC
                                |||||||||||||||||
                                ACGGACATTAGGGTCGATG

GAM380  LOC112724 5'  CCTGAGTAGCTGGGACTACAGG 57301
                                CCTGTAGTCCCAGCTACTCAGG
                                |||||||||||||||||||||
                                GGACATCAGGGTCGATGAGTCC

GAM380  LOC112817 3'  CCCGAGTAGCTGGGATTACAGG 57321               A
            C                   GCCTGTAGTCCCAGCTACTC GG
                                ||||||||||||||||||  ||
                                CGGACATTAGGGTCGATGAG CC
                                      C
GAM380  LOC113026 3'  GTAGCTGGGACTACAGGCA   56728
                                TGCCTGTAGTCCCAGCTAC
                                |||||||||||||||||
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                                ACGGACATCAGGGTCGATG

GAM380  LOC113523 3'  CCTGAGTAACTGAGATTACAGG 73419          C  C
              CA                TGCCTGTAGTC CAG TACTCAGG
                                |||||||||||  ||| ||||||||
                                ACGGACATTAG GTC ATGAGTCC
                                      A  A
GAM380  LOC115219 3'  CCAAGGTGCTGGGATTACAGGC 73693             T  CA
              A                 TGCCTGTAGTCCCAGC ACT  GG
                                |||||||||||||||  |||  ||
                                ACGGACATTAGGGTCG TGG  CC
                                         _  AA
GAM380  LOC115648 3'  CCTGAGTAGCTGGGATTACAG  60019
                                CTGTAGTCCCAGCTACTCAGG
                                ||||||||||||||||||||
                                GACATTAGGGTCGATGAGTCC

GAM380  LOC119392 3'  CCCGAGTAGCTGAGATTACAGG 59812          C       A
              C                 GCCTGTAGTC CAGCTACTC GG
                                ||||||||||  |||||||||  ||
                                CGGACATTAG GTCGATGAG CC
                                      A       C
GAM380  LOC120114 3'  CCAAAGTGCTGGGATTACAGGC 76042             T  CA
              A                 TGCCTGTAGTCCCAGC ACT  GG
                                |||||||||||||||  |||  ||
                                ACGGACATTAGGGTCG TGA  CC
                                         _  AA
GAM380  LOC120224 5'  CCCGAGTAGCTGGGACTACAGG 57885               A
              C                 GCCTGTAGTCCCAGCTACTC GG
                                ||||||||||||||||||  ||
                                CGGACATCAGGGTCGATGAG CC
                                           C
GAM380  LOC124216 3'  GTAGCTGGGATTACAGGCA   74739
                                TGCCTGTAGTCCCAGCTAC
                                |||||||||||||||||
                                ACGGACATTAGGGTCGATG

GAM380  LOC126133 3'  GTAGCTGGGGCCACAGACA   74913   C   A
                                TG CTGT GTCCCAGCTAC
                                ||  ||||  ||||||||||
                                AC GACA CGGGGTCGATG
                                 A   C
GAM380  LOC126364 3'  CCTGAGTAGCTGGGATTACAGC 76187    C
              A                 TGC TGTAGTCCCAGCTACTCAGG
                                |||  ||||||||||||||||||
                                ACG ACATTAGGGTCGATGAGTCC
                                  _
GAM380  LOC126661 3'  CCAAGTAGCTGGGATTACAG   75052            CA
                                CTGTAGTCCCAGCTACT  GG
                                ||||||||||||||||  ||
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                                GACATTAGGGTCGATGA  CC
                                      AC
GAM380  LOC126669 3'  CCCGAGTGCCTGGATTACAGGC 75930          CA  T   A
          A                    TGCCTGTAGTCC  GC ACTC GG
                               ||||||||||||  || |||| ||
                               ACGGACATTAGG  CG TGAG CC
                                     TC  _   C
GAM380  LOC128077 3'  CCCGAGTAGCTGGGATTACAG  75211              A
                               CTGTAGTCCCAGCTACTC GG
                               |||||||||||||||||| ||
                               GACATTAGGGTCGATGAG CC
                                      C
GAM380  LOC128077 3'  CCCGAGTAGCTGGGATTACAGG 75212               A
          CA                   TGCCTGTAGTCCCAGCTACTC GG
                               |||||||||||||||||||| ||
                               ACGGACATTAGGGTCGATGAG CC
                                      C
GAM380  LOC128387 3'  CCCAAGTAGCTGGGATTACAGG 75256               CA
          CA                   TGCCTGTAGTCCCAGCTACT  GG
                               |||||||||||||||||||  ||
                               ACGGACATTAGGGTCGATGA  CC
                                      AC
GAM380  LOC130813 3'  CCAAAGCACTGGGATTACAGGC 76267           CTA  CA
          A                    TGCCTGTAGTCCCAG   CT  GG
                               ||||||||||||||   ||  ||
                               ACGGACATTAGGGTC   GA  CC
                                     AC_  AA
GAM380  LOC130813 3'  CCTGAGTAGCTGGAATTACAGG 76271          C
          CA                   TGCCTGTAGT CCAGCTACTCAGG
                               |||||||||| ||||||||||||
                               ACGGACATTA GGTCGATGAGTCC
                                     A
GAM380  LOC131308 3'  CCCAAGTAGCTGGGACTACAGG 75493               CA
          CA                   TGCCTGTAGTCCCAGCTACT  GG
                               |||||||||||||||||||  ||
                               ACGGACATCAGGGTCGATGA  CC
                                      AC
GAM380  LOC131965 3'  CCTGAGTAGCTAGGACTACAGG 75522          C
          T                    GCCTGTAGTCC AGCTACTCAGG
                               ||||||||||| ||||||||||
                               TGGACATCAGG TCGATGAGTCC
                                     A
GAM380  LOC132241 3'  CCAAAGAACTGGGATTACAGGC 75555           CTA  CA
          A                    TGCCTGTAGTCCCAG   CT  GG
                               ||||||||||||||   ||  ||
                               ACGGACATTAGGGTC   GA  CC
                                     AA_  AA
GAM380  LOC132241 3'  CCCAAGTAGCTGGGACTACAGG 75557               CA
          CA                   TGCCTGTAGTCCCAGCTACT  GG
                               ||||||||||||||||||  ||
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                                ACGGACATCAGGGTCGATGA  CC
                                      AC
GAM380  LOC132625 3'  CCCAAGTAGCTGGGACTACAGG 76438              CA
          T                    GCCTGTAGTCCCAGCTACT  GG
                               ||||||||||||||||||  ||
                               TGGACATCAGGGTCGATGA  CC
                                     AC
GAM380  LOC133686 3'  AGTATTGGGATTACAGGCA   75610           C
                               TGCCTGTAGTCCCAG TACT
                               |||||||||||||| ||||
                               ACGGACATTAGGGTT ATGA
                                        _
GAM380  LOC133686 3'  CCCAAGTAGCTGGGATTACAGG 75614              CA
          CA                   TGCCTGTAGTCCCAGCTACT  GG
                               ||||||||||||||||||  ||
                               ACGGACATTAGGGTCGATGA  CC
                                     AC
GAM380  LOC134266 3'  AGTAGCTAGGACTACAGGC   75642          C
                               GCCTGTAGTCC AGCTACT
                               |||||||||| |||||||
                               CGGACATCAGG TCGATGA
                                     A
GAM380  LOC135154 3'  CCTGAGTAGCTGGGATTACAGA 75729    C
          CA                   TG CTGTAGTCCCAGCTACTCAGG
                               || ||||||||||||||||||||
                               AC GACATTAGGGTCGATGAGTCC
                                A
GAM380  LOC135293 3'  CCTAAAGTGCTGGGATTACAGG 76682            T  C_
          CA                   TGCCTGTAGTCCCAGC ACT  AGG
                               ||||||||||||||| |||  |||
                               ACGGACATTAGGGTCG TGA  TCC
                                     _  AA
GAM380  LOC135398 3'  CCCAAGTAGCTGGAACTATAGG 76467          C       CA
          CA                   TGCCTGTAGT CCAGCTACT  GG
                               |||||||||| |||||||||  ||
                               ACGGATATCA GGTCGATGA  CC
                                     A        AC
GAM380  LOC135763 3'  CCTGAGTAGCTGGAATTACAGG 57558        C
                               CCTGTAGT CCAGCTACTCAGG
                               |||||||| ||||||||||||
                               GGACATTA GGTCGATGAGTCC
                                    A
GAM380  LOC135818 3'  CCCAAGTAGGTGGGATTACAGG 75744            G    CA
          CA                   TGCCTGTAGTCCCA CTACT  GG
                               |||||||||||||| |||||  ||
                               ACGGACATTAGGGT GATGA  CC
                                     G    AC
GAM380  LOC138050 5'  CCTGAGTAGCTGGAACTGCAG  75814       C
                               CTGTAGT CCAGCTACTCAGG
                               ||||||| ||||||||||||
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                                GACGTCA GGTCGATGAGTCC
                                    A
GAM380  LOC138199 3'  CCTGAGTAGCTAGGACTGTAGG 75823          C
          CA                    TGCCTGTAGTCC AGCTACTCAGG
                                |||||||||||| ||||||||||
                                ACGGATGTCAGG TCGATGAGTCC
                                    A
GAM380  LOC143153 3'  GTAGCTAGGACTACAGGC    76981          C
                                GCCTGTAGTCC AGCTAC
                                |||||||||||| ||||||
                                CGGACATCAGG TCGATG
                                    A
GAM380  LOC143154 3'  GTAGCTAGGACTACAGGC    76992          C
                                GCCTGTAGTCC AGCTAC
                                |||||||||||| ||||||
                                CGGACATCAGG TCGATG
                                    A
GAM380  LOC143187 3'  CCCAAGTAGCTGGGACTACAGG 59756              CA
          CA                    TGCCTGTAGTCCCAGCTACT  GG
                                |||||||||||||||||||  ||
                                ACGGACATCAGGGTCGATGA  CC
                                      AC
GAM380  LOC144248 5'  CCCGAGTAGCTGGGATTACAGG 77252              A
          C                     GCCTGTAGTCCCAGCTACTC GG
                                |||||||||||||||||||| ||
                                CGGACATTAGGGTCGATGAG CC
                                      C
GAM380  LOC144305 3'  CCTACAAGTAGCTGGGACTACA 83970              C__
          GGC                     GCCTGTAGTCCCAGCTACT   AGG
                                |||||||||||||||||   |||
                                CGGACATCAGGGTCGATGA   TCC
                                      ACA
GAM380  LOC144317 5'  CCTGAGTAGCTGGGATGACAG  77292      A
                                CTGT GTCCCAGCTACTCAGG
                                |||| ||||||||||||||||
                                GACA TAGGGTCGATGAGTCC
                                  G
GAM380  LOC144742 5'  CTGAGTAGCTGGGACTACAGGC 77458
          A                     TGCCTGTAGTCCCAGCTACTCAG
                                |||||||||||||||||||||||
                                ACGGACATCAGGGTCGATGAGTC

GAM380  LOC144871 3'  AGTAGCTGGGACTATAGGCA   84117
                                TGCCTGTAGTCCCAGCTACT
                                ||||||||||||||||||||
                                ACGGATATCAGGGTCGATGA

GAM380  LOC145009 3'  CCAAAGTGCTGGGATTACAGGC 60970              T   CA
          A                     TGCCTGTAGTCCCAGC ACT  GG
                                |||||||||||||||| |||  ||
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                                ACGGACATTAGGGTCG TGA  CC
                                        _   AA
GAM380   LOC145009 3'  CCTGAGTAGTTGGGATTACAGG 60973
                CA                TGCCTGTAGTCCCAGCTACTCAGG
                                  ||||||||||||||||||||||||
                                  ACGGACATTAGGGTTGATGAGTCC

GAM380   LOC145082 5'  TAGCTGGGACTATAGGCA    84195
                                  TGCCTGTAGTCCCAGCTA
                                  ||||||||||||||||||
                                  ACGGATATCAGGGTCGAT

GAM380   LOC145127 3'  CCTACGCCTGGGCTACAGGCA  77542          T    CTACTC
                                  TGCCTGTAG CCCAG     AGG
                                  |||||||| |||||     |||
                                  ACGGACATC GGGTC     TCC
                                        _    CGCA__
GAM380   LOC145268 5'  CCCAAGTAGCTGGGATTACAG  77575               CA
                                  CTGTAGTCCCAGCTACT  GG
                                  ||||||||||||||||  ||
                                  GACATTAGGGTCGATGA  CC
                                        AC
GAM380   LOC145453 5'  CCAACGTGCTGGGATTACAGGC 77657               T  TCA
                CA                TGCCTGTAGTCCCAGC AC   GG
                                  |||||||||||||||  ||   ||
                                  ACGGACATTAGGGTCG TG   CC
                                        _  CAA
GAM380   LOC145622 3'  CCCAAGTAGCTGGGACTACAG  77812               CA
                                  CTGTAGTCCCAGCTACT  GG
                                  ||||||||||||||||  ||
                                  GACATCAGGGTCGATGA  CC
                                        AC
GAM380   LOC145725 3'  GAGTAGCTAGGACTACAGGCA  77884            C
                                  TGCCTGTAGTCC AGCTACTC
                                  |||||||||||| ||||||||
                                  ACGGACATCAGG TCGATGAG
                                        A
GAM380   LOC145732 3'  GAGTAGCTAGGACTACAGGCA  77896            C
                                  TGCCTGTAGTCC AGCTACTC
                                  |||||||||||| ||||||||
                                  ACGGACATCAGG TCGATGAG
                                        A
GAM380   LOC145757 5'  CCCGAGTAGCTGGGACTACAGA 77928    _             A
                GT                  GC CTGTAGTCCCAGCTACTC GG
                                    || |||||||||||||||| ||
                                    TG GACATCAGGGTCGATGAG CC
                                     A              C
GAM380   LOC145757 5'  CCTGAGTAGCTGGGATTACAGC 77929    C
                                  GC TGTAGTCCCAGCTACTCAGG
                                  || ||||||||||||||||||
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                                CG ACATTAGGGTCGATGAGTCC
                                   _
GAM380  LOC145813 5'  CCCAAGTAGCTGGAACTACAGG 84505          C        CA
              CA                  TGCCTGTAGT CCAGCTACT  GG
                                  |||||||||| |||||||||  ||
                                  ACGGACATCA GGTCGATGA  CC
                                        A         AC
GAM380  LOC146050 3'  CCAAAGTGCTGGGATTACAGGC 78107              T   CA
              A                   TGCCTGTAGTCCCAGC ACT  GG
                                  |||||||||||||||| |||  ||
                                  ACGGACATTAGGGTCG TGA  CC
                                        _  AA
GAM380  LOC146050 3'  CCCAAGTGGCTGGAATTACAAG 78111     C     C        CA
              CA                  TGC TGTAGT CCAGCTACT  GG
                                  ||| |||||| |||||||||  ||
                                  ACG ACATTA GGTCGGTGA  CC
                                    A     A         AC
GAM380  LOC146050 3'  CCTGAGTAGCTGGGATTACAGC 78113    C
              CA                  TG CTGTAGTCCCAGCTACTCAGG
                                  || ||||||||||||||||||||
                                  AC GACATTAGGGTCGATGAGTCC
                                   C
GAM380  LOC146229 3'  CCCAAGTAGCTGGGACTACAGG 78270                CA
              T                   GCCTGTAGTCCCAGCTACT  GG
                                  ||||||||||||||||||  ||
                                  TGGACATCAGGGTCGATGA  CC
                                        AC
GAM380  LOC146229 3'  CCCGAGGAGCTGGGATTACAGG 78271              A   A
              CA                  TGCCTGTAGTCCCAGCT CTC GG
                                  |||||||||||||||| ||| ||
                                  ACGGACATTAGGGTCGA GAG CC
                                        G   C
GAM380  LOC146336 3'  CCCGAGTAGCTGGGACTACAGG 78367                A
              T                   GCCTGTAGTCCCAGCTACTC GG
                                  |||||||||||||||||| ||
                                  TGGACATCAGGGTCGATGAG CC
                                        C
GAM380  LOC146346 5'  GTAGCTGGGATTACAGGCA    78405
                                  TGCCTGTAGTCCCAGCTAC
                                  |||||||||||||||||
                                  ACGGACATTAGGGTCGATG

GAM380  LOC146429 5'  CCTGAGTAGCTGGGATTACAGG 84663
              CA                  TGCCTGTAGTCCCAGCTACTCAGG
                                  ||||||||||||||||||||||
                                  ACGGACATTAGGGTCGATGAGTCC

GAM380  LOC146443 5'  CCCAAGTAGCTGGGATTACAGG 78439                CA
              C                   GCCTGTAGTCCCAGCTACT  GG
                                  ||||||||||||||||||  ||
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                                  CGGACATTAGGGTCGATGA  CC
                                                    AC
GAM380  LOC146603 5'  CCCGAGTAGCTGGGACTACAGG 78593                 A
              C                    GCCTGTAGTCCCAGCTACTC GG
                                   |||||||||||||||||||| ||
                                   CGGACATCAGGGTCGATGAG CC
                                                     C
GAM380  LOC146784 5'  CCAAAGTGCTGGGATTACAGGC 78707              T   CA
              A                    TGCCTGTAGTCCCAGC ACT  GG
                                   |||||||||||||||| |||  ||
                                   ACGGACATTAGGGTCG TGA  CC
                                                 _  AA
GAM380  LOC146820 5'  GTAGCTGGGATTACAGGCA   78739
                                   TGCCTGTAGTCCCAGCTAC
                                   ||||||||||||||||||
                                   ACGGACATTAGGGTCGATG

GAM380  LOC146839 3'  CCCAAGTAGCTGGGACTACAGG 84839                 CA
              C                    GCCTGTAGTCCCAGCTACT  GG
                                   |||||||||||||||||| ||
                                   CGGACATCAGGGTCGATGA  CC
                                                     AC
GAM380  LOC146894 3'  CCCAAATTGCCGGGATTACAGG 59856            A  TACTCA
              CA                     TGCCTGTAGTCCC GC     GG
                                   |||||||||||| ||     ||
                                   ACGGACATTAGGG CG     CC
                                             C  TTAAAC
GAM380  LOC146894 3'  CCCGAGTAGCTGGGATTACAGG 59857                 A
              CA                     TGCCTGTAGTCCCAGCTACTC GG
                                   |||||||||||||||||||| ||
                                   ACGGACATTAGGGTCGATGAG CC
                                                     C
GAM380  LOC146901 3'  CCAATGTGCTGGGATTACAGGC 84895              T  TCA
              A                    TGCCTGTAGTCCCAGC AC   GG
                                   |||||||||||||| ||   ||
                                   ACGGACATTAGGGTCG TG   CC
                                                _  TAA
GAM380  LOC146901 3'  CCCAAGTAGCTGAGATTACAG  84896         C       CA
                                   CTGTAGTC CAGCTACT  GG
                                   |||||||| ||||||||  ||
                                   GACATTAG GTCGATGA  CC
                                        A       AC
GAM380  LOC146909 3'  AGTAGCTGGGATTACAGGCA   78759
                                   TGCCTGTAGTCCCAGCTACT
                                   ||||||||||||||||||||
                                   ACGGACATTAGGGTCGATGA

GAM380  LOC146909 3'  CCAAAGTGCTGAGATTACAGGC 78762            C   T   CA
              A                    TGCCTGTAGTC CAGC ACT  GG
                                   |||||||||| |||| |||  ||
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                                ACGGACATTAG GTCG TGA  CC
                                      A   _  AA
GAM380  LOC146909 3'  CCCAAGTAGCTGGGACTACAGG 78765              CA
            C                  GCCTGTAGTCCCAGCTACT  GG
                               ||||||||||||||||||  ||
                               CGGACATCAGGGTCGATGA  CC
                                     AC
GAM380  LOC146952 5'  CCCAAGTAGCTGGGATTACAG  84925              CA
                               CTGTAGTCCCAGCTACT  GG
                               ||||||||||||||||  ||
                               GACATTAGGGTCGATGA  CC
                                     AC
GAM380  LOC147054 3'  CCCGAGTAGCTGGGACTACAGG 85003               A
            CA                  TGCCTGTAGTCCCAGCTACTC GG
                               ||||||||||||||||||| ||
                               ACGGACATCAGGGTCGATGAG CC
                                      C
GAM380  LOC147071 5'  CCTGAGTAGCTGGGATTGCAGG 73359
            TA                  TGCCTGTAGTCCCAGCTACTCAGG
                               ||||||||||||||||||||||
                               ATGGACGTTAGGGTCGATGAGTCC

GAM380  LOC147080 5'  CCCGAGCAGCTGGGACTACAGG 85029              A  A
            C                  GCCTGTAGTCCCAGCT CTC GG
                               |||||||||||||| ||| ||
                               CGGACATCAGGGTCGA GAG CC
                                     C  C
GAM380  LOC147093 5'  CCAAGGTGCTGGGACTACAGGC 85056              T  CA
                               GCCTGTAGTCCCAGC ACT  GG
                               |||||||||||||| |||  ||
                               CGGACATCAGGGTCG TGG  CC
                                     _  AA
GAM380  LOC147166 3'  CCCGAGTAGCTGGGATTACAG  78886              A
                               CTGTAGTCCCAGCTACTC GG
                               ||||||||||||||||| ||
                               GACATTAGGGTCGATGAG CC
                                      C
GAM380  LOC147276 3'  CCCGAAATGCTGGGATTACAGG 78955              TAC  A
            CA                  TGCCTGTAGTCCCAGC  TC GG
                               ||||||||||||||  || ||
                               ACGGACATTAGGGTCG  AG CC
                                     TAA  C
GAM380  LOC147276 3'  CCTGATTAGCTGGGATTACAGG 78957               C
            CA                  TGCCTGTAGTCCCAGCTA TCAGG
                               |||||||||||||||| |||||
                               ACGGACATTAGGGTCGAT AGTCC
                                      T
GAM380  LOC147694 3'  CCCGAGTAGCTGGGACTACAGG 79094               A
            T                   GCCTGTAGTCCCAGCTACTC GG
                               |||||||||||||||||| ||
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                                TGGACATCAGGGTCGATGAG CC
                                              C
GAM380  LOC147817 3'  CCCGAGTAGCTGGGACTACAGG 79171                A
          CA                    TGCCTGTAGTCCCAGCTACTC GG
                                |||||||||||||||||||| ||
                                ACGGACATCAGGGTCGATGAG CC
                                              C
GAM380  LOC147817 3'  CCTGAGTAGCTTGGATTACAGG 79175          C
          CA                    TGCCTGTAGTCC AGCTACTCAGG
                                |||||||||||| ||||||||||
                                ACGGACATTAGG TCGATGAGTCC
                                       T
GAM380  LOC147817 3'  GAGTAGCTGGGACTACAGACA  79178    C
                                TG CTGTAGTCCCAGCTACTC
                                || ||||||||||||||||
                                AC GACATCAGGGTCGATGAG
                                 A
GAM380  LOC147841 3'  GTAGCTGGGATTACAGGCA    79230
                                TGCCTGTAGTCCCAGCTAC
                                |||||||||||||||||
                                ACGGACATTAGGGTCGATG

GAM380  LOC147990 3'  CCCAAGTAGCTGGGACTATAG  85217              CA
                                CTGTAGTCCCAGCTACT  GG
                                ||||||||||||||||  ||
                                GATATCAGGGTCGATGA  CC
                                      AC
GAM380  LOC148137 3'  CCCGAGTAGCTGGGACTACAGG 59093                A
          T                     GCCTGTAGTCCCAGCTACTC GG
                                |||||||||||||||||||| ||
                                TGGACATCAGGGTCGATGAG CC
                                              C
GAM380  LOC148147 3'  AGTAGCTGGGACTACAGGC    79387
                                GCCTGTAGTCCCAGCTACT
                                |||||||||||||||||
                                CGGACATCAGGGTCGATGA

GAM380  LOC148189 5'  CCCAAGTATCTGGGACTACAGG 79447              C    CA
          CA                    TGCCTGTAGTCCCAG TACT  GG
                                |||||||||||||| ||||  ||
                                ACGGACATCAGGGTC ATGA  CC
                                       T    AC
GAM380  LOC148195 3'  CCCAAGTAGCTCCGATTACAGG 85275          CC       CA
          CA                    TGCCTGTAGTC  AGCTACT  GG
                                |||||||||||  |||||||  ||
                                ACGGACATTAG  TCGATGA  CC
                                      CC       AC
GAM380  LOC148195 5'  CCGAGGTAGCTGGGACTACAGG 85277                CA
          C                     GCCTGTAGTCCCAGCTACT  GG
                                |||||||||||||||||||  ||
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                                CGGACATCAGGGTCGATGG  CC
                                      AG
GAM380  LOC148198 3'  CCCAAGTAGCTGGGATTACAGG 71222                CA
          CA                    TGCCTGTAGTCCCAGCTACT  GG
                                |||||||||||||||||||  ||
                                ACGGACATTAGGGTCGATGA  CC
                                      AC
GAM380  LOC148443 3'  CCCAAGTAGCTAGGACTACAGC 79599     C       C       CA
          A                     TGC TGTAGTCC AGCTACT  GG
                                ||| |||||||| |||||||  ||
                                ACG ACATCAGG TCGATGA  CC
                                  _       A       AC
GAM380  LOC148645 5'  CCTGAGTAGCTGGGACGACAGG 85331        A
          C                     GCCTGT GTCCCAGCTACTCAGG
                                ||||||| ||||||||||||||||
                                CGGACA CAGGGTCGATGAGTCC
                                   G
GAM380  LOC148709 3'  CCCAAGTAGCTGGGATTACGGG 79689                CA
          CA                    TGCCTGTAGTCCCAGCTACT  GG
                                |||||||||||||||||||  ||
                                ACGGGCATTAGGGTCGATGA  CC
                                      AC
GAM380  LOC148887 5'  CCTGAGTAGCTGGGATTACAGG 85400
          C                     GCCTGTAGTCCCAGCTACTCAGG
                                ||||||||||||||||||||||
                                CGGACATTAGGGTCGATGAGTCC

GAM380  LOC148918 5'  CCTGAGAAGCTGGGACCACAGG 79824        A       A
          C                     GCCTGT GTCCCAGCT CTCAGG
                                |||||| ||||||||| ||||||
                                CGGACA CAGGGTCGA GAGTCC
                                   C        A
GAM380  LOC149113 3'  AGTAGCTGGAACTACAGGCA   79901          C
                                TGCCTGTAGT CCAGCTACT
                                |||||||||| |||||||||
                                ACGGACATCA GGTCGATGA
                                      A
GAM380  LOC149117 5'  CCCAAGTAGCTGGGATTACAG  85508              CA
                                CTGTAGTCCCAGCTACT  GG
                                ||||||||||||||||  ||
                                GACATTAGGGTCGATGA  CC
                                      AC
GAM380  LOC149127 3'  CCTGAGTAGCTGAAAGGATGAA 85498    GTA   ___
          G                     CT   GTCC   CAGCTACTCAGG
                                ||   ||||   ||||||||||||
                                GA   TAGG   GTCGATGAGTCC
                                 AG_    AAA
GAM380  LOC149171 5'  CCCGAGTAGCTGGGATTACAGG 79964                A
          CA                    TGCCTGTAGTCCCAGCTACTC GG
                                |||||||||||||||||||| ||
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                                ACGGACATTAGGGTCGATGAG CC
                                          C
GAM380  LOC149421 3'  CCAAAGTGCTGGGATTACAGGC 80141          T   CA
          A                    TGCCTGTAGTCCCAGC ACT  GG
                               ||||||||||||||| |||  ||
                               ACGGACATTAGGGTCG TGA  CC
                                       _   AA
GAM380  LOC149421 3'  CCCGAGTAGCTGGGACTACAGG 80143            A
          C                    GCCTGTAGTCCCAGCTACTC GG
                               |||||||||||||||||||| ||
                               CGGACATCAGGGTCGATGAG CC
                                          C
GAM380  LOC149478 3'  CCTGAGTAGCTGGGATTACAGA 80165    C
          CA                    TG CTGTAGTCCCAGCTACTCAGG
                               || ||||||||||||||||||||
                               AC GACATTAGGGTCGATGAGTCC
                                A
GAM380  LOC149506 3'  CCCGAGTAGCTGGGATTGCAG  85631            A
                               CTGTAGTCCCAGCTACTC GG
                               |||||||||||||||||| ||
                               GACGTTAGGGTCGATGAG CC
                                          C
GAM380  LOC149506 3'  CCTGAGTAGCTGGGATTACAGG 85632
          C                    GCCTGTAGTCCCAGCTACTCAGG
                               ||||||||||||||||||||||
                               CGGACATTAGGGTCGATGAGTCC

GAM380  LOC149577 3'  CCAAAGTGCTGGGATTACAGGC 85667          T   CA
          A                    TGCCTGTAGTCCCAGC ACT  GG
                               ||||||||||||||| |||  ||
                               ACGGACATTAGGGTCG TGA  CC
                                       _   AA
GAM380  LOC149577 3'  CCTGAGTAGCTGGGATTACAG  85672
                               CTGTAGTCCCAGCTACTCAGG
                               ||||||||||||||||||||
                               GACATTAGGGTCGATGAGTCC

GAM380  LOC149692 3'  CCAAAGTGCTGGCACTACAGGC 85728        C    T   CA
          A                    TGCCTGTAGT CCAGC ACT  GG
                               |||||||||| ||||| |||  ||
                               ACGGACATCA GGTCG TGA  CC
                                     C    _   AA
GAM380  LOC149692 3'  CCCAAGTAGCTGGGATTACAG  85730            CA
                               CTGTAGTCCCAGCTACT  GG
                               ||||||||||||||||  ||
                               GACATTAGGGTCGATGA  CC
                                          AC
GAM380  LOC149703 5'  CCCAAGTAGCTGGAATTACAGG 85818        C       CA
          C                    GCCTGTAGT CCAGCTACT  GG
                               |||||||| |||||||||  ||
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                                CGGACATTA GGTCGATGA  CC
                                     A        AC
GAM380  LOC149711 3'  CCAAGTAGCTGGGATTACAG   85845              CA
                                CTGTAGTCCCAGCTACT  GG
                                |||||||||||||||||  ||
                                GACATTAGGGTCGATGA  CC
                                        AC
GAM380  LOC150054 5'  AGTAGCTGGGAGTACAAGCA   85966     C    G
                                TGC TGTA TCCCAGCTACT
                                ||| |||| ||||||||||
                                ACG ACAT AGGGTCGATGA
                                  A    G
GAM380  LOC150166 5'  AGTGGCTAGAACTACAGGC    86030         CCC
                                GCCTGTAGT   AGCTACT
                                |||||||||   |||||||
                                CGGACATCA   TCGGTGA
                                     AGA
GAM380  LOC150225 3'  CCCGAGTAGCTGGGATTACAGG 86186                 A
          CA                      TGCCTGTAGTCCCAGCTACTC GG
                                  ||||||||||||||||||||| ||
                                  ACGGACATTAGGGTCGATGAG CC
                                              C
GAM380  LOC150282 5'  CCAAAGTGCTGGGATTACAGGC 80539              T   CA
          A                       TGCCTGTAGTCCCAGC ACT  GG
                                  |||||||||||||||| |||  ||
                                  ACGGACATTAGGGTCG TGA  CC
                                            _   AA
GAM380  LOC150282 5'  CCTGAGTAGCTGGGACTACAGG 80542
          C                       GCCTGTAGTCCCAGCTACTCAGG
                                  |||||||||||||||||||||||
                                  CGGACATCAGGGTCGATGAGTCC

GAM380  LOC150397 3'  CCCGAGTAGCTGGGATTATAGG 80658                 A
          C                       GCCTGTAGTCCCAGCTACTC GG
                                  |||||||||||||||||||| ||
                                  CGGATATTAGGGTCGATGAG CC
                                              C
GAM380  LOC150407 3'  CCAAAGTACTGGGATTACA    80637          C    CA
                                TGTAGTCCCAG TACT  GG
                                |||||||||| ||||  ||
                                ACATTAGGGTC ATGA  CC
                                      _   AA
GAM380  LOC150407 3'  CCCAAGTAGCTGGGACTACAGG 80640                CA
          CA                      TGCCTGTAGTCCCAGCTACT  GG
                                  ||||||||||||||||||||  ||
                                  ACGGACATCAGGGTCGATGA  CC
                                              AC
GAM380  LOC150587 3'  CCCAAGCAGCTGGGAAGATAGG 86240        AG       A  CA
          CA                      TGCCTGT  TCCCAGCT CT  GG
                                  |||||||  |||||||| ||  ||
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                                ACGGATA  AGGGTCGA GA  CC
                                   GA       C  AC
GAM380   LOC150630 5'  CCCGAGTAGCTGGGACTACAGG 86296                A
           C                     GCCTGTAGTCCCAGCTACTC GG
                                 |||||||||||||||||||| ||
                                 CGGACATCAGGGTCGATGAG CC
                                       C
GAM380   LOC150696 3'  CCCGAGTAGCTGGGACTGCAG  59157                A
                                 CTGTAGTCCCAGCTACTC GG
                                 |||||||||||||||||| ||
                                 GACGTCAGGGTCGATGAG CC
                                       C
GAM380   LOC150960 3'  CCCAAGTAGCTGGGACAACAG  80872      A         CA
                                 CTGT GTCCCAGCTACT  GG
                                 |||| ||||||||||  ||
                                 GACA CAGGGTCGATGA  CC
                                   A          AC
GAM380   LOC151057 3'  CCCGAGTAGCTGGGATTATAGA 86385    C             A
           CA                      TG CTGTAGTCCCAGCTACTC GG
                                 || |||||||||||||||| ||
                                 AC GATATTAGGGTCGATGAG CC
                                  A              C
GAM380   LOC151201 3'  CCCGAGTAGCTGGGACTACAGA 86471    C             A
           CA                      TG CTGTAGTCCCAGCTACTC GG
                                 || |||||||||||||||| ||
                                 AC GACATCAGGGTCGATGAG CC
                                  A              C
GAM380   LOC151475 5'  CCAAAGTGCTGGGATTACAGGC 86585              T   CA
           A                       TGCCTGTAGTCCCAGC ACT  GG
                                 |||||||||||||||| |||  ||
                                 ACGGACATTAGGGTCG TGA  CC
                                       _  AA
GAM380   LOC151475 5'  CCCGAGTAGCTGGGATTACAG  86588                A
                                 CTGTAGTCCCAGCTACTC GG
                                 |||||||||||||||| ||
                                 GACATTAGGGTCGATGAG CC
                                       C
GAM380   LOC151475 5'  CCGCAGTAGCTGGGACTACAGG 86589                CA
           CA                      TGCCTGTAGTCCCAGCTACT  GG
                                 |||||||||||||||||| ||
                                 ACGGACATCAGGGTCGATGA  CC
                                       CG
GAM380   LOC151701 3'  CCTGAGTAGCTGGGATTACAGG 86670
           CA                      TGCCTGTAGTCCCAGCTACTCAGG
                                 ||||||||||||||||||||||||
                                 ACGGACATTAGGGTCGATGAGTCC

GAM380   LOC151826 3'  CCAAAGTGCTGGGATTACAGGC 81177              T   CA
           A                       TGCCTGTAGTCCCAGC ACT  GG
                                 |||||||||||||||| |||  ||
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                                ACGGACATTAGGGTCG TGA  CC
                                        _   AA
GAM380  LOC151826 3'  CCCAAGTAGCTGGGATTACAGG 81179                CA
          CA                      TGCCTGTAGTCCCAGCTACT  GG
                                  ||||||||||||||||||  ||
                                  ACGGACATTAGGGTCGATGA  CC
                                        AC
GAM380  LOC151877 3'  CCAAAGTACTGGGACTACAGGC 86693            C   CA
                                  GCCTGTAGTCCCAG TACT  GG
                                  |||||||||||||| ||||  ||
                                  CGGACATCAGGGTC ATGA  CC
                                        _   AA
GAM380  LOC152137 3'  CCCAAGTAGCTGGAATTACAGG 81310          C       CA
          CA                      TGCCTGTAGT CCAGCTACT  GG
                                  |||||||||| |||||||||  ||
                                  ACGGACATTA GGTCGATGA  CC
                                        A       AC
GAM380  LOC152220 3'  CCTGAGTAGCTGAGACCACAGG 86762        A   C
          CA                      TGCCTGT GTC CAGCTACTCAGG
                                  |||||||| ||| ||||||||||||
                                  ACGGACA CAG GTCGATGAGTCC
                                      C   A
GAM380  LOC152282 5'  CCCAAGTAGCTGGGACTACAGA 81399    _           CA
          GC                      GC CTGTAGTCCCAGCTACT  GG
                                  || ||||||||||||||||  ||
                                  CG GACATCAGGGTCGATGA  CC
                                   A              AC
GAM380  LOC152343 3'  CCTGAGTAGCTGGGATTACAG  81424
                                  CTGTAGTCCCAGCTACTCAGG
                                  ||||||||||||||||||||
                                  GACATTAGGGTCGATGAGTCC

GAM380  LOC152445 3'  CCTGAGTAGCTAGGACCATAGG 86945        A   C
          CA                      TGCCTGT GTCC AGCTACTCAGG
                                  ||||||| |||| ||||||||||
                                  ACGGATA CAGG TCGATGAGTCC
                                      C   A
GAM380  LOC152582 5'  CCTGAGTAGCTGGATTACAGG  86989          C
                                  CCTGTAGTCC AGCTACTCAGG
                                  |||||||||| ||||||||||
                                  GGACATTAGG TCGATGAGTCC
                                        _
GAM380  LOC152620 3'  CCTGAGTAGCTGGGATTACAGG 60708
          CA                      TGCCTGTAGTCCCAGCTACTCAGG
                                  ||||||||||||||||||||||||
                                  ACGGACATTAGGGTCGATGAGTCC

GAM380  LOC152719 5'  CCGTGTAGCTGGGACTACAGGC 87020              TCA
                                  GCCTGTAGTCCCAGCTAC   GG
                                  ||||||||||||||||   ||
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                                CGGACATCAGGGTCGATG   CC
                                          TG_
GAM380   LOC152719 5'  CCTGAGTAGCTGGGATTACAG  87023
                                CTGTAGTCCCAGCTACTCAGG
                                ||||||||||||||||||||
                                GACATTAGGGTCGATGAGTCC

GAM380   LOC152794 5'  CCTGAGTAGCTGAGACTACAGG 81557          C
            CA                    TGCCTGTAGTC CAGCTACTCAGG
                                ||||||||||| ||||||||||||
                                ACGGACATCAG GTCGATGAGTCC
                                      A
GAM380   LOC152804 3'  CTGAGTAGCTGGGACTACAGGC 87078
            A                     TGCCTGTAGTCCCAGCTACTCAG
                                ||||||||||||||||||||||||
                                ACGGACATCAGGGTCGATGAGTC

GAM380   LOC152851 3'  CCCGAGTAGCTGGGATTACAGG 81589                A
            CA                    TGCCTGTAGTCCCAGCTACTC GG
                                |||||||||||||||||||| ||
                                ACGGACATTAGGGTCGATGAG CC
                                          C
GAM380   LOC153077 3'  CCTCGAGTAGCTGGGACTACAG 87119                 _
            GC                    GCCTGTAGTCCCAGCTACTC AGG
                                |||||||||||||||||| |||
                                CGGACATCAGGGTCGATGAG TCC
                                          C
GAM380   LOC153688 3'  CCAAAGTGCTAGGATTACAGGC 87303          C   T   CA
            A                     TGCCTGTAGTCC AGC ACT  GG
                                |||||||||||| ||| |||  ||
                                ACGGACATTAGG TCG TGA  CC
                                      A   _   AA
GAM380   LOC153811 3'  CCCGAGTAACTGGGACTACA   81829          C    A
                                TGTAGTCCCAG TACTC GG
                                |||||||||| ||||| ||
                                ACATCAGGGTC ATGAG CC
                                      A    C
GAM380   LOC153811 3'  CCGAGTAGCTGGATTTACAG   81830       TC        A
                                CTGTAG  CCAGCTACTC GG
                                ||||||  |||||||||| ||
                                GACATT  GGTCGATGAG CC
                                   TA         C
GAM380   LOC153811 5'  AGTAGCTGGGACCACAGGC    81823       A
                                GCCTGT GTCCCAGCTACT
                                ||||||| ||||||||||||
                                CGGACA CAGGGTCGATGA
                                   C
GAM380   LOC153883 5'  CCCAAGTAGCTGAGATTACAGG 81891          C       CA
            CA                    TGCCTGTAGTC CAGCTACT  GG
                                |||||||||| ||||||||  ||
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                                ACGGACATTAG GTCGATGA  CC
                                      A       AC
GAM380  LOC154282 5'  CCAAAGTGCTGGGATTACAGGC 87401             T   CA
          A                    TGCCTGTAGTCCCAGC ACT  GG
                               ||||||||||||||| |||  ||
                               ACGGACATTAGGGTCG TGA  CC
                                      _  AA
GAM380  LOC154282 5'  CCTGAGTAGCTGGGACTACAGG 87402
          CA                   TGCCTGTAGTCCCAGCTACTCAGG
                               ||||||||||||||||||||||||
                               ACGGACATCAGGGTCGATGAGTCC

GAM380  LOC154403 3'  AGTAGCTGGAACTACAGGCA   81967          C
                               TGCCTGTAGT CCAGCTACT
                               |||||||||| |||||||||
                               ACGGACATCA GGTCGATGA
                                     A
GAM380  LOC154726 5'  CCAAAGTGCTGGGATTACAGGC 82007             T   CA
          A                    TGCCTGTAGTCCCAGC ACT  GG
                               ||||||||||||||| |||  ||
                               ACGGACATTAGGGTCG TGA  CC
                                      _  AA
GAM380  LOC154739 3'  CCTGAGTAGCTGGGATTACAGG 87436
          CA                   TGCCTGTAGTCCCAGCTACTCAGG
                               ||||||||||||||||||||||||
                               ACGGACATTAGGGTCGATGAGTCC

GAM380  LOC154822 3'  CCTGAGTAGCTGGGATTACAG  87485
                               CTGTAGTCCCAGCTACTCAGG
                               ||||||||||||||||||||
                               GACATTAGGGTCGATGAGTCC

GAM380  LOC154877 3'  CCCAAGTAGCTGGGATTACAG  87539             CA
                               CTGTAGTCCCAGCTACT  GG
                               ||||||||||||||||  ||
                               GACATTAGGGTCGATGA  CC
                                      AC
GAM380  LOC154877 3'  CCCGAGTAGCTGGGATTACAGG 87540               A
          CA                   TGCCTGTAGTCCCAGCTACTC GG
                               |||||||||||||||||||  ||
                               ACGGACATTAGGGTCGATGAG CC
                                     C
GAM380  LOC154877 5'  CCTGAGAGCTGGGACTACAGGC 87543              A
                               GCCTGTAGTCCCAGCT CTCAGG
                               |||||||||||||||  ||||||
                               CGGACATCAGGGTCGA GAGTCC
                                     _
GAM380  LOC154930 3'  CCAGAATAGCTGGGACTACAGG 82087              C  A
          CA                   TGCCTGTAGTCCCAGCTA TC GG
                               |||||||||||||||||  ||  ||
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                                ACGGACATCAGGGTCGAT AG CC
                                      A  A
GAM380  LOC154992 3'  AGTAGCTGGAACTACAGGC   82129        C
                                GCCTGTAGT CCAGCTACT
                                ||||||||| |||||||||
                                CGGACATCA GGTCGATGA
                                    A
GAM380  LOC157247 5'  CCAAAGTGCTGGGATTACAGGC 82290            T   CA
          A                      TGCCTGTAGTCCCAGC ACT  GG
                                 |||||||||||||||| |||  ||
                                 ACGGACATTAGGGTCG TGA  CC
                                       _  AA
GAM380  LOC157506 3'  CCAAAGTGCTGGGATTACAGGC 82364            T   CA
          A                      TGCCTGTAGTCCCAGC ACT  GG
                                 |||||||||||||||| |||  ||
                                 ACGGACATTAGGGTCG TGA  CC
                                       _  AA
GAM380  LOC157506 3'  CCCAAGTAGCTGGGACTACAGG 82365               CA
          CA                     TGCCTGTAGTCCCAGCTACT  GG
                                 ||||||||||||||||||  ||
                                 ACGGACATCAGGGTCGATGA  CC
                                       AC
GAM380  LOC157507 5'  CCAAAGTGCTGGGATTACAGGC 82378            T   CA
          A                      TGCCTGTAGTCCCAGC ACT  GG
                                 |||||||||||||||| |||  ||
                                 ACGGACATTAGGGTCG TGA  CC
                                       _  AA
GAM380  LOC157798 5'  CCCAAGTAACTGGGACTGCAGG 87855            C   CA
          CA                     TGCCTGTAGTCCCAG TACT  GG
                                 |||||||||||||||| ||||  ||
                                 ACGGACGTCAGGGTC ATGA  CC
                                      A   AC
GAM380  LOC157798 5'  CCTGAAGTGCTGGGATTACAGG 87856            T  _
          CA                     TGCCTGTAGTCCCAGC ACT CAGG
                                 |||||||||||||||| ||| ||||
                                 ACGGACATTAGGGTCG TGA GTCC
                                       _  A
GAM380  LOC157858 5'  CCCGAGTAGCTGGGATTACAGG 87885               A
          CA                     TGCCTGTAGTCCCAGCTACTC GG
                                 ||||||||||||||||||| ||
                                 ACGGACATTAGGGTCGATGAG CC
                                       C
GAM380  LOC158310 5'  AGTAGCTGGGACTACAGGCA   88075
                                TGCCTGTAGTCCCAGCTACT
                                ||||||||||||||||||
                                ACGGACATCAGGGTCGATGA

GAM380  LOC158402 5'  CCCGAGTAACTGGGACTACAG  88144          C    A
                                CTGTAGTCCCAG TACTC GG
                                |||||||||||| ||||| ||
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                                GACATCAGGGTC ATGAG CC
                                      A    C
GAM380  LOC158476 3'  AGTAGCTGGGACTACAGGC   88184
                                GCCTGTAGTCCCAGCTACT
                                ||||||||||||||||||
                                CGGACATCAGGGTCGATGA

GAM380  LOC158476 3'  CCAAAGTGCTGGGATTACAGGC 88187              T  CA
          A                     TGCCTGTAGTCCCAGC ACT  GG
                                |||||||||||||||| |||  ||
                                ACGGACATTAGGGTCG TGA  CC
                                      _  AA
GAM380  LOC158476 3'  CCTGAGTAGCTGGGATCATAG  88191     A
                                CTGT GTCCCAGCTACTCAGG
                                |||| ||||||||||||||||
                                GATA TAGGGTCGATGAGTCC
                                  C
GAM380  LOC158549 5'  CCTGAGTAGCTGGGACTACAGG 88220
          C                     GCCTGTAGTCCCAGCTACTCAGG
                                ||||||||||||||||||||||
                                CGGACATCAGGGTCGATGAGTCC

GAM380  LOC158668 3'  CCTGAGTAGCTGGGATTACAGG 69898
          CA                    TGCCTGTAGTCCCAGCTACTCAGG
                                ||||||||||||||||||||||
                                ACGGACATTAGGGTCGATGAGTCC

GAM380  LOC159176 5'  GTAGCTGGGACTACAGGC    83008
                                GCCTGTAGTCCCAGCTAC
                                ||||||||||||||||||
                                CGGACATCAGGGTCGATG

GAM380  LOC160391 3'  CCGAAGTGTTGGGATTACAGGC 88439              T  CA
          A                     TGCCTGTAGTCCCAGC ACT  GG
                                |||||||||||||||| |||  ||
                                ACGGACATTAGGGTTG TGA  CC
                                      _  AG
GAM380  LOC161829 3'  CCTGAGTAGCTGGGATTACAG  83187
                                CTGTAGTCCCAGCTACTCAGG
                                |||||||||||||||||||||
                                GACATTAGGGTCGATGAGTCC

GAM380  LOC162461 5'  CCAGAGTAACTGGGACTACAGG 83236           C    A
                                CCTGTAGTCCCAG TACTC GG
                                |||||||||||| ||||| ||
                                GGACATCAGGGTC ATGAG CC
                                      A    A
GAM380  LOC169611 3'  CCAAAGTGTTGGGATTACAGGC 83640              T  CA
          A                     TGCCTGTAGTCCCAGC ACT  GG
                                |||||||||||||||| |||  ||
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                                ACGGACATTAGGGTTG TGA  CC
                                      _  AA
GAM380  LOC170082 5'  CCCAAGTAGCTAGGACTACAGG 83441          C      CA
          T                    GCCTGTAGTCC AGCTACT  GG
                               |||||||||||| |||||||  ||
                               TGGACATCAGG TCGATGA  CC
                                     A      AC
GAM380  LOC196047 5'  CCTGAGTAGCTGGAATTACAG  91150       C
                               CTGTAGT CCAGCTACTCAGG
                               ||||||| ||||||||||||
                               GACATTA GGTCGATGAGTCC
                                    A
GAM380  LOC196264 3'  CCAAAGTGTTGGGATTACAGGC 88981             T   CA
          A                    TGCCTGTAGTCCCAGC ACT  GG
                               |||||||||||||||| |||  ||
                               ACGGACATTAGGGTTG TGA  CC
                                     _  AA
GAM380  LOC196264 3'  GAGTAGCTGGGATTACAGGCA  88985
                               TGCCTGTAGTCCCAGCTACTC
                               |||||||||||||||||||||
                               ACGGACATTAGGGTCGATGAG

GAM380  LOC196529 3'  CCTGAGTAGCTGGTATTACAGG 89130         C
          CA                   TGCCTGTAGT CCAGCTACTCAGG
                               |||||||||| ||||||||||||
                               ACGGACATTA GGTCGATGAGTCC
                                     T
GAM380  LOC196957 3'  GAGTAGCTAGGACTACAGGCA  89189          C
                               TGCCTGTAGTCC AGCTACTC
                               |||||||||||| ||||||||
                               ACGGACATCAGG TCGATGAG
                                     A
GAM380  LOC196961 3'  GAGTAGCTAGGACTACAGGCA  89203          C
                               TGCCTGTAGTCC AGCTACTC
                               |||||||||||| ||||||||
                               ACGGACATCAGG TCGATGAG
                                     A
GAM380  LOC197138 3'  GAGTAGCTAGGACTACAGGCA  89252          C
                               TGCCTGTAGTCC AGCTACTC
                               |||||||||||| ||||||||
                               ACGGACATCAGG TCGATGAG
                                     A
GAM380  LOC197285 3'  CCTACGCCTGGGCTACAGGCA  89152        T    CTACTC
                               TGCCTGTAG CCCAG     AGG
                               ||||||||| |||||     |||
                               ACGGACATC GGGTC     TCC
                                     _    CGCA__
GAM380  LOC197358 3'  AGTAGCTGGGAATACAGGCA   89418        G
                               TGCCTGTA TCCCAGCTACT
                               |||||||| ||||||||||
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                                ACGGACAT AGGGTCGATGA
                                   A
GAM380  LOC197358 3'  CCAAAGTACTGGGATTACAGGC 89424            C   CA
          A                     TGCCTGTAGTCCCAG TACT  GG
                                |||||||||||||| ||||  ||
                                ACGGACATTAGGGTC ATGA  CC
                                      _   AA
GAM380  LOC197358 3'  CCCAAGTAGTTGGGTCTACAGG 89427        T       CA
          CA                    TGCCTGTAG CCCAGCTACT  GG
                                ||||||||| |||||||||  ||
                                ACGGACATC GGGTTGATGA  CC
                                     T        AC
GAM380  LOC199699 3'  CCCGAGTAGCTGGGACTACAGG 89671              A
          CA                    TGCCTGTAGTCCCAGCTACTC GG
                                |||||||||||||||||||| ||
                                ACGGACATCAGGGTCGATGAG CC
                                      C
GAM380  LOC199699 3'  CCTGAGTAGCTGGGACTACAGG 89672
          CA                    TGCCTGTAGTCCCAGCTACTCAGG
                                |||||||||||||||||||||||
                                ACGGACATCAGGGTCGATGAGTCC

GAM380  LOC199725 5'  CCAAAGTGCTGGGATTACAGGC 91413            T  CA
          A                     TGCCTGTAGTCCCAGC ACT  GG
                                |||||||||||||| |||  ||
                                ACGGACATTAGGGTCG TGA  CC
                                      _  AA
GAM380  LOC199786 3'  CCCGAGTAGCTGAGATTTCAGG 89745      T  C      A
          CA                    TGCCTG AGTC CAGCTACTC GG
                                ||||||  |||| |||||||| ||
                                ACGGAC TTAG GTCGATGAG CC
                                   T  A       C
GAM380  LOC200014 3'  CCTGAGTAGCTGGGATTACAGG 89929
          CA                    TGCCTGTAGTCCCAGCTACTCAGG
                                |||||||||||||||||||||||
                                ACGGACATTAGGGTCGATGAGTCC

GAM380  LOC200169 5'  CCAAAGTGCTGGGATTACAGGC 91553            T  CA
          A                     TGCCTGTAGTCCCAGC ACT  GG
                                |||||||||||||| |||  ||
                                ACGGACATTAGGGTCG TGA  CC
                                      _  AA
GAM380  LOC200301 5'  CCGAGAGTAGCTGGGACTACAG 90138              A_
          GC                     GCCTGTAGTCCCAGCTACTC  GG
                                 ||||||||||||||||||  ||
                                 CGGACATCAGGGTCGATGAG  CC
                                       AG
GAM380  LOC200310 3'  CCTAAGTAGCTGGCATTACAGG 66322        C       C
          CA                    TGCCTGTAGT CCAGCTACT AGG
                                |||||||||| ||||||||| |||
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                                ACGGACATTA GGTCGATGA TCC
                                      C        A
GAM380  LOC200314 3'  CCAAAGTGCTGGGATTACAGGC 91592              T   CA
              A                  TGCCTGTAGTCCCAGC ACT  GG
                                 |||||||||||||||| |||  ||
                                 ACGGACATTAGGGTCG TGA  CC
                                       _   AA
GAM380  LOC200314 3'  CCCGAGTAGCTGGGATTACAGG 91596                 A
              CA                   TGCCTGTAGTCCCAGCTACTC GG
                                   ||||||||||||||||||||| ||
                                   ACGGACATTAGGGTCGATGAG CC
                                         C
GAM380  LOC200845 5'  CCTGAATAGCTAGGATTACAG  90313          C    C
                                   CTGTAGTCC AGCTA TCAGG
                                   ||||||||| ||||| |||||
                                   GACATTAGG TCGAT AGTCC
                                      A    A
GAM380  LOC200860 3'  CCCGAGTAGCTGGGACCACAGG 91744        A          A
              T                    GCCTGT GTCCCAGCTACTC GG
                                   |||||| |||||||||||| ||
                                   TGGACA CAGGGTCGATGAG CC
                                     C          C
GAM380  LOC200860 3'  GCCCGAGTAGCTAAAGCTGAGA 91751          C   _______   A ___
              TTACAGGCA                TGCCTGTAGTC CAGCT     ACTC GG   C
                                   |||||||||| |||||     |||| ||   |
                                   ACGGACATTAG GTCGA     TGAG CC   G
                                      A    AATCGA   C ___
GAM380  LOC201164 3'  CCCGAGTAGCTGGGATTACAG  89490                A
                                   CTGTAGTCCCAGCTACTC GG
                                   |||||||||||||||| ||
                                   GACATTAGGGTCGATGAG CC
                                        C
GAM380  LOC201173 5'  CCTGAGTAGCTGGGATTGCAGG 88679
              TA                   TGCCTGTAGTCCCAGCTACTCAGG
                                   |||||||||||||||||||||||
                                   ATGGACGTTAGGGTCGATGAGTCC

GAM380  LOC201220 5'  CCTGAGTAGCTGGGATTGCAGG 88714
              TA                   TGCCTGTAGTCCCAGCTACTCAGG
                                   |||||||||||||||||||||||
                                   ATGGACGTTAGGGTCGATGAGTCC

GAM380  LOC201294 3'  CCCAAGTAGCTGGGACTACAGG 89581                CA
              CA                   TGCCTGTAGTCCCAGCTACT  GG
                                   |||||||||||||||||||  ||
                                   ACGGACATCAGGGTCGATGA  CC
                                        AC
GAM380  LOC201411 3'  CCCAAGTAGCTGAGATTACAG  63640         C       CA
                                   CTGTAGTC CAGCTACT  GG
                                   |||||||| ||||||||  ||
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                                GACATTAG GTCGATGA  CC
                                    A       AC
GAM380  LOC201626 3'  CCCGAGTAGCTGGGATTACAGG 90429                A
          C                      GCCTGTAGTCCCAGCTACTC GG
                                 |||||||||||||||||||| ||
                                 CGGACATTAGGGTCGATGAG CC
                                               C
GAM380  LOC201627 3'  CCTGAGTAGCTGGGATTACAGG 90452
          TA                     TGCCTGTAGTCCCAGCTACTCAGG
                                 |||||||||||||||||||||||||
                                 ATGGACATTAGGGTCGATGAGTCC

GAM380  LOC201696 3'  CCCGAGTAGCTGGGATTACAGG 63817                A
          CA                     TGCCTGTAGTCCCAGCTACTC GG
                                 |||||||||||||||||||| ||
                                 ACGGACATTAGGGTCGATGAG CC
                                               C
GAM380  LOC201702 5'  CCCGAGTAGCTGGTATTACAGG 90469          C     A
          C                      GCCTGTAGT CCAGCTACTC GG
                                 ||||||||| |||||||||| ||
                                 CGGACATTA GGTCGATGAG CC
                                       T         C
GAM380  LOC201868 3'  AGTAGCTGGAACTACAGGC    90514          C
                                 GCCTGTAGT CCAGCTACT
                                 ||||||||| |||||||||
                                 CGGACATCA GGTCGATGA
                                       A
GAM380  LOC202025 3'  CCTGAGTAGCTGGAACTACAGG 91885          C
          T                      GCCTGTAGT CCAGCTACTCAGG
                                 ||||||||| ||||||||||||
                                 TGGACATCA GGTCGATGAGTCC
                                       A
GAM380  LOC202459 5'  GGTAGCTGAGACTACAGGC    59931          C
                                 GCCTGTAGTC CAGCTACT
                                 |||||||||| ||||||||
                                 CGGACATCAG GTCGATGG
                                       A
GAM380  LOC202460 5'  CAAGTAGCTGGATTACA      90669          C      CA
                                 TGTAGTCC AGCTACT  G
                                 |||||||| ||||||| |
                                 ACATTAGG TCGATGA  C
                                       _       AC
GAM380  LOC202908 5'  AGTAGCTGGGACCACAGGC    90709        A
                                 GCCTGT GTCCCAGCTACT
                                 |||||| ||||||||||||
                                 CGGACA CAGGGTCGATGA
                                    C
GAM380  LOC202908 5'  CCCGAGTAGCTGGGATTACAG  90719                A
                                 CTGTAGTCCCAGCTACTC GG
                                 |||||||||||||||||| ||
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                                GACATTAGGGTCGATGAG CC
                                             C
GAM380  LOC202908 5'  CCTGAGTAGCTAGGACTGGT  90720    TGT   C
                                GCC  AGTCC AGCTACTCAGG
                                |||  ||||| ||||||||||
                                TGG  TCAGG TCGATGAGTCC
                                 ___    A
GAM380  LOC202908 5'  CCTGAGTAGCTGGGACTACAGG 90721
          C                      GCCTGTAGTCCCAGCTACTCAGG
                                 ||||||||||||||||||||||
                                 CGGACATCAGGGTCGATGAGTCC

GAM380  LOC202934 3'  CCTGAGTAGCTGGGACTATAGG 92037
          CA                       TGCCTGTAGTCCCAGCTACTCAGG
                                   ||||||||||||||||||||||
                                   ACGGATATCAGGGTCGATGAGTCC

GAM380  LOC203197 3'  CCCAAGTAGCTGGGACTACAGG 90807                CA
          T                        GCCTGTAGTCCCAGCTACT  GG
                                   ||||||||||||||||||  ||
                                   TGGACATCAGGGTCGATGA  CC
                                              AC
GAM380  LOC203276 3'  CCTGAGTAGCTGGGATTACAGG 92119
          CA                       TGCCTGTAGTCCCAGCTACTCAGG
                                   ||||||||||||||||||||||
                                   ACGGACATTAGGGTCGATGAGTCC

GAM380  LOC203297 5'  CCCGAGTAGCTGGGATTACAG  75871              A
                                CTGTAGTCCCAGCTACTC GG
                                |||||||||||||||| ||
                                GACATTAGGGTCGATGAG CC
                                             C
GAM380  LOC203305 3'  CCTGAGTAGCTGGGATTACAGG 92172
          CA                       TGCCTGTAGTCCCAGCTACTCAGG
                                   ||||||||||||||||||||||
                                   ACGGACATTAGGGTCGATGAGTCC

GAM380  LOC203339 3'  CCTGAGTAGCTGGGACTAGAGG 92209     G
          C                        GCCT TAGTCCCAGCTACTCAGG
                                   |||| ||||||||||||||||
                                   CGGA ATCAGGGTCGATGAGTCC
                                     G
GAM380  LOC203350 3'  CCTGAGTAGCTGGGATTACAGG 92234
          C                        GCCTGTAGTCCCAGCTACTCAGG
                                   ||||||||||||||||||||||
                                   CGGACATTAGGGTCGATGAGTCC

GAM380  LOC203369 3'  CCTGAGTAGCTGGGACTACAGG 90884
          C                        GCCTGTAGTCCCAGCTACTCAGG
                                   ||||||||||||||||||||||
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                                CGGACATCAGGGTCGATGAGTCC

GAM380  LOC203378 3'  CCAAAGTGCTGGGATTACAGGC 92285             T   CA
          A                    TGCCTGTAGTCCCAGC ACT  GG
                               |||||||||||||||| |||  ||
                               ACGGACATTAGGGTCG TGA  CC
                                        _   AA
GAM380  LOC204804 3'  CCCGAGTAGCTAGGATTACAGG 91038          C       A
          CA                    TGCCTGTAGTCC AGCTACTC GG
                               |||||||||||| ||||||| ||
                               ACGGACATTAGG TCGATGAG CC
                                      A       C
GAM380  LOC205251 5'  CCAAAGTGCTGGGATTACAGGC 92354             T   CA
          A                    TGCCTGTAGTCCCAGC ACT  GG
                               |||||||||||||||| |||  ||
                               ACGGACATTAGGGTCG TGA  CC
                                        _   AA
GAM380  LOC219294 3'  GTAGCTAGGACTACAGGC    94597          C
                               GCCTGTAGTCC AGCTAC
                               |||||||||| ||||||
                               CGGACATCAGG TCGATG
                                      A
GAM380  LOC219295 3'  GTAGCTAGGACTACAGGC    94588          C
                               GCCTGTAGTCC AGCTAC
                               |||||||||| ||||||
                               CGGACATCAGG TCGATG
                                      A
GAM380  LOC219445 5'  CCTGAGTAGCTGGGACTATAGG 93201
          C                    GCCTGTAGTCCCAGCTACTCAGG
                               |||||||||||||||||||||||
                               CGGATATCAGGGTCGATGAGTCC

GAM380  LOC219529 5'  CCCAAGTAGCTGGGACTACAGC 94564    C           CA
                               GC TGTAGTCCCAGCTACT  GG
                               || ||||||||||||||  ||
                               CG ACATCAGGGTCGATGA  CC
                                _            AC
GAM380  LOC219673 5'  CCAAAGTGCTAGGATTACAGGC 94617          C   T   CA
          A                    TGCCTGTAGTCC AGC ACT  GG
                               |||||||||||| ||| |||  ||
                               ACGGACATTAGG TCG TGA  CC
                                      A  _   AA
GAM380  LOC219673 5'  CCCAAGTAGCTGAGATTACAG  94620        C       CA
                               CTGTAGTC CAGCTACT  GG
                               |||||||| ||||||||  ||
                               GACATTAG GTCGATGA  CC
                                    A       AC
GAM380  LOC219731 5'  CCTGGGTAGCTGGGACTACAGG 94701
          C                    GCCTGTAGTCCCAGCTACTCAGG
                               |||||||||||||||||||||||
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                                CGGACATCAGGGTCGATGGGTCC

GAM380  LOC219735 3'  CCAAAGTGTTGGGATTACAGGC 94725            T   CA
          A                    TGCCTGTAGTCCCAGC ACT  GG
                               |||||||||||||||| |||  ||
                               ACGGACATTAGGGTTG TGA  CC
                                        _   AA
GAM380  LOC219735 3'  CCCGAGTAGCTGGGATTACAGG 94726              A
          C                    GCCTGTAGTCCCAGCTACTC GG
                               |||||||||||||||||||| ||
                               CGGACATTAGGGTCGATGAG CC
                                        C
GAM380  LOC219894 3'  CCCGAGTAGCTGGGACTACAGG 94903              A
          T                    GCCTGTAGTCCCAGCTACTC GG
                               |||||||||||||||||||| ||
                               TGGACATCAGGGTCGATGAG CC
                                        C
GAM380  LOC220074 3'  CCCAAGTAGCTGGGACTATAGG 59969              CA
          CA                    TGCCTGTAGTCCCAGCTACT  GG
                                |||||||||||||||||||  ||
                                ACGGATATCAGGGTCGATGA  CC
                                        AC
GAM380  LOC220074 3'  CCTGAGTAGCTGGGATTACAGG 59973
          C                    GCCTGTAGTCCCAGCTACTCAGG
                               |||||||||||||||||||||||
                               CGGACATTAGGGTCGATGAGTCC

GAM380  LOC220662 3'  CCAAAGTGTTGGGATTACAGGC 92811            T   CA
          A                    TGCCTGTAGTCCCAGC ACT  GG
                               |||||||||||||||| |||  ||
                               ACGGACATTAGGGTTG TGA  CC
                                        _   AA
GAM380  LOC220662 3'  GTAGCTGGGACTACAGGC    92829
                               GCCTGTAGTCCCAGCTAC
                               |||||||||||||||||
                               CGGACATCAGGGTCGATG

GAM380  LOC221174 5'  CCCAAGTAACTGGGATTACAGG 95151              C   CA
          CA                    TGCCTGTAGTCCCAG TACT  GG
                                |||||||||||||| ||||  ||
                                ACGGACATTAGGGTC ATGA  CC
                                        A    AC
GAM380  LOC221271 3'  CCAAAGTGTTGAGATTACAGGC 93503          C   T   CA
          A                    TGCCTGTAGTC CAGC ACT  GG
                               |||||||||| |||| |||  ||
                               ACGGACATTAG GTTG TGA  CC
                                        A   _   AA
GAM380  LOC221271 3'  CCTGAGTAGCTGGGATTACAGG 93507
          CA                    TGCCTGTAGTCCCAGCTACTCAGG
                                |||||||||||||||||||||||
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                                ACGGACATTAGGGTCGATGAGTCC

GAM380  LOC221296 3'  CCCGAGTAGCTGGGACTACAGG 93607                A
              C                GCCTGTAGTCCCAGCTACTC GG
                               |||||||||||||||||||| ||
                               CGGACATCAGGGTCGATGAG CC
                                          C
GAM380  LOC221540 3'  CCTGAGTAGCTGGGACTACAG  95477
                               CTGTAGTCCCAGCTACTCAGG
                               |||||||||||||||||||||
                               GACATCAGGGTCGATGAGTCC

GAM380  LOC221663 5'  CCAAAGTGCCGGGATTACAGGC 95458           A  T   CA
              A                TGCCTGTAGTCCC GC ACT  GG
                               |||||||||||| || |||  ||
                               ACGGACATTAGGG CG TGA  CC
                                        C  _   AA
GAM380  LOC221663 5'  CCCAAGTAGCTGGGACTACGGG 95460                CA
              CA                 TGCCTGTAGTCCCAGCTACT  GG
                                 |||||||||||||||||||  ||
                                 ACGGGCATCAGGGTCGATGA  CC
                                          AC
GAM380  LOC221760 5'  CCCAAGTAGCTAGGACTACAG  95428         C      CA
                               CTGTAGTCC AGCTACT  GG
                               |||||||| |||||||  ||
                               GACATCAGG TCGATGA  CC
                                     A      AC
GAM380  LOC221814 5'  CCTGAGTAGGTGGGATTACAAG 95554     C        G
              CA                 TGC TGTAGTCCCA CTACTCAGG
                                 ||| |||||||||| |||||||||
                                 ACG ACATTAGGGT GATGAGTCC
                                   A         G
GAM380  LOC221815 5'  CCTGAGTAGGTGGGATTACAAG 95551     C        G
              CA                 TGC TGTAGTCCCA CTACTCAGG
                                 ||| |||||||||| |||||||||
                                 ACG ACATTAGGGT GATGAGTCC
                                   A         G
GAM380  LOC221964 3'  CCCGAGTAGCGGGGATTACAGG 95602           A      A
              CA                 TGCCTGTAGTCCC GCTACTC GG
                                 |||||||||||| ||||||| ||
                                 ACGGACATTAGGG CGATGAG CC
                                        G      C
GAM380  LOC222068 3'  CCTGAGTAGCTGGGATTACAG  94274
                               CTGTAGTCCCAGCTACTCAGG
                               |||||||||||||||||||||
                               GACATTAGGGTCGATGAGTCC

GAM380  LOC222070 5'  CCCAAGTAGCCGGAATTACAGG 95812          C  A     CA
              CA                 TGCCTGTAGT CC GCTACT  GG
                                 |||||||||| || ||||||  ||
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                                ACGGACATTA GG CGATGA  CC
                                     A  C     AC
GAM380  LOC245771 5'  CCGAGTAGCTGGGATTACAGGC 94471                A
                A                TGCCTGTAGTCCCAGCTACTC GG
                                 |||||||||||||||||||| ||
                                 ACGGACATTAGGGTCGATGAG CC
                                                 _
GAM380  LOC253612 5'  CCTGAGTAGCTGGGATTACAGG 98546
                                 CCTGTAGTCCCAGCTACTCAGG
                                 |||||||||||||||||||||||
                                 GGACATTAGGGTCGATGAGTCC

GAM380  LOC253664 3'  CTAGTAGCTGAGATTACAGGCA 96465          C       C
                                 TGCCTGTAGTC CAGCTACT AG
                                 |||||||||| |||||||| ||
                                 ACGGACATTAG GTCGATGA TC
                                       A      _
GAM380  LOC253805 3'  AGTAACTGGGATTACAGGCA   98167            C
                                 TGCCTGTAGTCCCAG TACT
                                 |||||||||||||| ||||
                                 ACGGACATTAGGGTC ATGA
                                          A
GAM380  LOC253842 5'  CCTGAGTAGCTGGGACTACAGG 99237
                C                 GCCTGTAGTCCCAGCTACTCAGG
                                  |||||||||||||||||||||||
                                  CGGACATCAGGGTCGATGAGTCC

GAM380  LOC253868 3'  CCTGAACAGCTGGACAGCTGGG 97322      _ A   C   AC
                C                 GCCT GT GTCC AGCT  TCAGG
                                  |||| || |||| ||||  |||||
                                  CGGG CG CAGG TCGA  AGTCC
                                    T A   _    CA
GAM380  LOC253981 3'  CCCAAGTAGCTGGGATTACAGG 97533               CA
                CA                  TGCCTGTAGTCCCAGCTACT  GG
                                    |||||||||||||||||||  ||
                                    ACGGACATTAGGGTCGATGA  CC
                                                 AC
GAM380  LOC253981 3'  CCTGAGTAGCTGGGACTACAGG 97535
                T                 GCCTGTAGTCCCAGCTACTCAGG
                                  |||||||||||||||||||||||
                                  TGGACATCAGGGTCGATGAGTCC

GAM380  LOC254058 5'  CCCGAGTAGCTGGAACTATAGG 99145          C       A
                T                 GCCTGTAGT CCAGCTACTC GG
                                  ||||||||| |||||||||| ||
                                  TGGATATCA GGTCGATGAG CC
                                        A         C
GAM380  LOC254082 5'  CCCAAGTAGCTGGGACTACAGG 98995               CA
                C                 GCCTGTAGTCCCAGCTACT  GG
                                  |||||||||||||||||||  ||
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                                CGGACATCAGGGTCGATGA  CC
                                          AC
GAM380  LOC254243 3'  CCTGAGTAGCTGGGATTACAGG 99258
            CA                  TGCCTGTAGTCCCAGCTACTCAGG
                                |||||||||||||||||||||||
                                ACGGACATTAGGGTCGATGAGTCC

GAM380  LOC254268 3'  CCAAGCAGCTGAGATTACAG  97141        C    A  CA
                                CTGTAGTC CAGCT CT  GG
                                |||||||| ||||| ||  ||
                                GACATTAG GTCGA GA  CC
                                     A    C  AC
GAM380  LOC254532 5'  CCCAAGTAGCTGGGACCACCAT 98449    CT_  A         CA
            GC                  GC   GT GTCCCAGCTACT  GG
                                ||   || ||||||||||||  ||
                                CG   CA CAGGGTCGATGA  CC
                                 TAC  C          AC
GAM380  LOC254655 3'  CCCAAGTAGCTGGGATTACAGG 97217               CA
            C                   GCCTGTAGTCCCAGCTACT  GG
                                ||||||||||||||||||  ||
                                CGGACATTAGGGTCGATGA  CC
                                          AC
GAM380  LOC254685 3'  CCCAAGTAGCTGGCACTACAGG 98240          C       CA
            CA                  TGCCTGTAGT CCAGCTACT  GG
                                |||||||||| |||||||||  ||
                                ACGGACATCA GGTCGATGA  CC
                                      C        AC
GAM380  LOC255308 3'  CCCAAGTAGCTGAGATTACAG  96175        C       CA
                                CTGTAGTC CAGCTACT  GG
                                |||||||| ||||||||  ||
                                GACATTAG GTCGATGA  CC
                                     A       AC
GAM380  LOC255465 3'  CCTGAGTAGCTGGGACTATAGG 99111
            CA                  TGCCTGTAGTCCCAGCTACTCAGG
                                |||||||||||||||||||||||
                                ACGGATATCAGGGTCGATGAGTCC

GAM380  LOC255919 3'  GTAGCTGGGACTACAGGC    96748
                                GCCTGTAGTCCCAGCTAC
                                |||||||||||||||||
                                CGGACATCAGGGTCGATG

GAM380  LOC255975 5'  CCTATTGGCTGAGTCTACAGGC 97576         TCC     CTC
            A                   TGCCTGTAG   CAGCTA   AGG
                                |||||||||   ||||||   |||
                                ACGGACATC   GTCGGT   TCC
                                      TGA     TA_
GAM380  LOC256221 3'  CCCGAGTAGCTGGGACTACAGG 96907               A
            C                   GCCTGTAGTCCCAGCTACTC GG
                                |||||||||||||||||||| ||
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                                CGGACATCAGGGTCGATGAG CC
                                      C
GAM380  LOC256306 3'  CCCGAGTAGCTGGAATTACAG  98511        C         A
                                CTGTAGT CCAGCTACTC GG
                                ||||||| |||||||||| ||
                                GACATTA GGTCGATGAG CC
                                    A         C
GAM380  LOC256360 5'  CCCAAGCAGCTGGGATTATAGG 98326              A  CA
              C                  GCCTGTAGTCCCAGCT CT  GG
                                 |||||||||||||||| ||  ||
                                 CGGATATTAGGGTCGA GA  CC
                                       C  AC
GAM380  LOC256364 5'  CCAAAGTGCTGGGATTACAGGC 96442              T   CA
              A                  TGCCTGTAGTCCCAGC ACT  GG
                                 |||||||||||||||| |||  ||
                                 ACGGACATTAGGGTCG TGA  CC
                                       _  AA
GAM380  LOC257017 5'  CCACAGTGCTGGGATTACAGGC 99219              T   CA
              A                  TGCCTGTAGTCCCAGC ACT  GG
                                 |||||||||||||||| |||  ||
                                 ACGGACATTAGGGTCG TGA  CC
                                       _  CA
GAM380  LOC257054 5'  CGAGTAGCTGAGTCTACA    97372       TCC        A
                                 TGTAG   CAGCTACTC G
                                 |||||   ||||||||| |
                                 ACATC   GTCGATGAG C
                                    TGA        C
GAM380  LOC257463 3'  CCAAAGTGCTGGGATTACAAGC 71618     C          T   CA
              A                  TGC TGTAGTCCCAGC ACT  GG
                                 ||| |||||||||||| |||  ||
                                 ACG ACATTAGGGTCG TGA  CC
                                   A          _  AA
GAM380  LOC257463 3'  CCTGAACAGCTGGGACTACAGG 71620              AC
              T                  GCCTGTAGTCCCAGCT  TCAGG
                                 ||||||||||||||||  |||||
                                 TGGACATCAGGGTCGA  AGTCC
                                       CA
GAM380  LOC257465 3'  CCAAAGTGCTGGGATTACAGGC 82491              T   CA
              A                  TGCCTGTAGTCCCAGC ACT  GG
                                 |||||||||||||||| |||  ||
                                 ACGGACATTAGGGTCG TGA  CC
                                       _  AA
GAM380  LOC257486 3'  CCCGACTAGCTGGGACTACAGG 69769               C  A
              C                  GCCTGTAGTCCCAGCTA TC GG
                                 |||||||||||||||| || ||
                                 CGGACATCAGGGTCGAT AG CC
                                       C  C
GAM380  LOC257545 3'  CCTGAGTAGCTGGGACTACAG  99641
                                 CTGTAGTCCCAGCTACTCAGG
                                 |||||||||||||||||||
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                                GACATCAGGGTCGATGAGTCC

GAM380  LOC257598 3'  CCTGAGTAGCTGGGACTACAG  99749
                                CTGTAGTCCCAGCTACTCAGG
                                |||||||||||||||||||||
                                GACATCAGGGTCGATGAGTCC

GAM380  LOC51008  5'  CCCGAGTAGCTGGGATTACAGG 32530                A
          CA                    TGCCTGTAGTCCCAGCTACTC GG
                                |||||||||||||||||||| ||
                                ACGGACATTAGGGTCGATGAG CC
                                      C
GAM380  LOC51159  5'  CCAAAGTGTTGGGATTACAGGC 33028             T  CA
          A                     TGCCTGTAGTCCCAGC ACT  GG
                                |||||||||||||||| |||  ||
                                ACGGACATTAGGGTTG TGA  CC
                                      _  AA
GAM380  LOC51193  5'  CCCGAGTAGCTCAGATTACAGG 33363          CC      A
          CA                    TGCCTGTAGTC  AGCTACTC GG
                                ||||||||||  |||||||| ||
                                ACGGACATTAG  TCGATGAG CC
                                     AC       C
GAM380  LOC51193  3'  CCTGCATAGCTAGGACTACAGG 33364           C    CT
          CA                    TGCCTGTAGTCC AGCTA  CAGG
                                |||||||||||| |||||  ||||
                                ACGGACATCAGG TCGAT  GTCC
                                      A    AC
GAM380  LOC51219  5'  CCAAAGTGCTGGGATTACAGGC 33540             T  CA
          A                     TGCCTGTAGTCCCAGC ACT  GG
                                |||||||||||||||| |||  ||
                                ACGGACATTAGGGTCG TGA  CC
                                      _  AA
GAM380  LOC51219  5'  CCCGAGTAGCTGGGATTACAGG 33543                A
          CA                    TGCCTGTAGTCCCAGCTACTC GG
                                |||||||||||||||||||| ||
                                ACGGACATTAGGGTCGATGAG CC
                                      C
GAM380  LOC51601  5'  CCCGAGTAGCTGAGATTACAGG 32499          C      A
          C                     GCCTGTAGTC CAGCTACTC GG
                                |||||||||| ||||||||| ||
                                CGGACATTAG GTCGATGAG CC
                                     A       C
GAM380  LOC51696  3'  CCCAGGTAGCTGGGACTATAGG 33080                CA
          CA                    TGCCTGTAGTCCCAGCTACT  GG
                                |||||||||||||||||||  ||
                                ACGGATATCAGGGTCGATGG  CC
                                      AC
GAM380  LOC55954  5'  TAGCTGGGACTACAGGCA    39400
                                TGCCTGTAGTCCCAGCTA
                                ||||||||||||||||||
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                                ACGGACATCAGGGTCGAT

GAM380  LOC57107  3' CCCGAGTAGCTGGAATTACAGG 40184          C        A
             CA                  TGCCTGTAGT CCAGCTACTC GG
                                 |||||||||| |||||||||| ||
                                 ACGGACATTA GGTCGATGAG CC
                                       A        C
GAM380  LOC57146  3' CCCAAGTAGCTGGGATTACAGG 40294                CA
             CA                  TGCCTGTAGTCCCAGCTACT  GG
                                 |||||||||||||||||||  ||
                                 ACGGACATTAGGGTCGATGA  CC
                                           AC
GAM380  LOC81034  3' CCTGAGTAGCTGGGACTACAGG 48590
             CA                  TGCCTGTAGTCCCAGCTACTCAGG
                                 |||||||||||||||||||||||
                                 ACGGACATCAGGGTCGATGAGTCC

GAM380  LOC89231  3' CCGAGTAGCTAGGATTACAG  94295        C      A
                                 CTGTAGTCC AGCTACTC GG
                                 ||||||||| |||||||| ||
                                 GACATTAGG TCGATGAG CC
                                       A       C
GAM380  LOC89932  3' CCAAAGTGCTGGGATTACAGGC 61450             T   CA
             A                    TGCCTGTAGTCCCAGC ACT  GG
                                  |||||||||||||| |||  ||
                                  ACGGACATTAGGGTCG TGA  CC
                                           _  AA
GAM380  LOC89932  3' CCTGAGTAGCTGGGATTACAGG 61455
             TA                  TGCCTGTAGTCCCAGCTACTCAGG
                                 |||||||||||||||||||||||
                                 ATGGACATTAGGGTCGATGAGTCC

GAM380  LOC90038  3' CCTGAGTAGCTGGGATTACAGG 61801
             CA                  TGCCTGTAGTCCCAGCTACTCAGG
                                 |||||||||||||||||||||||
                                 ACGGACATTAGGGTCGATGAGTCC

GAM380  LOC90288  3' CCCGAATAGCTGGGACTACAGG 62780               C  A
             CA                  TGCCTGTAGTCCCAGCTA TC GG
                                 |||||||||||||||| || ||
                                 ACGGACATCAGGGTCGAT AG CC
                                           A  C
GAM380  LOC90288  3' CCTGAGTAGCTAGAACCACAGG 62784       A  CCC
             C                    GCCTGT GT   AGCTACTCAGG
                                  |||||| ||   ||||||||||
                                  CGGACA CA   TCGATGAGTCC
                                     C  AGA
GAM380  LOC90371  5' CCTGAGTAGCTGGGATTTCAGG 63160      T
             C                    GCCTG AGTCCCAGCTACTCAGG
                                  ||||| ||||||||||||||||
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                                CGGAC TTAGGGTCGATGAGTCC
                                  T
GAM380  LOC90408  5' CCAAGTAGCTGGGATTACAG  63339            CA
                                CTGTAGTCCCAGCTACT  GG
                                ||||||||||||||||  ||
                                GACATTAGGGTCGATGA  CC
                                    AC
GAM380  LOC90485  3' CCAAAGTGCTGGGACTACAGGC 63690           T  CA
                                GCCTGTAGTCCCAGC ACT  GG
                                |||||||||||||| |||  ||
                                CGGACATCAGGGTCG TGA  CC
                                    _  AA
GAM380  LOC90485  3' CCAAAGTGCTGGGATTACAGGC 63691           T  CA
          A                      TGCCTGTAGTCCCAGC ACT  GG
                                |||||||||||||| |||  ||
                                ACGGACATTAGGGTCG TGA  CC
                                    _  AA
GAM380  LOC90485  3' CCCGAGTAGCTGGGACTACAGG 63694             A
          C                      GCCTGTAGTCCCAGCTACTC GG
                                |||||||||||||||||| ||
                                CGGACATCAGGGTCGATGAG CC
                                    C
GAM380  LOC90591  3' CCCAAGTAGCTGGGATTACAG  64159           CA
                                CTGTAGTCCCAGCTACT  GG
                                ||||||||||||||||  ||
                                GACATTAGGGTCGATGA  CC
                                    AC
GAM380  LOC90591  3' CCTGAGTAGCTGGGACTACAGG 64163
          T                      GCCTGTAGTCCCAGCTACTCAGG
                                |||||||||||||||||||||||
                                TGGACATCAGGGTCGATGAGTCC

GAM380  LOC90918  3' CCAAAGTGCCGGGATTACAGGC 64998         A  T  CA
          A                      TGCCTGTAGTCCC GC ACT  GG
                                |||||||||||| || |||  ||
                                ACGGACATTAGGG CG TGA  CC
                                    C  _  AA
GAM380  LOC91115  3' AGTAACTGGGATTACAGGCA  65549           C
                                TGCCTGTAGTCCCAG TACT
                                |||||||||||||| ||||
                                ACGGACATTAGGGTC ATGA
                                    A
GAM380  LOC91115  3' CCTGAGTAGCTGGGACTACAGG 65559
          CA                      TGCCTGTAGTCCCAGCTACTCAGG
                                |||||||||||||||||||||||
                                ACGGACATCAGGGTCGATGAGTCC

GAM380  LOC91115  3' CGAGTAGCTGGGATTAC    65562            A
                                GTAGTCCCAGCTACTC G
                                |||||||||||||||| |
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                                CATTAGGGTCGATGAG C
                                                 C
GAM380  LOC91250  5'  CCAAAGTGCTGGGATTACAGGC 65912                T   CA
              A                   TGCCTGTAGTCCCAGC ACT  GG
                                  |||||||||||||||| |||  ||
                                  ACGGACATTAGGGTCG TGA  CC
                                                 _   AA
GAM380  LOC91250  5'  CCGAGTAGCTGGGATTACAG   65914                  A
                                  CTGTAGTCCCAGCTACTC GG
                                  |||||||||||||||||| ||
                                  GACATTAGGGTCGATGAG CC
                                                 C
GAM380  LOC91308  3'  CCCGAGTAGCTGAGACCACAGG 66166        A  C        A
              T                   GCCTGT GTC CAGCTACTC GG
                                  |||||| ||| ||||||||| ||
                                  TGGACA CAG GTCGATGAG CC
                                     C  A        C
GAM380  LOC91373  3'  CCTAGTAGCTGGGACTACAGGC 66410                  C
              A                   TGCCTGTAGTCCCAGCTACT AGG
                                  |||||||||||||||||| |||
                                  ACGGACATCAGGGTCGATGA TCC
                                                  _
GAM380  LOC91561  5'  CCCAAGTAGCTGGGACTACAGG 67041                  CA
              C                    GCCTGTAGTCCCAGCTACT  GG
                                   |||||||||||||||||  ||
                                   CGGACATCAGGGTCGATGA  CC
                                                 AC
GAM380  LOC91661  3'  GTAGCTGGGACTACAGGC    57217
                                  GCCTGTAGTCCCAGCTAC
                                  |||||||||||||||||
                                  CGGACATCAGGGTCGATG

GAM380  LOC91893  3'  CCCGAGTAGCTGGGACTACAGG 68071                  A
              CA                    TGCCTGTAGTCCCAGCTACTC GG
                                    |||||||||||||||||| ||
                                    ACGGACATCAGGGTCGATGAG CC
                                                   C
GAM380  LOC91917  3'  CCTACGCCTGGGCTACAGGCA  68140          T    CTACTC
                                  TGCCTGTAG CCCAG      AGG
                                  |||||||| |||||      |||
                                  ACGGACATC GGGTC      TCC
                                       _     CGCA__
GAM380  LOC92267  3'  CCCGAGTAGCTGGGATTGCAGG 69169                  A
              CA                    TGCCTGTAGTCCCAGCTACTC GG
                                    |||||||||||||||||| ||
                                    ACGGACGTTAGGGTCGATGAG CC
                                                   C
GAM380  LOC92283  3'  CCTGAGTAGCTGGGACTACAGG 69302
              CA                    TGCCTGTAGTCCCAGCTACTCAGG
                                    |||||||||||||||||||||||
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                                ACGGACATCAGGGTCGATGAGTCC

GAM380  LOC92303  3' CCCAAGTAGCTGGGATTACAGG 69387                CA
             CA                  TGCCTGTAGTCCCAGCTACT  GG
                                 ||||||||||||||||||  ||
                                 ACGGACATTAGGGTCGATGA  CC
                                       AC
GAM380  LOC92465  5' CTGAGTAGCTGGGACTAAAGGC 69948      G
             A                   TGCCT TAGTCCCAGCTACTCAG
                                 ||||| ||||||||||||||||
                                 ACGGA ATCAGGGTCGATGAGTC
                                   A
GAM380  LOC92661  5' CCAAAGTGCTGGGATTACAGGC 70621             T  CA
             A                   TGCCTGTAGTCCCAGC ACT  GG
                                 |||||||||||||||| |||  ||
                                 ACGGACATTAGGGTCG TGA  CC
                                       _  AA
GAM380  LOC92661  5' CCCGAGTAGCTGGGACTACAG  70626               A
                                 CTGTAGTCCCAGCTACTC GG
                                 |||||||||||||||||| ||
                                 GACATCAGGGTCGATGAG CC
                                       C
GAM380  LOC92689  3' CCTGAGTAGCTGGGACTACAGG 70773
             T                   GCCTGTAGTCCCAGCTACTCAGG
                                 |||||||||||||||||||||||
                                 TGGACATCAGGGTCGATGAGTCC

GAM380  LOC92697  5' CCAAAGTTCTGGGATTACAGGC 70805           CT  CA
             A                   TGCCTGTAGTCCCAG  ACT  GG
                                 ||||||||||||||  |||  ||
                                 ACGGACATTAGGGTC  TGA  CC
                                       T_  AA
GAM380  LOC92697  5' CCTGAGTAGCTGGGATTACAGG 70809
             CA                  TGCCTGTAGTCCCAGCTACTCAGG
                                 |||||||||||||||||||||||
                                 ACGGACATTAGGGTCGATGAGTCC

GAM380  LOC92841  3' CCAAAGTGCTGGGATTACAGGC 71248             T  CA
             A                   TGCCTGTAGTCCCAGC ACT  GG
                                 |||||||||||||||| |||  ||
                                 ACGGACATTAGGGTCG TGA  CC
                                       _  AA
GAM380  LOC92841  3' CCCAAGTAGCTGAGATTACAGG 71250         C      CA
             CA                  TGCCTGTAGTC CAGCTACT  GG
                                 ||||||||||| ||||||||  ||
                                 ACGGACATTAG GTCGATGA  CC
                                       A      AC
GAM380  LOC93070  3' CCCAAGTAGCTGGGATCACAGG 71804       A        CA
             C                   GCCTGT GTCCCAGCTACT  GG
                                 ||||||  ||||||||||||  ||
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                                CGGACA TAGGGTCGATGA  CC
                                   C          AC
GAM380  LOC93132  5'  AGTAGCTGGGACTACAAGCA  71977     C
                                TGC TGTAGTCCCAGCTACT
                                ||| ||||||||||||||||
                                ACG ACATCAGGGTCGATGA
                                  A
GAM380  LOC93349  3'  CCCAAGTAGCTGGGATTACAG  57265              CA
                                CTGTAGTCCCAGCTACT  GG
                                ||||||||||||||||  ||
                                GACATTAGGGTCGATGA  CC
                                          AC
GAM380  LOC93408  5'  CCAAAGTGCTGGGATTACAGGC 57284              T   CA
            A                    TGCCTGTAGTCCCAGC ACT  GG
                                ||||||||||||||| |||  ||
                                ACGGACATTAGGGTCG TGA  CC
                                          _  AA
GAM381  KIAA0857  3'  ATCCCCCAAGGATGGTCAGCCA 67247        AGGCGAG   AA
            T                    ATGGCTGA      TTG  GGAT
                                ||||||||      |||  ||||
                                TACCGACT      AAC  CCTA
                                     GGTAGG_   CC
GAM381  KPNA1    3'  ATCCACTCCCTCACCTTCAGCC 81130         C   TTGAA
                                GGCTGAAGG GAG     GGAT
                                ||||||||| |||     ||||
                                CCGACTTCC CTC     CCTA
                                     A   CCTCA
GAM381  LMO2     5'  CCCCCACCTGCCCTCAGCCGT  19935        A   G  T  AA
                                ATGGCTGA GGC AG TG  GG
                                |||||||| ||| || ||  ||
                                TGCCGACT CCG TC AC  CC
                                     C   _  C  CC
GAM381  PRIM1    3'  TCTTCTGCCTTCAACCA     8139      C       AGTT
                                TGG TGAAGGCG    GAAGG
                                ||| ||||||||    |||||
                                ACC ACTTCCGT    CTTCT
                                  A       _____
GAM381  RAI14    3'  CCTAGAACTTTCAGCCAT    32100         AGGC     GA
                                ATGGCTGA    GAGTT  AGG
                                ||||||||    |||||  |||
                                TACCGACT    TTCAA  TCC
                                     _____     GA
GAM381  RRM1     5'  ATCCTTCAGAGCCTCAGCCA  8279         A   GAGT
                                TGGCTGA GGC    TGAAGGAT
                                ||||||| |||    ||||||||
                                ACCGACT CCG    ACTTCCTA
                                     _  AG__
GAM381  FLJ12294 5'  ATCCTTCAACACCCCAACCCA  47707     CTGAA  CGA
                                TGG    GG   GTTGAAGGAT
                                |||    ||   ||||||||||
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                                ACC    CC   CAACTTCCTA
                                  CAAC_  CA_
GAM381  FLJ23186  3'  TCCTCCTCCCCCCCCACCAT   61046     C  AA  C   TTGA
                                ATGG TG  GG GAG    AGGA
                                |||| ||  || |||    ||||
                                TACC AC  CC CTC    TCCT
                                  _  CC  C   C___
GAM381  KIAA0556  3'  CCTTCTCCCCCTTCAGCCA   69645         CGAGTT
                                TGGCTGAAGG     GAAGG
                                ||||||||||     |||||
                                ACCGACTTCC     CTTCC
                                      CCCT__
GAM381  KIAA0720  3'  CCCCAGACTTCCCCACCTTCAG 62979         C____    GAA
           CCA                    TGGCTGAAGG    GAGTT   GG
                                ||||||||||    |||||   ||
                                ACCGACTTCC    TTCAG   CC
                                      ACCCC    ACC
GAM381  KIAA0961  5'  ATCCTCGTCCGCGCTTCAGCCA 30390         _   AGT   A
                                TGGCTGAAG GCG   TGA GGAT
                                ||||||||| |||   ||| ||||
                                ACCGACTTC CGC   GCT CCTA
                                     G   CT_  _
GAM381  KIAA1656  3'  ATCCTTCTGCCCTTCAGCC   66358         CGA  T
                                GGCTGAAGG   GT GAAGGAT
                                |||||||||   || |||||||
                                CCGACTTCC   CG CTTCCTA
                                      ___  T
GAM381  MGC19556  3'  CCTCTCCCCCTTCAGCCAT   54338         C_   TTGA
                                ATGGCTGAAGG  GAG    AGG
                                ||||||||||  |||    |||
                                TACCGACTTCC  CTC    TCC
                                      CC   _____
GAM381  NMT1      3'  CCCAGACCCCTTCAGCCA    41144         CGA   GAA
                                TGGCTGAAGG   GTT   GG
                                ||||||||||   |||   ||
                                ACCGACTTCC   CAG   CC
                                      C__   AC_
GAM381  p25       3'  CCTGCCTCGTCCTCAGCCAT   23830         A     TTGA
                                ATGGCTGA GGCGAG    AGG
                                |||||||| ||||||    |||
                                TACCGACT CTGCTC    TCC
                                    C     CG__
GAM381  LOC122773 3'  ATCCCTCAGTTTGGCCCCCACC 74634      C  AA   _  GT   A
           AT                     ATGG TG  GGC GA  TGA GGAT
                                |||| ||  ||| ||  ||| ||||
                                TACC AC  CCG TT  ACT CCTA
                                  _  CC   G  TG   C
GAM381  LOC152078 3'  TCCCCTGGCCTTCAGCC     81290         G  TTGAA
                                GGCTGAAGGC AG    GGA
                                |||||||||| ||    |||
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                                CCGACTTCCG TC     CCT
                                      G  C____
GAM381  LOC220635 3'  ATCCTTCAGACCCCTCCAGACA 92453     G   A   CGAG
           T                   ATG CTG AGG    TTGAAGGAT
                               ||| ||| |||    |||||||||
                               TAC GAC TCC    GACTTCCTA
                                 A   C   CCA_
GAM381  LOC91012  5'  TCCTTCGGCCCTCAGCC     65250       A   GAGT
                               GGCTGA GGC    TGAAGGA
                               |||||| |||    |||||||
                               CCGACT CCG    GCTTCCT
                                  C   ____
GAM382  A1BG      3'  AACTCCTGAGCTCAGGTGATC  56273          G
                               GATCACCTGAG TCAGGAGTT
                               |||||||||||| |||||||||
                               CTAGTGGACTC AGTCCTCAA
                                      G
GAM382  A1BG      3'  AACTCCTGAGCTCAGGTGATC  56273          G
                               GATCACCTGAG TCAGGAGTT
                               |||||||||||| |||||||||
                               CTAGTGGACTC AGTCCTCAA
                                      G
GAM382  ADAMTS4   3'  TCCTGACCTTAGGTGATC    18775
                               GATCACCTGAGGTCAGGA
                               ||||||||||||||||||
                               CTAGTGGATTCCAGTCCT

GAM382  ADAMTS4   3'  TCCTGACCTTAGGTGATC    18775
                               GATCACCTGAGGTCAGGA
                               ||||||||||||||||||
                               CTAGTGGATTCCAGTCCT

GAM382  ADAMTS4   3'  TGAACTCCTGACCTCAGGTAAT 18776     C
           C                    GAT ACCTGAGGTCAGGAGTTTG
                               ||| ||||||||||||||||||
                               CTA TGGACTCCAGTCCTCAAGT
                                 A
GAM382  ADAMTS4   3'  TGAACTCCTGACCTCAGGTAAT 18776     C
           C                    GAT ACCTGAGGTCAGGAGTTTG
                               ||| ||||||||||||||||||
                               CTA TGGACTCCAGTCCTCAAGT
                                 A
GAM382  ALDH1B1   3'  TGAACTCCTGACCTCAGGTGAT 7328
           C                    GATCACCTGAGGTCAGGAGTTTG
                               |||||||||||||||||||||||
                               CTAGTGGACTCCAGTCCTCAAGT

GAM382  ALDH1B1   3'  TGAACTCCTGACCTCAGGTGAT 7328
           C                    GATCACCTGAGGTCAGGAGTTTG
                               |||||||||||||||||||||||
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                                CTAGTGGACTCCAGTCCTCAAGT

GAM382  APM1    3'  TCAAACTCCTGACTTTGTGATC 17792       CT
                                GATCAC  GAGGTCAGGAGTTTGA
                                ||||||  ||||||||||||||||
                                CTAGTG  TTTCAGTCCTCAAACT
                                  —
GAM382  APM1    3'  TCAAACTCCTGACTTTGTGATC 17792       CT
                                GATCAC  GAGGTCAGGAGTTTGA
                                ||||||  ||||||||||||||||
                                CTAGTG  TTTCAGTCCTCAAACT
                                  —
GAM382  AQP6    3'  TCAAACTCCTGACCTGAGGCGA 55013     A  G
          TC                      GATC CCT AGGTCAGGAGTTTGA
                                ||||  |||  ||||||||||||||||
                                CTAG GGA TCCAGTCCTCAAACT
                                  C  G
GAM382  AQP6    3'  TCAAACTCCTGACCTGAGGCGA 55014     A  G
          TC                      GATC CCT AGGTCAGGAGTTTGA
                                ||||  |||  ||||||||||||||||
                                CTAG GGA TCCAGTCCTCAAACT
                                  C  G
GAM382  AQP6    3'  TCAAACTCCTGACCTGAGGCGA 55014     A  G
          TC                      GATC CCT AGGTCAGGAGTTTGA
                                ||||  |||  ||||||||||||||||
                                CTAG GGA TCCAGTCCTCAAACT
                                  C  G
GAM382  AQP6    3'  TCAAACTCCTGACCTGAGGCGA 9734      A  G
          TC                      GATC CCT AGGTCAGGAGTTTGA
                                ||||  |||  ||||||||||||||||
                                CTAG GGA TCCAGTCCTCAAACT
                                  C  G
GAM382  ARCN1   3'  CGAACTCCTGAGCTCAGGCAAT 9749     CA    G
          C                       GAT  CCTGAG TCAGGAGTTTG
                                |||  ||||||  ||||||||||
                                CTA  GGACTC AGTCCTCAAGC
                                  AC     G
GAM382  ARCN1   3'  CGAACTCCTGAGCTCAGGCAAT 9749     CA    G
          C                       GAT  CCTGAG TCAGGAGTTTG
                                |||  ||||||  ||||||||||
                                CTA  GGACTC AGTCCTCAAGC
                                  AC     G
GAM382  ARSF    5'  TCCCGACCTCAAGTGATC    65211       C     A
                                GATCAC TGAGGTC GGA
                                ||||||  |||||||  |||
                                CTAGTG ACTCCAG CCT
                                   A      C
GAM382  ARSF    5'  TCCCGACCTCAAGTGATC    65211       C     A
                                GATCAC TGAGGTC GGA
                                ||||||  |||||||  |||
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                                CTAGTG ACTCCAG CCT
                                   A      C
GAM382  ARSF     5'  TCGAACTCCCGACCTCAAGTGA 65212        C      A
                TC                  GATCAC TGAGGTC GGAGTTTGA
                                    |||||| ||||||| |||||||||
                                    CTAGTG ACTCCAG CCTCAAGCT
                                       A      C
GAM382  ARSF     5'  TCGAACTCCCGACCTCAAGTGA 65212        C      A
                TC                  GATCAC TGAGGTC GGAGTTTGA
                                    |||||| ||||||| |||||||||
                                    CTAGTG ACTCCAG CCTCAAGCT
                                       A      C
GAM382  ATP1B2   3'  TCGAACTCCCGACCTCAGGTGA 9841             A
                TC                  GATCACCTGAGGTC GGAGTTTGA
                                    |||||||||||||| |||||||||
                                    CTAGTGGACTCCAG CCTCAAGCT
                                           C
GAM382  ATP1B2   3'  TCGAACTCCCGACCTCAGGTGA 9841             A
                TC                  GATCACCTGAGGTC GGAGTTTGA
                                    |||||||||||||| |||||||||
                                    CTAGTGGACTCCAG CCTCAAGCT
                                           C
GAM382  ATP6V1A1 3'  TCCAGACCTCAGGTGATC    9876           A
                                    GATCACCTGAGGTC GGA
                                    |||||||||||||| |||
                                    CTAGTGGACTCCAG CCT
                                           A
GAM382  ATP6V1A1 3'  TCCAGACCTCAGGTGATC    9876           A
                                    GATCACCTGAGGTC GGA
                                    |||||||||||||| |||
                                    CTAGTGGACTCCAG CCT
                                           A
GAM382  ATP7A    3'  TAAACTCCTAACCTCAGGTGAT 5329            C
                C                    GATCACCTGAGGT AGGAGTTTG
                                    |||||||||||| |||||||||
                                    CTAGTGGACTCCA TCCTCAAAT
                                           A
GAM382  ATP7A    3'  TAAACTCCTAACCTCAGGTGAT 5329            C
                C                    GATCACCTGAGGT AGGAGTTTG
                                    |||||||||||| |||||||||
                                    CTAGTGGACTCCA TCCTCAAAT
                                           A
GAM382  AXL      3'  AAACTCCTGACCTCAAGTGATC 9893        C
                                    GATCAC TGAGGTCAGGAGTTT
                                    |||||| ||||||||||||||
                                    CTAGTG ACTCCAGTCCTCAAA
                                       A
GAM382  AXL      3'  AAACTCCTGACCTCAAGTGATC 41866       C
                                    GATCAC TGAGGTCAGGAGTTT
                                    |||||| ||||||||||||||
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                                CTAGTG ACTCCAGTCCTCAAA
                                   A
GAM382  AXL     3'  AAACTCCTGACCTCAAGTGATC 41866       C
                                GATCAC TGAGGTCAGGAGTTT
                                |||||| ||||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAA
                                   A
GAM382  C7      3'  AACTCCTGACCTCAGGTAATC  6972      C
                                GAT ACCTGAGGTCAGGAGTT
                                ||| ||||||||||||||||
                                CTA TGGACTCCAGTCCTCAA
                                  A
GAM382  C7      3'  AACTCCTGACCTCAGGTAATC  6972      C
                                GAT ACCTGAGGTCAGGAGTT
                                ||| ||||||||||||||||
                                CTA TGGACTCCAGTCCTCAA
                                  A
GAM382  CAMLG   3'  TCGAACTTCTGACCTCAGGTGA 10008
           TC                     GATCACCTGAGGTCAGGAGTTTGA
                                ||||||||||||||||||||||||
                                CTAGTGGACTCCAGTCTTCAAGCT

GAM382  CAMLG   3'  TCGAACTTCTGACCTCAGGTGA 10008
           TC                     GATCACCTGAGGTCAGGAGTTTGA
                                ||||||||||||||||||||||||
                                CTAGTGGACTCCAGTCTTCAAGCT

GAM382  CASP10  3'  TCAAACTCCTGGGCTCAAGCGA 53224      ACC   G
           TC                     GATC  TGAG TCAGGAGTTTGA
                                ||||  |||| ||||||||||||
                                CTAG  ACTC GGTCCTCAAACT
                                  CGA   G
GAM382  CASP10  3'  TCAAACTCCTGGGCTCAAGCGA 53262      ACC   G
           TC                     GATC  TGAG TCAGGAGTTTGA
                                ||||  |||| ||||||||||||
                                CTAG  ACTC GGTCCTCAAACT
                                  CGA   G
GAM382  CASP10  3'  TCAAACTCCTGGGCTCAAGCGA 53262      ACC   G
           TC                     GATC  TGAG TCAGGAGTTTGA
                                ||||  |||| ||||||||||||
                                CTAG  ACTC GGTCCTCAAACT
                                  CGA   G
GAM382  CASP10  3'  TCAAACTCCTGGGCTCAAGCGA 53263      ACC   G
           TC                     GATC  TGAG TCAGGAGTTTGA
                                ||||  |||| ||||||||||||
                                CTAG  ACTC GGTCCTCAAACT
                                  CGA   G
GAM382  CBFA2T2 3'  TCAAACCCCGGACCTCAGGTGA 18718          A  A
           TC                     GATCACCTGAGGTC GG GTTTGA
                                |||||||||||||| || ||||||
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                                CTAGTGGACTCCAG CC CAAACT
                                      G  C
GAM382  CBFA2T2  3'  TCAAACCCCGGACCTCAGGTGA 18718           A  A
           TC                   GATCACCTGAGGTC GG GTTTGA
                                |||||||||||||| || ||||||
                                CTAGTGGACTCCAG CC CAAACT
                                      G  C
GAM382  CCNF     3'  TCATGACCTCAAGTGATC    10088      C      G
                                GATCAC TGAGGTCA GA
                                |||||| |||||||| ||
                                CTAGTG ACTCCAGT CT
                                   A      A
GAM382  CCNF     3'  TCATGACCTCAAGTGATC    10088      C      G
                                GATCAC TGAGGTCA GA
                                |||||| |||||||| ||
                                CTAGTG ACTCCAGT CT
                                   A      A
GAM382  CDH1     3'  TCAAACTCCTGGGCTCAAGTGA 16407      C   G
           TC                   GATCAC TGAG TCAGGAGTTTGA
                                |||||| |||| ||||||||||||
                                CTAGTG ACTC GGTCCTCAAACT
                                   A   G
GAM382  CDH1     3'  TCAAACTCCTGGGCTCAAGTGA 16407      C   G
           TC                   GATCAC TGAG TCAGGAGTTTGA
                                |||||| |||| ||||||||||||
                                CTAGTG ACTC GGTCCTCAAACT
                                   A   G
GAM382  CDH17    3'  TCCTGACGTCAAGTGATC    15790      C  G
                                GATCAC TGA GTCAGGA
                                |||||| ||| |||||||
                                CTAGTG ACT CAGTCCT
                                   A  G
GAM382  CDH17    3'  TCCTGACGTCAAGTGATC    15790      C  G
                                GATCAC TGA GTCAGGA
                                |||||| ||| |||||||
                                CTAGTG ACT CAGTCCT
                                   A  G
GAM382  CHRNB4   3'  TCGAACTCCTGACCTCAGATGA 7450     C
                                TCA CTGAGGTCAGGAGTTTGA
                                ||| ||||||||||||||||||
                                AGT GACTCCAGTCCTCAAGCT
                                  A
GAM382  CHRNB4   3'  TCGAACTCCTGACCTCAGATGA 7450     C
                                TCA CTGAGGTCAGGAGTTTGA
                                ||| ||||||||||||||||||
                                AGT GACTCCAGTCCTCAAGCT
                                  A
GAM382  CLECSF12 3'  CGAACTCCTGACCTCAAGTGAT 77209      C
           C                    GATCAC TGAGGTCAGGAGTTTG
                                |||||| |||||||||||||||
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                                CTAGTG ACTCCAGTCCTCAAGC
                                   A
GAM382  CLECSF12  3'  CGAACTCCTGACCTCAAGTGAT 77209       C
           C                    GATCAC TGAGGTCAGGAGTTTG
                                |||||| ||||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAGC
                                   A
GAM382  CNGA1     5'  TGAACTCCTGATCTCAAGTGAT 60245       C
           C                    GATCAC TGAGGTCAGGAGTTTG
                                |||||| ||||||||||||||||
                                CTAGTG ACTCTAGTCCTCAAGT
                                   A
GAM382  CNGA1     5'  TGAACTCCTGATCTCAAGTGAT 60245       C
           C                    GATCAC TGAGGTCAGGAGTTTG
                                |||||| ||||||||||||||||
                                CTAGTG ACTCTAGTCCTCAAGT
                                   A
GAM382  COX15     3'  TGAACTCCTGACCTCAGGTAAT 55291     C
           C                    GAT ACCTGAGGTCAGGAGTTTG
                                ||| ||||||||||||||||||
                                CTA TGGACTCCAGTCCTCAAGT
                                   A
GAM382  COX15     3'  TGAACTCCTGACCTCAGGTAAT 55291     C
           C                    GAT ACCTGAGGTCAGGAGTTTG
                                ||| ||||||||||||||||||
                                CTA TGGACTCCAGTCCTCAAGT
                                   A
GAM382  CYP1A2    3'  TCAAACTCCTGACCTCAAGTGA 7527       C
           TC                     GATCAC TGAGGTCAGGAGTTTGA
                                  |||||| ||||||||||||||||
                                  CTAGTG ACTCCAGTCCTCAAACT
                                     A
GAM382  CYP1A2    3'  TCAAACTCCTGACCTCAAGTGA 7527       C
           TC                     GATCAC TGAGGTCAGGAGTTTGA
                                  |||||| ||||||||||||||||
                                  CTAGTG ACTCCAGTCCTCAAACT
                                     A
GAM382  CYP1A2    3'  TCGAACTCCTGACCCCAAGTTA 7528     C  C  A
           TC                     GAT AC TG GGTCAGGAGTTTGA
                                  ||| || || ||||||||||||||
                                  CTA TG AC CCAGTCCTCAAGCT
                                     T  A  C
GAM382  CYP1A2    3'  TCGAACTCCTGACCCCAAGTTA 7528     C  C  A
           TC                     GAT AC TG GGTCAGGAGTTTGA
                                  ||| || || ||||||||||||||
                                  CTA TG AC CCAGTCCTCAAGCT
                                     T  A  C
GAM382  CYP2B6    3'  TCCTGGCCTCAGGTGATC    7570
                                  GATCACCTGAGGTCAGGA
                                  ||||||||||||||||||
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                              CTAGTGGACTCCGGTCCT

GAM382  CYP2B6   3'  TCCTGGCCTCAGGTGATC    7570
                              GATCACCTGAGGTCAGGA
                              ||||||||||||||||||
                              CTAGTGGACTCCGGTCCT

GAM382  CYP4F3   3'  TGAACTCCTAACCTCAGGTGAT 8017            C
          C                    GATCACCTGAGGT AGGAGTTTG
                              |||||||||||| |||||||||
                              CTAGTGGACTCCA TCCTCAAGT
                                     A
GAM382  CYP4F3   3'  TGAACTCCTAACCTCAGGTGAT 8017            C
          C                    GATCACCTGAGGT AGGAGTTTG
                              |||||||||||| |||||||||
                              CTAGTGGACTCCA TCCTCAAGT
                                     A
GAM382  DFFB     3'  TCAAACTCCTGACCTCAGGTGA 88786
          TC                   GATCACCTGAGGTCAGGAGTTTGA
                              ||||||||||||||||||||||||
                              CTAGTGGACTCCAGTCCTCAAACT

GAM382  DFFB     3'  TCAAACTCCTGACCTCAGGTGA 88786
          TC                   GATCACCTGAGGTCAGGAGTTTGA
                              ||||||||||||||||||||||||
                              CTAGTGGACTCCAGTCCTCAAACT

GAM382  DFFB     3'  TCGAACTCCTGACCTCAGGTGA 88788
          TC                   GATCACCTGAGGTCAGGAGTTTGA
                              ||||||||||||||||||||||||
                              CTAGTGGACTCCAGTCCTCAAGCT

GAM382  DFFB     3'  TCGAACTCCTGACCTCAGGTGA 88788
          TC                   GATCACCTGAGGTCAGGAGTTTGA
                              ||||||||||||||||||||||||
                              CTAGTGGACTCCAGTCCTCAAGCT

GAM382  DIAPH2   3'  TCAAACTCCCAGGCTCAAGGGA 23012     A   GA   A_
          TC                   GATC CCT  GGTC  GGAGTTTGA
                              |||| |||  ||||  |||||||||
                              CTAG GGA  TCGG  CCTCAAACT
                                _  AC   AC
GAM382  DIAPH2   3'  TCAAACTCCCAGGCTCAAGGGA 24595     A   GA   A_
          TC                   GATC CCT  GGTC  GGAGTTTGA
                              |||| |||  ||||  |||||||||
                              CTAG GGA  TCGG  CCTCAAACT
                                _  AC   AC
GAM382  DISC1    3'  TCAAACTCCTGACCTCAGGCGA 38516     A
          TC                   GATC CCTGAGGTCAGGAGTTTGA
                              |||| ||||||||||||||||||
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                                CTAG GGACTCCAGTCCTCAAACT
                                  C
GAM382  DISC1    3'  TCAAACTCCTGACCTCAGGCGA 38516      A
                TC                GATC CCTGAGGTCAGGAGTTTGA
                                  |||| ||||||||||||||||||
                                CTAG GGACTCCAGTCCTCAAACT
                                  C
GAM382  EIF2S3   3'  TCCTGACCTCAGGGTGATC   9215        _
                                GATCACC TGAGGTCAGGA
                                ||||||| ||||||||||
                                CTAGTGG ACTCCAGTCCT
                                    G
GAM382  EIF2S3   3'  TCCTGACCTCAGGGTGATC   9215        _
                                GATCACC TGAGGTCAGGA
                                ||||||| ||||||||||
                                CTAGTGG ACTCCAGTCCT
                                    G
GAM382  EPB72    3'  CGAACTCCTAACCTCAGGTGAT 15870           C
                C                 GATCACCTGAGGT AGGAGTTTG
                                  |||||||||||| |||||||||
                                CTAGTGGACTCCA TCCTCAAGC
                                      A
GAM382  EPB72    3'  CGAACTCCTAACCTCAGGTGAT 15870           C
                C                 GATCACCTGAGGT AGGAGTTTG
                                  |||||||||||| |||||||||
                                CTAGTGGACTCCA TCCTCAAGC
                                      A
GAM382  F2RL2    3'  TCCTGACCTCAAGTGATC    15903       C
                                GATCAC TGAGGTCAGGA
                                ||||||| ||||||||||
                                CTAGTG ACTCCAGTCCT
                                    A
GAM382  F2RL2    3'  TCCTGACCTCAAGTGATC    15903       C
                                GATCAC TGAGGTCAGGA
                                ||||||| ||||||||||
                                CTAGTG ACTCCAGTCCT
                                    A
GAM382  F2RL2    3'  TGAACTCCTGACCTCAAGTGAT 15904       C
                C                 GATCAC TGAGGTCAGGAGTTTG
                                  |||||| ||||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAGT
                                    A
GAM382  F2RL2    3'  TGAACTCCTGACCTCAAGTGAT 15904       C
                C                 GATCAC TGAGGTCAGGAGTTTG
                                  |||||| ||||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAGT
                                    A
GAM382  F2RL3    3'  AACTCCTGCCCTCAAGTGATC  15481       C    T
                                GATCAC TGAGG CAGGAGTT
                                |||||| ||||| ||||||||
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                                CTAGTG ACTCC GTCCTCAA
                                   A    C
GAM382  F2RL3    3'  AACTCCTGCCCTCAAGTGATC  15481       C    T
                                GATCAC TGAGG CAGGAGTT
                                |||||| ||||| ||||||||
                                CTAGTG ACTCC GTCCTCAA
                                   A    C
GAM382  F3       3'  TCCTGACCTCAGTTGATC    67682       C
                                GATCA CTGAGGTCAGGA
                                ||||| ||||||||||||
                                CTAGT GACTCCAGTCCT
                                   T
GAM382  F3       3'  TCCTGACCTCAGTTGATC    67682       C
                                GATCA CTGAGGTCAGGA
                                ||||| ||||||||||||
                                CTAGT GACTCCAGTCCT
                                   T
GAM382  FANCE    3'  TGAACTCCTGAGCTCAAGTGAT 41903       C    G
            C                    GATCAC TGAG TCAGGAGTTTG
                                ||||||| |||| ||||||||||||
                                CTAGTG ACTC AGTCCTCAAGT
                                   A    G
GAM382  FANCE    3'  TGAACTCCTGAGCTCAAGTGAT 41903       C    G
            C                    GATCAC TGAG TCAGGAGTTTG
                                ||||||| |||| ||||||||||||
                                CTAGTG ACTC AGTCCTCAAGT
                                   A    G
GAM382  FCAR     3'  TCGAACTCCCGACCTCAGGTGA 56584            A
            TC                     GATCACCTGAGGTC GGAGTTTGA
                                ||||||||||||||| |||||||||
                                CTAGTGGACTCCAG CCTCAAGCT
                                         C
GAM382  FCAR     3'  TCGAACTCCTGACCTCAGGTGA 56585
            TC                     GATCACCTGAGGTCAGGAGTTTGA
                                ||||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAGCT

GAM382  FCAR     3'  TCGAACTCCTGACCTCAGGTGA 56585
            TC                     GATCACCTGAGGTCAGGAGTTTGA
                                ||||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAGCT

GAM382  FCAR     3'  TCGAACTCCTGACCTCAGGTGA 56598
            TC                     GATCACCTGAGGTCAGGAGTTTGA
                                ||||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAGCT

GAM382  FCAR     3'  TCGAACTCCTGACCTCAGGTGA 56610
            TC                     GATCACCTGAGGTCAGGAGTTTGA
                                ||||||||||||||||||||||||
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                                CTAGTGGACTCCAGTCCTCAAGCT

GAM382  FCAR    3'  TCGAACTCCTGACCTCAGGTGA 56622
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAGCT

GAM382  FCAR    3'  TCGAACTCCCGACCTCAGGTGA 56641           A
                TC                GATCACCTGAGGTC GGAGTTTGA
                                  |||||||||||||| |||||||||
                                  CTAGTGGACTCCAG CCTCAAGCT
                                        C
GAM382  FCAR    3'  TCGAACTCCTGACCTCAGGTGA 10595
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAGCT

GAM382  FMR2    3'  TCAAACTCTTTTGCCAGTGA  10700    CTGA  C_
                                  TCAC   GGT  AGGAGTTTGA
                                  ||||   |||  ||||||||||
                                  AGTG   CCG  TTCTCAAACT
                                    A___   TT
GAM382  FMR2    3'  TCAAACTCTTTTGCCAGTGA  10700    CTGA  C_
                                  TCAC   GGT  AGGAGTTTGA
                                  ||||   |||  ||||||||||
                                  AGTG   CCG  TTCTCAAACT
                                    A___   TT
GAM382  G6PC    3'  TCGAACTCCTGACCTCAAGTGA 5666       C
                TC                GATCAC TGAGGTCAGGAGTTTGA
                                  ||||||| ||||||||||||||||
                                  CTAGTG ACTCCAGTCCTCAAGCT
                                     A
GAM382  G6PC    3'  TCGAACTCCTGACCTCAAGTGA 5666       C
                TC                GATCAC TGAGGTCAGGAGTTTGA
                                  ||||||| ||||||||||||||||
                                  CTAGTG ACTCCAGTCCTCAAGCT
                                     A
GAM382  GLTSCR1  5'  TCAAACTCCTGGGCTCCAGTGA 32303      CT   G
                TC                GATCAC  GAG TCAGGAGTTTGA
                                  ||||||  ||| ||||||||||||
                                  CTAGTG  CTC GGTCCTCAAACT
                                     AC   G
GAM382  GLTSCR1  5'  TCAAACTCCTGGGCTCCAGTGA 32303      CT   G
                TC                GATCAC  GAG TCAGGAGTTTGA
                                  ||||||  ||| ||||||||||||
                                  CTAGTG  CTC GGTCCTCAAACT
                                     AC   G
GAM382  GNE     3'  TGAACTCCTGACCTCAGGTGAT 19681
                C                  GATCACCTGAGGTCAGGAGTTTG
                                   |||||||||||||||||||||||
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                                CTAGTGGACTCCAGTCCTCAAGT

GAM382  GNE      3'  TGAACTCCTGACCTCAGGTGAT 19681
                C                GATCACCTGAGGTCAGGAGTTTG
                                 ||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGT

GAM382  GPR81     3'  TCCTGACCTCAGGTGATC    51758
                                 GATCACCTGAGGTCAGGA
                                 |||||||||||||||||
                                 CTAGTGGACTCCAGTCCT

GAM382  GPR81     3'  TCCTGACCTCAGGTGATC    51758
                                 GATCACCTGAGGTCAGGA
                                 |||||||||||||||||
                                 CTAGTGGACTCCAGTCCT

GAM382  GRAF      3'  TCGAACTCCTGACCTCAAGTGA 31249       C
                TC                 GATCAC TGAGGTCAGGAGTTTGA
                                   |||||| ||||||||||||||||
                                   CTAGTG ACTCCAGTCCTCAAGCT
                                      A
GAM382  GRAF      3'  TCGAACTCCTGACCTCAAGTGA 31249       C
                TC                 GATCAC TGAGGTCAGGAGTTTGA
                                   |||||| ||||||||||||||||
                                   CTAGTG ACTCCAGTCCTCAAGCT
                                      A
GAM382  HUNK      3'  TCAAACTCCTGGGCTCCAACGA 28191      ACCT   G
                TC                 GATC    GAG TCAGGAGTTTGA
                                   ||||    ||| ||||||||||||
                                   CTAG    CTC GGTCCTCAAACT
                                     CAAC   G
GAM382  HUNK      3'  TCAAACTCCTGGGCTCCAACGA 28191      ACCT   G
                TC                 GATC    GAG TCAGGAGTTTGA
                                   ||||    ||| ||||||||||||
                                   CTAG    CTC GGTCCTCAAACT
                                     CAAC   G
GAM382  HYAL4     5'  TCCTGACCTCAAGTGATC    25372       C
                                   GATCAC TGAGGTCAGGA
                                   |||||| ||||||||||
                                   CTAGTG ACTCCAGTCCT
                                      A
GAM382  HYAL4     5'  TCCTGACCTCAAGTGATC    25372       C
                                   GATCAC TGAGGTCAGGA
                                   |||||| ||||||||||
                                   CTAGTG ACTCCAGTCCT
                                      A
GAM382  IFNAR2    3'  TCGAACTCCTGACCTCAAGTGA 7906        C
                TC                 GATCAC TGAGGTCAGGAGTTTGA
                                   |||||| ||||||||||||||||
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                                CTAGTG ACTCCAGTCCTCAAGCT
                                   A
GAM382  IFNAR2   3'  TCGAACTCCTGACCTCAAGTGA 7906        C
             TC                   GATCAC TGAGGTCAGGAGTTTGA
                                  |||||| ||||||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAGCT
                                   A
GAM382  IGF1     3'  TCAAACTCCTGACCTTGTGATT 7082        CT
                                GATCAC  GAGGTCAGGAGTTTGA
                                |||||| ||||||||||||||||
                                TTAGTG  TTCCAGTCCTCAAACT
                                   __
GAM382  IGF1     3'  TCAAACTCCTGACCTTGTGATT 7082        CT
                                GATCAC  GAGGTCAGGAGTTTGA
                                |||||| ||||||||||||||||
                                TTAGTG  TTCCAGTCCTCAAACT
                                   __
GAM382  IL11     3'  TCGAACTCCTGACCTCAGGTGA 7195
             TC                   GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAGCT

GAM382  IL11     3'  TCGAACTCCTGACCTCAGGTGA 7195
             TC                   GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAGCT

GAM382  JAK3     3'  TCGAACTCCTAACCTCAAGTGA 5833        C     C
             TC                   GATCAC TGAGGT AGGAGTTTGA
                                  |||||| |||||| ||||||||||
                                CTAGTG ACTCCA TCCTCAAGCT
                                   A     A
GAM382  JAK3     3'  TCGAACTCCTAACCTCAAGTGA 5833        C     C
             TC                   GATCAC TGAGGT AGGAGTTTGA
                                  |||||| |||||| ||||||||||
                                CTAGTG ACTCCA TCCTCAAGCT
                                   A     A
GAM382  KMO      3'  TCAAACTCCTGGCCTCATGTGA 14848       C
             TC                   GATCAC TGAGGTCAGGAGTTTGA
                                  |||||| ||||||||||||||||
                                CTAGTG ACTCCGGTCCTCAAACT
                                   T
GAM382  KMO      3'  TCAAACTCCTGGCCTCATGTGA 14848       C
             TC                   GATCAC TGAGGTCAGGAGTTTGA
                                  |||||| ||||||||||||||||
                                CTAGTG ACTCCGGTCCTCAAACT
                                   T
GAM382  MAK      3'  TCAAACTCCTGACCTCAGGTGA 20953
             TC                   GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
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                                CTAGTGGACTCCAGTCCTCAAACT

GAM382  MAK      3'  TCAAACTCCTGACCTCAGGTGA 20953
                TC                  GATCACCTGAGGTCAGGAGTTTGA
                                    ||||||||||||||||||||||||
                                    CTAGTGGACTCCAGTCCTCAAACT

GAM382  MEFV     3'  TCAAACTCCTGACCTCAGGTGA 5950
                T                   ATCACCTGAGGTCAGGAGTTTGA
                                    ||||||||||||||||||||||||
                                    TAGTGGACTCCAGTCCTCAAACT

GAM382  MEFV     3'  TCAAACTCCTGACCTCAGGTGA 5950
                T                   ATCACCTGAGGTCAGGAGTTTGA
                                    ||||||||||||||||||||||||
                                    TAGTGGACTCCAGTCCTCAAACT

GAM382  MEFV     3'  TCGAACTCCTGACCTCAGGTGA 5951
                TC                  GATCACCTGAGGTCAGGAGTTTGA
                                    ||||||||||||||||||||||||
                                    CTAGTGGACTCCAGTCCTCAAGCT

GAM382  MEFV     3'  TCGAACTCCTGACCTCAGGTGA 5951
                TC                  GATCACCTGAGGTCAGGAGTTTGA
                                    ||||||||||||||||||||||||
                                    CTAGTGGACTCCAGTCCTCAAGCT

GAM382  MICB     3'  TCAAACTCCTGACCTCAGGTGA 21025
                TC                  GATCACCTGAGGTCAGGAGTTTGA
                                    ||||||||||||||||||||||||
                                    CTAGTGGACTCCAGTCCTCAAACT

GAM382  MICB     3'  TCAAACTCCTGACCTCAGGTGA 21025
                TC                  GATCACCTGAGGTCAGGAGTTTGA
                                    ||||||||||||||||||||||||
                                    CTAGTGGACTCCAGTCCTCAAACT

GAM382  MLANA    3'  TCAAACTCCTGACCTCAGGTGA 19772
                TC                  GATCACCTGAGGTCAGGAGTTTGA
                                    ||||||||||||||||||||||||
                                    CTAGTGGACTCCAGTCCTCAAACT

GAM382  MLANA    3'  TCAAACTCCTGACCTCAGGTGA 19772
                TC                  GATCACCTGAGGTCAGGAGTTTGA
                                    ||||||||||||||||||||||||
                                    CTAGTGGACTCCAGTCCTCAAACT

GAM382  MPL      3'  TGAACTCCTAACCTCGGGTGAT 19362          C
                C                   GATCACCTGAGGT AGGAGTTTG
                                    |||||||||||| |||||||||
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                                CTAGTGGGCTCCA TCCTCAAGT
                                      A
GAM382  MPL      3'  TGAACTCCTAACCTCGGGTGAT 19362           C
            C                  GATCACCTGAGGT AGGAGTTTG
                               |||||||||||| |||||||||
                               CTAGTGGGCTCCA TCCTCAAGT
                                      A
GAM382  MRPL49   3'  TCAAACTCCTGACTCGAAGTGA 70173       CTGA
            TC                   GATCAC   GGTCAGGAGTTTGA
                               ||||||   ||||||||||||||
                               CTAGTG   TCAGTCCTCAAACT
                                  AAGC
GAM382  MRPL49   3'  TCAAACTCCTGACTCGAAGTGA 70173       CTGA
            TC                   GATCAC   GGTCAGGAGTTTGA
                               ||||||   ||||||||||||||
                               CTAGTG   TCAGTCCTCAAACT
                                  AAGC
GAM382  MYCL2    3'  TCCTGACCTAGGTGATC     19381         G
                               GATCACCT AGGTCAGGA
                               |||||||| |||||||||
                               CTAGTGGA TCCAGTCCT
                                      _
GAM382  NCOA6    5'  TCAAACTCCTGACCTCAAGTGA 26847       C
            TC                   GATCAC TGAGGTCAGGAGTTTGA
                               |||||| ||||||||||||||||
                               CTAGTG ACTCCAGTCCTCAAACT
                                  A
GAM382  NCOA6    5'  TCAAACTCCTGACCTCAAGTGA 26847       C
            TC                   GATCAC TGAGGTCAGGAGTTTGA
                               |||||| ||||||||||||||||
                               CTAGTG ACTCCAGTCCTCAAACT
                                  A
GAM382  NDRG3    3'  TCAAACTCCTGACCTCAGGTGA 50126
            TC                   GATCACCTGAGGTCAGGAGTTTGA
                               ||||||||||||||||||||||||
                               CTAGTGGACTCCAGTCCTCAAACT

GAM382  NDRG3    3'  TCAAACTCCTGACCTCAGGTGA 42771
            TC                   GATCACCTGAGGTCAGGAGTTTGA
                               ||||||||||||||||||||||||
                               CTAGTGGACTCCAGTCCTCAAACT

GAM382  NQO1     3'  TCAAACTCCTGACCTCAGGTGA 8056
            TC                   GATCACCTGAGGTCAGGAGTTTGA
                               ||||||||||||||||||||||||
                               CTAGTGGACTCCAGTCCTCAAACT

GAM382  NQO1     3'  TCAAACTCCTGACCTCAGGTGA 8056
            TC                   GATCACCTGAGGTCAGGAGTTTGA
                               ||||||||||||||||||||||||
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                                CTAGTGGACTCCAGTCCTCAAACT

GAM382  NT5C2    5' TCCTGACGTCAAGTGATC    25270       C   G
                                GATCAC TGA GTCAGGA
                                |||||| ||| |||||||
                                CTAGTG ACT CAGTCCT
                                   A   G
GAM382  NT5C2    5' TCCTGACGTCAAGTGATC    25270       C   G
                                GATCAC TGA GTCAGGA
                                |||||| ||| |||||||
                                CTAGTG ACT CAGTCCT
                                   A   G
GAM382  PDE6B    3' TCGAACTCCTGACCTCAGGTGA 6079
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                |||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAGCT

GAM382  PDE6B    3' TCGAACTCCTGACCTCAGGTGA 6079
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                |||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAGCT

GAM382  PER2     3' TCGAACTCCTGACCTCAAGCGA 43361      ACC
                TC                GATC   TGAGGTCAGGAGTTTGA
                                ||||   ||||||||||||||||
                                CTAG   ACTCCAGTCCTCAAGCT
                                  CGA
GAM382  PER2     3' TCGAACTCCTGACCTCAAGCGA 43361      ACC
                TC                GATC   TGAGGTCAGGAGTTTGA
                                ||||   ||||||||||||||||
                                CTAG   ACTCCAGTCCTCAAGCT
                                  CGA
GAM382  PIGR     3' TCCTGGCCTCAAGTGATC    73013       C
                                GATCAC TGAGGTCAGGA
                                |||||| ||||||||||
                                CTAGTG ACTCCGGTCCT
                                   A
GAM382  PIGR     3' TCCTGGCCTCAAGTGATC    73013       C
                                GATCAC TGAGGTCAGGA
                                |||||| ||||||||||
                                CTAGTG ACTCCGGTCCT
                                   A
GAM382  PIK3CD   3' TCGAACTCCTGACCTCAGGTGA 18502
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                |||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAGCT

GAM382  PIK3CD   3' TCGAACTCCTGACCTCAGGTGA 18502
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                |||||||||||||||||||||||
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                                CTAGTGGACTCCAGTCCTCAAGCT

GAM382  PPEF2    3'  TGAACTCCCAACCTCAGGTGAT 21780           CA
              C                  GATCACCTGAGGT  GGAGTTTG
                                 ||||||||||||  ||||||||
                                 CTAGTGGACTCCA  CCTCAAGT
                                       AC
GAM382  PPEF2    3'  TGAACTCCCAACCTCAGGTGAT 21780           CA
              C                  GATCACCTGAGGT  GGAGTTTG
                                 ||||||||||||  ||||||||
                                 CTAGTGGACTCCA  CCTCAAGT
                                       AC
GAM382  PRKR     3'  TCAAACTCCTGACCTCAAGTAA 12353     C  C
              TC                   GAT AC TGAGGTCAGGAGTTTGA
                                 ||| || ||||||||||||||||
                                 CTA TG ACTCCAGTCCTCAAACT
                                   A  A
GAM382  PRKR     3'  TCAAACTCCTGACCTCAAGTAA 12353     C  C
              TC                   GAT AC TGAGGTCAGGAGTTTGA
                                 ||| || ||||||||||||||||
                                 CTA TG ACTCCAGTCCTCAAACT
                                   A  A
GAM382  PRKWNK3  3'  TCAAACTCCTAACCTTGTGATC 62239       CT    C
                                 GATCAC  GAGGT AGGAGTTTGA
                                 ||||||  ||||| ||||||||||
                                 CTAGTG  TTCCA TCCTCAAACT
                                    __     A
GAM382  PRKWNK3  3'  TCAAACTCCTAACCTTGTGATC 62239       CT    C
                                 GATCAC  GAGGT AGGAGTTTGA
                                 ||||||  ||||| ||||||||||
                                 CTAGTG  TTCCA TCCTCAAACT
                                    __     A
GAM382  PTGES    3'  TCCTGGCCTCAAGTGATC    18073       C
                                 GATCAC TGAGGTCAGGA
                                 |||||| ||||||||||
                                 CTAGTG ACTCCGGTCCT
                                    A
GAM382  PTGES    3'  TCCTGGCCTCAAGTGATC    18073       C
                                 GATCAC TGAGGTCAGGA
                                 |||||| ||||||||||
                                 CTAGTG ACTCCGGTCCT
                                    A
GAM382  RAB36    3'  TCAGACTCCTGATCTCAGGTGA 18183
                                 TCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||
                                 AGTGGACTCTAGTCCTCAGACT

GAM382  RAB36    3'  TCAGACTCCTGATCTCAGGTGA 18183
                                 TCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||
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                                AGTGGACTCTAGTCCTCAGACT

GAM382  RBBP9   3'  TCCTGGCCTCAAGTGATC    70700       C
                                GATCAC TGAGGTCAGGA
                                |||||| ||||||||||
                                CTAGTG ACTCCGGTCCT
                                   A
GAM382  RBBP9   3'  TCCTGGCCTCAAGTGATC    70700       C
                                GATCAC TGAGGTCAGGA
                                |||||| ||||||||||
                                CTAGTG ACTCCGGTCCT
                                   A
GAM382  RGS9    5'  TCAAACTCCTGGGCTCAAGCGA 15174      ACC   G
            TC                    GATC   TGAG TCAGGAGTTTGA
                                |||| |||| ||||||||||||
                                CTAG   ACTC GGTCCTCAAACT
                                  CGA    G
GAM382  RGS9    5'  TCAAACTCCTGGGCTCAAGCGA 15174      ACC   G
            TC                    GATC   TGAG TCAGGAGTTTGA
                                |||| |||| ||||||||||||
                                CTAG   ACTC GGTCCTCAAACT
                                  CGA    G
GAM382  RHD     3'  TCAAACTCCTGACCTCAAGTGA 32839       C
            TC                    GATCAC TGAGGTCAGGAGTTTGA
                                |||||| ||||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAACT
                                   A
GAM382  RHD     3'  TCAAACTCCTGACCTCAAGTGA 32839       C
            TC                    GATCAC TGAGGTCAGGAGTTTGA
                                |||||| ||||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAACT
                                   A
GAM382  RHD     3'  TCAAACTCCTGACCTCAAGTGA 32840       C
            TC                    GATCAC TGAGGTCAGGAGTTTGA
                                |||||| ||||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAACT
                                   A
GAM382  RHD     3'  TCAAACTCCTGACCTCAAGTGA 33150       C
            TC                    GATCAC TGAGGTCAGGAGTTTGA
                                |||||| ||||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAACT
                                   A
GAM382  RP2     3'  TCGAACTCCTGACCTCAGGTGA 23607
            TC                    GATCACCTGAGGTCAGGAGTTTGA
                                |||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAGCT

GAM382  RP2     3'  TCGAACTCCTGACCTCAGGTGA 23607
            TC                    GATCACCTGAGGTCAGGAGTTTGA
                                |||||||||||||||||||||||
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                                CTAGTGGACTCCAGTCCTCAAGCT

GAM382  SAS     3'  TCGAACTCCTGACCTCAGGTGA 21109
                TC                  GATCACCTGAGGTCAGGAGTTTGA
                                    ||||||||||||||||||||||||
                                    CTAGTGGACTCCAGTCCTCAAGCT

GAM382  SAS     3'  TCGAACTCCTGACCTCAGGTGA 21109
                TC                  GATCACCTGAGGTCAGGAGTTTGA
                                    ||||||||||||||||||||||||
                                    CTAGTGGACTCCAGTCCTCAAGCT

GAM382  SCML2   3'  TCAAACTCCTGACCTCAGGTGA 21431
                TC                  GATCACCTGAGGTCAGGAGTTTGA
                                    ||||||||||||||||||||||||
                                    CTAGTGGACTCCAGTCCTCAAACT

GAM382  SCML2   3'  TCAAACTCCTGACCTCAGGTGA 21431
                TC                  GATCACCTGAGGTCAGGAGTTTGA
                                    ||||||||||||||||||||||||
                                    CTAGTGGACTCCAGTCCTCAAACT

GAM382  SCNN1G  3'  TCCTGGCCTCAAATGATC   8305      CC
                                    GATCA  TGAGGTCAGGA
                                    |||||  ||||||||||
                                    CTAGT  ACTCCGGTCCT
                                       AA
GAM382  SCNN1G  3'  TCCTGGCCTCAAATGATC   8305      CC
                                    GATCA  TGAGGTCAGGA
                                    |||||  ||||||||||
                                    CTAGT  ACTCCGGTCCT
                                       AA
GAM382  SEDL    3'  TCAAACTCCTGACCTCAGTTGA 28110     C
                TC                  GATCA CTGAGGTCAGGAGTTTGA
                                    |||||  ||||||||||||||||||
                                    CTAGT GACTCCAGTCCTCAAACT
                                       T
GAM382  SEDL    3'  TCAAACTCCTGACCTCAGTTGA 28110     C
                TC                  GATCA CTGAGGTCAGGAGTTTGA
                                    |||||  ||||||||||||||||||
                                    CTAGT GACTCCAGTCCTCAAACT
                                       T
GAM382  SEPN1   3'  GAACTTCTGACCTCAGGTGATC 66970
                                    GATCACCTGAGGTCAGGAGTTT
                                    |||||||||||||||||||||||
                                    CTAGTGGACTCCAGTCTTCAAG

GAM382  SEPN1   3'  GAACTTCTGACCTCAGGTGATC 66970
                                    GATCACCTGAGGTCAGGAGTTT
                                    |||||||||||||||||||||||
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                                CTAGTGGACTCCAGTCTTCAAG

GAM382  SH3BP2   3'  TCGAACTCCTGACCTCAGGTGA 13087
            TC                   GATCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGCT

GAM382  SH3BP2   3'  TCGAACTCCTGACCTCAGGTGA 13087
            TC                   GATCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGCT

GAM382  SH3BP2   3'  TGAACTCCTGACCTCAACTGAT 13088      CC
            C                    GATCA  TGAGGTCAGGAGTTTG
                                 |||||  ||||||||||||||||
                                 CTAGT  ACTCCAGTCCTCAAGT
                                    CA
GAM382  SH3BP2   3'  TGAACTCCTGACCTCAACTGAT 13088      CC
            C                    GATCA  TGAGGTCAGGAGTTTG
                                 |||||  ||||||||||||||||
                                 CTAGT  ACTCCAGTCCTCAAGT
                                    CA
GAM382  SHOX     3'  GAACTCCTGACCTCAGGTGATC 23518
                                 GATCACCTGAGGTCAGGAGTTT
                                 |||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAG

GAM382  SHOX     3'  TCGAACTCCTGACCTCAGGTGA 23523
            TC                   GATCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGCT

GAM382  SHOX     3'  GAACTCCTGACCTCAGGTGATC 6572
                                 GATCACCTGAGGTCAGGAGTTT
                                 |||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAG

GAM382  SHOX     3'  TCGAACTCCTGACCTCAGGTGA 6587
            TC                   GATCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGCT

GAM382  SIL      3'  TCAAACTCCCGACCTCAGGTGA 13162            A
            TC                   GATCACCTGAGGTC GGAGTTTGA
                                 |||||||||||||| |||||||||
                                 CTAGTGGACTCCAG CCTCAAACT
                                          C
GAM382  SIL      3'  TCAAACTCCCGACCTCAGGTGA 13162            A
            TC                   GATCACCTGAGGTC GGAGTTTGA
                                 |||||||||||||| |||||||||
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                                CTAGTGGACTCCAG CCTCAAACT
                                      C
GAM382  SIL     5'  TCCTGACTTCAGGTGATC    13163
                                GATCACCTGAGGTCAGGA
                                ||||||||||||||||||
                                CTAGTGGACTTCAGTCCT

GAM382  SIL     5'  TCCTGACTTCAGGTGATC    13163
                                GATCACCTGAGGTCAGGA
                                ||||||||||||||||||
                                CTAGTGGACTTCAGTCCT

GAM382  SLA2    3'  TCGAACTCCTGACCTCAGGTGA 50895
            TC                    GATCACCTGAGGTCAGGAGTTTGA
                                ||||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAGCT

GAM382  SLA2    3'  TCGAACTCCTGACCTCAGGTGA 50895
            TC                    GATCACCTGAGGTCAGGAGTTTGA
                                ||||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAGCT

GAM382  SLC3A2  5'  TCAACTCTTGGCCTCAAGTGAT 11526       C           T
            C                    GATCAC TGAGGTCAGGAGTT GA
                                ||||||| |||||||||||||| ||
                                CTAGTG ACTCCGGTTCTCAA CT
                                   A          _
GAM382  SLC3A2  5'  TCAACTCTTGGCCTCAAGTGAT 11526       C           T
            C                    GATCAC TGAGGTCAGGAGTT GA
                                ||||||| |||||||||||||| ||
                                CTAGTG ACTCCGGTTCTCAA CT
                                   A          _
GAM382  SMAC    5'  TCCTGACCTCAAGTGATC    58008       C
                                GATCAC TGAGGTCAGGA
                                ||||||| ||||||||||
                                CTAGTG ACTCCAGTCCT
                                   A
GAM382  SMAC    5'  TCCTGACCTCAAGTGATC    58029       C
                                GATCAC TGAGGTCAGGA
                                ||||||| ||||||||||
                                CTAGTG ACTCCAGTCCT
                                   A
GAM382  SNX15   3'  TCGAACTCCTGACCTCAAGTGA 74132       C
            TC                    GATCAC TGAGGTCAGGAGTTTGA
                                ||||||| ||||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAGCT
                                   A
GAM382  SNX15   3'  TCGAACTCCTGACCTCAAGTGA 74132       C
            TC                    GATCAC TGAGGTCAGGAGTTTGA
                                ||||||| ||||||||||||||||
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                                CTAGTG ACTCCAGTCCTCAAGCT
                                   A
GAM382  SPN     3'  TCAAACTCCTGACCTCAGGTGA 13381
                TC                  GATCACCTGAGGTCAGGAGTTTGA
                                    ||||||||||||||||||||||||
                                    CTAGTGGACTCCAGTCCTCAAACT

GAM382  SPN     3'  TCAAACTCCTGACCTCAGGTGA 13381
                TC                  GATCACCTGAGGTCAGGAGTTTGA
                                    ||||||||||||||||||||||||
                                    CTAGTGGACTCCAGTCCTCAAACT

GAM382  SULT2B1  5'  TCAAACTCCTGACCTCAGGTGA 17229
                TC                  GATCACCTGAGGTCAGGAGTTTGA
                                    ||||||||||||||||||||||||
                                    CTAGTGGACTCCAGTCCTCAAACT

GAM382  SULT2B1  5'  TCAAACTCCTGACCTCAGGTGA 17229
                TC                  GATCACCTGAGGTCAGGAGTTTGA
                                    ||||||||||||||||||||||||
                                    CTAGTGGACTCCAGTCCTCAAACT

GAM382  TAPBP   3'  TCCTGACCTCAGGTGATC   13589
                                    GATCACCTGAGGTCAGGA
                                    ||||||||||||||||||
                                    CTAGTGGACTCCAGTCCT

GAM382  TAPBP   3'  TCCTGACCTCAGGTGATC   13589
                                    GATCACCTGAGGTCAGGA
                                    ||||||||||||||||||
                                    CTAGTGGACTCCAGTCCT

GAM382  TAT     3'  TCAAACTCCTGACCTCAGGCAA 6260     CA
                TC                  GAT  CCTGAGGTCAGGAGTTTGA
                                    |||  ||||||||||||||||||||
                                    CTA  GGACTCCAGTCCTCAAACT
                                      AC
GAM382  TAT     3'  TCAAACTCCTGACCTCAGGCAA 6260     CA
                TC                  GAT  CCTGAGGTCAGGAGTTTGA
                                    |||  ||||||||||||||||||||
                                    CTA  GGACTCCAGTCCTCAAACT
                                      AC
GAM382  TBXA2R  3'  TCCTGACCTCAGGTGATT   8368
                                    GATCACCTGAGGTCAGGA
                                    ||||||||||||||||||
                                    TTAGTGGACTCCAGTCCT

GAM382  TBXA2R  3'  TCCTGACCTCAGGTGATT   8368
                                    GATCACCTGAGGTCAGGA
                                    ||||||||||||||||||
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                                TTAGTGGACTCCAGTCCT

GAM382  TES      3'  TCAAACTCCTGACCTCAGATGA 72467       C
            TC                    GATCA CTGAGGTCAGGAGTTTGA
                                  ||||| ||||||||||||||||||
                                  CTAGT GACTCCAGTCCTCAAACT
                                    A
GAM382  TES      3'  TCAAACTCCTGACCTCAGATGA 72467       C
            TC                    GATCA CTGAGGTCAGGAGTTTGA
                                  ||||| ||||||||||||||||||
                                  CTAGT GACTCCAGTCCTCAAACT
                                    A
GAM382  TIM3     3'  TCAAACTCCTGACCTCATGATT 52363       CC
                                  GATCA  TGAGGTCAGGAGTTTGA
                                  |||||  ||||||||||||||||
                                  TTAGT  ACTCCAGTCCTCAAACT
                                    __
GAM382  TIM3     3'  TCAAACTCCTGACCTCATGATT 52363       CC
                                  GATCA  TGAGGTCAGGAGTTTGA
                                  |||||  ||||||||||||||||
                                  TTAGT  ACTCCAGTCCTCAAACT
                                    __
GAM382  TMPRSS3  3'  TCAAACCCCTGACCTCAAATGA 51523      CC        A
            T                     ATCA  TGAGGTCAGG GTTTGA
                                  ||||  |||||||||| ||||||
                                  TAGT  ACTCCAGTCC CAAACT
                                    AA        C
GAM382  TMPRSS3  3'  TCAAACCCCTGACCTCAAATGA 51550      CC        A
            T                     ATCA  TGAGGTCAGG GTTTGA
                                  ||||  |||||||||| ||||||
                                  TAGT  ACTCCAGTCC CAAACT
                                    AA        C
GAM382  TMPRSS3  3'  TCAAACCCCTGACCTCAAATGA 44034      CC        A
            T                     ATCA  TGAGGTCAGG GTTTGA
                                  ||||  |||||||||| ||||||
                                  TAGT  ACTCCAGTCC CAAACT
                                    AA        C
GAM382  TMPRSS3  3'  TCAAACCCCTGACCTCAAATGA 44034      CC        A
            T                     ATCA  TGAGGTCAGG GTTTGA
                                  ||||  |||||||||| ||||||
                                  TAGT  ACTCCAGTCC CAAACT
                                    AA        C
GAM382  TNFRSF10B 3'  TCCTGACCTCAGGTGATC    15233
                                  GATCACCTGAGGTCAGGA
                                  ||||||||||||||||||
                                  CTAGTGGACTCCAGTCCT

GAM382  TNFRSF10B 3'  TCCTGACCTCAGGTGATC    15233
                                  GATCACCTGAGGTCAGGA
                                  ||||||||||||||||||
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                                CTAGTGGACTCCAGTCCT

GAM382  TNFRSF10B 3'  TCGAACTCCTGACCTCAGGTGA 15234
           TC                    GATCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGCT

GAM382  TNFRSF10B 3'  TCGAACTCCTGACCTCAGGTGA 15234
           TC                    GATCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGCT

GAM382  TP53    3'  TCAAACTCCTGGGCTCAGGCGA 6806      A     G
           TC                    GATC CCTGAG TCAGGAGTTTGA
                                 |||| |||||| ||||||||||||
                                 CTAG GGACTC GGTCCTCAAACT
                                   C     G
GAM382  TP53    3'  TCAAACTCCTGGGCTCAGGCGA 6806      A     G
           TC                    GATC CCTGAG TCAGGAGTTTGA
                                 |||| |||||| ||||||||||||
                                 CTAG GGACTC GGTCCTCAAACT
                                   C     G
GAM382  TPMT    3'  TCCTGACCTCAGGTGATC    6317
                                 GATCACCTGAGGTCAGGA
                                 ||||||||||||||||||
                                 CTAGTGGACTCCAGTCCT

GAM382  TPMT    3'  TCCTGACCTCAGGTGATC    6317
                                 GATCACCTGAGGTCAGGA
                                 ||||||||||||||||||
                                 CTAGTGGACTCCAGTCCT

GAM382  TRAF5   3'  TCAAACTCCTGACCTCAAGTGA 17284       C
           TC                    GATCAC TGAGGTCAGGAGTTTGA
                                 ||||||| ||||||||||||||||
                                 CTAGTG ACTCCAGTCCTCAAACT
                                    A
GAM382  TRAF5   3'  TCAAACTCCTGACCTCAAGTGA 17284       C
           TC                    GATCAC TGAGGTCAGGAGTTTGA
                                 ||||||| ||||||||||||||||
                                 CTAGTG ACTCCAGTCCTCAAACT
                                    A
GAM382  TRPM6   3'  TCAAACTCCTGACCTCAGATGA 35037      C
           TC                    GATCA CTGAGGTCAGGAGTTTGA
                                 ||||| |||||||||||||||||
                                 CTAGT GACTCCAGTCCTCAAACT
                                    A
GAM382  TRPM6   3'  TCAAACTCCTGACCTCAGATGA 35037      C
           TC                    GATCA CTGAGGTCAGGAGTTTGA
                                 ||||| |||||||||||||||||
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                                CTAGT GACTCCAGTCCTCAAACT
                                  A
GAM382  TRPV1    3'  TCGAACTCCTGACCTCAGGTGA 38706
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAGCT

GAM382  TRPV1    3'  TCGAACTCTTGACCTCAGGTGA 38707
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTTCTCAAGCT

GAM382  TRPV1    3'  TCGAACTCCTGACCTCAGGTGA 55690
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAGCT

GAM382  TRPV1    3'  TCGAACTCCTGACCTCAGGTGA 55690
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAGCT

GAM382  TRPV1    3'  TCGAACTCTTGACCTCAGGTGA 55691
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTTCTCAAGCT

GAM382  TRPV1    3'  TCGAACTCTTGACCTCAGGTGA 55692
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTTCTCAAGCT

GAM382  TRPV1    3'  TCGAACTCTTGACCTCAGGTGA 55692
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTTCTCAAGCT

GAM382  TRPV1    3'  TCGAACTCCTGACCTCAGGTGA 55722
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAGCT

GAM382  TRPV1    3'  TCGAACTCTTGACCTCAGGTGA 55723
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTTCTCAAGCT

GAM382  TRPV1    3'  TCGAACTCCTGACCTCAGGTGA 55753
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
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                              CTAGTGGACTCCAGTCCTCAAGCT

GAM382  TRPV1    3'  TCGAACTCTTGACCTCAGGTGA 55754
              TC                  GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTTCTCAAGCT

GAM382  TUFT1    3'  TCCTGACCTCAGGTGATC    39678
                              GATCACCTGAGGTCAGGA
                              ||||||||||||||||||
                              CTAGTGGACTCCAGTCCT

GAM382  TUFT1    3'  TCCTGACCTCAGGTGATC    39678
                              GATCACCTGAGGTCAGGA
                              ||||||||||||||||||
                              CTAGTGGACTCCAGTCCT

GAM382  VENTX2   3'  TCAAACTCCTGACCCTGTGATC 27867       CTGA
                              GATCAC   GGTCAGGAGTTTGA
                              ||||||   ||||||||||||||
                              CTAGTG   CCAGTCCTCAAACT
                                  TC__
GAM382  VENTX2   3'  TCAAACTCCTGACCCTGTGATC 27867       CTGA
                              GATCAC   GGTCAGGAGTTTGA
                              ||||||   ||||||||||||||
                              CTAGTG   CCAGTCCTCAAACT
                                  TC__
GAM382  VHL      3'  TCAAACTCCTGACCTCAGGTGA 6874
              TC                  GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAACT

GAM382  VHL      3'  TCAAACTCCTGACCTCAGGTGA 6874
              TC                  GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAACT

GAM382  XRCC2    3'  TCGAACTCCTGACCTCAAGTGA 19512       C
              TC                  GATCAC TGAGGTCAGGAGTTTGA
                                  ||||||| ||||||||||||||||
                                  CTAGTG ACTCCAGTCCTCAAGCT
                                     A
GAM382  XRCC2    3'  TCGAACTCCTGACCTCAAGTGA 19512       C
              TC                  GATCAC TGAGGTCAGGAGTTTGA
                                  ||||||| ||||||||||||||||
                                  CTAGTG ACTCCAGTCCTCAAGCT
                                     A
GAM382  ZNF157   3'  TCTAACTCCTGACCTCAGGTGA 14338                T
              TC                  GATCACCTGAGGTCAGGAGTT GA
                                  |||||||||||||||||||| ||
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                                CTAGTGGACTCCAGTCCTCAA CT
                                                    T
GAM382  ZNF157   3'  TCTAACTCCTGACCTCAGGTGA 14338                  T
           TC                    GATCACCTGAGGTCAGGAGTT GA
                                 |||||||||||||||||||| ||
                                 CTAGTGGACTCCAGTCCTCAA CT
                                                    T
GAM382  ZNF264   3'  TCAAACTCCTGACCTTGTGATC 14231       CT
                                 GATCAC  GAGGTCAGGAGTTTGA
                                 ||||||  ||||||||||||||||
                                 CTAGTG  TTCCAGTCCTCAAACT
                                   __
GAM382  ZNF264   3'  TCAAACTCCTGACCTTGTGATC 14231       CT
                                 GATCAC  GAGGTCAGGAGTTTGA
                                 ||||||  ||||||||||||||||
                                 CTAGTG  TTCCAGTCCTCAAACT
                                   __
GAM382  AAK1     3'  TCGAACTCCTGACCTCAGGTGA 30526
           TC                    GATCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGCT

GAM382  AAK1     3'  TCGAACTCCTGACCTCAGGTGA 30526
           TC                    GATCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGCT

GAM382  ARHGAP5  5'  TCGAACTCCCAACCTCAGGTGA 77606           CA
           TC                    GATCACCTGAGGT  GGAGTTTGA
                                 ||||||||||||  |||||||||
                                 CTAGTGGACTCCA  CCTCAAGCT
                                       AC
GAM382  ARHGAP5  5'  TCGAACTCCCAACCTCAGGTGA 77606           CA
           TC                    GATCACCTGAGGT  GGAGTTTGA
                                 ||||||||||||  |||||||||
                                 CTAGTGGACTCCA  CCTCAAGCT
                                       AC
GAM382  ASB16    3'  ACACTGACCTCAGGTGATC   55966             GA
                                 GATCACCTGAGGTCAG  GT
                                 ||||||||||||||||  ||
                                 CTAGTGGACTCCAGTC  CA
                                       A_
GAM382  ASB16    3'  ACACTGACCTCAGGTGATC   55966             GA
                                 GATCACCTGAGGTCAG  GT
                                 ||||||||||||||||  ||
                                 CTAGTGGACTCCAGTC  CA
                                       A_
GAM382  ATP1B4   3'  TCGAACTCCTGACCTCAAGTGA 24853       C
           TC                    GATCAC TGAGGTCAGGAGTTTGA
                                 ||||||  ||||||||||||||||
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                                CTAGTG ACTCCAGTCCTCAAGCT
                                   A
GAM382  ATP1B4   3'  TCGAACTCCTGACCTCAAGTGA 24853       C
           TC                    GATCAC TGAGGTCAGGAGTTTGA
                                 |||||| ||||||||||||||||
                                 CTAGTG ACTCCAGTCCTCAAGCT
                                   A
GAM382  BA108L7.2 3'  TCGAACTCCTGACCTCAGGTGA 49080
           TC                    GATCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGCT

GAM382  BA108L7.2 3'  TCGAACTCCTGACCTCAGGTGA 49080
           TC                    GATCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGCT

GAM382  BM045    5'  CTCCAACCTCAGGTGAT     78582          CA
                                 ATCACCTGAGGT  GGAG
                                 ||||||||||||  ||||
                                 TAGTGGACTCCA  CCTC
                                       A_
GAM382  C13orf1   3'  TCAAACTCCTGACCTCATGATC 40371      CC
                                 GATCA  TGAGGTCAGGAGTTTGA
                                 |||||  ||||||||||||||||
                                 CTAGT  ACTCCAGTCCTCAAACT
                                   __
GAM382  C13orf1   3'  TCAAACTCCTGACCTCATGATC 40371      CC
                                 GATCA  TGAGGTCAGGAGTTTGA
                                 |||||  ||||||||||||||||
                                 CTAGT  ACTCCAGTCCTCAAACT
                                   __
GAM382  C20orf142 3'  TCAAACTCCTGACCGCAGGTGA 75288         A
           TC                    GATCACCTG GGTCAGGAGTTTGA
                                 |||||||| ||||||||||||||
                                 CTAGTGGAC CCAGTCCTCAAACT
                                      G
GAM382  C20orf142 3'  TCAAACTCCTGACCGCAGGTGA 75288         A
           TC                    GATCACCTG GGTCAGGAGTTTGA
                                 |||||||| ||||||||||||||
                                 CTAGTGGAC CCAGTCCTCAAACT
                                      G
GAM382  C21orf25  3'  TCGAACTCCTGACCTCAGGTGA 64304
           TC                    GATCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGCT

GAM382  C21orf25  3'  TCGAACTCCTGACCTCAGGTGA 64304
           TC                    GATCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||||
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                                CTAGTGGACTCCAGTCCTCAAGCT

GAM382  C3F     3'  TCGAACTCCTGACCGCAAGTGA 20483       C  A
            TC                    GATCAC TG GGTCAGGAGTTTGA
                                  |||||| || ||||||||||||||
                                  CTAGTG AC CCAGTCCTCAAGCT
                                     A  G
GAM382  C3F     3'  TCGAACTCCTGACCGCAAGTGA 20483       C  A
            TC                    GATCAC TG GGTCAGGAGTTTGA
                                  |||||| || ||||||||||||||
                                  CTAGTG AC CCAGTCCTCAAGCT
                                     A  G
GAM382  C6orf33  3'  TGAACTCCTGAACTCAAGTGAT 56722       C   G
            C                     GATCAC TGAG TCAGGAGTTTG
                                  |||||| |||| ||||||||||
                                  CTAGTG ACTC AGTCCTCAAGT
                                     A   A
GAM382  C6orf33  3'  TGAACTCCTGAACTCAAGTGAT 56722       C   G
            C                     GATCAC TGAG TCAGGAGTTTG
                                  |||||| |||| ||||||||||
                                  CTAGTG ACTC AGTCCTCAAGT
                                     A   A
GAM382  CARD6    3'  TGAACTCCCGACCTCAGGTGAT 51850            A
            C                     GATCACCTGAGGTC GGAGTTTG
                                  |||||||||||||| ||||||||
                                  CTAGTGGACTCCAG CCTCAAGT
                                        C
GAM382  CARD6    3'  TGAACTCCCGACCTCAGGTGAT 51850            A
            C                     GATCACCTGAGGTC GGAGTTTG
                                  |||||||||||||| ||||||||
                                  CTAGTGGACTCCAG CCTCAAGT
                                        C
GAM382  CDC14B   3'  TCGAACTCCTGACCTCAAGTGA 54012       C
            TC                    GATCAC TGAGGTCAGGAGTTTGA
                                  |||||| ||||||||||||||||
                                  CTAGTG ACTCCAGTCCTCAAGCT
                                     A
GAM382  CDC14B   3'  TCGAACTCCTGACCTCAAGTGA 14779       C
            TC                    GATCAC TGAGGTCAGGAGTTTGA
                                  |||||| ||||||||||||||||
                                  CTAGTG ACTCCAGTCCTCAAGCT
                                     A
GAM382  CHRAC1   3'  TCAAACTCCTAACCTCAACTGA 34339      CC     C
            TC                    GATCA  TGAGGT AGGAGTTTGA
                                  |||||  |||||| ||||||||||
                                  CTAGT  ACTCCA TCCTCAAACT
                                     CA     A
GAM382  CHRAC1   3'  TCAAACTCCTAACCTCAACTGA 34339      CC     C
            TC                    GATCA  TGAGGT AGGAGTTTGA
                                  |||||  |||||| ||||||||||
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                                CTAGT  ACTCCA TCCTCAAACT
                                  CA     A
GAM382  CIP29    3'  TCGAACTCCTGAGCTCAGGTGA 51382          G
                TC                  GATCACCTGAG TCAGGAGTTTGA
                                    |||||||||||| ||||||||||||
                                    CTAGTGGACTC AGTCCTCAAGCT
                                          G
GAM382  CIP29    3'  TCGAACTCCTGAGCTCAGGTGA 51382          G
                TC                  GATCACCTGAG TCAGGAGTTTGA
                                    |||||||||||| ||||||||||||
                                    CTAGTGGACTC AGTCCTCAAGCT
                                          G
GAM382  COLEC12  3'  TCAAACTTCTGGCCTCAAGTGA 48621       C
                TC                  GATCAC TGAGGTCAGGAGTTTGA
                                    |||||| ||||||||||||||||
                                    CTAGTG ACTCCGGTCTTCAAACT
                                       A
GAM382  COLEC12  3'  TCAAACTTCTGGCCTCAAGTGA 48621       C
                TC                  GATCAC TGAGGTCAGGAGTTTGA
                                    |||||| ||||||||||||||||
                                    CTAGTG ACTCCGGTCTTCAAACT
                                       A
GAM382  CPSF2    3'  TCAAACTCCCGACCTCAGGTGA 62285           A
                TC                  GATCACCTGAGGTC GGAGTTTGA
                                    |||||||||||||| |||||||||
                                    CTAGTGGACTCCAG CCTCAAACT
                                          C
GAM382  CPSF2    3'  TCAAACTCCCGACCTCAGGTGA 62285           A
                TC                  GATCACCTGAGGTC GGAGTTTGA
                                    |||||||||||||| |||||||||
                                    CTAGTGGACTCCAG CCTCAAACT
                                          C
GAM382  CPSF2    3'  TCAAACTCCTGACCTCAAGCGA 62286      ACC
                TC                  GATC   TGAGGTCAGGAGTTTGA
                                    ||||   ||||||||||||||||
                                    CTAG   ACTCCAGTCCTCAAACT
                                      CGA
GAM382  CPSF2    3'  TCAAACTCCTGACCTCAAGCGA 62286      ACC
                TC                  GATC   TGAGGTCAGGAGTTTGA
                                    ||||   ||||||||||||||||
                                    CTAG   ACTCCAGTCCTCAAACT
                                      CGA
GAM382  CSL4     3'  TCAAACTCCTGGCCTCAAGTGG 32647       C
                TC                  GATCAC TGAGGTCAGGAGTTTGA
                                    |||||| ||||||||||||||||
                                    CTGGTG ACTCCGGTCCTCAAACT
                                       A
GAM382  CSL4     3'  TCAAACTCCTGGCCTCAAGTGG 32647       C
                TC                  GATCAC TGAGGTCAGGAGTTTGA
                                    |||||| ||||||||||||||||
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                                CTGGTG ACTCCGGTCCTCAAACT
                                   A
GAM382  DBR1     3'  AACTCCTGACCTCAGGCGATC  33053      A
                                GATC CCTGAGGTCAGGAGTT
                                |||| ||||||||||||||||
                                CTAG GGACTCCAGTCCTCAA
                                  C
GAM382  DBR1     3'  AACTCCTGACCTCAGGCGATC  33053      A
                                GATC CCTGAGGTCAGGAGTT
                                |||| ||||||||||||||||
                                CTAG GGACTCCAGTCCTCAA
                                  C
GAM382  DCOHM    3'  TCAAACTCCTGGCCTCAAGTGA 50536       C
           TC                     GATCAC TGAGGTCAGGAGTTTGA
                                |||||| ||||||||||||||||||
                                CTAGTG ACTCCGGTCCTCAAACT
                                   A
GAM382  DCOHM    3'  TCAAACTCCTGGCCTCAAGTGA 50536       C
           TC                     GATCAC TGAGGTCAGGAGTTTGA
                                |||||| ||||||||||||||||||
                                CTAGTG ACTCCGGTCCTCAAACT
                                   A
GAM382  DKFZp434A2417 3'  TCAAACTCCCAACCTCAGGTGA 66687            CA
           TC                     GATCACCTGAGGT  GGAGTTTGA
                                |||||||||||||  |||||||||
                                CTAGTGGACTCCA  CCTCAAACT
                                      AC
GAM382  DKFZp434A2417 3'  TCAAACTCCCAACCTCAGGTGA 66687            CA
           TC                     GATCACCTGAGGT  GGAGTTTGA
                                |||||||||||||  |||||||||
                                CTAGTGGACTCCA  CCTCAAACT
                                      AC
GAM382  DKFZP434B044 3'  TCGAACTCCTTACCTCAGGTGA 49723            C
           TC                     GATCACCTGAGGT AGGAGTTTGA
                                |||||||||||||  |||||||||
                                CTAGTGGACTCCA TCCTCAAGCT
                                      T
GAM382  DKFZP434B044 3'  TCGAACTCCTTACCTCAGGTGA 49723            C
           TC                     GATCACCTGAGGT AGGAGTTTGA
                                |||||||||||||  |||||||||
                                CTAGTGGACTCCA TCCTCAAGCT
                                      T
GAM382  DKFZp434C0923 3'  TCAAATTCCTGGCCTCAAGCGA 34653      ACC
           TC                     GATC   TGAGGTCAGGAGTTTGA
                                ||||   ||||||||||||||||||
                                CTAG   ACTCCGGTCCTTAAACT
                                  CGA
GAM382  DKFZp434C0923 3'  TCAAATTCCTGGCCTCAAGCGA 34653      ACC
           TC                     GATC   TGAGGTCAGGAGTTTGA
                                ||||   ||||||||||||||||||
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                                CTAG   ACTCCGGTCCTTAAACT
                                  CGA
GAM382  DKFZP434D146 3'  TCCTGCCCTCAAGTGATC    32142       C    T
                                GATCAC TGAGG CAGGA
                                |||||| ||||| |||||
                                CTAGTG ACTCC GTCCT
                                   A    C
GAM382  DKFZP434D146 3'  TCCTGCCCTCAAGTGATC    32142       C    T
                                GATCAC TGAGG CAGGA
                                |||||| ||||| |||||
                                CTAGTG ACTCC GTCCT
                                   A    C
GAM382  DKFZP434J037 3'  TCAAACTCCCGACCTCAGGTGA 48955             A
          TC                      GATCACCTGAGGTC GGAGTTTGA
                                |||||||||||||| |||||||||
                                CTAGTGGACTCCAG CCTCAAACT
                                      C
GAM382  DKFZP434J037 3'  TCAAACTCCCGACCTCAGGTGA 48955             A
          TC                      GATCACCTGAGGTC GGAGTTTGA
                                |||||||||||||| |||||||||
                                CTAGTGGACTCCAG CCTCAAACT
                                      C
GAM382  DKFZp547H025 3'  TCAAACTCTTGACTTCAAGTGA 39779         C
          TC                      GATCAC TGAGGTCAGGAGTTTGA
                                |||||| ||||||||||||||||
                                CTAGTG ACTTCAGTTCTCAAACT
                                   A
GAM382  DKFZp547H025 3'  TCAAACTCTTGACTTCAAGTGA 39779         C
          TC                      GATCAC TGAGGTCAGGAGTTTGA
                                |||||| ||||||||||||||||
                                CTAGTG ACTTCAGTTCTCAAACT
                                   A
GAM382  DKFZP564G092 5'  TGAACTCCTGACCTCAAGTAAT 32168     C  C
          C                       GAT AC TGAGGTCAGGAGTTTG
                                ||| || ||||||||||||||||
                                CTA TG ACTCCAGTCCTCAAGT
                                   A  A
GAM382  DKFZP564G092 5'  TGAACTCCTGACCTCAAGTAAT 32168     C  C
          C                       GAT AC TGAGGTCAGGAGTTTG
                                ||| || ||||||||||||||||
                                CTA TG ACTCCAGTCCTCAAGT
                                   A  A
GAM382  DKFZP564K0322 3'  TCAAACTTCTGGCCTCAAGTGA 50191         C
          TC                      GATCAC TGAGGTCAGGAGTTTGA
                                |||||| ||||||||||||||||
                                CTAGTG ACTCCGGTCTTCAAACT
                                   A
GAM382  DKFZP564K0322 3'  TCAAACTTCTGGCCTCAAGTGA 50191         C
          TC                      GATCAC TGAGGTCAGGAGTTTGA
                                |||||| ||||||||||||||||
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                                CTAGTG ACTCCGGTCTTCAAACT
                                   A
GAM382  DKFZP564O0423 3'  TCAAACTCCTGGCCTCAGGCGA 93359      A
           TC                   GATC CCTGAGGTCAGGAGTTTGA
                                |||| ||||||||||||||||||||
                                CTAG GGACTCCGGTCCTCAAACT
                                   C
GAM382  DKFZP564O0423 3'  TCAAACTCCTGGCCTCAGGCGA 93359      A
           TC                   GATC CCTGAGGTCAGGAGTTTGA
                                |||| ||||||||||||||||||||
                                CTAG GGACTCCGGTCCTCAAACT
                                   C
GAM382  DKFZP566I1024 3'  TCCTGGCCTCAAGCGATC    70653      ACC
                                GATC   TGAGGTCAGGA
                                ||||   ||||||||||
                                CTAG   ACTCCGGTCCT
                                   CGA
GAM382  DKFZP566I1024 3'  TCCTGGCCTCAAGCGATC    70653      ACC
                                GATC   TGAGGTCAGGA
                                ||||   ||||||||||
                                CTAG   ACTCCGGTCCT
                                   CGA
GAM382  DSCR6    3'  TGAACTCCTGACCTCAGGTGAT 39077
           C                     GATCACCTGAGGTCAGGAGTTTG
                                 ||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGT

GAM382  DSCR6    3'  TGAACTCCTGACCTCAGGTGAT 39077
           C                     GATCACCTGAGGTCAGGAGTTTG
                                 ||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGT

GAM382  EVI5     3'  TCAAACTTCTGACCTCAGGTGA 20216
           TC                    GATCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCTTCAAACT

GAM382  EVI5     3'  TCAAACTTCTGACCTCAGGTGA 20216
           TC                    GATCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCTTCAAACT

GAM382  EVI5     3'  TCGAACTCCTAACCTCAAGTGA 20219       C     C
           TC                    GATCAC TGAGGT AGGAGTTTGA
                                 |||||| |||||| ||||||||||
                                 CTAGTG ACTCCA TCCTCAAGCT
                                    A     A
GAM382  EVI5     3'  TCGAACTCCTAACCTCAAGTGA 20219       C     C
           TC                    GATCAC TGAGGT AGGAGTTTGA
                                 |||||| |||||| ||||||||||
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                                CTAGTG ACTCCA TCCTCAAGCT
                                   A     A
GAM382  FBP17    3'  TCAAACTCCTGACCTCAGGTGA 73160
                TC                  GATCACCTGAGGTCAGGAGTTTGA
                                    ||||||||||||||||||||||
                                    CTAGTGGACTCCAGTCCTCAAACT

GAM382  FBP17    3'  TCAAACTCCTGACCTCAGGTGA 73160
                TC                  GATCACCTGAGGTCAGGAGTTTGA
                                    ||||||||||||||||||||||
                                    CTAGTGGACTCCAGTCCTCAAACT

GAM382  FER1L4   3'  TGAACCCCTGACCTCAAGTGAT 48139       C        A
                C                   GATCAC TGAGGTCAGG GTTTG
                                    ||||||| |||||||||| |||||
                                    CTAGTG ACTCCAGTCC CAAGT
                                       A         C
GAM382  FER1L4   3'  TGAACCCCTGACCTCAAGTGAT 48139       C        A
                C                   GATCAC TGAGGTCAGG GTTTG
                                    ||||||| |||||||||| |||||
                                    CTAGTG ACTCCAGTCC CAAGT
                                       A         C
GAM382  FLB6421  3'  TGAACTCCTGAGCTCAAGTGAT 39647       C    G
                C                   GATCAC TGAG TCAGGAGTTTG
                                    ||||||| |||| ||||||||||
                                    CTAGTG ACTC AGTCCTCAAGT
                                       A    G
GAM382  FLB6421  3'  TGAACTCCTGAGCTCAAGTGAT 39647       C    G
                C                   GATCAC TGAG TCAGGAGTTTG
                                    ||||||| |||| ||||||||||
                                    CTAGTG ACTC AGTCCTCAAGT
                                       A    G
GAM382  FLJ10101 3'  TCAAACTCCGGGGCTCAGGCAG 45605     CA     G  A
                TC                  GAT  CCTGAG TC GGAGTTTGA
                                    |||  |||||| || |||||||||
                                    CTG  GGACTC GG CCTCAAACT
                                      AC     G  G
GAM382  FLJ10101 3'  TCAAACTCCGGGGCTCAGGCAG 45605     CA     G  A
                TC                  GAT  CCTGAG TC GGAGTTTGA
                                    |||  |||||| || |||||||||
                                    CTG  GGACTC GG CCTCAAACT
                                      AC     G  G
GAM382  FLJ10232 3'  CGAACTCCTGACCTCAGGTGAT 36377
                C                   GATCACCTGAGGTCAGGAGTTTG
                                    |||||||||||||||||||||||
                                    CTAGTGGACTCCAGTCCTCAAGC

GAM382  FLJ10232 3'  CGAACTCCTGACCTCAGGTGAT 36377
                C                   GATCACCTGAGGTCAGGAGTTTG
                                    |||||||||||||||||||||||
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                                CTAGTGGACTCCAGTCCTCAAGC

GAM382  FLJ10298 3' TCAAACTCCTGACCTAGTGATC 36464       CTG
                                GATCAC  AGGTCAGGAGTTTGA
                                ||||||  ||||||||||||||
                                CTAGTG  TCCAGTCCTCAAACT
                                   A__
GAM382  FLJ10298 3' TCAAACTCCTGACCTAGTGATC 36464       CTG
                                GATCAC  AGGTCAGGAGTTTGA
                                ||||||  ||||||||||||||
                                CTAGTG  TCCAGTCCTCAAACT
                                   A__
GAM382  FLJ10535 3' AACTCCTGACCTAAAGTGATC  36732       CTG
                                GATCAC  AGGTCAGGAGTT
                                ||||||  ||||||||||||
                                CTAGTG  TCCAGTCCTCAA
                                   AAA
GAM382  FLJ10535 3' AACTCCTGACCTAAAGTGATC  36732       CTG
                                GATCAC  AGGTCAGGAGTT
                                ||||||  ||||||||||||
                                CTAGTG  TCCAGTCCTCAA
                                   AAA
GAM382  FLJ10607 3' TCAAACTCCTGAGCTCAAGTGA 77644       C   G
           TC                     GATCAC TGAG TCAGGAGTTTGA
                                ||||||  ||||  ||||||||||||
                                CTAGTG ACTC AGTCCTCAAACT
                                   A   G
GAM382  FLJ10607 3' TCAAACTCCTGAGCTCAAGTGA 77644       C   G
           TC                     GATCAC TGAG TCAGGAGTTTGA
                                ||||||  ||||  ||||||||||||
                                CTAGTG ACTC AGTCCTCAAACT
                                   A   G
GAM382  FLJ10713 3' TCAAACTCCTGGACTCAAGTGA 37008       C   GT
           TC                     GATCAC TGAG  CAGGAGTTTGA
                                ||||||  ||||  ||||||||||||
                                CTAGTG ACTC  GTCCTCAAACT
                                   A   AG
GAM382  FLJ10713 3' TCAAACTCCTGGACTCAAGTGA 37008       C   GT
           TC                     GATCAC TGAG  CAGGAGTTTGA
                                ||||||  ||||  ||||||||||||
                                CTAGTG ACTC  GTCCTCAAACT
                                   A   AG
GAM382  FLJ10718 3' TCAAACTCTTAGGCTCAGGCGA 37033     A    G _
           TC                     GATC CCTGAG TC AGGAGTTTGA
                                ||||  ||||||  ||  ||||||||||
                                CTAG GGACTC GG TTCTCAAACT
                                  C    _  A
GAM382  FLJ10718 3' TCAAACTCTTAGGCTCAGGCGA 37033     A    G _
           TC                     GATC CCTGAG TC AGGAGTTTGA
                                ||||  ||||||  ||  ||||||||||
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                                CTAG GGACTC GG TTCTCAAACT
                                  C     _ A
GAM382  FLJ10901 3' TCGAACTCCTGACCTCAAGTGA 37372       C
                TC                GATCAC TGAGGTCAGGAGTTTGA
                                  |||||| ||||||||||||||||||
                                  CTAGTG ACTCCAGTCCTCAAGCT
                                    A
GAM382  FLJ10901 3' TCGAACTCCTGACCTCAAGTGA 37372       C
                TC                GATCAC TGAGGTCAGGAGTTTGA
                                  |||||| ||||||||||||||||||
                                  CTAGTG ACTCCAGTCCTCAAGCT
                                    A
GAM382  FLJ10956 3' GAACTCCTGAGCTCAAGTGATC 37466       C   G
                                  GATCAC TGAG TCAGGAGTTT
                                  |||||| |||| ||||||||||
                                  CTAGTG ACTC AGTCCTCAAG
                                    A   G
GAM382  FLJ10956 3' GAACTCCTGAGCTCAAGTGATC 37466       C   G
                                  GATCAC TGAG TCAGGAGTTT
                                  |||||| |||| ||||||||||
                                  CTAGTG ACTC AGTCCTCAAG
                                    A   G
GAM382  FLJ12363 3' TCAAACTCCTGACCTCAGGTGA 50642
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAACT

GAM382  FLJ12363 3' TCAAACTCCTGACCTCAGGTGA 50642
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAACT

GAM382  FLJ12668 3' TCAAACTCCTGACCTCAGGGGA 47162      A
                TC                GATC CCTGAGGTCAGGAGTTTGA
                                  |||| ||||||||||||||||||
                                  CTAG GGACTCCAGTCCTCAAACT
                                    G
GAM382  FLJ12668 3' TCAAACTCCTGACCTCAGGGGA 47162      A
                TC                GATC CCTGAGGTCAGGAGTTTGA
                                  |||| ||||||||||||||||||
                                  CTAG GGACTCCAGTCCTCAAACT
                                    G
GAM382  FLJ12687 3' TCAAACTCCTGACCTCAAGTGA 46758       C
                TC                GATCAC TGAGGTCAGGAGTTTGA
                                  |||||| ||||||||||||||||||
                                  CTAGTG ACTCCAGTCCTCAAACT
                                    A
GAM382  FLJ12687 3' TCAAACTCCTGACCTCAAGTGA 46758       C
                TC                GATCAC TGAGGTCAGGAGTTTGA
                                  |||||| ||||||||||||||||||
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                                CTAGTG ACTCCAGTCCTCAAACT
                                   A
GAM382  FLJ12747  3'  TCCCGACCTCAGGTGATC    50673           A
                                GATCACCTGAGGTC GGA
                                |||||||||||||| |||
                                CTAGTGGACTCCAG CCT
                                      C
GAM382  FLJ12747  3'  TCCCGACCTCAGGTGATC    50673           A
                                GATCACCTGAGGTC GGA
                                |||||||||||||| |||
                                CTAGTGGACTCCAG CCT
                                      C
GAM382  FLJ12787  3'  AAACTCCTGACCTCAAGTGATC 50683      C
                                GATCAC TGAGGTCAGGAGTTT
                                |||||| ||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAA
                                   A
GAM382  FLJ12787  3'  AAACTCCTGACCTCAAGTGATC 50683      C
                                GATCAC TGAGGTCAGGAGTTT
                                |||||| ||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAA
                                   A
GAM382  FLJ12903  3'  TGAACTCCTGACCTCAGGTGAT 43079
          C                      GATCACCTGAGGTCAGGAGTTTG
                                 ||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGT

GAM382  FLJ12903  3'  TGAACTCCTGACCTCAGGTGAT 43079
          C                      GATCACCTGAGGTCAGGAGTTTG
                                 ||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGT

GAM382  FLJ12973  3'  TCCTGACCTCAGGTGATC    46645
                                GATCACCTGAGGTCAGGA
                                ||||||||||||||||
                                CTAGTGGACTCCAGTCCT

GAM382  FLJ12973  3'  TCCTGACCTCAGGTGATC    46645
                                GATCACCTGAGGTCAGGA
                                ||||||||||||||||
                                CTAGTGGACTCCAGTCCT

GAM382  FLJ12975  3'  AACTCCTGAGCTCAGATGATC  70177      C    G
                                GATCA CTGAG TCAGGAGTT
                                ||||| ||||| |||||||||
                                CTAGT GACTC AGTCCTCAA
                                   A    G
GAM382  FLJ12975  3'  AACTCCTGAGCTCAGATGATC  70177      C    G
                                GATCA CTGAG TCAGGAGTT
                                ||||| ||||| |||||||||
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                                CTAGT GACTC AGTCCTCAA
                                  A     G
GAM382  FLJ13072  5'  TCGAACTCCTGACCTCAGGTAA 91401      C
              TC                  GAT ACCTGAGGTCAGGAGTTTGA
                                  ||| ||||||||||||||||||||
                                  CTA TGGACTCCAGTCCTCAAGCT
                                    A
GAM382  FLJ13072  5'  TCGAACTCCTGACCTCAGGTAA 91401      C
              TC                  GAT ACCTGAGGTCAGGAGTTTGA
                                  ||| ||||||||||||||||||||
                                  CTA TGGACTCCAGTCCTCAAGCT
                                    A
GAM382  FLJ13102  3'  TCCTGACCTCAGGTGATT    46535
                                  GATCACCTGAGGTCAGGA
                                  ||||||||||||||||||
                                  TTAGTGGACTCCAGTCCT

GAM382  FLJ13102  3'  TCCTGACCTCAGGTGATT    46535
                                  GATCACCTGAGGTCAGGA
                                  ||||||||||||||||||
                                  TTAGTGGACTCCAGTCCT

GAM382  FLJ13197  3'  TGAACTCCTGACCTCAAGTGAT 45188        C
              C                    GATCAC TGAGGTCAGGAGTTTG
                                   |||||| ||||||||||||||||
                                   CTAGTG ACTCCAGTCCTCAAGT
                                     A
GAM382  FLJ13197  3'  TGAACTCCTGACCTCAAGTGAT 45188        C
              C                    GATCAC TGAGGTCAGGAGTTTG
                                   |||||| ||||||||||||||||
                                   CTAGTG ACTCCAGTCCTCAAGT
                                     A
GAM382  FLJ13590  5'  TGAACTCCTGACCTCAAGTGAT 46210        C
              C                    GATCAC TGAGGTCAGGAGTTTG
                                   |||||| ||||||||||||||||
                                   CTAGTG ACTCCAGTCCTCAAGT
                                     A
GAM382  FLJ13590  5'  TGAACTCCTGACCTCAAGTGAT 46210        C
              C                    GATCAC TGAGGTCAGGAGTTTG
                                   |||||| ||||||||||||||||
                                   CTAGTG ACTCCAGTCCTCAAGT
                                     A
GAM382  FLJ13952  3'  TCCTGACGTCAGGTGATC    46022          G
                                  GATCACCTGA GTCAGGA
                                  |||||||||| |||||||
                                  CTAGTGGACT CAGTCCT
                                        G
GAM382  FLJ13952  3'  TCCTGACGTCAGGTGATC    46022          G
                                  GATCACCTGA GTCAGGA
                                  |||||||||| |||||||
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                                CTAGTGGACT CAGTCCT
                                      G
GAM382  FLJ14950 3' TGAACTCCTGACCGCAGGTAAT 52799     C     A
            C                    GAT ACCTG GGTCAGGAGTTTG
                                 ||| ||||| ||||||||||||
                                 CTA TGGAC CCAGTCCTCAAGT
                                   A     G
GAM382  FLJ14950 3' TGAACTCCTGACCGCAGGTAAT 52799     C     A
            C                    GAT ACCTG GGTCAGGAGTTTG
                                 ||| ||||| ||||||||||||
                                 CTA TGGAC CCAGTCCTCAAGT
                                   A     G
GAM382  FLJ14957 3' TGAACTCCTGACCTCAGGTGAT 52827
            C                    GATCACCTGAGGTCAGGAGTTTG
                                 |||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGT

GAM382  FLJ14957 3' TGAACTCCTGACCTCAGGTGAT 52827
            C                    GATCACCTGAGGTCAGGAGTTTG
                                 |||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGT

GAM382  FLJ20034 3' TCAAACTCCCGACCTCAGGTGA 34855           A
            TC                     GATCACCTGAGGTC GGAGTTTGA
                                   |||||||||||||| |||||||||
                                   CTAGTGGACTCCAG CCTCAAACT
                                         C
GAM382  FLJ20034 3' TCAAACTCCCGACCTCAGGTGA 34855           A
            TC                     GATCACCTGAGGTC GGAGTTTGA
                                   |||||||||||||| |||||||||
                                   CTAGTGGACTCCAG CCTCAAACT
                                         C
GAM382  FLJ20034 3' TCCCGACCTCAGGTGATC    34856          A
                                   GATCACCTGAGGTC GGA
                                   |||||||||||||| |||
                                   CTAGTGGACTCCAG CCT
                                         C
GAM382  FLJ20034 3' TCCCGACCTCAGGTGATC    34856          A
                                   GATCACCTGAGGTC GGA
                                   |||||||||||||| |||
                                   CTAGTGGACTCCAG CCT
                                         C
GAM382  FLJ20320 3' TCGAACTCCTTACCTCAGGTGA 35428           C
            TC                     GATCACCTGAGGT AGGAGTTTGA
                                   |||||||||||||| ||||||||||
                                   CTAGTGGACTCCA TCCTCAAGCT
                                         T
GAM382  FLJ20320 3' TCGAACTCCTTACCTCAGGTGA 35428           C
            TC                     GATCACCTGAGGT AGGAGTTTGA
                                   |||||||||||||| ||||||||||
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                                CTAGTGGACTCCA TCCTCAAGCT
                                       T
GAM382  FLJ20344  3'  TGAACTCCTGACCTCAAGTGAT 35490       C
            C                   GATCAC TGAGGTCAGGAGTTTG
                                |||||| ||||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAGT
                                   A
GAM382  FLJ20344  3'  TGAACTCCTGACCTCAAGTGAT 35490       C
            C                   GATCAC TGAGGTCAGGAGTTTG
                                |||||| ||||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAGT
                                   A
GAM382  FLJ20452  3'  TCGAACTCCTGACCTCAGGTGA 35653
            TC                    GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAGCT

GAM382  FLJ20452  3'  TCGAACTCCTGACCTCAGGTGA 35653
            TC                    GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAGCT

GAM382  FLJ20507  3'  GAACTCCTAACCTCAGGTTATC 35738     C       C
                                GAT ACCTGAGGT AGGAGTTT
                                ||| ||||||||| ||||||||
                                CTA TGGACTCCA TCCTCAAG
                                  T       A
GAM382  FLJ20507  3'  GAACTCCTAACCTCAGGTTATC 35738     C       C
                                GAT ACCTGAGGT AGGAGTTT
                                ||| ||||||||| ||||||||
                                CTA TGGACTCCA TCCTCAAG
                                  T       A
GAM382  FLJ20507  3'  GAACTCCTAACCTCAGGTTATC 60843     C       C
                                GAT ACCTGAGGT AGGAGTTT
                                ||| ||||||||| ||||||||
                                CTA TGGACTCCA TCCTCAAG
                                  T       A
GAM382  FLJ20813  3'  TCAAACTCCTGACCTCATGATC 36134      CC
                                GATCA  TGAGGTCAGGAGTTTGA
                                |||||  |||||||||||||||||
                                CTAGT  ACTCCAGTCCTCAAACT
                                  ——
GAM382  FLJ20813  3'  TCAAACTCCTGACCTCATGATC 36134      CC
                                GATCA  TGAGGTCAGGAGTTTGA
                                |||||  |||||||||||||||||
                                CTAGT  ACTCCAGTCCTCAAACT
                                  ——
GAM382  FLJ21324  5'  TCAAACTCCTGACCTCAAGTGA 92860       C
            TC                    GATCAC TGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||
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                                CTAGTG ACTCCAGTCCTCAAACT
                                   A
GAM382  FLJ21324  5'  TCAAACTCCTGACCTCAAGTGA 92860       C
                TC                  GATCAC TGAGGTCAGGAGTTTGA
                                    |||||| ||||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAACT
                                   A
GAM382  FLJ21459  3'  TCGAACTCCTGACCTCAGGTGA 44812
                TC                  GATCACCTGAGGTCAGGAGTTTGA
                                    ||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAGCT

GAM382  FLJ21459  3'  TCGAACTCCTGACCTCAGGTGA 44812
                TC                  GATCACCTGAGGTCAGGAGTTTGA
                                    ||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAGCT

GAM382  FLJ22329  3'  TCGAACTCCTGACCTCAAGTGA 45409       C
                TC                  GATCAC TGAGGTCAGGAGTTTGA
                                    |||||| ||||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAGCT
                                   A
GAM382  FLJ22329  3'  TCGAACTCCTGACCTCAAGTGA 45409       C
                TC                  GATCAC TGAGGTCAGGAGTTTGA
                                    |||||| ||||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAGCT
                                   A
GAM382  FLJ22529  3'  TCAAACCCCTGACCTTAGGTGG 45954             A
                TC                  GATCACCTGAGGTCAGG GTTTGA
                                    |||||||||||||||| ||||||
                                CTGGTGGATTCCAGTCC CAAACT
                                      C
GAM382  FLJ22529  3'  TCAAACCCCTGACCTTAGGTGG 45954             A
                TC                  GATCACCTGAGGTCAGG GTTTGA
                                    |||||||||||||||| ||||||
                                CTGGTGGATTCCAGTCC CAAACT
                                      C
GAM382  FLJ22529  3'  TCGAACTCCTGACCTCAAGTGA 45956       C
                TC                  GATCAC TGAGGTCAGGAGTTTGA
                                    |||||| ||||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAGCT
                                   A
GAM382  FLJ22529  3'  TCGAACTCCTGACCTCAAGTGA 45956       C
                TC                  GATCAC TGAGGTCAGGAGTTTGA
                                    |||||| ||||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAGCT
                                   A
GAM382  FLJ22625  3'  TCAAACTGCTGACTTCAGGTGA 45586           G
                TC                  GATCACCTGAGGTCAG AGTTTGA
                                    |||||||||||||||| |||||||
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                                CTAGTGGACTTCAGTC TCAAACT
                                       G
GAM382  FLJ22625  3'  TCAAACTGCTGACTTCAGGTGA 45586              G
            TC                   GATCACCTGAGGTCAG AGTTTGA
                                 ||||||||||||||| |||||||
                                 CTAGTGGACTTCAGTC TCAAACT
                                       G
GAM382  FLJ22684  3'  TCAAACTCCTGACCTCAGGTGA 47473
            TC                   GATCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAACT

GAM382  FLJ22684  3'  TCAAACTCCTGACCTCAGGTGA 47473
            TC                   GATCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAACT

GAM382  FLJ23392  3'  TCAAATTCCTGACCCCAGGTGA 45912         A
            TC                   GATCACCTG GGTCAGGAGTTTGA
                                 ||||||||| |||||||||||||
                                 CTAGTGGAC CCAGTCCTTAAACT
                                      C
GAM382  FLJ23392  3'  TCAAATTCCTGACCCCAGGTGA 45912         A
            TC                   GATCACCTG GGTCAGGAGTTTGA
                                 ||||||||| |||||||||||||
                                 CTAGTGGAC CCAGTCCTTAAACT
                                      C
GAM382  FLJ23556  3'  TCGAACTCCTGACCTCAGGTGA 46456
                                 TCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||
                                 AGTGGACTCCAGTCCTCAAGCT

GAM382  FLJ23556  3'  TCGAACTCCTGACCTCAGGTGA 46456
                                 TCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||
                                 AGTGGACTCCAGTCCTCAAGCT

GAM382  FLJ23563  3'  TCCTGACCTCAGGTGATC    68219
                                 GATCACCTGAGGTCAGGA
                                 ||||||||||||||||||
                                 CTAGTGGACTCCAGTCCT

GAM382  FLJ23563  3'  TCCTGACCTCAGGTGATC    68219
                                 GATCACCTGAGGTCAGGA
                                 ||||||||||||||||||
                                 CTAGTGGACTCCAGTCCT

GAM382  FLJ30532  3'  TCAAGCTCCTGACCTCAGATGA 59228       C
            TC                   GATCA CTGAGGTCAGGAGTTTGA
                                 ||||| ||||||||||||||||||
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                                CTAGT GACTCCAGTCCTCGAACT
                                  A
GAM382  FLJ30532  3'  TCAAGCTCCTGACCTCAGATGA 59228      C
           TC                    GATCA CTGAGGTCAGGAGTTTGA
                                 ||||| ||||||||||||||||||
                                 CTAGT GACTCCAGTCCTCGAACT
                                   A
GAM382  FLJ31153  3'  TGAACTCCTGACCTCAGGTGAT 58754
           C                     GATCACCTGAGGTCAGGAGTTTG
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGT

GAM382  FLJ31153  3'  TGAACTCCTGACCTCAGGTGAT 58754
           C                     GATCACCTGAGGTCAGGAGTTTG
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGT

GAM382  FLJ32499  3'  TCCTGGCCTCAAGTGATC    58783       C
                                 GATCAC TGAGGTCAGGA
                                 |||||| ||||||||||
                                 CTAGTG ACTCCGGTCCT
                                   A
GAM382  FLJ32499  3'  TCCTGGCCTCAAGTGATC    58783       C
                                 GATCAC TGAGGTCAGGA
                                 |||||| ||||||||||
                                 CTAGTG ACTCCGGTCCT
                                   A
GAM382  FLJ32865  3'  TCAAACCCCTGACCTCAGGCAA 58821     CA          A
           TC                    GAT  CCTGAGGTCAGG GTTTGA
                                 |||  |||||||||||| ||||||
                                 CTA  GGACTCCAGTCC CAAACT
                                   AC          C
GAM382  FLJ32865  3'  TCAAACCCCTGACCTCAGGCAA 58821     CA          A
           TC                    GAT  CCTGAGGTCAGG GTTTGA
                                 |||  |||||||||||| ||||||
                                 CTA  GGACTCCAGTCC CAAACT
                                   AC          C
GAM382  GAL3ST-4  3'  TGAACTCCTCACCTCAGGTGAT 45284            C
           C                     GATCACCTGAGGT AGGAGTTTG
                                 |||||||||||| |||||||||
                                 CTAGTGGACTCCA TCCTCAAGT
                                       C
GAM382  GAL3ST-4  3'  TGAACTCCTCACCTCAGGTGAT 45284            C
           C                     GATCACCTGAGGT AGGAGTTTG
                                 |||||||||||| |||||||||
                                 CTAGTGGACTCCA TCCTCAAGT
                                       C
GAM382  GGA2      3'  TCGAACTCCTGACCTCAGGTGA 31173
           TC                    GATCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||||
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                                CTAGTGGACTCCAGTCCTCAAGCT

GAM382  GGA2     3'  TCGAACTCCTGACCTCAGGTGA 31173
                TC                  GATCACCTGAGGTCAGGAGTTTGA
                                    ||||||||||||||||||||||||
                                    CTAGTGGACTCCAGTCCTCAAGCT

GAM382  GGA2     3'  TCGAACTCCTGACCTCAGGTGA 57684
                TC                  GATCACCTGAGGTCAGGAGTTTGA
                                    ||||||||||||||||||||||||
                                    CTAGTGGACTCCAGTCCTCAAGCT

GAM382  GGA2     3'  TCGAACTCCTGACCTCAGGTGA 57684
                TC                  GATCACCTGAGGTCAGGAGTTTGA
                                    ||||||||||||||||||||||||
                                    CTAGTGGACTCCAGTCCTCAAGCT

GAM382  GMPPB    5'  TCCTGACCTCAGGTGATC    97461
                                    GATCACCTGAGGTCAGGA
                                    ||||||||||||||||||
                                    CTAGTGGACTCCAGTCCT

GAM382  GMPPB    5'  TCCTGACCTCAGGTGATC    26225
                                    GATCACCTGAGGTCAGGA
                                    ||||||||||||||||||
                                    CTAGTGGACTCCAGTCCT

GAM382  GNG4     3'  TCAAACTCCTGACCTCGTGATC 16854       CT
                                    GATCAC  GAGGTCAGGAGTTTGA
                                    ||||||  ||||||||||||||||
                                    CTAGTG  CTCCAGTCCTCAAACT
                                       __
GAM382  GNG4     3'  TCAAACTCCTGACCTCGTGATC 16854       CT
                                    GATCAC  GAGGTCAGGAGTTTGA
                                    ||||||  ||||||||||||||||
                                    CTAGTG  CTCCAGTCCTCAAACT
                                       __
GAM382  GOLGA3   3'  TCCTGACCTCAAGTGATC    20897       C
                                    GATCAC TGAGGTCAGGA
                                    ||||||  ||||||||||
                                    CTAGTG ACTCCAGTCCT
                                       A
GAM382  GOLGA3   3'  TCCTGACCTCAAGTGATC    20897       C
                                    GATCAC TGAGGTCAGGA
                                    ||||||  ||||||||||
                                    CTAGTG ACTCCAGTCCT
                                       A
GAM382  GREB1    3'  TCCTGGCCTCAGGTGATC    28580
                                    GATCACCTGAGGTCAGGA
                                    ||||||||||||||||||
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                                CTAGTGGACTCCGGTCCT

GAM382  GREB1    3'  TCCTGGCCTCAGGTGATC    28580
                                GATCACCTGAGGTCAGGA
                                ||||||||||||||||||
                                CTAGTGGACTCCGGTCCT

GAM382  GRWD     3'  TCAAATTCTTGATCTCAAGTGA 49789       C
              TC                  GATCAC TGAGGTCAGGAGTTTGA
                                  |||||| ||||||||||||||||||
                                  CTAGTG ACTCTAGTTCTTAAACT
                                     A
GAM382  GRWD     3'  TCAAATTCTTGATCTCAAGTGA 49789       C
              TC                  GATCAC TGAGGTCAGGAGTTTGA
                                  |||||| ||||||||||||||||||
                                  CTAGTG ACTCTAGTTCTTAAACT
                                     A
GAM382  GTPBG3   3'  TGAACTCCTTGACCTCAGGTAA 51908     C
              TC                  GAT ACCTGAGGTCA GGAGTTTG
                                  ||| |||||||||| ||||||||
                                  CTA TGGACTCCAGT CCTCAAGT
                                     A         T
GAM382  GTPBG3   3'  TGAACTCCTTGACCTCAGGTAA 51908     C
              TC                  GAT ACCTGAGGTCA GGAGTTTG
                                  ||| |||||||||| ||||||||
                                  CTA TGGACTCCAGT CCTCAAGT
                                     A         T
GAM382  H2AV     3'  TCAAACTCCTGACCTCAGGCGA 57636      A
              TC                  GATC CCTGAGGTCAGGAGTTTGA
                                  |||| ||||||||||||||||||
                                  CTAG GGACTCCAGTCCTCAAACT
                                     C
GAM382  H2AV     3'  TCAAACTCCTGACCTCAGGCGA 25762      A
              TC                  GATC CCTGAGGTCAGGAGTTTGA
                                  |||| ||||||||||||||||||
                                  CTAG GGACTCCAGTCCTCAAACT
                                     C
GAM382  HCA4     3'  TCAAACTCCTGACTTTAGGTAA 57746     C
              TC                  GAT ACCTGAGGTCAGGAGTTTGA
                                  ||| ||||||||||||||||||
                                  CTA TGGATTTCAGTCCTCAAACT
                                     A
GAM382  HCA4     3'  TCAAACTCCTGACTTTAGGTAA 78045     C
              TC                  GAT ACCTGAGGTCAGGAGTTTGA
                                  ||| ||||||||||||||||||
                                  CTA TGGATTTCAGTCCTCAAACT
                                     A
GAM382  HSMPP8   3'  TGAACTCCTGACCTCAGGTGAT 95142
              C                    GATCACCTGAGGTCAGGAGTTTG
                                   |||||||||||||||||||||||
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                                CTAGTGGACTCCAGTCCTCAAGT

GAM382  HSMPP8   3'  TGAACTCCTGACCTCAGGTGAT 95142
              C                  GATCACCTGAGGTCAGGAGTTTG
                                 ||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGT

GAM382  HSPC232  3'  TCCTGGCCTCAAGTGATC    33658       C
                                 GATCAC TGAGGTCAGGA
                                 |||||| ||||||||||
                                 CTAGTG ACTCCGGTCCT
                                    A
GAM382  HSPC232  3'  TCCTGGCCTCAAGTGATC    33658       C
                                 GATCAC TGAGGTCAGGA
                                 |||||| ||||||||||
                                 CTAGTG ACTCCGGTCCT
                                    A
GAM382  JAM1     3'  TCAAACTCCTGACCTCTTGATC 34247      CCT
                                 GATCA   GAGGTCAGGAGTTTGA
                                 |||||   ||||||||||||||||
                                 CTAGT   CTCCAGTCCTCAAACT
                                    T__
GAM382  JAM1     3'  TCAAACTCCTGACCTCTTGATC 34248      CCT
                                 GATCA   GAGGTCAGGAGTTTGA
                                 |||||   ||||||||||||||||
                                 CTAGT   CTCCAGTCCTCAAACT
                                    T__
GAM382  JAM1     3'  TCAAACTCCTGACCTCTTGATC 58526      CCT
                                 GATCA   GAGGTCAGGAGTTTGA
                                 |||||   ||||||||||||||||
                                 CTAGT   CTCCAGTCCTCAAACT
                                    T__
GAM382  JAM1     3'  TCAAACTCCTGACCTCTTGATC 58553      CCT
                                 GATCA   GAGGTCAGGAGTTTGA
                                 |||||   ||||||||||||||||
                                 CTAGT   CTCCAGTCCTCAAACT
                                    T__
GAM382  JAM1     3'  TCAAACTCCTGACCTCTTGATC 58582      CCT
                                 GATCA   GAGGTCAGGAGTTTGA
                                 |||||   ||||||||||||||||
                                 CTAGT   CTCCAGTCCTCAAACT
                                    T__
GAM382  JAM1     3'  TCAAACTCCTGACCTCTTGATC 58583      CCT
                                 GATCA   GAGGTCAGGAGTTTGA
                                 |||||   ||||||||||||||||
                                 CTAGT   CTCCAGTCCTCAAACT
                                    T__
GAM382  KIAA0022 3'  TCAAACTCCTGACCTCAAGTGA 30285      C
              TC                   GATCAC TGAGGTCAGGAGTTTGA
                                   |||||| ||||||||||||||||
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                                CTAGTG ACTCCAGTCCTCAAACT
                                   A
GAM382  KIAA0022 3' TCAAACTCCTGACCTCAAGTGA 30285       C
           TC                    GATCAC TGAGGTCAGGAGTTTGA
                                 |||||| ||||||||||||||||||
                                 CTAGTG ACTCCAGTCCTCAAACT
                                   A
GAM382  KIAA0063 3' TCAAACTCCCGACCTCAAGTGA 30262       C      A
           TC                    GATCAC TGAGGTC GGAGTTTGA
                                 |||||| ||||||| |||||||||
                                 CTAGTG ACTCCAG CCTCAAACT
                                   A      C
GAM382  KIAA0063 3' TCAAACTCCCGACCTCAAGTGA 30262       C      A
           TC                    GATCAC TGAGGTC GGAGTTTGA
                                 |||||| ||||||| |||||||||
                                 CTAGTG ACTCCAG CCTCAAACT
                                   A      C
GAM382  KIAA0161 3' TCAAACTCCTGACCTCAGGTGA 29210
           TC                    GATCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAACT

GAM382  KIAA0161 3' TCAAACTCCTGACCTCAGGTGA 29210
           TC                    GATCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAACT

GAM382  KIAA0186 3' TCAAACTCCTGACCTCAAGTGA 41118      C
                                 TCAC TGAGGTCAGGAGTTTGA
                                 |||| ||||||||||||||||
                                 AGTG ACTCCAGTCCTCAAACT
                                   A
GAM382  KIAA0186 3' TCAAACTCCTGACCTCAAGTGA 41118      C
                                 TCAC TGAGGTCAGGAGTTTGA
                                 |||| ||||||||||||||||
                                 AGTG ACTCCAGTCCTCAAACT
                                   A
GAM382  KIAA0205 3' TCGAACTCCTGACCTCAGGTGA 30218
           TC                    GATCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGCT

GAM382  KIAA0205 3' TCGAACTCCTGACCTCAGGTGA 30218
           TC                    GATCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGCT

GAM382  KIAA0391 3' TCAAACTCCTGACCTCAGGTGA 28619
           TC                    GATCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||||
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                                CTAGTGGACTCCAGTCCTCAAACT

GAM382  KIAA0391 3' TCAAACTCCTGACCTCAGGTGA 28619
              TC                  GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAACT

GAM382  KIAA0459 3' TCAAACTCCTGACCTTGTGATC 61662       CT
                                  GATCAC  GAGGTCAGGAGTTTGA
                                  ||||||  ||||||||||||||||
                                  CTAGTG  TTCCAGTCCTCAAACT
                                    __
GAM382  KIAA0459 3' TCAAACTCCTGACCTTGTGATC 61662       CT
                                  GATCAC  GAGGTCAGGAGTTTGA
                                  ||||||  ||||||||||||||||
                                  CTAGTG  TTCCAGTCCTCAAACT
                                    __
GAM382  KIAA0472 5' TGAACTCCTGACCTCAAACGAT 72371     ACC
              C                   GATC   TGAGGTCAGGAGTTTG
                                  ||||   ||||||||||||||||
                                  CTAG   ACTCCAGTCCTCAAGT
                                    CAA
GAM382  KIAA0472 5' TGAACTCCTGACCTCAAACGAT 72371     ACC
              C                   GATC   TGAGGTCAGGAGTTTG
                                  ||||   ||||||||||||||||
                                  CTAG   ACTCCAGTCCTCAAGT
                                    CAA
GAM382  KIAA0475 3' TCCTGACCCCAGGTGATC    30131        A
                                  GATCACCTG GGTCAGGA
                                  ||||||||| ||||||||
                                  CTAGTGGAC CCAGTCCT
                                       C
GAM382  KIAA0475 3' TCCTGACCCCAGGTGATC    30131        A
                                  GATCACCTG GGTCAGGA
                                  ||||||||| ||||||||
                                  CTAGTGGAC CCAGTCCT
                                       C
GAM382  KIAA0513 3' TCGAACTCCTGACCTCAGGTGA 29051
              TC                  GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAGCT

GAM382  KIAA0513 3' TCGAACTCCTGACCTCAGGTGA 29051
              TC                  GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAGCT

GAM382  KIAA0513 5' TGAACTCCTGACCTCAGGTGA  29053
                                  TCACCTGAGGTCAGGAGTTTG
                                  |||||||||||||||||||||
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                                AGTGGACTCCAGTCCTCAAGT

GAM382  KIAA0513 5' TGAACTCCTGACCTCAGGTGA  29053
                                TCACCTGAGGTCAGGAGTTTG
                                |||||||||||||||||||||
                                AGTGGACTCCAGTCCTCAAGT

GAM382  KIAA0527 3' GAACTCCTGACCTCAAGTGATC 97496       C
                                GATCAC TGAGGTCAGGAGTTT
                                |||||| ||||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAG
                                   A
GAM382  KIAA0527 3' GAACTCCTGACCTCAAGTGATC 97496       C
                                GATCAC TGAGGTCAGGAGTTT
                                |||||| ||||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAG
                                   A
GAM382  KIAA0555 3' TCGAACTCCTGACCTCAAGTGA 29553       C
           TC                     GATCAC TGAGGTCAGGAGTTTGA
                                |||||| |||||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAGCT
                                   A
GAM382  KIAA0555 3' TCGAACTCCTGACCTCAAGTGA 60746       C
           TC                     GATCAC TGAGGTCAGGAGTTTGA
                                |||||| |||||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAGCT
                                   A
GAM382  KIAA0562 3' TCAAACTCCTGACCTTGTGATC 28831       CT
                                GATCAC  GAGGTCAGGAGTTTGA
                                ||||||  ||||||||||||||||
                                CTAGTG  TTCCAGTCCTCAAACT
                                   __
GAM382  KIAA0562 3' TCAAACTCCTGACCTTGTGATC 28831       CT
                                GATCAC  GAGGTCAGGAGTTTGA
                                ||||||  ||||||||||||||||
                                CTAGTG  TTCCAGTCCTCAAACT
                                   __
GAM382  KIAA0599 3' TCGAACTTCTGACCTCAGGTGA 77702
           TC                     GATCACCTGAGGTCAGGAGTTTGA
                                |||||||||||||||||||||||||
                                CTAGTGGACTCCAGTCTTCAAGCT

GAM382  KIAA0599 3' TCGAACTTCTGACCTCAGGTGA 77702
           TC                     GATCACCTGAGGTCAGGAGTTTGA
                                |||||||||||||||||||||||||
                                CTAGTGGACTCCAGTCTTCAAGCT

GAM382  KIAA0682 3' TCCTGACCTCAAGTGATC    30030       C
                                GATCAC TGAGGTCAGGA
                                |||||| ||||||||||
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                                CTAGTG ACTCCAGTCCT
                                   A
GAM382  KIAA0682 3' TCCTGACCTCAAGTGATC    30030       C
                                GATCAC TGAGGTCAGGA
                                |||||| ||||||||||
                                CTAGTG ACTCCAGTCCT
                                   A
GAM382  KIAA0682 3' TGAACTCCCAACCTCAAGTGAT 30031       C     CA
           C                     GATCAC TGAGGT  GGAGTTTG
                                |||||| ||||||  ||||||||
                                CTAGTG ACTCCA  CCTCAAGT
                                   A     AC
GAM382  KIAA0682 3' TGAACTCCCAACCTCAAGTGAT 30031       C     CA
           C                     GATCAC TGAGGT  GGAGTTTG
                                |||||| ||||||  ||||||||
                                CTAGTG ACTCCA  CCTCAAGT
                                   A     AC
GAM382  KIAA0720 3' TCCTGACCCCAAGTGTTC    62993    T   C  A
                                GA CAC TG GGTCAGGA
                                || ||| || ||||||||
                                CT GTG AC CCAGTCCT
                                 T   A  C
GAM382  KIAA0720 3' TCCTGACCCCAAGTGTTC    62993    T   C  A
                                GA CAC TG GGTCAGGA
                                || ||| || ||||||||
                                CT GTG AC CCAGTCCT
                                 T   A  C
GAM382  KIAA0841 3' TCGAACTCCTGACCTCAAGTGA 71906       C
           TC                     GATCAC TGAGGTCAGGAGTTTGA
                                |||||| ||||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAGCT
                                   A
GAM382  KIAA0841 3' TCGAACTCCTGACCTCAAGTGA 71906       C
           TC                     GATCAC TGAGGTCAGGAGTTTGA
                                |||||| ||||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAGCT
                                   A
GAM382  KIAA0889 3' TCGAACTCCCGACCTCAAGTGA 31788       C     A
           TC                     GATCAC TGAGGTC GGAGTTTGA
                                |||||| ||||||| |||||||||
                                CTAGTG ACTCCAG CCTCAAGCT
                                   A      C
GAM382  KIAA0889 3' TCGAACTCCCGACCTCAAGTGA 31788       C     A
           TC                     GATCAC TGAGGTC GGAGTTTGA
                                |||||| ||||||| |||||||||
                                CTAGTG ACTCCAG CCTCAAGCT
                                   A      C
GAM382  KIAA0924 3' TCAAACTCCTGACCTTGTGATC 30375       CT
                                GATCAC  GAGGTCAGGAGTTTGA
                                ||||||  ||||||||||||||||
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                                CTAGTG  TTCCAGTCCTCAAACT

                                  __
GAM382  KIAA0924  3'  TCAAACTCCTGACCTTGTGATC 30375       CT
                                GATCAC  GAGGTCAGGAGTTTGA
                                ||||||  ||||||||||||||||
                                CTAGTG  TTCCAGTCCTCAAACT

                                  __
GAM382  KIAA0931  3'  TGAACTCTTGACCTCAGGTGAT 68019
              C                  GATCACCTGAGGTCAGGAGTTTG
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTTCTCAAGT

GAM382  KIAA0931  3'  TGAACTCTTGACCTCAGGTGAT 68019
              C                  GATCACCTGAGGTCAGGAGTTTG
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTTCTCAAGT

GAM382  KIAA0961  3'  TCAACTCCTGACCTCAGGTGAT 30407                T
              C                  GATCACCTGAGGTCAGGAGTT GA
                                 |||||||||||||||||||| ||
                                 CTAGTGGACTCCAGTCCTCAA CT

                                    _
GAM382  KIAA0961  3'  TCAACTCCTGACCTCAGGTGAT 30407                T
              C                  GATCACCTGAGGTCAGGAGTT GA
                                 |||||||||||||||||||| ||
                                 CTAGTGGACTCCAGTCCTCAA CT

                                    _
GAM382  KIAA1026  3'  TCAACTCCTGACCTCAGGCGAT 71745      A          T
              C                  GATC CCTGAGGTCAGGAGTT GA
                                 |||| |||||||||||||| ||
                                 CTAG GGACTCCAGTCCTCAA CT
                                   C
GAM382  KIAA1026  3'  TCAACTCCTGACCTCAGGCGAT 71745      A          T
              C                  GATC CCTGAGGTCAGGAGTT GA
                                 |||| |||||||||||||| ||
                                 CTAG GGACTCCAGTCCTCAA CT
                                   C
GAM382  KIAA1040  3'  TGAACTCCTGACCTCAGGTGAT 72692
              C                  GATCACCTGAGGTCAGGAGTTTG
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGT

GAM382  KIAA1040  3'  TGAACTCCTGACCTCAGGTGAT 72692
              C                  GATCACCTGAGGTCAGGAGTTTG
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGT

GAM382  KIAA1054  3'  TCGAACTCCTGACCTCAAGTGA 68970       C
              TC                   GATCAC TGAGGTCAGGAGTTTGA
                                 ||||||  ||||||||||||||||
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                                CTAGTG ACTCCAGTCCTCAAGCT
                                   A
GAM382  KIAA1054 3' TCGAACTCCTGACCTCAAGTGA 68970       C
           TC                    GATCAC TGAGGTCAGGAGTTTGA
                                 |||||| ||||||||||||||||
                                 CTAGTG ACTCCAGTCCTCAAGCT
                                   A
GAM382  KIAA1128 3' TCGAACTCCTGACCTCAAGTGA 69012       C
           TC                    GATCAC TGAGGTCAGGAGTTTGA
                                 |||||| ||||||||||||||||
                                 CTAGTG ACTCCAGTCCTCAAGCT
                                   A
GAM382  KIAA1128 3' TCGAACTCCTGACCTCAAGTGA 69012       C
           TC                    GATCAC TGAGGTCAGGAGTTTGA
                                 |||||| ||||||||||||||||
                                 CTAGTG ACTCCAGTCCTCAAGCT
                                   A
GAM382  KIAA1161 5' TCAAACTCCTGACCTAGTGAT  82652      CTG
                                 ATCAC  AGGTCAGGAGTTTGA
                                 |||||  ||||||||||||||
                                 TAGTG  TCCAGTCCTCAAACT
                                   A__
GAM382  KIAA1161 5' TCAAACTCCTGACCTAGTGAT  82652      CTG
                                 ATCAC  AGGTCAGGAGTTTGA
                                 |||||  ||||||||||||||
                                 TAGTG  TCCAGTCCTCAAACT
                                   A__
GAM382  KIAA1170 3' TCAAACTCCTGACCTCAGGTGA 70424
           TC                    GATCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAACT

GAM382  KIAA1170 3' TCAAACTCCTGACCTCAGGTGA 70424
           TC                    GATCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAACT

GAM382  KIAA1198 3' TAAACTCTTGACCTCAAATGAT 64060      CC
           C                     GATCA  TGAGGTCAGGAGTTTG
                                 |||||  |||||||||||||||
                                 CTAGT  ACTCCAGTTCTCAAAT
                                   AA
GAM382  KIAA1198 3' TAAACTCTTGACCTCAAATGAT 64060      CC
           C                     GATCA  TGAGGTCAGGAGTTTG
                                 |||||  |||||||||||||||
                                 CTAGT  ACTCCAGTTCTCAAAT
                                   AA
GAM382  KIAA1198 3' TCAAACTCCTGACCTCAGGTGA 64065
           TC                    GATCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||||
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                                CTAGTGGACTCCAGTCCTCAAACT

GAM382  KIAA1198 3' TCAAACTCCTGACCTCAGGTGA 64065
              TC                  GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAACT

GAM382  KIAA1198 3' TGAACTCCTGACCTCAGGTAAT 64069     C
              C                   GAT ACCTGAGGTCAGGAGTTTG
                                  ||| ||||||||||||||||||
                                  CTA TGGACTCCAGTCCTCAAGT
                                    A
GAM382  KIAA1198 3' TGAACTCCTGACCTCAGGTAAT 64069     C
              C                   GAT ACCTGAGGTCAGGAGTTTG
                                  ||| ||||||||||||||||||
                                  CTA TGGACTCCAGTCCTCAAGT
                                    A
GAM382  KIAA1200 3' TCGAACTCCTGACCTCAGGTGA 63043
              TC                  GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAGCT

GAM382  KIAA1200 3' TCGAACTCCTGACCTCAGGTGA 63043
              TC                  GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAGCT

GAM382  KIAA1243 3' CAAAAGTACTTGACCTCAAGT  74023    C        AG__
                                  AC TGAGGTCAGG    TTTG
                                  || ||||||||||    ||||
                                  TG ACTCCAGTTC    AAAC
                                    A         ATGA
GAM382  KIAA1243 3' CAAAAGTACTTGACCTCAAGT  74023    C        AG__
                                  AC TGAGGTCAGG    TTTG
                                  || ||||||||||    ||||
                                  TG ACTCCAGTTC    AAAC
                                    A         ATGA
GAM382  KIAA1254 3' TCCTGACCTCAAGTGATC     70566        C
                                  GATCAC TGAGGTCAGGA
                                  ||||||| ||||||||||
                                  CTAGTG ACTCCAGTCCT
                                     A
GAM382  KIAA1254 3' TCCTGACCTCAAGTGATC     70566        C
                                  GATCAC TGAGGTCAGGA
                                  ||||||| ||||||||||
                                  CTAGTG ACTCCAGTCCT
                                     A
GAM382  KIAA1257 3' TCAAACTCCCGACTTCAGGTGA 63417             A
              TC                  GATCACCTGAGGTC GGAGTTTGA
                                  |||||||||||||| |||||||||
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                                CTAGTGGACTTCAG CCTCAAACT
                                       C
GAM382  KIAA1257 3' TCAAACTCCCGACTTCAGGTGA 63417            A
           TC                   GATCACCTGAGGTC GGAGTTTGA
                                |||||||||||||| |||||||||
                                CTAGTGGACTTCAG CCTCAAACT
                                       C
GAM382  KIAA1257 3' TCAAACTCCTGGTCACAAGTAA 63418     C  C  A GT
           TC                   GAT AC TG G  CAGGAGTTTGA
                                ||| || || |  ||||||||||
                                CTA TG AC C  GTCCTCAAACT
                                  A  A  A TG
GAM382  KIAA1257 3' TCAAACTCCTGGTCACAAGTAA 63418     C  C  A GT
           TC                   GAT AC TG G  CAGGAGTTTGA
                                ||| || || |  ||||||||||
                                CTA TG AC C  GTCCTCAAACT
                                  A  A  A TG
GAM382  KIAA1287 3' TCCTGGCCTCAGGTGATC    78942
                                GATCACCTGAGGTCAGGA
                                ||||||||||||||||||
                                CTAGTGGACTCCGGTCCT

GAM382  KIAA1287 3' TCCTGGCCTCAGGTGATC    78942
                                GATCACCTGAGGTCAGGA
                                ||||||||||||||||||
                                CTAGTGGACTCCGGTCCT

GAM382  KIAA1320 5' TCCTGACCTCAAGTGATC    69851       C
                                GATCAC TGAGGTCAGGA
                                |||||| ||||||||||
                                CTAGTG ACTCCAGTCCT
                                    A
GAM382  KIAA1320 5' TCCTGACCTCAAGTGATC    69851       C
                                GATCAC TGAGGTCAGGA
                                |||||| ||||||||||
                                CTAGTG ACTCCAGTCCT
                                    A
GAM382  KIAA1373 3' TCCTGACCTCTGATGATC    71513      CCT
                                GATCA   GAGGTCAGGA
                                |||||   ||||||||||
                                CTAGT   CTCCAGTCCT
                                   AGT
GAM382  KIAA1373 3' TCCTGACCTCTGATGATC    71513      CCT
                                GATCA   GAGGTCAGGA
                                |||||   ||||||||||
                                CTAGT   CTCCAGTCCT
                                   AGT
GAM382  KIAA1396 3' TCAAACTCCTGTGCTCAAGTGA 63674     C    GT
                                TCAC TGAG  CAGGAGTTTGA
                                |||| ||||  ||||||||||
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                                AGTG ACTC  GTCCTCAAACT
                                  A    GT
GAM382  KIAA1396 3' TCAAACTCCTGTGCTCAAGTGA 63674      C    GT
                                TCAC TGAG  CAGGAGTTTGA
                                |||| ||||  ||||||||||
                                AGTG ACTC  GTCCTCAAACT
                                  A    GT
GAM382  KIAA1465 3' CTCTTGACCTCAGGTGATC    61492
                                GATCACCTGAGGTCAGGAG
                                ||||||||||||||||||
                                CTAGTGGACTCCAGTTCTC

GAM382  KIAA1465 3' CTCTTGACCTCAGGTGATC    61492
                                GATCACCTGAGGTCAGGAG
                                ||||||||||||||||||
                                CTAGTGGACTCCAGTTCTC

GAM382  KIAA1493 3' TCAAACTCCTGACCTCAGGTGA 64844
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAACT

GAM382  KIAA1493 3' TCAAACTCCTGACCTCAGGTGA 64844
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAACT

GAM382  KIAA1508 3' TGAACTCCTGACCTCAGGTAAT 62565      C
                C                  GAT ACCTGAGGTCAGGAGTTTG
                                   ||| ||||||||||||||||||
                                   CTA TGGACTCCAGTCCTCAAGT
                                     A
GAM382  KIAA1508 3' TGAACTCCTGACCTCAGGTAAT 62565      C
                C                  GAT ACCTGAGGTCAGGAGTTTG
                                   ||| ||||||||||||||||||
                                   CTA TGGACTCCAGTCCTCAAGT
                                     A
GAM382  KIAA1571 3' TCAAACTCCTGACCTTGTGGTC 61624        CT
                                GATCAC  GAGGTCAGGAGTTTGA
                                ||||||  ||||||||||||||||
                                CTGGTG  TTCCAGTCCTCAAACT
                                  ——
GAM382  KIAA1571 3' TCAAACTCCTGACCTTGTGGTC 61624        CT
                                GATCAC  GAGGTCAGGAGTTTGA
                                ||||||  ||||||||||||||||
                                CTGGTG  TTCCAGTCCTCAAACT
                                  ——
GAM382  KIAA1607 3' CAAACTCCTGGTTGGTGAT    64534       TGA GT
                                ATCACC   G  CAGGAGTTTG
                                ||||||   |  ||||||||||
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                                TAGTGG   T  GTCCTCAAAC
                                   ___ TG
GAM382  KIAA1607 3' CAAACTCCTGGTTGGTGAT   64534       TGA GT
                                ATCACC   G  CAGGAGTTTG
                                ||||||   |  ||||||||||
                                TAGTGG   T  GTCCTCAAAC
                                   ___ TG
GAM382  KIAA1615 3' TCAAACTCCCGACCTCAGGTGA 69286            A
           TC                     GATCACCTGAGGTC GGAGTTTGA
                                ||||||||||||||| |||||||||
                                CTAGTGGACTCCAG CCTCAAACT
                                         C
GAM382  KIAA1615 3' TCAAACTCCCGACCTCAGGTGA 69286            A
           TC                     GATCACCTGAGGTC GGAGTTTGA
                                ||||||||||||||| |||||||||
                                CTAGTGGACTCCAG CCTCAAACT
                                         C
GAM382  KIAA1617 3' TGAACTCCCAACCTCAAGTGAT 93085       C     CA
           C                      GATCAC TGAGGT  GGAGTTTG
                                ||||||| ||||||  ||||||||
                                CTAGTG ACTCCA  CCTCAAGT
                                   A     AC
GAM382  KIAA1617 3' TGAACTCCCAACCTCAAGTGAT 93085       C     CA
           C                      GATCAC TGAGGT  GGAGTTTG
                                ||||||| ||||||  ||||||||
                                CTAGTG ACTCCA  CCTCAAGT
                                   A     AC
GAM382  KIAA1655 3' TCAAACTCCTGACCTCCAGTGA 67203       CT
           TC                     GATCAC  GAGGTCAGGAGTTTGA
                                ||||||  ||||||||||||||||
                                CTAGTG  CTCCAGTCCTCAAACT
                                   AC
GAM382  KIAA1655 3' TCAAACTCCTGACCTCCAGTGA 67203       CT
           TC                     GATCAC  GAGGTCAGGAGTTTGA
                                ||||||  ||||||||||||||||
                                CTAGTG  CTCCAGTCCTCAAACT
                                   AC
GAM382  KIAA1712 3' TCAAACTCCTGACCTCAGGTGA 68167
           TC                     GATCACCTGAGGTCAGGAGTTTGA
                                ||||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAACT

GAM382  KIAA1712 3' TCAAACTCCTGACCTCAGGTGA 68167
           TC                     GATCACCTGAGGTCAGGAGTTTGA
                                ||||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAACT

GAM382  KIAA1737 3' TCGAACTCCTGACCTCAGTTGA 67947       C
           TC                     GATCA CTGAGGTCAGGAGTTTGA
                                |||||  ||||||||||||||||||
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                                CTAGT GACTCCAGTCCTCAAGCT
                                  T
GAM382  KIAA1737 3'  TCGAACTCCTGACCTCAGTTGA 67947      C
           TC                    GATCA CTGAGGTCAGGAGTTTGA
                                 ||||| ||||||||||||||||||
                                 CTAGT GACTCCAGTCCTCAAGCT
                                   T
GAM382  KIAA1755 3'  TCAAACTCCTGGGCTCAAGTGA 62021       C   G
           TC                    GATCAC TGAG TCAGGAGTTTGA
                                 |||||| |||| ||||||||||||
                                 CTAGTG ACTC GGTCCTCAAACT
                                   A   G
GAM382  KIAA1755 3'  TCAAACTCCTGGGCTCAAGTGA 62021       C   G
           TC                    GATCAC TGAG TCAGGAGTTTGA
                                 |||||| |||| ||||||||||||
                                 CTAGTG ACTC GGTCCTCAAACT
                                   A   G
GAM382  KIAA1922 5'  TCGAACTCCTGACCTCAGGTGA 74007
           TC                    GATCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGCT

GAM382  KIAA1922 5'  TCGAACTCCTGACCTCAGGTGA 74007
           TC                    GATCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGCT

GAM382  KIAA1987 5'  TCGAACTTCTGACCTCAGGTGA 89393
           TC                    GATCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCTTCAAGCT

GAM382  KIAA1987 5'  TCGAACTTCTGACCTCAGGTGA 89393
           TC                    GATCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCTTCAAGCT

GAM382  LAMP3    3'  TGAACTCTTGACCTCAGGTGAT 60211
           C                     GATCACCTGAGGTCAGGAGTTTG
                                 |||||||||||||||||||||||
                                 CTAGTGGACTCCAGTTCTCAAGT

GAM382  LAMP3    3'  TGAACTCTTGACCTCAGGTGAT 60211
           C                     GATCACCTGAGGTCAGGAGTTTG
                                 |||||||||||||||||||||||
                                 CTAGTGGACTCCAGTTCTCAAGT

GAM382  MAP-1    3'  TCGAACTCCTGACCTCAAGTGA 42452       C
           TC                    GATCAC TGAGGTCAGGAGTTTGA
                                 |||||| ||||||||||||||||
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                                CTAGTG ACTCCAGTCCTCAAGCT
                                   A
GAM382  MAP-1    3'  TCGAACTCCTGACCTCAAGTGA 42452       C
                TC                  GATCAC TGAGGTCAGGAGTTTGA
                                    |||||| ||||||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAGCT
                                   A
GAM382  MCLC     3'  TCGAACTCCTGACCTCAAGTGA 31387      C
                                TCAC TGAGGTCAGGAGTTTGA
                                    |||| ||||||||||||||||
                                AGTG ACTCCAGTCCTCAAGCT
                                   A
GAM382  MCLC     3'  TCGAACTCCTGACCTCAAGTGA 31387      C
                                TCAC TGAGGTCAGGAGTTTGA
                                    |||| ||||||||||||||||
                                AGTG ACTCCAGTCCTCAAGCT
                                   A
GAM382  MCM10    3'  TCAAACTCCTGAGCACTAG   38180     AG _
                                CTG  G TCAGGAGTTTGA
                                    |||  | ||||||||||||
                                GAT  C AGTCCTCAAACT
                                  CA G
GAM382  MCM10    3'  TCAAACTCCTGAGCACTAG   38180     AG _
                                CTG  G TCAGGAGTTTGA
                                    |||  | ||||||||||||
                                GAT  C AGTCCTCAAACT
                                  CA G
GAM382  MEF-2    3'  TCAAACTCCTGACCTCGTGATC 65032       CT
                                GATCAC  GAGGTCAGGAGTTTGA
                                    ||||||  ||||||||||||||||
                                CTAGTG  CTCCAGTCCTCAAACT
                                   __
GAM382  MEF-2    3'  TCAAACTCCTGACCTCGTGATC 65032       CT
                                GATCAC  GAGGTCAGGAGTTTGA
                                    ||||||  ||||||||||||||||
                                CTAGTG  CTCCAGTCCTCAAACT
                                   __
GAM382  MGC13204 3'  TCAAAATCCTGACCTCAAGTCA 49633     C  C        G
                TC                  GAT AC TGAGGTCAGGA TTTGA
                                    ||| || |||||||||| |||||
                                CTA TG ACTCCAGTCCT AAACT
                                  C  A         A
GAM382  MGC13204 3'  TCAAAATCCTGACCTCAAGTCA 49633     C  C        G
                TC                  GAT AC TGAGGTCAGGA TTTGA
                                    ||| || |||||||||| |||||
                                CTA TG ACTCCAGTCCT AAACT
                                  C  A         A
GAM382  MGC14836 5'  CAAACTCCAGGCTCAGATGTC  54171    T  C    G  A
                                GA CA CTGAG TC GGAGTTTG
                                    || || ||||| || ||||||||
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                                CT GT GACTC GG CCTCAAAC
                                 _ A    _ A
GAM382  MGC14836 5' CAAACTCCAGGCTCAGATGTC  54171    T  C    G  A
                                GA CA CTGAG TC GGAGTTTG
                                || || ||||| || ||||||||
                                CT GT GACTC GG CCTCAAAC
                                 _ A    _ A
GAM382  MGC1842  3' TCGAACCCCTGAGCTCAGGTGA 66264          G    A
           TC                    GATCACCTGAG TCAGG GTTTGA
                                 |||||||||||| ||||| ||||||
                                 CTAGTGGACTC AGTCC CAAGCT
                                       G    C
GAM382  MGC1842  3' TCGAACCCCTGAGCTCAGGTGA 66264          G    A
           TC                    GATCACCTGAG TCAGG GTTTGA
                                 |||||||||||| ||||| ||||||
                                 CTAGTGGACTC AGTCC CAAGCT
                                       G    C
GAM382  MGC21675 3' TGAACTCCTGACCTCAGGTGAT 54599
           C                     GATCACCTGAGGTCAGGAGTTTG
                                 |||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGT

GAM382  MGC21675 3' TGAACTCCTGACCTCAGGTGAT 54599
           C                     GATCACCTGAGGTCAGGAGTTTG
                                 |||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGT

GAM382  MGC21738 3' TCGAACTCCTGACCTCAAGTGA 59580       C
           TC                    GATCAC TGAGGTCAGGAGTTTGA
                                 |||||| ||||||||||||||||
                                 CTAGTG ACTCCAGTCCTCAAGCT
                                    A
GAM382  MGC21738 3' TCGAACTCCTGACCTCAAGTGA 59580       C
           TC                    GATCAC TGAGGTCAGGAGTTTGA
                                 |||||| ||||||||||||||||
                                 CTAGTG ACTCCAGTCCTCAAGCT
                                    A
GAM382  MGC2474  3' TCCTGCCCTCAGGTGATC    43967          T
                                GATCACCTGAGG CAGGA
                                |||||||||||| |||||
                                CTAGTGGACTCC GTCCT
                                      C
GAM382  MGC2474  3' TCCTGCCCTCAGGTGATC    43967          T
                                GATCACCTGAGG CAGGA
                                |||||||||||| |||||
                                CTAGTGGACTCC GTCCT
                                      C
GAM382  MKRN4    3' TCGAACTCCTGACCTCAGGTGA 48476
           TC                    GATCACCTGAGGTCAGGAGTTTGA
                                 |||||||||||||||||||||||
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                                CTAGTGGACTCCAGTCCTCAAGCT

GAM382  MKRN4    3'  TCGAACTCCTGACCTCAGGTGA 48476
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAGCT

GAM382  moblak   3'  TCAAACTCCTGACTTCAGGTGA 56411
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTTCAGTCCTCAAACT

GAM382  moblak   3'  TCAAACTCCTGACTTCAGGTGA 56411
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTTCAGTCCTCAAACT

GAM382  MRPL44   3'  TGAACTCCTGACCTCAGGTGAT 43600
                C                 GATCACCTGAGGTCAGGAGTTTG
                                  |||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAGT

GAM382  MRPL44   3'  TGAACTCCTGACCTCAGGTGAT 43600
                C                 GATCACCTGAGGTCAGGAGTTTG
                                  |||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAGT

GAM382  MRPS27   3'  TCAACCTCCTGACCTCAAGTGA 31335      C        T
                TC                GATCAC TGAGGTCAGGAG TTGA
                                  |||||| |||||||||||| ||||
                                  CTAGTG ACTCCAGTCCTC AACT
                                     A         C
GAM382  MRPS27   3'  TCAACCTCCTGACCTCAAGTGA 31335      C        T
                TC                GATCAC TGAGGTCAGGAG TTGA
                                  |||||| |||||||||||| ||||
                                  CTAGTG ACTCCAGTCCTC AACT
                                     A         C
GAM382  NFAT5    3'  TCGAACTCCTAACCTCCAGTGA 57778      CT    C
                TC                GATCAC  GAGGT AGGAGTTTGA
                                  ||||||  ||||| ||||||||||
                                  CTAGTG  CTCCA TCCTCAAGCT
                                     AC    A
GAM382  NFAT5    3'  TCGAACTCCTAACCTCCAGTGA 57793      CT    C
                TC                GATCAC  GAGGT AGGAGTTTGA
                                  ||||||  ||||| ||||||||||
                                  CTAGTG  CTCCA TCCTCAAGCT
                                     AC    A
GAM382  NINJ2    3'  TGAACTCCTGACCTCAGGTGAT 33733
                C                 GATCACCTGAGGTCAGGAGTTTG
                                  |||||||||||||||||||||||
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                                CTAGTGGACTCCAGTCCTCAAGT

GAM382  NINJ2    3'  TGAACTCCTGACCTCAGGTGAT 33733
                C                GATCACCTGAGGTCAGGAGTTTG
                                 ||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGT

GAM382  Nup43    3'  TCGAACTCCTGACCACAGGTAA 45357     C    A
                TC                 GAT ACCTG GGTCAGGAGTTTGA
                                   ||| ||||| |||||||||||||
                                   CTA TGGAC CCAGTCCTCAAGCT
                                     A    A
GAM382  Nup43    3'  TCGAACTCCTGACCACAGGTAA 45357     C    A
                TC                 GAT ACCTG GGTCAGGAGTTTGA
                                   ||| ||||| |||||||||||||
                                   CTA TGGAC CCAGTCCTCAAGCT
                                     A    A
GAM382  NXN      3'  TCGAACTCCTGACCTCAGGTGA 42682
                TC                 GATCACCTGAGGTCAGGAGTTTGA
                                   ||||||||||||||||||||||||
                                   CTAGTGGACTCCAGTCCTCAAGCT

GAM382  NXN      3'  TCGAACTCCTGACCTCAGGTGA 42682
                TC                 GATCACCTGAGGTCAGGAGTTTGA
                                   ||||||||||||||||||||||||
                                   CTAGTGGACTCCAGTCCTCAAGCT

GAM382  OSBPL2   3'  TCAAACTCCCGACCTCAAGTAG 58494     C  C      A
                TC                 GAT AC TGAGGTC GGAGTTTGA
                                   ||| || ||||||| |||||||||
                                   CTG TG ACTCCAG CCTCAAACT
                                     A  A      C
GAM382  OSBPL2   3'  TCAAACTCCCGACCTCAAGTAG 58494     C  C      A
                TC                 GAT AC TGAGGTC GGAGTTTGA
                                   ||| || ||||||| |||||||||
                                   CTG TG ACTCCAG CCTCAAACT
                                     A  A      C
GAM382  OSBPL2   3'  TCAAACTCCCGACCTCAAGTAG 29907     C  C      A
                TC                 GAT AC TGAGGTC GGAGTTTGA
                                   ||| || ||||||| |||||||||
                                   CTG TG ACTCCAG CCTCAAACT
                                     A  A      C
GAM382  PASK     5'  TCCCAGCCTCAGGTGATC    31421            CA
                                   GATCACCTGAGGT  GGA
                                   ||||||||||||  |||
                                   CTAGTGGACTCCG  CCT
                                          AC
GAM382  PASK     5'  TCCCAGCCTCAGGTGATC    31421            CA
                                   GATCACCTGAGGT  GGA
                                   ||||||||||||  |||
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                                CTAGTGGACTCCG  CCT
                                      AC
GAM382  PELI1    5'  TCAAACTCCCAACCTCAAGTGA 40655       C     CA
          TC                    GATCAC TGAGGT  GGAGTTTGA
                                |||||| ||||||  |||||||||
                                CTAGTG ACTCCA  CCTCAAACT
                                   A     AC
GAM382  PELI1    5'  TCAAACTCCCAACCTCAAGTGA 40655       C     CA
          TC                    GATCAC TGAGGT  GGAGTTTGA
                                |||||| ||||||  |||||||||
                                CTAGTG ACTCCA  CCTCAAACT
                                   A     AC
GAM382  PELI1    5'  TCCTGACATCAAGTGATC    40656       C   G
                                GATCAC TGA GTCAGGA
                                |||||| ||| |||||||
                                CTAGTG ACT CAGTCCT
                                   A   A
GAM382  PELI1    5'  TCCTGACATCAAGTGATC    40656       C   G
                                GATCAC TGA GTCAGGA
                                |||||| ||| |||||||
                                CTAGTG ACT CAGTCCT
                                   A   A
GAM382  PELI1    5'  TGAACTCCTGACCTCAAGTGAT 40658       C
          C                     GATCAC TGAGGTCAGGAGTTTG
                                |||||| ||||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAGT
                                   A
GAM382  PELI1    5'  TGAACTCCTGACCTCAAGTGAT 40658       C
          C                     GATCAC TGAGGTCAGGAGTTTG
                                |||||| ||||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAGT
                                   A
GAM382  PIP3-E   3'  TCAAACTCCTGACCTCAGGTGA 67360
          TC                    GATCACCTGAGGTCAGGAGTTTGA
                                ||||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAACT

GAM382  PIP3-E   3'  TCAAACTCCTGACCTCAGGTGA 67360
          TC                    GATCACCTGAGGTCAGGAGTTTGA
                                ||||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAACT

GAM382  PRO0245  5'  TCAAACTCCCGAGCCCAAGTAA 26957     C  C  A  _  A
          TC                    GAT AC TG GG TC GGAGTTTGA
                                ||| || || || || |||||||||
                                CTA TG AC CC AG CCTCAAACT
                                  A  A  _  G  C
GAM382  PRO0245  5'  TCAAACTCCCGAGCCCAAGTAA 26957     C  C  A  _  A
          TC                    GAT AC TG GG TC GGAGTTTGA
                                ||| || || || || |||||||||
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                                CTA TG AC CC AG CCTCAAACT
                                  A  A  _  G  C
GAM382  PRO0365  5'  TCCTGACCTCAAGTGATC    26997       C
                                GATCAC TGAGGTCAGGA
                                |||||| ||||||||||
                                CTAGTG ACTCCAGTCCT
                                   A
GAM382  PRO0365  5'  TCCTGACCTCAAGTGATC    26997       C
                                GATCAC TGAGGTCAGGA
                                |||||| ||||||||||
                                CTAGTG ACTCCAGTCCT
                                   A
GAM382  PRO1992  3'  GAACTCAACCTCAGGTGATC   26903            CAG
                                GATCACCTGAGGT   GAGTTT
                                ||||||||||||   ||||||
                                CTAGTGGACTCCA   CTCAAG
                                      A__
GAM382  PRO1992  3'  GAACTCAACCTCAGGTGATC   26903            CAG
                                GATCACCTGAGGT   GAGTTT
                                ||||||||||||   ||||||
                                CTAGTGGACTCCA   CTCAAG
                                      A__
GAM382  PRO2955  3'  TCAAACTCCTGACCTCAGGTGA 38246
          TC                      GATCACCTGAGGTCAGGAGTTTGA
                                ||||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAACT

GAM382  PRO2955  3'  TCAAACTCCTGACCTCAGGTGA 38246
          TC                      GATCACCTGAGGTCAGGAGTTTGA
                                ||||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAACT

GAM382  PRO2964  5'  TCAAACTCCTAACAGCAAGT   38264    C  AG  C
                                AC TG  GT AGGAGTTTGA
                                || ||  || ||||||||||
                                TG AC  CA TCCTCAAACT
                                 A  GA  A
GAM382  PRO2964  5'  TCAAACTCCTAACAGCAAGT   38264    C  AG  C
                                AC TG  GT AGGAGTTTGA
                                || ||  || ||||||||||
                                TG AC  CA TCCTCAAACT
                                 A  GA  A
GAM382  PSTPIP2  3'  TCAAACTCCTGACCTCAGGTGA 44663
          TC                      GATCACCTGAGGTCAGGAGTTTGA
                                ||||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAACT

GAM382  PSTPIP2  3'  TCAAACTCCTGACCTCAGGTGA 44663
          TC                      GATCACCTGAGGTCAGGAGTTTGA
                                ||||||||||||||||||||||||
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                                CTAGTGGACTCCAGTCCTCAAACT

GAM382  RES4-25  3'  TCCCGACCTCAGGTAATC    65276    C       A
                                GAT ACCTGAGGTC GGA
                                ||| |||||||||| |||
                                CTA TGGACTCCAG CCT
                                  A        C
GAM382  RES4-25  3'  TCCCGACCTCAGGTAATC    65276    C       A
                                GAT ACCTGAGGTC GGA
                                ||| |||||||||| |||
                                CTA TGGACTCCAG CCT
                                  A        C
GAM382  RNF8     3'  TCAAATTCCTGACCTTAAGTGA 15576       C
                TC                GATCAC TGAGGTCAGGAGTTTGA
                                  |||||| ||||||||||||||||
                                  CTAGTG ATTCCAGTCCTTAAACT
                                     A
GAM382  RNF8     3'  TCAAATTCCTGACCTTAAGTGA 15576       C
                TC                GATCAC TGAGGTCAGGAGTTTGA
                                  |||||| ||||||||||||||||
                                  CTAGTG ATTCCAGTCCTTAAACT
                                     A
GAM382  SC4MOL   3'  TCAAACTTCTGACCTCAAGTGA 23106       C
                TC                GATCAC TGAGGTCAGGAGTTTGA
                                  |||||| ||||||||||||||||
                                  CTAGTG ACTCCAGTCTTCAAACT
                                     A
GAM382  SC4MOL   3'  TCAAACTTCTGACCTCAAGTGA 23106       C
                TC                GATCAC TGAGGTCAGGAGTTTGA
                                  |||||| ||||||||||||||||
                                  CTAGTG ACTCCAGTCTTCAAACT
                                     A
GAM382  SCAMP-4  3'  TCGAACTCCTGACCTCAAGTGA 55356       C
                TC                GATCAC TGAGGTCAGGAGTTTGA
                                  |||||| ||||||||||||||||
                                  CTAGTG ACTCCAGTCCTCAAGCT
                                     A
GAM382  SCAMP-4  3'  TCGAACTCCTGACCTCAAGTGA 55356       C
                TC                GATCAC TGAGGTCAGGAGTTTGA
                                  |||||| ||||||||||||||||
                                  CTAGTG ACTCCAGTCCTCAAGCT
                                     A
GAM382  SCYA22   3'  TCAAACTCCTGGGCTCAAGCGA 92612     ACC   G
                TC                GATC  TGAG TCAGGAGTTTGA
                                  ||||  |||| ||||||||||||
                                  CTAG  ACTC GGTCCTCAAACT
                                    CGA   G
GAM382  SCYA22   3'  TCAAACTCCTGGGCTCAAGCGA 92612     ACC   G
                TC                GATC  TGAG TCAGGAGTTTGA
                                  ||||  |||| ||||||||||||
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                                CTAG   ACTC GGTCCTCAAACT
                                  CGA    G
GAM382  SCYA22   3'  TCCTGTCCTCAGGTAATC    92613     C       T
                                GAT ACCTGAGG CAGGA
                                ||| |||||||| |||||
                                CTA TGGACTCC GTCCT
                                  A       T
GAM382  SCYA22   3'  TCCTGTCCTCAGGTAATC    92613     C       T
                                GAT ACCTGAGG CAGGA
                                ||| |||||||| |||||
                                CTA TGGACTCC GTCCT
                                  A       T
GAM382  SCYA22   3'  TGAACTCCTGACCTCAAGTGAT 92614       C
          C                      GATCAC TGAGGTCAGGAGTTTG
                                ||||||| ||||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAGT
                                   A
GAM382  SCYA22   3'  TGAACTCCTGACCTCAAGTGAT 92614       C
          C                      GATCAC TGAGGTCAGGAGTTTG
                                ||||||| ||||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAGT
                                   A
GAM382  SFXN2    3'  TCGAACTCCTGACCTCAGGTGA 74385
          TC                     GATCACCTGAGGTCAGGAGTTTGA
                                ||||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAGCT

GAM382  SFXN2    3'  TCGAACTCCTGACCTCAGGTGA 74385
          TC                     GATCACCTGAGGTCAGGAGTTTGA
                                ||||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAGCT

GAM382  SIRPB1   3'  TGAACTCCCGACCTCAGGTGAT 21370             A
          C                      GATCACCTGAGGTC GGAGTTTG
                                |||||||||||||| ||||||||
                                CTAGTGGACTCCAG CCTCAAGT
                                       C
GAM382  SIRPB1   3'  TGAACTCCCGACCTCAGGTGAT 21370             A
          C                      GATCACCTGAGGTC GGAGTTTG
                                |||||||||||||| ||||||||
                                CTAGTGGACTCCAG CCTCAAGT
                                       C
GAM382  SLC19A3  3'  TCAAACTCCTGACTTCAGGTGA 48250
          TC                     GATCACCTGAGGTCAGGAGTTTGA
                                ||||||||||||||||||||||||
                                CTAGTGGACTTCAGTCCTCAAACT

GAM382  SLC19A3  3'  TCAAACTCCTGACTTCAGGTGA 48250
          TC                     GATCACCTGAGGTCAGGAGTTTGA
                                ||||||||||||||||||||||||
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                                CTAGTGGACTTCAGTCCTCAAACT

GAM382  SLC2A10  3'  TGAACTCCTGAGCTCAAGTGAT 48559      C   G
            C                    GATCAC TGAG TCAGGAGTTTG
                                 |||||| |||| ||||||||||
                                 CTAGTG ACTC AGTCCTCAAGT
                                    A   G
GAM382  SLC2A10  3'  TGAACTCCTGAGCTCAAGTGAT 48559      C   G
            C                    GATCAC TGAG TCAGGAGTTTG
                                 |||||| |||| ||||||||||
                                 CTAGTG ACTC AGTCCTCAAGT
                                    A   G
GAM382  SLC6A14  3'  TGAACTCCCGACCTCAAGTGAT 24313      C     A
            C                    GATCAC TGAGGTC GGAGTTTG
                                 |||||| ||||||| ||||||||
                                 CTAGTG ACTCCAG CCTCAAGT
                                    A     C
GAM382  SLC6A14  3'  TGAACTCCCGACCTCAAGTGAT 24313      C     A
            C                    GATCAC TGAGGTC GGAGTTTG
                                 |||||| ||||||| ||||||||
                                 CTAGTG ACTCCAG CCTCAAGT
                                    A     C
GAM382  SPRY4    3'  TCAAACTTCTGGACTCAAGTGA 49031      C   GT
            TC                    GATCAC TGAG  CAGGAGTTTGA
                                  |||||| ||||  ||||||||||
                                  CTAGTG ACTC  GTCTTCAAACT
                                     A   AG
GAM382  SPRY4    3'  TCAAACTTCTGGACTCAAGTGA 49031      C   GT
            TC                    GATCAC TGAG  CAGGAGTTTGA
                                  |||||| ||||  ||||||||||
                                  CTAGTG ACTC  GTCTTCAAACT
                                     A   AG
GAM382  STAF65(gamma) 3'  AAACTCCTGACCTCAAGTGATC 30051      C
                                 GATCAC TGAGGTCAGGAGTTT
                                 |||||| |||||||||||||||
                                 CTAGTG ACTCCAGTCCTCAAA
                                    A
GAM382  STAF65(gamma) 3'  AAACTCCTGACCTCAAGTGATC 30051      C
                                 GATCAC TGAGGTCAGGAGTTT
                                 |||||| |||||||||||||||
                                 CTAGTG ACTCCAGTCCTCAAA
                                    A
GAM382  STAF65(gamma) 3'  AAACTCCTGACCTCAAGTGATC 30052      C
                                 GATCAC TGAGGTCAGGAGTTT
                                 |||||| |||||||||||||||
                                 CTAGTG ACTCCAGTCCTCAAA
                                    A
GAM382  STAF65(gamma) 3'  AAACTCCTGACCTCAAGTGATC 30052      C
                                 GATCAC TGAGGTCAGGAGTTT
                                 |||||| |||||||||||||||
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                                CTAGTG ACTCCAGTCCTCAAA
                                   A
GAM382  TBCC     3'  TCGAACTCCTGACCTCAGGTGA 13606
                TC                  GATCACCTGAGGTCAGGAGTTTGA
                                    ||||||||||||||||||||||||
                                    CTAGTGGACTCCAGTCCTCAAGCT

GAM382  TBCC     3'  TCGAACTCCTGACCTCAGGTGA 13606
                TC                  GATCACCTGAGGTCAGGAGTTTGA
                                    ||||||||||||||||||||||||
                                    CTAGTGGACTCCAGTCCTCAAGCT

GAM382  TCL6     3'  TCAAACTCCTGAGCTCAAGCGA 40493      ACC    G
                TC                  GATC   TGAG TCAGGAGTTTGA
                                    ||||   |||| ||||||||||||
                                    CTAG   ACTC AGTCCTCAAACT
                                      CGA    G
GAM382  TCL6     3'  TCAAACTCCTGAGCTCAAGCGA 40518      ACC    G
                TC                  GATC   TGAG TCAGGAGTTTGA
                                    ||||   |||| ||||||||||||
                                    CTAG   ACTC AGTCCTCAAACT
                                      CGA    G
GAM382  TCL6     3'  TCAAACTCCTGAGCTCAAGCGA 40533      ACC    G
                TC                  GATC   TGAG TCAGGAGTTTGA
                                    ||||   |||| ||||||||||||
                                    CTAG   ACTC AGTCCTCAAACT
                                      CGA    G
GAM382  THEA     3'  TCAAACTCCTGACTTCAAGTGA 66895        C
                TC                  GATCAC TGAGGTCAGGAGTTTGA
                                    ||||||| ||||||||||||||||
                                    CTAGTG ACTTCAGTCCTCAAACT
                                       A
GAM382  THEA     3'  TCAAACTCCTGACTTCAAGTGA 66895        C
                TC                  GATCAC TGAGGTCAGGAGTTTGA
                                    ||||||| ||||||||||||||||
                                    CTAGTG ACTTCAGTCCTCAAACT
                                       A
GAM382  TRIM16   3'  TCAAACTCCTGACCTCGTGAT  22378      CT
                                    ATCAC  GAGGTCAGGAGTTTGA
                                    |||||  ||||||||||||||||
                                    TAGTG  CTCCAGTCCTCAAACT
                                      __
GAM382  TRIM16   3'  TCAAACTCCTGACCTCGTGAT  22378      CT
                                    ATCAC  GAGGTCAGGAGTTTGA
                                    |||||  ||||||||||||||||
                                    TAGTG  CTCCAGTCCTCAAACT
                                      __
GAM382  TRIM35   3'  TCAAACTCATGGGCTCAAGTGA 61518        C   G   G
                TC                  GATCAC TGAG TCA GAGTTTGA
                                    |||||| |||| ||| ||||||||
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                                CTAGTG ACTC GGT CTCAAACT
                                   A   G   A
GAM382  TRIM35   3'  TCAAACTCATGGGCTCAAGTGA 61518       C   G   G
           TC                    GATCAC TGAG TCA GAGTTTGA
                                 |||||| |||| ||| ||||||||
                                 CTAGTG ACTC GGT CTCAAACT
                                   A   G   A
GAM382  TRIM6    3'  TCGAACTCCTGACCGCAAGTGA 55187       C  A
           TC                    GATCAC TG GGTCAGGAGTTTGA
                                 |||||| || ||||||||||||||
                                 CTAGTG AC CCAGTCCTCAAGCT
                                   A  G
GAM382  TRIM6    3'  TCGAACTCCTGACCGCAAGTGA 55187       C  A
           TC                    GATCAC TG GGTCAGGAGTTTGA
                                 |||||| || ||||||||||||||
                                 CTAGTG AC CCAGTCCTCAAGCT
                                   A  G
GAM382  TU12B1-TY 3'  TCAAACTCCTAGCCTCAAGTGT 33862    T   C    TC
           TC                    GA CAC TGAGG  AGGAGTTTGA
                                 || ||| |||||  ||||||||||
                                 CT GTG ACTCC  TCCTCAAACT
                                  T   A    GA
GAM382  TU12B1-TY 3'  TCAAACTCCTAGCCTCAAGTGT 33862    T   C    TC
           TC                    GA CAC TGAGG  AGGAGTTTGA
                                 || ||| |||||  ||||||||||
                                 CT GTG ACTCC  TCCTCAAACT
                                  T   A    GA
GAM382  TU12B1-TY 3'  TCGAACTCCTGACCTCAG    33863
                                 CTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||
                                 GACTCCAGTCCTCAAGCT

GAM382  TU12B1-TY 3'  TCGAACTCCTGACCTCAG    33863
                                 CTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||
                                 GACTCCAGTCCTCAAGCT

GAM382  TUCAN    3'  TCCTGGCCTCAAGTGATC    30990       C
                                 GATCAC TGAGGTCAGGA
                                 |||||| ||||||||||
                                 CTAGTG ACTCCGGTCCT
                                   A
GAM382  TUCAN    3'  TCCTGGCCTCAAGTGATC    30990       C
                                 GATCAC TGAGGTCAGGA
                                 |||||| ||||||||||
                                 CTAGTG ACTCCGGTCCT
                                   A
GAM382  TUSP     3'  TGAACTCCTGACCTCAGGTGAT 40030
           C                      GATCACCTGAGGTCAGGAGTTTG
                                 |||||||||||||||||||||||
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                                CTAGTGGACTCCAGTCCTCAAGT

GAM382  TUSP     3'  TGAACTCCTGACCTCAGGTGAT 40030
                C                GATCACCTGAGGTCAGGAGTTTG
                                 ||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGT

GAM382  UBCE7IP5  3'  TCAAACTCCTGGGCTCAAGCGA 30852     ACC    G
                T                ATC   TGAG TCAGGAGTTTGA
                                 |||   |||| ||||||||||||
                                 TAG   ACTC GGTCCTCAAACT
                                   CGA    G
GAM382  UBCE7IP5  3'  TCAAACTCCTGGGCTCAAGCGA 30852     ACC    G
                T                ATC   TGAG TCAGGAGTTTGA
                                 |||   |||| ||||||||||||
                                 TAG   ACTC GGTCCTCAAACT
                                   CGA    G
GAM382  UBF-fl   3'  TCAAACTCCTGACCTCAAGTGA 52635       C
                TC                 GATCAC TGAGGTCAGGAGTTTGA
                                   |||||| |||||||||||||||||
                                   CTAGTG ACTCCAGTCCTCAAACT
                                      A
GAM382  UBF-fl   3'  TCAAACTCCTGACCTCAAGTGA 52635       C
                TC                 GATCAC TGAGGTCAGGAGTTTGA
                                   |||||| |||||||||||||||||
                                   CTAGTG ACTCCAGTCCTCAAACT
                                      A
GAM382  VDU1     3'  TCAAACTCCTGACCTCAGGTGA 31129
                TC                 GATCACCTGAGGTCAGGAGTTTGA
                                   ||||||||||||||||||||||||
                                   CTAGTGGACTCCAGTCCTCAAACT

GAM382  VDU1     3'  TCAAACTCCTGACCTCAGGTGA 31129
                TC                 GATCACCTGAGGTCAGGAGTTTGA
                                   ||||||||||||||||||||||||
                                   CTAGTGGACTCCAGTCCTCAAACT

GAM382  VPS33A   3'  TCAAACTCCTGACCTCAGGTGA 43616
                TC                 GATCACCTGAGGTCAGGAGTTTGA
                                   ||||||||||||||||||||||||
                                   CTAGTGGACTCCAGTCCTCAAACT

GAM382  VPS33A   3'  TCAAACTCCTGACCTCAGGTGA 43616
                TC                 GATCACCTGAGGTCAGGAGTTTGA
                                   ||||||||||||||||||||||||
                                   CTAGTGGACTCCAGTCCTCAAACT

GAM382  WBSCR23  3'  TCAAACTCCTGACCTCAGGTGA 47442
                TC                 GATCACCTGAGGTCAGGAGTTTGA
                                   ||||||||||||||||||||||||
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                                CTAGTGGACTCCAGTCCTCAAACT

GAM382  WBSCR23  3'  TCAAACTCCTGACCTCAGGTGA 47442
              TC                 GATCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAACT

GAM382  ZNF17    3'  TCAAACTCCCGACCTCAAGTGA 83277      C      A
                                 TCAC TGAGGTC GGAGTTTGA
                                 |||| ||||||| |||||||||
                                 AGTG ACTCCAG CCTCAAACT
                                   A      C
GAM382  ZNF17    3'  TCAAACTCCCGACCTCAAGTGA 83277      C      A
                                 TCAC TGAGGTC GGAGTTTGA
                                 |||| ||||||| |||||||||
                                 AGTG ACTCCAG CCTCAAACT
                                   A      C
GAM382  ZNF177   5'  TCAAACTCCTGCTCTCAAGTGA 14357       C    GT
              TC                 GATCAC TGAG  CAGGAGTTTGA
                                 ||||||| ||||  ||||||||||
                                 CTAGTG ACTC  GTCCTCAAACT
                                    A    TC
GAM382  ZNF177   5'  TCAAACTCCTGCTCTCAAGTGA 14357       C    GT
              TC                 GATCAC TGAG  CAGGAGTTTGA
                                 ||||||| ||||  ||||||||||
                                 CTAGTG ACTC  GTCCTCAAACT
                                    A    TC
GAM382  ZNF338   3'  TGAACTCCTGACCTCAAGTGAT 42262       C
              C                  GATCAC TGAGGTCAGGAGTTTG
                                 ||||||| ||||||||||||||||
                                 CTAGTG ACTCCAGTCCTCAAGT
                                    A
GAM382  ZNF338   3'  TGAACTCCTGACCTCAAGTGAT 42262       C
              C                  GATCAC TGAGGTCAGGAGTTTG
                                 ||||||| ||||||||||||||||
                                 CTAGTG ACTCCAGTCCTCAAGT
                                    A
GAM382  ZTL1     3'  TGAACTCCTGACCTCAGGTGAT 43522
              C                  GATCACCTGAGGTCAGGAGTTTG
                                 ||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGT

GAM382  ZTL1     3'  TGAACTCCTGACCTCAGGTGAT 44143
              C                  GATCACCTGAGGTCAGGAGTTTG
                                 ||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGT

GAM382  LOC112687 3'  CAAACTCCTGACCTCATGTAAT 73221     C  C
              C                  GAT AC TGAGGTCAGGAGTTTG
                                 ||| || ||||||||||||||||
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                                CTA TG ACTCCAGTCCTCAAAC
                                  A  T
GAM382  LOC112687 3'  CAAACTCCTGACCTCATGTAAT 73221     C  C
            C                    GAT AC TGAGGTCAGGAGTTTG
                                 ||| || ||||||||||||||||
                                 CTA TG ACTCCAGTCCTCAAAC
                                   A  T
GAM382  LOC112817 3'  TGAACTCCTGACCTCAGGTGAT 57334
            C                    GATCACCTGAGGTCAGGAGTTTG
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGT

GAM382  LOC112817 3'  TGAACTCCTGACCTCAGGTGAT 57334
            C                    GATCACCTGAGGTCAGGAGTTTG
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGT

GAM382  LOC113026 3'  TCCTGACCTCAAGTGATC    56729       C
                                 GATCAC TGAGGTCAGGA
                                 |||||| ||||||||||
                                 CTAGTG ACTCCAGTCCT
                                    A
GAM382  LOC113026 3'  TCCTGACCTCAAGTGATC    56729       C
                                 GATCAC TGAGGTCAGGA
                                 |||||| ||||||||||
                                 CTAGTG ACTCCAGTCCT
                                    A
GAM382  LOC115219 5'  TCAAACTCCTGACGTCGTGATC 73708       CT  G
                                 GATCAC  GA GTCAGGAGTTTGA
                                 ||||||  || |||||||||||||
                                 CTAGTG  CT CAGTCCTCAAACT
                                    __  G
GAM382  LOC115219 5'  TCAAACTCCTGACGTCGTGATC 73708       CT  G
                                 GATCAC  GA GTCAGGAGTTTGA
                                 ||||||  || |||||||||||||
                                 CTAGTG  CT CAGTCCTCAAACT
                                    __  G
GAM382  LOC115648 3'  TCGAACTCCTGACCTCAGGTGA 60031
            TC                     GATCACCTGAGGTCAGGAGTTTGA
                                   ||||||||||||||||||||||||
                                   CTAGTGGACTCCAGTCCTCAAGCT

GAM382  LOC115648 3'  TCGAACTCCTGACCTCAGGTGA 60031
            TC                     GATCACCTGAGGTCAGGAGTTTGA
                                   ||||||||||||||||||||||||
                                   CTAGTGGACTCCAGTCCTCAAGCT

GAM382  LOC119392 3'  TCGAACTCCTGACCTCAGGTGA 59818
            TC                     GATCACCTGAGGTCAGGAGTTTGA
                                   ||||||||||||||||||||||||
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                                CTAGTGGACTCCAGTCCTCAAGCT

GAM382  LOC119392 3'  TCGAACTCCTGACCTCAGGTGA 59818
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAGCT

GAM382  LOC120114 3'  TCAAACTCCTGACCTCGTAATC 76052     C  CT
                                  GAT AC  GAGGTCAGGAGTTTGA
                                  ||| ||  ||||||||||||||||
                                  CTA TG  CTCCAGTCCTCAAACT
                                    A  __
GAM382  LOC120114 3'  TCAAACTCCTGACCTCGTAATC 76052     C  CT
                                  GAT AC  GAGGTCAGGAGTTTGA
                                  ||| ||  ||||||||||||||||
                                  CTA TG  CTCCAGTCCTCAAACT
                                    A  __
GAM382  LOC120224 5'  TCGAACTCCTGACCTCAGGTGA 57896
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAGCT

GAM382  LOC120224 5'  TCGAACTCCTGACCTCAGGTGA 57896
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAGCT

GAM382  LOC120939 3'  TCCTGACGTCAGGTGATC    76771          G
                                  GATCACCTGA GTCAGGA
                                  |||||||||| |||||||
                                  CTAGTGGACT CAGTCCT
                                        G
GAM382  LOC120939 3'  TCCTGACGTCAGGTGATC    76771          G
                                  GATCACCTGA GTCAGGA
                                  |||||||||| |||||||
                                  CTAGTGGACT CAGTCCT
                                        G
GAM382  LOC124216 3'  TCAAACTCCTGACCTCGTGATC 74741       CT
                                  GATCAC  GAGGTCAGGAGTTTGA
                                  ||||||  ||||||||||||||||
                                  CTAGTG  CTCCAGTCCTCAAACT
                                       __
GAM382  LOC124216 3'  TCAAACTCCTGACCTCGTGATC 74741       CT
                                  GATCAC  GAGGTCAGGAGTTTGA
                                  ||||||  ||||||||||||||||
                                  CTAGTG  CTCCAGTCCTCAAACT
                                       __
GAM382  LOC125194 5'  TCAAACTCCTGGCTTCAAGTGA 74860       C
                TC                GATCAC TGAGGTCAGGAGTTTGA
                                  ||||||  ||||||||||||||||
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                                CTAGTG ACTTCGGTCCTCAAACT
                                   A
GAM382  LOC125194 5'  TCAAACTCCTGGCTTCAAGTGA 74860       C
                TC                GATCAC TGAGGTCAGGAGTTTGA
                                  |||||| ||||||||||||||||
                                CTAGTG ACTTCGGTCCTCAAACT
                                   A
GAM382  LOC126364 3'  TCGAACTCCTGACCTCAAGCGA 76200      ACC
                TC                GATC   TGAGGTCAGGAGTTTGA
                                  ||||   ||||||||||||||||
                                CTAG   ACTCCAGTCCTCAAGCT
                                   CGA
GAM382  LOC126364 3'  TCGAACTCCTGACCTCAAGCGA 76200      ACC
                TC                GATC   TGAGGTCAGGAGTTTGA
                                  ||||   ||||||||||||||||
                                CTAG   ACTCCAGTCCTCAAGCT
                                   CGA
GAM382  LOC126661 3'  TGAACTTCTGACCTCAAGTGAT 75066       C
                C                 GATCAC TGAGGTCAGGAGTTTG
                                  |||||| |||||||||||||||
                                CTAGTG ACTCCAGTCTTCAAGT
                                   A
GAM382  LOC126661 3'  TGAACTTCTGACCTCAAGTGAT 75066       C
                C                 GATCAC TGAGGTCAGGAGTTTG
                                  |||||| |||||||||||||||
                                CTAGTG ACTCCAGTCTTCAAGT
                                   A
GAM382  LOC126669 3'  TCAAACTCCTGACCTCAAATGA 75950      CC
                TC                GATCA  TGAGGTCAGGAGTTTGA
                                  |||||  ||||||||||||||||
                                CTAGT  ACTCCAGTCCTCAAACT
                                   AA
GAM382  LOC126669 3'  TCAAACTCCTGACCTCAAATGA 75950      CC
                TC                GATCA  TGAGGTCAGGAGTTTGA
                                  |||||  ||||||||||||||||
                                CTAGT  ACTCCAGTCCTCAAACT
                                   AA
GAM382  LOC130639 5'  TCGAACTCCTGACCTCAAGTGA 75481       C
                TC                GATCAC TGAGGTCAGGAGTTTGA
                                  |||||| |||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAGCT
                                   A
GAM382  LOC130639 5'  TCGAACTCCTGACCTCAAGTGA 75481       C
                TC                GATCAC TGAGGTCAGGAGTTTGA
                                  |||||| |||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAGCT
                                   A
GAM382  LOC130813 3'  TCCCAACTTCAGGTGATC    76282        CA
                                GATCACCTGAGGT  GGA
                                |||||||||||||  |||
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                                CTAGTGGACTTCA  CCT
                                       AC
GAM382  LOC130813 3'  TCCCAACTTCAGGTGATC    76282           CA
                                GATCACCTGAGGT  GGA
                                |||||||||||||  |||
                                CTAGTGGACTTCA  CCT
                                       AC
GAM382  LOC132625 3'  TCAAACTCCTGACCTCCAGTGA 76445       CT
           TC                     GATCAC  GAGGTCAGGAGTTTGA
                                |||||||  ||||||||||||||||
                                CTAGTG  CTCCAGTCCTCAAACT
                                   AC
GAM382  LOC132625 3'  TCAAACTCCTGACCTCCAGTGA 76445       CT
           TC                     GATCAC  GAGGTCAGGAGTTTGA
                                |||||||  ||||||||||||||||
                                CTAGTG  CTCCAGTCCTCAAACT
                                   AC
GAM382  LOC135154 3'  TCGAACTCCTGACCTCAGTTGA 75737       C
           TC                     GATCA CTGAGGTCAGGAGTTTGA
                                |||||| ||||||||||||||||||
                                CTAGT GACTCCAGTCCTCAAGCT
                                   T
GAM382  LOC135154 3'  TCGAACTCCTGACCTCAGTTGA 75737       C
           TC                     GATCA CTGAGGTCAGGAGTTTGA
                                |||||| ||||||||||||||||||
                                CTAGT GACTCCAGTCCTCAAGCT
                                   T
GAM382  LOC135818 3'  TGAACTCCTGACCTCAGGTGAT 75750
           C                      GATCACCTGAGGTCAGGAGTTTG
                                |||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAGT

GAM382  LOC135818 3'  TGAACTCCTGACCTCAGGTGAT 75750
           C                      GATCACCTGAGGTCAGGAGTTTG
                                |||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAGT

GAM382  LOC138199 3'  TCAAACTCCTGGACTCAAGCGA 75828      ACC   GT
           TC                     GATC   TGAG  CAGGAGTTTGA
                                ||||   ||||  ||||||||||||
                                CTAG   ACTC  GTCCTCAAACT
                                  CGA    AG
GAM382  LOC138199 3'  TCAAACTCCTGGACTCAAGCGA 75828      ACC   GT
           TC                     GATC   TGAG  CAGGAGTTTGA
                                ||||   ||||  ||||||||||||
                                CTAG   ACTC  GTCCTCAAACT
                                  CGA    AG
GAM382  LOC142927 5'  TCAAACTCCTGGCCTCAAGTGA 76951       C
           TC                     GATCAC TGAGGTCAGGAGTTTGA
                                |||||| ||||||||||||||||||
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                                CTAGTG ACTCCGGTCCTCAAACT
                                   A
GAM382  LOC142927 5'  TCAAACTCCTGGCCTCAAGTGA 76951       C
                TC                GATCAC TGAGGTCAGGAGTTTGA
                                  |||||| ||||||||||||||||
                                  CTAGTG ACTCCGGTCCTCAAACT
                                     A
GAM382  LOC143916 3'  TCAAACTTCTGACCTCAGGTGA 77144
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCTTCAAACT

GAM382  LOC143916 3'  TCAAACTTCTGACCTCAGGTGA 77144
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCTTCAAACT

GAM382  LOC144317 5'  TCGAACTCCTGACCTCAGGTGA 77298
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAGCT

GAM382  LOC144317 5'  TCGAACTCCTGACCTCAGGTGA 77298
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAGCT

GAM382  LOC144519 3'  TCCTGACCTGAAGCGATC    77381     AC  G_
                                  GATC  CT  AGGTCAGGA
                                  ||||  ||  |||||||||
                                  CTAG  GA  TCCAGTCCT
                                    C_  AG
GAM382  LOC144519 3'  TCCTGACCTGAAGCGATC    77381     AC  G_
                                  GATC  CT  AGGTCAGGA
                                  ||||  ||  |||||||||
                                  CTAG  GA  TCCAGTCCT
                                    C_  AG
GAM382  LOC144524 5'  TCAAACTCCTGAACTCAGGTGA 84065          G
                TC                GATCACCTGAG TCAGGAGTTTGA
                                  |||||||||| ||||||||||
                                  CTAGTGGACTC AGTCCTCAAACT
                                        A
GAM382  LOC144524 5'  TCAAACTCCTGAACTCAGGTGA 84065          G
                TC                GATCACCTGAG TCAGGAGTTTGA
                                  |||||||||| ||||||||||
                                  CTAGTGGACTC AGTCCTCAAACT
                                        A
GAM382  LOC144742 5'  TCATGGCCTCAAATGATC    77468     CC      G
                                  GATCA  TGAGGTCA GA
                                  |||||  |||||||| ||
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                                CTAGT  ACTCCGGT CT
                                  AA       A
GAM382  LOC144742 5'  TCATGGCCTCAAATGATC    77468       CC       G
                                GATCA  TGAGGTCA GA
                                |||||  |||||||| ||
                                CTAGT  ACTCCGGT CT
                                  AA       A
GAM382  LOC145082 5'  TCAAACTCCTGGGCTCAAGGGA 84197      A  _  G
          TC                      GATC CCT GAG TCAGGAGTTTGA
                                |||| ||| ||| ||||||||||||
                                CTAG GGA CTC GGTCCTCAAACT
                                  _  A  G
GAM382  LOC145082 5'  TCAAACTCCTGGGCTCAAGGGA 84197      A  _  G
          TC                      GATC CCT GAG TCAGGAGTTTGA
                                |||| ||| ||| ||||||||||||
                                CTAG GGA CTC GGTCCTCAAACT
                                  _  A  G
GAM382  LOC145268 5'  TCGAACTCCTAACCTCGGGTGA 77587            C
          TC                      GATCACCTGAGGT AGGAGTTTGA
                                |||||||||||| ||||||||||
                                CTAGTGGGCTCCA TCCTCAAGCT
                                       A
GAM382  LOC145268 5'  TCGAACTCCTAACCTCGGGTGA 77587            C
          TC                      GATCACCTGAGGT AGGAGTTTGA
                                |||||||||||| ||||||||||
                                CTAGTGGGCTCCA TCCTCAAGCT
                                       A
GAM382  LOC145453 5'  TCAAACTCCTGACCTCAAGGAT 77669      ACC
          C                       GATC   TGAGGTCAGGAGTTTGA
                                ||||   ||||||||||||||||
                                CTAG   ACTCCAGTCCTCAAACT
                                  GA_
GAM382  LOC145453 5'  TCAAACTCCTGACCTCAAGGAT 77669      ACC
          C                       GATC   TGAGGTCAGGAGTTTGA
                                ||||   ||||||||||||||||
                                CTAG   ACTCCAGTCCTCAAACT
                                  GA_
GAM382  LOC145873 5'  TCGAACTCCTGAACTCAAGTAA 78014     C  C    G
          TC                      GAT AC TGAG TCAGGAGTTTGA
                                |||  ||  ||||  ||||||||||||
                                CTA TG ACTC AGTCCTCAAGCT
                                  A  A    A
GAM382  LOC145873 5'  TCGAACTCCTGAACTCAAGTAA 78014     C  C    G
          TC                      GAT AC TGAG TCAGGAGTTTGA
                                |||  ||  ||||  ||||||||||||
                                CTA TG ACTC AGTCCTCAAGCT
                                  A  A    A
GAM382  LOC146050 3'  TCAAACTCCCGACCTCAGGTGA 78126            A
          TC                      GATCACCTGAGGTC GGAGTTTGA
                                |||||||||||||| |||||||||
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                                CTAGTGGACTCCAG CCTCAAACT
                                      C
GAM382  LOC146050 3'  TCAAACTCCCGACCTCAGGTGA 78126            A
          TC                    GATCACCTGAGGTC GGAGTTTGA
                                |||||||||||||| |||||||||
                                CTAGTGGACTCCAG CCTCAAACT
                                      C
GAM382  LOC146229 3'  TCAAACTCCTGACCTCAAGTGA 78313       C
          TC                    GATCAC TGAGGTCAGGAGTTTGA
                                |||||| ||||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAACT
                                   A
GAM382  LOC146229 3'  TCAAACTCCTGACCTCAAGTGA 78313       C
          TC                    GATCAC TGAGGTCAGGAGTTTGA
                                |||||| ||||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAACT
                                   A
GAM382  LOC146229 3'  TCAAACTCCTGACCTCAGGTGA 78314
          TC                    GATCACCTGAGGTCAGGAGTTTGA
                                |||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAACT

GAM382  LOC146229 3'  TCAAACTCCTGACCTCAGGTGA 78314
          TC                    GATCACCTGAGGTCAGGAGTTTGA
                                |||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAACT

GAM382  LOC146229 3'  TCAAACTCCTGACTTCAAATGA 78315      CC
          TC                    GATCA  TGAGGTCAGGAGTTTGA
                                |||||  ||||||||||||||||
                                CTAGT  ACTTCAGTCCTCAAACT
                                   AA
GAM382  LOC146229 3'  TCAAACTCCTGACTTCAAATGA 78315      CC
          TC                    GATCA  TGAGGTCAGGAGTTTGA
                                |||||  ||||||||||||||||
                                CTAGT  ACTTCAGTCCTCAAACT
                                   AA
GAM382  LOC146894 3'  TGAACTCCTGACCTCAAATGA  59867     CC
                                TCA  TGAGGTCAGGAGTTTG
                                |||  ||||||||||||||||
                                AGT  ACTCCAGTCCTCAAGT
                                   AA
GAM382  LOC146894 3'  TGAACTCCTGACCTCAAATGA  59867     CC
                                TCA  TGAGGTCAGGAGTTTG
                                |||  ||||||||||||||||
                                AGT  ACTCCAGTCCTCAAGT
                                   AA
GAM382  LOC146901 3'  TCGAACTCCTGACCTCAGGTGA 84914
          TC                    GATCACCTGAGGTCAGGAGTTTGA
                                |||||||||||||||||||||||
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                                CTAGTGGACTCCAGTCCTCAAGCT

GAM382  LOC146901 3'  TCGAACTCCTGACCTCAGGTGA 84914
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAGCT

GAM382  LOC146909 3'  TGAACTCCTGACCTCAGGTGAT 78784
                C                 GATCACCTGAGGTCAGGAGTTTG
                                  |||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAGT

GAM382  LOC146909 3'  TGAACTCCTGACCTCAGGTGAT 78784
                C                 GATCACCTGAGGTCAGGAGTTTG
                                  |||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAGT

GAM382  LOC146952 5'  TCAAACTCCTGACCTCAGATGA 84936      C
                TC                GATCA CTGAGGTCAGGAGTTTGA
                                  ||||| ||||||||||||||||||
                                  CTAGT GACTCCAGTCCTCAAACT
                                    A
GAM382  LOC146952 5'  TCAAACTCCTGACCTCAGATGA 84936      C
                TC                GATCA CTGAGGTCAGGAGTTTGA
                                  ||||| ||||||||||||||||||
                                  CTAGT GACTCCAGTCCTCAAACT
                                    A
GAM382  LOC147054 3'  TCGAACTCCCGATCTCAGGTGA 85011            A
                TC                GATCACCTGAGGTC GGAGTTTGA
                                  |||||||||||||| |||||||||
                                  CTAGTGGACTCTAG CCTCAAGCT
                                        C
GAM382  LOC147054 3'  TCGAACTCCCGATCTCAGGTGA 85011            A
                TC                GATCACCTGAGGTC GGAGTTTGA
                                  |||||||||||||| |||||||||
                                  CTAGTGGACTCTAG CCTCAAGCT
                                        C
GAM382  LOC147276 3'  GAACTCCTGACCTCAAGTGATC 78960       C
                                  GATCAC TGAGGTCAGGAGTTT
                                  ||||||| ||||||||||||||
                                  CTAGTG ACTCCAGTCCTCAAG
                                    A
GAM382  LOC147276 3'  GAACTCCTGACCTCAAGTGATC 78960       C
                                  GATCAC TGAGGTCAGGAGTTT
                                  ||||||| ||||||||||||||
                                  CTAGTG ACTCCAGTCCTCAAG
                                    A
GAM382  LOC147407 5'  CAAACTCCAGGCTCAGATGAT  76819      C    G  A
                                  ATCA CTGAG TC GGAGTTTG
                                  |||| ||||| || ||||||||
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                                TAGT GACTC GG CCTCAAAC
                                  A    _  A
GAM382  LOC147407 5'  CAAACTCCAGGCTCAGATGAT  76819     C    G  A
                                ATCA CTGAG TC GGAGTTTG
                                |||| ||||| || ||||||||
                                TAGT GACTC GG CCTCAAAC
                                  A    _  A
GAM382  LOC147817 3'  TCAAACTCCTGGCTTCAAGTGA 79193       C
          TC                    GATCAC TGAGGTCAGGAGTTTGA
                                |||||| ||||||||||||||||
                                CTAGTG ACTTCGGTCCTCAAACT
                                  A
GAM382  LOC147817 3'  TCAAACTCCTGGCTTCAAGTGA 79193       C
          TC                    GATCAC TGAGGTCAGGAGTTTGA
                                |||||| ||||||||||||||||
                                CTAGTG ACTTCGGTCCTCAAACT
                                  A
GAM382  LOC147817 3'  TCATGACCTCAAGTGATC    79194       C      G
                                GATCAC TGAGGTCA GA
                                |||||| |||||||| ||
                                CTAGTG ACTCCAGT CT
                                  A       A
GAM382  LOC147817 3'  TCATGACCTCAAGTGATC    79194       C      G
                                GATCAC TGAGGTCA GA
                                |||||| |||||||| ||
                                CTAGTG ACTCCAGT CT
                                  A       A
GAM382  LOC147817 3'  TCCTGGCCTCAAGCGATC    79195     ACC
                                GATC   TGAGGTCAGGA
                                ||||   ||||||||||
                                CTAG   ACTCCGGTCCT
                                  CGA
GAM382  LOC147817 3'  TCCTGGCCTCAAGCGATC    79195     ACC
                                GATC   TGAGGTCAGGA
                                ||||   ||||||||||
                                CTAG   ACTCCGGTCCT
                                  CGA
GAM382  LOC147841 3'  TGAACTCCTGACCTCAGGTGAT 79232
          C                     GATCACCTGAGGTCAGGAGTTTG
                                ||||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAGT

GAM382  LOC147841 3'  TGAACTCCTGACCTCAGGTGAT 79232
          C                     GATCACCTGAGGTCAGGAGTTTG
                                ||||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAGT

GAM382  LOC147935 3'  TCAAACTCCTGGGCTCAAGTGA 85204       C   G
          TC                    GATCAC TGAG TCAGGAGTTTGA
                                |||||| |||| ||||||||||||
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                                CTAGTG ACTC GGTCCTCAAACT
                                   A   G
GAM382   LOC147935 3'  TCAAACTCCTGGGCTCAAGTGA 85204       C   G
            TC                   GATCAC TGAG TCAGGAGTTTGA
                                 |||||| |||| ||||||||||||
                                 CTAGTG ACTC GGTCCTCAAACT
                                   A   G
GAM382   LOC148195 3'  TGAACTCCTGACCTCAGGTGA  85293
                                 TCACCTGAGGTCAGGAGTTTG
                                 |||||||||||||||||||||
                                 AGTGGACTCCAGTCCTCAAGT

GAM382   LOC148195 3'  TGAACTCCTGACCTCAGGTGA  85293
                                 TCACCTGAGGTCAGGAGTTTG
                                 |||||||||||||||||||||
                                 AGTGGACTCCAGTCCTCAAGT

GAM382   LOC148645 5'  TCAAACTCCTGGGCTCAGGCCA 85339     CA     G
            TC                   GAT  CCTGAG TCAGGAGTTTGA
                                 |||  |||||| ||||||||||||
                                 CTA  GGACTC GGTCCTCAAACT
                                   CC     G
GAM382   LOC148645 5'  TCAAACTCCTGGGCTCAGGCCA 85339     CA     G
            TC                   GAT  CCTGAG TCAGGAGTTTGA
                                 |||  |||||| ||||||||||||
                                 CTA  GGACTC GGTCCTCAAACT
                                   CC     G
GAM382   LOC148709 3'  TCAAACTCCCGACCTTAGGTGA 79701            A
            T                     ATCACCTGAGGTC GGAGTTTGA
                                 |||||||||||||| |||||||||
                                 TAGTGGATTCCAG CCTCAAACT
                                         C
GAM382   LOC148709 3'  TCAAACTCCCGACCTTAGGTGA 79701            A
            T                     ATCACCTGAGGTC GGAGTTTGA
                                 |||||||||||||| |||||||||
                                 TAGTGGATTCCAG CCTCAAACT
                                         C
GAM382   LOC148918 5'  TCGAACTCCTGACCTCAGGTGA 79832
            TC                   GATCACCTGAGGTCAGGAGTTTGA
                                 |||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGCT

GAM382   LOC148918 5'  TCGAACTCCTGACCTCAGGTGA 79832
            TC                   GATCACCTGAGGTCAGGAGTTTGA
                                 |||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGCT

GAM382   LOC149171 5'  TCGAACTTCTGACCTCAGGTGA 79970
            TC                   GATCACCTGAGGTCAGGAGTTTGA
                                 |||||||||||||||||||||||
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                                CTAGTGGACTCCAGTCTTCAAGCT

GAM382  LOC149171 5'  TCGAACTTCTGACCTCAGGTGA 79970
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCTTCAAGCT

GAM382  LOC149577 3'  TCCTGACCTCAAGTGATC    85681       C
                                  GATCAC TGAGGTCAGGA
                                  |||||| ||||||||||
                                  CTAGTG ACTCCAGTCCT
                                     A
GAM382  LOC149577 3'  TCCTGACCTCAAGTGATC    85681       C
                                  GATCAC TGAGGTCAGGA
                                  |||||| ||||||||||
                                  CTAGTG ACTCCAGTCCT
                                     A
GAM382  LOC149577 3'  TCGAACTCCTGACCTCAAGTGA 85682       C
                TC                GATCAC TGAGGTCAGGAGTTTGA
                                  |||||| ||||||||||||||||
                                  CTAGTG ACTCCAGTCCTCAAGCT
                                     A
GAM382  LOC149577 3'  TCGAACTCCTGACCTCAAGTGA 85682       C
                TC                GATCAC TGAGGTCAGGAGTTTGA
                                  |||||| ||||||||||||||||
                                  CTAGTG ACTCCAGTCCTCAAGCT
                                     A
GAM382  LOC149692 3'  TCAAAGTCCTGACCTCAGGTGA 85746                G
                TC                GATCACCTGAGGTCAGGA TTTGA
                                  |||||||||||||||| |||||
                                  CTAGTGGACTCCAGTCCT AAACT
                                           G
GAM382  LOC149692 3'  TCAAAGTCCTGACCTCAGGTGA 85746                G
                TC                GATCACCTGAGGTCAGGA TTTGA
                                  |||||||||||||||| |||||
                                  CTAGTGGACTCCAGTCCT AAACT
                                           G
GAM382  LOC149692 3'  TCGAACTCCTGACCTCAGGTGA 85747
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAGCT

GAM382  LOC149692 3'  TCGAACTCCTGACCTCAGGTGA 85747
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAGCT

GAM382  LOC149711 3'  CAAACTCCTGACCTCAGGTGAT 85841
                C                  GATCACCTGAGGTCAGGAGTTTG
                                   |||||||||||||||||||||||
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                                CTAGTGGACTCCAGTCCTCAAAC

GAM382  LOC149711 3'  CAAACTCCTGACCTCAGGTGAT 85841
                C                GATCACCTGAGGTCAGGAGTTTG
                                 ||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAAC

GAM382  LOC150225 3'  TCAAACTCCTGACCTCAGATGA 86204      C
                TT                GATCA CTGAGGTCAGGAGTTTGA
                                  ||||| ||||||||||||||||||
                                  TTAGT GACTCCAGTCCTCAAACT
                                    A
GAM382  LOC150225 3'  TCAAACTCCTGACCTCAGATGA 86204      C
                TT                GATCA CTGAGGTCAGGAGTTTGA
                                  ||||| ||||||||||||||||||
                                  TTAGT GACTCCAGTCCTCAAACT
                                    A
GAM382  LOC150282 5'  TGAACTCCTGACCTCAGGTGAT 80546
                C                GATCACCTGAGGTCAGGAGTTTG
                                 ||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGT

GAM382  LOC150282 5'  TGAACTCCTGACCTCAGGTGAT 80546
                C                GATCACCTGAGGTCAGGAGTTTG
                                 ||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGT

GAM382  LOC150397 3'  TGAACCCCTGACCTCAGGTGAT 80668              A
                C                GATCACCTGAGGTCAGG GTTTG
                                 |||||||||||||||| |||||
                                 CTAGTGGACTCCAGTCC CAAGT
                                           C
GAM382  LOC150397 3'  TGAACCCCTGACCTCAGGTGAT 80668              A
                C                GATCACCTGAGGTCAGG GTTTG
                                 |||||||||||||||| |||||
                                 CTAGTGGACTCCAGTCC CAAGT
                                           C
GAM382  LOC150407 3'  TCAAACTCCTGGGCTCAAGTAA 80644     C  C    G
                TC                GAT AC TGAG TCAGGAGTTTGA
                                  ||| || |||| ||||||||||||
                                  CTA TG ACTC GGTCCTCAAACT
                                    A  A    G
GAM382  LOC150407 3'  TCAAACTCCTGGGCTCAAGTAA 80644     C  C    G
                TC                GAT AC TGAG TCAGGAGTTTGA
                                  ||| || |||| ||||||||||||
                                  CTA TG ACTC GGTCCTCAAACT
                                    A  A    G
GAM382  LOC150587 3'  TCAAACTCCTGGGCTCAAGCGA 86246      ACC    G
                TC                GATC   TGAG TCAGGAGTTTGA
                                  ||||   |||| ||||||||||||
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                                CTAG   ACTC GGTCCTCAAACT
                                  CGA    G
GAM382   LOC150587 3'  TCAAACTCCTGGGCTCAAGCGA 86246      ACC    G
           TC                     GATC   TGAG TCAGGAGTTTGA
                                  ||||   |||| ||||||||||||
                                CTAG   ACTC GGTCCTCAAACT
                                  CGA    G
GAM382   LOC150960 3'  TCAAATTCCTGACCTCAGGTGA 80878
           TC                     GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTTAAACT

GAM382   LOC150960 3'  TCAAATTCCTGACCTCAGGTGA 80878
           TC                     GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTTAAACT

GAM382   LOC151475 5'  TCAAACTCCTGACCTTAGGTGA 86605
           TC                     GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                CTAGTGGATTCCAGTCCTCAAACT

GAM382   LOC151475 5'  TCAAACTCCTGACCTTAGGTGA 86605
           TC                     GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                CTAGTGGATTCCAGTCCTCAAACT

GAM382   LOC151701 3'  TCGAACTCCTGACCTCAGATGA 86681       C
           TC                     GATCA CTGAGGTCAGGAGTTTGA
                                  ||||| ||||||||||||||||||
                                CTAGT GACTCCAGTCCTCAAGCT
                                   A
GAM382   LOC151701 3'  TCGAACTCCTGACCTCAGATGA 86681       C
           TC                     GATCA CTGAGGTCAGGAGTTTGA
                                  ||||| ||||||||||||||||||
                                CTAGT GACTCCAGTCCTCAAGCT
                                   A
GAM382   LOC151826 3'  TCCTGACATCAGGTGATC     81188          G
                                GATCACCTGA GTCAGGA
                                |||||||||| |||||||
                                CTAGTGGACT CAGTCCT
                                     A
GAM382   LOC151826 3'  TCCTGACATCAGGTGATC     81188          G
                                GATCACCTGA GTCAGGA
                                |||||||||| |||||||
                                CTAGTGGACT CAGTCCT
                                     A
GAM382   LOC152137 3'  TCGAACCCCTGACCTCAAGTGA 81325       C        A
           TC                     GATCAC TGAGGTCAGG GTTTGA
                                  |||||| |||||||||| ||||||
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                                CTAGTG ACTCCAGTCC CAAGCT
                                   A         C
GAM382  LOC152137 3'  TCGAACCCCTGACCTCAAGTGA 81325       C         A
                TC                  GATCAC TGAGGTCAGG GTTTGA
                                    |||||| |||||||||| ||||||
                                CTAGTG ACTCCAGTCC CAAGCT
                                   A         C
GAM382  LOC152794 5'  TGAACTCCTGACCTCAGGTGAT 81564
                C                   GATCACCTGAGGTCAGGAGTTTG
                                    ||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAGT

GAM382  LOC152794 5'  TGAACTCCTGACCTCAGGTGAT 81564
                C                   GATCACCTGAGGTCAGGAGTTTG
                                    ||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAGT

GAM382  LOC152851 3'  TCGAACTCCTGATCTCAGGTGA 81597
                TC                  GATCACCTGAGGTCAGGAGTTTGA
                                    ||||||||||||||||||||||
                                CTAGTGGACTCTAGTCCTCAAGCT

GAM382  LOC152851 3'  TCGAACTCCTGATCTCAGGTGA 81597
                TC                  GATCACCTGAGGTCAGGAGTTTGA
                                    ||||||||||||||||||||||
                                CTAGTGGACTCTAGTCCTCAAGCT

GAM382  LOC153077 3'  TGAACTCCTGACCTCAGGTGAT 87134
                C                   GATCACCTGAGGTCAGGAGTTTG
                                    |||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAGT

GAM382  LOC153077 3'  TGAACTCCTGACCTCAGGTGAT 87134
                C                   GATCACCTGAGGTCAGGAGTTTG
                                    |||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAGT

GAM382  LOC153443 3'  TCAAACTCCTGGGCTCAAGTGA 81691       C   G
                TC                  GATCAC TGAG TCAGGAGTTTGA
                                    |||||| |||| ||||||||||||
                                CTAGTG ACTC GGTCCTCAAACT
                                   A   G
GAM382  LOC153443 3'  TCAAACTCCTGGGCTCAAGTGA 81691       C   G
                TC                  GATCAC TGAG TCAGGAGTTTGA
                                    |||||| |||| ||||||||||||
                                CTAGTG ACTC GGTCCTCAAACT
                                   A   G
GAM382  LOC153688 3'  TCGAACTCCCAACCTCAGGTGA 87336           CA
                TC                  GATCACCTGAGGT  GGAGTTTGA
                                    ||||||||||||  |||||||||
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                                CTAGTGGACTCCA  CCTCAAGCT
                                      AC
GAM382  LOC153688 3'  TCGAACTCCCAACCTCAGGTGA 87336          CA
          TC                    GATCACCTGAGGT  GGAGTTTGA
                                ||||||||||||  |||||||||
                                CTAGTGGACTCCA  CCTCAAGCT
                                      AC
GAM382  LOC153811 3'  TCAAACTCCTGACCTCAAATGA 81852      CC
          TC                    GATCA  TGAGGTCAGGAGTTTGA
                                |||||  ||||||||||||||||
                                CTAGT  ACTCCAGTCCTCAAACT
                                  AA
GAM382  LOC153811 3'  TCAAACTCCTGACCTCAAATGA 81852      CC
          TC                    GATCA  TGAGGTCAGGAGTTTGA
                                |||||  ||||||||||||||||
                                CTAGT  ACTCCAGTCCTCAAACT
                                  AA
GAM382  LOC153811 3'  TCAAACTCCTGGGCTCCAGTGA 81853     CT  G
                                TCAC  GAG TCAGGAGTTTGA
                                ||||  ||| ||||||||||||
                                AGTG  CTC GGTCCTCAAACT
                                  AC  G
GAM382  LOC153811 3'  TCAAACTCCTGGGCTCCAGTGA 81853     CT  G
                                TCAC  GAG TCAGGAGTTTGA
                                ||||  ||| ||||||||||||
                                AGTG  CTC GGTCCTCAAACT
                                  AC  G
GAM382  LOC153883 5'  TGAACTCCTGACCTCAAGTGAT 81896      C
          C                     GATCAC TGAGGTCAGGAGTTTG
                                ||||||| |||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAGT
                                   A
GAM382  LOC153883 5'  TGAACTCCTGACCTCAAGTGAT 81896      C
          C                     GATCAC TGAGGTCAGGAGTTTG
                                ||||||| |||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAGT
                                   A
GAM382  LOC154007 3'  TCAAACTCCTAGGCTCAGGCGA 81931     A    G  _
          TC                    GATC CCTGAG TC AGGAGTTTGA
                                |||| |||||| || ||||||||||
                                CTAG GGACTC GG TCCTCAAACT
                                  C    _  A
GAM382  LOC154007 3'  TCAAACTCCTAGGCTCAGGCGA 81931     A    G  _
          TC                    GATC CCTGAG TC AGGAGTTTGA
                                |||| |||||| || ||||||||||
                                CTAG GGACTC GG TCCTCAAACT
                                  C    _  A
GAM382  LOC154726 3'  TCAAACTCCTGGGCTCAGATGA 82014     C    G
          TC                    GATCA CTGAG TCAGGAGTTTGA
                                ||||| ||||| ||||||||||||
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                                CTAGT GACTC GGTCCTCAAACT
                                  A     G
GAM382  LOC154726 3'  TCAAACTCCTGGGCTCAGATGA 82014      C     G
          TC                    GATCA CTGAG TCAGGAGTTTGA
                                |||||| ||||| ||||||||||||
                                CTAGT GACTC GGTCCTCAAACT
                                  A     G
GAM382  LOC154877 3'  TCAAACTCCTGGGCTCAAGTGA 87575       C    G
          TC                    GATCAC TGAG TCAGGAGTTTGA
                                |||||| |||| ||||||||||||
                                CTAGTG ACTC GGTCCTCAAACT
                                  A    G
GAM382  LOC154877 3'  TCAAACTCCTGGGCTCAAGTGA 87575       C    G
          TC                    GATCAC TGAG TCAGGAGTTTGA
                                |||||| |||| ||||||||||||
                                CTAGTG ACTC GGTCCTCAAACT
                                  A    G
GAM382  LOC154877 3'  TCGAACTCCCGACCTCAGGTGA 87578             A
          TC                    GATCACCTGAGGTC GGAGTTTGA
                                |||||||||||||| |||||||||
                                CTAGTGGACTCCAG CCTCAAGCT
                                       C
GAM382  LOC154877 3'  TCGAACTCCCGACCTCAGGTGA 87578             A
          TC                    GATCACCTGAGGTC GGAGTTTGA
                                |||||||||||||| |||||||||
                                CTAGTGGACTCCAG CCTCAAGCT
                                       C
GAM382  LOC154877 5'  TGAACTCCTGAGCTCAGGTGAT 87580           G
          C                     GATCACCTGAG TCAGGAGTTTG
                                |||||||||| ||||||||||
                                CTAGTGGACTC AGTCCTCAAGT
                                      G
GAM382  LOC154877 5'  TGAACTCCTGAGCTCAGGTGAT 87580           G
          C                     GATCACCTGAG TCAGGAGTTTG
                                |||||||||| ||||||||||
                                CTAGTGGACTC AGTCCTCAAGT
                                      G
GAM382  LOC155372 3'  AACTCCTGACCTCAGGTGATC  82254
                                GATCACCTGAGGTCAGGAGTT
                                |||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAA

GAM382  LOC155372 3'  AACTCCTGACCTCAGGTGATC  82254
                                GATCACCTGAGGTCAGGAGTT
                                |||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAA

GAM382  LOC157247 5'  TCGAACTCCTGACCTCAGGTGA 82308
          TC                    GATCACCTGAGGTCAGGAGTTTGA
                                ||||||||||||||||||||||||
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                                CTAGTGGACTCCAGTCCTCAAGCT

GAM382  LOC157247 5'  TCGAACTCCTGACCTCAGGTGA 82308
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAGCT

GAM382  LOC157858 5'  TCAAACTCCTGACCTCTGGTGA 87897       T
                TC                GATCACC GAGGTCAGGAGTTTGA
                                  |||||||  ||||||||||||||||
                                  CTAGTGG CTCCAGTCCTCAAACT
                                     T
GAM382  LOC157858 5'  TCAAACTCCTGACCTCTGGTGA 87897       T
                TC                GATCACC GAGGTCAGGAGTTTGA
                                  |||||||  ||||||||||||||||
                                  CTAGTGG CTCCAGTCCTCAAACT
                                     T
GAM382  LOC158310 5'  TCCTGACCTTAAGTGATC    88092       C
                                  GATCAC TGAGGTCAGGA
                                  ||||||  ||||||||||
                                  CTAGTG ATTCCAGTCCT
                                     A
GAM382  LOC158310 5'  TCCTGACCTTAAGTGATC    88092       C
                                  GATCAC TGAGGTCAGGA
                                  ||||||  ||||||||||
                                  CTAGTG ATTCCAGTCCT
                                     A
GAM382  LOC158476 3'  TGAACTCCTGACCCCAGGTGAT 88208         A
                C                  GATCACCTG GGTCAGGAGTTTG
                                   |||||||||  ||||||||||||
                                   CTAGTGGAC CCAGTCCTCAAGT
                                      C
GAM382  LOC158476 3'  TGAACTCCTGACCCCAGGTGAT 88208         A
                C                  GATCACCTG GGTCAGGAGTTTG
                                   |||||||||  ||||||||||||
                                   CTAGTGGAC CCAGTCCTCAAGT
                                      C
GAM382  LOC158629 5'  CAAACTCCTGGGCTCAAGTGAT 88240      C   G
                                  ATCAC TGAG TCAGGAGTTTG
                                  |||||  ||||  ||||||||||
                                  TAGTG ACTC GGTCCTCAAAC
                                     A   G
GAM382  LOC158629 5'  CAAACTCCTGGGCTCAAGTGAT 88240      C   G
                                  ATCAC TGAG TCAGGAGTTTG
                                  |||||  ||||  ||||||||||
                                  TAGTG ACTC GGTCCTCAAAC
                                     A   G
GAM382  LOC160646 3'  TCCTGACCTTCAGGTGATC   83123          _
                                  GATCACCTGA GGTCAGGA
                                  ||||||||||  ||||||||
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                                CTAGTGGACT CCAGTCCT
                                      T
GAM382  LOC160646 3'  TCCTGACCTTCAGGTGATC    83123          _
                                GATCACCTGA GGTCAGGA
                                |||||||||| ||||||||
                                CTAGTGGACT CCAGTCCT
                                      T
GAM382  LOC162427 3'  TCAAACTCCTGACCTCAAGTGA 83231      C
                                TCAC TGAGGTCAGGAGTTTGA
                                |||| ||||||||||||||||
                                AGTG ACTCCAGTCCTCAAACT
                                  A
GAM382  LOC162427 3'  TCAAACTCCTGACCTCAAGTGA 83231      C
                                TCAC TGAGGTCAGGAGTTTGA
                                |||| ||||||||||||||||
                                AGTG ACTCCAGTCCTCAAACT
                                  A
GAM382  LOC169611 3'  TCAAACTCCTGACCTCAGGTGA 83662
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                |||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAACT

GAM382  LOC169611 3'  TCAAACTCCTGACCTCAGGTGA 83662
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                |||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAACT

GAM382  LOC169611 3'  TCCTGACCTTAGGTGATC    83665
                                GATCACCTGAGGTCAGGA
                                ||||||||||||||||
                                CTAGTGGATTCCAGTCCT

GAM382  LOC169611 3'  TCCTGACCTTAGGTGATC    83665
                                GATCACCTGAGGTCAGGA
                                ||||||||||||||||
                                CTAGTGGATTCCAGTCCT

GAM382  LOC196047 5'  TCAAACTCCTGACCTCAGGTGA 91166
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                |||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAACT

GAM382  LOC196047 5'  TCAAACTCCTGACCTCAGGTGA 91166
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                |||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAACT

GAM382  LOC196529 3'  TGAACTCCTGATCTCAGGCAAT 89143     CA
                C                 GAT  CCTGAGGTCAGGAGTTTG
                                |||  ||||||||||||||||
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                                CTA  GGACTCTAGTCCTCAAGT
                                  AC
GAM382   LOC196529 3'  TGAACTCCTGATCTCAGGCAAT 89143     CA
           C                     GAT  CCTGAGGTCAGGAGTTTG
                                |||  ||||||||||||||||||
                                CTA  GGACTCTAGTCCTCAAGT
                                  AC
GAM382   LOC197358 3'  AACTCCTGACCTCAAGTGATC  89402       C
                                GATCAC TGAGGTCAGGAGTT
                                ||||||| ||||||||||||||
                                CTAGTG ACTCCAGTCCTCAA
                                   A
GAM382   LOC197358 3'  AACTCCTGACCTCAAGTGATC  89402       C
                                GATCAC TGAGGTCAGGAGTT
                                ||||||| ||||||||||||||
                                CTAGTG ACTCCAGTCCTCAA
                                   A
GAM382   LOC197358 3'  TCGAACTCCTGACCTCAGGTGA 89447
           TC                     GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAGCT

GAM382   LOC197358 3'  TCGAACTCCTGACCTCAGGTGA 89447
           TC                     GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAGCT

GAM382   LOC199699 3'  TCAAACTCCTGGCCTCAGGTGA 89685
           TC                     GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCGGTCCTCAAACT

GAM382   LOC199699 3'  TCAAACTCCTGGCCTCAGGTGA 89685
           TC                     GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCGGTCCTCAAACT

GAM382   LOC199775 5'  TCGAACTCCCGACCTCTGGTGA 89725       T     A
           TC                     GATCACC GAGGTC GGAGTTTGA
                                  ||||||| |||||| |||||||||
                                  CTAGTGG CTCCAG CCTCAAGCT
                                     T     C
GAM382   LOC199775 5'  TCGAACTCCCGACCTCTGGTGA 89725       T     A
           TC                     GATCACC GAGGTC GGAGTTTGA
                                  ||||||| |||||| |||||||||
                                  CTAGTGG CTCCAG CCTCAAGCT
                                     T     C
GAM382   LOC199906 3'  TCAAACTCCTGACCTCAGGCGA 89859     A
           TC                     GATC CCTGAGGTCAGGAGTTTGA
                                  |||| ||||||||||||||||||
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                                CTAG GGACTCCAGTCCTCAAACT
                                  C
GAM382  LOC199906 3'  TCAAACTCCTGACCTCAGGCGA 89859      A
          TC                    GATC CCTGAGGTCAGGAGTTTGA
                                |||| ||||||||||||||||||
                                CTAG GGACTCCAGTCCTCAAACT
                                  C
GAM382  LOC200107 3'  TCAAACTCCAGACCTCGGGTGA 89990            A
          TC                    GATCACCTGAGGTC GGAGTTTGA
                                |||||||||||||| |||||||||
                                CTAGTGGGCTCCAG CCTCAAACT
                                      A
GAM382  LOC200107 3'  TCAAACTCCAGACCTCGGGTGA 89990            A
          TC                    GATCACCTGAGGTC GGAGTTTGA
                                |||||||||||||| |||||||||
                                CTAGTGGGCTCCAG CCTCAAACT
                                      A
GAM382  LOC200314 3'  TCGAACTCCTGACCTCAGGTGA 91604
          TC                    GATCACCTGAGGTCAGGAGTTTGA
                                |||||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAGCT

GAM382  LOC200314 3'  TCGAACTCCTGACCTCAGGTGA 91604
          TC                    GATCACCTGAGGTCAGGAGTTTGA
                                |||||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAGCT

GAM382  LOC200316 3'  TGAACTCCTGACCTCAGGTGAT 90196
          C                     GATCACCTGAGGTCAGGAGTTTG
                                |||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAGT

GAM382  LOC200316 3'  TGAACTCCTGACCTCAGGTGAT 90196
          C                     GATCACCTGAGGTCAGGAGTTTG
                                |||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAGT

GAM382  LOC200339 3'  TCCTGGCCTCAAGCGATC    91618     ACC
                                GATC   TGAGGTCAGGA
                                ||||   ||||||||||
                                CTAG   ACTCCGGTCCT
                                  CGA
GAM382  LOC200339 3'  TCCTGGCCTCAAGCGATC    91618     ACC
                                GATC   TGAGGTCAGGA
                                ||||   ||||||||||
                                CTAG   ACTCCGGTCCT
                                  CGA
GAM382  LOC200407 3'  TCAAACTCCTGACCTCAGGTGA 91632
          TC                    GATCACCTGAGGTCAGGAGTTTGA
                                |||||||||||||||||||||||||
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                                CTAGTGGACTCCAGTCCTCAAACT

GAM382  LOC200407 3'  TCAAACTCCTGACCTCAGGTGA 91632
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAACT

GAM382  LOC200853 3'  TCAAACTCCTAGGCTCAAGCGA 90333     AC  GA   _
                TC                GATC  CT  GGTC AGGAGTTTGA
                                  ||||  ||  |||| ||||||||||
                                  CTAG  GA  TCGG TCCTCAAACT
                                    C_  AC    A
GAM382  LOC200853 3'  TCAAACTCCTAGGCTCAAGCGA 90333     AC  GA   _
                TC                GATC  CT  GGTC AGGAGTTTGA
                                  ||||  ||  |||| ||||||||||
                                  CTAG  GA  TCGG TCCTCAAACT
                                    C_  AC    A
GAM382  LOC200860 3'  CTCCACCTCAGGTGATC     91746          CA
                                  GATCACCTGAGGT  GGAG
                                  ||||||||||||  ||||
                                  CTAGTGGACTCCA  CCTC
                                        __
GAM382  LOC200860 3'  CTCCACCTCAGGTGATC     91746          CA
                                  GATCACCTGAGGT  GGAG
                                  ||||||||||||  ||||
                                  CTAGTGGACTCCA  CCTC
                                        __
GAM382  LOC201164 3'  TCAAACTCCTGACCTCAAGTGA 89503       C
                TC                GATCAC TGAGGTCAGGAGTTTGA
                                  ||||||  ||||||||||||||||
                                  CTAGTG ACTCCAGTCCTCAAACT
                                     A
GAM382  LOC201164 3'  TCAAACTCCTGACCTCAAGTGA 89503       C
                TC                GATCAC TGAGGTCAGGAGTTTGA
                                  ||||||  ||||||||||||||||
                                  CTAGTG ACTCCAGTCCTCAAACT
                                     A
GAM382  LOC201411 3'  TCCAGACCTCAGGTGATC     63648          A
                                  GATCACCTGAGGTC GGA
                                  ||||||||||||| |||
                                  CTAGTGGACTCCAG CCT
                                        A
GAM382  LOC201411 3'  TCCAGACCTCAGGTGATC     63648          A
                                  GATCACCTGAGGTC GGA
                                  ||||||||||||| |||
                                  CTAGTGGACTCCAG CCT
                                        A
GAM382  LOC201510 3'  TCAAACTCCTGGTCTCAAGTGA 89629       C   GT
                TC                GATCAC TGAG  CAGGAGTTTGA
                                  ||||||  ||||  ||||||||||
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                                CTAGTG ACTC  GTCCTCAAACT
                                   A    TG
GAM382   LOC201510 3'  TCAAACTCCTGGTCTCAAGTGA 89629       C    GT
                TC                  GATCAC TGAG  CAGGAGTTTGA
                                    |||||| ||||  ||||||||||
                                CTAGTG ACTC  GTCCTCAAACT
                                   A    TG
GAM382   LOC201626 3'  TGAACTCCTGACCTCAGGTGAT 90439
                C                   GATCACCTGAGGTCAGGAGTTTG
                                    ||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAGT

GAM382   LOC201626 3'  TGAACTCCTGACCTCAGGTGAT 90439
                C                   GATCACCTGAGGTCAGGAGTTTG
                                    ||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAGT

GAM382   LOC201627 3'  TCAAACTCCCGACCTCAGGTGA 90461             A
                TC                  GATCACCTGAGGTC GGAGTTTGA
                                    |||||||||||||| |||||||||
                                CTAGTGGACTCCAG CCTCAAACT
                                       C
GAM382   LOC201627 3'  TCAAACTCCCGACCTCAGGTGA 90461             A
                TC                  GATCACCTGAGGTC GGAGTTTGA
                                    |||||||||||||| |||||||||
                                CTAGTGGACTCCAG CCTCAAACT
                                       C
GAM382   LOC203197 3'  TCCTGACCTCAGGTGATC    90817
                                GATCACCTGAGGTCAGGA
                                ||||||||||||||||||
                                CTAGTGGACTCCAGTCCT

GAM382   LOC203197 3'  TCCTGACCTCAGGTGATC    90817
                                GATCACCTGAGGTCAGGA
                                ||||||||||||||||||
                                CTAGTGGACTCCAGTCCT

GAM382   LOC203197 3'  TGAACTCCTGACCTCAGGTGAT 90819
                C                   GATCACCTGAGGTCAGGAGTTTG
                                    ||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAGT

GAM382   LOC203197 3'  TGAACTCCTGACCTCAGGTGAT 90819
                C                   GATCACCTGAGGTCAGGAGTTTG
                                    ||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAGT

GAM382   LOC203378 3'  TCAAACTCCTCCACTCAGGTGA 92302           GTC
                TC                  GATCACCTGAG   AGGAGTTTGA
                                    ||||||||||   ||||||||||
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                                CTAGTGGACTC   TCCTCAAACT
                                      ACC
GAM382   LOC203378 3'  TCAAACTCCTCCACTCAGGTGA 92302          GTC
           TC                   GATCACCTGAG   AGGAGTTTGA
                                ||||||||||   ||||||||||
                                CTAGTGGACTC   TCCTCAAACT
                                      ACC
GAM382   LOC204804 3'  TCCTGGCCTCAGGTGATC    91054
                                GATCACCTGAGGTCAGGA
                                ||||||||||||||||||
                                CTAGTGGACTCCGGTCCT

GAM382   LOC204804 3'  TCCTGGCCTCAGGTGATC    91054
                                GATCACCTGAGGTCAGGA
                                ||||||||||||||||||
                                CTAGTGGACTCCGGTCCT

GAM382   LOC205251 5'  TCCTGACCTCAAGTGATC    92360       C
                                GATCAC TGAGGTCAGGA
                                |||||| ||||||||||
                                CTAGTG ACTCCAGTCCT
                                   A
GAM382   LOC205251 5'  TCCTGACCTCAAGTGATC    92360       C
                                GATCAC TGAGGTCAGGA
                                |||||| ||||||||||
                                CTAGTG ACTCCAGTCCT
                                   A
GAM382   LOC219529 5'  TCAAACTCCTGAGCCCAGGTGA 94568         A _
           TC                   GATCACCTG GG TCAGGAGTTTGA
                                ||||||||| || ||||||||||||
                                CTAGTGGAC CC AGTCCTCAAACT
                                     _ G
GAM382   LOC219529 5'  TCAAACTCCTGAGCCCAGGTGA 94568         A _
           TC                   GATCACCTG GG TCAGGAGTTTGA
                                ||||||||| || ||||||||||||
                                CTAGTGGAC CC AGTCCTCAAACT
                                     _ G
GAM382   LOC219673 5'  TCAAACGCCTGACCTCAAGTAA 94635    C  C        A
           TC                   GAT AC TGAGGTCAGG GTTTGA
                                ||| || |||||||||| ||||||
                                CTA TG ACTCCAGTCC CAAACT
                                  A  A         G
GAM382   LOC219673 5'  TCAAACGCCTGACCTCAAGTAA 94635    C  C        A
           TC                   GAT AC TGAGGTCAGG GTTTGA
                                ||| || |||||||||| ||||||
                                CTA TG ACTCCAGTCC CAAACT
                                  A  A         G
GAM382   LOC219731 5'  ACTCCTGAGCTCAAGTGATC  94695       C   G
                                GATCAC TGAG TCAGGAGT
                                |||||| |||| ||||||||
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                                CTAGTG ACTC AGTCCTCA
                                   A   G
GAM382  LOC219731 5'  ACTCCTGAGCTCAAGTGATC  94695       C   G
                                GATCAC TGAG TCAGGAGT
                                |||||| |||| ||||||||
                                CTAGTG ACTC AGTCCTCA
                                   A   G
GAM382  LOC220074 3'  TCAAACTCCTGACCTCAGGTGA 59997
           TC                    GATCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAACT

GAM382  LOC220074 3'  TCAAACTCCTGACCTCAGGTGA 59997
           TC                    GATCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAACT

GAM382  LOC220074 3'  TGAACTCCTGACCTCAGGTGAT 59998
           C                     GATCACCTGAGGTCAGGAGTTTG
                                 |||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGT

GAM382  LOC220074 3'  TGAACTCCTGACCTCAGGTGAT 59998
           C                     GATCACCTGAGGTCAGGAGTTTG
                                 |||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGT

GAM382  LOC221060 3'  TCGAACTCCTGACCTCAGGTGA 94837
           TC                    GATCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGCT

GAM382  LOC221060 3'  TCGAACTCCTGACCTCAGGTGA 94837
           TC                    GATCACCTGAGGTCAGGAGTTTGA
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGCT

GAM382  LOC221271 3'  TCAAACTCCTGATCTCAAGTGA 93528       C
           TC                    GATCAC TGAGGTCAGGAGTTTGA
                                 |||||| ||||||||||||||||
                                 CTAGTG ACTCTAGTCCTCAAACT
                                    A
GAM382  LOC221271 3'  TCAAACTCCTGATCTCAAGTGA 93528       C
           TC                    GATCAC TGAGGTCAGGAGTTTGA
                                 |||||| ||||||||||||||||
                                 CTAGTG ACTCTAGTCCTCAAACT
                                    A
GAM382  LOC221964 3'  TGAACTCCTGACCTCAGGTGAT 95613
           C                     GATCACCTGAGGTCAGGAGTTTG
                                 |||||||||||||||||||||||
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                                CTAGTGGACTCCAGTCCTCAAGT

GAM382   LOC221964 3'  TGAACTCCTGACCTCAGGTGAT 95613
                C                GATCACCTGAGGTCAGGAGTTTG
                                 ||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGT

GAM382   LOC222031 3'  TGAACTCCTGACCTCAGGTGAT 95688
                C                GATCACCTGAGGTCAGGAGTTTG
                                 ||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGT

GAM382   LOC222031 3'  TGAACTCCTGACCTCAGGTGAT 95688
                C                GATCACCTGAGGTCAGGAGTTTG
                                 ||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGT

GAM382   LOC222068 3'  TCCTGACCTCAGTTGATC    94280      C
                                 GATCA CTGAGGTCAGGA
                                 ||||| ||||||||||||
                                 CTAGT GACTCCAGTCCT
                                    T
GAM382   LOC222068 3'  TCCTGACCTCAGTTGATC    94280      C
                                 GATCA CTGAGGTCAGGA
                                 ||||| ||||||||||||
                                 CTAGT GACTCCAGTCCT
                                    T
GAM382   LOC245771 5'  TCGAACTCCTGACCTCAAGTGA 94487      C
                TC                 GATCAC TGAGGTCAGGAGTTTGA
                                   |||||| ||||||||||||||||
                                   CTAGTG ACTCCAGTCCTCAAGCT
                                      A
GAM382   LOC245771 5'  TCGAACTCCTGACCTCAAGTGA 94487      C
                TC                 GATCAC TGAGGTCAGGAGTTTGA
                                   |||||| ||||||||||||||||
                                   CTAGTG ACTCCAGTCCTCAAGCT
                                      A
GAM382   LOC253805 3'  TCCTGACCTCAGATGATT    98186      C
                                 GATCA CTGAGGTCAGGA
                                 ||||| ||||||||||||
                                 TTAGT GACTCCAGTCCT
                                    A
GAM382   LOC253805 3'  TCCTGACCTCAGATGATT    98186      C
                                 GATCA CTGAGGTCAGGA
                                 ||||| ||||||||||||
                                 TTAGT GACTCCAGTCCT
                                    A
GAM382   LOC253981 3'  TGAACTCCTGACCTCAGGCGAT 97540      A
                C                GATC CCTGAGGTCAGGAGTTTG
                                 |||| ||||||||||||||||||
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                                CTAG GGACTCCAGTCCTCAAGT
                                  C
GAM382  LOC253981 3'  TGAACTCCTGACCTCAGGCGAT 97540      A
          C                    GATC CCTGAGGTCAGGAGTTTG
                               |||| ||||||||||||||||||
                               CTAG GGACTCCAGTCCTCAAGT
                                  C
GAM382  LOC254268 3'  TCAAACTCCTGACCTCAAGTGA 97146       C
          TC                   GATCAC TGAGGTCAGGAGTTTGA
                               |||||| |||||||||||||||||
                               CTAGTG ACTCCAGTCCTCAAACT
                                  A
GAM382  LOC254268 3'  TCAAACTCCTGACCTCAAGTGA 97146       C
          TC                   GATCAC TGAGGTCAGGAGTTTGA
                               |||||| |||||||||||||||||
                               CTAGTG ACTCCAGTCCTCAAACT
                                  A
GAM382  LOC254351 5'  TCAAGCTCCTGACCTCGGGTGA 96694
          TC                   GATCACCTGAGGTCAGGAGTTTGA
                               ||||||||||||||||||||||||
                               CTAGTGGGCTCCAGTCCTCGAACT

GAM382  LOC254351 5'  TCAAGCTCCTGACCTCGGGTGA 96694
          TC                   GATCACCTGAGGTCAGGAGTTTGA
                               ||||||||||||||||||||||||
                               CTAGTGGGCTCCAGTCCTCGAACT

GAM382  LOC254532 5'  TCAAACTCCTGACCTCAAGTGA 98461       C
          TC                   GATCAC TGAGGTCAGGAGTTTGA
                               |||||| |||||||||||||||||
                               CTAGTG ACTCCAGTCCTCAAACT
                                  A
GAM382  LOC254532 5'  TCAAACTCCTGACCTCAAGTGA 98461       C
          TC                   GATCAC TGAGGTCAGGAGTTTGA
                               |||||| |||||||||||||||||
                               CTAGTG ACTCCAGTCCTCAAACT
                                  A
GAM382  LOC254655 3'  TCGAACTCCTGACCTCAGGTGA 97227
          TC                   GATCACCTGAGGTCAGGAGTTTGA
                               ||||||||||||||||||||||||
                               CTAGTGGACTCCAGTCCTCAAGCT

GAM382  LOC254655 3'  TCGAACTCCTGACCTCAGGTGA 97227
          TC                   GATCACCTGAGGTCAGGAGTTTGA
                               ||||||||||||||||||||||||
                               CTAGTGGACTCCAGTCCTCAAGCT

GAM382  LOC254778 3'  TCAAACTCCTGGGTTCAAGAGA 97837      ACC    G
          TC                   GATC   TGAG TCAGGAGTTTGA
                               ||||   |||| ||||||||||||
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                                CTAG   ACTT GGTCCTCAAACT
                                  AGA    G
GAM382  LOC254778 3'  TCAAACTCCTGGGTTCAAGAGA 97837      ACC    G
          TC                    GATC   TGAG TCAGGAGTTTGA
                                ||||   |||| ||||||||||||
                                CTAG   ACTT GGTCCTCAAACT
                                  AGA    G
GAM382  LOC255065 5'  TCAAACTCCTGACCTCAAGTAA 98372     C  C
          TC                    GAT AC TGAGGTCAGGAGTTTGA
                                ||| || ||||||||||||||||||
                                CTA TG ACTCCAGTCCTCAAACT
                                  A  A
GAM382  LOC255065 5'  TCAAACTCCTGACCTCAAGTAA 98372     C  C
          TC                    GAT AC TGAGGTCAGGAGTTTGA
                                ||| || ||||||||||||||||||
                                CTA TG ACTCCAGTCCTCAAACT
                                  A  A
GAM382  LOC255065 5'  TCCTGACCTCAAGTAATC     98373     C  C
                                GAT AC TGAGGTCAGGA
                                ||| || |||||||||||
                                CTA TG ACTCCAGTCCT
                                  A  A
GAM382  LOC255065 5'  TCCTGACCTCAAGTAATC     98373     C  C
                                GAT AC TGAGGTCAGGA
                                ||| || |||||||||||
                                CTA TG ACTCCAGTCCT
                                  A  A
GAM382  LOC255308 3'  TCCTGACCTCAGGGTGATC    96180        _
                                GATCACC TGAGGTCAGGA
                                ||||||| |||||||||||
                                CTAGTGG ACTCCAGTCCT
                                    G
GAM382  LOC255308 3'  TCCTGACCTCAGGGTGATC    96180        _
                                GATCACC TGAGGTCAGGA
                                ||||||| |||||||||||
                                CTAGTGG ACTCCAGTCCT
                                    G
GAM382  LOC255458 5'  TCAAACTCCTGGGCTCAAGCGA 98936      ACC    G
          TC                    GATC   TGAG TCAGGAGTTTGA
                                ||||   |||| ||||||||||||
                                CTAG   ACTC GGTCCTCAAACT
                                  CGA    G
GAM382  LOC255458 5'  TCAAACTCCTGGGCTCAAGCGA 98936      ACC    G
          TC                    GATC   TGAG TCAGGAGTTTGA
                                ||||   |||| ||||||||||||
                                CTAG   ACTC GGTCCTCAAACT
                                  CGA    G
GAM382  LOC256267 3'  TGAACTCCTGACCTCCGGTGAT 98614        T
          C                     GATCACC GAGGTCAGGAGTTTG
                                ||||||| |||||||||||||||
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                                CTAGTGG CTCCAGTCCTCAAGT
                                    C
GAM382  LOC256267 3'  TGAACTCCTGACCTCCGGTGAT 98614       T
          C                      GATCACC GAGGTCAGGAGTTTG
                                 ||||||| ||||||||||||||||
                                 CTAGTGG CTCCAGTCCTCAAGT
                                    C
GAM382  LOC257127 5'  TGAACTCCTGACCTCAGGTGAT 98497
          C                      GATCACCTGAGGTCAGGAGTTTG
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGT

GAM382  LOC257127 5'  TGAACTCCTGACCTCAGGTGAT 98497
          C                      GATCACCTGAGGTCAGGAGTTTG
                                 ||||||||||||||||||||||||
                                 CTAGTGGACTCCAGTCCTCAAGT

GAM382  LOC51008  5'  TGAACTCCCGACCTCAGGTGAT 32536          A
          C                      GATCACCTGAGGTC GGAGTTTG
                                 |||||||||||||| ||||||||
                                 CTAGTGGACTCCAG CCTCAAGT
                                       C
GAM382  LOC51008  5'  TGAACTCCCGACCTCAGGTGAT 32536          A
          C                      GATCACCTGAGGTC GGAGTTTG
                                 |||||||||||||| ||||||||
                                 CTAGTGGACTCCAG CCTCAAGT
                                       C
GAM382  LOC51193  5'  TCCCGACCTCAGGTGATC    33372          A
                                 GATCACCTGAGGTC GGA
                                 |||||||||||||| |||
                                 CTAGTGGACTCCAG CCT
                                       C
GAM382  LOC51193  5'  TCCCGACCTCAGGTGATC    33372          A
                                 GATCACCTGAGGTC GGA
                                 |||||||||||||| |||
                                 CTAGTGGACTCCAG CCT
                                       C
GAM382  LOC51200  3'  TCAAACTCCCAACCTCAGGTGA 33441          CA
          TC                     GATCACCTGAGGT  GGAGTTTGA
                                 ||||||||||||  |||||||||
                                 CTAGTGGACTCCA  CCTCAAACT
                                       AC
GAM382  LOC51200  3'  TCAAACTCCCAACCTCAGGTGA 33441          CA
          TC                     GATCACCTGAGGT  GGAGTTTGA
                                 ||||||||||||  |||||||||
                                 CTAGTGGACTCCA  CCTCAAACT
                                       AC
GAM382  LOC51219  5'  TCGAACTCCCGACCTCAGGTGA 33551          A
          TC                     GATCACCTGAGGTC GGAGTTTGA
                                 |||||||||||||| |||||||||
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                                CTAGTGGACTCCAG CCTCAAGCT
                                      C
GAM382  LOC51219  5'  TCGAACTCCCGACCTCAGGTGA 33551            A
            TC                  GATCACCTGAGGTC GGAGTTTGA
                                |||||||||||||| |||||||||
                                CTAGTGGACTCCAG CCTCAAGCT
                                      C
GAM382  LOC57107  3'  TCGAACTCCTGACCTCAGGTGA 40195
            TC                  GATCACCTGAGGTCAGGAGTTTGA
                                ||||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAGCT

GAM382  LOC57107  3'  TCGAACTCCTGACCTCAGGTGA 40195
            TC                  GATCACCTGAGGTCAGGAGTTTGA
                                ||||||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAAGCT

GAM382  LOC57146  3'  TCAAACTCCTGACCTCAGGTGC 40299    T
            TC                  GA CACCTGAGGTCAGGAGTTTGA
                                || ||||||||||||||||||||
                                CT GTGGACTCCAGTCCTCAAACT
                                 C
GAM382  LOC57146  3'  TCAAACTCCTGACCTCAGGTGC 40299    T
            TC                  GA CACCTGAGGTCAGGAGTTTGA
                                || ||||||||||||||||||||
                                CT GTGGACTCCAGTCCTCAAACT
                                 C
GAM382  LOC89894  5'  TCCTGGCCTCAAGTGATC    61232       C
                                GATCAC TGAGGTCAGGA
                                |||||| ||||||||||
                                CTAGTG ACTCCGGTCCT
                                   A
GAM382  LOC89894  5'  TCCTGGCCTCAAGTGATC    61232       C
                                GATCAC TGAGGTCAGGA
                                |||||| ||||||||||
                                CTAGTG ACTCCGGTCCT
                                   A
GAM382  LOC89932  3'  TCGAACTTCTGACCTCAGATGA 61475       C
            TC                  GATCA CTGAGGTCAGGAGTTTGA
                                ||||| ||||||||||||||||||
                                CTAGT GACTCCAGTCTTCAAGCT
                                   A
GAM382  LOC89932  3'  TCGAACTTCTGACCTCAGATGA 61475       C
            TC                  GATCA CTGAGGTCAGGAGTTTGA
                                ||||| ||||||||||||||||||
                                CTAGT GACTCCAGTCTTCAAGCT
                                   A
GAM382  LOC89932  3'  TGAACTCCCGACCTCAGGTAAT 61476    C        A
            C                   GAT ACCTGAGGTC GGAGTTTG
                                ||| |||||||||| ||||||||
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                                CTA TGGACTCCAG CCTCAAGT
                                  A         C
GAM382  LOC89932  3'  TGAACTCCCGACCTCAGGTAAT 61476     C         A
              C                   GAT ACCTGAGGTC GGAGTTTG
                                  ||| |||||||||| ||||||||
                                CTA TGGACTCCAG CCTCAAGT
                                  A         C
GAM382  LOC90072  3'  TCGAACTCCCGACCTCAAGTGA 61966       C       A
              TC                  GATCAC TGAGGTC GGAGTTTGA
                                  |||||| ||||||| |||||||||
                                CTAGTG ACTCCAG CCTCAAGCT
                                    A       C
GAM382  LOC90072  3'  TCGAACTCCCGACCTCAAGTGA 61966       C       A
              TC                  GATCAC TGAGGTC GGAGTTTGA
                                  |||||| ||||||| |||||||||
                                CTAGTG ACTCCAG CCTCAAGCT
                                    A       C
GAM382  LOC90408  5'  TCCTGACTTCAAGTGATC    63348       C
                                GATCAC TGAGGTCAGGA
                                |||||| ||||||||||
                                CTAGTG ACTTCAGTCCT
                                    A
GAM382  LOC90408  5'  TCCTGACTTCAAGTGATC    63348       C
                                GATCAC TGAGGTCAGGA
                                |||||| ||||||||||
                                CTAGTG ACTTCAGTCCT
                                    A
GAM382  LOC90459  3'  TCCTGACCTCAAGTGATT    63565       C
                                GATCAC TGAGGTCAGGA
                                |||||| ||||||||||
                                TTAGTG ACTCCAGTCCT
                                    A
GAM382  LOC90459  3'  TCCTGACCTCAAGTGATT    63565       C
                                GATCAC TGAGGTCAGGA
                                |||||| ||||||||||
                                TTAGTG ACTCCAGTCCT
                                    A
GAM382  LOC90485  3'  TCCTAACATCAGGCGATC    63713     A    G  C
                                GATC CCTGA GT AGGA
                                |||| ||||| || ||||
                                CTAG GGACT CA TCCT
                                  C    A  A
GAM382  LOC90485  3'  TCCTAACATCAGGCGATC    63713     A    G  C
                                GATC CCTGA GT AGGA
                                |||| ||||| || ||||
                                CTAG GGACT CA TCCT
                                  C    A  A
GAM382  LOC90591  3'  TCCTGACCTGAAGTGATC    64191       CTG
                                GATCAC   AGGTCAGGA
                                ||||||   |||||||||
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                              CTAGTG   TCCAGTCCT
                                 AAG
GAM382  LOC90591  3' TCCTGACCTGAAGTGATC    64191       CTG
                              GATCAC   AGGTCAGGA
                              ||||||   |||||||||
                              CTAGTG   TCCAGTCCT
                                 AAG
GAM382  LOC90591  3' TCGAACTCCTGACCTCAGGTGA 64193
           TC                   GATCACCTGAGGTCAGGAGTTTGA
                              ||||||||||||||||||||||||
                              CTAGTGGACTCCAGTCCTCAAGCT

GAM382  LOC90591  3' TCGAACTCCTGACCTCAGGTGA 64193
           TC                   GATCACCTGAGGTCAGGAGTTTGA
                              ||||||||||||||||||||||||
                              CTAGTGGACTCCAGTCCTCAAGCT

GAM382  LOC90918  3' TCAAACTCCTGACCTTAGTTGA 65004       C
           TC                   GATCA CTGAGGTCAGGAGTTTGA
                              |||||| ||||||||||||||||||
                              CTAGT GATTCCAGTCCTCAAACT
                                 T
GAM382  LOC90918  3' TCAAACTCCTGACCTTAGTTGA 65004       C
           TC                   GATCA CTGAGGTCAGGAGTTTGA
                              |||||| ||||||||||||||||||
                              CTAGT GATTCCAGTCCTCAAACT
                                 T
GAM382  LOC91115  3' AACTCCTGACCTCAGATGGTC  65531       C
                              GATCA CTGAGGTCAGGAGTT
                              |||||| |||||||||||||||
                              CTGGT GACTCCAGTCCTCAA
                                 A
GAM382  LOC91115  3' AACTCCTGACCTCAGATGGTC  65531       C
                              GATCA CTGAGGTCAGGAGTT
                              |||||| |||||||||||||||
                              CTGGT GACTCCAGTCCTCAA
                                 A
GAM382  LOC91291  5' TCAAACTCCTGACGCCAGGTGA 66095          AG
           TC                   GATCACCTG  GTCAGGAGTTTGA
                              |||||||||  ||||||||||||
                              CTAGTGGAC  CAGTCCTCAAACT
                                   CG
GAM382  LOC91291  5' TCAAACTCCTGACGCCAGGTGA 66095          AG
           TC                   GATCACCTG  GTCAGGAGTTTGA
                              |||||||||  ||||||||||||
                              CTAGTGGAC  CAGTCCTCAAACT
                                   CG
GAM382  LOC91561  5' TCGAACTCCTGACCTCAGGTGA 67047
           TC                   GATCACCTGAGGTCAGGAGTTTGA
                              ||||||||||||||||||||||||
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                                CTAGTGGACTCCAGTCCTCAAGCT

GAM382  LOC91561  5'  TCGAACTCCTGACCTCAGGTGA 67047
                TC                GATCACCTGAGGTCAGGAGTTTGA
                                  ||||||||||||||||||||||||
                                  CTAGTGGACTCCAGTCCTCAAGCT

GAM382  LOC91963  3'  TCAAACTCCTGAGCTCAAGTAA 68325     C  C    G
                TC                GAT AC TGAG TCAGGAGTTTGA
                                  ||| || |||| ||||||||||||
                                  CTA TG ACTC AGTCCTCAAACT
                                    A A    G
GAM382  LOC91963  3'  TCAAACTCCTGAGCTCAAGTAA 68325     C  C    G
                TC                GAT AC TGAG TCAGGAGTTTGA
                                  ||| || |||| ||||||||||||
                                  CTA TG ACTC AGTCCTCAAACT
                                    A A    G
GAM382  LOC92267  3'  TCAAACTCCTGACCTCAAGTGA 69178       C
                TC                GATCAC TGAGGTCAGGAGTTTGA
                                  |||||| ||||||||||||||||
                                  CTAGTG ACTCCAGTCCTCAAACT
                                     A
GAM382  LOC92267  3'  TCAAACTCCTGACCTCAAGTGA 69178       C
                TC                GATCAC TGAGGTCAGGAGTTTGA
                                  |||||| ||||||||||||||||
                                  CTAGTG ACTCCAGTCCTCAAACT
                                     A
GAM382  LOC92303  3'  TCCAGACCTCAGGTGATC    69398            A
                                  GATCACCTGAGGTC GGA
                                  |||||||||||||| |||
                                  CTAGTGGACTCCAG CCT
                                           A
GAM382  LOC92303  3'  TCCAGACCTCAGGTGATC    69398            A
                                  GATCACCTGAGGTC GGA
                                  |||||||||||||| |||
                                  CTAGTGGACTCCAG CCT
                                           A
GAM382  LOC92466  3'  TGAACTCCTGACCTCCGGTGAT 69970       T
                C                  GATCACC GAGGTCAGGAGTTTG
                                   |||||||| ||||||||||||||
                                   CTAGTGG CTCCAGTCCTCAAGT
                                      C
GAM382  LOC92466  3'  TGAACTCCTGACCTCCGGTGAT 69970       T
                C                  GATCACC GAGGTCAGGAGTTTG
                                   |||||||| ||||||||||||||
                                   CTAGTGG CTCCAGTCCTCAAGT
                                      C
GAM382  LOC92697  5'  TCGAACTCCCAACCTCAGGTGA 70817           CA
                TC                GATCACCTGAGGT  GGAGTTTGA
                                  ||||||||||||  |||||||||
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                                CTAGTGGACTCCA  CCTCAAGCT
                                      AC
GAM382  LOC92697  5'  TCGAACTCCCAACCTCAGGTGA 70817           CA
          TC                    GATCACCTGAGGT  GGAGTTTGA
                                ||||||||||||  |||||||||
                                CTAGTGGACTCCA  CCTCAAGCT
                                      AC
GAM382  LOC92841  3'  CGAACTCCTGACCTCAAGTGAT 71251       C
          C                     GATCAC TGAGGTCAGGAGTTTG
                                ||||||| ||||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAGC
                                   A
GAM382  LOC92841  3'  CGAACTCCTGACCTCAAGTGAT 71251       C
          C                     GATCAC TGAGGTCAGGAGTTTG
                                ||||||| ||||||||||||||||
                                CTAGTG ACTCCAGTCCTCAAGC
                                   A
GAM382  LOC92876  5'  GACTCCTGACCTCAGGTGATC  71348
                                GATCACCTGAGGTCAGGAGTT
                                ||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAG

GAM382  LOC92876  5'  GACTCCTGACCTCAGGTGATC  71348
                                GATCACCTGAGGTCAGGAGTT
                                ||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAG

GAM382  LOC93129  3'  TCAAACTCCTGGGCTCAAGTGA 71959     C   G
                                TCAC TGAG TCAGGAGTTTGA
                                |||| |||| ||||||||||||
                                AGTG ACTC GGTCCTCAAACT
                                  A   G
GAM382  LOC93129  3'  TCAAACTCCTGGGCTCAAGTGA 71959     C   G
                                TCAC TGAG TCAGGAGTTTGA
                                |||| |||| ||||||||||||
                                AGTG ACTC GGTCCTCAAACT
                                  A   G
GAM382  LOC93408  5'  TCAAACTCCTGGCCTCAAGTGA 57291       C
          TC                    GATCAC TGAGGTCAGGAGTTTGA
                                ||||||| ||||||||||||||||
                                CTAGTG ACTCCGGTCCTCAAACT
                                   A
GAM382  LOC93408  5'  TCAAACTCCTGGCCTCAAGTGA 57291       C
          TC                    GATCAC TGAGGTCAGGAGTTTGA
                                ||||||| ||||||||||||||||
                                CTAGTG ACTCCGGTCCTCAAACT
                                   A
GAM383  A1BG      3'  AGACAGGGTCTCACTGTGTT  56275         A   C
                                AACACGGTGA ACCC GTCT
                                |||||||||| |||| ||||
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                                TTGTGTCACT TGGG CAGA
                                      C   A
GAM383  A1BG     3'  AGATGGGGTTTCACCTTGTT  56279     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  T
GAM383  ADAMTS4  3'  AGACAGGGTTTCACCATGTT  18744     C        C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A         A
GAM383  ADAMTS4  3'  AGACGGGGTTTCACCATGTT  18747     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  ALOX15   3'  AGACGGGGCCTCACTATGTT  8539      CG    AA
                                AACA  GTGA  CCCCGTCT
                                ||||  ||||  ||||||||
                                TTGT  CACT  GGGGCAGA
                                  AT    CC
GAM383  APAF1    3'  AGACGGGGTTTCACCATGTT  25957     C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  APOL1    3'  AGATGGGGTTTCACCATGTT  14724     C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  APPBP2   3'  AGACGGAGTTTCGCTCTTGT  22114     C _      C
                                ACA G GTGAAAC CCGTCT
                                ||| | ||||||| ||||||
                                TGT C CGCTTTG GGCAGA
                                  T T      A
GAM383  APPL     3'  AGACGGGGTTTCACCGTGTT  24941
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGA

GAM383  ARCN1    3'  AGACGGGGTTTCACCGTGTT  9743
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGA

GAM383  ATP7A    3'  AGACGGGGTTTCGCCATGTT  5313      C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
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                                TTGT CCGCTTTGGGGCAGA
                                  A
GAM383  AXL     3'  AGACAGGGTTTCACCATGTT  41872     C       C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A        A
GAM383  BRIP1   3'  AGATGGGGTTTCACCATGTT  50203     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  C14orf1 3'  AGACGGGGTTTCACTCTGT   24161     C
                                ACA GGTGAAACCCCGTCT
                                ||| ||||||||||||||
                                TGT TCACTTTGGGGCAGA
                                  C
GAM383  C7      3'  AGATGGGTTTCACCATGTT   6978      C       C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG TAGA
                                  A       _
GAM383  CAMLG   3'  AGACAGAGTTTCGCTCTTGT  9992      C _     CCC
                                ACA G GTGAAAC  GTCT
                                ||| | |||||||  ||||
                                TGT C CGCTTTG  CAGA
                                  T T     AGA
GAM383  CASP10  3'  AGATGGGGTTTCACTATGTT  53197     CG
                                AACA  GTGAAACCCCGTCT
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGA
                                  AT
GAM383  CASP10  3'  AGATGGGGTTTCACTATGTT  53198     CG
                                AACA  GTGAAACCCCGTCT
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGA
                                  AT
GAM383  CASP2   3'  AGACAGGGTTTCACCATGTT  53315     C       C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A        A
GAM383  CASP2   3'  AGACAGGGTTTCACCATGTT  53316     C       C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A        A
GAM383  CASP2   3'  AGACAGGGTTTCACCATGTT  53317     C       C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
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                                TTGT CCACTTTGGG CAGA
                                  A         A
GAM383  CASP8    3'  AGACAGGGTTTCACTGTGTT  54067              C
                                AACACGGTGAAACCC GTCT
                                ||||||||||||||| ||||
                                TTGTGTCACTTTGGG CAGA
                                        A
GAM383  CASP8    3'  AGACAGGGTTTCACTGTGTT  8743               C
                                AACACGGTGAAACCC GTCT
                                ||||||||||||||| ||||
                                TTGTGTCACTTTGGG CAGA
                                        A
GAM383  CBFA2T2  3'  AGACGGGGTTTCTCCTTGTT  18698     C  T
                                AACA GG GAAACCCCGTCT
                                |||| || ||||||||||||
                                TTGT CC CTTTGGGGCAGA
                                  T  T
GAM383  CDC6     3'  AGACAGGGTTTTACCATGTT  8814      C        C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCATTTTGGG CAGA
                                  A         A
GAM383  CDH1     3'  AGACGGGGTCTCCCTGTGTT  16398       T  A
                                AACACGG GA ACCCCGTCT
                                ||||||| || |||||||||
                                TTGTGTC CT TGGGGCAGA
                                    C  C
GAM383  CLECSF11 5'  AGATGGGGTTTCACTATGTT  56144     CG
                                AACA  GTGAAACCCCGTCT
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGA
                                  AT
GAM383  CLECSF12 3'  AGACAGAGTTTCGCTCTTGT  77202     C _      CCC
                                ACA G GTGAAAC   GTCT
                                ||| | |||||||   ||||
                                TGT C CGCTTTG   CAGA
                                  T T      AGA
GAM383  CNN2     3'  AGATGGGGTTTCCCCATGTT  16452     C  T
                                AACA GG GAAACCCCGTCT
                                |||| || ||||||||||||
                                TTGT CC CTTTGGGGTAGA
                                  A  C
GAM383  COX15    3'  AGACAGAGTTTCACTCTTGT  55275     C _      CCC
                                ACA G GTGAAAC   GTCT
                                ||| | |||||||   ||||
                                TGT C CACTTTG   CAGA
                                  T T      AGA
GAM383  CR1      3'  AGACGGGGTTTCACCATGTT  6934      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
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                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  CRTAP   3' AGACGGGGTTTTGCCATGTT  22073     C  TG
                                AACA GG  AAACCCCGTCT
                                |||| ||  ||||||||||
                                TTGT CC  TTTGGGGCAGA
                                  A  GT
GAM383  CTF1    3' AGACGAGGTTTCGCCATGTT  9005      C       C
                                AACA GGTGAAACC CGTCT
                                |||| ||||||||| |||||
                                TTGT CCGCTTTGG GCAGA
                                  A       A
GAM383  CXCL16  3' AGACGGGGTTTCACCATGTT  42157     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  CYP1A2  3' AGACGAGGTTTCACTGTGTT  69654           C
                                AACACGGTGAAACC CGTCT
                                |||||||||||||| |||||
                                TTGTGTCACTTTGG GCAGA
                                      A
GAM383  CYP1A2  3' AGACGGGTTTCACCATGTT   69655     C       C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A       _
GAM383  CYP1A2  3' AGATGGGGTTTCACCATGTT  7499      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  CYP4F3  3' AGGCGGGGTTTCGCCATGTT  7991      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCGCTTTGGGGCGGA
                                  A
GAM383  CYP51   3' AGACGGGGGTTTCACTATGTT 7607      CG        _
                                AACA  GTGAAACCCC GTCT
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG CAGA
                                  AT        G
GAM383  DFFB    3' ACGGGGTTTCACCATGTT    88750     C
                                AACA GGTGAAACCCCGT
                                |||| ||||||||||||
                                TTGT CCACTTTGGGGCA
                                  A
GAM383  DFFB    3' AGACGGGGTTTCACCATGTT  88754     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
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                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  DHFR    3'  AGATGGGGTTTCACCATGTT  7638      C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  DSC3    3'  AGACGGGGTTTCACTGTGTT  44612
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGTCACTTTGGGGCAGA

GAM383  DSC3    3'  AGACGGGGTTTCACTGTGTT  10432
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGTCACTTTGGGGCAGA

GAM383  EHD2    3'  AGACGGGGTTTCACCATGTT  28210     C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  EIF2S3  3'  AGACGGGGTTTCAGCATGTT  9203      CGG
                                AACA  TGAAACCCCGTCT
                                ||||  ||||||||||||
                                TTGT  ACTTTGGGGCAGA
                                  ACG
GAM383  ENDOGL1 3'  AGATGTGGTCTCGCCGTGT   18819       A  C
                                ACACGGTGA ACC CGTCT
                                ||||||||| ||| |||||
                                TGTGCCGCT TGG GTAGA
                                     C  T
GAM383  EPB72   3'  AGACGGGGTTTCACCATGTT  15865     C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  F2RL2   3'  AGACGGGGTTTCACCATGTT  15889     C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  F2RL3   3'  AGACGGAGTTTCACCATGTT  15488     C      C
                                AACA GGTGAAAC CCGTCT
                                |||| |||||||| ||||||
                                TTGT CCACTTTG GGCAGA
                                  A      A
GAM383  FANCF   3'  AGACGGGGTTTCACCATG    42970    C
                                CA GGTGAAACCCCGTCT
                                || ||||||||||||||
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                                GT CCACTTTGGGGCAGA
                                 A
GAM383  FCAR     3'  AGATGGGGTTTCACTGTGTT   56560
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGTCACTTTGGGGTAGA

GAM383  FCAR     3'  AGACAGGGTTTCACCATGTT   10580     C        C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A         A
GAM383  FCGR2A   3'  AGACAGGGTTTCGCAATGTT   80023     CG       C
                                AACA  GTGAAACCC GTCT
                                ||||  ||||||||| ||||
                                TTGT  CGCTTTGGG CAGA
                                  AA        A
GAM383  FEZ1     3'  AGATGGGAGTTTCACCATGTT  18782     C        _
                                AACA GGTGAAAC CCCGTCT
                                |||| |||||||| |||||||
                                TTGT CCACTTTG GGGTAGA
                                  A       A
GAM383  FGF5     3'  AGACGGGGTTTCACCATGTT   53646     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  FGF5     3'  AGACGGGGTTTCACCATGTT   53647     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  FSHPRH1  5'  AGACATTGGTCTCACTGTGTT  23063         A   CC_
                                AACACGGTGA ACC   GTCT
                                |||||||||| |||   ||||
                                TTGTGTCACT TGG   CAGA
                                      C   TTA
GAM383  FUT1     3'  AGACAGGGTTTCACCATGTT   5577      C        C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A         A
GAM383  FUT1     3'  AGACGGGGTTTCATCGTGTT   5580
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCTACTTTGGGGCAGA

GAM383  GHR      3'  AGACGGGGTTTCACCATGTT   5688      C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
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                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  GM2A    3'  AGATGGGGTTTCACCATGTT  68371     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  GNE     3'  ACAGGGTTTCACCATGTT    19657     C       C
                                AACA GGTGAAACCC GT
                                |||| |||||||||| ||
                                TTGT CCACTTTGGG CA
                                  A        A
GAM383  GPR4    3'  AGACAGGGTCTCACTGTGTT  60573         A   C
                                AACACGGTGA ACCC GTCT
                                |||||||||| |||| ||||
                                TTGTGTCACT TGGG CAGA
                                     C   A
GAM383  GPR81   3'  AGACAGGGTTTTGCCATGTT  51734     C  TG    C
                                AACA GG  AAACCC GTCT
                                |||| ||  |||||| ||||
                                TTGT CC  TTTGGG CAGA
                                  A  GT     A
GAM383  GPR81   3'  AGACGGGGTTTCATTGTGTT  51735
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGTTACTTTGGGGCAGA

GAM383  GRM7    5'  AGATTGGGTTTCACCATGTT  7780      C       C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG TAGA
                                  A        T
GAM383  HCS     3'  AGATGGTGTTTCACCATGTT  38963     C      C
                                AACA GGTGAAAC CCGTCT
                                |||| |||||||| ||||||
                                TTGT CCACTTTG GGTAGA
                                  A       T
GAM383  HTR1D   3'  AGACGGGGTTTCATCATGTT  7835      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CTACTTTGGGGCAGA
                                  A
GAM383  HUNK    3'  ATGGGGTTTCGCCATGTT    28177     C
                                AACA GGTGAAACCCCGT
                                |||| ||||||||||||
                                TTGT CCGCTTTGGGGTA
                                  A
GAM383  HUS1    3'  AGACAGGGTCTCACTGTGTT  92735         A   C
                                AACACGGTGA ACCC GTCT
                                |||||||||| |||| ||||
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                                TTGTGTCACT TGGG CAGA
                                      C    A
GAM383  HYAL4    5'  AGATGGGGTTTCACCGTGTT  25362
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGTAGA

GAM383  IGF1     3'  AGACGGGGTTTTACCATGTT  7057       C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCATTTTGGGGCAGA
                                  A
GAM383  IL11     3'  AGACAGGGTTTCACCATGTT  7174       C         C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A         A
GAM383  IMPA2    5'  AGATGGGGCTTCGCCATG    96941    C     A
                                CA GGTGAA CCCCGTCT
                                || ||||||| ||||||||
                                GT CCGCTT GGGGTAGA
                                 A     C
GAM383  INMT     3'  AGACGGAGTTTCGCTCTGT   23204    C       C
                                ACA GGTGAAAC CCGTCT
                                ||| |||||||| ||||||
                                TGT TCGCTTTG GGCAGA
                                  C       A
GAM383  INMT     3'  ATGGGGTTTCACCGTGTT    23207
                                AACACGGTGAAACCCCGT
                                ||||||||||||||||||
                                TTGTGCCACTTTGGGGTA

GAM383  JAK3     3'  AGATGAGGTTTCACCATG    5823     C       C
                                CA GGTGAAACC CGTCT
                                || |||||||| |||||
                                GT CCACTTTGG GTAGA
                                 A        A
GAM383  JRK      3'  AGACAGGGTCTCACTGTGTT  87813          A   C
                                AACACGGTGA ACCC GTCT
                                |||||||||| |||| ||||
                                TTGTGTCACT TGGG CAGA
                                      C    A
GAM383  LLGL1    3'  AGATGGGGTTTCACCATGTT  67412      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  LNK      3'  AGACAGGGTTTCACCATGTT  19628      C       C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
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                                TTGT CCACTTTGGG CAGA
                                  A        A
GAM383  LTB4R    5'  AGACGGGGTTTCACCATGTT  7456      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  LYZ      3'  AGACAGGGTTTCACCGTGTT  5890             C
                                AACACGGTGAAACCC GTCT
                                ||||||||||||||| ||||
                                TTGTGCCACTTTGGG CAGA
                                       A
GAM383  MAGEA10  3'  AGACAGATTCTTCACTGTGTT  41083          ACCCC_
                                AACACGGTGAA     GTCT
                                ||||||||||      ||||
                                TTGTGTCACTT     CAGA
                                      CTTAGA
GAM383  MAK      3'  AGACAGGGTTTCACCATGTT  20937     C        C
                                AACA GGTGAAACCC GTCT
                                |||| ||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A        A
GAM383  MDM2     3'  AGACAGGGTTTCACCGTGTT  11489            C
                                AACACGGTGAAACCC GTCT
                                |||||||||||||| ||||
                                TTGTGCCACTTTGGG CAGA
                                       A
GAM383  MEF2A    5'  AGATGGAGTTTCACCATGTT  19988     C      C
                                AACA GGTGAAAC CCGTCT
                                |||| |||||||| ||||||
                                TTGT CCACTTTG GGTAGA
                                  A       A
GAM383  MEFV     3'  AGACGGGGGTTTCACCATGTT  5924      C        _
                                AACA GGTGAAACCCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGGG CAGA
                                  A         G
GAM383  MHC2TA   3'  AGACAGGGTTTTGCCGTGTT  5966        TG     C
                                AACACGG  AAACCC GTCT
                                |||||||  |||||| ||||
                                TTGTGCC  TTTGGG CAGA
                                   GT     A
GAM383  MLANA    3'  AGACGGGGTTTCTCCATGTT  19756     C  T
                                AACA GG GAAACCCCGTCT
                                |||| || ||||||||||||
                                TTGT CC CTTTGGGGCAGA
                                  A  T
GAM383  MPL      3'  AGACAGGGTTTTGCCATGTT  19335     C  TG     C
                                AACA GG  AAACCC GTCT
                                |||| ||  |||||| ||||
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                                TTGT CC  TTTGGG CAGA
                                  A  GT     A
GAM383  MRPL49   3'  AGATGGGGTTTCACCATGTT  70157     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  MTR      3'  AGACAGGATTTCACTGTGTT  6010          C  C
                                AACACGGTGAAA CC GTCT
                                |||||||||||| || ||||
                                TTGTGTCACTTT GG CAGA
                                      A  A
GAM383  NCOA6    5'  AGGCGGGGTTTCGCCATGTT  26825     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||||
                                TTGT CCGCTTTGGGGCGGA
                                  A
GAM383  NCOA6    5'  ATGGGGTTTCATCATGTT    26827     C
                                AACA GGTGAAACCCCGT
                                |||| ||||||||||||
                                TTGT CTACTTTGGGGTA
                                  A
GAM383  NDRG3    3'  AGATGGAGTTTCACCATGTT  42761     C       C
                                AACA GGTGAAAC CCGTCT
                                |||| |||||||| ||||||
                                TTGT CCACTTTG GGTAGA
                                  A       A
GAM383  NPR2L    3'  AGACGGGGTCTCACTCTGTT  22591     C    A
                                AACA GGTGA ACCCCGTCT
                                |||| ||||| |||||||||
                                TTGT TCACT TGGGGCAGA
                                  C    C
GAM383  NQO1     3'  AGACGGCGTTTCACCATGTT  8040      C       C
                                AACA GGTGAAAC CCGTCT
                                |||| |||||||| ||||||
                                TTGT CCACTTTG GGCAGA
                                  A       C
GAM383  PCDHA9   3'  AGATGGGGTTTCACCGTGTT  49831
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGTAGA

GAM383  PCDHA9   3'  AGATGGGGTTTCATCATGTT  26609     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||||
                                TTGT CTACTTTGGGGTAGA
                                  A
GAM383  PER2     3'  AGACAGGGTTTCACCATGTT  15314     C       C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
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                                TTGT CCACTTTGGG CAGA
                                  A         A
GAM383  PIGR     3'  AGACAAAGTCTCACTGTGT   72983          A  CCC
                                ACACGGTGA AC   GTCT
                                ||||||||| ||   ||||
                                TGTGTCACT TG   CAGA
                                    C  AAA
GAM383  PIGR     3'  AGACAGGGTTTCACCGTGTT  72985             C
                                AACACGGTGAAACCC GTCT
                                |||||||||||||| ||||
                                TTGTGCCACTTTGGG CAGA
                                       A
GAM383  PIGR     3'  AGACAGGGTTTCGCCATGTT  72986      C         C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCGCTTTGGG CAGA
                                  A         A
GAM383  PIK3C2B  3'  AGACGGGGTTTCACCATGTT  12087      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  PIK3CD   3'  AGACGGGGGTTTCACCATGTT  18483      C          _
                                AACA GGTGAAACCCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGGG CAGA
                                  A          G
GAM383  POU2AF1  3'  AGACGGGGTTTCACCATGTT  21728      C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  PRKR     3'  AGACAGGGTTTCACCATGTT  12340      C         C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A         A
GAM383  PRKWNK3  3'  ATGGGGTTTCACTATGTT   62224      CG
                                AACA  GTGAAACCCCGT
                                ||||  ||||||||||||
                                TTGT  CACTTTGGGGTA
                                  AT
GAM383  PTGIS    3'  AGACGGGGTTTCCCCATGTT  8188       C  T
                                AACA GG GAAACCCCGTCT
                                |||| ||  ||||||||||||
                                TTGT CC CTTTGGGGCAGA
                                  A  C
GAM383  RAB36    3'  AGAGAGGTTTCACCATGTT   18150      C        CCG
                                AACA GGTGAAACC   TCT
                                |||| |||||||||   |||
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                                TTGT CCACTTTGG  AGA
                                  A       AG_
GAM383  RAB36   3' AGATGGGGTTTCTCCATGTT  18153    C  T
                                AACA GG GAAACCCCGTCT
                                |||| || ||||||||||||
                                TTGT CC CTTTGGGGTAGA
                                  A  T
GAM383  RABL2A  3' AGACGGGGTTTCACCATGTT  23992    C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  RABL2B  3' AGACGGGGTTTCACCATGTT  23969    C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  RAD52   3' AGACGGGGTCTGGCTGTGTT  57018       GAA
                                AACACGGT  ACCCCGTCT
                                ||||||||  |||||||||
                                TTGTGTCG  TGGGGCAGA
                                    GTC
GAM383  RAD52   3' AGACGGGGTCTGGCTGTGTT  57019       GAA
                                AACACGGT  ACCCCGTCT
                                ||||||||  |||||||||
                                TTGTGTCG  TGGGGCAGA
                                    GTC
GAM383  RAD52   3' AGACGGGGTCTGGCTGTGTT  57020       GAA
                                AACACGGT  ACCCCGTCT
                                ||||||||  |||||||||
                                TTGTGTCG  TGGGGCAGA
                                    GTC
GAM383  RAD52   3' AGACGGGGTCTGGCTGTGTT  57021       GAA
                                AACACGGT  ACCCCGTCT
                                ||||||||  |||||||||
                                TTGTGTCG  TGGGGCAGA
                                    GTC
GAM383  RBBP9   3' AGACAGGGTTTCACCATGTT  70677    C       C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A       A
GAM383  RGS9    5' AGACGGGGTTTTGTCATGTT  15170    C  TG
                                AACA GG  AAACCCCGTCT
                                |||| ||  ||||||||||
                                TTGT CT  TTTGGGGCAGA
                                  A  GT
GAM383  RHD     3' ACAGGGTTTCACCATGTT   32802    C       C
                                AACA GGTGAAACCC GT
                                |||| |||||||||| ||
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                                TTGT CCACTTTGGG CA
                                  A        A
GAM383  RHD     3'  ACAGGGTTTCACCATGTT   32803     C        C
                                AACA GGTGAAACCC GT
                                |||| |||||||||| ||
                                TTGT CCACTTTGGG CA
                                  A        A
GAM383  RHD     3'  AGATGGGGTTTCACCATGTT  32808     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  RHD     3'  AGATGGGGTTTCACCATGTT  32810     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  RPH3AL  3'  AGATGGGGTTTCTCCATGTT  23727     C  T
                                AACA GG GAAACCCCGTCT
                                |||| || ||||||||||||
                                TTGT CC CTTTGGGGTAGA
                                  A  T
GAM383  RPP30   3'  AGACGGGGTTTCACCGTGTT  22189
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGA

GAM383  SAS     3'  AGACAGGGTTTCACCATGTT  21092     C        C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A        A
GAM383  SCML2   3'  AGATGGGGTTTCTCCATGTT  21421     C  T
                                AACA GG GAAACCCCGTCT
                                |||| || ||||||||||||
                                TTGT CC CTTTGGGGTAGA
                                  A  T
GAM383  SERPINB9 3' AGACGGGGTTTCACCGTGTT  16007
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGA

GAM383  SH3GL3  5'  AGATGGGTTTCACCATGTT   13102     C        C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG TAGA
                                  A        _
GAM383  SHOX    3'  AGACGGCGTTTCACCGTGTT  6559            C
                                AACACGGTGAAAC CCGTCT
                                |||||||||||| ||||||
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                                TTGTGCCACTTTG GGCAGA
                                      C
GAM383  SHOX     3'  AGATGGGGTTTGACCATGTT  6562      C  G
                                AACA GGT AAACCCCGTCT
                                |||| ||| ||||||||||
                                TTGT CCA TTTGGGGTAGA
                                  A  G
GAM383  SIGLEC11 3'  AGACAGGGTTTTGCCATGTT  54646     C TG    C
                                AACA GG  AAACCC GTCT
                                |||| ||  |||||| ||||
                                TTGT CC  TTTGGG CAGA
                                  A GT     A
GAM383  SIL      5'  AGACGGGGTTTCACCATGTT  13149     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  SLC15A1  3'  AGATGGGGTTTCACCATGTT  18634     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  SLC3A2   5'  AGACGGGGTCTGACTGTGTT  11515       GAA
                                AACACGGT   ACCCCGTCT
                                ||||||||   |||||||||
                                TTGTGTCA   TGGGGCAGA
                                    GTC
GAM383  SLC3A2   5'  AGTTGGGGTCTCACTGTGTT  11519       A    T
                                AACACGGTGA ACCCCG CT
                                |||||||||| |||||| ||
                                TTGTGTCACT TGGGGT GA
                                     C     T
GAM383  SMAC     5'  AGATGGGGTTTCACCATGTT  57992     C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  SNAP23   3'  AGACAGGGTTTCACCATGT   15133     C       C
                                ACA GGTGAAACCC GTCT
                                ||| |||||||||| ||||
                                TGT CCACTTTGGG CAGA
                                  A        A
GAM383  SNX15    3'  ACGGGGTTACACCATGTT    74113     C   A
                                AACA GGTG AACCCCGT
                                |||| |||| ||||||||
                                TTGT CCAC TTGGGGCA
                                  A   A
GAM383  SPN      3'  AGACAGAGTTTCGCTTTGT   13362     C      CCC
                                ACA GGTGAAAC  GTCT
                                ||| ||||||||  ||||
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                                TGT TCGCTTTG   CAGA
                                  T       AGA
GAM383  SPN     3'  AGATGGGGTTTCACCATGTT   13365     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  TAPBP   3'  AGACGGGGTTTCACCATGTT   13543     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  TAPBP   3'  AGACGGGGTTTCACCGTGTT   13546
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGA

GAM383  TAPBP   3'  AGACGGGGTTTCACCGTGTT   13547
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGA

GAM383  TAT     3'  AGACAGGGTTTCACCATGTT   6247      C       C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A        A
GAM383  TBXA2R  3'  AGACGGGGTTTCACCGTGTT   8340
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGA

GAM383  TEM7    3'  AGACAGGGTCTCACTGTGT    40241         A   C
                                ACACGGTGA ACCC GTCT
                                ||||||||| |||| ||||
                                TGTGTCACT TGGG CAGA
                                      C   A
GAM383  TERF1   3'  AGGCGGGGTTTCACCATG    34388    C
                                CA GGTGAAACCCCGTCT
                                || |||||||||||||||
                                GT CCACTTTGGGGCGGA
                                  A
GAM383  TERF2   3'  AGACGGGGTTTCACCGTGTT   20143
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGA

GAM383  TIM3    3'  AGACAGGGTTTCACCATGTT   52347     C       C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
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                                TTGT CCACTTTGGG CAGA
                                  A         A
GAM383  TMPRSS3  3'  AGACAGGGTTTCACCATGTT  44011      C         C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A         A
GAM383  TNFAIP2  3'  AGACAGGGTCTTGCTGTGTT  21916        TG A    C
                                AACACGG  A ACCC GTCT
                                |||||||  | |||| ||||
                                TTGTGTC  T TGGG CAGA
                                   GT C    A
GAM383  TNFRSF10B 3'  AGACGGGGTTTCACCATGTT  15211      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  TP53     3'  AGATGGGGTCTCACAGTGTT  6792       G    A
                                AACAC GTGA ACCCCGTCT
                                ||||| |||| |||||||||
                                TTGTG CACT TGGGGTAGA
                                   A    C
GAM383  TPMT     3'  AGACGGGGTTTCACCATGTT  6301       C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  TRAF5    3'  AGACGGAGTTTTGCCATGTT  17265      C  TG    C
                                AACA GG  AAAC CCGTCT
                                |||| ||  |||| ||||||
                                TTGT CC  TTTG GGCAGA
                                  A  GT    A
GAM383  TRIM9    5'  AGACGGAGTTTCGCTCTTGT  31438     C _      C
                                ACA G GTGAAAC CCGTCT
                                ||| | ||||||| ||||||
                                TGT C CGCTTTG GGCAGA
                                  T T       A
GAM383  TRPM6    3'  AGATGGGGTTTCACCATGTT  35023      C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  TRPV1    3'  AGACAGAGTTTCACTCTTGT  55648     C _      CCC
                                ACA G GTGAAAC   GTCT
                                ||| | |||||||   ||||
                                TGT C CACTTTG   CAGA
                                  T T       AGA
GAM383  TRPV1    3'  AGACAGAGTTTCACTCTTGT  55649     C _      CCC
                                ACA G GTGAAAC   GTCT
                                ||| | |||||||   ||||
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                                TGT C CACTTTG   CAGA
                                  T T      AGA
GAM383  TRPV1   3'  AGACGGGGTTTCACCATGTT  55651     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  TRPV1   3'  AGACGGGGTTTCACCATGTT  55652     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  TRPV1   3'  ATGGGGTTTCGCCATGTT   55658     C
                                AACA GGTGAAACCCCGT
                                |||| ||||||||||||
                                TTGT CCGCTTTGGGGTA
                                  A
GAM383  UGDH    3'  AGACAGGGTTTCACCATGT   13989     C       C
                                ACA GGTGAAACCC GTCT
                                ||| |||||||||| ||||
                                TGT CCACTTTGGG CAGA
                                  A        A
GAM383  VENTX2  3'  ATGGGGTTTCACCATGTT   27854     C
                                AACA GGTGAAACCCCGT
                                |||| ||||||||||||
                                TTGT CCACTTTGGGGTA
                                  A
GAM383  VHL     3'  AGACAGTGTTTCGCCATGTT  6824      C       CCC
                                AACA GGTGAAAC   GTCT
                                |||| ||||||||   ||||
                                TTGT CCGCTTTG   CAGA
                                  A       TGA
GAM383  VHL     3'  AGACGGGGTTTCACCATGTT  6826      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  VIPR2   3'  AGACAGGGTTTCACCATGTT  14055     C       C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A        A
GAM383  WBSCR5  5'  AGATGGAATTTCACCGTGTT  42107         CC
                                AACACGGTGAAA  CCGTCT
                                ||||||||||||  ||||||
                                TTGTGCCACTTT  GGTAGA
                                      AA
GAM383  XRCC2   3'  AGACGGGGTTTCACCATGTT  19488     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
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                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  YES1    3'  AGACGCAGTTTCACCGTGTT  19526          CC
                                AACACGGTGAAAC  CGTCT
                                |||||||||||||  |||||
                                TTGTGCCACTTTG  GCAGA
                                      AC
GAM383  ZNF157  3'  AGACGGGTTTCACCATGTT  14324    C       C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A       _
GAM383  ZNF264  3'  AGACGGGGTTTCACCATGTT  14190    C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  ZNF74   5'  AGACGGGGTTTTGCCATGTT  14253    C  TG
                                AACA GG  AAACCCCGTCT
                                |||| ||  ||||||||||
                                TTGT CC  TTTGGGGCAGA
                                  A  GT
GAM383  AAK1    3'  AGACAGAGTTTCACTCTTGT  30511    C _     CCC
                                ACA G GTGAAAC   GTCT
                                ||| | |||||||   ||||
                                TGT C CACTTTG   CAGA
                                  T T      AGA
GAM383  AAK1    3'  AGATGGGGTTTCTCCATGTT  30514    C  T
                                AACA GG GAAACCCCGTCT
                                |||| || ||||||||||||
                                TTGT CC CTTTGGGGTAGA
                                  A  T
GAM383  ANAPC11 5'  AGACGGAGTTTCGTCATGTT  33631    C GT    C
                                AACA G  GAAAC CCGTCT
                                |||| |  ||||| ||||||
                                TTGT C  CTTTG GGCAGA
                                  A TG    A
GAM383  ANKT    3'  AGACAGGGTCTCACTGTGTT  33454        A   C
                                AACACGGTGA ACCC GTCT
                                |||||||||| |||| ||||
                                TTGTGTCACT TGGG CAGA
                                     C   A
GAM383  AP3S2   3'  AGACAGGGTTTCACCATGTT  20639    C       C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A        A
GAM383  APOL2   3'  AGACGGGGTTTCACTGTGTT  48785
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
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                                TTGTGTCACTTTGGGGCAGA

GAM383  ARHF     3' AGACAGGGTTTCACCATGTT  39258      C        C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A         A
GAM383  ARHGAP5  5' AGATGGGGTTTCTCCATGTT  77595      C  T
                                AACA GG GAAACCCCGTCT
                                |||| || ||||||||||||
                                TTGT CC CTTTGGGGTAGA
                                  A  T
GAM383  ASB16    5' AGACGGGGTCTCACTCTGT   55968     C     A
                                ACA GGTGA ACCCCGTCT
                                ||| ||||| |||||||||
                                TGT TCACT TGGGGCAGA
                                  C    C
GAM383  ASB16    3' AGACGGGGTCTCGCCATGTT  55969      C     A
                                AACA GGTGA ACCCCGTCT
                                |||| ||||| |||||||||
                                TTGT CCGCT TGGGGCAGA
                                  A    C
GAM383  ATP1B4   3' AGACAGGGTTTCACCATGTT  24830      C        C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A         A
GAM383  BA108L7.2 3' AGATGGGGGTTTCACCATGTT 49064     C         _
                                AACA GGTGAAACCCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGGG TAGA
                                  A         G
GAM383  BAGE     3' AGATGGAGTTTCACTGTGT   8637          C
                                ACACGGTGAAAC CCGTCT
                                |||||||||||| ||||||
                                TGTGTCACTTTG GGTAGA
                                       A
GAM383  BNIP-S   3' AGACGGGGTTTCACCATGTT  57098      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  BRAG     3' AGATGGGGTCTCGCCGTGTT  30095         A
                                AACACGGTGA ACCCCGTCT
                                |||||||||| |||||||||
                                TTGTGCCGCT TGGGGTAGA
                                      C
GAM383  C11orf17 3' AGACGGGGTTTAACCATGTT  40573      C  G
                                AACA GGT AAACCCCGTCT
                                |||| ||| ||||||||||
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                                TTGT CCA TTTGGGGCAGA
                                  A   A
GAM383  C13orf1   3'  AGATGGGGTTTCACCATGTT  40349     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  C20orf142 3'  AGATGGGGTTTCTCCATGTT  75270     C  T
                                AACA GG GAAACCCCGTCT
                                |||| || ||||||||||||
                                TTGT CC CTTTGGGGTAGA
                                  A  T
GAM383  C22orf19  3'  AGACGGGGTCTTGCTCTGTT  14812     C  TG A
                                AACA GG  A ACCCCGTCT
                                |||| ||  | |||||||||
                                TTGT TC  T TGGGGCAGA
                                  C  GT C
GAM383  C6orf5    3'  AGACAGGGTTTCATATTG    31965    CG       C
                                CA  GTGAAACCC GTCT
                                ||  ||||||||| ||||
                                GT  TACTTTGGG CAGA
                                 TA        A
GAM383  C6orf5    3'  AGACAGGGTTTTGCCATGTT  31967     C  TG     C
                                AACA GG  AAACCC GTCT
                                |||| ||  |||||| ||||
                                TTGT CC  TTTGGG CAGA
                                  A  GT     A
GAM383  C9orf9    3'  AGACAGCGTTTCACCATGTT  39008     C       CCC
                                AACA GGTGAAAC   GTCT
                                |||| ||||||||   ||||
                                TTGT CCACTTTG   CAGA
                                  A       CGA
GAM383  CARD6     3'  AGACAGAGTTTCACTCTTGT  51836     C _     CCC
                                ACA G GTGAAAC   GTCT
                                ||| | |||||||   ||||
                                TGT C CACTTTG   CAGA
                                 T T      AGA
GAM383  CCRN4L    3'  AGACGGGGTTTCACCGTGTT  25065
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGA

GAM383  CDC14B    3'  AGACAGGGTTTCACCATGTT  14770     C        C
                                AACA GGTGAAACCC GTCT
                                |||| ||||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A        A
GAM383  CEACAM8   3'  AGACGGGGTTTCACTGTG    10175
                                CACGGTGAAACCCCGTCT
                                ||||||||||||||||||
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                                GTGTCACTTTGGGGCAGA

GAM383  CENPH    3'  AGACGGGGTTTCACCGTGTT   43562
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGA

GAM383  CHRAC1   3'  AGACGGGGTTCACCATGTT   34329     C     A
                                AACA GGTGAA CCCCGTCT
                                |||| |||||| ||||||||
                                TTGT CCACTT GGGGCAGA
                                  A     _
GAM383  CHSY1    3'  AGACGGGGTTTCACCATG    30559    C
                                CA GGTGAAACCCCGTCT
                                || ||||||||||||||
                                GT CCACTTTGGGGCAGA
                                 A
GAM383  CIP29    3'  AGACGGGGTTTCACCATGTT   51367     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  COLEC12  3'  AGAGGGGTTTCACAGTGTT   48605      G        G
                                AACAC GTGAAACCCC TCT
                                ||||| |||||||||| |||
                                TTGTG CACTTTGGGG AGA
                                   A        _
GAM383  CPSF2    3'  AGACAGGGTTTCACCATGTT   62256     C        C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A        A
GAM383  CPSF2    3'  AGACGGGGTTTCTCCATGTT   62259     C  T
                                AACA GG GAAACCCCGTCT
                                |||| || ||||||||||||
                                TTGT CC CTTTGGGGCAGA
                                  A  T
GAM383  DBR1     3'  ACAGGGTTTCACCGTGTT    33056            C
                                AACACGGTGAAACCC GT
                                |||||||||||||| ||
                                TTGTGCCACTTTGGG CA
                                         A
GAM383  DCOHM    3'  AGATGGGGTTTCGCCATGTT   50509     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCGCTTTGGGGTAGA
                                  A
GAM383  DKFZp434A2417 3'  AGACGGGGTTTCTCCATGTT   66672     C  T
                                AACA GG GAAACCCCGTCT
                                |||| || ||||||||||||
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                                TTGT CC CTTTGGGGCAGA
                                  A  T
GAM383  DKFZP434C212 3'  ACGGGGTTTCACCATGTT    69478      C
                                AACA GGTGAAACCCCGT
                                |||| ||||||||||||
                                TTGT CCACTTTGGGGCA
                                  A
GAM383  DKFZP434D146 3'  AGACAGGGTTTCATCATGTT   32129      C         C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CTACTTTGGG CAGA
                                  A         A
GAM383  DKFZP434F0318 3'  AGACAGGGTTTCGCCATGTT   48741      C         C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCGCTTTGGG CAGA
                                  A         A
GAM383  DKFZp434O0515 5'  AGACGGAGGGGTTTCATGGT   66508    G         ___
                                AC GTGAAACCCC   GTCT
                                || ||||||||||   ||||
                                TG TACTTTGGGG   CAGA
                                 G         AGG
GAM383  DKFZp547H025 3'  AGATGAGGTTTCACCATGTT   39767      C         C
                                AACA GGTGAAACC CGTCT
                                |||| ||||||||| |||||
                                TTGT CCACTTTGG GTAGA
                                  A         A
GAM383  DKFZP564G092 5'  AGACGGAGTTTCGCTCTTGT   32151     C _      C
                                ACA G GTGAAAC CCGTCT
                                ||| | ||||||| ||||||
                                TGT C CGCTTTG GGCAGA
                                  T T       A
GAM383  DKFZP564O0423 3'  AGATGGGGTCTCACTATGTT   93340      CG    A
                                AACA  GTGA ACCCCGTCT
                                ||||  |||| |||||||||
                                TTGT  CACT TGGGGTAGA
                                  AT    C
GAM383  DKFZP586A0522 3'  AGACAGGGTCTCACTGTGTT   26725           A    C
                                AACACGGTGA ACCC GTCT
                                |||||||||| |||| ||||
                                TTGTGTCACT TGGG CAGA
                                     C    A
GAM383  DKFZp761F2014 3'  AGCACCTGGTTTCACCATG    39937    C        CC  _
                                CA GGTGAAACC  GT CT
                                || |||||||||  || ||
                                GT CCACTTTGG  CA GA
                                 A         TC  C
GAM383  DKFZp761J139 5'  AGATGGGGTTTGACCATGTT   51097      C   G
                                AACA GGT AAACCCCGTCT
                                |||| ||| ||||||||||
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                                  TTGT CCA TTTGGGGTAGA
                                    A   G
GAM383  DKFZp761N1114 3'  AGACGGGATTTCACCGTGTT  79773          C
                                  AACACGGTGAAA CCCGTCT
                                  |||||||||||| |||||||
                                  TTGTGCCACTTT GGGCAGA
                                         A
GAM383  DKFZp761O0113 5'  AGACGGGGTTTCTCCATGTT  37886     C  T
                                  AACA GG GAAACCCCGTCT
                                  |||| || ||||||||||||
                                  TTGT CC CTTTGGGGCAGA
                                    A  T
GAM383  DKFZp762P2111 3'  AGACAGGGTTTCATCATGTT  87621     C       C
                                  AACA GGTGAAACCC GTCT
                                  |||| |||||||||| ||||
                                  TTGT CTACTTTGGG CAGA
                                    A        A
GAM383  DSCR6   3'  AGACTCGGTTTCACCATGTT  39055     C       CC
                                  AACA GGTGAAACC  GTCT
                                  |||| |||||||||  ||||
                                  TTGT CCACTTTGG  CAGA
                                    A        CT
GAM383  EREG    3'  AGGCGGGGTTTCACCATGTT  9300      C
                                  AACA GGTGAAACCCCGTCT
                                  |||| ||||||||||||||
                                  TTGT CCACTTTGGGGCGGA
                                    A
GAM383  ERO1L   3'  AGACAAGGTTTTGCTGTGTT  28152       TG    CC
                                  AACACGG  AAACC  GTCT
                                  |||||||  |||||  ||||
                                  TTGTGTC  TTTGG  CAGA
                                      GT    AA
GAM383  EVI5    3'  AGACAGGTGTCTCACTGTGTT  20192         A _ C
                                  AACACGGTGA AC CC GTCT
                                  |||||||||| || || ||||
                                  TTGTGTCACT TG GG CAGA
                                        C  T  A
GAM383  EVI5    3'  AGATGGGGTTTCACCATGTT  20195     C
                                  AACA GGTGAAACCCCGTCT
                                  |||| ||||||||||||||
                                  TTGT CCACTTTGGGGTAGA
                                    A
GAM383  FBP17   3'  AGACAGGGTTTCACCGTGTT  73141           C
                                  AACACGGTGAAACCC GTCT
                                  |||||||||||||| ||||
                                  TTGTGCCACTTTGGG CAGA
                                         A
GAM383  FER1L4  3'  AGACAGGGTTTCACCATGTT  48107     C       C
                                  AACA GGTGAAACCC GTCT
                                  |||| |||||||||| ||||
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                                TTGT CCACTTTGGG CAGA
                                  A        A
GAM383  FKBP9    3' AGACGGGGTTTCACCGTGTT  95710
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGA

GAM383  FLJ10298 3' AGACGGGGTTTCACCATGTT  36450     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  FLJ10346 5' AGGCAGGGTTTCACCATGTT  36520     C        C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CGGA
                                  A        A
GAM383  FLJ10535 3' AGACGGGGTTTCATTATGTT  36733     CG
                                AACA  GTGAAACCCCGTCT
                                ||||  ||||||||||||||
                                TTGT  TACTTTGGGGCAGA
                                  AT
GAM383  FLJ10535 3' AGATGGGGTTTCACCATGTT  36735     C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  FLJ10560 3' AGACGGGGTTTCACCGTGTT  36789
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGA

GAM383  FLJ10713 3' AGATGGGGTTTCACCATGTT  36995     C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  FLJ10901 3' AGATGGGGTTTCATCATGTT  37351     C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
                                TTGT CTACTTTGGGGTAGA
                                  A
GAM383  FLJ10956 3' AGACGGGGTTTCACCATGTT  37459     C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  FLJ11193 3' AGATGGGGTCTCACCATGTT  37744     C    A
                                AACA GGTGA ACCCCGTCT
                                |||| ||||| |||||||||
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                                TTGT CCACT TGGGGTAGA
                                  A    C
GAM383  FLJ12363  3'  ATGGGGTTTCACCATGTT    50627     C
                                AACA GGTGAAACCCCGT
                                |||| ||||||||||||
                                TTGT CCACTTTGGGGTA
                                  A
GAM383  FLJ12581  3'  AGACAGGGTTTCACTGTGTT  46328           C
                                AACACGGTGAAACCC GTCT
                                |||||||||||||| ||||
                                TTGTGTCACTTTGGG CAGA
                                       A
GAM383  FLJ12687  3'  AGACAGGGTTTCACCATGTT  46740     C       C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A        A
GAM383  FLJ12876  3'  AGACGGGGTTTCACTGTG    43084
                                CACGGTGAAACCCCGTCT
                                ||||||||||||||||||
                                GTGTCACTTTGGGGCAGA

GAM383  FLJ12891  3'  AGACGGGGTCTTGTTGTGT   46915       TG A
                                ACACGG  A ACCCCGTCT
                                ||||||  | |||||||||
                                TGTGTT  T TGGGGCAGA
                                   GT C
GAM383  FLJ12903  3'  AGACGGAGTTTCGCTGTTGT  43062    _      C
                                ACA CGGTGAAAC CCGTCT
                                ||| ||||||||| ||||||
                                TGT GTCGCTTTG GGCAGA
                                  T        A
GAM383  FLJ12973  3'  AGATGGGGTTTCATCATGTT  46637     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CTACTTTGGGGTAGA
                                  A
GAM383  FLJ12975  3'  AGACGGGGTTTCGCCTTGTT  70181     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCGCTTTGGGGCAGA
                                  T
GAM383  FLJ13072  5'  AGACAGGGTTTCACCATGTT  91382     C       C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A        A
GAM383  FLJ13114  3'  AGATGGAGTTTCACCATGTT  44892     C      C
                                AACA GGTGAAAC CCGTCT
                                |||| |||||||| ||||||
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                                TTGT CCACTTTG GGTAGA
                                  A       A
GAM383  FLJ13188 3' AGACAGAGTTTTGCTGTGTT  42186       TG   CCC
                                AACACGG  AAAC   GTCT
                                |||||||  ||||   ||||
                                TTGTGTC  TTTG   CAGA
                                   GT    AGA
GAM383  FLJ13197 3' AGACAAGAGTTTCACCATGTT 45171     C      CCC_
                                AACA GGTGAAAC    GTCT
                                ||||  ||||||||    ||||
                                TTGT CCACTTTG    CAGA
                                  A       AGAA
GAM383  FLJ13305 5' AGATGGGGTTTCACCATGTT  91703     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  FLJ13456 3' AGACAGAGTTTCACTCTGT   66524     C      CCC
                                ACA GGTGAAAC   GTCT
                                |||  ||||||||   ||||
                                TGT TCACTTTG   CAGA
                                  C       AGA
GAM383  FLJ13769 5' AGATGGGGTTTCACTATGTT  47240     CG
                                AACA  GTGAAACCCCGTCT
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGA
                                  AT
GAM383  FLJ14442 3' AGATGGGGTTTTACCATGTT  52374     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCATTTTGGGGTAGA
                                  A
GAM383  FLJ14950 3' AGACAGGGTTTCACCATGTT  52778     C        C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A        A
GAM383  FLJ14957 3' AGACGGGGTTTCACCATGTT  52805     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  FLJ20034 3' AGATGGGGTCTCTCCATGTT  34832     C  T  A
                                AACA GG GA ACCCCGTCT
                                |||| || || |||||||||
                                TTGT CC CT TGGGGTAGA
                                  A  T  C
GAM383  FLJ20136 3' AGATGAGTTTCACCATGTT   35090     C      CC
                                AACA GGTGAAAC  CGTCT
                                |||| ||||||||  |||||
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                                TTGT CCACTTTG  GTAGA
                                  A       A_
GAM383  FLJ20344  3'  AGACAGGGTTTCACCATGTT  35473     C        C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A        A
GAM383  FLJ20507  3'  AGACAGGGTTTCACCATGTT  35727     C        C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A        A
GAM383  FLJ20897  5'  AGACGGGGTTTCAACGTGTT  51473       G
                                AACACG TGAAACCCCGTCT
                                |||||| ||||||||||||
                                TTGTGC ACTTTGGGGCAGA
                                   A
GAM383  FLJ21302  3'  AGACAGGGTTTCACCATGTT  43500     C        C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A        A
GAM383  FLJ21324  5'  AGATGGGGTTTCACCATGTT  92839     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  FLJ21603  3'  AGATGGGGTTTCACCCTGTT  45765     C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  C
GAM383  FLJ22002  3'  AGATGAGGTTTCGCCATGTT  96359     C        C
                                AACA GGTGAAACC CGTCT
                                |||| ||||||||| |||||
                                TTGT CCGCTTTGG GTAGA
                                  A        A
GAM383  FLJ22060  3'  AGACAACACTATTTCATCGTGT 45158           CCCC___
          T                      AACACGGTGAAA      GTCT
                                ||||||||||||      ||||
                                TTGTGCTACTTT      CAGA
                                      ATCACAA
GAM383  FLJ22167  5'  AGATGGGGTCTCACTGTGTT  44859         A
                                AACACGGTGA ACCCCGTCT
                                |||||||||| |||||||||
                                TTGTGTCACT TGGGGTAGA
                                     C
GAM383  FLJ22329  3'  AGACGGGGTTTCACCATGTT  45390     C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
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                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  FLJ22529  3'  AGACAGGGTTTCATCATGTT  45937     C        C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CTACTTTGGG CAGA
                                  A        A
GAM383  FLJ22684  3'  AGACAGGGTTTCACCATGTT  47462     C        C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A        A
GAM383  FLJ22794  3'  AGACAGGGTTTCACCATGTT  93234     C        C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A        A
GAM383  FLJ22969  3'  AGACAGGGTTTCACCATGTT  69194     C        C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A        A
GAM383  FLJ23024  3'  AGACGGGGTTTCACCATGTT  46834     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  FLJ23392  3'  AGACAGGGTTTCACCATGTT  45872     C        C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A        A
GAM383  FLJ23392  3'  AGACAGGGTTTCACCGTGTT  45875              C
                                AACACGGTGAAACCC GTCT
                                |||||||||||||| ||||
                                TTGTGCCACTTTGGG CAGA
                                       A
GAM383  FLJ23392  3'  AGACGGGGTTTCACCGTGTT  45876
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGA

GAM383  FLJ23519  3'  AGATGGGGTTTCACCGTGTT  50943
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGTAGA

GAM383  FLJ23556  3'  AGACGGGGTTTCACCGTGTT  46423
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
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                                TTGTGCCACTTTGGGGCAGA

GAM383  FLJ25416  5'  AGATGGGGTTTCACCATGTT  59445     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  FLJ31153  3'  AGATGGGGTTTCACCATG    58740    C
                                CA GGTGAAACCCCGTCT
                                || ||||||||||||||
                                GT CCACTTTGGGGTAGA
                                 A
GAM383  FLJ32865  3'  AGACAGAGTTTCGCTCTTGT  58796    C _     CCC
                                ACA G GTGAAAC   GTCT
                                ||| | |||||||   ||||
                                TGT C CGCTTTG   CAGA
                                  T T      AGA
GAM383  FLJ32865  3'  AGACGGGGTTTCTCCGTGTT  58798       T
                                AACACGG GAAACCCCGTCT
                                ||||||| ||||||||||||
                                TTGTGCC CTTTGGGGCAGA
                                    T
GAM383  FLJ32894  3'  AGATGGGATTTCACTGTGTT  58990          C
                                AACACGGTGAAA CCCGTCT
                                |||||||||||| |||||||
                                TTGTGTCACTTT GGGTAGA
                                       A
GAM383  GMPPB     5'  AGACAGGGTTTCACCAGGTT  26216    AC       C
                                AAC  GGTGAAACCC GTCT
                                |||  |||||||||| ||||
                                TTG  CCACTTTGGG CAGA
                                  GA        A
GAM383  GNG4      3'  AGACGGGGTTTCACCATGTT  16838    C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  GOLGA3    3'  ATGGGGTTTCACCATGTT    20880    C
                                AACA GGTGAAACCCCGT
                                |||| ||||||||||||
                                TTGT CCACTTTGGGGTA
                                  A
GAM383  GREB1     3'  AGACGGGGTTTCACCATGTT  28552    C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  GRWD      3'  AGACGGGGTTTCACCATGTT  49771    C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||
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                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  GTF2E1   3'  AGGCAGGGTTTCACCATGTT  19791     C       C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CGGA
                                  A        A
GAM383  GTPBG3   3'  AGACAAGGTTTCACCATGTT  51886     C       CC
                                AACA GGTGAAACC  GTCT
                                |||| |||||||||  ||||
                                TTGT CCACTTTGG  CAGA
                                  A        AA
GAM383  H2AV     3'  AGACGTGGGGTTTCACCATGTT 25754     C        __
                                AACA GGTGAAACCCC  GTCT
                                |||| ||||||||||  ||||
                                TTGT CCACTTTGGGG  CAGA
                                  A         TG
GAM383  HARS2    3'  AGACGGGGTTTTACCATGTT  55861     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCATTTTGGGGCAGA
                                  A
GAM383  HCA4     3'  AGACGGGGTTTTGCCATGTT  57737     C  TG
                                AACA GG  AAACCCCGTCT
                                |||| ||  ||||||||||
                                TTGT CC  TTTGGGGCAGA
                                  A  GT
GAM383  HCGIV.9  3'  AGACAGGGTTTTTTGTTGTT  39128     _  T     C
                                AACA CGG GAAACCC GTCT
                                |||| ||| ||||||| ||||
                                TTGT GTT TTTTGGG CAGA
                                  T  _     A
GAM383  HRH4     3'  AGACAGGGTATTGCCGTGTT  41523       TG A   C
                                AACACGG  A ACCC GTCT
                                |||||||  | |||| ||||
                                TTGTGCC  T TGGG CAGA
                                    GT A   A
GAM383  HRH4     3'  AGATGAAGTCTCACTGTGTT  41525         A  CC
                                AACACGGTGA AC  CGTCT
                                |||||||||| ||  |||||
                                TTGTGTCACT TG  GTAGA
                                     C  AA
GAM383  HSMPP8   3'  AGACGGAGTTTCGCTCTTGT  95123     C _     C
                                ACA G GTGAAAC CCGTCT
                                ||| | ||||||| ||||||
                                TGT C CGCTTTG GGCAGA
                                  T T      A
GAM383  HSNOV1   3'  AGACATGGGGTTTCACCATGTT 34422     C        __
                                AACA GGTGAAACCCC  GTCT
                                |||| ||||||||||  ||||
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                                TTGT CCACTTTGGGG  CAGA
                                  A          TA
GAM383  HSNOV1   3' AGATGGGGTTTCGCCATGTT  34424      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCGCTTTGGGGTAGA
                                  A
GAM383  HSPC065  3' AGATGGGGTTTCACCATGTT  27134      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  HSPC065  3' AGATGGGGTTTCACGATGTT  27137      CG
                                AACA  GTGAAACCCCGTCT
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGA
                                  AG
GAM383  HSPC232  3' AGATGGGGTTCACCATGTT   33653      C     A
                                AACA GGTGAA CCCCGTCT
                                |||| |||||| ||||||||
                                TTGT CCACTT GGGGTAGA
                                  A     _
GAM383  HT002    3' ACAGGGTTTCACCGTGTT    26784             C
                                AACACGGTGAAACCC GT
                                |||||||||||||| ||
                                TTGTGCCACTTTGGG CA
                                      A
GAM383  ICK      3' AGACGGGGTTTCACTGTGTT  33678
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGTCACTTTGGGGCAGA

GAM383  JAM1     3' AGACAGGGTTTCACCATGTT  34208      C         C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A         A
GAM383  JAM1     3' AGACAGGGTTTCACCATGTT  34209      C         C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A         A
GAM383  KIAA0063 3' AGATGGGGTTTCTCCATGTT  30249      C  T
                                AACA GG GAAACCCCGTCT
                                |||| || ||||||||||||
                                TTGT CC CTTTGGGGTAGA
                                  A  T
GAM383  KIAA0161 3' AGACGGAGTTTCGCTTTTGT  29186      C_       C
                                ACA  GGTGAAAC CCGTCT
                                |||  |||||||| ||||||
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                                TGT  TCGCTTTG GGCAGA
                                  TT       A
GAM383  KIAA0161  3'  AGACGGGGTTTCACCATGTT  29187     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  KIAA0186  3'  AGACAGAGTTTTACCATGTT  41092     C       CCC
                                AACA GGTGAAAC   GTCT
                                |||| ||||||||   ||||
                                TTGT CCATTTTG   CAGA
                                  A       AGA
GAM383  KIAA0186  3'  AGATGGGGTTTCACCATGTT  41095     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  KIAA0205  3'  AGATGGGGTTTCACCATGTT  30199     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  KIAA0210  5'  AGACGGAGGAGTTTCACCATGT 29145      C      __ _
          T                      AACA GGTGAAA  CC CCGTCT
                                |||| |||||||  || ||||||
                                TTGT CCACTTT  GG GGCAGA
                                  A       GA  A
GAM383  KIAA0426  3'  AGACGGGGTTTCACCATGTT  28915     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  KIAA0459  3'  AGACGGGGTTTCACCATGTT  61641     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  KIAA0469  3'  AGACAGGGTCTTGCTGTGTT  29965       TG A    C
                                AACACGG  A ACCC GTCT
                                |||||||  | |||| ||||
                                TTGTGTC  T TGGG CAGA
                                    GT C    A
GAM383  KIAA0469  3'  AGACGGGATTTCACTGTGTT  29967          C
                                AACACGGTGAAA CCCGTCT
                                |||||||||||| |||||||
                                TTGTGTCACTTT GGGCAGA
                                       A
GAM383  KIAA0513  5'  AGACAGGGTTTCGCCATGTT  29008     C        C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
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                                TTGT CCGCTTTGGG CAGA
                                  A         A
GAM383  KIAA0513 3' AGATGGGGTTTCACCATG    29014    C
                                CA GGTGAAACCCCGTCT
                                || |||||||||||||||
                                GT CCACTTTGGGGTAGA
                                 A
GAM383  KIAA0527 3' AGATGGAGTTTCACCATGTT  97486     C       C
                                AACA GGTGAAAC CCGTCT
                                |||| |||||||| ||||||
                                TTGT CCACTTTG GGTAGA
                                  A       A
GAM383  KIAA0555 3' AGACAGGGTTTCACTATG    60734    CG       C
                                CA  GTGAAACCC GTCT
                                ||  ||||||||| ||||
                                GT  CACTTTGGG CAGA
                                 AT        A
GAM383  KIAA0557 3' AGACGGGGCCTTGCTGTGT   78542       TG AA
                                ACACGG  A  CCCCGTCT
                                ||||||  |  ||||||||
                                TGTGTC  T  GGGGCAGA
                                   GT CC
GAM383  KIAA0557 3' AGATGGGGTTTCTCCATGTT  78544     C  T
                                AACA GG GAAACCCCGTCT
                                |||| || ||||||||||||
                                TTGT CC CTTTGGGGTAGA
                                  A  T
GAM383  KIAA0561 3' AGACGGGGTTTCACCATGTT  66462     C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  KIAA0563 5' AGGCGGAGTTTCGCCATGTT  29867     C       C
                                AACA GGTGAAAC CCGTCT
                                |||| |||||||| ||||||
                                TTGT CCGCTTTG GGCGGA
                                  A       A
GAM383  KIAA0599 3' AGACGGGGTTTCGCCGTGTT  77684
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCGCTTTGGGGCAGA

GAM383  KIAA0682 3' AGACGGGGTTTCACCATGT   30011    C
                                ACA GGTGAAACCCCGTCT
                                ||| |||||||||||||||
                                TGT CCACTTTGGGGCAGA
                                  A
GAM383  KIAA0682 3' AGACTGGGTTTCACCATGT   30014    C       C
                                ACA GGTGAAACCC GTCT
                                ||| ||||||||| ||||
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                                TGT CCACTTTGGG CAGA
                                  A         T
GAM383  KIAA0737 3' AGACAGGGTTTCACCATGTT  29794     C         C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A         A
GAM383  KIAA0737 3' AGATGGGGTCTCACTATGTT  29799     CG    A
                                AACA  GTGA ACCCCGTCT
                                ||||  |||| |||||||||
                                TTGT  CACT TGGGGTAGA
                                  AT    C
GAM383  KIAA0798 3' AGACGGGGTTTCACTGTGTT  28439
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGTCACTTTGGGGCAGA

GAM383  KIAA0828 3' AGACAGGGTTTCACTATGTT  82107     CG        C
                                AACA  GTGAAACCC GTCT
                                ||||  ||||||||| ||||
                                TTGT  CACTTTGGG CAGA
                                  AT        A
GAM383  KIAA0831 3' AGACGGGGGTTTTCACCATGT 30625     C      __
                                ACA GGTGAAA  CCCCGTCT
                                ||| |||||||  ||||||||
                                TGT CCACTTT  GGGGCAGA
                                  A       TG
GAM383  KIAA0841 3' ACGGGGTTTCATCATGTT    71885     C
                                AACA GGTGAAACCCCGT
                                |||| ||||||||||||
                                TTGT CTACTTTGGGGCA
                                  A
GAM383  KIAA0861 3' AGACGGGGTTTCCCCGTGTT  90340       T
                                AACACGG GAAACCCCGTCT
                                ||||||| ||||||||||||
                                TTGTGCC CTTTGGGGCAGA
                                    C
GAM383  KIAA0884 3' AGGTGAGGTTTCACCATGTT  70747     C       C GT
                                AACA GGTGAAACC C  CT
                                |||| ||||||||| |  ||
                                TTGT CCACTTTGG G  GA
                                  A        A TG
GAM383  KIAA0889 3' AGACGGGGTTTCACCGTGTT  31751
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGA

GAM383  KIAA0931 3' AGACGGGGTTTCACCATGTT  68001     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
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                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  KIAA0961 3' AGATGGGGTTTCACCATGTT  30386     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  KIAA1041 3' AGATGGGGTTTCACCATGTT  30816     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  KIAA1054 3' AGGTGGGGTTTCACCGTGTT  68959           GT
                                AACACGGTGAAACCCC  CT
                                ||||||||||||||||  ||
                                TTGTGCCACTTTGGGG  GA
                                      TG
GAM383  KIAA1115 5' AGACAGGGTTTCGCCATGTT  30684     C       C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCGCTTTGGG CAGA
                                  A        A
GAM383  KIAA1143 3' AGACGGGGTTTCACTTTGTT  69227     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT TCACTTTGGGGCAGA
                                  T
GAM383  KIAA1161 5' AGATGGGGTTTACCATGTT   82636     C    A
                                AACA GGTGAA CCCCGTCT
                                |||| |||||| ||||||||
                                TTGT CCATTT GGGGTAGA
                                  A    _
GAM383  KIAA1170 3' ACAGGGTTTCACCATGTT    70404     C       C
                                AACA GGTGAAACCC GT
                                |||| |||||||||| ||
                                TTGT CCACTTTGGG CA
                                  A        A
GAM383  KIAA1170 3' AGACAGAGTTTCGCTCTTGT  70408     C _     CCC
                                ACA G GTGAAAC  GTCT
                                ||| | |||||||  ||||
                                TGT C CGCTTTG  CAGA
                                  T T      AGA
GAM383  KIAA1198 3' AGACAGTGTTTCACCATGTT  63984     C       CCC
                                AACA GGTGAAAC  GTCT
                                |||| ||||||||  ||||
                                TTGT CCACTTTG  CAGA
                                  A       TGA
GAM383  KIAA1198 3' AGACGGGGTTTCACCATGTT  63986     C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
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                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  KIAA1198 3' AGACGGGGTTTCACCATGTT  63987     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  KIAA1198 3' AGACGGGGTTTCACCGTGTT  63992
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGA

GAM383  KIAA1198 3' AGATGGGGTTTCACCATGTT  63998     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  KIAA1198 3' AGATGGGGTTTCTCCATGTT  64001     C  T
                                AACA GG GAAACCCCGTCT
                                |||| || ||||||||||||
                                TTGT CC CTTTGGGGTAGA
                                  A  T
GAM383  KIAA1200 3' AGACGGGGTTTCACCATGTT  63026     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  KIAA1210 3' AGACGGGGTTTCACCATGTT  98061     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  KIAA1254 3' AGATGGGGTTTCACCATGTT  70551     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  KIAA1443 3' AGACGGGTTTCATCATGTT   64564     C        C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CTACTTTGGG CAGA
                                  A       _
GAM383  KIAA1456 3' AGACGGGGTTTCACCGTGTT  67526
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGA

GAM383  KIAA1465 3' AGACGGGGTTTCACCATGTT  61482     C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
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                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  KIAA1467 3' AGACGGGGTTTCACCATGTT  72057     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  KIAA1493 3' AGATGGGGTTTCACCTTGTT  64832     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  T
GAM383  KIAA1497 5' AGACAGGGTTTCACCATGTT  68108     C        C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A        A
GAM383  KIAA1508 3' ACAAGGTTTCACCATGTT    62533     C       CC
                                AACA GGTGAAACC  GT
                                |||| |||||||||  ||
                                TTGT CCACTTTGG  CA
                                  A        AA
GAM383  KIAA1530 3' AGACGGGATTTCACTGTGTT  68542          C
                                AACACGGTGAAA CCCGTCT
                                |||||||||||| |||||||
                                TTGTGTCACTTT GGGCAGA
                                     A
GAM383  KIAA1530 3' AGATGAGGTCTCACTGTGTT  68545         A  C
                                AACACGGTGA ACC CGTCT
                                |||||||||| ||| |||||
                                TTGTGTCACT TGG GTAGA
                                    C  A
GAM383  KIAA1617 3' AGACAGGGTTTCACCATGTT  93067     C        C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A        A
GAM383  KIAA1649 3' AGATGAGGTTTCACCGTGTT  51215          C
                                AACACGGTGAAACC CGTCT
                                |||||||||||||| |||||
                                TTGTGCCACTTTGG GTAGA
                                     A
GAM383  KIAA1655 3' AGACAGGTTTCACCATGTT    67170     C       CC
                                AACA GGTGAAACC  GTCT
                                |||| |||||||||  ||||
                                TTGT CCACTTTGG  CAGA
                                  A        A_
GAM383  KIAA1668 3' AGACGGGGTTTCACCGTGTT  67056
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
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                                TTGTGCCACTTTGGGGCAGA

GAM383  KIAA1712 3' AGACAGGGTTTCACCATGTT  68146     C        C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A         A
GAM383  KIAA1737 3' ATGGGGTTTTACCGTGTT    67932
                                AACACGGTGAAACCCCGT
                                ||||||||||||||||||
                                TTGTGCCATTTTGGGGTA

GAM383  KIAA1751 3' AGACACAGGGTTTCGCCATGTT 72149     C        C__
                                AACA GGTGAAACCC   GTCT
                                |||| ||||||||||   ||||
                                TTGT CCGCTTTGGG   CAGA
                                  A         ACA
GAM383  KIAA1784 3' ACGGGGTTTCACCATGTT    65739     C
                                AACA GGTGAAACCCCGT
                                |||| ||||||||||||
                                TTGT CCACTTTGGGGCA
                                  A
GAM383  KIAA1821 3' AGACAGGGTCTCACTGTGTT  72255         A   C
                                AACACGGTGA ACCC GTCT
                                |||||||||| |||| ||||
                                TTGTGTCACT TGGG CAGA
                                     C    A
GAM383  KIAA1877 3' AGACAGGGTTTCACCGTGTT  66737           C
                                AACACGGTGAAACCC GTCT
                                |||||||||||||| ||||
                                TTGTGCCACTTTGGG CAGA
                                        A
GAM383  KIAA1922 5' AGACAAAGTTTCGCTCTTGT  73979    C _     CCC
                                ACA G GTGAAAC   GTCT
                                ||| | |||||||   ||||
                                TGT C CGCTTTG   CAGA
                                  T T       AAA
GAM383  KIAA1971 3' AGACAAGGTTTCGCTATGTT  74666     CG       CC
                                AACA  GTGAAACC  GTCT
                                ||||  ||||||||  ||||
                                TTGT  CGCTTTGG  CAGA
                                  AT        AA
GAM383  KIAA1971 3' AGACGAGGTTTCACCGTGTT  74667           C
                                AACACGGTGAAACC CGTCT
                                |||||||||||||| |||||
                                TTGTGCCACTTTGG GCAGA
                                        A
GAM383  KIAA1975 5' AGATGGGGTTTCACCATGTT  74411     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
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                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  KLK7     3'  AGACAGGGTTTCACCATGTT  18537     C        C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A         A
GAM383  LAMP3    3'  AGACGGGGTTTCACCATGTT  60194     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  LAMP3    3'  AGACGGAGTTTCACTCTTGT  60192     C _      C
                                ACA G GTGAAAC CCGTCT
                                ||| | ||||||| ||||||
                                TGT C CACTTTG GGCAGA
                                  T T      A
GAM383  LIECG3   3'  AGGGGGGTCTCACTGTGTT   88796          A    G
                                AACACGGTGA ACCCC TCT
                                |||||||||| ||||| |||
                                TTGTGTCACT TGGGG GGA
                                      C    _
GAM383  LY75     3'  AGATGGGGTTTCACCATGTT  11385     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  MAP-1    3'  AGACGGGGTTTCACCATGTT  42431     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  MCLC     3'  AGATGGGGTTTCACCATGTT  31375     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  MEF-2    3'  AGACTGGGTTTCACCATGTT  65014     C        C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A         T
GAM383  MGC10200 3'  AGATGGGGTTTCACCATGTT  59632     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  MGC11386 3'  AGATGGGGATCTCACTGTGTT  53054          AA_
                                AACACGGTGA   CCCCGTCT
                                ||||||||||   ||||||||
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                                TTGTGTCACT   GGGGTAGA
                                      CTA
GAM383  MGC12518 3'  AGTGAGGGTTTCACCATGTT   64773     C        _  T
                                AACA GGTGAAACCC CG CT
                                |||| |||||||||| || ||
                                TTGT CCACTTTGGG GT GA
                                  A         A  _
GAM383  MGC14436 5'  AGACGGGGTCTTGCCCTGT    52920     C  TG A
                                ACA GG  A ACCCCGTCT
                                ||| ||  | |||||||||
                                TGT CC  T TGGGGCAGA
                                  C  GT C
GAM383  MGC21675 3'  AGACAGAGTTTCGCTCTTGT   54580     C _      CCC
                                ACA G GTGAAAC   GTCT
                                ||| | |||||||   ||||
                                TGT C CGCTTTG   CAGA
                                  T T       AGA
GAM383  MGC21675 3'  AGATGGGGTTTCACCATGTT   54583     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  MGC2474  3'  AGATGGGGTTTCACCATGTT   43946     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  MGC4766  5'  AGACGGGGTTTCACCGTGTT   49553
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGA

GAM383  MMPL1    3'  AGACGGGGCCTTATTCTGT    15960     CG    AA
                                ACA  GTGA  CCCCGTCT
                                |||  ||||  ||||||||
                                TGT  TATT  GGGGCAGA
                                  CT    CC
GAM383  moblak   3'  AGACAGGGTTTCACCGTGTT   56382             C
                                AACACGGTGAAACCC GTCT
                                |||||||||||||| ||||
                                TTGTGCCACTTTGGG CAGA
                                        A
GAM383  MOCS3    3'  AGAGGGGGTTTCACCATGTT   27925     C         G
                                AACA GGTGAAACCCC TCT
                                |||| |||||||||| |||
                                TTGT CCACTTTGGGG AGA
                                  A         G
GAM383  MRPS27   3'  AGATGGGGTTTCACCATGTT   31317     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
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                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  MtFMT    3'  AGATGGGGTTTCACCATGTT  58327     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  MYO5C    3'  AGACAGGTTTCACCATGTT   38711     C       CC
                                AACA GGTGAAACC  GTCT
                                |||| |||||||||  ||||
                                TTGT CCACTTTGG  CAGA
                                  A       A_
GAM383  NDP52    3'  AGACAGGGTTTCACTATGTT  20662     CG       C
                                AACA  GTGAAACCC GTCT
                                ||||  ||||||||| ||||
                                TTGT  CACTTTGGG CAGA
                                  AT       A
GAM383  NDUFC2   3'  AGACGGGGTTTCACCATGTT  17022     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  NINJ2    3'  AGACGGGGTTTCTCCATGTT  33715     C  T
                                AACA GG GAAACCCCGTCT
                                |||| || ||||||||||||
                                TTGT CC CTTTGGGGCAGA
                                  A  T
GAM383  Nup43    3'  ACAGGGTTTCACCATGTT    45337     C       C
                                AACA GGTGAAACCC GT
                                |||| |||||||||| ||
                                TTGT CCACTTTGGG CA
                                  A       A
GAM383  Nup43    3'  AGATGGGGTTTCACTGTGTT  45342
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGTCACTTTGGGGTAGA

GAM383  NXN      3'  AGATGGGGTTTCACCATGTT  42663     C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  OCT11    3'  AGATGGGGTTTCACCATGTT  27580     C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  OR51E2   3'  AGACAGAGTTTCACCATGTT  48499     C       CCC
                                AACA GGTGAAAC   GTCT
                                |||| ||||||||   ||||
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                                TTGT CCACTTTG   CAGA
                                  A       AGA
GAM383  OSBPL2   3' AGACGGAGTTTCACTCTTGT  58477    C _     C
                                ACA G GTGAAAC CCGTCT
                                ||| | ||||||| ||||||
                                TGT C CACTTTG GGCAGA
                                  T T      A
GAM383  PASK     5' AGACAGAGTTTCGCTCTTGT  31402    C _     CCC
                                ACA G GTGAAAC   GTCT
                                ||| | |||||||   ||||
                                TGT C CGCTTTG   CAGA
                                  T T      AGA
GAM383  PASK     5' AGACGGGGTTTCTCCATGTT  31403    C  T
                                AACA GG GAAACCCCGTCT
                                |||| || ||||||||||||
                                TTGT CC CTTTGGGGCAGA
                                  A  T
GAM383  PELI1    5' AGACGGGGTTTCACCATGTT  40618    C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  PELI1    5' AGATGGGGTTTCACCATGTT  40622    C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  PIP3-E   3' AGACCGGGGTTTACCATGTT  67343    C    A    _
                                AACA GGTGAA CCCCG TCT
                                |||| |||||| ||||| |||
                                TTGT CCATTT GGGGC AGA
                                  A    _    C
GAM383  PRO0365  5' AGACGGGGTTTCACTATGTT  26975    CG
                                AACA  GTGAAACCCCGTCT
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGCAGA
                                  AT
GAM383  PRO0659  3' AGACGGAGCCGCCGTGTT    27073       AAACC
                                AACACGGTG    CCGTCT
                                |||||||||    ||||||
                                TTGTGCCGC    GGCAGA
                                     CGA__
GAM383  PRO1992  3' AGACAGAGTTTCGCTCTTGT  26893    C _     CCC
                                ACA G GTGAAAC   GTCT
                                ||| | |||||||   ||||
                                TGT C CGCTTTG   CAGA
                                  T T      AGA
GAM383  PRO2955  3' AGACAGGGTTTTACCATGTT  38231    C       C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
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                                TTGT CCATTTTGGG CAGA
                                  A         A
GAM383  PSPH     3'  AGACGGGGTTTGACCGTGTT  17128         G
                                AACACGGT AAACCCCGTCT
                                |||||||| ||||||||||
                                TTGTGCCA TTTGGGGCAGA
                                   G
GAM383  PSTPIP2  3'  AGACAGGGTTTTACCATGTT  44647      C         C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCATTTTGGG CAGA
                                  A         A
GAM383  RAB21    3'  AGACGGGGTTTCACCAGGTT  31079      AC
                                AAC  GGTGAAACCCCGTCT
                                |||  ||||||||||||||
                                TTG  CCACTTTGGGGCAGA
                                  GA
GAM383  RAB33B   3'  AGACGGGGTCTTGCTATGTT  49312      CG TG A
                                AACA  G  A ACCCCGTCT
                                ||||  |  | |||||||||
                                TTGT  C  T TGGGGCAGA
                                  AT GT C
GAM383  RAB33B   3'  AGATGGGGTTTCACCATGTT  49315      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  RAP140   3'  AGACAGGGTTTCACTGTGTT  31505            C
                                AACACGGTGAAACCC GTCT
                                |||||||||||||| ||||
                                TTGTGTCACTTTGGG CAGA
                                       A
GAM383  RES4-25  3'  AGACGGGGTTTCTCCATGTT  65258      C  T
                                AACA GG GAAACCCCGTCT
                                |||| || ||||||||||||
                                TTGT CC CTTTGGGGCAGA
                                  A  T
GAM383  RNF8     3'  AGACAGGGTTTCACCATGTT  15556      C         C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A         A
GAM383  RNO2     5'  AGATGGGGTGTCACCATGTT  53916      C     A
                                AACA GGTGA ACCCCGTCT
                                |||| ||||| |||||||||
                                TTGT CCACT TGGGGTAGA
                                  A     G
GAM383  SAMHD1   3'  AGACAAGGTTTTGCTCTGTT  61974      C  TG    CC
                                AACA GG  AAACC  GTCT
                                |||| ||  |||||  ||||
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                                TTGT TC  TTTGG  CAGA
                                  C  GT    AA
GAM383  SCAMP-4  3' AGACAGAGTTTCACTCTGT   55331    C      CCC
                                ACA GGTGAAAC   GTCT
                                ||| ||||||||   ||||
                                TGT TCACTTTG   CAGA
                                  C       AGA
GAM383  SCAMP-4  3' AGATGGGGTTTCACCATGTT   55333    C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  SCYA22   3' AGACGGGGTTTTGCCATGTT   92573    C  TG
                                AACA GG  AAACCCCGTCT
                                |||| ||  ||||||||||
                                TTGT CC  TTTGGGGCAGA
                                  A  GT
GAM383  SCYA28   3' AGACGGGGTTTCACCGTGTT   39536
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGA

GAM383  SERF1B   3' AGATGGGGTTTCACCATGTT   43687    C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  SFXN2    3' AGACGGGGTTTCACCATG    74369    C
                                CA GGTGAAACCCCGTCT
                                || ||||||||||||||
                                GT CCACTTTGGGGCAGA
                                 A
GAM383  SIRPB1   3' AGATGGGGTTTCTCCATGTT   21354    C  T
                                AACA GG GAAACCCCGTCT
                                |||| || ||||||||||
                                TTGT CC CTTTGGGGTAGA
                                  A  T
GAM383  SLC12A8  3' AGACAGGGTTTCACCATGTT   45230    C       C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A        A
GAM383  SLC16A4  3' AGGCGGGGTTTCACCATGTT   17446    C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCGGA
                                  A
GAM383  SLC19A3  3' AGATGGGGTTTCACAATGTT   48233    CG
                                AACA  GTGAAACCCCGTCT
                                ||||  ||||||||||||||
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                                TTGT  CACTTTGGGGTAGA
                                  AA
GAM383  SLC2A10  3'  AGATGGGGTTTCACTGTGTT  48543
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGTCACTTTGGGGTAGA

GAM383  SREC     3'  AGACAGGGTTTCACCATGTT  14895     C        C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A         A
GAM383  SS-56    3'  AGACGGAGTTTCACCATGTT  60342     C       C
                                AACA GGTGAAAC CCGTCT
                                |||| |||||||| ||||||
                                TTGT CCACTTTG GGCAGA
                                  A       A
GAM383  STAF65(gamma) 3'  AGATGAGGTTTCACCGTGTT  30059           C
                                AACACGGTGAAACC CGTCT
                                |||||||||||||| |||||
                                TTGTGCCACTTTGG GTAGA
                                        A
GAM383  STRBP    5'  AGACGGGGTTTTGCCATGTT  37815     C  TG
                                AACA GG  AAACCCCGTCT
                                |||| ||  ||||||||||
                                TTGT CC  TTTGGGGCAGA
                                  A  GT
GAM383  SULT1C2  3'  AGACGAGGTTTCACCGTGTT  22707           C
                                AACACGGTGAAACC CGTCT
                                |||||||||||||| |||||
                                TTGTGCCACTTTGG GCAGA
                                        A
GAM383  SUN1     3'  AGACAGGGTTTCACTGTGTT  47906           C
                                AACACGGTGAAACCC GTCT
                                |||||||||||||| ||||
                                TTGTGTCACTTTGGG CAGA
                                        A
GAM383  SYT13    3'  AGATGGGGTTTCACCATGTT  95092     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  TADA3L   3'  AGACGGGGTTTCACCGTGTT  22035
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGA

GAM383  TBCC     3'  AGACGGGGTTTCGCCATGTT  13599     C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
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                                TTGT CCGCTTTGGGGCAGA
                                  A
GAM383  TCL6     3'  AGACAGGGTTTCACCGTGTT  40456            C
                                AACACGGTGAAACCC GTCT
                                ||||||||||||||| ||||
                                TTGTGCCACTTTGGG CAGA
                                     A
GAM383  TCL6     5'  AGACGAGGTTTCACCATGTT  40457     C      C
                                AACA GGTGAAACC CGTCT
                                |||| ||||||||| |||||
                                TTGT CCACTTTGG GCAGA
                                  A       A
GAM383  THEA     3'  AGACACTTTCACTGTGTT    66867          CCCC
                                AACACGGTGAAA   GTCT
                                ||||||||||||   ||||
                                TTGTGTCACTTT   CAGA
                                      CA__
GAM383  THEA     3'  AGATGGGGTTTCACTGTGTT  66869
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGTCACTTTGGGGTAGA

GAM383  TRIM16   3'  AGATGGGGTTTCACCATGTT  22362     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  TRIM5    3'  AGACGGGGTTTCCCCATGTT  53462     C  T
                                AACA GG GAAACCCCGTCT
                                |||| || ||||||||||||
                                TTGT CC CTTTGGGGCAGA
                                  A  C
GAM383  TRIM5    3'  AGACGGGGTTTCCCCATGTT  53463     C  T
                                AACA GG GAAACCCCGTCT
                                |||| || ||||||||||||
                                TTGT CC CTTTGGGGCAGA
                                  A  C
GAM383  TRIM6    3'  AGATAGGGTTTCACCGTGTT  55172           CG
                                AACACGGTGAAACCC  TCT
                                |||||||||||||||  |||
                                TTGTGCCACTTTGGG  AGA
                                      AT
GAM383  TU12B1-TY 3'  AGACGGGGTTTCACCATGTT  33819     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  TU12B1-TY 3'  AGATGGGGTTTCACCATGTT  33824     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
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                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  UBF-fl   3'  ATGGGGTTTTACCATGTT    52617     C
                                AACA GGTGAAACCCCGT
                                |||| ||||||||||||
                                TTGT CCATTTTGGGGTA
                                  A
GAM383  VDU1     3'  AGATGGGGTTTCACCATGTT  31115     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  VPS33A   3'  ATGGTGTTTCACCATGTT    43608     C      C
                                AACA GGTGAAAC CCGT
                                |||| |||||||| ||||
                                TTGT CCACTTTG GGTA
                                  A       T
GAM383  WBSCR23  3'  AGACGGGGTTTCACCATGTT  47410     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  ZNF221   3'  ACGGGGTTTCACCGTGTT    26263
                                AACACGGTGAAACCCCGT
                                |||||||||||||||||
                                TTGTGCCACTTTGGGGCA

GAM383  LOC112817 3'  AGACAGAGTTTCACTCTGT   57312     C      CCC
                                ACA GGTGAAAC   GTCT
                                ||| ||||||||   ||||
                                TGT TCACTTTG   CAGA
                                  C       AGA
GAM383  LOC112817 3'  AGATGGGGTTTCACCGTGTT  57314
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGTAGA

GAM383  LOC113523 5'  AGACAGGGTTTCACCATGTT  73408     C        C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A         A
GAM383  LOC115219 5'  AGACGGGGTTTCATCATGTT  73684     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CTACTTTGGGGCAGA
                                  A
GAM383  LOC115648 3'  AGACGGGGTTTCACCATGTT  60014     C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
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                                  TTGT CCACTTTGGGGCAGA
                                    A
GAM383  LOC116411 5'  AGACGGGGTTTCGCTGTGTT  74292
                                  AACACGGTGAAACCCCGTCT
                                  ||||||||||||||||||||
                                  TTGTGTCGCTTTGGGGCAGA

GAM383  LOC120114 3'  AGATGGGGTTTCACCATGTT  76037     C
                                  AACA GGTGAAACCCCGTCT
                                  |||| ||||||||||||||
                                  TTGT CCACTTTGGGGTAGA
                                    A
GAM383  LOC120224 5'  AGACAGGGTTTCACCATGTT  57879     C        C
                                  AACA GGTGAAACCC GTCT
                                  |||| |||||||||| ||||
                                  TTGT CCACTTTGGG CAGA
                                    A         A
GAM383  LOC120939 3'  AGAGGGGGTTTCACCATGTT  76754     C         G
                                  AACA GGTGAAACCCC TCT
                                  |||| |||||||||| |||
                                  TTGT CCACTTTGGGG AGA
                                    A         G
GAM383  LOC121504 3'  ACGGGGTTTCACCATGTT    74537     C
                                  AACA GGTGAAACCCCGT
                                  |||| ||||||||||||
                                  TTGT CCACTTTGGGGCA
                                    A
GAM383  LOC126364 3'  AGATGGGGTTTCGCCATGTT  76181     C
                                  AACA GGTGAAACCCCGTCT
                                  |||| |||||||||||||||
                                  TTGT CCGCTTTGGGGTAGA
                                    A
GAM383  LOC126661 3'  AGATGGGGTTTCACCATGTT  75046     C
                                  AACA GGTGAAACCCCGTCT
                                  |||| |||||||||||||||
                                  TTGT CCACTTTGGGGTAGA
                                    A
GAM383  LOC126669 3'  AGACGAAGTCTCGCTGTGTT  75919          A  CC
                                  AACACGGTGA AC  CGTCT
                                  |||||||||| ||  |||||
                                  TTGTGTCGCT TG  GCAGA
                                       C  AA
GAM383  LOC128077 3'  AGACAGGGTTTCACCATGTT  75197     C        C
                                  AACA GGTGAAACCC GTCT
                                  |||| |||||||||| ||||
                                  TTGT CCACTTTGGG CAGA
                                    A         A
GAM383  LOC128077 3'  AGACGGGGTTTCACCATGTT  75200     C
                                  AACA GGTGAAACCCCGTCT
                                  |||| |||||||||||||||
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                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  LOC128989 3'  AGACGGGGTTTCACCATGTT  75307     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  LOC129880 3'  AGACGGGGTTTCGCTGTGTT  75403
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGTCGCTTTGGGGCAGA

GAM383  LOC130813 3'  AGATGGGGTTTCTCCATGTT  76263     C  T
                                AACA GG GAAACCCCGTCT
                                |||| || ||||||||||||
                                TTGT CC CTTTGGGGTAGA
                                  A  T
GAM383  LOC132241 5'  AGAGTGGGTTTCACTATGTT  75553     CG       CG
                                AACA  GTGAAACCC  TCT
                                ||||  |||||||||  |||
                                TTGT  CACTTTGGG  AGA
                                  AT        TG
GAM383  LOC132625 3'  AGATGGGGTTTCACCATGTT  76431     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  LOC135154 3'  AGACAAGGTTTCACCATGTT  75719     C        CC
                                AACA GGTGAAACC  GTCT
                                |||| |||||||||  ||||
                                TTGT CCACTTTGG  CAGA
                                  A        AA
GAM383  LOC142820 5'  AGACGGAGTTTTGCCATGTT  76911     C  TG   C
                                AACA GG  AAAC CCGTCT
                                |||| ||  |||| ||||||
                                TTGT CC  TTTG GGCAGA
                                  A  GT   A
GAM383  LOC143187 3'  AGATGGAGTTTCACCATGTT  59752     C       C
                                AACA GGTGAAAC CCGTCT
                                |||| |||||||| ||||||
                                TTGT CCACTTTG GGTAGA
                                  A       A
GAM383  LOC143916 3'  AGATGGGGTTTCACCTTGTT  77135     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  T
GAM383  LOC144317 5'  AGACTGGGGTTTCTCCATGTT  77287     C  T       _
                                AACA GG GAAACCCC GTCT
                                |||| || |||||||| ||||
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                                TTGT CC CTTTGGGG CAGA
                                  A T       T
GAM383  LOC144519 5'  AGACGGGGTTTTGCCATGTT  77365     C  TG
                                AACA GG  AAACCCCGTCT
                                |||| ||  ||||||||||||
                                TTGT CC  TTTGGGGCAGA
                                  A  GT
GAM383  LOC144524 5'  ACCGGGTTTCACCGTGTT    84046            C
                                AACACGGTGAAACCC GT
                                ||||||||||||||| ||
                                TTGTGCCACTTTGGG CA
                                         C
GAM383  LOC144871 3'  ATGGGGTTTCACTGTGTT    84119
                                AACACGGTGAAACCCCGT
                                ||||||||||||||||||
                                TTGTGTCACTTTGGGGTA

GAM383  LOC145082 5'  AGACGAGGTTTTGCCATGTT  84178     C  TG    C
                                AACA GG  AAACC CGTCT
                                |||| ||  ||||| |||||
                                TTGT CC  TTTGG GCAGA
                                  A  GT    A
GAM383  LOC145268 5'  AGACAGAGTTTCACCATGTT  77568     C       CCC
                                AACA GGTGAAAC   GTCT
                                |||| ||||||||   ||||
                                TTGT CCACTTTG   CAGA
                                  A       AGA
GAM383  LOC145453 5'  AGACAGGGTCTCACTGTGT   77651        A   C
                                ACACGGTGA ACCC GTCT
                                ||||||||| |||| ||||
                                TGTGTCACT TGGG CAGA
                                     C   A
GAM383  LOC146050 3'  AGATGGGGTTTCACCATGTT  78098     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  LOC146050 3'  AGATGGGGTTTCTCCATGTT  78101     C  T
                                AACA GG GAAACCCCGTCT
                                |||| || ||||||||||||
                                TTGT CC CTTTGGGGTAGA
                                  A  T
GAM383  LOC146229 3'  ACGGGGTTTCACCATGTT    78247     C
                                AACA GGTGAAACCCCGT
                                |||| ||||||||||||
                                TTGT CCACTTTGGGGCA
                                  A
GAM383  LOC146229 3'  AGACGGGGTTTCACCATGTT  78251     C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||
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                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383   LOC146229 3'  AGACGGGGTTTTACCGTGTT   78254
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCATTTTGGGGCAGA

GAM383   LOC146336 3'  AGACGGGGTCTCACCTGT    78363    C    A
                                ACA GGTGA ACCCCGTCT
                                ||| ||||| |||||||||
                                TGT CCACT TGGGGCAGA
                                  _    C
GAM383   LOC146346 5'  AGACGGGGTTTCACCGTGTT   78384
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGA

GAM383   LOC146429 5'  AGACAGGGTTTCACCATG    84659    C        C
                                CA GGTGAAACCC GTCT
                                || |||||||||| ||||
                                GT CCACTTTGGG CAGA
                                 A         A
GAM383   LOC146603 5'  AGACGGGGTTTCACCGTGTT   78587
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGA

GAM383   LOC146784 5'  AGATGGGGTTTCACCATGTT   78703     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383   LOC146839 3'  AGACGGGGTTTCACCGTGTT   84834
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGA

GAM383   LOC146894 3'  AGATGGGGTTTCACCATGTT   59850     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383   LOC146901 3'  AGACGGGGTTTCACCATGTT   84883     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383   LOC146909 3'  AGATGGGGTTTCACCGTGTT   78758
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
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                                TTGTGCCACTTTGGGGTAGA

GAM383  LOC147054 3' ATGGGGTTTCTCCATGTT    85001     C  T
                                AACA GG GAAACCCCGT
                                |||| || ||||||||||
                                TTGT CC CTTTGGGGTA
                                  A  T
GAM383  LOC147071 5' AGACGGAGTTTCACCATGTT   73346     C      C
                                AACA GGTGAAAC CCGTCT
                                |||| |||||||| ||||||
                                TTGT CCACTTTG GGCAGA
                                  A       A
GAM383  LOC147080 5' AGACAAGGTTTCACCATGTT   85023     C       CC
                                AACA GGTGAAACC  GTCT
                                |||| |||||||||  ||||
                                TTGT CCACTTTGG  CAGA
                                  A        AA
GAM383  LOC147166 3' AGATGGGGTTTCACCATGTT   78879     C
                                AACA GGTGAAACCCCCGTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  LOC147276 3' AGACGGGGCTTCTCCATGTT   78948     C  T   A
                                AACA GG GAA CCCCGTCT
                                |||| || ||| ||||||||
                                TTGT CC CTT GGGGCAGA
                                  A  T   C
GAM383  LOC147429 3' AGATGGGGTTTCACCATGTT   78988     C
                                AACA GGTGAAACCCCCGTCT
                                |||| |||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  LOC147694 3' AGACGGGGTTTCACCGTGTT   79088
                                AACACGGTGAAACCCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGA

GAM383  LOC147841 3' AGACAGAGTTTCACTCTTGT   79219     C _      CCC
                                ACA G GTGAAAC   GTCT
                                ||| | |||||||   ||||
                                TGT C CACTTTG   CAGA
                                  T T      AGA
GAM383  LOC147841 3' AGATGGAGTTTCACCATG     79221     C       C
                                CA GGTGAAAC CCGTCT
                                || |||||||| ||||||
                                GT CCACTTTG GGTAGA
                                 A       A
GAM383  LOC148137 3' AGACGGTGTTTCACTGTGTT   59085             C
                                AACACGGTGAAAC CCGTCT
                                |||||||||||| ||||||
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                                TTGTGTCACTTTG GGCAGA
                                      T
GAM383  LOC148189 5'  AGACGGGGTTTCACCATGTT  79442     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  LOC148645 5'  ACAGGGTCTCACTGTGTT   85326        A   C
                                AACACGGTGA ACCC GT
                                |||||||||| |||| ||
                                TTGTGTCACT TGGG CA
                                     C   A
GAM383  LOC148887 5'  AGACAGGGTTTCACCATGTT  85388     C       C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A        A
GAM383  LOC149171 5'  AGATGGGGTTTCTCCATGTT  79961     C  T
                                AACA GG GAAACCCCGTCT
                                |||| || ||||||||||||
                                TTGT CC CTTTGGGGTAGA
                                  A  T
GAM383  LOC149478 3'  AGACGGGGGTTTCACCATGTT  80162     C        _
                                AACA GGTGAAACCCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGGG CAGA
                                  A         G
GAM383  LOC149692 3'  AGACAGGGTTTCACCATGTT  85722     C       C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A        A
GAM383  LOC149703 5'  AGACGGGGTTTTGCCATGTT  85814     C  TG
                                AACA GG  AAACCCCGTCT
                                |||| ||  ||||||||||||
                                TTGT CC  TTTGGGGCAGA
                                  A  GT
GAM383  LOC149711 3'  AGATGGGGTTTTACCATGTT  85836     C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
                                TTGT CCATTTTGGGGTAGA
                                  A
GAM383  LOC149821 5'  AGACGGAGTTTCACCGTGTT  85927          C
                                AACACGGTGAAAC CCGTCT
                                |||||||||||| ||||||
                                TTGTGCCACTTTG GGCAGA
                                      A
GAM383  LOC150166 5'  ATGGGGTTTCACCATGTT    86033     C
                                AACA GGTGAAACCCCGT
                                |||| ||||||||||||
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                                TTGT CCACTTTGGGGTA
                                  A
GAM383  LOC150282 5'  AGATGGCGTTTCACCATGTT  80534     C       C
                                AACA GGTGAAAC CCGTCT
                                |||| |||||||| ||||||
                                TTGT CCACTTTG GGTAGA
                                  A       C
GAM383  LOC150397 3'  AGACGCAGTTTCACCGTGTT  80648           CC
                                AACACGGTGAAAC  CGTCT
                                ||||||||||||  |||||
                                TTGTGCCACTTTG  GCAGA
                                       AC
GAM383  LOC150630 5'  AGAGGGGGTTTCACCGTG    86285           G
                                CACGGTGAAACCCC TCT
                                |||||||||||||| |||
                                GTGCCACTTTGGGG AGA
                                       G
GAM383  LOC150696 3'  AGACGGGGTCTCGCTCTGT   59151    C    A
                                ACA GGTGA ACCCCGTCT
                                ||| ||||| |||||||||
                                TGT TCGCT TGGGGCAGA
                                  C    C
GAM383  LOC150696 3'  AGACGGGGTTTTGCCATGTT  59152     C  TG
                                AACA GG  AAACCCCGTCT
                                |||| ||  ||||||||||
                                TTGT CC  TTTGGGGCAGA
                                  A  GT
GAM383  LOC150960 3'  AGATGGGGTCTCACCCTGTT  80865     C    A
                                AACA GGTGA ACCCCGTCT
                                |||| ||||| |||||||||
                                TTGT CCACT TGGGGTAGA
                                  C    C
GAM383  LOC151050 5'  AGACAGAGTTTCACCATGTT  80912     C       CCC
                                AACA GGTGAAAC   GTCT
                                |||| ||||||||   ||||
                                TTGT CCACTTTG   CAGA
                                  A       AGA
GAM383  LOC151057 3'  AGACGGGGTTTCACCATGTT  86380     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  LOC151201 3'  AGACGGGGTTTCACCATGTT  86462     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  LOC151475 5'  AGACGAGGTTTCACCATGTT  86580     C       C
                                AACA GGTGAAACC CGTCT
                                |||| ||||||||| |||||
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                                TTGT CCACTTTGG GCAGA
                                  A        A
GAM383   LOC151701 3'  AGACGGGGTTTCACCATGTT  86661     C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383   LOC151826 3'  AGACAGGGTTTCACCGTGTT  81174            C
                                AACACGGTGAAACCC GTCT
                                |||||||||||||| ||||
                                TTGTGCCACTTTGGG CAGA
                                       A
GAM383   LOC151979 5'  AGACGGGGTTTCACCATGTT  81242     C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383   LOC152137 3'  AGAGCGGGTTTCACCATGTT  81306     C        CG
                                AACA GGTGAAACCC  TCT
                                |||| ||||||||||  |||
                                TTGT CCACTTTGGG  AGA
                                  A         CG
GAM383   LOC152343 3'  ACTGGGTTTCACCATGTT    81415     C        C
                                AACA GGTGAAACCC GT
                                |||| |||||||||| ||
                                TTGT CCACTTTGGG CA
                                  A         T
GAM383   LOC152445 3'  AGACAGGGTTTCACCATGTT  86926     C        C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A         A
GAM383   LOC152620 3'  AGGCGGGGTTACACCATG    60704    C   A
                                CA GGTG AACCCCGTCT
                                || |||| ||||||||||
                                GT CCAC TTGGGGCGGA
                                 A    A
GAM383   LOC152719 5'  AGACGGGGTTTCACCATGTT  87012     C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383   LOC152794 5'  AGATGGGGTTTCATCATGTT  81552     C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
                                TTGT CTACTTTGGGGTAGA
                                  A
GAM383   LOC153077 3'  AGATGGGGCTTCACCATGTT  87107     C     A
                                AACA GGTGAA CCCCGTCT
                                |||| |||||| ||||||||
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                                TTGT CCACTT GGGGTAGA
                                  A     C
GAM383  LOC153606 5'  AGATAGGGTTTCACCATGTT  87252     C        CG
                                AACA GGTGAAACCC  TCT
                                |||| ||||||||||  |||
                                TTGT CCACTTTGGG  AGA
                                  A         AT
GAM383  LOC153688 3'  AGACAGGATTTCATCGTGTT  87286          C  C
                                AACACGGTGAAA CC GTCT
                                |||||||||||| || ||||
                                TTGTGCTACTTT GG CAGA
                                       A  A
GAM383  LOC153688 3'  AGACAGGGTTTCACCATGTT  87288     C        C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A         A
GAM383  LOC153883 5'  ATGGGGTTTTACCATGTT    81888     C
                                AACA GGTGAAACCCCGT
                                |||| ||||||||||||
                                TTGT CCATTTTGGGGTA
                                  A
GAM383  LOC153910 5'  AGACAGGGTTTTGCCATGTT  81900     C  TG     C
                                AACA GG  AAACCC GTCT
                                |||| ||  |||||| ||||
                                TTGT CC  TTTGGG CAGA
                                  A  GT     A
GAM383  LOC154282 5'  AGATGGTGTTTCACCATGTT  87397     C       C
                                AACA GGTGAAAC CCGTCT
                                |||| |||||||| ||||||
                                TTGT CCACTTTG GGTAGA
                                  A       T
GAM383  LOC154726 5'  AGACAGAGTTTCGCTCTTGT  82005     C _      CCC
                                ACA G GTGAAAC   GTCT
                                ||| | |||||||   ||||
                                TGT C CGCTTTG   CAGA
                                  T T      AGA
GAM383  LOC154877 5'  AGACAGGGTTTCACCCTGTT  87523     C        C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  C         A
GAM383  LOC154877 3'  AGTCGGGGTTTCACCATGTT  87525     C          T
                                AACA GGTGAAACCCCG CT
                                |||| ||||||||||| ||
                                TTGT CCACTTTGGGGC GA
                                  A           T
GAM383  LOC154930 3'  AGACAGGATTTTACTGTGTT  82085          C  C
                                AACACGGTGAAA CC GTCT
                                |||||||||||| || ||||
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                                TTGTGTCATTTT GG CAGA
                                      A  A
GAM383  LOC157247 5'  AGACGGGGTTTCACCAGTGT   82283      _
                                ACAC GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TGTG CCACTTTGGGGCAGA
                                  A
GAM383  LOC157506 3'  AGACGGGGTTTCACCATGTT   82358      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  LOC157798 5'  AGACGGAGTCTTGCTGTGT    87848       TG A  C
                                ACACGG  A AC CCGTCT
                                ||||||  | || ||||||
                                TGTGTC  T TG GGCAGA
                                    GT C  A
GAM383  LOC157798 5'  AGACGGGGTTTCACCTTGTT   87850      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  T
GAM383  LOC157858 5'  AGACAGGGTTTCACTATGT    87881     CG        C
                                ACA  GTGAAACCC GTCT
                                |||  ||||||||| ||||
                                TGT  CACTTTGGG CAGA
                                  AT        A
GAM383  LOC158014 5'  AGACGGAGTTTCACCATGTT   82550      C       C
                                AACA GGTGAAAC CCGTCT
                                |||| |||||||| ||||||
                                TTGT CCACTTTG GGCAGA
                                  A       A
GAM383  LOC158310 5'  AGACAGGGTTTCACAATGTT   88071      CG        C
                                AACA  GTGAAACCC GTCT
                                ||||  ||||||||| ||||
                                TTGT  CACTTTGGG CAGA
                                  AA        A
GAM383  LOC158402 5'  AGGGGGGTTTCACCGTGTT    88141             G
                                AACACGGTGAAACCCC TCT
                                |||||||||||||||| |||
                                TTGTGCCACTTTGGGG GGA
                                                _
GAM383  LOC158476 3'  AGACAGGGTTTCACCATGTT   88180      C        C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A        A
GAM383  LOC158549 5'  AGATAGGGGTTTCACCGTGTT  88214                _
                                AACACGGTGAAACCCC GTCT
                                |||||||||||||||| ||||
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                                TTGTGCCACTTTGGGG TAGA
                                          A
GAM383   LOC158629 5'  AGACAGGGTTTTGCTATGTT  88237     CG TG     C
                                AACA  G  AAACCC GTCT
                                ||||  |  ||||||  ||||
                                TTGT  C  TTTGGG CAGA
                                  AT GT     A
GAM383   LOC158668 3'  AGGTGGGGTTTCACCATG    69893    C         GT
                                CA GGTGAAACCCC  CT
                                ||  ||||||||||  ||
                                GT CCACTTTGGGG  GA
                                 A          TG
GAM383   LOC158865 5'  AGATGGGGACTTCACCGTGTT  88303          A_
                                AACACGGTGAA  CCCCGTCT
                                ||||||||||  ||||||||
                                TTGTGCCACTT  GGGGTAGA
                                       CA
GAM383   LOC160646 3'  AGATGGGGCTTCACCATGTT  83102     C     A
                                AACA GGTGAA CCCCGTCT
                                ||||  ||||||  ||||||||
                                TTGT CCACTT GGGGTAGA
                                  A     C
GAM383   LOC161829 3'  AGATGGGGTTTCACCATGTT  83180     C
                                AACA GGTGAAACCCCGTCT
                                ||||  ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383   LOC162427 3'  ATGGGGTTTCACCATGTT    83221     C
                                AACA GGTGAAACCCCGT
                                ||||  |||||||||||||
                                TTGT CCACTTTGGGGTA
                                  A
GAM383   LOC169611 3'  AGACAGAGTTTCGCTTTTGTT  83631     C_      CCC
                                AACA  GGTGAAAC   GTCT
                                ||||  ||||||||   ||||
                                TTGT  TCGCTTTG   CAGA
                                  TT       AGA
GAM383   LOC170082 5'  AGATGGGGTTTCACCATGTT  83437     C
                                AACA GGTGAAACCCCGTCT
                                ||||  ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383   LOC196411 3'  AGATGGGGTTTCACTATGTT  89038     CG
                                AACA  GTGAAACCCCGTCT
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGA
                                  AT
GAM383   LOC196510 3'  ACGGGGTTAGGCTGGGTT    89089    A   GA
                                AAC CGGT  AACCCCGT
                                |||  ||||  ||||||||
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                                TTG GTCG  TTGGGGCA
                                  G    GA
GAM383   LOC196529 3'  AGACAGGGTCTCACTGTGTT  89118          A    C
                                AACACGGTGA ACCC GTCT
                                |||||||||| |||| ||||
                                TTGTGTCACT TGGG CAGA
                                     C    A
GAM383   LOC196529 3'  AGACAGGGTTTCACTACGTT  89120     AC         C
                                AAC  GGTGAAACCC GTCT
                                |||  |||||||||| ||||
                                TTG  TCACTTTGGG CAGA
                                  CA         A
GAM383   LOC197358 3'  AGACGGGGTTTCATCATGTT  89411      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CTACTTTGGGGCAGA
                                  A
GAM383   LOC197358 3'  AGATGGGGTTTCACCATGTT  89415      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383   LOC199699 3'  AGACAGGGTTTCACCGTGTT  89665            C
                                AACACGGTGAAACCC GTCT
                                |||||||||||||| ||||
                                TTGTGCCACTTTGGG CAGA
                                       A
GAM383   LOC199786 3'  AGACGGTGGTTTCACCATGTT 89735      C        _
                                AACA GGTGAAACC CCGTCT
                                |||| ||||||||| ||||||
                                TTGT CCACTTTGG GGCAGA
                                  A        T
GAM383   LOC199786 3'  AGATGGGGTTTCACCATGTT  89738      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383   LOC199906 3'  AGACAGGGTTTCATCATGTT  89843      C         C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CTACTTTGGG CAGA
                                  A         A
GAM383   LOC200014 3'  AGACGGTGTTTCACCATGTT  89914      C        C
                                AACA GGTGAAAC CCGTCT
                                |||| |||||||| ||||||
                                TTGT CCACTTTG GGCAGA
                                  A        T
GAM383   LOC200169 5'  AGACGGAGTTTCACCATGTT  91547      C        C
                                AACA GGTGAAAC CCGTCT
                                |||| |||||||| ||||||
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                                TTGT CCACTTTG GGCAGA
                                  A       A
GAM383   LOC200220 3'  ACGGGGTTAGGCTGGGTT    90031     A   GA
                                AAC CGGT  AACCCCGT
                                ||| ||||  ||||||||
                                TTG GTCG  TTGGGGCA
                                  G   GA
GAM383   LOC200301 5'  AGACGGGGTTTCACCGTGTT   90132
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGA

GAM383   LOC200310 3'  AGACGGGGTTTCACCATGTT   66316     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383   LOC200316 3'  ACTGGGTTTCACCATGTT    90166     C        C
                                AACA GGTGAAACCC GT
                                |||| |||||||||| ||
                                TTGT CCACTTTGGG CA
                                  A         T
GAM383   LOC200316 3'  AGACGGAGTTTCACTCTGT    90167     C      C
                                ACA GGTGAAAC CCGTCT
                                ||| |||||||| ||||||
                                TGT TCACTTTG GGCAGA
                                  C       A
GAM383   LOC200316 5'  AGACGGGGTTTCTCCATGTT   90169     C  T
                                AACA GG GAAACCCCGTCT
                                |||| || ||||||||||||
                                TTGT CC CTTTGGGGCAGA
                                  A  T
GAM383   LOC200407 3'  AGACAGGGTTTTGCCATGTT   91624     C  TG     C
                                AACA GG  AAACCC GTCT
                                |||| ||  |||||| ||||
                                TTGT CC  TTTGGG CAGA
                                  A  GT     A
GAM383   LOC200845 5'  AGATGGGGTTTCACTATGTT   90311     CG
                                AACA  GTGAAACCCCGTCT
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGA
                                  AT
GAM383   LOC200860 3'  AGACGGGGTTTCGCTCTTGT   91737     C _
                                ACA G GTGAAACCCCGTCT
                                ||| | ||||||||||||||
                                TGT C CGCTTTGGGGCAGA
                                  T T
GAM383   LOC200860 3'  AGACGGGGTTTCTCCATGTT   91738     C  T
                                AACA GG GAAACCCCGTCT
                                |||| || ||||||||||||
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                                TTGT CC CTTTGGGGCAGA
                                  A  T
GAM383   LOC201164 3'  AGACAGGGTTTCACCATGTT   89484      C         C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A         A
GAM383   LOC201173 5'  AGACGGAGTTTCACCATGTT   88665      C       C
                                AACA GGTGAAAC CCGTCT
                                |||| |||||||| ||||||
                                TTGT CCACTTTG GGCAGA
                                  A       A
GAM383   LOC201220 5'  AGATGGAGTTTCACCATGTT   88701      C       C
                                AACA GGTGAAAC CCGTCT
                                |||| |||||||| ||||||
                                TTGT CCACTTTG GGTAGA
                                  A       A
GAM383   LOC201294 3'  AGACGGGGTTTCACCATGTT   89570      C
                                AACA GGTGAAACCCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383   LOC201411 3'  AGACAGGGTTTCACCATGTT   63632      C         C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A         A
GAM383   LOC201627 3'  AGATGGGGTTTCTCCATGTT   90447      C  T
                                AACA GG GAAACCCCGTCT
                                |||| || ||||||||||||
                                TTGT CC CTTTGGGGTAGA
                                  A  T
GAM383   LOC202460 5'  AGATGGGGTTTCACCATGT    90661      C
                                ACA GGTGAAACCCCGTCT
                                ||| ||||||||||||||
                                TGT CCACTTTGGGGTAGA
                                  A
GAM383   LOC202908 5'  AGATGGGGTCTCACCCTGT    90705      C     A
                                ACA GGTGA ACCCCGTCT
                                ||| ||||| |||||||||
                                TGT CCACT TGGGGTAGA
                                  C     C
GAM383   LOC203197 3'  AGATGGGGTTTCGCCATGTT   90803      C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
                                TTGT CCGCTTTGGGGTAGA
                                  A
GAM383   LOC203339 3'  AGATGGGGTTTCACCATGTT   92204      C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
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                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383   LOC203350 3'  AGACGGGGTTTCACCGTGTT   92225
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGA

GAM383   LOC203369 3'  ATGGGGTTTCACTGTGTT    90881
                                AACACGGTGAAACCCCGT
                                ||||||||||||||||||
                                TTGTGTCACTTTGGGGTA

GAM383   LOC204804 3'  AGACAGGGTCTCACTGTGT   91030        A   C
                                ACACGGTGA ACCC GTCT
                                ||||||||| |||| ||||
                                TGTGTCACT TGGG CAGA
                                      C   A
GAM383   LOC205251 5'  ACAGGGTTTCACCATGTT    92352     C       C
                                AACA GGTGAAACCC GT
                                |||| ||||||||| ||
                                TTGT CCACTTTGGG CA
                                  A        A
GAM383   LOC219445 5'  ACGGGGTTTCACCGTGTT    93193
                                AACACGGTGAAACCCCGT
                                ||||||||||||||||||
                                TTGTGCCACTTTGGGGCA

GAM383   LOC219700 5'  AGACAGGGTTTTCACTGT    94647         _  C
                                ACGGTGAAA CCC GTCT
                                ||||||||| ||| ||||
                                TGTCACTTT GGG CAGA
                                      T  A
GAM383   LOC219735 3'  AGACGGGGTTTCACCGTGTT  94722
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGA

GAM383   LOC219894 3'  AGATGGGGTTTCACCGTGTT  94896
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGTAGA

GAM383   LOC220074 3'  AGACAAGGTTTCGCCATGTT  59953     C       CC
                                AACA GGTGAAACC  GTCT
                                |||| |||||||||  ||||
                                TTGT CCGCTTTGG  CAGA
                                  A        AA
GAM383   LOC220074 3'  AGACGGGGTTTCACCATGTT  59955     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
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                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  LOC220074 3'  AGATGGGGTTTCGCCATGTT  59960     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCGCTTTGGGGTAGA
                                  A
GAM383  LOC221042 3'  AGACGGGGTTTGCTGTGTT  94791       G
                                AACACGGT AAACCCCGTCT
                                |||||||| ||||||||||
                                TTGTGTCG TTTGGGGCAGA
                                    _
GAM383  LOC221060 3'  AGACGGTGTTTCACCATGTT  94826     C      C
                                AACA GGTGAAAC CCGTCT
                                |||| |||||||| ||||||
                                TTGT CCACTTTG GGCAGA
                                  A       T
GAM383  LOC221178 3'  AGACGGGGTTGACACAATG  95163    CG  A_
                                CA  GTG  AACCCCGTCT
                                ||  |||  ||||||||||
                                GT  CAC  TTGGGGCAGA
                                 AA   AG
GAM383  LOC221296 3'  AGACGGGGTTTCACCATG    93600    C
                                CA GGTGAAACCCCGTCT
                                || ||||||||||||||
                                GT CCACTTTGGGGCAGA
                                 A
GAM383  LOC221663 5'  AGACAAGGTTTCACTATGTT  95452     CG      CC
                                AACA  GTGAAACC  GTCT
                                ||||  ||||||||  ||||
                                TTGT  CACTTTGG  CAGA
                                  AT       AA
GAM383  LOC221964 3'  AGACAGGGTTTTGCCGTGTT  95598       TG    C
                                AACACGG  AAACCC GTCT
                                |||||||  ||||||  ||||
                                TTGTGCC  TTTGGG CAGA
                                    GT     A
GAM383  LOC222068 3'  AGATGGGGTTTTACCATGTT  94267     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCATTTTGGGGTAGA
                                  A
GAM383  LOC222070 5'  AGACGGTGTTTCACCATGTT  95805     C      C
                                AACA GGTGAAAC CCGTCT
                                |||| |||||||| ||||||
                                TTGT CCACTTTG GGCAGA
                                  A       T
GAM383  LOC222224 5'  AGACAGGGTTTCACCATGTT  95866     C       C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
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                                TTGT CCACTTTGGG CAGA
                                  A         A
GAM383   LOC245771 5'  AGATGGGGTTTCATCATGTT   94465      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||||
                                TTGT CTACTTTGGGGTAGA
                                  A
GAM383   LOC253664 3'  AGATGGGGTTTCCCCATGTT   96455      C  T
                                AACA GG GAAACCCCGTCT
                                |||| || ||||||||||||
                                TTGT CC CTTTGGGGTAGA
                                  A  C
GAM383   LOC253666 3'  AGACGGGGTTTCACCATGTT   96757      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383   LOC253805 3'  AGATAGGGTTTCACAATGTT   98165      CG        CG
                                AACA  GTGAAACCC  TCT
                                ||||  |||||||||  |||
                                TTGT  CACTTTGGG  AGA
                                  AA         AT
GAM383   LOC254018 5'  AGATGGGGTTTCGCCATGTT   98736      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||||
                                TTGT CCGCTTTGGGGTAGA
                                  A
GAM383   LOC254268 3'  AGATGGGGTTTCACCATGTT   97135      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383   LOC254295 5'  AGACGGGGTTTCACCGTGTT   97886
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGA

GAM383   LOC254351 3'  AGACGGAGTTTCACCCTTGT   96678      C_        C
                                ACA  GGTGAAAC CCGTCT
                                |||  |||||||| ||||||
                                TGT  CCACTTTG GGCAGA
                                  TC        A
GAM383   LOC254351 5'  AGACGGGGTTTCTCCGTGTT   96679         T
                                AACACGG GAAACCCCGTCT
                                ||||||| ||||||||||||
                                TTGTGCC CTTTGGGGCAGA
                                    T
GAM383   LOC254413 5'  AGACAGGGAGAGCTGTGTT    98910         GAAA   C
                                AACACGGT    CCC GTCT
                                ||||||||    ||| ||||
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                                TTGTGTCG   GGG CAGA
                                    AGA_  A
GAM383  LOC254559 3'  ACGGAAGCTCTTCACCGTGTT  98379          ACC___
                                AACACGGTGAA    CCGT
                                ||||||||||     ||||
                                TTGTGCCACTT    GGCA
                                   CTCGAA
GAM383  LOC254655 3'  AGACGGGGTTTCACCATGTT  97211     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  LOC254778 3'  AGACAGGATTTTGCTGTGTT  97827       TG  C  C
                                AACACGG  AAA CC GTCT
                                |||||||  ||| || ||||
                                TTGTGTC  TTT GG CAGA
                                    GT  A  A
GAM383  LOC255037 3'  AGACGAAGTCTCGCTGTGT   98435        A  CC
                                ACACGGTGA AC  CGTCT
                                |||||||||  ||  |||||
                                TGTGTCGCT TG  GCAGA
                                     C  AA
GAM383  LOC255308 3'  AGACGGGGTTTCGGCATGTT  96173     CGG
                                AACA   TGAAACCCCGTCT
                                ||||   ||||||||||||
                                TTGT   GCTTTGGGGCAGA
                                  ACG
GAM383  LOC255338 5'  AGACAGGGCATCACTGTGTT  97629         AA  C
                                AACACGGTGA  CCC GTCT
                                ||||||||||  ||| ||||
                                TTGTGTCACT  GGG CAGA
                                     AC  A
GAM383  LOC255465 3'  AGACGGGTTTCACCATGTT   99099     C        C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A       _
GAM383  LOC255497 3'  AGACGGGGTTTCACCATGTT  98980     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  LOC256221 3'  AGACGGGGTTTCACCGTGTT  96905
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGA

GAM383  LOC256306 3'  AGACGGGGTTTCACCATGTT  98501     C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
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                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  LOC257465 3'  AGATGGTGTTTCACCATGTT  82488     C      C
                                AACA GGTGAAAC CCGTCT
                                |||| |||||||| ||||||
                                TTGT CCACTTTG GGTAGA
                                  A       T
GAM383  LOC257486 3'  AGACGGGGTTTCACCATGTT  69762     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  LOC51008  5'  AGATGGGGTTTCTCCATGTT  32526     C  T
                                AACA GG GAAACCCCGTCT
                                |||| || ||||||||||||
                                TTGT CC CTTTGGGGTAGA
                                  A  T
GAM383  LOC51193  5'  AGACGGGGTTTCCCCATGTT  33356     C  T
                                AACA GG GAAACCCCGTCT
                                |||| || ||||||||||||
                                TTGT CC CTTTGGGGCAGA
                                  A  C
GAM383  LOC51219  5'  AGACGGGGTTTCTCCATGT   33538     C  T
                                ACA GG GAAACCCCGTCT
                                ||| || ||||||||||||
                                TGT CC CTTTGGGGCAGA
                                  A  T
GAM383  LOC51696  3'  AGACAGCGTTTCACCATGTT  33076     C      CCC
                                AACA GGTGAAAC   GTCT
                                |||| ||||||||   ||||
                                TTGT CCACTTTG   CAGA
                                  A       CGA
GAM383  LOC56181  5'  AGACAGGGCTTCACTGTGTT  97267          A  C
                                AACACGGTGAA CCC GTCT
                                |||||||||| ||| ||||
                                TTGTGTCACTT GGG CAGA
                                      C   A
GAM383  LOC57107  3'  AGATGGGGTTTCACTATGTT  40179     CG
                                AACA  GTGAAACCCCGTCT
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGA
                                  AT
GAM383  LOC57146  3'  AGATGGGGTTTCACCATGTT  40288     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  LOC81034  3'  ATGGGGTTTCACCATGTT    48582     C
                                AACA GGTGAAACCCCGT
                                |||| ||||||||||||
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                                TTGT CCACTTTGGGGTA
                                  A
GAM383  LOC89231  3' AGATGGGGTCTCACTATGTT  94292     CG   A
                                AACA  GTGA ACCCCGTCT
                                ||||  |||| |||||||||
                                TTGT  CACT TGGGGTAGA
                                  AT   C
GAM383  LOC89919  3' AGACGGGGTTTCACCATGTT  61367     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  LOC89932  3' AGACAGAGTTTCACTCTTGT  61437    C _     CCC
                                ACA G GTGAAAC   GTCT
                                ||| | |||||||   ||||
                                TGT C CACTTTG   CAGA
                                  T T      AGA
GAM383  LOC89932  3' AGACGGGGTTTCTCCATGTT  61439     C  T
                                AACA GG GAAACCCCGTCT
                                |||| || ||||||||||||
                                TTGT CC CTTTGGGGCAGA
                                  A  T
GAM383  LOC89932  3' AGATGGGGTTTCACCATGTT  61442     C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM383  LOC90288  3' AGACGGGGTTTCACAGTGTT  62766      G
                                AACAC GTGAAACCCCGTCT
                                ||||| |||||||||||||||
                                TTGTG CACTTTGGGGCAGA
                                   A
GAM383  LOC90288  3' AGAGGGAGTCTCACCGTGT   62768        A _   G
                                ACACGGTGA AC CCC TCT
                                ||||||||| || ||| |||
                                TGTGCCACT TG GGG AGA
                                     C  A  _
GAM383  LOC90333  3' AGACTGGGTTTCACCGTGTT  62955            C
                                AACACGGTGAAACCC GTCT
                                |||||||||||||| ||||
                                TTGTGCCACTTTGGG CAGA
                                        T
GAM383  LOC90459  3' AGGCGGGGTTTCACCATGTT  63547     C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
                                TTGT CCACTTTGGGGCGGA
                                  A
GAM383  LOC90485  3' AGGCAGGGTTTCACCATGTT  63686     C        C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
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                                TTGT CCACTTTGGG CGGA
                                  A         A
GAM383  LOC90485  3' AGGCGGGGTTTCACCATGTT  63687      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCGGA
                                  A
GAM383  LOC90591  3' AGACGGAGTTTCATCGTGTT  64139            C
                                AACACGGTGAAAC CCGTCT
                                |||||||||||| ||||||
                                TTGTGCTACTTTG GGCAGA
                                       A
GAM383  LOC90591  3' AGACGGGGCTTCACTATGTT  64140      CG    A
                                AACA  GTGAA CCCCGTCT
                                ||||  ||||| ||||||||
                                TTGT  CACTT GGGGCAGA
                                  AT    C
GAM383  LOC91012  5' AGACAAGGTTTTGCCATGTT  65240      C  TG    CC
                                AACA GG  AAACC  GTCT
                                |||| ||  |||||  ||||
                                TTGT CC  TTTGG  CAGA
                                  A  GT    AA
GAM383  LOC91115  3' AGATGGGGTTTCACTGTGTT  65544
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGTCACTTTGGGGTAGA

GAM383  LOC91115  3' AGATGGGGTTTCATCATGTT  65545      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||||
                                TTGT CTACTTTGGGGTAGA
                                  A
GAM383  LOC91250  5' AGATGGGGTTTCATCATGTT  65903      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||||
                                TTGT CTACTTTGGGGTAGA
                                  A
GAM383  LOC91291  5' AGACAAGGTTTCACCCTGTT  66083      C        CC
                                AACA GGTGAAACC  GTCT
                                |||| |||||||||  ||||
                                TTGT CCACTTTGG  CAGA
                                  C         AA
GAM383  LOC91373  3' AGACGGAGTTTCACTCTTGT  66402      C _      C
                                ACA G GTGAAAC CCGTCT
                                ||| | ||||||| ||||||
                                TGT C CACTTTG GGCAGA
                                  T T       A
GAM383  LOC91373  3' AGATGGGGTTTGACCGTGTT  66406         G
                                AACACGGT AAACCCCGTCT
                                |||||||| ||||||||||
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                                TTGTGCCA TTTGGGGTAGA
                                    G
GAM383  LOC91561  5' AGACGGGGTTTCTCCATGTT  67038    C  T
                                AACA GG GAAACCCCGTCT
                                |||| || ||||||||||||
                                TTGT CC CTTTGGGGCAGA
                                  A  T
GAM383  LOC91893  3' AGACGAGGTTTCACCGTGTT  68066          C
                                AACACGGTGAAACC CGTCT
                                |||||||||||||| |||||
                                TTGTGCCACTTTGG GCAGA
                                       A
GAM383  LOC92148  5' AGACGGGGTTTCACCGTGTT  68869
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGA

GAM383  LOC92303  3' AGATGGGTTTCACCATGTT  69383    C       C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG TAGA
                                  A       _
GAM383  LOC92661  5' AGGCGGGGTTTCACTGTGTT  70618
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGTCACTTTGGGGCGGA

GAM383  LOC92689  3' AGACAGGGTTTCACCATGTT  70767    C       C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A       A
GAM383  LOC92697  5' AGACGGGGTTTCGCTGTGTT  70803
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGTCGCTTTGGGGCAGA

GAM383  LOC92841  3' AGACAGGGTTTCACCATGTT  71240    C       C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A       A
GAM383  LOC92841  3' AGACGGGGTTTCACCATGTT  71243    C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM383  LOC93349  3' AGACGGGGTTTCACTATGTT  57260    CG
                                AACA  GTGAAACCCCGTCT
                                ||||  ||||||||||||||
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                                TTGT  CACTTTGGGGCAGA
                                  AT
GAM384  ADCY7    3'  TGGGTGCATGCAGAGGCTCC   8495          CC  TG
                                GGAGCCTCTGTA  TG  CCCA
                                ||||||||||||  ||  ||||
                                CCTCGGAGACGT  AC  GGGT
                                      __  GT
GAM384  ALDH1B1  3'  TGGGCATGGGATTTGTTTTTG  7331    TG   CTCT  A
                                C  GAGC   GT CCTGTGCCCA
                                |  ||||   || ||||||||||
                                G  TTTG   TA GGGTACGGGT
                                 TT   TT__  _
GAM384  ANK1     3'  TGGGTGCAGGTGCCAGGCTCGA 40417    G     CT      TG
            G                    CT GAGCCT  GTACCTG  CCCA
                                || ||||||  |||||||  ||||
                                GA CTCGGA  CGTGGAC  GGGT
                                 G     C_      GT
GAM384  ANK1     3'  TGGGTGCAGGTGCCAGGCTCGA 40418    G     CT      TG
            G                    CT GAGCCT  GTACCTG  CCCA
                                || ||||||  |||||||  ||||
                                GA CTCGGA  CGTGGAC  GGGT
                                 G     C_      GT
GAM384  ANXA8    3'  TGGGTGTGAGGGGGGTCCCAG  73468      AG   TGTA  _ TG
                                CTGG  CCTC    CCT G  CCCA
                                ||||  ||||    ||| |  ||||
                                GACC  GGGG    GGA T  GGGT
                                  CT    _____   G GT
GAM384  ASIP     3'  TGCAGGCGGGCGGAGGTTCCAG 9807            A__
                                CTGGAGCCTCTGT   CCTGTG
                                ||||||||||||   ||||||
                                GACCTTGGAGGCG   GGACGT
                                       GGC
GAM384  ATP5G1   5'  TGGGCCAAGCAGGGGTTGCAG  18981     G       ACC  T
                                CTG AGCCTCTGT   TG GCCCA
                                ||| |||||||||   || |||||
                                GAC TTGGGGACG   AC CGGGT
                                  G       A__  _
GAM384  AVPR2    3'  TGGGTGTAGGAGGGGCTGCAG  5340     G      GTA   TG
                                CTG AGCCTCT   CCTG  CCCA
                                ||| |||||||   ||||  ||||
                                GAC TCGGGGA   GGAT  GGGT
                                  G      ___    GT
GAM384  BAK1     3'  TGGGCACAGCCTAGGGTCTTGG 93635    TG AG  T   TAC
                                C  G  CC CTG   CTGTGCCCA
                                |  |  || |||   |||||||||
                                G  T  GG GAT   GACACGGGT
                                 GT CT  _   CC_
GAM384  BCL9     3'  GGGCATGGGTGGATTTAG    16321       G  TCTGT
                                CTGGA CC    ACCTGTGCCC
                                ||||| ||    ||||||||||
```

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                                GATTT GG    TGGGTACGGG
                                  A _____
GAM384  BMP1    3'  CGGAATGGGATGGGGGCTTCGG 21528          A    GC  A
                                CTGGAGCCTCTGT CCTGT  CC
                                |||||||||||| |||||  ||
                                GGCTTCGGGGGTA GGGTA  GG
                                      _    A_  CA
GAM384  BMP1    3'  GGAATGGGATGGGGGCTTCGG  21533          A    GC  A
                                CTGGAGCCTCTGT CCTGT  CC
                                |||||||||||| |||||  ||
                                GGCTTCGGGGGTA GGGTA  GG
                                      _    A_  C
GAM384  CD164   3'  GGACTAGTGCAGAGGCTTTA  21196          CT  G
                                TGGAGCCTCTGTAC  GT CC
                                ||||||||||||||  || ||
                                ATTTCGGAGACGTG  CA GG
                                      AT  _
GAM384  CD22    3'  TGGGCTGCAGCAGAGGCACTGG 10102   TG A     TAC   _
                                C  G GCCTCTG   CTGT GCCCA
                                |  | |||||||   |||| |||||
                                G  C CGGAGAC   GACG CGGGT
                                 GT A      ___    T
GAM384  CDK7    5'  GGGTGTTGGAGGCTTTA    10156          TACCT TG
                                TGGAGCCTCTG    G  CCC
                                ||||||||||    |  |||
                                ATTTCGGAGGT    T  GGG
                                      _____ GT
GAM384  CHST6   3'  GGATGTGTAGAGGGTTTAG   41503      G       CTGTG
                                CTGGA CCTCTGTAC    CC
                                ||||| |||||||||    ||
                                GATTT GGAGATGTG    GG
                                   G       TA___
GAM384  CLCN6   3'  TGGGTGTGAGCAGAGGCTCTGG 41706   TG       ACC  TG
                                C  GAGCCTCTGT   TG  CCCA
                                |  ||||||||||   ||  ||||
                                G  CTCGGAGACG   GT  GGGT
                                 GT        A__  GT
GAM384  CLCN6   3'  TGGGTGTGAGCAGAGGCTCTGG 8907    TG       ACC  TG
                                C  GAGCCTCTGT   TG  CCCA
                                |  ||||||||||   ||  ||||
                                G  CTCGGAGACG   GT  GGGT
                                 GT        A__  GT
GAM384  COG3    3'  TGGACATTGTCAGGGGTTCTGG 49500   TG       T  CT   C
                                C  GAGCCTCTG AC  GTG CCA
                                |  |||||||||  ||  ||| |||
                                G  CTTGGGGAC TG  TAC GGT
                                 GT        _  T_   A
GAM384  CPO     3'  GGCTGTGCAGGGGTTT      76254          CTGT
                                GAGCCTCTGTAC    GCC
                                ||||||||||||    |||
```

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                                TTTGGGGACGTG   CGG
                                       T___
GAM384  DCTN1   5'  GGCTGTGTGGAGGCTCTAG   43759        TG  CTGT
                                CTGGAGCCTC  TAC   GCC
                                ||||||||||  |||   |||
                                GATCTCGGAG  GTG   CGG
                                      GT  T___
GAM384  DLEC1   3'  TGGGCATGAAAAGGATGCTCCG 24725       C  GTACCT
          G                      CTGGAGC TCT    GTGCCCA
                                ||||||| |||    |||||||
                                GGCCTCG AGG    TACGGGT
                                    T  AAAAG_
GAM384  E2F1    3'  CAGGTGGGGAGGCTTTGG   85948   TG      G
                                C  GAGCCTCT TACCTG
                                |  |||||||| ||||||
                                G  TTCGGAGG GTGGAC
                                 GT       G
GAM384  EGFL4   3'  TGGGCCCCACATAGGGTTTTGG 62478   TG    T   ACCTGT
                                C  GAGCC CTGT    GCCCA
                                |  ||||| ||||    |||||
                                G  TTTGG GATA    CGGGT
                                 GT    _   CACCC_
GAM384  ESRRA   3'  TGGGACTGGTGGGGGTTCTGG  16726   TG      GT  T  G
                                C  GAGCCTCT  ACC GT CCCA
                                |  ||||||||  ||| || ||||
                                G  CTTGGGGG  TGG CA GGGT
                                 GT       __  T  _
GAM384  FANCC   3'  GGGCAGCCAGGGGTTCC    71047         TACCTG
                                GGAGCCTCTG    TGCCC
                                ||||||||||    |||||
                                CCTTGGGGAC    ACGGG
                                      CG____
GAM384  FLT1    3'  TGGGTGTGGGTGTATGTGTGTT 10666     CTC__      TG
          TT                    GGAGC    TGTACCTG  CCCA
                                |||||    ||||||||  ||||
                                TTTTG    ATGTGGGT  GGGT
                                   TGTGT      GT
GAM384  FSTL3   3'  TGGGTGAGTACGGAGGGTCTAG 20752      G       CTG
                                CTGGA CCTCTGTAC   TGCCCA
                                ||||| |||||||||   ||||||
                                GATCT GGAGGCATG   GTGGGT
                                   G       A__
GAM384  FSTL3   3'  TGGGTGAGTACGGAGGGTCTAG 20753      G       CTG
                                CTGGA CCTCTGTAC   TGCCCA
                                ||||| |||||||||   ||||||
                                GATCT GGAGGCATG   GTGGGT
                                   G       A__
GAM384  FSTL3   3'  TGGGTGAGTATGGAGGGTCTAG 20754      G       CTG
                                CTGGA CCTCTGTAC   TGCCCA
                                ||||| |||||||||   ||||||
```

```
                                GATCT GGAGGTATG   GTGGGT
                                   G       A__
GAM384   FSTL3    3'  TGGGTGAGTATGGAGGGTCTAG 20755      G       CTG
                                CTGGA CCTCTGTAC   TGCCCA
                                ||||| |||||||||   ||||||
                                GATCT GGAGGTATG   GTGGGT
                                   G       A__
GAM384   FSTL3    3'  TGGGTGAGTATGGAGGGTCTAG 20756      G       CTG
                                CTGGA CCTCTGTAC   TGCCCA
                                ||||| |||||||||   ||||||
                                GATCT GGAGGTATG   GTGGGT
                                   G       A__
GAM384   FSTL3    3'  TGGGTGAGTATGGAGGGTCTAG 20757      G       CTG
                                CTGGA CCTCTGTAC   TGCCCA
                                ||||| |||||||||   ||||||
                                GATCT GGAGGTATG   GTGGGT
                                   G       A__
GAM384   FSTL3    3'  TGGGTGTGTACGGAGGGTCTAG 20758      G       CT TG
                                CTGGA CCTCTGTAC  G  CCCA
                                ||||| |||||||||  |  ||||
                                GATCT GGAGGCATG  T  GGGT
                                   G       __ GT
GAM384   FSTL3    3'  TGGGTGTGTACGGAGGGTCTAG 20759      G       CT TG
                                CTGGA CCTCTGTAC  G  CCCA
                                ||||| |||||||||  |  ||||
                                GATCT GGAGGCATG  T  GGGT
                                   G       __ GT
GAM384   FSTL3    3'  TGGGTGTGTACGGAGGGTCTAG 20760      G       CT TG
                                CTGGA CCTCTGTAC  G  CCCA
                                ||||| |||||||||  |  ||||
                                GATCT GGAGGCATG  T  GGGT
                                   G       __ GT
GAM384   FSTL3    3'  TGGGTGTGTATGGAGGATCTAG 20761      G       CT TG
                                CTGGA CCTCTGTAC  G  CCCA
                                ||||| |||||||||  |  ||||
                                GATCT GGAGGTATG  T  GGGT
                                   A       __ GT
GAM384   FSTL3    3'  TGGGTGTGTATGGAGGGTCTAG 20762      G       CT TG
                                CTGGA CCTCTGTAC  G  CCCA
                                ||||| |||||||||  |  ||||
                                GATCT GGAGGTATG  T  GGGT
                                   G       __ GT
GAM384   FSTL3    3'  TGGGTGTGTATGGAGGGTCTAG 20763      G       CT TG
                                CTGGA CCTCTGTAC  G  CCCA
                                ||||| |||||||||  |  ||||
                                GATCT GGAGGTATG  T  GGGT
                                   G       __ GT
GAM384   GALGT    3'  TGGGCACAAAAGAAGGGGCACC 9422      A     GTACC
            AG                    CTGG GCCTCT    TGTGCCCA
                                ||||| ||||||    ||||||||
```

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                                GACC CGGGGA    ACACGGGT
                                  A     AGAAA
GAM384  GFRA2    3'  TGGGCTCTGGTGGGGGCTCC  9467        GT   TGT
                                GGAGCCTCT  ACC   GCCCA
                                |||||||||  |||   |||||
                                CCTCGGGGG  TGG   CGGGT
                                     __   TCT
GAM384  GNE      3'  TGGGTGTGGTGGCGGGTCCAG  19682      G  T  GT   T TG
                                CTGGA CC CT  ACC G  CCCA
                                ||||| || ||  ||| |  ||||
                                GACCT GG GG  TGG T  GGGT
                                   G  C  __   _ GT
GAM384  GYS1     3'  TGCGGTGGTGCCAGAGGTTTTA 89786          _   TG   CCA
           G                     CTGGAGCCTCTG TACC  TGC
                                ||||||||||| ||||  |||
                                GATTTTGGAGAC GTGG  GCG
                                      C    TG   T
GAM384  HDAC5    3'  GGTGAGAATGGAGGTTCTAG   19622          AC  G
                                CTGGAGCCTCTGT  CT TGCC
                                ||||||||||||  || ||||
                                GATCTTGGAGGTA  GA GTGG
                                      A_  _
GAM384  HMOX2    3'  TGGGTGTGGGTGGAAGCCTCAG 65760    GA  C   GT    TG
                                CTG  GC TCT  ACCTG  CCCA
                                |||  || |||  |||||  ||||
                                GAC  CG AGG  TGGGT  GGGT
                                  TC  A  __    GT
GAM384  HSD11B1  3'  TGGGCATGCTGAGGGATTTTGG 19829   TG  __   T  ACCT
                                C  GAG  CCTC GT   GTGCCCA
                                |  |||  |||| ||   |||||||
                                G  TTT  GGAG CG   TACGGGT
                                 GT   AG   T ____
GAM384  IDH1     3'  GGGCACAGGGAAGTTCTGG   62097   TG   C  TGTA
                                C  GAGC TC   CCTGTGCCC
                                |  |||| ||   |||||||||
                                G  CTTG AG   GGACACGGG
                                 GT   A  ____
GAM384  IFNGR2   5'  TGGGCGTCCCGCGGGGCTCCAG 19850       T   ACCTG
                                CTGGAGCC CTGT    TGCCCA
                                |||||||| ||||    ||||||
                                GACCTCGG GGCG    GCGGGT
                                     _   CCCT_
GAM384  IHPK1    3'  TGGGTGCAGGTGCCCACATTCT 97466     CCTCT     TG
                                GGAG    GTACCTG  CCCA
                                ||||    |||||||  ||||
                                TCTT    CGTGGAC  GGGT
                                  ACACC      GT
GAM384  IL1F9    3'  GGGTATGAAGATGCTTCAG   39513       C   GTACCT
                                CTGGAGC TCT    GTGCCC
                                ||||||| |||    ||||||
```

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                                GACTTCG AGA     TATGGG
                                   T  AG____
GAM384  IL6R    3'  TGGGCAGGTTGGTGGGGGCCTC 6917     GA    TG __   GT
            GG                   CTG  GCCTC  T  ACCT  GCCCA
                                |||  |||||  |  ||||  |||||
                                GGC  CGGGG  G  TGGA  CGGGT
                                  TC    GT GT   __
GAM384  KRT4    5'  TGGGCCCAGGCAGGGGCTTC   11229         TA   T
                                GGAGCCTCTG  CCTG GCCCA
                                ||||||||||  |||| |||||
                                CTTCGGGGAC  GGAC CGGGT
                                      __   C
GAM384  LDB3    3'  TGGGCAATTGCCAGGGCTCCAG 76928        T  TACCTG
                                CTGGAGCC CTG     TGCCCA
                                |||||||| |||     ||||||
                                GACCTCGG GAC     ACGGGT
                                   _  CGTTA_
GAM384  LENG4   3'  TGGGCCGCTGCGTGGGCTTCGG 44422        C   CC  T
                                CTGGAGCCT TGTA  TG GCCCA
                                |||||||| ||||  || |||||
                                GGCTTCGGG GCGT  GC CGGGT
                                     T   C_ _
GAM384  LIF     3'  TAAGTCAGGTGCAGAGGTTCT  11307            T  CCA
                                GGAGCCTCTGTACCTG GC
                                |||||||||||||||| ||
                                TCTTGGAGACGTGGAC TG
                                      _ AATC
GAM384  MAP1B   3'  TGGGTGAGCGTGTGTGGGGGTA 20965     A    TG  C  __
            CTAG                  CTGG GCCTC  TAC TGT  GCCCA
                                ||||  |||||  |||  |||  |||||
                                GATC TGGGG  GTG GCG  TGGGT
                                  A    GT  T  AG
GAM384  MAX     3'  TGGGTGGCATAGAGGTTTT   11477          A  TGT
                                GGAGCCTCTGT CC   GCCCA
                                ||||||||||| ||   |||||
                                TTTTGGAGATA GG   TGGGT
                                     C  ___
GAM384  MYCL2   3'  GGATGTTGTTGGGGGCTCCAG  19378          T  CTGTG
                                CTGGAGCCTCTG AC    CC
                                ||||||||||| ||    ||
                                GACCTCGGGGGT TG    GG
                                      _ TTGTA
GAM384  NRG1    3'  ATAGGTGTGTGAGGCTCCGG   16902         TG_
                                CTGGAGCCTC   TACCTGT
                                |||||||||   |||||||
                                GGCCTCGGAG   GTGGATA
                                      TGT
GAM384  NTF5    3'  TGGGTGAAACCACATGGGGTTT 21631    TG     _   ACCTG
            TGG                   C  GAGCCTC TGT    TGCCCA
                                |  ||||||| |||    ||||||
```

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                                G  TTTGGGG ACA    GTGGGT
                                 GT      T  CCAAA
GAM384  OPRD1    3'  TGGGCATGGGGTGGGCCTCTGG 8071    TG   C   TGTA
                                C  GAG CTC    CCTGTGCCCA
                                |  ||| |||    ||||||||||
                                G  CTC GGG    GGGTACGGGT
                                 GT   C   TG__
GAM384  PACE     3'  TGGCCCTGAGGTGTGGGGGCTG 11945     G     TG    GT__   CA
           CAG                    CTG AGCCTC  TACCT    GCC
                                ||| ||||||  |||||    |||
                                GAC TCGGGG  GTGGA    CGG
                                  G     GT    GTCC   T
GAM384  PLA2G2D  3'  GGGAGGCAGAGGTTTCAG    25720           ACCTGTG
                                CTGGAGCCTCTGT      CCC
                                ||||||||||||      |||
                                GACTTTGGAGACG      GGG
                                       GA_____
GAM384  POMZP3   3'  TGGGCGTAGGCCTGGCTGTGG  25277     G    TCTGTA
                                CTG AGCC     CCTGTGCCCA
                                ||| ||||     ||||||||||
                                GGT TCGG     GGATGCGGGT
                                  G    TCC___
GAM384  PSD      5'  TGGGCTCAAGGCAGGGCTCTGG 12441    TG    T    ACC  T
                                C  GAGCC CTGT   TG GCCCA
                                |  ||||| ||||   || |||||
                                G  CTCGG GACG   AC CGGGT
                                 GT    _    GA_  T
GAM384  PTGER2   5'  TGGGTGCGGGAAGGGGGCTCTG 8174    TG      GTA    TG
           G                     C  GAGCCTCT   CCTG  CCCA
                                |  ||||||||   ||||  ||||
                                G  CTCGGGGG   GGGC  GGGT
                                 GT      AA_    GT
GAM384  RFNG     3'  TGGGTGTCAAGGAGCAGGCTCC 89564         CT  A   __ TG
           AG                     CTGGAGCCT  GT CCT  G  CCCA
                                |||||||||  || |||  |  ||||
                                GACCTCGGA  CG GGA  T  GGGT
                                      __  A   AC GT
GAM384  RGS6     3'  TGGGCCCGGTGGAGGCTCC    16282         GT   T T
                                GGAGCCTCT  ACC G GCCCA
                                |||||||||  ||| | |||||
                                CCTCGGAGG  TGG C CGGGT
                                      __   _ C
GAM384  S100A11  5'  TGGGTTGAGGAGAGGCTCCAG  20056          GTA   GT
                                CTGGAGCCTCT   CCT  GCCCA
                                ||||||||||   |||  |||||
                                GACCTCGGAGA   GGA  TGGGT
                                       ___   GT
GAM384  SDHC     3'  GGGTTGGTGAGGCTTTGG    69913    TG      TGT   TGT
                                C  GAGCCTC   ACC   GCCC
                                |  |||||||   |||   ||||
```

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                              G  TTCGGAG   TGG   TGGG
                               GT      ___   T__
GAM384  SMURF1   3'  GGGCTGCTGAGGTTCTAG    94050         T   CCTGT
                              CTGGAGCCTC GTA    GCCC
                              |||||||||| |||    ||||
                              GATCTTGGAG CGT    CGGG
                                    T  _____
GAM384  SYNGR3   3'  TGCCCAGGTGTGGGTGGTTCTG 16124   TG    _ TG     T  CCA
           G                   C  GAGCC TC  TACCTG GC
                              |  ||||| ||  |||||| ||
                              G  CTTGG GG  GTGGAC CG
                               GT    T  GT     C  T
GAM384  TBXA2R   3'  TGGGCATCAGCAGCAGGGTTTT 8370    TG    T    AC   _
           GG                    C  GAGCC CTGT  CTG TGCCCA
                              |  ||||| ||||  ||| ||||||
                              G  TTTGG GACG  GAC ACGGGT
                               GT    _    AC   T
GAM384  TEM6     3'  GGGCATGGGTGCACCCCA    43039     AGCCTC
                              TGG     TGTACCTGTGCCC
                              |||     ||||||||||||
                              ACC     ACGTGGGTACGGG
                                CC____
GAM384  TGM2     3'  TGGGCAGCCTATGGGGGCTCT  17246           CCTG
                              GGAGCCTCTGTA   TGCCCA
                              ||||||||||||   ||||||
                              TCTCGGGGGTAT   ACGGGT
                                    CCG_
GAM384  TNFRSF7  3'  TGCAGGAGGGCGGGGGCTCTGG 8794    TG        A__
                              C  GAGCCTCTGT   CCTGTG
                              |  ||||||||||   ||||||
                              G  CTCGGGGGCG   GGACGT
                               GT        GGA
GAM384  TRAF1    3'  TAGAGCTACAGGGGTTCTGG   20178   TG        C  G
                              C  GAGCCTCTGTA CT TG
                              |  |||||||||| || ||
                              G  CTTGGGGACAT GA AT
                               GT         C  G
GAM384  TRPC5    5'  TGGGTGCGCTTGAAGGGGCTCA 25928     G      GTACC  TG
           G                   CTG AGCCTCT    TG  CCCA
                              ||| |||||||    ||  ||||
                              GAC TCGGGGA    GC  GGGT
                                _      AGTTC  GT
GAM384  ZP3A     3'  TGGGCGTAGGCCTGGCTGTGG  24099     G    TCTGTA
                              CTG AGCC     CCTGTGCCCA
                              ||| ||||     ||||||||||
                              GGT TCGG     GGATGCGGGT
                                G   TCC___
GAM384  AD-003   3'  GGGTGGAAGGGGCTCCAG    26779          GTA  TGT
                              CTGGAGCCTCT   CC   GCCC
                              ||||||||||   ||   ||||
```

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                                GACCTCGGGGA  GG  TGGG
                                      A__  ____
GAM384  APR-3    5'  TGGGCGTGGAAAGGGCTCTGG  55483   TG    T  GTAC TG
                                C  GAGCC CT   C  TGCCCA
                                |  ||||| ||   |  ||||||
                                G  CTCGG GA   G  GCGGGT
                                 GT    _  AA__ GT
GAM384  CBCIP2   3'  TGGGTGCAGGTGCACGCCAG  52662     AGCCTC      TG
                                CTGG     TGTACCTG  CCCA
                                ||||     ||||||||  ||||
                                GACC     ACGTGGAC  GGGT
                                  GC____       GT
GAM384  CDC42BPB 3'  TGGGCACCTGGGGGGTTCTGG  21241   TG     TGTA  T_
                                C  GAGCCTC   CC  GTGCCCA
                                |  |||||||   ||  |||||||
                                G  CTTGGGG   GG  CACGGGT
                                 GT      _____  TC
GAM384  CECR6    3'  TGGGTGTGGGGCAGGGCCTGG  49938   TG A  T   A   TG
                                C  G GCC CTGT CCTG  CCCA
                                |  | ||| |||| ||||  ||||
                                G  C CGG GACG GGGT  GGGT
                                 GT _  _   _   GT
GAM384  CFLAR    3'  TGGGTGTGGGTGTGGGTACC   15276    A   CTG     TG
                                GG GCCT   TACCTG  CCCA
                                || ||||   ||||||  ||||
                                CC TGGG   GTGGGT  GGGT
                                 A   T__     GT
GAM384  CLL-1    3'  GTAGGGGGTGGGGGTTCTAG   57177         TG A   G
                                CTGGAGCCTC  T CCT TGC
                                ||||||||||  | ||| |||
                                GATCTTGGGG  G GGG ATG
                                      GT _   G
GAM384  DKFZP434P1750 5'  GGGACTTGTGAGGCTCCGG    32027         TGT  CT  G
                                CTGGAGCCTC   AC  GT CCC
                                ||||||||||   ||  || |||
                                GGCCTCGGAG   TG  CA GGG
                                      ___  TT  _
GAM384  DKFZp547I094 3'  GCAGGGCAGGGGCTCCAG    50560           A
                                CTGGAGCCTCTGT CCTGT
                                |||||||||||| |||||
                                GACCTCGGGGACG GGACG
                                                _
GAM384  DKFZp586I021 3'  TGGGCATAGGTGGACAGGCTCT 51085    TG     CTG
           GG                    C  GAGCCT   TACCTGTGCCCA
                                |  ||||||  ||||||||||||
                                G  CTCGGA   GTGGATACGGGT
                                 GT     CAG
GAM384  DKFZp762A227 5'  TGGGCGGACGCGTGGGCTCTGG 34700    TG     C   A_  TGT
                                C  GAGCCT TGT  CC   GCCCA
                                |  |||||| |||  ||   |||||
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                              G  CTCGGG GCG  GG   CGGGT
                               GT     T   CA ___
GAM384  E2IG4    3'  TGGGCCTAGGAGAGGCTTTGG  92548   TG      GTA   T
                              C  GAGCCTCT   CCTG GCCCA
                              |  ||||||||   |||| |||||
                              G  TTCGGAGA   GGAT CGGGT
                               GT      ___   C
GAM384  EPB41L1  3'  TGGGTGTGGGTTGGCTCACAG  71121    _    TCTGT    TG
                              CTG GAGCC    ACCTG  CCCA
                              ||| |||||    |||||  ||||
                              GAC CTCGG    TGGGT  GGGT
                                A    T____    GT
GAM384  FAM3A    3'  TGGGGGCTATGGGGGCTGCAG  41734    G       CCT  G
                              CTG AGCCTCTGTA   GT CCCA
                              ||| ||||||||||   || ||||
                              GAC TCGGGGGTAT   CG GGGT
                                G        ___  G
GAM384  FLJ10520  5'  TGGGTATAGGTGCATTTCCA   36713     CCTC
                              TGGAG   TGTACCTGTGCCCA
                              |||||   ||||||||||||||
                              ACCTT   ACGTGGATATGGGT
                                 T___
GAM384  FLJ10904  5'  GGGTACGGGAGCGCTTTGG   37384   TG   CTCT  A
                              C  GAGC   GT CCTGTGCCC
                              |  ||||   || |||||||||
                              G  TTCG   CG GGGCATGGG
                               GT   _____  A
GAM384  FLJ10936  3'  TGGGATGTGGAGGTTGCAG   37452    G    TG  _
                              CTG AGCCTC  TA CCTG
                              ||| ||||||  || ||||
                              GAC TTGGAG  GT GGGT
                                G    GT  A
GAM384  FLJ11036  3'  TGGGTGTGGGGCCTGAGGCTTC 37558        TGTA   TG
            A                  TGGAGCCTC   CCTG  CCCA
                              |||||||||   ||||  ||||
                              ACTTCGGAG   GGGT  GGGT
                                    TCCG   GT
GAM384  FLJ11362  3'  TGGGAATCTGCAGAGGGCTCTG 41966   TG   _    CCTGTG
            G                  C  GAGCC TCTGTA    CCCA
                              |  ||||| ||||||     ||||
                              G  CTCGG AGACGT    GGGT
                               GT   G    CTAA__
GAM384  FLJ12171  3'  TGGGTGCGGGGGGAGGGTATCCG 45201     GC   GTA   TG
            G                  CTGGA  CTCT   CCTG  CCCA
                              |||||  ||||   ||||  ||||
                              GGCCT  GGGA   GGGC  GGGT
                                 AT   GG_   GT
GAM384  FLJ12221  5'  TGGGTGCGGTAGGGGTCCCGG  63226    AG    TAC   TG
                              CTGG  CCTCTG   CTG  CCCA
                              ||||  ||||||   |||  ||||
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                                GGCC  GGGGAT   GGC  GGGT
                                  CT     ___   GT
GAM384  FLJ12229  5' TGGGGACCATGTGGAGGTTCT  46408       TG  CCT  G
                                GGAGCCTC  TA   GT CCCA
                                ||||||||  ||   || ||||
                                TCTTGGAG  GT   CA GGGT
                                    GT  AC_  G
GAM384  FLJ12750  3' TGGGCAACGTTAGGGGTTT   45444        T  CTG
                                GAGCCTCTG AC   TGCCCA
                                |||||||||  ||   ||||||
                                TTTGGGGAT TG   ACGGGT
                                     _  CA_
GAM384  FLJ12788  3' TGGGTCTGCAGAAGGCTTTAG  42850        _    CCTGT
                                CTGGAGCCT CTGTA    GCCCA
                                |||||||||  |||||    |||||
                                GATTTCGGA GACGT    TGGGT
                                     A    C____
GAM384  FLJ13848  3' TGGGTGTAGAGGGCGGCTTCAG 45834       T  GTAC   TG
                                CTGGAGCC CT    CTG  CCCA
                                ||||||||  ||    |||  ||||
                                GACTTCGG GG    GAT  GGGT
                                    C  GA__   GT
GAM384  FLJ20036  5' TGGGCGGTTCGGCGGCTCTGG  34860   TG    T   T   TGT
                                C  GAGCC CTG ACC   GCCCA
                                |  ||||| ||| |||   |||||
                                G  CTCGG GGC TGG   CGGGT
                                 GT    C   T  ___
GAM384  FLJ20323  3' GCCTCATCAGGGCAGAGGTTTT 39180           A   _  CCCA
          AG                    CTGGAGCCTCTGT CCTG TG
                                |||||||||||||  |||| ||
                                GATTTTGGAGACG GGAC AC
                                       _   T  TCCGT
GAM384  FLJ20533  5' TGGAGTACGGGGCCTTCGG   35803       C      _
                                CTGGAG CTCTGTAC CTG
                                ||||||  ||||||||  |||
                                GGCTTC GGGGCATG GGT
                                    C       A
GAM384  FLJ20584  3' TGGGCACAGCCTCGGCTCTGG  35857   TG    TCTGTAC
                                C  GAGCC      CTGTGCCCA
                                |  |||||      |||||||||
                                G  CTCGG      GACACGGGT
                                 GT    CTCC___
GAM384  FLJ20825  5' TGGGCACAGGTGCAGAAGGTGC 36151     GA   _
          AG                    CTG  GCCT CTGTACCTGTGCCCA
                                |||  |||| ||||||||||||||
                                GAC  TGGA GACGTGGACACGGGT
                                  G_   A
GAM384  FLJ20825  5' TGGGCATAGGTGCAGTGAGTGC 36152    _  __
                                GC CTC  TGTACCTGTGCCCA
                                || |||  ||||||||||||||
```

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                                CG GAG  ACGTGGATACGGGT
                                 T   TG
GAM384   FLJ20825  5'  TGGGCATAGGTGCAGTGAGTGC 36153    _  __
                                GC CTC  TGTACCTGTGCCCA
                                || |||  ||||||||||||||
                                CG GAG  ACGTGGATACGGGT
                                 T   TG
GAM384   FLJ20825  5'  TGGGTGCAGGTGCAGTAGGTGC 36154    GA   _       TG
           AG                    CTG  GCCT CTGTACCTG  CCCA
                                ||| ||||  |||||||||  ||||
                                GAC  TGGA GACGTGGAC  GGGT
                                  G_   T       GT
GAM384   FLJ21019  3'  TGGGTGTGGGTAATTTTCTAG  46804       CCTCTG     TG
                                CTGGAG     TACCTG  CCCA
                                ||||||     ||||||  ||||
                                GATCTT     ATGGGT  GGGT
                                    TTA___     GT
GAM384   FLJ21742  3'  CAGATGCAGGGGCTCTGG    50813   TG         C
                                C  GAGCCTCTGTA CTG
                                |  ||||||||||| |||
                                G  CTCGGGGACGT GAC
                                 GT         A
GAM384   FLJ22795  3'  TGGGCGTGGCAAGGTTCC    47637        C  TAC TG
                                GGAGCCT TG   C  TGCCCA
                                ||||||| ||   |  ||||||
                                CCTTGGA AC   G  GCGGGT
                                    _  ___ GT
GAM384   FLJ22833  3'  GGGTACAGGTACATTTGG    43406    TC_
                                CC   TGTACCTGTGCCC
                                ||   ||||||||||||
                                GG   ACATGGACATGGG
                                 TTT
GAM384   FLJ23022  5'  TGGGTACAGAAGAGGCTTCAG  47502          GTAC
                                CTGGAGCCTCT    CTGTGCCCA
                                ||||||||||    |||||||||
                                GACTTCGGAGA    GACATGGGT
                                      A___
GAM384   FLJ23027  3'  TGGGTATAGGTATTTTCTTCC  50914      CCTCT
                                GGAG    GTACCTGTGCCCA
                                ||||    ||||||||||||
                                CCTT    TATGGATATGGGT
                                  CTTT_
GAM384   FLJ23251  5'  TGGGTGCACGTCCCCAGGGCTC 46101    TG    T   T__  C  TG
           TGG                   C  GAGCC CTG   AC TG  CCCA
                                |  ||||| |||   || ||  ||||
                                G  CTCGG GAC   TG AC  GGGT
                                 GT    _   CCC  C  GT
GAM384   FLJ23451  5'  TGGCACCTCCGGGTGTGGAAGG 45791         _ TG    _____     CA
           CTCCAG                CTGGAGCCT C  TACCT    GTGCC
                                |||||||||  |  |||||    |||||
```

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                                GACCTCGGA G  GTGGG    CACGG
                                     A GT    CCTC    T
GAM384  FLJ23506  5'  TGGGCCGCAGGTGGAGGTGTTG 46167   TG A    GT     _
          G                    C  G GCCTCT  ACCTGTG CCCA
                               |  | ||||||  ||||||| ||||
                               G  T TGGAGG  TGGACGC GGGT
                                GT G     __      C
GAM384  FLJ32356  3'  TGGGTGTGGGTGGCACAGGATC 59029   TG  G   C   _    TG
          TGG                   C  GA CCT TGT ACCTG  CCCA
                               |  || ||| ||| |||||  ||||
                               G  CT GGA ACG TGGGT  GGGT
                                GT  A   C   G    GT
GAM384  GMPPB    5'  GCCAGGTGCTGGGGGCTCTGG  26222   TG      _      T
                               C  GAGCCTCT GTACCTG GC
                               |  |||||||| ||||||| ||
                               G  CTCGGGGG CGTGGAC CG
                                GT       T     _
GAM384  GMPPB    5'  TGGGTTCAAAGGTGGAGGTTCC 26226          GT   GT__
          AG                    CTGGAGCCTCT  ACCT   GCCCA
                               ||||||||||  ||||   |||||
                               GACCTTGGAGG  TGGA   TGGGT
                                      __   AACT
GAM384  GNB4     5'  TGGGTGTGGCCGGCGGCTCTGG 41571   TG    T   TAC   TG
                               C  GAGCC CTG   CTG  CCCA
                               |  ||||| |||   |||  ||||
                               G  CTCGG GGC   GGT  GGGT
                                GT    C   C__   GT
GAM384  GNG4     3'  GGGCCCGCTGGGGTTTTAG    16848          T  ACCT T
                               CTGGAGCCTC GT    G GCCC
                               |||||||||| ||    | ||||
                               GATTTTGGGG CG    C CGGG
                                      T  _____ C
GAM384  GPS2     5'  TGGGCACAGGTGCACGCATTGG 88511    TG A  CTC
                               C  G GC   TGTACCTGTGCCCA
                               |  | ||   ||||||||||||||
                               G  T CG   ACGTGGACACGGGT
                                GT A  C__
GAM384  HIC2     3'  TGGGTCCAGTGGAGGCTCCGG  65875          TAC   TG
                               CTGGAGCCTCTG   CTG  CCCA
                               ||||||||||||   |||  ||||
                               GGCCTCGGAGGT   GAC  GGGT
                                      ____   CT
GAM384  HSNOV1   3'  TGGGTACAGATGAGGCCTCGG  34444     GA    TGTAC
                               CTG  GCCTC    CTGTGCCCA
                               |||  |||||    |||||||||
                               GGC  CGGAG    GACATGGGT
                                 TC    TA___
GAM384  HT001    5'  GGGTATTAGTGGCTTTAG    67243        T   TACCT
                               CTGGAGCC CTG    GTGCCC
                               |||||||| |||    ||||||
```

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                                GATTTCGG GAT    TATGGG
                                     T  _____
GAM384  HT002    3'  TGGGCTGCGGGGTCAGGGGCTC 26803          TA    _
            CAG                    CTGGAGCCTCTG  CCTGT GCCCA
                                   ||||||||||||  ||||| |||||
                                   GACCTCGGGGAC  GGGCG CGGGT
                                         TG    T
GAM384  KCND1    3'  TGGGATATGGAGCTTTGG    18350   TG   C    _
                                   C  GAGC TCTGTA CCTG
                                   |  |||| |||||| ||||
                                   G  TTCG AGGTAT GGGT
                                    GT   _     A
GAM384  KIAA0226 3'  TGGGCGTGGGTGCTGCCC    64266    A  CTCT    TG
                                   GG GC    GTACC  TGCCCA
                                   || ||    |||||  ||||||
                                   CC CG    CGTGG  GCGGGT
                                    _ T___     GT
GAM384  KIAA0329 3'  GCGGGCACAGGGGCTTCGG    29940          A
                                   CTGGAGCCTCTGT CCTGT
                                   |||||||||||| |||||
                                   GGCTTCGGGGACA GGGCG
                                         C
GAM384  KIAA0376 3'  GGGCACGGGGAGGGCTT     66215       CTGTA
                                   GAGCCT     CCTGTGCCC
                                   ||||||     |||||||||
                                   TTCGGG     GGGCACGGG
                                      AG___
GAM384  KIAA0450 3'  TGGGCGGCTCTGGAGGCCCAG  28376     A      TA_  TGT
                                   CTGG GCCTCTG   CC   GCCCA
                                   |||| |||||||   ||   |||||
                                   GACC CGGAGGT   GG   CGGGT
                                     _      CTC  ___
GAM384  KIAA0513 3'  GGGTGTAGGAGAGCTCTGG    29043    TG   C   GTA    TG
                                   C  GAGC TCT   CCTG  CCC
                                   |  |||| |||   ||||  |||
                                   G  CTCG AGA   GGAT  GGG
                                    GT   _  ___    GT
GAM384  KIAA0514 5'  TGGGCACGCAGTAGGGGCTCAG 28761     G       TACC
                                   CTG AGCCTCTG    TGTGCCCA
                                   ||| ||||||||    ||||||||
                                   GAC TCGGGGAT    GCACGGGT
                                     _       GAC_
GAM384  KIAA0767 3'  TGGGCCATCCGAGAGGCTCTGG 61260    TG       GTACC  T
                                   C  GAGCCTCT     TG GCCCA
                                   |  ||||||||     || |||||
                                   G  CTCGGAGA     AC CGGGT
                                    GT       GCCT_  _
GAM384  KIAA0798 3'  GGGAGGCAGAGGTTTCAG    28450           ACCTGTG
                                   CTGGAGCCTCTGT      CCC
                                   ||||||||||||       |||
```

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                                GACTTTGGAGACG      GGG
                                      GA_____
GAM384  KIAA0884  3'  TGGGATGTGGAGGTTGCAG   70761     G     TG  _
                                CTG AGCCTC  TA CCTG
                                ||| ||||||  || ||||
                                GAC TTGGAG  GT GGGT
                                  G     GT  A
GAM384  KIAA1130  3'  TGGGCATTGCTGGAGGTTT   63102        _  CCT
                                GAGCCTCT GTA   GTGCCCA
                                |||||||| |||   |||||||
                                TTTGGAGG CGT   TACGGGT
                                     T  ___
GAM384  KIAA1545  3'  TGGGCGGCTCCTGTGGGCTTCA 61337         CTGTACCTG
              G                  CTGGAGCCT       TGCCCA
                                |||||||||       ||||||
                                GACTTCGGG       GCGGGT
                                     TGTCCTCG_
GAM384  KIAA1550  3'  TGGGCAGTGCTGGAGGCTCT   67155         _   CTG
                                GGAGCCTCT GTAC   TGCCCA
                                ||||||||| ||||   ||||||
                                TCTCGGAGG CGTG   ACGGGT
                                     T   ___
GAM384  KIAA1655  5'  TGGGAGCTTAGGGCAGGGGCTC 67205           A   TG__
              CGG                  CTGGAGCCTCTGT CCTG   CCCA
                                |||||||||||| ||||   ||||
                                GGCCTCGGGGACG GGAT   GGGT
                                       _   TCGA
GAM384  KIAA1904  3'  GGGCTTCGTGGGGGGCTTCAG  73875         G  CTGT   A
                                CTGGAGCCTCT TAC   GCCC
                                |||||||||| |||   ||||
                                GACTTCGGGGG GTG   CGGG
                                       _  CTT_
GAM384  KIAA1932  3'  TGGGCAATGTCAAGAGAGGTTT 73826   TG      GTACCTG_
              TGG                  C  GAGCCTCT       TGCCCA
                                |  ||||||||       ||||||
                                G  TTTGGAGA       ACGGGT
                                 GT       GAACTGTA
GAM384  KIAA1951  5'  GGGTGTGTGTAGGCTTCAG   74162        CTGT  C  TG
                                CTGGAGCCT   AC TG  CCC
                                |||||||||   || ||  |||
                                GACTTCGGA   TG GT  GGG
                                     ____  T  GT
GAM384  KOC1      3'  TGGGTGTGGGTGGTCTCCA   92720      _ TCTGT    TG
                                TGGAG CC    ACCTG  CCCA
                                ||||| ||    |||||  ||||
                                ACCTC GG    TGGGT  GGGT
                                   T _____    GT
GAM384  LASP1     3'  TGGGCGATTTGGGGGCTCGGG  21581    G       TACCTG
                                CT GAGCCTCTG     TGCCCA
                                || |||||||||     ||||||
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                                GG CTCGGGGGT     GCGGGT
                                 G       TTA___
GAM384  LRRFIP2   3'  GGGCACTCGGAGGCCTTGG   21951   TG A     TACCT
                                C  G GCCTCTG    GTGCCC
                                |  | |||||||    ||||||
                                G  T CGGAGGC    CACGGG
                                 GT C      T____
GAM384  MANBAL    3'  GCTCCATCAGGTGCAGGGGATT 42219   TG  G        _  CCCA
           TGG                    C  GA CCTCTGTACCTG TG
                                |  || ||||||||||||| ||
                                G  TT GGGGACGTGGAC AC
                                 GT  A          T  CTCGT
GAM384  MGC12921  3'  TGGGCATCGATGAGGCTTTGG  64516   TG     TGTACCT
                                C  GAGCCTC      GTGCCCA
                                |  |||||||      |||||||
                                G  TTCGGAG      TACGGGT
                                 GT      TAGC___
GAM384  MGC23284  5'  GGGCGCGGCGAGGTCTGG    59360   TG  G   TGTAC
                                C  GA CCTC    CTGTGCCC
                                |  || ||||    ||||||||
                                G  CT GGAG    GGCGCGGG
                                 GT  _   C____
GAM384  MGC2452   5'  TGGAGCGTTGTCTGGAGGTTCC 51970          GT  CTG  _
           AG                    CTGGAGCCTCT  AC   TGC CCA
                                ||||||||||  ||   ||| |||
                                GACCTTGGAGG  TG   GCG GGT
                                      TC  TT_   A
GAM384  MGC3178   3'  TGGGTATCCAGGGAGGCTCT   48721        TGTA   __
                                GGAGCCTC    CCTG  TGCCCA
                                ||||||||    ||||  ||||||
                                TCTCGGAG    GGAC  ATGGGT
                                     _____   CT
GAM384  MGC4293   3'  TGGGACTCTGCGGGAGGCTCTG 49346   TG      _   CCT  G
           G                     C  GAGCCTCT GTA   GT CCCA
                                |  |||||||| |||   || ||||
                                G  CTCGGAGG CGT   CA GGGT
                                 GT       G   CT_  _
GAM384  MGC4655   3'  TGGGGATATGCAAGGGGCTCTG 53962   TG      _   CC   G
           G                     C  GAGCCTCT GTA  TGT CCCA
                                |  |||||||| |||  ||| ||||
                                G  CTCGGGGA CGT  ATA GGGT
                                 GT       A   __   G
GAM384  MGC5306   5'  GGTGTGTACAGAGCTCTAG    44372        C      CT TG
                                CTGGAGC TCTGTAC  G  CC
                                ||||||| |||||||  |  ||
                                GATCTCG AGACATG  T  GG
                                     _      __ GT
GAM384  MGLL      5'  TGGGTGCGGGAAGAGGGCTC   24419       _  GTA   TG
                                GAGCC TCT   CCTG  CCCA
                                ||||| |||   ||||  ||||
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                                CTCGG AGA   GGGC  GGGT
                                  G   A__    GT
GAM384  MRPL41    5'  TGGAGCTCGTGTGGGGTCTCCG 51648      C   TG   CTGT  _
           G                     CTGGAG CTC  TAC    GC CCA
                                 |||||| |||  |||    || |||
                                 GGCCTC GGG  GTG    CG GGT
                                    T   GT   CT__  A
GAM384  MRPL45    3'  TGGGCATGGACCAGCCTTCAG  51354      CCT   TA  T
                                 CTGGAG   CTG  CC GTGCCCA
                                 ||||||   |||  || |||||||
                                 GACTTC   GAC  GG TACGGGT
                                    C__   CA  _
GAM384  NCX       3'  GGGCTCTGAGGGGCTCTAG   32945          GTACCTGT
                                 CTGGAGCCTCT       GCCC
                                 ||||||||||        ||||
                                 GATCTCGGGGA       CGGG
                                       GTCT_____
GAM384  NYD-SP25  3'  TGGGCAAGTCAGTGGCTCCAG  54306        T   T  CTG
                                 CTGGAGCC CTG AC   TGCCCA
                                 |||||||| ||| ||   ||||||
                                 GACCTCGG GAC TG   ACGGGT
                                      T   _  A__
GAM384  P2RX1     3'  TGGGTGCAGCGTGAGGCTTCAG 67753          TGT  _   TG
                                 CTGGAGCCTC   AC CTG  CCCA
                                 ||||||||||   || |||  ||||
                                 GACTTCGGAG   TG GAC  GGGT
                                       ___  C   GT
GAM384  P37NB     5'  TGGGTGCAGCCAGAGAGGTCCA 20629      G    GTAC   TG
           G                      CTGGA CCTCT    CTG  CCCA
                                  ||||| |||||    |||  ||||
                                  GACCT GGAGA    GAC  GGGT
                                    _    GACC   GT
GAM384  PDE2A     3'  TGGGGGATACAGGGGCCCCAG  12007      A       _  TGTG
                                 CTGG GCCTCTGTA CC    CCCA
                                 |||| ||||||||| ||    ||||
                                 GACC CGGGGACAT GG    GGGT
                                   C       A  _____
GAM384  PGRMC2    3'  TGGGTGCATGGGGCTGTGG    21980     G     _
                                 CTG AGCCTC TGTACCTG
                                 ||| |||||| ||||||||
                                 GGT TCGGGG ACGTGGGT
                                   G     T
GAM384  PI4KII    3'  TGGGTCTCTGCAAGGGCTCTGG 37957    TG    TC    CCTGT
                                 C  GAGCC  TGTA    GCCCA
                                 |  |||||  ||||    |||||
                                 G  CTCGG  ACGT    TGGGT
                                  GT    GA   CTC__
GAM384  PRIC285   5'  TGGGCACACAGTAGGTGCTTTA 62122        C    TACC
           G                      CTGGAGC TCTG    TGTGCCCA
                                  ||||||| ||||    ||||||||
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                                GATTTCG GGAT    ACACGGGT
                                    T   GAC_
GAM384  PRO1048  3'  TGGGCAATAATGGGGGCTTT  38122          ACCTG
                                GGAGCCTCTGT    TGCCCA
                                ||||||||||    ||||||
                                TTTCGGGGGTA    ACGGGT
                                      ATA__
GAM384  PRO1048  3'  TGGGCATGGTGGCAGGCGCCAG 38123     A   CTG   T
                                CTGG GCCT   TACC GTGCCCA
                                |||| ||||   |||| |||||||
                                GACC CGGA   GTGG TACGGGT
                                  G   CG_   _
GAM384  RAB24    3'  CAGGTATGAGGCTTTAG    56257          T
                                CTGGAGCCTC GTACCTG
                                |||||||||| |||||||
                                GATTTCGGAG TATGGAC

                                      _
GAM384  SCAMP5   3'  GGCTGGTAGAGGCTCTAG    58061          GT   TGT
                                CTGGAGCCTCT  ACC   GCC
                                ||||||||||  |||   |||
                                GATCTCGGAGA  TGG   CGG
                                      __   T__
GAM384  SEMA4G   5'  TGGGCGTGGACGGGCTGCTGG  96335    TG _    CT  AC TG
                                C  G AGCCT  GT  C  TGCCCA
                                |  | |||||  ||  |  ||||||
                                G  C TCGGG  CA  G  GCGGGT
                                 GT G    __  __ GT
GAM384  SEPT3    3'  TGGGCATGGGAGGTGGGCGTTG 39407    TG A   _ GTA
           G                     C  G GCCT CT   CCTGTGCCCA
                                |  | |||| ||   ||||||||||
                                G  T CGGG GG   GGGTACGGGT
                                 GT G   T  A__
GAM384  SLC25A18 3'  TGGGCACAGCTACCAGGGGCTT 49752          _ C
           T                     GGAGCCTCTG TA CTGTGCCCA
                                |||||||||| || |||||||||
                                TTTCGGGGAC AT GACACGGGT
                                      C  C
GAM384  SPINLW1  3'  TGGGTGCAGGTAGTTTGTTTGA 40233    G   CTCTG    TG
           G                     CT GAGC    TACCTG  CCCA
                                || ||||    ||||||  ||||
                                GA TTTG    ATGGAC  GGGT
                                 G   TTTG_    GT
GAM384  SPRY4    3'  AGCAAGGTCAGAGGTTTTAG  48992          T   G   CCA
                                CTGGAGCCTCTG ACCT TGC
                                |||||||||||| |||| |||
                                GATTTTGGAGAC TGGA ACG
                                      _   _  AC
GAM384  TOLLIP   3'  TGGGTGCATGTGGGTTTTCGG  39201       _  CTGT  C  TG
                                CTGGAG CCT    AC TG  CCCA
                                |||||| |||   || ||  ||||
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                                GGCTTT GGG   TG AC  GGGT
                                   T  ____  T  GT
GAM384  U5-100K  3'  TGGGATATGGGGGCTTAG   60416    G       _
                                CTG AGCCTCTGTA CCTG
                                ||| |||||||||| ||||
                                GAT TCGGGGGTAT GGGT
                                  _       A
GAM384  USP20    3'  TGGGTGGGGAAGGGGCTCTGG  22903   TG      GTA   GT
                                C  GAGCCTCT   CCT  GCCCA
                                |  ||||||||   |||  |||||
                                G  CTCGGGGA   GGG  TGGGT
                                 GT       AG_  __
GAM384  VI       3'  GGGTTGTGGAGGTTGTGG    26487    G    TG  CCTGT
                                CTG AGCCTC  TA    GCCC
                                ||| ||||||  ||    ||||
                                GGT TTGGAG  GT    TGGG
                                  G     GT  _____
GAM384  LOC118738 3'  TGGGTGCAGCAGCCAGCCTTTG 76007   TG   C  __   TAC   TG
            G                    C  GAG CT  CTG   CTG  CCCA
                                |  ||| ||  |||   |||  ||||
                                G  TTC GA  GAC   GAC  GGGT
                                 GT   C  CC   ___   GT
GAM384  LOC118987 5'  TGGGCGCGGGAGTAGGGGCCCG 74397      A      TA
            G                    CTGG GCCTCTG  CCTGTGCCCA
                                |||| |||||||  ||||||||||
                                GGCC CGGGGAT  GGGCGCGGGT
                                  _      GA
GAM384  LOC126374 3'  ATGGGTGTGGGTGTGGAGGGAG 74992    AG___    TG     TG
            GGCC                   GG    CCTC  TACCTG  CCCA   T
                                ||    ||||  ||||||  ||||   |
                                CC    GGAG  GTGGGT  GGGT   A
                                 GGGAG   GT     GT
GAM384  LOC128933 5'  TGGGCCTTGTGCAGGGGCTCC  76775           CTGT
                                GGAGCCTCTGTAC    GCCCA
                                ||||||||||||    |||||
                                CCTCGGGGACGTG    CGGGT
                                       TTC_
GAM384  LOC129566 3'  GGGTGCGGGCAGGCTTGGG   76226    G    CTGTA   TG
                                CT GAGCCT    CCTG  CCC
                                || ||||||    ||||  |||
                                GG TTCGGA    GGGC  GGG
                                 G     C____    GT
GAM384  LOC138307 5'  GGGCGTGGGTGTCACCAG    75840     AGCCTC  _   TG
                                CTGG     TG TACC  TGCCC
                                ||||     || ||||  |||||
                                GACC     AC GTGG  GCGGG
                                  ______  T   GT
GAM384  LOC142972 3'  TGGGTGTGAGGGGGGTCCCAG  65723     AG   TGTA  _ TG
                                CTGG  CCTC   CCT G  CCCA
                                ||||  ||||   ||| |  ||||
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                                GACC  GGGG    GGA T  GGGT
                                  CT    ____    G GT
GAM384   LOC144519 3'  GGGCGTGGACCAGGCCCGG    77377      A    CT  AC TG
                                CTGG GCCT  GT  C  TGCCC
                                |||| ||||  ||  |  |||||
                                GGCC CGGA  CA  G  GCGGG
                                  _    C_  __ GT
GAM384   LOC145717 3'  TGGGCGTGGCAAGGTTCC     67378        C  TAC TG
                                GGAGCCT TG   C  TGCCCA
                                ||||||| ||   |  ||||||
                                CCTTGGA AC   G  GCGGGT
                                    _ ___ GT
GAM384   LOC145831 3'  TGGGCACAATCAGGGCTCTGG  77990    TG    T   TACC
                                C  GAGCC CTG    TGTGCCCA
                                |  ||||| |||    ||||||||
                                G  CTCGG GAC    ACACGGGT
                                 GT    _   TA__
GAM384   LOC145873 3'  TGGGTGTAGGAGGCAGGCCCCA 78015      A   _  GTA    TG
            G                    CTGG GCCT CT   CCTG  CCCA
                                |||| |||| ||   ||||  ||||
                                GACC CGGA GG   GGAT  GGGT
                                  C   C  A__    GT
GAM384   LOC146723 5'  GGGGAAAGATGGGTATAGGGGC 78685              G___   A
            TTCA                   TGGAGCCTCTGTACCTGT    CCC
                                |||||||||||||||||    |||
                                ACTTCGGGGATATGGGTA    GGG
                                       GAAA   GT
GAM384   LOC148132 3'  GGCTCAGGTGGAGGCTCCAG   85257          GT    T
                                CTGGAGCCTCT  ACCTG GCC
                                ||||||||||  ||||| |||
                                GACCTCGGAGG  TGGAC CGG
                                    __     T
GAM384   LOC149302 5'  TGGGTGTGGGTGAGGGCTTCGG 80045        T  G     TG
                                CTGGAGCC CT TACCTG  CCCA
                                |||||||| || ||||||  ||||
                                GGCTTCGG GA GTGGGT  GGGT
                                    _ _      GT
GAM384   LOC149465 3'  TTTCATAGGTATAGAGTTTTGG 80195    TG   C         CCCA
                                C  GAGC TCTGTACCTGTG
                                |  |||| ||||||||||||
                                G  TTTG AGATATGGATAC
                                 GT   _          TTTG
GAM384   LOC149506 5'  GGTGAGTGCGAAGGCTCTGG   85642    TG     C    CTG
                                C  GAGCCT TGTAC   TGCC
                                |  |||||| |||||   ||||
                                G  CTCGGA GCGTG   GTGG
                                 GT     A    A__
GAM384   LOC150378 5'  TGGGCCCACGGTGGAGGCCTCA 80561     GA     GT   _  T
            G                    CTG  GCCTCT  ACC TG GCCCA
                                |||  ||||||  ||| || |||||
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                                GAC  CGGAGG  TGG AC CGGGT
                                  TC     __   C  C
GAM384   LOC150418 5'  TGGGTGTGGTACCGAGGCTTCA 66117          T     T TG
                 G                 CTGGAGCCTC GTACC G  CCCA
                                   |||||||||| ||||| |  ||||
                                   GACTTCGGAG CATGG T  GGGT
                                         C    _ GT
GAM384   LOC150946 3'  TGGAATGCTGGTATGGGGGCCC 86350      A         T  GC_
                 CAG                 CTGG GCCTCTGTACC GT   CCA
                                   |||| |||||||||| ||   |||
                                   GACC CGGGGGTATGG CG   GGT
                                     C         T  TAA
GAM384   LOC151516 5'  TGGGTTGCTGCTGAGGTTCCAG 81071          T   CCTGT
                                   CTGGAGCCTC GTA     GCCCA
                                   |||||||||| |||     |||||
                                   GACCTTGGAG CGT     TGGGT
                                         T   CGT__
GAM384   LOC152762 3'  TGGGTAGAGAACAGAGGTCCAG 81539       G      AC  G
                                   CTGGA CCTCTGT  CT TGCCCA
                                   ||||| |||||||  || ||||||
                                   GACCT GGAGACA  GA ATGGGT
                                      _      A_  G
GAM384   LOC153811 3'  GGGCTGGCAGGGGCTCTGG    81840    TG        ACCTGT
                                   C  GAGCCTCTGT     GCCC
                                   |  ||||||||||     ||||
                                   G  CTCGGGGACG     CGGG
                                    GT         GT_____
GAM384   LOC154386 3'  TGTTTACTGGGTACAGAGTTTC 81991        C        _   CC
                 AG                  CTGGAGC TCTGTACCT GTG  CA
                                   |||||||  ||||||||| |||  ||
                                   GACTTTG AGACATGGG CAT  GT
                                      _        T   TT
GAM384   LOC155032 3'  TGGGGATGATGCAGGGGTTTTG 87600    TG         CC   G
                 G                  C  GAGCCTCTGTA  TGT CCCA
                                   |  ||||||||||  ||| ||||
                                   G  TTTGGGGACGT  GTA GGGT
                                    GT         A_   G
GAM384   LOC157773 5'  TGGATTGGATGTAGAGGCTTCA 82509             _  TGTG  CA
                 G                  CTGGAGCCTCTGTA CC    CC
                                   ||||||||||||| ||    ||
                                   GACTTCGGAGATGT GG    GG
                                         A  TTA_  T
GAM384   LOC197119 3'  TGGGTGGACGTGGAGGCTTCAG 91276          TG A_  TGT
                                   CTGGAGCCTC  T  CC   GCCCA
                                   ||||||||||  |  ||   |||||
                                   GACTTCGGAG  G  GG   TGGGT
                                         GT CA  ___
GAM384   LOC197414 3'  TGGGCAGCTCTGTGGGGGCTCT 89459         TG  CCTG
                                   GGAGCCTC  TA    TGCCCA
                                   ||||||||  ||    ||||||
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                                TCTCGGGG GT   ACGGGT
                                     GT CTCG
GAM384  LOC199953 3' TGGGCAGCGCCCACACAGGCTC 89886   TG    C  ACC _
           TGG                    C GAGCCT TGT  TG TGCCCA
                                | |||||| |||  || ||||||
                                G CTCGGA ACA  GC ACGGGT
                                 GT    C  CCC G
GAM384  LOC203069 3' GGGTGTGGTGGGCTTTAG    90762        _ TG
                                CTGGAGCCT C TACCT
                                ||||||||| |  |||||
                                GATTTCGGG G GTGGG
                                      T GT
GAM384  LOC203078 3' GCATGGGGGCGGGGGCTCTGG 90790   TG      TA
                                C GAGCCTCTG CCTGTGC
                                | |||||||||  |||||||
                                G CTCGGGGGC GGGTACG
                                 GT       GG
GAM384  LOC203080 5' TGGGTGTAGGGACTGGCCC   90775    A  TCT A   TG
                                GG GCC  GT CCTG CCCA
                                || |||  || ||||  ||||
                                CC CGG  CA GGAT GGGT
                                 _  T__ G   GT
GAM384  LOC204285 5' GCAGGTGCAGAGCTCTGG    91020   TG   C
                                C GAGC TCTGTACCTGT
                                | |||| ||||||||||
                                G CTCG AGACGTGGACG
                                 GT  _
GAM384  LOC219653 3' GGGTTCACAGCGGCTTTAG   92919       T   ACCTGT
                                CTGGAGCC CTGT     GCCC
                                |||||||| ||||     ||||
                                GATTTCGG GACA     TGGG
                                     C   CT____
GAM384  LOC219722 5' TGGGCATGGTGGCTCAGAGGTT 94690    G       ___   T
           TGGG                   CT GAGCCTCTG  TACC GTGCCCA
                                || |||||||||  |||| |||||||
                                GG TTTGGAGAC  GTGG TACGGGT
                                 G       TCG  _
GAM384  LOC219920 5' GGGTGCCCACAGGCTCCGG   94958        C TACCT TG
                                CTGGAGCCT TG    G CCC
                                ||||||||| ||    | |||
                                GGCCTCGGA AC    C GGG
                                     C C____ GT
GAM384  LOC220537 3' TGGGCGTGGCAAGGTTCC    92427       C TAC TG
                                GGAGCCT TG  C TGCCCA
                                ||||||| ||  | ||||||
                                CCTTGGA AC  G GCGGGT
                                    _ ___ GT
GAM384  LOC221463 3' GGGCTGGTGGGGGTGCTGG   93709   TG A    GT  TGT
                                C G GCCTCT ACC  GCCC
                                | | ||||||  |||  ||||
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                                G  C TGGGGG  TGG   CGGG
                                 GT G     __   T__
GAM384   LOC253219 3'  TGGGCGCGGAATCCGGGCTGCC 99349      _    CT  A  T
            GG                    CTGG AGCCT  GT CC GTGCCCA
                                  |||| |||||  || || |||||||
                                  GGCC TCGGG  TA GG CGCGGGT
                                    G    CC  A  _
GAM384   LOC253219 5'  TGGGCGCGGAATCCGGGCTGCC 99350      _    CT  A  T
            GG                    CTGG AGCCT  GT CC GTGCCCA
                                  |||| |||||  || || |||||||
                                  GGCC TCGGG  TA GG CGCGGGT
                                    G    CC  A  _
GAM384   LOC253451 5'  GGCGAGCAGGGGCTTCGG    97723           ACCTG
                                  CTGGAGCCTCTGT    TGCC
                                  ||||||||||||    ||||
                                  GGCTTCGGGGACG    GCGG
                                         A____
GAM384   LOC254719 3'  TGGGCACAGTGCTGGTTCTGG  97766   TG    TCT   C
                                  C  GAGCC   GTAC TGTGCCCA
                                  |  |||||   |||| ||||||||
                                  G  CTTGG   CGTG ACACGGGT
                                   GT    T__   _
GAM384   LOC254808 3'  TGGGTGTGGGCCGTGAGGTTTA 98812     G     TGTA    TG
            G                      CTG AGCCTC    CCTG  CCCA
                                  ||| ||||||    ||||  ||||
                                  GAT TTGGAG    GGGT  GGGT
                                    _     TGCC    GT
GAM384   LOC255031 3'  GGGAGGCAGAGGTTTCAG    99040           ACCTGTG
                                  CTGGAGCCTCTGT      CCC
                                  ||||||||||||       |||
                                  GACTTTGGAGACG      GGG
                                         GA_____
GAM384   LOC256451 3'  TGGGCGCCCTGAGGAGGCTCC  97805         GTACCT
                                  GGAGCCTCT     GTGCCCA
                                  |||||||||     |||||||
                                  CCTCGGAGG     CGCGGGT
                                       AGTCC_
GAM384   LOC257476 3'  TGGGTGCAGGTGCCCACATTCT 61925      CCTCT      TG
                                  GGAG    GTACCTG  CCCA
                                  ||||    |||||||  ||||
                                  TCTT    CGTGGAC  GGGT
                                    ACACC      GT
GAM384   LOC51157  5'  GGGTTAGTGGGGCTCTGG    33015    TG      TGTAC   T
                                  C  GAGCCTC    CTG GCCC
                                  |  |||||||    ||| ||||
                                  G  CTCGGGG    GAT TGGG
                                   GT      T_____   _
GAM384   LOC90346  3'  TGGGTATGGTGCTGGGCTGTTG 57201    TG _    CT    T
            G                      C  G AGCCT  GTACC GTGCCCA
                                  |  | |||||  ||||| |||||||
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                                G  T TCGGG  CGTGG TATGGGT
                                 GT G    T_    _
GAM384  LOC90637  5'  TGGGTGTGGGTGTGCCTCCG  64404      CCTCTG     TG
                                TGGAG     TACCTG  CCCA
                                |||||     ||||||  ||||
                                GCCTC     GTGGGT  GGGT
                                   CGT___     GT
GAM384  LOC90750  3'  TGGGCTTCGCATAGGCTTTAG  64635         C   ACCTGT
                                CTGGAGCCT TGT     GCCCA
                                |||||||||  |||     |||||
                                GATTTCGGA ACG     CGGGT
                                     T   CTT___
GAM384  LOC90982  5'  TGGGCATAGCCAAGGGGGTTCC 65148          GTAC
           AG                     CTGGAGCCTCT    CTGTGCCCA
                                ||||||||||    |||||||||
                                GACCTTGGGGG    GATACGGGT
                                      AACC
GAM384  LOC92305  3'  TGGGTAGGGGTGGGGGTTTGAG 57239    G      GT    G
                                CT GAGCCTCT  ACCT TGCCCA
                                || ||||||||  |||| ||||||
                                GA TTTGGGGG  TGGG ATGGGT
                                 G       __    G
GAM384  LOC93070  3'  TGGGATGTGGAGGTTGCAG   71817     G     TG  _
                                CTG AGCCTC  TA CCTG
                                ||| ||||||  || ||||
                                GAC TTGGAG  GT GGGT
                                  G     GT  A
GAM385  FMN2      3'  CCGTTTATAATCAGTGCTTTC  80130      A       A   TA
                                GAAA CACTGATTG TAA  GG
                                |||| |||||||| |||  ||
                                CTTT GTGACTAAT ATT  CC
                                  C       _   TG
GAM385  HSF2BP    3'  ATTAGTCAGCATTTTCTT    23842       CA
                                GAGAAAA  CTGATTGAT
                                |||||||  |||||||||
                                TTCTTTT  GACTGATTA
                                    AC
GAM385  ITPR1     3'  CTGGCCAATCAGTGTCATCTC  11072      AA        ATAA
                                GAGA  ACACTGATTG    TAG
                                ||||  ||||||||||    |||
                                CTCT  TGTGACTAAC    GTC
                                  AC        CG__
GAM385  ZFP103    5'  CTATTATTGGTTTTTTC     20224      CACT   TG
                                GAAAA    GAT  ATAATAG
                                |||||    |||  |||||||
                                CTTTT    TTG  TATTATC
                                   _____  GT
GAM385  FLJ14117  3'  CCTATTATCAAATTTGGGTTTC 43222    A    A TG __
           CT                     AG AAAC C  A  TTGATAATAGG
                                || |||| |  |  ||||||||||
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                                TC TTTG G  T  AACTATTATCC
                                 C   _ GT TA
GAM385  FLJ32332  3'  CCTATTATTAAATGTTTTCT  58943       CTGA
                                AGAAAACA   TTGATAATAGG
                                ||||||||   ||||||||||
                                TCTTTTGT   AATTATTATCC
                                    A___
GAM385  GIT2    3'  CCCATTGTCAGGTGCTCTC   29408     AAA   GAT     A
                                GAGA   CACT   TGATAAT GG
                                ||||   ||||   ||||||| ||
                                CTCT   GTGG   ACTGTTA CC
                                  C__   ___     C
GAM385  GIT2    3'  CCCATTGTCAGGTGCTCTC   55148     AAA   GAT     A
                                GAGA   CACT   TGATAAT GG
                                ||||   ||||   ||||||| ||
                                CTCT   GTGG   ACTGTTA CC
                                  C__   ___     C
GAM385  GIT2    3'  CCCATTGTCAGGTGCTCTC   55151     AAA   GAT     A
                                GAGA   CACT   TGATAAT GG
                                ||||   ||||   ||||||| ||
                                CTCT   GTGG   ACTGTTA CC
                                  C__   ___     C
GAM385  KIAA1336  3'  ATCAACCATGTTTTCTC     72783        C  A
                                GAGAAAACA TG TTGAT
                                ||||||||| || |||||
                                CTCTTTTGT AC AACTA
                                    _ C
GAM385  LAMB4    5'  CCTCAAGCAATCAGTATTTT   82081     C      ATAAT
                                AAAA ACTGATTG    AGG
                                |||| ||||||||    |||
                                TTTT TGACTAAC    TCC
                                  A      GAAC_
GAM385  MGC3146   3'  CCTACCACATCACCATCAGTGT 49263         __   AA__
          TT                    AAACACTGAT  TGAT   TAGG
                                ||||||||||  ||||   ||||
                                TTTGTGACTA  ACTA   ATCC
                                     CC   CACC
GAM385  LOC152762 3'  CCTACCGCTCAGTCGTTTTCTC 81531        _    T  ATAA
                                GAGAAAAC ACTGA TG   TAGG
                                |||||||| ||||| ||   ||||
                                CTCTTTTG TGACT GC   ATCC
                                    C    C  C___
GAM386  ABP1     5'  GCAGAGCGAACTGGGAGCAGAG 63799         CCGC    C
                                CTCTGTTCTT   CGCTC GC
                                ||||||||||   ||||| ||
                                GAGACGAGGG   GCGAG CG
                                     TCAA    A
GAM386  AHCY     3'  GGCAACTGAGAAAGAACAGAG  7304          _ _ ____
                                CTCTGTTCTT C C   GCC
                                |||||||||| | |   |||
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                                GAGACAAGAA G G   CGG
                                    A A TCAA
GAM386  BSN     3'  GGCAGAGGCAAGAGCAGAG   14387        CC  G _
                                CTCTGTTCTT  GCC CT CC
                                ||||||||||  ||| || ||
                                GAGACGAGAA  CGG GA GG
                                    __  A  C
GAM386  CSE1L   5'  GCGGAGCGGCGGCAGGAGC   62513      _
                                GTTCTT CCGCCGCTCCGC
                                |||||| ||||||||||||
                                CGAGGA GGCGGCGAGGCG
                                   C
GAM386  EHD4    3'  AGTGGCAAAAAAAATAGAG    58362       C  CC
                                CTCTGTT TT  GCCGCT
                                |||||||  ||  ||||||
                                GAGATAA AA  CGGTGA
                                    A  AA
GAM386  EIF2C1  3'  AGCCCAGCTGAAGAACAGA   25181        C  C__
                                TCTGTTCTTC GC   GCT
                                |||||||||| ||   |||
                                AGACAAGAAG CG   CGA
                                    T  ACC
GAM386  KCNK4   3'  GCGAGCAGCAGAGCAGG     33986       TCC  C    C
                                TCTGTTCT   GC GCTC GC
                                ||||||||   || |||| ||
                                GGACGAGA   CG CGAG CG
                                    ___  A    A
GAM386  MYO1D   3'  GCGGAACAGCCCATCCAGCAGA 72249       CTTCC_  CGC
          GT                    ACTCTGTT     GC   TCCGC
                                ||||||||     ||   |||||
                                TGAGACGA     CG   AGGCG
                                    CCTACC  ACA
GAM386  NUP62   3'  GGCAAAGCAGCACAGTGTGAAT 25650       TTCC___  C   CC
          AGA                   TCTGTTC      GC GCT  GCC
                                |||||||      || |||  |||
                                AGATAAG      CG CGA  CGG
                                    TGTGACA  A   AA
GAM386  RABIF   3'  GGCATGTGCAGAAAAACAGAGT 12728       C   C  C  TCC
                                ACTCTGTT TTC GC GC   GCC
                                |||||||| ||| || ||   |||
                                TGAGACAA AAG CG TG   CGG
                                    A   A  _  TA_
GAM386  RAX     3'  GCAGGGGAGGCGGAAAAATAGA 26466       C      G   _
          GT                    ACTCTGTT TTCCGCC CTCC GC
                                |||||||| ||||||| |||| ||
                                TGAGATAA AAGGCGG GGGG CG
                                    A      A   A
GAM386  RBM10   3'  GGCAGGGAAGGACAGAGT    20247          __
                                ACTCTGTTCTTCC  GCC
                                ||||||||||||  |||
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                                TGAGACAGGAAGG  CGG
                                       GA
GAM386  RGS16    3'  GGCAGGGCCCAGGAGAACAAAG 12869     C     T  GCC    C
             T                  ACT TGTTCT CC   GCTC GCC
                                ||| |||||| ||   |||| |||
                                TGA ACAAGA GG   CGGG CGG
                                  A     _ ACC    A
GAM386  ROM1     3'  GGAACAGCAAAGAACAGAGT   6165          CC  CGC
                                ACTCTGTTCTT  GC   TCC
                                ||||||||||  ||   |||
                                TGAGACAAGAA  CG   AGG
                                       A_  ACA
GAM386  SLC21A2  3'  GCAAAGCAAGTGATGAAGCAGA 20084        _ TTC   C_   CC
             GT                   ACTCTGTT C   CGC  GCT  GC
                                ||||||||  |   |||  |||  ||
                                TGAGACGA G   GTG  CGA  CG
                                     A TA_   AA   AA
GAM386  SMARCA5  5'  AGCCCCGCGGAAGAGCAGA    14588           C__
                                TCTGTTCTTCCGC   GCT
                                ||||||||||||   |||
                                AGACGAGAAGGCG   CGA
                                       CCC
GAM386  SYNGR1   3'  GGCAGAGCGGCAAGGACAGGG  17507          CC      C
                                CTCTGTTCTT  GCCGCTC GCC
                                ||||||||||  ||||||| |||
                                GGGACAGGAA  CGGCGAG CGG
                                      __       A
GAM386  TRAM     5'  AGCAGCTGGGAAGAGCAGA   27451           __ C
                                TCTGTTCTTCC  GC GCT
                                ||||||||||  || |||
                                AGACGAGAAGG  CG CGA
                                       GT  A
GAM386  VAT1     3'  AGCAGGGAAGTACAGAGT    22088        T    GCC
                                ACTCTGT CTTCC   GCT
                                ||||||| |||||   |||
                                TGAGACA GAAGG   CGA
                                     T    GA_
GAM386  CBX1     3'  AGCAATGGAAAAGAACAGA   23308         __   CC
                                TCTGTTCT  TCCG  GCT
                                ||||||||  ||||  |||
                                AGACAAGA  AGGT  CGA
                                      AA    AA
GAM386  CDC14A   5'  GGCGGAGCAGCAGCTGCAGCAG 53966    _   TCTTCC  C
                                CT CTGT     GC GCTCCGCC
                                || ||||     || ||||||||
                                GA GACG     CG CGAGGCGG
                                 C   TCGA__  A
GAM386  CDC14A   5'  GGCGGAGCAGCAGCTGCAGCAG 53967    _   TCTTCC  C
                                CT CTGT     GC GCTCCGCC
                                || ||||     || ||||||||
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                                GA GACG     CG CGAGGCGG
                                 C   TCGA__  A
GAM386  DKFZp547I224 5'  GATGGGGAAAAAACAGAG    39956       C_   G  C
                                CTCTGTT  TTCC CCG TC
                                |||||||  |||| ||| ||
                                GAGACAA  AAGG GGT AG
                                   AA   _  _
GAM386  ECE2     3'  GCAGGGAAAAGGAAGAACAGAG 28732          GCCG  C
          T                      ACTCTGTTCTTCC   CTC GC
                                 ||||||||||||    ||| ||
                                 TGAGACAAGAAGG   GGG CG
                                       AAAA  A
GAM386  FLJ10648  3'  CGAAGCAAACCAAGAACAGAG  36890        CCGCC  C
                                CTCTGTTCTT    GCT CG
                                ||||||||||    ||| ||
                                GAGACAAGAA    CGA GC
                                      CCAAA  A
GAM386  GRIN3A   3'  GCGGAGCAAGTGCCAAGCAGA  56783      CTTC  C_
                                TCTGTT   CGC  GCTCCGC
                                ||||||   |||  |||||||
                                AGACGA   GTG  CGAGGCG
                                   ACC_  AA
GAM386  INE1     3'  GCAGGTGTTAGACGAAAGAACA 14757        C  CC__  T  _
          GA                     TCTGTTCTT CG   GC CC GC
                                 |||||||| ||   || || ||
                                 AGACAAGAA GC   TG GG CG
                                      A  AGAT  T  A
GAM386  KIAA0410  3'  GCAGAGCTTAAGAATAGA    29426        CCGCC   C
                                TCTGTTCTT    GCTC GC
                                |||||||||    |||| ||
                                AGATAAGAA    CGAG CG
                                      TT___   A
GAM386  KIAA0964  5'  GCGGAACGGCAGAGCGGG    30448        TCC   C
                                TCTGTTCT   GCCG TCCGC
                                ||||||||   |||| |||||
                                GGGCGAGA   CGGC AGGCG
                                   ___   A
GAM386  KIAA1218  5'  AGCAGCACAAAAGAAACAGAGT 95958        _  CC__  C
                                ACTCTGTT CTT   GC GCT
                                |||||||| |||   || |||
                                TGAGACAA GAA   CG CGA
                                   A   AACA  A
GAM386  KIAA1322  3'  GGCAGCCGAGAAGAACAGA   73112         _ CC  _
                                TCTGTTCTTC CG  GCT CC
                                |||||||||| ||  ||| ||
                                AGACAAGAAG GC  CGA GG
                                      A  __  C
GAM386  KIAA1391  3'  AGTGGAGAAAAACAGAGT    67851        C  CG
                                ACTCTGTT TTC  CCGCT
                                |||||||| |||  |||||
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                                TGAGACAA AAG  GGTGA
                                    A   A_
GAM386  MGC13251  3'  AGCAGCCATAGAAAGGACAGA  52134        _ C___  C
                                TCTGTTCTT C    GC GCT
                                ||||||||| |    || |||
                                AGACAGGAA G    CG CGA
                                     A ATAC  A
GAM386  MYH7B     3'  GGCGGAGCAGCAGGCCAACA   71058     CTT  _  C
                                TGTT   CC GC GCTCCGCC
                                ||||   || || ||||||||
                                ACAA   GG CG CGAGGCGG
                                  CC_  A  A
GAM386  NCOA2     3'  GGCAAGGAGAAGAGCAAAGT   22572     C      CG  GCT
                                ACT TGTTCTTC  CC   CC
                                ||| ||||||||  ||   ||
                                TGA ACGAGAAG  GG   GG
                                  A       A_  AAC
GAM386  PTRF      3'  GGCAGTGGGGAAGACAGAG    64242      T    G    _
                                CTCTGT CTTCC CCGCT CC
                                |||||| ||||| ||||| ||
                                GAGACA GAAGG GGTGA GG
                                   _    _    C
GAM386  RHOBTB2   3'  AGCAGGAGGAAAAGCAGAGT   61593       C   G  _
                                ACTCTGTT TTCC CC GCT
                                |||||||| |||| || |||
                                TGAGACGA AAGG GG CGA
                                     A   A  A
GAM386  TAGAP     3'  AGACTGCAAGGAACAGAGT    55099         CC  CG_
                                ACTCTGTTCTT  GC   CT
                                ||||||||||  ||   ||
                                TGAGACAAGGA  CG   GA
                                      A_  TCA
GAM386  VELI1     3'  AGTGTAAGAAGAATAAAGT    17417     C      CGC
                                ACT TGTTCTTC   CGCT
                                ||| ||||||||   ||||
                                TGA ATAAGAAG   GTGA
                                  A       AAT
GAM386  LOC145783 5'  GCGGAGCGACGGAGACACAG   77949     TC    C
                                CTGT  TTCCG CGCTCCGC
                                ||||  ||||| ||||||||
                                GACA  GAGGC GCGAGGCG
                                  CA    A
GAM386  LOC150157 3'  AGCAAATGGAAAAGAACAGA   86020        __   CC_
                                TCTGTTCT  TCCG   GCT
                                ||||||||  ||||   |||
                                AGACAAGA  AGGT   CGA
                                     AA    AAA
GAM386  LOC151516 5'  GGCGGAGCTTCCAGAACAAAG  81068    C     TCCGCC
                                CT TGTTCT     GCTCCGCC
                                || ||||||     ||||||||
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                                GA ACAAGA     CGAGGCGG
                                 A     CCTT__
GAM386  LOC153769 3'  GGCGGAGCAGCATGAGAAAGA  81807     G    CC  C
                                TCT TTCTT  GC GCTCCGCC
                                ||| |||||  || ||||||||
                                AGA AAGAG  CG CGAGGCGG
                                  _    TA  A
GAM386  LOC161734 3'  GATGGGGAAAAAACAGAG    88467       C_   G   C
                                CTCTGTT  TTCC CCG TC
                                |||||||  |||| ||| ||
                                GAGACAA  AAGG GGT AG
                                    AA   _  _
GAM386  LOC167026 5'  GGCGGAGCGGCGGGCGGA    88620      TCTT
                                TCTGT   CCGCCGCTCCGCC
                                |||||   ||||||||||||
                                AGGCG   GGCGGCGAGGCGG
                                  _____
GAM386  LOC196890 3'  AGCAAATGGAAAAGAACAGA   91222        __   CC_
                                TCTGTTCT  TCCG   GCT
                                ||||||||  ||||   |||
                                AGACAAGA  AGGT   CGA
                                    AA    AAA
GAM386  LOC200731 5'  AGCACTGAAGAACAGAGT    91688          CGCC
                                ACTCTGTTCTTC    GCT
                                ||||||||||||   |||
                                TGAGACAAGAAG    CGA
                                      TCA_
GAM386  LOC221504 5'  CGGAGCGGCGGGGCAGGAG   94020     GTTC
                                CTCT   TTCCGCCGCTCCG
                                ||||   |||||||||||||
                                GAGG   GGGGCGGCGAGGC
                                  AC__
GAM386  LOC221663 5'  GCAAGCCCAGAACAGAGT    95463         TCCGCC   CC
                                ACTCTGTTCT     GCT  GC
                                ||||||||||     |||  ||
                                TGAGACAAGA     CGA  CG
                                     CC_____   AA
GAM386  LOC256310 3'  GGCAGAGCAGCGGGAGCAGGAG 98102     GTT     C   C
                                CTCT   CTTCCGC GCTC GCC
                                ||||   ||||||| |||| |||
                                GAGG   GAGGGCG CGAG CGG
                                  AC_      A   A
GAM386  LOC51762  3'  GGCCTAGCAAAAGAACAGA   33708        CCGCC   CC
                                TCTGTTCTT    GCT  GCC
                                |||||||||    |||  |||
                                AGACAAGAA    CGA  CGG
                                     AA___   TC
GAM386  LOC91266  5'  GGCTGAGGAAAAACAGAGT   66024        ___    C
                                ACTCTGT   TCTTC GCC
                                |||||||   ||||| |||
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                                TGAGACA   AGGAG CGG
                                   AAA    T
GAM387  C14orf1   3'  ACTTCTCCATGCCGGACACT   24160          ___
                                AGTGTCCGGCAT   GAAGT
                                ||||||||||||  |||||
                                TCACAGGCCGTA   CTTCA
                                      CCT
GAM387  IMPA1     3'  ATGTACTTTAGGAAAC     19852    G   GGCA
                                GT TCC    TGAAGTACAT
                                || |||    ||||||||||
                                CA AGG    ATTTCATGTA
                                 A  ____
GAM387  KIAA0426  3'  TACTTCATGTATAGCCTA    28933     T  CCG
                                TAG GT   GCATGAAGTA
                                ||| ||   ||||||||||
                                ATC CG   TGTACTTCAT
                                  _ ATA
GAM387  OSBPL1A   3'  ATGTACTTATTTGGAATACTA  36365      _   CATG
                                TAGTGT CCGG    AAGTACAT
                                |||||| ||||    ||||||||
                                ATCATA GGTT    TTCATGTA
                                   A   TA__
GAM387  OSBPL1A   3'  ATGTACTTATTTGGAATACTA  55489      _   CATG
                                TAGTGT CCGG    AAGTACAT
                                |||||| ||||    ||||||||
                                ATCATA GGTT    TTCATGTA
                                   A   TA__
GAM387  OSBPL1A   3'  ATGTACTTATTTGGAATACTA  56555      _   CATG
                                TAGTGT CCGG    AAGTACAT
                                |||||| ||||    ||||||||
                                ATCATA GGTT    TTCATGTA
                                   A   TA__
GAM387  SLC2A10   3'  GCATTCATGCCGAACCTA    48553     T  C      _
                                TAG GT CGGCATGAA GT
                                ||| || ||||||||| ||
                                ATC CA GCCGTACTT CG
                                  _ A       A
GAM387  ZF        3'  GACATCTTCACCGGACAC    41367       CA    TACA
                                GTGTCCGG  TGAAG   TC
                                ||||||||  |||||   ||
                                CACAGGCC  ACTTC   AG
                                     __    TAC_
GAM387  LOC122553 3'  ATGTACTTTAGGACATTA    74590       GGCA
                                TAGTGTCC   TGAAGTACAT
                                ||||||||   ||||||||||
                                ATTACAGG   ATTTCATGTA
                                     _____
GAM387  LOC149372 3'  GGATGTATTGATCAGACAC   80102      C  CATGA
                                GTGTC GG    AGTACATCC
                                ||||| ||    |||||||||
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                                CACAG CT    TTATGTAGG
                                  A  AG___
GAM387  LOC88523  3'  GACGTACCCGTTGGATAC    53574        ATGAA   A
                                GTGTCCGGC    GTAC TC
                                |||||||||    |||| ||
                                CATAGGTTG    CATG AG
                                     CC___   C
GAM388  DLX4    5'  GGCGCGCGTTCTCCGCTG    57113    A       A
                                CA CGGGGAACGC CGCT
                                || ||||||||||| ||||
                                GT GCCTCTTGCG GCGG
                                 C        C
GAM388  EP300    3'  ACCACCAGCCTTTCTTCCCCTT 9281     C    CGCAC   A
          TG                     CAA GGGGAA    GCTG TGGT
                                ||| ||||||    |||| |||||
                                GTT CCCCTT    CGAC ACCA
                                  T    CTTTC   C
GAM388  LOX     5'  TCCGCGCCGCTCCCCGTTG    11348        A  CA   T
                                CAACGGGGA CG  CGC GA
                                ||||||||| ||  ||| ||
                                GTTGCCCCT GC  GCG CT
                                     C  C_   C
GAM388  PLS1    3'  ACCATCAGTATTTTCCCC    12178       CGCAC
                                GGGGAA    GCTGATGGT
                                ||||||    |||||||||
                                CCCCTT    TGACTACCA
                                   TTA__
GAM388  DRG1    3'  ACCACAACAGCGTTCCCC    15971        ACGC  A
                                GGGGAACGC    TG TGGT
                                |||||||||    || ||||
                                CCCCTTGCG    AC ACCA
                                     ACA_  _
GAM388  FLJ14146  3'  ACCATCAGCGCACTCCCG    45564      AACGCA
                                CGGGG     CGCTGATGGT
                                |||||     ||||||||||
                                GCCCT     GCGACTACCA
                                   CAC___
GAM388  PCAF    5'  ACCATCAGCGCGCGGGGCCCG  15282     GAA   A
                                CGGG   CGC CGCTGATGGT
                                ||||   ||| ||||||||||
                                GCCC   GCG GCGACTACCA
                                  GGG   C
GAM388  LOC149935 5'  ACCATCAGCACATGCCCATCG  60931     _  AAC   C__
                                CGG GG   GCA   GCTGATGGT
                                ||| ||   |||   |||||||||
                                GCT CC   CGT   CGACTACCA
                                  A  ___   ACA
GAM388  LOC221250 5'  ACCATCAGCACCACCTCCACCG 93476     _   ACGCAC
                                CGG GGA     GCTGATGGT
                                ||| |||     |||||||||
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                                GCC CCT     CGACTACCA
                                  A   CCACCA
GAM389  AMPD3    3'  GTGAATCTCCTCATGAATACTT 6656       CCTC
                                AAGTG   CGTGAGGAGATTCAC
                                |||||   ||||||||||||||||
                                TTCAT   GTACTCCTCTAAGTG
                                  AA__
GAM389  ENPP1    3'  TGAATCTTTTTGAGAGAAC   21698    GC   CG
                                GT  CTC  TGAGGAGATTCA
                                ||  |||  ||||||||||||
                                CA  GAG  GTTTTTCTAAGT
                                 A_   A_
GAM389  LZTS1    3'  ATCTCTTCCCCAGAGAGGCACT 41025        CGT___
                                AGTGCCTC     GAGGAGAT
                                ||||||||     ||||||||
                                TCACGGAG     CTTCTCTA
                                     AGACCC
GAM389  RBM8A    3'  TGAATCTCCTCTTGGAGCATT  18815      C    T
                                AGTGC TCCG GAGGAGATTCA
                                ||||| |||| ||||||||||
                                TTACG AGGT CTCCTCTAAGT
                                   _    T
GAM389  TNFRSF6B 3'  GTGAGTGCCCACGGAGGC    33598         A  AG
                                GCCTCCGTG GG  ATTCAC
                                ||||||||| ||  ||||||
                                CGGAGGCAC CC  TGAGTG
                                      _ G_
GAM389  AD034    3'  TGAGTGTCCAGAGGCACT    49749        CGTGA   G
                                AGTGCCTC    GGA ATTCA
                                ||||||||    ||| |||||
                                TCACGGAG    CCT TGAGT
                                     A_____   G
GAM389  ATPW     5'  CTCCTCACGGAGGCTCTT    32259     T
                                AAG GCCTCCGTGAGGAG
                                ||| ||||||||||||||
                                TTC CGGAGGCACTCCTC
                                  T
GAM389  DKFZp761K1423 5'  GTGAAGAAACAAGGAGGCACTT 37939          G  AGGAGA
                                AAGTGCCTCC TG     TTCAC
                                |||||||||| ||     |||||
                                TTCACGGAGG AC     AAGTG
                                      A  AAAG__
GAM389  DRF1     5'  GAATGTAATACGGAGGCCT   47748    T       AGGAG
                                AG GCCTCCGTG    ATTC
                                || |||||||||    ||||
                                TC CGGAGGCAT    TAAG
                                 _       AATG_
GAM389  FLJ10901 3'  GAATCTCCTGCCTCAGCCTT   37361     T  CTCC  G
                                AAG GC    GT AGGAGATTC
                                ||| ||    || |||||||||
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                                TTC CG    CG TCCTCTAAG
                                  _ ACTC  _
GAM389  FLJ12895  3'  GTGAATCCCAGACGAGGCATT  43928        C  GA  A
                                AGTGCCTC GT  GG GATTCAC
                                ||||||| ||  || |||||||
                                TTACGGAG CA  CC CTAAGTG
                                    _ GA  _
GAM389  KIAA1656  5'  GTGAATCTCTGACAAGGC    66384     CC  GA
                                GCCT  GT  GGAGATTCAC
                                ||||  ||  ||||||||||
                                CGGA  CA  TCTCTAAGTG
                                  A_  G_
GAM389  LEP16     3'  TCTCCCCAGAAGGCACTT    51772        CCG  A
                                AAGTGCCT   TG GGAGA
                                ||||||||   || |||||
                                TTCACGGA   AC CCTCT
                                    AG_  C
GAM389  MCF2L     3'  CTCCCCATAAAGGCACTT    61528        CC   A
                                AAGTGCCT  GTG GGAG
                                ||||||||  ||| ||||
                                TTCACGGA  TAC CCTC
                                    AA   C
GAM389  MGC12966  5'  CTGCTCGCGGAGGCACTT    52087             G
                                AAGTGCCTCCGTGAG AG
                                |||||||||||||| ||
                                TTCACGGAGGCGCTC TC
                                       G
GAM389  MGC4655   3'  TGAACCTGGCAGGCACTT    53961        CC  G   AGA
                                AAGTGCCT  GT AGG   TTCA
                                ||||||||  || |||   ||||
                                TTCACGGA  CG TCC   AAGT
                                    __  G  ___
GAM389  NXPH3     3'  TGAATCTCCTAGCACT      66349      CTCCGTG
                                AGTGC      AGGAGATTCA
                                |||||      ||||||||||
                                TCACG      TCCTCTAAGT
                                  A_______
GAM389  NY-REN-25 3'  GTGAAGGATTTCCACGTAGACA 61265     C  C    AG  GA_
          C                      GTG CT CGTG  GA   TTCAC
                                ||| || ||||  ||   |||||
                                CAC GA GCAC  TT   AAGTG
                                  A  T    CT  AGG
GAM389  SUN1      3'  GTGAATCTCTCTCGAAAAGC   47920    CTCCG   _
                                GC    TGAG GAGATTCAC
                                ||    |||| |||||||||
                                CG    GCTC CTCTAAGTG
                                 AAAA_    T
GAM389  UBP1      3'  GTGAATCTCCTCACTGTCACT  27994      CCTCC
                                AGTG    GTGAGGAGATTCAC
                                ||||    ||||||||||||||
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                                TCAC    CACTCCTCTAAGTG
                                  TGT__
GAM389  LOC140275 3'  TGAATCTCCCTTAAAGTACTT  75296      CTCCG    _
                                AAGTGC    TGAGG AGATTCA
                                ||||||    ||||| |||||||
                                TTCATG    ATTCC TCTAAGT
                                   AA___    C
GAM389  LOC143188 5'  TGAACCTAGAGCTGGAGGCA  83795      _ GAGG  A
                                TGCCTCC GT    AG TTCA
                                ||||||| ||    || ||||
                                ACGGAGG CG    TC AAGT
                                    T  AGA_  C
GAM389  LOC145828 5'  GTGAATCCTGGGGCAGGGCACT 84539       __ GTGA  A
           T                     AAGTGCCT  CC    GG GATTCAC
                                ||||||||  ||    || |||||||
                                TTCACGGG  GG    TC CTAAGTG
                                    AC  GG__  _
GAM389  LOC245771 5'  GAATCTCCTGCCTCAGCCTT   94474    T  CTCC  G
                                AAG GC    GT AGGAGATTC
                                ||| ||    || |||||||||
                                TTC CG    CG TCCTCTAAG
                                  _  ACTC  _
GAM390  ABCC3    3'  CCTGCCCCATTTCCTCCT    39614     C       AAACCC
                                AGG AGGAGGTGG     CAGG
                                ||| |||||||||     ||||
                                TCC TCCTTTACC     GTCC
                                  _       CC_____
GAM390  ABCC3    3'  TCCTAAAGTTTCGTTTCTGTTT 39619        GTG    CCC
                                AGGCAGGAG   GAAAC   AGGG
                                |||||||||   |||||   ||||
                                TTTGTCTTT   CTTTG   TCCT
                                    G__     AAA
GAM390  ABCC3    3'  TCCTAAAGTTTCGTTTCTGTTT 39620        GTG    CCC
                                AGGCAGGAG   GAAAC   AGGG
                                |||||||||   |||||   ||||
                                TTTGTCTTT   CTTTG   TCCT
                                    G__     AAA
GAM390  ABCC3    3'  TCCTAAAGTTTCGTTTCTGTTT 39621        GTG    CCC
                                AGGCAGGAG   GAAAC   AGGG
                                |||||||||   |||||   ||||
                                TTTGTCTTT   CTTTG   TCCT
                                    G__     AAA
GAM390  ABCC5    3'  TCCTGGTGTCACTTACTGTTT  20297      G     AAACC
                                AGGCAG AGGTGG    CCAGGG
                                |||||| ||||||    ||||||
                                TTTGTC TTCACT    GGTCCT
                                   A     GT___
GAM390  ABCF1    3'  CTCTGAAGACTGCCTCTGGCCT 8448      A    TG AAACCC
                                AGGC GGAGG  G     CAGGG
                                |||| |||||  |     |||||
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                              TCCG TCTCC  C     GTCTC
                                G    GT AGAA__
GAM390  ABR     3'  CAGGGTTTTGTCTATGTTCTGT 41995        G    AA_______  CCAG
           TT                  AGGCAGGA GTGGA       CC   G
                               |||||||| |||||       ||   |
                               TTTGTCTT TATCT       GG   C
                                  G    GTTTT    GAC
GAM390  ABR     3'  CCAGGGTTTTGTCTATGTTCTG 41999        G    AA_______  CCAG
           TTT                  AGGCAGGA GTGGA       CC   G
                               |||||||| |||||       ||   |
                               TTTGTCTT TATCT       GG   C
                                  G    GTTTT    GACC
GAM390  ABR     3'  GGTTCTGGGGTTTACCTGTTCG 42008        _______  _
           GCCTCCTGCCT              AGGCAGGAGGT     GG AAACCCCAGGG   TT
                               ||||||||||     || ||||||||||   ||
                               TCCGTCCTCCG     CC TTTGGGGTCTT   GG
                                     GCTTGT  A
GAM390  ACAD8   3'  TTTTGTGTTTTTGTTTCCT   27667       TG    CC
                               AGGAGG  GAAAC  CAGGG
                               ||||||  |||||  |||||
                               TCCTTT  TTTTG  GTTTT
                                  GT    T_
GAM390  ACADS   3'  CCTTGGTGGGGTCTGTCTTTTC 5235      C     TG  AA  _
           CT                   AGG AGGAGG  GA  CC CCAGGG
                               ||| ||||||  ||  || ||||||
                               TCC TTTTCT  CT  GG GGTTCC
                                 _     GT  GG  T
GAM390  ACATN   3'  CCCCAGGGTTTTAAATGTATTT 17595          GAAA_________  CCAG
           CCTGCTT                AGGCAGGAGGTG         CC   GG
                               ||||||||||||         ||   ||
                               TTCGTCCTTTAT         GG   CC
                                     GTAAATTTT    GACC
GAM390  ACCN1   3'  CCAGGGTTTTGCTTCATTTTAT 8458       G      AA________  CCAG
           GCTT                   AGGCA GAGGTGGA       CC   G
                               ||||| ||||||||       ||   |
                               TTCGT TTTTACTT       GG   C
                                  A       CGTTTT    GACC
GAM390  ACHE    3'  CAGGGCCATTTCTGTCTCTTCT 32331     C    GT   A_______  CCAG
           T                    AGG AGGAG  GGAA      CC   G
                               ||| |||||  ||||      ||   |
                               TTC TTCTC  TCTT      GG   C
                                 _    TG    TACC    GAC
GAM390  ADAM19  3'  GTTTTCTTGCTTTTTGTTT   53845          __
                               AGGCAGGAGGT  GGAAAC
                               ||||||||||  ||||||
                               TTTGTTTTTCG  CTTTTG
                                     TT
GAM390  ADAMTS13 3'  CCTGGCGGCGCCTCCTTCT   58153     C       GAAA  _
                               AGG AGGAGGTG   CC CCAGG
                               ||| ||||||||   || |||||
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                                TCT TCCTCCGC    GG GGTCC
                                  _       ____ C
GAM390  ADAMTS5  3'  CCAGGGTTTTCTCCACCTTTTT 23859     C        AA_______  CCAG
            CTT                   AGG AGGAGGTGGA       CC    G
                                  ||| ||||||||||       ||    |
                                  TTC TTTTCCACCT       GG    C
                                    T         CTTTT     GACC
GAM390  ADAR     3'  CCAGGGCTTTGTCCAGTCTTTT 32356          _    AA_______  CCAG
            GTTT                    AGGCAGGAGG TGGA       CC    G
                                  |||||||||| ||||       ||    |
                                  TTTGTTTTCT ACCT       GG    C
                                        G    GTTTC     GACC
GAM390  ADAR     3'  CTCTGGCCAGCTGCCTCTTCTT 32359     C      TG AAACC
                                  AGG AGGAGG  G     CCAGGG
                                  ||| ||||||  |     ||||||
                                  TTC TTCTCC  C     GGTCTC
                                    _     GT GACC_
GAM390  ADCY2    3'  CCTGTATCTTTTATTTTCCTGT 65647          _    ACCC    G
            CT                    AGGCAGGAGG TGGAA    CAGG
                                  |||||||||| ||||||    ||||
                                  TCTGTCCTTT ATTTT    GTCC
                                        T     CTAT
GAM390  ADCY6    3'  CCTTGGGTGGCTTGTCTCTGCT 40949       G   TG AA_    C   G
            T                     AGGCAG AGG  G   ACCC AGG
                                  |||||| |||  |   |||| |||
                                  TTCGTC TCT  T   TGGG TCC
                                     _  GT CGG    T
GAM390  ADCY6    3'  CTCTAGATTCCCTTCCTGTCT  40950          T    ACCCC
                                  AGGCAGGAGG GGAA     AGGG
                                  |||||||||| ||||     ||||
                                  TCTGTCCTTC CCTT     TCTC
                                        _    AGA__
GAM390  ADCY6    5'  TTTTGGGCAAGTTTCTTGTC   40965        GG GGAAAC
                                  GGCAGGA  T     CCCAGGG
                                  |||||||  |     |||||||
                                  CTGTTCT  G     GGGTTTT
                                      TT AAC___
GAM390  ADD2     3'  CTTGGGCTCCCTCCTGCCT   34377          TG AAAC
                                  AGGCAGGAGG  G    CCCAGG
                                  ||||||||||  |    ||||||
                                  TCCGTCCTCC  C    GGGTTC
                                        CT ____
GAM390  ADD2     3'  CTTGGGCTCCCTCCTGCCT   34378          TG AAAC
                                  AGGCAGGAGG  G    CCCAGG
                                  ||||||||||  |    ||||||
                                  TCCGTCCTCC  C    GGGTTC
                                        CT ____
GAM390  ADH4     3'  CCAGGGTTCTCTCCACGTTTTG 7264          G     AA_______  CCAG
            TCT                     AGGCAGGA GTGGA       CC    G
                                  |||||||| |||||       ||    |
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                                TCTGTTTT CACCT       GG    C
                                     G    CTCTT    GACC
GAM390  ADK      3'  TTTGTTTTTTACATTTCTGCTT 22992          _      CCC
                                AGGCAGGAG GTGGAAA   CAGG
                                ||||||||| |||||||   ||||
                                TTCGTCTTT CATTTTT   GTTT
                                     A      T__
GAM390  ADPRT    3'  TTTTGGGGTTGTTTTTGTTTTT 9661      C     TG  ___
           TCTT                   AGG AGGAGG  GAA   ACCCCAGGG
                                ||| ||||||  |||   |||||||||
                                TTC TTTTTT  TTT   TGGGGTTTT
                                  _     GT   TGT
GAM390  ADRA2A   3'  CCAGGGTTCTGTCCATTTTTTT 7289      C        AA_______  CCAG
           CCT                    AGG AGGAGGTGGA       CC    G
                                ||| ||||||||||       ||    |
                                TCC TTTTTTACCT       GG    C
                                  T        GTCTT    GACC
GAM390  ADRA2B   3'  CTTGTGGTGTTTTCGTTTCTT  7296      GG     _ _   G
                                AGGA  TGGAAAC CC CAGG
                                ||||  ||||||| || ||||
                                TTCT  GCTTTTG GG GTTC
                                  TT      T  T
GAM390  ADSS     3'  TTTTGGGCTGTCTATTTTCTGC 72236           AAC
           T                     GGCAGGAGGTGGA   CCCAGGG
                                ||||||||||||   |||||||
                                TCGTCTTTTATCT   GGGTTTT
                                       GTC
GAM390  AGC1     3'  CCAGGGTCTTGTCGCTTTTTGT 25951          AAA_____  CCAG
           C                     GGCAGGAGGTGG       CC    G
                                ||||||||||||       ||    |
                                CTGTTTTTCGCT       GG    C
                                       GTTCT    GACC
GAM390  AGR2     3'  TTTGGGGGTGTTCTGTTT    22165        GGTGGAAA
                                AGGCAGGA       CCCCAGG
                                ||||||||       |||||||
                                TTTGTCTT       GGGGTTT
                                     GTG_____
GAM390  AIM1     3'  TCCTCCTTTCATTTCTTGCCT  93469            ACCCC
                                AGGCAGGAGGTGGAA    AGGG
                                ||||||||||||||    ||||
                                TCCGTTCTTTACTTT    TCCT
                                       CC___
GAM390  AKAP13   3'  TCTGACCTACCTTTGCCT    91254       G     AAACCC
                                AGGCAG AGGTGG     CAGG
                                |||||| ||||||     ||||
                                TCCGTT TCCATC     GTCT
                                  _     CA____
GAM390  AKR1C2   3'  CTCTGGTTAAATCTCTCCTGCT 71758          T  AAACC
           T                     AGGCAGGAGG GG     CCAGGG
                                |||||||||| ||     ||||||
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                                TTCGTCCTCT CT    GGTCTC
                                     _ AAATT
GAM390  ALDH1A3  3'  TTTTGGTTTTTGTTTTTTGTTT 7339         TG    CCAGGG
                                AGGCAGGAGG  GAAACC
                                ||||||||||  ||||||
                                TTTGTTTTTT  TTTTGG
                                     GT     TTTTT
GAM390  ALDH3B1  3'  CCTGAGTTTCGTCTCCTGTCT  93155        GT   ACCC
                                AGGCAGGAG  GGAA   CAGG
                                |||||||||  ||||   ||||
                                TCTGTCCTC  CTTT   GTCC
                                     TG   GA__
GAM390  ALDOC    3'  CCCTGGGCTCTCCTTCTTGCCT 18966         TG  AAC
                                AGGCAGGAGG  GA   CCCAGGG
                                ||||||||||  ||   |||||||
                                TCCGTTCTTC  CT   GGGTCCC
                                     CT  C__
GAM390  ALPP     3'  TCCTGCTCCCCACCTCCTGTC  69420          AAACCC
                                GGCAGGAGGTGG     CAGGG
                                ||||||||||||     |||||
                                CTGTCCTCCACC     GTCCT
                                      CCTC__
GAM390  ANG      3'  CCTGGACCTTTTGTTTTCTGTT 8556          TG   ACC    G
          T                      AGGCAGGAGG  GAA   CCAGG
                                ||||||||||  |||   |||||
                                TTTGTCTTTT  TTT   GGTCC
                                     GT   CCA
GAM390  ANKTM1   3'  CCAGGGTTCTATTTCTGTTTTT 24698      _____       AA__  CCAG
          GCTT                    AGGCA    GGAGGTGGA    CC    G
                                |||||    |||||||||    ||    |
                                TTCGT    TCTTTATCT    GG    C
                                   TTTTG       T     GACC
GAM390  ANKTM1   3'  CCCAGGGTTCTGTTTTTGCTTC 24699       TG    ________  CAG
          TT                     AGGAGG  GAAAC      CC   GG
                                ||||||  |||||      ||   ||
                                TTCTTC  TTTTG      GG   CC
                                   GT    TCTT    GAC
GAM390  ANXA4    3'  CCCAGGGTTACTTTCTACTTTG 63431       G        _________  CCA
          TGTTT                   AGGCA GAGGTGGAAA       CC   GG
                                ||||| ||||||||||       ||   ||
                                TTTGT TTTCATCTTT       GG   CC
                                   G         CATT   G  ACC
GAM390  AP3B1    3'  TCTTGACATTCTTGTCTCCTGC 14751          TG AAACCC
          TT                     AGGCAGGAGG  G     CAGGG
                                ||||||||||  |     |||||
                                TTCGTCCTCT  T     GTTCT
                                     GT CTTACA
GAM390  APBA2    3'  TCTGGACTGTCTTCTCCCT   19742     C     TG AAACC
                                AGG AGGAGG  G    CCAGG
                                ||| ||||||  |    |||||
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                                TCC TCTTCT  C     GGTCT
                                  C      GT A____
GAM390  APG5L    3'  CCAGGGCTTTGCATCACCTCTG 17937       G     AAA________  CCAG
              CTT                   AGGCAG AGGTGG         CC    G
                                |||||| ||||||         ||    |
                                TTCGTC TCCACT         GG    C
                                  _      ACGTTTC     GACC
GAM390  APM1     3'  CCCTGCACTACTCTACTTCCTC 17775     C        AACCC_
              TT                   AGG AGGAGGTGGA     CAGGG
                                ||| ||||||||||      |||||
                                TTC TCCTTCATCT     GTCCC
                                  _        CATCAC
GAM390  APXL     3'  CCCTGGTGCTCATCTTCTCTT  9712      C       AAACC
                                AGG AGGAGGTGG     CCAGGG
                                ||| |||||||||     ||||||
                                TTC TCTTCTACT     GGTCCC
                                  _        CGT__
GAM390  AQP1     3'  CCAGGGCTTTCTTTCTCTTTCT 6358          T    AC________ CCAG
              GTTT                   AGGCAGGAGG GGAA        C    G
                                |||||||||| ||||        |    |
                                TTTGTCTTTC CTTT        G    C
                                     T    CTTTC   G GACC
GAM390  AQP1     3'  GGTGTTTCTATCTCTTTCTT   6359      C          ____
                                AGG AGGAGGTGGAAAC    CC
                                ||| ||||||||||||    ||
                                TTC TTCTCTATCTTTG    GG
                                  T           T
GAM390  AQP6     3'  TTTTGGGGGGGTATATTTCCTCC 55024     C       GAAA
              T                   AGG AGGAGGTG    CCCCAGGG
                                ||| ||||||||    ||||||||
                                TCC TCCTTTAT    GGGGTTTT
                                  _       ATGG
GAM390  AQP6     3'  TTTTGGGGGGGTATATTTCCTCC 55025     C       GAAA
              T                   AGG AGGAGGTG    CCCCAGGG
                                ||| ||||||||    ||||||||
                                TCC TCCTTTAT    GGGGTTTT
                                  _       ATGG
GAM390  AR       5'  GGCTCTCTCCACCTCCTCCT   5275      C        AA_______
                                AGG AGGAGGTGGA       CC
                                ||| ||||||||||       ||
                                TCC TCCTCCACCT       GG
                                  _        CTCTC
GAM390  ARF3     3'  CAGGGTCTTCTCCAACTCTTGT 9770          G    AA_______  CCAG
              TT                   AGGCAGGAG TGGA       CC    G
                                |||||||||| ||||       ||    |
                                TTTGTTCTC ACCT       GG    C
                                     A    CTTCT     GAC
GAM390  ARF3     3'  CCCTGATTCCAGCTTTCTGCTT 9773          _     ACCC
                                AGGCAGGAGG TGGAA    CAGGG
                                |||||||||| |||||    |||||
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                                TTCGTCTTTC ACCTT   GTCCC
                                     G    A___
GAM390  ARF5    3'  TCTGCTCCTGCTCCTGCCT   9786        GT   AACCC
                                AGGCAGGAG GGA    CAGG
                                ||||||||| |||    ||||
                                TCCGTCCTC CCT    GTCT
                                    GT   C____
GAM390  ARHGEF6 3'  CTTTGGCTTTTGTTTTGTGTTT 68757     G   TG   ACC
                                AGGCA GAGG GAA   CCAGGG
                                ||||| |||| |||   ||||||
                                TTTGT TTTT TTT   GGTTTC
                                  G   GT   C__
GAM390  ARHH    5'  CGGGTTTTGTTTTCGCCTCCT 16299          ________ CAG
                                AGGAGGTGGAAAC     CC   G
                                ||||||||||||      ||   |
                                TCCTCCGCTTTTG     GG   C
                                      TTTT    GA
GAM390  ARPC2   5'  CCAGGGCTCTCCCTCCGTCCTT 20401     _____    TG  AA__  CCAG
            GCCT                AGGCA    GGAGG  GA   CC   G
                                |||||    |||||  ||   ||   |
                                TCCGT    CCTCC  CT   GG   C
                                  TCCTG    CT  C    GACC
GAM390  ARVCF   3'  CTTTGGGGACACCCTCCTGCC  9803        _  GAAA
                                GGCAGGAGG TG   CCCCAGGG
                                ||||||||| ||   ||||||||
                                CCGTCCTCC AC   GGGGTTTC
                                     C  A___
GAM390  ASB3    3'  CAGGGTTTTGATCATTTTCTGC 32773          AAA_______ CCAG
            TT                  AGGCAGGAGGTGG       CC   G
                                ||||||||||||        ||   |
                                TTCGTCTTTTACT       GG   C
                                      AGTTTT    GAC
GAM390  ASCL1   5'  CCAGGGTTTTGCTGCTGCTTCT 73134        __   _  A____  CCAG
            GCTT                AGGCAGGAG  GTGG AA    CC   G
                                |||||||||  |||| ||    ||   |
                                TTCGTCTTC  CGTC TT    GG   C
                                     GT   G  TT    GACC
GAM390  ASPH    3'  CCCTCCTTCCCCTTCCTGCTT  51632        T   ACCCC
                                AGGCAGGAGG GGAA    AGGG
                                |||||||||| ||||    ||||
                                TTCGTCCTTC CCTT    TCCC
                                     C   CC___
GAM390  ASTN    3'  CCCAAGACTTTCTTCCTCCTGT 69868         T    CCCCA
            TT                  AGGCAGGAGG GGAAA    GGG
                                |||||||||| |||||    |||
                                TTTGTCCTCC TCTTT    CCC
                                      T    CAGAA
GAM390  ASTN    3'  CTCTGTACCCTCTCCTTCTGTT 69870         T   AACCC
            T                   AGGCAGGAGG GGA    CAGGG
                                |||||||||| |||    |||||
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                                TTTGTCTTCC TCT    GTCTC
                                      _  CCCAT
GAM390  ATF7    3'  CTTTGGTCATTTTTCTGCTCCT 23401       G TG   CC___
            GCTT                  AGGCAGGA G  GAAA    CCAGGG
                                |||||||| |  ||||    ||||||
                                TTCGTCCT C  CTTT    GGTTTC
                                   _ GT   TTACT
GAM390  ATP2A3  3'  TCTGTCCCCACTTCCTTCT   18979    C      AAACCC
                                AGG AGGAGGTGG     CAGG
                                ||| |||||||||     ||||
                                TCT TCCTTCACC     GTCT
                                  _       CCT___
GAM390  ATP2B2  3'  GGGGAGGGGTTTTTGTTTGTTT 9851       _  TG      AGGG
            GTTT                  AGGCAGG AGG  GAAACCCC
                                ||||||| |||  ||||||||
                                TTTGTTT TTT  TTTTGGGG
                                   G   GT      AGGGGT
GAM390  ATP2B4  3'  CCTATTTCCATTTTCGTCT   70847     A       CCCC   G
                                AGGC GGAGGTGGAAA    AGG
                                |||| ||||||||||    |||
                                TCTG CTTTTACCTTT    TCC
                                  _         A___   A
GAM390  ATP5J   5'  CCCTCCACTTCCTCCTCCTGTT 9852         T    ACCCC
            T                   AGGCAGGAGG GGAA    AGGG
                                |||||||||| ||||    ||||
                                TTTGTCCTCC CCTT    TCCC
                                      T   CACC_
GAM390  ATP5J   5'  CCTGTTTGGCTTCTGTCT    9854         G GG AACCC
                                AGGCAGGAG T  A    CAGG
                                ||||||||| |  |    ||||
                                TCTGTCTTC G  T    GTCC
                                     G TT _____
GAM390  AVPR1A  5'  CAGGGTCTTTTGCATTTTTTGC 7375          _  A_____  CCAG
            CT                    AGGCAGGAGGTG GAA     CC   G
                                ||||||||||| |||     ||   |
                                TCCGTTTTTTAC TTT     GG   C
                                      G   TCT    GAC
GAM390  AVPR1A  5'  CCCTGAACCATTTCAATCTTCT 7377          G   CCC__
            GCCT                  AGGCAGGAGGT GAAA    CAGGG
                                |||||||||| ||||    |||||
                                TCCGTCTTCTA CTTT    GTCCC
                                      A   ACCAA
GAM390  AXL     3'  GGCTTTGCTGCATTCTGCCT   41888       G   _  A____
                                AGGCAGGA GTGG AA    CC
                                |||||||| |||| ||    ||
                                TCCGTCTT CGTC TT    GG
                                     A   G  TC
GAM390  AXUD1   3'  CCCTGCCCCCTCCACTTCCTGC 53440           AACCC
            C                   GGCAGGAGGTGGA    CAGGG
                                ||||||||||||    |||||
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                                CCGTCCTTCACCT    GTCCC
                                      CCCCC
GAM390  B4GALT2  3'  CTTTGGGGGGCCTCCTGCCT  48346         GGAAA
                                AGGCAGGAGGT    CCCCAGGG
                                ||||||||||    ||||||||
                                TCCGTCCTCCG    GGGGTTTC
                                      G____
GAM390  B4GALT2  3'  CTTTGGGGGGCCTCCTGCCT  48347         GGAAA
                                AGGCAGGAGGT    CCCCAGGG
                                ||||||||||    ||||||||
                                TCCGTCCTCCG    GGGGTTTC
                                      G____
GAM390  BAAT     5'  TTTTGGGGGCAGGTTCTCTTGC 9911         TGGAAA
           T                     GGCAGGAGG     CCCCAGGG
                                |||||||||     ||||||||
                                TCGTTCTCT     GGGGTTTT
                                     TGGACG
GAM390  BASP1    3'  CCAGGGCTCTCTCTATCTCCTC 76494     C       AA_______  CCAG
           TCT                    AGG AGGAGGTGGA       CC    G
                                ||| ||||||||||       ||    |
                                TCT TCCTCTATCT       GG    C
                                  C        CTCTC     GACC
GAM390  BAT1     5'  CCCTACTCTTCACCCCTTGTTT 17350       A     AACCCC
                                AGGCAGG GGTGGA     AGGG
                                ||||||| ||||||     ||||
                                TTTGTTC CCACTT     TCCC
                                    C     CTCA__
GAM390  BCAT1    5'  CTCTGATCTGTTTATTTCCTCC 66785     C       AACCC
           T                     AGG AGGAGGTGGA     CAGGG
                                ||| ||||||||||     |||||
                                TCC TCCTTTATTT     GTCTC
                                  _        GTCTA
GAM390  BCL11A   3'  TCCTACCTATCCACCTTCTGGC 43469     G        AACCCC
           T                     AG CAGGAGGTGGA     AGGG
                                || ||||||||||     ||||
                                TC GTCTTCCACCT     TCCT
                                 G         ATCCA_
GAM390  BCL11B   3'  CCCAGGTTTTTATTTTTT    57575           CCA
                                AGGAGGTGGAAACC   GGG
                                ||||||||||||||   |||
                                TTTTTTATTTTTGG   CCC
                                      A__
GAM390  BCL2     3'  CCTGTTTTGTCTTCTGTT    7234         TG   ACCC
                                GGCAGGAGG  GAA    CAGG
                                |||||||||  |||   ||||
                                TTGTCTTCT  TTT    GTCC
                                     GT  ____
GAM390  BCL2     3'  TTTGAGATTTTTATCTCTTG   7244           CCC    G
                                CAGGAGGTGGAAA   CAGG
                                ||||||||||||   ||||
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                                GTTCTCTATTTTT  GTTT
                                       AGA
GAM390  BCL9    3'  TCCTGGGATGCTTCTCTGTCT  16324      _    GAAAC
                                AGGCAG GAGGTG    CCCAGGG
                                ||||||| |||||||  |||||||
                                TCTGTC CTTCGT    GGGTCCT
                                   T     A____
GAM390  BCLG    3'  GGTGTTTCCACTTCCGTTT   57806     A        ____
                                AGGC GGAGGTGGAAAC   CC
                                |||| ||||||||||||   ||
                                TTTG CCTTCACCTTTG   GG
                                  _         T
GAM390  BCLG    3'  GGTGTTTCCACTTCCGTTT   57807     A        ____
                                AGGC GGAGGTGGAAAC   CC
                                |||| ||||||||||||   ||
                                TTTG CCTTCACCTTTG   GG
                                  _         T
GAM390  BMP8    3'  CTCTGTGCCTACTTCCTGTC  9946          AAACCC
                                GGCAGGAGGTGG    CAGGG
                                ||||||||||||    |||||
                                CTGTCCTTCATC    GTCTC
                                       CGT___
GAM390  BTD     3'  CCCTGGGACCATCTTTCTGCCT 5347       _    AAAC
                                AGGCAGGA GGTGG   CCCAGGG
                                |||||||| |||||   |||||||
                                TCCGTCTT CTACC   GGGTCCC
                                     T    A___
GAM390  BTEB1   3'  TTTTGGGTTTTTTGGTTTTTGT 8672        G GG   C
           TT                    AGGCAGGAG T  AAA CCCAGGG
                                |||||||||  |  ||| |||||||
                                TTTGTTTTT G  TTT GGGTTTT
                                     G TT   T
GAM390  C11orf8 5'  CCTGCTTCCATCTTTTGCT   9623           ACCC
                                GGCAGGAGGTGGAA   CAGG
                                ||||||||||||||   ||||
                                TCGTTTTCTACCTT   GTCC
                                       C___
GAM390  C14orf1 3'  CCAGGGTTTTATTCACTTTTAG 24164     AG      AA_______  CCAG
           CCT                   AGGC  GAGGTGGA      CC   G
                                ||||  ||||||||      ||   |
                                TCCG  TTTCACTT      GG   C
                                  AT      ATTTT    GACC
GAM390  C18orf1 3'  GGTTTTTGTTTGTTTGTTT   60868      _  TG
                                AGGCAGG AGG  GAAACC
                                ||||||| |||  ||||||
                                TTTGTTT TTT  TTTTGG
                                   G   GT
GAM390  C18orf1 3'  TCCTGCATCTATCTCCTGCT  60873          AACCC
                                GGCAGGAGGTGGA    CAGGG
                                ||||||||||||    |||||
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                                TCGTCCTCTATCT    GTCCT
                                      AC___
GAM390  C9      3'  TCCTGTGATGTTTCCATTTTTT 9979             CC__
            GTT                   GGCAGGAGGTGGAAAC   CAGGG
                                  ||||||||||||||||   |||||
                                  TTGTTTTTTACCTTTG   GTCCT
                                        TAGT
GAM390  CACNA2D2 3'  CCTGCTCACCACCTGCCT    21222       A    AAACCC
                                  AGGCAGG GGTGG     CAGG
                                  ||||||| |||||     ||||
                                  TCCGTCC CCACT     GTCC
                                     A    C_____
GAM390  CACNB1   3'  CCCTGAGCCCCTTCACTTACCT 7406        _      AACCC_
            GTCT                    AGGCAGG AGGTGGA     CAGGG
                                  ||||||| |||||||     |||||
                                  TCTGTCC TTCACTT     GTCCC
                                     A      CCCCGA
GAM390  CACNB1   3'  CCCTGGGGCATCCCTTTGCCT  7407       GA  T   AA
                                  AGGCAG  GG GGA  CCCCAGGG
                                  ||||||  || |||  ||||||||
                                  TCCGTT  TC CCT  GGGGTCCC
                                     __ _   AC
GAM390  CALCRL   3'  CCTTGTCAACCTCTTCCTGTCT 20527          T  AAACCC
                                  AGGCAGGAGG GG     CAGGG
                                  |||||||||| ||     |||||
                                  TCTGTCCTTC CC     GTTCC
                                        T  AACT__
GAM390  CALD1    5'  TCTGGCTGTGCTCCTGCTT   53699        _ TG AAACC
                                  AGGCAGGAG G  G    CCAGG
                                  ||||||||| |  |    |||||
                                  TTCGTCCTC T  C    GGTCT
                                       G GT _____
GAM390  CALM3    3'  TTTTGGTTTGTTTCCTCTTGTT 19006          TG _    CCAGGG
            T                    AGGCAGGAGG  G AAACC
                                  ||||||||||  | |||||
                                  TTTGTTCTCC  T TTTGG
                                        TT G    TTTT
GAM390  CAPG     3'  CCCTGCCCCCCACCACCTGCCT 10009       A    AAACCC
                                  AGGCAGG GGTGG     CAGGG
                                  ||||||| |||||     |||||
                                  TCCGTCC CCACC     GTCCC
                                     A    CCCC__
GAM390  CARPX    3'  CCCCAGGGTCCATTTGCTGTTT 39813       G      AA_  CCAG
                                  AGGCAG AGGTGGA   CC   GG
                                  |||||| |||||||   ||   ||
                                  TTTGTC TTTACCT   GG   CC
                                     G          GACC
GAM390  CASP2    3'  CTCTGTAACCACCTCTCTGTCT 8708        _      AAACCC
                                  AGGCAG GAGGTGG     CAGGG
                                  |||||| |||||||     |||||
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                                TCTGTC CTCCACC     GTCTC
                                   T      AAT___
GAM390  CASP2    3'  CTCTGTAACCACCTCTCTGTCT 53330       _      AAACCC
                                AGGCAG GAGGTGG     CAGGG
                                |||||| |||||||     |||||
                                TCTGTC CTCCACC     GTCTC
                                   T      AAT___
GAM390  CASP2    3'  CTCTGTAACCACCTCTCTGTCT 53331       _      AAACCC
                                AGGCAG GAGGTGG     CAGGG
                                |||||| |||||||     |||||
                                TCTGTC CTCCACC     GTCTC
                                   T      AAT___
GAM390  CASP7    3'  TTCTGGTGCTGTCTTTTGTT   54036         TG AAACC
                                GGCAGGAGG  G    CCAGGG
                                |||||||||  |    ||||||
                                TTGTTTTCT  C    GGTCTT
                                     GT GT___
GAM390  CASP7    3'  TTCTGGTGCTGTCTTTTGTT   54037         TG AAACC
                                GGCAGGAGG  G    CCAGGG
                                |||||||||  |    ||||||
                                TTGTTTTCT  C    GGTCTT
                                     GT GT___
GAM390  CASP8    3'  GGCTCTTTCATCTCTGCTT    54080       G      AC_____
                                AGGCAG AGGTGGAA      C
                                |||||| |||||||      |
                                TTCGTC TCTACTTT      G
                                   _       CTC   G
GAM390  CASP8    3'  GCTCTTTCATCTCTGCTT    8756        G      AC_____
                                AGGCAG AGGTGGAA      C
                                |||||| |||||||      |
                                TTCGTC TCTACTTT      G
                                   _       CTC   G
GAM390  CASP8    3'  GGCTCTTTCATCTCTGCTT    8757        G      AC_____
                                AGGCAG AGGTGGAA      C
                                |||||| |||||||      |
                                TTCGTC TCTACTTT      G
                                   _       CTC   G
GAM390  CASP8    5'  TCCTCCTTTTATCTTTTGT    8768            ACCCC
                                GCAGGAGGTGGAA    AGGG
                                ||||||||||||    ||||
                                TGTTTTCTATTTT    TCCT
                                      CC___
GAM390  CASQ1    3'  CCAGGGTCTTATCTGACTTCTG 8778          GT   AA_______  CCAG
          TTT                    AGGCAGGAG  GGA      CC    G
                                |||||||||  |||      ||   |
                                TTTGTCTTC  TCT      GG    C
                                     AG   ATTCT    GACC
GAM390  CAV1     3'  CAGGGCTCTGCTTGATTTTTGC 10023         _____  TG  AA__  CCAG
          CT                     AGGCAGGA   GG  GA   CC    G
                                ||||||||   ||  ||   ||   |
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                              TCCGTTTT   TC CT   GG   C
                                  TAGT GT C    GAC
GAM390  CBFA2T1  5' CAGGGCTCTCCATCTGTCTCTG 16359      ___     AA____ CCAG
           CCT                 AGGCAGG  AGGTGGA    CC   G
                              |||||||  |||||||    ||   |
                              TCCGTCT  TCTACCT    GG   C
                                 CTG     CTC    GAC
GAM390  CBFA2T1  3' GGTTTTTTTCCTGTTT     16361        TG
                              AGGCAGGAGG  GAAACC
                              ||||||||||  ||||||
                              TTTGTCCTTT  TTTTGG
                                       __
GAM390  CBFA2T1  5' TTCTGAATTTCACTTTTTGCTT 16362           ACCC
                              AGGCAGGAGGTGGAA   CAGGG
                              ||||||||||||||   |||||
                              TTCGTTTTTCACTTT   GTCTT
                                      AA__
GAM390  CBFA2T2  3' TTTTGGGTTTTGTTTTTTGTT  18721        TG  AC
                              GGCAGGAGG  GAA  CCCAGGG
                              |||||||||  |||  |||||||
                              TTGTTTTTT  TTT  GGGTTTT
                                   GT  __
GAM390  CCND2    5' CCAGGGTTCTGCTCCACCTTCT 10049    C       AA_______ CCAG
           CTCT                 AGG AGGAGGTGGA       CC   G
                              ||| ||||||||||       ||   |
                              TCT TCTTCCACCT       GG   C
                                C        CGTCTT    GACC
GAM390  CCND3    3' CCTGGGGGCTCTCATGTTT   10060    G  _ AA
                              GGA GTG GA  CCCCAGG
                              ||| ||| ||  |||||||
                              TTT TAC CT  GGGGTCC
                                G  T  CG
GAM390  CCNF     3' CCCTGCTGCCATCCACTTCTGT 10070      G     AACCC_
           TT                   AGGCAG AGGTGGA     CAGGG
                              ||||||  |||||||     |||||
                              TTTGTC TTCACCT     GTCCC
                                 _      ACCGTC
GAM390  CCNF     3' TTCTGGGCCATTCTTTTCCTGT 10090         T   AC_
           CT                   AGGCAGGAGG GGAA   CCCAGGG
                              ||||||||||  ||||   |||||||
                              TCTGTCCTTT  TCTT   GGGTCTT
                                   _    ACC
GAM390  CD34     3' CCCTGCCCCCACTTCCTGTTT  10104           AAACCC
                              AGGCAGGAGGTGG     CAGGG
                              ||||||||||||     |||||
                              TTTGTCCTTCACC     GTCCC
                                     CCC___
GAM390  CD4      3' CCCTATTTCCTTCTCCTCCTGT 7045          T___    CCCC
           CT                   AGGCAGGAGG    GGAAA    AGGG
                              |||||||||    |||||   ||||
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                                TCTGTCCTCC  CCTTT  TCCC
                                     TCTT   A___
GAM390  CD59    3'  TCCTGCGTAGTCCGCTTTCTCT 7031    C      AACCC
          T                   AGG AGGAGGTGGA   CAGGG
                              ||| ||||||||||   |||||
                              TTC TCTTTCGCCT   GTCCT
                                _      GATGC
GAM390  CD81    3'  TTTTGGGGTTTTGTTTTTGTT  16388      GTG
                              GGCAGGAG  GAAACCCCAGGG
                              ||||||||  ||||||||||||
                              TTGTTTTT  TTTTGGGGTTTT
                                   G__
GAM390  CDH12   3'  TTCTGATCTCCACCTTCTTCT  15779    C      AACCC
                              AGG AGGAGGTGGA   CAGGG
                              ||| ||||||||||   |||||
                              TCT TCTTCCACCT   GTCTT
                                _      CTA__
GAM390  CDK5R2  3'  CAGGGTTTTATCCATTTCCTTG 15444     _     AA_______ CCAG
          CCT                   AGGCA GGAGGTGGA     CC   G
                              ||||| |||||||||     ||   |
                              TCCGT CCTTTACCT     GG   C
                                 T      ATTTT   GAC
GAM390  CDK5R2  3'  CCCCAGGGTCTTCATTTTTCCT 15445       TG  A_________ CCAG
          CCTGTCT                AGGCAGGAGG  GAA      CC   GG
                              |||||||||| |||      ||   ||
                              TCTGTCCTCC  TTT      GG   CC
                                    TT   ACTTCT   GACC
GAM390  CDK5R2  3'  CCTGTCTGCCTTCTTCCT   15447    C    TG  AACCC
                              AGG AGGAGG  GA   CAGG
                              ||| ||||||  ||   ||||
                              TCC TCTTCC  CT   GTCC
                                T    GT  _____
GAM390  CENPB   3'  CCTGAGCCTGCTTCTGCCT   70112      GT  AAACCC
                              AGGCAGGAG  GG    CAGG
                              |||||||||  ||    ||||
                              TCCGTCTTC  CC    GTCC
                                   GT  GA____
GAM390  CENTD2  5'  CTCTGTCCCTTTATCTTTCTGT 31540      _    AACCC
          TT                   AGGCAGGA GGTGGA   CAGGG
                              ||||||| ||||||   |||||
                              TTTGTCTT CTATTT   GTCTC
                                   T    CCCT_
GAM390  CGB     5'  CCCTGGCCTTGTCTACCTCTTG 7426          AACC_
          CC                   GGCAGGAGGTGGA   CCAGGG
                              ||||||||||||    ||||||
                              CCGTTCTCCATCT   GGTCCC
                                     GTTCC
GAM390  CHAD    3'  CTTGCCCCACCCCTTGCTT   8853      A   AAACCC
                              AGGCAGG GGTGG    CAGG
                              ||||||| |||||    ||||
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                                TTCGTTC CCACC     GTTC
                                    C    CC____
GAM390  CHRNA2   5'  TCTGGGGTGACTTTTGTC   7431        GTGGAA
                                GGCAGGAG     ACCCCAGG
                                ||||||||     ||||||||
                                CTGTTTTC     TGGGGTCT
                                   AG____
GAM390  CHRNA4   3'  CCCTGGGGTTTCCACACAGGCC 7436     AGGAG
                                GGC    GTGGAAACCCCAGGG
                                |||    ||||||||||||||
                                CCG    CACCTTTGGGGTCCC
                                  GACA_
GAM390  CHRNA4   3'  CCTGGGGTACTTCTGT     7437        GTGGAA
                                GCAGGAG     ACCCCAGG
                                |||||||     ||||||||
                                TGTCTTC     TGGGGTCC
                                   A_____
GAM390  CHRNA7   3'  CCCCAGGGTTCAACATTTGCTT 7440         TG  AA_________  CCAG
           TTTGCTT                AGGCAGGAGG  GA       CC    GG
                                ||||||||||  ||       ||   ||
                                TTCGTTTTTC  TT       GG    CC
                                     GT  ACAACTT    GACC
GAM390  CHST1    3'  CCTGTTTCTGTTTCCAGTCT   14696     A    TG    CCC
                                AGGC GGAGG  GAAAC   AGG
                                |||| |||||  |||||   |||
                                TCTG CCTTT  CTTTG   TCC
                                  A    GT    ___
GAM390  CIAS1    5'  GGTTTTTTTCTTTCTGTTT   18101         T   A____
                                AGGCAGGAGG GGAA    CC
                                |||||||||| ||||    ||
                                TTTGTCTTTC TTTT    GG
                                     T   TT
GAM390  CIS4     3'  CCTTCGTTTTCATCTTCTAGTT 16167     _         CCC   G
           T                    AGGC AGGAGGTGGAAAC   AGG
                                |||| ||||||||||||   |||
                                TTTG TCTTCTACTTTTG   TCC
                                  A          CT_
GAM390  CISH     3'  TTCTGCTAGGTCTGCTTCCTGC 59671        TG  AACCC
           C                    GGCAGGAGG  GA    CAGGG
                                |||||||||  ||    |||||
                                CCGTCCTTC  CT    GTCTT
                                     GT  GGATC
GAM390  CKTSF1B1 3'  CCCTGAATACTCTTTTTGCCT  26292         T  AAACCC
                                AGGCAGGAGG GG     CAGGG
                                |||||||||| ||     |||||
                                TCCGTTTTTC TC     GTCCC
                                     _  ATAA__
GAM390  CKTSF1B1 3'  TCCTCACAATCCATCTCTTCTT 26296     C        AACCCC
                                AGG AGGAGGTGGA     AGGG
                                ||| ||||||||||     ||||
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                                TTC TTCTCTACCT     TCCT
                                  _        AACAC_
GAM390  CLASP2   3'  CTTGACCGTCTTCTGTTT    65203         GT  AAACCC
                                AGGCAGGAG  GG     CAGG
                                |||||||||  ||     ||||
                                TTTGTCTTC  CC     GTTC
                                     TG  A_____
GAM390  CLCN4    3'  CCGTTTTTACCTTTTGTC    10209             CCCA  G
                                GGCAGGAGGTGGAAAC    GG
                                ||||||||||||||||    ||
                                CTGTTTTCCATTTTTG    CC
                                          ____  A
GAM390  CLCN6    3'  TTTTGTGTTTCATCTCCAGCTT 41707      A         ACCC
                                AGGC GGAGGTGGAA    CAGGG
                                |||| ||||||||||    |||||
                                TTCG CCTCTACTTT    GTTTT
                                  A         GT__
GAM390  CLDN5    3'  CCTGGATCCGCTCCTGCCT    13816         G    AACC
                                AGGCAGGAG TGGA    CCAGG
                                ||||||||| ||||    |||||
                                TCCGTCCTC GCCT    GGTCC
                                     _    A___
GAM390  CLOCK    3'  CCTGTTTTTCCTTTTGTTT    18111          TG   ACCC
                                AGGCAGGAGG  GAA    CAGG
                                ||||||||||  |||    ||||
                                TTTGTTTTCC  TTT    GTCC
                                     TT   _____
GAM390  CLTA     3'  TTTTGGACCAAACCTTTTTGTC 10217         _   GGAAACC
           T                     AGGCAGGA GGT      CCAGGG
                                ||||||||| |||      ||||||
                                TCTGTTTT CCA      GGTTTT
                                     T   AACCA__
GAM390  CNN2     3'  TTCTGTGTTTTCATCTTTT    16467           CC
                                AGGAGGTGGAAAC  CAGGG
                                ||||||||||||  |||||
                                TTTTCTACTTTTG  GTCTT
                                       T_
GAM390  CNN3     3'  CCAGGGCCTTTTTCTGCCTCTT 60036     C     TG   A________  CCAG
           CCCT                    AGG AGGAGG  GAA       CC    G
                                ||| ||||||  |||       ||    |
                                TCC TTCTCC  CTT       GG    C
                                  C     GT   TTTCC    GACC
GAM390  CNN3     3'  CCTTTTTCCTTTTTCTGCCT   60037          T    CCCC
                                AGGCAGGAGG GGAAA    AGG
                                ||||||||||| |||||    |||
                                TCCGTCTTTT CCTTT    TCC
                                     T    T___
GAM390  CNP      3'  GCTCTGGGCTTTGATTCCATCT 53623       _        AC_____
           CCTTGTCT                 AGGCA GGAGGTGGAA     CCCAGGG   C
                                ||||| ||||||||||     |||||||   |
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                                TCTGT CCTCTACCTT     GGGTCTC   G
                                  T         AGTTTC
GAM390  CNTFR    3'  TCCTGCCCCAGCCTCCTGTCT  10239          _   AAACCC
                                AGGCAGGAGG TGG     CAGGG
                                |||||||||| |||     |||||
                                TCTGTCCTCC ACC     GTCCT
                                     G   CC____
GAM390  CNTN3    3'  CCCCAGGGTCAGTTTTTTACCT 67270     C         A_________  CCAG
           CTTTCCT                AGG AGGAGGTGGAA       CC    GG
                                ||| ||||||||||        ||    ||
                                TCC TTCTCCATTTT        GG    CC
                                  T         TTGACT     GACC
GAM390  COL4A6   3'  CCCTGCTGAGATCTGCTGTCCT 54437         _  TG  AACCC_
           GTTT                   AGGCAGGA GG  GA     CAGGG
                                |||||||| ||  ||      |||||
                                TTTGTCCT TC  CT     GTCCC
                                     G  GT  AGAGTC
GAM390  COL4A6   5'  TTTGGAGCACTTCTTATCT    54440    GC       GAAACC
                                AG  AGGAGGTG     CCAGG
                                ||  ||||||||     |||||
                                TC  TTCTTCAC     GGTTT
                                 TA       GA____
GAM390  COL5A3   3'  CGGGTTGTGTTTCTTTTCCTGC 32315          T     ________  CAG
           CT                     AGGCAGGAGG GGAAAC      CC   G
                                |||||||||| ||||||      ||   |
                                TCCGTCCTTT TCTTTG      GG   C
                                     _     TGTT     GA
GAM390  COL6A1   3'  TCCTGCCCGCCCTCCCTCCTGC 10249          TG AAACCC
           CT                     AGGCAGGAGG  G     CAGGG
                                ||||||||||  |     |||||
                                TCCGTCCTCC  C     GTCCT
                                     CT CCGCCC
GAM390  COLQ     3'  CCCTCATGTCCATTTCCTGTC  55421           AACCCC
                                GGCAGGAGGTGGA     AGGG
                                ||||||||||||      ||||
                                CTGTCCTTTACCT     TCCC
                                      GTAC__
GAM390  COLQ     3'  CCCTCATGTCCATTTCCTGTC  55422           AACCCC
                                GGCAGGAGGTGGA     AGGG
                                ||||||||||||      ||||
                                CTGTCCTTTACCT     TCCC
                                      GTAC__
GAM390  COLQ     3'  CCCTCATGTCCATTTCCTGTC  20253           AACCCC
                                GGCAGGAGGTGGA     AGGG
                                ||||||||||||      ||||
                                CTGTCCTTTACCT     TCCC
                                      GTAC__
GAM390  COX10    3'  CCAGGGCTCTATTCTGTTTCTT 8947      C     TG   A________  CCAG
           CCT                    AGG AGGAGG  GAA       CC    G
                                ||| ||||||  |||       ||    |
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                                TCC TTCTTT  CTT       GG    C
                                  _     GT   ATCTC    GACC
GAM390  COX11    3'  TTCTAAATATTTTCATTTTCTG 16487            CCCC_
              T                   GCAGGAGGTGGAAA    AGGG
                                  ||||||||||||||    ||||
                                  TGTCTTTTACTTTT    TCTT
                                        ATAAA
GAM390  CPB2     3'  CCCTGATTTTATCATTCTGCTT 10283        _     ACCC
                                  AGGCAGGA GGTGGAA    CAGGG
                                  |||||||| |||||||    |||||
                                  TTCGTCTT CTATTTT    GTCCC
                                       A      A___
GAM390  CPB2     3'  CCCTGATTTTATCATTCTGCTT 10284        _     ACCC
                                  AGGCAGGA GGTGGAA    CAGGG
                                  |||||||| |||||||    |||||
                                  TTCGTCTT CTATTTT    GTCCC
                                       A      A___
GAM390  CR1      3'  CCCAGGGTTTTGATTCATTTTC 6941            AA_______  CCAG
              TGCCT                AGGCAGGAGGTGGA       CC    GG
                                  ||||||||||||||       ||    ||
                                  TCCGTCTTTTACTT       GG    CC
                                        AGTTTT    GACC
GAM390  CR1L     5'  CCAGGGCCGTTTTCTATCATCT 90956       A      A_______  CCAG
              GCCT                  AGGCAGG GGTGGAA       CC    G
                                  |||||||| |||||||       ||    |
                                  TCCGTCT CTATCTT       GG    C
                                       A      TTGCC    GACC
GAM390  CRHR2    3'  CCCTGTCCTCCTCCACCTTCTT 10301     C        AACCC_
              CCT                   AGG AGGAGGTGGA     CAGGG
                                  ||| ||||||||||     |||||
                                  TCC TCTTCCACCT     GTCCC
                                    T        CCTCCT
GAM390  CRMP1    3'  CCAGGGCTCTTTCCCTTTTCTG 8972        _    T    A_______  CCAG
              TTT                   AGGCAG GAGG GGAA      CC    G
                                  |||||| |||| ||||      ||    |
                                  TTTGTC TTTC CCTT      GG    C
                                     T    _    TCTC    GACC
GAM390  CSE1L    3'  TCTTGTCCTTTATATTTTTTGT 62514           GAAACCC
              CT                    AGGCAGGAGGTG      CAGGG
                                  ||||||||||||      |||||
                                  TCTGTTTTTTAT      GTTCT
                                        ATTTCCT
GAM390  CSF3     3'  TTCTGAGTTTCATTCTCCTGCC 7486          TG    CC
              T                    AGGCAGGAGG  GAAAC  CAGGG
                                  ||||||||||  |||||  |||||
                                  TCCGTCCTCT  CTTTG  GTCTT
                                        TA    A_
GAM390  CSNK1A1  5'  CCGTGTTCCGTTTCCTGCC   10311       GG    ACCC  G
                                  GGCAGGA  TGGAA    CA GG
                                  |||||||  |||||    || ||
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                                CCGTCCT  GCCTT   GT CC
                                   TT    ____  G
GAM390  CSRP1   3'  CCAGGGTCTTCATTTATCTCTG 15811     A      AA_______  CCAG
           GCCT                  AGGC GGAGGTGGA       CC   G
                                ||||| |||||||||       ||   |
                                TCCG TCTCTATTT       GG   C
                                  G       ACTTCT    GACC
GAM390  CST1    3'  CCAGGGCCCTCCTTCCTTCTTG 10328       _ T_  AA____  CCAG
           CTT                   AGGCAGGA GG  GGA     CC   G
                                |||||||| ||  |||     ||   |
                                TTCGTTCT CC  CCT     GG   C
                                   T  TT   CCC    GACC
GAM390  CST3    3'  CCAGGGCCCTCCTTCCTTCTTG 5434        _ T_  AA____  CCAG
           CTT                   AGGCAGGA GG  GGA     CC   G
                                |||||||| ||  |||     ||   |
                                TTCGTTCT CC  CCT     GG   C
                                   T  TT   CCC    GACC
GAM390  CST4    3'  CCAGGGCCCTCCTTCCTTCTTG 10334       _ T_  AA____  CCAG
           CTT                   AGGCAGGA GG  GGA     CC   G
                                |||||||| ||  |||     ||   |
                                TTCGTTCT CC  CCT     GG   C
                                   T  TT   CCC    GACC
GAM390  CTBP1   3'  CCAGGGTTTTTTCTACCTGCTT 68537     _ G      A_______  CCAG
           GTCT                  AGGC AG AGGTGGAA      CC   G
                                |||| || ||||||||      ||   |
                                TCTG TC TCCATCTT      GG   C
                                  T  G       TTTT    GACC
GAM390  CTBP1   3'  TTTGAGGTTTTTTTTTTTGTTT 68538         T     C
                                AGGCAGGAGG GGAAACC CAGG
                                |||||||||| ||||||| ||||
                                TTTGTTTTTT TTTTTGG GTTT
                                      _     A
GAM390  CTF1    3'  CTTGGGGTGTCTCTGTTT   9015       GAGGT  A
                                AGGCAG    GGA ACCCCAGG
                                ||||||    ||| ||||||||
                                TTTGTC    TCT TGGGGTTC
                                   _____  G
GAM390  CTNNA2  3'  TCTGCATTCTGTTTCCTCTT  16525    C    TG  ACCC
                                AGG AGGAGG  GAA   CAGG
                                ||| ||||||  |||   ||||
                                TTC TCCTTT  CTT   GTCT
                                  _    GT  AC__
GAM390  CTNS    3'  CCTTGACACCGCCATCTCTTTT 18218    C      AAACCC
           CT                    AGG AGGAGGTGG     CAGGG
                                ||| |||||||||     |||||
                                TCT TTCTCTACC     GTTCC
                                  T       GCCACA
GAM390  CXCL1   3'  CTTGGACATTTTATGTCT    9496      G    GAAACC
                                AGGCA GAGGTG     CCAGG
                                ||||| ||||||     |||||
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                                TCTGT TTTTAC     GGTTC
                                  A     A_____
GAM390  CXCL16   3'  TCCTGGCTTCATTTTTTGCT   42179          AACC
                                GGCAGGAGGTGGA    CCAGGG
                                ||||||||||||    ||||||
                                TCGTTTTTTACTT    GGTCCT
                                      C___
GAM390  CXCR4    3'  TTGGATTTTTGTCTTGTGTTT  14414      G    TG    CC
                                AGGCA GAGG  GAAA  CCAG
                                ||||| ||||  ||||  ||||
                                TTTGT TTCT  TTTT  GGTT
                                  G    GT    A_
GAM390  CYB561   3'  TTCTGGGGCAGGTCTCCGCCT  10354      A     TGGAAA
                                AGGC GGAGG     CCCCAGGG
                                |||| |||||     ||||||||
                                TCCG CCTCT     GGGGTCTT
                                  _     GGAC__
GAM390  CYP4A11  3'  CAGGGTTCTGTCCCCTTCCTGT 7586          T   AA_______  CCAG
            CT                    AGGCAGGAGG GGA       CC    G
                                ||||||||||  |||       ||    |
                                TCTGTCCTTC CCT       GG    C
                                      C   GTCTT     GAC
GAM390  CYP4A11  3'  CCCCAGGGCCCATATCCTGTTT 7587         G    AAA_  CCAG
                                AGGCAGGA GTGG    CC    GG
                                ||||||||  ||||    ||    ||
                                TTTGTCCT TACC    GG    CC
                                     A    C     GACC
GAM390  CYP4A11  3'  CCCTGGACCCACTTTCTCTCT  7588      C       AAACC
                                AGG AGGAGGTGG     CCAGGG
                                |||  |||||||||     ||||||
                                TCT TCTTTCACC     GGTCCC
                                  C        CA___
GAM390  CYP4A11  3'  TCCTGTCTGCCCATATCCTGTT 7591         G    AAACCC
            T                    AGGCAGGA GTGG      CAGGG
                                ||||||||  ||||      |||||
                                TTTGTCCT TACC      GTCCT
                                     A    CGTCT_
GAM390  CYP51    3'  TTTTGGGCTCAGTTGTTCCCTG 7625         AG TG AAAC_
            CTT                    AGGCAGG  G  G    CCCAGGG
                                |||||||  |  |    |||||||
                                TTCGTCC  T  T    GGGTTTT
                                     CT GT GACTC
GAM390  D8S2298E  3'  CCTTAGAACTTTCCTTTCTGCC 20239          T    ACCCC_  G
            T                    AGGCAGGAGG GGAA     AGG
                                ||||||||||  ||||     |||
                                TCCGTCTTTC CTTT     TCC
                                      _    CAAGAT
GAM390  DAB2     3'  TGCTTTTCACTTTCTGTCT   9038             CCC
                                AGGCAGGAGGTGGAAA   CA
                                ||||||||||||||||   ||
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                                TCTGTCTTTCACTTTT  GT
                                      C__
GAM390  DAG1    3'  CCCTGGCTCTCTGCGTTTTGCC 16549       G TG  AACC
          T                    AGGCAGGA G  GA   CCAGGG
                               |||||||| |  ||   ||||||
                               TCCGTTTT C  CT   GGTCCC
                                   G GT  CTC_
GAM390  DAG1    5'  CTCTGGGACCAAGTCACTTGCT 16551       A __  AAAC
          T                    AGGCAGG GG  TGG   CCCAGGG
                               ||||||| ||  |||   |||||||
                               TTCGTTC CT  ACC   GGGTCTC
                                   A  GA  A___
GAM390  DAG1    3'  CTGATGTGTTTTTATTTCCTTC 16552    C         CC__  GG
          T                    AGG AGGAGGTGGAAAC   CAG
                               ||| ||||||||||||   |||
                               TCT TCCTTTATTTTTG   GTC
                                _          TGTA
GAM390  DBN1    3'  CCAGGGTTTTGACCCCTTCCTG 56017         T  AAA_______  CCAG
          TCT                   AGGCAGGAGG GG        CC   G
                               |||||||||| ||        ||   |
                               TCTGTCCTTC CC        GG   C
                                    _ CAGTTTT    GACC
GAM390  DBY     3'  GGCTCTTCCCCTCCTGCTT   17406         T   AC_____
                               AGGCAGGAGG GGAA      C
                               |||||||||| ||||      |
                               TTCGTCCTCC CCTT      G
                                    _   CTC   G
GAM390  DCK     3'  CCCCAGGGCCCACCTCTTACTT 7630          _  AA_______  CCAG
          CCTGCCT                AGGCAGGAGGT GGA       CC   GG
                               |||||||||||| |||       ||   ||
                               TCCGTCCTTCA TCT       GG   CC
                                     T  CCACCC    GACC
GAM390  DCK     3'  TCCTGAAAGCATTATTTTTTGT 7631           AAACCC
          T                    GGCAGGAGGTGG     CAGGG
                               ||||||||||||     |||||
                               TTGTTTTTTATT     GTCCT
                                     ACGAAA
GAM390  DCTN1   5'  TCCTGCCTAGGTTTCTACCTTT 15831    C         C___
          TCTCT                  AGG AGGAGGTGGAAACC   CAGGG
                               ||| ||||||||||||||   |||||
                               TCT TTTTCCATCTTTGG   GTCCT
                                 C          ATCC
GAM390  DDEF2   3'  TCTGTAGTTTTTTGTTTTTGTT 15290        GT    CC   G
          T                    AGGCAGGAG  GGAAAC  CAGG
                               |||||||||  ||||||  ||||
                               TTTGTTTTT  TTTTTG  GTCT
                                     GT     AT
GAM390  DDEF2   3'  TTTTGGCATTGTACTTTTTGTT 15293          G  ACC
          T                    AGGCAGGAGGTG AA   CCAGGG
                               |||||||||||| ||   ||||||
```

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                                TTTGTTTTTCAT TT   GGTTTT
                                      G  AC_
GAM390  DDX6    3'  CTTTGTGGGTTTTTCATCTTTT 16565          _  _
                                AGGAGGTGGAAA CCC CAGGG
                                |||||||||||| ||| |||||
                                TTTTCTACTTTT GGG GTTTC
                                      T   T
GAM390  DFNA5   3'  CTTGCATTCCACTTTTTGTT   16600           ACCC
                                GGCAGGAGGTGGAA   CAGG
                                ||||||||||||||   ||||
                                TTGTTTTTCACCTT   GTTC
                                       AC__
GAM390  DGAT2   3'  GGTTCTTTCACTTCCAGCTT   51777     A       AC_____
                                AGGC GGAGGTGGAA      C
                                |||| ||||||||||      |
                                TTCG CCTTCACTTT      G
                                  A        CTT   G
GAM390  DGCR2   3'  CCCTGGGCTCTTGCCTCCTGTT 18898         TG AAAC
                                GGCAGGAGG  G   CCCAGGG
                                |||||||||  |   |||||||
                                TTGTCCTCC  T   GGGTCCC
                                     GT CTC_
GAM390  DGCR2   3'  CTTTGGATCACTGTCTTCTCCT 18901     C     TG AAACC
                                AGG AGGAGG  G    CCAGGG
                                ||| ||||||  |    ||||||
                                TCC TCTTCT  C    GGTTTC
                                  _     GT ACTA_
GAM390  DIAPH2  3'  CTCTGTGGTTTATTTCTTTT   23005       TGG    C
                                AGGAGG   AAACC CAGGG
                                ||||||   ||||| |||||
                                TTTTCT   TTTGG GTCTC
                                   TTA    T
GAM390  DIAPH2  3'  CCAGGGCTTTCATTTTTTTCTG 24589         ___     AC___ CCAG
            TCT                   AGGCAGGAG   GTGGAA    C   G
                                |||||||||  ||||||    |   |
                                TCTGTCTTT   TACTTT    G   C
                                     TTT     C   G GACC
GAM390  DIO3    3'  CCCAGGGTTTTGTGTCTGTTTC 9069          TG  AA_________  CCAG
           CTGTC                  GGCAGGAGG  GA        CC    GG
                                |||||||||  ||        ||   ||
                                CTGTCCTTT  CT        GG    CC
                                     GT  GTGTTTT    GACC
GAM390  DIO3    3'  CCTGTTGCTTTTGTGTCT    9070       _    TG AAACCC
                                AGGCA GGAGG  G     CAGG
                                ||||| |||||  |     ||||
                                TCTGT TTTTC  T     GTCC
                                  G    GT _______
GAM390  DISC1   3'  TCCTGTGCCATTTGCCTTCTGC 38518         TG  AACCC
            T                   GGCAGGAGG  GA    CAGGG
                                |||||||||  ||    |||||
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                                TCGTCTTCC  TT    GTCCT
                                     GT  ACCGT
GAM390  DLEU1   3'  CCAGGGTTCTTTCCCTTTTTGC 20832         T    ________  CCA
             TT                   AGGCAGGAGG GGAAA      CC   G
                                  |||||||||| |||||      ||   |
                                  TTCGTTTTTC CCTTT      GG   C
                                       _    CTT   G  ACC
GAM390  DLEU1   3'  CTTTGTATTTCATCTCTTTCT  20833     C        ACCC
                                  AGG AGGAGGTGGAA    CAGGG
                                  ||| ||||||||||    |||||
                                  TCT TTCTCTACTTT    GTTTC
                                    _         AT__
GAM390  DLG4    3'  CCAGGGTTTTTTCCACTTTTTT 9079      C        A_______  CCAG
             TCT                    AGG AGGAGGTGGAA      CC    G
                                  ||| ||||||||||       ||    |
                                  TCT TTTTTCACCTT      GG    C
                                    T         TTTT     GACC
GAM390  DLG4    5'  TCCTGAACATTCCCTTCTGTCT 9090          T   AACCC
                                  AGGCAGGAGG GGA     CAGGG
                                  |||||||||| |||     |||||
                                  TCTGTCTTCC CTT     GTCCT
                                       _   ACAA_
GAM390  DLX2    3'  CCCTCCTTTTTATTTTTTCCT  16604     C        CCCC
                                  AGG AGGAGGTGGAAA   AGGG
                                  ||| ||||||||||||   ||||
                                  TCC TTTTTTATTTTT    TCCC
                                    _         CC__
GAM390  DNAJB1  3'  TCCTGGAGAATTCTGTCTTCTC 21567     C     TG   ACC_
             TT                    AGG AGGAGG  GAA    CCAGGG
                                  ||| ||||||  |||    ||||||
                                  TTC TCTTCT  CTT    GGTCCT
                                    _     GT   AAGA
GAM390  DPYSL3  3'  CTCTGGGGGAACTTTGTGTCT  9124       G    GGAAA
                                  AGGCA GAGGT    CCCCAGGG
                                  ||||| |||||    ||||||||
                                  TCTGT TTTCA    GGGGTCTC
                                     G    AG___
GAM390  DRIL1   3'  CTGTGTGTTTTCATTTTTGTCT 19078         G      CC_
                                  AGGCAGGAG TGGAAAC   CAG
                                  |||||||| |||||||   |||
                                  TCTGTTTTT ACTTTTG   GTC
                                       _      TGT
GAM390  DSC1    5'  TCCTACTGTTTATCACTTGCCT 18244        A     AACCCC
                                  AGGCAGG GGTGGA     AGGG
                                  ||||||| ||||||     ||||
                                  TCCGTTC CTATTT     TCCT
                                     A     GTCA__
GAM390  DUSP5   3'  CCAGGGCTTTTTTTTCTTTTTG 16630         T   A_______  CCAG
             TCT                    AGGCAGGAGG GGAA      CC    G
                                  |||||||||| ||||      ||    |
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                                TCTGTTTTTC TTTT      GG    C
                                      T    TTTC     GACC
GAM390  EBAF     3'  CCCTGTGTCCTTCCATTTCCTG 66026              ACCC_
            TCT                   AGGCAGGAGGTGGAA     CAGGG
                                  ||||||||||||||     |||||
                                  TCTGTCCTTTACCTT     GTCCC
                                        CCTGT
GAM390  EBAF     3'  CTTTGGCTCGTCATTTCCTCTT 66030     C        AAACC
                                  AGG AGGAGGTGG     CCAGGG
                                  ||| |||||||||     ||||||
                                  TTC TCCTTTACT     GGTTTC
                                    _       GCTC_
GAM390  EBP      5'  CCCCAGGGTTTTTTTTTAACTT 22700          _     A________  CCAG
            CCTGCCT                  AGGCAGGAGG TGGAA       CC    GG
                                  |||||||||| |||||       ||    ||
                                  TCCGTCCTTC ATTTT       GG    CC
                                        A     TTTTT     GACC
GAM390  EDAR     3'  CCTTGGGCCTTGTCTTTTCCT  42524     C      TG AAAC
                                  AGG AGGAGG  G    CCCAGGG
                                  ||| ||||||  |    |||||||
                                  TCC TTTTCT  T    GGGTTCC
                                    _     GT CC__
GAM390  EFG2     5'  CTTTGGCGCGGCTCGCGCCTCC 51481           _  AA  ___
            TGCTT                    AGGCAGGAGGTG GA  CC   CCAGGG
                                  ||||||||||||  ||  ||   ||||||
                                  TTCGTCCTCCGC CT  GG   GGTTTC
                                         G  C_  CGC
GAM390  EFNB1    3'  GGAAGGGTTTTTGTTTTTGTTT 16672         G TG       CAGGG
                                  AGGCAGGA G  GAAACCC
                                  ||||||||  |  |||||||
                                  TTTGTTTT T  TTTTGGG
                                       _ GT      AAGGC
GAM390  EGLN1    5'  CTCTGAATTTCCGTTTCCTCCT 42148     C    GG     CCC
                                  AGG AGGA  TGGAAA   CAGGG
                                  ||| ||||  ||||||   |||||
                                  TCC TCCT  GCCTTT   GTCTC
                                    _    TT      AA_
GAM390  EHD2     3'  CCAGGGTTCTGCTCCGCTTCCT 28220     C        AA________  CCAG
            CCT                    AGG AGGAGGTGGA        CC    G
                                  ||| ||||||||||        ||    |
                                  TCC TCCTTCGCCT        GG    C
                                    _         CGTCTT     GACC
GAM390  EHD4     3'  CCCCAGGGTTTTATTTTGTTTT 58363          TG   A________  CCAG
            CTGCT                    GGCAGGAGG  GAA       CC    GG
                                  |||||||||  |||       ||    ||
                                  TCGTCTTTT  TTT       GG    CC
                                       GT   ATTTT     GACC
GAM390  EHHADH   3'  TTCTGGTCTTTCCTCTTCTGTT 10502          T     CC
            T                     AGGCAGGAGG GGAAA  CCAGGG
                                  |||||||||| |||||  ||||||
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                                TTTGTCTTCT CCTTT  GGTCTT
                                      _    CT
GAM390  EIF1A    3'  CCCAGGGTTTTGTTTTTGTTTT 90005         TG   ________  CAG
            TTGTTT                AGGCAGGAGG  GAAAC      CC   GG
                                  ||||||||||  |||||      ||   ||
                                  TTTGTTTTTT  TTTTG      GG   CC
                                       GT     TTTT     GAC
GAM390  EIF1A    3'  GGTCCTTTTTATCTTTGCTT   90008       G      A_______
                                  AGGCAG AGGTGGAA      CC
                                  ||||||| ||||||||      ||
                                  TTCGTT TCTATTTT      GG
                                      _       TCCT
GAM390  EIF2C1   3'  CCCCAGGGCTTTGTACCACTGT 25185         _     AAA________  CCAG
            TTTGCCT                AGGCAGGA GGTGG        CC    GG
                                  ||||||||| |||||        ||    ||
                                  TCCGTTTT TCACC        GG    CC
                                       G    ATGTTTC     GACC
GAM390  EIF2C1   3'  CCTTGACTGTTCATTTTTTTCC 25186     C        AACCC
            T                     AGG AGGAGGTGGA     CAGGG
                                  ||| ||||||||||     |||||
                                  TCC TTTTTTACTT     GTTCC
                                    T        GTCA_
GAM390  EIF4EBP2 3'  CTCTGGGAGGAATGTCTTCTGT 15856         GT GAAAC
            CT                     AGGCAGGAG  G    CCCAGGG
                                  |||||||||  |    |||||||
                                  TCTGTCTTC  T    GGGTCTC
                                       TG AAGGA
GAM390  EIF4EBP2 3'  TTTGTTCTGTTTTCTGCC    15860         TG   ACCC
                                  GGCAGGAGG  GAA    CAGG
                                  |||||||||  |||    ||||
                                  CCGTCTTTT  CTT    GTTT
                                       GT   _____
GAM390  EIF4EBP2 3'  TTTTGAGGTCCACTTCCTTTCT 15861     C        AA  C
                                  AGG AGGAGGTGGA  CC CAGGG
                                  ||| ||||||||||  || |||||
                                  TCT TCCTTCACCT  GG GTTTT
                                    T        __ A
GAM390  EIF4G1   5'  TTCTGGCACCTACCTACCTGCT 18258       _     AAACC
            T                      AGGCAGG AGGTGG     CCAGGG
                                  |||||||| ||||||     ||||||
                                  TTCGTCC TCCATC     GGTCTT
                                      A      CAC__
GAM390  ELL      3'  CCTTGGGGTGGCGCGCCTGCCT 22556        AG   GAA
                                  AGGCAGG  GTG   ACCCCAGGG
                                  |||||||  |||   |||||||||
                                  TCCGTCC  CGC   TGGGGTTCC
                                      G_   GG_
GAM390  ELMO2    3'  TTCTGGTGCCTTGTCTTTTGCT 42245          TG AAACC
            T                      AGGCAGGAGG  G    CCAGGG
                                  ||||||||||  |    ||||||
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                                TTCGTTTTCT  T    GGTCTT
                                      GT CCGT_
GAM390  ELOVL4   5'  CTCTGGGTCTCCGCTTTCTCCT 42990    C       AAC
                                AGG AGGAGGTGGA   CCCAGGG
                                ||| ||||||||||   |||||||
                                TCC TCTTTCGCCT   GGGTCTC
                                  _       CT_
GAM390  EN2     3'  CCAGGGTCACTTTTTGTCT   9252           AAA  CCAG
                                AGGCAGGAGGTGG   CC   G
                                ||||||||||||   ||   |
                                TCTGTTTTTCACT   GG   C
                                          GACC
GAM390  EN2     3'  CCCCAGGGTCTTATCATCACTT 9253           AAA_________  CCAG
            TTTGTCT                 AGGCAGGAGGTGG        CC   GG
                                ||||||||||||         ||   ||
                                TCTGTTTTTCACT        GG   CC
                                       ACTATTCT    GACC
GAM390  EN2     3'  GGTTTCTGTTTTTTGTTT    9267         TG
                                AGGCAGGAGG  GAAACC
                                ||||||||||  ||||||
                                TTTGTTTTTT  CTTTGG
                                      GT
GAM390  ENO2    3'  TCCGCACTTTCCACTTCTTCCT 10521    C        CCCCA
                                AGG AGGAGGTGGAAA    GGG
                                ||| ||||||||||||    |||
                                TCC TTCTTCACCTTT    CCT
                                  _         CACG_
GAM390  EPB41L2  3'  TTTTGGTTTTGTTTTCTGTTT  9296         TG   ACC
                                AGGCAGGAGG  GAA   CCAGGG
                                ||||||||||  |||   ||||||
                                TTTGTCTTTT  TTT   GGTTTT
                                      GT  ___
GAM390  EPHB4    3'  CCCCGTTCCCTTTTTGTTT    16708         T    ACCCCA
                                AGGCAGGAGG GGAA     GGG
                                |||||||||| ||||     |||
                                TTTGTTTTTC CCTT     CCC
                                      _   GC_____
GAM390  EPM2A    3'  TTTTGGAATAAACTGTCTTTTT 20238    C     TG AAACC_
            CCT                   AGG AGGAGG  G     CCAGGG
                                ||| ||||||  |     ||||||
                                TCC TTTTCT  C     GGTTTT
                                  T     GT AAATAA
GAM390  ESD     5'  TCTTGAGCCCCGCCTTTTACTT 93400    C       AAACCC
                                AGG AGGAGGTGG     CAGGG
                                ||| |||||||||     |||||
                                TTC TTTTCCGCC     GTTCT
                                  A       CCGA__
GAM390  ESR1    3'  TCCTGAAGCTCTGCCTCTGGCT 5519      A    TG  AACCC
            T                    AGGC GGAGG  GA    CAGGG
                                |||| |||||  ||    |||||
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                                TTCG TCTCC  CT    GTCCT
                                  G    GT  CGAA_
GAM390  ESRRBL1  3'  CCAGGGCCTATTTTTACTTCCT 36323    C        A_______  CCAG
            TCT                   AGG AGGAGGTGGAA       CC    G
                                  ||| ||||||||||       ||    |
                                  TCT TCCTTCATTTT       GG    C
                                    _         TATCC     GACC
GAM390  ETS2    3'  TTTTGGGGGGTTTTCTTGCCT  19120         GTG  AA
                                  AGGCAGGAG   GA  CCCCAGGG
                                  |||||||||   ||  ||||||||
                                  TCCGTTCTT   TT  GGGGTTTT
                                       ___  GG
GAM390  ETV5    3'  CCTTGTTGCCTGCTTTGTGCTT 16727      G    TG A_   CCC
                                  AGGCA GAGG  G  AAC   AGG
                                  ||||| ||||  |  |||   |||
                                  TTCGT TTTC  C  TTG   TCC
                                     G    GT CG   T__
GAM390  ETV5    3'  CTTTGGGGTTTGTTTGTTTGCT 16728        AGGTGG
            T                      AGGCAGG     AAACCCCAGGG
                                  |||||||      ||||||||||
                                  TTCGTTT     TTTGGGGTTTC
                                      GTTTG_
GAM390  EXTL3   3'  CCAGGGCCACTTTCCACTCCCT 9332         A      A_______  CCAG
            GCTT                    AGGCAGG GGTGGAA       CC    G
                                  ||||||| |||||||       ||    |
                                  TTCGTCC TCACCTT       GG    C
                                      C      TCACC     GACC
GAM390  F2RL3   3'  CCTTCTTTTCACTTTCTGTC   15510            CCCC
                                  GGCAGGAGGTGGAAA    AGG
                                  ||||||||||||||    |||
                                  CTGTCTTTCACTTTT    TCC
                                           CT__
GAM390  F8      3'  CCTGGCTTGCCTTCTACCT    5527      C     TG AAACC
                                  AGG AGGAGG  G     CCAGG
                                  ||| ||||||  |     |||||
                                  TCC TCTTCC  T     GGTCC
                                    A     GT C____
GAM390  FAAH    3'  CCTTGGTGACCCACTTCTTCCT 97236     C        AAACC
                                  AGG AGGAGGTGG     CCAGGG
                                  ||| |||||||||     ||||||
                                  TCC TTCTTCACC     GGTTCC
                                    _        CAGT_
GAM390  FACL2   3'  CCTTGGGGTTTTGAATGTTTGC 41209        AGGTG
            TT                     AGGCAGG    GAAACCCCAGGG
                                  |||||||     ||||||||||||
                                  TTCGTTT     TTTTGGGGTTCC
                                      GTAAG
GAM390  FACL5   5'  CTCTGGGCCGGCCTTCTGCCT  64859          _  AAAC
                                  AGGCAGGAGGT GG    CCCAGGG
                                  |||||||||| ||    |||||||
```

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                                TCCGTCTTCCG CC    GGGTCTC
                                      G _____
GAM390  FANCG    5'  TCCTAAGTCCGCTTCTGGTCT  17337      A       AACCCC
                                AGGC GGAGGTGGA     AGGG
                                |||| |||||||||      ||||
                                TCTG TCTTCGCCT     TCCT
                                  G        GAA___
GAM390  FCAR     3'  TTCTGATTTTTTATATCCTGTT 56587        G      CCC
              T                  AGGCAGGA GTGGAAA   CAGGG
                                |||||||| |||||||   |||||
                                TTTGTCCT TATTTTT   GTCTT
                                     A      TA_
GAM390  FCMD     3'  CCCCAGGGCTCATTTCTACTTT 23032     _         A________  CCAG
              CTGCCCT                 AGG CAGGAGGTGGAA       CC    GG
                                ||| ||||||||||||       ||    ||
                                TCC GTCTTTCATCTT       GG    CC
                                  C          TACTC     GACC
GAM390  FGA      3'  CCTTGGGGGCAGGGCCTTTGTC 41850       G    GGAAA
              T                  AGGCAG AGGT     CCCCAGGG
                                |||||| ||||     ||||||||
                                TCTGTT TCCG     GGGGTTCC
                                   _   GGACG
GAM390  FGA      3'  TCCTGGTGGTCTTGCCTTCTG  41851        TG AA  _
                                CAGGAGG  G  ACC CCAGGG
                                |||||||  |  ||| ||||||
                                GTCTTCC  T  TGG GGTCCT
                                    GT C_  T
GAM390  FGF2     3'  TTTGGGGTCAGCTCTT      10624       G  GAA
                                AGGAG TG   ACCCCAGG
                                ||||| ||   ||||||||
                                TTCTC AC   TGGGGTTT
                                  G  ___
GAM390  FGF23    3'  CCAGGGTTCTGTTTTCATTTCC 40556            ________  CAG
              TGTT                  GGCAGGAGGTGGAAAC      CC   GG
                                |||||||||||||||      ||   ||
                                TTGTCCTTTACTTTTG      GG   CC
                                         TCTT     GAC
GAM390  FGF23    3'  TTTTGGCCCCATCTCTGGTTT  40560      A       AAACC
                                AGGC GGAGGTGG     CCAGGG
                                |||| ||||||||     ||||||
                                TTTG TCTCTACC     GGTTTT
                                  G       CC___
GAM390  FGF5     3'  GGCTCTCTTCACTTCCTTCT   53661     C        AA_______
                                AGG AGGAGGTGGA       CC
                                ||| ||||||||||       ||
                                TCT TCCTTCACTT       GG
                                  _        CTCTC
GAM390  FGF5     3'  GGCTCTCTTCACTTCCTTCT   53662     C        AA_______
                                AGG AGGAGGTGGA       CC
                                ||| ||||||||||       ||
```

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                                TCT TCCTTCACTT       GG
                                  _        CTCTC
GAM390  FGF7     3'  CAGGGTCCTATTCACCTTTTGT 10628           AA_______ CCAG
              TT                  AGGCAGGAGGTGGA       CC    G
                                  ||||||||||||||       ||    |
                                  TTTGTTTTCCACTT       GG    C
                                         ATCCT     GAC
GAM390  FGF7     3'  CTTTGGCATGTTTTTGTTTTTT 10631       TG    C__
                                  AGGAGG  GAAAC   CCAGGG
                                  ||||||  |||||   ||||||
                                  TTTTTT  TTTTG   GGTTTC
                                     GT     TAC
GAM390  FGFR2    3'  CTCTGGCAGCTGGCCTTCTGCT 43772          GGAAACC
              T                   AGGCAGGAGGT      CCAGGG
                                  ||||||||||       ||||||
                                  TTCGTCTTCCG      GGTCTC
                                        GTCGAC_
GAM390  FGFR2    3'  CTCTGGCAGCTGGCCTTCTGCT 43773          GGAAACC
              T                   AGGCAGGAGGT      CCAGGG
                                  ||||||||||       ||||||
                                  TTCGTCTTCCG      GGTCTC
                                        GTCGAC_
GAM390  FGFRL1   3'  CCTTGGCGGCTATTTTTGCCAC 41910        A  TG   ___  _
              CTGCCT                 AGGCAGG GG  GAAA   CC CCAGGG
                                  |||||||  ||  ||||   ||  ||||||
                                  TCCGTCC CC  TTTT   GG GGTTCC
                                     A  GT    ATC  C
GAM390  FKBP1B   3'  CCCCAGGGCTTTGCTGTCACTT 15924     C       AAA_________ CCAG
              TCTCTCT                AGG AGGAGGTGG         CC    GG
                                  |||  |||||||||          ||    ||
                                  TCT TCTTTCACT         GG    CC
                                    C        GTCGTTTC     GACC
GAM390  FKBP1B   3'  CCCCAGGGCTTTGCTGTCACTT 15925     C       AAA_________ CCAG
              TCTCTCT                AGG AGGAGGTGG         CC    GG
                                  |||  |||||||||          ||    ||
                                  TCT TCTTTCACT         GG    CC
                                    C        GTCGTTTC     GACC
GAM390  FLOT2    3'  TCCTGTCTGTCCACCTCCTCCT 16801     C       AACCC
                                  AGG AGGAGGTGGA     CAGGG
                                  |||  ||||||||||    |||||
                                  TCC TCCTCCACCT     GTCCT
                                    _        GTCT_
GAM390  FLRT2    3'  CCAGGGTTTGCTTCTGGTTTCT 25994          G     AC_______ CCAG
              GTTT                   AGGCAGGAG TGGAA        C    G
                                  |||||||||  |||||        |    |
                                  TTTGTCTTT GTCTT        G    C
                                       G     CGTTT   G GACC
GAM390  FMOD     3'  CTCTGGGCTCCCATTTGTTGCT 10672        G     AAAC
              T                   AGGCAG AGGTGG    CCCAGGG
                                  ||||||  ||||||    |||||||
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                                TTCGTT TTTACC   GGGTCTC
                                   G     CTC_
GAM390  FMR2    3' CCAGGGTTCTGAACCACCTTTT 10686    C       AAA_______  CCAG
            CTT                   AGG AGGAGGTGG        CC   G
                                ||| |||||||||        ||   |
                                TTC TTTTCCACC        GG   C
                                  _       AAGTCTT    GACC
GAM390  FMR2    3' CTCTGGCTCTGGCTTTTGCTT  10689        G   AACC
                                AGGCAGGAG TGGA   CCAGGG
                                ||||||||| ||||   ||||||
                                TTCGTTTTC GTCT   GGTCTC
                                     G   C___
GAM390  FMR2    3' CTTTGGTTATGTTTGTTTTTAT 10692      _    TG  AACC_
            GCTT                   AGGCA GGAGG  GA    CCAGGG
                                ||||| |||||  ||    ||||||
                                TTCGT TTTTT  TT    GGTTTC
                                   A    GT  GTATT
GAM390  FMR2    3' TTATAGGTTTTCTGTTTTCTAC 10702    C     TG   C  CAGGG
            TT                   AGG AGGAGG  GAAA CC
                                ||| ||||||  |||| ||
                                TTC TCTTTT  CTTT GG
                                  A     GT   T  ATATTC
GAM390  FMR2    3' TTCTGGCCCTTCTGTCTTTTGC 10703         TG   ACC
            CT                   AGGCAGGAGG  GAA   CCAGGG
                                |||||||||  |||   ||||||
                                TCCGTTTTCT  CTT   GGTCTT
                                     GT   CCC
GAM390  FMR2    3' TTCTGTTTTCTACTTTCT    10704          CCC
                                AGGAGGTGGAAA   CAGGG
                                ||||||||||||   |||||
                                TCTTTCATCTTT   GTCTT
                                       T__
GAM390  FNTB    3' CCAGGGCTCTAATTCCCTTTTG 10712         T   AA_______  CCAG
            CTT                   AGGCAGGAGG GGA       CC   G
                                |||||||||| |||       ||   |
                                TTCGTTTTCC CTT       GG   C
                                     _  AATCTC    GACC
GAM390  FOSB    3' CCCCAGGGTTTTGTCCTGCCTC 23055          _  AA______  CCAG
            TTGTTT                AGGCAGGAGGT GGA      CC   GG
                                |||||||||| |||      ||   ||
                                TTTGTTCTCCG CCT      GG   CC
                                      T  GTTTT    GACC
GAM390  FPRL1   3' CCCAGGGTTTTGTTTTTTGACT 9393         GT_    _______  CAG
            TCTGCCT               AGGCAGGAG  GGAAAC     CC  GG
                                |||||||||  ||||||     ||  ||
                                TCCGTCTTC  TTTTTG     GG  CC
                                     AGT     TTTT    GAC
GAM390  FRAT2   3' CCCTCACAATTTATTTCCTCCT 24900    C       AACCCC
                                AGG AGGAGGTGGA     AGGG
                                ||| ||||||||||     ||||
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                                TCC TCCTTTATTT     TCCC
                                  _        AACAC_
GAM390  FRDA    3'  GGTTTTTTTTATTCCTGCTT  5572         G    A_______
                                AGGCAGGAG TGGAA      CC
                                ||||||||| |||||      ||
                                TTCGTCCTT ATTTT      GG
                                     _    TTTT
GAM390  FVT1    3'  CCAGGGCTCTCTCTGTCTCTCT 10731       _   TG  AA_______  CCAG
          GTCT                    AGGCAG GAGG  GA       CC    G
                                |||||| ||||  ||       ||   |
                                TCTGTC CTCT  CT       GG    C
                                   T   GT  CTCTC    GACC
GAM390  FVT1    3'  CTCTGTCTCTCTGTCTCTCTGT 10732       _   TG  AACCC
          CT                      AGGCAG GAGG  GA     CAGGG
                                |||||| ||||  ||     |||||
                                TCTGTC CTCT  CT     GTCTC
                                   T   GT  CTCT_
GAM390  FVT1    3'  CTCTGTCTCTCTGTCTCTCTGT 10733       _   TG  AACCC
          CT                      AGGCAG GAGG  GA     CAGGG
                                |||||| ||||  ||     |||||
                                TCTGTC CTCT  CT     GTCTC
                                   T   GT  CTCT_
GAM390  FVT1    3'  CTCTGTCTCTCTGTCTCTCTGT 10734       _   TG  AACCC
          CT                      AGGCAG GAGG  GA     CAGGG
                                |||||| ||||  ||     |||||
                                TCTGTC CTCT  CT     GTCTC
                                   T   GT  CTCT_
GAM390  GAB2    3'  GGCTTTTTCATTCCTGTTT   25461         G    A_____
                                AGGCAGGAG TGGAA     CC
                                ||||||||| |||||     ||
                                TTTGTCCTT ACTTT     GG
                                     _    TTC
GAM390  GAB2    3'  TCCTCCCATCCACCTCCTCTCT 25466     C        AACCCC
                                AGG AGGAGGTGGA     AGGG
                                ||| ||||||||||     ||||
                                TCT TCCTCCACCT     TCCT
                                  C        ACCC__
GAM390  GABRE   3'  CCTTGCTGGCTCCATCTTTCGT 18281     AG       AA  C_
          CT                      AGGC  GAGGTGGA  CC  CAGGG
                                ||||  ||||||||  ||  |||||
                                TCTG  TTCTACCT  GG  GTTCC
                                  CT       C_  TC
GAM390  GCH1    3'  GGTCCTCTCTACTTCTGTTT   5679        G     AA_______
                                AGGCAG AGGTGGA       CC
                                |||||| |||||||       ||
                                TTTGTC TTCATCT       GG
                                   _      CTCCT
GAM390  GDI1    3'  CTGTTTTGTTTCTTGTCT    60641         TG   ACCC   GG
                                AGGCAGGAGG  GAA    CAG
                                ||||||||||  |||    |||
```

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                                TCTGTTCTTT  TTT   GTC
                                     GT  ____  G
GAM390  GGPS1   3'  CCCCAGGGCTTTTTTTTGTCTT 17905    _   GT   A_______  CCAG
           TTAGCCT                AGGC AGGAG  GGAA     CC   GG
                                |||| |||||  ||||      ||   ||
                                TCCG TTTTC  TTTT      GG   CC
                                  A   TG   TTTTC   GACC
GAM390  GJB3    5'  CCTTGAATCCACCTCTTGTTT  43993          AACCC
                                AGGCAGGAGGTGGA   CAGGG
                                ||||||||||||||   |||||
                                TTTGTTCTCCACCT   GTTCC
                                      AA___
GAM390  GLO1    3'  TCTGGGGTTTCAATTCCT   22963     GTG
                                AGGAG  GAAACCCCAGG
                                |||||  ||||||||||
                                TCCTT  CTTTGGGGTCT
                                  AA_
GAM390  GLS     3'  CTTTCATTTTCACTTCCAGTCT 30472     A       CCCC
                                AGGC GGAGGTGGAAA   AGG
                                |||| ||||||||||   |||
                                TCTG CCTTCACTTTT   TTC
                                  A        ACT_
GAM390  GLTSCR1  3'  CCCTGACGGTTTTTCTTGCCT  32300       GGTG    C_
                                AGGCAGGA   GAAACC  CAGGG
                                ||||||||   ||||||  |||||
                                TCCGTTCT   TTTTGG  GTCCC
                                     ____     CA
GAM390  GM2A    3'  CCAGGGCTAATTTTTATTTCCT 68377    C       A_______  CCAG
           TTCT                  AGG AGGAGGTGGAA      CC   G
                                ||| ||||||||||       ||   |
                                TCT TCCTTTATTTT      GG   C
                                  T        TAATC    GACC
GAM390  GNAI3   3'  TTCTGGAAATACTGTCTTCTGT 22446        TG AAACC
           TT                   AGGCAGGAGG  G    CCAGGG
                                ||||||||||  |    ||||||
                                TTTGTCTTCT  C    GGTCTT
                                     GT ATAAA
GAM390  GNAZ    3'  GCTCTGGCATTTTTTTTTGTTT 10828        TG   CC____
           TTTGTTT                AGGCAGGAGG  GAAA    CCAGGG  C
                                ||||||||||  ||||    ||||||  |
                                TTTGTTTTTT  TTTT    GGTCTC  G
                                     GT   TTTTAC
GAM390  GNB1    3'  CAGGGCTTTGTTTTCTTTTTTG 10834        T    _______  CAG
           TCT                   AGGCAGGAGG GGAAAC     CC  G
                                ||||||||||  ||||||     ||  |
                                TCTGTTTTTT CTTTTG     GG  C
                                     _    TTTC    GAC
GAM390  GNB1    3'  CCCTGGTTTTTAATTTTCTGTC 10836        GG  CC
           T                    AGGCAGGAGGT  AAA  CCAGGG
                                ||||||||||  |||  ||||||
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                                TCTGTCTTTTA  TTT  GGTCCC
                                      A_   TT
GAM390  GNB1    3'  CCCTTTCCACCTTTTGT     10837           ACCCC
                                GCAGGAGGTGGAA    AGGG
                                ||||||||||||    ||||
                                TGTTTTCCACCTT    TCCC
                                       _____   C
GAM390  GNE     3'  GGTGTTTTCACTTTTGGTCT   19677     AG        ____
                                AGGC  GAGGTGGAAAC   CC
                                ||||  ||||||||||   ||
                                TCTG  TTTCACTTTTG   GG
                                  GT         T
GAM390  GPC4    3'  GGTTCTGTCTCTTCCTGCTT   9355          T   AA_______
                                AGGCAGGAGG GGA       CC
                                |||||||||| |||       ||
                                TTCGTCCTTC TCT       GG
                                      _   GTCTT
GAM390  GPC4    3'  TTTTGGGATCCCAGTTTTTGTT 9358          G   AAAC
            T                    AGGCAGGAG TGG    CCCAGGG
                                |||||||||| |||    |||||||
                                TTTGTTTTT ACC    GGGTTTT
                                      G   CTA_
GAM390  GPR30   5'  TCCTGGGGAGTTTCCTGTCT   9494         GG GGAAA
                                AGGCAGGA  T    CCCCAGGG
                                ||||||||  |    ||||||||
                                TCTGTCCT  G    GGGGTCCT
                                     TT A____
GAM390  GPR4    5'  CCCTGCAAACCATCTCCTTCT  60576     C       AAACCC
                                AGG AGGAGGTGG     CAGGG
                                ||| |||||||||     |||||
                                TCT TCCTCTACC     GTCCC
                                  _       AAAC__
GAM390  GPR63   3'  TTTTGGGGTTTTTCCTT     48627     T
                                GAGG GGAAACCCCAGGG
                                |||| ||||||||||||
                                TTCC TTTTTGGGGTTTT
                                  _
GAM390  GPR81   5'  CCCTGGGTCTCTCATTTCCTGG 51744    G       _  AAC
            CT                    AG CAGGAGGTG GA   CCCAGGG
                                || |||||||| ||   |||||||
                                TC GTCCTTTAC CT   GGGTCCC
                                 G       T  CT_
GAM390  GRAF    3'  TCTGCTCCCACCCTTGCCT   31250        A    AAACCC
                                AGGCAGG GGTGG     CAGG
                                |||||||| |||||     ||||
                                TCCGTTC CCACC     GTCT
                                     _    CTC___
GAM390  GRB7    3'  CCCCAGGGTTCTCCTCTGCTTC 19190       _   TG  AA________  CCAG
            TTTGCCT                 AGGCAG GAGG  GA       CC   GG
                                |||||| ||||  ||       ||   ||
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                                TCCGTT CTTC  CT       GG    CC
                                   T   GT  CCTCTT    GACC
GAM390  GRF2    3'  GTCCTTTCACTTTCCGCTT   19200     A       AC_____
                                AGGC GGAGGTGGAA      C
                                |||| ||||||||||      |
                                TTCG CTTTCACTTT      G
                                  C        CCT   G
GAM390  GRF2    5'  TTCTGGGCACCGCCTTCTGCT  19203          AAAC
                                GGCAGGAGGTGG   CCCAGGG
                                ||||||||||||   |||||||
                                TCGTCTTCCGCC   GGGTCTT
                                       AC__
GAM390  GRF2    3'  TTCTGGTTTGGTTTTGTTTTCT 19204         TG  A ___
            GCTT                   AGGCAGGAGG  GAA CC   CCAGGG
                                |||||||||  ||| ||   ||||||
                                TTCGTCTTTT  TTT GG   GGTCTT
                                      GT   _  TTT
GAM390  GRINL1A  3'  CCAGGGTCTTCTCCTTTTTCTG 70060         T   AA_______  CCAG
            TCT                   AGGCAGGAGG GGA       CC    G
                                |||||||||| |||       ||    |
                                TCTGTCTTTT CCT       GG    C
                                      T   CTTCT    GACC
GAM390  GRINL1A  3'  CCAGGGTTTTTTCTGTTGCTTG 70061        A  TG   A_______  CCAG
            CTT                   AGGCAGG GG  GAA      CC    G
                                ||||||| ||  |||      ||    |
                                TTCGTTC TT  CTT      GG    C
                                   G  GT   TTTT    GACC
GAM390  GRLF1   3'  CCTTGGTTTTGCTTCCTGCT   79257         TG   ACC
                                GGCAGGAGG  GAA   CCAGGG
                                |||||||||  |||   ||||||
                                TCGTCCTTC  TTT   GGTTCC
                                      GT   ___
GAM390  GRM4    3'  TTCTGGCTCTTGCCTCCGCCT  7754       A     TG AAACC
                                AGGC GGAGG  G    CCAGGG
                                |||| |||||  |    ||||||
                                TCCG CCTCC  T    GGTCTT
                                  _    GT CTC__
GAM390  GRM6    3'  CTCTCCTTTCTTCCTCTTGCCT 7765          T    CCCC
                                AGGCAGGAGG GGAAA    AGGG
                                |||||||||| |||||    ||||
                                TCCGTTCTCC TCTTT    TCTC
                                      T    CC__
GAM390  GSTM5   3'  CCCTGGACCTGCCTTCTTCCT  7799      C     TG AAACC
                                AGG AGGAGG  G    CCAGGG
                                ||| ||||||  |    ||||||
                                TCC TCTTCC  C    GGTCCC
                                  T     GT CA___
GAM390  HADH2   3'  CCCTGGGGTACTACTCTCCAGC 16895      A   _   AA
            TT                    AGGC GGAG GTGG  ACCCCAGGG
                                |||| |||| ||||  |||||||||
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                                TTCG CCTC CATC  TGGGGTCCC
                                  A   T   A_
GAM390  HCFC1    3'  CCCTGCCCTCTGCCCTTTTGCC 71546        _ TG  AACCC
             T                   AGGCAGGAG G  GA    CAGGG
                                 ||||||||| |  ||    |||||
                                 TCCGTTTTC C  CT    GTCCC
                                     C GT  CCC__
GAM390  HD       3'  CCCTGGACCAGCCTCCTGTTT  10910         _  AAACC
                                 AGGCAGGAGG TGG    CCAGGG
                                 |||||||||| |||    ||||||
                                 TTTGTCCTCC ACC    GGTCCC
                                     G   A____
GAM390  HD       3'  CCTGGGGTGGCGTCTGCCT   10912       AG  GGAA
                                 AGGCAGG  GT   ACCCCAGG
                                 |||||||  ||   ||||||||
                                 TCCGTCT  CG   TGGGGTCC
                                    G_  G___
GAM390  HDAC4    3'  TCTTGTCTGTCTGTCTCTGTCT 21254      G   TG  AACCC
                                 AGGCAG AGG  GA    CAGGG
                                 ||||||| |||  ||    |||||
                                 TCTGTC TCT  CT    GTTCT
                                    _  GT  GTCT_
GAM390  HIVEP2   3'  TCTTGTATATTTTTTTGTCTCT 23076         TG   CCC___
             TGTTT                AGGCAGGAGG  GAAA    CAGGG
                                  |||||||||  ||||     |||||
                                  TTTGTTCTCT  TTTT    GTTCT
                                      GT   TTATAT
GAM390  HLA-DRA  3'  CCCTGTCTATTGCCTTTTCCT  68519    C     TG AAACCC
                                 AGG AGGAGG  G     CAGGG
                                 ||| ||||||  |     |||||
                                 TCC TTTTCC  T     GTCCC
                                   _     GT ATCT__
GAM390  HLA-DRA  3'  CCCTGTCTATTGCCTTTTCCT  68520    C     TG AAACCC
                                 AGG AGGAGG  G     CAGGG
                                 ||| ||||||  |     |||||
                                 TCC TTTTCC  T     GTCCC
                                   _     GT ATCT__
GAM390  HLF      3'  CCAGGGCCCTCCTTCACTCCTG 10932        GT__   AA____  CCAG
             CCT                   AGGCAGGAG   GGA    CC   G
                                   |||||||||   |||    ||   |
                                   TCCGTCCTC   CCT    GG   C
                                       ACTT   CCC    GACC
GAM390  HMG20A   3'  CTCTGGGGGTTATTTTTGCTT  37064        GTGGAAA
                                 AGGCAGGAG      CCCCAGGG
                                 |||||||||      ||||||||
                                 TTCGTTTTT      GGGGTCTC
                                     ATTG___
GAM390  HMG20A   3'  TTCTGGAGTTTTGTTTTTTCCT 37073       TG__    C
                                 AGGAGG   GAAAC CCAGGG
                                 ||||||   ||||| ||||||
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                                TCCTTT   TTTTG GGTCTT
                                   TTTG    A
GAM390  HOXA7   3'  CAGGGTTCTGCTCACTTCTTGC 23555          AAA_____ CCAG
           T                    GGCAGGAGGTGG       CC   G
                                ||||||||||||       ||   |
                                TCGTTCTTCACT       GG   C
                                      CGTCTT    GAC
GAM390  HOXB7   3'  CCTTGCTGCTGCTGCTTGCTT  16906       A  TG AAACCC
                                AGGCAGG GG  G     CAGGG
                                |||||||  ||  |     |||||
                                TTCGTTC TC  C     GTTCC
                                   G  GT GTC___
GAM390  HOXD4   3'  CCCTGGGGACTGCTCTTTGTTT 28257       AG TG AAA
                                AGGCAGG  G  G   CCCCAGGG
                                |||||||  |  |   ||||||||
                                TTTGTTT  C  C   GGGGTCCC
                                   CT GT A__
GAM390  HOXD4   3'  CTCTAGTCGTTTTTCTTCTGCC 28258         TG    CCC_
           T                    AGGCAGGAGG  GAAAC    AGGG
                                ||||||||||  |||||    ||||
                                TCCGTCTTCT  TTTTG    TCTC
                                      __     CTGA
GAM390  HPCAL1  3'  CAGGGCTCTCTTTGTCTGCCTG 10964       _  TG  AA_____ CCAG
           TTT                    AGGCAGG AGG  GA       CC   G
                                  |||||||  |||  ||       ||   |
                                  TTTGTCC TCT  TT       GG   C
                                     G   GT  CTCTC    GAC
GAM390  HPCAL1  3'  CCAGGGCTCTCTTTGTCTGCCT 10965       _  TG  AA_____ CCAG
           GTTT                    AGGCAGG AGG  GA       CC   G
                                   |||||||  |||  ||       ||   |
                                   TTTGTCC TCT  TT       GG   C
                                      G   GT  CTCTC    GACC
GAM390  HSD11B1  3'  TTTTGGGACTGTTCTGTCTCAT 19830      G   TG   AC__
           GTTT                    AGGCA GAGG  GAA    CCCAGGG
                                   |||||  ||||  |||    |||||||
                                   TTTGT CTCT  CTT    GGGTTTT
                                      A    GT   GTCA
GAM390  HTR1E   3'  CTGTTTTCTACCTCTGGTCT   7860      A        CCC
                                AGGC GGAGGTGGAAA   CAG
                                ||||  ||||||||||   |||
                                TCTG TCTCCATCTTT   GTC
                                  G         T__
GAM390  ICOS    3'  CAGGGTTTTCTCTACTTCCTGT 24923           AA_____ CCAG
           CT                    AGGCAGGAGGTGGA       CC   G
                                 ||||||||||||||       ||   |
                                 TCTGTCCTTCATCT       GG   C
                                        CTTTT    GAC
GAM390  IFIT1   3'  CCAGGGTCTTTTCTGCTTACTG 9549        G      A_____ CCAG
           TTT                    AGGCAG AGGTGGAA      CC   G
                                  ||||||  ||||||||      ||   |
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                                TTTGTC TTCGTCTT      GG    C
                                   A       TTCT     GACC
GAM390  IGF1     3'  CCAGGGTCATTTTTGCCCTCTG 7066         A  TG   A_______  CCAG
              CCT                  AGGCAGG GG  GAA      CC    G
                                |||||||  ||  |||       ||    |
                                TCCGTCT CC  TTT      GG    C
                                   C  GT   TACT     GACC
GAM390  IGF1     3'  CCAGGGTTCTTTTTATTTCTTG 7067     _         A_______  CCAG
              TCC                  GG CAGGAGGTGGAA      CC    G
                                ||  ||||||||||||       ||    |
                                CC GTTCTTTATTTT      GG    C
                                 T          TCTT     GACC
GAM390  IGF1     5'  TCTGGATTTCCTTTTGCTT    7085          TGGAAACC
                                AGGCAGGAGG       CCAGG
                                ||||||||||       |||||
                                TTCGTTTTCC       GGTCT
                                      TTTA____
GAM390  IGF2R    3'  CCAGGGCTCATTCTGTCTCTTT 7910      C     TG   A_______  CCAG
              TCT                  AGG AGGAGG  GAA      CC    G
                                |||  ||||||  |||       ||    |
                                TCT TTCTCT  CTT      GG    C
                                  T     GT   ACTC     GACC
GAM390  IGF2R    3'  CCAGGGTTCTCTTTTGCTTTCT 7911          TG   AC________ CCAG
              GTTT                  AGGCAGGAGG  GAA       C    G
                                ||||||||||  |||       |   |
                                TTTGTCTTTC  TTT       G    C
                                      GT   CTCTT   G GACC
GAM390  IGF2R    3'  TTCTGTCTCTTTTCTCTTTTGC 7916          T    CCC_
              TT                    AGGCAGGAGG GGAAA    CAGGG
                                ||||||||||  |||||    |||||
                                TTCGTTTTCT CTTTT    GTCTT
                                      _    CTCT
GAM390  IHPK1    3'  CTTGGGGGCTTTCCAGTCT    97464      A    TGGAAA
                                AGGC GGAGG     CCCCAGG
                                ||||  |||||     |||||||
                                TCTG CCTTT     GGGGTTC
                                  A    CG____
GAM390  IHPK3    3'  CCTGCTCTACTCTCTGCTT    55093       GA     AACCC
                                AGGCAG  GGTGGA    CAGG
                                ||||||  ||||||    ||||
                                TTCGTC  TCATCT    GTCC
                                   TC     C____
GAM390  IKBKG    3'  GGTTTTGTTCCCTTCTGTCT   14667          T   AA_______
                                AGGCAGGAGG GGA       CC
                                ||||||||||  |||       ||
                                TCTGTCTTCC CTT       GG
                                      _  GTTTT
GAM390  IL1F7    5'  CCAGGGTTCATTCCATTTTCTG 27815           A_______  CCAG
              TT                    GGCAGGAGGTGGAA      CC    G
                                ||||||||||||||       ||    |
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                                TTGTCTTTTACCTT      GG    C
                                      ACTT     GACC
GAM390  IL1R1    3'  TCTGTCTCTGCTCTTGCCT    7926         G TG  AACCC
                                AGGCAGGA G  GA     CAGG
                                |||||||| |  ||     ||||
                                TCCGTTCT C  CT     GTCT
                                    _ GT  CT___
GAM390  IL1RAP   3'  CTTGGATCTACTTTTT      57072          AACC
                                AGGAGGTGGA    CCAGG
                                ||||||||||    |||||
                                TTTTTCATCT    GGTTC
                                     A___
GAM390  IL20RA   3'  CCAGGGTCCTTTTGCCTTTTGT 27800          TG   AC_____ CCAG
            TT                   AGGCAGGAGG  GAA      C    G
                                |||||||||  |||      |   |
                                TTTGTTTTCC  TTT      G    C
                                     GT   CCT   G GACC
GAM390  ILF1     3'  CCCAGGGTTTTGTTTTTGTTTT 16919      A    TG    ________  CAG
            CAGCCT                AGGC GGAGG  GAAAC      CC   GG
                                |||| |||||  |||||      ||   ||
                                TCCG CTTTT  TTTTG      GG   CC
                                  A    GT    TTTT    GAC
GAM390  ING1     3'  CAGGGTTCTGTTTGCCTTTTGT 19856          TG  AA_______  CCAG
            TT                   AGGCAGGAGG  GA       CC    G
                                |||||||||  ||       ||   |
                                TTTGTTTTCC  TT       GG    C
                                     GT  GTCTT    GAC
GAM390  INHBC    3'  CCCCAGGGCCTTCATCCATTTT 19858           AA________  CCAG
            TTGTC                 GGCAGGAGGTGGA        CC    GG
                                ||||||||||||         ||    ||
                                CTGTTTTTTACCT        GG    CC
                                      ACTTCC    GACC
GAM390  INMT     3'  TCCTGGGTTGACGCCATTCTCC 23228          _   AAAC__
            TGCCT                 AGGCAGGAGG TGG     CCCAGGG
                                |||||||||| |||     |||||||
                                TCCGTCCTCT ACC     GGGTCCT
                                     T   GCAGTT
GAM390  IRTA2    3'  CCCTGCTGGACTGTCACCTGTT 49231        A  TG AAA  C_
            T                    AGGCAGG GG  G   CC  CAGGG
                                ||||||| ||  |   ||  |||||
                                TTTGTCC CT  C   GG  GTCCC
                                    A  GT A__  TC
GAM390  ITGA6    3'  CCCCAGGGTCCTACCGTCTTTT 5787         _______    AAA__  CCAG
            CCTGTTT                AGGCAGGA     GGTGG    CC    GG
                                ||||||||     |||||    ||   ||
                                TTTGTCCT     CCATC    GG   CC
                                    TTTCTG    CT    GACC
GAM390  ITGA6    3'  TCTGGGTTGCCTTTGTTT    5795        G   TG AAAC
                                AGGCAG AGG  G    CCCAGG
                                |||||| |||  |    ||||||
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                                TTTGTT TCC  T    GGGTCT
                                   _   GT _____
GAM390  ITGA6    3'  TTTTGGGGGGGGCTTTTTTTCT 5796      C      GGAAA
                                AGG AGGAGGT     CCCCAGGG
                                ||| |||||||     ||||||||
                                TCT TTTTTCG     GGGGTTTT
                                  T      GGG__
GAM390  ITGAM    3'  CCCCAGGGCTATTTTCATCTCT 72307            ________  CCA
             TGTT                   GGCAGGAGGTGGAAA      CC   GG
                                ||||||||||||||||      ||   ||
                                TTGTTCTCTACTTTT      GG   CC
                                        ATC   G  ACC
GAM390  ITGAM    3'  CTTTGGGAGAAAACGTCTTGCT 72310         G  GGAAAC
             T                   AGGCAGGA GT     CCCAGGG
                                ||||||||  ||     |||||||
                                TTCGTTCT CA     GGGTTTC
                                     G  AAAGA_
GAM390  ITGB3    3'  CCCAGGGTTTACCTTCTACCTC 5803     G          AC_________ CCAG
             TTGGCT                  AG CAGGAGGTGGAA        C    G
                                || ||||||||||||         |    |
                                TC GTTCTCCATCTT         G    C
                                 G          CCATTT   G GACC
GAM390  ITGB7    5'  TCTGGTCTGTTTCCTGTTT    7963           TG  AACC
                                AGGCAGGAGG  GA    CCAGG
                                ||||||||||  ||    |||||
                                TTTGTCCTTT  CT    GGTCT
                                     GT  _____
GAM390  ITPKB    3'  ACTTAGGGTTTTTGTTTTCTGT 11061          TG      C   G
             TT                    AGGCAGGAGG  GAAACCC AGG
                                ||||||||||  ||||||| |||
                                TTTGTCTTTT  TTTTGGG TTC
                                     GT      A   AT
GAM390  ITPKB    3'  CTTAGGGTTTTTGTTTTCTGTT 11064          TG      C   G
             T                    AGGCAGGAGG  GAAACCC AGG
                                ||||||||||  ||||||| |||
                                TTTGTCTTTT  TTTTGGG TTC
                                     GT      A
GAM390  JMJ      3'  CTTTGGCTGTCGTCTTCTGCC  18322         GT  AAACC
                                GGCAGGAG  GG    CCAGGG
                                |||||||  ||    ||||||
                                CCGTCTTC  CT    GGTTTC
                                     TG  GTC__
GAM390  JPH2     5'  CTTTGAACCTTTCCTTCCTGCT 96083          T    ACCC
             T                    AGGCAGGAGG GGAA    CAGGG
                                ||||||||||| ||||    |||||
                                TTCGTCCTTC CTTT    GTTTC
                                     _    CCAA
GAM390  JRK      3'  CCCTGGGCCCATTTCCTCTCT  87822     C       AAAC
                                AGG AGGAGGTGG    CCCAGGG
                                ||| |||||||||    |||||||
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                                TCT TCCTTTACC    GGGTCCC
                                  C        C___
GAM390  JRK      3'  TCCTGGAAGTGTGTGTTTCTTG 87836          GT GAA  C_
             CTT                    AGGCAGGAG  G   AC  CCAGGG
                                |||||||||  |   ||  ||||||
                                TTCGTTCTT  T   TG  GGTCCT
                                     TG GTG  AA
GAM390  JUN      5'  CCCCAGGGTTTTCTTTTCACCT 11101      C          A_________  CCAG
             TCTCTCT                 AGG AGGAGGTGGAA        CC    GG
                                ||| ||||||||||         ||    ||
                                TCT TCTTCCACTTT        GG    CC
                                  C          TCTTTT     GACC
GAM390  JUP      3'  CAGGGTTCTCTTCCCCTTCCTG 11106           T    AC________  CCAG
             TTT                    AGGCAGGAGG GGAA        C    G
                                ||||||||||  ||||         |    |
                                TTTGTCCTTC CCTT        G    C
                                     C    CTCTT   G GAC
GAM390  JUP      3'  TCTTGGGATAGTGTTCTGCTCC 11114          G TG   _  ___
             TGCTT                   AGGCAGGA G  GAA AC   CCCAGGG
                                ||||||||  |  |||  ||   |||||||
                                TTCGTCCT C  CTT TG   GGGTTCT
                                     _ GT   G  ATA
GAM390  KCNH2    3'  CTTGGGACCATCTTCTCCT    5884      C        AAAC
                                AGG AGGAGGTGG    CCCAGG
                                |||  |||||||||    ||||||
                                TCC TCTTCTACC    GGGTTC
                                  _        A___
GAM390  KCNJ6    3'  CCAGGGTTCTCTTTCTTTTTCT 11150           T    AC________  CCAG
             GTCT                    AGGCAGGAGG GGAA        C    G
                                ||||||||||  ||||         |    |
                                TCTGTCTTTT CTTT        G    C
                                     T    CTCTT   G GACC
GAM390  KCNK5    3'  TCCTGAATGTTTTTGTTATTTT 14971           ___    CC_
             TTGTTT                  AGGCAGGAGGTG   GAAAC   CAGGG
                                ||||||||||||   |||||  |||||
                                TTTGTTTTTTAT   TTTTG   GTCCT
                                      TGT    TAA
GAM390  KCNN3    3'  CCAGGGCTCTCCTTTCCTTTTG 11183          T__   AA____  CCAG
             TCT                    AGGCAGGAGG   GGA     CC    G
                                ||||||||||   |||     ||   |
                                TCTGTTTTCC   CCT     GG    C
                                     TTT   CTC     GACC
GAM390  KIAA0857 3'  CAGGGTTCTGCTTTGCTGTTT  67250       _   TG  AA__  CCAG
                                AGGCAG GAGG  GA   CC    G
                                ||||||  ||||  ||   ||   |
                                TTTGTC TTTC  CT    GG    C
                                   G    GT  T     GAC
GAM390  KIAA0857 3'  CCTTGCTCCTCTCCCTCCTGCC 67252          TG  AACCC
             T                   AGGCAGGAGG  GA    CAGGG
                                ||||||||||  ||    |||||
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                                TCCGTCCTCC CT    GTTCC
                                     CT CCTC_
GAM390  KIF2    3' CCTTGTCAGTTTTATTTTCT 16929         ACCC
                                AGGAGGTGGAA   CAGGG
                                ||||||||||   |||||
                                TCTTTTATTTT   GTTCC
                                     GACT
GAM390  KIF3B   3' GGCTCTTCCAATTTCTGCTT 17806       G    AC_____
                                AGGCAGGAG TGGAA     C
                                ||||||||| |||||     |
                                TTCGTCTTT ACCTT     G
                                     A   CTC  G
GAM390  KIF5C   3' CCCTACAGTTTCCATTTTTT 16933          CCC
                                AGGAGGTGGAAAC  AGGG
                                ||||||||||||  ||||
                                TTTTTTACCTTTG  TCCC
                                      ACA
GAM390  KL      3' CTCTGAGGTCTATTTTATGTTT 17742      G      AA  C
                                AGGCA GAGGTGGA  CC CAGGG
                                ||||| ||||||||  || |||||
                                TTTGT TTTTATCT  GG GTCTC
                                   A       __ A
GAM390  KLF8    3' CCAGGGTTCTTTTCCACTTTCT 24372    C        A_______ CCAG
            CCTT                  AGG AGGAGGTGGAA      CC   G
                                ||| ||||||||||       ||   |
                                TTC TCTTTCACCTT      GG   C
                                  C         TTCTT    GACC
GAM390  KLHL1   5' CCTGCCTCTGCTCCTGCCT   40871       G TG  AACCC
                                AGGCAGGA G  GA    CAGG
                                ||||||||  |  ||    ||||
                                TCCGTCCT C  CT    GTCC
                                    _ GT  CC___
GAM390  KLHL3   3' CTTGTTGTACTTCTTGTTT   88847         G  ACCC
                                AGGCAGGAGGTG AA   CAGG
                                ||||||||||| ||   ||||
                                TTTGTTCTTCAT TT   GTTC
                                      G  ____
GAM390  KLHL3   3' TTTGGGAGCATCTTGTCT    88856       G  GGAAAC
                                AGGCAGGA GT     CCCAGG
                                ||||||| ||     ||||||
                                TCTGTTCT CG     GGGTTT
                                    A  A_____
GAM390  KLK4    3' TTGGTTTTTCATTTTTTGTC  63533          CC
                                GGCAGGAGGTGGAAA  CCAG
                                |||||||||||||||  ||||
                                CTGTTTTTTACTTTT  GGTT
                                         T_
GAM390  KNSL1   3' CCTATTTCGCTTTCTCCT    16944     C       ACCCC
                                AGG AGGAGGTGGAA    AGG
                                ||| ||||||||||    |||
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                                TCC TCTTTCGCTTT    TCC
                                  _        A____
GAM390  KPNA1    3'  CAGGGTTTTATTTCATCTCCTG 81131          A_______  CCAG
                CT                  GGCAGGAGGTGGAA      CC   G
                                    ||||||||||||||      ||   |
                                    TCGTCCTCTACTTT      GG   C
                                           ATTTT    GAC
GAM390  KRTHB6   3'  CCCCAGGGTCTTCCTCCTACCT 11249        _  AA_______  CCAG
                TCTGTTT               AGGCAGGAGGT GGA      CC   GG
                                    |||||||||||| |||      ||   ||
                                    TTTGTCTTCCA CCT      GG   CC
                                           T  CCTTCT    GACC
GAM390  LALBA    3'  CCTGGAATACCTCTTCCCT   11256    C      GAAACC
                                    AGG AGGAGGTG     CCAGG
                                    ||| ||||||||     |||||
                                    TCC TTCTCCAT     GGTCC
                                      C       AA____
GAM390  LAMC1    3'  TCTTGATGATCCCACTTCCTGT 11272          AAACCC
                TT                  AGGCAGGAGGTGG     CAGGG
                                    ||||||||||||     |||||
                                    TTTGTCCTTCACC     GTTCT
                                           CTAGTA
GAM390  LANCL1   3'  GGTCCTATTATCTCCTGTTT  21332         ____  AA_
                                    AGGCAGGAGGT   GGA  CC
                                    ||||||||||    |||  ||
                                    TTTGTCCTCTA   CCT  GG
                                           TTAT
GAM390  LANGERIN 3'  CCCTGGGGTTTTCCACTCTT  32312      G    _
                                    AGGAG TGGAAA CCCCAGGG
                                    ||||| |||||| ||||||||
                                    TTCTC ACCTTT GGGGTCCC
                                      _     T
GAM390  LBX1     3'  TCCTGGCAGCCGCCTCTTCCCT 22670     C       AAACC
                                    AGG AGGAGGTGG    CCAGGG
                                    ||| |||||||||    ||||||
                                    TCC TTCTCCGCC    GGTCCT
                                      C       GAC__
GAM390  LCP1     5'  CCAGGGTTCTAGTCACTTCCTG 11281          AAA_______  CCAG
                CCT                   AGGCAGGAGGTGG       CC   G
                                    ||||||||||||||       ||   |
                                    TCCGTCCTTCACT       GG   C
                                           GATCTT    GACC
GAM390  LDB3     3'  CCAGGGTTCTGTCCTCACTCCT 76925        GT_  AA_______  CCAG
                GTTT                  AGGCAGGAG  GGA      CC   G
                                    |||||||||  |||      ||   |
                                    TTTGTCCTC  CCT      GG   C
                                         ACT  GTCTT    GACC
GAM390  LDB3     3'  TTTGGGTTGTCTTTGGCCT   76929     AG   TG AAAC
                                    AGGC  GAGG  G   CCCAGG
                                    ||||  ||||  |   ||||||
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                                TCCG  TTCT  T    GGGTTT
                                  GT    GT _____
GAM390  LDHB     5'  TTCTGGGGCTAAGCCTCCTTCT 11294     C      GGAAA
                                AGG AGGAGGT     CCCCAGGG
                                ||| |||||||     ||||||||
                                TCT TCCTCCG     GGGGTCTT
                                  _       AATC_
GAM390  LIMK1    3'  CTTTGGGTCTTTTTTTTGTTTC 11333     C     TG    C____
           TTTCTT                  AGG AGGAGG  GAAA    CCCAGGG
                                ||| ||||||  ||||    |||||||
                                TTC TTCTTT  TTTT    GGGTTTC
                                  T     GT    TTTCT
GAM390  LIMK1    3'  CTTTGGGTCTTTTTTTTGTTTC 11334     C     TG    C____
           TTTCTT                  AGG AGGAGG  GAAA    CCCAGGG
                                ||| ||||||  ||||    |||||||
                                TTC TTCTTT  TTTT    GGGTTTC
                                  T     GT    TTTCT
GAM390  LMO4     5'  GGTCCTCTCCTTTCCTGCTT   23186          T   AA_______
                                AGGCAGGAGG GGA       CC
                                |||||||||| |||       ||
                                TTCGTCCTTT CCT       GG
                                      _   CTCCT
GAM390  LOH11CR2A 3'  CTTTGTCTGTTCACTTTCTATC 28271     GC         AACCC
           T                     AG  AGGAGGTGGA     CAGGG
                                ||  ||||||||||     |||||
                                TC  TCTTTCACTT     GTTTC
                                  TA         GTCT_
GAM390  LPIN2    3'  CTCTGGTCGCCTCATTTCCTGC 28430           AAACC
           T                     GGCAGGAGGTGG     CCAGGG
                                ||||||||||||     ||||||
                                TCGTCCTTTACT     GGTCTC
                                      CCGCT
GAM390  LTB4R    5'  CTCTGGCTACCATACCTCCTTC 7462      C       GAAACC
           T                     AGG AGGAGGTG      CCAGGG
                                ||| ||||||||      ||||||
                                TCT TCCTCCAT      GGTCTC
                                  _       ACCATC
GAM390  LU       3'  CCCAGGGCTATTTTTACCTCCC 19941      A         ________  CCA
           GCCT                    AGGC GGAGGTGGAAA      CC   GG
                                |||| ||||||||||       ||   ||
                                TCCG CCTCCATTTTT      GG   CC
                                  C          ATC   G  ACC
GAM390  LZTS1    3'  CCCCAGGGTTCTTTTTTGCTTT 41028          _ TG   A________  CCAG
           CTTGTCT                  AGGCAGGAG G  GAA       CC    GG
                                |||||||||  |  |||       ||    ||
                                TCTGTTCTT C  TTT       GG    CC
                                      T GT   TTCTT    GACC
GAM390  LZTS1    3'  CCCTGGGGCCCAGCCCCTGTTT 41029        A  _   AAA
                                AGGCAGG GG TGG   CCCCAGGG
                                |||||||  ||  |||   ||||||||
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                                TTTGTCC CC ACC   GGGGTCCC
                                    _ G   C__
GAM390  M17S2    3'  GGCCATTTTTCTTTCTGCTT   20911          _____  AAA
                                AGGCAGGAGG    TGG   CC
                                ||||||||||    |||   ||
                                TTCGTCTTTC    ACC   GG
                                    TTTTT
GAM390  M6PR     3'  CTCTGATGCTTCCATCTTCCTG 11410        _      ACCC
           TTT                    AGGCAGGA GGTGGAA    CAGGG
                                ||||||||| |||||||    |||||
                                TTTGTCCT CTACCTT    GTCTC
                                    T      CGTA
GAM390  MADH7    3'  CAGGGTTATTTTCATCCTTGTC 20923        A       ________  CCA
           T                     AGGCAGG GGTGGAAA      CC   G
                                ||||||| ||||||||      ||   |
                                TCTGTTC CTACTTTT      GG   C
                                    _      ATT   G  AC
GAM390  MADH7    3'  CTTTGGTCGTTTTTTTTTTGTT 20926          TG    C_
           T                     AGGCAGGAGG  GAAAC  CCAGGG
                                ||||||||||  |||||  ||||||
                                TTTGTTTTTT  TTTTG  GGTTTC
                                    __     CT
GAM390  MAG      3'  CAGGGTTTATTGCTACTTCCTG 11420           AAA________  CCAG
           CCT                    AGGCAGGAGGTGG        CC    G
                                ||||||||||||         ||    |
                                TCCGTCCTTCATC        GG    C
                                    GTTATTT    GAC
GAM390  MAG      3'  CCAGGGTTTATTGCTACTTCCT 11422           AAA________  CCAG
           GCCT                    AGGCAGGAGGTGG        CC    G
                                ||||||||||||         ||    |
                                TCCGTCCTTCATC        GG    C
                                    GTTATTT    GACC
GAM390  MAGEA2   5'  CCTGCCCGCACTCCTGCCT   61108         _   AAACCC
                                AGGCAGGAG GTGG     CAGG
                                |||||||| ||||     ||||
                                TCCGTCCTC CGCC     GTCC
                                    A   C_____
GAM390  MAGEB4   5'  CCAGGGTTCTGCCTACACTCCT 11430         _   AAA_______  CCAG
           GCCT                    AGGCAGGAG GTGG        CC    G
                                ||||||||| ||||        ||    |
                                TCCGTCCTC CATC        GG    C
                                    A   CGTCTT    GACC
GAM390  MALT1    5'  GGTTCTTCCGCCCCTGCCT   23267        A      AC_____
                                AGGCAGG GGTGGAA      C
                                ||||||| |||||||      |
                                TCCGTCC CCGCCTT      G
                                    _      CTT   G
GAM390  MAN2A2   3'  CCTGCAACCGTTTCCGCCTCCT 21506           CC___   G
           GCT                    GGCAGGAGGTGGAAAC    CAGG
                                ||||||||||||||||    ||||
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                                TCGTCCTCCGCCTTTG    GTCC
                                      CCAAC
GAM390  MAN2A2   3'  CCTTGAAGCCTCACCTTTAGTC 21507     AG     AAACCC
            T                  AGGC  GAGGTGG     CAGGG
                               ||||  |||||||     |||||
                               TCTG  TTCCACT     GTTCC
                                 AT      CCGAA_
GAM390  MAN2A2   3'  CTCTGCCCTCATTTTCTGTTT  21508          AAACCC
                               AGGCAGGAGGTGG     CAGGG
                               ||||||||||||      |||||
                               TTTGTCTTTTACT     GTCTC
                                       CCC___
GAM390  MAN2C1   3'  CTCTGGGGACTCCTAATTTCTG 73299        GT_   AA
            CTT                  AGGCAGGAG   GGA  CCCCAGGG
                               |||||||||   |||  ||||||||
                               TTCGTCTTT   CCT  GGGGTCTC
                                     AAT   CA
GAM390  MAP2     3'  CCAGGGCTCATTTCACTATTCT 49819        _      A_______  CCAG
            GTTT                 AGGCAGGA GGTGGAA      CC    G
                               ||||||||| |||||||       ||    |
                               TTTGTCTT TCACTTT      GG    C
                                    A      ACTC     GACC
GAM390  MAP3K4   3'  CCTTGTTTTTAATCTCCTGTTT 22993          _     CCC
                               AGGCAGGAGGT GGAAAC   AGG
                               ||||||||||| ||||||   |||
                               TTTGTCCTCTA TTTTTG   TCC
                                     A     T__
GAM390  MAP4     3'  CCGTGTTCCCCTCTTGTCT    11446          T    ACCCCA
                               AGGCAGGAGG GGAA      GG
                               |||||||||| ||||      ||
                               TCTGTTCTCC CCTT      CC
                                     _    GTG___
GAM390  MAPK3    3'  CCCTGGGGCCTGGACCTGCCTC 73775          TG AAA____
            CTGCCT                 AGGCAGGAGG  G      CCCCAGGG
                               ||||||||||  |      ||||||||
                               TCCGTCCTCC  C      GGGGTCCC
                                     GT CAGGTCC
GAM390  MAPK9    3'  CAGGGTTTATTCTATCTTTTGT 58174          A_______  CCAG
                               GCAGGAGGTGGAA      CC    G
                               ||||||||||||      ||    |
                               TGTTTTCTATCTT      GG    C
                                      ATTT     GAC
GAM390  MAPK9    3'  CCAGGGTTTATTCTATCTTTTG 58175          A_______  CCAG
            T                   GCAGGAGGTGGAA      CC    G
                               ||||||||||||      ||    |
                               TGTTTTCTATCTT      GG    C
                                      ATTT     GACC
GAM390  MARK1    3'  CCAGGGTTCTGTTCATTTTCTG 38469          AA_______  CCAG
            TT                   GGCAGGAGGTGGA      CC    G
                               ||||||||||||      ||    |
```

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                              TTGTCTTTTACTT      GG   C
                                    GTCTT    GACC
GAM390  MARK3   5' CCCCAGGGTCCTCCTCCGCCTC 11461     _       AA_______ CCAG
          CTCGTTT                AGGC AGGAGGTGGA       CC   GG
                              |||| ||||||||||       ||   ||
                              TTTG TCCTCCGCCT       GG   CC
                                C        CCTCCT    GACC
GAM390  MBD3    3' CCCTGCCTCGGTTTCCCTTCTG 15390         TG    C___
          TTT                  AGGCAGGAGG  GAAACC   CAGGG
                              ||||||||||  ||||||   |||||
                              TTTGTCTTCC  CTTTGG   GTCCC
                                    __     CTCC
GAM390  MBL2    3' GGTTTTTCCATTTTTTTCT   5910     C        A_____
                              AGG AGGAGGTGGAA     CC
                              ||| ||||||||||     ||
                              TCT TTTTTTACCTT     GG
                                _         TTT
GAM390  MBNL    3' TCTTGGGCTGCAATTTGTTTTA 41073      G   TG  AAC___
          TGCTT                  AGGCA GAGG  GA     CCCAGGG
                              ||||| ||||  ||     |||||||
                              TTCGT TTTT  TT     GGGTTCT
                                A    GT  AACGTC
GAM390  MCC     3' GGTCCTCTTTCCTCCTGCTT   11482         T_   AA____
                              AGGCAGGAGG  GGA     CC
                              |||||||||  |||     ||
                              TTCGTCCTCC  TCT     GG
                                    TT   CCT
GAM390  MCM3    3' CTGTTTTCTGTTTGCTGTTT   11483      G   TG    CCC
                              AGGCAG AGG  GAAA   CAG
                              ||||||  |||  ||||   |||
                              TTTGTC TTT  CTTT   GTC
                                 G   GT    T__
GAM390  MCM3    3' TTTTGGGGGCACAACTGTTTTC 11485         TG AAA___
          TGTTT                  AGGCAGGAGG  G     CCCCAGGG
                              ||||||||||  |     ||||||||
                              TTTGTCTTTT  C     GGGGTTTT
                                    GT AACACG
GAM390  MECP2   3' CCTTCCATTTCTGCCTTTTGTT 18396         TG   CCCC   G
                              GGCAGGAGG  GAAA    AGG
                              |||||||||  ||||    |||
                              TTGTTTTCC  CTTT    TCC
                                   GT    ACCT
GAM390  MECP2   3' GTCCTGGGCTTTTGTTTTGCTT 18412     _     TG   AC____
          TTTAGTTT                AGGC AGGAGG  GAA     CCCAGGG   T
                              |||| ||||||  |||     |||||||  |
                              TTTG TTTTTC  TTT     GGGTCCT   G
                                A     GT   GTTTTC
GAM390  MEFV    3' CCTTGTTCTCTCTGCTTCTGTC 5936       G   TG  AACCC
          T                   AGGCAG AGG  GA    CAGGG
                              ||||||  |||  ||    |||||
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                                TCTGTC TTC  CT    GTTCC
                                   _  GT  CTCTT
GAM390  MEIS1   3'  CCTTATACATCACTTCCTGTTT 11534          AAACCCC
                                AGGCAGGAGGTGG      AGG
                                ||||||||||||      |||
                                TTTGTCCTTCACT      TCC
                                      ACATAT_
GAM390  MEL     3'  CCACTTCCACCTCTTCTCT   19327    C        ACCCCA
                                AGG AGGAGGTGGAA     GG
                                ||| ||||||||||     ||
                                TCT TTCTCCACCTT     CC
                                  C         CA____
GAM390  MEN1    3'  CAGGGTTTTATTTATTTCTTGC 56344          AA_______  CCAG
           T                     GGCAGGAGGTGGA       CC    G
                                ||||||||||||       ||   |
                                TCGTTCTTTATTT       GG    C
                                      ATTTT     GAC
GAM390  MEN1    3'  CCATTCTACTTTCTGTTT    56345           ACCCCA
                                AGGCAGGAGGTGGAA     GG
                                ||||||||||||||     ||
                                TTTGTCTTTCATCTT     CC
                                      A_____
GAM390  MEN1    3'  CCCAACACTTGTTATTTTCTGC 56346          AAACCCCA
           TT                    AGGCAGGAGGTGG       GGG
                                ||||||||||||       |||
                                TTCGTCTTTTATT       CCC
                                      GTTCACAA
GAM390  MEN1    5'  CCTTGGGGTTTGGGGGCTTGAC 56347    _   AGGTGG
           CT                     AGG CAGG     AAACCCCAGGG
                                ||| ||||     ||||||||||
                                TCC GTTC     TTTGGGGTTCC
                                  A   GGGGG_
GAM390  MFAP3   3'  TTGAGGTTTTTATTTTTGTTT  21002        G       C
                                AGGCAGGAG TGGAAACC CAG
                                ||||||||| ||||||| |||
                                TTTGTTTTT ATTTTTGG GTT
                                      _       A
GAM390  MGA     3'  CAGGGTCTTTCCTTTTCTGCTT 63464         T    _______  CCA
                                AGGCAGGAGG GGAAA     CC   G
                                |||||||||| |||||     ||   |
                                TTCGTCTTTT CCTTT     GG   C
                                      _    CT   G  AC
GAM390  MGA     3'  CCAGGGTCTTCTATATCTCCTG 63465          GAAA_______  CCAG
           TCT                    AGGCAGGAGGTG        CC    G
                                ||||||||||||        ||   |
                                TCTGTCCTCTAT        GG    C
                                      ATCTTCT    GACC
GAM390  MGAT1   3'  CTTGGTGGATTTTTGTTTCTTG 11553         TG   _ _    G
           CCT                    AGGCAGGAGG  GAAA CC CCAGG
                                ||||||||||  |||| || |||||
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                                TCCGTTCTTT  TTTT GG GGTTC
                                     GT    A  T
GAM390  MGAT1    3'  TCCTGCCCTTCTCTCCTGTCT  11556        GT    ACCC
                                AGGCAGGAG  GGAA    CAGGG
                                |||||||||  ||||    |||||
                                TCTGTCCTC  TCTT    GTCCT
                                     __    CCC_
GAM390  MGEA5    3'  GGTTTTCTTTACTTTTGTCT   25223        GT__    A___
                                AGGCAGGAG    GGAA    CC
                                |||||||||    ||||    ||
                                TCTGTTTTC    CTTT    GG
                                     ATTT    T
GAM390  MHC2TA   3'  CCCTGGGGAGAAAGTACTTCTT 5977         GAAA__
                                AGGAGGTG     CCCCAGGG
                                ||||||||     ||||||||
                                TTCTTCAT     GGGGTCCC
                                     GAAAGA
GAM390  MICB     3'  TTCTGTTGTTTTTTGTTTTTGTT 21026        G TG    CC
             T                   AGGCAGGA G  GAAAC  CAGGG
                                 ||||||||  |  |||||  |||||
                                 TTTGTTTT T  TTTTG  GTCTT
                                     _ GT     TT
GAM390  MJD      3'  CAGGGTTTGTTTTCTTTTTCTG 18421          T     _______ CAG
             TCT                   AGGCAGGAGG GGAAAC     CC   G
                                   ||||||||||  ||||||     ||   |
                                   TCTGTCTTTT CTTTTG     GG   C
                                        T     TTT     GAC
GAM390  MJD      3'  CGGGTTTGTTTTCTTTTTCTGT 18422          T     _______ CAG
             CT                    AGGCAGGAGG GGAAAC     CC   G
                                   ||||||||||  ||||||     ||   |
                                   TCTGTCTTTT CTTTTG     GG   C
                                        T     TTT     GA
GAM390  MKI67    3'  CAGGGCTGTTTTTACTTTTTCG 11591      _         _____ CAG
             CCT                    AGGC AGGAGGTGGAAAC    CC   G
                                    ||||  ||||||||||||    ||   |
                                    TCCG TTTTTCATTTTTG    GG   C
                                      C           TC     GAC
GAM390  MKI67    3'  CTCTGTACCTACCATCTCCTGC 11593           AAACCC
             CT                     AGGCAGGAGGTGG     CAGGG
                                    ||||||||||||      |||||
                                    TCCGTCCTCTACC     GTCTC
                                          ATCCAT
GAM390  MKPX     3'  CCTTGGTGTGGGTTTTATCTCT 39878      A        A ___
             GGTTT                   AGGC GGAGGTGGAA CC   CCAGGG
                                     ||||  ||||||||||  ||   ||||||
                                     TTTG TCTCTATTTT GG   GGTTCC
                                       G         G  TGT
GAM390  MLLT3    3'  TCTGTATTTTCCACCTTTTGTT 16963             CCC    G
             T                    AGGCAGGAGGTGGAAA   CAGG
                                  ||||||||||||||||   ||||
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                                TTTGTTTTCCACCTTT  GTCT
                                          TAT
GAM390  MLPH     5'  CCCTGCTTCGTCGCCTCCTTTC 44317     C       AAACCC
             T                   AGG AGGAGGTGG     CAGGG
                                 ||| |||||||||     |||||
                                 TCT TCCTCCGCT     GTCCC
                                   T       GCTTC_
GAM390  MMP12    3'  CTCTAATTGTCCATTCTTGCTT 11607         G   AACCCC
                                 AGGCAGGAG TGGA     AGGG
                                 ||||||||| ||||     ||||
                                 TTCGTTCTT ACCT     TCTC
                                       _   GTTAA_
GAM390  MMP19    3'  CAGGGCCCAACTCCATTTCCTG 11622           AA_______  CCAG
             TCT                   AGGCAGGAGGTGGA       CC   G
                                   ||||||||||||||       ||   |
                                   TCTGTCCTTTACCT       GG   C
                                         CAACCC    GAC
GAM390  MMP19    3'  CAGGGCCCAACTCCATTTCCTG 11623           AA_______  CCAG
             TCT                   AGGCAGGAGGTGGA       CC   G
                                   ||||||||||||||       ||   |
                                   TCTGTCCTTTACCT       GG   C
                                         CAACCC    GAC
GAM390  MMP19    3'  CCAGGGCCCAACTCCATTTCCT 11624           AA_______  CCAG
             GTCT                   AGGCAGGAGGTGGA       CC   G
                                   ||||||||||||||       ||   |
                                   TCTGTCCTTTACCT       GG   C
                                         CAACCC    GACC
GAM390  MMP19    3'  CCAGGGCCCAACTCCATTTCCT 11625           AA_______  CCAG
             GTCT                   AGGCAGGAGGTGGA       CC   G
                                   ||||||||||||||       ||   |
                                   TCTGTCCTTTACCT       GG   C
                                         CAACCC    GACC
GAM390  MOCS1    3'  TTTTGGGTTTTCTCTTCTCCTG 93669          T_    C
             CTT                   AGGCAGGAGG  GGAAA CCCAGGG
                                   ||||||||||  ||||| |||||||
                                   TTCGTCCTCT  TCTTT GGGTTTT
                                         TC    T
GAM390  MOG      3'  TTCTGTCATCTACCTTTTCTCT 11679     C       AACCC
                                 AGG AGGAGGTGGA     CAGGG
                                 ||| ||||||||||     |||||
                                 TCT TTTTCCATCT     GTCTT
                                   C         ACT__
GAM390  MPL      3'  CCAGGGTCCTCCTTTACTTCCT 19348     C       AA_______  CCAG
             CTCT                   AGG AGGAGGTGGA       CC   G
                                   ||| ||||||||||       ||   |
                                   TCT TCCTTCATTT       GG   C
                                     C         CCTCCT    GACC
GAM390  MPP3     5'  CCCCAGGGTCTTAGCTTTATTT 10410     C       AA_________  CCAG
             CCTTCCT                 AGG AGGAGGTGGA       CC   GG
                                     ||| ||||||||||       ||   ||
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                              TCC TCCTTTATTT       GG   CC
                                T       CGATTCT    GACC
GAM390  MPP3    3'  TGTTGTTGGTTTTTGTCTGTTG 10412      G  TG    C_  GG
           TTT                 AGGCAG AGG  GAAACC  CAG
                              |||||| |||  ||||||  |||
                              TTTGTT TCT  TTTTGG  GTT
                                 G  GT     TT   GTT
GAM390  MRPL49  3'  CTTTGGGGTCAGGCCTTGCTT  70167      GG   GGAA
                              AGGCA  AGGT    ACCCCAGGG
                              |||||  ||||   |||||||||
                              TTCGT  TCCG    TGGGGTTTC
                                 __   GAC_
GAM390  MS4A2   3'  CCAGGGTTCTTCTGTTTTCTGT 41975         TG   AC_____ CCAG
           TT                  AGGCAGGAGG  GAA     C   G
                              ||||||||||  |||      |   |
                              TTTGTCTTTT  CTT      G   C
                                    GT   CTT   G GACC
GAM390  MS4A2   3'  TTCTGTTTTCTGTTTCCT    41980       TG   CCC
                              AGGAGG  GAAA   CAGGG
                              ||||||  ||||   |||||
                              TCCTTT  CTTT   GTCTT
                                 GT    T__
GAM390  MS4A4A  3'  CCAGGGTTCTATTTCATCTTCT 44003     C        A_______  CCAG
           TCCT                  AGG AGGAGGTGGAA       CC   G
                              ||| ||||||||||       ||   |
                              TCC TCTTCTACTTT       GG   C
                                T        ATCTT    GACC
GAM390  MS4A4A  3'  CCTTTTTCCTTCTCCTGCTT   44004         T    CCCC
                              AGGCAGGAGG GGAAA    AGG
                              |||||||||| |||||    |||
                              TTCGTCCTCT CCTTT    TCC
                                    T    T___
GAM390  MSL3L1  3'  CTTGGGGCTCTGTTGTTT    23289       G   TGGAAA
                              AGGCAG AGG     CCCCAGG
                              |||||| |||     |||||||
                              TTTGTT TCT     GGGGTTC
                                 G   C_____
GAM390  MSR1    3'  TTCTGAATGTACACTTTCTGTC 11706          GAAACCC
           T                   AGGCAGGAGGTG      CAGGG
                              ||||||||||||      |||||
                              TCTGTCTTTCAC      GTCTT
                                    ATGTAA_
GAM390  MTIF2   5'  TTCTGGATTTCCGTTTCCT    11714     GG     CC
                              AGGA  TGGAAA  CCAGGG
                              ||||  ||||||  ||||||
                              TCCT  GCCTTT  GGTCTT
                                TT     A_
GAM390  MTMR3   3'  TCCTATATTTTTCATTTTTTGT 41170            CCCC
           C                   GGCAGGAGGTGGAAA   AGGG
                              ||||||||||||||    ||||
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                                CTGTTTTTTACTTTT  TCCT
                                      TATA
GAM390  MTR     3'  TCCTGGGTTCATGCCATTCTCC 6028        _  AAAC__
            TGCCT                 AGGCAGGAGG TGG     CCCAGGG
                                  |||||||||| |||     |||||||
                                  TCCGTCCTCT ACC     GGGTCCT
                                       T  GTACTT
GAM390  MUC4    3'  CCTGGGCGGCCTCTTGCT    37874         GGAAAC
                                  GGCAGGAGGT     CCCAGG
                                  ||||||||||     ||||||
                                  TCGTTCTCCG     GGGTCC
                                       GC____
GAM390  MUC4    3'  CCTTCCAACTTCACCCCTGTTT 37876       A     AACCCC
                                  AGGCAGG GGTGGA     AGG
                                  ||||||| ||||||     |||
                                  TTTGTCC CCACTT     TCC
                                      _     CAACCT
GAM390  MUT     3'  CCAGGGTTTTGTTTTAGCTTTT 6029         G    AC_______ CCAG
            GTCT                  AGGCAGGAG TGGAA       C   G
                                  ||||||||| |||||       |   |
                                  TCTGTTTTC ATTTT       G   C
                                       G    GTTTT  G GACC
GAM390  MXI1    3'  TCCTGTAGTTTTATTTTATGTT 56132      G     G   CC
            T                     AGGCA GAGGTG AAAC  CAGGG
                                  ||||| |||||| ||||  |||||
                                  TTTGT TTTTAT TTTG  GTCCT
                                     A     _   AT
GAM390  MXI1    3'  TCCTGTAGTTTTATTTTATGTT 56133      G     G   CC
            T                     AGGCA GAGGTG AAAC  CAGGG
                                  ||||| |||||| ||||  |||||
                                  TTTGT TTTTAT TTTG  GTCCT
                                     A     _   AT
GAM390  MYC     5'  CCTGGCTCCCCTCCTGCCT   11729         T   AACC
                                  AGGCAGGAGG GGA    CCAGG
                                  |||||||||| |||    |||||
                                  TCCGTCCTCC CCT    GGTCC
                                       _   C____
GAM390  MYEOV   3'  CTTTGGGCTCTGTCTCCTCCCT 57847     C     TG  AAC
                                  AGG AGGAGG  GA   CCCAGGG
                                  ||| ||||||  ||   |||||||
                                  TCC TCCTCT  CT   GGGTTTC
                                    C     GT  C__
GAM390  MYLK    3'  CCCAGGGCCAGTATTTTTCCTT 98795         TG   A_________  CCAG
            TTGCTT                AGGCAGGAGG  GAA       CC   GG
                                  ||||||||||  |||       ||   ||
                                  TTCGTTTTCC  TTT       GG   CC
                                       TT   ATGACC    GACC
GAM390  MYO15A  3'  CCCTGCCCCTAACTCCTGCCT  33181        GT_  AAACCC
                                  AGGCAGGAG   GG     CAGGG
                                  |||||||||   ||     |||||
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                                TCCGTCCTC  CC    GTCCC
                                     AAT  CC____
GAM390  MYO1C   3'  CAGGGTTCTGTCTGTTTACCTG 61857      _  TG  AA_____  CCAG
          TCT                  AGGCAGG AGG  GA      CC   G
                               ||||||| ||| ||       ||   |
                               TCTGTCC TTT  CT      GG   C
                                  A  GT  GTCTT    GAC
GAM390  MYO1C   3'  CCTTGGCACCTTGTCTTTCTGT 61862        TGGAAACC
          CT                   AGGCAGGAGG      CCAGGG
                               ||||||||||      ||||||
                               TCTGTCTTTC      GGTTCC
                                     TGTTCCAC
GAM390  MYO1F   3'  CCCTGGGATACTGCCTTCTCTT 83326    C     TG AAAC
                               AGG AGGAGG  G   CCCAGGG
                               ||| ||||||  |   |||||||
                               TTC TCTTCC  C   GGGTCCC
                                 _     GT ATA_
GAM390  MYOM2   5'  CCTTGCAATTTTCCTTTCTGTC 15607        T    CCC
          T                    AGGCAGGAGG GGAAA  CAGGG
                               |||||||||| |||||  |||||
                               TCTGTCTTTC CTTTT  GTTCC
                                     _    AAC
GAM390  NARS    3'  CATTGGGGTTTCTCTTTCTGTT 16998        T        GG
          T                    AGGCAGGAGG GGAAACCCCAG
                               |||||||||| ||||||||||
                               TTTGTCTTTC TCTTTGGGGTT
                                     _         ACT
GAM390  NAV2    3'  CCCCAGGGTTTTATTCCATCTT 60791          A_______  CCAG
          TTGC                 GCAGGAGGTGGAA      CC   GG
                               ||||||||||||       ||   ||
                               CGTTTTCTACCTT      GG   CC
                                     ATTTT    GACC
GAM390  NCL     3'  CTCTGGGGTTTTTACTGTTACC 60690    CAGGA
          T                    AGG    GGTGGAAACCCCAGGG
                               |||    ||||||||||||||||
                               TCC    TCATTTTTGGGGTCTC
                                 ATTG_
GAM390  NCOA4   3'  CCAGGGCTTAGTTCTTCTCCTG 19551        T  AA_____  CCAG
          CCT                  AGGCAGGAGG GGA      CC   G
                               |||||||||| |||      ||   |
                               TCCGTCCTCT CTT      GG   C
                                     T  GATTC    GACC
GAM390  NCSTN   3'  CCCAGGGTTTTGTTTTTGTCTT 74134    C    TG   _______  CAG
          TTTCCT                AGG AGGAGG  GAAAC     CC  GG
                               ||| ||||||  |||||     ||  ||
                               TCC TTTTCT  TTTTG     GG  CC
                                 T    GT    TTTT    GAC
GAM390  NCSTN   5'  GGTCCTTCGCCTTCTGTCT   74137          AA____
                               AGGCAGGAGGTGGA    CC
                               ||||||||||||||    ||
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                                TCTGTCTTCCGCTT     GG
                                        CCT
GAM390  NDP      3'  TCCTGGGACATCTTCTGTT   6045          GAAAC
                                GGCAGGAGGTG    CCCAGGG
                                ||||||||||    |||||||
                                TTGTCTTCTAC    GGGTCCT
                                      A____
GAM390  NDRG1    3'  CCCAGGGCTTTCCTTCCCTCTC 60309         T   AC_________ CCAG
            CTGCTT                 AGGCAGGAGG GGAA       C   G
                                ||||||||||| ||||        |   |
                                TTCGTCCTCT CCTT        G   C
                                      C   CCTTTC   G GACC
GAM390  NDUFA6   3'  TTCTGCAGCCTCTTTTTGCCT  11765         T  AAACCC
                                AGGCAGGAGG GG     CAGGG
                                |||||||||| ||     |||||
                                TCCGTTTTTC CC     GTCTT
                                      T  GAC___
GAM390  NEDD4    3'  CCTTAACATTTACCTCTTGT   70544          AACCCC
                                GCAGGAGGTGGA     AGG
                                ||||||||||||     |||
                                TGTTCTCCATTT     TCC
                                      ACAAT_
GAM390  NEDD4L   3'  TCTGTTTAGTCTCCTGTTT   31608         TG   ACCC
                                AGGCAGGAGG  GAA   CAGG
                                |||||||||  |||   ||||
                                TTTGTCCTCT  TTT   GTCT
                                      GA  _____
GAM390  NEO1     3'  TCCTGGGGTTGGCTTGTTTTTT 11776       TG A__
            G                   CAGGAGG  G   AACCCCAGGG
                                |||||||  |  ||||||||||
                                GTTTTTT  T   TTGGGGTCCT
                                    GT CGG
GAM390  NEUD4    3'  CTCTGGGGTGGTGCTCGCCTAC 17379       _    _ AA__
            CTGCCT                 AGGCAGG AGGTG G    ACCCCAGGG
                                ||||||| ||||| |    |||||||||
                                TCCGTCC TCCGC C    TGGGGTCTC
                                    A    T GTGG
GAM390  NFYC     3'  CCAGGGTTTTTTTCCATTTTTT 27246     C        A________  CCAG
            TCT                   AGG AGGAGGTGGAA       CC   G
                                ||| ||||||||||       ||   |
                                TCT TTTTTTACCTT       GG   C
                                  _         TTTTT    GACC
GAM390  NLGN3    3'  CCTTGGTGCTCGCCTTCGGCCT 39119     A       AA   CC
                                AGGC GGAGGTGG  ACC  AGG
                                |||| ||||||||  |||  |||
                                TCCG CTTCCGCT  TGG  TCC
                                  G       CG   T_
GAM390  NMB      3'  CCTGCTGTATTTCCTGCTT   74208          GGAA  CC
                                AGGCAGGAGGT    AC  CAGG
                                ||||||||||    ||  ||||
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                                TTCGTCCTTTA   TG  GTCC
                                      ____ TC
GAM390  NOS1    3'  CCCTCGCTCTGCCTCCTGTC  7092        TG  AACCCC
                                GGCAGGAGG  GA    AGGG
                                |||||||||  ||    ||||
                                CTGTCCTCC  CT    TCCC
                                     GT  CGC___
GAM390  NOTCH2  3'  CTTTGGGGATAGGTTTTTTTGT 44573        TGGAAA
           TT                    AGGCAGGAGG    CCCCAGGG
                                ||||||||||    ||||||||
                                TTTGTTTTTT    GGGGTTTC
                                     TGGATA
GAM390  NOTCH2  3'  CTTTGGTCTCCTTTCCCCTCCT 44574        T   CC___
           GTCT                   AGGCAGGAGG GGAAA    CCAGGG
                                |||||||||| |||||    ||||||
                                TCTGTCCTCC CCTTT    GGTTTC
                                     _    CCTCT
GAM390  NOTCH2  3'  GGCTTTGCTATTTTCTGCT   44576         A A_____
                                GGCAGGAGGTGG A    CC
                                ||||||||||||      ||
                                TCGTCTTTTATC T    GG
                                      G TTC
GAM390  NOVA1   3'  TCCTGTAAGTCTTACTTCCTGC 22421         _  AACCC
           TT                    AGGCAGGAGGTG GA    CAGGG
                                |||||||||||| ||    |||||
                                TTCGTCCTTCAT CT    GTCCT
                                      T  GAAT_
GAM390  NPDC1   5'  CCTTGGCATCCGCCTCTTCTT  31813    C       AACC
                                AGG AGGAGGTGGA   CCAGGG
                                ||| ||||||||||   ||||||
                                TTC TTCTCCGCCT   GGTTCC
                                  _       AC__
GAM390  NPR2L   3'  TTTTAGGTTTTAGTTTTTTGTT 22604        TG    CCAGGG
           T                     AGGCAGGAGG  GAAACC
                                ||||||||||  ||||||
                                TTTGTTTTTT  TTTTGG
                                     GA     ATTTT
GAM390  NPR3    3'  CCCCAGGGCCCACTTTTTTTTT 8061        ________    AAA_  CCAG
           TCTGCCT                AGGCAGGA     GGTGG   CC   GG
                                |||||||      |||||   ||   ||
                                TCCGTCTT     TCACC   GG   CC
                                    TTTTTTT    C    GACC
GAM390  NPTX1   3'  GGTGTTTCTGTCTTCTGTT   11840       TG   ____
                                GGCAGGAGG  GAAAC   CC
                                |||||||||  |||||   ||
                                TTGTCTTCT  CTTTG   GG
                                     GT    T
GAM390  NR1D1   3'  CTCTGATTTGTTCTGTTCCTGT 41669       G TG   ACCC_
           CT                    AGGCAGGA G  GAA    CAGGG
                                |||||||| |  |||    |||||
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                                TCTGTCCT T  CTT    GTCTC
                                    _ GT   GTTTA
GAM390  NRAS    3'  TCCTGTTGCTGTCTTCAGTCT  11845     A    TG AAACCC
                                AGGC GGAGG  G     CAGGG
                                |||| |||||  |     |||||
                                TCTG CTTCT  C     GTCCT
                                  A    GT GTT___
GAM390  NRGN    3'  CCCAATCTTCCTTCTTTTGCTT 21621         T   ACCCCA
                                AGGCAGGAGG GGAA     GGG
                                |||||||||| ||||     |||
                                TTCGTTTTCT CCTT     CCC
                                      T   CTAA__
GAM390  NT5C2   3'  CCAGGGTCCTTATTACCTTTTG 25260         _____  AA_  CCAG
            TTT                   AGGCAGGAGGT    GGA  CC   G
                                ||||||||||    |||  ||   |
                                TTTGTTTTCCA    CCT  GG   C
                                      TTATT      GACC
GAM390  NT5E    3'  CTCTGCTTTATTTCTTGTCT  11849           AACCC
                                AGGCAGGAGGTGGA    CAGGG
                                ||||||||||||||    |||||
                                TCTGTTCTTTATTT    GTCTC
                                      C____
GAM390  NUFIP1  3'  TTTGGGAAATTATCTGCCT   25639       AG  GGAAAC
                                AGGCAGG  GT    CCCAGG
                                |||||||  ||    ||||||
                                TCCGTCT  TA    GGGTTT
                                    AT  AA____
GAM390  NUP98   3'  GGCTGTTTTTGTTCCTGCCT  33327       G TG   _____
                                AGGCAGGA G  GAAAC    CC
                                |||||||| |  |||||    ||
                                TCCGTCCT T  TTTTG    GG
                                    _ GT    TC
GAM390  OAS2    3'  GGTCTTTCTGCCTTTGGCTT  11869     AG       A_____
                                AGGC  GAGGTGGAA     CC
                                ||||  |||||||||     ||
                                TTCG  TTCCGTCTT     GG
                                  GT       TCT
GAM390  OCRL    3'  CTCTGAGACCCATCTCCTGCCT 6059           AAACCC
                                AGGCAGGAGGTGG     CAGGG
                                ||||||||||||     |||||
                                TCCGTCCTCTACC     GTCTC
                                      CAGA__
GAM390  OGT     5'  TCTTGTTTTTATTTTCTCTCTT 14597         T    CCC___
            GTTT                  AGGCAGGAGG GGAAA     CAGGG
                                ||||||||||| |||||     |||||
                                TTTGTTCTCT CTTTT     GTTCT
                                      _    ATTTTT
GAM390  OPCML   3'  CCAGGGTTTGCTTTTATTTCCA 11895     A       AC_______ CCAG
            GCTT                  AGGC GGAGGTGGAA       C   G
                                |||| ||||||||||       |   |
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                                TTCG CCTTTATTTT       G   C
                                  A       CGTTT   G GACC
GAM390  ORC4L    3'  CTTGGCTGTGTCTTGCCT    62741        G TG AAACC
                                AGGCAGGA G  G    CCAGG
                                |||||||| |  |    |||||
                                TCCGTTCT T  C    GGTTC
                                    G GT _____
GAM390  OTOF     3'  CCTTGGGCCGAGCCTGCCTCCT 17829          _  AAAC_
           GCTT                   AGGCAGGAGGT GG    CCCAGGG
                                |||||||||||  ||    |||||||
                                TTCGTCCTCCG CC    GGGTTCC
                                      T  GAGCC
GAM390  OTP      3'  CCAGGGTTTGCTTCCTTTTCTG 50405         T   AC________ CCAG
           TTT                    AGGCAGGAGG GGAA       C   G
                                |||||||||| ||||       |   |
                                TTTGTCTTTT CCTT       G   C
                                      _   CGTTT   G GACC
GAM390  P23      3'  TTGGATTTTTTATTTCCT    22755          CC
                                AGGAGGTGGAAA  CCAG
                                ||||||||||||  ||||
                                TCCTTTATTTTT  GGTT
                                      TA
GAM390  P2RY1    3'  CAGGGTTTACTTTCTCTTTTGC 11930         T   AC________ CCAG
           CT                     AGGCAGGAGG GGAA       C   G
                                |||||||||| ||||       |   |
                                TCCGTTTTCT CTTT       G   C
                                      _   CATTT   G GAC
GAM390  PABPN1   3'  TTTTGTGTTTCTTTTTCTGTTT 17361         T    CC
                                AGGCAGGAGG GGAAAC  CAGGG
                                |||||||||| ||||||  |||||
                                TTTGTCTTTT TCTTTG  GTTTT
                                      _     T_
GAM390  PACE4    3'  CCTTGTTACCGTGTTCTGTCT  11948       GG   A   CCC
                                AGGCAGGA  TGG AAC   AGG
                                ||||||||  ||| |||   |||
                                TCTGTCTT  GCC TTG   TCC
                                    GT   A   T__
GAM390  PAFAH1B1 3'  CAGGGCTGTTTTCACCTTTTGT 6471              _____  CAG
           TT                     AGGCAGGAGGTGGAAAC    CC   G
                                |||||||||||||||||    ||   |
                                TTTGTTTTCCACTTTTG    GG   C
                                      TC    GAC
GAM390  PAFAH1B1 3'  CTCTCCCGTTCGCCTCTTTCT  6474     C       AACCCC
                                AGG AGGAGGTGGA     AGGG
                                ||| ||||||||||     ||||
                                TCT TTCTCCGCTT     TCTC
                                  _        GCCC__
GAM390  PAG      3'  CCAGGGTTTTGTTTCATTTCAT 38013      G       AC________ CCAG
           GCCT                   AGGCA GAGGTGGAA       C   G
                                ||||| |||||||||       |   |
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                                TCCGT CTTTACTTT       G   C
                                  A       GTTTT  G GACC
GAM390  PAG     3'  CCTGGAGTCTCTTCTGTCT   38014        GT  AACC
                                AGGCAGGAG  GGA   CCAGG
                                |||||||||  |||   |||||
                                TCTGTCTTC  TCT   GGTCC
                                     __  GA__
GAM390  PAK1    5'  TCCAGTTACCACCTCCTGCCT  11959          A  CCCA
                                AGGCAGGAGGTGG AAC   GGG
                                |||||||||||||| |||   |||
                                TCCGTCCTCCACC TTG   CCT
                                      A  A___
GAM390  PAM     3'  TTTTGGTTAAGTTGGCTTCTGT 57843        G  AAACC
            TT                   AGGCAGGAG TGG    CCAGGG
                                |||||||||  |||    ||||||
                                TTTGTCTTC GTT    GGTTTT
                                     G  GAATT
GAM390  PAP     3'  CAGGGTCTTATCTTTCTTCTGT 58037         T  AA_____  CCAG
            TT                   AGGCAGGAGG GGA      CC   G
                                |||||||||| |||       ||   |
                                TTTGTCTTCT TCT       GG   C
                                     T  ATTCT    GAC
GAM390  PAP     3'  CCAGGGTCTTATCTTTCTTCTG 58038         T  AA_____  CCAG
            TTT                  AGGCAGGAGG GGA      CC   G
                                |||||||||| |||       ||   |
                                TTTGTCTTCT TCT       GG   C
                                     T  ATTCT    GACC
GAM390  PARG    3'  CAGGGTTTTGTTTCTATTTTCT 14639    C        _____  CAG
            TCT                  AGG AGGAGGTGGAAAC     CC  G
                                ||| ||||||||||||      ||   |
                                TCT TCTTTTATCTTTG      GG  C
                                  _         TTTT    GAC
GAM390  PAX2    3'  TCCGTGTTTTCGCTTTTTCCT  15662    C        CCCA
                                AGG AGGAGGTGGAAAC   GGG
                                ||| ||||||||||||   |||
                                TCC TTTTTCGCTTTTG   CCT
                                  _         TG__
GAM390  PAX2    3'  TCCGTGTTTTCGCTTTTTCCT  15663    C        CCCA
                                AGG AGGAGGTGGAAAC   GGG
                                ||| ||||||||||||   |||
                                TCC TTTTTCGCTTTTG   CCT
                                  _         TG__
GAM390  PAX5    3'  CCTTGGGCCCCAGCCTCCTGCT 34128        _  AAAC
                                GGCAGGAGG TGG   CCCAGGG
                                |||||||||  |||   |||||||
                                TCGTCCTCC ACC   GGGTTCC
                                     G  CC__
GAM390  PAX9    5'  GGTCCTTTTACTTCTTCCT   21665    C       AC_____
                                AGG AGGAGGTGGAA     C
                                ||| ||||||||||      |
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                              TCC TTCTTCATTTT      G
                                _         CCT   G
GAM390  PBX2    3'  CCAGGGCTTTTTTCCATCTTTT 11977     C         A________  CCAG
            TCCT                  AGG AGGAGGTGGAA       CC    G
                              ||| ||||||||||       ||    |
                              TCC TTTTCTACCTT       GG    C
                                T         TTTTC     GACC
GAM390  PBX2    3'  CCCTGGGATCCATCTGTT    11979    G      AAC
                              AG AGGTGGA   CCCAGGG
                              || |||||||   |||||||
                              TT TCTACCT   GGGTCCC
                               G      A__
GAM390  PBX2    3'  CTTTGGGGTTGAACTTTTT    11980        GGA
                              AGGAGGT   AACCCCAGGG
                              |||||||   ||||||||||
                              TTTTTCA   TTGGGGTTTC
                                  AG_
GAM390  PCDH11X  3'  TTTTGGGCTTTCTTTTTGATTT 28019         GT_____    C
            TTGTTT                 AGGCAGGAG     GGAAA CCCAGGG
                              |||||||||      ||||| |||||||
                              TTTGTTTTT     TCTTT GGGTTTT
                                   AGTTTT    C
GAM390  PCDH11Y  3'  GTTTTGGGGCTTTCTTTTTGAT 53167         GT_____    _
            TTTTGTTT               AGGCAGGAG     GGAAA CCCCAGGG   T
                              |||||||||      ||||| ||||||||   |
                              TTTGTTTTT     TCTTT GGGGTTTT   G
                                   AGTTTT    C
GAM390  PCDH7    3'  TTCTGTAAAGTTTTGTCTTCTC 11994      _     TG   ACCC_
            GTTT                   AGGC AGGAGG  GAA     CAGGG
                              ||||  ||||||  |||     |||||
                              TTTG TCTTCT  TTT     GTCTT
                                C     GT   GAAAT
GAM390  PCDH9    5'  CCCATGTTTCCATCTCCTGTC  83692              CCCA
                              GGCAGGAGGTGGAAAC    GGG
                              ||||||||||||||||    |||
                              CTGTCCTCTACCTTTG    CCC
                                        TA__
GAM390  PCDHA1   3'  CCAGGGTCTTGTCTACTTTTAG 49411      AG       AA_______  CCAG
            CTT                    AGGC  GAGGTGGA       CC    G
                              ||||  ||||||||       ||    |
                              TTCG  TTTCATCT       GG    C
                                AT       GTTCT    GACC
GAM390  PCDHA1   3'  CTCTGGGGCTGCCTCTTGC   49412         TG AAA
                              GCAGGAGG  G   CCCCAGGG
                              ||||||||  |   ||||||||
                              CGTTCTCC  C   GGGGTCTC
                                   GT ____
GAM390  PCDHA10  3'  CCAGGGTCTTGTCTACTTTTAG 38788      AG       AA_______  CCAG
            CTT                    AGGC  GAGGTGGA       CC    G
                              ||||  ||||||||       ||    |
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                          TTCG  TTTCATCT     GG   C
                            AT      GTTCT    GACC
GAM390  PCDHA10  3' CTCTGGGGCTGCCTCTTGC   38789       TG AAA
                          GCAGGAGG  G   CCCCAGGG
                          ||||||||  |   ||||||||
                          CGTTCTCC  C   GGGGTCTC
                              GT ___
GAM390  PCDHA11  3' CCAGGGTCTTGTCTACTTTTAG 49859     AG      AA_______ CCAG
          CTT               AGGC  GAGGTGGA     CC   G
                          ||||  ||||||||      ||   |
                          TTCG  TTTCATCT     GG   C
                            AT      GTTCT    GACC
GAM390  PCDHA11  3' CTCTGGGGCTGCCTCTTGC   49860       TG AAA
                          GCAGGAGG  G   CCCCAGGG
                          ||||||||  |   ||||||||
                          CGTTCTCC  C   GGGGTCTC
                              GT ___
GAM390  PCDHA12  3' CCAGGGTCTTGTCTACTTTTAG 38796     AG      AA_______ CCAG
          CTT               AGGC  GAGGTGGA     CC   G
                          ||||  ||||||||      ||   |
                          TTCG  TTTCATCT     GG   C
                            AT      GTTCT    GACC
GAM390  PCDHA12  3' CTCTGGGGCTGCCTCTTGC   38797       TG AAA
                          GCAGGAGG  G   CCCCAGGG
                          ||||||||  |   ||||||||
                          CGTTCTCC  C   GGGGTCTC
                              GT ___
GAM390  PCDHA13  3' CCAGGGTCTTGTCTACTTTTAG 49867     AG      AA_______ CCAG
          CTT               AGGC  GAGGTGGA     CC   G
                          ||||  ||||||||      ||   |
                          TTCG  TTTCATCT     GG   C
                            AT      GTTCT    GACC
GAM390  PCDHA13  3' CTCTGGGGCTGCCTCTTGC   49868       TG AAA
                          GCAGGAGG  G   CCCCAGGG
                          ||||||||  |   ||||||||
                          CGTTCTCC  C   GGGGTCTC
                              GT ___
GAM390  PCDHA2   3' CCAGGGTCTTGTCTACTTTTAG 38803     AG      AA_______ CCAG
          CTT               AGGC  GAGGTGGA     CC   G
                          ||||  ||||||||      ||   |
                          TTCG  TTTCATCT     GG   C
                            AT      GTTCT    GACC
GAM390  PCDHA2   3' CTCTGGGGCTGCCTCTTGC   38804       TG AAA
                          GCAGGAGG  G   CCCCAGGG
                          ||||||||  |   ||||||||
                          CGTTCTCC  C   GGGGTCTC
                              GT ___
GAM390  PCDHA3   3' CCAGGGTCTTGTCTACTTTTAG 49804     AG      AA_______ CCAG
          CTT               AGGC  GAGGTGGA     CC   G
                          ||||  ||||||||      ||   |
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                                TTCG TTTCATCT     GG  C
                                  AT     GTTCT   GACC
GAM390  PCDHA3   3' CTCTGGGGCTGCCTCTTGC  49805       TG AAA
                                GCAGGAGG G  CCCCAGGG
                                |||||||| |  ||||||||
                                CGTTCTCC C  GGGGTCTC
                                    GT ___
GAM390  PCDHA4   3' CCAGGGTCTTGTCTACTTTTAG 38811    AG      AA_______ CCAG
          CTT                     AGGC  GAGGTGGA     CC   G
                                |||| ||||||||      ||   |
                                TTCG TTTCATCT     GG  C
                                  AT     GTTCT   GACC
GAM390  PCDHA4   3' CTCTGGGGCTGCCTCTTGC  38812       TG AAA
                                GCAGGAGG G  CCCCAGGG
                                |||||||| |  ||||||||
                                CGTTCTCC C  GGGGTCTC
                                    GT ___
GAM390  PCDHA5   3' CCAGGGTCTTGTCTACTTTTAG 49811    AG      AA_______ CCAG
          CTT                     AGGC  GAGGTGGA     CC   G
                                |||| ||||||||      ||   |
                                TTCG TTTCATCT     GG  C
                                  AT     GTTCT   GACC
GAM390  PCDHA5   3' CTCTGGGGCTGCCTCTTGC  49812       TG AAA
                                GCAGGAGG G  CCCCAGGG
                                |||||||| |  ||||||||
                                CGTTCTCC C  GGGGTCTC
                                    GT ___
GAM390  PCDHA6   3' CCAGGGTCTTGTCTACTTTTAG 38819    AG      AA_______ CCAG
          CTT                     AGGC  GAGGTGGA     CC   G
                                |||| ||||||||      ||   |
                                TTCG TTTCATCT     GG  C
                                  AT     GTTCT   GACC
GAM390  PCDHA6   3' CTCTGGGGCTGCCTCTTGC  38820       TG AAA
                                GCAGGAGG G  CCCCAGGG
                                |||||||| |  ||||||||
                                CGTTCTCC C  GGGGTCTC
                                    GT ___
GAM390  PCDHA7   3' CCAGGGTCTTGTCTACTTTTAG 49824    AG      AA_______ CCAG
          CTT                     AGGC  GAGGTGGA     CC   G
                                |||| ||||||||      ||   |
                                TTCG TTTCATCT     GG  C
                                  AT     GTTCT   GACC
GAM390  PCDHA7   3' CTCTGGGGCTGCCTCTTGC  49825       TG AAA
                                GCAGGAGG G  CCCCAGGG
                                |||||||| |  ||||||||
                                CGTTCTCC C  GGGGTCTC
                                    GT ___
GAM390  PCDHA8   3' CCAGGGTCTTGTCTACTTTTAG 38827    AG      AA_______ CCAG
          CTT                     AGGC  GAGGTGGA     CC   G
                                |||| ||||||||      ||   |
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                                TTCG  TTTCATCT      GG   C
                                  AT      GTTCT    GACC
GAM390  PCDHA8   3' CTCTGGGGCTGCCTCTTGC   38828        TG AAA
                                GCAGGAGG  G   CCCCAGGG
                                ||||||||  |   ||||||||
                                CGTTCTCC  C   GGGGTCTC
                                    GT ___
GAM390  PCDHA9   3' CCAGGGTCTTGTCTACTTTTAG 49835     AG      AA_______ CCAG
           CTT                    AGGC  GAGGTGGA      CC   G
                                ||||  ||||||||      ||   |
                                TTCG  TTTCATCT      GG   C
                                  AT      GTTCT    GACC
GAM390  PCDHA9   3' CTCTGGGGCTGCCTCTTGC   26618        TG AAA
                                GCAGGAGG  G   CCCCAGGG
                                ||||||||  |   ||||||||
                                CGTTCTCC  C   GGGGTCTC
                                    GT ___
GAM390  PCDHAC1  3' CCAGGGTCTTGTCTACTTTTAG 38778     AG      AA_______ CCAG
           CTT                    AGGC  GAGGTGGA      CC   G
                                ||||  ||||||||      ||   |
                                TTCG  TTTCATCT      GG   C
                                  AT      GTTCT    GACC
GAM390  PCDHAC1  3' CTCTGGGGCTGCCTCTTGC   38779        TG AAA
                                GCAGGAGG  G   CCCCAGGG
                                ||||||||  |   ||||||||
                                CGTTCTCC  C   GGGGTCTC
                                    GT ___
GAM390  PCDHAC2  3' CCAGGGTCTTGTCTACTTTTAG 38784     AG      AA_______ CCAG
           CTT                    AGGC  GAGGTGGA      CC   G
                                ||||  ||||||||      ||   |
                                TTCG  TTTCATCT      GG   C
                                  AT      GTTCT    GACC
GAM390  PCDHAC2  3' CTCTGGGGCTGCCTCTTGC   49876        TG AAA
                                GCAGGAGG  G   CCCCAGGG
                                ||||||||  |   ||||||||
                                CGTTCTCC  C   GGGGTCTC
                                    GT ___
GAM390  PCDHB13  3' CCCCAGGGCTTTAAATATGCTT 38935         GAAA_________ CCAG
           TTTGCTT                 AGGCAGGAGGTG         CC   GG
                                ||||||||||||         ||   ||
                                TTCGTTTTTCGT         GG   CC
                                     ATAAATTTC    GACC
GAM390  PCDHB16  3' CCAGGGTCCTATTCATTTTTTG 40905          AA_______ CCAG
           CT                    GGCAGGAGGTGGA      CC   G
                                ||||||||||||||      ||   |
                                TCGTTTTTTACTT      GG   C
                                     ATCCT    GACC
GAM390  PCDHB3   3' CCCCAGGGTCTTAATTCCGCCT 38939         A_________ CCAG
           TTT                    AGGAGGTGGAA       CC   GG
                                ||||||||||||       ||   ||
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                                TTTTCCGCCTT      GG   CC
                                     AATTCT    GACC
GAM390  PCDHGA1  3' CCCTGGGGACCAGTCTTCTGTT 38837       _  AAA
           T                  AGGCAGGAGG TGG  CCCCAGGG
                              |||||||||| |||  ||||||||
                              TTTGTCTTCT ACC  GGGGTCCC
                                   G  A__
GAM390  PCDHGA10 3' CCCTGGGGACCAGTCTTCTGTT 50312       _  AAA
           T                  AGGCAGGAGG TGG  CCCCAGGG
                              |||||||||| |||  ||||||||
                              TTTGTCTTCT ACC  GGGGTCCC
                                   G  A__
GAM390  PCDHGA11 3' CCCTGGGGACCAGTCTTCTGTT 38844       _  AAA
           T                  AGGCAGGAGG TGG  CCCCAGGG
                              |||||||||| |||  ||||||||
                              TTTGTCTTCT ACC  GGGGTCCC
                                   G  A__
GAM390  PCDHGA12 3' CCCTGGGGACCAGTCTTCTGTT 50319       _  AAA
           T                  AGGCAGGAGG TGG  CCCCAGGG
                              |||||||||| |||  ||||||||
                              TTTGTCTTCT ACC  GGGGTCCC
                                   G  A__
GAM390  PCDHGA2  3' CCCTGGGGACCAGTCTTCTGTT 38851       _  AAA
           T                  AGGCAGGAGG TGG  CCCCAGGG
                              |||||||||| |||  ||||||||
                              TTTGTCTTCT ACC  GGGGTCCC
                                   G  A__
GAM390  PCDHGA3  3' CCCTGGGGACCAGTCTTCTGTT 50095       _  AAA
           T                  AGGCAGGAGG TGG  CCCCAGGG
                              |||||||||| |||  ||||||||
                              TTTGTCTTCT ACC  GGGGTCCC
                                   G  A__
GAM390  PCDHGA4  3' CCCTGGGGACCAGTCTTCTGTT 38859       _  AAA
           T                  AGGCAGGAGG TGG  CCCCAGGG
                              |||||||||| |||  ||||||||
                              TTTGTCTTCT ACC  GGGGTCCC
                                   G  A__
GAM390  PCDHGA5  3' CCCTGGGGACCAGTCTTCTGTT 50293       _  AAA
           T                  AGGCAGGAGG TGG  CCCCAGGG
                              |||||||||| |||  ||||||||
                              TTTGTCTTCT ACC  GGGGTCCC
                                   G  A__
GAM390  PCDHGA6  3' CCCTGGGGACCAGTCTTCTGTT 38867       _  AAA
           T                  AGGCAGGAGG TGG  CCCCAGGG
                              |||||||||| |||  ||||||||
                              TTTGTCTTCT ACC  GGGGTCCC
                                   G  A__
GAM390  PCDHGA7  3' CCCTGGGGACCAGTCTTCTGTT 50300       _  AAA
           T                  AGGCAGGAGG TGG  CCCCAGGG
                              |||||||||| |||  ||||||||
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                                TTTGTCTTCT ACC   GGGGTCCC
                                    G   A__
GAM390  PCDHGA8  3' CCCTGGGGACCAGTCTTCTGTT 26601        _  AAA
          T                  AGGCAGGAGG TGG   CCCCAGGG
                             |||||||||| |||   ||||||||
                             TTTGTCTTCT ACC   GGGGTCCC
                                    G   A__
GAM390  PCDHGA9  3' CCCTGGGGACCAGTCTTCTGTT 50307        _  AAA
          T                  AGGCAGGAGG TGG   CCCCAGGG
                             |||||||||| |||   ||||||||
                             TTTGTCTTCT ACC   GGGGTCCC
                                    G   A__
GAM390  PCDHGB1  3' CCCTGGGGACCAGTCTTCTGTT 38876        _  AAA
          T                  AGGCAGGAGG TGG   CCCCAGGG
                             |||||||||| |||   ||||||||
                             TTTGTCTTCT ACC   GGGGTCCC
                                    G   A__
GAM390  PCDHGB2  3' CCCTGGGGACCAGTCTTCTGTT 50325        _  AAA
          T                  AGGCAGGAGG TGG   CCCCAGGG
                             |||||||||| |||   ||||||||
                             TTTGTCTTCT ACC   GGGGTCCC
                                    G   A__
GAM390  PCDHGB3  3' CCCTGGGGACCAGTCTTCTGTT 38884        _  AAA
          T                  AGGCAGGAGG TGG   CCCCAGGG
                             |||||||||| |||   ||||||||
                             TTTGTCTTCT ACC   GGGGTCCC
                                    G   A__
GAM390  PCDHGB4  3' CCCTGGGGACCAGTCTTCTGTT 50330        _  AAA
          T                  AGGCAGGAGG TGG   CCCCAGGG
                             |||||||||| |||   ||||||||
                             TTTGTCTTCT ACC   GGGGTCCC
                                    G   A__
GAM390  PCDHGB5  3' CCCTGGGGACCAGTCTTCTGTT 38891        _  AAA
          T                  AGGCAGGAGG TGG   CCCCAGGG
                             |||||||||| |||   ||||||||
                             TTTGTCTTCT ACC   GGGGTCCC
                                    G   A__
GAM390  PCDHGB6  3' CCCTGGGGACCAGTCTTCTGTT 50335        _  AAA
          T                  AGGCAGGAGG TGG   CCCCAGGG
                             |||||||||| |||   ||||||||
                             TTTGTCTTCT ACC   GGGGTCCC
                                    G   A__
GAM390  PCDHGB7  3' CCCTGGGGACCAGTCTTCTGTT 38900        _  AAA
          T                  AGGCAGGAGG TGG   CCCCAGGG
                             |||||||||| |||   ||||||||
                             TTTGTCTTCT ACC   GGGGTCCC
                                    G   A__
GAM390  PCDHGC3  3' CCCTGGGGACCAGTCTTCTGTT 51529        _  AAA
          T                  AGGCAGGAGG TGG   CCCCAGGG
                             |||||||||| |||   ||||||||
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                                TTTGTCTTCT ACC   GGGGTCCC
                                     G   A__
GAM390  PCDHGC4   3'  CCCTGGGGACCAGTCTTCTGTT 38906         _   AAA
           T                  AGGCAGGAGG TGG   CCCCAGGG
                              |||||||||| |||   ||||||||
                              TTTGTCTTCT ACC   GGGGTCCC
                                     G   A__
GAM390  PCDHGC5   3'  CCCTGGGGACCAGTCTTCTGTT 51556         _   AAA
           T                  AGGCAGGAGG TGG   CCCCAGGG
                              |||||||||| |||   ||||||||
                              TTTGTCTTCT ACC   GGGGTCCC
                                     G   A__
GAM390  PCLO     3'  TCCTGCTGTCCTTTCCTGTTT  95889         T   AACCC
                              AGGCAGGAGG GGA    CAGGG
                              |||||||||| |||    |||||
                              TTTGTCCTTT CCT    GTCCT
                                     _   GTC__
GAM390  PCOLN3   3'  CTTTGGGCACAGCCTGCTGTCT 12412       G   GGAAAC
                              AGGCAG AGGT     CCCAGGG
                              |||||| ||||     |||||||
                              TCTGTC TCCG     GGGTTTC
                                 G   ACAC__
GAM390  PCSK2    3'  CAGGGCTCTATTTCATTTTTTG 11999          A_______  CCAG
           C                   GCAGGAGGTGGAA      CC   G
                               ||||||||||||       ||   |
                               CGTTTTTTACTTT      GG   C
                                      ATCTC    GAC
GAM390  PCTK1    3'  CCAGGGCTCTGCCTGCTTTCCT 53415       _____  TG  AA__  CCAG
           GCCT                  AGGCAGGA    GG  GA   CC   G
                               ||||||||    ||  ||   ||   |
                               TCCGTCCT    CC  CT   GG   C
                                    TTCGT  GT  C    GACC
GAM390  PCTK1    5'  CCCTGGTGCCGTCTCCGGCTT  53416     A   GT  AAACC
                              AGGC GGAG  GG    CCAGGG
                              |||| ||||  ||    ||||||
                              TTCG CCTC  CC    GGTCCC
                                G   TG  GT___
GAM390  PCTK3    5'  CCCTCCCTTCTACCTCCTCTT  73325     C        ACCCC
                              AGG AGGAGGTGGAA    AGGG
                              ||| ||||||||||    ||||
                              TTC TCCTCCATCTT    TCCC
                                _         CCC__
GAM390  PCTP     3'  TCCTGGGCTGGGCTGCCTTCTT 41375     C     TG AAAC_
           CT                   AGG AGGAGG  G    CCCAGGG
                              ||| ||||||  |    |||||||
                              TCT TCTTCC  C    GGGTCCT
                                _     GT GGGTC
GAM390  PDCL     3'  CCCTGCTTGTCTTTGTCTCTT  19396       TG  A  CC_
                              AGGAGG  GA AC   CAGGG
                              ||||||  || ||   |||||
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                                TTCTCT  TT TG   GTCCC
                                   GT  C  TTC
GAM390  PDCL    3'  TTTGGTCTGTTTCCTGCC    19404        TG  AACC
                                GGCAGGAGG  GA   CCAGG
                                |||||||||  ||   |||||
                                CCGTCCTTT  CT   GGTTT
                                     GT  ____
GAM390  PDE4B   5'  CTTTGGTGCTTCTGCCTTTAGT 12012     AG   TG   ACC
           TT                    AGGC  GAGG  GAA   CCAGGG
                                ||||  ||||  |||   ||||||
                                TTTG  TTCC  CTT   GGTTTC
                                  AT   GT   CGT
GAM390  PDE7A   3'  CCTGGTTTGCCTTTTTCTT   66136    C     TG  AACC
                                AGG AGGAGG  GA   CCAGG
                                ||| ||||||  ||   |||||
                                TTC TTTTCC  TT   GGTCC
                                  T     GT  ____
GAM390  PDGFB   3'  TCTGATTCACCTCTTCCT    12027    C       AACCC
                                AGG AGGAGGTGGA    CAGG
                                ||| ||||||||||    ||||
                                TCC TTCTCCACTT    GTCT
                                  _        A____
GAM390  PDGFB   3'  TTTGGGGGCTTTCCTTTT    12028      T   AA
                                AGGAGG GGA  CCCCAGG
                                ||||||  |||  |||||||
                                TTTTCC TTT  GGGGTTT
                                   _  CG
GAM390  PER2    3'  CCAGGGTTCTGCATTATTCTTG 43347        ____ TG  AA__  CCAG
           TCT                   AGGCAGGAG   G  GA   CC   G
                                |||||||||   | ||   ||   |
                                TCTGTTCTT   C  CT   GG   C
                                     ATTA GT  T    GACC
GAM390  PER2    3'  TCTTGGGGACTGCTTTTTATCT 43362    GC     TG AAA
                                AG  AGGAGG  G   CCCCAGGG
                                ||  ||||||  |   ||||||||
                                TC  TTTTTC  C   GGGGTTCT
                                 TA     GT A__
GAM390  PFKFB2  3'  CCAGGGTTTTCCTTCACTTTTG 21699      G      AA_______  CCAG
           TCT                   AGGCA GAGGTGGA       CC   G
                                |||||  ||||||||       ||   |
                                TCTGT TTTCACTT       GG   C
                                  _      CCTTTT    GACC
GAM390  PFKL    3'  CCCTGCTCAGCCCATCCCCTGC 12055       A    AAACCC
           CT                    AGGCAGG GGTGG     CAGGG
                                |||||||  |||||     |||||
                                TCCGTCC CTACC     GTCCC
                                   C    CGACTC
GAM390  PFKM    3'  TCTGCTTGTTTTCTTCCT    60817       TG    CC_
                                AGGAGG  GAAAC   CAGG
                                ||||||  |||||   ||||
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                                TCCTTC  TTTTG   GTCT
                                  __    TTC
GAM390  PFN1    3'  TTTGGGGTTTTTTTTTTCT   18474       TG
                                AGGAGG  GAAACCCCAGG
                                ||||||  ||||||||||
                                TCTTTT  TTTTGGGGTTT
                                   TT
GAM390  PGD     3'  CAGGGCTTTGCCCTATTTTCTG 79548          AAA________  CCAG
          TT                     GGCAGGAGGTGG        CC   G
                                ||||||||||||        ||   |
                                TTGTCTTTTATC        GG   C
                                      CCGTTTC    GAC
GAM390  PHLDA3  3'  CCTGGGGGTCTCCTGCT    25692        GTGGAAA
                                GGCAGGAG     CCCCAGG
                                ||||||||     |||||||
                                TCGTCCTC     GGGGTCC
                                   TG_____
GAM390  PIAS3   3'  CCAGGGTTTTGGCCTCATCTCT 21443       ____   G   A___  CCAG
          GCCT                    AGGCAGG   AGGT GAA   CC   G
                                |||||||   |||| |||   ||   |
                                TCCGTCT   TCCG TTT   GG   C
                                   CTAC   G   T    GACC
GAM390  PIK3C2B 3'  TTTTGGGGGGGACTTTTCCTCTT 12113         TG  AA__
          GTCT                    AGGCAGGAGG  GA   CCCCAGGG
                                |||||||||  ||   ||||||||
                                TCTGTTCTCC  TT   GGGGTTTT
                                     TT  CAGG
GAM390  PIK3R3  3'  GGTTCTGTCCTTCCTGCCT   61710        _ _   AA__
                                AGGCAGGA GG TGGA   CC
                                |||||||| || ||||   ||
                                TCCGTCCT CC GTCT   GG
                                   T  T   T
GAM390  PIK4CB  3'  TCTTGGTCACTACCACCTCTTC 12134     C       AAACC_
          CCT                     AGG AGGAGGTGG     CCAGGG
                                ||| |||||||||     ||||||
                                TCC TTCTCCACC     GGTTCT
                                  C       ATCACT
GAM390  PIM1    3'  CCTGTTTTTGTTTCTTGTTT   92684         TG    CCC   G
                                AGGCAGGAGG  GAAAC   AGG
                                ||||||||||  |||||   |||
                                TTTGTTCTTT  TTTTG   TCC
                                     GT    ___   A
GAM390  PIM1    3'  GGCTCTTTTACCTGCTGCTT   92688       G       AC_____
                                AGGCAG AGGTGGAA      C
                                ||||||| ||||||||      |
                                TTCGTC TCCATTTT      G
                                   G       CTC   G
GAM390  PIM2    3'  GGTCCTCTCTTCTCCTGCCT   60656         T_   AA____
                                AGGCAGGAGG  GGA     CC
                                ||||||||||  |||     ||
```

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                                TCCGTCCTCT  TCT     GG
                                     TC   CCT
GAM390  PIP      5'  CTCTGGGACACATTGCCTTCTG 12135          TG AAAC_
             TTT                  AGGCAGGAGG  G    CCCAGGG
                                  ||||||||||  |    |||||||
                                  TTTGTCTTCC  T    GGGTCTC
                                       GT ACACA
GAM390  PK428    5'  CCAGGGTTTTCCTCCCTTTTCT 14600       __   T_   A____  CCAG
             GTTT                  AGGCAG  GAGG  GGAA    CC   G
                                   ||||||  ||||  ||||    ||   |
                                   TTTGTC  TTCC  CCTT    GG   C
                                      TT   CT   TT    GACC
GAM390  PKP2     3'  CCAGGGCTTTCTTTACTTTGTG 17108       G      AA_______  CCAG
             CTT                   AGGCA GAGGTGGA       CC   G
                                   |||||  ||||||||       ||   |
                                   TTCGT TTTCATTT       GG   C
                                      G       CTTTC    GACC
GAM390  PLAGL1   3'  CCAGGGTTTTCCTTTGCCTCTG 12151       G   ___   A____  CCAG
             TCT                   AGGCAG AGGT   GGAA    CC   G
                                   ||||||  ||||   ||||    ||   |
                                   TCTGTC TCCG   CCTT    GG   C
                                     _   TTT    TT    GACC
GAM390  PLAT     3'  TCCATGTTAGTTTTTACTTTCT 53397             CC_  _
             GTT                   GGCAGGAGGTGGAAAC   CA GGG
                                   ||||||||||||||||   || |||
                                   TTGTCTTTCATTTTTG   GT CCT
                                         ATT  A
GAM390  PLOD2    3'  TTTTGGGGGGGAGGGTTATTTGC 8126        AGGTGGAAA
             TT                    AGGCAGG        CCCCAGGG
                                   |||||||        ||||||||
                                   TTCGTTT        GGGGTTTT
                                      ATTGGGAGG
GAM390  PLSCR1   3'  CTCTGGTTGTATACTTTTGCTT 41193         _   G  ACC
                                   AGGCAGGAG GTG AA   CCAGGG
                                   |||||||||  ||| ||   ||||||
                                   TTCGTTTTC TAT TT   GGTCTC
                                        A   G  ___
GAM390  PMM2     3'  TCCTGGAGGCGTTCGCCTCTAG 72564      A       AA  _
             TTT                   AGGC GGAGGTGGA  CC CCAGGG
                                   ||||  |||||||||  || ||||||
                                   TTTG TCTCCGCTT  GG GGTCCT
                                     A        GC  A
GAM390  PMP2     3'  CAGGGTTTGTTTTTGCTTTTGT 12186       G   TG    _______  CAG
             CT                    AGGCAG AGG  GAAAC     CC   G
                                   ||||||  |||  |||||     ||   |
                                   TCTGTT TTC  TTTTG     GG   C
                                     _  GT     TTT     GAC
GAM390  PMX1     3'  CTCTGGGATACCACCACCACTT 23565        A     AAAC__
             GTTT                  AGGCAGG GGTGG     CCCAGGG
                                   |||||||  |||||     |||||||
```

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                                TTTGTTC CCACC     GGGTCTC
                                   A    ACCATA
GAM390  PMX1     3'  CTCTGGGATACCACCACCACTT 23566        A    AAAC__
             GTTT                  AGGCAGG GGTGG     CCCAGGG
                                ||||||| |||||     |||||||
                                TTTGTTC CCACC     GGGTCTC
                                   A    ACCATA
GAM390  PMX1     5'  GGTTCTCTCTTCTTCTGTTT   23570         T_   AA____
                                AGGCAGGAGG  GGA     CC
                                ||||||||||  |||     ||
                                TTTGTCTTCT  TCT     GG
                                     TC   CTT
GAM390  PNN      3'  CCCAGGGTTTTGAGTTTGTGTC 71662        G TG  AA_________  CCAG
             TTGTCT                AGGCAGGA G  GA        CC    GG
                                |||||||| |  ||        ||    ||
                                TCTGTTCT T  TT        GG    CC
                                   G GT  GAGTTTT    GACC
GAM390  PNOC     3'  TCCTGCTCACCCGCCTCTTGCC 21719           AAACCC
                                GGCAGGAGGTGG     CAGGG
                                ||||||||||||     |||||
                                CCGTTCTCCGCC     GTCCT
                                     CACTC_
GAM390  POLB     3'  CCAGGGTCTTCTTCATGCTTTT 12196         _    AA_______  CCAG
             GCTT                  AGGCAGGAG GTGGA       CC    G
                                |||||||| |||||       ||    |
                                TTCGTTTTC TACTT       GG    C
                                   G    CTTCT    GACC
GAM390  POLE2    5'  CTTGCTTCGTCTTCGCTT    12199     A   GT   AACCC
                                AGGC GGAG  GGA    CAGG
                                |||| ||||  |||    ||||
                                TTCG CTTC  CTT    GTTC
                                  _   TG   C____
GAM390  POLS     3'  TTTGCTATTTTCATTTCCTGTT 23784            CCC    G
                                GGCAGGAGGTGGAAA   CAGG
                                ||||||||||||||   ||||
                                TTGTCCTTTACTTTT   GTTT
                                     ATC
GAM390  PPARG    5'  CCTGCATTTCTGCATTCTGCTT 32424        G TG    CCC
                                AGGCAGGA G  GAAA   CAGG
                                |||||||| |  ||||   ||||
                                TTCGTCTT C  CTTT   GTCC
                                   A GT    AC_
GAM390  PPP1R12A 3'  TCTGGGGTGTTTTTGTTGT    11754      G   TGGAA
                                GCAG AGG    ACCCCAGG
                                |||| |||    ||||||||
                                TGTT TTT    TGGGGTCT
                                  G   TTG__
GAM390  PPP1R14B 3'  TTTTGGGGTTTTTTATTGTT   57704      GAGGT
                                GGCAG    GGAAACCCCAGGG
                                |||||    |||||||||||||
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                                TTGTT    TTTTTGGGGTTTT
                                  AT___
GAM390  PPP1R3C  3'  CCTTGCCTATTTTCATCTTGCT 19422      _       CCC_
            GTTT                  AGGCAG GAGGTGGAAA   CAGGG
                                  |||||| ||||||||||   |||||
                                  TTTGTC TTCTACTTTT   GTTCC
                                     G        ATCC
GAM390  PPP2R2B  5'  TGCCGGGTTTTTATTTTTTTTC 17125    C          CA  G
            T                   AGG AGGAGGTGGAAACCC  GG
                                ||| ||||||||||||||  ||
                                TCT TTTTTTATTTTTGGG  CC
                                  T           __ GTT
GAM390  PPP3CB   3'  CCTGTATGGTCTCCTGTCT   41216       GTGGAA   C__
                                AGGCAGGAG    ACC   CAGG
                                |||||||||    |||   ||||
                                TCTGTCCTC    TGG   GTCC
                                     _______  TAT
GAM390  PPT1     3'  GGCTTTGCCATCTTCTGTT   62446         A A_____
                                GGCAGGAGGTGG A     CC
                                |||||||||||| |     ||
                                TTGTCTTCTACC T     GG
                                      G TTC
GAM390  PRDM2    3'  CCTTGACCCTGCTTTTTGCTT  32416         TG AAACCC
                                AGGCAGGAGG  G     CAGGG
                                |||||||||  |     |||||
                                TTCGTTTTTC  C     GTTCC
                                     GT CCA___
GAM390  PREB     3'  CCCTGCCTCCTTTCTTCTGCCT 26328         T_   AACCC
                                AGGCAGGAGG  GGA    CAGGG
                                |||||||||  |||    |||||
                                TCCGTCTTCT  CCT    GTCCC
                                     TT   CC___
GAM390  PRG2     5'  CCTTCATCTTCATCTCTGTCT  12260       G      AACCCC
                                AGGCAG AGGTGGA     AGG
                                |||||| |||||||     |||
                                TCTGTC TCTACTT     TCC
                                   _      CTACT_
GAM390  PRKACG   3'  CCTTGCCCCAGCCCCCTTCTGC 12278          T  AAACCC
            CT                    AGGCAGGAGG GG     CAGGG
                                  |||||||||| ||     |||||
                                  TCCGTCTTCC CC     GTTCC
                                       C  GACCCC
GAM390  PRKAG2   3'  TCTGGGTCACGTTTTGCCT   33017        G    AAAC
                                AGGCAGGA GTGG    CCCAGG
                                |||||||| ||||    ||||||
                                TCCGTTTT CACT    GGGTCT
                                     G    _____
GAM390  PRKCB1   3'  CTTTGGGGTTTTGTTTCTGTT  71027        GTG
                                GGCAGGAG   GAAACCCCAGGG
                                |||||||   ||||||||||||
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                                TTGTCTTT   TTTTGGGGTTTC
                                    G__
GAM390  PRKCM    5'  TCCGGAAAGTTTTTATTTTCCG 12290      A         C__  A
            TCT                   AGGC GGAGGTGGAAAC   CC GGG
                                  |||| |||||||||||   || |||
                                  TCTG CTTTTATTTTTG   GG CCT
                                    C          AAA  _
GAM390  PRKCN    3'  CCCTGAAGCTAGTCTCCTGTCT 20562          _   AAACCC
                                  AGGCAGGAGG TGG     CAGGG
                                  |||||||||| |||     |||||
                                  TCTGTCCTCT ATC     GTCCC
                                       G   GAA___
GAM390  PRKY     3'  CCAGGGTCTTCTCCACCTCTTC 12368     C        AA_______  CCAG
            TT                    AGG AGGAGGTGGA       CC    G
                                  ||| ||||||||||       ||    |
                                  TTC TTCTCCACCT       GG    C
                                    _        CTTCT     GACC
GAM390  PRKY     3'  CCAGGGTTTTATTTCACCTTTA 12369     AG       A________  CCAG
            GTTT                    AGGC  GAGGTGGAA       CC    G
                                  ||||  |||||||||       ||    |
                                  TTTG  TTCCACTTT       GG    C
                                    AT       ATTTT     GACC
GAM390  PRKY     3'  CCCTGCCTTCATCTGTCTCCTT 12370     C     TG  AACCC_
            CT                    AGG AGGAGG  GA     CAGGG
                                  ||| ||||||  ||     |||||
                                  TCT TCCTCT  CT     GTCCC
                                    _     GT  ACTTCC
GAM390  PRKY     3'  CTTTGGGGTGTGTGCCTGTCT  12374        AGGTGGAA
                                  AGGCAGG       ACCCCAGGG
                                  |||||||       |||||||||
                                  TCTGTCC       TGGGGTTTC
                                      GTGTG___
GAM390  PROX1    3'  CCCCAGGGTTTTCTTTCTGCCT 12399      AG    TG   A_________  CCAG
            TTAGTTT                 AGGC  GAGG  GAA       CC    GG
                                  |||| ||||  |||       ||    ||
                                  TTTG  TTCC  CTT       GG    CC
                                    AT    GT   TCTTTT    GACC
GAM390  PRPF18   3'  CTGATTTTTCTTTCTTGCTT   14796          T    CCC
                                  AGGCAGGAGG GGAAA   CAG
                                  |||||||||| |||||   |||
                                  TTCGTTCTTT CTTTT   GTC
                                       _     TA_
GAM390  PRSS16   3'  CCAGGGTTCTAATCTCCTTCTG 20779          T   AA_______  CCAG
            TTT                     AGGCAGGAGG GGA        CC    G
                                  |||||||||| |||        ||    |
                                  TTTGTCTTCC TCT        GG    C
                                       _  AATCTT     GACC
GAM390  PRSS16   3'  CCAGGGTTCTGTCTATTTCTCT 20780       _       AA_______  CCAG
            GTTT                    AGGCAG GAGGTGGA       CC    G
                                  ||||||| ||||||||       ||    |
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                                TTTGTC CTTTATCT      GG   C
                                   T      GTCTT    GACC
GAM390  PRSS16   3'  CCCTGAGGCTCTATTTCTGTCT 20781       G      AA  C
                                AGGCAG AGGTGGA  CC CAGGG
                                |||||| |||||||  || |||||
                                TCTGTC TTTATCT  GG GTCCC
                                   _      C_  A
GAM390  PRSS16   3'  CCCTGAGGCTCTATTTCTGTCT 20782       G      AA  C
                                AGGCAG AGGTGGA  CC CAGGG
                                |||||| |||||||  || |||||
                                TCTGTC TTTATCT  GG GTCCC
                                   _      C_  A
GAM390  PRSS16   3'  TCTGTCTCTATTTCTGTCT   20785       G      AACCC
                                AGGCAG AGGTGGA    CAGG
                                |||||| |||||||    ||||
                                TCTGTC TTTATCT    GTCT
                                   _      CT___
GAM390  PSD      5'  CTCTGTGGTCATCTTCCGCTT  12436     A      GAA   C
                                AGGC GGAGGTG   ACC CAGGG
                                |||| |||||||   ||| |||||
                                TTCG CTTCTAC   TGG GTCTC
                                  C      ___   T
GAM390  PSMD2    3'  TTCTGGGGGAATTGTCGCCTCC 12516           AAA___
           TGCT                   GGCAGGAGGTGG     CCCCAGGG
                                |||||||||||     ||||||||
                                TCGTCCTCCGCT     GGGGTCTT
                                      GTTAAG
GAM390  PSMD9    3'  CCCTTTTATTTTTTGTCT    12524            AACCCC
                                AGGCAGGAGGTGGA     AGGG
                                ||||||||||||||     ||||
                                TCTGTTTTTTATTT     TCCC
                                      _______
GAM390  PSMD9    3'  TCTTGCACACCGCTTTCTGTTT 12531           AAACCC
                                AGGCAGGAGGTGG     CAGGG
                                ||||||||||||     |||||
                                TTTGTCTTTCGCC     GTTCT
                                      ACAC__
GAM390  PTBP1    3'  CAGGGCTCATTTCTGTGTTTTG 12538        GG    A________  CCAG
           CCT                   AGGCAGGA  TGGAA       CC    G
                                ||||||||  |||||       ||    |
                                TCCGTTTT  GTCTT       GG    C
                                   GT     TACTC     GAC
GAM390  PTBP1    3'  CCAGGGCTCATTTCTGTGTTTT 12539        GG    A________  CCAG
           GCCT                   AGGCAGGA  TGGAA       CC    G
                                ||||||||  |||||       ||    |
                                TCCGTTTT  GTCTT       GG    C
                                   GT     TACTC     GACC
GAM390  PTGS1    3'  CCTTGGGGTTAAGTCTCCTGTC 55473           GGA
           T                    AGGCAGGAGGT   AACCCCAGGG
                                ||||||||||   ||||||||||
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                                TCTGTCCTCTG   TTGGGGTTCC
                                      AA_
GAM390  PTHLH    3'  TTTTGGAGCCTCCCTTCTGCCT 12547          T_  AAACC
                                AGGCAGGAGG  GG    CCAGGG
                                ||||||||||  ||    ||||||
                                TCCGTCTTCC  CC    GGTTTT
                                      CT  GA___
GAM390  PTMA     3'  CCAGGGTTTTTTTCCTTTTTTG 12558          T    A_______  CCAG
             TCT                    AGGCAGGAGG GGAA      CC    G
                                ||||||||||| ||||      ||   |
                                TCTGTTTTTT CTTT      GG    C
                                      C    TTTT    GACC
GAM390  PTPN1    3'  CCCTCATCCTTTTACTTTTTGC 12575            ACCCC
             C                   GGCAGGAGGTGGAA     AGGG
                                ||||||||||||||     ||||
                                CCGTTTTTCATTTT     TCCC
                                      CCTAC
GAM390  PTPN1    3'  TCTTGCCAGCATTTTCACATTT 12579         G      CCC___
             TGCCT                  AGGCAGGA GTGGAAA     CAGGG
                                ||||||||| |||||||      |||||
                                TCCGTTTT CACTTTT      GTTCT
                                      A      ACGACC
GAM390  PTTG1IP  3'  CTTTGGGGTTTGGGCTTTTT   16348        GG
                                AGGAGGT  AAACCCCAGGG
                                |||||||  ||||||||||
                                TTTTTCG  TTTGGGGTTTC
                                     GG
GAM390  PXN      3'  TTTTGGGGGGCTGCTTCCTGTC 12678          TG AAA
             T                   AGGCAGGAGG  G   CCCCAGGG
                                ||||||||||  |   ||||||||
                                TCTGTCCTTC  C   GGGGTTTT
                                      GT GG_
GAM390  PYCR1    3'  CCTGCCACCACCTTCTCTT    70641     C       AAACCC
                                AGG AGGAGGTGG      CAGG
                                ||| |||||||||      ||||
                                TTC TCTTCCACC      GTCC
                                  _        ACC___
GAM390  RAB18    3'  CTCTGGGAAATTCCATCTCTTG 41450            AC_
             C                   GCAGGAGGTGGAA   CCCAGGG
                                ||||||||||||   |||||||
                                CGTTCTCTACCTT   GGGTCTC
                                      AAA
GAM390  RAB23    3'  TTTTGTGTTTTATCTTTTGTTT 33254            ACCC
                                AGGCAGGAGGTGGAA    CAGGG
                                ||||||||||||||    |||||
                                TTTGTTTTCTATTTT    GTTTT
                                      GT__
GAM390  RAB36    3'  CCTGGGAGTTTTCTGTTGT    18162      G  GTG    _
                                GCAG AG   GAAAC CCCAGG
                                |||| ||   ||||| ||||||
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                                TGTT TC   TTTTG GGGTCC
                                  G ___     A
GAM390  RAB4A    3'  CCCAGGGTTTTCCTTTCACTTT 17144      A        AC_________ CCAG
              CGGTTT                  AGGC GGAGGTGGAA        C    G
                                |||| ||||||||||         |    |
                                TTTG CTTTCACTTT         G    C
                                  G         CCTTTT   G GACC
GAM390  RAB4A    3'  CCTGTTTTTCACATCTTTTGTT 17145           _   CCC    G
              T                   AGGCAGGAGGTG GAAA   CAGG
                                ||||||||||||| ||||   ||||
                                TTTGTTTTCTAC CTTT   GTCC
                                       A    TT_
GAM390  RAB5B    3'  TCCTGTCCCTTCCCCTTCTGCT 12712          T    ACCC
              T                   AGGCAGGAGG GGAA    CAGGG
                                |||||||||| ||||    |||||
                                TTCGTCTTCC CCTT    GTCCT
                                      _    CCCT
GAM390  RAB6A    3'  CTTTGGTGATATTTATTTCTTT 12716       _       AACC_
              GCCT                    AGGCAG GAGGTGGA     CCAGGG
                                ||||||| ||||||||     |||||||
                                TCCGTT CTTTATTT     GGTTTC
                                   T       ATAGT
GAM390  RABGGTB  3'  CCGGTATTTTATTTTCTGCTT  17154             _   CCA
                                AGGCAGGAGGTGGAA ACC   GG
                                |||||||||||||| |||   ||
                                TTCGTCTTTTATTTT TGG   CC
                                       A   ___
GAM390  RABIF    3'  CCAGGGTCATTTCTATTTCCTT 12725     C         A_______  CCAG
              TTT                   AGG AGGAGGTGGAA      CC    G
                                ||| ||||||||||       ||    |
                                TTT TCCTTTATCTT      GG    C
                                  T         TACT     GACC
GAM390  RABL2A   3'  TTTTGGTGTTTTTGTTTTTGTT 24001         G TG     C
              T                   AGGCAGGA G  GAAAC CCAGGG
                                |||||||| |  ||||| ||||||
                                TTTGTTTT T  TTTTG GGTTTT
                                     _ GT     T
GAM390  RABL2B   3'  TTTTGGTGTTTTTGTTTTTGTT 23991         G TG     C
              T                   AGGCAGGA G  GAAAC CCAGGG
                                |||||||| |  ||||| ||||||
                                TTTGTTTT T  TTTTG GGTTTT
                                     _ GT     T
GAM390  RAD18    3'  CCTTGGGGTTTCTGATAATGT  39803     GGAGG
                                GCA     TGGAAACCCCAGGG
                                |||     ||||||||||||||
                                TGT     GTCTTTGGGGTTCC
                                  AATA_
GAM390  RAD51L3  3'  CCTTTTTTTTCTTTTGTCT    56886          TG    CCCC
                                AGGCAGGAGG  GAAA    AGG
                                |||||||||  ||||    |||
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                                TCTGTTTTCT  TTTT   TCC
                                     TT   ____
GAM390  RAD51L3  3' CCTTTTTTTTCTTTTGTCT   56887       TG   CCCC
                                AGGCAGGAGG  GAAA   AGG
                                ||||||||||  ||||   |||
                                TCTGTTTTCT  TTTT   TCC
                                     TT   ____
GAM390  RAD51L3  3' CCTTTTTTTTCTTTTGTCT   56888       TG   CCCC
                                AGGCAGGAGG  GAAA   AGG
                                ||||||||||  ||||   |||
                                TCTGTTTTCT  TTTT   TCC
                                     TT   ____
GAM390  RAD51L3  5' CTTGGTGCCGCCTCCTCCT   56889    C      AAACC
                                AGG AGGAGGTGG    CCAGG
                                ||| |||||||||    |||||
                                TCC TCCTCCGCC    GGTTC
                                  _       GT___
GAM390  RAD51L3  3' GGTCTTCTTCATCTCTGTTT  56890      G     AA_______
                                AGGCAG AGGTGGA      CC
                                ||||||| |||||||      ||
                                TTTGTC TCTACTT      GG
                                   _      CTTCT
GAM390  RAD51L3  3' GGTCTTCTTCATCTCTGTTT  56891      G     AA_______
                                AGGCAG AGGTGGA      CC
                                ||||||| |||||||      ||
                                TTTGTC TCTACTT      GG
                                   _      CTTCT
GAM390  RAD51L3  3' GGTCTTCTTCATCTCTGTTT  56892      G     AA_______
                                AGGCAG AGGTGGA      CC
                                ||||||| |||||||      ||
                                TTTGTC TCTACTT      GG
                                   _      CTTCT
GAM390  RAI14    3' CCAGGGCTCTTTTTGCCTTTGG 32099     A    TG   A_______  CCAG
           CTT                   AGGC GGAGG  GAA      CC   G
                                ||||  |||||  |||      ||   |
                                TTCG TTTCC  TTT      GG   C
                                  G    GT   TCTC    GACC
GAM390  RALBP1   3' CTCTGGTACCGTCACTCTTGCT 23274        G   AAACC
           T                    AGGCAGGAG TGG    CCAGGG
                                |||||||||  |||    ||||||
                                TTCGTTCTC ACT    GGTCTC
                                     _  GCCAT
GAM390  RB1CC1   3' TAAAATGGTTTTTGTTTTTTGG 29436    G     TG     CCAGGG
           TT                    AG CAGGAGG  GAAACC
                                ||  |||||||  ||||||
                                TT GTTTTTT  TTTTGG
                                  G      GT     TAAAATT
GAM390  RBBP9    3' CAGGGTCATTTCTGATTTCTGT 70685        G    A_______  CCAG
           TT                    AGGCAGGAG TGGAA      CC   G
                                |||||||||  |||||      ||   |
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                                TTTGTCTTT GTCTT      GG    C
                                     A    TACT    GAC
GAM390  RBM8A    3'  TCTTGGGCTCAAGCCATCCTTC 18814          _  AAAC__
            TGCCT                   AGGCAGGAGG TGG     CCCAGGG
                                ||||||||||  |||     |||||||
                                TCCGTCTTCC ACC     GGGTTCT
                                     T   GAACTC
GAM390  REGL     3'  CCAGGTGTTTCTGTCTCTTTCT 22499     C     TG    C  A
                                AGG AGGAGG  GAAAC CC GG
                                |||  ||||||  |||||  ||  ||
                                TCT TTCTCT  CTTTG GG CC
                                  _     GT    T  A
GAM390  REQ      3'  CCTTGGAATTTCTCATCTTCTG 21839           _   CC
            CCT                    AGGCAGGAGGTG GAAA  CCAGGG
                                ||||||||||||  ||||  ||||||
                                TCCGTCTTCTAC CTTT  GGTTCC
                                      T    AA
GAM390  RERE     3'  TCTTGGGGTTTGGCTTTAGTTT 25022      AG    G   A
                                AGGC  GAGGT GAA CCCCAGGG
                                ||||  |||||  |||  ||||||||
                                TTTG  TTTCG TTT GGGGTTCT
                                  A_    G  _
GAM390  RFPL1    3'  TCTTATGGTTCACATCTTGTTT 41051         G    AA   CC
                                AGGCAGGA GTGG  ACC  AGGG
                                ||||||||  ||||  |||  ||||
                                TTTGTTCT CACT  TGG  TTCT
                                     A   __   TA
GAM390  RFPL2    3'  TCCTATGGTTCACATCTTGTTT 22760         G    AA   CC
                                AGGCAGGA GTGG  ACC  AGGG
                                ||||||||  ||||  |||  ||||
                                TTTGTTCT CACT  TGG  TCCT
                                     A   __   TA
GAM390  RFPL3    3'  TCTTATGGTTCACATCTTGTTT 22758         G    AA   CC
                                AGGCAGGA GTGG  ACC  AGGG
                                ||||||||  ||||  |||  ||||
                                TTTGTTCT CACT  TGG  TTCT
                                     A   __   TA
GAM390  RFX5     3'  GTCCTTCCTTTTCCTGTTT    6551           T    AC_____
                                AGGCAGGAGG GGAA      C
                                ||||||||||  ||||      |
                                TTTGTCCTTT CCTT      G
                                     T    CCT   G
GAM390  RGL      3'  TTCTGCATCTCCATCATCTGTT 31431        GA     AACCC
              T                  AGGCAG  GGTGGA    CAGGG
                                ||||||  ||||||    |||||
                                TTTGTC  CTACCT    GTCTT
                                   TA     CTAC_
GAM390  RGS3     5'  CTCTGGGGGCAGTACCCCTGCC 56315         A   GAAA
              T                  AGGCAGG GGTG    CCCCAGGG
                                |||||||  ||||    ||||||||
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                                TCCGTCC CCAT    GGGGTCTC
                                   _    GACG
GAM390  RGS5     3'  CCTTCACTATTTCGCTTCCTGC 14622           ACCCC_  G
                                GCAGGAGGTGGAA     AGG
                                ||||||||||||      |||
                                CGTCCTTCGCTTT     TCC
                                     ATCACT
GAM390  RHO      3'  CCCTGGGCCTCACTTTCTTCT  6768      C       AAAC
                                AGG AGGAGGTGG    CCCAGGG
                                ||| |||||||||    |||||||
                                TCT TCTTTCACT    GGGTCCC
                                  _       CC__
GAM390  RNF14    3'  CCCAGGGCTTTGCCCTACCTTC 16272           AAA________  CCAG
           TGTTT                  AGGCAGGAGGTGG        CC    GG
                                ||||||||||||         ||    ||
                                TTTGTCTTCCATC        GG    CC
                                     CCGTTTC    GACC
GAM390  RNF26    3'  CCTGTCTGCTTCTGGTTT    50134      A    TG  AACCC
                                AGGC GGAGG  GA    CAGG
                                |||| |||||  ||    ||||
                                TTTG TCTTC  CT    GTCC
                                  G    GT  _____
GAM390  RNF26    3'  CTCTGGGGTTACCCCTGTCTGC 50135        _   T  A
           TT                    AGGCAGG AGG GG AACCCCAGGG
                                ||||||| ||| || ||||||||||
                                TTCGTCT TCC CC TTGGGGTCTC
                                   G   _  A
GAM390  RNF4     5'  CCTTGGTATAGATCACTTCCT  12881         AAACC_
                                AGGAGGTGG     CCAGGG
                                |||||||||     ||||||
                                TCCTTCACT     GGTTCC
                                     AGATAT
GAM390  RNH      5'  TTTTGGGGTGGGCTGTTCTCTG 60373        AG TG AA_
           CCT                    AGGCAGG  G  G   ACCCCAGGG
                                |||||||  |  |   |||||||||
                                TCCGTCT  T  C   TGGGGTTTT
                                   CT GT GGG
GAM390  RORB     5'  CCCCAGGGTTTTCTTTCTGTTT 23587     C     TG   A_________  CCAG
           CCTTTTT                AGG AGGAGG  GAA       CC    GG
                                ||| ||||||  |||       ||    ||
                                TTT TCCTTT  CTT       GG    CC
                                  T     GT   TCTTTT    GACC
GAM390  RP42     3'  CTGTTTTGTTTCCTGTCT    40566          TG   ACCC
                                AGGCAGGAGG  GAA   CAG
                                ||||||||||  |||   |||
                                TCTGTCCTTT  TTT   GTC
                                     GT  _____
GAM390  RPP30    3'  TCCTGGGTTCATGCCATTCTCC 22209          _   AAAC__
           TGCCT                  AGGCAGGAGG TGG     CCCAGGG
                                ||||||||||| |||     |||||||
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                                TCCGTCCTCT ACC     GGGTCCT
                                     T   GTACTT
GAM390  RPS6KA5  3'  CCAGGGTTTATTTTCATTTTCT 17649     C        A_______  CCAG
           ACTT                  AGG AGGAGGTGGAA       CC    G
                                 ||| ||||||||||       ||    |
                                 TTC TCTTTTACTTT       GG    C
                                   A         TATTT     GACC
GAM390  RTN2     3'  CTCTGGCCCCCTCCATCTCTTG 20053           AACC_
           TC                    GGCAGGAGGTGGA    CCAGGG
                                 ||||||||||||     ||||||
                                 CTGTTCTCTACCT    GGTCTC
                                       CCCCC
GAM390  RUNX1    3'  TTTTGGGTAGTTGTTTTTTTTT 10033         TGGA  __
           GTTT                  AGGCAGGAGG   AAC  CCCAGGG
                                 ||||||||||   |||  |||||||
                                 TTTGTTTTTT   TTG  GGGTTTT
                                      TTTG   AT
GAM390  SAFB     3'  TTTGGGGTTTTTTTTTTTT   12935       TG
                                 AGGAGG  GAAACCCCAGG
                                 ||||||  ||||||||||
                                 TTTTTT  TTTTGGGGTTT
                                    TT
GAM390  SALL2    3'  CTCTGGGGTGACCTTTCTGCT  64591        TGGAA
                                 GGCAGGAGG    ACCCCAGGG
                                 |||||||||    |||||||||
                                 TCGTCTTTC    TGGGGTCTC
                                      CAG__
GAM390  SCA1     3'  CCATTTCATTCTCTTGCTT   6176         _     ACCCCA
                                 AGGCAGGAG GTGGAA     GG
                                 |||||||||| ||||||     ||
                                 TTCGTTCTC TACTTT     CC
                                      T     A_____
GAM390  SCN3A    3'  CAGGGTTTATTTTACTTTATGC 23613      G       A______  CCAG
           TT                    AGGCA GAGGTGGAA      CC    G
                                 ||||| |||||||||      ||    |
                                 TTCGT TTTCATTTT      GG    C
                                   A       ATTT     GAC
GAM390  SCN3A    3'  CCCAGGGTTTTGTTTTTGTTTT 23614        TG    ________  CAG
           TTGCT                  GGCAGGAGG  GAAAC      CC   GG
                                  |||||||||  |||||      ||   ||
                                  TCGTTTTTT  TTTTG      GG   CC
                                       GT    TTTT    GAC
GAM390  SCN3A    3'  CTCTGGGGTTTTTTGTTTTTGT 23615        GT
           TT                     AGGCAGGAG  GGAAACCCCAGGG
                                  |||||||||  ||||||||||||
                                  TTTGTTTTT  TTTTTGGGGTCTC
                                       GT
GAM390  SCN3A    3'  GGCTTTGCCATCTTCTGCT   23617          A A_____
                                  GGCAGGAGGTGG A     CC
                                  |||||||||||| |     ||
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                                TCGTCTTCTACC T     GG
                                      G TTC
GAM390  SCN4A   3'  CCAGGGCTCTCCTCCCCTTCCT 6197          T   AA_______  CCAG
            GTTT                  AGGCAGGAGG GGA       CC    G
                                  |||||||||| |||       ||   |
                                  TTTGTCCTTC CCT       GG    C
                                      C   CCTCTC    GACC
GAM390  SCN4A   3'  CCCTGCTCCCTGCCTCCTGCCT 6198          TG AAACCC
                                  AGGCAGGAGG  G     CAGGG
                                  ||||||||||  |     |||||
                                  TCCGTCCTCC  C     GTCCC
                                      GT CCTC__
GAM390  SCN4A   3'  GTCCTTCCATCTCTTCCT    6204      C        AC_____
                                  AGG AGGAGGTGGAA      C
                                  ||| ||||||||||       |
                                  TCC TTCTCTACCTT      G
                                    _         CCT   G
GAM390  SDC1    3'  CTCTGCTTCTCTGACTTCTGCC 12988         GT   AACCC
            T                      AGGCAGGAG  GGA    CAGGG
                                  |||||||||  |||    |||||
                                  TCCGTCTTC  TCT    GTCTC
                                       AG   CTTC_
GAM390  SDC4    3'  CCCTTTCTGCCTTCTGTTT   12995          TG   ACCCC
                                  AGGCAGGAGG  GAA    AGGG
                                  ||||||||||  |||    ||||
                                  TTTGTCTTCC  CTT    TCCC
                                      GT  _____
GAM390  SDC4    3'  CTGGGTGGGTTTTTGCCTTTTT 12996     C     TG     ___   GG
            CT                     AGG AGGAGG  GAAACCC   CAG
                                  ||| ||||||  |||||||   |||
                                  TCT TTTTCC  TTTTGGG   GTC
                                    _     GT      TGG
GAM390  SEDL    3'  CTTTGGGGTTTTTTTTTTTT   28097       TG
                                  AGGAGG  GAAACCCCAGGG
                                  ||||||  ||||||||||||
                                  TTTTTT  TTTTGGGGTTTC
                                     TT
GAM390  SEDL    3'  TTTTGTGGGTTTTTGTTTTTGT 28117         G TG      _
            TT                     AGGCAGGA G  GAAACCC CAGGG
                                  |||||||| |  ||||||| |||||
                                  TTTGTTTT T  TTTTGGG GTTTT
                                      _ GT      T
GAM390  SEL1L   3'  CAGGGTTTTTTTTTTTTTCTGT 18598          T    A______  CCAG
            CT                     AGGCAGGAGG GGAA      CC    G
                                  |||||||||| ||||      ||   |
                                  TCTGTCTTTT TTTT      GG    C
                                      T    TTTT     GAC
GAM390  SEL1L   3'  CCCCAGGGTTCTAGTCTGTCTT 18599          _    AA_______  CCAG
            CCTGCCT                AGGCAGGAGG TGGA       CC    GG
                                  |||||||||| ||||       ||    ||
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                                TCCGTCCTTC GTCT       GG   CC
                                     T   GATCTT    GACC
GAM390  SEL1L   3'  CCCCAGGGTTTTTTTCTGTCTC 18600      _   GT   A_______  CCAG
          TGTGTTT                AGGCA GGAG  GGAA      CC   GG
                                |||||| ||||  ||||       ||   ||
                                TTTGT TCTC  TCTT      GG   CC
                                   G   TG   TTTTT    GACC
GAM390  SEL1L   3'  TTTGAAGTTTCAGTTTCTGTTT 18609        G  G   CC
                                AGGCAGGAG TG AAAC  CAGG
                                ||||||||| || ||||  ||||
                                TTTGTCTTT AC TTTG  GTTT
                                     G  _   AA
GAM390  SELP    3'  CCTGTCCCACCTCTTCTCT   13011    C       AAACCC
                                AGG AGGAGGTGG     CAGG
                                ||| |||||||||      ||||
                                TCT TTCTCCACC     GTCC
                                  C       CT_____
GAM390  SELPLG  3'  TTCTGAGGCTGTTTCCTGCT  60421        TG AAA  C
                                GGCAGGAGG  G   CC CAGGG
                                |||||||||  |   || |||||
                                TCGTCCTTT  C   GG GTCTT
                                     GT ___  A
GAM390  SERPINF2 3'  CCTTCCTTCCTCTCCTGTCT  8122         T   ACCCC
                                AGGCAGGAGG GGAA    AGG
                                |||||||||| ||||    |||
                                TCTGTCCTCT CCTT    TCC
                                     _   CCT__
GAM390  SET     3'  GGTTTTATCCCTTCCTGTCT  13019        T  AA_______
                                AGGCAGGAGG GGA       CC
                                |||||||||| |||       ||
                                TCTGTCCTTC CCT       GG
                                     _  ATTTT
GAM390  SEZ6L   5'  CTTTGGGTCCTTACCTCCTGCC 41204         AA   C   G
                                GGCAGGAGGTGG  ACCC AGG
                                ||||||||||||  |||| |||
                                CCGTCCTCCATT  TGGG TTC
                                     CC   T
GAM390  SF3A1   3'  GGTTTTGCCTCTCCTGTCT   20808        T  A A_____
                                AGGCAGGAGG GG A     CC
                                |||||||||| || |     ||
                                TCTGTCCTCT CC T     GG
                                     _  G TTT
GAM390  SFPQ    5'  GGTCTTCTTCGCTTTTGCCT  18612      G      AA_______
                                AGGCAG AGGTGGA       CC
                                |||||| |||||||       ||
                                TCCGTT TTCGCTT       GG
                                   _      CTTCT
GAM390  SFRS2IP 5'  GGTTCTCTCTCCTTTTGCTT  17545        T_   AA____
                                AGGCAGGAGG  GGA     CC
                                |||||||||  |||     ||
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                                TTCGTTTTCC  TCT     GG
                                      TC   CTT
GAM390  SH3BP2   3'  CCCTGGCGTTGCCGTCTGCTT  13058       GA   GGA   C
                                AGGCAG  GGT   AAC CCAGGG
                                ||||||  |||   ||| ||||||
                                TTCGTC  CCG   TTG GGTCCC
                                   TG   ___   C
GAM390  SH3GL3   3'  CAGGGTTCTTTTTTGCTTCCTG 13106         GG  A_______  CCAG
           TC                    GGCAGGAGGT  AA       CC    G
                                ||||||||||  ||       ||    |
                                CTGTCCTTCG  TT       GG    C
                                      TT  TTCTT     GAC
GAM390  SH3GL3   3'  GGTTGTTTTCTTTTTTGCTT   13114          T     _____
                                AGGCAGGAGG GGAAAC     CC
                                |||||||||| ||||||     ||
                                TTCGTTTTTT CTTTTG     GG
                                      _     TT
GAM390  SHANK2   3'  TCCTGAGACCTCCGTCCTCTGC 25533       G  _    AACCC
           TT                    AGGCAG AGG TGGA     CAGGG
                                ||||||| ||| ||||     |||||
                                TTCGTC TCC GCCT     GTCCT
                                   _  T    CCAGA
GAM390  SHOC2    3'  CAGGGTTTTCTTTGCTTCACTG 24781       _    TG  AA_______  CCAG
           CTT                    AGGCAG GAGG  GA       CC    G
                                ||||||| ||||  ||       ||    |
                                TTCGTC CTTC  TT       GG    C
                                   A    GT  CTTTT     GAC
GAM390  SHOX     3'  CCTACTCCATCTTCTGC     6568            AACCCC
                                GCAGGAGGTGGA     AGG
                                ||||||||||||     |||
                                CGTCTTCTACCT     TCC
                                      CA____
GAM390  SIX1     5'  CCCTACTCCTCCGCCTTCTCTT 21112     C        AACCCC
                                AGG AGGAGGTGGA     AGGG
                                ||| ||||||||||     ||||
                                TTC TCTTCCGCCT     TCCC
                                  _        CCTCA_
GAM390  SIX2     3'  CCCAGGGCTTTTTTCTGCTTTC 34188             A_______  CCAG
           TGTCT                   AGGCAGGAGGTGGAA       CC    GG
                                |||||||||||||||       ||    ||
                                TCTGTCTTTCGTCTT       GG    CC
                                         TTTTC     GACC
GAM390  SLC15A1  3'  TACCTTTGGGTTTTTGTTATTT 18646         _ TG      C
           TGTTT                   AGGCAGGA GG  GAAACCC AGGG
                                ||||||||  ||  ||||||| ||||
                                TTTGTTTT TT  TTTTGGG TTCC
                                      A  GT      T    ATT
GAM390  SLC16A1  3'  TTTGGTGTTTTTGTTTTTTTGT 13204         _ TG    C    G
           TT                    AGGCAGGAG G  GAAAC CCAGG
                                |||||||||  |  ||||| |||||
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                                TTTGTTTTT T  TTTTG GGTTT
                                     T GT    T
GAM390  SLC17A4  3'  TTTTGGACAGTTACCTTCTTTC 19720    C       AAACC
           T                  AGG AGGAGGTGG    CCAGGG
                              ||| |||||||||    ||||||
                              TCT TCTTCCATT    GGTTTT
                                T       GACA_
GAM390  SLC19A1  5'  TCCTGGGGAGTCTGCCTGCCT  13221     GGA  TG  AA
                              AGGCA   GG  GA  CCCCAGGG
                              |||||   ||  ||  ||||||||
                              TCCGT   CC  CT  GGGGTCCT
                                 ___  GT  GA
GAM390  SLC19A2  3'  CCTTCATTTTACATTCTGTCT  69551       G     ACCCC
                              AGGCAGGA GTGGAA    AGG
                              |||||||| ||||||    |||
                              TCTGTCTT CATTTT    TCC
                                   A     ACT__
GAM390  SLC19A2  3'  TTCTGTCTGTTTTTCTTTTTTT 69553        T_    CC_
           GCTT                  AGGCAGGAGG  GGAAAC   CAGGG
                              ||||||||||  ||||||   |||||
                              TTCGTTTTTT  TTTTTG   GTCTT
                                    TC     TCT
GAM390  SLC1A3   3'  CTCTGGGAAGAATGTCTCCTGC 16062       GT GAAAC
           C                   GGCAGGAG  G    CCCAGGG
                              ||||||||  |    |||||||
                              CCGTCCTC  T    GGGTCTC
                                   TG AAGAA
GAM390  SLC22A12  5'  CCTGGCCCACCTTCTCTT    58686    C       AAACC
                              AGG AGGAGGTGG    CCAGG
                              ||| |||||||||    |||||
                              TTC TCTTCCACC    GGTCC
                                _       C____
GAM390  SLC22A1L  5'  CCCTGCTCCGCCAGCCTCCTGC 11915         _   AAACCC
           TT                   AGGCAGGAGG TGG     CAGGG
                              |||||||||| |||     |||||
                              TTCGTCCTCC ACC     GTCCC
                                   G   GCCTC_
GAM390  SLC25A13  3'  CCCCAGGGTTTTACGTCCATCT 27287           AA_________  CCAG
           CTTGTTT               AGGCAGGAGGTGGA        CC    GG
                              ||||||||||||||        ||    ||
                              TTTGTTCTCTACCT        GG    CC
                                    GCATTTT    GACC
GAM390  SLC25A15  3'  TCTTGGGAATTTTGCTTTTTGT 27297         TG   AC
           CT                   AGGCAGGAGG  GAA  CCCAGGG
                              ||||||||||  |||  |||||||
                              TCTGTTTTTC  TTT  GGGTTCT
                                   GT   AA
GAM390  SLC25A5  5'  TCCTGCAGCAGTCTGCCTCCTC 8568     C     TG  AACCC_
           TT                   AGG AGGAGG  GA     CAGGG
                              ||| ||||||  ||     |||||
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                                TTC TCCTCC  CT     GTCCT
                                  _     GT  GACGAC
GAM390  SLC29A1  3'  CCTGTCTGCCTCCTGCC     18261        TG  AACCC
                                GGCAGGAGG  GA    CAGG
                                |||||||||  ||    ||||
                                CCGTCCTCC  CT    GTCC
                                     GT  _____
GAM390  SLC2A3   3'  TCCTGGACATCCTCTTCTGCTT 23646         T   AACC
                                AGGCAGGAGG GGA    CCAGGG
                                |||||||||| |||    ||||||
                                TTCGTCTTCT CCT    GGTCCT
                                     _   ACA_
GAM390  SLC38A2  3'  TCTGGGAGCTATCTTGTCT   39116        GG   AAAC
                                AGGCAGGA  TGG    CCCAGG
                                ||||||||  |||    ||||||
                                TCTGTTCT  ATC    GGGTCT
                                     __   GA__
GAM390  SLC6A12  3'  CTCTGCCTCTGTCTCCTGCC   13192        TG  AACCC
                                GGCAGGAGG  GA    CAGGG
                                |||||||||  ||    |||||
                                CCGTCCTCT  CT    GTCTC
                                     GT  CC___
GAM390  SLC7A8   5'  CCCAGGGTTCTCTTTTATCTGC 25301        _       AC_______ CCAG
           TTGCCT                 AGGCAGG AGGTGGAA       C   G
                                |||||||  ||||||||       |   |
                                TCCGTTC TCTATTTT       G   C
                                   G       CTCTT   G GACC
GAM390  SLC9A5   3'  CTCTGCCTCCACTTCCTGCTT  60475           AACCC
                                AGGCAGGAGGTGGA    CAGGG
                                ||||||||||||||    |||||
                                TTCGTCCTTCACCT    GTCTC
                                      CC___
GAM390  SLC9A5   3'  CTCTGCCTCCACTTCCTGCTT  60476           AACCC
                                AGGCAGGAGGTGGA    CAGGG
                                ||||||||||||||    |||||
                                TTCGTCCTTCACCT    GTCTC
                                      CC___
GAM390  SMCY     3'  TTGTGGTTGTTTTTGTTTGTTT 17389        _  TG    C_  GGG
           GTTT                   AGGCAGG AGG  GAAAC  CCA
                                |||||||  |||  |||||  |||
                                TTTGTTT TTT  TTTTG  GGT
                                   G   GT    TT   GTTT
GAM390  SMT3H1   3'  CTGAAATGTTCTCATTTCCTGT 60630          GA   CC__   GG
           TT                    AGGCAGGAGGTG  AAC   CAG
                                ||||||||||||  |||   |||
                                TTTGTCCTTTAC  TTG   GTC
                                      TC   TAAA
GAM390  SMURF1   3'  TCCTGGCCTCCGTCTCTGCTT  94052       G  GT   AACC
                                AGGCAG AG  GGA   CCAGGG
                                ||||||  ||  |||   ||||||
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                                TTCGTC TC  CCT    GGTCCT
                                   _ TG   CC__
GAM390  SMURF1   3'  TTCTGACACCATTTCCAGTTT  94054      A       AAACCC
                                AGGC GGAGGTGG     CAGGG
                                |||| ||||||||     |||||
                                TTTG CCTTTACC     GTCTT
                                  A       ACA___
GAM390  SNAI1    3'  CAGGGCTATTTCAGCCTCCTGT 21122          _    A_____  CCAG
           TT                    AGGCAGGAGG TGGAA     CC    G
                                |||||||||| |||||     ||   |
                                TTTGTCCTCC ACTTT     GG    C
                                      G    ATC    GAC
GAM390  SNCAIP   3'  TTCTGTCATTTCTACTTTTTGT 97610            CCC
                                GCAGGAGGTGGAAA   CAGGG
                                ||||||||||||||   |||||
                                TGTTTTTCATCTTT   GTCTT
                                         ACT
GAM390  SOS2     3'  CCAGGGCTTTGACCATCTTCTA 69062      _       AAA_______  CCAG
           GTTT                   AGGC AGGAGGTGG        CC    G
                                |||| |||||||||        ||   |
                                TTTG TCTTCTACC        GG    C
                                  A       AGTTTC    GACC
GAM390  SOX10    3'  CCTGTACATTCTGCCCTTGCCT 23672        A  TG   ACCC
                                AGGCAGG GG  GAA    CAGG
                                ||||||| ||  |||    ||||
                                TCCGTTC CC  CTT    GTCC
                                   _ GT   ACAT
GAM390  SOX10    3'  CCTTGCCTCTTACCCCTTGCCT 23674        A    AAACCC
                                AGGCAGG GGTGG     CAGGG
                                ||||||| |||||     |||||
                                TCCGTTC CCATT     GTTCC
                                   C    CTCC__
GAM390  SOX11    3'  CAGGGTCCTCCTCCACTCCCTG 13311        AG    AA________  CCAG
           CCT                    AGGCAGG  GTGGA       CC    G
                                |||||||  |||||       ||   |
                                TCCGTCC  CACCT       GG    C
                                   CT    CCTCCT    GAC
GAM390  SOX13    3'  CTCTGGGGGCCTCTTTCTGT   20280        T  AAA
                                GCAGGAGG GG   CCCCAGGG
                                |||||||| ||   ||||||||
                                TGTCTTTC CC   GGGGTCTC
                                    T  G__
GAM390  SOX4     5'  TTTGGGGACTTTTCTCTCT    13306      T    __
                                GGAGG GGAAA  CCCCAGG
                                ||||| |||||  |||||||
                                TCTCT CTTTT  GGGGTTT
                                   _    CA
GAM390  SOX9     3'  CTTTGGTTTGTGTTCGTGTTTT 6231         GG    A  C__
           GTTT                   AGGCAGGA  TGGA AC   CCAGGG
                                |||||||  |||| ||   ||||||
```

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                                TTTGTTTT  GCTT TG   GGTTTC
                                    GT    G  TTT
GAM390  SP3     3'  CCAGGGTCATTTTCCTTTTTTG 83383          T    A_______  CCAG
            CTT                   AGGCAGGAGG GGAA      CC    G
                                ||||||||||  ||||       ||    |
                                TTCGTTTTTT CTTT      GG    C
                                     C    TACT     GACC
GAM390  SP3     3'  CCTTTTTTGCTTCTTCCCT   83384     C     TG    CCCC
                                AGG AGGAGG  GAAA    AGG
                                |||  ||||||  ||||    |||
                                TCC TTCTTC  TTTT    TCC
                                  C     GT   _____
GAM390  SP3     5'  TCTGGAACACCTTCTGCT    83387           GAAACC
                                GGCAGGAGGTG     CCAGG
                                ||||||||||      |||||
                                TCGTCTTCCAC     GGTCT
                                      AA_____
GAM390  SPAG11   3'  TCCTCTTCCTGCCTCCTGTCT  33677           _    ACCCC
                                AGGCAGGAGGT GGAA     AGGG
                                ||||||||||  ||||     ||||
                                TCTGTCCTCCG CCTT     TCCT
                                      T    C_____
GAM390  SPAP1    3'  AGGAGGGGTTTCTGTCTCTTCC 57833     C     TG       AGGG
            T                    AGG AGGAGG  GAAACCCC
                                |||  ||||||  ||||||||
                                TCC TTCTCT  CTTTGGGG
                                  _     GT       AGGAT
GAM390  SPF30    3'  CTAAGGTGTTTTTGTTTTTTGT 20794         TG     C  AGGG
                                GCAGGAGG  GAAAC CC
                                ||||||||  |||||  ||
                                TGTTTTTT  TTTTG GG
                                     GT     T  AATCT
GAM390  SPOCK    3'  CTCTGGCCCACATATCTATCTC 63473            AACC_____
            TTGCCT                  AGGCAGGAGGTGGA       CCAGGG
                                ||||||||||||||       ||||||
                                TCCGTTCTCTATCT       GGTCTC
                                       ATACACCC
GAM390  SPOCK    3'  GGCTCTTTCATTTCTGCTT    63475       G       AC_____
                                AGGCAG AGGTGGAA      C
                                ||||||  ||||||||      |
                                TTCGTC TTTACTTT      G
                                   _       CTC   G
GAM390  SPON1    3'  TCTTGTTGGATTGTTATTTTTT 63124            AAA_  C_
            GTTT                    AGGCAGGAGGTGG    CC  CAGGG
                                ||||||||||||||    ||  |||||
                                TTTGTTTTTTATT    GG  GTTCT
                                       GTTA  TT
GAM390  SPRR2C   3'  TTTTGATGTCTTCTGTCTCTGT 22532       G   TG   _  CC
            CT                    AGGCAG AGG  GAA AC  CAGGG
                                ||||||  |||  |||  ||  |||||
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                                TCTGTC TCT  CTT TG  GTTTT
                                   _  GT   C  TA
GAM390  SPTBN1   3'  CCCCAGGGCTTTCCTTCACCTC 13389          AA_______  CCAG
           CTGCC                  GGCAGGAGGTGGA       CC   GG
                                |||||||||||||       ||   ||
                                CCGTCCTCCACTT       GG   CC
                                      CCTTTC    GACC
GAM390  SPTBN2   3'  CCCCAGGGCTCGCCTTCTGCCT 23692          AAA_  CCAG
                                AGGCAGGAGGTGG   CC   GG
                                |||||||||||||   ||   ||
                                TCCGTCTTCCGCT   GG   CC
                                      C    GACC
GAM390  SQSTM1   3'  TCTGGGGGTCCCTTGCTT    15330       A  TGGAAA
                                AGGCAGG GG     CCCCAGG
                                |||||||  ||     |||||||
                                TTCGTTC CC     GGGGTCT
                                   _  TG____
GAM390  SRD5A1   3'  CCAGGGTTCTCTCTGTCTTCTA 8315      _     TG  AA_______  CCAG
           GTCT                   AGGC AGGAGG  GA      CC   G
                                |||| ||||||  ||      ||   |
                                TCTG TCTTCT  CT      GG   C
                                  A     GT  CTCTT    GACC
GAM390  SREBF2   3'  CCCTACTCTCTCCTTTTTGCTT 17188         TG  AACCCC
                                AGGCAGGAGG  GA     AGGG
                                |||||||||  ||     ||||
                                TTCGTTTTTC  CT     TCCC
                                     CT  CTCA__
GAM390  SRGAP2   3'  CCCAGGGTTTTGTTGCTGTTTC 75108     _     TG A  ________  CAG
           CTGACCT                 AGG CAGGAGG  G AAC      CC   GG
                                ||| |||||||  | |||      ||   ||
                                TCC GTCCTTT  C TTG      GG   CC
                                  A      GT G   TTTT    GAC
GAM390  SRRM1    3'  TCTGTTCATATTTTTGTCT   20699        GTG   ACCC
                                AGGCAGGAG   GAA   CAGG
                                |||||||||   |||   ||||
                                TCTGTTTTT   CTT   GTCT
                                     ATA  _____
GAM390  SS18     3'  CCCAGGGTTTTGTTTTTGTTTT 20103        TG   ________  CAG
           TTGTT                   GGCAGGAGG  GAAAC     CC   GG
                                |||||||||  |||||      ||   ||
                                TTGTTTTTT  TTTTG      GG   CC
                                     GT    TTTT    GAC
GAM390  SSA1     3'  TCTGAACCACCTTTGTCT    13416       G     AAACCC
                                AGGCAG AGGTGG     CAGG
                                ||||||  ||||||     ||||
                                TCTGTT TCCACC     GTCT
                                   _     AA_____
GAM390  SSX4     3'  CCCTCACTCTGTTTCCTGTT   20099        TG  AACCCC
                                GGCAGGAGG  GA     AGGG
                                |||||||||  ||     ||||
```

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                                TTGTCCTTT CT     TCCC
                                     GT CAC___
GAM390 STAM    5' TCTGTTGCTCTTTTTGCCT  14422         T AAACCC
                                AGGCAGGAGG GG     CAGG
                                |||||||||| ||     ||||
                                TCCGTTTTTC TC     GTCT
                                     _ GTT___
GAM390 STARD4  3' CCAGGGTTTTATTTATTTTTTG 58245          AA_______ CCAG
           CC                    GGCAGGAGGTGGA      CC   G
                                ||||||||||||       ||   |
                                CCGTTTTTTATTT      GG   C
                                      ATTTT    GACC
GAM390 STAT1   3' CTGTATTTTTACCTTTTTCCT 24613    C        CCC
                                AGG AGGAGGTGGAAA  CAG
                                ||| ||||||||||||  |||
                                TCC TTTTCCATTTTT  GTC
                                  T         AT_
GAM390 STAU2   3' CTCTGAATTGATTTTTTGCTT 27671         G AACCC
                                AGGCAGGAGGT GA    CAGGG
                                |||||||||| ||    |||||
                                TTCGTTTTTTA TT    GTCTC
                                     G AA___
GAM390 STCH    3' TGCTTGGATTTCCATTATTCTG 23695       _      CC   G
           TTT                   AGGCAGGA GGTGGAAA CCAGG
                                |||||||| ||||||||  |||||
                                TTTGTCTT TTACCTTT  GGTTC
                                     A       A_    GTC
GAM390 STIM1   3' CCAGGGTCTTGTTTCTGTCTCT 60775         TG   ________ CAG
           TGCTT                  AGGCAGGAGG  GAAAC     CC  GG
                                ||||||||||  |||||     ||  ||
                                TTCGTTCTCT  CTTTG     GG  CC
                                     GT    TTCT    GAC
GAM390 STIM1   3' CTCTGGGGTTCAGCTTCTGTCT 60779        G  AA
                                AGGCAGGAG TGG  ACCCCAGGG
                                ||||||||| |||  |||||||||
                                TCTGTCTTC ACT  TGGGGTCTC
                                     G  __
GAM390 STIM1   3' TTTTGAGGTTTGGTTTCTTGTT 60787       GG G  A  C
           T                     AGGCAGGA  T GAA CC CAGGG
                                ||||||||  | ||| || |||||
                                TTTGTTCT  G TTT GG GTTTT
                                     TT G  _  A
GAM390 SUDD    5' CAGGGCTCTGCTCTGTTCTTGT 15156       ____ TG  AA__  CCAG
           CT                    AGGCAGGA   GG  GA   CC   G
                                ||||||||   ||  ||   ||   |
                                TCTGTTCT   TC  CT   GG   C
                                     TGTC  GT  C    GAC
GAM390 SUPT5H  3' TCTGGATTTCCTTTTGTTT  13491         TGGAAACC
                                AGGCAGGAGG      CCAGG
                                ||||||||||      |||||
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                                TTTGTTTTCC       GGTCT
                                     TTTA____
GAM390  SUV39H1  3'  CAGGGTTTTGCACCTGCTTCTG 13494        ___   G  A____  CCAG
            CCT                   AGGCAGGA   GGTG AA    CC    G
                                  ||||||||   |||| ||    ||   |
                                  TCCGTCTT   CCAC TT    GG    C
                                       CGT    G  TT    GAC
GAM390  SVIL    5'  TTTTGGGATTTTACTTTGTGCT 41711       G       AC
            T                     AGGCA GAGGTGGAA  CCCAGGG
                                  ||||| |||||||||  |||||||
                                  TTCGT TTTCATTTT  GGGTTTT
                                    G        A_
GAM390  TACC1   3'  CTTTGGGGTCTTCTCCACCACC 21872        A     A___
            TGTCT                   AGGCAGG GGTGGA    ACCCCAGGG
                                  |||||||  ||||||    |||||||||
                                  TCTGTCC CCACCT    TGGGGTTTC
                                       A     CTTC
GAM390  TACC1   3'  TTTGGTGTTTTCATGTTT    21881     G       C
                                  GGA GTGGAAAC CCAGG
                                  |||  ||||||||  |||||
                                  TTT TACTTTTG GGTTT
                                    G       T
GAM390  TAL1    3'  CCCTGGGGCTGGCTTTTCTGTT 13525          _  GGAAA
            T                     AGGCAGGAG GT     CCCCAGGG
                                  |||||||||  ||    ||||||||
                                  TTTGTCTTT CG     GGGGTCCC
                                       T  GTC__
GAM390  TAL1    3'  CCTGGCTAATTTTTACTTTTT  13526           CC__    G
                                  AGGAGGTGGAAA    CCAGG
                                  ||||||||||||    |||||
                                  TTTTTCATTTTT    GGTCC
                                         AATC
GAM390  TAP2    3'  CCAGGGTCTTGCCCATTTTCTG 6777            AAA_______  CCAG
            CT                      GGCAGGAGGTGG        CC    G
                                  ||||||||||||        ||   |
                                  TCGTCTTTTACC        GG    C
                                         CGTTCT     GACC
GAM390  TAT     5'  TCTTGGAGGCTGCTTTCTCCT  6261      C     TG AAA  _
                                  AGG AGGAGG  G   CC CCAGGG
                                  |||  ||||||  |   || ||||||
                                  TCC TCTTTC  C   GG GGTTCT
                                    _      GT ___  A
GAM390  TAZ     3'  CCAGGGCTCTCTTTCCTTCTTG 5484           TG  AA_______  CCAG
            CCT                     AGGCAGGAGG  GA       CC    G
                                  ||||||||||  ||       ||   |
                                  TCCGTTCTTC  TT       GG    C
                                       CT  CTCTC     GACC
GAM390  TBL1X   3'  CCTTGGGATTTTTTTTTTTTTG 20130          T_    C
            TTT                     AGGCAGGAGG  GGAAA CCCAGGG
                                  ||||||||||  |||||  |||||||
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                                TTTGTTTTTT  TTTTT GGGTTCC
                                      TT     A
GAM390  TBL1X    3'  TCTTGGGCTTGTTGTCTCTTCC 20139     C      TG A  C
              T                    AGG AGGAGG  G AA CCCAGGG
                                   ||| ||||||  | || |||||||
                                   TCC TTCTCT  T TT GGGTTCT
                                     _     GT G  C
GAM390  TCERG1   3'  TCTTGTAAACTATACTCCTGTT 22959          _    AAACCC
              T                    AGGCAGGAG GTGG     CAGGG
                                   ||||||||| ||||     |||||
                                   TTTGTCCTC TATC     GTTCT
                                       A    AAAT__
GAM390  TCF1     3'  CCCTGGGGCCTGTACTGCCTGC 6784         A    GAAA
              TT                    AGGCAGG GGTG    CCCCAGGG
                                   ||||||| ||||    ||||||||
                                   TTCGTCC TCAT    GGGGTCCC
                                      G    GTCC
GAM390  TCF21    5'  CCAGGGCTTTCTCTGTCTCTCT 13641       _    TG  AA_______  CCAG
              GTCT                   AGGCAG GAGG  GA       CC    G
                                   |||||| ||||  ||       ||    |
                                   TCTGTC CTCT  CT       GG    C
                                      T    GT  CTTTC     GACC
GAM390  TCF7L2   5'  CCTTGGACTCGTCTTTTTCTT  48439       T   AACC_
                                   AGGAGG GGA     CCAGGG
                                   |||||| |||     ||||||
                                   TTCTTT TCT     GGTTCC
                                      T   GCTCA
GAM390  TCF8     3'  TTCACGGTGGTTTTTGTTTTTT 48434     C      TG     _ AGGG
              CTT                    AGG AGGAGG  GAAACC CC
                                   ||| ||||||  |||||| ||
                                   TTC TTTTTT  TTTTGG GG
                                     _     GT     T  CACTTT
GAM390  TCL1A    3'  GGTTCTGTTCACCTTCGTTT   42018      A       AA_______
                                   AGGC GGAGGTGGA       CC
                                   |||| |||||||||       ||
                                   TTTG CTTCCACTT       GG
                                     _       GTCTT
GAM390  TCTA     3'  CCTGCCTACTTCCTTCCT     42493     C       AAACCC
                                   AGG AGGAGGTGG      CAGG
                                   ||| |||||||||      ||||
                                   TCC TCCTTCATC      GTCC
                                     T        C_____
GAM390  TCTEL1   3'  GGCCTTTCTCCTTTTGTCT    22536          T    AC____
                                   AGGCAGGAGG GGAA     C
                                   |||||||||| ||||     |
                                   TCTGTTTTCC CTTT     G
                                         T    CC   G
GAM390  TDGF1    5'  CCCTGGACGCCTTGCTCCTGCT 13655         GT_  AAACC
              T                    AGGCAGGAG   GG    CCAGGG
                                   |||||||||   ||    ||||||
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                                TTCGTCCTC  CC    GGTCCC
                                     GTT  GCA__
GAM390  TEGT    3'  GGTTCTGTGCTTTTTGCTT   65229          __  AA__
                                AGGCAGGAGGT  GGA   CC
                                ||||||||||  |||   ||
                                TTCGTTTTTCG  TCT   GG
                                     TG   T
GAM390  TEGT    3'  TTTGGTCTGTTACCTGTTT   65232       AG TG  AACC
                                AGGCAGG  G  GA   CCAGG
                                |||||||  |  ||   |||||
                                TTTGTCC  T  CT   GGTTT
                                   AT GT  ____
GAM390  TEK     5'  TTCTGTGCTGTTCCTTCTTGCC 6621          T   AACCC
           T                     AGGCAGGAGG GGA    CAGGG
                                ||||||||||  |||    |||||
                                TCCGTTCTTC CTT    GTCTT
                                     _  GTCGT
GAM390  TEM7    3'  CCCATGCATTTTTATCTACTGT 40251       G       CCC  _
           CT                     AGGCAG AGGTGGAAA   CA GGG
                                ||||||  |||||||||   ||  |||
                                TCTGTC TCTATTTTT   GT CCC
                                   A       AC_  A
GAM390  TERF2   3'  CCCTGCCCCCTGTCCCCTGCCT 20149       A  TG AAACCC
                                AGGCAGG GG  G     CAGGG
                                |||||||  ||  |     |||||
                                TCCGTCC CT  C     GTCCC
                                   C  GT CCCC__
GAM390  TEX14   3'  CCAGGGCTTTCTTCTCTTTCTG 49227         T   AA_______  CCAG
           CTT                    AGGCAGGAGG GGA       CC    G
                                ||||||||||  |||       ||    |
                                TTCGTCTTTC CTT       GG    C
                                     T   CTTTC    GACC
GAM390  TFPI2   3'  TCTTGGGGTCGTATTCCTG   95509       GTGGAA
                                CAGGAG     ACCCCAGGG
                                ||||||     |||||||||
                                GTCCTT     TGGGGTTCT
                                   ATGC__
GAM390  TGFA    3'  CCAGGGTTGTTTTCTGTCATTT 13705        A GT    A________  CCAG
           GCCT                    AGGCAGG G  GGAA       CC    G
                                |||||||  |  ||||       ||    |
                                TCCGTTT C  TCTT       GG    C
                                   A TG    TTGTT    GACC
GAM390  TGFB2   3'  CTTTGGAAGTTTGTGTTCTGTT 13714        G TG  AACC
           T                     AGGCAGGA G  GA    CCAGGG
                                ||||||||  |  ||    ||||||
                                TTTGTCTT T  TT    GGTTTC
                                     G GT  GAA_
GAM390  TGFBR2  5'  CCTTGGCCCTTTAGTTCCTGTC 13728         G    AACC
           T                     AGGCAGGAG TGGA    CCAGGG
                                |||||||||  ||||    ||||||
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                                TCTGTCCTT ATTT   GGTTCC
                                     G   CCC_
GAM390  TGFBR3   3'  CCAGGGCCTTATCAGCTTCCTG 13740         G  AA_____  CCAG
           TTT                  AGGCAGGAGGT GA       CC   G
                                |||||||||| ||       ||   |
                                TTTGTCCTTCG CT      GG   C
                                     A  ATTCC    GACC
GAM390  TIAM1    5'  TCTTGACAAAGCCTCTTCTGTT 13755         T  AAACCC
           T                   AGGCAGGAGG GG     CAGGG
                               |||||||||| ||     |||||
                               TTTGTCTTCT CC     GTTCT
                                     _  GAAACA
GAM390  TIMELESS  5'  TCCTGTTTCTCCACTTCCTTCT 15365     C        AACCC
                               AGG AGGAGGTGGA    CAGGG
                               ||| ||||||||||    |||||
                               TCT TCCTTCACCT    GTCCT
                                 _       CTTT_
GAM390  TIMP3    3'  CTTTGGGCATCTCTTCTGCCT  6285         GT   AAC
                               AGGCAGGAG  GGA   CCCAGGG
                               |||||||||  |||   |||||||
                               TCCGTCTTC  TCT   GGGTTTC
                                    __   AC_
GAM390  TK2      3'  CCTGGGCTGCCTCCTCCT    17248     C     TG AAAC
                               AGG AGGAGG  G    CCCAGG
                               ||| ||||||  |    ||||||
                               TCC TCCTCC  C    GGGTCC
                                 _     GT ____
GAM390  TLL2     3'  CTTTGGCTGGAATCATTTTCTT 25882     C       AAA  __
           TCT                   AGG AGGAGGTGG   CC  CCAGGG
                                 ||| |||||||||   ||  ||||||
                                 TCT TCTTTTACT   GG  GGTTTC
                                   T       AA_  TC
GAM390  TLR5     5'  CTCTGGGGTTTCCCTCTTCTCT 13788     C     T
           CT                    AGG AGGAGG GGAAACCCCAGGG
                                 ||| |||||| ||||||||||||
                                 TCT TCTTCT CCTTTGGGGTCTC
                                   C     C
GAM390  TLX1     5'  CTCTGGGAATGGTCGCTTCCTG 19820           AAAC_
           TTT                   AGGCAGGAGGTGG    CCCAGGG
                                 ||||||||||||     |||||||
                                 TTTGTCCTTCGCT    GGGTCTC
                                      GGTAA
GAM390  TMEFF2   5'  CCCTGGACTCCCGTCTCCTCCT 32997     C    GT  AAACC
                               AGG AGGAG  GG    CCAGGG
                               ||| |||||  ||    ||||||
                               TCC TCCTC  CC    GGTCCC
                                 _    TG  CTCA_
GAM390  TMEM1    3'  CCAGGGTTTTTTTTTCCTCCTG 13798         T   A_____  CCAG
           TCT                   AGGCAGGAGG GGAA      CC   G
                                 |||||||||| ||||      ||   |
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                                TCTGTCCTCC TTTT     GG   C
                                      T   TTTT    GACC
GAM390  TMEM2   3' GGTGTTTTTACTTTTTGT   26338           ____
                                GCAGGAGGTGGAAAC   CC
                                ||||||||||||||   ||
                                TGTTTTTCATTTTTG   GG
                                      T
GAM390  TMOD3   3' TTCTGAAACATTTCTACTTTCT 28021           CCC__
           GCT                  GGCAGGAGGTGGAAA    CAGGG
                                ||||||||||||||    |||||
                                TCGTCTTTCATCTTT    GTCTT
                                      ACAAA
GAM390  TNFAIP1 3' CTTTGGTTTTCATTCCTTTTTG 41229         ___      CC  GG
           TTT                   AGGCAGGAGG   TGGAAACC  AG
                                ||||||||||   ||||||||  ||
                                TTTGTTTTTC   ACTTTTGG  TC
                                      CTT       TT
GAM390  TNFAIP2 3' TCTGATGCTACTTCTGCCT   21929      G     AAACCC
                                AGGCAG AGGTGG     CAGG
                                |||||| ||||||     ||||
                                TCCGTC TTCATC     GTCT
                                   _     GTA___
GAM390  TNFSF4  3' CCAGGGTTTTCTTTACCATTTT 13910       _     AA_______  CCAG
           GCTT                  AGGCAGGA GGTGGA       CC    G
                                |||||||| ||||||       ||    |
                                TTCGTTTT CCATTT       GG    C
                                     A     CTTTT    GACC
GAM390  TNFSF4  3' TCCTGTTTTCTATTTCCTCTT  13915     C         CCC
                                AGG AGGAGGTGGAAA   CAGGG
                                ||| ||||||||||||   |||||
                                TTC TCCTTTATCTTT   GTCCT
                                  _         T__
GAM390  TNFSF4  3' TTGGATTTTTTTTTCCTGTTT  13917         TG    CC
                                AGGCAGGAGG  GAAA  CCAG
                                ||||||||||  ||||  ||||
                                TTTGTCCTTT  TTTT  GGTT
                                      TT    A_
GAM390  TNR     3' CCAGGGCCTTCCTTCTTTCCTG 13823         T__    AC____ CCAG
           CCT                   AGGCAGGAGG   GGAA     C    G
                                ||||||||||   ||||     |    |
                                TCCGTCCTTT   CCTT     G    C
                                      CTT    CC   G GACC
GAM390  TNS     3' CCCTGGGGAACCTACTTTCTGC 42948          AAA
           T                    GGCAGGAGGTGG   CCCCAGGG
                                ||||||||||||   ||||||||
                                TCGTCTTTCATC   GGGGTCCC
                                      CAA
GAM390  TOP2B   3' TCTTGTGTTGTCCTTTTGTCT  8410          TGGA   CC
                                AGGCAGGAGG    AAC  CAGGG
                                ||||||||||    |||  |||||
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                                TCTGTTTTCC   TTG  GTTCT
                                     TG__   T_
GAM390  TP53    3'  CCCTGGAGGATTTCATCTCTTG 6798           A  _
          T                   GCAGGAGGTGGAA CC CCAGGG
                              |||||||||||| || ||||||
                              TGTTCTCTACTTT GG GGTCCC
                                    A  A
GAM390  TPK1    3'  CCAGGGTTTTCATTACTTTCTG 42608         ___   A___  CCAG
          CTT                  AGGCAGGAGGT  GGAA   CC   G
                              ||||||||||  ||||  ||  |
                              TTCGTCTTTCA  CTTT   GG   C
                                    TTA   T   GACC
GAM390  TRHDE   3'  CCCAGGGTTTTGCCATCGTTTT 26313       ___   A A_____  CCAG
          CTGTC                 GGCAGGA  GGTGG A    CC   GG
                              |||||||  ||||| |    ||   ||
                              CTGTCTT  CTACC T    GG   CC
                                  TTG   G TTT   GACC
GAM390  TRHDE   3'  TTTTGGGGGATATTTTTT   26318       GAAA
                              AGGAGGTG   CCCCAGGG
                              ||||||||   ||||||||
                              TTTTTTAT   GGGGTTTT
                                  AG__
GAM390  TRIM14  3'  TTCTGAAGGTTCTGCGTCCTGT 29522       G TG  A  C_
          TT                   AGGCAGGA G  GAA CC  CAGGG
                              |||||||| |  ||| ||  |||||
                              TTTGTCCT C  CTT GG  GTCTT
                                  G GT  _  AA
GAM390  TRIM37  3'  CAGGGCTTTCATTTTTTTCTGC 31623       ___    AC___ CCAG
          CT                   AGGCAGGAG  GTGGAA   C   G
                              |||||||||  ||||||   |   |
                              TCCGTCTTT  TACTTT   G   C
                                  TTT    C  G GAC
GAM390  TRIM8   3'  CAGGGCTTGTTTCTCCTCTTGT 48850        T   _______  CAG
          TT                   AGGCAGGAGG GGAAAC    CC  G
                              |||||||||| ||||||    ||  |
                              TTTGTTCTCC TCTTTG    GG  C
                                    _    TTC    GAC
GAM390  TRPS1   5'  CTTGCTCTATTTCCTTTCT   26923    C       AACCC
                              AGG AGGAGGTGGA   CAGG
                              ||| ||||||||||   ||||
                              TCT TCCTTTATCT   GTTC
                                T       C____
GAM390  TRPS1   3'  GTTTGGGTTTTGTTTCTT   26925      TG  AC    G
                              AGGAGG  GAA  CCCAGG
                              ||||||  |||  ||||||
                              TTCTTT  TTT  GGGTTT
                                 GT  __    GT
GAM390  TSN     3'  TCTTGGTAAAGTCCTTTTCTTG 17306        T  AACC_
          CTT                  AGGCAGGAGG GGA   CCAGGG
                              |||||||||| |||   ||||||
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                                TTCGTTCTTT CCT    GGTTCT
                                     T  GAAAT
GAM390  TXK     3'  TTCTGGAAATGTCTTTTGTT  13918        GT GAAACC
                                GGCAGGAG  G     CCAGGG
                                ||||||||  |     ||||||
                                TTGTTTTC  T     GGTCTT
                                    TG AAA___
GAM390  U2AF1   3'  CCATTTTTACCTTATGTCT  64382      G       CCCCA
                                AGGCA GAGGTGGAAA    GG
                                ||||| ||||||||||    ||
                                TCTGT TTCCATTTTT    CC
                                  A       A____
GAM390  UBE1    3'  TCTTGCCACTGCCTTCTACCT  13926    C     TG AAACCC
                                AGG AGGAGG  G     CAGGG
                                ||| ||||||  |     |||||
                                TCC TCTTCC  C     GTTCT
                                  A     GT ACC___
GAM390  UBE2A   3'  TTCTGTTGTATTTCATTTCCAG 13931     A       _  CC
            TTT                   AGGC GGAGGTGGAA AC  CAGGG
                                ||||| |||||||||| ||  |||||
                                TTTG CCTTTACTTT TG  GTCTT
                                  A       A  TT
GAM390  UBE2L3  3'  CCCCAGGGCTTAAACTTTGCTT 13963         TG  AA_________  CCAG
            TTTGTTT               AGGCAGGAGG  GA       CC   GG
                                |||||||||  ||       ||   ||
                                TTTGTTTTTC  TT       GG   CC
                                     GT  CAAATTC    GACC
GAM390  UBL3    3'  CTCTGATTTTTTATTTCTTGT  24022           CCC
                                GCAGGAGGTGGAAA   CAGGG
                                ||||||||||||||  |||||
                                TGTTCTTTATTTTT   GTCTC
                                       TA_
GAM390  UBTF    3'  CCCTGGCCTCCCCCACTTTCTT 27255    C       AAACC_
            TCT                   AGG AGGAGGTGG     CCAGGG
                                ||| |||||||||     ||||||
                                TCT TCTTTCACC     GGTCCC
                                  T       CCCTCC
GAM390  USP6    3'  CCCAGGGTCTTTTTCTTGCTT  92780         T   AA_  CCAG
                                AGGCAGGAGG GGA   CC    GG
                                |||||||||| |||   ||    ||
                                TTCGTTCTTT TCT   GG    CC
                                     T       GACC
GAM390  UTY     3'  TTCTGAAAAAATCCACTTTTTG 24065           AACCC_
            TT                   GGCAGGAGGTGGA     CAGGG
                                ||||||||||||||     |||||
                                TTGTTTTTCACCT     GTCTT
                                       AAAAAA
GAM390  VANGL2  3'  CCAGGGTCTTATTTCCCTCTTG 72091         T    A________  CCAG
            TCT                   AGGCAGGAGG GGAA       CC    G
                                |||||||||| ||||       ||    |
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                                TCTGTTCTCC CTTT       GG    C
                                      _    ATTCT     GACC
GAM390  VANGL2   3'  TTCTGGGGGTCTGTCTCTTTTC 72096     C     TG  AA
           T                   AGG AGGAGG  GA  CCCCAGGG
                               ||| ||||||  ||  ||||||||
                               TCT TTCTCT  CT  GGGGTCTT
                                 T     GT  G_
GAM390  VASP     3'  CCCTCCCACCTTCACCTTTAGC 14027      AG       AACCCC
           TT                   AGGC  GAGGTGGA     AGGG
                               ||||  ||||||||     ||||
                               TTCG  TTCCACTT     TCCC
                                 AT       CCACCC
GAM390  VPREB3   5'  CCTTGCAGAACTTCTACTTGCC 26309        _       ACCC__
           TGCCT                  AGGCAGG AGGTGGAA     CAGGG
                               ||||||| ||||||||     |||||
                               TCCGTCC TTCATCTT     GTTCC
                                  G       CAAGAC
GAM390  WASF3    3'  CTTTGGTTTTTCCTTTTGTTT  22812          T      CC
                               AGGCAGGAGG GGAAACC  AG
                               |||||||||| |||||||  ||
                               TTTGTTTTCC TTTTTGG  TC
                                     _      TT
GAM390  WASF3    3'  TCCAGTGTTTCTGCTTTCAGTT 22815      A     TG     CCCA
           T                   AGGC GGAGG  GAAAC    GGG
                               |||| |||||  |||||    |||
                               TTTG CTTTC  CTTTG    CCT
                                 A    GT     TGA_
GAM390  WHSC1L1  5'  GGTTCCGCCTCCTCCT      35505     C         A
                               AGG AGGAGGTGGAA CC
                               ||| ||||||||||| ||
                               TCC TCCTCCGCCTT GG
                                 _         _
GAM390  WISP1    3'  CCTTGGCCTCCATTTCTGTCT  55940       G      AACC
                               AGGCAG AGGTGGA    CCAGGG
                               |||||| |||||||    ||||||
                               TCTGTC TTTACCT    GGTTCC
                                  _      CC__
GAM390  WNT5A    3'  CCAGGGCTTTTTTTCTTTTCTG 14117          TG   A_______  CCAG
           CCT                   AGGCAGGAGG  GAA      CC    G
                               |||||||||  |||      ||    |
                               TCCGTCTTTT  TTT      GG    C
                                     CT   TTTC     GACC
GAM390  WNT8B    3'  CCTGACCTACTTCCTCCT     60335     C       AAACCC
                               AGG AGGAGGTGG      CAGG
                               ||| |||||||||      ||||
                               TCC TCCTTCATC      GTCC
                                 _        CA_____
GAM390  WWP2     3'  CCCTGGGGCGAGGCCATCTCTG 61725       G      AAA__
           CCT                   AGGCAG AGGTGG     CCCCAGGG
                               |||||| ||||||     ||||||||
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                                TCCGTC TCTACC    GGGGTCCC
                                   _     GGAGC
GAM390  XBP1    3'  CCTGGCTTGCCTCCAGTTT   18675     A    TG AAACC
                                AGGC GGAGG  G    CCAGG
                                |||| |||||  |    |||||
                                TTTG CCTCC  T    GGTCC
                                  A    GT C____
GAM390  XK      3'  CCAGGGTCATTTTTTGTTTCTT 41154     C     TG  A________  CCAG
            CCT                   AGG AGGAGG  GAA       CC   G
                                ||| ||||||  |||       ||   |
                                TCC TTCTTT  TTT       GG   C
                                  _     GT   TTACT    GACC
GAM390  XPR1    3'  CCAGGGCTTTGTCTCATTTCTT 17619     C       _ AA_______  CCAG
            CCCT                   AGG AGGAGGTG GA       CC   G
                                ||| |||||||| ||       ||   |
                                TCC TTCTTTAC CT       GG   C
                                  C       T  GTTTC    GACC
GAM390  XPR1    3'  CCCTAACTATTCTGTTTTTTGA 17620    G     TG   ACCCC
            CT                    AG CAGGAGG  GAA    AGGG
                                || |||||||  |||    ||||
                                TC GTTTTTT  CTT    TCCC
                                 A      GT   ATCAA
GAM390  XRCC3   3'  CCCTGGGAGCCGCCTGCTTCTT 19516    C  G     AAAC
                                AGG AG AGGTGG   CCCAGGG
                                ||| || ||||||   |||||||
                                TTC TC TCCGCC   GGGTCCC
                                  T  G     GA__
GAM390  XRCC5   3'  CCAGGGTCTTGTCCTCATTCTT 41241        GT_  AA_______  CCAG
            GCCT                   AGGCAGGAG   GGA      CC   G
                                |||||||||  |||       ||   |
                                TCCGTTCTT   CCT      GG   C
                                     ACT   GTTCT    GACC
GAM390  XT3     3'  GGCTTCTGTCTCCTGCTT    39917         TG   A
                                AGGCAGGAGG  GAA CC
                                ||||||||||  ||| ||
                                TTCGTCCTCT  CTT GG
                                      GT   C
GAM390  YWHAZ   3'  TCCTGTTTTAGCCTTCTGTCT  14157         G    CCC
                                AGGCAGGAGGT GAAAC   AGGG
                                ||||||||||| |||||   ||||
                                TCTGTCTTCCG TTTTG   TCCT
                                      A    ___
GAM390  ZFH4    5'  CCCTGGGTTTGCTTCTT     45630       TG  AAC
                                AGGAGG  GA   CCCAGGG
                                ||||||  ||   |||||||
                                TTCTTC  TT   GGGTCCC
                                   GT  ___
GAM390  ZFP37   3'  CCTGTGTTTCTTCTTGTTT   14160        GGT     CC
                                AGGCAGGA   GGAAAC  CAGG
                                ||||||||   ||||||  ||||
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                                TTTGTTCT  TCTTTG  GTCC
                                   ___     T_
GAM390  ZNF10    3'  ATACATGGTTTTTCCCTTTTGC 31817         TG     CCAGGG
              CT                    AGGCAGGAGG  GAAACC
                                ||||||||||  ||||||
                                TCCGTTTTCC  TTTTGG
                                     CT     TACATAC
GAM390  ZNF144   3'  CTTGGCTGCTGTCCTGCCT   24074        _  TG AAACC
                                AGGCAGGA GG  G    CCAGG
                                ||||||||  ||  |    |||||
                                TCCGTCCT TC  C    GGTTC
                                    G  GT _____
GAM390  ZNF189   3'  CCTGTTTTGTTTTTCGCTT   14358     AG   TG   ACCC
                                AGGC  GAGG  GAA   CAGG
                                ||||  ||||  |||   ||||
                                TTCG  TTTT  TTT   GTCC
                                  CT   GT  _____
GAM390  ZNF189   3'  CTTTGGGAGTGCCTTTTTTGTT 14359          T  AA  _
              T                   AGGCAGGAGG GG  AC CCCAGGG
                                ||||||||||  ||  || |||||||
                                TTTGTTTTTT CC  TG GGGTTTC
                                     _  G_  A
GAM390  ZNF198   3'  TTTTGGGGTTTTGTTTTGTTT  14365        GGTG
                                AGGCAGGA   GAAACCCCAGGG
                                ||||||||   ||||||||||||
                                TTTGTTTT   TTTTGGGGTTTT
                                    G___
GAM390  ZNF207   5'  TTTTGGCCTCGTTTCTCCTGCT 14374          TGGAAACC
              T                   AGGCAGGAGG       CCAGGG
                                ||||||||||       ||||||
                                TTCGTCCTCT       GGTTTT
                                     TTGCTCC_
GAM390  ZNF24    5'  CCCTGAGGCTTATATTCTGCCT 23707         G   AAA  C
                                AGGCAGGA GTGG   CC CAGGG
                                |||||||| ||||   || |||||
                                TCCGTCTT TATT   GG GTCCC
                                    A   C__  A
GAM390  ZNF253   3'  TCCTGGGTTTAAGCCATTCTTC 41081          _   AAAC__
              TGCCT                 AGGCAGGAGG TGG     CCCAGGG
                                ||||||||| |||     |||||||
                                TCCGTCTTCT ACC     GGGTCCT
                                     T   GAATTT
GAM390  ZNF264   3'  GGTTCTATCACTTTTTGTTT   14223           AAA_____
                                AGGCAGGAGGTGG       CC
                                ||||||||||||       ||
                                TTTGTTTTTCACT       GG
                                       ATCTT
GAM390  ZNF36    3'  CCATTTCCCCCTTTTGTTT   95579          T    CCCCA
                                AGGCAGGAGG GGAAA    GG
                                |||||||||| |||||    ||
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                                TTTGTTTTCC CCTTT    CC
                                      C    A____
GAM390  ZNF42    5'  TTCTGTTGGCTCCACCTCCAGC 14245     A       AA  C_
            CT                    AGGC GGAGGTGGA  CC  CAGGG
                                  |||| |||||||||  ||  |||||
                                  TCCG CCTCCACCT  GG  GTCTT
                                    A       C_  TT
GAM390  ABCA8    3'  CCCAAATTCTGTGTTCCTGTTT 24135         _ TG   ACCCCA
                                  AGGCAGGAG G  GAA     GGG
                                  ||||||||| |  |||     |||
                                  TTTGTCCTT T  CTT     CCC
                                      G GT   AAA___
GAM390  ABHD3    3'  TTTGGGTGCATTTTGTCT    57183         G   GAAAC
                                  AGGCAGGA GTG    CCCAGG
                                  |||||||| |||    ||||||
                                  TCTGTTTT CGT    GGGTTT
                                     A  _____
GAM390  ABT1     3'  TCCTGGCCCTGCTCTGCTTCCT 26305          TG  AACC__
            GTCT                    AGGCAGGAGG  GA     CCAGGG
                                  ||||||||||  ||     ||||||
                                  TCTGTCCTTC  CT     GGTCCT
                                      GT  CGTCCC
GAM390  ACTR3    3'  CCCCAGGGCTCGCATTCTGTTT 20364          TG   A_________  CCAG
            CTTGCTT                 AGGCAGGAGG  GAA       CC    GG
                                  ||||||||||  |||       ||    ||
                                  TTCGTTCTTT  CTT       GG    CC
                                      GT   ACGCTC    GACC
GAM390  ACTR3    3'  TTCTGATTACTCGCATTCTGTT 20367         G    AAACCC
            T                     AGGCAGGA GTGG     CAGGG
                                  |||||||| ||||     |||||
                                  TTTGTCTT CGCT     GTCTT
                                     A    CATTA_
GAM390  AD-020   3'  CCAGGGTTTGTTTCATTTCTTG 60091     G          AC_______ CCAG
            ACT                     AG CAGGAGGTGGAA       C    G
                                  || ||||||||||||       |    |
                                  TC GTTCTTTACTTT       G    C
                                    A          GTTT   G GACC
GAM390  AF053356_CDS3 3'  CCTCTTCTCTTTCCTGCCT    43982          T    ACCCC
                                  AGGCAGGAGG GGAA     AGG
                                  |||||||||| ||||     |||
                                  TCCGTCCTTT TCTT     TCC
                                      C    C____
GAM390  AF9Q34   3'  CCCTGCCCCCACCCCTTCCTGT 51714         ___     AAACCC
            CT                      AGGCAGGA   GGTGG     CAGGG
                                  ||||||||   |||||     |||||
                                  TCTGTCCT   CCACC     GTCCC
                                       TCC    CCC___
GAM390  AFAP     3'  TCCTGGTTGTCACTGTCTTCTT 41613     C     TG AA  C_
            TCT                     AGG AGGAGG  G  AC  CCAGGG
                                  ||| ||||||  |  ||  ||||||
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                                TCT TCTTCT  C  TG  GGTCCT
                                  T     GT AC  TT
GAM390  AGPAT1   3'  CTCTGAGCCAGTTTTCATTTCT 22173     C          CC___
           TCCT                    AGG AGGAGGTGGAAAC    CAGGG
                                ||| |||||||||||||    |||||
                                TCC TTCTTTACTTTTG    GTCTC
                                  _          ACCGA
GAM390  AGPAT1   3'  CTCTGAGCCAGTTTTCATTTCT 22174     C          CC___
           TCCT                    AGG AGGAGGTGGAAAC    CAGGG
                                ||| |||||||||||||    |||||
                                TCC TTCTTTACTTTTG    GTCTC
                                  _          ACCGA
GAM390  AHCYL1   3'  TCCTATAATTTCATTCTTGTTT 22777         G    ACCCC
                                AGGCAGGAG TGGAA    AGGG
                                |||||||||| |||||    ||||
                                TTTGTTCTT ACTTT    TCCT
                                     _    AATA_
GAM390  AKAP11   3'  GGTTTTGGCCTTTCCTGTTT  58463       __   G  A___
                                AGGCAGG  AGGT GAA   CC
                                |||||||  |||| |||   ||
                                TTTGTCC  TCCG TTT   GG
                                    TT   G  T
GAM390  AKR7A2   3'  CAGGGTTTTTCTAGCTTCCTGC 14890          _   A_____  CCAG
           CT                     AGGCAGGAGGT GGAA     CC   G
                                |||||||||| ||||     ||   |
                                TCCGTCCTTCG TCTT     GG   C
                                      A   TTT    GAC
GAM390  ALOXE3   5'  CCTGTGCTCATCTCTGCCT   41558       G     AAACCC
                                AGGCAG AGGTGG     CAGG
                                |||||| ||||||     ||||
                                TCCGTC TCTACT     GTCC
                                   _     CGT___
GAM390  ALS2CR3  3'  CCTATTTTCCTTTCTGTTT   31181         T    CCCC
                                AGGCAGGAGG GGAAA   AGG
                                |||||||||| |||||   |||
                                TTTGTCTTTC CTTTT   TCC
                                     _    A___
GAM390  AMOT     5'  CCAGGGCTCTCTTTCGCCTCCT 56539     C        AC_______ CCAG
           CTT                     AGG AGGAGGTGGAA       C   G
                                ||| ||||||||||       |   |
                                TTC TCCTCCGCTTT       G   C
                                  _         CTCTC   G GACC
GAM390  AMOT     3'  CTTTGCATCTTTTTATCTTCTG 56542           CCC_
                                CAGGAGGTGGAAA   CAGGG
                                ||||||||||||   |||||
                                GTCTTCTATTTTT   GTTTC
                                       CTAC
GAM390  AMOTL1   3'  TCCTGTCTGCCTGGCTTCTTGT 74012          __  AAACCC
           CT                     AGGCAGGAGGT  GG     CAGGG
                                ||||||||||  ||     |||||
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                                TCTGTTCTTCG  CC     GTCCT
                                      GT  GTCT__
GAM390  AMOTL1   3'  TCTGAGTTCATCTCTGTCT   74014       G      AACCC
                                AGGCAG AGGTGGA     CAGG
                                ||||||| |||||||     ||||
                                TCTGTC TCTACTT     GTCT
                                   _       GA___
GAM390  AP3M1    3'  CCTGTGCTATCTTCTCTT    24935     C       AAACCC
                                AGG AGGAGGTGG      CAGG
                                ||| |||||||||      ||||
                                TTC TCTTCTATC      GTCC
                                  _        GT____
GAM390  AP3M2    3'  TTTTGCTAGTTTTATCTTCTGA 23303    G          ACCC
              CT                   AG CAGGAGGTGGAA    CAGGG
                                || ||||||||||||    |||||
                                TC GTCTTCTATTTT    GTTTT
                                 A          GATC
GAM390  APCL     3'  CCTGAGCTCACTTTCGCCT   20815      A       AAACCC
                                AGGC GGAGGTGG      CAGG
                                |||| ||||||||      ||||
                                TCCG CTTTCACT      GTCC
                                  _        CGA___
GAM390  APELIN   3'  CCAGGGCTTTGTCACTTCTCTT 34263          __    AAA_____  CCAG
              GCCT                    AGGCAGGAG  GTGG       CC    G
                                |||||||||  ||||       ||    |
                                TCCGTTCTC  CACT       GG    C
                                     TT    GTTTC     GACC
GAM390  APELIN   3'  GGCTTTCTCCCCTTTTGCTT   34268          T   AA_______
                                AGGCAGGAGG GGA       CC
                                |||||||||| |||       ||
                                TTCGTTTTCC CCT       GG
                                     _  CTTTC
GAM390  APEX2    3'  CCCTGAGCTGCCTCCTGCTT   27918          TG AAACCC
                                AGGCAGGAGG  G     CAGGG
                                ||||||||||  |     |||||
                                TTCGTCCTCC  C     GTCCC
                                     GT GA____
GAM390  APH2     3'  GGCTCTTCTACTTGCTGTCT   51302       G       AC_____
                                AGGCAG AGGTGGAA       C
                                ||||||| ||||||||      |
                                TCTGTC TTCATCTT       G
                                   G       CTC   G
GAM390  ARF6     3'  CTTGGGGGTTTTCTCTTTTGTT 9788           T       _   G
              T                    AGGCAGGAGG GGAAACCCC AGG
                                |||||||||| ||||||||| |||
                                TTTGTTTTCT CTTTTGGGG TTC
                                     _        G
GAM390  ARHGAP11A 3'  TCCTGGGTTCATGCCATTTTCC 29460          _   AAAC__
              TGCCT                   AGGCAGGAGG TGG     CCCAGGG
                                |||||||||| |||     |||||||
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                                TCCGTCCTTT ACC     GGGTCCT
                                     T  GTACTT
GAM390  ARHGDIG  3' CCCTGGGTGTCGTCTCTTTCTG 8619         T  AA  _
           CCT                  AGGCAGGAGG GG  AC CCCAGGG
                                |||||||||| ||  || |||||||
                                TCCGTCTTTC CT  TG GGGTCCC
                                     T  GC  T
GAM390  ARHGEF9  3' TTCTGGGCCTACATTTCTTGAC 31494    G       GAAAC
           T                    AG CAGGAGGTG    CCCAGGG
                                || |||||||||    |||||||
                                TC GTTCTTTAC    GGGTCTT
                                 A       ATCC_
GAM390  ARPP-21  3' TTTGGTTTTGCTTTTTTCCT  33298    C    TG  ACC
                                AGG AGGAGG  GAA  CCAGG
                                ||| ||||||  |||  |||||
                                TCC TTTTTC  TTT  GGTTT
                                  T     GT  ___
GAM390  ASTN2    3' TCCTGCCACACTCTGCTTTCTT 73562    C    TG  AACCC_
           CCT                  AGG AGGAGG  GA     CAGGG
                                ||| ||||||  ||     |||||
                                TCC TCTTTC  CT     GTCCT
                                  T     GT  CACACC
GAM390  ATP10B   3' TTGGTTCTGCTTTTTGCCT   64108         TG  ACC
                                AGGCAGGAGG  GAA  CCAG
                                ||||||||||  |||  ||||
                                TCCGTTTTTC  CTT  GGTT
                                     GT  ___
GAM390  ATP10D   3' TTTAGTTTTCTACCTTCTGCCT 73532          _   CCCAGGG
                                AGGCAGGAGGTGG AAAC
                                |||||||||||| ||||
                                TCCGTCTTCCATC TTTG
                                       T   ATTT
GAM390  ATP6V1B2 3' TCCTGAGTGTTTGCTTTCGGTT 9887      A    TG  A  CC
           T                    AGGC GGAGG  GA AC  CAGGG
                                |||| |||||  || ||  |||||
                                TTTG CTTTC  TT TG  GTCCT
                                  G    GT  G  A_
GAM390  ATP6V1B2 3' TTTGGTTCTGCTTTTTGACCT  9888     _     TG  ACC
                                AGG CAGGAGG  GAA  CCAGG
                                ||| |||||||  |||  |||||
                                TCC GTTTTTC  CTT  GGTTT
                                  A      GT  ___
GAM390  ATPAF2   3' CCCTGGGGGCTGGTCCTTTGCC 74857       G   TGGAAA
           T                    AGGCAG AGG     CCCCAGGG
                                |||||| |||     ||||||||
                                TCCGTT TCC     GGGGTCCC
                                   _  TGGTCG
GAM390  B3GNT5   3' GGTTTTTTTACCTTTTGGTT  50250    G         A_____
                                AG CAGGAGGTGGAA     CC
                                || ||||||||||||     ||
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                                TT GTTTTCCATTTT     GG
                                 G          TTT
GAM390  BAIAP1   5'  CCAAGTTTCTCTCTCCTGTTT  17639        GT     CCCA
                                AGGCAGGAG  GGAAAC    GG
                                |||||||||  ||||||    ||
                                TTTGTCCTC  TCTTTG    CC
                                     TC     AA__
GAM390  BAIAP1   3'  CTCTACACATTTCATCCTTTTG 17640         _    ACCCC
           CTT                    AGGCAGGAGG TGGAA     AGGG
                                |||||||||| |||||     ||||
                                TTCGTTTTCC ACTTT     TCTC
                                     T     ACACA
GAM390  BART1    3'  TCCTGTGATCACATCTTGTCT  25040        G    AAACCC
                                AGGCAGGA GTGG     CAGGG
                                |||||||| ||||      |||||
                                TCTGTTCT CACT     GTCCT
                                     A    AGT___
GAM390  BCAR3    3'  CTTTGGGAAAGCTTACTGTTT  14540       G    GGAAAC
                                AGGCAG AGGT     CCCAGGG
                                |||||| ||||     |||||||
                                TTTGTC TTCG     GGGTTTC
                                   A    AAA___
GAM390  BCMP1    3'  CCAGGGTCTTTTTTGCCTTTTG 49536    G      TG   A_____  CCAG
           GCT                    AG CAGGAGG  GAA      CC    G
                                || |||||||  |||      ||    |
                                TC GTTTTCC  TTT      GG    C
                                 G      GT   TTCT     GACC
GAM390  BDG-29   3'  TTTTGGGGTTTTTATGTTTT   72808      G
                                AGGA GTGGAAACCCCAGGG
                                |||| ||||||||||||||
                                TTTT TATTTTTGGGGTTTT
                                  G
GAM390  BIA2     3'  CCTTATTTTTTGTTTCTTACCT 71792     C     TG    CCCC
                                AGG AGGAGG  GAAA    AGG
                                ||| ||||||  ||||    |||
                                TCC TTCTTT  TTTT    TCC
                                  A     GT    TAT_
GAM390  BICD2    3'  TTCTGGGGTTTTTCATATTGT  70918      GAGGT
                                GCAG    GGAAACCCCAGGG
                                ||||    ||||||||||||
                                TGTT    TTTTTGGGGTCTT
                                  ATAC_
GAM390  BIRC1    3'  CCAGGGTTTTGTTTTACTTTCG 16990       _        AC________ CCAG
           TGCCT                   AGGCA GGAGGTGGAA       C    G
                                ||||| ||||||||||       |    |
                                TCCGT CTTTCATTTT       G    C
                                   G         GTTTT   G GACC
GAM390  BLCAP    3'  CCAGGGCTTTGCCCTTCCTCCT 22941         T_  AAA_______  CCAG
           GCCT                    AGGCAGGAGG  GG       CC    G
                                ||||||||||  ||       ||    |
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                                TCCGTCCTCC CC       GG   C
                                      TT CGTTTC    GACC
GAM390  BM-009   3' TCTTGCTTTTATTTCTTTCCT 62372    C        ACCC
                                AGG AGGAGGTGGAA   CAGGG
                                ||| ||||||||||    |||||
                                TCC TTCTTTATTTT   GTTCT
                                  T        C___
GAM390  BM046    3' TCTGAAATATTTTTTGCCT   38059          GAAACCC
                                AGGCAGGAGGTG      CAGG
                                ||||||||||||      ||||
                                TCCGTTTTTTAT      GTCT
                                      AAA____
GAM390  BMF      3' TTCTGGATATTACCTCTTCTT 54293    C       AAACC
                                AGG AGGAGGTGG    CCAGGG
                                ||| |||||||||    ||||||
                                TTC TTCTCCATT    GGTCTT
                                  _       ATA__
GAM390  BNIP-S   3' CTCTGGGTTTTTTTGTTTTTTG 57100         TG   C_
           TTT                   AGGCAGGAGG  GAAA  CCCAGGG
                                ||||||||||  ||||  |||||||
                                TTTGTTTTTT  TTTT  GGGTCTC
                                      GT   TT
GAM390  BNIP1    3' TTCTGGCCCTTTCAGCTCCTGT 26533        G    ACC
           TT                    AGGCAGGAG TGGAA   CCAGGG
                                ||||||||| |||||   ||||||
                                TTTGTCCTC ACTTT   GGTCTT
                                      G    CCC
GAM390  BPNT1    3' TTCTGGAATCTCACTCTTGTTT 65383        GT   AACC
                                AGGCAGGAG  GGA   CCAGGG
                                |||||||||  |||   ||||||
                                TTTGTTCTC  TCT   GGTCTT
                                      AC   AA__
GAM390  BRAG     5' CTCTGGGACATCACTTCCT   30098        AAAC
                                AGGAGGTGG   CCCAGGG
                                |||||||||   |||||||
                                TCCTTCACT   GGGTCTC
                                      ACA_
GAM390  BSMAP    3' TCTTGGGGGCTTGCTACTTTTT 25046          AAA__
           GTCT                   AGGCAGGAGGTGG    CCCCAGGG
                                ||||||||||||    ||||||||
                                TCTGTTTTTCATC    GGGGTTCT
                                      GTTCG
GAM390  C11orf11 5' GGTCTTGGCCTTCCTGTCT   94881       _   G  AA___
                                AGGCAGG AGGT GA    CC
                                ||||||| |||| ||    ||
                                TCTGTCC TCCG TT    GG
                                    T   G  CT
GAM390  C11orf9  3' TCTGGGGTTTGCCTGTT    26120       AGGTGG
                                GGCAGG    AAACCCCAGG
                                ||||||    ||||||||||
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                                TTGTCC     TTTGGGGTCT
                                   G_____
GAM390  C12orf22  3'  TCCTATTTGTTCCAGTTTTTGC 48712        G    ACCCC
            TT                   AGGCAGGAG TGGAA    AGGG
                                ||||||||| |||||    ||||
                                TTCGTTTTT ACCTT    TCCT
                                     G    GTTTA
GAM390  C12orf3   3'  CCCTGGGGCACCCTCTTGT   40163        _ GAAA
                                GCAGGAGG TG   CCCCAGGG
                                |||||||| ||   ||||||||
                                TGTTCTCC AC   GGGGTCCC
                                     C ____
GAM390  C14orf4   5'  TCCTGGGGGCCCCGCTTGTCT  67923       A  T  AAA
                                AGGCAGG GG GG   CCCCAGGG
                                ||||||| || ||   ||||||||
                                TCTGTTC CC CC   GGGGTCCT
                                     G  _  G__
GAM390  C16orf5   3'  CCCTGGGCCTCTGCTCTCTTGC 26349         _ TG  AAC
            CT                   AGGCAGGAG G  GA   CCCAGGG
                                ||||||||| |  ||   |||||||
                                TCCGTTCTC C  CT   GGGTCCC
                                     T GT  CC_
GAM390  C1orf16   3'  TTCTGGGTTTTGTTTTTTGTTT 29918         GT    ____
            TTGTCT                AGGCAGGAG  GGAAAC    CCCAGGG
                                |||||||||  ||||||   |||||||
                                TCTGTTTTT  TTTTTG    GGGTCTT
                                     GT     TTTT
GAM390  C1orf16   3'  TTTCTGGGTTTTGTTTTTTGTT 29919         TG   AC
            T                    AGGCAGGAGG  GAA  CCCAGGG
                                |||||||||||  |||  |||||||
                                TTTGTTTTTT  TTT  GGGTCTT
                                     GT   __      TT
GAM390  C1orf17   3'  CCTTGGGTATCTGGTTTTTGTT 68764         G   A   C   G
            T                    AGGCAGGAG TGGA ACCC AGG
                                |||||||||| |||| |||| |||
                                TTTGTTTTT GTCT TGGG TCC
                                     G   A   T
GAM390  C1orf19   3'  CCTTGTCACCCACTTCTGTTT  68748       G     AAACCC
                                AGGCAG AGGTGG     CAGGG
                                |||||| ||||||     |||||
                                TTTGTC TTCACC     GTTCC
                                   _     CACT__
GAM390  C1orf2    3'  CTCTGGGGTCTCTTGCTGCTTG 96267        A   _ A
            CCT                   AGGCAGG GGTG GA ACCCCAGGG
                                ||||||| |||| || |||||||||
                                TCCGTTC TCGT CT TGGGGTCTC
                                     G   T  C
GAM390  C1orf22   3'  CCCAGGGTTTTGTTCCATTTTT 48039          _    AC_______ CCAG
            CTGTCT                AGGCAGGAGG TGGAA       C   G
                                ||||||||| |||||       |   |
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                                TCTGTCTTTT ACCTT       G   C
                                     T    GTTTT   G GACC
GAM390  C1orf24   3'  CCTTGAATAATGGCTTCCTGCC 54788          GGAAACCC
              T                   AGGCAGGAGGT       CAGGG
                                  ||||||||||        |||||
                                  TCCGTCCTTCG       GTTCC
                                       GTAATAA_
GAM390  C1orf25   5'  CTGGTTCTTCATCTTTTGTCT  72940           AACC
                                  AGGCAGGAGGTGGA    CCAG
                                  ||||||||||||||    ||||
                                  TCTGTTTTCTACTT    GGTC
                                        CTT_
GAM390  C1orf28   3'  CTCTGAGCCATCTTCTG     44844          AAACCC
                                  CAGGAGGTGG     CAGGG
                                  ||||||||||     |||||
                                  GTCTTCTACC     GTCTC
                                       GA____
GAM390  C1orf29   3'  TTTTGTTCGTTTTGCCTTCTGT 23340         TG   ACCC
              C                    GGCAGGAGG  GAA    CAGGG
                                   |||||||||  |||    |||||
                                   CTGTCTTCC  TTT    GTTTT
                                        GT   GCTT
GAM390  C1orf35   3'  CTTGCTTGCCTCCTGCCT    44481          TG AAACCC
                                  AGGCAGGAGG  G     CAGG
                                  ||||||||||  |     ||||
                                  TCCGTCCTCC  T     GTTC
                                       GT C_____
GAM390  C1orf8    3'  TCTGTAGCTATTTTGTTTTTTG 18029         TG   ACCC__    G
              CTT                    AGGCAGGAGG  GAA     CAGG
                                     ||||||||||  |||     ||||
                                     TTCGTTTTTT  TTT     GTCT
                                          GT   ATCGAT
GAM390  C1QR1     3'  TCTGGGAGGCCTCATGTCT    24871       G    GGAAAC
                                  AGGCA GAGGT     CCCAGG
                                  |||||  |||||     ||||||
                                  TCTGT CTCCG     GGGTCT
                                     A    GA____
GAM390  C20orf141 5'  CTCTGAGCTCACCCTTCTGTCT 55788          TG  AACCC
                                  AGGCAGGAGG  GA    CAGGG
                                  ||||||||||  ||    |||||
                                  TCTGTCTTCC  CT    GTCTC
                                       CA  CGA__
GAM390  C20orf177 3'  CTTTGCTTGTTTACTTTCTGCC 62833            AACCC
              T                    AGGCAGGAGGTGGA    CAGGG
                                   ||||||||||||||    |||||
                                   TCCGTCTTTCATTT    GTTTC
                                         GTTC_
GAM390  C20orf18  3'  TTCTGGGGCTAACTTCTCTGCC 49175        _    GGAAA
              T                    AGGCAG GAGGT    CCCCAGGG
                                   ||||||  |||||    ||||||||
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                                TCCGTC CTTCA    GGGGTCTT
                                   T    ATC__
GAM390  C20orf18  3'  TTCTGGGGCTAACTTCTCTGCC 49184      _    GGAAA
            T                   AGGCAG GAGGT    CCCCAGGG
                                |||||| |||||    ||||||||
                                TCCGTC CTTCA    GGGGTCTT
                                   T    ATC__
GAM390  C20orf59  5'  TCCTGCGCCGGCTTTCTGTTT  42236         _ AAACCC
                                AGGCAGGAGGT GG     CAGGG
                                |||||||||||| ||     |||||
                                TTTGTCTTTCG CC     GTCCT
                                      G  GC____
GAM390  C20orf72  3'  CCCTGGGGAAGGGTTTTCTGTC 54605       GG GGAAA
            T                   AGGCAGGA  T    CCCCAGGG
                                ||||||||  |    ||||||||
                                TCTGTCTT  G    GGGGTCCC
                                     TT GGAA_
GAM390  C21orf108 3'  CCCTGGAGGCCACTTCTTCCT  90111     C       AAA  _
                                AGG AGGAGGTGG   CC CCAGGG
                                ||| |||||||||   || ||||||
                                TCC TTCTTCACC   GG GGTCCC
                                  _       ___ A
GAM390  C21orf25  3'  CCCAGGGTTTTGTTTTTGGCTT 64288        G GG   ________  CAG
            TTGTCT                 AGGCAGGAG T  AAAC      CC   GG
                                |||||||||  |  ||||      ||   ||
                                TCTGTTTTC G  TTTG      GG   CC
                                     G TT    TTTT     GAC
GAM390  C21orf25  3'  TCCAGGGTTTTTTTTCCTGCCT 64303         T       CA
                                AGGCAGGAGG GGAAACCC  GGG
                                |||||||||| ||||||||  |||
                                TCCGTCCTTT TTTTTGGG  CCT
                                     _       A_
GAM390  C21orf6   3'  TTCTGGGAAAACTTTTACTTCC 34203          AC___
            TG                    CAGGAGGTGGAA    CCCAGGG
                                ||||||||||||    |||||||
                                GTCCTTCATTTT    GGGTCTT
                                      CAAAA
GAM390  C22orf4   3'  GGTGTTTCTGCTTCTGTTT   61275       G   TG    ____
                                AGGCAG AGG  GAAAC   CC
                                |||||| |||  |||||   ||
                                TTTGTC TTC  CTTTG   GG
                                   _  GT    T
GAM390  C22orf5   3'  CCTGCCCCGCCATCTGCTT   25336       GA    AAACCC
                                AGGCAG  GGTGG     CAGG
                                ||||||  |||||     ||||
                                TTCGTC  CCGCC     GTCC
                                   TA    CC____
GAM390  C22orf5   3'  CTTTGGGCAGAGCCCTTGCTT  25339        A   GGAAAC
                                AGGCAGG GGT     CCCAGGG
                                ||||||| |||     |||||||
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                                TTCGTTC CCG     GGGTTTC
                                    _  AGAC__
GAM390  C3IP1    3'  CTTTGGGGAGCACTTTCCTGTC 41577       _  GAAA
                                GGCAGGAG GTG   CCCCAGGG
                                |||||||| |||   ||||||||
                                CTGTCCTT CAC   GGGGTTTC
                                    T  GA__
GAM390  C3orf4   5'  CCCCAGGGTCCTGACTCTTACC 39591    C    GT_  AA_  CCAG
          T                      AGG AGGAG  GGA  CC   GG
                                ||| |||||  |||  ||   ||
                                TCC TTCTC  CCT  GG   CC
                                  A    AGT      GACC
GAM390  C5orf7   3'  CCCCAGGGTTTTAATTTCACTT 64597          A_________  CCAG
          TCTGT                   GCAGGAGGTGGAA       CC   GG
                                ||||||||||||       ||   ||
                                TGTCTTTCACTTT       GG   CC
                                        AATTTT    GACC
GAM390  C6orf5   5'  CAGGGCAGCTTCCACTTCCTGC 31978           AC_______ CCAG
          TT                     AGGCAGGAGGTGGAA      C   G
                                ||||||||||||||       |   |
                                TTCGTCCTTCACCTT      G   C
                                        CGAC  G GAC
GAM390  C8orf13  3'  CTCTGTGACTGGCTCTTGCTT  82476        G  AAACCC
                                AGGCAGGAG TGG    CAGGG
                                |||||||| |||    |||||
                                TTCGTTCTC GTC    GTCTC
                                    G  AGT___
GAM390  C9orf14  3'  CAGGGTCCTACTTCATGTTT  87955      G     AAA__  CCAG
                                AGGCA GAGGTGG    CC   G
                                ||||| |||||||    ||   |
                                TTTGT CTTCATC    GG   C
                                   A     CT    GAC
GAM390  C9orf9   3'  GGCTCTCTCTCTTCTTGCTT  39027        T_  AA____
                                AGGCAGGAGG  GGA    CC
                                |||||||||  |||    ||
                                TTCGTTCTTC  TCT    GG
                                      TC  CTC
GAM390  CAMKK2   3'  CTCTGGTTATTTGTTTTTTCCT 22620    C    TG  AACC
                                AGG AGGAGG  GA   CCAGGG
                                ||| ||||||  ||   ||||||
                                TCC TTTTTT  TT   GGTCTC
                                  _    GT  ATT_
GAM390  CAMKK2   3'  TTCTGCAGGGCTTCTCTTGTTT 22633        TGGAAA  __
                                AGGCAGGAGG    CCC  CAGGG
                                ||||||||||    |||  |||||
                                TTTGTTCTCT    GGG  GTCTT
                                      TC____  AC
GAM390  CAP350   3'  TTCTGGAGTTTATTTCATTTCT 29709         ___  C
          T                     AGGAGGTGGAA  AC CCAGGG
                                ||||||||||  || ||||||
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                                TTCTTTACTTT   TG GGTCTT
                                      ATT  A
GAM390  CAPS2    3'  CTTTGCTAGTCATTTCTTCCT  71127     C       AAACCC
                                AGG AGGAGGTGG     CAGGG
                                ||| |||||||||     |||||
                                TCC TTCTTTACT     GTTTC
                                  _       GATC__
GAM390  CAPS2    3'  GGTTTTGCTACCTCTTCCT   71129     C       _  A____
                                AGG AGGAGGTGG AA    CC
                                ||| ||||||||| ||    ||
                                TCC TTCTCCATC TT    GG
                                  _       G  TT
GAM390  CAS1     3'  CAGGGTGTTTTTGCTTTTTGTT 43494          TG    ____  CAG
           T                     AGGCAGGAGG  GAAAC   CC   G
                                ||||||||||  |||||   ||   |
                                TTTGTTTTTC  TTTTG   GG   C
                                      GT    T    GAC
GAM390  caspr5   3'  CCAGGGTTCTCTTTATTTTCTG 56253            AA_______  CCAG
           CTT                    AGGCAGGAGGTGGA       CC    G
                                ||||||||||||||       ||   |
                                TTCGTCTTTTATTT       GG    C
                                      CTCTT    GACC
GAM390  CAT56    3'  CTTTGGGACCCATCTTTGCTT  48279       G     AAAC
                                AGGCAG AGGTGG   CCCAGGG
                                |||||| ||||||   |||||||
                                TTCGTT TCTACC   GGGTTTC
                                  _     CA__
GAM390  CBLN1    3'  TCTGGAATCCTTCTGCCT    16372          TGGAAACC
                                AGGCAGGAGG       CCAGG
                                ||||||||||       |||||
                                TCCGTCTTCC       GGTCT
                                      TAA_____
GAM390  CBX6     3'  CCTGGGCAGCTTCTGTTT    27412         G  GAAAC
                                AGGCAGGAG TG    CCCAGG
                                ||||||||| ||    ||||||
                                TTTGTCTTC AC    GGGTCC
                                      G  _____
GAM390  CDH24    3'  CTCTGTGTCTGTCTCCTGCC   96602         TG  AACCC
                                GGCAGGAGG  GA    CAGGG
                                |||||||||  ||    |||||
                                CCGTCCTCT  CT    GTCTC
                                      GT  GT___
GAM390  CEACAM8  3'  TCCTGGGTTCACACCATTCTCC 10189          _  AAAC__
           TGCCT                   AGGCAGGAGG TGG     CCCAGGG
                                |||||||||| |||     |||||||
                                TCCGTCCTCT ACC     GGGTCCT
                                      T   ACACTT
GAM390  CECR6    3'  CCTTGTCTTCTACCTTCTGTC  49932            ACCC
                                GGCAGGAGGTGGAA    CAGGG
                                ||||||||||||||   |||||
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                                CTGTCTTCCATCTT   GTTCC
                                      CT__
GAM390  cerk    3'  CTCGGATGTCTGTCTTTTGTCT 43165         TG  AAC  C
                                AGGCAGGAGG  GA   CC AG
                                ||||||||||  ||   || ||
                                TCTGTTTTCT  CT   GG TC
                                     GT  GTA  C
GAM390  CG012   5'  CTTTGGGGTTTTTGTTTGTTTT 84157    C  G   TG
          C                      GG AG AGG  GAAACCCCAGGG
                                 || || |||  ||||||||||||
                                 CT TT TTT  TTTTGGGGTTTC
                                  T  G   GT
GAM390  CGB5    5'  CCCTGGCCTTGTCTACCTCTTG 53488           AACC_
          CC                     GGCAGGAGGTGGA    CCAGGG
                                 ||||||||||||     ||||||
                                 CCGTTCTCCATCT    GGTCCC
                                       GTTCC
GAM390  CGB8    5'  CCCTGGCCTTGTCTACCTCTTG 53750           AACC_
          CC                     GGCAGGAGGTGGA    CCAGGG
                                 ||||||||||||     ||||||
                                 CCGTTCTCCATCT    GGTCCC
                                       GTTCC
GAM390  CGI-96  3'  CCAGGGTCCTTCCTGCTTCTTG 32292          _   AC_____ CCAG
          CCT                    AGGCAGGAGGT GGAA      C   G
                                 ||||||||||| ||||      |   |
                                 TCCGTTCTTCG CCTT      G   C
                                       T   CCT   G GACC
GAM390  CHERP   3'  TCTTGTGGATTTCATTGTTTTG 22135        _     A  C
          CCT                    AGGCAGGA GGTGGAA CC CAGGG
                                 |||||||| ||||||| || |||||
                                 TCCGTTTT TTACTTT GG GTTCT
                                     G      A  T
GAM390  CHK     3'  CCAGGGTTTATTTCATCTCTTG 8885            A_______  CCAG
          TTT                    AGGCAGGAGGTGGAA      CC   G
                                 ||||||||||||||      ||   |
                                 TTTGTTCTCTACTTT      GG   C
                                       ATTT    GACC
GAM390  CHL1    3'  TTCTGGTGTTATTCTGTCTCCT 22769     C     TG  __ C
          CTT                    AGG AGGAGG  GAA  AC CCAGGG
                                 ||| ||||||  |||  || ||||||
                                 TTC TCCTCT  CTT  TG GGTCTT
                                   _     GT   AT  T
GAM390  CHRNA9  3'  TCTGTGCTTTTTATTTTTAGCT 34553      AG        CCC   G
          T                      AGGC  GAGGTGGAAA   CAGG
                                 ||||  ||||||||||   ||||
                                 TTCG  TTTTATTTTT   GTCT
                                   AT        CGT
GAM390  CHST3   3'  CCCAGGGTTTTCTTTTGCTATT 16233         _ TG   AC________ CCAG
          TTGCCT                 AGGCAGGA GG  GAA       C   G
                                 ||||||||  ||  |||       |   |
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                                TCCGTTTT TC  TTT       G    C
                                    A  GT   CTTTT   G GACC
GAM390  CHST3    3'  CTGTGTTTTTGCTTTTGTTT   16238       G   TG    CC
                                AGGCAG AGG  GAAAC  CAG
                                |||||| |||  |||||  |||
                                TTTGTT TTC  TTTTG  GTC
                                   _  GT    T_
GAM390  CHST3    3'  TCTTGGGTTTTTTTTATTTTCT 16245           C__
                                AGGAGGTGGAAA   CCCAGGG
                                ||||||||||||   |||||||
                                TCTTTTATTTTT   GGGTTCT
                                       TTT
GAM390  CIP29    3'  CCCTGGGGTCTGTATGCCTTTG 51374       G    GAA__
           TCT                    AGGCAG AGGTG    ACCCCAGGG
                                |||||| |||||    |||||||||
                                TCTGTT TCCGT    TGGGGTCCC
                                   _    ATGTC
GAM390  CL25084  5'  CCAGGGTCCTCCTCCACCTCCT 32286     C        AA________  CCAG
           CCT                    AGG AGGAGGTGGA       CC    G
                                ||| ||||||||||       ||   |
                                TCC TCCTCCACCT       GG    C
                                  _       CCTCCT    GACC
GAM390  CLDN6    3'  CCCAGGGTTTTGTTTCTGCCTC 41334         TG    ________  CAG
           CTGCT                  GGCAGGAGG  GAAAC      CC   GG
                                |||||||||  |||||      ||   ||
                                TCGTCCTCC  CTTTG      GG   CC
                                     GT    TTTT    GAC
GAM390  CLDN6    3'  CTTTGGGATGGGTTCGTACCTT 41336           _  AC___
           TTGTTT                 AGGCAGGAGGTG GAA    CCCAGGG
                                |||||||||||| |||    |||||||
                                TTTGTTTTCCAT CTT    GGGTTTC
                                       G   GGGTA
GAM390  CLECSF9  3'  TTCTGACAAGTCTGTCTTCTCT 27625     C     TG  AACCC
           T                    AGG AGGAGG  GA    CAGGG
                                ||| ||||||  ||    |||||
                                TTC TCTTCT  CT    GTCTT
                                  _     GT  GAACA
GAM390  CNNM2    3'  GGCTCTGTGCCTCCTGCCT   34942           __  AA__
                                AGGCAGGAGGT  GGA   CC
                                ||||||||||  |||   ||
                                TCCGTCCTCCG  TCT   GG
                                       TG   C
GAM390  CNOT3    5'  TCTTGGGTACTGCCTTCTGCC  27988         TG AAAC
                                GGCAGGAGG  G   CCCAGGG
                                |||||||||  |   |||||||
                                CCGTCTTCC  C   GGGTTCT
                                     GT AT__
GAM390  CNOT8    3'  TCTGGTTGCCTCCTGCC     17709         TG AAACC
                                GGCAGGAGG  G    CCAGG
                                |||||||||  |    |||||
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                                CCGTCCTCC  T    GGTCT
                                     GT _____
GAM390  CNTNAP1   3'  CCCTGCCCCCCTCCTTTTGTTT 14642         T  AAACCC
                                AGGCAGGAGG GG     CAGGG
                                |||||||||| ||     |||||
                                TTTGTTTTCC CC     GTCCC
                                     T  CCCC__
GAM390  COLEC10   3'  CCCAGGGTTCTAGCTTTGTGTC 22237      G   _   AA__  CCAG
           T                    AGGCA GAGG TGGA   CC   GG
                                ||||| |||| ||||   ||   ||
                                TCTGT TTTC ATCT   GG   CC
                                   G   G   T   GACC
GAM390  COPS7A    3'  CCCAGGGTTTTGTTGGTACTTT 33322          GA  ________  CAG
           CTGTTT                 AGGCAGGAGGTG  AAC     CC   GG
                                ||||||||||||  |||     ||   ||
                                TTTGTCTTTCAT  TTG     GG   CC
                                      GG   TTTT    GAC
GAM390  COPS7B    3'  CTGCTTTCCCTCTCCTGCCT   42998         T    CCC
                                AGGCAGGAGG GGAAA   CAG
                                |||||||||| |||||   |||
                                TCCGTCCTCT CCTTT   GTC
                                     C    C__
GAM390  CORO1A    5'  CCAGGGTCCTCCTCCACCTCCG 23955      A       AA________  CCAG
           GCTT                   AGGC GGAGGTGGA       CC   G
                                |||| |||||||||       ||   |
                                TTCG CCTCCACCT       GG   C
                                  G       CCTCCT    GACC
GAM390  COTL1     3'  TCCTGGACCCTGCTTCCTGT   89293        TG AAACC
                                GCAGGAGG  G    CCAGGG
                                ||||||||  |    ||||||
                                TGTCCTTC  C    GGTCCT
                                     GT CCA__
GAM390  CRA       3'  TCCAAGTTCTATTTCTTCCCT  22938     C        ACCCCA
                                AGG AGGAGGTGGAA     GGG
                                ||| ||||||||||      |||
                                TCC TTCTTTATCTT     CCT
                                  C         GAA___
GAM390  CRSP3     3'  CCTATCTATATTTTTGTCT    61261         _    AACCCC
                                AGGCAGGAG GTGGA     AGG
                                |||||||| |||||     |||
                                TCTGTTTTT TATCT     TCC
                                     A    A_____
GAM390  CTCF      3'  CTGTTTTTTGCTTTTGCTT    22678       G   TG   CCC
                                AGGCAG AGG  GAAA   CAG
                                |||||| |||  ||||   |||
                                TTCGTT TTC  TTTT   GTC
                                   _  GT   T__
GAM390  CTCF      3'  TCCTGAAAGCTTTGCCTCTTTC 22680     C     TG  AACCC
           TT                     AGG AGGAGG  GA    CAGGG
                                ||| ||||||  ||    |||||
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                                TTC TTCTCC  TT    GTCCT
                                  T     GT  CGAAA
GAM390  CUGBP2   3'  CTCTGGAATCATTTTACTGTTT 22665       A      ACC__
            GTTT                  AGGCAGG GGTGGAA    CCAGGG
                                  ||||||| |||||||    ||||||
                                  TTTGTTT TCATTTT    GGTCTC
                                     G      ACTAA
GAM390  Cyt19    3'  CCAGGGTTTTTTTCTATTTCCT 73311     C        A________  CCAG
            ACTT                  AGG AGGAGGTGGAA      CC   G
                                  ||| ||||||||||       ||   |
                                  TTC TCCTTTATCTT       GG   C
                                    A         TTTTT    GACC
GAM390  D4ST-1   3'  CCAGCTTTCTGTGCTTCTGCCT 56197         _ TG   CCCCA
                                  AGGCAGGAG G  GAAA    GG
                                  ||||||||| |  ||||    ||
                                  TCCGTCTTC T  CTTT    CC
                                       G GT   CGA__
GAM390  DAMS     5'  CTAAGGTTTTCAATCTTTTGTC 42085          _     CC  GG
            T                      AGGCAGGAGGT GGAAACC  AG
                                  |||||||||| |||||||  ||
                                  TCTGTTTTCTA CTTTTGG  TC
                                       A      AA
GAM390  DCNP1    3'  CCCTGGGGTTTTGGGATTCTGT 56457       GGTG
                                  GCAGGA   GAAACCCCAGGG
                                  ||||||   ||||||||||||
                                  TGTCTT   TTTTGGGGTCCC
                                     AGGG
GAM390  DCOHM    3'  CTTTGGCTTTCTTCTGTTTTCT 50520     C     TG   ACC__
            TTCT                  AGG AGGAGG  GAA    CCAGGG
                                  ||| ||||||  |||    ||||||
                                  TCT TCTTTT  CTT    GGTTTC
                                    T     GT   CTTTC
GAM390  DCOHM    3'  TTTGGCATATTTCCTGCT    50540          GAAACC
                                  GGCAGGAGGTG    CCAGG
                                  ||||||||||     |||||
                                  TCGTCCTTTAT     GGTTT
                                       AC____
GAM390  DDM36    3'  CCCCAGGGTCATTTTTCATGTT 40917       _ G     A________  CCAG
            CTTGTTT                AGGCAGG A GTGGAA      CC   GG
                                  ||||||| | ||||||       ||   ||
                                  TTTGTTC T TACTTT       GG   CC
                                     T G     TTACT    GACC
GAM390  DDM36    3'  CTTGACTTCTATTTTCTGT   40923          ACCC
                                  GCAGGAGGTGGAA   CAGG
                                  ||||||||||||    ||||
                                  TGTCTTTTATCTT   GTTC
                                       CA__
GAM390  DDM36    3'  TTCTGGCTTCCCTGCATCTTGC 40931        G  __   ACC
            CT                     AGGCAGGA GT  GGAA   CCAGGG
                                  |||||||| ||  ||||   ||||||
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                                TCCGTTCT CG  CCTT   GGTCTT
                                    A  TC    C__
GAM390  DDX33    3'  TCCAGTTTTTGTTTTTTGTTT  39789          TG     CCCA
                                AGGCAGGAGG  GAAAC    GGG
                                ||||||||||  |||||    |||
                                TTTGTTTTTT  TTTTG    CCT
                                    GT     A___
GAM390  DDX33    3'  TTCTGAAAAGTTTTCCAGTTTT 39790          G  _    CC__
           TGTTT                  AGGCAGGAG TGG AAAC    CAGGG
                                |||||||||  ||| ||||    |||||
                                TTTGTTTTT ACC TTTG    GTCTT
                                    G  T    AAAA
GAM390  dJ309H15.1 3'  CCAGGGCTTTCTCCATCTATTG 57566        G      AA_______  CCAG
           TCT                    AGGCAG AGGTGGA       CC    G
                                ||||||  |||||||       ||    |
                                TCTGTT TCTACCT       GG    C
                                   A      CTTTC     GACC
GAM390  dJ55C23.6 3'  TTTTGGCTCTACCATCTGTTT  54509        GA     AACC
                                AGGCAG  GGTGGA    CCAGGG
                                ||||||  ||||||    ||||||
                                TTTGTC  CCATCT    GGTTTT
                                   TA     C___
GAM390  DKFZP434B1727 3'  TCCTGGGCTCAATACTCTTGCC 50481          GTG_  AAC
           T                    AGGCAGGAG    GA   CCCAGGG
                                |||||||||    ||   |||||||
                                TCCGTTCTC    CT   GGGTCCT
                                    ATAA  C__
GAM390  DKFZP434B195 3'  CTTTGGATGTGCTTTCTGCC   49247          GGAA  C_
                                GGCAGGAGGT    AC  CCAGGG
                                ||||||||||    ||  ||||||
                                CCGTCTTTCG    TG  GGTTTC
                                    _____  TA
GAM390  DKFZP434D1335 3'  GCACTGGGTTTTTGTTTTTTGT 65715          TG      C  GG
           TT                    AGGCAGGAGG  GAAACCC AG
                                ||||||||||  ||||||| ||
                                TTTGTTTTTT  TTTTGGG TC
                                    GT      _  ACGA
GAM390  DKFZp434E0519 3'  CCCCAGGGTTTTGCATCCTATT 50987          GT   AA_________  CCAG
           CTTGTTT                AGGCAGGAG  GGA        CC    GG
                                |||||||||  |||         ||    ||
                                TTTGTTCTT  CCT        GG    CC
                                    AT   ACGTTTT    GACC
GAM390  DKFZp434E0519 3'  CTTTGGTTTTCTTTCTTTTGTC 50989          T     CC
           T                    AGGCAGGAGG GGAAA  CCAGGG
                                ||||||||||| |||||  ||||||
                                TCTGTTTTCT TCTTT  GGTTTC
                                    T    T_
GAM390  DKFZP434E2135 3'  CTCTGCATGCTCTTTCTTGTTT 48684          T  AAACCC
                                AGGCAGGAGG GG     CAGGG
                                |||||||||| ||     |||||
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                                TTTGTTCTTT TC     GTCTC
                                      C  GTAC__
GAM390  DKFZP434E2135 3'  CTTGATGAGTTTTTGTTTCTGC 48685      G   TG    CC__   G
           TT                   AGGCAG AGG  GAAAC    CAGG
                                |||||| |||  |||||    ||||
                                TTCGTC TTT  TTTTG    GTTC
                                   _   GT     AGTA
GAM390  DKFZp434F142 3'  CCTTCCAGTCCCACCTCTTGCC 51033          AAACCCC   G
           T                    AGGCAGGAGGTGG      AGG
                                ||||||||||||       |||
                                TCCGTTCTCCACC      TCC
                                      CTGACCT
GAM390  DKFZp434F142 3'  TCTGGTTTTGCTCTTGCCT    51039       G TG   ACC
                                AGGCAGGA G  GAA   CCAGG
                                |||||||| |  |||   |||||
                                TCCGTTCT C  TTT   GGTCT
                                     _ GT   ___
GAM390  DKFZP434G156 3'  CTGACTTCCATCTCCTGCCT   70336           ACCC
                                AGGCAGGAGGTGGAA    CAG
                                ||||||||||||||    |||
                                TCCGTCCTCTACCTT    GTC
                                      CA__
GAM390  DKFZp434G179 3'  CCAGGGTTCTATTTGCTGTTT  80889      G      AA__  CCAG
                                AGGCAG AGGTGGA    CC    G
                                |||||| |||||||    ||    |
                                TTTGTC TTTATCT    GG    C
                                   G      T     GACC
GAM390  DKFZP434H0820 3'  TCTGGCGCATCTCTTCCCT    64586     C       GAAACC
                                AGG AGGAGGTG      CCAGG
                                ||| ||||||||      |||||
                                TCC TTCTCTAC      GGTCT
                                  C       GC_____
GAM390  DKFZp434H2226 5'  CCAGGGTCCTTTCCATCTTCTT 69131     C         A_______  CCAG
           CCT                    AGG AGGAGGTGGAA      CC    G
                                ||| ||||||||||       ||    |
                                TCC TCTTCTACCTT      GG    C
                                  T         TCCT     GACC
GAM390  DKFZP434J037 5'  CTTGCTCACCTCCTGCT     48948          AAACCC
                                GGCAGGAGGTGG      CAGG
                                ||||||||||||      ||||
                                TCGTCCTCCACT      GTTC
                                      C______
GAM390  DKFZP434K028 3'  CTCTGCCACCCCCTCCTGTCT  94859         T  AAACCC
                                AGGCAGGAGG GG      CAGGG
                                |||||||||| ||      |||||
                                TCTGTCCTCC CC      GTCTC
                                      _  CACC__
GAM390  DKFZp434K1210 5'  CCATTTCTGTTTGCTGCCT    34688       G   TG    CCCCA
                                AGGCAG AGG  GAAA     GG
                                |||||| |||  ||||     ||
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                                TCCGTC TTT  CTTT    CC
                                   G  GT   A____
GAM390  DKFZP434L1435 5'  CTCTGGGCCCCTGCCTCCTGC  99585        TG AAAC
                                GCAGGAGG  G   CCCAGGG
                                ||||||||  |   |||||||
                                CGTCCTCC  C   GGGTCTC
                                    GT CCC_
GAM390  DKFZP434L187 3'  TCTGGGGTTCTCTTTTCT    69355       T GA
                                AGGAGG G  AACCCCAGG
                                ||||||| |  |||||||||
                                TCTTTT C  TTGGGGTCT
                                   _ TC
GAM390  DKFZP434N161 3'  CCTTGTCCCCGTCTCCTCCCT  79215    C    GT  AAACCC
                                AGG AGGAG  GG     CAGGG
                                ||| |||||  ||     |||||
                                TCC TCCTC  CC     GTTCC
                                  C    TG  CCT___
GAM390  DKFZP434N178 3'  CCTTGGGAGGCGCTTCTTGCC  72398          GAAAC
                                GGCAGGAGGTG    CCCAGGG
                                ||||||||||    |||||||
                                CCGTTCTTCGC    GGGTTCC
                                     GGA__
GAM390  DKFZP434O125 3'  CTTTGGGACTAGTCTGTATCTT 65586        G TG  AAC__
           GTTT                  AGGCAGGA G  GA    CCCAGGG
                                ||||||||  |  ||    |||||||
                                TTTGTTCT T  CT    GGGTTTC
                                     A GT  GATCA
GAM390  DKFZP434O125 3'  TCTGAAAGTTGTTTTGCTTTTT 65590          TG   ACCC___   G
           GTTT                  AGGCAGGAGG  GAA      CAGG
                                ||||||||||  |||      ||||
                                TTTGTTTTTC  TTT      GTCT
                                     GT   GTTGAAA
GAM390  DKFZP434P0721 3'  CAGGGTTTTTTTGTCTTTTGGC 64460    G      TG   A_____  CCAG
           T                   AG CAGGAGG  GAA     CC    G
                                || |||||||  |||     ||   |
                                TC GTTTTCT  TTT     GG    C
                                 G      GT   TTT    GAC
GAM390  DKFZP434P0721 3'  TTTTGGATTTTTTTGTCTTTTG 64470    G      TG    CC_
           GCT                   AG CAGGAGG  GAAA   CCAGGG
                                || |||||||  ||||   ||||||
                                TC GTTTTCT  TTTT   GGTTTT
                                 G      GT    TTA
GAM390  DKFZp547D155 3'  CTTGGGGGGCTCCTGCCT    70947         GTGGAAA
                                AGGCAGGAG      CCCCAGG
                                |||||||||      |||||||
                                TCCGTCCTC      GGGGTTC
                                     GG_____
GAM390  DKFZP547E1010 3'  TTTGTTTTGCCCTTGTTT    67485        A  TG   ACCC
                                AGGCAGG GG  GAA    CAGG
                                ||||||| ||  |||    ||||
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                                TTTGTTC CC  TTT    GTTT
                                    _ GT  _____
GAM390  DKFZp547H236 3'  CCCTGAGCCCCACTTCTGCCT  79243       G     AAACCC
                                AGGCAG AGGTGG     CAGGG
                                ||||||| ||||||     |||||
                                TCCGTC TTCACC     GTCCC
                                   _     CCGA__
GAM390  DKFZp547M072 3'  CCCGTGTTTTCTGACCTCCTGC 61716          __     CCCA
          CT                    AGGCAGGAGGT  GGAAAC    GGG
                                ||||||||||  ||||||    |||
                                TCCGTCCTCCA  CTTTTG    CCC
                                      GT     TG__
GAM390  DKFZp547O146 3'  TTTGGGGTGTTTTTTTTTT    39969       TG  A
                                AGGAGG  GA ACCCCAGG
                                ||||||  || ||||||||
                                TTTTTT  TT TGGGGTTT
                                   TT  G
GAM390  DKFZP564B1162 3'  CCTGCTTTCGCCTGCTGTCT   49347       G       ACCC
                                AGGCAG AGGTGGAA    CAGG
                                ||||||| ||||||||    ||||
                                TCTGTC TCCGCTTT    GTCC
                                   G       C___
GAM390  DKFZP564D116 3'  CCAGGGTTTATTTCTGCCTTTT 72669     C     TG   A_______  CCAG
          TCTT                  AGG AGGAGG  GAA       CC    G
                                ||| ||||||  |||       ||    |
                                TTC TTTTCC  CTT       GG    C
                                  T     GT   TATTT     GACC
GAM390  DKFZP564D116 3'  CCCCAGGGCCCTACCATTTATT 72670        _______     AAA__  CCAG
          TCTGCCT                 AGGCAGGA     GGTGG    CC    GG
                                ||||||||     |||||    ||   ||
                                TCCGTCTT     CCATC    GG    CC
                                    TATTTA    CC    GACC
GAM390  DKFZP564D172 3'  CCAGGGTCCTTTTAGTTTTCTG 50195        GG G   A_______  CCAG
          CTT                   AGGCAGGA  T GAA      CC    G
                                ||||||||  | |||      ||    |
                                TTCGTCTT  G TTT      GG    C
                                    TT A   TCCT     GACC
GAM390  DKFZP564D172 3'  CTCGAGTTTCTGCCTCGTGCTT 50196      G    TG     CCCA
                                AGGCA GAGG  GAAAC    GGG
                                ||||| ||||  |||||    |||
                                TTCGT CTCC  CTTTG    CTC
                                   G    GT     AG__
GAM390  DKFZP564I0422 3'  CTTGCTTTTTATCTCCT     49514          CCC
                                AGGAGGTGGAAA   CAGG
                                ||||||||||||   ||||
                                TCCTCTATTTTT   GTTC
                                      C__
GAM390  DKFZP564I0422 3'  TCCTAAGGTTTTTTGTTTTCT  49520       TG   _  CC
                                AGGAGG  GAAA CC  AGGG
                                ||||||  |||| ||  ||||
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                                TCTTTT  TTTT GG  TCCT
                                   GT    T  AA
GAM390  DKFZP564O1664 3'  TCCTGAAAGCTTCACCTCTTCC 48669     C        AACCC
           CT                   AGG AGGAGGTGGA     CAGGG
                                ||| ||||||||||     |||||
                                TCC TTCTCCACTT     GTCCT
                                  C         CGAAA
GAM390  DKFZP566D1346 3'  TTCTGATGTGCCATTTTTTGTC 48739            AA  CC
           T                    AGGCAGGAGGTGG  AC  CAGGG
                                ||||||||||||||  ||  |||||
                                TCTGTTTTTTACC  TG  GTCTT
                                       G_  TA
GAM390  DKFZP566J091 3'  CCAGGGTTCTTTTCTTTTCTTG 48861          T    A________  CCAG
           CCT                    AGGCAGGAGG GGAA       CC    G
                                ||||||||||| ||||       ||    |
                                TCCGTTCTTT TCTT       GG    C
                                      _    TTCTT     GACC
GAM390  DKFZP586A0522 3'  TTTTGGGGGGGCGGTTTTTTTGG 26728    G      TGGAAA
           TT                    AG CAGGAGG      CCCCAGGG
                                || |||||||      ||||||||
                                TT GTTTTTT      GGGGTTTT
                                 G      TGGCGG
GAM390  DKFZP586B1621 3'  CCCCAGGGCTTTGTCACTTCCT 32037          T  AAA_________  CCAG
           TCTGCCT                  AGGCAGGAGG GG          CC    GG
                                ||||||||||| ||          ||    ||
                                TCCGTCTTCC TC          GG    CC
                                      T  ACTGTTTC     GACC
GAM390  DKFZP586F1524 3'  TCTTGTTCACTTTACCTTCTGC 32108            AACCC
           C                     GGCAGGAGGTGGA     CAGGG
                                ||||||||||||||     |||||
                                CCGTCTTCCATTT     GTTCT
                                       CACTT
GAM390  DKFZp586G0123 5'  TCCAGGAGTTTCTCCTTTTTGT 97148          TG     C  A
           TT                    AGGCAGGAGG  GAAAC CC GGG
                                ||||||||||  ||||| || |||
                                TTTGTTTTTC  CTTTG GG CCT
                                      CT     A  A
GAM390  DKFZp586H0623 3'  CCTTCATGTTTACCTTTTGCTT 34499             AACCCC   G
                                AGGCAGGAGGTGGA      AGG
                                ||||||||||||||      |||
                                TTCGTTTTCCATTT      TCC
                                       GTACT_
GAM390  DKFZp586H0623 3'  CTTGGGGCTTTTTAGTTT     34500      G     _
                                GAG TGGAAA CCCCAGG
                                ||| |||||| |||||||
                                TTT ATTTTT GGGGTTC
                                  G     C
GAM390  DKFZP727C091 3'  CTTTGGTATTTTTTTTTCTTGT 66794          TG    CC
           TT                    AGGCAGGAGG  GAAA  CCAGGG
                                ||||||||||  ||||  ||||||
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                                TTTGTTCTTT  TTTT  GGTTTC
                                     TT    AT
GAM390  DKFZP761C169 5'  CCCAGGGTTTTGTTTTTGCTTT 68418    G     TG    _______  CAG
           TTGGCT                  AG CAGGAGG  GAAAC      CC   GG
                                || |||||||  |||||      ||   ||
                                TC GTTTTTC  TTTTG      GG   CC
                                 G      GT     TTTT     GAC
GAM390  DKFZp761N0624 3'  GGTTTTTCAACCTCTTGCTT   51160          _    A____
                                AGGCAGGAGG TGGAA     CC
                                |||||||||| |||||     ||
                                TTCGTTCTCC ACTTT     GG
                                      A     TT
GAM390  DKFZp761O0113 5'  CCAGGGCTTATTTTTTCTTCTT 37891          T    A_______  CCAG
           GCTT                    AGGCAGGAGG GGAA       CC    G
                                |||||||||| ||||       ||    |
                                TTCGTTCTTC TTTT       GG    C
                                      T    TATTC     GACC
GAM390  DKFZp761O0113 5'  TCCTGGGGTCAGGCTGTTCTCC 37900         _ TG AA__
           TGCCT                   AGGCAGGAG G  G    ACCCCAGGG
                                |||||||||  |  |    |||||||||
                                TCCGTCCTC T  C    TGGGGTCCT
                                     T GT GGAC
GAM390  DKFZp761O132 5'  CCCTAATTTCTGCCCTCTTGTC 51168         _ TG    CCCC
           T                    AGGCAGGAG G  GAAA    AGGG
                                |||||||||  |  ||||    ||||
                                TCTGTTCTC C  CTTT    TCCC
                                     C GT    AA__
GAM390  DKFZp761O132 5'  GGCCTTCTCCATCTCTTCCT   51171     C        AA_______
                                AGG AGGAGGTGGA       CC
                                ||| ||||||||||       ||
                                TCC TTCTCTACCT       GG
                                  _        CTTCC
GAM390  DKFZp762L0311 3'  TCTGTTTGGTTTCTTGTCT    38675        GG G   ACCC
                                AGGCAGGA  T GAA    CAGG
                                ||||||||  | |||    ||||
                                TCTGTTCT  G TTT    GTCT
                                     TT G   ____
GAM390  DKFZp762P2111 3'  CCGGGTGCTTTCTGTTTCCTGT 87628          TG    C__   A  G
           TT                    AGGCAGGAGG  GAAA   CCC GG
                                |||||||||  ||||   ||| ||
                                TTTGTCCTTT  CTTT   GGG CC
                                     GT    CGT   _
GAM390  DMRTC2    3'  GGTGTTTTCATTTTGTGTCT   62481       G         ____
                                AGGCA GAGGTGGAAAC    CC
                                ||||| ||||||||||    ||
                                TCTGT TTTTACTTTTG    GG
                                   G          T
GAM390  DNAJC6    3'  CAGGGCTCTTTCTCTCTTTTGT 29491          T    A_______  CCAG
           TT                    AGGCAGGAGG GGAA       CC    G
                                |||||||||| ||||       ||    |
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                                TTTGTTTTCT TCTT      GG   C
                                      C   TCTC    GAC
GAM390  DNAJC8   3'  CCCTGCTATCTCCCTTCCTGCT 27346         T   AACCC
            T                  AGGCAGGAGG GGA    CAGGG
                               |||||||||| |||    |||||
                               TTCGTCCTTC CCT    GTCCC
                                     _  CTATC
GAM390  DOK4     3'  TTCTGCACAGGCTCCTTCCTGC 36666         TG AAACCC
            TT                  AGGCAGGAGG  G     CAGGG
                               ||||||||||  |     |||||
                               TTCGTCCTTC  C     GTCTT
                                     CT GGACAC
GAM390  DRIL2    3'  CCCTGACCCTGCCTTCTGCC  22346         TG AAACCC
                               GGCAGGAGG  G     CAGGG
                               |||||||||  |     |||||
                               CCGTCTTCC  C     GTCCC
                                     GT CCA___
GAM390  DRIL2    3'  TTCTGAAGACCGTTTTCTGCC  22357       GG   AAACCC
                               GGCAGGA  TGG     CAGGG
                               |||||||  |||     |||||
                               CCGTCTT  GCC     GTCTT
                                    TT   AGAA__
GAM390  DXS9879E 3'  TCCTGGGAGGGCCTCATGTTT  21181      G    GGAAAC
                               AGGCA GAGGT     CCCAGGG
                               ||||| |||||     |||||||
                               TTTGT CTCCG     GGGTCCT
                                  A    GGA___
GAM390  E1B-AP5  3'  GCCTTTTATTTTCTGTTT    59232           AC____
                               AGGCAGGAGGTGGAA     C
                               ||||||||||||||     |
                               TTTGTCTTTTATTTT     G
                                       CC   G
GAM390  E1B-AP5  3'  GGCCTTTTATTTTCTGTTT   23865           AC____
                               AGGCAGGAGGTGGAA     C
                               ||||||||||||||     |
                               TTTGTCTTTTATTTT     G
                                       CC   G
GAM390  ECE2     3'  TTTGGGGGTGCCCCTGCCT   28733       A   GGAAA
                               AGGCAGG GGT    CCCCAGG
                               ||||||| |||    |||||||
                               TCCGTCC CCG    GGGGTTT
                                  _   TG___
GAM390  EFA6R    3'  GGTTTTCTCTTGTTT      31637         GTG
                               AGGCAGGAG   GAAACC
                               |||||||||   ||||||
                               TTTGTTCTC   TTTTGG
                                     ___
GAM390  EFS2     3'  GGCTCTCTCTTTTCCTGTTT  20775         T_   AA____
                               AGGCAGGAGG  GGA     CC
                               ||||||||||  |||     ||
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                                TTTGTCCTTT  TCT     GG
                                      TC   CTC
GAM390  EHM2     3'  TTCTGCTCTTCACCTCCTGCT  39420          AACCC
                                GGCAGGAGGTGGA     CAGGG
                                ||||||||||||     |||||
                                TCGTCCTCCACTT     GTCTT
                                     CTC__
GAM390  EIF3S9   3'  CCGCTTCCACTTCTTTCTT   14986     C        ACCCCA
                                AGG AGGAGGTGGAA     GG
                                ||| ||||||||||      ||
                                TTC TTCTTCACCTT     CC
                                  T         CG____
GAM390  ELAC1    3'  TCCAGTTTTTTTATTTCTTGTT 92619            CCCCA
             T                   AGGCAGGAGGTGGAAA     GGG
                                ||||||||||||||||     |||
                                TTTGTTCTTTATTTTT     CCT
                                      TTGA_
GAM390  ELKS     3'  CCCCAGGGTCTTACTCTGCCTT 31189        _ TG  AA________  CCAG
             TCTGCTT                AGGCAGGA GG  GA       CC    GG
                                ||||||||  ||  ||       ||    ||
                                TTCGTCTT CC  CT       GG    CC
                                     T  GT  CATTCT    GACC
GAM390  ENPP4    3'  TTTGGGTGTCTCCTTCT     30720       T   AAC
                                AGGAGG GGA   CCCAGG
                                ||||||  |||   ||||||
                                TCTTCC TCT   GGGTTT
                                   _   GT_
GAM390  EPB41L1  3'  TCTTGCTGTCATTTTCTGTCT  71116          AAACCC
                                AGGCAGGAGGTGG     CAGGG
                                ||||||||||||      |||||
                                TCTGTCTTTTACT     GTTCT
                                      GTC___
GAM390  EPN2     3'  CCAGGGCTTTCTTTAGCTCCTG 31038         G    AA_______  CCAG
             TTT                   AGGCAGGAG TGGA       CC    G
                                |||||||||  ||||       ||    |
                                TTTGTCCTC ATTT       GG    C
                                     G    CTTTC     GACC
GAM390  EPN2     3'  TCCTGACCAGCCACCTTCTGCC 31044          AAACCC
                                GGCAGGAGGTGG     CAGGG
                                ||||||||||||     |||||
                                CCGTCTTCCACC     GTCCT
                                      GACCA_
GAM390  EPS15R   3'  CCCTGGGATTTTTGTCTCCT   41411       TG    C
                                AGGAGG  GAAA CCCAGGG
                                ||||||  ||||  |||||||
                                TCCTCT  TTTT GGGTCCC
                                   GT    A
GAM390  EPSIN    5'  CCTTGGCCTCCTGCCTCCCTGT 26209        _    _  AACC
             CT                    AGGCAGG AGGT GGA    CCAGGG
                                |||||||  ||||  |||    ||||||
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                                TCTGTCC TCCG CCT    GGTTCC
                                    C    T   CC__
GAM390  EREG     3'  CCAGGGTTATTTCTGTTTCCTA 9304      C     TG   A_______  CCAG
             TTT                   AGG AGGAGG  GAA      CC    G
                                |||  ||||||  |||      ||    |
                                TTT TCCTTT  CTT      GG    C
                                  A     GT   TATT    GACC
GAM390  ESDN     3'  CCTTGAATTTTTATCCTTTGCT 56057       GA      CCC
             T                    AGGCAG  GGTGGAAA   CAGGG
                                ||||||  ||||||||   |||||
                                TTCGTT  CTATTTTT   GTTCC
                                   TC       AA_
GAM390  EZF-2    3'  CCTGCCCTTTTCCTGCCT    37673          T  AAACCC
                                AGGCAGGAGG GG     CAGG
                                ||||||||||  ||     ||||
                                TCCGTCCTTT CC     GTCC
                                     T  C_____
GAM390  FAM3C    3'  CTTTGGAGTACTGTTTCTTCCT 30301     C     TG AA  C
                                AGG AGGAGG  G  AC CCAGGG
                                |||  ||||||  |  ||  ||||||
                                TCC TTCTTT  C  TG GGTTTC
                                  _     GT A_  A
GAM390  FAM8A1   3'  GTCTTGGGGTTGTAAGGTAGTC 33200          GGA_____
             TCCTGCTT                AGGCAGGAGGT       AACCCCAGGG   T
                                ||||||||||       ||||||||||   |
                                TTCGTCCTCTG       TTGGGGTTCT   G
                                     ATGGAATG
GAM390  FARP1    3'  TCCTGGAAGACGTTTCCTTTCT 20468     C    GG  GAAACC
                                AGG AGGA  TG      CCAGGG
                                |||  ||||  ||     ||||||
                                TCT TCCT  GC     GGTCCT
                                  T    TT  AGAA__
GAM390  FBX30    3'  CCTTGGAACTTGCCTCTTGTC  53744          TG AAACC
                                GGCAGGAGG  G    CCAGGG
                                |||||||||  |    ||||||
                                CTGTTCTCC  T    GGTTCC
                                     GT CAA__
GAM390  FBXO4    3'  TTTTGGTAATTTTTATATTTTC 25155           __   CC_
             TGTCT                   AGGCAGGAGGTG  GAAA   CCAGGG
                                ||||||||||||  ||||   ||||||
                                TCTGTCTTTTAT  TTTT   GGTTTT
                                      AT    AAT
GAM390  FGF19    3'  TCCTGAGTCCACGTTCTGTTT  18859        G    AACCC
                                AGGCAGGA GTGGA     CAGGG
                                ||||||||  |||||     |||||
                                TTTGTCTT CACCT     GTCCT
                                     G     GA___
GAM390  FHX      3'  GGCTCTCTTCCTTCCTGTTT   37922          T   AA_______
                                AGGCAGGAGG GGA       CC
                                ||||||||||  |||       ||
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                                TTTGTCCTTC CTT       GG
                                      _  CTCTC
GAM390  FLB6421  3' TTTGGGTGTCTTTTGTTT    39648         GT GAAAC
                                AGGCAGGAG  G    CCCAGG
                                |||||||||  |    ||||||
                                TTTGTTTTC  T    GGGTTT
                                     TG _____
GAM390  FLJ10044 3' TCCTGTTCCCTCATCCCTGCCT 36244        A    AAACCC
                                AGGCAGG GGTGG     CAGGG
                                ||||||| |||||     |||||
                                TCCGTCC CTACT     GTCCT
                                   _    CCCTT_
GAM390  FLJ10058 3' TCTGTCTTCAACCTCCTGTTT  36265          G   ACCC
                                AGGCAGGAGGT GAA    CAGG
                                |||||||||| |||    ||||
                                TTTGTCCTCCA CTT    GTCT
                                      A  CT__
GAM390  FLJ10079 3' CCTTGCCCTTCCACCTCCTCCT 60831     C         ACCC
                                AGG AGGAGGTGGAA    CAGGG
                                ||| ||||||||||    |||||
                                TCC TCCTCCACCTT    GTTCC
                                  _         CCC_
GAM390  FLJ10079 3' CCAGGGTTTTCTTCATCTCTTG 60830           AA_______  CCAG
          CT                  GGCAGGAGGTGGA       CC    G
                              ||||||||||||       ||   |
                              TCGTTCTCTACTT       GG    C
                                    CTTTT    GACC
GAM390  FLJ10103 3' GGTCCATTTCATTTTTGCTT  36299       _____       AA_
                                AGGCAG   GAGGTGGA  CC
                                ||||||   ||||||||  ||
                                TTCGTT   CTTTACCT  GG
                                   TTTA
GAM390  FLJ10241 3' TCTTGTTGGTTGTGCTTCTGCC 36392         GTGGA   C_
          T                   AGGCAGGAG    AACC  CAGGG
                              |||||||||    ||||  |||||
                              TCCGTCTTC    TTGG  GTTCT
                                   GTG__    TT
GAM390  FLJ10276 3' CCTGACCCACCTCCTTCCT   36420     C       AAACCC
                                AGG AGGAGGTGG     CAGG
                                ||| |||||||||     ||||
                                TCC TCCTCCACC     GTCC
                                  T       CA____
GAM390  FLJ10292 3' GGTCCTTTTACCTCCTTCCT  36433     C        AC_____
                                AGG AGGAGGTGGAA      C
                                ||| ||||||||||      |
                                TCC TCCTCCATTTT      G
                                  T        CCT  G
GAM390  FLJ10330 3' CTGCATTTTCATTTCCTCTT  36507     C         CCC
                                AGG AGGAGGTGGAAA   CAG
                                ||| ||||||||||||   |||
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                                TTC TCCTTTACTTTT   GTC
                                  _         AC_
GAM390  FLJ10335 3' TCTTGATATTTCTGTCTTCTCC 36512     C     TG    CCC
                T                  AGG AGGAGG  GAAA   CAGGG
                                   ||| ||||||  ||||   |||||
                                   TCC TCTTCT  CTTT   GTTCT
                                     _     GT    ATA
GAM390  FLJ10350 3' CCCTGGGGAGATCTTCCTCT   97246      T   AA_
                                   GGAGG GGA   CCCCAGGG
                                   ||||| |||   ||||||||
                                   TCTCC TCT   GGGGTCCC
                                      T   AGA
GAM390  FLJ10357 3' CCCTGCCACCACTATCTCTAGT 36551      A       AAACCC
                CT                   AGGC GGAGGTGG     CAGGG
                                   |||| ||||||||      |||||
                                   TCTG TCTCTATC     GTCCC
                                     A       ACCACC
GAM390  FLJ10407 5' CCTGGGGCCTTCCTGCCT    36579          TGGAAA
                                   AGGCAGGAGG     CCCCAGG
                                   ||||||||||     |||||||
                                   TCCGTCCTTC     GGGGTCC
                                         C_____
GAM390  FLJ10458 3' CCTGCCTCTGCTTTCTCCT    36602     C     TG  AACCC
                                   AGG AGGAGG  GA    CAGG
                                   ||| ||||||  ||    ||||
                                   TCC TCTTTC  CT    GTCC
                                     _     GT  CC___
GAM390  FLJ10468 3' CTCTGAGCTGCTGCCTTTTGCC 36632          TG AAACCC
                T                   AGGCAGGAGG  G     CAGGG
                                   ||||||||||  |     |||||
                                   TCCGTTTTCC  C     GTCTC
                                         GT GTCGA_
GAM390  FLJ10477 3' TTTGGGGTTTTTTTTTTT    36642       TG
                                   GGAGG  GAAACCCCAGG
                                   |||||  ||||||||||
                                   TTTTT  TTTTGGGGTTT
                                      TT
GAM390  FLJ10520 3' CCAGGGTTTTCTTTATTTTCTG 36703           AA_______  CCAG
                T                   GCAGGAGGTGGA       CC    G
                                   ||||||||||||       ||    |
                                   TGTCTTTTATTT       GG    C
                                         CTTTT     GACC
GAM390  FLJ10525 3' CCCCAGGGTTTTGTGACCAGTT 36723         G   AAA_________  CCAG
                TCTGTCT                AGGCAGGAG TGG         CC    GG
                                   |||||||||| |||         ||    ||
                                   TCTGTCTTT ACC         GG    CC
                                         G   AGTGTTTT     GACC
GAM390  FLJ10539 3' GGTGTTTATACCTTTTGTTT   36762           G    ____
                                   AGGCAGGAGGTG AAAC    CC
                                   |||||||||||| ||||    ||
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                                TTTGTTTTCCAT TTTG    GG
                                      A    T
GAM390  FLJ10620 3' TCTTGGAGGCTTATCTCTTCCC 36866     C       AAA  _
             T                   AGG AGGAGGTGG   CC CCAGGG
                                 ||| |||||||||   || ||||||
                                 TCC TTCTCTATT   GG GGTTCT
                                   C       C__  A
GAM390  FLJ10687 3' TCCGGATCTTTTTATTTCCT   36951           CC_  A
                                 AGGAGGTGGAAA   CC GGG
                                 ||||||||||||   || |||
                                 TCCTTTATTTTT   GG CCT
                                       CTA  _
GAM390  FLJ10687 3' TCTTGGGGTATATGACTGTCCT 36953         _   GGAA_
             GTTT                   AGGCAGGA GGT     ACCCCAGGG
                                 |||||||| |||     |||||||||
                                 TTTGTCCT TCA     TGGGGTTCT
                                     G   GTATA
GAM390  FLJ10697 3' CTCTGAGAGAGTTCTATTTTTT 36957           ACCC__
             G                   CAGGAGGTGGAA     CAGGG
                                 ||||||||||||     |||||
                                 GTTTTTTATCTT     GTCTC
                                       GAGAGA
GAM390  FLJ10700 3' CAGGGCCTTACCTTTCCTCTTG 36960          T__  AAA_____  CCAG
             TCT                   AGGCAGGAGG   GG       CC    G
                                 ||||||||||   ||       ||   |
                                 TCTGTTCTCC   CC       GG   C
                                      TTT  ATTCC     GAC
GAM390  FLJ10700 3' CTTGAATCTCTTCCTGTTT   36962          T   AACCC
                                 AGGCAGGAGG GGA     CAGG
                                 |||||||||| |||     ||||
                                 TTTGTCCTTC TCT     GTTC
                                      _   AA___
GAM390  FLJ10702 3' CAGGGTTATTTCTGTCTCTTGT 36968         GT    A_______  CCAG
             TT                    AGGCAGGAG  GGAA      CC    G
                                 |||||||||  ||||      ||   |
                                 TTTGTTCTC  TCTT      GG    C
                                      TG    TATT     GAC
GAM390  FLJ10702 3' CCCAGGGTTCTGTCTCTTGTTT 36969          TG  AA__  CCAG
                                 AGGCAGGAGG  GA   CC    GG
                                 |||||||||  ||   ||    ||
                                 TTTGTTCTCT  CT   GG    CC
                                      GT  T    GACC
GAM390  FLJ10709 3' TCTTGGGAGATGCATTTTCCGT 36990      A      GAAAC
             CT                    AGGC GGAGGTG     CCCAGGG
                                 |||| |||||||     |||||||
                                 TCTG CTTTTAC     GGGTTCT
                                   C      GTAGA
GAM390  FLJ10713 3' TCTGTTCTGTTTCCTTCCT    37009     C     TG   ACCC
                                 AGG AGGAGG  GAA    CAGG
                                 ||| ||||||  |||    ||||
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                                TCC TCCTTT  CTT    GTCT
                                  T     GT  ____
GAM390  FLJ10716 3' CCTTAGTGAATTTTGTCTCCTG 37015         TG  ___  CCC   G
                CTT                  AGGCAGGAGG  GAA   AC   AGG
                                |||||||||| |||  ||  |||
                                TTCGTCCTCT  TTT   TG   TCC
                                     GT   AAG  AT_
GAM390  FLJ10718 3' TTTGGGTTGTTTTCTCTCT    37035      T     __
                                GGAGG GGAAAC  CCCAGG
                                ||||| ||||||  ||||||
                                TCTCT CTTTTG  GGGTTT
                                   _     TT
GAM390  FLJ10724 3' CCTAGTGCTGCCTCCTGTTT   37039         TG AA  CCC
                                AGGCAGGAGG  G  AC   AGG
                                |||||||||| |  ||   |||
                                TTTGTCCTCC  C  TG   TCC
                                     GT G_  A__
GAM390  FLJ10743 3' CTCTGTCTCTACCTCTCTGCCT 37081       _       AACCC
                                AGGCAG GAGGTGGA     CAGGG
                                |||||| ||||||||     |||||
                                TCCGTC CTCCATCT     GTCTC
                                   T       CT___
GAM390  FLJ10743 3' TCCTGCCCCTGCTTTCTGCC   37089         TG AAACCC
                                GGCAGGAGG  G     CAGGG
                                |||||||||  |     |||||
                                CCGTCTTTC  C     GTCCT
                                     GT CCC___
GAM390  FLJ10751 3' TTCTGGAAGTTGTTTTCTCCT  37117       TGGA   C_
                                AGGAGG    AAC  CCAGGG
                                ||||||    |||  ||||||
                                TCCTCT    TTG  GGTCTT
                                   TTTG   AA
GAM390  FLJ10751 3' TTCTGGAAGTTGTTTTCTCCT  37278       TGGA   C_
                                AGGAGG    AAC  CCAGGG
                                ||||||    |||  ||||||
                                TCCTCT    TTG  GGTCTT
                                   TTTG   AA
GAM390  FLJ10761 3' CCTGGGGCCTTCCTGGCT    37127    G      TGGAAA
                                AG CAGGAGG      CCCCAGG
                                || |||||||      |||||||
                                TC GTCCTTC      GGGGTCC
                                 G      C_____
GAM390  FLJ10774 3' TCCTATAAGTTCATATTTTGCT 45418         G    AACCCC
                T                AGGCAGGA GTGGA      AGGG
                                |||||||| |||||      ||||
                                TTCGTTTT TACTT      TCCT
                                     A    GAATA_
GAM390  FLJ10829 3' CCCTTTCCATCTTCAGTTT    37258      A        ACCCC
                                AGGC GGAGGTGGAA     AGGG
                                |||| ||||||||||     ||||
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                                TTTG CTTCTACCTT    TCCC
                                  A       _____   A
GAM390  FLJ10830 3' CTTGATGCTTTCTGCCTTCTGT 37264        TG   CCC_   G
                CT                 AGGCAGGAGG  GAAA   CAGG
                                   ||||||||||  ||||   ||||
                                   TCTGTCTTCC  CTTT   GTTC
                                        GT   CGTA
GAM390  FLJ10842 3' CCCCAGGGTTTTTTTTTAGCTC 37270        G    _________ CCA
                TTGCTT               AGGCAGGAG TGGAAA      CC  GG
                                   |||||||||  ||||||      ||  ||
                                   TTCGTTCTC ATTTTT      GG  CC
                                        G     TTTT  G  ACC
GAM390  FLJ10853 3' GGTCTTATCCACCTTTGTCT  37317      G     AA_______
                                   AGGCAG AGGTGGA       CC
                                   ||||||  |||||||      ||
                                   TCTGTT TCCACCT       GG
                                      _      ATTCT
GAM390  FLJ10856 3' CTTTGTTGTTTGCTTCTTCCCT 37323    C     TG  AACCC
                                   AGG AGGAGG  GA    CAGGG
                                   |||  ||||||  ||    |||||
                                   TCC TTCTTC  TT    GTTTC
                                     C     GT  GTT__
GAM390  FLJ10898 3' CAGGGTCTTGTTTCCTTTTTTG 60127        T    ________ CAG
                TTT                  AGGCAGGAGG GGAAAC     CC  G
                                   ||||||||||  ||||||      ||  |
                                   TTTGTTTTTT CCTTTG      GG  C
                                        _     TTCT    GAC
GAM390  FLJ10898 3' CCAGGGTTCTGCTTTACCTTTT 60129    C       AA________ CCAG
                TCCT                   AGG AGGAGGTGGA       CC   G
                                   |||  ||||||||||       ||   |
                                   TCC TTTTCCATTT       GG   C
                                     T       CGTCTT    GACC
GAM390  FLJ10970 5' CTCAGGCGTTGCTGTTTCTTGT 37477        TG A  C  A
                CT                   AGGCAGGAGG  G AAC CC GGG
                                   ||||||||||  | ||| || |||
                                   TCTGTTCTTT  C TTG GG CTC
                                        GT G   C  A
GAM390  FLJ11099 3' CTCTGCCACATCACTTCCTTCT 37605    C       AAACCC
                T                   AGG AGGAGGTGG     CAGGG
                                   |||  |||||||||     |||||
                                   TTC TCCTTCACT     GTCTC
                                     T       ACACC_
GAM390  FLJ11101 3' CCAGGGTTTTGTTTTGCTTCCT 37612        TG  AC_______ CCAG
                GCTT                   AGGCAGGAGG  GAA       C   G
                                   ||||||||||  |||       |   |
                                   TTCGTCCTTC  TTT       G   C
                                        GT   GTTTT   G GACC
GAM390  FLJ11155 3' CCTGTTTTCTTCTTGTTT    37693         TG  AACCC
                                   AGGCAGGAGG  GA    CAGG
                                   ||||||||||  ||    ||||
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                              TTTGTTCTTC  TT    GTCC
                                    TT _____
GAM390  FLJ11193  3' CTGTTTTTTGCTTTTCTGTTT  37748      _   TG   CCC
                              AGGCAG GAGG  GAAA   CAG
                              ||||||| ||||  ||||   |||
                              TTTGTC TTTC  TTTT   GTC
                                 T   GT   T__
GAM390  FLJ11210  3' CCCCAGGGTTAATATTTCATCT 60318           A_________  CCAG
           TTTGCTT                AGGCAGGAGGTGGAA       CC   GG
                              ||||||||||||||||       ||   ||
                              TTCGTTTTCTACTTT       GG   CC
                                       ATAATT    GACC
GAM390  FLJ11275  3' TCTTGGGACATTTATTTGTTT  37783       _    GAAAC
                              AGGCAGG AGGTG    CCCAGGG
                              ||||||| |||||    |||||||
                              TTTGTTT TTTAC    GGGTTCT
                                  A    A____
GAM390  FLJ11286  3' CTTGATTCTTTTTTTGCCT   37794         T   ACCC
                              AGGCAGGAGG GGAA   CAGG
                              |||||||||| ||||   ||||
                              TCCGTTTTTT TCTT   GTTC
                                    _   A___
GAM390  FLJ11539  3' CCAGGGCTCTCTTCTACCTCCG 45706     A       AC_______ CCAG
           TCT                   AGGC GGAGGTGGAA       C   G
                              |||| ||||||||||       |   |
                              TCTG CCTCCATCTT       G   C
                                _       CTCTC   G GACC
GAM390  FLJ11565  3' CAGGGTCTTCTCTTATCTTCTG 45410          _ AA_______  CCAG
           TCT                   AGGCAGGAGGTG GA      CC   G
                              |||||||||||| ||       ||   |
                              TCTGTCTTCTAT CT       GG   C
                                    T  CTTCT    GAC
GAM390  FLJ11608  3' GGCTCTTTCTCTTCCTGCCT   44961         T   AC_____
                              AGGCAGGAGG GGAA      C
                              |||||||||| ||||      |
                              TCCGTCCTTC CTTT      G
                                    T   CTC   G
GAM390  FLJ11850  3' TCCTGGCCTTTGCTTCCTGGTT 43024    G      TG  AACC
                              AG CAGGAGG  GA   CCAGGG
                              || |||||||  ||   ||||||
                              TT GTCCTTC  TT   GGTCCT
                               G      GT  CC__
GAM390  FLJ11996  5' CCCCAGGGTTTTGTCTCCATTT 47058     C       AA_________  CCAG
           TTTCCCT                AGG AGGAGGTGGA       CC   GG
                              ||| ||||||||||       ||   ||
                              TCC TTTTTTACCT       GG   CC
                                C        CTGTTTT    GACC
GAM390  FLJ12076  3' CCAGGGTTCTGTCCATCTTTGG 48022      AG      AA_______  CCAG
           CCT                   AGGC  GAGGTGGA       CC   G
                              ||||  ||||||||       ||   |
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                                TCCG  TTCTACCT      GG   C
                                  GT       GTCTT    GACC
GAM390  FLJ12132  3' TTTGGTCGTTTCTAGCCT    47105     A  GG   AAACC
                                AGGC GGA  TGG    CCAGG
                                |||| |||  |||    |||||
                                TCCG TCT  GCT    GGTTT
                                  A  TT  _____
GAM390  FLJ12171  3' TCTGGGCAAATTCTTGTTT   45200        GTGGAAAC
                                AGGCAGGAG      CCCAGG
                                |||||||||      ||||||
                                TTTGTTCTT      GGGTCT
                                     AAAC____
GAM390  FLJ12221  3' CCCTTTCGCCTCCTGTCT    63219          AACCCC
                                AGGCAGGAGGTGGA     AGGG
                                ||||||||||||||     ||||
                                TCTGTCCTCCGCTT     TCCC
                                       ______   A
GAM390  FLJ12455  3' CTCTGGGCTTGCCCTTTGCCT  42224       GA  TG AAAC
                                AGGCAG  GG  G   CCCAGGG
                                ||||||  ||  |   |||||||
                                TCCGTT  CC  T   GGGTCTC
                                   TC  GT C___
GAM390  FLJ12484  3' CCTTGGAGCCCCATCTTTGCTT 70227       G     AAACC
                                AGGCAG AGGTGG    CCAGGG
                                |||||| ||||||    ||||||
                                TTCGTT TCTACC    GGTTCC
                                   _     CCGA_
GAM390  FLJ12505  3' TCTTGGAGTTACTTCCTTCTT  45719     C       GAA  C
                                AGG AGGAGGTG   AC CCAGGG
                                ||| ||||||||   || ||||||
                                TTC TCCTTCAT   TG GGTTCT
                                  T       ___  A
GAM390  FLJ12517  3' CCAGGGCTTTGCCACCTCCCTG 43717        _     _  A____  CCAG
           CCT                    AGGCAGG AGGTGG AA    CC    G
                                |||||||  |||||| ||    ||   |
                                TCCGTCC TCCACC TT    GG    C
                                   C     G  TC    GACC
GAM390  FLJ12529  3' GGTCTTTTCACCTTTTGACT   46088    G         A_____
                                AG CAGGAGGTGGAA     CC
                                || ||||||||||||     ||
                                TC GTTTTCCACTTT     GG
                                 A          TCT
GAM390  FLJ12568  3' CCAGGGTTTTTTTTTGTTTCCT 47140     C     TG   A_______  CCAG
           TCTT                   AGG AGGAGG  GAA       CC    G
                                ||| ||||||  |||       ||   |
                                TTC TCCTTT  TTT       GG    C
                                  T     GT   TTTTT    GACC
GAM390  FLJ12644  3' CAGGGTTTTCTTCTTTTTCTGC 43816         T__    A____  CCAG
           TT                     AGGCAGGAGG   GGAA    CC    G
                                ||||||||||   ||||    ||   |
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                                TTCGTCTTTT  TCTT   GG   C
                                     TCT   TT   GAC
GAM390  FLJ12650  3' CCACGGGTTTTTTGTTTTTTGT 44819        TG   C  AG
           TT                  AGGCAGGAGG  GAAA CCC  GG
                               ||||||||||  |||| |||  ||
                               TTTGTTTTTT  TTTT GGG  CC
                                     GT   T  CA
GAM390  FLJ12700  3' CCCAGGGTTCTTTCCATCTCTT 46654           _______  CCA
           GTCT                  AGGCAGGAGGTGGAAA     CC  GG
                               ||||||||||||||||     ||  ||
                               TCTGTTCTCTACCTTT     GG  CC
                                     CTT  G  ACC
GAM390  FLJ12747  3' TTCTGGGGGGTTTTTTTGTTT  50674       GTG  AA
                               AGGCAGGAG   GA  CCCCAGGG
                               |||||||||   ||  ||||||||
                               TTTGTTTTT   TT  GGGGTCTT
                                     ___  GG
GAM390  FLJ12787  3' CCTTGCTTAGCTTGCTTCCTGT 50693        TG AAACCC
           CT                   AGGCAGGAGG  G    CAGGG
                               ||||||||||  |     |||||
                               TCTGTCCTTC  T     GTTCC
                                     GT CGATTC
GAM390  FLJ12892  3' TAGAGGGTTTTTTTTTTCTGTT 68456        TG     CAGGG
           T                    AGGCAGGAGG  GAAACCC
                               ||||||||||  |||||||
                               TTTGTCTTTT  TTTTGGG
                                     TT      AGATC
GAM390  FLJ12895  3' CCTTGCCCCGATTCCTCCTGTT 43926        TGGAAACCC
           T                    AGGCAGGAGG       CAGGG
                               ||||||||||       |||||
                               TTTGTCCTCC       GTTCC
                                     TTAGCCCC_
GAM390  FLJ12934  3' CTCATGCCATTTTCTCTCTTGT 43489        T    CCC  _
           CT                   AGGCAGGAGG GGAAA   CA GGG
                               |||||||||| |||||   || |||
                               TCTGTTCTCT CTTTT   GT CTC
                                     _    ACC  A
GAM390  FLJ12934  3' TTTTGGTGGTTTTTGTTTTTT  43492      TG    _
                               AGGAGG  GAAACC CCAGGG
                               ||||||  |||||| ||||||
                               TTTTTT  TTTTGG GGTTTT
                                  GT     T
GAM390  FLJ12934  3' TTTTGTTTTTTTTTCATTTTCT 43493           CCC__
           GTT                    GGCAGGAGGTGGAAA    CAGGG
                               ||||||||||||||||    |||||
                               TTGTCTTTTACTTTT    GTTTT
                                     TTTTT
GAM390  FLJ12960  3' TCCTGGGTTCATGCCATTCTCC 45306        _  AAAC__
           TGCCT                  AGGCAGGAGG TGG     CCCAGGG
                               |||||||||| |||     |||||||
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                                TCCGTCCTCT ACC     GGGTCCT
                                     T   GTACTT
GAM390  FLJ12998  3' CTTGAGTCGGTTTCTGTTT   43149         G   AAACCC
                                AGGCAGGAG TGG     CAGG
                                ||||||||| |||     ||||
                                TTTGTCTTT GCT     GTTC
                                     G   GA____
GAM390  FLJ13031  5' CCAGGGTTCATTTTACCTCCTG 45512           A_______  CCAG
           TT                    GGCAGGAGGTGGAA      CC    G
                                ||||||||||||||      ||    |
                                TTGTCCTCCATTTT      GG    C
                                       ACTT    GACC
GAM390  FLJ13055  3' CCTTGGGGTACCCCTTTTCCT  43016     C     T  AA
                                AGG AGGAGG GG  ACCCCAGGG
                                ||| |||||| ||  |||||||||
                                TCC TTTTCC CC  TGGGGTTCC
                                 _     _ A_
GAM390  FLJ13072  5' TCCTGTGCACTCTGTGTCTTGT 91400        G TG  AACCC
           TT                    AGGCAGGA G  GA     CAGGG
                                ||||||||  |  ||     |||||
                                TTTGTTCT T  CT     GTCCT
                                    G GT  CACGT
GAM390  FLJ13111  3' TCCTGGTGCTGCCTCTGGCTT  47628      A     TG AAACC
                                AGGC GGAGG  G     CCAGGG
                                |||| |||||  |     ||||||
                                TTCG TCTCC  C     GGTCCT
                                  G     GT GT___
GAM390  FLJ13114  3' CCCCAGGGTTCTAATCTGCTTT 44898       _   TG  AA________  CCAG
           ACTGTCT                 AGGCAG GAGG  GA       CC    GG
                                |||||| ||||  ||       ||    ||
                                TCTGTC TTTC  CT       GG    CC
                                   A    GT  AATCTT    GACC
GAM390  FLJ13114  3' CTCTGGCAGCCTCTCCTGCCT  44900         T  AAACC
                                AGGCAGGAGG GG     CCAGGG
                                |||||||||| ||     ||||||
                                TCCGTCCTCT CC     GGTCTC
                                     _  GAC__
GAM390  FLJ13117  5' CCCCAGGGCCAATATTCTACTT 43808           A_________  CCAG
           TCTGTCT                 AGGCAGGAGGTGGAA       CC    GG
                                |||||||||||||||       ||    ||
                                TCTGTCTTTCATCTT       GG    CC
                                       ATAACC    GACC
GAM390  FLJ13154  3' CAGGGTCCTCTCTCTCTCTTGC 45103        GT   AA______  CCAG
           TT                    AGGCAGGAG  GGA      CC    G
                                |||||||||  |||      ||    |
                                TTCGTTCTC  TCT      GG    C
                                     TC   CTCCT    GAC
GAM390  FLJ13154  3' CCAGGGCTCTCTTCCCCTCCTG 45105         T   AC________ CCAG
           TCT                     AGGCAGGAGG GGAA       C    G
                                |||||||||| ||||       |    |
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                                TCTGTCCTCC CCTT       G    C
                                      _    CTCTC   G GACC
GAM390  FLJ13154  3'  CCAGGGCTCTCTTCCCTTCCTG 45106         T    AC________ CCAG
              TCT                  AGGCAGGAGG GGAA       C    G
                                   |||||||||| ||||       |    |
                                   TCTGTCCTTC CCTT       G    C
                                         _    CTCTC   G GACC
GAM390  FLJ13154  3'  CCAGGGTCTTCTCTCTCTCCTG 45107         GT   AA_______  CCAG
              TCT                  AGGCAGGAG  GGA       CC    G
                                   |||||||||  |||       ||    |
                                   TCTGTCCTC  TCT       GG    C
                                        TC   CTTCT    GACC
GAM390  FLJ13154  3'  CCTCCTCTATCTCTTCCT    45108     C        AACCCC
                                   AGG AGGAGGTGGA     AGG
                                   ||| ||||||||||     |||
                                   TCC TTCTCTATCT     TCC
                                     _        CC_____
GAM390  FLJ13154  3'  GGTTTTCTCCACTTCTTTCT   45111     C        AA_______
                                   AGG AGGAGGTGGA       CC
                                   ||| ||||||||||       ||
                                   TCT TTCTTCACCT       GG
                                     _        CTTTT
GAM390  FLJ13187  3'  CCAGGGTTTTGTTCATTTGCTT 45162         _      AA_______  CCAG
              GCTT                   AGGCAGG AGGTGGA       CC    G
                                     ||||||| |||||||       ||    |
                                     TTCGTTC TTTACTT       GG    C
                                        G      GTTTT     GACC
GAM390  FLJ13204  3'  CCAGGGTTCTGTACTACATCCT 45757         G    AAA________  CCAG
              GCCT                   AGGCAGGA GTGG         CC    G
                                     |||||||| ||||         ||    |
                                     TCCGTCCT CATC         GG    C
                                        A    ATGTCTT     GACC
GAM390  FLJ13204  3'  TTCGTATTTTTCCACTTATCTG 45761         _       CCCCA
              TCT                    AGGCAGG AGGTGGAAA     GGG
                                     ||||||| |||||||||     |||
                                     TCTGTCT TTCACCTTT     CTT
                                        A        TTATG
GAM390  FLJ13263  3'  CCCTGGAGGACTGCCTGCTTGC 47811         _  TG AAA  _
              TT                     AGGCAGG AGG  G   CC CCAGGG
                                     ||||||| |||  |   || ||||||
                                     TTCGTTC TCC  C   GG GGTCCC
                                        G   GT A__  A
GAM390  FLJ13310  3'  CCCCAGGGTTCTCCTTTGCCTT 47808         TG  AA________  CCAG
              TTGCC                   GGCAGGAGG  GA       CC    GG
                                      |||||||||  ||       ||    ||
                                      CCGTTTTCC  TT       GG    CC
                                           GT  CCTCTT    GACC
GAM390  FLJ13385  3'  CCTTGAAATTTACCTTTTGTT  46281           AACCC
                                      GGCAGGAGGTGGA     CAGGG
                                      ||||||||||||     |||||
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                                TTGTTTTCCATTT    GTTCC
                                      AAA__
GAM390  FLJ13397  5' GCCTTCTTCTTTCCTGCCT   46904        T_   AC____
                                AGGCAGGAGG  GGAA     C
                                ||||||||||  ||||     |
                                TCCGTCCTTT  TCTT     G
                                     CT    CC   G
GAM390  FLJ13409  3' TCTGGGGTTTCCCTCTCT    45195      T
                                GGAGG GGAAACCCCAGG
                                ||||| ||||||||||||
                                TCTCT CCTTTGGGGTCT
                                   C
GAM390  FLJ13441  5' TCCGTCGTCCATTTCTTGTCT  43917           AACCCCA
                                AGGCAGGAGGTGGA      GGG
                                ||||||||||||||      |||
                                TCTGTTCTTTACCT      CCT
                                      GCTG___
GAM390  FLJ13479  3' CCTGTACCTCCTTTTGCCT   45555         T  AAACCC
                                AGGCAGGAGG GG     CAGG
                                |||||||||| ||     ||||
                                TCCGTTTTCC CC     GTCC
                                     T  AT____
GAM390  FLJ13490  3' CTCTGGGGTTGTTAATATTATT 46871       AG   GA___
           TGTTT                AGGCAGG  GTG    AACCCCAGGG
                                |||||||  |||    ||||||||||
                                TTTGTTT  TAT    TTGGGGTCTC
                                    AT   AATTG
GAM390  FLJ13612  3' CCAGGGCCCACCTCTGTCTCCT 48087         TG  AA________  CCAG
           GCCT                 AGGCAGGAGG  GA       CC   G
                                ||||||||||  ||       ||   |
                                TCCGTCCTCT  CT       GG   C
                                     GT  CCACCC    GACC
GAM390  FLJ13693  3' CCTTGGCCTCATTTTTCCTGTC 46073         TG_  AACC
           T                    AGGCAGGAGG   GA   CCAGGG
                                ||||||||||   ||   ||||||
                                TCTGTCCTTT   CT   GGTTCC
                                     TTA  CC__
GAM390  FLJ13769  3' GGCTTTATTCATCTTTGTCT   47259       G      AA_______
                                AGGCAG AGGTGGA       CC
                                |||||| |||||||       ||
                                TCTGTT TCTACTT       GG
                                   _      ATTTC
GAM390  FLJ13840  5' TTCTGGCATTCTCTGCCTCTGC 45702       G   TG  _  CC
           CT                    AGGCAG AGG  GA AA  CCAGGG
                                 |||||| |||  || ||  ||||||
                                 TCCGTC TCC  CT TT  GGTCTT
                                    _  GT  C  AC
GAM390  FLJ13852  3' CTCTGGCCATCCTTTCCTGCCT 43839          T   AACC
                                AGGCAGGAGG GGA    CCAGGG
                                |||||||||| |||    ||||||
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                                TCCGTCCTTT CCT    GGTCTC
                                      _   ACC_
GAM390  FLJ13855 3' CCAGGGCTTTCTCTTCCTTCTG 43847          T   AA_______  CCAG
              CCT                  AGGCAGGAGG GGA       CC    G
                                   |||||||||| |||       ||    |
                                   TCCGTCTTCC TCT       GG    C
                                        T   CTTTC     GACC
GAM390  FLJ13910 3' TTGGTTGGGTTTTTGTTTGTTT 43254        _  TG      CAGGG
              GTTT                 AGGCAGG AGG  GAAACCC
                                   ||||||| |||  |||||||
                                   TTTGTTT TTT  TTTTGGG
                                      G   GT      TTGGTTT
GAM390  FLJ14007 3' CCTTTTTTTGTTTTCTGTT    45534          TG    CCCC
                                   GGCAGGAGG  GAAA    AGG
                                   |||||||||  ||||    |||
                                   TTGTCTTTT  TTTT    TCC
                                        GT    T___
GAM390  FLJ14075 3' GGTTTTTTTTTTTCCTGTTT   46583          T    A_____
                                   AGGCAGGAGG GGAA     CC
                                   |||||||||| ||||      ||
                                   TTTGTCCTTT TTTT     GG
                                        T    TTT
GAM390  FLJ14146 3' CTCTGGAGGGCTCTTCTGCCT  45570          TGGAAA  _
                                   AGGCAGGAGG     CC CCAGGG
                                   ||||||||||     || ||||||
                                   TCCGTCTTCT     GG GGTCTC
                                        CG____  A
GAM390  FLJ14213 3' CCCTGGGCCTTTCCATCTCCTG 46215             C_
              TTT                    AGGCAGGAGGTGGAAA  CCCAGGG
                                   ||||||||||||||||  |||||||
                                   TTTGTCCTCTACCTTT  GGGTCCC
                                             CC
GAM390  FLJ14326 3' CAGGGTTCATTCCACTTTCTGC 50761            A_______  CCAG
              T                     GGCAGGAGGTGGAA      CC    G
                                    ||||||||||||||      ||    |
                                    TCGTCTTTCACCTT      GG    C
                                          ACTT    GAC
GAM390  FLJ14326 3' CTTTGGGCCTTATTTTCTGGCT 50770    G        AAAC
                                   AG CAGGAGGTGG    CCCAGGG
                                   || ||||||||||    |||||||
                                   TC GTCTTTTATT    GGGTTTC
                                    G         CC__
GAM390  FLJ14327 3' CCTTGGGCCCATTTCCCTCCTG 46677          T    AC__
              TCT                    AGGCAGGAGG GGAA    CCCAGGG
                                   |||||||||| ||||    |||||||
                                   TCTGTCCTCC CTTT    GGGTTCC
                                        _    ACCC
GAM390  FLJ14346 3' CTTTGGTTGCACCTCCTGC    47365          G  ACC
                                   GCAGGAGGTG AA   CCAGGG
                                   |||||||||| ||   ||||||
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                                CGTCCTCCAC TT   GGTTTC
                                      G  ___
GAM390  FLJ14397  3'  CCTACCTTCCACTCCTGCCT   52321        G    ACCCC
                                AGGCAGGAG TGGAA    AGG
                                ||||||||| |||||    |||
                                TCCGTCCTC ACCTT    TCC
                                     _    CCA__
GAM390  FLJ14397  3'  CCTGCCGTTTTTTTCCTGCCT  52322        TG    CC
                                AGGCAGGAGG  GAAAC  CAGG
                                ||||||||||  |||||  ||||
                                TCCGTCCTTT  TTTTG  GTCC
                                     __    CC
GAM390  FLJ14457  3'  CCTTGTCTGGTGATTTTCTGCC 52404         GGAA   C__
           T                     AGGCAGGAGGT    ACC   CAGGG
                                ||||||||||    |||   |||||
                                TCCGTCTTTTA    TGG   GTTCC
                                      G___   TCT
GAM390  FLJ14525  3'  CCTGCCTCCACCTTCTGCCT   52481          AACCC
                                AGGCAGGAGGTGGA    CAGG
                                ||||||||||||||    ||||
                                TCCGTCTTCCACCT    GTCC
                                       CC___
GAM390  FLJ14525  3'  GCCTTGGGGTATAGTTTTATCT 52483        _     _____
           TTCTGCTT                AGGCAGGA GGTGGAA   ACCCCAGGG   C
                                |||||||| |||||||   |||||||||  |
                                TTCGTCTT CTATTTT   TGGGGTTCC   G
                                     T      GATA
GAM390  FLJ14642  3'  TTTTGGGAAAGACCCTTCTGTC 52584         TGGAAAC
           T                     AGGCAGGAGG      CCCAGGG
                                ||||||||||      |||||||
                                TCTGTCTTCC      GGGTTTT
                                      CAGAAA_
GAM390  FLJ14675  3'  CCCTGGAGGCTGCCTCCTGCC  52589         TG AAA  _
                                GGCAGGAGG  G   CC CCAGGG
                                |||||||||  |   || ||||||
                                CCGTCCTCC  C   GG GGTCCC
                                      GT ___  A
GAM390  FLJ14681  5'  TCCTGGCTCCTATCTCTGCCT  52598       G   _   AACC
                                AGGCAG AGGT GGA    CCAGGG
                                |||||| |||| |||    ||||||
                                TCCGTC TCTA CCT    GGTCCT
                                     _    T   C___
GAM390  FLJ14735  3'  CCTTGGGGCAGGGACATGTTTT 52666         G   GAAA__
           GTTT                   AGGCAGGA GTG     CCCCAGGG
                                |||||||| |||     |||||||||
                                TTTGTTTT TAC     GGGGTTCC
                                     G   AGGGAC
GAM390  FLJ14753  3'  CAGGGCTTTTTTTTTTTCCTGT 51763          T    A_______  CCAG
           TT                     AGGCAGGAGG GGAA      CC    G
                                |||||||||| ||||      ||    |
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                                TTTGTCCTTT TTTT      GG    C
                                      T    TTTC     GAC
GAM390  FLJ14753  3'  TTCTGCTCATCCTCCTCCTGTT 51767          T   AACCC
              T                  AGGCAGGAGG GGA     CAGGG
                                 |||||||||| |||     |||||
                                 TTTGTCCTCC CCT     GTCTT
                                       T   ACTC_
GAM390  FLJ14775  3'  TTTTGGGGAAACAAATTTTCTG 52683          GGAAA_
              TT                  GGCAGGAGGT     CCCCAGGG
                                 ||||||||||     ||||||||
                                 TTGTCTTTTA     GGGGTTTT
                                       AACAAA
GAM390  FLJ14816  3'  CCCTGGGTGAGTTACTTGCCT  52709       GGA     AAAC
                                 AGGCA   GGTGG    CCCAGGG
                                 |||||   |||||    |||||||
                                 TCCGT   TCATT    GGGTCCC
                                   ___     GAGT
GAM390  FLJ14824  3'  GGTTTTTCTACTTTCTTTTT   52717     C         A_____
                                 AGG AGGAGGTGGAA     CC
                                 ||| ||||||||||      ||
                                 TTT TCTTTCATCTT     GG
                                   T         TTT
GAM390  FLJ14840  5'  CTCTGTACCCCGCTTCCTCTT  52723     C        AAACCC
                                 AGG AGGAGGTGG     CAGGG
                                 ||| |||||||||     |||||
                                 TTC TCCTTCGCC     GTCTC
                                   _       CCAT__
GAM390  FLJ14840  5'  CTTTGTCCGCTGCCTTCTCCT  52724     C     TG AAACCC
                                 AGG AGGAGG  G     CAGGG
                                 ||| ||||||  |     |||||
                                 TCC TCTTCC  C     GTTTC
                                   _     GT GCCT__
GAM390  FLJ14917  3'  CCAGGGCTCAGTTCTACCTTTT 52764    GC         AC________ CCAG
              ATCT                  AG  AGGAGGTGGAA       C    G
                                 ||  ||||||||||        |   |
                                 TC  TTTTCCATCTT       G    C
                                  TA         GACTC   G GACC
GAM390  FLJ14950  3'  CCAGGGTTCTGCCTCAGCTCCT 52785         G   AAA________  CCAG
              GTCT                  AGGCAGGAG TGG         CC    G
                                 |||||||| |||         ||   |
                                 TCTGTCCTC ACT        GG    C
                                       G   CCGTCTT    GACC
GAM390  FLJ14957  3'  CCCAGGGCTTTTCTTCTGTTTT 52812          TG   AC_________ CCAG
              TTGCTT                  AGGCAGGAGG  GAA        C    G
                                 ||||||||||  |||         |   |
                                 TTCGTTTTTT  CTT        G    C
                                       GT   CTTTTC   G GACC
GAM390  FLJ14957  3'  CCCAGGGTTTTCTTCTGTTTTT 52813          TG   AC________ CCAG
              TGCTT                  AGGCAGGAGG  GAA       C    G
                                 ||||||||||  |||         |   |
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                                TTCGTTTTTT CTT       G   C
                                     GT  CTTTT  G GACC
GAM390  FLJ20010 3' GTCCTTCCATCTTTTCCT   39230    C       AC_____
                                AGG AGGAGGTGGAA     C
                                ||| ||||||||||      |
                                TCC TTTTCTACCTT     G
                                  _        CCT  G
GAM390  FLJ20034 3' CCCTGGAGGTGTTTCCTGTCT 34842        GG GGAA  _
                                AGGCAGGA  T   ACC CCAGGG
                                |||||||| |   ||| ||||||
                                TCTGTCCT  G   TGG GGTCCC
                                    TT ____  A
GAM390  FLJ20045 3' TTTTGGAAAGGACAATTTCTTG 34898         GGAAA ___
           TTT                    AGGCAGGAGGT   CC  CCAGGG
                                ||||||||||    ||  ||||||
                                TTTGTTCTTTA   GG  GGTTTT
                                      ACA__  AAA
GAM390  FLJ20081 3' CCAGGGTTTTATTCCATTTTCT 34988    C       A________  CCAG
           CTCT                    AGG AGGAGGTGGAA      CC   G
                                ||| ||||||||||      ||   |
                                TCT TCTTTTACCTT      GG   C
                                  C        ATTTT    GACC
GAM390  FLJ20093 3' TTTGGGGTTTTCTGCTTT   35042     TG  _
                                GAGG  GAAA CCCCAGG
                                ||||  |||| |||||||
                                TTTC  CTTT GGGGTTT
                                  GT   T
GAM390  FLJ20113 3' CCCCAGGGTTTTGCCTTCACCT 35055    C       AA_________  CCAG
           CTTTTCT                   AGG AGGAGGTGGA       CC   GG
                                ||| ||||||||||       ||   ||
                                TCT TTCTCCACTT       GG   CC
                                  T       CCGTTTT    GACC
GAM390  FLJ20113 3' TCTTGGAGGCCCCTCCTGCTT 35058         T  AAA  _
                                AGGCAGGAGG GG   CC CCAGGG
                                |||||||||| ||   || ||||||
                                TTCGTCCTCC CC   GG GGTTCT
                                      _ ___  A
GAM390  FLJ20136 3' TTCTAGTTTTTTCACCTTTTAG 35105     _        CCCC
           TTT                    AGGC AGGAGGTGGAAA   AGGG
                                |||| ||||||||||||   ||||
                                TTTG TTTTCCACTTTT   TCTT
                                  A          TTGA
GAM390  FLJ20136 3' TTTTGGGGTTTTTTTTTTTT  35108       TG
                                AGGAGG  GAAACCCCAGGG
                                ||||||  ||||||||||||
                                TTTTTT  TTTTGGGGTTTT
                                   TT
GAM390  FLJ20147 3' GTTTACTACCTTTTGCTT   35137          _
                                AGGCAGGAGGTGG AAAC
                                |||||||||||| ||||
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                                TTCGTTTTCCATC TTTG
                                      A
GAM390  FLJ20154  3' CCCTAACTCCATCTCCTTTCT  73303     C        AACCCC
                                AGG AGGAGGTGGA     AGGG
                                ||| ||||||||||     ||||
                                TCT TCCTCTACCT     TCCC
                                  T        CAA___
GAM390  FLJ20154  3' CCTGGGGACCCTTGTGCCT    73304      G    TGGAAA
                                AGGCA GAGG     CCCCAGG
                                ||||| ||||     |||||||
                                TCCGT TTCC     GGGGTCC
                                   G    CA____
GAM390  FLJ20170  3' TCCTGAAGCTGTTTCTGTTTTT 35169          TG     CC___
           TGTTT                  AGGCAGGAGG  GAAAC    CAGGG
                                ||||||||||  |||||    |||||
                                TTTGTTTTTT  CTTTG    GTCCT
                                      GT    TCGAA
GAM390  FLJ20171  3' CCAGGGTTCTCTTCATTTCCCT 35173        _      AA_______  CCAG
           GTCT                   AGGCAGG AGGTGGA       CC    G
                                ||||||| |||||||       ||    |
                                TCTGTCC TTTACTT       GG    C
                                   C      CTCTT     GACC
GAM390  FLJ20190  5' TTCTGGATGCATCATTTTTGCC 35209      G      AAACC
           T                   AGGCA GAGGTGG     CCAGGG
                                ||||| |||||||     ||||||
                                TCCGT TTTTACT     GGTCTT
                                   _      ACGTA
GAM390  FLJ20208  3' CCAGGGCTTTCTTTCTTTCTTG 35242        _  T_   A____  CCAG
           CTT                    AGGCAGG AGG  GGAA     CC    G
                                ||||||| |||  ||||    ||    |
                                TTCGTTC TTC  TCTT     GG    C
                                   T   TT    TC     GACC
GAM390  FLJ20208  3' CTTGCTTTCTTTCTTGCTT    35243         GT     CCC
                                AGGCAGGAG  GGAAA   CAGG
                                |||||||||  |||||   ||||
                                TTCGTTCTT  TCTTT   GTTC
                                     __     C__
GAM390  FLJ20208  3' CTTGCTTTCTTTCTTGCTT    35244         GT     CCC
                                AGGCAGGAG  GGAAA   CAGG
                                |||||||||  |||||   ||||
                                TTCGTTCTT  TCTTT   GTTC
                                     __     C__
GAM390  FLJ20208  3' TCTTGCTTTCTTTCTTTCTTGC 35247          T__     CCC
           TT                     AGGCAGGAGG   GGAAA   CAGGG
                                ||||||||||   |||||   |||||
                                TTCGTTCTTT   TCTTT   GTTCT
                                      CTT    C__
GAM390  FLJ20232  3' CTCTCGTTCATGCCTTCTGTTT 39184           GA   CCC
                                AGGCAGGAGGTG  AAC   AGGG
                                ||||||||||||  |||   ||||
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                                TTTGTCTTCCGT  TTG   TCTC
                                      AC   C__
GAM390  FLJ20232  3'  GGTCTTTTCTATTTTTTCCT   39187     C        A_______
                                AGG AGGAGGTGGAA      CC
                                ||| ||||||||||       ||
                                TCC TTTTTTATCTT      GG
                                  _         TTCT
GAM390  FLJ20232  3'  TTTTGGCCCATGTTTGCTGCCT 39190       __ G    AAACC
                                AGGCAG  GA GTGG    CCAGGG
                                ||||||  || ||||    ||||||
                                TCCGTC  TT TACC    GGTTTT
                                   GT  G    C____
GAM390  FLJ20294  5'  CCAGGGCCTTCCTTTATTCCTG 35347         GT__    AC____ CCAG
           TCT                    AGGCAGGAG    GGAA     C    G
                                |||||||||    ||||     |   |
                                TCTGTCCTT    CCTT     G    C
                                     ATTT    CC   G GACC
GAM390  FLJ20294  3'  GGTTCTTCCACCTCCTCCT    35359     C        AC_____
                                AGG AGGAGGTGGAA      C
                                ||| ||||||||||       |
                                TCC TCCTCCACCTT      G
                                  _         CTT   G
GAM390  FLJ20308  3'  ATTGGGGGGTTTTTGTTTTTTG 67389          TG       AGGG
           TTT                    AGGCAGGAGG  GAAACCCC
                                |||||||||  ||||||||
                                TTTGTTTTTT  TTTTGGGG
                                     GT       GGTTAC
GAM390  FLJ20366  3'  CCTTGCTTTGCTTTTTGCC    35529         TG  AACCC
                                GGCAGGAGG  GA    CAGGG
                                |||||||||  ||    |||||
                                CCGTTTTTC  TT    GTTCC
                                     GT  C____
GAM390  FLJ20436  3'  CAGGGTCCTCCTTCACCTTTGC 35623       G      AA________  CCAG
           TT                     AGGCAG AGGTGGA        CC    G
                                |||||| |||||||        ||    |
                                TTCGTT TCCACTT        GG    C
                                   _      CCTCCT     GAC
GAM390  FLJ20507  3'  CCCCAGGGTTCTGTCTTTATTT 35733           AA_________  CCAG
           TCTGT                   GCAGGAGGTGGA         CC    GG
                                ||||||||||||         ||    ||
                                TGTCTTTTATTT         GG    CC
                                      CTGTCTT    GACC
GAM390  FLJ20511  3'  TCCTGGGTTCATGCCATTCTCC 35784          _  AAAC__
           TGCTT                   AGGCAGGAGG TGG     CCCAGGG
                                |||||||||| |||     |||||||
                                TTCGTCCTCT ACC     GGGTCCT
                                     T   GTACTT
GAM390  FLJ20583  3'  CCAGGGTTCTGATCCCTTCCTG 35851          T   AA________  CCAG
           TCT                    AGGCAGGAGG GGA        CC    G
                                |||||||||| |||        ||    |
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                                TCTGTCCTTC CCT       GG   C
                                      _  AGTCTT    GACC
GAM390  FLJ20619  3'  CCCCAGGGTTTTGAATTATCTC 35893      _     AAA_______  CCAG
              ACTGTCT                AGGCAG GAGGTGG       CC   GG
                                |||||| |||||||        ||   ||
                                TCTGTC CTCTATT       GG   CC
                                   A      AAGTTTT    GACC
GAM390  FLJ20686  3'  CCCTGAACTGCTTTTCTGCCT  35953      _   TG AAACCC
                                AGGCAG GAGG  G     CAGGG
                                |||||| ||||  |     |||||
                                TCCGTC TTTC  C     GTCCC
                                   T   GT AA____
GAM390  FLJ20712  3'  CTCTGAGTTTCGGTCTCCTGTC 36033         G    CC
              T                  AGGCAGGAGGT GAAAC  CAGGG
                                |||||||||| |||||  |||||
                                TCTGTCCTCTG CTTTG  GTCTC
                                      G    A_
GAM390  FLJ20712  3'  CTCTGGAGTTGCTACCTGTCT  36034       A  GGA  C
                                AGGCAGG GGT   AAC CCAGGG
                                ||||||| |||   ||| ||||||
                                TCTGTCC TCG   TTG GGTCTC
                                   A  ___  A
GAM390  FLJ20736  3'  TTCTGGTTGCCATCTTTTTCT  36074     C       AAACC
                                AGG AGGAGGTGG    CCAGGG
                                ||| |||||||||    ||||||
                                TCT TTTTCTACC    GGTCTT
                                  _       GTT__
GAM390  FLJ20793  3'  CCTAGAATTTTCATTTTCTTTC 93449     C        CCCC  G
              T                  AGG AGGAGGTGGAAA   AGG
                                ||| ||||||||||||   |||
                                TCT TCTTTTACTTTT   TCC
                                  T         AAGA
GAM390  FLJ20793  3'  TTGGAATTTTTGCCTTCTCTT  93454     C    TG   CC
                                AGG AGGAGG  GAAA  CCAG
                                ||| ||||||  ||||  ||||
                                TTC TCTTCC  TTTT  GGTT
                                  _     GT   AA
GAM390  FLJ20811  5'  TCCTGCTAGTCGCCTCCGTCT  67710     A      AAACCC
                                AGGC GGAGGTGG     CAGGG
                                |||| ||||||||     |||||
                                TCTG CCTCCGCT     GTCCT
                                  _       GATC__
GAM390  FLJ21016  3'  GGTTTTTTTCCTTCCTGTCT   47962        TG   A_____
                                AGGCAGGAGG  GAA     CC
                                ||||||||||  |||     ||
                                TCTGTCCTTC  TTT     GG
                                      CT   TTT
GAM390  FLJ21032  3'  CCAGGGTTCAGTTTTGTCATTC 46618       _  TG   AC_______  CCAG
              TGTCT                AGGCAGGA GG  GAA       C    G
                                |||||||| ||  |||       |    |
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                                TCTGTCTT CT  TTT       G    C
                                    A  GT   GACTT   G GACC
GAM390  FLJ21087  3' CCCTGGTGTGCCATTTTCTCTT 93478     C       AA  C
                                AGG AGGAGGTGG  AC CCAGGG
                                ||| |||||||||  || ||||||
                                TTC TCTTTTACC  TG GGTCCC
                                  _       G_  T
GAM390  FLJ21162  5' CCTGTTTTTCTTTCTGCTT   46371         TG   ACCC
                                AGGCAGGAGG  GAA    CAGG
                                ||||||||||  |||    ||||
                                TTCGTCTTTC  TTT    GTCC
                                      TT  _____
GAM390  FLJ21269  3' CTTTTGGTTTTTGTTTCTTTCT 47780     C     TG     CC   G
            T                    AGG AGGAGG  GAAACC  AGG
                                ||| ||||||  ||||||  |||
                                TTC TTCTTT  TTTTGG  TTC
                                  T     GT     TT
GAM390  FLJ21269  3' TTTTGGTTTTTGTTTCTTTCTT 47781         GT     C____
            GTCT                    AGGCAGGAG  GGAAAC    CCAGGG
                                |||||||||  ||||||    ||||||
                                TCTGTTCTT  TCTTTG    GGTTTT
                                     __     TTTTT
GAM390  FLJ21290  3' CCAGGGTCTTCTCTATATTCTG 47396        G    AA_____  CCAG
            CCT                    AGGCAGGA GTGGA       CC    G
                                |||||||| |||||       ||    |
                                TCCGTCTT TATCT       GG    C
                                    A    CTTCT    GACC
GAM390  FLJ21308  5' CCCTGCATTTATTTTCTACTT  45192     C        AACCC
                                AGG AGGAGGTGGA    CAGGG
                                ||| ||||||||||    |||||
                                TTC TCTTTTATTT    GTCCC
                                  A        AC___
GAM390  FLJ21313  3' CCCAGGGTCTACATTTTGTCT  43930        G    AA_  CCAG
                                AGGCAGGA GTGGA   CC    GG
                                |||||||| |||||   ||    ||
                                TCTGTTTT CATCT   GG    CC
                                    A        GACC
GAM390  FLJ21596  3' GGTCATTCTGCCTTTTGTCT   46120         TG   A_____
                                AGGCAGGAGG  GAA     CC
                                ||||||||||  |||     ||
                                TCTGTTTTCC  CTT     GG
                                     GT   ACT
GAM390  FLJ21596  3' TTCTGGGCCTCCGTTTTCTGTT 46126        GG    AAC
            T                    AGGCAGGA  TGGA   CCCAGGG
                                ||||||||  ||||  |||||||
                                TTTGTCTT  GCCT   GGGTCTT
                                    TT    CC_
GAM390  FLJ21603  3' TCCTGGGTTCATGCCATTCTCC 45780         _   AAAC__
            TGCCT                   AGGCAGGAGG TGG     CCCAGGG
                                |||||||||| |||     |||||||
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                                TCCGTCCTCT ACC     GGGTCCT
                                     T   GTACTT
GAM390  FLJ21817  3'  TTTTGGGAGAAACTTTTTGTCT 42615          GGAAAC
                                AGGCAGGAGGT     CCCAGGG
                                ||||||||||      |||||||
                                TCTGTTTTTCA     GGGTTTT
                                     AAGA__
GAM390  FLJ21945  3'  CCTTGGGGACTCCTGTCTGTCT 48093        AGGT   AA
                                AGGCAGG   GGA  CCCCAGGG
                                |||||||   |||  ||||||||
                                TCTGTCT   CCT  GGGGTTCC
                                   GT__   CA
GAM390  FLJ21986  5'  CCTCATTCGCTCCTGCCT    46692         G   AACCCC
                                AGGCAGGAG TGGA     AGG
                                |||||||| ||||     |||
                                TCCGTCCTC GCTT     TCC
                                     _   AC_____
GAM390  FLJ22055  3'  CCTTGAGGCTTCCACTTTTT   45848          A  C
                                AGGAGGTGGAA CC CAGGG
                                |||||||||| || |||||
                                TTTTTCACCTT GG GTTCC
                                     C  A
GAM390  FLJ22167  5'  CTCTGCTCTCACCTCTCTGCTT 44869       _     _ AACCC
                                AGGCAG GAGGTG GA    CAGGG
                                |||||| |||||| ||    |||||
                                TTCGTC CTCCAC CT    GTCTC
                                   T     T  C_____
GAM390  FLJ22301  3'  TCCTGATTACTTTTGTTGTCCT 46182        _ TG   ACCC_
          GCCT                   AGGCAGGA GG  GAA    CAGGG
                                |||||||| ||  |||    |||||
                                TCCGTCCT TT  TTT    GTCCT
                                     G  GT   CATTA
GAM390  FLJ22316  5'  CCAGGGTTTTCTCCATTTTCTT 47615     C        AA_______  CCAG
          TCT                    AGG AGGAGGTGGA       CC    G
                                ||| ||||||||||       ||   |
                                TCT TCTTTTACCT       GG    C
                                  T        CTTTT     GACC
GAM390  FLJ22318  3'  TCCTGCTGTCTTTTCCTGTTT  43144          T   AACCC
                                AGGCAGGAGG GGA    CAGGG
                                |||||||||| |||    |||||
                                TTTGTCCTTT TCT    GTCCT
                                     _   GTC__
GAM390  FLJ22341  3'  TCCTGGGGCAGGGTCCTTTTCT 45116       T   AA___
          T                     AGGAGG GGA    CCCCAGGG
                                ||||||| |||    ||||||||
                                TTCTTT CCT    GGGGTCCT
                                   T   GGGAC
GAM390  FLJ22344  3'  CCCAGGGCTTTCTTTCTGCTT  45589          T_  AAA  CCAG
                                AGGCAGGAGG  GG   CC    GG
                                ||||||||||  ||   ||    ||
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                                TTCGTCTTTC  TC   GG    CC
                                      TT      GACC
GAM390  FLJ22408  3'  CCCTGCCTTCGACCTCCTGCCT 45984          G   ACCC
                                AGGCAGGAGGT GAA    CAGGG
                                |||||||||||| |||    |||||
                                TCCGTCCTCCA CTT    GTCCC
                                      G   CC__
GAM390  FLJ22408  5'  TCTGGCTGTTTTCTGTC     45988          TG AAACC
                                GGCAGGAGG  G    CCAGG
                                |||||||||  |    |||||
                                CTGTCTTTT  C    GGTCT
                                      GT _____
GAM390  FLJ22471  3'  GGCCCATTCTCCTTCTGCTT   47861          T   AA_____
                                AGGCAGGAGG GGA      CC
                                |||||||||| |||      ||
                                TTCGTCTTCC CTT      GG
                                      T   ACCC
GAM390  FLJ22582  3'  CCCTGGGGGGCCCACCTCTTGC 47455           AAA
          C                     GGCAGGAGGTGG   CCCCAGGG
                                ||||||||||||   ||||||||
                                CCGTTCTCCACC   GGGGTCCC
                                      CGG
GAM390  FLJ22671  3'  CTTGGAGCACCTCCTCCCT    46314     C       GAAACC
                                AGG AGGAGGTG     CCAGG
                                ||| ||||||||     |||||
                                TCC TCCTCCAC     GGTTC
                                  C       GA____
GAM390  FLJ22944  3'  CCCAGGGCCTTCCATTTACCCC 47869        A     AA_________  CCAG
          CTGCCT                  AGGCAGG GGTGGA        CC    GG
                                |||||||  ||||||         ||    ||
                                TCCGTCC CCATTT         GG    CC
                                    C     ACCTTCC     GACC
GAM390  FLJ22969  3'  CTTTGGGGTGCTGTTATTCTGC 69204         _  TG AA
          CT                    AGGCAGGA GG  G  ACCCCAGGG
                                |||||||| ||  |  |||||||||
                                TCCGTCTT TT  C  TGGGGTTTC
                                     A  GT G_
GAM390  FLJ23017  3'  CCCAGGGTCCAGATTTCTGCTT 43416         G_    AA_  CCAG
                                AGGCAGGAG  TGGA   CC    GG
                                |||||||||  ||||   ||    ||
                                TTCGTCTTT  ACCT   GG    CC
                                      AG        GACC
GAM390  FLJ23112  3'  CCTGGGGACGTCCTGTTT    46811         G  GGAAA
                                AGGCAGGA GT     CCCCAGG
                                |||||||| ||     |||||||
                                TTTGTCCT CA     GGGGTCC
                                     G  _____
GAM390  FLJ23120  3'  CTCTCTTTCTCTTTTCTGTCT  86327          T     CCCC
                                AGGCAGGAGG GGAAA    AGGG
                                |||||||||| |||||    ||||
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                                TCTGTCTTTT TCTTT    TCTC
                                      C    C___
GAM390  FLJ23186  3' CCAGGGTCCTCTTTATTTTCTG 61040          AA_______  CCAG
             C                   GCAGGAGGTGGA       CC    G
                                 ||||||||||||       ||    |
                                 CGTCTTTTATTT       GG    C
                                       CTCCT     GACC
GAM390  FLJ23556  5' TTCTGGAACTCACTGTTCTCTT 46464         _____   AAACC
             GCTT                  AGGCAGGAG   GTGG    CCAGGG
                                   |||||||||   ||||    ||||||
                                   TTCGTTCTC   CACT    GGTCTT
                                       TTGT    CAA__
GAM390  FLJ25193  3' CCTGCCCACTCTCTGCTT    59358       GA    AAACCC
                                 AGGCAG  GGTGG     CAGG
                                 ||||||  |||||     ||||
                                 TTCGTC  TCACC     GTCC
                                     TC    C_____
GAM390  FLJ25473  5' CCCTGGGTTCTGCCTCCGCCT  59137      A    TG   AC
                                 AGGC GGAGG  GAA  CCCAGGG
                                 |||| |||||  |||  |||||||
                                 TCCG CCTCC  CTT  GGGTCCC
                                   _    GT   __
GAM390  FLJ30294  3' CCAGGGTTTATTTTGTTTCTTG 58895         TG   A_______  CCAG
             CC                   GGCAGGAGG  GAA      CC    G
                                  |||||||||  |||      ||    |
                                  CCGTTCTTT  TTT      GG    C
                                       GT   ATTT     GACC
GAM390  FLJ30567  3' CCCTGGGGAGCTCCTCCGCCTT 59473    G         AA____
             TTGGCT                AG CAGGAGGTGGA     CCCCAGGG
                                   || ||||||||||      ||||||||
                                   TC GTTTTCCGCCT     GGGGTCCC
                                    G         CCTCGA
GAM390  FLJ30681  3' GGTTTTGGCTTTTTTGCCT   93437         _  G   A___
                                 AGGCAGGAG GT GAA    CC
                                 |||||||||  || |||    ||
                                 TCCGTTTTT CG TTT    GG
                                       T  G   T
GAM390  FLJ31121  3' TCCTGTGTTCTGCCTTTGTTT  59209      G    TG   ACCC
                                 AGGCA GAGG  GAA    CAGGG
                                 |||||  ||||  |||    |||||
                                 TTTGT TTCC  CTT    GTCCT
                                   _    GT   GT__
GAM390  FLJ31168  3' CCCTACCTTTTGGCTTCTGTCT 59179         G GG  ACCCC
                                 AGGCAGGAG T  AA     AGGG
                                 |||||||||  |  ||     ||||
                                 TCTGTCTTC G  TT     TCCC
                                       G TT  CCA__
GAM390  FLJ31737  3' CCAGGGCTCAATTTAGCTTCCT 59347          G   A________  CCAG
             GCTT                  AGGCAGGAGGT GAA       CC    G
                                   ||||||||||| |||       ||    |
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                                TTCGTCCTTCG TTT       GG    C
                                      A   AACTC     GACC
GAM390  FLJ32191  3'  CTCTGGTCTGCTTGCCTCCTGT 59078          TG AAACC
              TT                  AGGCAGGAGG  G     CCAGGG
                                  ||||||||||  |     ||||||
                                  TTTGTCCTCC  T     GGTCTC
                                        GT CGTCT
GAM390  FLJ32356  3'  CTTGGCTGCTTCATTGTCT    59022       _    TG AAACC
                                  AGGCAG GAGG  G     CCAGG
                                  ||||||  ||||  |     |||||
                                  TCTGTT CTTC  C     GGTTC
                                     A    GT _____
GAM390  FLJ32389  3'  CCTCCTCTACTTCCTTCT    58842     C        AACCCC
                                  AGG AGGAGGTGGA      AGG
                                  |||  ||||||||||      |||
                                  TCT TCCTTCATCT      TCC
                                    _         CC____
GAM390  FLJ32421  5'  GGCTCTTCTCTTCCTGTCT    59120          T   AA____
                                  AGGCAGGAGG GGA      CC
                                  ||||||||||  |||      ||
                                  TCTGTCCTTC CTT      GG
                                        T   CTC
GAM390  FLJ32818  3'  CCTTGGCCCTGCTGCCTCTGTC 59073        G   TG AAACC
              T                   AGGCAG AGG  G     CCAGGG
                                  ||||||  |||  |     ||||||
                                  TCTGTC TCC  C     GGTTCC
                                     _  GT GTCCC
GAM390  FLJ32865  3'  CTCTGCCACCACCGTTTCTTCC 58809     C    __     AAACCC
              T                   AGG AGGA  GGTGG      CAGGG
                                  |||  ||||  |||||      |||||
                                  TCC TCTT  CCACC      GTCTC
                                    T    TG     ACC___
GAM390  FLJ32894  3'  CCAGGGCTTTGACCACTTTCTT 58994     C        AAA_______  CCAG
              CTT                   AGG AGGAGGTGG        CC    G
                                  |||  |||||||||        ||    |
                                  TTC TCTTTCACC        GG    C
                                    T        AGTTTC     GACC
GAM390  FLJ32919  5'  CCCTGGAGTCTCCACCTTTTCC 58697     C        A  C
              T                   AGG AGGAGGTGGA AC CCAGGG
                                  |||  ||||||||||  ||  ||||||
                                  TCC TTTTCCACCT TG GGTCCC
                                    _         C  A
GAM390  FOXP1     3'  TTTTGATTTTTCTACTTTTTGT 52051             CCC
              T                   GGCAGGAGGTGGAAA   CAGGG
                                  ||||||||||||||||   |||||
                                  TTGTTTTTCATCTTT   GTTTT
                                            TTA
GAM390  FTCD      3'  CCCTGCCCAGCCAGCCTCCTGT 22838          _   AAACCC
              CT                    AGGCAGGAGG TGG      CAGGG
                                  ||||||||||  |||      |||||
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                                TCTGTCCTCC ACC     GTCCC
                                     G   GACCC_
GAM390  FUSIP1   3'  TTTTGGTGCCAGTGTTTTCTGC 55046          ___   AAACC
           TT                  AGGCAGGAGG   TGG    CCAGGG
                               ||||||||||   |||    ||||||
                               TTCGTCTTTT   ACC    GGTTTT
                                    GTG   GT___
GAM390  GAB3     3'  TTCTGGTGACATTATTTTCTTC 55524     C       AAACC
           CT                   AGG AGGAGGTGG    CCAGGG
                               ||| |||||||||    ||||||
                               TCC TCTTTTATT    GGTCTT
                                 T       ACAGT
GAM390  GC20     5'  CCAGGGTCCTCCTTCGCCTCTT 69473     C       AA________  CCAG
           CCT                   AGG AGGAGGTGGA       CC   G
                               ||| ||||||||||       ||   |
                               TCC TTCTCCGCTT       GG   C
                                _       CCTCCT    GACC
GAM390  GCHFR    3'  CCTGCCTCACCGTCTGCCT   19147      GA    AAACCC
                               AGGCAG  GGTGG     CAGG
                               ||||||  |||||     ||||
                               TCCGTC  CCACT     GTCC
                                  TG    CC____
GAM390  GFR      3'  TTTGCTTTTCCATCCTTGTCT  25452       A      CCC
                               AGGCAGG GGTGGAAA   CAGG
                               |||||||  ||||||||   ||||
                               TCTGTTC CTACCTTT   GTTT
                                  _      TC_
GAM390  GMEB2    3'  CAGGGTTTTTCCATCTGTTGCT 25660       G       _______  CCA
           T                    AGGCAG AGGTGGAAA     CC   G
                               ||||||  |||||||||     ||   |
                               TTCGTT TCTACCTTT     GG   C
                                  G       TT   G  AC
GAM390  GMPPB    5'  CCCTGCATCCTTTCCGTCTCCC 26218       _ GT    CCC__
           TGCTT                  AGGCAGG AG  GGAAA    CAGGG
                               |||||||  ||  |||||    |||||
                               TTCGTCC TC  CCTTT    GTCCC
                                  C  TG    CCTAC
GAM390  GOLGIN-67 3'  CCAGGGCTTTCCTCCATTTTCT 96656          AA________  CCAG
           GT                   GCAGGAGGTGGA       CC   G
                               ||||||||||||       ||   |
                               TGTCTTTTACCT       GG   C
                                     CCTTTC    GACC
GAM390  GOLPH2   3'  CCAGGGCTCTATTCATCTCATG 33768      G       AA_______  CCAG
           TTT                   AGGCA GAGGTGGA       CC   G
                               |||||  ||||||||       ||   |
                               TTTGT CTCTACTT       GG   C
                                 A       ATCTC    GACC
GAM390  GP5      3'  TTCTGATAATTTGCTTCTTCCT 16886     C     TG  AACCC
                               AGG AGGAGG  GA    CAGGG
                               ||| ||||||  ||    |||||
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                                TCC TTCTTC  TT    GTCTT
                                  _     GT  AATA_
GAM390  GPA33    3'  CCCACACACTTTCCATCTCTGC 20569       G       CCCCA_
              CT                   AGGCAG AGGTGGAAA     GGG
                                |||||| |||||||||     |||
                                TCCGTC TCTACCTTT     CCC
                                  _       CACACA
GAM390  GPR74    5'  TCTGCCCACCTCTTCTCT    54896    C       AAACCC
                                AGG AGGAGGTGG     CAGG
                                ||| |||||||||     ||||
                                TCT TTCTCCACC     GTCT
                                  C       C_____
GAM390  GPR88    3'  CCTGATTTTTACCCTTTGTTT  42135       GA      CCC
                                AGGCAG  GGTGGAAA   CAGG
                                ||||||  ||||||||   ||||
                                TTTGTT  CCATTTTT   GTCC
                                   TC       A__
GAM390  GREB1    5'  CCTTGCAGCTGTTTCACCTTCT 28565     C        ACCC__
              ACCT                   AGG AGGAGGTGGAA     CAGGG
                                ||| ||||||||||     |||||
                                TCC TCTTCCACTTT     GTTCC
                                  A         GTCGAC
GAM390  GRID1    3'  CCTTGTTTTTCATTTTCT    69023           CCC
                                AGGAGGTGGAAA   CAGGG
                                ||||||||||||   |||||
                                TCTTTTACTTTT   GTTCC
                                      T__
GAM390  GRO2     3'  CTTGGACATTTTATGTCT    60253       G     GAAACC
                                AGGCA GAGGTG      CCAGG
                                ||||| ||||||      |||||
                                TCTGT TTTTAC      GGTTC
                                  A     A_____
GAM390  GRO3     3'  CCTTAGACATTTTATGTCTTGC 63184         G     ACCCC_  G
              TT                   AGGCAGGA GTGGAA     AGG
                                |||||||| ||||||     |||
                                TTCGTTCT TATTTT     TCC
                                   G     ACAGAT
GAM390  GRWD     3'  CTCTGATCTTGCTTCCTGCTT  49780          TG AAACCC
                                AGGCAGGAGG  G     CAGGG
                                ||||||||||  |     |||||
                                TTCGTCCTTC  T     GTCTC
                                     GT CTA___
GAM390  GS3955   5'  CCTTGCAATTTTTCTTTTTTTT 41619          T    CCC__
              GTTT                   AGGCAGGAGG GGAAA     CAGGG
                                |||||||||| |||||    |||||
                                TTTGTTTTTT TCTTT     GTTCC
                                     T     TTAAC
GAM390  GTF2A1   5'  TCTTGGGGTTGCCCCCTCTTGT 32405          T  A
              TT                   AGGCAGGAGG GG AACCCCAGGG
                                |||||||||| || ||||||||||
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                                TTTGTTCTCC CC TTGGGGTTCT
                                      C  G
GAM390  GTPBP1   3'  CCCCAGGGCTTTCCTTTCCTCC 16264         T__    _____ CCA
          TGCTT                  AGGCAGGAGG  GGAAA    CC   GG
                                ||||||||||  |||||    ||  ||
                                TTCGTCCTCC  CCTTT    GG  CC
                                      TTT    C  G  ACC
GAM390  H_GS165L15.1 3'  CAGGGTTTTGACTTCCTTCT  18134    C     G  A___  CCAG
                                AGG AGGAGGT GAA   CC   G
                                ||| ||||||| |||   ||   |
                                TCT TCCTTCA TTT   GG   C
                                  _     G  T    GAC
GAM390  HAN11    3'  GGTTTTGTATTTCCTGCCT   20634          _  A___
                                AGGCAGGAGGTG GAA   CC
                                |||||||||||| |||   ||
                                TCCGTCCTTTAT TTT   GG
                                      G  T
GAM390  HAND1    3'  CCAGGGTTTTCCTTCCTTTTTG 17877        _ T_   A____  CCAG
          TTT                   AGGCAGGA GG  GGAA    CC   G
                                |||||||| ||  ||||    ||   |
                                TTTGTTTT CC  CCTT    GG   C
                                     T  TT    TT    GACC
GAM390  HCA127   3'  GGCTTTCTCCACTTCTGTCT  38568      G     AA_____
                                AGGCAG AGGTGGA      CC
                                |||||| |||||||      ||
                                TCTGTC TTCACCT      GG
                                   _     CTTTC
GAM390  HDAC9-PENDING 3'  CCTTGAAGGTGATCTCTTGTTT 28841          GGAA  C_
                                AGGCAGGAGGT   ACC  CAGGG
                                ||||||||||   |||  |||||
                                TTTGTTCTCTA   TGG  GTTCC
                                      G___   AA
GAM390  HDAC9-PENDING 3'  TTTGTATGTTTCCCTTCTTGCC 28845         T    CC_   G
          T                    AGGCAGGAGG GGAAAC   CAGG
                               |||||||||| ||||||   ||||
                               TCCGTTCTTC CCTTTG   GTTT
                                     _     TAT
GAM390  HEY2     3'  GGTCCTCTTCATTTTCTCCT  25323    C       AA_____
                                AGG AGGAGGTGGA      CC
                                ||| ||||||||||      ||
                                TCC TCTTTTACTT      GG
                                  _       CTCCT
GAM390  HINT1    3'  TTTTGGGGATAATTTTCTCTT  73592    C     GGAAA
                                AGG AGGAGGT    CCCCAGGG
                                ||| |||||||    ||||||||
                                TTC TCTTTTA    GGGGTTTT
                                  _     ATA__
GAM390  HLA-DOA  5'  GGTCTTCTTTACCTCCGCCT  10930     A       AA_____
                                AGGC GGAGGTGGA      CC
                                |||| |||||||||      ||
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                                TCCG CCTCCATTT       GG
                                  _       CTTCT
GAM390  HM74     3'  GGTCCATTCCTCTCTTGTTT  21203          T   A_______
                                AGGCAGGAGG GGAA      CC
                                |||||||||| ||||      ||
                                TTTGTTCTCT CCTT      GG
                                     _   ACCT
GAM390  HMP19    3'  CCAGGGTTTTCTTTGTCTTTTG 88859          TG  AA_______  CCAG
             CTT                   AGGCAGGAGG  GA       CC   G
                                |||||||||  ||      ||   |
                                TTCGTTTTCT  TT      GG   C
                                     GT  CTTTT    GACC
GAM390  HMT-1    3'  TCCTAACATTTTGATTCCTGTC 39411        G  G   CCCC
             T                    AGGCAGGA GT GAAA   AGGG
                                |||||||| || ||||   ||||
                                TCTGTCCT TA TTTT   TCCT
                                     _ G   ACAA
GAM390  HN1      3'  TCCTGAACGCTGTCGTTCTGTC 32990         _  TG AAACCC
             T                    AGGCAGGA GG  G     CAGGG
                                |||||||| ||  |     |||||
                                TCTGTCTT CT  C     GTCCT
                                     G  GT GCAA__
GAM390  HNRPL    3'  CCAGGGCTTTATGCCATTTTTT 9516            AAA________  CCAG
             GTTT                  AGGCAGGAGGTGG        CC   G
                                |||||||||||||        ||   |
                                TTTGTTTTTTACC        GG   C
                                       GTATTTC    GACC
GAM390  HRI      3'  CCAGGGTTCTCTCCACCTTCAG 27737      A       AA_______  CCAG
             TTT                   AGGC GGAGGTGGA       CC   G
                                |||| |||||||||       ||   |
                                TTTG CTTCCACCT       GG   C
                                  A       CTCTT    GACC
GAM390  HRIHFB2072 3'  CCCTGTCCACCATCTTGTGCCT 51695       G      AAACCC
                                AGGCA GAGGTGG     CAGGG
                                ||||| |||||||     |||||
                                TCCGT TTCTACC     GTCCC
                                   G      ACCT__
GAM390  HSA250839 3'  CTCTGTGCCTCCGTTTTCTGC  37850       GG   AACCC
                                GCAGGA  TGGA    CAGGG
                                ||||||  ||||    |||||
                                CGTCTT  GCCT    GTCTC
                                    TT   CCGT_
GAM390  HSH2     3'  TTTTGGGGTCTGTTCCTGC   52746       G TG  AA
                                GCAGGA G  GA  CCCCAGGG
                                |||||| |  ||  ||||||||
                                CGTCCT T  CT  GGGGTTTT
                                   _ GT  __
GAM390  HSJ001348 3'  TTCTGTTGATTACCTCTTGGTT 62862    G        AAACCC
                                AG CAGGAGGTGG     CAGGG
                                || ||||||||||     |||||
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                                TT GTTCTCCATT     GTCTT
                                 G        AGTT__
GAM390  HSPC039  3' CCAGGGTTTCTATTTATCTGTT 32738       _         CA  G
           T                    AGGCAGG AGGTGGAAACCC  GG
                                ||||||| |||||||||||  ||
                                TTTGTCT TTTATCTTTGGG  CC
                                   A          A_
GAM390  HSPC177  5' CTCTGCTTCCGTTTCTGGTTT  33524     A   GG    ACCC
                                AGGC GGA  TGGAA    CAGGG
                                |||| |||  |||||    |||||
                                TTTG TCT  GCCTT    GTCTC
                                  G  TT    C___
GAM390  HSPC195  3' CTCTCACAGATTTCATTCCTGT 81865        G    ACCCC_
           TT                    AGGCAGGAG TGGAA     AGGG
                                |||||||| |||||     ||||
                                TTTGTCCTT ACTTT     TCTC
                                   _    AGACAC
GAM390  HSPC228  3' GGTTTTTTGTTTTTTGTTT   33648         TG    C
                                AGGCAGGAGG  GAAA CC
                                ||||||||||  |||| ||
                                TTTGTTTTTT  TTTT GG
                                     GT    T
GAM390  HSRNAFEV 3' CCTCTTTCACCTTTTTTCT   34447     C        ACCCC
                                AGG AGGAGGTGGAA    AGG
                                ||| ||||||||||     |||
                                TCT TTTTCCACTTT    TCC
                                  T         C_____
GAM390  HT007    3' GGTTCTGTGCCTTTTGCCT   38077          __  AA__
                                AGGCAGGAGGT  GGA   CC
                                ||||||||||  |||   ||
                                TCCGTTTTCCG  TCT   GG
                                     TG   T
GAM390  HT010    3' TCTGCCTTTCCATCTTTTG   38068          CCC   G
                                CAGGAGGTGGAAA  CAGG
                                ||||||||||||  ||||
                                GTTTTCTACCTTT  GTCT
                                     CC_
GAM390  HTCD37   3' TTCTGTGATCTGCCTCTTGCT  68304        TG  AACCC
                                GGCAGGAGG  GA    CAGGG
                                |||||||||  ||    |||||
                                TCGTTCTCC  CT    GTCTT
                                   GT  AGT__
GAM390  HTEX4    5' CCAGGGCCCTCCTCAGTTTTCT 93721       _______   T  AAA_  CCAG
           GTTT                   AGGCAG     GAGG GG    CC    G
                                ||||||     |||| ||    ||    |
                                TTTGTC     CTCC CC    GG    C
                                   TTTTGA    T  C     GACC
GAM390  HTMP10   3' TTCTGTACTCTTCTTTTGCCT  53761         T   AACCC
                                AGGCAGGAGG GGA    CAGGG
                                |||||||||| |||    |||||
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                                TCCGTTTTCT TCT    GTCTT
                                      _  CAT__
GAM390  HUMAGCGB  3'  TTTTGGGGGATTTTTTTTTT  26138      TG  AA
                                AGGAGG  GA  CCCCAGGG
                                ||||||  ||  ||||||||
                                TTTTTT  TT  GGGGTTTT
                                   TT  AG
GAM390  HYPC    3'  TCCTGGGCCACCCTCACCGTCT 65220      GA    AAAC__
           GCCT                  AGGCAG  GGTGG    CCCAGGG
                                ||||||  |||||    |||||||
                                TCCGTC  CCACT    GGGTCCT
                                   TG    CCCACC
GAM390  ICK     3'  CCAGGGTTCTTTTGTCTCTCTG 33681      _   TG   AC_____ CCAG
           TTT                   AGGCAG GAGG  GAA     C   G
                                ||||||  ||||  |||     |   |
                                TTTGTC CTCT  TTT     G   C
                                   T   GT   CTT   G GACC
GAM390  ICK     3'  CCCAGGGTTTTAAATGTATCTC 33682          GAAA_________  CCAG
           TTGCCT                 AGGCAGGAGGTG         CC   GG
                                ||||||||||||         ||   ||
                                TCCGTTCTCTAT         GG   CC
                                      GTAAATTTT    GACC
GAM390  ICK     3'  CCCCAGGGTTTATTTTCATTTT 33683          _________  CCA
           CTGT                  GCAGGAGGTGGAAA      CC   GG
                                ||||||||||||||      ||   ||
                                TGTCTTTTACTTTT      GG   CC
                                      ATTT   G  ACC
GAM390  IL14    5'  CTTTGGGTGATCTCTTGTC   97164         GGAA   C
                                GGCAGGAGGT   ACCC AGG
                                ||||||||||   |||| |||
                                CTGTTCTCTA   TGGG TTC
                                      G___   T
GAM390  IRF5    3'  CCTGGGCTGTCTCTGGTCT   51960     A    TG AAAC
                                AGGC GGAGG  G   CCCAGG
                                ||||  |||||  |   ||||||
                                TCTG TCTCT  C   GGGTCC
                                  G    GT _____
GAM390  JAM1    3'  CTCTGGGGCCCACTCTCTTCTG 34226        ___   AAA
           TCT                   AGGCAGGAG   GTGG   CCCCAGGG
                                |||||||||   ||||   ||||||||
                                TCTGTCTTC   CACC   GGGGTCTC
                                     TCT   C__
GAM390  JAM1    3'  TCTTGGCTTGATTTTGCTTCTT 34249    C    TG   ACC__
           TCTT                   AGG AGGAGG  GAA    CCAGGG
                                |||  ||||||  |||    ||||||
                                TTC TTCTTC  TTT    GGTTCT
                                  T    GT   AGTTC
GAM390  JAM1    3'  TCTTGGCTTGATTTTGCTTCTT 34250    C    TG   ACC__
           TCTT                   AGG AGGAGG  GAA    CCAGGG
                                |||  ||||||  |||    ||||||
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                                TTC TTCTTC  TTT    GGTTCT
                                  T    GT   AGTTC
GAM390  JM11    3'  CCAGGGTCTTTTCTTCTTCTTG 54353        T_   A_____  CCAG
            TCT                   AGGCAGGAGG  GGAA     CC   G
                                  ||||||||||  ||||     ||   |
                                  TCTGTTCTTC  CTTT     GG   C
                                      TT   TCT    GACC
GAM390  JM11    3'  CCAGGGTCTTTTTCTGTGTCTT 54354       GG    A________  CCAG
            GTCT                    AGGCAGGA  TGGAA      CC   G
                                  ||||||||  |||||      ||   |
                                  TCTGTTCT  GTCTT      GG   C
                                      GT    TTTCT    GACC
GAM390  KALI    3'  GGTCCTTCAGTTTCCTGCTT   54695         _   AA____
                                  AGGCAGGAGG TGGA     CC
                                  ||||||||||  ||||     ||
                                  TTCGTCCTTT ACTT     GG
                                       G   CCT
GAM390  KBRAS2   3'  TCCTGGGAGTGTAGTTTTCTGT 34629       GG GGAA  _
            TT                    AGGCAGGA  T   AC CCCAGGG
                                  ||||||||  |   || |||||||
                                  TTTGTCTT  G   TG GGGTCCT
                                      TT ATG_  A
GAM390  KCNB2    5'  TTCTGTTCCAGCCCTCTCTTGT 97816         T  AAACCC
            CT                    AGGCAGGAGG GG     CAGGG
                                  ||||||||||  ||     |||||
                                  TCTGTTCTCT CC     GTCTT
                                       C  GACCTT
GAM390  KCNH8    3'  CCCCAGGGTTTTAGTTTGCCTT 58905       _  TG  AA________  CCAG
            TTTGCCT                 AGGCAGGA GG  GA       CC   GG
                                  ||||||||  ||  ||       ||   ||
                                  TCCGTTTT CC  TT       GG   CC
                                      T  GT  GATTTT    GACC
GAM390  KCNK13   3'  TACCTGTTTCTGTTTTTTGTT  42152        TG    CCC   G
                                  GGCAGGAGG  GAAAC   AGG
                                  |||||||||  |||||   |||
                                  TTGTTTTTT  CTTTG   TCC
                                       GT    ___   ATA
GAM390  KCNT1    3'  CCCTGTGCCACCTCCTGCCT   62489          AAACCC
                                  AGGCAGGAGGTGG     CAGGG
                                  ||||||||||||      |||||
                                  TCCGTCCTCCACC     GTCCC
                                        GT____
GAM390  KCNT1    3'  TCCTGGAAGCCATCTGCTGCTT 62497       G     AAACC
                                  AGGCAG AGGTGG    CCAGGG
                                  ||||||  ||||||    ||||||
                                  TTCGTC TCTACC    GGTCCT
                                     G     GAA__
GAM390  KIAA0008 5'  CCGAGTGTTCTTTACTTTTTGT 29239           _   CCCA  G
            TT                    AGGCAGGAGGTGGA AAC    GG
                                  ||||||||||||||  |||    ||
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                                TTTGTTTTTCATTT TTG   CC
                                      C  TGAG
GAM390  KIAA0010 3' CCCCAGGGTTCTATCTCCACTT 28590      G      AA_________ CCAG
            TGTGCCT               AGGCA GAGGTGGA        CC   GG
                                |||||| ||||||||        ||   ||
                                TCCGT TTTCACCT        GG   CC
                                  G       CTATCTT    GACC
GAM390  KIAA0014 3' CCCTGTGGAGTTCCTGTCTTCT 28540          TG A  _ _
            GTTT                  AGGCAGGAGG  G AAC CC CAGGG
                                |||||||||| | ||| || |||||
                                TTTGTCTTCT  C TTG GG GTCCC
                                      GT C   A  T
GAM390  KIAA0036 3' CTTTGGTTTCTTCTGTTT    28390       AGGT      CC
                                AGGCAGG    GGAAACC  AG
                                |||||||    |||||||  ||
                                TTTGTCT    TCTTTGG  TC
                                    ____      TT
GAM390  KIAA0040 3' CTCTGATTCCCTCTTCTGCCT  28490          T    ACCC
                                AGGCAGGAGG GGAA    CAGGG
                                |||||||||| ||||    |||||
                                TCCGTCTTCT CCTT    GTCTC
                                      C    A___
GAM390  KIAA0040 5' TTCTGGGGCTAAGCCTCCTTCT 28498     C      GGAAA
                                AGG AGGAGGT    CCCCAGGG
                                ||| |||||||    ||||||||
                                TCT TCCTCCG    GGGGTCTT
                                  _      AATC_
GAM390  KIAA0057 3' CCCTGCCTCCTCCTTCCTGCCT 25408         _  T   AACCC
                                AGGCAGGA GG GGA    CAGGG
                                |||||||| || |||    |||||
                                TCCGTCCT CC CCT    GTCCC
                                     T  T   CC___
GAM390  KIAA0057 3' TTCTGCTTGCTCTGTTTCTTGC 25428          TG  AACCC
            CT                  AGGCAGGAGG  GA    CAGGG
                                |||||||||  ||    |||||
                                TCCGTTCTTT  CT    GTCTT
                                      GT  CGTTC
GAM390  KIAA0077 3' CCCTGACTGGCTGTTTTTTCCC 67579     C     TG AAACCC
            T                   AGG AGGAGG  G     CAGGG
                                ||| ||||||  |     |||||
                                TCC TTTTTT  C     GTCCC
                                  C     GT GGTCA_
GAM390  KIAA0090 3' TTCTGACTTTTTCCATCTCTTG 89821             CCC_
            CTT                   AGGCAGGAGGTGGAAA   CAGGG
                                |||||||||||||||   |||||
                                TTCGTTCTCTACCTTT   GTCTT
                                        TTCA
GAM390  KIAA0101 5' CCAGGGCTCTCCTCTCTTCTTG 29087          T__   AA____  CCAG
            TTT                   AGGCAGGAGG   GGA     CC   G
                                |||||||||  |||     ||   |
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                              TTTGTTCTTC  CCT    GG   C
                                    TCT  CTC    GACC
GAM390  KIAA0125 3' CCTGGGTTGCCTCTTTTCT  29564    C    TG AAAC
                              AGG AGGAGG  G   CCCAGG
                              ||| ||||||  |   ||||||
                              TCT TTCTCC  T   GGGTCC
                                T    GT ____
GAM390  KIAA0125 3' TCCTGGGCAGGTGCTTCCTTTC 29577    C     GGAAAC
           T                   AGG AGGAGGT    CCCAGGG
                              ||| |||||||    |||||||
                              TCT TCCTTCG    GGGTCCT
                                T     TGGAC_
GAM390  KIAA0125 3' CCCTGGGGGCACCTTCCTCCT 61125      T_ AAA
                              AGGAGG  GG  CCCCAGGG
                              ||||||  ||  ||||||||
                              TCCTCC  CC  GGGGTCCC
                                  TT  ACG
GAM390  KIAA0133 3' TCTTGAAATGTCACATTTTCTG 29419         _ AACCC
           CCT                   AGGCAGGAGGTG GA    CAGGG
                              |||||||||||| ||    |||||
                              TCCGTCTTTTAC CT    GTTCT
                                    A  GTAAA
GAM390  KIAA0143 3' CCCAAAATGTTTTTCTTCCTGT 65409        T    CCCA_
           CT                   AGGCAGGAGG GGAAAC    GGG
                              |||||||||| ||||||    |||
                              TCTGTCCTTC TTTTTG    CCC
                                    _     TAAAA
GAM390  KIAA0152 3' CCAGGGTCTTCCTTCTTCTCCT 28968        T  AA_______  CCAG
           GCCT                  AGGCAGGAGG GGA       CC   G
                              |||||||||| |||       ||   |
                              TCCGTCCTCT CTT       GG   C
                                    T  CCTTCT    GACC
GAM390  KIAA0152 3' CCTGGGGACCACCTGCCT    28972       A  GGAAA
                              AGGCAGG GGT    CCCCAGG
                              ||||||| |||    |||||||
                              TCCGTCC CCA    GGGGTCC
                                  A  _____
GAM390  KIAA0152 3' CTCTGTTGTTCACCTTTTGCTT 28973          AACCC
                              AGGCAGGAGGTGGA    CAGGG
                              ||||||||||||||    |||||
                              TTCGTTTTCCACTT    GTCTC
                                     GTT__
GAM390  KIAA0172 3' TTTTGGATTTTTCTTTTGTCT  65601        TG   CC
                              AGGCAGGAGG  GAAA  CCAGGG
                              ||||||||||  ||||  ||||||
                              TCTGTTTTCT  TTTT  GGTTTT
                                    __   A_
GAM390  KIAA0179 3' TCTGGGGGCTTTTTCTTCT   65460      TG  AA
                              AGGAGG  GA  CCCCAGG
                              ||||||  ||  |||||||
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                              TCTTCT  TT  GGGGTCT
                                 TT  CG
GAM390  KIAA0189 5' TCCTGGGCTCGCCTCCTGCC  28945          AAAC
                              GGCAGGAGGTGG   CCCAGGG
                              ||||||||||||   |||||||
                              CCGTCCTCCGCT   GGGTCCT
                                    C___
GAM390  KIAA0211 3' TCTTGGTGCCCCATCTCTTGTC 28288          AAACC
           T                   AGGCAGGAGGTGG    CCAGGG
                              ||||||||||||||    ||||||
                              TCTGTTCTCTACC    GGTTCT
                                    CCGT_
GAM390  KIAA0211 3' TTCTGGGAGGTTCCCGCTTGCT 28289      G    A   __
           GCCT                  AGGCAG AGGTGG AACC  CCAGGG
                              |||||| |||||| ||||  ||||||
                              TCCGTC TTCGCC TTGG  GGTCTT
                                 G    C   AG
GAM390  KIAA0212 3' TTCTGTTTTGTTTCTGTTTTCT 28632       TG    CC__
           GT                   GCAGGAGG  GAAAC   CAGGG
                              ||||||||  |||||   |||||
                              TGTCTTTT  CTTTG   GTCTT
                                 GT    TTTT
GAM390  KIAA0222 3' CCCCAGGGTTCTGTCCCCACTC 28393       AG   AAA_________  CCAG
           TTTGCCT               AGGCAGG  GTGG        CC   GG
                              |||||||  ||||        ||   ||
                              TCCGTTT  CACC        GG   CC
                                 CT   CCTGTCTT    GACC
GAM390  KIAA0222 3' TTCTGCATTTTCTGGCTTTTGT 28401       G    CCC
           TT                   AGGCAGGAG TGGAAA   CAGGG
                              |||||||||  ||||||   |||||
                              TTTGTTTTC GTCTTT   GTCTT
                                 G     TAC
GAM390  KIAA0227 3' TTGGACACTTTTTGTTTTTTGC 61358       TG   CC__   GG
           T                   GGCAGGAGG  GAAA   CCAG
                              |||||||||  ||||   ||||
                              TCGTTTTTT  TTTT   GGTT
                                 GT   CACA
GAM390  KIAA0229 3' CCAGGGTTTTACTTCATTTCCT 94024          AA________  CCAG
           GCC                  GGCAGGAGGTGGA       CC   G
                              ||||||||||||||       ||   |
                              CCGTCCTTTACTT       GG   C
                                    CATTTT    GACC
GAM390  KIAA0232 3' GGTCTTTCTCTTCTTGCTT   73122         T   AC____
                              AGGCAGGAGG GGAA     C
                              ||||||||||| ||||     |
                              TTCGTTCTTC CTTT     G
                                    T   CT   G
GAM390  KIAA0237 3' CCCCAGGGTTTGTTCTTCATCT 29216          AA_________  CCAG
           CCTGTCT               AGGCAGGAGGTGGA       CC   GG
                              ||||||||||||||       ||   ||
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                              TCTGTCCTCTACTT       GG   CC
                                     CTTGTTT    GACC
GAM390  KIAA0237 3' CCCTGCTTCCCTGCCTCCTCCT 29217    C     __   ACCC
                              AGG AGGAGGT  GGAA   CAGGG
                              ||| |||||||  ||||   |||||
                              TCC TCCTCCG  CCTT   GTCCC
                                _     TC   C___
GAM390  KIAA0237 3' CTCTGCTTTGTTTTCTGTCT  29220        TG  AACCC
                              AGGCAGGAGG  GA    CAGGG
                              ||||||||||  ||    |||||
                              TCTGTCTTTT  TT    GTCTC
                                    GT  C____
GAM390  KIAA0240 3' CTCTGGCCTTGTTTATGCTTCT 94038          G   C___
           TGTCT                 AGGCAGGAGGTG AAAC   CCAGGG
                              ||||||||||||| ||||   ||||||
                              TCTGTTCTTCGT TTTG   GGTCTC
                                     A   TTCC
GAM390  KIAA0240 3' CTTTATTTATTTTTATTTCTTG 94041            CCCC__  G
           TC                   GGCAGGAGGTGGAAA     AGG
                              ||||||||||||||     |||
                              CTGTTCTTTATTTTT     TTC
                                      ATTTAT
GAM390  KIAA0247 3' CCCTCTTGCCTCCTGCCT    29067         TG AAACCCC
                              AGGCAGGAGG  G      AGGG
                              ||||||||||  |      ||||
                              TCCGTCCTCC  T      TCCC
                                    GT C_______
GAM390  KIAA0252 3' CTTTGGCAAGAACTACATTTTG 63455        G   AAACC_
           TTT                   AGGCAGGA GTGG     CCAGGG
                              ||||||||| ||||     ||||||
                              TTTGTTTT CATC     GGTTTC
                                  A   AAGAAC
GAM390  KIAA0255 5' CCATTCTACTTTTGGTCT    29131      AG       ACCCCA
                              AGGC  GAGGTGGAA     GG
                              ||||  |||||||||     ||
                              TCTG  TTTCATCTT     CC
                                GT       A_____
GAM390  KIAA0255 3' TTTTGTGGGTTGCTTTTTCTT  29140       T  A    _
                              AGGAGG GG AACCC CAGGG
                              |||||| || ||||| |||||
                              TTCTTT TC TTGGG GTTTT
                                 T  G    T
GAM390  KIAA0257 3' CTGCGTTTTCACCACCTGTCT  71372        A       CC
                              AGGCAGG GGTGGAAAC  CAG
                              ||||||| |||||||||  |||
                              TCTGTCC CCACTTTTG  GTC
                                  A       C_
GAM390  KIAA0275 3' CTTGGTGCAACTCCTGCCT   29326         G  GAAACC
                              AGGCAGGAG TG     CCAGG
                              |||||||| ||     |||||
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                                TCCGTCCTC AC     GGTTC
                                    A  GT____
GAM390  KIAA0280 3' CCAGGGCTTTTTCTAATCTCCT 93293         _   A_______ CCAG
            GCCT                  AGGCAGGAGGT GGAA      CC   G
                                  |||||||||| ||||      ||   |
                                  TCCGTCCTCTA TCTT      GG   C
                                      A   TTTC    GACC
GAM390  KIAA0284 3' CCAGGGTTATTTTTGTCTTTAG 63803     A    TG  A_______ CCAG
            CTT                   AGGC GGAGG  GAA      CC   G
                                  |||| |||||  |||      ||   |
                                  TTCG TTTCT  TTT      GG   C
                                    A    GT   TATT    GACC
GAM390  KIAA0295 3' CCCTAGGTTTCTGCCTCCTCGT 68662     _    TG     CC
            TT                    AGGC AGGAGG  GAAACC  AGGG
                                  |||| ||||||  ||||||  ||||
                                  TTTG TCCTCC  CTTTGG  TCCC
                                    C     GT     A_
GAM390  KIAA0295 3' GGTTCTCTCTACTTCCTCTT   68669    C       AA_______
                                  AGG AGGAGGTGGA       CC
                                  ||| ||||||||||       ||
                                  TTC TCCTTCATCT       GG
                                   _        CTCTT
GAM390  KIAA0295 3' TCTTGGTAACACATATTTTGTT 68675        G   GAAACC
            T                     AGGCAGGA GTG     CCAGGG
                                  |||||||| |||     ||||||
                                  TTTGTTTT TAC     GGTTCT
                                      A   ACAAT_
GAM390  KIAA0295 3' TTCTGGGCCTTTGTTGTTTGTT 68678       AG TG  AAC
            T                     AGGCAGG  G  GA   CCCAGGG
                                  |||||||  |  ||   |||||||
                                  TTTGTTT  T  TT   GGGTCTT
                                      GT GT  CC_
GAM390  KIAA0298 3' CTCTGGGCCTCTCCTCCTGCTT 77077         T   AAC
                                  AGGCAGGAGG GGA   CCCAGGG
                                  |||||||||| |||   |||||||
                                  TTCGTCCTCC TCT   GGGTCTC
                                       _   CC_
GAM390  KIAA0303 5' CCAGGGTTTTTTTTTATTTTTG 69989     A       A________ CCAG
            GCCT                  AGGC GGAGGTGGAA       CC   G
                                  |||| ||||||||||       ||   |
                                  TCCG TTTTTATTTT       GG   C
                                    G        TTTTT    GACC
GAM390  KIAA0332 3' GGTCTTTTCATTTCCTCTT   63365    C       A_____
                                  AGG AGGAGGTGGAA     CC
                                  ||| ||||||||||     ||
                                  TTC TCCTTTACTTT     GG
                                   _         TCT
GAM390  KIAA0332 3' TCCTGGGGTTTTTTGTTTGTTT 63367       AGGT
                                  AGGCAGG   GGAAACCCCAGGG
                                  |||||||   ||||||||||||
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                                TTTGTTT   TTTTTGGGGTCCT
                                   GT__
GAM390  KIAA0339 3' CCCTGGAGGCAGCTTCTGCCT 71961        G  GAAA _
                                AGGCAGGAG TG   CC CCAGGG
                                ||||||||| ||   || ||||||
                                TCCGTCTTC AC   GG GGTCCC
                                   G _____ A
GAM390  KIAA0350 3' CTTTGGATATTTATTTCCGCTT 61828     A       AACC
                                AGGC GGAGGTGGA   CCAGGG
                                |||| |||||||||   ||||||
                                TTCG CCTTTATTT   GGTTTC
                                  _       ATA_
GAM390  KIAA0355 5' TTTTGGACATCTTTTATTTTTT 28714            ACC__
           GTC                    GGCAGGAGGTGGAA    CCAGGG
                                |||||||||||||    ||||||
                                CTGTTTTTTATTTT    GGTTTT
                                       CTACA
GAM390  KIAA0379 3' TTTGGGGTTAATTTGGCTT   68717     AG  GGTGGA
                                AGGC  GA     AACCCCAGG
                                ||||  ||     |||||||||
                                TTCG  TT     TTGGGGTTT
                                  GT  AA____
GAM390  KIAA0410 3' CCAGGGTTTTCTTTCTCCTTTT 29423         T    AC_______ CCAG
           GTTT                   AGGCAGGAGG GGAA       C    G
                                |||||||||| ||||       |   |
                                TTTGTTTTCC CTTT       G    C
                                      T   CTTTT   G GACC
GAM390  KIAA0426 3' TCCTGGATGATTATCTCTGTTT 28935       G     AAACC
                                AGGCAG AGGTGG    CCAGGG
                                |||||| ||||||    ||||||
                                TTTGTC TCTATT    GGTCCT
                                   _     AGTA_
GAM390  KIAA0446 5' TCCTGAAAAGCTGCCCTTGCTT 69461       A  TG AAACCC
                                AGGCAGG GG  G     CAGGG
                                ||||||| ||  |     |||||
                                TTCGTTC CC  C     GTCCT
                                    _  GT GAAAA_
GAM390  KIAA0447 3' CCCGGATTTCCATTTCTT    72114          C  CA
                                AGGAGGTGGAAA CC  GGG
                                |||||||||||| ||  |||
                                TTCTTTACCTTT GG  CCC
                                       A  __
GAM390  KIAA0449 5' TTTTGTTATTTTTATTTTTTGC 34643            CCC
           T                    GGCAGGAGGTGGAAA   CAGGG
                                |||||||||||||||   |||||
                                TCGTTTTTTATTTTT   GTTTT
                                       ATT
GAM390  KIAA0450 3' CCTCTCTCTCTTCTGCTT    28346        GT   AACCCC
                                AGGCAGGAG  GGA     AGG
                                |||||||||  |||     |||
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                                TTCGTCTTC  TCT     TCC
                                     TC   C_____
GAM390  KIAA0451  5'  CCAGGGTCTTTTTCTGTGTTTT 29767        GG    A_______  CCAG
              GCTT                  AGGCAGGA  TGGAA       CC    G
                                    ||||||||  |||||       ||    |
                                    TTCGTTTT  GTCTT       GG    C
                                       GT    TTTCT    GACC
GAM390  KIAA0455  3'  TTCTGCATAGTTTTTCTTCTGC 72887         TG    CC__
              TT                     AGGCAGGAGG  GAAAC   CAGGG
                                    ||||||||||  |||||   |||||
                                    TTCGTCTTCT  TTTTG   GTCTT
                                       __    ATAC
GAM390  KIAA0459  3'  CTTGGATCATCTTTGTCT    61652       G     AAACC
                                    AGGCAG AGGTGG    CCAGG
                                    ||||||||||||     |||||
                                    TCTGTT TCTACT    GGTTC
                                       _     A____
GAM390  KIAA0461  3'  CCCTGCTTTTTTGTTTGTTTGT 71394        _  TG    CCC
              TT                     AGGCAGG AGG  GAAA   CAGGG
                                    |||||||  |||  ||||   |||||
                                    TTTGTTT TTT  TTTT   GTCCC
                                       G   GT    TC_
GAM390  KIAA0469  3'  CCTTGGCTTGAGTTTTTGTCCT 29979        A  TG    C____
              TGCCT                  AGGCAGG GG  GAAAC    CCAGGG
                                    |||||||  ||  |||||    ||||||
                                    TCCGTTC CT  TTTTG    GGTTCC
                                       _ GT    AGTTC
GAM390  KIAA0481  3'  GGTTCTGTTCTTTCTGCCT    72324         T__   AA__
                                    AGGCAGGAGG   GGA    CC
                                    ||||||||||   |||    ||
                                    TCCGTCTTTC   TCT    GG
                                         TTG   T
GAM390  KIAA0494  3'  TCTTGGTCCTTGTTTTCTTTTG 29404          TG AAACC_
              CCT                     AGGCAGGAGG  G     CCAGGG
                                    ||||||||||  |     ||||||
                                    TCCGTTTTCT  T     GGTTCT
                                         TT GTTCCT
GAM390  KIAA0495  3'  CTCTGGGACATGTCTTCTGCC  63264        GT GAAAC
                                    GGCAGGAG  G    CCCAGGG
                                    ||||||||  |    |||||||
                                    CCGTCTTC  T    GGGTCTC
                                       TG ACA__
GAM390  KIAA0530  3'  CCAGGGTCACATTTCATTTCTT 71430             A_______  CCAG
              GTTT                    AGGCAGGAGGTGGAA       CC    G
                                    ||||||||||||||||       ||    |
                                    TTTGTTCTTTACTTT       GG    C
                                          ACACT    GACC
GAM390  KIAA0537  3'  CCAGGGTTCAATTCCACCTCCT 29925     C         A_______  CCAG
              TCCT                    AGG AGGAGGTGGAA       CC    G
                                    |||  ||||||||||       ||    |
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                                TCC TCCTCCACCTT      GG   C
                                  T         AACTT    GACC
GAM390  KIAA0537 3' CCTTGCTGTTCACCTCCTCTT 29926    C       AACCC
                                AGG AGGAGGTGGA    CAGGG
                                ||| ||||||||||    |||||
                                TTC TCCTCCACTT    GTTCC
                                  _       GTC__
GAM390  KIAA0537 3' GGTTTTTGTTTCTGTTT    29933      G  TG
                                AGGCAG AGG  GAAACC
                                |||||| |||  ||||||
                                TTTGTC TTT  TTTTGG
                                   _  GT
GAM390  KIAA0545 3' TTTTGGTTTTGTTTTCTGTT  63848        TG  ACC
                                GGCAGGAGG  GAA  CCAGGG
                                |||||||||  |||  ||||||
                                TTGTCTTTT  TTT  GGTTTT
                                     GT  ___
GAM390  KIAA0551 3' TTTCAGGTTTTTACCTTTTTTC 67382    C         CCAGGG
           T                     AGG AGGAGGTGGAAACC
                                 ||| ||||||||||||||
                                 TCT TTTTCCATTTTTGG
                                   T          ACTTTT
GAM390  KIAA0553 3' CCAGGGTTTTGCCCCTCTTCTT 70444        T  AAA_______  CCAG
           GCCT                   AGGCAGGAGG GG       CC   G
                                  |||||||||| ||       ||   |
                                  TCCGTTCTTC CC       GG   C
                                       T  CCGTTTT    GACC
GAM390  KIAA0553 3' CCCCAGGGTCCTCCCTCTGCTT 70445     GA  T   AA_  CCAG
                                AGGCAG  GG GGA   CC   GG
                                ||||||  || |||   ||   ||
                                TTCGTC  CC CCT   GG   CC
                                   TC  T      GACC
GAM390  KIAA0553 3' TCTGGCTGCCTCTTTGCCT   70453      _   TG AAACC
                                AGGCAG GAGG  G    CCAGG
                                |||||| ||||  |    |||||
                                TCCGTT CTCC  C    GGTCT
                                   T   GT _____
GAM390  KIAA0555 3' CAGGGTTCTGACCTCTTCTTGT 60736        T  AAA______  CCAG
           TT                    AGGCAGGAGG GG       CC   G
                                 |||||||||| ||       ||   |
                                 TTTGTTCTTC CC       GG   C
                                      T  AGTCTT    GAC
GAM390  KIAA0555 3' CAGGGTTTTCTTCACTTTCTGT 60737         AA______  CCAG
           T                     GGCAGGAGGTGGA      CC   G
                                 ||||||||||||       ||   |
                                 TTGTCTTTCACTT      GG   C
                                       CTTTT    GAC
GAM390  KIAA0555 3' CAGGGCTTGTTTTTTCTTTTTG 29547        TG   _______  CAG
           CTT                    AGGCAGGAGG  GAAAC    CC   G
                                  |||||||||  |||||    ||   |
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                                TTCGTTTTTC  TTTTG     GG   C
                                      TT     TTC     GAC
GAM390  KIAA0557  3'  CCTTCACCTTCCAGCTTTTGTC 78553         G    ACCCC   G
              T                    AGGCAGGAG TGGAA     AGG
                                   ||||||||| |||||     |||
                                   TCTGTTTTC ACCTT     TCC
                                         G    CCACT
GAM390  KIAA0560  3'  CCCCAGGGTCTTACCTTTGTTT 62172       G   TG  AA_________  CCAG
              GCTGTCT                 AGGCAG AGG  GA        CC    GG
                                   |||||| |||  ||         ||    ||
                                   TCTGTC TTT  TT         GG    CC
                                      G   GT  CCATTCT     GACC
GAM390  KIAA0563  3'  TCTGCTTTCACCTTTGCTT    29891       G       ACCC
                                   AGGCAG AGGTGGAA    CAGG
                                   |||||| ||||||||    ||||
                                   TTCGTT TCCACTTT    GTCT
                                      _       C___
GAM390  KIAA0564  3'  CCAGGGTTATTTTTATTTTCTC 66791     C         A_______  CCAG
              CCT                    AGG AGGAGGTGGAA      CC    G
                                   ||| ||||||||||       ||    |
                                   TCC TCTTTTATTTT      GG    C
                                     C          TATT     GACC
GAM390  KIAA0574  3'  CTTTGGGGATTGCATTTCCTGC 69814           G  A
              CT                     AGGCAGGAGGTG AA CCCCAGGG
                                   |||||||||||| || ||||||||
                                   TCCGTCCTTTAC TT GGGGTTTC
                                         G  A
GAM390  KIAA0628  3'  TCTGTTCGTGCCTTTTGCCT   29537           _   ACCC
                                   AGGCAGGAGGTG GAA    CAGG
                                   |||||||||||| |||    ||||
                                   TCCGTTTTCCGT CTT    GTCT
                                         G   ____
GAM390  KIAA0630  3'  CCAGGGCTTTTTTTGCTTTCTC 90949     C     TG   A_______  CCAG
              CCT                     AGG AGGAGG  GAA      CC    G
                                   ||| ||||||  |||      ||    |
                                   TCC TCTTTC  TTT      GG    C
                                     C     GT   TTTC     GACC
GAM390  KIAA0633  3'  TTTTGGTGTTACTTTCTTGTCT 95705         GT  A   C
                                   AGGCAGGAG  GG AAC CCAGGG
                                   |||||||||  || ||| ||||||
                                   TCTGTTCTT  TC TTG GGTTTT
                                         __  A   T
GAM390  KIAA0648  3'  CTTGGTTCCAGTTCCTGCCT   83541         G    ACC
                                   AGGCAGGAG TGGAA   CCAGG
                                   ||||||||| |||||   |||||
                                   TCCGTCCTT ACCTT   GGTTC
                                         G    ___
GAM390  KIAA0650  3'  TTTTGGAACATTTCTTGTTT   89612           GAAACC
                                   AGGCAGGAGGTG     CCAGGG
                                   ||||||||||||     ||||||
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                                TTTGTTCTTTAC     GGTTTT
                                      AA____
GAM390  KIAA0652  3'  CCAGGGTCTTCTTCTCTCTCTT 29121        GT   AC_______ CCAG
                GCCT                  AGGCAGGAG  GGAA       C   G
                                      |||||||||  ||||       |   |
                                      TCCGTTCTC  TCTT       G   C
                                         TC    CTTCT   G GACC
GAM390  KIAA0652  3'  TCCTGCTGCCGGCCTCCTGCCT 29123          _  AAACCC
                                      AGGCAGGAGGT GG     CAGGG
                                      ||||||||||| ||     |||||
                                      TCCGTCCTCCG CC     GTCCT
                                            G  GTC___
GAM390  KIAA0657  3'  CCCTGCCATTGCTTTTTGCCT  72650          TG AAACCC
                                      AGGCAGGAGG  G      CAGGG
                                      ||||||||||  |      |||||
                                      TCCGTTTTTC  T      GTCCC
                                            GT ACC___
GAM390  KIAA0672  3'  CAGGGTTTTGATCCACTTTCAG 30047      A       AA_______  CCAG
                CCT                     AGGC GGAGGTGGA       CC   G
                                        |||| |||||||||       ||   |
                                        TCCG CTTTCACCT       GG   C
                                          A       AGTTTT    GAC
GAM390  KIAA0674  3'  TCCTGGGACATGTATCTTCTTC 61245     C       GAAAC
                TT                    AGG AGGAGGTG    CCCAGGG
                                      ||| ||||||||    |||||||
                                      TTC TCTTCTAT    GGGTCCT
                                        T       GTACA
GAM390  KIAA0677  3'  CCCTGGCCTTTACTTTCTTCCT 28530     C        AACC
                                      AGG AGGAGGTGGA   CCAGGG
                                      ||| ||||||||||   ||||||
                                      TCC TCTTTCATTT   GGTCCC
                                        T        CC__
GAM390  KIAA0689  3'  GGTTTTCTTTCTTTCTGTTT   31528          T__   A___
                                      AGGCAGGAGG   GGAA   CC
                                      ||||||||||   ||||   ||
                                      TTTGTCTTTC   CTTT   GG
                                            TTT    T
GAM390  KIAA0716  3'  CAGGGTTTTGAACTAGCTTTTG 28835         G   AAA_______  CCAG
                CTT                     AGGCAGGAG TGG        CC   G
                                        ||||||||| |||        ||   |
                                        TTCGTTTTC ATC        GG   C
                                           G   AAGTTTT    GAC
GAM390  KIAA0721  3'  CAGGGTCTTCCATCTGCTTTCT 97655     C  G       AC____ CCAG
                                      AGG AG AGGTGGAA     C   G
                                      ||| || ||||||||     |   |
                                      TCT TC TCTACCTT     G   C
                                        T  G       CT   G GAC
GAM390  KIAA0757  3'  TTTTGGGGTTTTGTTTTGTTTT 21262        GGTG__
                GTTT                    AGGCAGGA     GAAACCCCAGGG
                                        ||||||||     ||||||||||||
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                                TTTGTTTT     TTTTGGGGTTTT
                                     GTTTTG
GAM390  KIAA0759 3'  TCCACCACTTTTTACTTTCTGC 67892            CCCCA
             T                    GGCAGGAGGTGGAAA    GGG
                                  ||||||||||||||    |||
                                  TCGTCTTTCATTTTT    CCT
                                       CACCA
GAM390  KIAA0773 3'  CCCCAGGGTTCTCCATTTCACT 28721        ____    AA____  CCAG
             CTTGCTT                AGGCAGGAG   GTGGA    CC   GG
                                  |||||||||   |||||    ||   ||
                                  TTCGTTCTC   TACCT    GG   CC
                                       ACTT    CTT    GACC
GAM390  KIAA0783 3'  TCCTATTTTTCTTCTTTTTGCT 28505         T    CCCC
             T                    AGGCAGGAGG GGAAA    AGGG
                                  |||||||||| |||||    ||||
                                  TTCGTTTTTC TCTTT    TCCT
                                       T    TTA_
GAM390  KIAA0794 3'  GGCTTTCTCCTCTTCTGTTT  81233         T  AA_______
                                  AGGCAGGAGG GGA      CC
                                  |||||||||| |||      ||
                                  TTTGTCTTCT CCT      GG
                                       _  CTTTC
GAM390  KIAA0820 3'  CTTTGTTTTGCTTGCTTGTCT  69589       _  TG   ACCC
                                  AGGCAGG AGG  GAA    CAGGG
                                  ||||||| |||  |||    |||||
                                  TCTGTTC TTC  TTT    GTTTC
                                     G   GT  _____
GAM390  KIAA0820 3'  TTTGGGGATCATTTGCCT    69593       A   GGAAA
                                  AGGCAGG GGT    CCCCAGG
                                  ||||||| |||    |||||||
                                  TCCGTTT CTA    GGGGTTT
                                     A  ______
GAM390  KIAA0820 3'  TTTTGGGTCAAATTTTTCTTTT 69594         TG  AAC__
             GCTT                   AGGCAGGAGG  GA    CCCAGGG
                                  ||||||||||  ||    |||||||
                                  TTCGTTTTCT  TT    GGGTTTT
                                       TT  AAACT
GAM390  KIAA0828 3'  CCAGGGTTCAGTTCTTCCTTTT 82112         T   AC_______ CCAG
             GCCT                   AGGCAGGAGG GGAA       C   G
                                  |||||||||| ||||       |   |
                                  TCCGTTTTCC TCTT       G   C
                                       T   GACTT   G GACC
GAM390  KIAA0855 3'  CCAGGGCTTTCCTCCATTTTCT 31108          AA_______  CCAG
             GT                   GCAGGAGGTGGA       CC   G
                                  ||||||||||||       ||   |
                                  TGTCTTTTACCT       GG   C
                                       CCTTTC    GACC
GAM390  KIAA0871 3'  CCCATTTTTCGTATCCTGCTT  31019       GG     CCCCA
                                  AGGCAGGA  TGGAAA    GG
                                  ||||||||  ||||||    ||
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                              TTCGTCCT  GCTTTT    CC
                                 AT     TAC__
GAM390  KIAA0871  3'  TCCTGCAATTCCGCTTCCTACT 31021     C        ACCC
          T                   AGG AGGAGGTGGAA    CAGGG
                              ||| ||||||||||    |||||
                              TTC TCCTTCGCCTT    GTCCT
                                A         AAC_
GAM390  KIAA0872  3'  CTTTGTTTTTTACCTTCTGTCT 30755             CCC
                              AGGCAGGAGGTGGAAA   CAGGG
                              ||||||||||||||||   |||||
                              TCTGTCTTCCATTTTT   GTTTC
                                        T__
GAM390  KIAA0876  3'  TCCTGGGGTTTGTCTATCTTTG 65320       G     __
          TTT                   AGGCAG AGGTGGA  AACCCCAGGG
                              ||||||| |||||||  ||||||||||
                              TTTGTT TCTATCT  TTGGGGTCCT
                                 _      GT
GAM390  KIAA0882  3'  CTCATGACAGGTTTTTGCTTTT 83534       G   TG     C__ _
          GCTT                   AGGCAG AGG  GAAACC   CA GGG
                              |||||| |||  ||||||   || |||
                              TTCGTT TTC  TTTTGG   GT CTC
                                 _  GT     ACA  A
GAM390  KIAA0894  3'  CCAGGGTTTTGCTCACCTTTTG 30330           AAA_______  CCAG
          CCT                   AGGCAGGAGGTGG        CC    G
                              ||||||||||||        ||    |
                              TCCGTTTTCCACT       GG    C
                                    CGTTTT     GACC
GAM390  KIAA0912  3'  GGTTTTTCTATCTTTTCTT    65043     C        A_____
                              AGG AGGAGGTGGAA      CC
                              ||| ||||||||||      ||
                              TTC TTTTCTATCTT      GG
                                _         TTT
GAM390  KIAA0924  3'  TCCTGTCCTCCATGTTCTGCTT 30377         G     AACCC
                              AGGCAGGA GTGGA     CAGGG
                              |||||||| |||||     |||||
                              TTCGTCTT TACCT     GTCCT
                                   G    CCT__
GAM390  KIAA0931  3'  CCAGGGTCACTTTTTACTTCCT 68006     C        A________  CCAG
          TCT                   AGG AGGAGGTGGAA       CC    G
                              ||| ||||||||||       ||    |
                              TCT TCCTTCATTTT       GG    C
                                _         TCACT     GACC
GAM390  KIAA0931  3'  CCCTGGGTTCAAGCCATTCTCC 68008          _  AAAC__
          TGTCT                  AGGCAGGAGG TGG     CCCAGGG
                              |||||||||| |||     |||||||
                              TCTGTCCTCT ACC     GGGTCCC
                                    T   GAACTT
GAM390  KIAA0939  3'  TTCTGGGTCAGTTTTTTTTGCC 62725          TG__  AAC
          T                   AGGCAGGAGG    GA   CCCAGGG
                              ||||||||||    ||   |||||||
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                                TCCGTTTTTT   CT  GGGTCTT
                                     TTGA  ___
GAM390  KIAA0971  3'  TTCTGTGACTTTCACCTCTTTC 30678    C        ACCC
            T                   AGG AGGAGGTGGAA   CAGGG
                                ||| ||||||||||   |||||
                                TCT TTCTCCACTTT   GTCTT
                                  _        CAGT
GAM390  KIAA0977  3'  CCAGGGTTTTGATCTTTTTTTT 30434         T  AA_______  CCAG
            GCCT                  AGGCAGGAGG GGA       CC   G
                                ||||||||| |||       ||   |
                                TCCGTTTTTT TCT       GG   C
                                     T  AGTTTT   GACC
GAM390  KIAA0978  3'  CTTGCCTTGTTTCCTGCCT   70993         TG AAACCC
                                AGGCAGGAGG  G    CAGG
                                |||||||||  |    ||||
                                TCCGTCCTTT  T    GTTC
                                     GT CC____
GAM390  KIAA0982  3'  TTTATAGTTTTTCATGTTTTGC 26713       G  _    CCCAGGG
            TT                   AGGCAGGA GTG GAAAC
                                ||||||||| ||| |||||
                                TTCGTTTT TAC TTTTG
                                    G  T   ATATTTT
GAM390  KIAA0997  3'  CTTGTAGTTTTACTTCTTTCT  30888    C      G   CC
                                AGG AGGAGGTG AAAC  CAGG
                                ||| |||||||| ||||  ||||
                                TCT TTCTTCAT TTTG  GTTC
                                  _      _   AT
GAM390  KIAA1029  3'  CCTGTGTCCTGCCTCTTGCCT  24425         _  AACCC
                                AGGCAGGAGGT GGA    CAGG
                                ||||||||||| |||    ||||
                                TCCGTTCTCCG CCT    GTCC
                                     T  GT___
GAM390  KIAA1030  3'  CCTGTCCTCACCTCTGCTT   94976      G    AAACCC
                                AGGCAG AGGTGG     CAGG
                                |||||| ||||||     ||||
                                TTCGTC TCCACT     GTCC
                                   _     CCT___
GAM390  KIAA1042  3'  CCCACATGCTTTTCCTTCTTGT 31047         T   CCCCA_
            TT                   AGGCAGGAGG GGAAA     GGG
                                |||||||||| |||||     |||
                                TTTGTTCTTC CTTTT     CCC
                                     _    CGTACA
GAM390  KIAA1046  5'  GGTTTTCTCCTCTTTTGTTT   30663     __    T   A____
                                AGGCA  GGAGG GGAA    CC
                                |||||  ||||| ||||    ||
                                TTTGT  TCTCC TCTT    GG
                                   TT    _   TT
GAM390  KIAA1046  3'  TCCTGTTTATTTTTCTATGTTC 30664       G     CCC___
            TGTTT                 AGGCAGGA GTGGAAA     CAGGG
                                |||||||| |||||||     |||||
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                                TTTGTCTT TATCTTT     GTCCT
                                    G      TTATTT
GAM390  KIAA1056 3' CCCCAGGGTTTTCCCTCTATCT 30313          AA_________  CCAG
            TCTGT                GCAGGAGGTGGA        CC    GG
                                ||||||||||||        ||    ||
                                TGTCTTCTATCT        GG    CC
                                     CCCTTTT    GACC
GAM390  KIAA1061 3' CCTTTTTTTTTTCCTGCCT    71719         TG   ACCCC
                                AGGCAGGAGG  GAA    AGG
                                ||||||||||  |||    |||
                                TCCGTCCTTT  TTT    TCC
                                     TT  _____
GAM390  KIAA1061 3' GTCCTTTCACTCCTGCCT    71724         G    AC_____
                                AGGCAGGAG TGGAA      C
                                |||||||||| |||||      |
                                TCCGTCCTC ACTTT      G
                                    _    CCT   G
GAM390  KIAA1076 3' CAGGGTTCTGCTATTTTTTGCT 66119          AAA_____  CCAG
            T                    AGGCAGGAGGTGG       CC    G
                                ||||||||||||||       ||    |
                                TTCGTTTTTTATC       GG    C
                                      GTCTT     GAC
GAM390  KIAA1077 5' CTCTGCTCCTCTGCCTCCTCCC 73287     C     TG  AACCC
            T                    AGG AGGAGG  GA     CAGGG
                                ||| ||||||  ||     |||||
                                TCC TCCTCC  CT     GTCTC
                                  C     GT  CCTC_
GAM390  KIAA1077 3' GGTTTTGATTTTTTGCTT    73290          G
                                AGGCAGGAGGT GAAACC
                                |||||||||||| ||||||
                                TTCGTTTTTTA TTTTGG
                                      G
GAM390  KIAA1091 3' CCAGGGTCCTCTATCACCTCCT 70259           AAA________  CCAG
            GTCT                   AGGCAGGAGGTGG        CC    G
                                ||||||||||||||        ||    |
                                TCTGTCCTCCACT        GG    C
                                      ATCTCCT    GACC
GAM390  KIAA1096 3' TTCTGGGGTTTTGTTTTTTACC 69061     C     TG   A
            T                    AGG AGGAGG  GAA CCCCAGGG
                                ||| ||||||  ||| ||||||||
                                TCC TTTTTT  TTT GGGGTCTT
                                  A     GT  _
GAM390  KIAA1102 3' CTGGTTTTTTGTTTTTTGTT   69584         TG    CC
                                GGCAGGAGG  GAAA  CCAG
                                |||||||||  ||||  ||||
                                TTGTTTTTT  TTTT  GGTC
                                     GT    T_
GAM390  KIAA1128 3' CTTTGGTACCGCCTCCAGTTT  69004      A       AAACC
                                AGGC GGAGGTGG    CCAGGG
                                |||| ||||||||    ||||||
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                                TTTG CCTCCGCC    GGTTTC
                                  A      AT___
GAM390  KIAA1130 3' CCTGTTCTGTTTTTGCTT   63087      G   TG  ACCC
                                AGGCA GAGG  GAA   CAGG
                                ||||| ||||  |||   ||||
                                TTCGT TTTT  CTT   GTCC
                                  _   GT   ____
GAM390  KIAA1130 3' TTCTGTGCTACTCCCTTCCTGT 63104         T  AACCC_
           CT                    AGGCAGGAGG GGA     CAGGG
                                |||||||||| |||     |||||
                                TCTGTCCTTC CCT     GTCTT
                                      _  CATCGT
GAM390  KIAA1136 3' GTTCTTTTATCTCTTCCT   92961    C        AC_____
                                AGG AGGAGGTGGAA      C
                                ||| ||||||||||      |
                                TCC TTCTCTATTTT      G
                                  _        CTT   G
GAM390  KIAA1143 3' TCCTGGGTTCACACCATTCTCT 69252         _  AAAC__
           TGCCT                   AGGCAGGAGG TGG     CCCAGGG
                                |||||||||| |||     |||||||
                                TCCGTTCTCT ACC     GGGTCCT
                                      T   ACACTT
GAM390  KIAA1157 3' CCTTTGGTTTCCATTTCTTCTT 72698    C          CC   G
                                AGG AGGAGGTGGAAACC  AGG
                                ||| ||||||||||||  |||
                                TTC TTCTTTACCTTTGG  TCC
                                  _           TT
GAM390  KIAA1161 5' ATAAGAGGTTTCCCCTTTTGCT 82638         T     CCAGGG
           T                     AGGCAGGAGG GGAAACC
                                |||||||||| |||||||
                                TTCGTTTTCC CCTTTGG
                                      _      AGAATAT
GAM390  KIAA1161 3' ATAAGGGGTTTCCCCTTTTGCT 82639         T       AGGG
           T                     AGGCAGGAGG GGAAACCCC
                                |||||||||| |||||||||
                                TTCGTTTTCC CCTTTGGGG
                                      _       AATAA
GAM390  KIAA1161 3' CAGGGCTCTCATTCTCTCTTGT 82641         T  AA_______  CCAG
           CT                    AGGCAGGAGG GGA       CC   G
                                |||||||||| |||       ||   |
                                TCTGTTCTCT CTT       GG   C
                                      _  ACTCTC    GAC
GAM390  KIAA1161 5' CCAGGGTTCTCATTCTCTCTTG 82643         T  AA_______  CCAG
           CCT                    AGGCAGGAGG GGA       CC   G
                                |||||||||| |||       ||   |
                                TCCGTTCTCT CTT       GG   C
                                      _  ACTCTT    GACC
GAM390  KIAA1169 5' CCACAGGTTTCTGTGTTTTGCT 35879       G TG     CCA  G
           T                     AGGCAGGA G  GAAACC   GG
                                |||||||| |  ||||||   ||
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                                TTCGTTTT T  CTTTGG   CC
                                    G GT     ACA
GAM390  KIAA1170 3' CTTTGGTAGGACCTTTTCCTGC 70415          T  AAA  __
            TT                   AGGCAGGAGG GG   CC  CCAGGG
                                ||||||||||  ||   ||  ||||||
                                TTCGTCCTTT CC   GG  GGTTTC
                                     T  A__  AT
GAM390  KIAA1189 3' TCCACAATTTTTCATTTCATGC 72510       G        CCCCA
            TT                   AGGCA GAGGTGGAAA     GGG
                                ||||| ||||||||||     |||
                                TTCGT CTTTACTTTT     CCT
                                  A         TAACA
GAM390  KIAA1190 3' CTTGGGGCTCTCTGGTCT    71647      A    TGGAAA
                                AGGC GGAGG     CCCCAGG
                                |||| |||||     |||||||
                                TCTG TCTCT     GGGGTTC
                                  G    C_____
GAM390  KIAA1193 3' CCTTGGGGTAGCACCTCCTTCT 68265          T  AA__
            GCTT                   AGGCAGGAGG GG    ACCCCAGGG
                                ||||||||||  ||    |||||||||
                                TTCGTCTTCC CC    TGGGGTTCC
                                     T  ACGA
GAM390  KIAA1193 3' CTCGTTCGTTTCTGTTTCTGTT 68268       G   TG    CCCA
            T                    AGGCAG AGG  GAAAC    GGG
                                ||||||  |||  |||||    |||
                                TTTGTC TTT  CTTTG    CTC
                                   _  GT    CTTG   T
GAM390  KIAA1196 3' CCTTGCTTCTGTTTTCTACCT  62149     C     TG   ACCC
                                AGG AGGAGG  GAA    CAGGG
                                |||  ||||||  |||    |||||
                                TCC TCTTTT  CTT    GTTCC
                                  A     GT   C___
GAM390  KIAA1198 3' TCCTGGGTTCACGCCATTCTCC 64068          _  AAAC__
            TGCCT                  AGGCAGGAGG TGG     CCCAGGG
                                ||||||||||  |||     |||||||
                                TCCGTCCTCT ACC     GGGTCCT
                                     T   GCACTT
GAM390  KIAA1200 3' CCAGGGTTCTTTCATCTTTTGC 63034             AC_____ CCAG
            CT                   AGGCAGGAGGTGGAA      C    G
                                ||||||||||||||      |   |
                                TCCGTTTTCTACTTT      G    C
                                       CTT   G GACC
GAM390  KIAA1202 3' CTTTGGTCCTACCACCTCTTGT 72489            AAACC
            TT                   AGGCAGGAGGTGG    CCAGGG
                                ||||||||||||    ||||||
                                TTTGTTCTCCACC    GGTTTC
                                       ATCCT
GAM390  KIAA1205 3' CCCTGCTCCCACTACCCTTTGT 70581       GA    AAACCC
            CT                   AGGCAG  GGTGG     CAGGG
                                ||||||  |||||     |||||
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                              TCTGTT  CCATC     GTCCC
                                 TC    ACCCTC
GAM390  KIAA1238 3' CCAGGGTGTGTTTTGCTTTTTG 71632         TG   AC_______ CCAG
            TTT                AGGCAGGAGG  GAA       C    G
                              ||||||||||  |||       |   |
                              TTTGTTTTTC  TTT       G    C
                                   GT   GTGT   G GACC
GAM390  KIAA1238 3' CCCAGGGTTTGTTTTTTTCCTT 71633         T_     _______  CAG
            TTGTTT               AGGCAGGAGG  GGAAAC     CC   GG
                              ||||||||||  ||||||     ||   ||
                              TTTGTTTTCC  TTTTTG     GG   CC
                                   TT     TTT    GAC
GAM390  KIAA1243 3' TTCTGGGTTTGTGTTTTGCCT  74031        G TG  AAC
                              AGGCAGGA G  GA   CCCAGGG
                              ||||||||  |  ||   |||||||
                              TCCGTTTT T  TT   GGGTCTT
                                   G GT  ___
GAM390  KIAA1244 3' TCTGTTTGCCTTCAGTTT    72451      A    TG  AACCC
                              AGGC GGAGG  GA    CAGG
                              |||| |||||  ||    ||||
                              TTTG CTTCC  TT    GTCT
                                A    GT  _____
GAM390  KIAA1247 3' CCAGGGTCCATTTTTGCCCCTG 62507        A   GG  A_______  CCAG
            CTT                AGGCAGG GGT  AA       CC    G
                              |||||||  |||  ||       ||    |
                              TTCGTCC CCG  TT       GG    C
                                 _   TT  TACCT    GACC
GAM390  KIAA1254 3' CCCCAGGGTCTTACACTCACTT 70558          AAA_________  CCAG
            CTTGTCT               AGGCAGGAGGTGG         CC    GG
                              ||||||||||||||         ||    ||
                              TCTGTTCTTCACT         GG    CC
                                    CACATTCT    GACC
GAM390  KIAA1265 3' CTTTGGGGAGACATTTTTTGT  71337         GAAA
                              GCAGGAGGTG    CCCCAGGG
                              ||||||||||    ||||||||
                              TGTTTTTTAC    GGGGTTTC
                                   AGA_
GAM390  KIAA1266 3' CCCTCACCCTTTCACTTTCTCT 66693     C         ACCCC
            CT                 AGG AGGAGGTGGAA     AGGG
                              |||  ||||||||||     ||||
                              TCT TCTTTCACTTT     TCCC
                                C          CCCAC
GAM390  KIAA1271 3' CCAGGGCCTTACTTTATCTTGT 70133       G       AA_______  CCAG
            GCCT                 AGGCA GAGGTGGA        CC    G
                              |||||  ||||||||        ||    |
                              TCCGT TTCTATTT        GG    C
                                G       CATTCC    GACC
GAM390  KIAA1280 5' TCCTGATGCTTTTCACACTTCT 70290          _   CCC__
            TGTCT                AGGCAGGAGGTG GAAA     CAGGG
                              ||||||||||| ||||     |||||
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                                TCTGTTCTTCAC CTTT    GTCCT
                                      A   TCGTA
GAM390  KIAA1317 3' AATTTTGGTTTTTCCTTTTGTT 87206         T     CCAGGG
           T                   AGGCAGGAGG GGAAACC
                               |||||||||| |||||||
                               TTTGTTTTCC TTTTTGG
                                     _      TTTTAAT
GAM390  KIAA1319 3' TCCTATATTTTTGTCTTCTTCC 40792    C     TG   CCCC
           T                   AGG AGGAGG  GAAA   AGGG
                               ||| ||||||  ||||   ||||
                               TCC TCTTCT  TTTT   TCCT
                                 T    GT   ATA_
GAM390  KIAA1320 5' TCCTAGCAGGTTTTTTTTTTG 69850         T     CC__
           TTT                   AGGCAGGAGG GGAAACC   AGGG
                               |||||||||| |||||||   ||||
                               TTTGTTTTTT TTTTTGG   TCCT
                                     _      ACGA
GAM390  KIAA1323 3' CCAGGGCTTTGCATTTCTCTTG 63724         __ G  A____  CCAG
           TTT                   AGGCAGGAGG  TG AA    CC   G
                               ||||||||||  || ||    ||   |
                               TTTGTTCTCT  AC TT    GG   C
                                     TT  G  TC    GACC
GAM390  KIAA1324 5' CCCCAGGGTTTTTTTCCGCCTT 68649           _________  CCA
           CTGCC                 GGCAGGAGGTGGAAA      CC   GG
                               ||||||||||||||       ||   ||
                               CCGTCTTCCGCCTTT      GG   CC
                                     TTTT   G  ACC
GAM390  KIAA1332 3' CCAGGGTTTTCTTCTACCTTTT 71704    C        AC________ CCAG
           TTCT                   AGG AGGAGGTGGAA       C    G
                               ||| ||||||||||       |   |
                               TCT TTTTCCATCTT       G    C
                                 T        CTTTT   G GACC
GAM390  KIAA1332 3' TCTGTCAATTTCATTTTTTGTT 71708           ACCC    G
                               GGCAGGAGGTGGAA    CAGG
                               ||||||||||||||   ||||
                               TTGTTTTTTACTTT    GTCT
                                     AACT
GAM390  KIAA1332 3' TTTGGAGTGCTTCTTGT    71711         GGAA  C
                               GCAGGAGGT    AC CCAGG
                               |||||||||   || |||||
                               TGTTCTTCG    TG GGTTT
                                     ____  A
GAM390  KIAA1336 3' TCTTGGGGACCTTTGTCTTCTG 72788        TG  AA_
           T                   GCAGGAGG  GA   CCCCAGGG
                               ||||||||  ||   ||||||||
                               TGTCTTCT  TT   GGGGTTCT
                                    GT  CCA
GAM390  KIAA1348 3' GGTTTCCTGTTTTTTGTCT    69127        GG _
                               AGGCAGGA  T GGAAACC
                               ||||||||  | |||||||
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                                TCTGTTTT  G CCTTTGG
                                    TT T
GAM390  KIAA1349 3' CCAGGGTTCTATTCATTTATCT 71293       _     AA_______ CCAG
            GTCT                  AGGCAGG AGGTGGA       CC    G
                                  ||||||| |||||||       ||    |
                                  TCTGTCT TTTACTT       GG    C
                                     A      ATCTT     GACC
GAM390  KIAA1431 3' CCAGGGTCCTATCTGCTGCTT  63679       G     AAA__  CCAG
                                  AGGCAG AGGTGG     CC    G
                                  |||||| ||||||     ||    |
                                  TTCGTC TCTATC     GG    C
                                     G     CT     GACC
GAM390  KIAA1434 3' CCAGGGTTCTGTCCTATCTCTT 70210     C     _   AA_______ CCAG
            CCT                   AGG AGGAGGT GGA       CC    G
                                  ||| ||||||| |||       ||    |
                                  TCC TTCTCTA CCT       GG    C
                                   _      T   GTCTT     GACC
GAM390  KIAA1434 3' CCTGCTCACTTTCTGTC     70211           AAACCC
                                  GGCAGGAGGTGG     CAGG
                                  ||||||||||||     ||||
                                  CTGTCTTTCACT     GTCC
                                        C_____
GAM390  KIAA1437 3' TCCTGGGGAGGGAGGTTTTTTT 61220          TGGAAA__
            GTTT                  AGGCAGGAGG       CCCCAGGG
                                  ||||||||||       ||||||||
                                  TTTGTTTTTT       GGGGTCCT
                                       TGGAGGGA
GAM390  KIAA1437 3' TTGTGGCAGTTTTAGTTTTTTG 61223         TG    C_   GGG
            TTT                   AGGCAGGAGG  GAAAC  CCA
                                  ||||||||||  |||||  |||
                                  TTTGTTTTTT  TTTTG  GGT
                                       GA    AC   GTTT
GAM390  KIAA1449 3' CTTTGCTTCCTCCTTTTGTTT  40838         T    ACCC
                                  AGGCAGGAGG GGAA    CAGGG
                                  |||||||||| ||||    |||||
                                  TTTGTTTTCC CCTT    GTTTC
                                       T    C___
GAM390  KIAA1450 3' CCCACTGTTTTCATTTCTTCTT 66400     C          CCCA
                                  AGG AGGAGGTGGAAAC    GGG
                                  ||| ||||||||||||    |||
                                  TTC TTCTTTACTTTTG    CCC
                                    _          TCA_
GAM390  KIAA1456 3' TTTGGTTGTTTTTGTTTTCATG 67574      _    TG    C_    G
            TTT                   AGGCA GGAGG  GAAAC  CCAGG
                                  ||||| |||||  |||||  |||||
                                  TTTGT CTTTT  TTTTG  GGTTT
                                     A    GT    TT
GAM390  KIAA1463 3' CAGGGTTTTGTTTACTTTCTGT 72737           AA_______ CCAG
            C                     GGCAGGAGGTGGA       CC    G
                                  ||||||||||||       ||    |
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                                CTGTCTTTCATTT      GG   C
                                      GTTTT    GAC
GAM390  KIAA1463 3' CCTGGGCAATCCTTGCTT    72738       A   GGAAAC
                                AGGCAGG GGT     CCCAGG
                                ||||||| |||     ||||||
                                TTCGTTC CTA     GGGTCC
                                   _  AC_____
GAM390  KIAA1463 3' CCTTAGTGTTGTTTTTGTTGTC 72739       AG TG    CC ___
           TGCTT                AGGCAGG  G  GAAAC  CA   GGG
                                |||||||  |  |||||  ||   |||
                                TTCGTCT  T  TTTTG  GT   TCC
                                   GT GT    TT  GAT
GAM390  KIAA1463 3' TCCACAGTCTTTACTTCCTGCC 72743           A  CCCA
           T                    AGGCAGGAGGTGGA AC    GGG
                                ||||||||||||||  ||    |||
                                TCCGTCCTTCATTT TG    CCT
                                      C  ACA_
GAM390  KIAA1466 3' TTCTGTAAGCCTGCTTCCTGCT 72410         TG AAACCC
           T                    AGGCAGGAGG  G     CAGGG
                                ||||||||||  |     |||||
                                TTCGTCCTTC  C     GTCTT
                                     GT CGAAT_
GAM390  KIAA1485 3' CCCTGACCCTTACCATCTGCTT 90765       GA     AAACCC
                                AGGCAG  GGTGG     CAGGG
                                ||||||  |||||     |||||
                                TTCGTC  CCATT     GTCCC
                                   TA    CCCA__
GAM390  KIAA1486 3' TCTGGAATGTTTTCTCTCT    67980      T     C__
                                GGAGG GGAAAC   CCAGG
                                ||||| ||||||   |||||
                                TCTCT CTTTTG   GGTCT
                                   _     TAA
GAM390  KIAA1492 3' TCTTGGTCCTTTTACTTCTTTC 65129     C         ACC
           T                    AGG AGGAGGTGGAA   CCAGGG
                                ||| ||||||||||   ||||||
                                TCT TTCTTCATTTT   GGTTCT
                                  _         CCT
GAM390  KIAA1493 3' CCCTGACCCCTGCCATTCTGCC 64836        _  TG AAACCC
           T                    AGGCAGGA GG  G     CAGGG
                                |||||||  ||  |     |||||
                                TCCGTCTT CC  C     GTCCC
                                     A  GT CCCA__
GAM390  KIAA1494 3' TTTTGGGGTTATGTTTTGCTT  68986        G   GAA
                                AGGCAGGA GTG   ACCCCAGGG
                                ||||||||  |||   |||||||||
                                TTCGTTTT TAT   TGGGGTTTT
                                     G  ___
GAM390  KIAA1508 3' CCAGGGTTTTGCTCCATTTTTG 62545      AG       AA________  CCAG
           GCCT                    AGGC  GAGGTGGA       CC    G
                                ||||  ||||||||       ||    |
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                                TCCG  TTTTACCT       GG   C
                                  GT       CGTTTT    GACC
GAM390  KIAA1508 3' TTCTGGCTCTGATTTTTGCCT  62567        GT   AACC
                                AGGCAGGAG  GGA   CCAGGG
                                |||||||||  |||   ||||||
                                TCCGTTTTT  TCT   GGTCTT
                                     AG   C___
GAM390  KIAA1524 5' CCCAGGGTTCTGAGCTCACCTA 73838       G     AAA_________  CCAG
          TTGTCT                  AGGCAG AGGTGG         CC   GG
                                |||||| ||||||         ||   ||
                                TCTGTT TCCACT         GG   CC
                                   A     CGAGTCTT    GACC
GAM390  KIAA1529 5' TCCTGCTGGGCCGCTTCCTGC  71122          AAA   __
                                GCAGGAGGTGG   CCC  CAGGG
                                ||||||||||   |||  |||||
                                CGTCCTTCGCC   GGG  GTCCT
                                     ___   TC
GAM390  KIAA1545 3' TTCTGAGGGTGATCTTTTGTTT 61338          GGAA   _
                                AGGCAGGAGGT    ACCC CAGGG
                                ||||||||||    |||| |||||
                                TTTGTTTTCTA    TGGG GTCTT
                                     G___    A
GAM390  KIAA1546 3' CTTTGTAAGCTGGCTTTTGTCT 68497        G   AAACCC
                                AGGCAGGAG TGG     CAGGG
                                |||||||| |||     |||||
                                TCTGTTTTC GTC     GTTTC
                                     G   GAAT__
GAM390  KIAA1600 3' TCTGTTTTGCCTCCTGCCT   71943         TG   ACCC
                                AGGCAGGAGG  GAA   CAGG
                                ||||||||||  |||   ||||
                                TCCGTCCTCC  TTT   GTCT
                                     GT  ____
GAM390  KIAA1602 3' CCCAGGGCTCTGCTTCCTGCCT 65237          TG  AA__  CCAG
                                AGGCAGGAGG  GA   CC   GG
                                ||||||||||  ||   ||   ||
                                TCCGTCCTTC  CT   GG   CC
                                     GT  C    GACC
GAM390  KIAA1610 3' TCTTGGGTGATGTATTTTTGTC 67740         GTGGAAAC
            T                    AGGCAGGAG       CCCAGGG
                                |||||||||       |||||||
                                TCTGTTTTT       GGGTTCT
                                     ATGTAGT_
GAM390  KIAA1617 3' TCTTGGCTCACCCACGTTTTGC 93084         G   AAACC
            CT                    AGGCAGGA GTGG    CCAGGG
                                |||||||| ||||    ||||||
                                TCCGTTTT CACC    GGTTCT
                                     G   CACTC
GAM390  KIAA1617 3' CTCTGAGCGTCCCTTCTGTCT  93075          T  AAACCC
                                AGGCAGGAGG GG     CAGGG
                                |||||||||| ||     |||||
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                                TCTGTCTTCC CT     GTCTC
                                      _ GCGA__
GAM390  KIAA1649 3' TCCTGGCTCTCCATTTCTGGCC 51251     A       AACC
              T                  AGGC GGAGGTGGA    CCAGGG
                                 |||| |||||||||    ||||||
                                 TCCG TCTTTACCT    GGTCCT
                                   G       CTC_
GAM390  KIAA1656 3' TCCTGGGTGGCACTTCTGCCT  66386      G    GAAAC
                                 AGGCAG AGGTG    CCCAGGG
                                 |||||| |||||    |||||||
                                 TCCGTC TTCAC    GGGTCCT
                                    _    GGT__
GAM390  KIAA1668 3' CTCTGGGCCAAAGAATCTCTTG 67067          GGAAAC_
              TTT                  AGGCAGGAGGT      CCCAGGG
                                   ||||||||||       |||||||
                                   TTTGTTCTCTA      GGGTCTC
                                         AGAAACC
GAM390  KIAA1668 3' TCCTGGGGGGTTCTCTGGTTT  67083     A    TGGAAA
                                 AGGC GGAGG     CCCCAGGG
                                 |||| |||||     ||||||||
                                 TTTG TCTCT     GGGGTCCT
                                   G    TGG___
GAM390  KIAA1668 3' TCCTGGGTTCACGCCATCCTCC 67084          _  AAAC__
              TGCCT                AGGCAGGAGG TGG     CCCAGGG
                                   |||||||||| |||     |||||||
                                   TCCGTCCTCC ACC     GGGTCCT
                                         T   GCACTT
GAM390  KIAA1674 3' CCCCAGGGTTTGCTGTTTGTCT 69335          TG  AA_________  CCAG
              TCTGTCT                AGGCAGGAGG  GA        CC    GG
                                   ||||||||||  ||        ||   ||
                                   TCTGTCTTCT  TT        GG   CC
                                         GT  GTCGTTT    GACC
GAM390  KIAA1674 3' CTCTCCTTTTCACTTCTTGCCT 69339             CCCC
                                 AGGCAGGAGGTGGAAA   AGGG
                                 ||||||||||||||||   ||||
                                 TCCGTTCTTCACTTTT   TCTC
                                       CC__
GAM390  KIAA1679 3' TCCTAATATTTACTTCCTACCT 70714     C        AACCCC
                                 AGG AGGAGGTGGA     AGGG
                                 ||| ||||||||||     ||||
                                 TCC TCCTTCATTT     TCCT
                                   A        ATAA__
GAM390  KIAA1691 3' TTTGGGGGCTTTTTTTCTT   94139       TG  AA
                                 AGGAGG  GA  CCCCAGG
                                 ||||||  ||  |||||||
                                 TTCTTT  TT  GGGGTTT
                                    TT  CG
GAM390  KIAA1706 3' CCTCCTTCATCCCCTGCCT   94365        A     AACCCC
                                 AGGCAGG GGTGGA     AGG
                                 ||||||| ||||||     |||
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                                TCCGTCC CTACTT     TCC
                                   C     CC____
GAM390  KIAA1724 3' CCCAGGGTTTTCTTCTATTTCT 67612       _       AC_______ CCAG
              TTGTCT                 AGGCAG GAGGTGGAA       C    G
                                |||||| |||||||||       |   |
                                TCTGTT CTTTATCTT       G    C
                                   T       CTTTT   G GACC
GAM390  KIAA1724 3' TCTGGGTGTTTTTTTTTT    67623     TG    _
                                GAGG  GAAAC CCCAGG
                                ||||  ||||| ||||||
                                TTTT  TTTTG GGGTCT
                                  TT    T
GAM390  KIAA1728 3' GGTTTTGCCACTTTCTTCCT   68953     C       _ A____
                                AGG AGGAGGTGG AA    CC
                                ||| ||||||||| ||    ||
                                TCC TCTTTCACC TT    GG
                                  T       G  TT
GAM390  KIAA1729 3' CCTTGCCCACTGTTTCTTCCT  90589     C   __    AAACCC
                                AGG AGGA  GGTGG     CAGGG
                                ||| ||||  |||||     |||||
                                TCC TCTT  TCACC     GTTCC
                                  T   TG    C_____
GAM390  KIAA1729 3' GGTCCATTTTGTTTTTGCTT   90591         ____    AA_
                                AGGCAGGAG   GTGGA   CC
                                |||||||||   |||||   ||
                                TTCGTTTTT   TACCT   GG
                                     GTTT
GAM390  KIAA1735 3' CCTTGGGCTGCCTCTTCTGTCT 89004          T  AAAC
                                AGGCAGGAGG GG    CCCAGGG
                                |||||||||| ||    |||||||
                                TCTGTCTTCT CC    GGGTTCC
                                     _ GTC_
GAM390  KIAA1750 3' CCAGGGCTTTCCTCCTCTTCTG 68807      __    T   A____  CCAG
              CCT                   AGGCA  GGAGG GGAA    CC    G
                                |||||  ||||| ||||    ||   |
                                TCCGT  TCTCC CCTT    GG   C
                                   CT    T   TC    GACC
GAM390  KIAA1750 3' CCCCAGGGTCTTATTTTGCTTG 68808       _  TG   A_______  CCAG
              CCTGCCT                AGGCAGG AGG  GAA      CC    GG
                                ||||||| |||  |||      ||   ||
                                TCCGTCC TTC  TTT      GG    CC
                                   G   GT   ATTCT    GACC
GAM390  KIAA1750 3' TCTGCTTTTTTGTTTTTTGTT  68812        TG    CCC    G
                                GGCAGGAGG  GAAA   CAGG
                                |||||||||  ||||   ||||
                                TTGTTTTTT  TTTT   GTCT
                                     GT    TC_
GAM390  KIAA1784 3' CTTTGGGTTAAAGCTGCCTCCA 65749     A    TG AAAC__
              GCCT                   AGGC GGAGG  G     CCCAGGG
                                |||| |||||  |     |||||||
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                                TCCG CCTCC  C     GGGTTTC
                                  A    GT GAAATT
GAM390  KIAA1786 3' CCAGGGTTCTCCTCCCCTTCTT 66631         T  AA_______ CCAG
                GTCT                 AGGCAGGAGG GGA       CC   G
                                     |||||||||| |||       ||   |
                                     TCTGTTCTTC CCT       GG   C
                                          C  CCTCTT    GACC
GAM390  KIAA1789 5' CCTTGCAAGCAGTCTCCTGTTT 67700         _ GAAACCC
                                     AGGCAGGAGG TG      CAGGG
                                     |||||||||| ||      |||||
                                     TTTGTCCTCT AC      GTTCC
                                          G  GAAC___
GAM390  KIAA1798 3' TTCTGGGGTAAGTTCCACCTCT 61250     C        ___
                TCTT                 AGG AGGAGGTGGAA   ACCCCAGGG
                                     ||| ||||||||||   |||||||||
                                     TTC TTCTCCACCTT   TGGGGTCTT
                                      _        GAA
GAM390  KIAA1813 5' CTCTGAGCCTGTCTCCTTCCT  70823     C     TG AAACCC
                                     AGG AGGAGG  G     CAGGG
                                     ||| ||||||  |     |||||
                                     TCC TCCTCT  C     GTCTC
                                       T     GT CGA___
GAM390  KIAA1817 3' CCTGTGTCTGCCTCTGTTT   68776       G   TG  AACCC
                                     AGGCAG AGG  GA    CAGG
                                     |||||| |||  ||    ||||
                                     TTTGTC TCC  CT    GTCC
                                        _  GT  GT___
GAM390  KIAA1819 5' TTGCTGTGTGTTTCTGTCTCTT 70258         TG    CC_   GG
                GCT                  GGCAGGAGG  GAAAC   CAG
                                     |||||||||  |||||   |||
                                     TCGTTCTCT  CTTTG   GTC
                                          GT    TGT   GTTT
GAM390  KIAA1822 3' CCCTGGGGGCTCCTCTTGCCT  68183          TGGAAA
                                     AGGCAGGAGG     CCCCAGGG
                                     ||||||||||     ||||||||
                                     TCCGTTCTCC     GGGGTCCC
                                          TCG___
GAM390  KIAA1829 3' CCAATAAATTTCCTTTTTTTGC 62636         T    CCCCAG
                TT                   AGGCAGGAGG GGAAA     GG
                                     |||||||||| |||||     ||
                                     TTCGTTTTTT CCTTT     CC
                                          T    AAATAA
GAM390  KIAA1854 3' CCAGGGTTCTCTTCCGCTCCTG 72199         G    AC_______ CCAG
                CCT                  AGGCAGGAG TGGAA       C   G
                                     ||||||||| |||||       |   |
                                     TCCGTCCTC GCCTT       G   C
                                        _    CTCTT   G GACC
GAM390  KIAA1854 3' CTCTGAATCTCTCTCCTGTCT  72206         GT   AACCC
                                     AGGCAGGAG  GGA    CAGGG
                                     |||||||||  |||    |||||
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                                TCTGTCCTC  TCT    GTCTC
                                     TC   AA___
GAM390  KIAA1854  3'  TCCTGAATGACAACCTTCTGCT 72214          GGAAACCC
             T                    AGGCAGGAGGT       CAGGG
                                  ||||||||||        |||||
                                  TTCGTCTTCCA       GTCCT
                                       ACAGTAA_
GAM390  KIAA1854  3'  TTCTGACACCCACTTCTTTTCT 72217     C       AAACCC
                                  AGG AGGAGGTGG     CAGGG
                                  ||| |||||||||     |||||
                                  TCT TTCTTCACC     GTCTT
                                    T       CACA__
GAM390  KIAA1855  3'  CTCTGGGGTGCAGAAACCTCTT 93952          GGAA__
             GCCT                   AGGCAGGAGGT     ACCCCAGGG
                                  ||||||||||      |||||||||
                                  TCCGTTCTCCA     TGGGGTCTC
                                       AAGACG
GAM390  KIAA1856  3'  CCCAGGGTTATTTTTTATTTCC 94229           _________  CCA
             TGTT                   GGCAGGAGGTGGAAA       CC   GG
                                  ||||||||||||||       ||   ||
                                  TTGTCCTTTATTTTT       GG   CC
                                         TATT   G  ACC
GAM390  KIAA1857  3'  CCAGTTCCTTTTTTGTCT    51690         T    ACCCCA
                                  AGGCAGGAGG GGAA     GG
                                  |||||||||| ||||     ||
                                  TCTGTTTTTT CCTT     CC
                                       _   GA____
GAM390  KIAA1871  3'  GGCCTTTTTTTTTTTCTGTCT   61909         T    A_____
                                  AGGCAGGAGG GGAA     CC
                                  |||||||||| ||||     ||
                                  TCTGTCTTTT TTTT     GG
                                       T    TCC
GAM390  KIAA1871  3'  TCTTGGACATAATCACCTTTT  61912         AAACC_
                                  AGGAGGTGG     CCAGGG
                                  |||||||||     ||||||
                                  TTTTCCACT     GGTTCT
                                       AATACA
GAM390  KIAA1872  3'  TCCTGGGGTAGCTCCTGACCT  63624     _     G GGAA
                                  AGG CAGGAG T    ACCCCAGGG
                                  ||| |||||| |    |||||||||
                                  TCC GTCCTC A    TGGGGTCCT
                                    A     G ____
GAM390  KIAA1879  5'  CCCTGGAGTTCTGCTTCTGTCT 73936       G   TG   A C
                                  AGGCAG AGG  GAA C CCAGGG
                                  |||||| |||  ||| | ||||||
                                  TCTGTC TTC  CTT G GGTCCC
                                     _   GT   _ A
GAM390  KIAA1881  3'  CCCTGGTTTGTCCCTCTTGTCT 97083          T  AAACC
                                  AGGCAGGAGG GG     CCAGGG
                                  |||||||||| ||     ||||||
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                                TCTGTTCTCC CT    GGTCCC
                                     _ GTTT_
GAM390  KIAA1906 3' CCAGGGTTTATTTTTATTCTCT 73569      GA     A_______ CCAG
            GCTT                 AGGCAG  GGTGGAA      CC    G
                                |||||| |||||||      ||   |
                                TTCGTC  TTATTTT      GG    C
                                   TC      TATTT    GACC
GAM390  KIAA1915 3' TCTGAGTTGTTTTTATTTTCTT 73672     C         CC__   G
            CCT                  AGG AGGAGGTGGAAAC   CAGG
                                ||| ||||||||||||   ||||
                                TCC TCTTTTATTTTTG   GTCT
                                  T          TTGA
GAM390  KIAA1918 3' CTCTCATTATTCTGCCTCTTAC 73537     C     TG   ACCCC
            TT                   AGG AGGAGG  GAA    AGGG
                                ||| ||||||  |||    ||||
                                TTC TTCTCC  CTT    TCTC
                                  A     GT   ATTAC
GAM390  KIAA1937 3' CAGGGCTTTCCTTCACTCTTGC 74069        G    AA_______ CCAG
            CT                   AGGCAGGA GTGGA       CC    G
                                |||||||| |||||       ||   |
                                TCCGTTCT CACTT       GG    C
                                   _    CCTTTC    GAC
GAM390  KIAA1944 3' CCCCAGGGCTTTGAACCTATCT 76078     C       AAA_________ CCAG
            TCTCCCT                AGG AGGAGGTGG         CC    GG
                                ||| |||||||||         ||   ||
                                TCC TCTTCTATC         GG    CC
                                  C       CAAGTTTC    GACC
GAM390  KIAA1946 3' TCCAGGTGTTTCTATTTTTTGT 83358             C  A
                                GCAGGAGGTGGAAAC CC GGG
                                |||||||||||||| || |||
                                TGTTTTTTATCTTTG GG CCT
                                         T  A
GAM390  KIAA1971 3' TCCTGGGTTCACGCCATTCTCC 74697          _  AAAC__
            TGCCT                 AGGCAGGAGG TGG     CCCAGGG
                                |||||||||| |||     |||||||
                                TCCGTCCTCT ACC     GGGTCCT
                                     T   GCACTT
GAM390  KIAA1975 5' CAGGGTCTTCTCTGACCTTTTG 74416          _  AA_______ CCAG
            TCT                   AGGCAGGAGGT GGA       CC    G
                                |||||||||| |||       ||   |
                                TCTGTTTTCCA TCT       GG    C
                                     G   CTTCT    GAC
GAM390  KIAA1975 5' TCCTGGGTTCACCCCATTCTCC 74431          _  AAAC__
            TGTTT                 AGGCAGGAGG TGG     CCCAGGG
                                |||||||||| |||     |||||||
                                TTTGTCCTCT ACC     GGGTCCT
                                     T   CCACTT
GAM390  KIAA1977 5' CCAGGGTTTTTCTGCCTGCCTG 74764        _      A_____ CCAG
            CCT                   AGGCAGG AGGTGGAA     CC    G
                                ||||||| ||||||||     ||   |
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                                TCCGTCC TCCGTCTT     GG    C
                                   G       TTT     GACC
GAM390  KIAA1981  5'  CTCTGGCCGCCGCCTCCTCTT  89713     C       AAACC
                                AGG AGGAGGTGG     CCAGGG
                                ||| |||||||||     ||||||
                                TTC TCCTCCGCC     GGTCTC
                                  _       GCC__
GAM390  KIAA1985  3'  CCAGGGTTTTTTCCATTTCTTT 45017     C        A_______  CCAG
           CTT                    AGG AGGAGGTGGAA      CC    G
                                ||| ||||||||||      ||   |
                                TTC TTCTTTACCTT      GG    C
                                  T        TTTT     GACC
GAM390  KIF13B   3'  TCCTAGCATTTTCTCCTCTTGC 83719         T    CCCC
           CT                     AGGCAGGAGG GGAAA    AGGG
                                |||||||||| |||||    ||||
                                TCCGTTCTCC CTTTT    TCCT
                                     T    ACGA
GAM390  KIF13B   3'  CCCAGGGTTCTATCTTCTTTTC 31558        _______     AA__  CCAG
           TTGCCT                 AGGCAGGA     GGTGGA    CC    GG
                                ||||||||     ||||||    ||    ||
                                TCCGTTCT     CTATCT    GG    CC
                                   TTTCTT     T    GACC
GAM390  KIF13B   3'  CCCCAGGGTTCTATCTTCTTTT 31559        _______     AA__  CCAG
           CTTGCCT                AGGCAGGA     GGTGGA    CC    GG
                                ||||||||     ||||||    ||    ||
                                TCCGTTCT     CTATCT    GG    CC
                                   TTTCTT     T    GACC
GAM390  KIF13B   3'  TCCTAGCATTTTCTCCTCTTGC 31574         T    CCCC
           CT                     AGGCAGGAGG GGAAA    AGGG
                                |||||||||| |||||    ||||
                                TCCGTTCTCC CTTTT    TCCT
                                     T    ACGA
GAM390  KIF1C    3'  CCCTGTCCGTCTGTCTGTCTGT 61887        _  TG  AACCC
           CT                     AGGCAGG AGG  GA    CAGGG
                                ||||||| |||  ||    |||||
                                TCTGTCT TCT  CT    GTCCC
                                   G   GT  GCCT_
GAM390  KLHL8    5'  CAGGGTCTACATCTACCTTCTG 63508           AA________  CCAG
           CCT                    AGGCAGGAGGTGGA       CC    G
                                ||||||||||||||       ||   |
                                TCCGTCTTCCATCT       GG    C
                                      ACATCT    GAC
GAM390  KLHL8    3'  CCAGGGTTTTGCCTTTTCTTTT 63509       _____   TG  AA__  CCAG
           GCCT                   AGGCAG    GAGG  GA    CC    G
                                ||||||    ||||  ||    ||    |
                                TCCGTT    TTCC  TT    GG    C
                                   TTCTT    GT  T     GACC
GAM390  KLHL8    5'  CCCAGGGTCTACCTTCTGCCT  63511           AA_  CCAG
                                AGGCAGGAGGTGGA   CC    GG
                                ||||||||||||||   ||    ||
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                                TCCGTCTTCCATCT  GG   CC
                                             GACC
GAM390  KNSL6    3'  CCTGGGGTTGTCCTGGCT   23380   G   GGTGGA
                                AG CAGGA     AACCCCAGG
                                || |||||     |||||||||
                                TC GTCCT     TTGGGGTCC
                                 G   G_____
GAM390  KOC1     3'  TTCTGTCATATTTCACTTCTAG 92721      A       ACCC_
            CCT                   AGGC GGAGGTGGAA    CAGGG
                                |||| ||||||||||    |||||
                                TCCG TCTTCACTTT    GTCTT
                                  A        ATACT
GAM390  KRTAP4-12 3'  CCCCAGGGTTTGCATTCTACCT 49829           A_________  CCAG
            TTTGTC                  GGCAGGAGGTGGAA       CC   GG
                                ||||||||||||||       ||   ||
                                CTGTTTTCCATCTT       GG   CC
                                         ACGTTT    GACC
GAM390  KRTHB3   3'  CCCTGCCTCTCTGGCCTCTTGT 11246         _   AACCC
            CT                    AGGCAGGAGGT GGA    CAGGG
                                |||||||||| |||    |||||
                                TCTGTTCTCCG TCT    GTCCC
                                      G  CTCC_
GAM390  L3MBTL2  3'  TCCTGGGACCCGCCTGTTGCTT 90160       G     AAAC
                                AGGCAG AGGTGG   CCCAGGG
                                |||||| ||||||   |||||||
                                TTCGTT TCCGCC   GGGTCCT
                                   G    CA__
GAM390  LANO     3'  TCCAAGTTTTACCTCCTGT   47976          ACCCCA
                                GCAGGAGGTGGAA     GGG
                                ||||||||||||     |||
                                TGTCCTCCATTTT     CCT
                                       GAA___
GAM390  LAP1B    3'  TTTGGAATTTTTTTCTTTTGTT 65198         TG   CC    G
            T                    AGGCAGGAGG  GAAA  CCAGG
                                ||||||||||  ||||  |||||
                                TTTGTTTTCT  TTTT  GGTTT
                                      TT   AA
GAM390  LBP-9    3'  CCAGGGTTCTGACCACTCTCCT 28045        _   AAA_______  CCAG
            GCCT                   AGGCAGGAG GTGG       CC   G
                                ||||||||| ||||       ||   |
                                TCCGTCCTC CACC       GG   C
                                     T   AGTCTT    GACC
GAM390  LBP-9    3'  CCTTGGTCTGTCACTCCTGCTT 28046        G  AAACC
                                AGGCAGGAG TGG    CCAGGG
                                ||||||||| |||    ||||||
                                TTCGTCCTC ACT    GGTTCC
                                     _  GTCT_
GAM390  LBP-9    3'  TTCTGTGCCTTCTACCTCTTTC 28051     C        ACCC
            TT                    AGG AGGAGGTGGAA   CAGGG
                                ||| ||||||||||   |||||
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                                TTC TTCTCCATCTT   GTCTT
                                  T        CCGT
GAM390  LBP-9    3'  TTTGTGTGTTTTTACTTTTTGG 28053    G         CC_   G
                CT                  AG CAGGAGGTGGAAAC  CAGG
                                    || |||||||||||||  ||||
                                    TC GTTTTTCATTTTTG  GTTT
                                     G           TGT
GAM390  LCE      3'  CAGGGTTGTTTCTCTTTCTTGC 44258         T    _____ CAG
                TT                  AGGCAGGAGG GGAAAC    CC  G
                                    |||||||||| ||||||    ||  |
                                    TTCGTTCTTT TCTTTG    GG  C
                                          C     TT    GAC
GAM390  LCHN     3'  TTCTGCCACCATCTCCTGCC  87482          AAACCC
                                    GGCAGGAGGTGG     CAGGG
                                    ||||||||||||     |||||
                                    CCGTCCTCTACC     GTCTT
                                           ACC___
GAM390  LEC3     3'  CCAGGGCTTTTTTTCTTTTTTG 31534         TG  A______  CCAG
                CCT                   AGGCAGGAGG  GAA     CC   G
                                    ||||||||||  |||     ||   |
                                    TCCGTTTTTT  TTT     GG   C
                                          CT   TTTC    GACC
GAM390  LHPP     3'  CAGGGCTCTCCTCCACCCCTGC 42358       A    AA_______  CCAG
                CT                  AGGCAGG GGTGGA       CC   G
                                    |||||||  ||||||       ||   |
                                    TCCGTCC CCACCT       GG   C
                                       _     CCTCTC    GAC
GAM390  LHPP     3'  CCAGGGCTCTCCTCCACCCCTG 42359       A    AA_______  CCAG
                CCT                   AGGCAGG GGTGGA       CC   G
                                    |||||||  ||||||       ||   |
                                    TCCGTCC CCACCT       GG   C
                                       _     CCTCTC    GACC
GAM390  LHPP     3'  CCCTGACAGCCCTGCCTTCTGC 42362         TG AAACCC
                C                    GGCAGGAGG  G     CAGGG
                                    |||||||||  |     |||||
                                    CCGTCTTCC  C     GTCCC
                                         GT CCGACA
GAM390  LIPG     3'  CTTTGGAGCAAATCTCTTCTGT 21231         TGGAAACC
                TT                  AGGCAGGAGG       CCAGGG
                                    ||||||||||       ||||||
                                    TTTGTCTTCT       GGTTTC
                                         CTAAACGA
GAM390  LIPG     3'  TCCTGGTCACTTCTGACTTCTG 21233         GT   ACC_
                TTT                   AGGCAGGAG  GGAA   CCAGGG
                                    |||||||||  ||||   ||||||
                                    TTTGTCTTC  TCTT   GGTCCT
                                         AG   CACT
GAM390  LIPG     3'  TTAAGTGGTTTCTATTTCTTCT 21235     C         CCAGGG
                T                    AGG AGGAGGTGGAAACC
                                    ||| |||||||||||||
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                                TTC TTCTTTATCTTTGG
                                  _           TGAATTT
GAM390  LMOD1    3'  TTCTCACTTTCCTTTTCTTGTC 25109          T    CCCC
                T                AGGCAGGAGG GGAAA   AGGG
                                 |||||||||| |||||   ||||
                                 TCTGTTCTTT CCTTT   TCTT
                                       T    CAC_
GAM390  LNX      3'  TCCTGTGACTATCTCCTTCTT  51912     C       AAACCC
                                 AGG AGGAGGTGG     CAGGG
                                 ||| |||||||||     |||||
                                 TTC TCCTCTATC     GTCCT
                                   T       AGT___
GAM390  LRMP     3'  CTTACATTTCCTCTTTTTGCCT 21585          T    CCCC
                                 AGGCAGGAGG GGAAA   AGG
                                 |||||||||| |||||   |||
                                 TCCGTTTTTC CCTTT   TTC
                                       T    ACA_
GAM390  LRP15    5'  CCAGGGCTTTGCCTCTCTCCTG 54754          _ T  A A_____  CCAG
                TCT                AGGCAGGAG G GG A     CC   G
                                 ||||||||| | || |     ||   |
                                 TCTGTCCTC C CC T     GG   C
                                      T T  G TTC    GACC
GAM390  LRP1B    5'  TTTTGGGGTTGTTTTGCTTTCT 38279          TG  __
                GTTT                AGGCAGGAGG  GAA  ACCCCAGGG
                                 ||||||||||  |||  |||||||||
                                 TTTGTCTTTC  TTT  TGGGGTTTT
                                      GT   GT
GAM390  LRRFIP2  3'  TCCATGCTGTTTTTATTTTTTA 21952    GC          CC  _
                TCT                AG  AGGAGGTGGAAAC  CA GGG
                                 ||  ||||||||||||  || |||
                                 TC  TTTTTTATTTTTG  GT CCT
                                  TA          TC  A
GAM390  LSFR2    3'  CCTGGGGGGCCTGCTGCCT   61186       G   GGAAA
                                 AGGCAG AGGT    CCCCAGG
                                 |||||| ||||    |||||||
                                 TCCGTC TCCG    GGGGTCC
                                    G   G____
GAM390  LSM4     3'  CCCTGGCCCTTCGCTTCCTCTC 25566     C       AACC
                T                 AGG AGGAGGTGGA   CCAGGG
                                 ||| ||||||||||   ||||||
                                 TCT TCCTTCGCTT   GGTCCC
                                   C        CCC_
GAM390  LYSAL1   3'  TCCTGTGGTTTTGTTTTTTCT  18126       TG_     C
                                 AGGAGG   GAAACC CAGGG
                                 ||||||   |||||| |||||
                                 TCTTTT   TTTTGG GTCCT
                                    TTG     T
GAM390  MacGAP   3'  TTCTGGGTGAAAAAGCTTTTGT 54300          GTGGAAAC
                TT                 AGGCAGGAG       CCCAGGG
                                 |||||||||       |||||||
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                                TTTGTTTTC       GGGTCTT
                                     GAAAAAGT
GAM390  MAFB     3'  CAGACTGGTTTCTGTTTTTTGG 19590    G      TG     CCAGGG
             TT                   AG CAGGAGG  GAAACC
                                || |||||||  ||||||
                                TT GTTTTTT  CTTTGG
                                 G      GT     TCAGACT
GAM390  MAGE-E1  3'  TCCTGCTTTCATTTTGTGCTT  48677      G       ACCC
                                AGGCA GAGGTGGAA    CAGGG
                                ||||| |||||||||    |||||
                                TTCGT TTTTACTTT    GTCCT
                                   G       C___
GAM390  MAGEA1   5'  CCTGCCCACACTCCTGCCT    18378         _    AAACCC
                                AGGCAGGAG GTGG     CAGG
                                ||||||||| ||||     ||||
                                TCCGTCCTC CACC     GTCC
                                     A    C_____
GAM390  MAGEB1   5'  CCAGGGTTCTGCTCACTTTCCT 11426         _    AAA_____  CCAG
             GCCT                   AGGCAGGAG GTGG       CC    G
                                ||||||||| ||||       ||    |
                                TCCGTCCTT CACT       GG    C
                                     T    CGTCTT    GACC
GAM390  MAN1     3'  CCTGTTTGGCTTTTTGTCT    27482          G   ACCC
                                AGGCAGGAGGT GAA    CAGG
                                |||||||||| |||    ||||
                                TCTGTTTTTCG TTT    GTCC
                                     G  ____
GAM390  MAN1C1   3'  GTTTTGGTTTCTTGGTTTTTGT 40174        G TG     _______
             TTTTGCTT                AGGCAGGA G  GAAACC     CCAGGG   T
                                |||||||| |  ||||||     ||||||   |
                                TTCGTTTT T  TTTTGG     GGTTTT   G
                                    _ GT     TTCTTT
GAM390  MAP-1    3'  TTTGTCGTTTCTGTGCCT    42453      GGAGG      CC
                                AGGCA    TGGAAAC  CAGG
                                |||||    |||||||  ||||
                                TCCGT    GTCTTTG  GTTT
                                  ______      CT
GAM390  MAP2K3   3'  CTCTGTTGATTTTTTCTTTTGC 59685         TG   ACCC
             TT                   AGGCAGGAGG  GAA    CAGGG
                                |||||||||  |||    |||||
                                TTCGTTTTCT  TTT    GTCTC
                                     TT   AGTT
GAM390  MAPK8IP3 3'  CCCAGGGCTTTCCTTTCACCTC 54138           AC_________ CCAG
             CTGC                   GCAGGAGGTGGAA        C    G
                                ||||||||||||||        |   |
                                CGTCCTCCACTTT        G    C
                                       CCTTTC   G GACC
GAM390  MARCKS   5'  CCCCAGGGTTCTCCATTTTCCT 11413         _____    AA____  CCAG
             CTTGTCT                AGGCAGGAGG    TGGA     CC    GG
                                |||||||||   ||||     ||    ||
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                                TCTGTTCTCC  ACCT    GG  CC
                                     TTTT  CTT   GACC
GAM390  MAWBP   5' CCTTGGTAATTATTTCCT  42383       AAACC
                                AGGAGGTGG   CCAGGG
                                |||||||||   ||||||
                                TCCTTTATT   GGTTCC
                                     AAT__
GAM390  MBLL39  3' CTTGTTTTCTTTTTTCTGTTT 59260        T   CCC
                                AGGCAGGAGG GGAAA  CAGG
                                |||||||||| |||||  ||||
                                TTTGTCTTTT TCTTT  GTTC
                                     T   T__
GAM390  MCFP    5' CCCTGCAGCTGCCTTCTGCC  38735       TG AAACCC
                                GGCAGGAGG  G    CAGGG
                                |||||||||  |    |||||
                                CCGTCTTCC  C    GTCCC
                                     GT GAC___
GAM390  MEIS3   3' CTCTGAGCCCCGCTTCTGCCT  78869      G    AAACCC
                                AGGCAG AGGTGG    CAGGG
                                ||||||| ||||||     |||||
                                TCCGTC TTCGCC    GTCTC
                                   _     CCGA__
GAM390  METAP1  3' CAGGGCTTTCTTCCCTTTTCTG 73036        T   AC_______ CCAG
           TTT                  AGGCAGGAGG GGAA       C   G
                                |||||||||| ||||       |   |
                                TTTGTCTTTT CCTT       G   C
                                     C   CTTTC  G GAC
GAM390  METAP2  3' GGTTTTTCCCCTTCCTGTCT  60808       _  T   A_____
                                AGGCAGG AGG GGAA    CC
                                ||||||| ||| ||||    ||
                                TCTGTCC TCC CCTT    GG
                                   T  _   TTT
GAM390  MGC10200 3' TTTTGGATAAAGCTTATTTCTT 59653          _ AAACC_
           GTTT                 AGGCAGGAGGTG G    CCAGGG
                                ||||||||||| |    ||||||
                                TTTGTTCTTTAT C    GGTTTT
                                     T GAAATA
GAM390  MGC10818 3' CCTCCTTCATCCTTGTCT   48299       A    AACCCC
                                AGGCAGG GGTGGA    AGG
                                ||||||| ||||||    |||
                                TCTGTTC CTACTT    TCC
                                   _     CC____
GAM390  MGC10924 3' CAGGGCCTTATTTTCCTTTTGT 48310        TG  AA______  CCAG
           CT                   AGGCAGGAGG  GA      CC   G
                                ||||||||||  ||      ||   |
                                TCTGTTTTCC  TT      GG   C
                                     TT  ATTCC    GAC
GAM390  MGC11287 3' CTCTGTGGTCCACGTCCTGCCT 49614       G    AA  C
                                AGGCAGGA GTGGA  CC CAGGG
                                |||||||| |||||  || |||||
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                                TCCGTCCT CACCT  GG GTCTC
                                   G    __  T
GAM390  MGC11335 3' CCCTGGGGAGCCCTTCAGCCT  48768     AG   T  AAA
                                AGGC  GAGG GG   CCCCAGGG
                                ||||  |||| ||   ||||||||
                                TCCG  CTTC CC   GGGGTCCC
                                  A_   _ GA_
GAM390  MGC11386 3' CCAGGGTTACTATTTATTTCCT 53059           AA________  CCAG
           GCCT                  AGGCAGGAGGTGGA       CC   G
                                ||||||||||||||       ||   |
                                TCCGTCCTTTATTT       GG   C
                                      ATCATT    GACC
GAM390  MGC12837 3' CCTGATTTTCCACCTTTTTTCT 52170    C         CCC
                                AGG AGGAGGTGGAAA   CAGG
                                ||| ||||||||||||   ||||
                                TCT TTTTCCACCTTT   GTCC
                                  T          TA_
GAM390  MGC12921 5' CTCTGGGGGGCAGCTCTTGTCT  64513        G  GAAA
                                AGGCAGGAG TG    CCCCAGGG
                                |||||||||  ||    ||||||||
                                TCTGTTCTC AC    GGGGTCTC
                                   G  G___
GAM390  MGC13017 3' TCAGGGTTTTTTGTTTTTTGTT 55577         TG   C   AGGG
           T                    AGGCAGGAGG  GAAA CCC
                                ||||||||||  |||| |||
                                TTTGTTTTTT  TTTT GGG
                                      GT    T   ACTT
GAM390  MGC13204 3' TCCTAGGGTTTTTGTTTTTGTT 49634        G TG      C
           T                    AGGCAGGA G  GAAACCC AGGG
                                ||||||||  |  ||||||| ||||
                                TTTGTTTT T  TTTTGGG TCCT
                                   _ GT      A
GAM390  MGC14141 3' CCCTGGGGTGGTGTTTCTCCT  53041       TGGAA_
                                AGGAGG     ACCCCAGGG
                                ||||||     |||||||||
                                TCCTCT     TGGGGTCCC
                                   TTGTGG
GAM390  MGC14156 3' CTTGTTCTGCCCTTGTTT    52957       A  TG   ACCC
                                AGGCAGG GG  GAA    CAGG
                                ||||||| ||  |||    ||||
                                TTTGTTC CC  CTT    GTTC
                                   _ GT   _____
GAM390  MGC14156 3' GGTGTTTCTGTCTCTTCCT    52960     C     TG    _____
                                AGG AGGAGG  GAAAC    CC
                                ||| ||||||  |||||    ||
                                TCC TTCTCT  CTTTG    GG
                                  _     GT    T
GAM390  MGC14376 3' CTGTAATTTTCATCTTTGGTTT 52915      AG        CCC
                                AGGC  GAGGTGGAAA   CAG
                                ||||  ||||||||||   |||
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                                TTTG  TTCTACTTTT   GTC
                                  GT         AAT
GAM390  MGC14386 3' TTCTGTCAGTCATTTCCCTGCT 54328        _     AAACCC
           T                    AGGCAGG AGGTGG      CAGGG
                                ||||||| ||||||      |||||
                                TTCGTCC TTTACT      GTCTT
                                   C     GACT__
GAM390  MGC15429 3' GGTCTTTTCTACCTCTTTCT   52214     C        A_______
                                AGG AGGAGGTGGAA      CC
                                ||| ||||||||||       ||
                                TCT TTCTCCATCTT      GG
                                  _         TTCT
GAM390  MGC15429 3' TCCTGTTCTTCCACTTTCCTGC 52216         _     ACCC
           CT                    AGGCAGGAG GTGGAA    CAGGG
                                ||||||||| ||||||    |||||
                                TCCGTCCTT CACCTT    GTCCT
                                     T     CTT_
GAM390  MGC15504 3' CTTTGGGGAAATATTTATTTCC 52218           AA___
           TGC                    GCAGGAGGTGGA    CCCCAGGG
                                ||||||||||||    ||||||||
                                CGTCCTTTATTT    GGGGTTTC
                                      ATAAA
GAM390  MGC15631 3' TCCTGGGGCCTCAGTCTCCTGT 52236         TG  AA
           CT                    AGGCAGGAGG  GA  CCCCAGGG
                                ||||||||||  ||  ||||||||
                                TCTGTCCTCT  CT  GGGGTCCT
                                     GA  CC
GAM390  MGC15634 3' CCTTGGAGAAGTTTTATTTTTT 52240     C        ACC__
           TCT                    AGG AGGAGGTGGAA     CCAGGG
                                ||| ||||||||||     ||||||
                                TCT TTTTTTATTTT     GGTTCC
                                  _         GAAGA
GAM390  MGC15730 3' TCCGCGACCGGTTTTCATTTCT 52866     C          CCA___
           TTTCT                   AGG AGGAGGTGGAAACC     GGG
                                ||| ||||||||||||      |||
                                TCT TTCTTTACTTTTGG     CCT
                                  T           CCAGCG
GAM390  MGC20255 3' CCAGGGTCCTCTCCCTCTCCTG 54534         T   AA_______  CCAG
           TTT                    AGGCAGGAGG GGA       CC    G
                                ||||||||| |||       ||    |
                                TTTGTCCTCT CCT       GG    C
                                     C   CTCCT    GACC
GAM390  MGC20255 3' CCCAGGGCCCTGTCTCCTGCCT 54535         TG AAA__  CCAG
                                AGGCAGGAGG  G    CC    GG
                                ||||||||||  |    ||    ||
                                TCCGTCCTCT  C    GG    CC
                                     GT CC    GACC
GAM390  MGC20255 3' TTCTGTCTCTTTCTGTCTTTCT 54547         _     CCC_
           GTCT                    AGGCAGGAGG TGGAAA    CAGGG
                                ||||||||| ||||||    |||||
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                                TCTGTCTTTC GTCTTT    GTCTT
                                      T     CTCT
GAM390  MGC20460 5' CTCTGCCCATCGGCTTCTGCTT 54904         G   AAACCC
                                AGGCAGGAG TGG     CAGGG
                                ||||||||| |||     |||||
                                TTCGTCTTC GCT     GTCTC
                                     G   ACCC__
GAM390  MGC20460 5' CTCTGCCGACCGGCTTCTGCTT 54906         G   AAACCC
                                AGGCAGGAG TGG     CAGGG
                                ||||||||| |||     |||||
                                TTCGTCTTC GCC     GTCTC
                                     G   AGCC__
GAM390  MGC2452  5' GGTCCTCTTCACCTCTTCCT   51967     C        AA_______
                                AGG AGGAGGTGGA       CC
                                ||| ||||||||||       ||
                                TCC TTCTCCACTT       GG
                                  _        CTCCT
GAM390  MGC2454  3' CCCAGGGCTTAAGTTTTATCTT 48283            AC_________ CCAG
           CTGTC                  GGCAGGAGGTGGAA        C    G
                                ||||||||||||||        |    |
                                CTGTCTTCTATTTT        G    C
                                       GAATTC   G GACC
GAM390  MGC2541  3' CTCTGGGGCCTGCCCCTGCCT  55623       A  TG AAA
                                AGGCAGG GG  G   CCCCAGGG
                                ||||||| ||  |   ||||||||
                                TCCGTCC CC  C   GGGGTCTC
                                   _  GT C__
GAM390  MGC2628  3' CCTTGATGACCTCTGTTTCTTC 44197     C     TG  AACCC_
           CT                    AGG AGGAGG  GA     CAGGG
                                ||| ||||||  ||     |||||
                                TCC TTCTTT  CT     GTTCC
                                  _     GT  CCAGTA
GAM390  MGC2641  3' CCTTGGGTTTTTTTTTCCTGCC 51927         TG      C   G
           T                     AGGCAGGAGG  GAAACCC AGG
                                ||||||||||  ||||||| |||
                                TCCGTCCTTT  TTTTGGG TCC
                                      TT      T
GAM390  MGC26768 3' GGCTTTTCTGCTTGCTGCTT   58912       G       A______
                                AGGCAG AGGTGGAA     CC
                                |||||| ||||||||     ||
                                TTCGTC TTCGTCTT     GG
                                   G       TTC
GAM390  MGC26954 3' TCTTGGTTCTACTCATCTTCTG 59494           AAACC_
           TC                    GGCAGGAGGTGG     CCAGGG
                                ||||||||||||     ||||||
                                CTGTCTTCTACT     GGTTCT
                                       CATCTT
GAM390  MGC27434 3' CCCCAGGGTTACATTTCAATCT 59593         _    A________  CCAG
           TCTGTCT                AGGCAGGAGG TGGAA       CC   GG
                                ||||||||||| |||||       ||   ||
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                                TCTGTCTTCT ACTTT       GG    CC
                                     A     ACATT     GACC
GAM390  MGC2817  3' TCCTGAAATCCATTTTTGTTT  70740         G    AACCC
                                AGGCAGGAG TGGA     CAGGG
                                ||||||||| ||||     |||||
                                TTTGTTTTT ACCT     GTCCT
                                     _    AAA__
GAM390  MGC29956 3' CCTGGGGTTGGTCTGCTT    58922        AGGTGGA
                                AGGCAGG      AACCCCAGG
                                |||||||      |||||||||
                                TTCGTCT      TTGGGGTCC
                                   GG_____
GAM390  MGC3035  5' CTCTGGCAGCCTCGCTTTCTCC 44398     C        AAACC
           CT                     AGG AGGAGGTGG     CCAGGG
                                ||| |||||||||     ||||||
                                TCC TCTTTCGCT     GGTCTC
                                  C        CCGAC
GAM390  MGC3035  5' TTTGGCCTATTTTCTGCT     44407           AAACC
                                GGCAGGAGGTGG     CCAGG
                                ||||||||||||     |||||
                                TCGTCTTTTATC     GGTTT
                                      C____
GAM390  MGC3130  3' CCTTGGGTGTCCCTCTCCTGCC 44052          T   AAC
           T                     AGGCAGGAGG GGA   CCCAGGG
                                |||||||||| |||   |||||||
                                TCCGTCCTCT CCT   GGGTTCC
                                     C   GT_
GAM390  MGC32043 3' CTCTGGGCTCACTTGCCTGCCT 58663        _     AAAC
                                AGGCAGG AGGTGG    CCCAGGG
                                ||||||| ||||||    |||||||
                                TCCGTCC TTCACT    GGGTCTC
                                   G     C___
GAM390  MGC32043 3' CTCTGGTCTCATCACTTGCCT  58664        A   _  AACC
                                AGGCAGG GGTG GA    CCAGGG
                                ||||||| |||| ||    ||||||
                                TCCGTTC CTAC CT    GGTCTC
                                   A    T _____
GAM390  MGC32043 3' GGCTTATTCTATTCCTGTTT   58669         G    A_______
                                AGGCAGGAG TGGAA       CC
                                |||||||| |||||       ||
                                TTTGTCCTT ATCTT       GG
                                     _    ATTC
GAM390  MGC32043 3' TTCTGGGTCCCAGCCTCCTGT  58671          __  AAC
                                GCAGGAGGT  GGA   CCCAGGG
                                |||||||||  |||   |||||||
                                TGTCCTCCG  CCT   GGGTCTT
                                     AC   ___
GAM390  MGC4170  3' TTTGGGGATTTTTTTTTT    44476      TG   _
                                GAGG  GAAA CCCCAGG
                                ||||  |||| |||||||
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                                TTTT  TTTT GGGGTTT
                                  TT    A
GAM390  MGC4172  3' GGCCTTATCTATCTCCTTCT  44457     C        AA_______
                                AGG AGGAGGTGGA       CC
                                ||| ||||||||||       ||
                                TCT TCCTCTATCT       GG
                                  _        ATTCC
GAM390  MGC4251  3' CCAGGGTTTGTTTGATCTTTTG 51466          G   AC_______ CCAG
            CTT                   AGGCAGGAGGT GAA       C    G
                                ||||||||||| |||       |   |
                                TTCGTTTTCTA TTT       G    C
                                     G   GTTT   G GACC
GAM390  MGC4796  3' CCAGGGTTTTAATCTACCTCTG 62161        G      AA________  CCAG
            TCT                   AGGCAG AGGTGGA        CC    G
                                |||||| |||||||        ||    |
                                TCTGTC TCCATCT        GG    C
                                  _      AATTTT     GACC
GAM390  MGC4796  3' CCTGAGGCCCCTCCTGCCT   62162          T  AAA  C
                                AGGCAGGAGG GG   CC CAGG
                                |||||||||| ||   || ||||
                                TCCGTCCTCC CC   GG GTCC
                                     _ ___  A
GAM390  MGC4840  3' CCCCAGGGTCCGTCTCCTATTT 72020          _  AA________  CCAG
            CTTGCTT                 AGGCAGGAGGT GGA        CC    GG
                                ||||||||||| |||        ||    ||
                                TTCGTTCTTTA CCT        GG    CC
                                     T   CTGCCT     GACC
GAM390  MGC5139  5' CCAGGGCTTTGTACATTTCTTG 74568          GAAA_______  CCAG
            TTT                   AGGCAGGAGGTG         CC    G
                                ||||||||||||         ||    |
                                TTTGTTCTTTAC         GG    C
                                     ATGTTTC     GACC
GAM390  MGC5139  5' CTCTGTAAAGTCACTTTCTTCT 74570     C        AAACCC
                                AGG AGGAGGTGG      CAGGG
                                ||| |||||||||      |||||
                                TCT TCTTTCACT      GTCTC
                                  _        GAAAT_
GAM390  MGC5560  3' CAGGGTTGTTTTTGTCTTTTGG 39310    G      TG     _____  CAG
            TT                    AG CAGGAGG  GAAAC     CC   G
                                || |||||||  |||||     ||   |
                                TT GTTTTCT  TTTTG     GG   C
                                 G      GT     TT     GAC
GAM390  MGC5627  3' CCTGTTGTACCTTTTGCCT   44278          G  ACCC
                                AGGCAGGAGGTG AA    CAGG
                                |||||||||||| ||    ||||
                                TCCGTTTTCCAT TT    GTCC
                                     G  ____
GAM390  MGC7036  3' TCTTGGCATCACTTTCTCCCT  59619     C        AAACC
                                AGG AGGAGGTGG     CCAGGG
                                ||| |||||||||     ||||||
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                                TCC TCTTTCACT    GGTTCT
                                  C       AC___
GAM390  MGC8407  3' CAGGGTTTGTGTTATTTCCTGC 44110          AAA_______ CCAG
            CT                   AGGCAGGAGGTGG       CC   G
                                ||||||||||||        ||   |
                                TCCGTCCTTTATT       GG   C
                                     GTGTTT    GAC
GAM390  MGC8407  3' CCTTCCCCTTCCCTTCTTGCCT 44112         T   ACCCC
                                AGGCAGGAGG GGAA    AGG
                                |||||||||| ||||    |||
                                TCCGTTCTTC CCTT    TCC
                                     _   CCCCT
GAM390  MGC8407  3' CCTTGTGGCTTTTCTGTCTTTT 44113        TG   C_ _
            GCT                   GGCAGGAGG  GAAA  CC CAGGG
                                |||||||||  ||||  || |||||
                                TCGTTTTCT  CTTT  GG GTTCC
                                     GT   TC  T
GAM390  MIG-6    3' CCTGGGGATTGTTTGCTT    38999       AG  GGAAA
                                AGGCAGG  GT    CCCCAGG
                                |||||||  ||    |||||||
                                TTCGTTT  TA    GGGGTCC
                                    GT  _____
GAM390  MKP-7    3' GGTTTTGCCCTTTCTGCTT   67017         T  A A_____
                                AGGCAGGAGG GG A     CC
                                |||||||||| || |     ||
                                TTCGTCTTTC CC T     GG
                                     _  G TTT
GAM390  MKRN1    3' TTCTGTGGTTTTGGTCTCTTGT 26498         TG     C
            TT                   AGGCAGGAGG  GAAACC CAGGG
                                ||||||||||  |||||| |||||
                                TTTGTTCTCT  TTTTGG GTCTT
                                     GG     T
GAM390  MKRN2    3' CTCTGGGCACATTTCCTGTT   72847          GAAAC
                                GGCAGGAGGTG    CCCAGGG
                                ||||||||||     |||||||
                                TTGTCCTTTAC    GGGTCTC
                                     AC___
GAM390  MORF4    3' CCAGGGTTGATGTTTGTTTTCT 92470         TG  AA________  CCAG
            GTTT                   AGGCAGGAGG  GA       CC   G
                                ||||||||||  ||       ||   |
                                TTTGTCTTTT  TT       GG   C
                                     GT  GTAGTT    GACC
GAM390  MR       3' TCCTGGTCACATTCTCTGTCT  49150       AG  _  AACC
                                AGGCAGG  GTG GA    CCAGGG
                                |||||||  ||| ||    ||||||
                                TCTGTCT  TAC CT    GGTCCT
                                    CT   A  ____
GAM390  MRG15    3' CAGGGTTGATGTTTGTTTTCTG 23284         TG  AA________  CCAG
            TTT                   AGGCAGGAGG  GA       CC   G
                                ||||||||||  ||       ||   |
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                                TTTGTCTTTT TT       GG   C
                                     GT GTAGTT    GAC
GAM390  MRPL10   3' CCTTGGTCACTGCCTCTTGCT 59831         TG AAACC
                                GGCAGGAGG G    CCAGGG
                                ||||||||| |    ||||||
                                TCGTTCTCC C    GGTTCC
                                     GT ACT__
GAM390  MRPL37   3' CCTGAAACCCCTCTTGCCT   66842         T AAACCC
                                AGGCAGGAGG GG     CAGG
                                |||||||||| ||     ||||
                                TCCGTTCTCC CC     GTCC
                                     _ AAA___
GAM390  MRPS21   3' CCAGGGTTCTCTCCATCTCTTT 39161     C        AA_______ CCAG
           TCT                   AGG AGGAGGTGGA       CC   G
                                ||| ||||||||||       ||   |
                                TCT TTCTCTACCT       GG   C
                                  T        CTCTT    GACC
GAM390  MRPS21   5' CCCTGCTGCCATCTCTTTTCT 39162     C        AAACCC
                                AGG AGGAGGTGG     CAGGG
                                ||| |||||||||     |||||
                                TCT TTCTCTACC     GTCCC
                                  T       GTC___
GAM390  MTO1     5' CCCTGCAGATTGTCTCTTGTT 56934         TG AAACCC
                                GGCAGGAGG G     CAGGG
                                ||||||||| |     |||||
                                TTGTTCTCT T     GTCCC
                                     GT AGAC__
GAM390  MYNN     3' CAGGGTTTGTTTTTATTTTTGG 38480      AG         _______ CAG
           CTT                   AGGC  GAGGTGGAAAC     CC   G
                                |||| ||||||||||     ||   |
                                TTCG  TTTTATTTTTG     GG   C
                                  GT         TTT    GAC
GAM390  MYO5C    3' CCAATTGCACCTTCTGTTT   38715          G  ACCCCA
                                AGGCAGGAGGTG AA     GG
                                |||||||||||| ||     ||
                                TTTGTCTTCCAC TT     CC
                                      G  AA____
GAM390  MYT1     3' GGGTTCCTTTTGTTT       16981          TGGA
                                AGGCAGGAGG    AACCC
                                |||||||||    |||||
                                TTTGTTTTCC    TTGGG
                                     ____
GAM390  N4BP2    3' CCAGGGTTTTGCCCTTTCTTCT 36936         T_  AAA_______ CCAG
           GCTT                    AGGCAGGAGG  GG       CC   G
                                |||||||||  ||       ||   |
                                TTCGTCTTCT  CC       GG   C
                                     TT  CGTTTT    GACC
GAM390  N4BP2    3' CCTTGATCTTTTACCTTTTGTT 36939           ACCC
                                GGCAGGAGGTGGAA    CAGGG
                                ||||||||||||||    |||||
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                              TTGTTTTCCATTTT  GTTCC
                                     CTA_
GAM390  NAP1L1   3' TTTTGGGGTTGAACTTTTT  58305      GGA
                              AGGAGGT  AACCCCAGGG
                              |||||||  ||||||||||
                              TTTTTCA  TTGGGGTTTT
                                 AG_
GAM390  NAV1     3' CCCCAGGGCTTTCCCTTGACTT 40322        G  AA_________  CCAG
           CTTGTTT               AGGCAGGAGGT GA       CC   GG
                              |||||||||||  ||       ||   ||
                              TTTGTTCTTCA TT       GG   CC
                                    G  CCCTTTC    GACC
GAM390  NAV3     3' CCCCAGGGTTTTGTCCCTTCCT 30452        T__  AA_______  CCAG
           TTTGTTT               AGGCAGGAGG  GGA      CC   GG
                              ||||||||||  |||      ||   ||
                              TTTGTTTTCC  CCT      GG   CC
                                    TTC  GTTTT    GACC
GAM390  NDRG4    3' TCTTGGAATTTTGTTTTTTGCT 40384       TG  ACC
                              GGCAGGAGG  GAA  CCAGGG
                              |||||||||  |||  ||||||
                              TCGTTTTTT  TTT  GGTTCT
                                   GT  AA_
GAM390  NDRG4    3' TCTTGGAATTTTGTTTTTTGCT 40385       TG  ACC
                              GGCAGGAGG  GAA  CCAGGG
                              |||||||||  |||  ||||||
                              TCGTTTTTT  TTT  GGTTCT
                                   GT  AA_
GAM390  NECL1    3' CTCTGGGGCCTGAACTGCCTCT 41325      G  TG AAA___
           GCTT                  AGGCAG AGG  G     CCCCAGGG
                              ||||||  |||  |     ||||||||
                              TTCGTC TCC  C     GGGGTCTC
                                 _  GT AAGTCC
GAM390  NET-5    5' TCCTGGAACCTTCTTTTGTTT  22896        T  AAACC
                              AGGCAGGAGG GG    CCAGGG
                              ||||||||||  ||    ||||||
                              TTTGTTTTCT CC    GGTCCT
                                   T  AA___
GAM390  NETO1    5' CCAGGGCTTTATTTCCTTCTTG 58049        T   A________  CCAG
           CTT                   AGGCAGGAGG GGAA      CC   G
                              ||||||||||  ||||      ||   |
                              TTCGTTCTTC CTTT      GG   C
                                    _   ATTTC    GACC
GAM390  NETO2    3' TCTTGGCTAATCTCTGTACTTC 36596        _ TG  AACC__
           TGCCT                 AGGCAGGAG G  GA     CCAGGG
                              |||||||||  |  ||     ||||||
                              TCCGTCTTC T  CT     GGTTCT
                                   A GT  CTAATC
GAM390  NEUGRIN  3' CCCCAGGGTTCTGACCTCATTT 34061     C       AAA_________  CCAG
           CCTTCTT               AGG AGGAGGTGG        CC   GG
                              |||  |||||||||        ||   ||
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                                TTC TCCTTTACT         GG    CC
                                  T       CCAGTCTT    GACC
GAM390  NFAT5    5'  CCAGGGTCTTCCTCCATCTTTG 57763       G      AA________  CCAG
                CCT                  AGGCAG AGGTGGA       CC    G
                                |||||| |||||||       ||    |
                                TCCGTT TCTACCT       GG    C
                                  _      CCTTCT    GACC
GAM390  NFAT5    3'  CCAGGGTTACTTTTCACCTCTT 57764    C        A________  CCAG
                TTT                  GG AGGAGGTGGAA       CC    G
                                || ||||||||||       ||    |
                                TT TTCTCCACTTT       GG    C
                                  T         TCATT    GACC
GAM390  NFAT5    3'  CCAGGGTTTTCTCCATTTCTTC 22745    C        AA_______  CCAG
                CCT                  AGG AGGAGGTGGA       CC    G
                                ||| ||||||||||       ||    |
                                TCC TTCTTTACCT       GG    C
                                  C         CTTTT    GACC
GAM390  NFKBIE   3'  TCCTGGGTGAAGCCTGTTTGCC 17057        _   GGAAAC
                T                   AGGCAGG AGGT     CCCAGGG
                                ||||||| ||||     |||||||
                                TCCGTTT TCCG     GGGTCCT
                                   G    AAGT__
GAM390  NIP30    3'  CTTTGTAGGCACCTTCTGCTT  46898          GAAA  C_
                                AGGCAGGAGGTG    CC  CAGGG
                                ||||||||||||    ||  |||||
                                TTCGTCTTCCAC    GG  GTTTC
                                      _____  AT
GAM390  NLI-IF   3'  CCTGCCCCACCTCCTCCCT    41343     C       AAACCC
                                AGG AGGAGGTGG      CAGG
                                ||| |||||||||      ||||
                                TCC TCCTCCACC      GTCC
                                  C        CC_____
GAM390  NLI-IF   3'  TCCTGGGGGCAGGGTTCCTGCC 41345          GTGGAAA
                T                   AGGCAGGAG      CCCCAGGG
                                |||||||||      ||||||||
                                TCCGTCCTT      GGGGTCCT
                                     GGGACG_
GAM390  NPAS3    3'  CCTGCCGTTTTGTCTTCTTCT  42352     C     TG   ACCC
                                AGG AGGAGG  GAA    CAGG
                                ||| ||||||  |||    ||||
                                TCT TCTTCT  TTT    GTCC
                                  _     GT   GCC_
GAM390  NPC1L1   3'  CCTTGGGCAGTGCCTCCTCCT  26332     C      GGAAAC
                                AGG AGGAGGT     CCCAGGG
                                ||| |||||||     |||||||
                                TCC TCCTCCG     GGGTTCC
                                  _      TGAC__
GAM390  NR1H3    3'  TTCTGTCCCCATATTTTCTGTT 20303           GAAACCC
                T                   AGGCAGGAGGTG      CAGGG
                                ||||||||||||      |||||
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                                TTTGTCTTTTAT      GTCTT
                                      ACCCCT_
GAM390  NUDEL    3'  CTTTGGAGTGTTTTTGTTTTCT 48698     C     TG    C__
             CTT                    AGG AGGAGG  GAAAC   CCAGGG
                                ||| ||||||  |||||   ||||||
                                TTC TCTTTT  TTTTG   GGTTTC
                                  _     GT     TGA
GAM390  NX-17    5'  CCCCAGGGTTCTCACTTTGCCT 40703      G    TG  AA_________  CCAG
             TGTGTTT                AGGCA GAGG  GA        CC    GG
                                ||||| ||||  ||        ||    ||
                                TTTGT TTCC  TT        GG    CC
                                  G    GT  CACTCTT    GACC
GAM390  NXP-2    3'  CCAGGGTTTATTTTTACCTTTG 71658       G       A________  CCAG
             TTT                    AGGCAG AGGTGGAA       CC    G
                                |||||| ||||||||       ||    |
                                TTTGTT TCCATTTT       GG    C
                                  _       TATTT     GACC
GAM390  NY-REN-60 3'  CCTTTCAATTTTTTGTCT    51813          G   ACCCC
                                AGGCAGGAGGT GAA     AGG
                                ||||||||||| |||     |||
                                TCTGTTTTTTA CTT     TCC
                                      A   ______
GAM390  NYD-SP15  3'  CTCTGCTTTTGTTCCCTGCCT  48846       AG TG   ACCC
                                AGGCAGG  G  GAA    CAGGG
                                |||||||  |  |||    |||||
                                TCCGTCC  T  TTT    GTCTC
                                    CT GT   C___
GAM390  OAZ2     3'  CCCTGCTGTTGGCTTTCTGTTT 11874          G  AACCC
                                AGGCAGGAGGT GA     CAGGG
                                |||||||||||  ||     |||||
                                TTTGTCTTTCG TT     GTCCC
                                      G  GTC__
GAM390  OAZIN    5'  CCCGCGCCTTTCTTCTTTTGCC 32436          T     CCCCA
             T                     AGGCAGGAGG GGAAA     GGG
                                |||||||||| |||||     |||
                                TCCGTTTTCT TCTTT     CCC
                                      _     CCGCG
GAM390  OR7C1    3'  CCCCAGGGTCCATACTTCTGTT 34417          _     AA_  CCAG
             T                     AGGCAGGAG GTGGA   CC    GG
                                |||||||| |||||   ||    ||
                                TTTGTCTTC TACCT   GG    CC
                                      A         GACC
GAM390  OS4      5'  CCATTTCCTCCTCTTGTTT   20386          T     CCCCA
                                AGGCAGGAGG GGAAA     GG
                                |||||||||| |||||     ||
                                TTTGTTCTCC CCTTT     CC
                                      T     A____
GAM390  OS4      3'  TCTGGGTGTCTCCTGCTT    20396          GT GAAAC
                                AGGCAGGAG  G    CCCAGG
                                |||||||||  |    ||||||
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                                TTCGTCCTC  T    GGGTCT
                                     TG _____
GAM390  OS4      3'  TTCTGTTTAGCTTCCTCTTGCT 20400         T  AAACCC
            T                    AGGCAGGAGG GG     CAGGG
                                 |||||||||| ||     |||||
                                 TTCGTTCTCC TC     GTCTT
                                      T  GATTT_
GAM390  OSBPL10  3'  CCCAGGGCTAATTTTGTGCCTT 35522          _  A_______  CCAG
            TTGTCT                AGGCAGGAGGTG GAA      CC   GG
                                  |||||||||||| |||      ||   ||
                                  TCTGTTTTCCGT TTT      GG   CC
                                       G   TAATC    GACC
GAM390  OSBPL11  5'  CCAGGGTTTTTCCATCCTTGCT 43205       A      _______  CCA
            T                    AGGCAGG GGTGGAAA     CC   G
                                 ||||||| ||||||||     ||   |
                                 TTCGTTC CTACCTTT     GG   C
                                    _      TT   G  ACC
GAM390  OSBPL6   3'  TTTGGGATCCTTTCTGTTT   51688         T  AAAC
                                 AGGCAGGAGG GG    CCCAGG
                                 |||||||||| ||    ||||||
                                 TTTGTCTTTC CT    GGGTTT
                                      _  A___
GAM390  OSRF     3'  CCCTGGAAACAACTTACTTCTT 60268           AAACC__
            GCTT                   AGGCAGGAGGTGG      CCAGGG
                                   ||||||||||||      ||||||
                                   TTCGTTCTTCATT      GGTCCC
                                         CAACAAA
GAM390  P311     3'  CTTTGGGTTCTTTCTGTTT   17676         TGGA    C
                                 AGGCAGGAGG    AACCC AGG
                                 ||||||||||    ||||| |||
                                 TTTGTCTTTC    TTGGG TTC
                                      _____    T
GAM390  P38IP    3'  TTGAGTTTCTACTTTTTGTTT  34533            CC
                                 AGGCAGGAGGTGGAAAC  CAG
                                 |||||||||||||||||  |||
                                 TTTGTTTTTCATCTTTG  GTT
                                       A_
GAM390  PABPC5   3'  CTTATTTTTCTATTTTTTGT   55933          CCCC   G
                                 GCAGGAGGTGGAAA    AGG
                                 ||||||||||||||    |||
                                 TGTTTTTTATCTTT    TTC
                                       TTA_
GAM390  PABPC5   5'  TTCTGAGTCTGCTTTTAGCTT  55936     AG    TG  AACCC
                                 AGGC  GAGG  GA    CAGGG
                                 ||||  ||||  ||    |||||
                                 TTCG  TTTC  CT    GTCTT
                                   AT   GT  GA___
GAM390  PACSIN2  3'  CAGGGTTTTCACTCTATTCTTG 24297        _____     A___  CCAG
            CTT                    AGGCAGGAG   GTGGAA   CC    G
                                   |||||||||   ||||||   ||    |
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                                TTCGTTCTT   CACTTT   GG   C
                                     ATCT     T    GAC
GAM390  PADI3    3'  CTTTGGTCCAATTGCTTCCTCT 33174     C     TG AAACC
             CT                   AGG AGGAGG  G    CCAGGG
                                ||| ||||||  |    ||||||
                                TCT TCCTTC  T    GGTTTC
                                  C     GT AACCT
GAM390  PAPOLG   3'  TCCTGAACTCCTTTTTTGTTT  43472         T   AACCC
                                AGGCAGGAGG GGA    CAGGG
                                |||||||||| |||    |||||
                                TTTGTTTTTT CCT    GTCCT
                                     _  CAA__
GAM390  PASK     5'  TTCTGGGGTCGTCCTTTTT   31426       T  AA
                                AGGAGG GG  ACCCCAGGG
                                |||||| ||  |||||||||
                                TTTTTC CT  TGGGGTCTT
                                   _  GC
GAM390  PCBP4    5'  CCTGCCCCACTTTCTCTCT   40279     C       AAACCC
                                AGG AGGAGGTGG     CAGG
                                ||| |||||||||     ||||
                                TCT TCTTTCACC     GTCC
                                  C       CC____
GAM390  PCDH19   3'  GGCCCATTTATCTTTTGTCT  64446           AA_____
                                AGGCAGGAGGTGGA      CC
                                ||||||||||||||      ||
                                TCTGTTTTCTATTT      GG
                                       ACCC
GAM390  pcnp     3'  CCAGGGTTTTGTCCATTTTCCT 40142         _   AA_______  CCAG
             GTTT                  AGGCAGGAGG TGGA       CC    G
                                |||||||||| ||||       ||    |
                                TTTGTCCTTT ACCT       GG    C
                                     T   GTTTT    GACC
GAM390  PCQAP    3'  TCCTGCTTTTATCTTCTGCCT  32460           ACCC
                                AGGCAGGAGGTGGAA    CAGGG
                                ||||||||||||||    |||||
                                TCCGTCTTCTATTTT    GTCCT
                                       C___
GAM390  PDE4DIP  3'  CCAGGGTCCACTTTTCCTTTTG 97174         _____    AA_  CCAG
             CTT                   AGGCAGGAGG     TGGA   CC    G
                                |||||||||     ||||   ||    |
                                TTCGTTTTCC     ACCT   GG    C
                                     TTTTC        GACC
GAM390  PDZD2    5'  TTTGGGAACATCCCTGTTT   81739        A    GAAAC
                                AGGCAGG GGTG     CCCAGG
                                ||||||| ||||     ||||||
                                TTTGTCC CTAC     GGGTTT
                                   _    AA___
GAM390  PDZD2    3'  TTTTGTGGTTTCTGCTTTCTTG 81741         _ TG     C
             CCT                   AGGCAGGAG G  GAAACC CAGGG
                                |||||||||  |  |||||| |||||
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                                TCCGTTCTT C  CTTTGG GTTTT
                                     T GT     T
GAM390  PEGASUS   3'  CAGGGTTCTATCCATTTTCTGC 42689          AA_______  CCAG
            C                    GGCAGGAGGTGGA       CC    G
                                 ||||||||||||       ||    |
                                 CCGTCTTTTACCT       GG    C
                                       ATCTT     GAC
GAM390  PELI1     5'  CAGGGCTTTACTCTTTCTTCTG 40630         T  AA________  CCAG
            TCT                    AGGCAGGAGG GGA       CC    G
                                   |||||||||| |||       ||    |
                                   TCTGTCTTCT TCT       GG    C
                                         T   CATTTC     GAC
GAM390  PELI2     3'  CCAGGGTTTTGTTTCACTTCTT 41456     C        AC________ CCAG
            TTCT                    AGG AGGAGGTGGAA       C    G
                                    ||| ||||||||||       |    |
                                    TCT TTCTTCACTTT       G    C
                                      T         GTTTT   G GACC
GAM390  PELP1     3'  TTCTGCACCCCACTCTTTGTTT 73313        AG    AAACCC
                                   AGGCAGG  GTGG     CAGGG
                                   |||||||  ||||     |||||
                                   TTTGTTT  CACC     GTCTT
                                       CT    CCAC__
GAM390  PEX11B    3'  TCTTGAATATATTTACTTTGTG 15241       G       AACCC_
            TCT                    AGGCA GAGGTGGA     CAGGG
                                   ||||| ||||||||     |||||
                                   TCTGT TTTCATTT     GTTCT
                                      G       ATATAA
GAM390  PGR1      3'  GGTTCTCTTTTTTCCTGTCT   53907          T_   AA____
                                   AGGCAGGAGG  GGA     CC
                                   ||||||||||  |||     ||
                                   TCTGTCCTTT  TCT     GG
                                         TT   CTT
GAM390  PI15      5'  CCCTAACTCTACCTTTCTGCTT 32457         _     AACCCC
                                   AGGCAGGA GGTGGA     AGGG
                                   |||||||| ||||||     ||||
                                   TTCGTCTT CCATCT     TCCC
                                        T     CAA___
GAM390  PIP5K2B   3'  CCCTCGATCTATTTCCTTCTT  57693     C        AACCCC
                                   AGG AGGAGGTGGA     AGGG
                                   ||| ||||||||||     ||||
                                   TTC TCCTTTATCT     TCCC
                                     T         AGC___
GAM390  PIP5K2B   3'  CCCTGCTGCATTTGCTCTTGTC 57694         G TG  AACCC
            T                      AGGCAGGA G  GA     CAGGG
                                   |||||||| |  ||     |||||
                                   TCTGTTCT C  TT     GTCCC
                                        _ GT  ACGTC
GAM390  PISD      3'  TTCTGTTGGCCCCTTTTGTTT  27546          T  AAA  C_
                                   AGGCAGGAGG GG   CC  CAGGG
                                   |||||||||| ||   ||  |||||
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                                TTTGTTTTCC CC   GG  GTCTT
                                      _ ___  TT
GAM390  PJA1     5'  CCTTATTCTTTCTGTTACCTGC 42566       AG TG   CCCC_   G
             CT                   AGGCAGG  G  GAAA    AGG
                                  |||||||  |  ||||    |||
                                  TCCGTCC  T  CTTT    TCC
                                     AT GT    CTTAT
GAM390  PLAGL2   3'  CCTTGCCCCCACCTCCTGTCT  70958          AAACCC
                                  AGGCAGGAGGTGG     CAGGG
                                  ||||||||||||      |||||
                                  TCTGTCCTCCACC     GTTCC
                                        CCC___
GAM390  PM5      3'  CCTGGGGATTCATCTGTT    27380    G      AA
                                  AG AGGTGGA  CCCCAGG
                                  || |||||||  |||||||
                                  TT TCTACTT  GGGGTCC
                                   G      A_
GAM390  PMFBP1   3'  CAGGGTTTTGTCCACTTCCTGC 49271          AA_______  CCAG
             C                    GGCAGGAGGTGGA       CC    G
                                  ||||||||||||        ||    |
                                  CCGTCCTTCACCT       GG    C
                                        GTTTT     GAC
GAM390  POLE3    3'  GGCTCTGTGCCTCCTGCTT   34317          __   AA__
                                  AGGCAGGAGGT  GGA    CC
                                  ||||||||||  |||    ||
                                  TTCGTCCTCCG  TCT    GG
                                        TG   C
GAM390  POLE3    3'  TCCTGCTTCCTTTCTCTCCTGC 34321         T___    ACCC
             CT                    AGGCAGGAGG    GGAA    CAGGG
                                   ||||||||||    ||||    |||||
                                   TCCGTCCTCT    CCTT    GTCCT
                                         CTTT    C___
GAM390  POLR3F   3'  CAGGGCCATTTTCTGTTT    60617          AAA  CCAG
                                  AGGCAGGAGGTGG   CC    G
                                  ||||||||||||   ||    |
                                  TTTGTCTTTTACC   GG    C
                                          GAC
GAM390  POT1     3'  CCCAGGGTTTTGTTTTGCTTTC 31887         TG   AC________ CCAG
             TGTTT                  AGGCAGGAGG  GAA       C    G
                                    ||||||||||  |||       |    |
                                    TTTGTCTTTC  TTT       G    C
                                          GT   GTTTT   G GACC
GAM390  PP1201   3'  CCTTGCTTCAATCCCTTCTTGT 42456         T   AACCC_
             TT                     AGGCAGGAGG GGA     CAGGG
                                    ||||||||||  |||     |||||
                                    TTTGTTCTTC CCT     GTTCC
                                          _   AACTTC
GAM390  PPP1R13B 3'  CCTTGGGGGTTCCGCTTCCTGT 31657            A
             T                      GGCAGGAGGTGGAA CCCCAGGG
                                    |||||||||||||| ||||||||
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                                TTGTCCTTCGCCTT GGGGTTCC
                                      G
GAM390  PPP1R1A  3'  TTTTGGGGAAAATCTCTTGTTT 23098          GGAAA
                                AGGCAGGAGGT    CCCCAGGG
                                ||||||||||    ||||||||
                                TTTGTTCTCTA    GGGGTTTT
                                     AAA__
GAM390  PPP1R3B  3'  CAGGGCTCTTTTATTTTCTGTT 45134           AC_____ CCAG
          T                   AGGCAGGAGGTGGAA     C   G
                              ||||||||||||||     |   |
                              TTTGTCTTTTATTTT     G   C
                                    CTC   G GAC
GAM390  PPP1R3B  3'  CCAGGGTCCTCTTCACTTCTTT 45136    C       AA_______ CCAG
          CTT                   AGG AGGAGGTGGA      CC   G
                              ||| ||||||||||      ||   |
                              TTC TTCTTCACTT      GG   C
                                T       CTCCT    GACC
GAM390  PRDM7    3'  CCCTCCATTTTTTGTGTTTTGC 54844       G TG   CCCC
          CT                    AGGCAGGA G  GAAA   AGGG
                              |||||||| |  ||||   ||||
                              TCCGTTTT T  TTTT   TCCC
                                   G GT   TACC
GAM390  PRDM7    3'  TTTTGTGTTTTGCCTCCTGTT  54848        TG   ACCC
                              GGCAGGAGG  GAA   CAGGG
                              |||||||||  |||   |||||
                              TTGTCCTCC  TTT   GTTTT
                                   GT   GT__
GAM390  PRDM9    3'  GTTTGTTTTTTTGCCTCCTGTT 39977        TG   CCC   G
                              GGCAGGAGG  GAAA   CAGG
                              |||||||||  ||||   ||||
                              TTGTCCTCC  TTTT   GTTT
                                   GT   TT_   GT
GAM390  PRO0159  3'  CCCAGGGTTTTGTTTTCTGTTT 26946        GT    ________ CAG
          TTGCCT                AGGCAGGAG  GGAAAC     CC   GG
                              |||||||||  ||||||     ||   ||
                              TCCGTTTTT  CTTTTG     GG   CC
                                   GT     TTTT    GAC
GAM390  PRO0159  5'  TCTTGGTCACATCTTATTGTTT 26950      _    _ AACC
                              AGGCAG GAGGTG GA    CCAGGG
                              |||||| |||||| ||    ||||||
                              TTTGTT TTCTAC CT    GGTTCT
                                 A     A _____
GAM390  PRO0456  5'  CCAGGGTTCTTTCTACCTTTTG 27005    G        A_______ CCAG
          GCT                   AG CAGGAGGTGGAA      CC   G
                              || ||||||||||||      ||   |
                              TC GTTTTCCATCTT      GG   C
                               G          TCTT    GACC
GAM390  PRO0618  3'  CAGGGTTTTGTTTCTTTTTCTG 27049         T    ________ CAG
          TTT                   AGGCAGGAGG GGAAAC      CC   G
                              |||||||||| ||||||      ||   |
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                                TTTGTCTTTT TCTTTG      GG  C
                                      _     TTTT     GAC
GAM390  PRO0971  3' CCCCAGGGTTCATCATCTGCCT 38317          TG  AA_________  CCAG
             TCTGCTT                AGGCAGGAGG  GA        CC   GG
                                ||||||||||  ||         ||   ||
                                TTCGTCTTCC  CT        GG   CC
                                      GT  ACTACTT     GACC
GAM390  PRO0971  3' TCTGTAGTTTTATCTCCT    38318         G   CC
                                AGGAGGTG AAAC  CAGG
                                |||||||| ||||  ||||
                                TCCTCTAT TTTG  GTCT
                                     _   AT
GAM390  PRO1580  5' GGTTCTCTTCACTTCTGCTT   38125       G      AA_______
                                AGGCAG AGGTGGA       CC
                                |||||| |||||||       ||
                                TTCGTC TTCACTT       GG
                                   _      CTCTT
GAM390  PRO1598  5' TCTGGAATCCTTTTTGCCT    38132          T  AAACC
                                AGGCAGGAGG GG     CCAGG
                                |||||||||| ||     |||||
                                TCCGTTTTTC CT     GGTCT
                                      _  AA___
GAM390  PRO1617  5' TCTTGAGTATGTTTCATTTTCT 38339     C         ACCC__
             TTCT                  AGG AGGAGGTGGAA     CAGGG
                                ||| ||||||||||      |||||
                                TCT TCTTTTACTTT     GTTCT
                                  T         GTATGA
GAM390  PRO1728  5' CCTTATATATTTCCTGCTT    38135           GAAACCCC
                                AGGCAGGAGGTG       AGG
                                ||||||||||||       |||
                                TTCGTCCTTTAT       TCC
                                      ATAT____
GAM390  PRO1914  5' TTCTGTAAACCATTATCTTGCT 26889         _    AAACCC
             T                   AGGCAGGA GGTGG      CAGGG
                                |||||||| |||||      |||||
                                TTCGTTCT TTACC      GTCTT
                                     A     AAAT__
GAM390  PRO2325  3' CCTTGCCCATTCGCTCCTGCCT 98038         G   AACCC
                                AGGCAGGAG TGGA     CAGGG
                                ||||||||| ||||     |||||
                                TCCGTCCTC GCTT     GTTCC
                                     _    ACCC_
GAM390  PRO2325  5' GGTTCTTCTATGTTCTGCCT   98040         G     AC_____
                                AGGCAGGA GTGGAA       C
                                |||||||| ||||||       |
                                TCCGTCTT TATCTT       G
                                     G     CTT   G
GAM390  PRO2958  3' CTTTGTAGATTCCATTTTTTTT 38249     C         ACCC
             CT                    AGG AGGAGGTGGAA    CAGGG
                                ||| ||||||||||    |||||
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                                TCT TTTTTTACCTT   GTTTC
                                  T         AGAT
GAM390  PRRG1    3'  CTGTAGGGTTTTTACTTTTTTC 8150      C          __  GG
                TT                  AGG AGGAGGTGGAAACCC  CAG
                                    ||| ||||||||||||||  |||
                                    TTC TTTTTCATTTTTGGG  GTC
                                      T           AT
GAM390  PTBP2    3'  TTTTGGGGTTTCTTTTTTTT   41331       T
                                    AGGAGG GGAAACCCCAGGG
                                    |||||| ||||||||||||
                                    TTTTTT TCTTTGGGGTTTT
                                       T
GAM390  PTDSS2   3'  CCCCAGGGTCCTCCCTCCCCTT 48623         T   AA_________  CCAG
                TCTGCCT                 AGGCAGGAGG GGA        CC    GG
                                    |||||||||| |||         ||    ||
                                    TCCGTCTTTC CCT         GG    CC
                                          C   CCCTCCT     GACC
GAM390  PTK6     3'  CCTGTTTGTCTTGTGTCT    21073       G    TG  AACCC
                                    AGGCA GAGG  GA     CAGG
                                    ||||| ||||  ||     ||||
                                    TCTGT TTCT  TT     GTCC
                                      G    GT  _____
GAM390  PTPRT    3'  CCCCAGGGTTTGCATTCCACTT 56490          A_________  CCAG
                TCTG                   CAGGAGGTGGAA        CC    GG
                                    ||||||||||||        ||    ||
                                    GTCTTTCACCTT        GG    CC
                                          ACGTTT     GACC
GAM390  PYY      5'  CCCTCGCCTTCCACCTCCTGCT 16039           ACCCC
                                    GGCAGGAGGTGGAA     AGGG
                                    ||||||||||||||     ||||
                                    TCGTCCTCCACCTT     TCCC
                                          CCGC_
GAM390  PYY2     5'  TCCTCGCCTTCCACCTCCTGCT 41176           ACCCC
                                    GGCAGGAGGTGGAA     AGGG
                                    ||||||||||||||     ||||
                                    TCGTCCTCCACCTT     TCCT
                                          CCGC_
GAM390  QKI      3'  CCAGGGTTTTTTTTTTTTCCTG 66043          T   A_______  CCAG
                TTT                   AGGCAGGAGG GGAA       CC    G
                                    |||||||||| ||||       ||    |
                                    TTTGTCCTTT TTTT       GG    C
                                          T    TTTT     GACC
GAM390  RAB10    3'  CCCAGGGTTTTACTTCTATGTT 86351         G     AC_________ CCAG
                CTGCTT                  AGGCAGGA GTGGAA        C    G
                                    ||||||||| ||||||         |    |
                                    TTCGTCTT TATCTT         G    C
                                       G     CATTTT   G GACC
GAM390  Rab11-FIP2 3'  GGGTTTTTTTTTTTTGCTT    30456          TG
                                    AGGCAGGAGG  GAAACCC
                                    ||||||||||  |||||||
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                                TTCGTTTTTT  TTTTGGG
                                      TT
GAM390  RAB14    3'  TTTTGGGGAACTTTTTTGCC  33339        GT  AAA
                                GGCAGGAG  GG   CCCCAGGG
                                ||||||||  ||   ||||||||
                                CCGTTTTT  TC   GGGGTTTT
                                    __  AA_
GAM390  RAB1B    3'  CCCTCGTGCTGTCTCTTGCCT  49115          TG AA  CCC
                                AGGCAGGAGG  G  AC   AGGG
                                ||||||||||  |  ||   ||||
                                TCCGTTCTCT  C  TG   TCCC
                                      GT G_  C__
GAM390  RAB1B    3'  TCCTGGGCTCCCCATCTCCTTC 49118     C        AAAC
          T                      AGG AGGAGGTGG    CCCAGGG
                                ||| |||||||||    |||||||
                                TCT TCCTCTACC    GGGTCCT
                                  _       CCTC
GAM390  RAB35    3'  CCTGCTCTGGCTTTTGCCT   23412         G    AACCC
                                AGGCAGGAG TGGA     CAGG
                                |||||||||  ||||     ||||
                                TCCGTTTTC GTCT     GTCC
                                     G    C____
GAM390  RAB6B    5'  CCAGGGCCTTCCTCCGCCTCCG 33871      A        AA_______  CCAG
          CCT                     AGGC GGAGGTGGA        CC    G
                                ||||  |||||||||        ||    |
                                TCCG CCTCCGCCT        GG    C
                                  _       CCTTCC     GACC
GAM390  RAB6B    5'  CCCTGCTCCTTCGCTTTTTCCT 33872     C        AACCC
                                AGG AGGAGGTGGA     CAGGG
                                ||| ||||||||||     |||||
                                TCC TTTTTCGCTT     GTCCC
                                  _        CCTC_
GAM390  RAC6C    3'  CTTTGGCGATATTTCTTTGCTT 50484       _     GAAACC
                                AGGCAG GAGGTG      CCAGGG
                                ||||||  ||||||     ||||||
                                TTCGTT CTTTAT      GGTTTC
                                    T     AGC___
GAM390  RAI      3'  CCCAGGGCTCTCCCTCTGTTTT 22851          TG  AA_________  CCAG
          TTGCT                   GGCAGGAGG  GA        CC    GG
                                |||||||||  ||        ||    ||
                                TCGTTTTTT  CT        GG    CC
                                     GT  CCCTCTC     GACC
GAM390  RALGPS1A 3'  CCTGGGCTGTCTTTTTCT    28328     C     TG AAAC
                                AGG AGGAGG  G    CCCAGG
                                ||| ||||||  |    ||||||
                                TCT TTTTCT  C    GGGTCC
                                  _     GT ____
GAM390  RAP2B    3'  CCAGGGTTTTTTTCTATTTTCT 97522      C        A________  CCAG
          TTCT                    AGG AGGAGGTGGAA       CC    G
                                ||| ||||||||||       ||    |
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                                TCT TCTTTTATCTT       GG    C
                                  T         TTTTT     GACC
GAM390  RBAK     3'  CCCCAGGGTCCTCGCTCCATTT 41271           AA_________  CCAG
              CTTGCT                  GGCAGGAGGTGGA        CC    GG
                                |||||||||||||         ||    ||
                                TCGTTCTTTACCT        GG    CC
                                      CGCTCCT     GACC
GAM390  RERG     3'  GGTTCTTCCTTTCCTGCTT    53001          T    AC_____
                                AGGCAGGAGG GGAA      C
                                |||||||||| ||||      |
                                TTCGTCCTTT CCTT      G
                                      _    CTT   G
GAM390  RGPR     3'  CCAGGGCTTTGACTACTTCCTG 53594           AAA_______  CCAG
              TCT                   AGGCAGGAGGTGG        CC    G
                                |||||||||||||         ||    |
                                TCTGTCCTTCATC        GG    C
                                      AGTTTC     GACC
GAM390  RGS4     5'  TCCTGCCGCATTTCTTTCCTGC 20045          T    ACCC_
              TT                    AGGCAGGAGG GGAA     CAGGG
                                |||||||||| ||||     |||||
                                TTCGTCCTTT CTTT     GTCCT
                                      _    ACGCC
GAM390  RI58     3'  CAGGGTGTGTTTTACTTTTTGT 25775             AC_______ CCAG
              TT                    AGGCAGGAGGTGGAA       C    G
                                |||||||||||||||       |    |
                                TTTGTTTTTCATTTT       G    C
                                      GTGT   G GAC
GAM390  RNF10    3'  TCCATCTGGTTTTTGTTTTTGT 30162         G TG     CCAG
              TT                    AGGCAGGA G  GAAACC    GG
                                |||||||| |  ||||||    ||
                                TTTGTTTT T  TTTTGG    CC
                                     _ GT     TCTA  TC
GAM390  RNF11    3'  TTCTGACCTCCTTGCCTCTTGT 27654           __   AACCC
              CT                    AGGCAGGAGGT  GGA     CAGGG
                                ||||||||||  |||    |||||
                                TCTGTTCTCCG  CCT     GTCTT
                                      TT   CCA__
GAM390  RNF24    3'  CCCTCCTTCCATCTCTTCTCT  24278     C         ACCCC
                                AGG AGGAGGTGGAA     AGGG
                                ||| ||||||||||     ||||
                                TCT TTCTCTACCTT     TCCC
                                  C         CC___
GAM390  RNF40    3'  GGTTCGTTCCATCTTTTCCT   29366     C         AC_______
                                AGG AGGAGGTGGAA       C
                                ||| ||||||||||       |
                                TCC TTTTCTACCTT       G
                                  _         GCTT   G
GAM390  RNPC1    3'  CAGGGTCTTGCACCTTCTCCTG 34408          T  AAA________  CCAG
              CCT                   AGGCAGGAGG GG        CC    G
                                |||||||||| ||         ||    |
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                                TCCGTCCTCT CC        GG   C
                                     T  ACGTTCT    GAC
GAM390  RODH-4   5' CCTGCTCACTCTTTGCCT    14922        AG   AAACCC
                                AGGCAGG  GTGG     CAGG
                                |||||||  ||||     ||||
                                TCCGTTT  CACT     GTCC
                                    CT   C_____
GAM390  RoXaN    3' CCAGGGCTTTCTCTGTCTTTTC 47280     _     TG  AA_______ CCAG
           GCTT                   AGGC AGGAGG  GA      CC   G
                                |||| ||||||  ||       ||   |
                                TTCG TTTTCT  CT       GG   C
                                  C     GT  CTTTC    GACC
GAM390  RoXaN    3' CCTTCCTTCTGCCTCCTGCC  47286         TG   ACCCC
                                GGCAGGAGG  GAA    AGG
                                |||||||||  |||    |||
                                CCGTCCTCC  CTT    TCC
                                     GT   CCT__
GAM390  RPH3A    3' CCAGGGCTTTGTCTGTCTCTCT 30932       _   TG  AA_______ CCAG
           GTCT                   AGGCAG GAGG  GA      CC   G
                                |||||| ||||  ||       ||   |
                                TCTGTC CTCT  CT       GG   C
                                   T   GT  GTTTC    GACC
GAM390  RPL26L1  3' TCTGGAACATTTCATTTCCTGT 32735            ACC_    G
           TT                    AGGCAGGAGGTGGAA   CCAGG
                                |||||||||||||||   |||||
                                TTTGTCCTTTACTTT   GGTCT
                                      ACAA
GAM390  S164     3' CGGGTTTGTTTTCATTTTTGTC 61430         G      _______ CAG
           T                     AGGCAGGAG TGGAAAC     CC   G
                                |||||||||  |||||||     ||   |
                                TCTGTTTTT ACTTTTG     GG   C
                                     _      TTT     GA
GAM390  SARM     3' TCTGCCCGATCTTCTGTCT   31307          _ AAACCC
                                AGGCAGGAGGT GG     CAGG
                                ||||||||||| ||     ||||
                                TCTGTCTTCTA CC     GTCT
                                     G  C_____
GAM390  SCAMP5   3' CAGGGCTGTTTCTACTTTCAGT 58053      A         _____ CAG
           CT                    AGGC GGAGGTGGAAAC    CC   G
                                |||| ||||||||||||    ||   |
                                TCTG CTTTCATCTTTG    GG   C
                                  A          TC     GAC
GAM390  SCDGF-B  3' ACTGTTCTGATTTCCTGTTT  53631          _   ACCC   GG
                                AGGCAGGAGGT GGAA   CAG
                                |||||||||| ||||   |||
                                TTTGTCCTTTA TCTT   GTC
                                     G   ____   AC
GAM390  SCDGF-B  3' CTGTTCTGATTTCCTGTTT   53632          _   ACCC   GG
                                AGGCAGGAGGT GGAA   CAG
                                |||||||||| ||||   |||
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                                TTTGTCCTTTA TCTT    GTC
                                      G     ____    A
GAM390  SCOP     3'  CTTTGGGGGGAAAAGGCTTTTG 93426          GTGGAAA_
              TTT                   AGGCAGGAG       CCCCAGGG
                                    |||||||||       ||||||||
                                    TTTGTTTTC       GGGGTTTC
                                       GGAAAAGG
GAM390  SCYA21   3'  CCTTGCCACACTCTTTCTCCTG 12977          T   AACCC_
              CTT                   AGGCAGGAGG GGA     CAGGG
                                    |||||||||| |||     |||||
                                    TTCGTCCTCT TCT     GTTCC
                                       T   CACACC
GAM390  SCYA25   3'  CTCTCACTTTCTGTTTCTTGCC 20057          TG    CCCC
                                    GGCAGGAGG  GAAA    AGGG
                                    |||||||||  ||||    ||||
                                    CCGTTCTTT  CTTT    TCTC
                                       GT    CAC_
GAM390  SCYA25   3'  GGCTCTCTCACTTTCTGTTT   20058           _  AA____
                                    AGGCAGGAGGTG GA     CC
                                    ||||||||||| ||      ||
                                    TTTGTCTTTCAC CT     GG
                                       T  CTC
GAM390  SDC3     5'  CCCTGGCTCCCCTCCCTCCTGC 28467          TG AAACC
              CT                    AGGCAGGAGG  G    CCAGGG
                                    ||||||||||  |    ||||||
                                    TCCGTCCTCC  C    GGTCCC
                                       CT CCCTC
GAM390  SDC3     3'  CCCTGTGTCCCCTTCCTGCTT  28468          T   AACCC
                                    AGGCAGGAGG GGA     CAGGG
                                    ||||||||||| |||     |||||
                                    TTCGTCCTTC CCT     GTCCC
                                       C   GT___
GAM390  SDC3     3'  CCTGGGGTGCTGCTGTCT    28472       GA   GGAA
                                    AGGCAG  GGT    ACCCCAGG
                                    ||||||  |||    ||||||||
                                    TCTGTC  TCG    TGGGGTCC
                                       G_   _____
GAM390  SDF1     3'  TTCTGCTCATCATTCTCTGTCT 92522        AG    AAACCC
                                    AGGCAGG  GTGG     CAGGG
                                    |||||||  ||||     |||||
                                    TCTGTCT  TACT     GTCTT
                                       CT    ACTC__
GAM390  SDS3     3'  CTTTGTCAGTCTTTTCTGCCT  69747         GT   AACCC
                                    AGGCAGGAG  GGA    CAGGG
                                    |||||||||  |||    |||||
                                    TCCGTCTTT  TCT    GTTTC
                                       __   GACT_
GAM390  SDS3     3'  GGTTCATTTTACCTCTGCTT   69750       G      A_______
                                    AGGCAG AGGTGGAA      CC
                                    |||||| ||||||||      ||
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                                TTCGTC TCCATTTT      GG
                                   _       ACTT
GAM390  SDS3     3'  TTCTGGAGTGGGTTTTATTTTT 69754         GGTG      ____
             GTTT                   AGGCAGGA    GAAACCC    CAGGG
                                ||||||||    |||||||    |||||
                                TTTGTTTT    TTTTGGG    GTCTT
                                    TA__       TGAG
GAM390  SEC22C   3'  TCTATGTTTCTCTTTCTGCTT  16113          T     CCC
                                AGGCAGGAGG GGAAAC   AGG
                                ||||||||||| ||||||   |||
                                TTCGTCTTTC TCTTTG   TCT
                                    _      TA_
GAM390  SEMA3C   3'  CCCTGTGGTATTCCTTTCCTGC 22104          T   _   C
             TT                   AGGCAGGAGG GGAA ACC CAGGG
                                ||||||||||| |||| ||| |||||
                                TTCGTCCTTT CCTT TGG GTCCC
                                    _   A   T
GAM390  SEMA3C   3'  GGCTTTATTCACCTTTTCTT   22109     C        AA_______
                                AGG AGGAGGTGGA       CC
                                ||| ||||||||||       ||
                                TTC TTTTCCACTT       GG
                                  _        ATTTC
GAM390  SEMA4F   3'  CTTGGGGTGGTTCTGCTT    16208         GGTGGAA
                                AGGCAGGA      ACCCCAGG
                                ||||||||      ||||||||
                                TTCGTCTT      TGGGGTTC
                                    GG_____
GAM390  SEMA5A   3'  CCCAGGGTCCTCCATTTGCTT  15592        A  T   AA_  CCAG
                                AGGCAGG GG GGA   CC    GG
                                ||||||| || |||   ||    ||
                                TTCGTTT CC CCT   GG    CC
                                    A  T       GACC
GAM390  SEMA5A   3'  TTCTGCTGTTACTTGCTGCCT  15602       G     AAACCC
                                AGGCAG AGGTGG     CAGGG
                                ||||||| ||||||      |||||
                                TCCGTC TTCATT     GTCTT
                                    G     GTC___
GAM390  SEPT3    3'  CCAGGGTTCTGTCCCATCTCCT 39401     G        AAA________  CCAG
             GGTT                   AG CAGGAGGTGG         CC    G
                                || ||||||||||         ||    |
                                TT GTCCTCTACC         GG    C
                                 G         CTGTCTT    GACC
GAM390  SETMAR   3'  CTGACTTTTTGATTTCTGTCT  74017         GT    CCC
                                AGGCAGGAG  GGAAA   CAG
                                |||||||||  |||||   |||
                                TCTGTCTTT  TTTTT   GTC
                                     AG    CA_
GAM390  SETMAR   3'  TCCTGCCCTTCACCTCCTCTT  74018     C        AACCC
                                AGG AGGAGGTGGA     CAGGG
                                ||| ||||||||||     |||||
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                                TTC TCCTCCACTT    GTCCT
                                  _       CCC__
GAM390  SEZ6    3'  TTCTGGACAGTTCTGCCTCCTG 74832        TG  ACC_
            CC                   GGCAGGAGG  GAA   CCAGGG
                                |||||||||  |||   ||||||
                                CCGTCCTCC  CTT   GGTCTT
                                     GT   GACA
GAM390  SFRS10  3'  CAGGGTTTTTTATTGTCTCTTG 17180         TG A A_______  CCAG
            TTT                  AGGCAGGAGG  G A      CC   G
                                |||||||||| | |      ||   |
                                TTTGTTCTCT  T T      GG   C
                                     GT A TTTTT    GAC
GAM390  SFXN2   3'  GGTCTTCTTCGCTTCCTCCT   74382    C       AA______
                                AGG AGGAGGTGGA      CC
                                ||| ||||||||||      ||
                                TCC TCCTTCGCTT      GG
                                  _       CTTCT
GAM390  SHAPY   3'  CTTGAATTTTTTATTCCCTGCC 57910       AG     CCC   G
            T                    AGGCAGG  GTGGAAA   CAGG
                                |||||||  |||||||   ||||
                                TCCGTCC  TATTTTT   GTTC
                                    CT      TAA
GAM390  SIAT9   3'  CTCTGTTGGTCTGCCTTCTGCT 15315        TG  AA  C_
                                GGCAGGAGG  GA  CC  CAGGG
                                |||||||||  ||  ||  |||||
                                TCGTCTTCC  CT  GG  GTCTC
                                     GT  __  TT
GAM390  SIRPB1  3'  CCTTGGTGTTTGCCTCTTTCT  21364    C    TG  AACC
                                AGG AGGAGG  GA   CCAGGG
                                ||| ||||||  ||   ||||||
                                TCT TTCTCC  TT   GGTTCC
                                  _    GT  GT__
GAM390  SLC12A5 3'  CTCTGGGGCCGGGCCTCGCTGC 40769      _   __  AAA
            TT                   AGGCAG GAGGT  GG   CCCCAGGG
                                ||||||  |||||  ||   ||||||||
                                TTCGTC CTCCG  CC   GGGGTCTC
                                   G    GG  ___
GAM390  SLC19A3 3'  CCAGGGCTCTCTCTTTCTCCTG 48241         T   AA_______  CCAG
            CTT                  AGGCAGGAGG GGA       CC   G
                                |||||||||| |||       ||   |
                                TTCGTCCTCT TCT       GG   C
                                     T   CTCTC    GACC
GAM390  SLC26A7 3'  CCTTAAATTTCACCATTTGTCT 54511       A     ACCCC
                                AGGCAGG GGTGGAA    AGG
                                ||||||| |||||||    |||
                                TCTGTTT CCACTTT    TCC
                                    A      AAAT_
GAM390  SLC2A11 3'  TCCTGTCCTCTGCTTCCTGCC  48695        TG  AACCC
                                GGCAGGAGG  GA    CAGGG
                                |||||||||  ||    |||||
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                              CCGTCCTTC  CT    GTCCT
                                   GT  CCT__
GAM390  SLC2A13  3'  CTTTGGATTCCATATTTTTGTT 54658        _     ACC
           T                  AGGCAGGAG GTGGAA   CCAGGG
                              |||||||||  ||||||   ||||||
                              TTTGTTTTT TACCTT   GGTTTC
                                   A     A__
GAM390  SLC38A1  3'  CCAGGGCTCATTTCTATTTCTT 48422     C        A_______  CCAG
           CTT                  AGG AGGAGGTGGAA       CC    G
                              |||  ||||||||||       ||    |
                              TTC TTCTTTATCTT       GG    C
                                _        TACTC    GACC
GAM390  SLC38A5  5'  TCTTGGCCAGCCTGTGTCTCCT 54313         T___  AAACC
           GTCT                  AGGCAGGAGG    GG    CCAGGG
                              ||||||||||    ||    ||||||
                              TCTGTCCTCT    CC    GGTTCT
                                   GTGT  GACC_
GAM390  SLK     3'  CCAGGGTTCTGTTCTCATCTTC 28890          GA  ________  CAG
           TGCC                  GGCAGGAGGTG  AAC      CC   GG
                              ||||||||||  |||      ||   ||
                              CCGTCTTCTAC  TTG      GG   CC
                                    TC   TCTT    GAC
GAM390  SLK     3'  TTCTAGGTGTTTTCCTTTTTTG 28894          T     _  C
           TTT                   AGGCAGGAGG GGAAAC CC AGGG
                              ||||||||||  ||||||  ||  ||||
                              TTTGTTTTTT CTTTTG GG TCTT
                                   C     T  A
GAM390  SMARCF1  3'  CCTTGGGAAAAAGTCTCTCCTG 21187          T  AAAC__
           TTT                   AGGCAGGAGG GG     CCCAGGG
                              ||||||||||  ||      |||||||
                              TTTGTCCTCT CT     GGGTTCC
                                   _  GAAAAA
GAM390  SMARCF1  3'  CCTTGGGAAAAAGTCTCTCCTG 21188          T  AAAC__
           TTT                   AGGCAGGAGG GG     CCCAGGG
                              ||||||||||  ||      |||||||
                              TTTGTCCTCT CT     GGGTTCC
                                   _  GAAAAA
GAM390  SMUG1    3'  CAGGGTTTTGACACTACTCCTG 27469         __   GA A_____  CCAG
           TTT                   AGGCAGGA  GGTG  A     CC    G
                              ||||||||  ||||  |     ||    |
                              TTTGTCCT  TCAC  T     GG    C
                                   CA    AG TTT    GAC
GAM390  SNAPC1   3'  TCCTGGGCTCAAGCTATCCTCC 13280          _  AAAC__
           TGCCT                 AGGCAGGAGG TGG     CCCAGGG
                              ||||||||||  |||     |||||||
                              TCCGTCCTCC ATC     GGGTCCT
                                   T   GAACTC
GAM390  SNAPC3   3'  CCTAAATTTTTACTTTCTGT   13284           CCCC
                              GCAGGAGGTGGAAA   AGG
                              ||||||||||||||   |||
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                                TGTCTTTCATTTTT  TCC
                                      AAA_
GAM390  SPRY4   3'  CAGGGCTCGTTCCTCCTTCTGC 49003        T  AC_____ CCAG
          CT                  AGGCAGGAGG GGAA      C  G
                              |||||||||| ||||      |  |
                              TCCGTCTTCC CCTT      G  C
                                   T  GCTC  G GAC
GAM390  SPRY4   3'  CCAGGGTTTATTTCTACTTTTG 49006      G     A_______ CCAG
          TTT                 AGGCAG AGGTGGAA      CC  G
                              |||||| ||||||||      ||  |
                              TTTGTT TTCATCTT      GG  C
                                _      TATTT   GACC
GAM390  SPRY4   3'  TTCTGGGTTTTGGTTTGCTTTT 49040    C    TG  AAC___
          TCCT                  AGG AGGAGG  GA    CCCAGGG
                              ||| ||||||  ||    |||||||
                              TCC TTTTTC  TT    GGGTCTT
                                _    GT  GGTTTT
GAM390  SPTLC2  3'  CCAGGGCTTTTTCAACTTTTTG 17985        _   A_____  CCAG
          CTT                 AGGCAGGAGG TGGAA    CC  G
                              |||||||||| |||||    ||  |
                              TTCGTTTTTC ACTTT    GG  C
                                   A   TTC   GACC
GAM390  SPTLC2  3'  CCAGGGTCTTATTCCATTTTCT 17986    C       A_______  CCAG
          TCT                 AGG AGGAGGTGGAA      CC  G
                              ||| ||||||||||      ||  |
                              TCT TCTTTTACCTT      GG  C
                                _       ATTCT   GACC
GAM390  SRCRB4D  3'  CTCTGCAGACCACCTCTTCTT  55795    C       AAACCC
                              AGG AGGAGGTGG     CAGGG
                              ||| |||||||||     |||||
                              TTC TTCTCCACC     GTCTC
                                _       AGAC__
GAM390  SRP9    3'  CCTGCCCATTTTCTGTCT    79934           AAACCC
                              AGGCAGGAGGTGG     CAGG
                              ||||||||||||      ||||
                              TCTGTCTTTTACC     GTCC
                                     C_____
GAM390  SRPK2   3'  TCCTGGGGAAGGGTAGTCTTTT 13414         GGAAA__
          GTCT                  AGGCAGGAGGT      CCCCAGGG
                              ||||||||||       ||||||||
                              TCTGTTTTCTG      GGGGTCCT
                                     ATGGGAA
GAM390  SS-56   3'  TCCTGGGTTCACGCCATTCTCC 60361        _  AAAC__
          TGCCT                  AGGCAGGAGG TGG     CCCAGGG
                              |||||||||| |||     |||||||
                              TCCGTCCTCT ACC     GGGTCCT
                                   T  GCACTT
GAM390  SSBP2   3'  CCAGGGCCTTTTTATTTCCTGC 60273    _        A_____  CCAG
          TCT                   AG GCAGGAGGTGGAA     CC  G
                              || ||||||||||||     ||  |
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                                TC CGTCCTTTATTTT     GG   C
                                 T          TCC    GACC
GAM390  SSFA2    3'  GGTGTTTCTTTTTCTGTCT   74169         T    ____
                                AGGCAGGAGG GGAAAC   CC
                                |||||||||| ||||||   ||
                                TCTGTCTTTT TCTTTG   GG
                                     _     T
GAM390  SSH2     3'  CCAGGGTTTTTTTTTCTTTCTG 62889          T   A_______ CCAG
            CTT                   AGGCAGGAGG GGAA      CC   G
                                |||||||||| ||||      ||   |
                                TTCGTCTTTC TTTT      GG   C
                                     T   TTTT    GACC
GAM390  SSR3     3'  CCCAGGGTTTTCCCCTCTACTC 24033         GT____   A____  CCAG
            TTGTCT                AGGCAGGAG     GGAA    CC   GG
                                |||||||||     ||||    ||   ||
                                TCTGTTCTC     CCTT    GG   CC
                                     ATCTCC   TT    GACC
GAM390  SSX5     3'  CCCTCACTCTGTTTCCTGTT   41016        TG  AACCCC
                                GGCAGGAGG  GA     AGGG
                                |||||||||  ||     ||||
                                TTGTCCTTT  CT     TCCC
                                     GT  CAC___
GAM390  ST13     3'  TCTGTGTTTGCTTTCTGCTT   15433         TG  AACCC
                                AGGCAGGAGG  GA    CAGG
                                ||||||||||  ||    ||||
                                TTCGTCTTTC  TT    GTCT
                                     GT  GT___
GAM390  STARD7   5'  CCTGGCCATGCCTCTGCCT   39738       G    GAAACC
                                AGGCAG AGGTG     CCAGG
                                |||||| |||||     |||||
                                TCCGTC TCCGT     GGTCC
                                   _    ACC___
GAM390  STARD7   5'  CCTGGCCATGCCTCTGCCT   39739       G    GAAACC
                                AGGCAG AGGTG     CCAGG
                                |||||| |||||     |||||
                                TCCGTC TCCGT     GGTCC
                                   _    ACC___
GAM390  STK16    3'  TCCTGCATCTTTTCTTCTGCTT 72589          T_  AACCC
                                AGGCAGGAGG  GGA    CAGGG
                                ||||||||||  |||    |||||
                                TTCGTCTTCT  TCT    GTCCT
                                     TT   AC___
GAM390  STK17A   3'  CTTTGAATTCTACATCCTGTTT 17667         G     ACCC
                                AGGCAGGA GTGGAA    CAGGG
                                |||||||| ||||||    |||||
                                TTTGTCCT CATCTT    GTTTC
                                     A     AA__
GAM390  STK29    3'  TCTGTCTCTGCCTCTGCCT   88966       G   TG  AACCC
                                AGGCAG AGG  GA    CAGG
                                |||||| |||  ||    ||||
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                                TCCGTC TCC  CT    GTCT
                                   _  GT  CT___
GAM390  STRN3    3'  CAGGGTTTATTTCACTTTTTGT 28137           A_______  CCAG
              T                  GGCAGGAGGTGGAA      CC    G
                                 ||||||||||||||      ||   |
                                 TTGTTTTTCACTTT      GG    C
                                       ATTT     GAC
GAM390  STRN3    3'  CTTTCTTTCCTTCTTTTGCCT  28139         T     CCCC
                                 AGGCAGGAGG GGAAA    AGG
                                 ||||||||||| |||||    |||
                                 TCCGTTTTCT CCTTT    TTC
                                       T    CT__
GAM390  STX5A    3'  CCCTGATCCCCCACCCCTTGCC 13471        A     AAACCC
              T                  AGGCAGG GGTGG      CAGGG
                                 |||||||| |||||      |||||
                                 TCCGTTC CCACC      GTCCC
                                    C     CCCTA_
GAM390  SUCLG2   3'  TCCATGTGTTTTTACCATTTGC 66226        A        CC  _
              CT                   AGGCAGG GGTGGAAAC  CA GGG
                                 |||||||| |||||||||  || |||
                                 TCCGTTT CCATTTTTG  GT CCT
                                    A        T_  A
GAM390  SUPT4H1  3'  CCCTGCTTGTCTATTTTCTTCT 13484     C         AACCC
                                 AGG AGGAGGTGGA     CAGGG
                                 ||| ||||||||||     |||||
                                 TCT TCTTTTATCT     GTCCC
                                   _         GTTC_
GAM390  SV2B     3'  CTGATTTTTGATCTTTTGTTT  29949          G    CCC
                                 AGGCAGGAGGT GAAA   CAG
                                 |||||||||||| ||||   |||
                                 TTTGTTTTCTA TTTT   GTC
                                       G    TA_
GAM390  SV2B     3'  TTCTGGCCATCCACTTCTT    29954          AACC
                                 AGGAGGTGGA    CCAGGG
                                 ||||||||||    ||||||
                                 TTCTTCACCT    GGTCTT
                                       ACC_
GAM390  SYT13    3'  CCAGGGCTATTTTTCACCTTTT 95100     C         A________  CCAG
              TTTT                  AGG AGGAGGTGGAA       CC    G
                                 ||| ||||||||||       ||   |
                                 TTT TTTTCCACTTT       GG    C
                                   T         TTATC     GACC
GAM390  SYTL3    3'  CTCTGGTGGGTTATCTCCTCTT 81914     C       GAAA  _
                                 AGG AGGAGGTG    CC CCAGGG
                                 ||| ||||||||    || ||||||
                                 TTC TCCTCTAT    GG GGTCTC
                                   _       TG__  T
GAM390  SYTL4    3'  CAGGGCTTTTTATCTTCTGTCT 55782             _____  CCA
                                 AGGCAGGAGGTGGAAA     CC   G
                                 ||||||||||||||||     ||   |
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                                TCTGTCTTCTATTTTT    GG  C
                                          C  G AC
GAM390  SYTL4    3'  CCCTGTTATTCTGACTTCCTGC 55784          _   ACCC
            TT                  AGGCAGGAGGT GGAA   CAGGG
                                ||||||||||| ||||   |||||
                                TTCGTCCTTCA TCTT   GTCCC
                                      G   ATT_
GAM390  T2BP     3'  CCAGGGTTATTTTCTTTTTCTG 70534         T   A________  CCAG
            CTT                   AGGCAGGAGG GGAA      CC   G
                                ||||||||||| ||||       ||   |
                                TTCGTCTTTT TCTT       GG   C
                                      _   TTATT    GACC
GAM390  T2BP     3'  GCTTGATTTTCATCTTGTGTTT 70538      G       CCC   G
                                AGGCA GAGGTGGAAA   CAGG
                                ||||| ||||||||||   ||||
                                TTTGT TTCTACTTTT   GTTC
                                   G        A__   GT
GAM390  TA-KRP   3'  CCCAGTTTTATCTTCTGTTT   51672            ACCCCA
                                AGGCAGGAGGTGGAA     GGG
                                ||||||||||||||     |||
                                TTTGTCTTCTATTTT     CCC
                                       GA____
GAM390  TBLR1    3'  CTCTGTTGGTTTTGTTTTTTTG 45428         TG     C_
            TTT                   AGGCAGGAGG  GAAACC  CAGGG
                                ||||||||||  ||||||  |||||
                                TTTGTTTTTT  TTTTGG  GTCTC
                                      TG     TT
GAM390  TBLR1    3'  TTTTGGGTTTTTTGTTGTTTGT 45433       AG TG   C
            TT                    AGGCAGG  G  GAAA CCCAGGG
                                |||||||  |  |||| |||||||
                                TTTGTTT  T  TTTT GGGTTTT
                                    GT GT   T
GAM390  TBX19    3'  TTCTGGAAAGCCTCACTTCCT  18924         AAACC_
                                AGGAGGTGG     CCAGGG
                                |||||||||     ||||||
                                TCCTTCACT     GGTCTT
                                     CCGAAA
GAM390  TCF-3    3'  CCAGGGCTCTCTTGCACTTTCT 49241          G  AC________ CCAG
            GTCT                   AGGCAGGAGGTG AA       C   G
                                ||||||||||| ||       |   |
                                TCTGTCTTTCAC TT       G   C
                                      G  CTCTC   G GACC
GAM390  TCF-3    3'  TCTTGCACTTTCTGTCTCCTGT 49242         TG   CCC
            CT                    AGGCAGGAGG  GAAA   CAGGG
                                ||||||||||  ||||   |||||
                                TCTGTCCTCT  CTTT   GTTCT
                                      GT    CAC
GAM390  TED      3'  CTCTGTATATGTACTGCTTTCT 32266         TG AAACCC__
            GTTT                   AGGCAGGAGG  G       CAGGG
                                ||||||||||  |       |||||
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                                TTTGTCTTTC  C       GTCTC
                                      GT ATGTATAT
GAM390  TFEC     3'  CCAGGGCTCATTTCCATCTTCT 25313     C        A________  CCAG
              CTT                   AGG AGGAGGTGGAA       CC    G
                                ||| ||||||||||       ||    |
                                TTC TCTTCTACCTT       GG    C
                                  _         TACTC     GACC
GAM390  THEA     3'  CCTATGTCTACTTCTTTCT    66884     C        AACCCC
                                AGG AGGAGGTGGA     AGG
                                ||| ||||||||||     |||
                                TCT TTCTTCATCT     TCC
                                  _        GTA___
GAM390  THEA     3'  CCTGTGTTTTTTTTTGTTT    66886         GTG    CC
                                AGGCAGGAG   GAAAC  CAGG
                                |||||||||   |||||  ||||
                                TTTGTTTTT   TTTTG  GTCC
                                      ___     T_
GAM390  THEA     3'  TTTTGGAGGTTTTATTTGTTTG 66904        AGGTG     _
              TTT                   AGGCAGG     GAAACC CCAGGG
                                |||||||     |||||| ||||||
                                TTTGTTT     TTTTGG GGTTTT
                                    GTTTA     A
GAM390  TINF2    3'  CTCTGTACTCTAGTCTCCTGCC 25871          _    AACCC
              T                    AGGCAGGAGG TGGA     CAGGG
                                |||||||||| ||||     |||||
                                TCCGTCCTCT ATCT     GTCTC
                                      G    CAT__
GAM390  TJP4     3'  CCAGGGCTCATTTCCGTTTCCT 55504     C    GG     A________  CCAG
              ACCT                   AGG AGGA  TGGAA       CC    G
                                ||| ||||  |||||       ||    |
                                TCC TCCT  GCCTT       GG    C
                                  A    TT    TACTC     GACC
GAM390  TLOC1    5'  CTCTGATCCACTTCTCTGCTT  13774       _       AACCC
                                AGGCAG GAGGTGGA     CAGGG
                                |||||| ||||||||     |||||
                                TTCGTC CTTCACCT     GTCTC
                                    T       A____
GAM390  TLR10    5'  CAGGGTTCTATTTGTTTCCTGT 48977          TG  AA_______  CCAG
              TT                    AGGCAGGAGG  GA       CC    G
                                |||||||||  ||       ||    |
                                TTTGTCCTTT  TT       GG    C
                                      GT  ATCTT     GAC
GAM390  TMG3     3'  TTCTGTGATTTCTGTCCTTGCT 44226        A  TG    CCC
              T                    AGGCAGG GG  GAAA   CAGGG
                                |||||||  ||  ||||   |||||
                                TTCGTTC CT  CTTT   GTCTT
                                    _ GT    AGT
GAM390  TOLLIP   3'  CAGGGCTTTCCTTCATTTTATG 39192       G       AA________  CCAG
              CTT                   AGGCA GAGGTGGA       CC    G
                                ||||| ||||||||       ||    |
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                                TTCGT TTTTACTT       GG   C
                                  A       CCTTTC    GAC
GAM390  TOR1B    3'  CTTTGGGGTTTTGCCTGTTT  27973       AGGTG
                                AGGCAGG    GAAACCCCAGGG
                                |||||||    ||||||||||||
                                TTTGTCC    TTTTGGGGTTTC
                                   G____
GAM390  TOR2A    3'  CTCTGAGCCTCTGTCTCTGCTT 56186      G  TG  AACCC
                                AGGCAG AGG  GA    CAGGG
                                |||||| |||  ||    |||||
                                TTCGTC TCT  CT    GTCTC
                                   _  GT  CCGA_
GAM390  TREX1    5'  CCTCTCCAACTTCCTGCCT   50604         _  AACCCC
                                AGGCAGGAGGT GGA     AGG
                                |||||||||| |||     |||
                                TCCGTCCTTCA CCT     TCC
                                      A  C_____
GAM390  TRIM22   3'  TCTTGGGAAACAATTTTTTGTT 21389         GGAAAC
           T                     AGGCAGGAGGT     CCCAGGG
                                |||||||||||     |||||||
                                TTTGTTTTTTA     GGGTTCT
                                      ACAAA_
GAM390  TRIM26   3'  CCCCAGGGTCTTATTTCTGCCT 14345     A       A_________  CCAG
           CTAGTTT                 AGGC GGAGGTGGAA       CC   GG
                                |||| ||||||||||       ||   ||
                                TTTG TCTCCGTCTT       GG   CC
                                  A        TATTCT    GACC
GAM390  TRIM6    3'  CCCTTCTGATCTTCTGTTT   55177         _  AACCCC
                                AGGCAGGAGGT GGA     AGGG
                                |||||||||| |||     ||||
                                TTTGTCTTCTA TCT     TCCC
                                      G  _______
GAM390  TRIP-Br2 3'  CAGGGTTCTGCTCACTTCTTGC 29261          AAA_______  CCAG
           C                     GGCAGGAGGTGG       CC   G
                                ||||||||||||       ||   |
                                CCGTTCTTCACT       GG   C
                                      CGTCTT    GAC
GAM390  TRPC3    3'  CCCCAGGGCTTTGCACTACCTG 13858       _    AAA________  CCAG
           TTTGCCT                 AGGCAGG AGGTGG       CC   GG
                                ||||||| ||||||       ||   ||
                                TCCGTTT TCCATC       GG   CC
                                   G     ACGTTTC    GACC
GAM390  TTTY9    3'  CCCAGCATATTTCTGTTTTCTA 50021     C     TG   CCCCA_
           CCT                   AGG AGGAGG  GAAA     GGG
                                ||| ||||||  ||||     |||
                                TCC TCTTTT  CTTT     CCC
                                  A     GT    ATACGA
GAM390  TU12B1-TY 3'  CCAGGGCTTTCTTTCTTTTTTG 33835      __     T   A____  CCAG
           CCT                   AGGCA  GGAGG GGAA    CC   G
                                |||||  ||||| ||||    ||   |
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                                TCCGT  TTTCT TCTT    GG   C
                                  TT    T   TC    GACC
GAM390  TU12B1-TY 3'  CTCTGATTTTGCCTTTTTGTTT 33846     _    TG   ACCC
                                AGGC AGGAGG  GAA   CAGGG
                                |||| ||||||  |||   |||||
                                TTTG TTTTCC  TTT   GTCTC
                                  T     GT   A___
GAM390  TU12B1-TY 3'  GGCTTTTTTCATTTCTTTCT   33854     C        A_______
                                AGG AGGAGGTGGAA      CC
                                ||| ||||||||||       ||
                                TCT TTCTTTACTTT      GG
                                  _         TTTC
GAM390  TU3A    3'  CCAGGGTTTTTTTTTACTTTTT 24180     C        A________  CCAG
           CCT                    AGG AGGAGGTGGAA       CC   G
                                ||| ||||||||||       ||   |
                                TCC TTTTTCATTTT       GG   C
                                  _         TTTTT    GACC
GAM390  TUSP    5'  CCCAGGGCTCTGGCTTCTGCTT 40020         G   AA__  CCAG
                                AGGCAGGAG TGGA   CC   GG
                                ||||||||| ||||   ||   ||
                                TTCGTCTTC GTCT   GG   CC
                                     G   C    GACC
GAM390  TXN2    3'  TCCTGCTGCCTCCCTCCTGTCT 25933          T_  AAACCC
                                AGGCAGGAGG  GG    CAGGG
                                ||||||||||  ||    |||||
                                TCTGTCCTCC  CC    GTCCT
                                     CT  GTC___
GAM390  UBE2G1   3'  CTTTGCTTTTATCTCTTACCT  13953     C        ACCC
                                AGG AGGAGGTGGAA   CAGGG
                                ||| ||||||||||   |||||
                                TCC TTCTCTATTTT   GTTTC
                                  A         C___
GAM390  UBE3B   3'  CTCTGGGTTTTTTGTTTTTT   77442       TG   C
                                AGGAGG  GAAA CCCAGGG
                                ||||||  |||| |||||||
                                TTTTTT  TTTT GGGTCTC
                                   GT   T
GAM390  UCK1    3'  TCCTCATGTTTTCTGTTTTCTG 49502          TG   _ CCC
           TTT                   AGGCAGGAGG  GAAA C   AGGG
                                ||||||||||  |||| |   ||||
                                TTTGTCTTTT  CTTT G   TCCT
                                     GT   T TAC
GAM390  UNC5D   3'  CCCAGGGTCCACCTTTTACTT  56003     C        AA_  CCAG
                                AGG AGGAGGTGGA   CC   GG
                                ||| ||||||||||   ||   ||
                                TTC TTTTCCACCT   GG   CC
                                  A            GACC
GAM390  UNC5D   3'  TCCGTAGTTTCCACTGTTTTGT 56009         _       CCCA
           CT                    AGGCAGGA GGTGGAAAC    GGG
                                |||||||| |||||||||    |||
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                                TCTGTTTT TCACCTTTG   CCT
                                    G       ATG_
GAM390  USP15   3' CTTTGGGGTTTTTTTTTTCT  21962      TG
                                AGGAGG  GAAACCCCAGGG
                                ||||||  ||||||||||||
                                TCTTTT  TTTTGGGGTTTC
                                   TT
GAM390  USP15   3' TTTGAAACATTTTTATTTGCTG 21967      G      CCC__   G
           CTT                   AGGCAG AGGTGGAAA    CAGG
                                ||||||| |||||||||    ||||
                                TTCGTC TTTATTTTT    GTTT
                                   G       ACAAA
GAM390  USP16   3' TAGTGGTTTTTATTCCTGCTT  22247        G      CCAGGG
                                AGGCAGGAG TGGAAACC
                                ||||||||| ||||||||
                                TTCGTCCTT ATTTTTGG
                                    _       TGATA
GAM390  WAC     3' CCAGGGTCCTCTTTATCTCCTT 34032     C       AA_______  CCAG
           TCT                   AGG AGGAGGTGGA       CC   G
                                ||| ||||||||||       ||   |
                                TCT TCCTCTATTT       GG   C
                                  T       CTCCT    GACC
GAM390  WAC     3' CCCGTGTGTTTCCATTTCCTTC 34033     C         CCCA
           T                    AGG AGGAGGTGGAAAC   GGG
                                ||| ||||||||||||    |||
                                TCT TCCTTTACCTTTG   CCC
                                  _          TGTG
GAM390  WBSCR16  3' CCCCAGGGTCTATTTTCTGCCT 96148           AA_  CCAG
                                AGGCAGGAGGTGGA  CC   GG
                                ||||||||||||||  ||   ||
                                TCCGTCTTTTATCT  GG   CC
                                          GACC
GAM390  WBSCR23  3' TCCTGCAAAGTCTCTCCTGCTT 47447        GT   AACCC
                                AGGCAGGAG  GGA    CAGGG
                                |||||||||  |||    |||||
                                TTCGTCCTC  TCT    GTCCT
                                    __   GAAAC
GAM390  WDR7    3' TTCTGAAGTGCTCATCTCTTGC 31613          AA  CC
           TT                    AGGCAGGAGGTGG  AC  CAGGG
                                ||||||||||||  ||  |||||
                                TTCGTTCTCTACT  TG  GTCTT
                                      CG  AA
GAM390  WIRE    3' TTTGGGGGTATTTTGTTT    78909        GGTGGAAA
                                AGGCAGGA       CCCCAGG
                                ||||||||       |||||||
                                TTTGTTTT       GGGGTTT
                                   ATG_____
GAM390  WSB1    3' CCAGGGTCGATGTCCACTTTCT 56969           AA________  CCAG
           GCTT                   AGGCAGGAGGTGGA       CC   G
                                ||||||||||||||       ||   |
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                                TTCGTCTTTCACCT       GG   C
                                      GTAGCT    GACC
GAM390  WSB1    3'  TCTGCTTTTGCCTTCTGTT   56980        TG   ACCC
                                GGCAGGAGG  GAA   CAGG
                                |||||||||  |||   ||||
                                TTGTCTTCC  TTT   GTCT
                                     GT   C___
GAM390  WSB1    3'  TCTGCTTTTGCCTTCTGTT   56981        TG   ACCC
                                GGCAGGAGG  GAA   CAGG
                                |||||||||  |||   ||||
                                TTGTCTTCC  TTT   GTCT
                                     GT   C___
GAM390  YAP1    3'  CCTTGATGTGGTCTCTTGTTT  21459         TGGAA  CC
                                AGGCAGGAGG    AC  CAGGG
                                ||||||||||    ||  |||||
                                TTTGTTCTCT    TG  GTTCC
                                      GG___  TA
GAM390  YWHAQ   3'  CCAGGGTTCACTTACACCTCCT 23350          GAAA________  CCAG
           GCCT                  AGGCAGGAGGTG        CC   G
                                ||||||||||||         ||   |
                                TCCGTCCTCCAC         GG   C
                                      ATTCACTT    GACC
GAM390  ZAP3    3'  TCCACGTTTCAGTTCTTGTTT  77735         G    ACCCCA
                                AGGCAGGAG TGGAA     GGG
                                ||||||||| |||||     |||
                                TTTGTTCTT ACTTT     CCT
                                     G    GCA___
GAM390  ZDHHC2  3'  CCCCAGGGCTTAATTCCAGCCT 33446         _    A________  CCAG
           TTTGTTT               AGGCAGGAGG TGGAA      CC   GG
                                ||||||||||| |||||       ||   ||
                                TTTGTTTTCC ACCTT      GG   CC
                                     G    AATTC    GACC
GAM390  ZDHHC3  3'  CTTTGTTTCATCTGCTTCCTCT 33930    C     TG  AACCC
           CT                   AGG AGGAGG  GA    CAGGG
                                ||| ||||||  ||    |||||
                                TCT TCCTTC  CT    GTTTC
                                  C     GT  ACTTT
GAM390  ZDHHC9  5'  CCCTGGGACGGTCCGTTTCCTG 62353       GG   AAC_
           CC                   GGCAGGA  TGGA   CCCAGGG
                                |||||||  ||||   |||||||
                                CCGTCCT  GCCT   GGGTCCC
                                   TT   GGCA
GAM390  ZER6    3'  TCCTGCCAAAGTTCTGTCTCTG 64117      G   TG   ACCC__
           TCT                   AGGCAG AGG  GAA     CAGGG
                                ||||||  |||  |||     |||||
                                TCTGTC TCT  CTT     GTCCT
                                   _  GT   GAAACC
GAM390  ZER6    3'  TCTTGTTTCCTCTGCTTCTTCC 64118    C     TG  AACCC
           T                     AGG AGGAGG  GA    CAGGG
                                ||| ||||||  ||    |||||
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                              TCC TTCTTC  CT    GTTCT
                                _     GT  CCTTT
GAM390  ZFP106   3'  CCCCAGGGTCGCTTTCCAGCCT 42721         _   A_______  CCAG
           TTTGTTT                AGGCAGGAGGT GGAA       CC   GG
                              |||||||||| ||||       ||   ||
                              TTTGTTTTCCG CCTT       GG   CC
                                   A   TCGCT    GACC
GAM390  ZFP36L2  3'  GGTTTCCTCTTGTCT      23534        GGT
                              AGGCAGGA   GGAAACC
                              ||||||||   |||||||
                              TCTGTTCT   CCTTTGG
                                   ___
GAM390  ZFP91    3'  CCTTGCTTTTTGTTTCTTGCTT 54873         TG   CCC
                              AGGCAGGAGG  GAAA   CAGGG
                              ||||||||||  ||||   |||||
                              TTCGTTCTTT  TTTT   GTTCC
                                   GT   C__
GAM390  ZFP91    3'  GCTCTGGCTCCTTGCTTTTTGT 54876         TG   CC_______
           TTCTTGCTT               AGGCAGGAGG  GAAA      CCAGGG   C
                              ||||||||||  ||||       ||||||   |
                              TTCGTTCTTT  TTTT       GGTCTC   G
                                   GT    CGTTCCTC
GAM390  ZIM2     3'  CCAGGGCTTTGTGCGCTTCCTG 31720          GAAA_______  CCAG
           CCT                   AGGCAGGAGGTG        CC   G
                              ||||||||||||        ||   |
                              TCCGTCCTTCGC        GG   C
                                   GTGTTTC    GACC
GAM390  ZIM3     5'  TTTGGGTTGTTTCTTGACT    54642    G      TG AAAC
                              AG CAGGAGG  G   CCCAGG
                              || |||||||  |   ||||||
                              TC GTTCTTT  T   GGGTTT
                               A      GT ____
GAM390  ZIN      3'  CTCTATTTATTTCACTCTCTTG 26392         _     ACCCC
           TTT                   AGGCAGGAG GTGGAA    AGGG
                              |||||||||  ||||||    ||||
                              TTTGTTCTC CACTTT    TCTC
                                   T     ATTTA
GAM390  ZNF212   3'  CCAGGGCCCTCCATTTTTTCTT 25316         ___    AA____  CCAG
           GTTT                  AGGCAGGAG   GTGGA     CC   G
                              |||||||||  |||||     ||   |
                              TTTGTTCTT   TACCT     GG   C
                                   TTT    CCC    GACC
GAM390  ZNF220   3'  CCCAACCTTTCATTTCCTACTT 23155     C         ACCCCA
                              AGG AGGAGGTGGAA     GGG
                              ||| ||||||||||     |||
                              TTC TCCTTTACTTT     CCC
                                A         CCAA__
GAM390  ZNF237   3'  CCAGGGTTTTGCTCTACCACCT 27268        A     AA_______  CCAG
           GCCT                  AGGCAGG GGTGGA       CC   G
                              |||||||  ||||||       ||   |
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                                TCCGTCC CCATCT       GG   C
                                   A     CGTTTT    GACC
GAM390  ZNF313   3'  CAGGGTTCTTTTACCTTCTGCT 38563            AC_____ CCAG
           T                    AGGCAGGAGGTGGAA      C   G
                                |||||||||||||||      |   |
                                TTCGTCTTCCATTTT      G   C
                                      CTT   G GAC
GAM390  ZNF317   3'  CCCTGTATGTTTTGTTCTTTGC 72476       AG TG   ACCC
           TT                    AGGCAGG  G  GAA   CAGGG
                                |||||||  |  |||   |||||
                                TTCGTTT  T  TTT   GTCCC
                                   CT GT   GTAT
GAM390  ZNF337   3'  TCCTGTGGCCCTTCTATTTTCT 68652            AC_ _
           GCT                     GGCAGGAGGTGGAA   CC CAGGG
                                |||||||||||||||   || |||||
                                TCGTCTTTTATCTT   GG GTCCT
                                      CCC  T
GAM390  ZNF339   3'  CCCTGTAACCTGTGTCCTGTCT 41390        G TG AAACCC
                                AGGCAGGA G  G     CAGGG
                                ||||||||  |  |     |||||
                                TCTGTCCT T  C     GTCCC
                                   G GT CAAT__
GAM390  ZNF364   3'  GGTGTTTCCACCTCCTTCT   67311     C         ____
                                AGG AGGAGGTGGAAAC   CC
                                |||  ||||||||||||   ||
                                TCT TCCTCCACCTTTG   GG
                                  _          T
GAM390  ZTL1     3'  CCAGGGTTTTAGTCCATTTTTT 43516          AA_______  CCAG
           GC                     GCAGGAGGTGGA       CC   G
                                ||||||||||||       ||   |
                                CGTTTTTTACCT       GG   C
                                      GATTTT    GACC
GAM390  ZWINT    3'  CCTTGATCTTTCCCACTTTCTG 23903          _  CCC
           TTT                     AGGCAGGAGGTGG AAA   CAGGG
                                |||||||||||||  |||   |||||
                                TTTGTCTTTCACC TTT   GTTCC
                                      C   CTA
GAM390  ZWINT    3'  CCTTGATCTTTCCCACTTTCTG 23904          _  CCC
           TTT                     AGGCAGGAGGTGG AAA   CAGGG
                                |||||||||||||  |||   |||||
                                TTTGTCTTTCACC TTT   GTTCC
                                      C   CTA
GAM390  LOC112616 3'  GGTCCTCTCCATCTCTGCCT   57296      G      AA_______
                                AGGCAG AGGTGGA       CC
                                ||||||  |||||||      ||
                                TCCGTC TCTACCT       GG
                                   _      CTCCT
GAM390  LOC112885 3'  CTCTGGCTGACTTCCTTTCTGC 57338          T   AACC_
           TT                     AGGCAGGAGG GGA     CCAGGG
                                |||||||||  |||     ||||||
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                                TTCGTCTTTC CTT    GGTCTC
                                      _  CAGTC
GAM390  LOC113730 3'  TTCTGGACAACTTTCCCCTTCT 73502         T    CC___
            GCTT                   AGGCAGGAGG GGAAA    CCAGGG
                                |||||||||| |||||    ||||||
                                TTCGTCTTCC CCTTT    GGTCTT
                                      _    CAACA
GAM390  LOC115110 3'  CCATTTTCACCTTCTGTCT   72175             CCCCA
                                AGGCAGGAGGTGGAAA    GG
                                |||||||||||||||    ||
                                TCTGTCTTCCACTTTT    CC
                                      A____
GAM390  LOC115286 3'  TCTGATCTTTCATTTCCTGCC  73765            ACCC
                                GGCAGGAGGTGGAA   CAGG
                                ||||||||||||||   ||||
                                CCGTCCTTTACTTT   GTCT
                                      CTA_
GAM390  LOC115294 3'  TATAATGGTTTTCATTTTTTAC 73383    C          CCAGGG
            TT                   AGG AGGAGGTGGAAACC
                                ||| ||||||||||||||
                                TTC TTTTTTACTTTTGG
                                  A          TAATATC
GAM390  LOC115817 3'  CCTTGTCCTTCTTTTTACTTTT 57412             CCC___
            TGCCT                  AGGCAGGAGGTGGAAA    CAGGG
                                |||||||||||||||    |||||
                                TCCGTTTTTCATTTTT    GTTCC
                                      CTTCCT
GAM390  LOC115827 3'  CTTGGGAGCTTTCCTGTTT   57415        GT  AAAC
                                AGGCAGGAG  GG   CCCAGG
                                |||||||||  ||   ||||||
                                TTTGTCCTT  TC   GGGTTC
                                     __  GA__
GAM390  LOC116028 3'  GAATGTTGGGTTTCTGCTGTCT 74096       GA  TG     CAGGG
            GCTT                   AGGCAG  GG  GAAACCC
                                ||||||  ||  |||||||
                                TTCGTC  TC  CTTTGGG
                                   TG  GT     TTGTAAGT
GAM390  LOC119369 3'  CTCTGGCTTTTCCTTTTTGTTT 76023         T    CC
                                AGGCAGGAGG GGAAA  CCAGGG
                                |||||||||| |||||  ||||||
                                TTTGTTTTTC CTTTT  GGTCTC
                                      _    C_
GAM390  LOC119559 3'  CTCTGGGGTTTTTAAGGCTGGC 74453    G   GAGG
            T                   AG CAG   TGGAAACCCCAGGG
                                || |||   ||||||||||||||
                                TC GTC   ATTTTTGGGGTCTC
                                 G  GGA_
GAM390  LOC120224 5'  TCCTGAACACTTTGCTTTCTAT 57895    GC     TG  AACCC
            CT                   AG  AGGAGG  GA    CAGGG
                                ||  ||||||  ||    |||||
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                                TC  TCTTTC  TT    GTCCT
                                 TA     GT  CACAA
GAM390   LOC120939 3'  CCAGGGCTTTACTTCTTTCCT  76758     C        AA__  CCAG
                                AGG AGGAGGTGGA   CC   G
                                ||| ||||||||||   ||   |
                                TCC TTCTTCATTT   GG   C
                                  T        C    GACC
GAM390   LOC121219 5'  CTGTATTTTCGCCTTTTGTCT  74488             CCC
                                AGGCAGGAGGTGGAAA  CAG
                                ||||||||||||||||  |||
                                TCTGTTTTCCGCTTTT  GTC
                                          AT_
GAM390   LOC121504 3'  TCTTGACATTTGCCTCTTCTT  74554     C     TG  AACCC
                                AGG AGGAGG  GA    CAGGG
                                ||| ||||||  ||    |||||
                                TTC TTCTCC  TT    GTTCT
                                  _     GT  ACA__
GAM390   LOC121838 5'  CTTGTAGTTCTTTCTGTCT   76513         TGGA   CC
                                AGGCAGGAGG   AAC  CAGG
                                ||||||||||   |||  ||||
                                TCTGTCTTTC   TTG  GTTC
                                      _____  AT
GAM390   LOC121838 5'  GGTTCTGTCCTTTCTTGCTT   76514         T   AA_______
                                AGGCAGGAGG GGA       CC
                                |||||||||| |||       ||
                                TTCGTTCTTT CCT       GG
                                      _  GTCTT
GAM390   LOC124446 5'  CTTGGGAAGTCCTTTGTCT   74774        AGGT   AAC
                                AGGCAGG   GGA   CCCAGG
                                |||||||   |||   ||||||
                                TCTGTTT   CCT   GGGTTC
                                     _____  GAA
GAM390   LOC124753 5'  CCTGCAACCTTCTGTCTTTTGC 74801         TG   ACCC_   G
           C                     GGCAGGAGG  GAA    CAGG
                                |||||||||  |||    ||||
                                CCGTTTTCT  CTT    GTCC
                                      GT   CCAAC
GAM390   LOC124753 5'  CTGGCTTTCTTCTTCCTGCCT  74804         T    CC
                                AGGCAGGAGG GGAAA  CCAG
                                |||||||||| |||||  ||||
                                TCCGTCCTTC TCTTT  GGTC
                                      T    C_
GAM390   LOC124753 5'  TCCTAGATTTCTATCTCTTCCC 74807     C         CCCC
           T                     AGG AGGAGGTGGAAA   AGGG
                                ||| ||||||||||||   ||||
                                TCC TTCTCTATCTTT   TCCT
                                  C          AGA_
GAM390   LOC124961 3'  CCAGGGTTCTCTTTTCCTTCTG 76163         TG  AA_______  CCAG
           TTT                   AGGCAGGAGG  GA      CC   G
                                |||||||||  ||      ||   |
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                                TTTGTCTTCC TT      GG   C
                                     TT CTCTT    GACC
GAM390  LOC126122 3' CCTTGTCCTCTGCCTTCTGCT 74906        TG AACCC
                                GGCAGGAGG GA    CAGGG
                                ||||||||| ||    |||||
                                TCGTCTTCC CT    GTTCC
                                     GT CCT__
GAM390  LOC126282 3' CCAGGGTTTTTTTCCACCTCTT 74951    C        A_______ CCAG
          TTCT                    AGG AGGAGGTGGAA      CC   G
                                ||| ||||||||||       ||   |
                                TCT TTCTCCACCTT      GG   C
                                  T        TTTTT    GACC
GAM390  LOC126282 3' TTTGGGGCTCTCCTGCT    74974        TGGAAA
                                GGCAGGAGG    CCCCAGG
                                |||||||||    |||||||
                                TCGTCCTCT    GGGGTTT
                                     C_____
GAM390  LOC126299 5' CTCTGCTCCTGTCTCCTGTC  74979        TG AAACCC
                                GGCAGGAGG G    CAGGG
                                ||||||||| |    |||||
                                CTGTCCTCT C    GTCTC
                                     GT CTC___
GAM390  LOC126353 3' CCCTGCTGATTCTTTCTGCTT 74991        TGGAAACCC
                                AGGCAGGAGG       CAGGG
                                ||||||||||       |||||
                                TTCGTCTTTC       GTCCC
                                     TTAGTC___
GAM390  LOC126526 3' CTTTGTTCATTTCTCTTCTGTT 75038        T   ACCC
          T                      AGGCAGGAGG GGAA   CAGGG
                                |||||||||| ||||   |||||
                                TTTGTCTTCT CTTT   GTTTC
                                     _   ACTT
GAM390  LOC126603 5' TCCTGCAAGCTCCACTTTCTGT 75913          AACCC
                                GCAGGAGGTGGA    CAGGG
                                ||||||||||||    |||||
                                TGTCTTTCACCT    GTCCT
                                      CGAAC
GAM390  LOC126669 3' CTCTGGCTTTTTGTCATTTTGT 75932       _ TG   CC
          CT                     AGGCAGGA GG  GAAA  CCAGGG
                                |||||||| ||  ||||  ||||||
                                TCTGTTTT CT  TTTT  GGTCTC
                                    A  GT   C_
GAM390  LOC127002 5' CCTTGGGAGCAGTCTCTCTGTC 75124       _   _ GAAAC
          T                      AGGCAG GAGG TG    CCCAGGG
                                |||||| |||| ||    |||||||
                                TCTGTC CTCT AC    GGGTTCC
                                   T   G  GA___
GAM390  LOC128954 5' CCTGTGCTGCCTTCTGCCT   76302        TG AAACCC
                                AGGCAGGAGG  G    CAGG
                                ||||||||||  |    ||||
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                                TCCGTCTTCC  C     GTCC
                                      GT GT____
GAM390   LOC128954 5'  CCTGTGCTGCCTTCTGCCT   76303          TG AAACCC
                                AGGCAGGAGG  G     CAGG
                                ||||||||||  |     ||||
                                TCCGTCTTCC  C     GTCC
                                      GT GT____
GAM390   LOC128954 5'  TCTGTGCTGCCTTCTGCCT   76308          TG AAACCC
                                AGGCAGGAGG  G     CAGG
                                ||||||||||  |     ||||
                                TCCGTCTTCC  C     GTCT
                                      GT GT____
GAM390   LOC129198 3'  CCCTGTGACCTCCCTCCTGTCT 76613           TG AAACCC
                                AGGCAGGAGG  G     CAGGG
                                ||||||||||  |     |||||
                                TCTGTCCTCC  C     GTCCC
                                      CT CAGT__
GAM390   LOC129526 3'  TTCATGGTTTTTCTTTTGTTT  75389          TG     CCAGGG
                                AGGCAGGAGG  GAAACC
                                ||||||||||  ||||||
                                TTTGTTTTCT  TTTTGG
                                     __     TACTTT
GAM390   LOC129642 3'  CTCTGAGGGCTGTTTTTT    57923        TG AAA  _
                                AGGAGG  G   CCC CAGGG
                                ||||||  |   ||| |||||
                                TTTTTT  C   GGG GTCTC
                                   GT ___   A
GAM390   LOC129831 3'  TTTGGGGTTGTTTTGTTTT   75400      TG  __
                                GAGG  GAA  ACCCCAGG
                                ||||  |||  ||||||||
                                TTTT  TTT  TGGGGTTT
                                  GT   GT
GAM390   LOC130074 3'  TTCTGAGAAATTTGCTTTTTGT 76632         TG  AACCC
                                GCAGGAGG  GA    CAGGG
                                ||||||||  ||    |||||
                                TGTTTTTC  TT    GTCTT
                                     GT  AAAGA
GAM390   LOC130644 3'  CTCTGCTGTTTCCTTCTTGTTT 76251          GT     CC
                                AGGCAGGAG  GGAAAC  CAGGG
                                |||||||||  ||||||  |||||
                                TTTGTTCTT  CCTTTG  GTCTC
                                     __     TC
GAM390   LOC132112 3'  CCCAGGGTCCTACCTCCTCCTC 75532           T   AA_________  CCAG
            TTGCTT                  AGGCAGGAGG GGA        CC    GG
                                ||||||||||| |||        ||   ||
                                TTCGTTCTCC CCT        GG    CC
                                      T   CCATCCT    GACC
GAM390   LOC132235 5'  TCCTGGGGAGCCTGCCTCTGTT 76665       G   TG AAA
            T                    AGGCAG AGG  G   CCCCAGGG
                                ||||||  |||  |   ||||||||
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                                TTTGTC TCC  C   GGGGTCCT
                                   _  GT CGA
GAM390  LOC132241 5'  CTCTGAGCCTACTTCTCTGCTT 75559      _      AAACCC
                                AGGCAG GAGGTGG     CAGGG
                                |||||| |||||||     |||||
                                TTCGTC CTTCATC     GTCTC
                                   T      CGA___
GAM390  LOC132625 3'  TTGTGTAGTTTCCATTTCTTAG 76448     _         CC  G
           CTT                   AGGC AGGAGGTGGAAAC  CA GG
                                |||| ||||||||||||  || ||
                                TTCG TTCTTTACCTTTG  GT TT
                                  A           AT  G
GAM390  LOC132671 3'  CCCTGCCTGGCCACTTGCTGTT 59838      G     AAACCC
           T                    AGGCAG AGGTGG     CAGGG
                                ||||||| ||||||     |||||
                                TTTGTC TTCACC     GTCCC
                                   G     GGTCC_
GAM390  LOC133418 5'  CCCTCCCATTCCGCCTTTTCTT 75594     C         ACCCC
                                AGG AGGAGGTGGAA    AGGG
                                ||| ||||||||||     ||||
                                TTC TTTTCCGCCTT    TCCC
                                  _         ACCC_
GAM390  LOC133418 3'  CCTTGGGGAATTCTCTTAGTCT 75596     _     TGGAAA
                                AGGC AGGAGG     CCCCAGGG
                                |||| ||||||     ||||||||
                                TCTG TTCTCT     GGGGTTCC
                                  A     TAA___
GAM390  LOC133491 3'  CAGGGCTTTGTTCATCTCTTCT 75598     C        AA_______  CCAG
           T                    AGG AGGAGGTGGA       CC    G
                                ||| ||||||||||       ||    |
                                TTC TTCTCTACTT       GG    C
                                  _        GTTTC     GAC
GAM390  LOC133688 3'  CAGGGTTCTTTCTATTCTCTGC 75604       GA      A_______  CCAG
           CT                    AGGCAG  GGTGGAA      CC    G
                                ||||||  |||||||      ||    |
                                TCCGTC  TTATCTT      GG    C
                                   TC      TCTT     GAC
GAM390  LOC133688 3'  CCCAGGGTTCTATTCTCTGCCT 75606       AG     AA__  CCAG
                                AGGCAGG  GTGGA    CC    GG
                                |||||||  |||||    ||    ||
                                TCCGTCT  TATCT    GG    CC
                                   CT    T     GACC
GAM390  LOC134301 3'  TTCTGATCGGTTTTTGTTTCCT 75661          TG     C__
           GCTT                   AGGCAGGAGG  GAAACC   CAGGG
                                ||||||||||  ||||||   |||||
                                TTCGTCCTTT  TTTTGG   GTCTT
                                      GT     CTA
GAM390  LOC134553 3'  TCCTGTTTGGTTTTTTTCCTGC 75688          TG     C__
           TT                    AGGCAGGAGG  GAAACC   CAGGG
                                ||||||||||  ||||||   |||||
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                                TTCGTCCTTT  TTTTGG   GTCCT
                                   __       TTT
GAM390   LOC136345 3'  TTTTGGAGTTGTTTGGTTTTTG 76718         G GG _   C
                TTT                  AGGCAGGAG T  A AAC CCAGGG
                                |||||||||  |  | ||| ||||||
                                TTTGTTTTT G  T TTG GGTTTT
                                     G TT G   A
GAM390   LOC138389 5'  CCTGCCTTCCCTCTTGCCT   76732          T   AACCC   G
                                AGGCAGGAGG GGA    CAGG
                                |||||||||| |||    ||||
                                TCCGTTCTCC CTT    GTCC
                                     _  CC___   G
GAM390   LOC138389 5'  CCTGTCCTCATCTCTGCCT   76733       G    AAACCC
                                AGGCAG AGGTGG     CAGG
                                ||||||| ||||||     ||||
                                TCCGTC TCTACT     GTCC
                                   _     CCT___
GAM390   LOC138389 3'  CCTGTGTTCTTCCTGTCT    76734         TGGA   CC
                                AGGCAGGAGG    AAC  CAGG
                                ||||||||||    |||  ||||
                                TCTGTCCTTC    TTG  GTCC
                                     _____   T_
GAM390   LOC138389 5'  TTCTGTTCTCTGTTTCTTGCT  76747         TG  AACCC
                                GGCAGGAGG  GA    CAGGG
                                |||||||||  ||    |||||
                                TCGTTCTTT  CT    GTCTT
                                     GT  CTT__
GAM390   LOC138612 3'  CCTGTGCCCGCCCCTGCCT   76749        A    AAACCC
                                AGGCAGG GGTGG     CAGG
                                |||||||| |||||     ||||
                                TCCGTCC CCGCC     GTCC
                                   _    CGT___
GAM390   LOC138639 5'  CCTGTCTCTGTCTCTGTCT    75880       G   TG  AACCC
                                AGGCAG AGG  GA    CAGG
                                |||||| |||  ||    ||||
                                TCTGTC TCT  CT    GTCC
                                   _  GT  CT___
GAM390   LOC138639 5'  CTCTGTCTCTGTCTGTCTGTCT 75881        _  TG  AACCC
                                AGGCAGG AGG  GA    CAGGG
                                ||||||| |||  ||    |||||
                                TCTGTCT TCT  CT    GTCTC
                                     G   GT  CT___
GAM390   LOC138639 5'  CTCTGTCTGTCTGTCTCTTTCT 75882     C     TG  AACCC
                                AGG AGGAGG  GA    CAGGG
                                ||| ||||||  ||    |||||
                                TCT TTCTCT  CT    GTCTC
                                   _     GT  GTCT_
GAM390   LOC139202 3'  TTCTGCATTTCCTTTCTGCCT  76751          T   ACCC
                                AGGCAGGAGG GGAA    CAGGG
                                |||||||||| ||||    |||||
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                                TCCGTCTTTC CTTT    GTCTT
                                      _    AC__
GAM390   LOC139202 3'  TTCTGCTGTTTCTACTTTTTAT 76752     GC          CC
                 CT                    AG  AGGAGGTGGAAAC  CAGGG
                                       ||  ||||||||||||  |||||
                                       TC  TTTTTCATCTTTG  GTCTT
                                        TA           TC
GAM390   LOC139522 5'  TTCTGTCAGGCTGTCTGCTGCT 76366       G   TG AAACCC
                 T                     AGGCAG AGG  G     CAGGG
                                       ||||||  |||  |     |||||
                                       TTCGTC TCT  C     GTCTT
                                          G   GT GGACT_
GAM390   LOC139673 3'  CTTGGGCATTTTCTCTCT    76500       T    C_
                                       GGAGG GGAAA  CCCAGG
                                       |||||  |||||  ||||||
                                       TCTCT CTTTT  GGGTTC
                                          _    AC
GAM390   LOC142893 5'  CTCTGAGAACTGCTTCCTGTTT 83759          TG AAACCC
                                       AGGCAGGAGG  G     CAGGG
                                       ||||||||||  |     |||||
                                       TTTGTCCTTC  C     GTCTC
                                             GT AAGA__
GAM390   LOC143153 3'  CTCTGCGGGTCCAGCTCCTGCT 76977         G    AA   _
                 T                     AGGCAGGAG TGGA  CCC CAGGG
                                       |||||||||  ||||  ||| |||||
                                       TTCGTCCTC ACCT  GGG GTCTC
                                             G    __   C
GAM390   LOC143173 5'  CTTGACTTACCTTCTGTC    61018           AAACCC
                                       GGCAGGAGGTGG     CAGG
                                       ||||||||||||     ||||
                                       CTGTCTTCCATT     GTTC
                                             CA____
GAM390   LOC143282 5'  TCCTGGGGAATGCTCTTTGCCT 77024        AG   GAAA
                                       AGGCAGG  GTG    CCCCAGGG
                                       |||||||  |||    ||||||||
                                       TCCGTTT  CGT    GGGGTCCT
                                          CT   AA__
GAM390   LOC143286 5'  CTTTGCCATCTCCATCTCTGGT 83843      A        AACCC
                 TT                     AGGC GGAGGTGGA     CAGGG
                                       ||||  |||||||||     |||||
                                       TTTG TCTCTACCT     GTTTC
                                          G        CTACC
GAM390   LOC143310 5'  CCTTTTTTGTCCTTGCTT    77044        A  TG    CCCC   G
                                       AGGCAGG GG  GAAA    AGG
                                       |||||||  ||  ||||    |||
                                       TTCGTTC CT  TTTT    TCC
                                          _  GT    _____   A
GAM390   LOC143451 3'  CCAGGGTCTTCTCTTCTTCTTG 77069          T   AA_______  CCAG
                 CCT                     AGGCAGGAGG GGA       CC    G
                                       ||||||||||  |||       ||    |
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                                TCCGTTCTTC TCT      GG   C
                                     T  CTTCT    GACC
GAM390  LOC143916 3'  TCCTGGTCCTATTCTCTGCTT  77145       AG  _  AACC
                                AGGCAGG  GT GGA   CCAGGG
                                |||||||  || |||   ||||||
                                TTCGTCT  TA CCT   GGTCCT
                                   CT  T  ____
GAM390  LOC143916 5'  TCTGGGGTGTTTTTTTTT    77146      TG  A
                                GGAGG  GA ACCCCAGG
                                |||||  || ||||||||
                                TTTTT  TT TGGGGTCT
                                  TT  G
GAM390  LOC143943 5'  TTCTGGCTGTCTTCATCTCTGT 83923       G      A  C_
           CT                     AGGCAG AGGTGGA AC  CCAGGG
                                |||||| ||||||| ||  ||||||
                                TCTGTC TCTACTT TG  GGTCTT
                                  _      C  TC
GAM390  LOC144017 3'  TCCTGTTTTTTTTTGTTTTTTG 83932          TG   CCC_
           TTT                    AGGCAGGAGG  GAAA   CAGGG
                                ||||||||||  ||||   |||||
                                TTTGTTTTTT  TTTT   GTCCT
                                     GT   TTTT
GAM390  LOC144058 5'  TCTGGGGTTTGGGTCTCCT   77182       GG
                                AGGAGGT  AAACCCCAGG
                                |||||||  ||||||||||
                                TCCTCTG  TTTGGGGTCT
                                   GG
GAM390  LOC144114 5'  CCTTGGCCCTGCTGCTGCCTGC 83084       A  TG AAACC
           CT                     AGGCAGG GG  G    CCAGGG
                                |||||||  ||  |    ||||||
                                TCCGTCC TC  C    GGTTCC
                                   G  GT GTCCC
GAM390  LOC144193 3'  CTTAAAATTTCCATTTTGTGTC 77198      G       CCCC   G
           T                      AGGCA GAGGTGGAAA   AGG
                                |||||  ||||||||||   |||
                                TCTGT TTTTACCTTT   TTC
                                  G        AAAA
GAM390  LOC144195 3'  TCCTGGACATCCTCTTCTGCTT 60989         T   AACC
                                AGGCAGGAGG GGA   CCAGGG
                                |||||||||| |||   ||||||
                                TTCGTCTTCT CCT   GGTCCT
                                     _  ACA_
GAM390  LOC144501 3'  CTTGCCTCACCTCCTCTT    84030    C       AAACCC
                                AGG AGGAGGTGG     CAGG
                                ||| |||||||||     ||||
                                TTC TCCTCCACT     GTTC
                                  _       CC____
GAM390  LOC144509 3'  CAGGGTCTATTTCCTCTT    77359    C       AA_  CCAG
                                AGG AGGAGGTGGA   CC   G
                                ||| ||||||||||   ||   |
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                                TTC TCCTTTATCT   GG    C
                                  _            GAC
GAM390   LOC144563 5'  GGCTCATTTCCTTCCTGTCT   77401          T    A_______
                                AGGCAGGAGG GGAA       CC
                                |||||||||| ||||       ||
                                TCTGTCCTTC CTTT       GG
                                      _    ACTC
GAM390   LOC144571 3'  TCTTGGCTCAATCCTCCTGCTT 84080          TG_  AACC
                                AGGCAGGAGG   GA    CCAGGG
                                ||||||||||   ||    ||||||
                                TTCGTCCTCC   CT    GGTTCT
                                      TAA  C___
GAM390   LOC144577 3'  CCAGGGTCCGCTTCGCTTTCTG 77424            AA_______  CCAG
            TTT                   AGGCAGGAGGTGGA       CC    G
                                ||||||||||||||       ||    |
                                TTTGTCTTTCGCTT       GG    C
                                      CGCCT     GACC
GAM390   LOC144698 5'  CCCTGGAGCCACCTGCCTCTGG 77432      ___   _      AAACC
            CTT                   AGGC   AGG AGGTGG     CCAGGG
                                ||||   ||| ||||||     ||||||
                                TTCG   TCC TCCACC     GGTCCC
                                  GTC   G     GA___
GAM390   LOC145009 3'  TTTTGGCTCAGTTGTTCCCTGC 60984        AG TG AAACC
            TT                    AGGCAGG  G  G     CCAGGG
                                |||||||  |  |     ||||||
                                TTCGTCC  T  T     GGTTTT
                                    CT GT GACTC
GAM390   LOC145082 5'  CCTGCCTCTATCTTCTTCT    84186     C        AACCC
                                AGG AGGAGGTGGA     CAGG
                                ||| ||||||||||     ||||
                                TCT TCTTCTATCT     GTCC
                                  _        CC___
GAM390   LOC145098 3'  CCTTGTTCTCCACTTCTTTCCT 77534      C        AACCC
                                AGG AGGAGGTGGA     CAGGG
                                ||| ||||||||||     |||||
                                TCC TTCTTCACCT     GTTCC
                                  T        CTT__
GAM390   LOC145123 3'  CCAGGGTTTTTTTCCTTTTTTG 68136          T    A_______  CCAG
            TCT                   AGGCAGGAGG GGAA       CC    G
                                ||||||||||| ||||       ||    |
                                TCTGTTTTTT CTTT       GG    C
                                      C    TTTT     GACC
GAM390   LOC145125 3'  CCAGGGTCTTCTCTTCTTCTTG 77545          T   AA_______  CCAG
            CCT                   AGGCAGGAGG GGA       CC    G
                                ||||||||||| |||       ||    |
                                TCCGTTCTTC TCT       GG    C
                                      T   CTTCT     GACC
GAM390   LOC145135 5'  CTCTGGGTTCTCGCTGTTTGTT 84204        A    GA     C
            T                    AGGCAGG GGTG  AACCC AGGG
                                |||||||  ||||  |||||  ||||
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                                TTTGTTT TCGC  TTGGG TCTC
                                    G   TC    _
GAM390  LOC145225 3'  CCCTGGCACCATTTCCTCTCT  84265     C       AAACC
                                AGG AGGAGGTGG    CCAGGG
                                ||| |||||||||    ||||||
                                TCT TCCTTTACC    GGTCCC
                                  C       AC___
GAM390  LOC145439 3'  CAGGGCTTTGAGCCTCTCCTGT 77725         T  AAA_______  CCAG
           CT                     AGGCAGGAGG GG        CC   G
                                |||||||||| ||        ||   |
                                TCTGTCCTCT CC        GG   C
                                      _ GAGTTTC    GAC
GAM390  LOC145453 5'  CCTATTTTTTTATTTTTTGT  77658           CCCC  G
                                GCAGGAGGTGGAAA   AGG
                                ||||||||||||||   |||
                                TGTTTTTTATTTTT   TCC
                                      TTA_
GAM390  LOC145453 3'  TTCTGGGGATTATTCCTGTTT  77675         GTGGAAA
                                AGGCAGGAG      CCCCAGGG
                                |||||||||      ||||||||
                                TTTGTCCTT      GGGGTCTT
                                    ATTA___
GAM390  LOC145453 5'  TTTTGGTAATCTCTTTCTCTTG 77678         T  AACC_
           CTT                    AGGCAGGAGG GGA    CCAGGG
                                |||||||||| |||    ||||||
                                TTCGTTCTCT TCT    GGTTTT
                                      T  CTAAT
GAM390  LOC145501 3'  CCCTGGCTGCACTTCCTTGCCT 77765      _     GAAACC
                                AGGCA GGAGGTG     CCAGGG
                                ||||| |||||||     ||||||
                                TCCGT CCTTCAC     GGTCCC
                                   T      GTC___
GAM390  LOC145547 5'  CCTTGGGGCCCAAGGCCTCTTC 77781     C     ___  AAA
           CT                     AGG AGGAGGT   GG   CCCCAGGG
                                ||| |||||||   ||   ||||||||
                                TCC TTCTCCG   CC   GGGGTTCC
                                  _      GAA  C__
GAM390  LOC145601 3'  CTCTGATCTCCTTTCCTGCTT  84349         T  AACCC
                                AGGCAGGAGG GGA    CAGGG
                                |||||||||| |||    |||||
                                TTCGTCCTTT CCT    GTCTC
                                      _  CTA__
GAM390  LOC145609 5'  GGTTCTGTCCTTTCCTGTCT  84368         T  AA______
                                AGGCAGGAGG GGA       CC
                                |||||||||| |||       ||
                                TCTGTCCTTT CCT       GG
                                      _  GTCTT
GAM390  LOC145622 3'  CCCACTGTTTCCTCTTTCTGCT 77813         T     CCCA
           T                     AGGCAGGAGG GGAAAC    GGG
                                |||||||||| ||||||    |||
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                                TTCGTCTTTC CCTTTG    CCC
                                      T      TCA_
GAM390   LOC145623 3'  TCCTATTATTTCATTTTCTTGC 84395          _     ACCCC
                 CT                  AGGCAGGAGG TGGAA     AGGG
                                     |||||||||| |||||     ||||
                                     TCCGTTCTTT ACTTT     TCCT
                                           T     ATTA_
GAM390   LOC145623 3'  TCCTATTTCATCCATTTTTTGC 84396           AACCCC
                                     GCAGGAGGTGGA     AGGG
                                     ||||||||||||     ||||
                                     CGTTTTTTACCT     TCCT
                                           ACTTTA
GAM390   LOC145645 3'  GGCCTTCTCTCTTTCTGTCT   77841          T_    AC____
                                     AGGCAGGAGG  GGAA     C
                                     ||||||||||  ||||     |
                                     TCTGTCTTTC  TCTT     G
                                           TC    CC   G
GAM390   LOC145786 5'  CCTGTATAGTTCTCTTCCTGCT 84491          T   AACCC    G
                 T                   AGGCAGGAGG GGA     CAGG
                                     |||||||||| |||     ||||
                                     TTCGTCCTTC CTT     GTCC
                                           T   GATAT
GAM390   LOC145788 5'  CCCAGCTATTCATCTTCTGTTT 77960            AACCCCA
                                     AGGCAGGAGGTGGA      GGG
                                     ||||||||||||||      |||
                                     TTTGTCTTCTACTT      CCC
                                           ATCGA__
GAM390   LOC145788 5'  CCCCAGGGTTCATCTTCTGTTT 77961            AA_  CCAG
                                     AGGCAGGAGGTGGA   CC    GG
                                     ||||||||||||||   ||    ||
                                     TTTGTCTTCTACTT   GG    CC
                                           GACC
GAM390   LOC145813 5'  TTCTGTCTGCCCTGTCTCCTGT 84514          TG AAACCC
                 CT                  AGGCAGGAGG  G     CAGGG
                                     ||||||||||  |     |||||
                                     TCTGTCCTCT  C     GTCTT
                                           GT CCGTCT
GAM390   LOC145828 5'  TTCTGTTCTCATTTATCTTCTG 84541           AACCC_
                 CT                  GGCAGGAGGTGGA     CAGGG
                                     ||||||||||||      |||||
                                     TCGTCTTCTATTT     GTCTT
                                           ACTCTT
GAM390   LOC145831 3'  TCTGGTTTGCTTTCGTTT    77989      A    TG  AACC
                                     AGGC GGAGG  GA    CCAGG
                                     |||| |||||  ||    |||||
                                     TTTG CTTTC  TT    GGTCT
                                       _     GT  _____
GAM390   LOC145921 3'  GGCTCTGTCTCTCCTGCTT    76526          _ _    AA__
                                     AGGCAGGAG G TGGA    CC
                                     |||||||||  | ||||    ||
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                                TTCGTCCTC C GTCT    GG
                                     T T    C
GAM390   LOC145926 3'  CCCAGGGTTCAACATTTGCTTT 78031          TG  AA_________  CCAG
           TTGCTT                 AGGCAGGAGG  GA         CC    GG
                                ||||||||||  ||         ||    ||
                                TTCGTTTTTC  TT         GG    CC
                                     GT  ACAACTT     GACC
GAM390   LOC145982 3'  CTGGAATTTTTGTTTCTGCCT  61014       G   TG    CC
                                AGGCAG AGG  GAAA  CCAG
                                ||||||  |||  ||||  ||||
                                TCCGTC TTT  TTTT  GGTC
                                   _  GT    AA
GAM390   LOC145988 3'  CAGGGCTTTCCTCCATTTTCTG 78061           AA________  CCAG
           T                     GCAGGAGGTGGA        CC    G
                                ||||||||||||        ||    |
                                TGTCTTTTACCT        GG    C
                                      CCTTTC     GAC
GAM390   LOC145988 5'  CCAGGGTCCTCCTCCGCCTCCT 78064     C         AA________  CCAG
           CCT                     AGG AGGAGGTGGA        CC    G
                                ||| ||||||||||        ||    |
                                TCC TCCTCCGCCT        GG    C
                                 _        CCTCCT     GACC
GAM390   LOC146136 5'  CCAGGGCTTTATTCTGTCTTCC 73316     A    TG   A________  CCAG
           GTCT                    AGGC GGAGG  GAA       CC    G
                                |||| |||||  |||       ||    |
                                TCTG CTTCT  CTT       GG    C
                                  C    GT   ATTTC     GACC
GAM390   LOC146138 3'  CCTTCCTTTCTGCCGTTTTGTC 84591         _ TG    CCCC   G
           T                     AGGCAGGA GG  GAAA    AGG
                                ||||||||  ||  ||||    |||
                                TCTGTTTT CC  CTTT    TCC
                                    G  GT    CCT_
GAM390   LOC146159 5'  GGCTTTTACATTTCCTGCTT   78178           G  A______
                                AGGCAGGAGGTG AA     CC
                                ||||||||||||  ||     ||
                                TTCGTCCTTTAC TT     GG
                                      A  TTC
GAM390   LOC146224 5'  TCCTGCATCTTGTTCCTGCTT  78205         GT   AACCC
                                AGGCAGGAG  GGA    CAGGG
                                |||||||||  |||    |||||
                                TTCGTCCTT  TCT    GTCCT
                                     GT   AC____
GAM390   LOC146237 3'  TCTTGGGTGTGTGCCTTCTGCC 84616          GGAA  _
                                GGCAGGAGGT    AC CCCAGGG
                                ||||||||||    || |||||||
                                CCGTCTTCCG    TG GGGTTCT
                                      TG__  T
GAM390   LOC146268 3'  CCCTCATTCTTTTTGTCTCTTC 78336     C     TG    CCCC_
           TT                      AGG AGGAGG  GAAA    AGGG
                                ||| ||||||  ||||    ||||
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                                TTC TTCTCT  TTTT    TCCC
                                  _    GT   CTTAC
GAM390  LOC146268 3'  TCTGGCTCACCTCCGTCT   78344     A      AAACC
                                AGGC GGAGGTGG    CCAGG
                                |||| ||||||||    |||||
                                TCTG CCTCCACT    GGTCT
                                  _      C____
GAM390  LOC146268 3'  CCCCAGGGTTTTGTCTCTTCTT 78334         T  AA_________  CCAG
           TTTGCCT                AGGCAGGAGG GGA       CC   GG
                                |||||||||| |||       ||   ||
                                TCCGTTTTTC TCT       GG   CC
                                      T  CTGTTTT    GACC
GAM390  LOC146443 5'  CCCCAGGGTTCTCTTCGTGTCT 78440      G   T  AA_  CCAG
                                AGGCA GAGG GGA  CC   GG
                                ||||| |||| |||  ||   ||
                                TCTGT CTTC CTT  GG   CC
                                   G   T      GACC
GAM390  LOC146506 3'  CCCTGACCTCAGCTTCCTGCCT 78492          G  AACCC
                                AGGCAGGAGGT GA    CAGGG
                                ||||||||||| ||    |||||
                                TCCGTCCTTCG CT    GTCCC
                                      A  CCA__
GAM390  LOC146506 3'  CTCTGGCTGTCTTCTTCCTGTC 78493         T  AACC
           T                    AGGCAGGAGG GGA   CCAGGG
                                |||||||||| |||   ||||||
                                TCTGTCCTTC TCT   GGTCTC
                                      T  GTC_
GAM390  LOC146723 3'  CCCCAGGGTTCATTTTTTCTCT 78678         TG  A_________  CCAG
           CCTGTTT                AGGCAGGAGG  GAA      CC   GG
                                ||||||||||  |||       ||   ||
                                TTTGTCCTCT  TTT       GG   CC
                                      CT   TTACTT    GACC
GAM390  LOC146723 3'  TTTGTTTTGTTGTCTGCTT   78688       AG TG   ACCC
                                AGGCAGG  G  GAA   CAGG
                                |||||||  |  |||   ||||
                                TTCGTCT  T  TTT   GTTT
                                    GT GT  _____
GAM390  LOC146756 3'  CCCTGGTGGATCCTTTCTGTTT 84799         T  AAA  _
                                AGGCAGGAGG GG   CC CCAGGG
                                |||||||||| ||   || ||||||
                                TTTGTCTTTC CT   GG GGTCCC
                                      _  A__  T
GAM390  LOC146774 3'  GGTCTTTTCATCTTTTTCT   78698    C        A_____
                                AGG AGGAGGTGGAA     CC
                                ||| ||||||||||     ||
                                TCT TTTTCTACTTT     GG
                                  _         TCT
GAM390  LOC146795 3'  TTCTGGCAAGGTTTCCACCTCT 78724     C          ___
           TCCT                   AGG AGGAGGTGGAAACC   CCAGGG
                                ||| ||||||||||||||   ||||||
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                                TCC TTCTCCACCTTTGG   GGTCTT
                                  _           AAC
GAM390  LOC146819 3'  GGTCCTTCTTTTTCTTGCTT   78741          T    AC_____
                                AGGCAGGAGG GGAA       C
                                |||||||||| ||||       |
                                TTCGTTCTTT TCTT       G
                                      T    CCT   G
GAM390  LOC146821 3'  GTCCTTCTTTTTCTTGCTT    78732          T    AC_____
                                AGGCAGGAGG GGAA       C
                                |||||||||| ||||       |
                                TTCGTTCTTT TCTT       G
                                      T    CCT   G
GAM390  LOC146839 5'  CTTTGTGTGGTTTATTTTTGCC 84841         GGTGG     C__
          T                     AGGCAGGA     AAACC   CAGGG
                                ||||||||     |||||   |||||
                                TCCGTTTT     TTTGG   GTTTC
                                     TA___     TGT
GAM390  LOC146839 3'  TCCTGGGTTCATGCCATTCTCC 84855          _   AAAC__
          TGCCT                    AGGCAGGAGG TGG      CCCAGGG
                                |||||||||| |||      |||||||
                                TCCGTCCTCT ACC      GGGTCCT
                                     T   GTACTT
GAM390  LOC146909 3'  TTTTGGTGGTTTTTGTTTTTTG 78791           TG     _
          TTT                     AGGCAGGAGG  GAAACC CCAGGG
                                |||||||||  |||||| ||||||
                                TTTGTTTTTT  TTTTGG GGTTTT
                                     GT     T
GAM390  LOC146961 5'  CTCTGTCAGACTCACCTTTGTC 78823        G     AAACCC
          T                     AGGCAG AGGTGG      CAGGG
                                ||||||| ||||||      |||||
                                TCTGTT TCCACT      GTCTC
                                   _     CAGACT
GAM390  LOC147040 5'  CTCTGCTCTTTTCATCTCTTCT 78833      C          CCC
          CT                     AGG AGGAGGTGGAAA   CAGGG
                                ||| ||||||||||||   |||||
                                TCT TTCTCTACTTTT   GTCTC
                                  C          CTC
GAM390  LOC147057 3'  CCAGATTTTCTCGCTTTTTGTT 84977           _   CCCCA  G
          T                     AGGCAGGAGGTG GAAA     GG
                                |||||||||||| ||||     ||
                                TTTGTTTTTCGC CTTT     CC
                                      T    TAGA_
GAM390  LOC147071 3'  TCTGCTTTCACCTTTGCTT    73374        G       ACCC
                                AGGCAG AGGTGGAA    CAGG
                                |||||| ||||||||    ||||
                                TTCGTT TCCACTTT    GTCT
                                   _       C___
GAM390  LOC147077 3'  CCCCAGGGTCTTAGCTTAGCTT 78845          G  AA_________  CCAG
          TCTGTCT                  AGGCAGGAGGT GA        CC    GG
                                |||||||||| ||         ||    ||
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                                TCTGTCTTTCG TT        GG   CC
                                      A  CGATTCT    GACC
GAM390  LOC147165 5'  CCTGGGGGAGCCTCTTCTT   85083     C      GGAAA
                                AGG AGGAGGT    CCCCAGG
                                ||| |||||||    |||||||
                                TTC TTCTCCG    GGGGTCC
                                  _      AG___
GAM390  LOC147299 3'  CCCATTAATCTACTTTCTGTCT 78978             AACCCCA
                                AGGCAGGAGGTGGA      GGG
                                ||||||||||||||      |||
                                TCTGTCTTTCATCT      CCC
                                       AATTA__
GAM390  LOC147341 3'  GGTCTTTTTCACCTTTTCTT   85122     C         A_______
                                AGG AGGAGGTGGAA      CC
                                ||| ||||||||||      ||
                                TTC TTTTCCACTTT      GG
                                  _         TTCT
GAM390  LOC147622 3'  TTCTGGTTTGTTTTTGTTTTTG 85174         G TG     C__
           TTT                    AGGCAGGA G  GAAAC   CCAGGG
                                ||||||||  |  |||||   ||||||
                                TTTGTTTT T  TTTTG   GGTCTT
                                    _ GT     TTT
GAM390  LOC147671 3'  GGCTCTATCTATCCCTGTTT   79115        A     AA_______
                                AGGCAGG GGTGGA       CC
                                ||||||| ||||||       ||
                                TTTGTCC CTATCT       GG
                                    _     ATCTC
GAM390  LOC147694 3'  CCAGGGCTACTTCCACCTTTTG 79092             AC_______ CCAG
           CCT                    AGGCAGGAGGTGGAA       C    G
                                ||||||||||||||       |   |
                                TCCGTTTTCCACCTT       G    C
                                       CATC   G GACC
GAM390  LOC147694 3'  GGTTTTGGGGTTTTTTGTAGTG 79103          _______
           CCTTTTGTTT               AGGCAGGAGGT     GGAAACCCCAGGG   TT
                                ||||||||||     ||||||||||||   ||
                                TTTGTTTTCCG     TTTTTGGGGTTTT   GG
                                      TGATGT
GAM390  LOC147949 3'  CTTTGCACTTCCATTTCCTGCC 79278             ACCC
                                GGCAGGAGGTGGAA    CAGGG
                                ||||||||||||||   |||||
                                CCGTCCTTTACCTT    GTTTC
                                       CAC_
GAM390  LOC147991 3'  TTTGGGGGTTTTTTGTTT     79305         GG GGAAA
                                AGGCAGGA  T    CCCCAGG
                                ||||||||  |    |||||||
                                TTTGTTTT  G    GGGGTTT
                                     TT _____
GAM390  LOC148114 3'  TTCTGGGGTTTTGATTTTCCTT 79366     C     _ G
           CT                     AGG AGGAGG T GAAACCCCAGGG
                                ||| |||||| | ||||||||||||
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                                TCT TCCTTT A TTTTGGGGTCTT
                                  _     T G
GAM390  LOC148132 5'  CCTGGCCTGCCTCCTGCT    85255         TG AAACC
                                GGCAGGAGG  G    CCAGG
                                |||||||||  |    |||||
                                TCGTCCTCC  C    GGTCC
                                     GT C____
GAM390  LOC148181 5'  CCAGGGTTTTGCCCAACTTCTG 79431         G   AAA_______  CCAG
          TCT                     AGGCAGGAG TGG       CC    G
                                |||||||||  |||       ||   |
                                TCTGTCTTC ACC       GG    C
                                     A   CGTTTT    GACC
GAM390  LOC148195 5'  CCAGGGTTTTCTCCACTTCCTC 85272     C        AA_______  CCAG
          TCT                     AGG AGGAGGTGGA       CC    G
                                |||  ||||||||||       ||   |
                                TCT TCCTTCACCT       GG    C
                                  C         CTTTT    GACC
GAM390  LOC148195 5'  CCCCAGGGTTAATTTTCTGCCT 85276     A        A_________  CCAG
          CCAGTTT                   AGGC GGAGGTGGAA       CC    GG
                                ||||  ||||||||||       ||    ||
                                TTTG CCTCCGTCTT       GG    CC
                                  A        TTAATT    GACC
GAM390  LOC148195 5'  TCTTGAGTTAATTTTCTGCCT  85292          GGA   CC
                                AGGCAGGAGGT   AAC  CAGGG
                                ||||||||||   |||  |||||
                                TCCGTCTTTTA   TTG  GTTCT
                                     A__   A_
GAM390  LOC148223 3'  CCCAGTTTCTGCTTTCTGGCT  79484    G      TG    CCCA
                                AG CAGGAGG  GAAAC    GGG
                                || |||||||  |||||    |||
                                TC GTCTTTC  CTTTG    CCC
                                 G      GT    A___
GAM390  LOC148223 3'  CCTGACCCCACTTCCTTCT    79485     C       AAACCC
                                AGG AGGAGGTGG     CAGG
                                ||| |||||||||     ||||
                                TCT TCCTTCACC     GTCC
                                  _       CCA___
GAM390  LOC148438 3'  GGTTTTTCTTCCTCTTGCTT   85309          T_   A____
                                AGGCAGGAGG  GGAA    CC
                                ||||||||||  ||||    ||
                                TTCGTTCTCC  CTTT    GG
                                     TT   TT
GAM390  LOC148479 3'  CTTGAGTCTTTCTTTTTCTGTT 79613          T   _  CC    G
          T                      AGGCAGGAGG GGAA AC  CAGG
                                ||||||||||  |||| ||  ||||
                                TTTGTCTTTT CTTT TG  GTTC
                                     T   C  A_
GAM390  LOC148479 3'  TCTTAGGTTTCCTTCTGTTT   79617        GGT      CC
                                AGGCAGGA   GGAAACC  AGG
                                ||||||||   |||||||  |||
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                                TTTGTCTT  CCTTTGG  TCT
                                   ___      AT
GAM390  LOC148534 3'  CCAGGGTTCTGCCTTTCTTTTG 79635      ____   TG  AA__  CCAG
          CCT                   AGGCAG   GAGG  GA   CC   G
                                ||||||   ||||  ||   ||   |
                                TCCGTT   TTCC  CT   GG   C
                                  TTCT   GT  T    GACC
GAM390  LOC148645 5'  TCCTGGGCTCAGGCCATCCTCC 85340        _  AAAC__
          TGCCT                  AGGCAGGAGG TGG     CCCAGGG
                                ||||||||||  |||     |||||||
                                TCCGTCCTCC ACC     GGGTCCT
                                     T  GGACTC
GAM390  LOC148709 3'  TCCTGAACCAGTTTCATTTCTG 79704       G       ACCC__
          TCT                   AGGCAG AGGTGGAA     CAGGG
                                ||||||  ||||||||     |||||
                                TCTGTC TTTACTTT     GTCCT
                                  _       GACCAA
GAM390  LOC148809 5'  TCTTGGCTTGTCTCCTTGTCT  79764       _    TG AAACC
                                AGGCA GGAGG  G    CCAGGG
                                |||||  |||||  |    ||||||
                                TCTGT CCTCT  T    GGTTCT
                                   T    GT C____
GAM390  LOC148887 3'  CCCTGGGGTGGCCCCGTCCCTT 85399      __  _  T  AA
          GTTT                   AGGCA  GGA GG GG  ACCCCAGGG
                                |||||  ||| || ||  |||||||||
                                TTTGT  CCT CC CC  TGGGGTCCC
                                   TC   G  _  GG
GAM390  LOC148918 5'  TTCTGGCTTATTTACTTCTTAG 79836      _        AACC
          TTT                   AGGC AGGAGGTGGA    CCAGGG
                                ||||  ||||||||||    ||||||
                                TTTG TTCTTCATTT    GGTCTT
                                  A         ATTC
GAM390  LOC148936 5'  CTCTGCACAAGCTGTCTTTGTC 85451       G   TG AAACCC
          T                     AGGCAG AGG  G     CAGGG
                                ||||||  |||  |     |||||
                                TCTGTT TCT  C     GTCTC
                                   _  GT GAACAC
GAM390  LOC148936 3'  TCCTATATCTGTTTGTTTTCTG 85460         TG  AACCCC_
          TTT                   AGGCAGGAGG  GA      AGGG
                                ||||||||||  ||      ||||
                                TTTGTCTTTT  TT      TCCT
                                     GT  GTCTATA
GAM390  LOC148938 5'  CTCTGCACAAGCTGTCTTTGTC 85434       G   TG AAACCC
          T                     AGGCAG AGG  G     CAGGG
                                ||||||  |||  |     |||||
                                TCTGTT TCT  C     GTCTC
                                   _  GT GAACAC
GAM390  LOC148938 3'  TCCTATATCTGTTTGTTTTCTG 85442         TG  AACCCC_
          TTT                   AGGCAGGAGG  GA      AGGG
                                ||||||||||  ||      ||||
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                                TTTGTCTTTT  TT      TCCT
                                      GT  GTCTATA
GAM390  LOC149041 3'  TCCTACTTTTATCTTCTGCT   79871           ACCCC
                                GGCAGGAGGTGGAA    AGGG
                                ||||||||||||||    ||||
                                TCGTCTTCTATTTT    TCCT
                                      CA___
GAM390  LOC149086 3'  CTCTCAACTTCTGTTTCCTCTT 85493     C     TG   ACCCC
                                AGG AGGAGG  GAA    AGGG
                                ||| ||||||  |||    ||||
                                TTC TCCTTT  CTT    TCTC
                                  _     GT   CAAC_
GAM390  LOC149134 5'  TCCTGAGCGGTTCCGTCTCCTG 85522        GT    A  C__
           CT                     GGCAGGAG  GGAA CC   CAGGG
                                ||||||||  |||| ||   |||||
                                TCGTCCTC  CCTT GG   GTCCT
                                     TG    _  CGA
GAM390  LOC149153 5'  CCCAGGGTTTTGTTCTATTTCT 85526            AC________ CCAG
           TGTTT                    AGGCAGGAGGTGGAA       C    G
                                ||||||||||||||||       |   |
                                TTTGTTCTTTATCTT       G    C
                                       GTTTT   G GACC
GAM390  LOC149271 3'  TCCTGGGGTGTTCTGCCCTTTG 80013       GA  TG   _
           CTT                     AGGCAG  GG  GAA ACCCCAGGG
                                ||||||  ||  ||| |||||||||
                                TTCGTT  CC  CTT TGGGGTCCT
                                   TC  GT   G
GAM390  LOC149305 5'  CTCTGTTATCCATCTCCTGT   80038           AACCC
                                GCAGGAGGTGGA    CAGGG
                                ||||||||||||    |||||
                                TGTCCTCTACCT    GTCTC
                                      ATT__
GAM390  LOC149332 3'  CCTGAATTTTATTTCTGGCTT  85546      A        ACCC
                                AGGC GGAGGTGGAA    CAGG
                                ||||  ||||||||||    ||||
                                TTCG TCTTTATTTT    GTCC
                                  G         AA__
GAM390  LOC149332 5'  CTCTGCTTTTCATCTCTGCTT  85547       G       CCC
                                AGGCAG AGGTGGAAA   CAGGG
                                ||||||  |||||||||   |||||
                                TTCGTC TCTACTTTT   GTCTC
                                   _        C__
GAM390  LOC149422 3'  TCCTGGGTCACATTTCCTTCT  80135     C       _  AAC
                                AGG AGGAGGTG GA   CCCAGGG
                                ||| ||||||||  ||   |||||||
                                TCT TCCTTTAC CT   GGGTCCT
                                  _       A  ___
GAM390  LOC149448 3'  CCAGGGTTTTGCCTCATCCCTT 85578        A    AAA________  CCAG
           GCTT                     AGGCAGG GGTGG        CC    G
                                |||||||  |||||         ||    |
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                                TTCGTTC CTACT        GG   C
                                   C    CCGTTTT    GACC
GAM390  LOC149464 3'  CTCTGGGCATCAGTGTCCTTGT 85590      _  G TG  AAC
          CT                    AGGCA GGA G  GA   CCCAGGG
                                ||||| ||| |  ||   |||||||
                                TCTGT CCT T  CT   GGGTCTC
                                  T   G GA  AC_
GAM390  LOC149483 3'  CCAGGGTTCTGTACCTCTTCTG 80183         T  AAA_______  CCAG
          TTT                   AGGCAGGAGG GG        CC   G
                                |||||||||| ||        ||   |
                                TTTGTCTTCT CC        GG   C
                                   _ ATGTCTT    GACC
GAM390  LOC149668 5'  TCTTGGTCTCCTTCTGTCTGCT 85703       G   TG   ACC__
          GCCT                   AGGCAG AGG  GAA    CCAGGG
                                ||||||| |||  |||    ||||||
                                TCCGTC TCT  CTT    GGTTCT
                                   G   GT   CCTCT
GAM390  LOC149684 3'  CAGGGCTCATTCTCCCTTTTGC 85761         TG   A_______  CCAG
          CT                    AGGCAGGAGG  GAA      CC   G
                                ||||||||||  |||      ||   |
                                TCCGTTTTCC  CTT      GG   C
                                     CT   ACTC    GAC
GAM390  LOC149722 5'  CTCTAGGAGTTTCTGTTTTTTG 85751          TG    _ C
          TTT                   AGGCAGGAGG  GAAAC CC AGGG
                                |||||||||  ||||| || ||||
                                TTTGTTTTTT  CTTTG GG TCTC
                                     GT    A  A
GAM390  LOC149734 3'  CATTCTGGGTTTTTGTCTTCTG 85791        TG      C
          T                     GCAGGAGG  GAAACCC AGGG
                                ||||||||  ||||||| ||||
                                TGTCTTCT  TTTTGGG TCTT
                                     GT      _   ACT
GAM390  LOC149767 3'  CTCTAGCGCAGTTTTTTTTCTT 80312          T     CCC___
          GTCT                    AGGCAGGAGG GGAAAC     AGGG
                                ||||||||||  ||||||     ||||
                                TCTGTTCTTT TTTTTG     TCTC
                                     _     ACGCGA
GAM390  LOC149821 5'  CCTGGGTGTGTCTTTTCCT    85931       T   A  _
                                AGGAGG GGA AC CCCAGG
                                |||||| ||| || ||||||
                                TCCTTT TCT TG GGGTCC
                                   _   G  T
GAM390  LOC149837 5'  CAGGGTTCTGCTGTATTCCTGT 85891        ____  TG  AA__  CCAG
          CT                    AGGCAGGA    GG  GA    CC    G
                                ||||||||    ||  ||    ||    |
                                TCTGTCCT    TC  CT    GG    C
                                     TATG  GT  T     GAC
GAM390  LOC149837 3'  CCCCAGGGTTCTGATTTACACT 85893         _    AA_______  CCAG
          TCTGTTT                  AGGCAGGAG GTGGA       CC    GG
                                |||||||| |||||        ||    ||
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                                TTTGTCTTC CATTT       GG   CC
                                     A    AGTCTT    GACC
GAM390  LOC149837 3'  TTCTGGGGCCACCCTCCAGCCT 85912     A    _  AAA
                                AGGC GGAGG TGG   CCCCAGGG
                                |||| ||||| |||   ||||||||
                                TCCG CCTCC ACC   GGGGTCTT
                                  A    C   ___
GAM390  LOC150067 5'  TCCTGGGCCGCCGCCTCCTCCT 60964     C       AAAC
                                AGG AGGAGGTGG    CCCAGGG
                                ||| |||||||||    |||||||
                                TCC TCCTCCGCC    GGGTCCT
                                  _       GCC_
GAM390  LOC150082 5'  CCCTGTGCTTATCTTCAGTTT  80385     A       AAACCC
                                AGGC GGAGGTGG     CAGGG
                                |||| ||||||||      |||||
                                TTTG CTTCTATT     GTCCC
                                  A       CGT___
GAM390  LOC150150 5'  CCCAGGGTTTTGTTTACTGCCT 86010         TG _   ________  CAG
           CCTGTT                 GGCAGGAGG  G AAAC      CC   GG
                                |||||||||  | ||||      ||   ||
                                TTGTCCTCC  C TTTG      GG   CC
                                     GT A    TTTT    GAC
GAM390  LOC150150 5'  CCTGTTTTGTTTACTGCCT   86011       G   TG   ACCC
                                AGGCAG AGG  GAA    CAGG
                                |||||| |||  |||    ||||
                                TCCGTC TTT  TTT    GTCC
                                   A   GT  _____
GAM390  LOC150155 3'  CCTTCCGATTCCACCTCCGCCT 71410      A        ACCCC
                                AGGC GGAGGTGGAA     AGG
                                |||| ||||||||||     |||
                                TCCG CCTCCACCTT     TCC
                                  _        AGCCT
GAM390  LOC150295 3'  CCCTGCAGTTCCTTTTCTGTTT 86154         T    ACCC
                                AGGCAGGAGG GGAA    CAGGG
                                |||||||||| ||||    |||||
                                TTTGTCTTTT CCTT    GTCCC
                                     _   GAC_
GAM390  LOC150587 3'  CCCTGGTTGTCCCTTCTGCCT  86242         T  AAACC
                                AGGCAGGAGG GG     CCAGGG
                                |||||||||| ||     ||||||
                                TCCGTCTTCC CT     GGTCCC
                                     _  GTT__
GAM390  LOC150606 3'  TTTTGGGGATGCTTTTTTTCT  86278     C       GAAA
                                AGG AGGAGGTG    CCCCAGGG
                                ||| ||||||||    ||||||||
                                TCT TTTTTCGT    GGGGTTTT
                                  T       A___
GAM390  LOC150630 5'  CTCTGCATAATTTGTCTTCTGC 86299         TG  AACCC
              T                  GGCAGGAGG  GA     CAGGG
                                |||||||||  ||     |||||
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                                TCGTCTTCT TT    GTCTC
                                    GT  AATAC
GAM390  LOC150848 3'  CAGGGTTTTGTCTTTTTCTTGC 86317        T  AA_____ CCAG
          CT                    AGGCAGGAGG GGA      CC   G
                                |||||||||| |||      ||   |
                                TCCGTTCTTT TCT      GG   C
                                    T  GTTTT    GAC
GAM390  LOC150951 5'  TTTTGGGGTAAAATATTTTT  86345       GAA_
                                GGAGGTG   ACCCCAGGG
                                |||||||   |||||||||
                                TTTTTAT   TGGGGTTTT
                                   AAAA
GAM390  LOC150998 3'  CCCTGGCTTCTCAGCTTTTTGC 86357         G  AACC
          CT                    AGGCAGGAGGT GA   CCAGGG
                                |||||||||||  ||   ||||||
                                TCCGTTTTTCG CT   GGTCCC
                                    A  CTTC
GAM390  LOC151193 3'  CCAGGGTCTTGTTTACCATCTG 80973      GA    AA_____ CCAG
          TCT                   AGGCAG  GGTGGA      CC   G
                                ||||||  ||||||      ||   |
                                TCTGTC  CCATTT      GG   C
                                   TA    GTTCT    GACC
GAM390  LOC151193 3'  CTCTGACTCATTTCTCTGTTT  80975      _     AAACCC
                                AGGCAG GAGGTGG    CAGGG
                                |||||| |||||||    |||||
                                TTTGTC CTTTACT    GTCTC
                                   T     CA____
GAM390  LOC151195 5'  TTCTGGGAGCCATTCTTCTTGC 80972        __  AAAC
          CT                    AGGCAGGAGG  TGG   CCCAGGG
                                ||||||||||  |||   |||||||
                                TCCGTTCTTC  ACC   GGGTCTT
                                    TT  GA__
GAM390  LOC151277 5'  CTTTGGGTGTTATTTCTT    81006       AAAC
                                AGGAGGTGG   CCCAGGG
                                |||||||||   |||||||
                                TTCTTTATT   GGGTTTC
                                    GT__
GAM390  LOC151318 3'  CCATTTTCATTTTCTGCT    81028          CCCCA
                                GGCAGGAGGTGGAAA   GG
                                ||||||||||||||    ||
                                TCGTCTTTTACTTTT   CC
                                       A____
GAM390  LOC151391 3'  TCAAAATATTTCCGCCTTTTGC 86512          CCCCAG
          T                     GGCAGGAGGTGGAAA    GG
                                ||||||||||||||    ||
                                TCGTTTTCCGCCTTT    CT
                                       ATAAAA  T
GAM390  LOC151429 3'  CCCTGGGGGGCCCCTCCTGT  86531       T  AAA
                                GCAGGAGG GG  CCCCAGGG
                                |||||||| ||  ||||||||
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                                TGTCCTCC CC   GGGGTCCC
                                    _ GG_
GAM390  LOC151429 3'  CTTGCTGCTTCTCCTGCCT   86536         T  AAACCC
                                AGGCAGGAGG GG     CAGG
                                |||||||||| ||     ||||
                                TCCGTCCTCT TC     GTTC
                                    _ GTC___
GAM390  LOC151475 5'  CCTCTTTTACCTTCGTCT    86591      A        ACCCC
                                AGGC GGAGGTGGAA    AGG
                                |||| ||||||||||    |||
                                TCTG CTTCCATTTT    TCC
                                  _       C____
GAM390  LOC151512 5'  CCTTGGCTGTGCCTCCTGCT  86614         GGAA  C_
                                GGCAGGAGGT   AC  CCAGGG
                                ||||||||||   ||  ||||||
                                TCGTCCTCCG   TG  GGTTCC
                                    _____  TC
GAM390  LOC151516 3'  CCCCAGGGTTTTCTTTCTGTCA 81063        A GT   A_________  CCAG
            TTTGCTT                AGGCAGG G  GGAA       CC   GG
                                ||||||| |  ||||       ||   ||
                                TTCGTTT C  TCTT       GG   CC
                                   A TG   TCTTTT    GACC
GAM390  LOC151534 3'  CTTTGGCTTCTGTCTGTTCCTG 57485        ___  TG   ACC
            TCT                  AGGCAGGA   GG  GAA   CCAGGG
                                ||||||||   ||  |||   ||||||
                                TCTGTCCT   CT  CTT   GGTTTC
                                    TGT  GT   C__
GAM390  LOC151602 3'  CCAGGGCCTTTTTCTGTCT   81106         T  AAA  CCAG
                                AGGCAGGAGG GG   CC   G
                                |||||||||| ||   ||   |
                                TCTGTCTTTT CC   GG   C
                                      T      GACC
GAM390  LOC151602 3'  CCCGCTTTTCTATTTCTGGTTT 81107      A         CCCCA
                                AGGC GGAGGTGGAAA    GGG
                                |||| ||||||||||    |||
                                TTTG TCTTTATCTTT    CCC
                                  G         TCG__
GAM390  LOC151647 3'  CCAGGGTCTTCACTTTCTTTCT 81141        _____     AA___  CCAG
            GCTT                   AGGCAGGA   GGTGGA    CC   G
                                ||||||||   ||||||    ||   |
                                TTCGTCTT   TCACTT    GG   C
                                    TCTT     CT    GACC
GAM390  LOC151657 5'  CTTTGGGACCCCGTGCCTCCTG 86655         __  AAAC
            CC                   GGCAGGAGGT  GG   CCCAGGG
                                ||||||||||  ||   |||||||
                                CCGTCCTCCG  CC   GGGTTTC
                                    TG  CCA_
GAM390  LOC151720 5'  CCTTGCCCTTGCCTCTGGTCT  81151      A    TG AAACCC
                                AGGC GGAGG  G     CAGGG
                                |||| |||||  |     |||||
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                                TCTG TCTCC  T     GTTCC
                                  G    GT CCC___
GAM390  LOC151720 5'  TCTTGGTTTCTCTGTCTCTGTC 81159       G   TG  AACC
            T                    AGGCAG AGG  GA    CCAGGG
                                 |||||| |||  ||    ||||||
                                 TCTGTC TCT  CT    GGTTCT
                                   _  GT  CTTT
GAM390  LOC152110 5'  CCCAGGGTCCTCCTTTGCCTTC 81292         TG  AA_______  CCAG
            TGCT                   GGCAGGAGG  GA       CC    GG
                                 |||||||||  ||       ||    ||
                                 TCGTCTTCC  TT       GG    CC
                                      GT  CCTCCT    GACC
GAM390  LOC152137 5'  CCCGCCTTTCTGTCTCCTCTCT 81311     C     TG    CCCCA
                                 AGG AGGAGG  GAAA    GGG
                                 ||| ||||||  ||||    |||
                                 TCT TCCTCT  CTTT    CCC
                                   C     GT   CCG__
GAM390  LOC152137 3'  CTTTGTATTCCATCTCTTCTT  81315     C         ACCC
                                 AGG AGGAGGTGGAA   CAGGG
                                 ||| ||||||||||    |||||
                                 TTC TTCTCTACCTT   GTTTC
                                   _         AT__
GAM390  LOC152263 5'  CCAGGGTCAATTTTTCTCTCTT 86857         TG   A_______  CCAG
            GTTT                   AGGCAGGAGG  GAA       CC    G
                                 ||||||||||  |||       ||    |
                                 TTTGTTCTCT  TTT       GG    C
                                       CT   TAACT    GACC
GAM390  LOC152275 3'  CTCTAAGGTTTTCATCTGCTTG 86796       _         CC
            TTT                    AGGCAGG AGGTGGAAACC  AGGG
                                 ||||||| ||||||||||  ||||
                                 TTTGTTC TCTACTTTTGG  TCTC
                                    G         AA
GAM390  LOC152343 3'  CCAGGGCTGTCTTTGTTTCTTG 81423         TG  AA______  CCAG
            CTT                    AGGCAGGAGG  GA       CC    G
                                 ||||||||||  ||       ||    |
                                 TTCGTTCTTT  TT       GG    C
                                       GT  CTGTC    GACC
GAM390  LOC152426 5'  CTGTTTTCCATTTTTGCTT   86896      G       CCC
                                 AGGCA GAGGTGGAAA   CAG
                                 ||||| ||||||||||   |||
                                 TTCGT TTTTACCTTT   GTC
                                   _         T__
GAM390  LOC152426 5'  TTCTGGCTCTCACCTTTTCCT  86904     C      _  AACC
                                 AGG AGGAGGTG GA    CCAGGG
                                 ||| ||||||||  ||    ||||||
                                 TCC TTTTCCAC CT    GGTCTT
                                   _       T  C___
GAM390  LOC152445 3'  CTTTAAGGTTTTCTTTTTTGTT 86947         T      CC
            T                      AGGCAGGAGG GGAAACC  AGGG
                                 ||||||||||  |||||||  ||||
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                                TTTGTTTTTT CTTTTGG  TTTC
                                      _       AA
GAM390  LOC152453 5'  CCCTGCCTCTATCTTCTCTCT  81470     C        AACCC
                                AGG AGGAGGTGGA     CAGGG
                                ||| ||||||||||     |||||
                                TCT TCTTCTATCT     GTCCC
                                  C         CC___
GAM390  LOC152739 5'  GGTCTTATTCATCCTTGTTT   87044        A     AA_______
                                AGGCAGG GGTGGA       CC
                                ||||||| ||||||       ||
                                TTTGTTC CTACTT       GG
                                    _     ATTCT
GAM390  LOC152804 3'  TTTTGGATTTTCTGTTTCTTCC 87092     C     TG    CC
                T                AGG AGGAGG  GAAA  CCAGGG
                                ||| ||||||  ||||  ||||||
                                TCC TTCTTT  CTTT  GGTTTT
                                  _     GT    TA
GAM390  LOC152845 3'  CTCTGCACTCCTTGCCTCCTGT 60957          __   AACCC
                CT                 AGGCAGGAGGT  GGA     CAGGG
                                ||||||||||  |||     |||||
                                TCTGTCCTCCG  CCT     GTCTC
                                      TT   CAC__
GAM390  LOC152941 5'  GGTCCTATTTCCTTTTGCCT   81635          T____   AA_
                                AGGCAGGAGG     GGA   CC
                                ||||||||||     |||   ||
                                TCCGTTTTCC     CCT   GG
                                      TTTAT
GAM390  LOC153232 5'  CCAGGGTTCTCTTTATCTCTTT 87180        _       AA_______  CCAG
                GTCT                  AGGCAG GAGGTGGA       CC    G
                                ||||||| ||||||||       ||    |
                                TCTGTT CTCTATTT       GG    C
                                   T       CTCTT     GACC
GAM390  LOC153525 5'  CCAGGGCCTTATTTTCCTTTTG 87229          TG  AA_______  CCAG
                TCT                   AGGCAGGAGG  GA       CC    G
                                ||||||||||  ||       ||    |
                                TCTGTTTTCC  TT       GG    C
                                      TT  ATTCC     GACC
GAM390  LOC153525 5'  TCCTGATTTCTATTCTTGTCT  87230         G     CCC
                                AGGCAGGAG TGGAAA   CAGGG
                                ||||||||| ||||||   |||||
                                TCTGTTCTT ATCTTT   GTCCT
                                      _     A__
GAM390  LOC153606 3'  GGTGTTTTCATTCCTGTTT    87260         G      _____
                                AGGCAGGAG TGGAAAC    CC
                                ||||||||| |||||||    ||
                                TTTGTCCTT ACTTTTG    GG
                                      _       T
GAM390  LOC153642 3'  TCCTATTTCTATTCTTTGCCT  81794         AG       CCCC
                                AGGCAGG  GTGGAAA    AGGG
                                |||||||  |||||||    ||||
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                                TCCGTTT  TATCTTT    TCCT
                                   CT      A___
GAM390  LOC153643 3'  TCTGGGATGTTTACTGCTT   81780     AGGA     AAC
                                AGGC   GGTGGA   CCCAGG
                                ||||   ||||||   ||||||
                                TTCG   TCATTT   GGGTCT
                                  ____     GTA
GAM390  LOC153733 3'  AATGCAGTTTTCTTTTCTGCTT 81799         T     CC  GGG
                                AGGCAGGAGG GGAAAC  CA
                                |||||||||| ||||||  ||
                                TTCGTCTTTT CTTTTG  GT
                                      _     AC  AAT
GAM390  LOC153733 3'  CAGGGTTCTTTTCTGCTTCTGT 81800       G   TG   A_______  CCAG
           TT                    AGGCAG AGG  GAA       CC    G
                                ||||||  |||  |||       ||    |
                                TTTGTC TTC  CTT       GG    C
                                   _   GT   TTCTT     GAC
GAM390  LOC153883 5'  CCAGGGTTCTTTTTTTCTCTTG 81890         T    A______  CCAG
           TTT                    AGGCAGGAGG GGAA      CC    G
                                ||||||||||  ||||      ||    |
                                TTTGTTCTCT TTTT      GG    C
                                     T    TCTT     GACC
GAM390  LOC154449 5'  TCCTGGGTTCTGTCTGCTGCTT 81994       G   TG   AC
                                AGGCAG AGG  GAA  CCCAGGG
                                ||||||  |||  |||  |||||||
                                TTCGTC TCT  CTT  GGGTCCT
                                   G   GT   __
GAM390  LOC154789 5'  CTTTGCAGGCTTCATTCCCTGT 82027       AG     AA  C_
           CT                    AGGCAGG  GTGGA  CC  CAGGG
                                |||||||  |||||  ||  |||||
                                TCTGTCC  TACTT  GG  GTTTC
                                   CT    C_  AC
GAM390  LOC154865 3'  CTTTGCAGTTTATCGTCTGCTT 82062       GA     AACCC
                                AGGCAG  GGTGGA    CAGGG
                                ||||||  ||||||    |||||
                                TTCGTC  CTATTT    GTTTC
                                   TG     GAC__
GAM390  LOC154877 5'  CTCTGGGAAGAGCTCACTTCTG 87545         GT  AAAC_
           TTT                    AGGCAGGAG  GG    CCCAGGG
                                |||||||||  ||    |||||||
                                TTTGTCTTC  TC    GGGTCTC
                                     AC  GAGAA
GAM390  LOC154990 5'  CCAGGGTTTTGCCCAACTTCTG 82148         G   AAA_______  CCAG
           TCT                    AGGCAGGAG TGG       CC    G
                                |||||||||  |||       ||    |
                                TCTGTCTTC ACC       GG    C
                                     A   CGTTTT    GACC
GAM390  LOC155004 3'  CCCTCCCCTTCCCCTCCTGCCT 82155         T    ACCCC
                                AGGCAGGAGG GGAA    AGGG
                                ||||||||||  ||||    ||||
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                                TCCGTCCTCC CCTT    TCCC
                                      _   CCCC_
GAM390  LOC155032 5'  TTTTGGAGTTGTTTGGTTTTTG 87602        G GG _  C
                TTT                    AGGCAGGAG T  A AAC CCAGGG
                                       ||||||||| |  | ||| ||||||
                                       TTTGTTTTT G  T TTG GGTTTT
                                           G TT G   A
GAM390  LOC155036 5'  TTCTGGTTTTGTTTCTTGTT  87618        TG  ACC
                                       GGCAGGAGG  GAA  CCAGGG
                                       |||||||||  |||  ||||||
                                       TTGTTCTTT  TTT  GGTCTT
                                           GT  ___
GAM390  LOC155061 3'  CCTGTTTTGTTTTTTGTTT  82188        TG  ACCC
                                       AGGCAGGAGG  GAA   CAGG
                                       ||||||||||  |||   ||||
                                       TTTGTTTTTT  TTT   GTCC
                                           GT  ____
GAM390  LOC155064 3'  GGTTTTGCCACTTCTGTTT  82179      G    _ A____
                                       AGGCAG AGGTGG AA    CC
                                       |||||| |||||| ||    ||
                                       TTTGTC TTCACC TT    GG
                                          _    G  TT
GAM390  LOC155382 3'  TTCTGTATTTTTCTGTCCCTGT 87679       A  TG   CCC_
                CT                     AGGCAGG GG  GAAA   CAGGG
                                       ||||||| ||  ||||   |||||
                                       TCTGTCC CT  CTTT   GTCTT
                                          _ GT   TTAT
GAM390  LOC155434 3'  CCCCAGGGCTCTCCCTCCACCT 87689   G        AA_________  CCAG
                CCTGGCT                  AG CAGGAGGTGGA       CC   GG
                                       || ||||||||||        ||   ||
                                       TC GTCCTCCACCT        GG   CC
                                        G        CCCTCTC    GACC
GAM390  LOC157285 3'  CCCTGCCTAACCCTTTCCTGTC 87727         T  AAACCC
                T                      AGGCAGGAGG GG     CAGGG
                                       |||||||||| ||     |||||
                                       TCTGTCCTTT CC     GTCCC
                                             C  AATCC_
GAM390  LOC157349 3'  CCTGCGCCCCTCCTGCCT    82337         T  AAACCC
                                       AGGCAGGAGG GG     CAGG
                                       |||||||||| ||     ||||
                                       TCCGTCCTCC CC     GTCC
                                             _  GC____
GAM390  LOC157695 3'  CTCTCGCGTTCTTTTTCTGTCT 87811         T   ACCCC
                                       AGGCAGGAGG GGAA    AGGG
                                       |||||||||| ||||    ||||
                                       TCTGTCTTTT TCTT    TCTC
                                             _   GCGC_
GAM390  LOC157858 3'  CCAGGGTCGTTTTCTGTTTCTG 87884     A  GG    A________  CCAG
                GCTT                     AGGC GGA  TGGAA      CC   G
                                       |||| |||  |||||       ||   |
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                                TTCG TCT  GTCTT      GG   C
                                  G  TT    TTGCT    GACC
GAM390  LOC157867 5'  TTTTGGTTGCTCTTTTTCTGCT 87874         T  A_   CCAGGG
          T                    AGGCAGGAGG GG  AACC
                               ||||||||||  ||  ||||
                               TTCGTCTTTT CT  TTGG
                                    T  CG    TTTT
GAM390  LOC157922 3'  CTTTGGGTTCTTTCTGCCT    87927         TGGA    C
                               AGGCAGGAGG    AACCC AGG
                               ||||||||||    ||||| |||
                               TCCGTCTTTC    TTGGG TTC
                                    ____    T
GAM390  LOC158014 5'  TGGAAGTTTATCATTTTTTGCC 82570           _   C_  GGG
          T                    AGGCAGGAGGTGG AAAC  CCA
                               ||||||||||||| ||||  |||
                               TCCGTTTTTTACT TTTG  GGT
                                      A   AA
GAM390  LOC158116 3'  CAGGGTCCTATTCACCTTTTGT 60948           AA_______  CCAG
          TT                    AGGCAGGAGGTGGA       CC    G
                               ||||||||||||||       ||   |
                               TTTGTTTTCCACTT       GG    C
                                     ATCCT    GAC
GAM390  LOC158117 3'  CCCATTTTCTCACTTCCTGTTT 82610           _   CCCCA
                               AGGCAGGAGGTG GAAA    GGG
                               |||||||||||| ||||    |||
                               TTTGTCCTTCAC CTTT    CCC
                                     T   TA___
GAM390  LOC158156 3'  CCCAGGGTTTTTTTCACTTGCT 82624       G       ________  CCA
          GCTT                    AGGCAG AGGTGGAAA      CC   GG
                               ||||||| |||||||||       ||   ||
                               TTCGTC TTCACTTTT      GG   CC
                                  G        TTT   G  ACC
GAM390  LOC158187 3'  CCAGGGTTTTTTTTCTCTCTTG 87990         TG   A_______  CCAG
          CCT                    AGGCAGGAGG  GAA      CC    G
                               ||||||||||  |||      ||   |
                               TCCGTTCTCT  TTT      GG    C
                                     CT   TTTT    GACC
GAM390  LOC158235 3'  CCAGGGCTTTGCCTCATTTACT 88001       _____    TG  AA__  CCAG
          GCTT                    AGGCAG    GAGG  GA    CC    G
                               ||||||    ||||  ||   ||   |
                               TTCGTC    CTCC  TT   GG    C
                                  ATTTA    GT  C    GACC
GAM390  LOC158235 3'  CCAGGGTTTTCGTTTATTGTCT 88002       AG    AA________  CCAG
          GTCT                    AGGCAGG  GTGGA       CC    G
                               |||||||  |||||       ||   |
                               TCTGTCT  TATTT       GG    C
                                  GT    GCTTTT    GACC
GAM390  LOC158235 5'  CTTTGGTTTTCTTTTTGTCT   88005         TG     CC
                               AGGCAGGAGG  GAAACC  AG
                               ||||||||||  ||||||  ||
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                                TCTGTTTTTC  TTTTGG  TC
                                    __      TT
GAM390  LOC158267 3'  TCTTGGGCAAGTCATTTTCTGT 82724           AAAC
          CT                    AGGCAGGAGGTGG    CCCAGGG
                                ||||||||||||    |||||||
                                TCTGTCTTTTACT    GGGTTCT
                                    GAAC
GAM390  LOC158288 5'  GCCTGTCTTCATTTTTTGTCT  88023           AACCC    G
                                AGGCAGGAGGTGGA    CAGG
                                ||||||||||||||    ||||
                                TCTGTTTTTTACTT    GTCC
                                    CT___    GT
GAM390  LOC158293 3'  TCTTAGAGTTTTTATCTTTTAC 82748     C          CCC
          TT                    AGG AGGAGGTGGAAAC   AGGG
                                ||| ||||||||||||   ||||
                                TTC TTTTCTATTTTTG   TTCT
                                  A           AGA
GAM390  LOC158298 3'  CCTGTGCCCGCCCCTGCCT    88062        A    AAACCC
                                AGGCAGG GGTGG     CAGG
                                |||||||| |||||     ||||
                                TCCGTCC CCGCC     GTCC
                                   _    CGT___
GAM390  LOC158314 3'  CCTGGCTTATCTTCTGC     88095          AAACC
                                GCAGGAGGTGG    CCAGG
                                ||||||||||     |||||
                                CGTCTTCTATT    GGTCC
                                    C____
GAM390  LOC158332 3'  CCTTGAAGTCCACTTCCT    82764          AACCC
                                AGGAGGTGGA    CAGGG
                                ||||||||||    |||||
                                TCCTTCACCT    GTTCC
                                    GAA__
GAM390  LOC158402 5'  CTCTACAATGCCGCCTTCTGCC 88145           AAACCCC
          T                     AGGCAGGAGGTGG      AGGG
                                ||||||||||||      ||||
                                TCCGTCTTCCGCC      TCTC
                                    GTAACA_
GAM390  LOC158427 3'  CCAGGGCCTTCTTCATTTTCTG 58352           AA_____  CCAG
          TT                    GGCAGGAGGTGGA      CC    G
                                ||||||||||||       ||    |
                                TTGTCTTTTACTT      GG    C
                                    CTTCC    GACC
GAM390  LOC158563 5'  CCTTGCTGTCTGTCTCATTGTC 82844      _    TG  AACCC
          T                     AGGCAG GAGG  GA    CAGGG
                                |||||| ||||  ||    |||||
                                TCTGTT CTCT  CT    GTTCC
                                   A   GT  GTC__
GAM390  LOC158572 3'  CCTGAGTCAGCTCTTGCTT   82848        G   AAACCC
                                AGGCAGGAG TGG     CAGG
                                ||||||||| |||     ||||
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                                TTCGTTCTC ACT     GTCC
                                     G   GA____
GAM390   LOC158576 3'  TCCTGAGGTTTTTTTTTGTTT  82853        GTG     C
                                AGGCAGGAG   GAAACC CAGGG
                                |||||||||   |||||| |||||
                                TTTGTTTTT   TTTTGG GTCCT
                                     ___     A
GAM390   LOC159036 3'  CCCTACTCTCCACCTTTGCCT  88347      G      AACCCC
                                AGGCAG AGGTGGA     AGGG
                                |||||| |||||||     ||||
                                TCCGTT TCCACCT     TCCC
                                   _      CTCA__
GAM390   LOC159065 5'  CTTTGGTCTTCCTTTGTCTTCT 82955        TG  __  CC
            GCC                   GGCAGGAGG  GA  AA  CCAGGG
                                |||||||||  ||  ||  ||||||
                                CCGTCTTCT  TT  TT  GGTTTC
                                     GT  CC  CT
GAM390   LOC159090 5'  CAGGGTCCTCTCTGTCCTCCTG 82957         _   AA_______  CCAG
            CTT                   AGGCAGGAGG TGGA       CC    G
                                ||||||||||| ||||       ||    |
                                TTCGTCCTCC GTCT       GG    C
                                     T    CTCCT     GAC
GAM390   LOC159110 5'  CTCTCCGATTCCACCTCCTCCT 82990     C         ACCCC
                                AGG AGGAGGTGGAA     AGGG
                                ||| ||||||||||     ||||
                                TCC TCCTCCACCTT     TCTC
                                  _         AGCC_
GAM390   LOC159116 5'  CTCTCCGATTCCACCTCCTCCT 82973     C         ACCCC
                                AGG AGGAGGTGGAA     AGGG
                                ||| ||||||||||     ||||
                                TCC TCCTCCACCTT     TCTC
                                  _         AGCC_
GAM390   LOC159963 5'  TTTTGGAAACATCTTCTTCCT  83078     C       GAAACC
                                AGG AGGAGGTG      CCAGGG
                                ||| ||||||||      ||||||
                                TCC TCTTCTAC      GGTTTT
                                  T       AAA___
GAM390   LOC161003 3'  CCTGGGGATTTCATGTTT    59913     G     A
                                GGA GTGGAA CCCCAGG
                                ||| |||||| |||||||
                                TTT TACTTT GGGGTCC
                                  G      A
GAM390   LOC161247 5'  TCTGGGTGGCCTCTGCCT    83142       G    GGAAAC
                                AGGCAG AGGT     CCCAGG
                                |||||| ||||     ||||||
                                TCCGTC TCCG     GGGTCT
                                   _    GT____
GAM390   LOC161635 5'  CCGTGTTCCGCTTCCTGCC    98354            ACCC  G
                                GGCAGGAGGTGGAA    CA GG
                                ||||||||||||||    || ||
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                                CCGTCCTTCGCCTT   GT CC
                                      _____ G
GAM390  LOC163397 5'  CCCCAGGGTTTTACATCTGTTT 88394        TG  AA_________  CCAG
          TTTGCT                  GGCAGGAGG  GA        CC   GG
                                |||||||||  ||        ||   ||
                                TCGTTTTTT  CT        GG   CC
                                    GT  ACATTTT    GACC
GAM390  LOC165140 5'  CCCTGCCACCCCACCTCTTCCT 83354     C       AAACCC
                                AGG AGGAGGTGG     CAGGG
                                ||| |||||||||     |||||
                                TCC TTCTCCACC     GTCCC
                                  _       CCACC_
GAM390  LOC165140 5'  CCTCTTCATCTTCTGC      83355           AACCCC
                                GCAGGAGGTGGA     AGG
                                ||||||||||||     |||
                                CGTCTTCTACTT     TCC
                                      C_____
GAM390  LOC169436 5'  TCCTGGGCCAAGGCCTGCCTTT 83620          _  AAAC__
          TGCCT                   AGGCAGGAGGT GG     CCCAGGG
                                ||||||||||| ||     |||||||
                                TCCGTTTTCCG CC     GGGTCCT
                                      T  GGAACC
GAM390  LOC169611 3'  CAGGGTTCATTCTAGCTTTCTG 83639          _    A______  CCAG
          CTT                     AGGCAGGAGG TGGAA      CC   G
                                |||||||||| |||||      ||   |
                                TTCGTCTTTC ATCTT      GG   C
                                      G    ACTT    GAC
GAM390  LOC170127 3'  CCCTGGGGAGAGGCTTTCCTGC 83457         _  GGAAA
          CT                      AGGCAGGAG GT    CCCCAGGG
                                |||||||||  ||    ||||||||
                                TCCGTCCTT CG    GGGGTCCC
                                      T  GAGA_
GAM390  LOC170384 3'  CCCCAGGGTCTTTTTCTCATCT 83727          GA A_________  CCAG
          CTTGCTT                 AGGCAGGAGGTG  A       CC   GG
                                ||||||||||||  |       ||   ||
                                TTCGTTCTCTAC  T       GG   CC
                                      TC TTTTCT    GACC
GAM390  LOC170409 3'  TCGGTGGTTCTCATCTTCTGTT 83746          GA   _  AGGG
          T                       AGGCAGGAGGTG  AACC CC
                                ||||||||||||  ||||  ||
                                TTTGTCTTCTAC  TTGG GG
                                      TC    T  CT
GAM390  LOC196047 3'  CCCACACATTCCTCCTCCTGTC 91149          T    ACCCCA
          T                       AGGCAGGAGG GGAA     GGG
                                ||||||||||  ||||     |||
                                TCTGTCCTCC CCTT     CCC
                                      T    ACACA_
GAM390  LOC196047 5'  CTTTGGTGGCTGCTGTTTGTTT 91152        A  TG AAA  _
                                AGGCAGG GG  G   CC CCAGGG
                                |||||||  ||  |   ||  ||||||
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                                TTTGTTT TC  C   GG GGTTTC
                                    G  GT ___  T
GAM390  LOC196264 3'  CAGGGTTTGTTTCACCTCTTGT 88980           AC_______ CCAG
          TT                   AGGCAGGAGGTGGAA       C    G
                               ||||||||||||||       |   |
                               TTTGTTCTCCACTTT       G    C
                                     GTTT   G GAC
GAM390  LOC196264 3'  CCAGGGCTTTGTTATTTTCTGT 88982           AAA_____  CCAG
          CT                   AGGCAGGAGGTGG       CC    G
                               ||||||||||||       ||    |
                               TCTGTCTTTTATT       GG    C
                                     GTTTC     GACC
GAM390  LOC196320 5'  CTCTGGCCGCTTGCTTTTTGCT 89010         TG AAACC
                               GGCAGGAGG  G     CCAGGG
                               |||||||||  |     ||||||
                               TCGTTTTTC  T     GGTCTC
                                     GT CGCC_
GAM390  LOC196337 3'  TCCTCCCACCTCCGTCTCCTGC 89027         GT   AACCCC
          T                    GGCAGGAG  GGA     AGGG
                               ||||||||  |||     ||||
                               TCGTCCTC  CCT     TCCT
                                    TG   CCACCC
GAM390  LOC196527 3'  CCTGCTGCACTCCTGTCT    89098         _ TG AAACCC
                               AGGCAGGAG G  G     CAGG
                               |||||||||  |  |     ||||
                               TCTGTCCTC C  C     GTCC
                                    A GT _______
GAM390  LOC196529 3'  TTTTGGGGGGGCGGTTTTTTTGG 89148    G      TGGAAA
          TT                   AG CAGGAGG     CCCCAGGG
                               ||  |||||||     ||||||||
                               TT GTTTTTT     GGGGTTTT
                                G      TGGCGG
GAM390  LOC196540 5'  CCTGGACCACTTTCAGCCT    91199      A       AAACC
                               AGGC GGAGGTGG    CCAGG
                               ||||  ||||||||    |||||
                               TCCG CTTTCACC    GGTCC
                                 A       A____
GAM390  LOC196759 3'  CTTGCTCACCTTCTACTT    88911     C       AAACCC
                               AGG AGGAGGTGG     CAGG
                               |||  |||||||||     ||||
                               TTC TCTTCCACT     GTTC
                                 A       C_____
GAM390  LOC196860 5'  CCTTCCTTTCACTTCCTGTT   91216           ACCCC
                               GGCAGGAGGTGGAA    AGG
                               ||||||||||||||    |||
                               TTGTCCTTCACTTT    TCC
                                     CCT__
GAM390  LOC196955 5'  CCTGGTCTGTCTCTTGCT    77865         TG  AACC
                               GGCAGGAGG  GA    CCAGG
                               |||||||||  ||    |||||
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                                TCGTTCTCT  CT    GGTCC
                                     GT  ____
GAM390  LOC197131 3'  TCCTGGCTTTTGTTTTTTGT   89235        TG   ACC
                                GCAGGAGG  GAA   CCAGGG
                                ||||||||  |||   ||||||
                                TGTTTTTT  TTT   GGTCCT
                                     GT   C__
GAM390  LOC197131 3'  TCTTGGTTCCTGGCTTTTGTTT 89236         G _    ACC
                                AGGCAGGAG T GGAA   CCAGGG
                                |||||||||| | ||||   ||||||
                                TTTGTTTTC G CCTT   GGTTCT
                                     G T    ___
GAM390  LOC197201 3'  CCCCAGGGTCTTCCTTTTGTCT 89271          T   AA_  CCAG
                                AGGCAGGAGG GGA   CC    GG
                                |||||||||| |||   ||    ||
                                TCTGTTTTCC TCT   GG    CC
                                      T       GACC
GAM390  LOC197379 5'  CCAGGGTCCTCTCCTGCTTTCT 91314          _   AA_______  CCAG
           GCCT                    AGGCAGGAGGT GGA       CC    G
                                |||||||||||| |||       ||    |
                                TCCGTCTTTCG CCT       GG    C
                                      T   CTCCT     GACC
GAM390  LOC197379 5'  CCCTACTTTCCTCTCCTGCTT  91315         T    CCCC
                                AGGCAGGAGG GGAAA    AGGG
                                |||||||||| |||||    ||||
                                TTCGTCCTCT CCTTT    TCCC
                                     _     CA__
GAM390  LOC199786 3'  TTTTGGGGTTTTTTTCTCCGCT 89774      A    TG
           T                     AGGC GGAGG  GAAACCCCAGGG
                                ||||  |||||  ||||||||||||
                                TTCG CCTCT  TTTTGGGGTTTT
                                   _     TT
GAM390  LOC199864 3'  CTTGCTCACCTTCTACTT    91458     C       AAACCC
                                AGG AGGAGGTGG     CAGG
                                ||| |||||||||     ||||
                                TTC TCTTCCACT     GTTC
                                  A       C_____
GAM390  LOC199906 3'  CCCTGTTACCCTTTTTTTTGTT 89850          T_  AAACCC
           T                     AGGCAGGAGG  GG     CAGGG
                                ||||||||||  ||     |||||
                                TTTGTTTTTT  CC     GTCCC
                                     TT  CATT__
GAM390  LOC199907 3'  TTTTGGGGTTTTTTGTTTTTT  89835       TG   _
                                AGGAGG  GAAA CCCCAGGG
                                ||||||  |||| ||||||||
                                TTTTTT  TTTT GGGGTTTT
                                   GT    T
GAM390  LOC199923 5'  CAGGGCCTTCTCCACCTCCTGC 89866           AA_______  CCAG
           C                     GGCAGGAGGTGGA       CC    G
                                ||||||||||||       ||    |
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                                CCGTCCTCCACCT       GG    C
                                      CTTCC     GAC
GAM390   LOC199982 3'  CCAGGGTTTTATATATTTCCTG 89899          GAAA_______  CCAG
                CTT                    AGGCAGGAGGTG        CC    G
                                       ||||||||||||        ||    |
                                       TTCGTCCTTTAT        GG    C
                                             ATATTTT     GACC
GAM390   LOC199986 5'  CCCAGGGCTCAGCTTCTGCCTC 91506          TG   AC_________ CCAG
                CTGTCT                  AGGCAGGAGG  GAA        C    G
                                        ||||||||||  |||        |    |
                                        TCTGTCCTCC  CTT        G    C
                                              GT   CGACTC   G GACC
GAM390   LOC199986 5'  CCCTGGGGTTTCCACAGGC   91508    AGGAG
                                        GC     GTGGAAACCCCAGGG
                                        ||     ||||||||||||||
                                        CG     CACCTTTGGGGTCCC
                                         GA___
GAM390   LOC200081 3'  CCTTGGGGATTCTACTTCTTCC 89974     C          A
                T                       AGG AGGAGGTGGAA CCCCAGGG
                                        ||| |||||||||| ||||||||
                                        TCC TTCTTCATCTT GGGGTTCC
                                          _         A
GAM390   LOC200081 3'  GGTTTTTCTGCTTCCTGCC    89977             A_____
                                        GGCAGGAGGTGGAA      CC
                                        ||||||||||||||      ||
                                        CCGTCCTTCGTCTT      GG
                                              TTT
GAM390   LOC200091 3'  GGTCTTCTTCGCTTTTGCCT   91535       G      AA_______
                                        AGGCAG AGGTGGA       CC
                                        |||||| |||||||       ||
                                        TCCGTT TTCGCTT       GG
                                           _      CTTCT
GAM390   LOC200261 5'  CCTGGGAACCTTTTTTCT     90051     C      GGAAAC
                                        AGG AGGAGGT     CCCAGG
                                        ||| |||||||     ||||||
                                        TCT TTTTCCA     GGGTCC
                                          T      A_____
GAM390   LOC200269 3'  CCAGGGCTTTCTCTACCTTCAG 90071      A        AA_______  CCAG
                CTT                     AGGC GGAGGTGGA       CC    G
                                        |||| |||||||||       ||    |
                                        TTCG CTTCCATCT       GG    C
                                          A        CTTTC     GACC
GAM390   LOC200269 3'  CCTTGTCTCTACCTCCT     90072          A  CCC
                                        AGGAGGTGGA AC   AGG
                                        |||||||||| ||   |||
                                        TCCTCCATCT TG   TCC
                                              C  T__
GAM390   LOC200282 3'  CCAGGGTTTATTTTGTTTGCTG 90098       G   TG   A_______  CCAG
                TCT                     AGGCAG AGG  GAA      CC    G
                                        |||||| |||  |||      ||    |
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                                TCTGTC TTT  TTT      GG    C
                                   G   GT   ATTT    GACC
GAM390   LOC200301 3'  GGCTCATTCTTCTCCTGCTT   90145          T   AA_____
                                AGGCAGGAGG GGA      CC
                                |||||||||| |||      ||
                                TTCGTCCTCT CTT      GG
                                     T   ACTC
GAM390   LOC200316 3'  TCCTGCACCAGCTGTGCTTTTG 90195          _ TG AAACCC
            CCT                   AGGCAGGAG G  G     CAGGG
                                |||||||||  |  |     |||||
                                TCCGTTTTC T  C     GTCCT
                                     G GT GACCAC
GAM390   LOC200609 5'  CCTGCTTTTACTTTCTTCT    91661     C         ACCC
                                AGG AGGAGGTGGAA    CAGG
                                ||| ||||||||||    ||||
                                TCT TCTTTCATTTT    GTCC
                                  _         C___
GAM390   LOC200609 5'  CCTTATGGTTTTGCCTTTTCCT 91662     C     TG   A  CC
                                AGG AGGAGG  GAA CC  AGGG
                                ||| ||||||  ||| ||  ||||
                                TCC TTTTCC  TTT GG  TTCC
                                  _     GT   _  TA
GAM390   LOC200627 3'  CCAGGGCTTTCAGTTACTTTTT 90261           AAA_______  CCAG
            GTCT                  AGGCAGGAGGTGG         CC    G
                                ||||||||||||         ||    |
                                TCTGTTTTTCATT        GG    C
                                     GACTTTC     GACC
GAM390   LOC200830 3'  CCCAGGGCTTTCCCTTCGTCTT 91725        GT   AA_________  CCAG
            CTGCC                 GGCAGGAG  GGA        CC    GG
                                ||||||||  |||        ||    ||
                                CCGTCTTC  CTT        GG    CC
                                   TG   CCCTTTC     GACC
GAM390   LOC200860 3'  CTTTGGGGGATTTTTCTGCT   91747         TGGAAA
                                GGCAGGAGG     CCCCAGGG
                                |||||||||     ||||||||
                                TCGTCTTTT     GGGGTTTC
                                     TAG___
GAM390   LOC201115 5'  CTCTGCAACATCCACTTCCTGC 89478            AACCC
            T                  GGCAGGAGGTGGA     CAGGG
                                ||||||||||||     |||||
                                TCGTCCTTCACCT     GTCTC
                                     ACAAC
GAM390   LOC201158 3'  CCCATTAAATTTCATCTTTTAT 61085     GC         ACCCCA
            CT                   AG  AGGAGGTGGAA     GGG
                                ||  ||||||||||      |||
                                TC  TTTTCTACTTT     CCC
                                 TA         AAATTA
GAM390   LOC201173 3'  TCTGCTTTCACCTTTGCTT    88695       G       ACCC
                                AGGCAG AGGTGGAA    CAGG
                                ||||||  ||||||||    ||||
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                                TTCGTT TCCACTTT    GTCT
                                   _       C___
GAM390   LOC201220 3'  TCTGCTTTCACCTTTGCTT    88728       G       ACCC
                                AGGCAG AGGTGGAA    CAGG
                                ||||||| ||||||||    ||||
                                TTCGTT TCCACTTT    GTCT
                                   _       C___
GAM390   LOC201242 3'  CCAGCTTTTCACCTTTTCCT   88732     C         CCCCA
                                AGG AGGAGGTGGAAA    GG
                                ||| ||||||||||||    ||
                                TCC TTTTCCACTTTT    CC
                                  _         CGA__
GAM390   LOC201245 5'  CCTGCTCTGCCTCTTCCT    88734     C     TG  AACCC
                                AGG AGGAGG  GA    CAGG
                                ||| ||||||  ||    ||||
                                TCC TTCTCC  CT    GTCC
                                  _     GT  C____
GAM390   LOC201252 3'  CCCTGGGGCCCTGGCCTTCTGC 89551          __  AAA
            CT                    AGGCAGGAGGT  GG   CCCCAGGG
                                ||||||||||  ||   ||||||||
                                TCCGTCTTCCG  CC   GGGGTCCC
                                      GT  C__
GAM390   LOC201475 5'  TCCTGTTGCTGATTTTCTGTCT 89622           _  AAACCC
                                AGGCAGGAGGT GG     CAGGG
                                |||||||||| ||     |||||
                                TCTGTCTTTTA TC     GTCCT
                                      G  GTT___
GAM390   LOC201562 3'  CCCCAGGGTTTTCATTCACTCT 90413         _    AA_______  CCAG
            TCTGTTT                 AGGCAGGAG GTGGA       CC    GG
                                ||||||||| |||||       ||    ||
                                TTTGTCTTC CACTT       GG    CC
                                      T    ACTTTT    GACC
GAM390   LOC201633 3'  TTCTGGAAGATACACTTTTGTC 91828         _  GAAACC
            T                    AGGCAGGAG GTG     CCAGGG
                                ||||||||| |||     ||||||
                                TCTGTTTTC CAT     GGTCTT
                                      A   AGAA__
GAM390   LOC201685 3'  TTCTGGTTTGCATTTTATCATT 91850        A      ACC___
            TGCTT                   AGGCAGG GGTGGAA     CCAGGG
                                ||||||| |||||||     ||||||
                                TTCGTTT CTATTTT     GGTCTT
                                   A      ACGTTT
GAM390   LOC201895 3'  CTTGGGAAGCTTCTTTTCT   90545     C      GGAAAC
                                AGG AGGAGGT     CCCAGG
                                ||| |||||||     ||||||
                                TCT TTCTTCG     GGGTTC
                                  T      AA____
GAM390   LOC201965 3'  CCCCAGGGTCTTCATCTCTTCT 90572      ______       AA___  CCAG
            TTTGCTT                 AGGCA    GGAGGTGGA    CC    GG
                                |||||    |||||||||    ||    ||
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                                TTCGT    TCTCTACTT    GG   CC
                                  TTTCT       CT    GACC
GAM390  LOC201965 5'  CTCTGGGCCGCTGCCTTCGCTT 90573     A    TG AAAC
                                AGGC GGAGG  G   CCCAGGG
                                |||| |||||  |   |||||||
                                TTCG CTTCC  C   GGGTCTC
                                  _    GT GCC_
GAM390  LOC202741 3'  CTCTGCTTCTCATCTCCTACTT 90690     C      _  ACCC
                                AGG AGGAGGTG GAA   CAGGG
                                ||| |||||||| |||   |||||
                                TTC TCCTCTAC CTT   GTCTC
                                  A       T  C___
GAM390  LOC202775 5'  CTCTGATGTCATTTCCTGACCT 91964     _       AAACCC
                                AGG CAGGAGGTGG     CAGGG
                                ||| ||||||||||     |||||
                                TCC GTCCTTTACT     GTCTC
                                  A        GTA___
GAM390  LOC202868 5'  CCAGGGTCTTCCTTCACCTCCT 91994     C       AA________  CCAG
          CCT                    AGG AGGAGGTGGA       CC   G
                                ||| ||||||||||       ||   |
                                TCC TCCTCCACTT       GG   C
                                  _       CCTTCT    GACC
GAM390  LOC202908 3'  CAGGGTTTTGCCCAACTTCTGT 90715       G  AAA_______  CCAG
          CT                     AGGCAGGAG TGG       CC   G
                                ||||||||| |||       ||   |
                                TCTGTCTTC ACC       GG   C
                                     A  CGTTTT    GAC
GAM390  LOC202934 5'  CAGGGTGTTTCCATTTTCTGTT 92030            _____  CAG
          T                     AGGCAGGAGGTGGAAAC   CC   G
                                ||||||||||||||||   ||   |
                                TTTGTCTTTTACCTTTG   GG   C
                                          T    GAC
GAM390  LOC202934 3'  GGTTTTCTTTCTTTTTGTCT   92046        T__   A___
                                AGGCAGGAGG   GGAA   CC
                                ||||||||||   ||||   ||
                                TCTGTTTTTC   CTTT   GG
                                     TTT   T
GAM390  LOC202934 5'  TCCTGATTATTTTTGATTTCTG 92054        GT    CCC_
          TTT                    AGGCAGGAG  GGAAA   CAGGG
                                |||||||||  |||||   |||||
                                TTTGTCTTT  TTTTT   GTCCT
                                     AG    ATTA
GAM390  LOC202934 5'  TTTGGGAGACTTTTTGTT    92059         GGAAAC
                                GGCAGGAGGT     CCCAGG
                                ||||||||||     ||||||
                                TTGTTTTTCA     GGGTTT
                                     GA____
GAM390  LOC203069 5'  CTCTGGCCCCTGCCGCGCTCCT 90759        _   AAACC_
          GCCT                    AGGCAGGAG GTGG     CCAGGG
                                ||||||||| ||||     ||||||
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                                TCCGTCCTC CGCC     GGTCTC
                                    G   GTCCCC
GAM390  LOC203248 3'  CCCTGGGTTCTGCCGTCTTGCC 90843        _ TG   AC
          T                    AGGCAGGA GG  GAA  CCCAGGG
                               |||||||| ||  |||  |||||||
                               TCCGTTCT CC  CTT  GGGTCCC
                                   G  GT   __
GAM390  LOC203275 3'  CCCATTTTCTCACTTCCTGTTT 90852          _   CCCCA
                               AGGCAGGAGGTG GAAA    GGG
                               |||||||||||| ||||    |||
                               TTTGTCCTTCAC CTTT    CCC
                                     T   TA___
GAM390  LOC203276 3'  CCCAGGGTCTTGCACCCATCTC 92118          AAA_________  CCAG
          CTGC                   GCAGGAGGTGG        CC   GG
                               ||||||||||         ||   ||
                               CGTCCTCTACC         GG   CC
                                     CACGTTCT    GACC
GAM390  LOC203305 3'  CCCCAGGGTCTTGCACCCATCT 92171          AAA_________  CCAG
          CCTGC                  GCAGGAGGTGG        CC   GG
                               ||||||||||         ||   ||
                               CGTCCTCTACC         GG   CC
                                     CACGTTCT    GACC
GAM390  LOC203350 3'  TCTTGGGTCTCCTACTTCCTGT 92251          _  A   C   G
          CT                    AGGCAGGAGGT GGA ACCC AGG
                               |||||||||| ||| |||| |||
                               TCTGTCCTTCA CCT TGGG TCT
                                     T   C   T
GAM390  LOC203414 3'  CCCTAAACTCTTTTTGTCTTTT 90911        TG   CCCC__
          GC                    GCAGGAGG  GAAA     AGGG
                               ||||||||  ||||     ||||
                               CGTTTTCT  TTTT     TCCC
                                   GT   CTCAAA
GAM390  LOC203414 3'  CCTTGTGCTATTCAATTTTTGC 90912         G   AACCC
          TT                    AGGCAGGAG TGGA    CAGGG
                               ||||||||| ||||    |||||
                               TTCGTTTTT ACTT    GTTCC
                                   A   ATCGT
GAM390  LOC204084 5'  CAGGGTCTTGTACCACCTCCTG 90993          AAA_________  CCAG
          CT                    GGCAGGAGGTGG        CC   G
                               ||||||||||||        ||   |
                               TCGTCCTCCACC        GG   C
                                     ATGTTCT    GAC
GAM390  LOC204301 3'  CCAGGGCTTTCCTCCATTTTCT 91023          AA_________  CCAG
          GT                    GCAGGAGGTGGA       CC   G
                               ||||||||||||       ||   |
                               TGTCTTTTACCT       GG   C
                                     CCTTTC    GACC
GAM390  LOC205327 3'  TTCTGGGGTTTCTTGAATCTTG 91074        GGT_
          TC                    GGCAGGA   GGAAACCCCAGGG
                               |||||||   |||||||||||||
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                                CTGTTCT    TCTTTGGGGTCTT
                                    AAGT
GAM390   LOC206372 3'  CCAGGGTTCTTTTCACCTCTTG 91092    G         A_______  CCAG
           GTT                    AG CAGGAGGTGGAA      CC    G
                                || ||||||||||||      ||    |
                                TT GTTCTCCACTTT      GG    C
                                  G          TCTT     GACC
GAM390   LOC206372 3'  CCCAGGGTTCTGTTCTCACTTT 91093      AG     GA  ________  CAG
           TGGCTT                   AGGC  GAGGTG  AAC      CC   GG
                                |||||  ||||||  |||      ||   ||
                                TTCG  TTTCAC  TTG      GG   CC
                                  GT     TC   TCTT     GAC
GAM390   LOC206372 3'  CCTTGCCCCTTATTTCTTCCCT 91094     C        AAACCC
                                AGG AGGAGGTGG      CAGGG
                                ||| |||||||||      |||||
                                TCC TTCTTTATT      GTTCC
                                  C        CCCC__
GAM390   LOC219295 5'  CTCTGCGGGTCCAGCTCCTGCT 94584          G    AA  _
           T                     AGGCAGGAG TGGA  CCC CAGGG
                                |||||||||  ||||  |||  |||||
                                TTCGTCCTC ACCT  GGG GTCTC
                                     G    __   C
GAM390   LOC219445 5'  CCCTGGTTCAAACAATTCCTGC 93199          G  GAAACC
           CT                     AGGCAGGAG TG      CCAGGG
                                |||||||||  ||      ||||||
                                TCCGTCCTT AC      GGTCCC
                                     A  AAACTT
GAM390   LOC219445 3'  TCCTGACTTCATTTTGTGTTT  93218       G       AACCC
                                AGGCA GAGGTGGA     CAGGG
                                |||||  ||||||||     |||||
                                TTTGT TTTTACTT     GTCCT
                                   G       CA___
GAM390   LOC219505 5'  CCTTAAGTTCACCTCTTACCT  92895      C        AACCCC
                                AGG AGGAGGTGGA      AGG
                                ||| ||||||||||      |||
                                TCC TTCTCCACTT      TCC
                                  A         GAAT__
GAM390   LOC219731 5'  TCTGGTGGCCTCCTGCTT    94716           TGGAAA  _
                                AGGCAGGAGG      CC CCAGG
                                ||||||||||      || |||||
                                TTCGTCCTCC      GG GGTCT
                                      _______  T
GAM390   LOC219790 3'  CTTTGGATTCATTTTATGTTT  93005       G       AACC
                                AGGCA GAGGTGGA    CCAGGG
                                |||||  ||||||||    ||||||
                                TTTGT TTTTACTT    GGTTTC
                                   A       A___
GAM390   LOC219790 3'  TTTTGGGGTGTTCTTTTTCTT  93007        T   _
                                AGGAGG GGAA ACCCCAGGG
                                ||||||  ||||  |||||||||
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                                TTCTTT TCTT TGGGGTTTT
                                   T   G
GAM390  LOC219899 3'  TTTTGGTTCAGTTCCATTTTTT 93136          ACC__
                                AGGAGGTGGAA    CCAGGG
                                ||||||||||    ||||||
                                TTTTTTACCTT    GGTTTT
                                     GACTT
GAM390  LOC219920 5'  CCCAGGGTTCTGTTTCCTCCTT 94942       _ T    _______ CAG
          TCTGCCT               AGGCAGGA GG GGAAAC     CC  GG
                                |||||||| || ||||||     ||  ||
                                TCCGTCTT CC CCTTTG     GG  CC
                                     T  T    TCTT    GAC
GAM390  LOC219920 5'  TCCTATTTTTCTGTTTCCTCCT 94962    C    TG   CCCC
                                AGG AGGAGG  GAAA   AGGG
                                ||| ||||||  ||||   ||||
                                TCC TCCTTT  CTTT   TCCT
                                  _    GT   TTA_
GAM390  LOC219940 3'  TCTTGCTGTATTTTGTCTTCTT 95004    C    TG  _ CC
          TCT                   AGG AGGAGG  GAA AC  CAGGG
                                ||| ||||||  ||| ||  |||||
                                TCT TCTTCT  TTT TG  GTTCT
                                  T    GT   A  TC
GAM390  LOC220003 3'  CTCTGGGAGGCATTTTCCTGCT 93283         TGGAAAC
          T                     AGGCAGGAGG     CCCAGGG
                                ||||||||||     |||||||
                                TTCGTCCTTT     GGGTCTC
                                     TACGGA_
GAM390  LOC220143 5'  TCCTGGCACCACTTCCTGCC  95235          AAACC
                                GGCAGGAGGTGG   CCAGGG
                                ||||||||||||   ||||||
                                CCGTCCTTCACC   GGTCCT
                                     AC___
GAM390  LOC220431 5'  CCCTGGGAGACATCCTTGTCT  95994       A   GAAAC
                                AGGCAGG GGTG   CCCAGGG
                                ||||||| ||||   |||||||
                                TCTGTTC CTAC   GGGTCCC
                                   _   AGA__
GAM390  LOC220514 3'  CCAGGGTTTTCACTCTATTCTT 61073       ____    A___ CCAG
          GCTT                  AGGCAGGAG   GTGGAA   CC   G
                                |||||||||   ||||||   ||   |
                                TTCGTTCTT   CACTTT   GG   C
                                     ATCT    T    GACC
GAM390  LOC220565 3'  CCAGGGCTTTATTCTGTCTTCC 92439    A    TG  A_______ CCAG
          GTCT                  AGGC GGAGG  GAA      CC   G
                                |||| |||||  |||      ||   |
                                TCTG CTTCT  CTT      GG   C
                                  C    GT   ATTTC    GACC
GAM390  LOC220573 3'  CTTTGTCTTTCTTGCTTTTTGT 70205          _   CCC
          TT                    AGGCAGGAGGTG GAAA  CAGGG
                                |||||||||||| ||||  |||||
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                                TTTGTTTTTCGT CTTT   GTTTC
                                      T   CT_
GAM390   LOC220573 3'  TCTTGCTTTTTGTTTTTGCCT  70207      G   TG   CCC
                                AGGCA GAGG  GAAA   CAGGG
                                ||||| ||||  ||||   |||||
                                TCCGT TTTT  TTTT   GTTCT
                                  _   GT   C__
GAM390   LOC220705 3'  CCAGGGTTCTTTCATTTTCTGT 92867           AC_____ CCAG
           TT                    AGGCAGGAGGTGGAA      C   G
                                ||||||||||||||      |   |
                                TTTGTCTTTTACTTT      G   C
                                       CTT   G GACC
GAM390   LOC220739 5'  CTTTGGGGTTTCCTGTCTG   94520     AGGT
                                CAGG   GGAAACCCCAGGG
                                ||||   ||||||||||||
                                GTCT   CCTTTGGGGTTTC
                                  GT__
GAM390   LOC220753 3'  GGTTTTTTTCTCTTTTGCTT   94536         TG   A_____
                                AGGCAGGAGG  GAA     CC
                                ||||||||||  |||     ||
                                TTCGTTTTCT  TTT     GG
                                     CT   TTT
GAM390   LOC220758 5'  CCTGGAGCGCCTTCTGCC    92464          GAAACC
                                GGCAGGAGGTG     CCAGG
                                ||||||||||      |||||
                                CCGTCTTCCGC     GGTCC
                                      GA____
GAM390   LOC220776 3'  CCCTGCCTCCCACCTTCTATCT 68924    GC       AAACCC
                                AG  AGGAGGTGG     CAGGG
                                ||  |||||||||     |||||
                                TC  TCTTCCACC     GTCCC
                                 TA       CTCC__
GAM390   LOC220776 3'  CTCTGGGGTACTGTGACTTCTT 68927          GGAA__
           GCCT                    AGGCAGGAGGT     ACCCCAGGG
                                ||||||||||      |||||||||
                                TCCGTTCTTCA     TGGGGTCTC
                                      GTGTCA
GAM390   LOC220980 3'  CCTGTTTGTCTTTTGCCT    94767         TG  AACCC   G
                                AGGCAGGAGG  GA    CAGG
                                |||||||||  ||    ||||
                                TCCGTTTTCT  TT    GTCC
                                     GT  _____
GAM390   LOC221042 3'  CTCTGCGAACTTTGCCTTTTCC 94798     C     TG  AACCC
           T                     AGG AGGAGG  GA    CAGGG
                                ||| ||||||  ||    |||||
                                TCC TTTTCC  TT    GTCTC
                                  _     GT  CAAGC
GAM390   LOC221061 3'  TTTTGGGGTTTGCCTTTTTTTG 94843         T  _
           TT                    GGCAGGAGG GG AAACCCCAGGG
                                |||||||| || ||||||||||
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                                TTGTTTTTT CC TTTGGGGTTTT
                                     T  G
GAM390  LOC221178 3'  TCTTGGAATCACCTTCAGTCT  95177      A       AAACC
                                AGGC GGAGGTGG     CCAGGG
                                |||| ||||||||     ||||||
                                TCTG CTTCCACT     GGTTCT
                                  A       AA___
GAM390  LOC221179 3'  GGCTTTGATGCCTTTTGCTT   95195          G_  A____
                                AGGCAGGAGGTG  AA     CC
                                ||||||||||||  ||     ||
                                TTCGTTTTCCGT  TT     GG
                                      AG  TC
GAM390  LOC221271 3'  CCAGGGTTCTGCTTCACTTACT 93504       G      AA_______  CCAG
          GCCT                    AGGCAG AGGTGGA        CC    G
                                ||||||| |||||||        ||    |
                                TCCGTC TTCACTT        GG    C
                                   A      CGTCTT     GACC
GAM390  LOC221272 3'  CTTTGGGGTAATTTTTG     95248       GTGGAA
                                CAGGAG     ACCCCAGGG
                                |||||||     |||||||||
                                GTTTTT     TGGGGTTTC
                                   AA____
GAM390  LOC221288 3'  CCAGGGCTTTCTCCATCTTTGG 95257      AG       AA______  CCAG
          TCT                     AGGC  GAGGTGGA       CC    G
                                ||||  ||||||||       ||    |
                                TCTG  TTCTACCT       GG    C
                                  GT       CTTTC     GACC
GAM390  LOC221300 3'  CCAGGGTTTTTTTTTCCTTTTG 93575          T    A_______  CCAG
          CTT                     AGGCAGGAGG GGAA      CC    G
                                ||||||||||| ||||      ||    |
                                TTCGTTTTCC TTTT      GG    C
                                     T    TTTT     GACC
GAM390  LOC221301 3'  CCCTGCCTCTATTTTCTGGTT  93538    G         AACCC
                                AG CAGGAGGTGGA     CAGGG
                                || ||||||||||     |||||
                                TT GTCTTTTATCT     GTCCC
                                 G         CC___
GAM390  LOC221405 5'  GGCTCTTCCAATTTCTGCTT   95507         G    AC_____
                                AGGCAGGAG TGGAA       C
                                |||||||| |||||       |
                                TTCGTCTTT ACCTT       G
                                     A    CTC   G
GAM390  LOC221466 3'  CCAGGGCTTTGCCTTGCTGTCT 95311       _    TG  AA__  CCAG
                                AGGCAG GAGG  GA    CC    G
                                |||||| ||||  ||    ||    |
                                TCTGTC TTCC  TT    GG    C
                                   G   GT  C     GACC
GAM390  LOC221466 3'  TCCTCACCCCTTTGCCTTGCTG 95318       _    TG  AACCCC
          TCT                     AGGCAG GAGG  GA     AGGG
                                |||||| ||||  ||      ||||
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                                TCTGTC TTCC  TT     TCCT
                                   G   GT  CCCCAC
GAM390  LOC221486 3'  TCCTCACTTCTGTCTCCTGTCT 92660        TG   ACCCC
                                AGGCAGGAGG  GAA    AGGG
                                ||||||||||  |||    ||||
                                TCTGTCCTCT  CTT    TCCT
                                     GT   CAC__
GAM390  LOC221486 3'  TCCTGTTGCTCTGTTTCTTCCT 92661     C     TG  AACCC
                                AGG AGGAGG  GA    CAGGG
                                ||| ||||||  ||    |||||
                                TCC TTCTTT  CT    GTCCT
                                  _     GT  CGTT_
GAM390  LOC221573 3'  TTCTGGTGTTACTTTCTGTTT  93646          GAA  C
                                AGGCAGGAGGTG   AC CCAGGG
                                ||||||||||||   || ||||||
                                TTTGTCTTTCAT   TG GGTCTT
                                     ___  T
GAM390  LOC221692 5'  CTCTGGCTGGAACGGCTCTTGT 93852         G  GAAA  __
           TT                    AGGCAGGAG TG    CC  CCAGGG
                                ||||||||| ||    ||  ||||||
                                TTTGTTCTC GC    GG  GGTCTC
                                     G  AA__  TC
GAM390  LOC221692 3'  TTCTGGTTCTTGCTGTCTGCCT 93864       GA   _  ACC
                                AGGCAG  GGTG GAA   CCAGGG
                                ||||||  |||| |||   ||||||
                                TCCGTC  TCGT CTT   GGTCTT
                                   TG    T  ___
GAM390  LOC221738 3'  TCTGTTCGTCTCTTTCCT    95416     C    GT   AACCC
                                AGG AGGAG  GGA    CAGG
                                ||| |||||  |||    ||||
                                TCC TTCTC  CTT    GTCT
                                  T    TG  _____
GAM390  LOC221747 3'  CTCTCTTTTTGCCTCCTGCC   93963         TG   CCCC
                                GGCAGGAGG  GAAA   AGGG
                                |||||||||  ||||   ||||
                                CCGTCCTCC  TTTT   TCTC
                                     GT   C___
GAM390  LOC221751 5'  CCTTTTTCCCTTTCTGTTT   93676         T    CCCC
                                AGGCAGGAGG GGAAA   AGG
                                |||||||||| |||||   |||
                                TTTGTCTTTC CCTTT   TCC
                                     _    T___
GAM390  LOC221751 5'  TCCTGGGCCAGCTTCCTGCTT  93682         _  AAAC
                                AGGCAGGAGG TGG   CCCAGGG
                                |||||||||| |||   |||||||
                                TTCGTCCTTC ACC   GGGTCCT
                                     G  _____
GAM390  LOC221755 3'  CAGGGTCCTTTTAACTTTTTGC 94007          _____  AA_  CCAG
           CT                    AGGCAGGAGGT    GGA  CC   G
                                ||||||||||    |||  ||   |
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                                TCCGTTTTTCA    CCT  GG   C
                                      ATTTT      GAC
GAM390  LOC221773 3'  TCTTGGATGGGACATTTTTGTC 92698        G  GAAA  __
           T                   AGGCAGGAG TG   CC  CCAGGG
                               ||||||||| ||   ||  ||||||
                               TCTGTTTTT AC   GG  GGTTCT
                                     _  AG__  TA
GAM390  LOC221773 3'  TCTTGGGTACTCGCACCTCTTG 92700    G       _  AAC
           GCT                   AG CAGGAGGTG GA   CCCAGGG
                               || |||||||| ||   |||||||
                               TC GTTCTCCAC CT   GGGTTCT
                                G       G  CAT
GAM390  LOC221773 3'  TTCTGGAAAATGCTTCTTGGCT 92701    G       GAAACC
                               AG CAGGAGGTG     CCAGGG
                               || |||||||||     ||||||
                               TC GTTCTTCGT     GGTCTT
                                G       AAAA__
GAM390  LOC221810 3'  CCCCAGGGTTTTGATTCCACTT 95546    G         A_________  CCAG
           TTTGGTT                 AG CAGGAGGTGGAA       CC   GG
                               || ||||||||||||       ||   ||
                               TT GTTTTTCACCTT       GG   CC
                                G         AGTTTT    GACC
GAM390  LOC221810 3'  TTTTGGTTGAGTTTTTATGTTT 95549         _      C___
           TTGTTT                  AGGCAGGAG GTGGAAAC    CCAGGG
                               ||||||||| ||||||||   ||||||
                               TTTGTTTTT TATTTTTG    GGTTTT
                                     G       AGTT
GAM390  LOC221865 3'  CCTGGGGTTGGTTTTCCT    94087       TGGA
                               AGGAGG    AACCCCAGG
                               ||||||    |||||||||
                               TCCTTT    TTGGGGTCC
                                  TGG_
GAM390  LOC221935 3'  GGCTCTTTCTACCTCCTCTT   94204     C         A_______
                               AGG AGGAGGTGGAA      CC
                               ||| ||||||||||      ||
                               TTC TCCTCCATCTT      GG
                                 _         TCTC
GAM390  LOC221968 3'  CCCAGGGCTTAAGTTCTACTTC 94152     C         AC_________ CCAG
           CTTTCT                  AGG AGGAGGTGGAA        C    G
                               ||| ||||||||||        |   |
                               TCT TCCTTCATCTT        G    C
                                 T         GAATTC   G GACC
GAM390  LOC222031 3'  GGTTTTTTTTTCTTTTGCTT   95684          T    A_____
                               AGGCAGGAGG GGAA     CC
                               |||||||||| ||||     ||
                               TTCGTTTTCT TTTT     GG
                                     T    TTT
GAM390  LOC222031 3'  TCTGCTGCCTCTTTGCTT    95687       _    TG AAACCC
                               AGGCAG GAGG  G     CAGG
                               |||||| ||||  |     ||||
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                                TTCGTT CTCC  C     GTCT
                                   T   GT _______
GAM390  LOC222057 3'  CCAGGGTTTTGCCCAACTTCTG 94350        G   AAA_______  CCAG
                TCT                  AGGCAGGAG TGG       CC   G
                                     ||||||||| |||       ||   |
                                     TCTGTCTTC ACC       GG   C
                                        A  CGTTTT    GACC
GAM390  LOC222057 3'  CTTTGGACTCAGCTCCTGCCT  94352        G   AAACC
                                     AGGCAGGAG TGG    CCAGGG
                                     ||||||||| |||    ||||||
                                     TCCGTCCTC ACT    GGTTTC
                                        G  CA___
GAM390  LOC222066 3'  CCAGGGCTTTGTCGTACTTTCT 94317          _  AA_______  CCAG
                GTTT                 AGGCAGGAGGTG GA      CC   G
                                     |||||||||||| ||      ||   |
                                     TTTGTCTTTCAT CT      GG   C
                                        G  GTTTC    GACC
GAM390  LOC222066 5'  CCTGGGAGGCCTCTGCTT    94319      G   GGAAAC
                                     AGGCAG AGGT     CCCAGG
                                     |||||| ||||     ||||||
                                     TTCGTC TCCG     GGGTCC
                                        _   GA____
GAM390  LOC222068 3'  CCAGGGCTCTCCATTACCTTCT 94272          ___  AA____  CCAG
                GCTT                 AGGCAGGAGGT  GGA     CC   G
                                     ||||||||||  |||     ||   |
                                     TTCGTCTTCCA  CCT     GG   C
                                        TTA  CTC    GACC
GAM390  LOC222068 3'  GGTCCTGCTTCTTTTGCCT   94277      __    _  AA_
                                     AGGCA  GGAGGT GGA  CC
                                     |||||  |||||| |||  ||
                                     TCCGT  TCTTCG CCT  GG
                                        TT     T
GAM390  LOC222166 3'  GGGTTTTTGTTTTTTGGTT   95743    G     TG
                                     AG CAGGAGG  GAAACCC
                                     || |||||||  |||||||
                                     TT GTTTTTT  TTTTGGG
                                      G      GT
GAM390  LOC222234 3'  CAGGGTCATTTCTGTCTTCTGC 95900        GT   A_______  CCAG
                T                     GGCAGGAG  GGAA     CC   G
                                      ||||||||  ||||     ||   |
                                      TCGTCTTC  TCTT     GG   C
                                         TG   TACT    GAC
GAM390  LOC223029 5'  CAGGGTTCTGTCTTCTCTTCTG 96038        _ T  AA_______  CCAG
                TCT                  AGGCAGGAG G GGA      CC   G
                                     ||||||||| | |||      ||   |
                                     TCTGTCTTC C TCT      GG   C
                                        T T  GTCTT    GAC
GAM390  LOC253150 3'  TCCTGGCCTCCCCTCCTGTCT  97258         T   AACC
                                     AGGCAGGAGG GGA   CCAGGG
                                     |||||||||| |||   ||||||
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                                TCTGTCCTCC CCT    GGTCCT
                                      _   CC__
GAM390   LOC253264 3'  CTCTGATAGTGTTCATTTCTT  96337          A  CC_
                                AGGAGGTGGA AC   CAGGG
                                |||||||||| ||   |||||
                                TTCTTTACTT TG   GTCTC
                                     G  ATA
GAM390   LOC253681 5'  CTCTGCTCTTTTCATCTCTTCT 96838     C          CCC
           CT                     AGG AGGAGGTGGAAA   CAGGG
                                ||| ||||||||||||   |||||
                                TCT TTCTCTACTTTT   GTCTC
                                  C          CTC
GAM390   LOC253805 3'  TCCTGGGTTCAAACCATTCTCC 98187          _   AAAC__
           TGCCT                    AGGCAGGAGG TGG     CCCAGGG
                                |||||||||| |||     |||||||
                                TCCGTCCTCT ACC     GGGTCCT
                                     T   AAACTT
GAM390   LOC253827 3'  GGTTTTTTCTTCTTTTGCTT   96574          T    A_______
                                AGGCAGGAGG GGAA      CC
                                |||||||||| ||||      ||
                                TTCGTTTTCT TCTT      GG
                                     _    TTTT
GAM390   LOC253832 3'  CAGGGTTTTGCTTACCTTTTGT 96590           AAA_______  CCAG
           T                     GGCAGGAGGTGG       CC    G
                                ||||||||||||       ||    |
                                TTGTTTTCCATT       GG    C
                                     CGTTTT     GAC
GAM390   LOC253840 5'  CTCTGGATCCAGCTGGTTTTTG 97911        _____  G    AACC
           TTT                    AGGCAGG    AG TGGA    CCAGGG
                                |||||||    || ||||    ||||||
                                TTTGTTT    TC ACCT    GGTCTC
                                    TTGG  G    A___
GAM390   LOC253868 3'  CCCAGGGTCCTCCTTCGCCTTC 97321           AA________  CCAG
           TGCC                   GGCAGGAGGTGGA       CC    GG
                                ||||||||||||       ||    ||
                                CCGTCTTCCGCTT       GG    CC
                                     CCTCCT     GACC
GAM390   LOC253891 3'  CCCTGGGGGGGTGGTCTCCATGC 96065      _    TGGAAA
           CT                     AGGCA GGAGG     CCCCAGGG
                                ||||| |||||     ||||||||
                                TCCGT CCTCT     GGGGTCCC
                                   A    GGTGG_
GAM390   LOC253955 5'  CCTCGTCTGCTTCTTGTTT   96071          TG  AACCCC
                                AGGCAGGAGG  GA     AGG
                                ||||||||||  ||     |||
                                TTTGTTCTTC  CT     TCC
                                     GT  GC_____
GAM390   LOC253970 3'  CTTTGGTAGAAATAGCTTTTGC 98315          G  GAAACC
           TT                     AGGCAGGAG TG     CCAGGG
                                |||||||||| ||     ||||||
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                                TTCGTTTTC AT     GGTTTC
                                    G  AAAGAT
GAM390  LOC253981 3'  CCAGGGCTTTGTGTATTTCCTG 97532          GAAA_______  CCAG
                TTT                  AGGCAGGAGGTG        CC    G
                                     ||||||||||||        ||    |
                                     TTTGTCCTTTAT        GG    C
                                         GTGTTTC    GACC
GAM390  LOC254016 5'  CCCTGGCACTCTGCTTTCTTCT 98699     C     TG  AACC
                                     AGG AGGAGG  GA    CCAGGG
                                     ||| ||||||  ||    ||||||
                                     TCT TCTTTC  CT    GGTCCC
                                       _     GT  CAC_
GAM390  LOC254085 5'  CCAGGGTTTTTTCAGCTTCTGC 97820         G     _______  CCA
                TT                   AGGCAGGAG TGGAAA     CC   G
                                     |||||||||| ||||||     ||   |
                                     TTCGTCTTC ACTTTT     GG   C
                                         G     TT   G  ACC
GAM390  LOC254085 5'  CCTGGTTTGTGTTTTGCCT    97821        G TG  AACC
                                     AGGCAGGA G  GA    CCAGG
                                     |||||||| |  ||    |||||
                                     TCCGTTTT T  TT    GGTCC
                                         G GT  ____
GAM390  LOC254085 3'  TTTTGTTTTTCATTTTTTGTTT 97822              CCC
                                     AGGCAGGAGGTGGAAA   CAGGG
                                     ||||||||||||||||   |||||
                                     TTTGTTTTTTACTTTT   GTTTT
                                                T__
GAM390  LOC254115 5'  TCTGGACACCTCCTATCT    96373    GC      GAAACC
                                     AG  AGGAGGTG     CCAGG
                                     ||  ||||||||     |||||
                                     TC  TCCTCCAC     GGTCT
                                      TA       A_____
GAM390  LOC254268 3'  CAGGGCTTTCTATACTTTTTGC 97140          __   A____  CCAG
                CT                   AGGCAGGAGGTG  GAA    CC    G
                                     ||||||||||||  |||    ||    |
                                     TCCGTTTTTCAT  CTT    GG    C
                                           AT   TC    GAC
GAM390  LOC254358 3'  CCAGGGCTTTCCTCCATTTTCT 96654          AA________  CCAG
                GT                   GCAGGAGGTGGA        CC    G
                                     ||||||||||||        ||    |
                                     TGTCTTTTACCT        GG    C
                                           CCTTTC    GACC
GAM390  LOC254387 3'  CCAGGGTTTTCTTTCACGTTTC 96580         _     AC________ CCAG
                TGCTT                  AGGCAGGAG GTGGAA       C    G
                                       |||||||||| ||||||       |    |
                                       TTCGTCTTT CACTTT       G    C
                                           G     CTTTT   G GACC
GAM390  LOC254423 3'  TCTGCTCCCATCTTTGCCT    99302       G     AAACCC
                                     AGGCAG AGGTGG     CAGG
                                     |||||| ||||||     ||||
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                                TCCGTT TCTACC     GTCT
                                  _     CTC___
GAM390  LOC254428 3'  CCCTGGGCCCAGATTCTTTGTC 97194       _  G_  AAAC
          T                    AGGCAG GAG  TGG   CCCAGGG
                               |||||| |||  |||   |||||||
                               TCTGTT CTT  ACC   GGGTCCC
                                  T  AG  C___
GAM390  LOC254428 3'  CTCTGGACTTTTTTCATCTTTT 97195    C        CC__
          CCT                    AGG AGGAGGTGGAAA   CCAGGG
                               ||| ||||||||||||   ||||||
                               TCC TTTTCTACTTTT   GGTCTC
                                  _         TTCA
GAM390  LOC254440 3'  CCAGGGTCTTCTCTTCTTCTTG 98848        T  AA_______  CCAG
          CCT                    AGGCAGGAGG GGA      CC   G
                               |||||||||| |||      ||   |
                               TCCGTTCTTC TCT      GG   C
                                     T  CTTCT    GACC
GAM390  LOC254485 5'  CAGGGTCTTCCTTCACTTCTTG 96712          AA________  CCAG
          TT                     GGCAGGAGGTGGA      CC   G
                               ||||||||||||       ||   |
                               TTGTTCTTCACTT      GG   C
                                     CCTTCT    GAC
GAM390  LOC254532 5'  CCAGGGTTCTCCTTCTCCTTCC 98448        TG  AC_________ CCAG
          TGCTT                   AGGCAGGAGG  GAA       C   G
                               |||||||||  |||       |   |
                               TTCGTCCTTC  CTT       G   C
                                     CT   CCTCTT   G GACC
GAM390  LOC254552 3'  CCTCTCTGCCTCCTGCCT    96424        TG  AACCCC
                               AGGCAGGAGG  GA     AGG
                               ||||||||||  ||     |||
                               TCCGTCCTCC  CT     TCC
                                     GT  C_____
GAM390  LOC254556 5'  CCTTGGTATAGATCACTTCCT  96257        AAACC_
                               AGGAGGTGG     CCAGGG
                               |||||||||     ||||||
                               TCCTTCACT     GGTTCC
                                     AGATAT
GAM390  LOC254655 3'  CTTTGAAGGTTTTTTTGTTTTT 97218        GT_     C_
          GTTT                    AGGCAGGAG   GGAAACC  CAGGG
                               |||||||||   |||||||  |||||
                               TTTGTTTTT   TTTTTGG  GTTTC
                                     GTT      AA
GAM390  LOC254655 3'  GGTCCTTTCTCTTTTGCCT   97223      __    T_  AA_
                               AGGCA  GGAGG  GGA   CC
                               |||||  |||||  |||   ||
                               TCCGT  TCTCT  CCT   GG
                                  TT    TT
GAM390  LOC254734 3'  CCCAGGGCTCATTTTTGTTTTC 96624        GG GG  A________  CCAG
          TGTCT                   AGGCAGGA  T  AA      CC   GG
                               ||||||||  |  ||      ||   ||
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                                TCTGTCTT  G  TT      GG   CC
                                   TT TT  TACTC    GACC
GAM390  LOC254778 3'  CTCTGTGCCTATGTCTTGCTT  97830       G   AAACCC
                                AGGCAGGA GTGG     CAGGG
                                |||||||| ||||     |||||
                                TTCGTTCT TATC     GTCTC
                                   G   CGT___
GAM390  LOC254822 5'  CTTTGTTCTGCTTTTTGCC   99007       TG  ACCC
                                GGCAGGAGG  GAA   CAGGG
                                |||||||||  |||   |||||
                                CCGTTTTTC  CTT   GTTTC
                                     GT  ____
GAM390  LOC254822 5'  TTCTGCTTTTGCCCTTTGCCT  99009      GA  TG  ACCC
                                AGGCAG  GG  GAA   CAGGG
                                ||||||  ||  |||   |||||
                                TCCGTT  CC  TTT   GTCTT
                                   TC  GT  C___
GAM390  LOC254826 5'  ATCAGGGGTTTCTGCCTTTGCT 99048      G  TG      AGGG
           T                     AGGCAG AGG  GAAACCCC
                                |||||| |||  ||||||||
                                TTCGTT TCC  CTTTGGGG
                                   _  GT       ACTAT
GAM390  LOC255105 3'  TCTTGGGGACCCTTTTCTCTT  97795    C     T  AAA
                                AGG AGGAGG GG   CCCCAGGG
                                ||| |||||| ||   ||||||||
                                TTC TCTTTT CC   GGGGTTCT
                                  _     C  A__
GAM390  LOC255147 3'  CCTTCCCCCTCTATCTCCTTCT 97407    C       AACCCC  G
           T                     AGG AGGAGGTGGA     AGG
                                ||| ||||||||||     |||
                                TTC TCCTCTATCT     TCC
                                  T        CCCCCT
GAM390  LOC255158 3'  CTCTCAGTTTTGCCTCTTATCT 97880    GC     TG  ACCCC
                                AG  AGGAGG  GAA    AGGG
                                ||  ||||||  |||    ||||
                                TC  TTCTCC  TTT    TCTC
                                 TA     GT  GAC__
GAM390  LOC255177 3'  TTTTGGTGTTTTGTTTTTTTGT 98406         TG    C
           TT                     AGGCAGGAGG  GAAAC CCAGGG
                                |||||||||  ||||| ||||||
                                TTTGTTTTTT  TTTTG GGTTTT
                                     TG    T
GAM390  LOC255328 3'  CAGGGTTTTCCTCCTTTCTTGT 98335       __  T   A____  CCAG
           TT                     AGGCAGG  AGG GGAA    CC   G
                                |||||||  ||| ||||    ||   |
                                TTTGTTC  TCC CCTT    GG   C
                                   TT  T   TT    GAC
GAM390  LOC255360 5'  CAGGGCTTTCTCTTTCTTCTGC 98763         T  AA_______  CCAG
           CT                     AGGCAGGAGG GGA       CC   G
                                |||||||||| |||       ||   |
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                                TCCGTCTTCT TCT      GG   C
                                     T  CTTTC    GAC
GAM390  LOC255465 5'  CAGGGTGTTTCCATTTTCTGTT 99105            ____  CAG
                T                AGGCAGGAGGTGGAAAC   CC  G
                                 ||||||||||||||||   ||  |
                                 TTTGTCTTTTACCTTTG   GG  C
                                       T    GAC
GAM390  LOC255465 3'  GGTTTTCTTTCTTTTTGTCT  99121        T__   A___
                                 AGGCAGGAGG  GGAA   CC
                                 |||||||||  ||||   ||
                                 TCTGTTTTTC  CTTT   GG
                                      TTT   T
GAM390  LOC255465 5'  TCCTGATTATTTTTGATTTCTG 99128       GT    CCC_
                TTT                AGGCAGGAG  GGAAA   CAGGG
                                   |||||||||  |||||   |||||
                                   TTTGTCTTT  TTTTT   GTCCT
                                        AG    ATTA
GAM390  LOC255465 5'  TTTTGGGTCAGTTCACGTTTTC 99135       GG  _  AC__
                TGTTT                AGGCAGGA  TG GAA   CCCAGGG
                                     |||||||  || |||   |||||||
                                     TTTGTCTT  GC CTT   GGGTTTT
                                        TT  A   GACT
GAM390  LOC255536 3'  CCCCAGGGTTTTGTATTCATCT 96109          AA_________  CCAG
                TTTGT                GCAGGAGGTGGA       CC   GG
                                     ||||||||||||       ||   ||
                                     TGTTTTCTACTT       GG   CC
                                        ATGTTTT    GACC
GAM390  LOC255783 3'  TCCTGAGCTCTGTCTCCTGCC  96974       TG  AACCC
                                 GGCAGGAGG  GA    CAGGG
                                 |||||||||  ||    |||||
                                 CCGTCCTCT  CT    GTCCT
                                      GT  CGA__
GAM390  LOC255862 3'  CCTTAAAAATTCCCTTCTGTTT 96114         T   AACCCC
                                 AGGCAGGAGG GGA     AGG
                                 ||||||||||| |||     |||
                                 TTTGTCTTCC CTT     TCC
                                      _   AAAAAT
GAM390  LOC255975 5'  CCAGGGTTTTGCCTAACTTCTG 97575        GT_  A A_____  CCAG
                TCT                  AGGCAGGAG   GG A     CC   G
                                     |||||||||   || |     ||   |
                                     TCTGTCTTC   CC T     GG   C
                                          AAT  G TTT    GACC
GAM390  LOC255975 5'  CTCTGCAGGCCCAGCTCCTGCC 97579        G   AAA  C_
                T                  AGGCAGGAG TGG   CC  CAGGG
                                   |||||||||  |||   ||  |||||
                                   TCCGTCCTC ACC   GG  GTCTC
                                        G   C__  AC
GAM390  LOC255975 5'  TCCTCAAATCAGCCTTTTGCCT 97591          G  AACCCC
                                 AGGCAGGAGGT GA     AGGG
                                 ||||||||||| ||     ||||
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                                TCCGTTTTCCG CT     TCCT
                                      A  AAAC__
GAM390  LOC256019 3'  CTTTGCAGGCCCGGCCTCCTGC 97595         _  AAA  C_
          CT                    AGGCAGGAGG TGG   CC  CAGGG
                                |||||||||| |||   ||  |||||
                                TCCGTCCTCC GCC   GG  GTTTC
                                      G   C__  AC
GAM390  LOC256107 5'  CCCACTTTTCTCCCTCCTGTCT 98597          TG   CCCCA
                                AGGCAGGAGG  GAAA    GGG
                                ||||||||||  ||||    |||
                                TCTGTCCTCC  CTTT    CCC
                                      CT    TCA__
GAM390  LOC256337 3'  CTCTGAGGATTTGTTTTCTTCT 96343     C     TG  AA  C
                                AGG AGGAGG  GA  CC CAGGG
                                ||| ||||||  ||  || |||||
                                TCT TCTTTT  TT  GG GTCTC
                                  _     GT  A_  A
GAM390  LOC256364 5'  CCCCAGGGTTCTATCTTCGCCT 96444      G       AA_________  CCAG
          TGTGTCT                 AGGCA GAGGTGGA        CC    GG
                                |||||| ||||||||         ||    ||
                                TCTGT TTCCGCTT         GG    CC
                                   G       CTATCTT     GACC
GAM390  LOC256370 5'  CCCTGTTGAAGTTCATCTCTGC 99527       G      AACCC_
          CT                    AGGCAG AGGTGGA     CAGGG
                                |||||| |||||||     |||||
                                TCCGTC TCTACTT     GTCCC
                                   _      GAAGTT
GAM390  LOC256642 3'  CTTTATGTTTTCTGTGTTCTGC 98043        G TG _   CCC   G
          TT                    AGGCAGGA G  G AAAC   AGG
                                |||||||| |  | ||||   |||
                                TTCGTCTT T  C TTTG   TTC
                                    G GT T    TAT
GAM390  LOC256878 3'  CCAGGGTTTTGCCCAACTTCTG 98686         G   AAA_______  CCAG
          TCT                   AGGCAGGAG TGG        CC    G
                                ||||||||| |||        ||    |
                                TCTGTCTTC ACC        GG    C
                                      A   CGTTTT     GACC
GAM390  LOC256905 3'  GGTCATTCTGCCTCTTGTTT   98661          TG   A_____
                                AGGCAGGAGG  GAA     CC
                                ||||||||||  |||     ||
                                TTTGTTCTCC  CTT     GG
                                      GT   ACT
GAM390  LOC256946 3'  TTTTGGTGCCAGTGTTTTCTGC 96185          ___   AAACC
          TT                    AGGCAGGAGG   TGG    CCAGGG
                                ||||||||||   |||    ||||||
                                TTCGTCTTTT   ACC    GGTTTT
                                      GTG   GT___
GAM390  LOC257000 5'  TTTTGGAAGGCACTTCTCCTGC 98591          T  AAA  __
          CT                    AGGCAGGAGG GG   CC  CCAGGG
                                |||||||||| ||   ||  ||||||
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                                TCCGTCCTCT TC   GG  GGTTTT
                                      _  AC_  AA
GAM390   LOC257017 5'  TGGGAGTTTTTAGTTTTTTGTT 99222          _      _   GGG
           T                    AGGCAGGAGG TGGAAAC CCCA
                                |||||||||| ||||||| ||||
                                TTTGTTTTTT ATTTTTG GGGT
                                     G      A
GAM390   LOC257069 3'  CTTTGCAGGCCCGGCCTCCTGC 97303          _  AAA  C_
           CT                    AGGCAGGAGG TGG   CC  CAGGG
                                |||||||||| |||   ||  |||||
                                TCCGTCCTCC GCC   GG  GTTTC
                                     G   C__  AC
GAM390   LOC257109 3'  TCTTGAATTAATTTTCATTATC 97309         _      CCC___
           TTGCCT                  AGGCAGGA GGTGGAAA     CAGGG
                                |||||||| ||||||||     |||||
                                TCCGTTCT TTACTTTT     GTTCT
                                     A       AATTAA
GAM390   LOC257249 3'  CCTTATGTTTCTTTCTTGTTT  97612         GT     CCC
                                AGGCAGGAG  GGAAAC   AGG
                                |||||||||  ||||||   |||
                                TTTGTTCTT  TCTTTG   TCC
                                     __      TAT
GAM390   LOC257282 5'  TCCTGAGTCTACTTTCTGC    98137           AACCC
                                GCAGGAGGTGGA    CAGGG
                                ||||||||||||    |||||
                                CGTCTTTCATCT    GTCCT
                                      GA___
GAM390   LOC257302 5'  TTCTGGGGGCATGTCTCTTGCT 98000         GT GAAA
                                GGCAGGAG  G   CCCCAGGG
                                ||||||||  |   ||||||||
                                TCGTTCTC  T   GGGGTCTT
                                     TG ACG_
GAM390   LOC257319 3'  TTCTGAGTCCACTTCTT     97476          AACCC
                                AGGAGGTGGA    CAGGG
                                ||||||||||    |||||
                                TTCTTCACCT    GTCTT
                                      GA___
GAM390   LOC257319 3'  TTTTGGTAAAGATTGCCTTCTG 97477         TG AAACC_
           T                    GCAGGAGG  G     CCAGGG
                                ||||||||  |     ||||||
                                TGTCTTCC  T     GGTTTT
                                     GT AGAAAT
GAM390   LOC257358 3'  CTCTGTCTCTCCTGCCTTCTGC 98898          _  AACCC
           TT                    AGGCAGGAGGT GGA    CAGGG
                                |||||||||||| |||    |||||
                                TTCGTCTTCCG CCT    GTCTC
                                      T  CTCT_
GAM390   LOC257463 3'  CCTGATTTTTGTGTCTTGTTT  71621         G TG   CCC
                                AGGCAGGA G  GAAA   CAGG
                                |||||||| |  ||||   ||||
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                                TTTGTTCT T  TTTT   GTCC
                                    G GT    A__
GAM390  LOC257464 3'  TTTTGGCCTCCCCACTTCTTTC 91249     C        AAACC
              CT                  AGG AGGAGGTGG     CCAGGG
                                  ||| |||||||||     ||||||
                                  TCC TTCTTCACC     GGTTTT
                                    T       CCTCC
GAM390  LOC257471 3'  CCAGGGTCATTTTCCTTTTTTG 97389          T    A_______  CCAG
              CTT                   AGGCAGGAGG GGAA      CC    G
                                  |||||||||| ||||      ||   |
                                  TTCGTTTTTT CTTT      GG    C
                                       C    TACT     GACC
GAM390  LOC257471 3'  CCTTTTTTGCTTCTTCCCT   97390     C     TG    CCCC
                                  AGG AGGAGG  GAAA    AGG
                                  ||| ||||||  ||||    |||
                                  TCC TTCTTC  TTTT    TCC
                                    C     GT    ____
GAM390  LOC257471 5'  TCTGGAACACCTTCTGCT    97393          GAAACC
                                  GGCAGGAGGTG     CCAGG
                                  ||||||||||      |||||
                                  TCGTCTTCCAC     GGTCT
                                       AA____
GAM390  LOC257476 3'  CTTGGGGGCTTTCCAGTCT   61923      A     TGGAAA
                                  AGGC GGAGG      CCCCAGG
                                  |||| |||||      |||||||
                                  TCTG CCTTT      GGGGTTC
                                    A     CG____
GAM390  LOC257494 3'  CCCCAGGGTCTTATTTCTGCCT 99630      A        A_________  CCAG
              CTAGTTT                 AGGC GGAGGTGGAA       CC    GG
                                  |||| ||||||||||        ||    ||
                                  TTTG TCTCCGTCTT        GG    CC
                                    A        TATTCT     GACC
GAM390  LOC257522 3'  TTCTGGTGTTACTTTCTGTTT  99558          GAA  C
                                  AGGCAGGAGGTG   AC CCAGGG
                                  ||||||||||||   || ||||||
                                  TTTGTCTTTCAT   TG GGTCTT
                                       ___  T
GAM390  LOC257573 3'  TTCTGGTGTTACTTTCTGTTT  99679          GAA  C
                                  AGGCAGGAGGTG   AC CCAGGG
                                  ||||||||||||   || ||||||
                                  TTTGTCTTTCAT   TG GGTCTT
                                       ___  T
GAM390  LOC51008  3'  GGCCATTCTGCTTTCTGTCT   32534         TG   A_____
                                  AGGCAGGAGG  GAA     CC
                                  ||||||||||  |||     ||
                                  TCTGTCTTTC  CTT     GG
                                       GT   ACC
GAM390  LOC51064  3'  CCTGGGAGCTGTCTGTCT    32485       GA   GGAAAC
                                  AGGCAG  GGT     CCCAGG
                                  ||||||  |||     ||||||
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                                TCTGTC  TCG     GGGTCC
                                   TG   A_____
GAM390  LOC51072  5' TCCTGGGCCGCCGCCTCCTCCT 32549     C        AAAC
                                AGG AGGAGGTGG    CCCAGGG
                                ||| |||||||||    |||||||
                                TCC TCCTCCGCC    GGGTCCT
                                  _       GCC_
GAM390  LOC51087  3' CCAGCTTTTCACCTTTTCCT   32566     C         CCCCA
                                AGG AGGAGGTGGAAA    GG
                                ||| ||||||||||||    ||
                                TCC TTTTCCACTTTT    CC
                                  _         CGA__
GAM390  LOC51097  3' CCAGGGCTCTAATTTACTTTTT 32597          AA________  CCAG
             GT                   GCAGGAGGTGGA       CC    G
                                ||||||||||||       ||   |
                                TGTTTTTCATTT       GG   C
                                       AATCTC    GACC
GAM390  LOC51184  3' CTTATTTTCACTTTTTGT    33299           CCCC
                                GCAGGAGGTGGAAA   AGG
                                ||||||||||||||   |||
                                TGTTTTTCACTTTT   TTC
                                       A___
GAM390  LOC51186  3' GGTTTTTCTCCTTTTGCTT   33301         T   A_____
                                AGGCAGGAGG GGAA     CC
                                |||||||||| ||||     ||
                                TTCGTTTTCC TCTT     GG
                                     _   TTT
GAM390  LOC51193  3' CTTGATGTTTCATTTTCTGTT  33366         G   CC
                                GGCAGGAGGTG AAAC  CAGG
                                |||||||||| ||||  ||||
                                TTGTCTTTTAC TTTG  GTTC
                                     _   TA
GAM390  LOC51193  3' TCTTGGTGACTGTCATCCTGTT 33374        _  TG AAACC
             T                    AGGCAGGA GG  G    CCAGGG
                                ||||||||  ||  |    ||||||
                                TTTGTCCT CT  C    GGTTCT
                                    A  GT AGT__
GAM390  LOC51200  3' CCCAGGGTTTGTTTTTGTTTTT 33435         TG    _______  CAG
             TGCTT                  AGGCAGGAGG  GAAAC     CC   GG
                                ||||||||||  |||||     ||   ||
                                TTCGTTTTTT  TTTTG     GG   CC
                                     GT    TTT    GAC
GAM390  LOC51200  3' CCTCCCTCCTCTCCTGTTT   33436         T   AACCCC
                                AGGCAGGAGG GGA     AGG
                                |||||||||| |||     |||
                                TTTGTCCTCT CCT     TCC
                                     _  CCC___
GAM390  LOC51200  3' CTTTGGGGGGTTGTTTGTTTTT 33437        G TG  AA___
             GTTT                   AGGCAGGA G  GA    CCCCAGGG
                                ||||||||  |  ||    ||||||||
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                                TTTGTTTT T  TT    GGGGTTTC
                                   _ GT  GTTGG
GAM390  LOC51270  3' TTTTGTGTTTTCATTTTCT   60665          CC
                                AGGAGGTGGAAAC  CAGGG
                                |||||||||||||  |||||
                                TCTTTTACTTTTG  GTTTT
                                      T_
GAM390  LOC56181  5' TCCTGGGTTCACGCCATTCTCC 97286        _   AAAC__
           TGCCT                  AGGCAGGAGG TGG     CCCAGGG
                                |||||||||| |||     |||||||
                                TCCGTCCTCT ACC     GGGTCCT
                                     T   GCACTT
GAM390  LOC56832  3' CCTTGGAAGCCATTTCCTGCT  65446          AAACC
                                GGCAGGAGGTGG    CCAGGG
                                ||||||||||||    ||||||
                                TCGTCCTTTACC    GGTTCC
                                      GAA__
GAM390  LOC56851  3' CCCAGCTTTCATCTTTTGTCT  39751           ACCCCA
                                AGGCAGGAGGTGGAA     GGG
                                ||||||||||||||     |||
                                TCTGTTTTCTACTTT     CCC
                                      CGA___
GAM390  LOC56961  5' CCTCGTTCACCTTTTCCT    63577     C       AACCCC
                                AGG AGGAGGTGGA     AGG
                                ||| ||||||||||     |||
                                TCC TTTTCCACTT     TCC
                                  _        GC____
GAM390  LOC56961  5' GGTCCTCTCCACCTCCTCCT   63579     C       AA_______
                                AGG AGGAGGTGGA       CC
                                ||| ||||||||||       ||
                                TCC TCCTCCACCT       GG
                                  _        CTCCT
GAM390  LOC57100  3' CCCAGGGTCTTGCTCTATCATT 40160        _     AA________  CCAG
           CTGTTT                 AGGCAGGA GGTGGA       CC    GG
                                |||||||| ||||||       ||    ||
                                TTTGTCTT CTATCT       GG    CC
                                     A     CGTTCT     GACC
GAM390  LOC57107  3' CCTTGCACAAGTCACTTCCTTC 40186     C       AAACCC
           T                    AGG AGGAGGTGG     CAGGG
                                ||| |||||||||     |||||
                                TCT TCCTTCACT     GTTCC
                                  _        GAACAC
GAM390  LOC57333  3' CCCTGGCCCCAGCCCTCTCCTG 74091          T  AAACC_
           CCT                    AGGCAGGAGG GG     CCAGGG
                                |||||||||| ||     ||||||
                                TCCGTCCTCT CC     GGTCCC
                                     C  GACCCC
GAM390  LOC64182  3' CCAGGGCTCTTTTTGTCGCTTG 42554        A GT    A_______  CCAG
           TCT                    AGGCAGG G  GGAA      CC    G
                                |||||||  |  ||||      ||    |
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                                TCTGTTC C  TTTT      GG    C
                                   G TG    TCTC     GACC
GAM390  LOC64744  3' CTCTGGGTATTTTTGTTTTTGT 62442         GT    AC
           TT                   AGGCAGGAG  GGAA  CCCAGGG
                                |||||||||  ||||  |||||||
                                TTTGTTTTT  TTTT  GGGTCTC
                                    GT    AT
GAM390  LOC81034  3' CCAGGGTTTTTCTGCTTTTTGC 48587             A_____  CCAG
           CT                   AGGCAGGAGGTGGAA     CC    G
                                ||||||||||||||     ||    |
                                TCCGTTTTTCGTCTT     GG    C
                                       TTT     GACC
GAM390  LOC81034  3' CCCAGGGTCCTAGATCCAGTTC 48588          G    AA_________  CCAG
           TTGTTT                  AGGCAGGAG TGGA         CC    GG
                                |||||||||  ||||         ||    ||
                                TTTGTTCTT ACCT         GG    CC
                                    G    AGATCCT     GACC
GAM390  LOC81034  3' TCCTGCAATGTTTTTCTGCTTT 48597          TG    CCC____
           TTGCCT                  AGGCAGGAGG  GAAA      CAGGG
                                |||||||||  ||||      |||||
                                TCCGTTTTTC  CTTT      GTCCT
                                    GT    TTGTAAC
GAM390  LOC81569  5' TTCTGGTCCCACCCACCTCTGC 62677       G     AAACC_
           CT                   AGGCAG AGGTGG     CCAGGG
                                ||||||  ||||||     ||||||
                                TCCGTC TCCACC     GGTCTT
                                   _     CACCCT
GAM390  LOC84528  3' TCTGTGCCACTTTTTGCC    51664           AAACCC
                                GGCAGGAGGTGG     CAGG
                                ||||||||||||     ||||
                                CCGTTTTTCACC     GTCT
                                      GT____
GAM390  LOC89919  3' CCTTGGGCAGGTTCCATTTCTG 61372       G       AC__
           CTT                    AGGCAG AGGTGGAA    CCCAGGG
                                ||||||  ||||||||    |||||||
                                TTCGTC TTTACCTT    GGGTTCC
                                   _       GGAC
GAM390  LOC89919  5' TCCTGGGGAAGGCTCTCTTCCT 61383          T_  AAA_
           GCTT                    AGGCAGGAGG  GG    CCCCAGGG
                                |||||||||  ||    ||||||||
                                TTCGTCCTTC  TC    GGGGTCCT
                                     TC  GGAA
GAM390  LOC90019  3' CCCTGCAGCCCCGCCTTCGCCT 57524      A       AAACCC
                                AGGC GGAGGTGG      CAGGG
                                ||||  ||||||||      |||||
                                TCCG CTTCCGCC      GTCCC
                                   _       CCGAC_
GAM390  LOC90092  3' TCCTGGAGACCAGCCTTTTGCT 62076          _  AAACC
           T                    AGGCAGGAGG TGG     CCAGGG
                                ||||||||||  |||     ||||||
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                                TTCGTTTTCC ACC    GGTCCT
                                     G  AGA__
GAM390  LOC90110  5' GGTTTTCTCCATTCCTGTTT  62179       G   AA_____
                                AGGCAGGAG TGGA      CC
                                ||||||||| ||||      ||
                                TTTGTCCTT ACCT      GG
                                     _   CTTTT
GAM390  LOC90268  3' CTCTGGTAATCTTACCTTCTCC 62663    C       AAACC
          T                      AGG AGGAGGTGG    CCAGGG
                                 ||| |||||||||    ||||||
                                 TCC TCTTCCATT    GGTCTC
                                   _       CTAAT
GAM390  LOC90271  5' CCAGGGCTCATTTTTATTCCTG 62673       G   A_______  CCAG
          TCT                     AGGCAGGAG TGGAA      CC   G
                                 ||||||||| |||||      ||   |
                                 TCTGTCCTT ATTTT      GG   C
                                     _   TACTC    GACC
GAM390  LOC90288  3' CCAGGGCCTTCCTTCATCTCTT 62779    C       AA_______  CCAG
          CCCT                     AGG AGGAGGTGGA       CC   G
                                 ||| ||||||||||       ||   |
                                 TCC TTCTCTACTT       GG   C
                                   C       CCTTCC    GACC
GAM390  LOC90288  3' CCCTGCTCTATATTTTTTGTTT 62781          GAAACCC
                                AGGCAGGAGGTG     CAGGG
                                ||||||||||||     |||||
                                TTTGTTTTTTAT     GTCCC
                                     ATCTC__
GAM390  LOC90371  3' CCAGGGCTTTTTTCCTCTCCTG 63159       T   A_______  CCAG
          TCT                     AGGCAGGAGG GGAA      CC   G
                                 |||||||||| ||||      ||   |
                                 TCTGTCCTCT CTTT      GG   C
                                     C   TTTC    GACC
GAM390  LOC90379  3' CCTGGGGTGGCCTCTTCCT   63203       T  AA
                                AGGAGG GG  ACCCCAGG
                                |||||| ||  ||||||||
                                TCCTTC CC  TGGGGTCC
                                   T  GG
GAM390  LOC90408  5' CCCCAGGGTCCTCCTTATACTT 63341         ____  AA____  CCAG
          TCTGTCT                   AGGCAGGAGGT   GGA    CC   GG
                                 ||||||||||   |||    ||   ||
                                 TCTGTCTTTCA   CCT    GG   CC
                                      TATT  CCT    GACC
GAM390  LOC90591  3' TCCTGGGTTCACGCCATTCTCC 64192        _  AAAC__
          TGCCT                   AGGCAGGAGG TGG     CCCAGGG
                                 |||||||||| |||     |||||||
                                 TCCGTCCTCT ACC     GGGTCCT
                                      T  GCACTT
GAM390  LOC90639  3' TCAGGAGTTTCCACCTTTTCCC 64415    C         C  AGGG
          T                      AGG AGGAGGTGGAAAC CC
                                 ||| |||||||||||| ||
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                                TCC TTTTCCACCTTTG GG
                                  C          A  ACT
GAM390  LOC90750  3' CTCTGGGCTCATTCTTTGCCT  64627       AG    AAAC
                                AGGCAGG  GTGG    CCCAGGG
                                |||||||  ||||    |||||||
                                TCCGTTT  TACT    GGGTCTC
                                   CT    C___
GAM390  LOC90768  3' CCCTGGGATAGATCCATCTCCT 64653     C        AAC__
           TCT                    AGG AGGAGGTGGA    CCCAGGG
                                ||| ||||||||||    |||||||
                                TCT TCCTCTACCT    GGGTCCC
                                  _       AGATA
GAM390  LOC90777  3' TTTGGGATCTATCTGCT    64671    G      AAC
                                AG AGGTGGA   CCCAGG
                                || |||||||   ||||||
                                TC TCTATCT   GGGTTT
                                 G      A__
GAM390  LOC90786  5' CAGGGCTTTCTACCACTTCCTG 64727          AAA________  CCAG
           CCT                    AGGCAGGAGGTGG        CC    G
                                ||||||||||||         ||    |
                                TCCGTCCTTCACC        GG    C
                                      ATCTTTC    GAC
GAM390  LOC90786  5' GGTCCATTTTATTTTTGCCT   64732        ____    AA_
                                AGGCAGGAG   GTGGA   CC
                                |||||||||   |||||   ||
                                TCCGTTTTT   TACCT   GG
                                     ATTT
GAM390  LOC90829  5' CTTTATTTCCTTCTCCTGCTT  64792         T    CCCC
                                AGGCAGGAGG GGAAA    AGG
                                |||||||||| |||||    |||
                                TTCGTCCTCT CCTTT    TTC
                                      T    AT__
GAM390  LOC91115  3' TCTGCATAGGTTTCCACTTCTT 65579             C___    G
           GTC                    GGCAGGAGGTGGAAACC    CAGG
                                ||||||||||||||||    ||||
                                CTGTTCTTCACCTTTGG    GTCT
                                      ATAC
GAM390  LOC91138  5' CCTTGTTATCTCTTGCCT    65658          AAACCC
                                AGGCAGGAGGTGG     CAGGG
                                ||||||||||||     |||||
                                TCCGTTCTCTATT     GTTCC
                                     _______
GAM390  LOC91250  5' CCCAGGGTTTTGTTTTTGTTTT 65913        TG    ________  CAG
           TTGT                   GCAGGAGG  GAAAC      CC   GG
                                ||||||||  |||||      ||   ||
                                TGTTTTTT  TTTTG      GG   CC
                                   GT    TTTT    GAC
GAM390  LOC91308  5' CCAGGGCTTTAATCATTTTCTG 66164          AAA_______  CCAG
           TTT                    AGGCAGGAGGTGG       CC    G
                                ||||||||||||        ||    |
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                                TTTGTCTTTTACT       GG   C
                                      AATTTC    GACC
GAM390  LOC91408 3' TCCTGGTTTTTTTGTTTTTTGT 66519         TG   CC
            TT                  AGGCAGGAGG  GAAA  CCAGGG
                                ||||||||||  ||||  ||||||
                                TTTGTTTTTT  TTTT  GGTCCT
                                     GT    TT
GAM390  LOC91445 3' TCTGGAGTGTCTCTTCTCT   61173      T_   A  C
                                GGAGG  GGA AC CCAGG
                                |||||  ||| || |||||
                                TCTCT  TCT TG GGTCT
                                   TC   G  A
GAM390  LOC91496 5' TCTTGGAACCTGCTCTCCTGCT 66811         _ TG AAACC
            T                   AGGCAGGAG G  G    CCAGGG
                                |||||||||  |  |    ||||||
                                TTCGTCCTC C  C    GGTTCT
                                     T GT CAA__
GAM390  LOC91660 5' GGCTGTTTCTACTTTTGTCT   67404       G       _____
                                AGGCAG AGGTGGAAAC    CC
                                ||||||  ||||||||||    ||
                                TCTGTT TTCATCTTTG    GG
                                   _        TC
GAM390  LOC91663 3' CTCTGTTTTCCTCTTCCTGTCT 57223         T    CCC
                                AGGCAGGAGG GGAAA   CAGGG
                                ||||||||||  |||||  |||||
                                TCTGTCCTTC CCTTT   GTCTC
                                     T    T__
GAM390  LOC91689 3' CCAGGGTTTTCATCTATTTCCT 53976    G        AA________  CCAG
            GGCT                  AG CAGGAGGTGGA       CC   G
                                ||  ||||||||||        ||   |
                                TC GTCCTTTATCT       GG   C
                                 G         ACTTTT    GACC
GAM390  LOC91689 3' TCCTGACCTCCTTTCACCTGCT 53981       G      ACCC__
            GCTT                  AGGCAG AGGTGGAA     CAGGG
                                ||||||  ||||||||     |||||
                                TTCGTC TCCACTTT     GTCCT
                                   G       CCTCCA
GAM390  LOC91695 3' CCAGGGTCCTTCCCACCTCTTG 67510          AAA_______  CCAG
            CCT                   AGGCAGGAGGTGG       CC   G
                                ||||||||||||        ||   |
                                TCCGTTCTCCACC       GG   C
                                      CTTCCT    GACC
GAM390  LOC91759 3' CCAGGGCTCTATTTTGATTCCT 67690        _____    AA__  CCAG
            GCCT                  AGGCAGGAG    GTGGA   CC   G
                                |||||||||    |||||   ||   |
                                TCCGTCCTT    TATCT   GG   C
                                     AGTTT    C    GACC
GAM390  LOC91875 3' TCCTGTTGTTGCCTCCTTCCT  68034     C     TG AAACCC
                                AGG AGGAGG  G     CAGGG
                                ||| ||||||  |     |||||
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                                TCC TCCTCC  T     GTCCT
                                  T     GT GTT___
GAM390  LOC91875  3' TTCTGGCATATCTCTCCTGTCT 68036        GT   AACC
                                AGGCAGGAG  GGA    CCAGGG
                                |||||||||  |||    ||||||
                                TCTGTCCTC  TCT    GGTCTT
                                     __   ATAC
GAM390  LOC91923  5' GGCCATTCTACTTTCTGTCT   68174           A_____
                                AGGCAGGAGGTGGAA     CC
                                ||||||||||||||     ||
                                TCTGTCTTTCATCTT     GG
                                         ACC
GAM390  LOC91960  5' TCCTGGCGACCACTGCTTCTGT 68292         __   AAACC
             CT                   AGGCAGGAG  GTGG    CCAGGG
                                |||||||||  ||||    ||||||
                                TCTGTCTTC  CACC    GGTCCT
                                     GT    AGC__
GAM390  LOC91974  5' CCTTGGTGGACGTTTCTGTTT  68361         _  GGAAA  _
                                AGGCAGGAG GT     CC CCAGGG
                                |||||||||  ||     || ||||||
                                TTTGTCTTT CA     GG GGTTCC
                                     G  _____  T
GAM390  LOC92078  5' CCCTGGGCCTGTCCTTCTGCCT 68597          _   AAAC
                                AGGCAGGAGG TGG    CCCAGGG
                                |||||||||| |||    |||||||
                                TCCGTCTTCC GTC    GGGTCCC
                                     T   C___
GAM390  LOC92106  5' CCCTGCTTCTTATCGTCTGCTT 57226       GA    _   ACCC
                                AGGCAG  GGTG GAA    CAGGG
                                ||||||  |||| |||    |||||
                                TTCGTC  CTAT CTT    GTCCC
                                   TG    T   C___
GAM390  LOC92148  5' CCCCAGGGTCTATGTTCTGTTT 68874         G    AA_  CCAG
                                AGGCAGGA GTGGA   CC    GG
                                |||||||| |||||   ||    ||
                                TTTGTCTT TATCT   GG    CC
                                     G         GACC
GAM390  LOC92148  5' CTTGATCTATGTTCTGTTT    68878         G    AACCC
                                AGGCAGGA GTGGA     CAGG
                                |||||||| |||||     ||||
                                TTTGTCTT TATCT     GTTC
                                     G     A____
GAM390  LOC92148  5' TCTGATTCCTCTTCTGTCT    68889          T   ACCC
                                AGGCAGGAGG GGAA    CAGG
                                |||||||||| ||||    ||||
                                TCTGTCTTCT CCTT    GTCT
                                     _    A___
GAM390  LOC92218  3' CCAGGGTTTTTTTTTCTTTTTG 69031          T   A_______  CCAG
             CCT                   AGGCAGGAGG GGAA      CC    G
                                |||||||||| ||||      ||    |
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                                TCCGTTTTTC TTTT      GG    C
                                     T    TTTT     GACC
GAM390  LOC92230  5' CCTTGCCCACCTGCCTCTGGCC 69083      A     TG AAACCC
             T                   AGGC GGAGG  G      CAGGG
                                 |||| |||||  |      |||||
                                 TCCG TCTCC  C      GTTCC
                                   G     GT CACCC_
GAM390  LOC92293  3' CCAGGGTTCTTTTCCACTTTTT 69319     C         A________  CCAG
             CCTT                  AGG AGGAGGTGGAA       CC    G
                                 ||| ||||||||||        ||    |
                                 TTC TTTTTCACCTT       GG    C
                                   C         TTCTT     GACC
GAM390  LOC92299  5' GGCCTTCTCCACCTCCTCTT   69371     C         AA_______
                                 AGG AGGAGGTGGA       CC
                                 ||| ||||||||||       ||
                                 TTC TCCTCCACCT       GG
                                   _         CTTCC
GAM390  LOC92303  3' GGTGTTTTTTTTTCTGCTT    69396          T     _____
                                 AGGCAGGAGG GGAAAC    CC
                                 |||||||||| ||||||    ||
                                 TTCGTCTTTT TTTTTG    GG
                                      _      T
GAM390  LOC92340  3' CCCTGGCCAGGGCCATCTCCTG 69558            AAACC_
             TC                    GGCAGGAGGTGG      CCAGGG
                                   ||||||||||||      ||||||
                                   CTGTCCTCTACC      GGTCCC
                                         GGGACC
GAM390  LOC92340  3' CTCTGCCCCACTGCTTCCTGCC 69560          TG AAACCC
             T                     AGGCAGGAGG  G      CAGGG
                                   ||||||||||  |      |||||
                                   TCCGTCCTTC  C      GTCTC
                                         GT ACCCC_
GAM390  LOC92360  3' CCAGGGTCTTTTTCACTTTCTT 69624          _     A_______  CCAG
             GCCT                    AGGCAGGAG GTGGAA       CC    G
                                   ||||||||| ||||||       ||    |
                                   TCCGTTCTT CACTTT       GG    C
                                        T      TTCT     GACC
GAM390  LOC92399  3' GGTTCATTCTCTTCCTGCTT   57866          T   AA_____
                                   AGGCAGGAGG GGA       CC
                                   |||||||||| |||       ||
                                   TTCGTCCTTC CTT       GG
                                        T   ACTT
GAM390  LOC92573  5' TCTTGGTTGCTGTCTCCGTTT  70382      A     TG AAACC
                                   AGGC GGAGG  G     CCAGGG
                                   |||| |||||  |     ||||||
                                   TTTG CCTCT  C     GGTTCT
                                     _     GT GTT__
GAM390  LOC92606  3' CAGGGTCCAATTCAACCTTCTG 70528          G   A________  CCAG
             TCT                     AGGCAGGAGGT GAA       CC    G
                                   |||||||||| |||       ||    |
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                                TCTGTCTTCCA CTT       GG    C
                                      A   AACCT     GAC
GAM390  LOC92609  5' CCCTGGGCCCCCTTTATTTCTT 73208     C        AAC__
             TCT                  AGG AGGAGGTGGA     CCCAGGG
                                  ||| ||||||||||     |||||||
                                  TCT TTCTTTATTT     GGGTCCC
                                    _        CCCCC
GAM390  LOC92661  3' TCTTGGCCTCTGTATCCTGCCT 70636         G TG  AACC
                                  AGGCAGGA G  GA    CCAGGG
                                  |||||||| |  ||    ||||||
                                  TCCGTCCT T  CT    GGTTCT
                                      A GT  CC__
GAM390  LOC92719  3' CCAGTTTTTACTTTCTGTCT   70902              CCCA
                                  AGGCAGGAGGTGGAAAC    GG
                                  ||||||||||||||||    ||
                                  TCTGTCTTTCATTTTTG    CC
                                           A___
GAM390  LOC92771  3' CTCTGGGGTTCTAATTCTGGCT 54211     G     GG     A
                                  AG CAGGA  TGGAA CCCCAGGG
                                  || |||||  ||||| ||||||||
                                  TC GTCTT  ATCTT GGGGTCTC
                                   G    A_    _
GAM390  LOC92973  5' CTTTGGGCAGTGCCAGTCTCCT 71591          _   AAAC_
             GTTT                   AGGCAGGAGG TGG     CCCAGGG
                                  |||||||||| |||     |||||||
                                  TTTGTCCTCT ACC     GGGTTTC
                                       G   GTGAC
GAM390  LOC93052  5' CTCTGGGCCCAAAACTCCTGCC 71769         G__   AAAC
             T                    AGGCAGGAG   TGG    CCCAGGG
                                  |||||||||   |||    |||||||
                                  TCCGTCCTC   ACC    GGGTCTC
                                       AAA   C___
GAM390  LOC93259  5' CCTTTTCTGCCTTCTTTCT    72284     C     TG    CCCC
                                  AGG AGGAGG  GAAA    AGG
                                  ||| ||||||  ||||    |||
                                  TCT TCTTCC  CTTT    TCC
                                    T     GT    _____
GAM390  LOC93259  5' TCTTGTCTTTCTCCCTCCTGCT 72296          TG    CCC
             T                    AGGCAGGAGG  GAAA   CAGGG
                                  ||||||||||  ||||   |||||
                                  TTCGTCCTCC  CTTT   GTTCT
                                       CT    CT_
GAM390  LOC93380  3' CTTTGGGGTATGTCTTCGTTT  72652      A    GT GAA
                                  AGGC GGAG  G   ACCCCAGGG
                                  |||| ||||  |   |||||||||
                                  TTTG CTTC  T   TGGGGTTTC
                                    _    TG A__
GAM390  LOC93512  5' CCTGGGGGAGCCTCTTCTT    72875     C      GGAAA
                                  AGG AGGAGGT    CCCCAGG
                                  ||| |||||||    |||||||
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                                TTC TTCTCCG    GGGGTCC
                                  _     AG___
GAM390  LOC93613  5'  CCAGGGCTCTCGTTCACTTCCT 73071    C       AA_______  CCAG
                CCCT                AGG AGGAGGTGGA       CC   G
                                ||| ||||||||||       ||   |
                                TCC TCCTTCACTT       GG   C
                                  C        GCTCTC    GACC
GAM391  CDH12     3'  CTTATCATTTAAAGTGGTGTA  15777        CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM391  GOCAP1    3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA       G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM391  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT    98090      T    AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT     TTATTC
                                  _    GTCA_
GAM391  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
                A                    TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM391  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126        CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM391  HMP19     3'  CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
                TA                   TACA    TCC    GAAGAATAAG
                                ||||    |||    ||||||||||
                                ATGT    AGG    TTTCTTATTC
                                  AAA_   ATTG
GAM391  KIAA1579  3'  TACTCTTAGTGGTGTA     37154         CCCAAG    A
                                TACACCACT     AAGA TA
                                |||||||||     |||| ||
                                ATGTGGTGA     TTCT AT
                                     _______    C
GAM391  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68742             _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                        G
GAM391  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
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                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM391  KIAA1877 3' CTTATTCTTCTGCCATGAGT  66748     CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM391  KIAA1906 3' CTTATTCTTCTTGACTTTTGG 73571    CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM391  OSBPL11  3' CTTAATTTCCCAAGAGTGGTG 43206       CCAA   AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                     AACC   A_
GAM391  YME1L1   3' TCATTCTTGATGTGGTGTA   58438       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                     TA_    A
GAM391  YME1L1   3' TCATTCTTGATGTGGTGTA   27323       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                     TA_    A
GAM391  ZNF262   3' CTTATTTTGTTTGGGAGT    18723        A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                     G
GAM391  LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_    AAGA
                                TACACCAC  CCAAG   ATA
                                ||||||||  |||||   |||
                                ATGTGGTG  GGTTC   TGT
                                     CAA    GG__
GAM392  BRCA1    3' GCCTTCTAACAGCTACCCTT  24567     AACTA  C
                                AAGG    TGT TGGAAGGC
                                ||||    ||| ||||||||
                                TTCC    ACA ATCTTCCG
                                  CATCG  _
GAM392  CDKN2C   5' GCCCCGATCTATAGTTCCTT  55317        TC_  AA
                                AAGGAACTATG  TGG  GGC
                                ||||||||||   |||  |||
                                TTCCTTGATAT  GCC  CCG
                                     CTA   __
GAM392  CYP7A1   3' CCCTCACCACACAGTCCCTTT 7593      A  A  CTG  A
                                AAAGG ACT TGT  GA GG
                                ||||| ||| |||  || ||
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                                TTTCC TGA ACA  CT CC
                                  C  C  CCA  C
GAM392  DIAPH2   3' GCCCACAGATAATTCCTTT  23008      CTA    GAA
                                AAAGGAA  TGTCTG  GGC
                                |||||||  ||||||  |||
                                TTTCCTT  ATAGAC  CCG
                                   A__    AC_
GAM392  G6PT1    5' GCCTTCTGCTCCAGTTGCTTT 9404     G   AT_ CT
                                AAAG AACT  GT  GGAAGGC
                                |||| ||||  ||  |||||||
                                TTTC TTGA  CG  TCTTCCG
                                  G   CCT  __
GAM392  IDH3A    3' CCCTCAGGCATCTCCTTT   19844      ACT     AA
                                AAAGGA  ATGTCTGG  GG
                                ||||||  ||||||||  ||
                                TTTCCT  TACGGACT  CC
                                   C__     C_
GAM392  IL18     5' CCTTCCAGATCGCTTCCT   9591      CTAT
                                AGGAA   GTCTGGAAGG
                                |||||   ||||||||||
                                TCCTT   TAGACCTTCC
                                  CGC_
GAM392  KCNC3    3' CCTTTTGTCCAGACAGCTCCCT 18330     AACTA     ____
           T                     AAGG    TGTCTGGA   AGG
                                ||||    ||||||||   |||
                                TTCC    ACAGACCT   TCC
                                  CTCG_     GTTT
GAM392  KCNK3    3' GCCTTCCAGACACTGCCCTT  11177     AACTA
                                AAGG    TGTCTGGAAGGC
                                ||||    ||||||||||||
                                TTCC    ACAGACCTTCCG
                                  CGTC_
GAM392  LARS2    3' GCCCCCCAGATGTTGCCTCC  31696   A  AACT     AA
                                A AGG   ATGTCTGG  GGC
                                | |||   ||||||||  |||
                                C TCC   TGTAGACC  CCG
                                 C  GT__      CC
GAM392  MAOB     3' CCTTCCCTAGTTCTTT     60661       TGTCT
                                AAGGAACTA    GGAAGG
                                |||||||||    ||||||
                                TTTCTTGAT    CCTTCC
                                     C____
GAM392  MAP1B    3' CCTTTCACAGCTTCTTT    50090      CTA  CT
                                AAGGAA  TGT  GGAAGG
                                ||||||  |||  ||||||
                                TTTCTT  ACA  CTTTCC
                                   CG_  __
GAM392  MAP1B    3' CCTTTCACAGCTTCTTT    20962      CTA  CT
                                AAGGAA  TGT  GGAAGG
                                ||||||  |||  ||||||
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                                TTTCTT  ACA  CTTTCC
                                   CG_  __
GAM392  MAX     3'  CCTTCCAGCCTCCTTT     59704       ACTAT T
                                AAAGGA    G CTGGAAGG
                                ||||||    | ||||||||
                                TTTCCT    C GACCTTCC
                                   C_____ _
GAM392  MTMR2   3'  CCTTCCAGTGGTTCC      32910       TGT
                                GGAACTA   CTGGAAGG
                                |||||||   ||||||||
                                CCTTGGT   GACCTTCC
                                   ___
GAM392  NRBP    3'  GCCTTCTCAGCAGCCGCCTT  26341     AACTA  T  _
                                AAGG    TG CTG GAAGGC
                                ||||    || ||| ||||||
                                TTCC    AC GAC CTTCCG
                                  GCCG_ _   T
GAM392  NRXN1   5'  GCCTTTCCGGACAAGCCCCT  57829     AA  A      _
                                AGG  CT TGTCTGGAA GGC
                                |||  || |||||||| |||
                                TCC  GA ACAGGCCTT CCG
                                 CC  _       T
GAM392  PDGFB   3'  GCCTTCCAAAACCTGCTTCCTT 12026      C  T  C_
                                AAGGAA TA GT  TGGAAGGC
                                |||||| || ||  ||||||||
                                TTCCTT GT CA  ACCTTCCG
                                   C  C  AA
GAM392  PLA2G4C 3'  GCCTTCCACTGCTCCTTT   73808      ACTAT  C_
                                AAAGGA    GT  TGGAAGGC
                                ||||||    ||  ||||||||
                                TTTCCT    CG  ACCTTCCG
                                   ______ TC
GAM392  PNUTL1  3'  GCCCTCCAGACATAAGGAGGCC 12192    AA__ _      A
                                GG   CT ATGTCTGGA GGC
                                ||   || |||||||| |||
                                CC   GA TACAGACCT CCG
                                 GGAG  A       C
GAM392  PPP1R8  3'  GCCTTCCACTACCTCCTTT   12229      AC  TGTC
                                AAAGGA  TA   TGGAAGGC
                                ||||||  ||   ||||||||
                                TTTCCT  AT   ACCTTCCG
                                   CC  C___
GAM392  PPP1R8  3'  GCCTTCCACTACCTCCTTT   26919      AC  TGTC
                                AAAGGA  TA   TGGAAGGC
                                ||||||  ||   ||||||||
                                TTTCCT  AT   ACCTTCCG
                                   CC  C___
GAM392  PPP1R8  3'  GCCTTCCACTACCTCCTTT   57509      AC  TGTC
                                AAAGGA  TA   TGGAAGGC
                                ||||||  ||   ||||||||
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                                TTTCCT  AT    ACCTTCCG
                                   CC  C___
GAM392  PRKY     3'  GCCTTCCAGGAATTCCTT    12378       CTATG
                                AAGGAA    TCTGGAAGGC
                                ||||||    ||||||||||
                                TTCCTT    GGACCTTCCG
                                   AA___
GAM392  PSAP     3'  CCTGGCAGACATAGCTGCTT  69881     AA_       GA
                                AGG   CTATGTCTG  AGG
                                |||   |||||||||  |||
                                TTC   GATACAGAC  TCC
                                  GTC       GG
GAM392  PTGFRN   3'  CCAAGGACCTAGTTCCTT    67765         T    GGAA
                                AAGGAACTA GTCT    GG
                                |||||||||| ||||    ||
                                TTCCTTGAT CAGG    CC
                                     C    AA__
GAM392  RFX5     3'  CCCTCCAGATGTATCCTT    6549       AC        A
                                AAGGA  TATGTCTGGA GG
                                |||||  |||||||||| ||
                                TTCCT  ATGTAGACCT CC
                                   __         C
GAM392  SELL     3'  CCTGACCAACAGTTCCTT    7227         AT  C   A_
                                AAGGAACT  GT TGG  AGG
                                ||||||||  || |||  |||
                                TTCCTTGA  CA ACC  TCC
                                   __ _  AG
GAM392  SFRP5    3'  GCCTCGGCATAGACCCCCTT  13033      AA__      TGGA
                                AAGG   CTATGTC   AGGC
                                ||||   |||||||   ||||
                                TTCC   GATACGG   TCCG
                                  CCCA      C___
GAM392  SIM2     3'  CCCTCCAGGCCTCAGTTTCTT 24800        AT_      A
                                AAGGAACT   GTCTGGA GG
                                ||||||||   ||||||| ||
                                TTCTTTGA   CGGACCT CC
                                     CTC      C
GAM392  SLC4A4   3'  CCTCCAGACAGAGTCCCTT   14992      A  A      A
                                AAGG ACT TGTCTGGA GG
                                |||| ||| |||||||| ||
                                TTCC TGA ACAGACCT CC
                                  C  G       _
GAM392  TFRC     3'  CCTCCATTTAGTTCTTT     13701         TGTC   A
                                AAGGAACTA    TGGA GG
                                |||||||||    |||| ||
                                TTTCTTGAT    ACCT CC
                                     TT__    _
GAM392  TGFA     3'  GCCTCCCTAGAAGTGCCTT   13711      A  ATG   A_
                                AAGG ACT   TCTGG  AGGC
                                |||| |||   |||||  ||||
```

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                                TTCC TGA   AGATC  TCCG
                                  G  ___    CC
GAM392  TGFA     3'  GCCTTCCAAGTCAGTCCTTT   13712       A  AT TC
                                AAAGGA CT  G  TGGAAGGC
                                |||||| ||  |  ||||||||
                                TTTCCT GA  T  ACCTTCCG
                                   _  C_ GA
GAM392  XBP1     3'  GCCTCCAGTTTTAGGTCCTTT  18676       A   TGT    A
                                AAAGGA CTA   CTGGA GGC
                                |||||| |||   ||||| |||
                                TTTCCT GAT   GACCT CCG
                                   G   TTT    _
GAM392  XRCC3    3'  GCCTGGTTCAGACACAGCTCTT 19518   A    A  A      __
           CC                     A AGGA CT TGTCTGGA  AGGC
                                | |||| || ||||||||  ||||
                                C TTCT GA ACAGACTT  TCCG
                                 C   C  C       GG
GAM392  ASML3B   3'  GCCTTCCACCATTTCCTCC   27877   A    CT   TC
                                A AGGAA  ATG  TGGAAGGC
                                | |||||  |||  ||||||||
                                C TCCTT  TAC  ACCTTCCG
                                 C    __   C_
GAM392  C1orf34  3'  GCCTTCCAAGGTTTGCTTCTTT 61315       C  TG  _
                                AAGGAA TA  TCT GGAAGGC
                                |||||| ||  ||| |||||||
                                TTTCTT GT  GGA CCTTCCG
                                   C  TT   A
GAM392  CDCA7    3'  GCCCTCCTGCAGTTTCTT    50043        AT  CT   A
                                AAGGAACT  GT  GGA GGC
                                ||||||||  ||  ||| |||
                                TTCTTTGA  CG  CCT CCG
                                    __  T_   C
GAM392  CED-6    3'  GCCTTCTTGTTTAGTTTCTTT  33318         TGTCT
                                AAAGGAACTA    GGAAGGC
                                ||||||||||    |||||||
                                TTTCTTTGAT    TCTTCCG
                                     TTGT_
GAM392  dJ309H15.1 3'  GCCTTCCACAAATCCTTT    57569       ACTA   CT
                                AAAGGA    TGT  GGAAGGC
                                ||||||    |||  |||||||
                                TTTCCT    ACA  CCTTCCG
                                   AA__   __
GAM392  DKFZp434C0923 3'  GCCTCCTGCAGGTTCCTTT    34650         A   CT   A
                                AAAGGAACT TGT  GGA GGC
                                ||||||||| |||  ||| |||
                                TTTCCTTGG ACG  CCT CCG
                                     _  T_  _
GAM392  DKFZP434C131 3'  GCCCTCTTCGGGCAGCCCCCCT 69638      AACTA      A__
           T                     AAGG    TGTCTGGA   GGC
                                ||||    ||||||||  |||
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                                TTCC    ACGGGCTT   CCG
                                  CCCCG       CTC
GAM392  DKFZP434L0117 3'  GCCTTCCAGGTAGTCCCCTT   43243     A_    GT
                                AAGG  ACTAT  CTGGAAGGC
                                ||||  |||||  |||||||||
                                TTCC  TGATG  GACCTTCCG
                                  CC    __
GAM392  DRAP1    3'  CCCCCCAGACCATAGCCCCTTT 22244      AA    _    AA
                                AAAGG  CTATG TCTGG  GG
                                |||||  ||||| |||||  ||
                                TTTCC  GATAC AGACC  CC
                                   CC    C    CC
GAM392  DT1P1A10  3'  TTTTCCAGCATATTCC      62249      C    T
                                GGAA TATG CTGGAAGG
                                |||| |||| ||||||||
                                CCTT ATAC GACCTTTT

                                  _   _
GAM392  EAT2     3'  GCCTCCCAGACATATACC    80053    AAC       A
                                GG   TATGTCTGG AGGC
                                ||   ||||||||| ||||
                                CC   ATACAGACC TCCG
                                 AT_       C
GAM392  EPN2     3'  GCCTTCCAAGGCAGGCCCCTCA 31041    A   AA  A    _
                                A AGG  CT TGTCT GGAAGGC
                                | |||  || ||||| |||||||
                                A TCC  GG ACGGA CCTTCCG
                                 C   CC  _    A
GAM392  FLJ10420  3'  GCCCTCCAGAGGAGGGGTTTCT 36591        ATG__     A
           T                     AAGGAACT     TCTGGA GGC
                                ||||||||     |||||| |||
                                TTCTTTGG     AGACCT CCG
                                     GGAGG     C
GAM392  FLJ10751  3'  GCCCTCCAGACCCGGCCTTT   37114      AACTAT      A
                                AAAGG      GTCTGGA GGC
                                |||||      ||||||| |||
                                TTTCC      CAGACCT CCG
                                   GGCC__       C
GAM392  FLJ10751  3'  GCCCTCCAGACCCGGCCTTT   37277      AACTAT      A
                                AAAGG      GTCTGGA GGC
                                |||||      ||||||| |||
                                TTTCC      CAGACCT CCG
                                   GGCC__       C
GAM392  FLJ14082  3'  GCCTCTGCACTCACAGGTTCCT 47321        AT___  C    A
           T                     AAGGAACT     GT TGGA GGC
                                ||||||||     || |||| |||
                                TTCCTTGG     CA GTCT CCG
                                     ACACT  C    _
GAM392  FLJ22059  5'  CCTTACCAAGTTCCTTT     43054         ATGTC   _
                                AAAGGAACT     TGG AAGG
                                |||||||||     ||| ||||
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                                TTTCCTTGA    ACC TTCC
                                      _____  A
GAM392  FLJ22709  3'  GCCTTCCAGGACTTCCTCC   45020   A    CTATG
                                A AGGAA    TCTGGAAGGC
                                | |||||    ||||||||||
                                C TCCTT    GGACCTTCCG
                                 C    CA___
GAM392  FLJ23420  5'  GCCTTCTGTTACATCTCCTTT  47541      ACT   CT_
                                AAAGGA  ATGT  GGAAGGC
                                ||||||  ||||  |||||||
                                TTTCCT  TACA  TCTTCCG
                                   C__   TTG
GAM392  FLJ23590  5'  GCCTTCCAGACAGACCT    45366    AACTA
                                AGG    TGTCTGGAAGGC
                                |||    ||||||||||||
                                TCC    ACAGACCTTCCG
                                  AG___
GAM392  FLJ32356  3'  CCTTCTAGCAGGTTCC     59019      A  T
                                GGAACT TG CTGGAAGG
                                ||||||| || ||||||||
                                CCTTGG AC GATCTTCC
                                   _ _
GAM392  GOLGA1    3'  GCCTTCCAGAGGCCGCTTCTCC 10850   A   CTATG_
                                A GGAA     TCTGGAAGGC
                                | ||||     ||||||||||
                                C TCTT     AGACCTTCCG
                                 C   CGCCGG
GAM392  HT002     3'  GCCTTCCAGACATCTGCGTTC  26792     T___
                                GAAC   ATGTCTGGAAGGC
                                ||||   ||||||||||||
                                CTTG   TACAGACCTTCCG
                                  CGTC
GAM392  IL14      5'  CCTTCAGAAATAATCCTTT   97163      AC  G   G
                                AAAGGA  TAT TCTG AAGG
                                ||||||  ||| |||| ||||
                                TTTCCT  ATA AGAC TTCC
                                   A_  A   _
GAM392  KIAA0057  3'  GCCTTCCGAGCTTATGGTTCCT 25417          T_ _
           TT                    AAAGGAACTATG  CT GGAAGGC
                                ||||||||||||  || |||||||
                                TTTCCTTGGTAT  GA CCTTCCG
                                      TC  G
GAM392  KIAA0184  3'  GCCTCCTCTGCCAGTTCCTTT  65811        ATGTCT  A
                                AAAGGAACT     GGA GGC
                                |||||||||     ||| |||
                                TTTCCTTGA     CCT CCG
                                     CCGTCT  _
GAM392  KIAA0258  3'  CCCTGGTGCTAGTTCCTT    29468        T  _ TG AA
                                AAGGAACTA GT C  G  GG
                                ||||||||| || |  |  ||
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                                TTCCTTGAT CG G  C  CC
                                     _  T GT __
GAM392  KIAA0350  3'  GCCCCCAAGATGTTCCTTT   61830        TAT   _  AA
                                AAAGGAAC   GTCT GG  GGC
                                ||||||||   |||| ||  |||
                                TTTCCTTG   TAGA CC  CCG
                                     ___    A  C_
GAM392  KIAA0522  3'  GCCTTCCAGAGATCCTCG    72423   A   ACTA G
                                A AGGA    T TCTGGAAGGC
                                | ||||    | ||||||||||
                                G TCCT    A AGACCTTCCG
                                 C    _____ G
GAM392  KIAA0703  5'  GCCCCACTAGCAGTTCCTTT   30080         AT T    AA_
                                AAAGGAACT  G CTGG   GGC
                                |||||||||  | ||||   |||
                                TTTCCTTGA  C GATC   CCG
                                     __ _    ACC
GAM392  KIAA0852  5'  TTTATGACATAGTTCCTT    30767            _
                                AAGGAACTATGTC TGGA
                                |||||||||||| ||||
                                TTCCTTGATACAG ATTT
                                      T
GAM392  KIAA0934  3'  GCCCTCCAGATGGGTTCTTTT  64884         A       A
                                AAAGGAACT TGTCTGGA GGC
                                ||||||||| |||||||| |||
                                TTTTCTTGG GTAGACCT CCG
                                     _       C
GAM392  KIAA1554  3'  GCCTCCCTGGACAGTTCC    96859       AT    _  A
                                GGAACT  GTCT GG AGGC
                                ||||||  |||| || ||||
                                CCTTGA  CAGG CC TCCG
                                    __    T  C
GAM392  KIAA1762  5'  GCTGAAGACGTAGCTCCTCC   64532   A   A      GGAA
                                A AGGA CTATGTCT    GGC
                                | |||| ||||||||    |||
                                C TCCT GATGCAGA    TCG
                                 C    C       AG__
GAM392  KIAA1870  5'  CCCCCGGGAGTCATTCCTTT   52898       CT  GT    AA
                                AAAGGAA  AT  CTGG  GG
                                |||||||  ||  ||||  ||
                                TTTCCTT  TG  GGCC  CC
                                     AC  AG    C_
GAM392  KIAA1954  5'  GCCTTCAGGCATAGCTC     78226    A       G
                                GA CTATGTCTG AAGGC
                                || |||||||| |||||
                                CT GATACGGAC TTCCG
                                 C        _
GAM392  KIAA1954  5'  GCCTTCCAGCGCAGCTCCTCC  78227   A   A  A  T
                                A AGGA CT TG CTGGAAGGC
                                | |||| || || |||||||||
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                                C TCCT GA GC GACCTTCCG
                                 C   C C _
GAM392  LNIR     5' GCCTTCTGGGTCAGTTCCTT  48873       ATG  TG
                                AAGGAACT  TC  GAAGGC
                                ||||||||  ||  ||||||
                                TTCCTTGA  GG  CTTCCG
                                    CT_  GT
GAM392  MGC32043 3' CCTCCCTGGCTGTTCCTTT  58661       TAT  T  A
                                AAAGGAAC  GTC GG AGG
                                ||||||||  ||| || |||
                                TTTCCTTG  CGG CC TCC
                                    T__  T  C
GAM392  MGC4832  3' GCCTTCCCATCATCTCCTTT  59658      ACT  TCT
                                AAAGGA  ATG  GGAAGGC
                                ||||||  |||  |||||||
                                TTTCCT  TAC  CCTTCCG
                                   C__  TAC
GAM392  NIR3     3' CCTTCAGATTCCTTT      66826      ACTAT    G
                                AAAGGA    GTCTG AAGG
                                ||||||    ||||| ||||
                                TTTCCT    TAGAC TTCC
                                  _____   _
GAM392  PSKH1    3' CCTTTGGGACAGTTACTT    68793    G   AT   G
                                AAG AACT  GTCT GAAGG
                                ||| ||||  |||| |||||
                                TTC TTGA  CAGG TTTCC
                                  A   __   G
GAM392  RALGPS1A 3' GCCCTCCATGGGGTTCTTT   28332       ATGTC   A
                                AAGGAACT    TGGA GGC
                                ||||||||    |||| |||
                                TTTCTTGG    ACCT CCG
                                    GGT__   C
GAM392  RNP24    3' GCCTCCATTATATAGGTCCTT  23326     A    C_   A
                                AAGGA CTATGT  TGGA GGC
                                ||||| ||||||  |||| |||
                                TTCCT GATATA  ACCT CCG
                                   G     TT   _
GAM392  SCYA16   3' CCTTCCAGATGATCTTT     17170      ACTA
                                AAGGA   TGTCTGGAAGG
                                |||||   ||||||||||
                                TTTCT   GTAGACCTTCC
                                   A___
GAM392  SMUG1    3' CCTTTTAACATTGCCCCTTT  27470      AACT   C
                                AAAGG   ATGT TGGAAGG
                                |||||   |||| |||||||
                                TTTCC   TACA ATTTTCC
                                   CCGT   _
GAM392  STMN3    3' CCCTCTGGGCTGAGTTCCTT  32465       AT   TG  A
                                AAGGAACT  GTC  GA GG
                                ||||||||  |||  || ||
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                                TTCCTTGA  CGG  CT CC
                                    GT   GT  C
GAM392  TBC1D2   3'  CCTTGGACATGTCCCTT    37927     A  T     GG
                                AAGG AC ATGTCT  AAGG
                                |||| || ||||||  ||||
                                TTCC TG TACAGG  TTCC
                                  C  _     __
GAM392  VAMP4    3'  CAGAAATATAGTTCCTTT    61028          __
                                AAAGGAACTATG  TCTG
                                ||||||||||||  ||||
                                TTTCCTTGATAT  AGAC
                                      AA
GAM392  LOC115073 3'  GCCTTCTGAGCAGTTCTT    73581        AT  CT
                                AGGAACT  GT  GGAAGGC
                                |||||||  ||  |||||||
                                TTCTTGA  CG  TCTTCCG
                                   __  AG
GAM392  LOC126669 3'  GCCCTCCTGAAGATAGTTTCCT 75938      _   G_  T   A
                                AGGAA CTAT  TC GGA GGC
                                ||||| ||||  || ||| |||
                                TCCTT GATA  AG CCT CCG
                                   T   GA  T   C
GAM392  LOC146420 3'  CCAGGGCGACTACAGTTCCTTT 84652         A____   _
                                AAAGGAACT     TGTC TGG
                                |||||||||     |||| |||
                                TTTCCTTGA     GCGG ACC
                                     CATCA    G
GAM392  LOC146443 5'  GCCTTCCAAGGCTGGTCCTT   78447      A   T   _
                                AAGGA CTA GTCT GGAAGGC
                                ||||| ||| |||| |||||||
                                TTCCT GGT CGGA CCTTCCG
                                   _  _   A
GAM392  LOC146823 3'  GCATCCAGACATACTCCTTT   84827       AC        AG
                                AAAGGA  TATGTCTGGA  GC
                                ||||||  ||||||||||  ||
                                TTTCCT  ATACAGACCT  CG
                                   C_         A_
GAM392  LOC147276 3'  GCCTTCCAGCTCCTCCTCC    78966   A   ACTAT T
                                A AGGA     G CTGGAAGGC
                                | ||||     | |||||||||
                                C TCCT     C GACCTTCCG
                                 C    CCT__ _
GAM392  LOC147343 5'  GCCTTCTGCCATGTTCCTCC   85130   A     T   TC
                                A AGGAAC ATG  TGGAAGGC
                                | |||||| |||  ||||||||
                                C TCCTTG TAC  GTCTTCCG
                                 C      _  C_
GAM392  LOC147515 3'  CCTTCCAGCATTCTCCTTT    85148       ACT   T
                                AAAGGA   ATG CTGGAAGG
                                ||||||   ||| ||||||||
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                                TTTCCT   TAC GACCTTCC
                                   CT_  _
GAM392  LOC148181 5'  GCCTCCCAGTGGCCTCTTT   79435      A_  TGT   A
                                AAGGA  CTA   CTGG AGGC
                                |||||  |||   |||| ||||
                                TTTCT  GGT   GACC TCCG
                                   CC  ___   C
GAM392  LOC149995 3'  CCTTCCAGCATTCTCCTTT   85982      ACT   T
                                AAAGGA   ATG CTGGAAGG
                                ||||||   ||| ||||||||
                                TTTCCT   TAC GACCTTCC
                                   CT_  _
GAM392  LOC154834 3'  CCTTCCAGGTGGGTCC     87493     A   GT
                                GGA CTAT  CTGGAAGG
                                ||| ||||  ||||||||
                                CCT GGTG  GACCTTCC
                                  G   __
GAM392  LOC154834 3'  GCCTTCCACAACAGTCCCCTCG 87495   A   AACTA   C_
                                A AGG    TGT  TGGAAGGC
                                | |||    |||  ||||||||
                                G TCC    ACA  ACCTTCCG
                                 C   CCTG_   AC
GAM392  LOC154990 5'  GCCTCCCAGTGGCCTCTTT   82151      A_  TGT   A
                                AAGGA  CTA   CTGG AGGC
                                |||||  |||   |||| ||||
                                TTTCT  GGT   GACC TCCG
                                   CC  ___   C
GAM392  LOC157918 3'  CCTTCCAGAGTGCCTT     87930     A  TATG
                                AAGG AC    TCTGGAAGG
                                |||| ||    |||||||||
                                TTCC TG    AGACCTTCC
                                  G  ____
GAM392  LOC158191 3'  GCCTTTTTTTCATTAGTTCCTT 82678        _  TCT
                                AAGGAACTA TG   GGAAGGC
                                ||||||||| ||   |||||||
                                TTCCTTGAT AC   TTTTCCG
                                     T  TTT
GAM392  LOC158696 3'  GCCCTTTATCTAGTTCCT    82859       T  CT  AA
                                AGGAACTA GT  GG  GGC
                                |||||||| ||  ||  |||
                                TCCTTGAT TA  TC  CCG
                                     C  TT  __
GAM392  LOC158819 5'  GCCTGCTCCACAGTTCTTT   88279       ATGTC   __
                                AAGGAACT    TGGA  AGGC
                                ||||||||    ||||  ||||
                                TTTCTTGA    ACCT  TCCG
                                     C____    CG
GAM392  LOC167153 3'  CCTCCATCATAGTTGCTTT   83562     G      TC    A
                                AAAG AACTATG  TGGA GG
                                |||| |||||||  |||| ||
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                                TTTC TTGATAC  ACCT CC
                                  G      T_   _
GAM392   LOC196264 3'  GCCTTCCAGAATTTTTCTTT   88986       CTATG
                                AAAGGAA    TCTGGAAGGC
                                |||||||    ||||||||||
                                TTTCTTT    AGACCTTCCG
                                   TTA__
GAM392   LOC202754 3'  GCCTCTAGCGTCATAGTTTCCT 83589      _    T__    A
                                AGGAA CTATG   CTGGA GGC
                                ||||| |||||   ||||| |||
                                TCCTT GATAC   GATCT CCG
                                  T    TGC    _
GAM392   LOC202908 3'  GCCTCCCAGTGGCCTCTTT   90728      A_   TGT    A
                                AAGGA  CTA   CTGG AGGC
                                |||||  |||   |||| ||||
                                TTTCT  GGT   GACC TCCG
                                  CC   ____   C
GAM392   LOC204804 3'  GCCTTTGTTACATAGTTGCTCC 91046   A  G       CTG
                                A AG AACTATGT   GAAGGC
                                | || ||||||||   ||||||
                                C TC TTGATACA   TTTCCG
                                 C  G       TTG
GAM392   LOC220739 3'  GCCTTCCACCCTGGCTCCTT   94523      A   TGTC
                                AAGGA CTA    TGGAAGGC
                                ||||| |||    ||||||||
                                TTCCT GGT    ACCTTCCG
                                  C   CCC_
GAM392   LOC222057 3'  GCCTCCCAGTGGCCTCTTT   94356      A_   TGT    A
                                AAGGA  CTA   CTGG AGGC
                                |||||  |||   |||| ||||
                                TTTCT  GGT   GACC TCCG
                                  CC   ____   C
GAM392   LOC254219 3'  GCCCTCCAGGTGGTCCCT    98322     A    GT    A
                                AGG ACTAT  CTGGA GGC
                                ||| |||||  ||||| |||
                                TCC TGGTG  GACCT CCG
                                  C    __    C
GAM392   LOC254806 5'  GCCTTCCAGACGCTTC      97481     CTA
                                GAA   TGTCTGGAAGGC
                                |||   ||||||||||||
                                CTT   GCAGACCTTCCG
                                  C__
GAM392   LOC255975 3'  GCCTCCCAGTGGCCTCTTT   97585      A_   TGT    A
                                AAGGA  CTA   CTGG AGGC
                                |||||  |||   |||| ||||
                                TTTCT  GGT   GACC TCCG
                                  CC   ____   C
GAM392   LOC256878 3'  GCCTCCCAGTGGCCTCTTT   98689      A_   TGT    A
                                AAGGA  CTA   CTGG AGGC
                                |||||  |||   |||| ||||
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                                TTTCT  GGT   GACC TCCG
                                  CC  ___   C
GAM392  LOC55924  3' GCCCAACTCCAAGTTCCTTT  39393       ATGTC   A___
                                AAAGGAACT   TGGA   GGC
                                |||||||||   ||||   |||
                                TTTCCTTGA   ACCT   CCG
                                     _____  CAAC
GAM392  LOC90075  5' GCCTTTAGACTTAGTTCCTT  61994       T   G
                                AAGGAACTA GTCTG AAGGC
                                ||||||||| ||||| |||||
                                TTCCTTGAT CAGAT TTCCG
                                      T   _
GAM392  LOC90288  3' GCCTTCTTCCAGTAGTTCTT  62792       GTCT
                                AGGAACTAT   GGAAGGC
                                |||||||||   |||||||
                                TTCTTGATG   TCTTCCG
                                      ACCT
GAM392  LOC90333  3' CCATCAGACAATTCCTTT   62958      CTA     AA
                                AAAGGAA  TGTCTGG  GG
                                |||||||  |||||||  ||
                                TTTCCTT  ACAGACT  CC
                                    A__     A_
GAM392  LOC91548  5' GCCTTCCAAAGTTCTTCA   67010   A     ATGTC
                                A AGGAACT   TGGAAGGC
                                | |||||||   ||||||||
                                A TTCTTGA   ACCTTCCG
                                 C      A____
GAM393  ABCB8   3'  TCCTGCTCACAATAAAGC   24206   ATG     C
                                GC   TTATTG GAGCAGGA
                                ||   |||||| ||||||||
                                CG   AATAAC CTCGTCCT
                                 A__     A
GAM393  APXL    3'  GTCCCTGCTCGTTCAACA   9716      ATT       A
                                TGTT   GCGAGCAGG AC
                                ||||   ||||||||| ||
                                ACAA   TGCTCGTCC TG
                                  CT_       C
GAM393  HYAL1   3'  TTCCTGCTCCATATGCA    53705      TTAT  C
                                TGCATG   TG GAGCAGGAA
                                ||||||   || |||||||||
                                ACGTAT   AC CTCGTCCTT
                                     ____  _
GAM393  NID     3'  TTCCCCAAAACATGCA     11809        A   CGAGCA
                                TGCATGTT TTG     GGAA
                                |||||||| |||     ||||
                                ACGTACAA AAC     CCTT
                                     _  C_____
GAM393  DCTD    3'  TTCCTGCTCTCCCACTGCA   10394     T  TATTGC
                                TGCA GT     GAGCAGGAA
                                |||| ||     |||||||||
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                                ACGT CA     CTCGTCCTT
                                  _ CCCT__
GAM393  DNCI2    3'  TGTCCCTTTATATATAACATGC 61627         TGCG  C   A
            A                    TGCATGTTAT    AG AGG ACA
                                 ||||||||||    || ||| |||
                                 ACGTACAATA    TT TCC TGT
                                       TATA  _   C
GAM393  FLJ11160 3'  TGTTCCTGTTTACAACATGT   37695       TAT  CG
                                 GCATGT   TG  AGCAGGAACA
                                 ||||||   ||  ||||||||||
                                 TGTACA   AC  TTGTCCTTGT
                                    ___  AT
GAM393  KIAA0984 3'  TCTGTGTACCAATAACATGCA  66144          CGA_
                                 TGCATGTTATTG    GCAGG
                                 ||||||||||||    |||||
                                 ACGTACAATAAC    TGTCT
                                        CATG
GAM393  TSPEAR   3'  TCCTGCTTCTGCAACACA    59376     TA   __
                                 TGT  TTGC  GAGCAGGA
                                 |||  ||||  ||||||||
                                 ACA  AACG  TTCGTCCT
                                   C_   TC
GAM393  WBSCR22  3'  TGTTCCTGACTAATAACATG   34472         CGAG
                                 CATGTTATTG    CAGGAACA
                                 ||||||||||    ||||||||
                                 GTACAATAAT    GTCCTTGT
                                       CA__
GAM393  LOC151176 3'  TCCCCAAGTGCAGTAACACACA 86443    CA        AGCA_
                                 TG  TGTTATTGCG    GGA
                                 ||  ||||||||||     |||
                                 AC  ACAATGACGT    CCT
                                  AC         GAACC
GAM393  LOC196411 3'  CCTGTGGGCACAATAACAT    89046        __   GA
                                 ATGTTAT  TGC  GCAGG
                                 |||||||  |||  |||||
                                 TACAATA  ACG  TGTCC
                                     AC   GG
GAM393  LOC197342 3'  CCTGCCCAGCAGGCTGCA    89359     T  TA   GA_
                                 TGCA GT  TTGC   GCAGG
                                 |||| ||  ||||   |||||
                                 ACGT CG  GACG   CGTCC
                                   _ __    ACC
GAM394  DLG5     5'  TCACCCCCTCGCAAGGCCA    83823    A    _  A
                                 TG CCTTG GA GGGGTGG
                                 || ||||| || |||||||
                                 AC GGAAC CT CCCCACT
                                  C    G  C
GAM394  PNUTL1   3'  CCACCCCCTCCCAGGTCA    12189       T   A
                                 TGACCT GGA GGGGTGG
                                 |||||| ||| |||||||
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                                ACTGGA CCT CCCCACC
                                   C   C
GAM394  SLC1A3    5'  ATCTTCCACCCCTTACAAAATC 16061     CC   G       CCC
            A                    TGA  TTG AAGGGGTGG   GGT
                                 |||  ||| |||||||||   |||
                                 ACT  AAC TTCCCCACC   CTA
                                   AA   A       TT_
GAM394  C20orf126 3'  ACCAGCAACCCCCCAGGGTCA  48729         AA    G  CC
                                 TGACCTTGG  GGGGT GC  GGT
                                 |||||||||  ||||| ||  |||
                                 ACTGGGACC  CCCCA CG  CCA
                                      __    A  A_
GAM394  CGI-96    3'  ACCAGGCCACCCCTCGGGTC   32289      TG  A       C
                                 GACCT  GA GGGGTGGCC GGT
                                 |||||  || |||||||||| |||
                                 CTGGG  CT CCCCACCGG CCA
                                    __ _       A
GAM394  FLJ10058  3'  ACCAGGCATTTCTTCCAGG    36255        GG   G  C
                                 CTTGGAAG  GTG CC GGT
                                 ||||||||  ||| || |||
                                 GGACCTTC  TAC GG CCA
                                      TT   _  A
GAM394  GMEB2     3'  ACCAGGCTGAGGCCCCTCCAGG 25657       A    ___    C
                                 CTTGGA GGGGT   GGCC GGT
                                 ||||||| |||||   |||| |||
                                 GGACCT CCCCG   TCGG CCA
                                    _    GAG    A
GAM394  Grcc9     5'  ACCGAGCTCCCTTCCAGGTCA  51958       T      GT   C
                                 TGACCT GGAAGGG  GGC CGGT
                                 ||||||| |||||||  ||| ||||
                                 ACTGGA CCTTCCC  TCG GCCA
                                    _      __   A
GAM394  HSA250839 3'  ACCAGACTTGTCCCCAAGGTC  37847        GAA    TG CCC_
                                 GACCTTG   GGGG  G    GGT
                                 |||||||   ||||  |    |||
                                 CTGGAAC   CCCT  T    CCA
                                      ___    GT CAGA
GAM394  LHX6      3'  ACCAAGCCCTACCCAGGGTCA  27642         AA    GGCCC
                                 TGACCTTGG  GGGGT    GGT
                                 |||||||||  |||||    |||
                                 ACTGGGACC  TCCCG    CCA
                                      CA     AA___
GAM394  PPP2R3A   3'  CCATCGCCTTCCAAAGTCA    12241      C       _
                                 TGAC TTGGAAGG GGTGG
                                 |||| |||||||| |||||
                                 ACTG AACCTTCC CTACC
                                   A       G
GAM394  LOC91695  3'  ACCAGGCCACCCCTCGGGTC   67507      TG  A       C
                                 GACCT  GA GGGGTGGCC GGT
                                 |||||  || |||||||||| |||
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                                CTGGG  CT CCCCACCGG CCA
                                  __ _       A
GAM395  BCL11B   3'  TGTTTAAAAAACCAACACGGAA 43485        A   CTACGAT
              G                   CTTCCGTG TGGT      GACA
                                  |||||||| ||||      ||||
                                  GAAGGCAC ACCA      TTGT
                                     A   AAAAAT_
GAM395  CERD4    3'  TATCGCGCCATCACGGAAG   24882           CTA
                                  CTTCCGTGATGGT   CGATG
                                  ||||||||||||   |||||
                                  GAAGGCACTACCG   GCTAT
                                        C__
GAM395  JJAZ1    3'  TGTCATCGTAAAAGCTGGAA   31715     _  GATGGTC
                                  TTCC GT      TACGATGACA
                                  |||| ||      ||||||||||
                                  AAGG CG      ATGCTACTGT
                                    T  AAA____
GAM395  KCNF1    3'  GTCATCGACAGCACAGAAG   11147     C   ATG   TAC
                                  CTTC GTG   GTC   GATGAC
                                  |||| |||   |||   ||||||
                                  GAAG CAC   CAG   CTACTG
                                    A   GA_   ___
GAM395  PVR      3'  CATAGCAGACCACACAGAAG   22489     C   A     ACG
                                  CTTC GTG TGGTCT   ATG
                                  |||| ||| ||||||   |||
                                  GAAG CAC ACCAGA   TAC
                                    A   _     CGA
GAM395  KIAA0026  5'  TCTAGACCATCCCAGAAG    25392     CGT       C
                                  CTTC   GATGGTCTA GA
                                  ||||   ||||||||| ||
                                  GAAG   CTACCAGAT CT
                                    ACC       _
GAM395  LOC115129 3'  TCATCATACTGAGTCCTCACGG 73628         T  T  AC____
              AAG                   CTTCCGTGA GG CT     GATGA
                                  ||||||||| || ||     |||||
                                  GAAGGCACT CC GA     CTACT
                                       _  T  GTCATA
GAM395  LOC145384 3'  TCATCACTGGCCATCAGAGAA  77720     CG       TAC
                                  TTC  TGATGGTC   GATGA
                                  |||  ||||||||   |||||
                                  AAG  ACTACCGG   CTACT
                                    AG       TCA
GAM395  LOC162952 5'  TATCCTCCGACCATCACGGA   83264           TAC_
                                  TCCGTGATGGTC    GATG
                                  ||||||||||||    ||||
                                  AGGCACTACCAG    CTAT
                                         CCTC
GAM396  CAPN5    3'  TCCTAAGGCCCTGCTGTC    92550       TTAACAA
                                  GACAGT      GCCTTAGGA
                                  ||||||      |||||||||
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                                CTGTCG      CGGAATCCT
                                   TCC____
GAM396  EGFL5    5'  TCACAGGTGCTTGTTTAAACTG 87920    A      _    _  AG
            CCA                    TG CAGTTTAA CAAGC CTT  GA
                                || |||||||| ||||| |||  ||
                                AC GTCAAATT GTTCG GGA  CT
                                 C       T    T   CA
GAM396  MYLK2    3'  TTCCTAAGGCCCAGCTGCCA  53586    A    TAACAA
                                TG CAGTT     GCCTTAGGAA
                                || |||||     ||||||||||
                                AC GTCGA     CGGAATCCTT
                                 C    CC____
GAM396  NOVA1    3'  TTCCCAAGACCCAACAACTGTC 22422        TAACAAGC   A
            A                   TGACAGTT       CTT GGAA
                                ||||||||       ||| ||||
                                ACTGTCAA       GAA CCTT
                                     CAACCCA_   C
GAM396  NPAT     3'  TTCCTAAGGAACTAAATATCA  67812     CA    ACAAG
                                TGA  GTTTA    CCTTAGGAA
                                |||  |||||    |||||||||
                                ACT  TAAAT    GGAATCCTT
                                  A_    CAA__
GAM396  NYX      5'  TTCCTAATAGATCCAAACTGTC 42907        AACAAGCC
                                GACAGTTT       TTAGGAA
                                ||||||||       |||||||
                                CTGTCAAA       AATCCTT
                                     CCTAGAT_
GAM396  TAL1     3'  TTCCTAAGACCTGGGGTTGTCA 13534       TT AACAAGC
                                TGACAG  T      CTTAGGAA
                                ||||||  |      ||||||||
                                ACTGTT  G      GAATCCTT
                                   GG GTCCA__
GAM396  TRPC5    3'  CCTGCGTCGCTAAGACTGTCA  25927        AACA   CT__
                                TGACAGTTT    AGC    TAGG
                                |||||||||    |||    ||||
                                ACTGTCAGA    TCG    GTCC
                                     A___    CTGC
GAM396  ARFGEF2  3'  TTCCATTTTTCTGATTAAACTG 22217          CA  CCTTA_
            TCA                   TGACAGTTTAA  AG     GGAA
                                ||||||||||  ||     ||||
                                ACTGTCAAATT  TC     CCTT
                                      AG  TTTTTA
GAM396  ARHGEF10 3'  TTCCCAAGCTTCTCAAACTGTT 61057        AAC    C  A
            A                   TGACAGTTT   AAGC TT GGAA
                                |||||||||   |||| || ||||
                                ATTGTCAAA   TTCG AA CCTT
                                     CTC    _  C
GAM396  ELL2     3'  CCCAAGACTTGTGTTTGTTA   24892       TTTA    C   A
                                TGACAG    ACAAG CTT GG
                                ||||||    ||||| ||| ||
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                                ATTGTT    TGTTC GAA CC
                                   TG__     A   C
GAM396  EMILIN-2  3'  TTCCCAAAGCTTGTTGGGCTCC 50260    C          C  A
                                A AGTTTAACAAGC TT GGAA
                                | ||||||||||| || ||||
                                C TCGGGTTGTTCG AA CCTT
                                 C          A  C
GAM396  FLJ13909  3'  TTCCTAAGGCTCCTGGACT    47784       ACA
                                AGTTTA   AGCCTTAGGAA
                                ||||||   ||||||||||
                                TCAGGT   TCGGAATCCTT
                                   CC_
GAM396  MGC32043  3'  CCCAAGGCTCCGTGACTGTCA  58660         TAACA     A
                                TGACAGTT     AGCCTT GG
                                ||||||||     |||||| ||
                                ACTGTCAG     TCGGAA CC
                                     TGCC_     C
GAM396  LOC121504 3'  TTCAGGGCCCCCAAACTGTCA  74555          AACAA    A
                                TGACAGTTT     GCCTT GGA
                                |||||||||     ||||| |||
                                ACTGTCAAA     CGGGA CTT
                                     CCCC_    _
GAM396  LOC196955 5'  TCCCAAGGCTTGGCTGTC     77874        TTAA       A
                                GACAGT    CAAGCCTT GGA
                                ||||||    |||||||| |||
                                CTGTCG    GTTCGGAA CCT
                                   ____       C
GAM397  APAF1     3'  ACCTCATTGCAGCCTCAGACTC 25954      AG  A       T
           CT                     AGGA  CT AGGCTGCG TGGGGT
                                ||||  || |||||||| ||||||
                                TCCT  GA TCCGACGT ACTCCA
                                  CA  C       T
GAM397  CNN2      3'  TCTCCAGCCTCAGCCTCCT    16465      A   A     CGTT
                                AGGA GCT AGGCTG    GGGG
                                |||| ||| ||||||    ||||
                                TCCT CGA TCCGAC    CTCT
                                  C   C     ____
GAM397  ELA2      5'  ACCCCGGAGCCCCAGCCCC    10512    AA   AA    G GTT
                                GG  GCT  GGCT C   GGGGT
                                ||  |||  |||| |   |||||
                                CC  CGA  CCGA G   CCCCA
                                 C_   CC    G ___
GAM397  FZD1      5'  ACCCCGGCGCGCCCTAGCCACC 14495    AA    A   T
                                GG  GCTA GGC GCGTTGGGGT
                                ||  |||| ||| ||||||||||
                                CC  CGAT CCG CGCGGCCCCA
                                 AC    C   _
GAM397  ITGAM     3'  ACCCCCAGGCCTCAGTCTCC   72304     AG  A    GCGTT
                                GGA  CT AGGCT     GGGGT
                                |||  || |||||     |||||
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                                CCT  GA TCCGG    CCCCA
                                  CT  C    AC___
GAM397  JAK3    3'  ACCCCTTAAGCCCTGGCCCCCT 5821     AA   A   GCGTT
                                AGG  GCTA GGCT    GGGGT
                                |||  |||| ||||    |||||
                                TCC  CGGT CCGA    CCCCA
                                  CC   C   ATT__
GAM397  KCNK7   5'  ACCCCAGCCACCCCAGCCATCC 54051    A_  AA  C  C
                                GGA  GCT  GG TG GTTGGGGT
                                |||  |||  || || ||||||||
                                CCT  CGA  CC AC CGACCCCA
                                  AC   CC  _ _
GAM397  KRTHA1  3'  CCCAAAGCCTGTAGCCTCC   11235    A   _   GCG
                                GGA GCTA AGGCT   TTGGG
                                ||| |||| |||||   |||||
                                CCT CGAT TCCGA   AACCC
                                  C   G    ___
GAM397  PLXNB2  3'  CCAGCCCCAGCCCCAGCTCCCT 25726    A   AA    C_
                                AGG AGCT  GGCTG  GTTGG
                                ||| ||||  |||||  |||||
                                TCC TCGA  CCGAC  CGACC
                                  C   CC    CC
GAM397  RGS9    5'  ACCCTCTCACCTCAGCCTCC   15167    A  A   C  CGTT
                                GGA GCT AGG TG    GGGGT
                                ||| ||| ||| ||    |||||
                                CCT CGA TCC AC    TCCCA
                                  C   C   _  TC__
GAM397  SARDH   5'  CCCCACACCACCCCAGCTCCCT 24018    A   AA  C  C  _
                                AGG AGCT  GG TG GT TGGGG
                                ||| ||||  || || || |||||
                                TCC TCGA  CC AC CA ACCCC
                                  C   CC  _  _  C
GAM397  SLC22A12 3'  CCCCATGTCCCAGCTCCC    58684    A   AA  CT   T
                                GG AGCT  GG  GCGT GGGG
                                || ||||  ||  |||| ||||
                                CC TCGA  CC  TGTA CCCC
                                 C   __  C_   _
GAM397  ST7     3'  ACCTCTCAGCCTTAGCTCTCC  26471     _        CGTT
                                GGA AGCTAAGGCTG    GGGGT
                                ||| ||||||||||    |||||
                                CCT TCGATTCCGAC    CTCCA
                                  C          T___
GAM397  SYN3    3'  ACCCTCGCCTCACAGCCCCGGC 14476    AA  AA    C___  T
            CCCCT                   AGG  GCT  GGCTG   GT GGGGT
                                |||  |||  |||||   || |||||
                                TCC  CGG  CCGAC   CG TCCCA
                                  CC   CC    ACTC  C
GAM397  TBXA2R  3'  TTCACCAGCCTCAGCCTCC   8371     A  A     C  T
                                GGA GCT AGGCTG GT GGG
                                ||| ||| |||||| || |||
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                                CCT CGA TCCGAC CA CTT
                                  C  C     _ _
GAM397  VIPR1    3'  ACCCCAGTGGCCACTCAGCTTC 17308        AA__   TG GT
            CT                   AGGAAGCT   GGC  C  TGGGGT
                                 ||||||||   |||  |  ||||||
                                 TCCTTCGA   CCG  G  ACCCCA
                                     CTCA   GT __
GAM397  ACY-3    3'  CCCCAACCTCAGTCTTCC    55586     AGCTA     C_
                                 GGA    AGGCTG  GTTGGGG
                                 |||    ||||||  |||||||
                                 CCT    TCTGAC  CAACCCC
                                   _____     TC
GAM397  ATP1B4   3'  TCTCCAGCCTCAGCCTCCT   24854      A  A     CGTT
                                 AGGA GCT AGGCTG    GGGG
                                 |||| ||| ||||||    ||||
                                 TCCT CGA TCCGAC    CTCT
                                   C  C     _____
GAM397  BAD      5'  CCGACAGCCTCAGCTCCCT   53354     A   A    GC
                                 AGG AGCT AGGCT  GTTGG
                                 ||| |||| |||||  |||||
                                 TCC TCGA TCCGA  CAGCC
                                   C   C    __
GAM397  BCL2L1   3'  ACCCCCACACCTCAGTTCCCT  57583     A   A  CTGC  T
                                 AGG AGCT AGG    GT GGGGT
                                 ||| |||| |||    || |||||
                                 TCC TTGA TCC    CA CCCCA
                                   C   C  A___  C
GAM397  BG1      5'  ACCCCAGCTGCCCACAGCTTCC 88654        AA_   TGC
                                 GGAAGCT   GGC   GTTGGGGT
                                 |||||||   |||   ||||||||
                                 CCTTCGA   CCG   CGACCCCA
                                     CAC   T__
GAM397  CCR7     3'  CCCCAATCCCAGCTACCT    10221     A    AA  CTGC
                                 AGG AGCT  GG    GTTGGGG
                                 ||| ||||  ||    |||||||
                                 TCC TCGA  CC    TAACCCC
                                   A   C_  _____
GAM397  CGB5     5'  ACCCCAGCATCCTACAACCTCC 53487      AGCTA_   C   GT
            T                    AGGA     AGG TGC  TGGGGT
                                 ||||     ||| |||  ||||||
                                 TCCT     TCC ACG  ACCCCA
                                   CCAACA   T   __
GAM397  DKFZP434N014 3'  ACCCCAAGGCCCCAGCTTCC   61225        AA    GCG
                                 GGAAGCT  GGCT   TTGGGGT
                                 |||||||  ||||   |||||||
                                 CCTTCGA  CCGG   AACCCCA
                                     CC    ___
GAM397  FLJ00007 3'  ACCCCAGAAGCCCCAATTTCC  71773      CTAA    GCGT
                                 GGAAG    GGCT    TGGGGT
                                 |||||    ||||    ||||||
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                                CCTTT   CCGA   ACCCCA
                                  AACC   AG__
GAM397  FLJ12650  3' ACCCCAACTCTCCCCCAAGCCC 44814    AA  AA  CTGC_
             CT                   AGG  GCT  GG    GTTGGGGT
                                  |||  |||  ||    ||||||||
                                  TCC  CGA  CC    CAACCCCA
                                    C_   AC  CCTCT
GAM397  FLJ12891  3' CAGTGAGCCTCAGCCTCC    46919    A  A    G
                                  GGA GCT AGGCT CGTTG
                                  ||| ||| ||||| |||||
                                  CCT CGA TCCGA GTGAC
                                    C  C    _
GAM397  FLJ14299  3' ACCCCAGCCCCCTCACCCTCCT 47549     AGCTA  CTGC
                                  AGGA    AGG   GTTGGGGT
                                  ||||    |||   ||||||||
                                  TCCT    TCC   CGACCCCA
                                    CCCAC   CC__
GAM397  FLJ14950  3' ACCCCCCGGGCCTCAGTTTCCT 52777       A    G  TT
                                  AGGAAGCT AGGCT CG  GGGGT
                                  |||||||| ||||| ||  |||||
                                  TCCTTTGA TCCGG GC  CCCCA
                                       C    _ C_
GAM397  FLJ20509  5' ACCCCTGTCATCTCAGCCCCCT 35756    AA  A  CT  TT
                                  AGG  GCT AGG  GCG  GGGGT
                                  |||  ||| |||  |||  |||||
                                  TCC  CGA TCT  TGT  CCCCA
                                    CC   C   AC   __
GAM397  FLJ23024  3' TGGCACAACCTCAGCTCACT   46852    GA   A  C  C
                                  AG  AGCT AGG TG GTTG
                                  ||  |||| ||| || ||||
                                  TC  TCGA TCC AC CGGT
                                   AC    C   A  A
GAM397  FLJ23556  3' TCTCCAGCCTCAGCCTCCT    46457     A  A    CGTT
                                  AGGA GCT AGGCTG    GGGG
                                  |||| ||| ||||||    ||||
                                  TCCT CGA TCCGAC    CTCT
                                    C   C     _____
GAM397  FLJ32783  3' ACCCCAACCTCCCTGACTTCCT 59305       CTA   CTGC
                                  AGGAAG   AGG   GTTGGGGT
                                  ||||||   |||   ||||||||
                                  TCCTTC   TCC   CAACCCCA
                                     AG_   CTC_
GAM397  FOXN4    3' CCTCAGCCCCAGCCCGCT    76089    TAA    C_
                                  AGC   GGCTG  GTTGGGG
                                  |||   |||||  |||||||
                                  TCG   CCGAC  CGACTCC
                                    C__    CC
GAM397  GPA33    3' CCAGGCTGCAGCCTCCACTTCC 20568      CTA     _  TG
                                  GGAAG   AGGCTGC GT  GG
                                  |||||   ||||||| ||  ||
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                                CCTTC   TCCGACG CG  CC
                                   ACC      T  GA
GAM397  KIAA0406 3' ATCTCTATAGCCCCAGCTCCCT 61998     A    AA    CGTT
                                AGG AGCT  GGCTG    GGGGT
                                ||| ||||  |||||    |||||
                                TCC TCGA  CCGAT    CTCTA
                                  C   CC    AT__
GAM397  KIAA0441 3' ACCCTCCCACCTTAGCCTCC   29620     A      C  CGTT
                                GGA GCTAAGG TG    GGGGT
                                ||| ||||||| ||    |||||
                                CCT CGATTCC AC    TCCCA
                                  C      _  CC__
GAM397  KIAA1024 3' ACCCCAAGCTCACCCCAGCCTT 69613       _  AA  CT_  G
           CCT                    AGGAAG CT  GG   GC TTGGGGT
                                ||||||  ||  ||   || |||||||
                                TCCTTC GA  CC   CG AACCCCA
                                   C  CC  ACT  _
GAM397  KIAA1089 3' ACCCCAGTACTAGCCTAGCTTC 69427         A    CG_
           C                     GGAAGCTA GGCTG   TTGGGGT
                                |||||||| |||||   |||||||
                                CCTTCGAT CCGAT   GACCCCA
                                     _    CAT
GAM397  KIAA1467 3' TCTCCAGCCTTAGCCTCC    72078     A       CGTT
                                GGA GCTAAGGCTG    GGGG
                                ||| ||||||||||    ||||
                                CCT CGATTCCGAC    CTCT
                                  C         _____
GAM397  KIAA1553 5' CCCCAACATCTACTTCCT    93564       CTA   CTGC
                                AGGAAG   AGG    GTTGGGG
                                ||||||   |||    |||||||
                                TCCTTC   TCT    CAACCCC
                                   A__   A___
GAM397  KIAA1679 3' GGTGCAGCCTTGCCTCCT    70712      A  T
                                AGGA GC AAGGCTGCGTT
                                |||| || ||||||||||
                                TCCT CG TTCCGACGTGG
                                  C  _
GAM397  KIAA1829 3' ACCCTCCCACCTCAGCCTCCT  62625     A   A   C  CGTT
                                AGGA GCT AGG TG    GGGGT
                                |||| ||| ||| ||    |||||
                                TCCT CGA TCC AC    TCCCA
                                  C   C   _  CC__
GAM397  KIAA1855 3' CCCCAACACATGCCTTCC    93949     AGCTA   _  C
                                GGA     AGGC TG GTTGGGG
                                |||     |||| || |||||||
                                CCT     TCCG AC CAACCCC
                                  ______   T  A
GAM397  KIAA1944 3' ACCCTCCCAACCTTAGCCCT   76074     AA      C  CGTT
                                AGG  GCTAAGG TG    GGGGT
                                |||  ||||||| ||    |||||
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                                TCC  CGATTCC AC    TCCCA
                                  __      A  CC__
GAM397  MGC13170  5'  ACCCTTCCAGCCCCAGCCC   52127    AA   AA    CGTT
                                GG  GCT  GGCTG    GGGGT
                                ||  |||  |||||    |||||
                                CC  CGA  CCGAC    TCCCA
                                 __   CC    CT__
GAM397  MGC13186  5'  ACCCCAACCTGGACTGCTCCC  51295    A   TAAGG   C
                                GG AGC    CTG GTTGGGGT
                                || |||    ||| ||||||||
                                CC TCG    GGT CAACCCCA
                                 C   TCA__   C
GAM397  moblak    3'  TCCACCAGCCTCAGCCTCC    56412     A   A     C  T
                                GGA GCT AGGCTG GT GGG
                                ||| ||| |||||| || |||
                                CCT CGA TCCGAC CA CCT
                                  C   C     _ _
GAM397  MRPS27    3'  CAACAGCCTCAGCTTCCT     31324         A    GC
                                AGGAAGCT AGGCT  GTTG
                                |||||||| |||||  ||||
                                TCCTTCGA TCCGA  CAAC
                                     C    __
GAM397  PLA2G6    3'  ACCCCTGCCCCCAGCCCCAGCC 67086     A   AA    C__  T
           TCC                    GGA GCT  GGCTG   GT GGGGT
                                ||| |||  |||||   || |||||
                                CCT CGA  CCGAC   CG CCCCA
                                  C   CC    CCC  T
GAM397  POLR2D    3'  ACCCCGCTGCCTCAGCCTCC   17838     A   A    T  GTT
                                GGA GCT AGGC GC   GGGGT
                                ||| ||| |||| ||   |||||
                                CCT CGA TCCG CG   CCCCA
                                  C   C    T ____
GAM397  PSR       3'  ACCCCCACGCCCACAGCCCCCT 65771     AA   AA  CT    T
                                AGG  GCT  GG  GCGT GGGGT
                                |||  |||  ||  |||| |||||
                                TCC  CGA  CC  CGCA CCCCA
                                  CC   CA  __    C
GAM397  Rab11-FIP3 5'  ACCTCAGGCGCCTCAGCCTCCT 28782      A   A    T  G
                                AGGA GCT AGGC GC TTGGGGT
                                |||| ||| |||| || |||||||
                                TCCT CGA TCCG CG GACTCCA
                                  C   C    _ _
GAM397  RoXaN     3'  ACCCCTCAGAGCCTTGGCTTCC 47269             GCGTT
           T                     AGGAAGCTAAGGCT     GGGGT
                                ||||||||||||||     |||||
                                TCCTTCGGTTCCGA     CCCCA
                                         GACT_
GAM397  SERF1B    3'  TCTCCAGCCTCAGCTTCCT    43704         A     CGTT
                                AGGAAGCT AGGCTG    GGGG
                                |||||||| ||||||    ||||
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                                TCCTTCGA TCCGAC   CTCT
                                    C    ____
GAM397  TMG3     3' CAAAACAGCCTTAGCCTCCT  44220     A       CG
                                AGGA GCTAAGGCTG  TTG
                                |||| ||||||||||  |||
                                TCCT CGATTCCGAC  AAC
                                  C        AA
GAM397  LOC124739 5' CCATCAGCTCAGCTTCCT   74808       AA    CGT
                                AGGAAGCT  GGCTG   TGG
                                ||||||||  |||||   |||
                                TCCTTCGA  TCGAC   ACC
                                    C_    T__
GAM397  LOC135763 3' TCTCCAGCCTCAGCCTCCT   57564     A  A    CGTT
                                AGGA GCT AGGCTG   GGGG
                                |||| ||| ||||||   ||||
                                TCCT CGA TCCGAC   CTCT
                                  C  C    ____
GAM397  LOC142913 5' CCACTGCAGCCTCCACCTCCT 76930     AGCTA      T
                                AGGA    AGGCTGCG TGG
                                ||||    |||||||| |||
                                TCCT    TCCGACGT ACC
                                  CCACC       C
GAM397  LOC143162 5' CCTGGCACCTCAGCTTCCT   77005       A  CTGC  TG
                                AGGAAGCT AGG   GT  GG
                                |||||||| |||   ||  ||
                                TCCTTCGA TCC   CG  CC
                                    C  A___  GT
GAM397  LOC146227 3' ACCCCAGTACCCTCAGTCCCT 78213    AA  A  C  GT
                                AGG  GCT AGG TGC  TGGGGT
                                |||  ||| ||| |||  ||||||
                                TCC  TGA TCC ATG  ACCCCA
                                  C_  C  C  __
GAM397  LOC148137 3' CCCCGGCCTCCACCCCAGCTCC 59092   A   AA  C  C__
          C                      GG AGCT  GG TG   GTTGGGG
                                || ||||  || ||   |||||||
                                CC TCGA  CC AC   CGGCCCC
                                 C   CC  _  CTC
GAM397  LOC148443 3' ACCCTCCCACCTCAGCCTCC  79596    A  A  C  CGTT
                                GGA GCT AGG TG   GGGGT
                                ||| ||| ||| ||   |||||
                                CCT CGA TCC AC   TCCCA
                                  C  C   _  CC__
GAM397  LOC158364 3' CCCAGTGCAGCCCTGCTTCC  82753      TAA
                                GGAAGC  GGCTGCGTTGGG
                                ||||||  ||||||||||||
                                CCTTCG  CCGACGTGACCC
                                   TC_
GAM397  LOC196738 5' CCTGGCACCTCAGCTTCCT   88890       A  CTGC  TG
                                AGGAAGCT AGG   GT  GG
                                |||||||| |||   ||  ||
```

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                                TCCTTCGA TCC    CG  CC
                                    C   A___  GT
GAM397  LOC196955 3'  CAATGGCAGCCTCAGCTCCC   77861    A   A     _
                                GG AGCT AGGCTGC GTTG
                                || |||| ||||||| ||||
                                CC TCGA TCCGACG TAAC
                                 C   C      G
GAM397  LOC204084 5'  CAGCACAACCCGCAGCTTCCT  90992        AA  C_  C
                                AGGAAGCT  GG  TG GTTG
                                ||||||||  ||  || ||||
                                TCCTTCGA  CC  AC CGAC
                                     CG  CA  A
GAM397  LOC219649 3'  ACCTTCCTCAGCCTCAGCTCCC 94539     A   A     CGTT
           T                     AGG AGCT AGGCTG    GGGGT
                                ||| |||| ||||||    |||||
                                TCC TCGA TCCGAC    TTCCA
                                  C   C     TCC_
GAM397  LOC219942 3'  ACGCCCGCAGCCCCGACCTCCT 94990      AGCTAA      TT  G
                                AGGA     GGCTGCG  GG GT
                                ||||     |||||||  || ||
                                TCCT     CCGACGC  CC CA
                                  CCAGCC      __  G
GAM397  LOC253558 5'  ACCCCTACGGAGCCCCAGCTTG 97383    _    AA   G   T
           CC                    GG AAGCT  GGCT CGT GGGGT
                                || |||||  |||| ||| |||||
                                CC TTCGA  CCGA GCA CCCCA
                                 G    CC    G   T
GAM397  LOC253613 3'  CCCAGTGCAGCCCTGCTTCC   97915       TAA
                                GGAAGC   GGCTGCGTTGGG
                                ||||||   ||||||||||||
                                CCTTCG   CCGACGTGACCC
                                   TC_
GAM397  LOC257463 3'  ACCCTCCCACCTCAGCCTCCT  71617     A   A   C  CGTT
                                AGGA GCT AGG TG    GGGGT
                                |||| ||| ||| ||    |||||
                                TCCT CGA TCC AC    TCCCA
                                  C   C   _  CC__
GAM397  LOC90288  3'  ACCCCAACAGTAGTAATCTCCT 62764      AGCTAAG     _
                                AGGA      GCTGC GTTGGGGT
                                ||||      ||||| ||||||||
                                TCCT      TGATG CAACCCCA
                                  CTAA___     A
GAM397  LOC91115  3'  ACCATTCTCCTGCCTCAGCTTC 65537        A    TGCGTTGG
           CT                     AGGAAGCT AGGC       GGT
                                |||||||| ||||       |||
                                TCCTTCGA TCCG       CCA
                                     C    TCCTCTTA
GAM397  LOC91373  3'  ACCTCCAGGCCAGCCTCAGCCT 66401     A   A     C  _   _
           CC                     GGA GCT AGGCTG GT TGG GGT
                                ||| ||| |||||| || ||| |||
```

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                                CCT CGA TCCGAC CG ACC CCA
                                  C  C     _ G  T
GAM397  LOC92973  5'  GCTCAGCCTCAGCTTCCT    71593        A     CGTT  GG
                                AGGAAGCT AGGCTG   GG  T
                                |||||||| ||||||   ||  |
                                TCCTTCGA TCCGAC   TC  G
                                    C     ____  T
GAM398  ALPL     3'  CGCTTGTGGCCAGACCCAGAGG 6647         _  GC_______  CTTG
          CCCTG                  CAGGGCCTC GGG       CG   TG
                                |||||||||  |||       ||   ||
                                GTCCCGGAG CCC       GT   GC
                                     A  AGACC___G  GTTC
GAM398  ATP2B2   5'  CCACAAGCAGCCATCACCCGG  9848    A  CCTCGG  C
                                CC GGG     GGC GCTTGTGG
                                || |||     ||| ||||||||
                                GG CCC     CCG CGAACACC
                                 _  ACTA__  A
GAM398  COL1A1   3'  AGCACCCCCAGGCCCTGG    5389         C   CC
                                CCAGGGCCT GGGG  GCT
                                |||||||||  ||||  |||
                                GGTCCCGGA CCCC  CGA
                                     C   A_
GAM398  DGCR2    3'  CCACAAGCACTCAGGCCACTGG 18897     _    C  GCC
                                CCAG GGCCT GGG   GCTTGTGG
                                |||| ||||| |||   ||||||||
                                GGTC CCGGA CTC   CGAACACC
                                  A    _  A__
GAM398  EDN3     5'  CCACAAGCGGCCGTCCTCCTGG 5480       CCTC  __
                                CCAGGG   GG  GGCCGCTTGTGG
                                ||||||   ||  ||||||||||||
                                GGTCCT   CC  CCGGCGAACACC
                                   _____  TG
GAM398  FAAH     3'  CCACAGTCCACCCCAGACCCTG 44450       C  C   CC_  T
          G                     CCAGGG CT GGGG   GCT GTGG
                                |||||| || ||||   ||| ||||
                                GGTCCC GA CCCC   TGA CACC
                                   A  _   ACC  _
GAM398  GRB14    5'  AGTGGCCCCGAGCGCCCCGG   16892    A   _
                                CC GGGC CTCGGGGCCGCT
                                || |||| ||||||||||||
                                GG CCCG GAGCCCCGGTGA
                                 C   C
GAM398  LZTS1    3'  CCATAGACCCTGAGGCCCTGG  41027           CCGC
                                CCAGGGCCTCGGGG   TTGTGG
                                ||||||||||||||   ||||||
                                GGTCCCGGAGTCCC   GATACC
                                       A___
GAM398  WTAP     5'  CCATTGTGCCTCGAGGCCC   18138          C  TT
                                GGGCCTCGGGGC GC  GTGG
                                |||||||||||| ||  ||||
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                                CCCGGAGCTCCG TG  TACC
                                      _  T_
GAM398  ABTB1    3'  AGCCCCCAAGACCCTGG     51697       C  C    CC
                                CCAGGG CT GGGG  GCT
                                |||||| || ||||  |||
                                GGTCCC GA CCCC  CGA
                                   A  A   __
GAM398  FLJ22169  3'  CACAAGCAGCAGGCCCAGG   44229    A     CGGG  C
                                CC GGGCCT   GC GCTTGTG
                                || ||||||   || |||||||
                                GG CCCGGA   CG CGAACAC
                                 A     _____ A
GAM398  HEMK     3'  CCACAAGCAGGAGCCGGCCTCG 32952    AG   TC  GG  _
           G                     CC  GGCC  GG  CC GCTTGTGG
                                ||  ||||  ||  || ||||||||
                                GG  CCGG  CC  GG CGAACACC
                                 CT   __  GA  A
GAM398  HS6ST    3'  CAATGCCCCGAGGCCTGG    62727      G       CGCTTG
                                CCAGG CCTCGGGGC     TG
                                ||||| |||||||||     ||
                                GGTCC GGAGCCCCG     AC
                                   _       TA_____
GAM398  HS6ST1   3'  CAATGCCCCGAGGCCTGG    17847      G       CGCTTG
                                CCAGG CCTCGGGGC     TG
                                ||||| |||||||||     ||
                                GGTCC GGAGCCCCG     AC
                                   _       TA_____
GAM398  HSA249128 5'  GGGGCCCCGAGGCCTTGG    34561             G
                                CCAGGGCCTCGGGGCC CT
                                |||||||||||||||| ||
                                GGTTCCGGAGCCCCGG GG
                                                _
GAM398  HSJ001348 5'  AGCGGCCGCGAGGCCCTG    62855          G
                                CAGGGCCTCG GGCCGCT
                                |||||||||| |||||||
                                GTCCCGGAGC CCGGCGA
                                      G
GAM398  KIAA0447  3'  CCATCGAAGGCCCTGAGGCCCT 72111             GC  _
           GG                     CCAGGGCCTCGGGGCC  TTG TGG
                                |||||||||||||||  ||| |||
                                GGTCCCGGAGTCCCGG  AGC ACC
                                      A_   T
GAM398  KIAA1030  3'  AGCAGCCCAGAGGCCCTGG   94971         G   C
                                CCAGGGCCTC GGGC GCT
                                |||||||||| |||| |||
                                GGTCCCGGAG CCCG CGA
                                      A   A
GAM398  KIAA1169  5'  AGCAGCCCCGTGGCCCCGG   35875    A    T    C
                                CC GGGCC CGGGGC GCT
                                || ||||| |||||| |||
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                                GG CCCGG GCCCCG CGA
                                 C    T    A
GAM398  KIAA1862  3'  GGCGCCCCCAAGGCCCTGG   69513        C   C
                                CCAGGGCCT GGGG CGCT
                                ||||||||| |||| ||||
                                GGTCCCGGA CCCC GCGG
                                     A   C
GAM398  MAGE-E1   3'  CGATGGCCCCGAGGTCC    48674           C
                                GGGCCTCGGGGCCG TTG
                                |||||||||||||| |||
                                CCTGGAGCCCCGGT AGC
                                          _
GAM398  MGC16332  5'  TGAGCAGCCCGGAGGCCCTGG  57546        G   C
                                CCAGGGCCTC GGGC GCTTG
                                |||||||||| |||| |||||
                                GGTCCCGGAG CCCG CGAGT
                                     G   A
GAM398  MYL9      3'  CCACAGTGACCCCAGAGCCCTG 60612       _ C   C   T
          G                      CCAGGGC CT GGGG CGCT GTGG
                                ||||||| || |||| |||| ||||
                                GGTCCCG GA CCCC GTGA CACC
                                    A _   A   _
GAM398  NDP52     3'  CCACTGTGCTGGGCCCGAGGCC 20666         G _  TT_
          CTG                    CAGGGCCTCGGG CC GC   GTGG
                                ||||||||||| || ||   ||||
                                GTCCCGGAGCCC GG CG   CACC
                                      G  T  TGT
GAM398  NET-6     5'  GCAGCCCCAGGCCCCGG    27702    A    C   C
                                CC GGGCCT GGGGC GC
                                || |||||| ||||| ||
                                GG CCCGGA CCCCG CG
                                 C    _    A
GAM398  SEMA4F    5'  AGTAGCCCCGGGGCCCTG    16206          CG
                                CAGGGCCTCGGGGC  CT
                                |||||||||||||  ||
                                GTCCCGGGGCCCCG  GA
                                       AT
GAM398  LOC112703 3'  CCAGACTTGACCCCAAGACCTC 73877    _ C  C   C  CTTG
          TG                     CAG GG CT GGGG CG   TGG
                                ||| || || |||| ||   |||
                                GTC CC GA CCCC GT   ACC
                                  T  A  A   A  TCAG
GAM398  LOC115051 3'  CAATGCCCCGAGGCCTGG    60676      G       CGCTTG
                                CCAGG CCTCGGGGC     TG
                                ||||| |||||||||     ||
                                GGTCC GGAGCCCCG     AC
                                   _       TA____
GAM398  LOC143915 3'  CCACAGATACCAAAGCCCTGG  83903       CTCG  GCCG  T
                                CCAGGGC   GG   CT GTGG
                                |||||||   ||   || ||||
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                                GGTCCCG   CC   GA CACC
                                    AAA_  ATA_ _
GAM398  LOC148046 3'  GGCGGCCCCAAAGCCTCTGG  85247     _  CTC
                                CCAG GGC  GGGGCCGCT
                                |||| |||  |||||||||
                                GGTC CCG  CCCCGGCGG
                                  T  AAA
GAM398  LOC152283 5'  CCACAAGCCCCCCGACAACCCT 86869      CC_    CC
          GG                    CCAGGG  TCGGGG  GCTTGTGG
                                ||||||  ||||||  ||||||||
                                GGTCCC  AGCCCC  CGAACACC
                                   AAC    C_
GAM398  LOC152441 5'  ACAGCCCTGAAGCCCTG    86913      C     CGCT
                                CAGGGC TCGGGGC   TGT
                                |||||| |||||||   |||
                                GTCCCG AGTCCCG   ACA
                                   A     ____
GAM398  LOC152793 3'  CACCTCCCCAGGGCCCTGG   81547       TC   CCGCTT
                                CCAGGGCC  GGGG    GTG
                                ||||||||  ||||    |||
                                GGTCCCGG  CCCC    CAC
                                    GA   TC____
GAM398  LOC164582 5'  AGCACCCCAGGCCCTGG    83415       C   CC
                                CCAGGGCCT GGGG  GCT
                                ||||||||| ||||  |||
                                GGTCCCGGA CCCC  CGA
                                      _   A_
GAM398  LOC169611 3'  CAGGGGGCCTCGAGGCCCCGG  83638    A         G
                                CC GGGCCTCGGGGCC CTTG
                                || ||||||||||||| ||||
                                GG CCCGGAGCTCCGG GGAC
                                 C          G
GAM398  LOC199733 3'  CCACTAAGCCCCGAGGGCCTGG 91437      G       CGCTT
                                CCAGG CCTCGGGGC    GTGG
                                ||||| |||||||||    ||||
                                GGTCC GGAGCCCCG    CACC
                                   G       AAT__
GAM398  LOC222962 3'  CAGGGGCCCCGAGGCCT    94453          G
                                GGGCCTCGGGGCC CTTG
                                ||||||||||||| ||||
                                TCCGGAGCCCCGG GGAC
                                      _
GAM398  LOC254848 5'  CCACAAGCAAGCTACGCCC   98880     CTCGG  C_
                                GGGC    GGC  GCTTGTGG
                                ||||    |||  ||||||||
                                CCCG    TCG  CGAACACC
                                  CA___   AA
GAM398  LOC255452 3'  CCACGAGCCCCAAGCCCCTG  99390     C  C    CGC
                                CAGGG CT GGGGC   TTGTGG
                                ||||| || |||||   ||||||
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                                GTCCC GA CCCCG   AGCACC
                                  C  A    ___
GAM398  LOC84643  5'  CGCTTGTGGCCAACCCCAAGGG 51768         CG  G_________  CTTG
          CCCTGG                  CCAGGGCCT  GG       CCG    TG
                                |||||||||  ||       |||   ||
                                GGTCCCGGG  CC       GGT   GC
                                    AA  CCAACC___   GTTC
GAM398  LOC90639  3'  CCAGGGTGTGCTCCGAGACCC  64409     C      _    G
                                GGG CTCGGGGC CGCTT TGG
                                ||| |||||||| ||||| |||
                                CCC GAGCCTCG GTGGG ACC
                                  A       T    _
GAM398  LOC92080  3'  CAGGCCTAGCCCCGAAGCCTT  68622      C      C__
                                AGGGC TCGGGGC   GCTTG
                                ||||| |||||||   |||||
                                TTCCG AGCCCCG   CGGAC
                                   A      ATC
GAM398  LOC92305  3'  GCGGCCCCAAAGCCCCTG    57234      C  C_
                                CAGGG CT  GGGGCCGC
                                ||||| ||  ||||||||
                                GTCCC GA  CCCCGGCG
                                   C  AA
GAM399  ELF3      3'  TGACCTTGACCTTGACCAA    16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                   _    AGT  ___
GAM399  JAK2      3'  TGACCTTCATTCTGAGACCAA  18318       CAA       AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_       C_
GAM399  SLC10A2   5'  ACTCTCTGTCTTGACCAA    6590        CAA       A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___        C
GAM399  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM399  KIAA1958  5'  GTGACTTTGAACCCCAAACC   82788      CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM399  MARCKS    3'  ACTTTCCACCCTGCCCA     11411      TTCA    A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
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                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM399  TUB      5' GTGGGACCATCCCTTAAACC  13898     C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A       AG__
GAM399  LOC80298 3' ACTTTTACCTTGAACCA     48062         GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                     A___
GAM400  ELF3     3' TGACCTTGACCTTGACCAA    16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                  _    AGT  ___
GAM400  JAK2     3' TGACCTTCATTCTGAGACCAA  18318       CAA       AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_       C_
GAM400  SLC10A2  5' ACTCTCTGTCTTGACCAA    6590        CAA       A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___        C
GAM400  FLJ10803 3' GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM400  KIAA1958 5' GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM400  MARCKS   3' ACTTTCCACCCTGCCCA     11411     TTCA   A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM400  TUB      5' GTGGGACCATCCCTTAAACC   13898     C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A       AG__
GAM400  LOC80298 3' ACTTTTACCTTGAACCA     48062         GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
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                                ACCAAGTTCC    TTTTCA
                                     A___
GAM401  AF5Q31   5'  CCACTGCCGCAGCCAGGAG   27778       GT   _
                                CTCCTGGT  TGGC GTGG
                                ||||||||  |||| ||||
                                GAGGACCG  GCCG CACC
                                     AC    T
GAM401  AGRN     5'  CCACTGGGGACACCAGGA    79583        GG _
                                TCCTGGTGTT  C GTGG
                                ||||||||||  | ||||
                                AGGACCACAG  G CACC
                                     GG T
GAM401  AKT1     5'  CCATCTGTCACCAGGGG     18961        T  C
                                CTCCTGGTG TGG GTGG
                                ||||||||| ||| ||||
                                GGGGACCAC GTC TACC
                                     T  _
GAM401  ARVCF    5'  CCACGCTGCGCTCCAGGA    9801        T  _
                                TCCTGG GT TGGCGTGG
                                |||||| || ||||||||
                                AGGACC CG GTCGCACC
                                   T  C
GAM401  BCL2L2   5'  CCACGCTGGCCAGGAG     15756        GT
                                CTCCTGGT  TGGCGTGG
                                ||||||||  ||||||||
                                GAGGACCG  GTCGCACC
                                     __
GAM401  BDKRB2   3'  CCGGTAAAACACCGGAG     7109      T    G_  G
                                CTCC GGTGTT  GC TGG
                                |||| ||||||  || |||
                                GAGG CCACAA  TG GCC
                                  _     AA  _
GAM401  CAPN10   3'  CCATTCACAGCCAGGAG     43860        GT  C
                                CTCCTGGT  TGG GTGG
                                ||||||||  ||| ||||
                                GAGGACCG  ACT TACC
                                     AC  _
GAM401  CAPN10   3'  CCATTCACAGCCAGGAG     43863        GT  C
                                CTCCTGGT  TGG GTGG
                                ||||||||  ||| ||||
                                GAGGACCG  ACT TACC
                                     AC  _
GAM401  CAPN10   3'  CCATTCACAGCCAGGAG     43866        GT  C
                                CTCCTGGT  TGG GTGG
                                ||||||||  ||| ||||
                                GAGGACCG  ACT TACC
                                     AC  _
GAM401  CAPN10   3'  CCATTCACAGCCAGGAG     43869        GT  C
                                CTCCTGGT  TGG GTGG
                                ||||||||  ||| ||||
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                                GAGGACCG  ACT TACC
                                    AC  _
GAM401  CAPS    3'  CCACGCCATGCTGACCAGAG  15766    C  __ _
                                CTC TGGT  GT TGGCGTGG
                                ||| ||||  || ||||||||
                                GAG ACCA  CG ACCGCACC
                                  _   GT  T
GAM401  CD244   3'  CCAGTTGGCCACCAGGGG   33503       _ TG  G
                                CTCCTGGTG T  GC TGG
                                ||||||||| |  || |||
                                GGGGACCAC G  TG ACC
                                    C GT  _
GAM401  CD7     3'  CCACGCCGCCACCGGGAG   21542       T
                                CTCCTGGTG TGGCGTGG
                                ||||||||| ||||||||
                                GAGGGCCAC GCCGCACC
                                    C
GAM401  CELL    3'  CCACAGTGACCGACCAGGAG  10168       __   GC
                                CTCCTGGT  GTTG  GTGG
                                ||||||||  ||||  ||||
                                GAGGACCA  CAGT  CACC
                                    GC   GA
GAM401  CHST6   3'  CCATCAGCTACCAGGAG    41499       _   GC
                                CTCCTGGT GTTG  GTGG
                                |||||||| ||||  ||||
                                GAGGACCA CGAC  TACC
                                    T  __
GAM401  CKM     3'  CCACCCCAACCAGGAG     10199       GT  C
                                CTCCTGGT  TGG GTGG
                                ||||||||  ||| ||||
                                GAGGACCA  ACC CACC
                                    __  C
GAM401  CPLX2   5'  CCAGGCCAGCCAGGAG     22818       GT   G
                                CTCCTGGT  TGGC TGG
                                ||||||||  |||| |||
                                GAGGACCG  ACCG ACC
                                    __   G
GAM401  CRY2    3'  CCACAGTGCTGCCAGTGAG   72659    _   GTT  ___
                                CTC CTGGT  GGC  GTGG
                                ||| |||||  |||  ||||
                                GAG GACCG  TCG  CACC
                                  T   ___  TGA
GAM401  CSPG4   3'  CCTGGAGACACCAGGGG    10324        GG  T
                                CTCCTGGTGTT  CG GG
                                ||||||||||  || ||
                                GGGGACCACAG  GT CC
                                    AG  _
GAM401  DAG1    3'  CCATTGCCCACCGGGAG    16548        TT  _
                                CTCCTGGTG  GGCG TGG
                                |||||||||  |||| |||
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                                GAGGGCCAC  CCGT ACC
                                    __   T
GAM401  DDX11   3'  CCAGTTTCACCGGGAG     48386        TT  G
                                CTCCTGGTG  GGC TGG
                                |||||||||  ||| |||
                                GAGGGCCAC  TTG ACC
                                    T_  _
GAM401  F2RL3   3'  CCACCAGCAGCCAGGAG     15506       _    CG
                                CTCCTGG TGTTGG  TGG
                                |||||||  ||||||  |||
                                GAGGACC ACGACC  ACC
                                   G    __
GAM401  FGA     3'  CCATTCAGTACATCAGGA    6701         __  C
                                TCCTGGTGT  TGG GTGG
                                |||||||||  ||| ||||
                                AGGACTACA  ACT TACC
                                    TG  _
GAM401  FHL2    5'  CCACGCCCGGTGCCAGCGAG  9364     _   TG  _
                                CTC CTGG  TTGG CGTGG
                                |||  ||||  |||| |||||
                                GAG GACC  GGCC GCACC
                                  C   GT   C
GAM401  GTF2H1  3'  CCACGCCAACTCCCAGAG    19209    CT  T
                                CTC  GG GTTGGCGTGG
                                |||  ||  ||||||||||
                                GAG  CC CAACCGCACC
                                  AC  T
GAM401  IL1F5   5'  CCACAGCTCCCGCCAGGAG   25375       TT  _
                                CTCCTGGTG  GGC GTGG
                                |||||||||  ||| ||||
                                GAGGACCGC  TCG CACC
                                    CC   A
GAM401  ITGB2   5'  CCACGCCCAGCCAGGAG     5799        GTT
                                CTCCTGGT   GGCGTGG
                                ||||||||   |||||||
                                GAGGACCG   CCGCACC
                                   AC_
GAM401  KNSL1   5'  CCACGCAGCGCCCGAG      16942    CT     G
                                CTC  GGTGTTG CGTGG
                                |||  ||||||| |||||
                                GAG  CCGCGAC GCACC
                                  C_     _
GAM401  LFG     3'  CCTGAAACACCAGGAG      77232         GG  T
                                CTCCTGGTGTT  CG GG
                                ||||||||||  || ||
                                GAGGACCACAA  GT CC
                                    A_  _
GAM401  LGALS3BP 3' CCACTAGGGTCCACCAGGAG  69858        TT  ____
                                CTCCTGGTG  GGC   GTGG
                                |||||||||  |||   ||||
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                                GAGGACCAC  CTG   CACC
                                    __  GGAT
GAM401  LMNA    5'  CCACGCCTGCCAGGAG     19929       GTT
                                CTCCTGGT  GGCGTGG
                                ||||||||  |||||||
                                GAGGACCG  CCGCACC
                                   T__
GAM401  OVOL1   5'  CCACAGCCCTACCGGGAG    17062        TT  _
                                CTCCTGGTG  GGC GTGG
                                |||||||||  ||| ||||
                                GAGGGCCAT  CCG CACC
                                    C_  A
GAM401  PCTK1   3'  CCACGGCCAGCCAGGGG    21677        GT  _
                                CTCCTGGT  TGGC GTGG
                                ||||||||  |||| ||||
                                GGGGACCG  ACCG CACC
                                    __  G
GAM401  PCTK1   3'  CCACGGCCAGCCAGGGG    53414        GT  _
                                CTCCTGGT  TGGC GTGG
                                ||||||||  |||| ||||
                                GGGGACCG  ACCG CACC
                                    __  G
GAM401  PCTK1   3'  CCACGGCCAGCCAGGGG    53423        GT  _
                                CTCCTGGT  TGGC GTGG
                                ||||||||  |||| ||||
                                GGGGACCG  ACCG CACC
                                    __  G
GAM401  PFKL    5'  CCACGCCAAGCTGGAG     12054     T  G
                                CTCC GGT TTGGCGTGG
                                ||||  ||| |||||||||
                                GAGG TCG AACCGCACC
                                  _  _
GAM401  PLXNB3  5'  CCACGCCGCCCAGGAG     19407       T  T
                                CTCCTGG GT GGCGTGG
                                |||||||  ||  |||||||
                                GAGGACC CG CCGCACC
                                   _  _
GAM401  PYGB    3'  CCAGTGCCCACCAGGAG     12688        TT  _
                                CTCCTGGTG  GGCG TGG
                                |||||||||  ||||  |||
                                GAGGACCAC  CCGT ACC
                                    __  G
GAM401  RABIF   3'  CCACACAAGTCAGGAG     12724        G  GC
                                CTCCTGGT TTG  GTGG
                                ||||||||  |||  ||||
                                GAGGACTG AAC  CACC
                                    _  A_
GAM401  RNASEH1 5'  CCACGCTGGGCCGGGAG    12876        G TG
                                CTCCTGGT T  GCGTGG
                                ||||||||  |  ||||||
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                                GAGGGCCG G  CGCACC
                                     _ GT
GAM401  SCN4A    3'  CCACGCCAGGCCAGCAG     6196     C    G
                                CT CTGGT TTGGCGTGG
                                || ||||| |||||||||
                                GA GACCG GACCGCACC
                                 C    _
GAM401  SLC13A4  3'  CCACTAGGACCACCAGGAG   25860         _ GGC
                                CTCCTGGTG TT   GTGG
                                ||||||||| ||   ||||
                                GAGGACCAC AG   CACC
                                      C  GAT
GAM401  SLC22A12 5'  CCAAGTGACACCAGCAG     58682    C       G G
                                CT CTGGTGTTG C TGG
                                || ||||||||| | |||
                                GA GACCACAGT G ACC
                                 C        _ A
GAM401  SLC22A12 5'  CCACAGCCGCCAGGAG      58683        GTT  _
                                CTCCTGGT   GGC GTGG
                                ||||||||   ||| ||||
                                GAGGACCG   CCG CACC
                                     ____  A
GAM401  TCF2     3'  CCACAGCGATCCACGGAG    22403     _  T   GC
                                CTCC TGG GTTG  GTGG
                                |||| ||| ||||  ||||
                                GAGG ACC TAGC  CACC
                                  C  _   GA
GAM401  THY1     3'  CCACCCCTCATCAGGAG     21896        TT  C
                                CTCCTGGTG  GG GTGG
                                |||||||||  || ||||
                                GAGGACTAC  CC CACC
                                      TC  _
GAM401  TSG      3'  CCACCTAGAGCACCAGGA    40603         __  C
                                TCCTGGTGT  TGG GTGG
                                |||||||||  ||| ||||
                                AGGACCACG  ATC CACC
                                      AG  _
GAM401  ZNF76    3'  CCACACCATGCTGGAG      14268     T    T  C
                                CTCC GGTGT GG GTGG
                                |||| ||||| || ||||
                                GAGG TCGTA CC CACC
                                  _    _ A
GAM401  AGS3     5'  CCACGGCGAGCCCCAGGAG   73508       T   G  _
                                CTCCTGG GTT GC GTGG
                                ||||||| ||| || ||||
                                GAGGACC CGA CG CACC
                                     C  G  G
GAM401  AMOT     5'  CCACAGCAGCAGCCAGGAG   56538        _    GC
                                CTCCTGG TGTTG  GTGG
                                ||||||| |||||  ||||
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                                GAGGACC ACGAC  CACC
                                    G    GA
GAM401  APOARGC   3'  CCACACCGGCATCAGAG    44673    C      C
                                CTC TGGTGTTGG GTGG
                                ||| ||||||||| ||||
                                GAG ACTACGGCC CACC
                                  _       A
GAM401  ARHGEF16  5'  CCAGCTCTACCAGGAG     27819       TT  G
                                CTCCTGGTG  GGC TGG
                                |||||||||  ||| |||
                                GAGGACCAT  TCG ACC
                                     C_  _
GAM401  BCL2L1    3'  CCATTGCCACCAGGAG     57589       GTT   _
                                CTCCTGGT   GGCG TGG
                                ||||||||   |||| |||
                                GAGGACCA   CCGT ACC
                                    ____   T
GAM401  BICD2     3'  CCAGGCTCGCCAGGAG     70907       TT  G
                                CTCCTGGTG  GGC TGG
                                |||||||||  ||| |||
                                GAGGACCGC  TCG ACC
                                    __  G
GAM401  BM-002    3'  CTATGAAAACACCAGGAG   34007         GG
                                CTCCTGGTGTT  CGTGG
                                ||||||||||  |||||
                                GAGGACCACAA  GTATC
                                     AA
GAM401  BM046     3'  CCACGTTGTCACCGGAG    38057    T   T
                                CTCC GGTG TGGCGTGG
                                |||| |||| ||||||||
                                GAGG CCAC GTTGCACC
                                  _   T
GAM401  C11orf9   3'  CCACACCAGGGACCAGGGG  26117       G _  C
                                CTCCTGGT T TGG GTGG
                                |||||||| | ||| ||||
                                GGGGACCA G ACC CACC
                                    G G   A
GAM401  C9orf5    3'  CCTGAAATACCAGGAG     50105         GG  T
                                CTCCTGGTGTT  CG GG
                                ||||||||||  || ||
                                GAGGACCATAA  GT CC
                                     A_  _
GAM401  CENTG2    5'  CCACGCCACGGCCAGGAG   30537       GT
                                CTCCTGGT  TGGCGTGG
                                ||||||||  ||||||||
                                GAGGACCG  ACCGCACC
                                    GC
GAM401  CGI-96    3'  CCACACAGGCCAGGAG     32291       G  GC
                                CTCCTGGT TTG  GTGG
                                |||||||| |||  ||||
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                                GAGGACCG GAC  CACC
                                   _  A_
GAM401  DGKZ     3'  CCACGGGCAGCAGGAG      14678       G   GG
                                CTCCTG TGTT  CGTGG
                                ||||||| ||||  |||||
                                GAGGAC ACGG  GCACC
                                   G   __
GAM401  DKFZP586P0123 5'  CCATCTCACAGCACCAGGAG  96495          GC__
                                CTCCTGGTGTTG   GTGG
                                ||||||||||||   ||||
                                GAGGACCACGAC   TACC
                                      ACTC
GAM401  DLAD     5'  CCACCTTTCACCAGGAG     55263         TT  C
                                CTCCTGGTG  GG GTGG
                                |||||||||  || ||||
                                GAGGACCAC  TC CACC
                                     TT  _
GAM401  EAT2     3'  CCAGACATATACCAGGAG    80048          _ GCG
                                CTCCTGGTGT TG   TGG
                                |||||||||| ||   |||
                                GAGGACCATA AC   ACC
                                     T  AG_
GAM401  EPN2     5'  CCACGCCGGCCCGGAG      31037      T  T
                                CTCC GG GTTGGCGTGG
                                |||| || ||||||||||
                                GAGG CC CGGCCGCACC
                                  _ _
GAM401  FLJ11175  3'  CCTTGAGAACAGCCAGGAG   37715        _   GG  T
                                CTCCTGG TGTT  CG GG
                                ||||||| ||||  || ||
                                GAGGACC ACAA  GT CC
                                   G   GA  T
GAM401  FLJ11457  3'  CCATCTGTCATCAGGAG     45726         T   C
                                CTCCTGGTG TGG GTGG
                                ||||||||| ||| ||||
                                GAGGACTAC GTC TACC
                                     T  _
GAM401  FLJ11807  3'  CCACAAGGGCCAACCAGGAG  46943        GT   _____
                                CTCCTGGT  TGGC   GTGG
                                ||||||||  ||||   ||||
                                GAGGACCA  ACCG   CACC
                                     __   GGAA
GAM401  FLJ12242  5'  CCACGCGGAGCCAGGAG     45499        G  G
                                CTCCTGGT TT GCGTGG
                                |||||||| || ||||||
                                GAGGACCG AG CGCACC
                                     _ G
GAM401  FLJ12436  5'  CCACGCCAGATCTCAGGA    45414       TG_
                                TCCTGG   TTGGCGTGG
                                ||||||   |||||||||
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                                AGGACT   GACCGCACC
                                   CTA
GAM401   FLJ14001  5'  CCACTTCACGACACCGGAG   45489     T     GC__
                                CTCC GGTGTTG   GTGG
                                |||| |||||||   ||||
                                GAGG CCACAGC   CACC
                                  _     ACTT
GAM401   FLJ14146  3'  CCACTCTGTCACCAGGAG    45567       T  C
                                CTCCTGGTG TGG GTGG
                                ||||||||| ||| ||||
                                GAGGACCAC GTC CACC
                                     T  T
GAM401   FLJ14824  3'  CCACCTAAAGACCAGGAG    52715       G_  C
                                CTCCTGGT  TTGG GTGG
                                ||||||||  |||| ||||
                                GAGGACCA  AATC CACC
                                    GA  _
GAM401   FLJ20281  5'  CCATTCAACACCCAGAG     92622    CT     C
                                CTC  GGTGTTGG GTGG
                                |||  |||||||| ||||
                                GAG  CCACAACT TACC
                                  AC      _
GAM401   FLJ20506  5'  CCACGCGCCGCCAGGGG     35722       TTG
                                CTCCTGGTG   GCGTGG
                                |||||||||   ||||||
                                GGGGACCGC   CGCACC
                                     CG_
GAM401   FLJ22037  5'  CCACGCTCAGCCAGGAG     95533       GTT
                                CTCCTGGT   GGCGTGG
                                ||||||||   |||||||
                                GAGGACCG   TCGCACC
                                    AC_
GAM401   FLJ22282  5'  CCACGCGGCGCCAGCGAG    45964    _      G
                                CTC CTGGTGTTG CGTGG
                                ||| ||||||||| |||||
                                GAG GACCGCGGC GCACC
                                  C       _
GAM401   GBTS1    5'  CCAGCGGACACCGGAG      59721     T    G  G
                                CTCC GGTGTT GC TGG
                                |||| |||||| || |||
                                GAGG CCACAG CG ACC
                                  _     G  _
GAM401   HSU47926  3'  CTGTGTGACATCAGGAG     27308         G  TG
                                CTCCTGGTGTTG CG  G
                                ||||||||||||| ||  |
                                GAGGACTACAGT GT  C
                                       _ GT
GAM401   KIAA0140  3'  CCACGCAGCAGTCAGGGG    28507       _    G
                                CTCCTGG TGTTG CGTGG
                                ||||||| ||||| |||||
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                                GGGGACT ACGAC GCACC
                                   G    _
GAM401  KIAA0169 5' CCACGGCGCACCACGAG     73178     C     T G
                                CTC TGGTGT G CGTGG
                                ||| |||||| | |||||
                                GAG ACCACG C GCACC
                                  C     _ G
GAM401  KIAA0447 3' CCAGGGTCCACCGGGAG     72110         TT   G_
                                CTCCTGGTG  GGC  TGG
                                |||||||||  |||  |||
                                GAGGGCCAC  CTG  ACC
                                     __   GG
GAM401  KIAA0618 3' CCAGCTCACAGCAGGAG     29850       G   T   G
                                CTCCTG TGT GGC TGG
                                |||||| ||| ||| |||
                                GAGGAC ACA TCG ACC
                                   G   C   _
GAM401  KIAA0720 5' CCACGCCGACTGCCAGCAG   62978    C     _
                                CT CTGGT GTTGGCGTGG
                                || ||||| ||||||||||
                                GA GACCG CAGCCGCACC
                                 C     T
GAM401  KIAA0773 3' CCACGCCAGGCCCAAGAG    28720     C   TG
                                CTC TGG  TTGGCGTGG
                                ||| |||  |||||||||
                                GAG ACC  GACCGCACC
                                  A   CG
GAM401  KIAA0855 5' CCACTTCCCATCAGGAG     31107         TT  C_
                                CTCCTGGTG  GG  GTGG
                                |||||||||  ||  ||||
                                GAGGACTAC  CC  CACC
                                     __  TT
GAM401  KIAA1001 3' CCACGCCGACCCGAGAG     31004     C   T
                                CTC TGG GTTGGCGTGG
                                ||| ||| ||||||||||
                                GAG GCC CAGCCGCACC
                                  A   _
GAM401  KIAA1016 5' CCATCAGCACCACGGAG     93383      _      GC
                                CTCC TGGTGTTG  GTGG
                                |||| ||||||||  ||||
                                GAGG ACCACGAC  TACC
                                  C       __
GAM401  KIAA1026 3' CCAGAAATAACCACCAGGAG  71733          _  GCG_
                                CTCCTGGTG TTG    TGG
                                ||||||||| |||    |||
                                GAGGACCAC AAT    ACC
                                     C   AAAG
GAM401  KIAA1465 5' CCACGCCGGGTCTGGAG     61487      T  TG
                                CTCC GG  TTGGCGTGG
                                |||| ||  |||||||||
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                                GAGG TC  GGCCGCACC
                                  _ TG
GAM401  KIAA1615  5'  CCACGTGGAGCCGGGAG    69272       G  G
                                CTCCTGGT TT GCGTGG
                                |||||||| || ||||||
                                GAGGGCCG AG TGCACC
                                    _ G
GAM401  MGC14859  3'  CCTTGTACACTAGGAG     62599        TG   T
                                CTCCTGGTGT  GCG GG
                                ||||||||||  ||| ||
                                GAGGATCACA  TGT CC
                                     __  T
GAM401  MGC15716  3'  CCGGTGGATACCAGGAG    51403         G  G
                                CTCCTGGTGTT GC TGG
                                |||||||||| || |||
                                GAGGACCATAG TG GCC
                                     G _
GAM401  MGC2734   5'  CCACGCCGAGGCCACGAG   53578    C   G
                                CTC TGGT TTGGCGTGG
                                ||| |||| |||||||||
                                GAG ACCG AGCCGCACC
                                  C   G
GAM401  MGC33182  5'  CCACGCCCTGTAACACCGGGA  76093        ____
                                TCCTGGTGTT   GGCGTGG
                                ||||||||||   |||||||
                                AGGGCCACAA   CCGCACC
                                     TGTC
GAM401  MGC3771   5'  CCACACCAAGGACACCAGGAG  49051        ___  C
                                CTCCTGGTGT   TGG GTGG
                                ||||||||||   ||| ||||
                                GAGGACCACA   ACC CACC
                                     GGA   A
GAM401  MY050     3'  CCATTCCAAACCAGGAG     51917       G   C
                                CTCCTGGT TTGG GTGG
                                |||||||| |||| ||||
                                GAGGACCA AACC TACC
                                    _   T
GAM401  NIR3      3'  CCAGCCCCGCCAGGAG      66823        TT   G
                                CTCCTGGTG  GGC TGG
                                |||||||||  ||| |||
                                GAGGACCGC  CCG ACC
                                     C_  _
GAM401  PIP5K2B   3'  CCAGGTCAACACCAGAG     14528     C       G
                                CTC TGGTGTTGGC TGG
                                ||| |||||||||| |||
                                GAG ACCACAACTG ACC
                                  _       G
GAM401  PRO2900   3'  CCACGCCGGCTGAGGTAG    38438    _  GGT
                                CT CCT   GTTGGCGTGG
                                || |||   ||||||||||
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                                GA GGA   CGGCCGCACC
                                 T  GT_
GAM401  PRO2949   5' CCAGGTCAACACCAGTAG    38220    C        G
                                CT CTGGTGTTGGC TGG
                                || |||||||||| |||
                                GA GACCACAACTG ACC
                                  T         G
GAM401  RP4-622L5 3' CCAGCTCTCAGCCAGGAG    39423       _ TT   G
                                CTCCTGG TG  GGC TGG
                                ||||||| ||  ||| |||
                                GAGGACC AC  TCG ACC
                                    G  TC  _
GAM401  SH3BGRL2  5' CCACGCCAGCCCGGAG      49677      T  T
                                CTCC GG GTTGGCGTGG
                                |||| || ||||||||||
                                GAGG CC CGACCGCACC

                                  _ _
GAM401  SHAPY     3' CCACGGTGGGCCGGAG      57904      T   G   G
                                CTCC GGT TTG CGTGG
                                |||| ||| ||| |||||
                                GAGG CCG GGT GCACC
                                  _  _  G
GAM401  SIAT8C    5' CCACCTAGCCCATCAGGAG   32444         TT  ___
                                CTCCTGGTG  GGC   GTGG
                                |||||||||  |||   ||||
                                GAGGACTAC  CCG   CACC
                                     __  ATC
GAM401  SLC39A3   3' CCACAGCCACCAGGAG      58600         GTT  _
                                CTCCTGGT   GGC GTGG
                                ||||||||   ||| ||||
                                GAGGACCA   CCG CACC
                                    ___  A
GAM401  STK29     3' CCACGCCGCACCTGGAG     88961      T    T
                                CTCC GGTGT GGCGTGG
                                |||| ||||| |||||||
                                GAGG CCACG CCGCACC
                                  T    _
GAM401  LOC122886 3' CCAGTCACACCAAAGAG     76106     C_     T   G
                                CTC  TGGTGT GGC TGG
                                |||  |||||| ||| |||
                                GAG  ACCACA CTG ACC
                                  AA     _  _
GAM401  LOC124930 3' CCACGCCCAGGGCCAGGAG   74823         G   _
                                CTCCTGGT TTGG CGTGG
                                |||||||| |||| |||||
                                GAGGACCG GACC GCACC
                                     G   C
GAM401  LOC125268 3' CCACACCGAAGCCAGGGG    76572         G   C
                                CTCCTGGT TTGG GTGG
                                |||||||| |||| ||||
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                                GGGGACCG AGCC CACC
                                     A   A
GAM401   LOC143158 5'  CCACGTTCGTGACCGGGAG   76998       GT  _
                                CTCCTGGT  TGG CGTGG
                                ||||||||  ||| |||||
                                GAGGGCCA  GCT GCACC
                                     GT   T
GAM401   LOC144395 3'  CCACCTTGGCACCAGGAG    77320        TG C
                                CTCCTGGTGT  G GTGG
                                ||||||||||  | ||||
                                GAGGACCACG  T CACC
                                      GT C
GAM401   LOC145988 5'  CCACTTCCCATCAGGAG     78063       TT  C_
                                CTCCTGGTG  GG  GTGG
                                |||||||||  ||  ||||
                                GAGGACTAC  CC  CACC
                                     __  TT
GAM401   LOC146880 3'  CCATGTCCACCAATGAG     78747     C_    TT
                                CTC  TGGTG  GGCGTGG
                                |||  |||||  |||||||
                                GAG  ACCAC  CTGTACC
                                  TA    __
GAM401   LOC148148 5'  CCACAGCTAAGACACCAGGA   79378         __  _
                                TCCTGGTGTT  GGC GTGG
                                ||||||||||  ||| ||||
                                AGGACCACAG  TCG CACC
                                      AA   A
GAM401   LOC148753 3'  CCACGGGTAGGCACCAGGGG   85369          GG__
                                CTCCTGGTGTT    CGTGG
                                ||||||||||    |||||
                                GGGGACCACGG    GCACC
                                       ATGG
GAM401   LOC148764 3'  CCACGCCACTTCACACCAGGG  79734        ____
                                TCCTGGTGT    TGGCGTGG
                                |||||||||    ||||||||
                                GGGACCACA    ACCGCACC
                                     CTTC
GAM401   LOC149832 5'  CCACGGAGGGGCCAGGAG    85862        G  GG
                                CTCCTGGT TT  CGTGG
                                |||||||| ||  |||||
                                GAGGACCG GG  GCACC
                                     G  AG
GAM401   LOC150135 3'  CCAGCTGACACCAGGAG     80390         TG  G
                                CTCCTGGTGT  GC TGG
                                ||||||||||  || |||
                                GAGGACCACA  CG ACC
                                      GT  _
GAM401   LOC150135 3'  CCAGCTGACACCAGGAG     80391         TG  G
                                CTCCTGGTGT  GC TGG
                                ||||||||||  || |||
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                                GAGGACCACA  CG ACC
                                      GT  _
GAM401   LOC151361 3'  CCACGACTGCCAGGAG      86501        GTT  _
                                CTCCTGGT   GG CGTGG
                                ||||||||   || |||||
                                GAGGACCG   TC GCACC
                                    ____  A
GAM401   LOC152286 3'  CCACACTAGACAGCCAGGAG   86805        _  _  C
                                CTCCTGG TGT TGG GTGG
                                ||||||| ||| ||| ||||
                                GAGGACC ACA ATC CACC
                                    G   G   A
GAM401   LOC152317 5'  CCACACAGCGAGCCAGGGG   86826         __   GC
                                CTCCTGGT  GTTG  GTGG
                                ||||||||  ||||  ||||
                                GGGGACCG  CGAC  CACC
                                     AG    A_
GAM401   LOC152453 5'  CCACACAATGCCAGAG      81467     C       GC
                                CTC TGGTGTTG  GTGG
                                ||| ||||||||  ||||
                                GAG ACCGTAAC  CACC
                                  _       A_
GAM401   LOC153196 5'  CCACGCCATGGAGCCAGGGG   87165         GT__
                                CTCCTGGT    TGGCGTGG
                                ||||||||    ||||||||
                                GGGGACCG    ACCGCACC
                                     AGGT
GAM401   LOC157653 5'  CCACGTCAACCAGGAG      82443         GT
                                CTCCTGGT  TGGCGTGG
                                ||||||||  ||||||||
                                GAGGACCA  ACTGCACC
                                      __
GAM401   LOC157860 3'  CCATCGAGACACCATGGA    87877     _      GG  _
                                TCC TGGTGTT  CG TGG
                                ||| |||||||  || |||
                                AGG ACCACAG  GC ACC
                                  T      A_  T
GAM401   LOC159199 3'  CCACAGCCAACACCAGCAG    83058    C         _
                                CT CTGGTGTTGGC GTGG
                                || ||||||||||| ||||
                                GA GACCACAACCG CACC
                                 C          A
GAM401   LOC200597 3'  CCATTACCACCAGGAG      90256         T  GC
                                CTCCTGGTG TG  GTGG
                                |||||||||  ||  ||||
                                GAGGACCAC AT  TACC
                                      C  __
GAM401   LOC202404 5'  CCACGCCAAGTCCGCCCAGG   90649       _  ____
                                CCTGG TG   TTGGCGTGG
                                ||||| ||   |||||||||
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                                GGACC GC   AACCGCACC
                                   C  CTG
GAM401   LOC203113 3'  CCACAAGTTAACATCAAGA   90793    C       __
                                TC TGGTGTTGGC  GTGG
                                || ||||||||||  ||||
                                AG ACTACAATTG  CACC
                                 A         AA
GAM401   LOC204275 3'  CCATCATTAACACCAAGA    91004    C       C_
                                TC TGGTGTTGG  GTGG
                                || |||||||||  ||||
                                AG ACCACAATT  TACC
                                 A        AC
GAM401   LOC205418 5'  CCACGCATGCTGACCAGGG   92370       __ TG
                                TCCTGGT  GT  GCGTGG
                                |||||||  ||  ||||||
                                GGGACCA  CG  CGCACC
                                     GT  TA
GAM401   LOC253712 5'  CCACACCCTGCAGCGGGAG   98726      G  T_  C
                                CTCCTG TGT  GG GTGG
                                |||||| |||  || ||||
                                GAGGGC ACG  CC CACC
                                   G   TC  A
GAM401   LOC256306 5'  CCACGCCAAGGGGCTAGG    98506      G__
                                CCTGGT   TTGGCGTGG
                                ||||||   |||||||||
                                GGATCG   AACCGCACC
                                   GGG
GAM401   LOC51162  5'  CCACGCCTGGGCTCCAGCAG  66397    C   T  __
                                CT CTGG GTT  GGCGTGG
                                || |||| |||  |||||||
                                GA GACC CGG  CCGCACC
                                 C   T   GT
GAM401   LOC51162  5'  CCACGCCTGGGCTCCAGCAG  33049    C   T  __
                                CT CTGG GTT  GGCGTGG
                                || |||| |||  |||||||
                                GA GACC CGG  CCGCACC
                                 C   T   GT
GAM401   LOC55565  3'  CCACACCCACAGCCACGAG   34473    C  _  T  C
                                CTC TGG TGT GG GTGG
                                ||| ||| ||| || ||||
                                GAG ACC ACA CC CACC
                                  C  G  C  A
GAM401   LOC90906  3'  CCACAGCTGCTAGGAG      64949       GTT  _
                                CTCCTGGT   GGC GTGG
                                ||||||||   ||| ||||
                                GAGGATCG   TCG CACC
                                     ___   A
GAM401   LOC91145  3'  CCACACCATGCTGAGGTAG   65681    _  _   T  C
                                CT CCT GGTGT GG GTGG
                                || ||| ||||| || ||||
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                                GA GGA TCGTA CC CACC
                                 T  G    _ A
GAM401  LOC91695  3'  CCACACAGGCCAGGAG     67509        G  GC
                                CTCCTGGT TTG  GTGG
                                |||||||| |||  ||||
                                GAGGACCG GAC  CACC
                                     _  A_
GAM402  BRCA1    3'  GTACAGAGCCCAGGACCCCAAG 24449    C       CA  ___
          A                      TC TGGGGTCCTG  GGT   GTAC
                                || ||||||||||  |||   ||||
                                AG ACCCCAGGAC  CCG   CATG
                                 A         __   AGA
GAM402  BRCA1    3'  GTACAGAGCCACAGGACCCCAA 24461    C       CA  ___
          GA                     TC TGGGGTCCTG  GGT   GTAC
                                || ||||||||||  |||   ||||
                                AG ACCCCAGGAC  CCG   CATG
                                 A         A_   AGA
GAM402  BRCA1    3'  GTACAGGCCACAGGACCCCAAG 24472    C       CA  __
          A                      TC TGGGGTCCTG  GGT  GTAC
                                || ||||||||||  |||  ||||
                                AG ACCCCAGGAC  CCG  CATG
                                 A         A_   GA
GAM402  BRCA1    3'  GTACAAGCCACAGGACCCCAAG 24497    C       CA  __
          A                      TC TGGGGTCCTG  GGT  GTAC
                                || ||||||||||  |||  ||||
                                AG ACCCCAGGAC  CCG  CATG
                                 A         A_   AA
GAM402  BRCA1    3'  GTACAGAGCCACAGGACCCCAA 24507    C       CA  ___
          GA                     TC TGGGGTCCTG  GGT   GTAC
                                || ||||||||||  |||   ||||
                                AG ACCCCAGGAC  CCG   CATG
                                 A         A_   AGA
GAM402  DIBD1    3'  ACACCTGTGGCCCCAAAGGA  45693     CC      CT
                                TCT  TGGGGTC  GCAGGTGT
                                |||  |||||||  ||||||||
                                AGG  ACCCCGG  TGTCCACA
                                  AA      __
GAM402  MEF2D    5'  GCACTGAGGACCCCCGGAGA  20985      T      G  G
                                TCTCC GGGGTCCT CAG TGT
                                ||||| |||||||| ||| |||
                                AGAGG CCCCAGGA GTC ACG
                                   C       _  _
GAM402  NDUFS2   5'  GCACGAGGGCCCCAGGAGA   17043           GCAG
                                TCTCCTGGGGTCCT   GTGT
                                ||||||||||||||   ||||
                                AGAGGACCCCGGGA   CACG
                                         G___
GAM402  PKIG     3'  ACACCTAGGACCCAGGA     23924        G   GC
                                TCCTGGG TCCT  AGGTGT
                                ||||||| ||||  ||||||
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                                AGGACCC AGGA  TCCACA
                                      _   __
GAM402  SOX10    3'  GCAGCAAAGCCCCAGGAGA   23676          C___
                                TCTCCTGGGGT   CTGC
                                ||||||||||   ||||
                                AGAGGACCCCG   GACG
                                     AAAC
GAM402  SYT5     3'  ACACCCAGATGCCCCAGGG   13501        C_  CA
                                TCCTGGGGT  CTG  GGTGT
                                |||||||||  |||  |||||
                                GGGACCCCG  GAC  CCACA
                                     TA  __
GAM402  TP73     3'  GCACCTCACAGGCCCCAGGA  19472        T   C_
                                TCCTGGGG CCTG  AGGTGT
                                |||||||| ||||  ||||||
                                AGGACCCC GGAC  TCCACG
                                     _   AC
GAM402  WFDC1    3'  GCAGAGCAAGACCCCAGAGA  41339     C     C  AGG
                                TCTC TGGGGTC TGC   TGT
                                |||| ||||||| |||   |||
                                AGAG ACCCCAG ACG   ACG
                                  _     A  AG_
GAM402  APOARGC  3'  GCACAGTAGGACCTCAG     44675          AG
                                CTGGGGTCCTGC  GTGT
                                ||||||||||||  ||||
                                GACTCCAGGATG  CACG
                                      A_
GAM402  FLJ13204 3'  ACACCTACTCCCAGGA      45754        _ CCTGC
                                TCCTGGG GT    AGGTGT
                                ||||||| ||    ||||||
                                AGGACCC CA    TCCACA
                                    T _____
GAM402  HTMP10   3'  ACACCTGGCCTAGGAGA     53755        GTCCTG
                                TCTCCTGGG     CAGGTGT
                                |||||||||     |||||||
                                AGAGGATCC     GTCCACA
                                     G_____
GAM402  KIAA0356 3'  ATAGGCAGGACCCCAGAGA   66769     C         AG
                                TCTC TGGGGTCCTGC  GT
                                |||| ||||||||||  ||
                                AGAG ACCCCAGGACG  TA
                                  _         GA
GAM402  KIAA1858 3'  ACACCTTGACCCCAGGA     67719         CTGC
                                TCCTGGGGTC    AGGTGT
                                ||||||||||    ||||||
                                AGGACCCCAG    TCCACA
                                      T___
GAM402  MFN2     3'  ACACCTGCAGGTGTAAGGGA  30221     GGGGT
                                TCCT    CCTGCAGGTGT
                                ||||    ||||||||||
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                                AGGG    GGACGTCCACA
                                  AATGT
GAM402  MGC14161  5'  GTACACCTGCACCATCCAGAGA 52912     _    GTCC
           GA                     TCTC CTGGG    TGCAGGTGTAC
                                  |||| |||||    ||||||||||
                                  AGAG GACCT    ACGTCCACATG
                                    A    ACC_
GAM402  MGC2477   5'  GCTCACAGGACCCCGGAGA   44304      T       CA
                                  TCTCC GGGGTCCTG  GGT
                                  ||||| |||||||||  |||
                                  AGAGG CCCCAGGAC  TCG
                                    _       AC
GAM402  MGC26766  3'  ACGGCGAACCCCAGGAGA    59466          CC   AG
                                  TCTCCTGGGGT  TGC  GT
                                  ||||||||||  |||  ||
                                  AGAGGACCCCA  GCG  CA
                                        A_   G_
GAM402  ZFD25     5'  ACCCTAGAAAACCCCAGGAGA  33103          CCTGC   T
                                  TCTCCTGGGGT    AGG GT
                                  ||||||||||    ||| ||
                                  AGAGGACCCCA    TCC CA
                                        AAAGA   _
GAM402  LOC122618 5'  ACACCAAGGCAGGACCCCCAGA 57900      CT        A__
           GA                     TCTC  GGGGTCCTGC   GGTGT
                                  ||||  ||||||||||   |||||
                                  AGAG  CCCCAGGACG   CCACA
                                    AC         GAA
GAM402  LOC124842 5'  ACCCCTGCCCCCCAGGG     76157        TCCT    T
                                  TCCTGGGG    GCAGG GT
                                  ||||||||    ||||| ||
                                  GGGACCCC    CGTCC CA
                                       C___     C
GAM402  LOC137886 3'  GTACACCTTCCTCTCCAGAAGA 75799     C     TCCTGC
                                  TCT CTGGGG      AGGTGTAC
                                  ||| ||||||      ||||||||
                                  AGA GACCTC      TCCACATG
                                    A     TCCT__
GAM402  LOC145601 3'  GCACTGTGGAGAGACCCCAGGA 84350          _  G  _
                                  TCCTGGGGTC CT CA GGTGT
                                  |||||||||| || || |||||
                                  AGGACCCCAG GA GT TCACG
                                        A  G  G
GAM402  LOC157247 5'  CCTAAGGACCCCAAAAGA    82292     CC       GC
                                  TCT  TGGGGTCCT  AGG
                                  |||  |||||||||  |||
                                  AGA  ACCCCAGGA  TCC
                                    AA        A_
GAM402  LOC161158 5'  GCCGCAGGACCCCAGAAGG   88451     C          A
                                  TCT CTGGGGTCCTGC GGT
                                  ||| ||||||||||| |||
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                                GGA GACCCCAGGACG CCG
                                  A         _
GAM402  LOC164582 5'  TACACCTCTCCACAGAAGA   83416    C   G  TCCTGC
                                TCT CTG GG     AGGTGTA
                                ||| ||| ||     |||||||
                                AGA GAC CC     TCCACAT
                                  A   A  TC____
GAM402  LOC199988 5'  GCACCTCACAGGCCCCAGGA   91500        T   C_
                                TCCTGGGG CCTG  AGGTGT
                                |||||||| ||||  ||||||
                                AGGACCCC GGAC  TCCACG
                                     _    AC
GAM402  LOC204962 5'  GTACATGGGGACCCCAGAAGA  90958    C        GCAG
                                TCT CTGGGGTCCT    GTGTAC
                                ||| ||||||||||    ||||||
                                AGA GACCCCAGGG    TACATG
                                  A         G___
GAM402  LOC221486 3'  ACACCTTTTCCCCAGGAG    92654         TCCTGC
                                CTCCTGGGG     AGGTGT
                                |||||||||     ||||||
                                GAGGACCCC     TCCACA
                                     TTT___
GAM402  LOC253962 5'  GTACCCTCAAGACCCCAGAGA  98481     C      C  C   T
                                TCTC TGGGGTC TG AGG GTAC
                                |||| ||||||| || ||| ||||
                                AGAG ACCCCAG AC TCC CATG
                                  _      A  _   _
GAM402  LOC56965  3'  ATACTCAGGACCCCAAGA    39922    C        CA
                                TC TGGGGTCCTG  GGTGT
                                || ||||||||||  |||||
                                AG ACCCCAGGAC  TCATA
                                  A         __
GAM402  LOC56965  3'  ATACTCAGGACCCCAAGA    39929    C        CA
                                TC TGGGGTCCTG  GGTGT
                                || ||||||||||  |||||
                                AG ACCCCAGGAC  TCATA
                                  A         __
GAM402  LOC90594  5'  TACCAAAACCCCAGGAGA    64218          CC  CAGGT
                                TCTCCTGGGGT  TG    GTA
                                ||||||||||  ||    |||
                                AGAGGACCCCA  AC    CAT
                                     AA  _____
GAM403  HRH1      3'  TCCCTTCTCAGAAAACTTCT   7829     C    C       C
                                AG AGTT TCTGAGGAG GA
                                || |||| ||||||||| ||
                                TC TCAA AGACTCTTC CT
                                  T   A       C
GAM403  MEA       3'  CTTCTCAGAGACCCACTTT   28275      CAGT
                                AAAG    TCTCTGAGGAG
                                ||||    ||||||||||
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                                TTTC   AGAGACTCTTC
                                  ACCC
GAM403  NEDD4   3' CTCACAGAAAAACTGTTT   70545       C_   AG
                                AAGCAGTT  TCTG  GAG
                                ||||||||  ||||  |||
                                TTTGTCAA  AGAC  CTC
                                    AA   A_
GAM403  PCDH9   5' TTCCAGAGAATGCTCC     83698   A   G     A
                                A AGCA TTCTCTG GGA
                                | |||| ||||||| |||
                                C TCGT AAGAGAC CTT
                                 C   _     _
GAM403  UBE4A   3' CTAAATTAGAGAACTGCT   17732          GG_
                                AGCAGTTCTCTGA  AG
                                ||||||||||||  ||
                                TCGTCAAGAGATT  TC
                                       AAA
GAM403  BRD2    5' GCCCCAAAGAGACTGCTTT   18794       T   GA  A
                                AAAGCAGT CTCT  GG GC
                                |||||||| ||||  || ||
                                TTTCGTCA GAGA  CC CG
                                    _   AA  C
GAM403  BRI3    3' CTCAATAAAGCACTGCTTT   31794       T  C  AG
                                AAAGCAGT CT TG  GAG
                                |||||||| || ||  |||
                                TTTCGTCA GA AT  CTC
                                    C  A  AA
GAM403  FLJ20151 3' TCACTCCTTGGACTTGCTCC  35147   A    TTC  TG    C
                                A AGCAG   TC  AGGAG GA
                                | |||||   ||  ||||| ||
                                C TCGTT   AG  TCCTC CT
                                 C    C__  GT    A
GAM403  FLJ20507 3' CGCCCCCAGGCCACCTGCTCC 35736   A    TTC_   A  A
                                A AGCAG   TCTG GG GCG
                                | |||||   |||| || |||
                                C TCGTC   GGAC CC CGC
                                 C    CACC   _ C
GAM403  FLJ20507 3' CGCCCCCAGGCCACCTGCTCC 60842   A    TTC_   A  A
                                A AGCAG   TCTG GG GCG
                                | |||||   |||| || |||
                                C TCGTC   GGAC CC CGC
                                 C    CACC   _ C
GAM403  HDAC11  3' CGCCCCTTAGTGCTTT     46137      GTTCT     A
                                AAAGCA    CTGAGG GCG
                                ||||||    |||||| |||
                                TTTCGT    GATTCC CGC
                                    _____    C
GAM403  HSRNAFEV 3' TTCCCCAAGGAACTGCTCC   34455   A      TC  A
                                A AGCAGTTC  TG GGAG
                                | ||||||||  || ||||
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                                C TCGTCAAG  AC CCTT
                                 C       GA  C
GAM403  KIAA0022  3'  TCCAGAATGTAGAAACTGCTTT 30287          C    A_____
                                AAAGCAGTT TCTG      GGA
                                ||||||||| ||||      |||
                                TTTCGTCAA AGAT      CCT
                                      _    GTAAGA
GAM403  KIAA1054  3'  TTCAGGGAAAGAAAGCTGCTT  68975        _______
                                AAGCAGT     TCTCTGAG
                                |||||||     ||||||||
                                TTCGTCG     AGGGACTT
                                    AAAGAA
GAM403  KIAA1536  3'  ATTCTGTTCCCTAAGAACTGCT 40875          C  A    _
           T                     AAGCAGTTCT TG GGAGC GAAT
                                ||||||||||  || ||||| ||||
                                TTCGTCAAGA AT CCTTG CTTA
                                      _ C    T
GAM403  KIAA1615  3'  TCCAAATGAAGAGAACTCTTT  69287      C       GA____
                                AAAG AGTTCTCT      GGA
                                |||| ||||||||      |||
                                TTTC TCAAGAGA      CCT
                                  _       AGTAAA
GAM403  KIAA1813  5'  ATTCACTCCTCAGCCCTGTT   70822       TTCT       C
                                AGCAG    CTGAGGAG GAAT
                                |||||    |||||||| ||||
                                TTGTC    GACTCCTC CTTA
                                   CC__       A
GAM403  RHOBTB2   3'  GCAGCCCAGAGAACTCTCC    61602    A  C       A  A_
                                A AG AGTTCTCTG GG  GC
                                | || |||||||||  ||  ||
                                C TC TCAAGAGAC CC  CG
                                 C _        _ GA
GAM403  SERHL     3'  CCTCAAAGAGGACTACTT     97350     C       __
                                AAG AGTTCTCT  GAGG
                                ||| ||||||||  ||||
                                TTC TCAGGAGA  CTCC
                                  A       AA
GAM403  LOC151318 3'  TGCCCTGAAAACTGCTTT    81031          C  TG   A
                                AAAGCAGTT TC  AGG GCG
                                |||||||||  ||  ||| |||
                                TTTCGTCAA AG  TCC CGT
                                      A  __  _
GAM403  LOC158014 5'  TCTCAGAGCAACTGCTTT    82569          _
                                AAAGCAGTT CTCTGAGG
                                |||||||||  ||||||||
                                TTTCGTCAA GAGACTCT
                                      C
GAM403  LOC158376 3'  ATTCTGAAACCAAAGAGCTGCT 88134          C  AGGAGC
           T                     AAGCAGTTCT TG      GAAT
                                ||||||||||  ||      ||||
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                                TTCGTCGAGA AC     CTTA
                                     A  CAAAGT
GAM403  LOC158428 3'  ATTCTTTGCCCAGAGAGCTGC  71081          A  AGC_
                                GCAGTTCTCTG GG    GAAT
                                |||||||||| ||    ||||
                                CGTCGAGAGAC CC    CTTA
                                      _  GTTT
GAM403  LOC220431 5'  ATTCACCTCTTCAGAGACCACT 95993     CA  T        C_
          T                     AAG  GT CTCTGAGGAG  GAAT
                                |||  || ||||||||||  ||||
                                TTC  CA GAGACTTCTC  CTTA
                                  AC  _         CA
GAM404  C1orf22   3'  TTTTCCTAAAACACGGT     48044          T  TT
                                ACCGTGTTTTG GG  AG
                                |||||||||| ||  ||
                                TGGCACAAAAT CC  TT
                                      _  TT
GAM404  HT002     3'  GGATGCAACCACAACACACGG  26794       T       A  _
                                CCGTGT TTGTGGTT GC TCC
                                |||||| |||||||| || |||
                                GGCACA AACACCAA CG AGG
                                    C       _  T
GAM404  KIAA0475  3'  ACAGACTAGCACAAAACAC   30104         G   C  C
                                GTGTTTTGTG TTAG TC GT
                                |||||||||| |||| || ||
                                CACAAAACAC GATC AG CA
                                      _   _  A
GAM405  CDH12     3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM405  GOCAP1    3'  ATTGTTCTTGGGAGCAGTGTA  43007       CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM405  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090       T   AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT     TTATTC
                                   _   GTCA_
GAM405  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
          A                     TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM405  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
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                                ATGTGGTGA      TTTATTC
                                     AGACG___
GAM405  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
            TA                    TACA   TCC   GAAGAATAAG
                                  ||||   |||   ||||||||||
                                  ATGT   AGG   TTTCTTATTC
                                    AAA_   ATTG
GAM405  KIAA1719 3'  TCTGTCTTGGGAGTGGTGTA  68742           _
                                  TACACCACTCCCAAGA AGA
                                  |||||||||||||||| |||
                                  ATGTGGTGAGGGTTCT TCT
                                           G
GAM405  KIAA1853 3'  TTTTTCTTGGAAGCAGTG    69929    CA  C
                                  CAC  CT CCAAGAAGAA
                                  |||  || ||||||||||
                                  GTG  GA GGTTCTTTTT
                                    AC  A
GAM405  KIAA1877 3'  CTTATTCTTCTGCCATGAGT  66748    CCA__
                                  ACTC    AGAAGAATAAG
                                  ||||    ||||||||||
                                  TGAG    TCTTCTTATTC
                                    TACCG
GAM405  KIAA1906 3'  CTTATTCTTCTTGACTTTTGG  73571    CTCC_
                                  CCA    CAAGAAGAATAAG
                                  |||    ||||||||||||
                                  GGT    GTTCTTCTTATTC
                                    TTTCA
GAM405  OSBPL11  3'  CTTAATTTCCCAAGAGTGGTG  43206       CCAA   AA
                                  CACCACTC   GAAG  TAAG
                                  ||||||||   ||||  ||||
                                  GTGGTGAG   CTTT  ATTC
                                       AACC   A_
GAM405  YME1L1   3'  TCATTCTTGATGTGGTGTA   58438       TCC    _
                                  TACACCAC   CAAGAA GA
                                  ||||||||   |||||| ||
                                  ATGTGGTG   GTTCTT CT
                                       TA_     A
GAM405  ZNF262   3'  CTTATTTTGTTTGGGAGT    18723        A
                                  ACTCCCAAG AGAATAAG
                                  |||||||||  ||||||||
                                  TGAGGGTTT TTTTATTC
                                       G
GAM405  LOC91960 3'  TGTGGCTTGGAACGTGGTGTA  68294       TC_    AAGA
                                  TACACCAC   CCAAG    ATA
                                  ||||||||   |||||    |||
                                  ATGTGGTG   GGTTC    TGT
                                       CAA    GG__
GAM406  DMRT2    3'  CCACAACAAGCAACAAGAACAA 22648        AAC___
            G                      CTTGTTTTT     TGTTGTGG
                                  |||||||||     ||||||||
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                                GAACAAGAA     ACAACACC
                                     CAACGA
GAM406  PKHD1    3'  CAACAGAATTAAAAACGA    57714          __
                                TTGTTTTTAA  CTGTTG
                                ||||||||||  ||||||
                                AGCAAAAATT  GACAAC
                                      AA
GAM406  DKFZP434G2226 3'  CCACAACAAGTTGACTAGGA   49154      T   TTT   _
                                TCCT GTT   AACT GTTGTGG
                                |||| |||   |||| |||||||
                                AGGA CAG   TTGA CAACACC
                                  T  ___   A
GAM406  FIBL-6   3'  ACAACGAAAAACAAG       73296          AAC
                                CTTGTTTTT   TGTTGT
                                |||||||||   ||||||
                                GAACAAAAA   GCAACA
                                     ___
GAM406  KIAA0152  3'  CAGCTGACTGAAAACAAGGA   28966           ACT_
                                TCCTTGTTTTTA    GTTG
                                ||||||||||||    ||||
                                AGGAACAAAAGT    CGAC
                                      CAGT
GAM406  KIAA0416  3'  CAGCATCAAAAAGCAAAGATA  32087      C       AAC
                                TATC TTGTTTTT   TGTTG
                                |||| ||||||||   |||||
                                ATAG AACGAAAA   ACGAC
                                  A       ACT
GAM406  KIAA1912  3'  CCACAACAGTCAATCTCAAACA 73757         _____  A
          AGG                     CCTTGTTT    TT ACTGTTGTGG
                                |||||||||    || ||||||||||
                                GGAACAAA    AA TGACAACACC
                                     CTCT  C
GAM406  LOC122792 3'  CCAAGTGCTTAAACACAAGGAT 59822          T    CT  TG_
          A                      TATCCTTGT TTTAA  GT   TGG
                                |||||||||  |||||  ||   |||
                                ATAGGAACA AAATT  CG   ACC
                                      C    __  TGA
GAM406  LOC147649 3'  CCACAACAGTCAAAGGATGGAT 79057      TTG    A
                                ATCC   TTTTT ACTGTTGTGG
                                ||||   ||||| ||||||||||
                                TAGG   GGAAA TGACAACACC
                                  TA_    C
GAM407  HAL      5'  GCCACTCCTGCATAAAGCTC   10903          TGAAAA
                                GAGCTTTATGC     GGTGGC
                                ||||||||||     ||||||
                                CTCGAAATACG     TCACCG
                                      TCC___
GAM407  HMGN2    3'  GGCCACCTTGGCACAAAAGC   19809      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                |||||  ||  ||  |||||||||
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                                CGAAA AC AC  TTCCACCGG
                                  _ _ GG
GAM407  NMI     5' GGCCACCTCCTCAGGAAG    17436     ATG   AA
                                CTTT  CTGA  AGGTGGCC
                                ||||  ||||  ||||||||
                                GAAG  GACT  TCCACCGG
                                  ___   CC
GAM407  PACE    3' GGCCACCTCTCCAAGGGCTT  11944       A  CT  AAA
                                GAGCTTT TG  GA  GGTGGCC
                                ||||||| ||  ||  |||||||
                                TTCGGGA AC  CT  CCACCGG
                                    _ CT  ___
GAM407  PYCR1   3' CCACCTTCCTCTAGAGCTC   70639       TGCT  A_
                                GAGCTTTA   GA  AAGGTGG
                                ||||||||   ||  |||||||
                                CTCGAGAT   CT  TTCCACC
                                    _____ CC
GAM407  SDC1    3' GGCCACCTCCCCAGCATTCCAG 12991    TT_    AAA
          C                      GCT   ATGCTG   AGGTGGCC
                                |||   ||||||   ||||||||
                                CGA   TACGAC   TCCACCGG
                                  CCT     CCC
GAM407  FLJ11560 5' GCCCAGGCCCAGCATAAAG   48008        AAAA  ___
                                CTTTATGCTG   GGT   GGC
                                ||||||||||   |||   |||
                                GAAATACGAC   CCG   CCG
                                     _____  GAC
GAM407  KIAA0446 5' CCACCTTTTGAAGAGCTC    69446      ATGCTG
                                GAGCTTT     AAAAGGTGG
                                |||||||     |||||||||
                                CTCGAGA     TTTTCCACC
                                   AG_____
GAM407  KIAA0971 3' GTTGTTCTCAGCATAAAGT   30677         AAA  TG
                                GCTTTATGCTGA   GG  GC
                                ||||||||||||   ||  ||
                                TGAAATACGACT   TT  TG
                                      C__  GT
GAM407  KIAA1393 3' GGCCACCTTGGCACAAAAGC  72574      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _ GG
GAM407  KIAA1656 3' GGCCACCTCCTCCTAGAAGCC 66377   A    ATGCT  AA
                                G GCTTT    GA  AGGTGGCC
                                | |||||    ||  ||||||||
                                C CGAAG    CT  TCCACCGG
                                 _    ATC__  CC
GAM407  KIAA1884 3' GCCACCTTCATCTACCAAGGCT 73728       ATGCT  A_
          C                      GAGCTTT    GA  AAGGTGGC
                                |||||||    ||  ||||||||
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                                CTCGGAA    CT  TTCCACCG
                                    CCAT_  AC
GAM407  PP3501    3'  GGCCACCGTTGACAGCATAAAG 41683          AAAA_
                                CTTTATGCTG    GGTGGCC
                                ||||||||||    |||||||
                                GAAATACGAC    CCACCGG
                                      AGTTG
GAM407  SDCCAG3   3'  GGTGTTCTCAGCATGAAGCTC  22803            AAA  TG
                                GAGCTTTATGCTGA   GG  GCC
                                ||||||||||||||   ||  |||
                                CTCGAAGTACGACT   CT  TGG
                                       ___  TG
GAM407  SP140     3'  GGCCACCTCCATGCAGAAGC   24327      A   TGAAA
                                GCTTT TGC    AGGTGGCC
                                ||||| |||    ||||||||
                                CGAAG ACG    TCCACCGG
                                  _  TACC_
GAM407  LOC148760 3'  GGCCACCTTCTCCAACAAGCTC 85364       TA  CT  A
                                GAGCTT  TG  GA AAGGTGGCC
                                ||||||  ||  || |||||||||
                                CTCGAA  AC  CT TTCCACCGG
                                   CA  __  C
GAM407  LOC150170 5'  ACCTGTTTCACATAAAGC    80414        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                     _    G
GAM407  LOC150175 5'  ACCTGTTTCACATAAAGC    80453        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                     _    G
GAM407  LOC150215 5'  ACCTGTTTCACATAAAGC    80456        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                     _    G
GAM407  LOC150218 5'  ACCTGTTTCACATAAAGC    80525        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                     _    G
GAM407  LOC152065 3'  GGCCACCTTCTCCTTGGCAGGC 86737       TTA   ___  A
          TC                      GAGCT   TGCT   GA AAGGTGGCC
                                |||||   ||||   || |||||||||
                                CTCGG   ACGG   CT TTCCACCGG
                                   ___    TTC  C
GAM407  LOC152267 3'  GGCCACCTTGGCACAAAAGC   61036      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
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                                CGAAA AC AC  TTCCACCGG
                                  _ _ GG
GAM407  LOC158292 5'  CCTCTGGACCCAGCATAAGGCT 88046          AAAA_  T
          C                     GAGCTTTATGCTG    GG GG
                                ||||||||||||    || ||
                                CTCGGAATACGAC    TC CC
                                      CCAGG  T
GAM407  LOC219997 3'  GCCACCTCTTCAGCCTC    93256    CTTTAT    A
                                GAG    GCTGAA AGGTGGC
                                |||    |||||| |||||||
                                CTC    CGACTT TCCACCG
                                  _______    C
GAM407  LOC256269 3'  GGCCACCTTGGCACAAAAGC  96608     A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _ GG
GAM407  LOC91963  5'  GGCCACCTCCTCTGAGAAGC  68321     ATGCT  AA
                                GCTTT    GA  AGGTGGCC
                                |||||    ||  ||||||||
                                CGAAG    CT  TCCACCGG
                                   AGT__  CC
GAM408  CCND2     3'  TCCCCAGCAAATCATCGGGCCA 10056         CCACA  _  A
                                TGGCCTGATGAT    GC GG GA
                                ||||||||||||    || || ||
                                ACCGGGCTACTA    CG CC CT
                                      AA___  A  C
GAM408  GCN5L2    5'  CTCCGCTGCGGGGGAGGCC   60529     GATGA   A
                                GGCCT    TCC CAGCGGAG
                                |||||    ||| ||||||||
                                CCGGA    GGG GTCGCCTC
                                   GG___  C
GAM408  GJA5      3'  CTGACCAGATCATCAGCCA   19164     C      CACAG
                                TGGC TGATGATC    CGG
                                |||| ||||||||    |||
                                ACCG ACTACTAG    GTC
                                  _      ACCA_
GAM408  HIVEP3    3'  TCCCCGCTGTGGTTGGCAGCCA 44702     C  ATGAT       A
                                TGGC TG    CCACAGCGG GA
                                |||| ||    ||||||||| ||
                                ACCG AC    GGTGTCGCC CT
                                  _ GGTT_       C
GAM408  HOXD1     5'  CCGCCGGTATATTAGGCCA   44696        AT  ACA
                                TGGCCTGATG  CC   GCGG
                                ||||||||||  ||   ||||
                                ACCGGATTAT  GG   CGCC
                                      AT  C__
GAM408  SUFU      3'  CCTTGTGACCCATCAGGCCA  32934        ATC    C
                                TGGCCTGATG   CACAG GG
                                ||||||||||   ||||| ||
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                                ACCGGACTAC   GTGTT CC
                                     CCA    _
GAM408  ARHGEF15  3'  CTGTGGACCACAGGCCA     30953        A  A
                                TGGCCTG TG TCCACAG
                                ||||||| || |||||||
                                ACCGGAC AC AGGTGTC
                                   _  C
GAM408  DKFZP586J1624 3'  CTCCGCCCAGTCACCATCAGGC 32043          ATCCACA_
          CA                    TGGCCTGATG       GCGGAG
                                ||||||||||       ||||||
                                ACCGGACTAC       CGCCTC
                                     CACTGACC
GAM408  KIAA1671  3'  CTTTGCTTATGAATCATCAGAC 66282    C       C  C_
          C                     GG CTGATGAT CA  AGCGGAG
                                || |||||||| ||  |||||||
                                CC GACTACTA GT  TCGTTTC
                                 A       A  AT
GAM408  MGC18079  3'  CCGCGGACCTCAGGCCA     59033        TGA   ACA
                                TGGCCTGA   TCC   GCGG
                                ||||||||   |||   ||||
                                ACCGGACT   AGG   CGCC
                                     CC_   ___
GAM408  LOC115110 3'  TGCAGACATCAGGCCA      72186          A  CACA
                                TGGCCTGATG TC    GCG
                                |||||||||| ||    |||
                                ACCGGACTAC AG    CGT
                                     _  A___
GAM408  LOC159110 5'  TCTCCGCTGCCCCGGTCAACCA 82995     CCTGA    CA__
                                TGG    TGATC    CAGCGGAGA
                                |||    |||||   |||||||||
                                ACC    ACTGG    GTCGCCTCT
                                  A____     CCCC
GAM408  LOC159116 5'  TCTCCGCTGCCCCGGTCAACCA 82978     CCTGA    CA__
                                TGG    TGATC    CAGCGGAGA
                                |||    |||||   |||||||||
                                ACC    ACTGG    GTCGCCTCT
                                  A____     CCCC
GAM408  LOC165476 5'  CTCCGCTGCCTGCTCAGCCA   88550     C   TGATCCA
                                TGGC TGA      CAGCGGAG
                                |||| |||      ||||||||
                                ACCG ACT      GTCGCCTC
                                   _   CGTCC__
GAM408  LOC200032 5'  CTGACCAGATCATCAGCCA    85475      C       CACAG
                                TGGC TGATGATC     CGG
                                |||| ||||||||     |||
                                ACCG ACTACTAG     GTC
                                   _       ACCA_
GAM408  LOC219654 5'  CTCCGCTGCGGAGGGGGGCC   92932       GATGA   A
                                GGCCT     TCC CAGCGGAG
                                |||||     ||| ||||||||
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                                CCGGG    AGG GTCGCCTC
                                   GGG__  C
GAM408  LOC255862 3'  TCAAATGTAGACTATCAGGCCA 96115          A  C  GCG
                                TGGCCTGATG TC ACA  GA
                                |||||||||| || |||  ||
                                ACCGGACTAT AG TGT  CT
                                      C  A  AAA
GAM409  ARHGEF7  3'  GCACCCCCCATGTCGGTA   15322     _  _ CC
                                TGCC ATA GG  GGGGTGC
                                |||| ||| ||  |||||||
                                ATGG TGT CC  CCCCACG
                                  C  A __
GAM409  BACE    3'  TGGCACCTGTGGCCAGAGCA  58094    CATA   _
                                TGC   GGCCG GGGTGCCA
                                |||   ||||| ||||||||
                                ACG   CCGGT TCCACGGT
                                  AGA_    G
GAM409  BIN3    3'  TGGTCCTCCAGCCCTGGCA   38582     TA  C   TG
                                TGCCA  GGC GGGG  CCA
                                |||||  ||| ||||  |||
                                ACGGT  CCG CCTC  GGT
                                   C_  A   CT
GAM409  BSN     3'  TGGCATGTTTGACCTGTGGCA  14393        C  _
                                TGCCATAGG CGGG GTGCCA
                                |||||||| |||| ||||||
                                ACGGTGTCC GTTT TACGGT
                                      A   G
GAM409  CRK     5'  GGCACCCCAGCGTTTAGGC   60545    A   C__
                                GCC TAGGC  GGGGTGCC
                                ||| |||||  ||||||||
                                CGG ATTTG  CCCCACGG
                                  _    CGA
GAM409  CYB561   3'  TGGGCCCGGCCTTTGGCA    10353     T      GTG
                                TGCCA AGGCCGGG  CCA
                                ||||| ||||||||  |||
                                ACGGT TCCGGCCC  GGT
                                   T      G__
GAM409  DDOST    3'  TGGCATTTTTCCTATGTGCA  19068    _    CC
                                TGC CATAGG  GGGGTGCCA
                                ||| ||||||  |||||||||
                                ACG GTATCC  TTTTACGGT
                                  T    T_
GAM409  EGFL4    3'  TGGCACCCCTGCTGCTGACA  62477   C  TA  C
                                TG CA  GGC GGGGTGCCA
                                || ||  ||| |||||||||
                                AC GT  TCG CCCCACGGT
                                 A  CG  T
GAM409  HNF3B    3'  TGGCACCCCGGATCGAGG    41714   ATA  _
                                CC   GG CCGGGGTGCCA
                                ||   || ||||||||||
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                                GG   CT GGCCCCACGGT
                                 AG_  A
GAM409  LALBA    3'  TGGCACTTTCACTACAGCA   11258     CA   GCC
                                TGC  TAG   GGGGTGCCA
                                |||  |||   |||||||||
                                ACG  ATC   TTTCACGGT
                                  AC   AC_
GAM409  MAPK8IP1 3'  GGCATGCTGGCCTGTGGCA   19581           G
                                TGCCATAGGCCGG GTGCC
                                |||||||||||| |||||
                                ACGGTGTCCGGTC TACGG
                                       G
GAM409  NHLH1    5'  TGGCACCCTGACCATGG     20022      A  C
                                CCAT GG CGGGGTGCCA
                                |||| || ||||||||||
                                GGTA CC GTCCCACGGT
                                  _  A
GAM409  NOTCH3   3'  TGGCCCAGCCTTATGGCA    6483        _   CGG  T
                                TGCCATA GGC   GG GCCA
                                ||||||| |||   || ||||
                                ACGGTAT CCG   CC CGGT
                                    T   A__  _
GAM409  NUDT2    3'  TGGTATTTGGCTCATGACA   8598     C   AG     G
                                TG CAT  GCCGGG TGCCA
                                || |||  |||||| |||||
                                AC GTA  CGGTTT ATGGT
                                 A   CT     _
GAM409  PACSIN1  3'  TGGCACCCCGGGGACAGGCA  93887      ATAGG
                                TGCC    CCGGGGTGCCA
                                ||||    ||||||||||||
                                ACGG    GGCCCCACGGT
                                  ACAGG
GAM409  PAM      3'  GCATTCTTAGCCTGTGGCA   8087          C_
                                TGCCATAGGC  GGGGTGC
                                ||||||||||  |||||||
                                ACGGTGTCCG  TCTTACG
                                      AT
GAM409  SELENBP1 3'  TGGCACCCGACCCTTGGCA   15459      TA  C   G
                                TGCCA  GG CGGG TGCCA
                                |||||  || |||| |||||
                                ACGGT  CC GCCC ACGGT
                                   TC  A   _
GAM409  SLC10A2  5'  TGGCATGGTTCCTATGGC    6595         __ GGG
                                GCCATAGG  CC   GTGCCA
                                ||||||||  ||   ||||||
                                CGGTATCC  GG   TACGGT
                                    TT  ____
GAM409  SNX9     3'  GCACCCCGGCGTCTCTGGC   33122      T  __
                                GCCA AG  GCCGGGGTGC
                                |||| ||  ||||||||||
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                                CGGT TC  CGGCCCCACG
                                  C  TG
GAM409  SYNGR1   3'  TGGCACCCTCCTTTATGACA  17515    C     CC
                                TG CATAGG  GGGGTGCCA
                                || ||||||  |||||||||
                                AC GTATTT  TCCCACGGT
                                 A     CC
GAM409  TAPBP    3'  TGGCACGATCTCGGCTCACGGC 13591      ATA     ___
           A                     TGCC   GGCCGGG   GTGCCA
                                 ||||   |||||||   ||||||
                                 ACGG   TCGGCTC   CACGGT
                                   CAC      TAG
GAM409  UBE2B    3'  TGGCACTTCTGCCATGAGCA   13942    _  A   C
                                TGC CAT GGC GGGGTGCCA
                                ||| ||| ||| |||||||||
                                ACG GTA CCG CTTCACGGT
                                  A  _  T
GAM409  UBE2L3   3'  TGGCACCCCAGGGTTGGC    13966     TA G  _
                                GCCA  G CC GGGGTGCCA
                                ||||  | || |||||||||
                                CGGT  T GG CCCCACGGT
                                  __ G  A
GAM409  ACTR1A   3'  GGCACCCTCACCTGTGACA   63651    C     CC
                                TG CATAGG  GGGGTGCC
                                || ||||||  ||||||||
                                AC GTGTCC  TCCCACGG
                                 A     AC
GAM409  ATP6V1B1 3'  TGGCACCCCAACACCGGCA   9882      ATA  CC__
                                TGCC   GG   GGGGTGCCA
                                ||||   ||   |||||||||
                                ACGG   CC   CCCCACGGT
                                  ___  ACAA
GAM409  C22orf2  3'  TGGCACCCTTGGGTTGGCA   96089     TAG  __
                                TGCCA   GCC  GGGGTGCCA
                                |||||   |||  |||||||||
                                ACGGT   TGG  TCCCACGGT
                                  ____  GT
GAM409  CHSY1    3'  TGCTCCAGTCCTATGGCA    30575        _ C
                                TGCCATAGG C GGGGTG
                                ||||||||| | ||||||
                                ACGGTATCC G CCTCGT
                                     T A
GAM409  CXYorf1  5'  TGGCACCAAGATCGGCCCTGGC 82923      TA    _____
           A                     TGCCA  GGCCGG   GGTGCCA
                                 |||||  ||||||   |||||||
                                 ACGGT  CCGGCT   CCACGGT
                                   C_     AGAA
GAM409  DKFZp547C176 3'  TGGCATTTCATACCCATGGTA  67809       A  CC_ GG
                                TGCCAT GG   G  GTGCCA
                                |||||| ||   |  ||||||
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                                ATGGTA CC   C  TACGGT
                                   C  ATA TT
GAM409  DKFZP547L112 3'  GGCACCCTGGATATAGCA    67131     C   GG
                                TGC ATA  CCGGGGTGCC
                                ||| |||  ||||||||||
                                ACG TAT  GGTCCCACGG
                                  A   A_
GAM409  FLJ10521  3'  GCATCCTGGCCCCTGACA    36720    C  TA
                                TG CA  GGCCGGGGTGC
                                || ||  |||||||||||
                                AC GT  CCGGTCCTACG
                                 A  CC
GAM409  FLJ13952  3'  TGGCACGATCTCGGCTCACGGC 46023      ATA      ___
           A                     TGCC   GGCCGGG   GTGCCA
                                ||||   |||||||   ||||||
                                ACGG   TCGGCTC   CACGGT
                                  CAC      TAG
GAM409  FLJ20793  3'  TGATATTCTGCCTATGGCA   93451          C     C
                                TGCCATAGGC GGGGTG CA
                                |||||||||| |||||| ||
                                ACGGTATCCG TCTTAT GT
                                      _     A
GAM409  FLJ21709  3'  TGGCACGTGTTCTGTGGCA   78484        GC  GG
                                TGCCATAG  CG  GTGCCA
                                ||||||||  ||  ||||||
                                ACGGTGTC  GT  CACGGT
                                     TT  G_
GAM409  FLJ22318  3'  TGGCACCTGGCTCCATGGCA  43145       A_     G
                                TGCCAT  GGCCGGG TGCCA
                                ||||||  ||||||| |||||
                                ACGGTA  TCGGTCC ACGGT
                                   CC     _
GAM409  GIT2     3'  TGGACTTAAACCTTGGCA    29415       T   CCG    G
                                TGCCA AGG   GGGT CCA
                                ||||| |||   |||| |||
                                ACGGT TCC   TTCA GGT
                                   _  AAA   _
GAM409  ITGA8    5'  TGGCACCTGCTATGTAGCA   94845     C   _   CG
                                TGC ATA GGC  GGGTGCCA
                                ||| ||| |||  ||||||||
                                ACG TGT TCG  TCCACGGT
                                  A   A  __
GAM409  KIAA0152  3'  TGGCAGAGAGGGCCTTGGCA  28984       T     GGGG_
                                TGCCA AGGCC    TGCCA
                                ||||| |||||    |||||
                                ACGGT TCCGG    ACGGT
                                   _    GAGAG
GAM409  KIAA0173  5'  TGGCACCTTACCTCAGCA    28385     CAT   CC
                                TGC   AGG  GGGGTGCCA
                                |||   |||  |||||||||
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                                ACG   TCC  TTCCACGGT
                                  AC_  A_
GAM409  KIAA0295  3'  TGGCACTGGCCTGCAGCA    68676    CA     GG
                                TGC  TAGGCC  GGTGCCA
                                |||  ||||||  |||||||
                                ACG  GTCCGG  TCACGGT
                                  AC     __
GAM409  KIAA0555  3'  TGGCACAATCTCGGCTCATGGC 60747       AG     ___
            A                    TGCCAT  GCCGGG   GTGCCA
                                |||||||  ||||||   ||||||
                                ACGGTA  CGGCTC   CACGGT
                                   CT     TAA
GAM409  KIAA0574  3'  TGGACCCCAACTCTATGGCA   69824        CC_    G
                                TGCCATAGG   GGGGT CCA
                                |||||||||   ||||| |||
                                ACGGTATCT   CCCCA GGT
                                     CAA    _
GAM409  KIAA0792  3'  TGGCCTGGGGCCTTGGCA    28770      T    GG  T
                                TGCCA AGGCC  GG GCCA
                                |||||  |||||  ||  ||||
                                ACGGT TCCGG  TC CGGT
                                   _    GG  _
GAM409  KIAA1170  3'  TGGCATTTGACCCATGGCA   70426       A  C    G
                                TGCCAT GG CGGG TGCCA
                                ||||||  ||  ||||  |||||
                                ACGGTA CC GTTT ACGGT
                                   C  A   _
GAM409  KIAA1317  3'  TGGCACTCATCCCATGGTA   87216       A  CCG
                                TGCCAT GG   GGGTGCCA
                                ||||||  ||   ||||||||
                                ATGGTA CC   CTCACGGT
                                   C  TA_
GAM409  KIAA1881  3'  GGTCTCCGGCCTTAGCA     97087     CAT       T
                                TGC   AGGCCGGGG GCC
                                |||   |||||||||  |||
                                ACG   TCCGGCCTC TGG
                                  AT_       _
GAM409  LAMP3     3'  TGGCACGATCTCGGCTTATGGC 60213            ___
            A                    TGCCATAGGCCGGG   GTGCCA
                                ||||||||||||||   ||||||
                                ACGGTATTCGGCTC   CACGGT
                                       TAG
GAM409  MGC19556  3'  TGGCACCCTCCTGAATGG    54346     __  CC
                                CCAT  AGG  GGGGTGCCA
                                ||||  |||  |||||||||
                                GGTA  TCC  TCCCACGGT
                                  AG   __
GAM409  MGC2574   3'  TGGCACTCCAAACCCATGGC   44287      A  CC_
                                GCCAT GG   GGGGTGCCA
                                |||||  ||   |||||||||
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                                CGGTA CC   CCTCACGGT
                                   C  AAA
GAM409  MGC2647  3'  GGCACCCCAGTGGTGGCA    74079       AG  C
                                TGCCAT  GC GGGGTGCC
                                ||||||  || ||||||||
                                ACGGTG  TG CCCCACGG
                                   G_  A
GAM409  MIL1     3'  GGTTTCTCAGCCTTGGCA    31727      T   C   T
                                TGCCA AGGC GGGG GCC
                                ||||| |||| |||| |||
                                ACGGT TCCG CTCT TGG
                                   _   A   T
GAM409  NIP30    3'  TGACACTCTGGTGCCCATTGGC 46901      TA_  __     C
             A                   TGCCA   GGC  CGGGGTG CA
                                |||||   |||  ||||||| ||
                                ACGGT   CCG  GTCTCAC GT
                                   TAC   TG      A
GAM409  NR4A3    3'  GCACCCTGCTTCTACGCA    23720     CA   C_
                                TGC  TAGG  CGGGGTGC
                                |||  ||||  ||||||||
                                ACG  ATCT  GTCCCACG
                                  C_   TC
GAM409  PIB5PA   3'  TGGCACCTCAACTGTGACA   66652    C    GCC
                                TG CATAG   GGGGTGCCA
                                || |||||   |||||||||
                                AC GTGTC   CTCCACGGT
                                 A    AA_
GAM409  PPAP2A   5'  TGGCACACGAGCGCCTCGGCA 68443     AT   ___ GG
                                TGCC  AGGC   CG  GTGCCA
                                ||||  ||||   ||  ||||||
                                ACGG  TCCG   GC  CACGGT
                                  C_   CGA  A_
GAM409  PPP1R1A  3'  TGGCACTTGGCCCATGG     23096      A      G
                                CCAT GGCCGGG TGCCA
                                |||| ||||||| |||||
                                GGTA CCGGTTC ACGGT
                                   C      _
GAM409  RASSF2   3'  TGGCATGCGGCCCCTGGCA   29113      TA    GG
                                TGCCA  GGCCG  GTGCCA
                                |||||  |||||  ||||||
                                ACGGT  CCGGC  TACGGT
                                   CC    G_
GAM409  RCD-8    3'  TGGCATCTGACCTTGGCA    27525      T  C   G
                                TGCCA AGG CGGG TGCCA
                                ||||| ||| |||| |||||
                                ACGGT TCC GTCT ACGGT
                                   _  A   _
GAM409  SARM     3'  TGGCACCCAGTCCACTGGCA  31308      TA  CCG
                                TGCCA  GG   GGGTGCCA
                                |||||  ||   ||||||||
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                                ACGGT  CC   CCCACGGT
                                  CA  TGA
GAM409  TREX1    5'  TGGCACCCCCCTGCAGC     50619    CA   CC
                                GC  TAGG  GGGGTGCCA
                                ||  ||||  |||||||||
                                CG  GTCC  CCCCACGGT
                                 AC   __
GAM409  TSPEAR   3'  TGGGCCCAGCCTAGGGCA    59377     A    CG   G
                                TGCC TAGGC  GGGT CCA
                                |||| |||||  |||| |||
                                ACGG ATCCG  CCCG GGT
                                  G    A_   _
GAM409  ULK2     5'  GGCACCCCTGGCCCGGCA    28688     ATA   _
                                TGCC   GGCC GGGGTGCC
                                ||||   |||| ||||||||
                                ACGG   CCGG CCCCACGG
                                  C__    T
GAM409  LOC116028 3'  TGGCATTTCCTAACGGCA    74099     A_   CCG
                                TGCC  TAGG   GGGTGCCA
                                ||||  ||||   ||||||||
                                ACGG  ATCC   TTTACGGT
                                  CA   ___
GAM409  LOC126133 3'  TGGCACAATCTCGGCCCACTGC 74916     CATA     ___
          A                      TGC    GGCCGGG   GTGCCA
                                |||    |||||||   ||||||
                                ACG    CCGGCTC   CACGGT
                                  TCAC      TAA
GAM409  LOC146445 3'  TGGCACCCTCCACTCGGCA   84686     AT  GCC
                                TGCC  AG   GGGGTGCCA
                                ||||  ||   |||||||||
                                ACGG  TC   TCCCACGGT
                                  C_  ACC
GAM409  LOC148089 3'  TGGCACCCTTCTGAGGCA    79335     A   CC
                                TGCC TAGG  GGGGTGCCA
                                |||| ||||  |||||||||
                                ACGG GTCT  TCCCACGGT
                                  A   __
GAM409  LOC151534 5'  GGTCTCCGGCCTCGGCA     57487     AT       T
                                TGCC  AGGCCGGGG GCC
                                ||||  ||||||||| |||
                                ACGG  TCCGGCCTC TGG
                                  C_       _
GAM409  LOC153769 3'  TGGTCCTTCGGCCTCAGCA   81810     CAT      TG
                                TGC   AGGCCGGGG  CCA
                                |||   ||||||||  |||
                                ACG   TCCGGCTTC  GGT
                                  AC_       CT
GAM409  LOC158219 5'  TGGCACCCTTCCTCCAGCA   82693     CAT   CC
                                TGC   AGG  GGGGTGCCA
                                |||   |||  |||||||||
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                                ACG   TCC  TCCCACGGT
                                  ACC   T_
GAM409   LOC163994 5'  TGGCACCTCTTTTCGGCA    88426     AT   CC
                                TGCC  AGG  GGGGTGCCA
                                ||||  |||  |||||||||
                                ACGG  TTT  CTCCACGGT
                                  CT   __
GAM409   LOC197342 3'  TGGCGGGGGGGCCTGTGGCA   89374          GGGG
                                TGCCATAGGCC    TGCCA
                                ||||||||||    |||||
                                ACGGTGTCCGG    GCGGT
                                      GGG_
GAM409   LOC200093 5'  TGGCACCAAGATCGGCCCTGGC 63779      TA     ____
           A                     TGCCA  GGCCGG    GGTGCCA
                                |||||  ||||||    |||||||
                                ACGGT  CCGGCT    CCACGGT
                                   C_     AGAA
GAM409   LOC219818 3'  TGACACCCGCCTCACTGTGGCA 92540       ____   CG    C
                                TGCCAT    AGGC  GGGTG CA
                                ||||||    ||||  ||||| ||
                                ACGGTG    TCCG  CCCAC GT
                                   TCAC    __     A
GAM409   LOC255936 5'  TGGCACTCCCCCCATGCA    97964     C  A  CC
                                TGC AT GG  GGGGTGCCA
                                ||| || ||  |||||||||
                                ACG TA CC  CCTCACGGT
                                  _ _ CC
GAM409   LOC256789 3'  TGGCAAGTCGGACCTATGGC   99314        _   GG
                                GCCATAGG CCGG  TGCCA
                                |||||||| ||||  |||||
                                CGGTATCC GGCT  ACGGT
                                     A   GA
GAM409   LOC257481 3'  TGGCGTCTTGGCCTTCGGCA   61766     AT      GT
                                TGCC  AGGCCGGG  GCCA
                                ||||  ||||||||  ||||
                                ACGG  TCCGGTTC  CGGT
                                  CT       TG
GAM409   LOC51134  3'  TGACATTTTAACCTGTGGCA   32794         CC     C
                                TGCCATAGG  GGGGTG CA
                                |||||||||  ||||||  ||
                                ACGGTGTCC  TTTTAC GT
                                     AA     A
GAM409   LOC90693  3'  TGGATTATATCCTATGGCA    57858         CCGG   G
                                TGCCATAGG    GGT CCA
                                |||||||||    ||| |||
                                ACGGTATCC    TTA GGT
                                     TATA  _
GAM409   LOC91040  5'  TGGCACCAAGATCGGCCCTGGC 65354      TA     ____
           A                     TGCCA  GGCCGG    GGTGCCA
                                |||||  ||||||    |||||||
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                                ACGGT  CCGGCT   CCACGGT
                                  C_     AGAA
GAM409  LOC91464  5'  TGGCACCCTCCTTGGCCTA   66714      ____
                                TAGGCC   GGGGTGCCA
                                ||||||   |||||||||
                                ATCCGG   TCCCACGGT
                                   TTCC
GAM410  ADCY7    3'  TGAGTTGCCCCGGGCTG    8494        AACACT   __
                                CAGCCCGG    GGCA  TCA
                                ||||||||    ||||  |||
                                GTCGGGCC    CCGT  AGT
                                     _______  TG
GAM410  ADRBK1   3'  ATGATGCCACACCAAGCTGTG 9663       CC  AACAC
                                CACAGC  GG    TGGCATCAT
                                ||||||  ||    |||||||||
                                GTGTCG  CC    ACCGTAGTA
                                   AA  AC___
GAM410  BTEB1    5'  ATGTCAGTGTTCGAGGCTGT  8668       CG
                                ACAGCC  GAACACTGGCAT
                                ||||||  ||||||||||||
                                TGTCGG  CTTGTGACTGTA
                                   AG
GAM410  LAIR1    3'  GAGGACAGCCCGGGCTGTG   41662        AACA   GCA
                                CACAGCCCGG   CTG   TC
                                ||||||||||   |||   ||
                                GTGTCGGGCC   GAC   AG
                                     C___   AGG
GAM410  LILRB4   3'  TGATGTCTTCCTGGCTGT    23388       C   CACT
                                ACAGCC GGAA   GGCATCA
                                |||||| ||||   |||||||
                                TGTCGG CCTT   CTGTAGT
                                   T   _____
GAM410  P23      3'  ATGACTTGTCAGTGTTCCAGGT 22752     G  C        __
            GT                    ACA CC GGAACACTGGCA  TCAT
                                ||| || ||||||||||||  ||||
                                TGT GG CCTTGTGACTGT  AGTA
                                  _ A          TC
GAM410  PRV1     3'  TGAGCATTCAGGGCTGTG    73896        G   CACTG  A
                                CACAGCCC GAA    GC TCA
                                |||||||| |||    || |||
                                GTGTCGGG CTT    CG AGT
                                    A   A_____ _
GAM410  SOLH     5'  GGCGCCGCCGGGCTGTG     20094         AACAC   AT
                                CACAGCCCGG    TGGC  C
                                ||||||||||    ||||  |
                                GTGTCGGGCC    GCCG  G
                                     ______   CG
GAM410  SOX5     3'  ATGCCAGTAATTCAGCTG    23665      CC   AC
                                CAGC  GGA  ACTGGCAT
                                ||||  |||  ||||||||
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                                GTCG  CTT  TGACCGTA
                                  A_   AA
GAM410  ATP10B   3'  ATGATGCCAGCACTAGCCAGCT 64103     CC  AACA__
           G                     CAGC  GG     CTGGCATCAT
                                 ||||  ||     ||||||||||
                                 GTCG  CC     GACCGTAGTA
                                   A_  GATCAC
GAM410  C19orf7  3'  ATGCAGGTGTTCCAAGGTGTG  61776     G  C_      G
                                 CACA CC  GGAACACT GCAT
                                 |||| ||  |||||||| ||||
                                 GTGT GG  CCTTGTGG CGTA
                                   _  AA       A
GAM410  C1QR1    3'  ATGCCAGTGCTCCGAGCTCA  24867   C   C    A
                                 A AGC CGGA CACTGGCAT
                                 | ||| |||| |||||||||
                                 A TCG GCCT GTGACCGTA
                                  C   A   C
GAM410  CYP2A13  3'  ATGATGTCCTTCAGAGCTGTG  7546       CCG   CACT
                                 CACAGC   GAA   GGCATCAT
                                 ||||||   |||   ||||||||
                                 GTGTCG   CTT   CTGTAGTA
                                    AGA   C___
GAM410  KIAA0316 3'  ATGATGCCAATGAGCTGCTCTG 70243     CC   AA  C
                                 CAG  CGG  CA TGGCATCAT
                                 |||  |||  || |||||||||
                                 GTC  GTC  GT ACCGTAGTA
                                   TC   GA  A
GAM410  MGC4368  5'  ATGATGCCAGTGGCGCTGG   44723     AA_
                                 CCGG   CACTGGCATCAT
                                 ||||   ||||||||||||
                                 GGTC   GTGACCGTAGTA
                                   GCG
GAM410  NBL1     3'  ATGTTAGTGCCCCGCACTGTG  60045      CC   AA
                                 CACAG  CGG  CACTGGCAT
                                 |||||  |||  |||||||||
                                 GTGTC  GCC  GTGATTGTA
                                    AC   CC
GAM410  RNF13    5'  GCTAGTACTCCGGGCTGTG   24417          AC
                                 CACAGCCCGGA  ACTGGC
                                 ||||||||||  ||||||
                                 GTGTCGGGCCT  TGATCG
                                        CA
GAM410  RNPC1    3'  TGGGGCATCCAGGGCTGTG   34414        _  ACACTG  AT
                                 CACAGCCC GGA     GC  CA
                                 |||||||| |||     ||  ||
                                 GTGTCGGG CCT     CG  GT
                                     A  A_____  GG
GAM410  TIMM22   3'  ATGATGCCAGCCCCGGATCCGG 78911         ACA____
           GCTG                   CAGCCCGGA      CTGGCATCAT
                                 |||||||||      ||||||||||
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                                GTCGGGCCT      GACCGTAGTA
                                     AGGCCCC
GAM410  LOC143879 5'  ATGATGCCACTGATCAAACCTG 77157     CCCG  A  C
                                CAG    GA CA TGGCATCAT
                                |||    || || |||||||||
                                GTC    CT GT ACCGTAGTA
                                  CAAA  A  C
GAM410  LOC147858 5'  ATGCTGCACTCCGGAGCCGTG  79267     A  _    ACACT
                                CAC GC CCGGA    GGCAT
                                ||| || |||||    |||||
                                GTG CG GGCCT    TCGTA
                                  C  A    CACG_
GAM410  LOC149086 3'  ATGGGTTGGTGTCCGGGC    85491       A   TG  A
                                GCCCGGA CAC  GC TCAT
                                ||||||| |||  || ||||
                                CGGGCCT GTG  TG GGTA
                                    _  GT  _
GAM410  LOC200058 3'  TGTCGCAGCAGCCCGGGCTG   89965       AACA  __  AT
                                CAGCCCGG   CTG  GC  CA
                                ||||||||   |||  ||  ||
                                GTCGGGCC   GAC  CG  GT
                                     C___   GA  CT
GAM410  LOC257364 3'  ATGCTGGGCACCCAGGGCTGTG 96641        _  AACA TG
                                CACAGCCC GG    C  GCAT
                                |||||||| ||    |  ||||
                                GTGTCGGG CC    G  CGTA
                                     A  CACG GT
GAM410  LOC55893  5'  ATGATGCCAGGCTACCAGGC   38489     C  AACA
                                GCC GG    CTGGCATCAT
                                ||| ||    ||||||||||
                                CGG CC    GACCGTAGTA
                                  A  ATCG
GAM411  CELSR2    3'  CTCTCCTCCCCTCTCCTCA    9194      C  TTATT     A
                                TGAG AG    GGAGGA GAG
                                |||| ||    |||||| |||
                                ACTC TC    CCTCCT CTC
                                  C  TCC__     _
GAM411  CNP       3'  CTCTTCCCCTCTAATGCTCA   53619       G   TT  A
                                TGAGCA TTA  GG GGAAGAG
                                |||||| |||  || |||||||
                                ACTCGT AAT  CC CCTTCTC
                                    _  CT  _
GAM411  IGSF8     3'  CTCTCCCTCTGTCCACTCT    54613    C   TAT     A
                                AG AGT   TGGAGG AGAG
                                || |||   |||||| ||||
                                TC TCA   GTCTCC TCTC
                                 _  CCT     C
GAM411  IL2       5'  CTCTCTTTAATCACTACTCA   65251      C   T      GA
                                TGAG AGT ATTGGAG  AGAG
                                |||| ||| |||||||  ||||
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                                ACTC TCA TAATTTC  TCTC
                                  A  C     __
GAM411  LGTN    5'  CTCTCTTCCCCAGGCCAC    23552    TA_   A
                                GT  TTGG GGAAGAGAG
                                ||  |||| |||||||||
                                CA  GACC CCTTCTCTC
                                 CCG   _
GAM411  MYCL2   3'  CTTCCTCCCACTCTCA     19375     C   TATT
                                TGAG AGT   GGAGGAAG
                                |||| |||   ||||||||
                                ACTC TCA   CCTCCTTC
                                  _  C___
GAM411  PAX5    3'  CTCTCTTCCTCCAGGGACTCT  34129    C   A
                                AG AGTT TTGGAGGAAGAGAG
                                || |||| ||||||||||||||
                                TC TCAG GACCTCCTTCTCTC
                                 _   G
GAM411  PRKACA  3'  CTCCCTCCCTCCTTCCTCTACT 12268    C  TTATT    A  A
           C                     GAG AG    GGAGG AG GAG
                                ||| ||    ||||| || |||
                                CTC TC    CCTCC TC CTC
                                  A  TCCTT    C  C
GAM411  TBXA2R  5'  TCCCTAATAACCAGCCA    8367    A  A_      A
                                TG GC  GTTATTGG GGA
                                || ||  |||||||| |||
                                AC CG  CAATAATC CCT
                                 _ AC       _
GAM411  TXNIP   3'  TCTCTTCCTGGACACTCA    22384     CA   ATTGG
                                TGAG  GTT    AGGAAGAGA
                                ||||  |||    |||||||||
                                ACTC  CAG    TCCTTCTCT
                                  A_  G____
GAM411  C20orf32 3'  CTCCCTTCCTCCTCTGCTCA  40139       TTATT      A
                                TGAGCAG    GGAGGAAG GAG
                                |||||||    |||||||| |||
                                ACTCGTC    CCTCCTTC CTC
                                    T____       C
GAM411  ELOVL1  3'  CTCCCCTCCCCACAGCTGCTC  43371       ATT_    AA
                                GAGCAGTT   GGAGG  GAG
                                ||||||||   |||||  |||
                                CTCGTCGA   CCTCC  CTC
                                     CACC    C_
GAM411  FEM-2   3'  CTCCCCTCCCCCCGCTGCCCA  28311    A    TATT    AA
                                TG GCAGT   GGAGG  GAG
                                || |||||   |||||  |||
                                AC CGTCG   CCTCC  CTC
                                 C    CCCC    C_
GAM411  FLJ11320 3'  CTCCCTCTCCAGTCCCCTCA  37828     CAGTT      AA
                                TGAG    ATTGGAGG  GAG
                                ||||    ||||||||  |||
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                                ACTC    TGACCTCT  CTC
                                  CCC__       CC
GAM411  FLJ22671  3'  CTCTCTTCCTCTTTCTCCGGCC 46312    A  AGTTATT
            A                    TG GC      GGAGGAAGAGAG
                                 || ||      ||||||||||||
                                 AC CG      TCTCCTTCTCTC
                                  _  GCCTCTT
GAM411  KATNB1   3'  CTCTCTCCAGCAATAGCTGCCC 20831    A        GA   A
            A                    TG GCAGTTATTG  GGA GAGAG
                                 || ||||||||||  ||| |||||
                                 AC CGTCGATAAC  CCT CTCTC
                                  C         GA  _
GAM411  KIAA0296 3'  CTCTCTCCCCCCCAGGAGC    28774     A    A  A
                                 GTT TTGG GG AGAGAG
                                 ||| |||| || ||||||
                                 CGA GACC CC TCTCTC
                                   G    C  C
GAM411  KIAA0664 3'  CTCTTCCTCCACGTCTCA    64944      CA  TATT
                                 TGAG  GT    GGAGGAAGAG
                                 ||||  ||    ||||||||||
                                 ACTC  CA    CCTCCTTCTC
                                   TG  _____
GAM411  KIAA0747 3'  CTCCCTTCCTCCCAACTCCTCA 31620      C    ATT       A
                                 TGAG AGTT   GGAGGAAG GAG
                                 |||| ||||   |||||||| |||
                                 ACTC TCAA   CCTCCTTC CTC
                                   C    C__       C
GAM411  KIAA1884 3'  CTCCCTTCCCCCTTACACTC   73724     CA  TATT  A    A
                                 GAG  GT    GG GGAAG GAG
                                 |||  ||    || ||||| |||
                                 CTC  CA    CC CCTTC CTC
                                   A_  TT__  C    C
GAM411  KIAA1925 5'  CTCTCCCTCTCCGCCCTCGCCC 93713    A  _  TTAT     AA
            A                    TG GC AG    TGGAGG  GAGAG
                                 || || ||    ||||||  |||||
                                 AC CG TC    GCCTCT  CTCTC
                                  C  C  CC__      CC
GAM411  MARK2    5'  CTCCCTTCCTCCAAGCTTCTC  66220     C   TA        A
                                 GAG AGT  TTGGAGGAAG GAG
                                 ||| |||  |||||||||| |||
                                 CTC TCG  AACCTCCTTC CTC
                                   T   __          C
GAM411  TOB2     3'  CTCCCTTCCTCCTTCACACTC  33236     CA  TATT       A
                                 GAG  GT    GGAGGAAG GAG
                                 |||  ||    |||||||| |||
                                 CTC  CA    CCTCCTTC CTC
                                   A_  CTT_       C
GAM411  WBSCR23  3'  CTCCCCTCCTCCAATACATTCT 47433     C   _         A__
            C                    GAG AGT TATTGGAGGA   GAG
                                 ||| ||| ||||||||||   |||
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                                CTC TTA ATAACCTCCT   CTC
                                  _  C        CCC
GAM411  LOC126917 3'  CTCCCTTCCTCCTGAGCCAGCC 75088    A  A_   ATT      A
            CA                    TG GC  GTT   GGAGGAAG GAG
                                  || ||  |||   |||||||| |||
                                  AC CG  CGA   CCTCCTTC CTC
                                   C  AC   GT_       C
GAM411  LOC143437 5'  CTCTTCCTCCAACATGCAGCTC 83857      A  TA_
                                  GAGC GT   TTGGAGGAAGAG
                                  |||| ||   ||||||||||||
                                  CTCG CG   AACCTCCTTCTC
                                    A  TAC
GAM411  LOC143879 3'  CTCTCCTCCCCCCCTCTCA    77159      C  TTATT     A
                                  TGAG AG     GGAGGA GAG
                                  |||| ||     |||||| |||
                                  ACTC TC     CCTCCT CTC
                                    _  CCCC_     _
GAM411  LOC146488 3'  CTCTCCCCCTCCAGTCCTAGCC 71357    A  _  TT       AA
            CA                    TG GC AG  ATTGGAGG  GAGAG
                                  || || ||  ||||||||  |||||
                                  AC CG TC  TGACCTCC  CTCTC
                                   C  A  C_       CC
GAM411  LOC147180 5'  CTCTTCCTCTTCTCTGGTCA   85097     G   TTATT
                                  TGA CAG     GGAGGAAGAG
                                  ||| |||     ||||||||||
                                  ACT GTC     TCTCCTTCTC
                                    G   TCT__
GAM411  LOC148930 3'  CTCTCTTCCTCCCATCTTCTCA 79842      C  TTATT
                                  TGAG AG     GGAGGAAGAGAG
                                  |||| ||     ||||||||||||
                                  ACTC TC     CCTCCTTCTCTC
                                    T  TAC__
GAM411  LOC149466 3'  CTCTCTTGCTCAATAACTCTCA 80196      C       G  G
                                  TGAG AGTTATTG AG AAGAGAG
                                  |||| |||||||| || |||||||
                                  ACTC TCAATAAC TC TTCTCTC
                                    _       _ G
GAM411  LOC149699 5'  CTCTCTTCTAATCCACCACTCA 80325      CA  TATT  __
                                  TGAG  GT    GGA  GGAAGAGAG
                                  ||||  ||    |||  |||||||||
                                  ACTC  CA    CCT  TCTTCTCTC
                                    AC  ____   AA
GAM411  LOC149711 3'  CTCTCTTCCCCCTTTCTCTGC  85851      TTATT  A
                                  GCAG     GG GGAAGAGAG
                                  ||||     || |||||||||
                                  CGTC     CC CCTTCTCTC
                                    TCTTT  C
GAM411  LOC149721 3'  TCCTCCAACAAATGCTCA     80320       G  A
                                  TGAGCA TT TTGGAGGA
                                  |||||| || ||||||||
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                                ACTCGT AA AACCTCCT
                                   A  C
GAM411  LOC152762 3'  CTCTCTTCCCCTCCCTACCGCT 81532       A  TATT_  A
          CA                     TGAGC GT     GG GGAAGAGAG
                                 |||||| ||     || |||||||||
                                 ACTCG CA     CC CCTTCTCTC
                                   C  TCCCT  _
GAM411  LOC155179 3'  CTCTTCCTGGTGACACCCTCA  82229      CA_     GG
                                 TGAG   GTTATT  AGGAAGAG
                                 ||||   ||||||  ||||||||
                                 ACTC   CAGTGG  TCCTTCTC
                                   CCA     __
GAM411  LOC161734 3'  CTCTCCTCCTCCAAAGGAAC   88464     A__       A
                                 GTT   TTGGAGGA GAGAG
                                 |||   |||||||| |||||
                                 CAA   AACCTCCT CTCTC
                                   GGA       C
GAM411  LOC220021 3'  TCTCTTCCTCCCTTACTC    95025     CAGT  TT
                                 GAG    TA  GGAGGAAGAGA
                                 |||    ||  ||||||||||
                                 CTC    AT  CCTCCTTCTCT
                                   _____  TC
GAM411  LOC253531 5'  CTCTTCCTCCAACATGCAGCTC 98223      A  TA_
                                 GAGC GT   TTGGAGGAAGAG
                                 |||| ||   ||||||||||||
                                 CTCG CG   AACCTCCTTCTC
                                   A  TAC
GAM412  ALDH3A2   5'  CAGCCCGCTGCCAGAGCCGGGG 69796          ATG_  A
          A                      TCCCTGGCTT    AGC GGCTG
                                 ||||||||||    ||| |||||
                                 AGGGGCCGAG    TCG CCGAC
                                       ACCG   C
GAM412  CASP10    3'  CAGCCTGCTTTCACACTAAGGA 53245     C   CTTAT
                                 TCC TGG     GAGCAGGCTG
                                 ||| |||     ||||||||||
                                 AGG ATC     TTCGTCCGAC
                                   A   ACACT
GAM412  DYT1      3'  CAGCCCACTCATCGCAGGG    5477       G TT    CA
                                 CCCTG C  ATGAG  GGCTG
                                 ||||| |  |||||  |||||
                                 GGGAC G  TACTC  CCGAC
                                    _ C_     AC
GAM412  LPIN1     5'  CAGCCTGCTGAGAACTAG     67985      C  ATG
                                 CTGG TT   AGCAGGCTG
                                 |||| ||   |||||||||
                                 GATC AA   TCGTCCGAC
                                   _  GAG
GAM412  TNXB      5'  CTCAGCCTTGGGCCAAGCCTGG 51634     CT    TA  A  ___
          A                      TCC  GGCT  TG GC   AGGCTGAG
                                 |||  ||||  || ||   ||||||||
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                                AGG  CCGA  AC CG   TCCGACTC
                                  T_   __  _ GGT
GAM412  C20orf150 3'  CAGCCTGCCCTCAAGCCAAGGA 66009     C     ATGA
                                TCC TGGCTT   GCAGGCTG
                                ||| ||||||   ||||||||
                                AGG ACCGAA   CGTCCGAC
                                  A     CTCC
GAM412  C20orf39  5'  CAGCCTGCCGGCCAGGCGA   46571   _     TAT A
                                TC CCTGGCT   G GCAGGCTG
                                || |||||||  | ||||||||
                                AG GGACCGG   C CGTCCGAC
                                 C     ___ _
GAM412  CBX6    3'  CAGCCTGCCTGAAGCAAAGGA  27407    CTG   ATGA
                                TCC   GCTT   GCAGGCTG
                                |||   ||||   ||||||||
                                AGG   CGAA   CGTCCGAC
                                  AAA   GTC_
GAM412  CD84    3'  CTCAGCCTGTAAGCAAAGCAGG 81570     G   A  A__
                                CCTG CTT TG   GCAGGCTGAG
                                |||| ||| ||   ||||||||||
                                GGAC GAA AC   TGTCCGACTC
                                  _  _ GAA
GAM412  CYP2D6   3'  CAGCCTGCTCCTAGCCCAGAGG 5451    _   C   T
                                CC CTGG TTA GAGCAGGCTG
                                || |||| ||| ||||||||||
                                GG GACC GAT CTCGTCCGAC
                                 A   C   C
GAM412  DKFZP586J0619 3'  CTCAGCCTGCCCAGCAGGGA   82317       G  TAT A
                                TCCCTG CT   G GCAGGCTGAG
                                |||||| ||   | ||||||||||
                                AGGGAC GA   C CGTCCGACTC
                                   _ ___ C
GAM412  FKHL18   3'  CAGCCCTGGTGAGCCAAGGA   80370    C      G  CA
                                TCC TGGCTTAT AG  GGCTG
                                ||| |||||||| ||  |||||
                                AGG ACCGAGTG TC  CCGAC
                                  A       G __
GAM412  FLJ14800  3'  CAACCTGCTCAGGCACCACAGA 52684    CC   CTTA      C
                                TC  TGG    TGAGCAGG TG
                                ||  |||    |||||||| ||
                                AG  ACC    ACTCGTCC AC
                                 AC   ACGG       A
GAM412  FLJ14957  3'  CTCAGCCCACTCATACCTAGAG 52816    C    CT     CA
           A                     TC CTGG  TATGAG  GGCTGAG
                                || ||||  ||||||  |||||||
                                AG GATC  ATACTC  CCGACTC
                                 A   C_     AC
GAM412  KIAA1023  3'  CAGGCTCAGAAGCCAGGGA   34677          A    AGG
                                TCCCTGGCTT TGAGC   CTG
                                |||||||||| |||||   |||
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                                AGGGACCGAA ACTCG   GAC
                                      G    ___
GAM412  KIAA1655  5'  CTCAGCCCACTCCCAAACCAG  67183     C  AT   CA
                                CTGG TT  GAG  GGCTGAG
                                |||| ||  |||  |||||||
                                GACC AA  CTC  CCGACTC
                                  A  CC   AC
GAM412  MGC35521  3'  CTCAGGTGTCAGTAAGCCAG  59666        GA   GG
                                CTGGCTTAT  GCA  CTGAG
                                |||||||||  |||  |||||
                                GACCGAATG  TGT  GACTC
                                      AC   G_
GAM412  MGC5508   3'  CAGCCTGCCTCACCAGGGA   44264       CTTA   _
                                TCCCTGG    TGAG CAGGCTG
                                |||||||    |||| |||||||
                                AGGGACC    ACTC GTCCGAC
                                     ____   C
GAM412  RIN3      5'  CTCAGCCTGCCTCCCCAAGGGA 46162      _  CTTAT  _
                                TCCCT GG    GAG CAGGCTGAG
                                ||||| ||    ||| |||||||||
                                AGGGA CC    CTC GTCCGACTC
                                   A  C____   C
GAM412  SP140     3'  AGTATCTCATCAGCCAGGGA   24326        T    CAG
                                TCCCTGGCT ATGAG   GCT
                                ||||||||| |||||   |||
                                AGGGACCGA TACTC   TGA
                                      C    TA_
GAM412  VI        3'  CAGCCGCTAGGCCAGGGA    26486         ATG   A
                                TCCCTGGCTT   AGC GGCTG
                                ||||||||||   ||| |||||
                                AGGGACCGGA   TCG CCGAC
                                     ___   _
GAM412  LOC112817 5'  CAGTGGCCACAAGTCAGGGA   57319         A  A  AG
                                TCCCTGGCTT TG GC  GCTG
                                |||||||||| || ||  ||||
                                AGGGACTGAA AC CG  TGAC
                                      C  _  G_
GAM412  LOC129676 5'  CTCAGCCTGCAGACACAGGGA  76232       GCTTATGA
                                TCCCTG       GCAGGCTGAG
                                ||||||       ||||||||||
                                AGGGAC       CGTCCGACTC
                                   ACAGA___
GAM412  LOC134266 3'  CTCAGCCTACCAAGTAGCCAGG 75644        TATGAGC
                                CCTGGCT      AGGCTGAG
                                |||||||      ||||||||
                                GGACCGA      TCCGACTC
                                    TGAACCA
GAM412  LOC150248 3'  CCACCTCATCAGCCAGGGA    86126        T    CA
                                TCCCTGGCT ATGAG  GG
                                ||||||||| |||||  ||
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                                AGGGACCGA TACTC  CC
                                      C     CA
GAM412  LOC155179 3'  CAGGCTCAGAAGCCAGGGA   82225          A     AGG
                                TCCCTGGCTT TGAGC   CTG
                                |||||||||| |||||   |||
                                AGGGACCGAA ACTCG   GAC
                                      G    ___
GAM412  LOC158056 5'  CTCAGCCCAGGAGAGCCAGGGG 82589          ATGAGCA
                                TCCCTGGCTT      GGCTGAG
                                ||||||||||      |||||||
                                GGGGACCGAG      CCGACTC
                                      AGGAC__
GAM412  LOC219405 3'  CAGCCTGCTCTACCCAGAGA   92450    C    CTTAT
                                TC CTGG    GAGCAGGCTG
                                || ||||    ||||||||||
                                AG GACC    CTCGTCCGAC
                                 A   CAT__
GAM412  LOC221496 3'  TCAGCCTGCTCCCTGGGA    93643     T  CTTAT
                                TCCC GG    GAGCAGGCTGA
                                |||| ||    ||||||||||
                                AGGG CC    CTCGTCCGACT
                                  T  _____
GAM412  LOC222031 3'  CAGCCTGTCTAACCCAAAGA   95672    CC   C   T  G
                                TC  TGG TTA GA CAGGCTG
                                ||  ||| ||| || |||||||
                                AG  ACC AAT CT GTCCGAC
                                 AA   C   _  _
GAM412  LOC51320  3'  CTGCAACTAATAAGCCAAGGA  34028     C       GA___
                                TCC TGGCTTAT    GCAG
                                ||| ||||||||    ||||
                                AGG ACCGAATA    CGTC
                                  A       ATCAA
GAM413  HAL       5'  GCCACTCCTGCATAAAGCTC   10903          TGAAAA
                                GAGCTTTATGC     GGTGGC
                                ||||||||||     ||||||
                                CTCGAAATACG     TCACCG
                                      TCC___
GAM413  HMGN2     3'  GGCCACCTTGGCACAAAAGC   19809      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _  _  GG
GAM413  NMI       5'  GGCCACCTCCTCAGGAAG    17436     ATG   AA
                                CTTT   CTGA  AGGTGGCC
                                ||||   ||||  ||||||||
                                GAAG   GACT  TCCACCGG
                                  ___    CC
GAM413  PACE      3'  GGCCACCTCTCCAAGGGCTT   11944       A  CT  AAA
                                GAGCTTT TG  GA   GGTGGCC
                                |||||||  ||  ||   |||||||
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                                TTCGGGA AC  CT   CCACCGG
                                   _ CT  ___
GAM413  PYCR1    3' CCACCTTCCTCTAGAGCTC   70639       TGCT  A_
                                GAGCTTTA   GA  AAGGTGG
                                ||||||||   ||  |||||||
                                CTCGAGAT   CT  TTCCACC
                                   _____ CC
GAM413  SDC1     3' GGCCACCTCCCCAGCATTCCAG 12991     TT_     AAA
           C                     GCT   ATGCTG   AGGTGGCC
                                 |||   ||||||   ||||||||
                                 CGA   TACGAC   TCCACCGG
                                   CCT     CCC
GAM413  FLJ11560 5' GCCCAGGCCCAGCATAAAG   48008         AAAA  ___
                                CTTTATGCTG   GGT   GGC
                                ||||||||||   |||   |||
                                GAAATACGAC   CCG   CCG
                                     _____  GAC
GAM413  KIAA0446 5' CCACCTTTTGAAGAGCTC    69446       ATGCTG
                                GAGCTTT     AAAAGGTGG
                                |||||||     |||||||||
                                CTCGAGA     TTTTCCACC
                                   AG_____
GAM413  KIAA0971 3' GTTGTTCTCAGCATAAAGT   30677          AAA  TG
                                GCTTTATGCTGA   GG  GC
                                ||||||||||||   ||  ||
                                TGAAATACGACT   TT  TG
                                     C__  GT
GAM413  KIAA1393 3' GGCCACCTTGGCACAAAAGC  72574      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                   _ _  GG
GAM413  KIAA1656 3' GGCCACCTCCTCCTAGAAGCC 66377   A    ATGCT  AA
                                G GCTTT    GA  AGGTGGCC
                                | |||||    ||  ||||||||
                                C CGAAG    CT  TCCACCGG
                                _    ATC__  CC
GAM413  KIAA1884 3' GCCACCTTCATCTACCAAGGCT 73728       ATGCT  A_
           C                     GAGCTTT    GA  AAGGTGGC
                                 |||||||    ||  ||||||||
                                 CTCGGAA    CT  TTCCACCG
                                    CCAT_  AC
GAM413  PP3501   3' GGCCACCGTTGACAGCATAAAG 41683         AAAA_
                                CTTTATGCTG    GGTGGCC
                                ||||||||||    |||||||
                                GAAATACGAC    CCACCGG
                                     AGTTG
GAM413  SDCCAG3  3' GGTGTTCTCAGCATGAAGCTC  22803           AAA  TG
                                GAGCTTTATGCTGA   GG  GCC
                                ||||||||||||||   ||  |||
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                                CTCGAAGTACGACT   CT  TGG
                                      ___  TG
GAM413  SP140    3'  GGCCACCTCCATGCAGAAGC  24327      A   TGAAA
                                GCTTT TGC    AGGTGGCC
                                ||||| |||    ||||||||
                                CGAAG ACG    TCCACCGG
                                  _  TACC_
GAM413  LOC148760 3'  GGCCACCTTCTCCAACAAGCTC 85364       TA  CT  A
                                GAGCTT  TG  GA AAGGTGGCC
                                ||||||  ||  || |||||||||
                                CTCGAA  AC  CT TTCCACCGG
                                   CA  __  C
GAM413  LOC150170 5'  ACCTGTTTCACATAAAGC    80414        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                    _    G
GAM413  LOC150175 5'  ACCTGTTTCACATAAAGC    80453        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                    _    G
GAM413  LOC150215 5'  ACCTGTTTCACATAAAGC    80456        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                    _    G
GAM413  LOC150218 5'  ACCTGTTTCACATAAAGC    80525        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                    _    G
GAM413  LOC152065 3'  GGCCACCTTCTCCTTGGCAGGC 86737      TTA   ___  A
           TC                     GAGCT   TGCT   GA AAGGTGGCC
                                |||||   ||||   || |||||||||
                                CTCGG   ACGG   CT TTCCACCGG
                                  ___    TTC  C
GAM413  LOC152267 3'  GGCCACCTTGGCACAAAAGC   61036      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _  GG
GAM413  LOC158292 5'  CCTCTGGACCCAGCATAAGGCT 88046           AAAA_  T
           C                     GAGCTTTATGCTG     GG GG
                                ||||||||||||     || ||
                                CTCGGAATACGAC     TC CC
                                      CCAGG  T
GAM413  LOC219997 3'  GCCACCTCTTCAGCCTC     93256     CTTTAT     A
                                GAG     GCTGAA AGGTGGC
                                |||     |||||| |||||||
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                                CTC     CGACTT TCCACCG
                                  _______     C
GAM413  LOC256269 3'  GGCCACCTTGGCACAAAAGC   96608      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _ GG
GAM413  LOC91963  5'  GGCCACCTCCTCTGAGAAGC   68321      ATGCT  AA
                                GCTTT    GA  AGGTGGCC
                                |||||    ||  ||||||||
                                CGAAG    CT  TCCACCGG
                                   AGT__  CC
GAM414  CCND2     3'  TCCCAGCAAATCATCGGGCCA  10055          CCACA  _  A
                                TGGCCTGATGAT    GC GG GA
                                ||||||||||||    || || ||
                                ACCGGGCTACTA    CG CC CT
                                       AA___  A  C
GAM414  GCN5L2    5'  CTCCGCTGCGGGGGAGGCC    60529      GATGA   A
                                GGCCT    TCC CAGCGGAG
                                |||||    ||| ||||||||
                                CCGGA    GGG GTCGCCTC
                                   GG___  C
GAM414  GJA5      3'  CTGACCAGATCATCAGCCA    19164      C       CACAG
                                TGGC TGATGATC    CGG
                                |||| ||||||||    |||
                                ACCG ACTACTAG    GTC
                                  _       ACCA_
GAM414  HIVEP3    3'  TCCCCGCTGTGGTTGGCAGCCA 44702      C  ATGAT       A
                                TGGC TG    CCACAGCGG GA
                                |||| ||    ||||||||| ||
                                ACCG AC    GGTGTCGCC CT
                                  _ GGTT_       C
GAM414  HOXD1     5'  CCGCCGGTATATTAGGCCA    44696          AT  ACA
                                TGGCCTGATG  CC   GCGG
                                ||||||||||  ||   ||||
                                ACCGGATTAT  GG   CGCC
                                      AT  C__
GAM414  SUFU      3'  CCTTGTGACCCATCAGGCCA   32934          ATC    C
                                TGGCCTGATG   CACAG GG
                                ||||||||||   ||||| ||
                                ACCGGACTAC   GTGTT CC
                                      CCA    _
GAM414  DKFZP586J1624 3'  CTCCGCCCAGTCACCATCAGGC 32043          ATCCACA_
          CA                    TGGCCTGATG       GCGGAG
                                ||||||||||       ||||||
                                ACCGGACTAC       CGCCTC
                                      CACTGACC
GAM414  KIAA1671  3'  CTTTGCTTATGAATCATCAGAC 66282    C       C  C_
          C                     GG CTGATGAT CA  AGCGGAG
                                || |||||||| ||  |||||||
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                                CC GACTACTA GT  TCGTTTC
                                 A       A  AT
GAM414  LOC159110 5'  TCTCCGCTGCCCCGGTCAACCA 82995     CCTGA    CA__
                                TGG    TGATC   CAGCGGAGA
                                |||    |||||   |||||||||
                                ACC    ACTGG   GTCGCCTCT
                                  A____    CCCC
GAM414  LOC159116 5'  TCTCCGCTGCCCCGGTCAACCA 82978     CCTGA    CA__
                                TGG    TGATC   CAGCGGAGA
                                |||    |||||   |||||||||
                                ACC    ACTGG   GTCGCCTCT
                                  A____    CCCC
GAM414  LOC165476 5'  CTCCGCTGCCTGCTCAGCCA   88550     C   TGATCCA
                                TGGC TGA      CAGCGGAG
                                |||| |||      ||||||||
                                ACCG ACT      GTCGCCTC
                                  _   CGTCC__
GAM414  LOC200032 5'  CTGACCAGATCATCAGCCA    85475     C       CACAG
                                TGGC TGATGATC    CGG
                                |||| ||||||||    |||
                                ACCG ACTACTAG    GTC
                                  _       ACCA_
GAM414  LOC219654 5'  CTCCGCTGCGGAGGGGGGCC   92932      GATGA   A
                                GGCCT    TCC CAGCGGAG
                                |||||    ||| ||||||||
                                CCGGG    AGG GTCGCCTC
                                   GGG__   C
GAM414  LOC255862 3'  TCAAATGTAGACTATCAGGCCA 96115         A  C   GCG
                                TGGCCTGATG TC ACA   GA
                                |||||||||| || |||   ||
                                ACCGGACTAT AG TGT   CT
                                      C  A   AAA
GAM415  BAP1     3'  ATGCCAAGGGGTAATGGG    17395      C    GG
                                CCCAT ATCT  TTTGGCAT
                                ||||| ||||  ||||||||
                                GGGTA TGGG  GAACCGTA
                                   A   __
GAM415  FMR2     3'  CAGTATCAAATGAATGGGTCAA 10683         _  C   _
                                TTGACCCAT CAT TGGT TTG
                                ||||||||| ||| |||| |||
                                AACTGGGTA GTA ACTA GAC
                                      A  A   T
GAM415  FLJ11939  3'  ATGCCAAACCAATTTTGGGTCG 45494        TC  C
              A                  TTGACCCA  AT TGGTTTGGCAT
                                ||||||||  || ||||||||||
                                AGCTGGGT  TA ACCAAACCGTA
                                     TT  _
GAM415  MGC15606  3'  CCCTTAGAAGAATGGGTCAA   59522         _ A    TTT
                                TTGACCCAT C TCTGG   GG
                                |||||||| | |||||   ||
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                                AACTGGGTA G AGATT   CC
                                     A A    C__
GAM415  LOC126669 5'  ATGCCAAACGGACAAAGGGTCA 75924        ATCA   G
            A                    TTGACCC   TCTG TTTGGCAT
                                 |||||||   |||| ||||||||
                                 AACTGGG   AGGC AAACCGTA
                                     AAAC   _
GAM415  LOC145813 3'  CAAACTACAGACCACGGGCCAA 84503     A  ATCA   __
                                 TTG CCC   TCTG  GTTTG
                                 ||| |||   ||||  |||||
                                 AAC GGG   AGAC  CAAAC
                                   C   CACC   AT
GAM415  LOC148293 3'  GGGCAGATGATAGTCAA     79530      CC      G
                                 TTGAC  ATCATCTG TT
                                 |||||  |||||||| ||
                                 AACTG  TAGTAGAC GG
                                    A_      G
GAM416  CHAD     3'  GGAAGGCTGAGCCTCTC     8855       TA  CTGC
                                 GAGAG  CTC   GTCTTCC
                                 |||||  |||   |||||||
                                 CTCTC  GAG   CGGAAGG
                                    C_   T____
GAM416  DSG1     5'  AGGAAGGCAGAAACACCTC   10449    A  ACTC   GT
                                 GAG GT   CTGC  CTTCCT
                                 ||| ||   ||||  ||||||
                                 CTC CA   GACG  GAAGGA
                                   _  CAAA   __
GAM416  MID1     3'  AAGATGTAGAAGTCCCTC    6351     T_  C
                                 GAG  ACT CTGCGTCTT
                                 |||  ||| |||||||||
                                 CTC  TGA GATGTAGAA
                                   CC   A
GAM416  OTOF     3'  AGGAAGACTCCTGAAACCCTC  17828    A  AC  CTGC
                                 GAG GT  TC   GTCTTCCT
                                 ||| ||  ||   ||||||||
                                 CTC CA  AG   CAGAAGGA
                                   C  A_  TCCT
GAM416  RNMT     3'  AGGACATCCAAGGGTACTCTC  15047       T   GCGTCT
                                 GAGAGTAC CCT     TCCT
                                 |||||||| |||     ||||
                                 CTCTCATG GGA     AGGA
                                      _  ACCTAC
GAM416  SCN3A    5'  AGGAAGACACGTTATACCCT   23612    A   CTCC  C
                                 AG GTA   TG GTCTTCCT
                                 || |||   || ||||||||
                                 TC CAT   GC CAGAAGGA
                                  C   ATT_  A
GAM416  SFRS7    3'  GGAAGGCGATACTCTC      60148       CTCCTG
                                 GAGAGTA     CGTCTTCC
                                 |||||||     ||||||||
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                                CTCTCAT     GCGGAAGG
                                   A_____
GAM416  SLC13A4  5'  AAGACGAAGGAGGACTCTC   25857       A    G
                                GAGAGT CTCCT CGTCTT
                                |||||| ||||| ||||||
                                CTCTCA GAGGA GCAGAA
                                   G    A
GAM416  SSX2     3'  AGGAAGATGACGAGTAACTC  97962     _   CTG
                                GAGT ACTC   CGTCTTCCT
                                |||| ||||   |||||||||
                                CTCA TGAG   GTAGAAGGA
                                  A   CA_
GAM416  TGFBR2   3'  AAGATTCAAGAGTATTCTC   13725         C  C
                                GAGAGTACTC TG GTCTT
                                |||||||||| || |||||
                                CTCTTATGAG AC TAGAA
                                      A  T
GAM416  TNFRSF11A 3'  AGGAAGACCACCCGGCATTCTC 15187       A  CC_  C
                                GAGAGT CT   TG GTCTTCCT
                                |||||| ||   || ||||||||
                                CTCTTA GG   AC CAGAAGGA
                                   C  CCC  _
GAM416  AP3M2    3'  AGGAAGACCCGTACTCTC    23299        TCCT C
                                GAGAGTAC    G GTCTTCCT
                                ||||||||    | ||||||||
                                CTCTCATG    C CAGAAGGA
                                     _____ C
GAM416  CALN1    3'  AGGAAGACACAGAATTCTTTC  49658      TACTC   C
                                GAGAG     CTG GTCTTCCT
                                |||||     ||| ||||||||
                                CTTTC     GAC CAGAAGGA
                                   TTAA_   A
GAM416  DAMS     5'  AGGAAATTCAAGTACTCT    42084        CC  C  C
                                AGAGTACT  TG GT TTCCT
                                ||||||||  || || |||||
                                TCTCATGA  AC TA AAGGA
                                     __  T  _
GAM416  DKFZP727M111 5'  AGGCCAGGAGGACCCTC     32055     A  A     C
                                GAG GT CTCCTG GTCT
                                ||| || |||||| ||||
                                CTC CA GAGGAC CGGA
                                  C  G     _
GAM416  FLJ14486 5'  AGGAAGGTTCAAGTCTCTC   52434      T   CC  CG
                                GAGAG ACT  TG  TCTTCCT
                                ||||| |||  ||  |||||||
                                CTCTC TGA  AC  GGAAGGA
                                   _  __  TT
GAM416  FUSIP1   3'  AGGAAGACAGCCATAGTCTC  22780     T   CCT  _
                                GAG ACT   GC GTCTTCCT
                                ||| |||   || ||||||||
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                                CTC TGA   CG CAGAAGGA
                                  _   TAC  A
GAM416  HIC      3'  GAAGATTGAGTACTCT      68048         CTGC
                                AGAGTACTC    GTCTTC
                                |||||||||    ||||||
                                TCTCATGAG    TAGAAG
                                     T___
GAM416  IL22R    3'  AGGAAATGCAGGGAAACTC    41467      AC       C
                                GAGT  TCCTGCGT TTCCT
                                ||||  |||||||| |||||
                                CTCA  GGGACGTA AAGGA
                                  AA       _
GAM416  KIAA0472 3'  AGGAGGGGTAAGTACTCTC    72334         CC   G
                                GAGAGTACT  TGC TCTTCCT
                                |||||||||  ||| |||||||
                                CTCTCATGA  ATG GGGAGGA
                                       __   _
GAM416  KIAA1229 3'  AGGATGTAAAAGTTCTCTC    62750       T   CC
                                GAGAG ACT  TGCGTCTT
                                ||||| |||  ||||||||
                                CTCTC TGA  ATGTAGGA
                                   T   AA
GAM416  LAK-4P   3'  AGGAAGACAGTTTCGCCTCTC  24394       TACTCCT  _
                                GAGAG      GC GTCTTCCT
                                |||||      || ||||||||
                                CTCTC      TG CAGAAGGA
                                   CGCTT__  A
GAM416  MRPS35   3'  AGGTCCTCAGGAGTATTCTC   41819           CGTCTT
                                GAGAGTACTCCTG     CCT
                                ||||||||||||      |||
                                CTCTTATGAGGAC     GGA
                                       TCCT__
GAM416  OBTP     5'  AGGATCTGCAAGGAGGACCCTC 34663     A  A    _   TCT
                                GAG GT CTCCT GCG   TCCT
                                ||| || ||||| |||   ||||
                                CTC CA GAGGA CGT   AGGA
                                  C  G    A   CT_
GAM416  RI58     3'  AGATCAGGAATACTCTT     25774        C    C
                                GAGAGTA TCCTG GTCT
                                ||||||| ||||| ||||
                                TTCTCAT AGGAC TAGA
                                   A    _
GAM416  SMBP     3'  AAGACAGAAGTGTACTCTC    72620        TC  GC_
                                GAGAGTAC  CT   GTCTT
                                ||||||||  ||   |||||
                                CTCTCATG  GA   CAGAA
                                     T_  AGA
GAM416  SNTG1    5'  AGGACTCTGAGGAGTACTCTT  39099          G  TCT
                                GAGAGTACTCCT CG   TCCT
                                ||||||||||| ||   ||||
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                                TTCTCATGAGGA GT   AGGA
                                      _ CTC
GAM416  SNX11    3'  AGGACCAGGAGTATCTC     26169      G       C
                                GAGA TACTCCTG GTCTT
                                |||| |||||||| |||||
                                CTCT ATGAGGAC CAGGA
                                  _       _
GAM416  TTY7     3'  AGGAAGACACAGGTAGCT    50015     ACT    C
                                AGT   CCTG GTCTTCCT
                                |||   |||| ||||||||
                                TCG   GGAC CAGAAGGA
                                  AT_    A
GAM416  LOC123872 5' GGAAAGAGGGTACTCTC     74710          _ GCGTC
                                GAGAGTACTC CT     TTCC
                                |||||||||| ||     ||||
                                CTCTCATGGG GA     AAGG
                                      A ______
GAM416  LOC138389 3' AGGAAGACTTGCAAGTCTCTC 76725      T   CC   __
                                GAGAG ACT  TGC  GTCTTCCT
                                ||||| |||  |||  ||||||||
                                CTCTC TGA  ACG  CAGAAGGA
                                   _  __   TT
GAM416  LOC143943 3' AGGAAGATCAGCAGCCTCTC   83911      TA  C   C
                                GAGAG  CT CTG GTCTTCCT
                                |||||  || ||| ||||||||
                                CTCTC  GA GAC TAGAAGGA
                                   C_  C   _
GAM416  LOC145009 5' AAGAAACAAAGGAGTACTTTC  60965           GCG__
                                GAGAGTACTCCT     TCTT
                                ||||||||||||     ||||
                                CTTTCATGAGGA     AGAA
                                      AACAA
GAM416  LOC147976 5' AGGAAGACTGGGGTACCCTC   79285     A       TGC
                                GAG GTACTCC   GTCTTCCT
                                ||| |||||||   ||||||||
                                CTC CATGGGG   CAGAAGGA
                                  C      T__
GAM416  LOC151512 3' AGGAAGACAATGCTTGTACCTC 86611     A    TCCT  ___
                                GAG GTAC    GC   GTCTTCCT
                                ||| ||||    ||   ||||||||
                                CTC CATG    CG   CAGAAGGA
                                  _    TT__  TAA
GAM416  LOC158801 3' GAAAACACAAGAAGTATTCT   88255        _ C  C  C
                                AGAGTACT C TG GT TTC
                                |||||||| | || || |||
                                TCTTATGA G AC CA AAG
                                     A A  A  A
GAM416  LOC206426 3' GAAGCGAGGTGCACTCTC    91099       ACT   G  T
                                GAGAGT   CCT CG CTTC
                                ||||||   ||| || ||||
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                                CTCTCA   GGA GC GAAG
                                   CGT   _ _
GAM416   LOC254337 5'  GGAAAGGGGAGTATCTC     98012      G      GCGTC
                                GAGA TACTCCT     TTCC
                                |||| |||||||     ||||
                                CTCT ATGAGGG     AAGG
                                  _      GA____
GAM416   LOC256790 5'  AGTGCAGGAGTGCCCTC     96489     A         T
                                GAG GTACTCCTGCG CT
                                ||| |||||||||| ||
                                CTC CGTGAGGACGT GA
                                  C         _
GAM416   LOC256946 3'  AGGAAGACAGCCATAGTCTC   96182     T   CCT  _
                                GAG ACT   GC GTCTTCCT
                                ||| |||   || ||||||||
                                CTC TGA   CG CAGAAGGA
                                  _   TAC  A
GAM416   LOC257396 5'  GAAATGTAGGAGCATCTC     98922      GTA       C
                                GAGA   CTCCTGCGT TTC
                                ||||   ||||||||| |||
                                CTCT   GAGGATGTA AAG
                                   AC_        _
GAM416   LOC257408 3'  AGGGCACCAGGAGTACCTC    97797     A       C  CT
                                GAG GTACTCCTG GT  TCCT
                                ||| |||||||| ||  ||||
                                CTC CATGAGGAC CA  GGGA
                                  _        _ C_
GAM416   LOC257453 3'  AGGAAGATGACGAGTAACTC   82927      _   CTG
                                GAGT ACTC   CGTCTTCCT
                                |||| ||||   |||||||||
                                CTCA TGAG   GTAGAAGGA
                                  A    CA_
GAM416   LOC51066  3'  AGGAAGATGGCCGACACTCTC  32500       AC  CTG
                                GAGAGT  TC   CGTCTTCCT
                                ||||||  ||   |||||||||
                                CTCTCA  AG   GTAGAAGGA
                                   C_  CCG
GAM417   IRS1      3'  CCATAGATGGTTCTCAATTGTA 19874      C         TGAAC
                                TACA ATTGAGAACC     ATGG
                                |||| ||||||||||     ||||
                                ATGT TAACTCTTGG     TACC
                                  _         TAGA_
GAM417   SERPINF1  3'  CCTGTAAGGTTTCAATG     12038         A   GA   T
                                CATTGAGA CCT  ACA GG
                                |||||||| |||  ||| ||
                                GTAACTTT GGA  TGT CC
                                     _  A_  _
GAM417   HSA243396 3'  CCATGTTCAGCAATGTCAATG  37844       GAAC_
                                CATTGA    CTGAACATGG
                                ||||||    ||||||||||
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                                GTAACT    GACTTGTACC
                                   GTAAC
GAM417  KIAA1387  3'  CAGGAATTTTCAATATGTA   71444     C      __
                                TACA ATTGAGAA  CCTG
                                |||| ||||||||  ||||
                                ATGT TAACTTTT  GGAC
                                  A       AA
GAM417  MGC16063  3'  TTCAAATTCCAATGTGTA    54930        A   CC
                                TACACATTG GAA  TGAA
                                ||||||||| |||  ||||
                                ATGTGTAAC CTT  ACTT
                                     _  AA
GAM417  SMCR8     3'  CCATGCTCAGGTTTGACTATGT 59253     TGA_      A
                                ACAT   GAACCTGA CATGG
                                ||||   |||||||| |||||
                                TGTA   TTTGGACT GTACC
                                  TCAG       C
GAM417  UPLC1     3'  CCATGCTAGGCCCCAATGT   35227      AGAA   AA
                                ACATTG   CCTG  CATGG
                                ||||||   ||||  |||||
                                TGTAAC   GGAT  GTACC
                                   CCC_   C_
GAM417  ZNF334    3'  CCATAAGTCAACCCTCAATGT  36637       AACC   AC_
                                ACATTGAG   TGA   ATGG
                                ||||||||   |||   ||||
                                TGTAACTC   ACT   TACC
                                    CCA_   GAA
GAM417  LOC145082 3'  TATGGAATGCCCTTAATGTGTA 84196          AACCTGAA
                                TACACATTGAG       CATG
                                ||||||||||        ||||
                                ATGTGTAATTC       GTAT
                                      CCGTAAG_
GAM417  LOC157723 3'  CCAAGTAAGGTTCTCAAATGT  82465      _      GA  A
                                ACATT GAGAACCT  AC TGG
                                ||||| ||||||||  || |||
                                TGTAA CTCTTGGA  TG ACC
                                  A       A_  A
GAM417  LOC219988 5'  CCATGTTCGGCCCCCAATG   93262      AGAAC
                                CATTG    CTGAACATGG
                                |||||    ||||||||||
                                GTAAC    GGCTTGTACC
                                  CCCC_
GAM418  CDH12     3'  CTTATCATTTAAAGTGGTGTA  15777        CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM418  GOCAP1    3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
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                                ATGTG  GAGGGTTCTT TTA
                                  AC        G
GAM418  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090      T   AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                  _   GTCA_
GAM418  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
          A                      TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                  TACTCCC_
GAM418  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126        CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM418  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
          TA                     TACA   TCC   GAAGAATAAG
                                ||||   |||   ||||||||||
                                ATGT   AGG   TTTCTTATTC
                                  AAA_  ATTG
GAM418  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68742            _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                         G
GAM418  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM418  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748     CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM418  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM418  OSBPL11   3'  CTTAATTTCCCAAGAGTGGTG  43206        CCAA   AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                     AACC   A_
GAM418  YME1L1    3'  TCATTCTTGATGTGGTGTA   58438        TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   |||||| ||
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                                ATGTGGTG  GTTCTT CT
                                    TA_    A
GAM418  ZNF262   3' CTTATTTTGTTTGGGAGT   18723        A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                    G
GAM418  LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_   AAGA
                                TACACCAC  CCAAG   ATA
                                ||||||||  |||||   |||
                                ATGTGGTG  GGTTC   TGT
                                    CAA   GG__
GAM419  CDH12    3' CTTATCATTTAAAGTGGTGTA 15777        CCCAA  GA
                                TACACCACT   GAA  ATAAG
                                |||||||||   |||  |||||
                                ATGTGGTGA   TTT  TATTC
                                    AA___  AC
GAM419  GOCAP1   3' ATTGTTCTTGGGAGCAGTGTA 43007     CA       G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC       G
GAM419  DKFZp434N2435 5' CTTATTACTGTGGGGTGGT   98090     T   AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                   _   GTCA_
GAM419  DKFZP564I122 3' CTTATTCTTCTCCCTCATGTGT 63877     CACTCCCA
            A                    TACAC      AGAAGAATAAG
                                |||||      ||||||||||
                                ATGTG      TCTTCTTATTC
                                   TACTCCC_
GAM419  FLJ21791 3' CTTATTTGCAGAAGTGGTGTA 62126        CCCAAGAA
                                TACACCACT      GAATAAG
                                |||||||||      |||||||
                                ATGTGGTGA      TTTATTC
                                    AGACG___
GAM419  HMP19    3' CTTATTCTTTGTTAGGAAAATG 88860     CCAC  CAA_
            TA                   TACA   TCC   GAAGAATAAG
                                ||||   |||   ||||||||||
                                ATGT   AGG   TTTCTTATTC
                                  AAA_  ATTG
GAM419  KIAA1719 3' TCTGTCTTGGGAGTGGTGTA  68742           _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                        G
GAM419  KIAA1853 3' TTTTTCTTGGAAGCAGTG    69929    CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
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                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM419  KIAA1877 3'  CTTATTCTTCTGCCATGAGT  66748     CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM419  KIAA1906 3'  CTTATTCTTCTTGACTTTTGG  73571    CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM419  OSBPL11  3'  CTTAATTTCCCAAGAGTGGTG  43206       CCAA   AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                     AACC   A_
GAM419  YME1L1   3'  TCATTCTTGATGTGGTGTA   58438       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                     TA_    A
GAM419  ZNF262   3'  CTTATTTTGTTTGGGAGT    18723        A
                                ACTCCCAAG AGAATAAG
                                |||||||||  ||||||||
                                TGAGGGTTT TTTTATTC
                                     G
GAM419  LOC91960 3'  TGTGGCTTGGAACGTGGTGTA  68294       TC_   AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
                                ATGTGGTG   GGTTC   TGT
                                     CAA    GG__
GAM420  ADCY7    5'  ACGACACGCGTGCCAAG    8487        TG  C_
                                CTTGGCAC  GC  GTCGT
                                ||||||||  ||  |||||
                                GAACCGTG  CG  CAGCA
                                     __  CA
GAM420  LUM      5'  ACGAAAGCAGTGTCAAG    11377        G CG
                                CTTGGCACTG C  TCGT
                                ||||||||||  |  ||||
                                GAACTGTGAC G  AGCA
                                     _ AA
GAM420  ZNF134   5'  ACGACCGCGGTGCCAGG    14303         G C
                                CTTGGCACTG C GTCGT
                                ||||||||||  | |||||
                                GGACCGTGGC G CAGCA
                                     _ C
GAM420  AP4M1    3'  ACGACGGCCAAGGTGGCA   17548    G   __
                                TG CACT  GGCCGTCGT
                                ||  ||||  |||||||||
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                                AC GTGG  CCGGCAGCA
                                 G    AA
GAM420  C20orf98  5'  ACGACTCCAGTCCAAG      72004       C     CC
                                CTTGG ACTGG  GTCGT
                                ||||| |||||  |||||
                                GAACC TGACC  CAGCA
                                   _     T_
GAM420  EBF2      3'  ACGTAGTCAGTGCTAAG     42956           CGT
                                CTTGGCACTGGC   CGT
                                ||||||||||||   |||
                                GAATCGTGACTG   GCA
                                       AT_
GAM420  KIAA1950  3'  ACGGCGGCAGTGACAAG     94176      G     G
                                CTTG CACTG CCGTCGT
                                |||| ||||| |||||||
                                GAAC GTGAC GGCGGCA
                                  A     _
GAM420  MGC20496  3'  ACGACACTGCCAGTGCCA     54526          C__
                                TGGCACTGGC   GTCGT
                                ||||||||||   |||||
                                ACCGTGACCG   CAGCA
                                      TCA
GAM420  SDOS      5'  ACGAGGGTCAGTGCCAAG     51350            G
                                CTTGGCACTGGCC TCGT
                                |||||||||||| ||||
                                GAACCGTGACTGG AGCA
                                       G
GAM420  LOC149498 5'  ACGCTGTCAGTGCCAGG      80205           C T
                                CTTGGCACTGGC G CGT
                                |||||||||||| | |||
                                GGACCGTGACTG C GCA
                                       T _
GAM420  LOC150837 3'  ACGACGGTCCTGAGCAAG     80798      G_  CT
                                CTTG  CA  GGCCGTCGT
                                ||||  ||  |||||||||
                                GAAC  GT  CTGGCAGCA
                                  GA  C_
GAM420  LOC162417 5'  ACGAGGAGGTGCTCAAG      83212      _    GG  G
                                CTTG GCACT  CC TCGT
                                |||| |||||  || ||||
                                GAAC CGTGG  GG AGCA
                                  T    A_  _
GAM420  LOC164121 5'  ACGACAGCGGTGCCGAG      83047          G C
                                CTTGGCACTG C GTCGT
                                |||||||||| | |||||
                                GAGCCGTGGC G CAGCA
                                      _ A
GAM420  LOC164507 5'  ACGGTATCTCAGTGTCAAG    83413          ____
                                CTTGGCACTG    GCCGT
                                ||||||||||    |||||
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                                GAACTGTGAC    TGGCA
                                      TCTA
GAM420   LOC220070 5'  ACAACTGCCCAGTGCCCAG    59937    T      _ C  C
                                CT GGCACTGG C GT GT
                                || |||||||| | || ||
                                GA CCGTGACC G CA CA
                                  C       C T  A
GAM420   LOC221960 3'  ACGAGTTCAGTGCTAAG     92722          CCG
                                CTTGGCACTGG   TCGT
                                ||||||||||   ||||
                                GAATCGTGACT   AGCA
                                      TG_
GAM420   LOC51622  3'  ACGAGTTCAGTGCTAAG     32204          CCG
                                CTTGGCACTGG   TCGT
                                ||||||||||   ||||
                                GAATCGTGACT   AGCA
                                      TG_
GAM421   BAT5     3'  GAGACATGAGGAAAGACCCTCT 41266       AA  AGTG    C
              TA                   TAAGGG  TC    TTCA GTCTC
                                ||||||  ||    |||| |||||
                                ATTCTC  AG    GAGT CAGAG
                                   CC  AAAG    A
GAM421   DR1      5'  GAGACACGAAGGTGGTTCCC   60086        G G   AC
                                GGGAATCA T TTC  GTCTC
                                |||||||| | |||  |||||
                                CCCTTGGT G AAG  CAGAG
                                     _ G   CA
GAM421   MEST     3'  ATGTACACTGATTCCTTTA    70458            TC
                                TAAGGGAATCAGTGT  ACGT
                                ||||||||||||||  ||||
                                ATTTCCTTAGTCACA  TGTA
                                                __
GAM421   SH3BP2   3'  GGACAGGAACACTGGTCCCC   13078     A        AC
                                GGG ATCAGTGTTC  GTCT
                                ||| ||||||||||  ||||
                                CCC TGGTCACAAG  CAGG
                                  C         GA
GAM421   TP63     3'  AGACAAACTGCTTCCCTTA    14942        T    GTTCAC
                                TAAGGGAA CAGT     GTCT
                                |||||||| ||||     ||||
                                ATTCCCTT GTCA     CAGA
                                     C    AA_____
GAM421   ERAL1    3'  GAGACATGAACACTGACTGGCC 63311    AA__        C
                                GG    TCAGTGTTCA GTCTC
                                ||    |||||||||| |||||
                                CC    AGTCACAAGT CAGAG
                                 GGTC         A
GAM421   HINT3    3'  AACATAAAGTGGTTCTCTTA   57549          _____
                                TAAGGGAATCA    GTGTT
                                ||||||||||    |||||
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                                ATTCTCTTGGT   TACAA
                                      GAAA
GAM422  FACL4    3'  ACTGAAAAGCTGAGACCAAGAG 16742     CT_   CT   __
             C                   GCTC  GTCTT  GGCT  TCAGT
                                 ||||  |||||  ||||  |||||
                                 CGAG  CAGAG  TCGA  AGTCA
                                   AAC    __   AA
GAM422  FACL4    3'  ACTGAAAAGCTGAGACCAAGAG 43679     CT_   CT   __
             C                   GCTC  GTCTT  GGCT  TCAGT
                                 ||||  |||||  ||||  |||||
                                 CGAG  CAGAG  TCGA  AGTCA
                                   AAC    __   AA
GAM422  FSTL1    3'  AGACCGAAGCCAGGGGAAGAAG 24003     C  G         A
             C                   GCT CT TCTTCTGGCTTC GTCT
                                 ||| || ||||||||||| ||||
                                 CGA GA AGGGGACCGAAG CAGA
                                   A  _         C
GAM422  MSL3L1   5'  AGACTGAAGTGAAAGAAGA   23288       G__
                                 TCTTCT   GCTTCAGTCT
                                 ||||||   ||||||||||
                                 AGAAGA   TGAAGTCAGA
                                    AAG
GAM422  RDS      3'  AGACCGAGGCCAGAAGGCA   6148             A
                                 TGTCTTCTGGCTTC GTCT
                                 |||||||||||||| ||||
                                 ACGGAAGACCGGAG CAGA
                                       C
GAM422  RNGTT    3'  AGACTGAAGTTTTTTAGACAAG 15062    C    TCT_
             A                   TC TGTCT    GGCTTCAGTCT
                                 || |||||    ||||||||||
                                 AG ACAGA    TTGAAGTCAGA
                                  A    TTTT
GAM422  STAT6    3'  AGACACTGCACAGAAGACAGCA 13447     C        _ TTCA
             GC                    GCT CTGTCTTCTG GC    GTCT
                                 ||| ||||||||| ||    ||||
                                 CGA GACAGAAGAC CG    CAGA
                                   C        A  TCA_
GAM422  ANKRD6   3'  ACTGAAACCAGGGGAAGC    30768     CCTG       C
                                 GCT    TCTTCTGG TTCAGT
                                 |||    |||||||| ||||||
                                 CGA    AGGGGACC AAGTCA
                                   ____       A
GAM422  DKFZP727M111 5'  GACCGAAGCCAGGGGAGT    32058       GTCTT       A
                                 GCTCCT    CTGGCTTC GTC
                                 ||||||    |||||||| |||
                                 TGAGGG    GACCGAAG CAG
                                    _____       C
GAM422  FLJ11151 3'  AGACTGAAACCAAAGC     68465    T   C   C
                                 G CTT TGG TTCAGTCT
                                 | ||| ||| ||||||||
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                                C GAA ACC AAGTCAGA
                                 _  _  A
GAM422  FLJ13479  5'  AAGCCAGAGACAGAAGC    45554    C    T
                                GCT CTGTCT CTGGCTT
                                ||| |||||| |||||||
                                CGA GACAGA GACCGAA
                                  A    _
GAM422  FLJ14451  3'  AGACTGAAGCCAGCAGAGAGG  52395    G  T
                                CCT TCT CTGGCTTCAGTCT
                                ||| ||| ||||||||||||
                                GGA AGA GACCGAAGTCAGA
                                  G  C
GAM422  FLJ23191  5'  GCTGCCAGAGGACAGGAGC   45010           TTC
                                GCTCCTGTCTTCTGGC  AGT
                                ||||||||||||||||  |||
                                CGAGGACAGGAGACCG  TCG
                                                  ___
GAM422  HEI10    5'  AGACTGAAACCAGATCTGAGT  41292     CTGTCT    C
                                GCTC     TCTGG TTCAGTCT
                                ||||     ||||| ||||||||
                                TGAG     AGACC AAGTCAGA
                                  TCT___    A
GAM422  KIAA1867  5'  AGACCGAAGCCACCCGGAGGGA 96479     G  TC_     A
                                TCCT TCT   TGGCTTC GTCT
                                |||| |||   ||||||| ||||
                                AGGG AGG   ACCGAAG CAGA
                                  _  CCC      C
GAM422  KREMEN2   3'  AGACCAAAAGTCGGACAGGA   44717        TCT    CA_
                                TCCTGTCT   GGCTT   GTCT
                                ||||||||   |||||   ||||
                                AGGACAGG   CTGAA   CAGA
                                     ___    AAC
GAM422  RAB4B    5'  ACTGAAGGTCAGGAGC     32895       T TTCTGG
                                GCTCCTG C     CTTCAGT
                                ||||||| |     |||||||
                                CGAGGAC G     GAAGTCA
                                    T _______
GAM422  ZFP67    3'  GACTGAAGCAGCACAAGGC   32426      C __
                                GTCTT TG  GCTTCAGTC
                                ||||| ||  |||||||||
                                CGGAA AC  CGAAGTCAG
                                  C  GA
GAM422  LOC116068 3'  AGACCATCAGGAAAAGACAGGA 74106         ___    CTTCA
                                TCCTGTCT   TCTGG    GTCT
                                ||||||||   |||||    ||||
                                AGGACAGA   GGACT    CAGA
                                     AAA    AC___
GAM422  LOC148932 3'  ACTGAAGCCAGGAGAAGAAG   79846    C  G
                                CT CT TCTTCTGGCTTCAGT
                                || || ||||||||||||||
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                                GA GA AGAGGACCGAAGTCA
                                 A  _
GAM422  LOC151507 5'  AGACTGAAGTGAAAGAAGA   81061       G__
                                TCTTCT   GCTTCAGTCT
                                ||||||   ||||||||||
                                AGAAGA   TGAAGTCAGA
                                   AAG
GAM422  LOC157958 5'  AGACTGAAACTGTTTTAAAGAA 82528     C  GTCTTCT  C
           GC                     GCT CT      GG TTCAGTCT
                                ||| ||      || ||||||||
                                CGA GA      TC AAGTCAGA
                                  A  AATTTTG  A
GAM422  LOC164537 5'  AAGCCAGAAGCCAGAAGC    88572     C   T
                                GCT CTG CTTCTGGCTT
                                ||| ||| ||||||||||
                                CGA GAC GAAGACCGAA
                                  A   C
GAM422  LOC253971 3'  ACTGTGGCTGCAAAAGCAGAAG 97851     C   TC  CT_   T
           C                     GCT CTG  TT   GGCT CAGT
                                ||| |||  ||   |||| ||||
                                CGA GAC  AA   TCGG GTCA
                                  A   GA  ACG    T
GAM423  UBE2B    3'  CAGCCAGGGCAACATAATA    13935       C   GGGGA
                                TGTTATG TGT     CTGGCTG
                                ||||||| |||     |||||||
                                ATAATAC ACG     GACCGAC
                                    A   G____
GAM423  FLJ13441  3'  CCAGCCAACCGCTGCATGACA  43911        T    GGAC
                                TGTTATGC GTGG    TGGCTGG
                                |||||||| ||||    |||||||
                                ACAGTACG CGCC    ACCGACC
                                     T    A___
GAM423  FLJ23059  3'  CCAGCCAGTCCCCACAGCATAA 50915
           CA                     TGTTATGCTGTGGGGACTGGCTGG
                                |||||||||||||||||||||||
                                ACAATACGACACCCCTGACCGACC

GAM423  GBTS1    3'  CCAGCCACATCCACAGCACAAC 59720     A        GAC
                                GTT TGCTGTGGG   TGGCTGG
                                |||  |||||||||   |||||||
                                CAA ACGACACCT   ACCGACC
                                  C         AC_
GAM423  TLN1     3'  CCAGCCAGTCCCCACAGC    21902
                                GCTGTGGGGACTGGCTGG
                                ||||||||||||||||||
                                CGACACCCCTGACCGACC

GAM423  LOC115330 3'  CCAGCCCCCACAGATAACA    57404       G       A
                                TGTTAT CTGTGGGG CTGG
                                ||||||  |||||||| ||||
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                                ACAATA GACACCCC GACC
                                  _       C
GAM423  LOC147229 5'  CCAGCCAGCCTTGGGGACAAAA 78917      A _ G    A
          CA                      TGTT TG CT TGGGG CTGGCTGG
                                  |||| || || ||||| ||||||||
                                  ACAA AC GG GTTCC GACCGACC
                                    A A G    _
GAM423  LOC155179 3'  CCATCCCCACAGCAAAACA   82226      A        C
                                  TGTT TGCTGTGGGGA TGG
                                  |||| |||||||||| |||
                                  ACAA ACGACACCCCT ACC
                                    A         _
GAM423  LOC221100 5'  CCAAGCCCACAGCAGAACA   94867      A       GAC
                                  TGTT TGCTGTGGG   TGG
                                  |||| |||||||||   |||
                                  ACAA ACGACACCC   ACC
                                    G       GA_
GAM423  LOC257422 5'  CCAACATTCCAGAGCATAACA  98361        G    AC  GC
                                  TGTTATGCT TGGGG  TG  TGG
                                  |||||||| |||||  ||  |||
                                  ACAATACGA ACCTT  AC  ACC
                                       G    __  A_
GAM423  LOC90620  3'  CCAGCCAGCATTCAGCACAGCA 64327       G_  __
                                  TGCTGTG  GGA  CTGGCTGG
                                  |||||||  |||  ||||||||
                                  ACGACAC  CTT  GACCGACC
                                     GA   AC
GAM423  LOC91363  3'  TCAGTCACCACAGCATAACA   66352          G
                                  TGTTATGCTGTGG GACTGG
                                  |||||||||||| ||||||
                                  ACAATACGACACC CTGACT
                                         A
GAM424  ADCY2     3'  ACACTTTCTGACTGCAACTTCT 65638        A  C   TGAA
                                  AGAAGTTG CAG CAGG    TGT
                                  |||||||| ||| ||||    |||
                                  TCTTCAAC GTC GTCT    ACA
                                       _  A    TTC_
GAM424  COL18A1   3'  ACATTCACCTGCCCCAACTCTC 48340    _    ACA  C
                                  GA AGTTG   GC AGGTGAATGT
                                  || |||||   || ||||||||||
                                  CT TCAAC   CG TCCACTTACA
                                    C    CC_  _
GAM424  COL18A1   3'  ACATTCACCTGCCCCAACTCTC 56159    _    ACA  C
                                  GA AGTTG   GC AGGTGAATGT
                                  || |||||   || ||||||||||
                                  CT TCAAC   CG TCCACTTACA
                                    C    CC_  _
GAM424  COL18A1   3'  ACATTCACCTGCCCCAACTCTC 56164    _    ACA  C
                                  GA AGTTG   GC AGGTGAATGT
                                  || |||||   || ||||||||||
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                                CT TCAAC   CG TCCACTTACA
                                 C    CC_ _
GAM424  DRIL1    3'  ACACTCACCACTCCCAGCTTCT 19074        AC  CCA    A
                                AGAAGTTG  AG   GGTGA TGT
                                |||||||| ||   ||||| |||
                                TCTTCGAC  TC   CCACT ACA
                                     CC  A__    C
GAM424  FHIT     5'  ATTCCCAGCTGTCAACATC    10638    A       CA  T
                                GA GTTGACAGC  GG GAAT
                                || |||||||||  || ||||
                                CT CAACTGTCG  CC CTTA
                                 A        A_ _
GAM424  SIGLEC7  3'  CATGGCCTGGCTGCCCACTCCT 33745    A   TGA       GA
                                AG AGT   CAGCCAGGT  ATG
                                || |||   |||||||||  |||
                                TC TCA   GTCGGTCCG  TAC
                                 C  CCC        G_
GAM424  SPAM1    5'  ACATTGAGACCAGCCAACTTCT 13342        ACA  CA   G__
                                AGAAGTTG   GC  GGT   AATGT
                                ||||||||   ||  |||   |||||
                                TCTTCAAC   CG  CCA   TTACA
                                     ___  A_   GAG
GAM424  C2orf7   3'  ACACTCACCTGGCTCCAGCCTC 51270    A   AC        A
                                GA GTTG  AGCCAGGTGA TGT
                                || ||||  ||||||||||| |||
                                CT CGAC  TCGGTCCACT ACA
                                 C   C_        C
GAM424  FLJ14327 3'  ACCTGGTGTCAACCTCT     46669     A      G
                                AGA GTTGACA CCAGGT
                                ||| ||||||| ||||||
                                TCT CAACTGT GGTCCA
                                  C      _
GAM424  HRIHFB2436 3'  CACCCCTTATTGGCATGTCAAC 27568    A       _   _______
           TCCT                    AG AGTTGACA GCCA     GGTG
                                || |||||||| ||||     ||||
                                TC TCAACTGT CGGT     CCAC
                                 C       A    TATTCC
GAM424  KIAA1615 5'  ATGTGGTCATCAACTTCT    69268         CA   G
                                AGAAGTTGA  GCCA GT
                                |||||||||  |||| ||
                                TCTTCAACT  TGGT TA
                                     AC   G
GAM424  MGC955   3'  ACAGGACCTGGCTGTCAACCTC 44279    A           GAA
                                GA GTTGACAGCCAGGT   TGT
                                || ||||||||||||||   |||
                                CT CAACTGTCGGTCCA   ACA
                                 C            GG_
GAM424  TRIP-Br2 3'  ACATCCGAAAAGCAACCAACTT 29258        ACA  CAGG  A
           CT                    AGAAGTTG   GC    TG ATGT
                                ||||||||   ||    || ||||
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                                TCTTCAAC  CG   GC TACA
                                    CAA  AAAA  C
GAM424  TUBB5    3'  ACCTCTGACCCCAACTTCT   21410       A___  CC
                                AGAAGTTG   CAG  AGGT
                                ||||||||   |||  ||||
                                TCTTCAAC   GTC  TCCA
                                    CCCA  __
GAM424  LOC113444 3'  CATTGGCTGTCAATCTCT    57362    AG        G
                                AGA  TTGACAGCCAG TG
                                |||  |||||||||||  ||
                                TCT  AACTGTCGGTT AC
                                  CT         _
GAM424  LOC122553 3'  ACAGTTTTGACTTTCAACTTCT 74588        C  C   TGAA
                                AGAAGTTGA AG CAGG   TGT
                                |||||||||  ||  ||||   |||
                                TCTTCAACT TC GTTT   ACA
                                     T  A   TG__
GAM424  LOC153232 5'  CACTCTGCTCCACCAGCTTCT  87179       AC__  CA
                                AGAAGTTG   AGC  GGTG
                                ||||||||   |||  ||||
                                TCTTCGAC   TCG  TCAC
                                    CACC   TC
GAM424  LOC201702 5'  ATTCCCAGCTGTCAACATC   90467    A       CA  T
                                GA GTTGACAGC  GG GAAT
                                ||  |||||||||  ||  ||||
                                CT CAACTGTCG  CC CTTA
                                 A        A_  _
GAM425  ADAMTS5   3'  GGTCTGCAGCTATTTCAA    23860      _  ATG
                                TTGAAA GGC   TGCAGACC
                                ||||||  |||   ||||||||
                                AACTTT TCG   ACGTCTGG
                                   A   ___
GAM425  BCL7A    3'  TTTGCACACCCTCCAGA     40999     AA   CA
                                TTTG  AGG  TGTGCAGA
                                ||||  |||  ||||||||
                                AGAC  TCC  ACACGTTT
                                  C_   C_
GAM425  BMPR2    5'  GCCATTTGTCCTTTCAAA    8667         _  T   _
                                TTTGAAAGG CA GTG C
                                |||||||||  ||  |||  |
                                AAACTTTCC GT TAC G
                                     T  T   C
GAM425  CLOCK    3'  CTCACATGCCTTCTAAA     18112     A       C
                                TTTG AAGGCATGTG AG
                                ||||  ||||||||||  ||
                                AAAT TTCCGTACAC TC
                                  C        _
GAM425  EML1     3'  GGTCACAGAATGCCTTTTAAA  60450          GTGCA
                                TTTGAAAGGCAT    GACC
                                ||||||||||||    ||||
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                                AAATTTTCCGTA    CTGG
                                      AGACA
GAM425  FGFR3   3'  GGACTGCTACCTTTCAAA    5568         CATGT   A
                                TTTGAAAGG    GCAG CC
                                |||||||||    |||| ||
                                AAACTTTCC    CGTC GG
                                     AT___   A
GAM425  GRN     3'  GTTTGTACACTTTCAAA    10875        GCA
                                TTTGAAAG  TGTGCAGAC
                                ||||||||  |||||||||
                                AAACTTTC  ACATGTTTG
                                    ___
GAM425  HOXC5   3'  TTGCTCTATGCTTTCCAAA   39001     A      T_
                                TTTG AAGGCATG  GCAG
                                |||| ||||||||  ||||
                                AAAC TTTCGTAT  CGTT
                                  C       CT
GAM425  HPS1    3'  GGCTTTGATGTCTTTCAAA   5765          GTG   _
                                TTTGAAAGGCAT   CAGA CC
                                ||||||||||||   |||| ||
                                AAACTTTCTGTA   GTTT GG
                                       ___   C
GAM425  IL2RB   3'  CTGAGCGTGCTTTCCAAA    7938      A       G
                                TTTG AAGGCATGT CAG
                                |||| |||||||| |||
                                AAAC TTTCGTGCG GTC
                                  C       A
GAM425  LARGE   3'  TCTCAGGCCTTTCGAA     17627         A  TGC
                                TTTGAAAGGC TG   AGA
                                |||||||||| ||   |||
                                AAGCTTTCCG AC   TCT
                                     G  ___
GAM425  LARGE   3'  TCTCAGGCCTTTCGAA     56932         A  TGC
                                TTTGAAAGGC TG   AGA
                                |||||||||| ||   |||
                                AAGCTTTCCG AC   TCT
                                     G  ___
GAM425  LDB3    3'  GGTCTGCATCATCCTTTTCAAA 76927        C  _
                                TTTGAAAGG ATG TGCAGACC
                                ||||||||| ||| ||||||||
                                AAACTTTTC TAC ACGTCTGG
                                     C  T
GAM425  MOCS1   3'  GGTCTGGCTCCTTTCAGA    93668        CAT  G
                                TTTGAAAGG   GT CAGACC
                                |||||||||   || ||||||
                                AGACTTTCC   CG GTCTGG
                                     T__  _
GAM425  MORF    5'  TTGTAAATGACTTTCAAA    25606        G   G
                                TTTGAAAG CAT TGCAG
                                |||||||| ||| |||||
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                                AAACTTTC GTA ATGTT
                                    A   A
GAM425  MYO10    3'  GTCTGCACAGTTTCCAAA    25613     AA    A
                                TTTG  AGGC TGTGCAGAC
                                ||||  |||| |||||||||
                                AAAC  TTTG ACACGTCTG
                                  C_   _
GAM425  NPHP1    3'  GTCGCTTTTGCCTTTTCAAA  63149       _   TGT  A
                                TTTGAAA GGCA   GC GAC
                                ||||||| ||||   || |||
                                AAACTTT CCGT   CG CTG
                                    T   TTT  _
GAM425  PCK1     3'  TCTTAGCATGCCTCCAAA    60621     AA      GC
                                TTTG  AGGCATGT  AGA
                                ||||  ||||||||  |||
                                AAAC  TCCGTACG  TCT
                                  C_       AT
GAM425  PHTF1    3'  CTGTATTTTCATGCTTTTCAAA 22762           ____
                                TTTGAAAGGCATG    TGCAG
                                ||||||||||||    |||||
                                AAACTTTTCGTAC    ATGTC
                                       TTTT
GAM425  PPP1R12B 3'  TCTGTTTGTGCCTTTCAAA   50398           T
                                TTTGAAAGGCATG GCAGA
                                |||||||||||| |||||
                                AAACTTTCCGTGT TGTCT
                                       T
GAM425  PPP2R5C  3'  GGTCTCGGGTATCCTTTCAAA  12250        C_  G  C
                                TTTGAAAGG  AT TG AGACC
                                |||||||||  || || |||||
                                AAACTTTCC  TG GC TCTGG
                                     TA  G  _
GAM425  RAB5A    3'  GGTCAGTGTTCCTTTCAAA    16043        CAT TG A
                                TTTGAAAGG   G  C GACC
                                |||||||||   |  | ||||
                                AAACTTTCC   T  G CTGG
                                     T__ GT A
GAM425  UPK1B    3'  TCTGTTCACTTTCAAA      23705        GCA  T
                                TTTGAAAG   TG GCAGA
                                ||||||||   || |||||
                                AAACTTTC   AC TGTCT
                                     ___  T
GAM425  WASF3    3'  TCTGCACATGCCTGTCAAA   22816      A
                                TTTGA AGGCATGTGCAGA
                                ||||| |||||||||||||
                                AAACT TCCGTACACGTCT
                                   G
GAM425  ZNF264   3'  TCTGCAGATTTTTCAGA     14234        GC  G
                                TTTGAAAG  AT TGCAGA
                                ||||||||  || ||||||
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                                AGACTTTT  TA ACGTCT
                                    __  G
GAM425  ABCC13   3'  GGTCTGCCCCTTTTCAAA    57812        CATGT
                                TTTGAAAGG    GCAGACC
                                |||||||||    |||||||
                                AAACTTTTC    CGTCTGG
                                     CC___
GAM425  AFAP     3'  GGTCCATGGAGCCTTTCAAA   41611         A_   CA
                                TTTGAAAGGC  TGTG  GACC
                                ||||||||||  ||||  ||||
                                AAACTTTCCG  GTAC  CTGG
                                      AG   __
GAM425  CAMP-GEFII 3'  GTCCACAATCTTTCAAA     23811        CA   CA
                                TTTGAAAGG  TGTG  GAC
                                |||||||||  ||||  |||
                                AAACTTTCT  ACAC  CTG
                                     A_   __
GAM425  CDT6     3'  GTCTACACATTATTTTTAAA   41252        GC    C
                                TTTGAAAG  ATGTG AGAC
                                ||||||||  ||||| ||||
                                AAATTTTT  TACAC TCTG
                                     AT    A
GAM425  DKFZP564C196 3'  GGTCTGCAGTGTTTTAAA    70605       G  ATG
                                TTTGAAA GC   TGCAGACC
                                ||||||| ||   ||||||||
                                AAATTTT TG   ACGTCTGG
                                     G  ___
GAM425  FBXO9    5'  GTCTGTCTGTGCTCTCAAA   54257      AA    GT
                                TTTGA  GGCAT  GCAGAC
                                |||||  |||||  ||||||
                                AAACT  TCGTG  TGTCTG
                                   C_    TC
GAM425  FLJ10246 3'  GTCTGCTTGCTTCAAA      36410      AA   TGT
                                TTTGA  GGCA   GCAGAC
                                |||||  ||||   ||||||
                                AAACT  TCGT   CGTCTG
                                   __    T__
GAM425  FLJ10956 3'  GGCCTCAAGAGCCTTTCAAG   37469         ATG  C  A
                                TTTGAAAGGC   TG AG CC
                                ||||||||||   || || ||
                                GAACTTTCCG   AC TC GG
                                      AGA  _  C
GAM425  FLJ12891 3'  GGTCTGCAGCAGCCTCAA    46928     AA   A  _
                                TTGA  GGC TG TGCAGACC
                                ||||  ||| || ||||||||
                                AACT  CCG AC ACGTCTGG
                                   __  _  G
GAM425  FLJ13158 3'  GGTCCTGAAACCTTTCAAG   46652         CATGTG  _
                                TTTGAAAGG     CAG ACC
                                |||||||||     ||| |||
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                                GAACTTTCC     GTC TGG
                                     AAA___   C
GAM425  FLJ14075  3'  CTGCACACTTTCAAA      46582        GCA
                                TTTGAAAG   TGTGCAG
                                ||||||||   |||||||
                                AAACTTTC   ACACGTC
                                    ___
GAM425  FLJ14166  3'  GGTCTGTGCTCCTTTTAAA   44990        CAT TG
                                TTTGAAAGG   G  CAGACC
                                |||||||||   |  ||||||
                                AAATTTTCC   C  GTCTGG
                                     T__ GT
GAM425  FLJ14641  3'  GCATCTCTGCCTTTCAAA    52560         T__
                                TTTGAAAGGCA   GTGC
                                ||||||||||   ||||
                                AAACTTTCCGT   TACG
                                      CTC
GAM425  FLJ33069  3'  CACCAATGCGCTTTCAAA    58968        _   __
                                TTTGAAAG GCAT  GTG
                                |||||||| ||||  |||
                                AAACTTTC CGTA  CAC
                                     G    AC
GAM425  FN5       3'  GGTCCACTTCATGTGCCTTTCA 39818           CA___
          GA                    TTTGAAAGGCATGTG    GACC
                                ||||||||||||||    ||||
                                AGACTTTCCGTGTAC    CTGG
                                       TTCAC
GAM425  GOLPH3    3'  GGTCTACTTTGACTTTCAAA  42393        G  T_  GC
                                TTTGAAAG CA  GT  AGACC
                                |||||||| ||  ||  |||||
                                AAACTTTC GT  CA  TCTGG
                                     A  TT  __
GAM425  HIG2      5'  GGTCCAGAGGCCTTTCAGA   26204         ATG  CA
                                TTTGAAAGGC   TG  GACC
                                ||||||||||   ||  ||||
                                AGACTTTCCG   AC  CTGG
                                      GAG  __
GAM425  HSPC063   3'  TTGCTATGCCTTCTAAA     27123      A       T
                                TTTG AAGGCATG GCAG
                                |||| |||||||| ||||
                                AAAT TTCCGTAT CGTT
                                  C       _
GAM425  IRO039700 5'  GGTCTGCACAGGGAGTCAAG   38530       AAGGCA
                                TTTGA     TGTGCAGACC
                                |||||     ||||||||||
                                GAACT     ACACGTCTGG
                                   GAGGG_
GAM425  KIAA0367  3'  GTCTTCATATGCCCTTTAAA   67871        A       C
                                TTTGAA GGCATGTG AGAC
                                |||||| |||||||| ||||
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                                AAATTT CCGTATAC TCTG
                                   C       T
GAM425  KIAA0544  3' GTCAGCACCTTTCAGA      71474        CATG   A
                                TTTGAAAGG    TGC GAC
                                |||||||||    ||| |||
                                AGACTTTCC    ACG CTG
                                     ____   A
GAM425  KIAA0971  3' GGTCACATTTGCTTTCAAA    30675        G  T   CA
                                TTTGAAAG CA GTG  GACC
                                |||||||| || |||  ||||
                                AAACTTTC GT TAC  CTGG
                                     _ T   A_
GAM425  KIAA1030  3' GGTCCACATTGCTTTCAAG    94984        G  _   CA
                                TTTGAAAG CA TGTG  GACC
                                |||||||| || ||||  ||||
                                GAACTTTC GT ACAC  CTGG
                                     _ T    __
GAM425  KIAA1322  3' GGTCTGCACACTCCACTTCA   73114     A_  CA
                                TGAA  GG  TGTGCAGACC
                                ||||  ||  ||||||||||
                                ACTT  CC  ACACGTCTGG
                                  CA  TC
GAM425  KIAA1396  3' GCCACAGTGACCTTTCAAA    63671         _  _   _
                                TTTGAAAGG CA TGTG C
                                ||||||||| || |||| |
                                AAACTTTCC GT ACAC G
                                     A  G   C
GAM425  KIAA1822  3' GGCCTCCACTACTTTCAAA    68193        GCAT   C  A
                                TTTGAAAG    GTG AG CC
                                ||||||||    ||| || ||
                                AAACTTTC    CAC TC GG
                                     AT__   C  C
GAM425  LRPPRC    3' GTCTGCATAACTTTCGAA     56532        GCA
                                TTTGAAAG   TGTGCAGAC
                                ||||||||   |||||||||
                                AAGCTTTC   ATACGTCTG
                                     A__
GAM425  MGC2663   5' GTCTTTTTGCCTTTCAGA     44337          TGTGC
                                TTTGAAAGGCA     AGAC
                                ||||||||||     ||||
                                AGACTTTCCGT     TCTG
                                      TTT__
GAM425  MGC4415   3' GGCCTGCAGAAGCTTTCAGA   49764        G ATG    A
                                TTTGAAAG C   TGCAG CC
                                |||||||| |   ||||| ||
                                AGACTTTC G   ACGTC GG
                                     _ AAG    C
GAM425  MYBPC3    3' GGCCTGCTATGTCTTCCCAA   6030      A_      T   A
                                TTG  AAGGCATG GCAG CC
                                |||  |||||||| |||| ||
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                                AAC  TTCTGTAT CGTC GG
                                  CC       _    C
GAM425  RAB33B   3'  TCTGTTTATCGCTTTTCAAA  49336          _  T
                                TTTGAAAGGC ATG GCAGA
                                |||||||||| ||| |||||
                                AAACTTTTCG TAT TGTCT
                                      C   T
GAM425  SEEK1    3'  GTCTGTTAGCCTTTCAGA    26809          ATGT
                                TTTGAAAGGC    GCAGAC
                                |||||||||    ||||||
                                AGACTTTCCG    TGTCTG
                                      AT__
GAM425  SS18L2   3'  TCTGTGGCTCTTTCAAA     33304          _ ATG
                                TTTGAAAG GC   TGCAGA
                                |||||||| ||   ||||||
                                AAACTTTC CG   GTGTCT
                                     T ___
GAM425  TA-KRP   3'  GCCTATGCCTATCTTTCAAA  51674        ____      T
                                TTTGAA    AGGCATG GC
                                ||||||    ||||||| ||
                                AAACTT    TCCGTAT CG
                                    TCTA      C
GAM425  ZDHHC3   3'  GTCCCCACCCTTTCAAA     33935          CAT   CA
                                TTTGAAAGG   GTG  GAC
                                |||||||||   |||  |||
                                AAACTTTCC   CAC  CTG
                                      ___  CC
GAM425  LOC127428 3'  GGCCTGTCTCTGCCGTTCAAA  75161        A   TGT   A
                                TTTGAA GGCA   GCAG CC
                                |||||| ||||   |||| ||
                                AAACTT CCGT   TGTC GG
                                   G   CTC   C
GAM425  LOC129530 5'  GGTCCATTATGCCTTACAAA   75385      A       TGCA
                                TTTG AAGGCATG    GACC
                                |||| ||||||||    ||||
                                AAAC TTCCGTAT    CTGG
                                  A       TAC_
GAM425  LOC145268 5'  GGTCTTCTGGCTTTCAAA     77582          G  TGTGC
                                TTTGAAAG CA     AGACC
                                |||||||| ||     |||||
                                AAACTTTC GT     TCTGG
                                     G  CT___
GAM425  LOC149911 3'  TCTGCGTGCTTTCAAA      85875          G   GT
                                TTTGAAAG CAT  GCAGA
                                |||||||| |||  |||||
                                AAACTTTC GTG  CGTCT
                                      _  __
GAM425  LOC151963 3'  GGCCTGCTGATCTTTCAAA   81215          _ TGT   A
                                TTTGAAAGG CA   GCAG CC
                                ||||||||| ||   |||| ||
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                                AAACTTTCT GT   CGTC GG
                                    A ____    C
GAM425  LOC154215 3'  GCCCATGGACCTTTCAAA    81956         __    T
                                TTTGAAAGG  CATG GC
                                |||||||||  |||| ||
                                AAACTTTCC  GTAC CG
                                    AG    C
GAM425  LOC163115 3'  CTTTACTTGGCTTTCAAA    83315        G  T   C
                                TTTGAAAG CA GTG AG
                                |||||||| || ||| ||
                                AAACTTTC GT CAT TC
                                    G  T   T
GAM425  LOC200014 3'  GTCTGCTGCTTTGCTCTTTCAA 89943         _   T_  _
          A                      TTTGAAAG GCA  GT GCAGAC
                                |||||||| |||  || ||||||
                                AAACTTTC CGT  CG CGTCTG
                                    T   TT  T
GAM425  LOC200317 3'  TCTGCACACCTGTAGTCAA    90230     AAG   __
                                TTGA   GCA  TGTGCAGA
                                ||||   |||  ||||||||
                                AACT   TGT  ACACGTCT
                                  GA_   CC
GAM425  LOC220926 5'  GGCCTGCCTCTTTTCAAA    93023         CATGT    A
                                TTTGAAAGG     GCAG CC
                                |||||||||     |||| ||
                                AAACTTTTC     CGTC GG
                                    TC____    C
GAM425  LOC57149  3'  GGTCCAAGCTGGCTTTCAAA   40303        G  T  GCA
                                TTTGAAAG CA GT   GACC
                                |||||||| || ||   ||||
                                AAACTTTC GT CG   CTGG
                                    G  _  AAC
GAM425  LOC91828  5'  GGTCTATCTGCGTGCCTTCCA  67861    A        C__
                                TG AAGGCATGTG   AGACC
                                || ||||||||||   |||||
                                AC TTCCGTGCGT   TCTGG
                                 C         CTA
GAM425  LOC92405  5'  GGTCTGCGGGGCCGCCAAA    69716     AAA   ATG
                                TTTG   GGC   TGCAGACC
                                ||||   |||   ||||||||
                                AAAC   CCG   GCGTCTGG
                                  CG_   GG_
GAM426  CDH12     3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT     GAA  ATAAG
                                |||||||||     |||  |||||
                                ATGTGGTGA     TTT  TATTC
                                    AA____    AC
GAM426  GOCAP1    3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
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                                ATGTG  GAGGGTTCTT TTA
                                  AC        G
GAM426  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090      T   AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                  _   GTCA_
GAM426  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
          A                      TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                  TACTCCC_
GAM426  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126        CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM426  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
          TA                     TACA   TCC   GAAGAATAAG
                                ||||   |||   ||||||||||
                                ATGT   AGG   TTTCTTATTC
                                  AAA_  ATTG
GAM426  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68742            _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                         G
GAM426  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM426  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748     CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM426  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM426  OSBPL11   3'  CTTAATTTCCCAAGAGTGGTG  43206        CCAA   AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                     AACC   A_
GAM426  YME1L1    3'  TCATTCTTGATGTGGTGTA   58438        TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   |||||| ||
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                                ATGTGGTG  GTTCTT CT
                                    TA_    A
GAM426  ZNF262   3' CTTATTTTGTTTGGGAGT   18723       A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                    G
GAM426  LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_   AAGA
                                TACACCAC  CCAAG   ATA
                                ||||||||  |||||   |||
                                ATGTGGTG  GGTTC   TGT
                                    CAA   GG__
GAM427  LAMC1    3' TTGCAAAGTTTTCACGTCA  11275       C  CC_
                                TGACGTGGA AT  GCAA
                                ||||||||| ||  ||||
                                ACTGCACTT TG  CGTT
                                    T  AAA
GAM427  OPA1     3' TTGCGGGTGGAACAGTCA   56430     G  GA_
                                TGAC TG  CATCCGCAA
                                |||| ||  |||||||||
                                ACTG AC  GTGGGCGTT
                                  _ AAG
GAM427  OPA1     3' TTGCGGGTGGAACAGTCA   56432     G  GA_
                                TGAC TG  CATCCGCAA
                                |||| ||  |||||||||
                                ACTG AC  GTGGGCGTT
                                  _ AAG
GAM427  OPA1     3' TTGCGGGTGGAACAGTCA   56434     G  GA_
                                TGAC TG  CATCCGCAA
                                |||| ||  |||||||||
                                ACTG AC  GTGGGCGTT
                                  _ AAG
GAM427  OPA1     3' TTGCGGGTGGAACAGTCA   56436     G  GA_
                                TGAC TG  CATCCGCAA
                                |||| ||  |||||||||
                                ACTG AC  GTGGGCGTT
                                  _ AAG
GAM427  OPA1     3' TTGCGGGTGGAACAGTCA   56438     G  GA_
                                TGAC TG  CATCCGCAA
                                |||| ||  |||||||||
                                ACTG AC  GTGGGCGTT
                                  _ AAG
GAM427  PITX2    5' TTGCGGAGGGTGCGCTCA   6161     C  G  A_
                                TGA GTG AC  TCCGCAA
                                ||| ||| ||  |||||||
                                ACT CGC TG  AGGCGTT
                                  _  G  GG
GAM427  TLR4     5' TTGCGGGTTCTACATCA    57506    C    C
                                TGA GTGGA ATCCGCAA
                                ||| ||||| ||||||||
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                                ACT CATCT TGGGCGTT
                                  A    _
GAM427  KIAA1962  5'  TTGCGGATGCTGATGCA     82803    A  _  A
                                TG CGT GG CATCCGCAA
                                || ||| || |||||||||
                                AC GTA TC GTAGGCGTT
                                 _  G  _
GAM427  MGC861    3'  TTGAGGATGTCCAGTCA     44134     G       G
                                TGAC TGGACATCC CAA
                                |||| ||||||||| |||
                                ACTG ACCTGTAGG GTT
                                  _       A
GAM427  LOC132332 5'  TTGCGGATTGCCGTGCA     76669    A    AC
                                TG CGTGG  ATCCGCAA
                                || |||||  ||||||||
                                AC GTGCC  TAGGCGTT
                                 _    GT
GAM427  LOC144848 3'  TGGAGGATGTCCACATCA     73961     C        G_
                                TGA GTGGACATCC  CA
                                ||| ||||||||||  ||
                                ACT CACCTGTAGG  GT
                                  A         AG
GAM427  LOC165257 5'  TTGTGTGCCCCACGTCA     83373        A_  TC
                                TGACGTGG  CA  CGCAA
                                ||||||||  ||  |||||
                                ACTGCACC  GT  GTGTT
                                     CC  __
GAM427  LOC200269 3'  TTGCAGTGTCCACTCA      90079     C       CC
                                TGA GTGGACAT  GCAA
                                ||| ||||||||  ||||
                                ACT CACCTGTG  CGTT
                                  _       A_
GAM427  LOC221495 5'  TTGCAGGGGCATCACGTTA   95498        ACA  _
                                TGACGTGG   TCC GCAA
                                ||||||||   ||| ||||
                                ATTGCACT   GGG CGTT
                                     ACG   A
GAM427  LOC256520 3'  GCAGATTTTGTTCTACGTCA  97667         _ ____  C
                                TGACGTGGA CA   TC GC
                                ||||||||| ||   || ||
                                ACTGCATCT GT   AG CG
                                     T  TTT  A
GAM428  AQP7      5'  GACAGTCACGGAGGAACAAGAT 8605         A_
            CAA                    TTGATCTT  TCCTCCGTGACTGTC
                                ||||||||  ||||||||||||||||
                                AACTAGAA  AGGAGGCACTGACAG
                                     CA
GAM428  MMP14     5'  GACTAAGCAGAAGAAAGATCAA 18428         A  C  C  GACT
                                TTGATCTT TC TC GT    GTC
                                |||||||| || || ||    |||
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                                AACTAGAA AG AG CG    CAG
                                    _ A  A  AAT_
GAM428  KIAA0433  5'  ACAGTCATCATAATATCAA   31498      C    CCTCC
                                TTGAT TTAT    GTGACTGT
                                ||||| ||||    ||||||||
                                AACTA AATA    TACTGACA
                                   T   C____
GAM428  KIAA1915  5'  GACAGTATTTTAAAAATAAGGT 73667         CCTCCGTG_
           CAA                    TTGATCTTAT       ACTGTC
                                ||||||||||       ||||||
                                AACTGGAATA       TGACAG
                                    AAAATTTTA
GAM428  MGC5370   3'  CAGTTGAAAAGATCAA     52193        A  CTCCGT
                                TTGATCTT TC     GACTG
                                |||||||| ||     |||||
                                AACTAGAA AG     TTGAC
                                    A _______
GAM428  TREX1     5'  GACAGCTGGAGACAGAGATCAA 54382        ATC    TGA
                                TTGATCTT   CTCCG   CTGTC
                                ||||||||   |||||   |||||
                                AACTAGAG   GAGGT   GACAG
                                    ACA    C__
GAM428  TREX1     5'  GACAGCTGGAGACAGAGATCAA 54388        ATC    TGA
                                TTGATCTT   CTCCG   CTGTC
                                ||||||||   |||||   |||||
                                AACTAGAG   GAGGT   GACAG
                                    ACA    C__
GAM428  LOC127534 3'  ACAGCAGATAAGATCAA     75963         CTCCG  A  _
                                TTGATCTTATC    TG CTG T
                                ||||||||||     || ||| |
                                AACTAGAATAG    AC GAC A
                                    _____ _  T
GAM428  LOC150480 5'  GACAGTCACGGAGGAAGAAGAT 61025        A_
           CAA                    TTGATCTT  TCCTCCGTGACTGTC
                                ||||||||  ||||||||||||||||
                                AACTAGAA  AGGAGGCACTGACAG
                                    GA
GAM428  LOC158279 5'  GACAGTCACAGAGGAACAAGAT 60330        A_    C
           CAA                    TTGATCTT  TCCTC GTGACTGTC
                                ||||||||  ||||| |||||||||
                                AACTAGAA  AGGAG CACTGACAG
                                    CA    A
GAM428  LOC201522 3'  GACCTTCGGGAGAACGAGATCA 89637        ATC   G   CT
           A                     TTGATCTT   CTCC TGA  GTC
                                ||||||||   |||| |||  |||
                                AACTAGAG   GAGG GCT  CAG
                                    CAA    _   TC
GAM428  LOC220864 5'  GACAGTCACAGAGGAACAAGAT 92487        A_    C
           CAA                    TTGATCTT  TCCTC GTGACTGTC
                                ||||||||  ||||| |||||||||
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                                AACTAGAA  AGGAG CACTGACAG
                                    CA    A
GAM428  LOC254381 5'  GACAGTCACGACAGCAGACCAA 99328     A   TATCCTC
                                TTG TCT      CGTGACTGTC
                                ||| |||      ||||||||||
                                AAC AGA      GCACTGACAG
                                  C   CGACA__
GAM429  DKFZp547I224 3'  CCCCCACTGTCAACATT     39955          T   CCAG  C
                                AATGTTGACG TGG    GG G
                                |||||||||| |||    || |
                                TTACAACTGT ACC    CC C
                                      C   ____  A
GAM429  MGC20253  3'  ACACCCTGGAAGGTCAACAT   58672        G  GG     C
                                ATGTTGAC TT  CCAGGG GT
                                |||||||| ||  |||||| ||
                                TACAACTG AA  GGTCCC CA
                                    G  __     A
GAM429  MGC5391   3'  TGGCCAACATCCACACTG    52197    A   T  C
                                CA TGT GA GTTGGCCA
                                || ||| || ||||||||
                                GT ACA CT CAACCGGT
                                 C   C  A
GAM429  LOC92912  3'  GCAGCCAAGTCAACATCA    71407    A      G    CAGG
                                C ATGTTGAC TTGGC    GC
                                | |||||||| |||||    ||
                                A TACAACTG AACCG    CG
                                 C       _    A___
GAM430  ANXA8     3'  TGGGCACAGGTTATACAGACCC 73466     AGCC    ___
          CA                      TGG    TCTGT   ACCTGTGCCCA
                                |||    |||||  ||||||||||
                                ACC    AGACA   TGGACACGGGT
                                  CC__     TAT
GAM430  ANXA8     3'  TGGGCACAGGTTATACAGACCC 73467     AGCC    ___
          CA                      TGG    TCTGT   ACCTGTGCCCA
                                |||    |||||  ||||||||||
                                ACC    AGACA   TGGACACGGGT
                                  CC__     TAT
GAM430  ATP8A2    3'  CACAGGTACCTATCAG      95153      _ CCTCT
                                CTGG AG     GTACCTGTG
                                |||| ||     |||||||||
                                GACT TC     CATGGACAC
                                  A  _____
GAM430  CASP3     3'  TGGGCATGGTCAAAGGCTC    53356       C  T   T
                                GAGCCT TG ACC GTGCCCA
                                |||||| || ||| |||||||
                                CTCGGA AC TGG TACGGGT
                                   A  _   _
GAM430  CCND2     3'  TGGACACAGGTGATTGGCTCC  10057       TCTG       C
                                GGAGCC    TACCTGTG CCA
                                ||||||    |||||||| |||
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                                CCTCGG   GTGGACAC GGT
                                   TTA_      A
GAM430  DPEP1    5'  GGCCAGCACAGAGGCACCAG  16620     A      AC  T
                                CTGG GCCTCTGT  CTG GCC
                                |||| ||||||||  ||| |||
                                GACC CGGAGACA  GAC CGG
                                  A      C_  _
GAM430  EPHB4    3'  TGGGGACTCACAGAGGCCCC  16710    A      ACCT  G
                                GG GCCTCTGT   GT CCCA
                                || |||||||||   || ||||
                                CC CGGAGACA   CA GGGT
                                 C      CT__  G
GAM430  EVA1     5'  GGCACAGGTGAGGAACTC    59235    __    TGT
                                GAG  CCTC   ACCTGTGCC
                                |||  ||||   |||||||||
                                CTC  GGAG   TGGACACGG
                                  AA   ___
GAM430  FANCC    3'  TGGGCACAGGGGCAGCCGC   71053    CT   TA
                                GC  CTG  CCTGTGCCCA
                                ||  |||  ||||||||||
                                CG  GAC  GGACACGGGT
                                 CC   GG
GAM430  ITGA5    3'  CAGGGACAGAGGCCCCAG    61932     A      A
                                CTGG GCCTCTGT CCTG
                                |||| |||||||| ||||
                                GACC CGGAGACA GGAC
                                  C      G
GAM430  LDB3     3'  TGGGCAATTGCCAGGGCTCCAG 76928        T   TACCTG
                                CTGGAGCC CTG     TGCCCA
                                |||||||| |||     ||||||
                                GACCTCGG GAC     ACGGGT
                                    _  CGTTA_
GAM430  LZTS1    3'  TGGGCACAGTCCAGACCCA   41042    AGCC   TAC
                                TGG   TCTG   CTGTGCCCA
                                |||   ||||   |||||||||
                                ACC   AGAC   GACACGGGT
                                  C___   CT_
GAM430  MDM1     3'  TGAGCACATAAGCAGAGGCTGC 39684    G      ACC    C
           AG                    CTG AGCCTCTGT   TGTGC CA
                                ||| |||||||||   ||||| ||
                                GAC TCGGAGACG   ACACG GT
                                  G       AAT    A
GAM430  MHC2TA   3'  CACAGGCCCGGCTCCAG     5969        TCT TA
                                CTGGAGCC   G  CCTGTG
                                ||||||||   |  ||||||
                                GACCTCGG   C  GGACAC
                                    ___ CC
GAM430  NEURL    3'  GGACAGGCTGCAGAGGGCTCCA 16130        _    _    G
           G                     CTGGAGCC TCTGTA CCTGT CC
                                ||||||||| |||||| ||||| ||
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                                GACCTCGG AGACGT GGACA GG
                                    G     C    _
GAM430  ONECUT2  3'  GGGCACAAGTCACCTCCA    17943      CCTC  T  C
                                TGGAG   TG AC TGTGCCC
                                |||||   || || |||||||
                                ACCTC   AC TG ACACGGG
                                  C___  _  A
GAM430  PLOD     3'  GGCACAGGTGTTGCACCAG   6116      A  CTCTG
                                CTGG GC    TACCTGTGCC
                                ||||  ||    ||||||||||
                                GACC CG    GTGGACACGG
                                  A  TT___
GAM430  SCN4A    3'  TGAGCACCACCAGGGCTCCAG  6209        T   TACCT   C
                                CTGGAGCC CTG    GTGC CA
                                ||||||||  |||    ||||  ||
                                GACCTCGG GAC    CACG GT
                                    _   CAC__   A
GAM430  SYNGR3   3'  GGAGAGAGGCCCAGAGGCTCCA 16120          TA   GTG_
            G                    CTGGAGCCTCTG  CCT   CC
                                ||||||||||||  |||   ||
                                GACCTCGGAGAC  GGA   GG
                                      CC   GAGA
GAM430  SYNGR3   3'  GGCACAGACCAGGGCTCCA   16121       T   TAC
                                TGGAGCC CTG   CTGTGCC
                                |||||||  |||   |||||||
                                ACCTCGG GAC   GACACGG
                                   _   CA_
GAM430  BG1      3'  TGGGCACAGGCATTTCTGCCA  88655     AGCCTCT  A
                                TGG      GT CCTGTGCCCA
                                |||      || ||||||||||
                                ACC      TA GGACACGGGT
                                  GTCTT__  C
GAM430  CALN1    3'  TGAGCACAAGTAAAACTAAGGC 49671        CT  ___  C    C
            TTCAG                   CTGGAGCCT  GT   AC TGTGC CA
                                ||||||||  ||   || ||||| ||
                                GACTTCGGA  CA   TG ACACG GT
                                     AT  AAA  A    A
GAM430  DGKD     3'  GGGCACAGACACTGACCAG   60111     AGCC  T  AC
                                CTGG   TC GT  CTGTGCCC
                                ||||   || ||  ||||||||
                                GACC   AG CA  GACACGGG
                                  ____  T  CA
GAM430  DKFZP566G1424 3'  GGGAGGGGCACAGGGCTCCAG  85944       T   A   GTG
                                CTGGAGCC CTGT CCT   CCC
                                ||||||||  |||| |||   |||
                                GACCTCGG GACA GGG   GGG
                                    _   C   GA_
GAM430  EMILIN-2 3'  TGAGCTTGCCACAGAGGCTCC  50258          ACCTGT  C
                                GGAGCCTCTGT     GC CA
                                ||||||||||      || ||
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                                CCTCGGAGACA     CG GT
                                      CCGTT_  A
GAM430  FKSG28   3' CAGAGGTGCAGGCACCAG    48906     A   CT     G
                                CTGG GCCT  GTACCT TG
                                |||| ||||  |||||| ||
                                GACC CGGA  CGTGGA AC
                                  A   __     G
GAM430  FLJ11286 3' TGGGCACAGGCATGGTACCACC 37796     AGCCT   A
          AG                    CTGG    CTGT CCTGTGCCCA
                                ||||    |||| ||||||||||
                                GACC    GGTA GGACACGGGT
                                  ACCAT   C
GAM430  FLJ12056 3' GGGCACAGGCACGGGCACAG   46822    GA   CT  A
                                CTG  GCCT  GT CCTGTGCCC
                                |||  ||||  || |||||||||
                                GAC  CGGG  CA GGACACGGG
                                  A_   __  C
GAM430  FLJ13052 3' GGGCACAGGGGAAGCCCAG   43756     A  C   GTA
                                CTGG GC TCT   CCTGTGCCC
                                |||| || |||   |||||||||
                                GACC CG AGG   GGACACGGG
                                  _ A   ___
GAM430  FLJ14103 5' GGACAGCCAGAGGCTGCAG   97938     G      TAC   G
                                CTG AGCCTCTG   CTGT CC
                                ||| ||||||||   |||| ||
                                GAC TCGGAGAC   GACA GG
                                  G       C__   _
GAM430  KIAA0321 5' GCAGCCCAGAAAGCTCCAG   63054       C_   TAC
                                CTGGAGC  TCTG   CTGT
                                |||||||  ||||   ||||
                                GACCTCG  AGAC   GACG
                                    AA   CC_
GAM430  KIAA0352 3' ACAGCAGAGGCTCCA      29822          TAC
                                TGGAGCCTCTG   CTGT
                                ||||||||||   ||||
                                ACCTCGGAGAC   GACA
                                      ___
GAM430  KIAA0476 3' GCCCAGTCAAAGGCTCCA    30040        C  TAC   T
                                TGGAGCCT TG   CTG GC
                                |||||||| ||   ||| ||
                                ACCTCGGA AC   GAC CG
                                    A  T__   C
GAM430  KIAA0819 5' GGGAACCAGAGGCTCCAG    64334          TACCT  G
                                CTGGAGCCTCTG    GT CCC
                                ||||||||||||    || |||
                                GACCTCGGAGAC    CA GGG
                                      _____  A
GAM430  KIAA1001 3' GGCACAGGTGCCAGCTCCAG  31010       CTCT
                                CTGGAGC   GTACCTGTGCC
                                |||||||   ||||||||||
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                                GACCTCG   CGTGGACACGG
                                   AC__
GAM430  KIAA1076  3'  TGGGCACAGTGAGGAGACCCCA 66129    AGC   G  C
                                TGG  CTCT TAC TGTGCCCA
                                |||  |||| ||| ||||||||
                                ACC  GAGG GTG ACACGGGT
                                  CCA   A  _
GAM430  MYH7B   3'  CAGGCCACAGAGGCCCAG   71055     A      A_
                                CTGG GCCTCTGT  CCTG
                                |||| ||||||||  ||||
                                GACC CGGAGACA  GGAC
                                  _      CC
GAM430  NYD-SP25  3'  TGGGCAAGTCAGTGGCTCCAG  54306       T  T  CTG
                                CTGGAGCC CTG AC   TGCCCA
                                |||||||| ||| ||   ||||||
                                GACCTCGG GAC TG   ACGGGT
                                   T  _  A__
GAM430  PDE2A   3'  TGGGGGATACAGGGGCCCCAG  12007     A      _  TGTG
                                CTGG GCCTCTGTA CC   CCCA
                                |||| |||||||| ||   ||||
                                GACC CGGGGACAT GG   GGGT
                                  C       A  _____
GAM430  RoXaN   3'  CACAAGTAAATGCAGGCTGCAG 47275    G    CTG__  C
                                CTG AGCCT    TAC TGTG
                                ||| |||||    ||| ||||
                                GAC TCGGA    ATG ACAC
                                  G    CGTAA  A
GAM430  SPIB    3'  TGGCACACCCGAGGCTCC    13359       TGTACC   C
                                GGAGCCTC     TGTGC CA
                                ||||||||     ||||| ||
                                CCTCGGAG     ACACG GT
                                   CCC___    A
GAM430  TIX1    3'  GGGCACAGACACCTCC     62408     CCTC  AC
                                GGAG   TGT  CTGTGCCC
                                ||||   |||  ||||||||
                                CCTC   ACA  GACACGGG
                                  C___  __
GAM430  TREX1   5'  GGAGACACAATGGCTCCAG   50610       TC  ACCT  GC
                                CTGGAGCC  TGT   GT  CC
                                |||||||  |||   ||  ||
                                GACCTCGG  ACA   CA  GG
                                   TA  _____  GA
GAM430  TREX1   5'  GGAGACACAATGGCTCCAG   33502       TC  ACCT  GC
                                CTGGAGCC  TGT   GT  CC
                                |||||||  |||   ||  ||
                                GACCTCGG  ACA   CA  GG
                                   TA  _____  GA
GAM430  YKT6    3'  TGAGCCCACCACAGAGGCCACA 22645    GA      ACC  T  C
           G                    CTG  GCCTCTGT   TG GC CA
                                |||  ||||||||   || || ||
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                                GAC  CGGAGACA   AC CG GT
                                  AC       CC_  C  A
GAM430   LOC121629 5'  GGGTCACAAGAGGCTCCAG    76085          GTACC   _
                                CTGGAGCCTCT     TGTG CCC
                                ||||||||||     |||| |||
                                GACCTCGGAGA     ACAC GGG
                                      _____    T
GAM430   LOC127702 3'  GGGCAGCACAGAGGCCCC     75986    A       ACCTG
                                GG GCCTCTGT     TGCCC
                                || ||||||||     |||||
                                CC CGGAGACA     ACGGG
                                 C       CG___
GAM430   LOC142972 3'  TGGGCACAGGTTATACAGACCC 65722     AGCC    ___
            CA                    TGG    TCTGT   ACCTGTGCCCA
                                |||    |||||   ||||||||||
                                ACC    AGACA   TGGACACGGGT
                                  CC__     TAT
GAM430   LOC145317 3'  GCACAGACACAGAGGCCCAG   84280      A       AC
                                CTGG GCCTCTGT  CTGTGC
                                |||| ||||||||  ||||||
                                GACC CGGAGACA  GACACG
                                  _       CA
GAM430   LOC147160 5'  GGCACAGGGTCAGGCCCAG    85079      A    CTGTA
                                CTGG GCCT     CCTGTGCC
                                |||| ||||     ||||||||
                                GACC CGGA     GGACACGG
                                  _    CTG__
GAM430   LOC148114 5'  GGGCACAGACCAGCCCCA     79362     A  CTC  TAC
                                TGG GC   TG   CTGTGCCC
                                ||| ||   ||   ||||||||
                                ACC CG   AC   GACACGGG
                                  C  ___  CA_
GAM430   LOC153205 3'  ATATATACTAGAAGCTCCA    87152       C   _   CC
                                TGGAGC TCT GTA  TGT
                                |||||| ||| |||  |||
                                ACCTCG AGA CAT  ATA
                                    A   T   AT
GAM430   LOC153561 3'  TGAGCACAGGAGTTGGAGGCTG 81753     G       TA_      C
            CAG                    CTG AGCCTCTG   CCTGTGC CA
                                ||| ||||||||   ||||||| ||
                                GAC TCGGAGGT   GGACACG GT
                                  G       TGA      A
GAM430   LOC158263 5'  GGGCACCACTCAGAGGCTCCAG 82730           TACCT
                                CTGGAGCCTCTG     GTGCCC
                                ||||||||||||     ||||||
                                GACCTCGGAGAC     CACGGG
                                       TCAC_
GAM430   LOC167410 3'  CAGAGGTCCTCAGAGGCTCCAG 83563           T__    G
                                CTGGAGCCTCTG   ACCT TG
                                ||||||||||||   |||| ||
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                                GACCTCGGAGAC   TGGA AC
                                       TCC    G
GAM430   LOC170127 3'  TGGGCACAGATTCCGATTCCAG 83462       CC  TGTAC
                                CTGGAG  TC    CTGTGCCCA
                                ||||||  ||    |||||||||
                                GACCTT  AG    GACACGGGT
                                   __  CCTTA
GAM430   LOC197336 3'  TGGACACAGGCTTGGCAGAGGC 59925      A      A___     C
           GCCAG                    CTGG GCCTCTGT    CCTGTG CCA
                                ||||  ||||||||    ||||||  |||
                                GACC CGGAGACG    GGACAC GGT
                                  G       GTTC     A
GAM430   LOC200282 3'  TGCTGGAACAGAGGCTCCA    90102           A  T
                                TGGAGCCTCTGT CC GTG
                                ||||||||||||  ||  |||
                                ACCTCGGAGACA GG CGT
                                       A  T
GAM430   LOC201100 3'  GCCCAGCACAGAGGCTCCA    91324           AC   T
                                TGGAGCCTCTGT  CTG GC
                                ||||||||||||  |||  ||
                                ACCTCGGAGACA  GAC CG
                                       C_   C
GAM430   LOC203286 5'  ACAGGACAGCAGAGGCTCCAG  92139            A__
                                CTGGAGCCTCTGT   CCTGT
                                ||||||||||||   |||||
                                GACCTCGGAGACG   GGACA
                                        ACA
GAM430   LOC203636 3'  CAGGTCTTCACAGAGGCCCCGG 90975      A       _____
                                CTGG GCCTCTGT    ACCTG
                                ||||  ||||||||    |||||
                                GGCC CGGAGACA    TGGAC
                                  C       CTTC
GAM430   LOC219513 3'  GGACACAGAGTGCAGAGACCCC 95987      AGC       _    C
           GG                     CTGG   CTCTGTAC CTGTG CC
                                ||||   |||||||| ||||| ||
                                GGCC   GAGACGTG GACAC GG
                                  CCA       A     A
GAM430   LOC221822 5'  GGACTGGACAGAGGCACCAG   94451      A       A  T  G
                                CTGG GCCTCTGT CC GT CC
                                ||||  |||||||| ||  ||  ||
                                GACC CGGAGACA GG CA GG
                                  A       _  T  _
GAM430   LOC253027 3'  GGCACAGGTGCCCTGCCCA    98770     A  CTCT
                                TGG GC    GTACCTGTGCC
                                |||  ||    ||||||||||
                                ACC CG    CGTGGACACGG
                                  _  TCC_
GAM430   LOC255104 3'  GCACAGGTTAGAGTCCCAG    97128      AG C    T
                                CTGG  C TCTG ACCTGTGC
                                ||||  |  ||||  ||||||||
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                                GACC  G AGAT TGGACACG
                                  CT _   _
GAM430  LOC90092  5'  TGGGCACAGACACTCACAGCCC 62078    A  CTCT_  AC
          CA                      TGG GC    GT  CTGTGCCCA
                                ||| ||    ||  |||||||||
                                ACC CG    CA  GACACGGGT
                                  C  ACACT  CA
GAM430  LOC90917  3'  GGCACAGGCCTCAGAGCCCAG  64987     A  C    TA_
                                CTGG GC TCTG   CCTGTGCC
                                |||| || ||||   ||||||||
                                GACC CG AGAC   GGACACGG
                                  _ _   TCC
GAM430  LOC91516  5'  GCAGCTCAGAGGCTCCAG    66908          TAC
                                CTGGAGCCTCTG   CTGT
                                ||||||||||||   ||||
                                GACCTCGGAGAC   GACG
                                       TC_
GAM430  LOC91661  3'  GGTGCACAGAGGCCCCGG    57215     A      ACCT TG
                                CTGG GCCTCTGT    G  CC
                                |||| ||||||||    |  ||
                                GGCC CGGAGACA    C  GG
                                  C       ____ GT
GAM430  LOC92340  3'  TGGGCACAGGGCTAAGTCCAG  69569      GC  CT  A
                                CTGGA  CT  GT CCTGTGCCCA
                                |||||  ||  || ||||||||||
                                GACCT  GA  CG GGACACGGGT
                                   __  AT  _
GAM431  AQP5     5'  CAGCCAGGCCCCCGCCC     9718     A  A  T
                                GG GC GG GCCTGGCTG
                                || || || |||||||||
                                CC CG CC CGGACCGAC
                                 _  C  C
GAM431  ARNT2    3'  CAGAGACACAGAGGCACCTGCC 30083    A        GGC    C
          C                      GG GCAGGTGCCT   TGTC CTG
                                || ||||||||||   |||| |||
                                CC CGTCCACGGA   ACAG GAC
                                 _         GAC    A
GAM431  CARD15   3'  GGACAGCCCCTCCTCC      42471      C   TGCCT
                                GGAG AGG    GGCTGTCC
                                |||| |||    ||||||||
                                CCTC TCC    CCGACAGG
                                  C  _____
GAM431  COLQ     3'  GGACAGCCTTGGCTGGCTCC   55425      AGGT   T_
                                GGAGC   GCC  GGCTGTCC
                                |||||   |||  ||||||||
                                CCTCG   CGG  CCGACAGG
                                   GT__   TT
GAM431  EYA1     5'  GCGGCCAGGCGCCTGCCC    6697     A
                                GG GCAGGTGCCTGGCTGT
                                || ||||||||||||||||
```

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                                CC CGTCCGCGGACCGGCG
                                  _
GAM431  G6PD    5' CAGCCCAGGCGCCCGCCC   6385    A A      _
                                GG GC GGTGCCTGG CTG
                                || || ||||||||| |||
                                CC CG CCGCGGACC GAC
                                 _ C       C
GAM431  HD      3' CAGAGACATGGGCCTCCCACTC 10907    CA T_   GC   C
           C                     GGAG  GG  GCCTG  TGTC CTG
                                |||| || ||||| |||| |||
                                CCTC  CC  CGGGT  ACAG GAC
                                  AC  TC    __   A
GAM431  KIF5A   5' AGAGACTGAGCACCTGTCC   18373    G     CTGGCT   C
                                GGA CAGGTGC     GTC CT
                                ||| |||||||     ||| ||
                                CCT GTCCACG     CAG GA
                                 _      AGT___   A
GAM431  LYN     5' CAGAGACAGCCAGTTCCTCTCC 11402     C   TGC       C
                                GGAG AGG   CTGGCTGTC CTG
                                |||| |||   ||||||||| |||
                                CCTC TCC   GACCGACAG GAC
                                  _  TT_       A
GAM431  MAPRE3  3' CAGCCAGCCACCTGCTCC   25596         C
                                GGAGCAGGTG CTGGCTG
                                |||||||||| |||||||
                                CCTCGTCCAC GACCGAC
                                      C
GAM431  NEUROD2 3' CAGGGACACCCCCATCCTACC 21593   _ CA   CCT  C
                                GG AG  GGTG   GG TGTCCCTG
                                || ||  ||||   || ||||||||
                                CC TC  CTAC   CC ACAGGGAC
                                 A  __    C__  C
GAM431  PACSIN1 3' CAGGCTGCCGGCACCTGCCC  93878   A       T   TGTC
                                GG GCAGGTGCC GGC    CCTG
                                || ||||||||| |||    ||||
                                CC CGTCCACGG CCG    GGAC
                                 _        _   TC__
GAM431  PCDH9   5' CAGGGACAATGGGACCCCTCC  83691     CA  G   GC
                                GGAG  GGT CCTG  TGTCCCTG
                                ||||  ||| ||||  ||||||||
                                CCTC  CCA GGGT  ACAGGGAC
                                  C_  _    A_
GAM431  PTPN1   3' AGGGACACCCCCCGCCC    12573    A  A  TGCCT  C
                                GG GC GG    GG TGTCCCT
                                || || ||    || |||||||
                                CC CG CC    CC ACAGGGA
                                 _ C _____ C
GAM431  RAX     3' AGGGACAACCCCCCTCC     26465     CA  TGCCT  C
                                GGAG  GG    GG TGTCCCT
                                ||||  ||    || |||||||
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                                CCTC  CC    CC ACAGGGA
                                  C_ _____  A
GAM431  ROBO1    5'  CAGGGGTGCAGGCAGCTGCCC  56899    A   G     GC GT
                                GG GCAG TGCCTG  T  CCCTG
                                || |||| ||||||  |  |||||
                                CC CGTC ACGGAC  G  GGGAC
                                 _   G     __ TG
GAM431  SPOCK    5'  CAGCCGCAAGCACCTGCTCC   63471          C__
                                GGAGCAGGTGC   TGGCTG
                                ||||||||||   ||||||
                                CCTCGTCCACG   GCCGAC
                                      AAC
GAM431  VDR      3'  CAGGGACAGAGACACCTGCACC 6338     A      C  GG
                                GG GCAGGTG CT  CTGTCCCTG
                                || ||||||| ||  |||||||||
                                CC CGTCCAC GA  GACAGGGAC
                                 A      A __
GAM431  C20orf110 3'  CAGAGAGGCCAAACCCTGCTCC 80361        TGCC    G  C
                                GGAGCAGG    TGGCT TC CTG
                                ||||||||    ||||| || |||
                                CCTCGTCC    ACCGG AG GAC
                                     CAA_    _  A
GAM431  C20orf151 3'  CAGCCCAGCACCTGCTCC    90092          CT
                                GGAGCAGGTGC  GGCTG
                                ||||||||||  |||||
                                CCTCGTCCACG  CCGAC
                                      AC
GAM431  CCNE1    3'  GACAGTTGCGCGCCTGCTCC   55164          C
                                GGAGCAGGTGC TGGCTGTC
                                |||||||||| ||||||||
                                CCTCGTCCGCG GTTGACAG
                                      C
GAM431  CCNE1    3'  GACAGTTGCGCGCCTGCTCC   8790           C
                                GGAGCAGGTGC TGGCTGTC
                                |||||||||| ||||||||
                                CCTCGTCCGCG GTTGACAG
                                      C
GAM431  CLIPR-59  3'  GGACAGCTCACGACTGCCC   32018    A   __   CCT
                                GG GCAG  GTG   GGCTGTCC
                                || ||||  |||   ||||||||
                                CC CGTC  CAC   TCGACAGG
                                 _   AG  ___
GAM431  DKFZp434C0923 3'  CAGCCAGGCCCCTGCTCC    34645         T
                                GGAGCAGG GCCTGGCTG
                                |||||||| |||||||||
                                CCTCGTCC CGGACCGAC
                                     C
GAM431  DKFZp547J036 3'  AGAGAGGGGGCACCTCC     51118     GCA     TGG  G  C
                                GGA   GGTGCC   CT TC CT
                                |||   ||||||   || || ||
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                                CCT   CCACGG   GG AG GA
                                 ___     ___ G  A
GAM431   FLJ10813  3'  CAGAGATTCAGGCAGCCACTCC 37229      CA _      CT   C
                                GGAG  GG TGCCTGG  GTC CTG
                                ||||  || |||||||  ||| |||
                                CCTC  CC ACGGACT  TAG GAC
                                  A_  G      __   A
GAM431   FLJ10898  5'  AGGAGAAAGCACCTTCTCC   60123     C     CTGGCTG _
                                GGAG AGGTGC      TC CCT
                                |||| ||||||      || |||
                                CCTC TCCACG      AG GGA
                                  T     AA_____  A
GAM431   FLJ20200  5'  AGAGACAGCCAGACCCCC    35232    AGCA   GC       C
                                GG    GGT  CTGGCTGTC CT
                                ||    |||  |||||||||| ||
                                CC    CCA  GACCGACAG GA
                                 C___   __        A
GAM431   FLJ20464  3'  CAGGGACAGCAGCACCTGTCC  35691     G      CTG
                                GGA CAGGTGC   GCTGTCCCTG
                                ||| |||||||   ||||||||||
                                CCT GTCCACG   CGACAGGGAC
                                 _      A__
GAM431   FLJ21865  3'  AGGAAGCAGCACCTGCCC    43109    A      CTG   GTC
                                GG GCAGGTGC   GCT   CCT
                                || ||||||||   |||   |||
                                CC CGTCCACG   CGA   GGA
                                 _      A__   A__
GAM431   FLJ22477  3'  CAGCCCATGCACCTGCCC    45669    A      CT_
                                GG GCAGGTGC   GGCTG
                                || ||||||||   |||||
                                CC CGTCCACG   CCGAC
                                 _      TAC
GAM431   FLJ22578  3'  CAGGGACGGCCGCACCTGCCTC 46322      _      CT
           C                     GGAG CAGGTGC  GGCTGTCCCTG
                                ||||| |||||||  ||||||||||
                                CCTC GTCCACG  CCGGCAGGGAC
                                  C      __
GAM431   HCNGP     3'  CAGGCAAGCCCTGCTCC     26071        T  C  G
                                GGAGCAGG GC TG CTG
                                |||||||| || || |||
                                CCTCGTCC CG AC GAC
                                     _ A  G
GAM431   HSA243666 3'  CAACCAGCACCTGCCC      34555    A      C   C
                                GG GCAGGTGC TGG TG
                                || |||||||| ||| ||
                                CC CGTCCACG ACC AC
                                 _      _  A
GAM431   ISL2      3'  GACTGCAGACCCCTGCTCC   71399        TGC   G T
                                GGAGCAGG   CTG C GTC
                                ||||||||   ||| | |||
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                                CCTCGTCC   GAC G CAG
                                     CCA   _ T
GAM431  KIAA0682  3'  CAGGGAGCTAGAACCCCTGCTC 33007        TGC_    TG
            C                    GGAGCAGG    CTGGC  TCCCTG
                                 ||||||||    |||||  ||||||
                                 CCTCGTCC    GATCG  AGGGAC
                                     CCAA    __
GAM431  KIAA1553  3'  GACAGCTGTGGCCCTCTCC    93566      C   T   _
                                 GGAG AGG GCC TGGCTGTC
                                 |||| ||| ||| ||||||||
                                 CCTC TCC CGG GTCGACAG
                                   _   _   T
GAM431  KIAA1691  3'  CAGGGACACGTGCCACCTGCTC 94125         CCTG  _
                                 GAGCAGGTG    GC TGTCCCTG
                                 |||||||||    || ||||||||
                                 CTCGTCCAC    TG ACAGGGAC
                                      CG__  C
GAM431  KIAA1866  3'  GACAGCCAGCGTGCTC      61588       G TGC
                                 GAGCA G   CTGGCTGTC
                                 ||||| |   |||||||||
                                 CTCGT C   GACCGACAG
                                    G ___
GAM431  MGC21621  3'  AGGAATGGGCACCTGCTTC    59439            GCTGTC
                                 GGAGCAGGTGCCTG     CCT
                                 ||||||||||||||     |||
                                 CTTCGTCCACGGGT     GGA
                                       AA_____
GAM431  MY050     3'  AGGAAAAGAGGCCCTGCTCC   51916         T   GG  GTC
                                 GGAGCAGG GCCT  CT   CCT
                                 |||||||| ||||  ||   |||
                                 CCTCGTCC CGGA  GA   GGA
                                      _   __  AAA
GAM431  MYT1L     5'  CAGCCCCAGGAACCTGCTCC   67363         G   __
                                 GGAGCAGGT CCT  GGCTG
                                 ||||||||| |||  |||||
                                 CCTCGTCCA GGA  CCGAC
                                      A   CC
GAM431  OS4       3'  AGGGACACCACCCACTCA    20380    A    CC   C
                                 C GGTG  TGG TGTCCCT
                                 | ||||  ||| |||||||
                                 A TCAC  ACC ACAGGGA
                                  C    CC  _
GAM431  RAB40C    3'  GACACTGGCCTCCTGCTCC    41282         T_   T  C
                                 GGAGCAGG  GCC GG TGTC
                                 ||||||||  ||| || ||||
                                 CCTCGTCC  CGG TC ACAG
                                      TC   _  _
GAM431  RSP3      5'  GGACAGCCACCGTTGCCCC    50013    A   __   GCCT
                                 GG GCA  GGT    GGCTGTCC
                                 || |||  |||    ||||||||
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                                CC CGT  CCA    CCGACAGG
                                 C   TG  ____
GAM431  SIAT4B    5'  CAGGGACAGGACAGCCACTCC  23633    A    C   G_
                                C GGTG CTG  CTGTCCCTG
                                | |||| |||  |||||||||
                                C TCAC GAC  GACAGGGAC
                                 C    C   AG
GAM431  SPR1      3'  CAGGCATCTCCAGGCACCCACG 26811    AGCA       CT  C
           CC                     GG    GGTGCCTGG  GT CCTG
                                ||    |||||||||  || ||||
                                CC    CCACGGACC  TA GGAC
                                 GCAC        TC  C
GAM431  LOC121036 3'  CAGGAACAGCCAGGGGACCTCA 74480    C    G  _      C
                                G AGGT CC TGGCTGT CCTG
                                | |||| || ||||||| ||||
                                A TCCA GG ACCGACA GGAC
                                 C    G  G       A
GAM431  LOC123242 3'  CAGAGCCAGCAGGCACCGACCC 76110    AGCA       G   TCC
                                GG    GGTGCCTG CTG   CTG
                                ||    |||||||| |||   |||
                                CC    CCACGGAC GAC   GAC
                                 CAG_        _   CGA
GAM431  LOC127841 5'  CAGAACCCAGGCACTGCTCC   75185        G      ___
                                GGAGCAG TGCCTGG   CTG
                                ||||||| |||||||   |||
                                CCTCGTC ACGGACC   GAC
                                     _      CAA
GAM431  LOC142927 3'  AGAGAAGAAGCACCTGTCC    76941     G      CTGG  G  C
                                GGA CAGGTGC    CT TC CT
                                ||| |||||||    || || ||
                                CCT GTCCACG    GA AG GA
                                  _      AA__  _  A
GAM431  LOC145757 3'  CAGCCCAGGCACCTCCTCC    77918      C         _
                                GGAG AGGTGCCTGG CTG
                                |||| ||||||||| |||
                                CCTC TCCACGGACC GAC
                                   C        C
GAM431  LOC147669 5'  CAGAGGTTCAGGCACCTGCCC  85176    A          CTGT  _
                                GG GCAGGTGCCTGG    CC CTG
                                || ||||||||||||    || |||
                                CC CGTCCACGGACT    GG GAC
                                 _           T___  A
GAM431  LOC149653 3'  CAGGGAGCGAGACAGCTGCCC  85708    A   G  C  G  TG
                                GG GCAG TG CT GC  TCCCTG
                                || |||| || || ||  ||||||
                                CC CGTC AC GA CG  AGGGAC
                                 _   G  A  G  __
GAM431  LOC200078 3'  CAGCTCCAGGACCTGCCC     89979    A     G   __
                                GG GCAGGT CCTG  GCTG
                                || |||||| ||||  ||||
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                                CC CGTCCA GGAC  CGAC
                                 _    _   CT
GAM431   LOC200081 3'  CAGGGACAGCCAGGCACCTGCT 89972
            CC                    GGAGCAGGTGCCTGGCTGTCCCTG
                                  ||||||||||||||||||||||||
                                  CCTCGTCCACGGACCGACAGGGAC

GAM431   LOC200609 3'  AGCTGAATGCCAGGCACCCACA 91657    AGCA       TG  C_
            CC                    GG   GGTGCCTGGC  TC  CT
                                  ||   ||||||||||  ||  ||
                                  CC   CCACGGACCG  AG  GA
                                   ACAC        TA  TC
GAM431   LOC221178 3'  GACAGCCAAAGCAGTCCTGCTT 95171        __   C_
            C                     GGAGCAGG  TGC  TGGCTGTC
                                  ||||||||  |||  ||||||||
                                  CTTCGTCC  ACG  ACCGACAG
                                       TG   AA
GAM431   LOC221486 3'  CAGCCCAGCACCTGCTCC    92655          CT
                                  GGAGCAGGTGC  GGCTG
                                  ||||||||||  |||||
                                  CCTCGTCCACG  CCGAC
                                        AC
GAM431   LOC253001 3'  CAGAGCCAGCAGGCACCGACCC 97989    AGCA      G   TCC
                                  GG   GGTGCCTG CTG   CTG
                                  ||   |||||||| |||   |||
                                  CC   CCACGGAC GAC   GAC
                                   CAG_       _   CGA
GAM431   LOC254115 5'  CAGGGACAGCCACCGGCACT   96371       __
                                  GGTGCC  TGGCTGTCCCTG
                                  ||||||  ||||||||||||
                                  TCACGG  ACCGACAGGGAC
                                     CC
GAM431   LOC254848 5'  CAGAGAAGGCACCTGGTCC    98879     G       GG_
                                  GGA CAGGTGCCT   CTG
                                  ||| |||||||||   |||
                                  CCT GTCCACGGA   GAC
                                    G        AGA
GAM431   LOC255480 3'  CAGGGACCCCAGACACCTTGCT 98285       _   C    CT
            CC                    GGAGCA GGTG CTGG  GTCCCTG
                                  ||||||| |||| ||||  |||||||
                                  CCTCGT CCAC GACC  CAGGGAC
                                     T    A    C_
GAM431   LOC256158 5'  GGACAGCCAGGCCCTCTCC    99500     C   T
                                  GGAG AGG GCCTGGCTGTCC
                                  |||| ||| ||||||||||||
                                  CCTC TCC CGGACCGACAGG
                                    _  _
GAM431   LOC256158 5'  GGACGGGGCCCTGCTCC     99501         T   TGG
                                  GGAGCAGG GCC   CTGTCC
                                  |||||||| |||   ||||||
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                                CCTCGTCC CGG   GGCAGG
                                   _  ___
GAM431  LOC257458 5'  CAGCCCAAGCACCTGCTGC   68399   G       CT_
                                G AGCAGGTGC   GGCTG
                                | |||||||||   |||||
                                C TCGTCCACG   CCGAC
                                 G        AAC
GAM432  AVPR2    3'  ACAGCGGTCCCAGGGGCCTGA  5338     A      __
                                TCA GTCCCTGG  CTGTTGT
                                ||| ||||||||  |||||||
                                AGT CGGGGACC  GGCGACA
                                  C       CT
GAM432  BHLHB3   3'  ACAACAGTCTGACTATGA    48484    _   CCT
                                TCA AGTC   GGCTGTTGT
                                ||| ||||   |||||||||
                                AGT TCAG   CTGACAACA
                                  A   T__
GAM432  COG7     3'  ACAACTGGCTGGGCTCGA    68248    A    CT   _
                                TC AGTCC  GGCT GTTGT
                                || |||||  |||| |||||
                                AG TCGGG  TCGG CAACA
                                 C     __   T
GAM432  CORO2A   3'  ACAACAGTTTCTGAATTGA   54488     G  CCT
                                TCAA TC   GGCTGTTGT
                                |||| ||   |||||||||
                                AGTT AG   TTGACAACA
                                  A  TCT
GAM432  CORO2A   3'  ACAACAGTTTCTGAATTGA   14096     G  CCT
                                TCAA TC   GGCTGTTGT
                                |||| ||   |||||||||
                                AGTT AG   TTGACAACA
                                  A  TCT
GAM432  DUSP4    5'  ATGACAGCCAAGGACTGGA   55126    A    C      TG
                                TC AGTCC TGGCTGT  T
                                || ||||| |||||||  |
                                AG TCAGG ACCGACA  A
                                 G    A      GT
GAM432  G6PC     3'  ACAACCATGCCAGGGATTGA  5647      G      T__
                                TCAA TCCCTGGC   GTTGT
                                |||| ||||||||   |||||
                                AGTT AGGGACCG   CAACA
                                  _       TAC
GAM432  HAS2     3'  ACTGCTGCTGGGACTTGA    19228         T  T  T
                                TCAAGTCCC GGC GT GT
                                ||||||||| ||| || ||
                                AGTTCAGGG TCG CG CA
                                      _  T  T
GAM432  IL1R1    3'  ACAGTAGCAGGGAATTGA    7917      G     G
                                TCAA TCCCTG CTGTTGT
                                |||| |||||| |||||||
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                                AGTT AGGGAC GATGACA
                                  A     _
GAM432  KRTHA5   5'  GCTGTTGTACTGACAGGGACTT 11242          _________  TGTT
                GG                  TCAAGTCCCTG       GC    GT
                                    ||||||||||       ||    ||
                                    GGTTCAGGGAC       TG    CG
                                          AGTCA___  TTGT
GAM432  LIMD1    3'  ACAATTCTTGGACTTGA     27257        CT  CT
                                    TCAAGTCC  GG  GTTGT
                                    ||||||||  ||  |||||
                                    AGTTCAGG  TC  TAACA
                                         T_  T_
GAM432  NCAM2    3'  ACAATATTACAGGGGCTTGA   17000          GC_
                                    TCAAGTCCCTG   TGTTGT
                                    ||||||||||   ||||||
                                    AGTTCGGGGAC   ATAACA
                                          ATT
GAM432  PHLDA1   3'  ACAAGGTTTTGAGGACTTGA   24740        CT__   G
                                    TCAAGTCC    GGCT TTGT
                                    ||||||||    |||| ||||
                                    AGTTCAGG    TTGG AACA
                                         AGTT   _
GAM432  SCD      3'  ACGTTGCCAGGGGCTTGA    18587           TGT
                                    TCAAGTCCCTGGC   TGT
                                    ||||||||||||   |||
                                    AGTTCGGGGACCG   GCA
                                           TT_
GAM432  SLC22A3  3'  ACAACTCTTTGAGGATTTGA   42036        CT  CT_
                                    TCAAGTCC  GG   GTTGT
                                    ||||||||  ||   |||||
                                    AGTTTAGG  TT   CAACA
                                         AG  TCT
GAM432  SLC22A3  3'  ACAATCTGAGGACTTGG     42037        CT  CT
                                    TCAAGTCC  GG  GTTGT
                                    ||||||||  ||  |||||
                                    GGTTCAGG  TC  TAACA
                                         AG  __
GAM432  TLX1     3'  ACAACAGCCTCACTTGG     19814       CCCT
                                    TCAAGT    GGCTGTTGT
                                    ||||||    |||||||||
                                    GGTTCA    CCGACAACA
                                       CT__
GAM432  TPTE     5'  ACAACAGCTGCTACCTGA    26163     A  CCC
                                    TCA GT   TGGCTGTTGT
                                    ||| ||   ||||||||||
                                    AGT CA   GTCGACAACA
                                      C  TC_
GAM432  ZNF195   3'  ACAATGGAGGATTTGA      24097        CTGG
                                    TCAAGTCC    CTGTTGT
                                    ||||||||    |||||||
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                                AGTTTAGG  GGTAACA
                                   A___
GAM432  ZNF264   3' ACAACTTAGGGGGCTTGA   14178       GGCT
                                TCAAGTCCCT  GTTGT
                                ||||||||||  |||||
                                AGTTCGGGGG  CAACA
                                     ATT_
GAM432  ABCA9    3' ACAATAGCAAAGACTTGG   55363      CCTG
                                TCAAGTC  GCTGTTGT
                                |||||||  ||||||||
                                GGTTCAG  CGATAACA
                                   AAA_
GAM432  C11orf15 3' ACAAATCCTAAGGACTTGG  40592       C  CTG
                                TCAAGTCC TGG  TTGT
                                |||||||| |||  ||||
                                GGTTCAGG ATC  AACA
                                     A  CTA
GAM432  DKFZP434O047 5' ACAAAGTTCAATGGACTTGA  32119       C_  _ G
                                TCAAGTCC  TGG CT TTGT
                                ||||||||  ||| || ||||
                                AGTTCAGG  ACT GA AACA
                                     TA  T  _
GAM432  FLJ10895 3' ACAACAGCCAGTGCCTG    39357    A  CC
                                CA GT  CTGGCTGTTGT
                                || ||  ||||||||||||
                                GT CG  GACCGACAACA
                                 C  T_
GAM432  FLJ11068 3' ACAACAGTTAAAACTTTGA  37585     TCCC
                                TCAAG   TGGCTGTTGT
                                |||||   ||||||||||
                                AGTTT   ATTGACAACA
                                   CAAA
GAM432  FLJ11827 3' ACAATAGCCAGAAACTAGA  47676    A  CC
                                TC AGT  CTGGCTGTTGT
                                || |||  ||||||||||||
                                AG TCA  GACCGATAACA
                                 A  AA
GAM432  FLJ22635 3' ACAGGAGAGGGATTTGA    47668       GG  G
                                TCAAGTCCCT  CT TTGT
                                ||||||||||  || ||||
                                AGTTTAGGGA  GA GACA
                                     __  G
GAM432  KIAA1211 3' ACAAAGAAGGGACTTGG    69465       GG  G
                                TCAAGTCCCT  CT TTGT
                                ||||||||||  || ||||
                                GGTTCAGGGA  GA AACA
                                     A_  _
GAM432  KIAA1229 3' ACAATAGCAAAGACTTGG   62749      CCTG
                                TCAAGTC  GCTGTTGT
                                |||||||  ||||||||
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                                GGTTCAG   CGATAACA
                                   AAA_
GAM432  KIAA1871  3'  GCTGTTGTACTTACAGGGATTT 61907          _________ TGTT
            GA                   TCAAGTCCCTG      GC   GT
                                ||||||||||       ||   ||
                                AGTTTAGGGAC      TG   CG
                                     ATTCA___  TTGT
GAM432  MGC10646  3'  ACAACAGCCAAGGAACTT    52076     _  C
                                AAGT CC TGGCTGTTGT
                                |||| || ||||||||||
                                TTCA GG ACCGACAACA
                                  A  A
GAM432  MOST2     5'  ACATGTGCTAAGGACTTGA   40047       C   TGT
                                TCAAGTCC TGGC   TGT
                                |||||||| ||||   |||
                                AGTTCAGG ATCG   ACA
                                     A    TGT
GAM432  PRPF4     3'  ACAATGGGAAAAGGACTTGA  17462       CTGG_
                                TCAAGTCC    CTGTTGT
                                ||||||||    |||||||
                                AGTTCAGG    GGTAACA
                                     AAAAG
GAM432  SNT-1     5'  ACAGCGGCTGAGACTCGA    22827    A   CC
                                TC AGTC  TGGCTGTTGT
                                || ||||  ||||||||||
                                AG TCAG  GTCGGCGACA
                                 C    A_
GAM432  TRAF3     3'  ACAACAGCCAGTTGA       60451     GTCC
                                TCAA    CTGGCTGTTGT
                                ||||    ||||||||||
                                AGTT    GACCGACAACA
                                  ____
GAM432  LOC145188 3'  ACAACAGCACGAAGACTT    77560      CC  _
                                AAGTC  TG GCTGTTGT
                                |||||  || ||||||||
                                TTCAG  GC CGACAACA
                                   AA  A
GAM432  LOC145371 3'  ACAACAGCCAGGGCTGGA    77679    A  T
                                TC AG CCCTGGCTGTTGT
                                || || ||||||||||||
                                AG TC GGGACCGACAACA
                                 G  _
GAM432  LOC145384 3'  ACAATAGCAAAGACTTGG    77709       CCTG
                                TCAAGTC    GCTGTTGT
                                |||||||    ||||||||
                                GGTTCAG    CGATAACA
                                     AAA_
GAM432  LOC146336 3'  ACAGAGGCAGGGACTGGA    78361    A      G  G
                                TC AGTCCCTG CT TTGT
                                || |||||||| || ||||
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                                AG TCAGGGAC GA GACA
                                 G       G  _
GAM432   LOC148137 3'  AGCTGGCCAGGGACCTGG    59088     A         _
                                TCA GTCCCTGGCT GTT
                                ||| |||||||||| |||
                                GGT CAGGGACCGG CGA
                                  C         T
GAM432   LOC150481 3'  ACAATGTACAGGACTTGG    80688         C  GC
                                TCAAGTCC TG  TGTTGT
                                |||||||| ||  ||||||
                                GGTTCAGG AC  GTAACA
                                     _  AT
GAM432   LOC151040 3'  ACAATAGCAAAGACTTGG    80903        CCTG
                                TCAAGTC    GCTGTTGT
                                |||||||    ||||||||
                                GGTTCAG    CGATAACA
                                    AAA_
GAM432   LOC153129 5'  ACAATGTGAGGGACTTG     81653         G  T
                                CAAGTCCCT GC GTTGT
                                ||||||||| || |||||
                                GTTCAGGGA TG TAACA
                                     G  _
GAM432   LOC157531 3'  ACCTTGGCCAGGGCCTGA    87765     A T        TT
                                TCA G CCCTGGCTG  GT
                                ||| | |||||||||  ||
                                AGT C GGGACCGGT  CA
                                  C _        TC
GAM432   LOC158046 3'  ACAACAGCCAAGATTTGG    59899        CC
                                TCAAGTC  TGGCTGTTGT
                                |||||||  ||||||||||
                                GGTTTAG  ACCGACAACA
                                    A_
GAM432   LOC158191 3'  ACAATGTACAGGACTTGG    82659         C  GC
                                TCAAGTCC TG  TGTTGT
                                |||||||| ||  ||||||
                                GGTTCAGG AC  GTAACA
                                     _  AT
GAM432   LOC200081 3'  ACAACAGCCAGGGACTTGA   89968
                                TCAAGTCCCTGGCTGTTGT
                                ||||||||||||||||||
                                AGTTCAGGGACCGACAACA

GAM432   LOC222252 3'  ACAATAGCAAAGACTTGG    95963        CCTG
                                TCAAGTC    GCTGTTGT
                                |||||||    ||||||||
                                GGTTCAG    CGATAACA
                                    AAA_
GAM432   LOC255098 5'  ACAACATCCGGGGATTTGA   97130           C
                                TCAAGTCCCTGG TGTTGT
                                |||||||||||| ||||||
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                                AGTTTAGGGGCC ACAACA
                                       T
GAM433  RBBP9    3'  AGGTCTATAAATCACCCAACTA 70682     CA  A       AT
                                TAG  GG TGATTTATA  CCT
                                |||  || |||||||||  |||
                                ATC  CC ACTAAATAT  GGA
                                  AA  C       CT
GAM433  C1orf27  5'  AAAGGATTATGTGATTCTTGC  35720       TGATT
                                GCAGGA    TATAATCCTTT
                                ||||||    ||||||||||
                                CGTTCT    GTATTAGGAAA
                                   TAGT_
GAM433  FLJ10997 3'  AAGGATTATAAAACTCC     37512     TGA
                                GGA   TTTATAATCCTT
                                |||   ||||||||||||
                                CCT   AAATATTAGGAA
                                  CA_
GAM433  KIAA1229  3'  AAAGGACTATAAATCATGCTGC 62748       G        A
           TA                     TAGCAG ATGATTTATA TCCTTT
                                |||||| |||||||||| ||||||
                                ATCGTC TACTAAATAT AGGAAA
                                   G         C
GAM433  MGC32104  3'  AAAGGAATATAATCATTC    59057        T   A
                                GGATGATT ATA TCCTTT
                                |||||||| ||| ||||||
                                CTTACTAA TAT AGGAAA
                                     _  A
GAM433  RNF9     3'  AAGGACTATTATCCTCTA    54504     C       TTATAA
                                TAG AGGATGAT     TCCTT
                                ||| ||||||||     |||||
                                ATC TCCTATTA     AGGAA
                                  _       TC____
GAM433  LOC115294 3'  AAAGGATTATTATCTCTCTGCT 73379        AT   TT
           A                     TAGCAGG  GAT  ATAATCCTTT
                                |||||||  |||  ||||||||||
                                ATCGTCT  CTA  TATTAGGAAA
                                    CT   T_
GAM433  LOC142948 3'  AAAGGATTATAAACACACC    83769    A  A_
                                GG TG  TTTATAATCCTTT
                                || ||  ||||||||||||
                                CC AC  AAATATTAGGAAA
                                 _  AC
GAM433  LOC144766 3'  AAAGGATTATAAATCATGCTGC 77476       G
           TA                     TAGCAG ATGATTTATAATCCTTT
                                |||||| ||||||||||||||||
                                ATCGTC TACTAAATATTAGGAAA
                                   G
GAM433  LOC145384 3'  AAAGGATTATAAATCATGCTGC 77708       G
           TA                     TAGCAG ATGATTTATAATCCTTT
                                |||||| ||||||||||||||||
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                                ATCGTC TACTAAATATTAGGAAA
                                   G
GAM433  LOC151040 3'  AAAGGATTATAAATCATGCTGC 80902       G
           TA                    TAGCAG ATGATTTATAATCCTTT
                                 |||||| ||||||||||||||||||
                                 ATCGTC TACTAAATATTAGGAAA
                                   G
GAM433  LOC199907 3'  GATTAATACAGAACCATCCTGC 89828        A  A____
                                 GCAGGATG TTT    TAATC
                                 |||||||| |||    |||||
                                 CGTCCTAC AAG    ATTAG
                                     C  ACATA
GAM433  LOC222252 3'  AAAGGATTATAAATCATGCTGC 95962       G
           TA                    TAGCAG ATGATTTATAATCCTTT
                                 |||||| ||||||||||||||||||
                                 ATCGTC TACTAAATATTAGGAAA
                                   G
GAM433  LOC257396 5'  AAGGATTATAAGTGCACC    98921    A _
                                 GG TG ATTTATAATCCTT
                                 || || ||||||||||||
                                 CC AC TGAATATTAGGAA
                                  _ G
GAM433  LOC92539  3'  AAAGGATTACAACTCCTTGC  70218      AT  T  A
                                 GCAGG  GA TT TAATCCTTT
                                 |||||  || || |||||||||
                                 CGTTC  CT AA ATTAGGAAA
                                   __  C  C
GAM434  CELSR2    3'  TAAACTAGTTCTGTGCGGG   9198     A  ATGGTT
                                 TCC CA     GAACTAGTTTA
                                 ||| ||     ||||||||||
                                 GGG GT     CTTGATCAAAT
                                   C  GT____
GAM434  CTSL2     3'  TAAACCAGTTGAATCATTGAGG 9025     A      G    A
           A                     TCC CAATGGTT AACT GTTTA
                                 ||| |||||||| |||| |||||
                                 AGG GTTACTAA TTGA CAAAT
                                   A       G    C
GAM434  XRCC2     3'  ATTAGTTCAGCCATTGTGGA   19492
                                 TCCACAATGGTTGAACTAGT
                                 ||||||||||||||||||||
                                 AGGTGTTACCGACTTGATTA

GAM434  DKFZp761N0624 3'  AACCATTTCACACCATTGT   51157        _   CTA
                                 ACAATGGT TGAA   GTT
                                 |||||||| ||||   |||
                                 TGTTACCA ACTT   CAA
                                     C    TAC
GAM434  FLJ12985  3'  GTAATGCTACAACCATTG    46800         AAC   _
                                 CAATGGTTG   TAGT TTAC
                                 |||||||||   |||| ||||
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                                GTTACCAAC   ATCG AATG
                                     ___    T
GAM434  FLJ23556  5'  GTAAACTAGTTTTTGGTTTG   46450     TGGTT
                                CAA    GAACTAGTTTAC
                                |||    ||||||||||||
                                GTT    TTTGATCAAATG
                                  TGGTT
GAM434  KIAA1229  3'  GTAAATTAGTTCAACCACTGCG 62757     A  A
          GA                      TCC CA TGGTTGAACTAGTTTAC
                                ||| || ||||||||||||||||||
                                AGG GT ACCAACTTGATTAAATG
                                  C  C
GAM434  KIAA1866  3'  TGGTCGAACCATTGTAGA    61591    C       GA
                                TC ACAATGGTT  ACTA
                                || |||||||||  ||||
                                AG TGTTACCAA  TGGT
                                 A        GC
GAM434  KIAA1979  3'  GTAATGCTACAACCATTGT    89654          AAC   _
                                ACAATGGTTG   TAGT TTAC
                                ||||||||||   |||| ||||
                                TGTTACCAAC   ATCG AATG
                                     ___    T
GAM434  MGC32104  3'  GTAAATTAATTCAGCCATTGTG 59069              C
          GA                      TCCACAATGGTTGAA TAGTTTAC
                                |||||||||||||| ||||||||
                                AGGTGTTACCGACTT ATTAAATG
                                        A
GAM434  PRO2012   3'  ATTGGTCCAACCACTGTGGA   38388       A     A
                                TCCACA TGGTTG ACTAGT
                                |||||| |||||| ||||||
                                AGGTGT ACCAAC TGGTTA
                                   C     C
GAM434  Rabip4R   3'  TGGATTCAACCAACATGGA    36281      CAA      _
                                TCCA   TGGTTGAA CTA
                                ||||   |||||||| |||
                                AGGT   ACCAACTT GGT
                                  ACA       A
GAM434  LOC144766 3'  GTAAACTAGTTCAACCATTGTG 77484
          GA                      TCCACAATGGTTGAACTAGTTTAC
                                ||||||||||||||||||||||||
                                AGGTGTTACCAACTTGATCAAATG

GAM434  LOC145384 3'  GTAAACTGGTTCAACCATTGTG 77718
          GA                      TCCACAATGGTTGAACTAGTTTAC
                                ||||||||||||||||||||||||
                                AGGTGTTACCAACTTGGTCAAATG

GAM434  LOC146224 5'  GTAAACTAGCTGAGCCATTG   78203        GAA
                                CAATGGTT   CTAGTTTAC
                                ||||||||   |||||||||
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                                GTTACCGA   GATCAAATG
                                     GTC
GAM434   LOC149157 3'  GTAAATTAGTTCAACCATTGTG 79941
              GA                   TCCACAATGGTTGAACTAGTTTAC
                                   ||||||||||||||||||||||||
                                   AGGTGTTACCAACTTGATTAAATG

GAM434   LOC221300 3'  GTAAATTAGTATAACCACTATG 93577      CAA     A
              GA                   TCCA   TGGTTG ACTAGTTTAC
                                   ||||   |||||| ||||||||||
                                   AGGT   ACCAAT TGATTAAATG
                                     ATC     A
GAM434   LOC255624 3'  GTAATGCTACAACCATTG    96167         AAC   _
                                   CAATGGTTG   TAGT TTAC
                                   |||||||||   |||| ||||
                                   GTTACCAAC   ATCG AATG
                                       ___    T
GAM435   ATP11B    3'  TTAAAATTTTGGACCTGAGACA 81127         C  ___ TG
              CTGTG                  CACAGTGTC CA   T  AAATTTTAA
                                   ||||||||| ||   |  |||||||||
                                   GTGTCACAG GT   G  TTTAAAATT
                                        A  CCA GT
GAM435   CNTNAP2   3'  AAAATTTCAAACCTAGGACACT 27086        CA___
              G                    CAGTGTCC     TTGAAATTTT
                                   ||||||||     ||||||||||
                                   GTCACAGG     AACTTTAAAA
                                        ATCCA
GAM435   GCNT2     3'  TTAAAATATCCACTGGACACTG 9457          CATT  A
              TG                     CACAGTGTCC    GA ATTTTAA
                                   ||||||||||    || |||||||
                                   GTGTCACAGG    CT TAAAATT
                                         TCAC  A
GAM435   MS4A3     3'  AAAGGACAATGGGAAACTGT   21544       G       AAA
                                   ACAGT TCCCATTG   TTTT
                                   ||||| ||||||||   ||||
                                   TGTCA AGGGTAAC   GAAA
                                     A       AG_
GAM435   PSMD5     3'  AAAATTTTCATGGACAT     18550       C  T
                                   GTGTCC AT GAAATTTT
                                   |||||| || ||||||||
                                   TACAGG TA TTTTAAAA
                                     _  C
GAM435   PTEN      3'  AATGGCAATAGGACATTGTG   6137          C    AA
                                   CACAGTGTCC ATTG  ATT
                                   |||||||||| ||||  |||
                                   GTGTTACAGG TAAC  TAA
                                         A   GG
GAM435   SLC12A4   3'  TTTCAATAAAACATTGTG    18631         CCC
                                   CACAGTGT   ATTGAAA
                                   ||||||||   |||||||
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                                GTGTTACA   TAACTTT
                                     AAA
GAM435  ATP9A    3'  AAAATTGCAAATGGGACATGT  62733     G       GA_
                                ACA TGTCCCATT   AATTTT
                                ||| |||||||||   ||||||
                                TGT ACAGGGTAA   TTAAAA
                                  _       ACG
GAM435  DKFZP434A0225 3'  TTAAAATTCATATTGCTAAGAC 95527        C___  T__   A
           ACTGT                  ACAGTGTC    CA   TGAA TTTTAA
                                ||||||||    ||   |||| ||||||
                                TGTCACAG    GT   ACTT AAAATT
                                     AATC  TAT   _
GAM435  FLJ13193  3'  TAAAATCATAATGGGACAT    50734          AA
                                GTGTCCCATTG  ATTTTA
                                ||||||||||  ||||||
                                TACAGGGTAAT  TAAAAT
                                      AC
GAM435  FLJ32894  3'  AAAATTTGATATGGACATTG   58988        CATTG
                                CAGTGTCC    AAATTTT
                                ||||||||    |||||||
                                GTTACAGG    TTTAAAA
                                     TATAG
GAM435  KIAA0472  3'  TAAGACAGCAAGCGGGACACTG 72365         A_   AAA
                                CAGTGTCCC  TTG   TTTTA
                                |||||||||  |||   |||||
                                GTCACAGGG  AAC   AGAAT
                                     CG   GAC
GAM435  ZDHHC5    3'  AAAACTTCAAGACACTG     93183        CCA    A
                                CAGTGTC   TTGAA TTTT
                                |||||||   ||||| ||||
                                GTCACAG   AACTT AAAA
                                    ___    C
GAM436  GPR17     3'  CCAGAAGAGGGACCTGGG    19179       A  AAT
                                CCTAG TC   TTTCTTCTGG
                                ||||| ||   ||||||||||
                                GGGTC AG   GGAGAAGACC
                                   C  ___
GAM436  MAG       5'  CCAGAAGACGTCCCCAACTCAG 55493       _  ATCAATTT_
           GGA                    TCCCT AG        TCTTCTGG
                                ||||| ||        ||||||||
                                AGGGA TC        AGAAGACC
                                   C  AACCCCTGC
GAM436  MAG       5'  CCAGAAGACGTCCCCAACTCAG 11421       _  ATCAATTT_
           GGA                    TCCCT AG        TCTTCTGG
                                ||||| ||        ||||||||
                                AGGGA TC        AGAAGACC
                                   C  AACCCCTGC
GAM436  MTR       3'  CCTAAAATTGATCTATGGA   6017      C          CTTCT
                                TCC TAGATCAATTTT    GG
                                ||| ||||||||||||    ||
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                                AGG ATCTAGTTAAAA    CC
                                  T         T____
GAM436  RGS5    3'  TCCAGCTAAATTGGTCTA    14625         TCTT
                                TAGATCAATTT   CTGGA
                                ||||||||||   |||||
                                ATCTGGTTAAA   GACCT
                                      TC__
GAM436  SCD     3'  TCCAAAAAAAGGGAAGGATTTA 18596    C    AA  TT  C___
            AGGA                  TCC TAGATC  TT  CTT   TGGA
                                ||| ||||||  ||  |||   ||||
                                AGG ATTTAG  AA  GAA   ACCT
                                  A     G_  GG   AAAA
GAM436  ZNF36   3'  TCCAGAAGAGTATATCTA    95586      CAATT
                                TAGAT    TTCTTCTGGA
                                |||||    ||||||||||
                                ATCTA    GAGAAGACCT
                                   TAT__
GAM436  DKFZP434D0127 5'  CCAAAGGCCGACCTGGGGA   50495       A  AATTT   C
                                TCCCTAG TC    TCTT TGG
                                ||||||| ||    |||| |||
                                AGGGGTC AG    GGAA ACC
                                    C  CC___   _
GAM436  FLJ13590  5'  CCAGAAGTGGAATAATTCAGG  46203     A  TCA    _
                                CCT GA   ATTTT CTTCTGG
                                ||| ||   ||||| |||||||
                                GGA CT   TAAGG GAAGACC
                                  _  TAA    T
GAM436  FLJ13593  3'  CCAGAAGAAAATCCAAGG    45853     AGATCA
                                CCT     ATTTTCTTCTGG
                                |||     ||||||||||||
                                GGA     TAAAAGAAGACC
                                  ACC___
GAM436  FLJ20013  3'  TCCAGACTTGACTGATCCCGGG 34802      TA    A  TTCT
            A                    TCCC  GATCA TT    TCTGGA
                                ||||  ||||| ||    ||||||
                                AGGG  CTAGT AG    AGACCT
                                  CC    C  TTC_
GAM436  FLJ20509  3'  TCCTTCTTAAACTGTCCTAGGG 35761       AT  A   TCTTCT
            A                    TCCCTAG  CA TTT     GGA
                                |||||||  || |||     |||
                                AGGGATC  GT AAA     CCT
                                    CT  C   TTCTT_
GAM436  KIAA0133  3'  TCCTGAAAATTGACCCTGGG   29418      A_       TTCT
                                CCTAG  TCAATTTTC    GGA
                                |||||  |||||||||    |||
                                GGGTC  AGTTAAAAG    CCT
                                  CC       T___
GAM436  MGC14836  5'  TCCAGTTATCAAAATTGACTCA 54177    A  _      CTT__
            AG                    CT GA TCAATTTT    CTGGA
                                || || ||||||||     |||||
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                                GA CT AGTTAAAA    GACCT
                                 A  C       CTATT
GAM436  MUF1     5'  CCAAGTATAATTGATCTAGG  97241          TT_  TC
                                CCTAGATCAATT   CT  TGG
                                ||||||||||||  ||  |||
                                GGATCTAGTTAA   GA  ACC
                                       TAT  __
GAM436  SPATA1   5'  TCCAGAGGGGCCGATTAGGGA  42551      A   AATT
                                TCCCT GATC    TTCTTCTGGA
                                ||||| ||||    ||||||||||
                                AGGGA TTAG    GGGGAGACCT
                                   _   CC__
GAM436  TIP47    3'  TCCAGAAAAAATATCTTTCAGG 20607     CT__   CA    C
            A                    TCC    AGAT  ATTTT TTCTGGA
                                 |||    ||||  ||||| |||||||
                                 AGG    TCTA  TAAAA AAGACCT
                                   ACTT   __    _
GAM436  LOC133634 5'  TCCAGTGCACTGGTCTAGAGA  75601    C       ATTTTCTT
                                TC CTAGATCA       CTGGA
                                || ||||||||       |||||
                                AG GATCTGGT       GACCT
                                 A       CACGT___
GAM436  LOC143425 3'  CCAGAAGAATGGTCCCAGAGA  89012    C  A_    ATT
                                TC CT  GATCA   TTCTTCTGG
                                || ||  |||||   |||||||||
                                AG GA  CTGGT   AAGAAGACC
                                 A  CC    ___
GAM436  LOC170127 3'  CCAGAAGAAAATGCAGAGCAGG 83455      AGA  A__
            G                    CCCT   TC   ATTTTCTTCTGG
                                 ||||   ||   ||||||||||||
                                 GGGA   AG   TAAAAGAAGACC
                                   CG_  ACG
GAM436  LOC201283 3'  CCAGGAGAAAAATCATCTA    61050       CAA
                                TAGAT   TTTTCTTCTGG
                                |||||   ||||||||||
                                ATCTA   AAAAGAGGACC
                                   CTA
GAM436  LOC221955 3'  TCCAGAAGTGCGGGAATCCAGG 58269      A   _ AATTTT
            G                    CCCT GAT C      CTTCTGGA
                                 |||| ||| |      ||||||||
                                 GGGA CTA G      GAAGACCT
                                   C   A GGCGT_
GAM436  LOC253805 3'  TCCAACCAAAATTGATCTA    98185           CTTC
                                TAGATCAATTTT    TGGA
                                ||||||||||||    ||||
                                ATCTAGTTAAAA    ACCT
                                       CCA_
GAM436  LOC254638 5'  TCCAGAAGAATGAAGGTCTAGA 99467    C       AATT
            GA                   TC CTAGATC    TTCTTCTGGA
                                 || |||||||    ||||||||||
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                                AG GATCTGG    AAGAAGACCT
                                 A      AAGT
GAM436  LOC90594  5'  CCAGAAGAATCTCTACAGGGA  64216      __   TCAATT
                                TCCCT  AGA     TTCTTCTGG
                                |||||  |||     |||||||||
                                AGGGA  TCT     AAGAAGACC
                                   CA   CT____
GAM436  LOC90982  5'  CCAGAAGTAGATTAGGGA    65147      A    AATTTT
                                TCCCT GATC     CTTCTGG
                                ||||| ||||     |||||||
                                AGGGA TTAG     GAAGACC
                                   _    AT____
GAM437  DMRT2     3'  CCACAACAAGCAACAAGAACAA 22648         AAC___
              G                  CTTGTTTTT     TGTTGTGG
                                 |||||||||     |||||||||
                                 GAACAAGAA     ACAACACC
                                      CAACGA
GAM437  PKHD1     3'  CAACAGAATTAAAAACGA    57714          __
                                 TTGTTTTTAA  CTGTTG
                                 ||||||||||  ||||||
                                 AGCAAAAATT  GACAAC
                                       AA
GAM437  DKFZP434G2226 3'  CCACAACAAGTTGACTAGGA   49154      T   TTT   _
                                 TCCT GTT   AACT GTTGTGG
                                 |||| |||   |||| |||||||
                                 AGGA CAG   TTGA CAACACC
                                   T  ___   A
GAM437  FIBL-6    3'  ACAACGAAAAACAAG       73296          AAC
                                 CTTGTTTTT   TGTTGT
                                 |||||||||   ||||||
                                 GAACAAAAA   GCAACA
                                       ___
GAM437  KIAA0152  3'  CAGCTGACTGAAAACAAGGA   28966           ACT_
                                 TCCTTGTTTTTA    GTTG
                                 ||||||||||||    ||||
                                 AGGAACAAAAGT    CGAC
                                       CAGT
GAM437  KIAA0416  3'  CAGCATCAAAAAGCAAAGATA  32087      C       AAC
                                 TATC TTGTTTTT   TGTTG
                                 |||| ||||||||   |||||
                                 ATAG AACGAAAA   ACGAC
                                   A       ACT
GAM437  KIAA1912  3'  CCACAACAGTCAATCTCAAACA 73757         _____  A
              AGG                  CCTTGTTT    TT ACTGTTGTGG
                                   ||||||||    || ||||||||||
                                   GGAACAAA    AA TGACAACACC
                                       CTCT  C
GAM437  LOC122792 3'  CCAAGTGCTTAAACACAAGGAT 59822          T     CT  TG_
              A                    TATCCTTGT TTTAA  GT   TGG
                                   |||||||||  |||||  ||   |||
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                                ATAGGAACA AAATT  CG   ACC
                                      C     __ TGA
GAM437  LOC147649 3'  CCACAACAGTCAAAGGATGGAT 79057      TTG     A
                                ATCC   TTTTT ACTGTTGTGG
                                ||||   ||||| ||||||||||
                                TAGG   GGAAA TGACAACACC
                                  TA_    C
GAM438  SCAMP1    3'  GCTAAATAAATATTCTCC     18013     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C      A
GAM438  SCAMP1    3'  GCTAAATAAATATTCTCC     54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C      A
GAM438  NX-17     3'  TGAATATCAGCCCCTAATA    40706         ATA_
                                TATTAGGG    ATATTCA
                                ||||||||    |||||||
                                ATAATCCC    TATAAGT
                                     CGAC
GAM438  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
           TA                    TATTAGGGATAATATTCATTTAGC
                                 ||||||||||||||||||||||||
                                 ATAATCCCTATTATAAGTAAATCG

GAM439  ABCC12    5'  AGTGTCCCCAGGCCAAAAGC   53788     CCCA T     A  G
                                GCT    G CCTGGG GA GCT
                                |||    | |||||| || |||
                                CGA    C GGACCC CT TGA
                                  AAAC _      _  G
GAM439  ACCN1     5'  CCCGAGGACTGGGAGCTC     8459              _
                                GAGCTCCCAGTCCT GGG
                                |||||||||||||| |||
                                CTCGAGGGTCAGGA CCC
                                         G
GAM439  ATSV      3'  CCTCTCCTGCCAGACAGC     16309     CCCA   C__
                                GCT    GTC   TGGGAGAGG
                                |||    |||   |||||||||
                                CGA    CAG   GTCCTCTCC
                                  _____   ACC
GAM439  BCR       3'  AGATCTGCCCAGGTCTGGGAGC 41482         T     _   GG
                                GCTCCCAG CCTGGG AGA  CT
                                |||||||| |||||| |||  ||
                                CGAGGGTC GGACCC TCT  GA
                                     T     G   A_
GAM439  CNTN2     3'  AGCCCTGGGACCAAGAGCTC   18655       CCA    TG  AGAG
                                GAGCTC   GTCC  GG    GCT
                                ||||||   ||||  ||    |||
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                                CTCGAG  CAGG CC   CGA
                                   AAC   GT ____
GAM439  FMO5    3' TCCCTAGACTGGGAGCTC   9392          CT
                                GAGCTCCCAGTC GGGA
                                |||||||||||| ||||
                                CTCGAGGGTCAG CCCT
                                      AT
GAM439  ID3     3' CCTCTCCTGCCGGAAGCC   79806   A  C  A  CCT
                                G GCT CC GT  GGGAGAGG
                                | ||| || ||  ||||||||
                                C CGA GG CG  TCCTCTCC
                                 _  A  C ___
GAM439  MUC12   3' AGCCTCTCCATCCGGGAGCTT 95897       AGTCCTG
                                GAGCTCCC     GGAGAGGCT
                                ||||||||     |||||||||
                                TTCGAGGG     CCTCTCCGA
                                     CCTA___
GAM439  NLGN2   3' CTTCGCCAAGACTGGGG    89535       C   GA
                                TCCCAGTC TGG  GAGG
                                |||||||| |||  ||||
                                GGGGTCAG ACC  CTTC
                                     A  G_
GAM439  PML     3' AGCCCCTCCTTCCAGGAGCT  53794      CAGTCCT    A
                                AGCTCC      GGGAG GGCT
                                ||||||      ||||| ||||
                                TCGAGG      TCCTC CCGA
                                   ACCT___    C
GAM439  PPGB    3' AGCCTCTCCCGCTAGGAGAGTC 6124    G_   C  CCT
                                GA  CTCC AGT   GGGAGAGGCT
                                ||  |||| |||  ||||||||||
                                CT  GAGG TCG   CCCTCTCCGA
                                 GA   A  ___
GAM439  TRPV2   5' AGCCCCTGCTACTGAGAAGCTC 32770     _ C   CCT  G  A
                                GAGCT C CAGT   GG AG GGCT
                                ||||| | ||||  || || ||||
                                CTCGA G GTCA   TC TC CCGA
                                   A A   ___  G  C
GAM439  VENTX2  3' AGCCCCTCCCGGGGAGGACTC  27852    C  CAG      A
                                GAG TCC   TCCTGGGAG GGCT
                                ||| |||   ||||||||| ||||
                                CTC AGG   GGGGCCCTC CCGA
                                  _  A__       C
GAM439  WNT6    3' AGCCTCTCCCTGCCAAAGC   22540    CCCA  CCT
                                GCT   GT  GGGAGAGGCT
                                |||   ||  ||||||||||
                                CGA   CG  CCCTCTCCGA
                                  AAC_  T__
GAM439  ABTB1   3' AGCCCCAGGGGCCAGGAGCTC  51696       CA   G  AGA
                                GAGCTCC  GTCCT GG   GGCT
                                |||||||  ||||| ||   ||||
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                                CTCGAGG  CGGGG CC   CCGA
                                   AC    A ___
GAM439  AMSH     5'  CCTCTCCCAAGAGAACTT    22343     C  CCAG  C
                                GAG TC    TC TGGGAGAGG
                                ||| ||    || |||||||||
                                TTC AG    AG ACCCTCTCC
                                  A _____ A
GAM439  C22orf5  3'  AGCCCCTCCTCCCCGCGAGACT 25334     _  CCAGTCCT    A
           C                     GAG CTC       GGGAG GGCT
                                ||| |||       ||||| ||||
                                CTC GAG       TCCTC CCGA
                                  A  CGCCCC__    C
GAM439  EMR2     3'  AGCCTCTCCTTCCTACAAAGAC 26499     C  CCA  CCT_
           TC                    GAG TC   GT    GGGAGAGGCT
                                ||| ||   ||    ||||||||||
                                CTC AG   CA    TCCTCTCCGA
                                  _ AAA  TCCT
GAM439  FLJ10986 5'  AGCCAATTAAGAATTGGGAGC  37489         C  GG  GA
                                GCTCCCAGT CT  GA  GGCT
                                ||||||||| ||  ||  ||||
                                CGAGGGTTA GA  TT  CCGA
                                     A  A_  AA
GAM439  FLJ12671 5'  CTCCCAGGCCTAGGAGCTC    49108        C  T
                                GAGCTCC AG CCTGGGAG
                                ||||||| || ||||||||
                                CTCGAGG TC GGACCCTC
                                   A  C
GAM439  FLJ13265 3'  AGCCTCCCTGAGTACTGGGACT 46409     C      C  G  A
           C                     GAG TCCCAGT CT GG GAGGCT
                                ||| ||||||| || || ||||||
                                CTC AGGGTCA GA TC CTCCGA
                                  _      T  G  C
GAM439  FLJ13693 3'  AGCCTCTCCCAAGACTGAAGTG 46072    TCC_    C
           C                     GC    CAGTC TGGGAGAGGCT
                                ||    ||||| ||||||||||
                                CG    GTCAG ACCCTCTCCGA
                                  TGAA    A
GAM439  FLJ14525 3'  AGCCTCTGTTTCATCTGGGAGC 52476         TCCT  G
                                GCTCCCAG    GG AGAGGCT
                                ||||||||    || |||||||
                                CGAGGGTC    TT TCTCCGA
                                     TACT  G
GAM439  FLJ21709 3'  AGCTGCTCCCAGGGCTGGGAGC 78475                A
           TC                      GAGCTCCCAGTCCTGGGAG GGCT
                                ||||||||||||||||||| ||||
                                CTCGAGGGTCGGGACCCTC TCGA
                                           G
GAM439  GAL3ST2  3'  TCTCCCAGAACCAAGAGTTC   53485       CCA  C
                                GAGCTC   GT CTGGGAGA
                                ||||||   || ||||||||
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                                CTTGAG   CA GACCCTCT
                                   AAC  A
GAM439  HIG2     3'  AGCCTCTCTTCCACAAGAGCTC 26196       CCA  CCT
                                GAGCTC   GT   GGGAGAGGCT
                                ||||||   ||   ||||||||||
                                CTCGAG   CA   TTCTCTCCGA
                                   AA_  CC_
GAM439  KIAA0062 3'  GCCTGTGGGACTGGAAGT    70786     C       GGAG
                                GCT CCAGTCCTG    AGGC
                                ||| |||||||||    ||||
                                TGA GGTCAGGGT    TCCG
                                  A        G___
GAM439  KIAA0514 3'  AGCCTCTTCTGCACCTAGGAGC 28738       C  TCC
                                GCTCC AG   TGGGAGAGGCT
                                ||||| ||   ||||||||||
                                CGAGG TC   GTCTTCTCCGA
                                   A  CAC
GAM439  KIAA0552 3'  AGCCCCTCCCCCAACAAGATCT 28986     C  CCA  CCT    A
             C                    GAG TC   GT   GGGAG GGCT
                                ||| ||   ||   ||||| ||||
                                CTC AG   CA   CCCTC CCGA
                                  T  AA_  ACC    C
GAM439  LCHN     3'  AGCCAACAGGACTGGGAGCC   87466   A          GGAGA
                                G GCTCCCAGTCCTG     GGCT
                                | ||||||||||||     ||||
                                C CGAGGGTCAGGAC     CCGA
                                _           AA___
GAM439  MGC15882 3'  AGCCCTTGGATCAGGACTAGGG 52882        C       ___  A
             GCTC                    GAGCTCC AGTCCTGG   GAG GGCT
                                ||||||| ||||||||   ||| ||||
                                CTCGGGG TCAGGACT   TTC CCGA
                                   A       AGG  _
GAM439  MGC4638  3'  AGCCTCTCCCAAGATGAG    49732     CCA   C
                                CTC   GTC TGGGAGAGGCT
                                |||   ||| ||||||||||
                                GAG   TAG ACCCTCTCCGA
                                  ___  A
GAM439  OCT11    3'  CCCCTCCTAGGAGCTT      27586        CAGTCC     A
                                GAGCTCC     TGGGAG GG
                                |||||||     |||||| ||
                                TTCGAGG     ATCCTC CC
                                   _______     C
GAM439  PHYHIP   3'  GCCCCTCCCCGGGGAGTTC   29289         AGTCCT    A
                                GAGCTCCC     GGGAG GGC
                                ||||||||     ||||| |||
                                CTTGAGGG     CCCTC CCG
                                   GC____     C
GAM439  PKNOX2   3'  AGCCCTGGAGGAACTGGGGCTC 92524      T    _   GGG  A
                                GAGC CCCAGT CCT   AG GGCT
                                |||| |||||| |||   || ||||
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                                CTCG GGGTCA GGA   TC CCGA
                                  _     A   GG_ _
GAM439  SEC31B-1  3'  AGCCTCTCTTGCTAGGAG    31925      C   CCT
                                CTCC AGT   GGGAGAGGCT
                                |||| |||   ||||||||||
                                GAGG TCG   TTCTCTCCGA
                                  A  ____
GAM439  SLC39A3   3'  AGCCTCTCGGTGCCAAGAGCC  58597   A    CCA TC  GG
                                G GCTC   G  CT  GAGAGGCT
                                | ||||   |  ||  ||||||||
                                C CGAG   C  GG  CTCTCCGA
                                 _   AAC GT  __
GAM439  TM4SF11   3'  GCGTCCAAGACTGGGGC     32588    T      C    AGAG
                                GC CCCAGTC TGGG    GC
                                || ||||||| ||||    ||
                                CG GGGTCAG ACCT    CG
                                 _      A   G____
GAM439  TRIM11    3'  AGCCCTTACCAAAGCTGGGAGC 73188         CC  _  A
                                GCTCCCAGT  TGG GAG GGCT
                                |||||||||  ||| ||| ||||
                                CGAGGGTCG  ACC TTC CCGA
                                     AA   A   _
GAM439  TRIM26    3'  CCTCTCCTGCCTCGGGAGTTC  14346         _ TCC
                                GAGCTCCC AG   TGGGAGAGG
                                |||||||| ||   |||||||||
                                CTTGAGGG TC   GTCCTCTCC
                                     C  C__
GAM439  LOC115574 3'  AGCCTCCCCCAGGGTGGAAGCC 73847   A   C   G      A
                                G GCT CCA TCCTGGG GAGGCT
                                | ||| ||| ||||||| ||||||
                                C CGA GGT GGGACCC CTCCGA
                                 _   A   _      C
GAM439  LOC130612 5'  AGCCTCTTTCACTCAGAAGCTC 75464       _ CC   CCT GG
                                GAGCT C  AGT   G  AGAGGCT
                                ||||| |  |||   |  |||||||
                                CTCGA G  TCA   C  TCTCCGA
                                   A AC   ___ TT
GAM439  LOC144342 5'  AGCAAGACAAAACCAGGGAGCT 77301         A_  CC  GGAGAG
           C                     GAGCTCCC  GT  TG     GCT
                                |||||||  ||  ||     |||
                                CTCGAGGG  CA  AC     CGA
                                     AC  AA  AGAA__
GAM439  LOC149674 3'  AGCCCCTCCCAGGATGACTG   80331     ___        A
                                CAG   TCCTGGGAG GGCT
                                |||   ||||||||| ||||
                                GTC   AGGACCCTC CCGA
                                  AGT        C
GAM439  LOC199986 5'  AGCCCCTCCAGCTTCCTGGGAG 91503         TCCTG_   A
           T                     GCTCCCAG     GGAG GGCT
                                ||||||||     |||| ||||
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                                TGAGGGTC     CCTC CCGA
                                    CTTCGA    C
GAM439  LOC255426 3'  AGCCTCCATCCACAGGGAGCTC 98938        AGTCC    A_
                                GAGCTCCC    TGGG  GAGGCT
                                ||||||||    ||||  ||||||
                                CTCGAGGG    ACCT  CTCCGA
                                    AC___    AC
GAM439  LOC257494 3'  CCTCTCCTGCCTCGGGAGTTC  99631        _  TCC
                                GAGCTCCC AG   TGGGAGAGG
                                |||||||| ||   |||||||||
                                CTTGAGGG TC   GTCCTCTCC
                                    C  C__
GAM440  HAL      5'  GCCACTCCTGCATAAAGCTC   10903          TGAAAA
                                GAGCTTTATGC     GGTGGC
                                ||||||||||     ||||||
                                CTCGAAATACG     TCACCG
                                      TCC___
GAM440  HMGN2    3'  GGCCACCTTGGCACAAAAGC   19809      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _  GG
GAM440  NMI      5'  GGCCACCTCCTCAGGAAG    17436      ATG    AA
                                CTTT   CTGA  AGGTGGCC
                                ||||   ||||  ||||||||
                                GAAG   GACT  TCCACCGG
                                  ___    CC
GAM440  PACE     3'  GGCCACCTCTCCAAGGGCTT   11944       A  CT  AAA
                                GAGCTTT TG  GA   GGTGGCC
                                |||||||  ||  ||   |||||||
                                TTCGGGA AC  CT   CCACCGG
                                    _  CT  ___
GAM440  PYCR1    3'  CCACCTTCCTCTAGAGCTC    70639        TGCT  A_
                                GAGCTTTA    GA  AAGGTGG
                                ||||||||    ||  |||||||
                                CTCGAGAT    CT  TTCCACC
                                      _____  CC
GAM440  SDC1     3'  GGCCACCTCCCCAGCATTCCAG 12991     TT_     AAA
          C                      GCT   ATGCTG   AGGTGGCC
                                 |||   ||||||   ||||||||
                                 CGA   TACGAC   TCCACCGG
                                   CCT     CCC
GAM440  FLJ11560  5'  GCCCAGGCCCAGCATAAAG   48008         AAAA  ___
                                CTTTATGCTG    GGT   GGC
                                ||||||||||    |||   |||
                                GAAATACGAC    CCG   CCG
                                      _____  GAC
GAM440  KIAA0446  5'  CCACCTTTTGAAGAGCTC    69446        ATGCTG
                                GAGCTTT     AAAAGGTGG
                                |||||||     |||||||||
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                                CTCGAGA     TTTTCCACC
                                   AG____
GAM440  KIAA0971  3'  GTTGTTCTCAGCATAAAGT   30677          AAA  TG
                                GCTTTATGCTGA   GG  GC
                                ||||||||||||  ||  ||
                                TGAAATACGACT   TT  TG
                                      C__  GT
GAM440  KIAA1393  3'  GGCCACCTTGGCACAAAAGC   72574      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                   _ _  GG
GAM440  KIAA1656  3'  GGCCACCTCCTCCTAGAAGCC  66377   A    ATGCT  AA
                                G GCTTT    GA  AGGTGGCC
                                | |||||    ||  ||||||||
                                C CGAAG    CT  TCCACCGG
                                _    ATC__  CC
GAM440  KIAA1884  3'  GCCACCTTCATCTACCAAGGCT 73728       ATGCT  A_
            C                    GAGCTTT    GA  AAGGTGGC
                                |||||||    ||  ||||||||
                                CTCGGAA    CT  TTCCACCG
                                   CCAT_  AC
GAM440  PP3501    3'  GGCCACCGTTGACAGCATAAAG 41683         AAAA_
                                CTTTATGCTG    GGTGGCC
                                ||||||||||    |||||||
                                GAAATACGAC    CCACCGG
                                      AGTTG
GAM440  SDCCAG3   3'  GGTGTTCTCAGCATGAAGCTC  22803           AAA  TG
                                GAGCTTTATGCTGA   GG  GCC
                                ||||||||||||||  ||  |||
                                CTCGAAGTACGACT   CT  TGG
                                      ____  TG
GAM440  SP140     3'  GGCCACCTCCATGCAGAAGC   24327      A   TGAAA
                                GCTTT TGC    AGGTGGCC
                                ||||| |||    ||||||||
                                CGAAG ACG    TCCACCGG
                                   _  TACC_
GAM440  LOC148760 3'  GGCCACCTTCTCCAACAAGCTC 85364       TA  CT  A
                                GAGCTT  TG  GA AAGGTGGCC
                                ||||||  ||  || |||||||||
                                CTCGAA  AC  CT TTCCACCGG
                                   CA  __  C
GAM440  LOC150170 5'  ACCTGTTTCACATAAAGC    80414        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                      _    G
GAM440  LOC150175 5'  ACCTGTTTCACATAAAGC    80453        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
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                                CGAAATAC ACTTT TCCA
                                   _    G
GAM440  LOC150215 5'  ACCTGTTTCACATAAAGC    80456        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                   _    G
GAM440  LOC150218 5'  ACCTGTTTCACATAAAGC    80525        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                   _    G
GAM440  LOC152065 3'  GGCCACCTTCTCCTTGGCAGGC 86737      TTA   ___  A
          TC                     GAGCT   TGCT   GA AAGGTGGCC
                                |||||   ||||   || |||||||||
                                CTCGG   ACGG   CT TTCCACCGG
                                  ___   TTC  C
GAM440  LOC152267 3'  GGCCACCTTGGCACAAAAGC   61036      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _  GG
GAM440  LOC158292 5'  CCTCTGGACCCAGCATAAGGCT 88046           AAAA_  T
          C                     GAGCTTTATGCTG    GG GG
                                ||||||||||||    || ||
                                CTCGGAATACGAC    TC CC
                                      CCAGG  T
GAM440  LOC219997 3'  GCCACCTCTTCAGCCTC    93256    CTTTAT    A
                                GAG     GCTGAA AGGTGGC
                                |||     ||||||| |||||||
                                CTC     CGACTT TCCACCG
                                  _______     C
GAM440  LOC256269 3'  GGCCACCTTGGCACAAAAGC   96608      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _  GG
GAM440  LOC91963  5'  GGCCACCTCCTCTGAGAAGC   68321      ATGCT  AA
                                GCTTT    GA  AGGTGGCC
                                |||||    ||  ||||||||
                                CGAAG    CT  TCCACCGG
                                   AGT__  CC
GAM441  CCND2     3'  TCCCAGCAAATCATCGGGCCA  10055          CCACA  _  A
                                TGGCCTGATGAT    GC GG GA
                                ||||||||||||    || || ||
                                ACCGGGCTACTA    CG CC CT
                                      AA___  A  C
GAM441  GCN5L2    5'  CTCCGCTGCGGGGGAGGCC   60529      GATGA  A
                                GGCCT    TCC CAGCGGAG
                                |||||    ||| ||||||||
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                                CCGGA    GGG GTCGCCTC
                                  GG___  C
GAM441  GJA5     3'  CTGACCAGATCATCAGCCA   75167     C      CACAG
                                TGGC TGATGATC    CGG
                                |||| ||||||||    |||
                                ACCG ACTACTAG    GTC
                                  _      ACCA_
GAM441  HIVEP3   3'  TCCCCGCTGTGGTTGGCAGCCA 44702     C  ATGAT       A
                                TGGC TG    CCACAGCGG GA
                                |||| ||    ||||||||| ||
                                ACCG AC    GGTGTCGCC CT
                                  _ GGTT_       C
GAM441  HOXD1    5'  CCGCCGGTATATTAGGCCA   44696         AT  ACA
                                TGGCCTGATG  CC   GCGG
                                ||||||||||  ||   ||||
                                ACCGGATTAT  GG   CGCC
                                      AT  C__
GAM441  SUFU     3'  CCTTGTGACCCATCAGGCCA   32934         ATC    C
                                TGGCCTGATG   CACAG GG
                                ||||||||||   ||||| ||
                                ACCGGACTAC   GTGTT CC
                                      CCA    _
GAM441  DKFZP586J1624 3'  CTCCGCCCAGTCACCATCAGGC 32043          ATCCACA_
           CA                   TGGCCTGATG       GCGGAG
                                ||||||||||       ||||||
                                ACCGGACTAC       CGCCTC
                                      CACTGACC
GAM441  KIAA1671  3'  CTTTGCTTATGAATCATCAGAC 66282    C      C  C_
           C                    GG CTGATGAT CA  AGCGGAG
                                || |||||||| ||  |||||||
                                CC GACTACTA GT  TCGTTTC
                                 A       A  AT
GAM441  LOC159110 5'  TCTCCGCTGCCCCGGTCAACCA 82995     CCTGA    CA__
                                TGG    TGATC    CAGCGGAGA
                                |||    |||||   |||||||||
                                ACC    ACTGG    GTCGCCTCT
                                  A____     CCCC
GAM441  LOC159116 5'  TCTCCGCTGCCCCGGTCAACCA 82978     CCTGA    CA__
                                TGG    TGATC    CAGCGGAGA
                                |||    |||||   |||||||||
                                ACC    ACTGG    GTCGCCTCT
                                  A____     CCCC
GAM441  LOC165476 5'  CTCCGCTGCCTGCTCAGCCA   88550     C   TGATCCA
                                TGGC TGA      CAGCGGAG
                                |||| |||      ||||||||
                                ACCG ACT      GTCGCCTC
                                  _  CGTCC__
GAM441  LOC200032 5'  CTGACCAGATCATCAGCCA   85475     C      CACAG
                                TGGC TGATGATC    CGG
                                |||| ||||||||    |||
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                                ACCG ACTACTAG    GTC
                                  _      ACCA_
GAM441  LOC219654 5'  CTCCGCTGCGGAGGGGGGCC  92932      GATGA  A
                                GGCCT    TCC CAGCGGAG
                                |||||    ||| ||||||||
                                CCGGG    AGG GTCGCCTC
                                   GGG__  C
GAM441  LOC255862 3'  TCAAATGTAGACTATCAGGCCA 96115         A  C  GCG
                                TGGCCTGATG TC ACA  GA
                                |||||||||| || |||  ||
                                ACCGGACTAT AG TGT  CT
                                      C  A  AAA
GAM442  CDH12    3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA  GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                      AA___  AC
GAM442  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM442  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090      T   AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                   _   GTCA_
GAM442  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
            A                    TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM442  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126        CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                      AGACG___
GAM442  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860     CCAC  CAA_
            TA                    TACA   TCC   GAAGAATAAG
                                ||||   |||   ||||||||||
                                ATGT   AGG   TTTCTTATTC
                                  AAA_  ATTG
GAM442  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA  68742           _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                         G
GAM442  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
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                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM442  KIAA1877 3'  CTTATTCTTCTGCCATGAGT  66748     CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM442  KIAA1906 3'  CTTATTCTTCTTGACTTTTGG  73571    CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM442  OSBPL11  3'  CTTAATTTCCCAAGAGTGGTG  43206       CCAA   AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                     AACC   A_
GAM442  YME1L1   3'  TCATTCTTGATGTGGTGTA   58438       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                     TA_    A
GAM442  ZNF262   3'  CTTATTTTGTTTGGGAGT    18723        A
                                ACTCCCAAG AGAATAAG
                                |||||||||  ||||||||
                                TGAGGGTTT TTTTATTC
                                     G
GAM442  LOC91960 3'  TGTGGCTTGGAACGTGGTGTA  68294       TC_   AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
                                ATGTGGTG   GGTTC   TGT
                                     CAA    GG__
GAM443  CCND2    3'  TCCCCAGCAAATCATCGGGCCA 10056         CCACA  _  A
                                TGGCCTGATGAT    GC GG GA
                                ||||||||||||    || || ||
                                ACCGGGCTACTA    CG CC CT
                                       AA___  A  C
GAM443  GCN5L2   5'  CTCCGCTGCGGGGGAGGCC   60529     GATGA  A
                                GGCCT    TCC CAGCGGAG
                                |||||    ||| ||||||||
                                CCGGA    GGG GTCGCCTC
                                   GG___  C
GAM443  GJA5     3'  CTGACCAGATCATCAGCCA   19164     C      CACAG
                                TGGC TGATGATC    CGG
                                ||||  ||||||||    |||
                                ACCG ACTACTAG    GTC
                                  _       ACCA_
GAM443  HIVEP3   3'  TCCCCGCTGTGGTTGGCAGCCA 44702     C  ATGAT       A
                                TGGC TG    CCACAGCGG GA
                                ||||  ||    |||||||||  ||
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                                ACCG AC    GGTGTCGCC CT
                                  _ GGTT_       C
GAM443  HOXD1    5' CCGCCGGTATATTAGGCCA   44696         AT  ACA
                                TGGCCTGATG  CC   GCGG
                                ||||||||||  ||   ||||
                                ACCGGATTAT  GG   CGCC
                                      AT  C__
GAM443  SUFU     3' CCTTGTGACCCATCAGGCCA  32934         ATC    C
                                TGGCCTGATG   CACAG GG
                                ||||||||||   ||||| ||
                                ACCGGACTAC   GTGTT CC
                                      CCA    _
GAM443  ARHGEF15 3' CTGTGGACCACAGGCCA     30953        A  A
                                TGGCCTG TG TCCACAG
                                ||||||| || |||||||
                                ACCGGAC AC AGGTGTC
                                    _ C
GAM443  DKFZP586J1624 3'  CTCCGCCCAGTCACCATCAGGC 32043          ATCCACA_
          CA                    TGGCCTGATG       GCGGAG
                                ||||||||||       ||||||
                                ACCGGACTAC       CGCCTC
                                      CACTGACC
GAM443  KIAA1671  3' CTTTGCTTATGAATCATCAGAC 66282    C       C  C_
          C                     GG CTGATGAT CA  AGCGGAG
                                || |||||||| ||  |||||||
                                CC GACTACTA GT  TCGTTTC
                                 A       A  AT
GAM443  MGC18079  3' CCGCGGACCTCAGGCCA     59033        TGA   ACA
                                TGGCCTGA   TCC   GCGG
                                ||||||||   |||   ||||
                                ACCGGACT   AGG   CGCC
                                    CC_   ___
GAM443  LOC115110 3' TGCAGACATCAGGCCA      72186         A  CACA
                                TGGCCTGATG TC    GCG
                                |||||||||| ||    |||
                                ACCGGACTAC AG    CGT
                                      _ A___
GAM443  LOC159110 5' TCTCCGCTGCCCCGGTCAACCA 82995     CCTGA    CA__
                                TGG    TGATC    CAGCGGAGA
                                |||    |||||   |||||||||
                                ACC    ACTGG    GTCGCCTCT
                                  A_____    CCCC
GAM443  LOC159116 5' TCTCCGCTGCCCCGGTCAACCA 82978     CCTGA    CA__
                                TGG    TGATC    CAGCGGAGA
                                |||    |||||   |||||||||
                                ACC    ACTGG    GTCGCCTCT
                                  A_____    CCCC
GAM443  LOC165476 5' CTCCGCTGCCTGCTCAGCCA  88550     C   TGATCCA
                                TGGC TGA      CAGCGGAG
                                |||| |||      ||||||||
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                                ACCG ACT      GTCGCCTC
                                  _  CGTCC__
GAM443  LOC200032 5'  CTGACCAGATCATCAGCCA   85475     C      CACAG
                                TGGC TGATGATC    CGG
                                |||| ||||||||    |||
                                ACCG ACTACTAG    GTC
                                  _      ACCA_
GAM443  LOC219654 5'  CTCCGCTGCGGAGGGGGGCC   92932      GATGA   A
                                GGCCT    TCC CAGCGGAG
                                |||||    ||| ||||||||
                                CCGGG    AGG GTCGCCTC
                                   GGG__   C
GAM443  LOC255862 3'  TCAAATGTAGACTATCAGGCCA 96115         A  C   GCG
                                TGGCCTGATG TC ACA   GA
                                |||||||||| || |||   ||
                                ACCGGACTAT AG TGT   CT
                                      C  A   AAA
GAM444  ACLY    3'  GCACTTCCCTGCCACTCCTCTG 65685        CGA  T_   C_
          C                      GCAGAGGAG   GC  GGAA  GC
                                |||||||||   ||  ||||  ||
                                CGTCTCCTC   CG  CCTT  CG
                                     AC_  TC    CA
GAM444  BACE    3'  GGCGCTCGCTCCCATGC     58089     GA       TGGAAC
                                GCA  GGAGCGAGC     GCC
                                |||  |||||||||     |||
                                CGT  CCTCGCTCG     CGG
                                  AC        _______
GAM444  BACE    3'  GGCGCTCGCTCCCATGC     25033     GA       TGGAAC
                                GCA  GGAGCGAGC     GCC
                                |||  |||||||||     |||
                                CGT  CCTCGCTCG     CGG
                                  AC        _______
GAM444  BIG1    3'  GGCATTTACATCCCTCTGC   22218       AGC  GCTG   C
                                GCAGAGG   GA    GAA GCC
                                |||||||   ||    ||| |||
                                CGTCTCC   CT    TTT CGG
                                    ___  ACA_   A
GAM444  CEBPA   3'  GCCCCAGCCGCTCCTC      16428        A    AAC
                                GAGGAGCG GCTGG   GC
                                |||||||| |||||   ||
                                CTCCTCGC CGACC   CG
                                     _    C__
GAM444  GPI     5'  GGCGCTCCTTCCTCCTCGGC   5727     A     C   CT   A
                                GC GAGGAG GAG  GGA CGCC
                                || |||||| |||  ||| ||||
                                CG CTCCTC CTT  CCT GCGG
                                 G     _  ___  C
GAM444  GRB10   3'  GCTAGAGGCTCCTCCTCTGC   19196         C    GGAAC
                                GCAGAGGAG GAGCT    GC
                                |||||||| |||||    ||
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                                CGTCTCCTC CTCGG    CG
                                     _    AGAT_
GAM444  IL10RA   3'  CCATGCCTGCTCCTCTGC    60379         A  _
                                GCAGAGGAGCG GC TGG
                                |||||||||| || |||
                                CGTCTCCTCGT CG ACC
                                      C  T
GAM444  KRT4     5'  GCTCCCAGCTCGCTCTCTGC  11228      G       AAC
                                GCAGAG AGCGAGCTGG  GC
                                |||||| ||||||||||  ||
                                CGTCTC TCGCTCGACC  CG
                                   _       CT_
GAM444  MAP3K7IP1 3'  GGTGCCCCATCCTCTGC    21491       GCGAGC  AA
                                GCAGAGGA    TGG  CGCC
                                ||||||||    |||  ||||
                                CGTCTCCT    ACC  GTGG
                                     _______  CC
GAM444  NESG1    5'  TGGCATCCTGAGCTCCTCT   25620       GAGCT  AC
                                AGAGGAGC    GGA  GCCA
                                ||||||||    |||  ||||
                                TCTCCTCG    CCT  CGGT
                                     AGT__   A_
GAM444  PCSK5    5'  GGCGTAAGGCTCGCTGCTCTGC 21675      G      GGA
                                GCAGAG AGCGAGCT   ACGCC
                                |||||| ||||||||  |||||
                                CGTCTC TCGCTCGG   TGCGG
                                   G       AA_
GAM444  PCTP     3'  TCCAGCTCACTCGTCTGC    41373      G  C
                                GCAGA GAG GAGCTGGA
                                ||||| ||| ||||||||
                                CGTCT CTC CTCGACCT
                                  G  A
GAM444  PRKCG    3'  GCATTCCAGCTCTGCCCCCGC  12287    AGA  A  _      C
                                GC  GG GC GAGCTGGAA GC
                                ||  || || ||||||||| ||
                                CG  CC CG CTCGACCTT CG
                                 CC_  _  T       A
GAM444  PTGIS    3'  GCATTACCACTTCCCTGC    8214      A  GCG  C  _  C
                                GCAG GGA   AG TGG AA GC
                                |||| |||   || ||| || ||
                                CGTC CCT   TC ACC TT CG
                                  _  ____  _  A  A
GAM444  SCA2     5'  GCGCGCCGCCCGCTCCTC    12943       A  T  AA
                                GAGGAGCG GC GG  CGC
                                |||||||| || ||  |||
                                CTCCTCGC CG CC  GCG
                                     C  _  GC
GAM444  SDC1     3'  GCATTCCAGCCCCTCTG     12989       AGCGA     C
                                CAGAGG    GCTGGAA GC
                                ||||||    ||||||| ||
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                                GTCTCC    CGACCTT CG
                                   C____     A
GAM444  SMARCD3  3'  GGCTCCAGCATCACTCCTCTGC 13265        C _    AC
                                GCAGAGGAG GA GCTGGA  GCC
                                ||||||||| || ||||||  |||
                                CGTCTCCTC CT CGACCT  CGG
                                    A  A    __
GAM444  SRI      3'  TTCCAACTGGAGCTCTCCTTTG 13391        GC   _______
            C                    GCAGAGGA  GAGCT     GGAA
                                ||||||||  |||||     ||||
                                CGTTTCCT  CTCGA     CCTT
                                    __    GGTCAA
GAM444  SSR4     3'  GGCACCCCAGCCCTGCCCTTGC 21862     G  A  A_    AAC
                                GCA AGG GCG  GCTGG   GCC
                                ||| ||| |||  |||||   |||
                                CGT TCC CGT  CGACC   CGG
                                  _  _  CC    CCA
GAM444  TARBP2   5'  GGCGGAGGGCCCGCTCCTC    57003        A  GGAA
                                GAGGAGCG GCT    CGCC
                                |||||||| |||    ||||
                                CTCCTCGC CGG    GCGG
                                    C   GAG_
GAM444  TARBP2   5'  GGCGGAGGGCCCGCTCCTC    57005        A  GGAA
                                GAGGAGCG GCT    CGCC
                                |||||||| |||    ||||
                                CTCCTCGC CGG    GCGG
                                    C   GAG_
GAM444  VDR      3'  TGGGGTTCAGCCCCTCCTCTGC 6347         CGA   G  G
                                GCAGAGGAG   GCTG AAC CCA
                                |||||||||   |||| ||| |||
                                CGTCTCCTC   CGAC TTG GGT
                                    CC_    _   G
GAM444  AIF1     5'  GCATCCCCTCTAGCTCCTT    17926        __   CT   AC
                                GAGGAGC  GAG  GGA  GC
                                |||||||  |||  |||  ||
                                TTCCTCG  CTC  CCT  CG
                                    AT   C_   A_
GAM444  CHERP    3'  GGCACCCCAGCTCCTTCCTCCA 22132    A_    C      AAC
            GC                    GC  GAGGAG GAGCTGG   GCC
                                ||  |||||| |||||||   |||
                                CG  CTCCTT CTCGACC   CGG
                                 AC     C      CCA
GAM444  CNIL     5'  GGCGCCGCTCCCCGCTCCTC   20504        ___   T  AA
                                GAGGAGC   GAGC GG  CGCC
                                |||||||   |||| ||  ||||
                                CTCCTCG   CTCG CC  GCGG
                                    CCC   _ __
GAM444  DKFZP434B044 3'  GGCGTTCCTGGCTCTCCTGC   49720      AG    G GCT
                                GCAG  GAGC A   GGAACGCC
                                ||||  |||| |   ||||||||
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                                CGTC  CTCG T   CCTTGCGG
                                  CT    G ___
GAM444  DKFZP434K1772 5'  TGGCGCCCCATTTTCCTCTGC  68342        GC   C   AA
                                GCAGAGGA  GAG TGG  CGCCA
                                ||||||||  ||| |||  |||||
                                CGTCTCCT  TTT ACC  GCGGT
                                    __  _  CC
GAM444  FBXO2    5'  GCGCTCCGGCTCCTCCTC    25142       C       A
                                GAGGAG GAGCTGGA CGC
                                |||||| |||||||| |||
                                CTCCTC CTCGGCCT GCG
                                   _      C
GAM444  FEM1B    5'  GGCACTCGGCCTCCTCTGC   31679         CGA    AAC
                                GCAGAGGAG   GCTGG   GCC
                                |||||||||   |||||   |||
                                CGTCTCCTC   CGGCT   CGG
                                    ___    CA_
GAM444  FLJ10769  3'  GGCGCCCTTCGTTCCTCCTCTG 37147         C    T_  AA
          C                    GCAGAGGAG GAGC  GG  CGCC
                               |||||||||  ||||  ||  ||||
                               CGTCTCCTC CTTG  TC  GCGG
                                    _   CT  CC
GAM444  FLJ11280  3'  TGGCTAGTTGGCTTGCTCCCCC 37787    AGA       TG AAC
          GC                   GC   GGAGCGAGC  G   GCCA
                               ||   |||||||||  |   ||||
                               CG   CCTCGTTCG  T   CGGT
                                CCC        GT GAT
GAM444  FLJ14840  5'  GCGCCGACCCTCGCTCCCCGC  52726    AGA      C__   AA
                               GC   GGAGCGAG   TGG  CGC
                               ||   ||||||||   |||  |||
                               CG   CCTCGCTC   GCC  GCG
                                CC_       CCA   __
GAM444  HPCAL4   3'  GGCCCACCCAGTCCTCTGC   33209       AGCGA    AAC_
                               GCAGAGG    GCTGG    GCC
                               |||||||    |||||    |||
                               CGTCTCC    TGACC    CGG
                                   ______    CACC
GAM444  HRIHFB2436 5'  GACGCCACAGCGCTCGCTCCTC 27569    A         ________   AACG
          CGT                    GC GAGGAGCGAGC      TGG    C
                                 || ||||||||||       |||    |
                                 TG CTCCTCGCTCG      ACC    G
                                  C         CGAC___   GCAA
GAM444  KIAA0212  3'  TGGCGCTCCCCTCCTCT     28631        CGAGCT   A
                               AGAGGAG     GGA CGCCA
                               |||||||     ||| |||||
                               TCTCCTC     CCT GCGGT
                                   C_____   C
GAM444  KIAA0229  3'  TGGCATCCCGGTGCGCCTCTGC 94031         A  GA    AAC
                               GCAGAGG GC  GCTGG   GCCA
                               ||||||| ||  |||||   ||||
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                                CGTCTCC CG  TGGCC   CGGT
                                    G __    CTA
GAM444  KIAA0546 3' TTCTTTTGGTCCTCTGC    71840        G   CT
                                GCAGAGGA CGAG  GGAA
                                |||||||| ||||  ||||
                                CGTCTCCT GTTT  TCTT
                                    G   __
GAM444  KIAA0673 5' TGGCACCCCCAGAGCCCTCCTG 62950     _  A  GAG   AAC_
          C                      GCAG AGG GC   CTGG   GCCA
                                |||| ||| ||   ||||   ||||
                                CGTC TCC CG   GACC   CGGT
                                  C  _ A__   CCCA
GAM444  KIAA0792 3' GCATCCAGCTCCCTGC     28766     A    GAGC   AC
                                GCAG GGAGC   TGGA  GC
                                |||| |||||   ||||  ||
                                CGTC CCTCG   ACCT  CG
                                  _   _____   A_
GAM444  KIAA1813 5' GGCGTTCCCCAGTCGCCCC   70827    A   G __
                                GG GCGA CT  GGAACGCC
                                || |||| ||  ||||||||
                                CC CGCT GA  CCTTGCGG
                                 C   _ CC
GAM444  KIAA1863 5' TGGCGTCCCCACCTCCTCTGT  65500        CGAGCT   A
                                GCAGAGGAG     GGA CGCCA
                                |||||||||     ||| |||||
                                TGTCTCCTC     CCT GCGGT
                                    CACC__  _
GAM444  KIAA1913 5' GGCGACTCCCTCTCCCCTGC   74318     A  GC   CT   A_
                                GCAG GGA  GAG  GGA  CGCC
                                |||| |||  |||  |||  ||||
                                CGTC CCT  CTC  CCT  GCGG
                                  C  __  __  CA
GAM444  MGC10870 5' TGGCGTTCTCGCGCCCCTCGC  51181    A   A   AGCT
                                GC GAGG GCG   GGAACGCCA
                                || |||| |||   |||||||||
                                CG CTCC CGC   TCTTGCGGT
                                 _   C  GC__
GAM444  MGC2714  5' GGCGACTCTGCTCCTCCGC   51175    A     _  CTGGAA
                                GC GAGGAGC GAG     CGCC
                                || ||||||| |||     ||||
                                CG CTCCTCG CTC     GCGG
                                 C      T   A_____
GAM444  NPC1L1   3' GCACCACTGATGGCTCCTCTGC 26333         G___  C   AAC
                                GCAGAGGAGC   AG TGG   GC
                                ||||||||||   || |||   ||
                                CGTCTCCTCG   TC ACC   CG
                                    GTAG  _   A__
GAM444  PHACS    5' TGGCGCCGATCACACTTCCTCT 51854        C___  GC   AA
          GC                    GCAGAGGAG   GA  TGG  CGCCA
                                |||||||||   ||  |||  |||||
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                                CGTCTCCTT   CT  GCC  GCGGT
                                     CACA  A_  __
GAM444  PP1057   5'  GCACCAGTCACTCCTCTGT   49253        C  G   AAC
                                GCAGAGGAG GA CTGG   GC
                                ||||||||| || ||||  ||
                                TGTCTCCTC CT GACC   CG
                                     A  _   A__
GAM444  PPP2R3A  3'  TGGCATCCCTGAGTCCCCTCCG 12246   A_   A_ GAGCT   AC
          GC                   GC  GAGG  GC    GGA  GCCA
                                ||  ||||  ||    |||  ||||
                                CG  CTCC  TG    CCT  CGGT
                                 GC   CC  AGTC_  A_
GAM444  RAB11B   3'  GCGCCCACCCGCTCCTCCGC   74337    A      AGC   AA
                                GC GAGGAGCG   TGG  CGC
                                || ||||||||   |||  |||
                                CG CTCCTCGC   ACC  GCG
                                 C       CC_  C_
GAM444  RBPMS    5'  GCGTCCCAGCCGCGGCCCGC   23433    AGA  A_   A    A
                                GC   GG  GCG GCTGG ACGC
                                ||   ||  ||| ||||| ||||
                                CG   CC  CGC CGACC TGCG
                                 C__  GG   _    C
GAM444  SEMA5A   5'  GGCACCAGCGCTCCTCGC    15594    A     GA    AAC
                                GC GAGGAGC  GCTGG   GCC
                                || |||||||  |||||   |||
                                CG CTCCTCG  CGACC   CGG
                                 _      __    A__
GAM444  SIAT8C   5'  GGCGCTGCGCGCTCCTTCGC   32448    AG     A  TGGAA
                                GC  AGGAGCG GC    CGCC
                                ||  ||||||| ||    ||||
                                CG  TCCTCGC CG    GCGG
                                 CT      G  TC___
GAM444  SNAP29   3'  GCATTCCCACCCACTCTTCTGC 17714         CGAGCT   C
                                GCAGAGGAG     GGAA GC
                                |||||||||     |||| ||
                                CGTCTTCTC     CCTT CG
                                     ACCCAC    A
GAM444  SNRPD2   3'  CAGAACTCACTCCTCTGT    17187         C  __
                                GCAGAGGAG GAG  CTG
                                ||||||||| |||  |||
                                TGTCTCCTC CTC  GAC
                                     A   AA
GAM444  ZNF213   3'  GCGTTCCTCTTCCCCTCT    65699      AGC   CT
                                AGAGG   GAG  GGAACGC
                                |||||   |||  |||||||
                                TCTCC   CTT  CCTTGCG
                                   C__   CT
GAM444  LOC130355 5'  TGGCGGGCGGGACCCGCTCCTC 75435         AG__   GAA
                                GAGGAGCG   CTG   CGCCA
                                ||||||||   |||   |||||
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                                CTCCTCGC   GGC  GCGGT
                                    CCAG  GG_
GAM444  LOC139522 5'  TGGCGTTCCAGCCCAGATCC  76365    GCGA_
                                GGA   GCTGGAACGCCA
                                |||   ||||||||||||
                                CCT   CGACCTTGCGGT
                                  AGACC
GAM444  LOC146429 5'  TGGCATCCCTGCTGCTCCTCGC 84677   A    G  T_  AC
                                GC GAGGAGC AGC  GGA  GCCA
                                || ||||||| |||  |||  ||||
                                CG CTCCTCG TCG  CCT  CGGT
                                 _     _  TC  A_
GAM444  LOC149832 5'  TCCAGCTCACCTCCTCTGC   85870       C_
                                GCAGAGGAG  GAGCTGGA
                                |||||||||  ||||||||
                                CGTCTCCTC  CTCGACCT
                                     CA
GAM444  LOC152137 3'  GCATTCTTTAACACTTCCTCTG 81319       CGAGCT_   C
          C                      GCAGAGGAG      GGAA GC
                                |||||||||      |||| ||
                                CGTCTCCTT      TCTT CG
                                     CACAATT   A
GAM444  LOC154215 3'  GGCCATTGCTAACTCCTCTGC  81957       CG  TGGAAC
                                GCAGAGGAG  AGC     GCC
                                |||||||||  |||     |||
                                CGTCTCCTC  TCG     CGG
                                     AA  TTAC__
GAM444  LOC154877 3'  TCCCTGGCTTCTCTGC     87577        G  CT
                                GCAGAGGAGC AG  GGA
                                |||||||||| ||  |||
                                CGTCTCTTCG TC  CCT
                                     G  __
GAM444  LOC164945 5'  CCAGGCCCTGCTCCTCTGC   88538         A_ _
                                GCAGAGGAGCG  GC TGG
                                |||||||||||  || |||
                                CGTCTCCTCGT  CG ACC
                                      CC  G
GAM444  LOC220003 5'  GCGTCACTGTCGTCCTCTGC  93284       G  GCTG  A
                                GCAGAGGA CGA   GA CGC
                                |||||||| |||   || |||
                                CGTCTCCT GCT   CT GCG
                                     _  GTCA  _
GAM444  LOC255650 3'  GGCTGAGCTCGCTCCTTGC   98525    G       GGAAC
                                GCA AGGAGCGAGCT    GCC
                                ||| ||||||||||    |||
                                CGT TCCTCGCTCGA    CGG
                                  _        GT___
GAM444  LOC256158 5'  GGCGCCCCCATGGAGCTCCTCT 99507         GAGC  AA_
          GT                     GCAGAGGAGC   TGG  CGCC
                                |||||||||   |||  ||||
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                                TGTCTCCTCG   ACC  GCGG
                                     AGGT  CCC
GAM444  LOC256475 5' GGCGCCCCAGTGCCCGTGC  99354    GA A GA   AA
                                GCA  GG GC  GCTGG  CGCC
                                |||  || ||  |||||  ||||
                                CGT  CC CG  TGACC  GCGG
                                  G_  _ __    CC
GAM444  LOC256586 5' GCGCTCCCCGGCTCCCTCGC  96618   A   AGC    AA__
                                GC GAGG  GAGCTGG   CGC
                                || ||||  |||||||   |||
                                CG CTCC  CTCGGCC   GCG
                                 _   ___     CCTC
GAM444  LOC51177  5' GCGGGGCCGCCCCTCGGC   33246   A   A  A  GGAA
                                GC GAGG GCG GCT   CGC
                                || |||| ||| |||   |||
                                CG CTCC CGC CGG   GCG
                                 G   C  _  G___
GAM444  LOC91351  3' GGCACTCAGGCTCCTCTGC   66299       GAG   AAC
                                GCAGAGGAGC  CTGG  GCC
                                ||||||||||  ||||  |||
                                CGTCTCCTCG  GACT  CGG
                                     ___   CA_
GAM444  LOC92370  3' GGCATTCCAACTTTTTCTC   69666     C  C   C
                                GAGGAG GAG TGGAA GCC
                                |||||| ||| ||||| |||
                                CTCTTT TTC ACCTT CGG
                                   _  A   A
GAM445  FGF12    3' TTATGGATATTATCAATGAG  41064       CCAT
                                CTCATTGAT   TCCATAA
                                |||||||||   |||||||
                                GAGTAACTA   AGGTATT
                                     TTAT
GAM445  REV3L    5' TATGGAATAATATATCTGAGGA 12824     TT  CC___
                                TCCTCA  GAT   ATTCCATA
                                ||||||  |||   ||||||||
                                AGGAGT  CTA   TAAGGTAT
                                   __  TATAA
GAM445  RNTRE    3' TTATGGAATGTAGTCGACGGAT 28717    TCA   C_
           A                     TATCC  TTGAT  CATTCCATAA
                                |||||  |||||  ||||||||||
                                ATAGG  AGCTG  GTAAGGTATT
                                  C__    AT
GAM445  ZNF32    3' TATGGAATGAATGGAGA    93104   CT   GATC
                                TC  CATT   CATTCCATA
                                ||  ||||   |||||||||
                                AG  GTAA   GTAAGGTAT
                                 AG   ____
GAM445  GFR      3' ATGGAATGTGGCCCACAGGA  25444    CAT  A_ _
                                TCCT   TG  TC CATTCCAT
                                ||||   ||  || ||||||||
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                                AGGA   AC  GG GTAAGGTA
                                  C__  CC  T
GAM445  KIAA1128  3'  AGTGGTATCAATGAAGATA   68995     C      _
                                TATC TCATTGAT CCATT
                                |||| |||||||| |||||
                                ATAG AGTAACTA GGTGA
                                  A       T
GAM445  KIAA1724  3'  TTATGGAACAGATCTTGATAGA 67625     C_   TT    CA
           TG                     TATC  TCA  GATC  TTCCATAA
                                |||| |||  ||||  ||||||||
                                GTAG  AGT  CTAG  AAGGTATT
                                  AT   T_   AC
GAM445  PMS2L3    5'  TATGGAATGGATCTCATTGA   71850     TT__
                                TCA    GATCCATTCCATA
                                |||    ||||||||||||||
                                AGT    CTAGGTAAGGTAT
                                  TACT
GAM445  PRO2405   5'  ATGGTGTTCTGGATCAACAAGG 38415     CA      TT___
                                CCT  TTGATCCA    CCAT
                                |||  ||||||||    ||||
                                GGA  AACTAGGT    GGTA
                                  AC       CTTGT
GAM445  TIAF1     5'  TTATGAGGATTCAATGAGGA   55297         _   ATTC
                                TCCTCATTGA TCC    CATAA
                                |||||||||| |||    |||||
                                AGGAGTAACT AGG    GTATT
                                      T   A___
GAM445  LOC145652 3'  TTATGGAATGGAATTCAAT    84408      __
                                ATTGA  TCCATTCCATAA
                                |||||  ||||||||||||
                                TAACT  AGGTAAGGTATT
                                   TA
GAM445  LOC153077 3'  TATGGAATGAACAAACAGGA   87130     CA   ATC
                                TCCT  TTG   CATTCCATA
                                ||||  |||   |||||||||
                                AGGA  AAC   GTAAGGTAT
                                  CA   AA_
GAM445  LOC245787 5'  TATGGAATGGATCTCATTGA   82262     TT__
                                TCA    GATCCATTCCATA
                                |||    ||||||||||||||
                                AGT    CTAGGTAAGGTAT
                                  TACT
GAM445  LOC254747 3'  ATGGGGATCAATGAAGA     98972    C        ATT
                                TC TCATTGATCC   CCAT
                                || ||||||||||   ||||
                                AG AGTAACTAGG   GGTA
                                 A        ____
GAM446  GALNT7    3'  AAGTTAAGCATTTTTGATCCTG 34279         __     TACCC_
           TAATC                    GATTGCAGG  CAAAA     AACTT
                                |||||||||  |||||     |||||
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                                CTAATGTCC  GTTTT     TTGAA
                                     TA    TACGAA
GAM446  FLJ12270  3'  AAGTTGGGTATTGTCTGAAATC 48338     G     AA
                                GATT CAGGCA  ATACCCAACTT
                                |||| ||||||  ||||||||||
                                CTAA GTCTGT  TATGGGTTGAA
                                  A     __
GAM446  KIAA0853  3'  TTGGGTATTTTGGCAG     31216     AGG
                                TTGC   CAAAATACCCAA
                                ||||   ||||||||||||
                                GACG   GTTTTATGGGTT
                                  ___
GAM446  LOC145842 5'  AGCTGGGTATTGTAAAATC   77991     GCAG   AA     A
                                GATT    GCA  ATACCCA CT
                                ||||    |||  ||||||| ||
                                CTAA    TGT  TATGGGT GA
                                  AA__  __     C
GAM447  MARK3     5'  ATACTCCCCCCGGAACCCA   11460       AAA     A
                                TGGGTTCC   GGGGGAG TAT
                                ||||||||   ||||||| |||
                                ACCCAAGG   CCCCCTC ATA
                                     C__     _
GAM447  PLAA      3'  TGATATTTAATCCTTAAAACCC 16188     CCA    GG
                                GGGTT   AAGGG  AGATATCA
                                |||||   |||||  ||||||||
                                CCCAA   TTCCT  TTTATAGT
                                   AA_    AA
GAM447  PRO0650   3'  CTTCCCCTTTAGAACCCA    27072       C
                                TGGGTTC AAAGGGGGAG
                                ||||||| ||||||||||
                                ACCCAAG TTTCCCCTTC
                                     A
GAM447  SHAPY     3'  CTCCCCCTTTGAAACTCA    57909       C
                                TGGGTT CAAAGGGGGAG
                                |||||| ||||||||||
                                ACTCAA GTTTCCCCCTC
                                    A
GAM447  LOC124044 3'  ATTTCCCCACCCTCGGAACCCA 76531       AAAG__
                                TGGGTTCC     GGGGAGAT
                                ||||||||     ||||||||
                                ACCCAAGG     CCCCTTTA
                                     CTCCCA
GAM448  ACVRL1    5'  TTTATTAGGAGGGAGTGGTG   5240         AAGAAG
                                CACCACTCCC     AATAAG
                                ||||||||||     ||||||
                                GTGGTGAGGG     TTATTT
                                      AGGA__
GAM448  BCL11B    3'  TTTGTTTTTGGGGTGGGGGGTG 57582       A_ __      G  TAAG
           TG                     TACACC  CT  CCCAAGAA AA
                                ||||||  ||  |||||||| ||
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                                GTGTGG  GG  GGGTTTTT TT
                                   GG  TG      G  T
GAM448  C18orf1  3'  CTTCGTGTGGGAGTGGTGTG  60865          A__
                                TACACCACTCCCA  GAAG
                                ||||||||||||  ||||
                                GTGTGGTGAGGGT  CTTC
                                     GTG
GAM448  ITPR3    3'  CTTGTTTTTCTCCTTTTGGTGT 11085       CTCCCA
           A                    TACACCA     AGAAGAATAAG
                                |||||||     ||||||||||
                                ATGTGGT     TCTTTTTGTTC
                                   TTTCC_
GAM448  KCNAB1   3'  GTTTGTTTTTTTTTGAAGGGGG 61585         ____
           TGGTGTG                TACACCACTCCC   AAGAAGAATAAG  T
                                ||||||||||||  ||||||||||||  |
                                GTGTGGTGGGGG   TTTTTTTTGTTT  G
                                     AAGT
GAM448  KRAS2    3'  CTTATTTTTCTTACCAAGTGTG 54123    C  CCC_
                                CAC ACT   AAGAAGAATAAG
                                ||| |||   ||||||||||||
                                GTG TGA   TTCTTTTTATTC
                                  _  ACCA
GAM448  KRAS2    3'  CTTATTTTTCTTACCAAGTGTG 54124    C  CCC_
                                CAC ACT   AAGAAGAATAAG
                                ||| |||   ||||||||||||
                                GTG TGA   TTCTTTTTATTC
                                  _  ACCA
GAM448  LIFR     3'  TTTGTTTTTTTTGGTTGGTTG  11315   C   CTC
                                A ACCA  CCAAGAAGAATAAG
                                | ||||  ||||||||||||||
                                G TGGT  GGTTTTTTTTGTTT
                                 T   T__
GAM448  MEN1     5'  CTTGTTTTTTTCCTTTTGGTG  56348      CTCCCA
                                CACCA     AGAAGAATAAG
                                |||||     ||||||||||
                                GTGGT     TTTTTTTGTTC
                                   TTTCC_
GAM448  MLLT7    3'  TTGTGCCTGGGAGTGTGTG   21043    _      AGAAGA
                                CAC CACTCCCA     ATAA
                                ||| ||||||||     ||||
                                GTG GTGAGGGT     TGTT
                                  T       CCG___
GAM448  SIAH1    3'  TTTGTTTTTGCCGTGGGAGTGT 13128    _      AG__
           GTG                    CAC CACTCCCA    AAGAATAAG
                                ||| ||||||||   |||||||||
                                GTG GTGAGGGT    TTTTTGTTT
                                  T       GCCG
GAM448  SLC7A6   3'  TTTGTTTTTGTGGTGGGTGCTG 15646     C    _  AG
           TG                     TACA CACTC CCA  AAGAATAAG
                                ||||  |||||  |||  |||||||||
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                                GTGT GTGGG GGT  TTTTTGTTT
                                  C    T  G_
GAM448  STAT6    5'  ATTTTTCTTTTTGGTGGTGGTG 13448       TC        TAAG
                                CACCAC  CCAAGAAGAA
                                ||||||  ||||||||||
                                GTGGTG  GGTTTTTCTT
                                   GT        TTTAT
GAM448  TCF8     3'  CTTGTTTTTTTAAGAGTGTGTG 48429    _    CCA
                                CAC CACTC   AGAAGAATAAG
                                ||| |||||   ||||||||||
                                GTG GTGAG   TTTTTTTGTTC
                                  T    AA_
GAM448  B3GNT7   3'  TTGTTCTTGGCTGGTGGGTG   71685    A    C_     G
                                TAC CCACT  CCAAGAA AA
                                ||| |||||  ||||||| ||
                                GTG GGTGG  GGTTCTT TT
                                  _    TC      G
GAM448  BCDO     3'  TTATTCTTTCTGTGGGTG    34287      C  AG
                                CACTC CA  AAGAATAA
                                ||||| ||  ||||||||
                                GTGGG GT  TTCTTATT
                                   T  CT
GAM448  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
           A                     TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM448  EPN2     3'  TTTATTTTTCTTTGACTCGTGT 31046       CAC  CC
           G                     TACAC   TC  AAGAAGAATAAG
                                |||||   ||  ||||||||||||
                                GTGTG   AG  TTCTTTTTATTT
                                   CTC  T_
GAM448  FLJ13855  3'  GGGTATTTTTCTTGGGGGTGGA 43853     A              AG
           GTA                     TAC CCACTCCCAAGAAGAATA
                                ||| ||||||||||||||||||
                                ATG GGTGGGGGTTCTTTTTAT
                                  A              GGGA
GAM448  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126          CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM448  FLJ32865  3'  TTTGTTGGGGGTGGGGTG    58824     A        G
                                TAC CCACTCCCAA AAG
                                ||| |||||||||| |||
                                GTG GGTGGGGGTT TTT
                                  G        G
GAM448  GRP3     3'  TTGTTCTTCTTGGTGTG     31742     TC
                                CAC  CCAAGAAGAATAA
                                |||  ||||||||||||
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                                GTG  GGTTCTTCTTGTT
                                  T_
GAM448  HAND1     3'  TTTGTTCTTCGAATCGTGGTG  17880       TCCCAA
                                CACCAC     GAAGAATAAG
                                ||||||     ||||||||||
                                GTGGTG     CTTCTTGTTT
                                   CTAAG_
GAM448  KIAA0562  3'  TTTGTTTTGCGGGGGTGGTG   28834         AAGA
                                CACCACTCCC   AGAATAAG
                                ||||||||||   ||||||||
                                GTGGTGGGGG   TTTTGTTT
                                     CG__
GAM448  KIAA0871  5'  TTTATTTTTTTGGTGTGTGTGT 31023      _  TC       ATAAG
          G                      TACAC CAC  CCAAGAAGA
                                |||||  |||  |||||||||
                                GTGTG GTG  GGTTTTTTT
                                   T  T_       ATTT
GAM448  KIAA0970  3'  TTTGTTTTTTTTGTTAGGGTG  30622     A  CC
                                CACC CT  CAAGAAGAATAAG
                                ||||  ||  ||||||||||||
                                GTGG GA  GTTTTTTTTGTTT
                                  _  TT
GAM448  KIAA1240  3'  TTTATTTTTAGGGAGTGGGTA  67297     A       AAG
                                TAC CCACTCCC   AAGAATAAG
                                |||  ||||||||   |||||||||
                                ATG GGTGAGGG   TTTTTATTT
                                  _      A__
GAM448  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68742             _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||  |||
                                ATGTGGTGAGGGTTCT TCT
                                         G
GAM448  KIAA1750  3'  TTTATTTTTTTGTTCTAGGTGT 68815       ACTCCCA
          G                      TACACC      AGAAGAATAAG
                                ||||||      ||||||||||
                                GTGTGG      TTTTTTTATTT
                                   ATCTTG_
GAM448  MAP2K3    3'  CTTGTTTTTCTTGCATGGT    59686     CTCC
                                ACCA    CAAGAAGAATAAG
                                ||||    ||||||||||||
                                TGGT    GTTCTTTTTGTTC
                                  AC__
GAM448  MLN64     3'  CTTGTTGGGGAGTGGGTG    96062     A      _  G
                                TAC CCACTCCC AA AAG
                                |||  |||||||  ||  |||
                                GTG GGTGAGGG TT TTC
                                  _      G  G
GAM448  NY-REN-41 3'  TTTGTTTTTCTATCCTGGTGG  55564      CCCA_
                                CCACT    AGAAGAATAAG
                                |||||    ||||||||||
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                                GGTGG    TCTTTTTGTTT
                                   TCCTA
GAM448  PRO1489   5'  TTTGTTTTTCGTGTGTGTGTG  38334      _  TCCCAA
                                TACAC CAC     GAAGAATAAG
                                ||||| |||     ||||||||||
                                GTGTG GTG     CTTTTTGTTT
                                   T   TG____
GAM448  SEC15L    3'  TTTGTTCTACTTGGGTGGT    72731      CT     A
                                ACCA  CCCAAG AGAATAAG
                                ||||  |||||| ||||||||
                                TGGT  GGGTTC TCTTGTTT
                                   __     A
GAM448  SHAPY     3'  TTTGTTCTTTTTGGAACTGTG  57915     TC__
                                CAC    CCAAGAAGAATAAG
                                |||    ||||||||||||||
                                GTG    GGTTTTTCTTGTTT
                                  TCAA
GAM448  STAM2     3'  TGTTTTTCTTCCTGCAATGTGG 20709        TCC_  A     TAAG
            TGTG                   TACACCAC    CA GAAGAA
                                |||||||||    || ||||||
                                GTGTGGTG    GT CTTCTT
                                     TAAC  C     TTTGTT
GAM448  TUBGCP3   3'  TTTATTTTTTTTTAGTGTTGTA 21982      C    CCC
                                TACA CACT   AAGAAGAATAAG
                                |||| ||||   ||||||||||||
                                ATGT GTGA   TTTTTTTTATTT
                                   T    T__
GAM448  ZNF220    3'  CTTGTTTTTTTACCACCTGGTG 23157      CTCCCA
                                CACCA     AGAAGAATAAG
                                |||||     ||||||||||
                                GTGGT     TTTTTTTGTTC
                                   CCACCA
GAM448  LOC121219 5'  TTGTTCTATGGGTGGGTG    74493      ACT    AGA
                                CACC   CCCA   AGAATAA
                                ||||   ||||   |||||||
                                GTGG   GGGT   TCTTGTT
                                   GT_    A__
GAM448  LOC143146 3'  TTTGTTGGAGGTGGTGTA    60767        TC    G
                                TACACCAC  CCAA AAG
                                ||||||||  |||| |||
                                ATGTGGTG  GGTT TTT
                                     GA    G
GAM448  LOC146445 3'  TTGTTCTTTGTGTGGTTG    84687    C    TCCCAA
                                A ACCAC     GAAGAATAA
                                | |||||     |||||||||
                                G TGGTG     TTTCTTGTT
                                 T    TG____
GAM448  LOC150174 3'  TTTATTTTTTTTTACAATGGTG 80444      CTCCC
                                CACCA    AAGAAGAATAAG
                                |||||    ||||||||||||
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                                GTGGT    TTTTTTTTATTT
                                  AACAT
GAM448  LOC150213 3'  TTTATTTTTTTTACAATGGTG  75363      CTCCC
                                CACCA    AAGAAGAATAAG
                                |||||    ||||||||||||
                                GTGGT    TTTTTTTTATTT
                                  AACA_
GAM448  LOC150236 3'  TTTATTTTTTTTACAATGGTG  80505      CTCCC
                                CACCA    AAGAAGAATAAG
                                |||||    ||||||||||||
                                GTGGT    TTTTTTTTATTT
                                  AACA_
GAM448  LOC154084 3'  CTTGTTTTTTTTAGTAGGTGTG  87378       _  CCCA
                                TACACC ACT    AGAAGAATAAG
                                ||||||| |||    ||||||||||
                                GTGTGG TGA    TTTTTTTGTTC
                                   A  ____
GAM448  LOC170261 3'  TTTATTCTTTGTGAAAGTGGT  83472       CC  A
                                ACCACT  CA GAAGAATAAG
                                ||||||  || ||||||||||
                                TGGTGA  GT TTTCTTATTT
                                   AA  G
GAM448  LOC199692 3'  CTTGTTCTTCTGCTGTAGTGTG 59926       C  TCCCA
                                TACAC AC     AGAAGAATAAG
                                |||||| ||     ||||||||||
                                GTGTG TG     TCTTCTTGTTC
                                  A  TCG__
GAM448  LOC203414 3'  CTTGTCAACTGGGGGTGATGTG 90913      C       A AA  A
                                TACA CACTCCCA G  GA TAAG
                                |||| |||||||| |  || ||||
                                GTGT GTGGGGGT C  CT GTTC
                                  A       _ AA  _
GAM448  LOC222256 3'  TTTTTCTTGTGGTGT       95915        TCCC
                                ACACCAC    AAGAAGAA
                                |||||||    ||||||||
                                TGTGGTG    TTCTTTTT
                                             ____
GAM448  LOC257051 3'  TTTATTCTTTGTGAAAGTGGT  98054       CC  A
                                ACCACT  CA GAAGAATAAG
                                ||||||  || ||||||||||
                                TGGTGA  GT TTTCTTATTT
                                   AA  G
GAM448  LOC92303  3'  TTATTTTTTTTGAGGTGG    69400       CC
                                CCACT  CAAGAAGAATAA
                                |||||  ||||||||||||
                                GGTGG  GTTTTTTTTATT
                                  A_
GAM449  CDH12     3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
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                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM449  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM449  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090      T   AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                   _   GTCA_
GAM449  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
           A                     TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM449  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM449  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
           TA                    TACA   TCC   GAAGAATAAG
                                ||||   |||   ||||||||||
                                ATGT   AGG   TTTCTTATTC
                                  AAA_  ATTG
GAM449  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA  68742              _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                          G
GAM449  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM449  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748     CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM449  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM449  OSBPL11   3'  CTTAATTTCCCAAGAGTGGTG  43206        CCAA    AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
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                                GTGGTGAG   CTTT  ATTC
                                    AACC   A_
GAM449  YME1L1   3'  TCATTCTTGATGTGGTGTA   58438       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   |||||| ||
                                ATGTGGTG   GTTCTT CT
                                    TA_     A
GAM449  ZNF262   3'  CTTATTTTGTTTGGGAGT    18723        A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                     G
GAM449  LOC91960 3'  TGTGGCTTGGAACGTGGTGTA 68294       TC_    AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
                                ATGTGGTG   GGTTC   TGT
                                    CAA    GG__
GAM450  COL6A3   3'  TCCAAATTCCCTCTGG     16468    T  TC
                                CCA GG  GGAATTTGGA
                                ||| ||  ||||||||||
                                GGT TC  CCTTAAACCT
                                  C  __
GAM450  COL6A3   3'  TCCAAATTCCCTCTGG     55145    T  TC
                                CCA GG  GGAATTTGGA
                                ||| ||  ||||||||||
                                GGT TC  CCTTAAACCT
                                  C  __
GAM450  CPSF6    3'  CCAAATTCTAGGACAATG    23789    G  __
                                CAT GTC  GGAATTTGG
                                ||| |||  |||||||||
                                GTA CAG  TCTTAAACC
                                  A   GA
GAM450  GRIN2A   3'  TCCAAATTCCATTAAGGT    7725     A   C
                                ACC TGGT GGAATTTGGA
                                ||| |||| ||||||||||
                                TGG ATTA CCTTAAACCT
                                  A   _
GAM450  GRIN2A   3'  TCCAAACAGCCATGGTG     7724        CGGAA
                                TACCATGGT    TTTGGA
                                |||||||||    ||||||
                                GTGGTACCG    AAACCT
                                    AC____
GAM450  MKI67    3'  CCATTTCCACCATGGTA     11592       C   TT
                                TACCATGGT GGAA  TGG
                                ||||||||| ||||  |||
                                ATGGTACCA CCTT  ACC
                                    _   T_
GAM450  NCALD    3'  TCCAAATTTGTATGGTA     50193       GTCG
                                TACCATG   GAATTTGGA
                                |||||||   |||||||||
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                                ATGGTAT   TTTAAACCT
                                   G___
GAM450  ARHU     3'  CAGGTCAACCATGGTA     41359        CG  A
                                TACCATGGT  GA TTTG
                                |||||||||  || ||||
                                ATGGTACCA  CT GGAC
                                     A_  _
GAM450  C11orf24  3'  TCCAAATTCTTTTGGTG     42534      TGGTC
                                TACCA    GGAATTTGGA
                                |||||    ||||||||||
                                GTGGT    TCTTAAACCT
                                   TT___
GAM450  DKFZP564O0463 3'  TCCAAATTCAAGATGGTG    27126     G   G_
                                CAT GTC  GAATTTGGA
                                ||| |||  |||||||||
                                GTG TAG  CTTAAACCT
                                  G   AA
GAM450  FHX      3'  CCAAACTCTGCTTCTATGGTA  37921        T__    A
                                TACCATGG   CGGA TTTGG
                                ||||||||   |||| |||||
                                ATGGTATC   GTCT AAACC
                                     TTC    C
GAM450  FLJ10803  3'  TCCAAATTCCTATTTGGTG    37208      T   C
                                TACCA GGT GGAATTTGGA
                                ||||| ||| ||||||||||
                                GTGGT TTA CCTTAAACCT
                                   _   T
GAM450  FLJ12888  5'  TCCAAATTCTGTCATCA     46894    C    T
                                C ATGG CGGAATTTGGA
                                | |||| ||||||||||
                                A TACT GTCTTAAACCT
                                 C   _
GAM450  FLJ13262  3'  TCCAAATTCCCGGCCCGG    46696    AT     _
                                CC  GGTCGG AATTTGGA
                                ||  |||||| ||||||||
                                GG  CCGGCC TTAAACCT
                                 C_     C
GAM450  FLJ13291  3'  TCCAAACTCTGATAACGGT    50742     ATG     A
                                ACC   GTCGGA TTTGGA
                                |||   |||||| ||||||
                                TGG   TAGTCT AAACCT
                                  CAA     C
GAM450  KEAP1    3'  CCAAACCCTCTGGCCGGGTA   25429      A      A__
                                TACC TGGTCGGA   TTTGG
                                |||| ||||||||   |||||
                                ATGG GCCGGTCT   AAACC
                                   _       CCC
GAM450  KIAA0252  5'  CCGGGGGACCACCATGGTA   63452         C  AA_
                                TACCATGGT GG   TTTGG
                                ||||||||| ||   |||||
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                                ATGGTACCA CC   GGGCC
                                     _ AGG
GAM450  KIAA0798  3'  CCAATATGACCCATGGTA    28444        _  GAAT
                                TACCATGG TCG    TTGG
                                |||||||| |||    ||||
                                ATGGTACC AGT    AACC
                                     C   AT__
GAM450  KIAA0961  3'  TCCAAATTCAAATGGTG     30408      GGTCG
                                TACCAT    GAATTTGGA
                                ||||||    |||||||||
                                GTGGTA    CTTAAACCT
                                   AA___
GAM450  KIAA1786  3'  TCCAAATTCTGCTAGG      66636    A   T
                                CC TGG CGGAATTTGGA
                                || ||| ||||||||||
                                GG ATC GTCTTAAACCT
                                 _  _
GAM450  NAV3      3'  CCAAGGGCTAGGCCATGGTA   30451         _ AA
                                TACCATGGTC GG  TTTGG
                                |||||||||| ||  |||||
                                ATGGTACCGG TC  GAACC
                                      A  GG
GAM450  PDZ-GEF1  3'  TCCAAATTCCAAGATCATCA   27283   C     __
                                C ATGGTC  GGAATTTGGA
                                | ||||||  ||||||||||
                                A TACTAG  CCTTAAACCT
                                 C     AA
GAM450  PIP5K1C   3'  TCCAAATTCCTGTACTGT    71309      _ _
                                ATGGT C GGAATTTGGA
                                ||||| | ||||||||||
                                TGTCA G CCTTAAACCT
                                   T T
GAM450  SPARCL1   5'  TCCAAATTCTCGTCTGTCA   17432   C    T _
                                C ATGG CG GAATTTGGA
                                | |||| || |||||||||
                                A TGTC GC CTTAAACCT
                                 C    T  T
GAM450  LOC122553 3'  TCTGTGCCAATCATGGTA    74594        C  AATT
                                TACCATGGT GG    TGGA
                                |||||||| ||    ||||
                                ATGGTACTA CC    GTCT
                                      A  GT__
GAM450  LOC149271 3'  TCCAAATTCCTTCCATGGTA   80011        TC
                                TACCATGG  GGAATTTGGA
                                ||||||||  ||||||||||
                                ATGGTACC  CCTTAAACCT
                                      TT
GAM450  LOC149460 5'  TCCAGCCCCAATCATGGTA    85616        C  AAT
                                TACCATGGT GG   TTGGA
                                ||||||||| ||   |||||
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                                ATGGTACTA CC   GACCT
                                     A  CC_
GAM450  LOC151614 3'  CCAAATTCCACTTCTGGT    81119     T_  C
                                ACCA  GGT GGAATTTGG
                                ||||  ||| |||||||||
                                TGGT  TCA CCTTAAACC
                                  CT  _
GAM450  LOC158476 5'  TCCAAAGAACCATGGTG     88206        CGGAA
                                TACCATGGT    TTTGGA
                                |||||||||    ||||||
                                GTGGTACCA    AAACCT
                                     AG___
GAM450  LOC219333 3'  CCTTCCGATCATGGTA      95185          TTT
                                TACCATGGTCGGAA   GG
                                ||||||||||||||   ||
                                ATGGTACTAGCCTT   CC
                                                 ___
GAM450  LOC54516  3'  TCCAACTTTACCATGGTG    39286        CG   T
                                TACCATGGT  GAA TTGGA
                                |||||||||  ||| |||||
                                GTGGTACCA  TTT AACCT
                                     __  C
GAM450  LOC90589  3'  CCGAATCCAATCATGGTA    59773        C   A
                                TACCATGGT GGA TTTGG
                                |||||||||| ||| |||||
                                ATGGTACTA CCT AAGCC
                                     A  _
GAM450  LOC92017  5'  CCAAATTCCACACCCTGG    68488    T  C_
                                CCA GGT  GGAATTTGG
                                ||| |||  |||||||||
                                GGT CCA  CCTTAAACC
                                  C  CA
GAM451  UST       3'  CACCTATCAATGATGCCT    20348        C  C  _
                                GGGCATCAT GA AG TG
                                ||||||||| || || ||
                                TCCGTAGTA CT TC AC
                                     A  A  C
GAM452  CYP4F3    3'  CTGTATTCACAGCTGCTT    8004          CGTAAAAC
                                GAGCAGCTG       ATACAG
                                |||||||||       ||||||
                                TTCGTCGAC       TATGTC
                                     ACT_____
GAM452  EN2       5'  CTGCATGCGCGCAGCTCTC   9258     C      AAAA  A
                                GAG AGCTGCGT    CAT CAG
                                ||| ||||||||    ||| |||
                                CTC TCGACGCG    GTA GTC
                                  _       C___   C
GAM452  GPR44     3'  CTGTATGCAACAGGCACTC   17697    CA  GC  AAAA
                                GAG  GCT  GT    CATACAG
                                |||  |||  ||    |||||||
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                                CTC  CGG  CA    GTATGTC
                                  A_   A_  AC__
GAM452  NUCB1    3'  CCTGTATGCCCACAGCTACT   21639    C    CGTAAAA
                                AG AGCTG      CATACAGG
                                || |||||      ||||||||
                                TC TCGAC      GTATGTCC
                                 A    ACCC___
GAM452  SYNGR3   3'  CCTAGTACTCCACAAGCTGCTC 16118        GC  AAAACA  _
                                GAGCAGCT  GT     TAC AGG
                                ||||||||  ||     ||| |||
                                CTCGTCGA  CA     ATG TCC
                                     A_  CCTC__   A
GAM452  WBSCR14  3'  CCTGCTGCTCACTCAGCTGC   53094       C  AAAA  TA
                                GCAGCTG GT    CA  CAGG
                                ||||||| ||    ||  ||||
                                CGTCGAC CA    GT  GTCC
                                     T  CTC_  C_
GAM452  WBSCR14  3'  CCTGCTGCTCACTCAGCTGC   53096       C  AAAA  TA
                                GCAGCTG GT    CA  CAGG
                                ||||||| ||    ||  ||||
                                CGTCGAC CA    GT  GTCC
                                     T  CTC_  C_
GAM452  DKFZP434F1735 3'  ATGCTTTAGCAGCTGCTC    32114         G    A
                                GAGCAGCTGC TAAA CAT
                                |||||||||| |||| |||
                                CTCGTCGACG ATTT GTA
                                       _    C
GAM452  ELL2     3'  CTGCATTTCGAAGCTGCTC    24893        G  T   ACATA
                                GAGCAGCT CG AAA     CAG
                                |||||||| || |||     |||
                                CTCGTCGA GC TTT     GTC
                                     A  _   AC___
GAM452  FLJ20730  3'  CCTGTATGTTTACAGACT    36049    _  CGTA
                                AG CTG    AAACATACAGG
                                || |||    ||||||||||
                                TC GAC    TTTGTATGTCC
                                 A   A___
GAM452  HSPB7    3'  CCAGGGTGTCAACAGCTGCTC  27783         CGTAAA   ACA
                                GAGCAGCTG     ACAT   GG
                                |||||||||     ||||   ||
                                CTCGTCGAC     TGTG   CC
                                      AAC___    GGA
GAM452  KIAA0984  3'  TATGCTTTACGCAGTTGCTC   66143            A
                                GAGCAGCTGCGTAAA CATA
                                |||||||||||||| ||||
                                CTCGTTGACGCATTT GTAT
                                          C
GAM452  LOC201627 3'  CCTACATGTTTCACAGTTCAGC 90451        C___  A     AC
             TGCT                   AGCAGCTG   GT AAACAT  AGG
                                ||||||||   || ||||||  |||
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                                TCGTCGAC    CA TTTGTA  TCC
                                     TTGA  C      CA
GAM453  HOXC4     3'  CCCTCCCCTCACACAC      28245         A  TC  T
                                GTGTGTGA GG  GG GGG
                                |||||||| ||  || |||
                                CACACACT CC  CC CCC
                                     _  __  T
GAM453  CMG2      3'  CCCAAACCCACACACCAG     55199          AA   CGG
                                CTGGTGTGTG  GGT   TGGG
                                ||||||||||  |||   ||||
                                GACCACACAC  CCA   ACCC
                                     __   A__
GAM453  DKFZP727G051 3'  ACCCACCAGACACCACACAGCA 69999      G     AAG  _
          GA                      TCTG TGTGTG   GTC GGTGGGT
                                |||| ||||||   ||| |||||||
                                AGAC ACACAC   CAG CCACCCA
                                  G     CA_   A
GAM453  LOC113763 3'  CATACCCCCACACACCAG     57385          AA   CG
                                CTGGTGTGTG  GGT  GTG
                                ||||||||||  |||  |||
                                GACCACACAC  CCA  TAC
                                     CC   __
GAM453  LOC126964 3'  CCCCCATCACACACCA       75112          A  TCGGT
                                TGGTGTGTGA GG     GGG
                                |||||||||| ||     |||
                                ACCACACACT CC     CCC
                                     A  _____
GAM453  LOC158525 5'  ACCCAAATGGTCTCACACACCA 82836           A GT  G_
          G                      CTGGTGTGTGA G  CG  TGGGT
                                |||||||||||  |  ||  |||||
                                GACCACACACT C  GT  ACCCA
                                     _ TG  AA
GAM454  ABCG2     3'  GTATTCAATCAAGTTTTTT    17893           C   G
                                AAGGAGCTTGGTT GGA AC
                                |||||||||||| ||| ||
                                TTTTTTGAACTAA CTT TG
                                     _   A
GAM454  ADAM10    5'  GGAGGCTCCGGACCAAGCCCCT 8478       A          ACAGGC
          T                      AAGG GCTTGGTTCGGAG
                                |||| ||||||||||||
                                TTCC CGAACCAGGCCTC
                                  C           GGAGGT
GAM454  ADARB1    3'  GTCTGTCTAAACTTAGGTCTCT 32340       _     TTCGG
          TT                      AAGGAG CTTGG     AGACAGGC
                                ||||||| |||||     ||||||||
                                TTTCTC GGATT     TCTGTCTG
                                   T    CAAA_
GAM454  ADCY6     5'  GCCTGGTTTTGGGCAAGTTTCT 40957          G      A
          T                      AAGGAGCTTG TTCGGAG CAGGC
                                |||||||||| ||||||| |||||
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                                TTCTTTGAAC GGGTTTT GTCCG
                                      _      G
GAM454  ADRA2B   3'  GCCTGTTTCGGATCTGTGGTTC 7297        _  T  G
           CTT                   AAGGAGCT TGG TC GAGACAGGC
                                 |||||||| ||| || |||||||||
                                 TTCCTTGG GTC AG CTTTGTCCG
                                    T  T  G
GAM454  ALEX2    5'  GTCTGTCTTCCTTTTGGGCTCT 29438       TG TTC
                                 GGAGCT  G   GGAGACAGGC
                                 ||||||  |   ||||||||||
                                 TCTCGG  T   CTTCTGTCTG
                                    GT TTC
GAM454  ARHGEF7  3'  CTTTGAGCTGGGCACCTT    15320      A   TG
                                 AAGG GCT  GTTCGGAG
                                 |||| |||  ||||||||
                                 TTCC CGG  CGAGTTTC
                                   A   GT
GAM454  ATP1B1   3'  GTTTGTTTTTTGTTTTTTGGCT 9820         T_ TT     _
           CTTT                  AAGGAGCT  GG  CGGAGA CAGGC
                                 ||||||||  ||  |||||| |||||
                                 TTTCTCGG  TT  GTTTTT GTTTG
                                    TT  TT     T
GAM454  ATP2C1   3'  GCTATCATTTTTGTATCAAGTT 27663           T     CA__
           TTTT                  AAGGAGCTTGGT CGGAGA    GGC
                                 |||||||||||| ||||||    |||
                                 TTTTTTGAACTA GTTTTT    TCG
                                       T     ACTA
GAM454  BCL11B   3'  GCTTGTTCAAAACCAAGTTTGT 57577    G        CG   A
           T                     AA GAGCTTGGTT  GAG CAGGC
                                 || ||||||||||  ||| |||||
                                 TT TTTGAACCAA  CTT GTTCG
                                  G         AA  _
GAM454  BCL9     3'  GTTTGTTTTAAATTTTGTGGTT 16322         TGGTTCG__
           CCTT                  AAGGAGCT        GAGACAGGC
                                 ||||||||        |||||||||
                                 TTCCTTGG        TTTTGTTTG
                                    TGTTTTAAA
GAM454  BIN3     3'  GTTTGTTTTTGACTTTGGTTT  38581       T_  T
                                 GAGCT  GGT CGGAGACAGGC
                                 |||||  ||| ||||||||||
                                 TTTGG  TCA GTTTTTGTTTG
                                    TT  _
GAM454  BSN      3'  TGGCTTCAAGCTAAGTTTCTT  14394            C   A
                                 AAGGAGCTTGGTT GGAG CA
                                 |||||||||||| |||| ||
                                 TTCTTTGAATCGA CTTC GT
                                       A   G
GAM454  BST2     3'  GCCTGTTGTTATGGGTTTTTT  16339          GTTCGGA
                                 AAGGAGCTTG      GACAGGC
                                 ||||||||||      |||||||
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                                TTTTTTGGGT      TTGTCCG
                                      ATTG___
GAM454  CALCRL   3'  GTATCTGGGCTGATTTTTT   20528       C TG      G
                                AAGGAG T  GTTCGGA AC
                                ||||||  |  |||||||  ||
                                TTTTTT A  CGGGTCT TG
                                   _ GT      A
GAM454  CARD15   3'  CTTGTTAACTGAGTGCCTT   42469     A   TG   CGGA
                                AAGG GCT  GTT    GACAGG
                                ||||  |||  |||    ||||||
                                TTCC TGA  CAA    TTGTTC
                                  G   GT  _____
GAM454  CARD4    3'  GCACAAAGTTGGTGCCAAGCTT 21441           _    AGACAG
           CTT                    AAGGAGCTTGGT TCGG     GC
                                ||||||||||||  ||||      ||
                                TTCTTCGAACCG GGTT     CG
                                       T    GAAACA
GAM454  CBS      3'  GTTTGCGTGTTTGGGTTTTTT  5364         TG TT_  G
                                AAGGAGCT  G   CG AGAC
                                ||||||||  |   || ||||
                                TTTTTTGG  T   GC TTTG
                                     GT TGT  G
GAM454  CD2AP    3'  GTTTGTGACCACTAAGCTTCT  25080          TC  AG
                                AGGAGCTTGGT  GG  ACAGGC
                                ||||||||||  ||  ||||||
                                TCTTCGAATCA  CC  TGTTTG
                                      __ AG
GAM454  CENTD2   5'  GTCTGTCTCTGTTTCACTTCTT 58274       CT   TT
                                AAGGAG  TGG  CGGAGACAGGC
                                ||||||  |||  ||||||||||
                                TTCTTC  ACT  GTCTCTGTCTG
                                   __   TT
GAM454  CHD3     3'  GTCTGTAAACTGTGAATTAACC 8873        C       G  ___
           TCCTT                   AAGGAG TTGGTTCG AG   ACAGGC
                                ||||||  ||||||||  ||   ||||||
                                TTCCTC AATTAAGT TC   TGTCTG
                                   C       G  AAA
GAM454  CLTC     5'  CCCCCGACCCGAGCTCTTT    17957          T    AGACA
                                AAGGAGCTTGG TCGG     GG
                                ||||||||||  ||||     ||
                                TTTCTCGAGCC AGCC     CC
                                      C    C_____
GAM454  CNK      3'  GCTTGTCTTCGCTGGCTCCT   15804        TGGTT
                                AGGAGCT     CGGAGACAGGC
                                |||||||     ||||||||||
                                TCCTCGG     GCTTCTGTTCG
                                   TC___
GAM454  CPSF6    3'  GCTTGTTTTTGTAGTAGTTTGT 23792     G     TGGTT
           T                     AA GAGCT     CGGAGACAGGC
                                || |||||     ||||||||||
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                                TT TTTGA    GTTTTTGTTCG
                                 G    TGAT_
GAM454  CRSP6   5'  GTTGCTGGGCCAGCTCCTT   16222       T     AG
                                AAGGAGCT GGTTCGG  AC
                                |||||||| |||||||  ||
                                TTCCTCGA CCGGGTC  TG
                                    _     GT
GAM454  CTNS    3'  GCTTGTCAGTCCACTGAGTTTC 18221      _ TG  TC  __
          CT                     AGGAG CT  GT  GGA  GACAGGC
                                |||||  ||  ||  |||  |||||||
                                TCCTT GA  CA  CCT  CTGTTCG
                                  T  GT  __  GA
GAM454  CXorf6  3'  GCCACCCAGAACTGGGCTTCTT 19708       TG   _  AGACA
                                AAGGAGCT  GTTC GG    GGC
                                ||||||||  |||| ||    |||
                                TTCTTCGG  CAAG CC    CCG
                                    GT   A  CA___
GAM454  CXorf6  3'  GTTTGTCTTTGATGGTTTCT   19710       TGGT
                                AGGAGCT   TCGGAGACAGGC
                                |||||||   ||||||||||||
                                TCTTTGG   AGTTTCTGTTTG
                                    T___
GAM454  DGCR2   3'  GCTTGGAAGGAGGTTGAGCTCT 18903       TG __  GGAGA
          T                     AGGAGCT  G  TTC    CAGGC
                                |||||||  |  |||    |||||
                                TTCTCGA  T  AGG    GTTCG
                                    GT GG   AAG__
GAM454  DISC1   3'  GCCTGACACTGGGCTGACTTTC 38509      C TG    AGA
          TT                     AAGGAG T  GTTCGG   CAGGC
                                ||||||| |  ||||||   |||||
                                TTCTTT A  CGGGTC   GTCCG
                                   C GT     ACA
GAM454  DLG4    3'  GTCTGGGGGGGGAGCTGGGCTCC 9086        TG   GGAGA
          TT                     AAGGAGCT  GTTC    CAGGC
                                ||||||||  ||||    |||||
                                TTCCTCGG  CGAG    GTCTG
                                    GT   GGGGG
GAM454  DPP6    3'  CTTGGGAAACAAGCTCCTT   56320         G   GGAGA
                                AAGGAGCTTG TTC    CAGG
                                |||||||||| |||    ||||
                                TTCCTCGAAC AAG    GTTC
                                    A   G____
GAM454  DPP6    3'  GTACCGTATCAAGCTCTTT   56324          T   AG
                                AAGGAGCTTGGT CGG  AC
                                |||||||||||| |||  ||
                                TTTCTCGAACTA GCC  TG
                                    T   A_
GAM454  DSCR3   3'  CTGTTTTGAGCCAGGGTTTTT  21311      G       G     GC
                                AAGGA CTTGGTTCG AGACAG
                                ||||| ||||||||| ||||||
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                                TTTTT GGACCGAGT TTTGTC
                                  G       _     G
GAM454  DUSP11   3'  AGGTCTAATCAGGTTTCTT   14558          CGG   AGGC
                                AAGGAGCTTGGTT   AGAC
                                |||||||||||||   ||||
                                TTCTTTGGACTAA   TCTG
                                      ___    GAC
GAM454  DYRK2    3'  GCCAAGAAAGTTTCCGGTTAAG 14556         GG T     A_____
           TTCTTT                 AAGGAGCTT  T CGGAGAC     GGC
                                |||||||||  | |||||||     |||
                                TTTCTTGAA  G GCCTTTG     CCG
                                     TT _      AAAGAA
GAM454  EIF1A    3'  GCTTGTCTCAGCTTCAGGTTCT 90007          TTCG
           T                    AGGAGCTTGG    GAGACAGGC
                                ||||||||||    |||||||||
                                TTCTTGGACT    CTCTGTTCG
                                      TCGA
GAM454  EMD      3'  CTTCAGAGCTAGGTCTTT     5489       G      _
                                AAGGA CTTGGTTC GGAG
                                ||||| ||||||||| ||||
                                TTTCT GGATCGAG CTTC
                                  _       A
GAM454  EMP1     3'  TTCTAGTACTGTATTGGGCTTC 9242         TG  T   AG  _   C
           TT                    AAGGAGCT  GT CGG  AC AGG
                                |||||||||  || |||  || |||
                                TTCTTCGG  TA GTC  TG TCT
                                     GT  T   A_  A   TG
GAM454  ENAM     3'  CTTGTCTGAGTTAGTTTCCTT  49928       C  GG   GG     C
                                AAGGAG TT  TTC  AGACAGG
                                |||||| ||  |||  |||||||
                                TTCCTT GA  GAG  TCTGTTC
                                   T  TT   __      A
GAM454  ESR1     5'  GCCTCTAACCTCGGGCTGTGCT 5516         T       AGAC__
           CTTT                    AAGGAGC TGGTTCGG     AGGC
                                |||||||| ||||||||     ||||
                                TTTCTCG GTCGGGCT     TCCG
                                     T       CCAATC
GAM454  ESRRBL1  3'  GTTTCTGATTAGTTGGGTTTTT 36325         TG T___       AGGC
           T                     AAGGAGCT  G    TCGGAGAC
                                |||||||||  |    |||||||||
                                TTTTTTGG  T    AGTCTTTG
                                     GT GATT
GAM454  ETF1     3'  TATTGGTCTGAACCAGCTCCTT 17593         T       GA   GC
                                AAGGAGCT GGTTCGGA  CAG
                                |||||||| |||||||||  |||
                                TTCCTCGA CCAAGTCT  GTT
                                     _       G_   ATT
GAM454  ETS2     3'  GTTTGTTTTTGGGGGGTTTTCT 19119       _   GG
           T                     AAGGAG CTT  TTCGGAGACAGGC
                                |||||| |||  ||||||||||||
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                                TTCTTT GGG  GGGTTTTTGTTTG
                                   T  __
GAM454  EXTL3    3'  ACTGTTTTGAAGCTGGGCTCTT 9330         TG  CG      GC
                T                   AAGGAGCT  GTT  GAGACAG
                                    ||||||||  |||  |||||||
                                    TTTCTCGG  CGA  TTTTGTC
                                       GT   AG      AT
GAM454  FBLN1    3'  GTCCCCACTAGCCAGGCTCTTT 22415           C__  A
                                    AAGGAGCTTGGTT   GG GAC
                                    ||||||||||||||  || |||
                                    TTTCTCGGACCGA   CC CTG
                                           TCA  C
GAM454  FEZ1     3'  GTCTGTCTATCTTAAGCTTTCT 18788      _     TTCGG
                T                   AAGGA GCTTGG     AGACAGGC
                                    |||||  ||||||     ||||||||
                                    TTCTT CGAATT     TCTGTCTG
                                       T     CTA__
GAM454  FMN2     3'  GTTTTGTATGAGCTGGGTGTTT 80131      A   TG    ___     AGGC
                T                   AAGG GCT  GTTCG   GAGAC
                                    ||||  |||  |||||   |||||
                                    TTTT TGG  CGAGT   TTTTG
                                      G   GT     ATG       C
GAM454  FMR2     3'  TTTGTTTTTATGCTTCTT     10706        TTGGTTC
                                    AAGGAGC       GGAGACAGG
                                    |||||||       |||||||||
                                    TTCTTCG       TTTTTGTTT
                                       TA_____
GAM454  GFRA1    3'  GCCTACATTGATGCCAAGCTTT 19156           _    AGAC
                TT                   AAGGAGCTTGGT TCGG    AGGC
                                    ||||||||||||  ||||    ||||
                                    TTTTTCGAACCG AGTT    TCCG
                                           T    ACA_
GAM454  GLRX     3'  TTTTCTTCTGGATGAGCTCTTT 10805          G      ACAGGC
                                    AAGGAGCTTG TTCGGAG
                                    ||||||||||  |||||||
                                    TTTCTCGAGT AGGTCTT
                                          _      CTTTTG
GAM454  GNA15    5'  GCCACCGCCGAGCCGGGCTTCC 60590      _         AGACA
                T                   AGGA GCTTGGTTCGG     GGC
                                    ||||  ||||||||||     |||
                                    TCCT CGGGCCGAGCC     CCG
                                      T         GCCA_
GAM454  GRIN2B   3'  CTAGACGAGCAGGCTTCTT    7731           G    GAGACA
                                    AAGGAGCTTG TTCG      GG
                                    ||||||||||  ||||      ||
                                    TTCTTCGGAC GAGC      TC
                                          _    AGA___
GAM454  GRM7     3'  GTTTGTTTTCGAATGCCTTGTT 7790        TT   __
                TT                   GGAGC  GGT  TCGGAGACAGGC
                                    |||||  |||  ||||||||||||
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                                TTTTG  CCG  AGCTTTTGTTTG
                                   TT   TA
GAM454  GSPT1    5'  CCCCCGGGCCGGGCCCTT    10883     A        AGACA
                                AAGG GCTTGGTTCGG    GG
                                |||| ||||||||||    ||
                                TTCC CGGGCCGGGCC    CC
                                  _        C____
GAM454  HAS3     3'  TTTTCAGGTCAAGTTTTTT   57604         GT C
                                AAGGAGCTTG  T GGAGA
                                ||||||||||  | |||||
                                TTTTTTGAAC  G CTTTT
                                      TG A
GAM454  HDAC4    3'  GTTTGTTTCCTTTTATCTCCTT 21250       CT   TTC
                                AAGGAG  TGG   GGAGACAGGC
                                ||||||  |||   ||||||||||
                                TTCCTC  ATT   CCTTTGTTTG
                                   T_  TT_
GAM454  HEPH     5'  GCCTGCCTGGTTGGGCTTCCT  57832     _   GG TC  AGA
                                AGGA GCTT  T  GG   CAGGC
                                |||| ||||  |  ||   |||||
                                TCCT CGGG  G  CC   GTCCG
                                  T   TT GT  ___
GAM454  HK2      5'  TGGAGCCGGGCTGAGATTCTT  5752       G  TG     AGA
                                AAGGA CT  GTTCGG   CA
                                ||||| ||  ||||||   ||
                                TTCTT GA  CGGGCC   GT
                                   A  GT     GAG
GAM454  HOXB7    3'  GTCTGTCAGGTTTGGTTTTTT  16907        TGGT  GGA
                                AAGGAGCT   TC   GACAGGC
                                ||||||||   ||   |||||||
                                TTTTTTGG   GG   CTGTCTG
                                     TTT_  A__
GAM454  HSPG2    3'  CCTGTTTCTGCAGCCCTT    19839     A   TGGTT
                                AAGG GCT    CGGAGACAGG
                                |||| |||    ||||||||||
                                TTCC CGA    GTCTTTGTCC
                                  _  C____
GAM454  HTRA3    3'  GTCTGGGCTGCCAAGCTTCTT  90583          TC  AGA
                                AAGGAGCTTGGT  GG   CAGGC
                                ||||||||||||  ||   |||||
                                TTCTTCGAACCG  TC   GTCTG
                                      __  GG_
GAM454  IDH3A    3'  GTCTGTTTTCAAAGAACT    19846      ___
                                GGTTC   GGAGACAGGC
                                |||||   ||||||||||
                                TCAAG   CTTTTGTCTG
                                   AAA
GAM454  IDH3B    3'  GTCCTTGGGCCGGCTTCCTT   23560      _   T     GA
                                AAGGA GCT GGTTCG  GAC
                                ||||| ||| ||||||  |||
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                                TTCCT CGG CCGGGT  CTG
                                  T  _     TC
GAM454  IDS     3'  GTAATTGGACCAGTTTTTT   5777        T     AG
                                AAGGAGCT GGTTCGG  AC
                                |||||||| |||||||  ||
                                TTTTTTGA CCAGGTT  TG
                                    _      AA
GAM454  INHBB   3'  GTCCCGGGTGGGCTTCTT    11010       T G TT   A
                                AAGGAGC T G  CGG GAC
                                ||||||| | |  ||| |||
                                TTCTTCG G T  GCC CTG
                                   _ G GG  _
GAM454  IREB2   3'  CTCTGAACTGATTTCTT     67020       C TG
                                AAGGAG T  GTTCGGAG
                                ||||||| |  ||||||||
                                TTCTTT A  CAAGTCTC
                                   _ GT
GAM454  IRTA1   5'  GCTTGTCTCCTCAGAACTCCTT 49240       C_   TTC
                                AAGGAG  TTGG   GGAGACAGGC
                                ||||||  ||||   ||||||||||
                                TTCCTC  GACT   CCTCTGTTCG
                                   AA   ____
GAM454  ITGAL   3'  GCCTTTCTCCCAGGCCAGGCTC 11046           C_    C
            CTT                   AAGGAGCTTGGTT  GGAGA AGGC
                                ||||||||||||  ||||| ||||
                                TTCCTCGGACCGG  CCTCT TCCG
                                      AC    T
GAM454  ITGB3   3'  GTCCTGATAAGCTGAGCTCCTT 5805         TG ____   A
                                AAGGAGCT  GT   TCGG GAC
                                ||||||||  ||   |||| |||
                                TTCCTCGA  CG   AGTC CTG
                                   GT  AAT   _
GAM454  ITSN1   3'  CTGTTTGGTTTGAGTTCTTT   13093        TG TT  GA
                                AAGGAGCT  G  CG  GACAG
                                ||||||||  |  ||  |||||
                                TTTCTTGA  T  GT  TTGTC
                                   GT TG  __
GAM454  JAG1    3'  GTTTAGAACAGGTTTTTT    5814         G   GG
                                AAGGAGCTTG TTC  AGAC
                                |||||||||| |||  ||||
                                TTTTTTGGAC AAG  TTTG
                                      _   A_
GAM454  JAM3    3'  TCACTGAGTTGGGTTCCT    52492        GG    A
                                AGGAGCTT  TTCGG GA
                                ||||||||  |||||  ||
                                TCCTTGGG  GAGTC CT
                                   TT    A
GAM454  KCNA7   3'  GCCATGCTGAATTGAGTTCC  49901       TG     AGACA
                                GGAGCT  GTTCGG    GGC
                                ||||||  ||||||    |||
```

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                                CCTTGA  TAAGTC    CCG
                                   GT     GTA__
GAM454  KIAA0857  3'  GTTTGTCTTCCTAGTTAAGGCT 67255        GGTTC__
            CTTT                  AAGGAGCTT      GGAGACAGGC
                                  |||||||||      ||||||||||
                                  TTTCTCGGA      CTTCTGTTTG
                                     ATTGATC
GAM454  KL      3'  TTTGTTAGACTAGTTTCTT    17746        T    CGGA
                                  AAGGAGCT GGTT    GACAGG
                                  ||||||||| ||||    ||||||
                                  TTCTTTGA TCAG    TTGTTT
                                     _    A___
GAM454  LBR     3'  GTTTGTTTTTGACATGTTT    60071      TTG  T
                                  GAGC   GT CGGAGACAGGC
                                  ||||   || ||||||||||
                                  TTTG   CA GTTTTTGTTTG
                                    TA_  _
GAM454  LMCD1    3'  GTCTTAGGATGGAGTTCCTT   28149         G    G
                                  AAGGAGCTT GTTC GAGAC
                                  |||||||||  |||| |||||
                                  TTCCTTGAG TAGG TTCTG
                                     G    A
GAM454  MAF     5'  GCCGCGCACCGGGCCGGGCTCC 19312             AGACA
            T                      AGGAGCTTGGTTCGG     GGC
                                   ||||||||||||||     |||
                                   TCCTCGGGCCGGGCC     CCG
                                        ACGCG
GAM454  MAN1A1   3'  GTCTGTGATTAAGTTCTT    93556          T  G
                                  AGGAGCTTGGT CG AGAC
                                  |||||||||||  ||  ||||
                                  TTCTTGAATTA GT TCTG
                                     _  G
GAM454  MAN2A2   3'  GCCTCCGCTTGGGTTAGGGCTT 21513         GGT  G   AC_
            CTT                    AAGGAGCTT   TC GAG   AGGC
                                   |||||||||   ||  |||   ||||
                                   TTCTTCGGG   GG TTC   TCCG
                                      ATT  G   GCC
GAM454  MAT1A    3'  GTTTGCAGGTGGCCAAGTTCCT 92505           CGGAGA
                                  AGGAGCTTGGTT     CAGGC
                                  ||||||||||||     |||||
                                  TCCTTGAACCGG     GTTTG
                                     TGGAC_
GAM454  MBL2     3'  GTCTGTTTCTGGGCTGTCTATT 5911       GCT_
            CT                     AGGA    TGGTTCGGAGACAGGC
                                   ||||    ||||||||||||||||
                                   TCTT    GTCGGGTCTTTGTCTG
                                     ATCT
GAM454  MECP2    3'  TTGCACTTTTCTAAACTAGGCT 18419           CG    C  _
            CCTT                    AAGGAGCTTGGTT  GAGA AG GC
                                   ||||||||||||  |||| || ||
```

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                                TTCCTCGGATCAA  CTTT TC CG
                                      AT    _  A  TTT
GAM454   MEIS2    5'  TTGTCTAGACTGGGCTTTTT   39729        TG  T GG
                                AAGGAGCT  GT C  AGACAG
                                ||||||||  || |  ||||||
                                TTTTTCGG  CA G  TCTGTT
                                     GT  _ A_
GAM454   MEN1     5'  GCCTGTTTCAGAGGGTTGTTT  56351     G    TGG   G
                                AAG AGCT   TTC GAGACAGGC
                                ||| ||||   ||| |||||||||
                                TTT TTGG   GAG CTTTGTCCG
                                  G    ___   A
GAM454   MGAT2    5'  GTTGGGACCGCGGCTGAGCTTT 11558        TG  _  AGA   GC
           TT                     AAGGAGCT  GTT CGG   CAG
                                ||||||||  ||| |||   |||
                                TTTTTCGA  CGG GCC   GTT
                                     GT   C   AGG   G
GAM454   MS4A2    3'  GCTTGTGTTGTCACGCTTCTT  41977       T   TTCG  G
                                AAGGAGC TGG    GA ACAGGC
                                |||||||  |||    || ||||||
                                TTCTTCG ACT    TT TGTTCG
                                     C   G___  G
GAM454   MS4A2    3'  GTTCCTTGGATAGGCTTTTT   41978         G   _ AG
                                AAGGAGCTTG TTCG G  AC
                                |||||||||| ||||  |  ||
                                TTTTTCGGAT AGGT C  TG
                                       _    T CT
GAM454   MSX2     3'  GCTTGTTTCAAAGGGTTTCCT  66172      _   GGTTCG
                                AGGAG CTT     GAGACAGGC
                                |||||  |||     |||||||||
                                TCCTT GGG     CTTTGTTCG
                                   T   AAA___
GAM454   MTA1L1   5'  GCCTGGCAGGAGCCGAGCTTGT 17633    G         GGAGA
           T                     AA GAGCTTGGTTC     CAGGC
                                || ||||||||||     |||||
                                TT TTCGAGCCGAG    GTCCG
                                 G         GACG_
GAM454   MTMR8    3'  GTCTGTTAATACAGCTGAGCTT 31914         TG   CGGA_
           TTT                     AAGGAGCT  GTT    GACAGGC
                                ||||||||  |||    |||||||
                                TTTTTCGA  CGA    TTGTCTG
                                     GT   CATAA
GAM454   MYO1D    3'  CCTGGGTTTGGGTTCTTT    72242        TGGTT    GA
                                AAGGAGCT    CGGA  CAGG
                                ||||||||    ||||  ||||
                                TTTCTTGG    GTTT  GTCC
                                     _____    GG
GAM454   MYO9A    3'  TTGTATTTGAATTGAGATTTTT 23561      G  TG      G    GC
                                AAGGA CT  GTTCGGA ACAG
                                |||||  ||  ||||||| ||||
```

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                                TTTTT GA  TAAGTTT TGTT
                                   A  GT      A    G
GAM454  NAV2     3'  GTTTGTCTCTTGGCATCTTTTT 60797       CTTG  TC
                                AAGGAG    GT  GGAGACAGGC
                                ||||||    ||  ||||||||||
                                TTTTTC    CG  TCTCTGTTTG
                                   TA__   GT
GAM454  NDRG2    3'  GCTAAGCTTGGGCTGGGCTGCT 33194     G    TG     G  ACA
          T                      AAG AGCT  GTTCG AG   GGC
                                ||| ||||  ||||| ||   |||
                                TTC TCGG  CGGGT TC   TCG
                                  G    GT    _  GAA
GAM454  NEO1     3'  CTTGTTTTTTGGTTTC      11773       TGGTTC
                                GGAGCT     GGAGACAGG
                                ||||||     |||||||||
                                CTTTGG     TTTTTGTTC
                                   T_____
GAM454  NFATC1   3'  TCTGTCATCTCAGCTCTTT    21599        T GTTC   _
                                AAGGAGCT G    GGA GACAGG
                                |||||||| |    ||| ||||||
                                TTTCTCGA C    TCT CTGTCT
                                    _ ____   A
GAM454  NFE2L2   3'  CCTTTTCTGAGCTAGTTTTTT  21604        T        C   C
                                AAGGAGCT GGTTCGGAGA AGG
                                |||||||| |||||||||| |||
                                TTTTTTGA TCGAGTCTTT TCC
                                    _        _
GAM454  NGFR     3'  GCCTGGCAGAACTGAGCTCCT  11797        TG    GGAGA
                                AGGAGCT  GTTC     CAGGC
                                |||||||  ||||     |||||
                                TCCTCGA  CAAG     GTCCG
                                   GT    ACG__
GAM454  NUCB1    3'  CTGCTCCGGGCCAAGCTTCT   21641              A
                                AGGAGCTTGGTTCGGAG CAG
                                |||||||||||||||| |||
                                TCTTCGAACCGGGCCTC GTC
                                                 _
GAM454  NUFIP1   3'  GCCTGTTTTGGGTACAGGTTTT 25636          GT  G
          TT                     AAGGAGCTTG  TC GAGACAGGC
                                |||||||||  || |||||||||
                                TTTTTTGGAC  GG TTTTGTCCG
                                     AT  G
GAM454  OAS1     3'  GTTATCTGGACCAGTTCCTT   34147         T      _
                                AAGGAGCT GGTTCGGA GAC
                                |||||||| |||||||| |||
                                TTCCTTGA CCAGGTCT TTG
                                    _       A
GAM454  P2RY1    3'  GCTTAACAGAATCAAGTACTTT 11932      A        GGAGAC
                                AAGG GCTTGGTTC     AGGC
                                |||| |||||||||     ||||
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                                TTTC TGAACTAAG     TTCG
                                  A       ACAA__
GAM454  PAK4    3'  GCCTGAAGAACCAGGTTCCT  20827          GGAGA
                                AGGAGCTTGGTTC    CAGGC
                                ||||||||||||    |||||
                                TCCTTGGACCAAG    GTCCG
                                      AA___
GAM454  PAX2    3'  CCTGTTTGTTGGCTCTTT    15655        TGGTTCGG
                                AAGGAGCT      AGACAGG
                                ||||||||      |||||||
                                TTTCTCGG      TTTGTCC
                                    TTG_____
GAM454  PAX2    3'  CCTGTTTGTTGGCTCTTT    15656        TGGTTCGG
                                AAGGAGCT      AGACAGG
                                ||||||||      |||||||
                                TTTCTCGG      TTTGTCC
                                    TTG_____
GAM454  PCDH11X  5'  GTTTAGGGTTGGCTTCTT    28015        T  TT GG
                                AAGGAGCT GG  C  AGAC
                                |||||||| ||  |  ||||
                                TTCTTCGG TT  G  TTTG
                                    _  GG A_
GAM454  PDHB    3'  GTCTGTTACGGTTGCCATGTTC 88809        T   __  GA
           TTT                   AAGGAGC TGGT  TCG  GACAGGC
                                ||||||| ||||  |||  |||||||
                                TTTCTTG ACCG  GGC  TTGTCTG
                                    T   TT   A_
GAM454  PHGDH    5'  GCCAGGCCGAACCGCAGCTTCT 64919        _      AGACA
           T                    AAGGAGCT TGGTTCGG    GGC
                                |||||||| ||||||||    |||
                                TTCTTCGA GCCAAGCC    CCG
                                    C       GGA__
GAM454  PIAS3    3'  GTCTGTTTCTGGAAATGTTCTT 21449        TTGG
           T                    AAGGAGC   TTCGGAGACAGGC
                                |||||||   ||||||||||||
                                TTTCTTG   AGGTCTTTGTCTG
                                    TAA_
GAM454  PIK3R3   3'  GTCTGTTTCATTGGGGTTTTT  61711      G  TG  TCG
                                AAGGA CT  GT   GAGACAGGC
                                ||||| ||  ||   |||||||||
                                TTTTT GG  TA   CTTTGTCTG
                                   G  GT  ___
GAM454  PIM2    3'  GTCCCATATTGGGTCAAGCTGC 60657     G      TT _____  A   AGGC
           TT                    AAG AGCTTGG  C    GG GAC
                                ||| |||||||  |    || |||
                                TTC TCGAACT  G    CC CTG
                                  G      GG TTATA  _     C
GAM454  PLCG1    3'  CCGCGAACTGGGTTCTTT    12157        TG    GAGACA
                                AAGGAGCT  GTTCG     GG
                                ||||||||  |||||     ||
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                                TTTCTTGG  CAAGC     CC
                                    GT    G_____
GAM454  POLR2C   3'  GTCTACTGTTGGTTGAGCTTCT 12206        TG TT__  _   AGGC
           T                     AAGGAGCT  G   CGG AGAC
                                 |||||||| |   ||| ||||
                                 TTCTTCGA  T   GTC TCTG
                                    GT GGTT   A      C
GAM454  POU3F1   3'  TCTCCGGGCTTGGTTTTTT   60040        T
                                 AAGGAGCT GGTTCGGAGA
                                 |||||||| ||||||||||
                                 TTTTTTGG TCGGGCCTCT
                                    T
GAM454  POU5F1   3'  GCCAGGGTTTTTGGATTAAGTT 99602              A__
           CTT                     AGGAGCTTGGTTCGGAGAC   GGC
                                 ||||||||||||||||||   |||
                                 TTCTTGAATTAGGTTTTTG   CCG
                                       GGA
GAM454  PPARGC1  3'  GCTTGTTTTTCTTTGAAGTTTT 26082       GGTTC
                                 GGAGCTT    GGAGACAGGC
                                 |||||||    ||||||||||
                                 TTTTGAA    TTTTTGTTCG
                                    GTTTC
GAM454  PPIL1    5'  GTTCTTGAGCCCAGCTTCTT   32669        T      AG
                                 AAGGAGCT GGTTCGG  AC
                                 |||||||| |||||||  ||
                                 TTCTTCGA CCGAGTT  TG
                                    C      CT
GAM454  PPP1R12B 5'  GTTTGTTGAAAATTGGGCTTCT 50364       TG   CGGA
                                 AGGAGCT  GTT   GACAGGC
                                 |||||||  |||   |||||||
                                 TCTTCGG  TAA   TTGTTTG
                                    GT   AAG_
GAM454  PRKACA   3'  GCCTGTTTTAAACGAGTTTCT  12269        GTTCG
                                 AGGAGCTTG    GAGACAGGC
                                 |||||||||    |||||||||
                                 TCTTTGAGC    TTTTGTCCG
                                      AAA__
GAM454  PRKACG   3'  GCCTGTTTTAAACGAGTTTCT  12279        GTTCG
                                 AGGAGCTTG    GAGACAGGC
                                 |||||||||    |||||||||
                                 TCTTTGAGC    TTTTGTCCG
                                      AAA__
GAM454  PRLR     5'  GCCGGTTTTCTGGGCTGGGCTT 8144        TG       CA_
           T                     GGAGCT  GTTCGGAGA   GGC
                                 ||||||  |||||||||   |||
                                 TTTCGG  CGGGTCTTT   CCG
                                    GT       TGG
GAM454  PSAP     3'  CTGGCATGAGCCACAGTTTCTT 69882         _      GAGA   GC
                                 AAGGAGCT TGGTTCG    CAG
                                 |||||||| |||||||    |||
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                                TTCTTTGA ACCGAGT   GTC
                                    C      ACG_  G
GAM454  PSAP    3'  GCCTGGAATAATCAGGCTTTTT 69885          CGGAGA
                                AAGGAGCTTGGTT     CAGGC
                                ||||||||||||     |||||
                                TTTTTCGGACTAA     GTCCG
                                     TAAG__
GAM454  PTPN1   3'  TTCTGAGCTGGGCTTGTT    12580    G    TG
                                AA GAGCT  GTTCGGAG
                                || |||||  ||||||||
                                TT TTCGG  CGAGTCTT
                                 G    GT
GAM454  PTPRO   3'  GCTGGTTGGGCTGAGTTTTTT  48413       TG     AGACA
                                AAGGAGCT  GTTCGG    GGC
                                ||||||||  ||||||    |||
                                TTTTTTGA  CGGGTT    TCG
                                     GT     GG___
GAM454  PTPRO   3'  GCTGGTTGGGCTGAGTTTTTT  48414       TG     AGACA
                                AAGGAGCT  GTTCGG    GGC
                                ||||||||  ||||||    |||
                                TTTTTTGA  CGGGTT    TCG
                                     GT     GG___
GAM454  RAB38   3'  TTGCCTCTGAGTTAGCTCTTT  60928       T GG      A
                                AAGGAGC T  TTCGGAG CAG
                                |||||||  |  ||||||| |||
                                TTTCTCG A  GAGTCTC GTT
                                    _ TT      C
GAM454  RAB3B   3'  GCTTGTTTCCTATCGGGCTCC  12705         TC
                                GGAGCTTGGT  GGAGACAGGC
                                ||||||||||  ||||||||||
                                CCTCGGGCTA  CCTTTGTTCG
                                      T_
GAM454  RAB7L1  3'  GTACTAAATTGGGCAGGGCTTT 15413       TG    ___  _  AGGC
          TT                    AAGGAGCT  GTTCGG   AG AC
                                ||||||||  ||||||   || ||
                                TTTTTCGG  CGGGTT   TC TG
                                     GA     AAA  A    C
GAM454  RAD9    3'  GCTTGCTGGAGCTGAGCTGTTT 17158    G   TG   GG  A
                                AAG AGCT  GTTC  AG CAGGC
                                ||| ||||  ||||  || |||||
                                TTT TCGA  CGAG  TC GTTCG
                                  G   GT   G_  _
GAM454  RALB    3'  TTTTTGGGTAAGCTTCTT    12761         G TT
                                AAGGAGCTT G  CGGAGA
                                |||||||||  |  ||||||
                                TTCTTCGAA T  GTTTTT
                                      _ GG
GAM454  RBMS3   3'  GTCTGGGCTGTGCTAAGCTCTT 27920          T   AGA
          T                     AAGGAGCTTGGT CGG   CAGGC
                                ||||||||||| |||   |||||
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                                TTTCTCGAATCG GTC   GTCTG
                                      T   GG_
GAM454  RFP     3'  GTCATTTCTGGGCTAGGGCTCC 22512        _        CA
            TT                   AAGGAGCT TGGTTCGGAGA  GGC
                                 |||||||| ||||||||||  |||
                                 TTCCTCGG ATCGGGTCTTT  CTG
                                    G         A_
GAM454  RGS3    3'  CGCTTCGCGTTGACCAAGTTCC 56314           ____    ACAGGC
            TT                   AAGGAGCTTGGTT    CGGAG
                                 ||||||||||||    |||||
                                 TTCCTTGAACCAG    GCTTC
                                       TTGC    G   CG
GAM454  RGS3    3'  GCTTCGCGTTGACCAAGTTCCT 56316           ____    ACAGGC
            T                    AAGGAGCTTGGTT    CGGAG
                                 ||||||||||||    |||||
                                 TTCCTTGAACCAG    GCTTC
                                       TTGC    G   C
GAM454  RNPEPL1  3'  GCCTGTCTCTTGTAGCTTCCT  37216     _  TGGTTC
                                 AGGA GCT     GGAGACAGGC
                                 |||| |||     ||||||||||
                                 TCCT CGA     TCTCTGTCCG
                                   T   TGT___
GAM454  RP2     3'  CTATAAACTAAGTTCTTT    23600           CGG
                                 AAGGAGCTTGGTT   AG
                                 ||||||||||||   ||
                                 TTTCTTGAATCAA   TC
                                       ATA
GAM454  SACS    3'  GTTTGTCTCGCCATGCTTCTT  27634       T    TCG
                                 AAGGAGC TGGT   GAGACAGGC
                                 |||||||  ||||   |||||||||
                                 TTCTTCG ACCG   CTCTGTTTG
                                    T   ___
GAM454  SHOX    5'  GCTTGGAAAACTGGAGTTTCTT 6578        _ TG   CGGAGA
                                 AAGGAGC T  GTT     CAGGC
                                 |||||||  |  |||     |||||
                                 TTCTTTG G  CAA     GTTCG
                                    A GT   AAG___
GAM454  SIRT6   3'  GCTTGGGGAGGGTGGGGCTTTT 33739         G TT GGAGA
            T                    AAGGAGCTT G  C    CAGGC
                                 |||||||||  |  |    |||||
                                 TTTTTCGGG T  G    GTTCG
                                      G GG AGGG_
GAM454  SIX1    3'  CTTGTTTCTGGAGTTGTTT   21113     TTGG
                                 GAGC   TTCGGAGACAGG
                                 ||||   ||||||||||||
                                 TTTG   AGGTCTTTGTTC
                                   TTG_
GAM454  SLC13A3  3'  CCTGAGAAATAAGCTCCTT   61090         G   GGAGA
                                 AAGGAGCTTG TTC    CAGG
                                 |||||||||| |||    ||||
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                                TTCCTCGAAT AAG    GTCC
                                     A  A____
GAM454  SNAI1   3'  GCCTGTCTGCGTGGGTTTTT  21124        GTT  G
                                AGGAGCTTG  CG AGACAGGC
                                |||||||||  || ||||||||
                                TTTTTGGGT  GC TCTGTCCG
                                     ___  G
GAM454  SNX15   3'  GCCTGTCTTTTTGGGGTTTTT  74124      G  TG TTC
                                AAGGA CT  G  GGAGACAGGC
                                ||||| ||  |  ||||||||||
                                TTTTT GG  T  TTTCTGTCCG
                                   G  GT ___
GAM454  SORCS2  3'  CTGTTTGGGTTGGGTTTTT  40803       TG TT  GA
                                AGGAGCT  G  CG  GACAG
                                |||||||  |  ||  |||||
                                TTTTTGG  T  GT  TTGTC
                                     GT GG  __
GAM454  SOX11   3'  CTGCAGATGGACAGGTTTCTT  13315         G   GAGA
                                AAGGAGCTTG TTCG   CAG
                                |||||||||| ||||   |||
                                TTCTTTGGAC AGGT   GTC
                                     _   AGAC
GAM454  SPG4    3'  GTTTGTCTTCTGATGTTTTTT  30810       TTG  C
                                AAGGAGC  GTT GGAGACAGGC
                                |||||||  ||| ||||||||||
                                TTTTTTG  TAG CTTCTGTTTG
                                     ___  T
GAM454  STAU2   3'  CTCTGAATTGATTTTTT    27670       C TG
                                AAGGAG T  GTTCGGAG
                                ||||||  |  ||||||||
                                TTTTTT A  TAAGTCTC
                                   _ GT
GAM454  SUFU    3'  GCATTTTCTGAGCTAAGCTTT  32937             CAG
                                GGAGCTTGGTTCGGAGA  GC
                                ||||||||||||||||  ||
                                TTTCGAATCGAGTCTTT  CG
                                          TA_
GAM454  SURF5   3'  GCCAAGGCTGGGCCAGCCTTTT 56914       C       AGACA
           T                     AAGGAG TTGGTTCGG    GGC
                                ||||||  |||||||||    |||
                                TTTTTC GACCGGGTC    CCG
                                   C       GGAA_
GAM454  SUSP1   3'  TTTTGAACTAAGCATCTT   32097    GA
                                AAG  GCTTGGTTCGGAG
                                |||  ||||||||||||
                                TTC  CGAATCAAGTTTT
                                  TA
GAM454  TAT     5'  TTTCGGGGTTGGCTTCTT   6264         TGG
                                AAGGAGCT  TTCGGAG
                                ||||||||  |||||||
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                                TTCTTCGG   GGGCTTT
                                    TTG
GAM454  TCFL4    3'  GTTTGTTTTGTGAAAGCTTCT  64213        GGT  _
                                AGGAGCTT   TCG GAGACAGGC
                                ||||||||   ||| |||||||||
                                TCTTCGAA   AGT TTTTGTTTG
                                    ____  G
GAM454  TEM6     3'  GTTTGTGCAAGTCAGGCCCTT  43040      A    GT __  G
                                AAGG GCTTG  T  CG AGAC
                                |||| |||||  |  || ||||
                                TTCC CGGAC  A  GT TTTG
                                  _    TG AC  G
GAM454  TLX1     5'  GCCTTGTGGGCTGGACTCCTT  19825       C TG    G GAC
                                AAGGAG T  GTTCG A   AGGC
                                ||||||  |  |||||  |   ||||
                                TTCCTC G  CGGGT T   TCCG
                                   A GT    G ____
GAM454  TLX1     5'  TCTCTTGCACCGGGCTTTTT   19827          T  _
                                AAGGAGCTTGGT CG GAGA
                                ||||||||||||  || ||||
                                TTTTTCGGGCCA GT CTCT
                                      C  T
GAM454  TNFRSF1B 3'  CTCTTTCTGGGCCAAGTTCCT  8394              C  GC
                                AGGAGCTTGGTTCGGAGA AG
                                |||||||||||||||||  ||
                                TCCTTGAACCGGGTCTTT TC
                                      C  G
GAM454  TOX      5'  GCTTGGGGGAGAGTTGAGCGCT 28963     A   GG   GGAGA
           TT                    AAGG GCTT  TTC    CAGGC
                                ||||  ||||  |||    |||||
                                TTTC CGAG  GAG    GTTCG
                                  G   TT   AGGGG
GAM454  TRPM2    3'  CCTGTGCAGCTGGGCCCTT   13863     A   TG   CGGAG
                                AAGG GCT  GTT    ACAGG
                                |||| |||  |||    |||||
                                TTCC CGG  CGA    TGTCC
                                  _  GT   CG___
GAM454  TSG      3'  TAAAGACTTTGGAATAAGTTTC 40606         G      ACAGGC
           TT                    AAGGAGCTTG TTCGGAG
                                |||||||||| |||||||
                                TTCTTTGAAT AGGTTTC
                                     A      AGAAATG
GAM454  UBE2H    3'  TTTCTGAACCAGTTCTTT    13957        T
                                AAGGAGCT GGTTCGGAGA
                                |||||||| ||||||||||
                                TTTCTTGA CCAAGTCTTT
                                      _
GAM454  UGDH     3'  GCCTGGGCCCATGAACCAAGTG 13999      A       ___  AGA
           TTTT                    AAGG GCTTGGTTC   GG   CAGGC
                                |||| |||||||||   ||   |||||
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                                TTTT TGAACCAAG   CC   GTCCG
                                  G       TAC  GG_
GAM454  VDAC2    3'  TTTGTTTTTATGTTCCTT    14038        TTGGTTC
                                AAGGAGC      GGAGACAGG
                                |||||||      |||||||||
                                TTCCTTG      TTTTTGTTT
                                   TA_____
GAM454  WBSCR1   3'  CCTGTTTGTGCGTTTTTT    42480        TTGGTT  G
                                AAGGAGC     CG AGACAGG
                                |||||||     || |||||||
                                TTTTTTG     GT TTTGTCC
                                   C_____  G
GAM454  WNT3A    3'  GTTTTATGGTGGATGAGGCTTC 53611         G    ____    AGGC
           TT                    AAGGAGCTT GTTCG    GAGAC
                                |||||||| |||||    |||||
                                TTCTTCGGA TAGGT    TTTTG
                                     G    GGTA       C
GAM454  XPR1     3'  CCTTTTTGAATCGAGGTTTTT  17621      G         AC   C
                                AAGGA CTTGGTTCGGAG  AGG
                                ||||| ||||||||||||  |||
                                TTTTT GAGCTAAGTTTT  TCC
                                  G          __   C
GAM454  ZNF289   3'  CTCCTGGGGCTGAGCTCCTT   65928        TG   __
                                AAGGAGCT  GTTC  GGAG
                                ||||||||  ||||  ||||
                                TTCCTCGA  CGGG  CCTC
                                    GT   GT
GAM454  5T4      3'  GTTTCAGCATGAACATGGGCTT 22879         _    ____    AGGC
           CTT                   AAGGAGCTTG GTTCG    GAGAC
                                |||||||||| |||||    |||||
                                TTCTTCGGGT CAAGT    CTTTG
                                     A    ACGA       C
GAM454  AAK1     3'  CCTGTGCTACCAGCTCTTT   30521        T   TC  AG
                                AAGGAGCT GGT  GG  ACAGG
                                |||||||| |||  ||  |||||
                                TTTCTCGA CCA  TC  TGTCC
                                   _  __  G_
GAM454  ACAS2L   3'  GCCCAGTGAGCCGGGTCCCTT  68646      AG       GAGACA
                                AAGG  CTTGGTTCG     GGC
                                ||||  |||||||||     |||
                                TTCC  GGGCCGAGT     CCG
                                  CT       GAC___
GAM454  AIBZIP   5'  GCTTGACAGGGCTGGGCTCTT  56471        TG   GGAGA
                                AGGAGCT  GTTC    CAGGC
                                |||||||  ||||    |||||
                                TTCTCGG  CGGG    GTTCG
                                    GT   ACA__
GAM454  AK5      3'  GTTTGTTTCATATGGGCCCTT  24932      A    GTTCG
                                AAGG GCTTG    GAGACAGGC
                                |||| |||||    |||||||||
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                                TTCC CGGGT    CTTTGTTTG
                                  _    ATA__
GAM454  ANKRD6   3'  GAAACTTTGGACAAGCTTCTT  30772        G     ACAGGC
                                AAGGAGCTTG TTCGGAG
                                |||||||||| |||||||
                                TTCTTCGAAC AGGTTTC
                                     _      AAAGT
GAM454  AP1S2    3'  CTGGGCTGGATTAAGCTTT   15346          AGA
                                GGAGCTTGGTTCGG  CAG
                                |||||||||||||  |||
                                TTTCGAATTAGGTC  GTC
                                       GG_
GAM454  APBA2BP  3'  GTCTTGGGACCAGGCTTCT   49186          G
                                AGGAGCTTGGTTC GAGAC
                                |||||||||||| |||||
                                TCTTCGGACCAGG TTCTG
                                       G
GAM454  ARHGEF4  3'  GCTTGTTTCCCCAGGGTTCCTT 53374       _  TTC
                                AAGGAGCT TGG  GGAGACAGGC
                                |||||||| |||  ||||||||||
                                TTCCTTGG ACC  CCTTTGTTCG
                                     G  ___
GAM454  ARHV     3'  GTTTGGGAACCCAGTTTCTT  56912       T   GG
                                AAGGAGCT GGTTC  AGAC
                                |||||||| |||||  ||||
                                TTCTTTGA CCAAG  TTTG
                                     C    GG
GAM454  ARNTL2   3'  GCCTGTCTGGTGTGAGTTGTTT 39852    G    GT  GG
                                AAG AGCTTG  TC  AGACAGGC
                                ||| ||||||  ||  ||||||||
                                TTT TTGAGT  GG  TCTGTCCG
                                  G    GT  __
GAM454  ARSDR1   3'  GCAAATTTGAACTAGCTTCTT  32624       T      GACAG
                                AAGGAGCT GGTTCGGA    GC
                                |||||||| ||||||||    ||
                                TTCTTCGA TCAAGTTT    CG
                                     _      AAA__
GAM454  BCCIP    3'  GCTGAACTTTGAGTTAGTTTTC 33805      C  GG     ACA
           TT                    AAGGAG TT  TTCGGAG  GGC
                                |||||| ||  |||||||  |||
                                TTCTTT GA  GAGTTTC  TCG
                                   T  TT      AAG
GAM454  BLR1     3'  CCAAGCAGCCAAGCTCCTT   53112          CGGAGACA
                                AAGGAGCTTGGTT       GG
                                ||||||||||||       ||
                                TTCCTCGAACCGA       CC
                                       CGAA_____
GAM454  C11orf14 3'  GTCTTAGAATTAGAGTTTCTT  40599       _    G
                                AAGGAGCT TGGTTC GAGAC
                                |||||||| |||||| |||||
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                                TTCTTTGA ATTAAG TTCTG
                                    G     A
GAM454  C11orf17  3'  GTCTGTCTCTTTCAGTGCTTTT 40586       _   TTC
            T                    AAGGAGC TTGG   GGAGACAGGC
                                 ||||||| ||||  ||||||||||
                                 TTTTTCG GACT   TCTCTGTCTG
                                    T   T__
GAM454  C12orf22  3'  GCTTGTTTTTTCACCCAGGTTT 48707          TTC_
            TT                    AGGAGCTTGG    GGAGACAGGC
                                  ||||||||||    ||||||||||
                                  TTTTTGGACC    TTTTTGTTCG
                                      CACT
GAM454  C16orf7   3'  CCCCATGAACTAGTTTCTT    18144         T     GAGACA
                                 AAGGAGCT GGTTCG     GG
                                 |||||||| ||||||     ||
                                 TTCTTTGA TCAAGT     CC
                                    _     ACC___
GAM454  C17orf31  3'  GTCTCAGAAGACTGGGCTCTTT 34540         TG   CG__
                                 AAGGAGCT  GTT    GAGAC
                                 |||||||  |||    |||||
                                 TTTCTCGG  CAG    CTCTG
                                    GT   AAGA
GAM454  C1QR1     3'  CTCTGAGCTGAAGTTCTTT    24869          _
                                 AAGGAGCTT GGTTCGGAG
                                 ||||||||| |||||||||
                                 TTTCTTGAA TCGAGTCTC
                                     G
GAM454  C21orf25  3'  GCTTGTCTTGCTGGGTTTCTT  64297         TG  TCG
                                 AAGGAGCT  GT   GAGACAGGC
                                 |||||||  ||   |||||||||
                                 TTCTTTGG  CG   TTCTGTTCG
                                    GT  ___
GAM454  C22orf4   3'  CTGTGGACTGGTTCCTT     61274         T     G
                                 AAGGAGCT GGTTCG AG
                                 |||||||| |||||| ||
                                 TTCCTTGG TCAGGT TC
                                    _     G
GAM454  C5orf6    3'  TTTCTGAGCTGGCCTTTTT    33958       C TG
                                 AAGGAG T  GTTCGGAGA
                                 |||||| |  |||||||||
                                 TTTTTC G  CGAGTCTTT
                                    C GT
GAM454  C6orf33   3'  GCTTGAAAACATTAGGTTCTTT 56716           TCGGAGA
                                 AAGGAGCTTGGT      CAGGC
                                 ||||||||||||      |||||
                                 TTTCTTGGATTA      GTTCG
                                       CAAAA__
GAM454  CCNB3     5'  GTCTGGAACTGGATTACAGTTT 54469         _       AGA
            CTT                    AAGGAGCT TGGTTCGG   CAGGC
                                 |||||||| ||||||||   |||||
```

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                                TTCTTTGA ATTAGGTC   GTCTG
                                    C       AAG
GAM454  CD84-H1   3'  GTCCTGAGCTTGGTTTCTT    54225        T      A
                                AAGGAGCT GGTTCGG GAC
                                |||||||| ||||||| |||
                                TTCTTTGG TCGAGTC CTG
                                    T      _
GAM454  CHST3     3'  GTCATGGATCAGGTGCTTT    16241      A        GA
                                AAGG GCTTGGTTCG  GAC
                                |||| ||||||||||  |||
                                TTTC TGGACTAGGT  CTG
                                  G        A_
GAM454  CKAP2     3'  GTTTCAACCAACTGAGTTTTTT 37107         TG   CG__
                                AAGGAGCT  GTT    GAGAC
                                ||||||||  |||    |||||
                                TTTTTTGA  CAA    CTTTG
                                    GT   CCAA
GAM454  CNOT3     5'  GTCTTCCCTTGGACTAAAGCTC 27987          _    ____      AGGC
            CTT                   AAGGAGCTT GGTTC    GGAGAC
                                ||||||||| |||||    ||||||
                                TTCCTCGAA TCAGG    CTTCTG
                                     A     TTCC        C
GAM454  CPR2      3'  GCCTGTCTCTCCCAGCTTCTT  48833         T  TTC
                                AAGGAGCT GG   GGAGACAGGC
                                |||||||| ||   ||||||||||
                                TTCTTCGA CC   TCTCTGTCCG
                                    C  ___
GAM454  CSL4      3'  GCTAGGCACTGAGTCAGGTGCT 32646      A    GT    AGACA
            TT                    AAGG GCTTG  TCGG     GGC
                                |||| |||||  ||||     |||
                                TTTC TGGAC  AGTC     TCG
                                  G    TG    ACGGA
GAM454  CSMD1     5'  GTCTTGGGACCGGGCTCT     73517           G
                                GGAGCTTGGTTC GAGAC
                                |||||||||||| |||||
                                TCTCGGGCCAGG TTCTG
                                       G
GAM454  CTPS2     5'  GTTTGTGACCAGTGAAGTTCTT 39567          ____    T  G    AGGC
            T                     AAGGAGCT    TGGT CG AGAC
                                |||||||    |||| || ||||
                                TTTCTTGA    ACCA GT TTTG
                                    AGTG    _  G      C
GAM454  CTSO      3'  GTTTGTTTTTGTTTGCTT    9028       TTGGTT
                                GAGC     CGGAGACAGGC
                                ||||     ||||||||||
                                TTCG     GTTTTTGTTTG
                                  TTT___
GAM454  D21S2056E 3'  CTGTCTGGACGGGGCTCTTT   14866          G    GG
                                AAGGAGCTT GTTC  AGACAG
                                |||||||| ||||  ||||||
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                                TTTCTCGGG CAGG  TCTGTC
                                     G   __
GAM454  DAZAP1   3'  GTCGTCTGGACTGAGGTTTTT  39045      G  TG     _
                                AAGGA CT  GTTCGGA GAC
                                ||||| ||  ||||||| |||
                                TTTTT GA  CAGGTCT CTG
                                   G  GT      G
GAM454  DCAMKL1  3'  GTCTCCAGGCCTGAGTTTCTT  17604         _  TC
                                AAGGAGCTT GGT  GGAGAC
                                ||||||||| |||  ||||||
                                TTCTTTGAG CCG  CCTCTG
                                     T  GA
GAM454  DCLRE1B  3'  GTTTGTTTTTGGGGCCTACTTT 43403      CTT    _
           T                     AGGAG   GGTTC GGAGACAGGC
                                |||||   ||||| ||||||||||
                                TTTTC   CCGGG TTTTTGTTTG
                                   AT_    G
GAM454  DDX35    3'  GTTTGTTTGCTTGGGTTCTT   41930       TG TTCGG
                                AGGAGCT  G    AGACAGGC
                                |||||||  |    ||||||||
                                TTCTTGG  T    TTTGTTTG
                                    GT CG___
GAM454  DKFZP434C131 3'  CCTGGCGAGCAGGCTTCTT   69636         G   GAGA
                                AAGGAGCTTG TTCG   CAGG
                                |||||||||| ||||   ||||
                                TTCTTCGGAC GAGC   GTCC
                                     _   G___
GAM454  DKFZP434C212 3'  GTCTGTCTCTGAGATCTTT   69497     CTTGG
                                GGAG    TTCGGAGACAGGC
                                ||||    ||||||||||||||
                                TTTC    GAGTCTCTGTCTG
                                  TA___
GAM454  DKFZp434F1819 5'  GTCTCAGGAATTGGTTTCTT   51023        TGG   G
                                AAGGAGCT   TTC GAGAC
                                ||||||||   ||| |||||
                                TTCTTTGG   AGG CTCTG
                                     TTA   A
GAM454  DKFZp434G171 3'  GCCTGTGGGGTTGAGCTGTTT  80243     G    TG TT GGAG
                                AAG AGCT  G  C    ACAGGC
                                ||| ||||  |  |   ||||||
                                TTT TCGA  T  G    TGTCCG
                                  G    GT GG G___
GAM454  DKFZP434L187 3'  GTCTGTTTTCTCTGAAGGCCTT 69354      A   TGG      ___
           T                     AAGG GCT   TTCGGAGA   CAGGC
                                |||| |||   ||||||||   |||||
                                TTTC CGG   AAGTCTCT   GTCTG
                                  _  ___       TTT
GAM454  DKFZP434O125 3'  GTCTGTTTAGTCTGAGGTTTTT 65588      G  TG TTCGG
                                AAGGA CT  G    AGACAGGC
                                ||||| ||  |    ||||||||
```

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                                TTTTT GA  C    TTTGTCTG
                                  G  GT TGA__
GAM454  DKFZp547F072 5'  GCTCTACCTTTGAGTTAGGCCT 51088     A   GG     AC  _
          TT                     AAGG GCTT  TTCGGAG  AG GC
                                 |||| ||||  |||||||  || ||
                                 TTTC CGGA  GAGTTTC  TC CG
                                   _   TT      CA  T
GAM454  DKFZp547H236 3'  GCCTGGGACCCGAGCTGGGCTC 79247       TG     AGA_
          CT                     AGGAGCT  GTTCGG    CAGGC
                                 |||||||  ||||||    |||||
                                 TCCTCGG  CGAGCC    GTCCG
                                    GT     CAGG
GAM454  DKFZp564A176 3'  GCACCCTCAGCCGGGCTCTTT  50973          CG   ACAG
                                 AAGGAGCTTGGTT  GAG    GC
                                 ||||||||||||  |||    ||
                                 TTTCTCGGGCCGA  CTC    CG
                                        __  CCA_
GAM454  DKFZP564M082 3'  GCCAGGTCTGGTCTAAGTTTCT 26740          TT    GACA
          T                      AAGGAGCTTGG  CGGA    GGC
                                 ||||||||||  ||||    |||
                                 TTCTTTGAATC  GTCT    CCG
                                       TG    GGA_
GAM454  DKFZP564O0423 3'  GCTTCCTTTTAAGCTGGGCTTC 93355       TG   CG   AC
          TT                     AAGGAGCT  GTT  GAG  AGGC
                                 ||||||||  |||  |||  ||||
                                 TTCTTCGG  CGA  TTT  TTCG
                                    GT   AT   CC
GAM454  DKFZp566H0824 5'  GCCTAAGCTGCGAATTGAGTTT 34487      TG    G  AC_
          C                      GGAGCT  GTTCG AG   AGGC
                                 ||||||  ||||| ||   ||||
                                 CTTTGA  TAAGC TC   TCCG
                                    GT    G  GAA
GAM454  DKFZP586H2123 3'  GCTTGCAAGAAGTAAGTTTCTT 62612          G   GGAGA
                                 AAGGAGCTTG TTC     CAGGC
                                 ||||||||| |||     |||||
                                 TTCTTTGAAT AAG     GTTCG
                                       G   AAC__
GAM454  DKFZp761O132 3'  GCCCGGGATCGGACCAGGCTCC 51169            AGACA
                                 GGAGCTTGGTTCGG     GGC
                                 ||||||||||||||     |||
                                 CCTCGGACCAGGCT     CCG
                                       AGGGC
GAM454  DKFZp761O132 5'  GTCTGTCTACTCCTAATTCCTT 51174       C    TTCGG
                                 AAGGAG TTGG     AGACAGGC
                                 |||||| ||||     ||||||||
                                 TTCCTT AATC     TCTGTCTG
                                    _   CTCA_
GAM454  DKFZp762K2015 3'  CTCCATGGATTAATTCCTT    72889       C      __
                                 AAGGAG TTGGTTC  GGAG
                                 |||||| |||||||  ||||
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                                TTCCTT AATTAGG  CCTC
                                   _      TA
GAM454  DKFZp762K2015 3'  GCTTGTCTCATTTGAAGTTCTT 72892         GGTTCG
          T                     AAGGAGCTT     GAGACAGGC
                                |||||||||     |||||||||
                                TTTCTTGAA     CTCTGTTCG
                                    GTTTA_
GAM454  DNAM-1   3'  GTTGTCTGAATTGAGTTACTTT 22685     _   TG     _
                                AAGG AGCT  GTTCGGA GAC
                                |||| ||||  ||||||| |||
                                TTTC TTGA  TAAGTCT TTG
                                  A   GT      G
GAM454  DT1P1A10  3'  GCTTGGAAGAGCTGGGCTTT   62247       TG   GGAGA
                                GGAGCT  GTTC    CAGGC
                                ||||||  ||||    |||||
                                TTTCGG  CGAG    GTTCG
                                   GT   AAG__
GAM454  DTX2     3'  GTGGGTTCTGGGTCAGCTTCTT 72419        T  TT    A_  GGC
                                AAGGAGCT GG  CGGAG  CA
                                |||||||| ||  |||||  ||
                                TTCTTCGA CT  GTCTT  GT
                                    _ GG    GG  G
GAM454  ECG2     3'  CTCTGACTGAGTTTCTT     51778        TG  T
                                AAGGAGCT  GT CGGAG
                                ||||||||  || |||||
                                TTCTTTGA  CA GTCTC
                                    GT  _
GAM454  EFA6R    3'  GTCCTTGAAATTGAGTTCCTT  31638        TG   _  GA
                                AAGGAGCT  GTT CG  GAC
                                ||||||||  ||| ||  |||
                                TTCCTTGA  TAA GT  CTG
                                    GT   A  TC
GAM454  ELF2     3'  GCTTGTTTGTGTAAAGCTTTTT 23449         GGTT  G
                                AAGGAGCTT    CG AGACAGGC
                                |||||||||    || ||||||||
                                TTTTTCGAA    GT TTTGTTCG
                                    AT__  G
GAM454  EPB41L1   3'  GCTTGTCTGCCACAAGCTACTT 71111     G     GTTC  _
                                AAG AGCTTG    GG AGACAGGC
                                ||| ||||||    || ||||||||
                                TTC TCGAAC    CC TCTGTTCG
                                  A     A___  G
GAM454  EPHA7    3'  GCTTGTTTTTAAAGCTTT    16692        GGTTCG
                                GGAGCTT     GAGACAGGC
                                |||||||     |||||||||
                                TTTCGAA     TTTTGTTCG
                                    AT____
GAM454  ESDN     3'  GTATATTGGATTAAGTTTTTT  56060              AG_
                                AAGGAGCTTGGTTCGG   AC
                                ||||||||||||||||   ||
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                                TTTTTTGAATTAGGTT  TG
                                      ATA
GAM454  FBP17    3'  GTTTGCTTTTAGAGCCAAGTTT 73158          G  _
          CTT                   AAGGAGCTTGGTTC GAGA CAGGC
                                |||||||||||||| |||| |||||
                                TTCTTTGAACCGAG TTTT GTTTG
                                      A   C
GAM454  FBXW2    3'  TCTGTTATTAAAGCTTTTT   25140        GGTTCGGA
                                AAGGAGCTT      GACAGG
                                |||||||||      ||||||
                                TTTTTCGAA      TTGTCT
                                     ATTA____
GAM454  FLB6421  3'  GCCTGTTTTCCTGAAAAGTTCC 39645        GGTTC
          T                     AGGAGCTT    GGAGACAGGC
                                ||||||||    ||||||||||
                                TCCTTGAA    CTTTTGTCCG
                                     AAGTC
GAM454  FLJ00026 3'  TCTCTGGGACCAAGTTTCTT  65620          _
                                AAGGAGCTTGGTTC GGAGA
                                |||||||||||||| |||||
                                TTCTTTGAACCAGG TCTCT
                                      G
GAM454  FLJ10604 3'  GTCTGTCTCCGGGCCAGGGTC  36860    G
                                GA CTTGGTTCGGAGACAGGC
                                || ||||||||||||||||||
                                CT GGACCGGGCCTCTGTCTG
                                 G
GAM454  FLJ10656 3'  CTCTGAATCAGGGTTTTT    36907      G
                                AAGGA CTTGGTTCGGAG
                                ||||| ||||||||||||
                                TTTTT GGACTAAGTCTC
                                   G
GAM454  FLJ10718 3'  GCTTAGAGAGAATAAGCTTCTT 37030          G  GGAGAC
                                AAGGAGCTTG TTC     AGGC
                                |||||||||| |||     ||||
                                TTCTTCGAAT AAG     TTCG
                                      _  AGAGA_
GAM454  FLJ10743 3'  GCCTGTCTCCTTCCACCTCCTT 37084      CT  TTC
                                AAGGAG  TGG  GGAGACAGGC
                                ||||||  |||  ||||||||||
                                TTCCTC  ACC  CCTCTGTCCG
                                   C_  TT_
GAM454  FLJ10852 3'  GCCTGTTCCCCTTGGGTTTT  39253      TG TTC  AG
                                GGAGCT  G  GG  ACAGGC
                                ||||||  |  ||  ||||||
                                TTTTGG  T  CC  TGTCCG
                                   GT C__  CT
GAM454  FLJ10901 3'  TTTGTCTCTAAGCCCCTT   37378     AGCTT   CG
                                AAGG    GGTT  GAGACAGG
                                ||||    ||||  ||||||||
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                                TTCC    CCGA  CTCTGTTT
                                  _____   AT
GAM454  FLJ11101  3' GTTTGTTTTTGTTTTGCTTCCT 37614     _  TTGGTT
                                AGGA GC     CGGAGACAGGC
                                |||| ||     ||||||||||
                                TCCT CG     GTTTTTGTTTG
                                  T  TTTT__
GAM454  FLJ11362  3' GTCCCTTGGACTGGCCTCCTT  41964       C TG   __ A
                                AAGGAG T  GTTC  GG GAC
                                |||||| |  ||||  || |||
                                TTCCTC G  CAGG  CC CTG
                                   C GT   TT  _
GAM454  FLJ12409  3' CTTTAGGGTCAGGCCTTT    47769     A     TT _
                                AAGG GCTTGG  C GGAG
                                |||| ||||||  | ||||
                                TTTC CGGACT  G TTTC
                                  _     GG A
GAM454  FLJ12526  3' GTCTAGGACTGGGCTTCT    45930       TG   GG
                                AGGAGCT  GTTC  AGAC
                                |||||||  ||||  ||||
                                TCTTCGG  CAGG  TCTG
                                    GT   A_
GAM454  FLJ12586  3' GCAAACACTGAATCAACTTTTT 45211       C       AGACAG
                                AAGGAG TTGGTTCGG     GC
                                |||||| |||||||||     ||
                                TTTTTC AACTAAGTC     CG
                                   _       ACAAA_
GAM454  FLJ12707  3' GTGACTGAACTGGGTTTTT   42202       TG     AG
                                AGGAGCT  GTTCGG  AC
                                |||||||  ||||||  ||
                                TTTTTGG  CAAGTC  TG
                                    GT     AG
GAM454  FLJ12799  3' GCCTGAGAACAGCTAAGCTCC  42857          CGGAGA
                                GGAGCTTGGTT     CAGGC
                                ||||||||||     |||||
                                CCTCGAATCGA     GTCCG
                                       CAAGA_
GAM454  FLJ13057  3' CTCTGAATTGAGTGCCTT    42706     A   TG
                                AAGG GCT  GTTCGGAG
                                |||| |||  ||||||||
                                TTCC TGA  TAAGTCTC
                                  G   GT
GAM454  FLJ13193  3' GTTTGAGGACTAAGCCTTT    50733     A       GG
                                AAGG GCTTGGTTC  AGAC
                                |||| |||||||||  ||||
                                TTTC CGAATCAGG  TTTG
                                  _       AG
GAM454  FLJ13213  3' GTTTGTTTCACAAGGTTCTT   45730        GGTTCG
                                AGGAGCTT     GAGACAGGC
                                ||||||||     |||||||||
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                                TTCTTGGA     CTTTGTTTG
                                    ACA___
GAM454  FLJ13273  3'  TTTGTCTTACTGACTTTTT   45725       C TG  TCG
                                AAGGAG T  GT   GAGACAGG
                                ||||||  |  ||   ||||||||
                                TTTTTC A  CA   TTCTGTTT
                                   _ GT  ___
GAM454  FLJ13330  3'  CTCTCGGGTCAGTTCCTT    47665        T  TT  _
                                AAGGAGCT GG  CG GAG
                                |||||||| ||  || |||
                                TTCCTTGA CT  GC CTC
                                    _  GG  T
GAM454  FLJ13621  3'  GCTTGTTTTCTTAATATGCTTC 47224        TTG   C_
           TT                    AAGGAGC   GTT  GGAGACAGGC
                                |||||||   |||  ||||||||||
                                TTCTTCG   TAA  CTTTTGTTCG
                                    TA_   TT
GAM454  FLJ14124  3'  GCCTGTGGTGGAGCTGGGCTGC 46358     G    TG    GGAG
           TT                    AAG AGCT  GTTC    ACAGGC
                                ||| ||||  ||||    ||||||
                                TTC TCGG  CGAG    TGTCCG
                                  G    GT    GTGG
GAM454  FLJ14154  3'  CCTGTTCTTGCAGCTCCTT    46229        TG  TC    A
                                AAGGAGCT  GT  GGAG CAGG
                                ||||||||  ||  |||| ||||
                                TTCCTCGA  CG  TCTT GTCC
                                    ___  T_   _
GAM454  FLJ14326  5'  GCCTGGACAGGTGAACTGAGTT 50774      _    TG     GAGA__
           GCCTT                    AAGG AGCT  GTTCG     CAGGC
                                |||| ||||  |||||     |||||
                                TTCC TTGA  CAAGT     GTCCG
                                  G    GT    GGACAG
GAM454  FLJ14457  3'  GTCCTAACTGGGCTGGGCCTCT 52412     GA   TG     A___   AGGC
           T                     AAG  GCT  GTTCGG    GAC
                                |||  |||  ||||||    |||
                                TTC  CGG  CGGGTC    CTG
                                  TC   GT     AATC     C
GAM454  FLJ14594  3'  GCCCAGCTCCGGGCTGGCTTTT 52506         T        ACA
           T                     AAGGAGCT GGTTCGGAG   GGC
                                |||||||| |||||||||   |||
                                TTTTTCGG TCGGGCCTC   CCG
                                    _        GAC
GAM454  FLJ14708  3'  GTCCCTTGGGTCCAGGCTCCTT 52609           _   __  A
                                AAGGAGCTTGG TTC  GG GAC
                                |||||||||||| |||  || |||
                                TTCCTCGGACC GGG  CC CTG
                                     T   TT  _
GAM454  FLJ14917  3'  GTCATGTCTGGGTCAGTTCCTT 52765         T  TT   ____
                                AAGGAGCT GG  CGGA   GAC
                                |||||||| ||  ||||   |||
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                                TTCCTTGA CT  GTCT   CTG
                                    _ GG    GTA
GAM454   FLJ14950  3' GCTTGGAGGAGCTGGGCTCT   52793      TG    GGAGA
                                GGAGCT  GTTC    CAGGC
                                ||||||  ||||    |||||
                                TCTCGG  CGAG    GTTCG
                                   GT    GAG__
GAM454   FLJ20113  3' GTTTGAGGGGCCAGGCCTCTT  35057     GA       GG_
                                AAG  GCTTGGTTC   AGAC
                                |||  |||||||||  ||||
                                TTC  CGGACCGGG   TTTG
                                  TC        GAG
GAM454   FLJ20123  5' GCCTGTCTCCTGGGAGTGCTTT 35071      TTGG  _
                                GGAGC    TTC GGAGACAGGC
                                |||||    ||| ||||||||||
                                TTTCG    GGG CCTCTGTCCG
                                   TGA_   T
GAM454   FLJ20330  3' GTTGGTGGGCTGAGCTCCT    39145       TG    GA
                                AGGAGCT  GTTCG  GAC
                                |||||||  |||||  |||
                                TCCTCGA  CGGGT  TTG
                                    GT    GG
GAM454   FLJ20359  3' GCCTGGCCAGGACCGAGCTCTT 35518           GGAGA
                                AGGAGCTTGGTTC    CAGGC
                                ||||||||||||     |||||
                                TTCTCGAGCCAGG    GTCCG
                                       ACCG_
GAM454   FLJ20485  3' CTGTGCTGGCCGGGTTTTTT   39293          T   AG
                                AAGGAGCTTGGT CGG  ACAG
                                ||||||||||| |||  ||||
                                TTTTTTGGGCCG GTC  TGTC
                                       _  G_
GAM454   FLJ20507  3' GCCAAGGAACTGAACTAAGTCT 35742      G        AGACA_
           TT                   AAGGA CTTGGTTCGG     GGC
                                |||||  ||||||||||     |||
                                TTTCT GAATCAAGTC     CCG
                                   _        AAGGAA
GAM454   FLJ20574  5' GCCAAGTGGACTGGACTCTTT  35848      C TG    GAGACA
                                AAGGAG T  GTTCG     GGC
                                ||||||  |  |||||     |||
                                TTTCTC G  CAGGT     CCG
                                   A GT    GAA___
GAM454   FLJ20574  3' GCCAAGTGGACTGGACTCTTT  35849      C TG    GAGACA
                                AAGGAG T  GTTCG     GGC
                                ||||||  |  |||||     |||
                                TTTCTC G  CAGGT     CCG
                                   A GT    GAA___
GAM454   FLJ20686  3' TCTGTCTTCAGAGATTCTT   35958      G  GGTTC
                                AAGGA CTT    GGAGACAGG
                                |||||  |||    |||||||||
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                                TTCTT GAG    CTTCTGTCT
                                  A  A____
GAM454  FLJ20802  3'  GTTACACGGATAAGTTCTTT  36112        G   GA_
                                AAGGAGCTTG TTCG  GAC
                                |||||||||| ||||  |||
                                TTTCTTGAAT AGGC  TTG
                                      _   ACA
GAM454  FLJ20886  3'  GCCTTGCTGAACTAAGTTTT  48067           AGAC
                                GGAGCTTGGTTCGG   AGGC
                                ||||||||||||||   ||||
                                TTTTGAATCAAGTC   TCCG
                                       GT__
GAM454  FLJ20898  3'  GTCTGTTTTGCTCGATTCCTT  45117      C  _  TCG
                                AAGGAG TTG GT  GAGACAGGC
                                |||||| ||| ||  |||||||||
                                TTCCTT AGC CG  TTTTGTCTG
                                   _  T  ___
GAM454  FLJ21415  3'  GTTTTGATCCAGGCTCTTT   45690         T  G
                                AAGGAGCTTGG TCG AGAC
                                |||||||||| ||| ||||
                                TTTCTCGGACC AGT TTTG
                                      T  _
GAM454  FLJ21865  3'  GCCACTCTGAGCCGGGGCTCCT 43112        _       ACA
          T                    AAGGAGCTT GGTTCGGAG  GGC
                               ||||||||| |||||||||  |||
                               TTCCTCGGG CCGAGTCTC  CCG
                                    G       A__
GAM454  FLJ21940  3'  GTTACGAATGGGCTTTTT   43386       T G    GA
                                AAGGAGC T GTTCG  GAC
                                ||||||| | |||||  |||
                                TTTTTCG G TAAGC  TTG
                                   _ G    A_
GAM454  FLJ22116  5'  GCCCCGCCGATCAGGTTCCTT  45222          T  AGACA
                                AAGGAGCTTGGT CGG    GGC
                                |||||||||||| |||    |||
                                TTCCTTGGACTA GCC    CCG
                                      _  GCC__
GAM454  FLJ22418  3'  GCTTGTTGAGCTTCTAAGTTTC 45223          TTCGGA
          TT                   AAGGAGCTTGG     GACAGGC
                               ||||||||||     |||||||
                               TTCTTTGAATC     TTGTTCG
                                     TTCGAG
GAM454  FLJ22529  3'  GCCTGGGGAAGGAGCCAGTTTT 45945       T    GGAGA_
          TT                   AAGGAGCT GGTTC     CAGGC
                               ||||||||| |||||     |||||
                               TTTTTTGA CCGAG     GTCCG
                                   _    GAAGGG
GAM454  FLJ22529  5'  GTCAGCTCTGGGCTGGGCTTT  45950       TG       ACA
                                GGAGCT  GTTCGGAG  GGC
                                ||||||  ||||||||  |||
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                                TTTCGG  CGGGTCTC   CTG
                                   GT       GA_
GAM454  FLJ22649  3'  GTTTGTTTTTTGGTTTTGGGTT 41924        TG T_     _
              TTTT                  AAGGAGCT  G  TCGGAGA CAGGC
                                |||||||| |  ||||||| |||||
                                TTTTTTGG  T  GGTTTTT GTTTG
                                   GT TT      T
GAM454  FLJ22649  3'  TTTACCCTCTGAGTTATGTTTC 41925        T GG      ACAGGC
              TT                   AAGGAGC T  TTCGGAG
                                ||||||| |  |||||||
                                TTCTTTG A  GAGTCTC
                                   T TT      CCATTTG
GAM454  FLJ22969  3'  TTTGGGATACAAGTTCTTT   69221          _   G
                                AAGGAGCTTG GTTC GAG
                                |||||||||| |||| |||
                                TTTCTTGAAC TAGG TTT
                                     A   G
GAM454  FLJ23132  3'  GTTTTAGAATAGGGTTTCTT   97841        TG   G
                                AAGGAGCT  GTTC GAGAC
                                ||||||||  |||| |||||
                                TTCTTTGG  TAAG TTTTG
                                   GA   A
GAM454  FLJ23186  3'  GTTTGTTTTTGTTTTGTTTC   61045      TTGGTT
                                GGAGC     CGGAGACAGGC
                                |||||     ||||||||||
                                CTTTG     GTTTTTGTTTG
                                   TTTT__
GAM454  FLJ23235  3'  GCAAGTTGGACCGAGCCCTT   46880      A         AGACAG
                                AAGG GCTTGGTTCGG     GC
                                |||| ||||||||||     ||
                                TTCC CGAGCCAGGTT     CG
                                  _         GAA___
GAM454  FLJ23519  3'  CTTGTCTGGTGGTTTCTT    50949        TGGTTCGG
                                AAGGAGCT       AGACAGG
                                ||||||||       |||||||
                                TTCTTTGG       TCTGTTC
                                   TGG_____
GAM454  FLJ23519  3'  GCTAGATGGGCCGAGCTCCT   50954           GAGACA
                                AGGAGCTTGGTTCG     GGC
                                ||||||||||||||     |||
                                TCCTCGAGCCGGGT     TCG
                                      AGA___
GAM454  FLJ31121  3'  GTTTGTGTCTGATGAGTTTTTT 59208          GT    G
                                AAGGAGCTTG  TCGGA ACAGGC
                                ||||||||||  ||||| ||||||
                                TTTTTTGAGT  AGTCT TGTTTG
                                      __     G
GAM454  FLJ32499  3'  GTATTTCGAGTTTGGCTTTTT  58780        T GT     _
                                AAGGAGCT G  TCGGAG AC
                                |||||||| |  |||||| ||
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                                TTTTTCGG T  AGCTTT TG
                                     T TG     A
GAM454  FLJ32915  3'  GTTTGAGATAACCTAGCTCTTT 59436        T  __  GG
                                AAGGAGCT GGT  TC  AGAC
                                |||||||| |||  ||  ||||
                                TTTCTCGA CCA  AG  TTTG
                                     T   AT  AG
GAM454  GDAP2     3'  GTTTAAGGACTAAGGTTCCTT  35127       _     GG
                                AAGGAGC TTGGTTC  AGAC
                                ||||||| |||||||  ||||
                                TTCCTTG AATCAGG  TTTG
                                     G      AA
GAM454  GFR       3'  GTCTAGAAGATGGCTAAGCTCT 25449          __  GG__    AGGC
           TT                     AAGGAGCTTGGT  TC    AGAC
                                ||||||||||||  ||    ||||
                                TTTCTCGAATCG  AG    TCTG
                                       GT  AAGA      C
GAM454  GGA2      3'  CACTGCTCTGATTTGGGCTTTT 57653        TG T     A   GC
           T                      AAGGAGCT  G TCGGAG CAG
                                ||||||||  | ||||||  |||
                                TTTTTCGG  T AGTCTC GTC
                                     GT T      _   ACC
GAM454  GGA2      3'  CACTGCTCTGATTTGGGCTTTT 31159        TG T     A   GC
           T                      AAGGAGCT  G TCGGAG CAG
                                ||||||||  | ||||||  |||
                                TTTTTCGG  T AGTCTC GTC
                                     GT T      _   ACC
GAM454  H2AFY2    3'  GTTTTGATTCAGGCTTTTT    38466         GT   G
                                AAGGAGCTTG  TCG AGAC
                                ||||||||||  ||| ||||
                                TTTTTCGGAC  AGT TTTG
                                      TT  _
GAM454  HBXAP     5'  GTTTAGAATTAGGTTTTT     33882           GG
                                AGGAGCTTGGTTC  AGAC
                                ||||||||||||  ||||
                                TTTTTGGATTAAG  TTTG
                                       A_
GAM454  HH114     3'  GCTAGTATTTTTATGAGTCGAG 51668          GT   GAG____  A
           TTTTTT                   AAGGAGCTTG  TCG      AC GGC
                                ||||||||||  |||      || |||
                                TTTTTTGAGC  AGT      TG TCG
                                      TG   ATTTTTA  A
GAM454  HSJ1      3'  TGGTTTGGGCTGGGCTTTT    23088        TG      GA
                                AGGAGCT  GTTCGGA  CA
                                |||||||  |||||||  ||
                                TTTTCGG  CGGGTTT  GT
                                     GT      G_
GAM454  HSPF2     5'  GCCTGTCCAGGAATCAGTTTTT 19836         T    GGA
           T                      AAGGAGCT GGTTC   GACAGGC
                                ||||||||  |||||   |||||||
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                                TTTTTTGA CTAAG   CTGTCCG
                                      _    GAC
GAM454  HSU47926 3'  GTGGCTGAGCCAGCTCCTT   27310        T     AG
                                AAGGAGCT GGTTCGG  AC
                                |||||||| |||||||  ||
                                TTCCTCGA CCGAGTC  TG
                                      _      GG
GAM454  IDN3     3'  GTCTGTTTCCATTTGAATTTCT 56760       C TG TTC
           T                     AAGGAG T  G   GGAGACAGGC
                                |||||| |  |   ||||||||||
                                TTCTTT A  T   CCTTTGTCTG
                                   A GT TA_
GAM454  IL17D    3'  GTCTGTCTCTGAACACAA    57122     _
                                TTG GTTCGGAGACAGGC
                                ||| ||||||||||||||
                                AAC CAAGTCTCTGTCTG
                                  A
GAM454  jdp2     3'  GCCAGCATCAGCCGAGCTTTTT 56201           CG  GACA
                                AAGGAGCTTGGTT  GA   GGC
                                ||||||||||||  ||   |||
                                TTTTTCGAGCCGA  CT   CCG
                                       __ ACGA
GAM454  JFC1     5'  GCCTGTTGAGTCAGCCTTCTT  52839       C   GT  GGA
                                AAGGAG TTG  TC   GACAGGC
                                |||||| |||  ||   |||||||
                                TTCTTC GAC  AG   TTGTCCG
                                   C   TG  ___
GAM454  JIK      3'  GTTTCTCGGATCAAATTTTTT  33266       C      _
                                AAGGAG TTGGTTCG GAGAC
                                |||||| |||||||| |||||
                                TTTTTT AACTAGGC CTTTG
                                   A       T
GAM454  KCNMB3L  5'  CTTTAGGACTGGGCTCTTT   27713        TG   _
                                AAGGAGCT  GTTC GGAG
                                ||||||||  |||| ||||
                                TTTCTCGG  CAGG TTTC
                                     GT    A
GAM454  KCNMB3L  5'  GTGGCTTTAGGACTGGGCTCTT 27715        TG   _   A  GGC
           T                     AAGGAGCT  GTTC GGAG CA
                                |||||||  |||| |||| ||
                                TTTCTCGG  CAGG TTTC GT
                                     GT    A    G  G
GAM454  KIAA0062 3'  GCCTGTCTCTCCAGAAGCCTT  70785     AGC    TTC
                                AAGG   TTGG   GGAGACAGGC
                                ||||   ||||   ||||||||||
                                TTCC   GACC   TCTCTGTCCG
                                  GAA   ___
GAM454  KIAA0152 3'  GCCTAGCGAGGGCAGGTTTCTT 28977          G _   GAGAC
                                AAGGAGCTTG T TCG    AGGC
                                |||||||||| | |||    ||||
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                                TTCTTTGGAC G AGC    TCCG
                                     G G   GA___
GAM454  KIAA0210  5'  GTTCTAACTGGATTCAGGTTTT 29173          _    __  CAGGC
              TT                  AAGGAGCTTGG TTCGG  AGA
                                  |||||||||||| |||||  |||
                                  TTTTTTGGACT AGGTC  TCT
                                        T    AA   TG
GAM454  KIAA0237  3'  GTCTCCGTGGGCTGGTTTCCTT 29232       C TG  __
                                  AAGGAG T  GTT  CGGAGAC
                                  |||||| |  |||  |||||||
                                  TTCCTT G  CGG  GCCTCTG
                                     T GT   GT
GAM454  KIAA0276  3'  GTTTGTTTCATGCTAGGCTTTT 71523          TCG
                                  AGGAGCTTGGT   GAGACAGGC
                                  ||||||||||   |||||||||
                                  TTTTCGGATCG   CTTTGTTTG
                                        TA_
GAM454  KIAA0286  3'  GTCTGTCATTTACTTGGTTCTT 68859        T   TCGGA
              T                   AAGGAGCT GGT    GACAGGC
                                  |||||||| |||    |||||||
                                  TTTCTTGG TCA    CTGTCTG
                                       T   TTTA_
GAM454  KIAA0321  3'  CTCTGAACCAAGATTTTT    63049      G
                                  AAGGA CTTGGTTCGGAG
                                  ||||| ||||||||||||
                                  TTTTT GAACCAAGTCTC
                                     A
GAM454  KIAA0321  3'  GTTTGTCTGGAGATGGCCAGTT 63062        T   __  GG_
              CTTT                   AAGGAGCT GGT  TC   AGACAGGC
                                  |||||||| |||  ||   ||||||||
                                  TTTCTTGA CCG  AG   TCTGTTTG
                                       _  GT  AGG
GAM454  KIAA0349  3'  GTCTGGCACCCAGGCTTTTT   93917          TTCGG
                                  AAGGAGCTTGG    AGAC
                                  ||||||||||    ||||
                                  TTTTTCGGACC    TCTG
                                        CACGG
GAM454  KIAA0391  3'  GCTTTCAGTGAGCTAAACTTCT 28614       C       GA  C
              T                   AAGGAG TTGGTTCG  GA AGGC
                                  |||||| ||||||||  || ||||
                                  TTCTTC AATCGAGT  CT TTCG
                                     A       GA  _
GAM454  KIAA0436  3'  GCCGATCTGGGCTGAGTCTTT  60687      G  TG      GACA
                                  AAGGA CT  GTTCGGA    GGC
                                  ||||| ||  |||||||    |||
                                  TTTCT GA  CGGGTCT    CCG
                                     _  GT      AG__
GAM454  KIAA0451  3'  GTTGAGAGTGGGCGTGGGCTTC 29779          _    GA___   AGGC
              TT                   AAGGAGCTTG GTTCG    GAC
                                  |||||||||| |||||    |||
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                                TTCTTCGGGT CGGGT    TTG
                                      G    GAGAG
GAM454  KIAA0514 3' GCCTGTTTCTGGAGCCTCTTCT 28748      CTT   _
                                AGGAG  GGTTC GGAGACAGGC
                                |||||  ||||| ||||||||||
                                TCTTC  CCGAG TCTTTGTCCG
                                   T__    G
GAM454  KIAA0546 3' GCCTAATGGAATAGGCTCTTT 71838        G   GAGAC
                                AAGGAGCTTG TTCG    AGGC
                                |||||||||| ||||    ||||
                                TTTCTCGGAT AGGT    TCCG
                                      A   AA___
GAM454  KIAA0574 3' GTCCCTGGGCTGAGCCCTT   69822     A  TG    A
                                AAGG GCT  GTTCGG GAC
                                |||| |||  |||||| |||
                                TTCC CGA  CGGGTC CTG
                                  _  GT     C
GAM454  KIAA0628 3' GCTTATTGTTGACTCAAGTTCT 29532        GT   A  C
           TT                    AAGGAGCTTG  TCGG GA AGGC
                                |||||||||  |||| || ||||
                                TTTCTTGAAC  AGTT TT TTCG
                                      TC   G  A
GAM454  KIAA0628 3' TTCTGAGGTTGAACTGAGCTCT 29539       TG    AGA   C
           T                     AGGAGCT  GTTCGG   CAGG
                                |||||||  ||||||   ||||
                                TTCTCGA  CAAGTT   GTCT
                                    GT     GGA    TG
GAM454  KIAA0648 3' GTCTACTGAATTAATTTTTT   83543      C      _
                                AAGGAG TTGGTTCGG AGAC
                                |||||| ||||||||| ||||
                                TTTTTT AATTAAGTC TCTG
                                  _       A
GAM454  KIAA0676 3' GTTTATGAATTAGGCACCTT   31149     A       G
                                AAGG GCTTGGTTCG AGAC
                                |||| |||||||||| ||||
                                TTCC CGGATTAAGT TTTG
                                  A        A
GAM454  KIAA0680 3' GTCTGTCTCTGGCTGAGGTTTT 28896     G  TG  T
                                AGGA CT  GT CGGAGACAGGC
                                |||| ||  || ||||||||||
                                TTTT GA  CG GTCTCTGTCTG
                                  G  GT  _
GAM454  KIAA0694 3' TGACTTGGAACAAGTTTCTT   72975        G   G   A
                                AAGGAGCTTG TTC GAG CA
                                |||||||||| ||| ||| ||
                                TTCTTTGAAC AAG TTC GT
                                      _  G   A
GAM454  KIAA0720 3' GTCTTCAGGGCTGGGCTCCT   62991       TG   _
                                AGGAGCT  GTTC GGAGAC
                                |||||||  |||| ||||||
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                                TCCTCGG  CGGG CTTCTG
                                   GT    A
GAM454  KIAA0748 3' GTTTAGGGGACAAGTTTTTT  29617         GT  GG
                                AAGGAGCTTG  TC  AGAC
                                ||||||||||  ||  ||||
                                TTTTTTGAAC  GG  TTTG
                                     AG  GA
GAM454  KIAA0789 5' GCTTGGGAAACCAAGCCCCTT  64432      A       CGGAGA
                                AAGG GCTTGGTT     CAGGC
                                |||| ||||||||     |||||
                                TTCC CGAACCAA     GTTCG
                                  C       AGG___
GAM454  KIAA0825 3' TTTCTGAATCAGTTTTCTT   61694       C
                                AAGGAG TTGGTTCGGAGA
                                |||||| ||||||||||||
                                TTCTTT GACTAAGTCTTT
                                   T
GAM454  KIAA0830 3' GTTTGTCTTTACAATGGGTTTC 70270         GTTC
           T                     AGGAGCTTG    GGAGACAGGC
                                 |||||||||    ||||||||||
                                 TCTTTGGGT    TTTCTGTTTG
                                      AACA
GAM454  KIAA0844 3' GTTTGTTTGATTGAGGTTTTT  30897      G  TG   CGG
                                AAGGA CT  GTT   AGACAGGC
                                |||||  ||  |||   ||||||||
                                TTTTT GA  TAG   TTTGTTTG
                                   G  GT  ___
GAM454  KIAA0854 3' GCCTCACCATGAATTGATTTTT 30779       C TG    GAGAC
           TT                     AAGGAG T  GTTCG    AGGC
                                  ||||||  |  |||||    ||||
                                  TTTTTT A  TAAGT    TCCG
                                     T GT    ACCAC
GAM454  KIAA0869 3' GTTTGAAGATGAACCGACTTTT 71422       C       GAGA
           T                      AAGGAG TTGGTTCG    CAGGC
                                  ||||||  ||||||||    |||||
                                  TTTTTC AGCCAAGT    GTTTG
                                     _       AGAA
GAM454  KIAA0871 5' CGTTTCAGAGCTTTGTATTGGG 31020         _______    G    AGGC
           TTTTTT                  AAGGAGCTT      GGTTC GAGAC
                                   |||||||||      ||||| |||||
                                   TTTTTTGGG      TCGAG CTTTG
                                        TTATGTT    A       CG
GAM454  KIAA0939 3' GTCTGTTTTTCTGGGTCAGTTT 62720        T  TT   __
           TTT                     AAGGAGCT GG  CGGA  GACAGGC
                                   ||||||||  ||  ||||  |||||||
                                   TTTTTTGA CT  GTCT  TTGTCTG
                                        _ GG    TT
GAM454  KIAA0981 3' GCCTGTTTTTGAGTATGTTT   62089      TTG
                                GAGC   GTTCGGAGACAGGC
                                ||||   ||||||||||||||
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                                TTTG   TGAGTTTTTGTCCG
                                  TA_
GAM454  KIAA0993  3'  TTTGTTCAATCGGGTTTCTT   64824          CGGA
                                AAGGAGCTTGGTT    GACAGG
                                |||||||||||||    ||||||
                                TTCTTTGGGCTAA    TTGTTT
                                      C___
GAM454  KIAA1143  3'  AAAAGTTTTTGAATTAACTTTT 69222       C          AGGC
          T                      AAGGAG TTGGTTCGGAGAC
                                |||||| ||||||||||||
                                TTTTTC AATTAAGTTTTTG
                                   _          AAAAC
GAM454  KIAA1155  3'  GTCCCTTGGGTCTGGCTTTTT  62917        T  TT __  A
                                AAGGAGCT GG  C  GG GAC
                                |||||||| ||  |  || |||
                                TTTTTCGG CT  G  CC CTG
                                     T  GG TT  _
GAM454  KIAA1190  3'  GCTACATGTTTCCTAGTTAAGC 71650         GG  C     ___
          TCTTT                    AAGGAGCTT  TT GGAGACA   GGC
                                |||||||||  || |||||||   |||
                                TTTCTCGAA  GA CCTTTGT   TCG
                                     TT  T      ACA
GAM454  KIAA1196  3'  GTTTCTTGGTTTGGGTTTTTT  62153        TG TT  _
                                AAGGAGCT  G  CG GAGAC
                                ||||||||  |  || |||||
                                TTTTTTGG  T  GT CTTTG
                                     GT TG  T
GAM454  KIAA1198  3'  GCCACCATACCGAGCTAGTTTT 64043        T      AGACA_
          TT                     AAGGAGCT GGTTCGG     GGC
                                |||||||| |||||||     |||
                                TTTTTTGA TCGAGCC     CCG
                                   _      ATACCA
GAM454  KIAA1211  3'  ATTCTTCTGAATTGACTTTTT  69466       C TG       ACAGGC
                                AAGGAG T  GTTCGGAG
                                |||||| |  ||||||||
                                TTTTTC A  TAAGTCTT
                                   _ GT       CTTAA
GAM454  KIAA1237  3'  CCACAGACTAGGCTTCTT    81299          C__
                                AAGGAGCTTGGTT   GG
                                ||||||||||||   ||
                                TTCTTCGGATCAG   CC
                                      ACA
GAM454  KIAA1243  3'  GCCTGTCTCCAGGGCCAGGCT  74027          _
                                AGCTTGGTTC GGAGACAGGC
                                |||||||||| ||||||||||
                                TCGGACCGGG CCTCTGTCCG
                                     A
GAM454  KIAA1280  5'  GCCACCATGCCTGGCTGGGTTT 70283        TG  TC  AGACA_
          TTT                    AAGGAGCT  GT  GG     GGC
                                ||||||||  ||  ||     |||
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                              TTTTTTGG  CG  CC     CCG
                                  GT  GT  GTACCA
GAM454  KIAA1323  3'  TTTGTTTCTGAATTCTT     63729     CTT
                              GAG   GGTTCGGAGACAGG
                              |||   ||||||||||||||
                              TTC   TTAAGTCTTTGTTT
                                 ___
GAM454  KIAA1332  3'  GTTTTAACAGGGGCTGGGCTGC 71706     _   TG    G____     AGGC
          CTT                   AAGG AGCT  GTTC     GAGAC
                              |||| ||||  ||||     |||||
                              TTCC TCGG  CGGG     TTTTG
                                G    GT    GACAA       C
GAM454  KIAA1364  3'  GTTTGCTGGGCCGAGCTGCTT  64355     G          _
                              AAG AGCTTGGTTCGG AGAC
                              ||| ||||||||||| ||||
                              TTC TCGAGCCGGGTC TTTG
                                G           G
GAM454  KIAA1376  3'  GTTTGTTTATTTGGTTGGCTTT 64388         TGGTTCGG
          TT                    AAGGAGCT       AGACAGGC
                              ||||||||       ||||||||
                              TTTTTCGG       TTTGTTTG
                                  TTGGTTTA
GAM454  KIAA1432  5'  GTCTCAGGGATTAAGCACTTT  67309      A        G_
                              AAGG GCTTGGTTC  GAGAC
                              |||| |||||||||  |||||
                              TTTC CGAATTAGG  CTCTG
                                A        GA
GAM454  KIAA1437  3'  GTTTGTTTTTTGGGTTTTTT   61218         TG TTCG
                              AAGGAGCT  G    GAGACAGGC
                              ||||||||  |    |||||||||
                              TTTTTTGG  T    TTTTGTTTG
                                  GT ____
GAM454  KIAA1467  3'  CTTCAGGGATCCAGTTTCTT   72065         T    __
                              AAGGAGCT GGTTC  GGAG
                              |||||||| |||||  ||||
                              TTCTTTGA CTAGG  CTTC
                                  C     GA
GAM454  KIAA1560  3'  GTCATGAGATGAGTTCCTT    64852         GG    GA
                              AAGGAGCTT  TTCG  GAC
                              |||||||||  ||||  |||
                              TTCCTTGAG  GAGT  CTG
                                   TA    A_
GAM454  KIAA1671  3'  GCCCAGCTGAATTTGAGCTTTT 66283         TG _    AGACA
          T                     AAGGAGCT  G TTCGG     GGC
                              ||||||||  | |||||     |||
                              TTTTTCGA  T AAGTC     CCG
                                  GT T     GAC__
GAM454  KIAA1795  3'  GCCTGTTTCCTCTTAGCTTT   72616       T  TTC
                              GGAGCT GG   GGAGACAGGC
                              |||||| ||   ||||||||||
```

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                                TTTCGA TC   CCTTTGTCCG
                                   T  T__
GAM454  KIAA1841  3'  GTCAGGTAGCCAAGTTTTTT   80855          CGGA
                                AAGGAGCTTGGTT    GAC
                                ||||||||||||    |||
                                TTTTTTGAACCGA    CTG
                                      TGGA
GAM454  KIAA1862  3'  CCAATGGGCCAAGCTTCCT    69506     _       GAGACA
                                AGGA GCTTGGTTCG     GG
                                ||||| ||||||||||     ||
                                TCCT CGAACCGGGT     CC
                                  T        AA____
GAM454  KIAA1862  3'  GCCTTGAAGGGCTGGGCTCTT  69510       TG   GGAGAC
                                AGGAGCT  GTTC     AGGC
                                |||||||  ||||     ||||
                                TTCTCGG  CGGG     TCCG
                                    GT    AAGT__
GAM454  KIAA1877  3'  GCCTGTCTTTATTATACAGGTT 66752         GTTC__
            TCTT                   AAGGAGCTTG     GGAGACAGGC
                                ||||||||||     ||||||||||
                                TTCTTTGGAC     TTTCTGTCCG
                                      ATATTA
GAM454  KIAA1877  3'  GTTTCAGGATTGGTTTCTT    66760        T    G
                                AAGGAGCT GGTTC GAGAC
                                |||||||| ||||| |||||
                                TTCTTTGG TTAGG CTTTG
                                    _    A
GAM454  KIAA1879  5'  GTCTGGAATCAGGTTCCT    73944          GG
                                AGGAGCTTGGTTC  AGAC
                                ||||||||||||  ||||
                                TCCTTGGACTAAG  TCTG
                                      G_
GAM454  KIAA1924  3'  GTCTGGAGGCCGGACACAGGCT 74058         _     AGA_
            TCTT                   AAGGAGCTTG GTTCGG    CAGGC
                                ||||||||||| ||||||    |||||
                                TTCTTCGGAC CAGGCC    GTCTG
                                      A     GGAG
GAM454  KIAA1972  3'  GTTTGTTTTTTTGTTTTTTGGG 93413        TG TT__  __
            TTTTTT                 AAGGAGCT  G    CG  GAGACAGGC
                                |||||||  |    ||  |||||||||
                                TTTTTTGG  T    GT  TTTTGTTTG
                                    GT TTTT  TT
GAM454  KIAA1975  5'  GTCATGGGTTAAGCCCTT    74426      A     TT  GA
                                AAGG GCTTGG  CG  GAC
                                |||| ||||||  ||  |||
                                TTCC CGAATT  GT  CTG
                                  _     GG  A_
GAM454  KIAA1977  5'  GCCTGTGGTGGTCAGGGTTTTT 74766       G    GT CGGAG
                                AAGGA CTTG  T     ACAGGC
                                ||||| ||||  |     ||||||
```

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                                TTTTT GGAC  G    TGTCCG
                                  G   TG TGG__
GAM454  KIF13B   3'  TTTGTTTTTGGGTCCGCT    83720    TT  TT
                                AGC  GG  CGGAGACAGG
                                |||  ||  ||||||||||
                                TCG  CT  GTTTTTGTTT
                                  C_  GG
GAM454  KIF13B   3'  TTTGTTTTTGGGTCCGCT    31577    TT  TT
                                AGC  GG  CGGAGACAGG
                                |||  ||  ||||||||||
                                TCG  CT  GTTTTTGTTT
                                  C_  GG
GAM454  KLF12    3'  GTCAAGTCTTCTGACTGGGCTT 33280       TG   C     A_
            CTT                   AAGGAGCT  GTT GGAGAC  GGC
                                ||||||||  ||| ||||||  |||
                                TTCTTCGG  CAG CTTCTG  CTG
                                    GT   T     AA
GAM454  KOC1     3'  GCTGCTCTCTGAATTGATTTTT 92718      C TG       _  GC
            T                    AAGGAG T  GTTCGGAGA CAG
                                ||||||  |  |||||||| |||
                                TTTTTT A  TAAGTCTCT GTC
                                   _ GT       C   G
GAM454  KOC1     5'  GTTTGGGTTGTAGCTAGGCTTT 92719           _  AGA
            TT                    AAGGAGCTTGGTT CGG   CAGGC
                                ||||||||||||| |||   |||||
                                TTTTTCGGATCGA GTT   GTTTG
                                      T   GG_
GAM454  LGI3     3'  GCCCTTGAGCTGGGCGGGCTCC 58396         G    AGACA_
            TT                    AAGGAGCTTG TTCGG     GGC
                                ||||||||||  |||||     |||
                                TTCCTCGGGC GGGTC     CCG
                                     _    GAGTTC
GAM454  LNIR     5'  TTCCTGCCTTCTGGGTCAGTTC 48876        T  TT    A_   C
            CTT                   AAGGAGCT GG  CGGAG  CAGG
                                ||||||||  ||  |||||  ||||
                                TTCCTTGA CT  GTCTT  GTCC
                                   _ GG    CC    TTC
GAM454  MAD4     3'  GTCTGTCCCCCCAGGCTTC    22278        TTC  A
                                GGAGCTTGG   GG GACAGGC
                                |||||||||   || |||||||
                                CTTCGGACC   CC CTGTCTG
                                     C__  _
GAM454  MDN1     3'  GCTTTGCCTGGGCTGAGGTTTT 63359      G  TG     AGAC
            T                    AAGGA CT  GTTCGG    AGGC
                                |||||  ||  ||||||    ||||
                                TTTTT GA  CGGGTC    TTCG
                                  G  GT     CGT_
GAM454  MEIS3    3'  GCCTGGGACCCGAGCTGGGCTC 78871       TG     AGA_
            CT                    AGGAGCT  GTTCGG    CAGGC
                                |||||||  ||||||    |||||
```

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                                TCCTCGG  CGAGCC    GTCCG
                                   GT     CAGG
GAM454  MGC10960 3' GCCTGCTGAGATCAGGCTCTTT 51982          T GG  A
                                AAGGAGCTTGGT C  AG CAGGC
                                |||||||||||| |  || |||||
                                TTTCTCGGACTA G  TC GTCCG
                                      _ AG  _
GAM454  MGC12921 5' CCTCAACCGGGCTGAGTTCCT  64511       TG     AGAC   C
                                AGGAGCT  GTTCGG    AGG
                                |||||||  ||||||    |||
                                TCCTTGA  CGGGCC    TCC
                                   GT     AAC_
GAM454  MGC12992 3' TCCTTTGGAATTGAGTTCTTT  51343       TG    G  GAC   C
                                AAGGAGCT  GTTC GA   AGG
                                ||||||||  |||| ||   |||
                                TTTCTTGA  TAAG TT   TCC
                                   GT   G ___   TA
GAM454  MGC13007 3' GTTTGTGAAATTGGTTCTTT   51281       TGG    G
                                AAGGAGCT   TTCG AGAC
                                ||||||||   |||| ||||
                                TTTCTTGG   AAGT TTTG
                                   TTA    G
GAM454  MGC14156 3' GTTTGTTTAGCTTCAAGGTCTT 52961      G    TTCGG
          T                     AAGGA CTTGG    AGACAGGC
                                ||||| |||||    ||||||||
                                TTTCT GAACT    TTTGTTTG
                                  G    TCGA_
GAM454  MGC14289 3' GTTTGTTTAACTACTTGGCTTT 55594       T   TCGG
          TT                     AAGGAGCT GGT    AGACAGGC
                                ||||||||| |||    ||||||||
                                TTTTTCGG TCA    TTTGTTTG
                                   T   TCAA
GAM454  MGC14836 3' GTTATGGGCAAAGCTTTTT    54174       G    GA
                                AAGGAGCTT GTTCG  GAC
                                ||||||||| |||||  |||
                                TTTTTCGAA CGGGT  TTG
                                    A    A_
GAM454  MGC15429 3' GTTTGTCTTTTCTACCTCTTT  52215      CT   TTC
                                AAGGAG  TGG   GGAGACAGGC
                                ||||||  |||   ||||||||||
                                TTTCTC  ATC   TTTCTGTTTG
                                  C_   T__
GAM454  MGC15873 3' GCTTGTTTGCCTGTGCTTTTT  53007       TT_   TCGG
                                AAGGAGC   GGT    AGACAGGC
                                |||||||   |||   ||||||||
                                TTTTTCG   CCG    TTTGTTCG
                                   TGT   _____
GAM454  MGC16025 5' GCCAGTGAGTCCAGGCTCCTT  53023          _   GGAG  A
                                AAGGAGCTTGG TTC    AC GGC
                                |||||||||| |||    || |||
```

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                                TTCCTCGGACC GAG   TG CCG
                                      T  ____  A
GAM454  MGC20253  3'  GTCTTACAGAACTAAGATCTTT 58676     G      G__
                                AAGGA CTTGGTTC  GAGAC
                                ||||| ||||||||  |||||
                                TTTCT GAATCAAG  TTCTG
                                   A       ACA
GAM454  MGC2865   3'  CTCTAAATGGGTCAACTCCTT  51458      C   TT ____
                                AAGGAG TTGG  C   GGAG
                                |||||| ||||  |   ||||
                                TTCCTC AACT  G   TCTC
                                   _   GG TAAA
GAM454  MGC3222   3'  GCCTGTGCTATAAATGAGTTTC 44545        GTTCGG  _
           TT                    AAGGAGCTTG     AG ACAGGC
                                ||||||||||     || ||||||
                                TTCTTTGAGT     TC TGTCCG
                                      AAATA_  G
GAM454  MGC35558  3'  GCACTACTCTGGACTGGGTGCC 59413     A   TG      ACAG
           TT                    AAGG GCT  GTTCGGAG   GC
                                |||| |||  ||||||||   ||
                                TTCC TGG  CAGGTCTC   CG
                                  G  GT       ATCA
GAM454  MGC4677   5'  GTCTGTCTTTGGAAGTATCCTT 54616     GCTTGG
                                AAGGA     TTCGGAGACAGGC
                                |||||     |||||||||||||
                                TTCCT     AGGTTTCTGTCTG
                                   ATGA__
GAM454  MGC5338   3'  CTTTGTATTGAGTTCTTT    44152       TG  T
                                AAGGAGCT  GT CGGAG
                                ||||||||  || |||||
                                TTTCTTGA  TA GTTTC
                                     GT  T
GAM454  MGC5469   3'  GTCTGTGTATTAGCTCTTT   51362       T   T  G
                                AAGGAGCT GGT CG AGAC
                                |||||||| ||| || ||||
                                TTTCTCGA TTA GT TCTG
                                     _  T  G
GAM454  MGC9084   5'  GTTGTGAGGTGAGCTTTTT   54184        G   GA
                                AAGGAGCTTG TTCG  GAC
                                |||||||||| ||||  |||
                                TTTTTCGAGT GAGT  TTG
                                      G   G_
GAM454  MGC9753   3'  GCTTATGGCTGGGTCTGGTTTC 54195       T  TT   AGAC
           TT                    AAGGAGCT GG  CGG   AGGC
                                |||||||| ||  |||   ||||
                                TTCTTTGG CT  GTC   TTCG
                                     T  GG   GGTA
GAM454  MIC2L1    3'  GCCTGTCGGATGGCTAAGTCCT 49601      G      CGGA
           T                     AAGGA CTTGGTT   GACAGGC
                                ||||| |||||||   |||||||
```

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                                TTCCT GAATCGG   CTGTCCG
                                  _      TAGG
GAM454  MMP24    3'  TCTGGCCAGCCAGGCCCTT   22923     A      C  AGA
                                AAGG GCTTGGTT GG   CAGG
                                |||| |||||||| ||   ||||
                                TTCC CGGACCGA CC   GTCT
                                  _      _ G__
GAM454  MRPL43   3'  CTGTGATGGGCTAGGCACTTT  50410     A       GAG
                                AAGG GCTTGGTTCG   ACAG
                                |||| ||||||||||   ||||
                                TTTC CGGATCGGGT   TGTC
                                  A        AG_
GAM454  MRPS28   3'  CTTAGTGGATTGACTCCTT   26698      C TG   GGAG _
                                AAGGAG T  GTTC    AC AGG
                                |||||| |  ||||    || |||
                                TTCCTC A  TAGG    TG TTC
                                   _ GT   _____  A
GAM454  MSTP028  3'  GTTTAGGGATCAAGCCTTT   50067     A       GG
                                AAGG GCTTGGTTC  AGAC
                                |||| |||||||||  ||||
                                TTTC CGAACTAGG  TTTG
                                  _       GA
GAM454  NAF1     3'  GTCCCTGAACTGAGCTGTTT   21342     G   TG     A
                                AAG AGCT  GTTCGG GAC
                                ||| ||||  |||||| |||
                                TTT TCGA  CAAGTC CTG
                                  G   GT     C
GAM454  NET-7    3'  GCTTCCTTGAGCCTAGTTTTTT 25624        T     GA  CA
                                AAGGAGCT GGTTCG  GA  GGC
                                |||||||| ||||||  ||  |||
                                TTTTTTGA CCGAGT  CT  TCG
                                    T     TC  __
GAM454  NFASC    3'  CTGAGCTGGGCTTGGCTCCTT  70855        T      AGA
                                AAGGAGCT GGTTCGG   CAG
                                |||||||| |||||||   |||
                                TTCCTCGG TCGGGTC   GTC
                                    T      GA_
GAM454  NFAT5    3'  TCTTTGAATGGGCTCTTT    57779        T G
                                AAGGAGC T GTTCGGAGA
                                ||||||| | |||||||||
                                TTTCTCG G TAAGTTTCT
                                   _ G
GAM454  NFKBIE   3'  GCTTTCCAGGTGGACAGGGCTT 17053        TG   _____   CAGGC
          CTT                   AAGGAGCT  GTTC   GGAGA
                                ||||||||  ||||   |||||
                                TTCTTCGG  CAGG   CCTTT
                                    GA   TGGA    CG  C
GAM454  NPEPL1   3'  GCTTGTTTCTGTTTGTTACTT  45425    G   TTGGTT
                                AAG AGC     CGGAGACAGGC
                                ||| |||     ||||||||||
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                                TTC TTG     GTCTTTGTTCG
                                  A  TTT___
GAM454  NR6A1    3'  TCTGTCTTTGAACTCTTT    9450      CTT
                                GGAG  GGTTCGGAGACAGG
                                ||||  ||||||||||||||
                                TTTC  TCAAGTTTCTGTCT
                                   ___
GAM454  ORMDL3   3'  GTCATGGAATGGGCTGGGCTCC 74798       TG    GAGA _
           T                     AGGAGCT  GTTCG   CA GGC
                                |||||||  |||||   || |||
                                TCCTCGG  CGGGT   GT CTG
                                    GT    AAG_  A
GAM454  OS4      3'  GCCTGTCCTGTACCGAGCTCT  20390         T  A
                                GGAGCTTGGT CGG GACAGGC
                                |||||||||| ||| |||||||
                                TCTCGAGCCA GTC CTGTCCG
                                      T  _
GAM454  OSBPL2   3'  GTTGTGAACCGGCTCCTT    58493       T     GA
                                AAGGAGCT GGTTCG  GAC
                                |||||||| ||||||  |||
                                TTCCTCGG CCAAGT  TTG
                                   _     G_
GAM454  PAFAH2   3'  GCTTGGATAACTGGGTACTTT  6504      A  TG  CGGAGA
                                AAGG GCT  GTT     CAGGC
                                |||| |||  |||     |||||
                                TTTC TGG  CAA     GTTCG
                                  A  GT   TAG___
GAM454  PARG1    3'  CCTGTTTCAGAAGTTTTT    17867       TGGT  G
                                AGGAGCT    TC GAGACAGG
                                |||||||    || ||||||||
                                TTTTTGA    AG CTTTGTCC
                                   ____  A
GAM454  PARVA    3'  GTTTTGGGATTGAGTTCTTT   37184       TG   G
                                AAGGAGCT  GTTC GAGAC
                                ||||||||  |||| |||||
                                TTTCTTGA  TAGG TTTTG
                                    GT    G
GAM454  PARVA    3'  TGTTTTGGGATTGAGTTCTTT  37186       TG   G
                                AAGGAGCT  GTTC GAGACA
                                ||||||||  |||| ||||||
                                TTTCTTGA  TAGG TTTTGT
                                    GT    G
GAM454  PASK     5'  CTTGGGGCTAGGGTTCTT    31409      G      G
                                AAGGA CTTGGTTC GAG
                                |||||  |||||||| |||
                                TTCTT GGATCGGG TTC
                                  G       G
GAM454  PASK     5'  GTCTGTCCTTTATACAAGCTTT 31419         GTTC_  A
           TT                    AAGGAGCTTG    GG GACAGGC
                                |||||||||     || |||||||
```

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                                TTTTTTCGAAC    TC CTGTCTG
                                      ATATT  _
GAM454  PDE1C    3'  GCATCATTCTAGCTGAGCTTCT 18464       TG   C    ACAG
             T                   AAGGAGCT  GTT GGAG    GC
                                 ||||||||  ||| ||||    ||
                                 TTCTTCGA  CGA TCTT    CG
                                     GT   _    ACTA
GAM454  PELI2    3'  GTTTTTAACCAAGTTTTTT   41458          C
                                 AAGGAGCTTGGTT GGAGAC
                                 |||||||||||| ||||||
                                 TTTTTTGAACCAA TTTTTG
                                                _
GAM454  PGLYRP   3'  GCTTGTTTCGTCCCTGACTCCT 54671      CTT  TT  G
             T                   AAGGAG   GG  CG AGACAGGC
                                 ||||||   ||  || ||||||||
                                 TTCCTC   CC  GC TTTGTTCG
                                    AGT  CT  _
GAM454  POR1     3'  GCCCTCTGGCTTGGGCTCCTT  25730       TG TT    ACA
                                 AAGGAGCT  G  CGGAG   GGC
                                 ||||||||  |  |||||   |||
                                 TTCCTCGG  T  GTCTC   CCG
                                     GT CG    ___
GAM454  PORIMIN  3'  GTACTTTGAATGTAGGTTTTTT 54705         _      _
                                 AAGGAGCTTG GTTCGGAG AC
                                 |||||||||| |||||||| ||
                                 TTTTTTGGAT TAAGTTTC TG
                                       G       A
GAM454  PPP1R3B  3'  TTTTGTGGTTGGGTTAGGTTGT 45150    G      TT   AG    C
             TT                   AAG AGCTTGG  CGG  ACAGG
                                  ||| |||||||  |||  |||||
                                  TTT TTGGATT  GTT  TGTTT
                                    G      GG   GG    TG
GAM454  PRAX-1   3'  GCTCATTGGATTCAAGTTCTTT 17656         GT  G  GACA
                                 AAGGAGCTTG  TC GA    GGC
                                 ||||||||||  || ||    |||
                                 TTTCTTGAAC  AG TT    TCG
                                       TT  G  AC__
GAM454  PRKAG3   3'  CTATGATTCAGGCTTCTT    34288         GT   G
                                 AAGGAGCTTG  TCG AG
                                 ||||||||||  ||| ||
                                 TTCTTCGGAC  AGT TC
                                       TT   A
GAM454  PRO0082  3'  CCCCTGAGTCAGCCTCCTT   38345       C   GT    AGACA
                                 AAGGAG TTG  TCGG     GG
                                 ||||||| |||  ||||    ||
                                 TTCCTC GAC  AGTC     CC
                                    C   TG    C_____
GAM454  PRO1483  5'  ATATGACTTTGGGTCAGTTTCT 38330        T  TT    A  GGC
             T                   AAGGAGCT GG  CGGAG CA
                                 ||||||||  ||  ||||| ||
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                                TTCTTTGA CT  GTTTC GT
                                    _ GG    A  ATAC
GAM454  PRO2015  5'  CCTGCAGGATTGGCTTTTT   38160        T    GGAGA
                                AAGGAGCT GGTTC    CAGG
                                |||||||| |||||    ||||
                                TTTTTCGG TTAGG    GTCC
                                    _    AC___
GAM454  PRRG1    3'  GTTTTATAAACTGAGTTTCTT  8151        TG  CG_
                                AAGGAGCT  GTT  GAGAC
                                ||||||||  |||  |||||
                                TTCTTTGA  CAA  TTTTG
                                     GT  ATA
GAM454  PSKH1    3'  GTCGGCAGCCTGGGCCAGGCCC 68802      A       _ AGACA
            TT                   AAGG GCTTGGTTC GG    GGC
                                |||| |||||||| ||    |||
                                TTCC CGGACCGGG CC    CTG
                                  _       T  GACGG
GAM454  PSR      3'  TCTGTCTTAGGATTCCTT    65795      GCTTG   G
                                AAGGA    GTTC GAGACAGG
                                |||||    |||| ||||||||
                                TTCCT    TAGG TTCTGTCT
                                  _____   A
GAM454  PTR4     3'  GTTGCCTGGATTGATTTCTT   74495       C TG     A_
                                AAGGAG T  GTTCGG  GAC
                                |||||| |  ||||||  |||
                                TTCTTT A  TAGGTC  TTG
                                   _ GT     CG
GAM454  PYY2     3'  GCTTGCCTCCCCGGATCGGATT 41175       CT    __   A
            CCTT                  AAGGAG  TGGTTC  GGAG CAGGC
                                ||||||  ||||||  |||| |||||
                                TTCCTT  GCTAGG  CCTC GTTCG
                                   AG     CC   C
GAM454  RAB24    3'  GTAAGGGCTGGACCCAGCTCCT 56258        T     AG___  AGGC
            T                    AAGGAGCT GGTTCGG    AC
                                |||||||| |||||||    ||
                                TTCCTCGA CCAGGTC    TG
                                     C      GGGAA    C
GAM454  RAGB     5'  GCCTACGGCATGGGTCAGCTCT 34113        T  TT  GAGAC_
            TT                   AAGGAGCT GG  CG     AGGC
                                |||||||| ||  ||     ||||
                                TTTCTCGA CT  GT     TCCG
                                    _ GG  ACGGCA
GAM454  RALGPS1A 3'  CTGTGGAACAGGCTTTTT    28329         G   G
                                AAGGAGCTTG TTCG AG
                                |||||||||| |||| ||
                                TTTTTCGGAC AGGT TC
                                     A   G
GAM454  RASSF2   3'  GCCTGTCTCTATGGCGCTTCCT 29101      _ TTG   C_
            T                    AAGGA GC   GTT  GGAGACAGGC
                                ||||| ||   |||  ||||||||||
```

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                                TTCCT CG   CGG  TCTCTGTCCG
                                  T ___   TA
GAM454  RNF11    3'  CTTGTTTGCACAGTTCTTT   27652        TG  TCGG
                                AAGGAGCT  GT    AGACAGG
                                ||||||||  ||    |||||||
                                TTTCTTGA  CG    TTTGTTC
                                    CA  ____
GAM454  RNF38    3'  CTCCATGAACCTGGTTTTTT   43257        T    __
                                AAGGAGCT GGTTC  GGAG
                                |||||||| |||||  ||||
                                TTTTTTGG CCAAG  CCTC
                                    T    TA
GAM454  SAE1     3'  GCTTGTCTTTCAAGGCCAGGTT 19728          C__
             CC                   GGAGCTTGGTT   GGAGACAGGC
                                ||||||||||   ||||||||||
                                CCTTGGACCGG   TTTCTGTTCG
                                     AAC
GAM454  SCAND2   5'  GTTTGGGACCTGGGCTCGGGCT 54422          _     AGA_
             TCTT                  AAGGAGCTTG GTTCGG    CAGGC
                                |||||||||| ||||||    |||||
                                TTCTTCGGGC CGGGTC    GTTTG
                                    T     CAGG
GAM454  SCYA5    3'  GCCTGTTTCTGCTTGCTCTT   12968       TT   TC
                                AGGAGC  GGT  GGAGACAGGC
                                ||||||  |||  ||||||||||
                                TTCTCG  TCG  TCTTTGTCCG
                                   T_  __
GAM454  SDC3     3'  GCCTGTCTTTTCCAGGCTGGGC 28477       TG  TC  ___
             TCC                   GGAGCT  GT  GGA   GACAGGC
                                ||||||  ||  |||   |||||||
                                CCTCGG  CG  CCT   CTGTCCG
                                   GT  GA   TTT
GAM454  SEC8     3'  GCCTGTCTCTGAATTGTTCC   41737      TT
                                GGAGC  GGTTCGGAGACAGGC
                                |||||  ||||||||||||||
                                CCTTG  TTAAGTCTCTGTCCG
                                   __
GAM454  SEF      3'  GTCTGTTCTCTGGCATCAAGTT 69997          _     _
             TCTT                  AAGGAGCTTGGT TCGGAGA CAGGC
                                |||||||||||| ||||||| |||||
                                TTCTTTGAACTA GGTCTCT GTCTG
                                     C      T
GAM454  SENP2    3'  GTTTGTTTCTGTGTGTTTGTT  76834    G    TTGGTT
                                AA GAGC     CGGAGACAGGC
                                || ||||     ||||||||||
                                TT TTTG     GTCTTTGTTTG
                                 G   TGT___
GAM454  SFXN5    3'  GTTATGAGCCGACTTCTT    58657       C       GA
                                AAGGAG TTGGTTCG  GAC
                                |||||| ||||||||  |||
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                                TTCTTC AGCCGAGT  TTG
                                   _       A_
GAM454  SHANK3   3'  GTTTGGAGTCTGGACTAAGCTC 66111              GA_
            C                    GGAGCTTGGTTCGGA   CAGGC
                                 ||||||||||||||   |||||
                                 CCTCGAATCAGGTCT   GTTTG
                                       GAG
GAM454  SHAPY    3'  GCCTGTCTCTTCCCTGGGGTTT 57911          __  TTC
            CTT                   AAGGAGCTT  GG   GGAGACAGGC
                                  |||||||||  ||   ||||||||||
                                  TTCTTTGGG  CC   TCTCTGTCCG
                                       GT  CT_
GAM454  SLC31A2  3'  GTTGACAAACTAAGTTTTTT   60759            CGGA
                                 AAGGAGCTTGGTT    GAC
                                 ||||||||||||    |||
                                 TTTTTTGAATCAA    TTG
                                       ACAG
GAM454  SLC38A5  5'  GTTTGTTTCTGAGTCTGCCT   54312    A  TT GT
                                 GG GC  G  TCGGAGACAGGC
                                 || ||  |  ||||||||||||
                                 TC CG  C  AGTCTTTGTTTG
                                  _  T_ TG
GAM454  SLC6A14  3'  GCTTTATTTTGAACTAATTTCT 24310        C         AC
            T                    AAGGAG TTGGTTCGGAG  AGGC
                                 ||||||  ||||||||||  ||||
                                 TTCTTT AATCAAGTTTT  TTCG
                                    _          AT
GAM454  SMBP     3'  CTTTGGATCAATTTCTTT     72621        C
                                 AAGGAG TTGGTTCGGAG
                                 ||||||  ||||||||||
                                 TTTCTT AACTAGGTTTC
                                    T
GAM454  SNIP1    3'  TTTGTGGACCAGGTGTTTT    45538      A         G
                                 AAGG GCTTGGTTCG AGA
                                 ||||  ||||||||||  |||
                                 TTTT TGGACCAGGT TTT
                                   G         G
GAM454  SNRK     5'  GTTGGGTGCCGGCTCGGGCTCC 35282           TT   AGA_   GC
            TT                    AAGGAGCTTGG  CGG    CAG
                                  ||||||||||  |||    |||
                                  TTCCTCGGGCT  GCC    GTT
                                       CG   GTGG   G
GAM454  SPRY4    3'  GCCAGGCTGGGTTTGGGTTTCT 49018         TG TT_   AGACA
            T                     AAGGAGCT  G   CGG     GGC
                                  ||||||||  |   |||     |||
                                  TTCTTTGG  T   GTC     CCG
                                       GT TGG   GGA__
GAM454  SRP54    5'  GTCTGTCTGCTCCCAGCTTTCT 13403       _   T  TTC  _
            T                     AAGGA GCT GG   GG AGACAGGC
                                  |||||  ||| ||   || ||||||||
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                                TTCTT CGA CC   TC TCTGTCTG
                                   T   C ___  G
GAM454  SS-56    5'  CTGCGGAACCAGGCTTCTT    60350            _ G
                                AAGGAGCTTGGTTC G AG
                                |||||||||||||| | ||
                                TTCTTCGGACCAAG C TC
                                      G G
GAM454  STAF65(gamma) 5'  CCTGTTCTTCGTGCTCCTT    30068        TTGGTT    _
                                AAGGAGC     CGGAGA CAGG
                                |||||||     |||||| ||||
                                TTCCTCG     GCTTCT GTCC
                                   T_____      T
GAM454  STARD7    5'  GCCTGCGCCCCTCCGGACTGGT 39743         T       A____
           TCCTT                   AAGGAGCT GGTTCGGAG    CAGGC
                                |||||||| |||||||||    |||||
                                TTCCTTGG TCAGGCCTC    GTCCG
                                   _       CCCGC
GAM454  STK17A    3'  GCCTGTTTCTGCTGAGTTTCTT 17668         TG  TC
                                AAGGAGCT  GT  GGAGACAGGC
                                |||||||  ||  ||||||||||
                                TTCTTTGA  CG  TCTTTGTCCG
                                   GT  __
GAM454  STK25     3'  GTTTGTTTTTGTTCTGAGCTCC 22096       TG TT
                                GGAGCT  G  CGGAGACAGGC
                                ||||||  |  ||||||||||
                                CCTCGA  C  GTTTTTGTTTG
                                   GT TT
GAM454  STK3      3'  GTTCTCAAATGGGCTAGGCCTT 74102      A       ___   CAGGC
           T                    AAGG GCTTGGTTCG   GAGA
                                |||| ||||||||||   ||||
                                TTTC CGGATCGGGT   CTCT
                                  _       AAA   TG
GAM454  STMN3     3'  GCCCACACCCTCTGGGCTGAGT 32468         TG      ACA___
           TCCTT                   AAGGAGCT  GTTCGGAG     GGC
                                |||||||  ||||||||     |||
                                TTCCTTGA  CGGGTCTC     CCG
                                   GT       CCACAC
GAM454  SYTL4     3'  GTCTAGTGAGCTAAGTTTC    55786           G_
                                GGAGCTTGGTTCG  AGAC
                                ||||||||||||  ||||
                                CTTTGAATCGAGT  TCTG
                                      GA
GAM454  TADA3L    5'  GCCAGACACTGAACTGGGCTCT 22042        TG     AGACA
           T                    AGGAGCT  GTTCGG    GGC
                                |||||||  ||||||    |||
                                TTCTCGG  CAAGTC    CCG
                                   GT     ACAGA
GAM454  TBL1Y     5'  CTCCGGTGCGCCGGGCTCTTT  53859          ___
                                AAGGAGCTTGGT   TCGGAG
                                ||||||||||||   ||||||
```

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                                TTTCTCGGGCCG  GGCCTC
                                      CGT
GAM454  TP53INP1  3'  CTTCGTGAATGAGTTTCTT   53868        GTT_
                                AAGGAGCTTG   CGGAG
                                ||||||||||   |||||
                                TTCTTTGAGT   GCTTC
                                      AAGT
GAM454  TP53INP1  3'  CTTCGTGAATGAGTTTCTT   53869        GTT_
                                AAGGAGCTTG   CGGAG
                                ||||||||||   |||||
                                TTCTTTGAGT   GCTTC
                                      AAGT
GAM454  TRAF4     3'  GTCTGTCTTGAGATCTGATTTT 63320      C TG T  G_
           TT                    AAGGAG T  G TC  GAGACAGGC
                                ||||||  |  | ||  |||||||||
                                TTTTTT A  C AG  TTCTGTCTG
                                   _ GT T  AG
GAM454  TRIM36    3'  GTCTGTTTTTGAAAGGTGTTGC 38628    G   TTGG
           TT                    AAG AGC    TTCGGAGACAGGC
                                ||| |||    ||||||||||||
                                TTC TTG    AAGTTTTTGTCTG
                                  G   TGGA
GAM454  TRIP-Br2  3'  GCTTTGAATTTGAAGTGAGTTT 29268        G     GA  _
           TTT                    AAGGAGCTTG TTCGGA  CAG GC
                                ||||||||||  ||||||  ||| ||
                                TTTTTTGAGT AAGTTT  GTT CG
                                      G     AA   T
GAM454  TRIP-Br2  3'  GTCTTTACCAATTGAGCTTTTT 29269       TG   C  ___
                                AAGGAGCT  GTT GG   AGAC
                                ||||||||  ||| ||   ||||
                                TTTTTCGA  TAA CC   TCTG
                                     GT   _  ATT
GAM454  WBSCR20A  3'  GCAGAGGCTCCGGGCTGACTCC 50570      C TG       ACAG_
           TT                    AAGGAG T  GTTCGGAG    GC
                                ||||||  |  ||||||||    ||
                                TTCCTC A  CGGGCCTC    CG
                                   _ GT       GGAGA
GAM454  ZD52F10   3'  GCTTGTCTCTCCTTGTTTCTT  53974       TT  TTC
                                AAGGAGC  GG   GGAGACAGGC
                                |||||||  ||   ||||||||||
                                TTCTTTG  CC   TCTCTGTTCG
                                     TT  ___
GAM454  ZFP       3'  CTTTGAGTTAAGCTGTCTT    38471     _    GG
                                AAGG AGCTT  TTCGGAG
                                ||||  |||||  |||||||
                                TTCT TCGAA  GAGTTTC
                                  G    TT
GAM454  ZID       3'  TCATTGGGCCCGAGTTTCTT   22785         TT G  _
                                AAGGAGCTTGG  C GA GA
                                ||||||||||  | || ||
```

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                                TTCTTTGAGCC  G TT CT
                                     CG G  A
GAM454  ZNF33A    3'  GCTAAAATGGACCAATTCCTT  92998       C       GAGACA
                                AAGGAG TTGGTTCG      GGC
                                |||||| ||||||||      |||
                                TTCCTT AACCAGGT      TCG
                                   _       AAAA__
GAM454  ZNF340    5'  CCTGTATACCAGGCTTTT    85712           TCGGAG
                                AGGAGCTTGGT     ACAGG
                                ||||||||||      |||||
                                TTTTCGGACCA     TGTCC
                                     TA____
GAM454  LOC112687 3'  TTTGTCAGCTGGGCCCTT    73246      A   TG   CGGA
                                AAGG GCT  GTT    GACAGG
                                |||| |||  |||    ||||||
                                TTCC CGG  CGA    CTGTTT
                                  _  GT   _____
GAM454  LOC115219 5'  GCTTGTCACCCGCTGGGTTTCT 73698         TG  TC  A
           T                     AAGGAGCT  GT  GG GACAGGC
                                 ||||||||  ||  || |||||||
                                 TTCTTTGG  CG  CC CTGTTCG
                                      GT  C_  A
GAM454  LOC115343 5'  GCTCTGATTGGTCCAGGCTCTT 72533           T____      ACAGGC
           T                     AAGGAGCTTGG     TCGGAG
                                 ||||||||||      ||||||
                                 TTTCTCGGACC     AGTCTC
                                      TGGTT      G   C
GAM454  LOC118738 3'  GCCTGGATTCGAATCTGGGCTC 76004         TG _     GA
           TTT                     AAGGAGCT  G TTCGGA  CAGGC
                                   ||||||||  | ||||||  |||||
                                   TTTCTCGG  C AAGCTT  GTCCG
                                      GT T      AG
GAM454  LOC118851 5'  TGACTTTGAGTCGGGTTTCT   76020         GT      A
                                AGGAGCTTG  TCGGAG CA
                                |||||||||  |||||| ||
                                TCTTTGGGC  AGTTTC GT
                                      TG      A
GAM454  LOC124222 3'  GTCTGCAAGGGGCTGGCTCCTT 74756         T     GGAGA
                                AAGGAGCT GGTTC     CAGGC
                                |||||||| |||||     |||||
                                TTCCTCGG TCGGG     GTCTG
                                   _     GAAC_
GAM454  LOC125144 3'  GTTGGTGGGCAAAGTTCTTT   74854         G     GA
                                AAGGAGCTT GTTCG  GAC
                                ||||||||| |||||  |||
                                TTTCTTGAA CGGGT  TTG
                                      A     GG
GAM454  LOC128077 3'  GCTTGTCTTTGCAGCTTTGTT  75221     TT    _
                                AGC  GGTT CGGAGACAGGC
                                |||  |||| ||||||||||
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                                TTG  TCGA GTTTCTGTTCG
                                  TT    C
GAM454   LOC136015 3'  GCTTGTTACTCATAGTTTCTT  76704        TGGTTC  A
                                AAGGAGCT     GG GACAGGC
                                ||||||||     || |||||||
                                TTCTTTGA     TC TTGTTCG
                                     TAC___  A
GAM454   LOC138389 5'  GTAGCTGGACTGGGCTCTT    76742        TG     AG
                                AGGAGCT  GTTCGG  AC
                                |||||||  ||||||  ||
                                TTCTCGG  CAGGTC  TG
                                     GT     GA
GAM454   LOC143915 3'  CCTGGGGCTGGATCAGGCTTT  83905            AGA    C
                                GGAGCTTGGTTCGG   CAGG
                                ||||||||||||||   ||||
                                TTTCGGACTAGGTC   GTCC
                                         GGG    C
GAM454   LOC143943 3'  GCCTGTTATTTCTGGGTCCTT  83918      G  TG TTCGGA
                                AAGGA CT  G     GACAGGC
                                |||||  ||  |     |||||||
                                TTCCT GG  C     TTGTCCG
                                   _  GT TTTA__
GAM454   LOC144203 3'  GTTTGCAGTGGGCTATGGTTTC 77224          _      GAGA
           TT                     AAGGAGCT TGGTTCG    CAGGC
                                |||||||| |||||||    |||||
                                TTCTTTGG ATCGGGT    GTTTG
                                     T      GAC_
GAM454   LOC144395 3'  GTTATCTTGAATTGGGTTTT   77322        TG    _ _
                                GGAGCT  GTTCG GA GAC
                                ||||||  ||||| || |||
                                TTTTGG  TAAGT CT TTG
                                   GT    T  A
GAM454   LOC144455 3'  GCAATGCCGGGCCCGGTTTCTT 77332          T      AGACAG
                                AAGGAGCT GGTTCGG     GC
                                |||||||| |||||||     ||
                                TTCTTTGG CCGGGCC     CG
                                     C      GTAA__
GAM454   LOC144519 3'  TTTTTGTATCAAGCTCTTT    77382           T
                                AAGGAGCTTGGT CGGAGA
                                |||||||||||| ||||||
                                TTTCTCGAACTA GTTTTT
                                       T
GAM454   LOC144776 3'  GTCTGTCTTTCTTGCCTTCTT  77493      CTT   TC_
                                AGGAG   GGT   GGAGACAGGC
                                |||||   |||   ||||||||||
                                TTCTT   CCG   TTTCTGTCTG
                                   ___   TTC
GAM454   LOC145609 5'  GCCTGCAGGAGCCAGGCTCCT  84366            GGAGA
                                AGGAGCTTGGTTC    CAGGC
                                ||||||||||||     |||||
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                                TCCTCGGACCGAG    GTCCG
                                      GAC__
GAM454  LOC145813 3'  TTTGTTTTTGTTGTTCC    84515      TTGGTT
                                GGAGC     CGGAGACAGG
                                |||||     ||||||||||
                                CCTTG     GTTTTTGTTT
                                   TT____
GAM454  LOC145842 3'  GTTTGTTTCTTATTTAATAGGC 77995          GTTC___
          TTTTT                   AAGGAGCTTG      GGAGACAGGC
                                |||||||||      ||||||||||
                                TTTTTCGGAT      TCTTTGTTTG
                                      AATTTAT
GAM454  LOC146050 3'  CCACTGCGCCGGGCTTTTT   78108           T   AGACA
                                AAGGAGCTTGGT CGG    GG
                                |||||||||||| |||    ||
                                TTTTTCGGGCCG GTC    CC
                                      C   A____
GAM454  LOC146223 3'  GCCTGTCTCTCAGTCAAGTTTT 78207        GT C
                                GGAGCTTG  T GGAGACAGGC
                                ||||||||  | ||||||||||
                                TTTTGAAC  A TCTCTGTCCG
                                     TG C
GAM454  LOC146287 5'  GTTTGTTTTGCTTCAGTTTCTT 84634        T_   TCG
                                AAGGAGCT  GGT   GAGACAGGC
                                ||||||||  |||   |||||||||
                                TTCTTTGA  TCG   TTTTGTTTG
                                     CT   ___
GAM454  LOC146723 3'  GCTGACGCCCGAACTGACTTCT 78682       C TG     AGACA
          T                     AAGGAG T  GTTCGG    GGC
                                ||||||  |  ||||||    |||
                                TTCTTC A  CAAGCC    TCG
                                   _ GT     CGCAG
GAM454  LOC146880 3'  GCTTGTCCTCTGACTAGGTTTC 78750          T    _
          T                     AGGAGCTTGGT CGGAG ACAGGC
                                |||||||||| ||||| ||||||
                                TCTTTGGATCA GTCTC TGTTCG
                                      _    C
GAM454  LOC147239 5'  GGACCCTCCGAGCCAGTCTTTT 85115       C         ACAGGC
          T                     AAGGAG TTGGTTCGGAG
                                |||||| ||||||||||
                                TTTTTC GACCGAGCCTC
                                   T         CCAGGA
GAM454  LOC147276 3'  GCCCTACTCGAGGCGGGCTTTT 78965         G   G  ACA
          T                     AAGGAGCTTG TTCG AG   GGC
                                |||||||||| |||| ||   |||
                                TTTTTCGGGC GAGC TC   CCG
                                      G   _ ATC
GAM454  LOC147463 3'  CTTGTCTCTTTGGTCTTTT   79004      C TG TTC
                                AGGAG T  G   GGAGACAGG
                                ||||| |  |   |||||||||
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                                TTTTC G  T   TCTCTGTTC
                                  T GT ___
GAM454   LOC147694 3'  GTTGTTGAGTTGTAGTTCTTT  79106        _ GG    A
                                AAGGAGCT T  TTCGG GAC
                                |||||||| |  ||||| |||
                                TTTCTTGA G  GAGTT TTG
                                    T TT    G
GAM454   LOC147808 5'  GCCCCCGGAGCCAGGTTCTTT  85197           _  AGACA
                                AAGGAGCTTGGTTC GG    GGC
                                |||||||||||||| ||    |||
                                TTTCTTGGACCGAG CC    CCG
                                      G  C____
GAM454   LOC148438 3'  GTTTTTGCTGGTTAAGTTCTTT 85310         GG  __
                                AAGGAGCTT  TT  CGGAGAC
                                |||||||||  ||  |||||||
                                TTTCTTGAA  GG  GTTTTTG
                                     TT  TC
GAM454   LOC148894 5'  TCTGTAAAATGAGTTCTTT    85423          GTTCGGAG
                                AAGGAGCTTG       ACAGG
                                ||||||||||       |||||
                                TTTCTTGAGT       TGTCT
                                     AAAA____
GAM454   LOC149302 5'  GCCTTCTACTGACCCAAGTTTC 80041           T   _   C
          TT                     AAGGAGCTTGG TCGG AGA AGGC
                                |||||||||| |||| ||| ||||
                                TTCTTTGAACC AGTC TCT TCCG
                                      C    A  _
GAM454   LOC149483 3'  GCAGGTCAGGCTGAGCTCTTT  80187        TG   CGGA   AG
                                AAGGAGCT  GTT    GAC  GC
                                ||||||||  |||    |||  ||
                                TTTCTCGA  CGG    CTG  CG
                                    GT   A___   GA
GAM454   LOC149705 3'  GTTTGTTTTGACCAAAGTTT   85786       _    CG
                                GAGCTT GGTT  GAGACAGGC
                                |||||| ||||  |||||||||
                                TTTGAA CCAG  TTTTGTTTG
                                   A   __
GAM454   LOC149721 3'  GCCTGTCTCCATGTAGGTTCCT 80318         GTTC
                                AGGAGCTTG    GGAGACAGGC
                                |||||||||    ||||||||||
                                TCCTTGGAT    CCTCTGTCCG
                                     GTA_
GAM454   LOC149722 5'  GTTTGTGTTACAGCTCTTT    85757         T GTT  G
                                AAGGAGCT G   CG AGAC
                                |||||||| |   || ||||
                                TTTCTCGA C   GT TTTG
                                    _ ATT  G
GAM454   LOC150150 5'  TCTCTGGTTGAGTTTCTT     86014          GG T
                                AAGGAGCTT  T CGGAGA
                                |||||||||  | ||||||
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                                TTCTTTGAG  G GTCTCT
                                     TT _
GAM454   LOC150280 5'  GCCTGTTTCCAGAGAGCTCTT  80523        GGTTC
                                AGGAGCTT    GGAGACAGGC
                                ||||||||    ||||||||||
                                TTCTCGAG    CCTTTGTCCG
                                     AGA__
GAM454   LOC150311 5'  CTGTAGTAGCTGAGTTCTTT   80563        TG   CGGAG
                                AAGGAGCT  GTT    ACAG
                                ||||||||  |||    ||||
                                TTTCTTGA  CGA    TGTC
                                     GT   TGA__
GAM454   LOC150406 3'  GTCTGGGGCCAAGTTTCT    80674           GG
                                AGGAGCTTGGTTC  AGAC
                                ||||||||||||  ||||
                                TCTTTGAACCGGG  TCTG
                                       G_
GAM454   LOC150498 3'  GTCTCAGAATTTAGGTTCCTT  80722           _  G
                                AAGGAGCTTGG TTC GAGAC
                                ||||||||||| ||| |||||
                                TTCCTTGGATT AAG CTCTG
                                       T   A
GAM454   LOC151009 3'  GTCTGGAACTGGCTCCTT    86375        T    GG
                                AAGGAGCT GGTTC  AGAC
                                |||||||| |||||  ||||
                                TTCCTCGG TCAAG  TCTG
                                     _    G_
GAM454   LOC151414 3'  CCTGTCTCCTGACTGGGCTCCT 81036        TG   C       C
            T                    AAGGAGCT  GTT GGAGACAGG
                                ||||||||  ||| |||||||||
                                TTCCTCGG  CAG CCTCTGTCC
                                     GT   T       A
GAM454   LOC151484 3'  GCCAAGAAATGGGACTGGGCTC 81060        TG    GGAGACA_
            CTT                    AAGGAGCT  GTTC       GGC
                                ||||||||  ||||       |||
                                TTCCTCGG  CAGG       CCG
                                     GT    GTAAAGAA
GAM454   LOC151877 5'  GCCTGTTTCCGGATCCGCC    86699    AGCTT
                                GG    GGTTCGGAGACAGGC
                                ||    ||||||||||||||
                                CC    CTAGGCCTTTGTCCG
                                 GC___
GAM454   LOC152445 5'  GTCTGTTTCTGTCTATGGTTCC 86960        _  TT
            TT                    AAGGAGCT TGG  CGGAGACAGGC
                                |||||||| |||  ||||||||||
                                TTCCTTGG ATC  GTCTTTGTCTG
                                     T  T_
GAM454   LOC152804 3'  GTCTTTTTTTTTGAGTCAGGAT 87087      G   GT     C__
            CTTT                    AAGGA CTTG  TCGGAGA   AGGC
                                |||||  ||||  |||||||   ||||
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                                TTTCT GGAC  AGTTTTT   TCTG
                                   A    TG      TTT
GAM454   LOC154739 5'  GCTGATGGGCTAAGCTTGTT   87440    G          GAGACA
                                AA GAGCTTGGTTCG      GGC
                                || ||||||||||||      |||
                                TT TTCGAATCGGGT      TCG
                                 G           AG_____
GAM454   LOC154788 3'  GCTTGTTACTCATAGTTTCTT  87459         TGGTTC  A
                                AAGGAGCT     GG GACAGGC
                                ||||||||     || |||||||
                                TTCTTTGA     TC TTGTTCG
                                     TAC___  A
GAM454   LOC154877 5'  GTGCCAGACTAAGTTTTTT    87571           TC  AG
                                AAGGAGCTTGGT  GG  AC
                                ||||||||||||  ||  ||
                                TTTTTTGAATCA  CC  TG
                                       GA  G_
GAM454   LOC155100 5'  CTTTAGGACTGGGCTCTTT    73386         TG   _
                                AAGGAGCT  GTTC GGAG
                                ||||||||  |||| ||||
                                TTTCTCGG  CAGG TTTC
                                     GT    A
GAM454   LOC155100 5'  GTGGCTTTAGGACTGGGCTCTT 73387         TG   _    A  GGC
            T                    AAGGAGCT  GTTC GGAG CA
                                ||||||||  |||| |||| ||
                                TTTCTCGG  CAGG TTTC GT
                                     GT    A    G  G
GAM454   LOC157660 3'  GCCTGTTCTTTCTAGGTCTTT  87804      G    TTC    A
                                AAGGA CTTGG   GGAG CAGGC
                                |||||  |||||   ||||  |||||
                                TTTCT GGATC   TCTT GTCCG
                                   _     TT_   _
GAM454   LOC157918 3'  GTCTGTCCACCCGAGTTCT    87932         TTCGGA
                                GGAGCTTGG     GACAGGC
                                |||||||||     |||||||
                                TCTTGAGCC     CTGTCTG
                                     CAC___
GAM454   LOC157919 5'  GTCTGTCCACCCGAGTTCT    82522         TTCGGA
                                GGAGCTTGG     GACAGGC
                                |||||||||     |||||||
                                TCTTGAGCC     CTGTCTG
                                     CAC___
GAM454   LOC158187 3'  GTGACTCCGAAGCTAGGTTTTT 87997            _    A  GGC
            T                    AAGGAGCTTGGTT CGGAG CA
                                ||||||||||||| ||||| ||
                                TTTTTTGGATCGA GCCTC GT
                                       A    A  G
GAM454   LOC158549 5'  CTCCAGGAACCAGTTCCTT    88222         T    __
                                AAGGAGCT GGTTC  GGAG
                                |||||||| |||||  ||||
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                                TTCCTTGA CCAAG  CCTC
                                   _    GA
GAM454   LOC158576 3'  GTCTGTTTCTGGAGAAGTTCT  82852       GG
                                GGAGCTT  TTCGGAGACAGGC
                                |||||||  |||||||||||||
                                TCTTGAA  AGGTCTTTGTCTG
                                   G_
GAM454   LOC158801 5'  GTTGCGCGGGCTGGGTTTTT  88256       TG    GA_
                                AGGAGCT  GTTCG   GAC
                                |||||||  |||||  |||
                                TTTTTGG  CGGGC   TTG
                                   GT    GCG
GAM454   LOC158969 5'  GCCTGTTTTCCAAGGCTTCCT  82936     _   GGTTC
                                AGGA GCTT    GGAGACAGGC
                                |||| ||||    ||||||||||
                                TCCT CGGA    CTTTTGTCCG
                                  T   AC___
GAM454   LOC196540 5'  GCCCTTTAGATTGGGCTCCTT  91202       TG   CG   ACA
                                AAGGAGCT  GTT  GAG   GGC
                                ||||||||  |||  |||   |||
                                TTCCTCGG  TAG  TTC   CCG
                                   GT   AT   ___
GAM454   LOC199899 3'  CCGTGGAACAAGTTCTTT    91465         G   GGAG  A
                                AAGGAGCTTG TTC    AC GG
                                ||||||||||| |||    || ||
                                TTTCTTGAAC AAG    TG CC
                                   _   G___  A
GAM454   LOC199998 3'  GTCTTCATCTGAGTTAAATTCT 91519       C  GG     _  C
           TT                    AAGGAG TT  TTCGGA GA AGGC
                                ||||||  ||  ||||||  ||  ||||
                                TTTCTT AA  GAGTCT CT TCTG
                                   A  TT     A  _
GAM454   LOC200014 3'  CTTATGGGCTGAGTTTCT    89933        TG    _
                                AGGAGCT  GTTCG GAG
                                |||||||  |||||  |||
                                TCTTTGA  CGGGT TTC
                                   GT    A
GAM454   LOC200058 3'  GCCACCTTGGGCCAGGCTCCT  89961            G  ACA
                                AGGAGCTTGGTTCG AG   GGC
                                ||||||||||||||  ||   |||
                                TCCTCGGACCGGGT TC   CCG
                                      _  CA_
GAM454   LOC200149 5'  CTAATGGCCAGGTTTCTT    90972           CGG
                                AAGGAGCTTGGTT   AG
                                ||||||||||||   ||
                                TTCTTTGGACCGG   TC
                                      TAA
GAM454   LOC200150 3'  GCTTAGCATGAGGTGGGCTCTT 89995          G    GAGAC
           T                     AAGGAGCTTG TTCG     AGGC
                                ||||||||| ||||     ||||
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                                TTTCTCGGGT GAGT     TTCG
                                      G    ACGA_
GAM454   LOC200314 3'  CCGTTTCTCTAACCGGGCTTTT 91597            C     CA_  C
                T                    AAGGAGCTTGGTT GGAGA   GG
                                     |||||||||||| |||||   ||
                                     TTTTTCGGGCCAA TCTCT   CC
                                           _    TTG  T
GAM454   LOC200317 3'  GTCTGCTGAATTGGCTTCTT   90228         T      _
                                     AAGGAGCT GGTTCGG AGAC
                                     |||||||| ||||||| ||||
                                     TTCTTCGG TTAAGTC TCTG
                                        _      G
GAM454   LOC200854 5'  TCCTGTCCTGGATCAGTTCCTT 88812         T      A      C
                                     AAGGAGCT GGTTCGG GACAGG
                                     |||||||| ||||||| ||||||
                                     TTCCTTGA CTAGGTC CTGTCC
                                        _      _     TG
GAM454   LOC201456 3'  GTCCTCACTGGACCGAGTCTCT 89616       _         A  CA
                T                    AGGAG CTTGGTTCGG GA  GGC
                                     ||||| ||||||||| ||  |||
                                     TTCTC GAGCCAGGTC CT  CTG
                                        T        A  C_
GAM454   LOC201696 3'  GTTTGTTTTTTCCTTCTGGCTT 63828         T  TTC_
                CTT                    AAGGAGCT GG    GGAGACAGGC
                                     |||||||| ||    ||||||||||
                                     TTCTTCGG CT    TTTTTGTTTG
                                          T  TCCT
GAM454   LOC202934 3'  CCACTGTGCCAGGCTCCTT    92033           T   AGACA
                                     AAGGAGCTTGGT CGG     GG
                                     |||||||||||| |||     ||
                                     TTCCTCGGACCG GTC     CC
                                           T   A____
GAM454   LOC203221 5'  GCCTGTTTCTGGAGCATCTTC  91108      CT  G
                                     GGAG  TG TTCGGAGACAGGC
                                     ||||  || ||||||||||||
                                     CTTC  AC AGGTCTTTGTCCG
                                       T_  G
GAM454   LOC203274 5'  GTAGCTGGACTGGGCTCTT    92102        TG     AG
                                     AGGAGCT  GTTCGG  AC
                                     |||||||  ||||||  ||
                                     TTCTCGG  CAGGTC  TG
                                        GT     GA
GAM454   LOC219735 5'  GTTCGTACCTTTGGGTGAAGTT 94733         G TT    __  AG
                CTTT                    AAGGAGCTT G  CGGAG  AC  GC
                                     |||||||||  |  |||||  ||  ||
                                     TTTCTTGAA T  GTTTC  TG  TG
                                           G GG    CA  CT
GAM454   LOC219818 3'  GCTGCAGCGTTGCATTGGGCTT 92537         TG  T   AGACA_
                CTT                    AAGGAGCT  GT CGG     GGC
                                     ||||||||  || |||     |||
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                                TTCTTCGG  TA GTT     TCG
                                    GT  C   GCGACG
GAM454   LOC219920 5'  GCCTGTCTCCGGGCTCTGCCTC 94953     GA  TT
           TT                    AAG  GC  GGTTCGGAGACAGGC
                                 |||  ||  ||||||||||||||||
                                 TTC  CG  TCGGGCCTCTGTCCG
                                   TC  TC
GAM454   LOC219920 5'  GCTGTGATTTTGAACTGAGCTC 94955       TG      __    GC
           CT                    AGGAGCT  GTTCGGAG  ACAG
                                 |||||||  ||||||||  ||||
                                 TCCTCGA  CAAGTTTT  TGTC
                                    GT       AG    G
GAM454   LOC220018 5'  TGACTTTGGGCAAGTTCCTT   95031         G      A
                                 AAGGAGCTTG TTCGGAG CA
                                 ||||||||||| |||||||  ||
                                 TTCCTTGAAC GGGTTTC GT
                                      _      A
GAM454   LOC220115 5'  ACATTTTTTTTTGACGTTAAGTT 93401         GG _      CAGGC
           TCTT                    AAGGAGCTT  T TCGGAGA
                                 |||||||||  | |||||||
                                 TTCTTTGAA  G AGTTTTT
                                      TT C      TTTACAT
GAM454   LOC221416 3'  GTCTCCCCTGGGACTAGGTTCT 95409             ____     AGGC
           TT                    AAGGAGCTTGGTTC    GGAGAC
                                 ||||||||||||||    ||||||
                                 TTTCTTGGATCAGG    CCTCTG
                                       GTCC
GAM454   LOC221814 3'  GTCTGTTTTGTGTCTTTGATTT 95560       C TG TT_  _
           TCTT                    AAGGAG T  G   CG GAGACAGGC
                                 ||||||  |  |   ||  |||||||||
                                 TTCTTT A  T   GT TTTTGTCTG
                                    T GT TCT  G
GAM454   LOC221889 3'  CCTGTTTGTGCGTTTTTT     94107        TTGGTT  G
                                 AAGGAGC     CG AGACAGG
                                 |||||||      || |||||||
                                 TTTTTTG     GT TTTGTCC
                                    C_____  G
GAM454   LOC221955 3'  GTTTGTTTTTCAAACTGGGCTT 58268      _  TG   C_
           CCT                    AGGA GCT  GTT  GGAGACAGGC
                                 ||||  |||  |||  ||||||||||
                                 TCCT CGG  CAA  TTTTTGTTTG
                                   T   GT   AC
GAM454   LOC222070 5'  CCTGGAGAACAGGCTCCTT    95813         G   GGAGA
                                 AAGGAGCTTG TTC     CAGG
                                 |||||||||| |||     ||||
                                 TTCCTCGGAC AAG     GTCC
                                       _   AG___
GAM454   LOC222134 5'  GTTTGTTGTCATTCAGCTCTTT 95801         T  TTC GA
                                 AAGGAGCT GG   G  GACAGGC
                                 |||||||| ||   |  |||||||
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                                TTTCTCGA CT   C  TTGTTTG
                                    _  TA_ TG
GAM454   LOC222174 3'  GTTTAATTTTGTGTTAAGCTTT 95764          TT    AC
           TT                    AAGGAGCTTGG  CGGAG  AGGC
                                 ||||||||||  |||||  ||||
                                 TTTTTCGAATT  GTTTT  TTTG
                                       GT    AA
GAM454   LOC245771 3'  TTTGTCTCTAAGCCCCTT    94493     AGCTT   CG
                                 AAGG    GGTT  GAGACAGG
                                 ||||    ||||  ||||||||
                                 TTCC    CCGA  CTCTGTTT
                                   _____   AT
GAM454   LOC253289 3'  GCCTGGACAGGCAAAGCTCTTT 97764         G   CGGAGA
                                 AAGGAGCTT GTT     CAGGC
                                 |||||||||  |||     |||||
                                 TTTCTCGAA CGG     GTCCG
                                      A   ACAG__
GAM454   LOC254018 5'  CCTGCCTGACCGGTTTCTT    98739        T   C  AGA
                                 AAGGAGCT GGTT GG   CAGG
                                 ||||||||  |||| ||   ||||
                                 TTCTTTGG CCAG CC   GTCC
                                     _    T  ___
GAM454   LOC254122 3'  GTTCCCAGCTAGGCTCTTT    96396           C  AG
                                 AAGGAGCTTGGTT GG  AC
                                 ||||||||||||| ||  ||
                                 TTTCTCGGATCGA CC  TG
                                       _  CT
GAM454   LOC254128 3'  CTTGTGTGCGGAGCTCCTT    97358         G  TCGGAG
                                 AAGGAGCTT GT     ACAGG
                                 |||||||||  ||     |||||
                                 TTCCTCGAG CG     TGTTC
                                      G  TG____
GAM454   LOC254428 3'  TTTGGATGTAGGCTTTTT    97204          _
                                 AAGGAGCTTG GTTCGGA
                                 ||||||||||  |||||||
                                 TTTTTCGGAT TAGGTTT
                                       G
GAM454   LOC254944 3'  GCCTGTGAGACCAGTGGGCTCC 99003         ___    CGGAG
           TT                    AAGGAGCT   TGGTT    ACAGGC
                                 ||||||||   |||||    ||||||
                                 TTCCTCGG   ACCAG    TGTCCG
                                     GTG    AG___
GAM454   LOC255193 3'  GCCTTCAAGGATCGGGTTTTTT 97104            GGA  C
                                 AAGGAGCTTGGTTC   GA AGGC
                                 ||||||||||||||   || ||||
                                 TTTTTTGGGCTAGG   CT TCCG
                                       AA_  _
GAM454   LOC255231 3'  GCCTGTTTTCCTGTGGGTTTTC 97121       _  GGTTC
           TT                    AAGGAG CTT    GGAGACAGGC
                                 ||||||  |||    ||||||||||
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                                TTCTTT GGG    CTTTTGTCCG
                                   T  TGTC_
GAM454  LOC255242 3'  GTCTGTGTATTAGCTCTTT   97617       T  T  G
                                AAGGAGCT GGT CG AGAC
                                |||||||| ||| || ||||
                                TTTCTCGA TTA GT TCTG
                                    _  T  G
GAM454  LOC255326 3'  GTTTAGTGTATCAGGCTTTTT  98123         T  G_
                                AAGGAGCTTGGT CG  AGAC
                                |||||||||||| ||  ||||
                                TTTTTCGGACTA GT  TTTG
                                      T  GA
GAM454  LOC255328 3'  GTCAGCATGGGCTAAGTTTTTT 98346           GA__
                                AAGGAGCTTGGTTCG   GAC
                                ||||||||||||||   |||
                                TTTTTTGAATCGGGT   CTG
                                     ACGA
GAM454  LOC255391 5'  GTTTGCGCAGTCTGGGTTTCTT 99459       TG _ _ G
                                AAGGAGCT  G TT CG AGAC
                                ||||||||  | || || ||||
                                TTCTTTGG  C GA GC TTTG
                                   GT T  C  G
GAM454  LOC255465 3'  CCACTGTGCCAGGCTCCTT   99108         T  AGACA
                                AAGGAGCTTGGT CGG   GG
                                |||||||||||| |||   ||
                                TTCCTCGGACCG GTC   CC
                                     T  A____
GAM454  LOC256790 5'  GCCTTCCCAACTGGGACAGGCT 96493        GT   A___  C
          CTTT                   AAGGAGCTTG  TCGG   GA AGGC
                                ||||||||||  ||||   || ||||
                                TTTCTCGGAC  GGTC   CT TCCG
                                   AG   AACC  _
GAM454  LOC257109 3'  GCCTGTGGGAATGAGTCAGGCT 97306       GT   GAG__
          TCT                    AGGAGCTTG  TCG    ACAGGC
                                |||||||||  |||   ||||||
                                TCTTCGGAC  AGT    TGTCCG
                                   TG  AAGGG
GAM454  LOC257449 3'  GCCTGACATTGGTCAGGTTCTT 63378        GT CGGAGA
          T                     AAGGAGCTTG  T    CAGGC
                                ||||||||||  |    |||||
                                TTTCTTGGAC  G    GTCCG
                                   TG TTACA_
GAM454  LOC50999  3'  GTCTGTTTTTAACAGGTTCT  32639       GTTC
                                GGAGCTTG   GGAGACAGGC
                                ||||||||   ||||||||||
                                TCTTGGAC   TTTTTGTCTG
                                   AA__
GAM454  LOC51145  3'  GTCATTGATTGGGTTTTTT   32927       TG  T  A
                                AAGGAGCT  GT CGG GAC
                                ||||||||  || ||| |||
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                                TTTTTTGG  TA GTT CTG
                                    GT  _   A
GAM454  LOC51177  3' GTTGCTGGATAAAGCTTTTT  33247        G     AG
                                AAGGAGCTT GTTCGG  AC
                                ||||||||| ||||||  ||
                                TTTTTCGAA TAGGTC  TG
                                    A     GT
GAM454  LOC51204  5' CAATTCGGGTGAGTTCCTT   33463        G TT   GACAG
                                AAGGAGCTT G  CGGA    G
                                ||||||||| |  ||||    |
                                TTCCTTGAG T  GCTT    C
                                    _ GG   AA__
GAM454  LOC51233  5' CCTGGGGTCAGGCTGCTT    33611     G      TT GGAGA
                                AAG AGCTTGG  C    CAGG
                                ||| |||||||  |    ||||
                                TTC TCGGACT  G    GTCC
                                  G      GG _____
GAM454  LOC51301  3' GCCTGCAGTTGGCTAGGTTTTT 33906          T   AGA
            T                    AAGGAGCTTGGT CGG   CAGGC
                                ||||||||||| |||   |||||
                                TTTTTTGGATCG GTT   GTCCG
                                      _   GAC
GAM454  LOC51326  3' GTCTCCCTGAATTAAGCTTTT  34039          __
                                AGGAGCTTGGTTC  GGAGAC
                                ||||||||||||  ||||||
                                TTTTCGAATTAAG  CCTCTG
                                     TC
GAM454  LOC57019  3' GTTTCAGAATGGGATGGGTTTC 40093       ____ G   G    AGGC
            TT                    AAGGAGCT    T GTTC GAGAC
                                ||||||||    | |||| |||||
                                TTCTTTGG    G TAAG CTTTG
                                    GTAG G    A       C
GAM454  LOC89985  5' GCCTGTCTTAGCCTGAGCTGCT 61674     G    _   CG
            T                    AAG AGCTT GGTT  GAGACAGGC
                                ||| ||||| ||||  |||||||||
                                TTC TCGAG CCGA  TTCTGTCCG
                                  G    T   __
GAM454  LOC90288  5' CTTCTGCAGTCTGAGCTGAGCG 62787     A  TG     GA_   C
            CCTT                   AAGG GCT  GTTCGGA   CAGG
                                |||| |||  |||||||   ||||
                                TTCC CGA  CGAGTCT   GTCT
                                  G   GT      GAC    TCG
GAM454  LOC90639  5' GCTTTGGATGGATTGACTTCTT 64412       C TG    GAGA  _
                                AAGGAG T  GTTCG    CAG GC
                                |||||| |  |||||    ||| ||
                                TTCTTC A  TAGGT    GTT CG
                                   _ GT    AG__   T
GAM454  LOC90843  5' GCCTGTTTCCCTGTAGCAGCTC 64877        TGGTTC_
            CTT                    AAGGAGCT      GGAGACAGGC
                                ||||||||      ||||||||||
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                                TTCCTCGA      CCTTTGTCCG
                                     CGATGTC
GAM454  LOC90874  3' GCTTGGAGGACCAGGCACTTT  64918      A        GGAGA
                                AAGG GCTTGGTTC     CAGGC
                                |||| |||||||||     |||||
                                TTTC CGGACCAGG     GTTCG
                                  A        AG___
GAM454  LOC90917  3' GCCTGTCTTATTCATGCTTCTT 64986        T   TTCG
                                AAGGAGC TGG    GAGACAGGC
                                ||||||| |||    |||||||||
                                TTCTTCG ACT    TTCTGTCCG
                                     T   TA__
GAM454  LOC90981  3' TCTGTTTGAACCAAGTTTT    65143           GA     C
                                GGAGCTTGGTTCG  GACAGG
                                ||||||||||||  ||||||
                                TTTTGAACCAAGT  TTGTCT
                                        __      A
GAM454  LOC91056  3' GTCTAGGGTCTGAGACCAAGTT 96408           _    GAC_
           TTTT                    AAGGAGCTTGGT TCGGA    AGGC
                                ||||||||||| |||||    ||||
                                TTTTTTGAACCA AGTCT    TCTG
                                       G     GGGA
GAM454  LOC91156  3' GCCTGCAGGATGGGCCGGCTCC 65711         T     GAGA_
           TT                    AAGGAGCT GGTTCG     CAGGC
                                |||||||| ||||||     |||||
                                TTCCTCGG CCGGGT     GTCCG
                                     _      AGGAC
GAM454  LOC92710  5' GCCTCTTGGGGCAAGCTCCTT  70865         G   G    CA
                                AAGGAGCTTG TTC GAGA  GGC
                                |||||||||| ||| ||||  |||
                                TTCCTCGAAC GGG TTCT  CCG
                                       _   G    __
GAM454  LOC92710  3' GTCTGTCTTTGTGAGGCTGCTT 70868     G     G TT
                                AAG AGCTT G  CGGAGACAGGC
                                ||| ||||| |  ||||||||||
                                TTC TCGGA T  GTTTCTGTCTG
                                  G     G __
GAM454  LOC93259  5' GTCCTAGAGTGGACAGAGCTTT 72291         G   _____  A   AGGC
           TT                    AAGGAGCTT GTTC     GG GAC
                                ||||||||| ||||     || |||
                                TTTTTCGAG CAGG     TC CTG
                                       A    TGAGA  _      C
GAM454  LOC96573  5' GCCTGTTTTTCTCGCAGGCTCT 63872         GTTC
                                GGAGCTTG    GGAGACAGGC
                                ||||||||    ||||||||||
                                TCTCGGAC    TTTTTGTCCG
                                     GCTC
GAM454  LOC96810  3' TCGGCTGGACCAGCTTCTT    71087         T      A_
                                AAGGAGCT GGTTCGG  GA
                                |||||||| |||||||  ||
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                                TTCTTCGA CCAGGTC  CT
                                    _      GG
GAM455  ABCE1    3'  TTTTTCTGTTGGGCAGCCA   60263      AAGGA  TG
                                TGGC    CC  ATGGAGAAG
                                ||||    ||  |||||||||
                                ACCG    GG  TGTCTTTTT
                                  AC___  GT
GAM455  ADPRT    3'  TTTTTTTGTTTGCCTCTTGTGG 9662      G     ACCT  TG
              TG                  TAT GCAAGG    GA  GAGAAG
                                ||| ||||||   ||  ||||||
                                GTG TGTTCT    TT  TTTTTT
                                  G     CCGT  GT
GAM455  AGC1     3'  CTTCTTGTCGCTTTTTGTCATA 25952          CC   TG A
                                TATGGCAAGGA  TGA  G GAAG
                                ||||||||||  |||  | ||||
                                ATACTGTTTTT  GCT  T CTTC
                                      C_  GT _
GAM455  ANKH     5'  TTTTTCCCGGCAGATCTTTGTT 55079    TG      C   AT_
              GTG                   TA  GCAAGGA CTG   GGAGAAG
                                ||  ||||||| |||   |||||||
                                GT  TGTTTCT GAC   CCTTTTT
                                 GT      A   GGC
GAM455  ANXA4    3'  TTTTTTTAGGTTTTGTCCATA  63432      _   G     TG
                                TATGG CAAG ACCTGA  GAG
                                ||||| |||| ||||||  |||
                                ATACC GTTT TGGATT  TTT
                                   T   _     TT
GAM455  ARHC     5'  CTTTTCCGTGGACCTTTGCTAT 18970         AC  G
                                ATGGCAAGG  CT ATGGAGAAG
                                |||||||||  || |||||||||
                                TATCGTTTC  GG TGCCTTTTC
                                     CA  _
GAM455  ATP6V1C1 3'  CTTCCAGGATTTTGTTATA   9890          A    AT
                                TATGGCAAGG CCTG  GGAG
                                |||||||||| ||||  ||||
                                ATATTGTTTT GGAC  CTTC
                                     A   __
GAM455  BACH1    3'  TTTTTTTAACAGTTTGCTATA  8636          GAC   A
                                TATGGCAAG   CTG TGGAGAAG
                                |||||||||   ||| ||||||||
                                ATATCGTTT   GAC ATTTTTTT
                                     ___   A
GAM455  BACH2    3'  TTTTTCTCGTGGTTTTTATTGT 41793    TG C      _  T     G
              A                   TA  G AAGGACC TGA GGAGAA
                                ||  | ||||||| ||| ||||||
                                AT  T TTTTTGG GCT CTTTTT
                                 GT A      T  _
GAM455  BAZ2A    3'  CTTTTCTGTTTTATTTGCTA   26509        GACCT
                                TGGCAAG    GATGGAGAAG
                                |||||||    ||||||||||
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                                ATCGTTT    TTGTCTTTTC
                                   ATT__
GAM455  BCAT1    3'  CTTTTCCAAAACTTTTAGCCAT 66786       A   CCTGA
             A                   TATGGC AGGA    TGGAGAAG
                                 ||||||| ||||    ||||||||
                                 ATACCG TTTT    ACCTTTTC
                                    A   CAAA_
GAM455  BCL10    3'  CTTTTCCACTCCATTGTCGTA  15369        _  CCTGA
                                 TATGGCAA GGA    TGGAGAAG
                                 |||||||| |||    ||||||||
                                 ATGCTGTT CCT    ACCTTTTC
                                     A  C____
GAM455  C8A      5'  TTTTTTCATCCTACTTTGTTTT 6903     TG     ACCT
             A                   TA  GCAAGG   GATGGAGAAG
                                 ||  ||||||   ||||||||||
                                 AT  TGTTTC   CTACTTTTTT
                                  TT     ATC_
GAM455  CAPON    3'  CTTCTCCAGGCCCTTGCT    64660       A   GAT
                                 GGCAAGG CCT   GGAGAAG
                                 ||||||| |||   |||||||
                                 TCGTTCC GGA   CCTCTTC
                                    C   ___
GAM455  CAST     3'  TTTCTAGAATGGTTTTTGTT   10020         TGA_     AG
                                 GGCAAGGACC    TGGAGA
                                 ||||||||||    ||||||
                                 TTGTTTTTGG    ATCTTT
                                       TAAG
GAM455  CCND2    3'  TTTCTCCATCAGTGGGGGCCG  10058      AAGGAC
                                 TGGC     CTGATGGAGAAG
                                 ||||     ||||||||||||
                                 GCCG     GACTACCTCTTT
                                   GGGGT_
GAM455  CCNG1    3'  TTTCTCCACAACCTTGTTCTA  15775    TG     ACC  A
                                 TA  GCAAGG   TG TGGAGAAG
                                 ||  ||||||   || ||||||||
                                 AT  TGTTCC   AC ACCTCTTT
                                  CT     A__  _
GAM455  CD53     3'  TTTCTTTATTAGAGGGCC     6902      AAGGAC
                                 GGC     CTGATGGAGAAG
                                 |||     ||||||||||||
                                 CCG     GATTATTTCTTT
                                   GGA___
GAM455  CDC2L1   5'  CTTCTTCGGTGAAGTTCTTTTG 54258     TG C      CTGA_
             TA                    TA  G AAGGAC    TGGAGAAG
                                   ||  | ||||||    ||||||||
                                   AT  T TTCTTG    GCTTCTTC
                                    GT _     AAGTG
GAM455  CERD4    3'  TTTCTCTGTTGAGGATGC    24887     AGGA  _
                                 GCA    CCT GATGGAGAAG
                                 |||    ||| ||||||||||
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                                CGT   GGA TTGTCTCTTT
                                  A___  G
GAM455  CHD2    3'  CTTTTTCAGGTCTTGCTGT   8867        G    TG
                                ATGGCAAG ACCTGA  GAG
                                |||||||| ||||||  |||
                                TGTCGTTC TGGACT  TTC
                                    _     TT
GAM455  CHN2    3'  CTCAGGTTGGGTCTTTTGCTGT 15796        _   TG  G_   AAG
                  G                  TATGGCAAG GACC  AT  GAG
                                |||||||||| ||||  ||  |||
                                GTGTCGTTT CTGG  TG  CTC
                                     T   GT  GA
GAM455  CLN5    3'  TTCTTCATTGTTTCCTGT    22436     A   CC
                                GCA GGA  TGATGGAGAA
                                ||| |||  ||||||||||
                                TGT CCT  GTTACTTCTT
                                  _  TT
GAM455  CLOCK   3'  CTTCTCTGTCCTCTGCTTTGCT 18113         ACCT_
                  GT                  ATGGCAAGG    GATGGAGAAG
                                |||||||||    ||||||||||
                                TGTCGTTTC    CTGTCTCTTC
                                     GTCTC
GAM455  COL13A1  5'  TTTTTCCGTCCTCTTTGCCG   19043        CCT
                                TGGCAAGGA   GATGGAGAAG
                                |||||||||   ||||||||||
                                GCCGTTTCT   CTGCCTTTTT
                                     C__
GAM455  COL13A1  5'  TTTTTCCGTCCTCTTTGCCG   55852        CCT
                                TGGCAAGGA   GATGGAGAAG
                                |||||||||   ||||||||||
                                GCCGTTTCT   CTGCCTTTTT
                                     C__
GAM455  COL19A1  3'  TTTTTTCGTTTTCTTTCTTGT  10269       CCT_
                                GCAAGGA    GATGGAGAAG
                                |||||||    ||||||||||
                                TGTTCTT    TTGCTTTTTT
                                    TCTT
GAM455  CR2     3'  TTTCTTTAGCAGTTTTGTGATA 10292     G     AC   A
                                TAT GCAAGG  CTG TGGAGAAG
                                ||| ||||||  ||| ||||||||
                                ATA TGTTTT  GAC ATTTCTTT
                                  G     __  G
GAM455  CREBBP  3'  TTTTTCCGTTTTGTTTTTGTTT 16497   T       CT
                  G                  A GGCAAGGAC  GATGGAGAAG
                                | |||||||||  ||||||||||
                                G TTGTTTTTG  TTGCCTTTTT
                                 T       TT
GAM455  CSRP1   3'  TTTCTCTGTCAGCCCTGCCA   15816      A  AC
                                TGGCA GG  CTGATGGAGAAG
                                ||||| ||  ||||||||||||
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                                ACCGT CC  GACTGTCTCTTT
                                  _ C_
GAM455  CYP1A1   3'  CTTCTCTACACTCTTGTAATA  6689     G    ACC  A
                                TAT GCAAGG   TG TGGAGAAG
                                ||| ||||||   || ||||||||
                                ATA TGTTCT   AC ATCTCTTC
                                  A    C__  _
GAM455  CYP7B1   3'  TTTTTTTAGTTTCTCCTTGTTG 17876    TG     CCTGA
           TG                    TA  GCAAGGA    TGGAGAAG
                                ||  |||||||    ||||||||
                                GT  TGTTCCT    ATTTTTTT
                                 GT     CTTTG
GAM455  DAB2     5'  CTTCTCCATCGGGATCGCC   9036     AA  A
                                GGC  GG CCTGATGGAGAAG
                                |||  || ||||||||||||
                                CCG  CT GGGCTACCTCTTC
                                  __  A
GAM455  DAB2     3'  TTCTCCCATTTCTTGCTA    9039         CC  AT
                                TGGCAAGGA  TG  GGAGAA
                                |||||||||  ||  ||||||
                                ATCGTTCTT  AC  CCTCTT
                                     T_  __
GAM455  DAG1     3'  CTTTTTTATTTTTATTTTTTGC 16555        CCT__
           C                     GGCAAGGA    GATGGAGAAG
                                ||||||||    ||||||||||
                                CCGTTTTT    TTATTTTTTC
                                     TATTT
GAM455  DCT      3'  CTTTGACATAGGTTCTTCTATA 10396      C       A  GA
                                TATGG AAGGACCTG TG  GAAG
                                ||||| |||||||| ||  ||||
                                ATATC TTCTTGGAT AC  TTTC
                                  _       _ AG
GAM455  DMD      5'  TTTTTTTATCGCTGCCTTGATA 5469      G    ACC
           TA                    TATG CAAGG   TGATGGAGAAG
                                |||| |||||   ||||||||||
                                ATAT GTTCC   GCTATTTTTTT
                                  A    GTC
GAM455  DSC3     3'  CTACAATTAGGTCTTTGTCA   10438           GG_
                                TGGCAAGGACCTGAT   AG
                                ||||||||||||||   ||
                                ACTGTTTCTGGATTA   TC
                                       ACA
GAM455  DSC3     3'  CTACAATTAGGTCTTTGTCA   44620           GG_
                                TGGCAAGGACCTGAT   AG
                                ||||||||||||||   ||
                                ACTGTTTCTGGATTA   TC
                                       ACA
GAM455  DUSP5    3'  CTTTTCTGGATTTTTTTTGCCA 16631         CCTGA
           TG                    TATGGCAAGGA    TGGAGAAG
                                ||||||||||    ||||||||
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                                GTACCGTTTTT    GTCTTTTC
                                     TTTAG
GAM455  EFNA3    3'  CTTTTTCAAGTGCTTTGGCTGT 18252      _   AC  GA
              G                   TATGGC AAGG  CT  TGGAGAAG
                                  ||||||| ||||  ||  ||||||||
                                  GTGTCG TTTC  GA  ACTTTTTC
                                     G   GT  __
GAM455  EGLN1    3'  TTTTTTCATTCTTATATTTTGC 42150       ACCT__
              CA                   TGGCAAGG    GATGGAGAAG
                                  ||||||||     ||||||||||
                                  ACCGTTTT     TTACTTTTTT
                                       ATATTC
GAM455  EHD3     3'  CTTCTTCGGCAAACCTTGCT   28204       ACC  A
                                  GGCAAGG   TG TGGAGAAG
                                  |||||||   || ||||||||
                                  TCGTTCC   AC GCTTCTTC
                                       AA_  G
GAM455  EIF4G2   3'  CTTCTGCATAAGGTTTTTTTGT 9218     TG C      G   G
              A                    TA  G AAGGACCT ATG AGAAG
                                  ||  | |||||||| ||| |||||
                                  AT  T TTTTTGGA TAC TCTTC
                                   GT _      A   G
GAM455  ENTPD1   5'  CTTTTTTGTCAGCGATTGTCA  10112      GGAC   TG
                                  TGGCAA    CTGA  GAGAAG
                                  ||||||    ||||  ||||||
                                  ACTGTT    GACT  TTTTTC
                                     AGC_    GT
GAM455  EPHB4    3'  TTTTTCTACCGTCCTTGTCATA 16712          CTGA
                                  TATGGCAAGGAC    TGGAGAAG
                                  ||||||||||||    ||||||||
                                  ATACTGTTCCTG    ATCTTTTT
                                         CC__
GAM455  ERBB4    3'  TTTTTTCATTTTGTTTTGCT   19112       G  CT
                                  GGCAAG AC  GATGGAGAAG
                                  |||||| ||  ||||||||||
                                  TCGTTT TG  TTACTTTTTT
                                     _  TT
GAM455  EYA1     3'  TTCTTCATTAATTTTGT     6699        ACC
                                  GCAAGG   TGATGGAGAA
                                  ||||||   ||||||||||
                                  TGTTTT   ATTACTTCTT
                                     A__
GAM455  FABP2    3'  TTTTTTTAGAGATGGGGTCTTG 5538          GA   GA___
              CTATA                  TATGGCAAG  CCT    TGGAGAAG
                                  |||||||||  |||    ||||||||
                                  ATATCGTTC  GGG    ATTTTTTT
                                       TG   TAGAG
GAM455  FANCE    3'  TTTCTTCACCACCTTGTC    41906        ACC  A
                                  GGCAAGG   TG TGGAGAAG
                                  |||||||   || ||||||||
```

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                                CTGTTCC   AC ACTTCTTT
                                    ___  C
GAM455  FBXW1B   3'  TTTTTTGTTGTTTTTGC     25480        CT  TG
                                GCAAGGAC  GA  GAGAA
                                ||||||||  ||  |||||
                                CGTTTTTG  TT  TTTTT
                                    __  GT
GAM455  FGF5     3'  TTTCTAAGAGGGTTCTTGCTTA 16768   T        GA_
                                A GGCAAGGACCT   TGGAGA
                                | ||||||||||   ||||||
                                A TCGTTCTTGGG   ATCTTT
                                 T         AGA
GAM455  FGF5     3'  TTTCTAAGAGGGTTCTTGCTTA 53676   T        GA_
                                A GGCAAGGACCT   TGGAGA
                                | ||||||||||   ||||||
                                A TCGTTCTTGGG   ATCTTT
                                 T         AGA
GAM455  FGF8     3'  TTTGCTGTTGGGTTTTTGCTGT 21499          TG   AG  G
                                ATGGCAAGGACC  ATGG  AA
                                ||||||||||||  ||||  ||
                                TGTCGTTTTTGG  TGTC  TT
                                      GT   GT
GAM455  FKBP10   3'  TTTCTTTGTACTTCTTGTCAT  41940         CCTG TG
                                ATGGCAAGGA   A  GAGAAG
                                ||||||||||   |  ||||||
                                TACTGTTCTT   T  TTCTTT
                                     CA__ GT
GAM455  FMR2     3'  TTTTTAGTGGTTTTGTCATA   10707         G   TGA
                                TATGGCAAG ACC   TGGAGA
                                |||||||||| |||   ||||||
                                ATACTGTTT TGG   ATTTTT
                                     _  TG_
GAM455  FOXO1A   3'  CTTTTCTATTTTTTTTTGTTTA 10651   T      CCT
                                A GGCAAGGA   GATGGAGAAG
                                | ||||||||   ||||||||||
                                A TTGTTTTT   TTATCTTTTC
                                 T       TT_
GAM455  FPRL1    3'  TTTTTCTACTATCCTTGCTA   9396         CC  A
                                TGGCAAGGA  TG TGGAGAAG
                                |||||||||  || ||||||||
                                ATCGTTCCT  AT ATCTTTTT
                                     __  C
GAM455  FZD3     3'  TTTCTCTGTATTCATTGTTGTA 34261    TG   G  CCTG
                                TA  GCAA GA    ATGGAGAAG
                                ||  |||| ||    |||||||||
                                AT  TGTT CT    TGTCTCTTT
                                  GT    A  TA__
GAM455  FZD7     3'  TTTTTCCCCTTGTCTTTGTTGT 14508    TG      CTGAT
             A                   TA  GCAAGGAC    GGAGAAG
                                 ||  ||||||||    |||||||
```

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                                AT  TGTTTCTG    CCTTTTT
                                 GT      TTCC_
GAM455  GAS11    3'  TTTTCACATGTTCTTGCCAT   9433          C  A
                                ATGGCAAGGAC TG TGGAGA
                                |||||||||| || ||||||
                                TACCGTTCTTG AC ACTTTT
                                      T  _
GAM455  GDF8     3'  CTTTTTTATTTACTTTGGTATA 19149     G    ACCT
                                TATG CAAGG   GATGGAGAAG
                                |||| |||||   ||||||||||
                                ATAT GTTTC   TTATTTTTTC
                                  G    AT__
GAM455  GNAZ     3'  TTTTTGTGTCTGGCTTGCT   10830       GA  T   G
                                GGCAAG  CC GATG AGAAG
                                ||||||  || |||| |||||
                                TCGTTC  GG CTGT TTTTT
                                   __  T   G
GAM455  GNAZ     3'  TTTTTTCAGGTGGTCTTTTTTG 10831    TG C      TGA
             TG                   TA  G AAGGACC   TGGAGAAG
                                ||  | |||||||  ||||||||
                                GT  T TTTCTGG   ACTTTTTT
                                 GT T      TGG
GAM455  GORASP1  3'  TTCTCTGTAATCTGCTATG   49958       A  ACCTG
                                TATGGCA GG    ATGGAGAA
                                ||||||| ||    ||||||||
                                GTATCGT CT    TGTCTCTT
                                   _  AA___
GAM455  GRINL1A  3'  TTTTTTCATATTCATTGGCCAT 70075       AAG_  CCTG
             G                   TATGGC   GA   ATGGAGAAG
                                ||||||   ||   |||||||||
                                GTACCG   CT   TACTTTTTT
                                   GTTA  TA__
GAM455  GRM3     3'  AGTTTTTTGTAGGTCCTTGTTG 7744     TG       G TG    G
             TA                   TA  GCAAGGACCT A  GAGAA
                                ||  |||||||||| |  |||||
                                AT  TGTTCCTGGA T  TTTTT
                                 GT        _ GT    GAA
GAM455  GRM3     3'  TTTTTTGTAGGTCCTTGTTGTA 7750     TG       G TG    G
                                TA  GCAAGGACCT A  GAGAA
                                ||  |||||||||| |  |||||
                                AT  TGTTCCTGGA T  TTTTT
                                 GT        _ GT
GAM455  GSTZ1    3'  CTTTTCTCATCCGCTTTTGTTG 9499     TG     ACCT   _
             TG                   TA  GCAAGG   GATG GAGAAG
                                ||  ||||||   |||| ||||||
                                GT  TGTTTT   CTAC CTTTTC
                                 GT     CGC_   T
GAM455  HCFC1    3'  CTTTTTTGTTGTTGTTAGCTGT 71547       _  G   CT  TG
             G                   TATGGC AA GAC  GA  GAGAAG
                                |||||| || |||  ||  ||||||
```

```
                                GTGTCG TT TTG  TT  TTTTTC
                                   A  G  __ GT
GAM455  HEPH     3'  TTTCTTTAGTTTCTTTGCT   29654        CCTGA
                                GGCAAGGA    TGGAGAAG
                                ||||||||    ||||||||
                                TCGTTTCT    ATTTCTTT
                                    TTG__
GAM455  HLA-A    3'  CTTTTTCAAATTCTTGCCATG  10927          CC   TG
                                TATGGCAAGGA  TGA  GAG
                                ||||||||||  |||  |||
                                GTACCGTTCTT  ACT  TTC
                                      AA  TT
GAM455  HMG20A   3'  CTTCTCTTAGACTCCTTGTC  37066        C_  AT
                                GGCAAGGA  CTG  GGAGAAG
                                ||||||||  |||  |||||||
                                CTGTTCCT  GAT  TCTCTTC
                                    CA  __
GAM455  HMGB1    3'  TTTAAAGCAGGTTCTTGTT    10939          ATGG
                                GGCAAGGACCTG   AGA
                                ||||||||||||   |||
                                TTGTTCTTGGAC   TTT
                                      GAAA
GAM455  HMMR     3'  TTTCTTCAGAGTTTGTCATA   25949        AG  _   T
                                TATGGCA  GAC CTGA GGAGA
                                |||||||  ||| |||| |||||
                                ATACTGT  TTG GACT TCTTT
                                   __  A  _
GAM455  HNF4G    3'  CTTCTTCATTGGTGCTGTTATA 15953        A G  T
                                TATGGCA G ACC GATGGAGAAG
                                ||||||| | ||| ||||||||||
                                ATATTGT C TGG TTACTTCTTC
                                   _ G  _
GAM455  HNRPA2B1 3'  TTCTTCCTATTTGCCATG    10948        GACCTGAT
                                TATGGCAAG      GGAGAA
                                |||||||||      ||||||
                                GTACCGTTT      CTTCTT
                                     ATC_____
GAM455  HOXD4    3'  CTTTAGAAGGTTTCTGTTGTA  28259    TG  AG   GA
                                TA  GCA  GACCT  TGGAG
                                ||  |||  |||||  |||||
                                AT  TGT  TTGGA  ATTTC
                                 GT  CT   AG
GAM455  HS2ST1   3'  CTTTTTCAGTATTTTGACCATA 25329     _   AC   TG
                                TATGG CAAGG  CTGA  GAG
                                ||||| |||||  ||||  |||
                                ATACC GTTTT  GACT  TTC
                                   A   AT   TT
GAM455  IDH3B    5'  CTTGCTTCGGGTCTTTTCATG  23558     C       TG_
                                TATGG AAGGACCTGA  GAG
                                ||||| ||||||||||  |||
```

```
                                GTACT TTTCTGGGCT   TTC
                                  _        TCG
GAM455  IFNA10   3'  CTTTTTCATTAAATTTTTACTA 10980      C    CC
              TA                  TATGG AAGGA  TGATGGAGAAG
                                  ||||| |||||  ||||||||||
                                  ATATC TTTTT  ATTACTTTTTC
                                    A    AA
GAM455  IFNA17   3'  CTTTTTCATTAAATTTTTACTA 41477      C    CC
              TA                  TATGG AAGGA  TGATGGAGAAG
                                  ||||| |||||  ||||||||||
                                  ATATC TTTTT  ATTACTTTTTC
                                    A    AA
GAM455  IL22RA2  3'  CTTTTCTGTTTGTTTTTGTT   54772        CT
                                  GGCAAGGAC  GATGGAGAAG
                                  |||||||||  ||||||||||
                                  TTGTTTTTG  TTGTCTTTTC
                                       T_
GAM455  IMPG2    5'  CTTTTAAATGTTAGGTCTTTCC 33189      C        GG__
              TATA                  TATGG AAGGACCTGAT    AGAAG
                                  ||||| ||||||||||    |||||
                                  ATATC TTTCTGGATTG    TTTTC
                                    C          TAAA
GAM455  JDP1     5'  CTTAAAGCTAGTTTTTGCTATG 41723          CTGATG_
                                  TATGGCAAGGAC      GAG
                                  ||||||||||||      |||
                                  GTATCGTTTTTG      TTC
                                         ATCGAAA
GAM455  KCNJ6    3'  TTTTTCTGTCTCTCTTGCT    11151       ACCT
                                  GGCAAGG    GATGGAGAAG
                                  |||||||    ||||||||||
                                  TCGTTCT    CTGTCTTTTT
                                     CT__
GAM455  KCNS2    3'  CTTCTTAAGAGGTCCTTTTGTG 68847    TG C      GATG
                                  TA  G AAGGACCT    GAGAAG
                                  ||  | ||||||||    ||||||
                                  GT  T TTCCTGGA    TTCTTC
                                   GT _       GAA_
GAM455  KLK5     5'  TTTCTCTGTCCCCTCCTTGCC  25788        CCT
                                  GGCAAGGA   GATGGAGAAG
                                  ||||||||   ||||||||||
                                  CCGTTCCT   CTGTCTCTTT
                                       CCC
GAM455  KRTHA8   3'  TTCCATAGCTTCTTGCTATG   23194          C   A
                                  TATGGCAAGGA CTG TGGAG
                                  |||||||||||  ||| |||||
                                  GTATCGTTCTT GAT ACCTT
                                         C   _
GAM455  KTN1     3'  TTTTCTAATCCTTGTTA     18377          CCTGA
                                  TGGCAAGGA     TGGAGAA
                                  |||||||||     |||||||
```

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                                ATTGTTCCT    ATCTTTT
                                     A____
GAM455  LRP4    3'  TTTTTTTGTTTGTTTTTTTGCC 65066       CCT_  TG
                                GGCAAGGA   GA  GAGAAG
                                ||||||||   ||  ||||||
                                CCGTTTTT   TT  TTTTTT
                                    TTGT  GT
GAM455  MAF     5'  TTTTTTCATCTTCTAGCTGTA  19313      A   CCT
                                TATGGC AGGA   GATGGAGAAG
                                ||||||  ||||  ||||||||||
                                ATGTCG TCTT   CTACTTTTTT
                                   A   ___
GAM455  MAML1   3'  CTTTTTTGTTTCTGCTCTTTGT 29276       CCT__  TG
            CA                    TGGCAAGGA    GA  GAGAAG
                                |||||||||    ||  ||||||
                                ACTGTTTCT    TT  TTTTTC
                                     CGTCT  GT
GAM455  MAT1A   3'  CTTTTTTGTCAGTTTGTTTGT  92499     _ C   TG
                                GCAAG GA CTGA  GAGAAG
                                |||||  ||  ||||  ||||||
                                TGTTT TT GACT  TTTTTC
                                   G  T   GT
GAM455  MFAP3   3'  TTTTTCAGATGTTTTGCCATG  21003       AC_   TG
                                TATGGCAAGG   CTGA  GA
                                ||||||||||   ||||  ||
                                GTACCGTTTT   GACT  TT
                                     GTA   TT
GAM455  MSL3L1  5'  TTTCTTCGTTTCAGATTGTTG  23294    G  C   __
                                CAA GA CTGA  TGGAGAAG
                                |||  ||  ||||  ||||||||
                                GTT TT GACT  GCTTCTTT
                                  G  A   TT
GAM455  MTL5    3'  CTTCTCCATAATTATTGTTGTA 18198    TG   GGACCTG
                                TA  GCAA     ATGGAGAAG
                                ||  ||||     |||||||||
                                AT  TGTT     TACCTCTTC
                                  GT   ATTAA__
GAM455  MTM1    3'  CTTTTTCAGGTTGTTTTGTTTT 6005     TG    __     TG   AAG
            A                    TA  GCAAG  GACCTGA  GAG
                                ||  |||||  |||||||  |||
                                AT  TGTTT  TTGGACT  TTC
                                  TT    TG     TT
GAM455  MYF5    3'  CTTCTTTATTATTCTTTGCTTA 20007    T      CC
                                A GGCAAGGA  TGATGGAGAAG
                                | ||||||||  ||||||||||
                                A TCGTTTCT  ATTATTTCTTC
                                 T      T_
GAM455  NAV2    3'  CTTGCCTAGATCTTTGTTGTA  60795    TG     C   AT  AG
                                TA  GCAAGGA CTG  GG  AAG
                                ||  |||||||  |||  ||  |||
```

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                                AT  TGTTTCT GAT  CC  TTC
                                 GT      A  __  G_
GAM455  NAV2    3'  TTTTTTTAGTTTCTTACCATA  60802      C    C   TG
                                TATGG AAGGA CTGA  GAG
                                ||||| ||||| ||||  |||
                                ATACC TTCTT GATT  TTT
                                   A    T   TT
GAM455  NBEA    3'  TTTCTTCATGTTTCTTCTTTGT 96584       CCTG__
                                GCAAGGA     ATGGAGAAG
                                |||||||     |||||||||
                                TGTTTCT     TACTTCTTT
                                    TCTTTG
GAM455  NCOA6   5'  TTTTTTTATTGGGTTGTC    26854     AGG   TG
                                GGCA   ACC  ATGGAGAAG
                                ||||   |||  |||||||||
                                CTGT   TGG  TATTTTTTT
                                  ___   GT
GAM455  NDUFB3  5'  CTTCTCCGCTTTCCTGCCGTG  11766       A   CCTGA
                                TATGGCA GGA    TGGAGAAG
                                ||||||| |||    ||||||||
                                GTGCCGT CCT    GCCTCTTC
                                   _  TTC__
GAM455  NET1    3'  TTTCTTTGCTAAGCCTTGC   20767      ACC  AT
                                GCAAGG   TG  GGAGAAG
                                ||||||   ||  |||||||
                                CGTTCC   AT  TTTCTTT
                                   GA_  CG
GAM455  NID     3'  CTTCTTTATTATAGTCCT    11808      C_
                                AGGAC  TGATGGAGAAG
                                |||||  ||||||||||
                                TCCTG  ATTATTTCTTC
                                  AT
GAM455  NLGN3   3'  TTCTTTACAGTCTTTTGT    39122      AC   A
                                GCAAGG  CTG TGGAGAA
                                ||||||  ||| |||||||
                                TGTTTT  GAC ATTTCTT
                                   CT   _
GAM455  NONO    3'  TTTTTTCATTGGTGTACTGT   82895     AGG  _ TG
                                GCA   AC C  ATGGAGAAG
                                |||   || |  |||||||||
                                TGT   TG G  TACTTTTTT
                                  CA_  T GT
GAM455  NPY1R   3'  TTTTTTGGTGGTTTTTGTTTG  8064    T       TGA GG
                                A GGCAAGGACC   T  AGAA
                                | ||||||||||   |  ||||
                                G TTGTTTTTGG   G  TTTT
                                 T        TG_ TT
GAM455  NR1I2   5'  CTTTTCCTGTGTTTTTGTAGTG 15300     G      CTGAT
                                TAT GCAAGGAC    GGAGAAG
                                ||| ||||||||    |||||||
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                                GTG TGTTTTTG    CCTTTTC
                                  A      TGT__
GAM455  NR3C2    3'  TTTTTTGCAGTCTTTTGCTGTG 8026          AC   A GG
                                TATGGCAAGG  CTG T  AGAA
                                ||||||||||  ||| |  ||||
                                GTGTCGTTTT  GAC G  TTTT
                                     CT   _ TT
GAM455  NT5C2    3'  TTCTTCCATTCTTGTCAT    25273        GACCT    _
                                ATGGCAAG    GATGGA GAA
                                ||||||||    |||||| |||
                                TACTGTTC    TTACCT CTT
                                     _____     T
GAM455  OASL     3'  CTTCTCTGTACATTTCTGCCAT 14957        A   CCTG
          G                      TATGGCA GGA    ATGGAGAAG
                                |||||||  |||    |||||||||
                                GTACCGT CTT    TGTCTCTTC
                                   _   TACA
GAM455  PCDHA1   3'  TTTAACAGGTTTTGTCGTA   49415        G    A
                                TATGGCAAG ACCTG TGGA
                                ||||||||| ||||| ||||
                                ATGCTGTTT TGGAC ATTT
                                     _    A
GAM455  PCDHA10  3'  TTTAACAGGTTTTGTCGTA   38793        G    A
                                TATGGCAAG ACCTG TGGA
                                ||||||||| ||||| ||||
                                ATGCTGTTT TGGAC ATTT
                                     _    A
GAM455  PCDHA11  3'  TTTAACAGGTTTTGTCGTA   49863        G    A
                                TATGGCAAG ACCTG TGGA
                                ||||||||| ||||| ||||
                                ATGCTGTTT TGGAC ATTT
                                     _    A
GAM455  PCDHA12  3'  TTTAACAGGTTTTGTCGTA   49865        G    A
                                TATGGCAAG ACCTG TGGA
                                ||||||||| ||||| ||||
                                ATGCTGTTT TGGAC ATTT
                                     _    A
GAM455  PCDHA13  3'  TTTAACAGGTTTTGTCGTA   49871        G    A
                                TATGGCAAG ACCTG TGGA
                                ||||||||| ||||| ||||
                                ATGCTGTTT TGGAC ATTT
                                     _    A
GAM455  PCDHA2   3'  TTTAACAGGTTTTGTCGTA   38808        G    A
                                TATGGCAAG ACCTG TGGA
                                ||||||||| ||||| ||||
                                ATGCTGTTT TGGAC ATTT
                                     _    A
GAM455  PCDHA3   3'  TTTAACAGGTTTTGTCGTA   49808        G    A
                                TATGGCAAG ACCTG TGGA
                                ||||||||| ||||| ||||
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                                ATGCTGTTT TGGAC ATTT
                                    _    A
GAM455  PCDHA4   3' TTTAACAGGTTTTGTCGTA   38816       G    A
                                TATGGCAAG ACCTG TGGA
                                ||||||||| ||||| ||||
                                ATGCTGTTT TGGAC ATTT
                                    _    A
GAM455  PCDHA5   3' TTTAACAGGTTTTGTCGTA   49815       G    A
                                TATGGCAAG ACCTG TGGA
                                ||||||||| ||||| ||||
                                ATGCTGTTT TGGAC ATTT
                                    _    A
GAM455  PCDHA6   3' TTTAACAGGTTTTGTCGTA   38824       G    A
                                TATGGCAAG ACCTG TGGA
                                ||||||||| ||||| ||||
                                ATGCTGTTT TGGAC ATTT
                                    _    A
GAM455  PCDHA7   3' TTTAACAGGTTTTGTCGTA   49828       G    A
                                TATGGCAAG ACCTG TGGA
                                ||||||||| ||||| ||||
                                ATGCTGTTT TGGAC ATTT
                                    _    A
GAM455  PCDHA8   3' TTTAACAGGTTTTGTCGTA   38832       G    A
                                TATGGCAAG ACCTG TGGA
                                ||||||||| ||||| ||||
                                ATGCTGTTT TGGAC ATTT
                                    _    A
GAM455  PCDHA9   3' CTTCGCTTATTGAGTTTTTGTT 49841         CT    A_
          ATG                     TATGGCAAGGAC  GATGG  GAAG
                                ||||||||||||  |||||  ||||
                                GTATTGTTTTTG  TTATT  CTTC
                                      AG    CG
GAM455  PCDHA9   3' CTTTTTTATTTTTTTTTTTTGT 49843         CCT__
          CAT                     ATGGCAAGGA    GATGGAGAAG
                                ||||||||||    ||||||||||
                                TACTGTTTTT    TTATTTTTTC
                                     TTTTT
GAM455  PCDHA9   3' TTTAACAGGTTTTGTCGTA   49855       G    A
                                TATGGCAAG ACCTG TGGA
                                ||||||||| ||||| ||||
                                ATGCTGTTT TGGAC ATTT
                                    _    A
GAM455  PCDHAC1  3' TTTAACAGGTTTTGTCGTA   38783        G    A
                                TATGGCAAG ACCTG TGGA
                                ||||||||| ||||| ||||
                                ATGCTGTTT TGGAC ATTT
                                    _    A
GAM455  PCDHAC2  3' TTTAACAGGTTTTGTCGTA   49879        G    A
                                TATGGCAAG ACCTG TGGA
                                ||||||||| ||||| ||||
```

```
                                ATGCTGTTT TGGAC ATTT
                                    _    A
GAM455  PCDHB5   3'  CTTCTTGTTGGTATTTGTTGTG 32244    TG    G   TGATG
                                TA  GCAAG ACC    GAGAAG
                                ||  ||||| |||    ||||||
                                GT  TGTTT TGG    TTCTTC
                                 GT    A   TTG__
GAM455  PCDHB9   3'  CTTCTTTAATATATTCTTGTT  39443        CC  A
                                GGCAAGGA  TG TGGAGAAG
                                ||||||||  || ||||||||
                                TTGTTCTT  AT ATTTCTTC
                                     AT  A
GAM455  PCNA     3'  CTTTTCTGTCACCAAATTTGT  11996      GACC_
                                GCAAG    TGATGGAGAAG
                                |||||    ||||||||||
                                TGTTT    ACTGTCTTTTC
                                   AAACC
GAM455  PEX10    3'  CTCTCAGTTTTTTGTCATG   12039         C    TG
                                TATGGCAAGGA CTGA  GAG
                                |||||||||| ||||  |||
                                GTACTGTTTTT GACT  CTC
                                       T   __
GAM455  PHKA2    3'  TTTCTCTGGAACATTTGCTGTA 6091          GACCTGA
                                TATGGCAAG      TGGAGAAG
                                |||||||||      ||||||||
                                ATGTCGTTT      GTCTCTTT
                                      ACAAG__
GAM455  PIGC     5'  TTTTTCTAGGAACTTGGCTGTG 12082       _   GA   GAT
                                TATGGC AAG  CCT   GGAGAAG
                                |||||| |||  |||   |||||||
                                GTGTCG TTC  GGA   TCTTTTT
                                   G   AA  ____
GAM455  PITX2    5'  CTTCTCTGTCAGGGCTGCCG   6155       A GA
                                TGGCA G  CCTGATGGAGAAG
                                ||||| |  ||||||||||||
                                GCCGT C  GGACTGTCTCTTC
                                   _ G_
GAM455  PKHD1    3'  TTTCTCCATGCTTTTTGTTTG  57720    T      CCTG
                                A GGCAAGGA    ATGGAGAAG
                                | ||||||||    |||||||||
                                G TTGTTTTT    TACCTCTTT
                                 T       CG__
GAM455  PLS1     3'  TTTTTGCAGGTTCTGCTGTG   12181        A      A GG
                                TATGGCA GGACCTG T  AGA
                                ||||||| ||||||| |  |||
                                GTGTCGT CTTGGAC G  TTT
                                     _      _ TT
GAM455  POLB     3'  TTCTTCATGCTTTTGCTTG    12198    T     ACCTG
                                A GGCAAGG     ATGGAGAA
                                | |||||||     ||||||||
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                                G TCGTTTT    TACTTCTT
                                 T     CG___
GAM455  PPP1R2   3'  TTTTTGGGGGGTTTTTGTTTG  21790   T       GA GG
                                A GGCAAGGACCT  T  AGA
                                | ||||||||||  |  |||
                                G TTGTTTTTGGG  G  TTT
                                 T         GG TT
GAM455  PPT1     3'  TTTTTCCAAGTCTTGCCATA   62447         ACCTGA
                                TATGGCAAGG     TGGAGAAG
                                ||||||||||     ||||||||
                                ATACCGTTCT     ACCTTTTT
                                      GA____
GAM455  PRDM2    5'  TTTTTTAGGGACTTTGCTATA  32423         A_    TG
                                TATGGCAAGG  CCTGA  GA
                                ||||||||||  |||||  ||
                                ATATCGTTTC  GGATT  TT
                                      AG     TT
GAM455  PRKG2    3'  CTTTTCGAAAGTCCTTGTTA   21825         CTGATG
                                TGGCAAGGAC     GAGAAG
                                ||||||||||     ||||||
                                ATTGTTCCTG     CTTTTC
                                      AAAG__
GAM455  PRKWNK3  3'  TTTCTTCCTCTTGGGTTCTGTC 62244        A     __  T
           ATA                    TATGGCA GGACCT  GA GGAGAAG
                                ||||||| ||||||  || |||||||
                                ATACTGT CTTGGG  CT CTTCTTT
                                   _     TT  C
GAM455  PTGFRN   3'  TTTTCCATTTCTTTTGT     67774       ACCT
                                GCAAGG    GATGGAGAA
                                ||||||    |||||||||
                                TGTTTT    TTACCTTTT
                                   CT__
GAM455  PTHR2    3'  CTTCTTTGTAAACCATGTCATG 18563        A  ACCTG TG
                                TATGGCA GG     A  GAGAAG
                                ||||||| ||     |  ||||||
                                GTACTGT CC     T  TTCTTC
                                    A  AAA__ GT
GAM455  PTPRE    3'  TTTCTTTGTATATATTTTGTTA 22487         ACCTG TG
           TG                     TATGGCAAGG     A  GAGAAG
                                ||||||||||     |  ||||||
                                GTATTGTTTT     T  TTCTTT
                                      ATATA GT
GAM455  PTPRE    3'  TTTCTTTGTATATATTTTGTTA 56118         ACCTG TG
           TG                     TATGGCAAGG     A  GAGAAG
                                ||||||||||     |  ||||||
                                GTATTGTTTT     T  TTCTTT
                                      ATATA GT
GAM455  PTPRG    3'  CTTTTTTGAGGCCTTTTTTGCC 12613       _____   A   GA GG
           A                      TGGCA    AGG CCT  T  AGAAG
                                |||||    ||| |||  |  |||||
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                                ACCGT   TCC GGA  G  TTTTC
                                  TTTT  _  __ TT
GAM455  RAB5C    3'  TTTCTCCATATAATTTTGATCA 60527      _    ACCTG
            TA                   TATGG CAAGG    ATGGAGAAG
                                |||||| |||||    |||||||||
                                ATACT GTTTT    TACCTCTTT
                                  A    AATA_
GAM455  RAD23B   3'  TTTTTTCATCTCAGTTTTTTCT 12741      C     CT_
            GTG                  TATGG AAGGAC   GATGGAGAAG
                                |||||| ||||||   ||||||||||
                                GTGTC TTTTTG   CTACTTTTTT
                                  T     ACT
GAM455  RAP1GA1  3'  TTTCCAATTTGGGTTCTGCTGT 12777       A    TG __     AG
            G                    TATGGCA GGACC  A  TGGAGA
                                ||||||| |||||  |  ||||||
                                GTGTCGT CTTGG  T  ACCTTT
                                   _    GT TA
GAM455  SCAMP1   3'  CTTCTTCGTCTATATTTGTCA  54499       GACCT
                                TGGCAAG    GATGGAGAAG
                                |||||||    ||||||||||
                                ACTGTTT    CTGCTTCTTC
                                   ATAT_
GAM455  SCML2    3'  TTTCTCTTAGCAGTTTTTGTT  21435        C  AT_
                                GGCAAGGAC TG   GGAGAAG
                                |||||||| ||   |||||||
                                TTGTTTTTG AC   TCTCTTT
                                   _  GAT
GAM455  SCO1     3'  TTTCTCTAGGGGTTCTTTTATG 17163      C       GA
                                TATGG AAGGACCT  TGGAGAAG
                                ||||| ||||||||  ||||||||
                                GTATT TTCTTGGG  ATCTCTTT
                                  _       G_
GAM455  SERPINF2 3'  TTTTGTAAGGTTTTTGTAGTG  8124      G        G TG
                                TAT GCAAGGACCT A  GAG
                                ||| ||||||||||  |  |||
                                GTG TGTTTTTGGA T  TTT
                                  A         A GT
GAM455  SH3BP5   3'  TTTTTCAGAGCAGAGTTCTTGT 17921    TG       _  ATG_
            TGTG                   TA  GCAAGGAC CTG    GAGAAG
                                ||  |||||||| |||    ||||||
                                GT  TGTTCTTG GAC    CTTTTT
                                 GT       A   GAGA
GAM455  SH3GL2   3'  TTCTTCCCTCCTTGCTAT    13098          CCTGAT
                                ATGGCAAGGA     GGAGAA
                                ||||||||||     ||||||
                                TATCGTTCCT     CTTCTT
                                     CC____
GAM455  SIP      3'  TTTCTTCATTAGAACAGTTTT  27736       ____
                                AGGAC    CTGATGGAGAAG
                                |||||    ||||||||||||
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                                TTTTG   GATTACTTCTTT
                                  ACAA
GAM455  SLC11A3  5'  TTTCTTTTGTTCTTTGCCA   28168        CCTGAT
                                TGGCAAGGA    GGAGAAG
                                |||||||||    |||||||
                                ACCGTTTCT    TTTCTTT
                                   TGT___
GAM455  SLC15A1  3'  CTTTACCTTTGGGTTTTTGTTA 18641          TG T  A
           T                    ATGGCAAGGACC  A GG GAAG
                                ||||||||||||  | || ||||
                                TATTGTTTTTGG  T CC TTTC
                                      GT T  A
GAM455  SLC22A3  3'  TCTCCATTTCTCTGCTGTA   42040       AG  CCT      AG
                                TATGGCA  GA   GATGGAGA
                                |||||||  ||   ||||||||
                                ATGTCGT  CT   TTACCTCT
                                    CT  ___      C
GAM455  SLC4A4   3'  TTCTTCAATCCTTTTCATA   14999      C    CCTGA
                                TATGG AAGGA    TGGAGAA
                                ||||| |||||    |||||||
                                ATACT TTCCT    ACTTCTT
                                   T    A____
GAM455  SMURF1   3'  TTTCTTTGTTGTTGTTTTTGTT 94055   T       CT_  TG
           TG                    A GGCAAGGAC   GA  GAGAAG
                                | |||||||||   ||  ||||||
                                G TTGTTTTTG   TT  TTCTTT
                                 T       TTG  GT
GAM455  SORCS1   3'  TTTCTCTGTTCCACTTTCCATA 54686      C   GACCT
                                TATGG AAG    GATGGAGAAG
                                ||||| |||    ||||||||||
                                ATACC TTC    TTGTCTCTTT
                                   T   ACC__
GAM455  SOX9     3'  TTTCTTTGTTGTTTTTGTT   6235         CT  TG
                                GGCAAGGAC  GA  GAGAAG
                                |||||||||  ||  ||||||
                                TTGTTTTTG  TT  TTCTTT
                                     __  GT
GAM455  SP100    3'  TTTAAAGCAGGTTCTTGTTA   13340          ATGG
                                TGGCAAGGACCTG   AGA
                                ||||||||||||    |||
                                ATTGTTCTTGGAC    TTT
                                      GAAA
GAM455  SP4      3'  TTTCTTTGAAAGTACTTTGTTA 13336         AC  GA GG
           TA                    TATGGCAAGG  CT  T  AGAAG
                                ||||||||||  ||  |  |||||
                                ATATTGTTTC  GA  G  TCTTT
                                      AT  AA TT
GAM455  SRP46    3'  TTTTCTACCTTTTTGCCA    50340         CCTGA
                                TGGCAAGGA    TGGAGAA
                                |||||||||    |||||||
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                                ACCGTTTTT    ATCTTTT
                                     CC___
GAM455  ST7     3'  CTTAGTCTAGGTCCTTGTTGT  26472   TG       _  G
                                A  GCAAGGACCT GAT GAG
                                |  |||||||||| ||| |||
                                T  TGTTCCTGGA CTG TTC
                                 GT        T   A
GAM455  STAT1   3'  CTTTTCCATTGTAATTGCTAT  24614       GG  CT
                                ATGGCAA  AC  GATGGAGAAG
                                |||||||  ||  ||||||||||
                                TATCGTT  TG  TTACCTTTTC
                                    AA  __
GAM455  SULT1C1  3'  TTTTTTTAAAATAGGGTCTTGC 8326         GA   A__
           TATG                    TATGGCAAG  CCTG   TGGAGAAG
                                |||||||||  ||||  ||||||||
                                GTATCGTTC  GGAT   ATTTTTTT
                                     TG   AAA
GAM455  TCTEL1   3'  CTTTTCTCATTCTCTTTGTT   22535       CCT   _
                                GGCAAGGA   GATG GAGAAG
                                ||||||||   |||| ||||||
                                TTGTTTCT   TTAC CTTTTC
                                    C__   T
GAM455  TEX15    3'  TTTTTTCATGCTCTTGTCATA  49226         ACCTG
                                TATGGCAAGG    ATGGAGAAG
                                ||||||||||    |||||||||
                                ATACTGTTCT    TACTTTTTT
                                     CG___
GAM455  THBD     3'  TTTTTTTAAGTATTTAGGTTTT 6280    T        _____
           TGTTTG                   A GGCAAGGACCTGA    TGGAGAAG
                                | ||||||||||||||    ||||||||
                                G TTGTTTTTGGATT    ATTTTTTT
                                 T          TATGA
GAM455  TIRAP    3'  TTTTTTGTTTGGGTTTTTGTTG 54666   TG       _ TG    G
           T                     A  GCAAGGACCTG A  GAGAA
                                |  |||||||||| |  |||||
                                T  TGTTTTTGGGT T  TTTTT
                                 GT         T GT
GAM455  TJP1     3'  TTTTTTTATCGTCACTGCTTA  13769   T   AG   CT
                                A GGCA  GAC  GATGGAGAAG
                                | ||||  |||  ||||||||||
                                A TCGT  CTG  CTATTTTTTT
                                 T   CA  __
GAM455  TK2      3'  CTTTGCTAGTGTCTTTGTCATG 17249          _  AT
                                TATGGCAAGGAC CTG  GGAG
                                ||||||||||| |||  ||||
                                GTACTGTTTCTG GAT  TTTC
                                       T   CG
GAM455  TMEFF2   3'  TTTCTTTCCCATGTATTTGTTA 33000        G  C  AT
           TA                     TATGGCAAG AC TG  GGAGAAG
                                |||||||| || ||  |||||||
```

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                                ATATTGTTT TG AC  TTTCTTT
                                      A  T  CC
GAM455  TMPO     3'  CTTTTCTGTTAAGGTTGTT   13813    G    _
                                AA GACCT GATGGAGAAG
                                || ||||| ||||||||||
                                TT TTGGA TTGTCTTTTC
                                 G    A
GAM455  TNFAIP2  3'  TTTTTTTGAGACAGGGTCTTGC 21932         GA   A__ GG
           TGTG                    TATGGCAAG  CCTG   T  AGAAG
                                |||||||||  ||||  |  |||||
                                GTGTCGTTC  GGAC   G  TTTTT
                                      TG    AGA TT
GAM455  TNFRSF10B 3'  AGTTACATTAGGCTTTGCTATA 15215          A      GAGAAG
                                TATGGCAAGG CCTGATG
                                |||||||||| |||||||
                                ATATCGTTTC GGATTAC
                                      _      ATTGAT
GAM455  TOP2B    3'  CTTCTCTGTCTCAGACTTTTGT 8408        AC   ___
                                GCAAGG  CTGA  TGGAGAAG
                                ||||||  ||||  ||||||||
                                TGTTTT  GACT  GTCTCTTC
                                   CA    CT
GAM455  TOX      3'  TTTTATGTTGGTTTTTTGCTGT 28965          C TG   G    G
           G                     TATGGCAAGGA C  ATG AGAA
                                |||||||||| |  ||| ||||
                                GTGTCGTTTTT G  TGT TTTT
                                       T GT   A
GAM455  TRIP12   3'  TTTCTTTAGCAAGTTCTTGTTT 16180    T       C  A
           A                      A GGCAAGGAC TG TGGAGAAG
                                | |||||||| || ||||||||
                                A TTGTTCTTG AC ATTTCTTT
                                 T        A  G
GAM455  UBL3     5'  TTTCTTTGTTTGTTTTTTTCGT 24026       C     CT  TG
           A                      TATGG AAGGAC  GA  GAGAAG
                                |||||  ||||||  ||  ||||||
                                ATGCT TTTTTG  TT  TTCTTT
                                   T     T_  GT
GAM455  VPS41    3'  TTCTTCATCTATTCCTGT    27700     A   CCT
                                GCA GGA   GATGGAGAA
                                ||| |||   |||||||||
                                TGT CCT   CTACTTCTT
                                  _   TAT
GAM455  VRK1     3'  CTTTTCTGTTAGAACTGTTTTA 14079    TG   A GAC
                                TA  GCA G   CTGATGGAGAAG
                                ||  ||| |   ||||||||||||
                                AT  TGT C   GATTGTCTTTTC
                                 TT   _ AA_
GAM455  WHSC1    3'  CTTTTCCATTAAACTACTTTTG 24671        ACC___
           T                      GCAAGG     TGATGGAGAAG
                                ||||||     ||||||||||
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                                TGTTTT     ATTACCTTTTC
                                   CATCAA
GAM455  XT3     3'  CTTCTTATCAGAAGGTTCTTTT 39911      C      GA __
             ATG                    TATGG AAGGACCT  TG  GAGAAG
                                |||||| ||||||||  ||  ||||||
                                GTATT TTCTTGGA  AC  TTCTTC
                                   _       AG  TA
GAM455  YWHAG   3'  TTTCTTTGTTTCTTTGTTTTA  25946    TG     CCT  TG
                                TA  GCAAGGA   GA  GAGAAG
                                ||  |||||||   ||  ||||||
                                AT  TGTTTCT   TT  TTCTTT
                                 TT      ___  GT
GAM455  ZFX     5'  TCCGTCCGGTTCTTGCTATA   14165           T
                                TATGGCAAGGACC GATGGA
                                |||||||||||| ||||||
                                ATATCGTTCTTGG CTGCCT
                                        C
GAM455  ABHD2   3'  TTTCTCCATTGCATTGTTA   23797       GGACCT
                                TGGCAA     GATGGAGAAG
                                ||||||     ||||||||||
                                ATTGTT     TTACCTCTTT
                                   ACG___
GAM455  ABT1    3'  TTTTTCTATTTAATTTTTGTC  26307        CCT
                                GGCAAGGA   GATGGAGAAG
                                ||||||||   ||||||||||
                                CTGTTTTT   TTATCTTTTT
                                     AAT
GAM455  ACP33   3'  TTTCTTTTTATGTTGTTTGCTG 34037         _  C   T
             TA                   TATGGCAAG GAC TGA GGAGAAG
                                |||||||||| ||| ||| |||||||
                                ATGTCGTTT TTG ATT TTTCTTT
                                     G   T  _
GAM455  ADNP    3'  TTTTTTTAGTGTTGCCCTTGCT 31692          ___ _    TG   AAG
             GTG                    TATGGCAAGG   AC CTGA  GAG
                                ||||||||||   || ||||  |||
                                GTGTCGTTCC   TG GATT  TTT
                                      CGT  T    TT
GAM455  AND-1   3'  TGGTTCATTTGGTTTTTGTCAT 24010           T     GAAG
             G                   TATGGCAAGGACC GATGGA
                                |||||||||||| ||||||
                                GTACTGTTTTTGG TTACTT
                                        T     GGTT
GAM455  ANP32B  3'  TTTTTGTGTAAGATTCTTGCTG 22151          C  G   G
             TA                   TATGGCAAGGA CT ATG AGAAG
                                |||||||||||| || ||| |||||
                                ATGTCGTTCTT GA TGT TTTTT
                                      A  A   G
GAM455  AP3M2   3'  TTTTTTCATTTCTTACTTGTC  23304       GACCT
                                GGCAAG    GATGGAGAAG
                                ||||||    ||||||||||
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                                CTGTTC    TTACTTTTTT
                                   ATTCT
GAM455  APCL    3'  TTCTCCATCCCCTGCCGTG   20823       A  ACCT
                                TATGGCA GG   GATGGAGAA
                                ||||||| ||   |||||||||
                                GTGCCGT CC   CTACCTCTT
                                   C  ____
GAM455  ASTN2   3'  CTTCTCTCTCTTTTTTGCT   73558       CCT  T
                                GGCAAGGA   GA GGAGAAG
                                ||||||||   || |||||||
                                TCGTTTTT   CT TCTCTTC
                                     T__  C
GAM455  BBP     3'  TTTTTTGTGGTTTTTGTT    50140         TG TG
                                GGCAAGGACC  A  GAGAA
                                ||||||||||  |  |||||
                                TTGTTTTTGG  T  TTTTT
                                      __ GT
GAM455  BMF     3'  TTCTCTGTCAGGCCCTTG    54292      A
                                CAAGG CCTGATGGAGAA
                                ||||| ||||||||||||
                                GTTCC GGACTGTCTCTT
                                   C
GAM455  BOP     5'  TTCTTTGTCATTGTTAT     86233       GGACC   TG
                                ATGGCAA    TGA  GAGAA
                                |||||||    |||  |||||
                                TATTGTT    ACT  TTCTT
                                   ______  GT
GAM455  BOP     5'  TTTTTCCCTTCTTTGTCAT   86235         CCTGAT
                                ATGGCAAGGA     GGAGAAG
                                ||||||||||     |||||||
                                TACTGTTTCT     CCTTTTT
                                      TC____
GAM455  C11orf25  3'  TTTTTTTGTTAGGTACATGT   49469     AGG     TG
                                GCA   ACCTGA  GAGAAG
                                |||   ||||||  ||||||
                                TGT   TGGATT  TTTTTT
                                  ACA     GT
GAM455  C1orf22   3'  TTTTTTGGTTTGTTGTTGTTGT 48045    TG   G  CT   G
           A                     TA  GCAA GAC  GAT GAGAAG
                                ||  |||| |||  ||| ||||||
                                AT  TGTT TTG  TTG TTTTTT
                                  GT   G  T_  G
GAM455  C1orf34   3'  TTTTTTTAGAGACAGGGTCTTG 61327        GA   A___
           CTATG                   TATGGCAAG  CCTG   TGGAGAAG
                                |||||||||  ||||   ||||||||
                                GTATCGTTC  GGAC   ATTTTTTT
                                      TG   AGAG
GAM455  C1QR1   3'  TTTCTTTCTTCTTTGTCAT   24872         CCT  T
                                ATGGCAAGGA   GA GGAGA
                                ||||||||||   || |||||
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                                TACTGTTTCT   CT TCTTT
                                     T__  T
GAM455  C20orf180 3'  CTTCTCTGAATCTGTCCTTTTG 37973    TG C     CT  __
          TG                    TA  G AAGGAC  GAT  GGAGAAG
                                || | ||||||  |||  |||||||
                                GT  T TTCCTG  CTA  TCTCTTC
                                 GT _     T_  AG
GAM455  CARD14   3'  CTTCTGACCAGGGGTTTTTGC  44353         GA  __
                                GCAAGGACCT  TGG  AGAAG
                                ||||||||||  |||  |||||
                                CGTTTTTGGG  ACC  TCTTC
                                     G_  AG
GAM455  CD109    3'  TTTCTTCACCTGATCTTTGT   56864       CCTGA
                                GCAAGGA    TGGAGAAG
                                |||||||    ||||||||
                                TGTTTCT    ACTTCTTT
                                    AGTCC
GAM455  CEP3     3'  TTCTTCATCTGTTATCATA   22252      CAAG  CT
                                TATGG   GAC  GATGGAGAA
                                |||||   |||  |||||||||
                                ATACT   TTG  CTACTTCTT
                                   A___   T_
GAM455  CGR11    3'  TATCAGGTCTTTCTATG     22692      C
                                TATGG AAGGACCTGATG
                                ||||| ||||||||||||
                                GTATC TTTCTGGACTAT
                                  _
GAM455  CPEB1    3'  CTTTTTTACATTCCTTGC    48365       CC  A
                                GCAAGGA  TG TGGAGAAG
                                |||||||  || ||||||||
                                CGTTCCT  AC ATTTTTTC
                                    T_  _
GAM455  CYP4F2   3'  TTTTTCTGTCCAGGTTGTTCAT 8427       CA G     _
          A                     TATGG  A GACCTG ATGGAGAAG
                                |||||  | |||||| |||||||||
                                ATACT  T TTGGAC TGTCTTTTT
                                   __ G     C
GAM455  DCOHM    3'  CTGTTTATGTTTTTGCTATA  50519          CT_
                                TATGGCAAGGAC   GATGG
                                ||||||||||||   |||||
                                ATATCGTTTTTG   TTGTC
                                      TAT
GAM455  DD5      3'  TTTCAGCAAAGGTTCTTGT   32478         GA__
                                GCAAGGACCT    TGGAG
                                ||||||||||    |||||
                                TGTTCTTGGA    ACTTT
                                      AACG
GAM455  DKFZP434D0127 3'  CTTTTTCAGGTATTTTCTATA  50496      C   G     TG
                                TATGG AAG ACCTGA  GAG
                                ||||| ||| ||||||  |||
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                                ATATC TTT TGGACT  TTC
                                   T   A     TT
GAM455  DKFZP434F0318 3'  CTTCTCTGTTAGGTTCTGGGGC 48754     A__
           T                    GGC   AGGACCTGATGGAGAAG
                                |||   ||||||||||||||||
                                TCG   TCTTGGATTGTCTCTTC
                                  GGG
GAM455  DKFZP434I0714 3'  TTTCTTTGTCGCTTTGTCG    86994        ACC   TG
                                TGGCAAGG   TGA  GAGAAG
                                ||||||||   |||  |||||||
                                GCTGTTTC   GCT  TTCTTT
                                     ___   GT
GAM455  DKFZP434J154 3'  CTGCCGTTGGGTTTTTTCATA  32176      C      TG   _
                                TATGG AAGGACC  ATGG AG
                                ||||| |||||||  |||| ||
                                ATACT TTTTTGG  TGCC TC
                                   _      GT    G
GAM455  DKFZP434J193 3'  CTTCTCCACCACTCTCCTTGCC 71562          CC_  A
           ATG                    TATGGCAAGGA   TG TGGAGAAG
                                ||||||||||   || ||||||||
                                GTACCGTTCCT   AC ACCTCTTC
                                      CTC  C
GAM455  DKFZP564F013 3'  TTCTCCATCAATGCCGTG    95881        AGGACC
                                TATGGCA     TGATGGAGAA
                                |||||||     ||||||||||
                                GTGCCGT     ACTACCTCTT
                                   A_____
GAM455  DKFZP564G092 5'  TTTTTTGGGGGTCTTTGTTA   32170          GA GG
                                TGGCAAGGACCT  T  AGAA
                                ||||||||||||  |  ||||
                                ATTGTTTCTGGG  G  TTTT
                                      G_ TT
GAM455  DKFZP566D1346 3'  CTTGAGTTTGAGTCCTTGTTAT 48737          CT_   G_   AAG
           G                     TATGGCAAGGAC   GAT  GAG
                                ||||||||||||   |||  |||
                                GTATTGTTCCTG   TTG  TTC
                                      AGT   AG
GAM455  DKFZP566J091 3'  TTTTTCCAAACTACTTTTTGTC 48867        CCTGA_
           A                     TGGCAAGGA     TGGAGAAG
                                |||||||||     ||||||||
                                ACTGTTTTT     ACCTTTTT
                                   CATCAA
GAM455  DKFZP761G1913 3'  TTTCCTGGGTCTTGTGCTGTG  49701       _     GAT
                                TATGGCA AGGACCT   GGAGA
                                ||||||| |||||||   |||||
                                GTGTCGT TTCTGGG   CCTTT
                                   G      T__
GAM455  DKFZp761K1423 5'  TTTTTCCTAATTGGTTCTTGAC 37941      G       TGAT_
           GTG                    TATG CAAGGACC     GGAGAAG
                                ||||| ||||||||     |||||||
```

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                                GTGC GTTCTTGG    CCTTTTT
                                  A       TTAAT
GAM455  DRCTNNB1A 3'  CTTCTTCATAGTCCCTTGCTGT 51809          AC   A
           A                    TATGGCAAGG  CTG TGGAGAAG
                                |||||||||  ||| ||||||||
                                ATGTCGTTCC  GAT ACTTCTTC
                                     CT   _
GAM455  DRIL2    3'  CTCCATTCAGGTCCTGCTGTA  22348        A       _
                                TATGGCA GGACCTGA TGGAG
                                ||||||| |||||||| |||||
                                ATGTCGT CCTGGACT ACCTC
                                    _       T
GAM455  EDG2     3'  CTTTTTCATTGCAAAATTGCCA 9171         GGACCT
                                TGGCAA     GATGGAGAAG
                                ||||||     ||||||||||
                                ACCGTT     TTACTTTTTC
                                   AAAACG
GAM455  EFA6R    3'  CTTTAAAGGTTCTTTTGTG    31635    TG C       GA
                                TA  G AAGGACCT  TGGAG
                                ||  | ||||||||  |||||
                                GT  T TTCTTGGA  ATTTC
                                 GT _       A_
GAM455  ENAH     3'  TTTTTCTATCAGATATTCATTG 37160         _  C__
           TCATG                   TATGGCAA GGA   CTGATGGAGAAG
                                |||||||| |||   ||||||||||||
                                GTACTGTT CTT   GACTATCTTTTT
                                     A   ATA
GAM455  ERO1L    3'  TTTTTTTAGAGACAAGGTTTTG 28164          G    GA____
           CTGTG                   TATGGCAAG ACCT      TGGAGAAG
                                ||||||||| ||||     ||||||||
                                GTGTCGTTT TGGA     ATTTTTTT
                                     _   ACAGAG
GAM455  ESDN     3'  TTTTTCCTGGAGGTTTTTGTTG 56068    TG         GAT
           T                    A  GCAAGGACCT   GGAGAAG
                                |  ||||||||||   |||||||
                                T  TGTTTTTGGA   CCTTTTT
                                 GT         GGT
GAM455  FEM-2    3'  TTTCTCTTTTCTTTGCTA    28323          CCTGAT
                                TGGCAAGGA     GGAGAAG
                                |||||||||     |||||||
                                ATCGTTTCT     TCTCTTT
                                     TT_____
GAM455  FHX      3'  TTTCTCTGTCAGAGAAGCCA   37926      AAGGAC
                                TGGC     CTGATGGAGAAG
                                ||||     ||||||||||||
                                ACCG     GACTGTCTCTTT
                                  AAGA__
GAM455  FIGN     3'  TTTCTTTTAATGTTCTTGTC   36578          CTGAT
                                GGCAAGGAC    GGAGAAG
                                |||||||||    |||||||
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                                CTGTTCTTG    TTTCTTT
                                     TAAT_
GAM455  FLJ00024  3' CTTCTCCACTCAGGTCTTTGTT 64496          _
                                GGCAAGGACCTGA TGGAGAAG
                                ||||||||||||| ||||||||
                                TTGTTTCTGGACT ACCTCTTC
                                      C
GAM455  FLJ10040  3' ATGTTTTTATAGGGTTTTTGTT 36218    TG       G     AG
          GTA                    TA  GCAAGGACCT ATGGAGA
                                || ||||||||||| |||||||
                                AT  TGTTTTTGGG TATTTTT
                                 GT        A      GTAA
GAM455  FLJ10040  3' TTTTTATAGGGTTTTTGTTGTA 36223    TG       G     AG
                                TA  GCAAGGACCT ATGGAGA
                                || ||||||||||| |||||||
                                AT  TGTTTTTGGG TATTTTT
                                 GT        A
GAM455  FLJ10232  5' TTTTTTCGGAGATGGGGTTTTG 36389         G   G  ____
          CTATG                    TATGGCAAG ACCT AT    GGAGAAG
                                ||||||||| |||| ||    |||||||
                                GTATCGTTT TGGG TA    CTTTTTT
                                     _   G  GAGG
GAM455  FLJ10493  3' CTTTTTCATGCCCTTGTTTTA  36672    TG     ACCTG
                                TA  GCAAGG    ATGGAGAAG
                                || ||||||    |||||||||
                                AT  TGTTCC    TACTTTTTC
                                 TT     CG___
GAM455  FLJ10743  3' CTTCTCTGTTGGGGTGCC    37082     AGGA  TG
                                GGCA    CC  ATGGAGAAG
                                ||||    ||  |||||||||
                                CCGT    GG  TGTCTCTTC
                                  G___  GT
GAM455  FLJ11132  3' TTTTTCTATGGAGCTTGTCATA 37660         GA  TG
                                TATGGCAAG  CC  ATGGAGAAG
                                |||||||||  ||  |||||||||
                                ATACTGTTC  GG  TATCTTTTT
                                     GA  __
GAM455  FLJ11164  3' CTTCTCCGTTGTCGGGTGCCGT 37700       AG_  CT
                                ATGGCA   GAC  GATGGAGAAG
                                ||||||   |||  ||||||||||
                                TGCCGT   CTG  TTGCCTCTTC
                                   GGG   __
GAM455  FLJ11193  3' CTTTTCTGTTTTTGTTTTGCT  37749       ACCT
                                GGCAAGG    GATGGAGAAG
                                |||||||    ||||||||||
                                TCGTTTT    TTGTCTTTTC
                                    GTTT
GAM455  FLJ11259  3' TTTTTTTATCAGGAGAGC    37775    AAGGA
                                GC    CCTGATGGAGAAG
                                ||    ||||||||||||
```

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                              CG    GGACTATTTTTTT
                               AGA__
GAM455  FLJ11269 3' TTTTTTCATCAGTCGATTGT  73029     G_  C
                              GCAA  GAC TGATGGAGAAG
                              ||||  ||| ||||||||||
                              TGTT  CTG ACTACTTTTTT
                                AG  _
GAM455  FLJ11383 3' TTTCTTTGGGTTTTGTTGC   46857     __    TG T
                              GCAA  GGACC  A GGAGA
                              ||||  |||||  | |||||
                              CGTT  TTTGG  T TCTTT
                                GT    GT _
GAM455  FLJ12331 3' TTTTTCCTTGTTCTTGTCA   47117         CTGAT
                              TGGCAAGGAC    GGAGAAG
                              ||||||||||    |||||||
                              ACTGTTCTTG    CCTTTTT
                                    TT___
GAM455  FLJ12476 3' ATCATTCATCGTGTTTTTGTTA 43268          C     _  AG
           TA                   TATGGCAAGGAC TGATGGA GA
                              |||||||||||| ||||||| ||
                              ATATTGTTTTTG GCTACTT CT
                                     T      A  AT
GAM455  FLJ12644 3' TTTCTCTGCTCTTTGCCATG  43817          CCTGA
                              TATGGCAAGGA    TGGAGAAG
                              ||||||||||    ||||||||
                              GTACCGTTTCT    GTCTCTTT
                                     C_____
GAM455  FLJ12891 3' TTTTTTTGAGACGGGGTCTTGT 46938    TG    GA    A__ GG
           TGTG                 TA  GCAAG  CCTG   T  AGAAG
                              ||  |||||  ||||   |  |||||
                              GT  TGTTC  GGGC   G  TTTTT
                               GT    TG    AGA TT
GAM455  FLJ12985 3' CTTCTCCATCTATTTTGTTTA  46796   T     ACCT
                              A GGCAAGG    GATGGAGAAG
                              | |||||||    ||||||||||
                              A TTGTTTT    CTACCTCTTC
                               T      AT__
GAM455  FLJ12998 3' TTTCTCATTGGTTTTGCCGTG  43154        G   TGATG
                              TATGGCAAG ACC    GAGAAG
                              |||||||| |||    ||||||
                              GTGCCGTTT TGG    CTCTTT
                                    _  TTA__
GAM455  FLJ13096 3' CTTTTTTAAACTCTTGCTGTA  47174         ACC   TG
                              TATGGCAAGG   TGA  GAG
                              ||||||||||   |||  |||
                              ATGTCGTTCT   ATT  TTC
                                    CAA   TT
GAM455  FLJ13385 3' CTTCTCCATTAGGAGGGTTA   46283     AAGGA
                              TGGC    CCTGATGGAGAAG
                              ||||    ||||||||||||
```

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                                ATTG    GGATTACCTCTTC
                                  GGA__
GAM455  FLJ13576 3' TTTTTCTGATCCTTGTTA    42812        CCTGA
                                TGGCAAGGA    TGGAGAAG
                                |||||||||    ||||||||
                                ATTGTTCCT    GTCTTTTT
                                     A____
GAM455  FLJ13910 3' TTTGGTTGGGTTTTTGTTTG  43255   T       TG  G
                                A GGCAAGGACC  AT GAG
                                | ||||||||||  || |||
                                G TTGTTTTTGG  TG TTT
                                 T        GT  G
GAM455  FLJ20005 3' TTTTTTCATCTTTTTTGTTA  34772        CCT
                                TGGCAAGGA   GATGGAGAAG
                                |||||||||   ||||||||||
                                ATTGTTTTT   CTACTTTTTT
                                     T__
GAM455  FLJ20147 5' TTTTTCCCATGTCTTTGC    35139        C  AT
                                GCAAGGAC TG  GGAGAAG
                                |||||||| ||  |||||||
                                CGTTTCTG AC  CCTTTTT
                                     T  __
GAM455  FLJ20154 5' TTTTATTTCAGGTTTTTGCCA  73308           TG_   AG
                                TGGCAAGGACCTGA   GAGA
                                ||||||||||||||   ||||
                                ACCGTTTTTGGACT   TTTT
                                       TTA
GAM455  FLJ20273 3' CTTCTTCCTGGGTTTTTGTT   39248          GAT
                                GGCAAGGACCT   GGAGAAG
                                ||||||||||   |||||||
                                TTGTTTTTGGG   CTTCTTC
                                      TC_
GAM455  FLJ20280 5' TTTTTCTGGTTCCTTACTGTG  35336      C    _  TGAT
                                TATGG AAGGA CC    GGAGAAG
                                ||||| ||||| ||    |||||||
                                GTGTC TTCCT GG    TCTTTTT
                                   A    T  ____
GAM455  FLJ20509 3' CTTCTTCCTGCTGGGTTTTAGC 35759       A      AT_  _
           CATA                  TATGGC AGGACCTG   GGA GAAG
                                ||||||  ||||||||   ||| ||||
                                ATACCG TTTTGGGT   CCT CTTC
                                   A       CGT   T
GAM455  FLJ21272 3' CTTTTTTATTTACTTGCT    47393       GACCT
                                GGCAAG    GATGGAGAAG
                                ||||||    ||||||||||
                                TCGTTC    TTATTTTTTC
                                   AT___
GAM455  FLJ21276 3' TTTTTTCGTTTCATTTGTCAT  45263        GACCT
                                ATGGCAAG    GATGGAGAAG
                                ||||||||    ||||||||||
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                                TACTGTTT    TTGCTTTTTT
                                    ACT__
GAM455  FLJ21313  3'  TTTTTTCAGTTCTCCTGTTATG 43936       A   CCTGA
                                TATGGCA GGA    TGGAGAAG
                                ||||||| |||    ||||||||
                                GTATTGT CCT    ACTTTTTT
                                   _  CTTG_
GAM455  FLJ21817  3'  TTTTCTCAGCTAGTTTTTGT  42614        ___   T    AG
                                GCAAGGAC  CTGA GGAGA
                                ||||||||  |||| |||||
                                TGTTTTTG  GACT CTTTT
                                    ATC   _    C
GAM455  FLJ22174  5'  CTTTTTTGGAGTACTTGCTATA 41958        G  _ TG TG
                                TATGGCAAG AC C  A  GAG
                                ||||||||| || |  |  |||
                                ATATCGTTC TG G  T  TTC
                                     A  A GT TT
GAM455  FLJ22490  3'  TTTTTCCATCATCTGTATATA  45961     GCAA   CC
                                TATG   GGA  TGATGGAGAAG
                                ||||   |||  ||||||||||
                                ATAT   TCT  ACTACCTTTTT
                                  ATG_  __
GAM455  FLJ23356  3'  TTTTTTTATGGCTTAGCCATG  50929      A   A  TG
                                TATGGC AGG CC  ATGGAGAAG
                                |||||| ||| ||  |||||||||
                                GTACCG TTC GG  TATTTTTTT
                                   A  _ __
GAM455  FLJ25442  3'  CTTTTCCAGTTGATGTTTTTTG 59497          CCTGA___
          TCATG                 TATGGCAAGGA      TGGAGAAG
                                ||||||||||       ||||||||
                                GTACTGTTTTT      ACCTTTTC
                                     TGTAGTTG
GAM455  FLJ30046  3'  CTTTTTCATTTTTAATTTATTG 58723        GGACCT___
          TCATA                 TATGGCAA       GATGGAGAAG
                                ||||||||       ||||||||||
                                ATACTGTT       TTACTTTTTC
                                    ATTTAATTT
GAM455  GIT2    3'  TTTCTTTCTTTCCTTGTC    55154        CCT  T
                                GGCAAGGA   GA GGAGA
                                ||||||||   || |||||
                                CTGTTCCT   CT TCTTT
                                    TT_  T
GAM455  GIT2    3'  TTTCTTTCTTTCCTTGTC    29416        CCT  T
                                GGCAAGGA   GA GGAGA
                                ||||||||   || |||||
                                CTGTTCCT   CT TCTTT
                                    TT_  T
GAM455  GL004   3'  CTTCTTCATTAGGTACTTGT   66595      G
                                GCAAG ACCTGATGGAGAAG
                                ||||| ||||||||||||||
```

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                                TGTTC TGGATTACTTCTTC
                                   A
GAM455  GMEB2    3'  TTTCTCTGTTACATTTTTGTTT 25672    T      CC
                G                   A GGCAAGGA  TGATGGAGAAG
                                   | ||||||||  ||||||||||
                                   G TTGTTTTT  ATTGTCTCTTT
                                    T       AC
GAM455  GMEB2    3'  TTTTCCATCTGTTGCTTA    25673    T    AGG  CT
                                   A GGCA   AC  GATGGAGAA
                                   | ||||   ||  |||||||||
                                   A TCGT   TG  CTACCTTTT
                                    T    ___  T_
GAM455  GOLPH3   3'  TTTCTTTATCACTTTATTGT   42395      G  CC
                                   GCAA GA  TGATGGAGAAG
                                   |||| ||  ||||||||||
                                   TGTT TT  ACTATTTCTTT
                                      A  TC
GAM455  GRIN3A   3'  CTTTTCCATCTTCAGTTTCT   56781      C    ___
                                   AGGA CTGA   TGGAGAAG
                                   |||| ||||   ||||||||
                                   TCTT GACT   ACCTTTTC
                                      T    TCT
GAM455  H3F3A    3'  TTTTTCCATTTTCATTTGT    10901       GACCT
                                   GCAAG     GATGGAGAAG
                                   |||||     ||||||||||
                                   TGTTT     TTACCTTTTT
                                      ACTT_
GAM455  HCC8     3'  TTTTTTTACAGATCTTTCTATA 33696       C    C   A
                                   TATGG AAGGA CTG TGGAGAAG
                                   ||||| ||||| ||| ||||||||
                                   ATATC TTTCT GAC ATTTTTTT
                                      _     A   _
GAM455  HEY1     3'  TTTTTCATCATGTCATGT    92887     AG   C
                                   GCA  GAC TGATGGAGAA
                                   |||  ||| ||||||||||
                                   TGT  CTG ACTACTTTTT
                                     A_   T
GAM455  HMP19    3'  TTCTTTGTCTTTTGCTTG    88863    T     ACCT  TG
                                   A GGCAAGG    GA  GAGAA
                                   | |||||||    ||  |||||
                                   G TCGTTTT    CT  TTCTT
                                    T      _____  GT
GAM455  HMP19    3'  TTTTTTTGTGGCTTGCTGTG   88864         GA  TG TG
                                   TATGGCAAG  CC  A  GAGAAG
                                   |||||||||  ||  |  ||||||
                                   GTGTCGTTC  GG  T  TTTTTT
                                         __  __ GT
GAM455  HPCAL4   3'  CTTCTTCATCAGGTCTTTCTCC 33207    C_
                                   GG  AAGGACCTGATGGAGAAG
                                   ||  ||||||||||||||||||
```

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                                CC  TTTCTGGACTACTTCTTC
                                 TC
GAM455  HSA249128 3'  TTTCCATTGTAGGTTTTTGCTA 34563          __      AG
                                TGGCAAGGACCT  GATGGAGA
                                ||||||||||||  ||||||||
                                ATCGTTTTTGGA  TTACCTTT
                                      TG
GAM455  HSPC128  3'  CTATTAGGTTCTTCTGTG    27180      C
                                TATGG AAGGACCTGATGG
                                ||||| ||||||||||||
                                GTGTC TTCTTGGATTATC
                                  _
GAM455  HSPC177  3'  CTTTTTGATGGGTTTTGTTGTG 33525    TG    G   G  G
                                TA  GCAAG ACCT AT GAGAAG
                                ||  ||||| |||| || ||||||
                                GT  TGTTT TGGG TA TTTTTC
                                 GT    _   _ G
GAM455  HSU79252  5'  CTTCTCCATCTAGAGATTTTTG 26142        C  ___
           T                     GCAAGGA CT   GATGGAGAAG
                                |||||||  ||   ||||||||||
                                TGTTTTT GA   CTACCTCTTC
                                    A  GAT
GAM455  HYPH     3'  TTTTTTCATTCATATTTTTGTT 96572    TG      CC  _
           GT                     A  GCAAGGA  TGA TGGAGAAG
                                |  |||||||  |||  ||||||||
                                T  TGTTTTT  ACT ACTTTTTT
                                 GT      AT   T
GAM455  KIAA0061  3'  CATTGGGTTTTTACTGTA    68836      C      TG
                                TATGG AAGGACC  ATG
                                |||||  |||||||  |||
                                ATGTC TTTTTGG  TAC
                                   A      GT
GAM455  KIAA0121  3'  TTTTTTTGTCGTAGATTTGTC  73048       GACC   TG
                                GGCAAG    TGA  GAGAAG
                                ||||||    |||  ||||||
                                CTGTTT    GCT  TTTTTT
                                    AGAT   GT
GAM455  KIAA0179  3'  CTTCTGCTGAGGTCCTTGC    65454          GA  _
                                GCAAGGACCT  TGG AGAAG
                                ||||||||||  ||| |||||
                                CGTTCCTGGA  GTC TCTTC
                                      __  G
GAM455  KIAA0186  3'  TTTTTTCGTTTGTTTCTTTGTT 41133         CCT_
                                GGCAAGGA    GATGGAGAAG
                                ||||||||    ||||||||||
                                TTGTTTCT    TTGCTTTTTT
                                     TTGT
GAM455  KIAA0237  3'  CTTTTCCCTGCAATGGGTTTTT 29223      G       ___ AT_
           GGTATG                  TATG CAAGGACCT   G   GGAGAAG
                                |||| |||||||||   |   |||||||
```

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                                GTAT GTTTTTGGG  C   CCTTTTC
                                  G       TAA GTC
GAM455  KIAA0261 3' TTCTTCATTGGATTTGT     68746      GA  T
                                GCAAG  CC GATGGAGAA
                                ||||||  || |||||||||
                                TGTTT  GG TTACTTCTT
                                  A_  _
GAM455  KIAA0261 3' TTTTTTCATTCAGATTCTTTGT 68747      _     C_   _
           TCGTA                  TATGG CAAGGA  CTGA TGGAGAAG
                                ||||||  ||||||  ||||  ||||||||
                                ATGCT GTTTCT  GACT ACTTTTTT
                                  T     TA   T
GAM455  KIAA0352 3' TTTTTCCTAGACAGGTTTTTGC 29833           AT__
           TA                    TGGCAAGGACCTG   GGAGAAG
                                ||||||||||||||   |||||||
                                ATCGTTTTTGGAC   CCTTTTT
                                       AGAT
GAM455  KIAA0436 3' CTTCTCCATCTAAATTTTGCTT 60685   T     ACCT
           A                     A GGCAAGG   GATGGAGAAG
                                | |||||||   ||||||||||
                                A TCGTTTT   CTACCTCTTC
                                 T      AAAT
GAM455  KIAA0469 3' CTTTTTTGCGGCTTTGCTGTG  29980         A  T A GG
                                TATGGCAAGG CC G T  AGAAG
                                |||||||||| || | |  |||||
                                GTGTCGTTTC GG C G  TTTTC
                                      _  _ _ TT
GAM455  KIAA0470 3' TTTCTTCATTAGGGGACTTG   29718     GA_
                                CAAG   CCTGATGGAGAAG
                                ||||   ||||||||||||||
                                GTTC   GGATTACTTCTTT
                                  AGG
GAM455  KIAA0530 3' TTTTTTTATTTTGTGTTTGTTA 71433         G  CT
           TA                    TATGGCAAG AC  GATGGAGAAG
                                |||||||||  ||  ||||||||||
                                ATATTGTTT TG  TTATTTTTTT
                                      G  TT
GAM455  KIAA0557 3' TTTTTTTGAGACGGGGCCTTGC 78581          A   A__ GG
           TGTG                   TATGGCAAGG CCTG   T  AGAAG
                                |||||||||| ||||   |  |||||
                                GTGTCGTTCC GGGC   G  TTTTT
                                      G    AGA TT
GAM455  KIAA0618 3' CTTTTCTATTCCTCTTGCC   29852       ACCT
                                GGCAAGG   GATGGAGAAG
                                |||||||   ||||||||||
                                CCGTTCT   TTATCTTTTC
                                    CC__
GAM455  KIAA0628 3' CTTTTCCGTGTCGTCTTTTGT  29530      _  CTG
                                GCAAG GAC   ATGGAGAAG
                                ||||| |||   |||||||||
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                                TGTTT CTG   TGCCTTTTC
                                   T   CTG
GAM455  KIAA0836 3' TTTCTTTAAGTTTTTCTTTGCT 65170        CCTGA_
                                GGCAAGGA     TGGAGAAG
                                ||||||||     ||||||||
                                TCGTTTCT     ATTTCTTT
                                    TTTTGA
GAM455  KIAA0863 3' CTTCTTTGTAAGATCTTTGCTT 96952    T       C  G TG
            A                    A GGCAAGGA CT A  GAGAAG
                                | ||||||||| || |  ||||||
                                A TCGTTTCT GA T  TTCTTC
                                 T       A  A GT
GAM455  KIAA0863 3' CTTCTTTGTAAGATCTTTGCTT 96953    T       C  G TG
            A                    A GGCAAGGA CT A  GAGAAG
                                | ||||||||| || |  ||||||
                                A TCGTTTCT GA T  TTCTTC
                                 T       A  A GT
GAM455  KIAA0894 3' CTTCTTTGTTCTATGGTTTTTG 30332     GG       T___  TG
            ATGTA                TAT  CAAGGACC    GA  GAGAAG
                                ||| |||||||||   ||  ||||||
                                ATG  GTTTTTGG    TT  TTCTTC
                                  TA       TATC  GT
GAM455  KIAA0931 3' TTTTTCCATTGGAAGATTTGCT 68026    T     GAC_ TG
            TA                   A GGCAAG    C  ATGGAGAAG
                                | ||||||    |  |||||||||
                                A TCGTTT    G  TACCTTTTT
                                 T     AGAA GT
GAM455  KIAA0934 3' TTCTCTGCCTTTGCTATA     64886          ACCTGAT
                                TATGGCAAGG      GGAGAA
                                ||||||||||      ||||||
                                ATATCGTTTC      TCTCTT
                                     CG_____
GAM455  KIAA0934 3' TTTCTCTGTTTTAATGTGTCAT 64887        AGGACCT
            G                    TATGGCA      GATGGAGAAG
                                |||||||      ||||||||||
                                GTACTGT      TTGTCTCTTT
                                    GTAATT_
GAM455  KIAA0934 3' TTTTTTTGGTCCTTGCTA     64888          TGAT
                                TGGCAAGGACC    GGAGA
                                ||||||||||    |||||
                                ATCGTTCCTGG    TTTTT
                                      TT__
GAM455  KIAA1005 3' TTTCTCTATTCCCTCCTTCTCA 72746      C    CCT
            TA                    TATGG AAGGA   GATGGAGAAG
                                ||||| |||||   ||||||||||
                                ATACT TTCCT   TTATCTCTTT
                                   C    CCC
GAM455  KIAA1030 3' TTTCAAGGTCCCTGTTGTA    94989    TG  A    GA
                                TA  GCA GGACCT  TGGAG
                                ||  ||| ||||||  |||||
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                                AT  TGT CCTGGA  ACTTT
                                 GT   C     __
GAM455  KIAA1034  3'  TTTCTTTAAAAGTTTTTTGTTA 63136          C  GA
                                TGGCAAGGA CT  TGGAGAAG
                                |||||||||  ||  ||||||||
                                ATTGTTTTT GA  ATTTCTTT
                                     T  AA
GAM455  KIAA1041  3'  TTTCTCTGTCTTGGCATTCTTG 30837          __  T_
            CT                   GGCAAGGA  CC  GATGGAGAAG
                                |||||||||  ||  ||||||||||
                                TCGTTCTT  GG  CTGTCTCTTT
                                    AC  TT
GAM455  KIAA1049  3'  TTTCTCTGTTGGTCGGAGTCG  31066      AAG    T
                                TGGC   GACC GATGGAGAAG
                                ||||   |||| ||||||||||
                                GCTG   CTGG TTGTCTCTTT
                                  AGG   _
GAM455  KIAA1069  3'  TTTCTTTGTCAGACGTCTCCAT 68536      CAA   __    TG
            G                    TATGG   GGAC  CTGA  GAGAAG
                                ||||||   ||||  ||||  ||||||
                                GTACC   TCTG  GACT  TTCTTT
                                   ___    CA    GT
GAM455  KIAA1076  3'  CTTTTTTGTTGTTGGTGGTTTT 66123    TG     __   T__  TG
            GTTGTG                TA  GCAAGG  ACC   GA  GAGAAG
                                ||  ||||||  |||   ||  ||||||
                                GT  TGTTTT  TGG   TT  TTTTTC
                                 GT     GG   TTG  GT
GAM455  KIAA1077  3'  CTTTTTTGGTTTTCTTGGCATG 73289      G     C_ TG TG
                                TATG CAAGGA  C  A  GAG
                                |||| ||||||  |  |  |||
                                GTAC GTTCTT  G  T  TTC
                                  G     TT GT TT
GAM455  KIAA1084  3'  TTTTTCATGAGCTTCCATG    30507      C   GAC  G
                                TATGG AAG   CT ATGGAGAA
                                ||||| |||   || ||||||||
                                GTACC TTC   GA TACTTTTT
                                   _   ___  G
GAM455  KIAA1091  3'  CTTTTTTGTCAGTATTGTTTG  70262    T    GGAC    TG
                                A GGCAA    CTGA  GAGAAG
                                | |||||    ||||  ||||||
                                G TTGTT    GACT  TTTTTC
                                 T    AT__    GT
GAM455  KIAA1143  3'  TTTTTCCATTAGTATGGTCATA 69254        AAGGAC
                                TATGGC     CTGATGGAGAAG
                                ||||||     ||||||||||||
                                ATACTG     GATTACCTTTTT
                                   GTAT__
GAM455  KIAA1157  3'  CTTCTCTGTTTCTATTCTTTTA 72699      C    CCT_
            TG                   TATGG AAGGA    GATGGAGAAG
                                |||||  |||||    ||||||||||
```

```
                                GTATT TTCTT    TTGTCTCTTC
                                  _    ATCT
GAM455  KIAA1184  3'  CTTCTCCGTCAGGAGGCC    42928     AAGGA
                                GGC    CCTGATGGAGAAG
                                |||    ||||||||||||
                                CCG    GGACTGCCTCTTC
                                 GA___
GAM455  KIAA1185  3'  TTTTTCCAGATGATTCTGTCGT 63298        A   CCTGA
          A                      TATGGCA GGA    TGGAGAAG
                                |||||||  |||    ||||||||
                                ATGCTGT CTT    ACCTTTTT
                                   _  AGTAG
GAM455  KIAA1209  3'  CTTCTCCAAAGTATTCTTCTCA 61404      C    C_  GA
          TA                     TATGG AAGGA  CT  TGGAGAAG
                                ||||| |||||  ||  ||||||||
                                ATACT TTCTT  GA  ACCTCTTC
                                   C    AT  A_
GAM455  KIAA1238  3'  CTTTTTTAGGCCTTTTTGTG   71635    TG C    A    TG   AAG
                                TA  G AAGG CCTGA  GAG
                                ||  | |||| |||||  |||
                                GT  T TTCC GGATT  TTC
                                 GT T   _    TT
GAM455  KIAA1247  3'  TTTCTCCTAGTATTTCTTTGTT 62511          CC  AT_
          ATG                    TATGGCAAGGA  TG   GGAGAAG
                                ||||||||||  ||   |||||||
                                GTATTGTTTCT  AT   CCTCTTT
                                      TT  GAT
GAM455  KIAA1287  3'  CTTTTTCATCAGATTTGTT    78938       GAC
                                GGCAAG   CTGATGGAGAAG
                                ||||||   ||||||||||||
                                TTGTTT   GACTACTTTTTC
                                   A__
GAM455  KIAA1297  3'  CTTCTGAGAAGGTCTTTGTCA  72639           GATGG
                                TGGCAAGGACCT    AGAAG
                                ||||||||||||    |||||
                                ACTGTTTCTGGA    TCTTC
                                      AGAG_
GAM455  KIAA1305  3'  TTTTTTCATTTGATTTGTCA   47626        GACCT
                                TGGCAAG    GATGGAGAAG
                                |||||||    ||||||||||
                                ACTGTTT    TTACTTTTTT
                                    AGT__
GAM455  KIAA1321  3'  CTTTTCTAATTTCCTTCCATA  62900      C    CCTGA
                                TATGG AAGGA    TGGAGAAG
                                ||||| |||||    ||||||||
                                ATACC TTCCT    ATCTTTTC
                                   _    TTA__
GAM455  KIAA1323  3'  TTTCTTTATAGTATTTTTTGTT 63728          CCTG_
          ATA                    TATGGCAAGGA    ATGGAGAAG
                                ||||||||||    |||||||||
```

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                                ATATTGTTTTT    TATTTCTTT
                                      TATGA
GAM455  KIAA1354 3' TTTTCGTAGTTTTTGTCATG  61579         CTG
                                TATGGCAAGGAC  ATGGAGA
                                ||||||||||||  |||||||
                                GTACTGTTTTTG  TGCTTTT
                                      A__
GAM455  KIAA1363 3' ATATATCATTAGGTTTTTGTTG 69790    TG          AGAAG
           TG                   TA  GCAAGGACCTGATGG
                                ||  ||||||||||||||
                                GT  TGTTTTTGGATTACT
                                 GT           ATATAT
GAM455  KIAA1371 3' CTTTTTTGTTCTTCTGCTATA  90476       A  CCT  TG
                                TATGGCA GGA   GA  GAGAAG
                                ||||||| |||   ||  ||||||
                                ATATCGT CTT   TT  TTTTTC
                                    _  C__  GT
GAM455  KIAA1449 3' TTTTATATGCAGGTTTTTGTTG 40845    TG       _  G   G
           TA                   TA  GCAAGGACCTG ATG AGAA
                                ||  ||||||||||| ||| ||||
                                AT  TGTTTTTGGAC TAT TTTT
                                 GT         G  A
GAM455  KIAA1458 3' TTTCTCTGTCAGAGTTATTTCA 69574      CAAG  _
           TA                   TATGG   GAC CTGATGGAGAAG
                                |||||   ||| ||||||||||||
                                ATACT   TTG GACTGTCTCTTT
                                   TTA_  A
GAM455  KIAA1467 3' CTTCTCTGCATCTTTTTCTATA 72066      C    CC  A
                                TATGG AAGGA  TG TGGAGAAG
                                ||||| |||||  || ||||||||
                                ATATC TTTTT  AC GTCTCTTC
                                   _    CT  _
GAM455  KIAA1594 3' CTTTTTTGTCATTCTGCCATG  72552       A  CC  TG
                                TATGGCA GGA  TGA  GAGAAG
                                ||||||| |||  |||  ||||||
                                GTACCGT CTT  ACT  TTTTTC
                                    _  ___  GT
GAM455  KIAA1610 3' TTCTCCCATTCCTTGTC     67741        CC  AT
                                GGCAAGGA  TG  GGAGAA
                                ||||||||  ||  ||||||
                                CTGTTCCT  AC  CCTCTT
                                     T_  ___
GAM455  KIAA1673 3' TAATTTTCATCAGATTTTTGTT 71328          C       AG
           ATA                    TATGGCAAGGA CTGATGGAGA
                                  ||||||||||| ||||||||||
                                  ATATTGTTTTT GACTACTTTT
                                        A        AATA
GAM455  KIAA1766 3' TTTTTTCAGTTCTTGTCAT   71877          C  TG
                                ATGGCAAGGAC TGA  GAG
                                |||||||||| |||  |||
```

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                                TACTGTTCTTG ACT  TTT
                                      _  TT
GAM455  KIAA1795 3' CTTTTTTGTTTTTTTTTTGTTGT 72614   TG     CCT  TG
                                A  GCAAGGA   GA  GAGAAG
                                |  |||||||   ||  ||||||
                                T  TGTTTTT   TT  TTTTTC
                                 GT      TT_  GT
GAM455  KIAA1925 3' TTTTTCCTCATATTTGTCGTA  93716        GACC   T
                                TATGGCAAG    TGA GGAGAAG
                                |||||||||    ||| |||||||
                                ATGCTGTTT    ACT CCTTTTT
                                     AT__   _
GAM455  KIAA1972 3' TTTTTCCACCCCTTCTTGTT   93414        CCTGA
                                GGCAAGGA    TGGAGAAG
                                ||||||||    ||||||||
                                TTGTTCTT    ACCTTTTT
                                     CCCC_
GAM455  KIAA1979 3' CTTCTCTTCCATTCTTTGCCAT 89652         CC  AT
                                ATGGCAAGGA  TG  GGAGAAG
                                ||||||||||  ||  |||||||
                                TACCGTTTCT  AC  TCTCTTC
                                      T_  CT
GAM455  KIAA1979 3' TTTCTCTGTAAATTTGTTATA  89658         GACCTG
                                TATGGCAAG     ATGGAGAAG
                                |||||||||     |||||||||
                                ATATTGTTT     TGTCTCTTT
                                     AAA___
GAM455  KIAA1987 3' TTTCTTTAGCCAACTTTGCT   89397       ACC  A_
                                GGCAAGG   TG  TGGAGAAG
                                |||||||   ||  ||||||||
                                TCGTTTC   AC  ATTTCTTT
                                    A__  CG
GAM455  LDHL     3' TTTCTTTCATTCTTGCT     53753        CC   T
                                GGCAAGGA  TGA GGAGA
                                ||||||||  ||| |||||
                                TCGTTCTT  ACT TCTTT
                                     __   T
GAM455  LHFP     3' TTTCTCTGAGTAGCTTCTGCTA 20511       A   C   AT_
           TG                    TATGGCA GGA CTG   GGAGAAG
                                |||||||  ||| |||   |||||||
                                GTATCGT CTT GAT   TCTCTTT
                                    _  C   GAG
GAM455  LIG-1    3' CTACCTCAGTTCTTGTCATA   64612          C   T  _
                                TATGGCAAGGAC TGA GG AG
                                |||||||||||| ||| || ||
                                ATACTGTTCTTG ACT CC TC
                                      _  _  A
GAM455  LIN-7-C  3' CTTTTTCAAATGCAGATTTTGT 37754         AC   A___
           CATA                   TATGGCAAGG  CTG    TGGAGAAG
                                |||||||||  |||   ||||||||
```

```
                                ATACTGTTTT  GAC   ACTTTTTC
                                     A_  GTAA
GAM455  MADHIP   3'  TTTTTCTGTTCAGACTTGTTGC 17821     G  C_   _
                                GCAA GA  CTGA TGGAGAAG
                                |||| ||  |||| ||||||||
                                CGTT TT  GACT GTCTTTTT
                                  G  CA   T
GAM455  MADHIP   3'  TTTTTCTGTTCAGACTTGTTGC 17822     G  C_   _
                                GCAA GA  CTGA TGGAGAAG
                                |||| ||  |||| ||||||||
                                CGTT TT  GACT GTCTTTTT
                                  G  CA   T
GAM455  MARCKS   5'  TTTCTCCATTTTCCTCTTGTC  11415       ACCT
                                GGCAAGG   GATGGAGAAG
                                |||||||   ||||||||||
                                CTGTTCT   TTACCTCTTT
                                    CCTT
GAM455  MBLL39   3'  TTTTTCTGTTTTTTTCTTTGTT 59264        CCT_
            A                    TGGCAAGGA   GATGGAGAAG
                                |||||||||   ||||||||||
                                ATTGTTTCT   TTGTCTTTTT
                                     TTTT
GAM455  MGC12466 3'  TTTCTTCTGTTTTCTTTGCTA  79800        CCTGAT
                                TGGCAAGGA    GGAGAAG
                                |||||||||    |||||||
                                ATCGTTTCT    CTTCTTT
                                     TTTGT_
GAM455  MGC12466 3'  TTTCTTCTGTTTTCTTTGCTA  79801        CCTGAT
                                TGGCAAGGA    GGAGAAG
                                |||||||||    |||||||
                                ATCGTTTCT    CTTCTTT
                                     TTTGT_
GAM455  MGC13007 3'  CTTCTTCATTGTGAGATGCACA 51278     _  AGGACCT
            TA                   TATG GCA     GATGGAGAAG
                                |||| |||     ||||||||||
                                ATAC CGT     TTACTTCTTC
                                  A  AGAGTG_
GAM455  MGC14289 3'  TTTTTTGTAGAGAGGGTATTTT 55598         _   GA__  G
            GCCATG                TATGGCAAGG ACCT   TG AGAAG
                                |||||||||| ||||   || |||||
                                GTACCGTTTT TGGG   AT TTTTT
                                     A   AGAG  G    TT
GAM455  MGC14798 3'  TTTCTCTGTATCTTGTCATG  55546        ACCTG
                                TATGGCAAGG    ATGGAGAAG
                                ||||||||||    |||||||||
                                GTACTGTTCT    TGTCTCTTT
                                     A____
GAM455  MGC21688 3'  CTTCTCCGTTGTGTGTTTTGC  58915      _  C
                                GCAAGG AC TGATGGAGAAG
                                |||||| || ||||||||||
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                                CGTTTT TG GTTGCCTCTTC
                                   G  T
GAM455  MGC2404   3'  CTTTTCCACCCGTCTTTGGTAT 51361      G      CTGA
              G                    TATG CAAGGAC    TGGAGAAG
                                   |||| |||||||    ||||||||
                                   GTAT GTTTCTG    ACCTTTTC
                                     G      CCC_
GAM455  MGC26954  3'  CTTCTCCTATGGTTTTGCCGTG 59492         G   TGAT
                                   TATGGCAAG ACC    GGAGAAG
                                   ||||||||| |||    |||||||
                                   GTGCCGTTT TGG    CCTCTTC
                                         _  TAT_
GAM455  MGC4701   5'  CTTCTCTGTGGACTTGGTATA  65162      G    GA  TG
                                   TATG CAAG  CC  ATGGAGAAG
                                   |||| ||||  ||  |||||||||
                                   ATAT GTTC  GG  TGTCTCTTC
                                     G    A_  __
GAM455  MMD      3'  TTTCTCTATGCCTTTGCCA    60514         ACCTG
                                   TGGCAAGG     ATGGAGAAG
                                   ||||||||     |||||||||
                                   ACCGTTTC     TATCTCTTT
                                        CG___
GAM455  MRPS16    5'  CTTGCAGGTTCTTTCTGTG    32677       C        AT
                                   TATGG AAGGACCTG  GG
                                   ||||| |||||||||  ||
                                   GTGTC TTCTTGGAC  TC
                                      T        GT
GAM455  MYNN     3'  TTTCTCTATTAATATATTGTTA 38481        GGACC
                                   TGGCAA     TGATGGAGAAG
                                   ||||||     ||||||||||||
                                   ATTGTT     ATTATCTCTTT
                                       ATATA
GAM455  NPAS3     3'  TTTCTTCATAAAGATCTTGATA 42353      G     ACCTG
              TG                     TATG CAAGG     ATGGAGAAG
                                   |||| |||||     |||||||||
                                   GTAT GTTCT     TACTTCTTT
                                     A     AGAAA
GAM455  NPTXR     3'  TTCTCCAACTCTTGCTTG     27449    T      ACCTGA
                                   A GGCAAGG      TGGAGAA
                                   | |||||||      |||||||
                                   G TCGTTCT      ACCTCTT
                                    T      CA____
GAM455  NUCKS     3'  CTTTTTTATTTCATCACTTGTT 43002         _  CCT
              AT                     ATGGCAAG GA   GATGGAGAAG
                                   |||||||| ||   ||||||||||
                                   TATTGTTC CT   TTATTTTTTC
                                        A  ACT
GAM455  NUP107    3'  TTTCTCTGTGTGCTTGTTA    40238        G  CTG
                                   TGGCAAG AC   ATGGAGAAG
                                   ||||||| ||   |||||||||
```

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                                ATTGTTC TG   TGTCTCTTT
                                   G ___
GAM455  NXP-2    3'  TTTTGCCAGGATTTTGTTGTG  71661    TG     A    AT
                                TA  GCAAGG CCTG  GGAG
                                ||  |||||| ||||  ||||
                                GT  TGTTTT GGAC  TTTT
                                  GT     A    CG
GAM455  OLFM2    3'  TTTCTCCCCGCCTTTTTGCT   55169        CC  AT
                                GGCAAGGA  TG  GGAGAAG
                                ||||||||  ||  |||||||
                                TCGTTTTT  GC  CCTCTTT
                                     CC  C_
GAM455  OLFM3    3'  CTATCATGTCCTTGTCATG    83024           C
                                TATGGCAAGGAC TGATGG
                                |||||||||||| ||||||
                                GTACTGTTCCTG ACTATC
                                       T
GAM455  OR2C3    3'  TTGCGTTGTTGGTTTTTGCTAT 75978            T__    G  AAG
           A                     TATGGCAAGGACC   GATG AG
                                ||||||||||||   |||| ||
                                ATATCGTTTTTGG   TTGC TT
                                       TTG    G
GAM455  OSBPL10  3'  TTTTTCTATTTTTCACTTTGCC 35527         ACCT_
           A                     TGGCAAGG     GATGGAGAAG
                                ||||||||     ||||||||||
                                ACCGTTTC     TTATCTTTTT
                                     ACTTT
GAM455  OSBPL11  5'  TTTTTCCATCCTTGCTTTTGCC 43209         _ ACCT
           G                     TGGCAAG G    GATGGAGAAG
                                ||||||| |    ||||||||||
                                GCCGTTT C    CTACCTTTTT
                                   T GTTC
GAM455  p47      3'  TTTCCTGGGTTTTTGTGATG   32863     G        GAT
                                TAT GCAAGGACCT   GGAGA
                                ||| ||||||||||   |||||
                                GTA TGTTTTTGGG   CCTTT
                                  G        T__
GAM455  P66      3'  TTTTTTCATCACTGATTGCC   40747       GGACC
                                GGCAA     TGATGGAGAAG
                                |||||     ||||||||||
                                CCGTT     ACTACTTTTTT
                                   AGTC_
GAM455  PB1      3'  TTTCTTGGTTTTGGGTTTTTTT 36883       C       __   G
           ATA                     TATGG AAGGACCT  GAT GAGAAG
                                ||||| ||||||||  ||| ||||||
                                ATATT TTTTTGGG  TTG TTCTTT
                                   _       TT   G
GAM455  PDE2A    3'  TTCTCCGTTTCATTCTGT     12009     A   CCT
                                GCA GGA   GATGGAGAA
                                ||| |||   |||||||||
```

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                                TGT CTT   TTGCCTCTT
                                  _   ACT
GAM455  PDE4DIP  3'  CTTCTTCAGCCTTCTTTCCTGT 97176      C     CCTGA
            A                    TATGG AAGGA     TGGAGAAG
                                 ||||| |||||     ||||||||
                                 ATGTC TTTCT     ACTTCTTC
                                    C     TCCG_
GAM455  PDP      3'  CTTCTTTATCACAGGTGTCTTG 38029       _    __
                                 CAAGG ACCT  GATGGAGAAG
                                 ||||| ||||  ||||||||||
                                 GTTCT TGGA  CTATTTCTTC
                                    G    CA
GAM455  phospho1  3'  CTTTTCCCTTTGGCTTTGTTAT 83246          A  T  T
            G                    TATGGCAAGG CC GA GGAGAAG
                                 |||||||||| || || |||||||
                                 GTATTGTTTC GG TT CCTTTTC
                                       _  T  C
GAM455  PI4KII   3'  TTTCTTTTGGGTTTTTGCCA   37958           TG T
                                 TGGCAAGGACC  A GGAGA
                                 ||||||||||  | |||||
                                 ACCGTTTTTGG  T TCTTT
                                       GT T
GAM455  PLP1     3'  TTTTCCTGTTTTTGTTA     6762           CTGAT
                                 TGGCAAGGAC    GGAGAA
                                 |||||||||     ||||||
                                 ATTGTTTTTG    CCTTTT
                                       T_____
GAM455  PLSCR4   3'  TTTCTTTATATAATATTGTCAT 40136         GGACCTG
            A                    TATGGCAA      ATGGAGAAG
                                 ||||||||      |||||||||
                                 ATACTGTT      TATTTCTTT
                                     ATAATA_
GAM455  PP1044   5'  TTTCCGTCTTTGTTGTCA    41677       G  CCT
                                 TGGCAA GA   GATGGAGA
                                 |||||| ||   ||||||||
                                 ACTGTT TT   CTGCCTTT
                                    G  T__
GAM455  PPP1R14C  3'  TTTTAAAGGTTTTTGTTA    48931           GATG
                                 TGGCAAGGACCT    GAGA
                                 ||||||||||||    ||||
                                 ATTGTTTTTGGA    TTTT
                                       AA__
GAM455  PREI3    3'  GCTTCTTTGTTTAGTATAGGTT 66925          _______ TG
            TTTGT                  GCAAGGACCT     GA  GAGAAG   C
                                 ||||||||||     ||  ||||||   |
                                 TGTTTTTGGA     TT  TTCTTC   G
                                       TATGAT  GT
GAM455  PRO0149   5'  TTTTTCCATAAAAATCTTGCCA 26944         ACCTG
                                 TGGCAAGG    ATGGAGAAG
                                 ||||||||    |||||||||
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                                ACCGTTCT    TACCTTTTT
                                    AAAAA
GAM455  PRO2964  5'  TTTCTTCATAAATTTTTGTTGC 38266     G  CCTG__
                                GCAA GA     ATGGAGAAG
                                |||| ||     |||||||||
                                CGTT TT     TACTTCTTT
                                  G  TTTAAA
GAM455  PRRG1    3'  TTTCTTTAGTTTTGTTTCTTGT 8157          CCTGA__
          TATA                    TATGGCAAGGA      TGGAGAAG
                                |||||||||||      ||||||||
                                ATATTGTTCTT      ATTTCTTT
                                      TGTTTTG
GAM455  PSMA4    3'  CTGAATTGGGTCCTTGTCAT   12452          TG  GG
                                ATGGCAAGGACC  AT  AG
                                ||||||||||||  ||  ||
                                TACTGTTCCTGG  TA  TC
                                      GT  AG
GAM455  PSMD12   3'  TTTTTCTAAGCTTCTTTGTC   12536        CCTGA
                                GGCAAGGA    TGGAGAAG
                                ||||||||    ||||||||
                                CTGTTTCT    ATCTTTTT
                                    TCGA_
GAM455  PTPRR    5'  TTTTTCTCAGCATCTTTGTTAT 56452          C_   T    G
                                ATGGCAAGGA  CTGA GGAGAA
                                ||||||||||  |||| ||||||
                                TATTGTTTCT  GACT CTTTTT
                                    AC   _
GAM455  RAB33B   3'  GTTTTTTCATAGAGACGGGGTC 49334         GA   _____
          TTGCTATG                TATGGCAAG  CCTG    ATGGAGAAG   T
                                |||||||||  ||||    |||||||||  |
                                GTATCGTTC  GGGC    TACTTTTTT   G
                                    TG    AGAGA
GAM455  RAB6C    5'  CTTTTTCGTCAGCCGGCT    50485     AA  AC
                                GGC  GG  CTGATGGAGAAG
                                |||  ||  ||||||||||||
                                TCG  CC  GACTGCTTTTTC
                                  G_  __
GAM455  RBM12    3'  CTTCTTAAGGGTCCTTGCTGTA 21281            GATG
                                TATGGCAAGGACCT    GAGAAG
                                ||||||||||||||    ||||||
                                ATGTCGTTCCTGGG    TTCTTC
                                      AA__
GAM455  RFX4     3'  TTTTTCTGTCAGATTTGTAGTA 12859     G    GAC
                                TAT GCAAG   CTGATGGAGAAG
                                ||| |||||   ||||||||||||
                                ATG TGTTT   GACTGTCTTTTT
                                  A    A__
GAM455  RNF2     3'  TTTTTTTGTAATCTGTGCCATG 24259        A   CCTG TG
                                TATGGCA GGA    A  GAGAAG
                                |||||||  |||    |  ||||||
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```
                                GTACCGT TCT    T  TTTTTT
                                    G   AA__ GT
GAM455  RNF38    3'  TTTTTTGTGGGTTCTTGTTTG  43265    T         G TG
                                A GGCAAGGACCT A  GAGAA
                                | ||||||||||| |  |||||
                                G TTGTTCTTGGG T  TTTTT
                                 T         _ GT
GAM455  RNF8     3'  TTTCTTTATTACAGCTGCC    15581      AG ACC
                                GGCA  G   TGATGGAGAAG
                                ||||  |   ||||||||||
                                CCGT  C   ATTATTTCTTT
                                  __ GAC
GAM455  RNPC1    3'  TTCTCCATCAGGGCACGTG    34415      _  AAGGA
                                TATG GC    CCTGATGGAGAA
                                |||| ||    ||||||||||||
                                GTGC CG    GGACTACCTCTT
                                  A _____
GAM455  RPIA     3'  TTTCTCTGTTCCTTTGTTAT   58596          ACCT
                                ATGGCAAGG   GATGGAGAAG
                                |||||||||   ||||||||||
                                TATTGTTTC   TTGTCTCTTT
                                     C___
GAM455  RPL27    5'  TTCTTTCCTTTTTGCTGTA    8270           CCT  TG
                                TATGGCAAGGA   GA  GAGAA
                                ||||||||||   ||  |||||
                                ATGTCGTTTTT   CT  TTCTT
                                      C__  __
GAM455  RRN3     3'  CTTCTCTAAAGCCTCTTTTTGT 37959    TG C    AC  GA
           A                     TA  G AAGG  CT  TGGAGAAG
                                ||  | ||||  ||  ||||||||
                                AT  T TTCT  GA  ATCTCTTC
                                 GT T   CC  A_
GAM455  RRN3     3'  TTTTAACATGGGTTTTTGTCA  37962           G   GA
                                TGGCAAGGACCT ATG  GAAG
                                |||||||||||| |||  ||||
                                ACTGTTTTTGGG TAC  TTTT
                                       _  AA
GAM455  SCAND2   3'  TTTTTTCATTCTTATATTTTGC 54427         ACCT__
           CA                    TGGCAAGG     GATGGAGAAG
                                ||||||||     ||||||||||
                                ACCGTTTT     TTACTTTTTT
                                     ATATTC
GAM455  SEC15B   3'  CTTTTTTATCTAATTTGTC    67266        GACCT
                                GGCAAG    GATGGAGAAG
                                ||||||    ||||||||||
                                CTGTTT    CTATTTTTTC
                                   AAT__
GAM455  SEC24D   3'  CTTCTCTGTCATTGATGTTGC  29754      GGACC_
                                GCAA     TGATGGAGAAG
                                ||||     ||||||||||
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                                CGTT     ACTGTCTCTTC
                                  GTAGTT
GAM455  SERPING1  3'  CTTCTCCATGGCCCTGCCATG  5348        A  A  TG
                                TATGGCA GG CC  ATGGAGAAG
                                ||||||| || ||  |||||||||
                                GTACCGT CC GG  TACCTCTTC
                                   C  _  __
GAM455  SFRS11    5'  CTTTTCCGTTGCCGGTGCCG   17673      A_  ACC
                                TGGCA  GG   TGATGGAGAAG
                                |||||  ||   ||||||||||
                                GCCGT  CC   GTTGCCTTTTC
                                  GG  ____
GAM455  ShrmL     5'  TTGAATTGTCAGGTCTTTGTGG 40855     G          TG AGAAG
           TG                     TAT GCAAGGACCTGA  G
                                ||| ||||||||||||  |
                                GTG TGTTTCTGGACT  T
                                  G          GT AAGTTT
GAM455  SKIL      3'  TTTTTTTGTTTGTTGCTTGCT  19447       _  CT  TG
                                GGCAAG GAC  GA  GAGAAG
                                |||||| |||  ||  ||||||
                                TCGTTC TTG  TT  TTTTTT
                                   G  T_  GT
GAM455  SKIP      3'  CTTAAATACAGGTTTTTGTT   56247          ATG__   AAG
                                GGCAAGGACCTG    GAG
                                ||||||||||||    |||
                                TTGTTTTTGGAC    TTC
                                      ATAAA
GAM455  SMARCF1   3'  TTTTTCTGGGTTTTTGTT    21193          GAT
                                GGCAAGGACCT   GGAGAAG
                                ||||||||||   |||||||
                                TTGTTTTTGGG   TCTTTTT
                                      ___
GAM455  SMARCF1   3'  TTTTTCTGGGTTTTTGTT    21194          GAT
                                GGCAAGGACCT   GGAGAAG
                                ||||||||||   |||||||
                                TTGTTTTTGGG   TCTTTTT
                                      ___
GAM455  SMCR7     3'  TTTCTCTAGCTTTTTGCCA   58243        CCTGA
                                TGGCAAGGA    TGGAGAAG
                                |||||||||    ||||||||
                                ACCGTTTTT    ATCTCTTT
                                   CG___
GAM455  SMT3H2    3'  TTCTCCATTAGTGGCATG    23660      G  AGGAC
                                TATG CA    CTGATGGAGAA
                                ||||  ||    ||||||||||
                                GTAC GT    GATTACCTCTT
                                  G  _____
GAM455  SP2       3'  CTTCTTCCTTTCCTTGTTAT   13331          CCT  T
                                ATGGCAAGGA   GA GGAGAAG
                                |||||||||   ||  |||||||
```

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                                TATTGTTCCT   TT CTTCTTC
                                     ___  C
GAM455  SPRY4    3'  CTTTTGTGTGGGGTTCTTGCT  49012          G   G
                                GGCAAGGACCT ATG AGAAG
                                |||||||||||  ||| |||||
                                TCGTTCTTGGG TGT TTTTC
                                      G   G
GAM455  SRPK1    3'  TTTTTTTGTTGGTCTTGTT   13408       G   T  TG
                                GGCAAG ACC GA  GAGAAG
                                ||||||  ||| ||  ||||||
                                TTGTTC TGG TT  TTTTTT
                                   _  _  GT
GAM455  SSH1     3'  CTTTTCCCCTACTCTTGCCATA 39127          ACCTGAT
                                TATGGCAAGG      GGAGAAG
                                ||||||||||      |||||||
                                ATACCGTTCT      CCTTTTC
                                      CATCC__
GAM455  STK36    3'  CTTCCCAGCAGGTTTTTGCC   72583           A   A
                                GGCAAGGACCTG TGG GAAG
                                ||||||||||||  ||| ||||
                                CCGTTTTTGGAC ACC CTTC
                                      G   _
GAM455  STK38L   3'  TTTCTCTATTATATATTTCCCA 69691       C   GACC
           TA                     TATGG AAG    TGATGGAGAAG
                                |||||  |||    ||||||||||
                                ATACC TTT    ATTATCTCTTT
                                   C   ATAT
GAM455  STRN3    3'  TTTTGTAAGGTTTTTGTTTTA  28140    TG        G TG
                                TA  GCAAGGACCT A  GAG
                                ||  ||||||||||  |  |||
                                AT  TGTTTTTGGA T  TTT
                                 TT         A GT
GAM455  SURB7    3'  TTTTTTCATCCTTAATTTGCTT 16213    T     GACCT
           G                     A GGCAAG     GATGGAGAAG
                                |  ||||||     ||||||||||
                                G TCGTTT     CTACTTTTTT
                                 T      AATTC
GAM455  TBC1D2   5'  CTTCTCTGAGGCTCAGGTCCTT 37929    T          ____
           GCTTG                    A GGCAAGGACCTGA    TGGAGAAG
                                |  ||||||||||||    ||||||||
                                G TCGTTCCTGGACT    GTCTCTTC
                                 T           CGGA
GAM455  TGIF2    3'  TTTTTCCCTTTTTTTGCTGTG  41763           CCT  T
                                TATGGCAAGGA   GA GGAGAAG
                                ||||||||||   || |||||||
                                GTGTCGTTTTT   TT CCTTTTT
                                      ___  C
GAM455  TGIF2    3'  TTTTTTGTCTTTTGTCA     41764         ACCT  TG
                                TGGCAAGG    GA  GAGAA
                                ||||||||    ||  |||||
```

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                                ACTGTTTT   CT  TTTTT
                                     ____  GT
GAM455  TNFRSF21  3'  TTTCTCCATTTTGCCTTCTTAT 27828      C   ACCT
            G                    TATGG AAGG   GATGGAGAAG
                                 ||||| ||||   ||||||||||
                                 GTATT TTCC   TTACCTCTTT
                                   C   GTT_
GAM455  TRAF3    5'  TTTCTCCATCCCGTCATCTTGC 13856       __  CT
            T                    GGCAAG  GAC  GATGGAGAAG
                                 ||||||  |||  ||||||||||
                                 TCGTTC  CTG  CTACCTCTTT
                                    TA   CC
GAM455  TRIM35   3'  TTTTTTTAGAGACAGGGTCTTG 61522         GA   A___
            CTGTA                  TATGGCAAG  CCTG   TGGAGAAG
                                 |||||||||  ||||   ||||||||
                                 ATGTCGTTC  GGAC   ATTTTTTT
                                      TG   AGAG
GAM455  TRIM36   3'  TTTTTTGGTTGTCCTTGTTGT  38631   TG      CT   G
                                 A  GCAAGGAC  GAT GAGAAG
                                 |  ||||||||  ||| ||||||
                                 T  TGTTCCTG  TTG TTTTTT
                                  GT       __  G
GAM455  TRIP-Br2  3'  CTTTTCTGGCATTTTTGCC   29265        CC  AT
                                 GGCAAGGA  TG  GGAGAAG
                                 ||||||||  ||  |||||||
                                 CCGTTTTT  AC  TCTTTTC
                                      __  GG
GAM455  TSGA14   3'  CTTCTCCGGGCAGTCTTGGTGT 38666     G    AC   A_
            G                    TATG CAAGG  CTG  TGGAGAAG
                                 |||| |||||  |||  ||||||||
                                 GTGT GTTCT  GAC  GCCTCTTC
                                   G    __  GG
GAM455  TXNL2    3'  TTTTTTCATACAGCTTTGTC   22586        AC   _
                                 GGCAAGG  CTG ATGGAGAAG
                                 |||||||  ||| |||||||||
                                 CTGTTTC  GAC TACTTTTTT
                                      __  A
GAM455  VPS33A   3'  TTCTCCGTCTCTTTTGT     43619       ACCT
                                 GCAAGG   GATGGAGAA
                                 ||||||   |||||||||
                                 TGTTTT   CTGCCTCTT
                                    CT__
GAM455  WSB1     3'  CTTTGAGCAATGGTCTTTGCTG 56975            TGATGGA
            TG                     TATGGCAAGGACC      GAAG
                                 ||||||||||||||      ||||
                                 GTGTCGTTTCTGG      TTTC
                                        TAACGAG
GAM455  ZAK      3'  TTTTTGGTGGGTCTTTTTATG  34112      C      G  G
                                 TATGG AAGGACCT AT GAGAA
                                 ||||| |||||||| || |||||
```

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                                GTATT TTTCTGGG TG TTTTT
                                  _       _ G
GAM455  ZFP91    3'  TTTTTTTGGAGTCTTTGTTGCT 54882        ___    _ TG TG   AAG
            ATA                   TATGGCAA   GGAC C  A  GAG
                                  ||||||||   |||| |  |  |||
                                  ATATCGTT   TCTG G  T  TTT
                                     GTT    A GT TT     G
GAM455  ZMPSTE24  3'  TTTCTTCCCTTTCTTGCTA   20732         CCTGAT
                                  TGGCAAGGA     GGAGAAG
                                  |||||||||     |||||||
                                  ATCGTTCTT     CTTCTTT
                                       TCC___
GAM455  ZNF220   3'  TTTTTTTGGGTTCATTTTGTTG 23163    TG   ___    TG TG   AAG
            TG                    TA  GCAA   GGACC  A  GAG
                                  ||  ||||   |||||  |  |||
                                  GT  TGTT   CTTGG  T  TTT
                                   GT    TTA    GT TT
GAM455  ZNF297B  3'  TTTTTTTATCAGGCAGCCA   26679     AAGGA
                                  TGGC    CCTGATGGAGAAG
                                  ||||    ||||||||||||||
                                  ACCG    GGACTATTTTTTT
                                    AC___
GAM455  ZNF304   3'  CTTCTTTGTCAACTTAATTGTT 40681        GGACC_   TG
            ATG                   TATGGCAA     TGA  GAGAAG
                                  ||||||||     |||  ||||||
                                  GTATTGTT     ACT  TTCTTC
                                       AATTCA   GT
GAM455  ZWINT    3'  TTTCTTTGTGCTAAGGTTCTTG 23910     G        G___ TG
            CGGTG                    TAT GCAAGGACCT    A  GAGAAG
                                  |||  ||||||||||   |  ||||||
                                  GTG CGTTCTTGGA    T  TTCTTT
                                    G         ATCG GT
GAM455  LOC114932 3'  TTTCTCTGTTTTGTTTTTGT   73093        CT
                                  GCAAGGAC  GATGGAGAAG
                                  ||||||||  ||||||||||
                                  TGTTTTTG  TTGTCTCTTT
                                       TT
GAM455  LOC115817 3'  CTTCTTTTTACTTTTTGCC    57413        CCTGAT
                                  GGCAAGGA     GGAGAAG
                                  ||||||||     |||||||
                                  CCGTTTTT     TTTCTTC
                                       CATT__
GAM455  LOC116028 3'  CTTCTTCATCAGCAACTACCAT 74095      CA  GAC
            A                      TATGG  AG   CTGATGGAGAAG
                                  |||||  ||   ||||||||||||
                                  ATACC  TC   GACTACTTCTTC
                                     A_  AAC
GAM455  LOC120448 5'  CTTCTCTGTGTCCTCCTTGCTG 76067          CCTG
            TG                     TATGGCAAGGA    ATGGAGAAG
                                  ||||||||||    |||||||||
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                                GTGTCGTTCCT    TGTCTCTTC
                                      CCTG
GAM455   LOC122830 3'  CTTCTTTATATTTGACTTGCT  74631       GACCTG
                                GGCAAG     ATGGAGAAG
                                ||||||     |||||||||
                                TCGTTC     TATTTCTTC
                                   AGTTTA
GAM455   LOC124446 5'  CTTTTCCATCAGGCCGTCGC   74776    AA_  A
                                GC   GG CCTGATGGAGAAG
                                ||   || ||||||||||||
                                CG   CC GGACTACCTTTTC
                                 CTG  _
GAM455   LOC124944 5'  TTCTCCACCCTTCGCTGTG    74838       _    ACCTGA
                                TATGGC AAGG     TGGAGAA
                                |||||| ||||     |||||||
                                GTGTCG TTCC     ACCTCTT
                                   C    C_____
GAM455   LOC128989 3'  CTTCTGGCCAGTAGGTCTTTGT 75314           A   __
            T                    GGCAAGGACCTG TGG  AGAAG
                                ||||||||||| |||  |||||
                                TTGTTTCTGGAT ACC  TCTTC
                                      G   GG
GAM455   LOC130026 3'  CTTTTTCATACACTTGCTATA  57438         GACCTG
                                TATGGCAAG     ATGGAGAAG
                                |||||||||     |||||||||
                                ATATCGTTC     TACTTTTTC
                                     ACA___
GAM455   LOC130029 3'  CTTTTCCTATCTTTTGCCGTA  75414          ACCT   _
                                TATGGCAAGG    GAT GGAGAAG
                                ||||||||||    ||| |||||||
                                ATGCCGTTTT    CTA CCTTTTC
                                      _____   T
GAM455   LOC130497 3'  CTTTTTTATTTTTGTCTTTGAC 75449       _      CT_
            CATA                    TATGG CAAGGAC   GATGGAGAAG
                                ||||| |||||||   ||||||||||
                                ATACC GTTTCTG   TTATTTTTTC
                                   A      TTT
GAM455   LOC131308 3'  TTTTTTTGAGACAGTCTTGCTA 75500          AC   A__ GG
            TG                    TATGGCAAGG  CTG   T  AGAAG
                                ||||||||||  |||   |  |||||
                                GTATCGTTCT  GAC   G  TTTTT
                                      __   AGA TT
GAM455   LOC131377 3'  TTCTCCAGTGTTGCCATA     76783         GGACCTGA
                                TATGGCAA       TGGAGAA
                                ||||||||       |||||||
                                ATACCGTT       ACCTCTT
                                     GTG_____
GAM455   LOC133814 5'  CTTCTCTGTATAATCTTGTCA  76459         ACCTG
                                TGGCAAGG    ATGGAGAAG
                                ||||||||    |||||||||
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                                ACTGTTCT    TGTCTCTTC
                                    AATA_
GAM455  LOC133923 3'  TTTTCTATCAATGCCTTG    76462      ACC
                                CAAGG  TGATGGAGAA
                                |||||  ||||||||||
                                GTTCC  ACTATCTTTT
                                   GTA
GAM455  LOC135154 3'  TTTCTTTATATCCTTTATGTCG 75738       ___   CCTG
          TG                     TATGGCA  AGGA   ATGGAGAAG
                                |||||||  ||||   |||||||||
                                GTGCTGT  TCCT   TATTTCTTT
                                    ATT   A___
GAM455  LOC136345 3'  CTTCAAGGGGTCTTTCCATG  76713      C      GA
                                TATGG AAGGACCT  TGGAG
                                ||||| ||||||||  |||||
                                GTACC TTTCTGGG  ACTTC
                                   _      GA
GAM455  LOC136442 3'  TTTTTCTTGGATTTTTGCTA  55262        C TG T
                                TGGCAAGGA C  A GGAGAA
                                ||||||||| |  | ||||||
                                ATCGTTTTT G  T CTTTTT
                                     A GT _
GAM455  LOC139221 3'  CTCTTGGGCTCTTGTTATA   76328        GA  TG TG
                                TATGGCAAG  CC  A  GAG
                                |||||||||  ||  |  |||
                                ATATTGTTC  GG  T  CTC
                                     TC  GT __
GAM455  LOC144395 3'  CTTGAATTGGGTTTTCTGTCAT 77321       _    TG  G_   AAG
          G                     TATGGCA AGGACC  AT  GAG
                                |||||||  ||||||  ||  |||
                                GTACTGT TTTTGG  TA  TTC
                                    C     GT  AG
GAM455  LOC144501 3'  CTTCTCCGGAAGCTGCTCTTGC 84029        _ AC_  GA
          CATA                    TATGGCAAG G   CT  TGGAGAAG
                                |||||||||  |   ||  ||||||||
                                ATACCGTTC C   GA  GCCTCTTC
                                     T GTC  AG
GAM455  LOC144509 3'  CTTTTCTGTCGCTGAGTGCTA  77360      AGGACC
                                TGGCA     TGATGGAGAAG
                                |||||     ||||||||||
                                ATCGT     GCTGTCTTTTC
                                   GAGTC_
GAM455  LOC145547 3'  TTTTTTCATTTGATTTGTCA   77786       GACCT
                                TGGCAAG    GATGGAGAAG
                                |||||||    ||||||||||
                                ACTGTTT    TTACTTTTTT
                                    AGT__
GAM455  LOC145566 5'  TTTTTTCAGTCCACCTTGCTA  77791        ACCTGA
                                TGGCAAGG     TGGAGAAG
                                ||||||||     ||||||||
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                                ATCGTTCC     ACTTTTTT
                                     ACCTG_
GAM455  LOC145719 5'  CTTCTCTATCAGGTCTGGTGGC 84464     AA__
              T                   GGC   GGACCTGATGGAGAAG
                                  |||   ||||||||||||||||
                                  TCG   TCTGGACTATCTCTTC
                                    GTGG
GAM455  LOC145719 5'  CTTTTCCAGGAACCTTGCCA  84465       A_  GAT
                                  TGGCAAGG  CCT  GGAGAAG
                                  ||||||||  |||  |||||||
                                  ACCGTTCC  GGA  CCTTTTC
                                       AA  ___
GAM455  LOC145720 5'  CTTTTCCAGGAACCTTGCCA  84451       A_  GAT
                                  TGGCAAGG  CCT  GGAGAAG
                                  ||||||||  |||  |||||||
                                  ACCGTTCC  GGA  CCTTTTC
                                       AA  ___
GAM455  LOC145720 5'  CTTCTCTATCAGGTCTGGTGGC 84450     AA__
              T                   GGC   GGACCTGATGGAGAAG
                                  |||   ||||||||||||||||
                                  TCG   TCTGGACTATCTCTTC
                                    GTGG
GAM455  LOC145739 3'  TTTTTTCATACTCTGGCCATA  77908      AA  CCTG
                                  TATGGC  GGA   ATGGAGAAG
                                  ||||||  |||   |||||||||
                                  ATACCG  TCT   TACTTTTTT
                                     G_  CA__
GAM455  LOC145757 3'  CTTGATAGGTATTTTGCCGTG  77931         _   A G
                                  TATGGCAAGG ACCTG T GAG
                                  |||||||||| ||||| | |||
                                  GTGCCGTTTT TGGAT A TTC
                                        A    _ G
GAM455  LOC145828 5'  TTTCTTCTGTCTTCTTGTCA  84542       CCT    _
                                  TGGCAAGGA  GATGGA GAAG
                                  |||||||||  |||||| ||||
                                  ACTGTTCTT  CTGTCT CTTT
                                       ___     T
GAM455  LOC145945 5'  TTTTTTCATTGGCCGGTTAT  84576     AA  A  T
                                  ATGGC  GG CC GATGGAGAAG
                                  |||||  || || ||||||||||
                                  TATTG  CC GG TTACTTTTTT
                                    G_  _  _
GAM455  LOC146176 5'  TTTTAACAGGTTTTTGTAATA  78196    G        A
                                  TAT GCAAGGACCTG TGGAG
                                  ||| |||||||||| |||||
                                  ATA TGTTTTTGGAC ATTTT
                                    A         A
GAM455  LOC146229 3'  TTTCTCCATTCTAGGATCTTGT 78321       A  __
              TA                    TGGCAAGG CCT  GATGGAGAAG
                                  |||||||| |||  ||||||||||
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                                ATTGTTCT GGA  TTACCTCTTT
                                    A   TC
GAM455  LOC146455 3'  TTTTTCCATTGGTGTATTGT   78470     GG  _ TG
                                GCAA  AC C  ATGGAGAAG
                                ||||  || |  |||||||||
                                TGTT  TG G  TACCTTTTT
                                  A_  T GT
GAM455  LOC146517 3'  CTCAAATTGGGTTCTTGCC    78505        TG  G_
                                GGCAAGGACC  AT  GAG
                                ||||||||||  ||  |||
                                CCGTTCTTGG  TA  CTC
                                     GT  AA
GAM455  LOC146819 3'  TTTCTTTGTTGATCTTGTCA   78744       ACC   TG
                                TGGCAAGG   TGA  GAGAAG
                                ||||||||   |||  ||||||
                                ACTGTTCT   GTT  TTCTTT
                                    A__   GT
GAM455  LOC146821 3'  TTTCTTTGTTGATCTTGTCA   78734       ACC   TG
                                TGGCAAGG   TGA  GAGAAG
                                ||||||||   |||  ||||||
                                ACTGTTCT   GTT  TTCTTT
                                    A__   GT
GAM455  LOC146952 5'  CTTTTCCATAGCTTGTTTGCTA 84927        GACCTG
          TG                    TATGGCAAG     ATGGAGAAG
                                |||||||||     |||||||||
                                GTATCGTTT     TACCTTTTC
                                    GTTCGA
GAM455  LOC147160 3'  TTTCTCCATCATTAATGCTGTG 85080       AG  CC
                                TATGGCA  GA  TGATGGAGAAG
                                |||||||  ||  ||||||||||||
                                GTGTCGT  TT  ACTACCTCTTT
                                   AA  __
GAM455  LOC149182 3'  CTTTTCTACAGTATCTTTGTT  85534       C_  A
                                GGCAAGGA  CTG TGGAGAAG
                                ||||||||  ||| ||||||||
                                TTGTTTCT  GAC ATCTTTTC
                                    AT  _
GAM455  LOC149319 3'  TTTCTTCAGGTAATTTTTGTCA 80080        ___     T    AG
                                TGGCAAGG   ACCTGA GGAGA
                                ||||||||   |||||| |||||
                                ACTGTTTT   TGGACT TCTTT
                                    TAA     _
GAM455  LOC149606 3'  CTTTTCCAGAAATTCCTTGCTA 80262        CCTGA
                                TGGCAAGGA    TGGAGAAG
                                |||||||||    ||||||||
                                ATCGTTCCT    ACCTTTTC
                                     TAAAG
GAM455  LOC149767 3'  TTTAAAGCAGGTTCTTGTT   80313         ATGG
                                GGCAAGGACCTG   AGA
                                ||||||||||||   |||
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                                TTGTTCTTGGAC   TTT
                                      GAAA
GAM455  LOC150113 5'  CTTCTAAGGGTCTTTGCT    88566          GAT
                                GGCAAGGACCT  GGAG
                                ||||||||||  ||||
                                TCGTTTCTGGG  CTTC
                                      AAT
GAM455  LOC151162 5'  CTTTTTTGTGTGTTTGCTGTG  86429         G  CTG TG
                                TATGGCAAG AC  A  GAGAAG
                                |||||||| ||  |  ||||||
                                GTGTCGTTT TG  T  TTTTTC
                                     G ___ GT
GAM455  LOC151996 5'  CTTCTCTGGCTTTCCTGCTATA 86719        A  CCTGA
                                TATGGCA GGA    TGGAGAAG
                                ||||||| |||    ||||||||
                                ATATCGT CCT    GTCTCTTC
                                   _  TTCG_
GAM455  LOC152098 5'  TTTCTTCATGGAATTTTGCTA  81295         AC  G
                                TGGCAAGG  CT ATGGAGAAG
                                ||||||||  || |||||||||
                                ATCGTTTT  GG TACTTCTTT
                                     AA  _
GAM455  LOC152179 5'  CTTTTTCATAAGTTCTTTGTGA 86742     G      C  G
          TG                    TAT GCAAGGA CT ATGGAGAAG
                                ||| ||||||| || |||||||||
                                GTA TGTTTCT GA TACTTTTTC
                                  G      T  A
GAM455  LOC152275 3'  TTTTTTCATCTTTTTTTGTCG  86800         CCT
                                TGGCAAGGA   GATGGAGAAG
                                |||||||||   ||||||||||
                                GCTGTTTTT   CTACTTTTTT
                                     TT_
GAM455  LOC153642 3'  GTTTTTCTGTTGGTTGTTGGTC 81791          _______
          TTTGTT                GGCAAGGACC     TGATGGAGAAG   T
                                ||||||||||     ||||||||||  |
                                TTGTTTCTGG     GTTGTCTTTTT  G
                                     TTGTTG
GAM455  LOC153910 5'  GTTTTTTTGTAGAGACAGGGTT 81910         GA   _____ TG
          TTGCCATG               TATGGCAAG  CCTG    A  GAGAAG   T
                                |||||||||  ||||    |  ||||||  |
                                GTACCGTTT  GGAC    T  TTTTTT   G
                                     TG    AGAGA GT
GAM455  LOC154094 3'  TTTCTTCTGATTTTTGCCAT   61063         CCTGAT
                                ATGGCAAGGA     GGAGAAG
                                ||||||||||     |||||||
                                TACCGTTTTT     CTTCTTT
                                     AGT___
GAM455  LOC154547 3'  TTCTCCATTAGTGGCATG    76570      G  AGGAC
                                TATG CA    CTGATGGAGAA
                                |||| ||    ||||||||||
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                                GTAC GT     GATTACCTCTT
                                  G _____
GAM455  LOC155032 5'  CTTCAAGGGGTCTTTCCATG   87593       C       GA
                                TATGG AAGGACCT  TGGAG
                                ||||| ||||||||  |||||
                                GTACC TTTCTGGG  ACTTC
                                  _       GA
GAM455  LOC155072 3'  CTTCTCTGTCTCTTCCCTTGTT 87665         ACCT_
          A                      TGGCAAGG     GATGGAGAAG
                                ||||||||     ||||||||||
                                ATTGTTCC     CTGTCTCTTC
                                     CTTCT
GAM455  LOC157550 5'  CTTTTCTATGGCTTTTTGTTTG 82386    T       _  TG
                                A GGCAAGGA CC  ATGGAGAAG
                                | ||||||||  ||  |||||||||
                                G TTGTTTTT GG  TATCTTTTC
                                 T       C  __
GAM455  LOC157663 3'  CTTCTTTATCACAGGTGTCTTG 82451       _    __
                                CAAGG ACCT  GATGGAGAAG
                                ||||| ||||  ||||||||||
                                GTTCT TGGA  CTATTTCTTC
                                   G    CA
GAM455  LOC157681 5'  TTTTTTTAGAGGCGGGGGTCTT 82460          A_    ATG__
            GCCATG                 TATGGCAAGG  CCTG     GAGAAG
                                |||||||||  ||||     ||||||
                                GTACCGTTCT  GGGC     TTTTTT
                                      GG    GGAGA     T
GAM455  LOC157988 5'  TTTCTTCGTTATTCCTCCATA  82546       CA    CC
                                TATGG  AGGA  TGATGGAGAAG
                                |||||  ||||  ||||||||||||
                                ATACC  TCCT  ATTGCTTCTTT
                                   __    T_
GAM455  LOC158014 5'  TTTTATCATTAGGTGGCATA   82574      G AAGG        A
                                TATG C    ACCTGATGG GAAG
                                |||| |    ||||||||| ||||
                                ATAC G    TGGATTACT TTTT
                                  G ____         A
GAM455  LOC158363 3'  TTTTTTCATTGGCCAGGGCT   88118     AA_  A  T
                                GGC   GG CC GATGGAGAAG
                                |||   || || ||||||||||
                                TCG   CC GG TTACTTTTTT
                                  GGA  _  _
GAM455  LOC158402 5'  CTTTAAAATAGGTTTTTGTT   88147           A__     AAG
                                GGCAAGGACCTG   TGGAG
                                ||||||||||||   |||||
                                TTGTTTTTGGAT   ATTTC
                                       AAA
GAM455  LOC158969 3'  TTTTTTCATCAGGTGTTTTTGT 82940        __
                                GCAAGG  ACCTGATGGAGAAG
                                ||||||  ||||||||||||||
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                                TGTTTT  TGGACTACTTTTTT
                                   TG
GAM455  LOC158997 3'  TTCTCCATTAGTGGCATG    82953     G  AGGAC
                                TATG CA    CTGATGGAGAA
                                |||| ||    ||||||||||
                                GTAC GT    GATTACCTCTT
                                  G _____
GAM455  LOC159110 3'  TTTCTCTATTTATCTAGTTGTA 82998    TG  A   ACCT
                                TA  GC AGG    GATGGAGAAG
                                ||  || |||    ||||||||||
                                AT  TG TCT    TTATCTCTTT
                                 GT  A   AT__
GAM455  LOC159116 3'  TTTCTCTATTTATCTAGTTGTA 82981    TG  A   ACCT
                                TA  GC AGG    GATGGAGAAG
                                ||  || |||    ||||||||||
                                AT  TG TCT    TTATCTCTTT
                                 GT  A   AT__
GAM455  LOC160897 3'  CTTTTCTACTTTTCTTTGTCA  83132         CCTGA
                                TGGCAAGGA    TGGAGAAG
                                |||||||||    ||||||||
                                ACTGTTTCT    ATCTTTTC
                                     TTTC_
GAM455  LOC161725 3'  TTTTCCATTGTGTCGGTG    56472    AG   C
                                CA  GAC TGATGGAGAA
                                ||  ||| ||||||||||
                                GT  CTG GTTACCTTTT
                                 GG   T
GAM455  LOC161734 3'  CTTCTTTGTCCTTTTCCTTTGT 88465       _   CCT_  TG
           CA                    TGGCAA GGA    GA  GAGAAG
                                ||||||| |||    ||  ||||||
                                ACTGTT CCT    CT  TTCTTC
                                   T   TTTC  GT
GAM455  LOC163859 3'  TTTCTTTGTCTGGTTTTCTATA 83039      CA     T  TG
                                TATGG  AGGACC GA  GAGAAG
                                |||||  |||||| ||  ||||||
                                ATATC  TTTTGG CT  TTCTTT
                                   __     T  GT
GAM455  LOC164971 5'  CTTTTTCAGTGTATTTCTGTCA 83347       AG  CCTGA
           TA                    TATGGCA  GA    TGGAGAAG
                                |||||||  ||    ||||||||
                                ATACTGT  TT    ACTTTTTC
                                    CT  ATGTG
GAM455  LOC165693 5'  CTTCTCTATCAACTCTTGGCAT 83489     G    ACC
           A                     TATG CAAGG   TGATGGAGAAG
                                ||||  |||||   ||||||||||||
                                ATAC GTTCT   ACTATCTCTTC
                                  G    CA_
GAM455  LOC170063 3'  TTTTTTTGTTAGAGCCTCTATA 88599      CA   AC    TG
                                TATGG  AGG  CTGA  GAGAAG
                                |||||  |||  ||||  ||||||
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                                ATATC  TCC  GATT  TTTTTT
                                  __  GA   GT
GAM455  LOC196382 3'  TTTTTTAAAAAGGTTTTTGC  91190        GA_     G
                                GCAAGGACCT  TGGAGAA
                                ||||||||||  |||||||
                                CGTTTTTGGA  ATTTTTT
                                     AAA
GAM455  LOC197114 5'  CTTCTCTATCAGGTCTGGTGGC 91270    AA__
          T                      GGC   GGACCTGATGGAGAAG
                                 |||   ||||||||||||||||
                                 TCG   TCTGGACTATCTCTTC
                                   GTGG
GAM455  LOC197114 5'  CTTTTCCAGGAACCTTGCCATG 91271        A_  GAT
                                TATGGCAAGG  CCT  GGAGAAG
                                ||||||||||  |||  |||||||
                                GTACCGTTCC  GGA  CCTTTTC
                                     AA  ___
GAM455  LOC197117 5'  CTTCTCTATCAGGTCTGGTGGC 91281    AA__
          T                      GGC   GGACCTGATGGAGAAG
                                 |||   ||||||||||||||||
                                 TCG   TCTGGACTATCTCTTC
                                   GTGG
GAM455  LOC197131 5'  CTTCTTCAGTTAGTTCTTCCTA 89234     C     CTGA
          TA                     TATGG AAGGAC   TGGAGAAG
                                 ||||| ||||||   ||||||||
                                 ATATC TTCTTG   ACTTCTTC
                                    C     ATTG
GAM455  LOC199718 3'  TTTCTCCAGAATCTTTCCCATG 89705     C    CCTGA
                                TATGG AAGGA    TGGAGAAG
                                ||||| |||||    ||||||||
                                GTACC TTTCT    ACCTCTTT
                                   C    AAG__
GAM455  LOC199918 3'  TTTCTCTGTTTTAAACCTTGT  91476      ACCT_
                                GCAAGG    GATGGAGAAG
                                ||||||    ||||||||||
                                TGTTCC    TTGTCTCTTT
                                    AAATT
GAM455  LOC200010 3'  CTTCTCCCTTTGCTTGCCATG  91526       GACCT  T
                                TATGGCAAG    GA GGAGAAG
                                |||||||||    || |||||||
                                GTACCGTTC    TT CCTCTTC
                                     GT___  C
GAM455  LOC200339 3'  TTTTTCTATTTTTTCCTTCTAT 91619     C    CCT
          A                      TATGG AAGGA   GATGGAGAAG
                                 ||||| |||||   ||||||||||
                                 ATATC TTCCT   TTATCTTTTT
                                    _    TTT
GAM455  LOC200609 5'  CTTCTTTATCTTTTTTGTCAT  91663        CCT
                                ATGGCAAGGA   GATGGAGAAG
                                ||||||||||   ||||||||||
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                                TACTGTTTTT  CTATTTCTTC
                                      T__
GAM455  LOC200609 5'  CTTTTTCATGTTTTTGTGGTA  91665    G      C  TG
                                TAT GCAAGGAC TGA  GAG
                                ||| |||||||| |||  |||
                                ATG TGTTTTTG ACT  TTC
                                  G       T  TT
GAM455  LOC200845 5'  CTTCTCTATTTTCCTAGTTATA 90316      A   CCT
                                TATGGC AGGA  GATGGAGAAG
                                |||||| ||||  ||||||||||
                                ATATTG TCCT  TTATCTCTTC
                                   A   T__
GAM455  LOC200933 3'  CTTCTGAGTTCTTGCTGTA   91792         CTGAT
                                TATGGCAAGGAC    GGAG
                                ||||||||||||    ||||
                                ATGTCGTTCTTG    CTTC
                                      AGT__
GAM455  LOC201696 3'  TTTCTTCAGCTTCCCTTTCATA 63832     C   ACCTGA
                                TATGG AAGG     TGGAGAAG
                                ||||| ||||     ||||||||
                                ATACT TTCC     ACTTCTTT
                                   _   CTTCG_
GAM455  LOC202868 3'  CTTCTCTGTCTCTTCCCTTGTT 92003       ACCT_
          A                      TGGCAAGG    GATGGAGAAG
                                ||||||||    ||||||||||
                                ATTGTTCC    CTGTCTCTTC
                                     CTTCT
GAM455  LOC203276 3'  TTCTCTGTACCTTGTTTA    92137   T    ACCTG
                                A GGCAAGG    ATGGAGAA
                                | |||||||    ||||||||
                                A TTGTTCC    TGTCTCTT
                                 T      A____
GAM455  LOC203305 3'  TTCTCTGTACCTTGTTTA    92190   T    ACCTG
                                A GGCAAGG    ATGGAGAA
                                | |||||||    ||||||||
                                A TTGTTCC    TGTCTCTT
                                 T      A____
GAM455  LOC203377 5'  CTTTTTTGTGTGTTTGCTGTG  92258       G  CTG TG
                                TATGGCAAG AC   A  GAGAAG
                                ||||||||| ||   |  ||||||
                                GTGTCGTTT TG   T  TTTTTC
                                     G  ___ GT
GAM455  LOC203378 5'  TTCTCTGGCCCCTTCTGTA   92311     C   A_  TGAT
                                TATGG AAGG  CC    GGAGAA
                                ||||| ||||  ||    ||||||
                                ATGTC TTCC  GG    TCTCTT
                                   _    CC  ____
GAM455  LOC203427 3'  TTTTTTGGGGAGGTCTTGCTAT 90926       G   GA_ GG   G
          G                     TATGGCAAG ACCT   T  AGAA
                                |||||||| ||||   |  ||||
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                                GTATCGTTC TGGA   G  TTTT
                                     _    GGG TT
GAM455   LOC219654 3'  CTTCTCTGTTGCCAACCTTGCC 92934         ACCT_
              GT                  ATGGCAAGG     GATGGAGAAG
                                  |||||||||     ||||||||||
                                  TGCCGTTCC     TTGTCTCTTC
                                      AACCG
GAM455   LOC219654 3'  TTTTTGGTTGGTTTTTGTTTG  92945    T        T   G
                                  A GGCAAGGACC GAT GAGAA
                                  | ||||||||||  ||| |||||
                                  G TTGTTTTTGG TTG TTTTT
                                   T         _   G
GAM455   LOC219735 5'  CTTTGGGTGAAGTTCTTTGCTG 94727           C  GATGGA
              TG                  TATGGCAAGGA CT      GAAG
                                  ||||||||||| ||      ||||
                                  GTGTCGTTTCT GA      TTTC
                                        T  AGTGGG
GAM455   LOC219790 3'  CTTCACATCATTTTGCTAT    93004         ACC     GA
                                  ATGGCAAGG   TGATG  GAAG
                                  |||||||||   |||||  ||||
                                  TATCGTTTT   ACTAC  CTTC
                                      ___     A_
GAM455   LOC219899 3'  CTTCTCTACTATTTTGACCATG 93131       _     ACC  A
                                  TATGG CAAGG   TG TGGAGAAG
                                  ||||| |||||   || ||||||||
                                  GTACC GTTTT   AT ATCTCTTC
                                     A     ___  C
GAM455   LOC220739 5'  TTTCTCCTGGATTTTTGTC    94532         _  TGAT
                                  GGCAAGGA CC    GGAGAAG
                                  |||||||| ||    |||||||
                                  CTGTTTTT GG    CCTCTTT
                                       A  T___
GAM455   LOC220766 3'  TTTCTTCATTAGGGGACTTG   92477      GA_
                                  CAAG   CCTGATGGAGAAG
                                  ||||   ||||||||||||||
                                  GTTC   GGATTACTTCTTT
                                     AGG
GAM455   LOC220963 3'  CTTCTCTATGTTTGACTTGCTA 93099        GACCTG
                                  TGGCAAG      ATGGAGAAG
                                  |||||||      |||||||||
                                  ATCGTTC      TATCTCTTC
                                       AGTTTG
GAM455   LOC221395 3'  CTTCTCTGTCTATATTGTAATA 93662     G    GGACCT
                                  TAT GCAA     GATGGAGAAG
                                  ||| ||||     ||||||||||
                                  ATA TGTT     CTGTCTCTTC
                                    A   ATAT__
GAM455   LOC221561 3'  TTCTCCATTAGTGGCATG    93754      G  AGGAC
                                  TATG CA    CTGATGGAGAA
                                  |||| ||    ||||||||||
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                                GTAC GT     GATTACCTCTT
                                  G _____
GAM455  LOC221683 3'  CTTTGTAGGTTTTTGTTTG   95326   T        G TG
                                A GGCAAGGACCT A  GAG
                                | ||||||||||| |  |||
                                G TTGTTTTTGGA T  TTC
                                 T         _ GT
GAM455  LOC221751 5'  CTTCTCGAAGCATGTCTTTGCC 93678           C  ATG_
          ATG                     TATGGCAAGGAC TG    GAGAAG
                                ||||||||||||| ||    ||||||
                                GTACCGTTTCTG AC    CTCTTC
                                       T  GAAG
GAM455  LOC221751 5'  CTTTTTTGGAGTACTTGCTATA 93679         G  _ TG TG
                                TATGGCAAG AC C  A  GAG
                                ||||||||| || |  |  |||
                                ATATCGTTC TG G  T  TTC
                                      A  A GT TT
GAM455  LOC221833 3'  CTTTTTTGTTAGTCCGGCCGT  94114       AA    C   TG
                                ATGGC  GGAC TGA  GAGAAG
                                |||||  |||| |||  ||||||
                                TGCCG  CCTG ATT  TTTTTC
                                   G_   _  GT
GAM455  LOC253782 3'  CTTCTCCCCCTTTCTCTTGCTG 97399         _  CCTGAT
          TA                      TATGGCAAG GA     GGAGAAG
                                |||||||| ||     |||||||
                                ATGTCGTTC CT     CCTCTTC
                                      T  TTCCC_
GAM455  LOC253842 3'  TTTCTCTAAAATGTCTTGTAAT 99244     G     ACCTGA
          A                       TAT GCAAGG     TGGAGAAG
                                ||| ||||||     ||||||||
                                ATA TGTTCT     ATCTCTTT
                                  A     GTAAA_
GAM455  LOC254243 3'  TTCTCTGTACCTTGTTTA    99276   T      ACCTG
                                A GGCAAGG    ATGGAGAA
                                | |||||||    ||||||||
                                A TTGTTCC    TGTCTCTT
                                 T      A____
GAM455  LOC254249 5'  CTTTTCTACCTCATCATTTGTT 97183    TG    GACC  __
          GTA                     TA  GCAAG    TGA  TGGAGAAG
                                ||  |||||   |||  ||||||||
                                AT  TGTTT    ACT  ATCTTTTC
                                  GT    ACT_   CC
GAM455  LOC254249 5'  TTTCTTTAGTCTCTAGCTATG  97190       A  _   CTGA
                                TATGGC AG GAC    TGGAGAAG
                                |||||| || |||    ||||||||
                                GTATCG TC CTG    ATTTCTTT
                                   A  T  _____
GAM455  LOC254778 3'  TTTTTAAGACAGGATTTTGCTG 97838          A    ATG_    G
          TG                      TATGGCAAGG CCTG    GAGAA
                                ||||||||| ||||    |||||
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                                GTGTCGTTTT GGAC    TTTTT
                                     A    AGAA
GAM455   LOC255465 3'  TTTGTGTTTGGTTCTTTGTTAT 99134          _  T    G   AG
              G                    TATGGCAAGGA CC GATG AGA
                                   |||||||||||  || |||| |||
                                   GTATTGTTTCT GG TTGT TTT
                                         T  T    G
GAM455   LOC255520 3'  TTTCTTTATGGTTTTCTTTGTT 97555    T       ___  TG
              TG                    A GGCAAGGA   CC  ATGGAGAAG
                                   | ||||||||   ||  |||||||||
                                   G TTGTTTCT   GG  TATTTCTTT
                                    T       TTT  __
GAM455   LOC255624 3'  CTTCTCCATCTATTTTGTTTA  96163    T      ACCT
                                   A GGCAAGG    GATGGAGAAG
                                   | |||||||    ||||||||||
                                   A TTGTTTT    CTACCTCTTC
                                    T      AT__
GAM455   LOC256542 3'  CTTTTCTGGGGTTCCTGCTGTG 97290        A     GA
                                   TATGGCA GGACCT  TGGAGAAG
                                   ||||||| ||||||  ||||||||
                                   GTGTCGT CTTGGG  GTCTTTTC
                                       C     __
GAM455   LOC256940 5'  TTTCTTTGTCTGCTTGTGATG  98249     G    GACCT  TG
                                   TAT GCAAG    GA  GAGAAG
                                   ||| |||||    ||  ||||||
                                   GTA TGTTC    CT  TTCTTT
                                     G    GT___  GT
GAM455   LOC257017 5'  TTTCTCTGTTGATCTACCGTA  99224      CAA   CC
                                   TATGG   GGA  TGATGGAGAAG
                                   |||||   |||  ||||||||||
                                   ATGCC   TCT  GTTGTCTCTTT
                                      A__   A_
GAM455   LOC257206 3'  ATTCTTTTGTTGGGTTTTTGTT 98893    T        TG TG  _   G
              TG                    A GGCAAGGACC  A  GA GAA
                                   | ||||||||||  |  || |||
                                   G TTGTTTTTGG  T  TT CTT
                                    T        GT GT  T   AT
GAM455   LOC257428 5'  TTTCTCTATTAGAATACCGTA  95935      CAAGGAC
                                   TATGG      CTGATGGAGAAG
                                   |||||      ||||||||||||
                                   ATGCC      GATTATCTCTTT
                                      ATAA___
GAM455   LOC257443 3'  TTTCTCTGTCAGAGTTATTTCA 97549      CAAG   _
              TA                    TATGG    GAC CTGATGGAGAAG
                                   |||||    ||| ||||||||||||
                                   ATACT    TTG GACTGTCTCTTT
                                      TTA_   A
GAM455   LOC257463 3'  TTTTTTTGAGACAGGTTCTTGT 71628    TG        A__ GG
              TCTA                   TA  GCAAGGACCTG   T  AGAAG
                                   ||  ||||||||||  |  |||||
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                                AT  TGTTCTTGGAC   G  TTTTT
                                 CT         AGA TT
GAM455  LOC257490 3'  CTTTTTCAAATTCTTGCCATG  99560          CC   TG
                                TATGGCAAGGA  TGA  GAG
                                ||||||||||  |||  |||
                                GTACCGTTCTT  ACT  TTC
                                      AA   TT
GAM455  LOC257591 3'  TTCTCCATTAGTGGCATG    99674      G  AGGAC
                                TATG CA    CTGATGGAGAA
                                ||||  ||    ||||||||||
                                GTAC GT    GATTACCTCTT
                                  G  _____
GAM455  LOC51233  5'  TTGCACCTTTGGGTGCTTGTCA 33612         G   TG T  AGAAG
           TG                     TATGGCAAG ACC  A GG
                                ||||||||| |||  | ||
                                GTACTGTTC TGG  T CC
                                     G   GT T  ACGTTT
GAM455  LOC51313  3'  TTTCTCTAACATCATGCTATG  34000        A  ACC  A
                                TATGGCA GG   TG TGGAGAAG
                                |||||||  ||   || ||||||||
                                GTATCGT CT   AC ATCTCTTT
                                    A  ___  A
GAM455  LOC51652  3'  CTTTGTGCAGGTTTTTCTATG  32701       C        _ TG
                                TATGG AAGGACCTG A  GAG
                                |||||  |||||||||  |  |||
                                GTATC TTTTTGGAC T  TTC
                                   _        G GT
GAM455  LOC51667  3'  TTTCTTTGTTGTTGTTGTTGT  32781    TG    G   CT  TG
                                A  GCAA GAC  GA  GAGAAG
                                |  |||| |||  ||  ||||||
                                T  TGTT TTG  TT  TTCTTT
                                 GT    G   __  GT
GAM455  LOC54505  5'  TTTTTTTATCTGACTTTGTCA  68449         ACCT
                                TGGCAAGG    GATGGAGAAG
                                ||||||||    ||||||||||
                                ACTGTTTC    CTATTTTTTT
                                     AGT_
GAM455  LOC55885  3'  TAGAGTCTATCAGTGTTCTTGT 38444           _       GAAG
           TATA                    TATGGCAAGGAC CTGATGGA
                                ||||||||||| ||||||||
                                ATATTGTTCTTG GACTATCT
                                       T       GAGATT
GAM455  LOC56832  3'  TTTCTCTAATAAAGTCTTTGCC 65448          CTGA_
                                GGCAAGGAC     TGGAGAAG
                                |||||||||     ||||||||
                                CCGTTTCTG     ATCTCTTT
                                     AAATA
GAM455  LOC63928  3'  CTTAAATGGGTTTTTGCT    42270           ATG
                                GGCAAGGACCTG   GAG
                                ||||||||||||   |||
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                                TCGTTTTTGGGT  TTC
                                      AAA
GAM455  LOC90038  3' TTCTCTGTACCTTGTTTA   61820   T    ACCTG
                                A GGCAAGG   ATGGAGAA
                                | |||||||   ||||||||
                                A TTGTTCC   TGTCTCTT
                                 T     A____
GAM455  LOC90092  5' TTCTCTGCTTCGTGCCATG   62079      A  CCTGA
                                TATGGCA GGA   TGGAGAA
                                ||||||| |||   |||||||
                                GTACCGT CTT   GTCTCTT
                                    G  C____
GAM455  LOC90139  3' CTTCTTCAACATCCTTGCCA  56269       CC  A
                                TGGCAAGGA  TG TGGAGAAG
                                |||||||||  || ||||||||
                                ACCGTTCCT  AC ACTTCTTC
                                     __ A
GAM455  LOC91149  3' TTCTCCATTTTATTTTGT   65694      ACCT
                                GCAAGG   GATGGAGAA
                                ||||||   |||||||||
                                TGTTTT   TTACCTCTT
                                   ATT_
GAM455  LOC91149  3' TTTCTCCACACAGCCTGCTGTG 65695      A  ACC  A
                                TATGGCA GG   TG TGGAGAAG
                                ||||||| ||   || ||||||||
                                GTGTCGT CC   AC ACCTCTTT
                                   _ GAC  _
GAM455  LOC91351  3' CTTTAAAGGTGGGTTTTTGCTG 66298           ATGGA
          TG                  TATGGCAAGGACCTG   GAAG
                              ||||||||||||||    ||||
                              GTGTCGTTTTTGGGT   TTTC
                                     GGAAA
GAM455  LOC91445  3' TTCTTCATCAGAGCTTTG   61176     AC
                              CAAGG  CTGATGGAGAA
                              |||||  ||||||||||
                              GTTTC  GACTACTTCTT
                                 GA
GAM455  LOC91689  3' CTTGTTTTAGGCTTTTGTTATA 53978       GA   TG_
                              TATGGCAAG  CCTGA   GAG
                              |||||||||  |||||   |||
                              ATATTGTTT  GGATT   TTC
                                   TC    TTG
GAM455  LOC92181  3' CTTTTTATGGTTCTTGTTGT   68946   TG      TGATG
                              A  GCAAGGACC    GAGAAG
                              |  |||||||||    ||||||
                              T  TGTTCTTGG    TTTTTC
                               GT       TA___
GAM455  LOC92573  5' TTTTTTCAAAGTCCATGTTGTG 70384    TG  A   CTGA
                              TA  GCA GGAC   TGGAGAAG
                              ||  ||| ||||   ||||||||
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                                GT  TGT CCTG    ACTTTTTT
                                 GT   A    AA__
GAM455   LOC92606  3'  TTTCTTTATGTGTTTGCTGTA  70530         G  CTG
                                TATGGCAAG AC   ATGGAGAAG
                                |||||||||  ||   |||||||||
                                ATGTCGTTT TG   TATTTCTTT
                                     G  ___
GAM455   LOC92606  3'  TTTCTTTATTCTGCTTTTTTGC 70531         CCT__
           T                     GGCAAGGA    GATGGAGAAG
                                |||||||||    ||||||||||
                                TCGTTTTT    TTATTTCTTT
                                     TCGTC
GAM456   CD34      3'  GCAAGGCTGGGCAGTG      10109      _  ATG
                                CATT CC   CAGCCTTGC
                                ||||  ||   |||||||||
                                GTGA GG   GTCGGAACG
                                  C  ___
GAM456   CMKLR1    3'  GCATTTTGCATGGGATG     15802          CCT
                                CATTCCATGCAG   TGC
                                ||||||||||||   |||
                                GTAGGGTACGTT   ACG
                                       TT_
GAM456   EPAC      3'  GCAAGGCTCTCCGTGGAGTG  21454         C__
                                CATTCCATG   AGCCTTGC
                                |||||||||   ||||||||
                                GTGAGGTGC   TCGGAACG
                                     CTC
GAM456   LTBP2     3'  GCAAGGGCTGCCATGGGAT   6467          _    _
                                ATTCCATG CAGCC TTGC
                                |||||||| ||||| ||||
                                TAGGGTAC GTCGG AACG
                                     C    G
GAM456   PTGFR     3'  GCAAGGCTTTAAGGAGTG    8178        A  C
                                CATTCC TG AGCCTTGC
                                |||||| || ||||||||
                                GTGAGG AT TCGGAACG
                                    A  T
GAM456   RANBP3    5'  GCAAGGGGCATGAAATG     24638      C    AG
                                CATT CATGC  CCTTGC
                                ||||  |||||  ||||||
                                GTAA GTACG  GGAACG
                                  A    G_
GAM456   TGM2      3'  GCAAGGCTGGGTAATG      17243      _  ATG
                                CATT CC   CAGCCTTGC
                                ||||  ||   |||||||||
                                GTAA GG   GTCGGAACG
                                  T  ___
GAM456   TPX1      3'  CGCAAGACTGCATGGA      13842          C    ___
                                TCCATGCAG CTTGC   G
                                |||||||||  |||||   |
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                                AGGTACGTC GAACG   C
                                     A    ___
GAM456  BICD2    3'  GCAAGACTCGCAGTGGGATG   70911       _  _ C
                                CATTCCA TGC AG CTTGC
                                ||||||| ||| || |||||
                                GTAGGGT ACG TC GAACG
                                    G   C  A
GAM456  C1orf29  5'  CAAGATTGACATGGAATG    23338        _ GC
                                CATTCCATG CA  CTTG
                                ||||||||| ||  ||||
                                GTAAGGTAC GT  GAAC
                                     A  TA
GAM456  C20orf161 3'  GCAAGGCTGCAGGTCTG     54203    TT  A
                                CA  CC TGCAGCCTTGC
                                ||  || ||||||||||
                                GT  GG ACGTCGGAACG
                                 CT  _
GAM456  DKFZP586C1619 3'  GCAAGGGGTAGGGGATG     62619       A   AG
                                CATTCC TGC  CCTTGC
                                |||||| |||  ||||||
                                GTAGGG ATG  GGAACG
                                   G   G_
GAM456  FLJ10241  3'  GCGGGCTGCATGGAATG     36391            T
                                CATTCCATGCAGCCT GC
                                |||||||||||||| ||
                                GTAAGGTACGTCGGG CG
                                                _
GAM456  GS3955   3'  GCAAGAGGCGTGGGATG     41621          AGC
                                CATTCCATGC   CTTGC
                                ||||||||||   |||||
                                GTAGGGTGCG   GAACG
                                     GA_
GAM456  HCGIV.9  3'  GCAAGGCTCTGTAGATTG    39132    T  C   C
                                CA TC ATG AGCCTTGC
                                || || ||| ||||||||
                                GT AG TGT TCGGAACG
                                 T  A   C
GAM456  KIAA0514  3'  GCAAGGCTGTAGCCGATG    28747      CCA
                                CATT   TGCAGCCTTGC
                                ||||   ||||||||||
                                GTAG   ATGTCGGAACG
                                  CCG
GAM456  KIAA1266  3'  GCAAGGGCGAGCATGGGATG   66698          A_  _
                                CATTCCATGC  GCC TTGC
                                ||||||||||  ||| ||||
                                GTAGGGTACG  CGG AACG
                                     AG   G
GAM456  KIAA1904  3'  GCAAGGCTGGTCAGGGAG    73871      A  __
                                TTCC TG  CAGCCTTGC
                                ||||  ||  |||||||||
```

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                                GAGG AC  GTCGGAACG
                                  G  TG
GAM456  KRTHB2   3'  GCAAAGGGATATGGAATG    53453        CAG   _
                                CATTCCATG   CCTT GC
                                |||||||||   |||| ||
                                GTAAGGTAT   GGAA CG
                                     AG_    A
GAM456  MAP3K3   3'  CGCAAGGCTGTGGACCATGGAG 11538        _____       ___
          TG                     CATTCCATG    CAGCCTTGC   G
                                |||||||||    |||||||||  |
                                GTGAGGTAC    GTCGGAACG   C
                                     CAGGT       ___
GAM456  PDE2A    3'  GCAGAGGCTATGGAATG     12005        GC    _
                                CATTCCAT  AGCCT TGC
                                ||||||||  ||||| |||
                                GTAAGGTA  TCGGA ACG
                                     __     G
GAM456  R3HDM    3'  GCAAGGCTGTACAATG      31716      CCA
                                CATT   TGCAGCCTTGC
                                ||||   ||||||||||||
                                GTAA   ATGTCGGAACG
                                  C__
GAM456  SLC2A13  5'  GCAAGGCAAGCGAGAATG    54659      CA   A_
                                CATTC  TGC  GCCTTGC
                                |||||  |||  |||||||
                                GTAAG  GCG  CGGAACG
                                   A_   AA
GAM456  LOC143110 3'  GCAAAGCACTTATGGAATG   76785        CA_  C
                                CATTCCATG   GC TTGC
                                |||||||||   || ||||
                                GTAAGGTAT   CG AACG
                                     TCA  A
GAM456  LOC145757 3'  GCAAGGCCTGGGCAGGAATG  77933       A   A___
                                CATTCC TGC    GCCTTGC
                                ||||||  |||   |||||||
                                GTAAGG ACG    CGGAACG
                                   _   GGTC
GAM456  LOC149722 5'  GCAAGTCAGGCATGGAGTG   85754         AGC_
                                CATTCCATGC    CTTGC
                                ||||||||||    |||||
                                GTGAGGTACG    GAACG
                                     GACT
GAM456  LOC165246 5'  GCAAGAGCCATGGAGTG     83367        CA  _
                                CATTCCATG  GC CTTGC
                                |||||||||  ||  |||||
                                GTGAGGTAC  CG GAACG
                                     __  A
GAM456  LOC201304 3'  GCAAATGGTGGGCATGGAA   89605        A_   __
                                TTCCATGC  GCC  TTGC
                                ||||||||  |||  ||||
```

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                                AAGGTACG  TGG  AACG
                                    GG   TA
GAM456  LOC219406 3'  GCAAGGCTGGGTGCAGTG    95204     C   G
                                CATT CAT CAGCCTTGC
                                |||| ||| |||||||||
                                GTGA GTG GTCGGAACG
                                  C   G
GAM456  LOC219990 5'  GCAGCTGAGCATGGGATG    93230         __  CT
                                CATTCCATGC  AGC  TGC
                                ||||||||||  |||  |||
                                GTAGGGTACG  TCG  ACG
                                     AG  __
GAM456  LOC90631  5'  GCAAGGTTCTGCAGAATG    64394      CA    __
                                CATTC  TGCAG  CCTTGC
                                |||||  |||||  ||||||
                                GTAAG  ACGTC  GGAACG
                                  __    TT
GAM456  LOC91464  3'  GCAAGGCCCAGTGTGGAGTG   66711         A__
                                CATTCCATGC   GCCTTGC
                                ||||||||||   |||||||
                                GTGAGGTGTG   CGGAACG
                                     ACC
GAM456  LOC93589  3'  GCACTGACATGGGATG      73051         _  CCT
                                CATTCCATG CAG   TGC
                                |||||||| |||   |||
                                GTAGGGTAC GTC   ACG
                                     A  ___
GAM457  ANXA9     5'  GACACCCACCTCACCTCTG    14541     CA T  C
                                CAGA  G TG GGTGGGTGTC
                                ||||  | || ||||||||||
                                GTCT  C AC CCACCCACAG
                                  __ C  T
GAM457  BDNF      5'  GACACCCACCGCTGCTGT     60338      T
                                ACAGT GCGGTGGGTGTC
                                ||||| ||||||||||||
                                TGTCG CGCCACCCACAG
                                  T
GAM457  BMP1      3'  GACACCCAGGCCACCCTG     21522     ACA  T  GG
                                CAG   GT GC  TGGGTGTC
                                |||   || ||  ||||||||
                                GTC   CA CG  ACCCACAG
                                  C__  C  G_
GAM457  BMP1      3'  ACCTGTACCGCAGCCGCCTG   21525     ACA      __
                                CAG   GTTGCGGT  GGGT
                                |||   ||||||||  ||||
                                GTC   CGACGCCA  TCCA
                                  CGC       TG
GAM457  CDS2      3'  ACACCCATGTAGCTGCTG     15107     A      G
                                CAG CAGTTGCG TGGGTGT
                                ||| |||||||| |||||||
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                                GTC GTCGATGT ACCCACA
                                  _      _
GAM457  DKC1     3'  ACTGTCCGCAGCTGTCTG    9076            TG
                                CAGACAGTTGCGG  GGT
                                |||||||||||||  |||
                                GTCTGTCGACGCC  TCA
                                       TG
GAM457  HADHA    3'  ACCACACACACCTGTCTG    5732         T  CG  _
                                CAGACAG TG  GTG GGT
                                |||||||  ||  ||| |||
                                GTCTGTC AC  CAC CCA
                                    C  A_   A
GAM457  HLCS     5'  GCTCACCACAACCTCTG     6413       CA   C
                                CAGA  GTTG GGTGGGT
                                ||||  |||| |||||||
                                GTCT  CAAC CCACTCG
                                  C_    A
GAM457  LIMD1    3'  GACATTCAGAAACTGCCTG   27260     A    GCGG
                                CAG CAGTT    TGGGTGTC
                                |||  |||||    ||||||||
                                GTC GTCAA    ACTTACAG
                                  C    AG__
GAM457  MB       3'  GACAGTAGCAATTGTCTG    19323          GGTGGG
                                CAGACAGTTGC     TGTC
                                ||||||||||      ||||
                                GTCTGTTAACG     ACAG
                                       ATG___
GAM457  MECP2    3'  ACACCCACAGGCATGTC     18380     GT   G_
                                GACA  TGC  GTGGGTGT
                                ||||  |||  ||||||||
                                CTGT  ACG  CACCCACA
                                  __   GA
GAM457  MLC1     3'  GCATGGCCGCAACTTC      31469    C       GG
                                GA AGTTGCGGT  GTGT
                                || |||||||||  ||||
                                CT TCAACGCCG  TACG
                                 _       G_
GAM457  MLC1     3'  GCATGGCCGCAACTTC      58293    C       GG
                                GA AGTTGCGGT  GTGT
                                || |||||||||  ||||
                                CT TCAACGCCG  TACG
                                 _       G_
GAM457  MX1      3'  GACGTGCACGCACACTGTCTG  11721        _   G  G
                                CAGACAGT TGCG TG GTGTC
                                |||||||| |||| || |||||
                                GTCTGTCA ACGC AC TGCAG
                                     C    _  G
GAM457  P53AIP1  3'  GACACCCACTGAACTTTCTG   42337     C    G
                                CAGA AGTT CGGTGGGTGTC
                                |||| |||| ||||||||||
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                                GTCT TCAA GTCACCCACAG
                                  T   _
GAM457  PFKM     3'  GACACCCGGGTTACTGTCT   60815       T  GG
                                AGACAGT GC  TGGGTGTC
                                ||||||| ||  ||||||||
                                TCTGTCA TG  GCCCACAG
                                    T  G_
GAM457  PPARGC1  3'  GACACCCATGTAAATGTC    26078     G    G
                                GACA TTGCG TGGGTGTC
                                |||| ||||| ||||||||
                                CTGT AATGT ACCCACAG
                                  A    _
GAM457  RAD54B   3'  GACATTCAGGCAATGTCT    57063      G   GG
                                AGACA TTGC  TGGGTGTC
                                ||||| ||||  ||||||||
                                TCTGT AACG  ACTTACAG
                                  _   G_
GAM457  SAS      3'  GCTCACCGCAACCTCTG     21103     CA
                                CAGA  GTTGCGGTGGGT
                                ||||  ||||||||||||
                                GTCT  CAACGCCACTCG
                                  C_
GAM457  SCNN1G   3'  ACACTCACAACTGTC       8297        GCG
                                GACAGTT   GTGGGTGT
                                |||||||   ||||||||
                                CTGTCAA   CACTCACA
                                     ___
GAM457  SLC19A1  3'  GACACTCAGGGCAGCTGCCTG  13215     A      GG
                                CAG CAGTTGC  TGGGTGTC
                                ||| |||||||  ||||||||
                                GTC GTCGACG  ACTCACAG
                                  C      GG
GAM457  SLC3A2   5'  GACGGTCACGACTGCCT     11521    A    GCG   G
                                AG CAGTT   GTGG TGTC
                                || |||||   |||| ||||
                                TC GTCAG   CACT GCAG
                                 C    ___   G
GAM457  TGIF     3'  GATGCCCACATACTGTCT    13744       TGCG
                                AGACAGT   GTGGGTGTC
                                |||||||   |||||||||
                                TCTGTCA   CACCCGTAG
                                    TA__
GAM457  ZNF80    5'  ACACTCACCGCAAACGTCTG  24066      AG
                                CAGAC  TTGCGGTGGGTGT
                                |||||  ||||||||||||
                                GTCTG  AACGCCACTCACA
                                   CA
GAM457  C1orf24  3'  GACACCCAGAACACTGCTG   54789    A   TGCGG
                                CAG CAGT    TGGGTGTC
                                ||| ||||    ||||||||
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                                GTC GTCA    ACCCACAG
                                  _   CAAG_
GAM457  C20orf100 3'  GACACCCACCCCAGATGCATG  52878    GA  G   C
                                CA  CA TTG GGTGGGTGTC
                                ||  || ||| ||||||||||
                                GT  GT GAC CCACCCACAG
                                 AC  A   C
GAM457  C5orf6    3'  GACACTGGGTCAATGTCTG   33953       G   CGGTG
                                CAGACA TTG    GGTGTC
                                |||||| |||    ||||||
                                GTCTGT AAC    TCACAG
                                   _  TGGG_
GAM457  CARD6     3'  GCTCACCGCAACCTCTG     51844      CA
                                CAGA  GTTGCGGTGGGT
                                ||||  ||||||||||||
                                GTCT  CAACGCCACTCG
                                  C_
GAM457  CPSF2     3'  GCTCACCGCAACCTCTG     62273      CA
                                CAGA  GTTGCGGTGGGT
                                ||||  ||||||||||||
                                GTCT  CAACGCCACTCG
                                  C_
GAM457  Di-Ras2   3'  GACACCCACCGTCGTC      34612     AGTT
                                GAC   GCGGTGGGTGTC
                                |||   ||||||||||||
                                CTG   TGCCACCCACAG
                                 C___
GAM457  DNAJC6    3'  ACACCCATCACATTGTCTG   29488        T C
                                CAGACAGT G GGTGGGTGT
                                |||||||| | |||||||||
                                GTCTGTTA C CTACCCACA
                                    _ A
GAM457  EDR1      3'  GACACTCTCCACTGTC      16658       TGC  T
                                GACAGT   GG GGGTGTC
                                ||||||   || |||||||
                                CTGTCA   CC CTCACAG
                                   ___  T
GAM457  ELKS      3'  GACACCTGACAACCCTCTG   31190      CA   CGG
                                CAGA  GTTG   TGGGTGTC
                                ||||  ||||   ||||||||
                                GTCT  CAAC   GTCCACAG
                                  CC   A__
GAM457  FLJ12661  5'  ACACCTGCTGCAACTCCTG   47853     AC      TG
                                CAG  AGTTGCGG  GGTGT
                                |||  ||||||||  |||||
                                GTC  TCAACGTC  CCACA
                                 C_       GT
GAM457  FLJ13072  3'  ACACCCATATCAGTGTCTG   91378       G   CG
                                CAGACA TTG  GTGGGTGT
                                |||||| |||  ||||||||
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                                GTCTGT GAC  TACCCACA
                                   _  TA
GAM457  FLJ22056  3'  GACACCCAGCAGCCGCTG   42833    ACA    GG
                                CAG  GTTGC  TGGGTGTC
                                |||  |||||  ||||||||
                                GTC  CGACG  ACCCACAG
                                  GC_   __
GAM457  GFR       3'  ACACTCACCAACTGCTTG   25441    GA    GC
                                CA  CAGTT  GGTGGGTGT
                                ||  |||||  |||||||||
                                GT  GTCAA  CCACTCACA
                                 TC    __
GAM457  GMPPB     5'  GACACCCCCTCAACGTC    26220    A   C  T
                                GAC GTTG GG GGGTGTC
                                ||| |||| || |||||||
                                CTG CAAC CC CCCACAG
                                  _   T  _
GAM457  GMPPB     5'  GACACCCCCTCAACGTC    42023    A   C  T
                                GAC GTTG GG GGGTGTC
                                ||| |||| || |||||||
                                CTG CAAC CC CCCACAG
                                  _   T  _
GAM457  IL1F10    3'  GACACCCATTTCAGACTTCTG 51761     C   GC_
                                CAGA AGTT   GGTGGGTGTC
                                |||| ||||   ||||||||||
                                GTCT TCAG   TTACCCACAG
                                   _   ACT
GAM457  KIAA0574  3'  GACACCCAACGTGCTGCT   69815    A   T  G
                                AG CAGT GCG TGGGTGTC
                                || |||| ||| ||||||||
                                TC GTCG TGC ACCCACAG
                                 _   _  A
GAM457  KIAA1136  3'  ACACCCAAGTATCAACTGCT  92953    A    CGG__
                                AG CAGTTG    TGGGTGT
                                || ||||||    |||||||
                                TC GTCAAC    ACCCACA
                                 _     TATGA
GAM457  KIAA1712  3'  GCTCACCGCAACCTCTG    68159     CA
                                CAGA  GTTGCGGTGGGT
                                ||||  ||||||||||||
                                GTCT  CAACGCCACTCG
                                  C_
GAM457  KIAA1755  3'  GACACCCACCTGCAGCTCA   62015   C    _
                                A AGTTGC GGTGGGTGTC
                                | |||||| ||||||||||
                                A TCGACG CCACCCACAG
                                 C     T
GAM457  KIAA1944  5'  ACACCCAATGTCTGCTC    76073    _  TT  G
                                GA CAG  GCG TGGGTGT
                                || |||  ||| |||||||
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                                CT GTC  TGT ACCCACA
                                 C   __   A
GAM457  MGC11034 3'  GACTTTCACCACTGTCTG    49573        TGC     T
                                CAGACAGT   GGTGGG GTC
                                ||||||||   |||||| |||
                                GTCTGTCA   CCACTT CAG
                                     ___      T
GAM457  MGC4294  5'  ACACTCACACTACTGCCTG   44478     A   TGCG
                                CAG CAGT    GTGGGTGT
                                ||| ||||    ||||||||
                                GTC GTCA    CACTCACA
                                  C    TCA_
GAM457  MGC4294  5'  GACACCCACACGGGCCTTCTG  44479      CA  G  _
                                CAGA  GTT CG GTGGGTGTC
                                ||||  ||| || |||||||||
                                GTCT  CGG GC CACCCACAG
                                   TC   _  A
GAM457  PGR1     3'  GACAGTATGGAACTGTCTG    53906        G  GTGGG
                                CAGACAGTT CG     TGTC
                                |||||||||  ||     ||||
                                GTCTGTCAA GT     ACAG
                                     G  ATG__
GAM457  PNMA5    3'  GACACCCCCAAATATCT     73972     CA   GC  T
                                AGA  GTT  GG GGGTGTC
                                |||  |||  || |||||||
                                TCT  TAA  CC CCCACAG
                                  A_   A_  _
GAM457  POLR2D   3'  CACCTTCCCACTGTCTG     17840        T C  T
                                CAGACAGT G GG GGGTG
                                |||||||| | || |||||
                                GTCTGTCA C CC TCCAC
                                     _ _  T
GAM457  PTPN3    3'  GACACCCACAGAGCTGTT    12585        GCG
                                GACAGTT   GTGGGTGTC
                                |||||||   |||||||||
                                TTGTCGA   CACCCACAG
                                    GA_
GAM457  ROBO2    5'  GACACCCAGAACCCACCATCT  63154     CA  T C   ___
                                AGA  GT G GGT   GGGTGTC
                                |||  || | |||   |||||||
                                TCT  CA C CCA   CCCACAG
                                  AC  _ _   AGA
GAM457  SDFR1    3'  ACACCACAATGACTGTCT    25789        CG   G
                                AGACAGTTG  GTGG TGT
                                |||||||||  |||| |||
                                TCTGTCAGT  CACC ACA
                                     AA   _
GAM457  SDFR1    3'  ACACCACAATGACTGTCT    34358        CG   G
                                AGACAGTTG  GTGG TGT
                                |||||||||  |||| |||
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                                TCTGTCAGT  CACC ACA
                                     AA   _
GAM457  SLC26A9  3'  GACAAGTACAACTGTGCTG   54715    _    GCG   GG
                                CAG ACAGTT   GTG  TGTC
                                ||| ||||||   |||  ||||
                                GTC TGTCAA   CAT  ACAG
                                  G     ___   GA
GAM457  THG-1    5'  GACACCCACTCGCTGGCTG   48914     _  _
                                CAGTT GCG GTGGGTGTC
                                ||||| ||| |||||||||
                                GTCGG CGC CACCCACAG
                                   T  T
GAM457  UBCE7IP5 3'  GACACCCACAGTGTGCTCTG  30846     _ GT   G
                                CAGA CA  TGC GTGGGTGTC
                                |||| ||  ||| |||||||||
                                GTCT GT  GTG CACCCACAG
                                  C  __  A
GAM457  UTS2     5'  ACACAGCATGGCAACTCATCT  42079    C_    G  G_
                                AGA  AGTTGC GTG  GTGT
                                |||  |||||| |||  ||||
                                TCT  TCAACG TAC  CACA
                                  AC     G   GA
GAM457  WBSCR20A 5'  GCTCACCGCAACCTCTG    50571     CA
                                CAGA  GTTGCGGTGGGT
                                ||||  ||||||||||||
                                GTCT  CAACGCCACTCG
                                  C_
GAM457  LOC124216 3'  ACACCCACCACCAGTCTCTG  74731     CAG   C_
                                CAGA   TTG  GGTGGGTGT
                                ||||   |||  |||||||||
                                GTCT   GAC  CCACCCACA
                                  CT_   CA
GAM457  LOC126066 5'  GACACCCACAGACGTGTCTG  76175      _  GCG
                                CAGACA GTT   GTGGGTGTC
                                ||||||  |||  |||||||||
                                GTCTGT CAG   CACCCACAG
                                   G   A__
GAM457  LOC126392 5'  GACACCCAGGTGGGCCGTCTG  76205      A _ TG GG
                                CAGAC G T  C  TGGGTGTC
                                ||||| | |  |  ||||||||
                                GTCTG C G  G  ACCCACAG
                                   C G GT G_
GAM457  LOC129676 5'  ACACCCACCATCCAGGGTC   76230    AG   C__
                                GAC  TTG   GGTGGGTGT
                                |||  |||   |||||||||
                                CTG  GAC   CCACCCACA
                                  G_   CTA
GAM457  LOC135154 3'  GACACCCACCATTGCGCCTGGC 75731    A   T  ___
          T                      AG CAG TGC   GGTGGGTGTC
                                 || ||| |||   ||||||||||
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                                TC GTC GCG   CCACCCACAG
                                 G   C   TTA
GAM457   LOC138389 3'  GACACCCACCAGGGGTGCT   76739    A  G  GC
                                AG CA TT  GGTGGGTGTC
                                || || ||  ||||||||||
                                TC GT GG  CCACCCACAG
                                 _  G  GA
GAM457   LOC139248 5'  ACACCCACATCAGCCTG     76332     ACA    CG
                                CAG   GTTG  GTGGGTGT
                                |||   ||||  ||||||||
                                GTC   CGAC  CACCCACA
                                  ____   TA
GAM457   LOC147180 5'  ACACCTGTTTAAATGTCTG    85090       G   C  TG
                                CAGACA TTG GG  GGTGT
                                |||||| ||| ||  |||||
                                GTCTGT AAT TT  CCACA
                                    A   _  GT
GAM457   LOC149103 3'  ACACATGCAGACAACTGCTG   79936     A     CG_  GG
                                CAG CAGTTG   GT  GTGT
                                ||| ||||||   ||  ||||
                                GTC GTCAAC   CG  CACA
                                  _     AGA  TA
GAM457   LOC149465 3'  ACCCAGTCCCACACCTGCCTG  80191     A   T  C  ___
                                CAG CAG TG GG   TGGGT
                                ||| ||| || ||   |||||
                                GTC GTC AC CC   ACCCA
                                  C   C  A  CTG
GAM457   LOC150481 3'  GACACAACCCAAATGTC     80702      G   C   GG
                                GACA TTG GGT  GTGTC
                                |||| ||| |||  |||||
                                CTGT AAC CCA  CACAG
                                  A   _   A_
GAM457   LOC150538 5'  GACACCCACTGCGTATTG     80738      _
                                CAGT TGCGGTGGGTGTC
                                |||| ||||||||||||
                                GTTA GCGTCACCCACAG
                                  T
GAM457   LOC152317 5'  ACATAACTTGCAACTGTCT    86819          _  GG
                                AGACAGTTGCG GT  GTGT
                                |||||||||| ||  ||||
                                TCTGTCAACGT CA  TACA
                                       T  A_
GAM457   LOC152582 5'  GCTCACCGCAACCTCTG     86990      CA
                                CAGA  GTTGCGGTGGGT
                                ||||  ||||||||||||
                                GTCT  CAACGCCACTCG
                                  C_
GAM457   LOC152633 5'  GACACCCAGGGCTGTGCTG   86996     _     GCGG
                                CAG ACAGTT    TGGGTGTC
                                ||| ||||||    ||||||||
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                                GTC TGTCGG    ACCCACAG
                                  G     G___
GAM457   LOC158191 3'  GACACAACCCAAATGTC     82675      G   C   GG
                                GACA TTG GGT  GTGTC
                                |||| ||| |||  |||||
                                CTGT AAC CCA  CACAG
                                  A   _   A_
GAM457   LOC158332 3'  ACACCCATGCTGTGCT      82761    _     TGCG
                                AG ACAGT    GTGGGTGT
                                || |||||    ||||||||
                                TC TGTCG    TACCCACA
                                 G    _____
GAM457   LOC158527 5'  ACCATTCGACAACTGTCT     82837         _   TG
                                AGACAGTTG CGG  GGT
                                ||||||||| |||  |||
                                TCTGTCAAC GCT  CCA
                                      A   TA
GAM457   LOC170221 3'  ACACCCGCAGACTGCTG      83465     A     GCG
                                CAG CAGTT   GTGGGTGT
                                ||| |||||   ||||||||
                                GTC GTCAG   CGCCCACA
                                  _    A__
GAM457   LOC202986 3'  GACACCCGTAAAGCGTCTG    92066       A   GCG
                                CAGAC GTT   GTGGGTGTC
                                ||||| |||   |||||||||
                                GTCTG CGA   TGCCCACAG
                                   _   AA_
GAM457   LOC203350 3'  ACACCTTCACCTGTCTG      92222        T  CGGT
                                CAGACAG TG    GGGTGT
                                ||||||| ||    ||||||
                                GTCTGTC AC    TCCACA
                                    C  T___
GAM457   LOC219672 3'  GACACTTCAGCACCTGTC     92968       T   GGT
                                GACAG TGC   GGGTGTC
                                ||||| |||   |||||||
                                CTGTC ACG   TTCACAG
                                   C   AC_
GAM457   LOC221178 3'  ACATTCAAACAACTGTTTG    95161          CGG
                                CAGACAGTTG   TGGGTGT
                                |||||||||   |||||||
                                GTTTGTCAAC   ACTTACA
                                      AA_
GAM457   LOC253502 3'  GCCTACCAGAACTGCCTG     96220     A     GC
                                CAG CAGTT  GGTGGGT
                                ||| |||||  |||||||
                                GTC GTCAA  CCATCCG
                                  C    GA
GAM457   LOC253782 3'  GACACCCACAATTGTC       97400        GCG
                                GACAGTT   GTGGGTGTC
                                |||||||   |||||||||
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                                CTGTTAA   CACCCACAG
                                   ___
GAM457  LOC254827 5'  ACACTCATCAACTGTT      98773        CG
                                GACAGTTG  GTGGGTGT
                                ||||||||  ||||||||
                                TTGTCAAC  TACTCACA
                                   __
GAM457  LOC255019 3'  GACACCTTCCAAGTGTCTG    96780       G   C  T
                                CAGACA TTG GG GGGTGTC
                                |||||| ||| || |||||||
                                GTCTGT AAC CT TCCACAG
                                   G   _ _
GAM457  LOC257442 3'  GACAGTTTAGCAACTGTTCA   97809    A       GGT  G
                                C GACAGTTGC   GG TGTC
                                | |||||||||   || ||||
                                A TTGTCAACG   TT ACAG
                                 C        AT_  G
GAM457  LOC86651  3'  GACACTGTGGAGCAACATCTG  69310     CA    GGTG_
                                CAGA  GTTGC    GGTGTC
                                ||||  |||||    ||||||
                                GTCT  CAACG    TCACAG
                                  A_    AGGTG
GAM457  LOC90987  3'  GACAGTTTAGCAACTGTTCA   65150    A       GGT  G
                                C GACAGTTGC   GG TGTC
                                | |||||||||   || ||||
                                A TTGTCAACG   TT ACAG
                                 C        AT_  G
GAM457  LOC91960  3'  GACACCCAGAAGCTGTT     68284        GCGG
                                GACAGTT    TGGGTGTC
                                |||||||    ||||||||
                                TTGTCGA    ACCCACAG
                                   AG__
GAM458  ANK3      3'  CTGTAAAATTATTACTGT     8563       C       CC
                                GCAG AATAATTT  CAG
                                |||| ||||||||  |||
                                TGTC TTATTAAA  GTC
                                  A       AT
GAM458  CD80      5'  CACCTGGGAAGTGCCCTG     19023     CA   ATAA       A
                                CAG  GCA    TTTCCCAG TG
                                |||  |||    |||||||| ||
                                GTC  CGT    GAAGGGTC AC
                                  C_   _____        C
GAM458  EIF5A     3'  GCATCTGGGAGGGCCCTGC    10511      CAATAA
                                GCAG     TTTCCCAGATGC
                                ||||     ||||||||||||
                                CGTC     GGAGGGTCTACG
                                  CCG___
GAM458  HMMR      3'  CATCTGAGAAACCTGTTG     25947       CAATAA   C
                                CAGCAG     TTTC CAGATG
                                ||||||     |||| ||||||
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                                GTTGTC     AAAG GTCTAC
                                   C_____   A
GAM458  NESG1    3'  CATCCATAATTGCTGCT    25618        A  TTCCCA
                                AGCAGCAAT AT     GATG
                                ||||||||| ||     ||||
                                TCGTCGTTA TA     CTAC
                                    A  C_____
GAM458  PIGN     3'  GCATCCAAAGTCATTGCTGT  25603        A   CCCA
                                GCAGCAAT ATTT   GATGC
                                |||||||| ||||   |||||
                                TGTCGTTA TGAA   CTACG
                                    C   AC__
GAM458  TBL1X    3'  CACCTGGGAAAGGGATGCTGC 20129       ATAA      A
                                GCAGCA   TTTCCCAG TG
                                ||||||   |||||||| ||
                                CGTCGT   AAAGGGTC AC
                                   AGGG      C
GAM458  TCF8     3'  GCACCTCCCGTTTCCGCTGCTG 48432       AAT   TTCCC  A
                                CAGCAGC   AAT    AG TGC
                                |||||||   |||    || |||
                                GTCGTCG   TTG    TC ACG
                                    CCT   CCC__  C
GAM458  CDCA7    3'  GCATATGTAAACCATTGCTGT  50041        AAT  CC  G
                                GCAGCAAT   TT  CA ATGC
                                ||||||||   ||  || ||||
                                TGTCGTTA   AA  GT TACG
                                    CC_  AT  A
GAM458  CDT1     3'  GCACCTCTGTCCTTGCTGCTG  78161        TAATTTCC   __
                                CAGCAGCAA       CAGA  TGC
                                |||||||||       ||||  |||
                                GTCGTCGTT       GTCT  ACG
                                    CCT_____    CC
GAM458  DDX28    5'  CATCTGGGAAAACAGCTGC   37788      AATAA
                                GCAGC    TTTCCCAGATG
                                |||||    ||||||||||
                                CGTCG    AAAGGGTCTAC
                                   ACA__
GAM458  DKFZP434B044 3'  CATCTGGGAAACTTCTGGGTGC 49712      G_  ATAA
           TG                    CAGCA  CA    TTTCCCAGATG
                                 |||||  ||    ||||||||||
                                 GTCGT  GT    AAAGGGTCTAC
                                    GG  CTTC
GAM458  FLJ10232  3'  CACCTGGGGCTGTGCTACTG   36374     C   ATAATT     A
                                CAG AGCA     TCCCAG TG
                                ||| ||||     |||||| ||
                                GTC TCGT     GGGGTC AC
                                  A   GTC___     C
GAM458  FLJ10297  3'  GCACCTGGTGCCACGTGCTGCT 36440        ATAATTTC   A
           G                     CAGCAGCA       CCAG TGC
                                 ||||||||       |||| |||
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                                GTCGTCGT       GGTC ACG
                                    GCACCGT_    C
GAM458  FLJ10986  5'  CATCTGGGCTGCGTGCTG    37490       _   ATAATTT
                                CAGCA GCA      CCCAGATG
                                ||||| |||      ||||||||
                                GTCGT CGT      GGGTCTAC
                                   G   C_______
GAM458  FLJ20208  3'  GCATCTGGGGACACAGCTGC   35245       AATAAT
                                GCAGC     TTCCCAGATGC
                                |||||     ||||||||||
                                CGTCG     AGGGGTCTACG
                                   ACAC__
GAM458  FLJ20232  3'  GCACCTGGGGAGATCGGTGCT  39186      ATAA_       A
                                AGCA    TTTCCCAG TGC
                                ||||    |||||||| |||
                                TCGT    GAGGGGTC ACG
                                   GGCTA       C
GAM458  FLJ20450  3'  CACCTGGGACCTGTGTTGCTG  35637        ATAATT     A
                                CAGCAGCA     TCCCAG TG
                                ||||||||     |||||| ||
                                GTCGTTGT     AGGGTC AC
                                    GTCC__     C
GAM458  KIAA0513  3'  GCACCCCAGGAACCCTTGCTGC 29034         TAAT   CAGA_
          TG                    CAGCAGCAA   TTCC    TGC
                                |||||||||   ||||    |||
                                GTCGTCGTT   AAGG    ACG
                                    CCC_   ACCCC
GAM458  KIAA0673  3'  GCATCCAGCTTAGCTGCTGCTG 62946        A_   TTTCCCA
                                CAGCAGCA  TAA      GATGC
                                ||||||||  |||      |||||
                                GTCGTCGT  ATT      CTACG
                                    CG   CGAC___
GAM458  KIAA1164  3'  TTTGAAAGACTATTGCTGCTG  70056         A   CC
                                CAGCAGCAATA TTT  CAGA
                                |||||||||| |||  ||||
                                GTCGTCGTTAT AGA  GTTT
                                      C   AA
GAM458  KIAA1239  3'  CATCATGATTATTGATGCT    71847      G       TCCCA
                                AGCA CAATAATT     GATG
                                |||| ||||||||     ||||
                                TCGT GTTATTAG     CTAC
                                   A       TA___
GAM458  KIAA1691  3'  GCATCTGGCTGGTGCCTGCTGC 94130       ATA   TC
                                GCAGCA   ATT  CCAGATGC
                                ||||||   |||  ||||||||
                                CGTCGT   TGG  GGTCTACG
                                   CCG   TC
GAM458  KIAA1924  3'  GCATCTGGGACCTGGCCACCCT 74048     CA__  AATAATT
          G                     CAG    GC      TCCCAGATGC
                                |||    ||      ||||||||||
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                                GTC   CG      AGGGTCTACG
                                  CCAC  GTCC___
GAM458  LOC143243 3'  GCATCTGGGAAGGCCCTGC   60940      CAATAA
                                GCAG     TTTCCCAGATGC
                                ||||     ||||||||||||
                                CGTC     GAAGGGTCTACG
                                  CCG___
GAM458  LOC146517 3'  GCATCTGGGTCTTTGCAGCTG  78506      A   TAATTT
                                CAGC GCAA     CCCAGATGC
                                |||| ||||     |||||||||
                                GTCG CGTT     GGGTCTACG
                                  A   TCT___
GAM458  LOC150935 3'  GCATCTGGGAAGGCACAGCTG  80829      AATAA
                                CAGC     TTTCCCAGATGC
                                ||||     ||||||||||||
                                GTCG     GAAGGGTCTACG
                                  ACACG
GAM458  LOC158046 3'  GCATCTGGGACTACAGCCATTG 59905        AATT____
            CTGT                  GCAGCAAT       TCCCAGATGC
                                ||||||||       ||||||||||
                                TGTCGTTA       AGGGTCTACG
                                    CCGACATC
GAM458  LOC253805 3'  GCACCCGAGGCTCCTGCTGCTG 98177        ATAA   CCAGA
                                CAGCAGCA   TTTC    TGC
                                ||||||||   ||||    |||
                                GTCGTCGT   GGAG    ACG
                                    CCTC   CCC__
GAM458  LOC89932  5'  GCACCTACCTTGTTGCTGCT   61464         TTTCCC  A
                                AGCAGCAATAA     AG TGC
                                ||||||||||     || |||
                                TCGTCGTTGTT     TC ACG
                                    CCA___  C
GAM459  AIRE      3'  TGGGAGCCTGAGGCATGAGAA  7247      C     C
                                TTC CATGCC CAGGCTCCTG
                                ||| |||||| ||||||||||
                                AAG GTACGG GTCCGAGGGT
                                  A     A
GAM459  BCAS1     3'  CTCGGGAGCCCAACGCACGAGA 14711     CCA   CCCA      C
            A                   TTC   TGC   GGCTCCTG AG
                                |||   |||   |||||||| ||
                                AAG   ACG   CCGAGGGC TC
                                  AGC   CAAC      _
GAM459  DAG1      3'  CTGCAGGATGTAACATGG    16553      CCCCAG  _
                                CCATG     GC TCCTGCAG
                                |||||     || ||||||||
                                GGTAC     TG AGGACGTC
                                  AA____  T
GAM459  GPRK7     3'  CGGGAGCCTGAGGCAGGAGAA  58313     _  A   C
                                TTC CC TGCC CAGGCTCCTG
                                ||| || |||| ||||||||||
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                                AAG GG ACGG GTCCGAGGGC
                                  A _   A
GAM459  KIF1B   3'  TGGGAGCCTGAGGCAGGAGAA  31273    _ A   C
                                TTC CC TGCC CAGGCTCCTG
                                ||| || |||| ||||||||||
                                AAG GG ACGG GTCCGAGGGT
                                  A _   A
GAM459  NCAM1   5'  CTGCAGGGGGGGGGGCACAGAA 7040     CCA    AGG
                                TTC   TGCCCC   CTCCTGCAG
                                |||   ||||||   |||||||||
                                AAG   ACGGGG   GGGGACGTC
                                  AC_    GG_
GAM459  NOS1    3'  CTGCAGGGTCCCCAAGGATGG  7095     G  CCA_  CT
                                CCAT CC   GG  CCTGCAG
                                |||| ||   ||  |||||||
                                GGTA GG   CC  GGACGTC
                                  _ AACC  TG
GAM459  PDGFRB  3'  TGCCCCAGGGACATGGGAA   66584       _  CA  CTCCT
                                TTCCCATG CCC  GG   GCA
                                |||||||| |||  ||   |||
                                AAGGGTAC GGG  CC   CGT
                                    A  AC  _____
GAM459  RAB31   3'  CTGCAGGGGGCGGGGCAGGAA  23440    CA    AGG
                                TTCC  TGCCCC   CTCCTGCAG
                                ||||  ||||||   |||||||||
                                AAGG  ACGGGG   GGGGACGTC
                                  __     CG_
GAM459  SCN4A   3'  CTGCGTTCCCAGACCATGGGAA 6200       CCCCA  CTCC
                                TTCCCATG    GG   TGCAG
                                ||||||||    ||   |||||
                                AAGGGTAC    CC   GCGTC
                                    CAGAC  TT__
GAM459  WHSC1   3'  CTGCAATGACTGCAGGGCTGGG 24667      T   __  GCTCC
          AA                    TTCCCA GCCC  CAG    TGCAG
                                |||||| ||||  |||    |||||
                                AAGGGT CGGG  GTC    ACGTC
                                  _   AC   AGTA_
GAM459  WHSC1   3'  CTGCAATGACTGCAGGGCTGGG 24668      T   __  GCTCC
          AA                    TTCCCA GCCC  CAG    TGCAG
                                |||||| ||||  |||    |||||
                                AAGGGT CGGG  GTC    ACGTC
                                  _   AC   AGTA_
GAM459  WHSC1   3'  CTGCAATGACTGCAGGGCTGGG 24669      T   __  GCTCC
          AA                    TTCCCA GCCC  CAG    TGCAG
                                |||||| ||||  |||    |||||
                                AAGGGT CGGG  GTC    ACGTC
                                  _   AC   AGTA_
GAM459  ZFP36L1 3'  CTGCAGGAAGGAAGGCTG   18201    T  __  AGGC
                                CA GCC  CC   TCCTGCAG
                                || |||  ||   ||||||||
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                                GT CGG  GG   AGGACGTC
                                 _  AA  A___
GAM459  C20orf64  5'  CAAGAGCCCTTCCTGCAGGGAA 54334      A  CCCA__   C
                                TTCCC TGC     GGCTC TG
                                ||||| |||     ||||| ||
                                AAGGG ACG     CCGAG AC
                                   _  TCCTTC    A
GAM459  DRIL2    3'  CTGCAGGGTGTGGGCAGAGAA  22350    CCA    C G  T
                                TTC   TGCCC A GC CCTGCAG
                                |||   ||||| | || |||||||
                                AAG   ACGGG T TG GGACGTC
                                  AG_    _ G  _
GAM459  FEM-2    3'  CTGCAGGGCCAAGCCACAGGAA 28312     CAT_  CCCA   T
                                TTCC    GC    GGC CCTGCAG
                                ||||    ||    ||| |||||||
                                AAGG    CG    CCG GGACGTC
                                  ACAC  AA__   _
GAM459  FLJ10737  3'  CTGCAGTCCAAGCTGAACATGG 37054       CCCCA   C___
           GAA                    TTCCCATG    GGCT    CTGCAG
                                ||||||||    ||||   ||||||
                                AAGGGTAC    TCGA    GACGTC
                                    AAG__    ACCT
GAM459  FLJ10898  5'  CTGCCAAACCTGCAACATGGGA 60133       CCC    CTCCT
           A                    TTCCCATG   CAGG    GCAG
                                ||||||||   ||||    ||||
                                AAGGGTAC   GTCC    CGTC
                                    AAC    AAAC_
GAM459  FLJ11618  3'  CTGCAGGGGGAAGAGCCGGGAA 42624      AT  CCCAGG
                                TTCCC  GC     CTCCTGCAG
                                |||||  ||     |||||||||
                                AAGGG  CG     GGGGACGTC
                                   C_  AGAAG_
GAM459  FLJ12287  5'  TGCCTCTGGGGCCTGGGAA   42564       T       CTCCT
                                TTCCCA GCCCCAGG    GCA
                                |||||| ||||||||    |||
                                AAGGGT CGGGGTCT    CGT
                                    C       C_____
GAM459  FLJ14129  3'  TGGGAGCCTGGGGCAGGAGAA  48814     _  A
                                TTC CC TGCCCCAGGCTCCTG
                                ||| || ||||||||||||||
                                AAG GG ACGGGGTCCGAGGGT
                                  A  _
GAM459  KIAA0187  3'  CTGCAGGAGGAGGAACAGAGAA 29250     CCA  CC  AGG
                                TTC   TG  CC   CTCCTGCAG
                                |||   ||  ||   |||||||||
                                AAG   AC  GG   GAGGACGTC
                                  AG_  AA  AG_
GAM459  KIAA0416  5'  GGAAAGCCTGGGACACAGAA   32093     CCA  C       __
                                TTC   TG CCCAGGC  TCC
                                |||   || |||||||  |||
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                                AAG   AC GGGTCCG  AGG
                                  AC_  A      AA
GAM459  KIAA1266  3'  CTGCAAGGGCGAGCATGGGA   66695        CCCAG    C
                                TCCCATGC    GCTC TGCAG
                                ||||||||    |||| |||||
                                AGGGTACG    CGGG ACGTC
                                    AG___    A
GAM459  KIAA1483  3'  CTGCAGGGAAAAGGATATAGGA 70434      C   C  CAGG T
            A                    TTCC ATG CC    C CCTGCAG
                                ||||| ||| ||    | |||||||
                                AAGG TAT GG    G GGACGTC
                                  A   A  AAAA _
GAM459  KIAA1706  3'  TGCAGTGAGAGCATGGGA    94372        CCCAGG   _
                                TCCCATGC     CTC CTGCA
                                ||||||||     ||| |||||
                                AGGGTACG     GAG GACGT
                                    A_____   T
GAM459  KIAA1715  3'  CTCAGGAGCCTGAGGCAGGAGA 68684     _ A    C        C
            A                    TTC CC TGCC CAGGCTCCTG AG
                                ||| || |||| |||||||||| ||
                                AAG GG ACGG GTCCGAGGAC TC
                                  A  _    A        _
GAM459  KIAA1981  3'  CAGGAGCCAAGGTCACAGAA   89710     CCA  C  CA
                                TTC   TG CC  GGCTCCTG
                                |||   || ||  ||||||||
                                AAG   AC GG  CCGAGGAC
                                  AC_  T  AA
GAM459  MCAM      3'  CAGGAACCTGGGGGCCTGTGAA 22457     C  T    _   C
                                TTC CA GCCCC AGG TCCTG
                                ||| || ||||| ||| |||||
                                AAG GT CGGGG TCC AGGAC
                                  T  C    G   A
GAM459  MRPS24    3'  CTGCAGAGAATGGAAACGTGGG 50130        CC_   GG   C
            AA                    TTCCCATG   CCA  CTC TGCAG
                                ||||||||   |||  ||| |||||
                                AAGGGTGC   GGT  GAG ACGTC
                                    AAA   AA  _
GAM459  MSE55     3'  TGCAGGACAGACATGGGAG    23916        CCCCAGGC
                                TTCCCATG       TCCTGCA
                                ||||||||       |||||||
                                GAGGGTAC       AGGACGT
                                    AGAC_____
GAM459  OS4       3'  CTGCTTTGTGCTAAAAGCATGG 20388         CCCA   TCCT_
            GAA                    TTCCCATGC    GGC    GCAG
                                |||||||||   |||    ||||
                                AAGGGTACG   TCG    CGTC
                                     AAAA   TGTTT
GAM459  PASK      5'  CAGGGTCTCGCCTGGGGCATTA 31405     CC         _____
            GAA                    TTC  ATGCCCCAGGC    TCCTG
                                |||  ||||||||||   |||||
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                                AAG  TACGGGGTCCG    GGGAC
                                  AT         CTCT
GAM459  PRO1163   3'  CTGAATGAGCCTGGGGCA    38323           CTG
                                TGCCCCAGGCTC   CAG
                                ||||||||||||   |||
                                ACGGGGTCCGAG   GTC
                                       TAA
GAM459  THEA      3'  CTCAGGAAGCTGAGGCACAAGA 66887     CCA    C   GC     C
          A                      TTC   TGCC CAG  TCCTG AG
                                |||   |||| |||  ||||| ||
                                AAG   ACGG GTC  AGGAC TC
                                  AAC    A   GA    _
GAM459  WFDC3     3'  GCTGACCAGAGCATGGGAA    98702         CCCA  C  CT
                                TTCCCATGC    GG TC  GC
                                |||||||||    || ||  ||
                                AAGGGTACG    CC AG  CG
                                      AGA_  _  T_
GAM459  LOC122726 5'  CTGCAGGAAACACTGAGGCTTG 76103       T   C   GC__
          GGAA                      TTCCCA GCC CAG    TCCTGCAG
                                |||||| ||| |||    |||||||||
                                AAGGGT CGG GTC    AGGACGTC
                                   T   A   ACAA
GAM459  LOC129303 3'  CTGCAGGAATTGGGGGCTGGGA 75373       T     AG C
          A                      TTCCCA GCCCC  G TCCTGCAG
                                |||||| |||||  | |||||||||
                                AAGGGT CGGGG  T AGGACGTC
                                   _    GT A
GAM459  LOC132617 5'  CTGCAGATCGAGGCATGGGA   76415         CCA  CTC
                                TCCCATGCC   GG   CTGCAG
                                |||||||||   ||   ||||||
                                AGGGTACGG   CT   GACGTC
                                      AG_  A__
GAM459  LOC145945 5'  AGGGCCTGGACCATAGAA    84563     CC   CC     T
                                TTC  ATG  CCAGGC CCT
                                |||  |||  |||||| |||
                                AAG  TAC  GGTCCG GGA
                                  A_   CA     _
GAM459  LOC146332 3'  CAGGAGCCTGGGGCCTGTGGA  78353     _  T
                                TCC CA GCCCCAGGCTCCTG
                                ||| || ||||||||||||||
                                AGG GT CGGGGTCCGAGGAC
                                  T  C
GAM459  LOC146714 5'  TGCAGGGCAGGCACAGGGA   84754      A_    CCAG  T
                                TCCC  TGCC    GC CCTGCA
                                ||||  ||||    || ||||||
                                AGGG  ACGG    CG GGACGT
                                  AC    A___  _
GAM459  LOC147958 3'  CTGCAGGGCAGGCAGCAGAA   88523     CCA    CCAG  T
                                TTC   TGCC    GC CCTGCAG
                                |||   ||||    || |||||||
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                                AAG   ACGG    CG GGACGTC
                                  ACG    A___  _
GAM459   LOC149501 3'  CTGCAAGAGCCTGGCTGGGAA  75800       T   CC     C
                                TTCCCA GCC  AGGCTC TGCAG
                                |||||| |||  ||||||| |||||
                                AAGGGT CGG  TCCGAG ACGTC
                                   _  __     A
GAM459   LOC150397 3'  CAGGAGCCTGAGTGAAGGA   80655     CA   CC
                                TCC  TGC  CAGGCTCCTG
                                |||  |||  ||||||||||
                                AGG  GTG  GTCCGAGGAC
                                  AA   A_
GAM459   LOC150397 3'  GCAGGAGCCTGCAGGAGA    80664    _  A   CCC
                                TC CC TGC   AGGCTCCTGC
                                || || |||   ||||||||||
                                AG GG ACG   TCCGAGGACG
                                 A  _  ___
GAM459   LOC150517 5'  CTGCAGGTAGGAGCACAGAA   80725     CCA   C  AGGCT
                                TTC   TGC CC    CCTGCAG
                                |||   ||| ||    |||||||
                                AAG   ACG GG    GGACGTC
                                  AC_   A  AT___
GAM459   LOC153688 3'  TGGGAGGCTGGGGCATGAGAA  87341     C        G
                                TTC CATGCCCCAG CTCCTG
                                ||| |||||||||| ||||||
                                AAG GTACGGGGTC GAGGGT
                                  A         G
GAM459   LOC154849 3'  CTGCAGGAGGTGGAAGATG   60941     GCC   GG
                                CAT   CCA  CTCCTGCAG
                                |||   |||  |||||||||
                                GTA   GGT  GAGGACGTC
                                  GAA   G_
GAM459   LOC162137 3'  GCAGGAGCTTCCCATAAAGAA  88480     CC_   CCCC
                                TTC   ATG    AGGCTCCTGC
                                |||   |||    ||||||||||
                                AAG   TAC    TTCGAGGACG
                                  AAA   CC__
GAM459   LOC219654 3'  CAGGAGCCCAGGGGATGGGAA  92925        G   CA
                                TTCCCAT CCC  GGCTCCTG
                                ||||||| |||  ||||||||
                                AAGGGTA GGG  CCGAGGAC
                                    G   AC
GAM459   LOC255042 3'  CTCGGGAGCCTGAGGCAGGAGA 97042     _  A    C        C
            A                    TTC CC TGCC CAGGCTCCTG AG
                                ||| || |||| |||||||||| ||
                                AAG GG ACGG GTCCGAGGGC TC
                                  A  _    A        _
GAM459   LOC257000 3'  CTGCAGGACTCAGAGCATGG   98587       CCCA  C
                                CCATGC    GG TCCTGCAG
                                ||||||    || ||||||||
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                                GGTACG    TC AGGACGTC
                                   AGAC  _
GAM459  LOC91750  3'  TGGGGGCCTGAGGCACGAGAA  67659     CCA    C
                                TTC   TGCC CAGGCTCCTG
                                |||   |||| ||||||||||
                                AAG   ACGG GTCCGGGGGT
                                  AGC    A
GAM460  BLAME     3'  TTGGACAAAGGATCAGCACAG  39660        CC     CACA
                                CTGTGCTG  CCTTT    TCAA
                                ||||||||  |||||    ||||
                                GACACGAC  GGAAA    GGTT
                                     TA     CA__
GAM460  CNR1      3'  TGATGCCTCCCTGGCAGCACAG 32724          CCTTTCA
                                CTGTGCTGCC      CATCA
                                ||||||||||      |||||
                                GACACGACGG      GTAGT
                                      TCCCTCC
GAM460  FMOD      3'  TGATGTGGGAGGAGACAGCCA  10675    T    CC_   TT
                                TG GCTG   CCT  CACATCA
                                || ||||   |||  |||||||
                                AC CGAC   GGA  GTGTAGT
                                 _   AGA   GG
GAM460  ITPR2     3'  TTTGATATGTCTGCATGCAGCA 11083         CCCTTT_  C
           CAG                    CTGTGCTGC      CA ATCAAA
                                |||||||||      || ||||||
                                GACACGACG      GT TAGTTT
                                     TACGTCT  A
GAM460  TBXA2R    5'  ATGTGAAGGTCAACACAG    8344       C  CCC
                                CTGTG TG   CTTTCACAT
                                ||||| ||   |||||||||
                                GACAC AC   GGAAGTGTA
                                   A  T__
GAM460  DKFZp434A171 3'  TGCTGTGAAAGGAGCAGTACA  51026         C        T
                                TGTGCTGC CCTTTCACA CA
                                |||||||| ||||||||| ||
                                ACATGACG GGAAAGTGT GT
                                     A        C
GAM460  ESDN      3'  TTGATCTTAGGAAACAGCACAG 56066         CC_   TTCAC
                                CTGTGCTG   CCT     ATCAA
                                |||||||   |||    |||||
                                GACACGAC   GGA     TAGTT
                                     AAA   TTC__
GAM460  FLJ11186  3'  TGATAGTGAGAGGACAACAG   37730      GC  CC       _
                                CTGT  TG  CCTTTCAC ATCA
                                ||||  ||  |||||||| ||||
                                GACA  AC  GGAGAGTG TAGT
                                  __ A_       A
GAM460  FLJ20986  5'  GTAAAGGAGGCAGCACAG    44840          _    C
                                CTGTGCTGCC CCTTT AC
                                |||||||||| ||||| ||
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                                GACACGACGG GGAAA TG
                                     A    _
GAM460  KIAA0125  3'  TGATGCTGAAAACAGCACAG  29579       CCCC    _
                                CTGTGCTG   TTTCA CATCA
                                ||||||||   ||||| |||||
                                GACACGAC   AAAGT GTAGT
                                    A___    C
GAM460  KIAA0186  3'  TTTGATGTGAAATTTGGGAACA 41131     GCTG  C__
          G                      CTGT   CCC  TTTCACATCAAA
                                 ||||   |||  ||||||||||||
                                 GACA   GGG  AAAGTGTAGTTT
                                   A___  TTT
GAM460  KIAA0923  3'  GTGTGAAAGAAACAGCAGAG  26708   G   CCC
                                CT TGCTG  CTTTCACAT
                                || |||||  |||||||||
                                GA ACGAC  GAAAGTGTG
                                 G    AAA
GAM460  KIAA1719  3'  TTTGAGGGTGAGGGACAGCACA 68743       C  TT   A_
          G                      CTGTGCTG CCC  TCAC  TCAAA
                                 |||||||| |||  ||||  |||||
                                 GACACGAC GGG  AGTG  AGTTT
                                    A  __   GG
GAM460  MGC14425  3'  TTTGATGTTCAGAGCACACAG  52952     C  CC  TTC
                                CTGTG TGC  CT   ACATCAAA
                                ||||| |||  ||   ||||||||
                                GACAC ACG  GA   TGTAGTTT
                                  _  A_  CT_
GAM460  MGC20235  3'  TTTGACAATGTGGAGCAGCACA 59565       CCCT    ___
                                TGTGCTGC   TTCACA  TCAAA
                                ||||||||   ||||||  |||||
                                ACACGACG   AGGTGT  AGTTT
                                    _____    AAC
GAM460  MGC22014  3'  TTGATGTGAAAGAAAGGGCG  65122     ___
                                TGCCC  CTTTCACATCAA
                                |||||  ||||||||||||
                                GCGGG  GAAAGTGTAGTT
                                   AAA
GAM460  MGC26651  3'  TTTGATGTGAAAGATGTTATA  58953    CT  CC
                                TGTG  GC  CTTTCACATCAAA
                                ||||  ||  ||||||||||||
                                ATAT  TG  GAAAGTGTAGTTT
                                  __  TA
GAM460  PIK3C2G   3'  TTTGTTGTCAAAGACAGCACAG 17095       CCC   C  T
                                CTGTGCTG  CTTT ACA CAAA
                                ||||||||  |||| ||| ||||
                                GACACGAC  GAAA TGT GTTT
                                    A__   C  T
GAM460  PP1628    5'  TGACTTCTGAATACAGCACAG  48082       CCCCT   CA__
                                CTGTGCTG   TTCA   TCA
                                ||||||||   ||||   |||
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                                GACACGAC    AAGT   AGT
                                    AT___   CTTC
GAM460  SCAMP5   3' TGATGTAGGAGGGGCACACAG 58065     C      TC
                                CTGTG TGCCCCTT  ACATCA
                                ||||| ||||||||  ||||||
                                GACAC ACGGGGAG  TGTAGT
                                  _      GA
GAM460  LOC144184 5' GTGAGAAGAGGCAGCACGG   77196        C  _
                                CTGTGCTGCC CT TTCAC
                                |||||||||| || |||||
                                GGCACGACGG GA GAGTG
                                     A  A
GAM460  LOC157653 5' TGTAACAAGGGACACACAG   82448     C  C    TC_
                                CTGTG TG CCCTT   ACA
                                ||||| || |||||   |||
                                GACAC AC GGGAA   TGT
                                  _ A    CAA
GAM460  LOC201910 3' TTGAAAGCAAGGGGCAACAG  90553     GC      TCACA
                                CTGT  TGCCCCTT    TCAA
                                ||||  ||||||||    ||||
                                GACA  ACGGGGAA    AGTT
                                  __      CGAA_
GAM460  LOC221576 3' TTGATGTGATAACGCACAG   95325      TGCCCCTT
                                CTGTGC      TCACATCAA
                                ||||||      |||||||||
                                GACACG      AGTGTAGTT
                                   CAAT____
GAM460  LOC221882 5' TGATACTAAGAGCAGCACGG  94101       CC   TCAC
                                CTGTGCTGC  CTT   ATCA
                                |||||||||  |||   ||||
                                GGCACGACG  GAA   TAGT
                                     A_   TCA_
GAM460  LOC222234 5' TTGACTTGAGGCGGCACAG   95903       CCTT   CA
                                CTGTGCTGCC   TCA  TCAA
                                ||||||||||   |||  ||||
                                GACACGGCGG   AGT  AGTT
                                     ____   TC
GAM460  LOC254266 5' TTGACCTTGAGGACAGCATAG 99204       CC   TCACA
                                CTGTGCTG  CCTT    TCAA
                                ||||||||  ||||    ||||
                                GATACGAC  GGAG    AGTT
                                     A_   TTCC_
GAM460  LOC256158 5' ATGTGGCAGGTAGCACAG    99479       CCTT
                                CTGTGCTGCC   TCACAT
                                ||||||||||   ||||||
                                GACACGATGG   GGTGTA
                                     AC__
GAM460  LOC257515 3' TTGATGTGATAACGCACAG   99625      TGCCCCTT
                                CTGTGC      TCACATCAA
                                ||||||      |||||||||
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                                GACACG      AGTGTAGTT
                                   CAAT____
GAM460  LOC257572 3'  TTGATGTGATAACGCACAG   99745      TGCCCCTT
                                CTGTGC      TCACATCAA
                                ||||||      |||||||||
                                GACACG      AGTGTAGTT
                                   CAAT____
GAM460  LOC56965  3'  ATGGGAAAAGGACAGCACAG  39923       C  C   A
                                CTGTGCTG CC TTTC CAT
                                |||||||| || |||| |||
                                GACACGAC GG AAAG GTA
                                    A  A   G
GAM461  AEGL1     3'  CAAAGGCACCCCCGCCTTCCCC 8528         GT_________  TCAAA
           ATA                    TATGGGGAAGG       GTC    G
                                ||||||||||        |||    |
                                ATACCCCTTCC       CGG    C
                                      GCCCCCA___  AAAC
GAM461  BLTR2     5'  GCCTTTCTTTTCCCTTCCCC  39520       TGTCTC
                                GGGGAAGGG     AAAGGC
                                |||||||||     ||||||
                                CCCCTTCCC     TTTCCG
                                    TTTTC_
GAM461  C1QG      3'  CCCCCACTGCACCCCCTCCCCA 63151       A_     CTCAAA
           TG                    TATGGGGA  GGGTGT     GG
                                ||||||||  ||||||     ||
                                GTACCCCT  CCCACG     CC
                                    CC     TCACCC
GAM461  DRPLA     3'  GCCCCTTGCCCCTTCCCCA   10426        T  CTCAAA
                                TGGGGAAGGG GT     GGC
                                |||||||||| ||     |||
                                ACCCCTTCCC CG     CCG
                                    _  TTCC__
GAM461  FGFR4     3'  GCCTCTGAACCCCCTTTCCCCA 43629       _   T  C   A
                                TGGGGAA GGG GT TCA AGGC
                                ||||||| ||| || ||| ||||
                                ACCCCTT CCC CA AGT TCCG
                                    T   C  _   C
GAM461  GLP1R     3'  CCTTTGAAATTCCCCCA     10794      AA   GTC
                                TGGGG  GGGT   TCAAAGG
                                |||||  ||||   |||||||
                                ACCCC  CTTA   AGTTTCC
                                   __    A__
GAM461  KCNJ4     3'  GCCAGGACACCCCCTCCCA   18358      AA      CAAA
                                TGGGG  GGGTGTCT    GGC
                                |||||  ||||||||    |||
                                ACCCT  CCCACAGG    CCG
                                   CC       A___
GAM461  MEF2D     3'  GCAAGAGGACACCCCCCCCCA  20984      AA      CAAAG
                                TGGGG  GGGTGTCT    GC
                                |||||  ||||||||    ||
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                                ACCCC  CCCACAGG    CG
                                  CC       AGAA_
GAM461  MLLT7    3'  GCCCCCAAAGCAGCCCTTCCCC 21041         _  CTCAAA
                                GGGGAAGGG TGT     GGC
                                ||||||||| |||     |||
                                CCCCTTCCC ACG     CCG
                                    G   AAACCC
GAM461  NPTX2    3'  GCCCCCAAGACACCTGCCCCA  94084      AA      CAAA
                                TGGGG  GGGTGTCT   GGC
                                |||||  ||||||||   |||
                                ACCCC  TCCACAGA   CCG
                                  G_       ACCC
GAM461  NUCB1    3'  GCCCCCAGCCCCTTCCCCA   21643         T  CTCAAA
                                TGGGGAAGGG GT     GGC
                                |||||||||| ||     |||
                                ACCCCTTCCC CG     CCG
                                    _  ACCC__
GAM461  REGL     3'  GCCCCTGTTCTGGCCCTTCCCC 22501          GTCT_  AA
            AT                    ATGGGGAAGGGT    CA  GGC
                                ||||||||||||    ||  |||
                                TACCCCTTCCCG    GT  CCG
                                    GTCTT  CC
GAM461  SLC22A12 3'  CCCCTGGCCCCTCCCCATG   58685       A   T   TCAAA
                                TATGGGGA GGG GTC    GG
                                |||||||| ||| |||    ||
                                GTACCCCT CCC CGG    CC
                                    _   _   TCC__
GAM461  CENTB5   3'  GCCTTCACGCACCCCTTCCCCA 48381         _  CTCA
                                TGGGGAAGGG TGT    AAGGC
                                |||||||||| |||    |||||
                                ACCCCTTCCC ACG    TTCCG
                                    C   CAC_
GAM461  CENTG1   3'  GCCCCCTGCCCCTTCCCCA   29355         T  CTCAAA
                                TGGGGAAGGG GT     GGC
                                |||||||||| ||     |||
                                ACCCCTTCCC CG     CCG
                                    _  TCCC__
GAM461  CIC      3'  GCCCTTGCCCCCTTCCCCA   31368         T TCT   A
                                TGGGGAAGGG G   CAA GGC
                                |||||||||| |   ||| |||
                                ACCCCTTCCC C   GTT CCG
                                    C ___   C
GAM461  DKFZP586F1524 3'  CCTCCAAGGCTGGCCTCCTCAT 32105        A  G _   CAA
            A                    TATGGGGA GG T GTCT   AGG
                                |||||||| || | ||||   |||
                                ATACTCCT CC G CGGA   TCC
                                    _ G T    ACC
GAM461  ETL      3'  GCCTTTGAAACTAGTCCCC   42464       AG   GTC
                                GGGGA  GGT   TCAAAGGC
                                |||||  |||   ||||||||
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                                CCCCT  TCA   AGTTTCCG
                                   GA   A__
GAM461   FLJ14800  3'  CCTGGCCCCCTCCCCGTA    52685        A   T   TCAA
                                TATGGGGA GGG GTC    AGG
                                |||||||| ||| |||    |||
                                ATGCCCCT CCC CGG    TCC
                                     C   _   ____
GAM461   FLJ20442  3'  GCCCTCACTCCCCTTCCCCATG 35629           TGTCTCAAA
                                TATGGGGAAGGG        GGC
                                ||||||||||||        |||
                                GTACCCCTTCCC        CCG
                                       CTCACTC__
GAM461   FLJ22477  3'  CCTCTGATCTCAGCTTCCCCA  45672        G G  TC_   A
                                TGGGGAA G TG   TCA AGG
                                ||||||| | ||   ||| |||
                                ACCCCTT C AC   AGT TCC
                                    _ G  TCT   C
GAM461   KIAA0057  3'  GCCTTTCTGGCCCCTTCCCTCA 25418    _       T   TC
                                TG GGGAAGGG GTC  AAAGGC
                                || |||||||| |||  ||||||
                                AC CCCTTCCC CGG  TTTCCG
                                 T       _   TC
GAM461   KIAA0552  5'  GCCTACCCACCCTCCCCCA    28992      A     TCTCAA
                                TGGGG AGGGTG     AGGC
                                ||||| ||||||     ||||
                                ACCCC TCCCAC     TCCG
                                   C     CCA___
GAM461   KIAA0633  3'  CCTTTGAGACTTTTACCACATA 95702      G  A    T
                                TATG GG AGGG GTCTCAAAGG
                                |||| || |||| ||||||||||
                                ATAC CC TTTT CAGAGTTTCC
                                  A  A   _
GAM461   KIAA0976  3'  GCCTCCACCACATTCCCCATA  30551         GG   TCTCAA
                                TATGGGGAA  GTG     AGGC
                                |||||||||  |||     ||||
                                ATACCCCTT  CAC     TCCG
                                     A_   CACC__
GAM461   KIAA1500  3'  CCTTTGGTTCCCTCCCCCA    64808      A    TGT T
                                TGGGG AGGG   C CAAAGG
                                ||||| ||||   | ||||||
                                ACCCC TCCC   G GTTTCC
                                   C    TT_ _
GAM461   KIAA1607  3'  CCCCCAGGGCCTCCTTCCCCA  64535         T    CAAA
                                TGGGGAAGGG GTCT    GG
                                |||||||||| ||||    ||
                                ACCCCTTCCT CGGG    CC
                                      C    ACCC
GAM461   MCF2L    3'  GCCCTTGTGTGACCCTCCCCAT 61530        A    GTCT   A
            A                    TATGGGGA GGGT    CAA GGC
                                ||||||| ||||    ||| |||
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                                ATACCCCT CCCA   GTT CCG
                                    _   GTGT   C
GAM461  MKRN2    3'  CCTTTGATCTTTTCTTCCCCA  72846        TGTC
                                TGGGGAAGGG   TCAAAGG
                                ||||||||||   |||||||
                                ACCCCTTCTT   AGTTTCC
                                     TTCT
GAM461  RASD2    3'  GCCTCTGTCCCCTTCCCCA   27463        TGTCT  A
                                TGGGGAAGGG    CA AGGC
                                ||||||||||    || ||||
                                ACCCCTTCCC    GT TCCG
                                     CT___  C
GAM461  RNF8     3'  GCCTCTCACCCTTTCCCCA   15569       _    TCTCAA
                                TGGGGAA GGGTG     AGGC
                                |||||||| |||||     ||||
                                ACCCCTT CCCAC     TCCG
                                   T    TC_____
GAM461  SOX7     3'  GCCTCTATCCCCTTCCCCA   49531        TG CTCAA
                                TGGGGAAGGG  T     AGGC
                                ||||||||||  |     ||||
                                ACCCCTTCCC  A     TCCG
                                     CT TC___
GAM461  SSH-3    3'  GCCTCTGCAGCCCTTCCC    35792        GTCT  A
                                GGGAAGGGT    CA AGGC
                                |||||||||    || ||||
                                CCCTTCCCG    GT TCCG
                                     AC__  C
GAM461  ZNF220   3'  CCTCTTGAAACCCTTCCCCA  23156         GTC   _
                                TGGGGAAGGGT   TCAA AGG
                                ||||||||||   |||| |||
                                ACCCCTTCCCA   AGTT TCC
                                      A__    C
GAM461  LOC116113 3'  GCCCTCCGCCCCCTCCCCATG  93839       A_    TCTCAAA
                                TATGGGGA  GGGTG      GGC
                                ||||||||  |||||      |||
                                GTACCCCT  CCCGC      CCG
                                    CC    CTC_____
GAM461  LOC121344 3'  CCCCTAATCCTTCCCCATG    74501          GTCTCAAA
                                TATGGGGAAGGGT       GG
                                ||||||||||||        ||
                                GTACCCCTTCCTA       CC
                                      ATCC_____
GAM461  LOC129303 3'  GCCTCCACAGCACCCCACCCCA 75374       AA     CTCAA
          TA                    TATGGGG  GGGTGT     AGGC
                                |||||||  ||||||     ||||
                                ATACCCC  CCCACG     TCCG
                                   AC     ACACC
GAM461  LOC145333 3'  GCCTCTAAGACATCTCCCTTCC 84299          ___     CAA
          CCATG                  TATGGGGAAGGG   TGTCT   AGGC
                                ||||||||||||   |||||   ||||
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                                GTACCCCTTCCC  ACAGA  TCCG
                                      TCT   ATC
GAM461  LOC149069 3'  GCCCTGTGCCACCCTTCCCC  79884        TCT  AA
                                GGGGAAGGGTG  CA  GGC
                                ||||||||||  ||  |||
                                CCCCTTCCCAC  GT  CCG
                                      CGT  C_
GAM461  LOC163087 3'  GCCCCTGTCACCTTCCTCATA  83312        GTGTCT  AA
                                TATGGGGAAGG    CA  GGC
                                ||||||||||    ||  |||
                                ATACTCCTTCC    GT  CCG
                                      ACT___  CC
GAM461  LOC166341 3'  GCCTCTGAGCCAGCCTCCCCA  83516      A  G  T   A
                                TGGGGA GG TG CTCA AGGC
                                |||||| || || |||| ||||
                                ACCCCT CC AC GAGT TCCG
                                   _  G  C   C
GAM461  LOC220032 3'  CCTCTAAGAGATCCCCATG   93331       AGGGTG   AA__
                                TATGGGGA    TCTC   AGG
                                ||||||||    ||||   |||
                                GTACCCCT    AGAG   TCC
                                     _______   AATC
GAM462  BMP1    3'  CACCACAGTTTCCTGGGGC   21527    A  TCGCT
                                GCC CA    GACTGTGGTG
                                ||| ||    ||||||||||
                                CGG GT    TTGACACCAC
                                  G  CCT__
GAM462  HPCAL1   3'  CACCACAGCCGCTTGCACGTA  10963     CCA  TC  T A
                                TACG   CA  GC G CTGTGGTG
                                ||||   ||  || | ||||||||
                                ATGC   GT  CG C GACACCAC
                                  AC_  T_  _ C
GAM462  NDST1    3'  CACCACAGCCAGACTGAACGT  9527     CCA  TCG   A
                                ACG   CA   CTG CTGTGGTG
                                |||   ||   ||| ||||||||
                                TGC   GT   GAC GACACCAC
                                  AA_  CA_   C
GAM462  SDC1    3'  CACCACAGCCAGCACCTGGC   12986     CATC   A
                                GCCA   GCTG CTGTGGTG
                                ||||   |||| ||||||||
                                CGGT   CGAC GACACCAC
                                  CCA_   C
GAM462  SMG1    3'  CACCACAGTCGGTGGTGATGC  31341    CA
                                GC  CATCGCTGACTGTGGTG
                                ||  ||||||||||||||||
                                CG  GTGGTGGCTGACACCAC
                                 TA
GAM462  C20orf126 3'  CACCACAGCCATCTGTGGGGC  48730     A   CGC  A
                                GCC CAT   TG CTGTGGTG
                                ||| |||   || ||||||||
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                                CGG GTG   AC GACACCAC
                                  G   TCT  C
GAM462  DKFZP434B0335 5'  CACCGTGGGAGCAATGTGGC   94059        C   GA TG
                                GCCACAT GCT  C  TGGTG
                                ||||||| |||  |  |||||
                                CGGTGTA CGA  G  GCCAC
                                    A   G_ GT
GAM462  FOXN4    3'  CACCACAGTGGCCGTGGCG   76087       ATC   G
                                CGCCAC   GCT ACTGTGGTG
                                ||||||   ||| |||||||||
                                GCGGTG   CGG TGACACCAC
                                   C__   _
GAM462  MGC22776  3'  ACCACCGACGATGTGGGTA   59272     G       C  ACT
                                TAC CCACATCG TG   GTGGT
                                ||| ||||||| ||   |||||
                                ATG GGTGTAGC GC   CACCA
                                  _       A  ___
GAM462  TRPV5    5'  CACCACAGCCACACACTGTGC  39521    C   TCGC_  A
                                GC ACA     TG CTGTGGTG
                                || |||     || ||||||||
                                CG TGT     AC GACACCAC
                                 _   CACAC  C
GAM462  LOC152315 5'  CACCACAGATCAGACATGGC   81409      CATCG    _
                                GCCA     CTGA CTGTGGTG
                                ||||     |||| ||||||||
                                CGGT     GACT GACACCAC
                                  ACA__    A
GAM462  LOC158055 3'  CACCACAGCCTTGGTCACAGCG 82577       CACATC  TG __
           TG                     TACGC     GC  A  CTGTGGTG
                                |||||     ||  |  ||||||||
                                GTGCG     TG  T  GACACCAC
                                   ACAC__  GT CC
GAM462  LOC162918 5'  CACCACAGTTTGCGTGGCG   88515       ATC  T
                                CGCCAC   GC GACTGTGGTG
                                ||||||   || ||||||||||
                                GCGGTG   CG TTGACACCAC
                                   ___  T
GAM462  LOC201229 3'  CACACAGGATGTGGC       89518        G   AC
                                GCCACATC CTG  TGTG
                                |||||||| |||  ||||
                                CGGTGTAG GAC  ACAC
                                     _   __
GAM462  LOC92080  5'  CACCACAGTCCCTGGGC     68620     A  TCGCT
                                GCC CA     GACTGTGGTG
                                ||| ||     ||||||||||
                                CGG GT     CTGACACCAC
                                  _  CC____
GAM463  APOB48R   3'  GCCTGCCCTGGTTCCTCCCCA  38587     AA         ACCT
                                TG  GAGGAATCAGG    GGC
                                ||  ||||||||||    |||
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                                AC  CTCCTTGGTCC   CCG
                                 CC        CGT_
GAM463  ARHGDIB  5' GAGCCAGGGTTTCCTCTTCA  8615        TCAGGA
                                TGAAGAGGAA    CCTGGCTC
                                ||||||||||    ||||||||
                                ACTTCTCCTT    GGACCGAG
                                   TG____
GAM463  BAP1     3' AGCCAGGTCTTCTCTCTTCA  17393       AATC
                                TGAAGAGG   AGGACCTGGCT
                                ||||||||   ||||||||||
                                ACTTCTCT   TTCTGGACCGA
                                    C___
GAM463  LIMK1    3' GAGCCAGGCCCTGACTTGCCTT 11335     AG  A    A
           C                     GAAG  GA TCAGG CCTGGCTC
                                ||||  || ||||| ||||||||
                                CTTC  TT AGTCC GGACCGAG
                                  CG  C    C
GAM463  LIMK1    3' GAGCCAGGCCCTGACTTGCCTT 11336     AG  A    A
           C                     GAAG  GA TCAGG CCTGGCTC
                                ||||  || ||||| ||||||||
                                CTTC  TT AGTCC GGACCGAG
                                  CG  C    C
GAM463  NRXN2    5' GAACCAGGTCTCCGTCCCTCTT 57820       A  CA      C
           C                     GAAGAGG AT  GGACCTGG TC
                                ||||||| ||  |||||||| ||
                                CTTCTCC TG  TCTGGACC AG
                                    C  CC       A
GAM463  RAD1     5' GAGCCGCCTCGCTCCTCTTCA  12644       ATC   ACC
                                TGAAGAGGA   AGG   TGGCTC
                                |||||||||   |||   ||||||
                                ACTTCTCCT   TCC   GCCGAG
                                     CGC   ___
GAM463  RAD1     5' GAGCCGCCTCGCTCCTCTTCA  12645       ATC   ACC
                                TGAAGAGGA   AGG   TGGCTC
                                |||||||||   |||   ||||||
                                ACTTCTCCT   TCC   GCCGAG
                                     CGC   ___
GAM463  RAD1     5' GAGCCGCCTCGCTCCTCTTCA  12646       ATC   ACC
                                TGAAGAGGA   AGG   TGGCTC
                                |||||||||   |||   ||||||
                                ACTTCTCCT   TCC   GCCGAG
                                     CGC   ___
GAM463  RASAL1   3' AGCCAGGGGGCCCTCTTCA   17402       AA  AGGA
                                TGAAGAGG  TC   CCTGGCT
                                ||||||||  ||   |||||||
                                ACTTCTCC  GG   GGACCGA
                                     CG  ____
GAM463  SERPINB4 3' CCAAATCATACTTTCTCTTCA 65878        TCAG  CC
                                TGAAGAGGAA   GA  TGG
                                ||||||||||   ||  |||
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                                ACTTCTCTTT   CT  ACC
                                     CATA  AA
GAM463  SLC2A5   3'  AGCCAAATTCATCCTCTT   13177       ATCA  CC
                                AAGAGGA   GGA  TGGCT
                                |||||||   |||  |||||
                                TTCTCCT   CTT  ACCGA
                                   A___   AA
GAM463  SLC30A3  3'  GAGCCAGGTCCATACCCCTTC  14399     A  AATCA
                                GAAG GG    GGACCTGGCTC
                                |||| ||    ||||||||||
                                CTTC CC    CCTGGACCGAG
                                  _ CATA_
GAM463  TFE3     3'  GAGCCAGGCCCCACCCCTTC  22538     A  AATCA  A
                                GAAG GG    GG CCTGGCTC
                                |||| ||    || ||||||||
                                CTTC CC    CC GGACCGAG
                                  _ CACC_ _
GAM463  BM039    5'  AGCCAGGTCCTAACGGAGCCT  38048    AA  ___
                                AGG  TC   AGGACCTGGCT
                                |||  ||   ||||||||||
                                TCC  GG   TCCTGGACCGA
                                 GA  CAA
GAM463  C14orf4  5'  AGCCCCAATTCTTCTTCA    67896        CA  ACCT
                                TGAAGAGGAAT  GG   GGCT
                                ||||||||||  ||   ||||
                                ACTTCTTCTTA  CC   CCGA
                                   A_  _____
GAM463  CNNM3    3'  GACCAGGTGGATCCTCTTTA  34807       A  AGG    C
                                TGAAGAGGA TC   ACCTGG TC
                                |||||||| ||   |||||| ||
                                ATTTCTCCT AG   TGGACC AG
                                     _ G__     A
GAM463  CSTF3    3'  GAACCACATTTTGTTCCCTCTT 9001       AAT    CC  C
           CA                    TGAAGAGG   CAGGA  TGG TC
                                |||||||   |||||  ||| ||
                                ACTTCTCC   GTTTT  ACC AG
                                    CTT    AC   A
GAM463  DNAJC6   3'  GAACCAGGTCCCACCTCCCCA  29494    AA   AATCA      C
                                TG  GAGG    GGACCTGG TC
                                ||  ||||    |||||||| ||
                                AC  CTCC    CCTGGACC AG
                                 CC   AC___       A
GAM463  FLJ10415 3'  AGGCCTGACTCCCTTTCA    36584      A  A    A
                                TGAAG GGA TCAGG CCT
                                ||||| ||| ||||| |||
                                ACTTT CCT AGTCC GGA
                                  C  C    _
GAM463  FLJ20069 3'  CCAAATGGAATTTCTCTTCA  34949          _ AGGACC
                                TGAAGAGGAAT C     TGG
                                |||||||||| |     |||
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                                ACTTCTCTTTA G     ACC
                                      A GTAA__
GAM463  FLJ21276  3'  GAGCAGTTCCAATTCCTCTCA  45259     A     CA  C  G
                                TGA GAGGAAT  GGA CTG CTC
                                ||| |||||||  ||| ||| |||
                                ACT CTCCTTA  CCT GAC GAG
                                  _      A_  T  _
GAM463  FLJ21736  5'  GAGCCAAGTCCCTTCCATTCCT 46783    A      CA___   C
          TTCCA                    TG AGAGGAAT    GGAC TGGCTC
                                || ||||||||    |||| ||||||
                                AC TTTCCTTA    CCTG ACCGAG
                                 C       CCTTC   A
GAM463  FSD1      3'  GAGCCAGGCACCCTCCTCTGTC 44540    _     ATCA  A_
          A                     TGA AGAGGA   GG  CCTGGCTC
                                ||| ||||||   ||  ||||||||
                                ACT TCTCCT   CC  GGACCGAG
                                  G     C___  AC
GAM463  GTF3C4    5'  GAGCCAGGTCTCCACCTCTGCA 25207    A    AATCA
                                TG AGAGG    GGACCTGGCTC
                                || |||||    ||||||||||
                                AC TCTCC    TCTGGACCGAG
                                 G    ACC__
GAM463  KIAA0453  3'  GAGCCAGGCCAGTGCTTCC   69606     T  __  A
                                GGAA CA  GG CCTGGCTC
                                |||| ||  || ||||||||
                                CCTT GT  CC GGACCGAG
                                  C  GA  _
GAM463  KIAA0710  3'  GAGCCAGATTCATTCCTTCTTC 30187      _    CA  C
          A                     TGAAGA GGAAT  GGA CTGGCTC
                                |||||| |||||  ||| |||||||
                                ACTTCT CCTTA  CTT GACCGAG
                                   T    __   A
GAM463  KIAA0939  3'  AGCCAGCCACCCCTCTTCA   62708       AATCA  AC
                                TGAAGAGG    GG  CTGGCT
                                ||||||||    ||  ||||||
                                ACTTCTCC    CC  GACCGA
                                     CCA__  __
GAM463  KIAA1025  3'  AGCCAGGTCTCTCCTCTCA   64672    A    ATCA
                                TGA GAGGA   GGACCTGGCT
                                ||| |||||   ||||||||||
                                ACT CTCCT   TCTGGACCGA
                                  _    C___
GAM463  KIAA1463  3'  AGCCACTTTGTGACTCCCTTCA 72734      A  A  G  CC
                                TGAAG GGA TCA GA  TGGCT
                                ||||| ||| ||| ||  |||||
                                ACTTC CCT AGT TT  ACCGA
                                   _  C  G  TC
GAM463  KIAA1524  5'  AGGATCCTGATTCCTCTTCA  73836             _
                                TGAAGAGGAATCAGGA CCT
                                |||||||||||||||| |||
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                                ACTTCTCCTTAGTCCT GGA
                                        A
GAM463  LBP-9    3'  CAGGCTCCTGATTCCTCTTC  28044          _
                                GAAGAGGAATCAGGA CCTG
                                ||||||||||||||| ||||
                                CTTCTCCTTAGTCCT GGAC
                                        C
GAM463  MAPK8IP3 3'  AGCCAGGCCACTCCTTCA   54135   A    ATCA  A
                                A GAGGA   GG CCTGGCT
                                | |||||   || |||||||
                                A TTCCT   CC GGACCGA
                                 C    CA__ _
GAM463  MGC2628  3'  AGCCAGGTGTCCTCTTGCA   44194   _     ATCAGG
                                TG AAGAGGA     ACCTGGCT
                                || |||||||     ||||||||
                                AC TTCTCCT     TGGACCGA
                                  G      G_____
GAM463  p25      3'  GAGCCAGGAGAGCACCCTTC  23834     A  AA_  AGGA
                                GAAG GG   TC    CCTGGCTC
                                |||| ||   ||   ||||||||
                                CTTC CC   AG    GGACCGAG
                                  _ ACG  A___
GAM463  SMARCF1  3'  GAGCCAGGCCAGCCTCCTC   21189      ATCA  A
                                GAGGA   GG CCTGGCTC
                                |||||   || ||||||||
                                CTCCT   CC GGACCGAG
                                   CCGA  _
GAM463  TRIP-Br2 3'  AGCCAGGCCCCCAGGTCTTCTC 29259    A    ATCA_  A
           A                     TGA GAGGA    GG CCTGGCT
                                ||| |||||    || |||||||
                                ACT CTTCT    CC GGACCGA
                                  _    GGACC  C
GAM463  USP2     3'  AGCCAAGAGCCCTCTTCA    16107        AA  AGGACC
                                TGAAGAGG  TC     TGGCT
                                ||||||||  ||     |||||
                                ACTTCTCC  AG     ACCGA
                                     CG  A_____
GAM463  LOC147343 5'  AGCCATAACTCTTCTTCA   85123         ATCA GACC
                                TGAAGAGGA   G   TGGCT
                                |||||||||   |   |||||
                                ACTTCTTCT   C   ACCGA
                                     _____ AAT_
GAM463  LOC150333 5'  AGCCAGAGATTCCTCCTC   86211    A      AGGAC
                                GA GAGGAATC    CTGGCT
                                || ||||||||    ||||||
                                CT CTCCTTAG    GACCGA
                                 C       A_____
GAM463  LOC196527 3'  GAGCCAGGCCCTCTCACCCCT  89099    A  AATC   A
                                AG GG   AGG CCTGGCTC
                                || ||   ||| ||||||||
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                                TC CC    TCC GGACCGAG
                                 C  ACTC   C
GAM463   LOC220567 3'  GCCTGCCCTGGTTCCTCCCCA  92436    AA         ACCT
                                TG  GAGGAATCAGG    GGC
                                ||  ||||||||||    |||
                                AC  CTCCTTGGTCC    CCG
                                 CC          CGT_
GAM463   LOC253776 3'  AGCCAGGCCCTTTCCTCT    99292        TC   A
                                AGAGGAA  AGG CCTGGCT
                                |||||||  ||| |||||||
                                TCTCCTT  TCC GGACCGA
                                     __   C
GAM463   LOC253816 3'  GAGCCAGACCATTTCTTCCCCA 96041    AA     TCA  AC
                                TG  GAGGAA   GG  CTGGCTC
                                ||  ||||||   ||  |||||||
                                AC  CTTCTT   CC  GACCGAG
                                 CC     TA_  A_
GAM463   LOC254122 3'  AGCCAAGACTCCTCTTCA    96393          A  AGGACC
                                TGAAGAGGA TC      TGGCT
                                |||||||||  ||      |||||
                                ACTTCTCCT AG      ACCGA
                                     C  A_____
GAM463   LOC255299 5'  GAACCATGTACTGACGTCCTCT 99336          A_   G  C   C
            TCA                    TGAAGAGGA  TCAG AC TGG TC
                                |||||||||  ||||  ||  |||  ||
                                ACTTCTCCT  AGTC TG ACC AG
                                     GC    A  T   A
GAM463   LOC256283 5'  GAGCCAGGTCCTCCTCCTCCTC 98823    A    ATC
                                GA GAGGA   AGGACCTGGCTC
                                ||  |||||   ||||||||||||
                                CT CTCCT   TCCTGGACCGAG
                                 C    CC_
GAM463   LOC51125  3'  GAGTGTCCCTACCTCCTCTCCA 32742    A     ATCA_   CTG
                                TG AGAGGA    GGAC   GCTC
                                ||  ||||||    ||||   ||||
                                AC  TCTCCT    CCTG   TGAG
                                 C     CCATC   ____
GAM463   LOC51149  5'  AGCCAGGCCCCCGCTTCA    32971       A  AATCA  A
                                TGAAG GG     GG CCTGGCT
                                |||||  ||     ||  |||||||
                                ACTTC CC     CC GGACCGA
                                   G  _____  C
GAM463   LOC51161  3'  GAGCCAGGTCCTAGCTGTTCTC 33041       ATC__
                                GAGGA    AGGACCTGGCTC
                                |||||    ||||||||||||
                                CTCTT    TCCTGGACCGAG
                                   GTCGA
GAM463   LOC91663  3'  AGGCTCCCGTTCCCTCTCCA   57221    A    _   CA   _
                                TG AGAGG AAT  GGA CCT
                                ||  ||||| |||  ||| |||
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                                AC TCTCC TTG  CCT GGA
                                 C    C  C_  C
GAM463  LOC92249  3'  AGCCTCTATCTCCTCTTCA   69104        ATCA  CCT
                                TGAAGAGGA   GGA  GGCT
                                |||||||||   |||  ||||
                                ACTTCTCCT   TCT  CCGA
                                     CTA_  ___
GAM464  GJB1      3'  ACCTCCCATCCCACCCCCGA  60636     TTCAG       A
                                TTGG    GGGATGGGA GT
                                ||||    ||||||||| ||
                                AGCC    CCCTACCCT CA
                                  CCCA_       C
GAM464  KCNJ15    5'  ACTTCCCATCCAGCCAG     11158      CAGG
                                TTGGTT   GGATGGGAAGT
                                ||||||   ||||||||||
                                GACCGA   CCTACCCTTCA

                                    ____
GAM464  PER2      3'  GTGACTTCCCTTTGCAAACCAG 43359      CAGGGGAT
                                TTGGTT      GGGAAGTCAC
                                ||||||      ||||||||||
                                GACCAA      CCCTTCAGTG
                                   ACGTTT__
GAM464  HSA250839 3'  GTGACCCCCATTCCCCAAAGCA 37852    G  CA       AA
          A                      TTG TT  GGGGATGGG  GTCAC
                                ||| ||  |||||||||  |||||
                                AAC AA  CCCTTACCC  CAGTG
                                  G  AC       C_
GAM464  MGC19556  5'  GTGACTTCATGTCTCAAACCAA 54342      CAG    GG
                                TTGGTT   GGGAT  GAAGTCAC
                                ||||||   |||||  ||||||||
                                AACCAA   CTCTG  CTTCAGTG
                                   A__     TA
GAM464  MGC32104  3'  ACCCCCCAAGATTGAACCAA   59061        GGGA   AA
                                TTGGTTCAG    TGGG  GT
                                |||||||||    ||||  ||
                                AACCAAGTT    ACCC  CA
                                     AGA_    CC
GAM465  ANPEP     3'  GCTCCAGGGCCAGATGAGC    8565         _ AGGGG
                                GCTCATTTG C     GGAGC
                                ||||||||| |     |||||
                                CGAGTAGAC G     CCTCG
                                     C GGA__
GAM465  CLU       3'  GCTCCCCCCAAGATGAGC     10213        GCA
                                GCTCATTT   GGGGGGAGC
                                ||||||||   |||||||||
                                CGAGTAGA   CCCCCCTCG
                                     A__
GAM465  F13A1     3'  CTCAGCCTTGCAAATAGC     92710     C        GG
                                GCT ATTTGCAGGG  GAG
                                ||| ||||||||||  |||
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                                CGA TAAACGTTCC  CTC
                                  _       GA
GAM465  HRH2     3'  GCTCCCTTTTAAAAGGAGC   42510     A  GC
                                GCTC TTT  AGGGGGGAGC
                                |||| |||  ||||||||||
                                CGAG AAA  TTTTCCCTCG
                                  G  A_
GAM465  IFNGR2   3'  CTTGACTTTGGCAAATGAGC  19848        _   GG
                                GCTCATTTGC AGGG  GAG
                                |||||||||| ||||  |||
                                CGAGTAAACG TTTC  TTC
                                      G   AG
GAM465  PAK4     3'  TCCAGCCCCTGCAGCAAATGA  20829     ___      __
                                TCATT   TGCAGGGG  GGA
                                |||||   ||||||||  |||
                                AGTAA   ACGTCCCC  CCT
                                   ACG       GA
GAM465  PIM2     3'  CCCAATCCTACAAAGGAGC   60651     A   C   __
                                GCTC TTTG AGGG  GGG
                                |||| |||| ||||  |||
                                CGAG AAAC TCCT  CCC
                                  G   A   AA
GAM465  PKHD1    5'  TTTGGCTGGGACACAAACGAGT 57721     A   CAGGGGGG
                                GCTC TTTG       AGCCAAA
                                |||| ||||       |||||||
                                TGAG AAAC       TCGGTTT
                                  C   ACAGGG__
GAM465  PLAT     3'  CTCCTCAAAAGCAAATGAG   53395        AGG_
                                CTCATTTGC   GGGGAG
                                |||||||||   ||||||
                                GAGTAAACG   CTCCTC
                                      AAAA
GAM465  RAI2     3'  TTTGACTTTTCACAAATGAGT  41717        CAGG GG  C
                                GCTCATTTG   G  GAG CAAA
                                |||||||||   |  ||| ||||
                                TGAGTAAAC   C  TTC GTTT
                                      A___ TT  A
GAM465  TGFB3    3'  GGCTCCGGGCAAATGGC     13719    T     AGGGG
                                GC CATTTGC    GGAGCC
                                || |||||||    ||||||
                                CG GTAAACG    CCTCGG
                                 _     GG___
GAM465  BTN2A2   3'  TCCAGCCTACAGATGAGC    23771        C  GG
                                GCTCATTTG AGG  GGA
                                ||||||||| |||  |||
                                CGAGTAGAC TCC  CCT
                                      A  GA
GAM465  C20orf72 5'  TTCGACCGTTGCAAATAG    54609    C      G  G_
                                CT ATTTGCAG GG  GAG
                                || |||||||| ||  |||
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                                GA TAAACGTT CC  CTT
                                 _      G  AG
GAM465  C6orf37   3' CTAACTCTTGACAAATGAGT   68092        _     GG
                                GCTCATTTG CAGGGG  AG
                                ||||||||| ||||||  ||
                                TGAGTAAAC GTTCTC  TC
                                     A     AA
GAM465  DOC2A     3' GCTAGTCCCTGCAAATATGC   14563    TC        GG
                                GC  ATTTGCAGGGG  AGC
                                ||  ||||||||||  |||
                                CG  TAAACGTCCCT  TCG
                                 TA         GA
GAM465  FADS1     3' GCTCCATAAGCAAGTGAGC    26382         AGGGG
                                GCTCATTTGC    GGAGC
                                |||||||||     |||||
                                CGAGTGAACG    CCTCG
                                     AATA_
GAM465  FLJ20413  3' CTCAATCCCTGCAAATGA    35595          G_
                                TCATTTGCAGGGG  GAG
                                ||||||||||||  |||
                                AGTAAACGTCCCT  CTC
                                      AA
GAM465  HTATIP2   3' CTTATGACCGTGCAAATGAGC  22167         G  GG__
                                GCTCATTTGCA GG    GAG
                                |||||||||| ||    |||
                                CGAGTAAACGT CC    TTC
                                     G  AGTA
GAM465  KIAA1423  3' CCCAACCCACTAAATGAGC    62392        CA  __
                                GCTCATTTG  GGG  GGG
                                |||||||||  |||  |||
                                CGAGTAAAT  CCC  CCC
                                     CA   AA
GAM465  MFN1      3' TTCAACTTGAAAATGAGC     54322        G   GG
                                GCTCATTT CAGG  GGA
                                |||||||| ||||  |||
                                CGAGTAAA GTTC  CTT
                                     A    AA
GAM465  MGC15619  3' GCCTTAATTGAAAATGAGC    51402        G  GG  A
                                GCTCATTT CAG  GGG GC
                                |||||||| |||  ||| ||
                                CGAGTAAA GTT  TTC CG
                                     A   AA  _
GAM465  MGEA6     5' GCTCCCCCCGCAGCCGGC     21013     CAT   A
                                GCT   TTGC GGGGGGAGC
                                |||   |||| |||||||||
                                CGG   GACG CCCCCCTCG
                                  CC_   _
GAM465  NMT1      3' GCTCCCCTTCTGAATCAGC    41147     C  TG   _
                                GCT ATT  CAGG GGGGAGC
                                ||| |||  |||| |||||||
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                                CGA TAA  GTCT CCCCTCG
                                  C  __   T
GAM465  P114-RHO-GEF 3'  CTCAGCCCCCGGGAAATGAGC  31669       GCA   __
                                GCTCATTT  GGGGG  GAG
                                ||||||||  |||||  |||
                                CGAGTAAA  CCCCC  CTC
                                    GGG   GA
GAM465  TRPV5    5'  CTCAGCTCTGCAAAGAGC   39522     A      GG
                                GCTC TTTGCAGGG  GAG
                                |||| |||||||||  |||
                                CGAG AAACGTCTC  CTC
                                  _       GA
GAM465  LOC126961 3'  GGCTCCCCCCCGCGCGTGA   75121     T  A
                                TCAT TGC GGGGGGGAGCC
                                |||| ||| ||||||||||
                                AGTG GCG CCCCCCTCGG
                                  C  _
GAM465  LOC143915 3'  CTCCCCTCGGGCAACAAGC   83906    CAT   A_
                                GCT  TTGC  GGGGGGAG
                                |||  ||||  ||||||||
                                CGA  AACG  CTCCCCTC
                                  AC_   GG
GAM465  LOC145623 5'  TTGGCAGCTCCAGCAAATGAGC 84398        AG   GA
                                GCTCATTTGC  GGGG  GCCAA
                                ||||||||||  ||||  |||||
                                CGAGTAAACG  CCTC  CGGTT
                                     A_   GA
GAM465  LOC146268 3'  CCCGGGAATCTGCAAATGAGC  78335          _____
                                GCTCATTTGCAGG    GGG
                                ||||||||||||    |||
                                CGAGTAAACGTCT    CCC
                                       AAGGG
GAM465  LOC148887 3'  GGCTCCCCCGCATGCGC    85405    T  TT   AG
                                GC CA  TGC  GGGGGAGCC
                                || ||  |||  |||||||||
                                CG GT  ACG  CCCCCTCGG
                                 C  __  __
GAM465  LOC207043 3'  GCTCCCCCCCGGGTATCAGC   91078    CATT   A_
                                GCT   TGC  GGGGGGAGC
                                |||   |||  |||||||||
                                CGA   ATG  CCCCCCTCG
                                  CT__   GG
GAM465  LOC253786 5'  TTAACTTTTGCAAATGAGC   98836           GG
                                GCTCATTTGCAGGGG  AG
                                ||||||||||||||  ||
                                CGAGTAAACGTTTTC  TT
                                       AA
GAM465  LOC253974 3'  TTTGGCTCCCCCCCTGCAAATGA 99286
           GC                   GCTCATTTGCAGGGGGGAGCCAAA
                                |||||||||||||||||||||||||
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                                CGAGTAAACGTCCCCCCTCGGTTT

GAM465  LOC256905 3'  TCCATGTCCCTGCAAATGA   98663          ___
                                TCATTTGCAGGGG  GGA
                                |||||||||||||  |||
                                AGTAAACGTCCCT  CCT
                                     GTA
GAM465  LOC257395 3'  GGCTCCCCCCGCGCGTGA    97149     T  A
                                TCAT TGC GGGGGGAGCC
                                |||| ||| ||||||||||
                                AGTG GCG CCCCCCTCGG
                                  C  _
GAM465  LOC90233  3'  CCCAGGTCCTGCAAAGGAGC  57193     A      ___
                                GCTC TTTGCAGGG  GGG
                                |||| |||||||||  |||
                                CGAG AAACGTCCT  CCC
                                  G       GGA
GAM466  SACM1L    3'  GCTCAGTTTCATTATTGT    26695        __
                                ACAATGAT  AACTGAGC
                                ||||||||  ||||||||
                                TGTTATTA  TTGACTCG
                                    CT
GAM466  FLJ22104  3'  CGCTCAGTTTATATGCCATTGT 43625      AT_____     ___
                                ACAATG      AACTGAGC  G
                                ||||||      ||||||||  |
                                TGTTAC      TTGACTCG  C
                                   CGTATAT      ___
GAM466  KIAA0806  3'  GCCCAGGGATGTCATTGTA   29721        A__  A
                                TACAATGATA  CTG GC
                                ||||||||||  ||| ||
                                ATGTTACTGT  GAC CG
                                      AGG  C
GAM466  MGC30052  3'  GCTCAGTTGTTTATTGTA    59206       _
                                TACAATGA TAACTGAGC
                                |||||||| |||||||||
                                ATGTTATT GTTGACTCG
                                     T
GAM466  STAM2     3'  GCTCAGTTTATGTCATTGT   20704        ___
                                ACAATGATA  ACTGAGC
                                |||||||||  |||||||
                                TGTTACTGT  TGACTCG
                                      ATT
GAM466  TOR1B     3'  GCCAGTGTGAATCATTGTA   27975        A___  A
                                TACAATGAT   ACTG GC
                                |||||||||   |||| ||
                                ATGTTACTA   TGAC CG
                                      AGTG  _
GAM466  LOC158428 3'  GCTCAGCCCTTCTCGTTGTA  71083        T ___
                                TACAATGA AA  CTGAGC
                                |||||||| ||  ||||||
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                                ATGTTGCT TT   GACTCG
                                    C  CCC
GAM466  LOC257282 5'  GCCCAGTTCAAATCATTGT   98135        ___    A
                                ACAATGAT   AACTG GC
                                ||||||||   ||||| ||
                                TGTTACTA   TTGAC CG
                                    AAC    C
GAM467  BGN     3'  TGCATTTCCAGCCTTTCA    9927       A      CAGTG
                                TGAAA GTTGGAAA    GCA
                                ||||| ||||||||    |||
                                ACTTT CGACCTTT    CGT
                                  C       A____
GAM467  CACNA2D2  3'  TGCCACTGCCTGCACCTTTC   21226     A__  T  AAA
                                GAAA   GT GG   CAGTGGCA
                                ||||   || ||   ||||||||
                                CTTT   CG CC   GTCACCGT
                                  CCA  T  ___
GAM467  CAV2    3'  CCACTGTTCTGTTCATTTC   8783      AGT_    A
                                GAAA    TGGAA CAGTGG
                                ||||    ||||| ||||||
                                CTTT    GTCTT GTCACC
                                  ACTT    _
GAM467  CELSR3   3'  GTGCCACTGCCTCCTATGTTTA 9191      AAGTT   AA
                                TGAA    GGA  CAGTGGCAC
                                ||||    |||  |||||||||
                                ATTT    CCT  GTCACCGTG
                                  GTAT_  CC
GAM467  DAPK1    3'  GCTGGAATTCCTAACTTTTCA  18226        _   A__
                                TGAAAAGTT GGAA   CAGT
                                |||||||| ||||   ||||
                                ACTTTTCAA CCTT   GTCG
                                     T   AAG
GAM467  FMR2    5'  GTGCCACTGCCGCCGCTT    10698     T  AAA
                                AAGT GG   CAGTGGCAC
                                |||| ||   |||||||||
                                TTCG CC   GTCACCGTG
                                  _ GCC
GAM467  GDF5    3'  GTGCCACTGCCTCCTCAAATCA 6898     AAAGTT   AA
                                TGA     GGA  CAGTGGCAC
                                |||     |||  |||||||||
                                ACT     CCT  GTCACCGTG
                                  AAACT_   CC
GAM467  GSPT1    3'  TGCCACTGTTGAATTTTTC   10885       GGA
                                GAAAAGTT   AACAGTGGCA
                                ||||||||   ||||||||||
                                CTTTTTAA   TTGTCACCGT
                                    G__
GAM467  LZTS1    3'  GCCACCGTGCCTGGCTAACTTT 41032          AA____  A
            TCA                   TGAAAAGTTGG     AC GTGGC
                                ||||||||||     || |||||
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                                ACTTTTCAATC     TG CACCG
                                      GGTCCG  C
GAM467  MYH11   3'  GCAAACCTTTCCAACTTCTCA  11741    A       CAGTG
                                TGA AAGTTGGAAA    GC
                                ||| ||||||||||    ||
                                ACT TTCAACCTTT    CG
                                  C        CCAAA
GAM467  MYH11   3'  GCAAACCTTTCCAACTTCTCA  11742    A       CAGTG
                                TGA AAGTTGGAAA    GC
                                ||| ||||||||||    ||
                                ACT TTCAACCTTT    CG
                                  C        CCAAA
GAM467  MYH11   3'  GCAAACCTTTCCAACTTCTCA  11743    A       CAGTG
                                TGA AAGTTGGAAA    GC
                                ||| ||||||||||    ||
                                ACT TTCAACCTTT    CG
                                  C        CCAAA
GAM467  PIGN    3'  GTGCCACCGTCAATATTTATCA 25604    A   TG_  AACA
                                TGA AAGT   GA   GTGGCAC
                                ||| ||||   ||   |||||||
                                ACT TTTA   CT   CACCGTG
                                  A   TAA  GC__
GAM467  PIK3CD  3'  TGCTTGCTCTCCACTTTTCA  18504       T   AAC   _
                                TGAAAAGT GGA   AGTG GCA
                                |||||||| |||   |||| |||
                                ACTTTTCA CCT   TCGT CGT
                                     _   C__    T
GAM467  SALL2   3'  GTGCCAAGACCTCTCCAGCTTC 64593    A      AACAG__
          TCA                   TGA AAGTTGGA      TGGCAC
                                ||| ||||||||      ||||||
                                ACT TTCGACCT      ACCGTG
                                  C       CTCCAGA
GAM467  SLC26A3 3'  GCCACTGTTTTGAATCTCA   5472     AAA   G
                                TGA   GTT GAAACAGTGGC
                                |||   ||| ||||||||||
                                ACT   TAA TTTTGTCACCG
                                  C__   G
GAM467  SMARCAL1 5' TGCTTTTGCCAACTTTCCA   27085    A      AAA   T
                                TG AAAGTTGG   CAG GGCA
                                || ||||||||   ||| ||||
                                AC TTTCAACC   GTT TCGT
                                  C       ___   T
GAM467  SRRM2   3'  CCCCTCCCCCCAACTTTTCA  33385         AAAC  T
                                TGAAAAGTTGG    AG GG
                                ||||||||||    || ||
                                ACTTTTCAACC    TC CC
                                      CCCC  C
GAM467  VSNL1   3'  GCAACTTTCCAACTTTTCA   14081          AC   G
                                TGAAAAGTTGGAA  AGT GC
                                ||||||||||||  ||| ||
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                                ACTTTTCAACCTT  TCA CG
                                       __  A
GAM467  AAK1     3'  TGCCACTGCCCTCCAGCTT   30528        AA_
                                AAGTTGGA   CAGTGGCA
                                ||||||||   ||||||||
                                TTCGACCT   GTCACCGT
                                    CCC
GAM467  AP1GBP1  3'  CTGGATTTCCAACTTTTC    24348           __
                                GAAAAGTTGGAAA  CAG
                                ||||||||||||  |||
                                CTTTTCAACCTTT  GTC
                                       AG
GAM467  ARHGEF9  3'  CCTCTTTTTCCAACTTCTCA   31483     A        C  T
                                TGA AAGTTGGAAA AG GG
                                ||| ||||||||| || ||
                                ACT TTCAACCTTT TC CC
                                  C         T  T
GAM467  BICD2    3'  TGCCACTGCAATTCTTTTCA   70916       TTGGAAA
                                TGAAAAG      CAGTGGCA
                                |||||||      ||||||||
                                ACTTTTC      GTCACCGT
                                    TTAAC__
GAM467  C1QTNF2  3'  GCTATTTCCAACTTCTCA    49976     A       ACA
                                TGA AAGTTGGAA   GTGGC
                                ||| |||||||||   |||||
                                ACT TTCAACCTT   TATCG
                                  C       ___
GAM467  C5orf4   3'  TGCCTTTTCCAACTTTCA    51499      A      CAGT
                                TGAAA GTTGGAAA   GGCA
                                ||||| ||||||||   ||||
                                ACTTT CAACCTTT   CCGT
                                   _       T___
GAM467  C5orf4   3'  TGCCTTTTCCAACTTTCA    51500      A      CAGT
                                TGAAA GTTGGAAA   GGCA
                                ||||| ||||||||   ||||
                                ACTTT CAACCTTT   CCGT
                                   _       T___
GAM467  CHERP    3'  GCAAAATCTTCCAACTTTTCA  22131          ACAGTG
                                TGAAAAGTTGGAA     GC
                                ||||||||||||      ||
                                ACTTTTCAACCTT     CG
                                       CTAAAA
GAM467  FLJ12443 3'  TGCCACTGTGCATTTTCA    46147       GTTGGAA
                                TGAAAA      ACAGTGGCA
                                ||||||      |||||||||
                                ACTTTT      TGTCACCGT
                                   ACG_____
GAM467  FLJ20033 3'  TATTTTTCCAAGTTTTCA    34824       G      C
                                TGAAAA TTGGAAA AGTG
                                |||||| ||||||| ||||
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                                ACTTTT AACCTTT TTAT
                                   G     _
GAM467  FLJ20300  3' GTGCCACTGTCAGCTTTTC   35379        GAA
                                GAAAAGTTG  ACAGTGGCAC
                                |||||||||  ||||||||||
                                CTTTTCGAC  TGTCACCGTG
                                    ___
GAM467  KIAA0182  3' GCCTGTCCCCAACTTTTC    72501        AA  GT
                                GAAAAGTTGG ACA GGC
                                |||||||||| ||| |||
                                CTTTTCAACC TGT CCG
                                     CC  __
GAM467  KIAA0441  3' CAAAGTTTTTACCAACTTTTCA 29625         ___  AG
                                TGAAAAGTTGG  AAAC TG
                                |||||||||||  |||| ||
                                ACTTTTCAACC  TTTG AC
                                     ATT   AA
GAM467  KIAA0984  3' GTGAAGTTTTCCCAATTTTTCA 66142         __  AGTGG
                                TGAAAAGTTGG AAAC   CAC
                                |||||||||||  ||||   |||
                                ACTTTTTAACC TTTG   GTG
                                     CT   AA___
GAM467  KIAA1102  3' GTCACTTCCAAGTTTCCA   69585   A  G   AAC
                                TG AAA TTGGA  AGTGGC
                                || ||| |||||  ||||||
                                AC TTT AACCT  TCACTG
                                 C  G   ___
GAM467  KIAA1576  3' CACCTTGTTCAACTTTTCA   66490        AACA
                                TGAAAAGTTGGA   GTG
                                ||||||||||||   |||
                                ACTTTTCAACTT   CAC
                                     GTTC
GAM467  KIAA1729  5' GTGCAGCTCCTCCCAATTTTCA 90593      G   AAAC  G
                                TGAAAA TTGG   AGT GCAC
                                |||||| ||||   ||| ||||
                                ACTTTT AACC   TCG CGTG
                                   _  CTCC  A
GAM467  KIAA1789  5' GCAGTTTTTTTCCAACTTTT  67702        C  TG_
                                AAAAGTTGGAAA AG  GC
                                |||||||||||| ||  ||
                                TTTTCAACCTTT TT  CG
                                     T  TGA
GAM467  KIAA1813  3' GTGCCACTGCCAACCCTGTTCA 70831    AA__   AAA
                                TGAA   GTTGG  CAGTGGCAC
                                ||||   |||||  |||||||||
                                ACTT   CAACC  GTCACCGTG
                                  GTCC   ___
GAM467  LRP15     3' TGCCACTGCTGAACTTTT   54756       _ AAA
                                AAAAGTT GG  CAGTGGCA
                                |||||||  ||  ||||||||
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                                TTTTCAA TC   GTCACCGT
                                    G ___
GAM467  MGC3048   3'  GTACATTTGCTCCAAACTTTTC 44130         _  AAC   _
            A                    TGAAAAGTT GGA   AGTG GC
                                 ||||||||| |||   |||| ||
                                 ACTTTTCAA CCT   TTAC TG
                                      A   CGT    A
GAM467  nexilin   3'  GTGCCACTATGCTGACTTCTTA 58625     A    TG AAAC
                                 TGA AAGT  G    AGTGGCAC
                                 ||| |||| |    ||||||||
                                 ATT TTCA  C    TCACCGTG
                                   C    GT GTA_
GAM467  PRRG1     3'  CCACTTCCAAACTTTTCA     8148          _  AAC
                                 TGAAAAGTT GGA   AGTGG
                                 ||||||||| |||   |||||
                                 ACTTTTCAA CCT   TCACC
                                      A  ___
GAM467  QKI       3'  TGCCACTGCTTTGTCTTT     66051      TTG   A
                                 AAAG   GAA CAGTGGCA
                                 ||||   ||| ||||||||
                                 TTTC   TTT GTCACCGT
                                   TG_   C
GAM467  RHOBTB3   3'  CACAGTTTTTCCGACTTTTCA  30419           __  A
                                 TGAAAAGTTGGAA  AC GTG
                                 ||||||||||||  || |||
                                 ACTTTTCAGCCTT  TG CAC
                                        TT  A
GAM467  TLN1      3'  GTGCCACTACCAAAGCCTTC   21905     AAG_   AAAC
                                 GAA    TTGG    AGTGGCAC
                                 |||    ||||    ||||||||
                                 CTT    AACC    TCACCGTG
                                   CCGA    A___
GAM467  ZNF340    3'  ACTGCTTCCAACTTTGCA     85709     A         A
                                 TG AAAGTTGGAA CAGT
                                 || ||||||||| ||||
                                 AC TTTCAACCTT GTCA
                                  G         C
GAM467  LOC128553 3'  TGCCTTAGTTTCCACTTTCCA  75262     A     T      AGT
                                 TG AAAGT GGAAAC   GGCA
                                 || ||||| ||||||   ||||
                                 AC TTTCA CCTTTG   CCGT
                                  C     _      ATT
GAM467  LOC128977 3'  GTGCCACTGTGAATGTCTTTC  75330      AG TGGAA
                                 GAAA  T     ACAGTGGCAC
                                 ||||  |     ||||||||||
                                 CTTT  G     TGTCACCGTG
                                   CT TAAG_
GAM467  LOC145815 3'  GTTTTGTTTTCAACTTTTCA   84522               T
                                 TGAAAAGTTGGAAACAG GGC
                                 |||||||||||||||| |||
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                                ACTTTTCAACTTTTGTT TTG
                                                _
GAM467  LOC149566 3'  CCACCACTTCCACTCTGCTTTT 85651       ____    ACA
              C                  GAAAAGT   TGGAA  GTGG
                                 |||||||   |||||  ||||
                                 CTTTTCG   ACCTT  CACC
                                     TCTC    CAC
GAM467  LOC151584 3'  GTGCCACTATTTTCCACT    86628    T   C_
                                 AGT GGAAA  AGTGGCAC
                                 ||| |||||  ||||||||
                                 TCA CCTTT  TCACCGTG
                                   _    TA
GAM467  LOC154442 5'  GCCACTGTTTTTGTTTTCA   87422      GT GG
                                 TGAAAA  T  AAACAGTGGC
                                 ||||||  |  ||||||||||
                                 ACTTTT  G  TTTGTCACCG
                                    __ TT
GAM467  LOC154641 3'  TTACTTCCGAACTTTTCA    82000       _  AAC
                                 TGAAAAGTT GGA  AGTGG
                                 |||||||| |||  |||||
                                 ACTTTTCAA CCT  TCATT
                                      G  ___
GAM467  LOC155061 3'  TGCTGGCCCCAACTTTTC    82194        AAA
                                 GAAAAGTTGG  CAGTG
                                 ||||||||||  |||||
                                 CTTTTCAACC  GTCGT
                                      CCG
GAM467  LOC196527 3'  GTGCCACTGTTCCTCTCTTCA 89101     A  TT   A
                                 TGAA AG  GGAA CAGTGGCAC
                                 |||| ||  |||| |||||||||
                                 ACTT TC  CCTT GTCACCGTG
                                   C  T_   _
GAM467  LOC220045 3'  GTGCCACTGTGTTCCCCTT   95037    TT   _
                                 AAG  GGAA ACAGTGGCAC
                                 |||  |||| ||||||||||
                                 TTC  CCTT TGTCACCGTG
                                   C_   G
GAM467  LOC220729 3'  GTGCCACTGTCCCCCCAGC   72052      AA__
                                 GTTGG   ACAGTGGCAC
                                 |||||   ||||||||||
                                 CGACC   TGTCACCGTG
                                    CCCC
GAM467  LOC222174 3'  TACCTTTCCAACTTGTCA    95765    A       CA
                                 TGA AAGTTGGAAA  GTG
                                 ||| ||||||||||  |||
                                 ACT TTCAACCTTT  CAT
                                   G        C_
GAM468  BAZ2A    5'  TCCACTGAGTACTGCCGA    26515        G__  AAC
                                 TCGGCAGTG  GGT  GGA
                                 |||||||||  |||  |||
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                                AGCCGTCAT   TCA   CCT
                                     GAG   ___
GAM468  COL15A1  5'  CCGCCGCCGCCGCTGCCGA   10258         _   AA
                                TCGGCAGTGG GGT  CGG
                                |||||||||| |||  |||
                                AGCCGTCGCC CCG  GCC
                                     G   CC
GAM468  DXS1283E 3'  TCCATTTTCACACTGCTGA   71388         G  T  C
                                TCGGCAGTG GG AA GGA
                                ||||||||| || || |||
                                AGTCGTCAC CT TT CCT
                                     A  T  A
GAM468  GPRK5    5'  TCCGTTGCTGACCGCCGA    19186       A  G  G
                                TCGGC GT GG TAACGGA
                                ||||| || || |||||||
                                AGCCG CA TC GTTGCCT
                                   C  G  _
GAM468  MLC1     3'  CCAGGTTTCCCACTGCGGA   58290    G       T  __
                                TC GCAGTGGGG AAC  GG
                                || |||||||| |||  ||
                                AG CGTCACCCT TTG  CC
                                 G       _  GA
GAM468  MPP2     3'  TCCACAGCTTCTCACTGCCGA  60521           TAAC__
                                TCGGCAGTGGGG     GGA
                                ||||||||||||     |||
                                AGCCGTCACTCT     CCT
                                      TCGACA
GAM468  OTX1     3'  TCCATTGCCTGCACTGCCG   28059         _     C
                                CGGCAGTG GGGTAA GGA
                                |||||||| |||||| |||
                                GCCGTCAC TCCGTT CCT
                                     G     A
GAM468  RFNG     3'  TCCATTACCTGTTGCTGA    89562        TG  G   C
                                TCGGCAG  GG TAA GGA
                                |||||||  || ||| |||
                                AGTCGTT  CC ATT CCT
                                     GT  _  A
GAM468  S100A5   3'  TCCACCCTTTGCTGCTGA    12932         __    AAC
                                TCGGCAGT  GGGGT   GGA
                                ||||||||  |||||   |||
                                AGTCGTCG  TCCCA   CCT
                                     TT    ___
GAM468  SHOX2    3'  TCCGTTACCCCTTTGAGA    13126    GG   T
                                TC  CAG GGGGTAACGGA
                                ||  ||| ||||||||||
                                AG  GTT CCCCATTGCCT
                                 A_   T
GAM468  SMARCA1  5'  TCCAGTGCAGCCACTGCCG   58165         G_   AC
                                CGGCAGTGG  GTA  GGA
                                |||||||||  |||  |||
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                                GCCGTCACC  CGT  CCT
                                     GA   GA
GAM468  AGPAT1   5'  TCCGCCACCACCGCTGCCG   22180        _  AA
                                CGGCAGTGG GGT  CGGA
                                ||||||||| |||  ||||
                                GCCGTCGCC CCA  GCCT
                                     A   CC
GAM468  AKAP6    3'  TCACGTTTGTCACTGCCG    16253        GGT   _
                                CGGCAGTGG   AACG GA
                                |||||||||   |||| ||
                                GCCGTCACT   TTGC CT
                                     GT_   A
GAM468  C20orf162 5'  TCCGTTACATGCAGCAGA    55503    G  A   GG
                                TC GC GTG  GTAACGGA
                                || || |||  ||||||||
                                AG CG CGT  CATTGCCT
                                 A  A   A_
GAM468  COX4I2   5'  TCGCGCTCCCACTGCCGA    51883         _  AA
                                TCGGCAGTGGG GT  CGG
                                |||||||||| ||  |||
                                AGCCGTCACCC CG  GCT
                                      T  C_
GAM468  DKFZP434D1335 3'  TCCATTATATTCCATTGCC    65716          AC__
                                GGCAGTGGGGTA   GGA
                                ||||||||||||   |||
                                CCGTTACCTTAT   CCT
                                       ATTA
GAM468  DQX1     5'  CCGCTACTATGAGCTGCTGA   56909       GG__   A
                                TCGGCAGT   GGTA CGG
                                ||||||||   |||| |||
                                AGTCGTCG   TCAT GCC
                                     AGTA   C
GAM468  FLJ10847  5'  TCCGCGGTACCCACTGCCGG   37303         GTAA_
                                TCGGCAGTGGG    CGGA
                                ||||||||||    ||||
                                GGCCGTCACCC    GCCT
                                       ATGGC
GAM468  FLJ14326  3'  TCCATTTTCACACTGCTGA   50786        G  T  C
                                TCGGCAGTG GG AA GGA
                                ||||||||| || || |||
                                AGTCGTCAC CT TT CCT
                                     A  T  A
GAM468  FLJ21126  3'  TCCGTTACTATACCTGCC    91929      _  G
                                GGCAG TG GGTAACGGA
                                ||||| || |||||||||
                                CCGTC AT TCATTGCCT
                                   C  A
GAM468  FLJ22940  5'  CCGGCAGCTCCCACTGCCG   44996         _  AA_
                                CGGCAGTGGG GT   CGG
                                |||||||||| ||   |||
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                                GCCGTCACCC CG   GCC
                                      T  ACG
GAM468  FLJ23511  3'  TCCAATTACCCCACTGTC    50938          C_
                                GGCAGTGGGGTAA  GGA
                                ||||||||||||  |||
                                CTGTCACCCCATT  CCT
                                       AA
GAM468  KIAA0210  3'  TCCTGGGCCCCACTGCCGG   29179          AAC
                                TCGGCAGTGGGGT  GGA
                                ||||||||||||  |||
                                GGCCGTCACCCCG  CCT
                                       GGT
GAM468  KIAA0601  3'  TCCAGGTGCCCCACAGCCGA  63172      A      AC_
                                TCGGC GTGGGGTA  GGA
                                |||||  ||||||||  |||
                                AGCCG CACCCCGT  CCT
                                   A       GGA
GAM468  LBP-9     3'  TCCACTTGTCCCACTGCTGA  28049        GT  C_
                                TCGGCAGTGGG  AA  GGA
                                ||||||||||  ||  |||
                                AGTCGTCACCC  TT  CCT
                                       TG  CA
GAM468  MGC10485  3'  CCGTTACTTGCAACCTGA   54622     CAG  _
                                TCGG   TG GGGTAACGG
                                ||||   || |||||||||
                                AGTC   AC TTCATTGCC
                                  CA_  G
GAM468  NDP52     3'  TCCAAGTTGTCCCACTGCC   20678       GT  __
                                GGCAGTGGG  AAC  GGA
                                |||||||||  |||  |||
                                CCGTCACCC  TTG  CCT
                                      TG   AA
GAM468  PAK2      5'  CCATTATTGCCCCACCACCGG  67139     CA       C___
                                TCGG  GTGGGGTAA   GG
                                ||||  |||||||||   ||
                                GGCC  CACCCCGTT   CC
                                  AC        ATTA
GAM468  PHRET1    3'  TCCATTAGTTCTGCTGCCGA  41352       TG  _  C
                                TCGGCAG  GGG TAA GGA
                                |||||||  ||| ||| |||
                                AGCCGTC  CTT ATT CCT
                                    GT   G   A
GAM468  SC65      3'  TCCGCCCTCCTCACTGCTGA  22304         TAA_
                                TCGGCAGTGGGG   CGGA
                                ||||||||||||   ||||
                                AGTCGTCACTCC   GCCT
                                       TCCC
GAM468  SEMA4G    5'  TCCAGCTGCTCCCGCTACCGA  96333     C    _  AC_
                                TCGG AGTGGG GTA   GGA
                                |||| ||||||  |||   |||
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                                AGCC TCGCCC CGT   CCT
                                  A     T   CGA
GAM468  SERPINA10 5'  CCACCACCACTCACTGCCGG  32992        _ _  AAC
                                TCGGCAGTG G GGT   GG
                                ||||||||| | |||   ||
                                GGCCGTCAC C CCA   CC
                                     T A   CCA
GAM468  SPPL2A   5'  TCCGAGCCTACCCCGCCGA   52494      AGT     A___
                                TCGGC   GGGGTA    CGGA
                                |||||   ||||||    ||||
                                AGCCG   CCCCAT    GCCT
                                   ___     CCGA
GAM468  LOC133671 5'  CCGCTACCCTTCCTGCTGCTGA 76456        ____     A
                                TCGGCAGT    GGGGTA CGG
                                ||||||||    |||||| |||
                                AGTCGTCG    TCCCAT GCC
                                     TCCT     C
GAM468  LOC200035 3'  CCATTTGCCTCCCACTGCC    73635        __   C_
                                GGCAGTGGG  GTAA  GG
                                |||||||||  ||||  ||
                                CCGTCACCC  CGTT  CC
                                     TC    TA
GAM468  LOC201696 3'  CCATTGCTCTCCCACTGCAGA  63816    G      ___   C
                                TC GCAGTGGG   GTAA GG
                                || ||||||||   |||| ||
                                AG CGTCACCC   CGTT CC
                                 A       TCT    A
GAM468  LOC255270 3'  TCCACCCTTTGCTGCTGA    96245        __    AAC
                                TCGGCAGT  GGGGT   GGA
                                ||||||||  |||||   |||
                                AGTCGTCG  TCCCA   CCT
                                     TT    ___
GAM468  LOC91012  5'  TCCATTACAGATTTATTGCC   65249        ___   C
                                GGCAGTGGG   GTAA GGA
                                |||||||||   |||| |||
                                CCGTTATTT   CATT CCT
                                     AGA    A
GAM468  LOC92080  5'  CCATACCTCCACTGCTGA    68623         _   AC
                                TCGGCAGTGG GGTA  GG
                                |||||||||| ||||  ||
                                AGTCGTCACC CCAT  CC
                                     T    A_
GAM469  ALPP     3'  CACCACCTACAGCCCAGTG   69408         ATTTT  ACA
                                TACTGGGCTG    GG   GTG
                                ||||||||||    ||   |||
                                GTGACCCGAC    CC   CAC
                                     AT___  AC_
GAM469  FANCA    3'  CCACTGCACACCAGCCCAG   5540        ATTT  GA
                                CTGGGCTG    TG  CAGTGG
                                ||||||||    ||  ||||||
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                                GACCCGAC   AC  GTCACC
                                    C___  AC
GAM469  HSPA5    3'  CCACTGTACTCCAGCCCGG   19283       ATTTTGG
                                CTGGGCTG     ACAGTGG
                                ||||||||     |||||||
                                GGCCCGAC     TGTCACC
                                    CTCA___
GAM469  IGFBP1   5'  CCGCCCGCCGCCACCAGCCCAG 6995        ATTT  ACA
                                CTGGGCTG   TGG  GTGG
                                ||||||||   |||  ||||
                                GACCCGAC   GCC  CGCC
                                    CACC  GCC
GAM469  PRM2     5'  CCACTGCAGCCTCAGCCCAG  12396       TT  GA
                                CTGGGCTGA  TTG  CAGTGG
                                |||||||||  |||  ||||||
                                GACCCGACT  GAC  GTCACC
                                    CC  __
GAM469  TREM2    3'  CCACCAGGGACCAGCCCAG   39097       A   GGACA
                                CTGGGCTG TTTT    GTGG
                                |||||||| ||||    ||||
                                GACCCGAC AGGG    CACC
                                    C   AC___
GAM469  FLJ11286 3'  CCACCACGAAACTCAGCCCAGT 37791         _   GACA
          A                      TACTGGGCTGA TTTTG   GTGG
                                ||||||||||| |||||   ||||
                                ATGACCCGACT AAAGC   CACC
                                     C    AC__
GAM469  FLJ20208 3'  CACTGCACCCAGCCCAGT    35241       ATTTT  A_
                                ACTGGGCTG    GG  CAGTG
                                |||||||||    ||  |||||
                                TGACCCGAC    CC  GTCAC
                                     _____  AC
GAM469  KIAA0515 3'  CCACCGTCCAAATGCGTGGCCC 64546       AT__     A
          AG                     CTGGGCTG   TTTGGAC GTGG
                                ||||||||   ||||||| ||||
                                GACCCGGT   AAACCTG CACC
                                    GCGT     C
GAM470  CLCN6    3'  GGGACTTGGCCAAGGCA     8906         CGT
                                TGTCTTGGTT  GTCCC
                                ||||||||||  |||||
                                ACGGAACCGG  CAGGG
                                     TT_
GAM470  CLCN6    3'  GGGACTTGGCCAAGGCA     41698        CGT
                                TGTCTTGGTT  GTCCC
                                ||||||||||  |||||
                                ACGGAACCGG  CAGGG
                                     TT_
GAM470  CLCN6    3'  GGGACTTGGCCAAGGCA     41705        CGT
                                TGTCTTGGTT  GTCCC
                                ||||||||||  |||||
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                                ACGGAACCGG  CAGGG
                                     TT_
GAM470  CLECSF5  5' GGGATGCTACCAAGGCA    26040       TC
                                TGTCTTGGT  GTGTCCC
                                |||||||||  |||||||
                                ACGGAACCA  CGTAGGG
                                     T_
GAM470  ESRRA    3' GGGACATGGGGCAAGCCA    16721    T   G
                                TG CTTG TTCGTGTCCC
                                || |||| ||||||||||
                                AC GAAC GGGTACAGGG
                                 C   G
GAM470  ETF1     3' GGGACACAGCTTCTGGCA    17589     TT_   C
                                TGTC  GGTT GTGTCCC
                                ||||  |||| |||||||
                                ACGG  TCGA CACAGGG
                                  TCT   _
GAM470  MARS     3' GGGACATGGCCCAGGACA    96565       TT
                                TGTCTTGG  CGTGTCCC
                                ||||||||  ||||||||
                                ACAGGACC  GTACAGGG
                                     CG
GAM470  MASP1    5' GGGAGCACCCAAGGCA      58215       TTC  _
                                TGTCTTGG  GTG TCCC
                                ||||||||  ||| ||||
                                ACGGAACC  CAC AGGG
                                     ___  G
GAM470  MASP1    5' GGGAGCACCCAAGGCA      10296       TTC  _
                                TGTCTTGG  GTG TCCC
                                ||||||||  ||| ||||
                                ACGGAACC  CAC AGGG
                                     ___  G
GAM470  NFE2L1   5' GGGACACTCTGACCCAAGAC  13633       T ___
                                GTCTTGG TC  GTGTCCC
                                ||||||| ||  |||||||
                                CAGAACC AG  CACAGGG
                                     C  TCT
GAM470  NXF5     5' GGACCGCCAACTAAGACA    53089       C  _
                                TGTCTTGGTT GTG TCC
                                |||||||||| ||| |||
                                ACAGAATCAA CGC AGG
                                      C  C
GAM470  NXF5     5' GGACCGCCAACTAAGACA    53689       C  _
                                TGTCTTGGTT GTG TCC
                                |||||||||| ||| |||
                                ACAGAATCAA CGC AGG
                                      C  C
GAM470  NXF5     5' GGACCGCCAACTAAGACA    53691       C  _
                                TGTCTTGGTT GTG TCC
                                |||||||||| ||| |||
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                                ACAGAATCAA CGC AGG
                                      C   C
GAM470  NXF5     5'  GGACCGCCAACTAAGACA    53694          C  _
                                TGTCTTGGTT GTG TCC
                                |||||||||| ||| |||
                                ACAGAATCAA CGC AGG
                                      C   C
GAM470  NXF5     5'  GGACCGCCAACTAAGACA    53696          C  _
                                TGTCTTGGTT GTG TCC
                                |||||||||| ||| |||
                                ACAGAATCAA CGC AGG
                                      C   C
GAM470  TEL2     5'  GGGAGCGCTCAAGACA      32851         TT   G
                                TGTCTTGG  CGT TCCC
                                ||||||||  ||| ||||
                                ACAGAACT  GCG AGGG
                                     C_  _
GAM470  TESK1    3'  GGGATCACTGAACCAGACA    21888       T    _  _
                                TGTCT GGTTC GTG TCCC
                                ||||| ||||| ||| ||||
                                ACAGA CCAAG CAC AGGG
                                   _    T  T
GAM470  TGM1     3'  GGACATTGCCCCAAGATA     6272         TT  _
                                TGTCTTGG  CG TGTCC
                                ||||||||  || |||||
                                ATAGAACC  GT ACAGG
                                     CC  T
GAM470  TLL2     3'  GGGACATGTCAACCAAGA     25885         __
                                TCTTGGTT  CGTGTCCC
                                ||||||||  ||||||||
                                AGAACCAA  GTACAGGG
                                     CT
GAM470  ZFHX1B   3'  GGGCGGTTCAGCCAAGACA    29606          CG__
                                TGTCTTGGTT    TGTCC
                                ||||||||||    |||||
                                ACAGAACCGA    GCGGG
                                      CTTG
GAM470  CLECSF9  3'  GGGACACGGAGCCAAGACA    27622           _
                                TGTCTTGGTTC GTGTCCC
                                |||||||||||| |||||||
                                ACAGAACCGAG CACAGGG
                                       G
GAM470  DKFZP434K2235 5'  GGGACACGCAGTGACG      84498      _  GTT
                                TGTC TTG   CGTGTCCC
                                |||| |||   ||||||||
                                GCAG GAC   GCACAGGG
                                  T  ____
GAM470  DKFZp762K222 5'  GGGACACGACTCGGACA      71670       T  T
                                TGTCT GGT CGTGTCCC
                                ||||| ||| ||||||||
```

```
                                ACAGG TCA GCACAGGG
                                  C  _
GAM470  DSCR6    3'  GGGACACCCGAGCCAGGACA  39069          __
                                TGTCTTGGTTC  GTGTCCC
                                ||||||||||  |||||||
                                ACAGGACCGAG  CACAGGG
                                     CC
GAM470  FENS-1   3'  GGGATCGTACCAGGACA    40833        T  T
                                TGTCTTGGT CG GTCCC
                                ||||||||| || |||||
                                ACAGGACCA GC TAGGG
                                     T  _
GAM470  FLJ20651 3'  GGAACACAAGTATATCAAGATA 35921        TC____   _
                                TGTCTTGGT     GTGT CC
                                |||||||||     |||| ||
                                ATAGAACTA     CACA GG
                                     TATGAA    A
GAM470  FLJ21986 3'  GGGACTATGCAACCAAGA    46693        _  _
                                TCTTGGTT CGT GTCCC
                                |||||||| ||| |||||
                                AGAACCAA GTA CAGGG
                                     C   T
GAM470  GPS2     5'  GGGACATGGAGAAAGCA     16891    T   GG
                                TG CTT  TTCGTGTCCC
                                || |||  ||||||||||
                                AC GAA  AGGTACAGGG
                                 _  AG
GAM470  HEAB     5'  GGGACCTAGACCGAGACA    23361         CGT
                                TGTCTTGGTT   GTCCC
                                ||||||||||   |||||
                                ACAGAGCCAG   CAGGG
                                     ATC
GAM470  HTR3A    3'  GGGACATTTTCAAGACA     7877         TTC
                                TGTCTTGG   GTGTCCC
                                ||||||||   |||||||
                                ACAGAACT   TACAGGG
                                     TT_
GAM470  JM5      5'  GGGACACGCGGAGGTCA     23959    _   G TT
                                TG TCTT G  CGTGTCCC
                                || |||| |  ||||||||
                                AC GGAG C  GCACAGGG
                                 T   G __
GAM470  KIAA0255 3'  GGGACTCCCAACACAAGACA  29134        _  CGT_
                                TGTCTTG GTT    GTCCC
                                ||||||| |||    |||||
                                ACAGAAC CAA    CAGGG
                                     A   CCCT
GAM470  KIAA0453 3'  GGGACACAGGATGGAAAC    69609    C  G   _
                                GT TT GTTC GTGTCCC
                                || || |||| |||||||
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                                CA AG TAGG CACAGGG
                                 A G   A
GAM470  KIAA1775  3'  GGAACTTGGACCAAGGCA    53544          TG_
                                TGTCTTGGTTCG   TCC
                                ||||||||||||  |||
                                ACGGAACCAGGT   AGG
                                       TCA
GAM470  KIAA1908  3'  GGGACAGCTGGAAGGCA     73794      __  TCG
                                TGTCTT  GGT   TGTCCC
                                ||||||  |||   ||||||
                                ACGGAA  TCG   ACAGGG
                                   GG  ___
GAM470  MGC15631  3'  GGGACACGGCAGTAAGCA    52233    T   GT_
                                TG CTTG   TCGTGTCCC
                                || ||||   |||||||||
                                AC GAAT   GGCACAGGG
                                 _   GAC
GAM470  MGC3035   5'  GACACTGAGCCCCGAGACA   44400      __   _
                                TGTCTT  GGTTC GTGTC
                                ||||||  ||||| |||||
                                ACAGAG  CCGAG CACAG
                                   CC    T
GAM470  p25       3'  GACACGAAGTGCCGAGACA   23833        ___
                                TGTCTTGGT   TCGTGTC
                                |||||||||   |||||||
                                ACAGAGCCG   AGCACAG
                                      TGA
GAM470  P2RX5     3'  GGGACCTGCCCAAGATA     11922       TT  T
                                TGTCTTGG  CG GTCCC
                                ||||||||  || |||||
                                ATAGAACC  GT CAGGG
                                     C_  C
GAM470  PNMA5     3'  GGGACTTCACCAACCAAGAC   73975        C  ___
                                GTCTTGGTT GT   GTCCC
                                |||||||||  ||   |||||
                                CAGAACCAA CA   CAGGG
                                      C  CTT
GAM470  PRO1843   5'  GGGCTTGCAAACCAAGAT    38142        C  __
                                GTCTTGGTT GT  GTCC
                                |||||||||  ||  ||||
                                TAGAACCAA CG  CGGG
                                     A  TT
GAM470  RoXaN     3'  GGGACAGAGTCAGGACA     47297       GT  G
                                TGTCTTG  TC TGTCCC
                                |||||||  || ||||||
                                ACAGGAC  AG ACAGGG
                                   TG  _
GAM470  SLC17A3   5'  ACACAATGGCCACCAAGACA   22787        __ ___
                                TGTCTTGGT  TC   GTGT
                                |||||||||  ||   ||||
```

```
                                ACAGAACCA  GG   CACA
                                     CC  TAA
GAM470   LOC127255 3'  GGACACAACCTTGGGGCA    59836       __   C
                                TGTCTT  GGTT GTGTCC
                                ||||||  |||| ||||||
                                ACGGGG  CCAA CACAGG
                                   TT   _
GAM470   LOC132880 5'  GGGAGTGCTACCAGGACA    75582        TC  _
                                TGTCTTGGT  GTG TCCC
                                |||||||||  ||| ||||
                                ACAGGACCA  CGT AGGG
                                     T_   G
GAM470   LOC138389 3'  GGGAGGGGCCAGGACA     76741         GTG
                                TGTCTTGGTTC   TCCC
                                ||||||||||   ||||
                                ACAGGACCGGG   AGGG
                                      G__
GAM470   LOC144308 3'  GGGACACGCATGGGGCA     83983       GTT
                                TGTCTTG   CGTGTCCC
                                |||||||   ||||||||
                                ACGGGGT   GCACAGGG
                                    AC_
GAM470   LOC144742 5'  GGGATGCTTCTAAGACA     77462        TTC
                                TGTCTTGG   GTGTCCC
                                ||||||||   |||||||
                                ACAGAATC   CGTAGGG
                                     TT_
GAM470   LOC147495 3'  GGGACTGTGATCAAGACA    85144         CGT
                                TGTCTTGGTT   GTCCC
                                ||||||||||   |||||
                                ACAGAACTAG   CAGGG
                                      TGT
GAM470   LOC149684 3'  GGGACAGACCCCAGGACA    85768        T_  G
                                TGTCTTGG  TC TGTCCC
                                ||||||||  || ||||||
                                ACAGGACC  AG ACAGGG
                                    CC  _
GAM470   LOC152286 3'  GGGACACGGCACGGCA      86812      T  GT
                                TGTC TG  TCGTGTCCC
                                |||| ||  |||||||||
                                ACGG AC  GGCACAGGG
                                  C  __
GAM470   LOC152464 5'  GGGACACGCGGAGGTCA     60649    _   G TT
                                TG TCTT G  CGTGTCCC
                                || |||| |  ||||||||
                                AC GGAG C  GCACAGGG
                                 T   G __
GAM470   LOC153505 3'  GGGACGCGCGCCCAGACA    81707       T   T
                                TGTCT GGT CGTGTCCC
                                ||||| ||| ||||||||
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                                ACAGA CCG GCGCAGGG
                                   C   C
GAM470   LOC157867 3'  GGAATGCTTACCAAGATA    87872         TC    _
                                TGTCTTGGT  GTGT CC
                                |||||||||  |||| ||
                                ATAGAACCA  CGTA GG
                                     TT    A
GAM470   LOC201475 5'  GGGACACAGCAGGTCA      89621    T    G  C
                                TG CTTG TT GTGTCCC
                                || |||| || |||||||
                                AC GGAC GA CACAGGG
                                 T    _ _
GAM470   LOC205095 3'  GGGACCACCCCCAAGGCA    92386         TTC   _
                                TGTCTTGG   GTG TCCC
                                ||||||||   ||| ||||
                                ACGGAACC   CAC AGGG
                                     CC_   C
GAM470   LOC221718 3'  GGGACACGTGGGGGCA      95282       G TT
                                TGTCTT G  CGTGTCCC
                                ||||||| |  ||||||||
                                ACGGGG T  GCACAGGG
                                   G __
GAM470   LOC254155 5'  GGACTGCCCAACCAGGACA   99450          C_  _
                                TGTCTTGGTT  GT GTCC
                                ||||||||||  || ||||
                                ACAGGACCAA  CG CAGG
                                      CC  T
GAM470   LOC254826 3'  GGGATTGAACCAAACCA     99052    TC       T
                                TG  TTGGTTCG GTCCC
                                ||  |||||||| |||||
                                AC  AACCAAGT TAGGG
                                 CA       _
GAM470   LOC255328 3'  GGACACGTCTCCAAGATA     98342         TT_
                                TGTCTTGG   CGTGTCC
                                ||||||||   |||||||
                                ATAGAACC   GCACAGG
                                     TCT
GAM470   LOC256594 5'  GGGATGCCTCCCAAGACA     98867         TTC
                                TGTCTTGG   GTGTCCC
                                ||||||||   |||||||
                                ACAGAACC   CGTAGGG
                                     CTC
GAM470   LOC256789 5'  GGACAGGGCACAGAGACA     99308       G  _  G
                                TGTCTT GT TC TGTCC
                                |||||| || || |||||
                                ACAGAG CA GG ACAGG
                                   A  C  G
GAM470   LOC257482 3'  GGATGCTGCACCAAAACA     95896     C     T _
                                TGT TTGGT C GTGTCC
                                ||| ||||| | ||||||
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                                ACA AACCA G CGTAGG
                                  A    C T
GAM470  LOC51652  3'  GGGACATTCTTAAGATA    32702       TTC
                                TGTCTTGG  GTGTCCC
                                ||||||||  |||||||
                                ATAGAATT  TACAGGG
                                    CT_
GAM470  LOC90092  5'  GGGACATGGGAAGGCA     62069      GG
                                TGTCTT  TTCGTGTCCC
                                ||||||  ||||||||||
                                ACGGAA  GGGTACAGGG
                                  __
GAM470  LOC91522  3'  GGGACAAGATAGGACA     66918      GT  G
                                TGTCTTG  TC TGTCCC
                                |||||||  || ||||||
                                ACAGGAT  AG ACAGGG
                                   __ A
GAM471  GPD1      3'  TCATGCCACCACATTTG     60398      C      C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A      _
GAM471  IL5RA     5'  TCGCATGGCCACCGCATTT   6906         AT__
                                AAATGCGGTGGC   CGA
                                ||||||||||||   |||
                                TTTACGCCACCG   GCT
                                     GTAC
GAM471  MYO1C     3'  TGCCGATGCCAAATATTTG   61873      CGG      A
                                TAAATG  TGGCATCG CA
                                ||||||  |||||||| ||
                                GTTTAT  ACCGTAGC GT
                                   AA_      C
GAM471  C6orf37   3'  TGTCACACTGCATTTA      68097        GCATC
                                TAAATGCGGTG    GACA
                                ||||||||||    ||||
                                ATTTACGTCAC    CTGT
                                     A____
GAM471  DNAJC6    3'  TTGCAGAACCACCGCATT    29498        CA  GA
                                AATGCGGTGG  TC  CAA
                                |||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                     A_  AC
GAM471  FLJ11210  3'  GTCGATGTGCATGCTTTTA   60319     T  GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM471  FLJ12476  3'  TCGATCTTCTGCATTTA     43270        T  C
                                TAAATGCGG GG ATCGA
                                |||||||| || |||||
```

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                                ATTTACGTC TC TAGCT
                                     T  _
GAM471  KIAA1034  3'  TCGATGGCATCCGCATTTG   63134        _  G
                                TAAATGCGG TG CATCGA
                                ||||||||| || ||||||
                                GTTTACGCC AC GTAGCT
                                     T  G
GAM471  KIAA1987  3'  TCATGTAACTGCATTTA    89391         G   C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                     A   _
GAM471  MGC16063  3'  TGTCCTGGCCACTGCATT   54929          ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                      GTC
GAM471  LOC147949 3'  TGTCAGATGTCCACATTGCA  79279     __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM471  LOC150577 3'  GTCCTCACCGCATTTG      86258          CATC
                                TAAATGCGGTGG   GAC
                                ||||||||||||   |||
                                GTTTACGCCACT   CTG
                                      C___
GAM471  LOC158219 3'  TGTGTGTCACCACATTT     82694      C      CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                   A       __
GAM471  LOC202020 3'  TGTCTCACCACATTTA      90605       C    CATC
                                TAAATG GGTGG   GACA
                                |||||| |||||   ||||
                                ATTTAC CCACT   CTGT
                                    A    _____
GAM471  LOC90826  5'  TGTCGATGCAGGTTTATTTG  64788       CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                    TTGGA
GAM471  LOC93587  3'  TTGTCTTTACCTGCATTTA   73042       _    CATC
                                TAAATGC GGTGG   GACAA
                                ||||||| |||||   |||||
                                ATTTACG CCATT   CTGTT
                                    T    T___
GAM472  ELF3      3'  TGACCTTGACCTTGACCAA   16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
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                                AACCA GTTCC   TC   CAGT
                                  _    AGT  ___
GAM472  JAK2     3'  TGACCTTCATTCTGAGACCAA  18318       CAA       AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_       C_
GAM472  SLC10A2  5'  ACTCTCTGTCTTGACCAA    6590        CAA       A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM472  FLJ10803 3'  GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM472  KIAA1958 5'  GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM472  MARCKS   3'  ACTTTCCACCCTGCCCA     11411     TTCA    A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM472  TUB      5'  GTGGGACCATCCCTTAAACC   13898     C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A        AG__
GAM472  LOC80298 3'  ACTTTTACCTTGAACCA     48062         GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                     A___
GAM473  GPD1     3'  TCATGCCACCACATTTG      60398       C       C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A      _
GAM473  IL5RA    5'  TCGCATGGCCACCGCATTT    6906          AT__
                                AAATGCGGTGGC    CGA
                                ||||||||||||    |||
                                TTTACGCCACCG    GCT
                                      GTAC
GAM473  MYO1C    3'  TGCCGATGCCAAATATTTG    61873       CGG       A
                                TAAATG   TGGCATCG CA
                                ||||||   |||||||| ||
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                                GTTTAT   ACCGTAGC GT
                                   AA_      C
GAM473  C6orf37   3'  TGTCACACTGCATTTA     68097         GCATC
                                TAAATGCGGTG    GACA
                                ||||||||||    ||||
                                ATTTACGTCAC    CTGT
                                      A____
GAM473  DNAJC6    3'  TTGCAGAACCACCGCATT    29498        CA  GA
                                AATGCGGTGG  TC  CAA
                                |||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                      A_  AC
GAM473  FLJ11210  3'  GTCGATGTGCATGCTTTTA   60319     T   GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM473  FLJ12476  3'  TCGATCTTCTGCATTTA     43270        T  C
                                TAAATGCGG GG ATCGA
                                |||||||| || |||||
                                ATTTACGTC TC TAGCT
                                      T  _
GAM473  KIAA1034  3'  TCGATGGCATCCGCATTTG   63134        _  G
                                TAAATGCGG TG CATCGA
                                |||||||| || ||||||
                                GTTTACGCC AC GTAGCT
                                      T  G
GAM473  KIAA1987  3'  TCATGTAACTGCATTTA     89391         G   C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                      A   _
GAM473  MGC16063  3'  TGTCCTGGCCACTGCATT    54929          ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                      GTC
GAM473  LOC147949 3'  TGTCAGATGTCCACATTGCA  79279     __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM473  LOC150577 3'  GTCCTCACCGCATTTG      86258          CATC
                                TAAATGCGGTGG   GAC
                                ||||||||||||   |||
                                GTTTACGCCACT   CTG
                                      C___
GAM473  LOC158219 3'  TGTGTGTCACCACATTT     82694      C      CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
```

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                                TTTAC CCACTGTG  TGT
                                   A       __
GAM473  LOC202020 3'  TGTCTCACCACATTTA      90605       C    CATC
                                TAAATG GGTGG    GACA
                                |||||| |||||    ||||
                                ATTTAC CCACT    CTGT
                                   A    ____
GAM473  LOC90826  5'  TGTCGATGCAGGTTTATTTG   64788       CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                   TTGGA
GAM473  LOC93587  3'  TTGTCTTTACCTGCATTTA    73042       _    CATC
                                TAAATGC GGTGG    GACAA
                                ||||||| |||||    |||||
                                ATTTACG CCATT    CTGTT
                                    T    T___
GAM474  ELF3      3'  TGACCTTGACCTTGACCAA    16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                   _    AGT  ___
GAM474  JAK2      3'  TGACCTTCATTCTGAGACCAA  18318       CAA       AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_       C_
GAM474  SLC10A2   5'  ACTCTCTGTCTTGACCAA    6590        CAA       A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM474  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM474  KIAA1958  5'  GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM474  MARCKS    3'  ACTTTCCACCCTGCCCA     11411     TTCA    A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM474  TUB       5'  GTGGGACCATCCCTTAAACC   13898     C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
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```
                                CCAA TTCCCTACC    GGTG
                                  A       AG__
GAM474  LOC80298  3'  ACTTTTACCTTGAACCA     48062          GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                     A___
GAM475  A1BG      3'  CTGTCACCCAGGCTGGAGT    56289            C
                                ACTCCAGCCTGGG GACAG
                                |||||||||||| |||||
                                TGAGGTCGGACCC CTGTC
                                      A
GAM475  A1BG      3'  TTGCTCTTGTTGCCCAGGCTGG 56302                _
           AGT                    ACTCCAGCCTGGGCGACA GAGCAA
                                ||||||||||||||||| ||||||
                                TGAGGTCGGACCCGTTGT CTCGTT
                                       T
GAM475  AASS      3'  GCTCTGTCACCCAGGCTGGAGT 20461            C
                                ACTCCAGCCTGGG GACAGAGC
                                |||||||||||| ||||||||
                                TGAGGTCGGACCC CTGTCTCG
                                      A
GAM475  ABCD1     3'  TTGCTCCGCGGAGGAAGCTGGG 5262         ___ GG   ACA
           GT                     ACTCCAGC   CT  GCG   GAGCAA
                                ||||||||   ||  |||   ||||||
                                TGGGGTCG   GA  CGC   CTCGTT
                                    AAG  GG  ___
GAM475  ABCG1     3'  CTCTGCCCAGCTGGG       18190       C    GAC
                                TCCAGC TGGGC   AGAG
                                |||||| |||||   ||||
                                GGGTCG ACCCG   TCTC
                                   _    ___
GAM475  ACADSB    3'  CTCTGTCACCCAGGCTAGAGT  9646       C       C
                                ACTC AGCCTGGG GACAGAG
                                |||| |||||||| |||||||
                                TGAG TCGGACCC CTGTCTC
                                  A       A
GAM475  ADAMTS4   3'  GCTCTGTCGCCCAGGCTGGAGT 18765
                                ACTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTCG

GAM475  ADCY6     5'  CTCTGTCACCCAGGCTGGAGT  31588            C
                                ACTCCAGCCTGGG GACAGAG
                                |||||||||||| |||||||
                                TGAGGTCGGACCC CTGTCTC
                                      A
GAM475  ALDH1B1   3'  CTCTGTCGCCCAGGCTGGAGT  7322
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||||
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                                TGAGGTCGGACCCGCTGTCTC

GAM475  ALOX15   3' CTTTGACACCCAGGCTGGAGT  8546          CGA
                                ACTCCAGCCTGGG  CAGAG
                                |||||||||||||  |||||
                                TGAGGTCGGACCC  GTTTC
                                      ACA
GAM475  APAF1    3' TTGCACTATCACCCAGGCTGGA 8595          C  C  A
          GT                    ACTCCAGCCTGGG GA AG GCAA
                                |||||||||||||| || || ||||
                                TGAGGTCGGACCC CT TC CGTT
                                      A  A  A
GAM475  APAF1    3' TTGCTTTGTTGCCAGGCTGGAG 8596          G
          T                     ACTCCAGCCTGG CGACAGAGCAA
                                |||||||||||| ||||||||||
                                TGAGGTCGGACC GTTGTTTCGTT
                                      _
GAM475  APAF1    3' TTGCACTATCACCCAGGCTGGA 25988         C  C  A
          GT                    ACTCCAGCCTGGG GA AG GCAA
                                |||||||||||||| || || ||||
                                TGAGGTCGGACCC CT TC CGTT
                                      A  A  A
GAM475  APAF1    3' TTGCTTTGTTGCCAGGCTGGAG 25989         G
          T                     ACTCCAGCCTGG CGACAGAGCAA
                                |||||||||||| ||||||||||
                                TGAGGTCGGACC GTTGTTTCGTT
                                      _
GAM475  APM1     3' CTCTGTCACCCAGGCTGGAGT  17780         C
                                ACTCCAGCCTGGG GACAGAG
                                |||||||||||||| |||||||
                                TGAGGTCGGACCC CTGTCTC
                                      A
GAM475  APOL1    3' TTGCTCTGTCGCCAAGTTGGAG 14748       CTG
          T                     ACTCCAGC  GGCGACAGAGCAA
                                ||||||||  ||||||||||||
                                TGAGGTTG  CCGCTGTCTCGTT
                                    AA_
GAM475  APPL     3' TTGCTCTGTTGCCCAGGCTGGA 24962
          GT                    ACTCCAGCCTGGGCGACAGAGCAA
                                |||||||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTCGTT

GAM475  AQP6     5' TCAGGTCAGCTCAGGCTGGAG  55015         _  A_
                                CTCCAGCCTGGGC GAC  GA
                                |||||||||||||| |||  ||
                                GAGGTCGGACTCG CTG  CT
                                      A  GA
GAM475  AQP6     3' TTGATCTGTTACCCAGGCTGGA 55022         CG   G
          GT                    ACTCCAGCCTGGG  ACAGA CAA
                                |||||||||||||  ||||| |||
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                                TGAGGTCGGACCC  TGTCT GTT
                                      AT    A
GAM475  AQP6    5'  TCAGGTCAGCTCAGGCTGGAG  9735          _  A_
                                CTCCAGCCTGGGC GAC  GA
                                |||||||||||| |||  ||
                                GAGGTCGGACTCG CTG  CT
                                      A   GA
GAM475  AQP6    3'  TTGATCTGTTACCCAGGCTGGA 9738          CG    G
          GT                     ACTCCAGCCTGGG  ACAGA CAA
                                |||||||||||| ||||| |||
                                TGAGGTCGGACCC  TGTCT GTT
                                      AT    A
GAM475  ARCN1   3'  CTTTGTAACCCAGGCTGGA   9751          CG
                                TCCAGCCTGGG  ACAGAG
                                |||||||||| ||||||
                                AGGTCGGACCC  TGTTTC
                                      AA
GAM475  ATM     3'  CTCTGTCCGCCCAGGCTGGG  57143          _
                                TCCAGCCTGGGCG ACAGAG
                                |||||||||||| ||||||
                                GGGTCGGACCCGC TGTCTC
                                      C
GAM475  ATP1B2  3'  GCTCTTGTTGCCCAGGCTGGAG 9837              _
          T                     ACTCCAGCCTGGGCGACA GAGC
                                |||||||||||||||| ||||
                                TGAGGTCGGACCCGTTGT CTCG
                                        T
GAM475  ATP7A   3'  TTGCAGCCCAGGCTGGAGT   5332          GA
                                ACTCCAGCCTGGGC  CAG
                                |||||||||||| |||
                                TGAGGTCGGACCCG  GTT
                                       AC
GAM475  AXL     3'  CTGTGTCACCCAGGCTGGAGT  9904          C   G
                                ACTCCAGCCTGGG GACA AG
                                |||||||||||| |||| ||
                                TGAGGTCGGACCC CTGT TC
                                      A   G
GAM475  AXL     3'  CTGTGTCACCCAGGCTGGAGT  41885         C   G
                                ACTCCAGCCTGGG GACA AG
                                |||||||||||| |||| ||
                                TGAGGTCGGACCC CTGT TC
                                      A   G
GAM475  B4GALT5 3'  GCTCTGTCGCCTAAGCTGGAGT 17690       C
                                ACTCCAGC TGGGCGACAGAGC
                                |||||||| ||||||||||||
                                TGAGGTCG ATCCGCTGTCTCG
                                     A
GAM475  BCL10   3'  TTGCTCTATCGCCCAGGCTGGA 15375           C
          GT                    ACTCCAGCCTGGGCGA AGAGCAA
                                |||||||||||||||| |||||||
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                                TGAGGTCGGACCCGCT TCTCGTT
                                        A
GAM475  BRIP1    3'  TTGGTCTGTTGCCCAGGCTGGA 50216              G
                                TCCAGCCTGGGCGACAGA CAA
                                |||||||||||||||||| |||
                                AGGTCGGACCCGTTGTCT GTT
                                        G
GAM475  C14orf1  3'  CTCTGTCACCCAGGCTGGG   24167          C
                                TCCAGCCTGGG GACAGAG
                                |||||||||| |||||||
                                GGGTCGGACCC CTGTCTC
                                      A
GAM475  C7       3'  CTTTGTTGCCCAGGCTGGAG  6985
                                CTCCAGCCTGGGCGACAGAG
                                ||||||||||||||||||||
                                GAGGTCGGACCCGTTGTTTC

GAM475  CAMLG    3'  GCTCTTGTTGCCCAGGCTAGAG 10000      C          _
          T                      ACTC AGCCTGGGCGACA GAGC
                                |||| ||||||||||||| ||||
                                TGAG TCGGACCCGTTGT CTCG
                                  A          T
GAM475  CASP2    3'  GCTCTGTCGCCCAGGCTGGAG  8713
                                CTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||
                                GAGGTCGGACCCGCTGTCTCG

GAM475  CASP2    3'  GCTCTGTCGCCCAGGCTGGAG  53290
                                CTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||
                                GAGGTCGGACCCGCTGTCTCG

GAM475  CASP2    3'  GCTCTGTCGCCCAGGCTGGAG  53306
                                CTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||
                                GAGGTCGGACCCGCTGTCTCG

GAM475  CASP2    3'  GCTCTGTCGCCCAGGCTGGAG  53337
                                CTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||
                                GAGGTCGGACCCGCTGTCTCG

GAM475  CASP8    3'  GCTCTGTCGCCCAGGCTGGAGT 54079
                                ACTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTCG

GAM475  CASP8    3'  GCTCTGTCGCCCAGGCTGGAGT 54100
                                ACTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||||
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                                TGAGGTCGGACCCGCTGTCTCG

GAM475  CASP8    3'  GCTCTGTCGCCCAGGCTGGAGT 54116
                                ACTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTCG

GAM475  CASP8    3'  GCTCTGTCGCCCAGGCTGGAGT 8755
                                ACTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTCG

GAM475  CBFA2T2  3'  TTGTCTCCCAGGCTGGAGT   18720          C
                                ACTCCAGCCTGGG GACAG
                                |||||||||||| |||||
                                TGAGGTCGGACCC CTGTT
                                      T
GAM475  CCNF     3'  TTGCTCTTGTCTCCCCGGCTGG 10091        T  C  _
            AGT                   ACTCCAGCC GGG GACA GAGCAA
                                |||||||| ||| |||| ||||||
                                TGAGGTCGG CCC CTGT CTCGTT
                                     C  T   T
GAM475  CDC6     3'  CTGTTGCCCAGGCTGGAGT   8820
                                ACTCCAGCCTGGGCGACAG
                                |||||||||||||||||
                                TGAGGTCGGACCCGTTGTC

GAM475  CDC6     3'  GCTTCCCAGGTTGAAGT     8822     C      CGACA
                                ACT CAGCCTGGG    GAGC
                                ||| |||||||||    ||||
                                TGA GTTGGACCC    TTCG
                                  A      _____
GAM475  CDH1     3'  GCTCCATCGCCCAGGCCTGGG  16406     _      CA
                                TCCAG CCTGGGCGA  GAGC
                                ||||| |||||||||  ||||
                                GGGTC GGACCCGCT  CTCG
                                   C       AC
GAM475  CDH1     3'  TTCTATCGGCCAGGCTGGAGT  16412          G  C
                                ACTCCAGCCTGG CGA AGAG
                                |||||||||||| ||| ||||
                                TGAGGTCGGACC GCT TCTT
                                      G  A
GAM475  CDH17    3'  TTGCTCTGTCGCCCAGGCTGGA 15792
            GT                    ACTCCAGCCTGGGCGACAGAGCAA
                                |||||||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTCGTT

GAM475  CDK7     5'  TCGCCCTTTTCGGCTGGAGT   10158        T____
                                ACTCCAGCC    GGGCGA
                                |||||||||    ||||||
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                                TGAGGTCGG    CCCGCT
                                     CTTTT
GAM475  CHAT     5'  CTGCCGGGAACCCAGGCTGCAG 40967    C       ____  A
                                CT CAGCCTGGG   CG CAG
                                || |||||||||   || |||
                                GA GTCGGACCC   GC GTC
                                 C       AAGG  C
GAM475  CHI3L1   3'  TGCCCTGCTGAGTCCCAGGCTG 8883     C      _ GA__  A
             AG                   CTC AGCCTGGG C   CAG GCA
                                ||| |||||||| |   ||| |||
                                GAG TCGGACCC G   GTC CGT
                                  _      T AGTC   C
GAM475  CHRNB4   3'  TTGCTATATCGCCCAGGCTCAA 7453     CC        CAG
             GT                   ACT  AGCCTGGGCGA   AGCAA
                                |||  ||||||||||   |||||
                                TGA  TCGGACCCGCT   TCGTT
                                  AC         ATA
GAM475  CIAS1    5'  TTGCTGTGTCGCCTAGGCTGGA 18104              G
             GT                   ACTCCAGCCTGGGCGACA AGCAA
                                |||||||||||||||||| |||||
                                TGAGGTCGGATCCGCTGT TCGTT
                                          G
GAM475  CLECSF12 3'  CTTTGTTACCCAGGCTGGAGT  77210          CG
                                ACTCCAGCCTGGG  ACAGAG
                                ||||||||||||  ||||||
                                TGAGGTCGGACCC  TGTTTC
                                     AT
GAM475  CLECSF12 3'  GCTCTTGTTGCCCAGGCTGGAG 77213              _
             T                    ACTCCAGCCTGGGCGACA GAGC
                                |||||||||||||||||| ||||
                                TGAGGTCGGACCCGTTGT CTCG
                                          T
GAM475  CMAR     5'  GCTGTGTTGCCAAGGCTGGAGT 19034         G      G
                                ACTCCAGCCT GGCGACA AGC
                                |||||||||| ||||||| |||
                                TGAGGTCGGA CCGTTGT TCG
                                     A      G
GAM475  CMAR     5'  TTGCGCTGTCACCCAGGCTGGA 19038          C    A
             GT                   ACTCCAGCCTGGG GACAG GCAA
                                |||||||||||| ||||| ||||
                                TGAGGTCGGACCC CTGTC CGTT
                                     A    G
GAM475  CNGA1    5'  GCTCTTCGCCCAGGCTGGAGT  60243            C
                                ACTCCAGCCTGGGCGA AGAGC
                                |||||||||||||||| |||||
                                TGAGGTCGGACCCGCT TCTCG
                                          _
GAM475  CNP      3'  TGCTATTTCCCAAGCTGGAGT  53626        C   CGACAG
                                ACTCCAGC TGGG     AGCA
                                |||||||| ||||     ||||
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                                TGAGGTCG ACCC     TCGT
                                    A    TTTA__
GAM475  CORO2B   5'  TTCTGTTGCCCAAGCTGGAGT  65177        C
                                ACTCCAGC TGGGCGACAGAG
                                |||||||| ||||||||||||
                                TGAGGTCG ACCCGTTGTCTT
                                    A
GAM475  COX15    3'  CTCTTGTTGCCCAGGCTGGAGT 55283              _
                                ACTCCAGCCTGGGCGACA GAG
                                |||||||||||||||||| |||
                                TGAGGTCGGACCCGTTGT CTC
                                          T
GAM475  CR1      3'  CTGTCTCCCAGGCTGGAGT   6943           C
                                ACTCCAGCCTGGG GACAG
                                |||||||||||| |||||
                                TGAGGTCGGACCC CTGTC
                                       T
GAM475  CRTAP    3'  GCTCTCTTGCCCAGGCTGGAGT 22083            C
                                ACTCCAGCCTGGGCGA AGAGC
                                |||||||||||||| |||||
                                TGAGGTCGGACCCGTT TCTCG
                                         C
GAM475  CSNK2A2  5'  TGTCACCCAGGCTGGAGT    10322          C
                                ACTCCAGCCTGGG GACA
                                |||||||||||| ||||
                                TGAGGTCGGACCC CTGT
                                       A
GAM475  CTF1     3'  CTCTGTCGCCCAGGCTGGGGT  9013
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||
                                TGGGGTCGGACCCGCTGTCTC

GAM475  CTSB     5'  GCTCCGCTGCGCGCAGGCTGGG 65365        G  A ___
                                TCCAGCCTG GCG CA  GAGC
                                ||||||||| ||| ||  ||||
                                GGGTCGGAC CGC GT  CTCG
                                     G  _ CGC
GAM475  CXCL16   3'  GCTCTGTCATCCAGGCTGGAGT 42172          GC
                                ACTCCAGCCTGG  GACAGAGC
                                ||||||||||| ||||||||
                                TGAGGTCGGACC  CTGTCTCG
                                       TA
GAM475  CYP1A2   3'  CTCTGTTGCCAGGCTGGAGT  7512          G
                                ACTCCAGCCTGG CGACAGAG
                                |||||||||||| ||||||||
                                TGAGGTCGGACC GTTGTCTC
                                          _
GAM475  CYP1A2   3'  TCTGTCACCCAGGTTGGAGT  7529          C
                                ACTCCAGCCTGGG GACAGA
                                |||||||||||| ||||||
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                                TGAGGTTGGACCC CTGTCT
                                       A
GAM475  CYP2B6   3'  CTCTGTCACCCAGGTTCGAGT  7559      C       C
                                ACTC AGCCTGGG GACAGAG
                                |||| |||||||| |||||||
                                TGAG TTGGACCC CTGTCTC
                                  C       A
GAM475  CYP2B6   3'  CTGTTGCCCAGGCTGGAGT   7560
                                ACTCCAGCCTGGGCGACAG
                                ||||||||||||||||||
                                TGAGGTCGGACCCGTTGTC

GAM475  CYP2B6   3'  TTGCTCTGTCTCCCAGGCTGGA 7575              C
              GT                  ACTCCAGCCTGGG GACAGAGCAA
                                ||||||||||||| ||||||||||
                                TGAGGTCGGACCC CTGTCTCGTT
                                       T
GAM475  CYP4F3   3'  GCTCTGTTGCCCAGGCTGGAGT 8012
                                ACTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTCG

GAM475  CYP51    3'  GCTCTGTTGCCCAGGCTGGAGT 7618
                                ACTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTCG

GAM475  CYP8B1   3'  CTCTGTTGCCCAGGCTGCAGT  16537     C
                                ACT CAGCCTGGGCGACAGAG
                                ||| ||||||||||||||||
                                TGA GTCGGACCCGTTGTCTC
                                  C
GAM475  CYP8B1   3'  TTGCTCTGTCGCCGAGGCTGCA 16545     C     G
              GT                  ACT CAGCCT GGCGACAGAGCAA
                                ||| |||||| ||||||||||||
                                TGA GTCGGA CCGCTGTCTCGTT
                                  C     G
GAM475  DFFB     3'  CTCTGTCGCTCAGGCTGGAGT  88769
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||||
                                TGAGGTCGGACTCGCTGTCTC

GAM475  DFFB     3'  TTTTGTTGCCCAGGCTGGAGT  88793
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTTTT

GAM475  DHFR     3'  GCTCTTGTTGCCCAGGCT    7651              _
                                AGCCTGGGCGACA GAGC
                                |||||||||||| ||||
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                                TCGGACCCGTTGT CTCG
                                       T
GAM475  DIAPH2   3'  CTCTGTCACCCAGGCTGCAGT  23004     C        C
                                ACT CAGCCTGGG GACAGAG
                                ||| ||||||||| |||||||
                                TGA GTCGGACCC CTGTCTC
                                  C        A
GAM475  DISC1    3'  CTCTGTCACCCAAGTTGGAGT  38506         C    C
                                ACTCCAGC TGGG GACAGAG
                                |||||||| |||| |||||||
                                TGAGGTTG ACCC CTGTCTC
                                     A    A
GAM475  DRD1     5'  TGCTCTGTAGGGCTGAAG    7672     C     GGGCG
                                CT CAGCCT     ACAGAGCA
                                || ||||||     ||||||||
                                GA GTCGGG     TGTCTCGT
                                 A      A____
GAM475  DSC3     3'  GCTCTGACGCACAGGCTGGAGT 10443           G   A
                                ACTCCAGCCTG GCG CAGAGC
                                |||||||||||| ||| ||||||
                                TGAGGTCGGAC CGC GTCTCG
                                       A   A
GAM475  DSC3     3'  GCTCTGACGCACAGGCTGGAGT 44629           G   A
                                ACTCCAGCCTG GCG CAGAGC
                                |||||||||||| ||| ||||||
                                TGAGGTCGGAC CGC GTCTCG
                                       A   A
GAM475  DSCR3    3'  TCTGTCACCCAGGCTGGAGT   21324           C
                                ACTCCAGCCTGGG GACAGA
                                |||||||||||||| ||||||
                                TGAGGTCGGACCC CTGTCT
                                       A
GAM475  EDG8     3'  TGCTCTGTCACCCAGGCTGGAG 79152           C
          T                      ACTCCAGCCTGGG GACAGAGCA
                                |||||||||||| |||||||||
                                TGAGGTCGGACCC CTGTCTCGT
                                       A
GAM475  EGLN2    3'  TGCCCCATCATGGGGGCTGGGG 54924          _________
          T                      ACTCCAGCCT       GGGCG
                                ||||||||||       |||||
                                TGGGGTCGGG       CCCGT
                                     GGTACTAC
GAM475  EGLN2    3'  TGCCCCATCATGGGGGCTGGGG 34521          _________
          T                      ACTCCAGCCT       GGGCG
                                ||||||||||       |||||
                                TGGGGTCGGG       CCCGT
                                     GGTACTAC
GAM475  EGLN2    3'  TGCCCCATCATGGGGGCTGGGG 55777          _________
          T                      ACTCCAGCCT       GGGCG
                                ||||||||||       |||||
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                                TGGGGTCGGG       CCCGT
                                      GGTACTAC
GAM475  EHD2     3'  TTGCTCTGTCGCCCAGGCTGGA 28232
                GT                    ACTCCAGCCTGGGCGACAGAGCAA
                                      ||||||||||||||||||||||||
                                      TGAGGTCGGACCCGCTGTCTCGTT

GAM475  EIF2S3   3'  GCTCTGTCACCCAGGCTGGAGT 9209             C
                                      ACTCCAGCCTGGG GACAGAGC
                                      |||||||||||| ||||||||
                                      TGAGGTCGGACCC CTGTCTCG
                                            A
GAM475  ENDOGL1  3'  GCCGTGTCATCCAGGCTGGAGT 18825           GC   GA
                                      ACTCCAGCCTGG  GACA  GC
                                      ||||||||||||  ||||  ||
                                      TGAGGTCGGACC  CTGT  CG
                                            TA    GC
GAM475  EPB72    3'  CTCTTGTTGCCCAGGCTGGAGT 15871              _
                                      ACTCCAGCCTGGGCGACA GAG
                                      |||||||||||||||||| |||
                                      TGAGGTCGGACCCGTTGT CTC
                                                  T
GAM475  F2RL3    3'  GCGCTGTTGCCCAGGCTGGAGT 15517               A
                                      ACTCCAGCCTGGGCGACAG GC
                                      |||||||||||||||||| ||
                                      TGAGGTCGGACCCGTTGTC CG
                                                   G
GAM475  F3       3'  TTGCTCTGTTGCCCAGGCTGGA 67686
                GT                    ACTCCAGCCTGGGCGACAGAGCAA
                                      ||||||||||||||||||||||||
                                      TGAGGTCGGACCCGTTGTCTCGTT

GAM475  FABP2    3'  CTCTTTCACTCAGGCTGGA   5534           C  C
                                      TCCAGCCTGGG GA AGAG
                                      |||||||||| || ||||
                                      AGGTCGGACTC CT TCTC
                                            A  T
GAM475  FANCE    3'  TTGCTCTGTCATCCAGGCTGGA 41905           GC
                GT                    ACTCCAGCCTGG  GACAGAGCAA
                                      ||||||||||||  ||||||||||
                                      TGAGGTCGGACC  CTGTCTCGTT
                                            TA
GAM475  FANCF    3'  GCTCTGTCACCCAGTCTGGAGT 42981        C    C
                                      ACTCCAG CTGGG GACAGAGC
                                      ||||||| ||||| ||||||||
                                      TGAGGTC GACCC CTGTCTCG
                                          T    A
GAM475  FBXL11   3'  GCTCCACCGCCCTTTGTTGAG  25515     C   CT_    ACA
                                      CTC AGC   GGGCG   GAGC
                                      ||| |||   |||||   ||||
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                                GAG TTG   CCCGC   CTCG
                                  _  TTT    CAC
GAM475  FCAR    3'  GCTCTGTCACCCAGGCTGAAGT 56578    C       C
                                ACT CAGCCTGGG GACAGAGC
                                ||| ||||||||| ||||||||
                                TGA GTCGGACCC CTGTCTCG
                                  A       A
GAM475  FCAR    3'  GCTCTGTCACCCAGGCTGAAGT 56594    C       C
                                ACT CAGCCTGGG GACAGAGC
                                ||| ||||||||| ||||||||
                                TGA GTCGGACCC CTGTCTCG
                                  A       A
GAM475  FCAR    3'  GCTCTGTCACCCAGGCTGAAGT 56606    C       C
                                ACT CAGCCTGGG GACAGAGC
                                ||| ||||||||| ||||||||
                                TGA GTCGGACCC CTGTCTCG
                                  A       A
GAM475  FCAR    3'  GCTCTGTCACCCAGGCTGAAGT 56618    C       C
                                ACT CAGCCTGGG GACAGAGC
                                ||| ||||||||| ||||||||
                                TGA GTCGGACCC CTGTCTCG
                                  A       A
GAM475  FCAR    3'  TTGCTCTTTCGCCAAGGCTGGA 56643        G    C
          GT                      ACTCCAGCCT GGCGA AGAGCAA
                                ||||||||||| ||||| |||||||
                                TGAGGTCGGA CCGCT TCTCGTT
                                     A    T
GAM475  FCAR    3'  TTGCTCTTTCGCCAAGGCTGGA 56649        G    C
          GT                      ACTCCAGCCT GGCGA AGAGCAA
                                ||||||||||| ||||| |||||||
                                TGAGGTCGGA CCGCT TCTCGTT
                                     A    T
GAM475  FCAR    3'  GCTCTGTCACCCAGGCTGGAGT 10590          C
                                ACTCCAGCCTGGG GACAGAGC
                                |||||||||||| ||||||||
                                TGAGGTCGGACCC CTGTCTCG
                                     A
GAM475  FCGR2A  3'  TCTGTTACCCAGGCTGGAGT  80034          CG
                                ACTCCAGCCTGGG  ACAGA
                                ||||||||||||  |||||
                                TGAGGTCGGACCC  TGTCT
                                     AT
GAM475  FEZ1    3'  TTCTATCGCCCAGGCTGGAGT  42877          C
                                ACTCCAGCCTGGGCGA AGAG
                                |||||||||||||||| ||||
                                TGAGGTCGGACCCGCT TCTT
                                      A
GAM475  FGD1    5'  CTGCCCCCGCGGCTGGAG    16752       _  CGA
                                CTCCAGCC TGGG   CAG
                                |||||||| ||||   |||
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                                GAGGTCGG GCCC   GTC
                                    C    CC_
GAM475  FGF5    3'  TTGCTCTGTCACCAGGCTGGAG 16767          GC
            T                    ACTCCAGCCTGG  GACAGAGCAA
                                 ||||||||||||  ||||||||||
                                 TGAGGTCGGACC  CTGTCTCGTT
                                       A_
GAM475  FGF5    3'  TTGCTCTGTCACCAGGCTGGAG 53675          GC
            T                    ACTCCAGCCTGG  GACAGAGCAA
                                 ||||||||||||  ||||||||||
                                 TGAGGTCGGACC  CTGTCTCGTT
                                       A_
GAM475  FHL2    5'  GCTTTGTCGCCCAGGCTGGAGT 9368
                                 ACTCCAGCCTGGGCGACAGAGC
                                 |||||||||||||||||||||
                                 TGAGGTCGGACCCGCTGTTTCG

GAM475  FSHPRH1  5'  TTGCTCTGTCACCCAGGCTGGA 23071           C
            GT                   ACTCCAGCCTGGG GACAGAGCAA
                                 ||||||||||||| ||||||||||
                                 TGAGGTCGGACCC CTGTCTCGTT
                                       A
GAM475  FUT1    3'  GCTCTGTTGCCCAGGCTGGAGT 5600
                                 ACTCCAGCCTGGGCGACAGAGC
                                 |||||||||||||||||||||
                                 TGAGGTCGGACCCGTTGTCTCG

GAM475  FUT1    3'  TTGCTCTGTAGCCCAGGCCAGA 5617      CA      G
            GT                   ACTC  GCCTGGGC ACAGAGCAA
                                 ||||  |||||||| |||||||||
                                 TGAG  CGGACCCG TGTCTCGTT
                                   AC       A
GAM475  G1P3    3'  CTATATTGTCCAGGCTAGAGT  10743     C       CAG
                                 ACTC AGCCTGGGCGA   AG
                                 |||| ||||||||||   ||
                                 TGAG TCGGACCTGTT   TC
                                   A          ATA
GAM475  G1P3    3'  CTATATTGTCCAGGCTAGAGT  43454     C       CAG
                                 ACTC AGCCTGGGCGA   AG
                                 |||| ||||||||||   ||
                                 TGAG TCGGACCTGTT   TC
                                   A          ATA
GAM475  G1P3    3'  CTATATTGTCCAGGCTAGAGT  43458     C       CAG
                                 ACTC AGCCTGGGCGA   AG
                                 |||| ||||||||||   ||
                                 TGAG TCGGACCTGTT   TC
                                   A          ATA
GAM475  G6PC    3'  CTATCACCCAGGCTGGAGT   5659           C  C
                                 ACTCCAGCCTGGG GA AG
                                 ||||||||||||| || ||
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                                TGAGGTCGGACCC CT TC
                                      A  A
GAM475  G6PC     3'  TCACAAGCCCAGGCTGGAG   5663            GACA
                                CTCCAGCCTGGGC   GA
                                ||||||||||||   ||
                                GAGGTCGGACCCG   CT
                                      AACA
GAM475  GABRR2   5'  TTGCTCTGCCACAGGCTACTGG 10754     ___   _  GAC
              A                  TCCA  GCCTG GGC  AGAGCAA
                                ||||  ||||| |||  |||||||
                                AGGT  CGGAC CCG  TCTCGTT
                                  CAT   A  ___
GAM475  GAS11    3'  GCTCTGTTGAGGGCTGGG    9430         GGG
                                TCCAGCCT  CGACAGAGC
                                ||||||||  |||||||||
                                GGGTCGGG  GTTGTCTCG
                                    A__
GAM475  GHR      3'  GCTCTGTCGCCAGGCTAGAGT  5703      C     G
                                ACTC AGCCTGG CGACAGAGC
                                |||| ||||||| |||||||||
                                TGAG TCGGACC GCTGTCTCG
                                  A     _
GAM475  GM2A     3'  CTTTGTCACCAGGCTGGAGT  68381          GC
                                ACTCCAGCCTGG  GACAGAG
                                ||||||||||||  |||||||
                                TGAGGTCGGACC  CTGTTTC
                                      A_
GAM475  GPR4     3'  CTGTGTTGCCCAGGCTGGAGT  60577              G
                                ACTCCAGCCTGGGCGACA AG
                                |||||||||||||||||| ||
                                TGAGGTCGGACCCGTTGT TC
                                        G
GAM475  GPR56    5'  GCTCTGTCACACAGGCTGGAGT 20274          GGC
                                ACTCCAGCCTG  GACAGAGC
                                ||||||||||   ||||||||
                                TGAGGTCGGAC  CTGTCTCG
                                      ACA
GAM475  GPR81    3'  CTCTGTGTCCCAGGCTGGAGT  51748           CG
                                ACTCCAGCCTGGG  ACAGAG
                                ||||||||||||  ||||||
                                TGAGGTCGGACCC  TGTCTC
                                      TG
GAM475  GRAF     3'  CTCTGTGGCCCAGGCTGGAGT  31235            G
                                ACTCCAGCCTGGGC ACAGAG
                                |||||||||||||| ||||||
                                TGAGGTCGGACCCG TGTCTC
                                        G
GAM475  GRINL1A  3'  TTGCTCTGTCGCCCAGGCTGGA 70074
              GT                  ACTCCAGCCTGGGCGACAGAGCAA
                                ||||||||||||||||||||||||
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                                TGAGGTCGGACCCGCTGTCTCGTT

GAM475  HCS      3'  CTCTTGTTGCCCAGGCTGGAGT 38977                  _
                                ACTCCAGCCTGGGCGACA GAG
                                |||||||||||||||||| |||
                                TGAGGTCGGACCCGTTGT CTC
                                          T
GAM475  HCS      3'  CTGTGTCGCCAAGGCTGGAGT  38978          G      G
                                ACTCCAGCCT GGCGACA AG
                                |||||||||| ||||||| ||
                                TGAGGTCGGA CCGCTGT TC
                                      A      G
GAM475  HCS      3'  GCCCTTTTCGCCCAGGCTGAGT 38984      C         C_  A
                                ACTC AGCCTGGGCGA  AG GC
                                |||| ||||||||||  || ||
                                TGAG TCGGACCCGCT  TC CG
                                  _         TT  C
GAM475  HLCS     5'  GTTCTGTCGTCCAGGCTGGAGT 6418
                                ACTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||
                                TGAGGTCGGACCTGCTGTCTTG

GAM475  HMG20A   3'  TTGCTGTGTTGCCCAGGCTGGA 37074                 G
          GT                      ACTCCAGCCTGGGCGACA AGCAA
                                |||||||||||||||| |||||
                                TGAGGTCGGACCCGTTGT TCGTT
                                          G
GAM475  HOXB13   3'  TGCCAAGCCCAGGCTGGGG   22063           GACAGA
                                CTCCAGCCTGGGC     GCA
                                ||||||||||||     |||
                                GGGGTCGGACCCG     CGT
                                      AAC___
GAM475  HOXD4    3'  TGCAGTCCCTAGGCTG      28265         C   AGA
                                CAGCCTGGG GAC   GCA
                                ||||||||| |||   |||
                                GTCGGATCC CTG   CGT
                                     _  A__
GAM475  HTR1D    3'  TTGCCCTCTCGCCAGGCTGGAG 7852           G   C  A
          T                      ACTCCAGCCTGG CGA AG GCAA
                                |||||||||||| ||| || ||||
                                TGAGGTCGGACC GCT TC CGTT
                                      _  C  C
GAM475  HTR1E    5'  TCAGTCGCCCAGGCTGGAGT   7866              A
                                ACTCCAGCCTGGGCGAC GA
                                |||||||||||||||| ||
                                TGAGGTCGGACCCGCTG CT
                                          A
GAM475  HUNK     3'  TTGCTCTGTCACCCAGGCTGGA 28197           C
          GT                      ACTCCAGCCTGGG GACAGAGCAA
                                |||||||||||| ||||||||||
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                                TGAGGTCGGACCC CTGTCTCGTT
                                        A
GAM475  HYAL4    5'  CTCTGTTGCCCAGGCTGGAGT  25368
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTC

GAM475  ICAM1    3'  GCTCTGTCACCCAGGCTGGAGT 72039            C
                                ACTCCAGCCTGGG GACAGAGC
                                |||||||||||| ||||||||
                                TGAGGTCGGACCC CTGTCTCG
                                        A
GAM475  IFNAR2   3'  GTTCTGTCGCCCAAGCTGGAG  7905         C
                                CTCCAGC TGGGCGACAGAGC
                                ||||||| ||||||||||||
                                GAGGTCG ACCCGCTGTCTTG
                                    A
GAM475  IGF1     3'  CTGTCCCCCAGGCTGGAGT    7073             C
                                ACTCCAGCCTGGG GACAG
                                |||||||||||| |||||
                                TGAGGTCGGACCC CTGTC
                                        C
GAM475  IL11     3'  GCTCTGTTGCCTAGGCTGGAGT 7189
                                ACTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||
                                TGAGGTCGGATCCGTTGTCTCG

GAM475  INMT     3'  GCTCTGTCACCCAGGCTAGAGT 23218      C       C
                                ACTC AGCCTGGG GACAGAGC
                                |||| |||||||| ||||||||
                                TGAG TCGGACCC CTGTCTCG
                                  A       A
GAM475  INMT     3'  GCTCTGTCGCCCAGGCTGGAGT 23219
                                ACTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTCG

GAM475  ITGAM    3'  GCTCTGTCACCCAGGCTGGAGT 72313            C
                                ACTCCAGCCTGGG GACAGAGC
                                |||||||||||| ||||||||
                                TGAGGTCGGACCC CTGTCTCG
                                        A
GAM475  JRK      3'  CTCTGTTGACCAGGCTGGAGT  87825          G
                                ACTCCAGCCTGG CGACAGAG
                                |||||||||||| ||||||||
                                TGAGGTCGGACC GTTGTCTC
                                        A
GAM475  KMO      3'  CTCTGTTGACCAGGCTGGAGT  14843          G
                                ACTCCAGCCTGG CGACAGAG
                                |||||||||||| ||||||||
```

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                                TGAGGTCGGACC GTTGTCTC
                                       A
GAM475  LILRA3   3'  TTGCTCTGTCACCAGGCTGGA  97023          GC
                                TCCAGCCTGG  GACAGAGCAA
                                ||||||||||  ||||||||||
                                AGGTCGGACC  CTGTCTCGTT
                                       A_
GAM475  LLGL1    3'  TGCCCTGCTCGGAGCTGGAGT  67424         _     GAC  A
                                ACTCCAGC CTGGGC   AG GCA
                                |||||||| ||||||   || |||
                                TGAGGTCG GGCTCG   TC CGT
                                     A      ____  C
GAM475  LLGL1    3'  TTGCTCTGTCGCCCAGGCTGGA 67426
              GT                  ACTCCAGCCTGGGCGACAGAGCAA
                                ||||||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTCGTT

GAM475  LTB4R    5'  GCTCTGTCATTCAGGCTGGAGT 7467             C
                                ACTCCAGCCTGGG GACAGAGC
                                |||||||||||| ||||||||
                                TGAGGTCGGACTT CTGTCTCG
                                       A
GAM475  LYZ      3'  GCTCTGTCGCCCAGGCTGGAGT 5897
                                ACTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTCG

GAM475  LZTS1    3'  TTGCTCTGTCCCCCAGGCTGGA 41043            C
              GT                  ACTCCAGCCTGGG GACAGAGCAA
                                |||||||||||| ||||||||||
                                TGAGGTCGGACCC CTGTCTCGTT
                                       C
GAM475  MAD1L1   3'  TGCCCCGCCAGCCACAGGCTGG 88872         _  GACAGA_
              G                   TCCAGCCTG GGC      GCA
                                |||||||| |||      |||
                                GGGTCGGAC CCG      CGT
                                     A  ACCGCCC
GAM475  MAGEA3   5'  GCCTGTTGCCCTGACCAGAGT  19317     CAGCCT       A
                                ACTC     GGGCGACAG GC
                                ||||     ||||||||| ||
                                TGAG     CCCGTTGTC CG
                                  ACCAGT       _
GAM475  MAK      3'  CTCTTGTGTCCAGGCTGGAGT  20946            AC
                                ACTCCAGCCTGGGCG  AGAG
                                ||||||||||||||  ||||
                                TGAGGTCGGACCTGT  TCTC
                                       GT
GAM475  MDM2     3'  TTGCTCTGTTACCCAGGCTGGA 23465            CG
              GT                  ACTCCAGCCTGGG  ACAGAGCAA
                                ||||||||||||  |||||||||
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                                TGAGGTCGGACCC  TGTCTCGTT
                                       AT
GAM475  MDM2    3'  TTGCTCTGTTACCCAGGCTGGA 23478          CG
            GT                   ACTCCAGCCTGGG  ACAGAGCAA
                                ||||||||||||  |||||||||
                                TGAGGTCGGACCC  TGTCTCGTT
                                       AT
GAM475  MDM2    3'  TTGCTCTGTTACCCAGGCTGGA 23491          CG
            GT                   ACTCCAGCCTGGG  ACAGAGCAA
                                ||||||||||||  |||||||||
                                TGAGGTCGGACCC  TGTCTCGTT
                                       AT
GAM475  MDM2    3'  TTGCTCTGTTACCCAGGCTGGA 23505          CG
            GT                   ACTCCAGCCTGGG  ACAGAGCAA
                                ||||||||||||  |||||||||
                                TGAGGTCGGACCC  TGTCTCGTT
                                       AT
GAM475  MDM2    3'  TTGCTCTGTTACCCAGGCTGGA 11503          CG
            GT                   ACTCCAGCCTGGG  ACAGAGCAA
                                ||||||||||||  |||||||||
                                TGAGGTCGGACCC  TGTCTCGTT
                                       AT
GAM475  MDM4    3'  CTGTCTCCCAGGCTGAAGT   11510    C       C
                                ACT CAGCCTGGG GACAG
                                ||| ||||||||| |||||
                                TGA GTCGGACCC CTGTC
                                  A       T
GAM475  MEF2A   5'  CTCTACCCCCCAGGCTGAAGT  19999    C       CGAC
                                ACT CAGCCTGGG   AGAG
                                ||| |||||||||   ||||
                                TGA GTCGGACCC   TCTC
                                  A       CCCA
GAM475  MEFV    3'  TTGCTCTGTGGCCCAGGCTGGA 5957            G
            GT                   ACTCCAGCCTGGGC ACAGAGCAA
                                ||||||||||||| |||||||||
                                TGAGGTCGGACCCG TGTCTCGTT
                                       G
GAM475  MEFV    3'  TTGCTCTTGTCACCCAGGCTGG 5958           C  _
            AGT                   ACTCCAGCCTGGG GACA GAGCAA
                                ||||||||||||| |||| ||||||
                                TGAGGTCGGACCC CTGT CTCGTT
                                       A   T
GAM475  MHC2TA  3'  CTCTTATGCCCACGCTGGAGT  5979        C     AC
                                ACTCCAGC TGGGCG  AGAG
                                |||||||| ||||||  ||||
                                TGAGGTCG ACCCGT  TCTC
                                    C     AT
GAM475  MHC2TA  3'  CTGTTGCCCAGGCTGGCGT   5982     T
                                AC CCAGCCTGGGCGACAG
                                || ||||||||||||||||
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                                TG GGTCGGACCCGTTGTC
                                 C
GAM475  MICB     3'  CTCTGTCACCCAGGCTGCAGT  21022     C       C
                                ACT CAGCCTGGG GACAGAG
                                ||| ||||||||| |||||||
                                TGA GTCGGACCC CTGTCTC
                                  C        A
GAM475  MLANA    3'  GCTTTTGTTGCCCAGGCTGGAG 19765                 _
              T                  ACTCCAGCCTGGGCGACAGA GC
                                ||||||||||||||||||| ||
                                TGAGGTCGGACCCGTTGTTT CG
                                              T
GAM475  MN1      5'  GCTCTGTCGGTGCCCGGC    11655     T   ___
                                GCC GGGC   GACAGAGC
                                ||| ||||   ||||||||
                                CGG CCCG   CTGTCTCG
                                  _    TGG
GAM475  MPL      3'  CTCTGTCACCCAGGCTGCAGT  19352     C       C
                                ACT CAGCCTGGG GACAGAG
                                ||| ||||||||| |||||||
                                TGA GTCGGACCC CTGTCTC
                                  C        A
GAM475  MRPL49   3'  CTCTGTTGCCCAGGGTGGAGT  70166       G
                                ACTCCA CCTGGGCGACAGAG
                                |||||| ||||||||||||||
                                TGAGGT GGACCCGTTGTCTC
                                   G
GAM475  MTR      3'  GCTCTGTCGCCCAGGCTGGAGT 6021
                                ACTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTCG

GAM475  MYCL2    3'  TTGTCGCCCAGGCTGGAG    19384
                                CTCCAGCCTGGGCGACAG
                                ||||||||||||||||||
                                GAGGTCGGACCCGCTGTT

GAM475  MYD88    3'  TTGCTCCACTTTCAGCCAGGCT 11734          GC  CA___
              GGAG                  CTCCAGCCTGG  GA    GAGCAA
                                ||||||||||  ||    ||||||
                                GAGGTCGGACC  CT    CTCGTT
                                       GA  TTCAC
GAM475  NCKAP1   5'  GCTCTGTCGCCGGCGCGGG   26468     A_   TG
                                TCC  GCC  GGCGACAGAGC
                                |||  |||  ||||||||||
                                GGG  CGG  CCGCTGTCTCG
                                  CG   __
GAM475  NCOA6    5'  GCTCTGTCACCGAGGCTGGAGT 26839          G  C
                                ACTCCAGCCT GG GACAGAGC
                                |||||||||| || ||||||||
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                                TGAGGTCGGA CC CTGTCTCG
                                      G  A
GAM475  NCOA6    5'  TTGCTCTGTCGCCCAGGCTGGA 26853
                GT                    ACTCCAGCCTGGGCGACAGAGCAA
                                      ||||||||||||||||||||||||
                                      TGAGGTCGGACCCGCTGTCTCGTT

GAM475  NCOA6IP  3'  CTTTTACCGCCCAGGCTGGAGT 46154              AC_
                                      ACTCCAGCCTGGGCG   AGAG
                                      ||||||||||||||   ||||
                                      TGAGGTCGGACCCGC   TTTC
                                            CAT
GAM475  NCOA6IP  3'  TGTTGCCCAGGCTGGTGT    46160    T
                                      AC CCAGCCTGGGCGACA
                                      || ||||||||||||||
                                      TG GGTCGGACCCGTTGT
                                       T
GAM475  NDRG3    3'  CTGTTACCCAGGCTGGAGT    50121           CG
                                      ACTCCAGCCTGGG  ACAG
                                      ||||||||||||  ||||
                                      TGAGGTCGGACCC  TGTC
                                            AT
GAM475  NEU3     5'  GCTCTGTCACCCAGGCTGGAGT 22829            C
                                      ACTCCAGCCTGGG GACAGAGC
                                      |||||||||||| ||||||||
                                      TGAGGTCGGACCC CTGTCTCG
                                            A
GAM475  NGFR     3'  CTGCCGACCGAGGCTGGAG    11795         G _ A
                                      CTCCAGCCT GG CG CAG
                                      ||||||||| || || |||
                                      GAGGTCGGA CC GC GTC
                                           G  A  C
GAM475  NONO     3'  CTCTGTCGCCCAGGCTGGAGT  82888
                                      ACTCCAGCCTGGGCGACAGAG
                                      ||||||||||||||||||||
                                      TGAGGTCGGACCCGCTGTCTC

GAM475  NPEPPS   3'  CTCTATCCAGGCTGGG      63783          CGAC
                                      TCCAGCCTGGG    AGAG
                                      ||||||||||    ||||
                                      GGGTCGGACCT    TCTC
                                            A___
GAM475  NPR2L    3'  CTCTGTTACCCAGGCTGGA    22595          CG
                                      TCCAGCCTGGG  ACAGAG
                                      ||||||||||  ||||||
                                      AGGTCGGACCC  TGTCTC
                                            AT
GAM475  NQO1     3'  TTGCTCTGTTACCCAGGCTGGA 8059            CG
                GT                    ACTCCAGCCTGGG  ACAGAGCAA
                                      ||||||||||||  |||||||||
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                                TGAGGTCGGACCC  TGTCTCGTT
                                       AT
GAM475  NT5C2    5'  GCTCTGCTGCCCAGGCTGGAGT 25264            A
                                ACTCCAGCCTGGGCG CAGAGC
                                |||||||||||||| ||||||
                                TGAGGTCGGACCCGT GTCTCG
                                       C
GAM475  ORC1L    3'  TTGCTCTGTCGCCCAGGCTGGA 15990
              GT                  ACTCCAGCCTGGGCGACAGAGCAA
                                |||||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTCGTT

GAM475  PAICS    3'  CTGTCGCCCAGGCTGGAGT   22262
                                ACTCCAGCCTGGGCGACAG
                                |||||||||||||||||
                                TGAGGTCGGACCCGCTGTC

GAM475  PCDHA9   3'  GCTCTGTTGCCCAGGCTGGAGT 26623
                                ACTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTCG

GAM475  PCDHA9   3'  TTCTGCCACCCAGGCTGGAGT  26632          CGA
                                ACTCCAGCCTGGG  CAGAG
                                ||||||||||||  |||||
                                TGAGGTCGGACCC  GTCTT
                                       ACC
GAM475  PCDHB11  3'  CTGTCGCCCTGGCTGGAGT   38923        T
                                ACTCCAGCC GGGCGACAG
                                ||||||||| |||||||||
                                TGAGGTCGG CCCGCTGTC
                                      T
GAM475  PCDHB16  3'  CTCTTGTCACCCAGGCTGGAGT 40906          C  _
                                ACTCCAGCCTGGG GACA GAG
                                |||||||||||| |||| |||
                                TGAGGTCGGACCC CTGT CTC
                                       A   T
GAM475  PCDHB9   3'  GCTCTGTCGCCCAGGCTGGAGT 39447
                                ACTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTCG

GAM475  PDCL     3'  GCTCTGTCACCCAGGCTGGAGT 19399          C
                                ACTCCAGCCTGGG GACAGAGC
                                |||||||||||| ||||||||
                                TGAGGTCGGACCC CTGTCTCG
                                       A
GAM475  PDE6B    3'  TTGCTCTGTCACCCAGGCTGGA 6082           C
              GT                  ACTCCAGCCTGGG GACAGAGCAA
                                |||||||||||| ||||||||||
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                                TGAGGTCGGACCC CTGTCTCGTT
                                      A
GAM475  PDZK1    5'  TTCTGTTGCCCAGGCTGGAGT  12037
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTT

GAM475  PIGR     3'  CTGTCGCCCAGGCTGGAGT   72997
                                ACTCCAGCCTGGGCGACAG
                                |||||||||||||||||||
                                TGAGGTCGGACCCGCTGTC

GAM475  PIK3C2B  3'  GCCCTGTCGCCAGGCTGGAGT  12104          G     A
                                ACTCCAGCCTGG CGACAG GC
                                |||||||||||| |||||| ||
                                TGAGGTCGGACC GCTGTC CG
                                      _     C
GAM475  PIK3CD   3'  CTCTGTTGCCCAGGCTGGAGT  18490
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTC

GAM475  PKNOX1   3'  TTGCTCTTGTTGCCCAGGCTGG 17105                 _
           AG                     CTCCAGCCTGGGCGACA GAGCAA
                                ||||||||||||||| ||||||
                                GAGGTCGGACCCGTTGT CTCGTT
                                      T
GAM475  PMCHL1   3'  CTCTGTTGCCCAGGCTGGAGT  49915
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTC

GAM475  PON1     3'  CTCTGTTGCCCAGGCTGGAGT  6536
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTC

GAM475  POU2AF1  3'  CTCCATTGCCCAGGCTGGAGT  21741              CA
                                ACTCCAGCCTGGGCGA  GAG
                                ||||||||||||||  |||
                                TGAGGTCGGACCCGTT  CTC
                                      AC
GAM475  PPID     3'  TTGCTCTGTCACCCAGGCTGGA 88833            C
           GT                     ACTCCAGCCTGGG GACAGAGCAA
                                |||||||||||| ||||||||||
                                TGAGGTCGGACCC CTGTCTCGTT
                                      A
GAM475  PPP1R12B 5'  CTCTGCTCCGGGCTGAAG    50387    C       CGA
                                CT CAGCCTGGG   CAGAG
                                || |||||||||   |||||
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                                GA GTCGGGCCT   GTCTC
                                 A        C__
GAM475  PRKR     3'  GCTCTGTTGCCCAGGCTGGAGT 12348
                                ACTCCAGCCTGGGCGACAGAGC
                                ||||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTCG

GAM475  PRKWNK3  3'  CTCTGTCACCCAGGTTGGAGT  62232            C
                                ACTCCAGCCTGGG GACAGAG
                                |||||||||||| |||||||
                                TGAGGTTGGACCC CTGTCTC
                                       A
GAM475  PSMB2    3'  CTCTAGCCCAGGCTGGAGT   12469            GAC
                                ACTCCAGCCTGGGC   AGAG
                                ||||||||||||||   ||||
                                TGAGGTCGGACCCG   TCTC
                                       A__
GAM475  PSMD9    3'  TTGCTTTGTCACCCAGGCTGGA 12532           C
                GT                ACTCCAGCCTGGG GACAGAGCAA
                                ||||||||||||| ||||||||||
                                TGAGGTCGGACCC CTGTTTCGTT
                                       A
GAM475  PTGES    3'  TTGCTCTGTTGCCCAAGCTGGA 18076         C
                GT                ACTCCAGC TGGGCGACAGAGCAA
                                ||||||||| ||||||||||||||
                                TGAGGTCG ACCCGTTGTCTCGTT
                                    A
GAM475  PTGIS    3'  GCTCTGCTGCCCAGGCTAGAGT 8215       C        A
                                ACTC AGCCTGGGCG CAGAGC
                                |||| |||||||||| ||||||
                                TGAG TCGGACCCGT GTCTCG
                                  A        C
GAM475  RAB36    3'  CTCTGTCACCCAGGCTGGAGT  18166           C
                                ACTCCAGCCTGGG GACAGAG
                                |||||||||||| |||||||
                                TGAGGTCGGACCC CTGTCTC
                                       A
GAM475  RAB36    3'  TTGTTGCCCAGGCTGGAGT   18188
                                ACTCCAGCCTGGGCGACAG
                                |||||||||||||||||||
                                TGAGGTCGGACCCGTTGTT

GAM475  RABL2A   3'  GCTCTGTCGCCAGGCTGGAGT  26409           G
                                ACTCCAGCCTGG CGACAGAGC
                                |||||||||||| |||||||||
                                TGAGGTCGGACC GCTGTCTCG
                                        _
GAM475  RABL2B   3'  GCTCTGTCGCCAGGCTGGAGT  23980           G
                                ACTCCAGCCTGG CGACAGAGC
                                |||||||||||| |||||||||
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                                TGAGGTCGGACC GCTGTCTCG
                                          _
GAM475  RAI3    3'  TTGCTCTGTCACCCAGGCTTGA 15624      C       C
              GT                  ACTC AGCCTGGG GACAGAGCAA
                                  |||| |||||||| ||||||||||
                                  TGAG TCGGACCC CTGTCTCGTT
                                    T       A
GAM475  RBBP9   3'  TTGCTCTGTCTCCCAGGCTGGA 70705           C
              G                   CTCCAGCCTGGG GACAGAGCAA
                                  |||||||||||| ||||||||||
                                  GAGGTCGGACCC CTGTCTCGTT
                                         T
GAM475  RERE    3'  TGCCCTCGTTTCCAGGCTGCAG 25023    C       C  _  A
                                  CT CAGCCTGGG GAC AG GCA
                                  || ||||||||| ||| || |||
                                  GA GTCGGACCT TTG TC CGT
                                   C        _  C  C
GAM475  RHD     3'  CTCTGTCACCAGGCTGGAGT  32826          GC
                                  ACTCCAGCCTGG  GACAGAG
                                  ||||||||||||  |||||||
                                  TGAGGTCGGACC  CTGTCTC
                                         A_
GAM475  RHD     3'  CTCTGTCACCCAGGCTAGAGT  32827     C       C
                                  ACTC AGCCTGGG GACAGAG
                                  |||| |||||||| |||||||
                                  TGAG TCGGACCC CTGTCTC
                                    A       A
GAM475  RHD     3'  CTCTGTCACCAGGCTGGAGT  33141          GC
                                  ACTCCAGCCTGG  GACAGAG
                                  ||||||||||||  |||||||
                                  TGAGGTCGGACC  CTGTCTC
                                         A_
GAM475  RHD     3'  CTCTGTCACCCAGGCTAGAGT  33142     C       C
                                  ACTC AGCCTGGG GACAGAG
                                  |||| |||||||| |||||||
                                  TGAG TCGGACCC CTGTCTC
                                    A       A
GAM475  RP2     3'  CTCTTGTTGCCCAAGCTGGAGT 23601        C       _
                                  ACTCCAGC TGGGCGACA GAG
                                  |||||||| ||||||||| |||
                                  TGAGGTCG ACCCGTTGT CTC
                                      A       T
GAM475  RPH3AL  3'  GCTTTGTTGCCCAGGCTGGGGT 23736
                                  ACTCCAGCCTGGGCGACAGAGC
                                  |||||||||||||||||||||||
                                  TGGGGTCGGACCCGTTGTTTCG

GAM475  RPP30   3'  GCTCTGTCCCCCAGGCTGGAGT 22201          C
                                  ACTCCAGCCTGGG GACAGAGC
                                  |||||||||||| ||||||||
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                                TGAGGTCGGACCC CTGTCTCG
                                       C
GAM475  SAS      3'  TTGCTCTGTTGCCCAGGCTGGA 21111
              GT                  ACTCCAGCCTGGGCGACAGAGCAA
                                  |||||||||||||||||||||||||
                                  TGAGGTCGGACCCGTTGTCTCGTT

GAM475  SCML2    3'  CTCTTGTGCCCAGGCTGGAGT  21424            AC
                                  ACTCCAGCCTGGGCG  AGAG
                                  |||||||||||||||  ||||
                                  TGAGGTCGGACCCGT  TCTC
                                         GT
GAM475  SEDL     3'  CTCTGTTGCCAGGCTGGAGT   28096          G
                                  ACTCCAGCCTGG CGACAGAG
                                  |||||||||||| ||||||||
                                  TGAGGTCGGACC GTTGTCTC
                                              _
GAM475  SEDL     3'  GCTCTGTTGTCCAGGCTGGAGT 28100
                                  ACTCCAGCCTGGGCGACAGAGC
                                  |||||||||||||||||||||||
                                  TGAGGTCGGACCTGTTGTCTCG

GAM475  SEPN1    3'  TTGCTCTGTCACCCAGGCTGGA 66985           C
              GT                  ACTCCAGCCTGGG GACAGAGCAA
                                  |||||||||||| ||||||||||
                                  TGAGGTCGGACCC CTGTCTCGTT
                                         A
GAM475  SERPINB9 3'  CTCTGTCACCCAGGCTGGAGT  16018          C
                                  ACTCCAGCCTGGG GACAGAG
                                  |||||||||||| |||||||
                                  TGAGGTCGGACCC CTGTCTC
                                         A
GAM475  SERPINB9 3'  CTCTGTCGCCCAGGCTGGAGT  16019
                                  ACTCCAGCCTGGGCGACAGAG
                                  |||||||||||||||||||||
                                  TGAGGTCGGACCCGCTGTCTC

GAM475  SET      3'  TTGCTCTGCTGGAAGCTGGAG  13022       __ TG GCGA
                                  CTCCAGC  C  G   CAGAGCAA
                                  |||||||  |  |   ||||||||
                                  GAGGTCG  G  C   GTCTCGTT
                                      AA GT _____
GAM475  SH3BP2   3'  CTCTGTCGCCCAGGCTAGAGT  13066     C
                                  ACTC AGCCTGGGCGACAGAG
                                  |||| ||||||||||||||||
                                  TGAG TCGGACCCGCTGTCTC
                                    A
GAM475  SH3BP2   3'  CTGTCGCCCAGGCTGGAGT   13068
                                  ACTCCAGCCTGGGCGACAG
                                  |||||||||||||||||||
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                                TGAGGTCGGACCCGCTGTC

GAM475  SHOX    3'  TTGCTCTGTCACCCAGGCTGGA 23525          C
                G                CTCCAGCCTGGG GACAGAGCAA
                                 |||||||||||| ||||||||||
                                 GAGGTCGGACCC CTGTCTCGTT
                                        A
GAM475  SHOX    3'  TTGCTTTGTCGCCCAGGCTGGA 6589
                G                CTCCAGCCTGGGCGACAGAGCAA
                                 ||||||||||||||||||||||
                                 GAGGTCGGACCCGCTGTTTCGTT

GAM475  SIL     3'  TTGCTCTTGTAGCCCAGGCTGG 13166          G  _
                AGT                ACTCCAGCCTGGGC ACA GAGCAA
                                   |||||||||||||| ||| ||||||
                                   TGAGGTCGGACCCG TGT CTCGTT
                                          A  T
GAM475  SLA2    3'  TTGCCCTGTTGCCCATGCTGGA 50898        C       A
                GT                 ACTCCAGC TGGGCGACAG GCAA
                                   |||||||| |||||||||| ||||
                                   TGAGGTCG ACCCGTTGTC CGTT
                                       T       C
GAM475  SLC14A2  5'  TTGCTCTGTCACCCAGGCTGGA 24130          C
                GT                 ACTCCAGCCTGGG GACAGAGCAA
                                   |||||||||||| ||||||||||
                                   TGAGGTCGGACCC CTGTCTCGTT
                                          A
GAM475  SLC15A1  3'  TTGCTCTTGTTGTCCAGGCTGG 18651            _
                AGT                ACTCCAGCCTGGGCGACA GAGCAA
                                   |||||||||||||||| ||||||
                                   TGAGGTCGGACCTGTTGT CTCGTT
                                           T
GAM475  SLC39A1  5'  GCTCTGTTGCCCAGGCTGGAGT 27814
                                   ACTCCAGCCTGGGCGACAGAGC
                                   |||||||||||||||||||||
                                   TGAGGTCGGACCCGTTGTCTCG

GAM475  SMAC    5'  GCTCTGTTGCCCAGGCTGAAGT 58023    C
                                   ACT CAGCCTGGGCGACAGAGC
                                   ||| ||||||||||||||||
                                   TGA GTCGGACCCGTTGTCTCG
                                     A
GAM475  SMAC    5'  TGCCTCTGTCGCCCAGGCTGGA 58030              _
                GT                 ACTCCAGCCTGGGCGACAGAG CA
                                   |||||||||||||||||||| ||
                                   TGAGGTCGGACCCGCTGTCTC GT
                                          C
GAM475  SMG1    5'  TGCCCTGCGGGCTCAGGCGGA 31353    A      GA_  A
                                   TCC GCCTGGGC   CAG GCA
                                   ||| ||||||||   ||| |||
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                                AGG CGGACTCG   GTC CGT
                                  _      GGC   C
GAM475  SNAP23   3'  GCTCTCTTGTCCAGGCTGGAGT 56338              C
                                ACTCCAGCCTGGGCGA AGAGC
                                |||||||||||||||| |||||
                                TGAGGTCGGACCTGTT TCTCG
                                          C
GAM475  SNAP23   3'  GCTCTCTTGTCCAGGCTGGAGT 15141              C
                                ACTCCAGCCTGGGCGA AGAGC
                                |||||||||||||||| |||||
                                TGAGGTCGGACCTGTT TCTCG
                                          C
GAM475  SNX15    3'  GCTGTGTCGCCCAGACTGGAGT 74125        C         G
                                ACTCCAG CTGGGCGACA AGC
                                ||||||| |||||||||| |||
                                TGAGGTC GACCCGCTGT TCG
                                    A         G
GAM475  SPINT2   3'  GCCCTGTCGCCAAGAGGA    63851     AGC  G       A
                                TCC   CT GGCGACAG GC
                                |||   || |||||||| ||
                                AGG   GA CCGCTGTC CG
                                  A__  A       C
GAM475  SPN      3'  GCTTTGTCGCCCAGGCTGGAGT 13378
                                ACTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTTTCG

GAM475  SPTBN4   3'  TGCCCCAAGAAGCTGGGGT   48159         __  __
                                ACTCCAGC  CT  GGGCG
                                ||||||||  ||  |||||
                                TGGGGTCG  GA  CCCGT
                                    AA  AC
GAM475  SS18     3'  TTGCTCTTGTCGCCCAGGCTGG 20107                _
            AGT                   ACTCCAGCCTGGGCGACA GAGCAA
                                ||||||||||||||||| ||||||
                                TGAGGTCGGACCCGCTGT CTCGTT
                                          T
GAM475  STAU     5'  TTGCTCTTGTCGCCCAGGCTGG 17204                _
            AGT                   ACTCCAGCCTGGGCGACA GAGCAA
                                ||||||||||||||||| ||||||
                                TGAGGTCGGACCCGCTGT CTCGTT
                                          T
GAM475  SVIL     5'  TGCGTCCTCCCCAGGCTGAAGT 41709     C       C  CAGA
                                ACT CAGCCTGGG GA    GCA
                                ||| ||||||||| ||    |||
                                TGA GTCGGACCC CT    CGT
                                  A        _  CCTG
GAM475  TAF11    3'  TTGCTCTATCACCTAGGCTGGA 20124            C  C
            GT                    ACTCCAGCCTGGG GA AGAGCAA
                                ||||||||||||| || |||||||
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                                TGAGGTCGGATCC CT TCTCGTT
                                      A  A
GAM475  TAL1    3'  CTGTCACTCAGGCTGGAGT   13528          C
                                ACTCCAGCCTGGG GACAG
                                |||||||||||| |||||
                                TGAGGTCGGACTC CTGTC
                                      A
GAM475  TAPBP   3'  CTCTTCCGCCCAGGCTGCAGT  13560    C        AC
                                ACT CAGCCTGGGCG  AGAG
                                ||| ||||||||||  ||||
                                TGA GTCGGACCCGC  TCTC
                                  C         CT
GAM475  TAPBP   3'  GCTCTGTCGCCCAGGCTGGAGT 13569
                                ACTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTCG

GAM475  TAPBP   3'  GCTCTGTTGCCCAGGCTGGAGT 13570
                                ACTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTCG

GAM475  TAT     3'  TTGCTCTGTCGCCCATGCTGGA 6263         C
          GT                    ACTCCAGC TGGGCGACAGAGCAA
                                |||||||| ||||||||||||||
                                TGAGGTCG ACCCGCTGTCTCGTT
                                     T
GAM475  TBXA2R  3'  TTGCTCTGTCCCCCAGGCTGGA 8373           C
          GT                    ACTCCAGCCTGGG GACAGAGCAA
                                |||||||||||| |||||||||
                                TGAGGTCGGACCC CTGTCTCGTT
                                      C
GAM475  TCF2    3'  CTGTCACCCGAGCTGGAGT   22407        C   C
                                ACTCCAGC TGGG GACAG
                                |||||||| |||| |||||
                                TGAGGTCG GCCC CTGTC
                                     A   A
GAM475  TDGF1   3'  CTCTGTCACCCAGGCTGGA   13656          C
                                TCCAGCCTGGG GACAGAG
                                |||||||||| |||||||
                                AGGTCGGACCC CTGTCTC
                                      A
GAM475  TERF1   3'  CTCTGTTGCCCAGGCTGGAGT  34393
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTC

GAM475  TERF2   3'  GCTCTGTCACCCAGGCTGGAGT 20156           C
                                ACTCCAGCCTGGG GACAGAGC
                                |||||||||||| ||||||||
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                                TGAGGTCGGACCC CTGTCTCG
                                      A
GAM475  TIM3     3'  TTGCTCTGTTGCCCAGGCTGGA 52365
              GT                  ACTCCAGCCTGGGCGACAGAGCAA
                                  |||||||||||||||||||||||||
                                  TGAGGTCGGACCCGTTGTCTCGTT

GAM475  TJP1     5'  TTGCCCTGTGGTCCAGGCAGGA 13768      A      G   A
              GT                  ACTCC GCCTGGGC ACAG GCAA
                                  ||||| |||||||| |||| ||||
                                  TGAGG CGGACCTG TGTC CGTT
                                    A       G   C
GAM475  TLR5     5'  CTCTGCCGCCCAGGCTGGA   13787           A
                                  TCCAGCCTGGGCG CAGAG
                                  |||||||||||| |||||
                                  AGGTCGGACCCGC GTCTC
                                        C
GAM475  TMC1     5'  CTCTGTTGCCCAGGCTGGAGT  57709
                                  ACTCCAGCCTGGGCGACAGAG
                                  |||||||||||||||||||||
                                  TGAGGTCGGACCCGTTGTCTC

GAM475  TMPRSS3  3'  GCTCTGTTGCCCAGGCTGGAGT 51518
                                  ACTCCAGCCTGGGCGACAGAGC
                                  |||||||||||||||||||||||
                                  TGAGGTCGGACCCGTTGTCTCG

GAM475  TMPRSS3  3'  GCTCTGTTGCCCAGGCTGGAGT 51545
                                  ACTCCAGCCTGGGCGACAGAGC
                                  |||||||||||||||||||||||
                                  TGAGGTCGGACCCGTTGTCTCG

GAM475  TMPRSS3  3'  GCTCTGTTGCCCAGGCTGGAGT 44028
                                  ACTCCAGCCTGGGCGACAGAGC
                                  |||||||||||||||||||||||
                                  TGAGGTCGGACCCGTTGTCTCG

GAM475  TNFAIP2  3'  TTGCTGTGTTGCCCAGGCTGGA 21931             G
              GT                  ACTCCAGCCTGGGCGACA AGCAA
                                  |||||||||||||||| |||||
                                  TGAGGTCGGACCCGTTGT TCGTT
                                        G
GAM475  TNFRSF10B 3'  CTCTCTCGCCCAGGCTGGAGT  15224           C
                                  ACTCCAGCCTGGGCGA AGAG
                                  |||||||||||||| ||||
                                  TGAGGTCGGACCCGCT TCTC
                                        C
GAM475  TNFRSF10B 3'  CTCTGTCTCCCAGGCTGGAGT  15225          C
                                  ACTCCAGCCTGGG GACAGAG
                                  |||||||||||| |||||||
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                                TGAGGTCGGACCC CTGTCTC
                                        T
GAM475  TNFRSF11A 3'  TCTGGCCCAGGCTAGAGT    15197      C        GA
                                ACTC AGCCTGGGC  CAGA
                                |||| |||||||||  ||||
                                TGAG TCGGACCCG  GTCT
                                  A       __
GAM475  TNFRSF9   3'  CTCTGTCACCCAGGCTGGAGT  9583             C
                                ACTCCAGCCTGGG GACAGAG
                                |||||||||||| |||||||
                                TGAGGTCGGACCC CTGTCTC
                                        A
GAM475  TNFSF9    3'  TTGTTCTGTCAACCAGGCTAGA 15099    C      GC
                                TC AGCCTGG  GACAGAGCAA
                                || |||||||  ||||||||||
                                AG TCGGACC  CTGTCTTGTT
                                 A       AA
GAM475  TP53      3'  GCTTTGTTGCCCAGGCTGGAGT 6802
                                ACTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTTTCG

GAM475  TRAF5     3'  TTGTCACCCAGGCTGGAGT    17287            C
                                ACTCCAGCCTGGG GACAG
                                |||||||||||| |||||
                                TGAGGTCGGACCC CTGTT
                                        A
GAM475  TRIM9     5'  GCTCTGTCGCCCAGGCTGGG   31455
                                TCCAGCCTGGGCGACAGAGC
                                ||||||||||||||||||||
                                GGGTCGGACCCGCTGTCTCG

GAM475  TRIM9     5'  GCTCTTGTTGCTCAGACTGGAG 31456        C        _
          T                      ACTCCAG CTGGGCGACA GAGC
                                ||||||| |||||||||| ||||
                                TGAGGTC GACTCGTTGT CTCG
                                    A         T
GAM475  TRPM6     3'  CTCTTTTTACCCAGGCTGGAGT 35032            CG C_
                                ACTCCAGCCTGGG  A  AGAG
                                ||||||||||||  |  ||||
                                TGAGGTCGGACCC  T  TCTC
                                        AT TT
GAM475  TRPV1     3'  CTCTTCTCACCCAGGCTGGA   38694          C  C_
                                TCCAGCCTGGG GA  AGAG
                                |||||||||| ||  ||||
                                AGGTCGGACCC CT  TCTC
                                        A  CT
GAM475  TRPV1     3'  CTCTTGTTGCCCAGGCTGGAGT 38695                _
                                ACTCCAGCCTGGGCGACA GAG
                                |||||||||||||||| |||
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                                TGAGGTCGGACCCGTTGT CTC
                                       T
GAM475  TRPV1   3' CTCTTCTCACCCAGGCTGGA  55670        C  C_
                   TCCAGCCTGGG GA  AGAG
                   |||||||||| ||  ||||
                   AGGTCGGACCC CT  TCTC
                         A  CT
GAM475  TRPV1   3' CTCTTGTTGCCCAGGCTGGAGT 55671             _
                   ACTCCAGCCTGGGCGACA GAG
                   |||||||||||||||| |||
                   TGAGGTCGGACCCGTTGT CTC
                                       T
GAM475  TRPV1   3' CTCTTCTCACCCAGGCTGGA  55710        C  C_
                   TCCAGCCTGGG GA  AGAG
                   |||||||||| ||  ||||
                   AGGTCGGACCC CT  TCTC
                         A  CT
GAM475  TRPV1   3' CTCTTGTTGCCCAGGCTGGAGT 55711             _
                   ACTCCAGCCTGGGCGACA GAG
                   |||||||||||||||| |||
                   TGAGGTCGGACCCGTTGT CTC
                                       T
GAM475  TRPV1   3' CTCTTCTCACCCAGGCTGGA  55741        C  C_
                   TCCAGCCTGGG GA  AGAG
                   |||||||||| ||  ||||
                   AGGTCGGACCC CT  TCTC
                         A  CT
GAM475  TRPV1   3' CTCTTGTTGCCCAGGCTGGAGT 55742             _
                   ACTCCAGCCTGGGCGACA GAG
                   |||||||||||||||| |||
                   TGAGGTCGGACCCGTTGT CTC
                                       T
GAM475  TUFT1   3' CTCTGTCACCCAGGCTGGAGT  39673          C
                   ACTCCAGCCTGGG GACAGAG
                   |||||||||||| |||||||
                   TGAGGTCGGACCC CTGTCTC
                                A
GAM475  UGDH    3' CTGTTGCCCAGGCTGGAGT   13996
                   ACTCCAGCCTGGGCGACAG
                   |||||||||||||||||
                   TGAGGTCGGACCCGTTGTC

GAM475  UMPS    3' CTCTGTTGCCCAGGATGGAGT  6330       G
                   ACTCCA CCTGGGCGACAGAG
                   |||||| ||||||||||||||
                   TGAGGT GGACCCGTTGTCTC
                      A
GAM475  VENTX2  3' TTGCTCTGTCACCCAGGCTGGA 27871          C
           GT                ACTCCAGCCTGGG GACAGAGCAA
                             |||||||||||| ||||||||||
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                                TGAGGTCGGACCC CTGTCTCGTT
                                      A
GAM475  VHL     3'  CTCTGTTGCCCAGGCTGGAGT  6853
                                ACTCCAGCCTGGGCGACAGAG
                                ||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTC

GAM475  VIPR2   3'  TTGCTCTGTCGCCCAGGCTGGA 14078
                GT                ACTCCAGCCTGGGCGACAGAGCAA
                                  ||||||||||||||||||||||||
                                  TGAGGTCGGACCCGCTGTCTCGTT

GAM475  WHSC1   3'  CTGTTGGCCAGGCTGGAGT   56694          G
                                ACTCCAGCCTGG CGACAG
                                ||||||||||| ||||||
                                TGAGGTCGGACC GTTGTC
                                      G
GAM475  WIG1    5'  TTGCTCCGAGAAGAGGCTGGG  96106       GGG__  ACA
                                TCCAGCCT    CG   GAGCAA
                                ||||||||    ||   ||||||
                                GGGTCGGA    GC   CTCGTT
                                    GAAGA  ___
GAM475  XRCC2   3'  TTGCTCTGTCTCCCAGGCTGGA 19513           C
                GT                ACTCCAGCCTGGG GACAGAGCAA
                                  ||||||||||||| ||||||||||
                                  TGAGGTCGGACCC CTGTCTCGTT
                                        T
GAM475  YES1    3'  GCTCTGCCGCCCAGGCTGGAGT 19540            A
                                ACTCCAGCCTGGGCG CAGAGC
                                ||||||||||||||| ||||||
                                TGAGGTCGGACCCGC GTCTCG
                                       C
GAM475  ZNF133  5'  TTGCTCTGTTGCCCAGGCTGGA 14302
                GT                ACTCCAGCCTGGGCGACAGAGCAA
                                  ||||||||||||||||||||||||
                                  TGAGGTCGGACCCGTTGTCTCGTT

GAM475  ZNF157  3'  CTCTGTCACCCAGGCTGGAGT  14332           C
                                ACTCCAGCCTGGG GACAGAG
                                ||||||||||||| |||||||
                                TGAGGTCGGACCC CTGTCTC
                                      A
GAM475  ZNF253  3'  CTCTTGTCACCGAGGCTGGAGT 41078         G  C   _
                                ACTCCAGCCT GG GACA GAG
                                |||||||||| || |||| |||
                                TGAGGTCGGA CC CTGT CTC
                                     G  A   T
GAM475  ZNF264  3'  CTCTGTCACCCACGCTGGAGT  14210        C   C
                                ACTCCAGC TGGG GACAGAG
                                |||||||| |||| |||||||
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                                TGAGGTCG ACCC CTGTCTC
                                    C   A
GAM475  ZNF264   3'  CTCTGTCACCCAGGCTGGAGT  14211          C
                                ACTCCAGCCTGGG GACAGAG
                                |||||||||||| |||||||
                                TGAGGTCGGACCC CTGTCTC
                                      A
GAM475  20D7-FC4 5'  TCAGTCACCCAGGCTGGAGT   61571          C   A
                                ACTCCAGCCTGGG GAC GA
                                |||||||||||| ||| ||
                                TGAGGTCGGACCC CTG CT
                                      A   A
GAM475  AGMAT    3'  TTGCTTGTCACCCAGGCTGGAG 45746          C   G
          T                      ACTCCAGCCTGGG GACA AGCAA
                                |||||||||||| |||| |||||
                                TGAGGTCGGACCC CTGT TCGTT
                                      A   _
GAM475  ANKRD6   3'  TTGCTCTGTCACCCAGACTGGA 30776       C    C
          GT                      ACTCCAG CTGGG GACAGAGCAA
                                ||||||| ||||| ||||||||||
                                TGAGGTC GACCC CTGTCTCGTT
                                    A    A
GAM475  AP1S3    3'  CTCTGTCACCCAGGCTGGAGT  75426          C
                                ACTCCAGCCTGGG GACAGAG
                                |||||||||||| |||||||
                                TGAGGTCGGACCC CTGTCTC
                                      A
GAM475  AP3S2    3'  TTGCTCTGTCACCCAGGCTGGA 20660          C
          GT                      ACTCCAGCCTGGG GACAGAGCAA
                                |||||||||||| ||||||||||
                                TGAGGTCGGACCC CTGTCTCGTT
                                      A
GAM475  APOL2    3'  GCTCTATCGCCCAGGATGGAGT 48792       G       C
                                ACTCCA CCTGGGCGA AGAGC
                                |||||| ||||||||| |||||
                                TGAGGT GGACCCGCT TCTCG
                                   A       A
GAM475  APXL2    5'  CTTTGTCGCCAGGCTGGAGT   75679          G
                                ACTCCAGCCTGG CGACAGAG
                                |||||||||||| ||||||||
                                TGAGGTCGGACC GCTGTTTC
                                                _
GAM475  ARHF     3'  CTGTCACTCAGGCTAGAGT   39267      C       C
                                ACTC AGCCTGGG GACAG
                                |||| |||||||| |||||
                                TGAG TCGGACTC CTGTC
                                  A       A
GAM475  ARHGAP11A 3'  TGACTCTGTCGTCCAGGCTGGA 29461                  _
          GT                      ACTCCAGCCTGGGCGACAGAG CA
                                |||||||||||||||||||| ||
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                                TGAGGTCGGACCTGCTGTCTC GT
                                          A
GAM475  ARHGAP5  5'  CTCTTGTTGCCCAGGCTGGAGT 77600                  _
                                ACTCCAGCCTGGGCGACA GAG
                                |||||||||||||||||| |||
                                TGAGGTCGGACCCGTTGT CTC
                                          T
GAM475  ASB16    5'  CTCTGTCGCCCAGGCTGGAGT  70488
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTC

GAM475  ASB16    3'  CTCTGTGGCCCAGGCTGAAGT  70489     C        G
                                ACT CAGCCTGGGC ACAGAG
                                ||| |||||||||| ||||||
                                TGA GTCGGACCCG TGTCTC
                                  A         G
GAM475  ASB16    3'  CTCTGTTGCCCAGGCTGGAGT  55981
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTC

GAM475  ASE-1    3'  GCTCTGTCGCCCAGGTTGGAGT 24982
                                ACTCCAGCCTGGGCGACAGAGC
                                ||||||||||||||||||||||
                                TGAGGTTGGACCCGCTGTCTCG

GAM475  ASE-1    3'  TGTCACCCAGGCTGGAGT    24999           C
                                ACTCCAGCCTGGG GACA
                                |||||||||||| ||||
                                TGAGGTCGGACCC CTGT
                                          A
GAM475  ATP1B4   3'  GCTGTTGTCACCCAGGCTGGAG 24846           C    _
              T                  ACTCCAGCCTGGG GACAG AGC
                                ||||||||||||| ||||| |||
                                TGAGGTCGGACCC CTGTT TCG
                                          A    G
GAM475  BA108L7.2 3'  CTATTTTGCCCAGGCTGGAGT  49072             CAG
                                ACTCCAGCCTGGGCGA   AG
                                ||||||||||||||||  ||
                                TGAGGTCGGACCCGTT   TC
                                          TTA
GAM475  BMF      3'  TGCCAGGCCCAGGCTGGG    54288          GACAGA
                                TCCAGCCTGGGC     GCA
                                ||||||||||||     |||
                                GGGTCGGACCCG     CGT
                                       GAC___
GAM475  BNIP-S   3'  GCTCTGTCGCCAGGCTGGAGT  57091           G
                                ACTCCAGCCTGG CGACAGAGC
                                |||||||||||| |||||||||
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                                TGAGGTCGGACC GCTGTCTCG
                                           _
GAM475  BTN3A1    3'  CTCTGTTGCTAGGCTGGAGT   23891          G
                                ACTCCAGCCTGG CGACAGAG
                                |||||||||||| ||||||||
                                TGAGGTCGGATC GTTGTCTC
                                           _
GAM475  C(27)-3BETA-HSD 3'  TTGCTCTGTCACCCAGACTGGA 48057       C    C
           GT                     ACTCCAG CTGGG GACAGAGCAA
                                |||||||| ||||| ||||||||||
                                TGAGGTC GACCC CTGTCTCGTT
                                   A    A
GAM475  C11orf17  3'  CTCTGTTGCCCAGGCTGGAGT  40580
                                ACTCCAGCCTGGGCGACAGAG
                                ||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTC

GAM475  C13orf1   3'  TTGTCACCCAGGCTAGAGT   40375     C      C
                                ACTC AGCCTGGG GACAG
                                |||| |||||||| |||||
                                TGAG TCGGACCC CTGTT
                                  A       A
GAM475  C1orf24   3'  GCTCTGTCGCCAAGGCTGGAGT 54794         G
                                ACTCCAGCCT GGCGACAGAGC
                                |||||||||| ||||||||||
                                TGAGGTCGGA CCGCTGTCTCG
                                      A
GAM475  C1QTNF6   3'  TTGCTCTGTTGCCCAGGCTAGA 49999     C
           GT                     ACTC AGCCTGGGCGACAGAGCAA
                                |||| ||||||||||||||||||
                                TGAG TCGGACCCGTTGTCTCGTT
                                  A
GAM475  C20orf160 3'  GCTCTGCCGGGCTGGGG     55525          GCGA
                                CTCCAGCCTGG    CAGAGC
                                ||||||||||    ||||||
                                GGGGTCGGGCC    GTCTCG
                                          ____
GAM475  C21orf25  3'  CTCTGTTGCCCAGGCTGGAGT  64291
                                ACTCCAGCCTGGGCGACAGAG
                                ||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTC

GAM475  C21orf67  5'  GCGCTGTCGCCCAGGCTGGAG  55231              A
                                CTCCAGCCTGGGCGACAG GC
                                |||||||||||||||| ||
                                GAGGTCGGACCCGCTGTC CG
                                        G
GAM475  C22orf19  3'  TTGCTCTGTTGTCCAGGCTGGA 14838
           GT                     ACTCCAGCCTGGGCGACAGAGCAA
                                ||||||||||||||||||||||||
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                                TGAGGTCGGACCTGTTGTCTCGTT

GAM475  C3F      3'  TTGCTTTGTCACCCACGCTGGA 20484       C    C
                                TCCAGC TGGG GACAGAGCAA
                                |||||| |||| ||||||||||
                                AGGTCG ACCC CTGTTTCGTT
                                   C    A
GAM475  C6orf33   3'  CTCTGTCGCCCAGGCTGGAGT  56714
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTC

GAM475  C6orf5    3'  CTCTTTCCCAGGCTGCAGT    31988     C        CGAC
                                ACT CAGCCTGGG    AGAG
                                ||| |||||||||    ||||
                                TGA GTCGGACCC    TCTC
                                  C        TT__
GAM475  C6orf5    3'  GCTCTGTCGTCCAGGCTGGAGT 31996
                                ACTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||||
                                TGAGGTCGGACCTGCTGTCTCG

GAM475  C9orf9    3'  CTCTGTCTCCCAGGCTGGAGT  39018            C
                                ACTCCAGCCTGGG GACAGAG
                                |||||||||||| |||||||
                                TGAGGTCGGACCC CTGTCTC
                                         T
GAM475  C9orf9    3'  GCTCTGTCGCCCAGGCTGGAGT 39025
                                ACTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTCG

GAM475  CAC-1     3'  TGCTCTGTGACCAGGCCAGGA  54296     A_     GCG
                                TCC  GCCTGG   ACAGAGCA
                                |||  ||||||   ||||||||
                                AGG  CGGACC   TGTCTCGT
                                  AC     AG_
GAM475  CARD6     3'  CTCTTGTTGCCCAGGCTGGAGT 51840                 _
                                ACTCCAGCCTGGGCGACA GAG
                                |||||||||||||||| |||
                                TGAGGTCGGACCCGTTGT CTC
                                            T
GAM475  CDC14B    3'  TTGCTCTTGTTGTCCAGGCTGG 54013                 _
            AGT                   ACTCCAGCCTGGGCGACA GAGCAA
                                |||||||||||||||| ||||||
                                TGAGGTCGGACCTGTTGT CTCGTT
                                            T
GAM475  CEACAM8   3'  GCTCTGTCGCCCAGGCTGGAGT 10182
                                ACTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||
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                                TGAGGTCGGACCCGCTGTCTCG

GAM475  CENPH    3'  GCTTTGTTGCCCAGACTGGAG  43568       C
                                CTCCAG CTGGGCGACAGAGC
                                |||||| ||||||||||||||
                                GAGGTC GACCCGTTGTTTCG
                                   A
GAM475  CHRAC1   3'  CTCAGTTGCCCAGGCTGGA   34333             A
                                TCCAGCCTGGGCGAC GAG
                                ||||||||||||||| |||
                                AGGTCGGACCCGTTG CTC
                                      A
GAM475  CHSY1    3'  CTCTGTTACCCAGGCTGGA   30567          CG
                                TCCAGCCTGGG  ACAGAG
                                ||||||||||  ||||||
                                AGGTCGGACCC  TGTCTC
                                      AT
GAM475  CIP29    3'  TTGCTCTGTTGCCCAGCTGGAG 51385        C
                T                ACTCCAGC TGGGCGACAGAGCAA
                                 ||||||||| ||||||||||||||
                                 TGAGGTCG ACCCGTTGTCTCGTT
                                    _
GAM475  COLEC12  3'  CTCTGTCACCCAGGCTGGA   48609          C
                                TCCAGCCTGGG GACAGAG
                                |||||||||| |||||||
                                AGGTCGGACCC CTGTCTC
                                      A
GAM475  COLEC12  3'  CTCTGTTGCCCAGGCTGGAGT  48610
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTC

GAM475  COQ7     3'  GCTCTTTTGTCCAGGCCGGG  32857    A       C
                                TCC GCCTGGGCGA AGAGC
                                ||| |||||||||| |||||
                                GGG CGGACCTGTT TCTCG
                                  C        T
GAM475  CPSF2    3'  TTGCTCTTGTTGCCCAGACTGG 62288       C       _
                AGT                 ACTCCAG CTGGGCGACA GAGCAA
                                    ||||||| |||||||||| ||||||
                                    TGAGGTC GACCCGTTGT CTCGTT
                                       A        T
GAM475  CYLC2    3'  GCTCTGTTGCCCTGGCTGGAGT 9034          T
                                ACTCCAGCC GGGCGACAGAGC
                                ||||||||| ||||||||||||
                                TGAGGTCGG CCCGTTGTCTCG
                                      T
GAM475  DCOHM    3'  GCTCTTGTCGCCCAGGCTGGAG 50528                _
                T                ACTCCAGCCTGGGCGACA GAGC
                                 |||||||||||||||||| ||||
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                                TGAGGTCGGACCCGCTGT CTCG
                                           T
GAM475  DKFZP434B044 3'  CTCTGTTGCCCAAGGTAGAGT  49716      CA   _
                                ACTC  GCCT GGGCGACAGAG
                                ||||  |||| ||||||||||
                                TGAG  TGGA CCCGTTGTCTC
                                  A_   A
GAM475  DKFZp434C0923 3'  TTGCTCTGTCACCCAGGCTGGA 34655           C
          GT                     ACTCCAGCCTGGG GACAGAGCAA
                                ||||||||||||| |||||||||
                                TGAGGTCGGACCC CTGTCTCGTT
                                        A
GAM475  DKFZP434C212 3'  CTGTTGCCCAGGCTGGAGT   69486
                                ACTCCAGCCTGGGCGACAG
                                |||||||||||||||||
                                TGAGGTCGGACCCGTTGTC

GAM475  DKFZP434D146 3'  CTCTGTCGCCCAGGCTAGAGT  32134      C
                                ACTC AGCCTGGGCGACAGAG
                                |||| ||||||||||||||
                                TGAG TCGGACCCGCTGTCTC
                                  A
GAM475  DKFZp434E2220 5'  TCTGTTGCCCAGGCTGGAGT   34721
                                ACTCCAGCCTGGGCGACAGA
                                |||||||||||||||||
                                TGAGGTCGGACCCGTTGTCT

GAM475  DKFZP434F0318 3'  CTCTGTCACCTAGGCTGGAGT  48752           C
                                ACTCCAGCCTGGG GACAGAG
                                |||||||||||| |||||||
                                TGAGGTCGGATCC CTGTCTC
                                        A
GAM475  DKFZp434F1719 3'  TTGCTCTTGTTTCCCAGGCTGG 51020           C   _
          AGT                    ACTCCAGCCTGGG GACA GAGCAA
                                |||||||||||| |||| ||||||
                                TGAGGTCGGACCC TTGT CTCGTT
                                        T   T
GAM475  DKFZP434J037 3'  GCTCTTGGTGCCCAGGCTAGAG 48951      C        AC_
          T                     ACTC AGCCTGGGCG   AGAGC
                                |||| ||||||||||   |||||
                                TGAG TCGGACCCGT   TCTCG
                                  A         GGT
GAM475  DKFZp547H025 3'  GCTCCATTGCCCAGGCTGGA   39776           CA
                                TCCAGCCTGGGCGA  GAGC
                                ||||||||||||||  ||||
                                AGGTCGGACCCGTT  CTCG
                                        AC
GAM475  DKFZP564G092 5'  GCTCTTGTCGCCCAGGCTGTAG 32163     C          _
          T                     ACT CAGCCTGGGCGACA GAGC
                                ||| |||||||||||||| ||||
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                                TGA GTCGGACCCGCTGT CTCG
                                  T           T
GAM475  DKFZP564I122 3'  CTCTGTCACCTAGGCTGGAGT  63876            C
                                ACTCCAGCCTGGG GACAGAG
                                ||||||||||||| |||||||
                                TGAGGTCGGATCC CTGTCTC
                                        A
GAM475  DKFZP564K0322 3'  CTCTGTTGCCCAGGCTGGAGT  50185
                                ACTCCAGCCTGGGCGACAGAG
                                ||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTC

GAM475  DKFZP564O0523 3'  TTGCTCTGTTGCCCAGGCTGGA 50426
                                TCCAGCCTGGGCGACAGAGCAA
                                ||||||||||||||||||||||
                                AGGTCGGACCCGTTGTCTCGTT

GAM475  DKFZP566I1024 3'  CTCTGTTGCCCAGGCTAGAGT  70648      C
                                ACTC AGCCTGGGCGACAGAG
                                |||| ||||||||||||||||
                                TGAG TCGGACCCGTTGTCTC
                                  A
GAM475  DKFZp761J139 5'  TTGCTCTTGTCACCCAGGCTGG 51117            C   _
          AGT                     ACTCCAGCCTGGG GACA GAGCAA
                                ||||||||||||| |||| ||||||
                                TGAGGTCGGACCC CTGT CTCGTT
                                        A   T
GAM475  DKFZp761N1114 3'  CTCTGTTGCCAGGCTGGA    79782          G
                                TCCAGCCTGG CGACAGAG
                                |||||||||| ||||||||
                                AGGTCGGACC GTTGTCTC

                                  _
GAM475  DKFZp761O0113 5'  GCTCTTGTTGCCCAGGCTTGAG 37895      C          _
          T                      ACTC AGCCTGGGCGACA GAGC
                                |||| |||||||||||| ||||
                                TGAG TCGGACCCGTTGT CTCG
                                  T           T
GAM475  DKFZp762P2111 3'  CTCTTGTTGCCCAGGCTGGAGT 87632                _
                                ACTCCAGCCTGGGCGACA GAG
                                |||||||||||||||||| |||
                                TGAGGTCGGACCCGTTGT CTC
                                        T
GAM475  DSCR6    3'  TTGCTCTTGTCTCCCAGGCTGG 39079            C   _
          AGT                     ACTCCAGCCTGGG GACA GAGCAA
                                ||||||||||||| |||| ||||||
                                TGAGGTCGGACCC CTGT CTCGTT
                                        T   T
GAM475  EREG     3'  GCTCTGTTGCCCAGGTTGGAGT 9310
                                ACTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||||
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                                TGAGGTTGGACCCGTTGTCTCG

GAM475  ERO1L    3'  TTGCTGTGTTGCCCAAGCTGGA 28163       C       G
                                TCCAGC TGGGCGACA AGCAA
                                |||||| ||||||||| |||||
                                AGGTCG ACCCGTTGT TCGTT
                                   A       G
GAM475  EVI5     3'  CTGCACTCAGGCTGGAGT    20206           CGA
                                ACTCCAGCCTGGG  CAG
                                ||||||||||||  |||
                                TGAGGTCGGACTC  GTC
                                      AC_
GAM475  EVI5     3'  TTGTCACCCAGGCTGGAGT   20222           C
                                ACTCCAGCCTGGG GACAG
                                |||||||||||| |||||
                                TGAGGTCGGACCC CTGTT
                                      A
GAM475  FBP17    3'  GCTCTATTGTTCAGACTGGAGT 73152       C       C
                                ACTCCAG CTGGGCGA AGAGC
                                ||||||| |||||||| |||||
                                TGAGGTC GACTTGTT TCTCG
                                   A       A
GAM475  FER1L4   3'  GCTCTGTCTCCCAGGTTGGAGT 48123           C
                                ACTCCAGCCTGGG GACAGAGC
                                |||||||||||| ||||||||
                                TGAGGTTGGACCC CTGTCTCG
                                      T
GAM475  FER1L4   3'  GCTCTGTCTCCCAGGTTGGAGT 48124           C
                                ACTCCAGCCTGGG GACAGAGC
                                |||||||||||| ||||||||
                                TGAGGTTGGACCC CTGTCTCG
                                      T
GAM475  FKBP9    3'  TTGTCGCCAGGCTGGAGT    95726           G
                                ACTCCAGCCTGG CGACAG
                                |||||||||||| ||||||
                                TGAGGTCGGACC GCTGTT
                                      _
GAM475  FLJ00024 5'  GCTCTGTCACCCAGGCTGGAGT 64497           C
                                ACTCCAGCCTGGG GACAGAGC
                                |||||||||||| ||||||||
                                TGAGGTCGGACCC CTGTCTCG
                                      A
GAM475  FLJ00060 5'  TTGCTCTGTCACCCAGGCTGGA 61759           C
           GT                     ACTCCAGCCTGGG GACAGAGCAA
                                |||||||||||| ||||||||||
                                TGAGGTCGGACCC CTGTCTCGTT
                                      A
GAM475  FLJ10101 3'  TTGCTGTGTGGCCCAGGCTGGA 45607           G  G
           GT                     ACTCCAGCCTGGGC ACA AGCAA
                                |||||||||||||| ||| |||||
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                                TGAGGTCGGACCCG TGT TCGTT
                                       G   G
GAM475  FLJ10232  3'  TTGCTCTGTCACCCAGGCTGGA 36388           C
              GT                  ACTCCAGCCTGGG GACAGAGCAA
                                  |||||||||||| ||||||||||
                                  TGAGGTCGGACCC CTGTCTCGTT
                                         A
GAM475  FLJ10297  3'  CTGTGTTGCCCAGGCTAGAGT  36439     C          G
                                  ACTC AGCCTGGGCGACA AG
                                  |||| |||||||||||| ||
                                  TGAG TCGGACCCGTTGT TC
                                    A           G
GAM475  FLJ10298  3'  TTGCTCTGTTGCCCAGGCTGGA 36465
              GT                  ACTCCAGCCTGGGCGACAGAGCAA
                                  ||||||||||||||||||||||||
                                  TGAGGTCGGACCCGTTGTCTCGTT

GAM475  FLJ10346  5'  GCTCTGTCTCCCAGGCTGAAGT 36526     C       C
                                  ACT CAGCCTGGG GACAGAGC
                                  ||| ||||||||| ||||||||
                                  TGA GTCGGACCC CTGTCTCG
                                    A        T
GAM475  FLJ10535  3'  CTCTGTCACCCAGGCTGGAGT  36745           C
                                  ACTCCAGCCTGGG GACAGAG
                                  |||||||||||| |||||||
                                  TGAGGTCGGACCC CTGTCTC
                                         A
GAM475  FLJ10560  3'  TTGTTCTGTCGCCCAGGCTGGC 36803    T
              GT                  AC CCAGCCTGGGCGACAGAGCAA
                                  || ||||||||||||||||||||
                                  TG GGTCGGACCCGCTGTCTTGTT
                                   C
GAM475  FLJ10607  3'  CTCCATCACCCAGGCTGGAGT  77631           C  CA
                                  ACTCCAGCCTGGG GA  GAG
                                  |||||||||||| ||  |||
                                  TGAGGTCGGACCC CT  CTC
                                         A  AC
GAM475  FLJ10607  3'  CTGTTGCCCAGGCTAGAG    77634     C
                                  CTC AGCCTGGGCGACAG
                                  ||| ||||||||||||||
                                  GAG TCGGACCCGTTGTC
                                    A
GAM475  FLJ10713  3'  CTGTTGCCCAGGCTGGAGT   37001
                                  ACTCCAGCCTGGGCGACAG
                                  ||||||||||||||||||
                                  TGAGGTCGGACCCGTTGTC

GAM475  FLJ10716  5'  TTGCTCTCTTGCCCAGACTGGA 37023      C       C
                                  TCCAG CTGGGCGA AGAGCAA
                                  ||||| |||||||| |||||||
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                                AGGTC GACCCGTT TCTCGTT
                                  A       C
GAM475  FLJ10846 3' TTGCTCTGTCACCCAGGCTGGA 37294           C
            GT                    ACTCCAGCCTGGG GACAGAGCAA
                                  |||||||||||| ||||||||||
                                  TGAGGTCGGACCC CTGTCTCGTT
                                         A
GAM475  FLJ10847 3' TTGCTCTGTCATGCAGGCTGGA 37305         GGC
            GT                    ACTCCAGCCTG   GACAGAGCAA
                                  |||||||||||   ||||||||||
                                  TGAGGTCGGAC   CTGTCTCGTT
                                       GTA
GAM475  FLJ10901 3' GCTCTGTCGCCCAGGCTGGA   37366
                                  TCCAGCCTGGGCGACAGAGC
                                  ||||||||||||||||||||
                                  AGGTCGGACCCGCTGTCTCG

GAM475  FLJ10998 3' GCTCTGTCACCCAAGCAGGA   37521    A  C    C
                                  TCC GC TGGG GACAGAGC
                                  ||| || |||| ||||||||
                                  AGG CG ACCC CTGTCTCG
                                    A  A    A
GAM475  FLJ11004 5' TTGCTCTGTCGCCCAGACTGGA 37535       C
            GT                    ACTCCAG CTGGGCGACAGAGCAA
                                  ||||||| ||||||||||||||||
                                  TGAGGTC GACCCGCTGTCTCGTT
                                     A
GAM475  FLJ11125 5' TTGCTCTGCCTCCTAGGCAGGA 60326      A      CGA
            GT                    ACTCC GCCTGGG   CAGAGCAA
                                  ||||| |||||||   ||||||||
                                  TGAGG CGGATCC   GTCTCGTT
                                    A      TCC
GAM475  FLJ11467 3' CTGTCACCCAGGCTGGAGT    46975           C
                                  ACTCCAGCCTGGG GACAG
                                  |||||||||||| |||||
                                  TGAGGTCGGACCC CTGTC
                                         A
GAM475  FLJ11710 3' TTGCTCTGTCTCCCAGGCTGGA 46255           C
            GT                    ACTCCAGCCTGGG GACAGAGCAA
                                  |||||||||||| ||||||||||
                                  TGAGGTCGGACCC CTGTCTCGTT
                                         T
GAM475  FLJ12572 5' GCTCTGTCACCCAGGCTGGAGT 43544           C
                                  ACTCCAGCCTGGG GACAGAGC
                                  |||||||||||| ||||||||
                                  TGAGGTCGGACCC CTGTCTCG
                                         A
GAM475  FLJ12581 3' TTGCTCTGTCGCCCAGGCTGGA 46345
            GT                    ACTCCAGCCTGGGCGACAGAGCAA
                                  ||||||||||||||||||||||||
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                                TGAGGTCGGACCCGCTGTCTCGTT

GAM475  FLJ12649  3'  TTGCCCTGTCGCCCAGGCTGCA 45098     C           A
                GT                ACT CAGCCTGGGCGACAG GCAA
                                  ||| |||||||||||||| ||||
                                  TGA GTCGGACCCGCTGTC CGTT
                                    C           C
GAM475  FLJ12668  3'  TTGCTCTGTTGCCCAGGCTGGA 47165
                GT                ACTCCAGCCTGGGCGACAGAGCAA
                                  ||||||||||||||||||||||||
                                  TGAGGTCGGACCCGTTGTCTCGTT

GAM475  FLJ12687  3'  CTCTTGCCCAGGCTGGAGT   46750            AC
                                  ACTCCAGCCTGGGCG  AGAG
                                  ||||||||||||||  ||||
                                  TGAGGTCGGACCCGT  TCTC
                                                  __
GAM475  FLJ12747  3'  TTGCTCTTGTCACCCAGGCTGG 50675          C   _
                AGT                 ACTCCAGCCTGGG GACA GAGCAA
                                  |||||||||||| |||| ||||||
                                  TGAGGTCGGACCC CTGT CTCGTT
                                        A   T
GAM475  FLJ12787  3'  GCTTTATCGCCCAGGCTGGAGT 50694            C
                                  ACTCCAGCCTGGGCGA AGAGC
                                  |||||||||||||||| |||||
                                  TGAGGTCGGACCCGCT TTTCG
                                         A
GAM475  FLJ12876  3'  GCTCTGTCACCCAGGCTGGAGT 43095           C
                                  ACTCCAGCCTGGG GACAGAGC
                                  |||||||||||| ||||||||
                                  TGAGGTCGGACCC CTGTCTCG
                                        A
GAM475  FLJ12888  3'  TTGCTCTGTTGCCCAGGCTAGA 46895     C
                GT                ACTC AGCCTGGGCGACAGAGCAA
                                  |||| ||||||||||||||||||
                                  TGAG TCGGACCCGTTGTCTCGTT
                                    A
GAM475  FLJ12891  3'  TTGTGTCACCCAGGTTAGAGT  46936     C      C   G
                                  ACTC AGCCTGGG GACA AG
                                  |||| |||||||| |||| ||
                                  TGAG TTGGACCC CTGT TT
                                    A       A   G
GAM475  FLJ12903  3'  GCTGTTGTTGCCCAGGCTGGAG 43072              _
                T                  ACTCCAGCCTGGGCGACAG AGC
                                  |||||||||||||||||| |||
                                  TGAGGTCGGACCCGTTGTT TCG
                                           G
GAM475  FLJ12960  3'  TTGCTCTGTCGCCCAGGCTGGA 45309
                GT                ACTCCAGCCTGGGCGACAGAGCAA
                                  ||||||||||||||||||||||||
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                                TGAGGTCGGACCCGCTGTCTCGTT

GAM475  FLJ12973  3'  TTGCTCTTGTTGCCCAGGCTGG 46648                  _
              AGT                  ACTCCAGCCTGGGCGACA GAGCAA
                                   |||||||||||||||||| ||||||
                                   TGAGGTCGGACCCGTTGT CTCGTT
                                                T
GAM475  FLJ12975  3'  CTCTGTCACCCAGGCTGGAGT  70192             C
                                   ACTCCAGCCTGGG GACAGAG
                                   |||||||||||| |||||||
                                   TGAGGTCGGACCC CTGTCTC
                                             A
GAM475  FLJ12975  3'  TTGCTCTTGTTGCCCAGGCTGA 70199     C          _
              AGT                  ACT CAGCCTGGGCGACA GAGCAA
                                   ||| |||||||||||||| ||||||
                                   TGA GTCGGACCCGTTGT CTCGTT
                                     A           T
GAM475  FLJ13072  5'  TTGCTCTGTCGGCCAGGCTGGA 91403           G
              GT                   ACTCCAGCCTGG CGACAGAGCAA
                                   |||||||||||| ||||||||||
                                   TGAGGTCGGACC GCTGTCTCGTT
                                          G
GAM475  FLJ13114  3'  CTCTGTCGCCCAGGCTGGA   44901
                                   TCCAGCCTGGGCGACAGAG
                                   ||||||||||||||||||
                                   AGGTCGGACCCGCTGTCTC

GAM475  FLJ13188  3'  TTGCTCTGTCACCCAGGCTAGA 42199     C      C
              GT                   ACTC AGCCTGGG GACAGAGCAA
                                   |||| |||||||| ||||||||||
                                   TGAG TCGGACCC CTGTCTCGTT
                                     A       A
GAM475  FLJ13193  3'  CTGAACCCCCAGGCTGGAGT   50722           CGA_
                                   ACTCCAGCCTGGG   CAG
                                   ||||||||||||   |||
                                   TGAGGTCGGACCC   GTC
                                          CCAA
GAM475  FLJ13197  3'  CTCTGTTGCCCAGGCTGGAGT  45177
                                   ACTCCAGCCTGGGCGACAGAG
                                   ||||||||||||||||||||
                                   TGAGGTCGGACCCGTTGTCTC

GAM475  FLJ13456  3'  CTCTGTCGCCCAAGCTGGAGT  66544        C
                                   ACTCCAGC TGGGCGACAGAG
                                   |||||||| ||||||||||||
                                   TGAGGTCG ACCCGCTGTCTC
                                        A
GAM475  FLJ13848  3'  CTGTGGCAACAGGCTGGAG   45821         G_  G
                                   CTCCAGCCTG  GC ACAG
                                   |||||||||  || ||||
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                                GAGGTCGGAC  CG TGTC
                                     AA  G
GAM475  FLJ13952  3'  CTCTTGTTGCCCAGGCTGGA   46013                _
                                TCCAGCCTGGGCGACA GAG
                                |||||||||||||||| |||
                                AGGTCGGACCCGTTGT CTC
                                      T
GAM475  FLJ13984  5'  CTCTGTCACCTAGGCTGGAGT  45807             C
                                ACTCCAGCCTGGG GACAGAG
                                |||||||||||| |||||||
                                TGAGGTCGGATCC CTGTCTC
                                     A
GAM475  FLJ14351  3'  TTGCTTTGTCGCCCAGGCTGGA 45651
             GT                   ACTCCAGCCTGGGCGACAGAGCAA
                                ||||||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTTTCGTT

GAM475  FLJ14442  3'  CTCTGTTACCCAGGCTAGAGT  52382      C       CG
                                ACTC AGCCTGGG  ACAGAG
                                |||| ||||||||  ||||||
                                TGAG TCGGACCC  TGTCTC
                                  A       AT
GAM475  FLJ20004  3'  CTCTGTCGCCCAGGGTGGAGT  97004       G
                                ACTCCA CCTGGGCGACAGAG
                                |||||| ||||||||||||||
                                TGAGGT GGACCCGCTGTCTC
                                   G
GAM475  FLJ20034  3'  CTCTTGTTGCCCAGGCTGGAGT 34845                _
                                ACTCCAGCCTGGGCGACA GAG
                                |||||||||||||||| |||
                                TGAGGTCGGACCCGTTGT CTC
                                      T
GAM475  FLJ20079  3'  TTGCTCTTGTTGCCCAGGCTGG 34983                _
             AGT                   ACTCCAGCCTGGGCGACA GAGCAA
                                |||||||||||||||| ||||||
                                TGAGGTCGGACCCGTTGT CTCGTT
                                      T
GAM475  FLJ20136  3'  TTGCTCTGTCGCCCAGGCTGGA 35106
                                TCCAGCCTGGGCGACAGAGCAA
                                ||||||||||||||||||||||
                                AGGTCGGACCCGCTGTCTCGTT

GAM475  FLJ20147  3'  TTGCTGTGTTGCCCAGGCTAGA 35138      C          G
             GT                   ACTC AGCCTGGGCGACA AGCAA
                                |||| |||||||||||| |||||
                                TGAG TCGGACCCGTTGT TCGTT
                                  A          G
GAM475  FLJ20342  3'  GCTCTTGTCCCCCAGGCTGGAG 35466            C   _
             T                    ACTCCAGCCTGGG GACA GAGC
                                ||||||||||||| |||| ||||
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                                TGAGGTCGGACCC CTGT CTCG
                                      C    T
GAM475  FLJ20344  3'  TTGCTCTGTCATCCAAACTGGA 35492        CC   GC
          GT                    ACTCCAG  TGG  GACAGAGCAA
                                |||||||  |||  ||||||||||
                                TGAGGTC  ACC  CTGTCTCGTT
                                   AA   TA
GAM475  FLJ20485  3'  CTCTGTAGCACAGGCTGGA   39292         G  G
                                TCCAGCCTG GC ACAGAG
                                ||||||||| || ||||||
                                AGGTCGGAC CG TGTCTC
                                     A  A
GAM475  FLJ20507  3'  GCTCTGTCACCCGGGCTGGAGT 60848            C
                                ACTCCAGCCTGGG GACAGAGC
                                |||||||||||| ||||||||
                                TGAGGTCGGGCCC CTGTCTCG
                                      A
GAM475  FLJ20507  3'  GCTCTGTCACCCGGGCTGGAGT 35744            C
                                ACTCCAGCCTGGG GACAGAGC
                                |||||||||||| ||||||||
                                TGAGGTCGGGCCC CTGTCTCG
                                      A
GAM475  FLJ20511  3'  CTCTTGTCACCCAGGCTGGAGT 35772            C  _
                                ACTCCAGCCTGGG GACA GAG
                                |||||||||||| |||| |||
                                TGAGGTCGGACCC CTGT CTC
                                      A    T
GAM475  FLJ20671  3'  TTGGTCTGTTGCCCAGGCTGGA 35949                 G
          GT                    ACTCCAGCCTGGGCGACAGA CAA
                                |||||||||||||||||||| |||
                                TGAGGTCGGACCCGTTGTCT GTT
                                        G
GAM475  FLJ20695  3'  TTGCTGTGTTGCCCAGGCTGGA 35987              G
                                TCCAGCCTGGGCGACA AGCAA
                                |||||||||||||||| |||||
                                AGGTCGGACCCGTTGT TCGTT
                                       G
GAM475  FLJ20700  3'  GCTCTCTCGCCCAGGCTGGAGT 36011              C
                                ACTCCAGCCTGGGCGA AGAGC
                                |||||||||||||||| |||||
                                TGAGGTCGGACCCGCT TCTCG
                                       C
GAM475  FLJ20813  3'  CTCTTTCACCCAGGCTGGAGT  36131            C  C
                                ACTCCAGCCTGGG GA AGAG
                                |||||||||||| || ||||
                                TGAGGTCGGACCC CT TCTC
                                      A  T
GAM475  FLJ21324  5'  GCTCTGACACCCAGGCTGGCGT 92856    T        CGA
                                AC CCAGCCTGGG   CAGAGC
                                || ||||||||||   ||||||
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                                TG GGTCGGACCC   GTCTCG
                                 C         ACA
GAM475  FLJ21459  3'  CTCTGTCACCCAGGCTGGGGT  44803           C
                                ACTCCAGCCTGGG GACAGAG
                                ||||||||||||| |||||||
                                TGGGGTCGGACCC CTGTCTC
                                      A
GAM475  FLJ21603  3'  GCTCTGTCACCCAGGCTGGAGT 45774           C
                                ACTCCAGCCTGGG GACAGAGC
                                ||||||||||||| ||||||||
                                TGAGGTCGGACCC CTGTCTCG
                                      A
GAM475  FLJ21777  3'  TTGTGTCACCCAGGCTGGAGT  50853           C   G
                                ACTCCAGCCTGGG GACA AG
                                ||||||||||||| |||| ||
                                TGAGGTCGGACCC CTGT TT
                                      A   G
GAM475  FLJ21865  3'  CGCCCTTCAGGCTGGGGT    43111         ___
                                ACTCCAGCCT   GGGCG
                                ||||||||||   |||||
                                TGGGGTCGGA   CCCGC
                                     CTT
GAM475  FLJ22316  5'  TTGTCTCCCAGGCTGGAGT   47621           C
                                ACTCCAGCCTGGG GACAG
                                ||||||||||||| |||||
                                TGAGGTCGGACCC CTGTT
                                      T
GAM475  FLJ22329  3'  CTCTGTCACCCAGGCTGGAGT  45399           C
                                ACTCCAGCCTGGG GACAGAG
                                ||||||||||||| |||||||
                                TGAGGTCGGACCC CTGTCTC
                                      A
GAM475  FLJ22794  3'  CTCTGTCGCCTGGGCTGGAGT  93244         TG
                                ACTCCAGCC  GGCGACAGAG
                                |||||||||  ||||||||||
                                TGAGGTCGG  CCGCTGTCTC
                                     GT
GAM475  FLJ22965  3'  TTGCTCTTTCGCCCAGGATGGA 42303       G       C
          GT                      ACTCCA CCTGGGCGA AGAGCAA
                                ||||||| ||||||||| |||||||
                                TGAGGT GGACCCGCT TCTCGTT
                                   A        T
GAM475  FLJ23024  3'  TGCTCTGTCATTCCAGTGT   46850   _    C_
                                GC CTGGG  GACAGAGCA
                                || |||||  |||||||||
                                TG GACCT  CTGTCTCGT
                                 T    TA
GAM475  FLJ23024  3'  TTGCTCTGTCTCCCAGGCTAGA 46853      C       C
          GT                      ACTC AGCCTGGG GACAGAGCAA
                                |||| |||||||| ||||||||||
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                                TGAG TCGGACCC CTGTCTCGTT
                                  A       T
GAM475  FLJ23053  3'  TTGCTCTATTGCCCAGGCTGGA 43559              C
                GT                ACTCCAGCCTGGGCGA AGAGCAA
                                  ||||||||||||||| |||||||
                                  TGAGGTCGGACCCGTT TCTCGTT
                                           A
GAM475  FLJ23263  5'  CTCTGTCGCCCAGGCTGGAGT  47801
                                  ACTCCAGCCTGGGCGACAGAG
                                  ||||||||||||||||||||
                                  TGAGGTCGGACCCGCTGTCTC

GAM475  FLJ23356  3'  TTGCTCTGTTGCTGAGGCTGGA 50928          G
                GT                ACTCCAGCCT GGCGACAGAGCAA
                                  |||||||||| ||||||||||||
                                  TGAGGTCGGA TCGTTGTCTCGTT
                                       G
GAM475  FLJ23392  3'  CTCTGTCCCCCAGGCTGGAGT  45890           C
                                  ACTCCAGCCTGGG GACAGAG
                                  |||||||||||| |||||||
                                  TGAGGTCGGACCC CTGTCTC
                                        C
GAM475  FLJ23392  3'  TTGCTCTGTCACTGAGGCTGGA 45914          G  C
                GT                ACTCCAGCCT GG GACAGAGCAA
                                  |||||||||| || ||||||||||
                                  TGAGGTCGGA TC CTGTCTCGTT
                                       G  A
GAM475  FLJ23416  3'  CTCTGTTGCCCAGGCTGGAGT  50931
                                  ACTCCAGCCTGGGCGACAGAG
                                  ||||||||||||||||||||
                                  TGAGGTCGGACCCGTTGTCTC

GAM475  FLJ23519  3'  TTGCTCTGTCACCCAGGCTGGA 50968           C
                GT                ACTCCAGCCTGGG GACAGAGCAA
                                  |||||||||||| ||||||||||
                                  TGAGGTCGGACCC CTGTCTCGTT
                                        A
GAM475  FLJ23556  3'  TTGCTCTGTCACCCAGGCTGGA 46465           C
                GT                ACTCCAGCCTGGG GACAGAGCAA
                                  |||||||||||| ||||||||||
                                  TGAGGTCGGACCC CTGTCTCGTT
                                        A
GAM475  FLJ23556  3'  TTGCTCTGTCGCCCAGGCTGGA 46466
                GT                ACTCCAGCCTGGGCGACAGAGCAA
                                  ||||||||||||||||||||||||
                                  TGAGGTCGGACCCGCTGTCTCGTT

GAM475  FLJ23563  3'  CTCTTGTTGCCCAGGCTAGAGT 68215      C          _
                                  ACTC AGCCTGGGCGACA GAG
                                  |||| |||||||||||| |||
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                                TGAG TCGGACCCGTTGT CTC
                                  A          T
GAM475  FLJ25132  5' CTGCACGCCCAGGCCTGAG   78653    CA       A_
                                CTC  GCCTGGGCG  CAG
                                |||  |||||||||  |||
                                GAG  CGGACCCGC  GTC
                                  TC       AC
GAM475  FLJ25416  5' TTGCTCTGTCACCCAGGCTGGA 59460           C
           GT                    ACTCCAGCCTGGG GACAGAGCAA
                                |||||||||||||  ||||||||||
                                TGAGGTCGGACCC CTGTCTCGTT
                                       A
GAM475  FLJ25416  5' TTGCTCTTGTTGCCCAGGCTGA 59461    C          _
           AGT                    ACT CAGCCTGGGCGACA GAGCAA
                                |||  |||||||||||||  ||||||
                                TGA GTCGGACCCGTTGT CTCGTT
                                  A          T
GAM475  FLJ30532  3' GCTCTTGTTGCCCAGGCTGGAG 59221               _
           T                     ACTCCAGCCTGGGCGACA GAGC
                                |||||||||||||||||  ||||
                                TGAGGTCGGACCCGTTGT CTCG
                                          T
GAM475  FLJ31101  3' CTCTGTCGCCCAGGCTGGA   36160
                                TCCAGCCTGGGCGACAGAG
                                |||||||||||||||||
                                AGGTCGGACCCGCTGTCTC

GAM475  FLJ31153  3' GCTCTGTCACCCAGACTGGAGT 58750       C    C
                                ACTCCAG CTGGG GACAGAGC
                                |||||||  |||||  ||||||||
                                TGAGGTC GACCC CTGTCTCG
                                   A    A
GAM475  FLJ32499  3' TTGCTCTGTCACCCAGTCTGGA 58785       C    C
           GT                    ACTCCAG CTGGG GACAGAGCAA
                                |||||||  |||||  ||||||||||
                                TGAGGTC GACCC CTGTCTCGTT
                                   T    A
GAM475  FLJ32865  3' GCTCTTGTCACCCAGGCTGGAG 58814           C   _
           T                     ACTCCAGCCTGGG GACA GAGC
                                |||||||||||||  ||||  ||||
                                TGAGGTCGGACCC CTGT CTCG
                                       A   T
GAM475  FLJ32894  3' CTCTGTTGTCCAGGCTGGAGT  58996
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||||
                                TGAGGTCGGACCTGTTGTCTC

GAM475  GAL3ST-4  3' TTGCTCTGTCCCCCAGGCTGGA 45285           C
           GT                    ACTCCAGCCTGGG GACAGAGCAA
                                |||||||||||||  ||||||||||
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                                TGAGGTCGGACCC CTGTCTCGTT
                                      C
GAM475  GGA2    3'  CTCTGTCACTCAGGCTGGAGT  31165          C
                                ACTCCAGCCTGGG GACAGAG
                                ||||||||||||| |||||||
                                TGAGGTCGGACTC CTGTCTC
                                      A
GAM475  GGA2    3'  CTCTGTCACTCAGGCTGGAGT  57665          C
                                ACTCCAGCCTGGG GACAGAG
                                ||||||||||||| |||||||
                                TGAGGTCGGACTC CTGTCTC
                                      A
GAM475  GMPPB   5'  GCTCTGTTGCCCAGGCTGGAGT 97453
                                ACTCCAGCCTGGGCGACAGAGC
                                ||||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTCG

GAM475  GNG4    3'  GCTCTGTCACCCAGGCTGGAGT 16847          C
                                ACTCCAGCCTGGG GACAGAGC
                                ||||||||||||| ||||||||
                                TGAGGTCGGACCC CTGTCTCG
                                      A
GAM475  GOLGA3  3'  GCTTTGTTGCCCAGGCTGGAGT 20890
                                ACTCCAGCCTGGGCGACAGAGC
                                ||||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTTTCG

GAM475  GR6     5'  TTGCTCTGTCACCCAGGCTGGA 24754         C
                                TCCAGCCTGGG GACAGAGCAA
                                |||||||||||| ||||||||||
                                AGGTCGGACCC CTGTCTCGTT
                                      A
GAM475  GREB1   3'  GCTCTGTCACCCAGGCTGGAGT 28571          C
                                ACTCCAGCCTGGG GACAGAGC
                                ||||||||||||| ||||||||
                                TGAGGTCGGACCC CTGTCTCG
                                      A
GAM475  GRWD    3'  TTGGTCTGTCGCCCAGGCTGGA 49792              G
          GT                      ACTCCAGCCTGGGCGACAGA CAA
                                ||||||||||||||||||| |||
                                TGAGGTCGGACCCGCTGTCT GTT
                                         G
GAM475  GTF2E1  3'  CTCTTGTACCCCAGGCTGGAGT 19798          CG  _
                                ACTCCAGCCTGGG  ACA GAG
                                ||||||||||||  ||| |||
                                TGAGGTCGGACCC  TGT CTC
                                      CA   T
GAM475  GTPBG3  3'  GCTCTGTCACCCAGGCTGGAGT 51899          C
                                ACTCCAGCCTGGG GACAGAGC
                                ||||||||||||| ||||||||
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                                TGAGGTCGGACCC CTGTCTCG
                                      A
GAM475  GTPBG3   3'  TGTCTATTGCCCAGGCTGGAGT 51909            C  G
                                ACTCCAGCCTGGGCGA AGA CA
                                |||||||||||||||| ||| ||
                                TGAGGTCGGACCCGTT TCT GT
                                      A  _
GAM475  HCA4     3'  TTGCTCTTGTCGCCCAGGCTGG 78047             _
           AGT                   ACTCCAGCCTGGGCGACA GAGCAA
                                ||||||||||||||||| ||||||
                                TGAGGTCGGACCCGCTGT CTCGTT
                                      T
GAM475  HEMK     3'  TTGCCCTGCACTATGGCTGGAG 32969       _  GCGA  A
                                CTCCAGCC TGG   CAG GCAA
                                |||||||| |||   ||| ||||
                                GAGGTCGG ATC   GTC CGTT
                                     T  AC__  C
GAM475  HRH4     3'  TTGCTCTGTCACCCAGGCTGGA 41553           C
           GT                    ACTCCAGCCTGGG GACAGAGCAA
                                |||||||||||| ||||||||||
                                TGAGGTCGGACCC CTGTCTCGTT
                                      A
GAM475  HRH4     3'  TTGCTCTGTCTCCCAGGCTGGA 41554           C
           G                     CTCCAGCCTGGG GACAGAGCAA
                                |||||||||||| ||||||||||
                                GAGGTCGGACCC CTGTCTCGTT
                                      T
GAM475  HSMPP8   3'  GCTCTTGTTGCCCAGGCTGGAG 95138             _
           T                     ACTCCAGCCTGGGCGACA GAGC
                                |||||||||||||||| ||||
                                TGAGGTCGGACCCGTTGT CTCG
                                      T
GAM475  HSPC065  3'  TTGCTCTGTCCCCCATGCTGGA 27169       C   C
           GT                    ACTCCAGC TGGG GACAGAGCAA
                                |||||||| |||| ||||||||||
                                TGAGGTCG ACCC CTGTCTCGTT
                                     T   C
GAM475  ICK      3'  CTCTGTCACCCAGGCTGGAGT  30595          C
                                ACTCCAGCCTGGG GACAGAG
                                |||||||||||| |||||||
                                TGAGGTCGGACCC CTGTCTC
                                      A
GAM475  IMPACT   3'  TTGCTCTGTCACCTAGGCTGGA 38011           C
           GT                    ACTCCAGCCTGGG GACAGAGCAA
                                |||||||||||| ||||||||||
                                TGAGGTCGGATCC CTGTCTCGTT
                                      A
GAM475  JAM1     3'  GCTCTGTCACCCAGGCTGGAGT 58518           C
                                ACTCCAGCCTGGG GACAGAGC
                                |||||||||||| ||||||||
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                                TGAGGTCGGACCC CTGTCTCG
                                      A
GAM475  JAM1     3'  GCTCTGTCACCCAGGCTGGAGT 58546          C
                                ACTCCAGCCTGGG GACAGAGC
                                |||||||||||| ||||||||
                                TGAGGTCGGACCC CTGTCTCG
                                      A
GAM475  JAM1     3'  GCTCTGTCACCCAGGCTGGAGT 58575          C
                                ACTCCAGCCTGGG GACAGAGC
                                |||||||||||| ||||||||
                                TGAGGTCGGACCC CTGTCTCG
                                      A
GAM475  JAM1     3'  GCTCTGTCACCCAGGCTGGAGT 34232          C
                                ACTCCAGCCTGGG GACAGAGC
                                |||||||||||| ||||||||
                                TGAGGTCGGACCC CTGTCTCG
                                      A
GAM475  JM11     3'  TTGCTCTGTCACCAGGCTGGAG 54377          GC
              T                  ACTCCAGCCTGG  GACAGAGCAA
                                |||||||||||  ||||||||||
                                TGAGGTCGGACC  CTGTCTCGTT
                                      A_
GAM475  KIAA0022 3'  CTGTGCTGCCCAGGCTACAGT  30281     CC       A  G
                                ACT  AGCCTGGGCG CA AG
                                |||  |||||||||| || ||
                                TGA  TCGGACCCGT GT TC
                                  CA        C  G
GAM475  KIAA0063 3'  CTCTTGTTGCCCAGGCTGGAGT 30257              _
                                ACTCCAGCCTGGGCGACA GAG
                                |||||||||||||||||| |||
                                TGAGGTCGGACCCGTTGT CTC
                                      T
GAM475  KIAA0087 3'  TTCTGTCACCCAGGCTGGAGT  29351          C
                                ACTCCAGCCTGGG GACAGAG
                                |||||||||||| |||||||
                                TGAGGTCGGACCC CTGTCTT
                                      A
GAM475  KIAA0090 3'  CTCTGTCACCCAGGCTGGAG   89815          C
                                CTCCAGCCTGGG GACAGAG
                                |||||||||||| |||||||
                                GAGGTCGGACCC CTGTCTC
                                      A
GAM475  KIAA0161 3'  TTGTCCCCCAAGCTGGAGT   29213       C   C
                                ACTCCAGC TGGG GACAG
                                |||||||| |||| |||||
                                TGAGGTCG ACCC CTGTT
                                    A   C
GAM475  KIAA0186 3'  TTGTTCTGTCACCCAGGCTGGG 41130          C
              GT                  ACTCCAGCCTGGG GACAGAGCAA
                                |||||||||||| ||||||||||
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                                TGGGGTCGGACCC CTGTCTTGTT
                                      A
GAM475  KIAA0205 3' CTCTGTCACCCAGGCTGTAGT 30211     C       C
                                ACT CAGCCTGGG GACAGAG
                                ||| ||||||||| |||||||
                                TGA GTCGGACCC CTGTCTC
                                  T       A
GAM475  KIAA0210 5' GCTCTGTCGCCCAGGCTGGAGT 29162
                                ACTCCAGCCTGGGCGACAGAGC
                                ||||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTCG

GAM475  KIAA0210 5' GCTCTTGTCCAGGCTGGAGT  29163             AC
                                ACTCCAGCCTGGGCG  AGAGC
                                ||||||||||||||  |||||
                                TGAGGTCGGACCTGT  TCTCG
                                      __
GAM475  KIAA0418 5' GCTCTGTTGCTCAGGCTGGA  28296
                                TCCAGCCTGGGCGACAGAGC
                                ||||||||||||||||||||
                                AGGTCGGACTCGTTGTCTCG

GAM475  KIAA0426 3' TTGCTCCTGTCGCCCAGGCTGG 28938                 _
          AGT                   ACTCCAGCCTGGGCGACAG AGCAA
                                |||||||||||||||||| |||||
                                TGAGGTCGGACCCGCTGTC TCGTT
                                        C
GAM475  KIAA0435 5' TTGCTCTGTCACCCAGTTTGGA 29669       C    C
          GT                    ACTCCAG CTGGG GACAGAGCAA
                                ||||||| ||||| ||||||||||
                                TGAGGTT GACCC CTGTCTCGTT
                                    T    A
GAM475  KIAA0447 3' TTGCTCTGTCTGTCACCCAGGC 72138           C____
          TGGAGT                ACTCCAGCCTGGG    GACAGAGCAA
                                ||||||||||||    ||||||||||
                                TGAGGTCGGACCC    CTGTCTCGTT
                                      ACTGT
GAM475  KIAA0459 3' TTGCTTTGTTGCCCAGGCTGGA 61666
          GT                    ACTCCAGCCTGGGCGACAGAGCAA
                                ||||||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTTTCGTT

GAM475  KIAA0469 3' GCTCTGTCACCCAGGCTGGAGT 29985           C
                                ACTCCAGCCTGGG GACAGAGC
                                |||||||||||| ||||||||
                                TGAGGTCGGACCC CTGTCTCG
                                      A
GAM475  KIAA0469 3' TTGCTCTGTCACCCAGGCTGGA 30003           C
          GT                    ACTCCAGCCTGGG GACAGAGCAA
                                |||||||||||| ||||||||||
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                                TGAGGTCGGACCC CTGTCTCGTT
                                      A
GAM475  KIAA0475 3' CTCTGTTGCCCAGGCTGGAGT  30116
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTC

GAM475  KIAA0478 3' TTGCTCTGTCACCCAGACTGGA 30185       C     C
                                TCCAG CTGGG GACAGAGCAA
                                ||||| ||||| ||||||||||
                                AGGTC GACCC CTGTCTCGTT
                                   A     A
GAM475  KIAA0493 5' TTGCTCTCTTACCCAAGCTGGA 64940         C    CG C
           GT                     ACTCCAGC TGGG  A AGAGCAA
                                ||||||||| ||||  | |||||||
                                TGAGGTCG ACCC  T TCTCGTT
                                     A    AT C
GAM475  KIAA0495 3' TTGCCCTGTCACCCAGGCTGGA 63280             C     A
           GT                     ACTCCAGCCTGGG GACAG GCAA
                                |||||||||||| ||||| ||||
                                TGAGGTCGGACCC CTGTC CGTT
                                      A     C
GAM475  KIAA0513 3' TTGCTCTTGTTGCCCAGGCTGG 29057                  _
           AGT                      ACTCCAGCCTGGGCGACA GAGCAA
                                |||||||||||||||||| ||||||
                                TGAGGTCGGACCCGTTGT CTCGTT
                                         T
GAM475  KIAA0527 3' CTGTTGCCCAGGCTGGAGT   97495
                                ACTCCAGCCTGGGCGACAG
                                |||||||||||||||||||
                                TGAGGTCGGACCCGTTGTC

GAM475  KIAA0532 3' TTCTGTCACCCAGGCTAGAGT  71326      C       C
                                ACTC AGCCTGGG GACAGAG
                                |||| |||||||| |||||||
                                TGAG TCGGACCC CTGTCTT
                                   A       A
GAM475  KIAA0555 3' TTGCTCTGTTGCCCATGCTGGA 29555         C
           GT                     ACTCCAGC TGGGCGACAGAGCAA
                                |||||||| ||||||||||||||
                                TGAGGTCG ACCCGTTGTCTCGTT
                                     T
GAM475  KIAA0557 3' CTTCATTACCCAGGCTGGAGT  78560             CG CA
                                ACTCCAGCCTGGG  A  GAG
                                ||||||||||||  |  |||
                                TGAGGTCGGACCC  T  TTC
                                      AT AC
GAM475  KIAA0561 3' CTCTGTTGCCCGGGCTGGAGT  66474
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||||
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                                TGAGGTCGGGCCCGTTGTCTC

GAM475  KIAA0562  3'  TTGCTCTGTTGCCTAGGCTGGA 28833
                GT                ACTCCAGCCTGGGCGACAGAGCAA
                                  ||||||||||||||||||||||||
                                  TGAGGTCGGATCCGTTGTCTCGTT

GAM475  KIAA0594  3'  CTCTGTTGCCCAGGCTGGAGT  65511
                                  ACTCCAGCCTGGGCGACAGAG
                                  |||||||||||||||||||||
                                  TGAGGTCGGACCCGTTGTCTC

GAM475  KIAA0599  3'  TTCTGTCACCCAGGCTGGAGT  77704          C
                                  ACTCCAGCCTGGG GACAGAG
                                  |||||||||||| |||||||
                                  TGAGGTCGGACCC CTGTCTT
                                        A
GAM475  KIAA0599  3'  TTGCTCTGTCGCCCAGGCTGGA 77705
                G                  CTCCAGCCTGGGCGACAGAGCAA
                                   ||||||||||||||||||||||||
                                   GAGGTCGGACCCGCTGTCTCGTT

GAM475  KIAA0720  3'  CTCTGTCACCTAGGTTGGAGT  62982          C
                                  ACTCCAGCCTGGG GACAGAG
                                  |||||||||||| |||||||
                                  TGAGGTTGGATCC CTGTCTC
                                        A
GAM475  KIAA0737  3'  GCTCTGTCACCCAGGCTGGAGT 29812          C
                                  ACTCCAGCCTGGG GACAGAGC
                                  |||||||||||| ||||||||
                                  TGAGGTCGGACCC CTGTCTCG
                                        A
GAM475  KIAA0798  3'  TGCTCTTGTTGCCCAGGTTGGA 28456                _
                GT                ACTCCAGCCTGGGCGACA GAGCA
                                  |||||||||||||||| |||||
                                  TGAGGTTGGACCCGTTGT CTCGT
                                         T
GAM475  KIAA0831  3'  GCTCAGCTGCCCAGGCTGGAGT 30642          ACA
                                  ACTCCAGCCTGGGCG  GAGC
                                  |||||||||||||   ||||
                                  TGAGGTCGGACCCGT  CTCG
                                        CGA
GAM475  KIAA0861  3'  GCTCTGTCGCCCAGGCTGGAGT 90352
                                  ACTCCAGCCTGGGCGACAGAGC
                                  |||||||||||||||||||||||
                                  TGAGGTCGGACCCGCTGTCTCG

GAM475  KIAA0924  3'  TTGCTATGTTGCCCAGGCTAGA 30380     C         G
                GT                ACTC AGCCTGGGCGACA AGCAA
                                  |||| |||||||||||| |||||
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                                TGAG TCGGACCCGTTGT TCGTT
                                  A          A
GAM475  KIAA0931  3'  TTGCTCAGTCGCTCAGGCTGGA 68025              A
                GT                  ACTCCAGCCTGGGCGAC GAGCAA
                                    |||||||||||||||| ||||||
                                    TGAGGTCGGACTCGCTG CTCGTT
                                          A
GAM475  KIAA0961  3'  GCTCTTTCGCCCAGGCTGGCGT 30403    T          C
                                    AC CCAGCCTGGGCGA AGAGC
                                    || |||||||||||| |||||
                                    TG GGTCGGACCCGCT TCTCG
                                     C          T
GAM475  KIAA1028  3'  TTGCTCTGTCACCCAAGCTGGA 93596        C   C
                GT                  ACTCCAGC TGGG GACAGAGCAA
                                    |||||||| |||| ||||||||||
                                    TGAGGTCG ACCC CTGTCTCGTT
                                       A   A
GAM475  KIAA1040  3'  GCTCTGTCACCCAGGCTGGA   72689          C
                                    TCCAGCCTGGG GACAGAGC
                                    |||||||||| ||||||||
                                    AGGTCGGACCC CTGTCTCG
                                          A
GAM475  KIAA1041  3'  TTGCCCTGTTGCCCAGGCTGGA 30835              A
                GT                  ACTCCAGCCTGGGCGACAG GCAA
                                    |||||||||||||||||| ||||
                                    TGAGGTCGGACCCGTTGTC CGTT
                                             C
GAM475  KIAA1052  5'  TTGCTCTGTCACTCAGGCTGCA 30949    C       C
                GT                  ACT CAGCCTGGG GACAGAGCAA
                                    ||| ||||||||| ||||||||||
                                    TGA GTCGGACTC CTGTCTCGTT
                                      C        A
GAM475  KIAA1054  3'  CTCTGTTGCCCAGGCTGGAGT  68963
                                    ACTCCAGCCTGGGCGACAGAG
                                    ||||||||||||||||||||
                                    TGAGGTCGGACCCGTTGTCTC

GAM475  KIAA1128  3'  TTGCTCCATTGCCCAGGCTGGA 69014            CA
                                    TCCAGCCTGGGCGA  GAGCAA
                                    ||||||||||||||  ||||||
                                    AGGTCGGACCCGTT  CTCGTT
                                             AC
GAM475  KIAA1143  3'  GCTCTGTCACCCAGGCTGGAGT 69244           C
                                    ACTCCAGCCTGGG GACAGAGC
                                    |||||||||||| ||||||||
                                    TGAGGTCGGACCC CTGTCTCG
                                             A
GAM475  KIAA1155  3'  CTCTGTCACCCAGGCTGGAGT  62911           C
                                    ACTCCAGCCTGGG GACAGAG
                                    |||||||||||| |||||||
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                                TGAGGTCGGACCC CTGTCTC
                                      A
GAM475  KIAA1161  5'  TTGCTCTGTCACCCAGGTTGGA 82654          C
              GT                  ACTCCAGCCTGGG GACAGAGCAA
                                  |||||||||||| ||||||||||
                                  TGAGGTTGGACCC CTGTCTCGTT
                                      A
GAM475  KIAA1163  3'  CTTTTCTGCCCAGGCTGGAGT  79647           AC
                                  ACTCCAGCCTGGGCG  AGAG
                                  |||||||||||||||  ||||
                                  TGAGGTCGGACCCGT  TTTC
                                       CT
GAM475  KIAA1170  3'  GCTCTTGTTGCCCAAGCTGGAG 70417        C       _
              T                   ACTCCAGC TGGGCGACA GAGC
                                  |||||||| ||||||||| ||||
                                  TGAGGTCG ACCCGTTGT CTCG
                                     A       T
GAM475  KIAA1185  3'  GCTCTGTCGCCAGGCTGGAGT  63289          G
                                  ACTCCAGCCTGG CGACAGAGC
                                  |||||||||||| |||||||||
                                  TGAGGTCGGACC GCTGTCTCG
                                                _
GAM475  KIAA1193  3'  CTGTCGCCAGGCTGGAGT    68269          G
                                  ACTCCAGCCTGG CGACAG
                                  |||||||||||| ||||||
                                  TGAGGTCGGACC GCTGTC
                                                _
GAM475  KIAA1198  3'  CTCTGTTGCCCCAGGCTGGAGT 64031           _
                                  ACTCCAGCCTGGG CGACAGAG
                                  |||||||||||| ||||||||
                                  TGAGGTCGGACCC GTTGTCTC
                                       C
GAM475  KIAA1198  3'  CTCTGTTGCCTAGGCTGGAGT  64032
                                  ACTCCAGCCTGGGCGACAGAG
                                  ||||||||||||||||||||
                                  TGAGGTCGGATCCGTTGTCTC

GAM475  KIAA1198  3'  CTGTTGCCAGGCTGGAGT    64034          G
                                  ACTCCAGCCTGG CGACAG
                                  |||||||||||| ||||||
                                  TGAGGTCGGACC GTTGTC
                                                _
GAM475  KIAA1198  3'  GCTCTGTCACCAAGCTGGA   64045       C   GC
                                  TCCAGC TGG  GACAGAGC
                                  |||||| |||  ||||||||
                                  AGGTCG ACC  CTGTCTCG
                                     A  A_
GAM475  KIAA1198  3'  TTGCTCTTGTTGCCCAGGCTGG 64075              _
              AGT                 ACTCCAGCCTGGGCGACA GAGCAA
                                  |||||||||||||||||| ||||||
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                                TGAGGTCGGACCCGTTGT CTCGTT
                                          T
GAM475  KIAA1210 3' GCTCTGTTACCCAGATTGGAGT 98075      GC    CG
                                ACTCCA  CTGGG  ACAGAGC
                                ||||||  |||||  |||||||
                                TGAGGT  GACCC  TGTCTCG
                                   TA    AT
GAM475  KIAA1254 3' TTGCTTTGTCAGCCAGGCTGGA 70571          GC
           GT                    ACTCCAGCCTGG  GACAGAGCAA
                                ||||||||||||  ||||||||||
                                TGAGGTCGGACC  CTGTTTCGTT
                                      GA
GAM475  KIAA1257 3' TTGCTCTCTCACCCAGGCTGGA 63427          C  C
           GT                    ACTCCAGCCTGGG GA AGAGCAA
                                ||||||||||||| || |||||||
                                TGAGGTCGGACCC CT TCTCGTT
                                      A  C
GAM475  KIAA1257 3' TTGCTCTGTCGCCCAGGCTGGA 63428
           GT                    ACTCCAGCCTGGGCGACAGAGCAA
                                ||||||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTCGTT

GAM475  KIAA1257 3' TTGCTCTTGTTGCCCAGGCTGG 63429                _
           AGT                   ACTCCAGCCTGGGCGACA GAGCAA
                                ||||||||||||||||| ||||||
                                TGAGGTCGGACCCGTTGT CTCGTT
                                          T
GAM475  KIAA1280 5' TTGCTTTGTTGCCCAGGCTGGA 70297
           GT                    ACTCCAGCCTGGGCGACAGAGCAA
                                ||||||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTTTCGTT

GAM475  KIAA1287 3' CTGTTGCCCAGGCTGGAGT   78937
                                ACTCCAGCCTGGGCGACAG
                                |||||||||||||||||
                                TGAGGTCGGACCCGTTGTC

GAM475  KIAA1320 5' CTCTTTCACCCAGGCTGGAGT  69839          C  C
                                ACTCCAGCCTGGG GA AGAG
                                |||||||||||| || ||||
                                TGAGGTCGGACCC CT TCTC
                                      A  T
GAM475  KIAA1320 5' GCCCTGTCACCCAGGCTGGAGT 69842          C    A
                                ACTCCAGCCTGGG GACAG GC
                                |||||||||||| ||||| ||
                                TGAGGTCGGACCC CTGTC CG
                                      A    C
GAM475  KIAA1373 3' CTCTGTCGCCCAGGCTGGAGT  71505
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||
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                              TGAGGTCGGACCCGCTGTCTC

GAM475  KIAA1393  3'  TTGCTCTGTTGCCCAGGCTGGA 72577
              GT                ACTCCAGCCTGGGCGACAGAGCAA
                                |||||||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTCGTT

GAM475  KIAA1443  3'  TTGCTCTGTCGCCCAGGCTGTA 64580     C
              GT                ACT CAGCCTGGGCGACAGAGCAA
                                ||| ||||||||||||||||||
                                TGA GTCGGACCCGCTGTCTCGTT
                                  T
GAM475  KIAA1456  3'  GCTCTGTCGCCCAGGCTGGAGT 67559
                                ACTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTCG

GAM475  KIAA1464  3'  CTGGCCCCAGGGCTGGAG    68819        __   GA
                                CTCCAGCCT  GGGC  CAG
                                |||||||||  ||||  |||
                                GAGGTCGGG  CCCG  GTC
                                     AC   __
GAM475  KIAA1465  3'  TTGGTCTGTCGCCAGGCTGGAG 61512          G     G
              T                  ACTCCAGCCTGG CGACAGA CAA
                                 |||||||||||| ||||||| |||
                                 TGAGGTCGGACC GCTGTCT GTT
                                      _      G
GAM475  KIAA1467  3'  TTGCTCTTGTCGCCCAGGCTGG 72080              _
              AGT                  ACTCCAGCCTGGGCGACA GAGCAA
                                   |||||||||||||||||| ||||||
                                   TGAGGTCGGACCCGCTGT CTCGTT
                                             T
GAM475  KIAA1473  3'  TTGCTCTATCGCCCCCCCAGGC 71215          ____     C
              TGGAGT               ACTCCAGCCT   GGGCGA AGAGCAA
                                   ||||||||||   |||||| |||||||
                                   TGAGGTCGGA   CCCGCT TCTCGTT
                                        CCCC     A
GAM475  KIAA1493  3'  CTCTGTTGCCCAGTCTGGAGT  64839       C
                                ACTCCAG CTGGGCGACAGAG
                                ||||||| ||||||||||||
                                TGAGGTC GACCCGTTGTCTC
                                    T
GAM475  KIAA1497  5'  TTGCTCTGTTGCCCAGGCTGGA 68133
              GT                ACTCCAGCCTGGGCGACAGAGCAA
                                |||||||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTCGTT

GAM475  KIAA1508  3'  TTGCTCGTCACCCAGGCTGGAG 62568          C   A
              T                  ACTCCAGCCTGGG GAC GAGCAA
                                 |||||||||||| ||| ||||||
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                                TGAGGTCGGACCC CTG CTCGTT
                                      A   _
GAM475  KIAA1530 3' TTGCTCTGTCGCCAGGCTGGAG 68573          G
              T                  ACTCCAGCCTGG CGACAGAGCAA
                                 |||||||||||| ||||||||||
                                 TGAGGTCGGACC GCTGTCTCGTT
                                      _
GAM475  KIAA1530 3' TTGCTCTTACCCAGGCTGAGT  68574     C      CGAC
                                 ACTC AGCCTGGG    AGAGCAA
                                 |||| ||||||||    |||||||
                                 TGAG TCGGACCC    TCTCGTT
                                   _       AT__
GAM475  KIAA1559 3' CTTTGTCCCCCAGGCTGGAGT  73456           C
                                 ACTCCAGCCTGGG GACAGAG
                                 |||||||||||| |||||||
                                 TGAGGTCGGACCC CTGTTTC
                                      C
GAM475  KIAA1571 3' CTGTCTTGCCCAGGCTGGAGT  61616           __
                                 ACTCCAGCCTGGGC  GACAG
                                 |||||||||||||  |||||
                                 TGAGGTCGGACCCG  CTGTC
                                      TT
GAM475  KIAA1615 3' TTGCTCTGTCACCAGGCCGGAG 69292      A     GC
              T                  ACTCC GCCTGG  GACAGAGCAA
                                 |||||| ||||||  ||||||||||
                                 TGAGG CGGACC  CTGTCTCGTT
                                   C     A_
GAM475  KIAA1615 3' TTGCTCTTGTTGCCTAGGCTGG 69293              _
              AGT                  ACTCCAGCCTGGGCGACA GAGCAA
                                 |||||||||||||||||| ||||||
                                 TGAGGTCGGATCCGTTGT CTCGTT
                                       T
GAM475  KIAA1617 3' TTGCTCTGTCGCCCAGGTTG   93087
                                 CAGCCTGGGCGACAGAGCAA
                                 ||||||||||||||||||||
                                 GTTGGACCCGCTGTCTCGTT

GAM475  KIAA1649 3' CTCTGTTGCCAAGGCTGGAGT  51235          G
                                 ACTCCAGCCT GGCGACAGAG
                                 |||||||||| ||||||||||
                                 TGAGGTCGGA CCGTTGTCTC
                                      A
GAM475  KIAA1655 3' CTCTGTCGCCCAGGCTGGAGT  67184
                                 ACTCCAGCCTGGGCGACAGAG
                                 ||||||||||||||||||||
                                 TGAGGTCGGACCCGCTGTCTC

GAM475  KIAA1655 3' CTCTGTTGCCCAGGCTGGAGT  67185
                                 ACTCCAGCCTGGGCGACAGAG
                                 ||||||||||||||||||||
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                                TGAGGTCGGACCCGTTGTCTC

GAM475  KIAA1668  3'  GCTCTGTCGCCCAGGCTGGAGT 67073
                                ACTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTCG

GAM475  KIAA1671  3'  CTCTGTTGCTCAAGCTGGAGT  66278        C
                                ACTCCAGC TGGGCGACAGAG
                                |||||||| ||||||||||||
                                TGAGGTCG ACTCGTTGTCTC
                                     A
GAM475  KIAA1671  3'  TTGCTCTGTTGGCCAGGCTGGA 66293         G
                                TCCAGCCTGG CGACAGAGCAA
                                |||||||||| ||||||||||
                                AGGTCGGACC GTTGTCTCGTT
                                      G
GAM475  KIAA1712  3'  CTCTATTGCCCAGGCTGGAGT  68157             C
                                ACTCCAGCCTGGGCGA AGAG
                                |||||||||||||||| ||||
                                TGAGGTCGGACCCGTT TCTC
                                          A
GAM475  KIAA1712  3'  GCTGTTGTTGCCCAGGCTGGAG 68160                 _
          T                      ACTCCAGCCTGGGCGACAG AGC
                                 |||||||||||||||||| |||
                                 TGAGGTCGGACCCGTTGTT TCG
                                           G
GAM475  KIAA1715  5'  TGCTCTGGAGGCAGGCTGGG  68693        GGCGA
                                TCCAGCCTG    CAGAGCA
                                |||||||||    |||||||
                                GGGTCGGAC    GTCTCGT
                                     GGAG_
GAM475  KIAA1737  3'  GCTCTTGTTGCCCAGGCGGAGT 67945      A        _
                                ACTCC GCCTGGGCGACA GAGC
                                ||||| |||||||||||| ||||
                                TGAGG CGGACCCGTTGT CTCG
                                  _         T
GAM475  KIAA1751  3'  CTCTGTCGCCTAGGCTGGAGT  72155
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||||
                                TGAGGTCGGATCCGCTGTCTC

GAM475  KIAA1755  3'  CTCTGGTGTCCAGGCTGGAGT  62012             A
                                ACTCCAGCCTGGGCG CAGAG
                                |||||||||||||| |||||
                                TGAGGTCGGACCTGT GTCTC
                                          G
GAM475  KIAA1784  3'  CTGTGTCACCTAGGCTGGAGT  65748           C   G
                                ACTCCAGCCTGGG GACA AG
                                |||||||||||| |||| ||
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                                TGAGGTCGGATCC CTGT TC
                                      A   G
GAM475  KIAA1813 5' TGCTCTGCTGGGGGCTGGGGT 70834        GGG  A
                                ACTCCAGCCT   CG CAGAGCA
                                ||||||||||   || |||||||
                                TGGGGTCGGG   GT GTCTCGT
                                     G__  C
GAM475  KIAA1821 3' TTGCTCTGTTGCCCAGGCTGGA 72276
             GT                   ACTCCAGCCTGGGCGACAGAGCAA
                                ||||||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTCGTT

GAM475  KIAA1829 3' CTCTGTTATCCAGGCTGGA   62642         GC
                                TCCAGCCTGG  GACAGAG
                                ||||||||||  |||||||
                                AGGTCGGACC  TTGTCTC
                                      TA
GAM475  KIAA1829 3' GCTCTGTTGCCCAGGCTGGAGT 62647
                                ACTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTCG

GAM475  KIAA1871 3' CTATGTTGCCCAGGCTGGA   61902             G
                                TCCAGCCTGGGCGACA AG
                                |||||||||||||||| ||
                                AGGTCGGACCCGTTGT TC
                                      A
GAM475  KIAA1877 3' GCTCTGTCGCCCAGGCTAGAGT 66753     C
                                ACTC AGCCTGGGCGACAGAGC
                                |||| ||||||||||||||||
                                TGAG TCGGACCCGCTGTCTCG
                                  A
GAM475  KIAA1922 5' GCTCTTGTTGCCCAGGCTGGAG 73997                _
             T                   ACTCCAGCCTGGGCGACA GAGC
                                |||||||||||||||| ||||
                                TGAGGTCGGACCCGTTGT CTCG
                                      T
GAM475  KIAA1924 3' TTGCTCTGTCGCCCAGGATGGA 74064       G
             GT                   ACTCCA CCTGGGCGACAGAGCAA
                                ||||||| ||||||||||||||||
                                TGAGGT GGACCCGCTGTCTCGTT
                                   A
GAM475  KIAA1924 3' TTGTTCTGTCACCTAGGCTGGA 74065          C
                                TCCAGCCTGGG GACAGAGCAA
                                |||||||||| ||||||||||
                                AGGTCGGATCC CTGTCTTGTT
                                      A
GAM475  KIAA1956 3' CTGTCTGCCCAGGCTGGAGT   79077           _
                                ACTCCAGCCTGGGC GACAG
                                |||||||||||| |||||
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                                TGAGGTCGGACCCG CTGTC
                                        T
GAM475  KIAA1971  3'  CTCTGTCATCCAGGCTAGAGT  74676      C      GC
                                ACTC AGCCTGG  GACAGAG
                                |||| |||||||  |||||||
                                TGAG TCGGACC  CTGTCTC
                                  A       TA
GAM475  KIAA1971  3'  CTCTGTCGCCCAGGCTGGGGT  74677
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||||
                                TGGGGTCGGACCCGCTGTCTC

GAM475  KIAA1971  3'  GCTTCCCAGGCTGGGGT     74684            CGACA
                                ACTCCAGCCTGGG    GAGC
                                ||||||||||||    ||||
                                TGGGGTCGGACCC    TTCG
                                        _____
GAM475  KIAA1987  5'  TTGCTCTTGTTGCCCAGGTTAG 89396      C          _
              AGT                 ACTC AGCCTGGGCGACA GAGCAA
                                |||| |||||||||||| ||||||
                                TGAG TTGGACCCGTTGT CTCGTT
                                  A          T
GAM475  LAK-4P    3'  CTGCGCCTAGGCTGGAG     24395            A
                                CTCCAGCCTGGGCG CAG
                                |||||||||||||| |||
                                GAGGTCGGATCCGC GTC
                                        _
GAM475  LAMP3     3'  CTCTTGTCACCCAGGCTGGAGT 60202           C   _
                                ACTCCAGCCTGGG GACA GAG
                                |||||||||||| |||| |||
                                TGAGGTCGGACCC CTGT CTC
                                        A   T
GAM475  LIECG3    3'  TTGCTCCGTTGCCCAGGTTGGA 88804             A
              GT                  ACTCCAGCCTGGGCGAC GAGCAA
                                |||||||||||||||| ||||||
                                TGAGGTTGGACCCGTTG CTCGTT
                                          C
GAM475  LOH12CR1  5'  TGCCCTGTCGCCCGCCGCCGGA 55195      A  C_       A
              G                   CTCC GC  TGGGCGACAG GCA
                                |||| ||  |||||||||| |||
                                GAGG CG  GCCCGCTGTC CGT
                                  C  CC        C
GAM475  LY75      3'  CTCTGTTGCCCAGGCTGGAGT  11393
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTC

GAM475  MAIL      3'  TTGCTCTGGCGCCCAGGCTGGA 49475             A
              GT                  ACTCCAGCCTGGGCG CAGAGCAA
                                |||||||||||||| ||||||||
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                                TGAGGTCGGACCCGC GTCTCGTT
                                       G
GAM475  MAP-1    3'  GCTCTGTCACCCAGGCTGGAGT 42443           C
                                ACTCCAGCCTGGG GACAGAGC
                                ||||||||||||| ||||||||
                                TGAGGTCGGACCC CTGTCTCG
                                       A
GAM475  MCLC     3'  TTGCTCTGTCACCCAGGCTGGA 31389           C
              GT                  ACTCCAGCCTGGG GACAGAGCAA
                                ||||||||||||| ||||||||||
                                TGAGGTCGGACCC CTGTCTCGTT
                                       A
GAM475  MCM10    3'  CTATGTCACCCTGGCTGGAGT  38175        T  C  G
                                ACTCCAGCC GGG GACA AG
                                ||||||||| ||| |||| ||
                                TGAGGTCGG CCC CTGT TC
                                      T  A  A
GAM475  MGC10200 3'  TTGCTTTGTCACGCAGGCTAGA 59652     C     GGC
              GT                  ACTC AGCCTG  GACAGAGCAA
                                |||| ||||||  ||||||||||
                                TGAG TCGGAC  CTGTTTCGTT
                                  A     GCA
GAM475  MGC10818 3'  CTCTGTCGCCCAGGCTGGAGT  48302
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTC

GAM475  MGC11386 3'  GCTCTATCGCCTAGGCTGAAG  53069    C         C
                                CT CAGCCTGGGCGA AGAGC
                                || ||||||||||| |||||
                                GA GTCGGATCCGCT TCTCG
                                 A          A
GAM475  MGC13061 3'  CTAGGTTGCCCAGGCTGGTGT  51287    T          AG
                                AC CCAGCCTGGGCGAC  AG
                                || |||||||||||||  ||
                                TG GGTCGGACCCGTTG  TC
                                 T           GA
GAM475  MGC13138 3'  TGCTCTGTCACCCAGGCTGGAG 54164           C
              T                  ACTCCAGCCTGGG GACAGAGCA
                                |||||||||||| |||||||||
                                TGAGGTCGGACCC CTGTCTCGT
                                       A
GAM475  MGC13138 3'  TTGCTCTTGTTGCCCAGGCTGG 54166                _
              AGT                  ACTCCAGCCTGGGCGACA GAGCAA
                                |||||||||||||||||| ||||||
                                TGAGGTCGGACCCGTTGT CTCGTT
                                         T
GAM475  MGC13204 3'  TTGCTCTGTTGCCCAGGCTGGA 49636
              GT                  ACTCCAGCCTGGGCGACAGAGCAA
                                ||||||||||||||||||||||||
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                              TGAGGTCGGACCCGTTGTCTCGTT

GAM475  MGC14289 3' TTGCTCTGTTGCCCAGGCTGGA 55596
            GT                 ACTCCAGCCTGGGCGACAGAGCAA
                               ||||||||||||||||||||||||
                               TGAGGTCGGACCCGTTGTCTCGTT

GAM475  MGC14436 5' TTGCCCTGTCACCCAGGCTGGG 52932          C    A
            GT                 ACTCCAGCCTGGG GACAG GCAA
                               |||||||||||| ||||| ||||
                               TGGGGTCGGACCC CTGTC CGTT
                                     A    C
GAM475  MGC14836 3' TTGCTCTGTTGCCCAGGCTGGA 54179
            GT                 ACTCCAGCCTGGGCGACAGAGCAA
                               ||||||||||||||||||||||||
                               TGAGGTCGGACCCGTTGTCTCGTT

GAM475  MGC15606 5' TGCTCTGTTGCCCAGGCTGGAG 59527
            T                  ACTCCAGCCTGGGCGACAGAGCA
                               |||||||||||||||||||||||
                               TGAGGTCGGACCCGTTGTCTCGT

GAM475  MGC15873 5' CTCTGTCGCCCAGGCTGGCGT  53005    T
                               AC CCAGCCTGGGCGACAGAG
                               || ||||||||||||||||
                               TG GGTCGGACCCGCTGTCTC
                                C
GAM475  MGC1842  3' CTCTGTTGCCCAGACTGGAGT  66253       C
                               ACTCCAG CTGGGCGACAGAG
                               ||||||| ||||||||||||
                               TGAGGTC GACCCGTTGTCTC
                                  A
GAM475  MGC21675 3' GCTCTTGTTGCCCAGGCTGGAG 54594              _
            T                  ACTCCAGCCTGGGCGACA GAGC
                               |||||||||||||||| ||||
                               TGAGGTCGGACCCGTTGT CTCG
                                        T
GAM475  MGC2474  3' TTGCTCCTCACCCAGGCTGGA  43972          C  CA
                               TCCAGCCTGGG GA  GAGCAA
                               |||||||||| ||  ||||||
                               AGGTCGGACCC CT  CTCGTT
                                     A  C_
GAM475  MGC2474  3' TTGCTCTTGTTGCCCAGGCTGG 43973              _
            AGT                  ACTCCAGCCTGGGCGACA GAGCAA
                               |||||||||||||||| ||||||
                               TGAGGTCGGACCCGTTGT CTCGTT
                                        T
GAM475  MGC2477  5' CTCTGTTGCCCAGCTGGAGT  44300       C
                               ACTCCAGC TGGGCGACAGAG
                               |||||||| ||||||||||||
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                                TGAGGTCG ACCCGTTGTCTC
                                        _
GAM475  MGC2477  5' GCTCTGTCGCCCAGGGCTGGAG 44305        _
           T                    ACTCCAGCC TGGGCGACAGAGC
                                |||||||| ||||||||||||
                                TGAGGTCGG ACCCGCTGTCTCG
                                    G
GAM475  MGC2488  3' TTCTGTCACCCAGGTTAGAGT  44092     C      C
                                ACTC AGCCTGGG GACAGAG
                                |||| |||||||| |||||||
                                TGAG TTGGACCC CTGTCTT
                                  A       A
GAM475  MGC2562  3' CTCTGACCCAGCCAGAGT    51440     CA  C   CGA
                                ACTC  GC TGGG   CAGAG
                                ||||  || ||||   |||||
                                TGAG  CG ACCC   GTCTC
                                  AC  _    A__
GAM475  MGC2603  3' GCTCTGTCGCCAGGCTGGAGT  44076          G
                                ACTCCAGCCTGG CGACAGAGC
                                |||||||||||| |||||||||
                                TGAGGTCGGACC GCTGTCTCG
                                        _
GAM475  MGC29891 3' TGACTCTGTCACCCAGGCTGGA 58874           C     _
           GT                     ACTCCAGCCTGGG GACAGAG CA
                                  |||||||||||| ||||||| ||
                                  TGAGGTCGGACCC CTGTCTC GT
                                        A      A
GAM475  MGC29898 3' TTGCTTTGTTGCCCAGACTGGA 59589       C
           GT                     ACTCCAG CTGGGCGACAGAGCAA
                                  ||||||| ||||||||||||||||
                                  TGAGGTC GACCCGTTGTTTCGTT
                                     A
GAM475  MGC3329  3' CTCTTGTTGTCTAGGCTGGAGT 44246              _
                                ACTCCAGCCTGGGCGACA GAG
                                |||||||||||||||| |||
                                TGAGGTCGGATCTGTTGT CTC
                                           T
GAM475  MGC3771  5' GCTCTTCTTCCCATGCTGGAGT 49055       C   C_  C
                                ACTCCAGC TGGG  GA AGAGC
                                |||||||| ||||  || |||||
                                TGAGGTCG ACCC  CT TCTCG
                                     T   TT  _
GAM475  MGC4638  3' GCTCTGTCACCAGGCTGGAGT  49738          GC
                                ACTCCAGCCTGG  GACAGAGC
                                ||||||||||||  ||||||||
                                TGAGGTCGGACC  CTGTCTCG
                                        A_
GAM475  MGC9912  3' TTGCTCTGTCGCCAGACTGGAG 55611       C   G
           T                    ACTCCAG CTGG CGACAGAGCAA
                                ||||||| |||| ||||||||||
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                                TGAGGTC GACC GCTGTCTCGTT
                                   A   _
GAM475  MKRN4    3'  CTCTGTCACCCAGGCTGGAGT  48461          C
                                ACTCCAGCCTGGG GACAGAG
                                |||||||||||| |||||||
                                TGAGGTCGGACCC CTGTCTC
                                      A
GAM475  moblak   3'  CTGTCGCCCAGACTGGAGT   56399       C
                                ACTCCAG CTGGGCGACAG
                                ||||||| ||||||||||
                                TGAGGTC GACCCGCTGTC
                                   A
GAM475  MOCS3    3'  CTCTGTTGCCCAGGCTGGAGT  27931
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTC

GAM475  MRPL20   3'  GCGCTGTCACCCAGGCTGGAGT 36204          C    A
                                ACTCCAGCCTGGG GACAG GC
                                |||||||||||| ||||| ||
                                TGAGGTCGGACCC CTGTC CG
                                      A    G
GAM475  MRPL35   3'  TTGCTCTGTTGCCCAGGCTGGA 34026
          GT                      ACTCCAGCCTGGGCGACAGAGCAA
                                |||||||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTCGTT

GAM475  MRPL44   3'  CTCTGTCGCCCAGGCTGGA   43596
                                TCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||
                                AGGTCGGACCCGCTGTCTC

GAM475  MRPS27   3'  TTCTGTCACCCAGGCTGGAGT  31337          C
                                ACTCCAGCCTGGG GACAGAG
                                |||||||||||| |||||||
                                TGAGGTCGGACCC CTGTCTT
                                      A
GAM475  MtFMT    3'  CTCTGTCACCCAGGCTGGA   58335         C
                                TCCAGCCTGGG GACAGAG
                                |||||||||| |||||||
                                AGGTCGGACCC CTGTCTC
                                      A
GAM475  MYO5C    3'  GCTCTATCGCCAGGCTGGAGT  38721         G  C
                                ACTCCAGCCTGG CGA AGAGC
                                |||||||||||| ||| |||||
                                TGAGGTCGGACC GCT TCTCG
                                      _  A
GAM475  NAPG     5'  CTCTTTTGCCCAGGCTGGAGT  98537          C
                                ACTCCAGCCTGGGCGA AGAG
                                |||||||||||||||| ||||
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                                TGAGGTCGGACCCGTT TCTC
                                          T
GAM475  NDP52    3'  CTCTGTCACCCAGGCTGGCGT  20670    T        C
                                AC CCAGCCTGGG GACAGAG
                                || |||||||||| |||||||
                                TG GGTCGGACCC CTGTCTC
                                 C         A
GAM475  NDUFB1   5'  GCTGTATCCCCCAGGCTGGAGT 17014             C  CAG
                                ACTCCAGCCTGGG GA   AGC
                                |||||||||||||| ||   |||
                                TGAGGTCGGACCC CT   TCG
                                       C  ATG
GAM475  NDUFC2   3'  TTGCTCTGTCATCAGGCTGGAG 17039           GC
           T                    ACTCCAGCCTGG  GACAGAGCAA
                                |||||||||||  ||||||||||
                                TGAGGTCGGACT  CTGTCTCGTT
                                       A_
GAM475  NFAT5    3'  TTGCTCTGTCTCTCAGGCTAGA 57796     C       C
           G                    CTC AGCCTGGG GACAGAGCAA
                                ||| |||||||| ||||||||||
                                GAG TCGGACTC CTGTCTCGTT
                                 A       T
GAM475  NINJ2    3'  GCTCTTGTTGGCTAGGCTGGAG 33727           G    _
           T                    ACTCCAGCCTGG CGACA GAGC
                                |||||||||||| ||||| ||||
                                TGAGGTCGGATC GTTGT CTCG
                                       G    T
GAM475  NIR3     3'  GCCTGGAGCCCAGGCCAGT   66829     CCA      GA  A
                                ACT   GCCTGGGC  CAG GC
                                |||   ||||||||  ||| ||
                                TGA   CGGACCCG  GTC CG
                                 C__       AG  _
GAM475  NOSIP    5'  CTCTTGTTGCCTAGGCTGGAGT 32543               _
                                ACTCCAGCCTGGGCGACA GAG
                                |||||||||||||||||| |||
                                TGAGGTCGGATCCGTTGT CTC
                                          T
GAM475  NPTXR    3'  TGGGCCCAGGCTGAGT     27448     C       GA
                                ACTC AGCCTGGGC  CA
                                |||| |||||||||  ||
                                TGAG TCGGACCCG  GT
                                  _       G_
GAM475  NPTXR    3'  TGGGCCCAGGCTGAGT     55221     C       GA
                                ACTC AGCCTGGGC  CA
                                |||| |||||||||  ||
                                TGAG TCGGACCCG  GT
                                  _       G_
GAM475  NXN      3'  TTGCTCTGTCGCCCAGGCTGGA 42687
           GT                     ACTCCAGCCTGGGCGACAGAGCAA
                                |||||||||||||||||||||||||
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                                TGAGGTCGGACCCGCTGTCTCGTT

GAM475  OCT11    3'  TTGCTCCAGCCCAGGCTGGAGT 27597            GACA
                                ACTCCAGCCTGGGC   GAGCAA
                                |||||||||||||   ||||||
                                TGAGGTCGGACCCG   CTCGTT
                                      AC__
GAM475  OR51E2   3'  GCTCTGTCACCAGGCTGGAGT  48513          GC
                                ACTCCAGCCTGG  GACAGAGC
                                ||||||||||||  ||||||||
                                TGAGGTCGGACC  CTGTCTCG
                                      A_
GAM475  OSBPL2   3'  CTCTTGTTGCCCAGGCTGGAGT 29898              _
                                ACTCCAGCCTGGGCGACA GAG
                                |||||||||||||||||| |||
                                TGAGGTCGGACCCGTTGT CTC
                                       T
GAM475  OSBPL2   3'  CTCTTGTTGCCCAGGCTGGAGT 58484              _
                                ACTCCAGCCTGGGCGACA GAG
                                |||||||||||||||||| |||
                                TGAGGTCGGACCCGTTGT CTC
                                       T
GAM475  PELI1    5'  CTCTGTCGCCCAGGCTGGAGT  40638
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTC

GAM475  PELI1    5'  TTGCTCTGTCACCCAGGCTGGA 40666           C
           GT                     ACTCCAGCCTGGG GACAGAGCAA
                                |||||||||||| ||||||||||
                                TGAGGTCGGACCC CTGTCTCGTT
                                      A
GAM475  PELI1    5'  TTGCTCTGTTGCCCAGGTTGGA 40667
           GT                     ACTCCAGCCTGGGCGACAGAGCAA
                                |||||||||||||||||||||||
                                TGAGGTTGGACCCGTTGTCTCGTT

GAM475  PIG7     3'  CTATGTTGCCCAGGCTGGTGT  17968    T          G
                                AC CCAGCCTGGGCGACA AG
                                || ||||||||||||||| ||
                                TG GGTCGGACCCGTTGT TC
                                 T           A
GAM475  PIP3-E   3'  TTGCTCTGTTGCCCAGGCTGGA 67362
           GT                     ACTCCAGCCTGGGCGACAGAGCAA
                                |||||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTCGTT

GAM475  PME-1    3'  TGCCCTGGGCTGAGGCCAGG  32871    A_   G  GA  A
                                CC  GCCT GGC  CAG GCA
                                ||  |||| |||  ||| |||
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                                GG  CGGA TCG  GTC CGT
                                 AC    G  G_   C
GAM475  POFUT1    3'  TTGCTCTGTCTCCCAGGCTGGA 70987            C
              GT                  ACTCCAGCCTGGG GACAGAGCAA
                                  |||||||||||| ||||||||||
                                  TGAGGTCGGACCC CTGTCTCGTT
                                         T
GAM475  POLE3     3'  CTCTGTGGCCCAGGCTGGAGT  34315            G
                                  ACTCCAGCCTGGGC ACAGAG
                                  |||||||||||||| ||||||
                                  TGAGGTCGGACCCG TGTCTC
                                         G
GAM475  POR1      3'  CTCTTCAGGCTGGGGT      25729           GCGAC
                                  ACTCCAGCCTGG     AGAG
                                  ||||||||||||     ||||
                                  TGGGGTCGGACT     TCTC
                                                  _____
GAM475  PPIL2     3'  TGCCCTACACCCAGGCTGG    27540          CGAC  A
                                  CCAGCCTGGG    AG GCA
                                  ||||||||||    || |||
                                  GGTCGGACCC    TC CGT
                                        ACA_  C
GAM475  PRO0365   5'  GCTCTGTCGCCAGGCTGAAGT  26986     C       G
                                  ACT CAGCCTGG CGACAGAGC
                                  ||| |||||||| |||||||||
                                  TGA GTCGGACC GCTGTCTCG
                                    A       _
GAM475  PRO0902   3'  CTCTGTCACCCAGGCTGGAGT  54965            C
                                  ACTCCAGCCTGGG GACAGAG
                                  |||||||||||| |||||||
                                  TGAGGTCGGACCC CTGTCTC
                                         A
GAM475  PRO1048   3'  CTCTGCTGCCCAGGCTGGAGT  38112             A
                                  ACTCCAGCCTGGGCG CAGAG
                                  |||||||||||||| |||||
                                  TGAGGTCGGACCCGT GTCTC
                                          C
GAM475  PRO1992   3'  GCTCTTGTCACCCAGGCTGGAG 26908            C   _
              T                    ACTCCAGCCTGGG GACA GAGC
                                   |||||||||||| |||| ||||
                                   TGAGGTCGGACCC CTGT CTCG
                                          A    T
GAM475  PRO1992   5'  TTGCTCTGTCACCCAGACTGGA 26915        C     C
              GT                   ACTCCAG CTGGG GACAGAGCAA
                                   ||||||| ||||| ||||||||||
                                   TGAGGTC GACCC CTGTCTCGTT
                                       A    A
GAM475  PRO2955   3'  CTGTCCCCCAGGCTGAAGT   38238     C       C
                                   ACT CAGCCTGGG GACAG
                                   ||| ||||||||| |||||
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                                TGA GTCGGACCC CTGTC
                                  A       C
GAM475  PSPH     3'  TTGCTCTGTTGCCCAGGCTGGA 17142
                GT                  ACTCCAGCCTGGGCGACAGAGCAA
                                    ||||||||||||||||||||||||
                                    TGAGGTCGGACCCGTTGTCTCGTT

GAM475  PSTPIP2  3'  CTGTCCCCCAGGCTGAAGT   44654    C       C
                                    ACT CAGCCTGGG GACAG
                                    ||| ||||||||| |||||
                                    TGA GTCGGACCC CTGTC
                                      A       C
GAM475  RAB21    3'  GCTCTGTCACCCAGGCTGGAGT 31092           C
                                    ACTCCAGCCTGGG GACAGAGC
                                    |||||||||||| ||||||||
                                    TGAGGTCGGACCC CTGTCTCG
                                           A
GAM475  RAB33B   3'  GCTCTGTCTCCAGGCTGGAGT  49329           C
                                    ACTCCAGCCTGGG GACAGAGC
                                    |||||||||||| ||||||||
                                    TGAGGTCGGACCT CTGTCTCG
                                                _
GAM475  RAB39    3'  TTGTCACCCAGGCTGGAGT   77127           C
                                    ACTCCAGCCTGGG GACAG
                                    |||||||||||| |||||
                                    TGAGGTCGGACCC CTGTT
                                           A
GAM475  RALY     3'  TGCACTGCCCAGGCCAGAG   34117    CA      GAC  A
                                    CTC  GCCTGGGC   AG GCA
                                    |||  ||||||||   || |||
                                    GAG  CGGACCCG   TC CGT
                                      AC       ___  A
GAM475  RAP140   3'  GCTCTGTCGCCCAAGCTGGAGT 31519        C
                                    ACTCCAGC TGGGCGACAGAGC
                                    |||||||| ||||||||||||
                                    TGAGGTCG ACCCGCTGTCTCG
                                        A
GAM475  RES4-25  3'  TTGCTCTTGTTGCCCAGGCTGG 65280                 _
                AGT                   ACTCCAGCCTGGGCGACA GAGCAA
                                      |||||||||||||||||| ||||||
                                      TGAGGTCGGACCCGTTGT CTCGTT
                                             T
GAM475  RNF8     3'  TGACTCTGTTGCCCAAGCTGGA 15577        C        _
                GT                    ACTCCAGC TGGGCGACAGAG CA
                                      |||||||| |||||||||||| ||
                                      TGAGGTCG ACCCGTTGTCTC GT
                                        A          A
GAM475  RNO2     5'  GCTCTGTCACCAAGGCTGGAGT 53939          G  C
                                    ACTCCAGCCT GG GACAGAGC
                                    |||||||||| || ||||||||
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                                TGAGGTCGGA CC CTGTCTCG
                                      A  A
GAM475  SARM     3'  TTGCTCTGTTGTCCAGGCTGGA 31310
              G                  CTCCAGCCTGGGCGACAGAGCAA
                                 ||||||||||||||||||||||
                                 GAGGTCGGACCTGTTGTCTCGTT

GAM475  SCAMP-4  3'  CTCTGTCGCCCAGGCTGGAGT  55346
                                 ACTCCAGCCTGGGCGACAGAG
                                 |||||||||||||||||||||
                                 TGAGGTCGGACCCGCTGTCTC

GAM475  SCAND2   3'  TTCTATCACCCAGGCTGGAGT  42147           C  C
                                 ACTCCAGCCTGGG GA AGAG
                                 |||||||||||| || ||||
                                 TGAGGTCGGACCC CT TCTT
                                       A  A
GAM475  SCYA16   3'  CTCTGTCACCCAGGCTGGAGT  17171           C
                                 ACTCCAGCCTGGG GACAGAG
                                 |||||||||||| |||||||
                                 TGAGGTCGGACCC CTGTCTC
                                       A
GAM475  SCYA22   3'  CTCTGTCGCCCAGGCTGGAGT  92591
                                 ACTCCAGCCTGGGCGACAGAG
                                 |||||||||||||||||||||
                                 TGAGGTCGGACCCGCTGTCTC

GAM475  SCYA22   3'  GCTCTTGTCACCCACGCTGGAG 92598        C   C  _
              T                   ACTCCAGC TGGG GACA GAGC
                                  |||||||| |||| |||| ||||
                                  TGAGGTCG ACCC CTGT CTCG
                                       C   A   T
GAM475  SCYA28   3'  CTCTGTCACACAGGCTGGAG  39541         GGC
                                 CTCCAGCCTG  GACAGAG
                                 ||||||||||  |||||||
                                 GAGGTCGGAC  CTGTCTC
                                       ACA
GAM475  SERF2    5'  TTGCTCTGTTACCCATGCTGGA 20493        C   CG
              GT                   ACTCCAGC TGGG  ACAGAGCAA
                                   |||||||| ||||  |||||||||
                                   TGAGGTCG ACCC  TGTCTCGTT
                                        T   AT
GAM475  SFXN2    3'  TTGCTCTGTCGCCCAGGCTGGA 74387
                                 TCCAGCCTGGGCGACAGAGCAA
                                 |||||||||||||||||||||||
                                 AGGTCGGACCCGCTGTCTCGTT

GAM475  SIRPB1   3'  CTTATTCCCAGGCTGGAGT   21365          CGAC
                                 ACTCCAGCCTGGG   AG
                                 ||||||||||||   ||
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                                TGAGGTCGGACCC   TC
                                      TTAT
GAM475  SLC12A8  3'  GCCTTGTCACCCAGGCTGGAGT 45239          C    A
                                ACTCCAGCCTGGG GACAG GC
                                ||||||||||||| ||||| ||
                                TGAGGTCGGACCC CTGTT CG
                                      A    C
GAM475  SLC16A4  3'  GCTCTTTCGCCCAGGCTGGAGT 17454            C
                                ACTCCAGCCTGGGCGA AGAGC
                                |||||||||||||||| |||||
                                TGAGGTCGGACCCGCT TCTCG
                                       T
GAM475  SLC16A6  5'  TTGCTCTGTCATTCAGGCAAGA 17444     CA     C
            GT                    ACTC  GCCTGGG GACAGAGCAA
                                ||||  ||||||| ||||||||||
                                TGAG  CGGACTT CTGTCTCGTT
                                  AA      A
GAM475  SREC     3'  CTGTCCCCCAGGCTGGAGT    14902          C
                                ACTCCAGCCTGGG GACAG
                                ||||||||||||| |||||
                                TGAGGTCGGACCC CTGTC
                                      C
GAM475  SS-56    3'  CTCTGTTGCCCAGGCTGGAGT  60349
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTC

GAM475  STAF65(gamma) 3'  TTGCTCTGTCACCCAGGCTGGA 30079          C
            GT                    ACTCCAGCCTGGG GACAGAGCAA
                                ||||||||||||| ||||||||||
                                TGAGGTCGGACCC CTGTCTCGTT
                                      A
GAM475  STAM2    3'  GCTCTGTCACCCAGGCTGGAGT 20705          C
                                ACTCCAGCCTGGG GACAGAGC
                                ||||||||||||| ||||||||
                                TGAGGTCGGACCC CTGTCTCG
                                      A
GAM475  SULT1C2  3'  GCTCTGTCGCCCAGGCTGGAGT 22716
                                ACTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTCG

GAM475  SUN1     3'  CTCTGTTGCCCAGGCTGGAGT  47913
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTC

GAM475  SYT13    3'  TTGCTCTTTGTTGCCCAGGCTG 95110              __
            GAGT                    ACTCCAGCCTGGGCGACA  GAGCAA
                                |||||||||||||||||  ||||||
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                                TGAGGTCGGACCCGTTGT  CTCGTT
                                          TT
GAM475  TADA3L   3'  GCACTGTCACCCAGGCTGGAGT 56809          C    A
                                ACTCCAGCCTGGG GACAG GC
                                |||||||||||| ||||| ||
                                TGAGGTCGGACCC CTGTC CG
                                    A    A
GAM475  TCL6     5'  TTGCTCTGTCACTCAGGCTGGA 40497         C
                                TCCAGCCTGGG GACAGAGCAA
                                |||||||||| ||||||||||
                                AGGTCGGACTC CTGTCTCGTT
                                    A
GAM475  TCL6     5'  TTGCTCTGTCACTCAGGCTGGA 40521         C
                                TCCAGCCTGGG GACAGAGCAA
                                |||||||||| ||||||||||
                                AGGTCGGACTC CTGTCTCGTT
                                    A
GAM475  TCL6     5'  TTGCTCTGTCACTCAGGCTGGA 27772         C
                                TCCAGCCTGGG GACAGAGCAA
                                |||||||||| ||||||||||
                                AGGTCGGACTC CTGTCTCGTT
                                    A
GAM475  TCL6     5'  TTGCTCTGTCACTCAGGCTGGA 25920         C
                                TCCAGCCTGGG GACAGAGCAA
                                |||||||||| ||||||||||
                                AGGTCGGACTC CTGTCTCGTT
                                    A
GAM475  TERA     3'  TTGCTCTTGTTACCCAGGCTGG 41425          CG  _
            AGT                   ACTCCAGCCTGGG  ACA GAGCAA
                                |||||||||||||  ||| ||||||
                                TGAGGTCGGACCC  TGT CTCGTT
                                    AT   T
GAM475  TGIF2    3'  CTGTCACCCGGGCTGGAGT    41749          C
                                ACTCCAGCCTGGG GACAG
                                |||||||||||| |||||
                                TGAGGTCGGGCCC CTGTC
                                    A
GAM475  THEA     3'  TTGCTCTGTTGCCCAGGCTGGA 66903
            GT                    ACTCCAGCCTGGGCGACAGAGCAA
                                |||||||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTCGTT

GAM475  TIX1     3'  CTGGGGCGGCCCAGGCTGAAG  62407    C       GA___
                                CT CAGCCTGGGC    CAG
                                || ||||||||||    |||
                                GA GTCGGACCCG    GTC
                                 A        GCGGG
GAM475  TOR1B    3'  CTCCGTCATCCAAGCTGGAGT  27970       C  GC  A
                                ACTCCAGC TGG  GAC GAG
                                |||||||| |||  ||| |||
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                                TGAGGTCG ACC  CTG CTC
                                    A   TA   C
GAM475  TRIM35   3'  TTGCTGTATCACCCAGGCTGGA 61521            C  CAG
          GT                     ACTCCAGCCTGGG GA   AGCAA
                                 ||||||||||||| ||   |||||
                                 TGAGGTCGGACCC CT   TCGTT
                                       A  ATG
GAM475  TRIM5    3'  TTGCTCTTGTTCCCCAGGCTGG 53479            C   _
          AGT                    ACTCCAGCCTGGG GACA GAGCAA
                                 ||||||||||||| |||| ||||||
                                 TGAGGTCGGACCC TTGT CTCGTT
                                       C    T
GAM475  TRIM6    3'  GCTCTGTCGCCCAGGCTGGAGT 55182
                                 ACTCCAGCCTGGGCGACAGAGC
                                 |||||||||||||||||||||||
                                 TGAGGTCGGACCCGCTGTCTCG

GAM475  TU12B1-TY 3'  TTGCTCTTATTGCCCAGGCTGG 33868             C_
          AGT                    ACTCCAGCCTGGGCGA  AGAGCAA
                                 ||||||||||||||||  |||||||
                                 TGAGGTCGGACCCGTT  TCTCGTT
                                       AT
GAM475  TU12B1-TY 3'  TTGCTCTTTTTGCCCAGGCCGG 33869       A       C_
          AGT                    ACTCC GCCTGGGCGA  AGAGCAA
                                 ||||| ||||||||||  |||||||
                                 TGAGG CGGACCCGTT  TCTCGTT
                                    C         TT
GAM475  TUCAN    3'  CTCTGTTACCCAGGCTGGAGT  30975           CG
                                 ACTCCAGCCTGGG  ACAGAG
                                 ||||||||||||||  ||||||
                                 TGAGGTCGGACCC  TGTCTC
                                       AT
GAM475  TUCAN    3'  GCTCTGTCATCTAGGCTGGAGT 30981           GC
                                 ACTCCAGCCTGG  GACAGAGC
                                 ||||||||||||  ||||||||
                                 TGAGGTCGGATC  CTGTCTCG
                                       TA
GAM475  TUSP     3'  CTCTTGTCGCCCAACTAGAGT  40024      C  CC       _
                                 ACTC AG  TGGGCGACA GAG
                                 |||| ||  ||||||||| |||
                                 TGAG TC  ACCCGCTGT CTC
                                    A  A_        T
GAM475  TXNL2    3'  GCTCTGTCACCCAGGCTGGAGT 22582            C
                                 ACTCCAGCCTGGG GACAGAGC
                                 |||||||||||||| ||||||||
                                 TGAGGTCGGACCC CTGTCTCG
                                       A
GAM475  UBF-fl   3'  GCTCTGTCTCCCAGGCTAGAGT 52627      C       C
                                 ACTC AGCCTGGG GACAGAGC
                                 |||| |||||||| ||||||||
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                                TGAG TCGGACCC CTGTCTCG
                                  A       T
GAM475  VDU1     3'  TTGCTTTGTCACCCAGGCTGGA 31132            C
                GT                  ACTCCAGCCTGGG GACAGAGCAA
                                    |||||||||||| ||||||||||
                                    TGAGGTCGGACCC CTGTTTCGTT
                                          A
GAM475  VPS33A   3'  TTGCTCTGTCACCCAGACTAGA 43620      C  C     C
                GT                  ACTC AG CTGGG GACAGAGCAA
                                    |||| || ||||| ||||||||||
                                    TGAG TC GACCC CTGTCTCGTT
                                      A A     A
GAM475  ZNF17    3'  TTGCTCTGTTGCCCAGACTAGA 83280      C  C
                GT                  ACTC AG CTGGGCGACAGAGCAA
                                    |||| || ||||||||||||||||
                                    TGAG TC GACCCGTTGTCTCGTT
                                      A  A
GAM475  ZNF338   3'  GCTCTGTTTCCCAGGCTGGAGT 42258            C
                                    ACTCCAGCCTGGG GACAGAGC
                                    |||||||||||| ||||||||
                                    TGAGGTCGGACCC TTGTCTCG
                                          T
GAM475  ZNF339   3'  CTCTGTCACCCAGGCTGGAGT  41392            C
                                    ACTCCAGCCTGGG GACAGAG
                                    |||||||||||| |||||||
                                    TGAGGTCGGACCC CTGTCTC
                                          A
GAM475  ZTL1     3'  TTGCTCCATCGCCCAGGCTGCA 44145     C          CA
                GT                  ACT CAGCCTGGGCGA  GAGCAA
                                    ||| ||||||||||||  ||||||
                                    TGA GTCGGACCCGCT  CTCGTT
                                      C           AC
GAM475  LOC112687 3'  GCCCTGTCACCCAGGCTGGAGT 73237             C     A
                                    ACTCCAGCCTGGG GACAG GC
                                    |||||||||||| ||||| ||
                                    TGAGGTCGGACCC CTGTC CG
                                          A     C
GAM475  LOC112724 5'  CTCTGTCGCCAGGCTGGA    57304          G
                                    TCCAGCCTGG CGACAGAG
                                    |||||||||| ||||||||
                                    AGGTCGGACC GCTGTCTC
                                              _
GAM475  LOC112817 3'  CTCTGTCACCCAGGCTGGAGT  57324            C
                                    ACTCCAGCCTGGG GACAGAG
                                    |||||||||||| |||||||
                                    TGAGGTCGGACCC CTGTCTC
                                          A
GAM475  LOC113675 5'  TCTGTCACCCAGGCTGGAGT   57383            C
                                    ACTCCAGCCTGGG GACAGA
                                    |||||||||||| ||||||
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                                TGAGGTCGGACCC CTGTCT
                                       A
GAM475  LOC115196 3'  CTGCCACCCAGGCTGGAGT   73658          CGA
                                ACTCCAGCCTGGG  CAG
                                |||||||||||||  |||
                                TGAGGTCGGACCC  GTC
                                       ACC
GAM475  LOC115219 5'  TTGTCCCCCAGGCTGGAGT   73712          C
                                ACTCCAGCCTGGG GACAG
                                |||||||||||||| |||||
                                TGAGGTCGGACCC CTGTT
                                       C
GAM475  LOC115648 3'  GCTCTGTCGCCTGGCTGGAGT  60025        T
                                ACTCCAGCC GGGCGACAGAGC
                                ||||||||| ||||||||||||
                                TGAGGTCGG TCCGCTGTCTCG
                                          _
GAM475  LOC118471 5'  GCTCAGATCCAGGCCCGAGT   74354     CA     CGACA
                                ACTC  GCCTGGG    GAGC
                                ||||  |||||||    ||||
                                TGAG  CGGACCT    CTCG
                                  CC      AGA__
GAM475  LOC119392 3'  GCTCTTGTCATCCTGGCTGGAG 59815        T  GC   _
          T                      ACTCCAGCC GG  GACA GAGC
                                 ||||||||| ||  |||| ||||
                                 TGAGGTCGG CC  CTGT CTCG
                                       T  TA   T
GAM475  LOC120114 3'  TTGCTCTGTCACCCAGGCTAGA 76056     C      C
          GT                     ACTC AGCCTGGG GACAGAGCAA
                                 |||| |||||||| ||||||||||
                                 TGAG TCGGACCC CTGTCTCGTT
                                   A       A
GAM475  LOC120224 5'  TTGCTTTTGTCACCCAGGCTGG 57898          C    _
          AGT                     ACTCCAGCCTGGG GACAGA GCAA
                                  |||||||||||| |||||| ||||
                                  TGAGGTCGGACCC CTGTTT CGTT
                                         A     T
GAM475  LOC120526 3'  CTCTGTCGCGCCAGCTGGAGT  74464        C  _
                                ACTCCAGC TGG GCGACAGAG
                                |||||||| ||| |||||||||
                                TGAGGTCG ACC CGCTGTCTC
                                     _  G
GAM475  LOC120939 3'  TTGCTCTTGTAGCCCAGGCTGG 76772          G  _
          G                      TCCAGCCTGGGC ACA GAGCAA
                                 |||||||||||| ||| ||||||
                                 GGGTCGGACCCG TGT CTCGTT
                                        A  T
GAM475  LOC121504 3'  GCTCTGCCACCGAGGCTGGAGT 74549         G  CGA
                                ACTCCAGCCT GG   CAGAGC
                                |||||||||| ||   ||||||
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                                TGAGGTCGGA CC   GTCTCG
                                      G  ACC
GAM475   LOC125144 3'  TTGCTGTATTGCCCAGGCTGGA 74855              CAG
                GT                    ACTCCAGCCTGGGCGA   AGCAA
                                      ||||||||||||||||   |||||
                                      TGAGGTCGGACCCGTT   TCGTT
                                            ATG
GAM475   LOC126133 3'  GCTCTGTCACCCAGGCTGGAG  74911           C
                                      CTCCAGCCTGGG GACAGAGC
                                      |||||||||||| ||||||||
                                      GAGGTCGGACCC CTGTCTCG
                                            A
GAM475   LOC126364 3'  CTCTGTCACCCAGGCTGGAGT  76189           C
                                      ACTCCAGCCTGGG GACAGAG
                                      |||||||||||| |||||||
                                      TGAGGTCGGACCC CTGTCTC
                                            A
GAM475   LOC126661 3'  CTCAGTTGCCCAGGCTGGAGT  75055             A
                                      ACTCCAGCCTGGGCGAC GAG
                                      |||||||||||||||| |||
                                      TGAGGTCGGACCCGTTG CTC
                                            A
GAM475   LOC126669 3'  GCTGTGTTGCCCAGGCTGGAGT 75939               G
                                      ACTCCAGCCTGGGCGACA AGC
                                      |||||||||||||||| |||
                                      TGAGGTCGGACCCGTTGT TCG
                                            G
GAM475   LOC128077 3'  TTGCTCTGTCGCCCAGGCTAGA 75234      C
                GT                    ACTC AGCCTGGGCGACAGAGCAA
                                      |||| ||||||||||||||||||
                                      TGAG TCGGACCCGCTGTCTCGTT
                                        A
GAM475   LOC128387 3'  GCTGTTGTTGCCCAGGCTGGAG 75257                _
                T                     ACTCCAGCCTGGGCGACAG AGC
                                      |||||||||||||||| |||
                                      TGAGGTCGGACCCGTTGTT TCG
                                            G
GAM475   LOC128989 3'  TTGCTCTGTCACCCAGGCTGGA 75327           C
                GT                    ACTCCAGCCTGGG GACAGAGCAA
                                      |||||||||||| ||||||||||
                                      TGAGGTCGGACCC CTGTCTCGTT
                                            A
GAM475   LOC130813 3'  CTCTGTCACCTAGGCTAGAG   76273     C       C
                                      CTC AGCCTGGG GACAGAG
                                      ||| |||||||| |||||||
                                      GAG TCGGATCC CTGTCTC
                                        A       A
GAM475   LOC130813 3'  GCACTGTCGCCTAGGCTGGAGT 76276               A
                                      ACTCCAGCCTGGGCGACAG GC
                                      |||||||||||||||||| ||
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                                  TGAGGTCGGATCCGCTGTC CG
                                        A
GAM475  LOC131308 3'  TTGCTATGTCACTCAGGCTGGA 75499          C   G
          GT                    ACTCCAGCCTGGG GACA AGCAA
                                ||||||||||||| |||| |||||
                                TGAGGTCGGACTC CTGT TCGTT
                                      A   A
GAM475  LOC131583 5'  GCCCTTGCCCAGGCTGGGGT  76381           AC  A
                                ACTCCAGCCTGGGCG  AG GC
                                |||||||||||||||  || ||
                                TGGGGTCGGACCCGT  TC CG
                                      __  C
GAM475  LOC132625 3'  GCTCTGTCACCCAGGCTGGAGT 76441          C
                                ACTCCAGCCTGGG GACAGAGC
                                |||||||||||| ||||||||
                                TGAGGTCGGACCC CTGTCTCG
                                      A
GAM475  LOC133686 3'  TTGCTTTGTCACCCAGGCTGGA 75624          C
                                TCCAGCCTGGG GACAGAGCAA
                                |||||||||| ||||||||||
                                AGGTCGGACCC CTGTTTCGTT
                                      A
GAM475  LOC135293 3'  GCTCTGTTGCCCAGGCTGAAGT 76686    C
                                ACT CAGCCTGGGCGACAGAGC
                                ||| ||||||||||||||||
                                TGA GTCGGACCCGTTGTCTCG
                                  A
GAM475  LOC135763 3'  GCTCCGTCACCCAGGCTGGAGT 57560          C   A
                                ACTCCAGCCTGGG GAC GAGC
                                |||||||||||| ||| ||||
                                TGAGGTCGGACCC CTG CTCG
                                      A   C
GAM475  LOC135818 3'  TTGCTCTTGTTGCCCAGCCTGG 75756       C       _
          AGT                   ACTCCAG CTGGGCGACA GAGCAA
                                ||||||| |||||||||| ||||||
                                TGAGGTC GACCCGTTGT CTCGTT
                                   C        T
GAM475  LOC138050 5'  TTGCTATGTCACCCAGGCTGGA 75818          C   G
          GT                    ACTCCAGCCTGGG GACA AGCAA
                                ||||||||||||| |||| |||||
                                TGAGGTCGGACCC CTGT TCGTT
                                      A   A
GAM475  LOC138199 3'  GCTCTGTCTCCCAGGCCGGAGT 75825     A     C
                                ACTCC GCCTGGG GACAGAGC
                                ||||| ||||||| ||||||||
                                TGAGG CGGACCC CTGTCTCG
                                   C      T
GAM475  LOC139422 5'  GCTCTGTTGCCCAGACTGGAGT 76352       C
                                ACTCCAG CTGGGCGACAGAGC
                                ||||||| ||||||||||||||
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                                TGAGGTC GACCCGTTGTCTCG
                                   A
GAM475  LOC142913 5'  TTGCTCTCTCACCCAGGCTGGA 76935          C  C
                GT                  ACTCCAGCCTGGG GA AGAGCAA
                                    ||||||||||||| || |||||||
                                    TGAGGTCGGACCC CT TCTCGTT
                                          A  C
GAM475  LOC142927 5'  CTATGTTGCCCAAGCTGGTGT  76945    T    C       G
                                    AC CCAGC TGGGCGACA AG
                                    || ||||| ||||||||| ||
                                    TG GGTCG ACCCGTTGT TC
                                     T    A       A
GAM475  LOC142927 5'  CTGTCGCCCAGACTGTAGT   76946    C  C
                                    ACT CAG CTGGGCGACAG
                                    ||| ||| ||||||||||
                                    TGA GTC GACCCGCTGTC
                                      T  A
GAM475  LOC143153 3'  TGACTCTGTCACCCAGGCTGGA 76985          C     _
                GT                  ACTCCAGCCTGGG GACAGAG CA
                                    ||||||||||||| ||||||| ||
                                    TGAGGTCGGACCC CTGTCTC GT
                                          A      A
GAM475  LOC143154 3'  TGACTCTGTCACCCAGGCTGGA 76995          C     _
                GT                  ACTCCAGCCTGGG GACAGAG CA
                                    ||||||||||||| ||||||| ||
                                    TGAGGTCGGACCC CTGTCTC GT
                                          A      A
GAM475  LOC143187 3'  TTGCCCTGTCGCCTGGCTGGAG 59768        T       A
                T                    ACTCCAGCC GGGCGACAG GCAA
                                    ||||||||| ||||||||| ||||
                                    TGAGGTCGG TCCGCTGTC CGTT
                                       _       C
GAM475  LOC143241 5'  CTCTTGTTGCCCAGGCTGGAGT 57973                _
                                    ACTCCAGCCTGGGCGACA GAG
                                    |||||||||||||||||| |||
                                    TGAGGTCGGACCCGTTGT CTC
                                          T
GAM475  LOC144248 5'  GCTCTTTCGCCCAGGCTGGAGT 77255            C
                                    ACTCCAGCCTGGGCGA AGAGC
                                    |||||||||||||||| |||||
                                    TGAGGTCGGACCCGCT TCTCG
                                          T
GAM475  LOC144305 3'  GCTCTGTTGCCCAGGCTGGAGT 83972
                                    ACTCCAGCCTGGGCGACAGAGC
                                    ||||||||||||||||||||||
                                    TGAGGTCGGACCCGTTGTCTCG

GAM475  LOC144317 5'  CTGTCGCCCAGGCTGGAGT   77293
                                    ACTCCAGCCTGGGCGACAG
                                    ||||||||||||||||||
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                                TGAGGTCGGACCCGCTGTC

GAM475  LOC144524 5'  TTGCTCTTGTTGCCCAAGCTGG 84071         C       _
                AGT                    ACTCCAGC TGGGCGACA GAGCAA
                                       |||||||| ||||||||| ||||||
                                       TGAGGTCG ACCCGTTGT CTCGTT
                                           A        T
GAM475  LOC144667 3'  TTGCTCTGTCATCCAGGCTGGA 84093           GC
                G                       CTCCAGCCTGG  GACAGAGCAA
                                        ||||||||||  ||||||||||
                                        GAGGTCGGACC  CTGTCTCGTT
                                              TA
GAM475  LOC144742 5'  CTCTGTTGCCTAGGCTGGAGT  77457
                                        ACTCCAGCCTGGGCGACAGAG
                                        |||||||||||||||||||
                                        TGAGGTCGGATCCGTTGTCTC

GAM475  LOC144776 5'  CTCCATCACTCAGGCTGGAGT  77490           C  CA
                                        ACTCCAGCCTGGG GA  GAG
                                        ||||||||||||  ||  |||
                                        TGAGGTCGGACTC CT  CTC
                                              A  AC
GAM475  LOC144776 5'  TTCTGTTGCCCAGGCTGGAGT  77498
                                        ACTCCAGCCTGGGCGACAGAG
                                        |||||||||||||||||||
                                        TGAGGTCGGACCCGTTGTCTT

GAM475  LOC144817 5'  TTGCTCTGTCGCCCAGGCTGGA 77525
                GT                      ACTCCAGCCTGGGCGACAGAGCAA
                                        ||||||||||||||||||||||||
                                        TGAGGTCGGACCCGCTGTCTCGTT

GAM475  LOC144871 3'  TTGCTCTGTTGCCCAGGCTGGA 84132
                GT                      ACTCCAGCCTGGGCGACAGAGCAA
                                        ||||||||||||||||||||||||
                                        TGAGGTCGGACCCGTTGTCTCGTT

GAM475  LOC145009 3'  GCTCTGTCGCCCAGGCTGGAGT 60977
                                        ACTCCAGCCTGGGCGACAGAGC
                                        |||||||||||||||||||||
                                        TGAGGTCGGACCCGCTGTCTCG

GAM475  LOC145268 5'  CTCTTTTGCCCAGGCTGGAG   77577           C
                                        CTCCAGCCTGGGCGA AGAG
                                        |||||||||||||| ||||
                                        GAGGTCGGACCCGTT TCTC
                                                 T
GAM475  LOC145725 3'  GCTCTGTCACCAGGCTGGAGT  77885           GC
                                        ACTCCAGCCTGG  GACAGAGC
                                        ||||||||||  ||||||||
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                                TGAGGTCGGACC CTGTCTCG
                                      A_
GAM475  LOC145732 3'  GCTCTGTCACCAGGCTGGAGT 77897          GC
                                ACTCCAGCCTGG GACAGAGC
                                |||||||||||| ||||||||
                                TGAGGTCGGACC CTGTCTCG
                                      A_
GAM475  LOC145757 5'  GCTCTGTCGCCCAGGCTGGAGT 77936
                                ACTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTCG

GAM475  LOC145757 5'  TTGCTCTGTCGCCCAGGCTGGA 77945
                GT                ACTCCAGCCTGGGCGACAGAGCAA
                                |||||||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTCGTT

GAM475  LOC145813 5'  GCTCTGTCACCCAGGCTGGAGT 84510           C
                                ACTCCAGCCTGGG GACAGAGC
                                |||||||||||| ||||||||
                                TGAGGTCGGACCC CTGTCTCG
                                      A
GAM475  LOC146050 3'  CTCTGTCGTCCAGGCTGGAGT  78114
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||
                                TGAGGTCGGACCTGCTGTCTC

GAM475  LOC146050 3'  TTGCTCTTGTTGCCCAGGCTGG 78130                _
                AGT                ACTCCAGCCTGGGCGACA GAGCAA
                                |||||||||||||||| ||||||
                                TGAGGTCGGACCCGTTGT CTCGTT
                                         T
GAM475  LOC146229 3'  CTCTGTCGCCCAGGCTAGAGT  78278      C
                                ACTC AGCCTGGGCGACAGAG
                                |||| ||||||||||||||
                                TGAG TCGGACCCGCTGTCTC
                                  A
GAM475  LOC146229 3'  GCTCTGTCGCCCAGGCTGGAGT 78290
                                ACTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTCG

GAM475  LOC146229 3'  GCTCTGTTGCCTAGGCTGGAGT 78291
                                ACTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||
                                TGAGGTCGGATCCGTTGTCTCG

GAM475  LOC146346 5'  CTCCGTTGCCAGGCTGGAGT   78394          G   A
                                ACTCCAGCCTGG CGAC GAG
                                |||||||||||| |||| |||
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                                TGAGGTCGGACC GTTG CTC
                                      _   C
GAM475   LOC146346 5'  CTCGTTGCCCAGGCTGGAGT   78395              A
                                ACTCCAGCCTGGGCGAC GAG
                                |||||||||||||||| |||
                                TGAGGTCGGACCCGTTG CTC
                                                 _
GAM475   LOC146429 5'  GCTCTGTCACCAGGCTGGAGT  84669           GC
                                ACTCCAGCCTGG  GACAGAGC
                                ||||||||||||  ||||||||
                                TGAGGTCGGACC  CTGTCTCG
                                      A_
GAM475   LOC146443 5'  CTCCTAACCCCGGGCTGGAGT  78445           CGACA
                                ACTCCAGCCTGGG    GAG
                                ||||||||||||    |||
                                TGAGGTCGGGCCC    CTC
                                      CAATC
GAM475   LOC146455 3'  CTCTGTCGCCCAGGCTGGAGT  78458
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTC

GAM475   LOC146603 5'  GCTCTGTCGCCCAGGCTGGAGT 78598
                                ACTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTCG

GAM475   LOC146784 5'  CTCTTGTTGCCCAGGCTGGAGT 78711                _
                                ACTCCAGCCTGGGCGACA GAG
                                |||||||||||||||| |||
                                TGAGGTCGGACCCGTTGT CTC
                                      T
GAM475   LOC146839 3'  CTCTGTTGCCCAGGCTGGAGT  84840
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTC

GAM475   LOC146894 3'  CTGCTGCCCAGGCTGGAGT    59859           A
                                ACTCCAGCCTGGGCG CAG
                                ||||||||||||| |||
                                TGAGGTCGGACCCGT GTC
                                      C
GAM475   LOC146895 5'  CTCTGTCACCCAGGCTGGAGT  84867           C
                                ACTCCAGCCTGGG GACAGAG
                                |||||||||||| |||||||
                                TGAGGTCGGACCC CTGTCTC
                                      A
GAM475   LOC146909 3'  GCTCTGTCGCCCAGGCTGGAGT 78776
                                ACTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||||
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                                TGAGGTCGGACCCGCTGTCTCG

GAM475  LOC146909 3'  CTCTGTCGCCCAGGCTGGAGT  78769
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTC

GAM475  LOC146952 5'  GCTCTGTTGCCCAGGCTGGA   84929
                                TCCAGCCTGGGCGACAGAGC
                                ||||||||||||||||||||
                                AGGTCGGACCCGTTGTCTCG

GAM475  LOC147080 5'  CTGTCCGCCAGGCTGGAGT    85036          G  _
                                ACTCCAGCCTGG CG ACAG
                                |||||||||||| || ||||
                                TGAGGTCGGACC GC TGTC
                                       _  C
GAM475  LOC147166 3'  GCACTGTTGCCCAGGCTGGAGT 78890               A
                                ACTCCAGCCTGGGCGACAG GC
                                |||||||||||||||||| ||
                                TGAGGTCGGACCCGTTGTC CG
                                          A
GAM475  LOC147276 3'  CTCTTGTTGCCCACGCTGGAGT 78958        C       _
                                ACTCCAGC TGGGCGACA GAG
                                |||||||| ||||||||| |||
                                TGAGGTCG ACCCGTTGT CTC
                                     C       T
GAM475  LOC147343 5'  CTCTGTCACCCAGGCTAGAG   85127     C       C
                                CTC AGCCTGGG GACAGAG
                                ||| |||||||| |||||||
                                GAG TCGGACCC CTGTCTC
                                  A       A
GAM475  LOC147694 3'  TTGCTCTGTCACCCAGGCTGGA 79112            C
          GT                      ACTCCAGCCTGGG GACAGAGCAA
                                ||||||||||||| ||||||||||
                                TGAGGTCGGACCC CTGTCTCGTT
                                        A
GAM475  LOC147817 3'  CTCTGTCGCCCAGGCTGGAGT  79176
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTC

GAM475  LOC147817 3'  GCTCTGTCACCCAGGCTGTAGT 79183     C       C
                                ACT CAGCCTGGG GACAGAGC
                                ||| ||||||||| ||||||||
                                TGA GTCGGACCC CTGTCTCG
                                  T       A
GAM475  LOC147841 3'  CTCTTGTTGTCCAGTCTGGAGT 79226        C       _
                                ACTCCAG CTGGGCGACA GAG
                                ||||||| |||||||||| |||
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                                TGAGGTC GACCTGTTGT CTC
                                   T         T
GAM475   LOC147990 3'  CTCTGTCACCCAGGCTGGAGT  85221            C
                                ACTCCAGCCTGGG GACAGAG
                                ||||||||||||| |||||||
                                TGAGGTCGGACCC CTGTCTC
                                      A
GAM475   LOC147990 3'  TTGCTCTGTCACCCAGGCTAGA 85243    C       C
                                TC AGCCTGGG GACAGAGCAA
                                || |||||||| ||||||||||
                                AG TCGGACCC CTGTCTCGTT
                                 A       A
GAM475   LOC148137 3'  GCTCTGTCACCCAGGCTGGAGT 59104            C
                                ACTCCAGCCTGGG GACAGAGC
                                |||||||||||| ||||||||
                                TGAGGTCGGACCC CTGTCTCG
                                      A
GAM475   LOC148137 3'  TTGTTGCCCAGGCTGTAGT    59114     C
                                ACT CAGCCTGGGCGACAG
                                ||| ||||||||||||||
                                TGA GTCGGACCCGTTGTT
                                  T
GAM475   LOC148147 3'  CTCTGTCACCAGGCTGGAGT   79398           GC
                                ACTCCAGCCTGG  GACAGAG
                                ||||||||||||  |||||||
                                TGAGGTCGGACC  CTGTCTC
                                      A_
GAM475   LOC148195 5'  TTGCTCTGTCACCTAGGCTGCA 85298     C       C
            GT                    ACT CAGCCTGGG GACAGAGCAA
                                ||| ||||||||| ||||||||||
                                TGA GTCGGATCC CTGTCTCGTT
                                  C        A
GAM475   LOC148195 3'  TTGCTCTGTTATCCAGGCTGGT 85299    T       GC
            GT                    AC CCAGCCTGG  GACAGAGCAA
                                || |||||||||  ||||||||||
                                TG GGTCGGACC  TTGTCTCGTT
                                 T        TA
GAM475   LOC148198 3'  TTGCTCTGTCGCCCACCCAGGC 71230          ____
            TGGAGT                  ACTCCAGCCT    GGGCGACAGAGCAA
                                ||||||||||   ||||||||||||||
                                TGAGGTCGGA    CCCGCTGTCTCGTT
                                      CCCA
GAM475   LOC148443 3'  CTCTGTCACCCAGGCTGGG    79601           C
                                TCCAGCCTGGG GACAGAG
                                |||||||||||| |||||||
                                GGGTCGGACCC CTGTCTC
                                      A
GAM475   LOC148645 5'  CTCTGTTGCCAAGGCTGGA    85332         G
                                TCCAGCCT GGCGACAGAG
                                |||||||| ||||||||||
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                                AGGTCGGA CCGTTGTCTC
                                    A
GAM475  LOC148645 5'  CTGTGTTGGCCAGGCTGGAGT  85333          G    G
                                ACTCCAGCCTGG CGACA AG
                                |||||||||||| ||||| ||
                                TGAGGTCGGACC GTTGT TC
                                      G    G
GAM475  LOC148709 3'  GCTCTAGTTGCCCACACTAGAG 79695     C  CC      _
          T                    ACTC AG  TGGGCGAC AGAGC
                               |||| ||  |||||||| |||||
                               TGAG TC  ACCCGTTG TCTCG
                                 A  AC       A
GAM475  LOC148887 5'  GCTCTGTCGCCCAGGCTGGAGT 85404
                               ACTCCAGCCTGGGCGACAGAGC
                               |||||||||||||||||||||
                               TGAGGTCGGACCCGCTGTCTCG

GAM475  LOC149421 3'  CTCTGTCGCCCAGGCTGGAG   80144
                               CTCCAGCCTGGGCGACAGAG
                               ||||||||||||||||||
                               GAGGTCGGACCCGCTGTCTC

GAM475  LOC149422 3'  CTGGCTCCCAGGCTGGAGT    80134           CGA
                               ACTCCAGCCTGGG   CAG
                               ||||||||||||   |||
                               TGAGGTCGGACCC   GTC
                                     TCG
GAM475  LOC149478 3'  TTGCTCTGTCGTCGAGGCTGGA 80181          G
          GT                   ACTCCAGCCT GGCGACAGAGCAA
                               |||||||||| ||||||||||||
                               TGAGGTCGGA CTGCTGTCTCGTT
                                     G
GAM475  LOC149506 3'  CTGTTGCCCAGGCTGTAGT    85634     C
                               ACT CAGCCTGGGCGACAG
                               ||| ||||||||||||||
                               TGA GTCGGACCCGTTGTC
                                 T
GAM475  LOC149577 3'  CTCTGCCACCCAAGCTGGAGT  85673        C    CGA
                               ACTCCAGC TGGG   CAGAG
                               |||||||| ||||   |||||
                               TGAGGTCG ACCC   GTCTC
                                    A    ACC
GAM475  LOC149577 3'  GCTTTGTTGCCCAGGCTGGAGT 85680
                               ACTCCAGCCTGGGCGACAGAGC
                               |||||||||||||||||||||
                               TGAGGTCGGACCCGTTGTTTCG

GAM475  LOC149692 3'  GCTCTGTCACCCAGGCTGGAGT 85739           C
                               ACTCCAGCCTGGG GACAGAGC
                               |||||||||||| ||||||||
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                                TGAGGTCGGACCC CTGTCTCG
                                      A
GAM475  LOC149703 5'  CTGCTGCCCAAGCTGGAGT   85819       C     A
                                ACTCCAGC TGGGCG CAG
                                |||||||| ||||||| |||
                                TGAGGTCG ACCCGT GTC
                                    A     C
GAM475  LOC149734 3'  TTGCTCTGTCACCCAGGCTGGA 85799           C
          GT                      ACTCCAGCCTGGG GACAGAGCAA
                                |||||||||||| ||||||||||
                                TGAGGTCGGACCC CTGTCTCGTT
                                      A
GAM475  LOC150054 5'  CTCTGTCGCCCAGGCTGGAGT  85971
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTC

GAM475  LOC150225 3'  TTGCTCTGTCGCTCAGGCTGGA 86209
          GT                      ACTCCAGCCTGGGCGACAGAGCAA
                                |||||||||||||||||||||||
                                TGAGGTCGGACTCGCTGTCTCGTT

GAM475  LOC150290 3'  TGCTCTGTCACCCATCCTAGAG 80593     C  CC    C
          T                      ACTC AG  TGGG GACAGAGCA
                                |||| ||  |||| |||||||||
                                TGAG TC  ACCC CTGTCTCGT
                                  A  CT    A
GAM475  LOC150295 3'  GCTCCGTCTCCAGGCTGGA    86155          C   A
                                TCCAGCCTGGG GAC GAGC
                                |||||||||| ||| ||||
                                AGGTCGGACCT CTG CTCG
                                      _   C
GAM475  LOC150397 3'  CTCTGTCGTCCAGGTTAGAGT  80661      C
                                ACTC AGCCTGGGCGACAGAG
                                |||| ||||||||||||||||
                                TGAG TTGGACCTGCTGTCTC
                                  A
GAM475  LOC150407 3'  TTGCTCTGTTGTCCAGGCTAGA 80646      C
          GT                      ACTC AGCCTGGGCGACAGAGCAA
                                |||| ||||||||||||||||||
                                TGAG TCGGACCTGTTGTCTCGTT
                                  A
GAM475  LOC150696 3'  GCTCTGTCACCCAGGCTGGAGT 59160           C
                                ACTCCAGCCTGGG GACAGAGC
                                |||||||||||| ||||||||
                                TGAGGTCGGACCC CTGTCTCG
                                      A
GAM475  LOC150696 3'  TTGCCATGTTGCCCAGGCTGGA 59169             GA
                                TCCAGCCTGGGCGACA  GCAA
                                |||||||||||||||  ||||
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                                AGGTCGGACCCGTTGT  CGTT
                                      AC
GAM475  LOC150960 3'  TCTGTCACCCAGGCTGGAGT   80880          C
                                ACTCCAGCCTGGG GACAGA
                                |||||||||||| ||||||
                                TGAGGTCGGACCC CTGTCT
                                      A
GAM475  LOC151057 3'  CTCTGTCACCCAGGCTGGAGT  86387          C
                                ACTCCAGCCTGGG GACAGAG
                                |||||||||||| |||||||
                                TGAGGTCGGACCC CTGTCTC
                                      A
GAM475  LOC151195 3'  TGCGTTGTCCAGGCTGGAGT   80971            AGA
                                ACTCCAGCCTGGGCGAC   GCA
                                |||||||||||||||||   |||
                                TGAGGTCGGACCTGTTG   CGT
                                      ___
GAM475  LOC151201 3'  CTGTCACCAGGCTGGAGT    86474          GC
                                ACTCCAGCCTGG  GACAG
                                ||||||||||| |||||
                                TGAGGTCGGACC  CTGTC
                                      A_
GAM475  LOC151201 3'  TTCTGTCACCCAGGCTGGAGT  86493          C
                                ACTCCAGCCTGGG GACAGAG
                                |||||||||||| |||||||
                                TGAGGTCGGACCC CTGTCTT
                                      A
GAM475  LOC151475 5'  GCTCTGTCATCCAGGCTGGAGT 86596          GC
                                ACTCCAGCCTGG  GACAGAGC
                                ||||||||||| ||||||||
                                TGAGGTCGGACC  CTGTCTCG
                                      TA
GAM475  LOC151475 5'  TTGCTCTGTGGCCCAGGCTGGA 86608          G
          GT                    ACTCCAGCCTGGGC ACAGAGCAA
                                |||||||||||||| |||||||||
                                TGAGGTCGGACCCG TGTCTCGTT
                                      G
GAM475  LOC151701 3'  GCTCTGTCGCCCAGGCTGGAGT 86674
                                ACTCCAGCCTGGGCGACAGAGC
                                ||||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTCG

GAM475  LOC151826 3'  CTCTGTCACCCAGGCTGGAGT  81180          C
                                ACTCCAGCCTGGG GACAGAG
                                |||||||||||| |||||||
                                TGAGGTCGGACCC CTGTCTC
                                      A
GAM475  LOC151877 3'  TTGCTGTGTTGCCCAGGCT    86703          G
                                AGCCTGGGCGACA AGCAA
                                |||||||||||| |||||
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                                TCGGACCCGTTGT TCGTT
                                      G
GAM475  LOC151979 5'  TTGACTGTTGCCCAAGCTGGA  81257       C        AG
                                TCCAGC TGGGCGACAG  CAA
                                |||||| ||||||||||  |||
                                AGGTCG ACCCGTTGTC  GTT
                                   A        A_
GAM475  LOC152137 3'  GCCCTGTCACACAGGCTGGAGT 81320          GGC    A
                                ACTCCAGCCTG   GACAG GC
                                ||||||||||   ||||| ||
                                TGAGGTCGGAC   CTGTC CG
                                      ACA    C
GAM475  LOC152220 3'  CTCTGTCACTCAGGCTGGAGT  86764          C
                                ACTCCAGCCTGGG GACAGAG
                                |||||||||||| |||||||
                                TGAGGTCGGACTC CTGTCTC
                                      A
GAM475  LOC152245 3'  GCTCTGTAGCCCAGGCTGGAGT 86780           G
                                ACTCCAGCCTGGGC ACAGAGC
                                |||||||||||||| |||||||
                                TGAGGTCGGACCCG TGTCTCG
                                       A
GAM475  LOC152245 3'  GCTCTGTCGCCCAGGCTGGAGT 86781
                                ACTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTCG

GAM475  LOC152282 5'  TTGCCCTGTTGCCCAGGCTGGA 81408               A
          GT                    ACTCCAGCCTGGGCGACAG GCAA
                                |||||||||||||||||| ||||
                                TGAGGTCGGACCCGTTGTC CGTT
                                      C
GAM475  LOC152300 3'  CTTTGTCACCCAGGCTGGAGT  81384          C
                                ACTCCAGCCTGGG GACAGAG
                                |||||||||||| |||||||
                                TGAGGTCGGACCC CTGTTTC
                                      A
GAM475  LOC152343 3'  TTGCTGTGTCACCCAGGCTGGA 81443          C   G
          GT                    ACTCCAGCCTGGG GACA AGCAA
                                |||||||||||| |||| |||||
                                TGAGGTCGGACCC CTGT TCGTT
                                      A   G
GAM475  LOC152445 3'  TCTGTTGCCCAGGCTGGAGT   86967
                                ACTCCAGCCTGGGCGACAGA
                                ||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCT

GAM475  LOC152620 3'  CTCTGTTGCCCAGGCTGGAGT  60709
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||
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                                TGAGGTCGGACCCGTTGTCTC

GAM475  LOC152719 5'  CTCTGTCGCCCAGGCTGGA   87024
                                TCCAGCCTGGGCGACAGAG
                                ||||||||||||||||||
                                AGGTCGGACCCGCTGTCTC

GAM475  LOC152719 5'  GCTCTGTCGCCCAGCCTGGAGT 87033       C
                                ACTCCAG CTGGGCGACAGAGC
                                ||||||| |||||||||||||
                                TGAGGTC GACCCGCTGTCTCG
                                    C
GAM475  LOC152794 5'  TTGGTCTGTTACCCAGGCTGGA 81569          CG    G
          GT                     ACTCCAGCCTGGG  ACAGA CAA
                                ||||||||||||  ||||| |||
                                TGAGGTCGGACCC  TGTCT GTT
                                       AT    G
GAM475  LOC152851 3'  TTCTGGCCTAGGCTGGAGT   81600          GA
                                ACTCCAGCCTGGGC  CAGAG
                                ||||||||||||||  |||||
                                TGAGGTCGGATCCG  GTCTT
                                       __
GAM475  LOC152925 3'  GCTCAGTGGCCCAGGCTGGAGT 81620          G  A
                                ACTCCAGCCTGGGC AC GAGC
                                |||||||||||||| || ||||
                                TGAGGTCGGACCCG TG CTCG
                                       G  A
GAM475  LOC153077 3'  CTGATATCACCCAGGCTGGAGT 87124          C  ___
                                ACTCCAGCCTGGG GA   CAG
                                |||||||||||||| ||   |||
                                TGAGGTCGGACCC CT   GTC
                                       A  ATA
GAM475  LOC153443 3'  TTCTGTTGCCCAGACTAGAGT  81692     C  C
                                ACTC AG CTGGGCGACAGAG
                                |||| || ||||||||||||||
                                TGAG TC GACCCGTTGTCTT
                                  A  A
GAM475  LOC153688 3'  CTCTGTCACCCAGGCTGGAGT  87309          C
                                ACTCCAGCCTGGG GACAGAG
                                |||||||||||||| |||||||
                                TGAGGTCGGACCC CTGTCTC
                                       A
GAM475  LOC153811 3'  CTCTGTCGCCCAGACTGGAGT  81832       C
                                ACTCCAG CTGGGCGACAGAG
                                ||||||| ||||||||||||||
                                TGAGGTC GACCCGCTGTCTC
                                    A
GAM475  LOC153811 3'  CTCTGTTGCCCAGACTGGAGT  81833       C
                                ACTCCAG CTGGGCGACAGAG
                                ||||||| ||||||||||||||
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                                TGAGGTC GACCCGTTGTCTC
                                    A
GAM475  LOC153811 5'  GCTCTGTCACCCAGGCAGGAGT 81838      A      C
                                ACTCC GCCTGGG GACAGAGC
                                ||||| ||||||| ||||||||
                                TGAGG CGGACCC CTGTCTCG
                                   A      A
GAM475  LOC154282 5'  GCTCTGTCGCCAGGTTGGAGT  87407           G
                                ACTCCAGCCTGG CGACAGAGC
                                |||||||||||| |||||||||
                                TGAGGTTGGACC GCTGTCTCG
                                      _
GAM475  LOC154726 5'  GCTCTTGTTGCCCAGGCTGGAG 82010                _
             T                   ACTCCAGCCTGGGCGACA GAGC
                                ||||||||||||||||| ||||
                                TGAGGTCGGACCCGTTGT CTCG
                                        T
GAM475  LOC154822 3'  TTGTCAGCCAGGCTGGAGT    87489          GC
                                ACTCCAGCCTGG  GACAG
                                ||||||||||||  |||||
                                TGAGGTCGGACC  CTGTT
                                      GA
GAM475  LOC154877 5'  CTGTTTCCCAGGTTGGAGT    87546           C
                                ACTCCAGCCTGGG GACAG
                                |||||||||||| |||||
                                TGAGGTTGGACCC TTGTC
                                       T
GAM475  LOC154877 3'  GCTCTGTCGCCCAGGGTGGAGT 87557       G
                                ACTCCA CCTGGGCGACAGAGC
                                |||||| ||||||||||||||
                                TGAGGT GGACCCGCTGTCTCG
                                   G
GAM475  LOC155061 3'  TGCTCTGCCCAGTTGGGCTGAG 82193     C   ____   GAC
             T                   ACTC AGCCT   GGGC   AGAGCA
                                |||| |||||   ||||  ||||||
                                TGAG TCGGG   CCCG   TCTCGT
                                  _    TTGA   ___
GAM475  LOC157421 5'  CTCTTGCCAAGTTGGAGT    87738        CTG   AC
                                ACTCCAGC   GGCG  AGAG
                                ||||||||   ||||  ||||
                                TGAGGTTG   CCGT  TCTC
                                    AA_   __
GAM475  LOC157506 3'  GCTCTGTCACCAGGCTGGAGT  82369          GC
                                ACTCCAGCCTGG  GACAGAGC
                                ||||||||||||  ||||||||
                                TGAGGTCGGACC  CTGTCTCG
                                      A_
GAM475  LOC157798 5'  TTGCTGTGTCACCAGGCTGGAG 87869          GC   G
                                CTCCAGCCTGG  GACA AGCAA
                                ||||||||||  |||| |||||
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                                GAGGTCGGACC  CTGT TCGTT
                                      A_   G
GAM475  LOC158014 5'  CTCTTGTCACCCAGGCTGGAGT 82558           C   _
                                ACTCCAGCCTGGG GACA GAG
                                |||||||||||| |||| |||
                                TGAGGTCGGACCC CTGT CTC
                                      A   T
GAM475  LOC158056 3'  TGCCCCGCCCAGGCTGGG    82598          ACAGA
                                TCCAGCCTGGGCG    GCA
                                ||||||||||||    |||
                                GGGTCGGACCCGC    CGT
                                      CC___
GAM475  LOC158204 5'  TGCCTCATCCCAGGCTGAG   67714    C      CGAC  A
                                CTC AGCCTGGG   AG GCA
                                ||| ||||||||   || |||
                                GAG TCGGACCC   TC CGT
                                  _      TAC_  _
GAM475  LOC158310 5'  CTCTGTCGCCCAGGCTGGAGT  88080
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTC

GAM475  LOC158402 5'  CTCTGTTGCCCAGGCTGGAGT  88146
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTC

GAM475  LOC158476 3'  TTGCTCTGTCGCCCAGGCTGGA 88210
           GT                   ACTCCAGCCTGGGCGACAGAGCAA
                                |||||||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTCGTT

GAM475  LOC158510 5'  GCCTGTTGCCCTGACCAGAGT  82835     CAGCCT       A
                                ACTC     GGGCGACAG GC
                                ||||     ||||||||| ||
                                TGAG     CCCGTTGTC CG
                                  ACCAGT       _
GAM475  LOC158549 5'  TTGTCTCCCAGGCTGGAGT   88234          C
                                ACTCCAGCCTGGG GACAG
                                |||||||||||| |||||
                                TGAGGTCGGACCC CTGTT
                                      T
GAM475  LOC158668 3'  CTCTGTTGCCCAGGCTGGAGT  69899
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTC

GAM475  LOC160646 3'  TCTGTCACCCAGGCTGGAGT   83124          C
                                ACTCCAGCCTGGG GACAGA
                                |||||||||||| ||||||
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                                TGAGGTCGGACCC CTGTCT
                                      A
GAM475  LOC161829 3'  CTCTGTCACCCAGGCTGGAGT  83188          C
                                ACTCCAGCCTGGG GACAGAG
                                ||||||||||||| |||||||
                                TGAGGTCGGACCC CTGTCTC
                                      A
GAM475  LOC162427 3'  GCTCTGTTGCCCAGGCTGGAGT 83226
                                ACTCCAGCCTGGGCGACAGAGC
                                ||||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTCG

GAM475  LOC162962 3'  CTCTGTCGCCAGGCTGGA    83256        G
                                TCCAGCCTGG CGACAGAG
                                |||||||||| ||||||||
                                AGGTCGGACC GCTGTCTC

                                      _
GAM475  LOC196047 5'  CTCTGTCTCCCAGGCTGGAGT  91151          C
                                ACTCCAGCCTGGG GACAGAG
                                ||||||||||||| |||||||
                                TGAGGTCGGACCC CTGTCTC
                                      T
GAM475  LOC196264 3'  CTCTGTCGCCAGGCTGGAGT   88984         G
                                ACTCCAGCCTGG CGACAGAG
                                |||||||||||| ||||||||
                                TGAGGTCGGACC GCTGTCTC

                                      _
GAM475  LOC196529 3'  GCTCTTGTTGCCCAGGCTGGAG 89135                _
          T                      ACTCCAGCCTGGGCGACA GAGC
                                ||||||||||||||||| ||||
                                TGAGGTCGGACCCGTTGT CTCG
                                         T
GAM475  LOC196529 3'  TTGCTCTTGTTGCCCAGGCTGG 89146                _
          AGT                      ACTCCAGCCTGGGCGACA GAGCAA
                                |||||||||||||||| ||||||
                                TGAGGTCGGACCCGTTGT CTCGTT
                                         T
GAM475  LOC196957 3'  GCTCTGTCACCAGGCTGGAGT  89190          GC
                                ACTCCAGCCTGG  GACAGAGC
                                ||||||||||||  ||||||||
                                TGAGGTCGGACC  CTGTCTCG
                                      A_
GAM475  LOC196961 3'  GCTCTGTCACCAGGCTGGAGT  89204          GC
                                ACTCCAGCCTGG  GACAGAGC
                                ||||||||||||  ||||||||
                                TGAGGTCGGACC  CTGTCTCG
                                      A_
GAM475  LOC197138 3'  GCTCTGTCACCAGGCTGGAGT  89253          GC
                                ACTCCAGCCTGG  GACAGAGC
                                ||||||||||||  ||||||||
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                                TGAGGTCGGACC  CTGTCTCG
                                      A_
GAM475  LOC197358 3'  CTGTCACCCAGGCTGGAGT    89430           C
                                ACTCCAGCCTGGG GACAG
                                |||||||||||| |||||
                                TGAGGTCGGACCC CTGTC
                                      A
GAM475  LOC197358 3'  GCTCTTGTCGCCCAGGCTGGAG 89436                _
          T                      ACTCCAGCCTGGGCGACA GAGC
                                ||||||||||||||||| ||||
                                TGAGGTCGGACCCGCTGT CTCG
                                        T
GAM475  LOC199699 3'  CTCTGTCACCCAGGCTGGAGT  89673           C
                                ACTCCAGCCTGGG GACAGAG
                                |||||||||||| |||||||
                                TGAGGTCGGACCC CTGTCTC
                                      A
GAM475  LOC199699 3'  GCTCTGTCGCCCAGGCTGGAGT 89676
                                ACTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTCG

GAM475  LOC199725 5'  CTCTGTCACCTAGGCTGGA    91417          C
                                TCCAGCCTGGG GACAGAG
                                |||||||||| |||||||
                                AGGTCGGATCC CTGTCTC
                                      A
GAM475  LOC199786 3'  TTGCTCTGTCACCCGGGCTGGA 89772           C
            GT                    ACTCCAGCCTGGG GACAGAGCAA
                                |||||||||||| ||||||||||
                                TGAGGTCGGGCCC CTGTCTCGTT
                                      A
GAM475  LOC199899 5'  CTCTGTGTCTCAGGCTGGAGT  91467          _  G
                                ACTCCAGCCTG GGC ACAGAG
                                |||||||||| ||| ||||||
                                TGAGGTCGGAC CTG TGTCTC
                                      T  _
GAM475  LOC199906 3'  GCTGTGTTGTCCAGGCTGGAGT 89854                G
                                ACTCCAGCCTGGGCGACA AGC
                                |||||||||||||||| |||
                                TGAGGTCGGACCTGTTGT TCG
                                        G
GAM475  LOC199936 5'  GCTCTGTCACCCAGGCTGGAGT 91483           C
                                ACTCCAGCCTGGG GACAGAGC
                                |||||||||||| ||||||||
                                TGAGGTCGGACCC CTGTCTCG
                                      A
GAM475  LOC200014 3'  CTGCCAGCCAGGCTGGAGT    89930          G GA_
                                ACTCCAGCCTGG C   CAG
                                |||||||||||| |   |||
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                                TGAGGTCGGACC G   GTC
                                      _ ACC
GAM475   LOC200107 3'  GCTCTGTTGGCCAGGCTGGAGT 89989          G
                                ACTCCAGCCTGG CGACAGAGC
                                |||||||||||| |||||||||
                                TGAGGTCGGACC GTTGTCTCG
                                       G
GAM475   LOC200169 5'  TTCTGTCGTCCAGGCTGGAGT  91563
                                ACTCCAGCCTGGGCGACAGAG
                                ||||||||||||||||||||
                                TGAGGTCGGACCTGCTGTCTT

GAM475   LOC200268 3'  CTCTGTCGCCCAGGTTGGAGT  90085
                                ACTCCAGCCTGGGCGACAGAG
                                ||||||||||||||||||||
                                TGAGGTTGGACCCGCTGTCTC

GAM475   LOC200282 3'  GCTCTTAAGACATGGCTGGAG  90100        _ GGCGAC
                                CTCCAGCC TG     AGAGC
                                |||||||| ||     |||||
                                GAGGTCGG AC     TCTCG
                                     T  AGAAT_
GAM475   LOC200301 5'  GCTATCGCCCAGGCTGGAGT   90142           CAG
                                ACTCCAGCCTGGGCGA   AGC
                                ||||||||||||||||   |||
                                TGAGGTCGGACCCGCT   TCG
                                       A__
GAM475   LOC200310 3'  GCTCTTGTCACCTAGGCTGGAG 66329          C   _
           T                     ACTCCAGCCTGGG GACA GAGC
                                ||||||||||||| |||| ||||
                                TGAGGTCGGATCC CTGT CTCG
                                       A   T
GAM475   LOC200316 3'  CTCTGTCGCCCAGACTAGAGT  90179     C  C
                                ACTC AG CTGGGCGACAGAG
                                |||| || ||||||||||||
                                TGAG TC GACCCGCTGTCTC
                                  A  A
GAM475   LOC200860 3'  GCTCTTGTTGTCCAGGCTGGAG 91752            _
           T                     ACTCCAGCCTGGGCGACA GAGC
                                |||||||||||||||| ||||
                                TGAGGTCGGACCTGTTGT CTCG
                                       T
GAM475   LOC200860 3'  TTGCTCTGTCACCCAGGCTGGA 91763          C
           GT                    ACTCCAGCCTGGG GACAGAGCAA
                                |||||||||||| ||||||||||
                                TGAGGTCGGACCC CTGTCTCGTT
                                       A
GAM475   LOC201102 3'  TGCTCTGTCCTGACCAGGT   89474       GC__
                                GCCTGG   GACAGAGCA
                                ||||||   |||||||||
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                                TGGACC    CTGTCTCGT
                                   AGTC
GAM475   LOC201164 3'  CTCTGTGGCCCAGGCTGGAGT  89492            G
                                ACTCCAGCCTGGGC ACAGAG
                                |||||||||||||| ||||||
                                TGAGGTCGGACCCG TGTCTC
                                       G
GAM475   LOC201294 3'  GCTCTGTCGCCCAGGCTGGAGT 89586
                                ACTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTCG

GAM475   LOC201294 3'  TTGCTCTGTTGCCAGGCCAGAG 89599      CA     G
           T                     ACTC  GCCTGG CGACAGAGCAA
                                 ||||  |||||| ||||||||||
                                 TGAG  CGGACC GTTGTCTCGTT
                                   AC     _
GAM475   LOC201626 3'  CTCTTGTTGCCCAGGCTGGAGT 90431              _
                                ACTCCAGCCTGGGCGACA GAG
                                |||||||||||||||||| |||
                                TGAGGTCGGACCCGTTGT CTC
                                       T
GAM475   LOC201627 3'  TTGCTCTTGTTGCCCAGGCTGG 90466              _
           AGT                    ACTCCAGCCTGGGCGACA GAGCAA
                                  |||||||||||||||||| ||||||
                                  TGAGGTCGGACCCGTTGT CTCGTT
                                         T
GAM475   LOC201696 3'  CTCTTGTTGCCCAGGCTGGAGT 63818              _
                                ACTCCAGCCTGGGCGACA GAG
                                |||||||||||||||||| |||
                                TGAGGTCGGACCCGTTGT CTC
                                       T
GAM475   LOC201702 5'  CTCTTGTCACCCAGGCTGGAGT 90471            C   _
                                ACTCCAGCCTGGG GACA GAG
                                |||||||||||| |||| |||
                                TGAGGTCGGACCC CTGT CTC
                                      A   T
GAM475   LOC202025 3'  CTCTGTCAGCCAGGCTGGAGT  91888          GC
                                ACTCCAGCCTGG  GACAGAG
                                ||||||||||||  |||||||
                                TGAGGTCGGACC  CTGTCTC
                                      GA
GAM475   LOC202460 5'  TTGCTCTGTCACCAGGCTGGAG 90686          GC
           T                     ACTCCAGCCTGG  GACAGAGCAA
                                 ||||||||||||  ||||||||||
                                 TGAGGTCGGACC  CTGTCTCGTT
                                       A_
GAM475   LOC202908 5'  CTCTGTCACCCAGGCTGGAGT  90722            C
                                ACTCCAGCCTGGG GACAGAG
                                |||||||||||| |||||||
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                                TGAGGTCGGACCC CTGTCTC
                                      A
GAM475  LOC202934 3'  CTCTGTCACCCAGGCTGGAGT  92038          C
                                ACTCCAGCCTGGG GACAGAG
                                |||||||||||| |||||||
                                TGAGGTCGGACCC CTGTCTC
                                      A
GAM475  LOC202934 3'  GCTCTGTCACCAGGCTGGAGT  92041          GC
                                ACTCCAGCCTGG  GACAGAGC
                                ||||||||||||  ||||||||
                                TGAGGTCGGACC  CTGTCTCG
                                      A_
GAM475  LOC203197 3'  TTGCACTGTCACCCAGGCTGGA 90822          C    A
          GT                    ACTCCAGCCTGGG GACAG GCAA
                                |||||||||||| ||||| ||||
                                TGAGGTCGGACCC CTGTC CGTT
                                      A    A
GAM475  LOC203297 5'  GCTCTGTCACCCAGGCTGGAGT 75872          C
                                ACTCCAGCCTGGG GACAGAGC
                                |||||||||||| ||||||||
                                TGAGGTCGGACCC CTGTCTCG
                                      A
GAM475  LOC203350 3'  CTCTGTTGCCCAGGCTGGAGT  92236
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTC

GAM475  LOC203369 3'  TTGCCGCGTCTCCCAGGCTGGA 90894          C  AGA
          GT                    ACTCCAGCCTGGG GAC   GCAA
                                |||||||||||| |||   ||||
                                TGAGGTCGGACCC CTG   CGTT
                                      T  CGC
GAM475  LOC203378 3'  GCTCTGTCGCCCAGGCTGGAG  92292
                                CTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||
                                GAGGTCGGACCCGCTGTCTCG

GAM475  LOC203427 3'  TTGCTCTGTCACCCAGACTGGA 90925       C    C
          GT                    ACTCCAG CTGGG GACAGAGCAA
                                ||||||| ||||| ||||||||||
                                TGAGGTC GACCC CTGTCTCGTT
                                   A    A
GAM475  LOC204804 3'  CTGTGTCTCCCAGGCTGGAGT  91041          C   G
                                ACTCCAGCCTGGG GACA AG
                                |||||||||||| |||| ||
                                TGAGGTCGGACCC CTGT TC
                                      T   G
GAM475  LOC204804 3'  TCTGTCACCCAGGCTAGAGT  91055     C      C
                                ACTC AGCCTGGG GACAGA
                                |||| |||||||| ||||||
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                                TGAG TCGGACCC CTGTCT
                                  A       A
GAM475  LOC219294 3'  TGACTCTGTCACCCAGGCTGGA 94600          C     _
                GT                  ACTCCAGCCTGGG GACAGAG CA
                                    |||||||||||| ||||||| ||
                                    TGAGGTCGGACCC CTGTCTC GT
                                          A      A
GAM475  LOC219295 3'  TGACTCTGTCACCCAGGCTGGA 94590          C     _
                GT                  ACTCCAGCCTGGG GACAGAG CA
                                    |||||||||||| ||||||| ||
                                    TGAGGTCGGACCC CTGTCTC GT
                                          A      A
GAM475  LOC219445 5'  GCTTTGTTGCCCAGGCTGGAGT 93208
                                    ACTCCAGCCTGGGCGACAGAGC
                                    ||||||||||||||||||||||
                                    TGAGGTCGGACCCGTTGTTTCG

GAM475  LOC219731 5'  CTCTGTCATCCAGGCTGGAGT  94703          GC
                                    ACTCCAGCCTGG  GACAGAG
                                    ||||||||||||  |||||||
                                    TGAGGTCGGACC  CTGTCTC
                                          TA
GAM475  LOC219735 3'  TTGCTCTGTTGCCCAGGCTGGA 94739
                GT                  ACTCCAGCCTGGGCGACAGAGCAA
                                    ||||||||||||||||||||||||
                                    TGAGGTCGGACCCGTTGTCTCGTT

GAM475  LOC219894 3'  TTGCTCTGTTGCCCCAGGCTGG 94913          _
                AGT                   ACTCCAGCCTGGG CGACAGAGCAA
                                    |||||||||||| ||||||||||
                                    TGAGGTCGGACCC GTTGTCTCGTT
                                          C
GAM475  LOC219908 5'  GCCCCAGTCCAGGCTGAGT   95978     C       GACAGA
                                    ACTC AGCCTGGGC     GC
                                    |||| |||||||||     ||
                                    TGAG TCGGACCTG     CG
                                      _       ACCC__
GAM475  LOC220064 3'  CTCTGTCGCCGAGTTTGGAGT  95064       C  G
                                    ACTCCAG CT GGCGACAGAG
                                    ||||||| || ||||||||||
                                    TGAGGTT GA CCGCTGTCTC
                                       T  G
GAM475  LOC220074 3'  CTCGTCACCCCAGCTGGAGT   59974       CT   C   A
                                    ACTCCAGC  GGG GAC GAG
                                    ||||||||  ||| ||| |||
                                    TGAGGTCG  CCC CTG CTC
                                       AC   A  _
GAM475  LOC220074 3'  CTCTGTCACACAGGCTGGAGT  59975          GGC
                                    ACTCCAGCCTG   GACAGAG
                                    ||||||||||   |||||||
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                                TGAGGTCGGAC   CTGTCTC
                                      ACA
GAM475   LOC220074 3'  GCTCTGTCACCCAGGCTGGAGT 59985            C
                                ACTCCAGCCTGGG GACAGAGC
                                ||||||||||||| ||||||||
                                TGAGGTCGGACCC CTGTCTCG
                                       A
GAM475   LOC220662 3'  GCCGTTGCCCAGGCTGGAGT   92824              AGA
                                ACTCCAGCCTGGGCGAC   GC
                                ||||||||||||||||   ||
                                TGAGGTCGGACCCGTTG   CG
                                      C__
GAM475   LOC220739 3'  CTCTGCTTCCAGGCTGGGG   94519           CGA
                                CTCCAGCCTGGG   CAGAG
                                ||||||||||||   |||||
                                GGGGTCGGACCT   GTCTC
                                       TC_
GAM475   LOC221035 3'  TTGCTCTGTCACCAGGCTGGAG 94784           GC
           T                     ACTCCAGCCTGG  GACAGAGCAA
                                ||||||||||||  ||||||||||
                                TGAGGTCGGACC  CTGTCTCGTT
                                       A_
GAM475   LOC221060 3'  TTGCCCTTGTTGCCCAGGCTGG 94839                A_
           AGT                    ACTCCAGCCTGGGCGACAG  GCAA
                                ||||||||||||||||||  ||||
                                TGAGGTCGGACCCGTTGTT  CGTT
                                      CC
GAM475   LOC221271 3'  CTCTGTCACTCAGGCTGGAGT  93515            C
                                ACTCCAGCCTGGG GACAGAG
                                ||||||||||||| |||||||
                                TGAGGTCGGACTC CTGTCTC
                                       A
GAM475   LOC221296 3'  TTGCTCTGTCGCCCAGGTTGGA 93620
           GT                     ACTCCAGCCTGGGCGACAGAGCAA
                                ||||||||||||||||||||||||
                                TGAGGTTGGACCCGCTGTCTCGTT

GAM475   LOC221576 3'  CTGAGCTCCAGGCTGAAG    95320    C      _  GA
                                CT CAGCCTGG GC  CAG
                                || |||||||| ||  |||
                                GA GTCGGACC CG  GTC
                                 A       T  A_
GAM475   LOC221663 5'  GCTCTGTTGCCAAGGCTGGAGT 95465           G
                                ACTCCAGCCT GGCGACAGAGC
                                |||||||||| ||||||||||
                                TGAGGTCGGA CCGTTGTCTCG
                                       A
GAM475   LOC221773 3'  TTGCTCTGTCTCCCAGGCTGGA 92702            C
           GT                     ACTCCAGCCTGGG GACAGAGCAA
                                |||||||||||| ||||||||||
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                                TGAGGTCGGACCC CTGTCTCGTT
                                       T
GAM475  LOC221814 5'  TTGCTCTGTCGCCAAGCCAGAG 95563      CA  CTG
           T                    ACTC  GC   GGCGACAGAGCAA
                                ||||  ||   ||||||||||||
                                TGAG  CG   CCGCTGTCTCGTT
                                  AC  AA_
GAM475  LOC221960 3'  GCTCCGTGACCCAGGCTGGA   92726          CG  A
                                TCCAGCCTGGG  AC GAGC
                                ||||||||||  || ||||
                                AGGTCGGACCC  TG CTCG
                                       AG  C
GAM475  LOC221964 3'  CTCTGTCTCCCAGGCTGGA    95604          C
                                TCCAGCCTGGG GACAGAG
                                |||||||||| |||||||
                                AGGTCGGACCC CTGTCTC
                                       T
GAM475  LOC222068 3'  TTGCTCTTGTCGCCCAGGCTGG 94283                 _
           AGT                    ACTCCAGCCTGGGCGACA GAGCAA
                                  |||||||||||||||| ||||||
                                  TGAGGTCGGACCCGCTGT CTCGTT
                                         T
GAM475  LOC222070 5'  TTGCTCTGTCTCCCAGGCTGGA 95824           C
           GT                     ACTCCAGCCTGGG GACAGAGCAA
                                  |||||||||||| ||||||||||
                                  TGAGGTCGGACCC CTGTCTCGTT
                                         T
GAM475  LOC245771 5'  GCTCTGTCGCCCAGGCTGGA   94480
                                TCCAGCCTGGGCGACAGAGC
                                ||||||||||||||||||||
                                AGGTCGGACCCGCTGTCTCG

GAM475  LOC253612 5'  GCTCTGTCTCCCAGGCTGGAGT 98552           C
                                ACTCCAGCCTGGG GACAGAGC
                                |||||||||||| ||||||||
                                TGAGGTCGGACCC CTGTCTCG
                                       T
GAM475  LOC253664 3'  GCTCTGTTGCCCAGGCTGGAGT 96468
                                ACTCCAGCCTGGGCGACAGAGC
                                ||||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTCG

GAM475  LOC253779 3'  TTGCTCTGTCACCCAGGTTGGA 98928           C
           GT                     ACTCCAGCCTGGG GACAGAGCAA
                                  |||||||||||| ||||||||||
                                  TGAGGTTGGACCC CTGTCTCGTT
                                         A
GAM475  LOC253805 3'  CTCTGTTGCCCAGGCTGGAGT  98173
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||||
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                                TGAGGTCGGACCCGTTGTCTC

GAM475  LOC254013 3'  GCTCTGTCGTCCAGGCTGGAGT 96534
                                ACTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||
                                TGAGGTCGGACCTGCTGTCTCG

GAM475  LOC254082 5'  TTGCTGTGTCGCCCAAGCTAGA 98998      C  C       G
          GT                    ACTC AGC TGGGCGACA AGCAA
                                |||| ||| ||||||||| |||||
                                TGAG TCG ACCCGCTGT TCGTT
                                  A  A        G
GAM475  LOC254249 5'  CTCTGTCACCCAGGCTGGA   97182          C
                                TCCAGCCTGGG GACAGAG
                                |||||||||| |||||||
                                AGGTCGGACCC CTGTCTC
                                       A
GAM475  LOC254351 3'  TTGTTGTCCAGGCTGGAGT   96698
                                ACTCCAGCCTGGGCGACAG
                                |||||||||||||||||||
                                TGAGGTCGGACCTGTTGTT

GAM475  LOC254587 5'  CTGGCCCAGACTGAGAG     99524    _  C     GA
                                CTC CAG CTGGGC  CAG
                                ||| ||| ||||||  |||
                                GAG GTC GACCCG  GTC
                                  A  A    __
GAM475  LOC254655 3'  TTGTCTCCCAGGCTGGAGT   97228          C
                                ACTCCAGCCTGGG GACAG
                                |||||||||||| |||||
                                TGAGGTCGGACCC CTGTT
                                       T
GAM475  LOC254672 3'  CTCTGTTGCCCAGGCTGGAGT  96293
                                ACTCCAGCCTGGGCGACAGAG
                                |||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTC

GAM475  LOC255177 3'  CTCTCGTTGCCCAGGCTGGAGT 98392              _
                                ACTCCAGCCTGGGCGAC AGAG
                                |||||||||||||||| ||||
                                TGAGGTCGGACCCGTTG TCTC
                                          C
GAM475  LOC255196 5'  CTATTTTGCCCAGGCTGGAGT  98953            CAG
                                ACTCCAGCCTGGGCGA   AG
                                ||||||||||||||||   ||
                                TGAGGTCGGACCCGTT   TC
                                          TTA
GAM475  LOC255196 5'  TTGCTCTATTGCTCAGGCTGGA 98970             C
          GT                    ACTCCAGCCTGGGCGA AGAGCAA
                                |||||||||||||||| |||||||
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                                TGAGGTCGGACTCGTT TCTCGTT
                                       A
GAM475  LOC255465 3'  CTCTGTCACCCAGGCTGGAGT  99112          C
                                ACTCCAGCCTGGG GACAGAG
                                ||||||||||||| |||||||
                                TGAGGTCGGACCC CTGTCTC
                                       A
GAM475  LOC255465 3'  GCTCTGTCACCAGGCTGGAGT  99117          GC
                                ACTCCAGCCTGG  GACAGAGC
                                ||||||||||||  ||||||||
                                TGAGGTCGGACC  CTGTCTCG
                                       A_
GAM475  LOC255497 3'  GCTCTGTCGCCCTGGCTGGAGT 98986          T
                                ACTCCAGCC GGGCGACAGAGC
                                ||||||||| ||||||||||||
                                TGAGGTCGG CCCGCTGTCTCG
                                      T
GAM475  LOC255919 3'  GCTCTGTTGCCAGGCTGGAG   96747          G
                                CTCCAGCCTGG CGACAGAGC
                                |||||||||||  |||||||||
                                GAGGTCGGACC GTTGTCTCG
                                       _
GAM475  LOC256221 3'  GCTCTGTAACTCAGGCTGGAGT 96913          CG
                                ACTCCAGCCTGGG  ACAGAGC
                                |||||||||||||  |||||||
                                TGAGGTCGGACTC  TGTCTCG
                                       AA
GAM475  LOC256306 3'  TTGCTCTGTCGCCCAGGCTGGA 98523
                GT                    ACTCCAGCCTGGGCGACAGAGCAA
                                ||||||||||||||||||||||||
                                TGAGGTCGGACCCGCTGTCTCGTT

GAM475  LOC256360 5'  GCTCTGTTGCCCAGTCTGGAGT 98328        C
                                ACTCCAG CTGGGCGACAGAGC
                                ||||||| ||||||||||||||
                                TGAGGTC GACCCGTTGTCTCG
                                     T
GAM475  LOC256476 5'  TTCTGTCACCCAGGCTGGAGT  98627          C
                                ACTCCAGCCTGGG GACAGAG
                                |||||||||||| |||||||
                                TGAGGTCGGACCC CTGTCTT
                                       A
GAM475  LOC257054 5'  GCTCTCACCCAGGCTGGAGT   97374          C  CA
                                ACTCCAGCCTGGG GA  GAGC
                                |||||||||||| ||  ||||
                                TGAGGTCGGACCC CT  CTCG
                                       A  __
GAM475  LOC257463 3'  CTATCCCCAGGCTGGAGT    71622          C  C
                                ACTCCAGCCTGGG GA AG
                                |||||||||||| || ||
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                                TGAGGTCGGACCC CT TC
                                       _ A
GAM475  LOC257465 3'  CTCTGTCTTCCAGGCTGGAGT  82494           C
                                ACTCCAGCCTGGG GACAGAG
                                ||||||||||||| |||||||
                                TGAGGTCGGACCT CTGTCTC
                                       T
GAM475  LOC257486 3'  GCTCTGTTACCCAGATTGGAGT 69775       GC    CG
                                ACTCCA  CTGGG  ACAGAGC
                                ||||||  |||||  |||||||
                                TGAGGT  GACCC  TGTCTCG
                                   TA    AT
GAM475  LOC257515 3'  CTGAGCTCCAGGCTGAAG    99620    C      _ GA
                                CT CAGCCTGG GC  CAG
                                || ||||||| ||  |||
                                GA GTCGGACC CG  GTC
                                 A       T  A_
GAM475  LOC257572 3'  CTGAGCTCCAGGCTGAAG    99740    C      _ GA
                                CT CAGCCTGG GC  CAG
                                || ||||||| ||  |||
                                GA GTCGGACC CG  GTC
                                 A       T  A_
GAM475  LOC51030  5'  TTGCTCCCTCAAAGCTGAAGT  32698    C   C_   CGACA
                                ACT CAGC  TGGG    GAGCAA
                                ||| ||||  ||||    ||||||
                                TGA GTCG  ACTC    CTCGTT
                                  A   AA   C____
GAM475  LOC51031  5'  TTGCTCTGTCATCAGGCTGGAG 32713          GC
           T                     ACTCCAGCCTGG  GACAGAGCAA
                                ||||||||||||  ||||||||||
                                TGAGGTCGGACT  CTGTCTCGTT
                                       A_
GAM475  LOC51162  3'  TGCCCAGCGCCCCAGGCTGGA  33051          _ ACAGA
                                TCCAGCCTGGG CG    GCA
                                |||||||||| ||    |||
                                AGGTCGGACCC GC    CGT
                                       C  GACC_
GAM475  LOC51162  3'  TGCCCAGCGCCCCAGGCTGGA  66398          _ ACAGA
                                TCCAGCCTGGG CG    GCA
                                |||||||||| ||    |||
                                AGGTCGGACCC GC    CGT
                                       C  GACC_
GAM475  LOC51193  5'  CTCCTGTTACCCAGGCTGGAG  33365          CG   _
                                CTCCAGCCTGGG  ACAG AG
                                ||||||||||||  |||| ||
                                GAGGTCGGACCC  TGTC TC
                                       AT   C
GAM475  LOC51200  3'  TTGCTCTTGTTGCCCAGGCTGG 33442               _
           AGT                    ACTCCAGCCTGGGCGACA GAGCAA
                                ||||||||||||||||| ||||||
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                                TGAGGTCGGACCCGTTGT CTCGTT
                                          T
GAM475  LOC51219  5' TTGCCTTTGTCGCCCAGGCTGG 33552                  _
             AGT                  ACTCCAGCCTGGGCGACAGAG CAA
                                  |||||||||||||||||||| |||
                                  TGAGGTCGGACCCGCTGTTTC GTT
                                            C
GAM475  LOC51334  5' CTCTGTTGCCCAGGCTAGAGT  34059     C
                                  ACTC AGCCTGGGCGACAGAG
                                  |||| ||||||||||||||||
                                  TGAG TCGGACCCGTTGTCTC
                                    A
GAM475  LOC51336  3' CTCTGTTACCCAGGCTGGAGT  34070          CG
                                  ACTCCAGCCTGGG  ACAGAG
                                  ||||||||||||  ||||||
                                  TGAGGTCGGACCC  TGTCTC
                                          AT
GAM475  LOC51622  3' GCTCCGTGACCCAGGCTGGA   32209          CG  A
                                  TCCAGCCTGGG  AC GAGC
                                  ||||||||||  || ||||
                                  AGGTCGGACCC  TG CTCG
                                         AG  C
GAM475  LOC51696  3' CTCTTGTCACCCAGGCTGGAGT 33082          C   _
                                  ACTCCAGCCTGGG GACA GAG
                                  |||||||||||| |||| |||
                                  TGAGGTCGGACCC CTGT CTC
                                          A   T
GAM475  LOC56181  5' GCTCTGTCACCCAGGTTGGAGT 97277          C
                                  ACTCCAGCCTGGG GACAGAGC
                                  |||||||||||| ||||||||
                                  TGAGGTTGGACCC CTGTCTCG
                                          A
GAM475  LOC57107  3' TTGCTCTTGTTGCCCAGGCTGG 40198              _
             AGT                  ACTCCAGCCTGGGCGACA GAGCAA
                                  |||||||||||||||| ||||||
                                  TGAGGTCGGACCCGTTGT CTCGTT
                                            T
GAM475  LOC81034  3' TTGCTTTGTCGCCCAGGCTGGA 48600
             GT                   ACTCCAGCCTGGGCGACAGAGCAA
                                  ||||||||||||||||||||||||
                                  TGAGGTCGGACCCGCTGTTTCGTT

GAM475  LOC89231  3' CTCTTGTTGCCCAGGCTGGAGT 94296              _
                                  ACTCCAGCCTGGGCGACA GAG
                                  |||||||||||||||| |||
                                  TGAGGTCGGACCCGTTGT CTC
                                            T
GAM475  LOC89932  3' CTCTTGTTGCCCAGGCTGGAG  61458            _
                                  CTCCAGCCTGGGCGACA GAG
                                  |||||||||||||||| |||
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                                GAGGTCGGACCCGTTGT CTC
                                        T
GAM475  LOC90141  3' CTTTGTCACCTAAGCTGGAGT  62303        C    C
                                ACTCCAGC TGGG GACAGAG
                                |||||||| |||| |||||||
                                TGAGGTCG ATCC CTGTTTC
                                    A    A
GAM475  LOC90155  3' CTCTATGTCCCAGGCTAGAGT  62367      C       _  AC
                                ACTC AGCCTGGG CG  AGAG
                                |||| |||||||| ||  ||||
                                TGAG TCGGACCC GT  TCTC
                                  A       T  A_
GAM475  LOC90288  3' TGTCACCCAGGCTGGAGT    62805            C
                                ACTCCAGCCTGGG GACA
                                |||||||||||| ||||
                                TGAGGTCGGACCC CTGT
                                        A
GAM475  LOC90333  3' TTGCTCTGTCGCCCAGGTTGGA 62969
                GT                ACTCCAGCCTGGGCGACAGAGCAA
                                  ||||||||||||||||||||||||
                                  TGAGGTTGGACCCGCTGTCTCGTT

GAM475  LOC90371  5' GTTCTGTCACCCAGGCTGGAGT 63166            C
                                ACTCCAGCCTGGG GACAGAGC
                                |||||||||||| ||||||||
                                TGAGGTCGGACCC CTGTCTTG
                                        A
GAM475  LOC90485  3' CTCTGTCACCCAGGCTAGAGT  63697      C       C
                                ACTC AGCCTGGG GACAGAG
                                |||| |||||||| |||||||
                                TGAG TCGGACCC CTGTCTC
                                  A       A
GAM475  LOC90485  3' TTGCTCTGTCGCCCAGGCTGGA 63716
                GT                ACTCCAGCCTGGGCGACAGAGCAA
                                  ||||||||||||||||||||||||
                                  TGAGGTCGGACCCGCTGTCTCGTT

GAM475  LOC90591  3' GCTCTGTCACCCAGGCTGGAGT 64174            C
                                ACTCCAGCCTGGG GACAGAGC
                                |||||||||||| ||||||||
                                TGAGGTCGGACCC CTGTCTCG
                                        A
GAM475  LOC90591  3' TTGTTCTGTTGCCCAGGCTGGA 64198
                GT                ACTCCAGCCTGGGCGACAGAGCAA
                                  ||||||||||||||||||||||||
                                  TGAGGTCGGACCCGTTGTCTTGTT

GAM475  LOC90786  5' TTGCTCTGCACTGGCATGAAGT 64734     C  _   T  GCGA
                                ACT CA GCC GG    CAGAGCAA
                                ||| || ||| ||    ||||||||
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                                TGA GT CGG TC    GTCTCGTT
                                  A  A   _  AC__
GAM475  LOC90999  3'  CTCTGTTGCCCAGGCTGGAGT  65183
                                ACTCCAGCCTGGGCGACAGAG
                                ||||||||||||||||||||
                                TGAGGTCGGACCCGTTGTCTC

GAM475  LOC91115  3'  CTCTTGTCACCCAGGCTGGAGT 65563            C   _
                                ACTCCAGCCTGGG GACA GAG
                                |||||||||||| |||| |||
                                TGAGGTCGGACCC CTGT CTC
                                        A   T
GAM475  LOC91250  5'  GCTCTGTCACCCAGGCTGGAGT 65918            C
                                ACTCCAGCCTGGG GACAGAGC
                                |||||||||||| ||||||||
                                TGAGGTCGGACCC CTGTCTCG
                                        A
GAM475  LOC91291  5'  GCTCTGTCGCCCAGACTAGA   66091    C  C
                                TC AG CTGGGCGACAGAGC
                                || || ||||||||||||||
                                AG TC GACCCGCTGTCTCG
                                 A  A
GAM475  LOC91373  3'  CTCTTGTTGCCCAGGCTGGAGT 66413                _
                                ACTCCAGCCTGGGCGACA GAG
                                |||||||||||||||| |||
                                TGAGGTCGGACCCGTTGT CTC
                                          T
GAM475  LOC91661  3'  CTCTGTCGGCCAGGCTGGA   57213          G
                                TCCAGCCTGG CGACAGAG
                                |||||||||| ||||||||
                                AGGTCGGACC GCTGTCTC
                                      G
GAM475  LOC91893  3'  TTGCTCTGCCGCCCAGGCGGGA 68083      A       A
          GT                    ACTCC GCCTGGGCG CAGAGCAA
                                ||||| ||||||||| ||||||||
                                TGAGG CGGACCCGC GTCTCGTT
                                  G        C
GAM475  LOC92148  5'  GCCCTGCCGCCCAGGCTAGAGT 68883      C       A   A
                                ACTC AGCCTGGGCG CAG GC
                                |||| |||||||||| ||| ||
                                TGAG TCGGACCCGC GTC CG
                                  A        C   C
GAM475  LOC92303  3'  GCTCTTGTTGCCCGGGCTGGAG 69394                _
            T                    ACTCCAGCCTGGGCGACA GAGC
                                ||||||||||||||||| ||||
                                TGAGGTCGGGCCCGTTGT CTCG
                                          T
GAM475  LOC92609  3'  CTGTTGCCCAGGCTGGAGT   73209
                                ACTCCAGCCTGGGCGACAG
                                |||||||||||||||||||
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                                TGAGGTCGGACCCGTTGTC

GAM475  LOC92661  5'  CTGGCGCCCAGGCTGGAGT   70628            A
                                ACTCCAGCCTGGGCG CAG
                                ||||||||||||||| |||
                                TGAGGTCGGACCCGC GTC
                                          G
GAM475  LOC92689  3'  CTCTGTCGCCAGGCTGGAGT   70774          G
                                ACTCCAGCCTGG CGACAGAG
                                |||||||||||| ||||||||
                                TGAGGTCGGACC GCTGTCTC
                                           _
GAM475  LOC92697  5'  TGGTGCCCAGGCTGGAGT    70819           A
                                ACTCCAGCCTGGGCG CA
                                |||||||||||||| ||
                                TGAGGTCGGACCCGT GT
                                          G
GAM475  LOC92841  3'  GCTCTTGTTGCCCAGGCTGGAG 71256                _
          T                      ACTCCAGCCTGGGCGACA GAGC
                                 |||||||||||||||||| ||||
                                 TGAGGTCGGACCCGTTGT CTCG
                                            T
GAM475  LOC93132  5'  GCTCTGTCACCAGGCTGGAG   71993          GC
                                CTCCAGCCTGG  GACAGAGC
                                ||||||||||  ||||||||
                                GAGGTCGGACC  CTGTCTCG
                                      A_
GAM475  LOC93408  5'  GCTCTGTCGCCCAGGCTGGAG  57287
                                CTCCAGCCTGGGCGACAGAGC
                                |||||||||||||||||||||
                                GAGGTCGGACCCGCTGTCTCG

GAM476  FRAP1    3'  GCAGCAGAAATGTTTGCA    18272     C   CTCTAC
                                TGC AGC      TTCTGCTGC
                                ||| |||      |||||||||
                                ACG TTG      AAGACGACG
                                  T   TA____
GAM476  NPPB     5'  GCAGCAGAAGCAGCAGCAGCA  11830     CA  CT  A
                                TGC  GC  CT CTTCTGCTGC
                                |||  ||  || ||||||||||
                                ACG  CG  GA GAAGACGACG
                                  A_  AC  C
GAM476  P2RY6    3'  GCTGGAAGTACAGACTGGCA   15998       C  C     _
                                TGCCAG CT TACTTCT GC
                                |||||| || ||||||| ||
                                ACGGTC GA ATGAAGG CG
                                    A  C      T
GAM476  RYR2     5'  GCAGCAGAAGCAGAAGGCAGCG 8290      CA   _  A
                                TGC  GCCT CT CTTCTGCTGC
                                |||  |||| || ||||||||||
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                                GCG  CGGA GA GAAGACGACG
                                  A_   A  C
GAM476  SNX3     3'  GCATGCTGCACAGAAACTGGTA 15043        CC   ACTTCT  _
             TA                   TATGCCAG  TCT     GC TGC
                                  ||||||||  |||     || |||
                                  ATATGGTC  AGA     CG ACG
                                      AA   CACGT_  T
GAM476  TEM5     3'  CAGCAGGGTTCAGAGGTGGCA  52295      G    AC_
                                  TGCCA CCTCT   TTCTGCTG
                                  ||||| |||||   ||||||||
                                  ACGGT GGAGA   GGGACGAC
                                    _    CTT
GAM476  TNFAIP1  3'  GCAGCCCCTACAGAGGTGGCA  41231      G    ACTTCT
                                  TGCCA CCTCT     GCTGC
                                  ||||| |||||     |||||
                                  ACGGT GGAGA     CGACG
                                    _    CATCCC
GAM476  CNOT8    3'  GCAGCAGAAGCAGAAAAAGGCA 17707     AGCC   A
                                  TGCC    TCT CTTCTGCTGC
                                  ||||    ||| ||||||||||
                                  ACGG    AGA GAAGACGACG
                                    AAAA   C
GAM476  FLJ12598 3'  GCAGATAGTGGCTGGCA     45728        T   CT
                                  TGCCAGCC CTA  TCTGC
                                  |||||||| |||  |||||
                                  ACGGTCGG GAT  AGACG
                                      T   __
GAM476  FLJ30707 3'  CAGCAGAAAAATACTGGCAT   59463       CCTCTAC
                                  ATGCCAG      TTCTGCTG
                                  |||||||      ||||||||
                                  TACGGTC      AAGACGAC
                                      ATAAA__
GAM476  GTPBP2   3'  AGCAAAGGCTTGGCATA     39385       _   CTACTTC
                                  TATGCCA GCCT      TGCT
                                  ||||||| ||||      ||||
                                  ATACGGT CGGA      ACGA
                                      T   A_______
GAM476  IL18BP   3'  GCAGCAGGGTTAAGACTCAGCA 20312     C_  C  CT   T
                                  TGC  AG CT  ACT CTGCTGC
                                  |||  || ||  ||| |||||||
                                  ACG  TC GA  TGG GACGACG
                                    AC  A  AT   _
GAM476  KIAA0914 5'  GCAGCAGTAGACTGGC      30296      CC     T
                                  GCCAG  TCTACT CTGC
                                  |||||  |||||| ||||
                                  CGGTC  AGATGA GACG
                                     __     C
GAM476  KIAA1061 3'  GCCCGGAAGCAGAGGCTG    71721        A     CT
                                  CAGCCTCT CTTCTG  GC
                                  |||||||| ||||||  ||
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                                GTCGGAGA GAAGGC  CG
                                    C     C_
GAM476  KIAA1804  5'  CAGCAGAGGCGGCTGGC     70347        TCTA
                                GCCAGCC    CTTCTGCTG
                                |||||||    |||||||||
                                CGGTCGG    GGAGACGAC
                                   C___
GAM476  NAV1      3'  CAGCAGAACGCTGGCAT     40321        CTCTAC
                                ATGCCAGC     TTCTGCTG
                                ||||||||     ||||||||
                                TACGGTCG     AAGACGAC
                                    C_____
GAM476  PSKH1     3'  CAGAGTAGAGGTAGCA      68792     CA       T
                                TGC  GCCTCTACT CTG
                                |||  ||||||||| |||
                                ACG  TGGAGATGA GAC
                                  A_       _
GAM476  SPEC1     3'  GCTCAGTAGGGCTGACATA   40007     C    T    TCT
                                TATG CAGCC CTACT   GC
                                |||| ||||| |||||   ||
                                ATAC GTCGG GATGA   CG
                                  A    _    CT_
GAM476  ZNF263    3'  CAGCAGAGGATTGGCATA    20424        CCTCTA
                                TATGCCAG     CTTCTGCTG
                                ||||||||     |||||||||
                                ATACGGTT     GGAGACGAC
                                    A_____
GAM476  LOC121504 3'  GAAATAGAGTCTGGCATA    74544        C    C
                                TATGCCAG CTCTA TTC
                                |||||||| ||||| |||
                                ATACGGTC GAGAT AAG
                                    T    A
GAM476  LOC124044 3'  GCAGCAGGCCTAAGCCGGC   76533     A  CTC  CT
                                GCC GC   TA  TCTGCTGC
                                ||| ||   ||  ||||||||
                                CGG CG   AT  GGACGACG
                                  C  A__  CC
GAM476  LOC158308 3'  GCAGCAGGGCCCAGGCAGCA  88068     CA   CTAC
                                TGC  GCCT    TTCTGCTGC
                                |||  ||||    |||||||||
                                ACG  CGGA    GGGACGACG
                                  A_   CCC_
GAM476  LOC163412 5'  GCGGAAGCAGAAGCTGGCAT  83014        C   A
                                ATGCCAGC TCT CTTCTGC
                                |||||||| ||| |||||||
                                TACGGTCG AGA GAAGGCG
                                    A   C
GAM476  LOC163590 3'  CAGCAGAATGTATAAGCTAGCA 59509      C   CTC  _
           T                     ATGC AGC   TAC TTCTGCTG
                                |||| |||   ||| ||||||||
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                                TACG TCG   ATG AAGACGAC
                                  A  AAT   T
GAM476  LOC196205 5'  CAGCAGAAGCAGCAGCGC    88974    _ _ A
                                GC CT CT CTTCTGCTG
                                || || || |||||||||
                                CG GA GA GAAGACGAC
                                 C  C  C
GAM476  LOC253971 3'  GCTGCAAAAGCAGAAGCCGGCA 97853     A  C   A   C   T
                                TGCC GC TCT CTT TGC GC
                                |||| || ||| ||| ||| ||
                                ACGG CG AGA GAA ACG CG
                                  C A   C   A   T
GAM476  LOC64167  3'  CAGCAGGAAAATGGCATA    42536       GCCTCTAC
                                TATGCCA       TTCTGCTG
                                |||||||       ||||||||
                                ATACGGT       AGGACGAC
                                    AAA_____
GAM476  LOC91069  3'  CAGCAGAGTAGGCCAGCAT   65398     CA   CT   T
                                ATGC  GCCT  ACT CTGCTG
                                ||||  ||||  ||| ||||||
                                TACG  CGGA  TGA GACGAC
                                  AC   __  _
GAM477  EHF      3'  TCCAAAACCCAAGGTTGGCT   25127     AT   _   C
                                AGT  GCCT GGGT TTGGA
                                |||  |||| |||| |||||
                                TCG  TGGA CCCA AACCT
                                  GT   A   A
GAM477  EPHA2    3'  CCATCGGCCAAGAATACTTGAA 16675         GC  G   T_
           G                     CTTCAAGTAT  CT GGTC  TGG
                                ||||||||||  || ||||  |||
                                GAAGTTCATA  GA CCGG  ACC
                                     A_  A   CT
GAM477  ITGA5    3'  CCCAGAGACATACTTGAAG   61933          C__
                                CTTCAAGTATG   CTGGG
                                ||||||||||   |||||
                                GAAGTTCATAC   GACCC
                                      AGA
GAM477  TREM2    3'  TCCAAGACTGTCATATTT    39098       CCTG
                                AAGTATG   GGTCTTGGA
                                |||||||   |||||||||
                                TTTATAC   TCAGAACCT
                                   TG__
GAM477  UQCRB    3'  CCAACATAGGCATACTTAAG  21939     C        GGTC
                                CTT AAGTATGCCTG   TTGG
                                ||| ||||||||||   ||||
                                GAA TTCATACGGAT   AACC
                                  _        AC__
GAM477  ATP10D   3'  CAGAGACCACTTGAAG      73526        ATGCCTG   _
                                CTTCAAGT      GGTCT TG
                                ||||||||      ||||| ||
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                                GAAGTTCA      CCAGA AC
                                   _______    G
GAM477  B3GNT7   3'  CCCTTCCAGGCAACCTGAA   71678     A  A      TCTT
                                TTCA GT TGCCTGGG   GG
                                |||| || ||||||||   ||
                                AAGT CA ACGGACCT   CC
                                  C  _      TC__
GAM477  DKFZp547I224 3'  TCCAAAATTGACCACATACTTG 39963         CCTG   ____
          GA                    TTCAAGTATG   GGTC   TTGGA
                                ||||||||||   ||||   |||||
                                AGGTTCATAC   CCAG   AACCT
                                     A___   TTAA
GAM477  FLJ22341  3'  CCAAGCTCAGGCACACCCAAG  45114    CAA  A      T
                                CTT   GT TGCCTGGG CTTGG
                                |||   || |||||||| |||||
                                GAA   CA ACGGACTC GAACC
                                  CC_  C      _
GAM477  KIAA0779  3'  CCGAACAGCATACTTGAAG   86908          C  GGTC
                                CTTCAAGTATGC TG   TTGG
                                |||||||||||| ||   ||||
                                GAAGTTCATACG AC   AGCC
                                      _  A___
GAM477  LOC144233 3'  CCAAGGCACATAATTGAA    77246      G   CCTGG
                                TTCAA TATG    GTCTTGG
                                ||||| ||||    |||||||
                                AAGTT ATAC    CGGAACC
                                   A   A____
GAM477  LOC147341 3'  ACCCAGGCATAACTGAAG    85116      AG
                                CTTCA  TATGCCTGGGT
                                |||||  ||||||||||
                                GAAGT  ATACGGACCCA
                                   CA
GAM477  LOC221088 5'  TCCAAGGTGCTGGCCACTCGAA 94888     A   AT   TGGG
          G                     CTTC AGT  GCC    TCTTGGA
                                |||| |||  |||   |||||||
                                GAAG TCA  CGG    GGAACCT
                                  C   C_   TCGT
GAM478  TERF1    3'  CCCAAATCCTGTTCCAATGA   34391        C   TA   C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                     _   C_    A
GAM478  FLJ10159  3'  CCATGTCACGCCATCCAATGAC 36334         CA_   A   TC
                                GTCATTGGA   CGT GAT  GG
                                |||||||||   ||| |||  ||
                                CAGTAACCT   GCA CTG  CC
                                     ACC   _   TA
GAM478  FLJ14213  3'  CCGATGCTCCCAATGACG    46216         ACAC   GAT
                                CGTCATTGG   GTA   TCGG
                                |||||||||   |||   ||||
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                                GCAGTAACC   CGT  AGCC
                                    CT__  ___
GAM478  MGC10715  3'  ATTTACCAGACATCCAATGAC  44495       CAC___
                                GTCATTGGA    GTAGAT
                                |||||||||    ||||||
                                CAGTAACCT    CATTTA
                                    ACAGAC
GAM478  MOST2    5'  CCAGGACTGCCCAATGAC   40059      ACAC   A  _
                                GTCATTGG   GTAG TTC GG
                                ||||||||   |||| ||| ||
                                CAGTAACC   CGTC AGG CC
                                    ____   _  A
GAM478  LOC150370 3'  CCGGGTCTACGTGCCCATGAC  86123     T  A
                                GTCAT GG CACGTAGATTCGG
                                ||||| || ||||||||||||
                                CAGTA CC GTGCATCTGGGCC
                                  C  _
GAM478  LOC152620 3'  CCCAAATCCTGTTCCAATGA   60707      C   TA   C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                    _  C_   A
GAM478  LOC158668 3'  CCCAAATCCTGTTCCAATGA   69896      C   TA   C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                    _  C_   A
GAM479  AES      3'  AAAGGGGGGGCACGAGGG    8521      AAA   TGG
                                CCCTC   CCT   CTCCTTT
                                |||||   |||   |||||||
                                GGGAG   GGG   GGGGAAA
                                  CAC   ___
GAM479  BCL2     3'  AAAGGACATTTGTTGGAGGGGT 7147       A   CT_  GC
          G                      CACCCCTC AAC   TG  TCCTTT
                                |||||||| |||   ||  ||||||
                                GTGGGGAG TTG   AC  AGGAAA
                                    G   TTT  __
GAM479  CA3      5'  AAGGGAGTCAAACTTAGGGG   18994      CAAACC
                                CCCCT     TTGGCTCCTTT
                                |||||     ||||||||||
                                GGGGA     AACTGAGGGAA
                                  TTCA__
GAM479  DUSP3    3'  GAAGCTTGCCAAGGGGGG    15836     TCAAA     TC_
                                CCCC    CCTTGGC   CTTT
                                ||||    |||||||   ||||
                                GGGG    GGAACCG   GAAG
                                  _____      TTC
GAM479  FMOD     3'  AAAGGAGCTCCGATGTGAGGGG 10669       AACCTT
                                CCCCTCA     GGCTCCTTT
                                |||||||     |||||||||
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                                GGGGAGT     TCGAGGAAA
                                    GTAGCC
GAM479  IL1F5    5'  AAAGGAACATTCTGAGGGG   25374        AACCT  GC
                                CCCCTCA    TG  TCCTTT
                                |||||||    ||  ||||||
                                GGGGAGT    AC  AGGAAA
                                    CTT__  A_
GAM479  LAMB1    5'  AGAGGCGCCCCGGGGGGTG   11261        AAACCTT   T
                                CACCCCTC      GGC CCTTT
                                ||||||||      ||| |||||
                                GTGGGGGG      CCG GGAGA
                                    CC_____   C
GAM479  LFG      3'  AAAGGAGCCAAGAACTGGCGGG 77228      C   AAC
              TG                  CACCC TCA   CTTGGCTCCTTT
                                |||||  |||   ||||||||||||
                                GTGGG GGT   GAACCGAGGAAA
                                   C   CAA
GAM479  MGEA5    3'  GAGTGGGTTTCAGAAGTG    25218     CC  C     TG
                                CAC  CT AAACCT  GCTC
                                |||  ||  ||||||  ||||
                                GTG  GA TTTGGG  TGAG
                                  AA  C     __
GAM479  TLR9     5'  AGGAGCCAAGACCTGAGGG    34305       AAC
                                CCCTCA   CTTGGCTCCT
                                ||||||   ||||||||||
                                GGGAGT   GAACCGAGGA
                                   CCA
GAM479  TNFRSF1A 3'  AAAGGAGGGGTCCTGCAGGGG  8376       _  A_   TGG
                                CCCCT CA  ACCT   CTCCTTT
                                |||||  ||  ||||   |||||||
                                GGGGA GT  TGGG   GAGGAAA
                                   C  CC   ___
GAM479  TR2      5'  GGCCAGGGTTCAAGAAGTG   72778     CC  CA
                                CAC  CT  AACCTTGGCT
                                |||  ||  ||||||||||
                                GTG  GA  TTGGGACCGG
                                  AA  AC
GAM479  WBSCR5   3'  AAAGGAGCCAAGGCAAAGAGGG 42105      AAA_
                                CCCTC    CCTTGGCTCCTTT
                                |||||    ||||||||||||
                                GGGAG    GGAACCGAGGAAA
                                   AAAC
GAM479  WBSCR5   3'  AAAGGAGCCAAGGCAAAGAGGG 51625      AAA_
                                CCCTC    CCTTGGCTCCTTT
                                |||||    ||||||||||||
                                GGGAG    GGAACCGAGGAAA
                                   AAAC
GAM479  WBSCR5   3'  AAAGGAGCCAAGGCAAAGAGGG 27112      AAA_
                                CCCTC    CCTTGGCTCCTTT
                                |||||    ||||||||||||
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                                GGGAG   GGAACCGAGGAAA
                                  AAAC
GAM479  C20orf16  5'  AAAGGAGCGGTTCCTAGAAGGT 39238    C_ CA_   TTG
           G                     CACC  CT   AACC   GCTCCTTT
                                 |||| ||   ||||  ||||||||
                                 GTGG  GA   TTGG   CGAGGAAA
                                   AA  TCC   ___
GAM479  C20orf42  3'  GGCCAAGGTCTAGGGGT    35063      CAA
                                 ACCCCT   ACCTTGGCT
                                 ||||||   |||||||||
                                 TGGGGA   TGGAACCGG
                                    TC_
GAM479  C8orf6    5'  AGCCTGAGGTTTAAGGGG    90778     C     _
                                 CCCCT AAACCTT GGCT
                                 ||||| ||||||| ||||
                                 GGGGA TTTGGAG CCGA
                                    A      T
GAM479  ERp44     3'  AAGGGAGTTGATTTGAGG    82602      CC TG
                                 CCTCAAA  T  GCTCCTTT
                                 |||||||  |  ||||||||
                                 GGAGTTT  A  TGAGGGAA
                                     __ GT
GAM479  FLJ10157  3'  GGGAAGCCCGAGGGGTG    36332       AAACCTT   _
                                 CACCCCTC      GGCT CCT
                                 ||||||||      |||| |||
                                 GTGGGGAG      CCGA GGG
                                     C_______    A
GAM479  FLJ11618  3'  AAGGGGGTCGGCCCAGGGGTG  42621       CAAA  TT
                                 CACCCCT   CC  GGCTCCTTT
                                 |||||||   ||  |||||||||
                                 GTGGGGA   GG  CTGGGGGAA
                                     CCC_  __
GAM479  FLJ14154  3'  AGAAGCCTGGGGGGGTG     46224       AACCTT   C
                                 CACCCCTCA     GGCT CT
                                 |||||||||     |||| ||
                                 GTGGGGGGT     CCGA GA
                                       _______   A
GAM479  FLJ22795  3'  AAAGGAGTCAGGACTTGGAAGT 47630    CC T   AC
           G                     CAC  C CAA  CTTGGCTCCTTT
                                 |||  | |||  ||||||||||||
                                 GTG  G GTT  GGACTGAGGAAA
                                   AA _   CA
GAM479  HSPC054   3'  GAAGGGGCTTTGAGAGG    27118    C    ACCTT
                                 CC CTCAA    GGCTCCTTT
                                 || |||||    |||||||||
                                 GG GAGTT    TCGGGGAAG
                                  A   _____
GAM479  KIAA0016  3'  AAAGGAGGGCTGGCTGGAGGAG 29306    C   AAA  TTGG
           TG                      CAC CCTC   CC    CTCCTTT
                                 ||| ||||   ||   |||||||
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                                GTG GGAG   GG    GAGGAAA
                                  A    GTC  TCGG
GAM479  KIAA0022  3'  AAAGGAGTTCTTAAAGGAGTG  30271     C   CAAACCTT
                                CAC CCT       GGCTCCTTT
                                ||| |||       |||||||||
                                GTG GGA       TTGAGGAAA
                                  A   AATTC___
GAM479  KIAA0125  3'  GGGCCAAGGTCTGGGGGTG    29572       T  A
                                CACCCC CA ACCTTGGCTC
                                |||||| || ||||||||||
                                GTGGGG GT TGGAACCGGG
                                    _ C
GAM479  KIAA1029  5'  AAAGAAGCCAAGGCGCGGAG   24422     AAA_      C
                                CTC    CCTTGGCT CTTT
                                |||    |||||||| ||||
                                GAG    GGAACCGA GAAA
                                  GCGC       A
GAM479  LBP-9     3'  AGGAAACCAAGGCTCAGAGGGG 28042       AAA_     C_
                                CCCCTC    CCTTGG  TCCT
                                ||||||    ||||||  ||||
                                GGGGAG    GGAACC  AGGA
                                   ACTC     AA
GAM479  NCOA2     3'  AAGGAGCCTGTGAGAGGG    22571     _   AACCTT
                                CCC CTCA     GGCTCCTT
                                ||| ||||     ||||||||
                                GGG GAGT     CCGAGGAA
                                  A   GT____
GAM479  NRF       3'  AAAGGAGCCAAAGTTGA     34504      ACC
                                TCAA   TTGGCTCCTTT
                                ||||   ||||||||||
                                AGTT   AACCGAGGAAA
                                  GA_
GAM479  NRF       3'  AAAGGAGCTGTTGAAGATGTG  34505     CC  CA   CTT
                                CAC  CT  AAC   GGCTCCTTT
                                |||  ||  |||   |||||||||
                                GTG  GA  TTG   TCGAGGAAA
                                  TA  AG  ___
GAM479  PRO0618   3'  AGAGGGGCAGGGTTTGA     27044         G
                                TCAAACCTTG CTCCTTT
                                |||||||||| |||||||
                                AGTTTGGGAC GGGGAGA
                                       _
GAM479  PRO1855   3'  AAAGGAGTAGGCTTGGGGGTG  38144       T   A   TG
                                CACCCC CAA CCT  GCTCCTTT
                                |||||| ||| |||  ||||||||
                                GTGGGG GTT GGA  TGAGGAAA
                                    _   C   __
GAM479  PRO2214   5'  AAAGGGAAAGCTTGAGGGG   38168        AC   GG T
                                CCCCTCAA  CTT  C CCTTT
                                ||||||||  |||  | |||||
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                                GGGGAGTT  GAA  G GGAAA
                                    C_   A_ _
GAM479  TA-PP2C   3'  AGGTCCCAAGGCCTGAAGGGT  58402      C   AA     CT
                                ACCC TCA  CCTTGG  CCT
                                |||| |||  ||||||  |||
                                TGGG AGT  GGAACC  GGA
                                  A   CC     CT
GAM479  LOC116150 3'  AAGGAGCTCCAGAGGAGTG   57423     C    AAACCTT
                                CAC CCTC      GGCTCCTT
                                ||| ||||      ||||||||
                                GTG GGAG      TCGAGGAA
                                  A   ACC____
GAM479  LOC142779 5'  AAAGGAGCAGCTTTGAG     76896       C  TG
                                CTCAAA CT  GCTCCTTT
                                ||||||  ||  ||||||||
                                GAGTTT GA  CGAGGAAA
                                    C  __
GAM479  LOC145725 5'  AAAGGAGTCAGGACTTGGAAGT 77879     CC T   AC
          G                      CAC  C CAA  CTTGGCTCCTTT
                                |||  | |||  ||||||||||||
                                GTG  G GTT  GGACTGAGGAAA
                                  AA _   CA
GAM479  LOC145732 5'  AAAGGAGTCAGGACTTGGAAGT 77891     CC T   AC
          G                      CAC  C CAA  CTTGGCTCCTTT
                                |||  | |||  ||||||||||||
                                GTG  G GTT  GGACTGAGGAAA
                                  AA _   CA
GAM479  LOC157273 3'  AAAGACTATGAGGTTTGCAAGG 87712      CCT        GCTC
          TG                     CACC   CAAACCTTG    CTTT
                                ||||   |||||||||    ||||
                                GTGG   GTTTGGAGT    GAAA
                                  AAC        ATCA
GAM479  LOC158117 3'  AAAGGAGCCAAGGTGTAGTGGT 82608      C  CAA
          G                      CACC CT   ACCTTGGCTCCTTT
                                ||||  ||   ||||||||||||||
                                GTGG GA   TGGAACCGAGGAAA
                                  T  TG_
GAM479  LOC161528 3'  AAAGGAGTCAGGACTTGGAAGT 83153     CC T   AC
          G                      CAC  C CAA  CTTGGCTCCTTT
                                |||  | |||  ||||||||||||
                                GTG  G GTT  GGACTGAGGAAA
                                  AA _   CA
GAM479  LOC163033 5'  AAAGGAGCCAAGGAGGCGAGG  83282      AAA_
                                CCTC    CCTTGGCTCCTTT
                                ||||    ||||||||||||
                                GGAG    GGAACCGAGGAAA
                                  CGGA
GAM479  LOC164397 5'  AAAGGAGCTGTTTTTGAAGGTG 83405      CC     CCT
                                CACC  TCAAA   TGGCTCCTTT
                                ||||  |||||   ||||||||||
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                                GTGG  AGTTT   GTCGAGGAAA
                                  A_    TT_
GAM479  LOC196957 5'  AAAGGAGTCAGGACTTGGAAGT 89183    CC T   AC
          G                     CAC  C CAA  CTTGGCTCCTTT
                                |||  | |||  ||||||||||||
                                GTG  G GTT  GGACTGAGGAAA
                                  AA _   CA
GAM479  LOC196961 5'  AAAGGAGTCAGGACTTGGAAGT 89197    CC T   AC
          G                     CAC  C CAA  CTTGGCTCCTTT
                                |||  | |||  ||||||||||||
                                GTG  G GTT  GGACTGAGGAAA
                                  AA _   CA
GAM479  LOC203275 3'  AAAGGAGCCAAGGTGTAGTGGT 90851     C  CAA
          G                     CACC CT   ACCTTGGCTCCTTT
                                ||||  ||   ||||||||||||||
                                GTGG GA   TGGAACCGAGGAAA
                                  T  TG_
GAM479  LOC220537 3'  AAAGGAGTCAGGACTTGGAAGT 92418    CC T   AC
          G                     CAC  C CAA  CTTGGCTCCTTT
                                |||  | |||  ||||||||||||
                                GTG  G GTT  GGACTGAGGAAA
                                  AA _   CA
GAM479  LOC222183 3'  AAAGGGGTTCAGGTCAAGAGGT 95825     C  CAA    TG
          G                     CACC CT   ACCT  GCTCCTTT
                                ||||  ||   ||||  ||||||||
                                GTGG GA   TGGA  TGGGGAAA
                                  A  AC_   CT
GAM479  LOC245727 5'  AAAGGAGTCAGGACTTGGAAGT 92756    CC T   AC
          G                     CAC  C CAA  CTTGGCTCCTTT
                                |||  | |||  ||||||||||||
                                GTG  G GTT  GGACTGAGGAAA
                                  AA _   CA
GAM479  LOC255465 3'  AAGGAGCCAGGAGGGGGG    99097       AAAC
                                CCCCTC    CTTGGCTCCTT
                                ||||||    ||||||||||
                                GGGGGG    GGACCGAGGAA
                                   A___
GAM479  LOC51195  3'  AGCCTCAAGGCCTGAGGGGTG  33403         AA   __
                                CACCCCTCA  CCTT  GGCT
                                |||||||||  ||||  ||||
                                GTGGGGAGT  GGAA  CCGA
                                     CC    CT
GAM479  LOC57795  3'  AAAGGAGCCAAGGAAGAG    69862     AAA
                                CTC   CCTTGGCTCCTTT
                                |||   ||||||||||||
                                GAG   GGAACCGAGGAAA
                                  AA_
GAM480  ADAMTS4   3'  GCTCACTGCATCCTCCGCCTC  18764       G    A  T_
                                GAGGCGG AGGAT GC  TGAGC
                                ||||||| ||||| ||  |||||
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                                CTCCGCC TCCTA CG  ACTCG
                                   _    _ TC
GAM480  ADRBK1   3'  CCAGCCCTCCCGCCCCTT    9665      A       ATA   T A
                                AAG GGCGGGAGG   GCT G G
                                ||| |||||||||   ||| | |
                                TTC CCGCCCTCC   CGA C C
                                  C        ___   _ A
GAM480  AP2B1    3'  GCTTCAGTCACCTCCCACCTCT 8894        C     ATA   T
           T                     AAGAGG GGGAGG   GCT GAGC
                                ||||||| ||||||   ||| ||||
                                TTCTCC CCCTCC   TGA TTCG
                                   A     AC_   C
GAM480  CACNG6   5'  GCTCCTCGCTCCCGCCCCT   49948    A       _ T_
                                AG GGCGGGAG GA  AGC
                                || |||||||| ||  |||
                                TC CCGCCCTC CT  TCG
                                 C       G  CC
GAM480  CDH1     3'  GCTCAAGCTATCCTTGCACCTC 16405      CGG
                                GAGG   GAGGATAGCTTGAGC
                                ||||   ||||||||||||||||
                                CTCC   TTCCTATCGAACTCG
                                  ACG
GAM480  CLN2     3'  GCTCAAGCTGTTCCGTCCCCTT 6364       C  GA   _
                                GAGG GG  GGA TAGCTTGAGC
                                |||| ||  ||| ||||||||||
                                TTCC CC  CCT GTCGAACTCG
                                  _  TG   T
GAM480  COL6A2   3'  GCTCACTGCCCCCACGCCTC   55203       _  A  A   CT
                                GAGGCG GG GG TAG  TGAGC
                                |||||| || || |||  |||||
                                CTCCGC CC CC GTC  ACTCG
                                   A  _  C   __
GAM480  CSPG2    5'  GCATCCTCCCGCATCTT     16513      G        A
                                AAGA GCGGGAGGAT GC
                                |||| |||||||||| ||
                                TTCT CGCCCTCCTA CG
                                  A        _
GAM480  CTF1     3'  GCTCAAGCCATCCTTCCGCCTC 9017             A
                                GAGGCGGGAGGAT GCTTGAGC
                                |||||||||||| ||||||||
                                CTCCGCCTTCCTA CGAACTCG
                                        C
GAM480  DDX6     3'  GCTCTCTTTCTCCCCCACCTCT 16566       C   A   TAGCTT
           T                     AAGAGG GGG GGA     GAGC
                                ||||||| ||| |||     ||||
                                TTCTCC CCC CCT     CTCG
                                   A   _   CTTTCT
GAM480  DSCR3    3'  GCTCAAGCGATCCCTCCCCTC  21318      C  GA    A
                                GAGG GG  GGAT GCTTGAGC
                                |||| ||  |||| ||||||||
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                                CTCC CC  CCTA CGAACTCG
                                  _ TC   G
GAM480  ELMO1   3'  GCTCAAATCTCCTCCCACCTCT 56156     C     TAGC
                                AGAGG GGGAGGA   TTGAGC
                                ||||| |||||||   ||||||
                                TCTCC CCCTCCT   AACTCG
                                   A     CTA_
GAM480  ENG     3'  GCCTACCCTTCCCGCCTC   5499        _ A  _
                                GAGGCGGGA GG TAG C
                                ||||||||| || ||| |
                                CTCCGCCCT CC ATC G
                                      T C  C
GAM480  FAAH    5'  GCTCCGCCCCCCGCCGCCTC  44453      GA  ATA  TT
                                GAGGCGG  GG  GC  GAGC
                                |||||||  ||  ||  ||||
                                CTCCGCC  CC  CG  CTCG
                                    G_  CCC  C_
GAM480  GATA2   3'  TTCAACCCCCTCGCCTC    10769       A  ATAGC
                                GAGGCGGG GG   TTGAG
                                |||||||| ||   |||||
                                CTCCGCTC CC   AACTT
                                    _ CC___
GAM480  GLTSCR1  5'  GCTCAAGCCATCCATCCTCCT  32301    C   _   A
                                AGG GGGA GGAT GCTTGAGC
                                ||| |||| |||| ||||||||
                                TCC TCCT CCTA CGAACTCG
                                  _   A   C
GAM480  GMPS    5'  TTCCGGCACCCTCCCGCC    15266       ATA  T
                                GGCGGGAGG  GCT GAG
                                |||||||||  ||| |||
                                CCGCCCTCC  CGG CTT
                                     CA_  C
GAM480  LDLR    3'  GCCCATCCTCCCGACCCCT   6738    A _      A_
                                AG GG CGGGAGGAT  GC
                                || || |||||||||  ||
                                TC CC GCCCTCCTA  CG
                                 C  A       CC
GAM480  LU      3'  GCTATTTTTACCTCCCGCCTC  19947         _____
                                GAGGCGGGAGG   ATAGC
                                ||||||||||    |||||
                                CTCCGCCCTCC   TATCG
                                      ATTTT
GAM480  NCOA6   5'  GCTCAAGCAACCCTCCCACCTC 26838    C    ATA
                                GAGG GGGAGG  GCTTGAGC
                                |||| ||||||  ||||||||
                                CTCC CCCTCC  CGAACTCG
                                  A    CAA
GAM480  NESH    5'  GCCCTTTCCTCCCGCCTTCC  33572   A       TA__
                                A GAGGCGGGAGGA   GC
                                | ||||||||||||   ||
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                                C TTCCGCCCTCCT   CG
                                 C         TTCC
GAM480  NRXN2   5'  GCCCGGCCCCCTCCCGCC   31311       ATA  T A
                                GGCGGGAGG  GCT G GC
                                |||||||||  ||| | ||
                                CCGCCCTCC  CGG C CG
                                     CC_  _ C
GAM480  NRXN2   5'  GCCCGGCCCCCTCCCGCC   57821       ATA  T A
                                GGCGGGAGG  GCT G GC
                                |||||||||  ||| | ||
                                CCGCCCTCC  CGG C CG
                                     CC_  _ C
GAM480  PCDHB11  3'  GCTCACTGCACCCTCCGCCTCT 38926      GA  ATA  T_
                                AGAGGCGG  GG  GC  TGAGC
                                ||||||||  ||  ||  |||||
                                TCTCCGCC  CC  CG  ACTCG
                                     TC  A__  TC
GAM480  PCDHB16  3'  GCTCAAGCCATCCTCCCTCCTC 40907    C      A
                                GAGG GGGAGGAT GCTTGAGC
                                ||||  |||||||| ||||||||
                                CTCC CCCTCCTA CGAACTCG
                                  T       C
GAM480  PRex1   3'  GCCCAGCGTCCTCCCTGCCTC  40824     _      A  T A
                                GAGGC GGGAGGAT GCT G GC
                                |||||  |||||||| ||| | ||
                                CTCCG CCCTCCTG CGA C CG
                                  T       _  _ C
GAM480  PTPRG   5'  GCTCTCCGCTCCCCCTGCCTCT 12614       A  TA  TT_
                                AGAGGCGGG GGA  GC  GAGC
                                |||||||||  |||  ||  ||||
                                TCTCCGTCC CCT  CG  CTCG
                                     C  __  CCT
GAM480  RAD52   3'  GCCCAAGTGATACTCCCACCTC 12759     C   GATA   A
           T                     AGAGG GGGAG   GCTTG GC
                                 |||||  |||||   |||||  ||
                                 TCTCC CCCTC   TGAAC CG
                                   A    ATAG   C
GAM480  RAD52   3'  GCCCAAGTGATACTCCCACCTC 57037     C   GATA   A
           T                     AGAGG GGGAG   GCTTG GC
                                 |||||  |||||   |||||  ||
                                 TCTCC CCCTC   TGAAC CG
                                   A    ATAG   C
GAM480  RAD52   3'  GCCCAAGTGATACTCCCACCTC 57046     C   GATA   A
           T                     AGAGG GGGAG   GCTTG GC
                                 |||||  |||||   |||||  ||
                                 TCTCC CCCTC   TGAAC CG
                                   A    ATAG   C
GAM480  RAD52   3'  GCCCAAGTGATACTCCCACCTC 57052     C   GATA   A
           T                     AGAGG GGGAG   GCTTG GC
                                 |||||  |||||   |||||  ||
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                                TCTCC CCCTC   TGAAC CG
                                  A    ATAG    C
GAM480  RAPSN    3'  GCCCAGCTCCCCTCCCTGCCTC 51973       _    AT   T A
              TT                  AAGAGGC GGGAGG  AGCT G GC
                                  ||||||| ||||||  |||| | ||
                                  TTCTCCG CCCTCC  TCGA C CG
                                     T     CC   _ C
GAM480  RBM8A    3'  GCTCAAGCCATCCTTCTGCCTC 18809           A
                                  GAGGCGGGAGGAT GCTTGAGC
                                  |||||||||||| ||||||||
                                  CTCCGTCTTCCTA CGAACTCG
                                           C
GAM480  SCAP1    5'  GCCCGCGCCCCGTCCCGCCTCT 14948         _ ATA  T  A
                                  AGAGGCGGGA GG   GC TG GC
                                  |||||||||| ||   || || ||
                                  TCTCCGCCCT CC   CG GC CG
                                        G  C__  C  C
GAM480  SLC5A5   5'  GCCGAGCATCCTCCCACC    6596     C      A    A
                                  GG GGGAGGAT GCTTG GC
                                  || |||||||| ||||| ||
                                  CC CCCTCCTA CGAGC CG
                                   A      _    _
GAM480  SLC6A8   3'  GCCCAAACCATCCTCTCCTT   20071     C      AGC   A
                                  AGG GGGAGGAT   TTG GC
                                  ||| ||||||||   ||| ||
                                  TTC CTCTCCTA   AAC CG
                                    _       CCA   C
GAM480  TP73     3'  CAAGCTGCCTCCCCTC      19469      CG    A
                                  GAGG  GGAGG TAGCTTG
                                  ||||  ||||| |||||||
                                  CTCC  CCTCC GTCGAAC
                                          __    _
GAM480  VIPR1    3'  GCCCAAGGCGGCCCCTCCCGCC 17313     A       ATA_ _  A
              CCTT                   AAG GGCGGGAGG    GC TG GC
                                  ||| |||||||||    || ||| ||
                                  TTC CCGCCCTCC    CG AAC CG
                                    C        CCGG  G   C
GAM480  WNT7A    5'  CTCCTCCCTCCCTCCTC     17316      C     AT  CTT
                                  GAGG GGGAGG  AG   GAG
                                  |||| ||||||  ||   |||
                                  CTCC CCCTCC  TC   CTC
                                     T     C_  ___
GAM480  ZFX      5'  GCTCAAGCCGTTCTCCCGCCTC 14164           TA
                                  GAGGCGGGAGGA  GCTTGAGC
                                  ||||||||||||  ||||||||
                                  CTCCGCCCTCTT  CGAACTCG
                                           GC
GAM480  ZNFN2A1  3'  GCCCTGCTCCTCCTGCCTC   61394           TA  TTGA
                                  GAGGCGGGAGGA  GC    GC
                                  ||||||||||||  ||    ||
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                                CTCCGTCCTCCT  CG    CG
                                      __  TCC_
GAM480  AHCYL1   5'  GCCCTTTCTCCCCGCCTCTT  22776          _    TA_
                                AAGAGGCGGG AGGA   GC
                                |||||||||| ||||   ||
                                TTCTCCGCCC TCTT   CG
                                     C    TCC
GAM480  ARHGEF9  5'  CTCACAGGTTCCCCCCGCCTTT 31484         A   TA  __
                                AGAGGCGGG GGA  GCT  TGAG
                                ||||||||| |||  |||  ||||
                                TTTCCGCCC CCT  TGG  ACTC
                                     C   __   AC
GAM480  ASB16    5'  CTCAAGCGATCCTCCCACC   70487    C       A
                                GG GGGAGGAT GCTTGAG
                                || |||||||| |||||||
                                CC CCCTCCTA CGAACTC
                                 A       G
GAM480  C1orf34  3'  GCCCAAGCAATCTTCCCACCTC 61311       C       A    A
           T                     AGAGG GGGAGGAT GCTTG GC
                                ||||| |||||||| ||||| ||
                                TCTCC CCCTTCTA CGAAC CG
                                   A       A    C
GAM480  C1QTNF2  3'  CTCACCTCCTCCGCCTCTT   49973         G   TAGCT
                                AAGAGGCGG AGGA    TGAG
                                ||||||||| ||||    ||||
                                TTCTCCGCC TCCT    ACTC
                                     _   CC___
GAM480  C20orf18 5'  GCTCCTGGTCTCCCGCCTCT  49172          GA  CTT
                                AGAGGCGGGAG  TAG   GAGC
                                ||||||||||  |||   ||||
                                TCTCCGCCCTC  GTC   CTCG
                                      TG   ___
GAM480  C20orf18 5'  GCTCCTGGTCTCCCGCCTCT  49180          GA  CTT
                                AGAGGCGGGAG  TAG   GAGC
                                ||||||||||  |||   ||||
                                TCTCCGCCCTC  GTC   CTCG
                                      TG   ___
GAM480  C20orf35 3'  CTCAAGCCATGCTGCCTCCT  38074    C  G  G  A
                                AGG GG AG AT GCTTGAG
                                ||| || || || |||||||
                                TCC CC TC TA CGAACTC
                                  T  G  G  C
GAM480  C20orf98 3'  CTCAAGGCTCTCGCCCCT   72005    A      GATAG
                                AG GGCGGGAG    CTTGAG
                                || ||||||||    ||||||
                                TC CCGCTCTC    GAACTC
                                 C       G____
GAM480  CCNI     5'  GCCGGTCTCACCCCCCGCCTCT 23369         A  AT  C   A
                                AGAGGCGGG GG  AG TTG GC
                                ||||||||| ||  || ||| ||
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                                TCTCCGCCC CC  TC GGC CG
                                     C  AC  T  _
GAM480  EEA1     5'  GCCCAGTCCCTCCCGCC     14539         ATA   T A
                                GGCGGGAGG   GCT G GC
                                |||||||||   ||| | ||
                                CCGCCCTCC   TGA C CG
                                     C__   _ C
GAM480  ENDO180  3'  GCTCCCTCTCGCCCCTT     21267     A       AT
                                AAG GGCGGGAGG  AGC
                                ||| |||||||||  |||
                                TTC CCGCTCTCC  TCG
                                  C       C_
GAM480  FLJ10101 3'  GCTCAGGCAGTCCTCCCACCT  45601     C       A
                                AGG GGGAGGAT GCTTGAGC
                                ||| ||||||||  ||||||||
                                TCC CCCTCCTG CGGACTCG
                                  A       A
GAM480  FLJ10901 3'  GCTGAGACCCCCCCCACCCCT   37367    A  C   A  ATAG   G
                                AG GG GGG GG    CTT AGC
                                || || ||| ||    ||| |||
                                TC CC CCC CC    GAG TCG
                                 C  A   _  CCA_   _
GAM480  FLJ13102 3'  CTTTCCTATACCCCACCCGCCT 46531          A  ___    CTT
           CTT                    AAGAGGCGGG GG   ATAG   GAG
                                ||||||||||  ||   ||||   |||
                                TTCTCCGCCC CC   TATC   TTC
                                     A  CCA    CT_
GAM480  FLJ20584 3'  GCTCTGGGTCCCTCCGCCTC   35855       GA    AGCTT
                                GAGGCGG  GGAT    GAGC
                                |||||||  ||||    ||||
                                CTCCGCC  CCTG    CTCG
                                    TC    GGT__
GAM480  FLJ21777 3'  CTCAAGCGATCCACCCCC    50841    C   A    A
                                GG GGG GGAT GCTTGAG
                                || ||| |||| |||||||
                                CC CCC CCTA CGAACTC
                                 _   A    G
GAM480  FLJ23185 3'  GCCCCAAGTGATCCTCCCACCT 47516      C       A    A_
           CT                     AGAGG GGGAGGAT GCTTG  GC
                                ||||| |||||||| |||||  ||
                                TCTCC CCCTCCTA TGAAC  CG
                                   A       G     CC
GAM480  FLJ23191 5'  GCTGCGGCATCCTCCCGCC    45011          A   TG
                                GGCGGGAGGAT GCT  AGC
                                ||||||||||| |||  |||
                                CCGCCCTCCTA CGG  TCG
                                      _  CG
GAM480  FLJ23451 3'  GCTCCCTCCCCGCCTCTT    45788          _   AT
                                AAGAGGCGGG AGG  AGC
                                |||||||||| |||  |||
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                                TTCTCCGCCC TCC  TCG
                                      C   C_
GAM480  KIAA0057  3'  GCCCAGGCCCCCTCCCTGCCTC 25416      _     ATA    A
                                GAGGC GGGAGG   GCTTG GC
                                ||||| ||||||   ||||| ||
                                CTCCG CCCTCC   CGGAC CG
                                   T     CC_    C
GAM480  KIAA0552  3'  CTCTATTCCCCCAGCCTCTT   28990       _  A   TAGCTT
                                AAGAGGC GGG GGA     GAG
                                ||||||| ||| |||     |||
                                TTCTCCG CCC CCT     CTC
                                    A   _   TAT___
GAM480  KIAA1010  3'  GCTCAAGCAACCCTCCCGCCTC 72544          ATA
                                GAGGCGGGAGG   GCTTGAGC
                                ||||||||||   ||||||||
                                CTCCGCCCTCC   CGAACTCG
                                      CAA
GAM480  KIAA1138  3'  GCCCGCAGCCCCTCCTGCCCCT 62820    A       ATA  _  A
                                AG GGCGGGAGG   GCT TG GC
                                || |||||||||   ||| || ||
                                TC CCGTCCTCC   CGA GC CG
                                 C       C__   C  C
GAM480  KIAA1157  5'  GCCCGGCCCCCCGCCGCCTC   72702       GA  ATA   T A
                                GAGGCGG  GG   GCT G GC
                                |||||||  ||   ||| | ||
                                CTCCGCC  CC   CGG C CG
                                    G_  CC_   _ C
GAM480  KIAA1396  3'  GCTCAAGTGACCCTCCCACCTC 63672     C     ATA
                                GAGG GGGAGG   GCTTGAGC
                                |||| ||||||   ||||||||
                                CTCC CCCTCC   TGAACTCG
                                  A     CAG
GAM480  KIAA1754  3'  GCTCAGCAGCCCCCCCACCTCT  63931     C   A  ATA   T
                                AGAGG GGG GG   GCT GAGC
                                ||||| ||| ||   ||| ||||
                                TCTCC CCC CC   CGA CTCG
                                   A   C  GA_   _
GAM480  MGC17347  5'  TGAGCACCTCCCCCGCCTC   57173       A   TA_
                                GAGGCGGG GGA   GCTTG
                                |||||||| |||   |||||
                                CTCCGCCC CCT   CGAGT
                                     _   CCA
GAM480  MGC2306  3'  TTCAACCCCCTCGCCTC     51955       A  ATAGC
                                GAGGCGGG GG    TTGAG
                                |||||||| ||    |||||
                                CTCCGCTC CC    AACTT
                                     _ CC___
GAM480  MGC3413  3'  GCTGTGGATCGCTCCCGCCTC  52035         _   A_  TTG
                                GAGGCGGGAG GAT  GC   AGC
                                |||||||||| |||  ||   |||
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                                CTCCGCCCTC CTA  TG   TCG
                                     G   GG  ___
GAM480  MYO3B    3'  CTCTTCTCCATCCTCCCACCTT 58109      C      AGCTT_
            T                    AGAGG GGGAGGAT     GAG
                                 ||||| ||||||||     |||
                                 TTTCC CCCTCCTA     CTC
                                    A       CCTCTT
GAM480  NAPG     5'  GCTCAAGCCATCTGCCTGCCT  98539       A   A
                                 AGGCGGG GGAT GCTTGAGC
                                 ||||||| |||| ||||||||
                                 TCCGTCC TCTA CGAACTCG
                                     G   C
GAM480  NINJ2    3'  GCTCACTGCACCTCCGCCTC   33726       G   ATA  T_
                                 GAGGCGG AGG   GC  TGAGC
                                 ||||||| |||   ||  |||||
                                 CTCCGCC TCC   CG  ACTCG
                                     _   A__  TC
GAM480  NXN      3'  CAAGTGTCCAGCCTCT      42669       GGGA    G
                                 AGAGGC    GGATA CTTG
                                 ||||||    ||||| ||||
                                 TCTCCG    CCTGT GAAC
                                    A___    _
GAM480  OPN4     3'  GCCCAGGCCCTCCCACTTC    53852     C     ATA    A
                                 GAGG GGGAGG   GCTTG GC
                                 |||| ||||||   ||||| ||
                                 CTTC CCCTCC   CGGAC CG
                                   A     ___     C
GAM480  PDEF     3'  CTCCATCCCCCTGCCTC     25678        A   AGCTT
                                 GAGGCGGG GGAT    GAG
                                 |||||||| ||||    |||
                                 CTCCGTCC CCTA    CTC
                                     C   C____
GAM480  PFDN1    3'  GCTCTTCCTCCTGCCCCT    12050    A        T_
                                 AG GGCGGGAGGA  AGC
                                 || ||||||||||  |||
                                 TC CCGTCCTCCT  TCG
                                  C         TC
GAM480  RNF8     3'  CTCAAGCCATCCTCCCACCTC  15565     C       A
                                 GAGG GGGAGGAT GCTTGAG
                                 |||| |||||||| |||||||
                                 CTCC CCCTCCTA CGAACTC
                                   A       C
GAM480  SCYA28   3'  GCCCAAATTTTCCAGCCCCTT  39544     A  G      AGC   A
                                 AAG GGC GGAGGAT   TTG GC
                                 ||| ||| |||||||   ||| ||
                                 TTC CCG CCTTTTA   AAC CG
                                   C  A      ___   C
GAM480  SNAPC1   3'  GCTCAAGCTATCCTCCTGCCTC 13276
                                 GAGGCGGGAGGATAGCTTGAGC
                                 |||||||||||||||||||||
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                                CTCCGTCCTCCTATCGAACTCG

GAM480  TRIAD3   3'  CTCACCCTCCTCGCCTC    96133       _    ATAGCT
                                GAGGCG GGAGG     TGAG
                                |||||| |||||     ||||
                                CTCCGC CCTCC     ACTC
                                   T    C_____
GAM480  TSGA13   3'  CTCAGTCCTCCCGCCTC    54706          AGCT
                                GAGGCGGGAGGAT   TGAG
                                ||||||||||||   ||||
                                CTCCGCCCTCCTG   ACTC
                                      ____
GAM480  WDR9     5'  GCTCGCTCGCTCCCGCCTC   54457        GAT  TT
                                GAGGCGGGAG  AGC  GAGC
                                |||||||||  |||  ||||
                                CTCCGCCCTC  TCG  CTCG
                                     GC_  __
GAM480  WDR9     5'  GCTCGCTCGCTCCCGCCTC   39084        GAT  TT
                                GAGGCGGGAG  AGC  GAGC
                                |||||||||  |||  ||||
                                CTCCGCCCTC  TCG  CTCG
                                     GC_  __
GAM480  LOC115110 5' TGGGCTCCCCCCGCCTC    72188        A  TA
                                GAGGCGGG GGA  GCTTG
                                |||||||| |||  |||||
                                CTCCGCCC CCT  CGGGT
                                     C  __
GAM480  LOC122664 5' CTCTAAGTCCTCCCTCCCCCT  74615    C    _ TA  _
                                AGG GGGAGG A  GCTT GAG
                                ||| |||||| |  |||| |||
                                TCC CCCTCC T  TGAA CTC
                                  _    C CC   T
GAM480  LOC129080 3' CAGGCCCTCCCGCATCT    56792    G      ATA
                                AGA GCGGGAGG  GCTTG
                                ||| ||||||||  |||||
                                TCT CGCCCTCC  CGGAC
                                  A      ___
GAM480  LOC143384 5' CTCACAGCTCCCGCCCCTT   77063    A     GGATA  _
                                AAG GGCGGGA    GCT TGAG
                                ||| |||||||    ||| ||||
                                TTC CCGCCCT    CGA ACTC
                                  C      _____  C
GAM480  LOC144519 3' GCTCAAGCCATCCTCCCACC  77375   C      A
                                GG GGGAGGAT GCTTGAGC
                                || |||||||| ||||||||
                                CC CCCTCCTA CGAACTCG
                                 A       C
GAM480  LOC144667 3' GCTCAAGCCATCCTCCCACCCT 84088   A  C      A
                                AG GG GGGAGGAT GCTTGAGC
                                || || |||||||| ||||||||
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                                TC CC CCCTCCTA CGAACTCG
                                 _ A       C
GAM480  LOC145009 3'  GCTCACTGCATCCTCCGCCTC  60976        G    A  T_
                                GAGGCGG AGGAT GC  TGAGC
                                ||||||| ||||| ||  |||||
                                CTCCGCC TCCTA CG  ACTCG
                                   _    _ TC
GAM480  LOC146227 3'  CTCTGCCTCCCTCCCACCTCTT 78214        C     ATA  TT
                                AAGAGG GGGAGG   GC  GAG
                                |||||| ||||||   ||  |||
                                TTCTCC CCCTCC   CG  CTC
                                   A     CTC  T_
GAM480  LOC146443 5'  CTCAAACTGTCCTCCCCC    78444    C        C
                                GG GGGAGGATAG TTGAG
                                || |||||||||| |||||
                                CC CCCTCCTGTC AACTC
                                 _        A
GAM480  LOC146488 3'  GCCCAAACCATCCTCTCCTT   71358    C       AGC   A
                                AGG GGGAGGAT   TTG GC
                                ||| ||||||||   ||| ||
                                TTC CTCTCCTA   AAC CG
                                  _       CCA   C
GAM480  LOC147993 5'  GCCCAAACTCATACTCCCAGCC 88528    A  _    GAT_ C   A
           CTT                    AAG GGC GGGAG    AG TTG GC
                                ||| ||| |||||    || ||| ||
                                TTC CCG CCCTC    TC AAC CG
                                  _  A    ATAC  A   C
GAM480  LOC148181 5'  GCCCAGCTCCTCCTGCCTC    79434          TA   T A
                                GAGGCGGGAGGA  GCT G GC
                                ||||||||||||  ||| | ||
                                CTCCGTCCTCCT  CGA C CG
                                      __   _ C
GAM480  LOC150166 5'  GCTCAAGCCATCTGCCCGCCTC 86039        A   A
                                GAGGCGGG GGAT GCTTGAGC
                                |||||||| |||| ||||||||
                                CTCCGCCC TCTA CGAACTCG
                                     G   C
GAM480  LOC150166 5'  GCTCAAGCCATCTTTCCACCTC 86040     C       A
                                GAGG GGGAGGAT GCTTGAGC
                                |||| |||||||| ||||||||
                                CTCC CCTTTCTA CGAACTCG
                                  A       C
GAM480  LOC153443 3'  GCTCAAGTGATCCTCCCACCTC 81687      C       A
           T                    AGAGG GGGAGGAT GCTTGAGC
                                ||||| |||||||| ||||||||
                                TCTCC CCCTCCTA TGAACTCG
                                  A       G
GAM480  LOC154990 5'  GCCCAGCTCCTCCTGCCTC    82150          TA   T A
                                GAGGCGGGAGGA  GCT G GC
                                ||||||||||||  ||| | ||
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                                CTCCGTCCTCCT  CGA C CG
                                      __   _ C
GAM480   LOC160646 5'  GCCCAGGTGCCCCCCACTCT   83115     GC   A  ATA    A
                                AGAG  GGG GG   GCTTG GC
                                ||||  ||| ||   ||||| ||
                                TCTC  CCC CC   TGGAC CG
                                  A_   _  CG_    C
GAM480   LOC164826 5'  GCTCCTGGGTCCTCCCGCCATC 88531      _         AGCTT
           TT                    AAGA GGCGGGAGGAT     GAGC
                                ||||| ||||||||||     ||||
                                TTCT CCGCCCTCCTG     CTCG
                                  A          GGTC_
GAM480   LOC164945 5'  CTCCTTCCCTCCTGCCTC    88539          AT  CTT
                                GAGGCGGGAGG  AG   GAG
                                ||||||||||  ||   |||
                                CTCCGTCCTCC  TC   CTC
                                      CT  ____
GAM480   LOC196214 5'  CTCAGTCCACCCCCTCCGCCTC 91176        GA  ATA__   T
                                GAGGCGG  GG    GCT GAG
                                |||||||  ||    ||| |||
                                CTCCGCC  CC    TGA CTC
                                    TC  CCACC  _
GAM480   LOC199988 5'  CAAGCTGCCTCCCCTC     91498      CG    A
                                GAGG  GGAGG TAGCTTG
                                ||||  ||||| |||||||
                                CTCC  CCTCC GTCGAAC
                                  __    _
GAM480   LOC200853 3'  GCTCAAGCGATCCTCCCGCCTC 90331            A
           T                     AGAGGCGGGAGGAT GCTTGAGC
                                ||||||||||||| ||||||||
                                TCTCCGCCCTCCTA CGAACTCG
                                      G
GAM480   LOC202908 3'  GCCCAGCTCCTCCTGCCTC    90727          TA   T A
                                GAGGCGGGAGGA  GCT G GC
                                ||||||||||  ||| | ||
                                CTCCGTCCTCCT  CGA C CG
                                      __   _ C
GAM480   LOC222057 3'  GCCCAGCTCCTCCTGCCTC    94355          TA   T A
                                GAGGCGGGAGGA  GCT G GC
                                ||||||||||  ||| | ||
                                CTCCGTCCTCCT  CGA C CG
                                      __   _ C
GAM480   LOC245771 5'  GCTGAGACCCCCCCCACCCCT   94481    A  C   A  ATAG   G
                                AG GG GGG GG    CTT AGC
                                || || ||| ||    ||| |||
                                TC CC CCC CC    GAG TCG
                                 C  A   _  CCA_   _
GAM480   LOC253891 3'  GCTGACCCCACCGCCTCTT    96067         GA  A_
                                AAGAGGCGG  GG  TAGC
                                |||||||||  ||  ||||
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                                TTCTCCGCC  CC  GTCG
                                     AC  CA
GAM480  LOC254552 5'  GCCCCGCCTCGCCCCGCCTCTT 96425          ___  ATA_
                                AAGAGGCGGG  AGG   GC
                                ||||||||||  |||   ||
                                TTCTCCGCCC  TCC   CG
                                     CGC  GCCC
GAM480  LOC254896 5'  CTCGCTTGTCCTCCCACC    97860    C       _  TT
                                GG GGGAGGATA GC  GAG
                                || |||||||| ||  |||
                                CC CCCTCCTGT CG  CTC
                                 A       T __
GAM480  LOC255975 3'  GCCCAGCTCCTCCTGCCTC   97584          TA   T A
                                GAGGCGGGAGGA  GCT G GC
                                ||||||||||||  ||| | ||
                                CTCCGTCCTCCT  CGA C CG
                                      __  _ C
GAM480  LOC256878 3'  GCCCAGCTCCTCCTGCCTC   98688          TA   T A
                                GAGGCGGGAGGA  GCT G GC
                                ||||||||||||  ||| | ||
                                CTCCGTCCTCCT  CGA C CG
                                      __  _ C
GAM480  LOC257068 5'  CAAGCTATCAAACGCCTC    97504       GGAG
                                GAGGCG   GATAGCTTG
                                ||||||   |||||||||
                                CTCCGC   CTATCGAAC
                                   AAA_
GAM480  LOC55954  5'  GCTCAAGCTATCCTCCCACCTC 39397      C
                                GAGG GGGAGGATAGCTTGAGC
                                |||| ||||||||||||||||
                                CTCC CCCTCCTATCGAACTCG
                                  A
GAM480  LOC91012  5'  GCTCAAGCCATCCTTCGGCCCT 65246      _ G      A
          C                      GAGG C GGAGGAT GCTTGAGC
                                |||| | ||||||| ||||||||
                                CTCC G CTTCCTA CGAACTCG
                                  C G      C
GAM481  BAALC    5'  CTCCGGGGCTGAGCCGCCGC   46092        _ _  GG
                                GCGGCGGC C GC  CGGAG
                                |||||||| | ||  |||||
                                CGCCGCCG G CG  GCCTC
                                     A T  GG
GAM481  BSG      3'  CTCCACGTCTGCGCCGCCGCCG 68405    A      C   _ __
          G                      CC GCGGCGGC GCGG C  GGAG
                                || |||||||| |||| |  ||||
                                GG CGCCGCCG CGTC G  CCTC
                                 C       _    T CA
GAM481  BSG      3'  CTCCGCGTCTGCGCCGCCGCCG 9954     A      C  ___
          G                      CC GCGGCGGC GCG   GCGGAG
                                || |||||||| |||   ||||||
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                                GG CGCCGCCG CGT   CGCCTC
                                 C       _  CTG
GAM481  CHIC2    5'  CTCCGCCGCCTCGCCCGCCGGT 25048      A   _  CC
              A                   TACC GCGG CGG  GCGGCGGAG
                                  |||| |||| |||  |||||||||
                                  ATGG CGCC GCT  CGCCGCCTC
                                    C   C  C_
GAM481  FGF18    3'  CCGCCGCGGCCCTCAGGT    54451     AGC  C
                                  ACC   GG GGCCGCGGCGG
                                  |||   || ||||||||||
                                  TGG   TC CCGGCGCCGCC
                                   AC_  _
GAM481  HIVEP1   5'  CCGAGCCGCGGCCGCCGC    10921            __
                                  GCGGCGGCCGCGGC  GG
                                  ||||||||||||||  ||
                                  CGCCGCCGGCGCCG  CC
                                           AG
GAM481  HK3      3'  CTCCGCCGCAGCCTTGCTGG   10926       C   C
                                  CCAGCGG GGC GCGGCGGAG
                                  |||||||  ||| |||||||||
                                  GGTCGTT CCG CGCCGCCTC
                                      _  A
GAM481  HNRPD    5'  CGAGAGCGGCCGCCGCTGGTG  10949             GG_
                                  TACCAGCGGCGGCCGC   CG
                                  ||||||||||||||||   ||
                                  GTGGTCGCCGCCGGCG   GC
                                           AGA
GAM481  HNRPD    5'  CGAGAGCGGCCGCCGCTGGTG  49388             GG_
                                  TACCAGCGGCGGCCGC   CG
                                  ||||||||||||||||   ||
                                  GTGGTCGCCGCCGGCG   GC
                                           AGA
GAM481  HPCAL1   5'  CCGCTGCAGCCGCCGCCGG    10966    A       C
                                  CC GCGGCGGC GCGGCGG
                                  || ||||||||  |||||||
                                  GG CGCCGCCG CGTCGCC
                                   C       A
GAM481  IFITM2   5'  CCCGACCGCCGCTGGTCA     22232    T         C  C
                                  C ACCAGCGGCGG CG GG
                                  | ||||||||||  || ||
                                  A TGGTCGCCGCC GC CC
                                   C         A  _
GAM481  LBX1     3'  CCGGGCCGGCCGCCACCAGCGG 22667    A  ____       CGG
                                  CC GC    GGCGGCCG   CGG
                                  || ||    ||||||||   |||
                                  GG CG    CCGCCGGC   GCC
                                   _ ACCA       CGG
GAM481  PABPC4   5'  CCCCGCGCCCGCCGCCGC    15110         ___    C
                                  GCGGCGGC   CGCGG GG
                                  ||||||||   ||||| ||
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                                CGCCGCCG  GCGCC CC
                                    CCC   _
GAM481  RIMS1   5' TCCTGCCGCCGCCGCT     73031       CGC  _
                                AGCGGCGGC  GGC GGA
                                |||||||||  ||| |||
                                TCGCCGCCG  CCG CCT
                                    ___   T
GAM481  SOX12   3' CCACGCGTTCCCGTCGCTG  23682       C__  GC
                                CAGCGGCGG  CGCG  GG
                                |||||||||  ||||  ||
                                GTCGCTGCC  GCGC  CC
                                     CTT   A_
GAM481  TRAF5   5' CTCCGCTTCGCCGCCGCCGCCG 17273   A     C  __
          G                      CC GCGGCGGC GCG  GCGGAG
                                || ||||||| |||  ||||||
                                GG CGCCGCCG CGC  CGCCTC
                                 C      C   TT
GAM481  USP13   5' CCGCGCCGCCGCCGCCGGCAG  15452   A A     C  G
                                CT CC GCGGCGGC GCG CGG
                                || || |||||||| ||| |||
                                GA GG CGCCGCCG CGC GCC
                                 C  C      C  _
GAM481  USP14   5' CTCCGCCTCGGCCGCCGC   18933        C
                                GCGGCGGCCG GGCGGAG
                                |||||||||| |||||||
                                CGCCGCCGGC CCGCCTC
                                     T
GAM481  VGF     3' CCGCCGCGCGCGCGCGCCGG  14050   A  _  _ C
                                CC GCG GCG GC GCGGCGG
                                || ||| ||| || |||||||
                                GG CGC CGC CG CGCCGCC
                                 C  G  G  _
GAM481  WHSC1L1 5' CTCAGTGCCGGCCGCCATGGCA 35499   A  GC     CG  G
          G                      CT CCA  GGCGGCCG  GC GAG
                                || |||  ||||||||  || |||
                                GA GGT  CCGCCGGC  TG CTC
                                 C  A_      CG  A
GAM481  WHSC1L1 5' CTCAGTGCCGGCCGCCATGGCA 43780   A  GC     CG  G
          G                      CT CCA  GGCGGCCG  GC GAG
                                || |||  ||||||||  || |||
                                GA GGT  CCGCCGGC  TG CTC
                                 C  A_      CG  A
GAM481  BCAN    5' CTCCGCCGCAGTCTCAGCTGC  41969     ___  C
                                GCGGC  GGC GCGGCGGAG
                                |||||  ||| |||||||||
                                CGTCG  CTG CGCCGCCTC
                                   ACT  A
GAM481  C14orf4 5' CCGGGCCGCCGCCGCCGC   67913       C   __
                                GCGGCGGC GCGGC  GG
                                |||||||| |||||  ||
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                                CGCCGCCG CGCCG  CC
                                     C    GG
GAM481  CRELD1   3'  CGCGGCCACCACCTGTAG    31951     C  C_  C
                                CTAC AG  GG GGCCGCG
                                |||| ||  || |||||||
                                GATG TC  CC CCGGCGC
                                  _  CA  A
GAM481  DKFZP434J1813 5'  CCGGTACCGGCCGCGCGCTGGT 62436         _      CGG_
          AG                     CTACCAGCG GCGGCCG    CGG
                                |||||||| |||||||   |||
                                GATGGTCGC CGCCGGC    GCC
                                     G      CATG
GAM481  FLJ10724  5'  CCGCAGCCGCCGCCGATG    37038    G      C  G
                                CA CGGCGGC GC GCGG
                                || ||||||| || ||||
                                GT GCCGCCG CG CGCC
                                 A      C  A
GAM481  FLJ14596  3'  CCGCCGCGGGGTCCTGTCAG   52514    AC   C   GG
                                CT  CAG GGC  CCGCGGCGG
                                ||  ||| |||  |||||||||
                                GA  GTC CTG  GGCGCCGCC
                                 CT   _   G_
GAM481  FLJ14743  5'  CCGCCACCTCCGCCGCCGGCAG 68635    A  A      CCGC
                                CT CC GCGGCGG    GGCGG
                                || || |||||||    |||||
                                GA GG CGCCGCC    CCGCC
                                 C  C      TCCA
GAM481  FLJ23231  5'  CCGCCGGCCGCCGCTGG     47604           GC
                                CCAGCGGCGGCC  GGCGG
                                ||||||||||||  |||||
                                GGTCGCCGCCGG  CCGCC
                                      __
GAM481  HSPC189   5'  CTTCTCGCCGCCGCCTGC    96988    _     C    C
                                GC GGCGGC GCGG GGAG
                                || |||||| |||| ||||
                                CG CCGCCG CGCT CTTC
                                 T     C   _
GAM481  HTF9C     5'  CTCCGCCGCACGCGCTGGCGG  42994    TA     G  GCC
                                C  CCAGCG CG   GCGGCGGAG
                                |  |||||| ||   |||||||||
                                G  GGTCGC GC   CGCCGCCTC
                                 GC     _ A__
GAM481  KIAA0211  5'  CCGCCAATCCCCCGCCGCGGCA 28282    A  A      CCGC__
          G                     CT CC GCGGCGG     GGCGG
                                || || |||||||     |||||
                                GA GG CGCCGCC     CCGCC
                                 C  _      CCCTAA
GAM481  KIAA0211  5'  CCGCCGCGGCAGCCCCAGC    28283    ___   G
                                GC   GGC GCCGCGGCGG
                                ||   ||| ||||||||||
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                                CG   CCG CGGCGCCGCC
                                 ACC   A
GAM481  KIAA1755  5'  CGCCGCCCGCCGCTGGCAG   62011    A        CC
                                CT CCAGCGGCGG  GCGGCG
                                || ||||||||||  ||||||
                                GA GGTCGCCGCC  CGCCGC
                                 C         __
GAM481  moblak    3'  CTCCGCACTCCCCACTGGCAG  56398    A    C  C  CCGCG
                                CT CCAG GG GG    GCGGAG
                                || |||| || ||    ||||||
                                GA GGTC CC CC    CGCCTC
                                 C    A  _  TCA__
GAM481  MSE55     5'  CCGCGACGGCCGCCGCCGTG   23915     CA        CG
                                TAC  GCGGCGGCCG  GCGG
                                |||  ||||||||||  ||||
                                GTG  CGCCGCCGGC  CGCC
                                  C_         AG
GAM481  MYT1      5'  CTCCGCCAGCCCGTGCCACCGC 16979       C  _ __ _
                TG                  CAGCGG GGC C  GC GGCGGAG
                                    |||||| ||| |  || |||||||
                                    GTCGCC CCG G  CG CCGCCTC
                                       A   T CC  A
GAM481  NSE1      3'  CCGCCACGCGCGTCCGCCGCCG 59736       A      _ _   __
                GTGG                    CTACC GCGGCGG C CGC  GGCGG
                                        ||||| ||||||| | |||  |||||
                                        GGTGG CGCCGCC G GCG  CCGCC
                                           C       T C   CA
GAM481  PDE8B     5'  CCGCCGCGACCACCAGCAGG   68200    A  _  C  C
                                    CC GC GG GG CGCGGCGG
                                    || || || || ||||||||
                                    GG CG CC CC GCGCCGCC
                                     A  A  A  A
GAM481  PRKWNK2   5'  CCCCGCGCCCGCAGCGCTGGTA 92194          __    C     C
                G                    CTACCAGCG  GCGG CGCGG GG
                                     |||||||||  |||| ||||| ||
                                     GATGGTCGC  CGCC GCGCC CC
                                           GA    C    _
GAM481  RAI15     3'  CCACCACAGCTGTGGCTGGTA  67244        G     CGC  C
                                    TACCAGC GCGGC   GG GG
                                    ||||||| |||||   || ||
                                    ATGGTCG TGTCG   CC CC
                                        G     ACA  A
GAM481  SH3GLB1   5'  TCCGCCTCGCCGCCGCT     32601          C C
                                    AGCGGCGGC G GGCGGA
                                    ||||||||| | ||||||
                                    TCGCCGCCG C CCGCCT
                                          _ T
GAM481  SMPD2     5'  CCACCGCGGCCGTCGCTGG    13267               C
                                    CCAGCGGCGGCCGCGG GG
                                    ||||||||||||||| ||
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                                GGTCGCTGCCGGCGCC CC
                                       A
GAM481  TBL1Y    5'  CTCCGCTGCTGCCGCCACCGC  56951    ___     C
                                GC   GGCGGC GCGGCGGAG
                                ||   |||||| |||||||||
                                CG   CCGCCG CGTCGCCTC
                                 CCA     T
GAM481  TBL1Y    5'  CTCCGCTGCTGCCGCCACCGC  56954    ___     C
                                GC   GGCGGC GCGGCGGAG
                                ||   |||||| |||||||||
                                CG   CCGCCG CGTCGCCTC
                                 CCA     T
GAM481  TBL1Y    5'  CTCCGCTGCTGCCGCCACCGC  53858    ___     C
                                GC   GGCGGC GCGGCGGAG
                                ||   |||||| |||||||||
                                CG   CCGCCG CGTCGCCTC
                                 CCA     T
GAM481  LOC132166 3'  CCCCGCCAGCCGCTGGTG    75536         GGCC    C
                                TACCAGCGGC    GCGG GG
                                ||||||||||    |||| ||
                                GTGGTCGCCG    CGCC CC
                                      AC__    _
GAM481  LOC146990 5'  CTCCGCGCCGCCGCCGCCGGTG 84954      A       C   G
                                TACC GCGGCGGC GCG CGGAG
                                |||| |||||||| ||| |||||
                                GTGG CGCCGCCG CGC GCCTC
                                  C       C   _
GAM481  LOC148530 5'  CCCCGCCTGAGCAGCTGGTAG  85313        G  GGCC    C
                                CTACCAGC GC    GCGG GG
                                |||||||| ||    |||| ||
                                GATGGTCG CG    CGCC CC
                                     A  AGTC    _
GAM481  LOC199964 5'  CCGAGGGTCGCCGCTGGTAG   91495            G_
                                CTACCAGCGGCGGCC  CGG
                                ||||||||||||||  |||
                                GATGGTCGCCGCTGG  GCC
                                       GA
GAM481  LOC219908 5'  CTCCGCCGCGAATGCGGGC   95977    G_  GC
                                GC  GCG  CGCGGCGGAG
                                ||  |||  ||||||||||
                                CG  CGT  GCGCCGCCTC
                                 GG   AA
GAM481  LOC221424 5'  CCGCCGCAGCCTCCGCCGC   95268      ___  C
                                GCGGC   GGC GCGGCGG
                                |||||   ||| |||||||
                                CGCCG   CCG CGCCGCC
                                   CCT   A
GAM481  LOC221424 5'  CTCCGCCACAGCCGCCGC    95273        CGC
                                GCGGCGGC   GGCGGAG
                                ||||||||   |||||||
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                                CGCCGCCG   CCGCCTC
                                    ACA
GAM481  LOC221687 5'  CCCTGGGCCGCCGCCGG     93868    A       G   C
                                CC GCGGCGGCC CGG GG
                                || ||||||||| ||| ||
                                GG CGCCGCCGG GTC CC
                                 C       _  _
GAM481  LOC245726 5'  CTCCGCCGGCGACCGCTGACGG 74585    AG     C  _
                                CC  CGGCGG CGC GGCGGAG
                                ||  |||||| ||| |||||||
                                GG  GTCGCC GCG CCGCCTC
                                 CA     A  G
GAM481  LOC254617 5'  CTCCACCGCGGCCGCCGCGTGG 99279     _          C
                                CCA GCGGCGGCCGCGG GGAG
                                ||| |||||||||||| ||||
                                GGT CGCCGCCGGCGCC CCTC
                                  G          A
GAM481  LOC51308  3'  CTCCACCGCTGTTCCGCTGC   33964       CC__    C
                                GCGGCGG    GCGG GGAG
                                |||||||    |||| ||||
                                CGTCGCC    CGCC CCTC
                                    TTGT    A
GAM482  ARHGEF7   5'  GCTCTGTATTGCAGGTCTAC   15323          GATG
                                GTGGACCTGCGG    AGAGC
                                ||||||||||||    |||||
                                CATCTGGACGTT    TCTCG
                                       ATG_
GAM482  CHRNE     3'  GCTGGTGGCCCTCAGGCCCAC  5377      A    C   AT AG
                                GTGG CCTG GGG  G  AGC
                                |||| |||| |||  |  |||
                                CACC GGAC CCC  T  TCG
                                  C    T   GG GG
GAM482  CLN6      3'  CTCATCCCTCAGGCCCAC    35835      A    C
                                GTGG CCTG GGGATGAG
                                |||| |||| ||||||||
                                CACC GGAC CCCTACTC
                                  C    T
GAM482  DHCR24    3'  GCCTGGGCCTGCAGGCCCAC   29300      A       ATG  A
                                GTGG CCTGCGGG   AG GC
                                |||| ||||||||   || ||
                                CACC GGACGTCC   TC CG
                                  C       GGG  _
GAM482  EIF4EBP2  3'  GCTCCTAGAGCAGGTCCAT    15858          GGGA  A
                                GTGGACCTGC    TG GAGC
                                ||||||||||    || ||||
                                TACCTGGACG    AT CTCG
                                      AG__  C
GAM482  FOXD1     5'  CTCTCACCCGTCCCGC      16774      ACCT    A
                                GTGG    GCGGG TGAGAG
                                ||||    ||||| ||||||
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                                CGCC   TGCCC ACTCTC
                                  C___   _
GAM482  HLX1    5'  CTCTCATCCAGCCCGC     41984     ACCT  G
                                GTGG   GC GGATGAGAG
                                ||||   || |||||||||
                                CGCC   CG CCTACTCTC
                                  ____  A
GAM482  IL12A   5'  GCCCTCACCTGCCGCGGCCAC  7949      A  T__    A   A
                                GTGG CC   GCGGG TGAG GC
                                |||| ||   ||||| |||| ||
                                CACC GG   CGTCC ACTC CG
                                  _ CGC    _   C
GAM482  MB      3'  GCTCCCACCCCCACCCAT    19324     ACC  C   A  A
                                GTGG   TG GGG TG GAGC
                                ||||   || ||| || ||||
                                TACC   AC CCC AC CTCG
                                  C__  _   C  C
GAM482  MECP2   3'  CTCCCCCCAGGTCTAC      18399        C   ATGA
                                GTGGACCTG GGG    GAG
                                ||||||||| |||    |||
                                CATCTGGAC CCC    CTC
                                     _  C___
GAM482  MLLT4   3'  CTCTCATTGGGTTCCAC     72899      _  GCGG
                                GTGGA CCT    GATGAGAG
                                ||||| |||    ||||||||
                                CACCT GGG    TTACTCTC
                                  T  _____
GAM482  NIPSNAP1 3'  CTCATTCTGCAGGGCCAC    14657     A
                                GTGG CCTGCGGGATGAG
                                |||| ||||||||||||
                                CACC GGACGTCTTACTC
                                  G
GAM482  NUMA1   3'  GCCCTCACTCTTGAAGTCCA  95084      CTG    _   A
                                TGGAC   CGGGA TGAG GC
                                |||||   ||||| |||| ||
                                ACCTG   GTTCT ACTC CG
                                   AA_    C   C
GAM482  POLR2E  3'  GCTCCCACCTCGCGGGGCC   60597    A      A  A
                                GG CCTGCGGG TG GAGC
                                || |||||||| || ||||
                                CC GGGCGCTC AC CTCG
                                 G       C  C
GAM482  SLC38A3 3'  CTCATCCTGTTCTGTCTAC   23374      CT_
                                GTGGAC   GCGGGATGAG
                                ||||||   ||||||||||
                                CATCTG   TGTCCTACTC
                                   TCT
GAM482  SURF5   3'  GCTGTATCCCCCGCAGGCCC  23128    A    __     AG
                                GG CCTGC  GGGATG  AGC
                                || |||||  ||||||  |||
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                                CC GGACG  CCCTAT  TCG
                                 C    CC     G_
GAM482  TBL1X    5'  CTGGTCCACAGGTCCAT     20133         CG   G
                                GTGGACCTG  GGAT AG
                                |||||||||  |||| ||
                                TACCTGGAC  CCTG TC
                                     A_    G
GAM482  TCFL4    3'  GCCCTCATCCTCTCTAC     64212       CCTGC      A
                                GTGGA    GGGATGAG GC
                                |||||    |||||||| ||
                                CATCT    TCCTACTC CG
                                   C____       C
GAM482  TLR5     5'  CTCTCATCTGCTCCA       13786      CCT   G
                                TGGA   GCGG ATGAGAG
                                ||||   |||| |||||||
                                ACCT   CGTC TACTCTC
                                  ___   _
GAM482  C6orf9   3'  CTCCCCGCCCACAGGTCCAT   42326         C   ATGA
                                GTGGACCTG GGG    GAG
                                ||||||||| |||    |||
                                TACCTGGAC CCC    CTC
                                     A   GCCC
GAM482  CRELD1   5'  GCCCTCTATCTGCAGGTCC    31953          AT   A
                                GGACCTGCGGG  GAG GC
                                ||||||||||  ||| ||
                                CCTGGACGTCT  CTC CG
                                      AT   C
GAM482  DEPP     3'  GCTCCCACCCTCAAAGCCCAT  23806      ACC_  C   A  A
                                GTGG    TG GGG TG GAGC
                                ||||    || ||| || ||||
                                TACC    AC CCC AC CTCG
                                  CGAA  T   _  C
GAM482  DKFZP434P0111 3'  CTCTCATCAGGACCAC      67957      A   GCGG
                                GTGG CCT    GATGAGAG
                                |||| |||    ||||||||
                                CACC GGA    CTACTCTC
                                  A  ____
GAM482  DKFZp566H0824 5'  GCTCTTAAGGCAGGTCCA    34489          GGGA
                                TGGACCTGC    TGAGAGC
                                |||||||||    |||||||
                                ACCTGGACG    ATTCTCG
                                     GA__
GAM482  FAF1     5'  GCCCTCATCCTGGCCCGC    23898      A  TGC      A
                                GTGG CC   GGGATGAG GC
                                |||| ||   |||||||| ||
                                CGCC GG   TCCTACTC CG
                                  C ___       C
GAM482  FKBP8    3'  GCCCTCATTCCTTCAGACCCA  25161     AC   C_      A
                                TGG  CTG  GGGATGAG GC
                                |||  |||  |||||||| ||
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                                ACC  GAC  CCTTACTC CG
                                  CA   TT       C
GAM482  FLJ11848  3'  CTCTCATCCCAAGACCTAC   47930     AC  GC
                                GTGG  CT  GGGATGAGAG
                                ||||  ||  ||||||||||
                                CATC  GA  CCCTACTCTC
                                  CA  A_
GAM482  FLJ14827  5'  GCCCTCACCGACGGGTCCA   52720        _  GA   A
                                TGGACCTG CGG  TGAG GC
                                ||||||||  |||  |||| ||
                                ACCTGGGC GCC  ACTC CG
                                    A   __   C
GAM482  FLJ20507  3'  GCTCTCAGAACCGGAGGTCCAC 60847        G  GA_
                                GTGGACCT CGG   TGAGAGC
                                ||||||||  |||   |||||||
                                CACCTGGA GCC   ACTCTCG
                                    G   AAG
GAM482  FLJ20507  3'  GCTCTCAGAACCGGAGGTCCAC 35743        G  GA_
                                GTGGACCT CGG   TGAGAGC
                                ||||||||  |||   |||||||
                                CACCTGGA GCC   ACTCTCG
                                    G   AAG
GAM482  FLJ22635  3'  GCTCTCAGGGAAGGTCCAT   47671        GCGGGA
                                GTGGACCT     TGAGAGC
                                ||||||||     |||||||
                                TACCTGGA     ACTCTCG
                                    AGGG__
GAM482  FLJ22756  3'  GCTCCCTCCCTTCCTGCAGGCC 45962     A       T__ __
          CAC                     GTGG CCTGCGGGA   GA  GAGC
                                ||||  |||||||||   ||  ||||
                                CACC GGACGTCCT   CT  CTCG
                                  C        TCC  CC
GAM482  FOXJ1    5'  GCTCCCACCGTGGTCC      9378       T   GA  A
                                GGACC GCGG  TG GAGC
                                |||||  ||||  || ||||
                                CCTGG TGCC  AC CTCG
                                  _   __  C
GAM482  HSPF2    5'  CTCTGTCCACAGGTCCA     19834        CG   G
                                TGGACCTG  GGAT AGAG
                                ||||||||  ||||  ||||
                                ACCTGGAC  CCTG TCTC
                                    A_   _
GAM482  KIAA0557  3'  CTCTCATCCCTGGGCAC     78555     GA   C
                                GTG  CCTG GGGATGAGAG
                                |||  ||||  ||||||||||
                                CAC  GGGT CCCTACTCTC
                                  __   _
GAM482  KIAA0819  3'  GCTCCCATTTTGTAACCAC   64332     ACC       A
                                GTGG   TGCGGGATG GAGC
                                ||||   |||||||||  ||||
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                                CACC   ATGTTTTAC CTCG
                                  A__        C
GAM482  KIAA1613  3'  GCTCTCATTTCACAAATCCA   65440      CC  C GG
                                TGGA  TG G  ATGAGAGC
                                ||||  || |  ||||||||
                                ACCT  AC C  TACTCTCG
                                  AA  A TT
GAM482  KIAA1817  3'  GCCCTCACCTCCAGGTCCA   68782        C   A   A
                                TGGACCTG GGG TGAG GC
                                |||||||| ||| |||| ||
                                ACCTGGAC TCC ACTC CG
                                     C   _   C
GAM482  MGC3035   5'  GCTCTCATCCCCCCTCCAC   44404      CCTGC
                                GTGGA    GGGATGAGAGC
                                |||||    ||||||||||
                                CACCT    CCCTACTCTCG
                                   CCC__
GAM482  NGEF      3'  GCCCTCATCCCTGCCCAC    69682      ACCT  _      A
                                GTGG    GC GGGATGAG GC
                                ||||    || |||||||| ||
                                CACC    CG CCCTACTC CG
                                  _____  T       C
GAM482  PTGES2    5'  GCCCTCACCCCGGCCAACCCGC 47577      ACCT  _   A   A
                                GTGG    GC GGG TGAG GC
                                ||||    || ||| |||| ||
                                CGCC    CG CCC ACTC CG
                                  CAAC  G   C    C
GAM482  SDF1      3'  GCCCTCATCCCGAGCACC    92517    AC  G       A
                                GG  CT CGGGATGAG GC
                                ||  || ||||||||| ||
                                CC  GA GCCCTACTC CG
                                 AC  _        C
GAM482  TAF5L     3'  GCCCTCATTCCGGGCAGGTCC  27723         __       A
                                GGACCTGC  GGGATGAG GC
                                ||||||||  |||||||| ||
                                CCTGGACG  CCTTACTC CG
                                     GG       C
GAM482  LOC125206 3'  GCTCTGAGTCCTCAGGTCCAC  76167         C    G_
                                GTGGACCTG GGGAT  AGAGC
                                ||||||||| |||||  |||||
                                CACCTGGAC TCCTG  TCTCG
                                     _    AG
GAM482  LOC139046 5'  CTCACTCAGGTCCAC       76322         CG  A
                                GTGGACCTG  GG TGAG
                                |||||||||  || ||||
                                CACCTGGAC  TC ACTC
                                     __  _
GAM482  LOC144558 3'  GCTCCCATCCTGCTCTCCA   84077      CCT       A
                                TGGA   GCGGGATG GAGC
                                ||||   |||||||| ||||
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                                ACCT   CGTCCTAC CTCG
                                  CT_       C
GAM482   LOC151602 3'  CTCCATGTAGCAGGTCCAT   81110         GGG   A
                                GTGGACCTGC   ATG GAG
                                ||||||||||   ||| |||
                                TACCTGGACG   TAC CTC
                                     ATG   _
GAM482   LOC151623 3'  GCTCCCATCCTGCTCTCCA   86635     CCT       A
                                TGGA   GCGGGATG GAGC
                                ||||   |||||||| ||||
                                ACCT   CGTCCTAC CTCG
                                  CT_       C
GAM482   LOC153579 3'  GCCTGGGCCCGCAGACCAC   81770     AC      ATG  A
                                GTGG  CTGCGGG   AG GC
                                ||||  |||||||   || ||
                                CACC  GACGCCC   TC CG
                                  A_      GGG  _
GAM482   LOC157278 3'  GCTCCCATCCTGCTCTCCA   87708     CCT       A
                                TGGA   GCGGGATG GAGC
                                ||||   |||||||| ||||
                                ACCT   CGTCCTAC CTCG
                                  CT_       C
GAM482   LOC203083 5'  CTCTCATCCCAGGCAATCAC   92086     A__   GC
                                GTGG   CCT  GGGATGAGAG
                                ||||   |||  ||||||||||
                                CACT   GGA  CCCTACTCTC
                                  AAC   __
GAM482   LOC219919 5'  CTCTCATCCCAGGCAATCAC   94925     A__   GC
                                GTGG   CCT  GGGATGAGAG
                                ||||   |||  ||||||||||
                                CACT   GGA  CCCTACTCTC
                                  AAC   __
GAM482   LOC220522 3'  GCCCTCATCCTCAACATCC   61141     CC_  C       A
                                GGA   TG GGGATGAG GC
                                |||   || |||||||| ||
                                CCT   AC TCCTACTC CG
                                  ACA  _       C
GAM482   LOC221795 5'  CTCTCATCCCAGGCAATCAC   94074     A__   GC
                                GTGG   CCT  GGGATGAGAG
                                ||||   |||  ||||||||||
                                CACT   GGA  CCCTACTCTC
                                  AAC   __
GAM482   LOC221962 3'  GCTCCCATCCTGCTCTCCA   94241     CCT       A
                                TGGA   GCGGGATG GAGC
                                ||||   |||||||| ||||
                                ACCT   CGTCCTAC CTCG
                                  CT_       C
GAM482   LOC254176 5'  CTCTCATCCCAGGCAATCAC   99167     A__   GC
                                GTGG   CCT  GGGATGAGAG
                                ||||   |||  ||||||||||
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                                CACT   GGA  CCCTACTCTC
                                  AAC  __
GAM482  LOC255461 3'  GCTCCCATCCTGCTCTCCA   99140     CCT      A
                                TGGA   GCGGGATG GAGC
                                ||||   |||||||| ||||
                                ACCT   CGTCCTAC CTCG
                                  CT_      C
GAM482  LOC255516 3'  GCTCCCATCCTGCTCTCCA   99154     CCT      A
                                TGGA   GCGGGATG GAGC
                                ||||   |||||||| ||||
                                ACCT   CGTCCTAC CTCG
                                  CT_      C
GAM482  LOC256158 5'  GCCCTCACCTGCAGGTCCA   99497          A   A
                                TGGACCTGCGGG TGAG GC
                                |||||||||||| |||| ||
                                ACCTGGACGTCC ACTC CG
                                       _   C
GAM482  LOC256515 5'  CTCTCATCCCAGGCAATCAC   98211     A__   GC
                                GTGG   CCT  GGGATGAGAG
                                ||||   |||  ||||||||||
                                CACT   GGA  CCCTACTCTC
                                  AAC  __
GAM482  LOC51644  3'  GCCCTCATCCCAACAGCCCA   32666     AC   C_      A
                                TGG  CTG  GGGATGAG GC
                                |||  |||  |||||||| ||
                                ACC  GAC  CCCTACTC CG
                                  C_   AA       C
GAM482  LOC91035  5'  GCCCCTCAGTGCCCAGGTCCAC 65300         C  G _   A_
                                GTGGACCTG GG A TGAG  GC
                                ||||||||| || | ||||  ||
                                CACCTGGAC CC T ACTC  CG
                                      _ G G   CC
GAM482  LOC92399  3'  GCTCTCATAGCACAGTCTAC   57865       C_  GGG
                                GTGGAC  TGC   ATGAGAGC
                                ||||||  |||   ||||||||
                                CATCTG  ACG   TACTCTCG
                                   AC   A__
GAM483  AKAP2     3'  GAGCCAGATTTTCTCTGTGCT  24226         TA    __
                                AGCACAGAGA  AGGTC  GCTC
                                ||||||||||  |||||  ||||
                                TCGTGTCTCT  TTTAG  CGAG
                                      __     AC
GAM483  ALB       3'  GCCTCTTTTCTCTGTGCTT   6644           T    TC
                                AAGCACAGAGA AAGG  GC
                                |||||||||||| ||||  ||
                                TTCGTGTCTCT TTTC  CG
                                       _   TC
GAM483  ARNT2     3'  GAGCCCATGATCCCTGGCTT   30086     A   A   AA_  TC
                                AAGC CAG GAT   GG  GCTC
                                |||| ||| |||   ||  ||||
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                                TTCG GTC CTA   CC  CGAG
                                  _  C   GTA  __
GAM483  ATP7A    3'  AGTTTCCTAGCTCTGTGCT   5315         ATA  TC
                                AGCACAGAG   AGG  GCT
                                |||||||||   |||  |||
                                TCGTGTCTC   TCC  TGA
                                     GA_   TT
GAM483  BAZ2A    3'  AGCTGCCACCTCTGTGTT    26503         ATAA  C
                                AGCACAGAG    GGT GCT
                                |||||||||    ||| |||
                                TTGTGTCTC    CCG CGA
                                     CA__   T
GAM483  BNC      3'  GACCATCCCTGTGTTT      9942          A  AA
                                AAGCACAG GAT  GGTC
                                |||||||| |||  ||||
                                TTTGTGTC CTA  CCAG
                                     C  __
GAM483  BSN      3'  GAGATGCCATCTCTGTCT    14385    C      AA  CG
                                AG ACAGAGAT  GGT  CTC
                                || ||||||||  |||  |||
                                TC TGTCTCTA  CCG  GAG
                                 _      __   TA
GAM483  BZRP     3'  AGCAGTGTCCTGTGCTT     7388          A   AGGTC
                                AAGCACAG GATA    GCT
                                |||||||| ||||    |||
                                TTCGTGTC CTGT    CGA
                                     _   GA___
GAM483  BZRP     3'  AGCAGTGTCCTGTGCTT     24600         A   AGGTC
                                AAGCACAG GATA    GCT
                                |||||||| ||||    |||
                                TTCGTGTC CTGT    CGA
                                     _   GA___
GAM483  CDH7     5'  GATTATTATCTCTGGACT    54448    CA       _
                                AG  CAGAGATAA GGTC
                                ||  |||||||||  ||||
                                TC  GTCTCTATT TTAG
                                 AG        A
GAM483  CDH7     5'  GATTATTATCTCTGGACT    16413    CA       _
                                AG  CAGAGATAA GGTC
                                ||  |||||||||  ||||
                                TC  GTCTCTATT TTAG
                                 AG        A
GAM483  CDKN1A   3'  GAGTGGGGTTATCTCTGTGTT  55269           GG
                                AGCACAGAGATAA  TCGCTC
                                ||||||||||||  ||||||
                                TTGTGTCTCTATT  GGTGAG
                                      GG
GAM483  CHAC     5'  GAGCGACCGCCTCCGTCT    53955    C  A   ATAA
                                AG AC GAG    GGTCGCTC
                                || || |||    ||||||||
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                                TC TG CTC    CCAGCGAG
                                 _ C   CG__
GAM483  CHAC     5'  GAGCGACCGCCTCCGTCT    31496    C  A   ATAA
                                AG AC GAG    GGTCGCTC
                                || || |||    ||||||||
                                TC TG CTC    CCAGCGAG
                                 _ C   CG__
GAM483  CORO2A   5'  GGCATTTATCTCCATGTT    14104     CA      _
                                AGCA  GAGATAAG GTC
                                ||||  |||||||| |||
                                TTGT  CTCTATTT CGG
                                  AC       A
GAM483  EMR1     3'  CGACCATTTTATCTTCGTGCT  10516      AG     ___
                                AGCAC  AGATAA   GGTCG
                                |||||  ||||||   |||||
                                TCGTG  TCTATT   CCAGC
                                   CT     TTA
GAM483  HLA-A    3'  GGTGTCTCCATCTCTGTCT   10928    C      AA  T
                                AG ACAGAGAT  GG CGCT
                                || ||||||||  || ||||
                                TC TGTCTCTA  TC GTGG
                                 _       CC  T
GAM483  HPGD     3'  AGTGTATTTATATCTGTGCTT  7809         G    GT
                                AAGCACAGA ATAAG  CGCT
                                |||||||||| |||||  ||||
                                TTCGTGTCT TATTT  GTGA
                                     A    AT
GAM483  LIFR     3'  AGTATGCTTATTTCTGTGC   11309          GTC
                                GCACAGAGATAAG   GCT
                                ||||||||||||   |||
                                CGTGTCTTTATTC   TGA
                                       GTA
GAM483  MAZ      5'  AGGGGCCCTACATCTGCGCT   73777    A   GA  A   G
                                AGC CAGA  TA GGTC CT
                                ||| ||||  || |||| ||
                                TCG GTCT  AT CCGG GA
                                  C   AC  C   G
GAM483  MFRP     3'  AGTTCTGCCTCTCTGTGC    49503        TAA  C__
                                GCACAGAGA   GGT   GCT
                                |||||||||   |||   |||
                                CGTGTCTCT   CCG   TGA
                                     ___   TCT
GAM483  MPL      3'  AGTTCTTATCTCTAGCT     19340     AC       TC
                                AGC  AGAGATAAGG  GCT
                                |||  ||||||||||  |||
                                TCG  TCTCTATTCT  TGA
                                  A_         __
GAM483  PRKACB   3'  GATTTTATCTCTGCGTTT    12276     A
                                AAGC CAGAGATAAGGTC
                                |||| ||||||||||||
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                                TTTG GTCTCTATTTTAG
                                  C
GAM483  TBL2    3'  GAGTGCCCACTCTGTGC    53352       ATAA  T
                                GCACAGAG   GG CGCTC
                                ||||||||   || |||||
                                CGTGTCTC   CC GTGAG
                                    AC__  _
GAM483  TBL2    3'  GAGTGCCCACTCTGTGC    25866       ATAA  T
                                GCACAGAG   GG CGCTC
                                ||||||||   || |||||
                                CGTGTCTC   CC GTGAG
                                    AC__  _
GAM483  UBE3A   3'  GGCTTCTCATCCACTGTGCTT  56440       A_  A  TC
                                AAGCACAG  GAT AGG  GCT
                                ||||||||  ||| |||  |||
                                TTCGTGTC  CTA TCT  CGG
                                    AC  C  T_
GAM483  UBE3A   3'  GGCTTCTCATCCACTGTGCTT  56444       A_  A  TC
                                AAGCACAG  GAT AGG  GCT
                                ||||||||  ||| |||  |||
                                TTCGTGTC  CTA TCT  CGG
                                    AC  C  T_
GAM483  UBE3A   3'  GGCTTCTCATCCACTGTGCTT  6626        A_  A  TC
                                AAGCACAG  GAT AGG  GCT
                                ||||||||  ||| |||  |||
                                TTCGTGTC  CTA TCT  CGG
                                    AC  C  T_
GAM483  ZNF43   5'  GAGCGATTTGACTCTCCTGC  14248    CA   TA_
                                GCA  GAGA   AGGTCGCTC
                                |||  ||||   |||||||||
                                CGT  CTCT   TTTAGCGAG
                                  C_   CAG
GAM483  ZNF80   3'  GATTATTTCCTCTGTGCTT   24070       AT  _
                                AAGCACAGAG  AA GGTC
                                ||||||||||  || ||||
                                TTCGTGTCTC  TT TTAG
                                    CT  A
GAM483  AKT3    3'  GAGCATCTTTCCCCTGTGCTT  19606       A_  T   C
                                AAGCACAG  GA AAGGT GCTC
                                ||||||||  || ||||| ||||
                                TTCGTGTC  CT TTCTA CGAG
                                    CC  _    _
GAM483  APMCF1  3'  AGTTTTCTTATCTTCTGTGCTT 41357        _     TC
                                AAGCACAGA GATAAGG  GCT
                                |||||||||  |||||||  |||
                                TTCGTGTCT CTATTCT  TGA
                                    T      TT
GAM483  ARG99   3'  GATATATCTCTGTGCTT    50011          AG
                                AAGCACAGAGATA  GTC
                                ||||||||||||  |||
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                                TTCGTGTCTCTAT  TAG
                                      A_
GAM483  C20orf11  3'  AGTTTTTCCTTACCCCTGTGGT 35864    G    AGA    TC__
           T                   AA CACAG   TAAGG    GCT
                               || |||||   |||||    |||
                               TT GTGTC   ATTCC    TGA
                                 G    CCC    TTTT
GAM483  CBX6    3'  GCCCTCTCTCCCTGTGCTT   27417       A  TA_   TC
                               AAGCACAG GA   AGG  GC
                               |||||||| ||   |||  ||
                               TTCGTGTC CT   TCC  CG
                                    C  CTC   __
GAM483  CGR11   3'  AGGACCATCTCTGTGC      22690        AA   G
                               GCACAGAGAT  GGTC CT
                               ||||||||||  |||| ||
                               CGTGTCTCTA  CCAG GA
                                     __   _
GAM483  CSRP2BP  3'  GAGCTCTAATCTCTGTG     70655        A   TC
                               CACAGAGAT AGG  GCTC
                               |||||||| |||  ||||
                               GTGTCTCTA TCT  CGAG
                                    A  __
GAM483  FLJ10374  3'  GGTCCCTTCTCTGTGC     36555        TA   TC
                               GCACAGAGA  AGG  GCT
                               |||||||| |||  |||
                               CGTGTCTCT  TCC  TGG
                                     __  C_
GAM483  FLJ12960  3'  GAGGGATCCACCTTTGTGCT  45299        ATAA   G
                               AGCACAGAG   GGTC CTC
                               |||||||||   |||| |||
                               TCGTGTTTC   CTAG GAG
                                    CAC_   G
GAM483  FLJ13072  3'  AGTGCCTTTGTCTCTATGCTT  91386      C        T
                               AAGCA AGAGATAAGG CGCT
                               ||||| |||||||||| ||||
                               TTCGT TCTCTGTTTC GTGA
                                  A        C
GAM483  FLJ13265  3'  GAGTCCTCCATCTCTGT    46411        A_   TC
                               ACAGAGAT  AGG  GCTC
                               ||||||||  |||  ||||
                               TGTCTCTA  TCC  TGAG
                                    CC  __
GAM483  FLJ14564  3'  ACATTTATCACCTCTGTGC   77010        ___    _
                               GCACAGA   GATAAG GT
                               |||||||   |||||| ||
                               CGTGTCT   CTATTT CA
                                    CCA    A
GAM483  FLJ14641  3'  GAGTGGGCACCTCTGTGTTT  52558        ATAAG  _
                               AAGCACAGAG    GTC GCTC
                               ||||||||||    ||| ||||
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                                TTTGTGTCTC    CGG TGAG
                                     CA___   G
GAM483  FLJ14681  5'  GCTCCTATCTCTGCCTT    52596    CA      A  TC
                                AAG  CAGAGATA GG  GC
                                |||  |||||||| ||  ||
                                TTC  GTCTCTAT CC  CG
                                  C_       _  T_
GAM483  FLJ20054  3'  AGCGAATTCTACTGTGCTT   39307       _  TAAGG
                                AAGCACAG AGA    TCGCT
                                |||||||| |||    |||||
                                TTCGTGTC TCT    AGCGA
                                     A  TA___
GAM483  FLJ20986  5'  GCTTCCTTCCCTGTGCTT    44838       A  TA   TC
                                AAGCACAG GA  AGG  GC
                                |||||||| ||  |||  ||
                                TTCGTGTC CT  TCC  CG
                                     C  __   TT
GAM483  FLJ22688  3'  GCCCCTCTCCCCTCTGTGCTT  47823        ATA__  TC
                                AAGCACAGAG    AGG  GC
                                ||||||||||    |||  ||
                                TTCGTGTCTC    TCC  CG
                                     CCCTC   C_
GAM483  FLJ23375  3'  AGCACTTACCGCTGTGCTT    46945       AGATA   C
                                AAGCACAG    AGGT GCT
                                ||||||||    |||| |||
                                TTCGTGTC    TTCA CGA
                                     GCCA_   _
GAM483  GTF2H3    3'  CCTTTTCATCCTGTGCTT    9501        A  ___
                                AAGCACAG GAT   AAGG
                                |||||||| |||   ||||
                                TTCGTGTC CTA   TTCC
                                     _  CTT
GAM483  HES2      3'  AGTTCTCATTCCCTGTGCTT  39369       A  TAA  TC
                                AAGCACAG GA   GG  GCT
                                |||||||| ||   ||  |||
                                TTCGTGTC CT   TC  TGA
                                     C  TAC  T_
GAM483  HSA250839 3'  AGTCACGCCCTCTCTGTGC   37848       TAA   C__
                                GCACAGAGA   GGT   GCT
                                |||||||||   |||   |||
                                CGTGTCTCT   CCG   TGA
                                     C__   CAC
GAM483  HXCP2     3'  ACTTTGTACCTCTCTGTGCTT 51802        ____
                                AAGCACAGAGA   TAAGGT
                                ||||||||||    ||||||
                                TTCGTGTCTCT   GTTTCA
                                      CCAT
GAM483  JM11      3'  GAGCCCAACCCCCTCTGTGC  54361       ATAA   C__
                                GCACAGAG   GGT   GCTC
                                ||||||||   |||   ||||
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                                CGTGTCTC   CCA  CGAG
                                    CC__   ACC
GAM483  JM11     3' GAGCCCAACCCCCTCTGTGC  54362       ATAA  C__
                                GCACAGAG   GGT  GCTC
                                ||||||||   |||  ||||
                                CGTGTCTC   CCA  CGAG
                                    CC__   ACC
GAM483  KIAA0159 5' AGCCCTTTCTCTGTGC     30136       T   TC
                                GCACAGAGA AAGG  GCT
                                ||||||||| ||||  |||
                                CGTGTCTCT TTCC  CGA
                                      _   __
GAM483  KIAA0391 3' GATTCTTACCTCTATGCT   28612     C   A   _
                                AGCA AGAG TAAGG TC
                                |||| |||| ||||| ||
                                TCGT TCTC ATTCT AG
                                  A   C    T
GAM483  KIAA0419 3' GCATCATCTCTGTGCTT    28862        AA  C
                                AAGCACAGAGAT  GGT GC
                                ||||||||||||  ||| ||
                                TTCGTGTCTCTA  CTA CG
                                      __  _
GAM483  KIAA0555 5' AGTCTGCTCTCTGTGCT    60735       TAA  TC
                                AGCACAGAGA   GG  GCT
                                |||||||||   ||  |||
                                TCGTGTCTCT   TC  TGA
                                     CG_  __
GAM483  KIAA0676 3' GCCTCATACCTCTGTGCT   31144       A  __
                                AGCACAGAG TA  AGGT
                                ||||||||| ||  ||||
                                TCGTGTCTC AT  TCCG
                                     C  AC
GAM483  KIAA1025 5' GAGCATTTGTCCTGTGCTT  64677       A    GTC
                                AAGCACAG GATAAG   GCTC
                                |||||||| ||||||   ||||
                                TTCGTGTC CTGTTT   CGAG
                                   _     A__
GAM483  KIAA1189 3' GTCCTCTTAGCTCTGTGCT  72509       A    TC
                                AGCACAGAG TAAGG  GC
                                ||||||||| |||||  ||
                                TCGTGTCTC ATTCT  TG
                                     G    CC
GAM483  KIAA1649 3' GACTCTGCCATTTCTGTGC  51237        A__  _
                                GCACAGAGAT   AG GTC
                                ||||||||||   || |||
                                CGTGTCTTTA   TC CAG
                                     CCG  T
GAM483  KIAA1742 3' AGCAGGCTCCTGTGCTT    78135       A  TAAG  _
                                AAGCACAG GA   GTC GCT
                                |||||||| ||   ||| |||
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                                TTCGTGTC CT    CGG CGA
                                   _ _____   A
GAM483  KIAA1822  3'  GACTCCTCATACTCTGTGCTT  68184          _ A   __
                                AAGCACAGAG AT AGG  TC
                                |||||||||| || |||  ||
                                TTCGTGTCTC TA TCC  AG
                                    A  C   TC
GAM483  KIAA1877  3'  GAGCCATCACCCTGTGCTT   66750        AGATAA   C
                                AAGCACAG     GGT GCTC
                                ||||||||     ||| ||||
                                TTCGTGTC     CTA CGAG
                                   CCA___   C
GAM483  LBP-9     3'  GAGTGGGGCTATTCTGTGC   28047        A  AGG
                                GCACAGAG TA   TCGCTC
                                |||||||| ||   ||||||
                                CGTGTCTT AT   GGTGAG
                                   _ CGG
GAM483  MGC26684  3'  GACTTATCCTGTGCTT      58613        A     G
                                AAGCACAG GATAAG TC
                                |||||||| |||||| ||
                                TTCGTGTC CTATTC AG
                                   _     _
GAM483  MGC5242   3'  GGGGCTCTCTGTGCT       44054         TAAG   G
                                AGCACAGAGA    GTC CT
                                ||||||||||    ||| ||
                                TCGTGTCTCT    CGG GG
                                   _____   _
GAM483  MLZE      5'  AGGGCCCTCCTGTGCTT     49446        A  TAA    G
                                AAGCACAG GA   GGTC CT
                                |||||||| ||   |||| ||
                                TTCGTGTC CT   CCGG GA
                                   _ C__    _
GAM483  moblak    3'  GAGCAGGGACCATCTCTGT   56401        AA   ___
                                ACAGAGAT  GGTC   GCTC
                                ||||||||  ||||   ||||
                                TGTCTCTA  CCAG   CGAG
                                   __    GGA
GAM483  OS4       3'  GTTCCCATCTCTGTGTT     20394         AA  TC
                                AGCACAGAGAT  GG  GC
                                ||||||||||  ||  ||
                                TTGTGTCTCTA  CC  TG
                                   __ CT
GAM483  PIP3-E    3'  AGGGCCCTCTCTGTGCTT    67345         TAA   G
                                AAGCACAGAGA   GGTC CT
                                ||||||||||   |||| ||
                                TTCGTGTCTCT   CCGG GA
                                   C__    _
GAM483  PIP5K2B   3'  AGCACTGTCTCTGTGC      14526         AA   C
                                GCACAGAGAT  GGT GCT
                                |||||||||  ||| |||
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                                CGTGTCTCTG  TCA CGA
                                      __  _
GAM483  PIP5K2B  3'  AGCACTGTCTCTGTGC     14527        AA  C
                                GCACAGAGAT  GGT GCT
                                ||||||||||  ||| |||
                                CGTGTCTCTG  TCA CGA
                                      __  _
GAM483  PRO1386  5'  GAGTCTATTCTCTGTGCT   49217        TAA  TC
                                AGCACAGAGA  GG  GCTC
                                ||||||||||  ||  ||||
                                TCGTGTCTCT  TC  TGAG
                                     TA_  __
GAM483  PSKH1    3'  GCCCTTTCTCTGTGC      68799        T   TC
                                GCACAGAGA AAGG  GC
                                ||||||||| ||||  ||
                                CGTGTCTCT TTCC  CG
                                      _   __
GAM483  TBX19    3'  GGCAGGCATCTCTGTTCT   18922    C      AAG  _
                                AG ACAGAGAT  GTC GCT
                                || ||||||||  ||| |||
                                TC TGTCTCTA  CGG CGG
                                 T      ___  A
GAM483  WNT8A    3'  ACTTTCCCATCTTTGTGC   55255         ___
                                GCACAGAGAT  AAGGT
                                ||||||||||  |||||
                                CGTGTTTCTA  TTTCA
                                     CCC
GAM483  LOC115574 3'  GACTCCCGTCTCTGTGCTT   73853         AA_
                                AAGCACAGAGAT  GGTC
                                ||||||||||||  ||||
                                TTCGTGTCTCTG  TCAG
                                      CCC
GAM483  LOC116236 3'  GAGCTCCAGCTCTGTGCT   74245        ATAA  TC
                                AGCACAGAG   GG  GCTC
                                |||||||||   ||  ||||
                                TCGTGTCTC   CC  CGAG
                                     GA__  T_
GAM483  LOC118430 5'  AGCATTTTTGTCTGTGCT   55201       GAT   C
                                AGCACAGA  AAGGT GCT
                                ||||||||  ||||| |||
                                TCGTGTCT  TTTTA CGA
                                    GT_   _
GAM483  LOC121601 5'  GACTTTATCCCTCGCTT    74560     AC  A
                                AAGC  AG GATAAGGTC
                                ||||  || |||||||||
                                TTCG  TC CTATTTCAG
                                  C_  C
GAM483  LOC126074 3'  GACTACCTCTCTGTGCTT   74904         TAA
                                AAGCACAGAGA  GGTC
                                ||||||||||  ||||
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                                TTCGTGTCTCT   TCAG
                                      CCA
GAM483   LOC127937 5'  GAGCAGGCGTGTGATCTCTGT  75191        AAG__  _
                                ACAGAGAT    GTC GCTC
                                ||||||||    ||| ||||
                                TGTCTCTA    CGG CGAG
                                    GTGTG   A
GAM483   LOC144321 3'  GTTTCCATCTCTGTGTTT    83991          AA  TC
                                AAGCACAGAGAT  GG  GC
                                ||||||||||||  ||  ||
                                TTTGTGTCTCTA  CC  TG
                                      __  TT
GAM483   LOC145609 5'  AGTCCCTCTTCCTCTGTGC   84360        _ TA   TC
                                GCACAGAG A  AGG  GCT
                                |||||||| |  |||  |||
                                CGTGTCTC T  TCC  TGA
                                    C TC   C_
GAM483   LOC145623 5'  GGCTTCTCATCCACTGTGCTT  84393        A_   A   TC
                                AAGCACAG  GAT AGG  GCT
                                ||||||||  ||| |||  |||
                                TTCGTGTC  CTA TCT  CGG
                                    AC   C   T_
GAM483   LOC146433 5'  GAGTGACCACCTCTGCTGC   78437     _    ATAA
                                GCA CAGAG    GGTCGCTC
                                ||| |||||    ||||||||
                                CGT GTCTC    CCAGTGAG
                                  C    CA__
GAM483   LOC150819 5'  GCTCTTTCTCTGTGC       86310         T    TC
                                GCACAGAGA AAGG  GC
                                ||||||||| ||||  ||
                                CGTGTCTCT TTCT  CG
                                      _   __
GAM483   LOC152245 3'  AGCACTAATTCCTGTGCTT    86775        A  TAA   C
                                AAGCACAG GA   GGT GCT
                                |||||||| ||   ||| |||
                                TTCGTGTC CT   TCA CGA
                                    _  TAA   _
GAM483   LOC152283 5'  GAGCGACCTCCTCCTGC     86870     CA   ATA
                                GCA  GAG   AGGTCGCTC
                                |||  |||   |||||||||
                                CGT  CTC   TCCAGCGAG
                                  C_   C__
GAM483   LOC154222 3'  GAGATGGGTCATCTCTGTTCTT 87391     C       AA GT G__
                                AAG ACAGAGAT  G  C   CTC
                                ||| ||||||||  |  |   |||
                                TTC TGTCTCTA  C  G   GAG
                                  T       __ TG GTA
GAM483   LOC157556 3'  GAACGAAATTGGATCTTGTGCT 87781        _ GA   GG   C
           T                     AAGCACA GA  TAA  TCG TC
                                ||||||| ||  |||  ||| ||
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                                TTCGTGT CT  GTT  AGC AG
                                    T  AG   AA   A
GAM483   LOC199675 3'  GACATTTATCTCTGCACT    89639    CA        _
                                AG  CAGAGATAAG GTC
                                ||  |||||||||| |||
                                TC  GTCTCTATTT CAG
                                 AC         A
GAM483   LOC200316 3'  GATCTGCCCATCTCTGTCT    90184    C       A___
                                AG ACAGAGAT    AGGTC
                                || ||||||||    |||||
                                TC TGTCTCTA    TCTAG
                                 _       CCCG
GAM483   LOC200933 3'  GAGCGAAATCTTTGTACTT    91793     C       AAGG
                                AAG ACAGAGAT    TCGCTC
                                ||| ||||||||    ||||||
                                TTC TGTTTCTA    AGCGAG
                                  A       A___
GAM483   LOC219843 3'  GAGCAAATAATTCTCTGTGTTT 93137           TAAGGTC
                                AAGCACAGAGA       GCTC
                                ||||||||||       ||||
                                TTTGTGTCTCT       CGAG
                                      TAATAAA
GAM483   LOC219920 5'  GGCAGGCCCCTCTGTGC     94957         ATAA   _
                                GCACAGAG    GGTC GCT
                                ||||||||    |||| |||
                                CGTGTCTC    CCGG CGG
                                     C___    A
GAM483   LOC221405 5'  AGCCGCTTCCTCTCTGTGCTT  95505           TA   C
                                AAGCACAGAGA  AGGT GCT
                                ||||||||||  |||| |||
                                TTCGTGTCTCT  TTCG CGA
                                      CC    C
GAM483   LOC256997 5'  GAGCGACCTTGGGTGT      97079      AGAGA
                                GCAC     TAAGGTCGCTC
                                ||||     ||||||||||
                                TGTG     GTTCCAGCGAG
                                  G____
GAM483   LOC257449 3'  AGCAGGCTCCTGTGCTT     63371         A  TAAG   _
                                AAGCACAG GA    GTC GCT
                                |||||||| ||    ||| |||
                                TTCGTGTC CT    CGG CGA
                                    _ _____   A
GAM483   LOC51177  3'  GACTCTTATCTCCGTGTT    33245       A       _
                                AGCAC GAGATAAG GTC
                                ||||| |||||||| |||
                                TTGTG CTCTATTC CAG
                                  C       T
GAM483   LOC51580  3'  GGTACCATCTGTGCTT      32430          GATAA   C
                                AAGCACAGA     GGT GCT
                                |||||||||     ||| |||
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                                TTCGTGTCT    CCA TGG
                                     A____  _
GAM483  LOC90362  3'  GAGCGTGGGTCTCTGTGCTT  63113          AAGGT
                                AAGCACAGAGAT    CGCTC
                                ||||||||||||    |||||
                                TTCGTGTCTCTG    GCGAG
                                      GGT__
GAM484  GNAI3    3'  GAATTGGAAGAACTACTAAAGT 22443     GCG  C
           G                     TACT   AG AGTTCTTCCAATTC
                                ||||   || ||||||||||||||
                                GTGA   TC TCAAGAAGGTTAAG
                                  AA_  A
GAM484  NCOA6    5'  AATTGGAAGATCTGTCAACAG  26818    CGA    T
                                CTG   GCAG TCTTCCAATT
                                |||   |||| ||||||||||
                                GAC   TGTC AGAAGGTTAA
                                  AAC    T
GAM484  PCDH7    5'  GAATTGGACTCAACTCGAGTA  51620     G    CAGTTCT
                                TACT CGAG      TCCAATTC
                                |||| ||||      ||||||||
                                ATGA GCTC      AGGTTAAG
                                  _    AACTC__
GAM484  SHOX2    3'  TGTCTGGACTGCTGACAGTA   13127      CG       TTC
                                TACTG  AGCAGTTC   CA
                                |||||  ||||||||   ||
                                ATGAC  TCGTCAGG   GT
                                   AG       TCT
GAM484  SUV39H2  3'  GAATTGGAAATCTGTGTCGAGT 45456     G  _    TTC
           A                     TACT CGA GCAG   TTCCAATTC
                                |||| ||| ||||   |||||||||
                                ATGA GCT TGTC   AAGGTTAAG
                                  _  G   TA_
GAM484  FLJ20896 3'  GAACTGTACTACTCGCAGTG   45124        _____
                                TACTGCGAG    CAGTTC
                                |||||||||    ||||||
                                GTGACGCTC    GTCAAG
                                      ATCAT
GAM484  KIAA1724 3'  AATTGAGACTGCTCACA     67603    C      T  TC
                                TG GAGCAGT CT  CAATT
                                || ||||||| ||  |||||
                                AC CTCGTCA GA  GTTAA
                                 A     _ __
GAM484  KIAA1911 3'  AATTGGAAACAATGCAGTA   73886       AGCA   CT
                                TACTGCG   GTT  TCCAATT
                                |||||||   |||  |||||||
                                ATGACGT   CAA  AGGTTAA
                                    AA__   __
GAM484  LOC126302 3'  AAGAACTACTTCACAGTA    74981      C  _ C
                                TACTG GA G AGTTCTT
                                ||||| || | |||||||
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                                ATGAC CT C TCAAGAA
                                   A  T A
GAM484  LOC254808 3'  GAATTAAAAAAACTGTTCCAGT 98807      C       C  CC
                                ACTG GAGCAGTT TT  AATTC
                                |||| |||||||| ||  |||||
                                TGAC CTTGTCAA AA  TTAAG
                                  _       A  AA
GAM485  GPD1      3'  TCATGCCACCACATTTG     60398       C       C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A       _
GAM485  IL5RA     5'  TCGCATGGCCACCGCATTT    6906           AT__
                                AAATGCGGTGGC    CGA
                                ||||||||||||    |||
                                TTTACGCCACCG    GCT
                                      GTAC
GAM485  MYO1C     3'  TGCCGATGCCAAATATTTG    61873       CGG       A
                                TAAATG   TGGCATCG CA
                                ||||||   |||||||| ||
                                GTTTAT   ACCGTAGC GT
                                   AA_       C
GAM485  C6orf37   3'  TGTCACACTGCATTTA      68097          GCATC
                                TAAATGCGGTG     GACA
                                ||||||||||     ||||
                                ATTTACGTCAC     CTGT
                                      A_____
GAM485  DNAJC6    3'  TTGCAGAACCACCGCATT     29498         CA  GA
                                AATGCGGTGG  TC  CAA
                                ||||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                      A_  AC
GAM485  FLJ11210  3'  GTCGATGTGCATGCTTTTA    60319      T   GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM485  FLJ12476  3'  TCGATCTTCTGCATTTA     43270         T  C
                                TAAATGCGG GG ATCGA
                                ||||||||| || |||||
                                ATTTACGTC TC TAGCT
                                      T  _
GAM485  KIAA1034  3'  TCGATGGCATCCGCATTTG    63134         _  G
                                TAAATGCGG TG CATCGA
                                ||||||||| || ||||||
                                GTTTACGCC AC GTAGCT
                                      T  G
GAM485  KIAA1987  3'  TCATGTAACTGCATTTA     89391          G   C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
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                                ATTTACGTCA TGTA CT
                                     A   _
GAM485  MGC16063  3'  TGTCCTGGCCACTGCATT    54929          ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                     GTC
GAM485  LOC147949 3'  TGTCAGATGTCCACATTGCA   79279     __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T    A
GAM485  LOC150577 3'  GTCCTCACCGCATTTG      86258          CATC
                                TAAATGCGGTGG    GAC
                                ||||||||||||    |||
                                GTTTACGCCACT    CTG
                                     C___
GAM485  LOC158219 3'  TGTGTGTCACCACATTT     82694      C       CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                   A       __
GAM485  LOC202020 3'  TGTCTCACCACATTTA      90605       C    CATC
                                TAAATG GGTGG    GACA
                                |||||| |||||    ||||
                                ATTTAC CCACT    CTGT
                                   A    _____
GAM485  LOC90826  5'  TGTCGATGCAGGTTTATTTG  64788       CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                    TTGGA
GAM485  LOC93587  3'  TTGTCTTTACCTGCATTTA   73042       _    CATC
                                TAAATGC GGTGG    GACAA
                                ||||||| |||||    |||||
                                ATTTACG CCATT    CTGTT
                                     T    T___
GAM486  ADAM12    3'  GGCAGCATCCCCTTGAAC    14424         C   GAAA
                                GTTCAAGGG ATG    GTC
                                ||||||||| |||    |||
                                CAAGTTCCC TAC    CGG
                                     C   GA__
GAM486  CCND2     3'  GTGACTGACCCTTGAGC     10053         CATGGAA
                                GTTCAAGGG      AGTCAC
                                |||||||||      ||||||
                                CGAGTTCCC      TCAGTG
                                     AG_____
GAM486  FGFR1     3'  GACCTGTCCATGCCCCTGGAC  43886       A       AA_
                                GTTCA GGGCATGGA   GTC
                                ||||| |||||||||   |||
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                                CAGGT CCCGTACCT   CAG
                                   C        GTC
GAM486  GRINL1A  3'  GGTGACTTTCATGTGCTTGAA  70064       G    G
                                TTCAAG GCATG AAAGTCACC
                                |||||| ||||| |||||||||
                                AAGTTC TGTAC TTTCAGTGG
                                   G    _
GAM486  IL10     3'  GATATCATGCCCCTGTAC    6926     T  A      AAA
                                GT CA GGGCATGG   GTC
                                || || ||||||||   |||
                                CA GT CCCGTACT   TAG
                                 T  C       A__
GAM486  NOTCH2   3'  GGTGACTCTCTGCCCTTGGAC  44578          T   AA
                                GTTCAAGGGCA GGA  GTCACC
                                |||||||||||| |||  ||||||
                                CAGGTTCCCGT TCT  CAGTGG
                                      C  __
GAM486  Nrap     3'  TGACCTCCACCCTCCTTGGAC  58323        _ CA    AA
                                GTTCAAGG G  TGGA  GTCA
                                |||||||| |  ||||  ||||
                                CAGGTTCC C  ACCT  CAGT
                                     T CC    C_
GAM486  Nrap     3'  TGACCTCCACCCTCCTTGGAC  43624        _ CA    AA
                                GTTCAAGG G  TGGA  GTCA
                                |||||||| |  ||||  ||||
                                CAGGTTCC C  ACCT  CAGT
                                     T CC    C_
GAM486  PITX2    3'  GGCAACTCCGCCCTTGAA    6157          AT   AA_
                                TTCAAGGGC  GGA   GTC
                                |||||||||  |||   |||
                                AAGTTCCCG  CCT   CGG
                                     __   CAA
GAM486  RAB36    3'  GGTAACTCACTCTGCAGCCCTT 18174          AT_   A__   C
           GAAC                    GTTCAAGGGC   GGA   AGT ACC
                                |||||||||   |||   ||| |||
                                CAAGTTCCCG   TCT   TCA TGG
                                      ACG   CAC   A
GAM486  SCD      3'  ACTCTCTTTCCTTGAGC     18588         CAT   A
                                GTTCAAGGG   GGA AGT
                                |||||||||   ||| |||
                                CGAGTTCCT   TCT TCA
                                     T__   C
GAM486  AAMP     3'  TGACTTTCCAGCCTCTTCAAC  8437      C   _   A
                                GTT AAG GGC TGGAAAGTCA
                                ||| ||| ||| ||||||||||
                                CAA TTC CCG ACCTTTCAGT
                                  C   T   _
GAM486  dA141H5.1 3'  GTGTGTCAGCCCTTGAAC    59782          A   AAAGT
                                GTTCAAGGGC TGG     CAC
                                |||||||||| |||     |||
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                                CAAGTTCCCG ACT    GTG
                                      _  GT___
GAM486  DKFZp434A2417 3'  GATTTACCCTGCCCTTGAAC  66680         T  A
                                GTTCAAGGGCA GG AAGTC
                                |||||||||||  ||  |||||
                                CAAGTTCCCGT CC TTTAG
                                     C  A
GAM486  EPB41L1  3'  TGACTCTCCTTTGAA      71118        CAT   AA
                                TTCAAGGG   GGA  GTCA
                                ||||||||   |||  ||||
                                AAGTTTCC   TCT  CAGT
                                     ___   __
GAM486  FER1L4   3'  GTGACTCTCGCTGACCTTGGAC 48134       G  TG  A
                                GTTCAAGG CA  GA AGTCAC
                                ||||||||  ||  ||  ||||||
                                CAGGTTCC GT  CT TCAGTG
                                     A  CG  C
GAM486  FLJ21324  3'  GGTGACCTTCTGGATGCCTTTA 92858     C      __   A
          AC                    GTT AAGGGCAT  GGAA GTCACC
                                |||  ||||||||  ||||  ||||||
                                CAA TTTCCGTA  TCTT CAGTGG
                                  _      GG   C
GAM486  FLJ23168  3'  GGCAATATGCCCTTGAGC    47505          GAAA
                                GTTCAAGGGCATG   GTC
                                ||||||||||||   |||
                                CGAGTTCCCGTAT   CGG
                                       AA__
GAM486  KIAA0794  3'  GGTGACTTTCATTGTCCT    81234       TG
                                AGGGCA  GAAAGTCACC
                                ||||||  ||||||||||
                                TCCTGT  CTTTCAGTGG
                                   TA
GAM486  KIAA1023  3'  GTGAGGACCATGCCCTTGA   34683          AAAG
                                TCAAGGGCATGG   TCAC
                                ||||||||||||   ||||
                                AGTTCCCGTACC   AGTG
                                       AGG_
GAM486  SLC26A10  3'  GATGAGGACCATGACCCTTGAA 56846         _    AAA__
          C                     GTTCAAGGG CATGG    GTC
                                |||||||| |||||    |||
                                CAAGTTCCC GTACC    TAG
                                     A    AGGAG
GAM486  LOC120939 5'  GGTGACTTTCACCCTGCAAC  76767    CA   CATG
                                GTT  AGGG   GAAAGTCACC
                                |||  ||||   ||||||||||
                                CAA  TCCC   CTTTCAGTGG
                                  CG   A___
GAM486  LOC133584 3'  TGACTGTGTGACCTTGAAC   75599        G  GGAA
                                GTTCAAGG CAT   AGTCA
                                ||||||||  |||   |||||
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                                CAAGTTCC GTG    TCAGT
                                    A   TG__
GAM486   LOC136345 3'  GGTGACTGGGAGGCCTTGAAC  76716        G ATGGAA
                                GTTCAAGG C     AGTCACC
                                |||||||| |     |||||||
                                CAAGTTCC G     TCAGTGG
                                    _ GAGGG_
GAM486   LOC145761 5'  GACTCCATCTTGAAC       84479        GGC    AA
                                GTTCAAG   ATGGA  GTC
                                |||||||   |||||  |||
                                CAAGTTC   TACCT  CAG
                                   ___    __
GAM486   LOC146337 5'  GGCAACTCTAGCCTTTGAAC   84644         A    AA_
                                GTTCAAGGGC TGGA   GTC
                                |||||||||| ||||   |||
                                CAAGTTTCCG ATCT   CGG
                                    _   CAA
GAM486   LOC148930 3'  ACTTCCTCTCTTTGAAC     79837         CAT    A
                                GTTCAAGGG   GGAA GT
                                |||||||||   |||| ||
                                CAAGTTTCT   CCTT CA
                                    CT_   _
GAM486   LOC149684 5'  GGCTCCTGCCCTTGAAC     85767          T   AA
                                GTTCAAGGGCA GGA  GTC
                                |||||||||| |||  |||
                                CAAGTTCCCGT CCT  CGG
                                   _  __
GAM486   LOC151057 3'  GTGACCCTACCCTTGAGC    86397         CAT  AAA
                                GTTCAAGGG   GG   GTCAC
                                |||||||||   ||   |||||
                                CGAGTTCCC   CC   CAGTG
                                    AT_ ___
GAM486   LOC152018 3'  GACCTCCACCCCCTTGAAC    86729         CA    AA
                                GTTCAAGGG  TGGA  GTC
                                |||||||||  ||||  |||
                                CAAGTTCCC  ACCT  CAG
                                    CC    C_
GAM486   LOC152982 3'  TGACTTTCATGTGCTTGAA    81638       G    G
                                TTCAAG GCATG AAAGTCA
                                |||||| ||||| |||||||
                                AAGTTC TGTAC TTTCAGT
                                   G    _
GAM486   LOC155032 5'  GGTGACTGGGAGGCCTTGAAC  87597        G ATGGAA
                                GTTCAAGG C     AGTCACC
                                |||||||| |     |||||||
                                CAAGTTCC G     TCAGTGG
                                    _ GAGGG_
GAM486   LOC155179 3'  GTGAGGACCATGCCCTTGA    82233           AAAG
                                TCAAGGGCATGG    TCAC
                                ||||||||||||    ||||
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                                AGTTCCCGTACC    AGTG
                                      AGG_
GAM486  LOC155435 3'  GGTGACTTTGGTAGCCCTTGAG 82271          ATGG
          C                    GTTCAAGGGC    AAAGTCACC
                               ||||||||||    |||||||||
                               CGAGTTCCCG    TTTCAGTGG
                                     ATGG
GAM486  LOC170395 3'  GATGCTTCCTGCCCTTGAAC   76871          T    A_
                               GTTCAAGGGCA GGAA  GTC
                               ||||||||||| ||||  |||
                               CAAGTTCCCGT CCTT  TAG
                                     _   CG
GAM486  LOC253336 3'  GTAACTTTCTTCATCCCTTGAA 99182          CAT_      C
          T                    GTTCAAGGG    GGAAAGT AC
                               |||||||||    ||||||| ||
                               TAAGTTCCC    TCTTTCA TG
                                     TACT      A
GAM486  LOC253782 3'  TGACTTTCCTGTTACTAAAC   97405     CAAG    T
                               GTT    GGCA GGAAAGTCA
                               |||    |||| |||||||||
                               CAA    TTGT CCTTTCAGT
                                 ATCA   _
GAM486  LOC51279  3'  ACTTTCGCCTTGAAT       33748         G ATG
                               GTTCAAGG C   GAAAGT
                               |||||||| |   ||||||
                               TAAGTTCC G   CTTTCA
                                     _ ___
GAM486  LOC80298  3'  GTAACTTTTACCTTGAAC     48066         GCATG     C
                               GTTCAAGG     GAAAGT AC
                               ||||||||     |||||| ||
                               CAAGTTCC     TTTTCA TG
                                    A____     A
GAM487  BECN1     5'  TGGAGGCCTCGCTCCGGGGCCG 15005     A  A   ACC  _
          A                    TC GC CCG   GG GAGGCCTCCA
                               || || |||   || ||||||||||
                               AG CG GGC   TC CTCCGGAGGT
                                C  G   C__  G
GAM487  CDC25B    3'  GGAGGCCTCAGGTGCTG      41855         GACCGG
                               CAGCACC      GAGGCCTCC
                               |||||||      |||||||||
                               GTCGTGG      CTCCGGAGG
                                   A_____
GAM487  CSNK1G2   3'  TGGAGGCCCCCCCGGCCTGG    8992      A_    A
                               CCG  CCGGG GGCCTCCA
                               |||  ||||| ||||||||
                               GGT  GGCCC CCGGAGGT
                                 CC    C
GAM487  DNAJB1    3'  TGGAGGCCAGTCCAGTGCT    21569       C_   CGGGA
                               AGCAC  GAC    GGCCTCCA
                               |||||  |||    ||||||||
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                                TCGTG CTG    CCGGAGGT
                                  AC  A____
GAM487  GPR44    3'  TGAAGGCCTGGCCCACAGCAGG 17703        GACC__  __     C
            TGCTGA                 TCAGCACC     GGG AGGCCT CA
                                |||||||     |||  |||||| ||
                                AGTCGTGG     CCC  TCCGGA GT
                                    ACGACA   GG     A
GAM487  HEXA     3'  TGGAGAGAAAGGGGCCGGTGCT 6719          A  GGGAGGC
            GG                   TCAGCACCG CC      CTCCA
                                |||||||||  ||      |||||
                                GGTCGTGGC GG      GAGGT
                                    C  GGAAAGA
GAM487  IL1F9    5'  AGACCCTTTCTTGCCAGGTGCT 39511        GAC    ___  C
            GA                   TCAGCACC   CGGGA   GG CT
                                |||||||   |||||   || ||
                                AGTCGTGG   GTTCT   CC GA
                                    ACC    TTC  A
GAM487  POLR2E   3'  GGAGGCCTCCTCTAGGTC    60599     ___
                                GACC   GGGAGGCCTCC
                                ||||   ||||||||||
                                CTGG   TCCTCCGGAGG
                                  ATC
GAM487  TNFSF9   3'  GGAGACCCCTGGTGCTGG    15098        GACC   A  C
                                TCAGCACC    GGG GG CTCC
                                |||||||    ||| || ||||
                                GGTCGTGG    TCC CC GAGG
                                    _____   _  A
GAM487  XT3      3'  GAGGCCTCCATAAAGGGTCGGT 39914          G_________   GGCC
            GCTGA                TCAGCACCGACC       GGA   TC
                                ||||||||||||       |||   ||
                                AGTCGTGGCTGG       CCT   AG
                                      GAAAT___A   CCGG
GAM487  CBCIP2   3'  AGGCCTCCCAGCCGACACTGG  52648     CAC  ACC
                                TCAG   CG   GGGAGGCCT
                                ||||   ||   |||||||||
                                GGTC   GC   CCCTCCGGA
                                  ACA  CGA
GAM487  COE2     3'  AGGCCTCCTCATGCTGG     64902       CCGACC
                                TCAGCA     GGGAGGCCT
                                ||||||     |||||||||
                                GGTCGT     TCCTCCGGA
                                   AC_____
GAM487  FLJ13441 3'  TGGAGGCCCTGCTGCAGGCT   43921     ACCGAC   G  _
                                AGC     CGG AGG CCTCCA
                                |||     ||| ||| ||||||
                                TCG     GTC TCC GGAGGT
                                  GAC___   G   C
GAM487  FLJ14326 3'  GCCTCCCAGCCTCTCGTGCTGA 50773        C_  CC__
                                TCAGCAC  GA   GGGAGGC
                                |||||||  ||   |||||||
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                                AGTCGTG CT   CCCTCCG
                                    CT CCGA
GAM487  FLJ22202 3' TGGAGGCCGGGAGGCCAATGCT 46500      ____ GA GGGA
           GG                    TCAGCA   CC CC   GGCCTCCA
                                ||||||   || ||   ||||||||
                                GGTCGT   GG GG   CCGGAGGT
                                   AACC AG ____
GAM487  KIAA0514 3' GAGGCCTCCTGTGTGC     28746     CGAC
                                GCAC   CGGGAGGCCTC
                                ||||   ||||||||||
                                CGTG   GTCCTCCGGAG
                                  T___
GAM487  KIAA0542 3' TGAAGGCCTCCCGGCAGCAGCT 66669     ACCGA        C
           G                     CAGC    CCGGGAGGCCT CA
                                ||||    |||||||||| ||
                                GTCG    GGCCCTCCGGA GT
                                  ACGAC        A
GAM487  MGC4737  5' TGGAGGCCCGGGCCACACTGA 49653     CACCGA   GAG
                                TCAG    CCGG  GCCTCCA
                                ||||    ||||  |||||||
                                AGTC    GGCC  CGGAGGT
                                  ACACCG  ___
GAM487  MMP28    3' GAGGGGGTCGATGCTGG     44444      C    GGGAGG
                                TCAGCA CGACC    CCTC
                                |||||| |||||    ||||
                                GGTCGT GCTGG    GGAG
                                   A   G_____
GAM487  SLC5A6   5' TGAAGGCCTCCCCCGTCGCCGC 41180    AC   C_      C
                                GC  CGAC  GGGAGGCCT CA
                                ||  ||||  ||||||||| ||
                                CG  GCTG  CCCTCCGGA GT
                                 CC   CC       A
GAM487  STAT5A   5' GGGATTTCCCGGCAACGCCGA  13443    A  ACCGA     _
                                TC GC    CCGGGAGG CCT
                                || ||    |||||||| |||
                                AG CG    GGCCCTTT GGG
                                 C  CAAC_      A
GAM487  VPS33B   3' TTTCCCGGCCAGTGTTGA    38525       CGA
                                TCAGCAC   CCGGGAGG
                                |||||||   ||||||||
                                AGTTGTG   GGCCCTTT
                                   ACC
GAM487  LOC123242 5' GAGGCCCAGCTGGTGCTGA   76117        ACCGGGA
                                TCAGCACCG      GGCCTC
                                |||||||||      ||||||
                                AGTCGTGGT      CCGGAG
                                     CGAC___
GAM487  LOC125988 5' GAGGCCTCTGCGGCGCCGC   74899    AC  A  _
                                GC  CG CCG GGAGGCCTC
                                ||  || ||| |||||||||
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                                CG  GC GGC TCTCCGGAG
                                 CC  _  G
GAM487  LOC143101 5'  GGAGGCCTCAGGCCTCGGTGT  83786       __  GG
                                GCACCGA  CC  GAGGCCTCC
                                |||||||  ||  |||||||||
                                TGTGGCT  GG  CTCCGGAGG
                                    CC  A_
GAM487  LOC143666 5'  GGCTCCCGGTAGATGCTGA   83886      CCG      G
                                TCAGCA   ACCGGGAG CC
                                ||||||   |||||||| ||
                                AGTCGT   TGGCCCTC GG
                                   AGA      _
GAM487  LOC146435 5'  GAGGCCTCAAGTTTCGGGCTGA 78452      A   CCGG_
                                TCAGC CCGA    GAGGCCTC
                                ||||| ||||    ||||||||
                                AGTCG GGCT    CTCCGGAG
                                  _   TTGAA
GAM487  LOC146445 3'  GGAGGCCTCCACGGAGC    84683    A  ACCG
                                GC CCG   GGAGGCCTCC
                                || |||   ||||||||||
                                CG GGC   CCTCCGGAGG
                                 A  A___
GAM487  LOC153205 3'  GAGGCCTCATGAGTGCT    87159      CGAC  G
                                AGCAC   CG GAGGCCTC
                                |||||   || ||||||||
                                TCGTG   GT CTCCGGAG
                                   A___  A
GAM487  LOC155060 5'  TGGAGGCCCCCCGAGCCAGGCT 87608      ACCGAC   A
          GA                     TCAGC     CGGG GGCCTCCA
                                |||||     |||| ||||||||
                                AGTCG     GCCC CCGGAGGT
                                   GACCGA   C
GAM487  LOC158055 3'  GAGGCCTCCACCCAGTGCTGG  82582       CGACCG
                                TCAGCAC     GGAGGCCTC
                                |||||||     |||||||||
                                GGTCGTG     CCTCCGGAG
                                    ACCCA_
GAM487  LOC253001 5'  GAGGCCCAGCTGGTGCTGA   97995        ACCGGGA
                                TCAGCACCG      GGCCTC
                                |||||||||      ||||||
                                AGTCGTGGT      CCGGAG
                                     CGAC___
GAM487  LOC255187 5'  AGGCCTCCCTTGGCTCTCTGA  98974     CA__   CC
                                TCAG   CCGA  GGGAGGCCT
                                ||||   ||||  |||||||||
                                AGTC   GGTT  CCCTCCGGA
                                  TCTC   __
GAM487  LOC93550  5'  GGCTTTCCCGACGGGTGCTGA  72978       GAC    _
                                TCAGCACC   CGGGAG GCC
                                ||||||||   |||||| |||
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                                AGTCGTGG  GCCCTT CGG
                                    GCA    T
GAM488  ELF3    3'  TGACCTTGACCTTGACCAA   16685     T   GAT  AAA
                                TTGGT CAAGG  GG  GTCA
                                ||||| |||||  ||  ||||
                                AACCA GTTCC  TC  CAGT
                                  _    AGT  ___
GAM488  JAK2    3'  TGACCTTCATTCTGAGACCAA  18318      CAA      AA
                                TTGGTT  GGGATGGA  GTCA
                                ||||||  ||||||||  ||||
                                AACCAG  TCTTACTT  CAGT
                                   AG_      C_
GAM488  SLC10A2  5'  ACTCTCTGTCTTGACCAA    6590      CAA      A
                                TTGGTT  GGGATGGA AGT
                                ||||||  |||||||| |||
                                AACCAG  TTCTGTCT TCA
                                  ___       C
GAM488  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA  37205      CAAGG  G
                                TTGGTT   GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___  A
GAM488  KIAA1958  5'  GTGACTTTGAACCCCAAACC  82788     CAA  ATGG
                                GGTT  GGG   AAAGTCAC
                                ||||  |||   ||||||||
                                CCAA  CCC   TTTCAGTG
                                  A__  CAAG
GAM488  MARCKS   3'  ACTTTCCACCCTGCCCA    11411    TTCA   A
                                TGG   AGGG TGGAAAGT
                                |||   |||| ||||||||
                                ACC   TCCC ACCTTTCA
                                 CG__   _
GAM488  TUB     5'  GTGGGACCATCCCTTAAACC  13898     C       AAAG
                                GGTT AAGGGATGG   TCAC
                                |||| |||||||||   ||||
                                CCAA TTCCCTACC   GGTG
                                  A       AG__
GAM488  LOC80298  3'  ACTTTTACCTTGAACCA    48062        GATG
                                TGGTTCAAGG   GAAAGT
                                ||||||||||   ||||||
                                ACCAAGTTCC   TTTTCA
                                     A___
GAM489  GPD1    3'  TCATGCCACCACATTTG    60398       C       C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A       _
GAM489  IL5RA   5'  TCGCATGGCCACCGCATTT   6906           AT__
                                AAATGCGGTGGC   CGA
                                ||||||||||||   |||
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                                TTTACGCCACCG   GCT
                                      GTAC
GAM489  MYO1C    3'  TGCCGATGCCAAATATTTG   61873      CGG      A
                                TAAATG  TGGCATCG CA
                                ||||||  |||||||| ||
                                GTTTAT  ACCGTAGC GT
                                   AA_      C
GAM489  C6orf37  3'  TGTCACACTGCATTTA     68097         GCATC
                                TAAATGCGGTG    GACA
                                ||||||||||    ||||
                                ATTTACGTCAC    CTGT
                                      A____
GAM489  DNAJC6   3'  TTGCAGAACCACCGCATT    29498        CA  GA
                                AATGCGGTGG  TC  CAA
                                |||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                      A_  AC
GAM489  FLJ11210 3'  GTCGATGTGCATGCTTTTA   60319     T  GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM489  FLJ12476 3'  TCGATCTTCTGCATTTA     43270        T  C
                                TAAATGCGG GG ATCGA
                                |||||||| || |||||
                                ATTTACGTC TC TAGCT
                                      T  _
GAM489  KIAA1034 3'  TCGATGGCATCCGCATTTG   63134        _  G
                                TAAATGCGG TG CATCGA
                                |||||||| || ||||||
                                GTTTACGCC AC GTAGCT
                                      T  G
GAM489  KIAA1987 3'  TCATGTAACTGCATTTA     89391        G   C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                      A   _
GAM489  MGC16063 3'  TGTCCTGGCCACTGCATT    54929         ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                      GTC
GAM489  LOC147949 3'  TGTCAGATGTCCACATTGCA  79279     __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM489  LOC150577 3'  GTCCTCACCGCATTTG     86258         CATC
                                TAAATGCGGTGG   GAC
                                ||||||||||||   |||
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                                GTTTACGCCACT   CTG
                                      C___
GAM489  LOC158219 3'  TGTGTGTCACCACATTT    82694      C      CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                   A      __
GAM489  LOC202020 3'  TGTCTCACCACATTTA     90605      C    CATC
                                TAAATG GGTGG   GACA
                                |||||| |||||   ||||
                                ATTTAC CCACT   CTGT
                                   A    ____
GAM489  LOC90826  5'  TGTCGATGCAGGTTTATTTG  64788      CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                   TTGGA
GAM489  LOC93587  3'  TTGTCTTTACCTGCATTTA   73042      _    CATC
                                TAAATGC GGTGG   GACAA
                                ||||||| |||||   |||||
                                ATTTACG CCATT   CTGTT
                                    T    T___
GAM490  ELF3      3'  TGACCTTGACCTTGACCAA   16685     T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                   _    AGT  ___
GAM490  JAK2      3'  TGACCTTCATTCTGAGACCAA 18318      CAA      AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_      C_
GAM490  SLC10A2   5'  ACTCTCTGTCTTGACCAA    6590      CAA      A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM490  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA 37205      CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM490  KIAA1958  5'  GTGACTTTGAACCCCAAACC  82788     CAA   ATGG
                                GGTT   GGG   AAAGTCAC
                                ||||   |||   ||||||||
                                CCAA   CCC   TTTCAGTG
                                  A__   CAAG
GAM490  MARCKS    3'  ACTTTCCACCCTGCCCA    11411     TTCA   A
                                TGG   AGGG TGGAAAGT
                                |||   |||| ||||||||
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                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM490  TUB      5'  GTGGGACCATCCCTTAAACC   13898      C        AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A        AG__
GAM490  LOC80298 3'  ACTTTTACCTTGAACCA     48062          GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                      A___
GAM491  CACNG1   3'  AGGGGCCCAACTTCCCCTG    7411           CAGACTAA
                                TAGGGGAAGT       TCCCT
                                ||||||||||       |||||
                                GTCCCCTTCA       GGGGA
                                      ACCC____
GAM491  CYP3A43  3'  AGTGGACCCTGACTTTCCCTA  55121            ACTAA  _
                                TAGGGGAAGTCAG     TCC CT
                                ||||||||||||     ||| ||
                                ATCCCTTTCAGTC     AGG GA
                                       CC___   T
GAM491  ITGB7    5'  CAGAGAGAAAGTCTGACTTGCC 7960       _        AA_  C
           CC                     GGGG AAGTCAGACT   TC CTG
                                |||| ||||||||||   || |||
                                CCCC TTCAGTCTGA   AG GAC
                                  G         AAG  A
GAM491  TGFA     3'  CAGAGAATTTTGTCTTCCCCTA 13703          T    CTAA  C
                                TAGGGGAAG CAGA    TC CTG
                                ||||||||| ||||    || |||
                                ATCCCCTTC GTTT    AG GAC
                                      T    TA__  A
GAM491  C5orf3   5'  AGGTGACCTGACTTCCCC     38590          ACTAA  _
                                GGGGAAGTCAG     TC CCT
                                ||||||||||     || |||
                                CCCCTTCAGTC     AG GGA
                                       C____  T
GAM491  DKFZP564O0423 3'  CAGGAACCAGCTCCCTACGCTT 93344         CA___  _  AATC
           CCCC                    GGGGAAGT     GA CT    CCTG
                                ||||||||     || ||    ||||
                                CCCCTTCG     CT GA    GGAC
                                     CATCC  C  CCAA
GAM491  FLJ13840 5'  GGACTATTGCTTCCCT      45700        T   AC  A
                                GGGGAAG CAG  TA TCC
                                ||||||| |||  || |||
                                TCCCTTC GTT  AT AGG
                                     _  ___  C
GAM491  FLJ14834 3'  AGGGCAGCTGATTCCCCTA    52721         G    A  AAT
                                TAGGGGAA TCAG CT   CCCT
                                |||||||| |||| ||   ||||
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                                ATCCCCTT AGTC GA   GGGA
                                    _   _ C__
GAM491  KIAA1958  5'  CAGAGACTCTTGTGACTTCTCC 82778          GACTAA  C
          TA                    TAGGGGAAGTCA     TC CTG
                                ||||||||||||     || |||
                                ATCCTCTTCAGT     AG GAC
                                     GTTCTC  A
GAM491  MGC14793  3'  CAGAAATTAAATGGCTCACCT  53043     GA    GAC    CC
                                GGG  AGTCA   TAAT  CTG
                                |||  |||||   ||||  |||
                                TCC  TCGGT   ATTA  GAC
                                  AC    AA_    AA
GAM491  PORIMIN   3'  CAGGGATTGTGGGACTTCCCC  54701         AG  T
                                GGGGAAGTC  AC AATCCCTG
                                |||||||||  || ||||||||
                                CCCCTTCAG  TG TTAGGGAC
                                     GG  _
GAM491  SIAT4A    5'  AGAGATTAATGACCCCTTA   13133       AA    GAC    C
                                TAGGGG  GTCA   TAATC CT
                                ||||||  ||||   ||||| ||
                                ATTCCC  CAGT   ATTAG GA
                                   __    A__    A
GAM491  ZWINT     3'  AGGCCTCTGACTTCCCT     23902           CTAATC
                                GGGGAAGTCAGA     CCT
                                ||||||||||||     |||
                                TCCCTTCAGTCT     GGA
                                     CC____
GAM491  LOC145082 5'  CAGGGACCACACCCTTCCTCTA 84183          TCAGACTAA
                                TAGGGGAAG        TCCCTG
                                |||||||||        ||||||
                                ATCTCCTTC        AGGGAC
                                     CCACACC__
GAM491  LOC158332 3'  AGGAATCAGTTTCTCCTA    82762        AGTCA    A  C
                                TAGGGGA    GACT AT CCT
                                |||||||    |||| || |||
                                ATCCTCT    TTGA TA GGA
                                   _____   C  A
GAM491  LOC221543 3'  CAGGGTCCCTGACTTCCC    95368          ACTAAT
                                GGGAAGTCAG     CCCTG
                                ||||||||||     |||||
                                CCCTTCAGTC     GGGAC
                                     CCT___
GAM491  LOC257596 3'  CAGGGTCCCTGACTTCCC    99771          ACTAAT
                                GGGAAGTCAG     CCCTG
                                ||||||||||     |||||
                                CCCTTCAGTC     GGGAC
                                     CCT___
GAM492  CARD15    3'  GGATGTACAAGGACAGCCCCTC 42472       AC   GCAC_
                                GAGGG  CTG    GTACATCC
                                |||||  |||    ||||||||
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                                CTCCC  GAC    CATGTAGG
                                   C_   AGGAA
GAM492  CDKN2B   3'  GGGACTGACGCCAGGTTCC   55312         AC  A  _
                                GGGACCTGGC  GT CA TCCC
                                ||||||||||  || || ||||
                                CCTTGGACCG  CA GT AGGG
                                      __  _  C
GAM492  CERD4    3'  GGATGACCAGGTCCCTGG    24880   G       CACGTA
                                C AGGGACCTGG     CATCC
                                | ||||||||||     |||||
                                G TCCCTGGACC     GTAGG
                                 G        A_____
GAM492  FANCC    3'  TGCAGAGCCAGGTCCCTC    71052          AC_
                                GAGGGACCTGGC   GTA
                                ||||||||||||   |||
                                CTCCCTGGACCG   CGT
                                       AGA
GAM492  GNA11    3'  GGGATGTACATCTCTCCCTC   10814      CCT  CAC
                                GAGGGA   GG   GTACATCCC
                                ||||||   ||   |||||||||
                                CTCCCT   CT   CATGTAGGG
                                   CT_  A__
GAM492  RPS6KA2  3'  GGAACACACGGGTCCTTC    41224         GCAC  ACA
                                GAGGGACCTG    GT   TCC
                                ||||||||||    ||   |||
                                CTTCCTGGGC    CA   AGG
                                      ACA_  ___
GAM492  TRRAP    3'  ATGTACGTTCCTTCG       14492        CCTGGC
                                CGAGGGA     ACGTACAT
                                |||||||     ||||||||
                                GCTTCCT     TGCATGTA
                                     _______
GAM492  APELIN   3'  GGGATGGGGACCAGGTCTC   34269         CACGTA
                                GGGACCTGG     CATCCC
                                |||||||||     ||||||
                                CTCTGGACC     GTAGGG
                                      AGGG__
GAM492  BIRC5    3'  GTCCGCCCAGGTCCCCG     8604     A       CA  T
                                CG GGGACCTGG  CG AC
                                || |||||||||  || ||
                                GC CCCTGGACC  GC TG
                                 _       C_  C
GAM492  CGI-01   3'  GTGTGTGCAAGCCCCTC     32507       AC  G
                                GAGGG  CT GCACGTAC
                                |||||  || ||||||||
                                CTCCC  GA CGTGTGTG
                                   C_  A
GAM492  DKFZP434K1772 5'  GGAGTGTGCGTCAGGCCCCCCG 68336    A   A   GC      TC
                                CG GGG CCTG  ACGTACA  CC
                                || ||| ||||  |||||||  ||
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                                GC CCC GGAC  TGCGTGT  GG
                                 C  C   __     GA
GAM492  DKFZp547I014 5'  GGATGTTTACCTAGGTCCCTC  39945          CACGT
                                GAGGGACCTGG    ACATCC
                                ||||||||||    ||||||
                                CTCCCTGGATC    TGTAGG
                                      CATT_
GAM492  ELF4     3'  GGGTGTACCAATGCCCCTC   9234       ACCTG  C__
                                GAGGG    GCA  GTACATCC
                                |||||    |||  ||||||||
                                CTCCC    CGT  CATGTGGG
                                   _____  AAC
GAM492  FLJ11117  3'  GGACATGGACACTTCCAGGTCC 37636          CAC_  A  __
            CTC                   GAGGGACCTGG   GT CA  TCC
                                ||||||||||   || ||  |||
                                CTCCCTGGACC   CA GT  AGG
                                      TTCA  G  AC
GAM492  KIAA0323  3'  GGATTCCTGCCAGGTCCCCG  63949    A        CGTAC
                                CG GGGACCTGGCA    ATCC
                                || ||||||||||    ||||
                                GC CCCTGGACCGT    TAGG
                                 _        CCT__
GAM492  KIAA0924  5'  GATGCTCCCAAGTCCCTTG   30365        C   CACGTA
                                CGAGGGAC TGG     CATC
                                |||||||| |||     ||||
                                GTTCCCTG ACC     GTAG
                                    A  CTC___
GAM492  KIAA1344  5'  GGAACGGCCCAGGTCCCCG   72868    A       CA   ACA
                                CG GGGACCTGG  CGT   TCC
                                || |||||||||  |||   |||
                                GC CCCTGGACC  GCA   AGG
                                 _       CG  ____
GAM492  KIAA1622  3'  GGAATGTACGTTGTGGCCCTC  40910      A  TG  _     _
                                GAGGG CC  GCA CGTACAT CC
                                ||||| ||  ||| ||||||| ||
                                CTCCC GG  TGT GCATGTA GG
                                   _ __   T      A
GAM492  KIAA1924  3'  GGGCGTCTGTGCCAGGCCTCCC 74055      __       T  AT
                                GGGA  CCTGGCACG AC  CC
                                ||||  |||||||||| ||  ||
                                CCCT  GGACCGTGT TG  GG
                                   CC        C  CG
GAM492  XYLT1    5'  GGATGTGTCCAGACCGCCTC   78415     GAC_   C  GT
                                GAGG   CTGG AC  ACATCC
                                ||||   |||| ||  ||||||
                                CTCC   GACC TG  TGTAGG
                                   GCCA   _ __
GAM492  ZNF37A   5'  GATGTACGGATGCCCCC     65413     ACCT   __
                                GGG   GGCA  CGTACATC
                                |||   ||||  ||||||||
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                                CCC   CCGT  GCATGTAG
                                  _____   AG
GAM492  LOC125456 5'  GGAAGTGCTGCCAGGTTCCTC  76168          C   A
                                GAGGGACCTGGCA GTAC TCC
                                |||||||||||| |||| |||
                                CTCCTTGGACCGT CGTG AGG
                                       _   A
GAM492  LOC152580 3'  GATGCACACCAGGTCCC     86985        CAC  A
                                GGGACCTGG   GT CATC
                                |||||||||   || ||||
                                CCCTGGACC   CA GTAG
                                     A__  C
GAM492  LOC219818 3'  GGATACACAGCCTGCAGGTCCC 92538       ___   AC  AC
                                GGGACCT   GGC  GT  ATCC
                                |||||||   |||  ||  ||||
                                CCCTGGA   CCG  CA  TAGG
                                    CGT   A_  CA
GAM492  LOC51035  5'  GTCACACACCAGGTCCCCG   32393    A       CAC  _
                                CG GGGACCTGG   GT AC
                                || |||||||||   || ||
                                GC CCCTGGACC   CA TG
                                 _       ACA  C
GAM493  COL6A3    3'  TCCAAATTCCCTCTGG      16468     T  TC
                                CCA GG  GGAATTTGGA
                                ||| ||  ||||||||||
                                GGT TC  CCTTAAACCT
                                  C  __
GAM493  COL6A3    3'  TCCAAATTCCCTCTGG      55145     T  TC
                                CCA GG  GGAATTTGGA
                                ||| ||  ||||||||||
                                GGT TC  CCTTAAACCT
                                  C  __
GAM493  CPSF6     3'  CCAAATTCTAGGACAATG    23789     G  __
                                CAT GTC  GGAATTTGG
                                ||| |||  |||||||||
                                GTA CAG  TCTTAAACC
                                  A   GA
GAM493  GRIN2A    3'  TCCAAACAGCCATGGTG     7724          CGGAA
                                TACCATGGT    TTTGGA
                                |||||||||    ||||||
                                GTGGTACCG    AAACCT
                                     AC___
GAM493  GRIN2A    3'  TCCAAATTCCATTAAGGT    7725      A   C
                                ACC TGGT GGAATTTGGA
                                ||| |||| ||||||||||
                                TGG ATTA CCTTAAACCT
                                  A   _
GAM493  MKI67     3'  CCATTTCCACCATGGTA     11592         C   TT
                                TACCATGGT GGAA  TGG
                                ||||||||| ||||  |||
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                                ATGGTACCA CCTT  ACC
                                      _   T_
GAM493  NCALD    3'  TCCAAATTTGTATGGTA     50193       GTCG
                                TACCATG   GAATTTGGA
                                |||||||   |||||||||
                                ATGGTAT   TTTAAACCT
                                   G___
GAM493  ARHU     3'  CAGGTCAACCATGGTA      41359        CG  A
                                TACCATGGT  GA TTTG
                                |||||||||  || ||||
                                ATGGTACCA  CT GGAC
                                     A_  _
GAM493  C11orf24  3'  TCCAAATTCTTTTGGTG     42534      TGGTC
                                TACCA    GGAATTTGGA
                                |||||    ||||||||||
                                GTGGT    TCTTAAACCT
                                  TT___
GAM493  DKFZP564O0463 3'  TCCAAATTCAAGATGGTG    27126     G   G_
                                CAT GTC  GAATTTGGA
                                ||| |||  |||||||||
                                GTG TAG  CTTAAACCT
                                  G   AA
GAM493  FHX      3'  CCAAACTCTGCTTCTATGGTA  37921        T__   A
                                TACCATGG   CGGA TTTGG
                                ||||||||   |||| |||||
                                ATGGTATC   GTCT AAACC
                                     TTC   C
GAM493  FLJ10803  3'  TCCAAATTCCTATTTGGTG   37208      T   C
                                TACCA GGT GGAATTTGGA
                                ||||| ||| ||||||||||
                                GTGGT TTA CCTTAAACCT
                                   _  T
GAM493  FLJ12888  5'  TCCAAATTCTGTCATCA     46894    C    T
                                C ATGG CGGAATTTGGA
                                | |||| ||||||||||
                                A TACT GTCTTAAACCT
                                 C   _
GAM493  FLJ13262  3'  TCCAAATTCCCGGCCCGG    46696    AT     _
                                CC  GGTCGG AATTTGGA
                                ||  |||||| ||||||||
                                GG  CCGGCC TTAAACCT
                                 C_     C
GAM493  FLJ13291  3'  TCCAAACTCTGATAACGGT    50742     ATG     A
                                ACC   GTCGGA TTTGGA
                                |||   |||||| ||||||
                                TGG   TAGTCT AAACCT
                                  CAA     C
GAM493  KEAP1    3'  CCAAACCCTCTGGCCGGGTA   25429      A       A__
                                TACC TGGTCGGA   TTTGG
                                |||| ||||||||   |||||
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                                ATGG GCCGGTCT   AAACC
                                  _       CCC
GAM493  KIAA0252  5'  CCGGGGGACCACCATGGTA   63452         C  AA_
                                TACCATGGT GG   TTTGG
                                ||||||||| ||   |||||
                                ATGGTACCA CC   GGGCC
                                     _ AGG
GAM493  KIAA0798  3'  CCAATATGACCCATGGTA    28444         _  GAAT
                                TACCATGG TCG    TTGG
                                |||||||| |||    ||||
                                ATGGTACC AGT    AACC
                                    C   AT__
GAM493  KIAA0961  3'  TCCAAATTCAAATGGTG     30408       GGTCG
                                TACCAT    GAATTTGGA
                                ||||||    |||||||||
                                GTGGTA    CTTAAACCT
                                   AA___
GAM493  KIAA1786  3'  TCCAAATTCTGCTAGG      66636    A   T
                                CC TGG CGGAATTTGGA
                                || ||| ||||||||||
                                GG ATC GTCTTAAACCT
                                 _  _
GAM493  NAV3      3'  CCAAGGGCTAGGCCATGGTA   30451          _ AA
                                TACCATGGTC GG  TTTGG
                                |||||||||| ||  |||||
                                ATGGTACCGG TC  GAACC
                                     A  GG
GAM493  PDZ-GEF1  3'  TCCAAATTCCAAGATCATCA   27283   C     __
                                C ATGGTC  GGAATTTGGA
                                | ||||||  ||||||||||
                                A TACTAG  CCTTAAACCT
                                 C     AA
GAM493  PIP5K1C   3'  TCCAAATTCCTGTACTGT    71309      _ _
                                ATGGT C GGAATTTGGA
                                ||||| | ||||||||||
                                TGTCA G CCTTAAACCT
                                   T T
GAM493  SPARCL1   5'  TCCAAATTCTCGTCTGTCA   17432   C    T _
                                C ATGG CG GAATTTGGA
                                | |||| || |||||||||
                                A TGTC GC CTTAAACCT
                                 C   T  T
GAM493  LOC122553 3'  TCTGTGCCAATCATGGTA    74594         C  AATT
                                TACCATGGT GG    TGGA
                                ||||||||| ||    ||||
                                ATGGTACTA CC    GTCT
                                     A  GT__
GAM493  LOC149271 3'  TCCAAATTCCTTCCATGGTA   80011         TC
                                TACCATGG  GGAATTTGGA
                                ||||||||  ||||||||||
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                                ATGGTACC  CCTTAAACCT
                                    TT
GAM493  LOC149460 5'  TCCAGCCCCAATCATGGTA   85616       C  AAT
                                TACCATGGT GG   TTGGA
                                ||||||||| ||   |||||
                                ATGGTACTA CC   GACCT
                                    A  CC_
GAM493  LOC151614 3'  CCAAATTCCACTTCTGGT    81119     T_  C
                                ACCA  GGT GGAATTTGG
                                ||||  ||| |||||||||
                                TGGT  TCA CCTTAAACC
                                  CT  _
GAM493  LOC158476 5'  TCCAAAGAACCATGGTG     88206       CGGAA
                                TACCATGGT    TTTGGA
                                |||||||||    ||||||
                                GTGGTACCA    AAACCT
                                    AG___
GAM493  LOC219333 3'  CCTTCCGATCATGGTA      95185         TTT
                                TACCATGGTCGGAA  GG
                                ||||||||||||||  ||
                                ATGGTACTAGCCTT  CC
                                        ___
GAM493  LOC54516  3'  TCCAACTTTACCATGGTG    39286       CG  T
                                TACCATGGT  GAA TTGGA
                                |||||||||  ||| |||||
                                GTGGTACCA  TTT AACCT
                                    __  C
GAM493  LOC90589  3'  CCGAATCCAATCATGGTA    59773       C  A
                                TACCATGGT GGA TTTGG
                                ||||||||| ||| |||||
                                ATGGTACTA CCT AAGCC
                                    A  _
GAM493  LOC92017  5'  CCAAATTCCACACCCTGG    68488    T  C_
                                CCA GGT  GGAATTTGG
                                ||| |||  |||||||||
                                GGT CCA  CCTTAAACC
                                  C  CA
GAM494  DPYD     3'  CTCATTTATCTCCTCTTCAT   61070      C  AACC
                                ATGAAG AG   TGGATGAG
                                |||||| ||   ||||||||
                                TACTTC TC   ATTTACTC
                                   _ CTCT
GAM494  GOLGA5   3'  AGCTCAGCTCTGCTTTAT    18850       ACCTGGA
                                ATGAAGCAGA     TGAGCT
                                ||||||||||     ||||||
                                TATTTCGTCT     ACTCGA
                                    CG_____
GAM494  MAP1A    3'  TCCCCCAGACCCTGCTTTAT  11444       AAC   AT
                                ATGAAGCAG  CTGG  GA
                                |||||||||  ||||  ||
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                                TATTTCGTC   GACC  CT
                                     CCA    CC
GAM494  ZNFN2A1   3' AGCCCACCATCTGCTTC     61388        ACC   A  A
                                GAAGCAGA   TGG TG GCT
                                ||||||||   ||| || |||
                                CTTCGTCT   ACC AC CGA
                                     ___   _  C
GAM494  COE2      3' AAGCTCATCCAACAAAGGCCTC 64901    A  AGAACC
                                GA GC      TGGATGAGCTT
                                || ||      ||||||||||
                                CT CG      ACCTACTCGAA
                                 C  GAAACA
GAM494  DKFZP727G051 3' CATTCAAATTCTGCCTCAT    70003      A     CC
                                ATGA GCAGAA  TGGATG
                                |||| ||||||  ||||||
                                TACT CGTCTT  ACTTAC
                                  C      AA
GAM494  FLJ10704  3' CTTCCCCAGGCTCTGCTTC    36979         A     AT
                                GAAGCAGA CCTGG  GAG
                                |||||||| |||||  |||
                                CTTCGTCT GGACC  TTC
                                     C     CC
GAM494  FLJ14146  3' AAGCTGTGGAGCTAGACTCTGC 45563          AC    ATG___
           TTCA                    TGAAGCAGA  CTGG     AGCTT
                                |||||||||  ||||     |||||
                                ACTTCGTCT  GATC     TCGAA
                                     CA    GAGGTG
GAM494  FLJ14642  3' AAGCAACAAGGTTCTGCTCCAT 52571     A         GGATGA
                                ATG AGCAGAACCT      GCTT
                                ||| ||||||||||      ||||
                                TAC TCGTCTTGGA      CGAA
                                  C         ACAA__
GAM494  FLJ21438  3' AAGTCTGTCCAGGCCCTGCCTC 62188    A    AA      GA
                                GA GCAG  CCTGGAT  GCTT
                                || ||||  |||||||  ||||
                                CT CGTC  GGACCTG  TGAA
                                 C   CC      TC
GAM494  GAB3      3' AAGCTCATTCCTCTACCTCAT  55516      AGC   ACCT
                                ATGA   AGA    GGATGAGCTT
                                ||||   |||    ||||||||||
                                TACT   TCT    CTTACTCGAA
                                  CCA   C___
GAM494  HMGN4     3' AGCTCATACATGCCTCAT     22030      A   GAACC  G
                                ATGA GCA     TG ATGAGCT
                                |||| |||     || |||||||
                                TACT CGT     AC TACTCGA
                                  C   _____  A
GAM494  KIAA1388  5' CTCTCCAAACCCTGTTTCAT   95227          AACC    T
                                ATGAAGCAG    TGGA GAG
                                |||||||||    |||| |||
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                                TACTTTGTC   ACCT CTC
                                     CCAA   _
GAM494  OSBPL3    3'  AAGCATTTATCCAAATTCTGCT 32076    A    CC     __
          CA                    TGA GCAGAA  TGGATGA  GCTT
                                ||| ||||||  |||||||  ||||
                                ACT CGTCTT  ACCTATT  CGAA
                                  _     AA      TA
GAM494  LOC115219 5'  AAGCCCCTGTCCAGGCCCTGCT 73681    A   AA     A__
          CA                    TGA GCAG  CCTGGATG   GCTT
                                ||| ||||  ||||||||   ||||
                                ACT CGTC  GGACCTGT   CGAA
                                  _   CC       CCC
GAM494  LOC131873 3'  CATCAGGTTTGCTTCAT     76394         A   G
                                ATGAAGCAGA CCTG ATG
                                |||||||||| |||| |||
                                TACTTCGTTT GGAC TAC
                                     _   _
GAM494  LOC145725 5'  AAGCCCCAATCCCTGCTTCAT  77880        AACCT   GA__
                                ATGAAGCAG    GGAT   GCTT
                                |||||||||    ||||   ||||
                                TACTTCGTC    CCTA   CGAA
                                     _____   ACCC
GAM494  LOC145732 5'  AAGCCCCAATCCCTGCTTCAT  77892        AACCT   GA__
                                ATGAAGCAG    GGAT   GCTT
                                |||||||||    ||||   ||||
                                TACTTCGTC    CCTA   CGAA
                                     _____   ACCC
GAM494  LOC145873 3'  AGGCCCCAGGCTCTGCTTC   78010        A    ATGA
                                GAAGCAGA CCTGG   GCTT
                                |||||||| |||||   ||||
                                CTTCGTCT GGACC   CGGA
                                     C    C___
GAM494  LOC148343 5'  AGCTTGGGCTCTGCTTC     79536        A   GGAT
                                GAAGCAGA CCT   GAGCT
                                |||||||| |||   |||||
                                CTTCGTCT GGG   TTCGA
                                     C  _____
GAM494  LOC196957 5'  AAGCCCCAATCCCTGCTTCAT  89184        AACCT   GA__
                                ATGAAGCAG    GGAT   GCTT
                                |||||||||    ||||   ||||
                                TACTTCGTC    CCTA   CGAA
                                     _____   ACCC
GAM494  LOC196961 5'  AAGCCCCAATCCCTGCTTCAT  89198        AACCT   GA__
                                ATGAAGCAG    GGAT   GCTT
                                |||||||||    ||||   ||||
                                TACTTCGTC    CCTA   CGAA
                                     _____   ACCC
GAM494  LOC197138 5'  AAGCCCCAATCCCTGCTTCAT  89247        AACCT   GA__
                                ATGAAGCAG    GGAT   GCTT
                                |||||||||    ||||   ||||
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                                TACTTCGTC    CCTA   CGAA
                                     _____   ACCC
GAM495  AQP7     5'  GACAGTCACGGAGGAACAAGAT 8605        A_
            CAA                    TTGATCTT  TCCTCCGTGACTGTC
                                   ||||||||  ||||||||||||||||
                                   AACTAGAA  AGGAGGCACTGACAG
                                      CA
GAM495  MMP14    5'  GACTAAGCAGAAGAAAGATCAA 18428        A  C  C  GACT
                                   TTGATCTT TC TC GT   GTC
                                   |||||||| || || ||   |||
                                   AACTAGAA AG AG CG   CAG
                                      _  A  A  AAT_
GAM495  KIAA0433 5'  ACAGTCATCATAATATCAA   31498      C   CCTCC
                                   TTGAT TTAT    GTGACTGT
                                   ||||| ||||    ||||||||
                                   AACTA AATA    TACTGACA
                                     T   C____
GAM495  KIAA1915 5'  GACAGTATTTTAAAAATAAGGT 73667         CCTCCGTG_
            CAA                    TTGATCTTAT       ACTGTC
                                   ||||||||||       ||||||
                                   AACTGGAATA       TGACAG
                                       AAAATTTTA
GAM495  MGC5370  3'  CAGTTGAAAAGATCAA     52193        A  CTCCGT
                                   TTGATCTT TC     GACTG
                                   |||||||| ||     |||||
                                   AACTAGAA AG     TTGAC
                                      A _______
GAM495  TREX1    5'  GACAGCTGGAGACAGAGATCAA 54382        ATC    TGA
                                   TTGATCTT   CTCCG   CTGTC
                                   ||||||||   |||||   |||||
                                   AACTAGAG   GAGGT   GACAG
                                      ACA    C__
GAM495  TREX1    5'  GACAGCTGGAGACAGAGATCAA 54388        ATC    TGA
                                   TTGATCTT   CTCCG   CTGTC
                                   ||||||||   |||||   |||||
                                   AACTAGAG   GAGGT   GACAG
                                      ACA    C__
GAM495  LOC127534 3'  ACAGCAGATAAGATCAA     75963          CTCCG  A  _
                                   TTGATCTTATC    TG CTG T
                                   ||||||||||     || ||| |
                                   AACTAGAATAG    AC GAC A
                                         _____ _   T
GAM495  LOC150480 5'  GACAGTCACGGAGGAAGAAGAT 61025         A_
            CAA                    TTGATCTT  TCCTCCGTGACTGTC
                                   ||||||||  ||||||||||||||||
                                   AACTAGAA  AGGAGGCACTGACAG
                                      GA
GAM495  LOC158279 5'  GACAGTCACAGAGGAACAAGAT 60330         A_    C
            CAA                    TTGATCTT  TCCTC GTGACTGTC
                                   ||||||||  |||||  |||||||||
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                                AACTAGAA  AGGAG CACTGACAG
                                    CA    A
GAM495  LOC201522 3'  GACCTTCGGGAGAACGAGATCA 89637        ATC   G   CT
          A                      TTGATCTT   CTCC TGA  GTC
                                 ||||||||   |||| |||  |||
                                 AACTAGAG   GAGG GCT  CAG
                                    CAA   _   TC
GAM495  LOC220864 5'  GACAGTCACAGAGGAACAAGAT 92487        A_    C
          CAA                     TTGATCTT  TCCTC GTGACTGTC
                                 ||||||||  ||||| |||||||||
                                 AACTAGAA  AGGAG CACTGACAG
                                    CA    A
GAM495  LOC254381 5'  GACAGTCACGACAGCAGACCAA 99328     A   TATCCTC
                                 TTG TCT      CGTGACTGTC
                                 ||| |||      ||||||||||
                                 AAC AGA      GCACTGACAG
                                   C   CGACA__
GAM496  HRH1     3'  AAATGTGCCCTTTTGGCCGG   7812     A      A   TCA
                                 CC GGCCAAAA GGC   ACATTT
                                 || |||||||| |||   ||||||
                                 GG CCGGTTTT CCG   TGTAAA
                                  _       C   ___
GAM496  POLD2    5'  TTGAACCTCCTTGGCCTGG    21721         AA   C
                                 CCAGGCCAA  AGG TCAA
                                 |||||||||  ||| ||||
                                 GGTCCGGTT  TCC AGTT
                                      CC   A
GAM496  SCN7A    3'  AAATGTTGAAAGCCTAAGCC   12947     CAAAA   __
                                 GGC    AGGC  TCAACATTT
                                 |||    ||||  |||||||||
                                 CCG    TCCG  AGTTGTAAA
                                   AA___    AA
GAM496  SHANK2   3'  GTTGAACTTCTTCTTTGGCCTC 25531    C      _    C__
          A                       C AGGCCAAA AAGG   TCAAC
                                 | |||||||| ||||   |||||
                                 A TCCGGTTT TTCT   AGTTG
                                 C       C    TCA
GAM496  SIAT8E   3'  TGAGCCTCCTGGCCTGG     60552         AAA
                                 CCAGGCCA   AGGCTCA
                                 ||||||||   |||||||
                                 GGTCCGGT   TCCGAGT
                                      CC_
GAM496  SLC7A8   3'  GAGCCCTTCCTGGCCTGG    25304         AA   _
                                 CCAGGCCA  AAGG CTC
                                 ||||||||  |||| |||
                                 GGTCCGGT  TTCC GAG
                                      CC    C
GAM496  TFAP2C   3'  TGGGAACCCCTCCTGGCCTGG  13687         AAA  _____
                                 CCAGGCCA   AGG    CTCA
                                 ||||||||   |||    ||||
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                                GGTCCGGT  TCC   GGGT
                                    CC_  CCAA
GAM496  TRPM2    3'  GAGCCTTGCCTGGCCTGG   13864       AA_
                                CCAGGCCA  AAGGCTC
                                ||||||||  |||||||
                                GGTCCGGT  TTCCGAG
                                    CCG
GAM496  FLJ13189 3'  TTGAACCTTTTTTGCCTGG   46498     C     C
                                CCAGGC AAAAAGG TCAA
                                |||||| ||||||| ||||
                                GGTCCG TTTTTCC AGTT
                                   T     A
GAM496  FLJ20208 3'  AAATGCAGGCTTTTTAGCC   35240    C    G  CAA
                                GGC AAAAAG CT  CATTT
                                ||| |||||| ||  |||||
                                CCG TTTTTC GA  GTAAA
                                  A    G  C__
GAM496  FLJ22944 3'  AAATGTTGGGATTTGAACCC  47866   CCAA  GG
                                GG   AAA  CTCAACATTT
                                ||   |||  ||||||||||
                                CC   TTT  GGGTTGTAAA
                                 CAAG  A_
GAM496  HPRP8BP  3'  AAATGTTGGATGTCCAGGCT  60060     AAAAA  __
                                GGCC   GGC  TCAACATTT
                                ||||   |||  |||||||||
                                TCGG   CTG  GGTTGTAAA
                                  AC___  TA
GAM496  KIAA0872 3'  AAATGTTAAGCCTTTTGTTATT 30731    GCCA     C
           G                     CAG   AAAAGGCT AACATTT
                                |||   |||||||| |||||||
                                GTT   TTTTCCGA TTGTAAA
                                  ATTG      A
GAM496  KIAA1843 3'  AAATGTTGACTGAACCTGACCT 62880     C  AAAA_  C
           G                     CAGG CA    GG TCAACATTT
                                |||| ||    || |||||||||
                                GTCC GT    TC AGTTGTAAA
                                  A  CCAAG  _
GAM496  KIAA1975 3'  AAATGTTGATTTTTCTGACC  74407   C  A   C
                                GG CA AAAGG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM496  MRIP2    3'  AAATGTTGATTTTTCTGACC  56789   C  A   C
                                GG CA AAAGG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM496  SLC26A10 5'  TTGAACCCCTTTGGCCTG   56851       AA  C
                                CAGGCCAAA  GG TCAA
                                |||||||||  || ||||
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                                GTCCGGTTT  CC AGTT
                                     CC  A
GAM496  THEG     3'  TGAGCTTTTTGGCCTGG     33892          G
                                CCAGGCCAAAAAG CTCA
                                |||||||||||| ||||
                                GGTCCGGTTTTTC GAGT
                                          _
GAM496  LOC118704 3' AAATGTTGATTTTTCTGACC   74359    C  A    C
                                GG CA AAAGG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM496  LOC118706 3' AAATGTTGATTTTTCTGACC   74361    C  A    C
                                GG CA AAAGG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM496  LOC123036 3' AAATGTTTGCAGTTTTGGCT   74645        AG  TC
                                GGCCAAAA  GC  AACATTT
                                ||||||||  ||  |||||||
                                TCGGTTTT  CG  TTGTAAA
                                     GA  T_
GAM496  LOC123624 3' AAATGTTGGGCTTCTGTGCCT  76134     _  AAA
                                AGGC CA   AGGCTCAACATTT
                                |||| ||   ||||||||||||
                                TCCG GT   TTCGGGTTGTAAA
                                  T  C__
GAM496  LOC128338 3' AAATATTGAGCCTTTTTAATAG 75250    AGGCC          C
           G                     CC     AAAAAGGCTCAA ATTT
                                ||     |||||||||||| ||||
                                GG     TTTTTCCGAGTT TAAA
                                 ATAA_          A
GAM496  LOC143158 3' AAATGTTGATTTTTCTGACC   76997    C  A    C
                                GG CA AAAGG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM496  LOC195979 3' AAATGTTGATTTTTCTGACC   88928    C  A    C
                                GG CA AAAGG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM496  LOC219672 5' AATGGTGCTTTTTGGCTGG    92963     G       G TCAA
                                CCAG CCAAAAAG C    CATT
                                |||| |||||||| |    ||||
                                GGTC GGTTTTTC G    GTAA
                                  _       _ TG__
GAM496  LOC220466 3' AAATGTTGATTTTTCTGACC   74398    C  A    C
                                GG CA AAAGG TCAACATTT
                                || || ||||| |||||||||
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                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM496  LOC254105 3'  AGGTGTGGCCCCCTTGGCCTGG 96416         AAA    CA
                                CCAGGCCAA   GGCT  ACATTT
                                |||||||||   ||||  ||||||
                                GGTCCGGTT   CCGG  TGTGGA
                                     CCC    __
GAM496  LOC255319 3'  AAATGTTGATTTTTCTGACC   96152    C  A    C
                                GG CA AAAGG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM496  LOC91300  5'  GTTGAGCTTTTCTGGCCCGG   96238    A    A
                                CC GGCCA AAAGGCTCAAC
                                || ||||| ||||||||||
                                GG CCGGT TTTTCGAGTTG
                                 C    C
GAM496  LOC91300  5'  GTTGAGCTTTTCTGGCCCGG   57864    A    A
                                CC GGCCA AAAGGCTCAAC
                                || ||||| ||||||||||
                                GG CCGGT TTTTCGAGTTG
                                 C    C
GAM496  LOC91660  5'  AAATGTTTATCTTCTTTTTGGC 67399          CTC__
           TT                    AGGCCAAAAAGG    AACATTT
                                ||||||||||||    |||||||
                                TTCGGTTTTTCT    TTGTAAA
                                      TCTAT
GAM497  CDH12     3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM497  GOCAP1    3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM497  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT    98090      T    AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                   _   GTCA_
GAM497  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
           A                     TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM497  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
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                                ATGTGGTGA      TTTATTC
                                     AGACG___
GAM497  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
            TA                    TACA   TCC   GAAGAATAAG
                                  ||||   |||   ||||||||||
                                  ATGT   AGG   TTTCTTATTC
                                    AAA_   ATTG
GAM497  KIAA1719 3'  TCTGTCTTGGGAGTGGTGTA  68742           _
                                  TACACCACTCCCAAGA AGA
                                  |||||||||||||||| |||
                                  ATGTGGTGAGGGTTCT TCT
                                           G
GAM497  KIAA1853 3'  TTTTTCTTGGAAGCAGTG    69929    CA  C
                                  CAC  CT CCAAGAAGAA
                                  |||  || ||||||||||
                                  GTG  GA GGTTCTTTTT
                                    AC  A
GAM497  KIAA1877 3'  CTTATTCTTCTGCCATGAGT   66748     CCA__
                                  ACTC    AGAAGAATAAG
                                  ||||    ||||||||||
                                  TGAG    TCTTCTTATTC
                                    TACCG
GAM497  KIAA1906 3'  CTTATTCTTCTTGACTTTTGG  73571    CTCC_
                                  CCA    CAAGAAGAATAAG
                                  |||    ||||||||||||
                                  GGT    GTTCTTCTTATTC
                                    TTTCA
GAM497  OSBPL11  3'  CTTAATTTCCCAAGAGTGGTG 43206       CCAA   AA
                                  CACCACTC   GAAG  TAAG
                                  ||||||||   ||||  ||||
                                  GTGGTGAG   CTTT  ATTC
                                       AACC   A_
GAM497  YME1L1   3'  TCATTCTTGATGTGGTGTA   58438       TCC    _
                                  TACACCAC   CAAGAA GA
                                  ||||||||   |||||| ||
                                  ATGTGGTG   GTTCTT CT
                                       TA_     A
GAM497  ZNF262   3'  CTTATTTTGTTTGGGAGT    18723        A
                                  ACTCCCAAG AGAATAAG
                                  |||||||||  ||||||||
                                  TGAGGGTTT TTTTATTC
                                       G
GAM497  LOC91960 3'  TGTGGCTTGGAACGTGGTGTA 68294       TC_   AAGA
                                  TACACCAC   CCAAG   ATA
                                  ||||||||   |||||   |||
                                  ATGTGGTG   GGTTC   TGT
                                       CAA    GG__
GAM498  FLJ32861 3'  TCTACATCCAATCCCAACA   59384    _ TTT  ATC
                                  TGT GG   GA   GGATGTAGA
                                  ||| ||   ||   |||||||||
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                                ACA CC   CT   CCTACATCT
                                  A  ___  AA_
GAM498  KIAA0040  3'  TCTGTAAAATTCAAACACACA  28496      _      ____
                                TGTG GTTTGAAT   CGGA
                                |||| ||||||||   ||||
                                ACAC CAAACTTA   GTCT
                                  A       AAAT
GAM498  PIP3-E    3'  ACATGACCCCAGAACCACATA  67341          GAATC  __
                                TATGTGGTTT    GG  ATGT
                                ||||||||||    ||  ||||
                                ATACACCAAG    CC  TACA
                                      ACC__  AG
GAM499  CSF1R     3'  CAAGCAGGAAGCACAAACTCCC 19051      A    _  G  AT
                                GGGA GTTTG GC TC  TTGCTTG
                                |||| ||||| || ||  |||||||
                                CCCT CAAAC CG AG  GACGAAC
                                  _    A  A  __
GAM499  DKFZp761G0313 3'  CAAGCAAATCTGACCCAAACTC 66391      A     C   __
          CC                      GGGA GTTTGG GTCA  TTTGCTTG
                                |||| |||||| ||||  ||||||||
                                CCCT CAAACC CAGT  AAACGAAC
                                  _     _   CT
GAM500  NQO2      5'  TCAGAGAGAAGGAATCCAC    8060         T  C  GA   C
                                GTGGATT CC TC  TCT GA
                                ||||||| || ||  ||| ||
                                CACCTAA GG AG  AGA CT
                                    _ A  AG  _
GAM500  NUP62     3'  AGTCAGTTACAGTAAAATCCAC 33781          CC  CGAT  C
          T                      AGTGGATTT  CT    CT GACT
                                |||||||||  ||    || ||||
                                TCACCTAAA  GA    GA CTGA
                                     AT  CATT  _
GAM500  FLJ20436  3'  AGTCATGGATAGAAATCCACT  35622          CC  G  CTC
                                AGTGGATTTC  TC AT   GACT
                                ||||||||||  || ||   ||||
                                TCACCTAAAG  AG TA   CTGA
                                     AT  G  ___
GAM500  FLJ23231  3'  GTCGGGAAGGAAACCCAC    47608      A    CTCGA
                                GTGG TTTCC     TCTCGAC
                                ||||  |||||    |||||||
                                CACC AAAGG     AGGGCTG
                                  C    A____
GAM500  FLJ23360  3'  AGCCGAGATCGCGCCACCCACT 43821      ATTTCCCT      A
                                AGTGG       CGATCTCG CT
                                |||||       |||||||| ||
                                TCACC       GCTAGAGC GA
                                   CACCGC__       C
GAM500  TA-PP2C   3'  ATCGGGAGAAAAATCCATT    58403         __  C
                                AGTGGATT  TC CTCGAT
                                ||||||||  || ||||||
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                                TTACCTAA  AG GGGCTA
                                    AA  A
GAM500  LOC123876 5'  TCCAGATGAAATCCACT     74720         CCTCG    C
                                AGTGGATTTC    ATCT GA
                                ||||||||||    |||| ||
                                TCACCTAAAG    TAGA CT
                                     _____   C
GAM500  LOC154789 5'  GACGTCAAGAAAGATCCAC   82029        CC  C   C
                                GTGGATTT  CT GAT TC
                                ||||||||  || ||| ||
                                CACCTAGA  GA CTG AG
                                    AA  A   C
GAM500  LOC199221 3'  TCGGAAGAAAATCCAT     81169        CCC  GA  T
                                GTGGATTT   TC  TC CGA
                                ||||||||   ||  || |||
                                TACCTAAA   AG  AG GCT
                                    ___  A_  _
GAM501  CHRNB4    3'  TTCCCCTTGTCCAGTTC     7452     C       TATGT
                                GA CTGGACAAG    GGAA
                                || |||||||||    ||||
                                CT GACCTGTTC    CCTT
                                 T       C____
GAM501  DAZ       3'  ATTTCCTGCTTATCCAAGTT   15823    C   C    TGT
                                GAC TGGA AAGTA   GGAAAT
                                ||| |||| |||||   ||||||
                                TTG ACCT TTCGT   CCTTTA
                                  A   A    ___
GAM501  DAZ       3'  ATTTCCTGCTTATCCAAGTT   15824    C   C    TGT
                                GAC TGGA AAGTA   GGAAAT
                                ||| |||| |||||   ||||||
                                TTG ACCT TTCGT   CCTTTA
                                  A   A    ___
GAM501  HMMR      3'  TCCTTCTACTTGTCCAGTTC   25948    C        TGT
                                GA CTGGACAAGTA   GGA
                                || ||||||||||   |||
                                CT GACCTGTTCAT   CCT
                                 T         CTT
GAM501  PLOD2     3'  TATTTCTGAACACCTATGCAGG 8125       GACAA  ATG
           TC                     GACCTG    GT   TGGAAATA
                                ||||||    ||   ||||||||
                                CTGGAC    CA   GTCTTTAT
                                   GTATC  CAA
GAM501  SFRS7     3'  TATTTCCAATCCCCGTCGAGGT 60150      G   AAGTATG
           C                     GACCT GAC      TGGAAATA
                                |||||  |||      ||||||||
                                CTGGA CTG      ACCTTTAT
                                   G   CCCCTA_
GAM501  TSNAX     5'  CACTCCTCTTGCTCCAGGTC   21153        _   TAT_
                                GACCTGGA CAAG    GTG
                                |||||||| ||||    |||
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                                CTGGACCT GTTC   CAC
                                    C   TCCT
GAM501  FLJ10743  3'  TTCCCTCGGCTTCCAGGTC   37093       CA  ATGT
                                GACCTGGA AGT   GGAA
                                |||||||| |||   ||||
                                CTGGACCT TCG   CCTT
                                   __  GCTC
GAM501  FLJ12409  3'  ATTTCCACATACTTATCAG   47766     AC
                                CTGG AAGTATGTGGAAAT
                                |||| ||||||||||||||
                                GACT TTCATACACCTTTA
                                  A_
GAM501  FLJ12650  3'  TCCACCCCCTTCCAGGTC    44825       CA TAT
                                GACCTGGA AG  GTGGA
                                |||||||| ||  |||||
                                CTGGACCT TC  CACCT
                                   __ CCC
GAM501  HSNOV1    3'  ATTTCTCCATCACTCATTCCAG 34428       CA_ _  TG
          GTC                     GACCTGGA  AGT ATG  GAAAT
                                |||||||| ||| ||| |||||
                                CTGGACCT  TCA TAC  CTTTA
                                   TAC  C  CT
GAM501  LOC152580 5'  TTCCTGGACATACTTTCCA   86987     C     ___
                                TGGA AAGTATGT  GGAA
                                |||| ||||||||  ||||
                                ACCT TTCATACA  CCTT
                                  _     GGT
GAM501  LOC221540 3'  ATTTCCATGTGCTCCAGG   95474     CAA
                                CCTGGA  GTATGTGGAAAT
                                ||||||  ||||||||||||
                                GGACCT  CGTGTACCTTTA
                                   ___
GAM501  LOC222681 5'  TATTTCCCCTCACTCCAGG   94428     CAA ATGT
                                CCTGGA  GT   GGAAATA
                                ||||||  ||   |||||||
                                GGACCT  CA   CCTTTAT
                                   ___ CTCC
GAM501  LOC257507 5'  TATTTCCCCTCACTCCAGG   99615     CAA ATGT
                                CCTGGA  GT   GGAAATA
                                ||||||  ||   |||||||
                                GGACCT  CA   CCTTTAT
                                   ___ CTCC
GAM501  LOC257545 3'  ATTTCCATGTGCTCCAGG   99638     CAA
                                CCTGGA  GTATGTGGAAAT
                                ||||||  ||||||||||||
                                GGACCT  CGTGTACCTTTA
                                   ___
GAM501  LOC257598 3'  ATTTCCATGTGCTCCAGG   99746     CAA
                                CCTGGA  GTATGTGGAAAT
                                ||||||  ||||||||||||
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                                GGACCT  CGTGTACCTTTA
                                   ___
GAM501  LOC257625 5'  TATTTCCCCTCACTCCAGG   99735      CAA  ATGT
                                CCTGGA  GT   GGAAATA
                                ||||||  ||   |||||||
                                GGACCT  CA   CCTTTAT
                                   ___  CTCC
GAM501  LOC91571  3'  TTCCTGCCAATCCAGGTC    67104      CAA  TGT
                                GACCTGGA  GTA  GGAA
                                ||||||||  |||  ||||
                                CTGGACCT  CGT  CCTT
                                    AAC  ___
GAM502  ADORA1    3'  TGTCATCTGGGCCACCAGCT  7276       A  ATGTT
                                AGCTGGTG CC    TGACA
                                |||||||| ||    |||||
                                TCGACCAC GG    ACTGT
                                    C  GTCT_
GAM502  ATP2B2    5'  GCTCACCACCACTGTCACCAGC 9850       CA  TT  ACA
                                GCTGGTGAC  TG  TG   AGC
                                |||||||||  ||  ||   |||
                                CGACCACTG  AC  AC   TCG
                                    TC  C_  CAC
GAM502  CD34      3'  TGTGGACTTGGTCACCAGCT  10111        T   G
                                AGCTGGTGACCA GTTT ACA
                                |||||||||||| |||| |||
                                TCGACCACTGGT CAGG TGT
                                      T   _
GAM502  CHAC      3'  GCTCATCACAGAAATCATCAGC 53957      CCA_  TT  CA
           T                    AGCTGGTGA   TGT  GA  AGC
                                |||||||||   |||  ||  |||
                                TCGACTACT   ACA  CT  TCG
                                    AAAG  __  AC
GAM502  FBXL11    3'  GCTTAGAAGCCAGTCACCAGC  25517      CAT   GAC
                                GCTGGTGAC   GTTT   AAGC
                                |||||||||   ||||   ||||
                                CGACCACTG   CGAA   TTCG
                                    AC_   GA_
GAM502  NEO1      3'  GCTCCAGGCATGGCCACCTGC  11774   T   A      ACA
                                GC GGTG CCATGTTTG   AGC
                                || |||| |||||||||   |||
                                CG CCAC GGTACGGAC   TCG
                                 T   C       C__
GAM502  PODXL     3'  TTTGTCACGGTCACTAGCT    19421        ATGTT
                                AGCTGGTGACC    TGACAAG
                                ||||||||||    |||||||
                                TCGATCACTGG    ACTGTTT
                                      C____
GAM502  SCA1      3'  TGCCACCCACGGTCACCACT   6187    C      A  TT  A
                                AG TGGTGACC TG  TG CA
                                || |||||||| ||  || ||
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                                TC ACCACTGG AC  AC GT
                                 _      C  CC  C
GAM502  SDC4     3'  CTTGTCAGTATCTCCAGCT   12997       T  CCATGT
                                AGCTGG GA     TTGACAAG
                                ||||||| ||     ||||||||
                                TCGACC CT     GACTGTTC
                                   T  AT____
GAM502  SLC6A8   3'  TCAGCTCACATCACCAGCT   20076        CCA  T_
                                AGCTGGTGA   TG  TTGA
                                |||||||||   ||  ||||
                                TCGACCACT   AC  GACT
                                     AC_  TC
GAM502  C21orf108 3'  TCGAGCACAGCACCAGCT    90122        ACCA
                                AGCTGGTG    TGTTTGA
                                ||||||||    |||||||
                                TCGACCAC    ACGAGCT
                                     GAC_
GAM502  FIGN     3'  CTTGCCAAACATGTTACT    97363       C      A
                                GGTGAC ATGTTTG CAAG
                                ||||||| ||||||| ||||
                                TCATTG TACAAAC GTTC
                                   _      C
GAM502  FKBP4    5'  TCGCGCCGGCACCAGCT     10645        A  AT  T
                                AGCTGGTG CC  GT TGA
                                |||||||| ||  || |||
                                TCGACCAC GG  CG GCT
                                     _  C_  C
GAM502  FLJ20154  3'  GCTCGCCTTCAGGTCACCAGCT 73305          A  TTTGACA
                                AGCTGGTGACC TG      AGC
                                |||||||||||| ||      |||
                                TCGACCACTGG AC      TCG
                                      _  TTCCGC_
GAM502  HBOA     3'  GCTTGCCACCTGGTCACCAG   23932         T  TT A
                                CTGGTGACCA GT  G CAAGC
                                |||||||||| ||  | |||||
                                GACCACTGGT CA  C GTTCG
                                     C  __ C
GAM502  KCNH4    3'  GTCAGCAGCCACCAGCT     25391        ACCA   T
                                AGCTGGTG    TGTT GAC
                                ||||||||    |||| |||
                                TCGACCAC    ACGA CTG
                                     CG__    _
GAM502  KCNH8    3'  CTTGTGGGAGTAATACCAGCT  58906        ACCATG   G
                                AGCTGGTG     TTT ACAAG
                                ||||||||     ||| |||||
                                TCGACCAT     AGG TGTTC
                                     AATG__   G
GAM502  LY117    5'  CTTGAGGCAAGTCACCAGC   93961         CA    GA
                                GCTGGTGAC  TGTTT  CAAG
                                |||||||||  |||||  ||||
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                                CGACCACTG  ACGGA  GTTC
                                     A_    __
GAM502  LY117    5' CTTGAGGCAAGTCACCAGC   99586        CA    GA
                                GCTGGTGAC  TGTTT  CAAG
                                |||||||||  |||||  ||||
                                CGACCACTG  ACGGA  GTTC
                                     A_    __
GAM502  LY117    5' CTTGAGGCAAGTCACCAGC   99675        CA    GA
                                GCTGGTGAC  TGTTT  CAAG
                                |||||||||  |||||  ||||
                                CGACCACTG  ACGGA  GTTC
                                     A_    __
GAM502  MGC10715 5' TCTCCAGGGTCACCAGCT    44502          A  TTT
                                AGCTGGTGACC TG   GA
                                ||||||||||| ||   ||
                                TCGACCACTGG AC   CT
                                      G  CT_
GAM502  MGC11287 5' GCCTGGCCAACATGGTCCCAGC 49619       T       TGA  A
           T                     AGCTGG GACCATGTT   CA GC
                                |||||| |||||||||   || ||
                                TCGACC CTGGTACAA   GT CG
                                   _       CCG  C
GAM502  RPIA     5' GCTGGCAACACAAGCACCAGCT 58593        ACCA  _  ACA
                                AGCTGGTG   TGT TTG   AGC
                                ||||||||   ||| |||   |||
                                TCGACCAC   ACA AAC   TCG
                                    GA__   C   GG_
GAM502  LOC148183 5' GCCTGCAACAGCAAATCACCAG 85265         CCA  __  A  A
           CT                     AGCTGGTGA   TGT  TTG CA GC
                                |||||||||   |||  ||| || ||
                                TCGACCACT   ACG  AAC GT CG
                                    AA_   AC   _ C
GAM502  LOC149018 5' GCTTGTCAAGTTCACCA     79862       CCATG
                                TGGTGA    TTTGACAAGC
                                ||||||    ||||||||||
                                ACCACT    GAACTGTTCG
                                   T____
GAM502  LOC149935 3' GCCTGTCAGGTGAAAACCACAG 60936     __   GAC   GT     A
           CT                     AGC  TGGT   CAT  TTGACA GC
                                |||  ||||   |||  |||||| ||
                                TCG  ACCA   GTG  GACTGT CG
                                  AC    AAA   __     C
GAM502  LOC157292 5' TCACATCTGTAATACCAGCT   87701        AC_  T  T
                                AGCTGGTG   CA GT TGA
                                ||||||||   || || |||
                                TCGACCAT   GT TA ACT
                                    AAT  C  C
GAM502  LOC163231 5' TGTTTATGGTCACCA       83340          TTT
                                TGGTGACCATG   GACA
                                ||||||||||   ||||
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                                ACCACTGGTAT   TTGT
                                      ___
GAM502  LOC199221 3'  GCTTGTCAAGGAAGTCACCAGC 81167         CATG
                                GCTGGTGAC    TTTGACAAGC
                                |||||||||    ||||||||||
                                CGACCACTG    GAACTGTTCG
                                     AAG_
GAM502  LOC220883 3'  GCTTGCCACCTGGTCACCAG   92893         T  TT A
                                CTGGTGACCA GT  G CAAGC
                                |||||||||| ||  | |||||
                                GACCACTGGT CA  C GTTCG
                                      C  __ C
GAM503  MAPRE2    3'  CTGTTGCATATGCCAGCCA    27333      T     CA
                                TGGCT GGCATA  CAATGG
                                ||||| ||||||  ||||||
                                ACCGA CCGTAT  GTTGTC
                                   _     AC
GAM503  MEIS2     3'  TTCATATTTGCCAAGCCA     39727          TACACA
                                TGGCTTGGCA     ATGGA
                                ||||||||||     |||||
                                ACCGAACCGT     TACTT
                                      TTA___
GAM503  PUNC      5'  CGCCCCATTGTGTCCTGGAGCC 91229       __  CAT       A
                                GGCTT  GG   ACACAATGG GCG
                                |||||  ||   ||||||||| |||
                                CCGAG  CC   TGTGTTACC CGC
                                   GT  ___        C
GAM503  ROBO1     3'  TGCTTATATGCCAAGCTA     56901          CACAATG
                                TGGCTTGGCATA      GAGCG
                                ||||||||||||      |||||
                                ATCGAACCGTAT      TTCGT
                                      A_______
GAM503  ROBO1     3'  TGCTTATATGCCAAGCTA     12895          CACAATG
                                TGGCTTGGCATA      GAGCG
                                ||||||||||||      |||||
                                ATCGAACCGTAT      TTCGT
                                      A_______
GAM503  FLJ10998  3'  CGCTCCATTGCACTCCAGCC   37519     T  CATACA
                                GGCT GG     CAATGGAGCG
                                |||| ||     ||||||||||
                                CCGA CC     GTTACCTCGC
                                  _  TCAC__
GAM503  FLJ11577  3'  CGCTCCATTGCACTCCAGCC   47957     T  CATACA
                                GGCT GG     CAATGGAGCG
                                |||| ||     ||||||||||
                                CCGA CC     GTTACCTCGC
                                  _  TCAC__
GAM503  FLJ12476  3'  CGTGTTTTTGTTATACCAAGCC 43269        C   C    TGGA
            A                    TGGCTTGG ATA ACAA    GCG
                                |||||||| ||| ||||    |||
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                                ACCGAACC TAT TGTT    TGC
                                    A  _   TTTG
GAM503  MGC22014 3'  CCATGTTGCCAAGCCA     65111         TAC   A
                                TGGCTTGGCA   ACA TGG
                                ||||||||||   ||| |||
                                ACCGAACCGT   TGT ACC
                                    ____  _
GAM503  PTD004   3'  CTCCATCATGTATGCCAAGCC  26236           CA
                                GGCTTGGCATACA  ATGGAG
                                ||||||||||||  ||||||
                                CCGAACCGTATGT  TACCTC
                                      AC
GAM503  LOC165741 3'  CGCTCCATCACTGGGGCAATCC 88605     CTTG  ATA  CA_
          A                    TGG   GC   CA   ATGGAGCG
                               |||   ||   ||   ||||||||
                               ACC   CG   GT   TACCTCGC
                                 TAA_  GG_  CAC
GAM504  ADCY6    3'  GCAAGTGACTTTCTTTCTT   40955         A   A_
                                AAGAAAGAAA TTAC  GC
                                ||||||||| ||||  ||
                                TTCTTTCTTT AGTG  CG
                                     C   AA
GAM504  BACH2    3'  CAGGCTGACACATTCTTTCT   41778        AATTA
                                AGAAAGAA    CAGCCTG
                                ||||||||    |||||||
                                TCTTTCTT    GTCGGAC
                                    ACACA
GAM504  EPHA1    3'  CAGGAAATGATTTTCTGCCT   19097    AA       CAG
                                AG  AGAAAATTA   CCTG
                                ||  |||||||||   ||||
                                TC  TCTTTTAGT   GGAC
                                 CG       AAA
GAM504  HS2ST1   3'  GCAAATGTGGTTTTCTTTTTT  25330            GCC
                                AAGAAAGAAAATTACA   TGC
                                ||||||||||||||||   |||
                                TTTTTTCTTTTGGTGT   ACG
                                      AA_
GAM504  RDS      3'  CAGGAGTTTTCACTTTCTTTA  6149         __      ACAG
                                TAAAGAAA  GAAAATT    CCTG
                                ||||||||  |||||||    ||||
                                ATTTCTTT  CTTTTGA    GGAC
                                    CA      ____
GAM504  SYT4     3'  GCAGGAGAAATTTTCTTTCTTT 63109           ACAG  _
                                AAAGAAAGAAAATT    CCT GC
                                ||||||||||||||    ||| ||
                                TTTCTTTCTTTTAA    GGA CG
                                      AGA_   A
GAM504  TCL1B    3'  GCAAGCTGTGGGTTCTTTCT   18193        AAT     C
                                AGAAAGAA   TACAGC TGC
                                ||||||||   |||||| |||
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                                TCTTTCTT  GTGTCG ACG
                                    GG_     A
GAM504  TLR5     5'  CAGGCTGACAGTTCTTTCTCA  13779   A      AATTA
                                A AGAAAGAA    CAGCCTG
                                | ||||||||    |||||||
                                A TCTTTCTT    GTCGGAC
                                 C       GACA_
GAM504  UBE4A    3'  GCAAGCTTTTCTTCTTTTTTTA 17733          AATTAC  C
                                TAAAGAAAGAA     AGC TGC
                                ||||||||||     ||| |||
                                ATTTTTTTCTT     TCG ACG
                                      CTTT__  A
GAM504  UGDH     3'  TTGTAATTTTTTTCTTTA    14007          A
                                TAAAGAAAGAAA TTACAG
                                |||||||||||| ||||||
                                ATTTCTTTTTTT AATGTT
                                          _
GAM504  AKR1B10  3'  CAGGAGATTCTCTTTCTT    40078        A   ACAG
                                AAGAAAGA AATT   CCTG
                                |||||||| ||||   ||||
                                TTCTTTCT TTAG   GGAC
                                    C   A___
GAM504  DKFZP434L0117 3'  CAGGCTGTCCACCTTTCTT   43240       AAAATT
                                AAGAAAG     ACAGCCTG
                                |||||||     ||||||||
                                TTCTTTC     TGTCGGAC
                                    CACC__
GAM504  FLJ20309 3'  GCAGGCTGTAACTTCTCTC   35406   A   AA
                                GA AGAA  TTACAGCCTGC
                                || ||||  ||||||||||
                                CT TCTT  AATGTCGGACG
                                 C   C_
GAM504  FLJ22313 3'  AGGTGTTTTTTTTCTTTA    42576          TACA
                                TAAAGAAAGAAAAT   GCCT
                                ||||||||||||||   ||||
                                ATTTCTTTTTTTTG   TGGA
                                          _____
GAM504  FLJ22557 3'  GCAGACTGTATGAGGTCTTTTT 45582         AAAT_   C
           TTA                   TAAAGAAAGA    TACAG CTGC
                                ||||||||||    ||||| ||||
                                ATTTTTTTCT    ATGTC GACG
                                      GGAGT    A
GAM504  FLJ25438 3'  GCAGGCTGTCCACCCTCTTCT  59122     A  AAATT_
                                AGAA GA     ACAGCCTGC
                                |||| ||     |||||||||
                                TCTT CT     TGTCGGACG
                                  _ CCCACC
GAM504  HTATIP2  3'  CTGTAATTTTCTTTGTTTA   22166     G
                                TAAA AAAGAAAATTACAG
                                |||| ||||||||||||||
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                                ATTT TTTCTTTTAATGTC
                                  G
GAM504  KIAA0779  3'  AGGGTGCTTTTTTTCTTTA   86906          ATTA  G
                                TAAAGAAAGAAA   CA CCT
                                ||||||||||||   || |||
                                ATTTCTTTTTTT   GT GGA
                                      C___  G
GAM504  KIAA0979  3'  GCAGGTCTTTTTTTTTCTT   31140          TTACA
                                AAGAAAGAAAA    GCCTGC
                                ||||||||||    ||||||
                                TTCTTTTTTTT    TGGACG
                                      TC___
GAM504  KIAA1924  3'  GCAGGCTGTGGCCTTCTCTC  74047    A   AA
                                GA AGAA  TTACAGCCTGC
                                || ||||  ||||||||||
                                CT TCTT  GGTGTCGGACG
                                 C   CC
GAM504  MGC11034  3'  CAGGCTGTCGGTCTCCTCTCA 49570   A  A_  AAATT
                                A AGA  AGA    ACAGCCTG
                                | |||  |||    ||||||||
                                A TCT  TCT    TGTCGGAC
                                 C  CC  GGC__
GAM504  PCSK7    3'  CAGGCTGTGACTCTTCTCTC  17520    A   AA_
                                GA AGAA   TTACAGCCTG
                                || ||||   ||||||||||
                                CT TCTT   AGTGTCGGAC
                                 C   CTC
GAM504  PRO0246  5'  GCAGAACATAATCTCTTTCTTT 26959         AA   CAGC
           A                     TAAAGAAAGA  ATTA   CTGC
                                ||||||||||  ||||   ||||
                                ATTTCTTTCT  TAAT   GACG
                                      C_   ACAA
GAM504  RHOBTB3  3'  CAGACTGATAGTTTCTTTCTTT 30423          ATTA  C
                                AAAGAAAGAAA   CAG CTG
                                ||||||||||   ||| |||
                                TTTCTTTCTTT   GTC GAC
                                      GATA  A
GAM504  RICH1    3'  GCAGGCGAACCTCTTTCTTTG  36481         AAATTACA
                                TAAAGAAAGA      GCCTGC
                                ||||||||||      ||||||
                                GTTTCTTTCT      CGGACG
                                      CCAAG___
GAM504  Rpo1-2   3'  GCAAGCTGTAATGTAATTTT  39223     GAAA      C
                                GAAA   ATTACAGC TGC
                                ||||   |||||||| |||
                                TTTT   TAATGTCG ACG
                                  AATG      A
GAM504  Rpo1-2   3'  GCAGCTGTAATGTAATTTT   39224     GAAA      C
                                GAAA   ATTACAGC TGC
                                ||||   |||||||| |||
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                                TTTT    TAATGTCG ACG
                                  AATG       A
GAM504   TOB2     3'  GCAGGGTCATGAACTTTTTTCT 33238          AA   CA   _
             TTA                    TAAAGAAAGAA  TTA  GCC TGC
                                    ||||||||||  |||  ||| |||
                                    ATTTCTTTTTT  AGT  TGG ACG
                                          CA   AC   G
GAM504   WBP11    5'  GCAGAAGTGTTTTTCTTTTTTT 33315           T   AGC
             A                      TAAAGAAAGAAAA TAC   CTGC
                                    ||||||||||||| |||   ||||
                                    ATTTTTTTCTTTT GTG   GACG
                                            T   AA_
GAM504   ZFP106   3'  GCAAATAGTTTTCTTTCTT    42728           CA_
                                    AAGAAAGAAAATTA   GC
                                    ||||||||||||||   ||
                                    TTCTTTCTTTTGAT   CG
                                            AAA
GAM504   LOC112885 3'  TGTAGTTTTCCTTCTTTA     57343        A
                                    TAAAGAA GAAAATTACA
                                    |||||||  ||||||||||
                                    ATTTCTT CTTTTGATGT
                                         C
GAM504   LOC143914 5'  GCTTATAATTTTCTTTTTT    77111           C_
                                    AAGAAAGAAAATTA  AGC
                                    ||||||||||||||  |||
                                    TTTTTTCTTTTAAT  TCG
                                            AT
GAM504   LOC150605 5'  GCAAGCTGCTTCTCTTTTTT   86262        A  TTA    C
                                    AAGAAAGA AA   CAGC TGC
                                    ||||||||  ||   ||||  |||
                                    TTTTTTCT TT   GTCG ACG
                                         C  C__    A
GAM504   LOC151778 5'  CAGGCTGTGGCCATCTTC     71946     A  AAA
                                    GAA GA   TTACAGCCTG
                                    |||  ||   ||||||||||
                                    CTT CT   GGTGTCGGAC
                                      _  ACC
GAM504   LOC155340 5'  CAGGCTGTGGCCATCTTC     73768     A  AAA
                                    GAA GA   TTACAGCCTG
                                    |||  ||   ||||||||||
                                    CTT CT   GGTGTCGGAC
                                      _  ACC
GAM504   LOC161784 3'  GCCATTATTTTCTTTCTTTA   83172           TACA
                                    TAAAGAAAGAAAAT    GC
                                    ||||||||||||||    ||
                                    ATTTCTTTCTTTTA    CG
                                            TTAC
GAM504   LOC168346 5'  GCACTGGAATTTCTCTTTCTT  83578        _    A   CC
                                    AAGAAAGA AAATT CAG  TGC
                                    ||||||||  |||||  |||  |||
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                                TTCTTTCT TTTAA GTC  ACG
                                    C    G  __
GAM504  LOC255229 3'  GCCATTATTTTCTTTCTTTA  97171          TACA
                                TAAAGAAAGAAAAT   GC
                                ||||||||||||||  ||
                                ATTTCTTTCTTTTA   CG
                                      TTAC
GAM504  LOC255620 5'  CAGGCTGTGGCCATCTTC   98872    A  AAA
                                GAA GA   TTACAGCCTG
                                ||| ||  ||||||||||
                                CTT CT   GGTGTCGGAC
                                  _ ACC
GAM505  FLJ21438  5'  CAAAACGCTTCCCCCCATCCCA 62190      GAGATTATC
                                TGGGA       AAGCGTTTTG
                                |||||       ||||||||||
                                ACCCT       TTCGCAAAAC
                                   ACCCCCC__
GAM505  FLJ32334  3'  AAAACGCTATTCCTTCCCA   58605      A  TTATCA
                                TGGGAG GA     AGCGTTTT
                                |||||| ||     ||||||||
                                ACCCTT CT     TCGCAAAA
                                   C  TA____
GAM505  HHLA2    3'  CAATGTACTTTGTAATCTCCCC 23953     A      C   CG T
           CA                     TGGG GAGATTAT AAG  T TTG
                                |||| |||||||| |||  | |||
                                ACCC CTCTAATG TTC  G AAC
                                  C       T   AT T
GAM506  ADAT1    3'  CCAGCAAAGAATGAAGGC    24914    __       C
                                GTC  CATTCTTTGC GG
                                |||  |||||||||| ||
                                CGG  GTAAGAAACG CC
                                  AA        A
GAM506  M17S2    5'  CCGGTAGCGGACGGTCCTT   20910         ATTCT
                                AAGGACCGTCC    TTGCCGG
                                ||||||||||    |||||||
                                TTCCTGGCAGG    GATGGCC
                                      C_____
GAM506  ST14     5'  CCGGCAGGGACGACGCCT    42042    AC   CAT
                                AGG  CGTC   TCTTTGCCGG
                                |||  ||||   ||||||||||
                                TCC  GCAG   AGGGACGGCC
                                  __   C__
GAM506  HTGN29   5'  GCCAACTGTGTGGCGGTCC   39885       _  TC  T
                                GGACCGTC CAT  TT GC
                                |||||||| |||  || ||
                                CCTGGCGG GTG  AA CG
                                     T   TC  C
GAM506  PMAIP1   3'  GCAAGAATGGAAGACCCTT   41211     ACCG       T
                                AAGG    TCCATTCTT GC
                                ||||    ||||||||| ||
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                                TTCC    AGGTAAGAA CG
                                  CAGA       _
GAM506  LOC144278 3'  GCCAGCAAAGACTGCTCGATGG 77274          ___ T      C
            TCCT                   AGGACCGTC   CA TCTTTGC GGC
                                |||||||||   || ||||||| |||
                                TCCTGGTAG   GT AGAAACG CCG
                                     CTC  C      A
GAM506  LOC147976 3'  CCGGTGAATGAAGACCCT    79287     ACC   CA  _  TG
                                AGG   GTC  TTC TT  CCGG
                                |||   |||  ||| ||  ||||
                                TCC   CAG  AAG AA  GGCC
                                  ___   __   T  GT
GAM506  LOC254263 5'  GCCGGCAGCGGACGCGCC    96367    AC     ATTCT
                                GG  CGTCC    TTGCCGGC
                                ||  |||||    ||||||||
                                CC  GCAGG    GACGGCCG
                                 GC    C____
GAM507  B4GALT6   3'  ACAACCATATTGTTTATGCATA 60554     A    TTAT
                                TAT CATA    GTATGGTTGT
                                |||  ||||    ||||||||||
                                ATA GTAT    TATACCAACA
                                  C    TTGT
GAM507  BTAF1     3'  CAAACATACATGAATATGCATA 72870     A    _       G
                                TAT CATAT TATGTATG TTG
                                |||  ||||| |||||||| |||
                                ATA GTATA GTACATAC AAC
                                  C    A       A
GAM507  PDGFRA    3'  TTATACATCAATATGTATA    21697          _
                                TATACATATT ATGTATGG
                                |||||||||| ||||||||
                                ATATGTATAA TACATATT
                                      C
GAM507  SNAI2     3'  CAACCAAATAATATGTATA    13239           GTA
                                TATACATATTAT   TGGTTG
                                ||||||||||||   ||||||
                                ATATGTATAATA   ACCAAC
                                       A__
GAM507  KIAA1321  3'  TTATACATAATATATATA     62905      C
                                TATA ATATTATGTATGG
                                ||||  ||||||||||||
                                ATAT TATAATACATATT
                                  A
GAM507  KIAA1354  3'  CATACATACATATGTATA     61573          _
                                TATACATAT TATGTATG
                                |||||||||  ||||||||
                                ATATGTATA ATACATAC
                                      C
GAM507  PPIL4     3'  TACAAAAATACATAAACGTATA 58222       ATA       GG
                                TATAC   TTATGTAT  TTGTA
                                |||||   |||||||||  |||||
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                                ATATG   AATACATA  AACAT
                                   CA_       AA
GAM507  TRIM5    3'  ACCACATAAATATGTATA    53458         A   A
                                TATACATATT TGT TGGT
                                |||||||||| ||| ||||
                                ATATGTATAA ATA ACCA
                                      _  C
GAM507  TRIM5    3'  ACCACATAAATATGTATA    53536         A   A
                                TATACATATT TGT TGGT
                                |||||||||| ||| ||||
                                ATATGTATAA ATA ACCA
                                      _  C
GAM507  ZNF338   3'  ATTTTCTACATAATATG     42252         T  TT
                                CATATTATGTA GG  GT
                                |||||||||| ||  ||
                                GTATAATACAT CT  TA
                                      _ TT
GAM507  LOC153454 3'  TACACACATATATATGTATA   81695        TAT    GT
                                TATACATAT   GTATG  TGTA
                                |||||||||   |||||  ||||
                                ATATGTATA   TATAC  ACAT
                                      ___     AC
GAM507  LOC153577 5'  ACATCTATACATAATATGCATA 87234     A          T
                                TAT CATATTATGTATGG TGT
                                ||| |||||||||||||| |||
                                ATA GTATAATACATATC ACA
                                  C           T
GAM507  LOC154215 3'  CCATACATACATGTATA     81955       AT
                                TATACAT  TATGTATGG
                                |||||||  |||||||||
                                ATATGTA  ATACATACC
                                    C_
GAM507  LOC196411 3'  CATACACATATATGTATA    89043        TA_
                                TATACATAT   TGTATG
                                |||||||||   ||||||
                                ATATGTATA   ACATAC
                                      TAC
GAM508  HIVEP3   5'  CAAAAAACTCCCAAAGCCGTCT 44699     G   GTAC      C
           T                     AAGA GGT    GGGAGTTT TTG
                                |||| |||    |||||||| |||
                                TTCT CCG    CCCTCAAA AAC
                                  G   AAA_       A
GAM508  IL2RB    3'  GAGCTCCCTCACACCCCCT    7939     A     AC
                                AG GGGTGT  GGGAGTTT
                                || ||||||  ||||||||
                                TC CCCACA  CCCTCGAG
                                 C     CT
GAM508  KIT      3'  CAAAAAACTCCCCTTCCTC    5847       TGTAC      C
                                GAGGG    GGGAGTTT TTG
                                |||||    |||||||| |||
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                                CTCCT    CCCTCAAA AAC
                                  TC___      A
GAM508  BTBD3    3'  AAGCGTTCCACCACCCTCT   31025       TAC   _
                                AGAGGGTG   GGGA GTTT
                                ||||||||   |||| ||||
                                TCTCCCAC   CCTT CGAA
                                    CA_    G
GAM508  CLIPR-59 3'  AAGAAACCCCCAGTGCCTT   32011     TG AC   A
                                AGGG  T  GGG GTTTCTT
                                ||||  |  ||| |||||||
                                TTCC  G  CCC CAAAGAA
                                  GT A_   C
GAM508  FLJ14966 3'  CAAGTGCACCACACACCCTC   52833       ACG  A  TT
                                GAGGGTGT   GG GT  CTTG
                                ||||||||   || ||  ||||
                                CTCCCACA   CC CG  GAAC
                                    CA_  A  T_
GAM508  KIAA0759 3'  CAAGAAACTTACATCCCCTC   67883     TG ACGG
                                GAGGG  T   GAGTTTCTTG
                                |||||  |   ||||||||||
                                CTCCC  A   TTCAAAGAAC
                                  CT CA__
GAM508  PRO2325  5'  CAAAAAACTTTTCACACCACCT 38188    AG    AC      C
          T                      AAG  GGTGT  GGGAGTTT TTG
                                 |||  |||||  |||||||| |||
                                 TTC  CCACA  TTTTCAAA AAC
                                   CA    C_      A
GAM508  RALGPS1A 3'  AGACCCCACACGCCCTCT    28327       AC   A
                                AGAGGGTGT  GGG GTTT
                                |||||||||  ||| ||||
                                TCTCCCGCA  CCC CAGA
                                    CA   _
GAM508  LOC149267 3'  AAGAAACCCCCGGGACTTT   57472     GTA   A
                                AGGGT   CGGG GTTTCTT
                                |||||   |||| |||||||
                                TTTCA   GCCC CAAAGAA
                                  GG_    C
GAM508  LOC151171 5'  CAAGAAACCCCCCGCAGCAGACT 80944   GG   A_   A
                                AG  TGT  CGGG GTTTCTTG
                                ||  |||  |||| ||||||||
                                TC  ACG  GCCC CAAAGAAC
                                 AG   AC    C
GAM508  LOC152485 3'  AAGACCACACACCCTTT     81488       ACG  AGTT
                                AGAGGGTGT   GG    TCTT
                                |||||||||   ||    ||||
                                TTTCCCACA   CC    AGAA
                                    CA_  _____
GAM508  LOC153811 3'  AAGCTTCGACACACCCTC    81818       ACG
                                GAGGGTGT   GGAGTTT
                                ||||||||   |||||||
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                                CTCCCACA  CTTCGAA
                                    CAG
GAM508  LOC158856 5'  AGGCCCCCACACCCCTC    88289      _  AC  A
                                GAGGG TGT  GGG GTTT
                                ||||| |||  ||| ||||
                                CTCCC ACA  CCC CGGA
                                   C  C_  _
GAM508  LOC163915 5'  AGACCCCCACACCCTCT    88421        AC  A
                                AGAGGGTGT  GGG GTTT
                                |||||||||  ||| ||||
                                TCTCCCACA  CCC CAGA
                                    C_  _
GAM508  LOC203504 5'  AGGCTCCCACACCCCTC    92317      _  AC
                                GAGGG TGT  GGGAGTTT
                                ||||| |||  ||||||||
                                CTCCC ACA  CCCTCGGA
                                   C  __
GAM508  LOC255215 3'  GGGCTCCCCACACCCTCT    98667        AC
                                AGAGGGTGT  GGGAGTTT
                                |||||||||  ||||||||
                                TCTCCCACA  CCCTCGGG
                                    C_
GAM509  AVPR1A   5'  CTGCGAGTCTCCCAGCTCCA   7380        AA   A__
                                TGGAGCTG  AGAC   CAG
                                ||||||||  ||||   |||
                                ACCTCGAC  TCTG   GTC
                                    CC    AGC
GAM509  CDC34    3'  CGGTCCTGCCTGTCAGCTCCA  16389        A  ACA   AC
                                TGGAGCTGA AG   CAG  GCCG
                                ||||||||| ||   |||  ||||
                                ACCTCGACT TC   GTC  TGGC
                                    G  C__   C_
GAM509  EGR1     5'  CGGTGTCCCCTGCAGCTCCA   10490        AAAGACACA
                                TGGAGCTG       GACGCCG
                                ||||||||       |||||||
                                ACCTCGAC       CTGTGGC
                                    GTCCC____
GAM509  FGFR2    3'  CGGCAAGAGTCCTTCAGCTCC  43673        A   ACAGAC
                                GGAGCTGAA GAC     GCCG
                                ||||||||| |||     ||||
                                CCTCGACTT CTG     CGGC
                                    C  AGAA__
GAM509  LENG4    3'  TTGTGTCTTTCGCTCCA     44424       T
                                TGGAGC GAAAGACACAG
                                |||||| ||||||||||
                                ACCTCG CTTTCTGTGTT
                                   _
GAM509  MMP14    3'  TTTGTGTCTGTCCAGCCCCA   18433     A   AA_
                                TGG GCTG   AGACACAGA
                                ||| ||||   |||||||||
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                                ACC CGAC   TCTGTGTTT
                                  C    CTG
GAM509  NAP1L3   5'  CGGCCTCTGCATCCCCAGCTCC 16997        AAA  CA    C
             A                   TGGAGCTG   GA  CAGA GCCG
                                 |||||||||   ||  |||| |||||
                                 ACCTCGAC   CT  GTCT CGGC
                                     CC_  AC    C
GAM509  PTGS2    5'  GCGCCTCCTTCAGCTCCA    8247          A  CACA A
                                 TGGAGCTGAA GA    G CGC
                                 ||||||||||| ||    | |||
                                 ACCTCGACTT CT    C GCG
                                      C  ____ C
GAM509  PYCR1    5'  GGCGTCACCATCAGCTCCA   70643         AAGACACA
                                 TGGAGCTGA       GACGCC
                                 |||||||||       ||||||
                                 ACCTCGACT       CTGCGG
                                     ACCA____
GAM509  RCV1     5'  GCATCTCGGTCTTCAGCTC   12803        A   AC   C
                                 GAGCTGAA GAC  AGA GC
                                 |||||||| |||  ||| ||
                                 CTCGACTT CTG  TCT CG
                                     _   GC   A
GAM509  TCEA1    5'  CTGTGTCTTCCGCTCCA     81280       T   A
                                 TGGAGC GAA GACACAG
                                 |||||| ||| |||||||
                                 ACCTCG CTT CTGTGTC
                                    C   _
GAM509  TPTE     5'  CGGCGCCTACACTTAGCTCC   26164        AAGACAC  A
                                 GGAGCTGA      AG CGCCG
                                 ||||||||      || |||||
                                 CCTCGATT      TC GCGGC
                                     CACA___  C
GAM509  WDR1     5'  CGGTGCCGCCTTCCGGCTCCA  34405        A   ACACAGA
                                 TGGAGCTG AAG      CGCCG
                                 |||||||| |||      |||||
                                 ACCTCGGC TTC      GTGGC
                                     C   CGCC___
GAM509  WDR1     5'  CGGTGCCGCCTTCCGGCTCCA  18847        A   ACACAGA
                                 TGGAGCTG AAG      CGCCG
                                 |||||||| |||      |||||
                                 ACCTCGGC TTC      GTGGC
                                     C   CGCC___
GAM509  XT3      3'  TCTCATCTTCCAGCTTCA    39920         A    CAC
                                 TGGAGCTG AAGA   AGA
                                 |||||||| ||||   |||
                                 ACTTCGAC TTCT   TCT
                                     C    AC_
GAM509  DKFZP586M0122 3'  CGGCACCATCTGCCCAGCTCCA 31859         AA_   CACAGAC
                                 TGGAGCTG   AGA      GCCG
                                 ||||||||   |||      ||||
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                                ACCTCGAC  TCT     CGGC
                                    CCG  ACCA___
GAM509  FLJ10718  3'  CTGTGCCTTTCAGCCACA   37028   GA      A
                                TG  GCTGAAAG CACAG
                                ||  |||||||| |||||
                                AC  CGACTTTC GTGTC
                                 AC       C
GAM509  FLJ11151  3'  CTGTGTTTCTCAACTCCA   68476     C   A
                                TGGAG TGA AGACACAG
                                ||||| ||| ||||||||
                                ACCTC ACT TTTGTGTC
                                   A  C
GAM509  FLJ14466  3'  CTGTTCTCCCAGCTCCA    52428       AA  C
                                TGGAGCTG  AGA ACAG
                                ||||||||  ||| ||||
                                ACCTCGAC  TCT TGTC
                                    CC  _
GAM509  FLJ20374  5'  GGCGTCTGCGCTGCTCC    35552     TGAA  ACA
                                GGAGC   AG   CAGACGCC
                                |||||   ||  ||||||||
                                CCTCG   TC   GTCTGCGG
                                   _____ GC_
GAM509  HSPC142   3'  CTGTGTCTCCCAGCCCA    27186    A   AA
                                TGG GCTG  AGACACAG
                                ||| ||||  ||||||||
                                ACC CGAC  TCTGTGTC
                                  _   CC
GAM509  KIAA0556  3'  CGGCACCTCTGCTCAGCTCC  69647       AAGACA   C__
                                GGAGCTGA    CAGA   GCCG
                                ||||||||    ||||  ||||
                                CCTCGACT    GTCT   CGGC
                                    C_____   CCA
GAM509  KIAA0757  3'  CGGCCTCGCCCCTTCCAGCTCC 21257       A   ACACA  C
          A                    TGGAGCTG AAG    GA GCCG
                               |||||||| |||    || ||||
                               ACCTCGAC TTC    CT CGGC
                                    C  CCCG_  C
GAM509  KIAA1036  3'  GGACTGTCTTTCAGCTCC    30494          CAGACG
                                GGAGCTGAAAGACA    CC
                                ||||||||||||||    ||
                                CCTCGACTTTCTGT    GG
                                       CA____
GAM509  KIAA1364  3'  CTGACATGTCCCCAGCTCCA  64347       AAA   ___
                                TGGAGCTG   GACA   CAG
                                ||||||||   ||||   |||
                                ACCTCGAC   CTGT   GTC
                                    CC_    ACA
GAM509  KIAA1952  5'  CGGCGCCTGTGGGATCCAGTTC 73543       AAAGA    A
          CA                   TGGAGCTG    CACAG CGCCG
                               ||||||||    ||||| |||||
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                                ACCTTGAC    GTGTC GCGGC
                                    CTAGG    C
GAM509  MGC2963   5'  CGGCGCCGTGTTCCAGCTCC  49339       AAA    AGA
                                GGAGCTG  GACAC  CGCCG
                                |||||||  |||||  |||||
                                CCTCGAC  TTGTG  GCGGC
                                   C__    CC_
GAM509  NCKX3     3'  GTGACTTTTCCAGCTCCA    40726       __   A
                                TGGAGCTG  AAAG CAC
                                ||||||||  |||| |||
                                ACCTCGAC  TTTC GTG
                                    CT    A
GAM509  SERF1B    3'  TGGCGCCATCTCAGCTCCA   43707        AA  CACAGA
                                TGGAGCTGA  GA     CGCCG
                                |||||||||  ||     |||||
                                ACCTCGACT  CT     GCGGT
                                    __  ACC___
GAM509  SSAT2     5'  CGGCGCCGGAATCCCAGCTCCA 56858       AAA  CACAGA
                                TGGAGCTG   GA     CGCCG
                                ||||||||   ||     |||||
                                ACCTCGAC   CT     GCGGC
                                    C__  AAGGCC
GAM509  LOC148181 3'  CGTCTTTGGACTCAGCTCC   79432       AAGA  C
                                GGAGCTGA    CA AGACG
                                ||||||||    || |||||
                                CCTCGACT    GT TCTGC
                                    CAG_  T
GAM509  LOC162083 5'  GCATCCTGTCCAGCGCCA    83206     A   AAA    CA  C
                                TGG GCTG   GACA  GA GC
                                ||| ||||   ||||  || ||
                                ACC CGAC   CTGT  CT CG
                                  G   ___    C_  A
GAM509  LOC196214 5'  GCGTCTGTGTCCCTGCCC    91179    A  TGAAA
                                GG GC     GACACAGACGC
                                || ||     ||||||||||
                                CC CG     CTGTGTCTGCG
                                 _  TCC__
GAM509  LOC196472 5'  CTGTGCTCCTGACAGCTCCA   89059       AA  A__
                                TGGAGCTG  AG   CACAG
                                ||||||||  ||   |||||
                                ACCTCGAC  TC   GTGTC
                                    AG  CTC
GAM509  LOC200609 5'  GCGTCTGTGTTGCTACA     91666    G   TGAAA
                                TG AGC     GACACAGACGC
                                || |||     ||||||||||
                                AC TCG     TTGTGTCTGCG
                                 A  _____
GAM509  LOC201973 3'  GCATTTAATATTTCAGCTCCA  90575          GACAC   C
                                TGGAGCTGAAA     AGA GC
                                ||||||||||     ||| ||
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                                ACCTCGACTTT    TTT CG
                                     ATAA_  A
GAM509  LOC222057 3'  CGTCTTTGGACTCAGCTCC   94351       AAGA  C
                                GGAGCTGA   CA AGACG
                                ||||||||   || |||||
                                CCTCGACT   GT TCTGC
                                    CAG_  T
GAM509  LOC255671 3'  TCGTTCTCCCAGCTCCA    99078       AA  C  A
                                TGGAGCTG  AGA AC GA
                                ||||||||  ||| || ||
                                ACCTCGAC  TCT TG CT
                                    CC  _ _
GAM509  LOC92080  3'  GCATCCTGTCCCAGCTTCA   68631       AAA   CA  C
                                TGGAGCTG   GACA  GA GC
                                ||||||||   ||||  || ||
                                ACTTCGAC   CTGT  CT CG
                                    C__    C_  A
GAM510  AKAP1    3'  ACTATGGGTTCTCTTCGCAAA  14472     A  CTT      C
                                TTTGT GA   GGAACCCA AGT
                                ||||| ||   |||||||| |||
                                AAACG CT   TCTTGGGT TCA
                                   _ TC_      A
GAM510  AKAP1    3'  ACTATGGGTTCTCTTCGCAAA  58373     A  CTT      C
                                TTTGT GA   GGAACCCA AGT
                                ||||| ||   |||||||| |||
                                AAACG CT   TCTTGGGT TCA
                                   _ TC_      A
GAM510  EGF      3'  ACTATAGGTTTTGGTTCCACAA 10488     A  C TG    CAC
                                TTGT GA T  GAACC   AGT
                                |||| || |  |||||   |||
                                AACA CT G  TTTGG   TCA
                                  C  T GT    ATA
GAM510  EZH1     3'  GACTGTGGGTTCCAAATTAC   10551     AC
                                GTAG  TTGGAACCCACAGTC
                                ||||  ||||||||||||||
                                CATT  AACCTTGGGTGTCAG
                                  A_
GAM510  STAC     3'  GACTGTGGAGTAATAGCCACAA 13427     AGA  TGGA  _
          A                      TTTGT   CT    AC CCACAGTC
                                |||||   ||    || ||||||||
                                AAACA   GA    TG GGTGTCAG
                                   CC_  TAA_  A
GAM510  CCR1     3'  GACTGTGGGCTCCATTC     8927     CT   A
                                GA  TGGA CCCACAGTC
                                ||  |||| |||||||||
                                CT  ACCT GGGTGTCAG
                                 T_    C
GAM510  FLJ10483 3'  GACTGTGGAAGAGATTACAAA  36652       A   GGAAC
                                TTTGTAG CTT    CCACAGTC
                                |||||||  |||    ||||||||
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                                AAACATT GAG    GGTGTCAG
                                   A  AA___
GAM510  KIAA1871  3'  ACTGTAAGAGTCTACAAA   61890         GGAACCC
                                TTTGTAGACTT     ACAGT
                                ||||||||||      |||||
                                AAACATCTGAG     TGTCA
                                      AA_____
GAM510  LOC150821 3'  GGGTTCCACATCCACAAA   60944      A  CT
                                TTTGT GA  TGGAACCC
                                ||||| ||  ||||||||
                                AAACA CT  ACCTTGGG
                                   C  AC
GAM510  LOC151057 3'  ACTGTGGGTACACCTATAAA  86379       ACT  GA
                                TTTGTAG   TG  ACCCACAGT
                                |||||||   ||  |||||||||
                                AAATATC   AC  TGGGTGTCA
                                   C__  A_
GAM510  LOC157507 5'  ACTGTAAAAGTCTGCAAA   82377         GGAACCC
                                TTTGTAGACTT     ACAGT
                                ||||||||||      |||||
                                AAACGTCTGAA     TGTCA
                                      AA_____
GAM510  LOC203339 5'  GGATTCCCAGTCTACAAA   92214         T   C
                                TTTGTAGACT GGAA CC
                                |||||||||| |||| ||
                                AAACATCTGA CCTT GG
                                      C   A
GAM510  LOC51030  3'  ACTGTAAATTAAACCAATCTAC 32695       C   AACCC___
           AAA                    TTTGTAGA TTGG      ACAGT
                                |||||||| ||||       |||||
                                AAACATCT AACC       TGTCA
                                   _   AAATTAAA
GAM510  LOC90906  3'  GACTGTGGATCCCAAACTTTGC 64951      C_   AAC
           A                     TGTAGA  TTGG   CCACAGTC
                                ||||||  ||||   ||||||||
                                ACGTTT  AACC   GGTGTCAG
                                   CA   CTA
GAM511  NR2E1    5'  CAAGCAGCATTCCCAGCAGCT  13792        A  CTG   A
                                AGCTGCTGG GG   GCT CTTG
                                |||||||| ||   ||| ||||
                                TCGACGACC CT   CGA GAAC
                                      _ TA_   C
GAM511  STK13    5'  AGCCCAGCAGCCCAGCAGC   13467        AG_   _
                                GCTGCTGG   GCTGG CT
                                ||||||||   ||||| ||
                                CGACGACC   CGACC GA
                                      CGA    C
GAM511  DKFZp761K1423 5'  CAAGCAGCAGCTCTCCAGCATC 37937     C      _   G  A
           TC                     GAG TGCTGGAG GCTG CT CTTG
                                ||| |||||||| |||| || ||||
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                                CTC ACGACCTC CGAC GA GAAC
                                  T       T    _ C
GAM511  FLJ10597  3'  GGCCTCGCCTCCAGCAGC    36837           T_
                                GCTGCTGGAGGC  GGCT
                                ||||||||||||  ||||
                                CGACGACCTCCG  CCGG
                                      CT
GAM511  KIAA0217  3'  CAAGTAACCAGCTTCTCACTC  67597     C  CT       C
                                GAG TG  GGAGGCTGG TACTTG
                                ||| ||  |||||||||| ||||||
                                CTC AC  TCTTCGACC ATGAAC
                                  _ __        A
GAM511  RNF8      3'  AAGTAAACACCAGCAGCTC    15551           AGGC  GC
                                GAGCTGCTGG    TG  TACTT
                                ||||||||||    ||  |||||
                                CTCGACGACC    AC  ATGAA
                                      _____ AA
GAM511  TIEG      5'  CAAGCAGCCAGCAGCCTAGCAG 20169    A     _  AG      A
              CC                  G GCTGCT GG  GCTGGCT CTTG
                                | ||||||  ||  |||||||  ||||
                                C CGACGA CC  CGACCGA GAAC
                                _     T  GA      C
GAM511  LOC145990 3'  CAAGCAGCCAGCCATCATGC   78056    _  GA       A
                                GC TG  GGCTGGCT CTTG
                                || ||  ||||||||  ||||
                                CG AC  CCGACCGA GAAC
                                 T  TA       C
GAM511  LOC152282 3'  AGTAGCAGCTCCAGCAGC    81393           G   G
                                GCTGCTGGAG CTG CTACT
                                ||||||||||  |||  |||||
                                CGACGACCTC GAC GATGA
                                      _  _
GAM511  LOC152282 3'  AGTAGCAGCTCCAGCAGC    81394           G   G
                                GCTGCTGGAG CTG CTACT
                                ||||||||||  |||  |||||
                                CGACGACCTC GAC GATGA
                                      _  _
GAM511  LOC159090 5'  GCCAGTCCCCAGCAGCTC    82963           A
                                GAGCTGCTGG GGCTGGC
                                ||||||||||  |||||||
                                CTCGACGACC CTGACCG
                                      C
GAM511  LOC163782 5'  CAAGCAGCCAGCCTCCAAGCTC 83033       GC          A
                                GAGCT  TGGAGGCTGGCT CTTG
                                |||||  ||||||||||||  ||||
                                CTCGA  ACCTCCGACCGA GAAC
                                   __          C
GAM511  LOC200014 5'  AGCTTCAGCCCCAGCAGCTC   89917           A    __
                                GAGCTGCTGG GGCTG  GCT
                                ||||||||||  |||||  |||
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                                CTCGACGACC CCGAC  CGA
                                      _    TT
GAM511  LOC90459  5'  CAAGTGTCCGGCTCCAGCAACT 63549    C      G   C
            C                    GAG TGCTGGAG CTGG TACTTG
                                 ||| |||||||| |||| ||||||
                                 CTC ACGACCTC GGCC GTGAAC
                                   A      _   T
GAM512  BAT1     5'  CCATCCAGATCCCCCTTCCC   17349          CCTG   TT
                                 GGGAAGGGGGA   CTG  TGG
                                 ||||||||||    |||  |||
                                 CCCTTCCCCCT   GAC  ACC
                                       A___   CT
GAM512  CCNG1    5'  CCAGGACAGTCCCCCTCCC   15772     A     CTGC   _
                                 GGGA GGGGGAC   TGTT TGG
                                 |||| |||||||   |||| |||
                                 CCCT CCCCCTG   ACAG ACC
                                   _     _____   G
GAM512  CD34     3'  ACACAGGACCCCCTTCCC    10103          A   C
                                 GGGAAGGGGG CCTG TGT
                                 |||||||||| |||| |||
                                 CCCTTCCCCC GGAC ACA
                                       A   _
GAM512  CDH23    3'  GCCAAACAGGCCCTCCTCCCTC 42356     A     CCTG
            CC                     GGGA GGGGGA   CTGTTTGGC
                                   |||| ||||||   |||||||||
                                   CCCT CCTCCT   GACAAACCG
                                     C     CCCG
GAM512  CFL1     3'  GCCAAACAGACCCCCCACCCC  19746    AA    ACCTG
                                 GGG  GGGGG    CTGTTTGGC
                                 |||  |||||    |||||||||
                                 CCC  CCCCC    GACAAACCG
                                   CA    CA___
GAM512  ITGA6    5'  GCCGCTGCAGGTCCCCGCTCCC 5790      AG        T  TT
                                 GGGA  GGGGACCTGC GT  GGC
                                 ||||  |||||||||| ||  |||
                                 CCCT  CCCCTGGACG CG  CCG
                                   CG        T __
GAM512  LMO4     5'  GCCAGCCCAGGCGCCCCTTCCC 23184         GA   CT   T
                                 GGGAAGGGG  CCTG  GTT GGC
                                 |||||||||  ||||  ||| |||
                                 CCCTTCCCC  GGAC  CGA CCG
                                       GC    C_  _
GAM512  RASGRP2  5'  GCTCCCCACAGGTCCCTCTCCC 20630      A        C  TTT
                                 GGGA GGGGGACCTG TG   GGC
                                 |||| |||||||||| ||   |||
                                 CCCT CTCCCTGGAC AC   TCG
                                   _        _ CCC
GAM512  SLC39A1  3'  GCCAAACAAATCCCCTTCCT   27810          ACCTGC
                                 GGGAAGGGGG     TGTTTGGC
                                 ||||||||||     ||||||||
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                                TCCTTCCCCT     ACAAACCG
                                      AA____
GAM512  SORD     3'  GCCAAGTGAAGGACCCCCTCCC 13301      A    A   GC GT
                                GGGA GGGGG CCT  T  TTGGC
                                |||| ||||| |||  |  ||||||
                                CCCT CCCCC GGA  G  AACCG
                                  _    A   A_ TG
GAM512  WNT5A    3'  CAAACCTCCCTTCCC       14115          ACCTGCT
                                GGGAAGGGGGG      GTTTG
                                ||||||||||       |||||
                                CCCTTCCCTC       CAAAC
                                          ________
GAM512  ZNF200   3'  CAGGTCACAGATCCCCTTTCCC 14367           C   C  _
                                GGGAAGGGGGA CTG TG TTTG
                                |||||||||| ||| || ||||
                                CCCTTTCCCCT GAC AC GGAC
                                      A   _  T
GAM512  CARM1    3'  GCCCCTGCAGGTCCCCCCCC   64100     AA         TGTTT
                                GGG  GGGGGACCTGC    GGC
                                |||  ||||||||||     |||
                                CCC  CCCCCTGGACG    CCG
                                  __          TCC__
GAM512  DKFZp762K222 5'  GCGGCAGGTCGCCCTCCC    71669      A   G
                                GGGA GGG GACCTGCTGT
                                |||| ||| ||||||||||
                                CCCT CCC CTGGACGGCG
                                  _  G
GAM512  FLJ10701  3'  CCCTGCAGACCCCTCCTTCCC  36963          ACCTG    TT
                                GGGAAGGGGG    CTGT  GG
                                ||||||||||     ||||  ||
                                CCCTTCCTCC    GACG  CC
                                      CCA__    TC
GAM512  FLJ10738  3'  CCAAACAGCAACTTCCTGCC   37057    A     ACC
                                GG AGGGGG   TGCTGTTTGG
                                || ||||||   ||||||||||
                                CC TCCTTC   ACGACAAACC
                                 G     A__
GAM512  HRMT1L3   5'  GAACAGCCCCCCCTCCC     39559      A    ACCT
                                GGGA GGGGG    GCTGTTT
                                |||| |||||    |||||||
                                CCCT CCCCC    CGACAAG
                                  C    _____
GAM512  KIAA0125  3'  GCACAGACCCCCTTTCCC    29567          AC   C
                                GGGAAGGGGG  CTG TGT
                                ||||||||||  ||| |||
                                CCCTTTCCCC  GAC ACG
                                      CA   _
GAM512  KIAA0435  3'  GCCAGGCGCACAAATGCCCCTT 29660          GACC__   T
            CCC                   GGGAAGGGG     TGC GTTTGGC
                                |||||||||      ||| |||||||
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                                CCCTTCCCC     ACG CGGACCG
                                     GTAAAC  _
GAM512  KIAA0476 3' CCAATAATGGTCCCTCTTCCC 30037          TGCTGT
                                GGGAAGGGGGACC     TTGG
                                ||||||||||||     ||||
                                CCCTTCTCCCTGG     AACC
                                      TAAT__
GAM512  KIAA0750 3' CCAAAGAGTGCCCTCCTCCC  28305     A    ACC   G
                                GGGA GGGGG  TGCT TTTGG
                                |||| |||||  |||| |||||
                                CCCT CTCCC  GTGA AAACC
                                  C    ___   G
GAM512  KIAA1054 3' GCCTCTCAGGCTCCCCTTCCC 68966        GA   CTGTTT
                                GGGAAGGGG  CCTG     GGC
                                |||||||||  ||||     |||
                                CCCTTCCCC  GGAC     CCG
                                     TC   TCT___
GAM512  KIAA1190 5' GCCGGGCAGACCCCCCTCCCC 71649    A     ACCTG
                                GGG AGGGGG    CTGTTTGGC
                                ||| ||||||    |||||||||
                                CCC TCCCCC    GACGGGCCG
                                  C     CA___
GAM512  KIAA1493 3' CTACAAGCTCCCCTTCCC    64838         ACCT   GTT
                                GGGAAGGGGG   GCT   TGG
                                ||||||||||   |||  |||
                                CCCTTCCCCT   CGA   ATC
                                      _____  AC_
GAM512  KIAA1855 3' GCCAAACAGAATGTAACACCCC 93955     A   GACCTG___
           TCCC                  GGGA GGGG       CTGTTTGGC
                                ||||  ||||       |||||||||
                                CCCT CCCC       GACAAACCG
                                  _   ACAATGTAA
GAM512  KIAA1862 3' CCACCAGAGCCCCCTTCCC   69507         AC   CTGTT
                                GGGAAGGGGG  CTG    TGG
                                ||||||||||  |||    |||
                                CCCTTCCCCC  GAC    ACC
                                      GA   C_____
GAM512  MAP4K3   5' GCCCCCTGAGCGGCCCCCCTCC 14627     A    A  T   GTTT_
           C                   GGGA GGGGG CC GCT    GGC
                                |||| ||||| || |||    |||
                                CCCT CCCCC GG CGA    CCG
                                  C    _ _   GTCCC
GAM512  NYD-SP25 3' CCAGTGCAAGGACCCCCTTCCC 54302         A  _  TGT
                                GGGAAGGGGG CCT GC   TTGG
                                |||||||||| ||| ||   ||||
                                CCCTTCCCCC GGA CG   GACC
                                      A   A  T__
GAM512  OBSCN    3' CAGCAAGTCCCCCTCCC     71184      A      C
                                GGGA GGGGGAC TGCTG
                                |||| ||||||| |||||
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                                CCCT CCCCCTG ACGAC
                                  _      A
GAM512  POPX1    3'  CCAATACACAACCCCCTTCCC  30473          ACC  C  _
                                GGGAAGGGGG   TG TGT TTGG
                                ||||||||||   || ||| ||||
                                CCCTTCCCCC   AC ACA AACC
                                     A__  _   T
GAM512  SCAMP-4  3'  GCCAAGAGGCACCCCCTTCCC  55352          ACC    G
                                GGGAAGGGGG   TGCT TTTGGC
                                ||||||||||   |||| ||||||
                                CCCTTCCCCC   ACGG GAACCG
                                     ___   A
GAM512  SCAMP5   3'  CCAAGCAGGGTTCCCCCTTCCC 58055          _  TG
                                GGGAAGGGGGA CC  CTGTTTGG
                                |||||||||| ||  ||||||||
                                CCCTTCCCCCT GG  GACGAACC
                                      T  __
GAM512  SERPINA10 5'  AGCAGGTCTCCCCTTCCC    32991          _
                                GGGAAGGGG GACCTGCT
                                ||||||||| ||||||||
                                CCCTTCCCC CTGGACGA
                                     T
GAM512  SFXN5    3'  CCCCAGGCCTCCCTCCC     58647     A    A   CTGTTT
                                GGGA GGGGG CCTG     GG
                                |||| ||||| ||||     ||
                                CCCT CCTCC GGAC     CC
                                  C    _   C_____
GAM512  TRIM17   5'  GCTGTGCGGGCCCCCCTTCCC  32751          A    TGTTT
                                GGGAAGGGGG CCTGC    GGC
                                |||||||||| |||||    |||
                                CCCTTCCCCC GGGCG    TCG
                                     C    TG___
GAM512  LOC115129 3'  CCTCACTCAGATCCCTCCTCCC 73616      A     C  CT  TT
                                GGGA GGGGGA CTG  GT  GG
                                |||| |||||| |||  ||  ||
                                CCCT CTCCCT GAC  CA  CC
                                  C     A  T_  CT
GAM512  LOC116166 3'  GCCAAGTGAAGGACCCCCTCCC 60470      A    A  GC GT
                                GGGA GGGGG CCT  T  TTGGC
                                |||| ||||| |||  |  |||||
                                CCCT CCCCC GGA  G  AACCG
                                  _    A  A_ TG
GAM512  LOC143308 5'  GCATGCAATCCCCCTTCCC    83835          CC  _
                                GGGAAGGGGGA  TGC TGT
                                ||||||||||  ||| |||
                                CCCTTCCCCCT  ACG ACG
                                     A_  T
GAM512  LOC149670 3'  GCCAATACTGTGAACCCCCTTC 80304          ACC  T  _
          CC                      GGGAAGGGGG   TGC GT TTGGC
                                ||||||||||   ||| || |||||
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                                CCCTTCCCCC  GTG CA AACCG
                                      AA_   T  T
GAM512  LOC150372 5'  GCCAAGCAGAGCCCCCTCTCCC 80614     _     ACCTG
                                GGGA AGGGGG    CTGTTTGGC
                                |||| ||||||    |||||||||
                                CCCT TCCCCC    GACGAACCG
                                  C     GA___
GAM512  LOC203292 3'  CCCAGACCCCTCCTTCCC    92155         ACCTG   TTT
                                GGGAAGGGGG    CTG   GG
                                ||||||||||    |||   ||
                                CCCTTCCTCC    GAC   CC
                                      CCA__   ___
GAM512  LOC56930  5'  GCCAAGCCGGTCCTCCTTCCC  62745           T   GTT
                                GGGAAGGGGGACC GCT   TGGC
                                |||||||||||| |||   ||||
                                CCCTTCCTCCTGG CGA   ACCG
                                        C   ___
GAM512  LOC56961  5'  CCCCCAGCCCCCCTTCCC    63575         ACCT    TTT
                                GGGAAGGGGG   GCTG   GG
                                ||||||||||   ||||   ||
                                CCCTTCCCCC   CGAC   CC
                                      _____   CC_
GAM512  LOC90499  3'  CCCAGACCCCTCCTTCCC    63740         ACCTG   TTT
                                GGGAAGGGGG    CTG   GG
                                ||||||||||    |||   ||
                                CCCTTCCTCC    GAC   CC
                                      CCA__   ___
GAM512  LOC92249  3'  GCCAAACACACCGCCCCCACCC 69107     AA    ACC  C
          C                      GGG  GGGGG   TG TGTTTGGC
                                |||  |||||   || |||||||||
                                CCC  CCCCC   AC ACAAACCG
                                  CA    GCC  _
GAM513  ATP8A2    3'  ACCCAGTGTTAACACATCTTTG 95152         _____ T    TTAA
          TC                     GACAAAGAT    TA CACT    GGT
                                |||||||||    || ||||    |||
                                CTGTTTCTA    AT GTGA    CCA
                                      CACA  T    C___
GAM513  DNM1L     3'  ACCTGTGTAATAATCTTTGTT  24813           C  TTTA
                                GACAAAGATTAT AC    AGGT
                                ||||||||||| ||    ||||
                                TTGTTTCTAATA TG    TCCA
                                      A  TG__
GAM513  FLJ20371  3'  ACCTGCTTTGAGCGATAATCTT 35534    C        A   TA___
          TATC                    GA AAAGATTATC CTT     AGGT
                                || ||||||||| |||     ||||
                                CT TTTCTAATAG GAG     TCCA
                                 A        C   TTTCG
GAM513  KIAA0441  3'  ACCCTAAATTCTGAATTTTTGT 29619          ATCAC    A
          C                      GACAAAGATT     TTTA GGT
                                ||||||||||     |||| |||
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                                CTGTTTTTAA    AAAT CCA
                                      GTCTT   C
GAM513  KIAA1136  3'  ACCTTAAAGTATTTATTCTCA  92955   A   T  TC_
                                A AGA TA   ACTTTAAGGT
                                | ||| ||   ||||||||||
                                A TCT AT   TGAAATTCCA
                                 C   T  TTA
GAM513  STK17A    3'  ACCTTAAAGTAACTAATT    17665     TC_
                                GATTA   ACTTTAAGGT
                                |||||   ||||||||||
                                TTAAT   TGAAATTCCA
                                   CAA
GAM513  LOC150848 5'  ACCTTAAAAGTGACCCCTTTTC 86315    C    ATTA     _
                                GA AAAG    TCACTTT AAGGT
                                || ||||    ||||||| |||||
                                CT TTTC    AGTGAAA TTCCA
                                 _   CCC_      A
GAM513  LOC155038 3'  AGAGCATAATCTTTGTC     82181          CA
                                GACAAAGATTAT  CTTT
                                ||||||||||||  ||||
                                CTGTTTCTAATA  GAGA
                                       C_
GAM514  BTG2      3'  TAGGACAAGAGTTCT       23148        TC   A
                                AGAACTCT  TGT TCTA
                                ||||||||  ||| ||||
                                TCTTGAGA  ACA GGAT
                                      __  _
GAM514  CX3CR1    3'  AGACACAGAAGAGGCTGG    71178     AGAA       A
                                CCA    CTCTTCTGT TCT
                                |||    ||||||||| |||
                                GGT    GAGAAGACA AGA
                                  CG__        C
GAM514  LY9       3'  AGACACAGGCTCCTTCTTGGA  72144        CTCT    A
                                TCCAAGAA    TCTGT TCT
                                ||||||||    ||||| |||
                                AGGTTCTT    GGACA AGA
                                     CCTC    C
GAM514  MTMR3     5'  TAGTAGAAAAAGTTCTTGGG   41168         C_    TAT
                                TCCAAGAACT  TTCTG   CTA
                                ||||||||||  |||||   |||
                                GGGTTCTTGA  AAGAT   GAT
                                      AA    ____
GAM514  RFC1      3'  TGCAGAAGATTCTCAGA     12830    CA    C
                                TC  AGAA TCTTCTGTA
                                ||  |||| |||||||||
                                AG  TCTT AGAAGACGT
                                 AC    _
GAM514  SELE      5'  TTTGGGTGAAAAGAACTCTTG  6555       AC    CTG
                                CAAGA  TCTT   TATCTAAA
                                |||||  ||||   ||||||||
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                                GTTCT  AGAA   GTGGGTTT
                                   CA    AA_
GAM514  SELL     3'  TTGGTGAAAGAAAATTCTTGGA 7231         CTC    GTAT
                                TCCAAGAA   TTCT    CTAA
                                ||||||||   ||||    ||||
                                AGGTTCTT   AAGA    GGTT
                                     AA_    AAGT
GAM514  SHC1     3'  ATGCAAACAGTTCTTGGA    13121          C  C
                                TCCAAGAACT TT TGTAT
                                |||||||||| || |||||
                                AGGTTCTTGA AA ACGTA
                                      C  _
GAM514  WBSCR5   5'  TAGTTGCAACAGTTCTTGGA   42113         CTTC    T
                                TCCAAGAACT    TGTA CTA
                                ||||||||||    |||| |||
                                AGGTTCTTGA    ACGT GAT
                                      CA__    T
GAM514  BIRC2    5'  ACATTGAAGAGTTTTCAGA    67779    CA        __
                                TC  AGAACTCTTC  TGT
                                ||  ||||||||||  |||
                                AG  TTTTGAGAAG  ACA
                                 AC         TT
GAM514  C1orf29  3'  ACAGATTGTGAGTTCTTTGA   23335    C       T___
                                TC AAGAACTC    TCTGT
                                || ||||||||    |||||
                                AG TTCTTGAG    AGACA
                                 T       TGTT
GAM514  D123     5'  TTTAGGGACCGGAAGAGTCCTT 21214      A        TA_
           G                     CAAG ACTCTTCTG   TCTAAA
                                ||||| |||||||||   ||||||
                                GTTC TGAGAAGGC   GGATTT
                                  C        CAG
GAM514  dA141H5.1 3'  AGAGACTAGAAGAGTCTT    59778      A      _  A
                                AAGA CTCTTCT GT TCT
                                |||| ||||||| || |||
                                TTCT GAGAAGA CA AGA
                                  _      T  G
GAM514  FLJ12716  3'  TAGACTGAAAGTTTTTGGA    41943          C   TGTA
                                TCCAAGAACT TTC    TCTA
                                |||||||||| |||    ||||
                                AGGTTTTTGA AAG    AGAT
                                      _   TC__
GAM514  FLJ20701  3'  TTAGATACAGAATGAGTT    36027      _
                                AACTC TTCTGTATCTAA
                                ||||| ||||||||||||
                                TTGAG AAGACATAGATT
                                  T
GAM514  FLJ31978  3'  CAGAGACAGAGTTCTGGA    59007      A      ___
                                TCCA GAACTCT   TCTG
                                |||| |||||||   ||||
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                                AGGT CTTGAGA   AGAC
                                  _      CAG
GAM514  GAL3ST2   3'  CAGAACCAAGAGTTCTTGGG   53482          ____
                                TCCAAGAACTCT    TCTG
                                ||||||||||||   ||||
                                GGGTTCTTGAGA    AGAC
                                       ACCA
GAM514  LEAP-2    5'  TTTAGATACATGTCCTCCCTTG 54810       AACTCTTC
          GA                      TCCAAG       TGTATCTAAA
                                ||||||       ||||||||||
                                AGGTTC       ACATAGATTT
                                   CCTCCTGT
GAM514  MOCS3     3'  CAGTTAAGAAATTCTTGGA    27928        C_   __
                                TCCAAGAA  TCTT  CTG
                                ||||||||  ||||  |||
                                AGGTTCTT  AGAA  GAC
                                     AA    TT
GAM514  PRO1331   5'  TAGAAGCTGAAAGATTCTTGGA 48562        C   _ T  A
                                TCCAAGAA TCTT C GT TCTA
                                |||||||| |||| | || ||||
                                AGGTTCTT AGAA G CG AGAT
                                     _   A T  A
GAM514  PRO2893   5'  TTTAGATACAGGAGTTTTG    38436      ACT
                                CAAGA   CTTCTGTATCTAAA
                                |||||   ||||||||||||||
                                GTTTT   GAGGACATAGATTT
                                  ___
GAM514  PRO2893   3'  TTTGGATAGAAGAACTCTTG   38437      AC     GT
                                CAAGA  TCTTCT  ATCTAAA
                                |||||  ||||||  |||||||
                                GTTCT  AGAAGA  TAGGTTT
                                   CA     __
GAM514  LOC124411 3'  AGATGGGGGAACTCTAGGA    74770     A   AC     GT
                                TCC AGA  TCTTCT  ATCT
                                ||| |||  ||||||  ||||
                                AGG TCT  AGGGGG  TAGA
                                  A   CA     __
GAM514  LOC142893 5'  TTTAGAGCTGGAAGAGGCCTTG 83762       AA      GTA
          GA                      TCCAAG  CTCTTCT   TCTAAA
                                ||||||  |||||||   ||||||
                                AGGTTC  GAGAAGG   AGATTT
                                   CG      TCG
GAM514  LOC144395 3'  AGACACAGAAAATGACTCATGG 77318      A  ACTC__     A
          A                       TCCA GA     TTCTGT TCT
                                ||||  ||      |||||| |||
                                AGGT CT     AAGACA AGA
                                  A  CAGTAA     C
GAM514  LOC149830 3'  CAGAAGAAACTTCTTGGA    85886        C__
                                TCCAAGAA   TCTTCTG
                                ||||||||   |||||||
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                                AGGTTCTT   AGAAGAC
                                     CAA
GAM514  LOC158056 5'  TAGATGACCTAGAGTTCTGGGA 82594     A       TCTG
                                TCC AGAACTCT    TATCTA
                                ||| ||||||||    ||||||
                                AGG TCTTGAGA    GTAGAT
                                  G       TCCA
GAM514  LOC162137 5'  TGGAGCAGAAGAGCCGCT    88483    AA_       A
                                AG   CTCTTCTGT TCTA
                                ||   ||||||||| ||||
                                TC   GAGAAGACG AGGT
                                 GCC        _
GAM514  LOC200862 5'  TTAGATGTGGAAGCTCTTTGGA 91768       _ ACT    TG
                                TCCAA GA   CTTC  TATCTAA
                                ||||| ||   ||||  |||||||
                                AGGTT CT   GAAG  GTAGATT
                                   T  C__    GT
GAM514  LOC219972 3'  TTAGAGCCTGGAAGAGCCCT   93281    AA       TA_
                                AG  CTCTTCTG   TCTAA
                                ||  ||||||||   |||||
                                TC  GAGAAGGT   AGATT
                                 CC       CCG
GAM515  CDH12    3'  CTTATCATTTAAAGTGGTGTA  15777          CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM515  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007       CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC         G
GAM515  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT    98090       T    AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT     TTATTC
                                   _    GTCA_
GAM515  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
            A                    TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM515  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126          CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM515  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
            TA                    TACA   TCC    GAAGAATAAG
                                ||||   |||   ||||||||||
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                              ATGT   AGG   TTTCTTATTC
                                AAA_  ATTG
GAM515  KIAA1719 3' TCTGTCTTGGGAGTGGTGTA  68742           _
                              TACACCACTCCCAAGA AGA
                              |||||||||||||||| |||
                              ATGTGGTGAGGGTTCT TCT
                                       G
GAM515  KIAA1853 3' TTTTTCTTGGAAGCAGTG    69929    CA  C
                              CAC  CT CCAAGAAGAA
                              |||  || ||||||||||
                              GTG  GA GGTTCTTTTT
                                AC  A
GAM515  KIAA1877 3' CTTATTCTTCTGCCATGAGT  66748     CCA__
                              ACTC    AGAAGAATAAG
                              ||||    ||||||||||
                              TGAG    TCTTCTTATTC
                                TACCG
GAM515  KIAA1906 3' CTTATTCTTCTTGACTTTTGG 73571    CTCC_
                              CCA    CAAGAAGAATAAG
                              |||    ||||||||||||
                              GGT    GTTCTTCTTATTC
                                TTTCA
GAM515  OSBPL11  3' CTTAATTTCCCAAGAGTGGTG 43206       CCAA   AA
                              CACCACTC   GAAG  TAAG
                              ||||||||   ||||  ||||
                              GTGGTGAG   CTTT  ATTC
                                   AACC   A_
GAM515  YME1L1   3' TCATTCTTGATGTGGTGTA   58438       TCC    _
                              TACACCAC   CAAGAA GA
                              ||||||||   ||||||  ||
                              ATGTGGTG   GTTCTT CT
                                   TA_    A
GAM515  ZNF262   3' CTTATTTTGTTTGGGAGT    18723        A
                              ACTCCCAAG AGAATAAG
                              ||||||||| ||||||||
                              TGAGGGTTT TTTTATTC
                                   G
GAM515  LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_   AAGA
                              TACACCAC   CCAAG   ATA
                              ||||||||   |||||   |||
                              ATGTGGTG   GGTTC   TGT
                                   CAA    GG__
GAM516  CKN1     3' GGCTCTTAACTTTGTGAAA   5383        T  CC
                              TTTCACAA GT  GGAGCC
                              |||||||| ||  ||||||
                              AAAGTGTT CA  TCTCGG
                                   T  AT
GAM516  MGEA5    3' CCGGATTGTGAAAGCTTC    25217    A      AT
                              GAA CTTTCACA  GTCCGG
                              ||| ||||||||  ||||||
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                                CTT GAAAGTGT  TAGGCC
                                  C       __
GAM516  NELL2    3'  GCCCATTGGATCTGTGAAAG  21591        AT   ___  A
                                CTTTCACA  GTCC   GG GC
                                ||||||||  ||||   || ||
                                GAAAGTGT  TAGG   CC CG
                                    C_    TTA  _
GAM516  PDE6D    3'  GGCCCCTGGTTTTGGAAAAATT 12016    AC   A   TGT   A_
              C                  GAA  TTTC CAA   CCGG  GCC
                                 |||  |||| |||   ||||  |||
                                 CTT  AAAG GTT   GGTC  CGG
                                   AA    _   TT_    CC
GAM516  RAB6A    3'  GGCAAGGCACTGTAAAAGTTTT 12718        C   A  T  GGA
                                GAAACTTT ACA TG CC   GCC
                                |||||||| ||| || ||   |||
                                TTTTGAAA TGT AC GG   CGG
                                    A   C  _  AA_
GAM516  RARG     3'  GCTCCTTGTTTTTGCCAAAGTT 8264         CA   TGTCC_
              TC                  GAAACTTT  CAA     GGAGC
                                  ||||||||  |||     |||||
                                  CTTTGAAA  GTT     CCTCG
                                      CC   TTTGTT
GAM516  KIAA0836 3'  CCCCATTGTGACAGTTTC    65166       T       TCC
                                GAAACT TCACAATG   GG
                                ||||||  ||||||||   ||
                                CTTTGA AGTGTTAC   CC
                                   C       C__
GAM516  KIAA1223 3'  TTTCACATTGTAAAAGTTTT   71699        C      CC
                                GAAACTTT ACAATGT  GGAG
                                ||||||||  |||||||  ||||
                                TTTTGAAA TGTTACA  CTTT
                                    A      __
GAM516  PRO2032   5'  GCTCATACCGTGCAAAGTTTC  38391        _   AAT  CCG
                                GAAACTTT CAC   GT   GAGC
                                ||||||||  |||   ||   ||||
                                CTTTGAAA GTG   CA   CTCG
                                    C   C__   TA_
GAM516  LOC133634 5'  GCCCCGGACACCAGAGAGTTTC 75600          ACAA      A
                                GAAACTTTC    TGTCCGG GC
                                |||||||||    ||||||| ||
                                CTTTGAGAG    ACAGGCC CG
                                     ACC_      C
GAM516  LOC148426 5'  GCTCTGGCCATGAAGTCTC    85306    A    CACA   T
                                GA ACTTT    ATG CCGGAGC
                                || |||||    ||| |||||||
                                CT TGAAG    TAC GGTCTCG
                                 C     _____   C
GAM516  LOC150035 5'  GCCCACTGTGAAAGATTC    85958     A       AT  CC  A
                                GAA CTTTCACA  GT  GG GC
                                ||| ||||||||  ||  || ||
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                                CTT GAAAGTGT  CA  CC CG
                                  A       __  __  _
GAM516  LOC152667 3'  GGCATGCACTGTGAAAGCTTT  81525     A       A   CCGGA
                                GAA CTTTCACA TGT     GCC
                                ||| |||||||| |||     |||
                                TTT GAAAGTGT ACG     CGG
                                  C       C   TA___
GAM516  LOC90495  3'  CTTCAAATTGTGAAAGT     63736          GTCC
                                ACTTTCACAAT    GGAG
                                ||||||||||    ||||
                                TGAAAGTGTTA    CTTC
                                      AA__
GAM517  NCKAP1    3'  AAGTGTACCTGCCATAA     26467        ATAT
                                TTATGGCA    TGCACTT
                                ||||||||    |||||||
                                AATACCGT    ATGTGAA
                                     CC__
GAM517  SC5DL     3'  CGATATCACCATGATTTAA    92535          CA
                                TTAAATTATGG  ATATTG
                                ||||||||||  ||||||
                                AATTTAGTACC  TATAGC
                                      AC
GAM517  CAPN6     3'  AAGTGTAGTCCTGCCCTAA    27387     T    AT
                                TTA GGCA  ATTGCACTT
                                ||| ||||  |||||||||
                                AAT CCGT  TGATGTGAA
                                  C   CC
GAM517  SGKL      3'  AAGTGCAATATTGTATATTTTT 26045      TTATG
              AA                  TTAAA     GCAATATTGCACTT
                                ||||||    ||||||||||||||
                                AATTT     TGTTATAACGTGAA
                                   TTATA
GAM517  LOC144501 3'  AAGCTGCTCTTGCCATAAT    84025          TATT  _
                                ATTATGGCAA    GCA CTT
                                ||||||||||    ||| |||
                                TAATACCGTT    CGT GAA
                                      CT__   C
GAM517  LOC222161 5'  AAGTGCAACATTACTGTA     94374      C   A
                                TATGG AAT TTGCACTT
                                ||||| ||| ||||||||
                                ATGTC TTA AACGTGAA
                                   A   C
GAM518  AGTPBP1   3'  ACTGCAAAGAATAAATG      31536        G
                                CATTTAT TTTTTGCAGT
                                ||||||| ||||||||||
                                GTAAATA AGAAACGTCA
                                        _
GAM518  GRM8      3'  TGCTAAAAATAAATGCAA     7795           G    T
                                TTGCATTTAT TTTT GCA
                                |||||||||| |||| |||
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                                AACGTAAATA AAAA CGT
                                      _   T
GAM518  NSF      3'  ACTGCTGCTTAAAATGCAA   63748       AT_  TTTT
                                TTGCATTT  GT   GCAGT
                                ||||||||  ||   |||||
                                AACGTAAA  CG   CGTCA
                                    ATT  T___
GAM518  OXTR     3'  TGACTGCATTGAAATGCAA   8084        ATGTTTT
                                TTGCATTT     TGCAGTCA
                                ||||||||     ||||||||
                                AACGTAAA     ACGTCAGT
                                    GTT____
GAM518  SEMA3A   3'  CTGGAAAAACAAATGCAA   21405       TA     G
                                TTGCATT  TGTTTTT CAG
                                |||||||  ||||||| |||
                                AACGTAA  ACAAAAA GTC
                                   __     G
GAM518  VCY2     3'  TGACTGCAAAAACTGGGTAA  17430     ATTTAT
                                TTGC     GTTTTTGCAGTCA
                                ||||     ||||||||||||
                                AATG     CAAAAACGTCAGT
                                  GGT___
GAM518  VCY2     3'  TGACTGCAAAAACTGGGTAA  60895     ATTTAT
                                TTGC     GTTTTTGCAGTCA
                                ||||     ||||||||||||
                                AATG     CAAAAACGTCAGT
                                  GGT___
GAM518  ZFP106   3'  TGACTGCAAAAATGTTTAT   42743    TT
                                AT  ATGTTTTTGCAGTCA
                                ||  ||||||||||||||
                                TA  TGTAAAAACGTCAGT
                                 TT
GAM518  LOC196812 3'  CTGGGAATAACATAAATACAA  91124     C       _  G
                                TTG ATTTATGTT TTT CAG
                                ||| ||||||||| ||| |||
                                AAC TAAATACAA AAG GTC
                                  A       T  G
GAM518  LOC197423 5'  TTGACTACAATTGGAAATGC   78428       ATGTTT  C
                                GCATTT     TTG AGTCAA
                                ||||||     ||| ||||||
                                CGTAAA     AAC TCAGTT
                                   GGTT__   A
GAM519  DDEF1    3'  CTCAGTGTCAGGGCACATGTGA 60305      C  C   G  G
          A                      TTCAC TG GCT TG ACACTGAG
                                 ||||| || ||| || ||||||||
                                 AAGTG AC CGG AC TGTGACTC
                                   T  A   G  _
GAM519  EPM2A    5'  CCCAGCGCCCACAGGTGGA   20234       ____     T
                                TTCACCT    GCGCTG GG
                                |||||||    |||||| ||
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                                AGGTGGA   CGCGAC CC
                                   CACC    _
GAM519  MAPK14   3' CTCACCATCCACAGCAAGATGA 8977      C  GC      CAC
           A                    TTCA CT  GCTGTGGA   TGAG
                                |||| ||  ||||||||   ||||
                                AAGT GA  CGACACCT   ACTC
                                  A  A_       ACC
GAM519  MAPK14   3' CTCACCATCCACAGCAAGATGA 8978      C  GC      CAC
           A                    TTCA CT  GCTGTGGA   TGAG
                                |||| ||  ||||||||   ||||
                                AAGT GA  CGACACCT   ACTC
                                  A  A_       ACC
GAM519  FLJ20967 5' AGTGCCAGCACAGGTGGA    42205       C   GT  A
                                TTCACCTG GCT  GG CACT
                                |||||||| |||  || ||||
                                AGGTGGAC CGA  CC GTGA
                                   A  __ _
GAM519  KIAA1069 3' CTCAGCACCCACCCCTGCAGTG 68530     C    CT_   ACA
           AA                    TTCAC TGCG   GTGG   CTGAG
                                 ||||| ||||   ||||   |||||
                                 AAGTG ACGT   CACC   GACTC
                                   _   CCC    CAC
GAM519  KIAA1145 3' CTCAGTGTCCACAGCAGTCAG  66238    _ _
                                CTG C GCTGTGGACACTGAG
                                ||| | ||||||||||||||||
                                GAC G CGACACCTGTGACTC
                                  T A
GAM519  KIAA1719 3' TCAGTGTCCACAAATCAG    68735    CGC
                                CTG   TGTGGACACTGA
                                |||   ||||||||||||
                                GAC   ACACCTGTGACT
                                  TAA
GAM519  KIAA1795 3' CAGTGTCCACATTAATGAA   72613     CCTGCGC
                                TTCA      TGTGGACACTG
                                ||||      ||||||||||
                                AAGT      ACACCTGTGAC
                                  AATT___
GAM519  LHFPL2   3' CTCAGTGTCCTTACAAGT    70496    GC  __
                                GC  TGT  GGACACTGAG
                                ||  |||  ||||||||||
                                TG  ACA  CCTGTGACTC
                                 A_  TT
GAM519  MGC11386 3' CTCAGCATCCACAGTAGC    53063    _      CA
                                GC GCTGTGGA  CTGAG
                                || ||||||||  |||||
                                CG TGACACCT  GACTC
                                 A       AC
GAM519  LOC152674 5' CTCAATTATGTCAGCCACAGGT 87001        C_   TGGACAC
           GAA                    TTCACCTG  GCTG      TGAG
                                  ||||||||  ||||      ||||
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                                AAGTGGAC CGAC      ACTC
                                    AC    TGTATTA
GAM520  AKAP1    3'  ACTATGGGTTCTCTTCGCAAA  14472      A  CTT      C
                                TTTGT GA   GGAACCCA AGT
                                |||||| ||   |||||||| |||
                                AAACG CT   TCTTGGGT TCA
                                   _ TC_       A
GAM520  AKAP1    3'  ACTATGGGTTCTCTTCGCAAA  58373      A  CTT      C
                                TTTGT GA   GGAACCCA AGT
                                |||||| ||   |||||||| |||
                                AAACG CT   TCTTGGGT TCA
                                   _ TC_       A
GAM520  EGF      3'  ACTATAGGTTTTGGTTCCACAA 10488      A  C TG    CAC
                                TTGT GA T  GAACC   AGT
                                |||| || |  |||||   |||
                                AACA CT G  TTTGG   TCA
                                  C  T GT    ATA
GAM520  EZH1     3'  GACTGTGGGTTCCAAATTAC   10551      AC
                                GTAG  TTGGAACCCACAGTC
                                ||||  ||||||||||||||||
                                CATT  AACCTTGGGTGTCAG
                                  A_
GAM520  STAC     3'  GACTGTGGAGTAATAGCCACAA 13427      AGA  TGGA  _
           A                     TTTGT   CT    AC CCACAGTC
                                |||||   ||    || ||||||||
                                AAACA   GA    TG GGTGTCAG
                                   CC_  TAA_  A
GAM520  CCR1     3'  GACTGTGGGCTCCATTC     8927     CT    A
                                GA  TGGA CCCACAGTC
                                ||  |||| |||||||||
                                CT  ACCT GGGTGTCAG
                                 T_    C
GAM520  FLJ10483 3'  GACTGTGGAAGAGATTACAAA  36652       A   GGAAC
                                TTTGTAG CTT     CCACAGTC
                                ||||||| |||     ||||||||
                                AAACATT GAG     GGTGTCAG
                                    A   AA___
GAM520  KIAA1871 3'  ACTGTAAGAGTCTACAAA    61890          GGAACCC
                                TTTGTAGACTT      ACAGT
                                ||||||||||       |||||
                                AAACATCTGAG      TGTCA
                                      AA_____
GAM520  LOC150821 3'  GGGTTCCACATCCACAAA    60944      A  CT
                                TTTGT GA  TGGAACCC
                                ||||| ||  ||||||||
                                AAACA CT  ACCTTGGG
                                   C  AC
GAM520  LOC151057 3'  ACTGTGGGTACACCTATAAA  86379       ACT  GA
                                TTTGTAG   TG  ACCCACAGT
                                |||||||   ||  |||||||||
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                                AAATATC   AC  TGGGTGTCA
                                    C__  A_
GAM520  LOC157507 5'  ACTGTAAAAGTCTGCAAA    82377          GGAACCC
                                TTTGTAGACTT      ACAGT
                                ||||||||||       |||||
                                AAACGTCTGAA      TGTCA
                                      AA_____
GAM520  LOC203339 5'  GGATTCCCAGTCTACAAA    92214          T   C
                                TTTGTAGACT GGAA CC
                                |||||||||| |||| ||
                                AAACATCTGA CCTT GG
                                      C   A
GAM520  LOC51030  3'  ACTGTAAATTAAACCAATCTAC 32695        C   AACCC___
           AAA                    TTTGTAGA TTGG       ACAGT
                                ||||||||| ||||       |||||
                                AAACATCT AACC       TGTCA
                                    _   AAATTAAA
GAM520  LOC90906  3'  GACTGTGGATCCCAAACTTTGC 64951       C_   AAC
           A                     TGTAGA  TTGG   CCACAGTC
                                |||||||  ||||   ||||||||
                                ACGTTT  AACC   GGTGTCAG
                                   CA   CTA
GAM521  FGF13    3'  ACCAAGAAAATGTAAAAGACC  54441       CAGG  ___
                                GGTCTT   GC   TTCTTGGT
                                ||||||   ||   ||||||||
                                CCAGAA   TG   AAGAACCA
                                   AA__  TAA
GAM521  INSRR    3'  ACCCGTGGCCCTGAAGACGGTG 68987      G         TCTT
                                CACCG TCTTCAGGGCT   GGT
                                ||||| ||||||||||   |||
                                GTGGC AGAAGTCCCGG   CCA
                                   _         TGC_
GAM521  LOXL3    3'  ACCAAGAAACCCATGTCAGC   51865    CTT  _  C
                                GT   CA GGG TTCTTGGT
                                ||   || ||| ||||||||
                                CG   GT CCC AAGAACCA
                                 ACT  A   A
GAM521  RAP1GA1   3'  ACCTCTGCCCTGAAGACC    12767          TTCTT
                                GGTCTTCAGGGC    GGT
                                ||||||||||    |||
                                CCAGAAGTCCCG    CCA
                                      TCT__
GAM521  XRCC5     5'  ACCAAAGCGCCTGAGGACCGG  41239          _   CT
                                CCGGTCTTCAGG GCTT  TGGT
                                |||||||||| ||||  ||||
                                GGCCAGGAGTCC CGAA  ACCA
                                      G   __
GAM521  EDG1     5'  CCACCCCTGAAGCCAGTG    60049     C  T      CTTCT
                                CAC GG CTTCAGGG    TGG
                                ||| || ||||||||    |||
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                                GTG CC GAAGTCCC    ACC
                                  A _      C____
GAM521  KIAA0323  3'  CCAAGAAGGGAAACGGTG   63947     GTC  AGGG
                                CACCG  TTC   CTTCTTGG
                                |||||  |||   ||||||||
                                GTGGC  AGG   GAAGAACC
                                  AA_  ____
GAM521  MGC15875  5'  ACCAGCGCCCGAAGGCCG   53011       A   TTC
                                CGGTCTTC GGGC  TTGGT
                                |||||||| ||||  |||||
                                GCCGGAAG CCCG  GACCA
                                    _   C__
GAM521  LOC199786 3'  ACCAAGTTGCGGAGACCGGT  89730        AGG  TT
                                ACCGGTCTTC  GC  CTTGGT
                                ||||||||||  ||  ||||||
                                TGGCCAGAGG  CG  GAACCA
                                    ___  TT
GAM521  LOC200030 3'  ACCAAGAAGAGGAAGAAGACC  80119      AGGG_
                                GGTCTTC   CTTCTTGGT
                                |||||||   |||||||||
                                CCAGAAG   GAAGAACCA
                                   AAGGA
GAM521  LOC200030 3'  ACCAAGAAGAGGAAGAAGACC  80120      AGGG_
                                GGTCTTC   CTTCTTGGT
                                |||||||   |||||||||
                                CCAGAAG   GAAGAACCA
                                   AAGGA
GAM521  LOC200030 3'  ACCAAGAAGTGGAAGAAGACC  80121      AGG_
                                GGTCTTC   GCTTCTTGGT
                                |||||||   ||||||||||
                                CCAGAAG   TGAAGAACCA
                                   AAGG
GAM521  LOC200030 3'  ACCAAGAAGTGGAAGAAGACC  80122      AGG_
                                GGTCTTC   GCTTCTTGGT
                                |||||||   ||||||||||
                                CCAGAAG   TGAAGAACCA
                                   AAGG
GAM521  LOC200030 3'  ACCAAGAAGTGGAAGAAGACC  80123      AGG_
                                GGTCTTC   GCTTCTTGGT
                                |||||||   ||||||||||
                                CCAGAAG   TGAAGAACCA
                                   AAGG
GAM521  LOC204285 3'  ACCAAGAAGCTTCCAAACGAC  91009    TTCA__
                                GTC    GGGCTTCTTGGT
                                |||    ||||||||||||
                                CAG    TTCGAAGAACCA
                                  CAAACC
GAM521  LOC51629  3'  ACCAAGAAGCCCTCAGCCTGGT 32604      T  TC
            G                    CACCGG CT  AGGGCTTCTTGGT
                                |||||| ||  ||||||||||||
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                                GTGGTC GA  TCCCGAAGAACCA
                                   C  C_
GAM522  CDH12    3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM522  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM522  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090      T    AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                   _   GTCA_
GAM522  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
           A                     TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM522  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM522  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
           TA                    TACA   TCC    GAAGAATAAG
                                ||||   |||   ||||||||||
                                ATGT   AGG    TTTCTTATTC
                                  AAA_   ATTG
GAM522  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68742             _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                          G
GAM522  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM522  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748      CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM522  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
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                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM522  OSBPL11  3'  CTTAATTTCCCAAGAGTGGTG  43206       CCAA   AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                    AACC   A_
GAM522  YME1L1   3'  TCATTCTTGATGTGGTGTA   58438       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                    TA_    A
GAM522  ZNF262   3'  CTTATTTTGTTTGGGAGT    18723       A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                    G
GAM522  LOC91960 3'  TGTGGCTTGGAACGTGGTGTA  68294       TC_    AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
                                ATGTGGTG   GGTTC   TGT
                                    CAA    GG__
GAM523  CUBN     3'  GGCGTGGTGGCTCACCCC    8421     ATC     G
                                GGG   AGCCGTT ATGCC
                                |||   ||||||| |||||
                                CCC   TCGGTGG TGCGG
                                  CAC     _
GAM523  GAS7     5'  TGAGCATCCCTGATTCC     14672       CCGTT    C
                                GGGATCAG    GATGC CA
                                ||||||||    ||||| ||
                                CCTTAGTC    CTACG GT
                                    C____    A
GAM523  GEMIN5   3'  CATTCACTCTGGTCCCT     90642       CC  T
                                AGGGATCAG  GT GATG
                                |||||||||  || ||||
                                TCCCTGGTC  CA TTAC
                                    T_  C
GAM523  3-PAP    3'  TTGGGACAGCTGATCCCT    39321       C  TGATG
                                AGGGATCAGC GT    CCCAA
                                |||||||||| ||    |||||
                                TCCCTAGTCG CA    GGGTT
                                    A _____
GAM523  ARFRP1   3'  GGGACGGCTGGTCCC      13694         TGATG
                                GGGATCAGCCGT    CCC
                                ||||||||||||    |||
                                CCCTGGTCGGCA    GGG
                                                _____
GAM523  CNNM3    3'  CATCAATGCCTGGATCCT    34805       _  C
                                GGGATC AG CGTTGATG
                                |||||| || ||||||||
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                                TCCTAG TC GTAACTAC
                                   G  C
GAM523  DDR1     3'  TGGACAACACTGATTCCT    26561        CC   ATGC
                                AGGGATCAG  GTTG   CCA
                                |||||||||  ||||   |||
                                TCCTTAGTC  CAAC   GGT
                                     A_   A___
GAM523  DDR1     3'  TGGACAACACTGATTCCT    26563        CC   ATGC
                                AGGGATCAG  GTTG   CCA
                                |||||||||  ||||   |||
                                TCCTTAGTC  CAAC   GGT
                                     A_   A___
GAM523  DDR1     3'  TGGACAACACTGATTCCT    10478        CC   ATGC
                                AGGGATCAG  GTTG   CCA
                                |||||||||  ||||   |||
                                TCCTTAGTC  CAAC   GGT
                                     A_   A___
GAM523  DKFZP434C171 5'  TGGACAGGCGGCTGATCCT   32201          GA  C
                                GGGATCAGCCGTT  TG CCA
                                ||||||||||||  || |||
                                TCCTAGTCGGCGG  AC GGT
                                      __ A
GAM523  DKFZp434J0226 5'  GCTGAGATCGGCTGATCACC   72793    _       _  GAT
                                GG GATCAGCCG TT   GC
                                || |||||||| ||   ||
                                CC CTAGTCGGC AG   CG
                                 A        T  AGT
GAM523  DNAJC5   3'  GTCAGACTCCGGCTGATCCT   62141          ____
                                GGGATCAGCCG    TTGAT
                                ||||||||||    |||||
                                TCCTAGTCGGC    GACTG
                                      CTCA
GAM523  FLJ12895  5'  TGGGCATCTGGTCATCCCT   43929       CA    TT
                                AGGGAT  GCCG  GATGCCCA
                                ||||||  ||||  ||||||||
                                TCCCTA  TGGT  CTACGGGT
                                   C_   __
GAM523  FLJ22167  5'  GGAATCTGAGGGCTGATCCCT  44876          G  _  GC
                                AGGGATCAGCC TT GAT  CC
                                |||||||||| || |||  ||
                                TCCCTAGTCGG AG CTA  GG
                                      G  T   A_
GAM523  FLJ22596  5'  TGGACATTTCCTGATTCCT   47645         CCGTT   C
                                AGGGATCAG    GATG CCA
                                |||||||||    |||| |||
                                TCCTTAGTC    TTAC GGT
                                     CT___    A
GAM523  FLJ32389  3'  TGAGCACCCGCTCTGATTCC   58843         CC  TGA   C
                                GGGATCAG  GT   TGC CA
                                ||||||||  ||   ||| ||
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                                CCTTAGTC  CG   ACG GT
                                    T_  CCC   A
GAM523  GREAT    3'  TGAGGTGCAGCTGATCTCT   56375         C  TGAT  _
                                AGGGATCAGC GT   GCC CA
                                |||||||||| ||   ||| ||
                                TCTCTAGTCG CG   TGG GT
                                     A  ____   A
GAM523  H11      5'  GGGACACAACCGTCCCT    27637       CAGCC   A  _
                                AGGGAT    GTTG TG CCC
                                ||||||    |||| || |||
                                TCCCTG    CAAC AC GGG
                                   C____   _ A
GAM523  KIAA0420 3'  TGAGGCCGGCTGATCGCT   64096    G       TTGAT  _
                                AG GATCAGCCG    GCC CA
                                || |||||||||    ||| ||
                                TC CTAGTCGGC    CGG GT
                                 G       _____  A
GAM523  KIAA0711 3'  TGGCAACGGCTGATGCCC   30156    _        ATGC
                                GGG ATCAGCCGTTG   CCA
                                ||| ||||||||||   |||
                                CCC TAGTCGGCAAC   GGT
                                  G       ____
GAM523  LASP1    3'  TGGGCTGGGCTGAGCCCCT   21582     A_    GTTGAT
                                AGGG  TCAGCC    GCCCA
                                ||||  ||||||    |||||
                                TCCC  AGTCGG    CGGGT
                                  CG    GT____
GAM523  LGI4     5'  GGGTGTCAGCGAACCCCT   58411     ATCAGC
                                AGGG    CGTTGATGCCC
                                ||||    ||||||||||
                                TCCC    GCGACTGTGGG
                                  CAA___
GAM523  MGC10986 3'  GTTGGGCATCATAAATGCCCCT 48327     AT  GCCGT
                                AGGG  CA   TGATGCCCAAC
                                ||||  ||   ||||||||||
                                TCCC  GT   ACTACGGGTTG
                                  C_  AAAT_
GAM523  MGC4840  3'  TGGGCATGGTGGCTCACCCCT  72030     ATC    TT A
                                AGGG  AGCCG  G TGCCCA
                                ||||  |||||  | ||||||
                                TCCC  TCGGT  T ACGGGT
                                  CAC   GG _
GAM523  MRPS18A  3'  TGAGCATTGAGTCACTGATCTC 36783        CCG_ TG   C
           T                     AGGGATCAG   T  ATGC CA
                                 |||||||||   |  |||| ||
                                 TCTCTAGTC   A  TACG GT
                                      ACTG GT   A
GAM523  NUDEL    3'  TGAACAGCGGCGGCTGTCCCT  48702      T       A  CC
                                AGGGA CAGCCGTTG TG  CA
                                ||||| |||||||| ||  ||
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                                TCCCT GTCGGCGGC AC  GT
                                  _       G  AA
GAM523  PP1628    5'  TGGGCAGTGAGCCGGCCCCT   48083     ATCA   _  G _
                                AGGG   GCCG TT A TGCCCA
                                ||||   |||| || | ||||||
                                TCCC   CGGC GA T ACGGGT
                                  ____   C  G G
GAM523  PPP1R16B  3'  TGGGAATCCCAGCTGATTCC   62041        CGTT   G
                                GGGATCAGC    GAT CCCA
                                |||||||||    ||| ||||
                                CCTTAGTCG    CTA GGGT
                                     ACC_   A
GAM523  PTRF      5'  TGAGCATCAGCAAATCGCT   64247    G   CAGCC      C
                                AG GAT     GTTGATGC CA
                                || |||     |||||||| ||
                                TC CTA     CGACTACG GT
                                 G   AA___       A
GAM523  RALGPS1A  3'  GGCATCAAGCTACCCT     28335     ATC   CG
                                AGGG   AGC  TTGATGCC
                                ||||   |||  ||||||||
                                TCCC   TCG  AACTACGG
                                  A__   __
GAM523  LOC126528 3'  TTGAGCACCAGCTGGTCCCT   75034         CGT  A   C
                                AGGGATCAGC   TG TGC CAA
                                ||||||||||   || ||| |||
                                TCCCTGGTCG   AC ACG GTT
                                     ___ C   A
GAM523  LOC147123 5'  TGGGCATCTCTGTGGTCCCT   78856        GC  TT
                                AGGGATCA  CG  GATGCCCA
                                ||||||||  ||  ||||||||
                                TCCCTGGT  GT  CTACGGGT
                                     __  CT
GAM523  LOC148764 5'  TGGGCACCACCTACCCTGATCC 79740        CCGT__  A
                                GGATCAG     TG TGCCCA
                                |||||||     || ||||||
                                CCTAGTC     AC ACGGGT
                                    CCATCC  C
GAM523  LOC200904 3'  TTGGGCACCTGTAATCCC    91787      __  CCGTTGA
                                GGGAT  CAG      TGCCCAA
                                |||||  |||      |||||||
                                CCCTA  GTC      ACGGGTT
                                   AT   C_______
GAM523  LOC254826 3'  TTGGGCAACACCAACTGGTCCC 99054         CCGT  A
          T                     AGGGATCAG    TG TGCCCAA
                                |||||||||    || |||||||
                                TCCCTGGTC    AC ACGGGTT
                                     AACC  A
GAM523  LOC257354 3'  TGAGGCCGGCTGATCGCT    96798    G       TTGAT  _
                                AG GATCAGCCG    GCC CA
                                || |||||||||    ||| ||
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                                TC CTAGTCGGC     CGG GT
                                 G        _____   A
GAM524  THRB     5'  AAGGGATCCAGAATGATTACTA 6622          C   A   GA
                A                TTAGTAATTA TCT GGA  TTTT
                                 |||||||||| ||| |||  ||||
                                 AATCATTAGT AGA CCT  GGAA
                                       A   _   AG
GAM524  TRIM34   3'  AAAATCTCCCAGAGTAGT    56109         A
                                 ATTACTCT GGAGATTTT
                                 |||||||| |||||||||
                                 TGATGAGA CCTCTAAAA
                                      C
GAM524  LOC202266 3'  AAAATCTCCAGTGTTAACTA   91934      AATT  T  A
                                 TAGT    AC CT GGAGATTTT
                                 ||||    || || |||||||||
                                 ATCA    TG GA CCTCTAAAA
                                   AT__  T  _
GAM525  MRPL11   3'  ATCAGGCCTGAATAAACATCC  32649     CGG__
                                 GGA     GTTCAGGCCTGAT
                                 |||     ||||||||||||||
                                 CCT     TAAGTCCGGACTA
                                  ACAAA
GAM525  MYOZ2    5'  ATCAGGCCCAAGTGCCATCCAT 33938       CG   TCA__
                                 ATGGA  GGT     GGCCTGAT
                                 |||||  |||     ||||||||
                                 TACCT  CCG     CCGGACTA
                                    A_   TGAAC
GAM525  LOC145226 3'  TCAGGCCCAATCCATGCCA    77561     AC_    CA
                                 TGG   GGGTT  GGCCTGA
                                 |||   |||||  |||||||
                                 ACC   CCTAA  CCGGACT
                                  GTA     C_
GAM525  LOC146108 5'  ATCAGACCCAAGGGCCCGTTCA 78146           A__  C
                                 TGGACGGGTTC   GG CTGAT
                                 ||||||||||||   || |||||
                                 ACTTGCCCGGG   CC GACTA
                                       AAC  A
GAM526  CDH12    3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                 TACACCACT     GAA  ATAAG
                                 |||||||||     |||  |||||
                                 ATGTGGTGA     TTT  TATTC
                                      AA___    AC
GAM526  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007       CA         G
                                 TACAC  CTCCCAAGAA AAT
                                 |||||  |||||||||| |||
                                 ATGTG  GAGGGTTCTT TTA
                                    AC         G
GAM526  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT    98090       T    AGAAG
                                 ACCAC CCCA     AATAAG
                                 ||||| ||||     ||||||
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                                TGGTG GGGT    TTATTC
                                  _   GTCA_
GAM526  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
           A                      TACAC       AGAAGAATAAG
                                  |||||       ||||||||||
                                  ATGTG       TCTTCTTATTC
                                    TACTCCC_
GAM526  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                  TACACCACT       GAATAAG
                                  |||||||||       |||||||
                                  ATGTGGTGA       TTTATTC
                                       AGACG___
GAM526  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
           TA                     TACA   TCC   GAAGAATAAG
                                  ||||   |||   ||||||||||
                                  ATGT   AGG   TTTCTTATTC
                                    AAA_  ATTG
GAM526  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA  68742              _
                                  TACACCACTCCCAAGA AGA
                                  |||||||||||||||| |||
                                  ATGTGGTGAGGGTTCT TCT
                                            G
GAM526  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                  CAC  CT CCAAGAAGAA
                                  |||  || ||||||||||
                                  GTG  GA GGTTCTTTTT
                                    AC  A
GAM526  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748     CCA__
                                  ACTC    AGAAGAATAAG
                                  ||||    ||||||||||
                                  TGAG    TCTTCTTATTC
                                    TACCG
GAM526  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                                  CCA    CAAGAAGAATAAG
                                  |||    ||||||||||||
                                  GGT    GTTCTTCTTATTC
                                    TTTCA
GAM526  OSBPL11   3'  CTTAATTTCCCAAGAGTGGTG  43206        CCAA    AA
                                  CACCACTC    GAAG  TAAG
                                  ||||||||    ||||  ||||
                                  GTGGTGAG    CTTT  ATTC
                                       AACC    A_
GAM526  YME1L1    3'  TCATTCTTGATGTGGTGTA    58438        TCC     _
                                  TACACCAC   CAAGAA GA
                                  ||||||||   |||||| ||
                                  ATGTGGTG   GTTCTT CT
                                       TA_     A
GAM526  ZNF262    3'  CTTATTTTGTTTGGGAGT     18723         A
                                  ACTCCCAAG AGAATAAG
                                  ||||||||| ||||||||
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                                TGAGGGTTT TTTTATTC
                                     G
GAM526  LOC91960  3'  TGTGGCTTGGAACGTGGTGTA  68294        TC_    AAGA
                                TACACCAC  CCAAG   ATA
                                ||||||||  |||||   |||
                                ATGTGGTG  GGTTC   TGT
                                     CAA    GG__
GAM527  COL17A1   3'  AGCTGGAGTCTGTCAATGTCC  6684         __   TT
                                GGGCATTG  GGGC  TCCAGCT
                                ||||||||  ||||  |||||||
                                CCTGTAAC  TCTG  AGGTCGA
                                     TG   __
GAM527  CUTL1     3'  GAGAGCGAGCCCCCAATGCCC  10347          _  TCCA
                                GGGCATTGGGG CTT   GCTCTC
                                |||||||||| |||   ||||||
                                CCCGTAACCCC GAG   CGAGAG
                                      C  ____
GAM527  GGT2      5'  AGCTGAGGTCATCAATGCCC  74083         _    TC
                                GGGCATTGG GGCTT  CAGCT
                                |||||||| |||||  |||||
                                CCCGTAACT CTGGA  GTCGA
                                     A   __
GAM527  GIP       5'  AGAGCTGGAAAGGAAGTCTGCT 15936       TTGGGG
              C                  GGGCA     CTTTCCAGCTCT
                                 |||||     ||||||||||||
                                 CTCGT     GAAAGGTCGAGA
                                    CTGAAG
GAM527  HOXD4     3'  GGAAAAGCTCCAATGCCC    28263           _
                                GGGCATTGGGGCTTT CC
                                |||||||||||||| ||
                                CCCGTAACCTCGAAA GG
                                       A
GAM527  MAP1A     3'  GAGAGCCCAAGCCCCAATGCC  11438          TCCA
                                GGCATTGGGGCTT   GCTCTC
                                ||||||||||||   ||||||
                                CCGTAACCCCGAA   CGAGAG
                                      CC__
GAM527  SLC38A3   3'  AGAGCCAGGACCAAGGCCC   23371     A   GGCTT  A_
                                GGGC TTGG    TCC  GCTCT
                                |||| ||||    |||  |||||
                                CCCG AACC    AGG  CGAGA
                                  G   _____  AC
GAM527  TK2       3'  GAGAGCTGTTCCCCACCGCCC  17250     AT    CTTTC
                                GGGC  TGGGG    CAGCTCTC
                                ||||  |||||    ||||||||
                                CCCG  ACCCC    GTCGAGAG
                                  CC    TT___
GAM527  TMOD      3'  AGTGTTAAGCCACAATGCCC   13810       G    TC  G
                                GGGCATTG GGCTT  CA CT
                                |||||||| |||||  || ||
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                                CCCGTAAC CCGAA  GT GA
                                    A    TT  _
GAM527  FEZ2     3'  GAGAGCTGGCTACCATTACCC  18780     CAT   GGCTTT
                                GGG  TGG    CCAGCTCTC
                                |||  |||    |||||||||
                                CCC  ACC    GGTCGAGAG
                                  ATT  ATC___
GAM527  FLJ11274 5'  AGAACTGGAAAGCCCACTCTC  37779     CATTG        C
                                GGG    GGGCTTTCCAG TCT
                                |||    |||||||||||| |||
                                CTC    CCCGAAAGGTC AGA
                                  TCA__         A
GAM527  FLJ13154 3'  AGCCAGGCCTCCAATGC     45102       _    TCCA
                                GCATTGG GGCTT   GCT
                                ||||||| |||||   |||
                                CGTAACC CCGGA   CGA
                                    T    C___
GAM527  KIAA0556 3'  AGAACTCACCCCAGTGCCC   69643         CTTTCC  C
                                GGGCATTGGGG    AG TCT
                                ||||||||||     || |||
                                CCCGTGACCCC    TC AGA
                                      AC____  A
GAM527  KIAA1255 3'  GAGAGCTGAAAAATCGTGGCC  67743   G   TGG GC   C
                                GG CAT   G  TTT CAGCTCTC
                                || |||   |  ||| ||||||||
                                CC GTG   C  AAA GTCGAGAG
                                 G   ___ TA   A
GAM527  OBTP     5'  AGAAGACAGCCCCAAGCCC   34660     A      T  CAG
                                GGGC TTGGGGCT TC   CT
                                |||| |||||||| ||   ||
                                CCCG AACCCCGA AG   GA
                                  _       C  AA_
GAM527  PI4KII   3'  GAGAGCTGGATGTGCATGCCC  37952      TGGG  TT_
                                GGGCAT   GC   TCCAGCTCTC
                                ||||||   ||   ||||||||||
                                CCCGTA   CG   AGGTCGAGAG
                                    _____  TGT
GAM527  SARM     3'  GAGAGCTGGAGGACAATATCC  31293    GC   GGGCT
                                GG  ATTG    TTCCAGCTCTC
                                ||  ||||    ||||||||||
                                CC  TAAC    GAGGTCGAGAG
                                 TA   AG___
GAM527  LOC148166 5'  AGGGCTGAAAGCCCCAAGCCC  79410     A        C
                                GGGC TTGGGGCTTTC AGCTCT
                                |||| |||||||||| ||||||
                                CCCG AACCCCGAAAG TCGGGA
                                  _       _
GAM527  LOC200169 3'  GAAAGCACCCCAATGCCC    91555         __
                                GGGCATTGGG  GCTTTC
                                ||||||||||  ||||||
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                                CCCGTAACCC  CGAAAG
                                     CA
GAM527  LOC245771 5'  GAGAGCTGGTCGCCCACCACCC 94476     CATTG   TTT
                                GGG    GGGC   CCAGCTCTC
                                |||    ||||  |||||||||
                                CCC    CCCG   GGTCGAGAG
                                  ACCA_   CT_
GAM528  AQP6    3'  GAGCAAGGGTCCAGAGCA    55003      C   G
                                TGTTC GGA TTCTTGCTC
                                ||||| ||| |||||||||
                                ACGAG CCT GGGAACGAG
                                   A  _
GAM528  BTEB1   5'  GAGCAAGAGAATGCCGGAAC  8670        AG__
                                GTTCCGG   TTCTTGCTC
                                |||||||   |||||||||
                                CAAGGCC   GAGAACGAG
                                    GTAA
GAM528  CRY2    3'  GAGGGCTCCCTCGGAACA    72663       ___
                                TGTTCC  GGAGTTCTT
                                ||||||  |||||||||
                                ACAAGG  CCTCGGGAG
                                   CTC
GAM528  CXCR6   5'  GAGCAAGCTCATCTCTGGAACA 22676          TT___
                                TGTTCCGGAG    CTTGCTC
                                ||||||||||    |||||||
                                ACAAGGTCTC    GAACGAG
                                      TACTC
GAM528  FMNL    5'  GAGCCGGCTCCCGGAGCA    20868        _   CTT
                                TGTTCCGG AGTT   GCTC
                                |||||||| ||||  ||||
                                ACGAGGCC TCGG   CGAG
                                    C   C__
GAM528  GPR56   3'  AGCAAGAACTCCTGGAGC    20268      _
                                GTTCC GGAGTTCTTGCT
                                ||||| ||||||||||||
                                CGAGG CCTCAAGAACGA
                                   T
GAM528  LPIN2   3'  AGCGCTGGCCCGGAACA     28428        A   CT
                                TGTTCCGG GTT  TGCT
                                |||||||| |||  ||||
                                ACAAGGCC CGG  GCGA
                                     _  TC
GAM528  NT5E    3'  AGCAAGAGCTAAAGAGCA    11848      CGG
                                TGTTC   AGTTCTTGCT
                                |||||   ||||||||||
                                ACGAG   TCGAGAACGA
                                   AAA
GAM528  PLA2G2A 5'  GAGCAGGAGTGCAGAACA    6111       CGGA
                                TGTTC   GTTCTTGCTC
                                |||||   ||||||||||
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                                ACAAG   TGAGGACGAG
                                  ACG_
GAM528  RARA    3'  GAGCAAGGGCCCCGGGACA   8252        A
                                TGTTCCGG GTTCTTGCTC
                                |||||||| ||||||||||
                                ACAGGGCC CGGGAACGAG
                                    C
GAM528  RFX1    3'  GAGGGGGACTCCGAGACA    12850    TC       G
                                TGT  CGGAGTTCTT CTC
                                |||  |||||||||| |||
                                ACA  GCCTCAGGGG GAG
                                  GA       _
GAM528  RUNX1   3'  AGCAGGACTTCAGAACA     10026     C    T
                                TGTTC GGAGT CTTGCT
                                ||||| ||||| ||||||
                                ACAAG CTTCA GGACGA
                                   A   _
GAM528  SUV39H2 3'  AGCAAGGGGAATGGAGCA    45450       GAG
                                TGTTCCG   TTCTTGCT
                                |||||||   ||||||||
                                ACGAGGT   GGGAACGA
                                    AAG
GAM528  WHSC1   3'  GAGCAAGGTTGGAAACA     24673     _   AGT
                                TGTT CCGG   TCTTGCTC
                                |||| ||||   ||||||||
                                ACAA GGTT   GGAACGAG
                                  A   ____
GAM528  AKAP3   5'  GAGCAAGAACATCCCAGCA   22219     CC  _
                                TGTT  GGA GTTCTTGCTC
                                ||||  ||| ||||||||||
                                ACGA  CCT CAAGAACGAG
                                  C_   A
GAM528  AQP10   3'  GAGCAAGGCTGTGAAAC     55395     C  G   T
                                GTT CG AGT CTTGCTC
                                ||| || ||| |||||||
                                CAA GT TCG GAACGAG
                                  A  G   _
GAM528  C17orf1A 3' GGCAACTCCTGGAACA      49586       _    TCT
                                TGTTCC GGAGT   TGCT
                                |||||| |||||   ||||
                                ACAAGG CCTCA   ACGG
                                    T    ____
GAM528  C20orf54 3' GAGCAAGGGGCAGGAACA    54155       GGAG
                                TGTTCC    TTCTTGCTC
                                ||||||    |||||||||
                                ACAAGG    GGGAACGAG
                                    ACG_
GAM528  CLECSF9 3'  GAGCAAGAACATGGCCACA   27621     T_  GA
                                TGT  CCG  GTTCTTGCTC
                                |||  |||  ||||||||||
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                                ACA  GGT  CAAGAACGAG
                                  CC   A_
GAM528  CLIC6    3'  GAGCAAGGATACGAAAACA   83412     C_  GA
                                TGTT  CG  GTTCTTGCTC
                                ||||  ||  ||||||||||
                                ACAA  GC  TAGGAACGAG
                                  AA  A_
GAM528  DKFZP434G156 5'  AGCAAGAGGGTCCTGGAACA   70334       _   G _
                                TGTTCC GGA T TCTTGCT
                                |||||| ||| | |||||||
                                ACAAGG CCT G AGAACGA
                                    T   G G
GAM528  FLJ10326  3'  GAGCAAGAACCCTCCTGA    36501    C   __
                                TC GGA  GTTCTTGCTC
                                || |||  ||||||||||
                                AG CCT  CAAGAACGAG
                                 T   CC
GAM528  FLJ20727  3'  GAACATTATTCTGGAACA    36045          TCT  C
                                TGTTCCGGAGT   TG TC
                                ||||||||||   || ||
                                ACAAGGTCTTA   AC AG
                                      TT_  A
GAM528  HS747E2A  3'  GAACAAGAACTCATGGGAT    31732       _       C
                                GTTCCG GAGTTCTTG TC
                                |||||| |||||||| ||
                                TAGGGT CTCAAGAAC AG
                                   A        A
GAM528  KIAA0546  3'  AGCAAGAATCACTGAACA    71836      CG_  G
                                TGTTC   GA TTCTTGCT
                                |||||   || ||||||||
                                ACAAG   CT AAGAACGA
                                   TCA  _
GAM528  KIAA1255  3'  GAGCAAGAGATTCATACA    67744     TCCG   _
                                TGT    GAGT TCTTGCTC
                                |||    |||| ||||||||
                                ACA    CTTA AGAACGAG
                                  TA__    G
GAM528  KIAA1463  3'  AGCAAGAGTATTTGGAGCA   72733         GT_
                                TGTTCCGGA   TCTTGCT
                                |||||||||   |||||||
                                ACGAGGTTT   AGAACGA
                                     ATG
GAM528  KIAA1679  3'  AGCAAGTCTTTGGAACA     70708          TT
                                TGTTCCGGAG  CTTGCT
                                ||||||||||  ||||||
                                ACAAGGTTTC  GAACGA
                                      T_
GAM528  LENG1    5'  GAGCTGGCACGTCCGGAACA   85195         _  T  T
                                TGTTCCGGA GT CT GCTC
                                ||||||||| || || ||||
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                                ACAAGGCCT CA GG CGAG
                                     G  C  T
GAM528  SURB7     3'  GAGCAAGAAAGTTTTGGAA   16211        __
                                TTCCGGAG  TTCTTGCTC
                                ||||||||  |||||||||
                                AAGGTTTT  AAGAACGAG
                                    GA
GAM528  LOC146481 3'  GAGCAAGAACCTGCTATA    78486     TC   A
                                TGT  CGG GTTCTTGCTC
                                |||  ||| ||||||||||
                                ATA  GTC CAAGAACGAG
                                  TC   _
GAM528  LOC147043 5'  AGCAATGACAGCCGGGACA   88503         A_   C
                                TGTTCCGG  GTT TTGCT
                                ||||||||  ||| |||||
                                ACAGGGCC  CAG AACGA
                                    GA   T
GAM528  LOC147080 3'  GAGCAAGAAGTCTTAGAA    85039     C_   G
                                TTC  GGA TTCTTGCTC
                                |||  ||| |||||||||
                                AAG  TCT AAGAACGAG
                                  AT   G
GAM528  LOC148397 3'  GAGCAAGGCTGGGGAACA    79570       GG   T
                                TGTTCC  AGT CTTGCTC
                                ||||||  ||| |||||||
                                ACAAGG  TCG GAACGAG
                                   GG   _
GAM528  LOC149692 3'  GAGCAAGGAGATGGAATA    85736       GAG
                                TGTTCCG   TTCTTGCTC
                                |||||||   |||||||||
                                ATAAGGT   AGGAACGAG
                                    AG_
GAM528  LOC151234 3'  GAGCACAGGGCCTGGAACA   80977        A    _
                                TGTTCCGG GTTCT TGCTC
                                |||||||| ||||| |||||
                                ACAAGGTC CGGGA ACGAG
                                    _    C
GAM528  LOC163706 3'  GAGCCTCGACTCCGGACA    83030     T      CTT
                                TGT CCGGAGTT   GCTC
                                ||| ||||||||   ||||
                                ACA GGCCTCAG   CGAG
                                  _      CTC
GAM528  LOC201516 5'  GAACAAGATGGCTGGAACA   89630        AGT    C
                                TGTTCCGG   TCTTG TC
                                ||||||||   ||||| ||
                                ACAAGGTC   AGAAC AG
                                    GGT    A
GAM528  LOC205366 5'  GAGCAAGAACTTGAGAAC    92363      CG
                                GTTC  GAGTTCTTGCTC
                                ||||  ||||||||||||
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                                CAAG  TTCAAGAACGAG
                                  AG
GAM528  LOC253502 3'  GAGCCCGCGCTCCGGGACA   96219          TCTT
                                TGTTCCGGAGT   GCTC
                                ||||||||||   ||||
                                ACAGGGCCTCG   CGAG
                                     CGCC
GAM528  LOC255480 3'  AGCAGGGACCCCAGACA    98284     CC  A
                                TGTT  GG GTTCTTGCT
                                ||||  || |||||||||
                                ACAG  CC CAGGGACGA
                                  AC  _
GAM528  LOC256360 5'  GAGCAGGAACCAGAAC     98327     C  AG
                                GTTC GG  TTCTTGCTC
                                |||| ||  |||||||||
                                CAAG CC  AAGGACGAG
                                  A  __
GAM528  LOC92609  3'  AGCAAGAACTTGGGAATA    73204      G
                                TGTTCC GAGTTCTTGCT
                                |||||| ||||||||||
                                ATAAGG TTCAAGAACGA
                                   G
GAM528  LOC92661  3'  GAGCAGGGCCCAGAACA    70629     C  A  T
                                TGTTC GG GT CTTGCTC
                                ||||| || || |||||||
                                ACAAG CC CG GGACGAG
                                  A  _  _
GAM529  DKFZp547I094 3'  GTGCCCCCAGGGCACATCA   50565         CAT  A
                                TGATGTGCCC   GG CAT
                                ||||||||||   || |||
                                ACTACACGGG   CC GTG
                                     ACC  C
GAM529  KIAA1613  3'  GTGATATGGTAAGAAGCACCAT 65442      _  CCCATGGA
          CA                    TGATG TGC       CATATCAC
                                |||||| |||       ||||||||
                                ACTAC ACG       GTATAGTG
                                  C   AAGAATG_
GAM529  KIAA1877  3'  TCCACCAGGAGGCACATCA   66762         _ A__
                                TGATGTGCC CC   TGGA
                                |||||||| ||   ||||
                                ACTACACGG GG   ACCT
                                     A  ACC
GAM529  LOC145815 3'  TGACAGCTATGGGGCACACA  84524    A         ACATA
                                TG TGTGCCCCATGG    TCA
                                || ||||||||||||    |||
                                AC ACACGGGGTATC    AGT
                                 _          GAC__
GAM529  LOC159199 5'  TGTCCATGGAACACTCA     83070     T   CC
                                TGA GTG  CCATGGACA
                                ||| |||  |||||||||
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                                ACT CAC  GGTACCTGT
                                  _  AA
GAM530  SNTB1    5'  ACATGGCATTTTAAGAATGC  41044      G   TTT
                                GCATT TTGG  TGCCATGT
                                ||||| ||||  ||||||||
                                CGTAA AATT  ACGGTACA
                                   G   TT_
GAM530  SORCS2   3'  ACATAACAAAGAGACAATGC  40793       GG   CC
                                GCATTGTT  TTTTG  ATGT
                                ||||||||  |||||  ||||
                                CGTAACAG  GAAAC  TACA
                                    A_    AA
GAM530  CAMKK2   3'  TACACAGCTGCATCAGACAATG 22628       _   TTT  CA
           C                     GCATTGT TGGT  GC  TGTA
                                |||||||  ||||  ||  ||||
                                CGTAACA ACTA  CG  ACAT
                                    G   CGT  AC
GAM530  DPYSL4   3'  ACATGGCAGGGACAATGC    22224       GGT
                                GCATTGTT  TTTGCCATGT
                                ||||||||  ||||||||||
                                CGTAACAG  GGACGGTACA
                                          ___
GAM530  KIAA0750 3'  ACACAGCAAAACAAACAATG  28303       G     CA
                                CATTGTT GTTTTGC  TGT
                                |||||||  |||||||  |||
                                GTAACAA CAAAACG  ACA
                                    A     AC
GAM530  LATS1    3'  TACATGGCAACCTAACA    60911       TT
                                TGTTGG  TTGCCATGTA
                                ||||||  ||||||||||
                                ACAATC  AACGGTACAT
                                   C_
GAM530  LOC151446 3'  ACACAACAAAACCAGAATG   86562     G       CCA
                                CATT TTGGTTTTG  TGT
                                ||||  |||||||||  |||
                                GTAA GACCAAAAC  ACA
                                  _       AAC
GAM531  ARAF1    3'  ACCAAGAAGCACAGAATTCTGC 64641      CA___  CA
           TG                    CAGCAG    TG  CTTCTTGGT
                                ||||||    ||  |||||||||
                                GTCGTC    AC  GAAGAACCA
                                   TTAAG  AC
GAM531  CTNNA1   3'  CTAATGTACGCTGCTGCAG   66502        A   CTTC
                                CTGCAGCAGC TGCA   TTGG
                                ||||||||||  ||||   ||||
                                GACGTCGTCG ATGT   AATC
                                      C   ____
GAM531  CYP2B6   3'  ACCACAGTCACACACTGCTGTA 7550        CA  C_  TCT
           G                     CTGCAGCAG  TG  ACT   TGGT
                                |||||||||  ||  |||  ||||
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                                GATGTCGTC  AC  TGA   ACCA
                                     AC  AC   C__
GAM531  FLT1     3'  CCAAGAATATATGCTACAG   10659     C   GC   CAC
                                CTG AGCA  ATG   TTCTTGG
                                ||| ||||  |||   |||||||
                                GAC TCGT  TAT   AAGAACC
                                  A   A_  ___
GAM531  MYH13    5'  CCAAGAAGCCCTCTGCAG    15068       C  CATGCA
                                CTGCAG AG     CTTCTTGG
                                |||||| ||     ||||||||
                                GACGTC TC     GAAGAACC
                                   _ CC____
GAM531  NHP2L1   3'  CCAAAGAGATGTGCTGCAG   18449        G   GCA  TC
                                CTGCAGCA CAT   CT  TTGG
                                |||||||| |||   ||  ||||
                                GACGTCGT GTA   GA  AACC
                                     _  ___  GA
GAM531  RALBP1   3'  CAAGCCCATGCTGCTGCAG   23271           CACTT
                                CTGCAGCAGCATG    CTTG
                                ||||||||||||     ||||
                                GACGTCGTCGTAC    GAAC
                                       CC___
GAM531  SFRS7    3'  ACCAAAAAATGCATGTTTGAGG 60147    G   CA      C  C
                                CT CAG  GCATGCA TT TTGGT
                                || |||  ||||||| || |||||
                                GG GTT  TGTACGT AA AACCA
                                 A  __      A  A
GAM531  ALOX15B  3'  ACCAAGAAGTGGCTGC     8551       ATG
                                GCAGC   CACTTCTTGGT
                                |||||   ||||||||||||
                                CGTCG   GTGAAGAACCA
                                  ___
GAM531  C20orf130 3'  ACCAAAACCCATGCACAGTGCT 62411        _____     CACTTC
           GCAG                    CTGCAGCA   GCATG     TTGGT
                                |||||||    |||||     |||||
                                GACGTCGT    CGTAC     AACCA
                                     GACA    CCAA__
GAM531  FLJ10324  5'  ACCTGGAGGACACGCTGCTGCA 36496          A  CA    TT
           G                     CTGCAGCAGC TG  CTTC  GGT
                                |||||||||| ||  ||||  |||
                                GACGTCGTCG AC  GAGG  CCA
                                      C  AG   T_
GAM531  FLJ10581  3'  ACCAAGAAGCACTTTGTGCCCA 36829     CA_   CA   AC
           G                     CTG   GCAG  TGC  TTCTTGGT
                                |||   ||||  |||  ||||||||
                                GAC   TGTT  ACG  AAGAACCA
                                  CCG   TC   __
GAM531  FLJ22408  5'  ACCGCTTCGCCGCTGCTGCAG  45983          AT  ACTTCT
                                CTGCAGCAGC  GC     TGGT
                                ||||||||||  ||     ||||
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                                GACGTCGTCG CG     GCCA
                                     C_ CTTC__
GAM531  FLJ22944  5' ACCAAGAAAAAGACTGTACTGC 47867      CA  TGCAC_
          AG                   CTGCAG GCA     TTCTTGGT
                               |||||| |||     ||||||||
                               GACGTC TGT     AAGAACCA
                                  A_  CAGAAA
GAM531  KIAA1726  3' ACCAAAAAAAATCTGTTGCAG 67824        C GCACTTC
                               CTGCAGCAG AT      TTGGT
                               ||||||||| ||      |||||
                               GACGTTGTC TA      AACCA
                                     _ AAAAA__
GAM531  LOC115110 3' ACCAAGAGCTGGAAACCACTGC 72171      CAGCATG C
          A                    TGCAG      CA TTCTTGGT
                               |||||      || ||||||||
                               ACGTC      GT GAGAACCA
                                  ACCAAAG C
GAM531  LOC124470 3' ACTCTGGTGCATGCTGTCACAG 76145    CA         TCTT
                               CTG GCAGCATGCACT   GGT
                               ||| ||||||||||||   |||
                               GAC TGTCGTACGTGG   TCA
                                 AC         TC__
GAM531  LOC136442 3' ACCACTCCGCATGCTGCTG   55259         ACTTCT
                               CAGCAGCATGC     TGGT
                               ||||||||||     ||||
                               GTCGTCGTACG     ACCA
                                     CCTC__
GAM531  LOC199796 5' ACCAAGGTGAAGCCACTGCTGC 74920       CAT ACT_
          AG                   CTGCAGCAG  GC   TCTTGGT
                               |||||||||  ||   |||||||
                               GACGTCGTC  CG   GGAACCA
                                    AC_ AAGT
GAM531  LOC221576 3' ACCACGTGGCCACACGCTGCTG 95319       A CA_ TCT
          C                    GCAGCAGC TG  CT  TGGT
                               |||||||| ||  ||  ||||
                               CGTCGTCG AC  GG  ACCA
                                    C ACC TGC
GAM531  LOC257397 5' ACCAAGAAGAGCGCTCTGCAG  97951     C  AT A
                               CTGCAG AGC  GC CTTCTTGGT
                               |||||| |||  || |||||||||
                               GACGTC TCG  CG GAAGAACCA
                                  _  __ A
GAM531  LOC257515 3' ACCACGTGGCCACACGCTGCTG 99619       A CA_ TCT
          C                    GCAGCAGC TG  CT  TGGT
                               |||||||| ||  ||  ||||
                               CGTCGTCG AC  GG  ACCA
                                    C ACC TGC
GAM531  LOC257572 3' ACCACGTGGCCACACGCTGCTG 99739       A CA_ TCT
          C                    GCAGCAGC TG  CT  TGGT
                               |||||||| ||  ||  ||||
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                                CGTCGTCG AC   GG   ACCA
                                     C  ACC  TGC
GAM532  ADK      3'  CACAAGCCCAGGAGTGCAGA  8511        G  AAGA  GA
                                TCTGCACT CC    CT  GTG
                                |||||||| ||    ||  |||
                                AGACGTGA GG    GA  CAC
                                     _  ACCC  A_
GAM532  ADK      3'  CACAAGCCCAGGAGTGCAGA  22988       G  AAGA  GA
                                TCTGCACT CC    CT  GTG
                                |||||||| ||    ||  |||
                                AGACGTGA GG    GA  CAC
                                     _  ACCC  A_
GAM532  APPBP2   3'  CTCCTTAATAGTGCAGA     22118       CC   ACT
                                TCTGCACTG  AAG   GAG
                                |||||||||  |||   |||
                                AGACGTGAT  TTC   CTC
                                     AA   ___
GAM532  DISC1    3'  CACTCAATGCCAGGCAGTGCAG 38502         AAGAC_
                                CTGCACTGCC     TGAGTG
                                ||||||||||     ||||||
                                GACGTGACGG     ACTCAC
                                     ACCGTA
GAM532  FANCF    3'  CACCCAGTCTGGAGTGCAG   42975       G   A    A
                                CTGCACT CCA GACTG GTG
                                ||||||| ||| ||||| |||
                                GACGTGA GGT CTGAC CAC
                                     _  _    C
GAM532  FGFRL1   3'  ACTCACACACGTGCAGAT    41907       _  CCAAGAC
                                ATCTGCAC TG      TGAGT
                                |||||||| ||      |||||
                                TAGACGTG AC      ACTCA
                                     C  AC_____
GAM532  MPL      3'  CACCCAGGCTGCAGTGCA    19342       CA  A   A
                                TGCACTGC  AG CTG GTG
                                ||||||||  || ||| |||
                                ACGTGACG  TC GAC CAC
                                     __  G   C
GAM532  TRPV4    5'  CAGGCTGAGCAGTGCAGA    61328        CA  A
                                TCTGCACTGC  AG CTG
                                ||||||||||  || |||
                                AGACGTGACG  TC GAC
                                     AG  G
GAM532  CHRNA9   3'  CTCTTTGGCAGTACAGAT    34552      C       ACT
                                ATCTG ACTGCCAAG   GAG
                                ||||| |||||||||   |||
                                TAGAC TGACGGTTT   CTC
                                   A       ___
GAM532  DKFZp762P2111 3'  CTGAGGGGCAGTGCAGA     87633          AAGA  G
                                TCTGCACTGCC    CT AG
                                ||||||||||    || ||
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                                AGACGTGACGG   GA TC
                                      G___  G
GAM532  FLJ11715  3'  CACAAGTCAGCAGTGCAGA   44974        CAA   GA
                                TCTGCACTGC  GACT  GTG
                                ||||||||||  ||||  |||
                                AGACGTGACG  CTGA  CAC
                                      A__   A_
GAM532  FLJ12595  3'  CTCTCTGGCAATGCTGATG   47148    T  C    A  CT
                                CATC GCA TGCCA GA  GAG
                                |||| ||| ||||| ||  |||
                                GTAG CGT ACGGT CT  CTC
                                  T  A    _ __
GAM532  FLJ22167  5'  CACTCAGGCTGCAGTGCAG   44862        CA  A
                                CTGCACTGC  AG CTGAGTG
                                |||||||||  || |||||||
                                GACGTGACG  TC GACTCAC
                                     __  G
GAM532  FLJ22215  3'  CACCCAGGGTGCAGTGCAGA  98636         CAAGA  A
                                TCTGCACTGC    CTG GTG
                                ||||||||||    ||| |||
                                AGACGTGACG    GAC CAC
                                      TGG__  C
GAM532  KIAA1052  5'  CACTCAGGCTGCAGTGCAG   30938        CA  A
                                CTGCACTGC  AG CTGAGTG
                                |||||||||  || |||||||
                                GACGTGACG  TC GACTCAC
                                     __  G
GAM532  SFXN5     3'  ACTAAATGGCAGTGAGATG   58644      G      AGACTG
                                CATCT CACTGCCA     AGT
                                ||||| ||||||||     |||
                                GTAGA GTGACGGT     TCA
                                   _       AAA___
GAM532  SH3BGRL3  5'  CACGAGCCCGGCAGTGCAGCTG 49257    T        AAGA  GA
                                CA CTGCACTGCC   CT  GTG
                                || ||||||||||   ||  |||
                                GT GACGTGACGG   GA  CAC
                                 C        CCC_  G_
GAM532  LOC144161 5'  CACTCCCTCAGCAATGTAGATG 83934        C   CA  ACT
                                CATCTGCA TGC  AG   GAGTG
                                |||||||| |||  ||   |||||
                                GTAGATGT ACG  TC   CTCAC
                                     A   AC  C__
GAM532  LOC199725 5'  ACCCAGCCTTGGCGGGCA    91405    A      A  A
                                TGC CTGCCAAG CTG GT
                                ||| |||||||| ||| ||
                                ACG GGCGGTTC GAC CA
                                  _      C   C
GAM532  LOC219673 5'  CACCCAGTCTGGAGTGCAG   94612       G  A    A
                                CTGCACT CCA GACTG GTG
                                ||||||| ||| ||||| |||
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                                GACGTGA GGT CTGAC CAC
                                   _  _    C
GAM532  LOC221810 3'  CACAAGACTGACAGTGCAGA  95544        CCA  A  GA
                                TCTGCACTG  AG CT  GTG
                                |||||||||  || ||  |||
                                AGACGTGAC  TC GA  CAC
                                     AG_  A  A_
GAM532  LOC90271  5'  CACTCAGTCCGGCCGCG    62672    ACT  AA
                                TGC  GCC  GACTGAGTG
                                |||  |||  |||||||||
                                GCG  CGG  CTGACTCAC
                                  C__  C_
GAM532  LOC91661  3'  AGCGTGGCAGTGCAGAT    57208          AGA
                                ATCTGCACTGCCA  CT
                                ||||||||||||  ||
                                TAGACGTGACGGT  GA
                                      GC_
GAM533  BDKRB2    3'  GAGAAGCTAAAACCTGAGCTA  7110        AG__  ACCC
                                TAGCTCAGG   AGC   CTC
                                |||||||||   |||   |||
                                ATCGAGTCC   TCG   GAG
                                     AAAA  AA__
GAM533  CALB1     5'  TGGAGGAACGCTGAGCTG    18211       GGAGA  ACC
                                TAGCTCA    GC   CCTCCA
                                |||||||    ||   ||||||
                                GTCGAGT    CG   GGAGGT
                                     _____  CAA
GAM533  CSNK1G2   3'  TGGAGGGGTGCTGTGGAGCTG  8993       AGGAG
                                TAGCTC    AGCACCCCTCCA
                                ||||||    ||||||||||||
                                GTCGAG    TCGTGGGGAGGT
                                   GTG__
GAM533  GPR17     3'  GAGAGGCCTCTCTCCGCCTGAG 19181       ___     CAC  _
           CTA                    TAGCTCA  GGAGAG  CC CTC
                                |||||||  ||||||  || |||
                                ATCGAGT  CCTCTC  GG GAG
                                     CCG     TCC  A
GAM533  GUCA2B    3'  TTGGAGGGGGAGGCCCCTGAGG 24021    _    AGAGCA
           C                    GC TCAGG     CCCCTCCAA
                                || |||||     |||||||||
                                CG AGTCC     GGGGAGGTT
                                 G    CCGGAG
GAM533  IHH       3'  TGGAAGGGACCTGAGCTG    72586        AGAGCA  C
                                TAGCTCAGG     CCC TCCA
                                |||||||||     ||| ||||
                                GTCGAGTCC     GGG AGGT
                                     A_____   A
GAM533  IHPK3     3'  TGGAGGGGGCAGCCCAAGTTA  55098      CA  AGA  A
                                TAGCT  GG   GC CCCCTCCA
                                |||||  ||   || ||||||||
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                                ATTGA  CC   CG GGGGAGGT
                                  AC  GA_  _
GAM533  KRTHB1   3'  TGGAGAAGTGCTCAGCTA    11245      CAGGA     CC
                                TAGCT    GAGCAC  CTCCA
                                |||||    ||||||  |||||
                                ATCGA    CTCGTG  GAGGT
                                  _____     AA
GAM533  MMP15    3'  TGGCAGAGATGCCTCCCTGAGC 11614         _  A   CCC  _
          TA                     TAGCTCAGG AG GCA   CT CCA
                                |||||||| || |||   || |||
                                ATCGAGTCC TC CGT   GA GGT
                                    C  _   AGA  C
GAM533  NAV2     3'  TGAAGATGACTTCCTGAGC   60799         AG  CCC  C
                                GCTCAGGAG  CA   CT CA
                                |||||||||  ||   || ||
                                CGAGTCCTT  GT   GA GT
                                    CA  A__  A
GAM533  OPHN1    3'  TGGAAGATATTCCTGAGTTA  11912          AGCACCCC
                                TAGCTCAGGAG       TCCA
                                ||||||||||        ||||
                                ATTGAGTCCTT       AGGT
                                     ATAGA___
GAM533  PRex1    3'  TGGAGGGGTGCTGGAG      40826     AGGAG
                                CTC     AGCACCCCTCCA
                                |||     ||||||||||||
                                GAG     TCGTGGGGAGGT
                                  G____
GAM533  PSEN1    5'  TGGAAGGAACCTGAGCTA    5243          AGAGCAC  C
                                TAGCTCAGG      CC TCCA
                                |||||||||      || ||||
                                ATCGAGTCC      GG AGGT
                                    AA_____  A
GAM533  TTN      3'  TTGGAAAAGTAACATCTCCTGG 56754    T      GC__  CCC
          C                      GC CAGGAGA    AC   TCCAA
                                || |||||||    ||   |||||
                                CG GTCCTCT    TG   AGGTT
                                 _      ACAA  AAA
GAM533  TTN      3'  TTGGAAAAGTAACATCTCCTGG 56757    T      GC__  CCC
          C                      GC CAGGAGA    AC   TCCAA
                                || |||||||    ||   |||||
                                CG GTCCTCT    TG   AGGTT
                                 _      ACAA  AAA
GAM533  TTN      3'  TTGGAAAAGTAACATCTCCTGG 56763    T      GC__  CCC
          C                      GC CAGGAGA    AC   TCCAA
                                || |||||||    ||   |||||
                                CG GTCCTCT    TG   AGGTT
                                 _      ACAA  AAA
GAM533  ZAP70    3'  GGAGGGCCCTGAGCTG      71377         AGAGCAC
                                TAGCTCAGG      CCCTCC
                                |||||||||      ||||||
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                                GTCGAGTCC      GGGAGG
                                     C_______
GAM533  AF9Q34   3'  TGGAGGGGTGGCCCAGAGC   51726      A  AGAG
                                GCTC GG    CACCCCTCCA
                                |||| ||    ||||||||||
                                CGAG CC    GTGGGGAGGT
                                  A  CG__
GAM533  DKFZP434D146 5'  GGCGGCAGCGCTCTCCTAAGCT 32136      C       ACC_  T
                                AGCT AGGAGAGC    CC CC
                                |||| ||||||||    || ||
                                TCGA TCCTCTCG    GG GG
                                  A       CGAC  C
GAM533  FLJ12891  5'  TGGAAGGGGCACACCTCCTGAG 46932          AGCA_    _
           CTA                    TAGCTCAGGAG     CCCCT CCA
                                ||||||||||     ||||| |||
                                ATCGAGTCCTC     GGGGA GGT
                                      CACAC     A
GAM533  FLJ14502  3'  TTGGTCAGCCCTCCTGAGC    63370         A  ACCCCT
                                GCTCAGGAG GC      CCAA
                                |||||||| ||      ||||
                                CGAGTCCTC CG      GGTT
                                     C  ACT___
GAM533  FLJ23071  3'  TTGGAGCCTTTCTGCTGAGCTA 48047        G    CACCC
                                TAGCTCAG AGAG     CTCCAA
                                |||||||| ||||     ||||||
                                ATCGAGTC TCTT     GAGGTT
                                     G    TCC__
GAM533  FLJ32865  3'  GGGTACTCCCTGAGCTA     58817         A   C
                                TAGCTCAGG GAG ACCC
                                ||||||||| ||| ||||
                                ATCGAGTCC CTC TGGG
                                     _   A
GAM533  INPP5E    3'  TGGAGGAGCCCTGAGCTG     73507         AGA  ACC
                                TAGCTCAGG   GC   CCTCCA
                                |||||||||   ||   ||||||
                                GTCGAGTCC   CG   GGAGGT
                                     ___  A__
GAM533  KIAA0010  3'  GAGGCTCTCCTAAGCT      28591      C       ACCC
                                AGCT AGGAGAGC    CTC
                                |||| ||||||||    |||
                                TCGA TCCTCTCG    GAG
                                  A       _____
GAM533  KIAA0082  3'  TGAAGGAAGCTGCTCCTGAGGC 93785    _      _  ACC   C
                                GC TCAGGAG AGC   CCT CA
                                || ||||||| |||   ||| ||
                                CG AGTCCTC TCG   GGA GT
                                 G      G   AA_   A
GAM533  KIAA1041  3'  AGGGGCATGTTGCTCCTGAGC  30818          _    __
                                GCTCAGGAG AGCA  CCCCT
                                |||||||| ||||  |||||
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                                CGAGTCCTC TTGT  GGGGA
                                     G   AC
GAM533  KIAA1813  5'  GGGGGGTGCTCCTGGGC     70829        GA
                                GCTCAGGA  GCACCCCTC
                                ||||||||  |||||||||
                                CGGGTCCT  CGTGGGGGG
                                     __
GAM533  KIAA1940  5'  TGGAGGAGCGCGCGTCTGAGCT 80792        AGA  ACC
                                AGCTCAGG   GC   CCTCCA
                                ||||||||   ||   ||||||
                                TCGAGTCT   CG   GGAGGT
                                     GCG  CGA
GAM533  NXPH3     3'  GGCTGCTCTCCTCAGCTA    66343      C       C
                                TAGCT AGGAGAGCA CC
                                ||||| ||||||||| ||
                                ATCGA TCCTCTCGT GG
                                   C       C
GAM533  POFUT1    3'  TGGAGGGACCAGAGTCTGAGCT 70985        AGAGCAC
              G                  TAGCTCAGG      CCCTCCA
                                |||||||||      |||||||
                                GTCGAGTCT      GGGAGGT
                                     GAGACCA
GAM533  TMLHE     3'  TTGGAGAGGCGGGACTCTGAGT 37050        AGAGCA  C
              TA                  TAGCTCAGG     CC CTCCAA
                                |||||||||     || ||||||
                                ATTGAGTCT     GG GAGGTT
                                     CAGGGC  A
GAM533  LOC150606 5'  TGAAGGGACGTCCCTGAGC    86276       A  G AC    C
                                GCTCAGG GA C  CCCT CA
                                ||||||| || |  |||| ||
                                CGAGTCC CT G  GGGA GT
                                     _ _ CA    A
GAM533  LOC157556 3'  TGGAGGGGTGCTCTGTGGA    87785     AGG
                                TC   AGAGCACCCCTCCA
                                ||   ||||||||||||||
                                AG   TCTCGTGGGGAGGT
                                  GTG
GAM533  LOC164733 5'  AGGACTCTCCTGGCTA      83345      T       CACC
                                TAGC CAGGAGAG    CCT
                                |||| ||||||||    |||
                                ATCG GTCCTCTC    GGA
                                   _       A___
GAM533  LOC219855 3'  TTGAAGGGGCACTCCCTCTTGG 93145         __   CA     C
              GC                   GCTCAGGA  GAG  CCCCT CAA
                                |||||||||  |||  ||||| |||
                                CGGGTTCT  CTC  GGGGA GTT
                                     CC   AC    A
GAM533  LOC221025 3'  TGGAAAATGCTTTCCTGA    94789          CCCC
                                TCAGGAGAGCA    TCCA
                                ||||||||||    ||||
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                                AGTCCTTTCGT   AGGT
                                      AAA_
GAM533  LOC51580  3'  TTGGAGGGGGTAGCCTAGC   32432    C  AGA  A
                                GCT AGG  GC CCCCTCCAA
                                ||| |||  || |||||||||
                                CGA TCC  TG GGGGAGGTT
                                  _  GA_  _
GAM533  LOC90371  5'  TTGGAGAAACCTTCTGAGC   63168       AGCACCC
                                GCTCAGGAG     CTCCAA
                                |||||||||     ||||||
                                CGAGTCTTC     GAGGTT
                                      CAAA___
GAM533  LOC91397  5'  GTGCCCACTCTCCTGAGCT   66501         ____
                                AGCTCAGGAGA   GCAC
                                ||||||||||   ||||
                                TCGAGTCCTCT   CGTG
                                      CACC
GAM534  ADH7      3'  CCAGAGTAATATTCACTT    7269          GC
                                AGGTGAATATTG  TTGG
                                ||||||||||| ||||
                                TTCACTTATAAT  GACC
                                       GA
GAM534  APBA1     3'  AGCCAGCACCCACCTGGTA   70473       AATA
                                TACCAGGTG   TTGGCT
                                |||||||||   ||||||
                                ATGGTCCAC   GACCGA
                                      CCAC
GAM534  EPM2A     3'  CCAAGCCAACCACTTTCACCTG 20233       TA___
          G                    CCAGGTGAA   TTGGCTTGG
                               |||||||||   |||||||||
                               GGTCCACTT   AACCGAACC
                                     TCACC
GAM534  MAPT      3'  TTCCAAGCCTGGGCCACTGG  34179    G  AATATT
                                CCAG TG     GGCTTGGAA
                                |||| ||     |||||||||
                                GGTC AC     CCGAACCTT
                                  _ CGGGT_
GAM534  RNF4      3'  TCCAGCGTCCTTCACCTGG   12887       TATT  _
                                CCAGGTGAA   GGC TTGGA
                                |||||||||   ||| |||||
                                GGTCCACTT   CTG GACCT
                                      C___   C
GAM534  WNT7A     3'  TTCCAAGCTGCGGGCTCCCTGG 17322     T  ATATT_
                                CCAGG GA     GGCTTGGAA
                                ||||| ||     |||||||||
                                GGTCC CT     TCGAACCTT
                                  _ CGGGCG
GAM534  13CDNA73  3'  TTCCAAGTCTTTTCACCTG   43789       TATT
                                CAGGTGAA   GGCTTGGAA
                                ||||||||   |||||||||
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                                GTCCACTT   CTGAACCTT
                                    TT__
GAM534  FAM3D    5'  CCAAGCCACCCTTCACCTGG  57946       TAT
                                CCAGGTGAA  TGGCTTGG
                                |||||||||  ||||||||
                                GGTCCACTT  ACCGAACC
                                    CCC
GAM534  FLJ20557  3'  TCCAAGTCACCACCTAGTA  62571    C    AATAT
                                TAC AGGTG   TGGCTTGGA
                                ||| |||||   |||||||||
                                ATG TCCAC   ACTGAACCT
                                  A   C____
GAM534  FLJ20802  3'  TCCAAAATGGCATACTCACCTG 36113       A  TG  ____
          G                      CCAGGTGA TAT  GCT   TGGA
                                ||||||||| |||  |||   ||||
                                GGTCCACT ATA  CGG   ACCT
                                    C  __  TAAA
GAM534  KIAA1674  3'  TTCCAAGGTGCTCACCTGGT  69351       A  TGG
                                ACCAGGTGA TAT  CTTGGAA
                                |||||||||| |||  |||||||
                                TGGTCCACT GTG  GAACCTT
                                    C  ___
GAM534  LSR68    3'  CCCAGTTACATTCACCTGGT  38554       AT   T
                                ACCAGGTGAAT  TGGCT GG
                                ||||||||||  ||||| ||
                                TGGTCCACTTA  ATTGA CC
                                    C_   C
GAM534  MGC13523  3'  TCCAGAATTTTCACCTGGTA  54170        T  GGC
                                TACCAGGTGAA ATT  TTGGA
                                |||||||||||| |||  |||||
                                ATGGTCCACTT TAA  GACCT
                                    T  ___
GAM534  MGC3178   3'  TTCCAAGCCAACACACTCT   48722   _  AATA
                                AG GTG   TTGGCTTGGAA
                                || |||   ||||||||||
                                TC CAC   AACCGAACCTT
                                 T  AC__
GAM534  PRO0800   5'  TTCCAAATTTCTTCACCTGG  38351       TATT  C
                                CCAGGTGAA   GG TTGGAA
                                |||||||||   || ||||||
                                GGTCCACTT   TT AACCTT
                                    CT__  A
GAM534  LOC112687 3'  CCCCACACTTCACCTGGTA   73230        TAT  CTT
                                TACCAGGTGAA  TGG  GG
                                ||||||||||  |||  ||
                                ATGGTCCACTT  ACC  CC
                                    CAC  ___
GAM534  LOC139397 5'  TTCCAAGCTGGTCCACCT   76337     AAT  TG
                                AGGTG  AT  GCTTGGAA
                                |||||  ||  ||||||||
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                                TCCAC   TG  CGAACCTT
                                  C__  GT
GAM534  LOC149837 3'  TCCAGGTGTCCACCTGGTA   85906        A  ATTG
                                TACCAGGTG AT   GCTTGGA
                                ||||||||| ||   |||||||
                                ATGGTCCAC TG   TGGACCT
                                   C  _____
GAM534  LOC158301 3'  TTCCAAACCTGTGGTTCCACCT 82751      _  ATT_  C
                                AGGTG AAT   GG TTGGAA
                                ||||| |||   || ||||||
                                TCCAC TTG   CC AACCTT
                                  C  GTGT  A
GAM534  LOC158402 5'  TTCCAAGCCAAGAACTTGG   88155       GAATA
                                CCAGGT    TTGGCTTGGAA
                                ||||||    ||||||||||
                                GGTTCA    AACCGAACCTT
                                   AG___
GAM534  LOC200197 3'  TCCAAATGCTCACCTGG     90022        A   GGCT
                                CCAGGTGA TATT   TGGA
                                |||||||| ||||   ||||
                                GGTCCACT GTAA   ACCT
                                   C   _____
GAM534  LOC219722 5'  TTCCACAAGTATTTACC     94692         GGCT
                                GGTGAATATT   TGGAA
                                |||||||||   |||||
                                CCATTTATGA   ACCTT
                                   AC__
GAM534  LOC254556 3'  TCCAGCGTCCTTCACCTGG   96262        TATT  _
                                CCAGGTGAA   GGC TTGGA
                                |||||||||   ||| |||||
                                GGTCCACTT   CTG GACCT
                                   C___  C
GAM534  LOC256158 5'  CCCCAAACATCACCTGGT    99486        ATA   CTT
                                ACCAGGTGA  TTGG  GG
                                |||||||||  ||||  ||
                                TGGTCCACT  AACC  CC
                                   ACA   ___
GAM534  LOC91531  5'  TCCAGATCACTCAGCTAGTA  66942    C  G  ATAT  GC
                                TAC AG TGA   TG  TTGGA
                                ||| || |||   ||  |||||
                                ATG TC ACT   AC  GACCT
                                  A  G  C___  TA
GAM535  CDH12    3'  CTTATCATTTAAAGTGGTGTA  15777        CCCAA  GA
                                TACACCACT   GAA  ATAAG
                                |||||||||   |||  |||||
                                ATGTGGTGA   TTT  TATTC
                                   AA___  AC
GAM535  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA       G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
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                                ATGTG  GAGGGTTCTT TTA
                                  AC        G
GAM535  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090      T   AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                  _   GTCA_
GAM535  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
          A                      TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                  TACTCCC_
GAM535  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126        CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM535  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
          TA                     TACA   TCC   GAAGAATAAG
                                ||||   |||   ||||||||||
                                ATGT   AGG   TTTCTTATTC
                                  AAA_  ATTG
GAM535  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68742            _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                         G
GAM535  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM535  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748     CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM535  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM535  OSBPL11   3'  CTTAATTTCCCAAGAGTGGTG  43206        CCAA   AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                     AACC   A_
GAM535  YME1L1    3'  TCATTCTTGATGTGGTGTA   58438        TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   |||||| ||
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                                ATGTGGTG  GTTCTT CT
                                    TA_    A
GAM535  ZNF262   3' CTTATTTTGTTTGGGAGT   18723        A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                    G
GAM535  LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_   AAGA
                                TACACCAC  CCAAG   ATA
                                ||||||||  |||||   |||
                                ATGTGGTG  GGTTC   TGT
                                    CAA   GG__
GAM536  CDH12    3' CTTATCATTTAAAGTGGTGTA 15777        CCCAA  GA
                                TACACCACT   GAA  ATAAG
                                |||||||||   |||  |||||
                                ATGTGGTGA   TTT  TATTC
                                    AA___  AC
GAM536  GOCAP1   3' ATTGTTCTTGGGAGCAGTGTA 43007     CA       G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC       G
GAM536  DKFZp434N2435 5' CTTATTACTGTGGGGTGGT   98090     T   AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                   _   GTCA_
GAM536  DKFZP564I122 3' CTTATTCTTCTCCCTCATGTGT 63877     CACTCCCA
            A                    TACAC      AGAAGAATAAG
                                |||||      ||||||||||
                                ATGTG      TCTTCTTATTC
                                   TACTCCC_
GAM536  FLJ21791 3' CTTATTTGCAGAAGTGGTGTA 62126       CCCAAGAA
                                TACACCACT      GAATAAG
                                |||||||||      |||||||
                                ATGTGGTGA      TTTATTC
                                    AGACG___
GAM536  HMP19    3' CTTATTCTTTGTTAGGAAAATG 88860     CCAC  CAA_
            TA                   TACA   TCC   GAAGAATAAG
                                ||||   |||   ||||||||||
                                ATGT   AGG   TTTCTTATTC
                                  AAA_  ATTG
GAM536  KIAA1719 3' TCTGTCTTGGGAGTGGTGTA  68742          _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                        G
GAM536  KIAA1853 3' TTTTTCTTGGAAGCAGTG    69929    CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
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                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM536  KIAA1877 3' CTTATTCTTCTGCCATGAGT  66748     CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM536  KIAA1906 3' CTTATTCTTCTTGACTTTTGG 73571    CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM536  OSBPL11  3' CTTAATTTCCCAAGAGTGGTG 43206       CCAA   AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                     AACC   A_
GAM536  YME1L1   3' TCATTCTTGATGTGGTGTA   58438       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                     TA_    A
GAM536  ZNF262   3' CTTATTTTGTTTGGGAGT    18723       A
                                ACTCCCAAG AGAATAAG
                                |||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                      G
GAM536  LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_   AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
                                ATGTGGTG   GGTTC   TGT
                                     CAA    GG__
GAM537  DXYS155E 3' CAAGAAGCACGCCTACAAGGA 18685    C  GA_  AACTA
                                TCC TG   GC    TGCTTCTTG
                                ||| ||   ||    |||||||||
                                AGG AC   CG    ACGAAGAAC
                                  A  ATC  C____
GAM537  GYPC     3' AAGAGGCCACTCCCAGGGA   10898      _  CAACTAT
                                TCCCTGG AG      GCTTCTT
                                |||||||  ||      |||||||
                                AGGGACC TC      CGGAGAA
                                    C  AC_____
GAM537  GYPC     3' AAGAGGCCACTCCCAGGGA   34142      _  CAACTAT
                                TCCCTGG AG      GCTTCTT
                                |||||||  ||      |||||||
                                AGGGACC TC      CGGAGAA
                                    C  AC_____
GAM537  ICOS     3' CAAGAATATTTTTGCTCCAG  24922       CT   C
                                CTGGAGCAA  ATG TTCTTG
                                |||||||||  ||| ||||||
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                                GACCTCGTT  TAT AAGAAC
                                     TT   _
GAM537  LCP1     3'  GGCACAGATGCTCCAGGGA   11283          A  A
                                TCCCTGGAGCA CT TGCT
                                |||||||||||  ||  ||||
                                AGGGACCTCGT GA ACGG
                                      A  C
GAM537  APEX2    3'  GGACACTAGCTGCCCCAGG   27919      A   A   _  C
                                CCTGG GCA CTA TG TTC
                                |||||  |||  |||  ||  |||
                                GGACC CGT GAT AC AGG
                                   C   C   C  _
GAM537  DKFZP434J193 5'  CAAGGGGAGACATTGCTCCAGG 71557          CTATG
                                CCTGGAGCAA    CTTCTTG
                                ||||||||||    |||||||
                                GGACCTCGTT    GGGGAAC
                                      ACAGA
GAM537  DKFZP434K028 3'  AAGGAGCAACTGTCCCCAGGGA 94857        A_   ACTA
                                TCCCTGG  GCA   TGCTTCTT
                                |||||||  |||   ||||||||
                                AGGGACC  TGT   ACGAGGAA
                                     CC   CA__
GAM537  FLJ10581  3'  CAAGAAGCACTTTGTGCCCAG  36830      A   ACTA_
                                CTGG GCA    TGCTTCTTG
                                ||||  |||    |||||||||
                                GACC CGT    ACGAAGAAC
                                  _  GTTTC
GAM537  FLJ11700  3'  CAAGAAGCCACAGCTCAGAGA  46556    C   G   AACTAT
                                TC CTG AGC     GCTTCTTG
                                ||  |||  |||     ||||||||
                                AG GAC TCG     CGAAGAAC
                                 A   _   ACAC__
GAM537  FLJ13984  5'  CAAGAAGCTGGGACCACAGGGA 45802       GAGCAA   T
                                TCCCTG     CTA GCTTCTTG
                                ||||||     |||  ||||||||
                                AGGGAC     GGT CGAAGAAC
                                    ACCAG_  _
GAM537  KIAA0319  3'  CAAGAAGTAGTGGCTCCA    29698       A   AT
                                TGGAGC ACT  GCTTCTTG
                                ||||||  |||  ||||||||
                                ACCTCG TGA  TGAAGAAC
                                   G   __
GAM537  KIAA0710  3'  CAAGTCACCAACTGCTTCAGGG 30186          ACTATGCTT
           A                     TCCCTGGAGCA        CTTG
                                ||||||||||         ||||
                                AGGGACTTCGT        GAAC
                                      CAACCACT_
GAM537  MGC5391   5'  CAAGAAGCATGGGATCCAGG   52195       GCAA
                                CCTGGA   CTATGCTTCTTG
                                ||||||   ||||||||||||
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                                GGACCT   GGTACGAAGAAC
                                   AG__
GAM537  RAB40A   3'  AAGCTGGAATCGCTCCAGG   56014       AA__  T
                                CCTGGAGC   CTA GCTT
                                ||||||||   ||| ||||
                                GGACCTCG   GGT CGAA
                                    CTAA  _
GAM537  RAB40A   3'  AAGCTGGAATCGCTCCAGG   82941       AA__  T
                                CCTGGAGC   CTA GCTT
                                ||||||||   ||| ||||
                                GGACCTCG   GGT CGAA
                                    CTAA  _
GAM537  SLC26A9  3'  GGAAGTCCTCCAGGGA     57009       CAACTAT
                                TCCCTGGAG     GCTTCT
                                |||||||||     ||||||
                                AGGGACCTC     TGAAGG
                                    C_______
GAM537  SLC26A9  3'  GGAAGTCCTCCAGGGA     54719       CAACTAT
                                TCCCTGGAG     GCTTCT
                                |||||||||     ||||||
                                AGGGACCTC     TGAAGG
                                    C_______
GAM537  LOC138654 5'  CAAGAACTATGACCACTCCAGG 76488       CAAC   C
          G                    CCCTGGAG   TATG TTCTTG
                               ||||||||   |||| ||||||
                               GGGACCTC   GTAT AAGAAC
                                   ACCA   C
GAM537  LOC153232 3'  CAAGAACAGTGTTGCTCCAGGG 87178          TA  C
          G                    TCCCTGGAGCAAC  TG TTCTTG
                               ||||||||||||  || ||||||
                               GGGGACCTCGTTG  AC AAGAAC
                                      TG  _
GAM537  LOC257020 5'  AAGAAGCCGCTCAAGGGA   99355      G   AACTAT
                               TCCCT GAGC     GCTTCTT
                               ||||| ||||     |||||||
                               AGGGA CTCG     CGAAGAA
                                  A   C_____
GAM537  LOC89932  5'  AGGGAGCCGGCCCAGGGA   61445       A  AACTAT
                               TCCCTGG GC     GCTTCTT
                               ||||||| ||     |||||||
                               AGGGACC CG     CGAGGGA
                                  _  GC____
GAM538  BMP1     3'  TGGCCCAAGGAGTACCCCCCCA 21538     ACA  C  GATTA
                               TGG   GG AT    TTGGGCCA
                               |||   || ||    ||||||||
                               ACC   CC TG    AACCCGGT
                                 CCC  A  AGG__
GAM538  BMP1     3'  TGGCCCAAGGAGTACCCCCCCA 21539     ACA  C  GATTA
                               TGG   GG AT    TTGGGCCA
                               |||   || ||    ||||||||
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                                ACC   CC TG    AACCCGGT
                                  CCC  A  AGG__
GAM538  CXCL16   3'  TGACCTGGTGATCTGCCCACCC 42181    ACA   T    TG  C
            A                    TGG   GGCA GATTAT  GG CA
                                 |||   |||| ||||||  || ||
                                ACC   CCGT CTAGTG  CC GT
                                  CAC    _     GT  A
GAM538  DEDD     3'  GCCTAGTCATGCCTCCCA    53379     AC       TAT
                                TGG  AGGCATGAT   TGGGC
                                |||  |||||||||   |||||
                                ACC  TCCGTACTG   ATCCG
                                  C_       ___
GAM538  ESRRA    5'  GGCCCCCATGCCTGCCC     16720    A      ATTATT
                                GG CAGGCATG     GGGCC
                                || ||||||||     |||||
                                CC GTCCGTAC     CCCGG
                                  C       C_____
GAM538  ITPKB    3'  GCCTGGAAGACCGTGCCTGCCC 11066     A      ATTA_ TG
            A                    TGG CAGGCATG    T  GGC
                                 ||| ||||||||    |  |||
                                ACC GTCCGTGC    G  CCG
                                  C       CAGAA GT
GAM538  MDH2     3'  CATCATCATGCCTTCCA     20977      C       TAT
                                TGGA AGGCATGAT   TG
                                |||| |||||||||   ||
                                ACCT TCCGTACTA   AC
                                  _       CT_
GAM538  PLEK     5'  TGACCTTTGCATCTGCCTGTCC 12169         T   TATT   C
            A                    TGGACAGGCA GAT    GGG CA
                                 ||||||||||| |||    ||| ||
                                ACCTGTCCGT CTA    TCC GT
                                      _  CGTT   A
GAM538  DKFZP564D0462 3'  CATCAATCATCCCTGTCCA    71019        C     AT
                                TGGACAGG ATGATT  TG
                                |||||||| ||||||  ||
                                ACCTGTCC TACTAA  AC
                                     C     CT
GAM538  FLJ12747  3'  GGCCACCATGCCTGCCCA    50668     A      ATTATTG  _
                                TGG CAGGCATG      GGC C
                                ||| ||||||||      ||| |
                                ACC GTCCGTAC      CCG G
                                  C       CA_____   A
GAM538  FLJ12800  3'  GCCTCATCATGCCCTCCA    43530      CA      TATT
                                TGGA  GGCATGAT    GGGC
                                ||||  ||||||||    ||||
                                ACCT  CCGTACTA    TCCG
                                  C_       C___
GAM538  G2       5'  GCCCACAGAGAATCATGCCTCC 67242     AC        AT___
            CCA                    TGG  AGGCATGATT    TGGGC
                                   |||  ||||||||||    |||||
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                                ACC  TCCGTACTAA    ACCCG
                                  CC        GAGAC
GAM538  HN1L     3'  CAAAGTCACACCTGTCCA    58614        CA    A
                                TGGACAGG  TGATT TTG
                                ||||||||  ||||| |||
                                ACCTGTCC  ACTGA AAC
                                    AC    _
GAM538  KIAA0337 3'  TGGCCCAGGACTCGCCCGCCCA 29484     ACA   AT  TTA
                                TGG   GGC  GA   TTGGGCCA
                                |||   |||  ||   ||||||||
                                ACC   CCG  CT   GACCCGGT
                                  CGC   __  CAG
GAM538  MGC2574  3'  TCTAACTCATGCCTGTCCA   44286           TTA
                                TGGACAGGCATGA   TTGGG
                                ||||||||||||   |||||
                                ACCTGTCCGTACT   AATCT
                                       C__
GAM538  RINZF    3'  GCCCAATCACTCTGTCCA    43937        CA   TAT   C
                                TGGACAGG  TGAT   TGGG C
                                ||||||||  ||||   |||| |
                                ACCTGTCT  ACTA   ACCC G
                                    C_    ___    A
GAM538  LOC123242 5'  TGACCCAGACATGCCTGTCC   76121          ATTA    C
                                GGACAGGCATG    TTGGG CA
                                ||||||||||    ||||| ||
                                CCTGTCCGTAC    GACCC GT
                                      A___     A
GAM538  LOC253001 5'  TGACCCAGACATGCCTGTCC   97999          ATTA    C
                                GGACAGGCATG    TTGGG CA
                                ||||||||||    ||||| ||
                                CCTGTCCGTAC    GACCC GT
                                      A___     A
GAM538  LOC256158 5'  GGCCTCCCAGACCTGTCCA    99506        CA  ATTATT
                                TGGACAGG  TG     GGGCC
                                ||||||||  ||     |||||
                                ACCTGTCC  AC     TCCGG
                                    AG  CC____
GAM538  LOC91689  3'  GCTTCAATCATCCCTATCCA   53979     C   C     ATT
                                TGGA AGG ATGATT   GGGC
                                |||| ||| ||||||   ||||
                                ACCT TCC TACTAA   TTCG
                                  A  C     C__
GAM539  LOC165693 5'  ACAAAGGCGGCCTCCTTGTCCA 83485     _  AATTA      C
                                TGG CAA     GTCGCCTT GT
                                ||| |||     |||||||| ||
                                ACC GTT     CGGCGGAA CA
                                  T   CCTC_       A
GAM540  CDH12    3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
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                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM540  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM540  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090      T   AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                   _   GTCA_
GAM540  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
           A                     TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM540  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM540  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
           TA                    TACA   TCC   GAAGAATAAG
                                ||||   |||   ||||||||||
                                ATGT   AGG   TTTCTTATTC
                                  AAA_  ATTG
GAM540  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA  68742             _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                          G
GAM540  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM540  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748     CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM540  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM540  OSBPL11   3'  CTTAATTTCCCAAGAGTGGTG  43206        CCAA    AA
                                CACCACTC    GAAG  TAAG
                                ||||||||    ||||  ||||
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                                GTGGTGAG   CTTT  ATTC
                                    AACC   A_
GAM540  YME1L1   3'  TCATTCTTGATGTGGTGTA   58438       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                    TA_    A
GAM540  ZNF262   3'  CTTATTTTGTTTGGGAGT    18723       A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                     G
GAM540  LOC91960 3'  TGTGGCTTGGAACGTGGTGTA 68294       TC_    AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
                                ATGTGGTG   GGTTC   TGT
                                    CAA    GG__
GAM541  CD244    3'  CTTCCAATTTACAGATCAGA   33504       A    GC  T
                                TCTGATCT TAAAT  GG GG
                                |||||||| |||||  || ||
                                AGACTAGA ATTTA  CC TC
                                    C    A_  T
GAM541  RNF12    5'  CCACCGCAAAACTCAGATG    32786       TCTATAAA
                                CATCTGA      TGCGGTGG
                                |||||||      ||||||||
                                GTAGACT      ACGCCACC
                                   CAAA____
GAM541  SCGB3A2  3'  ACCAATTATAGATCAAATG    55047    C       ATGC
                                CAT TGATCTATAA   GGT
                                ||| ||||||||||   |||
                                GTA ACTAGATATT   CCA
                                  A        AA__
GAM541  COL12A1  3'  TCTCATTTACAGGTCAGAT    16472        A    C
                                ATCTGATCT TAAATG GG
                                ||||||||| ||||||  ||
                                TAGACTGGA ATTTAC CT
                                     C    T
GAM541  DKFZP586C1619 3'  CGTCATATTTATGGACCAGA   62617     A       C  TG
                                TCTG TCTATAAATG GG  G
                                |||| ||||||||||  ||  |
                                AGAC AGGTATTTAT CT  C
                                  C        A  GT
GAM541  DKFZp761D081 3'  ACCCATATAAATCAGATG    34695       C   AA  C
                                CATCTGAT TATA  TG GGT
                                |||||||| ||||  || |||
                                GTAGACTA ATAT  AC CCA
                                    A   __  _
GAM541  KIAA0483  3'  CCACCATGTGATCATTGATCAG 31473        TATAA__  GC
           ATG                   CATCTGATC     AT  GGTGG
                                |||||||||      ||  |||||
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                                GTAGACTAG     TG  CCACC
                                     TTACTAG  TA
GAM541  KIAA1297  5'  GCCACCGCATCCAGAGCAG   72642    A   ATAA
                                CTG TCT   ATGCGGTGGC
                                ||| |||   ||||||||||
                                GAC AGA   TACGCCACCG
                                  G   CC__
GAM541  MGC2603   3'  GCCACCGCGCCCAGCCAGATG  44075      AT  ATAAA
                                CATCTG  CT    TGCGGTGGC
                                ||||||  ||    |||||||||
                                GTAGAC  GA    GCGCCACCG
                                   C_  CCC__
GAM541  MOST2     5'  GCCATCGTTATACACCAGA   40066     ATC   AAT
                                TCTG   TATA   GCGGTGGC
                                ||||   ||||   ||||||||
                                AGAC   ATAT   TGCTACCG
                                  CAC    ____
GAM541  TCL6      5'  GCCACCGCACCTGGCCTCA   40481     T_   TAAA
                                TGA  CTA    TGCGGTGGC
                                |||  |||    |||||||||
                                ACT  GGT    ACGCCACCG
                                  CC   CC__
GAM541  LOC139673 3'  CCCCTTTTATAGATCAGA    76499          TGC  T
                                TCTGATCTATAAA   GG GG
                                ||||||||||||   || ||
                                AGACTAGATATTT   CC CC
                                       T__  _
GAM541  LOC144866 5'  GCCATGTTTATTACAGATCAGA 84136         A   AT_   G
           T                     ATCTGATCT TAA   GCG TGGC
                                ||||||||| |||   ||| ||||
                                TAGACTAGA ATT   TGT ACCG
                                     C   ATT   _
GAM541  LOC157798 5'  GCCTTAGTTATTTATAATTCAA 87860     C   TC       _ GGT
           ATG                    CAT TGA  TATAAATG C   GGC
                                ||| |||  |||||||| |   |||
                                GTA ACT  ATATTTAT G   CCG
                                  A   TA       T ATT
GAM541  LOC203248 3'  ACCGCATTTTATAGATGAGAT  90841      G        _
                                ATCT ATCTATAAA TGCGGT
                                |||| ||||||||| ||||||
                                TAGA TAGATATTT ACGCCA
                                  G        T
GAM542  EHF       3'  CCAAAACCCAAGGTTGGCT    25122     ATT   _   C
                                AGT   GCCT GGGT TTGG
                                |||   |||| |||| ||||
                                TCG   TGGA CCCA AACC
                                  GT_    A    A
GAM542  IGF1      3'  CCAAAACGGTAATACGTGAAA  7063       A       TGG  C
                                TTTCA GTATTGCC   GT TTGG
                                ||||| ||||||||   || ||||
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                                AAAGT CATAATGG  CA AACC
                                  G      ___  A
GAM542  DKFZp586H0623 3'  CCCAGGAAATACTTGAAA   34498         G
                                TTTCAAGTATT CCTGGG
                                |||||||||| ||||||
                                AAAGTTCATAA GGACCC
                                       A
GAM542  FLJ23153  3'  CCCAGGCAATACTCAAGA   45266    CA
                                TTT  AGTATTGCCTGGG
                                |||  ||||||||||||
                                AGA  TCATAACGGACCC
                                  AC
GAM542  MBLL39   3'  CCAAAGAGACAAGCACTTGAAA 20448       ATT  C  GG   _
                                TTTCAAGT   GC TG  TCTT GG
                                ||||||||   || ||  |||| ||
                                AAAGTTCA   CG AC  AGAA CC
                                     ___  A  AG   A
GAM542  PRO2955   3'  CCAACCACGGCAATACTGAAA  38235     A      _  GTC
                                TTTCA GTATTGCC TGG   TTGG
                                ||||| |||||||| |||   ||||
                                AAAGT CATAACGG ACC   AACC
                                   _       C  ___
GAM543  AHCY     3'  CACCTGGTCTGTGGACT     7303     C        A
                                AG CCACAGGCCA GGTG
                                || ||||||||| ||||
                                TC GGTGTCTGGT CCAC
                                 A        _
GAM543  CD2      3'  CACCTCCTGAGGCTGTGGGC   10092        G  A____
                                GCCCACAG CC     AGGTG
                                |||||||| ||     |||||
                                CGGGTGTC GG     TCCAC
                                     _  AGTCC
GAM543  MCL1     3'  CACCTTGGTTCTGGTTAA    41987       CACA
                                TTAGCC    GGCCAAGGTG
                                ||||||    ||||||||||
                                AATTGG    TTGGTTCCAC
                                    TC__
GAM543  TMPRSS3   5'  CACCTTTCTTTGGGCTGA    44017        C   CC
                                TTAGCCCA AGG  AAGGTG
                                |||||||| |||  ||||||
                                AGTCGGGT TCT  TTCCAC
                                     T  __
GAM543  BET3     3'  CACCTTTGGTTGGACTAG    27717     C   CAG    _
                                TTAG CCA   GCCAA GGTG
                                |||| |||   ||||| ||||
                                GATC GGT   TGGTT CCAC
                                  A  ___    T
GAM543  C20orf81  3'  CACCTCAGGTACTGGGCTAG   43117        CAG   A_
                                TTAGCCCA   GCC  AGGTG
                                ||||||||   |||  |||||
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                                GATCGGGT  TGG  TCCAC
                                    CA_  AC
GAM543  DKFZP586A011 3'  CACCTTCACTGGCATGGGCTAA 31839       CAG  ____
                                TTAGCCCA  GCCA   AGGTG
                                ||||||||  ||||   |||||
                                AATCGGGT  CGGT   TCCAC
                                    A__   CACT
GAM543  FLJ10101  3'  CTTTGGCCTACGGACTAA   45599     C  AC
                                TTAG CC  AGGCCAAGG
                                |||| ||  |||||||||
                                AATC GG  TCCGGTTTC
                                  A  CA
GAM543  HCRTR1   5'  CACCCTGAAGGGAGTGGGCTGA 9510         AGGC__  A
                                TTAGCCCAC     CA GGTG
                                |||||||||     || ||||
                                AGTCGGGTG     GT CCAC
                                     AGGGAA  C
GAM543  KCNT1    3'  CACCTTCTCCACCGTGGGCTA  62486       A__  CC
                                TAGCCCAC  GG  AAGGTG
                                ||||||||  ||  ||||||
                                ATCGGGTG  CC  TTCCAC
                                    CCA  TC
GAM543  KIAA0767  3'  CACCTTGGCGCCTGAGGC    61253     CA   __
                                GCC  CAGGC  CAAGGTG
                                |||  |||||  |||||||
                                CGG  GTCCG  GTTCCAC
                                  A_    CG
GAM543  MGC16491  3'  CACGAGGCCCCTGTGGGCT   54737       __   AAG
                                AGCCCACA  GGCC   GTG
                                ||||||||  ||||   |||
                                TCGGGTGT  CCGG   CAC
                                    CC    AG_
GAM543  PDK2     3'  CACCCTGGCCTTGGTCTGCTGA 12031      ___  C    A
                                TTAGC   CCA AGGCCA GGTG
                                |||||   ||| |||||| ||||
                                AGTCG   GGT TCCGGT CCAC
                                   TCT  _     C
GAM543  PRAX-1   3'  CACCTTGACCTTGGTCT     17653    C  C  C
                                AG CCA AGG CAAGGTG
                                || ||| ||| |||||||
                                TC GGT TCC GTTCCAC
                                 T  _  A
GAM543  SCAND2   5'  CACCTCAAGCCTGCTGGGCTAA 54414       _    CA_
                                TTAGCCCA CAGGC   AGGTG
                                |||||||| |||||   |||||
                                AATCGGGT GTCCG   TCCAC
                                    C     AAC
GAM543  U5-100K  3'  CACTCTTCCTGTGGGCTGA   60413         CC  _
                                TTAGCCCACAGG  AAG GTG
                                ||||||||||||  ||| |||
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                                AGTCGGGTGTCC  TTC CAC
                                      __   T
GAM543   LOC130752 3'  CACCTTGGCCTCAACTAA    75483     CCCAC
                                TTAG    AGGCCAAGGTG
                                ||||    ||||||||||
                                AATC    TCCGGTTCCAC
                                  AAC__
GAM543   LOC135932 5'  CACCTGGAGCATGGGCTAA   76695       CAGG   A
                                TTAGCCCA   CCA GGTG
                                ||||||||   ||| ||||
                                AATCGGGT   GGT CCAC
                                     ACGA  _
GAM543   LOC145652 3'  CACCTCTGCTGTAAGTTAA   84405     CC   G CA
                                TTAGC  ACAG C  AGGTG
                                |||||  |||| |  |||||
                                AATTG  TGTC G  TCCAC
                                   AA   _ TC
GAM543   LOC154739 5'  CACTTGCTGATGGGCTAA    87431       CA   CA
                                TTAGCCCA  GGC  AGGTG
                                ||||||||  |||  |||||
                                AATCGGGT  TCG  TTCAC
                                     AG  __
GAM543   LOC154760 5'  CACCTGGAGCATGGGCTAA   87452       CAGG   A
                                TTAGCCCA   CCA GGTG
                                ||||||||   ||| ||||
                                AATCGGGT   GGT CCAC
                                     ACGA  _
GAM543   LOC164633 3'  CACCCTGGCCTGTAAGGAGC  83423   _ __      A
                                GC CC  ACAGGCCA GGTG
                                || ||  |||||||| ||||
                                CG GG  TGTCCGGT CCAC
                                 A  AA       C
GAM543   LOC200583 5'  CACCTCTTCGTGGGCTA     90252       _  CCA
                                TAGCCCAC AGG   AGGTG
                                |||||||| |||   |||||
                                ATCGGGTG TTC   TCCAC
                                     C  ___
GAM543   LOC203276 3'  CACCTGTGGGTGGGCTAA    92110       AGG  _
                                TTAGCCCAC   CCA AGGTG
                                |||||||||   ||| |||||
                                AATCGGGTG   GGT TCCAC
                                     ___  G
GAM543   LOC203305 3'  CACCTGTGGGTGGGCTAA    92163       AGG  _
                                TTAGCCCAC   CCA AGGTG
                                |||||||||   ||| |||||
                                AATCGGGTG   GGT TCCAC
                                     ___  G
GAM543   LOC221178 3'  CTTTGGCCTGCGGACTAG    95170     C  A
                                TTAG CC CAGGCCAAGG
                                |||| || ||||||||||
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                                GATC GG GTCCGGTTTC
                                  A  C
GAM543  LOC253891 3'  CATCTCCTCGTGGGCTAA    96064        _  CCA
                                TTAGCCCAC AGG   AGGTG
                                ||||||||| |||   |||||
                                AATCGGGTG TCC   TCTAC
                                     C  ___
GAM543  LOC254243 3'  CACCTGTGGGTGGGCTAA    99249        AGG  _
                                TTAGCCCAC   CCA AGGTG
                                |||||||||   ||| |||||
                                AATCGGGTG   GGT TCCAC
                                     ___  G
GAM543  LOC254824 3'  CATTTGCCCATGGGCTAA    98410        CA   CA
                                TTAGCCCA  GGC  AGGTG
                                ||||||||  |||  |||||
                                AATCGGGT  CCG  TTTAC
                                     AC  __
GAM543  LOC255000 3'  CACCTTGGAGGTGGTTAA    98631       C  AGG
                                TTAGCC AC   CCAAGGTG
                                ||||||  ||   ||||||||
                                AATTGG TG   GGTTCCAC
                                   _  GA_
GAM543  LOC90038  3'  CACCTGTGGGTGGGCTAA    61792        AGG  _
                                TTAGCCCAC   CCA AGGTG
                                |||||||||   ||| |||||
                                AATCGGGTG   GGT TCCAC
                                     ___  G
GAM544  ITGA1     3'  CCAATGAGACAGTCCCTGA    64271      A   CAT  CA
                                TCAGG GAC   TG  TCATTGG
                                |||||  |||   ||  |||||||
                                AGTCC CTG   AC  AGTAACC
                                   _  ___  AG
GAM544  SH3GL3    5'  GCCAATATGGTCTCGATCTCCT 13111        CCATT  ATC
            GA                    TCAGGAGA    GC   ATTGGC
                                  ||||||||    ||  ||||||
                                  AGTCCTCT    TG   TAACCG
                                      AGCTC  GTA
GAM544  ARHGEF15  3'  GCCAATGAAAACGGCCGCCTGA 30954      AGA  ATTGCA
                                TCAGG   CC     TCATTGGC
                                |||||   ||     ||||||||
                                AGTCC   GG     AGTAACCG
                                   GCC  CAAA__
GAM544  DKFZp434F2322 3'  CCACCGACGATCTCCTGA    70299        CCA   CA  AT
                                TCAGGAGA   TTG  TC  TGG
                                ||||||||   |||  ||  |||
                                AGTCCTCT   AGC  AG  ACC
                                     ___   __  CC
GAM544  FLJ10716  3'  GCCACGTATCAACAATCTTCTG 37018        CCA   C  CAT
            A                     TCAGGAGA   TTG AT   TGGC
                                  ||||||||   ||| ||   ||||
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                                AGTCTTCT   AAC TA   ACCG
                                     AAC   _  TGC
GAM544   KIAA0527  3'  GCCACCTGCAATAGTCTCCTG  97499        C     TCAT
                                CAGGAGAC ATTGCA    TGGC
                                |||||||| ||||||    ||||
                                GTCCTCTG TAACGT    ACCG
                                     A     CC__
GAM544   KIAA1111  3'  GCCAATGACGCAGATAACCCTG 97946      AGACCA    A
           G                     TCAGG     TTGC TCATTGGC
                                |||||      |||| ||||||||
                                GGTCC     GACG AGTAACCG
                                   CAATA_    C
GAM544   Kv6.3     3'  GCCAATGATGCAAAGGTCCCC  56855    A    A
                                GG GACC TTGCATCATTGGC
                                || |||| ||||||||||||
                                CC CTGG AACGTAGTAACCG
                                 C    A
GAM544   LOC145547 3'  GCCAATGGAGACAATTCCTGA  77782       GACC    CA_
                                TCAGGA    ATTG   TCATTGGC
                                ||||||    ||||   ||||||||
                                AGTCCT    TAAC   GGTAACCG
                                     _____    AGA
GAM544   LOC162333 5'  GCCAATGACTGAGAACGCCCCT 88494       AGACCATTG  _
           GA                     TCAGG        CA TCATTGGC
                                |||||        || ||||||||
                                AGTCC        GT AGTAACCG
                                   CCGCAAGA_  C
GAM545   SLC4A1    3'  GGATGGTTACTGAGGACC    6223     _  A   AC
                                GG CC TCA  GTGGCCATCC
                                || || |||  ||||||||||
                                CC GG AGT  CATTGGTAGG
                                 A  _   __
GAM545   FLJ20273  3'  CGGGATTTTTGTTGATGGCTGA 39247            TGGCC
                                TCGGCCATCAACG    ATCCCG
                                ||||||||||||     ||||||
                                AGTCGGTAGTTGT    TAGGGC
                                       TTT__
GAM545   KIAA0146  5'  CGGAATGGCAGCTGATGGCTGA 82321          AC  G    C
                                TCGGCCATCA  GT GCCAT CCG
                                ||||||||||  || ||||| |||
                                AGTCGGTAGT  CG CGGTA GGC
                                      __ A    A
GAM545   KIAA1297  5'  GATGCATTTCGATGGCCG    72641        AAC   GC
                                CGGCCATC   GTG  CATC
                                ||||||||   |||  ||||
                                GCCGGTAG   TAC  GTAG
                                     CTT   __
GAM545   LOC254076 3'  GATGATGCTGATGGCC      98992        A   GGC
                                GGCCATCA CGT   CATC
                                |||||||| |||   ||||
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                                CCGGTAGT GTA   GTAG
                                     C  ___
GAM545  LOC91291  5' CGGGAGCCACCATGATGGCC  66088       AC    CA
                                GGCCATCA  GTGGC  TCCCG
                                ||||||||  |||||  |||||
                                CCGGTAGT  CACCG  AGGGC
                                     AC    __
GAM546  AGRP    5' CTTCATTAGGCCCTGCCATA  24616       A  A
                                TATGGCA GG CCTGATGGAG
                                ||||||| || ||||||||||
                                ATACCGT CC GGATTACTTC
                                     C  _
GAM546  CGTHBA   3' CTTCCCTCCAGTCCTTGCCG  24890        C  AT  A
                                TGGCAAGGAC TG  GG GAAG
                                |||||||||| ||  || ||||
                                GCCGTTCCTG AC  CC CTTC
                                      _  CT  _
GAM546  COL5A3   3' CTCCCCAGGCTCACCTTGCCAT 32318        A___   AT
           G                     TATGGCAAGG   CCTG  GGAG
                                ||||||||||   ||||  ||||
                                GTACCGTTCC   GGAC  CCTC
                                      ACTC   C_
GAM546  FGF23   3' CTTCTCTGGGGTCCCTTCCA  40557    CAA    GA
                                TGG   GGACCT  TGGAGAAG
                                |||   ||||||  ||||||||
                                ACC   CCTGGG  GTCTCTTC
                                 TTC    __
GAM546  FUT3    3' CTCCCAGAGACCTTGCCA   5621        AC_  AT
                                TGGCAAGG   CTG  GGAG
                                ||||||||   |||  ||||
                                ACCGTTCC   GAC  CCTC
                                     AGA   __
GAM546  FUT5    3' CTCCCAGAGACCTTGCCA   10726        AC_  AT
                                TGGCAAGG   CTG  GGAG
                                ||||||||   |||  ||||
                                ACCGTTCC   GAC  CCTC
                                     AGA   __
GAM546  TCF12   3' TCTCCTATCCTCTTGCCATA  13639         ACCT  _
                                TATGGCAAGG   GAT GGAGA
                                ||||||||||   ||| |||||
                                ATACCGTTCT   CTA CCTCT
                                      C___   T
GAM546  WSX1    3' CTCCCCCACATCCTTTCCTTGC 17915        CCT  _____
           C                     GGCAAGGA  GAT    GGAG
                                ||||||||  |||    ||||
                                CCGTTCCT  CTA    CCTC
                                     TTC  CACCC
GAM546  ZAP70   3' CTTCCCCACCCTCAGCCCCACC 71375    CAA  AC   ___  A
           CCA                    TGG  GG  CTGA  TGG GAAG
                                |||  ||  ||||  ||| ||||
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                                ACC   CC  GACT   ACC CTTC
                                  CCA  CC    CCC   C
GAM546  C1orf34   3'  CCTCTGGCCATTGCCATA    61303        _  A  T  T
                                TATGGCAA GG CC GA GG
                                |||||||| || || || ||
                                ATACCGTT CC GG CT CC
                                     A  _  T  _
GAM546  CLSTN1    3'  CTCCCCAGAGCACCCCCTGCCA 30787       A  AC____   AT
           T                     ATGGCA GG     CTG  GGAG
                                |||||| ||     |||  ||||
                                TACCGT CC     GAC  CCTC
                                   C  CCACGA   C_
GAM546  DKFZP434J193 3'  CTTCTCCACCACTCTCCTTGCC 71562          CC_  A
           ATG                     TATGGCAAGGA   TG TGGAGAAG
                                |||||||||||   || ||||||||
                                GTACCGTTCCT   AC ACCTCTTC
                                      CTC  C
GAM546  DNAJC6    3'  CTCCAAAGTTCCCACCATA    29492      CAA   C  GA
                                TATGG   GGA CT  TGGAG
                                |||||   ||| ||  |||||
                                ATACC   CCT GA  ACCTC
                                   AC_   T  A_
GAM546  FLJ12122  5'  CTGCCAGCTCAGGTCCCTGCCA 47092       A      __  _
                                TGGCA GGACCTGA  TGG AG
                                ||||| ||||||||  ||| ||
                                ACCGT CCTGGACT  ACC TC
                                   C       CG   G
GAM546  FLJ14642  3'  CTTCTCCGTAGTCCCCGCC   52575     AA    CTG
                                GGC  GGAC   ATGGAGAAG
                                |||  ||||   |||||||||
                                CCG  CCTG   TGCCTCTTC
                                  CC    A__
GAM546  FLJ20275  3'  CTGTCAGATCCTTGCCAT    35308          C
                                ATGGCAAGGA CTGATGG
                                |||||||||| |||||||
                                TACCGTTCCT GACTGTC
                                      A
GAM546  FLJ21369  3'  CTTCTCCATCAAGTTTCACCA  46051     CAA    C
                                TGG   GGAC TGATGGAGAAG
                                |||   |||| ||||||||||
                                ACC   TTTG ACTACCTCTTC
                                  AC_    A
GAM546  HSPC016   3'  TCTCTATTCCCTGCCATA    32503       A   CCTG
                                TATGGCA GGA    ATGGAGA
                                ||||||| |||    |||||||
                                ATACCGT CCT    TATCTCT
                                    C  _____
GAM546  HT014     3'  CTTCCTAATAAATCCTTGCCA  40153        CC  A   A
                                TGGCAAGGA  TG TGG GAAG
                                |||||||||  || ||| ||||
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                                ACCGTTCCT  AT ATC CTTC
                                     AA  A  _
GAM546  KIAA0773  3'  CTTCTCCACGACCTCACC    28722    CA   ACC  A
                                GG  AGG   TG TGGAGAAG
                                ||  |||   || ||||||||
                                CC  TCC   GC ACCTCTTC
                                 AC   A__  _
GAM546  KIAA1181  3'  CTCCATCAGCTGGTCA      68911      A  GAC
                                TGGC AG   CTGATGGAG
                                ||||  ||   |||||||||
                                ACTG TC   GACTACCTC
                                  G  ____
GAM546  KIAA1493  3'  CTTCTCCACCTAGTCTGCC   64840      AG   CTGA
                                GGCA  GAC    TGGAGAAG
                                ||||  |||    ||||||||
                                CCGT  CTG    ACCTCTTC
                                  __   ATCC
GAM546  KIAA1535  3'  CTCTGTGGTCCTTGCC      80212          TG
                                GGCAAGGACC  ATGGAG
                                ||||||||||  ||||||
                                CCGTTCCTGG  TGTCTC
                                          __
GAM546  KIAA1819  5'  CTTCTCCACGGCTCCCCCA   70252     CAA   C   A
                                TGG   GGA CTG TGGAGAAG
                                |||   ||| ||| ||||||||
                                ACC   CCT GGC ACCTCTTC
                                  C__   C   _
GAM546  LAT1-3TM  3'  CTCCATCAGTGTCATCACCA   49143     CAAG   _
                                TGG    GAC CTGATGGAG
                                |||    ||| |||||||||
                                ACC    CTG GACTACCTC
                                  ACTA   T
GAM546  LAT1-3TM  5'  CTCCATCAGTGTCATTACCA   49144     CAAG   _
                                TGG    GAC CTGATGGAG
                                |||    ||| |||||||||
                                ACC    CTG GACTACCTC
                                  ATTA   T
GAM546  OS4       3'  CTTCCCCATCATCCCTTCCATT 20389        _   CC___     A
            GCCA                    TGGCAA GGA     TGATGG GAAG
                                |||||| |||     |||||| ||||
                                ACCGTT CCT     ACTACC CTTC
                                   A   TCCCT     C
GAM546  RASSF2    3'  CTTCTCCACCTTCTCTCCA   29097     CA    CCTGA
                                TGG  AGGA    TGGAGAAG
                                |||  ||||    ||||||||
                                ACC  TCTT    ACCTCTTC
                                  TC   CC___
GAM546  SARM      3'  CTCCCCCAGGCCCTGCCAT   31285       A  A   AT
                                ATGGCA GG CCTG  GGAG
                                |||||| || ||||  ||||
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                                TACCGT CC GGAC  CCTC
                                   C  _   CC
GAM546  SELB     3'  CTCCCCCAGGGCCTCCTTGCC  62591        ___   AT
                                GGCAAGGA  CCTG  GGAG
                                ||||||||  ||||  ||||
                                CCGTTCCT  GGAC  CCTC
                                    CCG   CC
GAM546  SERPING1 3'  CTTCTCCATGGCCCTGCCATG  5348        A  A  TG
                                TATGGCA GG CC  ATGGAGAAG
                                ||||||| || ||  |||||||||
                                GTACCGT CC GG  TACCTCTTC
                                    C  _  __
GAM546  ZDHHC8   3'  TCCCCACCAACTTCTCTGCC  64622     _   CC  A   A
                                GGCA AGGA  TG TGG GA
                                |||| ||||  || ||| ||
                                CCGT TCTT  AC ACC CT
                                  C   CA  C   C
GAM546  LOC112868 5'  CTCCCAGCCCTTGCCA     73268        AC   AT
                                TGGCAAGG  CTG  GGAG
                                ||||||||  |||  ||||
                                ACCGTTCC  GAC  CCTC
                                    C_  __
GAM546  LOC150319 3'  CTTCTCCATCCTCCTGCCAT  80471       A   CCT
                                ATGGCA GGA   GATGGAGAAG
                                ||||||| |||  ||||||||||
                                TACCGT CCT   CTACCTCTTC
                                   _  C__
GAM546  LOC197423 5'  CTCCATCAGTGTCATTACCA  78424     CAAG  _
                                TGG   GAC CTGATGGAG
                                |||   ||| |||||||||
                                ACC   CTG GACTACCTC
                                  ATTA  T
GAM546  LOC199923 5'  CTTCTCCACCTCCTGCCA    89871      A   CCTGA
                                TGGCA GGA    TGGAGAAG
                                ||||| |||    ||||||||
                                ACCGT CCT    ACCTCTTC
                                   _  CC___
GAM546  LOC220565 5'  CTCCATCAGTGTCATCACCA  92441     CAAG  _
                                TGG   GAC CTGATGGAG
                                |||   ||| |||||||||
                                ACC   CTG GACTACCTC
                                  ACTA  T
GAM546  LOC221975 5'  CTTCTCCATGGAGCCTGCC   94192     A  AC  G
                                GGCA GG  CT ATGGAGAAG
                                ||||  ||  || |||||||||
                                CCGT CC  GG TACCTCTTC
                                   _  GA  _
GAM546  LOC257239 5'  CTTCTCCACCTCAACCACCA  98844     CAA  ACC  __
                                TGG   GG   TGA  TGGAGAAG
                                |||   ||   |||  ||||||||
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                                ACC   CC   ACT  ACCTCTTC
                                  A__  A__   CC
GAM546  LOC90499  3'  CTTCTCCATGGCCCCCTCCA  63741    CAA  A  TG
                                TGG   GG CC  ATGGAGAAG
                                |||   || ||  |||||||||
                                ACC   CC GG  TACCTCTTC
                                  TCC  C  __
GAM547  CELSR1   3'  GTCCTTTGCAAAGGCACCC   27276       CTA_   CTT
                                GGGTGCCT   AAAG   GAC
                                ||||||||   ||||   |||
                                CCCACGGA   TTTC   CTG
                                    AACG   ___
GAM547  EDG8     3'  TGCAAGGGTGGGGCACCC    79151       TAAAAG   A
                                GGGTGCCTC     CTTG CA
                                |||||||||     |||| ||
                                CCCACGGGG     GAAC GT
                                     TGG___   C
GAM547  GPD1     3'  TGTCAAGCCACTGGCAGCCT  60399    G   TCTAAAA
                                AGG TGCC      GCTTGACA
                                ||| ||||      ||||||||
                                TCC ACGG      CGAACTGT
                                  G   TCAC___
GAM547  GRAF     3'  GTCAAGCTCCCCAGGAGCCCCT 31241     T  CT  AAA_
           T                     AAGGG GC  CT   AGCTTGAC
                                |||||  ||  ||   ||||||||
                                TTCCC CG  GA   TCGAACTG
                                  _  AG  CCCC
GAM547  NEUROD2  3'  GGGCTCCCTGGAGGCACCC   21594         AA_
                                GGGTGCCTCTA   AGCTT
                                ||||||||||   |||||
                                CCCACGGAGGT   TCGGG
                                      CCC
GAM547  SET      3'  GTCAAACTTTGTCACCCT    13020       CCTCTA   C
                                AGGGTG     AAAG TTGAC
                                ||||||     |||| |||||
                                TCCCAC     TTTC AACTG
                                   TG____   A
GAM547  SLC6A5   5'  GTCAAACCAAGGGCACCTT   16142       T  AAAAGC
                                AGGGTGCC CT     TTGAC
                                |||||||| ||     |||||
                                TTCCACGG GA     AACTG
                                    _  ACCA__
GAM547  DKFZp434D177 3'  TGTCCCTTTTAGAGACACCTT  80252       C       CTT
                                AGGGTG CTCTAAAAG   GACA
                                |||||| |||||||||   ||||
                                TTCCAC GAGATTTTC   CTGT
                                   A       C__
GAM547  DKFZp761F2014 3'  TGTCAGCTCTAGAGGCACCCT  39942          AA   T
                                AGGGTGCCTCTA  AGCT GACA
                                ||||||||||||  |||| ||||
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                                TCCCACGGAGAT  TCGA CTGT
                                      C_   _
GAM547  EDG1     3'  TGTCAAGCTCCTAAAGGGTTC  60053    GG G   C  AA
                                G  T CCT TA  AGCTTGACA
                                |  | ||| ||  |||||||||
                                C  G GGA AT  TCGAACTGT
                                 TT _   A  CC
GAM547  FLJ30655  5'  GTCAAGCTCCCGCGGCACTCT  58955         TCTAAA
                                AGGGTGCC     AGCTTGAC
                                ||||||||     ||||||||
                                TCTCACGG     TCGAACTG
                                     CGCCC_
GAM547  KLHL6    3'  TGTCAAGCCTTGAGGACACCC  56179       _    TAAAA
                                GGGTG CCTC     GCTTGACA
                                ||||| ||||     ||||||||
                                CCCAC GGAG     CGAACTGT
                                   A    TTC__
GAM547  OATL1    5'  TGTCAAGCCCTTCAAGCCACCC 71017       C  CT  AA
                                GGGTG CT  AA  GCTTGACA
                                ||||| ||  ||  ||||||||
                                CCCAC GA  TT  CGAACTGT
                                   C  AC  CC
GAM547  P114-RHO-GEF 3'  TGTCAAGCCTTGTTCTGCACCC 31678        CTCTA  A
                                GGGTGC     AA GCTTGACA
                                ||||||     || ||||||||
                                CCCACG     TT CGAACTGT
                                    TCTTG  C
GAM547  PTRF     3'  TGGGCTCTTGGAGGCACCC    64249            A
                                GGGTGCCTCTAA AGCTTG
                                |||||||||||| ||||||
                                CCCACGGAGGTT TCGGGT
                                      C
GAM547  RNB6     3'  TGGGTTTCTAGAGACGCCC    33400       C     A
                                GGGTG CTCTA AAGCTTG
                                ||||| ||||| |||||||
                                CCCGC GAGAT TTTGGGT
                                   A    C
GAM547  LOC125297 5'  TCAAGGAGGAGGCGCCCTT    74868           AAAAG
                                AAGGGTGCCTCT     CTTGA
                                ||||||||||||     |||||
                                TTCCCGCGGAGG     GAACT
                                      AG___
GAM547  LOC143287 3'  TCCAGAACTTAGAGTGCACCCT 83830         _     AAG  T
          T                      AAGGGTGC CTCTAA   CT GA
                                 ||||||||  ||||||   || ||
                                 TTCCCACG GAGATT   GA CT
                                      T     CAA  C
GAM547  LOC149010 3'  TGTCCCTTTTAGAGACACCTT  79855       C        CTT
                                AGGGTG CTCTAAAAG   GACA
                                ||||||  |||||||||   ||||
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                                TTCCAC GAGATTTTC   CTGT
                                   A       C__
GAM547   LOC149013 3'  TGTCCCTTTTAGAGACACCTT  79860       C       CTT
                                AGGGTG CTCTAAAAG   GACA
                                |||||| |||||||||   ||||
                                TTCCAC GAGATTTTC   CTGT
                                   A       C__
GAM547   LOC149317 3'  TGTCCCTTTTAGAGACACCTT  80062       C       CTT
                                AGGGTG CTCTAAAAG   GACA
                                |||||| |||||||||   ||||
                                TTCCAC GAGATTTTC   CTGT
                                   A       C__
GAM547   LOC150951 5'  CAAGCTTTCCTGACCACCT    86342      CC  TA_
                                GGGTG  TC   AAAGCTTG
                                |||||  ||   ||||||||
                                TCCAC  AG   TTTCGAAC
                                  C_  TCC
GAM547   LOC204970 3'  TGTGGAGCTGAAAGGCACCC   90970        CTAAA    G
                                GGGTGCCT    AGCTT ACA
                                ||||||||    ||||| |||
                                CCCACGGA    TCGAG TGT
                                    AAG__    G
GAM547   LOC221463 3'  GCTACCTGGAGGCACCCTT    93704          AA_
                                AAGGGTGCCTCTA   AGC
                                ||||||||||||   |||
                                TTCCCACGGAGGT   TCG
                                      CCA
GAM547   LOC256940 5'  TCAAACTGAAGGGCACCC     98247        T  AAA  C
                                GGGTGCC CT   AG TTGA
                                ||||||| ||   || ||||
                                CCCACGG GA   TC AACT
                                   _  AG_  A
GAM548   BCL11A    3'  CCCTACATTCCAGCATCTTA   43465         A   ATTCAAT
                                TAAGATGCT GAA      GGG
                                ||||||||| |||      |||
                                ATTCTACGA CTT      CCC
                                     C   ACAT___
GAM548   ELK4      3'  CCCATTGAAAACATCTT     10514       CTAGAAA
                                AAGATG      TTCAATGGG
                                ||||||      |||||||||
                                TTCTAC      AAGTTACCC
                                   AA_____
GAM548   FUT6      5'  CCCCGAGTCCCTCTAGCATCT  5633          A__   AAT
                                AGATGCTAGA   ATTC   GGG
                                ||||||||||   ||||   |||
                                TCTACGATCT   TGAG   CCC
                                     CCC    C__
GAM548   TNFSF6    3'  CCCACTGGCAGCATCTT     7168         AGAAAT   A
                                AAGATGCT     TCA TGGG
                                ||||||||     ||| ||||
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                                TTCTACGA     GGT ACCC
                                    C_____   C
GAM548  WNT1     3'  CCCACCAGTGTAGCATCTT   19477        GAA   CAA
                                AAGATGCTA   ATT   TGGG
                                |||||||||   |||   ||||
                                TTCTACGAT   TGA   ACCC
                                    G__   CC_
GAM548  CG012    5'  CCCATTAAAAAGCACTAGCATT 84155        AAATTC__
           T                     AGATGCTAG       AATGGG
                                |||||||||       ||||||
                                TTTACGATC       TTACCC
                                    ACGAAAAA
GAM548  GR6      5'  TCCCATTGCCCTATTCTAGCAT 24750         ATT__
           C                     GATGCTAGAA    CAATGGGA
                                ||||||||||    ||||||||
                                CTACGATCTT    GTTACCCT
                                    ATCCC
GAM548  NIR3     3'  TCCCACTGAATTTCTACTCT   66833     TGC        A
                                AGA   TAGAAATTCA TGGGA
                                |||   |||||||||| |||||
                                TCT   ATCTTTAAGT ACCCT
                                  C__         C
GAM548  RAB9B    5'  TCCCATTGTGTTGGCACCCT   33478    A_     AAATT
                                AG  TGCTAG    CAATGGGA
                                ||  ||||||    ||||||||
                                TC  ACGGTT    GTTACCCT
                                  CC     GT___
GAM548  SLC31A2  3'  TCCCATTGAACTCCTAGT    60761      AAA
                                GCTAG   TTCAATGGGA
                                |||||   ||||||||||
                                TGATC   AAGTTACCCT
                                   CTC
GAM548  LOC147180 5'  TCCCAGAAGTATCCCTAGCATC 85106        AA  TCAA_
                                GATGCTAG  AT    TGGGA
                                ||||||||  ||    |||||
                                CTACGATC  TA    ACCCT
                                    CC  TGAAG
GAM548  LOC157657 3'  TCCCTCAAAATTTCTAGCTC   82438    T        CAAT
                                GA GCTAGAAATT    GGGA
                                || ||||||||||    ||||
                                CT CGATCTTTAA    CCCT
                                  _         AACT
GAM548  LOC158267 3'  TCCCACCAGGGACAGCGTCTTA 82723         AGAAA   AA__
                                TAAGATGCT    TTC    TGGGA
                                |||||||||    |||    |||||
                                ATTCTGCGA    AGG    ACCCT
                                    C_____   GACC
GAM548  LOC158364 5'  CCCACCTCTAGCATGTTA    82752     G       AATTCAA
                                TAA ATGCTAGA      TGGG
                                ||| ||||||||      ||||
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                                ATT TACGATCT      ACCC
                                  G       CC_____
GAM548  LOC220776 3'  CCCAGCATTTCTAGCTC     68922     T       TCAA
                                GA GCTAGAAAT    TGGG
                                || |||||||||    ||||
                                CT CGATCTTTA    ACCC
                                 _       CG__
GAM548  LOC91115  3'  TCCATCACCTCTAGCATTT    65578          AATTCA
                                AGATGCTAGA     ATGGG
                                ||||||||||     |||||
                                TTTACGATCT     TACCT
                                      CCAC__
GAM549  ITPKB     3'  CCTCGTCACCACAGGGACT    11062         AATAA  _
                                AGTCCCTGT     GAT AGG
                                |||||||||     ||| |||
                                TCAGGGACA     CTG TCC
                                      CCA__   C
GAM549  PKIA      3'  CTGCATTGCAGGAACCTGCT   23343      A  C       A_
                                AGCA GT CCTGTAAT  AG
                                |||| || ||||||||  ||
                                TCGT CA GGACGTTA  TC
                                  C  A       CG
GAM549  DKFZp547H236 3'  CCTACCTCCCTAGGGCCCTGCT 79244      AGT     TAATA  A
                                AGCA   CCCTG     AG TAGG
                                ||||   |||||     || ||||
                                TCGT   GGGAT     TC ATCC
                                  CCC     CCC__  C
GAM549  FLJ20273  5'  CCATCCACATAAGGATTTGC   39246         C   AATAA   A
                                GCAAGTCC TGT     GAT GG
                                |||||||| |||     ||| ||
                                CGTTTAGG ATA     CTA CC
                                     A   CAC__   C
GAM549  KIAA0534  3'  CTGATTACAGGAATTGCT     71930       GTC       A
                                AGCAA   CCTGTAAT AG
                                |||||   |||||||| ||
                                TCGTT   GGACATTA TC
                                  AA_       G
GAM549  KIAA0555  3'  CTTACTACAGGGATTTGCT    60740             A
                                AGCAAGTCCCTGTA TAAG
                                |||||||||||||| ||||
                                TCGTTTAGGGACAT ATTC
                                       C
GAM549  KIAA1068  3'  CCTGCATTCCAGGGACTTGCT  31685           T   AAGA
                                AGCAAGTCCCTG AAT    TAGG
                                |||||||||||| |||    ||||
                                TCGTTCAGGGAC TTA    GTCC
                                       C   C___
GAM549  KIAA1956  3'  CCCATCTCGTCATGTACAGGGA 79076          ____ TA    A
            CT                    AGTCCCTGTA    A  AGAT GG
                                ||||||||||    |  |||| ||
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                                TCAGGGACAT    T  TCTA CC
                                      GTAC GC    C
GAM549  LEPROTL1  3'  CTATTTTCACAGAGACTTGCT  31701        C    AAT
                                AGCAAGTC CTGT   AAGATAG
                                |||||||| ||||   |||||||
                                TCGTTCAG GACA   TTTTATC
                                     A    C__
GAM549  MEIS3     3'  CCTACCTCCCTAGGGCCCTGCT 78868      AGT    TAATA  A
                                AGCA   CCCTG    AG TAGG
                                ||||   |||||    || ||||
                                TCGT   GGGAT    TC ATCC
                                  CCC    CCC__  C
GAM549  LOC145980 5'  CCCATCTCACAATTTGGATTTG 84581         CT  AATA    A
           CT                     AGCAAGTCC  GT    AGAT GG
                                |||||||||  ||    |||| ||
                                TCGTTTAGG  TA    TCTA CC
                                     TT  ACAC    C
GAM549  LOC147669 3'  CCTACCTTATGGATTTGGGACT 85181         TGTA__     A
           TGC                    GCAAGTCCC     ATAAG TAGG
                                |||||||||      ||||| ||||
                                CGTTCAGGG     TATTC ATCC
                                     TTTAGG    C
GAM550  PROK1     3'  CACCAACCTGCTGGCTTTAGAA 51567      TCAC  G    AGC
                                TTCT    GG CAGCA   TGGTG
                                ||||    || |||||   |||||
                                AAGA    TC GTCGT   ACCAC
                                  TT__  G    CCA
GAM550  HSA404617 5'  CACCAGCTCGCCCTTCTGAGAA 73089      CAC_   AGCA
                                TTCTT    GGGC    AGCTGGTG
                                |||||    ||||    ||||||||
                                AAGAG    CCCG    TCGACCAC
                                   TCTT    C___
GAM550  KIAA0431  3'  CACCAGCTTGGGCAACATAAGA 31546      CACGG  AG
           A                      TTCTT    GC  CAAGCTGGTG
                                |||||    ||  ||||||||||
                                AAGAA    CG  GTTCGACCAC
                                   TACAA  G_
GAM550  PAK6      5'  ACCAGCCTGCAGTGGAGAA    39806        GG    CAA
                                TTCTTCAC  GCAG   GCTGGT
                                |||||||  ||||   ||||||
                                AAGAGGTG  CGTC   CGACCA
                                     A_    ___
GAM550  LOC90670  3'  TTTGCTGCCCTGAAGAA     64486        C
                                TTCTTCA GGGCAGCAAG
                                ||||||| ||||||||||
                                AAGAAGT CCCGTCGTTT
                                     _
GAM551  C20orf1   3'  GAGAAAGCATACTTGACA    25052    C   T      GTA
                                TG CAA GTATGCTT   CTC
                                || ||| ||||||||   |||
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                                AC GTT CATACGAA   GAG
                                 A   _       A__
GAM551   TCF12     3'  CTGATGCCAGCATACATT     13638          T   CTC
                                AATGTATGCT GTA   CAG
                                |||||||||| |||   |||
                                TTACATACGA CGT   GTC
                                     C   A__
GAM551   WHSC1     3'  AGAGCAGCATGACATTGGCA   56688          _    T  A
                                TGCCAATGT ATGCT GT CT
                                ||||||||| ||||| || ||
                                ACGGTTACA TACGA CG GA
                                     G    _ A
GAM551   DRF1      3'  GAGCACAATGTATAGGCA     47749      AATG    _   A
                                TGCC    TATGC TTGT CTC
                                ||||    ||||| |||| |||
                                ACGG    ATATG AACA GAG
                                  _____     T    C
GAM551   FLJ12668  3'  CTGGAGTACAGTGGTCACTGCA 47158     CAA  TA    T
                                TGC   TG  TGCT GTACTCCAG
                                |||   ||  |||| |||||||||
                                ACG   AC  GTGA CATGAGGTC
                                  TC_  TG    _
GAM551   KIAA0435  5'  TGGGTAGCATTACATTGGCA   29667          _   TGT  T
                                TGCCAATGTA TGCT   AC CCA
                                |||||||||| ||||   || |||
                                ACGGTTACAT ACGA   TG GGT
                                     T   ____ _
GAM551   SEZ6      3'  CTGGAGCACAAGCATCAACAGC 74829    CAA  T       A
                                GC   TG ATGCTTGT CTCCAG
                                ||   || |||||||| ||||||
                                CG   AC TACGAACA GAGGTC
                                 ACA  _       C
GAM551   TRIM2     3'  CTGGAATAGCAGTACACTAGCA 31599     CAA   _   TGTAC
                                TGC   TGTA TGCT     TCCAG
                                |||   |||| ||||     |||||
                                ACG   ACAT ACGA     AGGTC
                                  ATC    G    TA___
GAM551   LOC169026 3'  AGACACATACATTGGCA     83598           CT   A
                                TGCCAATGTATG  TGT CT
                                ||||||||||||  ||| ||
                                ACGGTTACATAC  ACA GA
                                      __   _
GAM552   CLECSF2   5'  CTTTGAAGAGAGTTTCTGC    18877    T  T   A_
                                GC GA GGC  TCTTCAAAG
                                || || |||  |||||||||
                                CG CT TTG  AGAAGTTTC
                                 T  _   AG
GAM552   FLJ20340  3'  CAGCTTTGAAAAACTTTTCAGC 35452       TGGCATC
                                GCTGA      TTCAAAGCTG
                                |||||      ||||||||||
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                                CGACT      AAGTTTCGAC
                                   TTTCAAA
GAM552  FLJ21709  5'  AGCTTTGAAAGCCAACA     50812    A   ATC
                                TG TGGC   TTCAAAGCT
                                || ||||   |||||||||
                                AC ACCG   AAGTTTCGA
                                 A   A__
GAM552  FLJ21709  3'  AGCTTTGAAAGCCAACA     78476    A   ATC
                                TG TGGC   TTCAAAGCT
                                || ||||   |||||||||
                                AC ACCG   AAGTTTCGA
                                 A   A__
GAM552  FLJ22794  5'  CAGCTTTGAAGATACTGCTAT  93240       ___
                                ATGGCA   TCTTCAAAGCTG
                                ||||||   ||||||||||||
                                TATCGT   AGAAGTTTCGAC
                                   CAT
GAM552  KIAA0280  3'  CAGCTTTGGGCCTGACCCCAGC 93291     AT  _  TC
                                GCTG  GG CA  TTCAAAGCTG
                                ||||  || ||  ||||||||||
                                CGAC  CC GT  GGGTTTCGAC
                                  C_  A  CC
GAM552  SGKL     3'  AGCCTGGGTGCCACAGCGA   26050       A       TCAAA
                                TCGCTG TGGCATCT    GCT
                                |||||| ||||||||    |||
                                AGCGAC ACCGTGGG    CGA
                                   _       TC___
GAM552  SMCR7    3'  CAGCTTCGAAGATGTGAACAAG 58237    GC  ATG       A
           A                     TC  TG   GCATCTTC AAGCTG
                                 ||  ||   |||||||| |||||||
                                 AG  AC   TGTAGAAG TTCGAC
                                  A_  AAG       C
GAM552  WNT16    3'  CAGCCTTGGGCAAGATGCCTCA 32729      T     ___    A
           GC                      GCTGA GGCATCT   TCAA GCTG
                                 |||||| |||||||   |||| ||||
                                 CGACT CCGTAGA   GGTT CGAC
                                   _      ACG    C
GAM552  WNT16    3'  CAGCCTTGGGCAAGATGCCTCA 55147      T     ___    A
           GC                      GCTGA GGCATCT   TCAA GCTG
                                 |||||| |||||||   |||| ||||
                                 CGACT CCGTAGA   GGTT CGAC
                                   _      ACG    C
GAM552  ZER6     3'  CAGCTTCCTTGAGCCATCAGAG 64114    G       A  TTCA
           A                      TC CTGATGGC TC    AAGCTG
                                  || |||||||| ||    ||||||
                                  AG GACTACCG AG    TTCGAC
                                   A       _ TTCC
GAM552  LOC124976 3'  CAGCTTTGAAGACTCAACAG   74840     A   CA
                                CTG TGG  TCTTCAAAGCTG
                                ||| |||  ||||||||||||
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                                GAC ACT  AGAAGTTTCGAC
                                  A   C_
GAM552  LOC148638 3'  GTGAGAAGATGCCATCCGC   79667    T         AAA
                                GC GATGGCATCTTC   GC
                                || ||||||||||||   ||
                                CG CTACCGTAGAAG   TG
                                 C          AG_
GAM552  LOC203378 3'  AGCTCTGATCATCAGT     92273        CATCT   A
                                GCTGATGG    TCA AGCT
                                ||||||||    ||| ||||
                                TGACTACT    AGT TCGA
                                     _____  C
GAM552  LOC90249  3'  CAGCTTTGGCACCCACCAAGGA 62609    GC  A   CATCT
                                TC  TG TGG    TCAAAGCTG
                                ||  || |||    |||||||||
                                AG  AC ACC    GGTTTCGAC
                                 GA  C   CAC__
GAM552  LOC91097  5'  AGCTTTGAAGCTCCAGAG    65462    GA   CAT
                                CT  TGG   CTTCAAAGCT
                                ||  |||   ||||||||||
                                GA  ACC   GAAGTTTCGA
                                 G_   TC_
GAM553  HAL      5'  GCCACTCCTGCATAAAGCTC   10903          TGAAAA
                                GAGCTTTATGC     GGTGGC
                                ||||||||||     ||||||
                                CTCGAAATACG     TCACCG
                                      TCC___
GAM553  HMGN2    3'  GGCCACCTTGGCACAAAAGC   19809      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                   _ _  GG
GAM553  NMI      5'  GGCCACCTCCTCAGGAAG    17436     ATG   AA
                                CTTT   CTGA  AGGTGGCC
                                ||||   ||||  ||||||||
                                GAAG   GACT  TCCACCGG
                                  ___    CC
GAM553  PACE     3'  GGCCACCTCTCCAAGGGCTT   11944       A  CT  AAA
                                GAGCTTT TG  GA   GGTGGCC
                                ||||||| ||  ||   |||||||
                                TTCGGGA AC  CT   CCACCGG
                                   _  CT  ___
GAM553  PYCR1    3'  CCACCTTCCTCTAGAGCTC    70639       TGCT  A_
                                GAGCTTTA    GA  AAGGTGG
                                ||||||||    ||  |||||||
                                CTCGAGAT    CT  TTCCACC
                                     _____  CC
GAM553  SDC1     3'  GGCCACCTCCCCAGCATTCCAG 12991     TT_     AAA
            C                    GCT   ATGCTG   AGGTGGCC
                                 |||   ||||||   ||||||||
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                                CGA  TACGAC  TCCACCGG
                                  CCT    CCC
GAM553  FLJ11560  5' GCCCAGGCCCAGCATAAAG  48008       AAAA  ___
                                CTTTATGCTG  GGT  GGC
                                ||||||||||  |||  |||
                                GAAATACGAC  CCG  CCG
                                      _____  GAC
GAM553  KIAA0446  5' CCACCTTTTGAAGAGCTC  69446      ATGCTG
                                GAGCTTT    AAAAGGTGG
                                |||||||    |||||||||
                                CTCGAGA    TTTTCCACC
                                   AG____
GAM553  KIAA0971  3' GTTGTTCTCAGCATAAAGT  30677        AAA  TG
                                GCTTTATGCTGA  GG  GC
                                ||||||||||||  ||  ||
                                TGAAATACGACT  TT  TG
                                      C__  GT
GAM553  KIAA1393  3' GGCCACCTTGGCACAAAAGC  72574     A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _  GG
GAM553  KIAA1656  3' GGCCACCTCCTCCTAGAAGCC  66377   A    ATGCT  AA
                                G GCTTT    GA  AGGTGGCC
                                | |||||    ||  ||||||||
                                C CGAAG    CT  TCCACCGG
                                _    ATC__  CC
GAM553  KIAA1884  3' GCCACCTTCATCTACCAAGGCT 73728       ATGCT  A_
           C                     GAGCTTT    GA  AAGGTGGC
                                |||||||    ||  ||||||||
                                CTCGGAA    CT  TTCCACCG
                                   CCAT_  AC
GAM553  PP3501    3' GGCCACCGTTGACAGCATAAAG 41683        AAAA_
                                CTTTATGCTG    GGTGGCC
                                ||||||||||    |||||||
                                GAAATACGAC    CCACCGG
                                      AGTTG
GAM553  SDCCAG3   3' GGTGTTCTCAGCATGAAGCTC  22803          AAA  TG
                                GAGCTTTATGCTGA  GG  GCC
                                ||||||||||||||  ||  |||
                                CTCGAAGTACGACT  CT  TGG
                                      ___  TG
GAM553  SP140     3' GGCCACCTCCATGCAGAAGC  24327     A  TGAAA
                                GCTTT TGC    AGGTGGCC
                                ||||| |||    ||||||||
                                CGAAG ACG    TCCACCGG
                                  _  TACC_
GAM553  LOC148760 3' GGCCACCTTCTCCAACAAGCTC 85364      TA  CT  A
                                GAGCTT  TG  GA AAGGTGGCC
                                ||||||  ||  || |||||||||
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                                CTCGAA  AC  CT TTCCACCGG
                                   CA  __  C
GAM553  LOC150170 5'  ACCTGTTTCACATAAAGC    80414        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                     _    G
GAM553  LOC150175 5'  ACCTGTTTCACATAAAGC    80453        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                     _    G
GAM553  LOC150215 5'  ACCTGTTTCACATAAAGC    80456        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                     _    G
GAM553  LOC150218 5'  ACCTGTTTCACATAAAGC    80525        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                     _    G
GAM553  LOC152065 3'  GGCCACCTTCTCCTTGGCAGGC 86737       TTA   ___  A
           TC                    GAGCT   TGCT   GA AAGGTGGCC
                                |||||   ||||   || |||||||||
                                CTCGG   ACGG   CT TTCCACCGG
                                   ___    TTC  C
GAM553  LOC152267 3'  GGCCACCTTGGCACAAAAGC   61036      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                   _ _  GG
GAM553  LOC158292 5'  CCTCTGGACCCAGCATAAGGCT 88046            AAAA_  T
           C                     GAGCTTTATGCTG    GG GG
                                ||||||||||||    || ||
                                CTCGGAATACGAC    TC CC
                                        CCAGG  T
GAM553  LOC219997 3'  GCCACCTCTTCAGCCTC     93256     CTTTAT     A
                                GAG     GCTGAA AGGTGGC
                                |||     |||||| |||||||
                                CTC     CGACTT TCCACCG
                                  _____     C
GAM553  LOC256269 3'  GGCCACCTTGGCACAAAAGC   96608      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                   _ _  GG
GAM553  LOC91963  5'  GGCCACCTCCTCTGAGAAGC   68321      ATGCT  AA
                                GCTTT    GA  AGGTGGCC
                                |||||    ||  ||||||||
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                                CGAAG    CT  TCCACCGG
                                   AGT__  CC
GAM554  CCND2    3'  TCCCAGCAAATCATCGGGCCA  10055          CCACA  _  A
                                TGGCCTGATGAT    GC GG GA
                                ||||||||||||    || || ||
                                ACCGGGCTACTA    CG CC CT
                                       AA___  A  C
GAM554  GCN5L2   5'  CTCCGCTGCGGGGGAGGCC   60529      GATGA  A
                                GGCCT    TCC CAGCGGAG
                                |||||    ||| ||||||||
                                CCGGA    GGG GTCGCCTC
                                   GG___  C
GAM554  GJA5     3'  CTGACCAGATCATCAGCCA   19164      C      CACAG
                                TGGC TGATGATC    CGG
                                |||| ||||||||    |||
                                ACCG ACTACTAG    GTC
                                  _      ACCA_
GAM554  HIVEP3   3'  TCCCCGCTGTGGTTGGCAGCCA 44702      C  ATGAT       A
                                TGGC TG    CCACAGCGG GA
                                |||| ||    ||||||||| ||
                                ACCG AC    GGTGTCGCC CT
                                  _ GGTT_       C
GAM554  HOXD1    5'  CCGCCGGTATATTAGGCCA   44696         AT  ACA
                                TGGCCTGATG  CC   GCGG
                                ||||||||||  ||   ||||
                                ACCGGATTAT  GG   CGCC
                                      AT  C__
GAM554  SUFU     3'  CCTTGTGACCCATCAGGCCA  32934         ATC    C
                                TGGCCTGATG   CACAG GG
                                ||||||||||   ||||| ||
                                ACCGGACTAC   GTGTT CC
                                      CCA    _
GAM554  DKFZP586J1624 3'  CTCCGCCCAGTCACCATCAGGC 32043          ATCCACA_
           CA                   TGGCCTGATG       GCGGAG
                                ||||||||||       ||||||
                                ACCGGACTAC       CGCCTC
                                      CACTGACC
GAM554  KIAA1671  3'  CTTTGCTTATGAATCATCAGAC 66282    C      C  C_
           C                    GG CTGATGAT CA  AGCGGAG
                                || |||||||| ||  |||||||
                                CC GACTACTA GT  TCGTTTC
                                 A       A  AT
GAM554  LOC159110 5'  TCTCCGCTGCCCCGGTCAACCA 82995     CCTGA    CA__
                                TGG    TGATC    CAGCGGAGA
                                |||    |||||   |||||||||
                                ACC    ACTGG    GTCGCCTCT
                                  A_____    CCCC
GAM554  LOC159116 5'  TCTCCGCTGCCCCGGTCAACCA 82978     CCTGA    CA__
                                TGG    TGATC    CAGCGGAGA
                                |||    |||||   |||||||||
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                                ACC    ACTGG   GTCGCCTCT
                                  A____    CCCC
GAM554  LOC165476 5'  CTCCGCTGCCTGCTCAGCCA  88550     C  TGATCCA
                                TGGC TGA     CAGCGGAG
                                |||| |||     ||||||||
                                ACCG ACT     GTCGCCTC
                                  _  CGTCC__
GAM554  LOC200032 5'  CTGACCAGATCATCAGCCA   85475     C      CACAG
                                TGGC TGATGATC    CGG
                                |||| ||||||||    |||
                                ACCG ACTACTAG    GTC
                                  _      ACCA_
GAM554  LOC219654 5'  CTCCGCTGCGGAGGGGGGCC  92932      GATGA  A
                                GGCCT    TCC CAGCGGAG
                                |||||    ||| ||||||||
                                CCGGG    AGG GTCGCCTC
                                   GGG__  C
GAM554  LOC255862 3'  TCAAATGTAGACTATCAGGCCA 96115         A  C  GCG
                                TGGCCTGATG TC ACA  GA
                                |||||||||| || |||  ||
                                ACCGGACTAT AG TGT  CT
                                      C  A  AAA
GAM555  CCND2    3'  CCAGCAAATCATCGGGCCA   10048          CCACA
                                TGGCCTGATGAT    GCTGG
                                ||||||||||||    |||||
                                ACCGGGCTACTA    CGACC
                                      AA___
GAM555  COG7     3'  CCAGATGGATCATGAAGCCA  68250     CTG      CAG
                                TGGC  ATGATCCA  CTGG
                                ||||  ||||||||  ||||
                                ACCG  TACTAGGT  GACC
                                  AAG      A__
GAM555  GJA5     3'  CCCTGACCAGATCATCAGCCA 19163     C      CA__  CT
                                TGGC TGATGATC   CAG  GG
                                |||| ||||||||   |||  ||
                                ACCG ACTACTAG   GTC  CC
                                  _      ACCA  __
GAM555  LAMC1    3'  TCCAGCAAGTCTCAGGCCA   11270       T  CCACA
                                TGGCCTGA GAT    GCTGGA
                                |||||||| |||    ||||||
                                ACCGGACT CTG    CGACCT
                                     _  AA___
GAM555  MB       5'  CCAGCTGTTGGGGCCAGGACA 19322   G   ATGA  _
                                TG CCTG   TCCA CAGCTGG
                                || ||||   |||| |||||||
                                AC GGAC   GGGT GTCGACC
                                 A   CG__   T
GAM555  MYCL1    3'  CTCCAGCTTTCTGCCATCTAGC 19365     CT   ATCCAC
            CA                   TGGC  GATG    AGCTGGAG
                                ||||  ||||    ||||||||
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                                ACCG  CTAC     TCGACCTC
                                  AT   CGTCTT
GAM555  PKM2     3'  CCAGCCCATCCATTAGGCCA  12141         ATCCACA
                                TGGCCTGATG      GCTGG
                                ||||||||||      |||||
                                ACCGGATTAC      CGACC
                                     CTACC__
GAM555  RAD51L3  3'  TCCAGCTGCTTCAGGCTA    56895        TGATCCA
                                TGGCCTGA      CAGCTGGA
                                ||||||||      ||||||||
                                ATCGGACT      GTCGACCT
                                    TC_____
GAM555  RHBG     3'  CTCCAGCTGCAAGAAGGGAGCC 40274      _  GATGATCCA
          A                      TGGC CT       CAGCTGGAG
                                ||||  ||       |||||||||
                                ACCG GG       GTCGACCTC
                                  A  GAAGAAC__
GAM555  SUFU     3'  TTGTGACCCATCAGGCCA    32942         ATC
                                TGGCCTGATG   CACAG
                                ||||||||||   |||||
                                ACCGGACTAC   GTGTT
                                     CCA
GAM555  FLJ12389 3'  CTCCAGCTGTGAGCCCAGGC   60898      ATGATC
                                GCCTG     CACAGCTGGAG
                                |||||     ||||||||||
                                CGGAC     GTGTCGACCTC
                                   CCGA__
GAM555  FLJ12788 3'  CTCCAGCATCTGTCTCAGGCCA 42847        T   CCACA
                                TGGCCTGA GAT    GCTGGAG
                                |||||||| |||    |||||||
                                ACCGGACT CTG    CGACCTC
                                     _  TCTA_
GAM555  KIAA1171 3'  CCAGCTGTGAAATGGGGCCA   89340       G  GATC
                                TGGCCT AT    CACAGCTGG
                                |||||| ||    |||||||||
                                ACCGGG TA    GTGTCGACC
                                   G  AA__
GAM555  KIAA1742 3'  CTCCAGCTGTGGATGTTAAACC 78138    CC    G
                                GG  TGAT ATCCACAGCTGGAG
                                ||  |||| ||||||||||||||
                                CC  ATTG TAGGTGTCGACCTC
                                 AA   _
GAM555  KIAA1822 3'  CCACCTCAGATCATCAGGC    68182          CAC  C
                                GCCTGATGATC   AG TGG
                                ||||||||||   || |||
                                CGGACTACTAG   TC ACC
                                      AC_  C
GAM555  MGC18079 3'  CCGCGGACCTCAGGCCA     59033        TGA   ACA  T
                                TGGCCTGA   TCC   GC GG
                                ||||||||   |||   || ||
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                                ACCGGACT  AGG  CG CC
                                   CC_  ___  C
GAM555  P5-1     5'  TCCAGCCACTATTAGGCCA  22890       ATCCACA
                                TGGCCTGATG    GCTGGA
                                ||||||||||    ||||||
                                ACCGGATTAT    CGACCT
                                    CAC____
GAM555  PGS1     5'  CCAGCTGTTCCCCAGGTCA  44593      AT  TCC
                                TGGCCTG  GA  ACAGCTGG
                                |||||||  ||  ||||||||
                                ACTGGAC  CT  TGTCGACC
                                   CC  ___
GAM555  WBSCR16  3'  CTCCAGCTGCAGGTGAGGCC  96149     G TGAT  A_
                                GGCCT A   CC  CAGCTGGAG
                                ||||| |   ||  |||||||||
                                CCGGA T   GG  GTCGACCTC
                                  G ____  AC
GAM555  LOC150245 3'  CTCCAGCTGTAGCAAAGACA  86111   GC  GA  ATCC
                                TG  CT  TG   ACAGCTGGAG
                                ||  ||  ||   ||||||||||
                                AC  GA  AC   TGTCGACCTC
                                 A_  A_  GA__
GAM555  LOC200032 5'  CCCTGACCAGATCATCAGCCA  85474     C      CA__  CT
                                TGGC TGATGATC   CAG  GG
                                |||| ||||||||   |||  ||
                                ACCG ACTACTAG   GTC  CC
                                  _      ACCA  __
GAM555  LOC220936 3'  TCCAACTATGTGTCAGGC   93046       ATC  C  C
                                GCCTGATG  CA AG TGGA
                                ||||||||  || || ||||
                                CGGACTGT  GT TC ACCT
                                    ___  A  A
GAM555  LOC255862 3'  CAAATGTAGACTATCAGGCCA  96113        A  C  GC
                                TGGCCTGATG TC ACA  TG
                                |||||||||| || |||  ||
                                ACCGGACTAT AG TGT  AC
                                      C  A  AA
GAM555  LOC257449 3'  CTCCAGCTGTGGATGTTAAACC 63374   CC   G
                                GG  TGAT ATCCACAGCTGGAG
                                ||  |||| ||||||||||||||
                                CC  ATTG TAGGTGTCGACCTC
                                 AA   _
GAM556  EPS15    3'  TGTAAAAACTTTCACTGA    10533        GTACTG
                                TCAGTGAAAGT    TTTACA
                                ||||||||||    ||||||
                                AGTCACTTTCA    AAATGT
                                      A_____
GAM556  TEGT     3'  ATGGCTCACTTTCACTGA    65226         TA
                                TCAGTGAAAGTG  CTGT
                                ||||||||||  ||||
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                                AGTCACTTTCAC  GGTA
                                      TC
GAM556  TEK      3'  TGTAGGCACACTTTGCACTGA  6620       _     ACT
                                TCAGTG AAAGTGT   GTTTACA
                                |||||| |||||||   |||||||
                                AGTCAC TTTCACA   CGGATGT
                                   G     ____
GAM556  DKFZP434N093 3'  ATGTAAACAGAAGGTCTTCA   80743     AG GTA
                                TGAA  T   CTGTTTACAT
                                ||||  |   ||||||||||
                                ACTT  G   GACAAATGTA
                                  CT GAA
GAM556  FLJ21302  3'  ATGCAAACAGTACATTAAAAAC 43504     GAA_         A
             TG                   CAGT    AGTGTACTGTTT CAT
                                ||||    |||||||||||| |||
                                GTCA    TTACATGACAAA GTA
                                  AAAA          C
GAM556  FRAG1    3'  ACAGTCACCTTTCACTGA    27943         T  _
                                TCAGTGAAAG GT ACTGT
                                |||||||||| || |||||
                                AGTCACTTTC CA TGACA
                                      _  C
GAM556  GPR105   5'  TGGGCAAAACACCTTCACTGA  30269        A    AC
                                TCAGTGAA GTGT  TGTTTA
                                |||||||| ||||  ||||||
                                AGTCACTT CACA  ACGGGT
                                     C    AA
GAM556  KIAA1673  3'  TAGGCACACTTTTCACTGA   71329         _   A_
                                TCAGTGAAA GTGT  CTG
                                ||||||||| ||||  |||
                                AGTCACTTT CACA  GAT
                                      T    CG
GAM556  KIAA1946  3'  TGTAAACAAGTTCAGTGA    83359     G    AGTGTAC
                                TCA TGAA      TGTTTACA
                                ||| ||||      ||||||||
                                AGT ACTT      ACAAATGT
                                  G    GA_____
GAM556  LOC203339 5'  TGTGGACACGCCCCCACTGA   92220       AAA    ACT
                                TCAGTG   GTGT   GTTTACA
                                ||||||   ||||   |||||||
                                AGTCAC   CGCA   CAGGTGT
                                   CCC    ___
GAM556  LOC219561 3'  ATGCAAACAGTAATATCTCATT 93409      AAGTG       A
                                AGTGA     TACTGTTT CAT
                                |||||     |||||||| |||
                                TTACT     ATGACAAA GTA
                                   CTATA       C
GAM557  AMACR    3'  TTGTATGCATGGAAACATGGA  69103      ATC        G
                                TCCAT   TCCATGCATG CGG
                                |||||   |||||||||| |||
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                                AGGTA  AGGTACGTAT GTT
                                  CAA       _
GAM557  BCL2L11  3'  TCGCCCAGAGATATGGA    57615        CA  CAT   G
                                TCCATATCTC  TG  GGCG A
                                ||||||||||  ||  |||| |
                                AGGTATAGAG  AC  CCGC T
                                    __ ____   G
GAM557  BCL2L11  3'  TCGCCCAGAGATATGGA    57616        CA  CAT   G
                                TCCATATCTC  TG  GGCG A
                                ||||||||||  ||  |||| |
                                AGGTATAGAG  AC  CCGC T
                                    __ ____   G
GAM557  FGFR2    5'  CGTCCACATGGAGATATGGA  5559           CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                    __  T
GAM557  FGFR2    5'  CGTCCACATGGAGATATGGA  43633          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                    __  T
GAM557  FGFR2    5'  CGTCCACATGGAGATATGGA  43638          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                    __  T
GAM557  FGFR2    5'  CGTCCACATGGAGATATGGA  43642          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                    __  T
GAM557  FGFR2    5'  CGTCCACATGGAGATATGGA  43652          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                    __  T
GAM557  FGFR2    5'  CGTCCACATGGAGATATGGA  43665          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                    __  T
GAM557  FGFR2    5'  CGTCCACATGGAGATATGGA  43674          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                    __  T
GAM557  FGFR2    5'  CGTCCACATGGAGATATGGA  43678          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
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                                AGGTATAGAGGTAC  ACC GC
                                      __   T
GAM557  FGFR2    5'  CGTCCACATGGAGATATGGA   43763          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __   T
GAM557  FGFR2    5'  CGTCCACATGGAGATATGGA   43767          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __   T
GAM557  FGFR2    5'  CGTCCACATGGAGATATGGA   43771          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __   T
GAM557  MAP3K14  3'  ATCCGCCACGTGAAGAGA    15541     CA  A
                                TCTC  TGC TGGCGGAT
                                ||||  ||| ||||||||
                                AGAG  GTG ACCGCCTA
                                  AA  C
GAM557  KIAA0819 3'  CCCCAGCATCACAGGAGACATG 64330      A   ____   A  C
           GA                     TCCAT TCTCC   ATGC TGG GG
                                ||||| |||||   |||| ||| ||
                                AGGTA AGAGG   TACG ACC CC
                                  C    ACAC   _  _
GAM557  PORIMIN  3'  CATACATGGAGTATGGA     54702       T     C
                                TCCATA CTCCATG ATG
                                ||||||| ||||||| |||
                                AGGTAT GAGGTAC TAC
                                   _     A
GAM557  RDC1     3'  CCGGCACGGGATATGGA     72832        T  A  A
                                TCCATATC CC TGC TGG
                                |||||||| || ||| |||
                                AGGTATAG GG ACG GCC
                                     _ C  _
GAM557  VEZATIN  3'  ATCCGCCACAACAGACAATG   34656    A_  CCA  CA
                                CAT  TCT   TG  TGGCGGAT
                                |||  |||   ||  ||||||||
                                GTA  AGA   AC  ACCGCCTA
                                  AC   CA_ __
GAM557  LOC147645 5'  ATCCGCTGGTGGCAGAGACACG 79065    ATA   CA  AT__
           G                     CC   TCTC  TGC   GGCGGAT
                                ||   ||||  |||   |||||||
                                GG   AGAG  ACG   TCGCCTA
                                 CAC    __   GTGG
GAM557  LOC199775 3'  TTGCTGCATCAGAGATATG   89726        C_    TG
                                CATATCTC  ATGCA  GCGG
                                ||||||||  |||||  ||||
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                                GTATAGAG  TACGT  CGTT
                                    AC    __
GAM557  LOC51279  3'  CCGCTATTAGAGTATGGA    33752       T   CATGC
                                TCCATA CTC    ATGGCGG
                                ||||||| |||    |||||||
                                AGGTAT GAG    TATCGCC
                                   _   AT___
GAM558  FLJ22332  5'  GGAAAGAAAACTACATCACA   45637     G  A      _______
                                TGTG AT TAGTTTTC     CC
                                |||| || ||||||||     ||
                                ACAC TA ATCAAAAG     GG
                                  _ C       AAA___
GAM559  IRS2      3'  GACCCTGCTGAAAGCAGTGTA  60440         C    C  A
                                TATACTGCT TTAGC AG GTC
                                ||||||||| ||||| || |||
                                ATGTGACGA AGTCG TC CAG
                                      A    _ C
GAM559  LZTS1     3'  ACTCCAGGAAAGAGCAGTCA   41023   T       AG  A_
                                A ACTGCTCTT  CC  GAGT
                                | |||||||||  ||  ||||
                                A TGACGAGAA  GG  CTCA
                                 C        A_  AC
GAM559  PCOLN3    3'  GACTCTGGGGCAGCAG      12413      _ TAG
                                CTGCT CT   CCAGAGTC
                                ||||| ||   ||||||||
                                GACGA GG   GGTCTCAG
                                   C  ___
GAM559  STC1      3'  GACTCTGCTTAAACAAAGCAGT 13462         C___    C
            ATA                   TATACTGCT    TTAG CAGAGTC
                                |||||||||    |||| |||||||
                                ATATGACGA    AATT GTCTCAG
                                      AACA    C
GAM559  CYorf14   3'  ACTCTGGCCAGGTGCAGTA   38201       T   A
                                TACTGC CTT GCCAGAGT
                                |||||| ||| ||||||||
                                ATGACG GGA CGGTCTCA
                                    T   C
GAM559  DKFZP434C131 3'  GACTCTGGGAGAACAG     69637     C    AG
                                CTG TCTT  CCAGAGTC
                                ||| ||||  ||||||||
                                GAC AGAG  GGTCTCAG
                                  A   __
GAM559  FLJ12298  5'  GACTCCAGGAAGGGCAG     50598        AG  A_
                                CTGCTCTT  CC  GAGTC
                                ||||||||  ||  |||||
                                GACGGGAA  GG  CTCAG
                                     __  AC
GAM559  FLJ21477  3'  ACTCTTAAGAGAGCAGTAT   47902          AGCC
                                ATACTGCTCTT    AGAGT
                                ||||||||||    |||||
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                                TATGACGAGAG   TCTCA
                                      AAT_
GAM559  FYCO1    3'  GACTCTGGCCAAGCTGATG   44771    ACT   CTTA
                                TAT   GCT   GCCAGAGTC
                                |||   |||   |||||||||
                                GTA   CGA   CGGTCTCAG
                                  GT_   AC__
GAM559  KIAA1819  3'  ACTCCAAGCACTAAAAGGCAGT 70249       T   A____  CA_
          ATA                     TATACTGC CTT    GC   GAGT
                                |||||||| |||    ||   ||||
                                ATATGACG GAA    CG   CTCA
                                     _  AATCA  AAC
GAM559  SUPT4H1   3'  GACTGTTGAGAGAGCAG     13487       AGC   _
                                CTGCTCTT   CAG AGTC
                                ||||||||   ||| ||||
                                GACGAGAG   GTT TCAG
                                     A__   G
GAM559  LOC134553 3'  TTGCCTAAGAGCATATA     75689     C       C
                                TATA TGCTCTTAG CAG
                                |||| |||||||||| |||
                                ATAT ACGAGAATC GTT
                                  _       C
GAM559  LOC145474 3'  GACTCTGAAAGGCAGTATG    77729       T   AGC
                                TATACTGC CTT   CAGAGTC
                                |||||||| |||   |||||||
                                GTATGACG GAA   GTCTCAG
                                     _  A__
GAM559  LOC202934 3'  ACCCTGTTTAGAGCAGTCA    92023    T      T   C  A
                                A ACTGCTCT AGC AG GT
                                | |||||||| ||| || ||
                                A TGACGAGA TTG TC CA
                                 C       T   _  C
GAM559  LOC91250  5'  ACTCTGAGAAGCAGTATG     65901        _  TAGC
                                TATACTGCT CT    CAGAGT
                                ||||||||| ||    ||||||
                                GTATGACGA GA    GTCTCA
                                     A  _____
GAM560  BCRP2    3'  TCTGAATGTCTAGCTGGCCA   63071      G   GGCT
                                TGGCC AGT    CATTCAGA
                                ||||| |||    ||||||||
                                ACCGG TCG    GTAAGTCT
                                  _   ATCT
GAM560  CD81     3'  CTGGGAGCCACTCGCCCA     16385     C       AT
                                TGG CGAGTGGCTC  TCAG
                                ||| ||||||||||  ||||
                                ACC GCTCACCGAG  GGTC
                                  C         __
GAM560  CDH13    3'  TCTGAATGCTGCCACAACCA   8840      CCGA    T_
                                TGG    GTGGC  CATTCAGA
                                |||    |||||  ||||||||
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                                ACC   CACCG  GTAAGTCT
                                  AA__    TC
GAM560  CIT     3'  TCCAAATGAGCCTTTCCC   70306   CC  T     CA
                                GG  GAG GGCTCATT  GA
                                ||  ||| ||||||||  ||
                                CC  CTT CCGAGTAA  CT
                                 __  T      AC
GAM560  CRAT    3'  CTGGGATGGGCCACCCACCA  7477    CCGA       _
                                TGG   GTGGCTCATTC AG
                                |||   |||||||||||| ||
                                ACC   CACCGGGTAGG TC
                                  ACC_        G
GAM560  DNM2    3'  CTGAATGAGGGGTCCAGCC   18235   CGAG  ____
                                GGC   TGG   CTCATTCAG
                                |||   |||   |||||||||
                                CCG   ACC   GAGTAAGTC
                                 ____  TGGG
GAM560  DUSP4   5'  TCCAAATGAGCCCAGTCCCCC  9154    CC  G  _    CA
                                GG  GA TGG CTCATT  GA
                                ||  || ||| ||||||  ||
                                CC  CT ACC GAGTAA  CT
                                 CC  G   C     AC
GAM560  ITGA9   3'  CTGAGGCAGCCACTTCGGCCA  11035      _    CA
                                TGGCCGA GTGGCT  TTCAG
                                ||||||| ||||||  |||||
                                ACCGGCT CACCGA  GAGTC
                                    T     CG
GAM560  MAP3K9  3'  CTGCAGAGTCACTCAGCCA   61362    C      ATT
                                TGGC GAGTGGCTC   CAG
                                |||| |||||||||   |||
                                ACCG CTCACTGAG   GTC
                                  A       AC_
GAM560  NOTCH3  3'  TCTGTGGGCCCATTCGGCCA  6482         _   TT
                                TGGCCGAGTGG CTCA  CAGA
                                |||||||||||| ||||  ||||
                                ACCGGCTTACC GGGT  GTCT
                                      C   __
GAM560  P2RX4   3'  TCTGTTTGCCCACTCGGCC   11920        CT  TT
                                GGCCGAGTGG  CA  CAGA
                                ||||||||||  ||  ||||
                                CCGGCTCACC  GT  GTCT
                                      C_  TT
GAM560  PLEK    3'  TCTGAATGTAACTCACCA    12168    CC   GGCT
                                TGG  GAGT   CATTCAGA
                                |||  ||||   ||||||||
                                ACC  CTCA   GTAAGTCT
                                  A_   AT__
GAM560  PRKCABP 3'  TCTGTTCCCCCAGCTCGGCCA  25749       _  CTCATT
                                TGGCCGAG TGG     CAGA
                                |||||||| |||     ||||
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                                ACCGGCTC ACC     GTCT
                                    G  CCCTT_
GAM560  PTPN7    3'  TCTAGAAGCCACTCCAGCCA  55464     C_      CAT  _
                                TGGC  GAGTGGCT   TC AGA
                                ||||  ||||||||   || |||
                                ACCG  CTCACCGA   AG TCT
                                  AC       ____  A
GAM560  PTPN7    3'  TCTAGAAGCCACTCCAGCCA  12595     C_      CAT  _
                                TGGC  GAGTGGCT   TC AGA
                                ||||  ||||||||   || |||
                                ACCG  CTCACCGA   AG TCT
                                  AC       ____  A
GAM560  TCTA     3'  TCTGCTGGGCCACCAGCCA  42505     CGA      TT
                                TGGC   GTGGCTCA  CAGA
                                ||||   ||||||||  ||||
                                ACCG   CACCGGGT  GTCT
                                  AC_      C_
GAM560  TNFAIP1  5'  TCTGGCCTCCACTGGCCA   41233     G    CTCAT
                                TGGCC AGTGG    TCAGA
                                ||||| |||||    |||||
                                ACCGG TCACC    GGTCT
                                   _    TCC__
GAM560  ZNF219   3'  TTGAGGAGCCACTCTGCCA  33558     C       A
                                TGGC GAGTGGCTC TTCAG
                                |||| ||||||||| |||||
                                ACCG CTCACCGAG GAGTT
                                  T       _
GAM560  C20orf51 3'  TCTGAATGAGTATTGAGCTA  42289     _  GTG
                                TGGC CGA   GCTCATTCAGA
                                |||| |||   ||||||||||
                                ATCG GTT   TGAGTAAGTCT
                                  A  A__
GAM560  CCR7     3'  TCTGAATGAACCTTCTGGCC  10228     _  T  C
                                GGCC GAG GG TCATTCAGA
                                |||| ||| || |||||||||
                                CCGG CTT CC AGTAAGTCT
                                  T  _  A
GAM560  CPR2     3'  TCTGATGCTTGGCCACTCACCC 48841    CC      CAT__
           A                     TGG  GAGTGGCT    TCAGA
                                |||  ||||||||    |||||
                                ACC  CTCACCGG    AGTCT
                                  CA       TTCGT
GAM560  CXorf1   3'  CTGAATGGCAATCGCCCA   17487    C  GTG  T
                                TGG CGA   GC CATTCAG
                                ||| |||   || |||||||
                                ACC GCT   CG GTAAGTC
                                  C  AA_  _
GAM560  FLJ21551 3'  TCTGGTAGCCACTTAACCA  46042    CC      CAT
                                TGG  GAGTGGCT   TCAGA
                                |||  ||||||||   |||||
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                                ACC  TTCACCGA   GGTCT
                                  AA       T__
GAM560  GMFB     3'  CTGAATAGTTAACTAAACCA   15939     CCG  _   C
                                TGG   AGT GGCT ATTCAG
                                |||   ||| |||| ||||||
                                ACC   TCA TTGA TAAGTC
                                  AAA   A   _
GAM560  IMAGE:4907098 3'  CTGAGGACCACTCGGCTA    57755          C  A
                                TGGCCGAGTGG TC TTCAG
                                |||||||||||| || |||||
                                ATCGGCTCACC AG GAGTC
                                                _ _
GAM560  KIAA0700  3'  CTGGGACCCACGCGGCCA    72519       A    C  AT
                                TGGCCG GTGG TC  TCAG
                                |||||| |||| ||  ||||
                                ACCGGC CACC AG  GGTC
                                   G    C  __
GAM560  KIAA1437  3'  TCTGAACTTGTAGACTCGGTCA 61221         G_  TCA
                                TGGCCGAGT  GC   TTCAGA
                                |||||||||  ||   ||||||
                                ACTGGCTCA  TG   AAGTCT
                                     GA  TTC
GAM560  MGC13090  3'  TCTGGAGTGGCCACTTGGCCA  52124           CA
                                TGGCCGAGTGGCT  TTCAGA
                                ||||||||||||  ||||||
                                ACCGGTTCACCGG  AGGTCT
                                       TG
GAM560  ZNF282    3'  TCTGAATGGACGCCCAGCTC   90697      __  __
                                GAGT  GGC  TCATTCAGA
                                ||||  |||  |||||||||
                                CTCG  CCG  GGTAAGTCT
                                  AC   CA
GAM560  ZNF387    3'  TCTGAATGATTACTTCAAACA  28684    GCC_     C
                                TG    GAGTGG TCATTCAGA
                                ||    |||||| |||||||||
                                AC    TTCATT AGTAAGTCT
                                 AAAC     _
GAM560  LOC144465 3'  TCTGAATGCAGCTCAGCC    77353     C    GGCT
                                GGC GAGT    CATTCAGA
                                ||| ||||    ||||||||
                                CCG CTCG    GTAAGTCT
                                  A   AC__
GAM560  LOC149127 5'  TCTGAATGAATAAGTAGCCA   85504      CGAG  GC
                                TGGC    TG  TCATTCAGA
                                ||||    ||  |||||||||
                                ACCG    AT  AGTAAGTCT
                                  ATGA  A_
GAM560  LOC196955 3'  TCTCGGAGCCACTGGCCA     77875       G       ATTC
                                TGGCC AGTGGCTC    AGA
                                ||||| ||||||||    |||
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                                ACCGG TCACCGAG    TCT
                                  _       GC__
GAM560  LOC201109 3'  CTGGAGGTGCCCTCGGCCA   91327        T   TCA
                                TGGCCGAG GGC   TTCAG
                                |||||||| |||   |||||
                                ACCGGCTC CCG   AGGTC
                                     _  TGG
GAM560  LOC203350 3'  CTGCTGGTGCACTCAGCCA   92237      C    _  T  TT
                                TGGC GAGTG GC CA  CAG
                                |||| ||||| || ||  |||
                                ACCG CTCAC TG GT  GTC
                                  A    G  _  C_
GAM560  LOC253512 3'  TCTGAATGATATCTCTACCA  96586     CC   TGGC
                                TGG  GAG    TCATTCAGA
                                |||  |||    |||||||||
                                ACC  CTC    AGTAAGTCT
                                  AT   TAT_
GAM560  LOC254312 5'  TCTGTGGCCTCTCGGCCA    98129        T   T  TT
                                TGGCCGAG GGC CA  CAGA
                                |||||||| ||| ||  ||||
                                ACCGGCTC CCG GT  GTCT
                                     T   _  __
GAM560  LOC55971  3'  TCTAATGACCAGCTCAGCCA  38733      C   _   C    C
                                TGGC GAG TGG TCATT AGA
                                |||| ||| ||| ||||| |||
                                ACCG CTC ACC AGTAA TCT
                                  A   G   _    _
GAM560  LOC90019  3'  TCTGAACCCCAACTCGGCCA  57537         _  CTCA
                                TGGCCGAGT GG    TTCAGA
                                |||||||||  ||    ||||||
                                ACCGGCTCA CC    AAGTCT
                                     A  CC__
GAM561  ANGPT4    3'  GTACCTTGAATGGGCT      32572        GGCA
                                AGCCCATT    GGGGTAC
                                ||||||||    |||||||
                                TCGGGTAA    TTCCATG
                                     G___
GAM561  ASS       5'  GGCACCCCTGCCAGTCCTGCTC 55026      CC_         A
                                GAGC   ATTGGCAGGGGT CC
                                ||||   |||||||||||| ||
                                CTCG   TGACCGTCCCCA GG
                                  TCC          C
GAM561  BAK1      3'  TACCCTTGTGAGAGCCCA    93634    A  CCA  G
                                TG GC   TT GCAGGGGTA
                                || ||   || |||||||||
                                AC CG   GA TGTTCCCAT
                                 C  A__  G
GAM561  DNASE1L1  3'  GGTACCGATATGCCAATGGGCC 23018    A        A________  GGTA
          A                      TG GCCCATTGGC       GG    C
                                || ||||||||||       ||    |
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                                AC CGGGTAACCG       CC    G
                                 _        TATAG___  ATGG
GAM561  DUSP6    3'  ACACCAAATCATGGGCTCA   66576         T  CAG  _
                                TGAGCCCAT GG   GG GT
                                ||||||||| ||   || ||
                                ACTCGGGTA CT   CC CA
                                      _ AAA  A
GAM561  MN1      3'  ACACTTTGCCAATTAGCTCA   11647      CC        _
                                TGAGC  ATTGGCAGGG GT
                                |||||  |||||||||| ||
                                ACTCG  TAACCGTTTC CA
                                   AT         A
GAM561  MPP2     3'  GCAGGGGCCAGTGGGCTCA   60520           AGGG
                                TGAGCCCATTGGC    GT
                                ||||||||||||    ||
                                ACTCGGGTGACCG    CG
                                        GGGA
GAM561  SULT1A2  3'  CCCTGACCAATGGGCTCA    72672           _
                                TGAGCCCATTGG CAGGG
                                |||||||||||| |||||
                                ACTCGGGTAACC GTCCC
                                        A
GAM561  SULT1A3  3'  CCCTGACCAATGGGCTCA    13483           _
                                TGAGCCCATTGG CAGGG
                                |||||||||||| |||||
                                ACTCGGGTAACC GTCCC
                                        A
GAM561  TRPM2    3'  GGCACCCCTGCAGAGGCTC    13868      CATTG       A
                                GAGCC     GCAGGGGT CC
                                |||||     |||||||| ||
                                CTCGG     CGTCCCCA GG
                                   AGA__       C
GAM561  XBP1     3'  ACTTTTGCCAATGAACTC     18674     CC
                                GAG  CATTGGCAGGGGT
                                |||  ||||||||||||
                                CTC  GTAACCGTTTTCA
                                  AA
GAM561  BMF      3'  GGTACCGGTGCCATATGGGCTC 54286         _   A_____  GGTA
           A                     TGAGCCCAT TGGC      GG    C
                                |||||||| ||||     ||   |
                                ACTCGGGTA ACCG     CC    G
                                      T    TGG___  ATGG
GAM561  DKFZP727M111 5'  GCTTTTGCCAGTGAGCCCA    32061    A  C
                                TG GC CATTGGCAGGGGT
                                || || ||||||||||||
                                AC CG GTGACCGTTTTCG
                                 C  A
GAM561  FLJ13162  5'  GCACCCTCCATGGGCTCA    47185         T  C   _
                                TGAGCCCAT GG AGGG GT
                                |||||||| || |||| ||
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                                ACTCGGGTA CC TCCC CG
                                    _ _   A
GAM561  GMPPB    5' ACTTCTGCAATAAGCCCA   97429   A CC   G
                                TG GC  ATTG CAGGGGT
                                || ||  |||| |||||||
                                AC CG  TAAC GTCTTCA
                                 C  AA   _
GAM561  KIAA0444 3' TGCCCCATGGGCTCA      63006        TGGCA
                                TGAGCCCAT    GGGGTA
                                |||||||||    ||||||
                                ACTCGGGTA    CCCCGT
                                    _____
GAM561  KIAA0963 3' GACCCACAAGGGCTCA     31033       A  GCAG   A
                                TGAGCCC TTG   GGGT C
                                ||||||| |||   |||| |
                                ACTCGGG AAC   CCCA G
                                   _  A___   C
GAM561  KIAA1649 5' GCTTATGACCAATGGGCCA  51243   A      _ GG
                                TG GCCCATTGG CA  GGT
                                || |||||||| ||  |||
                                AC CGGGTAACC GT  TCG
                                 _       A  AT
GAM561  KIAA1649 3' GCTTATGACCAATGGGCCA  67517   A      _ GG
                                TG GCCCATTGG CA  GGT
                                || |||||||| ||  |||
                                AC CGGGTAACC GT  TCG
                                 _       A  AT
GAM561  KIAA1813 3' GCTTCTGCCAAGAACTCA   70825    CCCA
                                TGAG   TTGGCAGGGGT
                                ||||   ||||||||||
                                ACTC   AACCGTCTTCG
                                  AAG_
GAM561  KIAA1813 5' GGCTCCCCCCACCAATGGGC 70828       CA_   TA
                                GCCCATTGG  GGGG  CC
                                |||||||||  ||||  ||
                                CGGGTAACC  CCCC  GG
                                     ACC   TC
GAM561  MAP1LC3A 3' ACCCCTGCTGTGTGGTTCA  51679      _  T
                                TGAGCC CAT GGCAGGGGT
                                |||||| ||| |||||||||
                                ACTTGG GTG TCGTCCCCA
                                   T  _
GAM561  MGC11316 3' GGTGCATTGCCAAGGACTCA 53047    C A    GG
                                TGAG CC TTGGCAG  GTACC
                                |||| || |||||||  |||||
                                ACTC GG AACCGTT  CGTGG
                                  A _     A_
GAM561  PDE8B    5' GGCACCCCTGCCCGGCCTC   68203    C  ATT      A
                                GAG CC   GGCAGGGGT CC
                                ||| ||   |||||||| ||
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                                CTC GG   CCGTCCCCA GG
                                  C  C__       C
GAM561  PRO0529  3'  TACTCACCAATGGGACCA    26857    AG      CAG
                                TG  CCCATTGG   GGGTA
                                ||  ||||||||   |||||
                                AC  GGGTAACC   CTCAT
                                 CA       A__
GAM561  RAB17    3'  CCCCTGCCTGGGCCA      42617    A    TT
                                TG GCCCA  GGCAGGGG
                                || |||||  ||||||||
                                AC CGGGT  CCGTCCCC
                                 _    __
GAM561  UBE2G1   3'  ACTCCTGCCAAGAGCCCA    13950    A  CCA
                                TG GC   TTGGCAGGGGT
                                || ||   ||||||||||
                                AC CG   AACCGTCCTCA
                                 C  AG_
GAM561  LOC115708 3'  GGTACCCCTACCCCTCA     73920      CCCATT  C
                                TGAG     GG AGGGGTACC
                                ||||     || |||||||||
                                ACTC     CC TCCCCATGG
                                  C_____  A
GAM561  LOC150481 3'  GCACCTAACAATGGGTCA    80705     G      GC   G
                                TGA CCCATTG  AGG GT
                                ||| |||||||  ||| ||
                                ACT GGGTAAC  TCC CG
                                  _      AA   A
GAM561  LOC153196 5'  GGCACTGCCTTGCCATCGGGCC 87171    A    AT       __  A
           CA                     TG GCCC  TGGCAGGG  GT CC
                                || ||||  ||||||||  || ||
                                AC CGGG  ACCGTTCC  CA GG
                                 C   CT       GT  C
GAM561  LOC153711 5'  ACCTGTTAGCCGATGGGCCCA  87342    A        AG__
                                TG GCCCATTGGC    GGGT
                                || ||||||||||    ||||
                                AC CGGGTAGCCG    TCCA
                                 C         ATTG
GAM561  LOC157860 3'  GGCACCCCCTCCTGGGCTC    87878        TT  CA    A
                                GAGCCCA  GG  GGGGT CC
                                |||||||  ||  ||||| ||
                                CTCGGGT  CC  CCCCA GG
                                    __  TC    C
GAM561  LOC158014 5'  GTGCCACCCATGGGCTCA    82566         T  CAGG
                                TGAGCCCAT GG    GGTAC
                                |||||||||  ||    |||||
                                ACTCGGGTA CC    CCGTG
                                      _  CA__
GAM561  LOC158191 3'  GCACCTAACAATGGGTCA    82677     G      GC   G
                                TGA CCCATTG  AGG GT
                                ||| |||||||  ||| ||
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                                ACT GGGTAAC  TCC CG
                                  _      AA   A
GAM561   LOC203378 5'  ATCTCTGCCAACAGTCTCA   92276      CCCA
                                TGAG    TTGGCAGGGGT
                                ||||    ||||||||||
                                ACTC    AACCGTCTCTA
                                  TGAC
GAM561   LOC203378 3'  GGTATTTTGCCCAAAGGCTCA  92295       CATT      G
                                TGAGCC    GGCAGGG TACC
                                ||||||    ||||||| ||||
                                ACTCGG    CCGTTTT ATGG
                                   AAAC      _
GAM561   LOC204970 3'  GGCACCCCTGCGGGCTCA    90964       ATTG      A
                                TGAGCCC    GCAGGGGT CC
                                |||||||    |||||||| ||
                                ACTCGGG    CGTCCCCA GG
                                   ____       C
GAM561   LOC219700 5'  GGCTTCCCTGCCATGGACTCA  94653     C    T      TA
                                TGAG CCAT GGCAGGGG  CC
                                |||| |||| ||||||||  ||
                                ACTC GGTA CCGTCCCT  GG
                                  A   _       TC
GAM561   LOC256126 3'  GCCCCTGCCATAGGCCCA    97015    A   CAT
                                TG GCC   TGGCAGGGGT
                                || |||   ||||||||||
                                AC CGG   ACCGTCCCCG
                                 C   AT_
GAM561   LOC51246  3'  ACCTGGGCCAATGGGCCA    33636    A       AG
                                TG GCCCATTGGC  GGGT
                                || ||||||||||  ||||
                                AC CGGGTAACCG  TCCA
                                 _        GG
GAM561   LOC90190  3'  ACTGTTACCAATGGGCTC    62421          C  G
                                GAGCCCATTGG AG GGT
                                |||||||||||  || |||
                                CTCGGGTAACC TT TCA
                                       A  G
GAM562   LDLR      3'  GGGATTGGCAATTGTCCCCA   6741       A  C      GT
                                TGGG AC ATTGCCAA  CT
                                |||| || ||||||||  ||
                                ACCC TG TAACGGTT  GG
                                  C  T       AG
GAM562   NRIP1     3'  TACCAAACTCAGGTGATTCC   60624     ACC  TG  A_   C
                                GGA   AT  CC  AGT TGGTA
                                |||   ||  ||  ||| |||||
                                CCT   TA  GG  TCA ACCAT
                                  ___  GT  AC   A
GAM562   PSEN2     3'  ACCAGACTTTGGCTCCC     25950      ACCATT    _
                                GGGA     GCCAA GTCTGGT
                                ||||     ||||| |||||||
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                                CCCT     CGGTT CAGACCA
                                  _______    T
GAM562  PSEN2    3'  ACCAGACTTTGGCTCCC     6542      ACCATT    _
                                GGGA     GCCAA GTCTGGT
                                ||||     ||||| |||||||
                                CCCT     CGGTT CAGACCA
                                  _______    T
GAM562  FLJ12604 3'  ACATGGTAAAATGGTTCCCA  65059          __    A
                                TGGGAACCAT  TGCCA GT
                                ||||||||||  ||||| ||
                                ACCCTTGGTA  ATGGT CA
                                      AA    A
GAM562  FLJ13081 3'  ACATGGCAGTGGTTCCCA    46169            A
                                TGGGAACCATTGCCA GT
                                |||||||||||||| ||
                                ACCCTTGGTGACGGT CA
                                         A
GAM562  FLJ23093 3'  ACCAGACTCCTCAGGTTCC   45321      AT  CCA
                                GGAACC  TG   AGTCTGGT
                                ||||||  ||   ||||||||
                                CCTTGG  AC   TCAGACCA
                                   __ TCC
GAM562  GP5      3'  ACCAGACTCACGGTCTCCA   16857     GA   AT  CCA
                                TGG  ACC  TG   AGTCTGGT
                                |||  |||  ||   ||||||||
                                ACC  TGG  AC   TCAGACCA
                                  TC   C_  ___
GAM562  KIAA0286 3'  ACCAGACTTACTGGCTCACCA  68855     _  A   TTGCC
                                TGG GA CCA     AAGTCTGGT
                                ||| || |||     |||||||||
                                ACC CT GGT     TTCAGACCA
                                  A  C   CA___
GAM562  MGC10540 3'  ACCAGACTCAAAAGGACTCCA  51356      AA  A  GCCA
                                TGGG  CC TT    AGTCTGGT
                                ||||  || ||    ||||||||
                                ACCT  GG AA    TCAGACCA
                                  CA  A  AC__
GAM562  LOC157226 5'  TACCGCAGGCAAAGGTTCCCA  64640         A    AAGTC
                                TGGGAACC TTGCC     TGGTA
                                |||||||| |||||     |||||
                                ACCCTTGG AACGG     GCCAT
                                     A     AC___
GAM563  ADCY6    3'  GGGAGCAGGGGAGGGGTCAG   40959     C      G   ATG
                                CTG CCCCTCT CTG   CCC
                                ||| ||||||| |||   |||
                                GAC GGGGAGG GAC   GGG
                                  T      G   GA_
GAM563  ADCY6    3'  GGGAGCAGGGGAGGGGTCAG   31590     C      G   ATG
                                CTG CCCCTCT CTG   CCC
                                ||| ||||||| |||   |||
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                                GAC GGGGAGG GAC   GGG
                                  T      G   GA_
GAM563   AGRN     3'  GGGGCAGGTGCAGAGGTGGCAG 79588       C      TGA
                                CTGCC CCTCTGC   TGCCCC
                                ||||| |||||||   ||||||
                                GACGG GGAGACG   ACGGGG
                                   T      TGG
GAM563   AKAP2    3'  TGGGGGCATTTTTAGAGCGGCA 24231      CC     CT
                                TGCC  CTCTG  GATGCCCCCA
                                ||||  |||||  ||||||||||
                                ACGG  GAGAT  TTACGGGGGT
                                  C_    TT
GAM563   AQP6     3'  GGGACAGAGCAGAGGAAGGCAG 9731       C_       GA  _
                                CTGCC  CCTCTGCT  TG CCC
                                |||||  ||||||||  || |||
                                GACGG  GGAGACGA  AC GGG
                                   AA       G_  A
GAM563   AQP6     3'  GGGACAGAGCAGAGGAAGGCAG 55009      C_       GA  _
                                CTGCC  CCTCTGCT  TG CCC
                                |||||  ||||||||  || |||
                                GACGG  GGAGACGA  AC GGG
                                   AA       G_  A
GAM563   AQP6     3'  TGGGGACAGGGGCAGGGGCAG  55018       CTC    GA  C
                                CTGCCCC   TGCT  TG CCCCA
                                |||||||   ||||  || |||||
                                GACGGGG   ACGG  AC GGGGT
                                    ___    GG  A
GAM563   ASIC4    5'  GCGGCAGCAGAGGCAGCAG   38537      CC       A
                                CTGC  CCTCTGCTG TGC
                                ||||  ||||||||| |||
                                GACG  GGAGACGAC GCG
                                  AC       G
GAM563   ATOX1    3'  GGATGGACCAAAGGGGGCAG   15749         C  CTGATG  C_
                                CTGCCCCCT TG     CC  CC
                                ||||||||| ||     ||  ||
                                GACGGGGGA AC     GG  GG
                                     A  CA____  TA
GAM563   ATP1A2   3'  GGGTAGCAGCAGAGGCAG    7367       CCC      A
                                CTGCC   TCTGCTG TGCCC
                                |||||   ||||||| |||||
                                GACGG   AGACGAC ATGGG
                                   ___      G
GAM563   ATRN     3'  TGAGGACACAGCCAGGACGGCA 58447      C_   CT    A  C  C
           G                     CTGCC  CCT  GCTG TG CC CA
                                |||||  |||  |||| || || ||
                                GACGG  GGA  CGAC AC GG GT
                                   CA   C_    _  A  A
GAM563   AVP      5'  GCCAGCAGAGGCAGCAG     6675       CC       AT
                                CTGC  CCTCTGCTG  GC
                                ||||  |||||||||  ||
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                                GACG  GGAGACGAC  CG
                                  AC       __
GAM563  B3GNT3   3'  TGGAGGTGTGGGCAGAGGAGGG 27306    _      G    C
                                CCC CCTCTGCT ATGCC CCA
                                ||| |||||||| ||||| |||
                                GGG GGAGACGG TGTGG GGT
                                  A       G    A
GAM563  CBFA2T2  3'  GGAGTCGGCAGAGAAGCAG   18712     CCC        G
                                CTGC   CTCTGCTGAT CC
                                ||||   |||||||||| ||
                                GACG   GAGACGGCTG GG
                                  AA_        A
GAM563  CDS2     3'  GGAACAGAACTGAGCAGGGGCA 15108        __  TG__  ATG
          G                      CTGCCCC  CTC   CTG   CC
                                |||||||  |||   |||   ||
                                GACGGGG  GAG   GAC   GG
                                    AC   TCAA   AA_
GAM563  CEP2     3'  TGGGGGCAGGGGAAGAGACAG  23250    CCCC   G  GA
                                CTG    CTCT CT  TGCCCCCA
                                |||    |||| ||  ||||||||
                                GAC    GAGA GG  ACGGGGGT
                                  A___    A  GG
GAM563  COPA     5'  GGGGGGACAGAGGGGCAG    16479       C   CTGATG
                                CTGCCCC TCTG     CCCCC
                                ||||||| ||||     |||||
                                GACGGGG AGAC     GGGGG
                                    _   AG_____
GAM563  DAG1     3'  TGGGGGCACCTGGGAGGTCA   16557   T  _  TCTGCTGA
                                C GCC CCC       TGCCCCCA
                                | ||| |||       ||||||||
                                A TGG GGG       ACGGGGGT
                                 C   A   TCC_____
GAM563  DBCCR1   5'  GGGAGGCAGAGGGAGTAG    28243     C       GATG
                                CTGC CCCTCTGCT    CCC
                                |||| |||||||||    |||
                                GATG GGGAGACGG    GGG
                                  A       A___
GAM563  DDB2     3'  TGGGTGGTAGCAGAGGGATCA  5458     CC       GAT  _
                                TG  CCCTCTGCT   GCC CCCA
                                ||  |||||||||   ||| ||||
                                AC  GGGAGACGA   TGG GGGT
                                  TA        ___   T
GAM563  DTNA     3'  GCCAGCAGGGGGGAGCAG     9146      C        AT
                                CTGC CCCTCTGCTG  GC
                                |||| ||||||||||  ||
                                GACG GGGGGACGAC  CG
                                  A        __
GAM563  DTNA     3'  GCCAGCAGGGGGGAGCAG     53270     C        AT
                                CTGC CCCTCTGCTG  GC
                                |||| ||||||||||  ||
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                                GACG GGGGGACGAC  CG
                                  A        __
GAM563  DTNA    3'  GCCAGCAGGGGGAGCAG    53272     C       AT
                                CTGC CCCTCTGCTG  GC
                                |||| ||||||||||  ||
                                GACG GGGGGACGAC  CG
                                  A        __
GAM563  DTNA    3'  GCCAGCAGGGGGAGCAG    53277     C       AT
                                CTGC CCCTCTGCTG  GC
                                |||| ||||||||||  ||
                                GACG GGGGGACGAC  CG
                                  A        __
GAM563  DTR     3'  GGGGTCAGTGCAGCAGAGGACA 10457    CCC       AT___
              G                  CTG   CCTCTGCTG    GCCCC
                                |||   |||||||||    |||||
                                GAC   GGAGACGAC    TGGGG
                                  A__       GTGAC
GAM563  DUSP3   3'  GGGGGCTCAGAGGGGG     15837        CTGAT
                                CCCCCTCTG    GCCCCC
                                |||||||||    ||||||
                                GGGGGAGAC    CGGGGG
                                     T_____
GAM563  EGFL4   3'  GGGGATCCAGGAGGAGCAG   62470     CC    GCT   G
                                CTGC  CCTCT   GAT CCCC
                                ||||  |||||   ||| ||||
                                GACG  GGAGG   CTA GGGG
                                  A_    AC_  _
GAM563  EHD2    3'  TGGAAGCATTTAGAGGGG    28231       CT    CC
                                CCCCTCTG  GATGC  CCA
                                ||||||||  |||||  |||
                                GGGGAGAT  TTACG  GGT
                                     __    AA
GAM563  EIF2B5  3'  GGGAACAGCAGAGAGCAG    62205     CCC      ATG
                                CTGC   CTCTGCTG   CCC
                                ||||   ||||||||   |||
                                GACG   GAGACGAC   GGG
                                  A__       AA_
GAM563  EPHA8   3'  TGGAGGCATCATGGCAGAG   40441       __     C
                                CTCTGCT  GATGCC CCA
                                |||||||  |||||| |||
                                GAGACGG  CTACGG GGT
                                    TA     A
GAM563  EZH1    3'  TGGGAGTGTTACAGTAGGGAGC 10558     C   _  C     C
              AG                  CTGC CCCT CTG TGATGC CCCA
                                |||| |||| ||| |||||| ||||
                                GACG GGGA GAC ATTGTG GGGT
                                  A   T  _     A
GAM563  FGFR4   5'  GGAGGAGCCAGGAAGGCAG   10637     C_  CT   GATG  C
                                CTGCC  CCT  GCT   CC CC
                                |||||  |||  |||   || ||
```

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                                GACGG  GGA  CGA    GG GG
                                  AA   C_   ____   A
GAM563  FGFR4    5'  GGAGGAGCCAGGAAGGCAG   43630      C_   CT   GATG  C
                                CTGCC  CCT  GCT    CC CC
                                |||||  |||  |||    || ||
                                GACGG  GGA  CGA    GG GG
                                  AA   C_   ____   A
GAM563  GCNT2    5'  GGGGAGGCAGAGGGAGG     9455     _       GATG
                                CC CCCTCTGCT    CCCC
                                || |||||||||    ||||
                                GG GGGAGACGG    GGGG
                                 A        A___
GAM563  GDF5     3'  GGAATCACAGAGGGGTCAG   6896      C       C    G
                                CTG CCCCTCTG TGAT CC
                                ||| |||||||| |||| ||
                                GAC GGGGAGAC ACTA GG
                                  T       _    A
GAM563  GRLF1    3'  TGGGGACAGAGGCAGGGGCA  79263       CTC    GA  C
                                TGCCCC   TGCT  TG CCCCA
                                ||||||   ||||  || |||||
                                ACGGGG   ACGG  AC GGGGT
                                   ___    AG  A
GAM563  H1F0     5'  GGCAGAGGCAGAGGCAG     19219       CCC     GA
                                CTGCC   TCTGCT  TGCC
                                |||||   ||||||  ||||
                                GACGG   AGACGG  ACGG
                                   ___     AG
GAM563  H1F0     5'  TGGGAAAAGGGAGGCAGAGGAG 19220       C       GATG  ____
            GCAG                    CTGCC CCTCTGCT    CC    CCCA
                                |||||  ||||||||    ||    ||||
                                GACGG GGAGACGG    GG    GGGT
                                   A       AG__  AAAA
GAM563  HMG20A   3'  TGGGGGCAGAGAAAGAGTGCAG 37072      CCC    GCTGA
                                CTGC   CTCT    TGCCCCCA
                                ||||   ||||    ||||||||
                                GACG   GAGA    ACGGGGGT
                                  T__    AAGAG
GAM563  HNRPD    5'  GGGAGGCGAAGGGGGCAG    10950         CTGCTGA   _
                                CTGCCCCCT      TGCC CCC
                                |||||||||      |||| |||
                                GACGGGGGA      GCGG GGG
                                     A_______    A
GAM563  HNRPD    5'  GGGAGGCGAAGGGGGCAG    49389         CTGCTGA   _
                                CTGCCCCCT      TGCC CCC
                                |||||||||      |||| |||
                                GACGGGGGA      GCGG GGG
                                     A_______    A
GAM563  HOXB3    5'  GGGGGGCAGAGAGGGG      10955      _     TGATG
                                CCCC CTCTGC    CCCCC
                                |||| ||||||    |||||
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                                GGGG GAGACG    GGGGG
                                  A    _____
GAM563  ISG20    5'  GGCAGCAGAGAGGCAG     11022      CC     GAT
                                CTGCC  CTCTGCT   GCC
                                |||||  |||||||   |||
                                GACGG  GAGACGA   CGG
                                  A_     ___
GAM563  ITIH1    3'  GGGGCCAAGGCAGAGGAGG   11058    C      GAT
                                CC CCTCTGCT   GCCCC
                                || ||||||||   |||||
                                GG GGAGACGG   CGGGG
                                 A       AAC
GAM563  JRK      5'  GGATCAGCAGAGCAGGCAG   87829      CC        G
                                CTGCC  CTCTGCTGAT CC
                                |||||  |||||||||| ||
                                GACGG  GAGACGACTA GG
                                  AC        _
GAM563  LEP      3'  GGGGTGATTTCAGAGAGGGCAG 5866       C    CT  _
                                CTGCCC CTCTG  GAT GCCCC
                                ||||||| |||||  ||| |||||
                                GACGGG GAGAC  TTA TGGGG
                                   A    T_  G
GAM563  LMO2     5'  GGAGGCCGAGCAAGCGGAGGCA 19938      _ _ C   GAT  C
          G                      CTGCC CC CT TGCT   GCC CC
                                |||||  || || ||||   ||| ||
                                GACGG GG GA ACGA   CGG GG
                                  A  C  _   GC_   A
GAM563  LUZP1    5'  GGGGCCGCAGAGGGGACA    54404    C       TGAT
                                TG CCCCTCTGC    GCCCC
                                || |||||||||    |||||
                                AC GGGGAGACG    CGGGG
                                 A       C___
GAM563  MAP3K9   3'  GGGGCGGGCAAGGGGGACAG   61365    _     C   GA
                                CTG CCCCCT TGCT  TGCCCC
                                |||  ||||||  ||||  ||||||
                                GAC GGGGGA ACGG  GCGGGG
                                  A     _   __
GAM563  MGEA5    5'  GGAGGGCAGCAGAGGCAG    25220      CCC     GAT   _
                                CTGCC   TCTGCT   GCCC CC
                                |||||   ||||||   |||| ||
                                GACGG   AGACGA   CGGG GG
                                   ___     ___    A
GAM563  MMP14    3'  GGCAGAACAGCCAGAGGGGGCA 18430          _   A__
          G                      CTGCCCCCTCTG CTG   TGCC
                                ||||||||||||  |||   ||||
                                GACGGGGGAGAC GAC   ACGG
                                       C   AAG
GAM563  MSL3L1   3'  GGAAGTCAGCAGCAGGGGAGGC 55322      _   __       GC
          AG                     CTGCC CCCT  CTGCTGAT  CC
                                |||||  ||||  ||||||||  ||
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                                GACGG GGGG  GACGACTG  GG
                                  A   AC      AA
GAM563  NCOA6IP  5' GGGGGCAGGGGCAGGGGCAG  46155      CTC   GA
                                CTGCCCC  TGCT  TGCCCCC
                                |||||||  ||||  |||||||
                                GACGGGG  ACGG  ACGGGGG
                                   ___   GG
GAM563  NCSTN    5' GCTCAGCAGAGAGGCA    74136    CC      T
                                TGCC  CTCTGCTGA GC
                                ||||  |||||||| ||
                                ACGG  GAGACGACT CG
                                  A_      _
GAM563  NR4A2    3' TGGAAACTGTCAAGAGGGGGCA 21647        GC   GCCC_
                                TGCCCCCTCT  TGAT   CCA
                                ||||||||||  ||||   |||
                                ACGGGGGAGA  ACTG   GGT
                                     __   TCAAA
GAM563  P2RY6    3' GGAAGCTTCTTAGAAGAGGCAG 15999     CCC   CT  T  CC
                                CTGCC  TCTG  GA GC  CC
                                |||||  ||||  || ||  ||
                                GACGG  AGAT  CT CG  GG
                                  AGA   T_  T  AA
GAM563  PCSK5    5' GGGCCAGCAGAGGGGGC    21676          AT
                                GCCCCCTCTGCTG  GCCC
                                ||||||||||||  ||||
                                CGGGGGGAGACGAC  CGGG
                                      __
GAM563  PEX13    5' GGGAGCCGAGAGGAGGCGG   12043     C   GCTGAT  C
                                CTGCC CCTCT    GC CCC
                                ||||| |||||     || |||
                                GGCGG GGAGA    CG GGG
                                  A   GC____  A
GAM563  PGF      3' TGAAGGCAGTGGCAGGGGAGCA 12067    C  T   GA   CC
          G                      CTGC CCC CTGCT  TGCC  CA
                                ||||  ||| |||||  ||||  ||
                                GACG GGG GACGG  ACGG  GT
                                  A  _    TG   AA
GAM563  PHLDA3   5' GGAGGCATCTGGCAGAGGCGG  25694   _     _    C
                                CC CCTCTGCT GATGCC CC
                                || |||||||| |||||| ||
                                GG GGAGACGG CTACGG GG
                                 C      T     A
GAM563  PLAB     5' TGGGGGCACCCTGAGGGGGCA  66428       TGCTGA
                                TGCCCCCTC    TGCCCCCA
                                |||||||||    ||||||||
                                ACGGGGGAG    ACGGGGGT
                                     TCCC__
GAM563  PPP2R2B  5' GGGCAGCGGAGGCAG      17122     CCC    GAT  C
                                CTGCC  TCTGCT  GCC C
                                |||||  ||||||  ||| |
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                                GACGG   AGGCGA   CGG G
                                  ___     ___   A
GAM563  PROK1    3'  TGGGAGCAAGGGACAGGGAGCA 51571     C    CTG  GA   C
            G                    CTGC CCCT   CT  TGC CCCA
                                 |||| ||||   ||  ||| ||||
                                 GACG GGGA   GG  ACG GGGT
                                   A    CA_  GA   A
GAM563  PSCD3    3'  GGAAGGCGTGGCAGGGAGGCAG 16164      C  T    G    C_
                                 CTGCC CC CTGCT ATGCC  CC
                                 ||||| || ||||| |||||  ||
                                 GACGG GG GACGG TGCGG  GG
                                   A  _    _     AA
GAM563  PTCRA    3'  GGGGCATTTAGGGAGCAG    57154      C   CTGCT
                                 CTGC CCCT    GATGCCCC
                                 |||| ||||    ||||||||
                                 GACG GGGA    TTACGGGG
                                   A   T____
GAM563  PTGS1    3'  GCATACAACAGAGGGGGCA   55474          C  _
                                 TGCCCCCTCTG TG ATGC
                                 |||||||||| || ||||
                                 ACGGGGGAGAC AC TACG
                                       A  A
GAM563  PTGS1    3'  GCATACAACAGAGGGGGCA   8242           C  _
                                 TGCCCCCTCTG TG ATGC
                                 |||||||||| || ||||
                                 ACGGGGGAGAC AC TACG
                                       A  A
GAM563  RAP1GA1  3'  GGGATTGCTCAGTGGAAGCAG  12774     CCCC  TG    T  C__
                                 CTGC   TC  CTGA GC   CCC
                                 ||||   ||  |||| ||   |||
                                 GACG   AG  GACT CG   GGG
                                   A___  GT   _  TTA
GAM563  RIMS1    5'  GCGAGCAGAGGGGGCGG     73030            GA
                                 CTGCCCCCTCTGCT  TGC
                                 ||||||||||||||  |||
                                 GGCGGGGGAGACGA  GCG
                                                 __
GAM563  RPA2     5'  GGAGCATGGGCAGAGGAGACAG 12899     CCC      G   C
                                 CTG   CCTCTGCT ATGC CC
                                 |||   |||||||| |||| ||
                                 GAC   GGAGACGG TACG GG
                                   AGA       G   A
GAM563  RPS6KA2  3'  GGCACAGGTGGGAGGGCAG   41225      C   TG   A
                                 CTGCCC CTC  CTG TGCC
                                 |||||| |||  ||| ||||
                                 GACGGG GGG  GAC ACGG
                                    A  TG  _
GAM563  S100A10  5'  GGGGGCAGGAAGAGGGGG    60048        GCTGA
                                 CCCCCTCT    TGCCCCC
                                 ||||||||    |||||||
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                                GGGGGAGA    ACGGGGG
                                    AGG__
GAM563  SIRT1    5'  GGGAGCAGAGGAGGCG      25289      C       GATG
                                TGCC CCTCTGCT    CCC
                                |||| ||||||||    |||
                                GCGG GGAGACGA    GGG
                                  A      _____
GAM563  SLC12A4  5'  GGGGACAGCGGCGGGGACAG  18629     C    T     ATG
                                CTG CCCC CTGCTG   CCCC
                                ||| |||| ||||||   ||||
                                GAC GGGG GGCGAC   GGGG
                                  A   C     A__
GAM563  SLC22A12 3'  GGAGAGCAGAGGGGTCAG    58690     C        GATG
                                CTG CCCCTCTGCT    CC
                                ||| ||||||||||    ||
                                GAC GGGGAGACGA    GG
                                  T        GA__
GAM563  SLC5A5   5'  GGGGCGGACGCAGAGACAG   6597      CCCC     TGA
                                CTG    CTCTGC   TGCCCC
                                |||    ||||||   ||||||
                                GAC    GAGACG   GCGGGG
                                  A___      CAG
GAM563  SOX11    3'  CAAAGGCAGAGGGGGCGG    13310            GA
                                CTGCCCCCTCTGCT  TG
                                ||||||||||||||  ||
                                GGCGGGGGGAGACGG  AC
                                       AA
GAM563  SPAG8    3'  GGGGGCAGAGCGGGGCAG    25841       CTCT   GA
                                CTGCCCC    GCT  TGCCCCC
                                |||||||    |||  |||||||
                                GACGGGG    CGA  ACGGGGG
                                    _____  G_
GAM563  STK11    3'  GGGCCGGGCAGGGGGACAG    6599      C    T    GAT
                                CTG CCCC CTGCT   GCCC
                                ||| |||| |||||   ||||
                                GAC GGGG GACGG   CGGG
                                  A    _    GC_
GAM563  STX1A    3'  GGGAAGAGGCAGAGGGAGGCAG 17214       _       GATG
                                CTGCC CCCTCTGCT    CCC
                                ||||| |||||||||    |||
                                GACGG GGGAGACGG    GGG
                                   A        AGAA
GAM563  TTYH1    3'  GGGAGTAGCTGAGGGGGCAG   40685         T    ATG
                                CTGCCCCCTC GCTG   CCC
                                |||||||||| ||||   |||
                                GACGGGGGAG CGAT   GGG
                                      T   GA_
GAM563  UBE2G2   3'  GGGAGGCAGAGGTAGCAG    65490      CC       GATG
                                CTGC  CCTCTGCT    CCC
                                ||||  ||||||||    |||
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                                GACG  GGAGACGG   GGG
                                  AT      A___
GAM563  USP5    3'  GGGCAGAGCAGAGGGGCAG   14448       C     GA
                                CTGCCCC TCTGCT  TGCCC
                                ||||||| ||||||  |||||
                                GACGGGG AGACGA  ACGGG
                                   _     G_
GAM563  WHSC1   3'  TGGGGACATTGGGAAGGTGGGC 56703       _  CTG TG   C
          AG                      CTGCCC CCT   C  ATG CCCCA
                                ||||||| |||   |  ||| |||||
                                GACGGG GGA   G  TAC GGGGT
                                   T   AG_ GT   A
GAM563  ZNF219  3'  GCCAGCAGGGGGCAG      33555         CT    AT
                                CTGCCCCCT  GCTG  GC
                                |||||||||  ||||  ||
                                GACGGGGGA  CGAC  CG
                                     __    __
GAM563  20D7-FC4 3'  GGACCCACCAGCAGGGAGCAG  61564     CC  T     A  CCC
                                CTGC  CC CTGCTG TG   CC
                                ||||  || ||||||  ||   ||
                                GACG  GG GACGAC AC   GG
                                  A_ _     C  CCA
GAM563  ABIN-2  3'  GGAACATCTGGCAGAGGG    44461         _   CC
                                CCCTCTGCT GATG  CC
                                ||||||||| ||||  ||
                                GGGAGACGG CTAC  GG
                                     T    AA
GAM563  AIP     5'  GGAAGTTGCCGAAAGGGAGCAG 15615     _  C_  T  T   GC
                                CTGC CCC  TC GC GAT  CC
                                |||| |||  || || |||  ||
                                GACG GGG  AG CG TTG  GG
                                  A   AA  C  _   AA
GAM563  ASB13   3'  TGGGGAGCACAGAGGAGGC   45547     C     CTGA  _
                                GCC CCTCTG    TGC CCCCA
                                ||| ||||||    ||| |||||
                                CGG GGAGAC    ACG GGGGT
                                  A      _____  A
GAM563  BATF    5'  GGGCAGGCAGAGGAGGCA    22147      C       GA
                                TGCC CCTCTGCT  TGCCC
                                |||| ||||||||  |||||
                                ACGG GGAGACGG  ACGGG
                                  A       __
GAM563  BCDO2   3'  TGAGGACTCCAAAAGGGGGGCA 50036        T  GC  ATGC  C
                                TGCCCCC CT  TG    CC CA
                                ||||||| ||  ||    || ||
                                ACGGGGG GA  AC    GG GT
                                   _ AA  CTCA  A
GAM563  BRP44I  5'  TGGGAAGCGGCAGCAGAGGCAG 32740       CCC      A  C_
                                CTGCC   TCTGCTG TGC  CCCA
                                |||||   ||||||| |||  ||||
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                                GACGG  AGACGAC GCG  GGGT
                                  ___     G  AA
GAM563  C12orf22  3'  GGAGGCAGTAGGGAGCA    48708    C   CT  GAT  C
                                TGC CCCT  GCT  GCC CC
                                ||| ||||  |||  ||| ||
                                ACG GGGA  TGA  CGG GG
                                  A  __  ___  A
GAM563  C12orf3   3'  GGGGTCTTGAAGAGGGGGCAG  40166         GC  T
                                CTGCCCCCTCT  TGA GCCCC
                                ||||||||||  ||| |||||
                                GACGGGGGAGA  GTT TGGGG
                                      A_  C
GAM563  C17orf31  5'  TGAAGGTGGCAGAGGATGCAG  34545     CC      GAT  CC
                                CTGC  CCTCTGCT  GCC  CA
                                ||||  ||||||||  |||  ||
                                GACG  GGAGACGG  TGG  GT
                                  TA       ___  AA
GAM563  C20orf110 3'  TGGGGGAGACAGAAGGGGCAG  80367       C  _  GATG
                                CTGCCCC TCTG CT   CCCCCA
                                ||||||| |||| ||   ||||||
                                GACGGGG AGAC GA   GGGGGT
                                    A   A ____
GAM563  C20orf39  5'  TGAGGGGAGGGCAGAGGAGG  46579    C      GATG  _
                                CC CCTCTGCT   CCCC CA
                                || ||||||||   |||| ||
                                GG GGAGACGG   GGGG GT
                                 A      GA__   A
GAM563  C8orf13   3'  GGGGTGTCAGAGGAAGC    82481    CC    GCT
                                GC  CCTCT  GATGCCCC
                                ||  |||||  ||||||||
                                CG  GGAGA  CTGTGGGG
                                 AA   ___
GAM563  CAMTA1    3'  GGAAATTTGCAGAGGGGCAG  68506       C    T  GC
                                CTGCCCC TCTGC GAT  CC
                                ||||||| ||||| |||  ||
                                GACGGGG AGACG TTA  GG
                                    _   T  AA
GAM563  CBLN1     5'  GGGAACACAGCGCGGAGGGG  16369       __   A  CC
                                CCCCTCT  GCTG TG  CCC
                                |||||||  |||| ||  |||
                                GGGGAGG  CGAC AC  GGG
                                    CG   _  AA
GAM563  CENTG3    3'  GGAAGAGGGCAGAGGGGCCAG  50047    C       GATG_
                                CTG CCCCTCTGCT    CC
                                ||| ||||||||||    ||
                                GAC GGGGAGACGG    GG
                                  C        GAGAA
GAM563  cerk      3'  TGGGGGCAGTCAGGAGGAAGC  43172    CC   TG   _
                                GC  CCTC  CTGA TGCCCCCA
                                ||  ||||  |||| ||||||||
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                                CG  GGAG  GACT ACGGGGGT
                                 AA   __   G
GAM563  COASTER   3'  TGGGGGCAGGGCAAGAGGAGAC 32083     CCC    _  GA
          AG                     CTG   CCTCT GCT  TGCCCCCA
                                |||   ||||| |||  ||||||||
                                GAC   GGAGA CGG  ACGGGGGT
                                  AGA    A  G_
GAM563  CXYorf1   3'  TGGGGGCATCGGCAAGG     82925     C
                                CCT TGCTGATGCCCCCA
                                ||| ||||||||||||||
                                GGA ACGGCTACGGGGGT
                                 _
GAM563  DIO2      3'  TGGAGAAATGAAGCAGAGGAAG 26558    C_      G_  GCCC
          G                      CC  CCTCTGCT  AT   CCA
                                ||  ||||||||  ||   |||
                                GG  GGAGACGA  TA   GGT
                                 AA       AG  AAGA
GAM563  DIO2      3'  TGGAGAAATGAAGCAGAGGAAG 7668     C_      G_  GCCC
          G                      CC  CCTCTGCT  AT   CCA
                                ||  ||||||||  ||   |||
                                GG  GGAGACGA  TA   GGT
                                 AA       AG  AAGA
GAM563  DKFZP564B1162 5'  GGGGGTGCTATAAAAGAAGCAG 49350      CCCC   GC__  AT
                                CTGC    TCT    TG  GCCCCC
                                ||||    |||    ||  ||||||
                                GACG    AGA    AT  TGGGGG
                                  A___   AAAT  CG
GAM563  DKFZP564C103 3'  GGGGGCACTGAGGAAGCAG    32241     CC    TGCTGA
                                CTGC  CCTC     TGCCCCC
                                ||||  ||||     |||||||
                                GACG  GGAG     ACGGGGG
                                  AA   TC____
GAM563  DKFZP667O116 3'  CAGAAGCAGAGGAGGCAG    95939      C       GA
                                CTGCC CCTCTGCT  TG
                                ||||| ||||||||  ||
                                GACGG GGAGACGA  AC
                                   A       AG
GAM563  DKFZP761C169 5'  GGGGCACCTCTGGTGGGGCAG  68424        C  TGCTGA
                                CTGCCCC TC     TGCCCC
                                ||||||| ||     ||||||
                                GACGGGG GG     ACGGGG
                                    T  TCTCC_
GAM563  DKFZp762K222 5'  GGGGACTGCAGCGGAGGCAG   71671      CCC      ATG_
                                CTGCC   TCTGCTG   CCCC
                                |||||   |||||||   ||||
                                GACGG   AGGCGAC   GGGG
                                   ___     GTCA
GAM563  DKFZp762O076 5'  GGCAGCAGAGGCAGCAG     73957      CC       GAT
                                CTGC  CCTCTGCT   GCC
                                ||||  ||||||||   |||
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                                GACG  GGAGACGA   CGG
                                  AC       ___
GAM563  DPCR1    3'  TGGGGGCACCAATGCAGA    56000       __  A
                                TCTGC  TG TGCCCCCA
                                |||||  || ||||||||
                                AGACG  AC ACGGGGGT
                                   TA  C
GAM563  DRF1     3'  TGGAGGAGGCAGTGGGGGCAG  47762         T    GATG  C
                                CTGCCCCC CTGCT    CC CCA
                                |||||||| |||||    || |||
                                GACGGGGG GACGG    GG GGT
                                     T    A___  A
GAM563  FAM3D    3'  GGGGCTGAGGAGGAGGAGCAG  57947      _ _    GCTGAT
                                CTGC CC CCTCT     GCCCC
                                |||| || |||||     |||||
                                GACG GG GGAGG     CGGGG
                                  A  A    AGT___
GAM563  FBP17    3'  TGGGAGCATCTGGCAGGCAGGG 73163          ___    _    C
           GGGCAG                  CTGCCCCCT   CTGCT GATGC CCCA
                                |||||||||   ||||| ||||| ||||
                                GACGGGGGG   GACGG CTACG GGGT
                                     ACG    T    A
GAM563  FBXO9    5'  GGGGGCGGTGCAGAGGGGGCA  54251           TGA
                                TGCCCCCTCTGC   TGCCCCC
                                ||||||||||||   |||||||
                                ACGGGGGAGACG   GCGGGGG
                                       TG_
GAM563  FLJ10415 3'  CAGCAGCAGAGGCAGCAG    36586     CC       A
                                CTGC  CCTCTGCTG TG
                                ||||  ||||||||| ||
                                GACG  GGAGACGAC AC
                                  AC        G
GAM563  FLJ10415 3'  GGGAGGAACAGCAGCAGAGGCA 36588      CC  _     ATG  _
           G                     CTGCC  CT CTGCTG   CC CCC
                                |||||  || ||||||   || |||
                                GACGG  GA GACGAC   GG GGG
                                   A_  C     AA_  A
GAM563  FLJ10468 3'  ATCAGCAGAGCAGGACAG    36631     _ CC
                                CTG CC  CTCTGCTGAT
                                |||  ||  ||||||||||
                                GAC GG  GAGACGACTA
                                  A  AC
GAM563  FLJ11126 3'  GGCAGCAGAGAGGCCAG     37652     C  C      GAT
                                CTG CC CTCTGCT   GCC
                                |||  || |||||||   |||
                                GAC GG GAGACGA   CGG
                                  C  A      ___
GAM563  FLJ12242 3'  GGGGAGAGGCAGCAGAAGGGGC 45504       C      ATG__
                                GCCCC TCTGCTG    CCCC
                                |||||  |||||||     ||||
```

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                                CGGGG AGACGAC    GGGG
                                  A      GGAGA
GAM563  FLJ12547  3'  TGGAAGCACAGCGTGAGGGGGC 47136         _    A  CC
              A                   TGCCCCCTC TGCTG TGC  CCA
                                  ||||||||| ||||| |||  |||
                                  ACGGGGGAG GCGAC ACG  GGT
                                      T    _  AA
GAM563  FLJ12577  3'  GGTGAGCAGGGGAGCA     48886    C  T   GA
                                  TGC CCC CTGCT  TGCC
                                  ||| ||| |||||  ||||
                                  ACG GGG GACGA  GTGG
                                    A  _    __
GAM563  FLJ12700  5'  GGGGCAGTCAGGGAGCAG    46658     C   CTGCT  _
                                  CTGC CCCT    GA TGCCCC
                                  |||| ||||    || ||||||
                                  GACG GGGA    CT ACGGGG
                                    A   _____  G
GAM563  FLJ12770  3'  GGGGCAGTTGATGAGGCAG    50680      CCC  T  GAT
                                  CTGCC   TC GCT   GCCCC
                                  |||||   || |||   |||||
                                  GACGG   AG TGA   CGGGG
                                     AGT  T  ___
GAM563  FLJ12998  3'  TGGAGGGACAGAGCAGAGGGGC 43152     C        GA  _  _
              CAG                   CTG CCCCTCTGCT  TG CCC CCA
                                  ||| ||||||||||  || ||| |||
                                  GAC GGGGAGACGA  AC GGG GGT
                                    C        G_  A  A
GAM563  FLJ13111  3'  TGAGGGACACACAGAGGTGACA 47629     CCC     C  A  _  C
              G                    CTG   CCTCTG TG TG CCC CA
                                  |||   |||||| || || ||| ||
                                  GAC   GGAGAC AC AC GGG GT
                                    AGT     _  _  A  A
GAM563  FLJ13114  3'  GGAGCTTGGGCAGCAGGGGCAG 44905        CT    GAT  C
                                  CTGCCCC  CTGCT   GC CC
                                  |||||||  |||||   || ||
                                  GACGGGG  GACGG   CG GG
                                      AC    GTT  A
GAM563  FLJ14249  3'  TGGGGACATCGGTGTGAAGGG  42647     C  _      C
                                  CCC TC TGCTGATG CCCCA
                                  ||| || |||||||| |||||
                                  GGG AG GTGGCTAC GGGGT
                                    A  T       A
GAM563  FLJ14594  3'  GGAGCAGGCTAGGGGGCAG   52507         CT   GA   C
                                  CTGCCCCCT  GCT  TGC CC
                                  |||||||||  |||  ||| ||
                                  GACGGGGGA  CGG  ACG GG
                                      T_   __   A
GAM563  FLJ14642  3'  GGGAAGCAGAGGTGGCAG    52577      C       GATG
                                  CTGCC CCTCTGCT    CCC
                                  ||||| ||||||||    |||
```

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                                GACGG GGAGACGA   GGG
                                  T      A___
GAM563  FLJ14810  3'  TGGGGACAGAGAGCAGGGGGCA 52705        CT  GA_  C
          G                    CTGCCCCCT  GCT   TG CCCCA
                               |||||||||  |||   || |||||
                               GACGGGGGA  CGA   AC GGGGT
                                    __   GAG  A
GAM563  FLJ20296  3'  GGGCACAGCAGGGGACAG    35366    CC   T    A
                               CTG  CCC CTGCTG TGCCC
                               |||  ||| |||||| |||||
                               GAC  GGG GACGAC ACGGG
                                 A_  _    _
GAM563  FLJ20619  5'  GGGTGAGGCCAGGGGAGCAG   35894     _   CT   GAT
                               CTGC CCCCT  GCT   GCCC
                               |||| |||||  |||   ||||
                               GACG GGGGA  CGG   TGGG
                                 A    C_   AG_
GAM563  FLJ20700  3'  GGGAGGCCAAGGGGGCAG    36013       C  CTGAT  _
                               CTGCCCCCT TG    GCC CCC
                               |||||||||  ||    ||| |||
                               GACGGGGGA AC    CGG GGG
                                    _ _____  A
GAM563  FLJ22160  3'  GGGCATCAGGGACGCAG     45034     CCCC   G
                               CTGC    TCT CTGATGCCC
                               ||||    ||| |||||||||
                               GACG    AGG GACTACGGG
                                 C___   _
GAM563  FLJ23058  5'  GGCATCTCGGGGCAGGGGGCAG 45527        ___   CT
                               CTGCCCCCT   CTG  GATGCC
                               |||||||||   |||  ||||||
                               GACGGGGGA   GGC  CTACGG
                                    CGG   T_
GAM563  FLJ23403  3'  CAACAGCAATAGGGGGCAG   42204        C_    A
                               CTGCCCCCT  TGCTG TG
                               |||||||||  |||||  ||
                               GACGGGGGA  ACGAC AC
                                    TA    A
GAM563  FLJ32818  5'  GGGGGTGCCAGGGAAGCAG   59074     C_   CT  TGAT
                               CTGC  CCCT  GC   GCCCCC
                               ||||  ||||  ||   ||||||
                               GACG  GGGA  CG   TGGGGG
                                 AA   C_  _____
GAM563  FREQ     3'  TGGGAGCTGGAAGAAGGGGCA  27378      C   G  GAT  C
                               TGCCCC TCT CT   GC CCCA
                               ||||||  ||| ||   ||  ||||
                               ACGGGG AGA GG   CG GGGT
                                  A   A  T__  A
GAM563  GMPPB    5'  GGGCATAGCAGATGGGGCAG   97455       C      A
                               CTGCCCC TCTGCTG TGCCC
                               |||||||  |||||||  |||||
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                                GACGGGG AGACGAT ACGGG
                                   T     _
GAM563  HIC2     3' GGTGATGCAGCAGCAGGGGCA 65873      CT     AT__
                                TGCCCC  CTGCTG   GCC
                                ||||||  ||||||   |||
                                ACGGGG  GACGAC   TGG
                                   AC     GTAG
GAM563  KBRAS2   3' TGAGGGCAAAGTAGAGG    34631       GA    C
                                CCTCTGCT  TGCCC CA
                                ||||||||  ||||| ||
                                GGAGATGA  ACGGG GT
                                   A_    A
GAM563  KIAA0057 3' TGGGGGCCGAGCAGGGGGCA  25426       CT   GAT
                                TGCCCCCT  GCT   GCCCCCA
                                ||||||||  |||   |||||||
                                ACGGGGGA  CGA   CGGGGGT
                                   __   GC_
GAM563  KIAA0265 5' GGGCTGGGACAGTGGGGGCAG 70442       T  _  GAT
                                CTGCCCCC CTG CT   GCCC
                                ||||||||  ||| ||   ||||
                                GACGGGGG GAC GG   CGGG
                                   T   A  GT_
GAM563  KIAA0280 3' GGGAATCCAGAGAGGGGCAG  93307       _    CT   G
                                CTGCCCC CTCTG  GAT CCC
                                |||||||  |||||  ||| |||
                                GACGGGG GAGAC  CTA GGG
                                   A    __   A
GAM563  KIAA0321 5' GGGTCTTTGCAGCAGGGGCAG 63059       CT    T  T
                                CTGCCCC  CTGC GA GCCC
                                |||||||  ||||  || ||||
                                GACGGGG  GACG TT TGGG
                                   AC    T  C
GAM563  KIAA0329 3' GGTGGCAGCAGAGGCAG    29941      CCC     AT
                                CTGCC   TCTGCTG  GCC
                                |||||   |||||||  |||
                                GACGG   AGACGAC  TGG
                                  ____     GG
GAM563  KIAA0540 3' GGGAACACCCCGGGGTGGGCAG 64616      C    CTGA  CC
                                CTGCCC CTCTG    TG  CCC
                                ||||||  |||||    ||  |||
                                GACGGG GGGGC    AC  GGG
                                   T    CCC_  AA
GAM563  KIAA0557 3' GGGCAGCGTATGGGGGCAG   78572       TC   TGA
                                CTGCCCCC  TGC   TGCCC
                                ||||||||  |||   |||||
                                GACGGGGG  ATG   ACGGG
                                   T_   CG_
GAM563  KIAA0620 3' GGGGGCTGGAGGGGGGCAG   62813       T  G  GAT
                                CTGCCCCC CT CT   GCCCCC
                                |||||||  || ||   ||||||
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                                GACGGGGG GA GG   CGGGGG
                                    _ _  T__
GAM563  KIAA0720  3'  GGCCGAGCAGAGGGGGCA    62988           GAT
                                TGCCCCCTCTGCT   GCC
                                |||||||||||||   |||
                                ACGGGGGAGACGA   CGG
                                      GC_
GAM563  KIAA0769  3'  GGAGCAAAGAGGGGGGCAG   29758        T  G  GA   C
                                CTGCCCCC CT CT  TGC CC
                                |||||||| || ||  ||| ||
                                GACGGGGG GA GA  ACG GG
                                    _ _  A_   A
GAM563  KIAA0836  3'  GCATCAAAGGGGGCAG      65167         CTGC
                                CTGCCCCCT    TGATGC
                                |||||||||    ||||||
                                GACGGGGGA    ACTACG
                                     A___
GAM563  KIAA0913  5'  TGGGGGCGAGGAAGAGAAGGC  69535     CC    G  GA
                                GCC  CTCT CT  TGCCCCCA
                                |||  |||| ||  ||||||||
                                CGG  GAGA GG  GCGGGGGT
                                  AA    A  A_
GAM563  KIAA0945  3'  TGGGGGCGGGAAGGAGGGGCA  30907       CT  GCTGA
                                TGCCCC  CT    TGCCCCCA
                                ||||||  ||    ||||||||
                                ACGGGG  GA    GCGGGGGT
                                   AG  AGG__
GAM563  KIAA0980  3'  TGGGAGCTGTCAGCAAGGAGCA 47999      CC   C      _  C
          G                      CTGC  CCT TGCTGAT GC CCCA
                                ||||  ||| ||||||| || ||||
                                GACG  GGA ACGACTG CG GGGT
                                  A_  _      T  A
GAM563  KIAA1130  3'  GGGAGGCAGAGGTAGCAG    63099      CC       GATG
                                CTGC  CCTCTGCT    CCC
                                ||||  ||||||||    |||
                                GACG  GGAGACGG    GGG
                                  AT       A___
GAM563  KIAA1136  3'  GGCATGGGTAGAAGAGGACCAG 92959     CC  _  _    G
                                CTG  CC CT CTGCT ATGCC
                                |||  || || ||||| |||||
                                GAC  GG GA GATGG TACGG
                                  CA  A  A    G
GAM563  KIAA1193  3'  GGGGCACAGAGGGCAG      68275        CC   CTGA    C
                                CTGCCC  TCTG    TGCCC C
                                ||||||  ||||    ||||| |
                                GACGGG  AGAC    ACGGG G
                                   __   _____    A
GAM563  KIAA1199  3'  GGCCCAGCAGAGGGAGTAG    72931      C         AT
                                CTGC CCCTCTGCTG  GCC
                                ||||  ||||||||||  |||
```

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                                GATG GGGAGACGAC  CGG
                                  A        C_
GAM563  KIAA1259  3'  GGGCGGAGAGAGGGGGCAG   50800          G  GA
                                CTGCCCCCTCT CT  TGCCC
                                |||||||||| ||  |||||
                                GACGGGGGAGA GA  GCGGG
                                      _ G_
GAM563  KIAA1277  3'  GCTGTCCTGCAGCGGGGACAG  65079     C   T   T_  _
                                CTG CCCC CTGC  GAT GC
                                ||| |||| ||||  ||| ||
                                GAC GGGG GACG  CTG CG
                                  A   C   TC  T
GAM563  KIAA1277  3'  GGGACAGCGGGGAGGCAG    65080      C  T     ATG
                                CTGCC CC CTGCTG   CCC
                                ||||| || ||||||   |||
                                GACGG GG GGCGAC   GGG
                                   A _     A__
GAM563  KIAA1277  3'  GGGGACAGTGGGGACAG     65082     C   TCT   ATG
                                CTG CCCC   GCTG   CCCC
                                ||| ||||   ||||   ||||
                                GAC GGGG   TGAC   GGGG
                                  A   ____   A__
GAM563  KIAA1363  5'  GGACACCGTAGAGGGGGCA   69791          T A  _
                                TGCCCCCTCTGC G TG CC
                                |||||||||||| | || ||
                                ACGGGGGAGATG C AC GG
                                      _ C  A
GAM563  KIAA1399  3'  GGAGCCAACAGAGGGAGCAG  70793     C     C  AT  C
                                CTGC CCCTCTG TG  GC CC
                                |||| ||||||| ||  || ||
                                GACG GGGAGAC AC  CG GG
                                  A      A __ A
GAM563  KIAA1610  5'  GGGAGCGGCAGAGACGGCAG  67739      CC       ATG
                                CTGCC  CTCTGCTG   CCC
                                |||||  ||||||||   |||
                                GACGG  GAGACGGC   GGG
                                   CA       GA_
GAM563  KIAA1879  5'  TGGAGGACGTGCAGAGGGTGCA 73949     C      TG  _  C
          G                      CTGC CCCTCTGC  ATG CC CCA
                                |||| ||||||||  ||| || |||
                                GACG GGGAGACG  TGC GG GGT
                                  T       __   A  A
GAM563  KIAA1957  3'  GGTGGGCGCGGAGGGAGCAG  76217     C      TGAT   _
                                CTGC CCCTCTGC    GCCC CC
                                |||| ||||||||    |||| ||
                                GACG GGGAGGCG    CGGG GG
                                  A       _____   T
GAM563  KIF13B   3'  CAGCAGCAGAGGGGACAG    83713     C        A
                                CTG CCCCTCTGCTG TG
                                ||| ||||||||||| ||
```

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                                GAC GGGGAGACGAC AC
                                  A         G
GAM563  KIF13B   3'  CAGCAGCAGAGGGGACAG    31557     C         A
                                CTG CCCCTCTGCTG TG
                                ||| |||||||||| ||
                                GAC GGGGAGACGAC AC
                                  A         G
GAM563  KRTHB2   3'  TGGGGACAGACGGCAGAG    53454        A_  C
                                CTCTGCTG  TG CCCCA
                                ||||||||  || |||||
                                GAGACGGC  AC GGGGT
                                     AG  A
GAM563  LIN-28   3'  TGGGGGCAACCAGGAGGGGGG  45473        G   A_
                                CCCCTCT CTG  TGCCCCCA
                                ||||||| |||  ||||||||
                                GGGGGGA GAC  ACGGGGGT
                                    G   CA
GAM563  MESDC2   3'  GGCAGGCAGAGGAAACAG    72918     CCC       GA
                                CTG   CCTCTGCT  TGCC
                                |||   ||||||||  ||||
                                GAC   GGAGACGG  ACGG
                                  AAA       __
GAM563  MGC10334 5'  GGGTGCGGTGCAGAGCAGAGCA 48321      CCC_     TGA   C
           G                     CTGC    CTCTGC   TGC CCC
                                ||||    ||||||   ||| |||
                                GACG    GAGACG   GCG GGG
                                  AGAC     TG_   T
GAM563  MGC10765 3'  GGGAGGCAGAGGGTGCAG    44564     C        GATG
                                CTGC CCCTCTGCT    CCC
                                |||| |||||||||    |||
                                GACG GGGAGACGG    GGG
                                  T        A____
GAM563  MGC13010 5'  TGGAGGCACGGCAGAGGAGGCA 52062       C        A    C
           G                     CTGCC CCTCTGCTG TGCC CCA
                                ||||| ||||||||| |||| |||
                                GACGG GGAGACGGC ACGG GGT
                                  A        _    A
GAM563  MGC15416 5'  TGGGGGCAGCCAGGGAGAGGGC 57349       C    G   A_
           A                     TGCCC CTCT CTG  TGCCCCCA
                                ||||| |||| |||  ||||||||
                                ACGGG GAGG GAC  ACGGGGGT
                                  A    _   CG
GAM563  MGC16025 3'  TGGAAGGTTTTAGCAGAAAAAG 53029     CCC_      T   C_
           G                     CC    TCTGCTGA GCC  CCA
                                ||    |||||||| |||  |||
                                GG    AGACGATT TGG  GGT
                                  AAAA       T   AA
GAM563  MGC21688 3'  GTGTTTGGAGAGGAGGCAG    58917       C     GCT
                                CTGCC CCTCT   GATGC
                                ||||| |||||   |||||
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                                GACGG GGAGA   TTGTG
                                  A     GGT
GAM563  MGC35558 3'  TGAGGGCATCGTGGAAGGG   59422     C  TG T      C
                                CCC TC  C GATGCCC CA
                                ||| ||  | ||||||| ||
                                GGG AG  G CTACGGG GT
                                  A  GT _      A
GAM563  MGC5566  3'  TGGAAGCATTGCCAGAGGGG   44125        CT    CC
                                CCCCTCTG  GATGC  CCA
                                ||||||||  |||||  |||
                                GGGGAGAC  TTACG  GGT
                                     CG    AA
GAM563  NOPAR    5'  GGGGGGAGCAGAGGAGGCAG   54860      C       GATG
                                CTGCC CCTCTGCT    CCCCC
                                ||||| ||||||||    |||||
                                GACGG GGAGACGA    GGGGG
                                  A       G___
GAM563  NOPAR    5'  TGGAGACAAGGTAGGGGGGAGC 54861      _        GA  CCC
           AG                     CTGC CCCCTCTGCT  TG   CCA
                                ||||| ||||||||||  ||   |||
                                GACG GGGGGGATGG  AC   GGT
                                  A         A_  AGA
GAM563  OBTP     3'  GGAAGCCTCCAAGCAGAGGACA 34667     CCC       __  T  CC
           G                     CTG   CCTCTGCT  GA GC  CC
                                |||   ||||||||  || ||  ||
                                GAC   GGAGACGA  CT CG  GG
                                  A__       AC  C  AA
GAM563  P114-RHO-GEF 3'  GGGGGGCATGGGCAGAGAGGGC  31674      C      G
                                GCCC CTCTGCT ATGCCCCC
                                |||| ||||||| ||||||||
                                CGGG GAGACGG TACGGGGG
                                  A      G
GAM563  p25      3'  TGGGGGTGACAAGAGGAGACAG 23839     CCC    GC  A
                                CTG   CCTCT  TG TGCCCCCA
                                |||   |||||  || ||||||||
                                GAC   GGAGA  AC GTGGGGGT
                                  AGA    __  A
GAM563  P2RXL1   3'  TGGAGGTCTGGGAGAGAGAGCA 19565     CCC    G  GAT   C
           G                     CTGC   CTCT CT   GCC CCA
                                ||||   |||| ||   ||| |||
                                GACG   GAGA GG   TGG GGT
                                  AGA    G  TC_   A
GAM563  P2RXL1   3'  TGGGAGAGAGAGCAGAGGGCGG 19566      _       GATGCC
           CAG                     CTGCC CCCTCTGCT     CCCA
                                ||||| |||||||||     ||||
                                GACGG GGGAGACGA     GGGT
                                  C        GAGAGA
GAM563  PP591    5'  TGGAGGGCCTTGCAGAGGGGCA 48152       C    TGAT   _
           G                     CTGCCCC TCTGC    GCCC CCA
                                ||||||| |||||    |||| |||
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                                GACGGGG AGACG   CGGG GGT
                                   _    TTC_   A
GAM563  PRO1257  5'  TGAGGGCATGAGCAGAGG    38327        G     C
                                CCTCTGCT ATGCCC CA
                                |||||||| |||||| ||
                                GGAGACGA TACGGG GT
                                     G     A
GAM563  REPRIMO  3'  TGGGGGCAGGTGGAGAGGGCGG 39532       C   TG  GA
                                CTGCCC CTC  CT  TGCCCCCA
                                |||||| |||  ||  ||||||||
                                GGCGGG GAG  GG  ACGGGGGT
                                   A  GT  __
GAM563  RINZF    5'  GGGGGCGAGACAGAGGGGG   43939         _  GA
                                CCCCCTCTG CT  TGCCCCC
                                ||||||||| ||  |||||||
                                GGGGGAGAC GA  GCGGGGG
                                     A  __
GAM563  RP4-622L5 3'  GGATATACAGACGGGGGCAG   39428        _   CTG  G
                                CTGCCCCC TCTG   AT CC
                                |||||||| ||||   || ||
                                GACGGGGG AGAC   TA GG
                                     C    ATA  _
GAM563  SIAT8A   5'  GGAGCATCGCTCGGAGGGGACA 13144    C       C_     C
                                TG CCCCTCTG  TGATGC CC
                                || ||||||||  |||||| ||
                                AC GGGGAGGC  GCTACG GG
                                  A       TC     A
GAM563  SKIP     3'  TGGGGGCAGGCAGAAGGG    33713     C     GA
                                CCC TCTGCT  TGCCCCCA
                                ||| ||||||  ||||||||
                                GGG AGACGG  ACGGGGGT
                                  A     __
GAM563  SKIP     3'  TGGGGGCAGGCAGAAGGG    56248     C     GA
                                CCC TCTGCT  TGCCCCCA
                                ||| ||||||  ||||||||
                                GGG AGACGG  ACGGGGGT
                                  A     __
GAM563  SLC16A6  3'  GGGGACACAAGGAGGCAG    17441      C  CTGC  A  C
                                CTGCC CCT    TG TG CCCC
                                ||||| |||    || || ||||
                                GACGG GGA    AC AC GGGG
                                   A  _____  _  A
GAM563  SLC2A10  5'  GGAGGGCAGGGCAGGAGGGACA 48556     C  CT    GA    _
           G                     CTG CCC  CTGCT  TGCCC CC
                                ||| |||  |||||  ||||| ||
                                GAC GGG  GACGG  ACGGG GG
                                  A  AG    G_     A
GAM563  SLC37A1  3'  GGCCAGCAGAGAAGCAG     39092      CCC       AT
                                CTGC   CTCTGCTG  GCC
                                ||||   ||||||||  |||
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                                GACG  GAGACGAC  CGG
                                  AA_      __
GAM563  SPRY4   3'  GGATAGCAGGGGAGGCAG   49021     C      ATG
                                CTGCC CCTCTGCTG  CC
                                ||||| |||||||||  ||
                                GACGG GGGGACGAT  GG
                                   A       A__
GAM563  SPRY4   3'  GGGCATCATCAGGCAG    49027     CCCTC  C
                                CTGCC    TG TGATGCCC
                                |||||    || ||||||||
                                GACGG    AC ACTACGGG
                                   _____ T
GAM563  SSH-3   3'  GGAGCAGGAGCAGGGGCAG  37418      CTC   GA  C
                                CTGCCCC  TGCT  TGC CC
                                |||||||  ||||  ||| ||
                                GACGGGG  ACGA  ACG GG
                                   ___   GG  A
GAM563  SSH-3   3'  GGAGCAGGGGCAGGGGCAG  37419      CTC   GA  C
                                CTGCCCC  TGCT  TGC CC
                                |||||||  ||||  ||| ||
                                GACGGGG  ACGG  ACG GG
                                   ___   GG  A
GAM563  SSH-3   3'  GGGGCAGGGGCAGGGGCAG  37420      CTC   GA
                                CTGCCCC  TGCT  TGCCCC
                                |||||||  ||||  ||||||
                                GACGGGG  ACGG  ACGGGG
                                   ___   GG
GAM563  STAT2   3'  GGGTACAGAGGGGACA    19454   C     CTGA
                                TG CCCCTCTG   TGCCC
                                || ||||||||   |||||
                                AC GGGGAGAC   ATGGG
                                 A     _____
GAM563  STC2    3'  GGAGAAGGGTGGAGAGGAGGCA 14934     C   G  GAT  _____
          G                      CTGCC CCTCT CT  GCCC   CC
                                ||||| ||||| ||  ||||   ||
                                GACGG GGAGA GG  TGGG   GG
                                   A   _ ___   AAGA
GAM563  STX1B2  5'  GGAGCAGCAGCAGAGGCAG  54619     CCC     A  C
                                CTGCC  TCTGCTG TGC CC
                                |||||  ||||||| ||| ||
                                GACGG  AGACGAC ACG GG
                                   ___     G  A
GAM563  SYT13   3'  GGCTGGCAGAGTAGGCAG   95102     CC     GAT
                                CTGCC  CTCTGCT  GCC
                                |||||  |||||||  |||
                                GACGG  GAGACGG  CGG
                                   AT     T__
GAM563  TED     3'  GGGGGCACAGAGGGG     32273       CTGA
                                CCCCTCTG   TGCCCCC
                                ||||||||   |||||||
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                                GGGGAGAC   ACGGGGG
                                    ____
GAM563  TGIF2    3'  GCCACAGCAGGGGGCAG     41751        CT   AT
                                CTGCCCCCT  GCTG  GC
                                |||||||||  ||||  ||
                                GACGGGGGA  CGAC  CG
                                     __    AC
GAM563  THTPA    5'  TGAGGACATCAGCAGCAGTGG  44511    C _      C  C
                                CC CT CTGCTGATG CC CA
                                || || |||||||| || ||
                                GG GA GACGACTAC GG GT
                                 T  C       A  A
GAM563  TM4-B    5'  GGACACAGAGGGGCAG      25889       C   C  ATG
                                CTGCCCC TCTG TG   CC
                                ||||||| |||| ||   ||
                                GACGGGG AGAC AC   GG
                                   _   _  A__
GAM563  YKT6     3'  GGTAGCTGCAGAGGGGGGAG   22642    G        TGA
                                CT CCCCCTCTGC   TGCC
                                || ||||||||||   ||||
                                GA GGGGGAGACG   ATGG
                                 G         TCG
GAM563  ZIC5     5'  TGAAGGCGGGCAGAGGG     53615        GA   CC
                                CCCTCTGCT  TGCC  CA
                                |||||||||  ||||  ||
                                GGGAGACGG  GCGG  GT
                                     __    AA
GAM563  ZNF263   3'  GGAATTGGCAGAGGAAGTAG   20427     CC     TG  G
                                CTGC  CCTCTGC  AT CC
                                ||||  |||||||  || ||
                                GATG  GGAGACG  TA GG
                                  AA      GT  A
GAM563  ZNF263   3'  GGGAGGTGCAGAGGCAGCAG   20428     CC     TGAT  _
                                CTGC  CCTCTGC    GCC CCC
                                ||||  |||||||    ||| |||
                                GACG  GGAGACG    TGG GGG
                                  AC      _____  A
GAM563  LOC116173 3'  GCCAGCCAGAGAGGACAG    57427    C  C    _  AT
                                CTG CC CTCTG CTG  GC
                                ||| || ||||| |||  ||
                                GAC GG GAGAC GAC  CG
                                 A  A    C  __
GAM563  LOC124470 3'  TGGAAAGGCAGGCAGAGGG   76149        GA   C__
                                CCCTCTGCT  TGCC   CCA
                                |||||||||  ||||   |||
                                GGGAGACGG  ACGG   GGT
                                     __    AAA
GAM563  LOC124590 3'  TGGAGGCACCAGAGGGGCA   76153       C   CTGA   C
                                TGCCCC TCTG    TGCC CCA
                                ||||||  ||||    |||| |||
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                                ACGGGG AGAC    ACGG GGT
                                   _   C___    A
GAM563   LOC124997 3'  GCCTTCAGCTGAGGGGGCAG   74848          T    T_
                                CTGCCCCCTC GCTGA  GC
                                |||||||||| |||||  ||
                                GACGGGGGAG CGACT  CG
                                     T    TC
GAM563   LOC127841 5'  GCCCAGGCAGAGAGGGCAG    75188       C      GAT
                                CTGCCC CTCTGCT   GC
                                |||||| |||||||   ||
                                GACGGG GAGACGG   CG
                                   A      ACC
GAM563   LOC129181 5'  TGGGGGCTGCAGCAGGGAGGCA 76315      C  T     AT
                                TGCC CC CTGCTG  GCCCCCA
                                |||| || ||||||  |||||||
                                ACGG GG GACGAC  CGGGGGT
                                  A _     GT
GAM563   LOC129303 3'  GGGAACAGCAGAGGGGATAG   75375     C         ATG
                                CTG CCCCTCTGCTG   CCC
                                ||| ||||||||||   |||
                                GAT GGGGAGACGAC   GGG
                                  A         AA_
GAM563   LOC130940 5'  GGGGGTGGCGGAGAGGACAG   57939     C  C      GAT
                                CTG CC CTCTGCT   GCCCCC
                                ||| || |||||||   ||||||
                                GAC GG GAGGCGG   TGGGGG
                                  A  A      ___
GAM563   LOC143437 5'  TGGGGATACAGCAGGGAGCA   83861     CC  T     A  C
                                TGC  CC CTGCTG TG CCCCA
                                |||  || |||||| || |||||
                                ACG  GG GACGAC AT GGGGT
                                  A_ _     _ A
GAM563   LOC145241 5'  TGAAGGTGATCAGCAGGGGCAG 63529         CTC      _   CC
                                CTGCCCC   TGCTGAT GCC  CA
                                |||||||   ||||||| |||  ||
                                GACGGGG   ACGACTA TGG  GT
                                     ___      G   AA
GAM563   LOC146802 3'  GCAGCAGCAGAGAGCAG     78726      CCC       A
                                CTGC   CTCTGCTG TGC
                                ||||   |||||||| |||
                                GACG   GAGACGAC ACG
                                  A__       G
GAM563   LOC147043 5'  GGCATCAGAAGGGGAGC     88504    _    CTG
                                GC CCCCT   CTGATGCC
                                || |||||   ||||||||
                                CG GGGGA   GACTACGG
                                 A    A__
GAM563   LOC147645 5'  CACGGTTGGGGGAGGCAG    79066       _    T   A
                                CTGCC CCCTC GCTG TG
                                ||||| ||||| |||| ||
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                                GACGG GGGGG TGGC AC
                                  A    T   _
GAM563  LOC147912 5'  TGGGGGCGAAAAGGGGGGACAG 79266    C     GCTGA
                                CTG CCCCTCT    TGCCCCCA
                                ||| |||||||    ||||||||
                                GAC GGGGGGA    GCGGGGGT
                                  A      AAA__
GAM563  LOC148413 3'  GGGGCATCGGGGGGGCAG     79581         CTGCT
                                CTGCCCCCT    GATGCCCC
                                |||||||||    ||||||||
                                GACGGGGGGG    CTACGGGG
                                      _____
GAM563  LOC149386 5'  TGGGGGCGTCAGCAGAGGGGCA 85565        C
          G                      CTGCCCC TCTGCTGATGCCCCCA
                                |||||||| ||||||||||||||||
                                GACGGGG AGACGACTGCGGGGGT
                                      _
GAM563  LOC150481 3'  TGAGGGGATGGGCAGAGGAGGC 80717    C      G  G   _
                                GCC CCTCTGCT AT CCCC CA
                                ||| |||||||| || |||| ||
                                CGG GGAGACGG TA GGGG GT
                                  A       G  _   A
GAM563  LOC152220 3'  TGGGACTAGCAGCAGAGGCAG  86771      CCC      ATGCC
                                CTGCC   TCTGCTG    CCCA
                                |||||   |||||||    ||||
                                GACGG   AGACGAC    GGGT
                                   ___      GATCA
GAM563  LOC152627 3'  GGGAGGCAGAGGGTGCAG    81512     C       GATG
                                CTGC CCCTCTGCT    CCC
                                |||| |||||||||    |||
                                GACG GGGAGACGG    GGG
                                  T       A___
GAM563  LOC155066 5'  GGACCCGGCCAGAGGGACAG   82210    CC     _  ATG
                                CTG  CCCTCTG CTG   CC
                                |||  ||||||| |||   ||
                                GAC  GGGAGAC GGC   GG
                                  A_      C   CCA
GAM563  LOC157860 3'  GGGGCATCTGGGCGCAG     87880     C   TCTGCT
                                CTGC CCC     GATGCCCC
                                |||| |||     ||||||||
                                GACG GGG     CTACGGGG
                                  C   T_____
GAM563  LOC158062 3'  GGGGAGAGCCACAGAGGAGCAG 87964     CC     C  AT  ___
                                CTGC  CCTCTG TG  GC   CCCC
                                ||||  |||||| ||  ||   ||||
                                GACG  GGAGAC AC  CG   GGGG
                                  A_     _  __  AGA
GAM563  LOC158191 3'  TGAGGGGATGGGCAGAGGAGGC 82686    C      G  G   _
                                GCC CCTCTGCT AT CCCC CA
                                ||| |||||||| || |||| ||
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                                CGG GGAGACGG TA GGGG GT
                                  A       G _    A
GAM563  LOC159121 3'  TGGGGGCAAGGGCAAGAGG    88389      _   GA
                                CCTCT GCT  TGCCCCCA
                                ||||| |||  ||||||||
                                GGAGA CGG  ACGGGGGT
                                   A   GA
GAM563  LOC159199 5'  GGGCAGCAGAGTGAGCAG    83066     CCC      GAT
                                CTGC   CTCTGCT   GCCC
                                ||||   |||||||   ||||
                                GACG   GAGACGA   CGGG
                                  AGT      ___
GAM563  LOC162083 3'  GGAAAGCTGAGGGGGCAG    83208          T   GATG
                                CTGCCCCCTC GCT    CC
                                |||||||||| |||    ||
                                GACGGGGGAG CGA    GG
                                      T   AA__
GAM563  LOC163682 3'  GGGGGCACAGGGGGCAG     88412         CTGCT A
                                CTGCCCCCT    G TGCCCCC
                                |||||||||    | |||||||
                                GACGGGGGA    C ACGGGGG
                                     _____ _
GAM563  LOC164714 3'  GGCAGCAGGGGGGGCAG     88586            GAT
                                CTGCCCCCTCTGCT   GCC
                                ||||||||||||||   |||
                                GACGGGGGGGGACGA   CGG
                                      ___
GAM563  LOC169693 5'  GGGAAGCAGAGGAGCAG     88630      CC       GATG
                                CTGC  CCTCTGCT    CCC
                                ||||  ||||||||    |||
                                GACG  GGAGACGA    GGG
                                  A_       A___
GAM563  LOC196214 5'  GTACAGCAAGGGGGGCAG     91183          C    A
                                CTGCCCCCT TGCTG TGC
                                ||||||||| ||||| |||
                                GACGGGGGA ACGAC ATG
                                     _    _
GAM563  LOC196410 3'  TGGGGGCACCAGGGAGAATCAG 89034     CCCC    G   A
                                CTG    CTCT CTG TGCCCCCA
                                |||    |||| ||| ||||||||
                                GAC    GAGG GAC ACGGGGGT
                                  TAA_    _   C
GAM563  LOC196955 5'  TGAGGGCATTGTAAAAGG    77876     C_   T      C
                                CCT  TGC GATGCCC CA
                                |||  ||| ||||||| ||
                                GGA  ATG TTACGGG GT
                                  AA   _      A
GAM563  LOC200093 3'  TGGGGGCATCGGCAAGG     63781     C
                                CCT TGCTGATGCCCCCA
                                ||| ||||||||||||||
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                                GGA ACGGCTACGGGGGT
                                  _
GAM563  LOC200563 5'  GCATCAGTCAGTGGACAG    91656     CCC  T  _
                                CTG   CC CTG CTGATGC
                                |||   || ||| |||||||
                                GAC   GG GAC GACTACG
                                  A__  T  T
GAM563  LOC200734 3'  TGAAGGCATCGGTTAAGGGCA  90284       CCTCT       CC
                                TGCCC    GCTGATGCC  CA
                                |||||    |||||||||  ||
                                ACGGG    TGGCTACGG  GT
                                   AAT__       AA
GAM563  LOC201685 5'  GCCAGCAGACAGGGCAG     91842       CC      AT
                                CTGCCC  TCTGCTG  GC
                                ||||||  |||||||  ||
                                GACGGG  AGACGAC  CG
                                    AC      __
GAM563  LOC203238 3'  GTTTCAGCAGAAGTGGCAG    90824       CCC       T
                                CTGCC   TCTGCTGA GC
                                |||||   |||||||| ||
                                GACGG   AGACGACT TG
                                   TGA       T
GAM563  LOC203554 5'  GGGAGGCAGCAGAGGGG     92328          GAT  _
                                CCCCTCTGCT   GCC CCC
                                ||||||||||   ||| |||
                                GGGGAGACGA   CGG GGG
                                      ___   A
GAM563  LOC220024 5'  GGGAGCTGAGCGCAGCAGAGAG 95032      CCC       AT____  C
          CAG                     CTGC   CTCTGCTG     GC CCC
                                ||||   ||||||||      || |||
                                GACG   GAGACGAC     CG GGG
                                  A__       GCGAGT  A
GAM563  LOC221184 5'  TGGGGGTGCCCCAGCAGCGGGG 93411         T     A__
          GCAG                    CTGCCCCC CTGCTG   TGCCCCCA
                                |||||||| ||||||   ||||||||
                                GACGGGGG GACGAC   GTGGGGGT
                                     C     CCC
GAM563  LOC221922 5'  GGGAGGGTCAGGAGGGCAG    94255       CCTC G     G  _
                                CTGCCC    T CTGAT CC CCC
                                ||||||    | ||||| || |||
                                GACGGG    A GACTG GG GGG
                                   ____ G     _  A
GAM563  LOC221922 5'  GGGGGAGCAGGAGGGCAG    94258       C T     GATG
                                CTGCCC C CTGCT    CCCCC
                                |||||| | |||||    |||||
                                GACGGG G GACGA    GGGGG
                                   A _     _____
GAM563  LOC221922 5'  GGGGGAGCAGGAGGGCAG    94259       C T     GATG
                                CTGCCC C CTGCT    CCCCC
                                |||||| | |||||    |||||
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                                GACGGG G GACGA   GGGGG
                                   A _   _____
GAM563  LOC221964 3'  GGGGCAGGGGCAGGGGCAG   95607       CTC   GA
                                CTGCCCC  TGCT  TGCCCC
                                |||||||  ||||  ||||||
                                GACGGGG  ACGG  ACGGGG
                                    ___   GG
GAM563  LOC253367 3'  GGGGAGTTTCGAGGGGGCA   99438        TGCT  T  _
                                TGCCCCCTC   GA GC CCCC
                                |||||||||   || || ||||
                                ACGGGGGAG   CT TG GGGG
                                     _____  T  A
GAM563  LOC253531 5'  TGGGGATACAGCAGGGAGCA  98227    CC  T    A  C
                                TGC  CC CTGCTG TG CCCCA
                                |||  || |||||| || |||||
                                ACG  GG GACGAC AT GGGGT
                                  A_  _    _  A
GAM563  LOC253974 3'  TGGGGGCATCAGCAGAGGGGGC 99284
           AG                   CTGCCCCCTCTGCTGATGCCCCCA
                                |||||||||||||||||||||||||
                                GACGGGGGGAGACGACTACGGGGGT

GAM563  LOC254050 3'  GGAAGGCAGAGGTGGCAG    96562      C      GATG
                                CTGCC CCTCTGCT   CC
                                ||||| ||||||||   ||
                                GACGG GGAGACGG   GG
                                   T      AA__
GAM563  LOC254181 5'  GGGCCCCAGCAGAGCAGGCAG  99442      CC      AT
                                CTGCC  CTCTGCTG  GCCC
                                |||||  ||||||||  ||||
                                GACGG  GAGACGAC  CGGG
                                   AC      CC
GAM563  LOC254263 3'  GGCTCAGCAGGGGGGCAG    96369       T     T
                                CTGCCCCC CTGCTGA GCC
                                |||||||| ||||||| |||
                                GACGGGGG GACGACT CGG
                                     _     _
GAM563  LOC255394 5'  TGAGGGCCCCAGAGGGGG    96544        CTGAT   C
                                CCCCCTCTG    GCCC CA
                                |||||||||    |||| ||
                                GGGGGAGAC    CGGG GT
                                     CC___   A
GAM563  LOC256073 5'  GGAAGCTCCAAGAGGGCAG   98487      CC   GCT  T  CC
                                CTGCCC  TCT   GA GC  CC
                                ||||||  |||   || ||  ||
                                GACGGG  AGA   CT CG  GG
                                   __  AC_  _  AA
GAM563  LOC256254 3'  GTTTCAGCAGAAGTGGCAG   97902      CCC      T
                                CTGCC   TCTGCTGA GC
                                |||||   |||||||| ||
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                                GACGG   AGACGACT TG
                                   TGA       T
GAM563  LOC256530 3'  GGGAGTTCAGTGGGGACAG   98622    C   TCT    T C
                                CTG CCCC   GCTGA GC CCC
                                ||| ||||   ||||| || |||
                                GAC GGGG   TGACT TG GGG
                                  A   ___    _ A
GAM563  LOC256949 5'  GGCTGCGGAGGAGGCAG    96985     C     TGAT
                                CTGCC CCTCTGC    GCC
                                ||||| |||||||    |||
                                GACGG GGAGGCG    CGG
                                   A      T___
GAM563  LOC257095 5'  GGGCAGCGGGGGCAG      98721       TCT   GAT   C
                                CTGCCCCC   GCT   GCC C
                                ||||||||   |||   ||| |
                                GACGGGGG   CGA   CGG G
                                     ___   ___   A
GAM563  LOC257450 3'  GGGGTCAAGCAGAGGAGG    91451    C      GAT
                                CC CCTCTGCT   GCCCC
                                || ||||||||   |||||
                                GG GGAGACGA   TGGGG
                                 A       AC_
GAM563  LOC51125  5'  GGAGGGCAGAGGAGGCGG    32743     C    GCTGAT   _
                                CTGCC CCTCT     GCCC CC
                                ||||| |||||     |||| ||
                                GGCGG GGAGA     CGGG GG
                                   A    _______    A
GAM563  LOC56832  3'  GGCTATCAGCAGAAGGATCAG  65447    CC  C       _
                                CTG  CC TCTGCTGAT GCC
                                |||  || |||||||| |||
                                GAC  GG AGACGACTA CGG
                                  TA  A        T
GAM563  LOC56964  5'  GGACAGTCAGTGGGAGCAG   63252    C   T   _   ATG
                                CTGC CCC CTG CTG   CC
                                |||| ||| ||| |||   ||
                                GACG GGG GAC GAC   GG
                                  A  T   T   A__
GAM563  LOC90119  5'  GGGGAGGGCAGAGGGGTCAG   62211    C       GATG
                                CTG CCCCTCTGCT    CCCC
                                ||| ||||||||||    ||||
                                GAC GGGGAGACGG    GGGG
                                  T        GA__
GAM563  LOC90462  3'  GGCCCAGCAGAGGGCAG     63572      CC     AT
                                CTGCCC  TCTGCTG  GCC
                                ||||||  |||||||  |||
                                GACGGG  AGACGAC  CGG
                                   __      C_
GAM563  LOC90494  5'  GGAGTAGGCAGAGGGATCAG   63734    CC       GA   C
                                CTG  CCCTCTGCT  TGC CC
                                |||  |||||||||  ||| ||
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                                GAC  GGGAGACGG  ATG GG
                                  TA       __   A
GAM563  LOC91040  3'  TGGGGGCATCGGCAAGG     65356     C
                                CCT TGCTGATGCCCCCA
                                ||| ||||||||||||||
                                GGA ACGGCTACGGGGGT
                                  _
GAM563  LOC91974  5'  TGGGAGCAAACTTCAGAGAAGG 68365      CC    CTGA_  C
           CAG                    CTGCC  CTCTG    TGC CCCA
                                ||||||  |||||    ||| ||||
                                GACGG  GAGAC    ACG GGGT
                                   AA    TTCAA  A
GAM563  LOC92230  5'  GGGGGCAAAAGGGGCAG     69087       CTCTGC GA
                                CTGCCCC     T  TGCCCCC
                                |||||||     |  |||||||
                                GACGGGG     A  ACGGGGG
                                   _______ AA
GAM563  LOC92340  3'  TGGGGACCTCAGTGGGGGCAG  69570       TCT    TGC
                                CTGCCCCC   GCTGA   CCCCA
                                ||||||||   |||||   |||||
                                GACGGGGG   TGACT   GGGGT
                                     ___    CCA
GAM563  LOC92710  3'  GGGTGCAGAGAGGCAG      70866      CC     TGAT
                                CTGCC  CTCTGC   GCCC
                                |||||  ||||||   ||||
                                GACGG  GAGACG   TGGG
                                   A_    _____
GAM564  BCL2L2    3'  AACTCGCAGTCCTCTAGA    15753       TT  GG
                                TCTGGAG  GA  TGCGAGTT
                                |||||||  ||  ||||||||
                                AGATCTC  CT  ACGCTCAA
                                     __ G_
GAM564  CA3       5'  AACTCGCACAAGTGTCCAGAG  18993       GTTGAG
                                CTCTGGA     GTGCGAGTT
                                |||||||     |||||||||
                                GAGACCT     CACGCTCAA
                                    GTGAA_
GAM564  KIT       3'  AACTTGCATCCAACTCCAGGAT 5846     CT       A
              A                  TA  CTGGAGTTG GGTGCGAGTT
                                ||  ||||||||| ||||||||||
                                AT  GACCTCAAC CTACGTTCAA
                                  AG       _
GAM564  UBE4A     3'  ACCAAAACCAACCCCAGAGTG  17727        A   A____
                                TACTCTGG GTTG    GGT
                                |||||||| ||||    |||
                                GTGAGACC CAAC    CCA
                                     C   CAAAA
GAM564  ACTR2     3'  AACTCATTCAACTCCAGG    20368          GTGC
                                TCTGGAGTTGAG   GAGTT
                                ||||||||||||   |||||
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                                GGACCTCAACTT   CTCAA
                                      A___
GAM564  LOC146159 5'  ACCCGCACTTCCCAGA     78171      AGTT      A
                                TCTGG   GAGGTGCG GT
                                |||||   |||||||| ||
                                AGACC   CTTCACGC CA
                                  ____      C
GAM564  LOC196746 3'  AACTCAACAAACTTCAGAGTA  88896          GAG  GC
                                TACTCTGGAGTT   GT  GAGTT
                                ||||||||||||   ||  |||||
                                ATGAGACTTCAA   CA  CTCAA
                                      A__  A_
GAM565  HAL       5'  GCCACTCCTGCATAAAGCTC   10903          TGAAAA
                                GAGCTTTATGC     GGTGGC
                                ||||||||||      ||||||
                                CTCGAAATACG     TCACCG
                                      TCC___
GAM565  HMGN2     3'  GGCCACCTTGGCACAAAAGC   19809      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _ GG
GAM565  NMI       5'  GGCCACCTCCTCAGGAAG    17436      ATG   AA
                                CTTT   CTGA  AGGTGGCC
                                ||||   ||||  ||||||||
                                GAAG   GACT  TCCACCGG
                                  ___    CC
GAM565  PACE      3'  GGCCACCTCTCCAAGGGCTT   11944       A  CT  AAA
                                GAGCTTT TG  GA   GGTGGCC
                                ||||||| ||  ||   |||||||
                                TTCGGGA AC  CT   CCACCGG
                                   _ CT  ___
GAM565  PYCR1     3'  CCACCTTCCTCTAGAGCTC    70639       TGCT  A_
                                GAGCTTTA    GA  AAGGTGG
                                ||||||||    ||  |||||||
                                CTCGAGAT    CT  TTCCACC
                                   _____ CC
GAM565  SDC1      3'  GGCCACCTCCCCAGCATTCCAG 12991     TT_     AAA
          C                      GCT   ATGCTG   AGGTGGCC
                                 |||   ||||||   ||||||||
                                 CGA   TACGAC   TCCACCGG
                                   CCT     CCC
GAM565  FLJ11560  5'  GCCCAGGCCCAGCATAAAG   48008         AAAA  ___
                                CTTTATGCTG   GGT   GGC
                                ||||||||||   |||   |||
                                GAAATACGAC   CCG   CCG
                                     _____  GAC
GAM565  KIAA0446  5'  CCACCTTTTGAAGAGCTC    69446       ATGCTG
                                GAGCTTT     AAAAGGTGG
                                |||||||     |||||||||
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                                CTCGAGA     TTTTCCACC
                                   AG____
GAM565  KIAA0971  3'  GTTGTTCTCAGCATAAAGT   30677          AAA  TG
                                GCTTTATGCTGA   GG  GC
                                ||||||||||||  ||  ||
                                TGAAATACGACT   TT  TG
                                      C__  GT
GAM565  KIAA1393  3'  GGCCACCTTGGCACAAAAGC   72574      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                   _ _  GG
GAM565  KIAA1656  3'  GGCCACCTCCTCCTAGAAGCC  66377   A    ATGCT  AA
                                G GCTTT    GA  AGGTGGCC
                                | |||||    ||  ||||||||
                                C CGAAG    CT  TCCACCGG
                                _    ATC__  CC
GAM565  KIAA1884  3'  GCCACCTTCATCTACCAAGGCT 73728       ATGCT  A_
             C                   GAGCTTT    GA  AAGGTGGC
                                |||||||    ||  ||||||||
                                CTCGGAA    CT  TTCCACCG
                                   CCAT_  AC
GAM565  PP3501    3'  GGCCACCGTTGACAGCATAAAG 41683         AAAA_
                                CTTTATGCTG    GGTGGCC
                                ||||||||||    |||||||
                                GAAATACGAC    CCACCGG
                                      AGTTG
GAM565  SDCCAG3   3'  GGTGTTCTCAGCATGAAGCTC  22803           AAA  TG
                                GAGCTTTATGCTGA   GG  GCC
                                ||||||||||||||  ||  |||
                                CTCGAAGTACGACT   CT  TGG
                                      ____  TG
GAM565  SP140     3'  GGCCACCTCCATGCAGAAGC   24327      A   TGAAA
                                GCTTT TGC    AGGTGGCC
                                ||||| |||    ||||||||
                                CGAAG ACG    TCCACCGG
                                   _  TACC_
GAM565  LOC148760 3'  GGCCACCTTCTCCAACAAGCTC 85364       TA  CT  A
                                GAGCTT  TG  GA AAGGTGGCC
                                ||||||  ||  || |||||||||
                                CTCGAA  AC  CT TTCCACCGG
                                   CA  __  C
GAM565  LOC150170 5'  ACCTGTTTCACATAAAGC    80414        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                      _    G
GAM565  LOC150175 5'  ACCTGTTTCACATAAAGC    80453        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
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                                CGAAATAC ACTTT TCCA
                                   _    G
GAM565  LOC150215 5'  ACCTGTTTCACATAAAGC    80456        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                   _    G
GAM565  LOC150218 5'  ACCTGTTTCACATAAAGC    80525        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                   _    G
GAM565  LOC152065 3'  GGCCACCTTCTCCTTGGCAGGC 86737      TTA   ___  A
          TC                     GAGCT   TGCT   GA AAGGTGGCC
                                |||||   ||||   || |||||||||
                                CTCGG   ACGG   CT TTCCACCGG
                                  ___   TTC  C
GAM565  LOC152267 3'  GGCCACCTTGGCACAAAAGC   61036      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _  GG
GAM565  LOC158292 5'  CCTCTGGACCCAGCATAAGGCT 88046           AAAA_  T
          C                     GAGCTTTATGCTG    GG GG
                                ||||||||||||    || ||
                                CTCGGAATACGAC    TC CC
                                      CCAGG  T
GAM565  LOC219997 3'  GCCACCTCTTCAGCCTC    93256    CTTTAT    A
                                GAG     GCTGAA AGGTGGC
                                |||     |||||| |||||||
                                CTC     CGACTT TCCACCG
                                  _______     C
GAM565  LOC256269 3'  GGCCACCTTGGCACAAAAGC   96608      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _  GG
GAM565  LOC91963  5'  GGCCACCTCCTCTGAGAAGC   68321      ATGCT  AA
                                GCTTT    GA  AGGTGGCC
                                |||||    ||  ||||||||
                                CGAAG    CT  TCCACCGG
                                   AGT__  CC
GAM566  AK3     3'  CAGCTGGTTTTTGACAGC    26396     CCCTG      A
                                GCTG    GGGAACCA CTG
                                ||||    |||||||| |||
                                CGAC    TTTTTGGT GAC
                                  AG___       C
GAM566  BCL11A   3'  CCAGTTGGTGTTCAAATAGCA  43464      CCC   GA
                                TGCTG   TGGG  ACCAACTGG
                                |||||   ||||  |||||||||
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                                ACGAT   ACTT  TGGTTGACC
                                  AA_   G_
GAM566  CDX2     5'  CCAGCGTCGGTCCCCAGGCAGC 8850         C     A  AA__
             AT                   ATGCTGCC TGGGGA CC    CTGG
                                  |||||||| |||||| ||    ||||
                                  TACGACGG ACCCCT GG    GACC
                                     _     _ CTGC
GAM566  LDB3     3'  CCAGTCTCCCCCAGGGAGCAT  76926       G       AACCA
                                  ATGCT CCCTGGGG     ACTGG
                                  ||||| ||||||||     |||||
                                  TACGA GGGACCCC     TGACC
                                     _       CTC__
GAM566  MAK      3'  CAGCTGGTTCCCCCAAGC    20941     GCCCT       A
                                  GCT    GGGGAACCA CTG
                                  |||    ||||||||| |||
                                  CGA    CCCCTTGGT GAC
                                    AC___        C
GAM566  MAP3K14  3'  CCACTCTTCCCCAGAGCAGCA  15543       C       CCAAC
                                  TGCTGC CTGGGGAA    TGG
                                  |||||| ||||||||    |||
                                  ACGACG GACCCCTT    ACC
                                     A       CTC__
GAM566  MYLK2    3'  CAGATCCCCAGGGCAGC     53580           ACCAA
                                  GCTGCCCTGGGGA    CTG
                                  ||||||||||||    |||
                                  CGACGGGACCCCT    GAC
                                         A____
GAM566  SORCS2   3'  TGGTTCTCCCCAGGGCAG    40810           __
                                  CTGCCCTGGGGA  ACCA
                                  ||||||||||||  ||||
                                  GACGGGACCCCT  TGGT
                                         CT
GAM566  C1orf2   3'  CCAGCTGGTTGGGACCAGCAGC 22728       CC   GG__    A
                                  GCTGC  TGG    AACCA CTGG
                                  |||||  |||    ||||| ||||
                                  CGACG  ACC    TTGGT GACC
                                     __  AGGG    C
GAM566  C1orf2   3'  CCAGCTGGTTGGGACCAGCAGC 96266       CC   GG__    A
                                  GCTGC  TGG    AACCA CTGG
                                  |||||  |||    ||||| ||||
                                  CGACG  ACC    TTGGT GACC
                                     __  AGGG    C
GAM566  CDC14B   3'  CCAGTTACTGCAGGGCAGC   14774         G  AACC
                                  GCTGCCCTG GG    AACTGG
                                  ||||||||| ||    ||||||
                                  CGACGGGAC TC    TTGACC
                                        G  A___
GAM566  DKFZP434B195 5'  CCAGTTGGTCCAAAGCTACAT  49246     CT  CC   GGA
                                  ATG  GC  TGG   ACCAACTGG
                                  |||  ||  |||   |||||||||
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                                TAC  CG  ACC   TGGTTGACC
                                  AT  AA  ___
GAM566  FLJ12525  3'  CCAGCCGTGCCAGGGCAACA  49131    C      GGA  CAA
                                TG TGCCCTGG   AC   CTGG
                                || ||||||||   ||   ||||
                                AC ACGGGACC   TG   GACC
                                  A       G__  CC_
GAM566  FLJ12541  3'  CAGTTGAGCCAGGGCAGC    42568         GGAAC
                                GCTGCCCTGG    CAACTG
                                ||||||||||    ||||||
                                CGACGGGACC    GTTGAC
                                      GA___
GAM566  FLJ22471  3'  CCAACCTTTCCCAGGGCGGCA  47858           CCAAC
                                TGCTGCCCTGGGGAA    TGG
                                ||||||||||||||    |||
                                ACGGCGGGACCCTTT    ACC
                                        CCA__
GAM566  FLJ30473  3'  CCAGGATCCCCCAGGGCAG    59139         AACCAA
                                CTGCCCTGGGG     CTGG
                                ||||||||||      ||||
                                GACGGGACCCC     GACC
                                      CTAG__
GAM566  GLTP      3'  TGTGTCCCCCAGAGCAGC    33591      C     A  _
                                GCTGC CTGGGG AC CA
                                ||||| |||||| || ||
                                CGACG GACCCC TG GT
                                   A     C  T
GAM566  KIAA1068  3'  CAGCCACTGCAGGCAGCAT   31684       C   G  AACCAA
                                ATGCTG CCTG GG     CTG
                                |||||| |||| ||     |||
                                TACGAC GGAC TC     GAC
                                   _   G  ACC___
GAM566  KIAA1211  3'  CCAGTTGGCTCCCAGGGAACAT 69468     CTG       AA
                                ATG   CCCTGGGG  CCAACTGG
                                |||   ||||||||  ||||||||
                                TAC   GGGACCCT  GGTTGACC
                                  AA_       C_
GAM566  MGC21738  5'  CACTGGCCTTTCCGCAGGGCAG 59574          _   A_____  AACT
          CA                    TGCTGCCCTG GGGA     CC    G
                                |||||||||| ||||     ||    |
                                ACGACGGGAC CCTT     GG    C
                                      G    TCC___  TCAA
GAM566  RAB20     5'  CCAGCTGCGCCCAGGGCGCA  35619     T      GAAC  A
                                TGC GCCCTGGG    CA CTGG
                                ||| ||||||||    || ||||
                                ACG CGGGACCC    GT GACC
                                  _       GC__  C
GAM566  WBSCR17   3'  CCAGGGCTTCTCCAGGGCAGCA 82214             _  AA
                                TGCTGCCCTGGGGAA CC  CTGG
                                |||||||||||||| ||  ||||
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                                ACGACGGGACCTCTT GG  GACC
                                        C ___
GAM566  WDR9     3'  CCAGTCAGCTCTTGTACAGACA 39083     _  CCCT    AACCA
              T                  ATG CTG    GGGG     ACTGG
                                 ||| |||    ||||     |||||
                                 TAC GAC    TCTC     TGACC
                                   A   ATGT    GAC__
GAM566  LOC129450 5'  CCAGTTGGTCCAGAGGGCAGC  75379        GG   A
                                 GCTGCCCT  GGA CCAACTGG
                                 ||||||||  ||| ||||||||
                                 CGACGGGA  CCT GGTTGACC
                                      GA  _
GAM566  LOC153769 3'  TGTGTCCTCCCAAGGCAGCAT  81811        C   _ A  _
                                 ATGCTGCC TGGG G AC CA
                                 |||||||| |||| | || ||
                                 TACGACGG ACCC C TG GT
                                      A    T C  T
GAM566  LOC157273 5'  CCAGCTAGTCTACTCCAGGGCA 87718            A__  CAA
              GCAT                   ATGCTGCCCTGGGG   AC   CTGG
                                 ||||||||||||||   ||   ||||
                                 TACGACGGGACCTC   TG   GACC
                                        ATC  ATC
GAM566  LOC257081 3'  TGGGCTCCCAAGGCAGCAT   98594        C    AA
                                 ATGCTGCC TGGGG  CCA
                                 |||||||| |||||  |||
                                 TACGACGG ACCCT  GGT
                                      A    CG
GAM567  CCND2    3'  TCCCAGCAAATCATCGGGCCA  10055          CCACA  _  A
                                 TGGCCTGATGAT    GC GG GA
                                 ||||||||||||    || || ||
                                 ACCGGGCTACTA    CG CC CT
                                        AA___  A  C
GAM567  GCN5L2   5'  CTCCGCTGCGGGGGAGGCC   60529      GATGA   A
                                 GGCCT    TCC CAGCGGAG
                                 |||||    ||| ||||||||
                                 CCGGA    GGG GTCGCCTC
                                    GG___   C
GAM567  GJA5     3'  CTGACCAGATCATCAGCCA   75167      C       CACAG
                                 TGGC TGATGATC    CGG
                                 |||| ||||||||    |||
                                 ACCG ACTACTAG    GTC
                                    _       ACCA_
GAM567  HIVEP3   3'  TCCCCGCTGTGGTTGGCAGCCA 44702      C  ATGAT       A
                                 TGGC TG    CCACAGCGG GA
                                 |||| ||    ||||||||| ||
                                 ACCG AC    GGTGTCGCC CT
                                    _ GGTT_       C
GAM567  HOXD1    5'  CCGCCGGTATATTAGGCCA   44696          AT  ACA
                                 TGGCCTGATG  CC   GCGG
                                 |||||||||  ||   ||||
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                                ACCGGATTAT  GG   CGCC
                                      AT  C__
GAM567  SUFU     3'  CCTTGTGACCCATCAGGCCA   32934          ATC    C
                                TGGCCTGATG   CACAG GG
                                ||||||||||   ||||| ||
                                ACCGGACTAC   GTGTT CC
                                      CCA    _
GAM567  DKFZP586J1624 3'  CTCCGCCCAGTCACCATCAGGC 32043          ATCCACA_
          CA                    TGGCCTGATG       GCGGAG
                                ||||||||||       ||||||
                                ACCGGACTAC       CGCCTC
                                      CACTGACC
GAM567  KIAA1671  3'  CTTTGCTTATGAATCATCAGAC 66282    C       C  C_
          C                     GG CTGATGAT CA  AGCGGAG
                                || ||||||||  ||  |||||||
                                CC GACTACTA GT  TCGTTTC
                                 A       A  AT
GAM567  LOC159110 5'  TCTCCGCTGCCCCGGTCAACCA 82995     CCTGA    CA__
                                TGG    TGATC    CAGCGGAGA
                                |||    |||||    |||||||||
                                ACC    ACTGG    GTCGCCTCT
                                  A____     CCCC
GAM567  LOC159116 5'  TCTCCGCTGCCCCGGTCAACCA 82978     CCTGA    CA__
                                TGG    TGATC    CAGCGGAGA
                                |||    |||||    |||||||||
                                ACC    ACTGG    GTCGCCTCT
                                  A____     CCCC
GAM567  LOC165476 5'  CTCCGCTGCCTGCTCAGCCA   88550     C   TGATCCA
                                TGGC TGA      CAGCGGAG
                                |||| |||      ||||||||
                                ACCG ACT      GTCGCCTC
                                  _   CGTCC__
GAM567  LOC200032 5'  CTGACCAGATCATCAGCCA    85475     C       CACAG
                                TGGC TGATGATC     CGG
                                |||| ||||||||     |||
                                ACCG ACTACTAG     GTC
                                  _       ACCA_
GAM567  LOC219654 5'  CTCCGCTGCGGAGGGGGGCC   92932      GATGA   A
                                GGCCT     TCC CAGCGGAG
                                |||||     ||| ||||||||
                                CCGGG     AGG GTCGCCTC
                                   GGG__   C
GAM567  LOC255862 3'  TCAAATGTAGACTATCAGGCCA 96115          A  C   GCG
                                TGGCCTGATG TC ACA   GA
                                |||||||||| || |||   ||
                                ACCGGACTAT AG TGT   CT
                                      C  A   AAA
GAM568  BSN      3'  TGCAGGGCACCACCTTCAA    14392       A   CC  AGA
                                TTGAA GTG  TG   TCCTGCA
                                ||||| |||  ||   |||||||
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                                AACTT CAC  AC   GGGACGT
                                  C   C_  ___
GAM568  CA12     3'  CTGCAGGATCCCTACTGCCAA  8689      AA    CCTGA
                                TTG  AGTG    GATCCTGCAG
                                |||  ||||    ||||||||||
                                AAC  TCAT    CTAGGACGTC
                                  CG   CC___
GAM568  CSDA     3'  CAGGCTCCTCAGGCACCTTCA  14686      A       AT_
                                TGAA GTGCCTGAG   CCTG
                                |||| |||||||||   ||||
                                ACTT CACGGACTC   GGAC
                                  C       CTC
GAM568  HMGA2    5'  TGCCCAAGGCACTTTCAA    14459           GAGATCCT
                                TTGAAAGTGCCT      GCA
                                ||||||||||||      |||
                                AACTTTCACGGA      CGT
                                       ACC_____
GAM568  KCNA7    3'  CTGCAGGACCTCACAC      49899     CC    A
                                GTG  TGAG TCCTGCAG
                                |||  |||| ||||||||
                                CAC  ACTC AGGACGTC
                                  __    C
GAM568  RAB30    3'  GTCCACAGGCACTTTCAA    27939           A_
                                TTGAAAGTGCCTG  GAT
                                ||||||||||||  |||
                                AACTTTCACGGAC  CTG
                                       AC
GAM568  S100B    3'  CTGCAGGATCCTTGCCTCCAA  21849     AA  T  CTGA
                                TTG  AG GC    GATCCTGCAG
                                |||  || ||    ||||||||||
                                AAC  TC CG    CTAGGACGTC
                                  C_  _  TTC_
GAM568  SPON2    3'  CTGCAGGATAAAGTCATCCCCA 25851     AAA   C  GAG
           A                     TTG   GTG CT   ATCCTGCAG
                                |||   ||| ||   |||||||||
                                AAC   TAC GA   TAGGACGTC
                                  CCC   T  AA_
GAM568  FLJ10997 3'  CAGTATCTCAGGCACCTTC    37513     A         C
                                GAA GTGCCTGAGAT CTG
                                ||| ||||||||||| |||
                                CTT CACGGACTCTA GAC
                                  C         T
GAM568  FLJ21657 5'  CTGCAGGAGAGGATGACACTTT 42798          ____   GAGA
           CGA                    TTGAAAGTG    CCT    TCCTGCAG
                                |||||||||    |||    ||||||||
                                AGCTTTCAC    GGA    AGGACGTC
                                     AGTA   G___
GAM568  FLJ21988 3'  CTGCAGGACCAGGACTCCCAG  42852     AA   G    AGA
                                TTG  AGT CCTG   TCCTGCAG
                                |||  ||| ||||   ||||||||
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                                GAC  TCA GGAC   AGGACGTC
                                  CC   _    C__
GAM568  KIAA0146  3'  GCAGGATCTGTGAACTTTGCAA 82322     _    GCCTG
                                TTG AAAGT    AGATCCTGC
                                ||| |||||    |||||||||
                                AAC TTTCA    TCTAGGACG
                                  G    AGTG_
GAM568  KIAA1677  3'  CTGCAGCATGCAAGCACTTTTA 67663         C  AG  C
          A                      TTGAAAGTGC TG  AT CTGCAG
                                ||||||||||  ||  || ||||||
                                AATTTTCACG AC  TA GACGTC
                                      A  G_  C
GAM568  MYT1     5'  TGCAGGACCTCAAGACAC    16982     C  _  A
                                GTG CT GAG TCCTGCA
                                ||| || ||| |||||||
                                CAC GA CTC AGGACGT
                                  A  A   C
GAM568  PPFIBP2   3'  CTCAGCTCTCAGGCAC      77099          TC   C
                                GTGCCTGAGA  CTG AG
                                ||||||||||  ||| ||
                                CACGGACTCT  GAC TC
                                      C_   _
GAM568  RASGRP4   3'  CTGCAGGAGCTGGTGGCCCTCC 54745     AA  T   TG_  A
          AA                    TTG  AG GCC   AG TCCTGCAG
                                |||  || |||   || ||||||||
                                AAC  TC CGG   TC AGGACGTC
                                  C_  C   TGG  G
GAM568  LOC121506 5'  GCAGGAAGAACACTTTCA    74533        C_  GAGA
                                TGAAAGTG  CT    TCCTGC
                                ||||||||  ||    ||||||
                                ACTTTCAC  GA    AGGACG
                                    AA  ____
GAM568  LOC127540 5'  CTGCAAGTACAGCACTTTC    75171        C  AG  CC
                                GAAAGTGC TG  AT  TGCAG
                                |||||||| ||  ||  |||||
                                CTTTCACG AC  TG  ACGTC
                                    _  A_  A_
GAM568  LOC145919 3'  CTGCTGACTAAACACTTTCAA  78026         CCTG  A  CT
                                TTGAAAGTG    AG TC  GCAG
                                |||||||||    || ||  ||||
                                AACTTTCAC    TC AG  CGTC
                                      AAA_  _  T_
GAM568  LOC152274 3'  TGCAGGAGCAGCCTCCAA    81347     AA  T  C  AGA
                                TTG  AG GC TG   TCCTGCA
                                |||  || || ||   |||||||
                                AAC  TC CG AC   AGGACGT
                                  C_  _  _  G__
GAM568  LOC157923 5'  CAGCCTCAGGCACTCTCA    82524     A        ATC
                                TGA AGTGCCTGAG   CTG
                                ||| ||||||||||   |||
```

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                                ACT TCACGGACTC   GAC
                                  C        C__
GAM569  ABCC3    3'  GCCACATCACGGCAACTGA   39615      G   TTTGAG
                                TCAGT GCC     GATGTGGC
                                ||||| |||     ||||||||
                                AGTCA CGG     CTACACCG
                                   A   CA____
GAM569  AP2M1    3'  AGCTCCCCCAAAGGCCA     15798         A  ATGT
                                TGGCCTTTG GG    GGCT
                                ||||||||| ||    ||||
                                ACCGGAAAC CC    TCGA
                                      _ CC__
GAM569  CACNA2D2 3'  AGCCACATCCCCAAGCCCAC   21220      C   T A
                                GTGG CTT G GGATGTGGCT
                                |||| ||| | ||||||||||
                                CACC GAA C CCTACACCGA
                                  C   _ C
GAM569  GGA3     3'  GCCACATCCTCACACCTGA    26586     _  GCCTT
                                TCAG TG     TGAGGATGTGGC
                                |||| ||     ||||||||||||
                                AGTC AC     ACTCCTACACCG
                                  C  _____
GAM569  GGA3     3'  GCCACATCCTCACACCTGA    57609     _  GCCTT
                                TCAG TG     TGAGGATGTGGC
                                |||| ||     ||||||||||||
                                AGTC AC     ACTCCTACACCG
                                  C  _____
GAM569  GPR30    3'  AGCCACACGGAGAGGCCACTG  9489           GAGGA
                                CAGTGGCCTTT     TGTGGCT
                                ||||||||||     |||||||
                                GTCACCGGAGA     ACACCGA
                                      GGC__
GAM569  EIF3S8   3'  CCACACCTCAGTCACT      14989       CTT     A
                                AGTGGC   TGAGG TGTGG
                                ||||||   ||||| |||||
                                TCACTG   ACTCC ACACC
                                   ___    _
GAM569  KIAA1128 3'  GCATCCCAAGGCCACT      69006         T A
                                AGTGGCCTT G GGATGT
                                ||||||||| | ||||||
                                TCACCGGAA C CCTACG
                                   _ _
GAM569  MGC13090 3'  TCCCCCAGAAGCCACTGA    52123        C    A_
                                TCAGTGGC TTTG  GGA
                                |||||||| ||||  |||
                                AGTCACCG AGAC  CCT
                                     A    CC
GAM569  NCKX3    3'  AGCCACTGGGCAAGGCCAC    40723        T AGGAT
                                GTGGCCTT G     GTGGCT
                                |||||||| |     ||||||
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```
                                CACCGGAA C    CACCGA
                                    _ GGGT_
GAM569  LOC221362 5'  ACTCCCAAAGCCACTGA    95397       C   A  T
                                TCAGTGGC TTTG GGA GT
                                |||||||| |||| ||| ||
                                AGTCACCG AAAC CCT CA
                                    _   _  _
GAM570  AXIN1    3'  ACCAGAAAATCATGCAGTG   61532       CC__
                                CACTGCGTGA   TTGGT
                                ||||||||||   |||||
                                GTGACGTACT   GACCA
                                     AAAA
GAM570  B4GALT4  5'  GCCACGGAACTCACGCAGTG  15028        ___ T
                                CACTGCGTGA  CC TGGT
                                ||||||||||  || ||||
                                GTGACGCACT  GG ACCG
                                     CAA  C
GAM570  CMAR     3'  GCTGGTCTAGTCACGCA     19033       CT  TT
                                TGCGTGAC  TGG  CAGC
                                ||||||||  |||  ||||
                                ACGCACTG  ATC  GTCG
                                    __  TG
GAM570  COL17A1  3'  CTGAACCAGGCCAGAGCA    6685     G_  A  T
                                TGC  TG CCT GGTTCAG
                                |||  || ||| |||||||
                                ACG  AC GGA CCAAGTC
                                  AG  C  _
GAM570  COL17A1  3'  CTGAACCAGGCCAGAGCA    56256    G_  A  T
                                TGC  TG CCT GGTTCAG
                                |||  || ||| |||||||
                                ACG  AC GGA CCAAGTC
                                  AG  C  _
GAM570  CRY2     3'  GCCAGTGGAGTCAGGCAGTG   72664      G   _ __
                                CACTGC TGAC CT  TGGT
                                |||||| |||| ||  ||||
                                GTGACG ACTG GG  ACCG
                                   G   A  TG
GAM570  CSPG2    5'  GCCGAACCCAGTCGCGCAG    16514       CTT   A
                                CTGCGTGAC   GGTTC GC
                                |||||||||   ||||| ||
                                GACGCGCTG   CCAAG CG
                                     AC_    C
GAM570  EMS1     3'  GCCAAATTGACTGTCACGCGG  19094       C_ TG  CA
                                CTGCGTGAC  T  GTT  GC
                                |||||||||  |  |||  ||
                                GGCGCACTG  A  TAA  CG
                                     TC GT   AC
GAM570  EMS1     3'  GCCAAATTGACTGTCACGCGG  57519       C_ TG  CA
                                CTGCGTGAC  T  GTT  GC
                                |||||||||  |  |||  ||
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                                GGCGCACTG  A  TAA  CG
                                     TC GT   AC
GAM570  FBXL7   3'  CTGAATCAGAGGCCACACAG  25495    C  A  _
                                CTG GTG CCT TGGTTCAG
                                ||| ||| ||| ||||||||
                                GAC CAC GGA ACTAAGTC
                                  A  C  G
GAM570  FGF18   3'  CTGAACCAAAACTCTTGGGG  15258   G  T  CC_
                                CT CG GA   TTGGTTCAG
                                || || ||   |||||||||
                                GG GT CT   AACCAAGTC
                                 G  T  CAA
GAM570  GARP    3'  CTGACTCAAGGTCACACAGTG  19779     C       GT
                                CACTG GTGACCTTG  TCAG
                                ||||| |||||||||  ||||
                                GTGAC CACTGGAAC  AGTC
                                   A        TC
GAM570  HDLBP   3'  CTAAACCAAGGTCATGAG   68508   G         C
                                CT CGTGACCTTGGTT AG
                                || ||||||||||||| ||
                                GA GTACTGGAACCAA TC
                                 _          A
GAM570  KCNJ16  5'  GCTGGTCAGTCACGCAGT   38486         CTTGGT
                                ACTGCGTGAC     TCAGC
                                ||||||||||     |||||
                                TGACGCACTG     GGTCG
                                      ACT___
GAM570  MHC2TA  3'  CTGAAGTCACACAGTG     5980       C    CTTGG
                                CACTG GTGAC    TTCAG
                                ||||| |||||    |||||
                                GTGAC CACTG    AAGTC
                                   A   _____
GAM570  PCDH7   5'  GCCGAACCCGCGGCGCGCAGTG 11990         A  TT_   A
                                CACTGCGTG CC   GGTTC GC
                                ||||||||| ||   ||||| ||
                                GTGACGCGC GG   CCAAG CG
                                      _ CGC    C
GAM570  PCDH7   5'  GCCGAACCCGCGGCGCGCAGTG 51617         A  TT_   A
                                CACTGCGTG CC   GGTTC GC
                                ||||||||| ||   ||||| ||
                                GTGACGCGC GG   CCAAG CG
                                      _ CGC    C
GAM570  PCDH7   5'  GCCGAACCCGCGGCGCGCAGTG 51621         A  TT_   A
                                CACTGCGTG CC   GGTTC GC
                                ||||||||| ||   ||||| ||
                                GTGACGCGC GG   CCAAG CG
                                      _ CGC    C
GAM570  SPG7    3'  GCTGGTCTAGTCACGCA    13347        CT   TT
                                TGCGTGAC  TGG  CAGC
                                ||||||||  |||  ||||
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                                ACGCACTG  ATC  GTCG
                                    __   TG
GAM570  TESK1    3'  CTGAACCAGACACAGCA     21886     _  ACC
                                TGC GTG   TTGGTTCAG
                                ||| |||   |||||||||
                                ACG CAC   GACCAAGTC
                                  A   A__
GAM570  TOP3A    3'  GCTGAAAAGTCACGCAG     17260         CTTGG
                                CTGCGTGAC    TTCAGC
                                |||||||||    ||||||
                                GACGCACTG    AAGTCG
                                     AA___
GAM570  AP1GBP1  3'  GCTGGGGATAAAAGCCACTGCA 24351       _  AC   GG___
           GTG                     CACTGC GTG  CTT    TTCAGC
                                |||||| |||  |||    ||||||
                                GTGACG CAC  GAA    GGGTCG
                                   T   C_   AATAG
GAM570  AP1GBP1  3'  GCTGGGGATAAAAGCCACTGCA 55440       _  AC   GG___
           GTG                     CACTGC GTG  CTT    TTCAGC
                                |||||| |||  |||    ||||||
                                GTGACG CAC  GAA    GGGTCG
                                   T   C_   AATAG
GAM570  C16orf7  3'  TGAGCCGGCCAGCAGTG     18146       G  A  TT
                                CACTGC TG CC  GGTTCA
                                |||||| || ||  ||||||
                                GTGACG AC GG  CCGAGT
                                   _  C  __
GAM570  CEACAM7  3'  GCTGTCTGAGTCAGCACAGT   23542      C _    C TG TT
                                ACTG G TGAC T  G  CAGC
                                |||| | |||| |  |  ||||
                                TGAC C ACTG A  C  GTCG
                                  A G    _ GT T_
GAM570  CENTG2   3'  GCCGAGGAGGTAGTCACGCGG  30539        _______
                                CTGCGTGA     CCTTGGT
                                ||||||||     |||||||
                                GGCGCACT     GGAGCCG
                                     GATGGA
GAM570  DCOHM    3'  GCTGCTTAGGTCACGCAG    50529           T  TT
                                CTGCGTGACCT GG  CAGC
                                |||||||||| ||  ||||
                                GACGCACTGGA TC  GTCG
                                       T  __
GAM570  DGKD     3'  GCCGAACCAAGAACATGATGTG 60109     TG    AC       A
                                CAC  CGTG  CTTGGTTC GC
                                |||  ||||  |||||||| ||
                                GTG  GTAC  GAACCAAG CG
                                  TA    AA       C
GAM570  DKFZP434K2235 5'  GCTGAGAGGGACACGCAGTG   84496          A    GG
                                CACTGCGTG CCTT  TTCAGC
                                ||||||||| ||||  ||||||
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                                GTGACGCAC GGGA  GAGTCG
                                     A   __
GAM570  DKFZp566D234 5' GCTGAACCTGAGACGCG     62520      GAC  _
                                TGCGT   CTT GGTTCAGC
                                |||||   ||| ||||||||
                                GCGCA   GAG CCAAGTCG
                                  ____  T
GAM570  FLJ11457  3' GCTTCTATGAGGTCACCAG    45727     C       GTTC
                                CTG GTGACCTTG    AGC
                                ||| |||||||||    |||
                                GAC CACTGGAGT    TCG
                                  _       ATCT
GAM570  FLJ11806  5' GCCAAGCGCCGCGCAGTG    46127         AC_
                                CACTGCGTG   CTTGGT
                                |||||||||   ||||||
                                GTGACGCGC   GAACCG
                                     CGC
GAM570  FLJ21588  5' GCCGAGGAGGGTCACGCAG    50804          GG   A
                                CTGCGTGACCTT  TTC GC
                                ||||||||||||  ||| ||
                                GACGCACTGGGA  GAG CG
                                      G_   C
GAM570  FLJ22639  5' GCCAAACCCAGCCACGCAGT   45996        AC  T    CA
                                ACTGCGTG  CT GGTT  GC
                                ||||||||  || ||||  ||
                                TGACGCAC  GA CCAA  CG
                                     C_  C    AC
GAM570  FLJ30681  3' GCTGAACCAATATACAGTG    93436      CG  ACC
                                CACTG  TG   TTGGTTCAGC
                                |||||  ||   ||||||||||
                                GTGAC  AT   AACCAAGTCG
                                   AT  ____
GAM570  KIAA0415  3' GCTATTCGAGGTCACCCAGTG  94165      C        TTC
                                CACTG GTGACCTTGG   AGC
                                ||||| ||||||||||   |||
                                GTGAC CACTGGAGCT   TCG
                                   C         TA_
GAM570  KIAA0472  3' GCCAAAGAAGGGTCACAAAGTG 72357     GC      ______
                                CACT  GTGACCT     TGGT
                                ||||  |||||||     ||||
                                GTGA  CACTGGG     ACCG
                                  AA      AAGAA
GAM570  KIAA0513  3' GCCAGAGTCACAGCAGTG    29035       _    C
                                CACTGC GTGAC TTGGT
                                |||||| ||||| |||||
                                GTGACG CACTG GACCG
                                   A    A
GAM570  KIAA0545  3' GCTCCAGGAGGTCACACAG   63846     C      __   TTC
                                CTG GTGACCT  TGG   AGC
                                ||| |||||||  |||   |||
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                                GAC CACTGGA  ACC   TCG
                                  A      GG  ___
GAM570  KIAA0877 3' GCTGAACCAAGATTTCTGC   62483    T  C__
                                GCG GA   CTTGGTTCAGC
                                ||| ||   ||||||||||
                                CGT CT   GAACCAAGTCG
                                  _  TTA
GAM570  KIAA0976 3' GCTTCCAGAGGTCACCCA    30552    C     _  TTC
                                TG GTGACCT TGG   AGC
                                || ||||||| |||   |||
                                AC CACTGGA ACC   TCG
                                 C      G  T__
GAM570  KIAA1136 3' ACCGACATGATCATGCAGTG  92954        CC___
                                CACTGCGTGA    TTGGT
                                ||||||||||    |||||
                                GTGACGTACT    AGCCA
                                      AGTAC
GAM570  KIAA1243 3' GCTCTCCAAAAATACACAGTG 74028     C   ACC   TTC
                                CACTG GTG   TTGG   AGC
                                ||||| |||   ||||   |||
                                GTGAC CAT   AACC   TCG
                                   A   AAA   TC_
GAM570  KIAA1957 3' GCTGGGAGCGACACGCAGTG  76216       ACC   G_
                                CACTGCGTG   TTG  TTCAGC
                                |||||||||   |||  ||||||
                                GTGACGCAC   AGC  GGGTCG
                                     ___   GA
GAM570  MEGF10   3' CTGAACCAAATCCATCAG    51607    C   ACC
                                CTG GTG   TTGGTTCAG
                                ||| |||   |||||||||
                                GAC TAC   AACCAAGTC
                                  _   CTA
GAM570  MGC20255 3' CTGAATTGTCCCAGCAGTG   54537      GT_   CTT
                                CACTGC   GAC   GGTTCAG
                                ||||||   |||   |||||||
                                GTGACG   CTG   TTAAGTC
                                   ACC   ___
GAM570  MGC33547 3' GCCAAGTATACCATGCAGTG  58986       AC___
                                CACTGCGTG    CTTGGT
                                |||||||||    ||||||
                                GTGACGTAC    GAACCG
                                     CATAT
GAM570  ORMDL3   3' GCTGAACATGGACCACGCAGT 74797       A_  TTG
                                ACTGCGTG  CC   GTTCAGC
                                ||||||||  ||   |||||||
                                TGACGCAC  GG   CAAGTCG
                                     CA  TA_
GAM570  RGS11    3' GCTGAACCCAGCACCAGTG   15164     C   AC  T
                                CACTG GTG  CT GGTTCAGC
                                ||||| |||  || ||||||||
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                                GTGAC CAC  GA CCAAGTCG
                                  _  __  C
GAM570  TCL6     5'  GCCAAGTCCAAGGTCACACAG  40480    C       _  CA
                                CTG GTGACCTTGG TT  GC
                                ||| |||||||||| ||  ||
                                GAC CACTGGAACC GA  CG
                                  A        T  AC
GAM570  TCL6     5'  GCCAAGTCCAAGGTCACACAG  40512    C       _  CA
                                CTG GTGACCTTGG TT  GC
                                ||| |||||||||| ||  ||
                                GAC CACTGGAACC GA  CG
                                  A        T  AC
GAM570  TCL6     5'  GCCAAGTCCAAGGTCACACAG  25909    C       _  CA
                                CTG GTGACCTTGG TT  GC
                                ||| |||||||||| ||  ||
                                GAC CACTGGAACC GA  CG
                                  A        T  AC
GAM570  TCL6     5'  GCCAAGTCCAAGGTCACACAG  27761    C       _  CA
                                CTG GTGACCTTGG TT  GC
                                ||| |||||||||| ||  ||
                                GAC CACTGGAACC GA  CG
                                  A        T  AC
GAM570  TLN2     3'  GCTGAACTGGACAGACAGTG  62356     CG  A  TT
                                CACTG  TG CC  GGTTCAGC
                                |||||  || ||  ||||||||
                                GTGAC  AC GG  TCAAGTCG
                                   AG  A  __
GAM570  LOC144893 5'  GCTGAAGGAGCCAGGCAG   84111     G  AC   GG
                                CTGC TG  CTT  TTCAGC
                                ||||  ||  |||  ||||||
                                GACG AC  GAG  AAGTCG
                                  G  C_   G_
GAM570  LOC146756 3'  GCTACGTGGATACGCAGTG   84807        A  TTG  TC
                                CACTGCGTG CC   GT  AGC
                                |||||||||  ||   ||  |||
                                GTGACGCAT GG   CA  TCG
                                     A  TG_  __
GAM570  LOC147057 3'  GCTGAACCAGTGCCGCAG    84986      TG  CT
                                CTGCG  AC  TGGTTCAGC
                                |||||  ||  |||||||||
                                GACGC  TG  ACCAAGTCG
                                   CG  __
GAM570  LOC148147 3'  GCTAAACCCTGGAAAGCCACAA 79401     GC   A____  TT   C
          GTG                    CACT  GTG    CC  GGTT AGC
                                ||||  |||    ||  |||| |||
                                GTGA  CAC    GG  CCAA TCG
                                  A_   CGAAA  TC   A
GAM570  LOC149478 5'  GCTGAACCTTTTTCCGCAG   80172      T  CCTT
                                CTGCG GA    GGTTCAGC
                                ||||| ||    ||||||||
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                                GACGC CT    CCAAGTCG
                                   _ TTTT
GAM570   LOC149734 3'  GCTGAACCAGTTCCACAAG   85796    GC   ACC
                                CT  GTG   TTGGTTCAGC
                                ||  |||   ||||||||||
                                GA  CAC   GACCAAGTCG
                                 A_   CTT
GAM570   LOC149951 3'  GCTGAACCAGCTGGGCGCGCA  85951       A  ___
                                TGCGTG CCT   TGGTTCAGC
                                ||||||  |||   |||||||||
                                ACGCGC GGG   ACCAAGTCG
                                   _   TCG
GAM570   LOC150538 3'  CTAAACCAAGGTCAAGGGG   80737    GCG        C
                                CT   TGACCTTGGTT AG
                                ||   ||||||||||| ||
                                GG   ACTGGAACCAA TC
                                 GGA          A
GAM570   LOC164714 5'  GCTGAACCACTACGCA      88585       ACCT
                                TGCGTG    TGGTTCAGC
                                ||||||    |||||||||
                                ACGCAT    ACCAAGTCG
                                   C___
GAM570   LOC219920 3'  CTAGAGCCACACAGCAG     94946     _  ACCT     _
                                CTGC GTG    TGGTTC AG
                                ||||  |||    ||||||  ||
                                GACG CAC    ACCGAG TC
                                  A  _____      A
GAM570   LOC220824 5'  GCCAAACCCAGCCACGCAGT   92480        AC  T    CA
                                ACTGCGTG  CT GGTT  GC
                                ||||||||  ||  ||||  ||
                                TGACGCAC  GA CCAA  CG
                                     C_  C    AC
GAM570   LOC254659 5'  GCTGAACCAAACAGCCCACG   96821      AC  ___
                                CGTG  CT   TGGTTCAGC
                                ||||  ||   |||||||||
                                GCAC  GA   ACCAAGTCG
                                  CC  CAA
GAM570   LOC257007 5'  GCTGCCCGGGTCACGCGTG    99444     T       T  TT
                                CAC GCGTGACCT GG  CAGC
                                |||  |||||||||  ||  ||||
                                GTG CGCACTGGG CC  GTCG
                                  _        C  __
GAM571   APM1     3'  CAAAGCTCAAAACAATCAAGA  17763    A   AGGG_
                                TC TTGG     TTGAGCTTTG
                                ||  ||||     ||||||||||
                                AG AACT     AACTCGAAAC
                                 _    AACAA
GAM571   ATF7     3'  TCAAAGCTTGTTCCATCAA    23403     GA   TT
                                TTG  GGG  GAGCTTTGA
                                |||  |||  |||||||||
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                                AAC  CCT  TTCGAAACT
                                  TA   TG
GAM571  ATP6V1G2  3'  TCAAAGAAATCCTCCAAT    56194          GAG
                                ATTGGAGGGTT   CTTTGA
                                ||||||||||   ||||||
                                TAACCTCCTAA   GAAACT
                                      A__
GAM571  ATP6V1G2  3'  TCAAAGAAATCCTCCAAT    57117          GAG
                                ATTGGAGGGTT   CTTTGA
                                ||||||||||   ||||||
                                TAACCTCCTAA   GAAACT
                                      A__
GAM571  DGKB      3'  CAAAGCTCAATAGATGA     94108       GGAGG
                                TCATT    GTTGAGCTTTG
                                |||||    ||||||||||
                                AGTAG    TAACTCGAAAC
                                   A____
GAM571  NONO      3'  CAAACATCCCCCAATGA     82883        A   T  AGC
                                TCATTGG GGG TG   TTTG
                                ||||||| ||| ||   ||||
                                AGTAACC CCC AC   AAAC
                                    _   T  ___
GAM571  PIK3R1    3'  TCAAAGCTGCTTTATTCAAT   69135        __    TG
                                ATTGGA  GGGT  AGCTTTGA
                                ||||||  ||||  ||||||||
                                TAACTT  TTCG  TCGAAACT
                                   AT    __
GAM571  SLC21A9   3'  TCAAAGTCTCCTTCAA      24382         TTGA
                                TTGGAGGG    GCTTTGA
                                ||||||||    |||||||
                                AACTTCCT    TGAAACT
                                     C___
GAM571  SLC7A8    5'  TCAAAGCTCTCTCCCAAT    25305      A   TT
                                ATTGG GGG  GAGCTTTGA
                                ||||| |||  |||||||||
                                TAACC CTC  CTCGAAACT
                                   _   T_
GAM571  SPON1     3'  CAAAGCCCCCCCAATG      63117       A   TTGA
                                CATTGG GGG    GCTTTG
                                |||||| |||    ||||||
                                GTAACC CCC    CGAAAC
                                   _   C___
GAM571  VAMP8     3'  TCAGGGACAACCCTCCA     15002          AG
                                TGGAGGGTTG  CTTTGA
                                ||||||||||  ||||||
                                ACCTCCCAAC  GGGACT
                                      A_
GAM571  YWHAZ     3'  CAAAGCTCACTTTACAA     14154     G    T
                                TTG AGGGT GAGCTTTG
                                ||| ||||| ||||||||
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                                AAC TTTCA CTCGAAAC
                                  A    _
GAM571  DAPK2    3'  CAAAGCTCTTAATTCTCCA   27510         __
                                TGGAGGGTT  GAGCTTTG
                                |||||||||  ||||||||
                                ACCTCTTAA  CTCGAAAC
                                     TT
GAM571  FACTP140 3'  TCAAAGCTGTATTTCCAAGA  24210    A     GTTG
                                TC TTGGAGG   AGCTTTGA
                                || |||||||   |||||||||
                                AG AACCTTT   TCGAAACT
                                 _     ATG_
GAM571  FLJ11186 3'  TCAAAGCTTTCTCCTCCAAGA  37729    A      TT
                                TC TTGGAGGG  GAGCTTTGA
                                || ||||||||  |||||||||
                                AG AACCTCCT  TTCGAAACT
                                 _      CT
GAM571  HH114    5'  CAAAGCTCAGTACGACGA    51666    A  GAGGG
                                TC TTG    TTGAGCTTTG
                                || |||    ||||||||||
                                AG AGC    GACTCGAAAC
                                 C  AT___
GAM571  KIAA1872 3'  GAAGCTCAACCCCCCTATGA   63611     T  A
                                TCAT GG GGGTTGAGCTTT
                                |||| || ||||||||||||
                                AGTA CC CCCAACTCGAAG
                                  T  C
GAM571  MGC15705 3'  CAAAGGAACGCCTCCAAGGA   52245    A     _  GAG
                                TC TTGGAGG GTT   CTTTG
                                || ||||||| |||   |||||
                                AG AACCTCC CAA   GAAAC
                                 G     G  G__
GAM571  MGC16279 5'  TCAAAACTGCCCTCTAAT    52993         TG  C
                                ATTGGAGGGT  AG TTTGA
                                ||||||||||  || |||||
                                TAATCTCCCG  TC AAACT
                                      __  A
GAM571  MGC16279 3'  TCAAAACTGCCCTCTAAT    63543         TG  C
                                ATTGGAGGGT  AG TTTGA
                                ||||||||||  || |||||
                                TAATCTCCCG  TC AAACT
                                      __  A
GAM571  NYD-SP21 3'  CAAAGCTCAGTACAAGA     51861    A  GAGGG
                                TC TTG    TTGAGCTTTG
                                || |||    ||||||||||
                                AG AAC    GACTCGAAAC
                                 _  AT___
GAM571  OPN4     3'  TCAAAACTCCTGCCCCATAA   53854     GA   T_  C
                                TTG  GGGT  GAG TTTGA
                                |||  ||||  ||| |||||
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                                AAT  CCCG  CTC AAACT
                                  AC    TC   A
GAM571  PP35     3'  TCAAAACTTCTGGTCCTCCAAA 23799    A      GT __   C
              GA                   TC TTGGAGG  T  GAG TTTGA
                                || |||||||  |  ||| |||||
                                AG AACCTCC  G  TTC AAACT
                                 A      TG TC   A
GAM571  SGK2     3'  AAAGCTCCCCCCAATGA     33248        A   TT
                                TCATTGG GGG  GAGCTTT
                                ||||||| |||  |||||||
                                AGTAACC CCC  CTCGAAA
                                     _  __
GAM571  LOC145623 3'  CAAAGTGCCTCCAATG      84388         GTTGA
                                CATTGGAGG    GCTTTG
                                |||||||||    ||||||
                                GTAACCTCC    TGAAAC
                                     G____
GAM571  LOC150886 5'  TCAAAACTTAATCCCCAATG   86332       A       C
                                CATTGG GGGTTGAG TTTGA
                                |||||| |||||||| |||||
                                GTAACC CCTAATTC AAACT
                                    _       A
GAM571  LOC254065 5'  CAAAGCTTATACCTCTAAT    99288        GT
                                ATTGGAGG  TGAGCTTTG
                                ||||||||  |||||||||
                                TAATCTCC  ATTCGAAAC
                                     AT
GAM571  LOC257480 3'  GTGACATCCCTCCAATGA     78434          T  A_
                                TCATTGGAGGG TG  GC
                                |||||||||||  ||  ||
                                AGTAACCTCCC AC  TG
                                      T  AG
GAM572  AK1      3'  CCTCCCCCTGTGTGGCCCTG   6638     A       A  T   T
                                CA GGCCACACA GG GGA GG
                                || |||||||| || ||| ||
                                GT CCGGTGTGT CC CCT CC
                                 C        C  _  _
GAM572  ARSD     3'  CCTTCCTTCTATGGCCTTG    24811        CACA   T   T
                                CAAGGCCA    AGG GGA GG
                                ||||||||    ||| ||| ||
                                GTTCCGGT    TCT CCT CC
                                     A___    T   T
GAM572  ATP7B    3'  CCTGGCCTTGTGTGGCTT     5334            GGAT
                                AGGCCACACAAGGT    GG
                                ||||||||||||||    ||
                                TTCGGTGTGTTCCG    CC
                                       GT__
GAM572  AVPR2    3'  CTGGGACACTGTGTGGCCCTG  5339     A       AG   GA_
                                CA GGCCACACA  GTG   TGG
                                || |||||||||  |||   |||
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                                GT CCGGTGTGT  CAC   GTC
                                 C        __  AGG
GAM572  BAP1    3'  CCACTCTTGCCGTGTGGCC   17397        ___  _
                                GGCCACAC   AAG GTGG
                                ||||||||   ||| ||||
                                CCGGTGTG   TTC CACC
                                    CCG   T
GAM572  BCL7A   3'  GTCCACCGGGGAGTGGCCTTG  40991         ACAA_
                                CAAGGCCAC    GGTGGAT
                                |||||||||    |||||||
                                GTTCCGGTG    CCACCTG
                                     AGGGG
GAM572  CBFA2T2  3'  CCATGCTTTACTTTGTACAGCC 18706    A   CAC        ___
           CTG                    CA GGC   ACAAGGTGGA   TGG
                                || |||   ||||||||||   |||
                                GT CCG   TGTTTCATTT   ACC
                                 C   ACA         CGT
GAM572  CHN2    3'  TTACCCTGTGTACCTTG     15797      CC    A
                                CAAGG  ACACA GGTGG
                                |||||  ||||| |||||
                                GTTCC  TGTGT CCATT
                                   A_    C
GAM572  DAAM2   3'  GTCCATCTCATGCTGGCCTTG  93905         _ CA
                                CAAGGCCA CA  AGGTGGAT
                                |||||||| ||  ||||||||
                                GTTCCGGT GT  TCTACCTG
                                     C  AC
GAM572  EGFL4   3'  CCAGGGCCTTGTGGGCC     62460      A       GGA
                                GGCC CACAAGGT   TGG
                                |||| ||||||||   |||
                                CCGG GTGTTCCG   ACC
                                   _       GG_
GAM572  EXTL3   3'  GTCCATCCACCCCACCCCTT   9336       CCACACAA
                                AAGG       GGTGGATGGAC
                                ||||       ||||||||||||
                                TTCC       CCACCTACCTG
                                   CCACC___
GAM572  F3      3'  TCCACCCACCTTGGCCTCC   67681   A     CACA     A
                                C AGGCCA    AGGTGG TGGA
                                | ||||||    |||||| ||||
                                C TCCGGT    TCCACC ACCT
                                 C      ____      C
GAM572  FCAR    3'  TCCACCCACCTTGGCCTCC   56581   A     CACA     A
                                C AGGCCA    AGGTGG TGGA
                                | ||||||    |||||| ||||
                                C TCCGGT    TCCACC ACCT
                                 C      ____      C
GAM572  FCAR    3'  TCCACCCACCTTGGCCTCC   56597   A     CACA     A
                                C AGGCCA    AGGTGG TGGA
                                | ||||||    |||||| ||||
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                                C TCCGGT   TCCACC ACCT
                                 C     ____     C
GAM572  FCAR    3'  TCCACCCACCTTGGCCTCC   56609   A    CACA    A
                                C AGGCCA   AGGTGG TGGA
                                | ||||||   |||||| ||||
                                C TCCGGT   TCCACC ACCT
                                 C     ____     C
GAM572  FCAR    3'  TCCACCCACCTTGGCCTCC   56621   A    CACA    A
                                C AGGCCA   AGGTGG TGGA
                                | ||||||   |||||| ||||
                                C TCCGGT   TCCACC ACCT
                                 C     ____     C
GAM572  FCAR    3'  TCCACCCACCTTGGCCTCC   10593   A    CACA    A
                                C AGGCCA   AGGTGG TGGA
                                | ||||||   |||||| ||||
                                C TCCGGT   TCCACC ACCT
                                 C     ____     C
GAM572  FLOT2   3'  GTCCATCCTCCCTATGGCCCTG 16800    A    CACAA  T
                                CA GGCCA    GG GGATGGAC
                                || |||||    || ||||||||
                                GT CCGGT    CC CCTACCTG
                                 C    ATC__  T
GAM572  HCS     3'  TCCACCCACCTTGGCCTCC   38992   A    CACA    A
                                C AGGCCA   AGGTGG TGGA
                                | ||||||   |||||| ||||
                                C TCCGGT   TCCACC ACCT
                                 C     ____     C
GAM572  HLCS    3'  GTCCACCCGGTGGTGTGGCC  6415       AA___
                                GGCCACAC    GGTGGAT
                                ||||||||    |||||||
                                CCGGTGTG    CCACCTG
                                     GTGGC
GAM572  HS3ST2  3'  GTCCACCCAGGAGTGGCCTTG  21278       ACAA_
                                CAAGGCCAC    GGTGGAT
                                |||||||||    |||||||
                                GTTCCGGTG    CCACCTG
                                      AGGAC
GAM572  KIFAP3  5'  CCCCGCCTTGCAGGCCTCA   31065   A    ACA     AT
                                C AGGCC   CAAGGTGG  GG
                                | |||||   ||||||||  ||
                                A TCCGG   GTTCCGCC  CC
                                 C    AC_      __
GAM572  LFG     3'  GTCAATCCCTGTGCCGCC    77241    CA   AG T   G
                                GGC  CACA  G GGAT GAC
                                |||  ||||  | |||| |||
                                CCG  GTGT  C CCTA CTG
                                  CC    __ _   A
GAM572  MPL     3'  TCCACCCACCTTGGCCTCC   19361   A    CACA    A
                                C AGGCCA   AGGTGG TGGA
                                | ||||||   |||||| ||||
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                                C TCCGGT   TCCACC ACCT
                                 C    ____    C
GAM572  NID     3'  CCCTTCCCTGTGGCCTT    11806       CAA  T   T
                                AAGGCCACA   GG GGA GG
                                |||||||||   || ||| ||
                                TTCCGGTGT   CC CTT CC
                                     ___ _   C
GAM572  Nrap    3'  TCCATCCACCTATTAGCCCTG  43622    A   CACACA
                                CA GGC     AGGTGGATGGA
                                || |||     ||||||||||
                                GT CCG     TCCACCTACCT
                                 C   ATTA__
GAM572  Nrap    3'  TCCATCCACCTATTAGCCCTG  58321    A   CACACA
                                CA GGC     AGGTGGATGGA
                                || |||     ||||||||||
                                GT CCG     TCCACCTACCT
                                 C   ATTA__
GAM572  PPP1R8  5'  TCCCTCGTGCGGCACTTG    12230     _   A   A   T
                                CAAG GCC CAC AGG GG
                                |||| ||| ||| ||| ||
                                GTTC CGG GTG TCC CT
                                  A   C   C   _
GAM572  RNMT    3'  CCATCCACCACCTGCAGCTT   15051     CA  CAA
                                AGGC  CA   GGTGGATGG
                                ||||  ||   |||||||||
                                TTCG  GT   CCACCTACC
                                  AC  CCA
GAM572  SDC4    3'  CCCCGCTCCTCATGGCCTTG   12994       CACAA    AT
                                CAAGGCCA    GGTGG  GG
                                ||||||||    |||||  ||
                                GTTCCGGT    TCGCC  CC
                                    ACTCC    __
GAM572  SLA2    3'  TCCACCCACCTTGGCCTCC    50894    A    CACA     A
                                C AGGCCA    AGGTGG TGGA
                                | ||||||    |||||| ||||
                                C TCCGGT    TCCACC ACCT
                                 C    ____    C
GAM572  SLC12A4 3'  CCAGGTCTTGTGGGACCCTG   18627    A  _  A     TGGA
                                CA GG CC CACAAGG    TGG
                                || || || |||||||    |||
                                GT CC GG GTGTTCT    ACC
                                 C  A  _      GG__
GAM572  TCP10   3'  CCCTCTTCCCCGTGTGGCC    17236       AA  T   T
                                GGCCACAC  GG GGA GG
                                ||||||||  || ||| ||
                                CCGGTGTG  CC TCT CC
                                     CC  T   C
GAM572  TM4SF2  3'  GTCCATTTTGTGAAGCCCTG   17253    A   CA
                                CA GGC  CACAAGGTGGAT
                                || |||  ||||||||||||
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                                GT CCG  GTGTTTTACCTG
                                 C   AA
GAM572  WFS1     3'  CCTTTCCCCAGTGTGGCC    21165        AA  T   T_
                                GGCCACAC  GG GGA  GG
                                ||||||||  || |||  ||
                                CCGGTGTG  CC CCT  CC
                                    A_  _   TT
GAM572  ZNF85    5'  CCAGCCTCTGTGGCCCTG    14274    A      CA  _
                                CA GGCCACA  AGG TGG
                                || |||||||  ||| |||
                                GT CCGGTGT  TCC ACC
                                 C      C_   G
GAM572  ZNF91    5'  CCAGCCTGTGTGGCCCTG    14278    A       A  _
                                CA GGCCACACA GG TGG
                                || |||||||||| || |||
                                GT CCGGTGTGT CC ACC
                                 C        _  G
GAM572  ARS2     3'  ATCCATACTTGTACTACCTTG  32482      CCAC    _
                                CAAGG    ACAAG GTGGAT
                                |||||    ||||| ||||||
                                GTTCC    TGTTC TACCTA
                                   ATCA    A
GAM572  BOC      5'  ATCTCTTTGTGTGACCCTG   53826    A  C       T
                                CA GG CACACAAGG GGAT
                                || || |||||||||| ||||
                                GT CC GTGTGTTTC TCTA
                                 C  A       _
GAM572  BSPECV   3'  CCAGGCCCATGTGGCCTCC   34045   A      CAA   GGA
                                C AGGCCACA   GGT   TGG
                                | ||||||||   |||   |||
                                C TCCGGTGT   CCG   ACC
                                 C       AC_   G__
GAM572  BTEB5    3'  CCATCCACCAGGCGGACCTTG  57712      _  ACACAA
                                CAAGG CC     GGTGGATGG
                                ||||| ||     |||||||||
                                GTTCC GG     CCACCTACC
                                   A  CGGA__
GAM572  C11orf17 3'  TCCACCCACCTTGGCCTCC   40590   A    CACA     A
                                C AGGCCA    AGGTGG TGGA
                                | ||||||    |||||| ||||
                                C TCCGGT    TCCACC ACCT
                                 C      ____      C
GAM572  C11orf21 3'  CCATGGAGCCCTGTGGCCTTG 27102         CAA   GG_
                                CAAGGCCACA   GGT   ATGG
                                ||||||||||   |||   ||||
                                GTTCCGGTGT   CCG   TACC
                                      C__   AGG
GAM572  C20orf121 5' CCAGCCCTTCTGTGGCCTCA   44523   A      C    TGGA
                                C AGGCCACA AAGG    TGG
                                | |||||||| ||||    |||
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                                A TCCGGTGT TTCC   ACC
                                 C      C   CG__
GAM572  C21orf25  3'  TCCACCCACCTTGGCCTCC   64302   A    CACA    A
                                C AGGCCA   AGGTGG TGGA
                                | ||||||   |||||| ||||
                                C TCCGGT   TCCACC ACCT
                                 C     ____     C
GAM572  C9orf7    3'  CCCTCTCCCTGGTGTGGCC   34580       A  TG  T
                                GGCCACAC AGG  GA GG
                                |||||||| |||  || ||
                                CCGGTGTG TCC  CT CC
                                     G  CT  C
GAM572  CBX5      5'  CCGGGGACCTGGTGGCCTT   25061       A  A  GGA
                                AAGGCCAC CA GGT  TGG
                                |||||||| || |||  |||
                                TTCCGGTG GT CCA  GCC
                                    _ _  GGG
GAM572  CDH24     3'  TCCATTACTCATGGCCTCA   96607   A    CACAA   G
                                C AGGCCA    GGTG ATGGA
                                | ||||||    |||| |||||
                                A TCCGGT    TCAT TACCT
                                 C    AC___   _
GAM572  CLSTN1    3'  GTCTCACCGTGTGCAGCCTTG  30792      CA   A   _
                                CAAGGC  CACA GGTG GAT
                                ||||||  |||| |||| |||
                                GTTCCG  GTGT CCAC CTG
                                   AC   G   T
GAM572  CPLX1     3'  ATCCACCTGGTGGCCCTG    22820    A    A  A
                                CA GGCCAC CA GGTGGAT
                                || |||||| || |||||||
                                GT CCGGTG GT CCACCTA
                                 C    _ _
GAM572  CSEN      3'  CCACACCCCTGCCGGCCTTG  26457       ACACA  T  A_
                                CAAGGCC    AGG GG  TGG
                                |||||||    ||| ||  |||
                                GTTCCGG    TCC CC  ACC
                                    CCG__  _  AC
GAM572  D4ST-1    3'  TTTATCCACCCCATGTGCCTCA 56200   A   C   CAA
                                C AGGC ACA   GGTGGATGGA
                                | |||| |||   ||||||||||
                                A TCCG TGT   CCACCTATTT
                                 C   _   ACC
GAM572  DKFZP434B044 3'  TCCACCCACCTTGGCCTCC   49722   A    CACA    A
                                C AGGCCA   AGGTGG TGGA
                                | ||||||   |||||| ||||
                                C TCCGGT   TCCACC ACCT
                                 C     ____     C
GAM572  DKFZp761O132 5'  GTCCATCCCTTTATTTGTGCAT 51172   A  C__   C__   T
            CCTCA                C AGG   CACA   AAGG GGATGGAC
                                | |||   ||||  |||| ||||||||
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                              A TCC   GTGT   TTTC CCTACCTG
                               C   TAC    TTA   _
GAM572  FADS2    3'  CCTTTCACCACATGGCCTTG  16215        CACAA     T
                              CAAGGCCA    GGTGGA GG
                              ||||||||    |||||| ||
                              GTTCCGGT    CCACTT CC
                                   ACA__     T
GAM572  FLJ11362 3'  CCTGGGCCCTGGATGGCCTTG  41962        CA  A   GGAT
                              CAAGGCCA  CA GGT   GG
                              ||||||||  || |||   ||
                              GTTCCGGT  GT CCG   CC
                                   AG  C   GGT_
GAM572  FLJ12875 3'  CTGTCCATGTGCAGCCTCA   44917   A   CA   AGG
                              C AGGC  CACA   TGGATGG
                              | ||||  ||||   |||||||
                              A TCCG  GTGT   ACCTGTC
                               C    AC    ___
GAM572  FLJ13114 3'  TCCACCCACCTTGGCCTCC   44911   A    CACA    A
                              C AGGCCA    AGGTGG TGGA
                              | ||||||    |||||| ||||
                              C TCCGGT    TCCACC ACCT
                               C     _____     C
GAM572  FLJ13614 5'  GTCCTCTTGTGTAGCCT    58200     C      T
                              AGGC ACACAAGG GGAT
                              |||| |||||||| ||||
                              TCCG TGTGTTCT CCTG
                                A      _
GAM572  FLJ20045 3'  TCCACCCACCTTGGCCTCC   34892   A    CACA    A
                              C AGGCCA    AGGTGG TGGA
                              | ||||||    |||||| ||||
                              C TCCGGT    TCCACC ACCT
                               C     _____     C
GAM572  FLJ20507 3'  TCCACCCACCTTGGCCTCC   35752   A    CACA    A
                              C AGGCCA    AGGTGG TGGA
                              | ||||||    |||||| ||||
                              C TCCGGT    TCCACC ACCT
                               C     _____     C
GAM572  FLJ20507 3'  TCCACCCACCTTGGCCTCC   60854   A    CACA    A
                              C AGGCCA    AGGTGG TGGA
                              | ||||||    |||||| ||||
                              C TCCGGT    TCCACC ACCT
                               C     _____     C
GAM572  FLJ22002 3'  TCCATCCACCTCGGCCTCC   46199   A   ACACA
                              C AGGCC    AGGTGGATGGA
                              | |||||    ||||||||||
                              C TCCGG    TCCACCTACCT
                               C    C_____
GAM572  GRWD     3'  CCAGAGACTTGTGTGGCCT   49778         GTGGA
                              AGGCCACACAAG    TGG
                              ||||||||||||    |||
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                                TCCGGTGTGTTC    ACC
                                      AGAG_
GAM572  KIAA0022 3' TCCACCCACCTTGGTCTCC   30286   CC  A      A
                                GG  AC CAAGGTGG TGGA
                                ||  || |||||||| ||||
                                CC  TG GTTCCACC ACCT
                                 TC  _      C
GAM572  KIAA0355 3' CCAACCCTGCGTGGCTCTTG  28702     _    A  A  _
                                CAAG GCCAC CA GGT GG
                                |||| ||||| || ||| ||
                                GTTC CGGTG GT CCA CC
                                   T    C  C   A
GAM572  KIAA0376 3' GTCCATTCAGGTCATGTGGGCT 66217   A    A    A __
           CA                     A GGCC CACA GG  TGGATGGAC
                                | |||| |||| ||  |||||||||
                                A TCGG GTGT CT  ACTTACCTG
                                 C   _   A  GG
GAM572  KIAA0682 3' TCCACCCACCTTGTTCTCCC  30029   CCAC       A
                                GG   ACAAGGTGG TGGA
                                ||   ||||||||| ||||
                                CC   TGTTCCACC ACCT
                                 CTCT       C
GAM572  KIAA1093 5' TCTACCTTGTATGCCTCA    67146   A   CAC
                                C AGGC   ACAAGGTGGA
                                | ||||   ||||||||||
                                A TCCG   TGTTCCATCT
                                 C   TA_
GAM572  KIAA1128 3' TCCACCCACCTCGTCTATGG   69011    C__  A     A
                                CCA   AC AGGTGG TGGA
                                |||   || |||||| ||||
                                GGT   TG TCCACC ACCT
                                  ATC  C     C
GAM572  KIAA1171 3' CCGGGAACCCTGTGTGGCTTTG 89341           A   GGA
                                CAAGGCCACACA GGT   TGG
                                |||||||||||| |||   |||
                                GTTTCGGTGTGT CCA   GCC
                                       C   AGG
GAM572  KIAA1183 3' CCACCGCTCAGCGCTGGCCTTG 63189        CACAA_    A
                                CAAGGCCA     GGTGG TGG
                                ||||||||     ||||| |||
                                GTTCCGGT     TCGCC ACC
                                     CGCGAC    _
GAM572  KIAA1198 3' TCCACCCACCTTGGCCTCC   64067   A     CACA     A
                                C AGGCCA    AGGTGG TGGA
                                | ||||||    |||||| ||||
                                C TCCGGT    TCCACC ACCT
                                 C     _____     C
GAM572  KIAA1203 3' TCCATTGCACTCAGCCCTG   72089    A  CACACAA   _
                                CA GGC      GGTG GATGGA
                                || |||      |||| ||||||
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                                GT CCG      TCAC TTACCT
                                 C  AC_____   G
GAM572  KIAA1300 5' TCCACCCACCCTGTGTAGT  63525   C    A    A
                                GC ACACA GGTGG TGGA
                                || ||||| ||||| ||||
                                TG TGTGT CCACC ACCT
                                 A    C    C
GAM572  KIAA1571 3' TCCAGGTTATTTTGTGGCCTT 61625        CA    A_
                                AAGGCCACA  AGGTGG  TGGA
                                |||||||||  ||||||  ||||
                                TTCCGGTGT  TTTATT  ACCT
                                      __     GG
GAM572  KIAA1668 3' TCCACCCACCTTGGCCTCC   67081   A    CACA    A
                                C AGGCCA   AGGTGG TGGA
                                | ||||||   |||||| ||||
                                C TCCGGT   TCCACC ACCT
                                 C     ____     C
GAM572  KLK7    3' TCCACCCACCTTGGCCTCC   58394   A    CACA    A
                                C AGGCCA   AGGTGG TGGA
                                | ||||||   |||||| ||||
                                C TCCGGT   TCCACC ACCT
                                 C     ____     C
GAM572  KLK7    3' TCCACCCACCTTGGCCTCC   18549   A    CACA    A
                                C AGGCCA   AGGTGG TGGA
                                | ||||||   |||||| ||||
                                C TCCGGT   TCCACC ACCT
                                 C     ____     C
GAM572  LCHN    3' CTGTCCCCTGTGGCCTT    87469        CAA  T
                                AAGGCCACA   GG GGATGG
                                |||||||||   || ||||||
                                TTCCGGTGT   CC CCTGTC
                                      ___  _
GAM572  LEC3    3' ATCCATTTTGTATGGTCTCA  31532   A    C
                                C AGGCCA ACAAGGTGGAT
                                | |||||| ||||||||||
                                A TCTGGT TGTTTTACCTA
                                 C    A
GAM572  LSM10   3' CCAGAATCCTATATGTGGCCTT 52868        CA_  TGGA
            G                    CAAGGCCACA  AGG   TGG
                                |||||||||   |||   |||
                                GTTCCGGTGT  TCC   ACC
                                      ATA   TAAG
GAM572  MFN2    3' GTCCTGGACTTGTGCAGGCCT  30227     A_    GTGGAT
                                AGGCC  CACAAG     GGAC
                                |||||  ||||||     ||||
                                TCCGG  GTGTTC     CCTG
                                   AC     AGGT__
GAM572  MGC35521 3' CCAGCCCCATGGCCTTG    59664       CACAA  T  A
                                CAAGGCCA    GG GG TGG
                                ||||||||    || || |||
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                                GTTCCGGT    CC CC ACC
                                    A____  _  G
GAM572  PRAX-1   3'  GTCCACCCACCTCGTCT    17658     CACACA    A
                                AGGC     AGGTGG TGGAC
                                ||||     |||||| |||||
                                TCTG     TCCACC ACCTG
                                  C_____     C
GAM572  PRKWNK2  3'  GTCCATCCGTGACCGCGTGGCC 92200        ACAA  ___
           TTG                    CAAGGCCAC   GGT  GGATGGAC
                                |||||||||   |||  ||||||||
                                GTTCCGGTG   CCA  CCTACCTG
                                    CG__  GTG
GAM572  RAP140   5'  ATCCATCCTTGTACCTTG   31507      CCAC    _
                                CAAGG   ACAAGG TGGAT
                                |||||   |||||| |||||
                                GTTCC   TGTTCC ACCTA
                                  A___     T
GAM572  RNF9     3'  CCAGTACCATGTGGCTT    23236       CAA   GA
                                AGGCCACA  GGTG  TGG
                                ||||||||  ||||  |||
                                TTCGGTGT  CCAT  ACC
                                    A__   G_
GAM572  SARM     3'  GTCCACTGCCCTGTGTGGCCTT 31303         A  TG A
                                AAGGCCACACA GG  G TGGAC
                                |||||||||||  ||  | |||||
                                TTCCGGTGTGT CC  C ACCTG
                                     C  GT _
GAM572  SCYA21   3'  CCACCCCATGCTGGCCTTG   12975       _  CAA
                                CAAGGCCA CA   GGTGG
                                ||||||||  ||   |||||
                                GTTCCGGT GT   CCACC
                                    C  ACC
GAM572  SEC61A1  3'  CTATCACACGTGGCCTTG    26229       ACAAG  _
                                CAAGGCCAC    GTG GATGG
                                |||||||||    ||| |||||
                                GTTCCGGTG    CAC CTATC
                                     _____  A
GAM572  SPAF     3'  CCAGGCTTATGTGGCCTTG   83520        C  G_
                                CAAGGCCACA AAG  TGG
                                |||||||||| |||  |||
                                GTTCCGGTGT TTC  ACC
                                     A  GG
GAM572  ZTL1     3'  GTCCATTTTTTGCATAGCCT  43520     CACA    TG
                                AGGC   CAAGG  GATGGAC
                                ||||   |||||  |||||||
                                TCCG   GTTTT  TTACCTG
                                  ATAC    __
GAM572  LOC121219 3'  CCGGTTACCTTGACAGCCCTG  74486   A  CACA     A
                                CA GGC   CAAGGTGG TGG
                                || |||   |||||||| |||
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                                GT CCG    GTTCCATT GCC
                                 C   ACA_       G
GAM572   LOC130644 5'  GTCCACCTGCGTGGCCTTG    76253          A  A
                                CAAGGCCAC CA GGTGGAT
                                ||||||||| || |||||||
                                GTTCCGGTG GT CCACCTG
                                     C  _
GAM572   LOC143308 5'  GTCCTAGAACTCAGTGGCCTT  83837         ACAA   GGAT
                                AAGGCCAC    GGT    GGAC
                                ||||||||    |||    ||||
                                TTCCGGTG    TCA    CCTG
                                     AC__   AGAT
GAM572   LOC144742 5'  TCCACCCACCTTGGCCTCC    77469    A     CACA     A
                                C AGGCCA    AGGTGG TGGA
                                | ||||||    |||||| ||||
                                C TCCGGT    TCCACC ACCT
                                 C      _____      C
GAM572   LOC145231 3'  GTCCATCCCTTGACAAAACCTT 84257      CCACACA   T
                                AAGG       AGG GGATGGAC
                                ||||       ||| ||||||||
                                TTCC       TTC CCTACCTG
                                  AAAACAG   _
GAM572   LOC145323 5'  CCGTTCACCTGTGTGCCCT    77615     C     A
                                AGG CACACA GGTGGATGG
                                ||| |||||| |||||||||
                                TCC GTGTGT CCACTTGCC
                                  C     _
GAM572   LOC146229 3'  TCCACCCACCTTGGCCTCC    78316    A     CACA     A
                                C AGGCCA    AGGTGG TGGA
                                | ||||||    |||||| ||||
                                C TCCGGT    TCCACC ACCT
                                 C      _____      C
GAM572   LOC146337 5'  TCCACCCACCTTGGCCTT     84646        CACA     A
                                AAGGCCA    AGGTGG TGGA
                                |||||||    |||||| ||||
                                TTCCGGT    TCCACC ACCT
                                     _____      C
GAM572   LOC146346 5'  GTCCACCCACCTTGGCCTCA   78406    A     CACA     A
                                C AGGCCA    AGGTGG TGGAC
                                | ||||||    |||||| |||||
                                A TCCGGT    TCCACC ACCTG
                                 C      _____      C
GAM572   LOC149706 3'  TCCACCCACCTTTCCCTCA    85810    A   CCACAC      A
                                C AGG      AAGGTGG TGGA
                                | |||      ||||||| ||||
                                A TCC      TTCCACC ACCT
                                 C   CT_____       C
GAM572   LOC150967 5'  ATCCTGGCTTTGTGACCTCA   80883    A   CCA       __
                                C AGG   CACAAGGT  GGAT
                                | |||   ||||||||  ||||
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                                A TCC   GTGTTTCG  CCTA
                                 C   A__       GT
GAM572   LOC151162 5'  CCAGATTTTGTGGAGCCTT   86428      CA       GGA
                                AAGGC  CACAAGGT   TGG
                                |||||  ||||||||   |||
                                TTCCG  GTGTTTTA   ACC
                                   AG       G__
GAM572   LOC152343 3'  TCCACCCACCTTGGTCTCC   81436    CC  A       A
                                GG  AC CAAGGTGG TGGA
                                ||  || |||||||| ||||
                                CC  TG GTTCCACC ACCT
                                 TC  _       C
GAM572   LOC152620 3'  TCCACCCACCTTGGCCTCC   60713    A     CACA     A
                                C AGGCCA    AGGTGG TGGA
                                | ||||||    |||||| ||||
                                C TCCGGT    TCCACC ACCT
                                 C      ____      C
GAM572   LOC158310 5'  TCCACCCACCTTGGCCTCC   88091    A     CACA     A
                                C AGGCCA    AGGTGG TGGA
                                | ||||||    |||||| ||||
                                C TCCGGT    TCCACC ACCT
                                 C      ____      C
GAM572   LOC158668 3'  TCCACCCACCTTGGCCTCC   69908    A     CACA     A
                                C AGGCCA    AGGTGG TGGA
                                | ||||||    |||||| ||||
                                C TCCGGT    TCCACC ACCT
                                 C      ____      C
GAM572   LOC196985 3'  CCACGAACATCCCAGTGTGGCC 91235    A       AA_    GA__
            CTG                    CA GGCCACAC   GGTG    TGG
                                || ||||||||   ||||    |||
                                GT CCGGTGTG   CTAC    ACC
                                 C       ACC    AAGC
GAM572   LOC200470 3'  ATCCAGCCTGTGTGGCACT   91639    _       A  _
                                AG GCCACACA GG TGGAT
                                || |||||||| || |||||
                                TC CGGTGTGT CC ACCTA
                                 A       _  G
GAM572   LOC203377 5'  CCAGATTTTGTGGAGCCTT   92257      CA       GGA
                                AAGGC  CACAAGGT   TGG
                                |||||  ||||||||   |||
                                TTCCG  GTGTTTTA   ACC
                                   AG       G__
GAM572   LOC221495 3'  ATCACGCCTTGTATGACCCTT  95490      C_  C       _
                                AAGG  CA ACAAGGTG GAT
                                ||||  || |||||||| |||
                                TTCC  GT TGTTCCGC CTA
                                  CA  A       A
GAM572   LOC221903 3'  ATCCACCTGTATGACTTTG   95567      C  C   A
                                CAAGG CA ACA GGTGGAT
                                ||||| || ||| |||||||
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                                GTTTC GT TGT CCACCTA
                                  A  A  _
GAM572  LOC222493 5'  TCCATCAGGCCTGGCCTCA   96011   A    CACAA  G_
                                C AGGCCA    GGT  GATGGA
                                | ||||||    |||  ||||||
                                A TCCGGT    CCG  CTACCT
                                 C     _____  GA
GAM572  LOC254532 5'  TCCACCCACCTTGGCCTCC   98462   A    CACA    A
                                C AGGCCA   AGGTGG TGGA
                                | ||||||   |||||| ||||
                                C TCCGGT   TCCACC ACCT
                                 C     ____     C
GAM572  LOC255707 3'  TCCACCCACCTTGGCCTCC   98732   A    CACA    A
                                C AGGCCA   AGGTGG TGGA
                                | ||||||   |||||| ||||
                                C TCCGGT   TCCACC ACCT
                                 C     ____     C
GAM572  LOC56965  5'  CCATCTCGTTGGCCTTG     39930       C  A
                                CAAGGCCA AC AGGTGG
                                |||||||| || ||||||
                                GTTCCGGT TG TCTACC
                                     _  C
GAM572  LOC90297  5'  GTCTCCCTTGTCTGGCCTTG  62854       C    TG
                                CAAGGCCA ACAAGG  GAT
                                |||||||| ||||||  |||
                                GTTCCGGT TGTTCC  CTG
                                     C     CT
GAM572  LOC96652  3'  CCACCTGTCTCTGCAGGGCCCT 66074   A   ACA  _   TG A
          G                     CA GGCC   CA AGG  G TGG
                                || ||||   || |||  | |||
                                GT CCGG   GT TCT  C ACC
                                 C   GAC  C   GT C
GAM573  KCNK4    3'  CCGTTGGGGCAGAACCATGGAG 33980       A_  __  G TG  C
          GA                    TTCTCCATG  TC  CC C  GC GG
                                ||||||||| ||  || |  || ||
                                AGGAGGTAC  AG  GG G  TG CC
                                     CA  AC  _ GT  _
GAM573  KRT3     3'  CCCGGCCAAGCCCAGTCACGAG 55102     CA   CCC  _
          AA                    TTCTC  TGAT   GCT GGCCGGG
                                |||||  ||||   ||| |||||||
                                AAGAG  ACTG   CGA CCGGCCC
                                  C_    ACC   A
GAM573  TNFRSF1B  3'  CCCAGCCATTACCATGGAGA   8390       ATCCCGC   C
                                TCTCCATG      TGGC GGG
                                ||||||||      |||| |||
                                AGAGGTAC      ACCG CCC
                                     CATT___    A
GAM573  FLJ10307  3'  CCCAGCCAGCAGAGATGGAGAG 36475       GA  CC     C
                                TTCTCCAT  TC  GCTGGC GGG
                                ||||||||  ||  |||||| |||
```

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                                GAGAGGTA  AG  CGACCG CCC
                                    G_  A_     A
GAM573  FLJ10546  3'  CTAGTACAAGACATGGAGAA  60180        A  CC__
                                TTCTCCATG TC    GCTGG
                                |||||||||  ||    |||||
                                AAGAGGTAC AG    TGATC
                                    _  AACA
GAM573  FLJ12526  3'  CCCGATCAAGAACATGGAGAA  45926        A  CCGC  GC
                                TTCTCCATG TC    TG  CGGG
                                |||||||||  ||    ||  ||||
                                AAGAGGTAC AG    AC  GCCC
                                    A  A___  TA
GAM573  GAPCENA  3'  CCAGGTAGACATGGAGAA    25176        A  CCG
                                TTCTCCATG TC   CTGG
                                |||||||||  ||   ||||
                                AAGAGGTAC AG   GACC
                                    _  ATG
GAM573  GPS2     5'  CCAAGGGGACATGGAGAA    16887        A   GC
                                TTCTCCATG TCCC  TGG
                                |||||||||  ||||  |||
                                AAGAGGTAC AGGG  ACC
                                    _   GA
GAM573  KIAA0256  5'  CCCGAGCGGGGGGCCATGGAGA 65049        AT   G   GC
          A                      TTCTCCATG  CCC CTG  CGGG
                                 |||||||||  ||| |||  ||||
                                 AAGAGGTAC  GGG GGC  GCCC
                                     CG   _   GA
GAM573  KIAA1938  3'  CCCGGCTGCAGATTACGGAGAA 93822       A    CC  T
                                TTCTCC TGATC  GC GGCCGGG
                                ||||||  |||||  ||  |||||||
                                AAGAGG ATTAG  CG TCGGCCC
                                   C    A_  _
GAM573  NDRG4    3'  CCCAAGGAAGACAGAACATGGA 40377        A  CCG  GG  __
          GAA                     TTCTCCATG TC   CT  CC  GGG
                                  |||||||||  ||   ||  ||  |||
                                  AAGAGGTAC AG   GA  GG  CCC
                                      A  ACA  A_  AA
GAM573  NDRG4    3'  CCCAAGGAAGACAGAACATGGA 43576        A  CCG  GG  __
          GAA                     TTCTCCATG TC   CT  CC  GGG
                                  |||||||||  ||   ||  ||  |||
                                  AAGAGGTAC AG   GA  GG  CCC
                                      A  ACA  A_  AA
GAM573  OATPRP4  3'  CGGTTAGCAAAACCATGGGAA  48983     T    ATCCC
                                TTC CCATG    GCTGGCCG
                                |||  |||||    ||||||||
                                AAG GGTAC    CGATTGGC
                                  _    CAAAA
GAM573  LOC164173 3'  CCCAAACTAGCAAAACCTATGG 83051        ATCCC_    CC_
          AGAA                    TTCTCCATG    GCTGG   GGG
                                  |||||||||    |||||  |||
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                                AAGAGGTAT     CGATC   CCC
                                     CCAAAA     AAA
GAM573  LOC257438 3'  CCCAGCCAGCAGAGATGGAGAG 95591         GA  CC     C
                                TTCTCCAT  TC  GCTGGC GGG
                                ||||||||  ||  |||||| |||
                                GAGAGGTA  AG  CGACCG CCC
                                     G_  A_     A
GAM574  ACTN2    5'  GAGGTCACCCCGCGCCCG    8470          CGCTAGAC   _
                                CGGGCGCGGG       GCCT C
                                ||||||||||       |||| |
                                GCCCGCGCCC       TGGA G
                                     CAC_____    A
GAM574  AP3S1    5'  CGAGGCTCGCGCGCCCGCCCCC 8896      C       TA  C
           G                     CGGG GCGGGCGC  GA GCCTCG
                                ||||  ||||||||  ||  ||||||
                                GCCC CGCCCGCG  CT CGGAGC
                                  C       CG  _
GAM574  CALB1    5'  GGCAGCGCCCGCGCCC      18208           AGAC
                                GGGCGCGGGCGCT    GCC
                                ||||||||||||    |||
                                CCCGCGCCCGCGA    CGG
                                          ____
GAM574  CAPN5    5'  GCTCCAGCGCCCGCGCC     92549           A  C
                                GGCGCGGGCGCT GA GC
                                |||||||||||| || ||
                                CCGCGCCCGCGA CT CG
                                     C  _
GAM574  IRAK1    5'  GGCCCAGGCCCGCGCCCG    9614           G  AGAC
                                CGGGCGCGGGC CT    GCC
                                ||||||||||| ||    |||
                                GCCCGCGCCCG GA    CGG
                                     _  CC__
GAM574  LMNA     5'  CGAGGTCCGACAGCGCCCGGCC 19930      G       AGAC_
           C                     GGGC CGGGCGCT    GCCTCG
                                ||||  ||||||||    ||||||
                                CCCG GCCCGCGA     TGGAGC
                                  _       CAGCC
GAM574  SIRT2    5'  GGGCTTCAGCACCGCGCCC    48362         GC   A  C
                                GGGCGCGG  GCT GA GCCT
                                ||||||||  ||| || ||||
                                CCCGCGCC  CGA CT CGGG
                                     A_   _  T
GAM574  SLC21A2  5'  CGAGGCGCCCCGACCCCGCGCC 20082         CGCTAGA
                                GGCGCGGG      CGCCTCG
                                ||||||||      |||||||
                                CCGCGCCC      GCGGAGC
                                     CAGCCCC
GAM574  SREBF1   5'  CGAGTGGATGCTAGCGCCAGCG 96075        G       ACG __
           CCCG                     CGGGCGC GGCGCTAG   CC  TCG
                                ||||||| ||||||||   ||  |||
```

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                                GCCCGCG CCGCGATC   GG  AGC
                                    A       GTA  TG
GAM574  BAG3     5'  CGGAGCCAGCGCCCCGCACCCG 16257      C    _   AGAC  CT
                                CGGG GCGGG CGCT    GC  CG
                                |||| ||||| ||||    ||  ||
                                GCCC CGCCC GCGA    CG  GC
                                  A    C   C___  AG
GAM574  CCNI     5'  CGAGCGCCAGCGCCCGCGCCCG 23368           AGA   C
                                CGGGCGCGGGCGCT   CGC TCG
                                ||||||||||||||   ||| |||
                                GCCCGCGCCCGCGA   GCG AGC
                                        CC_  _
GAM574  DDM36    5'  GAGGCCGCGCCCCCGCCCG    40924       C     TAGAC
                                CGGGCG GGGCGC     GCCTC
                                ||||||| ||||||     |||||
                                GCCCGC CCCGCG     CGGAG
                                    C     C_____
GAM574  DKFZP564K1964 5'  AGGCCCGCGCCCGCGCCCG    32070           TAGAC
                                CGGGCGCGGGCGC     GCCT
                                ||||||||||||     ||||
                                GCCCGCGCCCGCG     CGGA
                                        CC___
GAM574  FLJ22169  3'  AGGCACCCTGAGCCCGTGCCCG 44227          GC   AC_
                                CGGGCGCGGGC  TAG   GCCT
                                ||||||||||  |||   ||||
                                GCCCGTGCCCG  GTC   CGGA
                                      A_   CCA
GAM574  KIAA0227  5'  CGAGGCGCGGGGCCGGCGCCCG 61345       G   G  AGA
                                CGGGCGC GGC CT   CGCCTCG
                                ||||||| ||| ||   |||||||
                                GCCCGCG CCG GG   GCGGAGC
                                    G   G  C__
GAM574  KIAA1971  5'  GAGGCCAGGCCCGCGCCCG    74682          G  AGAC
                                CGGGCGCGGGC CT    GCCTC
                                |||||||||| ||    |||||
                                GCCCGCGCCCG GA    CGGAG
                                      _  C___
GAM574  MGC2628   5'  CGAAGCTGCGCCCGGCGCCCG  44198        _     TAGAC  C
                                CGGGCGC GGGCGC     GC TCG
                                ||||||| ||||||     || |||
                                GCCCGCG CCCGCG     CG AGC
                                    G     T_____  A
GAM574  PPP1R15A  5'  AGACGCTGCACGACCCCGCGCC 60571          C_____  T  A  C
          CG                      CGGGCGCGGG     GC AG CG CT
                                ||||||||||     || || || ||
                                GCCCGCGCCC     CG TC GC GA
                                      CAGCA  _  _  A
GAM574  PSIP2     5'  CGAGGCATCCTCCCCCGCCCG  53780       C   CGCTA  C
                                CGGGCG GGG     GA GCCTCG
                                |||||| |||     || ||||||
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                                GCCCGC CCC    CT CGGAGC
                                   _  CTC__  A
GAM574  PSKH1    5'  CGAGACGCCGAAGAGCCCGCCG 68795      _    G  AGA_  C
           CCCG                   CGGGCG CGGGC CT    CG CTCG
                                |||||| ||||| ||    || ||||
                                GCCCGC GCCCG GA    GC GAGC
                                   C    A  AGCC  A
GAM574  Rab11-FIP3 5'  GAGGGGATGCCCGCGCCCG   28785          _ AGACG
                                CGGGCGCGGGCG CT    CCTC
                                |||||||||||| ||    ||||
                                GCCCGCGCCCGT GG    GGAG
                                      A _____
GAM574  SCAMP-4   5'  CGAAGCGCTGCGCTCGCGCCCG 55345          T  A   C
                                CGGGCGCGGGCGC AG CGC TCG
                                |||||||||||| || ||| |||
                                GCCCGCGCTCGCG TC GCG AGC
                                      _ _   A
GAM574  LOC155060 5'  CGAGTGCACCTACACCCGCGCC 87604        CGC   AC  _
           C                    GGGCGCGGG   TAG  GC CTCG
                                |||||||||   |||  || ||||
                                CCCGCGCCC   ATC  CG GAGC
                                     AC_   CA  T
GAM574  LOC197342 5'  CGAGCCCCAGCGCCCGGCCCG  89360      G       AGAC  C
                                CGGGC CGGGCGCT    GC TCG
                                ||||| ||||||||    || |||
                                GCCCG GCCCGCGA    CG AGC
                                   _       CCC_  _
GAM574  LOC254351 3'  GAGGTCAGGCCCGCGCCCG    96690          G  AGAC
                                CGGGCGCGGGC CT    GCCTC
                                |||||||||| ||    |||||
                                GCCCGCGCCCG GA    TGGAG
                                      _ C____
GAM575  LZTR1     3'  ACCCATCTACCCAGTTTCCA   23164    AT       C    A
                                TG  AACTGGGTA GTGG GT
                                ||  ||||||||| |||| ||
                                AC  TTGACCCAT TACC CA
                                 CT        C   _
GAM575  PEPP3     3'  ACCTACCCAGTTCCATGA    30705      AT       C
                                TCATG  AACTGGGTA GT
                                |||||  ||||||||| ||
                                AGTAC  TTGACCCAT CA
                                   C_        C
GAM575  LOC222031 3'  ACCCCTGAGCCACTATCATGA  95664        ACTG   A  T  A
                                TCATGATA    GGT CG GG GT
                                ||||||||    ||| || || ||
                                AGTACTAT    CCG GT CC CA
                                     CA__   A  C  _
GAM576  ADAM12    3'  CATGTTTCACAAGGTCTT    14423          TGGCT
                                AAGACTTTGTG    ACATG
                                ||||||||||     |||||
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                                TTCTGGAACAC    TGTAC
                                      TT___
GAM576  CELSR1   3'  TCATCCAGACACAAAGGTCTT  27278       G   G  AC
                                AAGACTTT TGTG CT  ATGA
                                |||||||| |||| ||  ||||
                                TTCTGGAA ACAC GA  TACT
                                     _   A  CC
GAM576  GAN      3'  GTCTGAAAGCACACAAAGTCTT 42121          G  ACAT
                                AAGACTTTGTGTG CT   GAC
                                |||||||||||| ||   |||
                                TTCTGAAACACAC GA   CTG
                                      _ AAGT
GAM576  HFE      3'  GTCATACAGATTTGCAAAGTTT 58121         TGG  AC
                                AGACTTTGTG   CT  ATGAC
                                ||||||||||   ||  |||||
                                TTTGAAACGT   GA  TACTG
                                      TTA  CA
GAM576  HFE      3'  GTCATACAGATTTGCAAAGTTT 6400          TGG  AC
                                AGACTTTGTG   CT  ATGAC
                                ||||||||||   ||  |||||
                                TTTGAAACGT   GA  TACTG
                                      TTA  CA
GAM576  KCNS2    3'  GTCATGTGAAAACAAAATCT   68851    C    GTGGC
                                AGA TTTGT    TACATGAC
                                ||| |||||    ||||||||
                                TCT AAACA    GTGTACTG
                                  A    AAA__
GAM576  RAB38    3'  GTCATGTAGCTGACCAAAATC  60926    C   TG
                                GA TTTG  TGGCTACATGAC
                                || ||||  ||||||||||||
                                CT AAAC  GTCGATGTACTG
                                 A   CA
GAM576  RCN2     3'  GCCATATGACAACAAAGTCTT  12798        _______
                                AAGACTTTGT     GTGGC
                                ||||||||||     |||||
                                TTCTGAAACA     TACCG
                                      ACAGTA
GAM576  SLC26A3  5'  CACATAGTTGCAAAGGTCTT   5470        G  TG   CA
                                AAGACTTT TG  GCTA  TG
                                |||||||| ||  ||||  ||
                                TTCTGGAA AC  TGAT  AC
                                     _ GT    AC
GAM576  TCF2     3'  GCCACACAGGAAGAAAGTCTT  22408       _______
                                AAGACTT     TGTGTGGC
                                |||||||     ||||||||
                                TTCTGAA     ACACACCG
                                    AGAAGG
GAM576  ALK7     3'  ATGGACCCGCACAAAATCT    76241     C       CTA
                                AGA TTTGTGTGG   CAT
                                ||| |||||||||   |||
```

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                                TCT AAACACGCC   GTA
                                  A        CAG
GAM576  AQP10    3'  GTCTGCTCAACACAAAGCCT   55397    A      __   T_
                                AG CTTTGTGT  GGC  AC
                                || ||||||||  |||  ||
                                TC GAAACACA  TCG  TG
                                 C       AC   TC
GAM576  DKFZP434P0721 3'  TCATGTAGACTAAAGTCTT   64466         T  GG
                                AAGACTTTG GT  CTACATGA
                                ||||||||| ||  ||||||||
                                TTCTGAAAT CA  GATGTACT
                                     _ __
GAM576  DKFZP564D0462 3'  GCCACAGCACAAAGTTTT    71022           ___
                                AAGACTTTGTGT   GGC
                                ||||||||||||   |||
                                TTTTGAAACACG   CCG
                                       ACA
GAM576  FLJ14936  3'  CAGGAGCCACTCAAAGTCT   51127         T     ACA
                                AGACTTTG GTGGCT   TG
                                |||||||| ||||||   ||
                                TCTGAAAC CACCGA   AC
                                     T     GG_
GAM576  FLJ21551  3'  CACGTAGTTACCAAAACTCT   46031     C_   T       A
                                AGA  TTTG GTGGCTAC TG
                                |||  |||| |||||||| ||
                                TCT  AAAC CATTGATG AC
                                  CA   _       C
GAM576  FLJ21709  3'  GTCTCACCGCACAAAGCCT   78482    A        CTACAT
                                AG CTTTGTGTGG     GAC
                                || ||||||||||     |||
                                TC GAAACACGCC     CTG
                                 C        ACT___
GAM576  GRID1    3'  TCATGGAGAAATACAAAGTC   69027          GG  A
                                GACTTTGTGT  CT CATGA
                                ||||||||||  || |||||
                                CTGAAACATA  GA GTACT
                                      AA  G
GAM576  KIAA0179  3'  GTCATATAGCCAAACGGG    65458      G     C
                                TTTGT TGGCTA ATGAC
                                ||||| |||||| |||||
                                GGGCA ACCGAT TACTG
                                   A     A
GAM576  KRTAP1-1  3'  TCACACAGCCACATAAATTC   49046    C         ACA
                                GA TTTGTGTGGCT   TGA
                                || ||||||||||   |||
                                CT AAATACACCGA   ACT
                                 T         CAC
GAM576  LOXL4    3'  CATGCCCTTCACAGAGTC    50857         T_  CTA
                                GACTTTGTG  GG   CATG
                                |||||||||  ||   ||||
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                                CTGAGACAC  CC   GTAC
                                     TT  C__
GAM576  MISS     3'  GTCATACAGCACTAAAGTCT   58641        T   G  AC
                                AGACTTTG GTG CT  ATGAC
                                |||||||| ||| ||  |||||
                                TCTGAAAT CAC GA  TACTG
                                     _  _  CA
GAM576  NXP-2    3'  TCACGGTTAAACACAAAGTGTT 71660    G       GGCT  A_
                                AA ACTTTGTGT    AC  TGA
                                || |||||||||    ||  |||
                                TT TGAAACACA    TG  ACT
                                 G        AAT_  GC
GAM576  PTD011   3'  GTCACATAAAGGAAGTCTT    26760        ____
                                AAGACTTT    GTGTGGC
                                ||||||||    |||||||
                                TTCTGAAG    TACACTG
                                     GAAA
GAM576  SDFR1    3'  GTCATGTAAATTCATAAATC   34359    C     TGGC
                                GA TTTGTG    TACATGAC
                                || ||||||    ||||||||
                                CT AAATAC    ATGTACTG
                                 _     TTAA
GAM576  SDFR1    3'  GTCATGTAAATTCATAAATC   25793    C     TGGC
                                GA TTTGTG    TACATGAC
                                || ||||||    ||||||||
                                CT AAATAC    ATGTACTG
                                 _     TTAA
GAM576  LOC124842 3'  GTCACAGGCTGCACAAAGACTT 76159     A      TG   ACA
                                AAG CTTTGTG  GCT   TGAC
                                ||| |||||||  |||   ||||
                                TTC GAAACAC  CGG   ACTG
                                  A      GT   AC_
GAM576  LOC146310 5'  CATGCAGCCACATCTTCT    78350     CTTT      A
                                AGA    GTGTGGCT CATG
                                |||    |||||||| ||||
                                TCT    TACACCGA GTAC
                                  TC__       C
GAM576  LOC147040 3'  CACGTAGCCAGGAGGGGCCT   78831    A   GTG      A
                                AG CTTT   TGGCTAC TG
                                || ||||   ||||||| ||
                                TC GGGG   ACCGATG AC
                                 C    AGG      C
GAM576  LOC148534 3'  CATCAGTACCAAAGTCTT    79633         T   G  AC
                                AAGACTTTG GTG CT  ATG
                                ||||||||| ||| ||  |||
                                TTCTGAAAC CAT GA  TAC
                                     _  _  C_
GAM576  LOC150112 3'  CATGTAGCCCCAGTCT      80388       TTGT T
                                AGACT    G GGCTACATG
                                |||||    | |||||||||
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                                TCTGA   C CCGATGTAC
                                  ____ C
GAM576  LOC153894 3'  GTCATACAGCCCTAAAGTCT  81879       TGT   AC
                                AGACTTTG  GGCT  ATGAC
                                ||||||||  ||||  |||||
                                TCTGAAAT  CCGA  TACTG
                                    C__   CA
GAM576  LOC253389 5'  CATGTTGCTCACACAAAGCCT  97646   A       _  T
                                AG CTTTGTGTG GC ACATG
                                || |||||||| || |||||
                                TC GAAACACAC CG TGTAC
                                 C       T  T
GAM576  LOC253681 3'  CACGTAGCCAGGAGGGGCCT  96836   A   GTG     A
                                AG CTTT  TGGCTAC TG
                                || ||||  ||||||| ||
                                TC GGGG  ACCGATG AC
                                 C   AGG     C
GAM576  LOC253805 3'  TCATATATTTGTGCAAAGTTTT 98184         TG C  C
                                AAGACTTTGTG  G TA ATGA
                                ||||||||||  | || ||||
                                TTTTGAAACGT  T AT TACT
                                      GT T  A
GAM576  LOC255349 3'  TCATGTAGCCAACTTCAAATC  97352   C   TG__
                                GA TTTG   TGGCTACATGA
                                || ||||   ||||||||||
                                CT AAAC   ACCGATGTACT
                                 _   TTCA
GAM577  INHBB   3'  CAGTCAAAACCAGAGCGAGA  11005         CG  T
                                TCTCGCTCTGGT  TG CTG
                                ||||||||||||  || |||
                                AGAGCGAGACCA  AC GAC
                                      AA  T
GAM577  FLJ20241  3'  TGGACAACAGAGCGAGA    35292        GTCG
                                TCTCGCTCTG   TGTCTG
                                ||||||||||   ||||||
                                AGAGCGAGAC   ACAGGT
                                      A___
GAM577  KIAA0057  3'  ACAGACACAGCAGGAGGAGA  25395    G   G  C
                                TCTC CTCT GT GTGTCTGT
                                |||| |||| || ||||||||
                                AGAG GAGG CG CACAGACA
                                  _   A  A
GAM577  KIAA0227  3'  TGACAGACCAGAACCAGA    61354      _ GT
                                TCTGGT C  GTCTGTCA
                                |||||| |  ||||||||
                                AGACCA G  CAGACAGT
                                   A AC
GAM577  KIAA1950  3'  GACAAACAGGGCAGCCAGAGCC 94182    C      ___ G   C
            AGA                   TCT GCTCTGGT   C TGT TGTC
                                ||| ||||||||   | ||| ||||
```

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                                AGA CGAGACCG   G ACA ACAG
                                  C       ACG G   A
GAM577  WSB1     3'  TGGACAACAGAGCGAGA     56986          GTCG
                                TCTCGCTCTG    TGTCTG
                                ||||||||||    ||||||
                                AGAGCGAGAC    ACAGGT
                                     A___
GAM577  WSB1     3'  TGGACAACAGAGCGAGA     56998          GTCG
                                TCTCGCTCTG    TGTCTG
                                ||||||||||    ||||||
                                AGAGCGAGAC    ACAGGT
                                     A___
GAM577  LOC128008 5'  TGACAGACATCCTGAAGA    75989    GC  T  TC
                                TC  TC GG  GTGTCTGTCA
                                ||  || ||  ||||||||||
                                AG  AG CC  TACAGACAGT
                                 A_  T  __
GAM577  LOC143286 5'  TGACAGACAGTGGAAAAGA   83850     GG_  _
                                TCT   TCG TGTCTGTCA
                                |||   ||| |||||||||
                                AGA   GGT ACAGACAGT
                                  AAA   G
GAM577  LOC148946 5'  ACGGAAAACAGAGCGAGA    85462          GTCGTG
                                TCTCGCTCTG     TCTGT
                                ||||||||||     |||||
                                AGAGCGAGAC     AGGCA
                                     AAA___
GAM577  LOC150889 3'  ACAGACACTTTACAGAAGAGA  80807     GC    GTC_
                                TCTC  TCTG    GTGTCTGT
                                ||||  ||||    ||||||||
                                AGAG  AGAC    CACAGACA
                                  A_    ATTT
GAM577  LOC154525 3'  ACAGATGTCACCAAAGAAGA   87424     CG  C    C TG
                                TCT  CT TGGT G  TCTGT
                                |||  || |||| |  |||||
                                AGA  GA ACCA T  AGACA
                                  A_  A    C GT
GAM577  LOC90917  3'  ACAGACACTGCCAAGGAAGA   64981     CG TC    C
                                TCT  C  TGGT GTGTCTGT
                                |||  |  |||| ||||||||
                                AGA  G  ACCG CACAGACA
                                  A_ GA    T
GAM578  ADCY7    3'  TGAGTTGCCCCGGGCTG     8494          AACACT   __
                                CAGCCCGG     GGCA  TCA
                                ||||||||     ||||  |||
                                GTCGGGCC     CCGT  AGT
                                     _______   TG
GAM578  ADRBK1   3'  ATGATGCCACACCAAGCTGTG  9663        CC  AACAC
                                CACAGC  GG    TGGCATCAT
                                ||||||  ||    |||||||||
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                                GTGTCG  CC    ACCGTAGTA
                                   AA  AC___
GAM578  BTEB1    5'  ATGTCAGTGTTCGAGGCTGT  8668       CG
                                ACAGCC  GAACACTGGCAT
                                ||||||  ||||||||||||
                                TGTCGG  CTTGTGACTGTA
                                   AG
GAM578  LAIR1    3'  GAGGACAGCCCGGGCTGTG   41662        AACA   GCA
                                CACAGCCCGG   CTG   TC
                                ||||||||||   |||  ||
                                GTGTCGGGCC   GAC   AG
                                      C___   AGG
GAM578  LILRB4   3'  TGATGTCTTCCTGGCTGT    23388      C   CACT
                                ACAGCC GGAA   GGCATCA
                                |||||| ||||   |||||||
                                TGTCGG CCTT   CTGTAGT
                                   T   _____
GAM578  P23      3'  ATGACTTGTCAGTGTTCCAGGT 22752     G  C         __
             GT                   ACA CC GGAACACTGGCA  TCAT
                                ||| || ||||||||||||  ||||
                                TGT GG CCTTGTGACTGT  AGTA
                                  _ A          TC
GAM578  PRV1     3'  TGAGCATTCAGGGCTGTG    73896        G   CACTG  A
                                CACAGCCC GAA    GC TCA
                                |||||||| |||    || |||
                                GTGTCGGG CTT    CG AGT
                                     A   A____  _
GAM578  SOLH     5'  GGCGCCGCCGGGCTGTG     20094         AACAC   AT
                                CACAGCCCGG    TGGC  C
                                ||||||||||    ||||  |
                                GTGTCGGGCC    GCCG  G
                                      ______   CG
GAM578  SOX5     3'  ATGCCAGTAATTCAGCTG    23665      CC   AC
                                CAGC  GGA  ACTGGCAT
                                ||||  |||  ||||||||
                                GTCG  CTT  TGACCGTA
                                  A_   AA
GAM578  ATP10B   3'  ATGATGCCAGCACTAGCCAGCT 64103      CC  AACA__
             G                    CAGC  GG     CTGGCATCAT
                                ||||  ||     ||||||||||
                                GTCG  CC     GACCGTAGTA
                                  A_  GATCAC
GAM578  C19orf7  3'  ATGCAGGTGTTCCAAGGTGTG  61776      G  C_      G
                                CACA CC  GGAACACT GCAT
                                |||| ||  |||||||| ||||
                                GTGT GG  CCTTGTGG CGTA
                                  _ AA       A
GAM578  C1QR1    3'  ATGCCAGTGCTCCGAGCTCA  24867   C   C    A
                                A AGC CGGA CACTGGCAT
                                | ||| |||| |||||||||
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                                A TCG GCCT GTGACCGTA
                                 C  A   C
GAM578  CYP2A13  3'  ATGATGTCCTTCAGAGCTGTG  7546       CCG  CACT
                                CACAGC  GAA  GGCATCAT
                                ||||||  |||  ||||||||
                                GTGTCG  CTT  CTGTAGTA
                                   AGA  C___
GAM578  KIAA0316 3'  ATGATGCCAATGAGCTGCTCTG 70243    CC  AA  C
                                CAG  CGG  CA TGGCATCAT
                                |||  |||  || |||||||||
                                GTC  GTC  GT ACCGTAGTA
                                  TC  GA  A
GAM578  MGC4368  5'  ATGATGCCAGTGGCGCTGG  44723    AA_
                                CCGG  CACTGGCATCAT
                                ||||  ||||||||||||
                                GGTC  GTGACCGTAGTA
                                  GCG
GAM578  NBL1     3'  ATGTTAGTGCCCCGCACTGTG  60045     CC  AA
                                CACAG  CGG  CACTGGCAT
                                |||||  |||  |||||||||
                                GTGTC  GCC  GTGATTGTA
                                   AC  CC
GAM578  RNF13    5'  GCTAGTACTCCGGGCTGTG  24417        AC
                                CACAGCCCGGA  ACTGGC
                                ||||||||||  ||||||
                                GTGTCGGGCCT  TGATCG
                                      CA
GAM578  RNPC1    3'  TGGGGCATCCAGGGCTGTG  34414       _  ACACTG  AT
                                CACAGCCC GGA    GC  CA
                                |||||||| |||    ||  ||
                                GTGTCGGG CCT    CG  GT
                                    A  A_____  GG
GAM578  TIMM22   3'  ATGATGCCAGCCCCGGATCCGG 78911        ACA____
           GCTG                 CAGCCCGGA     CTGGCATCAT
                                |||||||||     ||||||||||
                                GTCGGGCCT     GACCGTAGTA
                                     AGGCCCC
GAM578  LOC143879 5'  ATGATGCCACTGATCAAACCTG 77157    CCCG  A  C
                                CAG   GA CA TGGCATCAT
                                |||   || || |||||||||
                                GTC   CT GT ACCGTAGTA
                                  CAAA  A  C
GAM578  LOC147858 5'  ATGCTGCACTCCGGAGCCGTG  79267    A  _   ACACT
                                CAC GC CCGGA    GGCAT
                                ||| || |||||    |||||
                                GTG CG GGCCT    TCGTA
                                  C  A    CACG_
GAM578  LOC149086 3'  ATGGGTTGGTGTCCGGGC    85491       A  TG  A
                                GCCCGGA CAC  GC TCAT
                                ||||||| |||  || ||||
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                                CGGGCCT GTG  TG GGTA
                                   _  GT  _
GAM578  LOC200058 3'  TGTCGCAGCAGCCCGGGCTG  89965       AACA  __ AT
                                CAGCCCGG   CTG  GC  CA
                                ||||||||   |||  ||  ||
                                GTCGGGCC   GAC  CG  GT
                                   C___   GA  CT
GAM578  LOC257364 3'  ATGCTGGGCACCCAGGGCTGTG 96641       _  AACA TG
                                CACAGCCC GG   C  GCAT
                                |||||||| ||   |  ||||
                                GTGTCGGG CC   G  CGTA
                                   A  CACG GT
GAM578  LOC55893  5'  ATGATGCCAGGCTACCAGGC  38489    C  AACA
                                GCC GG   CTGGCATCAT
                                ||| ||   ||||||||||
                                CGG CC   GACCGTAGTA
                                  A  ATCG
GAM579  KCNK4    3'  CCGTTGGGGCAGAACCATGGAG 33980       A_  __  G TG  C
          GA                    TTCTCCATG  TC  CC C  GC GG
                                |||||||||  ||  || |  || ||
                                AGGAGGTAC  AG  GG G  TG CC
                                   CA  AC  _ GT  _
GAM579  KRT3     3'  CCCGGCCAAGCCCAGTCACGAG 55102     CA   CCC  _
          AA                    TTCTC  TGAT   GCT GGCCGGG
                                |||||  ||||   ||| |||||||
                                AAGAG  ACTG   CGA CCGGCCC
                                  C_   ACC   A
GAM579  TNFRSF1B  3'  CCCAGCCATTACCATGGAGA  8390       ATCCCGC   C
                                TCTCCATG      TGGC GGG
                                ||||||||      |||| |||
                                AGAGGTAC      ACCG CCC
                                   CATT___    A
GAM579  FLJ10307  3'  CCCAGCCAGCAGAGATGGAGAG 36475       GA  CC    C
                                TTCTCCAT  TC  GCTGGC GGG
                                |||||||  ||  |||||| |||
                                GAGAGGTA  AG  CGACCG CCC
                                   G_  A_     A
GAM579  FLJ10546  3'  CTAGTACAAGACATGGAGAA  60180       A  CC__
                                TTCTCCATG TC   GCTGG
                                |||||||| ||   |||||
                                AAGAGGTAC AG   TGATC
                                   _  AACA
GAM579  FLJ12526  3'  CCCGATCAAGAACATGGAGAA  45926       A  CCGC  GC
                                TTCTCCATG TC   TG  CGGG
                                |||||||| ||   ||  ||||
                                AAGAGGTAC AG   AC  GCCC
                                   A  A___  TA
GAM579  GAPCENA  3'  CCAGGTAGACATGGAGAA   25176       A  CCG
                                TTCTCCATG TC   CTGG
                                |||||||| ||   ||||
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                                AAGAGGTAC AG   GACC
                                     _ ATG
GAM579  GPS2     5' CCAAGGGGACATGGAGAA    16887         A    GC
                                TTCTCCATG TCCC  TGG
                                ||||||||| ||||  |||
                                AAGAGGTAC AGGG  ACC
                                     _   GA
GAM579  KIAA0256 5' CCCGAGCGGGGGGCCATGGAGA 65049         AT   G   GC
           A                     TTCTCCATG  CCC CTG  CGGG
                                 |||||||||  ||| |||  ||||
                                 AAGAGGTAC  GGG GGC  GCCC
                                      CG   _   GA
GAM579  KIAA1938 3' CCCGGCTGCAGATTACGGAGAA 93822       A    CC  T
                                 TTCTCC TGATC  GC GGCCGGG
                                 |||||| |||||  || |||||||
                                 AAGAGG ATTAG  CG TCGGCCC
                                     C    A_ _
GAM579  NDRG4    3' CCCAAGGAAGACAGAACATGGA 40377         A  CCG  GG  __
           GAA                     TTCTCCATG TC   CT  CC  GGG
                                 ||||||||| ||   ||  ||  |||
                                 AAGAGGTAC AG   GA  GG  CCC
                                      A  ACA  A_  AA
GAM579  OATPRP4  3' CGGTTAGCAAAACCATGGGAA  48983     T    ATCCC
                                 TTC CCATG    GCTGGCCG
                                 ||| |||||    ||||||||
                                 AAG GGTAC    CGATTGGC
                                   _    CAAAA
GAM579  LOC164173 3' CCCAAACTAGCAAAACCTATGG 83051         ATCCC_    CC_
           AGAA                    TTCTCCATG     GCTGG   GGG
                                 |||||||||     |||||  |||
                                 AAGAGGTAT     CGATC   CCC
                                      CCAAAA    AAA
GAM579  LOC257438 3' CCCAGCCAGCAGAGATGGAGAG 95591         GA  CC     C
                                 TTCTCCAT  TC  GCTGGC GGG
                                 |||||||  ||  |||||| |||
                                 GAGAGGTA  AG  CGACCG CCC
                                      G_  A_     A
GAM580  CCND2    3' CATTTCAGGCACAACGATA   10047     T C  C
                                 TATC G TG GCCTGAGATG
                                 |||| | || ||||||||||
                                 ATAG C AC CGGACTTTAC
                                   _ A  A
GAM580  SLC16A2  3' ACTCATCTCAGGCTGAGC    22521     GC
                                 GCT  GCCTGAGATGAGT
                                 |||  ||||||||||||
                                 CGA  CGGACTCTACTCA
                                   GT
GAM580  SURF5    3' TACTCATTAACTCAGCAGA   23129        CGCCTGA
                                 TCTGCTG      GATGAGTA
                                 |||||||      ||||||||
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                                AGACGAC      TTACTCAT
                                    TCAA___
GAM580  BANP     5'  TACCCAGATCACACAGCTGATA 66803     T   CGCC   GA  A
                                TATC GCTG   TGA  TG GTA
                                |||| ||||   |||  || |||
                                ATAG CGAC   ACT  AC CAT
                                  T   AC__   AG  C
GAM580  LOXL4    3'  ACTCATCTCTACAGAGATA   50854      G   CGCCT
                                TATCT CTG    GAGATGAGT
                                ||||| |||    |||||||||
                                ATAGA GAC    CTCTACTCA
                                  _  AT___
GAM580  LOC127881 5'  TACTCAAGGCCACACAGCAAGT 75988    TC    C___   GAGA
            A                    TA  TGCTG   GCCT   TGAGTA
                                || |||||   ||||   ||||||
                                AT  ACGAC   CGGA   ACTCAT
                                 GA    ACAC   _____
GAM580  LOC142779 3'  ACCCATCTCCGTAGCAG     76898        CCT     A
                                CTGCTGCG   GAGATG GT
                                ||||||||   |||||| ||
                                GACGATGC   CTCTAC CA
                                    ___     C
GAM581  CDH12    3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM581  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                  AC        G
GAM581  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT    98090      T    AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                  _   GTCA_
GAM581  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
            A                    TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM581  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126        CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM581  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
            TA                    TACA   TCC   GAAGAATAAG
                                ||||   |||   ||||||||||
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                              ATGT   AGG   TTTCTTATTC
                                AAA_  ATTG
GAM581  KIAA1579 3' TACTCTTAGTGGTGTA     37154        CCCAAG   A
                              TACACCACT     AAGA TA
                              |||||||||     |||| ||
                              ATGTGGTGA     TTCT AT
                                    _______   C
GAM581  KIAA1719 3' TCTGTCTTGGGAGTGGTGTA  68742             _
                              TACACCACTCCCAAGA AGA
                              |||||||||||||||| |||
                              ATGTGGTGAGGGTTCT TCT
                                        G
GAM581  KIAA1853 3' TTTTTCTTGGAAGCAGTG    69929    CA  C
                              CAC  CT CCAAGAAGAA
                              |||  || ||||||||||
                              GTG  GA GGTTCTTTTT
                                AC  A
GAM581  KIAA1877 3' CTTATTCTTCTGCCATGAGT  66748     CCA__
                              ACTC    AGAAGAATAAG
                              ||||    ||||||||||
                              TGAG    TCTTCTTATTC
                                TACCG
GAM581  KIAA1906 3' CTTATTCTTCTTGACTTTTGG 73571    CTCC_
                              CCA    CAAGAAGAATAAG
                              |||    ||||||||||||
                              GGT    GTTCTTCTTATTC
                                TTTCA
GAM581  OSBPL11  3' CTTAATTTCCCAAGAGTGGTG 43206       CCAA   AA
                              CACCACTC   GAAG  TAAG
                              ||||||||   ||||  ||||
                              GTGGTGAG   CTTT  ATTC
                                   AACC   A_
GAM581  YME1L1   3' TCATTCTTGATGTGGTGTA   58438       TCC    _
                              TACACCAC   CAAGAA GA
                              ||||||||   |||||| ||
                              ATGTGGTG   GTTCTT CT
                                   TA_    A
GAM581  YME1L1   3' TCATTCTTGATGTGGTGTA   27323       TCC    _
                              TACACCAC   CAAGAA GA
                              ||||||||   |||||| ||
                              ATGTGGTG   GTTCTT CT
                                   TA_    A
GAM581  ZNF262   3' CTTATTTTGTTTGGGAGT    18723        A
                              ACTCCCAAG AGAATAAG
                              ||||||||| ||||||||
                              TGAGGGTTT TTTTATTC
                                   G
GAM581  LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_   AAGA
                              TACACCAC   CCAAG   ATA
                              ||||||||   |||||   |||
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                                ATGTGGTG  GGTTC   TGT
                                    CAA   GG__
GAM582  ADRBK1   3'  GCCAGGTGGGCGGGCAGCACAG 9667    GA     AA   C___
          C                  GC  TGCTGCCC  GTCC   GGC
                             ||  ||||||||  ||||   |||
                             CG  ACGACGGG  CGGG   CCG
                              AC       __   TGGA
GAM582  APOB48R  3'  CCAGCCTGGGCAGCATAGC   38583   G       A  CCC
                             GC ATGCTGCCCA GT   GG
                             || ||||||||||  ||   ||
                             CG TACGACGGGT CG   CC
                              A        C  A__
GAM582  DHFR     3'  CCAGCTTGGGCAACATGGC   7646    G   C       CCC
                             GC ATG TGCCCAAGT   GG
                             || ||| |||||||||   ||
                             CG TAC ACGGGTTCG   CC
                              G   A       A__
GAM582  IL2RA    3'  CCAGCCTGGGCAGCATAGC   6450    G       A  CCC
                             GC ATGCTGCCCA GT   GG
                             || ||||||||||  ||   ||
                             CG TACGACGGGT CG   CC
                              A        C  A__
GAM582  NR2E1    5'  GCCGGGACTCGGGCAGCG    13793       A
                             TGCTGCCC AGTCCCGGC
                             ||||||||  |||||||||
                             GCGACGGG TCAGGGCCG
                                  C
GAM582  SFRS2IP  5'  CCAGCTTGGGCAACATGGC   17538   G   C       CCC
                             GC ATG TGCCCAAGT   GG
                             || ||| |||||||||   ||
                             CG TAC ACGGGTTCG   CC
                              G   A       A__
GAM582  T        5'  GCCGGGACCCGGGACCCGGGA  13506   G  ATGCTG   AA
                             TC CG     CCC  GTCCCGGC
                             || ||     |||  ||||||||
                             AG GC     GGG  CAGGGCCG
                              G  CCA___   CC
GAM582  C1orf34  3'  CCGGGACTTGGTGTCTCCACGT 61302     A  CT_  _
                             GCG TG   GC CCAAGTCCCGG
                             ||| ||   || ||||||||||
                             TGC AC   TG GGTTCAGGGCC
                               _  CTC  T
GAM582  C20orf154 3'  CCAACCTTGGGCAACATAGC   90048   G   C       TCCC
                             GC ATG TGCCCAAG    GG
                             || ||| ||||||||    ||
                             CG TAC ACGGGTTC    CC
                              A  A       CAA_
GAM582  DDX12    3'  GCCGGGACCCAGGCACAGGCG  60424     GA  C   CAA
                             CGC  TG TGCC   GTCCCGGC
                             |||  || ||||   ||||||||
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                                GCG  AC ACGG   CAGGGCCG
                                  G_ _    ACC
GAM582  DKFZP586M1120 3'  GCCGGGACCTGGAGAATC    49283     G  GC   A
                                GAT CT  CCA GTCCCGGC
                                ||| ||  ||| ||||||||
                                CTA GA  GGT CAGGGCCG
                                  A __   C
GAM582  KIAA0514  3'  CCAGCTTGGGCAGCATGGCGA  28742      G          CCC
                                TCGC ATGCTGCCCAAGT   GG
                                |||| ||||||||||||   ||
                                AGCG TACGACGGGTTCG   CC
                                  G          A__
GAM582  KIAA1297  3'  CGTACTGGGCAGCATC      72637          A  CC
                                GATGCTGCCCA GT  CG
                                |||||||||| ||  ||
                                CTACGACGGGT CA  GC
                                       _ T_
GAM582  MGC2562   3'  CCAGTTTGGGCAACATGGCGA  51435     G   C       TCCC
                                TCGC ATG TGCCCAAG    GG
                                |||| ||| ||||||||    ||
                                AGCG TAC ACGGGTTT    CC
                                  G   A       GA__
GAM582  NOPAR     5'  GCCGGGCAGCGGCAGCATC    54859         CAA T
                                GATGCTGCC   G CCCGGC
                                |||||||||   | ||||||
                                CTACGACGG   C GGGCCG
                                     CGA _
GAM582  NY-REN-25 5'  GCCGAGACTTGGGGCGGGCGA  61263      GA   TG       C
                                TCGC  TGC  CCCAAGTC CGGC
                                ||||  |||  |||||||| ||||
                                AGCG  GCG  GGGTTCAG GCCG
                                  G_  __       A
GAM582  PTD012    3'  CCAGCTTGGGCAACATAGC    26735    G   C       CCC
                                GC ATG TGCCCAAGT   GG
                                || ||| |||||||||   ||
                                CG TAC ACGGGTTCG   CC
                                 A   A        A__
GAM582  TNFAIP3   5'  CCAGGACTTGGGACTTTGCGA  21907       TGCTG       C
                                TCGCGA     CCCAAGTCC GG
                                ||||||     ||||||||| ||
                                AGCGTT     GGGTTCAGG CC
                                   TCA__         A
GAM582  LOC145375 5'  CCGCAGGGCAGCACCGGA    60635    G  A       AAGTCC
                                TC CG TGCTGCCC      CGG
                                || || ||||||||      |||
                                AG GC ACGACGGG      GCC
                                 _ C       AC_____
GAM582  LOC152447 3'  CCGGGACTCGGGACTCCCGGGA 81458    G  ATGCTG   A
                                TC CG      CCC AGTCCCGG
                                || ||      ||| ||||||||
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                                AG GC     GGG TCAGGGCC
                                 G  CCTCA_  C
GAM582  LOC220058 5'  GCCAGGACCCAGACATCTGGGA 93379    G _   _  CCCAA   C
                                TC C GATG CTG    GTCC GGC
                                || | |||| |||    |||| |||
                                AG G CTAC GAC    CAGG CCG
                                 G T   A  C____   A
GAM582  LOC220567 3'  CCAGCCTGGGCAGCATAGC   92432    G       A  CCC
                                GC ATGCTGCCCA GT  GG
                                || |||||||||| ||  ||
                                CG TACGACGGGT CG  CC
                                 A        C  A__
GAM583  CYP2F1   5'  CCAGCCAGTGTCTCCTG    7581        T    C
                                CAGGAGA CGCTG GCTGG
                                ||||||| ||||| |||||
                                GTCCTCT GTGAC CGACC
                                   _    _
GAM583  ETS2     5'  CCCGGCCAGCGTCCGGCCTCC  19116     AT  CT       A
                                GGAG  CG  GCGCTGGCC GG
                                ||||  ||  |||||||||| ||
                                CCTC  GC  TGCGACCGG CC
                                  CG  C_       C
GAM583  EXTL1    5'  CTGGCCAAGCCGCCTCCTG   16735       ATC  T  GC
                                CAGGAG   GC GC  TGGCCAG
                                ||||||   || ||  |||||||
                                GTCCTC   CG CG  ACCGGTC
                                   ___  C  A_
GAM583  FLOT2    3'  CCCAGCCAGCGCTCATACCCTG 16797     AG  CGCT      CA
                                CAGG  AT   GCGCTGGC  GG
                                ||||  ||   ||||||||  ||
                                GTCC  TA   CGCGACCG  CC
                                  CA  CT__      AC
GAM583  LEP      3'  CTGGCCAGGCACCCCCTG    5860      AGATCGC   G
                                CAGG      TGC CTGGCCAG
                                ||||      ||| ||||||||
                                GTCC      ACG GACCGGTC
                                  CCC_____  _
GAM583  OVOL1    3'  CCTGGCCAGCCCACCCTCCTG  17066       ATCGC  C
                                CAGGAG    TG GCTGGCCAGG
                                ||||||    || ||||||||||
                                GTCCTC    AC CGACCGGTCC
                                   CC___  C
GAM583  SORCS2   3'  CTGGCCAGCAGGCCGCCTG   40802     AGATC   GC
                                CAGG    GCT  GCTGGCCAG
                                ||||    |||  |||||||||
                                GTCC    CGG  CGACCGGTC
                                  GC___   A_
GAM583  TAT      3'  CCTGACCTCAGGCAATCTGCC  6254     _   C   GCGCT  C
                                GG AGAT GCT    GG CAGG
                                || |||| |||    || ||||
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                                CC TCTA CGG    CC GTCC
                                 G   A  ACT__  A
GAM583  TRIM8    3'  CCTGGATTTTGACACAGCAACT 48851      ATC   CGCTGG___
            TCCTG                  CAGGAG  GCTG       CCAGG
                                |||||| ||||       |||||
                                GTCCTT  CGAC       GGTCC
                                   CAA   ACAGTTTTA
GAM583  AP1GBP1  3'  CCTGGCCAACACAATGAAACC  24347    AGA  C  CGC
                                GG  TCG TG  TGGCCAGG
                                ||  ||| ||  ||||||||
                                CC  AGT AC  ACCGGTCC
                                 AA_  A  ACA
GAM583  CDH24    3'  CTGGCCCTGCGATCTCTCA   96603   A      TGCGCT
                                C GGAGATCGC     GGCCAG
                                | |||||||||     ||||||
                                A TCTCTAGCG     CCGGTC
                                 C       TC_____
GAM583  CNK1     3'  CCTGGCCAGCACTCTAGCTCCT 21968      ATCGCTGC
            G                   CAGGAG      GCTGGCCAGG
                                ||||||      ||||||||||
                                GTCCTC      CGACCGGTCC
                                   GATCTCA_
GAM583  CNNM4    3'  CCTGGCCAGTCTGAGGTCTCCT 39862       GCTGC
                                AGGAGATC    GCTGGCCAGG
                                ||||||||    ||||||||||
                                TCCTCTGG    TGACCGGTCC
                                     AGTC_
GAM583  DJ971N18.2 3'  CCAGCCCTCTGAATCTCCTG  41262       _  CTGC
                                CAGGAGAT CG    GCTGG
                                |||||||| ||    |||||
                                GTCCTCTA GT    CGACC
                                     A  CTCC
GAM583  EZF-2    3'  CCGGCCAGCGCCATCTCC    37672      CGCT       A
                                GGAGAT    GCGCTGGCC GG
                                ||||||    ||||||||| ||
                                CCTCTA    CGCGACCGG CC
                                   C___        C
GAM583  FKSG28   3'  CCTGGCCAGTAGGACCTCC   48907     A  G  GC
                                GGAG TC CT  GCTGGCCAGG
                                |||| || ||  ||||||||||
                                CCTC AG GA  TGACCGGTCC
                                  C  _  __
GAM583  FLJ10922 3'  CCAGCAGTAACATCTCCTG   37397       CGC  _
                                CAGGAGAT   TGC GCTGG
                                ||||||||   ||| |||||
                                GTCCTCTA   ATG CGACC
                                     CA_   A
GAM583  FLJ11560 3'  CCTGGCCAGACTCTGACCCACC 48006     AGA_   CTGCG
            T                    AGG    TCG    CTGGCCAGG
                                 |||    |||    |||||||||
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                                TCC   AGT    GACCGGTCC
                                  ACCC  CTCA_
GAM583  FLJ11722  3'  CCTGGCCAACACAGTGAAACCC 46997    AGA_    CGC
             C                   GG   TCGCTG  TGGCCAGG
                                 ||   ||||||  ||||||||
                                 CC   AGTGAC  ACCGGTCC
                                  CCAA    ACA
GAM583  FLJ12671  3'  CCTGGCCAACATGGCGAATTCC 49107     A     CGC
                                 GGAG TCGCTG  TGGCCAGG
                                 |||| ||||||  ||||||||
                                 CCTT AGCGGT  ACCGGTCC
                                   A     ACA
GAM583  FLJ20456  3'  CCTGGCCAACACTGGTCTCT  35664       C  CGC
                                 GGAGATCG TG  TGGCCAGG
                                 |||||||| ||  ||||||||
                                 TCTCTGGT AC  ACCGGTCC
                                      C  A__
GAM583  FLJ20509  5'  CCTAACCAGCGCGTCTACC   35758   _   CGCT     CC
                                 GG AGAT   GCGCTGG  AGG
                                 || ||||   |||||||  |||
                                 CC TCTG   CGCGACC  TCC
                                  A   _____     AA
GAM583  FLJ22692  3'  CCTGGCCAACACAGTAAACCCT 47480     AGATC   CGC
             G                   CAGG   GCTG  TGGCCAGG
                                 ||||   ||||  ||||||||
                                 GTCC   TGAC  ACCGGTCC
                                   CAAA_   ACA
GAM583  FLJ23047  3'  CCTGGCTCAAGTGATCTCC   44932        GCGCT
                                 GGAGATCGCT    GGCCAGG
                                 ||||||||||    |||||||
                                 CCTCTAGTGA    TCGGTCC
                                      AC___
GAM583  HN1L     3'  CCTGGCTGCTCAGCGTCTCCTG 58615       T    C  T
                                 CAGGAGA CGCTG GC GGCCAGG
                                 ||||||| ||||| || |||||||
                                 GTCCTCT GCGAC CG TCGGTCC
                                     _    T  _
GAM583  KIAA0217  3'  CCTAGCCAGCAGCAGTCTTCTG 67598       ATC    _    C
                                 CAGGAG   GCTGC GCTGGC AGG
                                 ||||||   ||||| |||||| |||
                                 GTCTTC   TGACG CGACCG TCC
                                    ___    A     A
GAM583  KIAA0298  3'  CCTGGCCAACAGCATCTCTCA  77076   A    C   CGC
                                 C GGAGAT GCTG   TGGCCAGG
                                 | |||||| ||||   ||||||||
                                 A TCTCTA CGAC   ACCGGTCC
                                  C     _   A__
GAM583  KIAA0349  3'  CCAGCCAGCATTTCCTG     93915        C   C
                                 CAGGAGAT GCTG GCTGG
                                 |||||||| |||| |||||
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                                GTCCTTTA CGAC CGACC
                                     _   _
GAM583  KIAA1530  3'  CCTAGCCTCAAGCGATCCTCCT 68555      _     GCGCT   C
            G                    CAGGAG ATCGCT    GGC AGG
                                 |||||| ||||||    ||| |||
                                 GTCCTC TAGCGA    CCG TCC
                                    C     ACT__   A
GAM583  MGC29891  3'  CCTGGCCAACATGGTGACACCC 58860    AGA_     CGC
            C                    GG   TCGCTG   TGGCCAGG
                                 ||   ||||||   ||||||||
                                 CC   AGTGGT   ACCGGTCC
                                  CCAC     ACA
GAM583  MKNK1     3'  CCTGGCCAGGCATTGTCCCCTG 14877     A  T  C   G
                                 CAGG GA CG TGC CTGGCCAGG
                                 |||| || || ||| |||||||||
                                 GTCC CT GT ACG GACCGGTCC
                                   C  _  T   _
GAM583  N4BP2     3'  CCTGGCCAACATGGTGAATCCC 36938    A   _    CGC
            C                    GG GAT CGCTG   TGGCCAGG
                                 || ||| |||||   ||||||||
                                 CC CTA GTGGT   ACCGGTCC
                                  C   A    ACA
GAM583  RPIA      3'  CCACCAGCAGTGATCTCCTG   58589            GC_
                                 CAGGAGATCGCTGC   TGG
                                 ||||||||||||||   |||
                                 GTCCTCTAGTGACG   ACC
                                         ACC
GAM583  TRIM35    3'  CCTGGCCAACGTCATCTTCCTG 61516      _  CGCT   C
                                 CAGGA GAT    GCG TGGCCAGG
                                 ||||| |||    ||| ||||||||
                                 GTCCT CTA    TGC ACCGGTCC
                                    T   C___   A
GAM583  LOC147299 5'  CCTGGCCAGCACCCGGCCTCTC 78979      TC    C__
            T                    GGAGA  GCTG   GCTGGCCAGG
                                 |||||  ||||   ||||||||||
                                 TCTCT  CGGC   CGACCGGTCC
                                    C_    CCA
GAM583  LOC148809 5'  CCTGGCCAACACAGTGAAACCC 79751    AGA_     CGC
            C                    GG   TCGCTG   TGGCCAGG
                                 ||   ||||||   ||||||||
                                 CC   AGTGAC   ACCGGTCC
                                  CCAA     ACA
GAM583  LOC148887 3'  CCAGCGCCAGCGCCCTCCTG   85397       AT    _
                                 CAGGAG  CGCTG CGCTGG
                                 ||||||  ||||| ||||||
                                 GTCCTC  GCGAC GCGACC
                                    CC    C
GAM583  LOC150358 3'  CCTGGCCAACATGGTGATACCC 86093    AG      CGC
                                 GG  ATCGCTG   TGGCCAGG
                                 ||  |||||||   ||||||||
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                                CC  TAGTGGT   ACCGGTCC
                                 CA      ACA
GAM583  LOC150372 5'  CCTGGCCAACACAGCTATCTCC 80609       C    CGC
           T                     AGGAGAT GCTG   TGGCCAGG
                                 ||||||| ||||   ||||||||
                                 TCCTCTA CGAC   ACCGGTCC
                                    T   ACA
GAM583  LOC157421 5'  CCGGCTGCAGCGATCTCC    87737          GCT    A
                                 GGAGATCGCTGC   GGCC GG
                                 ||||||||||||   |||| ||
                                 CCTCTAGCGACG   TCGG CC
                                        ___    G
GAM583  LOC158187 3'  CCTGGCCAACATGGTGACACCC 87992     AGA     CGC
           TG                    CAGG   TCGCTG   TGGCCAGG
                                 ||||   ||||||   ||||||||
                                 GTCC   AGTGGT   ACCGGTCC
                                   CAC     ACA
GAM583  LOC165257 5'  CCCGGCCAGCGCAAGCACTCCC 83369     A  TC  _       A
           TG                    CAGG GA  GCT GCGCTGGCC GG
                                 |||| ||  ||| |||||||||  ||
                                 GTCC CT  CGA CGCGACCGG CC
                                   _ CA   A       C
GAM583  LOC170394 5'  CCGGTCATCAAGATCTCCT    83736        GC  CGC    A
                                 AGGAGATC  TG   TGGCC GG
                                 ||||||||  ||   ||||| ||
                                 TCCTCTAG  AC   ACTGG CC
                                      A_  T__    C
GAM583  LOC197319 3'  CCTGGCCAACACAGTGAAACCT 89319     A__     CGC
           C                      GAG   TCGCTG   TGGCCAGG
                                  |||   ||||||   ||||||||
                                  CTC   AGTGAC   ACCGGTCC
                                    CAA     ACA
GAM583  LOC201161 5'  CCGGGCGCAGCGCCCCCTG    89506     AGAT       _
                                 CAGG    CGCTGCGCT GG
                                 ||||    ||||||||| ||
                                 GTCC    GCGACGCGG CC
                                   CCC_       G
GAM583  LOC202052 3'  CCTGGCCAACACAGTGAAACCC 91896    AGA_     CGC
           C                      GG    TCGCTG   TGGCCAGG
                                  ||    ||||||   ||||||||
                                  CC    AGTGAC   ACCGGTCC
                                   CCAA     ACA
GAM583  LOC204970 5'  CCTGGCCAGCGCGCAGATCCCC 90961    A   _  T
                                 GG GATC GC GCGCTGGCCAGG
                                 || |||| || ||||||||||||
                                 CC CTAG CG CGCGACCGGTCC
                                  C   A  _
GAM583  LOC219673 3'  CCTGGCCGCAAGCAATCCTCCT 94623       _  C   GC  T
           G                      CAGGAG AT GCT  GC GGCCAGG
                                  |||||| || |||  || |||||||
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                                GTCCTC TA CGA  CG CCGGTCC
                                   C  A   A_  _
GAM583  LOC91380  3'  CCTGGCCAACATAGCAATACCC 66444     AG  C    CGC
           TG                    CAGG  AT GCTG   TGGCCAGG
                                ||||  || ||||  ||||||||
                                GTCC  TA CGAT   ACCGGTCC
                                  CA  A    ACA
GAM583  LOC92340  3'  CCTGGCCAGGGCCATCTCCTG  69559        CGCT  G
                                CAGGAGAT   GC CTGGCCAGG
                                ||||||||   || |||||||||
                                GTCCTCTA   CG GACCGGTCC
                                     C___  G
GAM584  ITGA1     3'  CCAATGAGACAGTCCCTGA   64271      A  CAT  CA
                                TCAGG GAC   TG  TCATTGG
                                ||||| |||   ||  |||||||
                                AGTCC CTG   AC  AGTAACC
                                  _  ___  AG
GAM584  SH3GL3    5'  GCCAATATGGTCTCGATCTCCT 13111        CCATT  ATC
           GA                    TCAGGAGA    GC   ATTGGC
                                ||||||||    ||   ||||||
                                AGTCCTCT    TG   TAACCG
                                     AGCTC  GTA
GAM584  ARHGEF15  3'  GCCAATGAAAACGGCCGCCTGA 30954      AGA  ATTGCA
                                TCAGG   CC     TCATTGGC
                                |||||   ||     ||||||||
                                AGTCC   GG     AGTAACCG
                                   GCC  CAAA__
GAM584  DKFZp434F2322 3'  CCACCGACGATCTCCTGA    70299        CCA   CA  AT
                                TCAGGAGA   TTG  TC  TGG
                                ||||||||   |||  ||  |||
                                AGTCCTCT   AGC  AG  ACC
                                     ___   __  CC
GAM584  FLJ10716  3'  GCCACGTATCAACAATCTTCTG 37018        CCA   C  CAT
           A                     TCAGGAGA   TTG AT   TGGC
                                ||||||||   ||| ||   ||||
                                AGTCTTCT   AAC TA   ACCG
                                     AAC   _  TGC
GAM584  KIAA0527  3'  GCCACCTGCAATAGTCTCCTG  97499        C     TCAT
                                CAGGAGAC ATTGCA    TGGC
                                |||||||| ||||||    ||||
                                GTCCTCTG TAACGT    ACCG
                                     A     CC__
GAM584  KIAA1111  3'  GCCAATGACGCAGATAACCCTG 97946      AGACCA   A
           G                     TCAGG     TTGC TCATTGGC
                                |||||     |||| ||||||||
                                GGTCC     GACG AGTAACCG
                                   CAATA_   C
GAM584  Kv6.3     3'  GCCAATGATGCAAAGGTCCCC  56855    A   A
                                GG GACC TTGCATCATTGGC
                                || |||| ||||||||||||
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                                CC CTGG AACGTAGTAACCG
                                 C   A
GAM584  LOC145547 3'  GCCAATGGAGACAATTCCTGA  77782      GACC   CA_
                                TCAGGA   ATTG  TCATTGGC
                                ||||||   ||||  ||||||||
                                AGTCCT   TAAC  GGTAACCG
                                   ____   AGA
GAM584  LOC162333 5'  GCCAATGACTGAGAACGCCCCT 88494      AGACCATTG  _
          GA                     TCAGG       CA TCATTGGC
                                |||||        || ||||||||
                                AGTCC        GT AGTAACCG
                                  CCGCAAGA_  C
GAM585  GNL1    5'  CCTCGCTGGAAAACACCACA  93671       CTG  _  TTTC
                                TGTGGTGT  TCC GC   AGG
                                ||||||||  ||| ||   |||
                                ACACCACA  AGG CG   TCC
                                    AA_   T  C___
GAM585  GNL1    5'  CCTCGCTGGAAAACACCACA  99715       CTG  _  TTTC
                                TGTGGTGT  TCC GC   AGG
                                ||||||||  ||| ||   |||
                                ACACCACA  AGG CG   TCC
                                    AA_   T  C___
GAM585  RLN1    5'  TCCTGAAAGGCTGCAACACCCA 23582    T    C   CCG
                                TG GGTGT TGT  CTTTCAGGA
                                || ||||| |||  |||||||||
                                AC CCACA ACG  GAAAGTCCT
                                 _    _  TCG
GAM585  RORB    5'  TCCTGAAAACAAACAAACAAAC 23592    GG   C   CCGC
          A                     TGT  TGT TGT   TTTCAGGA
                                |||  ||| |||   ||||||||
                                ACA  ACA ACA   AAAGTCCT
                                  A_   A   AACA
GAM585  ATP9A   3'  CCTGAAAGCAAAACTCACA   62736      T  CTGTCC
                                TGTGG GT     GCTTTCAGG
                                ||||| ||     |||||||||
                                ACACT CA     CGAAAGTCC
                                   _  AAA___
GAM585  KIAA0275  3'  TCCCAGGGGAGAGACACCACA  29333        G   G  TTCA
                                TGTGGTGTCT TCC CT   GGA
                                |||||||||| ||| ||   |||
                                ACACCACAGA AGG GA   CCT
                                     G   G  C___
GAM585  OSBPL2   3'  CTTGAGGACAGACACCA    29899          GCTT
                                TGGTGTCTGTCC   TCAGG
                                ||||||||||||   |||||
                                ACCACAGACAGG   AGTTC
                                          _____
GAM585  OSBPL2   3'  CTTGAGGACAGACACCA    58485          GCTT
                                TGGTGTCTGTCC   TCAGG
                                ||||||||||||   |||||
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                                ACCACAGACAGG   AGTTC
                                      ____
GAM585  PPP4R1L  3'  CCTGAGTTACAAATACCACA  80323       C  CCGCT
                                TGTGGTGT TGT    TTCAGG
                                |||||||| |||    ||||||
                                ACACCATA ACA    GAGTCC
                                    A  TT___
GAM585  PRO2032  5'  TCCAGGCAAACCAAACACCACA 38393       C  TCC_   TCA
                                TGTGGTGT TG   GCTT  GGA
                                |||||||| ||   ||||  |||
                                ACACCACA AC   CGGA  CCT
                                    A  CAAA   ___
GAM585  LOC128843 5'  TCCTGAAGTTCAGACATCACA  76293         TCC   T
                                TGTGGTGTCTG   GCTT CAGGA
                                ||||||||||   |||| |||||
                                ACACTACAGAC   TGAA GTCCT
                                      T__   _
GAM585  LOC245727 5'  AGGACAGACAGACACCATA   92757          CG_
                                TGTGGTGTCTGTC   CTT
                                ||||||||||||   |||
                                ATACCACAGACAG   GGA
                                       ACA
GAM585  LOC257447 3'  AGGACAGACAGACACCATA   84456          CG_
                                TGTGGTGTCTGTC   CTT
                                ||||||||||||   |||
                                ATACCACAGACAG   GGA
                                       ACA
GAM585  LOC257541 5'  CCTCGCTGGAAAACACCACA   99596       CTG  _  TTTC
                                TGTGGTGT   TCC GC   AGG
                                ||||||||   ||| ||   |||
                                ACACCACA   AGG CG   TCC
                                    AA_   T  C___
GAM586  LDB3     3'  CAGATCGTGCATTTGCAT    76924      TTC      A
                                ATGC   GGATGCAC ATCTG
                                ||||   |||||||| |||||
                                TACG   TTTACGTG TAGAC
                                  ___       C
GAM586  MLLT2    3'  ATGCAGATTGTGCCAGAGCAT  21027      TC GAT
                                ATGCT  G   GCACAATCTGCAT
                                |||||  |  ||||||||||||
                                TACGA  C   CGTGTTAGACGTA
                                   GA ___
GAM586  DGS-A    3'  ATGCAGACTGTGCATCCCCGGT 86050     TC       A
                                GCT  GGATGCACA TCTGCAT
                                |||  ||||||||| |||||||
                                TGG  CCTACGTGT AGACGTA
                                  CC        C
GAM586  HYPH     3'  ATGCAGATTACAGGTATTAAAG 96566      CG    AC__
            CA                    TGCTT  GATGC    AATCTGCAT
                                |||||  |||||   |||||||||
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                                ACGAA  TTATG    TTAGACGTA
                                  A_     GACA
GAM586  MSRA     3'  CAGATTGGGTTTACCGAAGTAT 25607         AT_  A
                                ATGCTTCGG   GC CAATCTG
                                |||||||||   || |||||||
                                TATGAAGCC   TG GTTAGAC
                                     ATT  G
GAM586  PRO1386  3'  ATGCAGATTGCTGCAGAAG   49212      GGA   _
                                CTTC   TGCA CAATCTGCAT
                                ||||   |||| ||||||||||
                                GAAG   ACGT GTTAGACGTA
                                  ___    C
GAM586  LOC157657 3'  ATGCAGACTGCACATTCGGACA 82430    C       CA  A
                                TG TTCGGATG  CA TCTGCAT
                                || ||||||||  || |||||||
                                AC AGGCTTAC  GT AGACGTA
                                 _       AC  C
GAM586  LOC257017 5'  CAGATTGTTTAAAAAGCA    99217       CGGA  C
                                TGCTT    TG ACAATCTG
                                |||||    || ||||||||
                                ACGAA    AT TGTTAGAC
                                   AA__  T
GAM586  LOC257428 3'  CAGTTAGTGCATCCGAAGC   95932            AAT
                                GCTTCGGATGCAC   CTG
                                ||||||||||||   |||
                                CGAAGCCTACGTG   GAC
                                      ATT
GAM586  LOC90826  3'  CAGTGTACATCTGAAACAT   64783     C       C   AT
                                ATG TTCGGATG ACA  CTG
                                ||| |||||||| |||  |||
                                TAC AAGTCTAC TGT  GAC
                                  A       A  __
GAM586  LOC92606  3'  ATGCAAATTGATTACCTGAAGC 70527         A  CA    C
             AT                   ATGCTTCGG TG  CAAT TGCAT
                                |||||||||  ||  |||| |||||
                                TACGAAGTC AT  GTTA ACGTA
                                     C  TA    A
GAM587  BPHL     3'  AAGAGTTTTTCAAAATTA    16331      G       G
                                TAAT TTTGAAAAA CTCTT
                                |||| |||||||| |||||
                                ATTA AAACTTTTT GAGAA
                                  _       _
GAM587  CYBB     3'  TGAGAGCACTTTTACAAACATT 76854         _   A_
             A                    TAATGTTTG AAAA  GCTCTTG
                                |||||||||  ||||  |||||||
                                ATTACAAAC TTTT  CGAGAGT
                                     A    CA
GAM587  LGI1     3'  TTGCAAATGAATGCCTTTCAAA 18736           AA  __  __
             CATTG                  TAATGTTTGAAA  GC  TC  TTGCAA
                                ||||||||||||  ||  ||  ||||||
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                                GTTACAAACTTT CG AG AACGTT
                                      C_ TA TA
GAM587  MS4A2    3' TGTTTCCTTTTTTAAACATTA 41979            CTCTT
                                TAATGTTTGAAAAAG    GCA
                                |||||||||||||||    |||
                                ATTACAAATTTTTTC    TGT
                                     CTT__
GAM587  MYBPC1   3' TTGCAAGGCGTACCTCCAAACA 11725       AAAAA__ T
           T                    ATGTTTG      GC CTTGCAA
                                |||||||      || |||||||
                                TACAAAC      CG GAACGTT
                                   CTCCATG _
GAM587  RAG2     3' TTGCAAAAGCCTTTCAGAT   83076        AA  C
                                GTTTGAAA GCT TTGCAA
                                ||||||||  ||| ||||||
                                TAGACTTT CGA AACGTT
                                     C_  A
GAM587  TRIM14   3' TGCAAGAGCTTCTTAGCA    29521     TGAAA
                                TGTT    AAGCTCTTGCA
                                ||||    ||||||||||
                                ACGA    TTCGAGAACGT
                                  TTC__
GAM587  VHL      3' AGCTTTTCACAAACATTA    6831         A_
                                TAATGTTTG AAAAGCT
                                |||||||||  |||||||
                                ATTACAAAC TTTTCGA
                                     AC
GAM587  BHMT     3' TGCAGCTTTCTAAACATTA   9934         AA    CTT
                                TAATGTTTG AAAGCT  GCA
                                |||||||||  ||||||  |||
                                ATTACAAAT TTTCGA  CGT
                                     C_    ____
GAM587  DKFZP564L0864 3' TTGCAGTACTTTTAAACATTA 72950          AA  CTT
                                TAATGTTTGAAA GCT  GCAA
                                ||||||||||| |||  ||||
                                ATTACAAATTTT TGA  CGTT
                                       CA  ___
GAM587  FLJ13614 3' AAGTACTTTTTCAAACAT    58196          CT
                                ATGTTTGAAAAAG CTT
                                ||||||||||||  |||
                                TACAAACTTTTTC GAA
                                       AT
GAM587  FLJ14775 3' TTGCAAGAGCTTTTTTTTTTT 52682     TGTTT
           TA                    TAA    GAAAAAGCTCTTGCAA
                                |||    ||||||||||||||||
                                ATT    TTTTTTCGAGAACGTT
                                  TTTTT
GAM587  FLJ20254 5' TTGCAAGAGCTGGATAAGACA 35299      GAAAA
                                TGTTT    AGCTCTTGCAA
                                |||||    ||||||||||
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                                ACAGA    TCGAGAACGTT
                                  ATAGG
GAM587  KIAA0543  3'  TGCAAGAGCCCCCAGAGGCATT 69523        GAAAAA
            G                    TAATGTTT     GCTCTTGCA
                                 ||||||||     |||||||||
                                 GTTACGGA     CGAGAACGT
                                    GACCCC
GAM587  KIAA0625  3'  TTGCAAAAGCTTTCAGAGGGCA 31180        GAA_     C
            TTG                    TAATGTTT    AAAGCT TTGCAA
                                   ||||||||    |||||| ||||||
                                   GTTACGGG    TTTCGA AACGTT
                                      AGAC     A
GAM587  MEGF10    3'  CAGGACTTTTCAAACAT     51606          A C
                                 ATGTTTGAAAA G TCTTG
                                 |||||||||||| | |||||
                                 TACAAACTTTT C AGGAC
                                      _ _
GAM587  P115      3'  TTGCAAAGAGCTTCAAACA    14938       AAA      _
                                 TGTTTGA   AGCTCTT GCAA
                                 |||||||   ||||||| ||||
                                 ACAAACT   TCGAGAA CGTT
                                     ___      A
GAM587  RAB27B    3'  TGAGGCCCTTTCAAACAT    16046         AA  T
                                 ATGTTTGAAA  GC CTTG
                                 ||||||||||  || ||||
                                 TACAAACTTT  CG GAGT
                                      CC  _
GAM587  SMCR5     3'  AGTGCTCCTCAAACATTA    59245         AAA   T
                                 TAATGTTTGA   AGC CT
                                 ||||||||||   ||| ||
                                 ATTACAAACT   TCG GA
                                      CC_   T
GAM587  WAP1      3'  TTGCAGAGTTTTCCAAACAT   80342        AA       T
                                 ATGTTTG  AAAGCTCT GCAA
                                 |||||||  |||||||| ||||
                                 TACAAAC  TTTTGAGA CGTT
                                    C_       _
GAM587  LOC126282 3'  TGTAGCAGCTGTTTCAAACA   74972         A    C
                                 TGTTTGAAA AGCT TTGCA
                                 ||||||||| |||| |||||
                                 ACAAACTTT TCGA GATGT
                                      G    C
GAM587  LOC153856 3'  CAAGAGCTTTTTCTTGCA    81873     TT
                                 TGT  GAAAAAGCTCTTG
                                 |||  ||||||||||||
                                 ACG  CTTTTTCGAGAAC
                                   TT
GAM587  LOC154877 3'  TTGCAAGAGCCTTCAGCA    87586      T   AAA
                                 TGTT GAA   GCTCTTGCAA
                                 |||| |||   ||||||||||
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                                ACGA CTT   CGAGAACGTT
                                  _  C__
GAM587  LOC51759  3'  TGCTGGATTTTTCAAGCA    73175          GC   T
                                TGTTTGAAAAA  TCT GCA
                                ||||||||||  ||| |||
                                ACGAACTTTTT  AGG CGT
                                      __   T
GAM588  A1BG     3'  GGCTGGTCTCCAACTC      56293     C       AG
                                GAG TGGAGACCA  GCC
                                ||| |||||||||  |||
                                CTC ACCTCTGGT  CGG
                                  A       __
GAM588  ADRA2A   3'  GCCCTCACAGCTCTTC      7292          _  ACCAA
                                GAAGAGCTG GAG     GGC
                                ||||||||| |||     |||
                                CTTCTCGAC CTC     CCG
                                     A  _____
GAM588  CA4      3'  GCCTCTCTGTTGCCTCAGCTCT 7391        _ A_   CA__
                                AGAGCTG G  GAC    AGGC
                                ||||||| |  |||    ||||
                                TCTCGAC C  TTG    TCCG
                                    T CG   TCTC
GAM588  CIAS1    5'  CGGCCTTGGCTAACTTTTC    18096       CTGG  A
                                GAAGAG    AG CCAAGGCCG
                                ||||||    || |||||||||
                                CTTTTC    TC GGTTCCGGC
                                   AA__  _
GAM588  DVL1     3'  GCCTGGCTGCTCCAGCTC     60058         A__   A
                                GAGCTGGAG   CCA GGC
                                |||||||||   ||| |||
                                CTCGACCTC   GGT CCG
                                     GTC  _
GAM588  RXRA     3'  GCCCTGACCTTCGGTTTTCCGA 12920     A         AC  A
                                TCG AGAGCTGGAG  CA GGC
                                ||| ||||||||||  || |||
                                AGC TTTTGGCTTC  GT CCG
                                  C         CA  C
GAM588  TRIM14   3'  CCTTAGGCCCAGCTTTC     29510    A      AGA  _
                                GA GAGCTGG   CC AAGG
                                || |||||||   || ||||
                                CT TTCGACC   GG TTCC
                                  _      C__  A
GAM588  TRIM9    5'  CGGCCTTGGCCTCCCAAAGT   31448     ___    A
                                GCT   GGAG CCAAGGCCG
                                |||   |||| |||||||||
                                TGA   CCTC GGTTCCGGC
                                  AAC    C
GAM588  VIPR2    3'  GCCTTGCCCAGCTTTC      14067    A      AGAC
                                GA GAGCTGG    CAAGGC
                                || |||||||    ||||||
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                                CT TTCGACC    GTTCCG
                                 _      C___
GAM588  BLCAP     3'  CGGCCTTGATCCCCTTGATAGA 22942    GAA_   CT  A  C
                                TC    GAG  GG GA CAAGGCCG
                                ||    |||  || || ||||||||
                                AG    TTC  CC CT GTTCCGGC
                                 ATAG   __ _  A
GAM588  DBR1      3'  GGCTGGTCTCCAACTC      33067     C        AG
                                GAG TGGAGACCA  GCC
                                ||| |||||||||  |||
                                CTC ACCTCTGGT  CGG
                                  A        __
GAM588  FLJ10535  3'  GGCTGGTCTCCAACTC      36751     C        AG
                                GAG TGGAGACCA  GCC
                                ||| |||||||||  |||
                                CTC ACCTCTGGT  CGG
                                  A        __
GAM588  HRD1      3'  GCCTTCCTCTCCAACTCTTC   70151       C     CC
                                GAAGAG TGGAGA  AAGGC
                                |||||| ||||||  |||||
                                CTTCTC ACCTCT  TTCCG
                                   A     CC
GAM588  HRIHFB2122 3'  CCCTGGTCCCCCTCTGTC    23843    _    CT  A     A
                                GA AGAG  GG GACCA GG
                                || ||||  || ||||| ||
                                CT TCTC  CC CTGGT CC
                                 G    C_  _     C
GAM588  KIAA1052  5'  CGGCCTTGACCTCCTGTGCTC  30940      T__    AC
                                GAGC   GGAG  CAAGGCCG
                                ||||   ||||  ||||||||
                                CTCG   CCTC  GTTCCGGC
                                  TGT    CA
GAM588  RAB39     3'  GGCTGGTCTCCAACTCCTCG   77123     A   C        AG
                                CGA GAG TGGAGACCA  GCC
                                ||| ||| |||||||||  |||
                                GCT CTC ACCTCTGGT  CGG
                                  C   A        __
GAM588  SPINT1    5'  CGGCCGAGCCCCAGCTCTCCGA 63332     A       AGACCAA
                                TCG AGAGCTGG       GGCCG
                                ||| ||||||||       |||||
                                AGC TCTCGACC       CCGGC
                                  C        CCGAG__
GAM588  LOC116411 5'  CGGGCTGGTCTCCAGCTC    74299            A G
                                GAGCTGGAGACCA G CCG
                                |||||||||||||| | |||
                                CTCGACCTCTGGT C GGC
                                          _ G
GAM588  LOC124460 3'  GCCCTGTGTGCTCTCCAGCTC  76564           ___ _  A
                                GAGCTGGAGA   C CA GGC
                                ||||||||||   | || |||
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                                CTCGACCTCT   G GT CCG
                                     CGT T  C
GAM588  LOC129880 3'  CGGGCTGGTCTCCAGCTC    75405           A G
                                GAGCTGGAGACCA G CCG
                                |||||||||||| | |||
                                CTCGACCTCTGGT C GGC
                                       _ G
GAM588  LOC152220 3'  GGCTGGTCTCCAACTC      86766     C       AG
                                GAG TGGAGACCA  GCC
                                ||| |||||||||  |||
                                CTC ACCTCTGGT  CGG
                                  A       __
GAM588  LOC154562 3'  GCCTTGGTCCCTAAGCCTC    81997     _ __  A
                                GAG CT  GG GACCAAGGC
                                ||| ||  || |||||||||
                                CTC GA  CC CTGGTTCCG
                                  C  AT  _
GAM588  LOC168451 5'  CGGCCCCGGTCTCCAGGGGCCT 83585     _____       AA
            C                    GAG   CTGGAGACC  GGCCG
                                |||   |||||||||  |||||
                                CTC   GACCTCTGG  CCGGC
                                  CGGG       CC
GAM588  LOC199958 3'  CCTTTACAGTTCCAGCTCCTCG 91491      A       ACC__
            G                    TCGA GAGCTGGAG     AAGG
                                |||| |||||||||     ||||
                                GGCT CTCGACCTT     TTCC
                                  C        GACAT
GAM588  LOC254100 3'  GGCTGGTCTCCAACTC      98158     C       AG
                                GAG TGGAGACCA  GCC
                                ||| |||||||||  |||
                                CTC ACCTCTGGT  CGG
                                  A       __
GAM588  LOC92697  5'  GGCTGGTCTCCAGCTC      70814           AG
                                GAGCTGGAGACCA  GCC
                                ||||||||||||  |||
                                CTCGACCTCTGGT  CGG
                                       __
GAM589  ACAA1     3'  TGGATGAGAAGTGCAATGGGCA 9636          T  _ C  C
                                TGCCCATTGC CT C CA TCCA
                                |||||||||| || | || ||||
                                ACGGGTAACG GA G GT AGGT
                                     T  A A  _
GAM589  CALB2     5'  GGGAGCGGGAGCGGTG      9981        TC    A    A
                                CATTGC  TCCC CTCC C
                                ||||||  |||| |||| |
                                GTGGCG  AGGG GAGG G
                                   __    C    C
GAM589  DAZ       3'  CGTGGAATGGTAGCAATGGG   83005         CTC   C
                                CCCATTGCT   CCA TCCACG
                                |||||||||   ||| ||||||
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                                GGGTAACGA   GGT AGGTGC
                                     T__   A
GAM589  FXYD6    3'  GTAGGGTAAGAGCACGGGCA  42095      AT    __  _
                                TGCCC  TGCTCT  CCC AC
                                |||||  ||||||  ||| ||
                                ACGGG  ACGAGA  GGG TG
                                   C_     AT   A
GAM589  MTR      3'  GTGAAGAGCAGTGAGCA     6025      C       CC
                                TGC CATTGCTCT  CAC
                                ||| |||||||||  |||
                                ACG GTGACGAGA  GTG
                                  A       A_
GAM589  PTPN18   3'  CGCAGAATGGAAACAGTGGGC  27649        CTCTC   C  CA
                                GCCCATTG    CCA TC  CG
                                ||||||||    ||| ||  ||
                                CGGGTGAC    GGT AG  GC
                                     AAA__   A  AC
GAM589  RORB     5'  CGCGGAGCGGGAGAGCGGC   23588     CATT      A   A
                                GCC    GCTCTCCC CTCC CG
                                |||    |||||||| |||| ||
                                CGG    CGAGAGGG GAGG GC
                                 _____       C   C
GAM589  SIX3     3'  CGAGGACAAGAGGGCAATGAGC 19439     C        CCAC   A
           A                     TGC CATTGCTCTC    TCC CG
                                |||  ||||||||||    ||| ||
                                ACG GTAACGGGAG    AGG GC
                                  A        AAC_   A
GAM589  ERAP140  5'  AGTAGATGCAGAGGGCA     75700      A   _   CCC
                                TGCCC TTGC TCT   ACT
                                |||||  |||| |||   |||
                                ACGGG GACG AGA   TGA
                                   A   T   ___
GAM589  KIAA1691 3'  TGAAGTGGGAGCGAGGC     94137     CA   TC      C
                                GCC  TTGC  TCCCACT CA
                                |||  ||||  ||||||| ||
                                CGG  AGCG  AGGGTGA GT
                                  __   __      A
GAM589  MAD4     3'  CGCAGAGTGGGAGAGGCTGCAG 22273     CCATT  _        CA
           CA                     TGC    GC TCTCCCACTC  CG
                                |||    || ||||||||||  ||
                                ACG    CG AGAGGGTGAG  GC
                                  ACGT_  G         AC
GAM589  MGC15438 3'  CGTGGAGTGGAAGCCTGGGGGC 52851      ATT_   CTC
                                GCCC    GCT   CCACTCCACG
                                ||||    |||   ||||||||||
                                CGGG    CGA   GGTGAGGTGC
                                  GGTC   A__
GAM589  PSR      3'  GAGTGGGAACGGTGTGCA    65786     C    CTC
                                TGC CATTG   TCCCACTC
                                ||| |||||   ||||||||
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                                ACG GTGGC   AGGGTGAG
                                  T    A__
GAM589  PTPN3    3'  GTGGGAAAGGAATGGGCA    12588        G  C
                                TGCCCATT CT TCCCAC
                                |||||||| || ||||||
                                ACGGGTAA GA AGGGTG
                                     G  A
GAM589  TRIP-Br2  5'  TGGAGCGGGAGTAGCTGAGG   29270    ATT  _    A
                                CC   GCT CTCCC CTCCA
                                ||   ||| ||||| |||||
                                GG   CGA GAGGG GAGGT
                                 AGT   T    C
GAM589  LOC142948 3'  TGGAGTAGGGCGGGAAGGGGCA 83781       ATTG   T  _
                                TGCCC    CTC CCC ACTCCA
                                |||||    ||| ||| ||||||
                                ACGGG    GGG GGG TGAGGT
                                   GAA_   C   A
GAM589  LOC147219 5'  GTGGTATGGGAGAGCAAAAGGC 85113      CA         CT
           A                     TGCC  TTGCTCTCCCA  CCAC
                                ||||  ||||||||||  ||||
                                ACGG  AACGAGAGGGT  GGTG
                                   AA          AT
GAM589  LOC196872 3'  CGTGGAGTGAGACCAGTGG    89156       C    CC
                                CCATTG TCTC  ACTCCACG
                                |||||| ||||  ||||||||
                                GGTGAC AGAG  TGAGGTGC
                                   C   __
GAM589  LOC197125 3'  TGGAGTGGGAGGGAGGCGCA   89246     _ ATTG
                                TGC CC    CTCTCCCACTCCA
                                ||| ||    ||||||||||||
                                ACG GG    GGGAGGGTGAGGT
                                  C  A___
GAM589  LOC221755 5'  CGCGGAGTAGGAGAGTAGG    94008    AT       C    A
                                CC  TGCTCTCC ACTCC CG
                                ||  |||||||| ||||| ||
                                GG  ATGAGAGG TGAGG GC
                                 __       A    C
GAM589  LOC253664 5'  CGCAGAGTGGGAGCAGCA     96464      _        CA
                                TGCT CTCCCACTC  CG
                                |||| |||||||||  ||
                                ACGA GAGGGTGAG  GC
                                   C        AC
GAM589  LOC253912 3'  CGTGGAGTGGAAGTCAGG     99207    AT  CT  C
                                CC  TG  CT CCACTCCACG
                                ||  ||  || ||||||||||
                                GG  AC  GA GGTGAGGTGC
                                 __ T_  A
GAM589  LOC57795  5'  GGAGCGGGAGAGCGTGGCG    69865      CAT        A
                                TGCC   TGCTCTCCC CTCC
                                ||||   ||||||||| ||||
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                                GCGG   GCGAGAGGG GAGG
                                  T__        C
GAM590  GNB1     3'  ACTTTTCCACCAGTGTATTTGA 10832         A   TATTT
            A                    TTCAAATA ACT     GAAAAGT
                                 |||||||| |||     |||||||
                                 AAGTTTAT TGA     CTTTTCA
                                    G   CCAC_
GAM590  RNGTT    3'  ACCTTTCAAATGAGTTACGTGA 15061      AATA          A
            A                    TTCA    AACTTATTTGAAA GT
                                 ||||    |||||||||||||| ||
                                 AAGT    TTGAGTAAACTTT CA
                                   GCA_           C
GAM590  WRB      3'  TTTAAGTAAGTTCTTTGAA    17330       TA
                                 TTCAAA  AACTTATTTGAA
                                 ||||||  ||||||||||||
                                 AAGTTT  TTGAATGAATTT
                                    C_
GAM590  ARTS-1   3'  ACTTTTCAAATCTAGTAATTTG 33606        AA   T_
            AA                    TTCAAAT  ACT  ATTTGAAAAGT
                                  |||||||  |||  ||||||||||||
                                  AAGTTTA  TGA  TAAACTTTTCA
                                     A_   TC
GAM590  FLJ12085 3'  ACTCTTGCAAAAAGTTTATTTG 43180           A   _  A
            AA                    TTCAAATAAACTT TTTG AA AGT
                                  |||||||||||||| |||| || |||
                                  AAGTTTATTTGAA AAAC TT TCA
                                        _    G  C
GAM590  LEPROTL1 3'  ACTTTTCAAATATAGTTTA   31699       _
                                 TAAACT TATTTGAAAAGT
                                 |||||| ||||||||||||
                                 ATTTGA ATAAACTTTTCA
                                    T
GAM590  LOC115207 3'  TTTCATGCAGTTTGTTTGAA   57402           TATT
                                 TTCAAATAAACT    TGAAA
                                 ||||||||||||    |||||
                                 AAGTTTGTTTGA    ACTTT
                                        CGT_
GAM590  LOC154084 5'  CTTTTCTAGTTTATTTGA     87379          TATTT
                                 TCAAATAAACT     GAAAAG
                                 ||||||||||||    ||||||
                                 AGTTTATTTGA     CTTTTC
                                        T_____
GAM590  LOC201696 3'  ACTTTTCAAATAAAATACTTGA 63809       A  AAC
            A                    TTCAA TA   TTATTTGAAAAGT
                                 ||||| ||   ||||||||||||
                                 AAGTT AT   AATAAACTTTTCA
                                    C  AA_
GAM590  LOC253912 3'  ACTTCTCAAATAAGAACGTGAA 99205      AATAAA        A
                                 TTCA      CTTATTTGA AAGT
                                 ||||      |||||||| ||||
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                                AAGT     GAATAAACT TTCA
                                  GCAA__       C
GAM591  CDH12    3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM591  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                  AC         G
GAM591  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT    98090      T    AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||     ||||||
                                TGGTG GGGT     TTATTC
                                  _    GTCA_
GAM591  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
          A                      TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM591  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM591  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
          TA                     TACA    TCC    GAAGAATAAG
                                ||||    |||    ||||||||||
                                ATGT    AGG    TTTCTTATTC
                                  AAA_   ATTG
GAM591  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68742              _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                          G
GAM591  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM591  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748      CCA__
                                ACTC     AGAAGAATAAG
                                ||||     ||||||||||
                                TGAG     TCTTCTTATTC
                                  TACCG
GAM591  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                                CCA     CAAGAAGAATAAG
                                |||     ||||||||||||
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                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM591  OSBPL11  3' CTTAATTTCCCAAGAGTGGTG 43206       CCAA   AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                    AACC   A_
GAM591  YME1L1   3' TCATTCTTGATGTGGTGTA   58438       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                    TA_    A
GAM591  ZNF262   3' CTTATTTTGTTTGGGAGT    18723       A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                    G
GAM591  LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_    AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
                                ATGTGGTG   GGTTC   TGT
                                    CAA    GG__
GAM592  AGTR1    5' GCGCGCCGCTAGCAGCTCTGC  7301     AAACCA  G
                                GCA    GC TGGCGGCGCGC
                                |||    || ||||||||||
                                CGT    CG ATCGCCGCGCG
                                  CTCGA_ _
GAM592  AGTR1    5' GCGCGCCGCTAGCAGCTCTGC  17899    AAACCA  G
                                GCA    GC TGGCGGCGCGC
                                |||    || ||||||||||
                                CGT    CG ATCGCCGCGCG
                                  CTCGA_ _
GAM592  AGTR1    5' GCGCGCCGCTAGCAGCTCTGC  24794    AAACCA  G
                                GCA    GC TGGCGGCGCGC
                                |||    || ||||||||||
                                CGT    CG ATCGCCGCGCG
                                  CTCGA_ _
GAM592  AGTR1    5' GCGCGCCGCTAGCAGCTCTGC  49822    AAACCA  G
                                GCA    GC TGGCGGCGCGC
                                |||    || ||||||||||
                                CGT    CG ATCGCCGCGCG
                                  CTCGA_ _
GAM592  DNAH9    5' GTCTGCCATGGTTTTACA    17411    C     GCG    C
                                TG AAAACCA   TGGCGG GC
                                || |||||||   |||||| ||
                                AC TTTTGGT   ACCGTC TG
                                 A     ____    _
GAM592  FBXL5    5' GCGCGCCGCCTCTGCCCCGC  25136    AAAAC   CGT
                                GC    CAG   GGCGGCGCGC
                                ||    |||   ||||||||||
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                              CG    GTC  CCGCCGCGCG
                               CCCC_  T__
GAM592  FBXL5    5' GCGCGCCGCCTCTGCCCCGC  54318   AAAAC  CGT
                              GC    CAG  GGCGGCGCGC
                              ||    |||  ||||||||||
                              CG    GTC  CCGCCGCGCG
                               CCCC_  T__
GAM592  MAF      5' CGCGCCGCCCTGCCTGCA    19309     AAACCA  T
                              TGCA     GCG GGCGGCGCG
                              ||||     ||| |||||||||
                              ACGT     CGT CCGCCGCGC
                                C_____  C
GAM592  RAB26    5' CGCGCCGCCCAACGGGCCTTGC 27601      AA  AGCGT
           A                   TGCAA  CC    GGCGGCGCG
                              |||||  ||    |||||||||
                              ACGTT  GG    CCGCCGCGC
                                 CC  GCAAC
GAM592  RPS18    5' CGCCGCCGCTTGTGCTGCA   42881     AA  C   GT
                              TGCA  AC AGC  GGCGGCG
                              ||||  || |||  |||||||
                              ACGT  TG TCG  CCGCCGC
                                CG  T   __
GAM592  ABIN-2   5' GCGCAGCTGCCGCGCTCTGCA  44460     AAACC        _
                              TGCA    AGCGTGGCGGC GCGC
                              ||||    |||||||||||| ||||
                              ACGT    TCGCGCCGTCG CGCG
                                C____         A
GAM592  ADAMTS18 5' GCGCGCCGCCCGTGCGCT    58169      ___
                              AGCGT   GGCGGCGCGC
                              |||||   ||||||||||
                              TCGCG   CCGCCGCGCG
                                 TGC
GAM592  HBOA     3' CTGCAGACGCTGGTTCTG    23930    A       G_
                              CA AACCAGCGT  GCGG
                              || |||||||||  ||||
                              GT TTGGTCGCA  CGTC
                               C        GA
GAM592  KIAA0649 5' GCGGAGCGCGCTGGCCCTGCA  29713     AAA      G GG
                              TGCA   CCAGCGTG C  CGC
                              ||||   |||||||| |  |||
                              ACGT   GGTCGCGC G  GCG
                                CCC       _ AG
GAM592  SPRY4    3' GCTGTGGCCACGCTGGTT    49019          G  _
                              AACCAGCGTGGC GC GC
                              |||||||||||| || ||
                              TTGGTCGCACCG TG CG
                                     G  T
GAM592  URKL1    5' GCGCGCCGCCCGGCCAGGCCCG 35794     AAAA  A_  GT
           CA                   TGC   CC  GC  GGCGGCGCGC
                              |||   ||  ||  ||||||||||
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                                ACG   GG  CG  CCGCCGCGCG
                                  CCC_  AC  GC
GAM592  LOC145813 5'  GCCCACGCTGGTCTTG     84509     A        CG
                                CAA ACCAGCGTGG  GC
                                ||| ||||||||||  ||
                                GTT TGGTCGCACC  CG
                                  C        __
GAM592  LOC148697 3'  GCCACGCTGTGTCTTGCA    79677      A  _
                                TGCAA AC CAGCGTGGC
                                ||||| || |||||||||
                                ACGTT TG GTCGCACCG
                                   C  T
GAM592  LOC205095 3'  CGCCACCAGTGGCTTCTGC   92383     A  _  G G   C
                                GCA AA CCA C TGG GGCG
                                ||| || ||| | ||| ||||
                                CGT TT GGT G ACC CCGC
                                  C  C  _ _  A
GAM592  LOC221143 5'  GCGCGCCGCCGAGGCGTTTTG  95215       CA  G_
                                CAAAAC  GC  TGGCGGCGCGC
                                ||||||  ||  ||||||||||
                                GTTTTG  CG  GCCGCCGCGCG
                                   __  GA
GAM592  LOC221296 3'  GCGCGCCGCCACGCCCGG    93610    A_
                                CC  GCGTGGCGGCGCGC
                                ||  ||||||||||||||
                                GG  CGCACCGCCGCGCG
                                 CC
GAM592  LOC255391 5'  GCGGGCACGCTGGTCTTGC   99457     A       G GG
                                GCAA ACCAGCGTG C  CGC
                                |||| ||||||||| |  |||
                                CGTT TGGTCGCAC G  GCG
                                  C       _ G_
GAM592  LOC255452 3'  GCCGCCACGCGGGCTCCGCA  99395     AAAA  A
                                TGC   CC GCGTGGCGGC
                                |||   || ||||||||||
                                ACG   GG CGCACCGCCG
                                  CCTC  G
GAM593  ABCA3    5'  GTGTTCCCAAACCTCAGGGT   8446          CTGCC
                                GCCCTGGGGTTT    CGC
                                ||||||||||||    |||
                                TGGGACTCCAAA    GTG
                                      CCCTT
GAM593  ACPT     3'  GTGCCTGCGGGCCTTGGGG   53521     TG   TT   CC
                                CCC  GGGT  CTGC  GCAC
                                |||  ||||  ||||  ||||
                                GGG  TCCG  GGCG  CGTG
                                  GT   __   TC
GAM593  ACPT     3'  GTGCCTGCGGGCCTTGGGG   53522     TG   TT   CC
                                CCC  GGGT  CTGC  GCAC
                                |||  ||||  ||||  ||||
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                                GGG  TCCG  GGCG  CGTG
                                  GT   __    TC
GAM593  ADAM12   3'  TGCAGACAGGAATCTTAAGGT  14425     C         CCC   C
                                GCC TGGGGTTTCTG   GCA
                                ||| ||||||||||   |||
                                TGG ATTCTAAGGAC   CGT
                                  A         AGA   T
GAM593  ADAM15   3'  GTGTCTTAAGACTCCGGGCA   15104       T      CTGCC
                                TGCCC GGGGTTT    CGC
                                ||||| |||||||    |||
                                ACGGG CCTCAGA    GTG
                                   _      ATTCT
GAM593  ADAM19   3'  GTGTCTGGGATCCAGGGCA   53844         GT    CC
                                TGCCCTGGG  TTCTG  CGC
                                |||||||||  |||||  |||
                                ACGGGACCT  AGGGT  GTG
                                     __    CT
GAM593  ADAMTS9  3'  GTCTACCAGTGACCTCAGGGCA 40045           T   CCC_  AC
                                TGCCCTGGGGTT CTG    GC
                                |||||||||||| |||    ||
                                ACGGGACTCCAG GAC    TG
                                      T   CATC
GAM593  ADCY3    3'  GCATAGGGGTCTTAGGCA    15744     C    TT    CCC
                                TGCC TGGGG  TCTG   GC
                                |||| |||||  ||||   ||
                                ACGG ATTCT  GGAT   CG
                                  _    GG    A__
GAM593  ADCY6    5'  GGGCGGGGGCCCAGGGCA    40960         G TT
                                TGCCCTGGG T  CTGCCC
                                |||||||||  |  ||||||
                                ACGGGACCC G  GGCGGG
                                     _ GG
GAM593  ADCY8    5'  GTGCGTTTCAGAGCTCCAGGGT 8504           T   CC_
                                GCCCTGGGGTT CTG   CGCAC
                                |||||||||| |||   |||||
                                TGGGACCTCGA GAC   GCGTG
                                      _   TTT
GAM593  ADCY9    3'  GTGTGCCCAGGCCTCGGGG    8508         TT   CC
                                CCCTGGGGT  CTG  CGCAC
                                |||||||||  |||  |||||
                                GGGGCTCCG  GAC  GTGTG
                                     __    CC
GAM593  AGPAT2   3'  GTGCAGCTGGGCTCCAGGGT   22182           CT  CC
                                GCCCTGGGGTTT  GC  GCAC
                                ||||||||||||  ||  ||||
                                TGGGACCTCGGG  CG  CGTG
                                      T_  A_
GAM593  AKAP2    3'  GTGTGTATTAAAATTCCAGAGT 24230     C        CTGCC
                                GC CTGGGGTTT     CGCAC
                                || |||||||||     |||||
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                                TG GACCTTAAA    GTGTG
                                 A       ATTAT
GAM593  AKT1    5'  AGCGTCGCGGGAGCCTCGGGCA 18960      T       C_  AC
                                TGCCC GGGGTTTCTGC  CGC
                                ||||| ||||||||||  |||
                                ACGGG CTCCGAGGGCG  GCG
                                   _        CT   AG
GAM593  ANKRD3  3'  GTGATGAAGCCCCAGGCGT   40563   _       TGCC
                                GC CCTGGGGTTTC   CGC
                                || ||||||||||   |||
                                TG GGACCCCGAAG   GTG
                                 C        TA__
GAM593  AOX1    5'  GTGCCGCCGGGTCCCAGG    8573       TT   CCC
                                CCTGGGG  TCTG   GCAC
                                |||||||  ||||   ||||
                                GGACCCT  GGGC   CGTG
                                   __   CGC
GAM593  AREG    5'  GCCCCAGAGGTCCCGGGACA  9764    C    GT    CCC
                                TG CCTGGG  TTCTG   GC
                                || ||||||  |||||   ||
                                AC GGGCCC  GAGAC   CG
                                 A     TG    CC_
GAM593  ARF3    3'  GTGTGGCCAGGGCCCTGGGTA  9779      T    T   C
                                TGCCC GGGGTT CTG CCGCAC
                                ||||| |||||| ||| ||||||
                                ATGGG TCCCGG GAC GGTGTG
                                   _     _  C
GAM593  ARF3    3'  GTGTGTTAGGGACCCAGGGCA  9780         G TT   CC
                                TGCCCTGGG T  CTG  CGCAC
                                |||||||||  |  |||  |||||
                                ACGGGACCC A  GAT  GTGTG
                                     _ GG   T_
GAM593  ARHGEF7  3'  GTGCACTCAGGACCACAGGGCA 15325       G    T   CCC
                                TGCCCTG GGTT CTG   GCAC
                                ||||||| |||| |||   ||||
                                ACGGGAC CCAG GAC   CGTG
                                   A    _   TCA
GAM593  ATP5G1   5'  GTGGGCCAAGCAGGGGTTGCAG 18980       G  TT  _____     AC
           GGCA                 TGCCCTG GG  TCT    GCCCGC
                                ||||||| ||  |||    ||||||
                                ACGGGAC TT  GGA    CGGGTG
                                   G  GG   CGAAC
GAM593  B3GNT3   3'  GTGTGGGCAGAGGAGGGAGGCA 27305     _ GGGG
                                TGCC CT    TTTCTGCCCGCAC
                                |||| ||    ||||||||||||
                                ACGG GG    GGAGACGGGTGTG
                                  A  GA__
GAM593  B4GALT1  3'  GTGTGTGGATTCCAGGGCA   9472          TT  TG C
                                TGCCCTGGGG  TC  C CGC
                                ||||||||||  ||  | |||
```

```
                                ACGGGACCTT  AG  G GTG
                                      __  GT T
GAM593  BACH2    3'  GCATTTGGGAGCTTCAGG    41785          CCC
                                CCTGGGGTTTCTG   GC
                                ||||||||||||   ||
                                GGACTTCGAGGGT   CG
                                      TTA
GAM593  BAP1     5'  GTGTGGGACTGAGGGGCCCCGG 17398        TT  G___
           GG                    CCCTGGGGT  CT    CCCGCAC
                                |||||||||  ||   |||||||
                                GGGGCCCCG  GA    GGGTGTG
                                     GG  GTCA
GAM593  BAZ2A    3'  GCAGCAGAGACCCTGGAGCA   26511     C TG        CC
                                TGC C  GGGTTTCTGC  GC
                                ||| |  ||||||||||  ||
                                ACG G  CCCAGAGACG  CG
                                  A GT         A_
GAM593  BCL2     3'  GTGCGGGTGGGCTCCTGGGCA  7240       T     TT TG
                                TGCCC GGGGT  C  CCCGCAC
                                ||||| |||||  |  |||||||
                                ACGGG CCTCG  G  GGGCGTG
                                   T     __ GT
GAM593  BCL7A    3'  GTGCAGGGGGACCTTAGGCA   40992      C     TT TG  C
                                TGCC TGGGGT  C  CC GCAC
                                |||| ||||||  |  || ||||
                                ACGG ATTCCA  G  GG CGTG
                                   _     GG __  A
GAM593  BCL7A    3'  GTGGCCTCAAGGGCTCCCAGGG 40993         _   TC  C__    AC
           CA                    TGCCCTGGG GTT  TG   CCGC
                                |||||||||  |||  ||   ||||
                                ACGGGACCC CGG  AC   GGTG
                                     T   GA  TCC
GAM593  BDKRB2   3'  GTGGAGGAGGCCTGGGGGCA   7115        G       GC
                                TGCCCT GGGTTTCT  CCGC
                                ||||||  ||||||||  ||||
                                ACGGGG TCCGGAGG  GGTG
                                   G       A_
GAM593  BIN1     3'  GTGTGCCTGGCCGCAGGGC    16290       G    TCT  C
                                GCCCTG GGTT   GC CGC
                                ||||||  ||||   || |||
                                CGGGAC CCGG   CG GTG
                                   G    TC_  T
GAM593  BIN3     3'  GCACCAGGAGCCCTAGGCA    38577      C         CCC
                                TGCC TGGGGTTTCTG   GC
                                ||||  ||||||||||   ||
                                ACGG ATCCCGAGGAC   CG
                                   _         CA_
GAM593  BYSL     5'  GTGCGGGCGGGGGTCCGGG    15763     TG   TT
                                CCC  GGG  TCTGCCCGCAC
                                |||  |||  ||||||||||
```

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                                GGG  CCT  GGGCGGGCGTG
                                  __  GG
GAM593  C18orf2  3'  GTGGAGGGAGCCCTGGGT    49462     T       GC
                                GCCC GGGGTTTCT  CCGC
                                |||| |||||||||  ||||
                                TGGG TCCCGAGGG  GGTG
                                  _       A_
GAM593  C1orf6   3'  GTGGGAACTGTTGGAAATTCCA 39697            _______    AC
           GGGTA                  TGCCCTGGGGTTTCTG     CCCGC
                                |||||||||||||||     |||||
                                ATGGGACCTTAAAGGT     GGGTG
                                        TGTCAA
GAM593  C20orf1  5'  GTGCGAGCAGGGGCTTCGGGC  25053     T    TT   C
                                GCCC GGGGT  CTGC CGCAC
                                |||| |||||  |||| |||||
                                CGGG CTTCG  GACG GCGTG
                                  _    GG   A
GAM593  C21orf2  3'  GTGGTCTGGAGGTTCTAGGC   18206    C   GG    C_   AC
                                GCC TGG  TTTCTG  CCGC
                                ||| |||  ||||||  ||||
                                CGG ATC  GGAGGT  GGTG
                                  _  TT     CT
GAM593  CACNA1C  3'  GCGGCGAGGGTCCCGGGGC   7400        GT TC   C
                                GCCCTGGG  T  TGCC GC
                                ||||||||  |  |||| ||
                                CGGGGCCC  G  GCGG CG
                                     TG GA   _
GAM593  CACNA1S  3'  GTGGGGAAGTTGCTGGGGT   5362      GG   TT  G_
                                GCCCT  GGT  CT  CCCGC
                                |||||  |||  ||  |||||
                                TGGGG  TCG  GA  GGGTG
                                  __  TT  AG
GAM593  CALCB    5'  GTGTGGTGTTCATCCCGGGTCG 88960    C      TTCT  _
                                TG CCTGGGGGT   GC CCGCAC
                                || ||||||||   || ||||||
                                GC GGGCCCTA   TG GGTGTG
                                 T      CT__  T
GAM593  CARD10   3'  GCCTATGGGAGTCCCGGGACA  28038    C    GT    CCC
                                TG CCTGGG  TTCTG   GC
                                || ||||||  |||||   ||
                                AC GGGCCC  AGGGT   CG
                                 A     TG    ATC
GAM593  CASP10   3'  GTGAACTGGAATGCCTTGGGGC 53205     TG   _    CC_  AC
                                GCCC  GGGT TTCTG   CGC
                                ||||  |||| |||||   |||
                                CGGG  TCCG AAGGT   GTG
                                  GT   T    CAA
GAM593  CASP10   3'  GTGAACTGGAATGCCTTGGGGC 53261     TG   _    CC_  AC
                                GCCC  GGGT TTCTG   CGC
                                ||||  |||| |||||   |||
```

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                                CGGG  TCCG AAGGT   GTG
                                  GT    T    CAA
GAM593  CASP4    5'  GTGTTGGAATCCCTGGGCA   8725       T      TGCC
                                TGCCC GGGGTTTC   CGC
                                ||||| ||||||||   |||
                                ACGGG CCCTAAGG   GTG
                                   T       TT__
GAM593  CASP4    5'  GTGTTGGAATCCCTGGGCA   8726       T      TGCC
                                TGCCC GGGGTTTC   CGC
                                ||||| ||||||||   |||
                                ACGGG CCCTAAGG   GTG
                                   T       TT__
GAM593  CCR2     3'  GTGCCCAGGAACCTCAGGGC  7223             CCC
                                GCCCTGGGGTTTCTG  GCAC
                                ||||||||||||||  ||||
                                CGGGACTCCAAGGAC  CGTG
                                         C__
GAM593  CDH6     3'  GTGCAGTCATCAGAAATTCCAG 18212    C         CCC___
          CGTA                    TGC CTGGGGTTTCTG    GCAC
                                ||| ||||||||||||    ||||
                                ATG GACCTTAAAGAC     CGTG
                                  C          TACTGA
GAM593  CDK10    3'  GTTGGCTGTGGGGACCCCAGG  14793        TT ___  C  AC
                                CCTGGGGT  CT   GCC GC
                                ||||||||  ||   ||| ||
                                GGACCCCA  GG   CGG TG
                                     GG  TGT   T
GAM593  CDK10    3'  GTTGGCTGTGGGGACCCCAGG  14794        TT ___  C  AC
                                CCTGGGGT  CT   GCC GC
                                ||||||||  ||   ||| ||
                                GGACCCCA  GG   CGG TG
                                     GG  TGT   T
GAM593  CDK10    3'  GTTGGCTGTGGGGACCCCAGG  54836        TT ___  C  AC
                                CCTGGGGT  CT   GCC GC
                                ||||||||  ||   ||| ||
                                GGACCCCA  GG   CGG TG
                                     GG  TGT   T
GAM593  CDK7     5'  GTGTTGGAGGCTTTAAGGTA  10157     C        GCC
                                TGCC TGGGGTTTCT   CGC
                                |||| ||||||||||   |||
                                ATGG ATTTCGGAGG   GTG
                                  A        TT_
GAM593  CEP2     3'  GCACCCAGGAGCCCCAGGTCG 23245    C          CCC
                                TG CCTGGGGTTTCTG   GC
                                || ||||||||||||   ||
                                GC GGACCCCGAGGAC   CG
                                 T          CCA
GAM593  CEP2     5'  GTTGGCAGAAATCCTGGG    23247    TG        C
                                CC  GGGTTTCTGCC GC
                                ||  |||||||||| ||
```

```
                                GG  CCTAAAGACGG TG
                                 GT         T
GAM593  CHST1    3'  GTGCGGGTGGGGGGCGGGAGGCG 14703     _  GGG  TT TG
             CA                   TGC CCT   GT  C  CCCGCAC
                                  ||| |||   ||  |  |||||||
                                  ACG GGA   CG  G  GGGCGTG
                                    C   GGG  GG GT
GAM593  CLASP1   3'  GTGCAGCCGGTCCTCGGGGCA  65895         TT  T  CC
                                  TGCCCTGGGG  TC GC  GCAC
                                  ||||||||||  || ||  ||||
                                  ACGGGGCTCC  GG CG  CGTG
                                        T_  C  A_
GAM593  CLASP1   5'  GTTAGGAGACTCCAGGAGCA   65896     _         GCCC
                                  TGC CCTGGGGTTTCT    GC
                                  ||| ||||||||||||    ||
                                  ACG GGACCTCAGAGG    TG
                                    A          AT__
GAM593  CNK      3'  GTGCCTCACTGGGGGCTTTGGG 15805      T    TT  GCCC__
             C                    GCCC GGGGT  CT     GCAC
                                  |||| |||||  ||     ||||
                                  CGGG TTTCG  GG     CGTG
                                    _    GG  TCACTC
GAM593  CNR1     3'  GTGCAGATGAAGGCTCAGGGT  32721        G   TGCCC
                                  GCCCTGGG TTTC     GCAC
                                  |||||||| ||||    ||||
                                  TGGGACTC GAAG     CGTG
                                      G   TAGA_
GAM593  CORO1C   5'  GCAGCGGGGACTTCGGCGGC   27506     _     TT   CC
                                  GCC CTGGGGT  CTGC  GC
                                  ||| |||||||  ||||  ||
                                  CGG GGCTTCA  GGCG  CG
                                    C      GG   A_
GAM593  CRIM1    3'  GCTGTAGAGATATTTGGGGT   33603      TG  _      CC
                                  GCCC  GG GTTTCTGC  GC
                                  ||||  || ||||||||  ||
                                  TGGG  TT TAGAGATG  CG
                                    GT  A       T_
GAM593  CRKL     5'  GCCCGAGAACCCCGGGGT    19045          TC  CCC
                                  GCCCTGGGGTT  TG   GC
                                  ||||||||||  ||   ||
                                  TGGGGCCCCAA  GC   CG
                                        GA  C__
GAM593  CRKL     5'  GTGTGGCGGCCCCGGAGCA   19046     C     TTT    _
                                  TGC CTGGGG   CTGCC CGC
                                  ||| ||||||   ||||| |||
                                  ACG GGCCCC   GGCGG GTG
                                    A      ___     T
GAM593  CTNS     5'  GTGCGGAGTGCGGGGCTCCGGG 18222         TT _   _
             G                    CCCTGGGGT  C TGC CCGCAC
                                  |||||||||  | ||| ||||||
```

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                                GGGGCCTCG  G GTG GGCGTG
                                     GG C   A
GAM593  CTPS    3'  GTGCTGGGAACCTCAGGGTA  90000          TCTG  _
                                TGCCCTGGGGTT   CCC GCAC
                                ||||||||||||   ||| ||||
                                ATGGGACTCCAA   GGG CGTG
                                     _____  T
GAM593  CYBB    3'  GTCTCCCAGAATCCTCAGGGCA 76852         T    CCC_  AC
                                TGCCCTGGGG TTCTG   GC
                                |||||||||| |||||   ||
                                ACGGGACTCC AAGAC   TG
                                      T    CCTC
GAM593  CYP19   5'  GTGTCAGAAACCCTGTGGT   5441     C        CC
                                GCC TGGGGTTTCTG  CGC
                                ||| ||||||||||  |||
                                TGG GTCCCAAAGAC  GTG
                                  T         T_
GAM593  CYP51   5'  GTTTAGTAGGAGACCTGGGGCA 7622      TG  G     CC_  AC
                                TGCCC  GG TTTCTGC   GC
                                |||||  || |||||||   ||
                                ACGGG  CC GAGGATG   TG
                                   GT  A      ATT
GAM593  DBN1    5'  GCTGCAGAGGCTCCGAGGC   56019    C         CC
                                GCC TGGGGTTTCTGC  GC
                                ||| ||||||||||||  ||
                                CGG GCCTCGGAGACG  CG
                                  A          T_
GAM593  DCTN1   5'  GTGTGGAGGCTCTAGGCA    15830    C       TG CC
                                TGCC TGGGGTTTC  C  GC
                                |||| |||||||||  |  ||
                                ACGG ATCTCGGAG  G  TG
                                  _       GT __
GAM593  DFFA    3'  GTGTGCCAAGGAAGCTCTGTGG 16597    C        GCC_
          C                      GCC TGGGGTTTCT    CGCAC
                                ||| ||||||||||    |||||
                                CGG GTCTCGAAGG    GTGTG
                                  T         AACC
GAM593  DIO3    3'  TGAGGGGAGTCCTAGGCA    9074     C    TTT  G   G
                                TGCC TGGGG   CT CCC CA
                                |||| |||||   || ||| ||
                                ACGG ATCCT   GA GGG GT
                                  _    ___  G   A
GAM593  DLG5    5'  GTGCGGCGGAGGAAGTCCCTGG 83822     T   GT    GC__
          GT                     GCCC GGG  TTCT    CCGCAC
                                |||| |||  ||||   ||||||
                                TGGG CCC  AAGG    GGCGTG
                                  T  TG    AGGC
GAM593  DPEP1   5'  GCACAGAGGCACCAGGGCA   16619        G      CCC
                                TGCCCTGG GTTTCTG   GC
                                |||||||| |||||||   ||
```

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                                ACGGGACC CGGAGAC   CG
                                    A      A__
GAM593  DUSP4    5'  GCCCTGGAGATTCTGGGC    9152      T       CCC
                                GCCC GGGGTTTCTG   GC
                                |||| ||||||||||   ||
                                CGGG TCTTAGAGGT   CG
                                  _        CC_
GAM593  DVL1     3'  GTGCCCAGGCCCCCAGGGT   60059        TT   CCC
                                GCCCTGGGG  TCTG   GCAC
                                |||||||||  ||||   ||||
                                TGGGACCCC  GGAC   CGTG
                                     C_    C__
GAM593  EDAR     5'  TGTGCCAGGTCCCAGGCA    42532     C    TT   CC
                                TGCC TGGGG  TCTG  CGCA
                                |||| |||||  ||||  ||||
                                ACGG ACCCT  GGAC  GTGT
                                  _    __    C_
GAM593  EDG8     5'  CCAGGGCGCAGACCTTGGGGC  79147     TG    C    GCAC
                                GCCC  GGGTTT TGCCC
                                ||||  |||||| |||||
                                CGGG  TCCAGA GCGGG
                                  GT     C    ACCA
GAM593  EFNB1    3'  GTGGGGAAACAGAGGCCCAGGG 16673       G    ____    AC
          T                      GCCCTGGG TTTCTG   CCCGC
                                |||||||| ||||||   |||||
                                TGGGACCC GGAGAC   GGGTG
                                   _     AAAG
GAM593  EGFL4    3'  GCAAAGGCAGAGGCCCTGGGGT 62466     TG       C__  AC
                                GCCC  GGGTTTCTGCC   GC
                                ||||  ||||||||||   ||
                                TGGG  CCCGGAGACGG   CG
                                  GT         AAA
GAM593  EGLN2    5'  GTGCTGAGGCCTTGTGGT    34520     C       T  CC
                                GCC TGGGGTTTC GC  GC
                                ||| ||||||||| ||  ||
                                TGG GTTCCGGAG CG  TG
                                  T       T  __
GAM593  EN2      5'  GTGCGGGCGGGGACGGCCGGGC 9269      T  G_  TT
                                GCCC GG  GT  CTGCCCGCAC
                                |||| ||  ||  ||||||||||
                                CGGG CC  CA  GGCGGGCGTG
                                  _ GG  GG
GAM593  EN2      5'  GTGCGGGCGGTGGCGGGC    9270      TGGG  TT
                                GCCC   GT  CTGCCCGCAC
                                ||||   ||  ||||||||||
                                CGGG   CG  GGCGGGCGTG
                                  ____  GT
GAM593  EP300    5'  GTGCGGCGCGGGGACCCCGGGC 9287      T    TT   _
                                GCCC GGGGT  CTGC CCGCAC
                                |||| |||||  |||| ||||||
```

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                                CGGG CCCCA  GGCG GGCGTG
                                  _    GG   C
GAM593  EP300   5' GTGGCAGGGGGCCCGGGGC  9288       G TT   C
                                GCCCTGGG T  CTGCC GC
                                |||||||| |  ||||| ||
                                CGGGGCCC G  GACGG TG
                                    G GG    _
GAM593  ERCC1   5' GTGCTGCGAGCCCTGGGC   10540    T     CT  CC
                                GCCC GGGGTTT  GC  GCAC
                                |||| |||||||  ||  ||||
                                CGGG TCCCGAG  CG  CGTG
                                  _     __ T_
GAM593  ESR1    3' GTGCCCTGGGATCCCTGGGGTA 5518      TG  TTTCTG  ___
                                TGCCC  GGG    CCC   GCAC
                                |||||  |||    |||   ||||
                                ATGGG  CCC    GGG   CGTG
                                   GT   TA____   TCC
GAM593  ESRRA   3' GTGTGTCCAGGCTCTGGGCA  16724     T    TT   CC
                                TGCCC GGGGT  CTG  CGCAC
                                ||||| |||||  |||  |||||
                                ACGGG TCTCG  GAC  GTGTG
                                  _    __   CT
GAM593  FAAH    3' GTGCTGAGGGGGCCCTGAGGCA 97239     CT    TT  GCCC
                                TGCC  GGGGT  CT   GCAC
                                ||||  |||||  ||   ||||
                                ACGG  TCCCG  GG   CGTG
                                  AG    GG  AGT_
GAM593  FACL6   5' GTGTCGGGGGGCTTCTGGGTA  31579     T   TTT  G   _
                                TGCCC GGGG   CT CCCG CAC
                                ||||| ||||   || |||| |||
                                ATGGG CTTC   GG GGGC GTG
                                   T   ___  G   T
GAM593  FANCE   3' GCTCCAGGAGGTCTGGGGTA  41899     TG  G    CCC
                                TGCCC  GG TTTCTG   GC
                                |||||  || ||||||   ||
                                ATGGG  CT GAGGAC   CG
                                   GT  G    CT_
GAM593  FBXL7   5' CTCTGGGCGGCCCCGGGGC   25494       TTT     CAC
                                GCCCTGGGG   CTGCCCG
                                |||||||||   |||||||
                                CGGGGCCCC   GGCGGGT
                                     ___      CTCC
GAM593  FBXL7   5' GTGCGGGGACCTCTCCAGGCCG 25498   C      TTTCTG
                                TG CCTGGGG     CCCGCAC
                                || |||||||     |||||||
                                GC GGACCTC     GGGCGTG
                                 C      TCCAG_
GAM593  FCRH1   3' GTTCTTCAGAGATCCTGGGGCA 54731     TG       CCC_  AC
                                TGCCC  GGGTTTCTG   GC
                                |||||  |||||||||   ||
```

```
                                ACGGG CCTAGAGAC  TG
                                  GT      TTCT
GAM593  FGF1    3' GTAAGCAGAGGCTTTGGGGT 53642    TG      CC
                                GCCC GGGTTTCTGC GC
                                |||| |||||||||| ||
                                TGGG TTCGGAGACG TG
                                  GT      AA
GAM593  FGF1    3' GTAAGCAGAGGCTTTGGGGT 53643    TG      CC
                                GCCC GGGTTTCTGC GC
                                |||| |||||||||| ||
                                TGGG TTCGGAGACG TG
                                  GT      AA
GAM593  FGFR2   3' GTTGGGGAGACCTCAGGG   5565        G C
                                CCCTGGGGTTTCT CC GC
                                |||||||||||| || ||
                                GGGACTCCAGAGG GG TG
                                      _ T
GAM593  FGFR3   3' GTGGAGGGAGGCCCCAGGG  5569        GC
                                CCCTGGGGTTTCT CCGC
                                |||||||||||| ||||
                                GGGACCCCGGAGG GGTG
                                    GA
GAM593  FLOT2   3' GCATGGGCAGGGGTTCTGGGTA 16799     T GG TT   __ AC
                                TGCCC GG T CTGCCC GC
                                ||||| || | |||||| ||
                                ATGGG TC G GACGGG CG
                                  _ TT GG   TA
GAM593  FMOD    3' GTCAGGAGACCCCAAGGCA  10674    C       GCCC
                                TGCC TGGGGTTTCT  GC
                                |||| |||||||||  ||
                                ACGG ACCCCAGAGG  TG
                                  A       AC__
GAM593  FOXD2   5' GTGTCCAGTCCTCAGGGCA  16792       TTT  CC
                                TGCCCTGGGG  CTG CGC
                                |||||||||  ||| |||
                                ACGGGACTCC  GAC GTG
                                    T__  CT
GAM593  FOXD2   5' TGCGGCGCTGTCGGGGCA  16794       GGTTTCT _
                                TGCCCTGG    GC CCGCA
                                ||||||||    || |||||
                                ACGGGGCT    CG GGCGT
                                  GT_____ C
GAM593  FRAP1   5' GCCGCGCGAACCTCAGGGCA 18273        C  CC
                                TGCCCTGGGGTTT TGC GC
                                |||||||||||| ||| ||
                                ACGGGACTCCAAG GCG CG
                                    C  C_
GAM593  FUT7    3' GTGTGGGTGGAAGGGCTGGGT 16807    T GG  TG
                                GCCC GG TTTC CCCGCAC
                                |||| || |||| |||||||
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```
                                TGGG TC  GAAG  GGGTGTG
                                  _ GG   GT
GAM593  GABPA   5' GTGCGGGCGGGGGCGACAGGGC 10750      GG  TT
                                GCCCTG  GT  CTGCCCGCAC
                                ||||||  ||  ||||||||||
                                CGGGAC  CG  GGCGGGCGTG
                                   AG  GG
GAM593  GADD45G 3' GTGGTGACGCCCCGGGGC   22957        T  TGC
                                GCCCTGGGGT TC   CCGC
                                ||||||||||  ||   ||||
                                CGGGGCCCCG AG   GGTG
                                      C  T__
GAM593  GCGR    3' GTGAGCAGAGGAGTCCAGGGC  5676       G_     C   AC
                                GCCCTGGG  TTTCTGC CGC
                                ||||||||  |||||||  |||
                                CGGGACCT  GGAGACG GTG
                                     GA      A
GAM593  GCNT3   3' GTGTGGGTGGGAGACCAGGGC  17645      GG    TG
                                GCCCTGG  TTTC  CCCGCAC
                                |||||||  ||||  |||||||
                                CGGGACC  GAGG  GGGTGTG
                                   A_   GT
GAM593  GGA1    3' TGTGGGGGCTCAAGGGTA    26280      G    TCTG
                                TGCCCT GGGTT    CCCGCA
                                ||||||  |||||   ||||||
                                ATGGGA CTCGG    GGGTGT
                                   A    _____
GAM593  GGA3    3' GTGGAACAGGGGCCCTGGGCA  26591     T    TT   C_
                                TGCCC GGGGT  CTG  CCGC
                                |||||  |||||  |||  ||||
                                ACGGG TCCCG  GAC  GGTG
                                  _    GG   AA
GAM593  GLDC    3' CTGTGGGAAATCCCAGGGCA   64895         CTG     C
                                TGCCCTGGGGTTT   CCCGCA
                                ||||||||||||   ||||||
                                ACGGGACCCTAAA   GGGTGT
                                      ___     CT
GAM593  GMPR    3' GCCTGGAGGCTTCGGGGC    92651          CCC
                                GCCCTGGGGTTTCTG   GC
                                ||||||||||||||   ||
                                CGGGGCTTCGGAGGT   CG
                                       C__
GAM593  GNA11   3' TGTTGCAGGCCCAGGGCA    10818       GTT    CC
                                TGCCCTGGG   TCTGC  GCA
                                |||||||||   |||||  |||
                                ACGGGACCC   GGACG  TGT
                                      ___    T_
GAM593  GNA15   5' GCCAGCAGGGGCCCGGGGGC  60591     G   TT   CC
                                GCCCT GGGT  CTGC  GC
                                |||||  ||||  ||||  ||
```

```
                                CGGGG CCCG  GACG  CG
                                  G   GG   AC
GAM593  GNAI1   3'  GTGGCAACTTAGGATTTTAGGG 10821          C____   C  AC
              T                  GCCCTGGGGTTT    TGCC GC
                                 ||||||||||||    |||| ||
                                 TGGGATTTTAGG    ACGG TG
                                       ATTCA   _
GAM593  GNB1    5'  TGTGGGCGCGTCAGGCCG    10840    C    G  TTCT
                                 TG CCTGG GT   GCCCGCA
                                 || ||||| ||   |||||||
                                 GC GGACT CG   CGGGTGT
                                  C    G  ____
GAM593  GPRC5B  3'  GTGGGTGGGATTCCAAGGT   33178    C     TT T
                                 GCC TGGGGT  C GCCCGC
                                 ||| ||||||  | ||||||
                                 TGG ACCTTA  G TGGGTG
                                   A     GG _
GAM593  GRAF    3'  GTGTGAACAGGAAACTTTAGGG 31246           GCC_
              TA                  TGCCCTGGGGTTTCT   CGCAC
                                  ||||||||||||||   |||||
                                  ATGGGATTTCAAAGG   GTGTG
                                        ACAA
GAM593  GTF2E2  5'  GTGCGGGCAGGCGGGGGC    10886     GGG  TT
                                 GCCCT   GT  CTGCCCGCAC
                                 |||||   ||  ||||||||||
                                 CGGGG   CG  GACGGGCGTG
                                   G__  __
GAM593  GUK1    3'  GTGGTTGGAACATCCTGGGGT  7805     TG   _   GC   AC
                                 GCCC  GGGT TTCT  CCGC
                                 ||||  |||| ||||  ||||
                                 TGGG  CCTA AAGG  GGTG
                                   GT   C   TT
GAM593  HADHA   3'  GTGTGCAGAATTCTAGGCA   5736     C     T   C
                                 TGCC TGGGGTT CTGC CGC
                                 |||| ||||||| |||| |||
                                 ACGG ATCTTAA GACG GTG
                                   _     _   T
GAM593  HCN4    5'  TGCGGCGGGAGCCCCGGG    19686          C   C
                                 CCTGGGGTTTCTGCC GCA
                                 |||||||||||||| |||
                                 GGGCCCCGAGGGCGG CGT
                                       _
GAM593  HDAC7A  3'  GTCTTTAGAGATCCTGTGGGCA 31835     _        CCC  AC
                                 TGCCC TGGGGTTTCTG   GC
                                 ||||| ||||||||||   ||
                                 ACGGG GTCCTAGAGAT   TG
                                   T         TTC
GAM593  HEXA    3'  GTGTGAATGGCGTTAGGGTA  6718        G   TCTGCC
                                 TGCCCTGG GTT     CGCAC
                                 |||||||| |||     |||||
```

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                                ATGGGATT CGG     GTGTG
                                    G   TAA___
GAM593  HIVEP1   5'  GTGAAGGAGGGATCCCAGGC   10923     C     TT  G  CG
                                GCC TGGGGT  CT CC  CAC
                                ||| ||||||  || ||  |||
                                CGG ACCCTA  GA GG  GTG
                                  _     GG  _  AA
GAM593  HKE4     3'  GTTGGTGGAGGCTTCAGGG   23713          TG  C
                                CCCTGGGGTTTC  CC GC
                                ||||||||||||  || ||
                                GGGACTTCGGAG  GG TG
                                      GT  T
GAM593  HMGA2    5'  GTGCTGGGCAGCTCCGGGGC   14456         TTT     _
                                GCCCTGGGG   CTGCCC GCAC
                                |||||||||   |||||| ||||
                                CGGGGCCTC   GACGGG CGTG
                                    ___      T
GAM593  HMGCS1   3'  GTGAGGTGCAAGACTTCAGGGT 10940           C  _  G
                                GCCCTGGGGTTT TGC CC CAC
                                |||||||||||| ||| || |||
                                TGGGACTTCAGA ACG GG GTG
                                      _  T  A
GAM593  HMOX2    3'  CGTGTGGGTGGAAGCCTCAGAG 65759     _        TG
          GC                    GCC CTGGGGTTTC  CCCGCAC   G
                                ||| ||||||||||  |||||||   |
                                CGG GACTCCGAAG  GGGTGTG   C
                                  A         GT
GAM593  HMX1     3'  GCCATGCAGAGACTCTGGGC   38946     T         CC_  AC
                                GCCC GGGGTTTCTGC   GC
                                |||| ||||||||||   ||
                                CGGG TCTCAGAGACG   CG
                                  _         TAC
GAM593  HNF4A    5'  GAGGGCGGGGGCCTTCGGGGT  6607        _  TT     GCAC
                                GCCCTGG GGT  CTGCCC
                                ||||||| |||  ||||||
                                TGGGGCT CCG  GGCGGG
                                    T  GG     AG
GAM593  HNRPA1   3'  GTCTTCGGAAACCTTGGTGTA  49121     C TG       CCC
                                TGC C  GGGTTTCTG   GC
                                ||| |  |||||||||   ||
                                ATG G  TCCAAAGGC   TG
                                  T GT        TTC
GAM593  HOXD1    3'  GTGGCCTGCAGAAGTCCCAGGC 44698     C    GT     ___    AC
                                GCC TGGG  TTCTGC   CCGC
                                ||| ||||  ||||||   ||||
                                CGG ACCC  AAGACG   GGTG
                                  _   TG     TCC
GAM593  HSPA4    3'  GCATGGAGGCCTCGAGGCA   90652      C         CCC
                                TGCC TGGGGTTTCTG   GC
                                |||| ||||||||||   ||
```

```
                                ACGG GCTCCGGAGGT   CG
                                  A         A__
GAM593  HSPA5    3'  GTGCTGTGTACCCTGGGGCA  19287      TG    TTCT  CC
                                TGCCC  GGGT    GC  GCAC
                                |||||  ||||    ||  ||||
                                ACGGG  CCCA    TG  CGTG
                                   GT    TG__  T_
GAM593  HTR1D    5'  GCCAAAGGCAAGAATCCCAGGG 7844           TC    C___  AC
           CA                     TGCCCTGGGGTT  TGCC    GC
                                |||||||||||  ||||    ||
                                ACGGGACCCTAA  ACGG    CG
                                      GA    AAAC
GAM593  ID1      3'  GTCACCAGAGACTTTAGGG   70573            CCC
                                CCCTGGGGTTTCTG   GC
                                ||||||||||||||   ||
                                GGGATTTCAGAGAC   TG
                                      CAC
GAM593  IK       5'  GTGTGGGTTGATTCTGAGG   76836     G   TT  T
                                CCT GGG  TC GCCCGCAC
                                ||| |||  || ||||||||
                                GGA TCT  AG TGGGTGTG
                                  G   T_  T
GAM593  IL10RA   3'  GTAGGAATGGAAGCTTCAGGGC 60383            G__  CG AC
                                GCCCTGGGGTTTCT   CC  C
                                ||||||||||||||   ||  |
                                CGGGACTTCGAAGG   GG  G
                                      TAA  AT
GAM593  IL1F5    3'  GTGTGGCTGGAATCTCTGGGTA 25377      T      T  _  AC
                                TGCCC GGGGTTTC GCC CGC
                                ||||| |||||||| ||| |||
                                ATGGG CTCTAAGG CGG GTG
                                   T      T  T
GAM593  IL27     3'  GTGGCTGAAGCCCTGGGGCA   65327      TG     T  C
                                TGCCC  GGGTTTC GCC GC
                                |||||  ||||||| ||| ||
                                ACGGG  CCCGAAG CGG TG
                                   GT     T  _
GAM593  IPF1     3'  GTGCCAGTTGGGGCCCCGCGGG 5782       _     TT T  CC
           TA                     TGCCC TGGGGT  C GC  GCAC
                                ||||| ||||||  | ||  ||||
                                ATGGG GCCCCG  G TG  CGTG
                                   C     GG T  AC
GAM593  IRS2     3'  GTGCTAGCAATTCCAGGGT   60442         TTC   CC
                                GCCCTGGGGT   TGC  GCAC
                                ||||||||||   |||  ||||
                                TGGGACCTTA   ACG  CGTG
                                      ___   AT
GAM593  ISLR     3'  GTGGTGGAATTCCAGGCA    19882      C       TGC
                                TGCC TGGGGTTTC   CCGC
                                ||||  |||||||||   ||||
```

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                                ACGG ACCTTAAGG   GGTG
                                  _       T__
GAM593  ITGAM    3'  TGTGGGTAGGTGACGGCA    72317     CTGGG  _
                                TGCC    GTT TCTGCCCGCA
                                ||||    ||| ||||||||||
                                ACGG    CAG GGATGGGTGT
                                  _____  T
GAM593  ITPKB    3'  GTGTGGGTATCTTGTAGGGTA  11069       G  TTTC
                                TGCCCTG GG    TGCCCGCAC
                                ||||||| ||    |||||||||
                                ATGGGAT TT    ATGGGTGTG
                                    G  CT__
GAM593  JPH2     3'  GTGTGCTAGGAACTCCAGAGT  96085    C        _ C   AC
                                GC CTGGGGTTTCT GC CGC
                                || ||||||||||| || |||
                                TG GACCTCAAGGA CG GTG
                                 A         T  T
GAM593  KCND2    3'  GTGTGGCCAGGTTTTAGG    25386       TT    C
                                CCTGGGG  TCTG CCGCAC
                                |||||||  |||| ||||||
                                GGATTTT  GGAC GGTGTG
                                   __    C
GAM593  KCNK7    3'  GTGGGCGGGAGGCCTCAGGG   54057          _     AC
                                CCCTGGGGTTTCT GCCCGC
                                |||||||||||| ||||||
                                GGGACTCCGGAGG CGGGTG
                                      G
GAM593  KCNK7    3'  GTGGGCGGGAGGCCTCAGGG   54058          _     AC
                                CCCTGGGGTTTCT GCCCGC
                                |||||||||||| ||||||
                                GGGACTCCGGAGG CGGGTG
                                      G
GAM593  KCNK7    3'  GTGGGCGGGAGGCCTCAGGG   54059          _     AC
                                CCCTGGGGTTTCT GCCCGC
                                |||||||||||| ||||||
                                GGGACTCCGGAGG CGGGTG
                                      G
GAM593  KCNK7    3'  GTGGGCGGGAGGCCTCAGGG   20346          _     AC
                                CCCTGGGGTTTCT GCCCGC
                                |||||||||||| ||||||
                                GGGACTCCGGAGG CGGGTG
                                      G
GAM593  KCNN3    3'  GTCTACGGAAGCCTCTGGGT   11187     T        CCC
                                GCCC GGGGTTTCTG   GC
                                ||||  ||||||||||   ||
                                TGGG CTCCGAAGGC   TG
                                  T         ATC
GAM593  KIFC3    3'  GTGGGCGAGGAGCCTCTGGGCA 19892      T       _     AC
                                TGCCC GGGGTTTCT GCCCGC
                                |||||  ||||||||| ||||||
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                                ACGGG CTCCGAGGA CGGGTG
                                  T       G
GAM593  KLK5    5'  TGCCTGGGTCTCAGCGCA   25786    C   GTTTCT  __
                                TGC CTGGG    GCCC  GCA
                                ||| |||||    ||||  |||
                                ACG GACTC    TGGG  CGT
                                  C   _____   TC
GAM593  LDHB    5'  GTGGAGGGAAGTCCCAGGG   11292      GT   GC
                                CCCTGGG  TTCT  CCGC
                                |||||||  ||||  ||||
                                GGGACCC  AAGG  GGTG
                                    TG   GA
GAM593  LEF1    5'  GTGCCCTTCGGCCTCGGGGC  33224        TCTGCCC
                                GCCCTGGGGTT     GCAC
                                ||||||||||      ||||
                                CGGGGCTCCGG     CGTG
                                      CTTCC__
GAM593  LGR6    5'  GTTCGAGCAGGGGTCCTAGGC  85357    C    TT    C  C
                                GCC TGGGG  TCTGC CG AC
                                ||| |||||  ||||| || ||
                                CGG ATCCT  GGACG GC TG
                                  _    GG    A  T
GAM593  LIF     3'  GTGGCTGGGGCCCAGGGCA   11306       G TT T   C
                                TGCCCTGGG T  C GCC GC
                                |||||||| |  | ||| ||
                                ACGGGACCC G  G CGG TG
                                     _ GG T  _
GAM593  LZTS1   3'  GCCCTTAGAGACCCCGAGGTA  41033    C        CCC
                                TGCC TGGGGTTTCTG   GC
                                |||| ||||||||||   ||
                                ATGG GCCCCAGAGAT   CG
                                  A         TCC
GAM593  MADD    3'  GTGAGGGAACCCTGGGGC    56216     TG      GCC
                                GCCC  GGGTTTCT   CGC
                                ||||  ||||||||   |||
                                CGGG  CCCAAGGG   GTG
                                  GT       A__
GAM593  MADD    3'  GTGAGGGAACCCTGGGGC    56217     TG      GCC
                                GCCC  GGGTTTCT   CGC
                                ||||  ||||||||   |||
                                CGGG  CCCAAGGG   GTG
                                  GT       A__
GAM593  MAK     3'  GTGCGTTCAGCTGCTGGGGCA 20951      GG   TT   CC
                                TGCCCT  GGT  CTG  CGCAC
                                ||||||  |||  |||  |||||
                                ACGGGG  TCG  GAC  GCGTG
                                    __   TC   TT
GAM593  MAPK1   3'  CTGGGGATGTCCCAGGGT    12297        TT  TG   CAC
                                GCCCTGGGG  TC  CCCG
                                |||||||||  ||  ||||
```

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                                TGGGACCCT  AG  GGGT
                                    GT  __   CT
GAM593  MAPK14   3'  GTTGTGGATGCTCCAGGGCA  8980          T  TG CC
                                TGCCCTGGGGT TC  C  GC
                                |||||||||||  ||  |  ||
                                ACGGGACCTCG AG  G  TG
                                      T  GT T_
GAM593  MAPK14   3'  GTTGTGGATGCTCCAGGGCA  8981          T  TG CC
                                TGCCCTGGGGT TC  C  GC
                                |||||||||||  ||  |  ||
                                ACGGGACCTCG AG  G  TG
                                      T  GT T_
GAM593  MCM3     3'  GTGGAGAGAAGCTCTGAGGCA  11484     CT       GC
                                TGCC  GGGGTTTCT  CCGC
                                ||||  |||||||||  ||||
                                ACGG  TCTCGAAGA  GGTG
                                  AG        GA
GAM593  MECP2    3'  GTGAAGGAGGCTCCAGGCA   18413     C        GCC
                                TGCC TGGGGTTTCT   CGC
                                |||| ||||||||||   |||
                                ACGG ACCTCGGAGG   GTG
                                  _         AA_
GAM593  MEF2D    3'  GGGTAGGGGCTCCTGGGC    20987     T    TT
                                GCCC GGGGT  CTGCCC
                                |||| |||||  ||||||
                                CGGG CCTCG  GATGGG
                                  T    GG
GAM593  MFNG     3'  GTGGCCAGAGAGGCTCCAGGG  11546         __    C   AC
                                CCCTGGGGT  TTCTG CCGC
                                |||||||||  ||||| ||||
                                GGGACCTCG  GAGAC GGTG
                                     GA    C
GAM593  MFNG     3'  GTGTGATGGCTGGATCTGGGGC 11547      TG  GT   T  __
          A                      TGCCC  GG  TTC GCC  CGCAC
                                 |||||  ||  ||| |||  |||||
                                 ACGGG  CT  AGG CGG  GTGTG
                                    GT  __   T   TA
GAM593  MFNG     3'  TTGGGCAGAGACTTCTGGGT   11549     T          CAC
                                GCCC GGGGTTTCTGCCCG
                                |||| ||||||||||||||
                                TGGG CTTCAGAGACGGGT
                                  T           TG
GAM593  MFRP     5'  GTGGGCCCTTGGGGGTCTTGGG 49505     T   G TT T___     AC
          C                      GCCC GGG T  C    GCCCGC
                                 |||| ||| |  |    ||||||
                                 CGGG TCT G  G    CGGGTG
                                   T  G GG TTCC
GAM593  MGEA5    3'  GTGGGTTTCAGAAGTGTCAGGG 25226       GG     ___     AC
          T                      GCCCTGG  TTTCTG   CCCGC
                                 |||||||  ||||||   |||||
```

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                                TGGGACT  GAAGAC   GGGTG
                                   GT     TTT
GAM593  MHC2TA   3'  GTTGGCTGGGGGCCTCAGTGCA 5995     C      TT  _   C  AC
                                TGC CTGGGGT  CT GCC GC
                                ||| |||||||  || ||| ||
                                ACG GACTCCG  GG CGG TG
                                  T      GG  T   T
GAM593  MMP11    5'  GCCCAGCAGCCCCGGGGC    21045          T   CCC
                                GCCCTGGGGTT CTG   GC
                                |||||||||||| |||   ||
                                CGGGGCCCCGA GAC   CG
                                       C   C__
GAM593  MMP19    5'  GCTCCCAGAAATCTCAGGTCA  11631    C          CCC
                                TG CCTGGGGTTTCTG   GC
                                || ||||||||||||   ||
                                AC GGACTCTAAAGAC   CG
                                 T           CCT
GAM593  MMP19    5'  GCTCCCAGAAATCTCAGGTCA  11632    C          CCC
                                TG CCTGGGGTTTCTG   GC
                                || ||||||||||||   ||
                                AC GGACTCTAAAGAC   CG
                                 T           CCT
GAM593  MMP25    3'  GTGGGTGGAACCTGGGGGCA   42697       G     T TG
                                TGCCCT GGGTT C  CCCGC
                                |||||| ||||| |  |||||
                                ACGGGG TCCAA G  GGGTG
                                   G    _ GT
GAM593  MSI1     3'  GTGAATGTGAAGCCCCAGGCCG 11700    C         T  CCG
                                TG CCTGGGGTTTC GC   CAC
                                || ||||||||||| ||   |||
                                GC GGACCCCGAAG TG   GTG
                                 C          _  TAA
GAM593  MTF1     3'  GCTCTGCAGAGGCCCTAGGCA  21050     C          CC_
                                TGCC TGGGGTTTCTGC   GC
                                |||| ||||||||||||   ||
                                ACGG ATCCCGGAGACG   CG
                                  _           TCT
GAM593  MUCDHL   3'  GCTGGCGGAAGCCCCACGGC   88642     C          C
                                GCC TGGGGTTTCTGCC GC
                                ||| ||||||||||||| ||
                                CGG ACCCCGAAGGCGG CG
                                  C           T
GAM593  MUCDHL   3'  GTGCGGGACACTCCGGGG    88647         TTCTG
                                CCCTGGGGT    CCCGCAC
                                |||||||||    |||||||
                                GGGGCCTCA    GGGCGTG
                                      CA___
GAM593  MYOZ1    5'  GTGAAGGGGAGTCCCTGGGCA  41435      T   TTT  G   G_
                                TGCCC GGGG   CT CCC  CAC
                                ||||| ||||   || |||  |||
```

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                                ACGGG CCCT   GA GGG  GTG
                                  T   ___ G   AA
GAM593  NDP     3'  GTGTGCTATAGCTTTAGCGT   6044     C      TCT  C
                                GC CTGGGGTT   GC CGC
                                || ||||||||   || |||
                                TG GATTTCGA   CG GTG
                                 C       TAT  T
GAM593  NDUFA6   3'  GTCTTTGGAAACCCTGGTGTA  11764     C TG       CCC
                                TGC C  GGGTTTCTG   GC
                                ||| |  |||||||||   ||
                                ATG G  CCCAAAGGT   TG
                                  T GT        TTC
GAM593  NEO1     3'  GTGTGGGTCGTTCCTGGGGT   11775     TG   TTTCT
                                GCCC  GGG    GCCCGCAC
                                ||||  |||    ||||||||
                                TGGG  CCT    TGGGTGTG
                                  GT   TGC__
GAM593  NEURL    3'  GTGTGCCAGGACCTCAGGC    16135     C      T   CC
                                GCC TGGGGTT CTG  CGCAC
                                ||| ||||||| |||  |||||
                                CGG ACTCCAG GAC  GTGTG
                                 _      _  C_
GAM593  NEUROD1  5'  GTCCGGAGGCCCCAGGGT    11779            CCC
                                GCCCTGGGGTTTCTG   GC
                                ||||||||||||||   ||
                                TGGGACCCCGGAGGC   TG
                                       C__
GAM593  NFE2     3'  GTGTTTGGAAGTTCCAAGGT   21602     C   GG     CC
                                GCC TGG  TTTCTG  CGC
                                ||| |||  ||||||  |||
                                TGG ACC  GAAGGT  GTG
                                  A  TT     TT
GAM593  NFIA     5'  GTGTAGGGAAACTCTAGGC    70888     C       TG  CG
                                GCC TGGGGTTTC  CC  CAC
                                ||| |||||||||  ||  |||
                                CGG ATCTCAAAG  GG  GTG
                                 _        __ AT
GAM593  NFIC     3'  GTCCCAGGAATCCCAGGG     20013           CCC
                                CCCTGGGGTTTCTG   GC
                                ||||||||||||||   ||
                                GGGACCCTAAGGAC   TG
                                       CC_
GAM593  NOL3     3'  TGCCCAGGAACTTAGGGT     15464        G     CCC   C
                                GCCCTGGG TTTCTG   GCA
                                |||||||| ||||||   |||
                                TGGGATTC AAGGAC   CGT
                                     _     C__
GAM593  NOX4     5'  GTGCGGGTGGGAGTCAGGGC   34187       GG    TG
                                GCCCTGG  TTTC  CCCGCAC
                                |||||||  ||||  |||||||
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                                CGGGACT  GAGG  GGGCGTG
                                   __    GT
GAM593  NR1D1    5'  GTGCGGCCCGGGAACCCTGGGC 41670      T        C_
                                GCCC GGGGTTTCTG  CCGCAC
                                |||| ||||||||||  ||||||
                                CGGG TCCCAAGGGC  GGCGTG
                                  _        CC
GAM593  NR1H2    3'  GTGGAAGGGGCCCTGGGC    70606      T    TT  GC
                                GCCC GGGGT  CT  CCGC
                                |||| |||||  ||  ||||
                                CGGG TCCCG  GA  GGTG
                                  _    GG  A_
GAM593  OAS3     3'  GCACTCTAGGAATCTTAGGCA  21653      C         CCC_
                                TGCC TGGGGTTTCTG    GC
                                |||| ||||||||||    ||
                                ACGG ATTCTAAGGAT    CG
                                  _         CTCA
GAM593  OGDH     3'  GCTGGCAGAGGTTTCTAGGGT  92751       _ GG TT     C  AC
                                GCCCT G  G  TCTGCC GC
                                ||||| |  |  |||||| ||
                                TGGGA C  T  AGACGG CG
                                   T TT GG     T
GAM593  OPHN1    5'  GTCAGGAAACTCTAAGGTA    11911      C         GCCC
                                TGCC TGGGGTTTCT    GC
                                |||| ||||||||||    ||
                                ATGG ATCTCAAAGG    TG
                                  A         AC__
GAM593  PCDH12   3'  GCCTGAGAACTTTAGGGT    33886          _   T_
                                GCCCTGGGGT TTC  GC
                                |||||||||| |||  ||
                                TGGGATTTCA GAG  CG
                                     A   TC
GAM593  PCDH12   5'  GTGTGGGCAGGGACTGCCCCAG 33887          ___
          GGC                    GCCCTGGGGT   TTCTGCCCGCAC
                                ||||||||||   ||||||||||||
                                CGGGACCCCG   GGGACGGGTGTG
                                     TCA
GAM593  PDE4A    5'  GTGTGCAGCAGCCCCAGGC    21686      C      T    C
                                GCC TGGGGTT CTGC CGC
                                ||| ||||||| |||| |||
                                CGG ACCCCGA GACG GTG
                                  _      C    T
GAM593  PGF      5'  GGCCGGGGCCTCGGGGCA     12066          TT T
                                TGCCCTGGGGT  C GCC
                                ||||||||||  | |||
                                ACGGGGCTCCG  G CGG
                                     GG C
GAM593  PHLDA3   5'  GCTTTCCGCGAACCTCGGGGC  25693           C  CCC_  AC
                                GCCCTGGGGTTT TG    GC
                                |||||||||||| ||    ||
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                                CGGGGCTCCAAG GC    CG
                                      C  CTTT
GAM593  PIGH     5'  GTGCGGGCGGCCGAGTGGGGGC 17092      GGGGTTT
                                GCCCT      CTGCCCGCAC
                                |||||      ||||||||||
                                CGGGG      GGCGGGCGTG
                                   GTGAGCC
GAM593  PIK3C2B  5'  GCAGAGGCCCTCAGGGTA    12103       _
                                TGCCCTG GGGTTTCTGC
                                ||||||| ||||||||||
                                ATGGGAC CCCGGAGACG
                                    T
GAM593  PIK4CB   3'  GTGGTGGGGGGTCCGGGGCA  12133        G TT TG  C
                                TGCCCTGGG T  C  CC GC
                                ||||||||| |  |  || ||
                                ACGGGGCCT G  G  GG TG
                                      G GG GT  _
GAM593  PLXNA1   3'  GCCAGGGGCCCCGGGTCG    72772    C      TT   CCC
                                TG CCTGGGGT  CTG   GC
                                || ||||||||  |||   ||
                                GC GGGCCCCG  GAC   CG
                                 T       GG   ___
GAM593  PMP22    3'  GTGTGGGTAGAAACCCCA    6121
                                TGGGGTTTCTGCCCGCAC
                                ||||||||||||||||||
                                ACCCCAAAGATGGGTGTG

GAM593  PNUTL2   3'  GTGGAAGTGGAAAACCCAGGGC 55376        G    TG __    AC
           A                     TGCCCTGGG TTTC  C  CCGC
                                ||||||||| ||||  |  ||||
                                ACGGGACCC AAAG  G  GGTG
                                      A    GT AA
GAM593  PNUTL2   3'  GTGGAAGTGGAAAACCCAGGGC 55377        G    TG __    AC
           A                     TGCCCTGGG TTTC  C  CCGC
                                ||||||||| ||||  |  ||||
                                ACGGGACCC AAAG  G  GGTG
                                      A    GT AA
GAM593  POU2AF1  5'  GTGTGGGGCGCTCTGGGC    21750     T    TTCTG
                                GCCC GGGGT     CCCGCAC
                                |||| |||||     |||||||
                                CGGG TCTCG     GGGTGTG
                                  _     CG___
GAM593  PPP1R12B 3'  GCCATTCCAGAGATTCTGGGGC 50360      TG       CCC__  AC
                                GCCC  GGGTTTCTG    GC
                                ||||  |||||||||    ||
                                CGGG  CTTAGAGAC    CG
                                  GT       CTTAC
GAM593  PPP1R12B 3'  GTTATGCAAATCTCAGGGT   50363         TC   CC_
                                GCCCTGGGGTT  TGC   GC
                                ||||||||||  |||   ||
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                                TGGGACTCTAA ACG  TG
                                     __  TAT
GAM593  PPP1R12B  5'  GCCAGCAGCCCTGGGGCA   50359     TG   T  CCC
                                TGCCC GGGTT CTG  GC
                                ||||| ||||| |||  ||
                                ACGGG CCCGA GAC  CG
                                   GT   C  ___
GAM593  PPP2R5B  5'  GTTGCAGGAGGCCCTGGGG  21801    TG    _  CC
                                CCC GGGTTTC TGC GC
                                ||| ||||||| |||  ||
                                GGG CCCGGAG ACG TG
                                  GT     G  T_
GAM593  PPP3CB   3'  GTGAGCAAGGGGCTTGGGGCA 41217     TG G TC  C
                                TGCCC GG TT TGC CGC
                                ||||| || ||  ||| |||
                                ACGGG TC GG ACG GTG
                                   GT G GA  A
GAM593  PRDM2    3'  GTGTGGTTGAGGCCTTGGGGT 32420     TG     TGC
                                GCCC GGGTTTC  CCGCAC
                                ||||  |||||||  ||||||
                                TGGG TCCGGAG  GGTGTG
                                  GT     TT_
GAM593  PRDM4    3'  GCCACTTGGAAGTTTAGGGTA 25742       G   TGCCC
                                TGCCCTGGG TTTC    GC
                                ||||||||| ||||    ||
                                ATGGGATTT AAGG    CG
                                     G   TTCAC
GAM593  PRKCABP  5'  GCCTGGAGACCCGTGGGGC   25747      _      CCC
                                GCCCTG GGGTTTCTG  GC
                                |||||| |||||||||  ||
                                CGGGGT CCCAGAGGT  CG
                                   G       C__
GAM593  PSAP     3'  GTGTGGATTGGATGCTGGGGT 69886     TG G   CTGC
                                GCCC G GTTT   CCGCAC
                                ||||  | ||||  ||||||
                                TGGG C TAGG   GGTGTG
                                  GT G   TTA_
GAM593  PSD      5'  GCTCAAGGCAGGGCTCTGGGGT 12438     TG   T   C___  AC
                                GCCC GGGTT CTGCC   GC
                                ||||  ||||| |||||   ||
                                TGGG  CTCGG GACGG   CG
                                  GT    _    AACT
GAM593  PTGES    3'  GTGGAGGACCGGGAGCTTTGGG 18069    TG      C____   AC
                                CC  GGGTTTCTG    CCGC
                                ||  |||||||||    ||||
                                GG  TTCGAGGGC    GGTG
                                 GT       CAGGA
GAM593  PTGFRN   3'  GGGCGAGAAATCCCAGGGCA  67771          _
                                TGCCCTGGGGTTTCT GCCC
                                |||||||||||||| ||||
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                                ACGGGACCCTAAAGA CGGG
                                       G
GAM593  PTPRJ    5' CCGGGGAAGCCCGGGGC     12619        G   TG   CAC
                                GCCCTGGG TTTC  CCCG
                                |||||||| ||||  ||||
                                CGGGGCCC GAAG  GGGC
                                    _   ___   CT
GAM593  RAB26    3' GTTTTCAGGAGCCCCAGGTCA  27605    C         CCC
                                TG CCTGGGGTTTCTG   GC
                                || ||||||||||||   ||
                                AC GGACCCCGAGGAC   TG
                                 T          TTT
GAM593  RAD51L3  3' GTGCTGCAGGAGCTCCGAGGCA 56893     C         CC
                                TGCC TGGGGTTTCTGC  GCAC
                                |||| ||||||||||||  ||||
                                ACGG GCCTCGAGGACG  CGTG
                                  A          T_
GAM593  RAD51L3  3' GTGCTGCAGGAGCTCCGAGGCA 56894     C         CC
                                TGCC TGGGGTTTCTGC  GCAC
                                |||| ||||||||||||  ||||
                                ACGG GCCTCGAGGACG  CGTG
                                  A          T_
GAM593  RAGE     5' GTGCGGGACCCCGCCTCAGGG  27251        TTCTG
                                CCCTGGGGT    CCCGCAC
                                |||||||||    |||||||
                                GGGACTCCG    GGGCGTG
                                     CCCCA
GAM593  RB1      3' GTGTTCTGCCAGATCTTAGG   92555         CT  CC_
                                CCTGGGGTTT  GC   GCAC
                                ||||||||||  ||   ||||
                                GGATTCTAGA  CG   TGTG
                                     C_  TCT
GAM593  RECQL    5' GTGGGGAGAGGCTCTGGG    53075    TG      G
                                CC  GGGTTTCT CCCGC
                                ||  |||||||| |||||
                                GG  CTCGGAGA GGGTG
                                 GT       G
GAM593  RET      3' GTGTGTAATAGAGCCTTGTGGT 40543     C     T   CC_
                                GCC TGGGGTT CTG   CGCAC
                                ||| ||||||| |||   |||||
                                TGG GTTCCGA GAT   GTGTG
                                  T      _   AAT
GAM593  RET      3' GTGTGTAATAGAGCCTTGTGGT 40544     C     T   CC_
                                GCC TGGGGTT CTG   CGCAC
                                ||| ||||||| |||   |||||
                                TGG GTTCCGA GAT   GTGTG
                                  T      _   AAT
GAM593  RET      3' GTGTGTAATAGAGCCTTGTGGT 40545     C     T   CC_
                                GCC TGGGGTT CTG   CGCAC
                                ||| ||||||| |||   |||||
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                                TGG GTTCCGA GAT   GTGTG
                                  T      _   AAT
GAM593  RET     3'  GTGTGTAATAGAGCCTTGTGGT 6152      C      T   CC_
                                GCC TGGGGTT CTG   CGCAC
                                ||| ||||||| |||   |||||
                                TGG GTTCCGA GAT   GTGTG
                                  T      _   AAT
GAM593  RNGTT    5'  GTGTCTCGGACCCCGGTGT   15067    C     TT    CCC
                                GC CTGGGG  TCTG   GCAC
                                || ||||||  ||||   ||||
                                TG GGCCCC  AGGC   TGTG
                                 T      __    TC_
GAM593  RNH     5'  GTGCCTGGGGAGGCTTCAGGGT 60370           TG   __
                                GCCCTGGGGTTTC  CCC  GCAC
                                ||||||||||||  |||  ||||
                                TGGGACTTCGGAG  GGG  CGTG
                                       __   TC
GAM593  RNH     5'  GTGCCTGGGGAGGCTTCAGGGT 60371           TG   __
                                GCCCTGGGGTTTC  CCC  GCAC
                                ||||||||||||  |||  ||||
                                TGGGACTTCGGAG  GGG  CGTG
                                       __   TC
GAM593  RPA2    3'  GTGAACATGAAGTTCTGCGGTA 12900      C   GG    _  CC   AC
                                TGCC TGG  TTTC TG  CGC
                                |||| |||  |||| ||  |||
                                ATGG GTC  GAAG AC  GTG
                                  C   TT    T  AA
GAM593  RRAS    3'  GTGAGGGGCTCCGGGTCA    21845    C       TT  GCC
                                TG CCTGGGGT  CT   CGC
                                || ||||||||  ||   |||
                                AC GGGCCTCG  GA   GTG
                                 T       GG  ____
GAM593  SACM1L  3'  GTGTGTTAGATCTTAAGGTA   26696     C       CT  C
                                TGCC TGGGGTTT  GC CGC
                                |||| ||||||||  || |||
                                ATGG ATTCTAGA  TG GTG
                                  A       T_  T
GAM593  SDC1    3'  GCCTGGAGACTTAGGGCA    12990         G     CCC
                                TGCCCTGGG TTTCTG   GC
                                |||||||| ||||||   ||
                                ACGGGATTC AGAGGT   CG
                                      _     C__
GAM593  SFRP5   3'  GTGGAGGGGCTCAGGGCA    13035         G TT  GC
                                TGCCCTGGG T  CT  CCGC
                                |||||||| |  ||  ||||
                                ACGGGACTC G  GA  GGTG
                                      _ GG  __
GAM593  SFTPA2  3'  GCAGTGAGGCCTTGGGGTA   23628      TG      T  CC
                                TGCCC  GGGTTTC GC  GC
                                |||||  ||||||| ||  ||
```

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                                ATGGG  TCCGGAG TG  CG
                                  GT      _  A_
GAM593  SGT     3'  GTGTTTTCTAGAATCCTGGGGT 13041     TG    T  CCC_
                                GCCC  GGGTT CTG   GCAC
                                ||||  ||||| |||   ||||
                                TGGG  CCTAA GAT   TGTG
                                  GT    _  CTTT
GAM593  SIM1    3'  TGTGGGCTCCTTTAGGCA   18620     CT   TTTCT
                                TGCC  GGGG   GCCCGCA
                                ||||  ||||   |||||||
                                ACGG  TTCC   CGGGTGT
                                  AT   T____
GAM593  SIRT6   3'  GTCCCCGGGAGCCTCAGGGC  33740          CCC
                                GCCCTGGGGTTTCTG  GC
                                ||||||||||||||  ||
                                CGGGACTCCGAGGGC  TG
                                        CCC
GAM593  SLC19A1  5'  GTCCGGGAGCCCCAGGGCA  13218          CCC
                                TGCCCTGGGGTTTCTG  GC
                                ||||||||||||||  ||
                                ACGGGACCCCGAGGGC  TG
                                        C__
GAM593  SLC19A1  5'  GTGTCGGGGGCTGCGGGGT  13219     G  TT  CC
                                GCCCTG GGT  CTG  CGC
                                |||||| |||  |||  |||
                                TGGGGC TCG  GGC  GTG
                                   G  GG  T_
GAM593  SLC1A2   3'  GTGTGGTACACTCCAGGG   62615       TTC   _
                                CCCTGGGGT  TGCC CGC
                                |||||||||  |||| |||
                                GGGACCTCA  ATGG GTG
                                     C__   T
GAM593  SLC30A3  5'  GCCCTGCGGGGATCCCGGGG  14400       TT   CC_
                                CCCTGGGGT  CTGC  GC
                                |||||||||  ||||  ||
                                GGGGCCCTA  GGCG  CG
                                     GG   TCC
GAM593  SLC6A8   3'  GTGCATGGTGGGGGCCTCGGGG 20074        TT TG  C_
            C                    GCCCTGGGGT  C  CC  GCAC
                                ||||||||||  |  ||  ||||
                                CGGGGCTCCG  G  GG  CGTG
                                      GG GT  TA
GAM593  SMARCD1  3'  TGACACTGGACAACCTTGGGGC 58188      TG   _  GCCCG  C
            A                    TGCCC  GGGTT TCT    CA
                                |||||  ||||| |||    ||
                                ACGGG  TCCAA AGG    GT
                                  GT    C  TCACA  T
GAM593  SMN1    5'  GCTCCCAGAAGCCCCGGGC   43461     T       CCC
                                GCCC GGGGTTTCTG  GC
                                ||||  ||||||||||  ||
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                                CGGG CCCCGAAGAC   CG
                                  _       CCT
GAM593  SMURF1   3'  GCCTGGGAGGCCCGGGGC    94048       G     CCC
                                GCCCTGGG TTTCTG   GC
                                |||||||| ||||||   ||
                                CGGGGCCC GAGGGT   CG
                                    G     C__
GAM593  SOCS5    3'  GTGAGGCAACTCTGGGGCA   26683      TG    TTC   _
                                TGCCC  GGGT   TGCC CGC
                                |||||  ||||   |||| |||
                                ACGGG  CTCA   ACGG GTG
                                  GT   ____   A
GAM593  SOLH     5'  GTGTGCCCAGGCCCTGAGGT   20095     CT    TT   CC
                                GCC  GGGGT  CTG  CGCAC
                                |||  |||||  |||  |||||
                                TGG  TCCCG  GAC  GTGTG
                                  AG    __   CC
GAM593  SOLH     3'  GTGTGGAGCGGCGAGTCCCGGG 20096        GT  _   _
            GC                    GCCCTGGG  TT CTGC CCGCAC
                                |||||||  || |||| ||||||
                                CGGGGCCC  AG GGCG GGTGTG
                                    TG  C    A
GAM593  SOX12    3'  GCTGGGTGTCCCAGGGCA    23686         TTTC    _
                                TGCCCTGGGG    TGCCC GC
                                ||||||||||    ||||| ||
                                ACGGGACCCT    GTGGG CG
                                      ____    T
GAM593  SP3      5'  GTGTGAGTGTGGGCCCCAGCGT 83386    C       TC   C
                                GC CTGGGGTT  TGC CGCAC
                                || ||||||||  ||| |||||
                                TG GACCCCGG  GTG GTGTG
                                 C       GT   A
GAM593  SURF5    3'  GTGGCTGAGAGGGGTCCTAGGG 56917         TT   GC___   AC
            T                    GCCCTGGGG  TCT    CCGC
                                |||||||||  |||    ||||
                                TGGGATCCT  GGA    GGTG
                                     GG   GAGTC
GAM593  SURF6    3'  GTCCTAGGAGACTCCAGGACA  23133    C         GCCC
                                TG CCTGGGGTTTCT    GC
                                || ||||||||||||    ||
                                AC GGACCTCAGAGG    TG
                                 A          ATCC
GAM593  SYNGR1   3'  GCACTAGGAGACCTCAGGGTA  17505            GCCC
                                TGCCCTGGGGTTTCT    GC
                                ||||||||||||||    ||
                                ATGGGACTCCAGAGG    CG
                                          ATCA
GAM593  SYNGR1   3'  GTGCAAGTATATCCCAGGGCA  17510          TTC   CC
                                TGCCCTGGGGT   TGC  GCAC
                                ||||||||||   |||  ||||
```

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                                ACGGGACCCTA  ATG  CGTG
                                      T__  AA
GAM593  SYNGR1   3'  GTGGAGGAAGCCCTGGTGGTA  17511     _ TG      GC
                                TGCC C  GGGTTTCT  CCGC
                                |||| |  ||||||||  ||||
                                ATGG G  CCCGAAGG  GGTG
                                  T GT      A_
GAM593  TCF2     3'  GTGCACTCCCTAAGAAACCCCA 6619            GCCC____
           GGGCA                 TGCCCTGGGGTTTCT      GCAC
                                |||||||||||||||      ||||
                                ACGGGACCCCAAAGA      CGTG
                                       ATCCCTCA
GAM593  TCP10    3'  GTGTGGCCCACCCCAGGCA   17238     C    TTCT  _
                                TGCC TGGGGT   GCC CGC
                                |||| ||||||   ||| |||
                                ACGG ACCCCA   CGG GTG
                                  _     CC__  T
GAM593  TEF      5'  GTGCGCGAGCCGAGTCCGGGGC 13680        GT  T  C__
           A                    TGCCCTGGG  TTC GC  CGCAC
                                |||||||||  ||| ||  |||||
                                ACGGGGCCT  GAG CG  GCGTG
                                     __  C  AGC
GAM593  TEGT     3'  GTGTCAAGCCAGAGATTCGGGG 65230        G    _ CC_
           CA                     TGCCCTGGG TTTCTG C  GCAC
                                |||||||||  |||||| |  ||||
                                ACGGGGCTT AGAGAC G  TGTG
                                     _     C AAC
GAM593  THY1     3'  GTCCCTCAGAGGCCTTGGGGCA 21899      TG       CCC_  AC
                                TGCCC  GGGTTTCTG   GC
                                |||||  |||||||||   ||
                                ACGGG  TCCGGAGAC   TG
                                  GT       TCCC
GAM593  TIMM44   3'  GTGCCAAGAGGCCCCAGGGC  71924           GCCC
                                GCCCTGGGGTTTCT   GCAC
                                ||||||||||||||   ||||
                                CGGGACCCCGGAGA   CGTG
                                       AC__
GAM593  TIMP3    3'  GTGAGGAGGCCCTGGGCA    6290      T       GCC
                                TGCCC GGGGTTTCT  CGC
                                ||||| |||||||||  |||
                                ACGGG TCCCGGAGG  GTG
                                  _       A__
GAM593  TJP1     5'  GCGTGGGAGTTGCTGGGGCA  13764      GG  TT  G  _
                                TGCCCT  GGT  CT CC CGC
                                ||||||  |||  || || |||
                                ACGGGG  TCG  GA GG GCG
                                   __  TT  G  T
GAM593  TNFAIP1  3'  GTGCTGTAGAGGCCCTGGTGCA 41232     C TG       CC
                                TGC C  GGGTTTCTGC  GCAC
                                ||| |  ||||||||||  ||||
```

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                                ACG G  CCCGGAGATG  CGTG
                                  T GT        T_
GAM593  TNFAIP2  3'  GTGCCCAGCAAGCCTTGGGCA  21926      T     _  CCC
                                TGCCC GGGGTTT CTG   GCAC
                                ||||| ||||||| |||   ||||
                                ACGGG TTCCGAA GAC   CGTG
                                  _      C  C__
GAM593  TRAF1    3'  GCACCCAAGACCTCAGGGCA   20175          C  CCC
                                TGCCCTGGGGTTT TG   GC
                                |||||||||||| ||   ||
                                ACGGGACTCCAGA AC   CG
                                       _ CCA
GAM593  TRPM2    5'  GTGTCTCTAGAACCCCAGTGTA 13869    C       T   CCC
                                TGC CTGGGGTT CTG   GCAC
                                ||| |||||||| |||   ||||
                                ATG GACCCCAA GAT   TGTG
                                  T       _  CTC
GAM593  TRPM4    3'  GCTGCAGGGTCCTTGGGGTA   34868      TG  T     CC
                                TGCCC  GGG TTCTGC  GC
                                |||||  ||| ||||||  ||
                                ATGGG  TCC GGGACG  CG
                                   GT  T     T_
GAM593  TRPV3    5'  TGCGGTGATCTCAGGGCA    96817          TCTGC    C
                                TGCCCTGGGGTT    CCGCA
                                ||||||||||||    |||||
                                ACGGGACTCTAG    GGCGT
                                       T____
GAM593  TSG101   5'  GTGTGGGACGGTCTGGGGCA   21933      TG  GTTT  _
                                TGCCC  GG    CTG CCCGCAC
                                |||||  ||    ||| |||||||
                                ACGGG  CT    GGC GGGTGTG
                                   GT  ____   A
GAM593  TSSC4    5'  GTGTGGCGTGGCCCTGGGG   20328     TG    TC   _
                                CCC  GGGTT  TGCC CGC
                                |||  |||||  |||| |||
                                GGG  CCCGG  GCGG GTG
                                  GT    T_   T
GAM593  USP18    3'  GCCTGTGGGAACTTCAGGG   64384          TG CC
                                CCCTGGGGTTTC  C  GC
                                ||||||||||||  |  ||
                                GGGACTTCAAGG  G  CG
                                       GT TC
GAM593  VEGF     3'  TGGGGAGCTTCAGGACA     14044    C       CTG
                                TG CCTGGGGTTT   CCCG
                                || ||||||||||   ||||
                                AC GGACTTCGAG   GGGT
                                 A        ___
GAM593  WDR4     5'  GTGCGGACAGGAAGAGGCTCTG 54460      T    _____     C
             GGC                   GCCC GGGGT    TTCTG CCGCAC
                                |||| |||||    ||||| ||||||
```

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                                CGGG TCTCG    AGGAC GGCGTG
                                  _    GAGA    A
GAM593  WFS1     5'  GCCCAGAGGCCCCAGGGC    21167            CCC
                                GCCCTGGGGTTTCTG   GC
                                ||||||||||||||   ||
                                CGGGACCCCGGAGAC   CG
                                       C__
GAM593  WHSC1    3'  GTGTGTGGCGCTTTAGGGT   24685         TTCT  _
                                GCCCTGGGGT    GCC CGCAC
                                ||||||||||    ||| |||||
                                TGGGATTTCG    CGG GTGTG
                                      _____  T
GAM593  XRCC3    3'  GTGCCCCACAAAACTTCAGTGT 19522    C       CTGCCC
                                GC CTGGGGTTT     GCAC
                                || |||||||||     ||||
                                TG GACTTCAAA     CGTG
                                 T       ACACCC
GAM593  XYLB     3'  GTGCCCGTGTGCCCCAGGGCA  18829          TTCT  CC
                                TGCCCTGGGGT    GC  GCAC
                                ||||||||||    ||  ||||
                                ACGGGACCCCG    TG  CGTG
                                       TG__  CC
GAM593  ZNF179   3'  GTGATGCCAGGGATTCCAAGGC 24089     C     TT   CCCG
          A                     TGCC TGGGGT  CTG    CAC
                                ||||  ||||||  |||    |||
                                ACGG ACCTTA  GAC    GTG
                                  A     GG   CGTA
GAM593  ZNF264   5'  GCCTGGAAGCCCCGGGCA    14216      T        CCC
                                TGCCC GGGGTTTCTG   GC
                                |||||  ||||||||||   ||
                                ACGGG CCCCGAAGGT   CG
                                  _         C__
GAM593  ZNF264   3'  GTGCGTGGCATGGAAGTTTTTG 14228      TG GG    __  _
          GGT                     GCCC  G  TTTCT  GCC CGCAC
                                ||||  |  |||||  ||| |||||
                                TGGG  T  GAAGG  CGG GCGTG
                                  TT TT    TA   T
GAM593  ZNFN2A1  3'  GTGTGACATGAGCCCTGGAGT  61396    C TG     C  CC
                                GC C  GGGTTT TG  CGCAC
                                || |  ||||||  ||  |||||
                                TG G  CCCGAG AC  GTGTG
                                 A GT     T  A_
GAM593  20D7-FC4 3'  GTGGGGGGGCCCCGTGGGCA   61568      _     TT TG
                                TGCCC TGGGGT  C  CCCGC
                                |||||  ||||||  |  |||||
                                ACGGG GCCCCG  G  GGGTG
                                   T     GG __
GAM593  A        5'  GTGAGTGGGGCTCCTGGGT   27338      T    TT T  C
                                GCCC GGGGT  C GC CGC
                                |||| |||||  | || |||
```

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                                TGGG CCTCG  G TG GTG
                                  T    GG _  A
GAM593  ACTR1A   3'  GTGCCCTGAGGCCCCAGGCA  63653     C       TGCCC
                                TGCC TGGGGTTTC    GCAC
                                |||| |||||||||    ||||
                                ACGG ACCCCGGAG    CGTG
                                  _       TCC__
GAM593  AD-003   3'  GTGGAAGGGGCTCCAGGGC   26780         TT  GC
                                GCCCTGGGGT  CT  CCGC
                                ||||||||||  ||  ||||
                                CGGGACCTCG  GA  GGTG
                                      GG  A_
GAM593  AKAP11   3'  GTGTGGGTAGAGGCTTTAAGCA 58464     CC
                                TGC  TGGGGTTTCTGCCCGCAC
                                |||  ||||||||||||||||||
                                ACG  ATTTCGGAGATGGGTGTG
                                  A_
GAM593  ALLC     5'  GTGCAAAGGCCCTGGGGCA   37981      TG     C   CC
                                TGCCC  GGGTTT TGC  GC
                                |||||  ||||||  |||  ||
                                ACGGG  CCCGGA ACG  TG
                                   GT     A  __
GAM593  AP1G2    5'  GTGAGGCTGGAGTCCTGGGGTA 15356      TG  GT   T  _   AC
                                TGCCC  GG  TTC GCC CGC
                                |||||  ||  ||| ||| |||
                                ATGGG  CC  AGG CGG GTG
                                   GT  TG   T   A
GAM593  APELIN   3'  GCATGGAAGTGCCAGGGT    34267       G      CCC
                                GCCCTGG GTTTCTG   GC
                                |||||||  |||||||   ||
                                TGGGACC TGAAGGT   CG
                                    G      A__
GAM593  APXL2    5'  GTTCCAGGAGGTCTCAGGGTA  75685         GT    GCCC
                                TGCCCTGGG  TTCT    GC
                                |||||||||  ||||    ||
                                ATGGGACTC  GAGG    TG
                                      TG    ACCT
GAM593  ARHF     5'  TGCTGCGGGCTCCGGGCA    39280      T    TT   CC
                                TGCCC GGGGT  CTGC  GCA
                                |||||  |||||  ||||  |||
                                ACGGG CCTCG  GGCG  CGT
                                  _    ___    T_
GAM593  ARHGEF9  3'  GTGAGTTAGGGGCCCAGGGGCA 31492       G    TT   _ C   AC
                                TGCCCT GGGT  CTG C CGC
                                ||||||  ||||  |||  |  |||
                                ACGGGG CCCG  GAT G GTG
                                   A   GG   T A
GAM593  ARPC5    3'  GTGTAATTTAAACTCTGGGCA  20359      T      CTGCCC
                                TGCCC GGGGTTT     GCAC
                                |||||  |||||||     ||||
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```
                                ACGGG TCTCAAA     TGTG
                                  _       TTTAA_
GAM593  AUTL1    5'  GTGCGGGCTGGTTTTGTGGC  52727     C GG  TT  T
                                GCC T  GG  TC GCCCGCAC
                                ||| |  ||  || ||||||||
                                CGG G  TT  GG CGGGCGTG
                                  T TT  __  T
GAM593  BCL2L1   3'  GCTATGGGAGCCCCAGGGT   57594            CCC
                                GCCCTGGGGTTTCTG   GC
                                ||||||||||||||   ||
                                TGGGACCCCGAGGGT   CG
                                        AT_
GAM593  BLR1     3'  GTGGAGAACTCCTAGGGT    53118        GT    GC
                                GCCCTGGG  TTCT  CCGC
                                ||||||||  ||||  ||||
                                TGGGATCC  AAGA  GGTG
                                    TC   __
GAM593  BSMAP    3'  GCCCAGGAGTCCAAGGGCA   25045       G  GT    CCC
                                TGCCCT GG  TTCTG   GC
                                |||||| ||  |||||   ||
                                ACGGGA CC  AGGAC   CG
                                   A  TG    C__
GAM593  BSPECV   3'  GTGCAACACCAAACTTCAGGG  34047          CTGCCC
                                CCCTGGGGTTT     GCAC
                                ||||||||||     ||||
                                GGGACTTCAAA     CGTG
                                      CCACAA
GAM593  C11orf21  3'  GCCAGGTGGAAGCCATTGGGGT 27104      TG _     TG  C_  AC
                                GCCC  G GGTTTC  CC  GC
                                ||||  | ||||||  ||  ||
                                TGGG  T CCGAAG  GG  CG
                                  GT A     GT  AC
GAM593  C11orf21  3'  GTGAACCTGGGGAGCCTCGGGG 27108       _       GCCCG_
           GCA                    TGCCCT GGGGTTTCT     CAC
                                ||||||| |||||||||     |||
                                ACGGGG CTCCGAGGG     GTG
                                   G        GTCCAA
GAM593  C11orf9   3'  GCTCCCAAGAAGTCCCAGGGCA 26119         GT    GCCC_  AC
                                TGCCCTGGG  TTCT    GC
                                |||||||||  ||||    ||
                                ACGGGACCC  AAGA    CG
                                     TG    ACCCT
GAM593  C12orf22  5'  GTGAGTAGGGGCTTTGGGGC   48711     TG    TT    C
                                GCCC  GGGT  CTGC CGC
                                ||||  ||||  |||| |||
                                CGGG  TTCG  GATG GTG
                                  GT    GG    A
GAM593  C19orf7   3'  GTTTCTAGAACCCTAGGGT   61783          T   CCC
                                GCCCTGGGGTT CTG   GC
                                |||||||||| |||   ||
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                                TGGGATCCCAA GAT   TG
                                      _  CTT
GAM593  C20orf124 3'  GTGCGGGTGTCTTTCCTGGGGC 45843      TG   TTTCT
           A                   TGCCC  GGG    GCCCGCAC
                               |||||  |||    ||||||||
                               ACGGG  CCT    TGGGCGTG
                                  GT   TTCTG
GAM593  C20orf150 3'  GCCCCACAGAAGGCTCAGGGCA 66013         G     CCC_  AC
                               TGCCCTGGG TTTCTG    GC
                               |||||||||  ||||||    ||
                               ACGGGACTC GAAGAC    CG
                                     G     ACCC
GAM593  C20orf60  3'  GTGTGGTGGCACAGTCCTGGTG 54807    C TG  GT TC   __
           T                   GC C  GG  T  TGCC  CGCAC
                               || |  ||  |  ||||  |||||
                               TG G  CC  A  ACGG  GTGTG
                                T GT  TG C_   TG
GAM593  C21orf93  3'  GTGCAAGGAGCCTTGGGC    59746     T       GCC
                               GCCC GGGGTTTCT   CGC
                               ||||  |||||||||   |||
                               CGGG TTCCGAGGA   GTG
                                 _       AC_
GAM593  C5orf6    5'  GTGTGCAAGTCAAATCCTGGGG 33955     TG     C___   C   AC
                               CCC  GGGTTT    TGC CGC
                               |||  ||||||    ||| |||
                               GGG  CCTAAA    ACG GTG
                                 GT     CTGA   T
GAM593  C5orf7    5'  GTGCGGAGGGAGGCCTTGCGGG 64599      _        GC
           C                   GCCC TGGGGTTTCT  CCGCAC
                               ||||  ||||||||||  ||||||
                               CGGG GTTCCGGAGG  GGCGTG
                                 C         GA
GAM593  C6orf33   5'  GTGGCCGGGACCCCGAGGC    56720     C     TT T   C
                               GCC TGGGGT  C GCC GC
                               ||| ||||||  | ||| ||
                               CGG GCCCCA  G CGG TG
                                 A     GG C   _
GAM593  CAMKK2    3'  GTGCTAGGGAAGTTTCAGGGTA 22626         GG    GCCC
                               TGCCCTGG  TTTCT    GCAC
                               ||||||||  |||||    ||||
                               ATGGGACT  GAAGG    CGTG
                                    TT    GAT_
GAM593  CBLN1     5'  GTGCGGGCAGGAGGCGGCGGCA 16371      _  GGG
                               TGCC CTG   TTTCTGCCCGCAC
                               ||||  |||   ||||||||||||
                               ACGG GGC   GAGGACGGGCGTG
                                 C   G__
GAM593  CCRK      5'  GTGGAGTTTGGAAGTTCAGGGG 25077       G GG    __  _    AC
           CA                    TGCCCT G  TTTCT  GC CCGC
                               ||||||  |  |||||  ||  ||||
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                                ACGGGG C  GAAGG  TG GGTG
                                   A TT    TT  A
GAM593  CDC16    5'  GTGTGGGTGGGGACCTGCGGC  15339     CTG   TT TG
                                GCC   GGGT  C  CCCGCAC
                                |||   ||||  |  |||||||
                                CGG   TCCA  G  GGGTGTG
                                  CG_   GG GT
GAM593  CDT1     3'  GTGAAGGGGGCTCTGTGGCA   78165      C     TT  GCC
                                TGCC TGGGGT  CT   CGC
                                |||| ||||||  ||   |||
                                ACGG GTCTCG  GG   GTG
                                  T     GG  AA_
GAM593  CDT6     3'  GGGAGGAAACTCCAGGGCA   41251             G
                                TGCCCTGGGGTTTCT CCC
                                |||||||||||||| |||
                                ACGGGACCTCAAAGG GGG
                                         A
GAM593  CECR2    5'  GCGGCGGGAGTCCCAGGTCG   49434    C     GT      C
                                TG CCTGGG  TTCTGCC GC
                                || ||||||  ||||||| ||
                                GC GGACCC  AGGGCGG CG
                                 T     TG      _
GAM593  CENTA1   3'  GTGGCCCTGGGGGGTCCCGGGCA 23447      T   TT   C__   AC
                                TGCCC GGGG  TCTG   CCGC
                                ||||| ||||  ||||   ||||
                                ACGGG CCCT  GGGT   GGTG
                                   _   GG    CCC
GAM593  CENTG1   3'  GAGGGGAAGCCCAGGGT     29354        G    G  CG
                                GCCCTGGG TTTCT CC  C
                                |||||||| ||||| ||  |
                                TGGGACCC GAAGG GG  G
                                     _    _  AT
GAM593  CENTG1   3'  GTGGGGAGGGCGTTTTGGGGTA 29358      TG GG _   G    AC
                                TGCCC  G  T TTCT CCCGC
                                |||||  |  | |||| |||||
                                ATGGG  T  G GGGA GGGTG
                                   GT TT C    G
GAM593  CENTG2   5'  GCGCGGGGGCCCCGGCGC    30540    C     TT   CC
                                GC CTGGGGT  CTGC  GC
                                || |||||||  ||||  ||
                                CG GGCCCCG  GGCG  CG
                                 C      GG   __
GAM593  CEP3     5'  GTGCGCCCGCGGGAGGCCCGGG 22250         G     C__
            GCA                    TGCCCTGGG TTTCTGC   CGCAC
                                |||||||||| |||||||   |||||
                                ACGGGGCCC GAGGGCG   GCGTG
                                      G      CCC
GAM593  CEZANNE  3'  GAGGTGGGCAGAAGTCTTGGGG 39895     TG  GT        AC
                                CCC  GG  TTCTGCCCGC
                                |||  ||  ||||||||||
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                                GGG  TC  AAGACGGGTG
                                  GT  TG        GAGG
GAM593  CITED1    5'  GTGCGGGCTTTTCCCAGGC   15970     C    TTTCT
                                GCC TGGGG    GCCCGCAC
                                ||| |||||    ||||||||
                                CGG ACCCT    CGGGCGTG
                                  _    TTT__
GAM593  CLL-1     3'  GTGTAGGGGGTGGGGGTTCTAG 57178     C   GG TT TG  ___
           GC                     GCC TGG  T  C  CCC   GCAC
                                ||| |||  |  |  |||   ||||
                                CGG ATC  G  G  GGG   TGTG
                                  _  TT GG GT   GGA
GAM593  CPLX1     3'  GTGCGGGCGGGGCGAGGGCG   22824      GGG  TT T
                                TGCCCT   GT  C GCCCGCAC
                                ||||||   ||  | ||||||||
                                GCGGGA   CG  G CGGGCGTG
                                   G__  GG _
GAM593  CSEN      3'  GCCAGGGAGCCCGGGGCA    26459        G TT   CCC
                                TGCCCTGGG T  CTG   GC
                                |||||||| |  |||   ||
                                ACGGGGCCC A  GAC   CG
                                     G GG   ___
GAM593  DC-TM4F2  3'  GCTCAGAAGCTCCAGGCA    48901     C         CCC
                                TGCC TGGGGTTTCTG   GC
                                |||| ||||||||||   ||
                                ACGG ACCTCGAAGAC   CG
                                  _         T__
GAM593  DDX18     5'  GTGTGGCGCCTTATTCTAGGCA 23198     C     TTCT  _
                                TGCC TGGGGT    GC CCGCAC
                                |||| ||||||    || ||||||
                                ACGG ATCTTA    CG GGTGTG
                                  _     TTC_  C
GAM593  DDX31     3'  GTGGAACCTGGAAGCCCCGGGT 57613      T        C___    AC
                                GCCC GGGGTTTCTG    CCGC
                                |||| ||||||||||    ||||
                                TGGG CCCCGAAGGT    GGTG
                                  _         CCAA
GAM593  DDX33     3'  GTGTGGGCGGGGGGGGGTGGGGG 39787       GGGG__ TT
           GCA                     TGCCCT     T  CTGCCCGCAC
                                ||||||     |  ||||||||||
                                ACGGGG     G  GGCGGGTGTG
                                   GGTGGG GG
GAM593  DDX34     3'  GTGCTGCCTGAGGGGTCCTGGG 28676      T   TT  ___  CC
           TA                      TGCCC GGGG  TCT   GC  GCAC
                                ||||| ||||  |||   ||  ||||
                                ATGGG TCCT  GGA   CG  CGTG
                                  _   GG   GTC  T_
GAM593  DJ102H19.4 3'  GTGGGTTGGGGATCCCAAGGCA 42243     C     TT  _    AC
                                TGCC TGGGGT  CTG CCCGC
                                |||| ||||||  ||| |||||
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                                ACGG ACCCTA  GGT GGGTG
                                  A     GG   T
GAM593  DKFZP434A0131 3'  GCCAGGAGTCCCAGAGCA    39151     C    GT    CCC
                                TGC CTGGG  TTCTG   GC
                                ||| |||||  |||||   ||
                                ACG GACCC  AGGAC   CG
                                  A    TG    ___
GAM593  DKFZP434A0225 3'  GCATCCTAGAGTGCTCCAGGGC 95523          _    CCC_  AC
          A                      TGCCCTGGGGT TTCTG    GC
                                ||||||||||| |||||    ||
                                ACGGGACCTCG GAGAT    CG
                                       T    CCTA
GAM593  DKFZP434A1319 5'  GCCCTGCAGGCCTCGGGGCA   50460          TT    CC_
                                TGCCCTGGGGT  CTGC   GC
                                ||||||||||  ||||   ||
                                ACGGGGCTCCG  GACG   CG
                                       __    TCC
GAM593  DKFZP434B0335 5'  TGCGAGGAGTCCCGGGGT    94060        GT    GCC    C
                                GCCCTGGG  TTCT   CGCA
                                ||||||||  ||||   ||||
                                TGGGGCCC  AGGA   GCGT
                                     TG    ___
GAM593  DKFZP434B103 5'  GCCTTGGGGACATTTAGGGCA  32225         _ TT   CCC
                                TGCCCTGGG GT  CTG   GC
                                |||||||| ||  |||   ||
                                ACGGGATTT CA  GGT   CG
                                      A  GG   TC_
GAM593  DKFZP434B103 5'  GTGCTGTCAGAGGCCTTGGGGA 32226    _   TG       CCC
          CA                     TG CCC  GGGTTTCTG   GCAC
                                || |||  |||||||||   ||||
                                AC GGG  TCCGGAGAC   CGTG
                                 A  GT       TGT
GAM593  DKFZP434B103 5'  GTGTGTTAGAGGTCCCAGGGGC 32227      _   GT    CC
          A                      TGCCC TGGG  TTCTG  CGCAC
                                ||||| ||||  |||||  |||||
                                ACGGG ACCC  GAGAT  GTGTG
                                   G    TG    T_
GAM593  DKFZP434C131 3'  GTGGGGAGAGTCTGGGGC    69641     TG  GT   G
                                GCCC  GG  TTCT CCCGC
                                ||||  ||  |||| |||||
                                CGGG  CT  GAGA GGGTG
                                   GT  __    G
GAM593  DKFZP434P0316 5'  GTGCGGGCGTTCGATAGGGT   50453       GGGTTTC
                                GCCCTG      TGCCCGCAC
                                ||||||      |||||||||
                                TGGGAT      GCGGGCGTG
                                    AGCTT__
GAM593  DKFZP434P211 5'  GTGTGCTCCGAGTTCCAGGGC  28030       GG   CT_  C   AC
                                GCCCTGG  TTT   GC CGC
                                |||||||  |||   || |||
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                                CGGGACC  GAG   CG GTG
                                    TT   CCT  T
GAM593   DKFZp547I094 3'  GCAGGGCAGGGGCTCCAGG    50561         TT     _
                                CCTGGGGT  CTGCCC GC
                                ||||||||  |||||| ||
                                GGACCTCG  GACGGG CG
                                    GG      A
GAM593   DKFZP564I0422 5'  GCCTCAGTAGAGACCTAAGGGC 49517       G         CC__  AC
                                GCCCT GGGTTTCTGC    GC
                                ||||| ||||||||||    ||
                                CGGGA TCCAGAGATG    CG
                                   A          ACTC
GAM593   DKFZP566J091 3'  GTGGCTCTGGGGATGCCAGGGC 48865         G  TT   C__    AC
            A                      TGCCCTGG GT  CTG   CCGC
                                ||||||||  ||  |||   ||||
                                ACGGGACC TA  GGT   GGTG
                                     G  GG   CTC
GAM593   DKFZP586I2223 3'  GTGCGGGCAGGAGGCGGG    55772      GGG
                                CCTG   TTTCTGCCCGCAC
                                ||||   ||||||||||||
                                GGGC   GAGGACGGGCGTG
                                  G__
GAM593   DKFZP586J1624 3'  GTGCAGAGCCAGGGGTCTGAGG 32048        G   TT    _ CC_
            GCA                    TGCCCT GGG  TCTG C   GCAC
                                ||||||  |||  |||| |   ||||
                                ACGGGA TCT  GGAC G   CGTG
                                    G   GG    C AGA
GAM593   DKFZP586P0123 3'  GTCAAGGAAATCCTAGGGC    96496             GCCC
                                GCCCTGGGGTTTCT    GC
                                ||||||||||||||    ||
                                CGGGATCCTAAAGG    TG
                                         AAC_
GAM593   DKFZP761C169 3'  GCTTTAGAAATCTTAGTGT    68422     C          CCC
                                GC CTGGGGTTTCTG   GC
                                || ||||||||||||   ||
                                TG GATTCTAAAGAT   CG
                                 T          TT_
GAM593   DKFZP761I2123 3'  GCTTCAAGCAGAGGCCTCGGGG 49547               CC___  AC
            T                      GCCCTGGGGTTTCTGC     GC
                                ||||||||||||||||     ||
                                TGGGGCTCCGGAGACG     CG
                                         AACTT
GAM593   DKFZp761O0113 5'  GTGCAAACAGGTCTCATGGT   37897     C     TT    CCC
                                GCC TGGGG  TCTG   GCAC
                                ||| |||||  ||||   ||||
                                TGG ACTCT  GGAC   CGTG
                                  T     __    AAA
GAM593   DNAJA4    3'  GTGTGGCATCACAGGCCCGGGG 38362          G  TC__    _   AC
            CA                     TGCCCTGGG TT    TGCC CGC
                                ||||||||| ||    |||| |||
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                                ACGGGGCCC GA   ACGG GTG
                                     G  CACT   T
GAM593  DPYSL4   3'  GCCGCGGGGGCCCCAGGGCA  22228         TT   CC
                                TGCCCTGGGGT  CTGC  GC
                                ||||||||||  ||||  ||
                                ACGGGACCCCG  GGCG  CG
                                      GG   C_
GAM593  DRG1     5'  GTGTGGAGGCCACAGGGTA   15973       G     TG CC
                                TGCCCTG GGTTTC  C  GC
                                |||||||  ||||||  |  ||
                                ATGGGAC CCGGAG  G  TG
                                   A     GT __
GAM593  DXS9928E 3'  GTGTCACCGGGACTCCAGGCA 17475     C     TT TGCCC
                                TGCC TGGGGT  C    GCAC
                                ||||  ||||||  |    ||||
                                ACGG ACCTCA  G    TGTG
                                  _     GG CCAC_
GAM593  E2IG4    3'  GCCTCTGGAAGCTTAGGGCA  92547        G   TGCCC
                                TGCCCTGGG TTTC    GC
                                |||||||||  ||||    ||
                                ACGGGATTC AAGG    CG
                                     G   TCTC_
GAM593  FBP17    3'  GTGCCTGCGAGCCTCGGGT   73156     T     CT  CC
                                GCCC GGGGTTT  GC  GCAC
                                ||||  |||||||  ||  ||||
                                TGGG CTCCGAG  CG  CGTG
                                  _      __  TC
GAM593  FBX30    3'  GTACAGGATGTCCCAGGGTA  53748         TT   GCCC
                                TGCCCTGGGG  TCT   GC
                                ||||||||||  |||   ||
                                ATGGGACCCT  AGG   TG
                                     GT   ACA_
GAM593  FEM-2    3'  GTGCACGTGGGACCCTGGGGC 28320     TG   TT T  CC
                                GCCC  GGGT  C GC  GCAC
                                ||||  ||||  | ||  ||||
                                CGGG  CCCA  G TG  CGTG
                                  GT   GG _  CA
GAM593  FER1L4   5'  GCTGCAGGAGCTCCAGGG    48125           CC  AC
                                CCCTGGGGTTTCTGC  GC
                                ||||||||||||||  ||
                                GGGACCTCGAGGACG  CG
                                        T_  C
GAM593  FKBP4    3'  GTGGAGAGGGAGACTCCTGGGC 10643      T       GC__   AC
          A                      TGCCC GGGGTTTCT   CCGC
                                |||||  |||||||||   ||||
                                ACGGG CCTCAGAGG   GGTG
                                   T       GAGA
GAM593  FLJ00007 3'  GCTCTGCAGAAGCTCTGGGGT  71778     TG       CC_  AC
                                GCCC  GGGTTTCTGC   GC
                                ||||  ||||||||||   ||
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                                TGGG  CTCGAAGACG   CG
                                  GT         TCT
GAM593  FLJ00024  3' GTGCAGTCAGGCTCTGGGT   64503     T    TT   CCC
                                GCCC GGGGT  CTG   GCAC
                                |||| |||||  |||   ||||
                                TGGG TCTCG  GAC   CGTG
                                  _    __   TGA
GAM593  FLJ00058  5' GTGACCCGGGGGGGGCTTCCGGG 79508     T    TT TG   ___
           T                     GCCC GGGGT  C  CCCG   CAC
                                |||| |||||  |  ||||   |||
                                TGGG CTTCG  G  GGGC   GTG
                                  C    GG __    CCA
GAM593  FLJ10040  5' GCAGCAGGAGCTCCAGGC    36220     C         CC
                                GCC TGGGGTTTCTGC  GC
                                ||| ||||||||||||  ||
                                CGG ACCTCGAGGACG  CG
                                  _         A_
GAM593  FLJ10079  3' GTGGTGCAGGTCTCAGGGCA   60834         TT    _
                                TGCCCTGGGG  TCTGC CCGC
                                ||||||||||  ||||| ||||
                                ACGGGACTCT  GGACG GGTG
                                      __     T
GAM593  FLJ10081  3' GTGTCTAGGAGTCTCAGGCA   36293     C   GT    CC
                                TGCC TGGG  TTCTG  CGC
                                |||| ||||  |||||  |||
                                ACGG ACTC  AGGAT  GTG
                                  _   TG    CT
GAM593  FLJ10297  3' GTGTGGGCAGGGGCTGCA    36443    G   TT
                                TG GGT  CTGCCCGCAC
                                || |||  ||||||||||
                                AC TCG  GACGGGTGTG
                                 G   GG
GAM593  FLJ10350  5' TGCGGGCGCGGGGCTCCGGGGC 97254          TT _      C
                                GCCCTGGGGT  C TGCCCGCA
                                ||||||||||  | ||||||||
                                CGGGGCCTCG  G GCGGGCGT
                                      GG C       C
GAM593  FLJ10375  3' GGCAGGGGGGGGTACCCGGGGCA 36559         GTT   G   _  AC
                                TGCCCTGGG   TCT CCC GC
                                |||||||||   ||| ||| ||
                                ACGGGGCCC   GGG GGG CG
                                     AT_   G   A  GT
GAM593  FLJ10716  3' TGTGAGTGCTCTGGGGCA    37022      TG    TTCT  C
                                TGCCC  GGGT    GC CGCA
                                |||||  ||||    || ||||
                                ACGGG  CTCG    TG GTGT
                                  GT    _____  A
GAM593  FLJ10748  5' GTGGAGGAAGCCCTGGGG    37103     TG      GC
                                CCC  GGGTTTCT  CCGC
                                |||  ||||||||  ||||
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                                GGG  CCCGAAGG  GGTG
                                  GT       A_
GAM593  FLJ10759  3'  GTGGCCACTGGAGACCTCAGGC 37124    C          ___ C    AC
            CA                    TG CCTGGGGTTTCT   G CCGC
                                  || ||||||||||||   | ||||
                                  AC GGACTCCAGAGG   C GGTG
                                   C          TCA C
GAM593  FLJ10769  3'  GCTGGGCAGGGGTCCCCGGGT  37145     T   _ TT     _  AC
                                  GCCC GGGG T  CTGCCC GC
                                  |||| |||| |  |||||| ||
                                  TGGG CCCC G  GACGGG CG
                                    _   T GG     T
GAM593  FLJ10811  3'  GCACCGGAGATCTTGAGGCA   37223     CT        CCC
                                  TGCC  GGGGTTTCTG   GC
                                  ||||  ||||||||||   ||
                                  ACGG  TTCTAGAGGC   CG
                                    AG         CA_
GAM593  FLJ10842  3'  GTGTCGTCAGAGGGTCCCCAGG 37272          __      CC  _
            GCA                     TGCCCTGGGG  TTTCTG  CG CAC
                                  ||||||||||  ||||||  || |||
                                  ACGGGACCCC  GGAGAC  GC GTG
                                        TG     T_  T
GAM593  FLJ10853  5'  GTGCACGGAGGAGTTCCGGGG  37318       GG     G  C_
                                  CCCTGG  TTTCT CC  GCAC
                                  ||||||  ||||| ||  ||||
                                  GGGGCC  GAGGA GG  CGTG
                                     TT     _  CA
GAM593  FLJ10996  5'  AGCTGGGCATTTCAGGGCA    39303       GG TTTC     _  AC
                                  TGCCCTG  G    TGCCC GC
                                  |||||||  |    ||||| ||
                                  ACGGGAC  T    ACGGG CG
                                     TT _____     T  AC
GAM593  FLJ11099  3'  GCCATGGACCTCAGGGCA    37607           TC  CCC
                                  TGCCCTGGGGTT  TG   GC
                                  ||||||||||||  ||   ||
                                  ACGGGACTCCAG  AC   CG
                                        GT  ____
GAM593  FLJ11259  3'  GTGTAGGGAGTTCGGGGTA    37771         G TT    CC
                                  TGCCCTGGG T  CTGC  GC
                                  |||||||| |  ||||  ||
                                  ATGGGGCTT A  GATG  TG
                                       G GG    __
GAM593  FLJ11618  3'  GTGTGGCTCATCTCGGGG     42626         TTCT   _
                                  CCCTGGGGT    GCC CGC
                                  |||||||||    ||| |||
                                  GGGGCTCTA    CGG GTG
                                       CT__   T
GAM593  FLJ11726  3'  GTGTGGGTAGCAGGCCTAGGG  47030        G  T
                                  CCCTGGG TT CTGCCCGCAC
                                  ||||||| || ||||||||||
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                                GGGATCC GA GATGGGTGTG
                                    G  C
GAM593  FLJ12078  3'  GTGAAGTGGAAAATCCAGGGCA 47085        GG    TG C_   AC
                                TGCCCTGG  TTTC  C  CGC
                                ||||||||  ||||  |  |||
                                ACGGGACC  AAAG  G  GTG
                                     TA    GT AA
GAM593  FLJ12221  5'  GTGCGGTAGGGGTCCCGGGGC  63225         TT     C
                                GCCCTGGGG  TCTGCC GCAC
                                |||||||||  ||||||  ||||
                                CGGGGCCCT  GGATGG CGTG
                                     GG     _   G
GAM593  FLJ12587  3'  GCAGAGGGACCCCAGGGT    42779          __
                                GCCCTGGGGTT  TCTGC
                                ||||||||||  |||||
                                TGGGACCCCAG  AGACG
                                      GG
GAM593  FLJ12671  3'  GTGCTAACCACAGGTGTCCCAG 49111         TT   CCC___
          GGT                     GCCCTGGGG  TCTG     GCAC
                                |||||||||  ||||     ||||
                                TGGGACCCT  GGAC     CGTG
                                     GT    ACCAAT
GAM593  FLJ12747  5'  GCTATGAGAGCTCCAGGGT   50667          T  GCCC
                                GCCCTGGGGTT CT    GC
                                ||||||||||| ||    ||
                                TGGGACCTCGA GA    CG
                                      _  GTAT
GAM593  FLJ12750  3'  GTGCCAAGGGCTCTGGGGC   45441      TG    TC  CCC
                                GCCC  GGGTT  TG   GCAC
                                ||||  |||||  ||   ||||
                                CGGG  CTCGG  AC   CGTG
                                  GT    GA  ___
GAM593  FLJ12750  3'  GTGGCTGGGCCTCAGGGT    45442          CT   C
                                GCCCTGGGGTTT  GCC GC
                                ||||||||||||  ||| ||
                                TGGGACTCCGGG  CGG TG
                                      T_  _
GAM593  FLJ13055  3'  GGCAGGGTCCTTGGGGTA    43019      TG   T
                                TGCCC  GGG TTCTGCC
                                |||||  ||| |||||||
                                ATGGG  TCC GGGACGG
                                   GT   T
GAM593  FLJ13114  3'  GTGAGGCAAGCCTCAGGGTA   44909          TC   _
                                TGCCCTGGGGTT  TGCC CGC
                                ||||||||||||  |||| |||
                                ATGGGACTCCGA  ACGG GTG
                                      __   A
GAM593  FLJ13262  5'  GTGCGGGATGTGGAGGGGCCCG 46695        G TT  G_____
          GGGC                    GCCCTGGG T  CT     CCCGCAC
                                |||||||| |  ||     |||||||
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                                CGGGGCCC G  GA     GGGCGTG
                                    _ GG  GGTGTA
GAM593  FLJ13855  5'  GGGCGGCGGGCCCCGGGGC   43852          _
                                GCCCTGGGGTTT CTGCCC
                                |||||||||||| ||||||
                                CGGGGCCCCGGG GGCGGG
                                      C
GAM593  FLJ13855  5'  GTGTGGGCGGCGGCGGCGGCA 43855     _ GGG  TT
                                TGCC CT   GT  CTGCCCGCAC
                                |||| ||   ||  ||||||||||
                                ACGG GG   CG  GGCGGGTGTG
                                  C ___  GC
GAM593  FLJ13964  3'  GTGCAATGTGAATTTTAGGG   50755          CT  CC_
                                CCCTGGGGTTT  GC   GCAC
                                ||||||||||  ||   ||||
                                GGGATTTTAAG  TG   CGTG
                                      __ TAA
GAM593  FLJ14082  3'  GTGAAGCAGAAGCCCCTGGGGT 47323       _        C_  AC
          A                      TGCCCT GGGGTTTCTGC  CGC
                                |||||| ||||||||||  |||
                                ATGGGG CCCCGAAGACG  GTG
                                    T          AA
GAM593  FLJ14154  3'  GCACAGGAGCCTCGGGACA   46233    C          CCC
                                TG CCTGGGGTTTCTG   GC
                                || ||||||||||||   ||
                                AC GGGCTCCGAGGAC   CG
                                 A           A__
GAM593  FLJ14594  3'  GGGCAGGGACCCCCGGGC    52509     T    TT
                                GCCC GGGGT  CTGCCC
                                |||| |||||  ||||||
                                CGGG CCCCA  GACGGG
                                  C    GG
GAM593  FLJ14600  3'  GTGGGGTGGAAGTTTCAGG   52527      GG   TG  G
                                CCTGG  TTTC  CCC CAC
                                |||||  ||||  ||| |||
                                GGACT  GAAG  GGG GTG
                                   TT   GT  _
GAM593  FLJ20004  3'  GTGCAAAGGCCCTGAGGCA   34764     CT     C  CC
                                TGCC  GGGGTTT TGC  GC
                                ||||  ||||||| |||  ||
                                ACGG  TCCCGGA ACG  TG
                                  AG      A  __
GAM593  FLJ20006  5'  GTGTGGGTCCCCACTCCCAGGG 34787       _ TTCT
                                CCCTGGG GT    GCCCGCAC
                                |||||||  ||    ||||||||
                                GGGACCC CA    TGGGTGTG
                                    T  CCCC
GAM593  FLJ20034  3'  GTGATGGGGGAGGTTTGGGGT  34852     TG  G   TG   _
                                GCCC  GG TTTC  CCCG CAC
                                ||||  || ||||  |||| |||
```

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                                TGGG  TT GAGG  GGGT GTG
                                  GT  G   __   A
GAM593  FLJ20080  5' GTGGGATGGGGGTCCCGCGGCA 34985     C    TT   _    AC
                                TGCC TGGGG  TCTG CCCGC
                                |||| |||||  |||| |||||
                                ACGG GCCCT  GGGT GGGTG
                                  C    GG   A
GAM593  FLJ20084  5' GTCTGGTACAGGTTTCAGGGCA 34998       GG TT C   C_  AC
                                TGCCCTG  G  T TGCC  GC
                                |||||||  |  | ||||  ||
                                ACGGGAC  T  A ATGG  TG
                                    TT GG C   TC
GAM593  FLJ20257  5' GTGCGCATGCGTGGTTCCGGGG 39491       GG  TC   C__
          C                      GCCCTGG  TT  TGC   CGCAC
                                |||||||  ||  |||   |||||
                                CGGGGCC  GG  GCG   GCGTG
                                    TT  T_   TAC
GAM593  FLJ20296  3' GTGTGGTTCTGGAGCTTTGGGG 35367     TG     TGC_
          TA                     TGCCC  GGGTTTC   CCGCAC
                                |||||  |||||||   ||||||
                                ATGGG  TTCGAGG   GGTGTG
                                  GT     TCTT
GAM593  FLJ20371  5' GTGCGGCCGGCCTTGGGACA  35539   C  TG   TTT   C
                                TG CC  GGG   CTG CCGCAC
                                || ||  |||   ||| ||||||
                                AC GG  TCC   GGC GGCGTG
                                 A  GT  ____  C
GAM593  FLJ20378  3' GGCAGGGGCTGTGGGGTA   35557       G   TT
                                TGCCCTG GGT  CTGCC
                                ||||||| |||  |||||
                                ATGGGGT TCG  GACGG
                                    G   GG
GAM593  FLJ20419  5' GTGTGAGGAGGACCCCGGGC  35608     T     T  G  _
                                GCCC GGGGTT CT CC CGCAC
                                |||| |||||| || || |||||
                                CGGG CCCCAG GA GG GTGTG
                                  _     _ _  A
GAM593  FLJ20604  5' GTGGAGAAGTGTCCGGGGTA  35868        GT_   GC
                                TGCCCTGGG   TTCT  CCGC
                                |||||||||   ||||  ||||
                                ATGGGGCCT   AAGA  GGTG
                                     GTG   __
GAM593  FLJ20718  3' GTGCGAAGGAATCTCAGG    36042          GCC
                                CCTGGGGTTTCT   CGCAC
                                ||||||||||||   |||||
                                GGACTCTAAGGA   GCGTG
                                       A__
GAM593  FLJ20793  3' GTGTGTGAACTTTATGGTA   93450      C      CT  C
                                TGCC TGGGGTTT  GC CGC
                                |||| ||||||||  || |||
```

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                                ATGG ATTTCAAG  TG GTG
                                  T       __ T
GAM593  FLJ20886  5' GTGATGGGCCACCGGGGCA   48068        GGTTTCT    _
                                TGCCCTGG      GCCCG CAC
                                ||||||||      ||||| |||
                                ACGGGGCC      CGGGT GTG
                                    AC_____     A
GAM593  FLJ21308  5' GTCCAGCGATCCCAGGGC    45193          T   CCC
                                GCCCTGGGGTT CTG   GC
                                |||||||||||| |||   ||
                                CGGGACCCTAG GAC   TG
                                      C   C__
GAM593  FLJ21369  3' GTGTGTAAAGAGCTTGGGGCA  46055      TG  G   C   C
                                TGCCC  GG TTT TGC CGC
                                |||||  || ||| ||| |||
                                ACGGG  TC AGA ATG GTG
                                   GT  G   A   T
GAM593  FLJ21438  5' GTGGCCATGGGGAACTTCAGGG 62200           ___ C    AC
                                CCCTGGGGTTTCT   G CCGC
                                ||||||||||||   | ||||
                                GGGACTTCAAGGG   C GGTG
                                       GTA C
GAM593  FLJ21596  3' GTGTCCTTGAGCTCTAGAGCA  46122     C        CTGCC
                                TGC CTGGGGTTT     CGC
                                ||| |||||||||     |||
                                ACG GATCTCGAG     GTG
                                  A        TTCCT
GAM593  FLJ22127  3' GCCTTAGGGTGGAGACTTTAGT 43201     C        TG  _____  AC
           GTA                    TGC CTGGGGTTTC  CCC    GC
                                |||  ||||||||||  |||    ||
                                ATG GATTTCAGAG  GGG    CG
                                  T        GT   ATTC
GAM593  FLJ22246  3' GTGCCCTGCAGGGCTCCAGGGC 48215          T    CC_
                                GCCCTGGGGTT CTGC   GCAC
                                |||||||||||  ||||   ||||
                                CGGGACCTCGG GACG   CGTG
                                      _    TCC
GAM593  FLJ22283  5' GCTATGCTGGGGTCCCAGGGT  50903         TT  T  CC_  AC
                                GCCCTGGGG  TC GC   GC
                                |||||||||  || ||   ||
                                TGGGACCCT  GG CG   CG
                                     GG  T  TAT
GAM593  FLJ22283  5' TGTGGGAGCCCTGGGGT     50905     TG    TCTG     C
                                GCCC  GGGTT    CCCGCA
                                ||||  |||||    ||||||
                                TGGG  CCCGA    GGGTGT
                                  GT     _____      C
GAM593  FLJ22378  3' TGTGGGGTGTCTCAGGGT    47602         TTTCTG     C
                                GCCCTGGGG     CCCGCA
                                |||||||||     ||||||
```

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                                TGGGACTCT     GGGTGT
                                    GTG___     C
GAM593  FLJ22393  3'  GTGCATCCTCAGAAGCTCTGGG 47778     T        CCC__
          T                  GCCC GGGGTTTCTG     GCAC
                             |||| ||||||||||     ||||
                             TGGG TCTCGAAGAC     CGTG
                               _        TCCTA
GAM593  FLJ22672  3'  GTGTGGGGAGGAGGGTCCTAGG 46599     C    __    G
          C                  GCC TGGGG  TTTCT CCCGCAC
                             ||| |||||  ||||| |||||||
                             CGG ATCCT  GAGGA GGGTGTG
                               _    GG    G
GAM593  FLJ22833  5'  GTGAGCGGGACTCAGGGCA   43407         GT     C
                             TGCCCTGGG  TTCTGC CGC
                             |||||||||  |||||| |||
                             ACGGGACTC  AGGGCG GTG
                                   __     A
GAM593  FLJ23093  5'  GTGCCCGAGGGCCTCAGGC   45328     C      TC  CCC
                             GCC TGGGGTT  TG   GCAC
                             ||| |||||||  ||   ||||
                             CGG ACTCCGG  GC   CGTG
                               _      GA  C__
GAM593  FLJ23185  3'  CAGTGGGTAGAAGACTCGGGGC 47512         G         AC
          A                  TGCCCTGGG TTTCTGCCCGC
                             ||||||||| ||||||||||
                             ACGGGGCTC GAAGATGGGTG
                                   A          ACT
GAM593  FLJ23399  5'  GTGGCTGTGAGGTCTCAGAGTA 43146     C    GT   TGC_   AC
                             TGC CTGGG  TTC    CCGC
                             ||| |||||  |||    ||||
                             ATG GACTC  GAG    GGTG
                               A    TG   TGTC
GAM593  FLJ23436  3'  GTGGGGAGTGGGGCCCCGGGGT 45464          TT __ G    AC
                             GCCCTGGGGT  C  T CCCGC
                             ||||||||||  |  | |||||
                             TGGGGCCCCG  G  A GGGTG
                                   GG TG G
GAM593  FLJ23436  3'  GTGTGGGCAGAAGATAAGGGGC 45465      GGGG
                             GCCCT    TTTCTGCCCGCAC
                             |||||    ||||||||||||||
                             CGGGG    GAAGACGGGTGTG
                                AATA
GAM593  FLJ23519  5'  GTGCCTGGGGAGGCTTCAGGGT 50958           TG   __
                             GCCCTGGGGTTTC  CCC  GCAC
                             ||||||||||||||  |||  ||||
                             TGGGACTTCGGAG  GGG  CGTG
                                     __   TC
GAM593  FLJ23519  5'  GTGCCTGGGGAGGCTTCAGGGT 50959           TG   __
                             GCCCTGGGGTTTC  CCC  GCAC
                             ||||||||||||||  |||  ||||
```

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                                TGGGACTTCGGAG  GGG  CGTG
                                       __   TC
GAM593  FLJ23590  3'  GTGGGAAGTTCCCAGGGCA   45367         TTT  G
                                TGCCCTGGGG   CT CCCGC
                                ||||||||||   || |||||
                                ACGGGACCCT   GA GGGTG
                                      T__  A
GAM593  FLJ23816  5'  GTGCCACAACCTCCAGGGCA  58979        _   TC  CCC
                                TGCCCTGG GGTT  TG   GCAC
                                |||||||| ||||  ||   ||||
                                ACGGGACC CCAA  AC   CGTG
                                     T   C_ ____
GAM593  FLJ23816  3'  GTGCGTCAGCGAGACCTTGGGT 58980    C  TG      T  C__
          CA                     TG CC  GGGTTTC GC   CGCAC
                                || ||  ||||||| ||   |||||
                                AC GG  TCCAGAG CG   GCGTG
                                 T  GT      _  ACT
GAM593  FLJ30567  3'  GTGGTTGGAGAGTTTGGGGTA  59477      TG  G    GC
                                TGCCC  GG TTTCT  CCGC
                                |||||  || |||||  ||||
                                ATGGG  TT AGAGG  GGTG
                                   GT  G    TT
GAM593  FLJ30567  3'  GTGTGGACAGAGTCCTGGGCA  59478      TG   T    C
                                TGCCC  GGG TTCTG CCGCAC
                                |||||  ||| ||||| ||||||
                                ACGGG  TCC GAGAC GGTGTG
                                   __   T    A
GAM593  FLJ31300  3'  GTGTGGGCAGCAATATAGGGTA 58932       GG   T
                                TGCCCTG  GTT CTGCCCGCAC
                                |||||||  ||| ||||||||||
                                ATGGGAT  TAA GACGGGTGTG
                                    A_  C
GAM593  FLJ31951  3'  GTGGGAAGGGCTTTAGGGCA  59230          T  G
                                TGCCCTGGGGTT CT CCCGC
                                |||||||||||| || |||||
                                ACGGGATTTCGG GA GGGTG
                                       _  A
GAM593  FLJ32332  3'  GTGGCTTGTAGAAACCTTTGGG 58946      TG       ___   AC
          CA                     TGCCC  GGGTTTCTGC   CCGC
                                |||||  ||||||||||   ||||
                                ACGGG  TCCAAAGATG   GGTG
                                   TT        TTC
GAM593  FLJ32356  3'  GTGTGGGTGGCACAGGATCTGG 59028      TG  GTTT___ TG
          GGCA                    TGCCC  GG      C  CCCGCAC
                                |||||  ||      |  |||||||
                                ACGGG  CT      G  GGGTGTG
                                   GT  AGGACAC GT
GAM593  FLJ32780  5'  GTTGGCAGAGGCCTCGGGGT   59298             C
                                GCCCTGGGGTTTCTGCC GC
                                |||||||||||||||| ||
```

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                                TGGGGCTCCGGAGACGG TG
                                                 T
GAM593  FLJ32818  5'  GTGTGGCCTGGGGGTTTGGGGG 59075      G GG TT __  _  AC
           T                     GCCCT G  T  CT  GCC CGC
                                 ||||| |  |  ||  ||| |||
                                 TGGGG T  G  GG  CGG GTG
                                    G TT GG  TC   T
GAM593  FPGT     5'  GTGCGGCGCGGTCTCAGGG   15181        TTT   _
                                 CCCTGGGG   CTGC CCGCAC
                                 ||||||||   |||| ||||||
                                 GGGACTCT   GGCG GGCGTG
                                      ___   C
GAM593  FREQ     3'  GTGAGTCCTCAGAGGCCCTGGG 27376     T       CCCG__
           C                     GCCC GGGGTTTCTG     CAC
                                 |||| ||||||||||     |||
                                 CGGG TCCCGGAGAC     GTG
                                   _        TCCTGA
GAM593  FRSB     3'  GTGTGGGTAGAGACCATCC    20292    __
                                 GG  GGTTTCTGCCCGCAC
                                 ||  ||||||||||||||
                                 CC  CCAGAGATGGGTGTG
                                  TA
GAM593  G4       5'  GTGAGTGAAACTTGGGGT    92640     TG  G    T  C
                                 GCCC  GG TTTC GC CGC
                                 ||||  || |||| || |||
                                 TGGG  TC AAAG TG GTG
                                   GT  _   _  A
GAM593  G4       3'  GTGGTTGGGAAACCCAGGGT   92641        G    GC
                                 GCCCTGGG TTTCT  CCGC
                                 |||||||| |||||  ||||
                                 TGGGACCC AAGGG  GGTG
                                      A     TT
GAM593  GAL3ST-4  3'  GTGAGCCACAGGAAGTTTGGGG 45282      TG  G    ___  C   AC
           C                     GCCC  GG TTTCT   GC CGC
                                 ||||  || |||||   || |||
                                 CGGG  TT AAGGA   CG GTG
                                   GT  G    CAC  A
GAM593  GMPPA    5'  GCTGGGAGCCCCGAGGCA    72649     C        _
                                 TGCC TGGGGTTTCT GC
                                 |||| |||||||||| ||
                                 ACGG GCCCCGAGGG CG
                                   A         T
GAM593  GOLGA2LY  5'  GTGTGGGAAGACAGCTCCAGGC 64946     C      _  G
                                 GCC TGGGGTT TCT CCCGCAC
                                 ||| ||||||| ||| |||||||
                                 CGG ACCTCGA AGA GGGTGTG
                                   _      C  A
GAM593  GPS2     5'  GTGTGGGTGTTCGTCGGGG   88510       _ TTTCT
                                 CCCTGG GG    GCCCGCAC
                                 |||||| ||    ||||||||
```

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                                GGGGCT CT    TGGGTGTG
                                   G  TG___
GAM593  GR6     5'  GTGGCCATGGAGCTCCTGGGT  24749     T      _  C   AC
                                GCCC GGGGTTTC TG CCGC
                                |||| |||||||| || ||||
                                TGGG CCTCGAGG AC GGTG
                                  T       T  C
GAM593  GRIN3A  5'  GGCGGAGACCTCAGGCA     56785     C
                                TGCC TGGGGTTTCTGCC
                                |||| ||||||||||||
                                ACGG ACTCCAGAGGCGG
                                  _
GAM593  GTPBG3  3'  GTGGAGACCCAGGAGCCTCGGG 51906           C____   AC
           G                     CCCTGGGGTTTCTG    CCGC
                                ||||||||||||||    ||||
                                GGGGCTCCGAGGAC    GGTG
                                      CCAGA
GAM593  GTPBP5  3'  GCAGAGGAGCCCCAGGGCA   65976          __
                                TGCCCTGGGGTT  TCTGC
                                ||||||||||||  |||||
                                ACGGGACCCCGA  AGACG
                                      GG
GAM593  HAIK1   5'  TGCGAAGGCCCAGGGGCA    31956       G     CTGCC
                                TGCCCT GGGTTT    CGCA
                                |||||| ||||||    ||||
                                ACGGGG CCCGGA    GCGT
                                   A     A____
GAM593  HES2    3'  GCTTCAGCAGCTCCAGGGTA  39376          T   CCC
                                TGCCCTGGGGTT CTG   GC
                                |||||||||||| |||   ||
                                ATGGGACCTCGA GAC   CG
                                      C   TT_
GAM593  HEYL    3'  GTGAGTTTGCAGAAACCTTGGG 28133    TG        CCG__
           G                     CCC  GGGTTTCTGC    CAC
                                |||  ||||||||||    |||
                                GGG  TCCAAAGACG    GTG
                                  GT         TTTGA
GAM593  HIG2    3'  GTGTGGGTGGGCTGTTGGGAGT 26205    _  TG _   TT TG
                                GC CC  G GGT  C  CCCGCAC
                                || ||  | |||  |  |||||||
                                TG GG  T TCG  G  GGGTGTG
                                 A  GT G   __ GT
GAM593  HIP-55  5'  GGGCGGAGACTGCGGGGC    26776       G
                                GCCCTG GGTTTCTGCCC
                                |||||| ||||||||||
                                CGGGGC TCAGAGGCGGG
                                   G
GAM593  HNK-1ST 5'  CGCGGCGCGGAGGCCTCGGGGC 17947              _    AC
           A                     TGCCCTGGGGTTTCTGC CCGC
                                |||||||||||||||| ||||
```

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                                ACGGGGCTCCGGAGGCG GGCG
                                          C    CC
GAM593  HNK-1ST  3'  GTGCCGCCGAGCCCGGGGT   17950        GT   T  CC
                                GCCCTGGG  TTC GC  GCAC
                                ||||||||  ||| ||  ||||
                                TGGGGCCC  GAG CG  CGTG
                                     __   C  C_
GAM593  HRD1     3'  GCCATGGGGATCTCGGGTCA   70149    C       TT   CCC
                                TG CCTGGGGT  CTG   GC
                                || ||||||||  |||   ||
                                AC GGGCTCTA  GGT   CG
                                 T       GG   AC_
GAM593  HSA243396 5'  GTGGAAGCTGGAGTTCCGGGGT 37845        GG    T __    AC
                                GCCCTGG  TTTC GC  CCGC
                                |||||||  |||| ||  ||||
                                TGGGGCC  GAGG CG  GGTG
                                     TT    T  AA
GAM593  HSJ1     3'  GTGGGGGGTGTCAGGGCA    23086         G TTT  G
                                TGCCCTGG G   CT CCCGC
                                |||||||| |   || |||||
                                ACGGGACT T   GG GGGTG
                                     G ___  G
GAM593  HSPB7    3'  GTTAGCAGGGGTCCCCAGGGCA 27785          _ TT    CC  AC
                                TGCCCTGGGG T  CTGC  GC
                                |||||||||| |  ||||  ||
                                ACGGGACCCC G  GACG  TG
                                       T GG    AT
GAM593  HT011    5'  GTGCCAAAGTTGAGAGACCCTG 38069      TG       __ CC__
           GGGTA                  TGCCC  GGGTTTCT  GC    GCAC
                                |||||  ||||||||  ||    ||||
                                ATGGG  CCCAGAGA  TG    CGTG
                                   GT       GT  AAAC
GAM593  HUMAGCGB 3'  GTGGGGGGGTCCAAGGGCA   26134       GG  TT   G
                                TGCCCT  GG  TCT CCCGC
                                ||||||  ||  ||| |||||
                                ACGGGA  CC  GGG GGGTG
                                    A_  T_   G
GAM593  IMP-1    3'  GTGTCAGAAATTCTAGCGCA   22605     C         CC
                                TGC CTGGGGTTTCTG  CGC
                                ||| ||||||||||||  |||
                                ACG GATCTTAAAGAC  GTG
                                  C          T_
GAM593  IMP-2    3'  TTGGGAGGTCTCACGGT     22612     C    TT   G    CAC
                                GCC TGGGG  TCT CCCG
                                ||| |||||  ||| ||||
                                TGG ACTCT  GGA GGGT
                                  C     __  _    TT
GAM593  ING5     3'  GTGCGGGCGGGGACATGGTA   51304      CTGGG  TT
                                TGCC    GT  CTGCCCGCAC
                                ||||    ||  ||||||||||
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                                ATGG    CA  GGCGGGCGTG
                                  TA___  GG
GAM593  ITM3     5'  GCACCGGCAGAGGCTGCGGGGC 48890       G        C__  AC
                                GCCCTG GGTTTCTGCC   GC
                                |||||| ||||||||||   ||
                                CGGGGC TCGGAGACGG   CG
                                   G         CCA
GAM593  JM11     3'  GTGGAGGGGATCTTGGGCA   54372      T    TT  GC
                                TGCCC GGGGT  CT  CCGC
                                ||||| |||||  ||  ||||
                                ACGGG TTCTA  GG  GGTG
                                  _    GG  A_
GAM593  KDELR3   5'  GCAGGCAGGGCTCTGGGGCA  23397      TG    T    C
                                TGCCC  GGGTT CTGCC GC
                                |||||  ||||| ||||| ||
                                ACGGG  CTCGG GACGG CG
                                   GT    _    A
GAM593  KHSRP    3'  GTGGGGGGGACTTGGGGGCA  14882      G    TT  G
                                TGCCCT GGGT  CT CCCGC
                                |||||| ||||  || |||||
                                ACGGGG TTCA  GG GGGTG
                                   G    GG  _
GAM593  KIAA0014 3'  GTGTGGCCACGCCCAGGGC   28544        _  TTCT   _
                                GCCCTGGG GT    GCC CGC
                                |||||||| ||    ||| |||
                                CGGGACCC CA    CGG GTG
                                     G  C___   T
GAM593  KIAA0100 3'  GCTCCAGGGACTTGTGGGGT  28652       _   TT   CCC
                                GCCCTG GGGT  CTG   GC
                                |||||| ||||  |||   ||
                                TGGGGT TTCA  GAC   CG
                                   G    GG   CT_
GAM593  KIAA0140 3'  GTGAGAGACAGAATCCCTGGGG 28519     TG   T    CCCG_
          T                     GCCC  GGG TTCTG    CAC
                                ||||  ||| |||||    |||
                                TGGG  CCC AAGAC    GTG
                                  GT   T    AGAGA
GAM593  KIAA0173 3'  CGTGTGGTTTGTCTGGGGGCCC 28382    C TG    TT __ ___
            TGGTGT                GC C  GGGT  CT  GC   CCGCAC   G
                                || |  ||||  ||  ||   ||||||   |
                                TG G  CCCG  GG  TG   GGTGTG   C
                                 T GT    GG  TC  TTT
GAM593  KIAA0193 3'  GTGCTTTGAAATTTTAGG    29317          TGCCC
                                CCTGGGGTTTC    GCAC
                                ||||||||||    ||||
                                GGATTTTAAAG    CGTG
                                      TTT__
GAM593  KIAA0194 3'  CGTGTGGGTCAGGGTGGAGGTC 66589      T   GT   _______
            CTGGGT                GCCC GGG  TTCT     GCCCGCAC   G
                                |||| |||  ||||     ||||||||   |
```

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                                TGGG TCC  GAGG     TGGGTGTG   C
                                  _  TG    TGGGAC
GAM593  KIAA0212  3'  GTGTTCTGAAATCCTGGGTA  28628      T      TGCC
                                TGCCC GGGGTTTC    CGC
                                ||||| ||||||||    |||
                                ATGGG TCCTAAAG    GTG
                                   _       TCTT
GAM593  KIAA0237  5'  CGCGGGGCGGGGTCCCGGGGCA 29218         GT T     _  AC
                                TGCCCTGGG  T CTGCCC GC
                                |||||||||  | ||||||  ||
                                ACGGGGCCC  G GGCGGG CG
                                      TG _     G  CT
GAM593  KIAA0237  3'  GTAAGGAGGTTCTGTGGGTA  29231      _  GG    GCCC
                                TGCCC TGG  TTTCT    GC
                                ||||| |||  |||||    ||
                                ATGGG GTC  GGAGG    TG
                                   T   TT    AA__
GAM593  KIAA0252  3'  GCTGGAGCCCCTGGGGCA    63457      _      T
                                TGCCCT GGGGTTTC GC
                                |||||| |||||||| ||
                                ACGGGG CCCCGAGG CG
                                    T       T
GAM593  KIAA0254  5'  GTGTCCGTGGGCCCCAGGGC  29283         TC  CC
                                GCCCTGGGGTT  TG  CGC
                                ||||||||||  ||  |||
                                CGGGACCCCGG  GC  GTG
                                      GT  CT
GAM593  KIAA0255  5'  GTGAAGGAGACTCCGGGAGC  29136    _         GCC
                                GC CCTGGGGTTTCT   CGC
                                || ||||||||||||   |||
                                CG GGGCCTCAGAGG   GTG
                                 A          AA_
GAM593  KIAA0376  3'  GTGCGGGCACGCCAGGGC    66218       G  TTCT
                                GCCCTGG GT    GCCCGCAC
                                ||||||| ||    ||||||||
                                CGGGACC CA    CGGGCGTG
                                   G  _____
GAM593  KIAA0397  3'  GCTCTGAGGAATCCCAGGGT  62351           GCCC
                                GCCCTGGGGTTTCT    GC
                                ||||||||||||||    ||
                                TGGGACCCTAAGGA    CG
                                      GTCT
GAM593  KIAA0415  3'  GTGGCCAGGGACTTCGGTGCA  94168     C      TT   C
                                TGC CTGGGGT  CTG CCGC
                                ||| |||||||  ||| ||||
                                ACG GGCTTCA  GAC GGTG
                                  T      GG   C
GAM593  KIAA0415  3'  GTGTGGTCACCGCTCTGGGT   94169     T    TTC  C
                                GCCC GGGGT   TG CCGCAC
                                |||| |||||   || ||||||
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                                TGGG TCTCG   AC GGTGTG
                                  _    CC_  T
GAM593  KIAA0445  5'  GCTACAGGAGGTTCGGGGCA  28640        G     CCC
                                TGCCCTGGG TTTCTG   GC
                                ||||||||| ||||||   ||
                                ACGGGGCTT GAGGAC   CG
                                     G     AT_
GAM593  KIAA0450  3'  GCTCTGGAGGCCCAGGGCA   28361        G   TGCCC
                                TGCCCTGGG TTTC    GC
                                ||||||||| ||||    ||
                                ACGGGACCC GAGG    CG
                                     G   TCT__
GAM593  KIAA0514  5'  GTGGTTGTGGAAGCCCAGGGT  28754        G   TG __   AC
                                GCCCTGGG TTTC  C  CCGC
                                |||||||| ||||  |  ||||
                                TGGGACCC GAAG  G  GGTG
                                     _   GT TT
GAM593  KIAA0522  3'  GTGTCCGGAGCTGTCGGGGT   72427       _   T   CC
                                GCCCTGG GGTT CTG  CGC
                                ||||||| |||| |||  |||
                                TGGGGCT TCGA GGC  GTG
                                    G   _  CT
GAM593  KIAA0537  3'  GTGCTTCAAGACCCCAGG    29934         C  CCC
                                CCTGGGGTTT TG   GCAC
                                |||||||||| ||   ||||
                                GGACCCCAGA AC   CGTG
                                     _  TT_
GAM593  KIAA0542  3'  GCCTCTGGGAGCTCTGGGC   66663     T        CCC
                                GCCC GGGGTTTCTG   GC
                                |||| ||||||||||   ||
                                CGGG TCTCGAGGGT   CG
                                  _        CTC
GAM593  KIAA0542  3'  GTCGGGGAGGCCTCAGGCCA  66667    C         TG   _
                                TG CCTGGGGTTTC  CCCG C
                                || ||||||||||  |||| |
                                AC GGACTCCGGAG  GGGC G
                                 C          __   T
GAM593  KIAA0552  5'  GTGCATGGAGCCCTGGGG    28997     TG      _  CC
                                CCC  GGGTTTC TGC  GC
                                |||  ||||||| |||  ||
                                GGG  CCCGAGG ACG  TG
                                  GT      T  __
GAM593  KIAA0564  3'  GCAAAATCAGAAACGTTAGGGC 66792        G      CCC__  AC
            A                    TGCCCTGG GTTTCTG    GC
                                ||||||||| |||||||    ||
                                ACGGGATT CAAAGAC    CG
                                     G      TAAAA
GAM593  KIAA0618  5'  GCCTCTCGGGAGCCGTGGGGCA 29855       G       CCC_  AC
                                TGCCCTG GGTTTCTG    GC
                                ||||||| ||||||||   ||
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                                ACGGGGT CCGAGGGC   CG
                                    G       TCTC
GAM593  KIAA0618  3'  GTAAACAGAGACCCCAGGC   29858    C        CCC
                                GCC TGGGGTTTCTG   GC
                                ||| ||||||||||   ||
                                CGG ACCCCAGAGAC   TG
                                  _         AAA
GAM593  KIAA0632  3'  GTGCTCTGTGGGAGCCCCAGGA 32072    C        TG CC_
            CA                    TG CCTGGGGTTTC  C   GCAC
                                || ||||||||||  |   ||||
                                AC GGACCCCGAGG  G   CGTG
                                 A          GT TCT
GAM593  KIAA0668  3'  TGTGGGGACGTTCAGGGTA   67125         _  TCTG     C
                                TGCCCTGGG GTT    CCCGCA
                                ||||||||| |||    ||||||
                                ATGGGACTT CAG    GGGTGT
                                     G  ____     T
GAM593  KIAA0676  3'  GTGACCGCAGGGGGCCCCAGGG 31147         TT _   CCG
            C                     GCCCTGGGGT  C TGC   CAC
                                ||||||||||  | |||   |||
                                CGGGACCCCG  G ACG   GTG
                                      GG G   CCA
GAM593  KIAA0711  5'  GTGAGGCTGGAAACCCCGGAGT 30152    C        _  _  AC
            A                     TGC CTGGGGTTTCT GCC CGC
                                ||| ||||||||||| ||| |||
                                ATG GGCCCCAAAGG CGG GTG
                                  A          T  A
GAM593  KIAA0737  3'  GTGAAGAGAGTAGAAACCCTAG 29818           CCG___
            GG                    CCCTGGGGTTTCTGC     CAC
                                ||||||||||||||     |||
                                GGGATCCCAAAGATG     GTG
                                       AGAGAA
GAM593  KIAA0759  3'  GTGTGGCCTTGGGAGATCCTGG 67890     T       ____  _  AC
            GC                    GCCC GGGGTTTCT    GCC CGC
                                |||| |||||||||    ||| |||
                                CGGG TCCTAGAGG    CGG GTG
                                  _        GTTC   T
GAM593  KIAA0790  5'  GTGGCCGGGGCCGCCGGGGCA  69258       _  TT T   C
                                TGCCCTGG GGT  C GCC GC
                                |||||||| |||  | ||| ||
                                ACGGGGCC CCG  G CGG TG
                                     G   GG C   _
GAM593  KIAA0819  3'  GTGCAGTGGGGAGCCCCAGG   64335          GCCC
                                CCTGGGGTTTCT    GCAC
                                ||||||||||||    ||||
                                GGACCCCGAGGG    CGTG
                                       GTGA
GAM593  KIAA0930  3'  GTGTGGGGACAGAGCCTCAGGG 71073          T  __
                                CCCTGGGGTT CTG  CCCGCAC
                                ||||||||| |||  |||||||
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                                GGGACTCCGA GAC  GGGTGTG
                                      _  AG
GAM593  KIAA0931  3'  GTGCAATGGTGGGGTCTCGGGT 68016    C     TT  T   C__
          CA                    TG CCTGGGG  TC GCC   GCAC
                                || |||||||  || |||   ||||
                                AC GGGCTCT  GG TGG   CGTG
                                 T      GG  _   TAA
GAM593  KIAA0939  3'  GTGCGGGCAGGGATCTGAG   62722    G   TT
                                CT GGGT  CTGCCCGCAC
                                || ||||  ||||||||||
                                GA TCTA  GACGGGCGTG
                                 G   GG
GAM593  KIAA0939  3'  GTGTGGGTGTGGCCTGGGGT   62723     TG  G  TCT
                                GCCC  GG TT   GCCCGCAC
                                ||||  || ||   ||||||||
                                TGGG  CC GG   TGGGTGTG
                                  GT  _  TG_
GAM593  KIAA1032  3'  GGGTGGGAATTCCAGGCCA   66730    C        TG
                                TG CCTGGGGTTTC  CCC
                                || ||||||||||  |||
                                AC GGACCTTAAGG  GGG
                                 C         GT
GAM593  KIAA1032  3'  GTGCACATAGGACCTTAGGG   66731         T   CCC
                                CCCTGGGGTT CTG   GCAC
                                |||||||||| |||   ||||
                                GGGATTCCAG GAT   CGTG
                                      _  ACA
GAM593  KIAA1033  5'  TGTGGGAGGCGCCGGGGT    65132       G   CTG    C
                                GCCCTGG GTTT   CCCGCA
                                ||||||| ||||   ||||||
                                TGGGGCC CGGA   GGGTGT
                                   G   ___     C
GAM593  KIAA1036  3'  GTGTGGGCAGAGGAGGGGT   30495      GGGGT
                                GCCCT    TTCTGCCCGCAC
                                |||||    ||||||||||||
                                TGGGG    GAGACGGGTGTG
                                  AG___
GAM593  KIAA1076  3'  GCCTCTCGGAGGCCCCAGTGCA 66124     C         CCC_  AC
                                TGC CTGGGGTTTCTG   GC
                                ||| ||||||||||||   ||
                                ACG GACCCCGGAGGC   CG
                                  T          TCTC
GAM593  KIAA1076  3'  GTCTGCAGAGGCCTCAGTGT   66125    C         CC
                                GC CTGGGGTTTCTGC  GC
                                || ||||||||||||  ||
                                TG GACTCCGGAGACG  TG
                                 T          TC
GAM593  KIAA1084  3'  GCACAGATACCTTAGGGCA   30501         T   CCC
                                TGCCCTGGGGT TCTG   GC
                                |||||||||| ||||   ||
```

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                                ACGGGATTCCA AGAC   CG
                                      T   A__
GAM593  KIAA1183 3' GCCCTGGAGGTTCCAGAGTA  63198    C   GG    CCC
                                TGC CTGG  TTTCTG   GC
                                ||| ||||  ||||||   ||
                                ATG GACC  GGAGGT   CG
                                  A   TT    CC_
GAM593  KIAA1196 3' GTCAGGCAGGGAGTCCAGGGT 62152       G TT    C_ AC
                                GCCCTGGG T  CTGCC  GC
                                |||||||| |  |||||  ||
                                TGGGACCT A  GACGG  TG
                                    G GG    AC
GAM593  KIAA1199 3' GTGTCTACCTGGAGCCCCTGGG 72933     _      TGCCC_
           GC                   GCCCT GGGGTTTC     GCAC
                                ||||| ||||||||     ||||
                                CGGGG CCCCGAGG     TGTG
                                   T       TCCATC
GAM593  KIAA1272 3' GTGTGGCTGCTCTGGGCA    70733     T    TTCT  _
                                TGCCC GGGGT   GCC CGC
                                ||||| |||||   ||| |||
                                ACGGG TCTCG   CGG GTG
                                   _    T___  T
GAM593  KIAA1277 3' GTGTGGGTGGGGACTAGGGGG 65084     GG   TT TG
                                CCCT  GGT  C  CCCGCAC
                                ||||  |||  |  |||||||
                                GGGG  TCA  G  GGGTGTG
                                  GA   GG GT
GAM593  KIAA1322 3' GTAACAGGAGCCTTGGGC    73115     T       CCC
                                GCCC GGGGTTTCTG   GC
                                |||| ||||||||||   ||
                                CGGG TTCCGAGGAC   TG
                                  _        AA_
GAM593  KIAA1357 3' GTGCTGTGGGCCCCGGGGT   72433        TT TG CC
                                GCCCTGGGGT  C  C  GCAC
                                ||||||||||  |  |  ||||
                                TGGGGCCCCG  G  G  CGTG
                                      __ GT T_
GAM593  KIAA1364 3' TGTGGGGCTTCAGGACA     64360    C      TTCTG     C
                                TG CCTGGGGT    CCCGCA
                                || ||||||||    ||||||
                                AC GGACTTCG    GGGTGT
                                 A      _____     C
GAM593  KIAA1372 5' GTGTGGAGGGGCGAGACTTGGG 93320     TG  G   T   ____
           GT                   GCCC  GG TTTC GCCC    GCAC
                                ||||  || |||| ||||    ||||
                                TGGG  TC AGAG CGGG    TGTG
                                  GT  _   _   GAGG
GAM593  KIAA1399 3' TGGCGGGAGCCCTGGGGTA   70795      TG        CGCAC
                                TGCCC  GGGTTTCTGCC
                                |||||  ||||||||||
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                                ATGGG  CCCGAGGGCGG
                                  GT        T_____
GAM593  KIAA1437 3' GTGAGTTGGAGTCTCAGGGCA 61217        GT   T  C
                                TGCCCTGGG  TTC GC CGC
                                |||||||||  ||| || |||
                                ACGGGACTC  AGG TG GTG
                                     TG   T  A
GAM593  KIAA1548 3' GTTGAAGAGACCCTGGGGCA  40881      TG      GCCC
                                TGCCC  GGGTTTCT   GC
                                |||||  ||||||||   ||
                                ACGGG  CCCAGAGA   TG
                                  GT      AGT_
GAM593  KIAA1613 3' GCCCAAGCAGGGGCTCTGGGCA 65439      T    TT   CC__  AC
                                TGCCC GGGGT  CTGC   GC
                                ||||| |||||  ||||   ||
                                ACGGG TCTCG  GACG   CG
                                  _    GG   AACC
GAM593  KIAA1655 3' GCTTGGAGAGCCCGGGGT   67190       G     CCC
                                GCCCTGGG TTTCTG   GC
                                |||||||| ||||||   ||
                                TGGGGCCC AGAGGT   CG
                                     G     T__
GAM593  KIAA1655 5' GTGTGGGCCAGTCTTGGGTCA  67198    C  TG  GT TCT
                                TG CC  GG  T   GCCCGCAC
                                || ||  ||  |   ||||||||
                                AC GG  TC  A   CGGGTGTG
                                 T  GT  TG C__
GAM593  KIAA1655 5' GTGTGGGTTTGCTTGGGC    67199     TG    TTCT
                                GCCC  GGGT   GCCCGCAC
                                ||||  ||||   ||||||||
                                CGGG  TTCG   TGGGTGTG
                                  __   TT__
GAM593  KIAA1735 3' GCACAATAGAAACCATGGGGC  89007      GG      CCC_  AC
                                GCCCT  GGTTTCTG   GC
                                |||||  ||||||||   ||
                                CGGGG  CCAAAGAT   CG
                                  TA       AACA
GAM593  KIAA1786 3' GCAGCAGAGACCTCAGGG    66633           CC
                                CCCTGGGGTTTCTGC  GC
                                ||||||||||||||  ||
                                GGGACTCCAGAGACG  CG
                                         A_
GAM593  KIAA1789 5' GTAGGCCCCACAAGTTTCAGGG 67705       GG   CT___   CG AC
           TA                    TGCCCTGG  TTT    GCC  C
                                ||||||||  |||    |||  |
                                ATGGGACT  GAA    CGG  G
                                     TT   CACCC   AT
GAM593  KIAA1789 5' GTGTGGTGTAAAGAATTCTGGG 67706      T      C_  _
           CA                    TGCCC GGGGTTT  TGC CCGCAC
                                ||||| |||||||  ||| ||||||
```

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                                ACGGG TCTTAAG  ATG GGTGTG
                                  _      AA   T
GAM593  KIAA1795 3' GCCTGGAAACTTTGGAGCA   72615     C TG       CCC
                                TGC C  GGGTTTCTG   GC
                                ||| |  |||||||||   ||
                                ACG G  TTCAAAGGT   CG
                                  A GT       C__
GAM593  KIAA1814 3' GCTCGGCAGAAGTTCCGGGG   70880      GG      C_
                                CCCTGG  TTTCTGCC  GC
                                ||||||  ||||||||  ||
                                GGGGCC  GAAGACGG  CG
                                   TT       CT
GAM593  KIAA1822 3' GCTGGGCAGGCCTTGGGGCA   68187      TG   TT    _ AC
                                TGCCC  GGGT  CTGCCC GC
                                |||||  ||||  |||||| ||
                                ACGGG  TCCG  GACGGG CG
                                   GT   __     T  G
GAM593  KIAA1822 3' GTGCGGGTGTGTGCTGTCCTGG 68195    TG ___  TTC
            GG                    CCC  GG   GT   TGCCCGCAC
                                ||| ||   ||   |||||||||
                                GGG  CC   CG   GTGGGCGTG
                                  GT  TGT  TGT
GAM593  KIAA1855 3' GTGTGGGCTGCCTTCCTGGGCA 93958      T   TTTCT
                                TGCCC GGGG    GCCCGCAC
                                ||||| ||||    ||||||||
                                ACGGG TCCT    CGGGTGTG
                                   _   TCCGT
GAM593  KIAA1878 3' GTGTCAAGCCCCGGCGCA    93370    C       CTGCC
                                TGC CTGGGGTTT    CGC
                                ||| |||||||||    |||
                                ACG GGCCCCGAA    GTG
                                  C       CT___
GAM593  KIAA1884 3' GCGTAGGCAGCTTCGGGGCA   73729         TTT    __
                                TGCCCTGGGG   CTGCC  CGC
                                ||||||||||   |||||  |||
                                ACGGGGCTTC   GACGG  GCG
                                      ___     AT
GAM593  KIAA1889 3' GTGTCTTTTAGAGGCTTTGGGA 73883    C  TG       CCC_
            CA                    TG CC  GGGTTTCTG    GCAC
                                || ||  |||||||||   ||||
                                AC GG  TTCGGAGAT    TGTG
                                 A  GT       TTTC
GAM593  KIAA1908 3' GCATGGTGGTCTCAGGGTA   73790         TTT TG  C_
                                TGCCCTGGGG   C  CC  GC
                                ||||||||||   |  ||  ||
                                ATGGGACTCT   G  GG  CG
                                      ___ GT  TA
GAM593  KIAA1908 3' GTGGCTGTTCAGAAGCCTTGGG 73798     TG       C_____   AC
            GC                    GCCC  GGGTTTCTG    CCGC
                                ||||  |||||||||    ||||
```

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                                CGGG  TCCGAAGAC    GGTG
                                  GT       TTGTC
GAM593  KIAA1908  3'  GTTCAGAAGCCTTGGGGC    73799     TG       CCC
                                GCCC  GGGTTTCTG   GC
                                ||||  |||||||||   ||
                                CGGG  TCCGAAGAC   TG
                                  GT       T__
GAM593  KIAA1938  3'  GTGGAGGGGGCCACCGGGGCA  93824        _   TT  GC
                                TGCCCTGG GGT  CT  CCGC
                                |||||||| |||  ||  ||||
                                ACGGGGCC CCG  GG  GGTG
                                    A   GG  A_
GAM593  KIAA1944  3'  GTGTGGAGTTGGGGGGGTTCTG 76081     T  GG TT  ___  _
            GGT                   GCCC GG  T  CT   GC CCGCAC
                                |||| ||  |  ||   || ||||||
                                TGGG TC  G  GG   TG GGTGTG
                                  _  TT GG  GGT  A
GAM593  KIAA1949  3'  GCCCGGAAGATTCAGGGCA   99695        G     CCC
                                TGCCCTGGG TTTCTG   GC
                                |||||||| ||||||   ||
                                ACGGGACTT GAAGGC   CG
                                    A     C__
GAM593  KIAA1951  3'  GTGTGGGTACCTCTGGGG    74164     TG   TTTC
                                CCC  GGG   TGCCCGCAC
                                |||  |||   |||||||||
                                GGG  CTC   ATGGGTGTG
                                  GT   C___
GAM593  LANCL2    3'  GTGTTTTAAAGAAGCCTCAGAG 38621    C        GCCC_
            T                   GC CTGGGGTTTCT    GCAC
                                || ||||||||||    ||||
                                TG GACTCCGAAGA    TGTG
                                 A         AATTT
GAM593  LGALS8    3'  GTGTATTTGAACTTAGGGCA   22450        GT   TGCCC
                                TGCCCTGGG  TTC    GCAC
                                |||||||||  |||    ||||
                                ACGGGATTC  AAG    TGTG
                                    __   TTTA_
GAM593  LGI2      3'  GTGCAGGCTGGGGATCTCAGGC 36929     C     TT  _   C
                                GCC TGGGGT  CT GCC GCAC
                                ||| ||||||  || ||| ||||
                                CGG ACTCTA  GG CGG CGTG
                                  _     GG  T   A
GAM593  LGP2      3'  GCCACACAGGAGTCCTGGGCA  44379      T  GT    CCC_
                                TGCCC GGG  TTCTG   GC
                                |||||  |||  |||||   ||
                                ACGGG TCC  AGGAC    CG
                                  _  TG    ACAC
GAM593  LIMK2     3'  GCTGGGCAGGATCCCAGGGT   19924         T     _
                                GCCCTGGGGTT CTGCCC GC
                                |||||||||| |||||| ||
```

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                                TGGGACCCTAG GACGGG CG
                                      _     T
GAM593  LRRFIP1   3'  GTGCACAGGAAGTCTCAGTGT  17616    C    GT   GCCC
                                GC CTGGG  TTCT   GCAC
                                || |||||  ||||   ||||
                                TG GACTC  AAGG   CGTG
                                 T    TG   ACA_
GAM593  LW-1      5'  GTGCCTGGCTCAGGAGCTCTAG 60886    C        __  C_
           GACA                   TG CCTGGGGTTTCT  GCC  GCAC
                                || ||||||||||||  |||  ||||
                                AC GGATCTCGAGGA  CGG  CGTG
                                 A          CT   TC
GAM593  LW-1      5'  GTGCCTGGCTCAGGAGCTCTAG 60887    C        __  C_
           GACA                   TG CCTGGGGTTTCT  GCC  GCAC
                                || ||||||||||||  |||  ||||
                                AC GGATCTCGAGGA  CGG  CGTG
                                 A          CT   TC
GAM593  MAP2K1IP1 5'  GCCCAGAAACCCCAGGCGT   42021    _        CCC
                                GC CCTGGGGTTTCTG   GC
                                || ||||||||||||   ||
                                TG GGACCCCAAAGAC   CG
                                 C          C__
GAM593  MAP2K5    5'  GTGTGGCGGCCCTGGGGC    12328     TG   TTT    _
                                GCCC  GGG   CTGCC CGC
                                ||||  |||   ||||| |||
                                CGGG  CCC   GGCGG GTG
                                  GT   ____    T
GAM593  MAPK8IP3  3'  GTGCGCGGGGCCTCAGGCA   54145     C     TT T  C
                                TGCC TGGGGT  C GC CGC
                                |||| ||||||  | || |||
                                ACGG ACTCCG  G CG GTG
                                  _     GG _  C
GAM593  MAPKAP1   5'  GTGTGGAAGCAGCTTCAGG   44375        T  GC
                                CCTGGGGTT CT  CCGCAC
                                |||||||| ||  ||||||
                                GGACTTCGA GA  GGTGTG
                                      C  A_
GAM593  MFN2      3'  GTGTGGGCTCCCCCAGGGGCA  30228      _    TTTCT
                                TGCCC TGGGG    GCCCGCAC
                                ||||| |||||    ||||||||
                                ACGGG ACCCC    CGGGTGTG
                                   G    CT___
GAM593  MGC10200  3'  GTTCAGGGAGCTTCAGGGT   59648           GCCC
                                GCCCTGGGGTTTCT   GC
                                ||||||||||||||   ||
                                TGGGACTTCGAGGG   TG
                                         ACT_
GAM593  MGC10334  5'  GTGAAGTCACAGGTCCCGGGGT 48322        GT  C  CCCG
                                GCCCTGGG  TT TG   CAC
                                ||||||||  || ||   |||
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                                TGGGGCCC  GA AC    GTG
                                    TG  C  TGAA
GAM593  MGC11352  5'  GCTCAGAAGCTCCAGGCA    65433      C         CCC
                                TGCC TGGGGTTTCTG   GC
                                |||| ||||||||||   ||
                                ACGG ACCTCGAAGAC   CG
                                  _        T__
GAM593  MGC13010  5'  GTGTGCAGTGGCCTCAGGG   52061         TT    C
                                CCCTGGGGT  CTGC CGC
                                |||||||||  |||| |||
                                GGGACTCCG  GACG GTG
                                     GT    T
GAM593  MGC13053  5'  GCCTGCAGGCCCCGGGGCA   52111          TT    CC
                                TGCCCTGGGGT  CTGC  GC
                                ||||||||||  ||||  ||
                                ACGGGGCCCCG  GACG  CG
                                      __   TC
GAM593  MGC13053  3'  TGTTGGAGATTTTAGGGC    52117           CCC   C
                                GCCCTGGGGTTTCTG   GCA
                                ||||||||||||||   |||
                                CGGGATTTTAGAGGT   TGT
                                        ____   T
GAM593  MGC13114  3'  GTGGGGCTGGGAGCACTGGGGC 51393      TG G     _    G
                                GCCC  G GTTTCT GCCC CAC
                                ||||  | |||||| |||| |||
                                CGGG  C CGAGGG CGGG GTG
                                  GT A     T   _
GAM593  MGC15476  3'  GCTTGGAAGCCCTTGGGCA   59611       T        CCC
                                TGCCC GGGGTTTCTG   GC
                                ||||| ||||||||||   ||
                                ACGGG TCCCGAAGGT   CG
                                   T        T__
GAM593  MGC15631  3'  TGCCCTGGACCTCGGGCA    52238       T      CTGCCC
                                TGCCC GGGGTTT     GCA
                                ||||| |||||||     |||
                                ACGGG CTCCAGG     CGT
                                   _      TCC___
GAM593  MGC15875  3'  GCTTTCAGAGGCTCAGGGT    53016         G     CCC
                                GCCCTGGG TTTCTG   GC
                                |||||||| ||||||   ||
                                TGGGACTC GGAGAC   CG
                                     _     TTT
GAM593  MGC16025  5'  GCCCTCAGGAGCCCTGGGGT   53024      TG       CCC
                                GCCC  GGGTTTCTG   GC
                                ||||  |||||||||   ||
                                TGGG  CCCGAGGAC   CG
                                  GT        TCC
GAM593  MGC16186  5'  GCTTTCGGGAGCCCCAGGC    51409     C         CCC
                                GCC TGGGGTTTCTG   GC
                                ||| ||||||||||   ||
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                                CGG ACCCCGAGGGC  CG
                                  _        TTT
GAM593  MGC16279  5'  GCAACTTAGACAGCCCCAGGGT 52983          _   CCC_  AC
                                GCCCTGGGGTT TCTG   GC
                                |||||||||| ||||   ||
                                TGGGACCCCGA AGAT   CG
                                      C   TCAA
GAM593  MGC21688  3'  TGCCCGGGGCCTCTGGGGCA  58919     TG  TTTCT  ___  C
                                TGCCC  GGG   GCCC  GCA
                                |||||  |||   ||||  |||
                                ACGGG  CTC   CGGG  CGT
                                  GT  _____  GCC
GAM593  MGC23284  5'  GTGCGGAGAGTGGACCTCGGTG 59361   C       _ GC
          T                    GC CTGGGGTTT CT  CCGCAC
                               || |||||||| ||  ||||||
                               TG GGCTCCAGG GA  GGCGTG
                                T       T  GA
GAM593  MGC23445  5'  GTGGGCTTGGGGGGCTCTGGGT  58774    T   TT __    AC
                                GCCC GGGGT  CT  GCCCGC
                                |||| |||||  ||  ||||||
                                TGGG TCTCG  GG  CGGGTG
                                  _    GG  TT
GAM593  MGC2656   3'  GTGTCGGGGACACCGGGGCA  44721       G  TT  CC
                                TGCCCTGG GT  CTG  CGC
                                |||||||| ||  |||  |||
                                ACGGGGCC CA  GGC  GTG
                                     A  GG   T_
GAM593  MGC2749   3'  GTGCCTTGAGGGGGTCTCAGGG 44172        TT  GCCC_
          CA                   TGCCCTGGGG  TCT   GCAC
                               ||||||||||  |||   ||||
                               ACGGGACTCT  GGG   CGTG
                                     GG   AGTTC
GAM593  MGC29654  5'  GTGGCGGGGTCTCGCGGC   67209    C   GT T   C
                                GCC TGGG  T CTGCC GC
                                ||| ||||  | ||||| ||
                                CGG GCTC  G GGCGG TG
                                  C   TG _   _
GAM593  MGC3101   3'  GTGGCCCACGGCGGCCTTGGGG 44104    TG   TT  C___   AC
          T                    GCCC  GGGT  CTG   CCGC
                               ||||  ||||  |||   ||||
                               TGGG  TCCG  GGC   GGTG
                                 GT   GC   ACCC
GAM593  MGC3295   5'  GCTTTGCAGACTTCGGGGT   48257       TT   CC_
                                GCCCTGGGG  TCTGC   GC
                                |||||||||  |||||   ||
                                TGGGGCTTC  AGACG   CG
                                     __    TTT
GAM593  MGC33182  5'  GGCCTGGCGGAAATCCTGGTGT 76096   C TG        C_  AC
                                GC C  GGGTTTCTGCC  GC
                                || |  ||||||||||  ||
```

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                                TG G  CCTAAAGGCGG  CG
                                 T GT         TC  GT
GAM593  MGC34869  5'  GCCCACGGCAGCTTCGGGGT  58715        TTT    C___
                                GCCCTGGGG  CTGCC   GC
                                |||||||||  |||||   ||
                                TGGGGCTTC  GACGG   CG
                                     ___    CACC
GAM593  MGC35558  3'  GCTCCCAGGGGCTCCAGGCA  59414     C     TT  CCC
                                TGCC TGGGGT  CTG   GC
                                |||| ||||||  |||   ||
                                ACGG ACCTCG  GAC   CG
                                  _     GG   CCT
GAM593  MGC35558  3'  GTGGAATGAGGCCCCAGG    59418         TGC
                                CCTGGGGTTTC   CCGC
                                ||||||||||   ||||
                                GGACCCCGGAG   GGTG
                                      TAA
GAM593  MGC4172   5'  GTGACGGGGGCCTCGGGG    44458        TT   CC
                                CCCTGGGGT  CTG  CGC
                                |||||||||  |||  |||
                                GGGGCTCCG  GGC  GTG
                                     GG   A_
GAM593  MGC4281   3'  GCAAAGCAGAAGCCGCCAGGGC 55601        _       CC_  AC
          A                      TGCCCTGG GGTTTCTGC   GC
                                |||||||| |||||||||   ||
                                ACGGGACC CCGAAGACG   CG
                                     G        AAA
GAM593  MGC4368   5'  GTGTGGGCGGGGATGGCTCGGC 44728    CT   __  TT
                                GCC  GGG  GT  CTGCCCGCAC
                                |||  |||  ||  ||||||||||
                                CGG  CTC  TA  GGCGGGTGTG
                                  __   GG  GG
GAM593  MGC4607   5'  GCGGCGGGGCTCCCGGGGC   49541        GT     C
                                GCCCTGGG  TTCTGCC GC
                                ||||||||  ||||||| ||
                                CGGGGCCC  GGGGCGG CG
                                     TC     _
GAM593  MGC4643   3'  GTGCAGCCCGGAGGCTTAGGGT 52143        G   T_  CC
                                GCCCTGGG TTTC  GC  GCAC
                                |||||||| ||||  ||  ||||
                                TGGGATTC GAGG  CG  CGTG
                                     G   CC  A_
GAM593  MGC4737   3'  GTGCTCCCTGGCCCCAGGGT   49648         TCTGCCC
                                GCCCTGGGGTT      GCAC
                                ||||||||||      ||||
                                TGGGACCCCGG      CGTG
                                      TCCCT__
GAM593  MGC4737   5'  GTGGAGCTCGGAGGTTCCAGGG 49649        GG    __ _   AC
          CA                     TGCCCTGG  TTTCT  GC CCGC
                                ||||||||  |||||  || ||||
```

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                                ACGGGACC  GGAGG  CG GGTG
                                    TT    CT  A
GAM593  MGC4796  3'  GAGGGCAGGTGATCTTAGGGT  62165          _      GCAC
                                GCCCTGGGGTT TCTGCCC
                                |||||||||| |||||||
                                TGGGATTCTAG GGACGGG
                                      T      AG
GAM593  MGC8407  3'  GTGTGGGCTGCTCTAGGAGCA  44116     _      TTCT
                                TGC CCTGGGGT   GCCCGCAC
                                ||| ||||||||   ||||||||
                                ACG GGATCTCG   CGGGTGTG
                                  A       T___
GAM593  MGC9753  3'  CAGGGTGGCCCCAGGGCA    54186          TCT   GCAC
                                TGCCCTGGGGTT   GCCC
                                ||||||||||||   ||||
                                ACGGGACCCCGG   TGGG
                                       ___    ACC
GAM593  MKRN1    5'  GTGATCCCGGAAGTTCCGGGGC 26496        GG    CCCG
                                GCCCTGG  TTTCTG    CAC
                                |||||||  ||||||    |||
                                CGGGGCC  GAAGGC    GTG
                                    TT     CCTA
GAM593  MKRN4    5'  GTGATTCCGGAAGTTCCGGGGC 48474        GG    CCCG
                                GCCCTGG  TTTCTG    CAC
                                |||||||  ||||||    |||
                                CGGGGCC  GAAGGC    GTG
                                    TT     CTTA
GAM593  MMP28    3'  GTCGATGCTGGAGGTTCCGGGG 44446        GG    _  C_  _ AC
          C                      GCCCTGG  TTTCT GC  CG C
                                |||||||  ||||| ||  || |
                                CGGGGCC  GGAGG CG  GC G
                                    TT     T  TA  T
GAM593  MO25     5'  GCCGCGGGAGCCCCTGGGCA   33290       T         CC
                                TGCCC GGGGTTTCTGC  GC
                                ||||| ||||||||||  ||
                                ACGGG CCCCGAGGGCG  CG
                                   T          C_
GAM593  MR       5'  GTGGCAGGGATCCTGGAGCA   49149     C TG    TT    C
                                TGC C  GGGT  CTGCC GC
                                ||| |  ||||  ||||| ||
                                ACG G  CCTA  GACGG TG
                                  A GT    GG    _
GAM593  MRPL35   3'  GTTACAGGGGCCTCAGAGCA   34021     C      TT   CCC
                                TGC CTGGGGT  CTG   GC
                                ||| |||||||  |||   ||
                                ACG GACTCCG  GAC   TG
                                  A      GG   AT_
GAM593  MRPL41   5'  GTGTGGGGTCTCCGGTCCAGGG 51647        GTTTCTG_
          C                      GCCCTGGG       CCCGCAC
                                ||||||||       |||||||
```

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                                CGGGACCT      GGGTGTG
                                    GGCCTCTG
GAM593  MRPS18A  3'  GTGCAGGGGGTCCTGGGCA   36782      T  G TT   CC
                                TGCCC GGG T  CTGC  GC
                                ||||| ||| |  ||||  ||
                                ACGGG CCT G  GACG  TG
                                   T  G GG   __
GAM593  MRPS21   5'  GTGTGGTGGTTGGGACCCTGTG 39163    C     TT T  __
          GC                    GCC TGGGGT  C GCC  CGCAC
                                ||| ||||||  | |||  |||||
                                CGG GTCCCA  G TGG  GTGTG
                                  T     GG T   TG
GAM593  MRPS26   3'  GTGTGTACAGCCTCAGCGCA   48724    C     TTT   CC
                                TGC CTGGGG   CTG  CGCAC
                                ||| ||||||   |||  |||||
                                ACG GACTCC   GAC  GTGTG
                                  C      ___   AT
GAM593  N4BP3    3'  GCAACGGGGCTCTAGGGCA   66852          TT __
                                TGCCCTGGGGT  C  TGC
                                ||||||||||  |  |||
                                ACGGGATCTCG  G  ACG
                                      GG CA
GAM593  N4BP3    3'  GTGCCAAGCACAGGGACTCCAG 66861         TT   CCC___
          GG                    CCCTGGGGT  CTG     GCAC
                                |||||||||  |||     ||||
                                GGGACCTCA  GAC     CGTG
                                     GG   ACGAAC
GAM593  NBL1     3'  GTTCCAGAGGCCCTAGGC    60046     C         CCC
                                GCC TGGGGTTTCTG   GC
                                ||| ||||||||||   ||
                                CGG ATCCCGGAGAC   TG
                                  _         CT_
GAM593  NCE2     5'  GTCTCGGGGAGCCCAGGGTA   55630         G TT   CCC
                                TGCCCTGGG T  CTG   GC
                                ||||||||| |  |||   ||
                                ATGGGACCC A  GGC   TG
                                     G GG   TC_
GAM593  NINJ2    5'  GTGTGAAGGGACTTGAGGGCA  33730       G    TT  GCC
                                TGCCCT GGGT  CT   CGCAC
                                |||||| ||||  ||   |||||
                                ACGGGA TTCA  GA   GTGTG
                                   G    GG  A__
GAM593  NMT1     3'  GTGCCTCAAGCCCCAGAGT    41151    C       CTGCCC
                                GC CTGGGGTTT     GCAC
                                || |||||||||     ||||
                                TG GACCCCGAA     CGTG
                                 A        CTC___
GAM593  NUDC     3'  GCACACAGGTCCCGGGGCA    22748          TT   CCC
                                TGCCCTGGGG  TCTG   GC
                                ||||||||||  ||||   ||
```

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                                ACGGGGCCCT  GGAC   CG
                                      __    ACA
GAM593  NUDEL    3'  GTGCGCCTCAGACTCGGGGT   48701        GTT    CC_
                                GCCCTGGG   TCTG   CGCAC
                                ||||||||   ||||   |||||
                                TGGGGCTC   AGAC   GCGTG
                                     ____    TCC
GAM593  OAZ2     3'  GCCTGGGAATTGTGGGGCA   11879       G       CCC
                                TGCCCTG GGTTTCTG   GC
                                ||||||| ||||||||   ||
                                ACGGGGT TTAAGGGT   CG
                                    G       C__
GAM593  OBSCN    3'  GTGACGGAGGAGTCCCAGGACA 71192    C     GT    GC   _
                                TG CCTGGG  TTCT  CCG CAC
                                || ||||||  ||||  ||| |||
                                AC GGACCC  AGGA  GGC GTG
                                 A     TG   __  A
GAM593  OS-9     3'  GTGGGTGTGGGGGCCCTGGGT  23319     T    TT  __     AC
                                GCCC GGGGT  CT  GCCCGC
                                |||| |||||  ||  ||||||
                                TGGG TCCCG  GG  TGGGTG
                                  _    GG  TG
GAM593  OS4      3'  GTGCCTATGGGGTCCCGGTGTA 20393     C     TT  TGCCC
                                TGC CTGGGG  TC    GCAC
                                ||| ||||||  ||    ||||
                                ATG GGCCCT  GG    CGTG
                                  T     GG  TATC_
GAM593  P101-PI3K 3'  CTGGACAGAAGCCCTGGGGCA  27458      TG       C   CAC
                                TGCCC  GGGTTTCTG CCG
                                |||||  ||||||||| |||
                                ACGGG  CCCGAAGAC GGT
                                   GT       A   CA
GAM593  P114-RHO-GEF 3'  GTGCTGGGACATCCCAGGGT   31675         TTCTG  _
                                GCCCTGGGGT    CCC GCAC
                                ||||||||||    ||| ||||
                                TGGGACCCTA    GGG CGTG
                                      CA___   T
GAM593  P17.3    5'  GTGGGCGAGGGAACTCGGGGC  39313       G TT  _     AC
                                GCCCTGGG T  CT GCCCGC
                                |||||||  |  || ||||||
                                CGGGGCTC A  GA CGGGTG
                                     A GG  G
GAM593  p25      3'  GCAGAGCAGAAGCCCCAGGGC  23835            CC_  AC
                                GCCCTGGGGTTTCTGC   GC
                                ||||||||||||||||   ||
                                CGGGACCCCGAAGACG   CG
                                          AGA
GAM593  p25      3'  GTGCATCCCAAACCCTAGGCCA 23837    C        CTGCCC
                                TG CCTGGGGTTT     GCAC
                                || ||||||||||     ||||
```

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                                AC GGATCCCAAA     CGTG
                                 C        CCCTA_
GAM593  P2RX5    3'  GCCTTTGGGAATCCCAGG    11921           CCC
                                CCTGGGGTTTCTG   GC
                                ||||||||||||   ||
                                GGACCCTAAGGGT   CG
                                      TTC
GAM593  PALM     3'  GTGCTAATTTGGGGACCCCAGG 11968         TT  GCCC__
          G                      CCCTGGGGT  CT     GCAC
                                |||||||||  ||     ||||
                                GGGACCCCA  GG     CGTG
                                     GG  TTTAAT
GAM593  PCBP4    3'  TGCGGCAGCCCCAGGGCA    40282          TTT    C
                                TGCCCTGGGG   CTGCC GCA
                                ||||||||||   ||||| |||
                                ACGGGACCCC   GACGG CGT
                                    ____   _
GAM593  PCDH10   3'  AACTGTAGAAACTTTAGAGGCA 53100      _          CCGCAC
                                TGCC CTGGGGTTTCTGC
                                |||| ||||||||||||
                                ACGG GATTTCAAAGATG
                                  A           TCAAG
GAM593  PCYT2    3'  GTGCAGAGCAGGGGGCTTTAGG 12684         TT _   CC_
          G                      CCCTGGGGT  C TGC   GCAC
                                |||||||||  | |||   ||||
                                GGGATTTCG  G ACG   CGTG
                                     GG G   AGA
GAM593  PDCD7    5'  GTGTTCGGGACCCCGCGGC   72610     C      T   CC
                                GCC TGGGGTT CTG  CGC
                                ||| ||||||| |||  |||
                                CGG GCCCCAG GGC  GTG
                                  C       _  TT
GAM593  PDE11A   5'  AACAGCTAGAGGCCTCGGGGCA 34254             _ CCGCAC
                                TGCCCTGGGGTTTCT GC
                                |||||||||||||| ||
                                ACGGGGCTCCGGAGA CG
                                       T  ACAAG
GAM593  PDE11A   5'  GCTAGAGGCCTCGGGGCA    34255            _
                                TGCCCTGGGGTTTCT GC
                                |||||||||||||| ||
                                ACGGGGCTCCGGAGA CG
                                       T
GAM593  PDE4DIP  3'  GTAGGAGGAATCTTGGTGTA   97177     C TG       G  CG
                                TGC C  GGGTTTCT CC  C
                                ||| |  |||||||| ||  |
                                ATG G  TCTAAGGA GG  G
                                  T GT       _  AT
GAM593  PDE7B    5'  GCTCAGAGATTTCACGGCA   38951      C  GG      CCC
                                TGCC TG  GTTTCTG   GC
                                ||||  ||  |||||||   ||
```

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                                ACGG AC  TAGAGAC   CG
                                  C  TT      T__
GAM593  PEPP3    3'  GTGTGGTCAGCCTTGGGGC   30711     TG   TTT   C
                                GCCC  GGG   CTG CCGCAC
                                ||||  |||   ||| ||||||
                                CGGG  TCC   GAC GGTGTG
                                  GT   ___   T
GAM593  phospho1 5'  GCCCAGAAATCCGGGGGT    83249      G       CCC
                                GCCCT GGGTTTCTG   GC
                                ||||| |||||||||   ||
                                TGGGG CCTAAAGAC   CG
                                  G       C__
GAM593  PIPPIN   3'  GTGCCCCAAGACCGCAGGGTA  80511       G    C  CCC
                                TGCCCTG GGTTT TG   GCAC
                                ||||||| ||||| ||   ||||
                                ATGGGAC CCAGA AC   CGTG
                                    G    _ CC_
GAM593  PISD     5'  GGCAGAGGCCCTGGAGCA    27544     C TG
                                TGC C  GGGTTTCTGCC
                                ||| |  ||||||||||
                                ACG G  CCCGGAGACGG
                                  A GT
GAM593  PKNOX2   3'  GTGTCGCCGGGAGGCCTTCAGG 92533        _     __ C_   AC
           GT                     GCCCTGG GGTTTCT  GC  CGC
                                ||||||| |||||||  ||  |||
                                TGGGACT CCGGAGG  CG  GTG
                                    T      GC  CT
GAM593  PLU-1    5'  GGTATGGAGTCCCAGGGTA    88806         GT  _
                                TGCCCTGGG  TTC TGCC
                                |||||||||  ||| ||||
                                ATGGGACCC  AGG ATGG
                                     TG   T
GAM593  POLR2D   3'  GTGACATGGAATCTTGGAGCA  17844     C TG      _  CC
                                TGC C  GGGTTTC TG  CGC
                                ||| |  ||||||| ||  |||
                                ACG G  TCTAAGG AC  GTG
                                  A GT      T  A_
GAM593  PP1201   3'  GTGCGGGCAGGGAGAATGCCTG 42458     TG  G____ TT
           GGG                    CCC  GG    T  CTGCCCGCAC
                                |||  ||    |  ||||||||||
                                GGG  CC    A  GACGGGCGTG
                                  GT  GTAAG GG
GAM593  PP1665   3'  GTGTCCAGCAGACCTCAAGGCA 48640      C       _  CC   AC
                                TGCC TGGGGTTT CTG  CGC
                                |||| |||||||| |||  |||
                                ACGG ACTCCAGA GAC  GTG
                                  A       C   CT
GAM593  PP3501   3'  GTGTGGGTGGGCAAGGCCAGGG 41686        GG  _  TG
           C                     GCCCTGG  TT TC  CCCGCAC
                                |||||||  || ||  |||||||
```

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                                CGGGACC  AA GG  GGGTGTG
                                    GG  C  GT
GAM593  PPAP2C   3'  GCTCCAGGAACCCTGGGC    14930     T       CCC
                                GCCC GGGGTTTCTG   GC
                                |||| ||||||||||   ||
                                CGGG TCCCAAGGAC   CG
                                  _       CT_
GAM593  PPFIA4   3'  GTGCGGATCTTGACTCTAGGGC 70845          TCTGC
          A                      TGCCCTGGGGTT    CCGCAC
                                ||||||||||||    ||||||
                                ACGGGATCTCAG    GGCGTG
                                      TTCTA
GAM593  PRO0641  3'  GTGGTTTGGGATTTTCAGGGTA 27067       GG T   GC_   AC
                                TGCCCTG  G TTCT   CCGC
                                |||||||  | ||||   ||||
                                ATGGGAC  T AGGG   GGTG
                                    TT T    TTT
GAM593  PRO0659  3'  GTGTGGGCCCATTTTGGGG   27075    TG   TTCT
                                CCC  GGGT   GCCCGCAC
                                |||  ||||   ||||||||
                                GGG  TTTA   CGGGTGTG
                                  GT   CC__
GAM593  PRO1496  3'  GTTGAGGGAACTTTAGGG    38367          GCCC
                                CCCTGGGGTTTCT   GC
                                ||||||||||||   ||
                                GGGATTTCAAGGG   TG
                                      AGT_
GAM593  PRO1777  5'  GTGTGACGGGCCTTAGGGC   38375        TT   CC
                                GCCCTGGGGT  CTG  CGCAC
                                ||||||||||  |||  |||||
                                CGGGATTCCG  GGC  GTGTG
                                    __   A_
GAM593  PRO2266  5'  GTGTGGGATGCGGCCCCTGGGG 38186      _     TCTG
          T                     GCCCT GGGGTT    CCCGCAC
                                |||||  ||||||    |||||||
                                TGGGG CCCCGG    GGGTGTG
                                   T     CGTA
GAM593  PRO2900  3'  GTGCTTTCAGACCCCACGGCA  38440     C    TT   CCC
                                TGCC TGGGG  TCTG   GCAC
                                ||||  |||||  ||||   ||||
                                ACGG ACCCC  AGAC   CGTG
                                  C     __    TTT
GAM593  PRSS25   5'  GTCACCCGGAAGCCTGGGGGC  59675      G       CCC_  AC
                                GCCCT GGGTTTCTG    GC
                                |||||  |||||||||    ||
                                CGGGG TCCGAAGGC    TG
                                   G        CCAC
GAM593  PSR      3'  GTGGTACTGGGATGTTTAGGGT 65793        _  TT TGC_    AC
                                GCCCTGGG GT  C    CCGC
                                |||||||  ||  |    ||||
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                                TGGGATTT TA  G    GGTG
                                     G  GG TCAT
GAM593  PTPN21   5'  GTGCGGGTGCGGCTGCGGC   23864     CT G    TC
                                GCC  G GGTT  TGCCCGCAC
                                |||  | ||||  |||||||||
                                CGG  C TCGG  GTGGGCGTG
                                  __ G    C_
GAM593  PTPRT    3'  GCTCAGGAGCTCTGAGGT    56497     CT        CCC
                                GCC  GGGGTTTCTG   GC
                                |||  ||||||||||   ||
                                TGG  TCTCGAGGAC   CG
                                  AG         T__
GAM593  Rab11-FIP2 5'  GTGCTAGGGAACTCGGGGGCA  30457       G       GCCC
                                TGCCCT GGGTTTCT    GCAC
                                |||||| ||||||||    ||||
                                ACGGGG CTCAAGGG    CGTG
                                    G       AT__
GAM593  RAB27B   5'  GTGGAGCCCGGGAGTTCCAGGG 16045       GG    __ _    AC
           C                     GCCCTGG  TTTCT  GC CCGC
                                |||||||  |||||  || ||||
                                CGGGACC  GAGGG  CG GGTG
                                     TT    CC  A
GAM593  RAB3IL1  3'  GTGGCTGGATCTCCAGGGTA   26369          TT   GC
                                TGCCCTGGGG  TCT  CCGC
                                ||||||||||  |||  ||||
                                ATGGGACCTC  AGG  GGTG
                                      T_   TC
GAM593  RAB40C   3'  GTAAGGGAACCCCAGGCA    41284      C        GCCC
                                TGCC TGGGGTTTCT    GC
                                |||| ||||||||||    ||
                                ACGG ACCCCAAGGG    TG
                                  _         AA__
GAM593  RABEX5   3'  GTGCATGAGGCCCCAGGGCA   27963             _   CC
                                TGCCCTGGGGTTTC TGC  GC
                                |||||||||||||| |||  ||
                                ACGGGACCCCGGAG ACG  TG
                                        T   __
GAM593  RASSF2   3'  GTGGCCAGGAAGTTTCAGG    29108      GG _     C    AC
                                CCTG  G TTTCTG CCGC
                                ||||  | |||||| ||||
                                GGAC  T AAGGAC GGTG
                                   TT G     C
GAM593  RBAK     5'  GCCTCTCGGGAGCCGTGGGGCA 41272        G       CCC_  AC
                                TGCCCTG GGTTTCTG    GC
                                |||||||  ||||||||    ||
                                ACGGGGT CCGAGGGC    CG
                                    G       TCTC
GAM593  RBM5     3'  GTGCTGTTAATAGATCTTAGGG 20506           CT__  CC
           T                     GCCCTGGGGTTT    GC  GCAC
                                ||||||||||||    ||  ||||
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                                TGGGATTCTAGA   TG  CGTG
                                      TAAT  T_
GAM593  REM     3'  GTGCATTCTGGGCTCCAGGG  26688         CTGCCC
                                CCCTGGGGTTT     GCAC
                                ||||||||||     ||||
                                GGGACCTCGGG     CGTG
                                      TCTTA_
GAM593  RGS19   3'  GTGGCCAAGCAGGAACTCCAGG 20802           ____   AC
                                CCTGGGGTTTCTGC   CCGC
                                ||||||||||||||   ||||
                                GGACCTCAAGGACG   GGTG
                                       AACC
GAM593  RIL     3'  GTGTCCTAGACTCCGGGTCG  14888   C       CTGCC
                                TG CCTGGGGTTT    CGC
                                || ||||||||||    |||
                                GC GGGCCTCAGA    GTG
                                 T        TCCT_
GAM593  RNF20   3'  GTGAAGAAATCTTGTGGGTA  39462     _       GCC
                                TGCCC TGGGGTTTCT  CGC
                                ||||| ||||||||||  |||
                                ATGGG GTTCTAAAGA  GTG
                                   T        A__
GAM593  RNPC1   3'  TGCAGGCGCTCCAGGGCA   34413         TTCT  C
                                TGCCCTGGGGT   GCC GCA
                                ||||||||||   ||| |||
                                ACGGGACCTCG   CGG CGT
                                      ____  A
GAM593  RPH3A   3'  GTGAGAGAAGCATTGGGGCA  30936     TG G    GCC
                                TGCCC  G GTTTCT   CGC
                                |||||  | ||||||   |||
                                ACGGG  T CGAAGA   GTG
                                   GT A     GA_
GAM593  RPS6KB2 3'  GTTCCAGAGACCTGGGGGT   15535     G       CCC
                                GCCCT GGGTTTCTG   GC
                                ||||| |||||||||   ||
                                TGGGG TCCAGAGAC   TG
                                   G        CT_
GAM593  SCYA22  3'  GTGAAGGAATCCTGGGTA    92608     T       GCC
                                TGCCC GGGGTTTCT   CGC
                                ||||| |||||||||   |||
                                ATGGG TCCTAAGGA   GTG
                                   _        A__
GAM593  SDS3    3'  GCCCAGAAGCTTGGGGCA    69749     TG  G    CCC
                                TGCCC  GG TTTCTG   GC
                                |||||  || ||||||   ||
                                ACGGG  TC GAAGAC   CG
                                   GT _     C__
GAM593  SEC14L1 3'  GTAAGGGAATTCTGGGGCA   13006     TG      GCCC
                                TGCCC  GGGTTTCT   GC
                                |||||  ||||||||   ||
```

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                                ACGGG  CTTAAGGG    TG
                                  GT       AA__
GAM593  SEC24D   5'  GCTCGGAAGCCCGCGGGGT   29755       _       CCC
                                GCCCTG GGGTTTCTG   GC
                                |||||| |||||||||   ||
                                TGGGGC CCCGAAGGC   CG
                                   G        T__
GAM593  SEMA4B   5'  CCGGAGGCGGGGGCCCCCGGGG 69597         _ TT    CGCAC
           C                     GCCCTGGGG T  CTGCC
                                |||||||||  |  |||||
                                CGGGGCCCC G  GGCGG
                                     C GG    AGGCCT
GAM593  SEMA4B   3'  GCCCTTGGGAGCCTTGGGGC   69598     TG       CCC
                                GCCC  GGGTTTCTG   GC
                                ||||  |||||||||   ||
                                CGGG  TCCGAGGGT   CG
                                  GT        TCC
GAM593  SHAPY    3'  GTTTGCTGGGAACCCCAGGTCA 57913    C         _  CC  AC
                                TG CCTGGGGTTTCT GC  GC
                                || ||||||||||| ||  ||
                                AC GGACCCCAAGGG CG  TG
                                 T          T  TT
GAM593  SIMRP7   3'  GCCCCAGGAACCCCAGGGC   93976            CCC
                                GCCCTGGGGTTTCTG   GC
                                ||||||||||||||   ||
                                CGGGACCCCAAGGAC   CG
                                       CC_
GAM593  SKB1     5'  GTATCAAGGAATCCCGGCGT   21472    C        GCCC
                                GC CTGGGGTTTCT    GC
                                || ||||||||||    ||
                                TG GGCCCTAAGGA    TG
                                 C         ACTA
GAM593  SLC12A5  3'  GCCCGGAGGCCCGCGGGGT   40770       _       CCC
                                GCCCTG GGGTTTCTG   GC
                                |||||| |||||||||   ||
                                TGGGGC CCCGGAGGC   CG
                                   G        C__
GAM593  SLC39A3  3'  GTGTGGCAGAGTAGAGTTCCAG 58603        GG  ____     _  AC
           GGT                    GCCCTGG  TT    TCTGCC CGC
                                |||||||  ||    |||||| |||
                                TGGGACC  GA    AGACGG GTG
                                    TT  GATG     T
GAM593  SNRK     3'  GTGTGGTTGACCCTTGGGGTA  35281      TG   TT  TGC
                                TGCCC  GGG  TC   CCGCAC
                                |||||  |||  ||   ||||||
                                ATGGG  TCC  AG   GGTGTG
                                   GT   C_  TT_
GAM593  Spir-1   3'  TGTGGGAGTTTCAGGACA    65331    C    GG TTT  G
                                TG CCTG  G   CT CCCGCA
                                || ||||  |   || ||||||
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                                AC GGAC  T   GA GGGTGT
                                 A    TT ____ _
GAM593  SSB-4    3'  GTGTCAGGGTCTCTGGGCA    55963      T    T    CC
                                TGCCC GGGG TTCTG  CGC
                                ||||| |||| |||||  |||
                                ACGGG TCTC GGGAC  GTG
                                   _    T    T_
GAM593  STAT2    3'  GTACTTGGAGGGCTCAGGGCA  19455        G     CCC
                                TGCCCTGGG TTTCTG   GC
                                |||||||||| ||||||   ||
                                ACGGGACTC GGAGGT   TG
                                     G     TCA
GAM593  STIM2    3'  GTGAGAAGGGAGCTCTGGAGCA 40862     C TG       GCC_   AC
                                TGC C  GGGTTTCT    CGC
                                ||| |  ||||||||    |||
                                ACG G  CTCGAGGG    GTG
                                  A GT       AAGA
GAM593  SUCLG2   3'  GTGTTTTGCAGACTTTGGGG   66225     TG   TT    CC_
                                CCC  GGG  TCTGC   GCAC
                                |||  |||  |||||   ||||
                                GGG  TTC  AGACG   TGTG
                                  GT   __     TTT
GAM593  SV2      3'  GTGTGTAAACCCCGTGGGCA   29959      _      TC   C
                                TGCCC TGGGGTT  TGC CGC
                                ||||| |||||||  ||| |||
                                ACGGG GCCCCAA  ATG GTG
                                   T      __   T
GAM593  SYNPO2   3'  GTGTGTGGAGACTGTAGGGT   72389       G     TG C
                                GCCCTG GGTTTC  C CGC
                                |||||| ||||||  | |||
                                TGGGAT TCAGAG  G GTG
                                   G     GT T
GAM593  SYT12    3'  GTGTCCAGGGCCCCAGGGT    96386          T   CC
                                GCCCTGGGGTT CTG  CGC
                                |||||||||||| |||  |||
                                TGGGACCCCGG GAC  GTG
                                      _  CT
GAM593  TAS1R1   3'  GTGTCCGGGAGGTCTTTGGGCA 57724      T_   G     CC   AC
                                TGCCC  GGG TTTCTG  CGC
                                |||||  ||| ||||||  |||
                                ACGGG  TCT GAGGGC  GTG
                                   TT   G     CT
GAM593  TGIF2    3'  GTGGCAGGAAACTTTGGGG    41758     TG       GC
                                CCC  GGGTTTCT  CCGC
                                |||  ||||||||  ||||
                                GGG  TTCAAAGG  GGTG
                                  GT       AC
GAM593  THTPA    3'  GTGCCTCCTGTGGAAGTTTAGG 44510       G GG    TG CC___
            GGCA                   TGCCCT G  TTTC  C     GCAC
                                |||||| |  ||||  |    ||||
```

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                                ACGGGG T  GAAG  G    CGTG
                                   A TT   GT TCCTC
GAM593  TIEG2    5'  GTGCCGGCCGCAGGAGCTCCGG 14584          __  _
           G                    CCTGGGGTTTCTGC  CCG CAC
                                |||||||||||||  ||| |||
                                GGGCCTCGAGGACG  GGC GTG
                                      CC   C
GAM593  TIGD5    5'  GCGCAGGGGACCCCGGGGC   52769        TT  GCC
                                GCCCTGGGGT  CT   CGC
                                ||||||||||  ||   |||
                                CGGGGCCCCA  GG   GCG
                                     GG  AC_
GAM593  TLN1     3'  GTGCCTGCCAAACCCCAGGGC  21906         CT  CC
                                GCCCTGGGGTTT  GC  GCAC
                                ||||||||||||  ||  ||||
                                CGGGACCCCAAA  CG  CGTG
                                      C_  TC
GAM593  TMSNB    3'  GTGTTTGTAGAGATTTTAGGC  42077    C        CC
                                GCC TGGGGTTTCTGC  GCAC
                                |||  ||||||||||||  ||||
                                CGG ATTTTAGAGATG  TGTG
                                  _         TT
GAM593  TNFRSF21 3'  GTGTGGGTGGGGTTTGTGGGTA 27826     TGGGGT   TG
                                TGCCC     TTC  CCCGCAC
                                |||||     |||  |||||||
                                ATGGG     GGG  GGGTGTG
                                   TGTTT_   GT
GAM593  TNRC4    3'  GCTCGAAGGCTCCGGGGTA   24193         C  CCC
                                TGCCCTGGGGTTT TG   GC
                                ||||||||||||| ||   ||
                                ATGGGGCCTCGGA GC   CG
                                      A  T__
GAM593  TOLLIP   3'  GTGCTGGGAGGTCTCAGCGC   39200    C     TT   G  C
                                GC CTGGGG  TCT CC GCAC
                                || ||||||  ||| || ||||
                                CG GACTCT  GGA GG CGTG
                                 C     __   G  T
GAM593  TRAD     5'  GTGCCATGCGGGAGCGCTGGGG 23921     TG G       CC_
           C                    GCCC  G GTTTCTGC   GCAC
                                ||||  | ||||||||   ||||
                                CGGG  C CGAGGGCG   CGTG
                                  GT G       TAC
GAM593  TRAP-1   5'  GTGGGCGGGGCCCCAGGCCG   16194    C       TT T
                                TG CCTGGGGT  C GCCCGC
                                || ||||||||  | ||||||
                                GC GGACCCCG  G CGGGTG
                                 C       GG _
GAM593  TREX2    5'  GCTTGGAGATCCTAGAGT    55642    C         CCC
                                GC CTGGGGTTTCTG   GC
                                || ||||||||||||   ||
```

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                                TG GATCCTAGAGGT   CG
                                 A          T__
GAM593   TRIM31    3'  GTGCTCCACGGACTTCGGAGCA 92650     C       TC  CCC
                                TGC CTGGGGTT  TG   GCAC
                                ||| ||||||||  ||   ||||
                                ACG GGCTTCAG  AC   CGTG
                                  A       GC  CT_
GAM593   Ubc6p     3'  GCGGGTGGGAACCTCGGGGC   55192           TG
                                GCCCTGGGGTTTC  CCCGC
                                ||||||||||||  |||||
                                CGGGGCTCCAAGG  GGGCG
                                        GT
GAM593   ULK2      5'  GCGGTGCGGGTTCTAGGGC    28687        GG TT   _
                                GCCCTGG  T  CTGC CCGC
                                |||||||  |  |||| ||||
                                CGGGATC  G  GGCG GGCG
                                    TT __    T
GAM593   UPK1A     3'  GTGTGCCCTGAAACCCCAGGGC 23786           TGCC
                                GCCCTGGGGTTTC    CGCAC
                                ||||||||||||    |||||
                                CGGGACCCCAAAG    GTGTG
                                        TCCC
GAM593   UREB1     5'  GTGTTAAACCAGATCCTACGGC 49390      C       CTGCCC
           A                     TGCC TGGGGTTT     GCAC
                                ||||| ||||||||     ||||
                                ACGG ATCCTAGA     TGTG
                                  C       CCAAAT
GAM593   USP19     3'  GGGCAGAGTATCCTAGGGT    90403          _
                                GCCCTGGGGT TTCTGCCC
                                |||||||||| ||||||||
                                TGGGATCCTA GAGACGGG
                                      T
GAM593   VAMP4     5'  GTTCCCCGGGAGCCTCAGG    61030           CCC_
                                CCTGGGGTTTCTG    GC
                                ||||||||||||    ||
                                GGACTCCGAGGGC    TG
                                        CCCT
GAM593   VI        3'  GTGGGGAGGTCCCAGAGGT    26488     _     TT   G
                                GCC CTGGGG  TCT CCCGC
                                ||| ||||||  ||| |||||
                                TGG GACCCT  GGA GGGTG
                                  A     __   G
GAM593   WASPIP    3'  GTGTGGGTGGGAATCGGTA    14086      CTGG     TG
                                TGCC    GGTTTC  CCCGCAC
                                ||||    ||||||  |||||||
                                ATGG    CTAAGG  GGGTGTG
                                  ____      GT
GAM593   WBSCR18   3'  GTTCCTGGAGTCTCTAGGGT   51263         T    CCC
                                GCCCTGGGG TTCTG   GC
                                |||||||| |||||   ||
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                                TGGGATCTC GAGGT   TG
                                      T    CCT
GAM593  WBSCR20A  3'  GCACATAGCAGAGGCTCCGGGC 50569     T        CC___  AC
                                GCCC GGGGTTTCTGC    GC
                                |||| ||||||||||    ||
                                CGGG CCTCGGAGACG    CG
                                  _         ATACA
GAM593  WDR7    3'  GCTGCAAAACCCTGGGGT    31611     TG    C   CC
                                GCCC  GGGTTT TGC  GC
                                ||||  |||||| |||  ||
                                TGGG  CCCAAA ACG  CG
                                  GT     _   T_
GAM593  YAP1    5'  GGGCGGAGGCGCCGGGGC    21462       G
                                GCCCTGG GTTTCTGCCC
                                ||||||| ||||||||||
                                CGGGGCC CGGAGGCGGG
                                    G
GAM593  ZDHHC4   3'  GTGTCTCTAAACTCTGGGCA   36644     T     CTGCC
                                TGCCC GGGGTTT    CGC
                                ||||| |||||||    |||
                                ACGGG TCTCAAA    GTG
                                  _      TCTCT
GAM593  ZFD25   5'  GTGTGGGCTTTATTTGGGC   33114     TG   TTCT
                                GCCC  GGGT   GCCCGCAC
                                ||||  ||||   ||||||||
                                CGGG  TTTA   CGGGTGTG
                                  __   TTT_
GAM593  ZIC4    5'  GTACAGGGAGCTCCGGGG    50542          GCCC
                                CCCTGGGGTTTCT   GC
                                ||||||||||||   ||
                                GGGGCCTCGAGGG   TG
                                       ACA_
GAM593  ZIC4    5'  GTGCCCCGGAGAGCCCCGGGGT 50543        _    CCC
                                GCCCTGGGG TTTCTG   GCAC
                                ||||||||| ||||||   ||||
                                TGGGGCCCC AGAGGC   CGTG
                                     G    CC_
GAM593  ZNF263   3'  CTGAGGTGACCTCAGGGT    20425         TCT  _  CAC
                                GCCCTGGGGTT   GCC CG
                                ||||||||||   ||| ||
                                TGGGACTCCAG   TGG GT
                                      ___   A  CT
GAM593  ZNF31   5'  GTGTCTCGGTGGAGCCTTGGGG 65616    TG    T TG  C__
                                CCC  GGGTT C  CC   GCAC
                                |||  ||||| |  ||   ||||
                                GGG  TCCGA G  GG   TGTG
                                  GT    _ GT  CTC
GAM593  ZNF339   3'  GTGTGATGTTTAACTTCAGG   41397        TCT  C_
                                CCTGGGGTT   GC  CGCAC
                                |||||||||   ||  |||||
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                                GGACTTCAA   TG  GTGTG
                                    TT_  TA
GAM593   LOC112868 3'  GTGTGGGGTGGCCCCAGGGC   73270          TCTG
                                GCCCTGGGGTT    CCCGCAC
                                ||||||||||    |||||||
                                CGGGACCCCGG    GGGTGTG
                                    TG__
GAM593   LOC113230 5'  GCAAAGGGCGGAGGTCCAGGGG 73341       G  GT      ___  AC
           CA                     TGCCCT GG  TTCTGCCC   GC
                                ||||||  ||  ||||||||   ||
                                ACGGGG CC  GAGGCGGG   CG
                                   A  TG       AAA
GAM593   LOC113386 5'  GTGTGGGTGCCCTCCAGGTGT  57869    _      TTTC
                                GC CCTGGGG    TGCCCGCAC
                                || |||||||    |||||||||
                                TG GGACCTC    GTGGGTGTG
                                 T      CC__
GAM593   LOC115098 3'  GTGTGTAGAGCCTCAGGGC    57395          T    C
                                GCCCTGGGGTT CTGC CGC
                                |||||||||||  |||| |||
                                CGGGACTCCGA GATG GTG
                                    _    T
GAM593   LOC115110 5'  GCTGGGAAACCTCAGGGT    72180           TG  C
                                GCCCTGGGGTTTC  CC GC
                                ||||||||||||  || ||
                                TGGGACTCCAAAG  GG CG
                                     __  T
GAM593   LOC115110 5'  GTGCTCTGGAGGCTTTGGGCA  72184      T        CCC
                                TGCCC GGGGTTTCTG   GCAC
                                |||||  ||||||||||   ||||
                                ACGGG TTTCGGAGGT   CGTG
                                   _         CT_
GAM593   LOC115110 5'  GTGGGAGGGATCTGGGGCA    72185      TG  G TT  G
                                TGCCC  GG T  CT CCCGC
                                |||||  || |  || |||||
                                ACGGG  CT A  GA GGGTG
                                   GT  _ GG  _
GAM593   LOC115264 3'  GCCCTGGTGGACTCCAGGGT   73739         TT  TG  C__
                                GCCCTGGGG  TC  CC   GC
                                |||||||||  ||  ||   ||
                                TGGGACCTC  AG  GG   CG
                                     __  GT  TCC
GAM593   LOC115704 3'  GCTCCTCAGGGCCCCGGGGCA  73909           T   CCC_
                                TGCCCTGGGGTT CTG    GC
                                ||||||||||||  |||    ||
                                ACGGGGCCCCGG GAC    CG
                                     _   TCCT
GAM593   LOC115817 3'  GTGTGTCCGTGGTGAGTTCTGG 57414      TG GG   _ TG C__
           GGT                    GCCC  G  TTT C  C   CGCAC
                                ||||  |  ||| |  |   |||||
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                                TGGG  C  GAG G  G   GTGTG
                                  GT TT   T GT CCT
GAM593   LOC121629 5'  GTCACAAGAGGCTCCAGGG   76086          GCCC
                                CCCTGGGGTTTCT   GC
                                ||||||||||||   ||
                                GGGACCTCGGAGA   TG
                                       ACAC
GAM593   LOC122792 5'  GTCCGCGGAGACTCTGGGG   59826    TG       CC
                                CCC  GGGTTTCTGC  GC
                                |||  ||||||||||  ||
                                GGG  CTCAGAGGCG  TG
                                  GT        CC
GAM593   LOC123792 3'  GTGCCCATGAACTGCTGGGGC  74705     TG _    C  CCC
                                GCCC  G GGTTT TG   GCAC
                                ||||  | |||||  ||   ||||
                                CGGG  C TCAAG AC   CGTG
                                  GT G    T  C__
GAM593   LOC124944 5'  GTGCGCTAGGGCCCCGGCGC   74837    C       CT  C
                                GC CTGGGGTTT  GC CGC
                                || |||||||||  || |||
                                CG GGCCCCGGG  CG GTG
                                 C        AT  C
GAM593   LOC124968 5'  GTGACCAGCGGGGGTCCCTGGG 74833     TG  _ TT   CCG_
           GC                    GCCC  GGG T  CTGC   CAC
                                ||||  ||| |  ||||   |||
                                CGGG  CCC G  GGCG   GTG
                                  GT   T GG   ACCA
GAM593   LOC125268 3'  GTGCGTGTCAGGGCCCCAGGCA 76578     C     T  _ C
                                TGCC TGGGGTT CTG C CGCAC
                                |||| ||||||| ||| | |||||
                                ACGG ACCCCGG GAC G GCGTG
                                  _      _  T T
GAM593   LOC125704 5'  GTGCCAGGACTACCAGGGC   74882       GGT    CCC
                                GCCCTGG   TTCTG   GCAC
                                |||||||   |||||   ||||
                                CGGGACC   AGGAC   CGTG
                                    ATC    ___
GAM593   LOC125875 5'  GCTGGGGGCCTCGGGGTA    74887          TT  _
                                TGCCCTGGGGT  CT GC
                                ||||||||||  || ||
                                ATGGGGCTCCG  GG CG
                                       GG  T
GAM593   LOC125875 5'  GTGTCTAAGGAGCCCTAGGGCA 74889            GCCC
                                TGCCCTGGGGTTTCT   GCAC
                                ||||||||||||||   ||||
                                ACGGGATCCCGAGGA   TGTG
                                         ATC_
GAM593   LOC126005 5'  GTGTGAGTACTTCTGGGGTA   76174      TG   TTTC   C
                                TGCCC  GGG   TGC CGCAC
                                |||||  |||   ||| |||||
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                                ATGGG  CTT    ATG GTGTG
                                   GT   C___   A
GAM593   LOC126129 5'  GTGACGGTGATCTCGGGGT   74919          T   CC
                                GCCCTGGGGTT CTG  CGC
                                |||||||||| |||  |||
                                TGGGGCTCTAG GGC  GTG
                                      T   A_
GAM593   LOC126208 3'  GTGCGATGGACCCCGCGGCA   74931      C       CTGCC
                                TGCC TGGGGTTT     CGCAC
                                |||| ||||||||     |||||
                                ACGG GCCCCAGG     GCGTG
                                  C       TA___
GAM593   LOC126549 5'  GCCCAGAGTTTTCAGGGCA    76210        GG T     CCC
                                TGCCCTG  G TTCTG   GC
                                |||||||  | |||||   ||
                                ACGGGAC  T GAGAC   CG
                                    TT T     C__
GAM593   LOC126549 5'  GTGTATTGTGGAAGCCCTAGGG 76211           TG CC_
                                CCCTGGGGTTTC  C   GCAC
                                ||||||||||| |   ||||
                                GGGATCCCGAAG  G   TGTG
                                      GT TTA
GAM593   LOC126917 3'  GTGGTATGGGAGTTTCGTGGGC 75099       _  GG     GC_    AC
           A                     TGCCC TGG  TTTCT   CCGC
                                ||||| |||  |||||   ||||
                                ACGGG GCT  GAGGG   GGTG
                                   T   TT     TAT
GAM593   LOC127435 3'  GTGCTGCTGGGGCCTTGGGGCA 76609       TG    TT T  CC
                                TGCCC  GGGT  C GC  GCAC
                                |||||  ||||  | ||  ||||
                                ACGGG  TCCG  G CG  CGTG
                                   GT    GG T  T_
GAM593   LOC127435 3'  GTGGGGGAAGTTCCGGGT    76610      T  GG     G
                                GCCC GG  TTTCT CCCGC
                                |||| ||  ||||| |||||
                                TGGG CC  GAAGG GGGTG
                                  _  TT    _
GAM593   LOC128077 5'  GCTGGCAGGCTCCGGGGC    75220          TT     C
                                GCCCTGGGGT  CTGCC GC
                                ||||||||||  ||||| ||
                                CGGGGCCTCG  GACGG CG
                                      __     T
GAM593   LOC128272 5'  GCAACCCCAGAGCCCCCAGGGT 75243          T     CCC__  AC
                                GCCCTGGGG TTCTG     GC
                                |||||||||| |||||     ||
                                TGGGACCCC GAGAC     CG
                                      C     CCCAA
GAM593   LOC128402 3'  GCGCAGGGACCCCAAGGT    76289     C      TT    CC
                                GCC TGGGGT  CTGC  GC
                                ||| ||||||  ||||  ||
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                                TGG ACCCCA  GACG  CG
                                  A     GG   __
GAM593   LOC129433 5'  GTGAGTGGGATCCTGGGCA   76222      T    TT T  C
                                TGCCC GGGGT  C GC CGC
                                ||||| |||||  | || |||
                                ACGGG TCCTA  G TG GTG
                                   _    GG _  A
GAM593   LOC129446 3'  GCCTCAGCAGAGGCCTTATGGT 76616     C         CC__  AC
           A                     TGCC TGGGGTTTCTGC   GC
                                |||| ||||||||||||   ||
                                ATGG ATTCCGGAGACG   CG
                                  T         ACTC
GAM593   LOC129566 3'  GTGCGGGCAGGCTTGGGGG   76227     G   TT
                                CCCT GGGT  CTGCCCGCAC
                                |||| ||||  ||||||||||
                                GGGG TTCG  GACGGGCGTG
                                  G   __
GAM593   LOC129676 5'  GTGCTTGGACGGGAGTGTCTGG 76236      TG  GT_    _  C_
           GGCA                   TGCCC  GG   TTCTG CC  GCAC
                                ||||| ||   ||||| ||  ||||
                                ACGGG  CT   AGGGC GG  CGTG
                                   GT  GTG    A  TT
GAM593   LOC129676 5'  GTGTGGAAGTAGAGATTCTGGG 76237     T        __
           C                     GCCC GGGGTTTCTGC  CCGCAC
                                |||| ||||||||||  ||||||
                                CGGG TCTTAGAGATG  GGTGTG
                                  _         AA
GAM593   LOC130327 3'  GTGTGCCCTGGGAGTCTCAGGG 75423       GT    CC_
           C                     GCCCTGGG  TTCTG   CGCAC
                                ||||||||  |||||   |||||
                                CGGGACTC  AGGGT   GTGTG
                                    TG    CCC
GAM593   LOC130497 3'  GCCCTAGGGACCGCGGGGCA   75451       G   TT   CCC
                                TGCCCTG GGT  CTG   GC
                                ||||||| |||  |||   ||
                                ACGGGGC CCA  GAT   CG
                                   G   GG   CC_
GAM593   LOC130576 3'  GTGCACATTGGACCTCAAGGC  75460     C       CTGCCC
                                GCC TGGGGTTT     GCAC
                                ||| ||||||||     ||||
                                CGG ACTCCAGG     CGTG
                                  A       TTACA_
GAM593   LOC138429 3'  GTGGGAGAAGCAGGGGTCCTGG 75866     TG   TT    _____   AC
           GG                    CCC  GGG  TCTGC    CCGC
                                |||  |||  |||||    ||||
                                GGG  CCT  GGACG    GGTG
                                  GT   GG    AAGAG
GAM593   LOC139341 3'  GCCAGAGTCTCTAGGGCA    75899         T    CCC
                                TGCCCTGGGG TTCTG   GC
                                |||||||||| |||||   ||
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                                ACGGGATCTC GAGAC   CG
                                      T    ___
GAM593   LOC139840 5'  GCTCCAGGGCAGGGATCTTGGG 76776      T    TT    _____ AC
            TA                   TGCCC GGGGT  CTGCCC    GC
                                 ||||| |||||  ||||||    ||
                                 ATGGG TTCTA  GACGGG    CG
                                   _    GG     ACCT
GAM593   LOC142972 5'  GTGTGGCGCTGCCCTGGGC    65721     T    TTCT  _
                                 GCCC GGGGT    GC CCGCAC
                                 |||| |||||    || ||||||
                                 CGGG TCCCG    CG GGTGTG
                                   _    T___  C
GAM593   LOC143162 3'  GTGTGGCGAACTTGGGGCA    77008      TG  GT   T  _
                                 TGCCC  GG  TTC GCC CGC
                                 |||||  ||  ||| ||| |||
                                 ACGGG  TC  AAG CGG GTG
                                    GT  __  _  T
GAM593   LOC143451 5'  GTGTTACAGAATCCTGAGG    77071     G   T    CCC
                                 CCT GGG TTCTG   GCAC
                                 ||| ||| |||||   ||||
                                 GGA TCC AAGAC   TGTG
                                   G   T    AT_
GAM593   LOC143666 5'  GTGTGGATTTGGCTCCAGGTCG 83888    C       TCTGC
                                 TG CCTGGGGTT    CCGCAC
                                 || |||||||||    ||||||
                                 GC GGACCTCGG    GGTGTG
                                  T       TTTA_
GAM593   LOC143915 3'  GAGGAGGGAGCCTTAGGGT    83907           G  CG
                                 GCCCTGGGGTTTCT CC  C
                                 |||||||||||||| ||  |
                                 TGGGATTCCGAGGG GG  G
                                          A  AT
GAM593   LOC144558 3'  AGTGGGAGTTGTCGGGGCA    84073        GGTTT  G    AC
                                 TGCCCTGG    CT CCCGC
                                 ||||||||    || |||||
                                 ACGGGGCT    GA GGGTG
                                      GTT__  _    AT
GAM593   LOC145125 5'  GTGTTACAGAATCCTGAGG    77548     G   T    CCC
                                 CCT GGG TTCTG   GCAC
                                 ||| ||| |||||   ||||
                                 GGA TCC AAGAC   TGTG
                                   G   T    AT_
GAM593   LOC145241 5'  GTGGATGGGACCCTAGTGTA   63526     C      TT TGC
                                 TGC CTGGGGT  C   CCGC
                                 ||| |||||||  |   ||||
                                 ATG GATCCCA  G   GGTG
                                   T      GG TA_
GAM593   LOC145333 5'  GTGTGAGATGGCTCTGGTGT   84303    C TG    _   GCC
                                 GC C  GGGTT TCT   CGCAC
                                 || |  ||||| |||   |||||
```

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                                TG G  CTCGG AGA   GTGTG
                                 T GT    T  ___
GAM593  LOC145438 5'  TGCGGCCACTTGGGGGCA    84320       G   TTCT  C
                                TGCCCT GGGT   GCC GCA
                                |||||| ||||   ||| |||
                                ACGGGG TTCA   CGG CGT
                                   G   C___  _
GAM593  LOC145453 3'  GAGGAGAGGTCTGAGGGCA   77665       G  GT   G  CG
                                TGCCCT GG  TTCT CC  C
                                |||||| ||  |||| ||  |
                                ACGGGA TC  GAGA GG  G
                                   G  TG   _ AT
GAM593  LOC145623 3'  TGTTTTAGAGATTTCAGTGT  84397    C  GG     CCC  C
                                GC CTG  GTTTCTG   GCA
                                || |||  |||||||   |||
                                TG GAC  TAGAGAT   TGT
                                 T  TT     TT_  A
GAM593  LOC145725 3'  GTGTGCCACTTGCCCCCAGGGC 77889         TTTCTGCC
           A                     TGCCCTGGGG       CGCAC
                                ||||||||||       |||||
                                ACGGGACCCC       GTGTG
                                      CGTTCACC
GAM593  LOC145732 3'  GTGTGCCACTTGCCCCCAGGGC 77900         TTTCTGCC
           A                     TGCCCTGGGG       CGCAC
                                ||||||||||       |||||
                                ACGGGACCCC       GTGTG
                                      CGTTCACC
GAM593  LOC145853 5'  GCACACCGGGGGCTCTCGGGCA 84549      T    TT  CCC_  AC
                                TGCCC GGGGT  CTG   GC
                                ||||| |||||  |||   ||
                                ACGGG TCTCG  GGC   CG
                                   C    GG  CACA
GAM593  LOC146237 3'  GTGTTAGCCGGGAAACTCCGGG 84614           __  CC
           GC                    GCCCTGGGGTTTCT  GC  GCAC
                                |||||||||||||  ||  ||||
                                CGGGGCCTCAAAGG  CG  TGTG
                                        GC  AT
GAM593  LOC146268 5'  TGGGGGACTTGGGGGCA     78346       G    TCTG  G
                                TGCCCT GGGTT    CCC CA
                                |||||| |||||    ||| ||
                                ACGGGG TTCAG    GGG GT
                                   G    _____  A
GAM593  LOC146272 5'  GCTCTCCGGAAGCTTCAGG   78328          CCC_
                                CCTGGGGTTTCTG   GC
                                ||||||||||||    ||
                                GGACTTCGAAGGC   CG
                                        CTCT
GAM593  LOC146337 3'  GTGCCCAGAGACCCCGGGGTA  84645             CCC
                                TGCCCTGGGGTTTCTG   GCAC
                                ||||||||||||||||   ||||
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                                ATGGGGCCCCAGAGAC   CGTG
                                      C__
GAM593   LOC146488 3'  GTGCATGGTGGGGGCCTCGGGG 71360         TT TG  C_
           C                    GCCCTGGGGT  C  CC  GCAC
                                ||||||||||  |  ||  ||||
                                CGGGGCTCCG  G  GG  CGTG
                                      GG GT  TA
GAM593   LOC146714 5'  GTGTGGGCAGGTGGATAAGGGC 84752       GGGGTT
           A                    TGCCCT     TCTGCCCGCAC
                                ||||||     ||||||||||
                                ACGGGA     GGACGGGTGTG
                                   ATAGGT
GAM593   LOC147054 5'  GTGTGCTGCGGGACCCTTGGGT 85009     T     T    C_
                                GCCC GGGGTT CTGC  CGCAC
                                |||| |||||| ||||  |||||
                                TGGG TCCCAG GGCG  GTGTG
                                  T     _   TC
GAM593   LOC147180 5'  GCATCAGAGTTCCAGGGCA    85101        GG  T   CCC
                                TGCCCTGG  TT CTG   GC
                                ||||||||  || |||   ||
                                ACGGGACC  GA GAC   CG
                                     TT  _   TA_
GAM593   LOC147791 5'  GTGAAGTTATGGGGGCTCTATG 85192     C     TT ___  C_   AC
           GCA                    TGCC TGGGGT  CT   GC  CGC
                                |||| ||||||  ||   ||  |||
                                ACGG ATCTCG  GG   TG  GTG
                                  T     GG  TAT  AA
GAM593   LOC147958 5'  GTGCCCCCCAGAGCTCCCAGGG 88527        GT    CCC_
           CA                     TGCCCTGGG  TTCTG   GCAC
                                |||||||||  |||||   ||||
                                ACGGGACCC  GAGAC   CGTG
                                     TC    CCCC
GAM593   LOC147990 3'  GTGTCACTGGGACCCCAGGCA  85233     C     TT TGCCC
                                TGCC TGGGGT  C    GCAC
                                |||| ||||||  |    ||||
                                ACGG ACCCCA  G    TGTG
                                  _     GG TCAC_
GAM593   LOC148089 3'  GCACTGAGGGCCCCGGGGCA   79332          _  ___
                                TGCCCTGGGGTT TC  TGC
                                ||||||||||| ||  |||
                                ACGGGGCCCCGG AG  ACG
                                      G  TC
GAM593   LOC148137 3'  GTGCTAAGAGCCCATAGGGCA  59112       _    T  GCCC
                                TGCCCTG GGGTT CT   GCAC
                                ||||||| ||||| ||   ||||
                                ACGGGAT CCCGA GA   CGTG
                                     A    _  AT__
GAM593   LOC148195 3'  GCAATACCAGAAACCTACAGGG 85284       _       CCC__  AC
           TA                     TGCCCTG GGGTTTCTG    GC
                                ||||||| |||||||||    ||
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                                ATGGGAC TCCAAAGAC     CG
                                   A        CATAA
GAM593   LOC148426 5'  GTGTGGCCGGGGCCCCAGGGGC 85307      _     TT T   _   AC
             A                      TGCCC TGGGGT  C GCC CGC
                                    ||||| ||||||  | ||| |||
                                    ACGGG ACCCCG  G CGG GTG
                                       G     GG C   T
GAM593   LOC148530 5'  GTGTTTTTGAATCCCGGGGC   85317           CTGCC
                                    GCCCTGGGGTTT     CGC
                                    ||||||||||||     |||
                                    CGGGGCCCTAAG     GTG
                                           TTTTT
GAM593   LOC148710 3'  TGCACACAGAAGTCCCAGGG   85351        GT    CCC   C
                                    CCCTGGG  TTCTG   GCA
                                    |||||||  |||||   |||
                                    GGGACCC  AAGAC   CGT
                                       TG     ACA
GAM593   LOC148764 5'  TGTGGGCTTTCCATGGCA    79741      C    TTTCT
                                    TGCC TGGGG     GCCCGCA
                                    |||| |||||     |||||||
                                    ACGG ACCTT     CGGGTGT
                                      T     T____
GAM593   LOC148887 5'  GCCTGGAAACCCCGGGACA    85403    C          CCC
                                    TG CCTGGGGTTTCTG   GC
                                    || ||||||||||||   ||
                                    AC GGGCCCCAAAGGT   CG
                                     A           C__
GAM593   LOC148887 3'  GTGCATGAGCCCCTGGGGT    85411      _      C   CC
                                    GCCCT GGGGTTT TGC  GC
                                    ||||| ||||||| |||  ||
                                    TGGGG CCCCGAG ACG  TG
                                      T      T  __
GAM593   LOC148930 3'  GTGCCCCAGAGATGCCCCAGGG 79845          __    CCC
             T                      GCCCTGGGGT  TTCTG   GCAC
                                    ||||||||||  |||||   ||||
                                    TGGGACCCCG  GAGAC   CGTG
                                          TA    CC_
GAM593   LOC149072 5'  GTGATCCTGGGAGCCCTGGGGC 79887      TG       GCCCG
                                    GCCC  GGGTTTCT     CAC
                                    ||||  ||||||||     |||
                                    CGGG  CCCGAGGG     GTG
                                      GT       TCCTA
GAM593   LOC149086 3'  TGCTGGACCCCAGAGGCA    85496      _      TTCTG  C
                                    TGCC CTGGGGT     CC GCA
                                    |||| |||||||     || |||
                                    ACGG GACCCCA     GG CGT
                                      A       _____  T
GAM593   LOC149194 3'  GTGCGGAGGTCCTGTGGCA    79988      C    GT     CC
                                    TGCC TGGG  TTCTGC  GC
                                    |||| ||||  ||||||  ||
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                                ACGG GTCC  GAGGCG  TG
                                  T   TG     __
GAM593  LOC149276 5'  GCCCAGGAACTTGGGGGT    85535      G       CCC
                                GCCCT GGGTTTCTG   GC
                                ||||| |||||||||   ||
                                TGGGG TTCAAGGAC   CG
                                   G       C__
GAM593  LOC149297 5'  GTGTGGTCCGGCTACGGGGC   85543      GG   TCTGC
                                GCCCTG  GTT    CCGCAC
                                ||||||  |||    ||||||
                                CGGGGC  CGG    GGTGTG
                                   AT   CCT__
GAM593  LOC149460 5'  GTGTGGAAAGAGGCCCCAAGGT 85614     C        GC
          A                      TGCC TGGGGTTTCT  CCGCAC
                                 |||| ||||||||||  ||||||
                                 ATGG ACCCCGGAGA  GGTGTG
                                   A         AA
GAM593  LOC149579 5'  GCTACAGGAGGTTCGGGGCA   71694        G     CCC
                                TGCCCTGGG TTTCTG   GC
                                ||||||||| ||||||   ||
                                ACGGGGCTT GAGGAC   CG
                                     G     AT_
GAM593  LOC149684 5'  GGATTGGCAGCAGCTTCGGGGC 85766          T    CGCAC
          A                      TGCCCTGGGGTT CTGCC
                                 |||||||||||| |||||
                                 ACGGGGCTTCGA GACGG
                                       C     TTAGGT
GAM593  LOC149706 5'  GCCTGTGGAAACCCTGGGTA   85806      T       TG CC
                                TGCCC GGGGTTTC  C  GC
                                ||||| ||||||||  |  ||
                                ATGGG TCCCAAAG  G  CG
                                  _       GT TC
GAM593  LOC149837 3'  GCCCAGGAACCTCAGGGT    85898            CCC
                                GCCCTGGGGTTTCTG   GC
                                ||||||||||||||   ||
                                TGGGACTCCAAGGAC   CG
                                       C__
GAM593  LOC150005 3'  GCAGCAGGATCCCCAGGGCA   85963         T     CC
                                TGCCCTGGGG TTCTGC  GC
                                |||||||||| ||||||  ||
                                ACGGGACCCC AGGACG  CG
                                     T     A_
GAM593  LOC150005 3'  GTGTTAGACTGGAGGCCCCGGG 85964           GCCC__
          G                      CCCTGGGGTTTCT     GCAC
                                 ||||||||||||      ||||
                                 GGGGCCCCGGAGG     TGTG
                                       TCAGAT
GAM593  LOC150113 5'  GTGTCCAGGAACTCCAGTGCA  88570     C          CC
                                TGC CTGGGGTTTCTG  CGC
                                ||| ||||||||||||  |||
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                                ACG GACCTCAAGGAC  GTG
                                  T          CT
GAM593   LOC150174 5'  GTGCTCCGAGTTCCAGGGCA   80440        GG   CTGCCC
                                TGCCCTGG  TTT     GCAC
                                ||||||||  |||     ||||
                                ACGGGACC  GAG     CGTG
                                    TT   CCT___
GAM593   LOC150213 5'  GTGTGCTCCGAGTTCCAGGGC  75359       GG   CT_  C   AC
                                GCCCTGG  TTT   GC CGC
                                |||||||  |||   || |||
                                CGGGACC  GAG   CG GTG
                                    TT   CCT  T
GAM593   LOC150290 3'  GTGCTCCAGGAATCCTGGGG   80591     TG       CCC
                                CCC  GGGTTTCTG   GCAC
                                |||  |||||||||   ||||
                                GGG  CCTAAGGAC   CGTG
                                  GT        CT_
GAM593   LOC150343 5'  GTCACAGGAGCCTGGGGCA    80495      TG  G     CCC
                                TGCCC  GG TTTCTG   GC
                                |||||  || ||||||   ||
                                ACGGG  CC GAGGAC   TG
                                   GT  _     AC_
GAM593   LOC150370 3'  GCTCATTAGAAACTCTTGGGCA 86125       T        CCC_  AC
                                TGCCC GGGGTTTCTG    GC
                                ||||| ||||||||||    ||
                                ACGGG TCTCAAAGAT    CG
                                   T         TACT
GAM593   LOC150372 3'  GTGGCAGGGAACTTCAGGGT   80621            GC    AC
                                GCCCTGGGGTTTCT  CCGC
                                ||||||||||||||  ||||
                                TGGGACTTCAAGGG  GGTG
                                        AC
GAM593   LOC150378 5'  GCCCACGGTGGAGGCCTCAGGC 80558      C        TG  C___  AC
           A                     TGCC TGGGGTTTC  CC    GC
                                ||||  |||||||||  ||    ||
                                ACGG ACTCCGGAG  GG    CG
                                  _        GT  CACC
GAM593   LOC150519 5'  GCCGGGGGCTTCGGGGT     80731         TT   CCC  AC
                                GCCCTGGGGT  CTG   GC
                                ||||||||||  |||   ||
                                TGGGGCTTCG  GGC   CG
                                     GG   ___  C
GAM593   LOC151249 3'  GTCTTCGGAAACCTTGGTGTA  60689     C TG       CCC
                                TGC C  GGGTTTCTG   GC
                                |||  |  |||||||||   ||
                                ATG G  TCCAAAGGC   TG
                                  T GT        TTC
GAM593   LOC151278 5'  GTGTGGGCGCAGCCGGGACA   81012    _   TGG    TC
                                TG CCC   GGTT  TGCCCGCAC
                                || |||   ||||  |||||||||
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                                AC GGG   CCGA  GCGGGTGTG
                                 A  ___   C_
GAM593  LOC151720 5'  GCCCCAGGGACCCAGGGCA   81156        G TT   CCC  AC
                                TGCCCTGGG T  CTG   GC
                                |||||||||  |  |||   ||
                                ACGGGACCC A  GAC   CG
                                      _ GG   CC_  A
GAM593  LOC152300 5'  GTTACAGAAACTTCGTGGCA   81390     C         CCC
                                TGCC TGGGGTTTCTG   GC
                                |||| ||||||||||   ||
                                ACGG GCTTCAAAGAC   TG
                                  T         AT_
GAM593  LOC152317 5'  GTGAGGGGGATCCTGGGGACA  86836    _   TG     CTG   G
                                TG CCC  GGGTTT   CCC CAC
                                || |||  ||||||   ||| |||
                                AC GGG  CCTAGG   GGG GTG
                                 A  GT     ___   A
GAM593  LOC152674 5'  GTGTGGGCAGAGGCCTTA    87004
                                TGGGGTTTCTGCCCGCAC
                                ||||||||||||||||||
                                ATTCCGGAGACGGGTGTG

GAM593  LOC152992 5'  GTGCCCCTGAGGGACTCCGGGC 81645      T    TT  GCCC_
          A                      TGCCC GGGGT  CT    GCAC
                                |||||  |||||  ||    ||||
                                ACGGG CCTCA  GA    CGTG
                                   _    GG  GTCCC
GAM593  LOC153396 5'  GCCCCGGCAACTCCAGGGT   81683         TTC   C__
                                GCCCTGGGGT   TGCC   GC
                                ||||||||||   ||||   ||
                                TGGGACCTCA   ACGG   CG
                                      ___    CCC
GAM593  LOC153546 5'  CGCGGGCCGGAAGCCTCGGGC  81742     T        _    AC
                                GCCC GGGGTTTCTG CCCGC
                                |||| |||||||||| |||||
                                CGGG CTCCGAAGGC GGGCG
                                   _        C    CG
GAM593  LOC153546 5'  TGCGGGAGGCCTCGGTGC    81746    C       CTG
                                GC CTGGGGTTT   CCCGCA
                                || |||||||||   ||||||
                                CG GGCTCCGGA   GGGCGT
                                 T       ___
GAM593  LOC153572 3'  GTGGCCGCAAGACGCCCCAGGG 87233          T  _ __   AC
          CA                     TGCCCTGGGGT TCT GC  CCGC
                                ||||||||||| ||| ||  ||||
                                ACGGGACCCCG AGA CG  GGTG
                                      C   A  CC
GAM593  LOC153577 5'  GTGATGGGGAGCTTTGGGG   87243    TG     CTG   _
                                CCC  GGGTTT   CCCG CAC
                                |||  ||||||   |||| |||
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                                GGG  TTCGAG   GGGT GTG
                                  GT     ___    A
GAM593   LOC153592 3'  GTGGTGGAACCTCAGGCA    87249     C       TGC
                                TGCC TGGGGTTTC   CCGC
                                |||| |||||||||   ||||
                                ACGG ACTCCAAGG   GGTG
                                  _       T__
GAM593   LOC153817 3'  GTCTTCAGAAACCTTGGTGTA  61702     C TG       CCC
                                TGC C  GGGTTTCTG   GC
                                ||| |  |||||||||   ||
                                ATG G  TCCAAAGAC   TG
                                  T GT        TTC
GAM593   LOC154043 5'  GTGCCCGGGATCCCGGCGGC   81935     _      T   CCC
                                GCC CTGGGGTT CTG   GCAC
                                ||| |||||||| |||   ||||
                                CGG GGCCCTAG GGC   CGTG
                                  C       _   C__
GAM593   LOC154215 3'  GTGTGCCCAAGAATCCCAGTGC 81958     C       TC  CC
           A                     TGC CTGGGGTT  TG  CGCAC
                                ||| ||||||||  ||  |||||
                                ACG GACCCTAA  AC  GTGTG
                                  T       GA  CC
GAM593   LOC154739 5'  GTGTGATGCTGAGATTTGGGGT 87442      TG  G    T  C_
           A                     TGCCC  GG TTTC GC  CGCAC
                                |||||  || |||| ||  |||||
                                ATGGG  TT AGAG CG  GTGTG
                                   GT  _    T  TA
GAM593   LOC154760 5'  GTGTGCACTGAAGCCCCAGGCA 87455     C       __  C   AC
                                TGCC TGGGGTTTC  TGC CGC
                                |||| |||||||||  ||| |||
                                ACGG ACCCCGAAG  ACG GTG
                                  _       TC   T
GAM593   LOC154881 3'  GTGTAAACAAAGATTCCAGGGC 82076          C  CCC
                                GCCCTGGGGTTT TG   GCAC
                                |||||||||||| ||   ||||
                                CGGGACCTTAGA AC   TGTG
                                       A  AAA
GAM593   LOC155032 3'  GCAACCAGCAACTCCAGGGTA  87594          T   CCC
                                TGCCCTGGGGTT CTG   GC
                                |||||||||||| |||   ||
                                ATGGGACCTCAA GAC   CG
                                       C   CAA
GAM593   LOC155061 3'  GCGTGGAAGCTTCAGGCA    82190     C       TG CC
                                TGCC TGGGGTTTC  C  GC
                                |||| |||||||||  |  ||
                                ACGG ACTTCGAAG  G  CG
                                  _       GT __
GAM593   LOC155435 3'  GTGTGACACAGGCCCTGGGGT  82273     TG     C  CC
                                GCCC  GGGTTT TG  CGCAC
                                ||||  |||||| ||  |||||
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                                TGGG  CCCGGA AC  GTGTG
                                  GT     C  A_
GAM593   LOC157292 3'  GCTACATGGCAGCCCCAGGGCA 87699          TTT    C____  AC
                                TGCCCTGGGG   CTGCC    GC
                                ||||||||||   |||||    ||
                                ACGGGACCCC   GACGG    CG
                                      ___     TACAT
GAM593   LOC157567 5'  GTGGTCCGGGGAACCCCTGGGC 82393      T       GC__   AC
           A                     TGCCC GGGGTTTCT   CCGC
                                 |||||  |||||||||   ||||
                                 ACGGG CCCCAAGGG    GGTG
                                    T       GCCT
GAM593   LOC157623 5'  GTGTGGGTGGAGTGCAGAGCA  82415    C   GGGT   TG
                                TGC CTG    TTC  CCCGCAC
                                |||  |||    |||  |||||||
                                ACG GAC    GAG  GGGTGTG
                                  A   GT__   GT
GAM593   LOC157638 5'  GCCCTAGAAGTCTCGGGGC    82423        GT    CCC
                                GCCCTGGG  TTCTG   GC
                                ||||||||  |||||   ||
                                CGGGGCTC  AAGAT   CG
                                     TG    CC_
GAM593   LOC157927 5'  GTGGGATGGGGGATTCCGTGGC 87948      C     TT  G__    AC
           A                     TGCC TGGGGT  CT   CCCGC
                                 ||||  ||||||  ||   |||||
                                 ACGG GCCTTA  GG   GGGTG
                                   T     GG  GTA
GAM593   LOC158046 5'  GTGTGGGCGCATCTAGGGCA   59906         GTTTC
                                TGCCCTGGG     TGCCCGCAC
                                |||||||||     |||||||||
                                ACGGGATCT     GCGGGTGTG
                                     AC___
GAM593   LOC158236 5'  GTGCAAAGTGGAGCTCCGGGGC 88011             TGCCC
           A                     TGCCCTGGGGTTTC     GCAC
                                 ||||||||||||||     ||||
                                 ACGGGGCCTCGAGG     CGTG
                                       TGAAA
GAM593   LOC158435 5'  GCTAACGCGGAAGCCCTAGAGC 57501     C          CC__  AC
           A                     TGC CTGGGGTTTCTGC    GC
                                 |||  ||||||||||||    ||
                                 ACG GATCCCGAAGGCG    CG
                                   A           CAAT
GAM593   LOC158662 3'  GGGAGGAAACTTTGGGGCA   82854       TG       G
                                TGCCC  GGGTTTCT CCC
                                |||||  |||||||| |||
                                ACGGG  TTCAAAGG GGG
                                   GT       A
GAM593   LOC158674 3'  GTGACCGAGGAGGAATTTCAGG 82857       GG     G  _  __
           GT                    GCCCTG  GTTTCT CC CG  CAC
                                 ||||||  |||||| || ||  |||
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                                TGGGAC  TAAGGA GG GC  GTG
                                  TT     _ A  CA
GAM593   LOC158678 3'  GTGACCAAGGAGGAATTTCAGG 61134       GG     G  CG___
           GT                     GCCCTG  GTTTCT CC    CAC
                                |||||| ||||||  ||    |||
                                TGGGAC  TAAGGA GG    GTG
                                  TT     _  AACCA
GAM593   LOC159089 5'  GCCTCAGGTGCCTTGGGGTA   88381      TG    T    CCC
                                TGCCC  GGGT TCTG   GC
                                |||||  |||| ||||   ||
                                ATGGG  TCCG GGAC   CG
                                  GT    T    TC_
GAM593   LOC159184 3'  GCCAGCAGCCCTGGGGCA    60682      TG    T   CCC
                                TGCCC  GGGTT CTG   GC
                                |||||  ||||| |||   ||
                                ACGGG  CCCGA GAC   CG
                                  GT    C   ___
GAM593   LOC161527 5'  GTGTGGGAAGACAGCTCCAGGC 83150     C      _   G
                                GCC TGGGGTT TCT CCCGCAC
                                |||  ||||||| ||| |||||||
                                CGG ACCTCGA AGA GGGTGTG
                                  _      C   A
GAM593   LOC161642 5'  GTGCGGGTCTGCACTTGGGGT  83164      TG  _  TTCT
                                GCCC  GG GT    GCCCGCAC
                                ||||  || ||    ||||||||
                                TGGG  TC CG    TGGGCGTG
                                  GT  A  TC__
GAM593   LOC162417 5'  GTGCGGGGCCAGCCCTGGGG   83214     TG     TCTG
                                CCC  GGGTT    CCCGCAC
                                |||  |||||    |||||||
                                GGG  CCCGA    GGGCGTG
                                  GT    CCG_
GAM593   LOC164121 5'  GTGTGGATGTGGTCCTGGGC   83049     T    TTT TG __
                                GCCC GGGG   C  C  CCGCAC
                                |||| ||||   |  |  ||||||
                                CGGG TCCT   G  G  GGTGTG
                                  _    ___ GT TA
GAM593   LOC164295 5'  GTGTGAACTGGGTCCCTGGGGC 83396      TG   T   TGCC
                                GCCC  GGG TTC    CGCAC
                                ||||  ||| |||    |||||
                                CGGG  CCC GGG    GTGTG
                                  GT   T   TCAA
GAM593   LOC164295 5'  GTGTTAGAAAACTCTGGGGC   83397      TG     _   CC
                                GCCC  GGGTTT CTG  CGC
                                ||||  |||||| |||  |||
                                CGGG  CTCAAA GAT  GTG
                                  GT     A   T_
GAM593   LOC164397 3'  GTGCAGGAGGCTTTGAGGGTA  83411       _       GCC
                                TGCCCT GGGGTTTCT   CGC
                                ||||||  |||||||||   |||
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                                ATGGGA TTTCGGAGG   GTG
                                   G       AC_
GAM593   LOC165552 3'  GTGGCTTCAGAACTTCAGGGCA 83379          T   C__    AC
                                TGCCCTGGGGTT CTG   CCGC
                                |||||||||||| |||   ||||
                                ACGGGACTTCAA GAC   GGTG
                                      _   TTC
GAM593   LOC165741 3'  GCTGGAACATCTCAGGGCA    88607          TTCTG  C
                                TGCCCTGGGGT    CC GC
                                ||||||||||    || ||
                                ACGGGACTCTA    GG CG
                                      CAA__  T
GAM593   LOC166341 3'  GCACCAGGAGCTGTAGGGCA   83515       G       CCC
                                TGCCCTG GGTTTCTG   GC
                                ||||||| ||||||||   ||
                                ACGGGAT TCGAGGAC   CG
                                   G       CA_
GAM593   LOC166713 5'  GTGTGGTCCTGCAACTCCAGGG 88614          TTC  ____
            CA                    TGCCCTGGGGT   TGC    CCGCAC
                                ||||||||||   |||    ||||||
                                ACGGGACCTCA   ACG    GGTGTG
                                      ___   TCCT
GAM593   LOC169026 3'  GTGTGGTCAGAACTCCAGGTCA 83604    C       T   C
                                TG CCTGGGGTT CTG CCGCAC
                                || |||||||| ||| ||||||
                                AC GGACCTCAA GAC GGTGTG
                                 T        _   T
GAM593   LOC196214 5'  GTGTACAGTGCCCCAGGGCA   91184          TT   CC
                                TGCCCTGGGGT  CTG  CGC
                                ||||||||||  |||  |||
                                ACGGGACCCCG  GAC  GTG
                                      T_   AT
GAM593   LOC196463 3'  TGGGAAGGTCCTGGGGCA    89058       TG   TT   G
                                TGCCC  GGG  TCT CCCG
                                |||||  |||  ||| ||||
                                ACGGG  CCT  GGA GGGT
                                   GT   __   A
GAM593   LOC196510 3'  GTGTGCAAAGGAGATTTTGGGT 89095       T       GCC_
            A                     TGCCC GGGGTTTCT    CGCAC
                                ||||| |||||||||    |||||
                                ATGGG TTTTAGAGG    GTGTG
                                   _        AAAC
GAM593   LOC196738 3'  GTGTGGCGAACTTGGGGCA   88893       TG  GT   T  _
                                TGCCC  GG  TTC GCC CGC
                                |||||  ||  ||| ||| |||
                                ACGGG  TC  AAG CGG GTG
                                   GT  __   _   T
GAM593   LOC196955 5'  GTGATAAGCCAGAGGCTCTGGG 77872     TG       _ CCG_
            G                     CCC  GGGTTTCTG C    CAC
                                |||  ||||||||| |    |||
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                                GGG  CTCGGAGAC G    GTG
                                  GT        C AATA
GAM593   LOC196957 3'  GTGTGCCACTTGTCCCCAGGGC 89195          TTTCTGCC
           A                     TGCCCTGGGG       CGCAC
                                 ||||||||||       |||||
                                 ACGGGACCCC       GTGTG
                                       TGTTCACC
GAM593   LOC196961 3'  GTGTGCCACTTGCCCCCAGGGC 89208          TTTCTGCC
           A                     TGCCCTGGGG       CGCAC
                                 ||||||||||       |||||
                                 ACGGGACCCC       GTGTG
                                       CGTTCACC
GAM593   LOC197085 5'  GTGAACAGGAGAAGCTGCCAGG 89222          _      G  CG__
           GCA                     TGCCCTGG GGTTTCT CC    CAC
                                 |||||||| ||||||| ||    |||
                                 ACGGGACC TCGAAGA GG    GTG
                                      G      _ ACAA
GAM593   LOC197115 5'  GTGTGAACAGGAGAAGCTGCCA 89227          _      G _____
           GGGCA                   TGCCCTGG GGTTTCT CC    CGCAC
                                 |||||||| ||||||| ||    |||||
                                 ACGGGACC TCGAAGA GG    GTGTG
                                      G      _ ACAA
GAM593   LOC197138 3'  GTGTGCCACTTGCCCCCAGGGC 89256          TTTCTGCC
           A                     TGCCCTGGGG       CGCAC
                                 ||||||||||       |||||
                                 ACGGGACCCC       GTGTG
                                       CGTTCACC
GAM593   LOC197342 5'  GCCCTGGAGGCCCTGGGC    89368      T        CCC
                                 GCCC GGGGTTTCTG   GC
                                 |||| ||||||||||   ||
                                 CGGG TCCCGGAGGT   CG
                                   _         CC_
GAM593   LOC197342 3'  GTGGAGGAGGCCTGGGGGCA   89373       G       GC
                                 TGCCCT GGGTTTCT  CCGC
                                 |||||| ||||||||  ||||
                                 ACGGGG TCCGGAGG  GGTG
                                    G       A_
GAM593   LOC200205 3'  GCTCAGGGGCCCCAGGCA    90026      C     TT   CCC
                                 TGCC TGGGGT  CTG   GC
                                 |||| ||||||  |||   ||
                                 ACGG ACCCCG  GAC   CG
                                   _     GG   T__
GAM593   LOC200205 3'  GTGGTCTAGAGGGGTCTGGGGC 90027       TG  G  _   C_   AC
           A                     TGCCC  GG TT TCTG  CCGC
                                 |||||  || || ||||  ||||
                                 ACGGG  CT GG AGAT  GGTG
                                    GT  G  G    CT
GAM593   LOC200220 3'  GTGTGCAAAGGAGATTTTGGGT 90039       T       GCC_
           A                     TGCCC GGGGTTTCT    CGCAC
                                 ||||| |||||||||    |||||
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                                ATGGG TTTTAGAGG   GTGTG
                                  _       AAAC
GAM593  LOC200860 3'  GTGTCCCAGACCCTAAGGCA  91757     C    TT   CCC
                                TGCC TGGGG  TCTG   GCAC
                                |||| |||||  ||||   ||||
                                ACGG ATCCC  AGAC   TGTG
                                  A    __    CC_
GAM593  LOC201562 3'  GTCTATGAAGCTTCGGGGTA  90415          TGCCC
                                TGCCCTGGGGTTTC    GC
                                ||||||||||||||    ||
                                ATGGGGCTTCGAAG    TG
                                        TATC_
GAM593  LOC201917 5'  GCTTGCAGGGATCCGGGGGT  91873      G   TT   CC
                                GCCCT GGGT  CTGC  GC
                                ||||| ||||  ||||  ||
                                TGGGG CCTA  GACG  CG
                                   G    GG    TT
GAM593  LOC201952 5'  GTGTTACAAACCTTAGGCA   91879     C      CTGCC
                                TGCC TGGGGTTT    CGC
                                |||| ||||||||    |||
                                ACGG ATTCCAAA    GTG
                                  _       CATT_
GAM593  LOC203246 3'  GCCAGCAAGCTCTGGGGT    90833     TG    _  CCC
                                GCCC  GGGTTT CTG   GC
                                ||||  |||||| |||   ||
                                TGGG  CTCGAA GAC   CG
                                  GT     C  ___
GAM593  LOC203248 3'  GTGAGGTGCCTTAGGGCA    90844         TTCT  _
                                TGCCCTGGGGT    GCC CGC
                                ||||||||||    ||| |||
                                ACGGGATTCCG    TGG GTG
                                       ____  A
GAM593  LOC203276 3'  GTGTGATGCTGAGATTTGGGGT 92129      TG  G    T  C_
           A                     TGCCC  GG TTTC GC  CGCAC
                                |||||  || |||| ||  |||||
                                ATGGG  TT AGAG CG  GTGTG
                                   GT  _    T  TA
GAM593  LOC203305 3'  GTGTGATGCTGAGATTTGGGGT 92182      TG  G    T  C_
           A                     TGCCC  GG TTTC GC  CGCAC
                                |||||  || |||| ||  |||||
                                ATGGG  TT AGAG CG  GTGTG
                                   GT  _    T  TA
GAM593  LOC203429 3'  GTGTGGTTGCAATCTCAGGC   90934     C     TTC  __
                                GCC TGGGGT   TGC  CCGCAC
                                ||| ||||||   |||  ||||||
                                CGG ACTCTA   ACG  GGTGTG
                                  _     ___   TT
GAM593  LOC203504 5'  GCATAGGGCTCCTAGGGCA   92324         TTTCT   ___
                                TGCCCTGGGG    GCCC   GC
                                ||||||||||    ||||   ||
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                                ACGGGATCCT    CGGG   CG
                                      _____    ATA
GAM593   LOC203636 3'  GTGCTCTGAGCTCTCAGGGC   90981        GT   TGCCC
                                GCCCTGGG  TTC    GCAC
                                ||||||||  |||    ||||
                                CGGGACTC  GAG    CGTG
                                     TC   TCT__
GAM593   LOC205037 5'  GCTTCCAGAAAGCCCAGGGCA  92333         G     CCC
                                TGCCCTGGG TTTCTG   GC
                                |||||||||| ||||||   ||
                                ACGGGACCC AAAGAC   CG
                                      G     CTT
GAM593   LOC206480 5'  GCCGGTGGGGGCTTCAGGGT   92407         TT TG  C
                                GCCCTGGGGT  C  CC GC
                                ||||||||||  |  || ||
                                TGGGACTTCG  G  GG CG
                                       GG GT  C
GAM593   LOC219397 3'  GTGCCCGGAATCTCAGGGC    95120          T   CCC
                                GCCCTGGGGTT CTG   GCAC
                                |||||||||||| |||   ||||
                                CGGGACTCTAA GGC   CGTG
                                      _   C__
GAM593   LOC219653 3'  GTGTCCCTGGAGTTCAGGGGCA 92921       G GG    TGCCC
                                TGCCCT G  TTTC    GCAC
                                |||||| |  ||||    ||||
                                ACGGGG C  GAGG    TGTG
                                    A TT    TCCC_
GAM593   LOC219700 5'  GGCAGTGACCCTAGGGCA     94652           T
                                TGCCCTGGGGTT CTGCC
                                |||||||||||| |||||
                                ACGGGATCCCAG GACGG
                                       T
GAM593   LOC219700 3'  GTGACCAGGAGCTTTGGTGCA  94658     C TG        CC
                                TGC C  GGGTTTCTG  CGC
                                ||| |  |||||||||  |||
                                ACG G  TTCGAGGAC  GTG
                                  T GT        CA
GAM593   LOC219701 3'  GTGACCAGGAGCTTTGGTGCA  94645     C TG        CC
                                TGC C  GGGTTTCTG  CGC
                                ||| |  |||||||||  |||
                                ACG G  TTCGAGGAC  GTG
                                  T GT        CA
GAM593   LOC219920 5'  AGTGGGGAGACCTTGGGCA    94938       T       TG    AC
                                TGCCC GGGGTTTC  CCCGC
                                ||||| ||||||||  |||||
                                ACGGG TTCCAGAG  GGGTG
                                  _       __    AG
GAM593   LOC219920 3'  GTGGGCCCTGGGAATCCCGGTG 94961     C          ___      AC
           T                    GC CTGGGGTTTCT   GCCCGC
                                || ||||||||||   ||||||
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                                TG GGCCCTAAGGG   CGGGTG
                                 T          TCC
GAM593   LOC220446 5'  GTGAGATACCTTGGGGTA    94405      TG    T   GCC
                                TGCCC  GGGT TCT   CGC
                                |||||  |||| |||   |||
                                ATGGG  TCCA AGA   GTG
                                   GT    T  ___
GAM593   LOC220739 5'  GTGCATTACAAGGCCCCAGGAC 94527    C         CTGCCC
           A                     TG CCTGGGGTTT     GCAC
                                || ||||||||||      ||||
                                AC GGACCCCGGA     CGTG
                                 A         ACATTA
GAM593   LOC220840 3'  GTCTTCGGAAACCTTGGTGTA  92483     C TG        CCC
                                TGC C  GGGTTTCTG   GC
                                ||| |  |||||||||   ||
                                ATG G  TCCAAAGGC   TG
                                  T GT        TTC
GAM593   LOC220936 3'  GTGCAAAGATCCTGTGGCA    93044      C       C   CC
                                TGCC TGGGGTTT TGC  GC
                                |||| |||||||| |||  ||
                                ACGG GTCCTAGA ACG  TG
                                   T       A  __
GAM593   LOC220980 5'  GTGGCTTGAAGTTCCAGAGCA  94771     C    GG    TGC
                                TGC CTGG  TTTC   CCGC
                                ||| ||||  ||||   ||||
                                ACG GACC  GAAG   GGTG
                                  A   TT    TTC
GAM593   LOC221088 5'  GTGGAAGGAGACCTCGGGG   94887            GC
                                CCCTGGGGTTTCT  CCGC
                                ||||||||||||  ||||
                                GGGGCTCCAGAGG  GGTG
                                        AA
GAM593   LOC221486 3'  GTGGGCAGGAGGCCCCAGGC   92658     C       _      AC
                                GCC TGGGGTTTC TGCCCGC
                                ||| |||||||| |||||||
                                CGG ACCCCGGAG ACGGGTG
                                  _        G
GAM593   LOC221496 3'  GCGGGCAGCCCCAGGGC     93641          TTT      _
                                GCCCTGGGG   CTGCCCG C
                                |||||||||   ||||||| |
                                CGGGACCCC   GACGGGC G
                                     ___       T
GAM593   LOC221656 3'  GTGCAGTGAACCTCAGGCA   93850      C       _   CC
                                TGCC TGGGGTTT CTGC  GC
                                |||| |||||||| ||||  ||
                                ACGG ACTCCAAG GACG  TG
                                  _        T   __
GAM593   LOC221752 5'  GTGGGCCGGGAGCCGTGGGGC  95424        G       _    AC
                                GCCCTG GGTTTCTG CCCGC
                                |||||| |||||||| |||||
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                                CGGGGT CCGAGGGC GGGTG
                                   G       C
GAM593   LOC221922 5'  TGTGGGCAGAAGGCTGCA    94262     CCTG  G
                                TGC    GG TTTCTGCCCGCA
                                |||    || ||||||||||||
                                ACG    TC GAAGACGGGTGT
                                 _____  G
GAM593   LOC221931 3'  GTGTGCTCAGAGCCTGGGGT   95635      TG  GT    CC
                                GCCC  GG  TTCTG  CGCAC
                                ||||  ||  |||||  |||||
                                TGGG  CC  GAGAC  GTGTG
                                  GT  __    TC
GAM593   LOC221935 3'  GTGCCAGGGCAGAGATTCCAGG 94205      C           __
            CA                    TGCC TGGGGTTTCTGCCC  GCAC
                                |||| ||||||||||||||  ||||
                                ACGG ACCTTAGAGACGGG  CGTG
                                  _           AC
GAM593   LOC221962 3'  GTTCCAGAGCACCCCAGGGCA  94242           _    CCC
                                TGCCCTGGGGT TTCTG   GC
                                ||||||||||| |||||   ||
                                ACGGGACCCCA GAGAC   TG
                                      C     CT_
GAM593   LOC222133 5'  GCTGGCAGGAGCTCTCGGGC   95762      T          C
                                GCCC GGGGTTTCTGCC GC
                                |||| ||||||||||| ||
                                CGGG TCTCGAGGACGG CG
                                  C           T
GAM593   LOC245727 5'  GTGAACCTGCAGGAGCTGCGGG 92763        G        CCG__
            GCA                    TGCCCTG GGTTTCTGC     CAC
                                |||||||| |||||||||     |||
                                ACGGGGC TCGAGGACG     GTG
                                   G        TCCAA
GAM593   LOC245727 3'  GTGTGCCACTTGCCCCCAGGGC 92764          TTTCTGCC
            A                     TGCCCTGGGG       CGCAC
                                ||||||||||       |||||
                                ACGGGACCCC       GTGTG
                                      CGTTCACC
GAM593   LOC245757 3'  GTGACCAAGGAGGAATTTCAGG 92457       GG     G  CG___
            GT                    GCCCTG  GTTTCT CC     CAC
                                ||||||  |||||| ||     |||
                                TGGGAC  TAAGGA GG     GTG
                                   TT     _  AACCA
GAM593   LOC253027 3'  GTGCTGCGGAGGCTGCAGGGC  98771       G        CC
                                GCCCTG GGTTTCTGC  GCAC
                                |||||| |||||||||  ||||
                                CGGGAC TCGGAGGCG  CGTG
                                   G        T_
GAM593   LOC253115 3'  GTGGGCAGGGAATCCTGGAGCA 96125     C TG      _      AC
                                TGC C  GGGTTTC TGCCCGC
                                ||| |  ||||||| |||||||
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                                ACG G  CCTAAGG ACGGGTG
                                  A GT      G
GAM593   LOC253150 3'  GTGAAGGGGGCGCCCAGGGC   97257        _  TT  GCC
                                GCCCTGGG GT  CT   CGC
                                ||||||| ||  ||   |||
                                CGGGACCC CG  GG   GTG
                                     G  GG  AA_
GAM593   LOC253216 3'  GTGCCCCTGAGCTCTAGGC    96632     C       CTGCCC
                                GCC TGGGGTTT     GCAC
                                ||| ||||||||     ||||
                                CGG ATCTCGAG     CGTG
                                  _       TCCC__
GAM593   LOC253258 5'  GTGTGGATTTGGCTCCAGGTCG 98232    C       TCTGC
                                TG CCTGGGGTT    CCGCAC
                                || |||||||||    ||||||
                                GC GGACCTCGG    GGTGTG
                                 T       TTTA_
GAM593   LOC253286 5'  GCCTTGGAGGGTTTGGGGCA   99422      TG  G     CCC
                                TGCCC  GG TTTCTG   GC
                                |||||  || ||||||   ||
                                ACGGG  TT GGAGGT   CG
                                   GT  G     TC_
GAM593   LOC253502 3'  GTGTGAAGGCATCCAGGGC    96224        GTTTC   __
                                GCCCTGGG    TGCC  CGCAC
                                ||||||||    ||||  |||||
                                CGGGACCT    ACGG  GTGTG
                                     _____   AA
GAM593   LOC253891 3'  GGCGGCAGGGCGTCCCAGGGT  96068         TT_     C  AC
                                GCCCTGGGG   TCTGCC GC
                                |||||||||   |||||| ||
                                TGGGACCCT   GGACGG CG
                                     GCG     _  GT
GAM593   LOC254173 3'  GTTCCGGGGGCCTCAGGCGC   98646    _      TT   CCC
                                GC CCTGGGGT  CTG   GC
                                || ||||||||  |||   ||
                                CG GGACTCCG  GGC   TG
                                 C       GG   CT_
GAM593   LOC254185 5'  GTGAAGGAGCCTCAGGTCA    97988    C         GCC
                                TG CCTGGGGTTTCT   CGC
                                || ||||||||||||   |||
                                AC GGACTCCGAGGA   GTG
                                 T          A__
GAM593   LOC254243 3'  GTGTGATGCTGAGATTTGGGGT 99268      TG  G    T  C_
           A                    TGCCC  GG TTTC GC  CGCAC
                                |||||  || |||| ||  |||||
                                ATGGG  TT AGAG CG  GTGTG
                                   GT  _    T  TA
GAM593   LOC254402 5'  GTGTTTGGAGAGGCCCCAGGG  99411           G  C_
                                CCCTGGGGTTTCT CC  GCAC
                                |||||||||||| ||  ||||
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                                GGGACCCCGGAGA GG  TGTG
                                        _ TT
GAM593   LOC254440 5'  GTGTTACAGAATCCTGAGG    98850     G   T    CCC
                                CCT GGG TTCTG   GCAC
                                ||| ||| |||||   ||||
                                GGA TCC AAGAC   TGTG
                                  G   T    AT_
GAM593   LOC254532 5'  GTGTGGGTGGGGGGCGCTCTGGG 98459      T  _  TT TG
           T                     GCCC GGG GT  C  CCCGCAC
                                |||| ||| ||  |  |||||||
                                TGGG CTC CG  G  GGGTGTG
                                  T  G  GG GT
GAM593   LOC254547 5'  TGCGGGAGGCCCCGGGCA    96370      T      CTG     C
                                TGCCC GGGGTTT   CCCGCA
                                ||||| |||||||   ||||||
                                ACGGG CCCCGGA   GGGCGT
                                  _     ____
GAM593   LOC254947 5'  GTGTGGGAAGACAGCTCCAGGC 98364     C      _   G
                                GCC TGGGGTT TCT CCCGCAC
                                ||| ||||||| ||| |||||||
                                CGG ACCTCGA AGA GGGTGTG
                                  _      C   A
GAM593   LOC254964 5'  GTGTGAACAGGAGAAGCTGCCA 96701         _      G  ____
             GGGCA                  TGCCCTGG GGTTTCT CC    CGCAC
                                |||||||| ||||||| ||    |||||
                                ACGGGACC TCGAAGA GG    GTGTG
                                     G       _ ACAA
GAM593   LOC255004 3'  GTGTCCAAGAGACTCCAGGC   97292     C        _ CC   AC
                                GCC TGGGGTTTCT G  CGC
                                ||| ||||||||| |  |||
                                CGG ACCTCAGAGA C  GTG
                                  _        A CT
GAM593   LOC255043 3'  GAGGAGAGGCCTCGGGG     97070            G  CG
                                CCCTGGGGTTTCT CC  C
                                |||||||||||| ||  |
                                GGGGCTCCGGAGA GG  G
                                        _ AT
GAM593   LOC255104 3'  GTGCGCTGCATAACTCCAGGG  97129          TC   C_
                                CCCTGGGGTT  TGC  CGCAC
                                |||||||||  |||  |||||
                                GGGACCTCAA  ACG  GCGTG
                                     T_   TC
GAM593   LOC255158 3'  GCCCCCAGAAGTGCTGGGGTA  97882       TG G      CCC
                                TGCCC  G GTTTCTG   GC
                                |||||  | |||||||   ||
                                ATGGG  C TGAAGAC   CG
                                   GT G      CCC
GAM593   LOC255452 3'  GTGAACAGGGGCCTGGGGGT   99400       G    TT   CC
                                GCCCT GGGT  CTG  CGC
                                ||||| ||||  |||  |||
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                                TGGGG TCCG  GAC  GTG
                                   G   GG   AA
GAM593   LOC255524 3'  GTGTCTTCAGGATCCTGGGGC  98408     TG    T   CCC
                                GCCC  GGGTT CTG   GCAC
                                ||||  ||||| |||   ||||
                                CGGG  CCTAG GAC   TGTG
                                  GT    _   TTC
GAM593   LOC255779 3'  GTGAGGAGGGGCCCTGGGC   97716     T    TT  G  _
                                GCCC GGGGT  CT CC CGC
                                |||| |||||  || || |||
                                CGGG TCCCG  GA GG GTG
                                  _    GG  _  A
GAM593   LOC256044 5'  GTGCGACGGCGGGCCCTGGGGC 98008     TG   TT    __
                                GCCC  GGGT  CTGCC  CGCAC
                                ||||  ||||  |||||  |||||
                                CGGG  CCCG  GGCGG  GCGTG
                                  GT   __    CA
GAM593   LOC256158 5'  GTGAGAGGGGAGCCCCAGGG  99512          GCC_  AC
                                CCCTGGGGTTTCT   CGC
                                ||||||||||||   |||
                                GGGACCCCGAGGG   GTG
                                       GAGA
GAM593   LOC256685 5'  GTGCTAAGTGAATCCCAGG   97921        _  GCCC
                                CCTGGGGTTT CT   GCAC
                                |||||||||| ||   ||||
                                GGACCCTAAG GA   CGTG
                                     T  AT__
GAM593   LOC256867 5'  GCGGGGGGAGTTCTGGGGTA  96514     TG GG   G
                                TGCCC  G  TTTCT CCCGC
                                |||||  |  ||||| |||||
                                ATGGG  C  GAGGG GGGCG
                                   GT TT    _
GAM593   LOC256867 5'  GTCCCCAGAAGTCCTGAGGGC  96516     G  _    CCC  AC
                                GCCCT GGG TTTCTG   GC
                                ||||| ||| ||||||   ||
                                CGGGA TCC GAAGAC   TG
                                   G   T    CCC
GAM593   LOC256903 5'  GTGTGTCTAGGGCCCGGGGT   99431       GT    CC
                                GCCCTGGG  TTCTG  CGCAC
                                ||||||||  |||||  |||||
                                TGGGGCCC  GGGAT  GTGTG
                                     __    CT
GAM593   LOC256950 3'  GTGTCCAGGGCTCAGGGCA   97157        GT    CC
                                TGCCCTGGG  TTCTG  CGC
                                |||||||||  |||||  |||
                                ACGGGACTC  GGGAC  GTG
                                     __    CT
GAM593   LOC257000 3'  GTGCGTTGTGGGAATTCCGGGT 98588     T      TG C_
                                GCCC GGGGTTTC  C  CGCAC
                                |||| ||||||||  |  |||||
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                                  TGGG CCTTAAGG  G  GCGTG
                                    _       GT TT
GAM593   LOC257000 3'  TTCCGGGTGGAGACCCTCAGGG 98590        _      TG    CAC
           CA                       TGCCCTG GGGTTTC  CCCG
                                  ||||||| |||||||  ||||
                                  ACGGGAC CCCAGAG  GGGC
                                     T      GT    CTTA
GAM593   LOC257177 3'  GTGAAACAGGGAAATTTTGGGG 97124      TG       GCCCG_
           T                        GCCC  GGGTTTCT      CAC
                                  ||||  ||||||||      |||
                                  TGGG  TTTAAAGG     GTG
                                    GT       GACAAA
GAM593   LOC257406 5'  GCCCTGGGAGCTGCCAGGGC   99305        _       CCC
                                  GCCCTGG GGTTTCTG   GC
                                  ||||||| ||||||||   ||
                                  CGGGACC TCGAGGGT   CG
                                     G       CC_
GAM593   LOC257431 5'  GTGTGGGAAGACAGCTCCAGGC 83007     C      _  G
                                  GCC TGGGGTT TCT CCCGCAC
                                  ||| ||||||| ||| |||||||
                                  CGG ACCTCGA AGA GGGTGTG
                                    _      C   A
GAM593   LOC257447 5'  GTGTGGGAAGACAGCTCCAGGC 84457     C      _  G
                                  GCC TGGGGTT TCT CCCGCAC
                                  ||| ||||||| ||| |||||||
                                  CGG ACCTCGA AGA GGGTGTG
                                    _      C   A
GAM593   LOC257471 5'  GTGTGAGTGTGGGCCCCAGCGT 97392    C       TC   C
                                  GC CTGGGGTT  TGC CGCAC
                                  || ||||||||  ||| |||||
                                  TG GACCCCGG  GTG GTGTG
                                    C       GT   A
GAM593   LOC257489 3'  GTGTTTTGCAGACTTTGGGG   66229     TG   TT    CC_
                                  CCC  GGG  TCTGC   GCAC
                                  |||  |||  |||||   ||||
                                  GGG  TTC  AGACG   TGTG
                                    GT   __     TTT
GAM593   LOC257554 5'  GTGAGTGAAACTTGGGGT    99535      TG  G    T  C
                                  GCCC  GG TTTC GC CGC
                                  ||||  || |||| || |||
                                  TGGG  TC AAAG TG GTG
                                    GT  _    _  A
GAM593   LOC257554 3'  GTGGTTGGGAAACCCAGGGT   99536         G     GC
                                  GCCCTGGG TTTCT  CCGC
                                  |||||||| |||||  ||||
                                  TGGGACCC AAGGG  GGTG
                                       A     TT
GAM593   LOC257556 3'  GTGGGCAGGGAATCCTGGAGCA 99553     C TG      _      AC
                                  TGC C  GGGTTTC TGCCCGC
                                  ||| |  ||||||| |||||||
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                                ACG G  CCTAAGG ACGGGTG
                                  A GT      G
GAM593  LOC257608 3'  GTGCTCCACGGACTTCGGAGCA 99665     C       TC  CCC
                                TGC CTGGGGTT  TG   GCAC
                                ||| ||||||||  ||   ||||
                                ACG GGCTTCAG  AC   CGTG
                                  A       GC  CT_
GAM593  LOC257617 3'  GTGGGCAGGGAATCCTGGAGCA 99647     C TG      _      AC
                                TGC C  GGGTTTC TGCCCGC
                                ||| |  ||||||| |||||||
                                ACG G  CCTAAGG ACGGGTG
                                  A GT      G
GAM593  LOC51104  5'  GTGAGCGGGGCCCCTGGGGC  32602     TG   TT    C
                                GCCC  GGG  TCTGC CGC
                                ||||  |||  ||||| |||
                                CGGG  CCC  GGGCG GTG
                                   GT   CG    A
GAM593  LOC51267  5'  GCCCGGGGGCCCAGGGCA    33674        G TT   CCC
                                TGCCCTGGG T  CTG   GC
                                |||||||||  |  |||   ||
                                ACGGGACCC G  GGC   CG
                                     _ GG   C__
GAM593  LOC51279  3'  GCACAGTGGAGGCCCCAGGCA  33759     C       TG CC_
                                TGCC TGGGGTTTC  C   GC
                                |||| |||||||||  |   ||
                                ACGG ACCCCGGAG  G   CG
                                  _       GT ACA
GAM593  LOC54466  5'  GCACCAGAGGCACTCAGGGCA  39174        _     CCC
                                TGCCCTGGG GTTTCTG   GC
                                |||||||||  |||||||   ||
                                ACGGGACTC CGGAGAC   CG
                                     A      CA_
GAM593  LOC56920  3'  GTGTGGGTGCGTCTAGGG    39799       _  TTCT
                                CCCTGGG GT    GCCCGCAC
                                |||||||  ||    ||||||||
                                GGGATCT CG    TGGGTGTG
                                   G  _____
GAM593  LOC56926  5'  GTGCCCACAGGACCTCAGGGC  73127         T   CCC
                                GCCCTGGGGTT CTG   GCAC
                                ||||||||||| |||   ||||
                                CGGGACTCCAG GAC   CGTG
                                     _   ACC
GAM593  LOC56930  5'  GTGGCTGGGGGTCCCAGGG   62746        TT   GC
                                CCCTGGGG  TCT  CCGC
                                ||||||||  |||  ||||
                                GGGACCCT  GGG  GGTG
                                     GG   TC
GAM593  LOC57105  3'  GCTACTGGAAGCCCCAGAGCA  40170     C          CCC
                                TGC CTGGGGTTTCTG   GC
                                ||| ||||||||||||   ||
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                                ACG GACCCCGAAGGT   CG
                                  A          CAT
GAM593  LOC57107  3' GCACCAGGCAGGATCCTAGGGC 40189          T    C___  AC
                                GCCCTGGGGTT CTGCC   GC
                                |||||||||| |||||   ||
                                CGGGATCCTAG GACGG   CG
                                      _    ACCA
GAM593  LOC83985  5' GTGCTCTGTGCTTCAGGGCA  50176          TTCTGCCC
                                TGCCCTGGGGT       GCAC
                                ||||||||||        ||||
                                ACGGGACTTCG       CGTG
                                      TGTCT___
GAM593  LOC85028  5' GTCTACAGAGATCCCGGCGTA  54898     C          CCC
                                TGC CTGGGGTTTCTG   GC
                                ||| ||||||||||||   ||
                                ATG GGCCCTAGAGAC   TG
                                  C          ATC
GAM593  LOC85028  5' GTGATCGAGGACTTCCGGGGTA 54899         _  TC  CC   AC
                                TGCCCTGGG GTT  TG  CGC
                                ||||||||| |||  ||  |||
                                ATGGGGCCT CAG  GC  GTG
                                     T   GA  TA
GAM593  LOC85569  3' GTTGGGAGATTCTGGGGTA   53573      TG      TG  C
                                TGCCC  GGGTTTC  CC GC
                                |||||  |||||||  || ||
                                ATGGG  CTTAGAG  GG TG
                                   GT       __  T
GAM593  LOC89919  3' AGCCATGGGAGCTACTGGGGT  61369     TG _      CCC  AC
                                GCCC  G GGTTTCTG   GC
                                ||||  | ||||||||   ||
                                TGGG  C TCGAGGGT   CG
                                  GT A       AC_  AT
GAM593  LOC89932  5' GTGCAGGCAGCCCTGGGGCA  61471      TG   TTT    C
                                TGCCC  GGG   CTGCC GCAC
                                |||||  |||   ||||| ||||
                                ACGGG  CCC   GACGG CGTG
                                   GT   ___     A
GAM593  LOC90010  5' GCTGCAGGAACCCTGGGC    61721     T         CC
                                GCCC GGGGTTTCTGC  GC
                                |||| ||||||||||  ||
                                CGGG TCCCAAGGACG  CG
                                  _         T_
GAM593  LOC90019  3' TGCCCGGGCCTCGGGGCA    57538          TT   CCC
                                TGCCCTGGGGT  CTG   GCA
                                ||||||||||  |||   |||
                                ACGGGGCTCCG  GGC   CGT
                                      __  C__
GAM593  LOC90038  3' GTGTGATGCTGAGATTTGGGGT 61812      TG  G    T  C_
          A                      TGCCC  GG TTTC GC  CGCAC
                                |||||  || |||| ||  |||||
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                                ATGGG  TT AGAG CG  GTGTG
                                  GT  _    T  TA
GAM593  LOC90170  5' GTCTTTGGAGATCCCCGGGCA  62381      T        CCC
                                TGCCC GGGGTTTCTG   GC
                                ||||| ||||||||||   ||
                                ACGGG CCCTAGAGGT   TG
                                   C         TTC
GAM593  LOC90829  5' GTTAAGGAGATTTTGGGC    64794     T       GCCC
                                GCCC GGGGTTTCT    GC
                                |||| |||||||||    ||
                                CGGG TTTTAGAGG    TG
                                  _        AAT_
GAM593  LOC90979  5' GTGTGGGAAAACCTTTGGGCA  65139      TG     CTG
                                TGCCC  GGGTTT   CCCGCAC
                                |||||  ||||||   |||||||
                                ACGGG  TCCAAA   GGGTGTG
                                   TT     A__
GAM593  LOC91050  3' GTGAGTCCCAGAGAATCTAGGG 65378       GG     CCCG_
          T                     GCCCTGG  TTTCTG     CAC
                                |||||||  ||||||     |||
                                TGGGATC  AGAGAC     GTG
                                    TA     CCTGA
GAM593  LOC91064  5' GTGTGGCACCTGCCCTGGGACA 65390    C  TG    TTC   _   AC
                                TG CC  GGGT   TGCC CGC
                                || ||  ||||   |||| |||
                                AC GG  CCCG   ACGG GTG
                                 A  GT    TCC    T
GAM593  LOC91149  3' GTGCAAAGGCCCCGAGGT    65693     C       C   CC
                                GCC TGGGGTTT TGC  GC
                                ||| |||||||| |||  ||
                                TGG GCCCCGGA ACG  TG
                                  A       A   __
GAM593  LOC91582  3' GTGGGCCGGAAGTCCTGGGG   67144     TG  GT    _    AC
                                CCC  GG  TTCTG CCCGC
                                |||  ||  ||||| |||||
                                GGG  CC  AAGGC GGGTG
                                  GT  TG    C
GAM593  LOC91585  5' AAAGGGGTGGGAGCCCCGAGGT 67156     C       TG   GCAC
                                GCC TGGGGTTTC  CCC
                                ||| |||||||||  |||
                                TGG GCCCCGAGG  GGG
                                  A        GT   GAAAT
GAM593  LOC91966  5' GCTACGGGAGGCCCGGGGC    68331        G     CCC
                                GCCCTGGG TTTCTG   GC
                                |||||||| ||||||   ||
                                CGGGGCCC GAGGGC   CG
                                    G     AT_
GAM593  LOC92078  5' GCTTGGAAACACTAGGGT    68605        G      CCC
                                GCCCTGG GTTTCTG   GC
                                ||||||| |||||||   ||
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                                TGGGATC CAAAGGT   CG
                                   A     T__
GAM593  LOC92080  5' GTGCCTTAGAGACTCCGGG   68634          CCC
                                CCTGGGGTTTCTG   GCAC
                                ||||||||||||   ||||
                                GGGCCTCAGAGAT   CGTG
                                      TC_
GAM593  LOC92181  3' TAGAGGTGGAGATATTAGGGTA 68948       G    TG  CGCAC
                                TGCCCTGG GTTTC  CC
                                |||||||| |||||  ||
                                ATGGGATT TAGAG  GG
                                   A    GT  AGATT
GAM593  LOC92305  3' GTGTGGGAGCAGTCCTGGGGC  57237     TG  GT T  G
                                GCCC  GG  T CT CCCGCAC
                                ||||  ||  | || |||||||
                                CGGG  CC  A GA GGGTGTG
                                  GT  TG C  _
GAM593  LOC92482  3' GCTACTCGGGAGTCTCAGGCA  70022     C   GT    CCC_
                                TGCC TGGG  TTCTG   GC
                                |||| ||||  |||||   ||
                                ACGG ACTC  AGGGC   CG
                                  _   TG    TCAT
GAM593  LOC93109  3' GTGCTGGGGGGCCTTGGGTCA  71923   C  TG   TT TG  C
                                TG CC  GGGT  C  CC GCAC
                                || ||  ||||  |  || ||||
                                AC GG  TCCG  G  GG CGTG
                                 T  GT   GG __  T
GAM593  LOC93166  5' GCGGGAGGTTTCCGGGC    72081     TG   TT   G   _
                                GCCC  GGG  TCT CCCG C
                                ||||  |||  ||| |||| |
                                CGGG  CCT  GGA GGGC G
                                  __   TT   _   T
GAM593  LOC93589  3' GCATGCAGGGCTTTTGGGGC  73052     TG   T    CC
                                GCCC  GGG TTCTGC  GC
                                ||||  ||| ||||||  ||
                                CGGG  TTT GGGACG  CG
                                  GT   C     TA
GAM593  LOC93622  3' GTGTTTGCTGACTTTGGGGTA  57731     TG    TCT  CC
                                TGCCC  GGGTT   GC  GCAC
                                |||||  |||||   ||  ||||
                                ATGGG  TTCAG   CG  TGTG
                                   GT    T__  TT
GAM593  LOC93626  3' TGTTGCAGGCCCAGGGCA    73132        GTT    CC
                                TGCCCTGGG   TCTGC  GCA
                                |||||||||   |||||  |||
                                ACGGGACCC   GGACG  TGT
                                      ___    T_
GAM594  EHF     3' TCCAAAACCCAAGGTTGGCT   25127     AT   _   C
                                AGT  GCCT GGGT TTGGA
                                |||  |||| |||| |||||
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                                TCG  TGGA CCCA AACCT
                                  GT   A   A
GAM594  EPHA2    3'  CCATCGGCCAAGAATACTTGAA 16675         GC  G   T_
            G                    CTTCAAGTAT  CT GGTC  TGG
                                 ||||||||||  || ||||  |||
                                 GAAGTTCATA  GA CCGG  ACC
                                       A_  A   CT
GAM594  ITGA5    3'  CCCAGAGACATACTTGAAG   61933          C__
                                 CTTCAAGTATG  CTGGG
                                 ||||||||||   |||||
                                 GAAGTTCATAC  GACCC
                                       AGA
GAM594  TREM2    3'  TCCAAGACTGTCATATTT    39098       CCTG
                                 AAGTATG   GGTCTTGGA
                                 |||||||   |||||||||
                                 TTTATAC   TCAGAACCT
                                     TG__
GAM594  UQCRB    3'  CCAACATAGGCATACTTAAG  21939    C        GGTC
                                 CTT AAGTATGCCTG   TTGG
                                 ||| ||||||||||   ||||
                                 GAA TTCATACGGAT   AACC
                                   _         AC__
GAM594  ATP10D   3'  CAGAGACCACTTGAAG      73526        ATGCCTG   _
                                 CTTCAAGT      GGTCT TG
                                 ||||||||      ||||| ||
                                 GAAGTTCA      CCAGA AC
                                     ________    G
GAM594  B3GNT7   3'  CCCTTCCAGGCAACCTGAA   71678     A  A      TCTT
                                 TTCA GT TGCCTGGG   GG
                                 |||| || ||||||||   ||
                                 AAGT CA ACGGACCT   CC
                                   C  _       TC__
GAM594  DKFZp547I224 3'  TCCAAAATTGACCACATACTTG 39963          CCTG  _____
            GA                    TTCAAGTATG   GGTC   TTGGA
                                  ||||||||||   ||||   |||||
                                  AGGTTCATAC   CCAG   AACCT
                                       A___    TTAA
GAM594  FLJ22341 3'  CCAAGCTCAGGCACACCCAAG  45114    CAA  A      T
                                 CTT   GT TGCCTGGG CTTGG
                                 |||   || |||||||| |||||
                                 GAA   CA ACGGACTC GAACC
                                   CC_  C       _
GAM594  KIAA0779 3'  CCGAACAGCATACTTGAAG   86908          C  GGTC
                                 CTTCAAGTATGC TG   TTGG
                                 |||||||||||| ||   ||||
                                 GAAGTTCATACG AC   AGCC
                                       _  A___
GAM594  LOC144233 3'  CCAAGGCACATAATTGAA    77246      G   CCTGG
                                 TTCAA TATG    GTCTTGG
                                 ||||| ||||    |||||||
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                                AAGTT ATAC    CGGAACC
                                  A   A____
GAM594  LOC147341 3'  ACCCAGGCATAACTGAAG    85116      AG
                                CTTCA  TATGCCTGGGT
                                |||||  ||||||||||
                                GAAGT  ATACGGACCCA
                                  CA
GAM594  LOC221088 5'  TCCAAGGTGCTGGCCACTCGAA 94888     A   AT   TGGG
          G                      CTTC AGT  GCC   TCTTGGA
                                |||| |||  |||   |||||||
                                GAAG TCA  CGG   GGAACCT
                                  C   C_   TCGT
GAM595  AKT1    3'  GGTGACTGTCCCACCGGAG   18964     AA  GAT
                                TTCC  GG   GGACAGTCACC
                                ||||  ||   ||||||||||
                                GAGG  CC   CCTGTCAGTGG
                                  __  AC_
GAM595  AXIN1   3'  GGTGACCCCCCCCCATCCCCCG 61542    AA      ACA___
          G                      CC  GGGATGG     GTCACC
                                ||  |||||||     ||||||
                                GG  CCCTACC     CAGTGG
                                 CC      CCCCCC
GAM595  CBFA2T2  3'  GTGGATCATCTCTTGGAA    18716          ACAG
                                TTCCAAGGGATGG   TCAC
                                ||||||||||||   ||||
                                AAGGTTCTCTACT   GGTG
                                       A___
GAM595  FHL1    3'  GTGACTAGTTGAATCCCTTG   9361        G_  _
                                CAAGGGAT  GAC AGTCAC
                                ||||||||  ||| ||||||
                                GTTCCCTA  TTG TCAGTG
                                    AG   A
GAM595  GGA3    3'  GCTATCCTCCCCTTGGAA    26588        AT   C
                                TTCCAAGGG  GGA AGT
                                |||||||||  ||| |||
                                AAGGTTCCC  CCT TCG
                                     CT   A
GAM595  GMFG    3'  GGTGACTGGGGACTTGGAA   60592       GGATGGA
                                TTCCAAG      CAGTCACC
                                |||||||      ||||||||
                                AAGGTTC      GTCAGTGG
                                   AGGG___
GAM595  GTF2I   3'  GTGACTGTGGGTCTGGAA    53386      AGG   GG
                                TTCCA   GAT  ACAGTCAC
                                |||||   |||  ||||||||
                                AAGGT   CTG  TGTCAGTG
                                  ___   GG
GAM595  HD      3'  GGTAACTGCCAGCCTTGGAG   10918       GA   A    C
                                TTCCAAGG  TGG CAGT ACC
                                ||||||||  ||| |||| |||
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                                GAGGTTCC  ACC GTCA TGG
                                    G_  _   A
GAM595  KCNA3   3' GTAACTGTTTAACCTCAGAA  11135    CA  GA     C
                                TTC  AGG  TGGACAGT AC
                                ||| |||  |||||||| ||
                                AAG  TCC  ATTTGTCA TG
                                  AC  A_      A
GAM595  MME     3' ACTGTCTAACTTTAGAA    8028     C   GA
                                TTC AAGG  TGGACAGT
                                ||| ||||  ||||||||
                                AAG TTTC  ATCTGTCA
                                  A   A_
GAM595  PDGFRB  5' GGTGACTGTCCAGAGCCTGGAA 66583      A  GA_
                                TTCCA GG   TGGACAGTCACC
                                ||||| ||   ||||||||||||
                                AAGGT CC   ACCTGTCAGTGG
                                   _ GAG
GAM595  RGS14   3' GGTGAGTCCAGCCCCTTGGAA  22400        A_   AG
                                TTCCAAGGG  TGGAC  TCACC
                                |||||||||  |||||  |||||
                                AAGGTTCCC  ACCTG  AGTGG
                                     CG   __
GAM595  TGFA    3' GATAGCTCATCCCTAGGAA   13710     A      ACA
                                TTCC AGGGATGG   GTC
                                |||| ||||||||   |||
                                AAGG TCCCTACT   TAG
                                  A       CGA
GAM595  UCP2    3' GCGTCCCGTCCCTTGGAA    13978           _ A
                                TTCCAAGGGATGG AC GT
                                |||||||||||||| || ||
                                AAGGTTCCCTGCC TG CG
                                       C _
GAM595  USP14   3' GTGCTGCTGTCCATCCCATGGA 18938      A        __
          A                      TTCCA GGGATGGACAGT  CAC
                                |||||  ||||||||||||  |||
                                AAGGT CCCTACCTGTCG  GTG
                                   A          TC
GAM595  AFAP    3' GGTGGATGTCCATCCTTGAA  41612    CA        GT
                                TTC  AGGGATGGACA  CACC
                                |||  ||||||||||  ||||
                                AAG  TTCCTACCTGT  GTGG
                                  __         AG
GAM595  BRD2    5' GGTGACTGACACCTTGGAA   18798        GA  GA
                                TTCCAAGG  TG  CAGTCACC
                                ||||||||  ||  ||||||||
                                AAGGTTCC  AC  GTCAGTGG
                                     __ A_
GAM595  DAPK3   5' GGTGACTGCACTTTCCCTGGAG 9049       A   T  A_
                                TTCCA GGGA GG  CAGTCACC
                                ||||| |||| ||  ||||||||
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                                GAGGT CCCT TC  GTCAGTGG
                                  _   T  AC
GAM595  DKFZP434L1435 3'  GTGACTGTGGTGTCCTTGAGA  99686   _    ATGG
                                TC CAAGGG   ACAGTCAC
                                || ||||||   ||||||||
                                AG GTTCCT   TGTCAGTG
                                 A     GTGG
GAM595  DKFZP566E144 3'  GGTCATGTCCATCCCTTGG   31957          GTC
                                CCAAGGGATGGACA  ACC
                                ||||||||||||||  |||
                                GGTTCCCTACCTGT  TGG
                                        AC_
GAM595  DSCR6    3'  GGTGACTGTTTGGGGCCTGG  39070    A  GA_ GG
                                CCA GG   T  ACAGTCACC
                                ||| ||   |  |||||||||
                                GGT CC   G  TGTCAGTGG
                                  _  GGG TT
GAM595  EDG1     3'  GCTGTCCACCCACCGGAA    60052     AA_  A
                                TTCC   GGG TGGACAGT
                                ||||   ||| ||||||||
                                AAGG   CCC ACCTGTCG
                                  CCA  _
GAM595  FLJ10008  3'  GGCAACCTGTCCCTTGAGA   36191   _       ACA
                                TC CAAGGGATGG   GTC
                                || ||||||||||   |||
                                AG GTTCCCTGTC   CGG
                                 A         CAA
GAM595  FLJ10044  3'  GACCCACCTCCATCCTTCGGAA 36241     A       CA___
                                TTCC AGGGATGGA    GTC
                                |||| |||||||||    |||
                                AAGG TTCCTACCT    CAG
                                  C       CCACC
GAM595  FLJ10811  3'  GTGAGACCTCATCTCTTAGAA  37226    C       ACAG
                                TTC AAGGGATGG   TCAC
                                ||| |||||||||   ||||
                                AAG TTCTCTACT   AGTG
                                  A       CCAG
GAM595  FLJ12891  3'  GGTGACCGCAGCCCCTTGGA   46929        A_  GACA
                                TCCAAGGG  TG   GTCACC
                                ||||||||  ||   ||||||
                                AGGTTCCC  AC   CAGTGG
                                    CG  GC__
GAM595  FLJ23093  3'  GGTAACTGCCAAAGGTGGAA   45327     AGGGA  A   C
                                TTCCA    TGG CAGT ACC
                                |||||    ||| |||| |||
                                AAGGT    ACC GTCA TGG
                                  GGAA_  _   A
GAM595  KIAA0731  3'  GACCTTTCCATCCTTGAA    67479    CA       CA_
                                TTC  AGGGATGGA   GTC
                                |||  |||||||||  |||
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                                AAG  TTCCTACCT   CAG
                                  __        TTC
GAM595  KIAA1040  3'  ACTGTGCCACCCTTGGAA    72676         A  _
                                TTCCAAGGG TGG ACAGT
                                ||||||||| ||| |||||
                                AAGGTTCCC ACC TGTCA
                                     _  G
GAM595  KIAA1076  3'  GTGACTGTTGTGACCCGGAG   66127     AA   ATG_
                                TTCC  GGG   GACAGTCAC
                                ||||  |||   |||||||||
                                GAGG  CCC   TTGTCAGTG
                                  __  AGTG
GAM595  KIAA1266  3'  GGTGACTGCAGATTCTGGAA   66701      AG GA  GA
                                TTCCA  G  TG  CAGTCACC
                                |||||  |  ||  ||||||||
                                AAGGT  T  AC  GTCAGTGG
                                   CT AG  __
GAM595  KIAA1764  3'  GTAACTGCTATGACTTTGAA   69828    C   GG    A    C
                                TTC AAG  ATGG CAGT AC
                                ||| |||  |||| |||| ||
                                AAG TTC  TATC GTCA TG
                                  T  AG   _   A
GAM595  MGC17330  3'  GTGCTCCTTGTCCATCCCTTGG 54631              T___
            AG                    TTCCAAGGGATGGACAG    CAC
                                |||||||||||||||||    |||
                                GAGGTTCCCTACCTGTT    GTG
                                      CCTC
GAM595  MGC4171   5'  GGTGACTGGCGCCCCCTGGAG  44455      A   A  GA
                                TTCCA GGG TG  CAGTCACC
                                ||||| ||| ||  ||||||||
                                GAGGT CCC GC  GTCAGTGG
                                   C   C  G_
GAM595  SIAT8C    5'  ATTGTCCATCCACTGGAA    32442      AG
                                TTCCA  GGATGGACAGT
                                |||||  ||||||||||
                                AAGGT  CCTACCTGTTA
                                   CA
GAM595  LOC112724 5'  GGCCACCATCCCTGGGAA    57305     A       ACA
                                TTCC AGGGATGG   GTC
                                |||| ||||||||   |||
                                AAGG TCCCTACC   CGG
                                   G       AC_
GAM595  LOC134121 3'  TGAATGGATCCCTTGGAA    75639          GGA  G
                                TTCCAAGGGAT   CA TCA
                                ||||||||||   || |||
                                AAGGTTCCCTA   GT AGT
                                      G__  A
GAM595  LOC143943 3'  GGCTACCCCCACCCCTTGGA   83919         A   AC__
                                TCCAAGGG TGG    AGTC
                                |||||||| |||    ||||
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                                AGGTTCCC ACC    TCGG
                                     C   CCCA
GAM595  LOC148223 3'  GGTGCTGTGCACCCCCTGGAG  79487      A   A  G    T
                                TTCCA GGG TG ACAG CACC
                                ||||| ||| || |||| ||||
                                GAGGT CCC AC TGTC GTGG
                                   C   C  G   _
GAM595  LOC157931 3'  GGTCTAAGCCACCCCTTGGGA  87944         A   ACAGTC
                                TTCCAAGGG TGG     ACC
                                ||||||||| |||     |||
                                AGGGTTCCC ACC     TGG
                                     C   GAATC_
GAM595  LOC253336 3'  GTAACTTTCTTCATCCCTTG   99179          C__   C
                                CAAGGGATGGA   AGT AC
                                ||||||||||   ||| ||
                                GTTCCCTACTT   TCA TG
                                      CTT   A
GAM595  LOC51301  3'  GGAACTGTCCAACTGGAA    33907      AGG A       CA
                                TTCCA   G TGGACAGT  CC
                                |||||   | ||||||||  ||
                                AAGGT   C ACCTGTCA  GG
                                   ___ A       AC
GAM595  LOC81569  3'  GACAAGATGTCATCCTTGGAA  62674         ATG   _____
                                TTCCAAGGG   GACA   GTC
                                |||||||||   ||||   |||
                                AAGGTTCCT   CTGT   CAG
                                     A__   AGAA
GAM596  KIAA1500  3'  GACATCCATCCCTGACCAA   64810      T       CACAC
                                TTGGT CAGGGATGG    GTC
                                ||||| |||||||||    |||
                                AACCA GTCCCTACC    CAG
                                   _       TA___
GAM596  PRRDH     3'  GATCCCCATCCCTGAAC     32324           CACAC
                                GTTCAGGGATGG    GTC
                                ||||||||||||    |||
                                CAAGTCCCTACC    TAG
                                      CC___
GAM596  LOC149951 3'  GACATGCAGCAGCTGAACCAG  85950         GGATG   CAC
                                TTGGTTCAG    GCA   GTC
                                |||||||||    |||   |||
                                GACCAAGTC    CGT   CAG
                                     GACGA   A__
GAM597  ASH1      3'  CCATCTATTCTCTGT      38086      A  ATAC
                                ACAGA GA    ATAGATGG
                                ||||| ||    ||||||||
                                TGTCT CT    TATCTACC
                                   _ _____
GAM597  ATP4A     3'  GCCCCACCAGTATCTGCTTCTG 7373         A__    ATAGA   A
           TA                    TACAGAAG   ATAC     TGG GC
                                ||||||||   ||||     ||| ||
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                                ATGTCTTC  TATG    ACC CG
                                    GTC   ACC__  C
GAM597  BCAS1   3'  GCTCCATGTATATATTCTTCTG 14713        C  G
                                CAGAAGAATA ATA ATGGAGC
                                |||||||||| ||| |||||||
                                GTCTTCTTAT TAT TACCTCG
                                     A  G
GAM597  CHAC    3'  CTCCATCTTTTTCTCTGTA   53953      A  TACAT
                                TACAGA GAA    AGATGGAG
                                |||||| |||    ||||||||
                                ATGTCT CTT    TCTACCTC
                                   _  TT___
GAM597  CHC1L   5'  GCAAATCATATATTCTTCTGTG 8856          C A  GGA
                                TACAGAAGAATA AT GAT  GC
                                |||||||||||| || |||  ||
                                GTGTCTTCTTAT TA CTA  CG
                                     A _  AA_
GAM597  DFFB    3'  GCTCCATCCTCTTGACTCTTCT 88773      ATA  TA__
                                AGAAGA  CA   GATGGAGC
                                ||||||  ||   ||||||||
                                TCTTCT  GT   CTACCTCG
                                   CA_  TCTC
GAM597  DLG4    5'  CCTAAGTGTATTCTTCTG    9080          AGAT
                                CAGAAGAATACAT   GG
                                ||||||||||||   ||
                                GTCTTCTTATGTG   CC
                                     AAT_
GAM597  EIF2C1  3'  CTCCATCCTTCCTCTGTG    25188      A  TACATA
                                TACAGA GAA    GATGGAG
                                |||||| |||    |||||||
                                GTGTCT CTT    CTACCTC
                                   C  C_____
GAM597  GABRE   3'  CTCCATCTTTCGTCTG      18282     A  TACAT
                                CAGA GAA    AGATGGAG
                                |||| |||    ||||||||
                                GTCT CTT    TCTACCTC
                                  G  _____
GAM597  GABRE   3'  CTCCATCTTTCGTCTG      42057     A  TACAT
                                CAGA GAA    AGATGGAG
                                |||| |||    ||||||||
                                GTCT CTT    TCTACCTC
                                  G  _____
GAM597  GABRE   3'  CTCCATCTTTCGTCTG      42061     A  TACAT
                                CAGA GAA    AGATGGAG
                                |||| |||    ||||||||
                                GTCT CTT    TCTACCTC
                                  G  _____
GAM597  GABRE   3'  CTCCATCTTTCGTCTG      42072     A  TACAT
                                CAGA GAA    AGATGGAG
                                |||| |||    ||||||||
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                                GTCT CTT    TCTACCTC
                                  G  _____
GAM597  MADH4    3'  CAGTAGTTGTATTCTTCTGTA  19306           TAGA_
                                TACAGAAGAATACA    TG
                                ||||||||||||||    ||
                                ATGTCTTCTTATGT    AC
                                       TGATG
GAM597  NAT1     3'  CTATCATGTATCTTCTGTA   7260         A    A
                                TACAGAAGA TACAT GATGG
                                ||||||||| ||||| |||||
                                ATGTCTTCT ATGTA CTATC
                                          _    _
GAM597  P53AIP1  3'  GCCTCATTTTGCATCCTTCTGT 42338        A  A  T    GA
           A                     TACAGAAG AT CA AGATG  GC
                                ||||||||| || || |||||  ||
                                ATGTCTTC TA GT TTTAC  CG
                                     C  C  _    TC
GAM597  PRELP    3'  CCATCTATTCTTCTG      12256        ATAC
                                CAGAAGA   ATAGATGG
                                |||||||   ||||||||
                                GTCTTCT   TATCTACC
                                          ____
GAM597  PTER     3'  CTATCTATATATTCTTCT    48408         C
                                AGAAGAATA ATAGATGG
                                ||||||||| ||||||||
                                TCTTCTTAT TATCTATC
                                      A
GAM597  SLC30A3  3'  CTCCATCCATGTGTCTGT    14398      AGAA    A
                                ACAGA   TACAT GATGGAG
                                |||||   ||||| |||||||
                                TGTCT   GTGTA CTACCTC
                                   ____    C
GAM597  TAL1     3'  GCCCCATCTGTGCATTCTCCTG 13529     A    A       A
                                CAG AGAAT CATAGATGG GC
                                ||| ||||| ||||||||| ||
                                GTC TCTTA GTGTCTACC CG
                                  C    C       C
GAM597  USP1     3'  GCTCGTATTTGTATTCT     14019        TA   _
                                AGAATACA  GATG GAGC
                                ||||||||  |||| ||||
                                TCTTATGT  TTAT CTCG
                                     __   G
GAM597  AB026190 3'  TCTTGTATATATTCCTCTGTA  27831       A    C   GAT
                                TACAGA GAATA ATA   GGA
                                |||||| ||||| |||   |||
                                ATGTCT CTTAT TAT   TCT
                                   C    A  GT_
GAM597  AKAP11   3'  CTTCATTTATTCTTCT      33191         CATA
                                AGAAGAATA   GATGGAG
                                |||||||||   |||||||
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                              TCTTCTTAT   TTACTTC
                                          ____
GAM597  AP3M1    3'  GCTCCATGCTCCATTCTCACTG 24937      A_    ACAT  _
             TA                   TACAG  AGAAT   AG ATGGAGC
                                  |||||  |||||   || |||||||
                                  ATGTC  TCTTA   TC TACCTCG
                                     AC    CC__  G
GAM597  ATIP1    3'  GTCTATACATTCTCTGTA    40775       A   AC
                                  TACAGA GAAT  ATAGAT
                                  ||||||| ||||  ||||||
                                  ATGTCT CTTA  TATCTG
                                     _   CA
GAM597  BCAA     3'  CTGTATATGTATTCCCTTGTA  33494      AA       G
                                  TACAG  GAATACATA ATGG
                                  |||||  ||||||||| ||||
                                  ATGTT  CTTATGTAT TGTC
                                     CC       A
GAM597  BOP      5'  GCTCCATCTATTATTGCTTCT  86230      _   C
                                  AGAAG AATA ATAGATGGAGC
                                  ||||| |||| ||||||||||
                                  TCTTC TTAT TATCTACCTCG
                                     G   _
GAM597  FLJ20188 3'  CTCAATTATATTTTCTGTA   35205        ATAC   ATG
                                  TACAGAAGA   ATAG   GAG
                                  |||||||||   ||||  |||
                                  ATGTCTTTT   TATT   CTC
                                        A___   AA_
GAM597  HSPCAL3  3'  GCTCGAGTCACATTCTTCTTA  77066   C      ACATA   G_
                                  A AGAAGAAT    GAT  GAGC
                                  | ||||||||    |||  ||||
                                  A TCTTCTTA    CTG  CTCG
                                   T      CA___   AG
GAM597  IDN3     3'  CCGTTTATACATCCTTTTGTA  31799        A  AC
                                  TACAGAAG AT  ATAGATGG
                                  |||||||| ||  ||||||||
                                  ATGTTTTC TA  TATTTGCC
                                       C  CA
GAM597  KIAA0256 3'  TTGTCATGTATTTTCTGTA   65053        A    A  TG
                                  TACAGAAGA TACAT GA  G
                                  ||||||||| ||||| ||  |
                                  ATGTCTTTT ATGTA CT  T
                                        _    _ GT
GAM597  KIAA0894 3'  CAATTACGTATTCTTCTG    30326         A   A
                                  CAGAAGAATAC TAG TG
                                  |||||||||||| ||| ||
                                  GTCTTCTTATG ATT AC
                                         C   A
GAM597  KIAA1157 3'  GCCCCATCCCACTTTTCTGTA  72701         ATACATA    A
                                  TACAGAAGA      GATGG GC
                                  |||||||||      ||||| ||
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                                ATGTCTTTT      CTACC CG
                                     CACC___     C
GAM597  KIAA1719 3'  CCCTCCTGCTTCTTCTGTA   68730         TACA   AT  A
                                TACAGAAGAA    TAG  GG G
                                ||||||||||    |||  || |
                                ATGTCTTCTT    GTC  CC C
                                     C___   CT  _
GAM597  KIAA1817 3'  CCAATGTTTCTTCTGTA     68774         T    AGA
                                TACAGAAGAA ACAT   TGG
                                |||||||||| ||||   |||
                                ATGTCTTCTT TGTA   ACC
                                     _   ___
GAM597  MGC14156 3'  CCAGTGTATGTATTCTTC    52956          G _
                                GAAGAATACATA A TGG
                                |||||||||||| | |||
                                CTTCTTATGTAT T ACC
                                      G G
GAM597  MGC26651 3'  CATTTGCATTCTTCTG      58949         ACA
                                CAGAAGAAT   TAGATG
                                |||||||||   ||||||
                                GTCTTCTTA   GTTTAC
                                     C__
GAM597  MGC2941  3'  CCATTTATTTTCTTCT      44413        TAC
                                AGAAGAA   ATAGATGG
                                |||||||   ||||||||
                                TCTTCTT   TATTTACC
                                    T__
GAM597  PCBP3    5'  GCCCCATCTGTCCTTCCTC   40444    A   TAC      A
                                GA GAA   ATAGATGG GC
                                || |||   |||||||| ||
                                CT CTT   TGTCTACC CG
                                 C  CC_       C
GAM597  PFTK1    5'  GCTCCCATTCTGTATTCTTCTG 25689           TAGAT
                                CAGAAGAATACA    GGAGC
                                ||||||||||||    |||||
                                GTCTTCTTATGT    CCTCG
                                      CTTAC
GAM597  PRO1575  5'  GCCCCATCTATTTTCATTCTGT 26872        _  TAC      A
            A                    TACAGAA GAA   ATAGATGG GC
                                |||||||| |||   |||||||| ||
                                ATGTCTT CTT   TATCTACC CG
                                    A  T__       C
GAM597  SQV7L    5'  GCTCCATCCATGTCCCTG    71097     AAGAAT    A
                                CAG     ACAT GATGGAGC
                                |||     |||| ||||||||
                                GTC     TGTA CTACCTCG
                                  CC_____    C
GAM597  TRIM4    3'  GCTCCATCCATGTTGCTG    53407     AAGAAT    A
                                CAG     ACAT GATGGAGC
                                |||     |||| ||||||||
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                                GTC      TGTA CTACCTCG
                                  GT____    C
GAM597  LOC150319 3'  GCCCCAGTCTCCTCTTCTGTA  80474          ATACAT  _  A
                                TACAGAAGA     AGA TGG GC
                                |||||||||     ||| ||| ||
                                ATGTCTTCT     TCT ACC CG
                                     CC____   G   C
GAM597  LOC154866 3'  TCAGCATGTTTCTTCTGTA    82060          T   AGA
                                TACAGAAGAA ACAT   TGG
                                |||||||||| ||||   |||
                                ATGTCTTCTT TGTA   ACT
                                      _   CG_
GAM597  LOC200081 3'  GCTCCATCCATGTCTAGACCTT 89976      AAT___   A
          C                      GAAG      ACAT GATGGAGC
                                ||||      |||| ||||||||
                                CTTC      TGTA CTACCTCG
                                  CAGATC    C
GAM597  LOC221656 5'  CTCCTCAGAAATGTATTCCTC  93849    A       A___  T
                                GA GAATACAT    GA GGAG
                                || |||||||    || ||||
                                CT CTTATGTA    CT CCTC
                                 C       AAGA  _
GAM598  CBFA2T2   3'  CAGCCCCATCCCTACCTTG    18703      GCTTCC   AC
                                TAAGG     GGA  GGGGCTG
                                |||||     |||  |||||||
                                GTTCC     CCT  CCCCGAC
                                   ATC___   A_
GAM598  LBX1      3'  GCCGCCCCGGAAGCCCT     22668          AAC  _
                                AGGGCTTCCGG   GG GGC
                                ||||||||||   || |||
                                TCCCGAAGGCC   CC CCG
                                      ___  G
GAM598  OPA1      3'  ACAGCCCCATTGCTACTCCCC  56426     CTTCC  _  C
                                GGG     GG AA GGGGCTGT
                                |||     || || ||||||||
                                CCC     TC TT CCCCGACA
                                  CTCA_  G  A
GAM598  PPP1R12B  3'  ACAACCCAGTGTCCCGGAAGCC 50341          A  __  C
          CT                      AGGGCTTCCGG ACG  GGG TGT
                                ||||||||||| |||  ||| |||
                                TCCCGAAGGCC TGT  CCC ACA
                                      C   GA   A
GAM598  PSG4      3'  CTCTGTTCCAGAAGCCCT    12442          C
                                AGGGCTTC GGAACGGGG
                                |||||||| |||||||||
                                TCCCGAAG CCTTGTCTC
                                    A
GAM598  PSG7      3'  CTCTGTTCCAGAAGCCCT    12448          C
                                AGGGCTTC GGAACGGGG
                                |||||||| |||||||||
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                                TCCCGAAG CCTTGTCTC
                                    A
GAM598  SLC22A12  3'  ACAGCTTTACCCAGAAGCCCT  58680       C  AAC
                                AGGGCTTC GG   GGGGCTGT
                                |||||||| ||   ||||||||
                                TCCCGAAG CC   TTTCGACA
                                    A  CA_
GAM598  SMAC      5'  ACAGCCCCGCCTCCGCCCCCT  57990     CTTC   A_
                                AGGG   CGGA  CGGGGCTGT
                                ||||   ||||  |||||||||
                                TCCC   GCCT  GCCCCGACA
                                  CC__   CC
GAM598  TACC1     3'  ACAGCCCTGGAAGAAACCCT   21866     C   CGGAA
                                AGGG TTC    CGGGGCTGT
                                |||| |||    |||||||||
                                TCCC AAG    GTCCCGACA
                                  A  AAG__
GAM598  DKFZp762E1511 3'  CAGCCCCACCAGGCCTCA    60249   A    CC  AAC
                                A GGGCTT  GG   GGGGCTG
                                | ||||||  ||   |||||||
                                A TCCGGA  CC   CCCCGAC
                                 C     __ A__
GAM598  FLJ11294  3'  CCTGAATCCCAGGAACCCT   37797     C   __   A_
                                AGGG TTCC  GGA  CGGG
                                |||| ||||  |||  ||||
                                TCCC AAGG  CCT  GTCC
                                  _   AC   AA
GAM598  FLJ22184  3'  ACAGCCCCGCCTGCTACACCCC 47684    CTTC__   AA
                                GGG     CGG  CGGGGCTGT
                                |||     |||  |||||||||
                                CCC     GTC  GCCCCGACA
                                  CACATC   C_
GAM598  KIAA0748  3'  ACAGCCCCACCCCTATCTCCCT 29610      CTTCC  AAC
          T                      AAGGG    GG   GGGGCTGT
                                |||||    ||   ||||||||
                                TTCCC    CC   CCCCGACA
                                   TCTAT  CCA
GAM598  KIAA1196  3'  ATAGGCCTCCAGGAGCCCT   62146       C   ACG  G
                                AGGGCTTC GGA   GG CTGT
                                |||||||| |||   || ||||
                                TCCCGAGG CCT   CC GATA
                                    A  ___  G
GAM598  PRRG2     3'  CCGGATTCCGGAAGCCGCT   8159    _       __
                                AG GGCTTCCGGAA  CGG
                                || ||||||||||  |||
                                TC CCGAAGGCCTT  GCC
                                 G         AG
GAM598  LOC115817 5'  ACAGCCCCACTCAGCCC     57410      TCCG  AC
                                GGGCT   GA  GGGGCTGT
                                |||||   ||  ||||||||
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                                CCCGA   CT  CCCCGACA
                                   _____ CA
GAM598  LOC129102 5'  ACAGCCCCACTCCAGCCC    76314      TCC   AC
                                GGGCT   GGA  GGGGCTGT
                                |||||   |||  ||||||||
                                CCCGA   CCT  CCCCGACA
                                   ____  CA
GAM598  LOC132660 5'  ACAGAAATCCAGAAGCCTTTA  75574         C   ACGGGG
                                TAAGGGCTTC GGA     CTGT
                                |||||||||| |||     ||||
                                ATTTCCGAAG CCT     GACA
                                      A   AAA___
GAM598  LOC152992 3'  ACAGTTACTCGGAAGCCC    81640         AACGG
                                GGGCTTCCGG    GGCTGT
                                ||||||||||    ||||||
                                CCCGAAGGCT    TTGACA
                                      CA___
GAM598  LOC196337 3'  ACAGCCCCATCCACCCTGCCTT 89018      TTCC_   AC
                                AGGGC    GGA  GGGGCTGT
                                |||||    |||  ||||||||
                                TTCCG    CCT  CCCCGACA
                                   TCCCA   A_
GAM598  LOC221466 3'  ACAGCCCCATCCTCACCCCTT  95310      CTTCC   AC
                                AAGGG    GGA  GGGGCTGT
                                |||||    |||  ||||||||
                                TTCCC    CCT  CCCCGACA
                                   CACT_   A_
GAM598  LOC254266 5'  ACAACCTTCCAGAAGCCCT    99189        C   AC   GC
                                AGGGCTTC GGA  GGG  TGT
                                |||||||| |||  |||  |||
                                TCCCGAAG CCT  TCC  ACA
                                     A   __   A_
GAM598  LOC91301  5'  ACAGCCCCTACAAGAAACCTCA 66145   A   C   CGGAAC
                                A GGG TTC     GGGGCTGT
                                | ||| |||     ||||||||
                                A TCC AAG     CCCCGACA
                                 C   A   AACAT_
GAM599  EN2       5'  GGTGACTCACACCCCTGAACCG 9266          A  GAA
          C                      GTGGTTCAGGG TG   AGTCACC
                                ||||||||||| ||   |||||||
                                CGCCAAGTCCC AC   TCAGTGG
                                      C  AC_
GAM599  PER2      3'  GGTGACTTCCCTTTGCAAACCA 43358       __    AT    A
                                TGGTT  CAGGG  GGAA GTCACC
                                |||||  |||||  |||| ||||||
                                ACCAA  GTTTC  CCTT CAGTGG
                                   AC    __   _
GAM599  PPT1      3'  GACTTCCATCCCCAAAACAC   62445     GTTCA       A
                                GTG    GGGATGGAA GTC
                                |||    ||||||||| |||
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                                CAC    CCCTACCTT CAG
                                  AAAAC       _
GAM599  FLJ14298  5'  GGTATTTCATCCCCGAAGCCAC 45786       _ A       AG
                                GTGGTT C GGGATGGAA  TC
                                |||||| | |||||||||  ||
                                CACCGA G CCCTACTTT  GG
                                   A C        AT
GAM599  KIAA1881  3'  GTGACCTTCTTAACTGAGCCAC 97088        GGAT    A
                                GTGGTTCAG    GGAA GTCAC
                                |||||||||    |||| |||||
                                CACCGAGTC    TCTT CAGTG
                                     AAT_    C
GAM599  KIAA1958  5'  GTGACTTTGAACCCCAAACC   82787     CA   ATGG
                                GGTT  GGG    AAAGTCAC
                                ||||  |||    ||||||||
                                CCAA  CCC    TTTCAGTG
                                  AC   AAG_
GAM599  PEG10     3'  ACTCAGAAAGTCCCTGATCCAC 31196     T       GGAA__
                                GTGG TCAGGGAT     AGT
                                |||| ||||||||      |||
                                CACC AGTCCCTG     TCA
                                  T       AAAGAC
GAM599  PRRDH     3'  GATCCCCATCCCTGAAC     32325          AAA
                                GTTCAGGGATGG   GTC
                                ||||||||||||   |||
                                CAAGTCCCTACC   TAG
                                     CC_
GAM599  LOC115399 3'  GGTGACCTCTGCTTCTGAACC  73816        AT   AA
                                GGTTCAGGG  GGA  GTCACC
                                |||||||||  |||  ||||||
                                CCAAGTCTT  TCT  CAGTGG
                                     CG   C_
GAM599  LOC130507 3'  TGACCCTCATGAATGAGCCAC  75456        GGG    AAA
                                GTGGTTCA   ATGG   GTCA
                                ||||||||   ||||   ||||
                                CACCGAGT   TACT   CAGT
                                    AAG    CC_
GAM599  LOC245806 3'  TGACTTTTGGCCGAATCAC    93544        AG  ATG
                                GTGGTTC  GG   GAAAGTCA
                                |||||||  ||   ||||||||
                                CACTAAG  CC   TTTTCAGT
                                   __  GG_
GAM599  LOC253782 3'  TGACTTTCCTGTTACTAAAC   97405     C  GG  _
                                GTT AG  AT GGAAAGTCA
                                ||| ||  || |||||||||
                                CAA TC  TG CCTTTCAGT
                                  A  AT  T
GAM599  LOC90620  3'  ACTTCCCATTTCTGAACC     64323        GG    A
                                GGTTCAG  ATGG AAGT
                                |||||||  |||| ||||
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                                CCAAGTC  TACC TTCA
                                    TT    C
GAM600  AXIN1    3'  TGGTGAGGGGCCGCGCTGTCA  61544      ACACAT
                                TGACA     CCCCTCACCA
                                |||||     ||||||||||
                                ACTGT     GGGGAGTGGT
                                   CGCGCC
GAM600  BLNK     3'  TGGTGAGGTTGAGTTATCATG  26162      C   A  TCC
                                CATGA AAC CA   CCTCACCA
                                ||||| ||| ||   ||||||||
                                GTACT TTG GT   GGAGTGGT
                                   A   A  T__
GAM600  EZH1     3'  TGGTGAGGGGCTAAATTGCA   10559    A   CACAT
                                TG CAA    CCCCTCACCA
                                || |||    ||||||||||
                                AC GTT    GGGGAGTGGT
                                 _   AAATC
GAM600  FCMD     3'  GGGAAGGCAATGTGTTGCCAT  23042    A      CC   CA
                                ATG CAACACAT  CCT  CC
                                ||| ||||||||  |||  ||
                                TAC GTTGTGTA  GGA  GG
                                  C       AC   AG
GAM600  FUT5     3'  GTGCCTGTGGATGTGTTGCGAT 10730    GA       CCT__
          G                      CAT  CAACACATCC    CAC
                                |||  ||||||||||    |||
                                GTA  GTTGTGTAGG    GTG
                                  GC         TGTCC
GAM600  MMP10    3'  GGTGAGAGAATGTATTTTCAT  11605    C  C    CCC
                                ATGA AA ACAT   CTCACC
                                |||| || ||||   ||||||
                                TACT TT TGTA   GAGTGG
                                  T  A    AGA
GAM600  ATP10B   3'  GTGAGGGGATTGAGTCA     64107     AA  C
                                TGAC  CA ATCCCCTCAC
                                ||||  || ||||||||||
                                ACTG  GT TAGGGGAGTG
                                  A_  _
GAM600  BRUNOL6  3'  TGGTGAGGAGTGACTGTC    54523     A_   ATCC
                                GACA  CAC    CCTCACCA
                                ||||  |||    ||||||||
                                CTGT  GTG    GGAGTGGT
                                  CA   A___
GAM600  CAGE     5'  GGGAAAATGTGGTTGTCATG   83579        _   ___
                                CATGACAAC ACA   TCCC
                                ||||||||| |||   ||||
                                GTACTGTTG TGT   AGGG
                                     G   AAA
GAM600  CSRP2BP  3'  GGCCATTGATGTGTTGTCAT   70656          CCCTCA
                                ATGACAACACATC     CC
                                ||||||||||||     ||
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                                TACTGTTGTGTAG     GG
                                       TTACC_
GAM600  DOCK3    3'  TGAACTCATGTGTTGCCATG  67100     A      CCCC
                                CATG CAACACAT    TCA
                                |||| ||||||||    |||
                                GTAC GTTGTGTA    AGT
                                  C       CTCA
GAM600  DRF1     3'  GTGAGGATGATGGTCACCGTG  47755     ACA  A   C_
                                CATG   AC CATC  CCTCAC
                                ||||   || ||||  ||||||
                                GTGC   TG GTAG  GGAGTG
                                  CAC  _   TA
GAM600  FLJ20321 3'  GGTGACTTTGTATTGTCATG  35430       C   TCCCC
                                CATGACAA ACA    TCACC
                                |||||||| |||    |||||
                                GTACTGTT TGT    AGTGG
                                     A   TTC__
GAM600  FLJ20811 3'  TGGTGAGGGGATCACTTCA   67711    CAACAC
                                TGA     ATCCCCTCACCA
                                |||     ||||||||||||
                                ACT     TAGGGGAGTGGT
                                  TCAC__
GAM600  FLJ21369 3'  TGGTAAGATGATTGCAAGTTGT 46057        A__  _  CC  C
           CATG                   CATGACAAC   CA TC  CT ACCA
                                |||||||||   || ||  || ||||
                                GTACTGTTG   GT AG  GA TGGT
                                     AAC  T  TA  A
GAM600  KIAA1937 3'  TGGTGAGGGTGCTTGTC     74075      _  CATC
                                GACAA CA    CCCTCACCA
                                ||||| ||    |||||||||
                                CTGTT GT    GGGAGTGGT
                                  C  ____
GAM600  MADHIP   3'  GTGAGGGCCCCGTTGTCATG   24643        ACATC
                                CATGACAAC    CCCTCAC
                                |||||||||    |||||||
                                GTACTGTTG    GGGAGTG
                                     CCCC_
GAM600  MGC11386 3'  TGGTGAGGCTTGGTTGTATG   53074     A   A  TCC
                                CATG CAAC CA   CCTCACCA
                                |||| |||| ||   ||||||||
                                GTAT GTTG GT   GGAGTGGT
                                  _   _  TC_
GAM600  MGC1842  3'  GTGCCGTGTGTTGTCATG    66260          CCCCT
                                CATGACAACACAT    CAC
                                ||||||||||||    |||
                                GTACTGTTGTGTG    GTG
                                       CC___
GAM600  PELI2    3'  AGTGGTGTGTTGCATG     41454      A     T  C
                                CATG CAACACA CC CT
                                |||| ||||||| || ||
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                                GTAC GTTGTGT GG GA
                                  _      _ T
GAM600  RALGPS1A  3'  TGGTGAGGAAAGTAGTTGTCA  28340        _ ATCC
                                TGACAAC AC    CCTCACCA
                                ||||||| ||    ||||||||
                                ACTGTTG TG    GGAGTGGT
                                    A  AAA_
GAM600  RBT1      3'  TGACAGGGATGTGCTGCCA   26282    A  A      C_
                                TG CA CACATCCC  TCA
                                || || ||||||||  |||
                                AC GT GTGTAGGG  AGT
                                 C  C       AC
GAM600  TCL6      5'  GGTGAGGCCAGTTTCATG    27764      C   ACATCC
                                CATGA AAC     CCTCACC
                                ||||| |||     |||||||
                                GTACT TTG     GGAGTGG
                                   _   ACC___
GAM600  TCL6      5'  GGTGAGGCCAGTTTCATG    25912      C   ACATCC
                                CATGA AAC     CCTCACC
                                ||||| |||     |||||||
                                GTACT TTG     GGAGTGG
                                   _   ACC___
GAM600  TCL6      5'  GGTGAGGCCAGTTTCATG    40485      C   ACATCC
                                CATGA AAC     CCTCACC
                                ||||| |||     |||||||
                                GTACT TTG     GGAGTGG
                                   _   ACC___
GAM600  TCL6      5'  GGTGAGGCCAGTTTCATG    40514      C   ACATCC
                                CATGA AAC     CCTCACC
                                ||||| |||     |||||||
                                GTACT TTG     GGAGTGG
                                   _   ACC___
GAM600  VPS4B     3'  TGAGGATGTGTTTCAT      18026      C       CC
                                ATGA AACACATCC  TCA
                                |||| |||||||||  |||
                                TACT TTGTGTAGG  AGT
                                   _       __
GAM600  LOC128966 5'  TGGTGAGGACAGAGTGTCATG  76310        ACACATCC
                                CATGACA       CCTCACCA
                                |||||||       ||||||||
                                GTACTGT       GGAGTGGT
                                    GAGACA__
GAM600  LOC149670 3'  TGGTGAGGGTCCTGCAGTCATG 80310        AA  CATC
                                CATGAC  CA    CCCTCACCA
                                ||||||  ||    |||||||||
                                GTACTG  GT    GGGAGTGGT
                                   AC  CCT_
GAM600  LOC158288 5'  GGTGAGGGTGGTCGCATG    88028      ACA  A  TC
                                CATG   AC CA  CCCTCACC
                                ||||   || ||  ||||||||
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                                GTAC   TG GT  GGGAGTGG
                                  GC_  _  __
GAM600  LOC201617 5'  TGAAGGATGTGTTATCA     91827     C        CC
                                TGA AACACATCC  TCA
                                ||| |||||||||  |||
                                ACT TTGTGTAGG  AGT
                                  A        A_
GAM600  LOC221496 3'  TGGTGAGGCCATGTTCTCAT   93645      C    CATCC
                                ATGA AACA    CCTCACCA
                                |||| ||||    ||||||||
                                TACT TTGT    GGAGTGGT
                                  C    ACC__
GAM600  LOC255565 3'  GTGAGGGGCAGTTCTCATG    96803      C   ACAT
                                CATGA AAC    CCCCTCAC
                                ||||| |||    ||||||||
                                GTACT TTG    GGGGAGTG
                                   C   AC__
GAM600  LOC256730 3'  TGAGTTTGGATGTGTTGCAT   96939     A        C__
                                ATG CAACACATCC   CTCA
                                ||| ||||||||||   ||||
                                TAC GTTGTGTAGG   GAGT
                                  _        TTT
GAM600  LOC90233  3'  TGGTGAGGGGAATCTGTTG    57200      CA_
                                CAACA   TCCCCTCACCA
                                |||||   ||||||||||
                                GTTGT   AGGGGAGTGGT
                                   CTA
GAM600  LOC91252  3'  GGTGAGGGCTCCACGTTGTCA  65940       ACATC_
                                TGACAAC     CCCTCACC
                                |||||||     ||||||||
                                ACTGTTG     GGGAGTGG
                                    CACCTC
GAM601  ELAVL2    5'  AGAACTGCACCGTTACTTTA   16679        T  CCA  _
                                TAAAGTAA CG   TGC GTTCT
                                |||||||| ||   ||| |||||
                                ATTTCATT GC   ACG CAAGA
                                     _  C__   T
GAM601  ORC3L     3'  ACCTGTGGAGTACTTTAGA    25656        ATCG    C
                                TCTAAAGTA    CCATG GT
                                |||||||||    ||||| ||
                                AGATTTCAT    GGTGT CA
                                     GA__     C
GAM601  C5orf3    5'  AGAACGCATGTTTGCTCATCTA 38589     A___    TCGC
           GA                     TCTA    AGTAA    CATGCGTTCT
                                ||||    |||||    ||||||||||
                                AGAT    TCGTT    GTACGCAAGA
                                  CTAC     T___
GAM601  FLJ20152  3'  GCTTTAATGATTACTTTAGA   39165          CCAT_
                                TCTAAAGTAATCG    GC
                                ||||||||||||     ||
```

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                                AGATTTCATTAGT    CG
                                      AATTT
GAM601  MRPS35   3' ATGGCAATGATTACTCCAGA  41820    AA     ___
                                TCT  AGTAATC   GCCAT
                                |||  |||||||   |||||
                                AGA  TCATTAG   CGGTA
                                  CC      TAA
GAM601  PAK2     5' AGAACACTGGGCTCGATTACTA 67137    AA     __  ATGC
           CAGA                   TCT  AGTAATC  GCC   GTTCT
                                |||  |||||||  |||   |||||
                                AGA  TCATTAG  CGG   CAAGA
                                  CA      CT   GTCA
GAM601  LOC144766 3' GTGTGGCGATTCCTCAGA    77485    AA  T
                                TCT  AG AATCGCCATGC
                                |||  ||  ||||||||||||
                                AGA  TC TTAGCGGTGTG
                                  C_  C
GAM601  LOC199958 3' AGAACGCACAGCCCGCAACTTT 91487       AATC_  CA
           A                     TAAAGT    GC  TGCGTTCT
                                ||||||    ||  ||||||||
                                ATTTCA    CG  ACGCAAGA
                                    ACGCC  AC
GAM602  AMACR    3' GCCCACGGCTCAAGTGAATTTG 69101      A   CACCA
                                CAAA TCAC    CCGTGGGC
                                ||||  ||||    ||||||||
                                GTTT AGTG    GGCACCCG
                                  A   AACTC
GAM602  CCRL1    3' GCTTTGTGGTGATAATTTTG   33794       CAC     CGT
                                CAAAAT   CACCAC   GGGC
                                ||||||   ||||||   ||||
                                GTTTTA   GTGGTG   TTCG
                                    ATA     T__
GAM602  GALNS    3' GCCCACGGCGCCTCAGATTTCA 6704     A_    ACCACCA
           GG                     CC  AAATC      CCGTGGGC
                                ||  |||||      ||||||||
                                GG  TTTAG      GGCACCCG
                                 AC     ACTCCGC
GAM602  GEMIN5   5' GCCGAGGGGTGATGATTTTG   90643        C   A  GTG
                                CAAAATCA CACC CC   GGC
                                |||||||| |||| ||   |||
                                GTTTTAGT GTGG GG   CCG
                                    A   _  AG_
GAM602  LIFR     3' CCCAGGCAGTGGTGATCTTTG  11310      _      CA  G
                                CAAA ATCACCAC  CC TGGG
                                ||||  ||||||||  || ||||
                                GTTT TAGTGGTG  GG ACCC
                                  C       AC  _
GAM602  RNF12    5' ACAGTGGGTGATTTCAGA    32785    CA      AC   C
                                TC  AAATCACC  CAC GT
                                ||  ||||||||  ||| ||
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                                AG  TTTAGTGG  GTG CA
                                 AC       __  A
GAM602  SOX4     3'  CGCGGCGGCGTTTTGGA     13304        CACCA  A
                                TCCAAAAT    CC CCGTG
                                ||||||||    || |||||
                                AGGTTTTG    GG GGCGC
                                    C____  C
GAM602  TRPM8    3'  CATGGTGGATGATTTT      44205        CCA
                                AAAATCA   CCACCGTG
                                |||||||   ||||||||
                                TTTTAGT   GGTGGTAC
                                   A__
GAM602  BART1    3'  CCCAGTTTGAGATTTTGGA   25037         AC  CC  CG
                                TCCAAAATC  CA  AC  TGGG
                                |||||||||  ||  ||  ||||
                                AGGTTTTAG  GT  TG  ACCC
                                     A_  T_  __
GAM602  BIVM     3'  TTATGGTGGGTGATTTCAGA   35161    CA      AC
                                TC  AAATCACC  CACCGTGG
                                ||  ||||||||  ||||||||
                                AG  TTTAGTGG  GTGGTATT
                                 AC       __
GAM602  C6orf5   3'  CCCTCAGGTTGATAATTTTGGA 31984        CAC  CC   GT_
                                TCCAAAAT   CA  ACC   GGG
                                |||||||   ||  |||   |||
                                AGGTTTTA   GT  TGG   CCC
                                     ATA  __  ACT
GAM602  DKFZP762N2316 3'  CCCTGTGGTGGTCTTGGA    67712      AATC      CGT
                                TCCAA   ACCACCAC   GGG
                                |||||   ||||||||   |||
                                AGGTT   TGGTGGTG   CCC
                                   C___       T__
GAM602  FLJ10936 3'  GCCCTACTATGGTGATGAT    37445      C    CC  _
                                ATCA CACCA  GT GGGC
                                |||| |||||  || ||||
                                TAGT GTGGT  CA CCCG
                                   A    AT  T
GAM602  FLJ21120 5'  GCTTCTTTGATTGGTGATTTTG 45792          CCACCGT
                                CAAAATCACCA      GGGC
                                ||||||||||       ||||
                                GTTTTAGTGGT      TTCG
                                      TAGTTTC
GAM602  GDF10    3'  CCACATAGTGATTTTGGA    18296          CACCACC
                                TCCAAAATCAC      GTGG
                                ||||||||||       ||||
                                AGGTTTTAGTG      CACC
                                      ATA____
GAM602  HSPC195  3'  CCCAACAGTGATTTTGGA    81862          CACCACCG
                                TCCAAAATCAC      TGGG
                                ||||||||||       ||||
```

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                                AGGTTTTAGTG       ACCC
                                      ACA_____
GAM602  ICB-1    3'  GCCATTCTTGGTGGTGAGCCTG 17933      AAA       CCGTG
            GA                    TCCA   TCACCACCA    GGC
                                  ||||   |||||||||    |||
                                  AGGT   AGTGGTGGT    CCG
                                    CCG        TCTTA
GAM602  KIAA1950 5'  GCCCACGGTGGGCTGGACTTTG 94183      A  ACCA
                                  CAAA TC    CCACCGTGGGC
                                  |||| ||    ||||||||||
                                  GTTT AG    GGTGGCACCCG
                                    C  GTCG
GAM602  LANCL2   3'  GTTCTGTGGTGATGACCTATGG 38622      AAA_   C     CGT
            A                     TCCA    TCA CACCAC   GGGC
                                  ||||    ||| ||||||   ||||
                                  AGGT    AGT GTGGTG   CTTG
                                    ATCC   A     T__
GAM602  MGC4701   5'  GCGTCGCGGTGGTGGACTCTGG 65163      AAATCA          _
            A                     TCCA     CCACCACCGTGG GC
                                  ||||     |||||||||||| ||
                                  AGGT     GGTGGTGGCGCT CG
                                    CTCA__           G
GAM602  PCCX2    3'  GGTAGTGGTGTTTTGGA     66587        T     C
                                  TCCAAAA CACCAC ACC
                                  ||||||| |||||| |||
                                  AGGTTTT GTGGTG TGG
                                      _     A
GAM602  PRDM14   5'  GCTCCGCGGTGGCGCTCTTGGA 44706      AATCACCA       _
                                  TCCAA       CCACCGTGG GC
                                  |||||       ||||||||| ||
                                  AGGTT       GGTGGCGCC CG
                                     CTCGC___        T
GAM602  SHAPY    3'  CCATCTGGTGGTGATTTCGG   57905    A          CC
                                  CC AAATCACCACCA  GTGG
                                  || ||||||||||||  ||||
                                  GG TTTAGTGGTGGT  TACC
                                   C          C_
GAM602  SSR1     3'  CTCTGGAGTGATTTTAGA    13417    C      CA   CCGT
                                  TC AAAATCAC  CCA    GGG
                                  || ||||||||  |||    |||
                                  AG TTTTAGTG  GGT    CTC
                                   A       A_   _____
GAM602  LOC145719 5'  TCCAGTGGTGATCTAGGA    84469     AAA       CACCG
                                  TCC   ATCACCAC    TGGG
                                  |||   ||||||||    ||||
                                  AGG   TAGTGGTG    ACCT
                                    ATC       ______
GAM602  LOC145720 5'  TCCAGTGGTGATCTAGGA    84455     AAA       CACCG
                                  TCC   ATCACCAC    TGGG
                                  |||   ||||||||    ||||
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                                AGG  TAGTGGTG    ACCT
                                  ATC      _____
GAM602  LOC146336 3'  CCCACACCGTGATTTTGGA   78366          CACCACC
                                TCCAAAATCAC      GTGGG
                                ||||||||||      |||||
                                AGGTTTTAGTG      CACCC
                                     CCA____
GAM602  LOC157273 3'  ACAGTGGAGTGATTTTG     87713        CA   C
                                CAAAATCAC  CCAC GT
                                |||||||||  |||| ||
                                GTTTTAGTG  GGTG CA
                                     A_   A
GAM602  LOC197114 5'  TCCAGTGGTGATCTAGGA    91275     AAA      CACCG
                                TCC  ATCACCAC    TGGG
                                |||  ||||||||    ||||
                                AGG  TAGTGGTG    ACCT
                                  ATC      _____
GAM602  LOC197117 5'  TCCAGTGGTGATCTAGGA    91286     AAA      CACCG
                                TCC  ATCACCAC    TGGG
                                |||  ||||||||    ||||
                                AGG  TAGTGGTG    ACCT
                                  ATC      _____
GAM602  LOC256158 5'  GCCCACGGCTGCAGGTCCTGGA 99496      AAATC  AC  _
                                TCCA    ACC  CA CCGTGGGC
                                ||||    |||  || ||||||||
                                AGGT    TGG  GT GGCACCCG
                                  CC___   AC  C
GAM602  LOC91373  3'  GCCCACACCTTGTGATTTTTGA 66416    C      CACCACC
                                TC AAAATCAC      GTGGGC
                                || ||||||||      ||||||
                                AG TTTTAGTG      CACCCG
                                 T       TTCCA__
GAM602  LOC93070  3'  GCCCTACTATGGTGATGAT    71810      C    CC  _
                                ATCA CACCA  GT GGGC
                                |||| |||||  || ||||
                                TAGT GTGGT  CA CCCG
                                  A    AT  T
GAM603  BSND     5'  GGCCAGGGACTGGCCAGG    55161        CA   AA_
                                CCTGGCCA  GTTC   GCC
                                ||||||||  ||||   |||
                                GGACCGGT  CAGG   CGG
                                     __    GAC
GAM603  CTSL     5'  GGCCCAGCTGTGGCCGG     10344          CAA
                                CTGGCCACAGTT   GCC
                                ||||||||||||   |||
                                GGCCGGTGTCGA   CGG
                                     CC_
GAM603  DBCCR1   5'  GGCTGCTAGGAGCCAGGTA   28241        CAC_  TCA
                                TACCTGGC   AGT   AGCC
                                ||||||||   |||   ||||
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                                ATGGACCG   TCG  TCGG
                                    AGGA  ___
GAM603  HEM1    3'  GCTTGAGCTCTGACAGG    19240     GC  C
                                CCTG  CA AGTTCAAGC
                                ||||  || |||||||||
                                GGAC  GT TCGAGTTCG
                                  A_  C
GAM603  KCND2   5'  GGCGCGCACTTGGCCAGGTA  25384        C   TCAA
                                TACCTGGCCA AGT   GCC
                                |||||||||| |||   |||
                                ATGGACCGGT TCA   CGG
                                      _  CGCG
GAM603  LEP     3'  GCATTACGTGAGCCAGGTA   5863        _   A  TCAA
                                TACCTGGC CAC GT   GC
                                |||||||| ||| ||   ||
                                ATGGACCG GTG CA   CG
                                    A  _  TTA_
GAM603  LTB4R   5'  GCTTGAACTGAAGCCAAGG   7468     _   CA
                                CCT GGC  CAGTTCAAGC
                                ||| |||  ||||||||||
                                GGA CCG  GTCAAGTTCG
                                  A  AA
GAM603  NGB     3'  GCTAGCTGGCCAGGTG     41464        CA   CA
                                TACCTGGCCA  GTT  AGC
                                ||||||||||  |||  |||
                                GTGGACCGGT  CGA  TCG
                                      __  __
GAM603  NOC4    3'  GGTGTTTCTGTGGTCAGGTA  21376          TTCAA
                                TACCTGGCCACAG    GCC
                                ||||||||||||     |||
                                ATGGACTGGTGTC    TGG
                                       TTTG_
GAM603  PRKY    3'  GGCTCCACTCTGTAGCCAGGTG 12380       C    TTCA_
                                TACCTGGC ACAG    AGCC
                                |||||||| ||||    ||||
                                GTGGACCG TGTC    TCGG
                                    A   TCACC
GAM603  RANBP2L1 5'  GGCTTGAACCTAATCAGGT   51050      CCACA
                                ACCTGG    GTTCAAGCC
                                ||||||    |||||||||
                                TGGACT    CAAGTTCGG
                                   AATC_
GAM603  RNMT    3'  GCCATGAGATGGCCAGGTA   15054        CAG   A_
                                TACCTGGCCA   TTCA  GC
                                ||||||||||   ||||  ||
                                ATGGACCGGT   GAGT  CG
                                     A__    AC
GAM603  TCERG1  3'  GGCTTGAACTTGCCAG     22958      CAC
                                CTGGC   AGTTCAAGCC
                                |||||   ||||||||||
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                                GACCG   TCAAGTTCGG
                                  T__
GAM603  TMPRSS2  3'  GCCCTGGATGGTGGCCAG    20172        A    A_
                                CTGGCCAC GTTCA  GC
                                |||||||| |||||  ||
                                GACCGGTG TAGGT  CG
                                     G    CC
GAM603  TNFAIP2  3'  GGCCAGGAAGTGGCCGGTA   21924     T    AG   AA
                                TACC GGCCAC  TTC  GCC
                                |||| ||||||  |||  |||
                                ATGG CCGGTG  AGG  CGG
                                  _    A_   AC
GAM603  TP63     3'  AGCTGCCATGGCTAGGTA    14943          ___
                                TACCTGGCCA   CAGTT
                                ||||||||||   |||||
                                ATGGATCGGT   GTCGA
                                      ACC
GAM603  TRIM14   3'  GGCCCAAACTGAATTGTGACAG 53775      GC       A_____
          G                      CCTG  CACAGTTCA     GCC
                                ||||  |||||||||     |||
                                GGAC  GTGTTAAGT     CGG
                                  A_        CAAACC
GAM603  WHSC1    3'  GCTTCCTCTGGCCAGGTA    24675         C  TTC
                                TACCTGGCCA AG   AAGC
                                |||||||||| ||   ||||
                                ATGGACCGGT TC   TTCG
                                      C  C__
GAM603  ZNF289   3'  GCTTGATGCTGGCCAGG     65931         _ GT
                                CCTGGCCA CA  TCAAGC
                                |||||||| ||  ||||||
                                GGACCGGT GT  AGTTCG
                                     C  __
GAM603  ARFGAP1  3'  GCGGACGTGGCCAGG       37140         A   AA
                                CCTGGCCAC GTTC  GC
                                ||||||||| ||||  ||
                                GGACCGGTG CAGG  CG
                                      _   __
GAM603  ARHGEF16 5'  GGCCTGGGGAAGCCAGGTG   27822         CACAG   A
                                TACCTGGC    TTCA GCC
                                ||||||||    |||| |||
                                GTGGACCG    GGGT CGG
                                     AAG__   C
GAM603  C20orf106 3' GGCTTGAACCCTGGAGG     55907     GG   CA
                                CCT  CCA  GTTCAAGCC
                                |||  |||  |||||||||
                                GGA  GGT  CAAGTTCGG
                                  __  CC
GAM603  CLDN4    3'  GGCTTCTGCTGGCCAGG      8956         _  TTC
                                CCTGGCCA CAG   AAGCC
                                |||||||| |||   |||||
```

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                                GGACCGGT GTC   TTCGG
                                    C  ___
GAM603  DC-TM4F2  3'  GGCTCCTCTTGTGGCCATGTA  48903     C       TTCA
                                TAC TGGCCACAG    AGCC
                                ||| |||||||||    ||||
                                ATG ACCGGTGTT    TCGG
                                  T       CTCC
GAM603  FLJ10713  3'  CTTGAGTAGCTAGGTA      37002        C  AGT
                                TACCTGGC AC   TCAAG
                                |||||||| ||   |||||
                                ATGGATCG TG   AGTTC
                                    A  ___
GAM603  FLJ10811  3'  GGCTCGAATATGGGGGCCAGGT 37224         A_ _   A
          G                      TACCTGGCC  CA GTTC AGCC
                                |||||||||  || |||| ||||
                                GTGGACCGG  GT TAAG TCGG
                                     GG  A    C
GAM603  FLJ10922  3'  GGCTTCTGTAAACCGCCAGGTA 37405        C____   TTC
                                TACCTGGC    ACAG   AAGCC
                                ||||||||    ||||   |||||
                                ATGGACCG    TGTC   TTCGG
                                    CCAAA   ___
GAM603  FLJ12484  3'  GGCTTCCGGTGTGGCCGGTA   70228     T     GTTC
                                TACC GGCCACA    AAGCC
                                |||| |||||||    |||||
                                ATGG CCGGTGT    TTCGG
                                  _      GGCC
GAM603  FLJ21156  3'  AGCTGGCATGGTCAGGTA    45118         ___
                                TACCTGGCCA   CAGTT
                                ||||||||||   |||||
                                ATGGACTGGT   GTCGA
                                     ACG
GAM603  FLJ21657  3'  GGCTTGAACCTGGGAGG     42801     GG  A  _
                                CCT  CC CAG TTCAAGCC
                                |||  || ||| ||||||||
                                GGA  GG GTC AAGTTCGG
                                  __  _  C
GAM603  FLJ22167  5'  GATCCTGTGAGCCAGGTA    44874        _    T_
                                TACCTGGC CACAG  TC
                                ||||||| |||||  ||
                                ATGGACCG GTGTC  AG
                                    A    CT
GAM603  FOXP1     5'  GGCTCAGCATGGCCAGGTG   52046         CA   CA
                                TACCTGGCCA  GTT  AGCC
                                ||||||||||  |||  ||||
                                GTGGACCGGT  CGA  TCGG
                                     A_   C_
GAM603  GAB3      3'  GCTACCTGTAGCCAGGTA    55521        C    TTCA
                                TACCTGGC ACAG    AGC
                                |||||||| ||||    |||
```

```
                                ATGGACCG TGTC    TCG
                                    A    CA__
GAM603  KIAA0427  3'  GCTTGCCATCGTGGCCAGG   29386        A  T_
                                CCTGGCCAC GT  CAAGC
                                ||||||||| ||  |||||
                                GGACCGGTG TA  GTTCG
                                    C  CC
GAM603  KIAA0481  3'  GGCACCTGTGGCCAAGTG    72322    C       TTCAA
                                TAC TGGCCACAG    GCC
                                ||| |||||||||    |||
                                GTG ACCGGTGTC    CGG
                                  A       CA___
GAM603  KIAA0557  3'  GCTAGATGTGGCCAGG     78568         GT  A
                                CCTGGCCACA  TC AGC
                                ||||||||||  || |||
                                GGACCGGTGT  AG TCG
                                    __  A
GAM603  KIAA0729  3'  GGCTTAATTCTTGGTCAGG   97412        C_   C
                                CCTGGCCA  AGTT AAGCC
                                ||||||||  |||| |||||
                                GGACTGGT  TTAA TTCGG
                                    TC   _
GAM603  KIAA0794  3'  GGCTTGAACCTGGGAGG    81232    GG  A  _
                                CCT  CC CAG TTCAAGCC
                                |||  || ||| ||||||||
                                GGA  GG GTC AAGTTCGG
                                  __  _  C
GAM603  KIAA0872  3'  GGTGTGTCTGTGGCCAG    30761         TT  A
                                CTGGCCACAG  CA GCC
                                ||||||||||  || |||
                                GACCGGTGTC  GT TGG
                                    T_  G
GAM603  KIAA1202  3'  GCCTGAATCCACCGTGGCTAGG 72490        A____    A
                                CCTGGCCAC    GTTCA GC
                                |||||||||    ||||| ||
                                GGATCGGTG    TAAGT CG
                                    CCACC    C
GAM603  KIAA1297  5'  GGCCCGGCTGCTGGCCAGG   72643        _    CAA
                                CCTGGCCA CAGTT   GCC
                                |||||||| |||||   |||
                                GGACCGGT GTCGG   CGG
                                    C    CC_
GAM603  KIAA1841  3'  GGCCTAAACTGTCAGGTA    80853      GCC     CAA
                                TACCTG   ACAGTT   GCC
                                ||||||   ||||||   |||
                                ATGGAC   TGTCAA   CGG
                                   ___     ATC
GAM603  KIAA1924  3'  GGCCTGGGGCACCGGCCAGGTG 74053        ACA   AA_
                                TACCTGGCC   GTTC   GCC
                                |||||||||   ||||   |||
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                              GTGGACCGG  CGGG  CGG
                                   CCA   GTC
GAM603  LNIR    3'  GGCTTGAACTGTTACAG    48874    GCC
                              CTG  ACAGTTCAAGCC
                              |||  ||||||||||||
                              GAC  TGTCAAGTTCGG
                                AT_
GAM603  MACF1   3'  GCTTGAACCTGGTAGGTG   53430      G  CA
                              TACCTG CCA  GTTCAAGC
                              |||||| |||  ||||||||
                              GTGGAT GGT  CAAGTTCG
                                 _  C_
GAM603  MCC2    3'  GGCCTGATGGGGTGTGGCCAGG 72527        G   A___
                              CCTGGCCACA TTCA   GCC
                              |||||||||| ||||   |||
                              GGACCGGTGT GGGT   CGG
                                    G   AGTC
GAM603  MGC11352 5'  GGCTCCTCTTGTGGCCATGTA  65434    C      TTCA
                              TAC TGGCCACAG   AGCC
                              ||| |||||||||   ||||
                              ATG ACCGGTGTT   TCGG
                                T       CTCC
GAM603  MGC16025 3'  GGCTCAGATCTGGCCAGGTG  53026        CA  CA
                              TACCTGGCCA  GTT  AGCC
                              ||||||||||  |||  ||||
                              GTGGACCGGT  TAG  TCGG
                                    C_  AC
GAM603  MGC23244 3'  GGCTTGAACCTGGGAGG    58835    GG  A  _
                              CCT  CC CAG TTCAAGCC
                              |||  || ||| ||||||||
                              GGA  GG GTC AAGTTCGG
                                __ _  C
GAM603  MGC2396  3'  GGCTTGAACCCTGGAGG    54560    GG  CA
                              CCT  CCA  GTTCAAGCC
                              |||  |||  |||||||||
                              GGA  GGT  CAAGTTCGG
                                __  CC
GAM603  MGC33630 5'  GGCTTGGGTGGCAACCAG    59004    ___   AGT
                              CTG  GCCAC  TCAAGCC
                              |||  |||||  |||||||
                              GAC  CGGTG  GGTTCGG
                                CAA   ___
GAM603  MYBPC3   3'  GGCTCCTGGGGATGGCCAGGTA 6031        CAG  __
                              TACCTGGCCA  TTCA  AGCC
                              ||||||||||  ||||  ||||
                              ATGGACCGGT  GGGT  TCGG
                                    AG_   CC
GAM603  MYO1G    5'  GGCCTGAGGCCATCGCCAGGTA 94305       CACA  _  A
                              TACCTGGC   GT TCA GCC
                              ||||||||   || ||| |||
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                                ATGGACCG   CG AGT CGG
                                    CTAC  G   C
GAM603  POFUT1   3'  GGCTTGAACCTGGGAGGTG   70979      GG  A  _
                                TACCT  CC CAG TTCAAGCC
                                ||||||  || ||| ||||||||
                                GTGGA  GG GTC AAGTTCGG
                                  __  _   C
GAM603  Rab11-FIP2 5'  GGCCTGCACGGCGCGGCCAGGT 30455         ACA__  T  A
          G                      TACCTGGCC    GT CA GCC
                                |||||||||     || || |||
                                GTGGACCGG    CA GT CGG
                                    CGCGG  C  C
GAM603  RES4-22  3'  GGCCTGGGCCGTGGCCAG    14917        A    A
                                CTGGCCAC GTTCA GCC
                                |||||||| ||||| |||
                                GACCGGTG CGGGT CGG
                                    C    C
GAM603  SEC24C   3'  GGCTTGATGGTGGCCAGG    18196        AGT
                                CCTGGCCAC   TCAAGCC
                                |||||||||   |||||||
                                GGACCGGTG   AGTTCGG
                                    GT_
GAM603  SLC26A9  3'  GCCTGGACAGTGGCCAGG    54717        A    A
                                CCTGGCCAC GTTCA GC
                                ||||||||| ||||| ||
                                GGACCGGTG CAGGT CG
                                    A    C
GAM603  SLC26A9  3'  GCCTGGACAGTGGCCAGG    54718        A    A
                                CCTGGCCAC GTTCA GC
                                ||||||||| ||||| ||
                                GGACCGGTG CAGGT CG
                                    A    C
GAM603  SSR3     3'  GGCCTGAGTGGCCAGG      24038        AGT  A
                                CCTGGCCAC   TCA GCC
                                |||||||||   ||| |||
                                GGACCGGTG   AGT CGG
                                    ___  C
GAM603  TBL1Y    5'  GGCTCAGAACACGGCCAGGTA  53862        ACA   A_
                                TACCTGGCC   GTTC  AGCC
                                |||||||||   ||||  ||||
                                ATGGACCGG   CAAG  TCGG
                                    CA_   AC
GAM603  TLK1     5'  GGCTCGGCGGCGGCGGCCAGGT 25435        ACA  __  A
                                ACCTGGCC   GT  TC AGCC
                                ||||||||   ||  || ||||
                                TGGACCGG   CG  GG TCGG
                                    CGG  GC  C
GAM603  ULK2     3'  GGCTTGTTGAGCCAGGTA    28689        CA   TT
                                TACCTGGC  CAG  CAAGCC
                                ||||||||  |||  ||||||
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                                ATGGACCG  GTT  GTTCGG
                                    A_  __
GAM603  LOC113444 3'  GGCTGCTCCTTGATGGCCAGG  57363       _  TTCA_
                                CCTGGCCA CAG    AGCC
                                |||||||| |||    ||||
                                GGACCGGT GTT    TCGG
                                    A  CCTCG
GAM603  LOC138389 3'  GGCTTGAACCCTGGAGG    76740    GG  CA
                                CCT  CCA  GTTCAAGCC
                                |||  |||  |||||||||
                                GGA  GGT  CAAGTTCGG
                                  __  CC
GAM603  LOC145098 5'  GGCATGCTTCTGTGGCCAG   77537        TT_  A
                                CTGGCCACAG   CA GCC
                                ||||||||||   || |||
                                GACCGGTGTC   GT CGG
                                     TTC  A
GAM603  LOC145601 3'  GGCCTGACACCCAGCAGCCAGG 84352       CACA__  _  A
          TG                     TACCTGGC     GT TCA GCC
                                |||||||||     || ||| |||
                                GTGGACCG     CA AGT CGG
                                    ACGACC  C   C
GAM603  LOC147004 3'  GCTCAACATGGCCAGGTG    84968        CA  CA
                                TACCTGGCCA  GTT  AGC
                                ||||||||||  |||  |||
                                GTGGACCGGT  CAA  TCG
                                     A_  C_
GAM603  LOC147515 3'  GGCTTCTATGGCCAGG     85151       C  TTC
                                CCTGGCCA AG   AAGCC
                                |||||||| ||   |||||
                                GGACCGGT TC   TTCGG
                                    A  ___
GAM603  LOC148413 3'  CTCAGGGTGGGTCAGGTA    79579        A  G  CA
                                TACCTGGCC CA TT  AG
                                ||||||||| || ||  ||
                                ATGGACTGG GT GG  TC
                                     _  G  AC
GAM603  LOC149466 3'  GGCTTAAAGGTTGGCCAGG   80197       _ AG  C
                                CCTGGCCA C  TT AAGCC
                                |||||||| |  || |||||
                                GGACCGGT G  AA TTCGG
                                    T GA  _
GAM603  LOC149995 3'  GGCTTCTATGGCCAGG     85986       C  TTC
                                CCTGGCCA AG   AAGCC
                                |||||||| ||   |||||
                                GGACCGGT TC   TTCGG
                                    A  ___
GAM603  LOC150935 5'  GGCTCAGCTGTGGCCGG    80833         CA
                                CTGGCCACAGTT  AGCC
                                ||||||||||||  ||||
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                                GGCCGGTGTCGA  TCGG
                                      C_
GAM603  LOC151102 3'  GGCCTGGGATCTGGCCAGG   86409       CAG   A
                                CCTGGCCA   TTCA GCC
                                ||||||||   |||| |||
                                GGACCGGT   GGGT CGG
                                     CTA   C
GAM603  LOC152271 3'  GGCTTGAAATGTCCAG     81362     CC  G
                                CTGG  ACA TTCAAGCC
                                ||||  ||| ||||||||
                                GACC  TGT AAGTTCGG
                                  __  A
GAM603  LOC152359 3'  GCACCTACTACGTGCCAGGTA 86883       C __  TCAA
                                TACCTGGC AC  AGT   GC
                                |||||||| ||  |||   ||
                                ATGGACCG TG  TCA   CG
                                     _ CA   TCCA
GAM603  LOC152804 3'  GGCTTGAACCTGGGAGG    87085    GG  A  _
                                CCT  CC CAG TTCAAGCC
                                |||  || ||| ||||||||
                                GGA  GG GTC AAGTTCGG
                                  __ _  C
GAM603  LOC155036 3'  GCTTGTCGGTGGCCGGTA   87614     T    AGTT
                                TACC GGCCAC   CAAGC
                                |||| ||||||   |||||
                                ATGG CCGGTG   GTTCG
                                  _     GCT_
GAM603  LOC158125 5'  GACTGTCAAGGCCAGGTA   82619        ___
                                TACCTGGCC   ACAGTT
                                |||||||||   ||||||
                                ATGGACCGG   TGTCAG
                                     AAC
GAM603  LOC161356 5'  GCTGGAGACGTGGCCAGG   83144        AG   A
                                CCTGGCCAC  TTC AGC
                                |||||||||  ||| |||
                                GGACCGGTG  GAG TCG
                                     CA   G
GAM603  LOC197135 3'  GGTTCCCTGGGCCAGGTA   89238        A   TTCA
                                TACCTGGCC CAG   AGCC
                                ||||||||| |||   ||||
                                ATGGACCGG GTC   TTGG
                                     _  CC__
GAM603  LOC197320 3'  CTTGAGGAATGTGGCTAGG   89307        GT__
                                CCTGGCCACA   TCAAG
                                ||||||||||   |||||
                                GGATCGGTGT   AGTTC
                                     AAGG
GAM603  LOC200492 3'  GTGTGTCTGTGGCCAGGT   91654         TT  A
                                ACCTGGCCACAG  CA GC
                                ||||||||||||  || ||
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                                TGGACCGGTGTC  GT TG
                                      T_  G
GAM603  LOC220522 3'  GGCCAGGACGGCCAGGT     61143        ACA    AA
                                ACCTGGCC   GTTC  GCC
                                ||||||||   ||||  |||
                                TGGACCGG   CAGG  CGG
                                   ___    AC
GAM603  LOC220930 3'  GGCCAAACTGTGGACAAGTA   94751     C  G      CAA
                                TAC TG CCACAGTT   GCC
                                ||| || ||||||||   |||
                                ATG AC GGTGTCAA   CGG
                                  A  A       AC_
GAM603  LOC220980 3'  CTAGAATTGGCTAGGTA     94768          CA    A
                                TACCTGGCCA  GTTC AG
                                ||||||||||  |||| ||
                                ATGGATCGGT  TAAG TC
                                   __    A
GAM603  LOC221296 3'  GGCTAGAGGCATGGGCCAGGTA 93611          A  _  _  A
                                TACCTGGCC CA GT TC AGCC
                                ||||||||| || || || ||||
                                ATGGACCGG GT CG AG TCGG
                                   _  A  G  A
GAM603  LOC221865 3'  GGCTTGCAGTGTGGCCAGG    94089          GTT
                                CCTGGCCACA   CAAGCC
                                ||||||||||   ||||||
                                GGACCGGTGT   GTTCGG
                                     GAC
GAM603  LOC222968 5'  GGCCCTCTGGTGGCCAGGTG   94459           _  TTCAA
                                TACCTGGCCAC AG    GCC
                                |||||||||||  ||    |||
                                GTGGACCGGTG TC    CGG
                                     G  TCC__
GAM603  LOC253196 3'  GGCTTGGAGGTGGCCAGG    98670         AG
                                CCTGGCCAC  TTCAAGCC
                                |||||||||  ||||||||
                                GGACCGGTG  AGGTTCGG
                                   G_
GAM603  LOC253891 3'  GGCTCCTGACAGTGGCCAGG   96069         A   CA_
                                CCTGGCCAC GTT   AGCC
                                |||||||||  |||   ||||
                                GGACCGGTG CAG   TCGG
                                     A   TCC
GAM603  LOC256594 5'  GGCTTGAAATGTCCAG      98864      CC   G
                                CTGG  ACA TTCAAGCC
                                ||||  ||| ||||||||
                                GACC  TGT AAGTTCGG
                                  __   A
GAM603  LOC90198  5'  GGCCTGAACTGTGGGTGG    62448     G         A
                                CTG CCACAGTTCA GCC
                                ||| ||||||||||  |||
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                                GGT GGTGTCAAGT CGG
                                  G        C
GAM603  LOC91266  5'  GGCTCAATGAGCAGCCAGGTA  66023        CACA    ___
                                TACCTGGC   GTTCA   AGCC
                                ||||||||   |||||  ||||
                                ATGGACCG   CGAGT   TCGG
                                    A___    AAC
GAM603  LOC91355  5'  GGCTGGTGTGTGGCCAGG    66308         GT   A
                                CCTGGCCACA  TCA GCC
                                ||||||||||  ||| |||
                                GGACCGGTGT  GGT CGG
                                     GT   _
GAM603  LOC92249  5'  GGCTTAGATCTTGTGGCCA    69109         T_ _
                                TGGCCACAG  TC AAGCC
                                |||||||||  || |||||
                                ACCGGTGTT  AG TTCGG
                                     CT  A
GAM604  ARHH     5'  CTGAAGCCGTGGAGAACGC    16300     CTGCCGG
                                GCG      CCGCGGCTTCAG
                                |||      ||||||||||||
                                CGC      GGTGCCGAAGTC
                                  AAGA___
GAM604  CSK      3'  GGCCACGGAGCGGGCGGCAGCG 16507         G   GG  TCA
          C                      GCGCTGCCG CCGC  CT   GCC
                                |||||||| ||||  ||   |||
                                CGCGACGGC GGCG  GG   CGG
                                     G   A_  CAC
GAM604  CSRP1    3'  GGCTGCGGCCAGCAGAGC    15815    G   C
                                GC CTGC GGCCGCGGCT
                                || |||| ||||||||||
                                CG GACG CCGGCGTCGG
                                 A   A
GAM604  DNMT3B   5'  GCTGCCCGGCCGGCAGCGC    23549          C   TTC
                                GCGCTGCCGGCCG GGC   AGC
                                |||||||||||| |||   |||
                                CGCGACGGCCGGC CCG   TCG
                                          _  ___
GAM604  EDNRA    5'  GCCGAAGCCGCCGCCGCGC    64801     TGCC   C      A
                                GCGC    GGC GCGGCTTC GC
                                ||||    ||| ||||||||  ||
                                CGCG    CCG CGCCGAAG CG
                                  ____   C       C
GAM604  FGFR2    5'  CTGCAGCAGCAGCGGCAGCGC  43634         G C  G   T
                                GCGCTGCCG C GC GCT CAG
                                ||||||||| | || ||| |||
                                CGCGACGGC G CG CGA GTC
                                     _ A  A   C
GAM604  FGFR2    5'  CTGCAGCAGCAGCGGCAGCGC  43639         G C  G   T
                                GCGCTGCCG C GC GCT CAG
                                ||||||||| | || ||| |||
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                                CGCGACGGC G CG CGA GTC
                                     _ A  A   C
GAM604   FGFR2    5'  CTGCAGCAGCAGCGGCAGCGC  43643        G C  G   T
                                GCGCTGCCG C GC GCT CAG
                                |||||||||  |  ||  |||  |||
                                CGCGACGGC G CG CGA GTC
                                     _ A  A   C
GAM604   FGFR2    5'  CTGCAGCAGCAGCGGCAGCGC  43653        G C  G   T
                                GCGCTGCCG C GC GCT CAG
                                |||||||||  |  ||  |||  |||
                                CGCGACGGC G CG CGA GTC
                                     _ A  A   C
GAM604   FGFR2    5'  CTGCAGCAGCAGCGGCAGCGC  43666        G C  G   T
                                GCGCTGCCG C GC GCT CAG
                                |||||||||  |  ||  |||  |||
                                CGCGACGGC G CG CGA GTC
                                     _ A  A   C
GAM604   FGFR2    5'  CTGCAGCAGCAGCGGCAGCGC  43675        G C  G   T
                                GCGCTGCCG C GC GCT CAG
                                |||||||||  |  ||  |||  |||
                                CGCGACGGC G CG CGA GTC
                                     _ A  A   C
GAM604   FGFR2    5'  CTGCAGCAGCAGCGGCAGCGC  43764        G C  G   T
                                GCGCTGCCG C GC GCT CAG
                                |||||||||  |  ||  |||  |||
                                CGCGACGGC G CG CGA GTC
                                     _ A  A   C
GAM604   FGFR2    5'  CTGCAGCAGCAGCGGCAGCGC  5560         G C  G   T
                                GCGCTGCCG C GC GCT CAG
                                |||||||||  |  ||  |||  |||
                                CGCGACGGC G CG CGA GTC
                                     _ A  A   C
GAM604   GYG      5'  GGCCGCCTGCGCACCCGGCAGC 15948        C__  _   TTCA
                                GCTGCCGG   CGC GGC   GCC
                                ||||||||   |||  |||   |||
                                CGACGGCC   GCG CCG   CGG
                                     CAC   T   C___
GAM604   HOXA3    3'  GGCCGAGGCGAGCCGGCAGAGC 48402    G      CG  G   A
                                GC CTGCCGGC  CG CTTC GCC
                                ||  ||||||||  ||  ||||  |||
                                CG GACGGCCG  GC GGAG CGG
                                 A       A_  _   C
GAM604   IRS1     5'  CTCAGCCAACTGCAGCGGCAGC 19876         G C C________   TTCA
            GC                    GCGCTGCCG C G       GGC   G
                                |||||||||  |  |       |||   |
                                CGCGACGGC G C       CCG   C
                                     _ A GTCAA___   ACTT
GAM604   JAG2     5'  GGCCGGGCAGCCGGAGCGC   11097      G    C  __
                                GCGCT CCGGC GC  GGCT
                                |||||  |||||  ||  ||||
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                                CGCGA GGCCG CG  CCGG
                                  _    A  GG
GAM604  KCNF1    5'  GCTGAAGCGGCGGAGCGC    11145      GCCGG   G
                                GCGCT    CCGC GCTTCAGC
                                |||||    |||| ||||||||
                                CGCGA    GGCG CGAAGTCG
                                  _____   G
GAM604  LAMC3    5'  GCCGAGCGGGGCCGGCAGAGC  21345    G       G  G   CA
                                GC CTGCCGGCC CG CTT  GC
                                || |||||||| || |||  ||
                                CG GACGGCCGG GC GAG  CG
                                 A       G  _  C_
GAM604  LMNA     5'  GCTTCAGCCAGCCAGCCGGCCG 19931       _    C_ C____   TTCA
           GCGC                  GCGCTG CCGGC  G    GGC   GC
                                |||||| |||||  |    |||   ||
                                CGCGGC GGCCG  C    CCG   CG
                                   C    AC GA___   ACTT
GAM604  MAP4K5   5'  AGCTGCCGGCCGGCGCGC    22695     T      _
                                GCGC GCCGGCCG CGGCT
                                |||| |||||||| |||||
                                CGCG CGGCCGGC GTCGA
                                  _       C
GAM604  NOS1     5'  GCTGAAGCCTTGTCAGC     7096      C   CCGC
                                GCTG CGG    GGCTTCAGC
                                |||| |||    |||||||||
                                CGAC GTT    CCGAAGTCG
                                  T  _____
GAM604  PFN1     5'  AGCCGCGGTCCGGACGGCAGCG 18473          _____
           C                     GCGCTGCCG    GCCGCGGCT
                                |||||||||    |||||||||
                                CGCGACGGC    TGGCGCCGA
                                     AGGCC
GAM604  TOP3A    5'  CTGAAGCTCCAAAGGCCAGCAG 17259    G   C   GC___
           GC                    GC CTGC GGCC    GGCTTCAG
                                || |||| ||||    ||||||||
                                CG GACG CCGG    TCGAAGTC
                                 _   A   AAACC
GAM604  WW45     5'  CTGAGCGGCGGCCGGCGCGC   41812     T      G   T
                                GCGC GCCGGCCGC GCT CAG
                                |||| |||||||| ||| |||
                                CGCG CGGCCGGCG CGA GTC
                                  _       G  _
GAM604  13CDNA73 5'  GCTGGTGGGCGGCCGGCAGC   43788          GGCT
                                GCTGCCGGCCGC   TCAGC
                                ||||||||||||   |||||
                                CGACGGCCGGCG   GGTCG
                                       GGT_
GAM604  CAM-KIIN 3'  GCCTCGCAGCGGCCAGGAGCGC 53834      G  _    G  TTCA
                                GCGCT CC GGCCGC GC   GC
                                ||||| || |||||| ||   ||
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                                CGCGA GG CCGGCG CG    CG
                                  _ A     A  CTC_
GAM604  DKFZP564O0423 3'  GCTGAGGCAGCAGCCAGCAGGC 93354    G    C   C  G
                                GC CTGC GGC GC GCTTCAGC
                                || |||| ||| || ||||||||
                                CG GACG CCG CG CGGAGTCG
                                 _   A  A  A
GAM604  DRF1     5'  CTGAAGCCGCGGCCGAAAACGC 47747     CTGC
                                GCG   CGGCCGCGGCTTCAG
                                |||   ||||||||||||||
                                CGC   GCCGGCGCCGAAGTC
                                  AAAA
GAM604  FLJ10300  5'  GCTTCAGCCGACACGCGACCGG 36472        C   _________  TTCA
           CAGC                   GCTGCCGG CGCG      GC   GC
                                |||||||| ||||       ||   ||
                                CGACGGCC GCGC      CG   CG
                                     A   ACAG___C  ACTT
GAM604  HH114    3'  GCTGAAGCCACAAAGTCCAAAG 51669     GCC   CGC__
           C                    GCT   GGC    GGCTTCAGC
                                |||   |||    |||||||||
                                CGA   CTG    CCGAAGTCG
                                  AAC   AAACA
GAM604  HSRNAFEV  5'  GGCCGAGGCGGCAGCGC     34451         G  G
                                GCGCTGCCG CC CGGCT
                                ||||||||| || |||||
                                CGCGACGGC GG GCCGG
                                     _ A
GAM604  IL-17RE   3'  GGCTGAACTGCTACGGGCAGCG 58940        GGCC   C
           C                    GCGCTGCC   GCGG TTCAGCC
                                ||||||||   |||| |||||||
                                CGCGACGG   CGTC AAGTCGG
                                    GCAT   _
GAM604  KIAA0014  3'  GGCTGCTGGGCAGCCGGCGGCG 28542          C  GG  T_
           C                    GCGCTGCCGGC GC  CT  CAGCC
                                |||||||||| ||  ||  |||||
                                CGCGGCGGCCG CG  GG  GTCGG
                                      A  __  TC
GAM604  KIAA0237  5'  GGCTGCTGCGGAGCCGGCAGCG 29228          __     TTC
           C                    GCGCTGCCGGC  CGCGGC   AGCC
                                ||||||||||  ||||||   ||||
                                CGCGACGGCCG  GCGTCG   TCGG
                                      AG     ___
GAM604  KIAA0557  5'  CTGCCCACGGCCGGCAGCGC   78557          C  CTT
                                GCGCTGCCGGCCG GG   CAG
                                |||||||||||| ||   |||
                                CGCGACGGCCGGC CC   GTC
                                      A  C__
GAM604  KIAA1579  5'  GGCTGAAGAGGTCCAGCAGGC  37151    G   C  _  GCGG
                                GC CTGC GG CC    CTTCAGCC
                                || |||| || ||    ||||||||
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                                CG GACG CC GG   GAAGTCGG
                                 _   A  T  A___
GAM604  MGC10870  5'  GCTTCAGCCGACGCGAGGCCGG 51179          __  ______  TTCA
            CAGCGC                GCGCTGCCGGCC  GCG    GC   GC
                                ||||||||||||  |||    ||   ||
                                CGCGACGGCCGG  CGC    CG   CG
                                      AG   AG___C  ACTT
GAM604  MIC2L1   3'  GGCTGAAGGGGGACCTGCAGC  49602     C  _  GCGG
                                GCTGC GG CC   CTTCAGCC
                                ||||| || ||   ||||||||
                                CGACG CC GG   GAAGTCGG
                                   T  A  GG__
GAM604  NBR2     3'  GGCACACCGCGGCCAGCAGGC  20620   G   C     CTTCA
                                GC CTGC GGCCGCGG    GCC
                                || |||| ||||||||    |||
                                CG GACG CCGGCGCC    CGG
                                 _   A      ACA__
GAM604  OPN4     3'  GCTGAAGCCGAGCACAG    53853    CCG  CG
                                CTG   GC  CGGCTTCAGC
                                |||   ||  ||||||||||
                                GAC   CG  GCCGAAGTCG
                                  A__  A_
GAM604  SCYB11   5'  GCTGAAGTAGCAGCAGCAGC   88836     CG  C  G
                                GCTGC  GC GC GCTTCAGC
                                |||||  || || ||||||||
                                CGACG  CG CG TGAAGTCG
                                   A_  A  A
GAM604  LOC126031 5'  AGCTTGGGGCCAGCAGCGC   74901      C   G _
                                GCGCTGC GGCC C GGCT
                                ||||||| |||| | ||||
                                CGCGACG CCGG G TCGA
                                    A   G T
GAM604  LOC148887 3'  GGCTGAAGCCGCCCACTCAGC  85406    CC_  CC
                                GCTG   GG  GCGGCTTCAGCC
                                ||||   ||  ||||||||||||
                                CGAC   CC  CGCCGAAGTCGG
                                  TCA  __
GAM604  LOC150155 5'  GGCTGCAACCGCCAGCGC    71415      C   CC
                                GCGCTG CGG  GCGGCT
                                ||||||  |||  ||||||
                                CGCGAC GCC  CGTCGG
                                   C   AA
GAM604  LOC152441 5'  GCCACTCTGCAGCCGGCAGGC  86918    G     C   CTTCA
                                GC CTGCCGGC GCGG    GC
                                || ||||||||  ||||    ||
                                CG GACGGCCG CGTC    CG
                                 _      A   TCAC_
GAM604  LOC158170 5'  GGCTGCAGCGGCCGGCA     82657        GGCTT
                                TGCCGGCCGC    CAGCC
                                ||||||||||    |||||
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                                ACGGCCGGCG    GTCGG
                                     AC___
GAM604  LOC163412 5'  GGCCGAAGTTGCTCCACAGC   83017     CC  CC      A
                                GCTG  GG  GCGGCTTC GCC
                                ||||  ||  |||||||| |||
                                CGAC  CC  CGTTGAAG CGG
                                  A_  T_      C
GAM604  LOC164537 5'  GGCCTCGCAGACGGCAGCGC   88576        GC__  C
                                GCGCTGCCG   CG GGCT
                                |||||||||   || ||||
                                CGCGACGGC   GC CCGG
                                     AGAC  T
GAM604  LOC165476 5'  GCTGAAGTTCCTACAGC     88553     CC  CCGC
                                GCTG  GG   GGCTTCAGC
                                ||||  ||   |||||||||
                                CGAC  CC   TTGAAGTCG
                                  AT  _____
GAM604  LOC200488 5'  CTGAAGCCCTCTGACAGC    91650     C   CCGC
                                GCTG CGG   GGCTTCAG
                                |||| |||   ||||||||
                                CGAC GTC   CCGAAGTC
                                  A  TC__
GAM604  LOC200597 3'  GCTGGAGCAGCGGCAGCA    90257     CG    G
                                TGC  GCCGC GCTTCAGC
                                |||  ||||| ||||||||
                                ACG  CGGCG CGAGGTCG
                                  A_    A
GAM604  LOC203429 3'  GGCTGAAGCAAGCATCAGC   90931      CCG  CGCG
                                GCTG   GC   GCTTCAGCC
                                ||||   ||   |||||||||
                                CGAC   CG   CGAAGTCGG
                                  TA_  AA__
GAM604  LOC219333 5'  GGCCGGCGGCCGGCAGGC    95186    G        _
                                GC CTGCCGGCCGC GGCT
                                || ||||||||||| ||||
                                CG GACGGCCGGCG CCGG
                                 _         G
GAM604  LOC221576 3'  GGCTGAAGCCTCTGCCGGCGCG 95321      T     CGC
          C                      GCGC GCCGGC   GGCTTCAGCC
                                |||| ||||||   ||||||||||
                                CGCG CGGCCG   CCGAAGTCGG
                                  _     TCT
GAM604  LOC222193 5'  GCTGCAGCCGCCGGCAGC    95844        CGC   T
                                GCTGCCGGC   GGCT CAGC
                                |||||||||   |||| ||||
                                CGACGGCCG   CCGA GTCG
                                     ___    C
GAM604  LOC254263 5'  GGCCCGGGCAGCCGGCAGCG   96368         C  ___
                                CGCTGCCGGC GC   GGCT
                                |||||||||| ||   ||||
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                                GCGACGGCCG CG   CCGG
                                     A  GGC
GAM604  LOC257515 3'  GGCTGAAGCCTCTGCCGGCGCG 99621     T     CGC
          C                   GCGC GCCGGC   GGCTTCAGCC
                              |||| ||||||   ||||||||||
                              CGCG CGGCCG   CCGAAGTCGG
                                _     TCT
GAM604  LOC257572 3'  GGCTGAAGCCTCTGCCGGCGCG 99741     T     CGC
          C                   GCGC GCCGGC   GGCTTCAGCC
                              |||| ||||||   ||||||||||
                              CGCG CGGCCG   CCGAAGTCGG
                                _     TCT
GAM604  LOC51207  5'  GCTGAAAGCCGGCAGC      33474         CGCGGC
                              GCTGCCGGC     TTCAGC
                              |||||||||     ||||||
                              CGACGGCCG     AAGTCG
                                   A_____
GAM604  LOC91661  3'  GCTGACAGCGGCCAACAGGC   57214    G   CC     GGCT
                              GC CTG  GGCCGC    TCAGC
                              || |||  ||||||    |||||
                              CG GAC  CCGGCG    AGTCG
                               _  AA     AC__
GAM605  LOC155036 5'  TGGACACGGAGACCAGGA    87616    G  A       AT GC
                              TC CT GTCTCCGT  G  CCG
                              || || ||||||||  |  |||
                              AG GA CAGAGGCA  C  GGT
                               _ C       __ A_
GAM606  COL19A1   3'  CAGACCAAAGAGTTCACA    10261     T   C      C
                              TGT GAGC TTTTTGG CTG
                              ||| |||| ||||||| |||
                              ACA CTTG AGAAACC GAC
                                _   _      A
GAM606  RRM2B     3'  CAAAAACTTAACATTTA     68431          CC
                              TAAATGTTGAG  TTTTTG
                              ||||||||||  ||||||
                              ATTTACAATTC  AAAAAC
                                           __
GAM606  TCF2      3'  CAGGCTGGAGCCCAGCATT   22402        A  CTT  TG
                              AATGTTG GC   TT  GCCTG
                              ||||||| ||   ||  |||||
                              TTACGAC CG   AG  CGGAC
                                  C  ___  GT
GAM606  BY55      3'  AGACAGACCTCAACATT     60061         CCTT   GC
                              AATGTTGAG    TTTG  CT
                              |||||||||    ||||  ||
                              TTACAACTC    AGAC  GA
                                   C___    A_
GAM606  C8orf2    3'  CAAGTCAGGCTGAACATT    24145       G    T_
                              AATGTT AGCCT  TTTG
                              |||||| |||||  ||||
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                                TTACAA TCGGA  GAAC
                                   G    CT
GAM606  FLJ13409  3'  CAGGCTTCAACTTAACATTTA  45194          CCTTTTT
                                TAAATGTTGAG      GGCCTG
                                ||||||||||       ||||||
                                ATTTACAATTC      TCGGAC
                                      AACT___
GAM606  FLJ22774  3'  CTAAAAAGGCTGAACATTTA   64471         G
                                TAAATGTT AGCCTTTTTGG
                                |||||||| ||||||||||
                                ATTTACAA TCGGAAAAATC
                                     G
GAM606  HSOBRGRP  3'  CAGACCAAGAGCCTCAACATTT 34462          C    T  C
                                AAATGTTGAG CTTTT GG CTG
                                |||||||||| ||||| || |||
                                TTTACAACTC GAGAA CC GAC
                                      C    _  A
GAM606  KIAA0435  3'  GCTAGAACTCAGCATT      29661          CCT
                                AATGTTGAG   TTTTGGC
                                |||||||||   |||||||
                                TTACGACTC   AAGATCG
                                     ___
GAM606  MGC10940  3'  CAAAAAGTAAAAAAAGCTCAAC 51183         _________
           A                     TGTTGAGC       CTTTTTG
                                 ||||||||       |||||||
                                 ACAACTCG       GAAAAAC
                                      AAAAAAAT
GAM606  ZIN      3'  CAGGCCAGGGATTGCCCAACA  26391       A  C_
                                TGTTG GC  TTTTTGGCCTG
                                ||||| ||  ||||||||||
                                ACAAC CG  AGGGACCGGAC
                                   C  TT
GAM606  LOC256158 5'  CAGGCCACTGGAGAGCCCACA  99482     T A  _    T_
                                TGT G GC CTTT  TGGCCTG
                                ||| | || ||||  |||||||
                                ACA C CG GAGG  ACCGGAC
                                  _ C  A    TC
GAM607  ASC      5'  GCCTGGGGCCCCAATCCA    26069    A        GA  T
                                TG GATTGGGGCC  CG GC
                                || ||||||||||  || ||
                                AC CTAACCCCGG  GT CG
                                  _         G_  C
GAM607  MECP2    3'  GCCCCACACCAGCCCCAATCCA 18404    A        CGAC   CAA
                                TG GATTGGGGC    GTG   GC
                                || |||||||||    |||   ||
                                AC CTAACCCCG    CAC   CG
                                  _        ACCA   CC_
GAM607  PTPRM    3'  GCTTGCACTGCCCAATCCCA   12621    A      G CGAC
                                TG GATTGGG C    GTGCAAGC
                                || ||||||| |    ||||||||
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                                AC CTAACCC G    CACGTTCG
                                 C      _ T___
GAM607  RET     3'  GCCTCAGCCCCAGTCCCA    40548    A       C  CGT
                                TG GATTGGGGC GA   GC
                                || ||||||||| ||   ||
                                AC CTGACCCCG CT   CG
                                 C       A  C__
GAM607  SH3BP2  3'  CTTGCCCTGTCCCAATCCCA  13069    A       CGACGT
                                TG GATTGGGGC     GCAAG
                                || |||||||||     |||||
                                AC CTAACCCTG     CGTTC
                                 C       TCC___
GAM607  SH3BP2  3'  GCTCAGGCCCAGCCCCAATCCA 13076    A       CGAC  GCA
                                TG GATTGGGGC    GT   AGC
                                || |||||||||    ||   |||
                                AC CTAACCCCG    CG   TCG
                                 _       ACC_  GAC
GAM607  FLJ23516 5' GCTCGCAGCTCCCCAGTCTCA  44887          CCGACG   A
                                TGAGATTGGGG     TGC AGC
                                ||||||||||      ||| |||
                                ACTCTGACCCC     ACG TCG
                                       TCG___   C
GAM607  JM11    3'  TGCACCCAGCCCCAATCCA   54374    A       CGAC
                                TG GATTGGGGC    GTGCA
                                || |||||||||    |||||
                                AC CTAACCCCG    CACGT
                                 _       ACC_
GAM607  KIAA0172 5' ACATCAACTCCAATCTCA    65591          CC  C
                                TGAGATTGGGG  GA GT
                                ||||||||||  || ||
                                ACTCTAACCTC  CT CA
                                       AA  A
GAM607  KIAA0557 3' GCCTGCTGCTTGGCCCCATCTC 78567       T      C  _   A
           A                     TGAGAT GGGGCCGA GT GCA GC
                                ||||||| |||||||| || ||| ||
                                ACTCTA CCCCGGTT CG CGT CG
                                   _       _ T   C
GAM607  KIAA1402 3' GCCTGGGGGCCCTAACCTCA   66992     A      GA  T
                                TGAG TTGGGGCC  CG GC
                                |||| ||||||||  || ||
                                ACTC AATCCCGG  GT CG
                                  C       GG  C
GAM607  PI4KII  3'  CTGCCTGCCCCAATCCCA    37950    A       CGACGT   A
                                TG GATTGGGGC     GCA G
                                || |||||||||     ||| |
                                AC CTAACCCCG     CGT C
                                 C       TC_____  C
GAM607  PPY2    3'  GCCCCATCTCCAGCCCCAGTCC 41174    A       C_  C   CAA
           CA                     TG GATTGGGGC  GA GTG   GC
                                || |||||||||  || |||   ||
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                                AC CTGACCCCG  CT TAC   CG
                                 C       AC  C   CC_
GAM607  YAP      5'  TGCAACCCCAATCTCA     58207          CCGACG
                                TGAGATTGGGG     TGCA
                                ||||||||||     ||||
                                ACTCTAACCCC     ACGT
                                      A_____
GAM607  LOC157280 3'  GCCTAGGCTCCAATCTCA    74345           GACGT
                                TGAGATTGGGGCC    GC
                                ||||||||||||    ||
                                ACTCTAACCTCGG    CG
                                      ATC__
GAM607  LOC255448 3'  GCCTAGGCTCCAATCTCA    96305           GACGT
                                TGAGATTGGGGCC    GC
                                ||||||||||||    ||
                                ACTCTAACCTCGG    CG
                                      ATC__
GAM608  ABCB4    5'  GAATAGACTGAGAAGTCCAA   6532        AC
                                TTGGAT  TTTAGTCTATTC
                                ||||||  ||||||||||||
                                AACCTG  GAGTCAGATAAG
                                   AA
GAM608  ABCB4    5'  GAATAGACTGAGAAGTCCAA   38759       AC
                                TTGGAT  TTTAGTCTATTC
                                ||||||  ||||||||||||
                                AACCTG  GAGTCAGATAAG
                                   AA
GAM608  MLLT2    3'  GAATGGGAAAAGTATCTAA   21030          AG
                                TTGGATACTTT  TCTATTC
                                ||||||||||  |||||||
                                AATCTATGAAA  GGGTAAG
                                      A_
GAM608  TSN      3'  GAATAATATGAAGTATCTAA  17300          GTC
                                TTGGATACTTTA   TATTC
                                ||||||||||||   |||||
                                AATCTATGAAGT   ATAAG
                                      ATA
GAM608  FLJ10283  3'  AATAGACTAAAGTTCACAG   36428     GAT
                                TTG   ACTTTAGTCTATT
                                |||   |||||||||||||
                                GAC   TGAAATCAGATAA
                                  ACT
GAM608  FLJ10830  3'  GAACAGACACAAGTGTATCCAG 37265         TTTA__    A
                                TTGGATAC     GTCT TTC
                                ||||||||     |||| |||
                                GACCTATG     CAGA AAG
                                     TGAACA    C
GAM608  FLJ11218  3'  AATAGACTAAATCTA      37755       ACT
                                TGGAT   TTAGTCTATT
                                |||||   ||||||||||
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                                ATCTA   AATCAGATAA
                                  ___
GAM608  FLJ20452  3'  GAATGGAAAAAGTATTCAA   35649          AG
                                TTGGATACTTT  TCTATTC
                                ||||||||||  |||||||
                                AACTTATGAAA  AGGTAAG
                                      A_
GAM608  KIAA1016  5'  AGACTGGTTGAAGTTCCAA   93380      T    ____
                                TTGGA ACTTT    AGTCT
                                ||||| |||||    |||||
                                AACCT TGAAG    TCAGA
                                   _    TTGG
GAM608  KIAA1023  3'  GAAGAGACTAAAATAGCCAA   34680     A  C      A
                                TTGG TA TTTAGTCT TTC
                                |||| || |||||||| |||
                                AACC AT AAATCAGA AAG
                                  G  A       G
GAM608  SLC2A12   3'  GAATAGACTATGTCC       59738      CTT
                                GGATA   TAGTCTATTC
                                |||||   ||||||||||
                                CCTGT   ATCAGATAAG
                                  ___
GAM608  LOC151126 3'  AATAACTCTGGTATCCAA    80935        TT   C
                                TTGGATACT  AGT TATT
                                |||||||||  ||| ||||
                                AACCTATGG  TCA ATAA
                                      TC  _
GAM608  LOC155179 3'  GAAGAGACTAAAATAGCCAA   82230     A  C      A
                                TTGG TA TTTAGTCT TTC
                                |||| || |||||||| |||
                                AACC AT AAATCAGA AAG
                                  G  A       G
GAM608  LOC166867 5'  AATAGATTGCTTGATCCAA    83552       ACTT
                                TTGGAT    TAGTCTATT
                                ||||||    |||||||||
                                AACCTA    GTTAGATAA
                                   GTTC
GAM609  CACNA1C   3'  ACAGCGTCTTCATTCA      7396         TCCT  A
                                TGAATGGAG    GC CTGT
                                |||||||||    || ||||
                                ACTTACTTC    TG GACA
                                      ____  C
GAM609  CHAC      3'  ACAATGCCTACTTTCCATTCA  53952        TCCT_  C
                                TGAATGGAG     GCA TGT
                                |||||||||     ||| |||
                                ACTTACCTT     CGT ACA
                                      TCATC   A
GAM609  IRAK4     3'  GACAGAGTGAGACTCCATCA   61844     A      CT  A
                                TGA TGGAGTC  GC CTGTC
                                |||  |||||||  ||  |||||
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                                ACT ACCTCAG  TG GACAG
                                  _     AG  A
GAM609  LETM1    3'  GACCACGTGGACTCCGCCCA  25554    AA      T  ACT
                                TG  TGGAGTCC GC   GTC
                                ||  |||||||| ||   |||
                                AC  GCCTCAGG TG   CAG
                                 CC       _  CAC
GAM609  MS4A2    3'  GACAATACAGAACCCATTC   41976      A  C   CAC
                                GAATGG GT CTG   TGTC
                                |||||| || |||   ||||
                                CTTACC CA GAC   ACAG
                                   _ A   ATA
GAM609  NOVA1    3'  GACAGTCATTACTCCATT    11817       CC  C
                                AATGGAGT  TG ACTGTC
                                ||||||||  || ||||||
                                TTACCTCA  AC TGACAG
                                     TT  _
GAM609  NOVA1    3'  GACAGTCATTACTCCATT    22420       CC  C
                                AATGGAGT  TG ACTGTC
                                ||||||||  || ||||||
                                TTACCTCA  AC TGACAG
                                     TT  _
GAM609  SERPINB9 3'  ACAGTAAAAATTCCATTCA   16004         CCTGC
                                TGAATGGAGT    ACTGT
                                ||||||||||    |||||
                                ACTTACCTTA    TGACA
                                     AAAA_
GAM609  SLC19A2  3'  ACAGCATCTGCCTCTATTCA  69548        TCCT  ____
                                TGAATGGAG   GCA   CTGT
                                |||||||||   |||   ||||
                                ACTTATCTC   CGT   GACA
                                     ____  CTAC
GAM609  SORBS1   3'  GACAGTGCAGCTGCATTTA   31804      G  TC
                                TGAATG AG  CTGCACTGTC
                                ||||||  ||  ||||||||||
                                ATTTAC TC  GACGTGACAG
                                   G  __
GAM609  TCF15    3'  GCTGTGAGGATCCATTCA    17233       G   G   T
                                TGAATGGA TCCT CAC GT
                                |||||||| |||| ||| ||
                                ACTTACCT AGGA GTG CG
                                     _   _  T
GAM609  AKR1B10  5'  ACAGTGCAAGACTGTCTCA   40076    ATGG   C
                                TGA   AGTC TGCACTGT
                                |||   |||| ||||||||
                                ACT   TCAG ACGTGACA
                                  CTG_   A
GAM609  ARNTL2   3'  GACAGTGCAATTTATAGTCA  39849    ATG_   CC
                                TGA   GAGT  TGCACTGTC
                                |||   ||||  |||||||||
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                                ACT   TTTA  ACGTGACAG
                                  GATA   __
GAM609  BCL2L12  5' ACACAGAACTTCCATTCA    57640       _  C   CAC
                                TGAATGGA GT CTG   TGT
                                |||||||| || |||   |||
                                ACTTACCT CA GAC   ACA
                                     T  A  ____
GAM609  FLJ10898 5' GACACCGGACTCCATTC     60134         TGCAC
                                GAATGGAGTCC    TGTC
                                ||||||||||     ||||
                                CTTACCTCAGG    ACAG
                                      CC___
GAM609  FLJ10932 3' GACAGTGCCTTTCCATCCG   37427    A     TCCT
                                TG ATGGAG   GCACTGTC
                                || ||||||   ||||||||
                                GC TACCTT   CGTGACAG
                                 C     TC__
GAM609  FLJ11726 3' GACCTTTGAGGTCTCCATTCA 47021        T   G  CT_
                                TGAATGGAG CCT CA   GTC
                                ||||||||| ||| ||   |||
                                ACTTACCTC GGA GT   CAG
                                     T   _  TTC
GAM609  FLJ12800 3' GACAGTAGGCCCCATGCA    43529    A   A T   GC
                                TG ATGG G CCT  ACTGTC
                                || |||| | |||  ||||||
                                AC TACC C GGA  TGACAG
                                 G   C _  __
GAM609  FLJ12891 3' ACAGTGCAGATGCATTC     46914      GA   C
                                GAATG  GTC TGCACTGT
                                |||||  ||| ||||||||
                                CTTAC  TAG ACGTGACA
                                   G_  _
GAM609  FLJ13576 3' ACAGTAGGTTTCATCCA     42805    A     T   GC
                                TG ATGGAG CCT  ACTGT
                                || |||||| |||  |||||
                                AC TACTTT GGA  TGACA
                                 C     _  __
GAM609  FLJ20306 3' GACAGAGCAAGACTCCAT    35394        C   A
                                ATGGAGTC TGC CTGTC
                                |||||||| ||| |||||
                                TACCTCAG ACG GACAG
                                     A   A
GAM609  FLJ23047 3' ACACTAGTCTCCATTCA     44929        TC   CAC
                                TGAATGGAG  CTG   TGT
                                |||||||||  |||   |||
                                ACTTACCTC  GAT   ACA
                                     T_   C__
GAM609  FLJ30927 3' ACAATGCCTTCATTCA      59080        TCCT   C
                                TGAATGGAG    GCA TGT
                                |||||||||    ||| |||
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                                ACTTACTTC   CGT ACA
                                     ____   A
GAM609  GLTP    3' GACAGCACAGACTGACTTTA  33585      ___  CA
                                TGGAGTC  CTG  CTGTC
                                |||||||  |||  |||||
                                ATTTCAG  GAC  GACAG
                                    TCA  AC
GAM609  HML2    5' GACCAGCAGGACTCCAGTCA  22023    A       ACT
                                TGA TGGAGTCCTGC  GTC
                                ||| ||||||||||  |||
                                ACT ACCTCAGGACG  CAG
                                  G        AC_
GAM609  HSPC065 3' AGTTCAGGACTCCTCTCA    27140    AT      C
                                TGA  GGAGTCCTG ACT
                                |||  ||||||||| |||
                                ACT  CCTCAGGAC TGA
                                  CT       T
GAM609  KIAA0237 3' GACTTGGGGCCTCCATTCA  29224       T  G  CT
                                TGAATGGAG CCT CA  GTC
                                ||||||||| ||| ||  |||
                                ACTTACCTC GGG GT  CAG
                                     C  _ T_
GAM609  KIAA1340 3' GACAGTGCAAGACTCTGT   69696       C
                                ATGGAGTC TGCACTGTC
                                |||||||| |||||||||
                                TGTCTCAG ACGTGACAG
                                    A
GAM609  KIAA1371 3' GACAGTGCATTTTGTCATTCA 90477      AGTCC
                                TGAATGG    TGCACTGTC
                                |||||||    |||||||||
                                ACTTACT    ACGTGACAG
                                   GTTTT
GAM609  KIAA1449 3' ACAGTACATTCCATTCA    40836       TCC  C
                                TGAATGGAG   TG ACTGT
                                |||||||||   || |||||
                                ACTTACCTT   AC TGACA
                                    ___  A
GAM609  KIAA1463 3' GACAGTGCAGATCTATACTCA 72740    A  G  TC
                                TGA TG AG  CTGCACTGTC
                                ||| || ||  ||||||||||
                                ACT AT TC  GACGTGACAG
                                  C  A  TA
GAM609  KIAA1951 3' ACAGTGCAAGACCCTGTCA   74142    AT  A   C
                                TGA  GG GTC TGCACTGT
                                |||  || ||| ||||||||
                                ACT  CC CAG ACGTGACA
                                  GT  _   A
GAM609  MACF1   3' GACAGTGCATGCACTCCA    53495      CC_
                                TGGAGT   TGCACTGTC
                                ||||||   |||||||||
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                                ACCTCA   ACGTGACAG
                                   CGT
GAM609  MAWBP    3' ACAGAGTAAGACTCCATCCA  42371    A      C   A
                                TG ATGGAGTC TGC CTGT
                                || |||||||| ||| ||||
                                AC TACCTCAG ATG GACA
                                 C       A   A
GAM609  MGC3101  5' GACAGAGCGAGACTCCAT    44103        C   A
                                ATGGAGTC TGC CTGTC
                                |||||||| ||| |||||
                                TACCTCAG GCG GACAG
                                     A   A
GAM609  MGC32104 3' AGTAAGAACTTCATTCA     59064         C  GC
                                TGAATGGAGT CT  ACT
                                |||||||||| ||  |||
                                ACTTACTTCA GA  TGA
                                      A  A_
GAM609  PRDM10   3' GACACTGTAGACTTCATTCA  39979          C   C
                                TGAATGGAGTC TGCA TGTC
                                |||||||||| |||| ||||
                                ACTTACTTCAG ATGT ACAG
                                       _   C
GAM609  PTPN21   5' GACAGTGTTCGTCCCATCCG  23863    A   AG CCT
                                TG ATGG  T   GCACTGTC
                                || ||||  |  ||||||||
                                GC TACC  G   TGTGACAG
                                 C   CT CT_
GAM609  RAP140   3' ACAGTGCAGTTTCATTTA    31504        TC
                                TGAATGGAG  CTGCACTGT
                                |||||||||  |||||||||
                                ATTTACTTT  GACGTGACA
                                       __
GAM609  RNF9     3' AGTACAGGACTCATTCA     23234       G     C
                                TGAATG AGTCCTG ACT
                                |||||| ||||||| |||
                                ACTTAC TCAGGAC TGA
                                   _     A
GAM609  SERPINA10 3' GACAATGCAAGATTCCAT    32993        C   C
                                ATGGAGTC TGCA TGTC
                                |||||||| |||| ||||
                                TACCTTAG ACGT ACAG
                                     A   A
GAM609  SIAT8D   3' ACAGTGCACTCATCATT     20229     __   CCT
                                AATG  GAGT   GCACTGT
                                ||||  ||||   |||||||
                                TTAC  CTCA   CGTGACA
                                  TA   ____
GAM609  SPTLC2   3' ACAGTGCAGAACTGCCAGTC  17973    A  _  C
                                GA TGG AGT CTGCACTGT
                                || ||| ||| |||||||||
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                                CT ACC TCA GACGTGACA
                                 G   G   A
GAM609   LOC122830 3'  ACACTGAAAGACTCCATTCA   74626          CTG  C
                                TGAATGGAGTC   CA TGT
                                ||||||||||   || |||
                                ACTTACCTCAG   GT ACA
                                      AAA  C
GAM609   LOC127262 3'  GACAGAGCGAGACTCCAT    76598        C   A
                                ATGGAGTC TGC CTGTC
                                |||||||| ||| |||||
                                TACCTCAG GCG GACAG
                                     A   A
GAM609   LOC149460 3'  GACAGAGCAAGACTCCATCA   85610     A      C   A
                                TGA TGGAGTC TGC CTGTC
                                ||| ||||||| ||| |||||
                                ACT ACCTCAG ACG GACAG
                                  _      A   A
GAM609   LOC150311 5'  GACCTGAGGACTCCACTCA    80564     A       G  CT
                                TGA TGGAGTCCT CA  GTC
                                ||| ||||||||| ||  |||
                                ACT ACCTCAGGA GT  CAG
                                  C        _ C_
GAM609   LOC150960 3'  ACAAAGTGAGACTCCATCA    80860     A      CT  AC
                                TGA TGGAGTC  GC  TGT
                                ||| |||||||  ||  |||
                                ACT ACCTCAG  TG  ACA
                                  _      AG  AA
GAM609   LOC161877 5'  GACAGTGCAGAAGGCACC    83197    A  __
                                GG GTC  CTGCACTGTC
                                || |||  ||||||||||
                                CC CGG  GACGTGACAG
                                 A   AA
GAM609   LOC199907 3'  GACAGTGCAGAGATTCTCCA   89827      __ _
                                TGGAG  TC CTGCACTGTC
                                |||||  || ||||||||||
                                ACCTC  AG GACGTGACAG
                                   TT  A
GAM609   LOC201595 3'  ACAGTTCATCCATTCA      90419        GTCC  C
                                TGAATGGA    TG ACTGT
                                ||||||||    || |||||
                                ACTTACCT    AC TGACA
                                     _____  T
GAM609   LOC219623 5'  GACATTGGGACTCCATCA    93089     A        CAC
                                TGA TGGAGTCCTG   TGTC
                                ||| ||||||||||   ||||
                                ACT ACCTCAGGGT   ACAG
                                  _        T__
GAM609   LOC220980 5'  ACAGTGTGTCCACCTCA     94762     A_    GTCC
                                TGA  TGGA    TGCACTGT
                                |||  ||||    ||||||||
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                                ACT  ACCT   GTGTGACA
                                  CC   ____
GAM609  LOC221490 5'  ACAGTGCAGCCCATACA     95294    A   A TC
                                TG ATGG G  CTGCACTGT
                                || |||| |  |||||||||
                                AC TACC C  GACGTGACA
                                 A   _ __
GAM609  LOC221810 3'  GACAGTGCAGAACATTTTTC   95547     TG A  C
                                GAA  G GT CTGCACTGTC
                                |||  | || ||||||||||
                                CTT  T CA GACGTGACAG
                                  TT A  A
GAM609  LOC222678 5'  ACAGCAGTATTACTTCCATTCA 94416         _ CC   A_
                                TGAATGGA GT  TGC  CTGT
                                |||||||| ||  |||  ||||
                                ACTTACCT CA  ATG  GACA
                                     T  TT   AC
GAM609  LOC257475 3'  GACAGTGTCTGCTCCATGCA   72853    A      CCT
                                TG ATGGAGT   GCACTGTC
                                || |||||||   ||||||||
                                AC TACCTCG   TGTGACAG
                                 G      TC_
GAM609  LOC55829  3'  ACAGTGATTGCATTCA      38032       G    CTGC
                                TGAATG AGTC    ACTGT
                                |||||| ||||    |||||
                                ACTTAC TTAG    TGACA
                                   G   ____
GAM609  LOC90918  5'  AGCTGGAGGACTCACACTCA   64994     A _      G _
                                TGA TG GAGTCCT CA CT
                                ||| || ||||||| || ||
                                ACT AC CTCAGGA GT GA
                                  C  A      G  C
GAM609  LOC93190  3'  GACAGAGTGAGACTCCAT    72098         CT  A
                                ATGGAGTC  GC CTGTC
                                ||||||||  || |||||
                                TACCTCAG  TG GACAG
                                     AG  A
GAM610  CA7      3'  CCAGTCACCAAAGCCACCT    60828     A_      TCGGA   A
                                AGG  GCTTTGGT    GAC GG
                                |||  ||||||||    ||| ||
                                TCC  CGAAACCA    CTG CC
                                  AC       _____   A
GAM610  E2F3     3'  CTGTCTCCATGAACCACTC    10467     CTT     __
                                GAG   TGGTTC  GGAGACAG
                                |||   ||||||  ||||||||
                                CTC   ACCAAG  CCTCTGTC
                                  ___     TA
GAM610  HD       3'  CCTATCCCCAGGACAGGTCCCT 10911     AG   TG   _  A  C
                                AGG  CTT  GTTC GG GA AGG
                                |||  |||  |||| || || |||
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                                TCC  GGA  CAGG CC CT TCC
                                  CT   __    A  C  A
GAM610  LZTR1    3'  CTGTCACCCAAGGCTCCT    23170          TTCG A
                                AGGAGCTTTGG    G GACAG
                                ||||||||||    | |||||
                                TCCTCGGAACC    C CTGTC
                                      ____ A
GAM610  MECP2    3'  CCCGTCTAACCACAGCTCCTT  18394        T    CGG    A
                                AAGGAGCT TGGTT   AGAC GG
                                |||||||| |||||   |||| ||
                                TTCCTCGA ACCAA   TCTG CC
                                     C     ___    C
GAM610  PLA2G2A  5'  CTGTCTCCAAACAGCCTT    6110      A   TTG   C
                                AGG GCT   GTT GGAGACAG
                                ||| |||   ||| ||||||||
                                TTC CGA   CAA CCTCTGTC
                                  _   ___    A
GAM610  PLOD     3'  CCTGAAAAACCAAGGCCCC    6114     A       CGGAGA
                                GG GCTTTGGTT     CAGG
                                || |||||||||      ||||
                                CC CGGAACCAA     GTCC
                                 C        AAA___
GAM610  POLR2A   3'  CCTGTCCCCAAATTGAAGATCC 8128       G   TG   C  A
           TT                     AAGGA CTT  GTT GG GACAGG
                                |||||| |||  ||| || ||||||
                                TTCCT GAA  TAA CC CTGTCC
                                   A   GT   A  C
GAM610  RAB36    3'  CCTGTCTCCAACACCGCCTCCT 18163      CTT    TC_
                                AGGAG   TGGT   GGAGACAGG
                                |||||   ||||   |||||||||
                                TCCTC   GCCA   CCTCTGTCC
                                   C__    CAA
GAM610  RAP1     3'  CCTGTCCTTTGGCAGAAGCTCC 39111          G  T    _
           TT                     AAGGAGCTTT GT CGGAG ACAGG
                                |||||||||| || ||||| |||||
                                TTCCTCGAAG CG GTTTC TGTCC
                                     A  _    C
GAM610  SFRP5    3'  CCTGCCCCAAGGCCCAGAGCTC 13032          TT __  AGA
           C                      GGAGCTTTGG  C  GG   CAGG
                                ||||||||||  |  ||   ||||
                                CCTCGAGACC  G  CC   GTCC
                                     CG AA  CC_
GAM610  SORCS2   3'  CCTGTCCCCCAGACCCAAAGCT 40800          T  _  A_
           CT                     GGAGCTTTGG TC GG  GACAGG
                                |||||||||| || ||  ||||||
                                TCTCGAAACC AG CC  CTGTCC
                                     C  A  CC
GAM610  TFR2     3'  CCCGTCCCCCAGTCAAGAGCTC 13698          _ GT C  A   A
           CT                     AGGAGCTTT G  T GG GAC GG
                                |||||||||  |  | || ||| ||
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                                TCCTCGAGA C  A CC CTG CC
                                     A TG C  C   C
GAM610  C1orf35   3'  CTGCCTCGGAAGCTCCTT    44480        TTGGT  G   A
                                AAGGAGCT    TC GAG CAG
                                ||||||||    || ||| |||
                                TTCCTCGA    AG CTC GTC
                                     _____  G   C
GAM610  DKFZp434J1015 3'  CCGCCTCCACCTGAAAAGCTCC 94209          ___  TC    ACA
           TT                    AAGGAGCTTT   GGT  GGAG   GG
                                ||||||||||   |||  ||||   ||
                                TTCCTCGAAA   CCA  CCTC   CC
                                     AGT   __    CG_
GAM610  EFS2     3'  CTGCCTGCCAAAGCCCC     20773    A      TC  AGA
                                GG GCTTTGGT  GG   CAG
                                || ||||||||  ||   |||
                                CC CGAAACCG  CC   GTC
                                 C       T_  ___
GAM610  FLJ10350  5'  CCGCCTCCGAGTCGCTACTT   97248    G   TTT GT     ACA
                                AAG AGC   G  TCGGAG   GG
                                ||| |||   |  ||||||   ||
                                TTC TCG   C  AGCCTC   CC
                                  A   ___ TG     CG_
GAM610  HRI      3'  CTGCCCCACAAGCTCCTT    27738         _   TT
                                AAGGAGCTT TGG  CGG
                                |||||||| |||  |||
                                TTCCTCGAA ACC  GTC
                                     C   CC
GAM610  KIAA0057  3'  CCTGTCTCTTGCAAGCTCC   25409       TG  TC
                                GGAGCTT  GT  GGAGACAGG
                                |||||||  ||  |||||||||
                                CCTCGAA  CG  TCTCTGTCC
                                     __  T_
GAM610  KIAA0189  3'  CCTGTCCCCTTTCCTAAAGCTC 28941          TTC_  A
           CT                    AGGAGCTTTGG    GG GACAGG
                                ||||||||||    || ||||||
                                TCCTCGAAATC    CC CTGTCC
                                      CTTT  C
GAM610  KIAA1203  3'  CCTGCCCTCCCACCAAAGCCTC 72087      _      TC    A_
           CT                    AGGAG CTTTGGT  GGAG  CAGG
                                ||||| |||||||  ||||  ||||
                                TCCTC GAAACCA  CCTC  GTCC
                                   C      C_   CC
GAM610  KIAA1533  5'  CCTGCCCCCAAGCCGGCCCC   74140    A   TT    C  AGA
                                GG GCT  GGTT GG   CAGG
                                || |||  |||| ||   ||||
                                CC CGG  CCGA CC   GTCC
                                 C   __    A  CCC
GAM610  SAMHD1    3'  CCTGCCCCCGTGAAGAGTTCC  61981        GGTT   AGA
                                GGAGCTTT   CGG   CAGG
                                ||||||||   |||   ||||
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                                CCTTGAGA   GCC   GTCC
                                    AGT_   CCC
GAM610  SCGN     3'  CCTGTCTCACTGAAAGCCCCT  23775     A    _   TCG
                                AGG GCTTT GGT   GAGACAGG
                                ||| ||||| |||   ||||||||
                                TCC CGAAA TCA   CTCTGTCC
                                  C    G  ___
GAM610  SYT6     3'  CATCTCCGAAACCACCTC    79517     CTT    _     CA
                                GAG   TGGTT CGGAGA  G
                                |||   ||||| ||||||  |
                                CTC   ACCAA GCCTCT  C
                                  C__    A     AC
GAM610  UBXD2    3'  CTGCCTCCATCAGCTTCTT    68892        TT   TC    A
                                AAGGAGCT  GGT  GGAG CAG
                                ||||||||  |||  |||| |||
                                TTCTTCGA  CTA  CCTC GTC
                                    __   __    C
GAM610  LOC113146 3'  CCTAAAATGGAACCAAAGCTTC 73334            GGAGAC
                                GGAGCTTTGGTTC     AGG
                                ||||||||||||      |||
                                CTTCGAAACCAAG     TCC
                                      GTAAAA
GAM610  LOC113521 5'  CCCGTCTCCGAGCTGCTCC    73402       TTT         A
                                GGAGC   GGTTCGGAGAC GG
                                |||||   |||||||||| ||
                                CCTCG   TCGAGCCTCTG CC
                                  ___          C
GAM610  LOC115704 3'  CCTGCAGCGGAAACCAAAGTCC 73906    AG      __   GAGA
            C                    GG  CTTTGGT  TCG    CAGG
                                ||  |||||||  |||    ||||
                                CC  GAAACCA  GGC    GTCC
                                 CT      AA   GAC_
GAM610  LOC136345 3'  CCTACCCCACCCAAAGCTGCCT 76712     _       TTC  AGAC
                                AGG AGCTTTGG   GG    AGG
                                ||| ||||||||   ||    |||
                                TCC TCGAAACC   CC    TCC
                                  G       CA_  CCA_
GAM610  LOC144231 5'  CCTGTCTTCCTTGACCAAAGCT 83938           C__
            CT                    GGAGCTTTGGTT   GGAGACAGG
                                ||||||||||||   |||||||||
                                TCTCGAAACCAG   CTTCTGTCC
                                      TTC
GAM610  LOC146856 5'  CTGTCTCCATGAACCACTC    83700     CTT     __
                                GAG   TGGTTC  GGAGACAG
                                |||   ||||||  ||||||||
                                CTC   ACCAAG  CCTCTGTC
                                  ___     TA
GAM610  LOC147669 5'  CCGCCTCCTGGGCAAGCTCC   85180        TG   _   ACA
                                GGAGCTT  GTTC GGAG   GG
                                |||||||  |||| ||||   ||
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                                CCTCGAA  CGGG CCTC   CC
                                   __   T   CG_
GAM610  LOC148021 5'  CTACCTCCAGAGCTACTT    79316    G      TTC  _
                                AAG AGCTTTGG   GG AG
                                ||| ||||||||   || ||
                                TTC TCGAGACC   CC TC
                                  A       T__  A
GAM610  LOC153688 3'  CCTGCCCCCAAACCAAGGCCT  87307    A       C  AGA
                                GG GCTTTGGTT GG   CAGG
                                || |||||||| ||   ||||
                                TC CGGAACCAA CC   GTCC
                                  _       A  CCC
GAM610  LOC155032 5'  CCTACCCCACCCAAAGCTGCCT 87592     _      TTC  AGAC
                                AGG AGCTTTGG   GG    AGG
                                ||| ||||||||   ||    |||
                                TCC TCGAAACC   CC    TCC
                                  G       CA_  CCA_
GAM610  LOC157349 5'  CCCGTCTCCGGCAGCCCCT    82334    A   TTG  T      A
                                AGG GCT   GT CGGAGAC GG
                                ||| |||   || ||||||| ||
                                TCC CGA   CG GCCTCTG CC
                                  C  ___  _      C
GAM610  LOC157349 5'  CCGTCTCCGGCAGCCCCT    82335    A   TTG  T      A
                                AGG GCT   GT CGGAGAC GG
                                ||| |||   || ||||||| ||
                                TCC CGA   CG GCCTCTG CC
                                  C  ___  _      C
GAM610  LOC199991 3'  CCTGTCCACCCTCAAAGCCCT  91515    A      TTC  A_
                                AGG GCTTTGG   GG  GACAGG
                                ||| |||||||   ||  ||||||
                                TCC CGAAACT   CC  CTGTCC
                                  _      C__  AC
GAM611  AGRP     5'  CTTCATTAGGCCCTGCCATA   24616       A  A
                                TATGGCA GG CCTGATGGAG
                                ||||||| || ||||||||||
                                ATACCGT CC GGATTACTTC
                                    C  _
GAM611  CGTHBA   3'  CTTCCCTCCAGTCCTTGCCG   24890         C  AT  A
                                TGGCAAGGAC TG  GG GAAG
                                |||||||||| ||  || ||||
                                GCCGTTCCTG AC  CC CTTC
                                     _  CT  _
GAM611  COL5A3   3'  CTCCCCAGGCTCACCTTGCCAT 32318         A___   AT
           G                    TATGGCAAGG   CCTG  GGAG
                                ||||||||||   ||||  ||||
                                GTACCGTTCC   GGAC  CCTC
                                     ACTC   C_
GAM611  FGF23    3'  CTTCTCTGGGGTCCCTTCCA  40557    CAA    GA
                                TGG   GGACCT  TGGAGAAG
                                |||   ||||||  ||||||||
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                                ACC  CCTGGG  GTCTCTTC
                                 TTC    __
GAM611  FUT3    3'  CTCCCAGAGACCTTGCCA   5621       AC_  AT
                                TGGCAAGG  CTG  GGAG
                                ||||||||  |||  ||||
                                ACCGTTCC  GAC  CCTC
                                    AGA  __
GAM611  FUT5    3'  CTCCCAGAGACCTTGCCA   10726      AC_  AT
                                TGGCAAGG  CTG  GGAG
                                ||||||||  |||  ||||
                                ACCGTTCC  GAC  CCTC
                                    AGA  __
GAM611  TCF12   3'  TCTCCTATCCTCTTGCCATA  13639       ACCT  _
                                TATGGCAAGG   GAT GGAGA
                                ||||||||||   ||| |||||
                                ATACCGTTCT   CTA CCTCT
                                     C___  T
GAM611  WSX1    3'  CTCCCCCACATCCTTTCCTTGC 17915      CCT  _____
           C                     GGCAAGGA  GAT   GGAG
                                ||||||||  |||   ||||
                                CCGTTCCT  CTA   CCTC
                                    TTC  CACCC
GAM611  ZAP70   3'  CTTCCCCACCCTCAGCCCCACC 71375    CAA  AC   ___  A
           CCA                    TGG  GG  CTGA  TGG GAAG
                                |||  ||  ||||  ||| ||||
                                ACC  CC  GACT  ACC CTTC
                                 CCA  CC   CCC  C
GAM611  C1orf34 3'  CCTCTGGCCATTGCCATA   61303       _  A  T  T
                                TATGGCAA GG CC GA GG
                                |||||||| || || || ||
                                ATACCGTT CC GG CT CC
                                    A  _  T  _
GAM611  CLSTN1  3'  CTCCCCAGAGCACCCCCTGCCA 30787      A  AC____  AT
           T                    ATGGCA GG    CTG  GGAG
                                ||||||  ||    |||  ||||
                                TACCGT CC    GAC  CCTC
                                   C  CCACGA  C_
GAM611  DKFZP434J193 3'  CTTCTCCACCACTCTCCTTGCC 71562        CC_  A
           ATG                    TATGGCAAGGA  TG TGGAGAAG
                                ||||||||||  ||  ||||||||
                                GTACCGTTCCT  AC ACCTCTTC
                                     CTC  C
GAM611  DNAJC6  3'  CTCCAAAGTTCCCACCATA   29492     CAA  C  GA
                                TATGG  GGA CT  TGGAG
                                |||||  ||| ||  |||||
                                ATACC  CCT GA  ACCTC
                                   AC_  T  A_
GAM611  FLJ12122 5'  CTGCCAGCTCAGGTCCCTGCCA 47092     A     __  _
                                TGGCA GGACCTGA  TGG AG
                                ||||| ||||||||  ||| ||
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                                ACCGT CCTGGACT  ACC TC
                                  C       CG   G
GAM611  FLJ14642  3'  CTTCTCCGTAGTCCCCGCC   52575    AA   CTG
                                GGC  GGAC   ATGGAGAAG
                                |||  ||||   |||||||||
                                CCG  CCTG   TGCCTCTTC
                                  CC    A__
GAM611  FLJ20275  3'  CTGTCAGATCCTTGCCAT    35308         C
                                ATGGCAAGGA CTGATGG
                                |||||||||| |||||||
                                TACCGTTCCT GACTGTC
                                      A
GAM611  FLJ21369  3'  CTTCTCCATCAAGTTTCACCA  46051    CAA   C
                                TGG   GGAC TGATGGAGAAG
                                |||   |||| ||||||||||
                                ACC   TTTG ACTACCTCTTC
                                  AC_   A
GAM611  HSPC016   3'  TCTCTATTCCCTGCCATA    32503       A   CCTG
                                TATGGCA GGA    ATGGAGA
                                |||||||  |||    |||||||
                                ATACCGT CCT    TATCTCT
                                    C  _____
GAM611  HT014     3'  CTTCCTAATAAATCCTTGCCA  40153        CC  A   A
                                TGGCAAGGA  TG TGG GAAG
                                |||||||||  ||  ||| ||||
                                ACCGTTCCT  AT ATC CTTC
                                      AA  A  _
GAM611  KIAA0773  3'  CTTCTCCACGACCTCACC    28722    CA   ACC  A
                                GG  AGG   TG TGGAGAAG
                                ||  |||   || ||||||||
                                CC  TCC   GC ACCTCTTC
                                 AC   A__  _
GAM611  KIAA1181  3'  CTCCATCAGCTGGTCA      68911      A  GAC
                                TGGC AG   CTGATGGAG
                                ||||  ||   |||||||||
                                ACTG TC   GACTACCTC
                                  G  ____
GAM611  KIAA1321  3'  CTCCTTAGGTCCTCACA     62899    GCA       T
                                TG   AGGACCTGA GGAG
                                ||   ||||||||| ||||
                                AC   TCCTGGATT CCTC
                                 AC_        _
GAM611  KIAA1348  3'  CTTCTTAGGTCTTGCCA     69122        G     T
                                TGGCAAG ACCTGA GGAG
                                ||||||| |||||| ||||
                                ACCGTTC TGGATT CTTC
                                      _     _
GAM611  KIAA1493  3'  CTTCTCCACCTAGTCTGCC   64840      AG   CTGA
                                GGCA  GAC    TGGAGAAG
                                ||||  |||    ||||||||
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                              CCGT  CTG   ACCTCTTC
                                __  ATCC
GAM611  KIAA1535 3' CTCTGTGGTCCTTGCC     80212        TG
                              GGCAAGGACC  ATGGAG
                              ||||||||||  ||||||
                              CCGTTCCTGG  TGTCTC
                                          __
GAM611  KIAA1819 5' CTTCTCCACGGCTCCCCCA   70252    CAA  C  A
                              TGG   GGA CTG TGGAGAAG
                              |||   ||| ||| ||||||||
                              ACC   CCT GGC ACCTCTTC
                                C__   C  _
GAM611  LAT1-3TM 3' CTCCATCAGTGTCATCACCA  49143    CAAG  _
                              TGG   GAC CTGATGGAG
                              |||   ||| |||||||||
                              ACC   CTG GACTACCTC
                                ACTA  T
GAM611  LAT1-3TM 5' CTCCATCAGTGTCATTACCA  49144    CAAG  _
                              TGG   GAC CTGATGGAG
                              |||   ||| |||||||||
                              ACC   CTG GACTACCTC
                                ATTA  T
GAM611  OS4     3' CTTCCCCATCATCCCTTCCATT 20389      _  CC___    A
           GCCA                  TGGCAA GGA    TGATGG GAAG
                              |||||| |||    |||||| ||||
                              ACCGTT CCT    ACTACC CTTC
                                 A  TCCCT    C
GAM611  RASSF2   3' CTTCTCCACCTTCTCTCCA   29097    CA   CCTGA
                              TGG  AGGA    TGGAGAAG
                              |||  ||||    ||||||||
                              ACC  TCTT    ACCTCTTC
                                TC   CC___
GAM611  SARM     3' CTCCCCCAGGCCCTGCCAT   31285      A  A   AT
                              ATGGCA GG CCTG  GGAG
                              |||||| || ||||  ||||
                              TACCGT CC GGAC  CCTC
                                 C  _   CC
GAM611  SELB     3' CTCCCCCAGGGCCTCCTTGCC  62591       ___   AT
                              GGCAAGGA  CCTG  GGAG
                              ||||||||  ||||  ||||
                              CCGTTCCT  GGAC  CCTC
                                   CCG   CC
GAM611  SERPING1 3' CTTCTCCATGGCCCTGCCATG  5348       A  A  TG
                              TATGGCA GG CC  ATGGAGAAG
                              ||||||| || ||  |||||||||
                              GTACCGT CC GG  TACCTCTTC
                                 C  _  __
GAM611  SLIT1    3' TCTCCGGAAGTCCTTGC     13233        C GA
                              GCAAGGAC T  TGGAGA
                              |||||||| |  ||||||
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                                CGTTCCTG A  GCCTCT
                                    _ AG
GAM611  ZDHHC8    3'  TCCCCACCAACTTCTCTGCC  64622     _   CC  A   A
                                GGCA AGGA  TG TGG GA
                                |||| ||||  || ||| ||
                                CCGT TCTT  AC ACC CT
                                  C   CA  C   C
GAM611  LOC112868 5'  CTCCCAGCCCTTGCCA     73268       AC   AT
                                TGGCAAGG  CTG  GGAG
                                ||||||||  |||  ||||
                                ACCGTTCC  GAC  CCTC
                                    C_  __
GAM611  LOC142946 3'  CCATGGTCCTTGCCATA     83783          TG
                                TATGGCAAGGACC  ATGG
                                ||||||||||||  ||||
                                ATACCGTTCCTGG  TACC

                                      __
GAM611  LOC150319 3'  CTTCTCCATCCTCCTGCCAT  80471      A   CCT
                                ATGGCA GGA   GATGGAGAAG
                                ||||||| |||   ||||||||||
                                TACCGT CCT   CTACCTCTTC
                                   _  C__
GAM611  LOC159319 5'  TTCTCCACACCCCTGCC     83073     A  ACC  A
                                GGCA GG   TG TGGAGAA
                                |||| ||   || |||||||
                                CCGT CC   AC ACCTCTT
                                  C  C__  _
GAM611  LOC197423 5'  CTCCATCAGTGTCATTACCA  78424     CAAG  _
                                TGG    GAC CTGATGGAG
                                |||    ||| |||||||||
                                ACC    CTG GACTACCTC
                                  ATTA   T
GAM611  LOC199923 5'  CTTCTCCACCTCCTGCCA    89871      A   CCTGA
                                TGGCA GGA    TGGAGAAG
                                ||||| |||    ||||||||
                                ACCGT CCT    ACCTCTTC
                                   _  CC___
GAM611  LOC206657 5'  CTTCTCAGTCTTGCCA      91105        AC   T
                                TGGCAAGG  CTGA GGAG
                                ||||||||  |||| ||||
                                ACCGTTCT  GACT CTTC

                                    __   _
GAM611  LOC220565 5'  CTCCATCAGTGTCATCACCA  92441     CAAG  _
                                TGG    GAC CTGATGGAG
                                |||    ||| |||||||||
                                ACC    CTG GACTACCTC
                                  ACTA   T
GAM611  LOC221975 5'  CTTCTCCATGGAGCCTGCC   94192      A  AC  G
                                GGCA GG  CT ATGGAGAAG
                                |||| ||  || |||||||||
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                                CCGT CC  GG TACCTCTTC
                                  _ GA  _
GAM611  LOC222160 5'  TCCCATTAGGCCCCCA     95793     CAA  A       A
                                TGG   GG CCTGATGG GA
                                |||   || |||||||| ||
                                ACC   CC GGATTACC CT
                                  C__  _       _
GAM611  LOC257239 5'  CTTCTCCACCTCAACCACCA  98844     CAA  ACC   __
                                TGG   GG   TGA  TGGAGAAG
                                |||   ||   |||  ||||||||
                                ACC   CC   ACT  ACCTCTTC
                                  A__  A__   CC
GAM611  LOC90499  3'  CTTCTCCATGGCCCCCTCCA  63741     CAA  A  TG
                                TGG   GG CC  ATGGAGAAG
                                |||   || ||  |||||||||
                                ACC   CC GG  TACCTCTTC
                                  TCC  C  __
GAM612  ATP11A    3'  TGGCCCACATGTGGATGCCACA 77558       G    TG     A
                                TGTGGCA TTAC  ATGTGG CCA
                                ||||||| ||||  |||||| |||
                                ACACCGT GGTG  TACACC GGT
                                    A   __     C
GAM612  CAMLG     3'  ACTCAGTAACTGCCATA     9991            T
                                TGTGGCAGTTACTGA GT
                                |||||||||||||| ||
                                ATACCGTCAATGACT CA
                                                _
GAM612  DGKG      3'  TGGCTTAGGCAGCAACCTCCAC 9043       CA   A   ATGT  A
            A                    TGTGG  GTT CTG    GG CCA
                                |||||  ||| |||    || |||
                                ACACC  CAA GAC    TC GGT
                                   TC   C   GGAT  _
GAM612  GFAP      3'  ACCCCAGTAAGCCACTGCCACA 10774         ____     AT
                                TGTGGCAGT    TACTG  GT
                                |||||||||    |||||  ||
                                ACACCGTCA    ATGAC  CA
                                     CCGA     CC
GAM612  NONO      3'  CCCAGAGAAACTGCCACA    82886         A  GA  T
                                TGTGGCAGTT CT  TG GG
                                |||||||||| ||  || ||
                                ACACCGTCAA GA  AC CC
                                     A  G_  _
GAM612  NUMB      3'  CATATCAGCAACTGCCCA    14979    T     A
                                TG GGCAGTT CTGATGTG
                                || ||||||| ||||||||
                                AC CCGTCAA GACTATAC
                                  _      C
GAM612  RAB36     3'  TGGCCCACATCAGCAGTCA    18185     AGTTA       A
                                TGGC    CTGATGTGG CCA
                                ||||    ||||||||| |||
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                                ACTG    GACTACACC GGT
                                  AC___       C
GAM612  ACAA2    3'  ACCTTCAGAGCAGCTGCCACA  93421         A__   T_
                                TGTGGCAGTT  CTGA  GT
                                ||||||||||  ||||  ||
                                ACACCGTCGA  GACT  CA
                                      CGA   TC
GAM612  BM046    3'  TCCACATGGTCTACCA     38058     C  TT   G
                                TGG AG  ACT ATGTGGA
                                ||| ||  ||| |||||||
                                ACC TC  TGG TACACCT
                                  A __  _
GAM612  C1orf17  3'  GGCCCACATCAGTTCAAC    68767     __        A
                                GTT  ACTGATGTGG CC
                                |||  |||||||||| ||
                                CAA  TGACTACACC GG
                                  CT        C
GAM612  HYPC     5'  GCAGCAGCAGCTGCCACA    65218          A   A
                                TGTGGCAGTT CTG TGT
                                |||||||||| ||| |||
                                ACACCGTCGA GAC ACG
                                      C   G
GAM612  KIAA0788 3'  CACATCAGCACTACCACA    71851       C   TA
                                TGTGG AGT  CTGATGTG
                                |||||| |||  ||||||||
                                ACACC TCA  GACTACAC
                                   A   C_
GAM612  MGC16025 3'  TGGCCCACATCAGCATTGACCA 53030      _    TA       A
            C                    GTGG CAGT  CTGATGTGG CCA
                                |||| ||||  |||||||||| |||
                                CACC GTTA  GACTACACC GGT
                                  A   C_       C
GAM612  PEPP2    3'  GTCAGCAGTTACTGCCACA   39203         T    ATGTG
                                TGTGGCAGT ACTG    GAC
                                ||||||||| ||||    |||
                                ACACCGTCA TGAC    CTG
                                      T   GA___
GAM612  SHANK3   3'  CTGTAACAGACTGCCACA    66105         TA   A  TG
                                TGTGGCAGT  CTG TG  G
                                |||||||||  ||| ||  |
                                ACACCGTCA  GAC AT  C
                                      __   A  GT
GAM612  LOC138130 5' GTCCACAAGGGGACTGCCAC   76482         TA  GA
                                GTGGCAGT  CT  TGTGGAC
                                ||||||||  ||  |||||||
                                CACCGTCA  GG  ACACCTG
                                     GG  A_
GAM612  LOC146455 3' GTCCCAGAGAAACTGCCACA   78463          A  GA  T
                                TGTGGCAGTT CT  TG GGAC
                                |||||||||| ||  || ||||
```

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                                ACACCGTCAA GA  AC CCTG
                                     A  G_  _
GAM612  LOC201283 3'  GGTCCTTACACTACCAC     61052      C   TAC   TGT
                                GTGG AGT   TGA   GGACC
                                |||| |||   |||   |||||
                                CACC TCA   ATT   CCTGG
                                  A  C__   ___
GAM612  LOC219894 3'  ATATACAGTACTGCCACA    94897         T   _
                                TGTGGCAGT ACTG ATGT
                                ||||||||| |||| ||||
                                ACACCGTCA TGAC TATA
                                     _   A
GAM612  LOC222865 3'  CAGTTCAGCCACTGCCACA   94442         TA    TG
                                TGTGGCAGT  CTGA  TG
                                |||||||||  ||||  ||
                                ACACCGTCA  GACT  AC
                                     CC    TG
GAM612  LOC255870 3'  ACCTTCAGAGCAGCTGCCACA 96311          A__    T_
                                TGTGGCAGTT   CTGA  GT
                                ||||||||||   ||||  ||
                                ACACCGTCGA   GACT  CA
                                     CGA    TC
GAM613  DIRC1    5'  CCTTCCAAGATGTTTTCC     54751          C  AGCGAT
                                GGAAGACATC TG     GAGG
                                |||||||||| ||     ||||
                                CCTTTTGTAG AC     TTCC
                                     A  C_____
GAM613  FLJ11783  5'  ACCTCATCCGAGCAAGATTCCT 46547     A  C   C  AG  _
           CC                     GGA GA ATC TG  CG ATGAGGT
                                ||| || ||| ||  || |||||||
                                CCT CT TAG AC  GC TACTCCA
                                  C  _   A  GA  C
GAM613  FLJ20174  3'  ACCTCATCACTCTGACTCTGCC 35188    A   CA  CT   C
                                GG AGA  TC  GAG GATGAGGT
                                || |||  ||  ||| ||||||||
                                CC TCT  AG  CTC CTACTCCA
                                 G   C_  T_   A
GAM613  JDD1     3'  ACCTCATCAAATAGATGTCATT 63907      _     CTGAGC
           CC                     GGAA GACATC     GATGAGGT
                                |||| ||||||     ||||||||
                                CCTT CTGTAG     CTACTCCA
                                  A     ATAAA_
GAM613  KIAA0179  3'  ACGGCAAGCCCAAAGTGTCTTC 65452         CC  A  GA  AG
           C                      GGAAGACAT  TG GC  TG  GT
                                |||||||||  || ||  ||  ||
                                CCTTCTGTG  AC CG  AC  CA
                                     AA  C  A_  GG
GAM613  KIAA0232  3'  ACCTCATCACCCAGAGAAATCT 73119     CA  _   AGC
                                AGA  TC CTG   GATGAGGT
                                |||  || |||   ||||||||
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                                TCT  AG GAC   CTACTCCA
                                  AA  A   CCA
GAM613  KRT6     3'  CTTACCCAGGATGTTTCC    83094     A       AGCGA
                                GGA GACATCCTG     TGAG
                                ||| |||||||||     ||||
                                CCT TTGTAGGAC     ATTC
                                  _       CC___
GAM613  NR6A1    3'  ACCTTATCCCAGGACGTGTTCC 54015     G  A    AGC
                                GGAA AC TCCTG   GATGAGGT
                                |||| || |||||   ||||||||
                                CCTT TG AGGAC   CTATTCCA
                                  G  C    C__
GAM613  NR6A1    3'  ACCTTATCCCAGGACGTGTTCC 54021     G  A    AGC
                                GGAA AC TCCTG   GATGAGGT
                                |||| || |||||   ||||||||
                                CCTT TG AGGAC   CTATTCCA
                                  G  C    C__
GAM613  NR6A1    3'  ACCTTATCCCAGGACGTGTTCC 9442      G  A    AGC
                                GGAA AC TCCTG   GATGAGGT
                                |||| || |||||   ||||||||
                                CCTT TG AGGAC   CTATTCCA
                                  G  C    C__
GAM613  PFDN1    3'  ACCTCTGCCCAGGACACTCTTC 12044      CA_    A   AT
          C                      GGAAGA   TCCTG GCG  GAGGT
                                ||||||   ||||| |||  |||||
                                CCTTCT   AGGAC CGT  CTCCA
                                   CAC    C  __
GAM613  LOC145790 3'  ACCTCATTATAGATGTCTT   77953        CTGAGC
                                AAGACATC     GATGAGGT
                                ||||||||     ||||||||
                                TTCTGTAG     TTACTCCA
                                    ATA___
GAM613  LOC146728 5'  ACCTGCTTCACGATGTCTTCC  84757         C  _  GATG
                                GGAAGACATC TGA GC    AGGT
                                |||||||||| ||| ||    ||||
                                CCTTCTGTAG ACT CG    TCCA
                                      C   T  _____
GAM613  LOC147949 3'  ACCTTGTTCCAGGTTACCTTCC 79275      ACAT    AGC  TG
                                GGAAG    CCTG   GA  AGGT
                                |||||    ||||   ||  ||||
                                CCTTC    GGAC   TT  TCCA
                                   CATT    C__  GT
GAM613  LOC149668 5'  ACCTCATCGCCTCCACGTCCCC 85688    AA   ATCCT  _
          C                     GG  GAC    GAG CGATGAGGT
                                ||  |||    ||| |||||||||
                                CC  CTG    CTC GCTACTCCA
                                 CC   CAC__   C
GAM613  LOC157584 3'  ACCTCACCGTGGCTGCTGTCTT 82402        TCCTGA   A
          CC                      GGAAGACA     GCG TGAGGT
                                ||||||||     ||| ||||||
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                                CCTTCTGT     TGC ACTCCA
                                     CGTCGG   C
GAM613  LOC196214 3'  ACCCCAGTGTCCAGGTGTCTTC 91170        T   AG  A  A
          C                       GGAAGACA CCTG  CG TG GGT
                                |||||||| ||||  || || |||
                                CCTTCTGT GGAC  GT AC CCA
                                     _   CT  G  C
GAM614  IRS1     3'  CCATAGATGGTTCTCAATTGTA 19874      C        TGAAC
                                TACA ATTGAGAACC    ATGG
                                |||| ||||||||||    ||||
                                ATGT TAACTCTTGG    TACC
                                  _        TAGA_
GAM614  SERPINF1  3'  CCTGTAAGGTTTCAATG     12038        A   GA   T
                                CATTGAGA CCT  ACA GG
                                |||||||| |||  ||| ||
                                GTAACTTT GGA  TGT CC
                                     _  A_  _
GAM614  HSA243396 3'  CCATGTTCAGCAATGTCAATG  37844       GAAC_
                                CATTGA    CTGAACATGG
                                ||||||    ||||||||||
                                GTAACT    GACTTGTACC
                                   GTAAC
GAM614  KIAA1387  3'  CAGGAATTTTCAATATGTA    71444      C      __
                                TACA ATTGAGAA  CCTG
                                |||| ||||||||  ||||
                                ATGT TAACTTTT  GGAC
                                  A       AA
GAM614  MGC16063  3'  TTCAAATTCCAATGTGTA    54930         A   CC
                                TACACATTG GAA  TGAA
                                ||||||||| |||  ||||
                                ATGTGTAAC CTT  ACTT
                                     _  AA
GAM614  SMCR8     3'  CCATGCTCAGGTTTGACTATGT 59253      TGA_      A
                                ACAT    GAACCTGA CATGG
                                ||||    |||||||| |||||
                                TGTA    TTTGGACT GTACC
                                  TCAG       C
GAM614  UPLC1     3'  CCATGCTAGGCCCCAATGT    35227       AGAA    AA
                                ACATTG    CCTG  CATGG
                                ||||||    ||||  |||||
                                TGTAAC    GGAT  GTACC
                                   CCC_    C_
GAM614  ZNF334    3'  CCATAAGTCAACCCTCAATGT  36637        AACC   AC_
                                ACATTGAG    TGA   ATGG
                                ||||||||    |||   ||||
                                TGTAACTC    ACT   TACC
                                     CCA_   GAA
GAM614  LOC145082 3'  TATGGAATGCCCTTAATGTGTA 84196          AACCTGAA
                                TACACATTGAG       CATG
                                ||||||||||        ||||
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                                ATGTGTAATTC       GTAT
                                      CCGTAAG_
GAM614  LOC157723 3'  CCAAGTAAGGTTCTCAAATGT  82465       _      GA  A
                                ACATT GAGAACCT  AC TGG
                                ||||| ||||||||  || |||
                                TGTAA CTCTTGGA  TG ACC
                                   A       A_  A
GAM614  LOC219988 5'  CCATGTTCGGCCCCCAATG   93262       AGAAC
                                CATTG    CTGAACATGG
                                |||||    ||||||||||
                                GTAAC    GGCTTGTACC
                                   CCCC_
GAM615  SLC25A15  3'  CCTTATGCACCTAATTCAA   27293         A   AT_
                                TTGAATTAG TGCA   GG
                                ||||||||| ||||   ||
                                AACTTAATC ACGT   CC
                                      C    ATT
GAM615  KIAA0682  3'  TGGTTTCAACATCTAATTCAA  30034          CAAT
                                TTGAATTAGATG    GGATCA
                                ||||||||||||    ||||||
                                AACTTAATCTAC    TTTGGT
                                      AAC_
GAM615  UNC5D     3'  GTCTTTGCTACATGTAATTCAA 56007        G ___    T
                                TTGAATTA AT   GCAA GGAT
                                |||||||| ||   |||| ||||
                                AACTTAAT TA   CGTT TCTG
                                     G  CAT   _
GAM615  LOC149386 3'  GTGATCCATACAATTTAA    85561       GCA
                                TTAGAT   ATGGATCAC
                                ||||||   |||||||||
                                AATTTA   TACCTAGTG
                                   ACA
GAM615  LOC253782 3'  CCATTCACATTTAATTCAA   97397          C_
                                TTGAATTAGATG  AATGG
                                ||||||||||||  |||||
                                AACTTAATTTAC  TTACC
                                      AC
GAM616  ALDH1A3   3'  TGTGTGTTCTGCAAGCAGGGC  7337         C  AAA_
                                GCCCTGTTT CA    ACGCG
                                ||||||||| ||    |||||
                                CGGGACGAA GT    TGTGT
                                      C  CTTG
GAM616  APAF1     3'  TGTTTTTGGAGACAGAGT    25987    C
                                GC CTGTTTCCAAAAACG
                                || ||||||||||||||
                                TG GACAGAGGTTTTTGT
                                 A
GAM616  AQP3      3'  TGTGTGTGTGGGGGGGGT    60334      GT    AAA
                                GCCCT  TTCCA   ACGCG
                                |||||  |||||   |||||
```

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                                TGGGG  GGGGT   TGTGT
                                  __     GTG
GAM616  ATP8A2   3'  TGTGTAATTGGAGCAGGGC   95160        T    AA
                                GCCCTGTT CCAA  ACGCG
                                |||||||| ||||  |||||
                                CGGGACGA GGTT  TGTGT
                                    _    AA
GAM616  ATSV     3'  TGTATGTGTGGGAGAGTGGGG  16313      _    AAAA
                                CCCTG TTTCC    ACGCGTACA
                                ||||| |||||    |||||||||
                                GGGGT AGAGG    TGTGTATGT
                                  G    G___
GAM616  B4GALT5  3'  TGTATGTGTGTGGGTTAGGGC  17694       TT    AAA
                                GCCCTG  TCCA   ACGCGTACA
                                ||||||  ||||   |||||||||
                                CGGGAT  GGGT   TGTGTATGT
                                   T_    G__
GAM616  BCL7A    3'  TGTGTGTTACTGGGGGTGGGGT 40996     TG TT   AA       CA
                                GCCC  T  CCA  AACGCGTA
                                ||||  |  |||  ||||||||
                                TGGG  G  GGT  TTGTGTGT
                                  GT GG   CA
GAM616  C14orf1  3'  TGTTTTTTTAGAGACGGGGT   24174         C    C
                                GCCCTGTTTC AAAAA GCG
                                |||||||||| ||||| |||
                                TGGGGCAGAG TTTTT TGT
                                     A    T
GAM616  CACNG6   3'  TGTATGTGGGTTGCTTGGGGGT 49950    TG TT   ___ AA
           GGG                   CC  T  CCAA   A  CGCGTACA
                                || |  ||||   |  ||||||||
                                GG  G  GGTT   T  GTGTATGT
                                 GT GG    CGT GG
GAM616  CD81     3'  GTATGAGTGGAGACGGGC     16386      T      AAAACG
                                GCCC GTTTCCA     CGTAC
                                |||| |||||||     |||||
                                CGGG CAGAGGT     GTATG
                                  _      GA____
GAM616  CDC25A   3'  TGTGTGACATTTGGAGAGGGGG 10131       G       AACG
           C                    GCCCT TTTCCAAA    CGTACA
                                ||||| ||||||||    ||||||
                                CGGGG AGAGGTTT    GTGTGT
                                  G       ACA_
GAM616  CLN5     5'  TGTGTGTTTGGGGCAGGGT   22435         T    A
                                GCCCTGTT CCAAA ACGCG
                                |||||||| ||||| |||||
                                TGGGACGG GGTTT TGTGT
                                    _    G
GAM616  CNP      3'  TGTTTTTAGAGACAGGGT    53627          C
                                GCCCTGTTTC AAAAACG
                                |||||||||| |||||||
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                                TGGGACAGAG TTTTTGT
                                      A
GAM616  CRYBA2   5'  TGTGTGTGGCTCGAAACGGGGC 19048          CAAAAA
                                GCCCTGTTTC     CGCGTACA
                                ||||||||||     ||||||||
                                CGGGGCAAAG     GTGTGTGT
                                      CTCG__
GAM616  CTSD     3'  TGTATTGGCCTGGAGGTGGGGT 10343      TG     AAAA  C
                                GCCC  TTTCCA    CG GTACA
                                ||||  ||||||    || |||||
                                TGGG  GGAGGT    GT TATGT
                                  GT     CCG_ _
GAM616  CYP51    3'  TGTGTGTGTGAGGATGGAAGGG 7624       GTT_   AAAA
           T                     GCCCT    TCC    ACGCGTACA
                                 |||||    |||    |||||||||
                                 TGGGA    AGG    TGTGTGTGT
                                    AGGT   AG__
GAM616  DFFB     3'  TGTATGTTTAGTAGAAACGGGG 88790          CAAAAAC
           T                     GCCCTGTTTC      GCGTACA
                                 ||||||||||      |||||||
                                 TGGGGCAAAG      TGTATGT
                                       ATGATT_
GAM616  DGCR2    3'  TGTGTGTGCGGGACAGGGT    18909       TT _  AAA
                                 GCCCTGT  C CA   ACGCG
                                 |||||||  | ||   |||||
                                 TGGGACA  G GT   TGTGT
                                     GG C  G__
GAM616  EGLN2    5'  TGTGTGTTGGGAGGGAGTGGGC 54925      __ G    AAAA    TACA
                                 GCCC  T TTTCC    ACGCG
                                 ||||  | |||||    |||||
                                 CGGG  A GGAGG    TGTGT
                                   TG G     GTTG
GAM616  EIF2C1   3'  TGTACCTTTCTTTGGGGAATGG 25200          AAAAACGC_
           GGT                     GCCCTGTTTCC        GTACA
                                   ||||||||||||       |||||
                                   TGGGGTAAGGG        CATGT
                                         GTTTCTTTC
GAM616  F2RL3    3'  TGTGACCTTATTTGGAAATAGG 15531           AACGCG
           GT                      GCCCTGTTTCCAAA     TACA
                                   ||||||||||||||     ||||
                                   TGGGATAAAGGTTT     GTGT
                                         ATTCCA
GAM616  FACL4    3'  TGTGCAGTAACTTGGGAGTGTG 43681     C GT     AA_  GC
           GT                      GCC T  TTCCAA   AC  GTACA
                                   ||| |  ||||||   ||  |||||
                                   TGG G  AGGGTT   TG  CGTGT
                                     T TG     CAA  A_
GAM616  FSTL1    3'  GTTTTTGGAAAGCAGGGT    24006          _
                                   GCCCTGTTT CCAAAAAC
                                   ||||||||| ||||||||
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                                TGGGACGAA GGTTTTTG
                                     A
GAM616  FUT7    3'  TGTAGGCTGGGGCGGGGC    16809        T  AAAAC  G
                                GCCCTGTT CCA    GC TACA
                                |||||||| |||    || ||||
                                CGGGGCGG GGT    CG ATGT
                                   _  _____  G
GAM616  FZD3    5'  TGTGGTTTGGGAATGTGGT   34260    C        AA
                                GCC TGTTTCCAAA  CGCG
                                ||| ||||||||||  ||||
                                TGG GTAAGGGTTT  GTGT
                                  T        G_
GAM616  GGCX    3'  GCTTTTTGGGGGCTGGGT    7704      T  TT      C
                                GCCC GT  CCAAAAA GC
                                |||| ||  ||||||| ||
                                TGGG CG  GGTTTTT CG
                                  T  GG      _
GAM616  GPM6B   5'  TGTGTGTTGGGGGGAACAGGG  67669          AAA
                                CCCTGTTTCC   AACGCGTA
                                ||||||||||   ||||||||
                                GGGACAAGGG   TTGTGTGT
                                     GGG
GAM616  GPR63   3'  GTATGTGTGTGAGCAGTGT   48626    C    TC AAAA
                                GC CTGTT  C    ACGCGTAC
                                || |||||  |    ||||||||
                                TG GACGA  G    TGTGTATG
                                 T    GT _____
GAM616  GRINL1A  3'  TGTGTTTTTTTTTGAGATGGGG 70073          C___       TACA
            T                    GCCCTGTTTC    AAAAACGCG
                                ||||||||||    |||||||||
                                TGGGGTAGAG    TTTTTGTGT
                                     TTTT
GAM616  GRM6    3'  TGTGTTCGGGTTGGGGATGGGT 7776      T  TT    AAA  CG
                                GCCC GT  CCAA   CG  TACA
                                |||| ||  ||||   ||  ||||
                                TGGG TA  GGTT   GC  GTGT
                                  _  GG    GG_  TT
GAM616  HCS     3'  TGTATTTGATTGGGAATGGTGC 38997    C        AAA  C
                                GC CTGTTTCCAA   CG GTACA
                                || ||||||||||   || |||||
                                CG GGTAAGGGTT   GT TATGT
                                  T        A__  T
GAM616  HIS1    3'  TGTGACTGCATTTTTGGGGAGG 22342      G TT      C  __
            GGT                    GCCCT T  CCAAAAA GCG  TACA
                                ||||| |  ||||||| |||  ||||
                                TGGGG A  GGTTTTT CGT  GTGT
                                  _ GG      A   CA
GAM616  HOXC4   5'  TGTGTGTGTGGAGCTGAGACAG 28252     C     CAAAA_
            GC                    GCC TGTTTC     ACGCGTACA
                                ||| ||||||     |||||||||
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                                CGG ACAGAG     TGTGTGTGT
                                  _     TCGAGG
GAM616  HPS4     3'  TGTGTTTTGGGGGCAGGG    42229       TT     A
                                CCCTGT  CCAAAA CGCG
                                ||||||  |||||| ||||
                                GGGACG  GGTTTT GTGT
                                   GG     _
GAM616  HSD17B1  3'  TGTGTGGTCCCTGGGGATGGGG 6430        TT   AAA  G
           C                     GCCCTGT  CCA   AC CGTACA
                                 |||||||  |||   || ||||||
                                 CGGGGTA  GGT   TG GTGTGT
                                    GG   CCC  _
GAM616  HSPA4    3'  TGTGTGTGTGTGGGGAAGGGT  90655      G TT   AAA
                                GCCCT T  CCA   ACGCGTACA
                                ||||| |  |||   |||||||||
                                TGGGA A  GGT   TGTGTGTGT
                                  _ GG   G__
GAM616  HSPA9B   3'  TGTGCCATGTTTGTAGATGGGG 15955         C    AACGC
           C                     GCCCTGTTT CAAA     GTACA
                                 |||||||||| ||||     |||||
                                 CGGGGTAGA GTTT     CGTGT
                                      T    GTAC_
GAM616  IGFBP4   3'  TGTGTGTGTTTGTGAGCATGGG 9556       _   TC   AA
           T                     GCCC TGTT  CAA  ACGCGTACA
                                 |||| ||||  |||  |||||||||
                                 TGGG ACGA  GTT  TGTGTGTGT
                                   T   GT  __
GAM616  IL2RB    3'  GTGTGTGTTGCAGGGGGGC   7944       GTTT  AAA
                                GCCCT    CC   AACGCGTAC
                                |||||    ||   |||||||||
                                CGGGG    GG   TTGTGTGTG
                                   _____  ACG
GAM616  INHBB    3'  TGTGTGTGTTTTTGGGGTGGGG 11012     TG  T
                                CCC  TT CCAAAAACGCGTACA
                                |||  || ||||||||||||||
                                GGG  GG GGTTTTTGTGTGTGT
                                  GT  _
GAM616  INSR     3'  TGTGTGTGTCCATTAGACACGG 71541     C    CCAAAA
           C                     GCC TGTTT     ACGCGTACA
                                 ||| |||||     |||||||||
                                 CGG ACAGA     TGTGTGTGT
                                   C    TTACC_
GAM616  KIAA0857 3'  TGTGCCTTTGGTGGGCGGGGT  67259         _    AA
                                GCCCTGTTT CCAAA  CGCG
                                ||||||||| |||||  ||||
                                TGGGGCGGG GGTTT  GTGT
                                     T    CC
GAM616  KIF3C    3'  TGTGCGTGTTTACCTCCACAGG 11208       TTCCAA
           G                     CCCTGT     AAACGCGTACA
                                 ||||||     ||||||||||
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                                GGGACA     TTTGTGCGTGT
                                   CCTCCA
GAM616  MSF      3'  TGTGTGTGCATGGAAGTTGGGG 89470      GT_    AAAA
              C                    GCCCT   TTCCA    CGCGTACA
                                   |||||   |||||    ||||||||
                                   CGGGG   AAGGT    GTGTGTGT
                                     TTG     AC__
GAM616  MSL3L1   3'  TGTGTGGAGGTGGAAACAGAGC 23293    C       AAA__
                                   GC CTGTTTCCA     ACGCG
                                   || |||||||||     |||||
                                   CG GACAAAGGT     TGTGT
                                    A        GGAGG
GAM616  NPR2L    3'  TGTATTTTGCTTTTTTGAGACG 22602          C    C ___
              GGGT                    GCCCTGTTTC AAAAA GC   GTACA
                                   |||||||||| ||||| ||   |||||
                                   TGGGGCAGAG TTTTT CG   TATGT
                                         _     T  TTT
GAM616  ORC1L    3'  GGTTTTGTTTTTTTGAGACAGGG 15985          C      CGTACA
              T                    GCCCTGTTTC AAAAACG
                                   |||||||||| |||||||
                                   TGGGACAGAG TTTTTGT
                                        T      TTTGGG
GAM616  PITX2    5'  GTGCGCGTTGCGGAGGGT    6159      TGTT   AAA
                                   GCCC    TCC   AACGCGTAC
                                   ||||    |||   |||||||||
                                   TGGG    AGG   TTGCGCGTG
                                     _____   CG_
GAM616  PNOC     5'  TGTATGTGTCATGGAGGTGGGC 21720      T TT    AAA
                                   GCCC G  TCCA   ACGCGTACA
                                   |||| |  ||||   |||||||||
                                   CGGG T  AGGT   TGTGTATGT
                                     _ GG    AC_
GAM616  PPP1R3D  3'  TGTGTAATGAGTTGGGGCAGGG 21792        T    AA____    TACA
              T                    GCCCTGTT CCAA     ACGCG
                                   |||||||| ||||     |||||
                                   TGGGACGG GGTT     TGTGT
                                        _    GAGTAA
GAM616  PRKY     3'  TGTACAGATTTGAAATGGGGT  12391          C   AACGC
                                   GCCCTGTTTC AAA    GTACA
                                   |||||||||| |||    |||||
                                   TGGGGTAAAG TTT    CATGT
                                        _   AGA__
GAM616  RGS16    3'  TGTGCTGTCTCTTGGAGGCAGG 12874           AA_   C
              GC                     GCCCTGTTTCCAA   ACG GTACA
                                   ||||||||||||||   ||| |||||
                                   CGGGACGGAGGTT   TGT CGTGT
                                          CTC   _
GAM616  SP3      5'  TGTGCGCGTGTGAGTGTGGGC  83388      TGT   CAAAA
                                   GCCC   TTC    ACGCGTACA
                                   ||||   |||    |||||||||
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                                CGGG  GAG    TGCGCGTGT
                                  TGT  TG___
GAM616  TAL1     3'  TGTGTGTGTGAGAGACGGTGT  13533    C      CAAAA
                                GC CTGTTTC    ACGCGTACA
                                || |||||||    |||||||||
                                TG GGCAGAG    TGTGTGTGT
                                 T      AG___
GAM616  TIMM17B  5'  TGTGCGTCTACGCTGGGGGCGT 20691    C   TT   AAAAC_
           GGC                    GCC TGT  CCA     GCGTACA
                                ||| |||  |||     |||||||
                                CGG GCG  GGT     TGCGTGT
                                  T  GG  CGCATC
GAM616  TMEM1    3'  TGTATGTGTTTGAGACAAGCAG 13807        CCAA_
           G                     CCTGTTT    AAACGCGTACA
                                |||||||    ||||||||||
                                GGACGAA    TTTGTGTATGT
                                    CAGAG
GAM616  TNFRSF11A 3'  TGTAAACACTTTTGGGAAAGGG 15198      G        ACGCG
           C                     GCCCT TTTCCAAAA    TACA
                                ||||| |||||||||    ||||
                                CGGGA AAGGGTTTT    ATGT
                                  _       CACAA
GAM616  UBQLN2   3'  TGTGATTTTTGGAAACAGG   26493          _
                                CCTGTTTCCAAAAA CGCG
                                |||||||||||||| ||||
                                GGACAAAGGTTTTT GTGT
                                       A
GAM616  VNN1     3'  TGTGACTGTATTTGGAGACAGG 17424           A   CG
           GT                    GCCCTGTTTCCAAA ACG  TACA
                                |||||||||||||| |||  ||||
                                TGGGACAGAGGTTT TGT  GTGT
                                       A   CA
GAM616  AP3S2    3'  TGTATGTTTAGTAGAGACAGGG 20659         CAAAAAC
           T                     GCCCTGTTTC      GCGTACA
                                ||||||||||      |||||||
                                TGGGACAGAG      TGTATGT
                                     ATGATT_
GAM616  BIRC2    3'  TGTATGTGTACCTAAGGGAGTA 67781    C       AAAA__
           GTGT                    GC CTGTTTCC     ACGCGTACA
                                || ||||||||     |||||||||
                                TG GATGAGGG     TGTGTATGT
                                 T       AATCCA
GAM616  BMF      3'  TGTGTGCGTGCCCTGGTGTGGG 54291      TG TT   AAA_
           GC                    GCCC  T  CCA    ACGCGTACA
                                ||||  |  |||    |||||||||
                                CGGG  G  GGT    TGCGTGTGT
                                  GT T_   CCCG
GAM616  C(27)-3BETA-HSD 3'  TGTTTTTAGAGACAGGGT    48056          C
                                GCCCTGTTTC AAAAACG
                                |||||||||| |||||||
```

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                                TGGGACAGAG TTTTTGT
                                     A
GAM616  C1QTNF7  3'  GTATGTGTTTAAGGGGGT    50006      G  TCCAA
                                GCCCT TT    AAACGCGTAC
                                ||||| ||    ||||||||||
                                TGGGG AA    TTTGTGTATG
                                  G _____
GAM616  C6orf35  3'  TGTGTGCGTGCTGGGGGAGGGT 38047      G TT   AAA
                                GCCCT T  CCA   ACGCGTACA
                                ||||| |  |||   |||||||||
                                TGGGA G  GGT   TGCGTGTGT
                                  _ GG   CG_
GAM616  C8orf17  5'  GTGCGGCTGAGGGCGGGGT   39999        TC  AAAAC  _
                                GCCCTGTT  CA    GC GTAC
                                ||||||||  ||    || ||||
                                TGGGGCGG  GT    CG CGTG
                                    GA _____  G
GAM616  C9orf5   3'  TGTGTGTGTGTTGGGGGTGGGG 50109     TG TT    AA
                                CCC  T  CCAA  ACGCGTACA
                                |||  |  ||||  |||||||||
                                GGG  G  GGTT  TGTGTGTGT
                                 GT GG    G_
GAM616  CAMTA1   5'  TGTGCGTGGGCCGCGGGGCGGG 68507        TT CAAAAA
           GC                    GCCCTGT  C     CGCGTACA
                                |||||||  |     ||||||||
                                CGGGGCG  G     GTGCGTGT
                                   GG CGCCGG
GAM616  COLEC12  3'  GTATGTATGGGACAGGGT    56106        T   AAAAC
                                GCCCTGTT CCA    GCGTAC
                                |||||||| |||    ||||||
                                TGGGACAG GGT    TGTATG
                                   _  A____
GAM616  COQ7     3'  TATGTTTTTTGGAGACAGGGC  32860             C
                                GCCCTGTTTCCAAAAA GCGTA
                                |||||||||||||||| |||||
                                CGGGACAGAGGTTTTT TGTAT
                                                 _
GAM616  DAPK2    3'  TGTATTTGGAGATGGGGT    27517            A
                                GCCCTGTTTCCAAA ACG
                                |||||||||||||| |||
                                TGGGGTAGAGGTTT TGT
                                      A
GAM616  Di-Ras2  3'  TGTGTTAGCTTGGGGATAGG   34615      TT   A__
                                CCTGT  CCAA   AACGCG
                                |||||  ||||   ||||||
                                GGATA  GGTT   TTGTGT
                                  GG   CGA
GAM616  DKFZP586M1120 3'  TGTGTGTGTTGGGCAGGCAGG  49289        _  AAA
                                CCTGTTT CC   AACGCGTACA
                                |||||||  ||   ||||||||||
```

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                                GGACGGA GG   TTGTGTGTGT
                                   C  G__
GAM616  EFA6R    3'  TGTGCGTGTGTGGGCATGGGGT 31642       T    AAA
                                GCCCTGT TCCA   ACGCGTACA
                                ||||||| ||||   |||||||||
                                TGGGGTA GGGT   TGTGCGTGT
                                   C    G__
GAM616  FGF19    5'  GTGTGCGGGGGGCGGAGGC    18858    _   TT  AAAAA
                                GCC CTGT  CC    CGCGTAC
                                ||| ||||  ||    |||||||
                                CGG GGCG  GG    GCGTGTG
                                  A    GG  _____
GAM616  FKBP5    3'  TGTGTGTGGGGAGGGGAAGGGT 15934      G TT  AAAAA
                                GCCCT T  CC    CGCGTACA
                                ||||| |  ||    ||||||||
                                TGGGA A  GG    GTGTGTGT
                                  _ GG  AGGG_
GAM616  FLJ10483 3'  TGTGTGTGTTTTGCCACAGAGC 36659    C    TTCCA
                                GC CTGT    AAAACGCGTACA
                                || ||||    ||||||||||||
                                CG GACA    TTTTGTGTGTGT
                                 A   CCG__
GAM616  FLJ10525 5'  TGTGTGTGGCGCGAGGCAGGG  36726        CAAAAA
                                CCCTGTTTC     CGCGTACA
                                |||||||||     ||||||||
                                GGGACGGAG     GTGTGTGT
                                     CGCG__
GAM616  FLJ10743 3'  TGTGTGTGTTAGGGAGTGAGGG 37092      GT    AAA
           T                     GCCCT  TTCC   AACGCGTACA
                                |||||  ||||   ||||||||||
                                TGGGA  GAGG   TTGTGTGTGT
                                  GT   GA_
GAM616  FLJ10997 3'  TGTGTGTGGGAGGGGGGC    37515      G     AAA
                                GCCCT TTTCCA   ACGCG
                                ||||| ||||||   |||||
                                CGGGG GAGGGT   TGTGT
                                  G     G__
GAM616  FLJ12355 3'  TGTATTTGGAGATAAGGC    47121     C        A
                                GCC TGTTTCCAAA ACG
                                ||| ||||||||||| |||
                                CGG ATAGAGGTTT TGT
                                  A         A
GAM616  FLJ12610 3'  TGTGTGTGGAGACAAGGC    45862     C       AAA
                                GCC TGTTTCCA   ACGCG
                                ||| ||||||||   |||||
                                CGG ACAGAGGT   TGTGT
                                  A       G__
GAM616  FLJ12891 3'  TGTTTTTTTGAGACGGGGT   46933         C    C
                                GCCCTGTTTC AAAAA GCG
                                |||||||||| ||||| |||
```

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                                TGGGGCAGAG TTTTT TGT
                                      _    T
GAM616  FLJ14251  3'  TGTGTGTGTTTTTTGCCTTGG  46495   TGTTTC
                                CC     CAAAAACGCGTACA
                                ||     ||||||||||||||
                                GG     GTTTTTGTGTGTGT
                                 TTCC__
GAM616  FLJ20013  3'  TGTGTTGGATTAGGGAACAGGG 34804          AAA___     TACA
          T                      GCCCTGTTTCC     AACGCG
                                 ||||||||||||     ||||||
                                 TGGGACAAGGG     TTGTGT
                                       ATTAGG
GAM616  FLJ20793  3'  TGTGTGTGTTTTGCTTTGGG  93452    TGTTTCCA
                                CCC      AAAACGCGTACA
                                |||      ||||||||||||
                                GGG      TTTTGTGTGTGT
                                  TTTCG___
GAM616  FLJ21272  5'  TGTGTGCTGTTTGGAGACTGGG 47394     T       AAC
          T                      GCCC GTTTCCAAA   GCGTACA
                                 |||| |||||||||   |||||||
                                 TGGG CAGAGGTTT   CGTGTGT
                                   T       GT_
GAM616  FLJ21459  3'  TGTATTTTTTGTGGAAACAGGG 44813          A   CGC
          T                      GCCCTGTTTCCA AAA   GTACA
                                 |||||||||||| |||   |||||
                                 TGGGACAAAGGT TTT   TATGT
                                       G   TT_
GAM616  FLJ22246  3'  TGTGTGTGTTGGTGAGTGAGG  48216    GT   C AA
                                CCT  TTC A  AACGCGTACA
                                |||  ||| |  ||||||||||
                                GGA  GAG T  TTGTGTGTGT
                                  GT   _ GG
GAM616  FLJ23186  3'  TGTTTTTTGAGACAGGGT    61047         C
                                GCCCTGTTTC AAAAACG
                                |||||||||| |||||||
                                TGGGACAGAG TTTTTGT
                                      T
GAM616  FLJ25416  5'  TGTATTTAGTGGAGATGGGGT  59459          AAAACGC
                                GCCCTGTTTCCA      GTACA
                                ||||||||||||      |||||
                                TGGGGTAGAGGT      TATGT
                                       GATT___
GAM616  FOXP1     3'  TGTGTGTGTATTGGGGGGAGGG 52050     G TT    AA
                                CCCT T  CCAA  ACGCGTACA
                                ||||  |  ||||  |||||||||
                                GGGA G  GGTT  TGTGTGTGT
                                  G GG    A_
GAM616  FXYD3     3'  TGTGTGCATTGGGGTGGGGC   21062     TG  T    AA_
                                GCCC  TT CCAA   ACGCG
                                ||||  || ||||   |||||
```

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                                CGGG  GG GGTT   TGTGT
                                  GT  _    ACG
GAM616  GGA2     3'  TGTGTGTGTTCGGGGAGAGGGT 57688      G TT  AAA
                                GCCCT T  CC   AACGCGTACA
                                |||||| |  ||   ||||||||||
                                TGGGA A  GG   TTGTGTGTGT
                                  G GG  C__
GAM616  GGA2     3'  TGTGTGTGTTCGGGGAGAGGGT 57689      G TT  AAA
                                GCCCT T  CC   AACGCGTACA
                                |||||| |  ||   ||||||||||
                                TGGGA A  GG   TTGTGTGTGT
                                  G GG  C__
GAM616  GLP      3'  TGTGTATTGGGGATGGGAGT   38474    _    TT    AA
                                GC CCTGT  CCAA  ACGCG
                                || |||||  ||||  |||||
                                TG GGGTA  GGTT  TGTGT
                                 A    GG    A_
GAM616  GPR108   3'  TGTGTGTGGCGGGGGCGCGGGC 69634      _   TT  AAAAA
                                GCCC TGT  CC    CGCGTACA
                                |||| |||  ||    ||||||||
                                CGGG GCG  GG    GTGTGTGT
                                  C   GG  CG___
GAM616  HIF1AN   3'  TGCGTTTTTTGGGGAGGGGT   62671      G TT      _
                                GCCCT T  CCAAAAA CGCG
                                |||||| |  ||||||| ||||
                                TGGGG A  GGTTTTT GCGT
                                  _ GG      T
GAM616  KIAA0090 3'  TGCTTTTTTTTTGGAGGCAGGG 89820             C___   TACA
           T                     GCCCTGTTTCCAAAAA   GCG
                                ||||||||||||||||   |||
                                TGGGACGGAGGTTTTT   CGT
                                        TTTT
GAM616  KIAA0186 3'  TGTATTTTTTGTGGAGATGGGG 41125           A   CGC
           T                     GCCCTGTTTCCA AAA   GTACA
                                |||||||||||| |||   |||||
                                TGGGGTAGAGGT TTT   TATGT
                                      G   TT_
GAM616  KIAA0186 3'  TGTGAAATTTGGGAACAGG    41126           AA_
                                CCTGTTTCCAAA   CGCG
                                ||||||||||||   ||||
                                GGACAAGGGTTT   GTGT
                                      AAA
GAM616  KIAA0232 3'  TGTGTGTGGTGGGTTGGGGC   73125      TT   AAA
                                GCCCTG  TCCA   ACGCGTA
                                ||||||  ||||   |||||||
                                CGGGGT  GGGT   TGTGTGT
                                   T_   GG_
GAM616  KIAA0284 3'  TGTGTGTGTGAGGGGGGGCGGG 63806       TT  AAAA
           G                     CCCTGT  CC    ACGCGTACA
                                ||||||  ||    |||||||||
```

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                                GGGGCG GG   TGTGTGTGT
                                   GG GGAG
GAM616  KIAA0342 3' TGTATGTGCCCAGGGGTGGGC 71143    TGTT  AAAAA
                                GCCC   TCC    CGCGTACA
                                ||||   |||    ||||||||
                                CGGG   GGG    GTGTATGT
                                  T___  GACCC
GAM616  KIAA0513 5' TGTGTGTGGGCAGAGAGACATG 29055    C     CAAAAA
           GC                    GCC TGTTTC     CGCGTACA
                                ||| ||||||     ||||||||
                                CGG ACAGAG     GTGTGTGT
                                  T     AGACGG
GAM616  KIAA0537 3' TGTGTGTGTGGGGGGGGGTGGG 29935    TG TT  AAAA
           G                     CCC  T  CC    ACGCGTACA
                                ||| |  ||   |||||||||
                                GGG  G  GG   TGTGTGTGT
                                  GT GG  GGGG
GAM616  KIAA0635 3' TGTGTGTGTATACCTGGGGGTG 28425   TG TT   AAA__
           GG                    CC  T  CCA    ACGCGTACA
                                || |  |||    |||||||||
                                GG  G  GGT    TGTGTGTGT
                                 GT GG   CCATA
GAM616  KIAA0682 3' TGTATTTTTGGTAGACGGGGT  30035        _     CG
                                GCCCTGTTT CCAAAAA  CG
                                ||||||||| |||||||  ||
                                TGGGGCAGA GGTTTTT  GT
                                     T      AT
GAM616  KIAA0711 3' TGTAAACGATTTGGAAATAGG  30157          AA  CG
                                CCTGTTTCCAAA  CG  TACA
                                ||||||||||||  ||  ||||
                                GGATAAAGGTTT  GC  ATGT
                                      A_  AA
GAM616  KIAA0864 3' TGTGCTGGTGTGGAAACGGGGC 63943          AAAA  C
                                GCCCTGTTTCCA    CG GTACA
                                ||||||||||||    || |||||
                                CGGGGCAAAGGT    GT CGTGT
                                      GTG_  _
GAM616  KIAA1041 3' GTGTGTGTTTTAATGGAG    30827      __
                                TTCCA  AAAACGCGTAC
                                |||||  ||||||||||||
                                GAGGT  TTTTGTGTGTG
                                   AA
GAM616  KIAA1280 5' TGTTTTGTTTTTGAGACAGGGT 70294         C      CGT
                                GCCCTGTTTC AAAAACG   ACA
                                |||||||||| |||||||   |||
                                TGGGACAGAG TTTTTGT   TGT
                                     _      TT_
GAM616  KIAA1465 3' TGTGTGTGTCGGGGGGGTAGGG  61511      TT   AAAA
                                CCCTG  TCC    ACGCGTACA
                                |||||  |||    |||||||||
```

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                                GGGAT  GGG   TGTGTGTGT
                                  GG  GC__
GAM616  KIAA1484  3'  TGTGTGTGTGTTGGGGGAGGGT 70526     G TT   AA
                                GCCCT T  CCAA  ACGCGTACA
                                ||||| |  ||||  |||||||||
                                TGGGA G  GGTT  TGTGTGTGT
                                  _ GG   G_
GAM616  KIAA1494  5'  GTGCGCGCGTGAGGGGGGC   68983     G  TC  AAAA
                                GCCCT TT  CA   CGCGTAC
                                ||||| ||  ||   |||||||
                                CGGGG GA  GT   GCGCGTG
                                  G  __  GC__
GAM616  KIAA1559  3'  TGTATAATTTTTTTGAGACAGG 73464       C    CGC
          GT                    GCCCTGTTTC AAAAA  GTACA
                                ||||||||||  |||||  |||||
                                TGGGACAGAG TTTTT  TATGT
                                     T    TAA
GAM616  KIAA1822  3'  TGTGTGTTGGGGGCGGTGT   68198   C   TT   AA
                                GC CTGT  CCAA  ACGCG
                                || ||||  ||||  |||||
                                TG GGCG  GGTT  TGTGT
                                 T   GG   G_
GAM616  MESDC2   3'  TGTTTTTGTTTTTGAGACAGGG 72926       C     CGT
          T                     GCCCTGTTTC AAAAACG  ACA
                                ||||||||||  |||||||  |||
                                TGGGACAGAG TTTTTGT  TGT
                                     _     TTT
GAM616  MGC13138  3'  GTGTGTGTGTGATGGGGT   54161       TCCAAAA
                                GCCCTGTT     ACGCGTAC
                                ||||||||     ||||||||
                                TGGGGTAG     TGTGTGTG
                                   TG_____
GAM616  MGC22014  3'  TGTGTGTGTGGTGAATGGGG  65119       _  AAA
                                CCCTGTTT CCA  ACGCG
                                |||||||| |||  |||||
                                GGGGTAAG GGT  TGTGT
                                   T  GTG
GAM616  MGC2306   3'  TGTATGCGGTGACGGCGGGGT  51954       TC  AAAA
                                GCCCTGTT  CA   CGCGTACA
                                ||||||||  ||   ||||||||
                                TGGGGCGG  GT   GCGTATGT
                                   CA  G___
GAM616  MGC2477   5'  TGTTTTTGGAGACAAGGT   44316   C
                                GCC TGTTTCCAAAAACG
                                ||| ||||||||||||||
                                TGG ACAGAGGTTTTTGT
                                  A
GAM616  MGC2508   3'  TGGGCTTTTGGGGATGGGGC  44508      TT    AC  G
                                GCCCTGT  CCAAAA  GC TA
                                |||||||  ||||||  || ||
```

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                                CGGGGTA  GGTTTT  CG GT
                                   GG     __  G
GAM616  MGC2742  3'  TGTGTGTGTGGAGGGGGGGC  43979      G     AAA
                                GCCCT TTTCCA   ACGCG
                                ||||| ||||||   |||||
                                CGGGG GGAGGT   TGTGT
                                   G     GTG
GAM616  MGC4549  3'  GTGCGTGTGGGTGTGGGT    51472     TGTT   AAAA
                                GCCC    TCC    ACGCGTAC
                                ||||    |||    ||||||||
                                TGGG    GGG    TGTGCGTG
                                  TGT_  _____
GAM616  MLZE     5'  TGTATGTGAAAGGAAATGGGTG 49456    _       AAAAA
           T                     GC CCTGTTTCC     CGCGTACA
                                || |||||||||     ||||||||
                                TG GGGTAAAGG     GTGTATGT
                                 T       AAA__
GAM616  NEIL1    3'  TGAATTTTTGGGAGCAGG    45153            CG
                                CCTGTTTCCAAAAA  CG
                                ||||||||||||||  ||
                                GGACGAGGGTTTTT  GT
                                        AA
GAM616  NT5C1B   5'  TGTGCCTGTTGTGGGAGCAGGG 71751           AA   C
           C                     GCCCTGTTTCCA  AACG GTACA
                                ||||||||||||  |||| |||||
                                CGGGACGAGGGT  TTGT CGTGT
                                       G_   C
GAM616  P2RX5    3'  TGTGCGTGTCCGGAAAAGGGC  11923      G    AAAA
                                GCCCT TTTCC    ACGCGTACA
                                ||||| |||||    |||||||||
                                CGGGA AAAGG    TGTGCGTGT
                                   _    CC__
GAM616  PDE2A    3'  TGTGTGCGTTGTGGGGTGGGG  12008     TG TT CAAA
                                CCC  T  C    AACGCGTACA
                                |||  |  |   ||||||||||
                                GGG  G  G    TTGCGTGTGT
                                  GT GG TG__
GAM616  PIP5K2A  3'  TGTGTGTGTGTTGGGGGGGGGT 18520      G TT    AA
                                GCCCT T  CCAA  ACGCGTACA
                                ||||| |  ||||  |||||||||
                                TGGGG G  GGTT  TGTGTGTGT
                                  _ GG    G_
GAM616  POLR3F   3'  TGTGATGGTATTTGGAGGTGGG 60620      TG       A  G  _
           GC                     GCCC  TTTCCAAA AC CGT ACA
                                ||||  |||||||| || ||| |||
                                CGGG  GGAGGTTT TG GTA TGT
                                  GT       A  _   G
GAM616  PRO0618  3'  TGTGTGTAAAAAGAGGGGCAGG 27057        TT CAAAAAC
           GT                     GCCCTGT  C      GCGTACA
                                |||||||  |      |||||||
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                                TGGGACG G      TGTGTGT
                                    GG AGAAAAA
GAM616  PRO2730  3'  TGTGGCATTTGGGGATAAGGT  48190     C   TT    AAC  G
                                GCC TGT  CCAAA   GC TACA
                                ||| |||  |||||   || ||||
                                TGG ATA  GGTTT   CG GTGT
                                  A  GG    A__  _
GAM616  PTPRT    3'  TGTGTGGTCAGTGGGAGGGGGT 56513      G     AAA  G
                                GCCCT TTTCCA   AC CGTACA
                                ||||| ||||||   || ||||||
                                TGGGG GAGGGT   TG GTGTGT
                                  _     GAC  _
GAM616  SHANK3   3'  TGTGTGTGGGTGAAACTGGGT  66113     T    CAAAAA
                                GCCC GTTTC     CGCGTACA
                                |||| |||||     ||||||||
                                TGGG CAAAG     GTGTGTGT
                                  T    TGG___
GAM616  SMARCA4  5'  TGTGTGTGAAGGGGGGGCGGTG 13249     _   TT  AAAAA
            GC                    GCC CTGT  CC     CGCGTACA
                                ||| ||||  ||     ||||||||
                                CGG GGCG  GG     GTGTGTGT
                                  T   GG  GGAA_
GAM616  SP2      5'  GTGTGCGATGAAGGGGGC    13333      G   CCAAAAA
                                GCCCT TTT      CGCGTAC
                                ||||| |||      |||||||
                                CGGGG AAG      GCGTGTG
                                  G   TA_____
GAM616  SSB-4    3'  TGTGTGCCCCGTTGCAGACAGG 55965         C   AAAC
            GC                    GCCCTGTTT CAA    GCGTACA
                                ||||||||| |||    |||||||
                                CGGGACAGA GTT    CGTGTGT
                                     C   GCCC
GAM616  STAF65(gamma) 3'  TGTAAAATGTGGAGGCAGGGC  30076           AAAACGCG
                                GCCCTGTTTCCA       TACA
                                ||||||||||||       ||||
                                CGGGACGGAGGT       ATGT
                                       GTAAA___
GAM616  STI2     3'  TGTGGATTTTGTGGGATGGGGT 90409        TT _    A_
                                GCCCTGT  C CAAAA  CGCG
                                |||||||  | |||||  ||||
                                TGGGGTA  G GTTTT  GTGT
                                    GG T    AG
GAM616  STK22B   3'  TGTGTGTGGTGGGGGTCGGGGT 54869       _ TT   AAA
                                GCCCTG T  CCA   ACGCGTA
                                ||||||  |  |||   |||||||
                                TGGGGC G  GGT   TGTGTGT
                                   T GG   GG_
GAM616  SUN1     3'  TGTAAATATTTTTTGGAAGCGG 47927    C          CGCG_
            AGT                   GC CTGTTTCCAAAAA     TACA
                                || ||||||||||||     ||||
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                                TG GGCGAAGGTTTTT    ATGT
                                 A          TATAA
GAM616  TOR1B    3'  TGTGTGTGTGGGGGGGGGTGGG 27979     TG TT  AAAA
                GC                 GCCC  T  CC   ACGCGTACA
                                   |||| | ||   |||||||||
                                   CGGG  G  GG   TGTGTGTGT
                                     GT GG  GGGG
GAM616  TOR1B    3'  TGTGTGTGTGTGGGGGGGGGT  27980      G TT   AAA
                                   GCCCT T  CCA   ACGCGTACA
                                   ||||| |  |||   |||||||||
                                   TGGGG G  GGT   TGTGTGTGT
                                     _ GG   G__
GAM616  UBE4B    3'  TGTGTGAGTTTGAGGCAGGGT  21287         C  AA_
                                   GCCCTGTTTC AA   ACGCG
                                   |||||||||| ||   |||||
                                   TGGGACGGAG TT   TGTGT
                                         T  GAG
GAM616  LOC121838 5'  TGTGACTGTATTTGGGGATAGG 76519        TT    A   CG
                GT                 GCCCTGT  CCAAA ACG  TACA
                                   |||||||  ||||| |||  ||||
                                   TGGGATA  GGTTT TGT  GTGT
                                      GG    A   CA
GAM616  LOC122553 3'  TGTGTGTGTGAAAAAGCTGGGT 74595      T    CCAAAA
                                   GCCC GTTT     ACGCGTACA
                                   |||| ||||     |||||||||
                                   TGGG CGAA     TGTGTGTGT
                                     T   AAAG__
GAM616  LOC122726 3'  TGTGTGCTTGGGAATATGGT   76105     C        AA
                                   GCC TGTTTCCAA  ACGCG
                                   ||| |||||||||  |||||
                                   TGG ATAAGGGTT  TGTGT
                                     T        CG
GAM616  LOC126528 3'  TGTACGTGGTGCCCGTGGGTGG 75033      TG TT   AAAA___
                GGT                  GCCC  T  CCA      CGCGTACA
                                     |||| | |||      ||||||||
                                     TGGG  G  GGT      GTGCATGT
                                       GT __   GCCCGTG
GAM616  LOC126755 3'  TGTGATGGTATTTGGAGGTGGG 75076      TG       A  G   _
                GC                   GCCC  TTTCCAAA AC CGT ACA
                                     ||||  |||||||| || ||| |||
                                     CGGG  GGAGGTTT TG GTA TGT
                                       GT       A  _   G
GAM616  LOC130612 3'  TGTATGTGTGTGGGGGTGGG   75474    TG TT   AAA
                                   CC  T  CCA   ACGCGTACA
                                   ||  |  |||   |||||||||
                                   GG  G  GGT   TGTGTATGT
                                    GT GG   G__
GAM616  LOC137964 5'  TGTGGACTTTGGAATGGGGT   75803        T    AA_
                                   GCCCTGTT CCAAA   CGCG
                                   ||||||||  |||||   ||||
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                                TGGGGTAA GGTTT   GTGT
                                    _    CAG
GAM616   LOC144667 3'  TGTTTTTGTTTTTGAGGCAGGG 84092         C      CGT
             T                   GCCCTGTTTC AAAAACG   ACA
                                 |||||||||| |||||||   |||
                                 TGGGACGGAG TTTTTGT   TGT
                                     _      TTT
GAM616   LOC145891 3'  TGTGCTCTTTTGGAAACTGGGT 78019     T        ACGC
                                 GCCC GTTTCCAAAA   GTACA
                                 |||| ||||||||||   |||||
                                 TGGG CAAAGGTTTT   CGTGT
                                   T        CT__
GAM616   LOC146287 5'  TGTGTGTAAGGAAATGGGT   84635     T     AAAA
                                 GCCC GTTTCC   ACGCG
                                 |||| ||||||   |||||
                                 TGGG TAAAGG   TGTGT
                                   _     AATG
GAM616   LOC146517 5'  TGTATACCAATTTGGGAATAGG 78512           AACGC
             G                   CCCTGTTTCCAAA    GTACA
                                 ||||||||||||    |||||
                                 GGGATAAGGGTTT    TATGT
                                       AACCA
GAM616   LOC146728 5'  TGTGACTATTTGGAGATAGGGT 84778           AA__
                                 GCCCTGTTTCCAAA   CGCG
                                 ||||||||||||   ||||
                                 TGGGATAGAGGTTT   GTGT
                                       ATCA
GAM616   LOC150311 5'  GTACTCTTGGAAGCTGGGC   80566     T      AAACGC
                                 GCCC GTTTCCAA     GTAC
                                 |||| ||||||||     ||||
                                 CGGG CGAAGGTT     CATG
                                   T       CT____
GAM616   LOC151190 5'  TGTGTGTGTGTGGGAGGGGGGT 80965      G     AAA
                                 GCCCT TTTCCA   ACGCGTACA
                                 ||||| ||||||   |||||||||
                                 TGGGG GAGGGT   TGTGTGTGT
                                   G     G__
GAM616   LOC151614 5'  TGTGTGTGTTGCAGATAAGGGC 81124      GTT  CAAA
                                 GCCCT   TC    AACGCGTACA
                                 |||||   ||    ||||||||||
                                 CGGGA   AG    TTGTGTGTGT
                                   AT_  ACG_
GAM616   LOC151904 3'  TGTGTGTGTAAGCCGGGAGGTG 81211    TG    AAAA__
             GG                    CC  TTTCC     ACGCGTACA
                                   ||  |||||     |||||||||
                                   GG  GGAGG     TGTGTGTGT
                                    GT    GCCGAA
GAM616   LOC151987 5'  TGTGTGCGAGGGAGGGGGAGGG 68084      G TT  AAAAA
             C                     GCCCT T  CC     CGCGTACA
                                   ||||| |  ||     ||||||||
```

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                                CGGGA G  GG    GCGTGTGT
                                  _ GG  AGGGA
GAM616  LOC152453 5'  TGTGTGTGTAGCATTGGGGACA 81485      TT   AA__
                GG                 CCTGT  CCAA   ACGCGTACA
                                   |||||  ||||   |||||||||
                                   GGACA  GGTT   TGTGTGTGT
                                     GG   ACGA
GAM616  LOC152794 5'  TGTATTTTTTGTGGAGATGGGG 81567          A  CGC
                T                  GCCCTGTTTCCA AAA  GTACA
                                   ||||||||||| |||  |||||
                                   TGGGGTAGAGGT TTT  TATGT
                                          G  TT_
GAM616  LOC153277 5'  TGTGCGCGCACCGAGGCAGGAG 87190   _      CAAAAA
                C                  GC CCTGTTTC     CGCGTACA
                                   || ||||||||     ||||||||
                                   CG GGACGGAG     GCGCGTGT
                                    A       CCAC__
GAM616  LOC154877 5'  GCTCCTGTTTTTTGAGACAGGG 87556        C      CGTACA
                T                  GCCCTGTTTC AAAAACG
                                   |||||||||| |||||||
                                   TGGGACAGAG TTTTTGT
                                         T      CCTCGG
GAM616  LOC157503 3'  GTGCGTAGGGAACGGTGT    87764    C       AAAAAC
                                   GC CTGTTTCC     GCGTAC
                                   || ||||||||     ||||||
                                   TG GGCAAGGG     TGCGTG
                                    T       A_____
GAM616  LOC157627 3'  TGTGTGTTGGAGGCTGGGC   82420     T       AA
                                   GCCC GTTTCCAA  ACGCG
                                   |||| ||||||||  |||||
                                   CGGG CGGAGGTT  TGTGT
                                     T       G_
GAM616  LOC161734 3'  TGTGATTTGGGAGTAGGG    88472          AA
                                   CCCTGTTTCCAAA  CGCG
                                   ||||||||||||  ||||
                                   GGGATGAGGGTTT  GTGT
                                          A_
GAM616  LOC170396 3'  TGTGTTGGGAGGTGGGGT    83731     TG    AAA
                                   GCCC  TTTCC   AACGCG
                                   ||||  |||||   ||||||
                                   TGGG  GGAGG   TTGTGT
                                     GT    G__
GAM616  LOC201475 5'  TGTGTGTGTGAGCGGGGAGTGG 89624    TG    AAAA_
                G                  CC  TTTCC    ACGCGTACA
                                   ||  |||||    |||||||||
                                   GG  GAGGG    TGTGTGTGT
                                    GT    GCGAG
GAM616  LOC201562 3'  TGCCTTTTTTTGGGGGCAGGGT 90416       TT      C__   TACA
                                   GCCCTGT  CCAAAAA   GCG
                                   |||||||  |||||||   |||
```

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                                TGGGACG  GGTTTTT   CGT
                                   GG      TTC
GAM616   LOC202908 5'  TGTGTGTGTCTTGAGACAGGGT 90734         CAAAA
                                GCCCTGTTTC    ACGCGTACA
                                ||||||||||    |||||||||
                                TGGGACAGAG    TGTGTGTGT
                                    TTC__
GAM616   LOC203286 5'  TGTATGTGAAAGTGGGGTGAGG 92151     GT    AAAA
                                CCT  TTCCA    CGCGTACA
                                |||  |||||    ||||||||
                                GGA  GGGGT    GTGTATGT
                                  GT    GAAA
GAM616   LOC203427 3'  TGTTTTGTTTTTAGAGACAGGG 90924         C      CGT
            T                    GCCCTGTTTC AAAAACG   ACA
                                |||||||||| |||||||   |||
                                TGGGACAGAG TTTTTGT   TGT
                                    A      TT_
GAM616   LOC204804 3'  TGTTTTGTTTTTAGAGACAGGG 91056         C      CGT
            T                    GCCCTGTTTC AAAAACG   ACA
                                |||||||||| |||||||   |||
                                TGGGACAGAG TTTTTGT   TGT
                                    A      TT_
GAM616   LOC219445 3'  GTGTGCGTTAGAAAGGGC    93215      GT   CAAA
                                GCCCT  TTC    AACGCGTAC
                                |||||  |||    |||||||||
                                CGGGA  AAG    TTGCGTGTG
                                  __   A___
GAM616   LOC219654 3'  TGTGTGTGTTGACAAACAGTGT 92942    C     CCAAA
                                GC CTGTTT     AACGCGTACA
                                || ||||||     ||||||||||
                                TG GACAAA     TTGTGTGTGT
                                 T     CAG__
GAM616   LOC220538 3'  TGTGTATTGGGGATGGGAGT   92431    _    TT    AA
                                GC CCTGT  CCAA  ACGCG
                                || |||||  ||||  |||||
                                TG GGGTA  GGTT  TGTGT
                                 A    GG    A_
GAM616   LOC221540 3'  TGTGCGTGCCCCGGGGTGGGT  95481     TGTT   AAAAA
                                GCCC    TCC     CGCGTACA
                                ||||    |||     ||||||||
                                TGGG    GGG     GTGCGTGT
                                  T___   GCCCC
GAM616   LOC221683 3'  TGTGCTGGTATTAGGAGGTGGG 95334     TG    A  A  GC
            GC                   GCCC  TTTCC AA AC  GTACA
                                ||||  ||||| || ||  |||||
                                CGGG  GGAGG TT TG  CGTGT
                                  GT    A  A  GT
GAM616   LOC253070 3'  TGTGTGTGTTTATGGGAGAGGT 98789     TG__     A
            GGGT                   GCCC    TTTCCA AAACGCGTACA
                                ||||    |||||| ||||||||||
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                                TGGG   GAGGGT TTTGTGTGTGT
                                  TGGA     A
GAM616  LOC253868 3'  TGTGTTCAGCTTTGTGAGTGGG 97329     TG  TC   ____     TACA
            GC                    GCCC  TT  CAAA    AACGCG
                                  ||||  ||  ||||    ||||||
                                  CGGG  GA  GTTT    TTGTGT
                                    GT  GT    CGAC        A
GAM616  LOC254249 5'  TGTGTGTGATGGGGGATAGGG  97188       TT  AAAAA
                                  CCCTGT  CC    CGCGTACA
                                  ||||||  ||    ||||||||
                                  GGGATA  GG    GTGTGTGT
                                     GG  GTA__
GAM616  LOC254685 3'  TGTGTGTGTTTTTGAGACAGAG 98243    C      C
            T                      GC CTGTTTC AAAAACGCGTACA
                                  ||  |||||||  ||||||||||||
                                  TG GACAGAG TTTTTGTGTGTGT
                                   A      _
GAM616  LOC257286 3'  TGTGTATTGGGGATGGGAGT   96197    _    TT    AA
                                  GC CCTGT  CCAA  ACGCG
                                  ||  |||||  ||||  |||||
                                  TG GGGTA  GGTT  TGTGT
                                   A    GG    A_
GAM616  LOC257471 5'  TGTGCGCGTGTGAGTGTGGGC  97394     TGT   CAAAA
                                  GCCC   TTC    ACGCGTACA
                                  ||||   |||    |||||||||
                                  CGGG   GAG    TGCGCGTGT
                                    TGT   TG___
GAM616  LOC257545 3'  TGTGCGTGCCCCGGGGTGGGT  99645     TGTT   AAAAA
                                  GCCC    TCC    CGCGTACA
                                  ||||    |||    ||||||||
                                  TGGG    GGG    GTGCGTGT
                                    T___   GCCCC
GAM616  LOC257598 3'  TGTGCGTGCCCCGGGGTGGGT  99753     TGTT   AAAAA
                                  GCCC    TCC    CGCGTACA
                                  ||||    |||    ||||||||
                                  TGGG    GGG    GTGCGTGT
                                    T___   GCCCC
GAM616  LOC51195  3'  GTGTGTGCTGGGGAGGGGT   33409      G TT   AAAA
                                  GCCCT T  CCA    CGCGTAC
                                  |||||  |  |||    |||||||
                                  TGGGG A  GGT    GTGTGTG
                                     _ GG   C___
GAM616  LOC54466  3'  TGTGTTTGGTAGATGGGGC    39179         _    AA
                                  GCCCTGTTT CCAA  ACGCG
                                  |||||||||  ||||  |||||
                                  CGGGGTAGA GGTT  TGTGT
                                        T    __
GAM616  LOC55580  5'  TGTGGCTTTGGTGGATGGGGT  34535          _     AA
                                  GCCCTGTTT CCAAA  CGCG
                                  |||||||||  |||||  ||||
```

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                                TGGGGTAGG GGTTT  GTGT
                                     T    CG
GAM616  LOC90631  3'  TGTGTGTGGGCGCAGGGC    64398       T   AAA
                                GCCCTGT TCCA   ACGCG
                                ||||||| ||||   |||||
                                CGGGACG GGGT   TGTGT
                                    C   G__
GAM616  LOC92379  3'  TGTAATTGGTTTGGGAGGGGGC 69678      G      AACGCG
                                GCCCT TTTCCAAA     TACA
                                ||||| ||||||||     ||||
                                CGGGG GAGGGTTT     ATGT
                                  _       GGTTA_
GAM617  CLN5      3'  TCCAATCACCAGCATCTGTTT  22433     T  TTT       CA
                                AAGC GG   TGCTGGTGAT  GA
                                |||| ||   ||||||||||  ||
                                TTTG CT   ACGACCACTA  CT
                                  T ____        AC
GAM617  FCGR2A    3'  CTGAGCAAACAAAACCACCT   80028    C      CTGG  A
                                AG TGGTTTTG    TG TCAG
                                || ||||||||    || ||||
                                TC ACCAAAAC    AC AGTC
                                 C       AA__  G
GAM617  G6PT1     5'  CTGACCACCAGCACGAGACC   9402       __      A
                                GGTTT  TGCTGGTG TCAG
                                |||||  |||||||| ||||
                                CCAGA  ACGACCAC AGTC
                                   GC       C
GAM617  PCTK3     3'  CTGATCCCAATACCAGCTT    73326       TTTGC   T
                                AAGCTGGT    TGG GATCAG
                                ||||||||    ||| ||||||
                                TTCGACCA    ACC CTAGTC
                                     TA____  _
GAM617  SLC24A1   5'  TCTGATCACCAACCTGAATC   17569     TGC_
                                GGTTT   TGGTGATCAGA
                                |||||   ||||||||||
                                CTAAG   ACCACTAGTCT
                                   TCCA
GAM617  ZNF278    3'  CAAGGCAAAACCAGTCC     27498   A        GG
                                A GCTGGTTTTGCT  TG
                                | ||||||||||  ||
                                C TGACCAAAACGG  AC
                                 C          A_
GAM617  ZNF278    3'  CAAGGCAAAACCAGTCC     50264   A        GG
                                A GCTGGTTTTGCT  TG
                                | ||||||||||  ||
                                C TGACCAAAACGG  AC
                                 C          A_
GAM617  ZNF278    3'  CAAGGCAAAACCAGTCC     50285   A        GG
                                A GCTGGTTTTGCT  TG
                                | ||||||||||  ||
```

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                                C TGACCAAAACGG  AC
                                 C          A_
GAM617  DKFZp762E1312 5'  CTGGTGACCCAGCGAAACCAGC 37902              _ G
           TT                     AAGCTGGTTTTGCTGG T ATCAG
                                  ||||||||||||||| | |||||
                                  TTCGACCAAAGCGACC A TGGTC
                                        C G
GAM617  FLJ21125  3'  TCTGCGCTGAGCAGAACCAGCT 45226            _   AT
                                  AGCTGGTTTTGCT GGTG  CAGA
                                  |||||||||||| ||||  ||||
                                  TCGACCAAGACGA TCGC  GTCT
                                        G   __
GAM617  FLJ21939  3'  CTGATCATTGAAGCCAACTT   42651     C      GCT
                                  AAG TGGTTTT   GGTGATCAG
                                  ||| |||||||   |||||||||
                                  TTC ACCGAAG   TTACTAGTC
                                    A     ____
GAM617  FREQ     3'  TCTTTTGGCAGCAAAACCACCT 27377    C        G   TC
                                  AG TGGTTTTGCTG TGA  AGA
                                  || ||||||||||| |||  |||
                                  TC ACCAAAACGAC GTT  TCT
                                   C         G   T_
GAM617  KIAA0444  3'  CTGACATCCCAAAACCATCTT  62999     C      CT    A
                                  AAG TGGTTTTG  GGTG TCAG
                                  ||| ||||||||  |||| ||||
                                  TTC ACCAAAAC  CTAC AGTC
                                    T       C_   _
GAM617  KIAA0630  3'  CTGACCTCAAACCAGCTT    90951          TGCT  TGA
                                  AAGCTGGTTT    GG   TCAG
                                  ||||||||||    ||   ||||
                                  TTCGACCAAA    CC   AGTC
                                        CT__  ____
GAM617  MIDORI    3'  TCTGGCTACAGCAAGACCAGC  74220           G  AT
                                  GCTGGTTTTGCTG TG  CAGA
                                  |||||||||||| ||  ||||
                                  CGACCAGAACGAC AT  GTCT
                                        _  CG
GAM617  WBSCR21   5'  TCGGCAGCAAAACTAACTT    49307     C        G
                                  AAG TGGTTTTGCTG TGA
                                  ||| |||||||||| |||
                                  TTC ATCAAAACGAC GCT
                                    A         G
GAM617  LOC145919 3'  CTGAGGCAGCAAGACCAGC    78025           GTGA
                                  GCTGGTTTTGCTG    TCAG
                                  ||||||||||||    ||||
                                  CGACCAGAACGAC    AGTC
                                        GG__
GAM617  LOC150928 3'  CGATGACCAAACCAGC      74581        TTGC   G   A
                                  GCTGGTT    TGGT ATC G
                                  |||||||    |||| ||| |
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                                CGACCAA    ACCA TAG C
                                    _____   G   C
GAM617   LOC153442 3'  CTGCAACAGAAACCAGCTT   87228         TG   G  AT
                                AAGCTGGTTT  CTG TG  CAG
                                ||||||||||  ||| ||  |||
                                TTCGACCAAA  GAC AC  GTC
                                     __   A  __
GAM617   LOC161054 5'  TCTGATCCTGGCTAAAACTAGC 88447          _  TG T
                                GCTGGTTTT GC  G GATCAGA
                                ||||||||| ||  | |||||||
                                CGATCAAAA CG  C CTAGTCT
                                      T  GT _
GAM617   LOC253549 3'  CAAGGGAAAAACCAGCTT    98575          G  GG
                                AAGCTGGTTTT CT  TG
                                |||||||||| ||  ||
                                TTCGACCAAAA GG  AC
                                       A  GA
GAM617   LOC253649 5'  CTGATCACCAGCTTTTCTACC  97876     TTT___
                                GGT     GCTGGTGATCAG
                                |||     ||||||||||||
                                CCA     CGACCACTAGTC
                                  TCTTTT
GAM617   LOC253650 5'  CTGATCACCAGCTTTTCTACC  97872     TTT___
                                GGT     GCTGGTGATCAG
                                |||     ||||||||||||
                                CCA     CGACCACTAGTC
                                  TCTTTT
GAM618   CMKLR1    3'  AACCCAGGGACACCCAAGGA   15801        C      CT
                                TCCTTGGG GTCCTTG  GTT
                                |||||||| |||||||  |||
                                AGGAACCC CAGGGAC  CAA
                                     A      C_
GAM618   TCP10     3'  ACTACAAGGACACCCAAGGG   17235        C      CT
                                TCCTTGGG GTCCTTG  GT
                                |||||||| |||||||  ||
                                GGGAACCC CAGGAAC  CA
                                     A      AT
GAM618   TEM7      3'  GGCAAGGATGCCCAAAGA    40266    C
                                TC TTGGGCGTCCTTGCT
                                || ||||||||||||||
                                AG AACCCGTAGGAACGG
                                 A
GAM618   BTN3A2    5'  GGTAAAGACACTCAAGGA    23879        C   C
                                TCCTTGGG GTC TTGCT
                                |||||||| ||| |||||
                                AGGAACTC CAG AATGG
                                     A   A
GAM618   BTN3A3    5'  GGTAAAGACACTCAAGGA    23766        C   C
                                TCCTTGGG GTC TTGCT
                                |||||||| ||| |||||
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                                AGGAACTC CAG AATGG
                                    A   A
GAM618  DKFZp434N074 5'  AAAGCCAGGGAGACCCAAGGA  63327        CG     CT
                                TCCTTGGG  TCCTTG  GTTTT
                                ||||||||  ||||||  |||||
                                AGGAACCC  AGGGAC  CGAAA
                                    AG     __
GAM618  DKFZp762A227 3'  CAAAATAAAGACACACAAGGA  26880       GGC   CTTGC
                                TCCTTG   GTC    TGTTTTG
                                ||||||   |||    |||||||
                                AGGAAC   CAG    ATAAAAC
                                   ACA   AA___
GAM618  HT002    3'  AGCCAAGGAACCCAAGGA    26786        CG     _
                                TCCTTGGG  TCCTTG CT
                                ||||||||  ||||||  ||
                                AGGAACCC  AGGAAC GA
                                    A_     C
GAM618  MGC11082  5'  CAAAACAGCAAAAAGTTTTCCA 52072        ___  GTCC
           GGGA                     TCCTTGG   GC    TTGCTGTTTTG
                                |||||||   ||   ||||||||||
                                AGGGACC   TG    AACGACAAAAC
                                    TTT  AAA_
GAM618  OPTC     3'  GGGTGACAAAGAAGCCCAAGGA 27628         G  C   CT TT
                                TCCTTGGGC TC TTG  G  T
                                |||||||| || |||  |  |
                                AGGAACCCG AG AAC  T  G
                                     A  A   AG GG
GAM618  OPTC     3'  GGGTGACAAAGAAGCCCAAGGA 27629         G  C   CT TT
                                TCCTTGGGC TC TTG  G  T
                                |||||||| || |||  |  |
                                AGGAACCCG AG AAC  T  G
                                     A  A   AG GG
GAM618  PIK4CA   3'  CAAAATAGTAAAAACCCAA   55167      CGTCC
                                TTGGG    TTGCTGTTTTG
                                |||||    ||||||||||
                                AACCC    AATGATAAAAC
                                   AAA__
GAM618  LOC222488 3'  CAAAACCAACACACCCAAGGA  96007        C  CC   CT
                                TCCTTGGG GT  TTG  GTTTTG
                                |||||||| ||  |||  ||||||
                                AGGAACCC CA  AAC  CAAAAC
                                    A  C_   __
GAM618  LOC90334  5'  CAAAGCAGAGGAGACCCAAGGA 62971         CG    TG
                                TCCTTGGG  TCCT  CTGTTTTG
                                ||||||||  ||||  ||||||||
                                AGGAACCC  AGGA  GACGAAAC
                                    AG    __
GAM619  ALDH8A1   3'  ATTCCAGCTATGCCTTGA    42913      A       AA
                                TCAA GCATGGCT  GAGT
                                ||||  ||||||||  ||||
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                                AGTT CGTATCGA  CTTA
                                  C       C_
GAM619  DEC1     5'  TGAACACTCTGCGGCTTCTCTG 34277     A  CAT    A_
              A                   TCA AG   GGCT  AGAGTGTTCA
                                  ||| ||   ||||  ||||||||||
                                  AGT TC   TCGG  TCTCACAAGT
                                    C  T__    CG
GAM619  KCNJ10   3'  GAAGGCCTCAGCCATGCTTGGA 11156    A        A  A  G
                                  TC AAGCATGGCT AG GT TTC
                                  || ||||||||||  || || |||
                                  AG TTCGTACCGA TC CG AAG
                                   G        C  _  G
GAM619  PCDH11X  3'  AGCAGTTCCAACCATGCTTTGG 53134          CTAA  G
                                  TCAAAGCATGG    GA TGTT
                                  ||||||||||    || ||||
                                  GGTTTCGTACC    TT ACGA
                                         AACC  G
GAM619  PCDH11X  3'  AGCAGTTCCAACCATGCTTTGG 53141          CTAA  G
                                  TCAAAGCATGG    GA TGTT
                                  ||||||||||    || ||||
                                  GGTTTCGTACC    TT ACGA
                                         AACC  G
GAM619  TRIM9    3'  GCTTCTTAGCTATACTTT    54830      C         T
                                  AAAG ATGGCTAAGAG GT
                                  |||| ||||||||||| ||
                                  TTTC TATCGATTCTT CG
                                    A          _
GAM619  ARHGAP8  3'  GAACACTCTGTATGTTTCGA   31724    A      G TA
                                  TC AAGCATG C  AGAGTGTTC
                                  || |||||||  |  |||||||||
                                  AG TTTGTAT G  TCTCACAAG
                                   C      _ __
GAM619  C1orf9   3'  AACACTACAATGCTTTGA    33156          GGCTAAG
                                  TCAAAGCAT      AGTGTT
                                  |||||||||      ||||||
                                  AGTTTCGTA      TCACAA
                                        ACA____
GAM619  DC-TM4F2 3'  GGATCCTCAGCCATGTT     48902          AA   TG
                                  AGCATGGCT  GAG  TTC
                                  |||||||||  |||  |||
                                  TTGTACCGA  CTC  AGG
                                        __   CT
GAM619  DKFZp547M236 5'  AACACTCTTAATACAACTT   38659     CA  GC_
                                  AAG  TG   TAAGAGTGTT
                                  |||  ||   ||||||||||
                                  TTC  AC   ATTCTCACAA
                                    A_  ATA
GAM619  DKFZp761J1523 3'  CACTCAGCCAGCTCTGA     51149     A   A    AA
                                  TCA AGC TGGCT  GAGTG
                                  ||| ||| |||||  |||||
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                                AGT TCG ACCGA  CTCAC
                                  C  _    __
GAM619  FLJ21415  3'  GACCTGTTAGCCATATCCTGA  45687     AAGC       G  T
                                TCA   ATGGCTAA AG GTT
                                |||   |||||||| || |||
                                AGT   TACCGATT TC CAG
                                  CCTA       G  _
GAM619  HIC2      3'  AACACTCTTAACAGTGTT    65855      GGC
                                AGCAT   TAAGAGTGTT
                                |||||   ||||||||||
                                TTGTG   ATTCTCACAA
                                   ACA
GAM619  KIAA1034  3'  TGAACGTAATCCATGCTTT   63135         CTAAGAG
                                AAAGCATGG      TGTTCA
                                |||||||||      ||||||
                                TTTCGTACC      GCAAGT
                                     TAAT___
GAM619  LIPG      3'  TGCTCAGCCTGCTTTGA     21234         T   AA
                                TCAAAGCA GGCT  GAGTG
                                |||||||| ||||  |||||
                                AGTTTCGT CCGA  CTCGT
                                     _   __
GAM619  MAFB      3'  TGAGAGGCTTAGCCATCCCTGA 19594     AAGC       AGTG
                                TCA   ATGGCTAAG   TTCA
                                |||   |||||||||   ||||
                                AGT   TACCGATTC   GAGT
                                  CCC_       GGA_
GAM619  TLR10     5'  TTCTCAGCCAATGCTCTGA   48978     A   _   A
                                TCA AGCAT GGCT AGAG
                                ||| ||||| |||| ||||
                                AGT TCGTA CCGA TCTT
                                  C    A   C
GAM619  WBSCR20A  5'  TGAACACTCTCAAGACCTGCT  50574      T  _  A_
                                AGCA GG CT  AGAGTGTTCA
                                |||| || ||  ||||||||||
                                TCGT CC GA  TCTCACAAGT
                                  _ A  AC
GAM619  LOC132617 3'  ATTCACCATGCTTTGA      76409          CTAA
                                TCAAAGCATGG   GAGT
                                ||||||||||    ||||
                                AGTTTCGTACC   CTTA
                                      A___
GAM619  LOC146243 3'  TGAACACTCTGTACATCTTT   84624      C   GCTA
                                AAAG ATG   AGAGTGTTCA
                                |||| |||   ||||||||||
                                TTTC TAC   TCTCACAAGT
                                  _  ATG_
GAM619  LOC150837 3'  AACATGGCCATAGCTTGA    80797      A  _     AAGA
                                TCAA GC ATGGCT   GTGTT
                                |||| || ||||||   |||||
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                                AGTT CG TACCGG    TACAA
                                  _ A     _____
GAM619  LOC153396 3'  CAAACTGAGCCATGCTTT    81682          A  AG
                                AAAGCATGGCT AG  TG
                                |||||||||| ||  ||
                                TTTCGTACCGA TC  AC
                                      G  AA
GAM619  LOC92421  3'  TGAACACTCCCAGGCCATTATG 69731    AAGC     AA_
          A                     TCA   ATGGCT   GAGTGTTCA
                                |||   ||||||  |||||||||
                                AGT   TACCGG   CTCACAAGT
                                  AT__     ACC
GAM620  CDH12    3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                      AA___   AC
GAM620  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM620  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090      T    AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                   _   GTCA_
GAM620  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
          A                     TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM620  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126        CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                      AGACG___
GAM620  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
          TA                    TACA   TCC    GAAGAATAAG
                                ||||   |||   ||||||||||
                                ATGT   AGG    TTTCTTATTC
                                  AAA_   ATTG
GAM620  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68742           _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                          G
GAM620  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
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                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM620  KIAA1877 3'  CTTATTCTTCTGCCATGAGT  66748     CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM620  KIAA1906 3'  CTTATTCTTCTTGACTTTTGG  73571    CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM620  OSBPL11  3'  CTTAATTTCCCAAGAGTGGTG  43206       CCAA   AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                     AACC   A_
GAM620  YME1L1   3'  TCATTCTTGATGTGGTGTA   58438       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                     TA_    A
GAM620  ZNF262   3'  CTTATTTTGTTTGGGAGT    18723        A
                                ACTCCCAAG AGAATAAG
                                |||||||||  ||||||||
                                TGAGGGTTT TTTTATTC
                                     G
GAM620  LOC91960 3'  TGTGGCTTGGAACGTGGTGTA  68294       TC_   AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
                                ATGTGGTG   GGTTC   TGT
                                     CAA    GG__
GAM621  CDH12    3'  CTTATCATTTAAAGTGGTGTA  15777       CCCAA  GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM621  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007     CA       G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM621  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090     T   AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                   _   GTCA_
GAM621  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877     CACTCCCA
            A                    TACAC       AGAAGAATAAG
                                |||||       ||||||||||
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                              ATGTG      TCTTCTTATTC
                                 TACTCCC_
GAM621  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126        CCCAAGAA
                              TACACCACT      GAATAAG
                              |||||||||      |||||||
                              ATGTGGTGA      TTTATTC
                                   AGACG___
GAM621  HMP19     3'  CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
           TA                   TACA   TCC   GAAGAATAAG
                              ||||   |||   ||||||||||
                              ATGT   AGG   TTTCTTATTC
                                AAA_  ATTG
GAM621  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA  68742             _
                              TACACCACTCCCAAGA AGA
                              |||||||||||||||| |||
                              ATGTGGTGAGGGTTCT TCT
                                        G
GAM621  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                              CAC  CT CCAAGAAGAA
                              |||  || ||||||||||
                              GTG  GA GGTTCTTTTT
                                AC  A
GAM621  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748     CCA__
                              ACTC    AGAAGAATAAG
                              ||||    ||||||||||
                              TGAG    TCTTCTTATTC
                                TACCG
GAM621  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                              CCA    CAAGAAGAATAAG
                              |||    ||||||||||||
                              GGT    GTTCTTCTTATTC
                                TTTCA
GAM621  OSBPL11   3'  CTTAATTTCCCAAGAGTGGTG  43206        CCAA    AA
                              CACCACTC   GAAG  TAAG
                              ||||||||   ||||  ||||
                              GTGGTGAG   CTTT  ATTC
                                   AACC   A_
GAM621  YME1L1    3'  TCATTCTTGATGTGGTGTA   58438        TCC     _
                              TACACCAC   CAAGAA GA
                              ||||||||   ||||||  ||
                              ATGTGGTG   GTTCTT CT
                                   TA_     A
GAM621  ZNF262    3'  CTTATTTTGTTTGGGAGT    18723         A
                              ACTCCCAAG AGAATAAG
                              ||||||||| ||||||||
                              TGAGGGTTT TTTTATTC
                                   G
GAM621  LOC91960  3'  TGTGGCTTGGAACGTGGTGTA  68294        TC_    AAGA
                              TACACCAC   CCAAG   ATA
                              ||||||||   |||||   |||
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                                ATGTGGTG  GGTTC   TGT
                                    CAA    GG__
GAM622  CD83    3'  GGTGAGATGCAGCTGGAAAA  16171      T   A    GG
                                TTTTCC AGCT CATCT  TACC
                                |||||| |||| |||||  ||||
                                AAAAGG TCGA GTAGA  GTGG
                                   _   C    __
GAM622  DSPG3   3'  ACCAGATGAGTTAGGAA    60814        A
                                TTCCTAGCT CATCTGGT
                                ||||||||| ||||||||
                                AAGGATTGA GTAGACCA
                                    _
GAM622  IL1RAP  3'  CCAAATGTAGCTAAAAAAA   10985     CC       C
                                TTTT  TAGCTACAT TGG
                                ||||  ||||||||| |||
                                AAAA  ATCGATGTA ACC
                                  AA       A
GAM622  OAS3    3'  TACACACGCAATAGCTAGGAAA 21656          CATC_ _
            A                    TTTTCCTAGCTA    TG GTA
                                ||||||||||||    || |||
                                AAAAGGATCGAT    AC CAT
                                      AACGC  A
GAM622  PLS3    3'  TACATCGTAGCTAGAAGA    18526      C     ATCTG
                                TTTTC TAGCTAC    GTA
                                ||||| |||||||    |||
                                AGAAG ATCGATG    CAT
                                   _     CTA__
GAM622  STAT4   3'  TACCAGGTTCTAGGAAA    13441       CTAC
                                TTTCCTAG   ATCTGGTA
                                ||||||||   ||||||||
                                AAAGGATC   TGGACCAT
                                     T___
GAM622  THBS1   3'  CAGATGTAGCAGGAAAA    13746       A
                                TTTTCCT GCTACATCTG
                                ||||||| ||||||||||
                                AAAAGGA CGATGTAGAC
                                    _
GAM622  CED-6   3'  AGGTACATTTTCACTAGGAAAA 33316        CTACATCTG
                                TTTTCCTAG       GTACCT
                                |||||||||       ||||||
                                AAAAGGATC       CATGGA
                                     ACTTTTA__
GAM622  DKFZP566F2124 3'  AGATTCATAGCTAGGAAA   32214         C__
                                TTTCCTAGCTA  ATCT
                                ||||||||||  ||||
                                AAAGGATCGAT  TAGA
                                       ACT
GAM622  FBXO24  3'  AGATACGGGCAGCTAGGAA   25146        ACAT  G   C
                                TTCCTAGCT   CT GTA CT
                                |||||||||   || ||| ||
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                                AAGGATCGA   GG CAT GA
                                    C___  G   A
GAM622  FLJ10895  3'  GGTACCAGCACCAGGAAGA   39359       AGCTACAT
                                TTTTCCT      CTGGTACC
                                |||||||      ||||||||
                                AGAAGGA      GACCATGG
                                   CCAC____
GAM622  FLJ11996  3'  AGGTGCCTACAGGTAGGAAAA  47055       G  ACATCT
                                TTTTCCTA CT    GGTACCT
                                |||||||| ||    |||||||
                                AAAAGGAT GA    CCGTGGA
                                    G  CAT___
GAM622  KIAA0433  3'  AGGTACCAGATGTAAGAG    31499    AGC
                                CT   TACATCTGGTACCT
                                ||   ||||||||||||||
                                GA   ATGTAGACCATGGA
                                 GA_
GAM622  KIAA1110  3'  CAGATGTAAGCAAGAAAA    62499      CTA  _
                                TTTTC   GCT ACATCTG
                                |||||   ||| |||||||
                                AAAAG   CGA TGTAGAC
                                   AA_   A
GAM622  PSR       3'  CAGGTGTAACCAGGAAAA    65779       AGC
                                TTTTCCT   TACATCTG
                                |||||||   ||||||||
                                AAAAGGA   ATGTGGAC
                                    CCA
GAM622  SYTL2     3'  AGATATTTGAACAAGCTAGGAA 53076         ACA  TG   C
           AA                    TTTTCCTAGCT   TC  GTA CT
                                ||||||||||   ||  ||| ||
                                AAAAGGATCGA   AG  TAT GA
                                      ACA  TT   A
GAM622  TA-KRP    3'  AGGTACCAGATGAATCAGGA   51670     AGCTA
                                TCCT    CATCTGGTACCT
                                ||||    ||||||||||||
                                AGGA    GTAGACCATGGA
                                  CTAA_
GAM622  LOC139767 5'  AGGTACCAGATGCCATAG    76367     GCTA
                                CTA    CATCTGGTACCT
                                |||    ||||||||||||
                                GAT    GTAGACCATGGA
                                  ACC_
GAM622  LOC147080 3'  GTATAAGCAGGTAGGAAAA   85048       G  ACAT  G
                                TTTTCCTA CT    CT GTAC
                                |||||||| ||    || ||||
                                AAAAGGAT GA    GA TATG
                                    G  C___  A
GAM622  LOC199918 3'  ACCTTGTATAAATAGGAAAA  91474       GC__   TCT
                                TTTTCCTA    TACA   GGT
                                ||||||||    ||||   |||
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                                AAAAGGAT   ATGT  CCA
                                    AAAT   T__
GAM622  LOC257428 5'  ACAACGTGAAGCTAGGAAAA  95929          A  CTG
                                TTTTCCTAGCT CAT  GT
                                |||||||||| |||  ||
                                AAAAGGATCGA GTG  CA
                                    A  CAA
GAM623  FLJ21438  5'  CAAAACGCTTCCCCCCATCCCA 62190      GAGATTATC
                                TGGGA       AAGCGTTTTG
                                |||||       ||||||||||
                                ACCCT       TTCGCAAAAC
                                  ACCCCCC__
GAM623  FLJ32334  3'  AAAACGCTATTCCTTCCCA   58605       A  TTATCA
                                TGGGAG GA    AGCGTTTT
                                |||||| ||    ||||||||
                                ACCCTT CT    TCGCAAAA
                                   C  TA____
GAM623  HHLA2     3'  CAATGTACTTTGTAATCTCCCC 23953     A      C  CG T
           CA                     TGGG GAGATTAT AAG  T TTG
                                |||| |||||||| |||  | |||
                                ACCC CTCTAATG TTC  G AAC
                                  C       T  AT T
GAM624  ADAT1     3'  CCAGCAAAGAATGAAGGC    24914     __        C
                                GTC  CATTCTTTGC GG
                                |||  |||||||||| ||
                                CGG  GTAAGAAACG CC
                                  AA         A
GAM624  M17S2     5'  CCGGTAGCGGACGGTCCTT   20910          ATTCT
                                AAGGACCGTCC    TTGCCGG
                                ||||||||||     |||||||
                                TTCCTGGCAGG    GATGGCC
                                      C____
GAM624  ST14      5'  CCGGCAGGGACGACGCCT    42042     AC   CAT
                                AGG  CGTC   TCTTTGCCGG
                                |||  ||||   ||||||||||
                                TCC  GCAG   AGGGACGGCC
                                  __    C__
GAM624  HTGN29    5'  GCCAACTGTGTGGCGGTCC   39885        _  TC  T
                                GGACCGTC CAT  TT GC
                                |||||||| |||  || ||
                                CCTGGCGG GTG  AA CG
                                     T  TC  C
GAM624  PMAIP1    3'  GCAAGAATGGAAGACCCTT   41211     ACCG       T
                                AAGG    TCCATTCTT GC
                                ||||    ||||||||| ||
                                TTCC    AGGTAAGAA CG
                                  CAGA       _
GAM624  LOC144278 3'  GCCAGCAAAGACTGCTCGATGG 77274         ___  T      C
           TCCT                    AGGACCGTC   CA TCTTTGC GGC
                                |||||||||   || ||||||| |||
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                                TCCTGGTAG   GT AGAAACG CCG
                                     CTC  C      A
GAM624  LOC147976 3'  CCGGTGAATGAAGACCCT    79287     ACC   CA  _  TG
                                AGG   GTC  TTC TT  CCGG
                                |||   |||  ||| ||  ||||
                                TCC   CAG  AAG AA  GGCC
                                 ____  __   T  GT
GAM624  LOC254263 5'  GCCGGCAGCGGACGCGCC    96367    AC    ATTCT
                                GG  CGTCC    TTGCCGGC
                                ||  |||||    ||||||||
                                CC  GCAGG    GACGGCCG
                                 GC    C____
GAM625  ADCY8    5'  GCTCACAGCGCTGCGGCTCCT  8501      A  AT   CAA
                                AGGA CC  GGC   CTGTGAGC
                                ||||  ||  |||   ||||||||
                                TCCT GG  TCG   GACACTCG
                                  C  CG   C__
GAM625  CIT      5'  GCTCACAGAGCTACAGCTCTCC 70304     ACCA__    CAA
                                GGA     TGGC   CTGTGAGC
                                |||     ||||   ||||||||
                                CCT     ATCG   GACACTCG
                                 CTCGAC    A__
GAM625  FAAH     5'  GCGGTCTCCGGCCATGGCCCC  97238    AA       A___
                                GG  CCATGGCC    ACTGT
                                ||  ||||||||    |||||
                                CC  GGTACCGG    TGGCG
                                 CC       CCTC
GAM625  GSTM3    5'  GCTCACAGTTTCCCTAGTCCT  68638     ACCAT  CC
                                AGGA    GG  AACTGTGAGC
                                ||||    ||  ||||||||||
                                TCCT    CC  TTGACACTCG
                                  GAT__  CT
GAM625  HSD11B2  3'  GCTCCGTGAGCCTTGGTTCCT  5771         T   CA  T T
                                AGGAACCA GGC  AC G GAGC
                                |||||||| |||  || | ||||
                                TCCTTGGT CCG  TG C CTCG
                                     T   AG  _ _
GAM625  HYAL1    5'  CTCCAGTGGCCATGCTCC    53703     AC       A   T
                                GGA  CATGGCCA CTG GAG
                                |||  |||||||| ||| |||
                                CCT  GTACCGGT GAC CTC
                                 C_       _   _
GAM625  NPTX2    3'  GCTGGAGTGGCCATGTCCCTT  94085      AAC       A  G G
                                AAGG   CATGGCCA CT T AGC
                                ||||   |||||||| || | |||
                                TTCC   GTACCGGT GA G TCG
                                  CT_       _  G _
GAM625  RFX2     3'  GCCCCACCAGACCATGGGTTCC 7158          _    CCAA   _  A_
           TT                    AAGGAACC ATGG    CTG TG  GC
                                ||||||||  ||||    |||  ||  ||
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                                TTCCTTGG TACC   GAC AC  CG
                                    G   A___   C  CC
GAM625  SMAP    5' GCCCCACAGAGCCATGGTCC  22932    A     CAA    A_
                                GGA CCATGGC  CTGTG  GC
                                ||| |||||||  |||||  ||
                                CCT GGTACCG  GACAC  CG
                                  _     A__    CC
GAM625  SMURF1  3' GCTCACAGCCCTGAGCTCTTT 94049     AC_  T   CAAC
                                AAGGA  CA GGC   TGTGAGC
                                |||||  || |||   |||||||
                                TTTCT  GT CCG   ACACTCG
                                   CGA  C  ____
GAM625  DC-TM4F2 3' ACTGTTGGCCAGGGCTCCT  48895     A  A      T
                                AGGA CC TGGCCAAC GT
                                |||| || |||||||| ||
                                TCCT GG ACCGGTTG CA
                                  C  G       T
GAM625  DKFZp566H0824 5' GCTCACAAACCCCATAGTTGCC 34488    _  C   CCAAC
           T                     AGG AAC ATGG    TGTGAGC
                                |||  ||| ||||    |||||||
                                TCC TTG TACC    ACACTCG
                                  G  A   CCAA_
GAM625  FLJ10292 3' GCCCACAGTTGTTGGTTGTTCC 36432      C  GGC      A
           T                     AGGAAC AT   CAACTGTG GC
                                ||||||  ||   |||||||| ||
                                TCCTTG TG   GTTGACAC CG
                                   T  GTT      C
GAM625  FLJ20085 3' GCTCATGGTGCCACAGCCCCT  35009    AACCA   CA
                                AGG    TGGC  ACTGTGAGC
                                |||    ||||  |||||||||
                                TCC    ACCG  TGGTACTCG
                                  CCGAC   __
GAM625  FLJ22690 3' GCTCACAGCCGACCTGTGGCCT 45575    AA    CCAA_
                                AGG  CCATGG    CTGTGAGC
                                |||  ||||||    ||||||||
                                TCC  GGTGTC    GACACTCG
                                  __     CAGCC
GAM625  FLJ32449 3' GCATTTGGCCATGGTTCCTT  59378            C
                                AAGGAACCATGGCCAA TGT
                                |||||||||||||||| |||
                                TTCCTTGGTACCGGTT ACG
                                          T
GAM625  HPIP    3' GCTCACAGCTGCCTTGGCCCC  40425   AA  T  CAA
                                GG  CCA GGC   CTGTGAGC
                                ||  ||| |||   ||||||||
                                CC  GGT CCG   GACACTCG
                                 CC   T   TC_
GAM625  ILF3    3' GCTCACAGTCGAACTACAGCTC 25234    ACCA   CCA_
           C                     GGA   TGG   ACTGTGAGC
                                |||   |||   |||||||||
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                                CCT   ATC   TGACACTCG
                                  CGAC  AAGC
GAM625  KIAA1190  3'  GCTCACAGAGCACCCCAGTTCC 71651      CAT  CCAA
            T                    AGGAAC  GG   CTGTGAGC
                                 ||||||  ||   ||||||||
                                 TCCTTG  CC   GACACTCG
                                    ACC  ACGA
GAM625  MGC11266  3'  GCTCACAGTGGTCAGGGCCC  44488   AA  A    A
                                 GG  CC TGGCCA CTGTGAGC
                                 ||  || |||||| ||||||||
                                 CC  GG ACTGGT GACACTCG
                                  CG  _    _
GAM625  MGC11352  5'  ACTGTTGGCCAGGGCTCCT   65424     A  A      T
                                 AGGA CC TGGCCAAC GT
                                 |||| || |||||||| ||
                                 TCCT GG ACCGGTTG CA
                                   C  G       T
GAM625  MGC5590   3'  CACAACTTTGGTTTCTT     44149        T  CCAAC
                                 AAGGAACCA GG    TGTG
                                 |||||||||  ||    ||||
                                 TTCTTTGGT TC    ACAC
                                       T  A____
GAM625  MKP-7     3'  GCTTCTCTTGGCCATGGTCCC  67015    A        CTGT
                                 GG ACCATGGCCAA   GAGC
                                 ||  ||||||||||   ||||
                                 CC TGGTACCGGTT   TTCG
                                  C         CTC_
GAM625  MSP       3'  GCTCAGGCAGGCCATGGCC   50245    AA      AA  G
                                 GG  CCATGGCC  CT TGAGC
                                 ||  ||||||||  || |||||
                                 CC  GGTACCGG  GG ACTCG
                                   __       AC  _
GAM625  PGR1      3'  CTCACAGTTGGAGTTCTCC   53905   A    CATGG
                                 A GGAAC    CCAACTGTGAG
                                 | |||||    ||||||||||
                                 C TCTTG    GGTTGACACTC
                                  C    A____
GAM625  PTPRT     3'  GCTTCGTGTTGGCCAAGACTCC 56502      ACCA       TGT
            TT                    AAGGA   TGGCCAAC   GAGC
                                  |||||   ||||||||  ||||
                                  TTCCT   ACCGGTTG   TTCG
                                     CAGA       TGC
GAM625  TRF4-2    3'  CTCAAACAAGCCATGGTTCCTT 42611          CAACTG
                                 AAGGAACCATGGC     TGAG
                                 ||||||||||||     ||||
                                 TTCCTTGGTACCG     ACTC
                                        AACAA_
GAM625  LOC122786 3'  GCCTTTGGCCATGATTCT    74622      C       CT
                                 GGAA CATGGCCAA  GT
                                 |||| |||||||||  ||
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                                TCTT GTACCGGTT  CG
                                  A        TC
GAM625   LOC138428 3'  TAGTGGCCATGGCTGCCT    75862     AA_       A
                                AGG   CCATGGCCA CTG
                                |||   ||||||||| |||
                                TCC   GGTACCGGT GAT
                                  GTC        _
GAM625   LOC145581 3'  GCTCCATTAGACCATGGTTC   77794         CCAAC  T
                                GAACCATGG     TG GAGC
                                |||||||||     || ||||
                                CTTGGTACC     AC CTCG
                                     AGATT  _
GAM625   LOC146268 5'  GCTCACAGTCGGCTTGCTGCCT 78342     AAC  T    A
                                AGG   CA GGCC ACTGTGAGC
                                |||   || |||| |||||||||
                                TCC   GT TCGG TGACACTCG
                                  GTC  _    C
GAM625   LOC147299 3'  GCTGTGAGCCGCCATGGTCCC  78981    A       CAA  GTG
                                GG ACCATGGC   CT   AGC
                                || ||||||||   ||   |||
                                CC TGGTACCG   GA   TCG
                                 C       CC_  GTG
GAM625   LOC159199 3'  GCTCACAGCTGGCGGCCCT    83062     AA  ATG    A
                                AGG  CC   GCCA CTGTGAGC
                                |||  ||   |||| ||||||||
                                TCC  GG   CGGT GACACTCG
                                  C_  ____    C
GAM625   LOC200982 5'  AGTTGGCCATGGCTCTTT     91807      A
                                AAGGA CCATGGCCAACT
                                ||||| ||||||||||||
                                TTTCT GGTACCGGTTGA
                                   C
GAM625   LOC253842 3'  GCTCATAGAAGCCTGGTCCCT  99238     A    T   CAA
                                AGG ACCA GGC   CTGTGAGC
                                ||| |||| |||   ||||||||
                                TCC TGGT CCG   GATACTCG
                                  C    _   AA_
GAM625   LOC254778 3'  GCCCTGTGTTGGCCAAGGTTCC 97831       A       TGTGA
                                GGAACC TGGCCAAC     GC
                                |||||| ||||||||     ||
                                CCTTGG ACCGGTTG     CG
                                    A       TGTCC
GAM625   LOC255231 3'  CTCACAGTTAGCCAGCTGACC  97119    AACCA    C
                                GG     TGGC AACTGTGAG
                                ||     |||| |||||||||
                                CC     ACCG TTGACACTC
                                 AGTCG    A
GAM625   LOC257358 5'  GCTCGTGAAGAGCATGGTTCCT 98900           G CAACTG
           T                     AAGGAACCATG C      TGAGC
                                ||||||||||| |      |||||
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                                TTCCTTGGTAC G     GCTCG
                                      _ AGAAGT
GAM625  LOC90190  3'  CGCCCACAGAGCAATTGGCCAT 62422     AC       _____     A ___
            GCCTCC                  GGA  CATGGCCAA    CTGTG GC   G
                                ||| |||||||||    ||||| ||  |
                                CCT  GTACCGGTT    GACAC CG   C
                                  CC        AACGA    C __
GAM625  LOC90495  3'  GCTCACAGTCAACTGCTTTCTT 63737       CCAT   CA___
            T                    AAGGAA    GGC    ACTGTGAGC
                                ||||||   |||    |||||||||
                                TTTCTT    TCG    TGACACTCG
                                    ____  TCAAC
GAM625  LOC90750  3'  GCTCACAGCCCTGCCCTGCCCC 64630    AAC  T   CAA_
            C                    GG   CA GGC    CTGTGAGC
                                ||   || |||    ||||||||
                                CC   GT CCG    GACACTCG
                                 CCC  C   TCCC
GAM626  PDGFB    3'  AGCCACGACTGCCATGTA    12018         A   GG
                                TACATGGCA TCG  GGCT
                                ||||||||| |||  ||||
                                ATGTACCGT AGC  CCGA
                                     C   A_
GAM626  ATP6V1B2  3'  ACATGATTACAATTGCCAGTAG 9883      A      CGG  GC
                                CTAC TGGCAAT   GG  TATGT
                                |||| |||||||   ||  |||||
                                GATG ACCGTTA   TT  GTACA
                                  _      ACA  A_
GAM626  DKFZp434F1719 3'  ACACAGCTAGTCTGCCATGTA  51006         ATCGGG   A
                                TACATGGCA     GGCT TGT
                                |||||||||     |||| |||
                                ATGTACCGT     TCGA ACA
                                     CTGA__    C
GAM626  E2IG4    3'  ACATAGCCCTTTCTTTGCCATG 92546         TC_
                                CATGGCAA   GGGGGCTATGT
                                ||||||||   ||||||||||||
                                GTACCGTT   TTCCCGATACA
                                     TCT
GAM626  FLJ25193  3'  ACATAGCCCCCAACCTGTGTA  59353       CAATC
                                TACATGG    GGGGGCTATGT
                                |||||||    ||||||||||||
                                ATGTGTC    CCCCCGATACA
                                   CAA__
GAM626  TMLHE    3'  ACATAACCATATGTCATGTAG  37046         ATCGG  GC
                                CTACATGGCA    GG  TATGT
                                ||||||||||    ||  |||||
                                GATGTACTGT    CC  ATACA
                                     ATA__  A_
GAM626  LOC158997 3'  CATAGCTGCTACATGTAG    82951        GCAATC  G
                                CTACATG     GG GGCTATG
                                |||||||     || |||||||
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                                GATGTAC     TC TCGATAC
                                   A_____ G
GAM627  FBN2     3'  CAACATTTCATATCACCAGAC  10577      ___       CA
                                GTCT   GATATGAAA  TTG
                                ||||   |||||||||  |||
                                CAGA   CTATACTTT  AAC
                                  CCA        AC
GAM627  HIVEP3   5'  CAATGTGGCCAAAGCTGGACA  44700        T  GATATGAA
                                TGTCCAG CT       ACATTG
                                ||||||| ||       ||||||
                                ACAGGTC GA       TGTAAC
                                   _ AACCGG__
GAM627  AFAP     3'  CAATGTTTCAATGTTAAACT   41603     C     _
                                AGT TGATAT GAAACATTG
                                ||| |||||| |||||||||
                                TCA ATTGTA CTTTGTAAC
                                  A     A
GAM627  FLJ14442 3'  CAATGTTCCACATCCTGTTGGA 52377        TCT   A  A
           CA                     TGTCCAG   GAT TG AACATTG
                                ||||||||   ||| || |||||||
                                ACAGGTT   CTA AC TTGTAAC
                                   GTC   C  C
GAM627  LOC158055 3'  TGGATGTATCAGATTAAACA   82583     CC         AAA
                                TGT  AGTCTGATATG   CA
                                |||  ||||||||||   ||
                                ACA  TTAGACTATGT   GT
                                  AA         AG_
GAM627  LOC165741 3'  CAGTGTTTACCAGACCAGA    88603    CA    ATATG
                                TC  GTCTG    AAACATTG
                                ||  |||||    |||||||||
                                AG  CAGAC    TTTGTGAC
                                 AC    CA___
GAM628  MYLK     5'  CATTAACGCACACATCAGTTCC 98793         AT  C  _  CTC
           AG                     CTGGAACT  TG TG GT   AATG
                                |||||||  || || ||   ||||
                                GACCTTGA  AC AC CG   TTAC
                                    CT  _  A  CAA
GAM628  SLA2     3'  CATTGAGGACAACAGCCCCAG  50882      AACTA   C  GT
                                CTGG    TTG TG  CTCAATG
                                ||||    ||| ||  |||||||
                                GACC    GAC AC  GAGTTAC
                                  CC___   A  AG
GAM628  SLC25A14 3'  ATTGAGACTCTGGCCCCAG    15532      AA   TTGCT
                                CTGG  CTA    GGTCTCAAT
                                ||||  |||    |||||||||
                                GACC  GGT    TCAGAGTTA
                                  CC   C____
GAM628  DARS     3'  CATTGAGATAAGAATAATTCAG 9050        AC    G  G
                                CTGGA  TATT CT GTCTCAATG
                                |||||  |||| || |||||||||
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                                GACTT  ATAA GA TAGAGTTAC
                                  A_   _ A
GAM628  FLJ10201  3'  GGACCTGCAACAGTTCCAG   36354        A   T
                                CTGGAACT TTGC GGTCT
                                |||||||| |||| |||||
                                GACCTTGA AACG CCAGG
                                    C   T
GAM628  GRP3      3'  CATTAAGGCAAAGTAGTTCCAG 31738          GCTG   C
                                CTGGAACTATT   GTCT AATG
                                ||||||||||    |||| ||||
                                GACCTTGATGA   CGGA TTAC
                                      AA__   A
GAM628  LOC219793 5'  CATTGAGGACCCCAAAGCCCCA 93018     AA  A   CT   _
                                TGG  CT TTG  GGTC TCAATG
                                |||  || |||  |||| ||||||
                                ACC  GA AAC  CCAG AGTTAC
                                  CC  _  C_   G
GAM628  LOC221154 3'  AGGCCAGCATCAATTCCAG   95191       CTAT
                                CTGGAA   TGCTGGTCT
                                ||||||   |||||||||
                                GACCTT   ACGACCGGA
                                   AACT
GAM628  LOC92399  3'  TGGGGCCAGCAATACTCCAG   57867      AC
                                CTGGA  TATTGCTGGTCTCA
                                |||||  ||||||||||||||
                                GACCT  ATAACGACCGGGGT
                                  C_
GAM629  ABR       3'  CCAGGGCCGCATCCCACCTCCT 8453          AAA________  CCAG
           GCC                   GGCAGGAGGTGG        CC   G
                                ||||||||||||        ||   |
                                CCGTCCTCCACC        GG   C
                                      CTACGCC___  GACC
GAM629  ABR       3'  CCAGGGCCGCATCCCACCTCCT 41998          AAA________  CCAG
           GCC                   GGCAGGAGGTGG        CC   G
                                ||||||||||||        ||   |
                                CCGTCCTCCACC        GG   C
                                      CTACGCC___  GACC
GAM629  ACY1      3'  CCCTGGGGCTTCCATCCCAACC 7262     CA  A      A
                                GG  GG GGTGGAA CCCCAGGG
                                ||  || ||||||| ||||||||
                                CC  CC CTACCTT GGGGTCCC
                                 AA  _      C
GAM629  ADCY7     5'  CCCTGGGGCCTCCTTAACGGCC 8489      AG__   T  AAA
                                GGC   GAGG GG   CCCCAGGG
                                |||   |||| ||   ||||||||
                                CCG   TTCC CC   GGGGTCCC
                                  GCAA   T ___
GAM629  ADCY9     3'  CCTGGAAACCCCGCTGCCT   8506       GA  T  AAACC
                                AGGCAG  GG GG    CCAGG
                                ||||||  || ||    |||||
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                                TCCGTC  CC CC    GGTCC
                                   G_  _  AAA__
GAM629  AIM1    5'  CCCTGGGGCCCCGCAACGCC  93461    AGGAG   AAA
                                GGC    GTGG  CCCCAGGG
                                |||    ||||  ||||||||
                                CCG    CGCC  GGGGTCCC
                                  CAA__   CC_
GAM629  ALPP    3'  CCAGGGGGCCCTCTGCCT   69411      GA  GGAAA   A
                                AGGCAG  GGT    CCCC GG
                                ||||||  |||    |||| ||
                                TCCGTC  CCG    GGGG CC
                                   TC  _____   A
GAM629  APLP2   3'  CCCTCACCTCCACCCCCTCCT  92542    C  A    AACCCC
                                AGG AGG GGTGGA     AGGG
                                ||| ||| ||||||     ||||
                                TCC TCC CCACCT     TCCC
                                  _  C     CCAC__
GAM629  AR      5'  CCCACTCTCTCTCCACCTCCTC 5272     C       AACCCCA_
            CT                    AGG AGGAGGTGGA       GGG
                                ||| ||||||||||       |||
                                TCC TCCTCCACCT       CCC
                                  _        CTCTCTCA
GAM629  AXUD1   3'  GGCCCCTCCACTTCCTGCC   53444          AA_____
                                GGCAGGAGGTGGA      CC
                                ||||||||||||       ||
                                CCGTCCTTCACCT      GG
                                       CCCC___
GAM629  BAX     3'  CCCTGGAGCCTCCACTGCCT   16315       GA  T  AAACC
                                AGGCAG  GG GG    CCAGGG
                                ||||||  || ||    ||||||
                                TCCGTC  CC CC    GGTCCC
                                   A_  T  GA___
GAM629  BDNF    5'  GGCCCCTCCACCTCCTGCT   60339          AA_____
                                GGCAGGAGGTGGA      CC
                                ||||||||||||       ||
                                TCGTCCTCCACCT      GG
                                       CCCC___
GAM629  BICD1   5'  CCCGTAACCCCCTCCTGCCT   9936         T  AAACCCCA
                                AGGCAGGAGG GG       GGG
                                |||||||||| ||       |||
                                TCCGTCCTCC CC       CCC
                                      _  CAATG___
GAM629  BTD     3'  CCCTGGGACCATCTTTCTGCCT 5347         _    AAAC
                                AGGCAGGA GGTGG    CCCAGGG
                                |||||||| |||||    |||||||
                                TCCGTCTT CTACC    GGGTCCC
                                     T    A___
GAM629  CACNA1S 5'  CCTGCCCCCCCACTCCTGCC   5361         G   AAACCC
                                GGCAGGAG TGG     CAGG
                                |||||||| |||     ||||
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                                CCGTCCTC ACC     GTCC
                                    _  CCCC__
GAM629  CACNA2D2  3'  CCAGGGCCTTTCCCACCCTCCT 21221       _    AAA_______  CCAG
           GCC                   GGCAGGA GGTGG       CC   G
                                 ||||||| |||||       ||   |
                                 CCGTCCT CCACC       GG   C
                                    C    CTTTCC___  GACC
GAM629  CALM3    3'  CCCCACCCCCCACCCCCTGCTT 19002       A    AAACCCCA
                                 AGGCAGG GGTGG       GGG
                                 ||||||| |||||       |||
                                 TTCGTCC CCACC       CCC
                                    C    CCCCAC__
GAM629  CAPG     3'  CCCTGCCCCCCCACCACCTGCCT 10009       A    AAACCC
                                 AGGCAGG GGTGG     CAGGG
                                 ||||||| |||||     |||||
                                 TCCGTCC CCACC     GTCCC
                                    A    CCCC__
GAM629  CAPON    5'  CCCCGGGGTCTCGCCAGCCCCT 64658     C  A  _  AA__    A
           TCCT                  AGG AGG GG TGG    ACCCC GGG
                                 ||| ||| || |||    ||||| |||
                                 TCC TCC CC ACC    TGGGG CCC
                                   T  _  G  GCTC    C
GAM629  CASP10   3'  CCAGGGTAACCTCCAGCCTCCT 53220         _   AA_______  CCAG
           GCC                   GGCAGGAGG TGGA       CC   G
                                 ||||||||| ||||       ||   |
                                 CCGTCCTCC ACCT       GG   C
                                      G   CCAAT___  GACC
GAM629  CASP10   3'  CCAGGGTAACCTCCAGCCTCCT 53250         _   AA_______  CCAG
           GCC                   GGCAGGAGG TGGA       CC   G
                                 ||||||||| ||||       ||   |
                                 CCGTCCTCC ACCT       GG   C
                                      G   CCAAT___  GACC
GAM629  CDK2     3'  CTGACGTCCACCTCCTACC   10154    C       AACCC
                                 GG AGGAGGTGGA     CAG
                                 || ||||||||||     |||
                                 CC TCCTCCACCT     GTC
                                   A        GCA__
GAM629  CHC1     3'  CCCTGGGGTTTTGTGCCCACTC 8859     C  GA   _
           T                     GG AG  GGTG GAAACCCCAGGG
                                 || ||  |||| ||||||||||||
                                 TC TC  CCGT TTTTGGGGTCCC
                                  _  AC   G
GAM629  CHRNA4   3'  CCCTGGGGTTTCCACACAGGCC 7436      AGGAG
                                 GGC    GTGGAAACCCCAGGG
                                 |||    ||||||||||||||||
                                 CCG    CACCTTTGGGGTCCC
                                   GACA_
GAM629  CLCN7    3'  CCCTGGAAGGGCCCCTCTGCCT 8908       G  T  AAACC
                                 AGGCAG AGG GG    CCAGGG
                                 |||||| ||| ||    ||||||
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                                TCCGTC TCC CC    GGTCCC
                                   _  _  GGGAA
GAM629  CNTN2    3'  CCCTGGGACCAAGAGCTCTCCC 18658     A   _  GGAAAC_
            GCCT                  AGGC GGAG GT      CCCAGGG
                                |||| |||| ||      |||||||
                                TCCG CCTC CG      GGGTCCC
                                  C   T  AGAACCA
GAM629  CNTN2    3'  CTAGGGGCTCCTGCCT      18659         GTGGAAA   _
                                AGGCAGGAG      CCCC AG
                                |||||||||      |||| ||
                                TCCGTCCTC      GGGG TC
                                   ________   A
GAM629  CSPG3    3'  CCCTGGGTCCCACTCCTGCC   16517        GT   AAC
                                GGCAGGAG  GGA   CCCAGGG
                                ||||||||  |||   |||||||
                                CCGTCCTC  CCT   GGGTCCC
                                    AC   ___
GAM629  CTF1     3'  CCAGGGCCATCCCCACTTCCTG 9011           AAA_______  CCAG
            CCT                   AGGCAGGAGGTGG       CC   G
                                ||||||||||||        ||   |
                                TCCGTCCTTCACC       GG   C
                                      CCTACC___  GACC
GAM629  CYP24    5'  CCCCAGGGCCCCACCCCATCCT 7596          _  AAA________  CCAG
            CCTGCCT                AGGCAGGAGG TGG        CC   GG
                                |||||||||| |||         ||   ||
                                TCCGTCCTCC ACC        GG   CC
                                      T   CCACCCC___  GACC
GAM629  DHCR24   3'  CCCAAGGCCAGCTCCCATCT   29298     CA   G   AAAC  CA
                                AGG  GGAG TGG    CC  GGG
                                |||  |||| |||    ||  |||
                                TCT  CCTC ACC    GG  CCC
                                  AC    G   _____  AA
GAM629  DLEC1    3'  CCCTGAGGACCACCTCCT    24721         AAA  C
                                AGGAGGTGG   CC CAGGG
                                |||||||||   || |||||
                                TCCTCCACC   GG GTCCC
                                    A__  A
GAM629  DLEC1    3'  CCCTGAGGACCACCTCCT    24731         AAA  C
                                AGGAGGTGG   CC CAGGG
                                |||||||||   || |||||
                                TCCTCCACC   GG GTCCC
                                    A__  A
GAM629  DRD2     3'  CCCTGGGGCTGGGCCCCCCAGC 7675      A  A  T  AAA__
            T                    GGC GG GG GG     CCCCAGGG
                                ||| || || ||     ||||||||
                                TCG CC CC CC     GGGGTCCC
                                  A  _  _  GGGTC
GAM629  EGFL4    3'  CTGGGCTCCCACCTCCCGCCT  62465      A       AAAC
                                AGGC GGAGGTGG    CCCAG
                                |||| ||||||||    |||||
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                                TCCG CCTCCACC   GGGTC
                                  C      CTC_
GAM629  EGR3    5'  CCCTGGGGCCCTCTCCCGCC  60301    A    T  AAA
                                GGC GGAGG GG  CCCCAGGG
                                ||| ||||| ||  ||||||||
                                CCG CCTCT CC  GGGGTCCC
                                  C    C  ___
GAM629  ELAVL3  3'  CCCGCCCCATCCTCCTGCC   9226         _  AAACCCCA
                                GGCAGGAGG TGG      GGG
                                ||||||||| |||      |||
                                CCGTCCTCC ACC      CCC
                                     T  CCG_____
GAM629  ENTPD6  3'  CCCAGGGCAGAGCTCCCCTTCC 8806       T  AAC___  A
           T                     AGGAGG GGA    CCC GGG
                                ||||||| |||    ||| |||
                                TCCTTC CCT    GGG CCC
                                   C  CGAGAC  A
GAM629  F2RL3   3'  CTGGTCTCCAACTCCTGCC   15513       G   AACC
                                GGCAGGAG TGGA   CCAG
                                |||||||| ||||   ||||
                                CCGTCCTC ACCT   GGTC
                                    A   CT__
GAM629  FMR2    3'  CCCTGGGGCCCGTGCCTGGCCT 10688    _  AGG  AAA
                                AGGC AGG  TGG  CCCCAGGG
                                |||| |||  |||  ||||||||
                                TCCG TCC  GCC  GGGGTCCC
                                  G  GT_  C__
GAM629  G6PD    3'  CCCTGGGCACCCACCTCCACC  6387    CA     AAAC
                                GG  GGAGGTGG   CCCAGGG
                                ||  ||||||||   |||||||
                                CC  CCTCCACC   GGGTCCC
                                 A_      CAC_
GAM629  GFRA1   5'  CCCTAAAAGCGGAACCGCCTCC 19155    A     AAA  CC____
           CGCC                  GGC GGAGGTGG  CC    AGGG
                                ||| ||||||||  ||    ||||
                                CCG CCTCCGCC  GG    TCCC
                                  C      AA_  CGAAAA
GAM629  GJA4    5'  CCATCGTCCCCACCTCCACCT  60082    CA     AA  CCCA
                                AGG  GGAGGTGG  AC   GG
                                |||  |||||||  ||   ||
                                TCC  CCTCCACC  TG   CC
                                  A_      CC  CTA_
GAM629  GLRA1   5'  CCCTGGGGCTCTCCCTCCGCGC 5720     A_   TG  AA
           C                     GGC  GGAGG  GA  CCCCAGGG
                                |||  |||||  ||  ||||||||
                                CCG  CCTCC  CT  GGGGTCCC
                                  CG    CT  C_
GAM629  GNA15   5'  CCCTGGCCTCCCCACCTCCTCC 60588   C      AAACC
                                GG AGGAGGTGG    CCAGGG
                                || |||||||||    ||||||
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                                CC TCCTCCACC    GGTCCC
                                 _       CCTCC
GAM629  GNA15    5'  CCCTGGGGCCCCCACCTCACCC 60589    CAG      AAA
              T                   AGG   GAGGTGG   CCCCAGGG
                                  |||   |||||||   ||||||||
                                  TCC   CTCCACC   GGGGTCCC
                                    CA_      CCC
GAM629  GNB2     3'  CCCTGGGGTTGGGGCCTCACCC 19170    CAG    GGA
                                  GG   GAGGT   AACCCCAGGG
                                  ||   |||||   ||||||||||
                                  CC   CTCCG   TTGGGGTCCC
                                   CA_    GGG
GAM629  GYS1     5'  CCCCGGAGCCCCCCTTCCTGC  89781        T  AAACC  A
                                  GCAGGAGG GG    CC GGG
                                  |||||||| ||    || |||
                                  CGTCCTTC CC    GG CCC
                                       _ CCCGA  C
GAM629  HAP1     3'  CCCTACCCCCAACCCCTGCCT  15474        A  _  AAACCCC
                                  AGGCAGG GGT GG      AGGG
                                  ||||||| ||| ||      ||||
                                  TCCGTCC CCA CC      TCCC
                                      _  A  CCCA___
GAM629  HD       3'  CCAGGGCCCCACCCGCCTCCCG 10908     A      AAA_______  CCAG
             CCT                   AGGC GGAGGTGG       CC   G
                                   |||| ||||||||       ||   |
                                   TCCG CCTCCGCC       GG   C
                                     C       CACCCC___  GACC
GAM629  HD       3'  CCCTAAAGGACACCCCTCGCC  10909    _  A   GAAA  CC_
                                  GGC AGG GGTG   CC   AGGG
                                  ||| ||| ||||   ||   ||||
                                  CCG TCC CCAC   GG   TCCC
                                    C  _   A___  AAA
GAM629  HR       5'  CCTGGGGGGCACCCCGCC    18916     A  A   GAAA
                                  GGC GG GGTG   CCCCAGG
                                  ||| || ||||   |||||||
                                  CCG CC CCAC   GGGGTCC
                                    _ _   GG__
GAM629  IGF2     3'  CCCTGGGGCTTCTCCTGACC   7034     _      TGGAAA
                                  GG CAGGAGG     CCCCAGGG
                                  || |||||||     ||||||||
                                  CC GTCCTCT     GGGGTCCC
                                   A      TC_____
GAM629  IGF2R    5'  GGCCGTCTCCACCTCCGCCT   7915      A       AA_______
                                  AGGC GGAGGTGGA       CC
                                  |||| |||||||||       ||
                                  TCCG CCTCCACCT       GG
                                    _       CTGCC___
GAM629  IL8RA    3'  CCCTGGGGCTTTAACTCCTGCT 7152         GTG   A
                                  GGCAGGAG   GAA CCCCAGGG
                                  ||||||||   ||| ||||||||
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                                TCGTCCTC  TTT GGGGTCCC
                                    AA_  C
GAM629  KCNH1   5'  CCCGAGGCCAGTTTCCTGCT  11148       _  AAAC  CA
                                GGCAGGAGG TGG   CC  GGG
                                ||||||||| |||   ||  |||
                                TCGTCCTTT ACC   GG  CCC
                                    G  ____  AG
GAM629  KCNK3   3'  CCCTGGGGCCCCCATCGGAGCC 11171    AGGA    AAA
                                GGC   GGTGG  CCCCAGGG
                                |||   |||||  ||||||||
                                CCG   CTACC  GGGGTCCC
                                  AGG_    CCC
GAM629  KCNK5   3'  CCCTGAACAAGGACCTCACTGC 14967     _   GGAAACCC
          C                      GGCAG GAGGT      CAGGG
                                |||||  |||||      |||||
                                CCGTC CTCCA      GTCCC
                                   A    GGAACAA_
GAM629  KCNN4   5'  CCCTGGGGCCTCCCCTGCC   11189      A  T  AAA
                                GGCAGG GG GG   CCCCAGGG
                                ||||||  ||  ||  ||||||||
                                CCGTCC CC CC   GGGGTCCC
                                   _  T  ___
GAM629  KLK2    3'  CCTGTCCCACCCCTACCT    19895    C   A    AAACCC
                                AGG AGG GGTGG     CAGG
                                |||  |||  |||||     ||||
                                TCC TCC CCACC     GTCC
                                  A  _    CT____
GAM629  KRT8    5'  CCTGCCTCCACTCCTGCCT   11230        G   AACCC
                                AGGCAGGAG TGGA    CAGG
                                |||||||||  ||||    ||||
                                TCCGTCCTC ACCT    GTCC
                                     _   CC___
GAM629  LAD1    3'  CCCTGGGGCCTGCTCCCAGCC  19901    A  AG TG AAA
                                GGC GG  G  G   CCCCAGGG
                                |||  ||  |  |  ||||||||
                                CCG CC  C  C   GGGGTCCC
                                  A  CT GT C__
GAM629  LAG3    5'  CCTGGGACACCCCCGCC    11252    A  A   GAAAC
                                GGC GG GGTG    CCCAGG
                                |||  ||  ||||    ||||||
                                CCG CC CCAC    GGGTCC
                                  C  _   A____
GAM629  LCN1    3'  CCCTTCCTACCACCCCCCGCCT 11279     A  A    AAACCCC
                                AGGC GG GGTGG      AGGG
                                ||||  ||  |||||      ||||
                                TCCG CC CCACC      TCCC
                                  C  C    ATCCT__
GAM629  LCN1    3'  CCCTTCCTACCACCCCCCGCCT 64889     A  A    AAACCCC
                                AGGC GG GGTGG      AGGG
                                ||||  ||  |||||      ||||
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                                TCCG CC CCACC      TCCC
                                  C  C    ATCCT__
GAM629  LETM1    3'  CCAGGGCACCTCCATCCTCCTG 25551         _   AA_____  CCAG
              CC                  GGCAGGAGG TGGA      CC   G
                                ||||||||| ||||      ||   |
                                CCGTCCTCC ACCT      GG   C
                                     T   CCAC___  GACC
GAM629  LLGL1    3'  CCTGGGGGCCCACTGCCT    67418       GA   GGAAA
                                AGGCAG  GGT    CCCCAGG
                                ||||||  |||    |||||||
                                TCCGTC  CCG    GGGGTCC
                                  AC  _____
GAM629  LU       3'  CCTGGTCCCACTCCTGCC    19944        GT   AACC
                                GGCAGGAG  GGA    CCAGG
                                ||||||||  |||    |||||
                                CCGTCCTC  CCT    GGTCC
                                     AC  ____
GAM629  MAGEA12  5'  CCCCGGAGCAGCACTAGCTCCT 19321         G   AAACC__  A
              GCC                 GGCAGGAG TGG      CC GGG
                                ||||||||| |||      || |||
                                CCGTCCTC ATC      GG CCC
                                     G   ACGACGA  C
GAM629  MAML1    3'  CCCCGGGGCTCGCTGGCCCTGC 29274       A__    AAA    A
                                GCAGG   GGTGG   CCCC GGG
                                |||||   |||||   |||| |||
                                CGTCC   TCGCT   GGGG CCC
                                   CGG    C__    C
GAM629  MAP3K7   5'  CCCCGGAGTTTACGGCCCTCCT 13519     C     TGG__    C  A
              CCT                 AGG AGGAGG     AAAC CC GGG
                                ||| ||||||     |||| || |||
                                TCC TCCTCC     TTTG GG CCC
                                  _     CGGCA    A  C
GAM629  MAPK3    3'  CCCTGGGGCCTGGACCTGCCT  73774        AGGT  AAA
                                AGGCAGG    GG   CCCCAGGG
                                |||||||    ||   ||||||||
                                TCCGTCC    CC   GGGGTCCC
                                     AGGT  ___
GAM629  MFGE8    3'  CCCTCTTTCCCACCCTCCACCT 21006     CA    T__    CCCC
                                AGG  GGAGG   GGAAA   AGGG
                                |||  |||||   |||||   ||||
                                TCC  CCTCC   CCTTT   TCCC
                                  A_    CAC    C___
GAM629  MFRP     3'  CCCTGAAGCCGGCCCCTGCC   49504       A  _  AAACCC
                                GGCAGG GGT GG     CAGGG
                                |||||| ||| ||     |||||
                                CCGTCC CCG CC     GTCCC
                                     _  G  GAA___
GAM629  MMP19    3'  CCCTGAGGCTCCACCACCCACC 43303     CA  A     AA  C
                                GG  GG GGTGGA  CC CAGGG
                                ||  || ||||||  || |||||
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                                CC  CC CCACCT  GG GTCCC
                                 AC  A     C_  A
GAM629  MMP19    3' CCCTGAGGCTCCACCACCCACC 43311    CA  A     AA  C
                                GG  GG GGTGGA  CC CAGGG
                                ||  || ||||||  || |||||
                                CC  CC CCACCT  GG GTCCC
                                 AC  A     C_  A
GAM629  MMP19    3' CCCTGAGGCTCCACCACCCACC 43314    CA  A     AA  C
                                GG  GG GGTGGA  CC CAGGG
                                ||  || ||||||  || |||||
                                CC  CC CCACCT  GG GTCCC
                                 AC  A     C_  A
GAM629  MMP19    3' CCCTGAGGCTCCACCACCCACC 11627    CA  A     AA  C
                                GG  GG GGTGGA  CC CAGGG
                                ||  || ||||||  || |||||
                                CC  CC CCACCT  GG GTCCC
                                 AC  A     C_  A
GAM629  MMP25    3' CCCGCCACCCACCTCCTCCT   42696     C       AAACCCCA
                                AGG AGGAGGTGG       GGG
                                ||| |||||||||       |||
                                TCC TCCTCCACC       CCC
                                  _       CACCG___
GAM629  MUC3B    3' CCAGGGCCCCATCCCATCTCCT 95920          AAA________  CCAG
           GCC                    GGCAGGAGGTGG        CC   G
                                  ||||||||||||        ||   |
                                  CCGTCCTCTACC        GG   C
                                         CTACCCC___  GACC
GAM629  MVK      3' CCCTGAAGCTCCCACAGTCCCA 61278     CA  G_   AAACCC
           TCT                    AGG  GGA  GTGG     CAGGG
                                  |||  |||  ||||     |||||
                                  TCT  CCT  CACC     GTCCC
                                   AC   GA   CTCGAA
GAM629  MYC      5' CCTGGCTCCCCTCCTGCCT    11729          T   AACC
                                  AGGCAGGAGG GGA    CCAGG
                                  |||||||||| |||    |||||
                                  TCCGTCCTCC CCT    GGTCC
                                        _   C___
GAM629  MYO1C    3' CCAGGGCAATCTCCCACCTCCT 61859          AAA________  CCAG
           GCC                    GGCAGGAGGTGG        CC   G
                                  ||||||||||||        ||   |
                                  CCGTCCTCCACC        GG   C
                                         CTCTAAC___  GACC
GAM629  NDRG2    3' CCCTGGGGCTTCTGACCCCCCT 33193     CA  A  _   A
                                  AGG  GG GGT GGAA CCCCAGGG
                                  |||  || ||| |||| ||||||||
                                  TCC  CC CCA TCTT GGGGTCCC
                                    __  _  G   C
GAM629  NIPSNAP1 3' CCTACACCTCCACCTCCTTCC  14656    C       AACCCC
                                  GG AGGAGGTGGA     AGG
                                  || ||||||||||     |||
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                                CC TCCTCCACCT     TCC
                                 T        CCACA_
GAM629  NLGN3    5'  CCCTGGAGTCTGCCTCTCCTGC 39118         T  AA_  C
            C                    GGCAGGAGG GG   AC CCAGGG
                                 ||||||||| ||   || ||||||
                                 CCGTCCTCT CC   TG GGTCCC
                                      _  GTC  A
GAM629  OXCT     3'  CCCTAGAACATCCCCCTTCCT  6486     C   A  T   AACCCC
                                 AGG AGG GG GGA     AGGG
                                 ||| ||| || |||     ||||
                                 TCC TTC CC CCT     TCCC
                                  _  _ _  ACAAGA
GAM629  PAG      3'  CCTGGAGTCTCTTCTGTCT   38014         GT   AACC
                                 AGGCAGGAG  GGA   CCAGG
                                 |||||||||  |||   |||||
                                 TCTGTCTTC  TCT   GGTCC
                                      __  GA__
GAM629  PAK1     5'  CCAGTTACCACCTCCTGCCT   11957           A   CCCA
                                 AGGCAGGAGGTGG AAC   GG
                                 |||||||||||| |||   ||
                                 TCCGTCCTCCACC TTG   CC
                                       A   A___
GAM629  PAX2     3'  CCCAGGGCCCGGCACCTCCTGC 15651          GAAAC   A
            T                    GGCAGGAGGTG    CCC GGG
                                 ||||||||||     ||| |||
                                 TCGTCCTCCAC    GGG CCC
                                       GGCCC   A
GAM629  PAX2     3'  CCCAGGGCCCGGCACCTCCTGC 15665          GAAAC   A
            T                    GGCAGGAGGTG    CCC GGG
                                 ||||||||||     ||| |||
                                 TCGTCCTCCAC    GGG CCC
                                       GGCCC   A
GAM629  PDE1B    3'  CCCTGGGACCTCCCCCATCCT  8110      _  T   AAC
                                 AGGA GG GGA   CCCAGGG
                                 |||| || |||   |||||||
                                 TCCT CC CCT   GGGTCCC
                                   A  C   CCA
GAM629  PFKL     3'  CCCTGCTCAGCCCATCCCCTGC 12055       A    AAACCC
            CT                    AGGCAGG GGTGG     CAGGG
                                 |||||||  |||||     |||||
                                 TCCGTCC CTACC     GTCCC
                                    C    CGACTC
GAM629  PFKL     3'  CCCTGGGGCATCCACCTTCCTG 12056       _     AA
            CC                    GGCAGGA GGTGGA  CCCCAGGG
                                 |||||||  ||||||  ||||||||
                                 CCGTCCT CCACCT  GGGGTCCC
                                    T     AC
GAM629  PIN1     3'  CCCTGGGGTCCCCACTCCCTGT 21706       AG   AA
            C                    GGCAGG  GTGG  ACCCCAGGG
                                 ||||||  ||||  |||||||||
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                                CTGTCC  CACC  TGGGGTCCC
                                   CT    CC
GAM629  PIN1L    3'  CCCTGGGGTTCCCCACTCCCT  21709     AG    A_
                                AGG  GTGG  AACCCCAGGG
                                |||  ||||  ||||||||||
                                TCC  CACC  TTGGGGTCCC
                                  CT    CC
GAM629  PMM2     3'  CCCTGGGGCCGGTTCTTACC   72558    C     G   AAA
                                GG AGGAG TGG   CCCCAGGG
                                || ||||| |||   ||||||||
                                CC TTCTT GCC   GGGGTCCC
                                 A    G   ___
GAM629  PPP1R12B 3'  CCCTGAGGTTTCCATGCCTCTC 50385    CA     __      C
             C                   GG  GGAGGT  GGAAACC CAGGG
                                ||  ||||||  ||||||| |||||
                                CC  TCTCCG  CCTTTGG GTCCC
                                 __     TA      A
GAM629  PPP2R1A  3'  CCCATTTACTTCTCCACCTCCC 27248     A       AACCCCA__
             GTC                   GGC GGAGGTGGA        GGG
                                ||| |||||||||        |||
                                CTG CCTCCACCT        CCC
                                  C        CTTCATTTA
GAM629  PRKCN    3'  CCCTGAAGCTAGTCTCCTGTCT 20562          _  AAACCC
                                AGGCAGGAGG TGG     CAGGG
                                |||||||||| |||     |||||
                                TCTGTCCTCT ATC     GTCCC
                                      G   GAA___
GAM629  PTBP1    3'  CCCCAGGGCCTTCCCTTCTGCC 50082         T   AA   CA
                                GGCAGGAGG GGA  CCC  GGG
                                |||||||||| |||  |||  |||
                                CCGTCTTCC CTT  GGG  CCC
                                      _  CC   AC
GAM629  PTBP1    3'  CCCCAGGGCCTTCCCTTCTGCC 12540         T   AA   CA
                                GGCAGGAGG GGA  CCC  GGG
                                |||||||||| |||  |||  |||
                                CCGTCTTCC CTT  GGG  CCC
                                      _  CC   AC
GAM629  PTMS     5'  CCCCGGGACCCCGCCTCCCCGC 12562     A_      AAAC   A
             C                   GGC  GGAGGTGG    CCC GGG
                                |||  ||||||||    ||| |||
                                CCG  CCTCCGCC    GGG CCC
                                  CC       CCA_   C
GAM629  PTPN1    3'  CCCTCCTCCACTCCACCTCCAC 12576    CA       AACCCC_
             C                   GG  GGAGGTGGA      AGGG
                                ||  |||||||||      ||||
                                CC  CCTCCACCT      TCCC
                                 A_        CACCTCC
GAM629  RAD51L3  5'  CCTGGGGCTGTTCCGGCCT   12753      A   G TG AAA
                                AGGC GGA G  G   CCCCAGG
                                |||| ||| |  |   |||||||
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                                TCCG CCT T  C   GGGGTCC
                                  G   _ GT ___
GAM629  RAD51L3  5'  CCTGGGGCTGTTCCGGCCT   56885     A   G TG AAA
                                AGGC GGA G  G   CCCCAGG
                                |||| ||| |  |   |||||||
                                TCCG CCT T  C   GGGGTCC
                                  G   _ GT ___
GAM629  RAD51L3  5'  CCTGGGGCTGTTCCGGCCT   56896     A   G TG AAA
                                AGGC GGA G  G   CCCCAGG
                                |||| ||| |  |   |||||||
                                TCCG CCT T  C   GGGGTCC
                                  G   _ GT ___
GAM629  RAD51L3  5'  CCTGGGGCTGTTCCGGCCT   56897     A   G TG AAA
                                AGGC GGA G  G   CCCCAGG
                                |||| ||| |  |   |||||||
                                TCCG CCT T  C   GGGGTCC
                                  G   _ GT ___
GAM629  RAD54L   5'  CCTGGTTTCCACCTCCAGCC   14552     A          CC
                                GGC GGAGGTGGAAACC  AGG
                                ||| ||||||||||||  |||
                                CCG CCTCCACCTTTGG  TCC
                                  A          __
GAM629  RANBP3   3'  CCCCAGGGTCCCCTGACTCCCG 14634      A   GT_  AA   CA
           TCT                    AGGC GGAG   GG  ACCC  GGG
                                |||| ||||   ||  ||||  |||
                                TCTG CCTC   CC  TGGG  CCC
                                  C    AGT  CC    AC
GAM629  RDS     3'  CCCTGGGGCCCCTCCCCTCC   6150       T   AA__
                                GGAGG GGA    CCCCAGGG
                                ||||| |||    ||||||||
                                CCTCC CCT    GGGGTCCC
                                  _   CCCC
GAM629  RNH     3'  CCCTGGGGCCCACCAGCCCCTG 12890       A___    AAA
           CC                     GGCAGG   GGTGG   CCCCAGGG
                                ||||||   |||||  ||||||||
                                CCGTCC   CCACC   GGGGTCCC
                                   CCGA    C__
GAM629  RNH     3'  CCCTGGGGCCCACCAGCCCCTG 60369       A___    AAA
           CC                     GGCAGG   GGTGG   CCCCAGGG
                                ||||||   |||||  ||||||||
                                CCGTCC   CCACC   GGGGTCCC
                                   CCGA    C__
GAM629  RXRA    3'  CCCGCCGCCCTCCACCCCTGCC 12917        A     AACCCCA
           T                     AGGCAGG GGTGGA      GGG
                                |||||||  ||||||      |||
                                TCCGTCC CCACCT      CCC
                                   _     CCCGCCG
GAM629  RXRG    3'  CCCTGCACTTTCCTCCACCTCC 23609    CA       AACCC___
           CACC                    GG  GGAGGTGGA       CAGGG
                                ||  |||||||||       |||||
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                              CC  CCTCCACCT      GTCCC
                               AC       CCTTTCAC
GAM629  RYR2    3' CAGGGCTGTTTCCTCCCCCCAC 8289     CA  A  T    _____ CAG
           CT                   AGG  GG GG GGAAAC    CC   G
                              |||  || || ||||||    ||   |
                              TCC  CC CC CCTTTG    GG   C
                               AC  C  T     TC___  GAC
GAM629  SALL2   3' CCCTGGAATTCCAGCTCCACCT 64590    CA   G    ACC
                              AGG  GGAG TGGAA   CCAGGG
                              |||  |||| |||||   ||||||
                              TCC  CCTC ACCTT   GGTCCC
                               A_   G    AA_
GAM629  SF3A1   3' CCCTGAGGCTTTGCCTTGCCT  20806     GG   TG  AA  C
                              AGGCA  AGG  GA  CC CAGGG
                              |||||  |||  ||  || |||||
                              TCCGT  TCC  TT  GG GTCCC
                                 __  GT  C_  A
GAM629  SLC17A7 3' CCCTAAAGGTTCCCTCTCCACC 40083   CA    T   A  CC_
                              GG  GGAGG GGAA CC   AGGG
                              ||  ||||| |||| ||   ||||
                              CC  CCTCT CCTT GG   TCCC
                               A_    C    _ AAA
GAM629  SLC18A3  5' CCCGAAGTCCCGCTGCCCTCGC 13212     _  A_    AA  CCCA
           CT                   AGGC AGG  GGTGG  AC   GGG
                              |||| |||  |||||  ||   |||
                              TCCG TCC  TCGCC  TG   CCC
                                C   CG    C_  AAG_
GAM629  SLC2A3   3' CCTCCTTCCACCTCCCTCC   23639    CA       ACCCC
                              GG  GGAGGTGGAA    AGG
                              ||  ||||||||||    |||
                              CC  CCTCCACCTT    TCC
                               TC        CC___
GAM629  SLC38A3  3' CCTGGGGCCTCATCTCC     23373        AAA
                              GGAGGTGG   CCCCAGG
                              ||||||||   |||||||
                              CCTCTACT   GGGGTCC
                                   CC_
GAM629  SLC6A8   3' CCCTGCCACGCCCACCCCCTGC 20070       A    AAACCC
           C                    GGCAGG GGTGG     CAGGG
                              ||||||  |||||     |||||
                              CCGTCC CCACC     GTCCC
                                 C    CGCACC
GAM629  SOD3    3' CCCGAGGCCCCCCTCTGCCT   13299      GA  T  AAAC  CA
                              AGGCAG  GG GG   CC  GGG
                              ||||||  || ||   ||  |||
                              TCCGTC  CC CC   GG  CCC
                                 TC  _  C___  AG
GAM629  SOX11   3' CCAGGGCCTCCTCCACTCCCTG 13312       AG    AA_______  CCAG
           CCT                    AGGCAGG  GTGGA      CC   G
                              |||||||  |||||      ||   |
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                                TCCGTCC  CACCT      GG   C
                                   CT    CCTCC___  GACC
GAM629  SPTBN1   3'  CCCCAGGGCCTTTCCTTCACCT 13388          AA_________  CCAG
           CCTGCC                GGCAGGAGGTGGA        CC   GG
                                ||||||||||||        ||   ||
                                CCGTCCTCCACTT       GG   CC
                                      CCTTTCC___  GACC
GAM629  SYNGR1   3'  CCCTGGCCACCCACCTCCTACC 17499    C       AAACC
                                GG AGGAGGTGG    CCAGGG
                                || |||||||||    ||||||
                                CC TCCTCCACC    GGTCCC
                                 A       CACC_
GAM629  TCF1     3'  CCTGGGGCCTGTACTGCCT   6785       GAGGT  AAA
                                AGGCAG    GG   CCCCAGG
                                ||||||    ||   |||||||
                                TCCGTC    CC   GGGGTCC
                                   ATGT_ ___
GAM629  TCTA     3'  CCCTGGGGTAGCCTCCTATC   42492   GC     GGAA
                                G  AGGAGGT    ACCCCAGGG
                                |  |||||||    |||||||||
                                C  TCCTCCG    TGGGGTCCC
                                 TA      A___
GAM629  TFAP4    3'  CCCCAGCCCCCACCTCTGCCT  13689       G     AAACCCCA
                                AGGCAG AGGTGG       GGG
                                |||||| ||||||       |||
                                TCCGTC TCCACC       CCC
                                   _     CCCGAC__
GAM629  TIMM23   3'  CCAGGGCAACCTCCACCTCCCA 60772     A_       AA_______  CCAG
           GCC                   GGC  GGAGGTGGA       CC    G
                                |||  |||||||||       ||    |
                                CCG  CCTCCACCT      GG    C
                                  AC        CCAAC___  GACC
GAM629  TKTL1    3'  CCTGGAATTCCCTTCGCT    25314     A    T   AACC
                                GGC GGAGG GGA    CCAGG
                                ||| ||||| |||    |||||
                                TCG CTTCC CTT    GGTCC
                                  _    _   AA__
GAM629  TRPV4    3'  CCCTGGGGTGGGGGCTCCCGGC 61330     A  AG  GGAA
           C                     GGC GG  GT    ACCCCAGGG
                                ||| ||  ||    |||||||||
                                CCG CC  CG    TGGGGTCCC
                                  G  CT  GGGG
GAM629  VEGF     5'  CCCAGTTACCACCTCCTCCC   14041    C       A   CCCA
                                GG AGGAGGTGG AAC    GGG
                                || |||||||| |||    |||
                                CC TCCTCCACC TTG    CCC
                                 C        A   A___
GAM629  VHL      3'  GGACTTCCACCTCCAGCCT    6864       A        AC
                                AGGC GGAGGTGGAA  CC
                                ||||  ||||||||||  ||
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                                TCCG CCTCCACCTT  GG
                                  A        CA
GAM629  WNT11    3'  CCTGGGGTCTGAGCCTGCT   17324       AGG   AA
                                GGCAGG  TGGA  CCCCAGG
                                ||||||  ||||  |||||||
                                TCGTCC  GTCT  GGGGTCC
                                  GA_   __
GAM629  WT1      5'  CCCCAGGGCCGCTCCCCCACTT 44639    A      AAA_________  CCAG
            CCCGCC                GGC GGAGGTGG        CC   GG
                                ||| ||||||||        ||   ||
                                CCG CCTTCACC        GG   CC
                                  C      CCCTCGCC___  GACC
GAM629  WT1      5'  CCCCAGGGCCGCTCCCCCACTT 44640    A      AAA_________  CCAG
            CCCGCC                GGC GGAGGTGG        CC   GG
                                ||| ||||||||        ||   ||
                                CCG CCTTCACC        GG   CC
                                  C      CCCTCGCC___  GACC
GAM629  WT1      5'  CCCCAGGGCCGCTCCCCCACTT 44641    A      AAA_________  CCAG
            CCCGCC                GGC GGAGGTGG        CC   GG
                                ||| ||||||||        ||   ||
                                CCG CCTTCACC        GG   CC
                                  C      CCCTCGCC___  GACC
GAM629  WT1      5'  CCCCAGGGCCGCTCCCCCACTT 6349     A      AAA_________  CCAG
            CCCGCC                GGC GGAGGTGG        CC   GG
                                ||| ||||||||        ||   ||
                                CCG CCTTCACC        GG   CC
                                  C      CCCTCGCC___  GACC
GAM629  XPNPEP2  3'  CCCTGAGCCCACCTCCCAGCC  14141    A_      AAACCC
                                GGC  GGAGGTGG     CAGGG
                                |||  ||||||||     |||||
                                CCG  CCTCCACC     GTCCC
                                  AC       CGA___
GAM629  ZNF216   5'  CCAGGGCCTCCCTCCACCTCCT 21171    C       AA________  CCAG
            CCT                   AGG AGGAGGTGGA       CC   G
                                ||| ||||||||||       ||   |
                                TCC TCCTCCACCT       GG   C
                                  _        CCCTCC___  GACC
GAM629  ZNF24    5'  CCCTGAGGCTTATATTCTGCCT 23707        G   AAA  C
                                AGGCAGGA GTGG   CC CAGGG
                                |||||||| ||||   || |||||
                                TCCGTCTT TATT   GG GTCCC
                                     A   C__  A
GAM629  ZYX      3'  CCCTGGGGTCTGGTCCTCGCC  14403     AG    TGGAA
                                GGC  GAGG    ACCCCAGGG
                                |||  ||||    |||||||||
                                CCG  CTCC    TGGGGTCCC
                                  __    TGGTC
GAM629  ABT1     3'  CCCTGAAAATCCCACTTCCTGC 26300           AAACCC
            C                    GGCAGGAGGTGG     CAGGG
                                ||||||||||||     |||||
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                                CCGTCCTTCACC     GTCCC
                                      CTAAAA
GAM629  ACTR1A   3'  CCCTGAGGCCCCAGGCAGCTGC 63649       G  G  GAAAC__  _
           TGCCT                  AGGCAG AG TG      CC CAGGG
                                |||||| || ||      || |||||
                                TCCGTC TC AC      GG GTCCC
                                   G  G  GGACCCC  A
GAM629  AFAP     3'  CCCAGGAACAAGCACCCCTTGC 41605       A   GAAACC  A
           CT                   AGGCAGG GGTG     CC GGG
                                ||||||| ||||     || |||
                                TCCGTTC CCAC     GG CCC
                                   C   GAACAA  A
GAM629  AGPAT1   3'  CTTGACCCCCACCTCCTACT   22176    C       AAACCC
                                GG AGGAGGTGG     CAGG
                                || |||||||||     ||||
                                TC TCCTCCACC     GTTC
                                 A       CCCA__
GAM629  AGPAT1   3'  CTTGACCCCCACCTCCTACT   52200    C       AAACCC
                                GG AGGAGGTGG     CAGG
                                || |||||||||     ||||
                                TC TCCTCCACC     GTTC
                                 A       CCCA__
GAM629  APBA2BP  3'  CCCCGGGACCCTGCCTGCCT   49185       A  T  AAAC   A
                                AGGCAGG GG GG    CCC GGG
                                ||||||| || ||    ||| |||
                                TCCGTCC TC CC    GGG CCC
                                   G  _  A___   C
GAM629  ARHGAP4  3'  CCGCTCCACATCCTGCCT    9794        G    AACCCCA
                                AGGCAGGA GTGGA      GG
                                |||||||| |||||      ||
                                TCCGTCCT CACCT      CC
                                    A    CG_____
GAM629  ARHU     3'  GCCCTGGAGGGGACTTCCACAC 41360          __   A___  _    ___
           CTCCTGCCT               AGGCAGGAGGT  GGAA   CC CCAGGG   C
                                |||||||||||  ||||   || ||||||   |
                                TCCGTCCTCCA  CCTT   GG GGTCCC   G
                                      CA   CAGG  A    ___
GAM629  B3GNT7   3'  GGTTGCCACCTCCTACCT    71681     C       A
                                AGG AGGAGGTGG AACC
                                ||| ||||||||| ||||
                                TCC TCCTCCACC TTGG
                                  A       G
GAM629  BC002942 3'  CCCCAGGACTCCCACTATTGCC 66071       GA    AAAC  CA
           T                    AGGCAG  GGTGG   CC  GGG
                                ||||||  |||||   ||  |||
                                TCCGTT  TCACC   GG  CCC
                                   A_    CTCA  AC
GAM629  BMF      3'  CCCTGGGGTCTGGGCACTCTGC 54279       AG  GGAA
           CT                   AGGCAGG  GT   ACCCCAGGG
                                |||||||  ||   |||||||||
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                                TCCGTCT  CG    TGGGGTCCC
                                    CA  GGTC
GAM629  BRPF3    3'  CCCCAGGACACCACCTCCCACC 93928    CA       AAAC  CA
                                GG  GGAGGTGG    CC  GGG
                                ||  ||||||||    ||  |||
                                CC  CCTCCACC    GG  CCC
                                 AC       ACA_  AC
GAM629  C19orf7   3'  CCTGGGGTGGCTCCTGGCC   61780     _    G GGAA
                                GGC AGGAG T    ACCCCAGG
                                ||| ||||| |    ||||||||
                                CCG TCCTC G    TGGGGTCC
                                  G    G ____
GAM629  C1orf16   3'  CCCATTCTACTTCCCACCCTCC 29911         T__    ACCCCA_
           TGCC                    GGCAGGAGG   GGAA      GGG
                                |||||||||   ||||      |||
                                CCGTCCTCC   CCTT      CCC
                                     CAC    CATCTTA
GAM629  C20orf18  3'  CCCTGCGGCTCCCACCTCTGCC 49169       G     AAA  C
           T                     AGGCAG AGGTGG   CC CAGGG
                                ||||||  ||||||   || |||||
                                TCCGTC TCCACC   GG GTCCC
                                   _     CTC  C
GAM629  C20orf18  3'  CCCTGCGGCTCCCACCTCTGCC 49176       G     AAA  C
           T                     AGGCAG AGGTGG   CC CAGGG
                                ||||||  ||||||   || |||||
                                TCCGTC TCCACC   GG GTCCC
                                   _     CTC  C
GAM629  C20orf39  5'  CCCCGGGGCCCGCGCCCGCTGC 46573       GA    GAAA    A
           CT                     AGGCAG  GGTG    CCCC GGG
                                ||||||  ||||    |||| |||
                                TCCGTC  CCGC    GGGG CCC
                                   GC    GCCC    C
GAM629  C22orf4   3'  CCTGGACCACTCCTGCC     61271         G   AAACC
                                GGCAGGAG TGG     CCAGG
                                |||||||| |||     |||||
                                CCGTCCTC ACC     GGTCC
                                     _   A_____
GAM629  C6orf33   3'  CCAGGGCCCCAAGGCTTCTGTC 56711         G__    AAA__  CCAG
           T                     AGGCAGGAG   TGG    CC    G
                                |||||||||   |||    ||    |
                                TCTGTCTTC   ACC    GG    C
                                     GGA   CC____  GACC
GAM629  CACNA1H   3'  CCCTGGGGTCTGGGGGCCCCGC 41185     A  A   GGAA__
           T                     GGC GG GGT      ACCCCAGGG
                                ||| || |||      |||||||||
                                TCG CC CCG      TGGGGTCCC
                                  _  _   GGGGTC
GAM629  CACNA1I   3'  CCCCGGCCGCCCACCGCCCGCC 41183     A  A    AAACC  A
                                GGC GG GGTGG    CC GGG
                                ||| || |||||    || |||
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                                CCG CC CCACC    GG CCC
                                  C  G    CGCC_  C
GAM629  CARM1   3'  CCCTAACCCCCACCTCCCGGCC 64097    A_      AAACCCC
                                GGC  GGAGGTGG      AGGG
                                |||  ||||||||      ||||
                                CCG  CCTCCACC      TCCC
                                  GC       CCCAA__
GAM629  CARM1   3'  CCCTCGTCCCCCCTCCTGCC   64098         T  AA  CCC
                                GGCAGGAGG GG  AC   AGGG
                                |||||||||  ||  ||   ||||
                                CCGTCCTCC CC  TG   TCCC
                                      _  CC  C__
GAM629  CCNI    5'  CCGGTCTCACCCCCCGCCT   23367     A  A    AA   CCA
                                AGGC GG GGTGG  ACC   GG
                                ||||  ||  |||||  |||   ||
                                TCCG CC CCACT  TGG   CC
                                  C  C    C_   ___
GAM629  CECR7   5'  CCCTAGGGCCCCTGCCTGCCT  80447        _   T  AAA   C
                                AGGCAGG AGG GG   CCC AGGG
                                |||||||  |||  ||   |||  ||||
                                TCCGTCC TCC CC   GGG TCCC
                                   G   _  ___   A
GAM629  CHST3   3'  CCCTGAAGTCTCCATCTCAGCT 16234     AG       A  CC
                                GGC  GAGGTGGA AC  CAGGG
                                |||  ||||||||  ||  |||||
                                TCG  CTCTACCT TG  GTCCC
                                  A_       C  AA
GAM629  CL25084  5'  GGCCTCCTCCACCTCCTCCT   32288     C        AA_______
                                AGG AGGAGGTGGA       CC
                                |||  ||||||||||       ||
                                TCC TCCTCCACCT       GG
                                  _        CCTCC___
GAM629  CLECSF9  3'  CCAGGGCCTCTCCCTCCTCCTA 27619     C     T_   AA_____  CCAG
            CCT                   AGG AGGAGG  GGA      CC    G
                                |||  ||||||  |||      ||    |
                                TCC TCCTCC  CCT      GG    C
                                  A     TC   CTCC___  GACC
GAM629  CLECSF9  3'  CCCTGGGGCTTCCTTTGCTCTG 27620       _ AGGT    A
            CCT                   AGGCAG G    GGAA CCCCAGGG
                                ||||||  |    ||||  ||||||||
                                TCCGTC C    CCTT GGGGTCCC
                                   T GTTT    C
GAM629  CPLX1   3'  CCCTGGGGAGGACCCCTGCC   22821       A   GGAAA
                                GGCAGG GGT     CCCCAGGG
                                ||||||  |||    ||||||||
                                CCGTCC CCA     GGGGTCCC
                                   _   GGA__
GAM629  CXYorf1  3'  CCCTGTTCCCCACCTCCCGGCT 82909     A_       AAACCC
                                GGC  GGAGGTGG     CAGGG
                                |||  ||||||||     |||||
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                                TCG  CCTCCACC     GTCCC
                                  GC       CCTT__
GAM629  CYP2A7   5'  CCCTGGGGTCCCCTTATCCTCC 7539      C    GGT  AA
            CT                    AGG AGGA   GG  ACCCCAGGG
                                  ||| ||||   ||  |||||||||
                                  TCC TCCT   CC  TGGGGTCCC
                                    C    ATT  CC
GAM629  CYP2A7   5'  CCCTGGGGTCCCCTTATCCTCC 48352     C    GGT  AA
            CT                    AGG AGGA   GG  ACCCCAGGG
                                  ||| ||||   ||  |||||||||
                                  TCC TCCT   CC  TGGGGTCCC
                                    C    ATT  CC
GAM629  DDM36    3'  CCTACGTTTCCACCTCCTCCC  40918    C          CCC
                                  GG AGGAGGTGGAAAC   AGG
                                  || ||||||||||||   |||
                                  CC TCCTCCACCTTTG   TCC
                                   C           CA_
GAM629  DDX39    3'  CCCTGCCCGCCCCTCCCACCT  58116     CA     T  AAACCC
                                  AGG  GGAGG GG     CAGGG
                                  |||  ||||| ||     |||||
                                  TCC  CCTCC CC     GTCCC
                                    AC     _  GCCC__
GAM629  DKFZP434G156 3'  CTGACTTCCATCTCCTGCCT   70336             ACCC
                                  AGGCAGGAGGTGGAA    CAG
                                  ||||||||||||||    |||
                                  TCCGTCCTCTACCTT    GTC
                                            CA__
GAM629  DKFZP434J037 3'  GGCTATTTCCACCTCCTCC    48952    C         A_______
                                  GG AGGAGGTGGAA      CC
                                  || ||||||||||       ||
                                  CC TCCTCCACCTT      GG
                                   _          TATC___
GAM629  DKFZP434K1772 3'  CCCTAGCCCCACTCCCTGCCT  68334        AG    AAACCCC
                                  AGGCAGG  GTGG      AGGG
                                  |||||||  ||||      ||||
                                  TCCGTCC  CACC      TCCC
                                      CT    CCGA___
GAM629  DKFZP434K1772 5'  CCCTGGGGTCTCCAGCTGC    68335      GAGG    A
                                  GCAG    TGGA ACCCCAGGG
                                  ||||    |||| |||||||||
                                  CGTC    ACCT TGGGGTCCC
                                    G___    C
GAM629  DKFZP547L112 5'  CCTGAACTACTCCTGCC     67128         G    AAACCC
                                  GGCAGGA GTGG      CAGG
                                  ||||||| ||||      ||||
                                  CCGTCCT CATC      GTCC
                                      _    AA_____
GAM629  DKFZP564J157 3'  CCTTGTGCTCCCCACCCCCTAC 38052     C   A     AAACCC
            CT                    AGG AGG GGTGG      CAGGG
                                  ||| ||| |||||      |||||
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                                TCC TCC CCACC     GTTCC
                                  A  C    CCTCGT
GAM629  DSCR6    3'  CCAGGGCCCACTCCACCTCCTA 39061    C       AA_______  CCAG
            CTT                   AGG AGGAGGTGGA      CC   G
                                ||| ||||||||||      ||   |
                                TTC TCCTCCACCT      GG   C
                                  A        CACCC___  GACC
GAM629  EFS2     5'  CCGCTCCTCCTCCTGCCT    20771         T  AACCCCA
                                AGGCAGGAGG GGA      GG
                                |||||||||| |||      ||
                                TCCGTCCTCC CCT      CC
                                      T  CG_____
GAM629  ENAH     5'  CCCTCCTCCTCCACCACCTCCT 37156          AAACCCC__
            GCC                   GGCAGGAGGTGG       AGGG
                                ||||||||||||       ||||
                                CCGTCCTCCACC       TCCC
                                       ACCTCCTCC
GAM629  FLJ00001  3'  CCTGGGGGTGGACCCTGCC    82712      AG  GGAA
                                GGCAGG  GT   ACCCCAGG
                                ||||||  ||   ||||||||
                                CCGTCC  CA   TGGGGTCC
                                   __  GG__
GAM629  FLJ00007  3'  CCCTGGGGCTCCAGGACCTTCC 71775    C   AGG    AA
                                GG AGG   TGGA  CCCCAGGG
                                || |||   ||||  ||||||||
                                CC TCC   ACCT  GGGGTCCC
                                 T   AGG    C_
GAM629  FLJ10040  3'  CCTGGACAACCTCCTGCT    36219         GGAAACC
                                GGCAGGAGGT      CCAGG
                                ||||||||||      |||||
                                TCGTCCTCCA      GGTCC
                                      ACA____
GAM629  FLJ10276  3'  CCTGACCCACCTCCTTCCT    36420     C       AAACCC
                                AGG AGGAGGTGG     CAGG
                                ||| |||||||||     ||||
                                TCC TCCTCCACC     GTCC
                                  T       CA____
GAM629  FLJ10297  3'  CCCTGGGGCCCCAGGATCCACC 36438     CA   GG_   AAA
            T                    AGG  GGA   TGG   CCCCAGGG
                                ||| |||   |||   ||||||||
                                TCC  CCT   ACC   GGGGTCCC
                                  A_   AGG   CC_
GAM629  FLJ10307  3'  GGCCCCAAAACTTCCACCTCCC 36478     CA_       ACCCCA  ___
            TCCCT                  AGG   GGAGGTGGAA     GGG   CC
                                |||   ||||||||||     |||   ||
                                TCC   CCTCCACCTT     CCC   GG
                                  CTC        CAAAAC  ___
GAM629  FLJ10314  5'  CCCAAGGCCAGCTTACTGCCT  36487       _   G   AAAC  CA
                                AGGCAG GAG TGG    CC  GGG
                                |||||| ||| |||    ||  |||
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                                TCCGTC TTC ACC    GG  CCC
                                   A   G   ____  AA
GAM629  FLJ10324  5' CCCTGGGGCTCTACTACCTGCT 36498       A     AA
                                GGCAGG GGTGGA  CCCCAGGG
                                |||||| ||||||  ||||||||
                                TCGTCC TCATCT  GGGGTCCC
                                   A     C_
GAM629  FLJ10743  3' CCTGTCTCCTTCCACCTCCTTC 37080    C         ACCC_
          C                     GG AGGAGGTGGAA    CAGG
                                || ||||||||||    ||||
                                CC TCCTCCACCTT    GTCC
                                 T         CCTCT
GAM629  FLJ11078  3' CCCTGGGGTGCCCTCCTTCC  37594    C     TGGAA
                                GG AGGAGG    ACCCCAGGG
                                || ||||||    |||||||||
                                CC TCCTCC    TGGGGTCCC
                                 T     CG___
GAM629  FLJ11362  3' CCTCTCCTCCCACCTCCTCCCT 41961     C        AAACCCC
                                AGG AGGAGGTGG      AGG
                                ||| |||||||||      |||
                                TCC TCCTCCACC      TCC
                                  C       CTCCTC_
GAM629  FLJ12229  5' CCCTGGGGCCTGGGCCCCACC  46403    CA  A   GGAAA
                                GG  GG GGT    CCCCAGGG
                                ||  || |||    ||||||||
                                CC  CC CCG    GGGGTCCC
                                 A_  _   GGTCC
GAM629  FLJ12770  3' CCCTGAGGTTTCCTCCTTCCC  50677    CA    T     C
                                GG  GGAGG GGAAACC CAGGG
                                ||  ||||| ||||||| |||||
                                CC  CTTCC CCTTTGG GTCCC
                                 __    T     A
GAM629  FLJ13241  3' CCCCAGGGCTCCCATCCTTCTG 47650        _  AAA   CA
          C                     GCAGGAGG TGG   CCC  GGG
                                |||||||| |||   |||  |||
                                CGTCTTCC ACC   GGG  CCC
                                     T   CTC   AC
GAM629  FLJ14351  3' CCAGGGCCGCTCTCCACCCCCT 45646       A     AA________  CCAG
          GCTT                    AGGCAGG GGTGGA       CC    G
                                ||||||| ||||||       ||   |
                                TTCGTCC CCACCT       GG    C
                                   C     CTCGCC___  GACC
GAM629  FLJ14360  5' CCCGCCTCCCGCCTCCCGCCT  52292     A      AAACCCCA
                                AGGC GGAGGTGG       GGG
                                |||| ||||||||       |||
                                TCCG CCTCCGCC       CCC
                                  C       CTCCG___
GAM629  FLJ14397  3' CCTACCTTCCACTCCTGCCT   52321         G    ACCCC
                                AGGCAGGAG TGGAA    AGG
                                ||||||||| |||||    |||
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                                TCCGTCCTC ACCTT    TCC
                                      _    CCA__
GAM629  FLJ14525  3'  CCTGCCTCCACCTTCTGCCT  52481          AACCC
                                AGGCAGGAGGTGGA    CAGG
                                ||||||||||||||    ||||
                                TCCGTCTTCCACCT    GTCC
                                      CC___
GAM629  FLJ20048  3'  CCCCAGGGCCCCACCCCCATCC 34899       A    AAA_________  CCAG
          CCTGCCT                AGGCAGG GGTGG         CC   GG
                                |||||||  |||||         ||   ||
                                TCCGTCC CTACC         GG   CC
                                   C    CCCACCCC___  GACC
GAM629  FLJ20294  3'  CCGTTCTTCCACCTCCTCCT  35350    C        ACCCCA
                                AGG AGGAGGTGGAA     GG
                                |||  ||||||||||     ||
                                TCC TCCTCCACCTT     CC
                                  _         CTTG__
GAM629  FLJ20477  5'  CCAGGGCCTTTCCAGCCTCCCG 35707    A    _   A_____  CCAG
          CC                    GGC GGAGGT GGAA     CC   G
                                |||  ||||||  ||||     ||   |
                                CCG CCTCCG CCTT     GG   C
                                  C     A   TCC___  GACC
GAM629  FLJ20507  5'  CCCTGGGGCCTGCTGACTGCC  35734      GA  TG AAA
                                GGCAG  GG  G   CCCCAGGG
                                |||||  ||  |   ||||||||
                                CCGTC  TC  C   GGGGTCCC
                                   AG  GT C__
GAM629  FLJ20507  5'  CCCTGGGGCCTGCTGACTGCC  60841      GA  TG AAA
                                GGCAG  GG  G   CCCCAGGG
                                |||||  ||  |   ||||||||
                                CCGTC  TC  C   GGGGTCCC
                                   AG  GT C__
GAM629  FLJ20699  3'  CCAGGGAGGCCCCCACCTGCTG 35989       G     AAA_______  CCAG
          CCT                   AGGCAG AGGTGG        CC   G
                                ||||||  ||||||        ||   |
                                TCCGTC TCCACC        GG   C
                                   G     CCCGGA___  GACC
GAM629  FLJ21478  3'  GGAAGCTTCCCCTCCTGCCT  45197          T   AC_______
                                AGGCAGGAGG GGAA       C
                                ||||||||||  ||||       |
                                TCCGTCCTCC CCTT       G
                                      _    CGAA___G
GAM629  FLJ22408  3'  CCCTGCCTTCGACCTCCTGCCT 45984          G   ACCC
                                AGGCAGGAGGT GAA    CAGGG
                                ||||||||||| |||    |||||
                                TCCGTCCTCCA CTT    GTCCC
                                      G   CC__
GAM629  FLJ22551  5'  CCGGGATCGCCACCTCCTGCCT 45560           AAAC   A
                                AGGCAGGAGGTGG    CCC GG
                                ||||||||||||    ||| ||
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                                TCCGTCCTCCACC   GGG CC
                                      GCTA  _
GAM629  FLJ22582  3' CCCTGGGGGGCCCACCTCTTGC 47455          AAA
           C                   GGCAGGAGGTGG  CCCCAGGG
                               ||||||||||||  ||||||||
                               CCGTTCTCCACC  GGGGTCCC
                                     CGG
GAM629  FLJ22644  3' CCCAGGCCTCCACCTCCAGCC  47698    A      AA  CCA
                               GGC GGAGGTGGA  CC  GGG
                               ||| |||||||||  ||  |||
                               CCG CCTCCACCT  GG  CCC
                                 A       CC  A__
GAM629  FLJ22671  3' CCCAGGCATCCCCACCTCCTAC 46310    C       AAACC  A
           CT                   AGG AGGAGGTGG    CC GGG
                               ||| |||||||||    || |||
                               TCC TCCTCCACC    GG CCC
                                 A       CCTAC  A
GAM629  FLJ23306  3' CCCCAGGGTATGGCTCCTGCT  44847       G  GAA   CA
                               GGCAGGAG TG   ACCC  GGG
                               ||||||| ||   ||||  |||
                               TCGTCCTC GT   TGGG  CCC
                                    G  A__   AC
GAM629  FLJ23322  3' CCCAGTTGCACCCCCTGACT   90214   G   A   GA   CCCA
                               AG CAGG GGTG  AAC   GGG
                               || |||| ||||  |||   |||
                               TC GTCC CCAC  TTG   CCC
                                A   C   G_  A___
GAM629  FLJ23519  3' CCCTGGGGCCCACCAGCCCCTG 69721       A___    AAA
           CC                   GGCAGGG   GGTGG  CCCCAGGG
                               ||||||   |||||  ||||||||
                               CCGTCC   CCACC  GGGGTCCC
                                  CCGA    C__
GAM629  FLJ32771  3' CCCAGGGGAACACCCCTGCC   59442       A   GAAA   A
                               GGCAGG GGTG   CCCC GGG
                               |||||| ||||   |||| |||
                               CCGTCC CCAC   GGGG CCC
                                  _   AA__   A
GAM629  FLJ32919  5' CCCTGGAGTCTCCACCTTTTCC 58697    C       A  C
           T                    AGG AGGAGGTGGA AC CCAGGG
                               ||| |||||||||| || ||||||
                               TCC TTTTCCACCT TG GGTCCC
                                 _       C  A
GAM629  FUK     3' CCAGGGGAACCTCCACCTCCTA 59625    C       AA_______  CCAG
           CT                   GG AGGAGGTGGA      CC   G
                               || ||||||||||      ||   |
                               TC TCCTCCACCT      GG   C
                                A       CCAAG___  GACC
GAM629  FUK     3' CCCATGGGAACCTCCACCTCCT 59626    C       AAC_   _
           ACT                   GG AGGAGGTGGA   CCCA GGG
                               || ||||||||||   |||| |||
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                                TC TCCTCCACCT    GGGT CCC
                                 A         CCAA    A
GAM629  GABARAPL3 5'  CCCTCCCACCCCACCTTCTGCC 51780            AAACCCC
                                GGCAGGAGGTGG       AGGG
                                ||||||||||||       ||||
                                CCGTCTTCCACC       TCCC
                                       CCACCC_
GAM629  HEYL     3'  GCCCTGGGAAGATTCTCCCACC 28129     C        AAAC_____      ___
           TCCTCCCT                  AGG AGGAGGTGG        CCCAGGG   C
                                ||| |||||||||        |||||||   |
                                TCC TCCTCCACC        GGGTCCC   G
                                  C        CTCTTAGAA      ___
GAM629  HSPC023  3'  CCCCAGGGCCAACATCCCACCC 26757     C   A     AAA_________  CCAG
           CCTACCT                   AGG AGG GGTGG         CC    GG
                                ||| ||| |||||         ||    ||
                                TCC TCC CCACC         GG    CC
                                  A   C     CTACAACC___  GACC
GAM629  HU-K4    3'  CCCTGCTCTCCCACCTCTACCT 25360     CA       AAACCC
                                AGG  GGAGGTGG      CAGGG
                                |||  |||||||||      |||||
                                TCC  TCTCCACC      GTCCC
                                  A_       CTCTC_
GAM629  HYPC     3'  CCTGAGGCTCCACCACTT    65217     A     AA  C
                                AGG GGTGGA  CC CAGG
                                ||| ||||||  || ||||
                                TTC CCACCT  GG GTCC
                                  A     C_  A
GAM629  KCNT1    3'  CCCTGTGCCACCTCCTGCCT   62489            AAACCC
                                AGGCAGGAGGTGG      CAGGG
                                ||||||||||||||     |||||
                                TCCGTCCTCCACC      GTCCC
                                       GT_____
GAM629  KIAA0290 3'  CCCTGGGGCCTCCCACCCCAGC 66715      A  A     AAA_
           CT                      AGGC GG GGTGG    CCCCAGGG
                                |||| || |||||    ||||||||
                                TCCG CC CCACC    GGGGTCCC
                                  A  _     CTCC
GAM629  KIAA0450 5'  CCAGCTACTTCCACCTCTGCC  28344       G       ACCCCA
                                GGCAG AGGTGGAA      GG
                                ||||| ||||||||      ||
                                CCGTC TCCACCTT      CC
                                   _        CATCGA
GAM629  KIAA0475 3'  GGGAATTTCCACCTCTGCCT   30120       G       A_______
                                AGGCAG AGGTGGAA       CC
                                ||||||| ||||||||      ||
                                TCCGTC TCCACCTT       GG
                                   _        TAAG___
GAM629  KIAA0544 3'  CCCTGGGGCCCGACTCCTGCT  71462         G   AAA
                                GGCAGGAG TGG   CCCCAGGG
                                |||||||| |||   ||||||||
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                                TCGTCCTC GCC   GGGGTCCC
                                    A   C__
GAM629  KIAA0700 3' CCCTGGGGCTCAGCCCCACC  72516    CA  A   G  AA
                                GG  GG GGT GA  CCCCAGGG
                                ||  || ||| ||  ||||||||
                                CC  CC CCG CT  GGGGTCCC
                                 A_  _   A  C_
GAM629  KIAA0821 5' CCCTCGTCCCGCCACCTCCTAC 30604    C       AAACCCC
            C                    GG AGGAGGTGG      AGGG
                                || |||||||||      ||||
                                CC TCCTCCACC      TCCC
                                 A       GCCCTGC
GAM629  KIAA1075 5' CCCTGGGGCCAGCACCCCAGCC 62385     A  A   GAAA
                                GGC GG GGTG   CCCCAGGG
                                ||| || ||||   ||||||||
                                CCG CC CCAC   GGGGTCCC
                                  A  _   GACC
GAM629  KIAA1100 3' CCCTGGCTCCCACCTCCCGCC  30440     A      AAACC
                                GGC GGAGGTGG    CCAGGG
                                ||| ||||||||    ||||||
                                CCG CCTCCACC    GGTCCC
                                  C       CTC__
GAM629  KIAA1266 3' GGCCCCTCCACCTCCTCCCT   66700     C       AA_____
                                AGG AGGAGGTGGA      CC
                                ||| ||||||||||      ||
                                TCC TCCTCCACCT      GG
                                  C        CCCC___
GAM629  KIAA1655 5' CCCCAGGGCTCCAACTCCTCCT 67178      _    ___   AA   CA
            TGCCT                 AGGCA GGAGG   TGGA  CCC  GGG
                                ||||| |||||   ||||  |||  |||
                                TCCGT CCTCC   ACCT  GGG  CCC
                                   T    TCA    C_   AC
GAM629  KIAA1691 3' CCCTGGGGCCAGGCTCTGCC  94127       AGG   AAA
                                GGCAGG   TGG   CCCCAGGG
                                ||||||   |||   ||||||||
                                CCGTCT   ACC   GGGGTCCC
                                   CGG   ___
GAM629  KIAA1691 3' CCTGGGGCCAGCTCTGCC    94129      G  G   AAA
                                GGCAG AG TGG   CCCCAGG
                                ||||| || |||   |||||||
                                CCGTC TC ACC   GGGGTCC
                                  _ G   ___
GAM629  KIAA1867 3' CCAGGGCCCCACCCACCTCCTG 96481           AAA_______  CCAG
            CTT                   AGGCAGGAGGTGG       CC    G
                                ||||||||||||       ||   |
                                TTCGTCCTCCACC       GG    C
                                      CACCCC___  GACC
GAM629  KIAA1938 3' CCCAATCTCCTTCCACCTCCCT 93819    CA       ACCCCA_
            CC                    GG  GGAGGTGGAA      GGG
                                ||  ||||||||||      |||
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                                CC  CCTCCACCTT      CCC
                                 TC        CCTCTAA
GAM629  KIF13B   3'  GGCCTCCACCTCCTGGCT    83718    G        AA
                                AG CAGGAGGTGGA  CC
                                || ||||||||||  ||
                                TC GTCCTCCACCT  GG
                                 G         CC
GAM629  KIF13B   3'  GGCCTCCACCTCCTGGCT    31568    G        AA
                                AG CAGGAGGTGGA  CC
                                || ||||||||||  ||
                                TC GTCCTCCACCT  GG
                                 G         CC
GAM629  KNSL6    3'  CCTGGGGTTGTCCTGGCT    23380    G    GGTGGA
                                AG CAGGA     AACCCCAGG
                                || |||||     |||||||||
                                TC GTCCT     TTGGGGTCC
                                 G    G_____
GAM629  KPTN     3'  CCCTGGGGCCCCAGCTAACCC  73804    CAGG  G   AAA
                                GG   AG TGG   CCCCAGGG
                                ||   || |||   ||||||||
                                CC   TC ACC   GGGGTCCC
                                 CAA_  G   CC_
GAM629  LENEP    3'  CCTTCATTCCCAACCCCTGCCT 38478        A  __    ACCCC
                                AGGCAGG GGT  GGAA    AGG
                                ||||||| |||  ||||    |||
                                TCCGTCC CCA  CCTT    TCC
                                    _  AC    ACT__
GAM629  LHPP     3'  CCCCACCTCCTCCACCCCTGCC 42360        A     AACCCCA
           T                     AGGCAGG GGTGGA      GGG
                                ||||||| ||||||      |||
                                TCCGTCC CCACCT      CCC
                                    _     CCTCCAC
GAM629  LHPP     3'  CCCGCCTCCTCCACCCCTGCCT 42361        A     AACCCCA
                                AGGCAGG GGTGGA      GGG
                                ||||||| ||||||      |||
                                TCCGTCC CCACCT      CCC
                                    _     CCTCCG_
GAM629  LHPP     3'  CCCTGCCTCTCCTCCACCCCTG 42363        A     AACCC__
            CCT                   AGGCAGG GGTGGA      CAGGG
                                ||||||| ||||||      |||||
                                TCCGTCC CCACCT      GTCCC
                                    _     CCTCTCC
GAM629  LHPP     3'  CCCTGCCTCTCCTCCACCCCTG 42364        A     AACCC__
            CCT                   AGGCAGG GGTGGA      CAGGG
                                ||||||| ||||||      |||||
                                TCCGTCC CCACCT      GTCCC
                                    _     CCTCTCC
GAM629  LHPP     3'  GGCCCCTCCACCCCTGCCT   42367        A     AA_____
                                AGGCAGG GGTGGA      CC
                                ||||||| ||||||      ||
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                                TCCGTCC CCACCT      GG
                                   _     CCCC___
GAM629  LSFR2    3'  CCTGGGGGGCCTGCTGCCT   61186       G   GGAAA
                                AGGCAG AGGT    CCCCAGG
                                ||||||| ||||    |||||||
                                TCCGTC TCCG    GGGGTCC
                                   G   G____
GAM629  LYPLA3   3'  GCCCTGGGACATCTCACTCCAC 25562     C    _____  _ AAC      ___
           TCCTACCT                AGG AGGAG   GTG GA   CCCAGGG   C
                                ||| |||||   ||| ||   |||||||  |
                                TCC TCCTC   CAC CT   GGGTCCC   G
                                  A    ACCT   T  ACA     ___
GAM629  MFN2     5'  CCAGGGCCACTTCCCTCCTCCC 30223      A    T_   AC_______ CCAG
           GCCT                   AGGC GGAGG  GGAA       C   G
                                |||| |||||  ||||       |   |
                                TCCG CCTCC  CCTT       G   C
                                  C    TC   CACC___G GACC
GAM629  MGC11115 3'  CCCCAGGGCTCCATCTCCGCCT 51204      A       AA   CA
                                AGGC GGAGGTGGA  CCC  GGG
                                |||| |||||||||  |||  |||
                                TCCG CCTCTACCT  GGG  CCC
                                  _       C_   AC
GAM629  MGC12217 3'  CCTTTCCCACCTCCTTCC    52287    C       A  CCCC
                                GG AGGAGGTGG AA    AGG
                                || |||||||| ||    |||
                                CC TCCTCCACC TT    TCC
                                 T       C  _____
GAM629  MGC14376 3'  CCTACTTCCACCTCCGCC    52914     A        ACCCC
                                GGC GGAGGTGGAA     AGG
                                ||| ||||||||||     |||
                                CCG CCTCCACCTT     TCC
                                  _        CA___
GAM629  MGC16025 5'  CCCTGGGGTGGGTCTCCTTGCC 53022      _    TGGAA
                                GGCA GGAGG     ACCCCAGGG
                                |||| |||||    |||||||||
                                CCGT CCTCT     TGGGGTCCC
                                  T    GGG__
GAM629  MGC2941  3'  CCCTGAAGGAGTCCCTCCTGCT 44414         T  AAA  C_
                                GGCAGGAGG GG   CC  CAGGG
                                |||||||| ||   ||  |||||
                                TCGTCCTCC CT   GG  GTCCC
                                     _ GA_  AA
GAM629  MGC3329  3'  CCCATACCCCCACCTCCAGCCT 44242      A       AAACCCCA
                                AGGC GGAGGTGG       GGG
                                |||| ||||||||       |||
                                TCCG CCTCCACC       CCC
                                  A       CCCATA__
GAM629  MGC34869 5'  CCTGGGGCGGGCTCCTGCC    58714         GTGGAAA
                                GGCAGGAG      CCCCAGG
                                ||||||||      |||||||
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                                CCGTCCTC      GGGGTCC
                                    GGGC___
GAM629  MGC35521  3'  CCTGGGGCCCCCTGCTGCT   59665      G  T  AAA
                                GGCAG AGG GG   CCCCAGG
                                ||||| ||| ||   |||||||
                                TCGTC TCC CC   GGGGTCC
                                  G   _  C__
GAM629  MGC4701   5'  CCCTGGGGCTTGCCGCTGCCT  65161      GA  TG AAA
                                AGGCAG  GG  G   CCCCAGGG
                                ||||||  ||  |   ||||||||
                                TCCGTC  CC  T   GGGGTCCC
                                   G_  GT C__
GAM629  MGC4796   3'  CCTGAGGCCCCTCCTGCCT   62162        T  AAA  C
                                AGGCAGGAGG GG   CC CAGG
                                |||||||||| ||   || ||||
                                TCCGTCCTCC CC   GG GTCC
                                      _  ___  A
GAM629  MKNK1     3'  CCCTGAGGTTCCCATCAACCCC 14876    CA  A_    A    C
                                GG  GG  GGTGG AACC CAGGG
                                ||  ||  ||||| |||| |||||
                                CC  CC  CTACC TTGG GTCCC
                                 __ AA    C    A
GAM629  N4BP3     3'  CCCGCACCCACCTCCTGTCT   66847          AAACCCCA
                                AGGCAGGAGGTGG       GGG
                                ||||||||||||        |||
                                TCTGTCCTCCACC       CCC
                                      CACG_____
GAM629  N4BP3     3'  CCCTAAAACCCACACCTGCCT  66848       AG    AAACCCC
                                AGGCAGG  GTGG      AGGG
                                |||||||  ||||      ||||
                                TCCGTCC  CACC      TCCC
                                   A_    CAAAA__
GAM629  N4BP3     3'  CCCTTCTTGGCCCCACCCTCTA 66849    C  GA    AAA  CC__
              CC                  GG AG  GGTGG   CC    AGGG
                                || ||  |||||   ||    ||||
                                CC TC  CCACC   GG    TCCC
                                 A  TC    CC_  TTCT
GAM629  NESCA     3'  CCCTGGGACCCTTTCCTGC    27518        T  AAAC
                                GCAGGAGG GG    CCCAGGG
                                ||||||| ||    |||||||
                                CGTCCTTT CC    GGGTCCC
                                    C  A___
GAM629  NIR3      3'  CCCCACGCCCCCACCACCTGCCT 66824        A    AAACCCCA
                                AGGCAGG GGTGG       GGG
                                ||||||| |||||       |||
                                TCCGTCC CCACC       CCC
                                   A    CCGCAC__
GAM629  NLI-IF    3'  CCTGCCCCACCTCCTCCCT    41343     C       AAACCC
                                AGG AGGAGGTGG     CAGG
                                ||| |||||||||     ||||
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                                TCC TCCTCCACC     GTCC
                                  C       CC____
GAM629  NPEPL1   3'  CCCCGGGGTGAGGCCTCCTGCC 45421          GGAA    A
                T                  AGGCAGGAGGT   ACCCC GGG
                                   ||||||||||    ||||| |||
                                   TCCGTCCTCCG   TGGGG CCC
                                         GAG_    C
GAM629  P114-RHO-GEF 5'  CCCCGGGGCACCCTCCTGTC  31668         _ GAAA   A
                                   GGCAGGAGG TG   CCCC GGG
                                   |||||||||  ||   |||| |||
                                   CTGTCCTCC AC   GGGG CCC
                                         C  ____   C
GAM629  PARVB    3'  CCTGCCCCACCCCCTGCCT   26190       A    AAACCC
                                   AGGCAGG GGTGG     CAGG
                                   |||||||  |||||     ||||
                                   TCCGTCC CCACC     GTCC
                                      C    CC____
GAM629  PFDN1    3'  CCCTGGAGTTTTTACCCGGCT  12047     AGGA       C
                                   GGC   GGTGGAAAC CCAGGG
                                   |||   |||||||||  ||||||
                                   TCG   CCATTTTTG GGTCCC
                                     GC__       A
GAM629  PLAGL2   3'  CCTGTGCCCCCACCCCCGCCT  70957     A  A    AAACCC
                                   AGGC GG GGTGG     CAGG
                                   ||||  ||  |||||     ||||
                                   TCCG CC CCACC     GTCC
                                     C  _    CCCGT_
GAM629  PLAGL2   3'  CCTTGCCCCCACCTCCTGTCT  70958          AAACCC
                                   AGGCAGGAGGTGG     CAGGG
                                   ||||||||||||      |||||
                                   TCTGTCCTCCACC     GTTCC
                                         CCC___
GAM629  PPP1R16B 3'  CCTGCCTCCACCTCCCACC   62036    CA       AACCC
                                   GG  GGAGGTGGA     CAGG
                                   ||  |||||||||     ||||
                                   CC  CCTCCACCT     GTCC
                                    AC       CC___
GAM629  PTD008   3'  CCCTAGGCTTACCCCTCCTGCC 32865         T  A  C  C
                T                  AGGCAGGAGG GG AA CC AGGG
                                   ||||||||||  ||  ||  ||  ||||
                                   TCCGTCCTCC CC TT GG TCCC
                                         _  A  C  A
GAM629  PYY      5'  CCCTCGCCTTCCACCTCCTGCT 16039           ACCCC
                                   GGCAGGAGGTGGAA    AGGG
                                   ||||||||||||||    ||||
                                   TCGTCCTCCACCTT    TCCC
                                         CCGC_
GAM629  RAB40C   3'  CCCTGGGGTCCCCACAGCTGC  41277     GAG    AA
                                   GCAG   GTGG  ACCCCAGGG
                                   ||||   ||||  |||||||||
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                                CGTC   CACC  TGGGGTCCC
                                  GA_    CC
GAM629  RASSF2   3'  CCTGGGCACCCTCCTGCC    29095         _  GAAAC
                                GGCAGGAGG TG    CCCAGG
                                ||||||||| ||    ||||||
                                CCGTCCTCC AC    GGGTCC
                                    C  _____
GAM629  SEMA4B   5'  CCCTGTTTCCCACCTCCCGCC  69596     A      _   CCC
                                GGC GGAGGTGG AAAC   AGGG
                                ||| |||||||| ||||   ||||
                                CCG CCTCCACC TTTG   TCCC
                                  C       C   ___
GAM629  SFXN5    3'  CCCCGGGGTCTCCACCTC    58648        A    A
                                GAGGTGGA ACCCC GGG
                                |||||||| ||||| |||
                                CTCCACCT TGGGG CCC
                                    C    C
GAM629  SLC38A5  3'  CCTAGGGTCCCTCCTGCC    54308         T GAA    C
                                GGCAGGAGG G   ACCC AGG
                                ||||||||| |   |||| |||
                                CCGTCCTCC C   TGGG TCC
                                    _ ___    A
GAM629  SSI-1    3'  CCTGAACTCGCACCTCCTACCT 14984     C       _  AACCC
                                AGG AGGAGGTG GA    CAGG
                                ||| |||||||| ||    ||||
                                TCC TCCTCCAC CT    GTCC
                                  A       G  CAA__
GAM629  STX5A    3'  CCCTGATCCCCCACCCCTTGCC 13471        A    AAACCC
           T                     AGGCAGG GGTGG     CAGGG
                                |||||||| |||||     |||||
                                TCCGTTC CCACC     GTCCC
                                   C    CCCTA_
GAM629  SYT12    3'  CCCAGGGTCTGCTCCTGCT   96377       G TG  AA   CA
                                GGCAGGA G  GA  CCC  GG
                                ||||||| |  ||  |||  ||
                                TCGTCCT C  CT  GGG  CC
                                   _ GT  __   AC
GAM629  TNRC4    3'  CCTCCCACCCCCCTGCCT    24192        A_    AAACCCC
                                AGGCAGG  GGTGG      AGG
                                |||||||  |||||      |||
                                TCCGTCC  CCACC      TCC
                                   CC    C_______
GAM629  TOMM40   3'  CCCTTCCGATTCCACCTCCACC 21483     CA        ACCCC
           T                     AGG  GGAGGTGGAA    AGGG
                                |||  ||||||||||    ||||
                                TCC  CCTCCACCTT    TCCC
                                  A_         AGCCT
GAM629  TPRA40   3'  CCCTGGGGCTCCCAATCCCCT  33486    CA   GG   AAA
                                AGG  GGA  TGG   CCCCAGGG
                                |||  |||  |||   ||||||||
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                                TCC  CCT  ACC   GGGGTCCC
                                  __   A_   CTC
GAM629  TUBB4    3'  CCCTAGGGCTCCCTTGCCGCCC 71148     C   A_   ___   AA   C
            TCCT                   AGG AGG  GGT   GGA  CCC AGGG
                                |||  |||  |||   |||  |||  ||||
                                TCC TCC  CCG   CCT  GGG TCCC
                                  _   CG   TTC   C_   A
GAM629  TUBB5    3'  CCTGAGCCCCAGCTCCTACCT  21412     C    G   AAACCC
                                AGG AGGAG TGG     CAGG
                                |||  |||||  |||     ||||
                                TCC TCCTC ACC     GTCC
                                  A    G   CCGA__
GAM629  U5-116KD 3'  CCCCAGGGAAGCCGCCTGCCT  16183       A   GGAAA   CA
                                AGGCAGG GGT    CCC  GGG
                                |||||||  |||    |||  |||
                                TCCGTCC CCG    GGG  CCC
                                    G   AA___   AC
GAM629  URKL1    3'  CCCCACCACCCTCCTCCTGCCT 35793         T  AAACCCCA
                                AGGCAGGAGG GG       GGG
                                ||||||||||  ||       |||
                                TCCGTCCTCC CC       CCC
                                      T  CACCAC__
GAM629  WBSCR23  3'  GGCACCTCCACCTCCAGCCT   47436      A       AA_____
                                AGGC GGAGGTGGA      CC
                                ||||  |||||||||      ||
                                TCCG CCTCCACCT      GG
                                  A        CCAC___
GAM629  ZNF212   3'  CCAGGGCCTCTTCCCACCTCCT 25317     C       AAA________  CCAG
            CCT                    AGG AGGAGGTGG        CC    G
                                |||  |||||||||        ||    |
                                TCC TCCTCCACC        GG    C
                                  _       CTTCTCC___  GACC
GAM629  LOC112817 5'  CCCTGGGGCCTATAGGCCTTGC 57322      _  AG_    AAA
            C                     GGCA GG   GTGG   CCCCAGGG
                                ||||  ||   ||||   ||||||||
                                CCGT CC   TATC   GGGGTCCC
                                  T  GGA    C__
GAM629  LOC115574 3'  CCTGCTCTTCACCTCCCACCT  73851     CA       AACCC
                                AGG  GGAGGTGGA     CAGG
                                |||  |||||||||     ||||
                                TCC  CCTCCACTT     GTCC
                                  AC        CTC__
GAM629  LOC118738 3'  CCCTGAAGCTATACCTGCTACC 76002     C  G    GAAACCC
            T                     AGG AG AGGTG       CAGGG
                                |||  ||  |||||       |||||
                                TCC TC TCCAT       GTCCC
                                  A  G     ATCGAA_
GAM629  LOC121642 5'  CCTAGGGTCCCTTCCGGCT    74562     A    T   AA   C
                                GGC GGAGG GGA  CCC AGG
                                |||  |||||  |||  |||  |||
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                                TCG CCTTC CCT  GGG TCC
                                  G    _  __   A
GAM629  LOC123242 3'  CCCTGAGGCCCGGAGCCATGCC 76113      _ AGG   AAA  C
              T                    AGGCA GG   TGG   CC CAGGG
                                   ||||| ||   |||   || |||||
                                   TCCGT CC   GCC   GG GTCCC
                                     A  GAG   C__  A
GAM629  LOC124402 3'  CCCCAGGGCCCTGCCTCCTCCC 59829    C     TG AAA   CA
                                   GG AGGAGG  G   CCC  GGG
                                   || ||||||  |   |||  |||
                                   CC TCCTCC  C   GGG  CCC
                                    C     GT CC_   AC
GAM629  LOC124842 3'  CTCAGGACTCCCACCTCTGCC  76158      G     AAAC  CA
                                   GGCAG AGGTGG    CC  GG
                                   ||||| ||||||    ||  ||
                                   CCGTC TCCACC    GG  TC
                                     _     CTCA  AC
GAM629  LOC125268 3'  CCTGCCCCACTCCTGCC     76574         G   AAACCC
                                   GGCAGGAG TGG     CAGG
                                   |||||||| |||     ||||
                                   CCGTCCTC ACC     GTCC
                                       _   CC____
GAM629  LOC128402 3'  CCCTGGGGTGACCCCCCAGCCT 76286      A  A  T  AA
                                   AGGC GG GG GG  ACCCCAGGG
                                   |||| || || ||  |||||||||
                                   TCCG CC CC CC  TGGGGTCCC
                                     A  _  _  AG
GAM629  LOC130644 3'  CCCTGAGGCTTTTCTTCTCCTG 76250         T    C  _
              CC                     GGCAGGAGG GGAAA CC CAGGG
                                   ||||||||| ||||| || |||||
                                   CCGTCCTCT CTTTT GG GTCCC
                                        T    C  A
GAM629  LOC132112 3'  CCCCAGGGCCCATCCTCCAACT 75533     C    G    AA_________  CCAG
              CCTACCT                  AGG AGGAG TGGA         CC    GG
                                   ||| ||||| ||||         ||    ||
                                   TCC TCCTC ACCT         GG    CC
                                     A    A   CCTACCC___  GACC
GAM629  LOC144195 3'  CCTCCTTCCACCTCCCTCC    60985    CA        ACCCC
                                   GG  GGAGGTGGAA    AGG
                                   ||  ||||||||||    |||
                                   CC  CCTCCACCTT    TCC
                                    TC         CC___
GAM629  LOC144202 5'  CCCTGAGGCCCCAGAACTATCT 77225    GC  GA__  T  AAA  C
                                   AG  AG    GG GG   CC CAGGG
                                   ||  ||    || ||   || |||||
                                   TC  TC    CC CC   GG GTCCC
                                    TA  AAGA  _  ___  A
GAM629  LOC144231 5'  CCCTATCTTTTCTCCCACCTCC 83937     C        AAACCCC___
              TTCCT                    AGG AGGAGGTGG         AGGG
                                   ||| |||||||||         ||||
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                                TCC TCCTCCACC         TCCC
                                  T       CTCTTTTCTA
GAM629  LOC144248 5'  CCAGGGCAACCTCCACCTCCTG 77250    G        AA_______  CCAG
                GCT                   AG CAGGAGGTGGA       CC    G
                                ||  ||||||||||       ||    |
                                TC GTCCTCCACCT       GG    C
                                 G         CCAAC___  GACC
GAM629  LOC144473 3'  CCTTATTTCCACCCCCCACC   83993    CA  A      CCCC
                                GG  GG GGTGGAAA    AGG
                                ||  ||  ||||||||    |||
                                CC  CC CCACCTTT    TCC
                                 AC  C       AT__
GAM629  LOC145468 3'  CCCTTCCGATTCCACCTCCACC 74251     CA        ACCCC
                T                  AGG  GGAGGTGGAA    AGGG
                                |||  ||||||||||     ||||
                                TCC  CCTCCACCTT    TCCC
                                  A_         AGCCT
GAM629  LOC146381 5'  CCCTGGGGCCTCAGGCCTCC   78429       G_  AA
                                GGAGGT  GA  CCCCAGGG
                                ||||||  ||  ||||||||
                                CCTCCG  CT  GGGGTCCC
                                    GA  CC
GAM629  LOC146452 3'  CCCTGGGGCAGGACCCCAGCCT 78471      A  A   GGAAA
                                AGGC GG GGT     CCCCAGGG
                                ||||  ||  |||     ||||||||
                                TCCG CC CCA     GGGGTCCC
                                  A  _   GGAC_
GAM629  LOC146488 3'  CCCTGCCACGCCCACCCCCTGC 71356       A     AAACCC
                C                  GGCAGG GGTGG      CAGGG
                                ||||||  |||||      |||||
                                CCGTCC CCACC      GTCCC
                                    C     CGCACC
GAM629  LOC147343 5'  CCCTGGGGCTCCCACACTCTGC 85124       AG    AAA
                                GCAGG  GTGG   CCCCAGGG
                                |||||  ||||   ||||||||
                                CGTCT  CACC   GGGGTCCC
                                   CA    CTC
GAM629  LOC148014 3'  GCCCTGAGTCATTCTTTCCACC 79310     _  A       CCC_____     ___
                CCCTGGCC                GGC AGG GGTGGAAA       CAGGG   C
                                |||  |||  ||||||||       |||||   |
                                CCG TCC CCACCTTT       GTCCC   G
                                  G   C       CTTACTGA    ___
GAM629  LOC148479 5'  CCCTGCAGCCACTCTCCCGCCT 79610      A   _   AAACCC
                                AGGC GGAG GTGG      CAGGG
                                ||||  ||||  ||||      |||||
                                TCCG CCTC CACC      GTCCC
                                  C    T    GAC___
GAM629  LOC149483 3'  CCTGCCCCCACCTCCTGCT    80185           AAACCC
                                GGCAGGAGGTGG      CAGG
                                ||||||||||||      ||||
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                                TCGTCCTCCACC     GTCC
                                      CCC___
GAM629  LOC150155 3'  CCCTTCCGATTCCACCTCCGCC 71409     A        ACCCC
            T                  AGGC GGAGGTGGAA    AGGG
                               |||| ||||||||||    ||||
                               TCCG CCTCCACCTT    TCCC
                                 _        AGCCT
GAM629  LOC151996 5'  CCTGGAGCTCCTCCTGC    86717        T  AAACC
                               GCAGGAGG GG    CCAGG
                               |||||||| ||    |||||
                               CGTCCTCC TC    GGTCC
                                    _ GA___
GAM629  LOC152189 5'  CCAGGGCCCCTCGCACCTCCTG 81327          _  AA_____  CCAG
            CC                   GGCAGGAGGTG GA     CC   G
                               |||||||||| ||      ||   |
                               CCGTCCTCCAC CT      GG   C
                                      G  CCCC___  GACC
GAM629  LOC153243 5'  CCTGCCTCCACTCCTGCCT   81661        G   AACCC
                               AGGCAGGAG TGGA    CAGG
                               ||||||||| ||||    ||||
                               TCCGTCCTC ACCT    GTCC
                                    _   CC___
GAM629  LOC153565 5'  CCCAAGGCCCCCGCCGCCT   81756     A  A  T  AAAC  CA
                               AGGC GG GG GG   CC  GGG
                               |||| || || ||   ||  |||
                               TCCG CC CC CC   GG  CCC
                                 _  G  _  C___  AA
GAM629  LOC155036 5'  CCCTGGGGACTTCACCTGCTGC 87612      G      AA
            C                   GGCAG AGGTGGA  CCCCAGGG
                               ||||| |||||||  ||||||||
                               CCGTC TCCACTT  GGGGTCCC
                                  G      CA
GAM629  LOC155434 3'  CCTCTCCCTCCACCTCCTGGCT 87690    G         AACCCC
                               AG CAGGAGGTGGA     AGG
                               || ||||||||||      |||
                               TC GTCCTCCACCT     TCC
                                G         CCCTC_
GAM629  LOC157349 5'  CCCCGGGGTTCCTGAACGCCT  82332     AGGAGGT   A   A
                               AGGC      GGAA CCCC GGG
                               ||||      |||| |||| |||
                               TCCG      CCTT GGGG CCC
                                 CAAGT__   _   C
GAM629  LOC157349 3'  CCTGCGCCCCTCCTGCCT    82337         T  AAACCC
                               AGGCAGGAGG GG     CAGG
                               |||||||||| ||     ||||
                               TCCGTCCTCC CC     GTCC
                                     _ GC_____
GAM629  LOC157737 3'  CCCTGGAACCTGGATCTCCTGG 87844    G      GGAAACC
            CT                   AG CAGGAGGT      CCAGGG
                               || ||||||||      ||||||
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                                TC GTCCTCTA      GGTCCC
                                 G       GGTCCAA
GAM629  LOC158056 5'  CCCCGGAGCTTCCACCTTCTCA 82587    C         ACC  A
                                G AGGAGGTGGAA   CC GGG
                                | ||||||||||   || |||
                                A TCTTCCACCTT   GG CCC
                                 C          CGA  C
GAM629  LOC158230 3'  CCCTGGGAGGCCCAACCTCCTG 82699          _  AAAC
           CC                     GGCAGGAGGT GG    CCCAGGG
                                ||||||||| ||    |||||||
                                CCGTCCTCCA CC    GGGTCCC
                                      A  CGGA
GAM629  LOC158230 3'  GGCCTTTCCACCTCCCTCCT   82702     CA        A_____
                                AGG  GGAGGTGGAA     CC
                                |||  ||||||||||      ||
                                TCC  CCTCCACCTT     GG
                                  TC         TCC___
GAM629  LOC158490 3'  CCTGGAGCACCTCCTGGCC    82821     _       GAAACC
                                GGC AGGAGGTG      CCAGG
                                ||| ||||||||      |||||
                                CCG TCCTCCAC      GGTCC
                                  G       GA____
GAM629  LOC158825 5'  CCCAGGGCCGGCCACCTCCCAG 82880     A_       AAAC   A
           CC                     GGC  GGAGGTGG    CCC GGG
                                |||  ||||||||    ||| |||
                                CCG  CCTCCACC    GGG CCC
                                  AC       GGCC   A
GAM629  LOC158828 3'  CCCGGAGCCATTCCTCCCT    82896     C    G   AAACC  A
                                AGG AGGAG TGG     CC GG
                                ||| ||||| |||     || ||
                                TCC TCCTT ACC     GG CC
                                  C    _   GA___  C
GAM629  LOC164118 3'  CCCCAGGGCCCACCCCCACCCG 83045        A_     AAA________  CCAG
           CCTGCCT                 AGGCAGG  GGTGG        CC    GG
                                |||||||  |||||        ||    ||
                                TCCGTCC  CCACC        GG    CC
                                    GC     CCCACCC___  GACC
GAM629  LOC164375 5'  CCCTGGAGTCGTCTCCGGCC   88556     A   GT  AAACC
                                GGC GGAG  GG     CCAGGG
                                ||| ||||  ||     ||||||
                                CCG CCTC  CT     GGTCCC
                                  G    TG  GA___
GAM629  LOC197083 3'  CCAGGCCCCCACCTGCTACCT  89224     C  G     AAACC  A
                                AGG AG AGGTGG     CC GG
                                ||| || ||||||     || ||
                                TCC TC TCCACC     GG CC
                                  A  G     CCC__  A
GAM629  LOC197439 5'  CCCTGGGGCCTCAGGCCTCC   89461       G_  AA
                                GGAGGT  GA  CCCCAGGG
                                ||||||  ||  ||||||||
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                                CCTCCG  CT  GGGGTCCC
                                   GA  CC
GAM629  LOC199232 5'  CCCTGGGGCCTCCCCAGTCTCC 90412     C   A_  T   AA
                CT                  AGG AGG  GG GGA  CCCCAGGG
                                    ||| |||  || |||  ||||||||
                                    TCC TCT  CC CCT  GGGGTCCC
                                      C   GA  _   CC
GAM629  LOC199678 3'  CCCTCCACCCCACCCTCCACCT 91365     CA    _   AAACCCC
                                    AGG  GGAGG TGG      AGGG
                                    |||  ||||| |||      ||||
                                    TCC  CCTCC ACC      TCCC
                                      A_    C   CCACC__
GAM629  LOC199923 5'  CCTTCTCCACCTCCTGCC    89869            AACCCC
                                    GGCAGGAGGTGGA     AGG
                                    ||||||||||||      |||
                                    CCGTCCTCCACCT     TCC
                                           CT____
GAM629  LOC199927 3'  CCCTGGGGCTCCCAGCCTTC   91478       __   AA
                                    GGAGGT  GGA  CCCCAGGG
                                    ||||||  |||  ||||||||
                                    CTTCCG  CCT  GGGGTCCC
                                       AC   C_
GAM629  LOC199986 5'  CCCTAGAAGGTAACCACCTCCT 91507    G        AA   CC__
                CT                    AG CAGGAGGTGG  ACC    AGGG
                                    || ||||||||||  |||    ||||
                                    TC GTCCTCCACC  TGG    TCCC
                                      G         AA   AAGA
GAM629  LOC200093 3'  CCCTGTTCCCCACCTCCCGGCT 63766     A_      AAACCC
                                    GGC  GGAGGTGG     CAGGG
                                    |||  ||||||||     |||||
                                    TCG  CCTCCACC     GTCCC
                                      GC       CCTT__
GAM629  LOC200213 5'  CCCCGGGCCGGCCAGCCTCCTG 90029          _   AAAC   A
                CCT                   AGGCAGGAGG TGG    CCC GGG
                                    |||||||||| |||    ||| |||
                                    TCCGTCCTCC ACC    GGG CCC
                                          G   GGCC   C
GAM629  LOC200812 5'  CCCTGACTCCCACCTCCCC    90302    CA      AAACCC
                                    GG  GGAGGTGG     CAGGG
                                    ||  ||||||||     |||||
                                    CC  CCTCCACC     GTCCC
                                      __       CTCA__
GAM629  LOC201252 3'  CCCTGGGGCCCTGGCCTTCTGC 89551           __  AAA
                CT                    AGGCAGGAGGT  GG   CCCCAGGG
                                    ||||||||||  ||   ||||||||
                                    TCCGTCTTCCG  CC   GGGGTCCC
                                           GT  C__
GAM629  LOC201707 5'  CCGGGAGGCTCCCATCTCCCGC 90474     A       AAA  _  A
                C                     GGC GGAGGTGG   CC CC GG
                                    ||| ||||||||   || || ||
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                                CCG CCTCTACC   GG GG CC
                                  C       CTC  A  G
GAM629   LOC204275 5'  CCCTGAGGCCCCAGAACTATCT 91005    GC  GA__  T  AAA  C
                                AG  AG    GG GG   CC CAGGG
                                ||  ||    || ||   || |||||
                                TC  TC    CC CC   GG GTCCC
                                 TA  AAGA  _  ___  A
GAM629   LOC204804 3'  CCCTGGGGCTTGGCTCCAGCCT 91039      A    G   AAA
                                AGGC GGAG TGG   CCCCAGGG
                                |||| |||| |||   ||||||||
                                TCCG CCTC GTT   GGGGTCCC
                                  A   G   C__
GAM629   LOC205948 5'  CCCTGGAGCTCCCCGTTTCCCT 91086      A__   GG   AAACC_
           CGCCT                  AGGC   GGA  TGG     CCAGGG
                                ||||   |||  |||     ||||||
                                TCCG   CCT  GCC     GGTCCC
                                  CTC   TT   CCTCGA
GAM629   LOC206389 5'  CCCTGGGGCCCCCACCAGCC   92402     AGGA    AAA
                                GGC    GGTGG   CCCCAGGG
                                |||    |||||   ||||||||
                                CCG    CCACC   GGGGTCCC
                                  A___     CCC
GAM629   LOC220739 3'  CCCTGGGGTCTGGCTCACTGCC 94518        _   G    AA
           T                    AGGCAG GAG TGGA  CCCCAGGG
                                ||||||  ||| ||||  ||||||||
                                TCCGTC CTC GTCT  GGGGTCCC
                                   A   G   __
GAM629   LOC221418 5'  CCCTGGGGCTCCCTCCTAGCC  95285     _     TG AAA
                                GGC AGGAGG  G   CCCCAGGG
                                ||| ||||||  |   ||||||||
                                CCG TCCTCC  C   GGGGTCCC
                                  A     CT ___
GAM629   LOC221491 5'  CCCCAACACCCCCACCTCCGGC 93656      A       AAACCCCA
           CT                     AGGC GGAGGTGG       GGG
                                ||||  ||||||||       |||
                                TCCG CCTCCACC       CCC
                                  G       CCCACAAC
GAM629   LOC222133 5'  CCCTGGGGCCCTGGCCTCC    95760       __  AAA
                                GGAGGT  GG   CCCCAGGG
                                ||||||  ||   ||||||||
                                CCTCCG  CC   GGGGTCCC
                                   GT  C__
GAM629   LOC253001 3'  CCCTGAGGCCCGGAGCCATGCC 97992      _  AGG   AAA  C
           T                     AGGCA GG   TGG   CC CAGGG
                                |||||  ||   |||   || |||||
                                TCCGT CC   GCC   GG GTCCC
                                   A  GAG   C__  A
GAM629   LOC253216 3'  CCCTGAGACCCAGCCACTGCCT 96629       GA  _   AAACCC
                                AGGCAG  GG TGG     CAGGG
                                ||||||  || |||     |||||
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                                TCCGTC  CC ACC     GTCCC
                                   A_  G   CAGA__
GAM629  LOC253992 3'  CCCTAAGACTCCATCTCTTCTC 98422       ____      AACCCC
           TGCCT                   AGGCAG   GAGGTGGA     AGGG
                                |||||||  ||||||||     ||||
                                TCCGTC   CTCTACCT     TCCC
                                   TCTT       CAGAA_
GAM629  LOC254295 3'  CCCTAAGATCTTCACCTCTCTG 97889       _      AACCCC
           CCT                    AGGCAG GAGGTGGA     AGGG
                                |||||| ||||||||     ||||
                                TCCGTC CTCCACTT     TCCC
                                   T       CTAGAA
GAM629  LOC254428 3'  CCCTCCTCCACCCCACACTCCC 97193     CA   _   AAACCCC_
           ACCT                    AGG  GGAG GTGG       AGGG
                                |||  |||| ||||       ||||
                                TCC  CCTC CACC       TCCC
                                  AC    A    CCACCTCC
GAM629  LOC255102 3'  CCCTGACTCCCACCTCCACACC 97801    CA_      AAACCC
                                GG   GGAGGTGG     CAGGG
                                ||   ||||||||     |||||
                                CC   CCTCCACC     GTCCC
                                 ACA       CTCA__
GAM629  LOC255736 3'  CCTTGTGCTCCCCACCCCCTAC 97073     C   A     AAACCC
           CT                     AGG AGG GGTGG     CAGGG
                                ||| ||| |||||     |||||
                                TCC TCC CCACC     GTTCC
                                  A   C     CCTCGT
GAM629  LOC256974 3'  CCCTGGGACCCCGGGTCCTTCC 99056     C    GG   AAAC
           T                      AGG AGGA  TGG    CCCAGGG
                                ||| ||||  |||   |||||||
                                TCC TCCT  GCC    GGGTCCC
                                  T   GG   CCA_
GAM629  LOC257106 3'  CCCCAGGGCCAGCTCCCCACCC 97126       GA     AAA_________  CCAG
           TCTGCCT                  AGGCAG  GGTGG         CC    GG
                                ||||||  |||||         ||    ||
                                TCCGTC  CCACC         GG    CC
                                   TC     CCTCGACC___  GACC
GAM629  LOC257438 3'  CCCCAAAACTTTCACCTCCCTC 95592    CA        ACCCCA
           C                       GG  GGAGGTGGAA     GGG
                                ||  ||||||||||     |||
                                CC  CCTCCACTTT     CCC
                                 TC         CAAAAC
GAM629  LOC51308  3'  CCCTGGGGTCCATCCCCTCTTG 33963         T   A__
           CC                      GGCAGGAGG GGA   ACCCCAGGG
                                |||||||||  |||   |||||||||
                                CCGTTCTCC CCT   TGGGGTCCC
                                      _   ACC
GAM629  LOC56930  5'  CCCTGGGGCTCGGCCTCCTCC  62742    C      G  AA
                                GG AGGAGGT GA  CCCCAGGG
                                || |||||| ||  ||||||||
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                                CC TCCTCCG CT  GGGGTCCC
                                 _      G  C_
GAM629  LOC56961  5' CCCTTCCTCTCCACCTCCTCCT 63576     C        AACCCC
                                AGG AGGAGGTGGA      AGGG
                                ||| ||||||||||      ||||
                                TCC TCCTCCACCT      TCCC
                                  _         CTCCT_
GAM629  LOC58512  3' CCCCAGGGCTTTGTCCCCACCT 65282     C        AAA_________  CCAG
          CCTCCC                  GG AGGAGGTGG          CC    GG
                                || |||||||||          ||    ||
                                CC TCCTCCACC          GG    CC
                                 C        CCTGTTTC___  GACC
GAM629  LOC90133  5' CCTGCTGCCTCCACTCCTGCCT 62290          G    AACCC
                                AGGCAGGAG TGGA     CAGG
                                ||||||||| ||||     ||||
                                TCCGTCCTC ACCT     GTCC
                                      _    CCGTC
GAM629  LOC90230  3' CCTGGGGTCTCTGCTGC     62526      G   T GAA
                                GCAG AGG G   ACCCCAGG
                                |||| ||| |   ||||||||
                                CGTC TCT C   TGGGGTCC
                                  G   _ ___
GAM629  LOC90678  3' CCCGGGGCCCTCCTGCT     57202          TGGAAA    A
                                GGCAGGAGG     CCCC GG
                                |||||||||     |||| ||
                                TCGTCCTCC     GGGG CC
                                     C_____    C
GAM629  LOC90784  5' CCTCCCCACCTCCTGCC     64694           AAACCCC
                                GGCAGGAGGTGG       AGG
                                ||||||||||||       |||
                                CCGTCCTCCACC       TCC
                                       CC_____
GAM629  LOC91040  3' CCCTGTTCCCCACCTCCCGGCT 65341     A_       AAACCC
                                GGC  GGAGGTGG      CAGGG
                                |||  ||||||||      |||||
                                TCG  CCTCCACC      GTCCC
                                  GC       CCTT__
GAM629  LOC91156  5' CCCTGGGGTTCTGGGCCCTCC  65707       ___     A
                                GGAGG   TGGAA CCCCAGGG
                                |||||   ||||| ||||||||
                                CCTCC   GTCTT GGGGTCCC
                                   CGG    _
GAM629  LOC91695  3' GGCCTTCCCACCTCTTGCCT   67511           AAA_____
                                AGGCAGGAGGTGG       CC
                                ||||||||||||       ||
                                TCCGTTCTCCACC       GG
                                       CTTCC___
GAM629  LOC91948  3' CCTGAGGACACCTCTACCT    68234     CA      GAAA  C
                                AGG  GGAGGTG    CC CAGG
                                |||  |||||||    || ||||
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                                TCC  TCTCCAC    GG GTCC
                                  A_      A___  A
GAM629  LOC92080  3'  CCCCAGGCCCACCTCCTGGCC  68624     _       AAAC  CA
                                GGC AGGAGGTGG    CC  GGG
                                ||| |||||||||    ||  |||
                                CCG TCCTCCACC    GG  CCC
                                  G        C___  AC
GAM629  LOC92080  3'  CCTCTTCCCTCCACCTCCTCCC 68627    C        AACCCC
                                GG AGGAGGTGGA      AGG
                                || ||||||||||      |||
                                CC TCCTCCACCT      TCC
                                 C         CCCTTC
GAM629  LOC92340  3'  CCCCGGAGCCGCCTCCTGC    69557           AAACC  A
                                GCAGGAGGTGG     CC GGG
                                ||||||||||     || |||
                                CGTCCTCCGCC     GG CCC
                                       GA___  C
GAM629  LOC92697  5'  CCAGGGCAACCTCCACCTCCCA 70807     A_       AA_______  CCAG
            GCT                   GGC  GGAGGTGGA       CC    G
                                |||  |||||||||       ||    |
                                TCG  CCTCCACCT       GG    C
                                  AC        CCAAC___  GACC
GAM629  LOC96597  3'  CCCTGGGGCCTCTGACCCCACC 67453     CA  A   _   AA
            T                    AGG  GG GGT GGA  CCCCAGGG
                                |||  || ||| |||  ||||||||
                                TCC  CC CCA TCT  GGGGTCCC
                                  A_  _   G   CC
GAM629  LOC96652  3'  CCCTGGGGCTGGCCCTGCC    66076       AG  GGAAA
                                GGCAGG  GT     CCCCAGGG
                                ||||||  ||     ||||||||
                                CCGTCC  CG     GGGGTCCC
                                   __  GTC__
GAM630  ADAR     3'  AACACCAAAGCATCCCAAGGAA 32354     G    _   TTT
                                TT CTTGG ATG   CTTTGGTGTT
                                || ||||| |||   ||||||||||
                                AA GAACC TAC   GAAACCACAA
                                 G    C   ___
GAM630  CAST     3'  AACACCAAAAAAACAAAAGAAA 10017      GGA___     C
            AGC                   GCTT      TGTTT TTTGGTGTT
                                ||||      ||||| |||||||||
                                CGAA      ACAAA AAACCACAA
                                  AAGAAA     A
GAM630  CSDA     3'  AACACCAAAGAAACATCCAAGC 14685
            AA                    TTGCTTGGATGTTTCTTTGGTGTT
                                |||||||||||||||||||||||||
                                AACGAACCTACAAAGAAACCACAA

GAM630  MECP2    3'  AACACCAAAAAAATCCAG     18379        GTTTC
                                TTGGAT     TTTGGTGTT
                                ||||||     |||||||||
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                                GACCTA    AAACCACAA
                                   AAA__
GAM630  PTP4A2   3'  ACACCAAAAAAACAGCAG    14435      TGGAT   C
                                TTGCT    GTTT TTTGGTGT
                                |||||    |||| ||||||||
                                GACGA    CAAA AAACCACA
                                   _____   A
GAM630  FLJ20152 3'  AACACCAAAAAAATTTCAAACA 39164    C    T   C
           A                     TTG TTGGA GTTT TTTGGTGTT
                                 ||| ||||| |||| |||||||||
                                 AAC AACTT TAAA AAACCACAA
                                   A    _   A
GAM630  TRAF3    3'  AACACCAAAAAAACACACACAC 13846    CT  GA    C
           A                     TG  TG  TGTTT TTTGGTGTT
                                 ||  ||  ||||| |||||||||
                                 AC  AC  ACAAA AAACCACAA
                                   AC  AC    A
GAM630  TRAF3    5'  AACACCAAAAAAACACACACAC 13847    CT  GA    C
           A                     TG  TG  TGTTT TTTGGTGTT
                                 ||  ||  ||||| |||||||||
                                 AC  AC  ACAAA AAACCACAA
                                   AC  AC    A
GAM630  LOC166793 5' ACCTTTTAAACACCCAAGCAA  59916        A    CTTT
                                 TTGCTTGG TGTTT    GGT
                                 |||||||| |||||    |||
                                 AACGAACC ACAAA    CCA
                                      C    TTTT
GAM630  LOC220558 3'  AACACCAAAGAAACATCCAAGC 92769
           AA                      TTGCTTGGATGTTTCTTTGGTGTT
                                   ||||||||||||||||||||||||
                                   AACGAACCTACAAAGAAACCACAA

GAM630  LOC221178 3'  CAAAAAACATTCAAACAA    95165    C        C
                                 TTG TTGGATGTTT TTTG
                                 ||| |||||||||| ||||
                                 AAC AACTTACAAA AAAC
                                   A        _
GAM631  CORO2A   3'  CCAAACCACAAGTCCCCTC    14101    TTA
                                 GAG   ACTTGTGGTTTGG
                                 |||   |||||||||||||
                                 CTC   TGAACACCAAACC
                                   CCC
GAM631  CORO2A   3'  CCAAACCACAAGTCCCCTC    54493    TTA
                                 GAG   ACTTGTGGTTTGG
                                 |||   |||||||||||||
                                 CTC   TGAACACCAAACC
                                   CCC
GAM631  MAT2A    3'  GCCAAACCTCACCAACTC    20969      AACT  T
                                 GAGTT    TG GGTTTGGC
                                 |||||    || ||||||||
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                                CTCAA    AC CCAAACCG
                                   CC__  T
GAM631  PPBP     3'  GCCAAACTTCTTTAACTC    12220        CTTGT
                                GAGTTAA    GGTTTGGC
                                |||||||    ||||||||
                                CTCAATT    TCAAACCG
                                    TCT__
GAM631  OAZ2     3'  GCCAAACTCTAATTAATTCT   11878        C   T
                                AGAGTTAA TTG GGTTTGGC
                                |||||||| ||| ||||||||
                                TCTTAATT AAT TCAAACCG
                                      _  C
GAM631  LOC113523 3'  CCAAAATGTGGTGAACTCTTAA 73417         A   TGTGG
                                TTAAGAGTT ACT    TTTGG
                                ||||||||| |||    |||||
                                AATTCTCAA TGG    AAACC
                                      G  TGTA_
GAM631  LOC201164 3'  GCCAGCTTGGAAGTTAACTTTT 89497           G   T
            AA                    TTAAGAGTTAACTT TGG TTGGC
                                |||||||||||||| ||| |||||
                                AATTTTCAATTGAA GTT GACCG
                                        G  C
GAM631  LOC92539  5'  GCCATATGAAATAAACTCTTAA 70221         AACT___
                                TTAAGAGTT      TGTGGT
                                |||||||||      ||||||
                                AATTCTCAA      ATACCG
                                      ATAAAGT
GAM632  DUT      3'  CCACCCAGTTTGTGGAAGCAC  10461           A   AGA
                                GTGCTTTCACAAA TGG   GTGG
                                |||||||||||| |||   ||||
                                CACGAAGGTGTTT ACC   CACC
                                        G  ___
GAM632  KIF3C    3'  CCACTCTCCACTTTCTGAGC   11204     TCAC   A
                                GCTT    AAA TGGAGAGTGG
                                ||||    ||| ||||||||||
                                CGAG    TTT ACCTCTCACC
                                  TC__   C
GAM632  PCSK2    3'  ACATCTCTGAAAGCAC      11997         CAAAATG   _
                                GTGCTTTCA      GAGA GT
                                |||||||||      |||| ||
                                CACGAAAGT      CTCT CA
                                      _______   A
GAM632  RECK     3'  CTTTCCATTCGTGAAAACAC   41198     C     AA
                                GTG TTTCAC  AATGGAGAG
                                ||| ||||||  |||||||||
                                CAC AAAGTG  TTACCTTTC
                                  A     C_
GAM632  SLC6A12  3'  CCACCCTCCATTCTCAGCG   13190     TTCACAA      A
                                TGCT      AATGGAG GTGG
                                ||||      ||||||| ||||
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                                GCGA      TTACCTC CACC
                                  CTC_____      C
GAM632  SYNGR3   3'  CCACTCTCCACTTTCTCTCAC  16116    CTTTCAC   A
                                GTG      AAA TGGAGAGTGG
                                |||      ||| ||||||||||
                                CAC      TTT ACCTCTCACC
                                  TCTC___   C
GAM632  SYT4     3'  CCACTCGGCATCTCTGTGAAAG 63108         AA_   GA
            CA                    TGCTTTCACA   ATG  GAGTGG
                                |||||||||   |||  ||||||
                                ACGAAAGTGT   TAC  CTCACC
                                      CTC   GG
GAM632  DKFZP761D0211 5'  CCACCTGGGCTTGCGAAGGCAC 50177        A   AATGG  A
                                GTGCTTTC CAA     AG GTGG
                                |||||||| |||     || ||||
                                CACGGAAG GTT     TC CACC
                                     C   CGGG_ _
GAM632  KIAA1671  3'  CTGCATTTGTGAAAGCAC    66280           A  G
                                GTGCTTTCACAAA TG AG
                                |||||||||||| || ||
                                CACGAAAGTGTTT AC TC
                                       _ G
GAM632  MPHOSPH10 5'  CACCCTCCTGCGAAAGCGC    62923        A  AAAT    A
                                GTGCTTTC CA    GGAG GTG
                                |||||||| ||    |||| |||
                                CGCGAAAG GT    CCTC CAC
                                     C _____    C
GAM632  ZFP95    3'  CACTTCTCTGTGAAACAC    59681     C      AAATG   _
                                GTG TTTCACA    GAGA GTG
                                ||| |||||||    |||| |||
                                CAC AAAGTGT    CTCT CAC
                                  _      ______    T
GAM632  ZFP95    3'  CACTTCTCTGTGAAACAC    28119     C      AAATG   _
                                GTG TTTCACA    GAGA GTG
                                ||| |||||||    |||| |||
                                CAC AAAGTGT    CTCT CAC
                                  _      ______    T
GAM632  LOC144289 5'  CCACTTCTCCCTGTGAAAGC   83955         AAAT    _
                                GCTTTCACA    GGAGA GTGG
                                |||||||||    ||||| ||||
                                CGAAAGTGT    CCTCT CACC
                                     C___     T
GAM632  LOC144755 3'  CCACTCTCCATCCTCTGCCGCG 84099      TTT  CAAA
            C                     GTGC   CA    ATGGAGAGTGG
                                ||||   ||   ||||||||||
                                CGCG   GT    TACCTCTCACC
                                  CC_  CTCC
GAM632  LOC254381 5'  CCAACTCCACCCTAAGAAAGCA 99325         ACAAAA     AG
            C                     GTGCTTTC     TGGAG  TGG
                                ||||||||     |||||  |||
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                                CACGAAAG     ACCTC  ACC
                                     AATCCC     A_
GAM632  LOC93380  3'  CCACATCTTTTGTAAAAGCC   72651   T    C    AT   GA
                                G GCTTT ACAAA  GGA  GTGG
                                | ||||| |||||  |||  ||||
                                C CGAAA TGTTT  TCT  CACC
                                 _    A    __   A_
GAM633  APRT     3'  CACACAGCGGGAGAACGCAGT  6664          ACA  A
                                ACTGCGTTCTC   CT GTGTG
                                ||||||||||   || |||||
                                TGACGCAAGAG   GA CACAC
                                      GGC  _
GAM633  CD3Z     3'  GCACAAAGTGGCATAAAAAACA 7423       CG  CTCA__   AG
           GTG                    CACTG  TT     CACT  TGTGC
                                |||||  ||     ||||  |||||
                                GTGAC  AA     GTGA  ACACG
                                   AA  AATACG    A_
GAM633  GCG      5'  GCACACTACCAGAAGACAGCA  10773     _  TC  ACAC
                                TGC GT  TC    TAGTGTGC
                                ||| ||  ||    ||||||||
                                ACG CA  AG    ATCACACG
                                  A  GA  ACC_
GAM633  MECP2    3'  ACACTTATCCACGAGAGCGCAG 18381          ACACT__
                                CTGCGTTCTC      AGTGT
                                ||||||||||      |||||
                                GACGCGAGAG      TCACA
                                      CACCTAT
GAM633  WHSC1    3'  CACACTGGAGAAAAGGCAGT   24653      G  C  ACA
                                ACTGC TT TC   CTAGTGTG
                                |||||  || ||   ||||||||
                                TGACG AA AG   GGTCACAC
                                   G  A  A__
GAM633  DKFZP564O0423 3'  GCCAGATGTGAGAACGAG    93353    G       _  A
                                CT CGTTCTCACA CT GT
                                || |||||||||| || ||
                                GA GCAAGAGTGT GA CG
                                 _        A  C
GAM633  FLJ12572  3'  GCACACTATCGTGTACACAG   43543     C  TCT   AC
                                CTG GT   CAC  TAGTGTGC
                                |||  ||   |||  ||||||||
                                GAC CA   GTG  ATCACACG
                                  A  T__   CT
GAM633  KIAA0590  3'  GCTGGGCGAGAACGCAG     28864          ACA
                                CTGCGTTCTC   CTAGT
                                ||||||||||   |||||
                                GACGCAAGAG   GGTCG
                                      CG_
GAM633  KIAA0976  3'  GCACAGATCTGGTGAGAACACA 30550     C       ACTAG_
           G                     CTG GTTCTCAC      TGTGC
                                |||  ||||||||      |||||
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                                GAC CAAGAGTG     ACACG
                                  A       GTCTAG
GAM633  LOC127180 3'  GCACACTTTGTGAGAACCAATG 75131    C  C       CT
                                CA TG GTTCTCACA  AGTGTGC
                                || || |||||||||  |||||||
                                GT AC CAAGAGTGT  TCACACG
                                 A  _       T_
GAM633  LOC146957 3'  ACACGGAGAAGCAGTG      78811       G    ACACTA
                                CACTGC TTCTC     GTGT
                                ||||||| |||||     ||||
                                GTGACG AAGAG     CACA
                                   _    G_____
GAM633  LOC152200 3'  GCACACCAGTGTGTTAGGCACT 86754    C   G  CT     A
          G                      CA TGC TT  CACACT GTGTGC
                                || ||| ||  |||||| ||||||
                                GT ACG GA  GTGTGA CACACG
                                 C  _ TT     C
GAM633  LOC152573 3'  GCATGCTAGGAAAACACAG   81496     C   C  ACA
                                CTG GTT TC   CTAGTGTGC
                                ||| ||| ||   |||||||||
                                GAC CAA AG   GATCGTACG
                                  A  A  ___
GAM633  LOC91408  3'  GCACTGGTAAAACACAGT    66517      C   CTCAC
                                ACTG GTT     ACTAGTGT
                                |||| |||     ||||||||
                                TGAC CAA     TGGTCACG
                                  A  AA___
GAM634  BLMH      3'  ACTGAAGCCAAAGTTATGCAA  6360        _    _
                                TTGTG GACTT GGCTTCAGT
                                ||||| ||||| |||||||||
                                AACGT TTGAA CCGAAGTCA
                                   A    A
GAM634  SHANK2    3'  ACTGAGTTGTGTCCACAACATG 25521     __      T    T
                                CAT  TGTGGAC TGGCT CAGT
                                |||  ||||||| ||||| ||||
                                GTA  ACACCTG GTTGA GTCA
                                  CA      T    _
GAM634  LOC154421 3'  ACTGGATCAACCCACAATG    87418        AC   C
                                CATTGTGG  TTGG TTCAGT
                                ||||||||  |||| ||||||
                                GTAACACC  AACT AGGTCA
                                    C_   _
GAM635  ADCY1     5'  ACGACAATGTGAGCATC     94336          AG
                                GATGCTCACAT  GTTGT
                                ||||||||||  |||||
                                CTACGAGTGTA  CAGCA
                                      A_
GAM635  C8orf1    3'  ATAGCATGATGTGAGCATC   16343          AG_
                                GATGCTCACAT   GTTGT
                                ||||||||||   |||||
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                                CTACGAGTGTA   CGATA
                                      GTA
GAM635  CDH12    3'  ATAGCTATGTGGCATCA     15776       T      G
                                TGATGC CACATAG TTGT
                                |||||| ||||||| ||||
                                ACTACG GTGTATC GATA
                                  _      _
GAM635  HIP1     3'  ACAAACTTGTGAGCATCA     19242          T  G
                                TGATGCTCACA AG TTGT
                                |||||||||||| || ||||
                                ACTACGAGTGT TC AACA
                                      _ A
GAM635  DKFZp547I224 5'  ATGGCCTATGTGAGATCA     39948      G         TG
                                TGAT CTCACATAGGT  T
                                |||| ||||||||||  |
                                ACTA GAGTGTATCCG  A
                                  _         GT
GAM635  DKFZp761P1010 3'  GGCACAAATAAGCTCA      37943     T   CACA  GG
                                TGA GCT    TA  TTGTGCC
                                ||| |||    ||  |||||||
                                ACT CGA    AT  AACACGG
                                  _  _____  A_
GAM635  FLJ13114  3'  ACAGGCCAGGTGAGCATCA    44889          ATA   _
                                TGATGCTCAC   GGT TGT
                                ||||||||||   ||| |||
                                ACTACGAGTG   CCG ACA
                                      GA_   G
GAM635  FLJ23024  3'  TGGCACAACCTCAGCTCA     46851     T   CACAT
                                TGA GCT     AGGTTGTGCCA
                                ||| |||     ||||||||||||
                                ACT CGA     TCCAACACGGT
                                  _   C_____
GAM635  HNK-1ST   5'  ACAGCAAGGAAATGTGAGCCCC 17946     AT       AG_____
            A                    TG  GCTCACAT      GTTGT
                                ||  ||||||||      |||||
                                AC  CGAGTGTA      CGACA
                                 CC        AAGGAA
GAM635  KIAA0459  3'  ACAATCATGTGAGCTCA     61639     T      A
                                TGA GCTCACAT GGTTGT
                                ||| |||||||| ||||||
                                ACT CGAGTGTA CTAACA
                                  _       _
GAM635  KIAA1466  3'  ATAACCTATGAAACATCA     72405      CTCA
                                TGATG    CATAGGTTGT
                                |||||    ||||||||||
                                ACTAC    GTATCCAATA
                                   AAA_
GAM635  KIAA1954  5'  ACAGCTTACTGAGCATCA     78220         CA
                                TGATGCTCA  TAGGTTGT
                                |||||||||  ||||||||
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                                ACTACGAGT  ATTCGACA
                                     C_
GAM635  PACSIN2  3'  ATGGCACAGATTGATGCGCACC 24296    A   T  _  TAGG
            A                    TG TGC CA CA    TTGTGCCAT
                                 || ||| || ||    |||||||||
                                 AC ACG GT GT    GACACGGTA
                                  C   C  A  TA__
GAM635  PARVA    3'  GGCCCATGTGAGCATCA     37183          A  TTGT
                                 TGATGCTCACAT GG    GCC
                                 ||||||||||||| ||    |||
                                 ACTACGAGTGTA CC    CGG
                                          _  _____
GAM635  RoXaN    3'  GCACACATGTGAGCACA     47292    A       AGGT
                                 TG TGCTCACAT    TGTGC
                                 || |||||||||    |||||
                                 AC ACGAGTGTA    ACACG
                                  _       C___
GAM635  LOC148638 3'  ATGGCCATGTGAGCACA     79665    A       A   TG
                                 TG TGCTCACAT GGT  T
                                 || ||||||||| |||  |
                                 AC ACGAGTGTA CCG  A
                                  _       _  GT
GAM635  LOC148696 5'  GGCCAGCATTGAGCATCA     85348         CATAG    T
                                 TGATGCTCA    GTTG GCC
                                 |||||||||    |||| |||
                                 ACTACGAGT    CGAC CGG
                                       TA___   _
GAM635  LOC200609 5'  ATAACACTGTGCAATCATCA   91658      CTCA    _
                                 TGATG    CATAG GTTGT
                                 |||||    ||||| |||||
                                 ACTAC    GTGTC CAATA
                                    TAAC     A
GAM635  LOC203235 3'  ATGACACAACCTGAGAGGCACC 92097    A    CACA       C
            A                    TG TGCT    TAGGTTGTG CAT
                                 || ||||    ||||||||| |||
                                 AC ACGG    GTCCAACAC GTA
                                  C    AGA_       A
GAM635  LOC219667 3'  GCCAGCCTATGCAACATCA    92948      CTCA       T
                                 TGATG    CATAGGTTG GC
                                 |||||    ||||||||| ||
                                 ACTAC    GTATCCGAC CG
                                    AAC_       _
GAM635  LOC220514 3'  ATGGCACAGATTGATGCGCACC 61072    A   T  _  TAGG
            A                    TG TGC CA CA    TTGTGCCAT
                                 || ||| || ||    |||||||||
                                 AC ACG GT GT    GACACGGTA
                                  C   C  A  TA__
GAM635  LOC221463 3'  GGCATGGCACGTGAGCAGCA   93706    A      ATAG  TG
                                 TG TGCTCAC    GT  TGCC
                                 || |||||||    ||  ||||
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                                AC ACGAGTG   CG  ACGG
                                 G      CA__  GT
GAM636  ASL     3'  GTTTGACACAGCCTGGGCAACA 72396     GA   A       C
                                TGT  CCCA GCTGTGTC AAT
                                |||  |||| |||||||| |||
                                ACA  GGGT CGACACAG TTG
                                  AC   C       T
GAM636  DHFR    3'  GACCAGCTTGGGCAACA     7647      GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM636  MMP19   3'  GACCAGCTTGGGCAACA     11630     GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM636  MMP19   3'  GACCAGCTTGGGCAACA     43304     GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM636  NR1I2   5'  AGATCAAAGTGGTGGGGTCACA 15294         AA  TG GTCCA
                                TGTGACCC  GC  T    ATCT
                                ||||||||  ||  |    ||||
                                ACACTGGG  TG  G    TAGA
                                     G_  GT AAAC_
GAM636  PRKY    3'  GACCAGCTTGGGCAACA     12375     GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM636  RAD54B  3'  AGATTGTCAGCTTGGTCCACA  57062      AC       TGTC
                                TGTG  CCAAGCTG    CAATCT
                                ||||  ||||||||    ||||||
                                ACAC  GGTTCGAC    GTTAGA
                                  CT       T___
GAM636  RCE1    3'  GATTTAACTTGGGTAACA     18890     G      C  T
                                TGT ACCCAAG TG GTC
                                ||| ||||||| || |||
                                ACA TGGGTTC AT TAG
                                  A      A  T
GAM636  SFRS2IP 5'  GACCAGCTTGGGCAACA     17540     GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM636  TEM7    3'  GACCAGCTTGGGCAACA     40259     GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
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                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM636  FLJ13263  3'  AGATTGCTCCTTCAGCTCAGGG 47809     A  A_    TGTC__
            CCACA                  TGTG CCC  AGCTG     CAATCT
                                |||| |||  |||||     ||||||
                                ACAC GGG  TCGAC     GTTAGA
                                  C   AC    TTCCTC
GAM636  FLJ14327  3'  GACCAGCTTGGGCAACA     46679     GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM636  KIAA0172  3'  GACTGCTAGCCTGGGCACA   65596     A   A  _ _
                                TGTG CCCA GCT GT GTC
                                |||| |||| ||| || |||
                                ACAC GGGT CGA CG CAG
                                  _   C   T  T
GAM636  KIAA1833  3'  GGACCACAGCCTGGGCACA   90753     A   A    _
                                TGTG CCCA GCTGTG TCC
                                |||| |||| ||||||| |||
                                ACAC GGGT CGACAC AGG
                                  _   C     C
GAM636  KIAA1870  3'  GACCAGCTTGGGCAACA     52901     GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM636  MEGF11    3'  ATTGGACAAATGTGGATACA   51599     AC   AGCTG
                                TGTG  CCA    TGTCCAAT
                                ||||  |||    ||||||||
                                ACAT  GGT    ACAGGTTA
                                  A_   GTAA_
GAM636  MGC15631  3'  GACCAGCCTGGGTGACA     52230     G    A   T
                                TGT ACCCA GCTG GTC
                                ||| ||||| |||| |||
                                ACA TGGGT CGAC CAG
                                  G    C   _
GAM636  MGC32043  3'  GACCAGGTCTTGGGCACA    58665     A     __  T
                                TGTG CCCAAG  CTG GTC
                                |||| ||||||  ||| |||
                                ACAC GGGTTC  GAC CAG
                                  _     TG  _
GAM636  PLP1      3'  ATTGGACATTAAGCATCACA   6755      CCCAA  __
                                TGTGA    GCT  GTGTCCAAT
                                |||||    |||  |||||||||
                                ACACT    CGA  TACAGGTTA
                                   A_____   AT
GAM636  PTD012    3'  GACCAGCTTGGGCAACA     26738     GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
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                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM636  STAF42   3'  ATTGAATGTTTTTTGGGTCCA  54942    T      CT TG C
                                TG GACCCAAG  G  T CAAT
                                || ||||||||  |  | ||||
                                AC CTGGGTTT  T  A GTTA
                                 _       TT GT A
GAM636  TRIM31   3'  ACGCCAGCCTGGGTCACA    92649         A   _
                                TGTGACCCA GCTG TGT
                                ||||||||| |||| |||
                                ACACTGGGT CGAC GCA
                                      C   C
GAM636  LOC142893 5'  ATTGGAACATTTTTGGGTCCA  83757    T      CT   _
                                TG GACCCAAG  GTGT CCAAT
                                || ||||||||  |||| |||||
                                AC CTGGGTTT  TACA GGTTA
                                 _       T_   A
GAM636  LOC143503 5'  AGACTGGACAAAGGGGGTCACA 83882         AAGCTG     A
                                TGTGACCC     TGTCCA TCT
                                ||||||||     |||||| |||
                                ACACTGGG     ACAGGT AGA
                                     GGAA__     C
GAM636  LOC145824 5'  GACTTGCAGCTTGGATACACA  77986      AC_       __
                                TGTG   CCAAGCTGT  GTC
                                ||||   |||||||||  |||
                                ACAC   GGTTCGACG  CAG
                                  ATA        TT
GAM636  LOC157603 3'  GACCAGCTTGGGCAACA     87786     GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM636  LOC221300 3'  GACCAGCTTGGGTAACA     93576     G        T
                                TGT ACCCAAGCTG GTC
                                ||| |||||||||| |||
                                ACA TGGGTTCGAC CAG
                                  A        _
GAM636  LOC257608 3'  ACGCCAGCCTGGGTCACA    99664         A   _
                                TGTGACCCA GCTG TGT
                                ||||||||| |||| |||
                                ACACTGGGT CGAC GCA
                                      C   C
GAM636  LOC51337  3'  GACCAGAGCATCCTGGGTACA  34081      A   A___   G  _
                                TGTG CCCA    GCT TG TC
                                |||| ||||    ||| || ||
                                ACAT GGGT    CGA AC AG
                                  _    CCTA   G  C
GAM637  DLEC1    3'  CATCTGGCCCTCCCTTG     24716       A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
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                                GTTCC TCCCG TC TAC
                                  C    G  _
GAM637  DLEC1    3'  CATCTGGCCCTCCCTTG    24728      A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                  C    G  _
GAM637  PIP5K1A  3'  TATCCCACCCTGCCTTGATA  14520       A   CA  C
                                TATCAAGG AGGG  GG GTG
                                |||||||| ||||  || |||
                                ATAGTTCC TCCC  CC TAT
                                    G   A_  C
GAM637  SOX11    3'  ACCCACCCCCCCCTTGGTA    13308       AA   CA  C
                                TATCAAGG  GGG  GG GT
                                ||||||||  |||  || ||
                                ATGGTTCC  CCC  CC CA
                                    CC   A_  _
GAM637  CHL1     3'  TGTTACCTTTCCTCAATA    22768     CA      CA
                                TAT  AGGAAGGG  GGCG
                                |||  ||||||||  ||||
                                ATA  TCCTTTCC  TTGT
                                  AC       A_
GAM637  EPB41L1  3'  CATTCTGCCCTTCCCTGA    71104     A        C
                                TCA GGAAGGGCAGG GTG
                                ||| ||||||||||| |||
                                AGT CCTTCCCGTCT TAC
                                  C         _
GAM637  FLJ00060 3'  CATACCCCCTGCCCTCCTCTGA 61741     _   A      CGTG
                                TCA AGGA GGGCAGG    ATG
                                ||| |||| |||||||    |||
                                AGT TCCT CCCGTCC    TAC
                                  C    _      CCCA
GAM637  FLJ10898 5'  CACCACAGCCCTTTCTCAATA  60126     CA       AGGC
                                TAT  AGGAAGGGC    GTG
                                |||  |||||||||    |||
                                ATA  TCTTTCCCG    CAC
                                  AC        ACAC
GAM637  FLJ22557 3'  ATCATCCCATCCTTAATA    45581     C    A   CAGGC
                                TAT AAGGA GGG     GTGAT
                                ||| ||||| |||     |||||
                                ATA TTCCT CCC     TACTA
                                  A    A  _____
GAM637  KIAA0574 3'  CATCCCCTGCCCTCCCCTGA   69808     A  A      CGT
                                TCA GG AGGGCAGG   GATG
                                ||| || ||||||||   ||||
                                AGT CC TCCCGTCC   CTAC
                                  C  C       C__
GAM637  KIAA0632 3'  CACCTCAGAAACCCTTCCTTGA 32071          CA___  C
                                TCAAGGAAGGG    GG GTG
                                ||||||||||     || |||
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                                AGTTCCTTCCC    CT CAC
                                     AAAGA  C
GAM637  KIAA1045  3'  CATCACATGTCCTTCC     71599        GGC
                                GGAAGGGCA  GTGATG
                                |||||||||  ||||||
                                CCTTCCTGT  CACTAC
                                    A__
GAM637  KIAA1354  5'  CAGTGACTGCCTTCCCTTGATA 61572       A     G _
                                TATCAAGG AGGGCAG CG TG
                                |||||||| ||||||| || ||
                                ATAGTTCC TTCCGTC GT AC
                                    C      A  G
GAM637  MGC20460  5'  CACCGCCTCCTACCCTTCTT  54901       C___    _
                                AGGAAGGG   AGGCG TG
                                ||||||||   ||||| ||
                                TTCTTCCC   TCCGC AC
                                    ATCC    C
GAM637  LOC158476 3'  CACGCCCGCCCCCCCCCATTGA  88186     _ AA_   A
                                TCAA GG  GGGC GGCGTG
                                |||| ||  |||| ||||||
                                AGTT CC  CCCG CCGCAC
                                  A  CCC   C
GAM637  LOC90459  3'  CACACCCGCCTAATTTTTG   63550      A_   A  C
                                CAAGGA  GGGC GG GTG
                                ||||||  |||| || |||
                                GTTTTT  TCCG CC CAC
                                   AA   C  A
GAM638  ASB2      3'  CCCTCCACTTGTTCTGG     32873      CT
                                TCAGG  GCAAGTGGAGGG
                                |||||  ||||||||||||
                                GGTCT  TGTTCACCTCCC
                                  __
GAM638  ATP5G2    3'  TCCCCAGGCAGCCTGGGGAA  18982          AAG   A
                                TTCCTCAGGCTGC   TGG GGG
                                ||||||||||||   ||| |||
                                AAGGGGTCCGACG   ACC CCT
                                     G__   _
GAM638  CHRM1     3'  TCCCTCCACCCCAGTCCCCGGG 96435      CA  _   CAA
          AA                    TTCCT  GG CTG   GTGGAGGGA
                                |||||  || |||   |||||||||
                                AAGGG  CC GAC   CACCTCCCT
                                  CC  T   CC_
GAM638  DLEC1     3'  CCCCCAAAACAGCCTGAG    96280        CAAG   A
                                CTCAGGCTG    TGG GGG
                                |||||||||    ||| |||
                                GAGTCCGAC    ACC CCC
                                     AAA_   _
GAM638  DLEC1     3'  CCCCCAAAACAGCCTGAG    24720        CAAG   A
                                CTCAGGCTG    TGG GGG
                                |||||||||    ||| |||
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                                GAGTCCGAC    ACC CCC
                                     AAA_  _
GAM638  IGF2     3'  CCCTCCATCGGGCTGAGGAA  7033         G   CAA
                                TTCCTCAG CTG   GTGGAGGG
                                |||||||| |||   ||||||||
                                AAGGAGTC GGC   TACCTCCC
                                     G  ____
GAM638  SPOCK    3'  TCTTGTAGCCTGCAGGCTGAGG 63477        G    A  GGA
             AA                   TTCCTCAG CTGCA GT   GGGA
                                |||||||| ||||| ||   ||||
                                AAGGAGTC GACGT CG   TTCT
                                     G    C  ATG
GAM638  SYN3     3'  CCATCCGCAACCTGAGGAA   14480         C   AA
                                TTCCTCAGG TGC  GTGG
                                |||||||||| |||  ||||
                                AAGGAGTCC ACG  TACC
                                     A   CC
GAM638  SYN3     3'  CCATCCGCAACCTGAGGAA   14481         C   AA
                                TTCCTCAGG TGC  GTGG
                                |||||||||| |||  ||||
                                AAGGAGTCC ACG  TACC
                                     A   CC
GAM638  TAF4     3'  CCCTCCACTCCGCTGAG     13513       G TGCA
                                CTCAG C    AGTGGAGGG
                                ||||| |    |||||||||
                                GAGTC G    TCACCTCCC
                                   _ CC__
GAM638  XT3      3'  CCCCCCACTGAGACAGCCTGAG 39908         CA__    A
                                CTCAGGCTG    AGTGG GGG
                                |||||||||    ||||| |||
                                GAGTCCGAC    TCACC CCC
                                     AGAG    C
GAM638  CDW92    3'  TCCCTCCAAAGTGACCTGATGG 42331     _    CT  AAG
             AA                   TTCC TCAGG  GC   TGGAGGGA
                                |||| |||||  ||   ||||||||
                                AAGG AGTCC  TG   ACCTCCCT
                                   T    AG  AA_
GAM638  FLJ10743 3'  CCCTCCACCCGCTGCGGGCTGA 37079        G    A___
             GGGA                   TTCCTCAG CTGCA    GTGGAGGG
                                |||||||| |||||    ||||||||
                                AGGGAGTC GGCGT    CACCTCCC
                                     G    CGCC
GAM638  FLJ12529 3'  TCCCTCCAGACACCCAGGGAA  46091      CA  C  CAAG
                                TTCCT  GG TG    TGGAGGGA
                                |||||  || ||    ||||||||
                                AAGGG  CC AC    ACCTCCCT
                                   AC  _  AG__
GAM638  FLJ13852 3'  CCTGCCCTGCAGCCTGGAGAA  43838     CT       A T  A
                                TTC  CAGGCTGCA G GG GGG
                                |||  ||||||||| | || |||
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                                AAG  GTCCGACGT C CC TCC
                                  AG        _ _  G
GAM638  FLJ14621  3'  TCCCACTATTACAGCCTGAG   52543         CA    A
                                CTCAGGCTG  AGTGG GGGA
                                |||||||||  ||||| ||||
                                GAGTCCGAC  TTATC CCCT
                                     A_    A
GAM638  FLJ22635  3'  CCCTGCACCGCTGTCAGCCTGA 47670           CA    ___
          GGAA                    TTCCTCAGGCTG  AGTGG   AGGG
                                |||||||||||  |||||   ||||
                                AAGGAGTCCGAC  TCGCC   TCCC
                                       TG    ACG
GAM638  HDAC9-PENDING 5'  CCCTAGCAGCCTGAAGAA    28840     C       A  T
                                TTC TCAGGCTGC AG GG
                                ||| |||||||| || ||
                                AAG AGTCCGACG TC CC
                                  A        A _
GAM638  KIAA0450  3'  TCCCCCCACTGTGCAGCCTGG  28370          _    A
                                TCAGGCTGCA AGTGG GGGA
                                ||||||||| ||||| ||||
                                GGTCCGACGT TCACC CCCT
                                     G    C
GAM638  KIAA1668  3'  TCCCTCCAGGTGCCCGAG    67082     A  CT   AG
                                CTC GG  GCA  TGGAGGGA
                                ||| ||  |||  ||||||||
                                GAG CC  CGT  ACCTCCCT
                                  _ __   GG
GAM638  MGC10485  3'  CCCGTTACTTGCAACCTGA   54621       C       A
                                TCAGG TGCAAGTGG GGG
                                ||||| ||||||||| |||
                                AGTCC ACGTTCATT CCC
                                   A        G
GAM638  MGC15631  5'  CCCCCCAAGCCCGAGGAG    52226       A   GCAAG   A
                                TTCCTC GGCT    TGG GGG
                                |||||| ||||    ||| |||
                                GAGGAG CCGA    ACC CCC
                                   C   _____  C
GAM638  PP1628    5'  TCCCTTGCAGCCCAGGGAA   48080      CA       T
                                TTCCT  GGCTGCAAG GGA
                                |||||  ||||||||| |||
                                AAGGG  CCGACGTTC CCT
                                   AC       _
GAM638  PRO1580   5'  TCCCAGCTTCTACAGGCTGAGG 38126        G   C__   GGA
          AA                     TTCCTCAG CTG   AAGT   GGGA
                                |||||||| |||   ||||   ||||
                                AAGGAGTC GAC   TTCG   CCCT
                                     G   ATC    A__
GAM638  TNKS1BP1  3'  CCCTCCACCTCTGAGGAG    54147         CTGCAA
                                TTCCTCAGG     GTGGAGGG
                                |||||||||     ||||||||
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                                GAGGAGTCT     CACCTCCC
                                    C_____
GAM638  WDR13     5'  TCTTGCCTGGAGCCTGAG    35844        G  AGT  AG
                                CTCAGGCT CA   GG  GGA
                                |||||||| ||   ||  |||
                                GAGTCCGA GT   CC  TCT
                                    G  ___  GT
GAM638  LOC132228 3'  CCCCACAGCCCTGAGGAA    75544         CT  AA   A
                                TTCCTCAGG  GC  GTGG GG
                                |||||||||  ||  |||| ||
                                AAGGAGTCC  CG  CACC CC
                                    __ A_   _
GAM638  LOC145989 5'  TCGGCCAGCAGCCTGAAGAA   60297     C        AA  G
                                TTC TCAGGCTGC  GT GA
                                ||| |||||||||  || ||
                                AAG AGTCCGACG  CG CT
                                  A        AC  G
GAM638  LOC146146 5'  TCCCTCCACCTCACCGCCTGGG 78169      T     TGCAA_
          AA                      TTCC CAGGC     GTGGAGGGA
                                |||| |||||     |||||||||
                                AAGG GTCCG     CACCTCCCT
                                  _    CCACTC
GAM638  LOC146795 5'  CCCCTCGCCCAGCCTGAG    78723         CAA   GA
                                CTCAGGCTG   GTG  GGG
                                |||||||||   |||  |||
                                GAGTCCGAC   CGC  CCC
                                    C__   TC
GAM638  LOC147779 3'  TCCCCAGGGTGCAGCCTGAG   79155          AG_   A
                                CTCAGGCTGCA   TGG GGG
                                ||||||||||   ||| |||
                                GAGTCCGACGT   ACC CCT
                                     GGG  _
GAM638  LOC149506 5'  CCCCGCGCAGCCTGGGAA    85630      T       AA    A
                                TTCC CAGGCTGC  GTGG GG
                                |||| ||||||||  |||| ||
                                AAGG GTCCGACG  CGCC CC
                                  _      __   _
GAM638  LOC163126 5'  CCCGGCACAGCCTGAGGAG   83319          GCAA   GA
                                TTCCTCAGGCT    GTG  GGG
                                ||||||||||    |||  |||
                                GAGGAGTCCGA    CAC  CCC
                                     ____  GG
GAM638  LOC200812 3'  CCCTTCATCTACAGCCTGAG   90303         CAA
                                CTCAGGCTG   GTGGAGGG
                                |||||||||   ||||||||
                                GAGTCCGAC   TACTTCCC
                                    ATC
GAM638  LOC219445 3'  CCCTTCATCTGCAGCCTGAG   93200          AG
                                CTCAGGCTGCA  TGGAGGG
                                ||||||||||  |||||||
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                                GAGTCCGACGT  ACTTCCC
                                      CT
GAM638  LOC253196 3'  CCCTCCACTTGGGAAGGAA   98669      CAGG  G
                                TTCCT   CT CAAGTGGAGGG
                                |||||   || ||||||||||
                                AAGGA   GG GTTCACCTCCC
                                  A___  _
GAM638  LOC253933 3'  CCCTTCGTCTACAGCCTGAG  97753        CA  _
                                CTCAGGCTG  AG TGGAGGG
                                |||||||||  || |||||||
                                GAGTCCGAC  TC GCTTCCC
                                      A_  T
GAM638  LOC254266 3'  TCCAGCCCCACAGCCTGAGGGA 99202           CAAGT  AG
                                TTCCTCAGGCTG    GG  GGA
                                ||||||||||||    ||  |||
                                AGGGAGTCCGAC    CC  CCT
                                       ACC__  GA
GAM638  LOC255105 3'  CCCTTCATCTACAGCCTGAG  97793        CAA
                                CTCAGGCTG   GTGGAGGG
                                |||||||||   ||||||||
                                GAGTCCGAC   TACTTCCC
                                      ATC
GAM638  LOC57105  3'  TCCATTTTACAGCTGAAGAA  40172     C   G   C_
                                TTC TCAG CTG  AAGTGGA
                                ||| |||| |||  |||||||
                                AAG AGTC GAC  TTTACCT
                                  A   _  AT
GAM638  LOC57862  3'  TCCCTTTAGCAACCTGAG    41323      C  AAG
                                CTCAGG TGC   TGGAGGGA
                                ||||||| |||   ||||||||
                                GAGTCC ACG   ATTTCCCT
                                   A  ___
GAM638  LOC93132  5'  TCACCCTGCAGACCTGAGGAA  71999        _    A_
                                TTCCTCAGG CTGCA  GTGG
                                ||||||||| |||||  ||||
                                AAGGAGTCC GACGT  CACT
                                      A    CC
GAM638  LOC93395  5'  CCCTAAGCAGCCTGAGG     61121         AAGTGG
                                CCTCAGGCTGC     AGGG
                                ||||||||||      ||||
                                GGAGTCCGACG     TCCC
                                       AA_____
GAM639  DUSP6    3'  CACCAGCTGTCTGTACTAG    66577      AAATC
                                TTAGTA    CAGCTGGTG
                                ||||||    |||||||||
                                GATCAT    GTCGACCAC
                                   GTCT_
GAM639  KLHL1    5'  CACCACCTTCCCTACTAAGGC  40869        AAATCC  C
                                GCCTTAGTA     AG TGGTG
                                |||||||||     || |||||
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                                CGGAATCAT     TC ACCAC
                                     CCCT__  C
GAM639  LPIN1    3'  CAGTAAATATTACTAAGGCA  67986          A  CCA
                                TGCCTTAGTAA AT   GCTG
                                |||||||||| ||   ||||
                                ACGGAATCATT TA   TGAC
                                      A  AA_
GAM639  NESH     3'  ACCAGCTGACCTAGAAGCA   33567     C_    TAAAATC
                                TGC  TTAG      CAGCTGGT
                                |||  ||||      ||||||||
                                ACG  GATC      GTCGACCA
                                  AA    CA_____
GAM639  RPL10    3'  CTGGACTTTACCAGGCA     21178       TA     A
                                TGCCT  GTAAA TCCAG
                                |||||  ||||| |||||
                                ACGGA  CATTT AGGTC
                                   C_     C
GAM639  TRPC5    3'  CACCAGCTATCAGATAAGGCA  25925        GTAAAATCC
                                TGCCTTA        AGCTGGTG
                                |||||||        ||||||||
                                ACGGAAT        TCGACCAC
                                     AGACTA___
GAM639  DKFZP434O047 5'  CAGATGTGGATTTTACTGA    32120            G__
                                TTAGTAAAATCCA   CTG
                                ||||||||||||   |||
                                AGTCATTTTAGGT   GAC
                                       GTA
GAM639  ICK      5'  CGGGATGGATTTCTCTAAGGCA 33686         TA      G_
                                TGCCTTAG  AAATCCA  CTG
                                ||||||||  |||||||  |||
                                ACGGAATC  TTTAGGT  GGC
                                     TC       AG
GAM639  KIAA1784  3'  CCAGCTGGCCAGGGCA      65745        A TAAAAT
                                TGCCTT G     CCAGCTGG
                                |||||| |     ||||||||
                                ACGGGA C     GGTCGACC
                                   C _______
GAM639  LIP8     5'  CTGGACTTTGCTAAAGCA     89524      C       A
                                TGC TTAGTAAA TCCAG
                                ||| |||||||| |||||
                                ACG AATCGTTT AGGTC
                                  A       C
GAM639  MRPS27    3'  CACCAGCTGAATACCTTAAGG  31325        TAAAATC
                                CCTTAG       CAGCTGGTG
                                ||||||       |||||||||
                                GGAATT       GTCGACCAC
                                   CCATAA_
GAM639  NUDEL    3'  CACCTTCTGATTTTACTTAAGC 48696     CTT        C  CT
             A                   TGC   AGTAAAATC AG  GGTG
                                |||   ||||||||| ||  ||||
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                                ACG   TCATTTTAG TC  CCAC
                                  AAT        _ TT
GAM639  LOC146229 3'  CACCAGCTGGATGACCTCAGGC 78264       T  TAAA
           A                     TGCCT AG    ATCCAGCTGGTG
                                 |||||| ||    ||||||||||||
                                 ACGGA TC    TAGGTCGACCAC
                                   C  CAG_
GAM640  AQP3    3'  TGGAACCGGAATTTGGGTCA   60333          _ AAAA
                                 TGACCCAGGT CC    GTTCCA
                                 |||||||||| ||    ||||||
                                 ACTGGGTTTA GG    CAAGGT
                                       A  C___
GAM640  CD81    3'  TGGAGACGGGCCTGGGTC    16387          AAAAG
                                 GACCCAGGTCC    TTCCA
                                 ||||||||||     |||||
                                 CTGGGTCCGGG    GAGGT
                                       CA___
GAM640  CUL5    3'  TGGAACTTCCTAATTTTGGGTC 14432          TCCAA_
           AT                     ATGACCCAGG     AAGTTCCA
                                  ||||||||||     ||||||||
                                  TACTGGGTTT     TTCAAGGT
                                       TAATCC
GAM640  EN2     3'  TGGGGCTAAAGGCCTGGGGTGT 9275      GA       CAAA
           G                      TAT  CCCAGGTC    AGTTCCA
                                  |||  ||||||||    |||||||
                                  GTG  GGGTCCGG    TCGGGGT
                                    TG       AAA_
GAM640  ENC1    3'  TGGGATTTCATGGGGTTTGGTT 14652    TG   C  G    A_
           GTG                      TA  ACC AG TCCA  AAGTTCCA
                                  ||  ||| || ||||  ||||||||
                                  GT  TGG TT GGGT  TTTAGGGT
                                   GT   T  G    AC
GAM640  EPHB2   3'  GGAGTGAGATTTGGGT      16700          _ AAAG
                                 ACCCAGGTC CA    TTCC
                                 |||||||||  ||    ||||
                                 TGGGTTTAG GT    GAGG
                                       A  _____
GAM640  FBXL4   3'  TGGGATTGGTTTTGGGTT    25135         T   AAA
                                 GACCCAGG CCA   GTTCCA
                                 ||||||||  |||   ||||||
                                 TTGGGTTT GGT   TAGGGT
                                       T  ____
GAM640  FGF23   3'  GGGACTGCTCTGGGTTA     40559          _ CCAAA
                                 TGACCCAG GT    AGTTCC
                                 ||||||||  ||    ||||||
                                 ATTGGGTC CG    TCAGGG
                                       T  ______
GAM640  GDI1    3'  GGGGAAGGCTTGGGCATG    60643      A       CAAAAG
                                 TATG CCCAGGTC     TTCC
                                 ||||  ||||||||     ||||
```

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                                GTAC GGGTTCGG     GGGG
                                  _       AA____
GAM640  GGA1    3'  GGAAGAACTTGGGTCATG    26278          _ CAAAAG
                                TATGACCCAGGT C     TTCC
                                |||||||||||| |     ||||
                                GTACTGGGTTCA G     AAGG
                                       A _______
GAM640  HUS1    3'  TGGGGCCAGTTTTGGGTTTAGG 92744    TG   C  GT    ___
          TTGTA                    TA  ACC AG  CCAAAA   GTTCCA
                                ||  ||| ||  ||||||   ||||||
                                AT  TGG TT  GGTTTT   CGGGGT
                                 GT   A  TG     GAC
GAM640  LPL     3'  TAAATTTCTGGATTTGGGTTGT 5883     TG        A    CCA
          G                       TA  ACCCAGGTCCA AAGTT
                                ||  ||||||||||| |||||
                                GT  TGGGTTTAGGT TTTAA
                                 GT         C     AT
GAM640  MBP     3'  TGGGGTTCAACACTGGGTTATG 91352         GTCCAAA  TT
                                TATGACCCAG      AG  CCA
                                ||||||||||      ||  |||
                                GTATTGGGTC      TT  GGT
                                      ACAAC__  GG
GAM640  MECP2   3'  TGGGGTTTTTCTGTTTGGGTTT 18416   T     GG CC    TT
          G                      A GACCCA  T  AAAAG  CCA
                                | ||||||  |  |||||  |||
                                G TTGGGT  G  TTTTT  GGT
                                 T     TT TC     GG
GAM640  MEF2D   3'  TGGGGCTCTTCCTGGGTC    20990        TCCAAA
                                GACCCAGG     AGTTCCA
                                ||||||||     |||||||
                                CTGGGTCC     TCGGGGT
                                     TTC___
GAM640  NFKBIA  3'  TGGGGTTTTTGGAGAAGGTTAT 40447       CAGG       TT
                                ATGACC    TCCAAAAG  CCA
                                ||||||    ||||||||  |||
                                TATTGG    AGGTTTTT  GGT
                                   AAG_       GG
GAM640  NHP2L1  3'  TGGGGCAGTTGACCTGGGTC   18450         C  AA
                                GACCCAGGTC AA  GTTCCA
                                |||||||||| ||  ||||||
                                CTGGGTCCAG TT  CGGGGT
                                      _  GA
GAM640  RXRB    3'  TGGGGAAGGGGCCTGGGCTGTG 42033     GA        AAAAG
                                TAT  CCCAGGTCC     TTCCA
                                |||  |||||||||     |||||
                                GTG  GGGTCCGGG     GGGGT
                                  TC        GAA__
GAM640  SEPX1   3'  GGGACAGGCCTGGGCTGTG   33379     GA       CAAAA
                                TAT  CCCAGGTC     GTTCC
                                |||  ||||||||     |||||
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                                GTG  GGGTCCGG    CAGGG
                                  TC       A____
GAM640  SLC21A2   3'  TGGAACAGCTGGGCATGGGTCA 20089         G    AAA
              TG                    TATGACCCA GTCCA   GTTCCA
                                |||||||||| |||||   ||||||
                                GTACTGGGT CGGGT   CAAGGT
                                     A    CGA
GAM640  SLC9A5    3'  TGGGGCCAGAAGGGCCTGGGTT 60479          AAAA_
                                GACCCAGGTCC    GTTCCA
                                ||||||||||    ||||||
                                TTGGGTCCGGG    CGGGGT
                                      AAGAC
GAM640  SPTBN4    3'  TGGGGAGTCGGGGGATTGGGTT 48160    TG    GT  AAAAG_
              GTG                   TA  ACCCAG  CC     TTCCA
                                ||  ||||||  ||     |||||
                                GT  TGGGTT  GG     GGGGT
                                 GT     AG  GGCTGA
GAM640  ST14      3'  TGGGGCTGCCGGATCTGGGCTG 42044     GA       AAA
              TG                    TAT  CCCAGGTCC   AGTTCCA
                                |||  |||||||||  |||||||
                                GTG  GGGTCTAGG   TCGGGGT
                                  TC       CCG
GAM640  WNT11     3'  TGGAATCACTAGCTTGGGTTGT 17327    TG       CCAAAA
              A                     TA  ACCCAGGT     GTTCCA
                                ||  ||||||||     ||||||
                                AT  TGGGTTCG     TAAGGT
                                 GT       ATCAC_
GAM640  AF053356_CDS3 5'  GGGGCCCTGGGCCTGGGTC    43983           AAA    A
                                GACCCAGGTCCA   GTTCC
                                ||||||||||||   |||||
                                CTGGGTCCGGGT   CGGGG
                                      CC_    G
GAM640  ARAP3     3'  TGGAAACCAGAGGCCTGGGTGA 42789     G       CAAAAG
              TG                    TAT ACCCAGGTC     TTCCA
                                |||  |||||||||      |||||
                                GTA TGGGTCCGG     AAGGT
                                  G        AGACCA
GAM640  ARTS-1    3'  TGGGGCTCCAGCTTGGGTCGT  33608          CCAAA
                                ATGACCCAGGT    AGTTCCA
                                ||||||||||    |||||||
                                TGCTGGGTTCG    TCGGGGT
                                      ACC__
GAM640  DDX18     3'  TGGAGCAAAAACTATGGGTTGT 23199    TG    _  CCAAAA
              A                     TA  ACCCA GGT     GTTCCA
                                ||  ||||| |||     ||||||
                                AT  TGGGT TCA     CGAGGT
                                 GT    A   AAAA__
GAM640  DKFZP434K2235 3'  TGGAACTTTTCCCAAAGGGTT  84499      A__  TCC
                                GACCC   GG   AAAAGTTCCA
                                |||||   ||   ||||||||||
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                                TTGGG  CC  TTTTCAAGGT
                                   AAA  C__
GAM640  DKFZP564O0423 3'  GGAACTTTTATGGGTTA    93356       GGTCC
                                TGACCCA    AAAAGTTCC
                                |||||||    |||||||||
                                ATTGGGT    TTTTCAAGG
                                    A_____
GAM640  DKFZP586J1624 3'  TGGGGCTGGGCCCTGGGTT   32049       _   AAA
                                GACCCAGG TCCA  GTTCCA
                                |||||||| ||||  ||||||
                                TTGGGTCC GGGT  CGGGGT
                                     C   ___
GAM640  DKFZP761D0211 3'  TGGAATGCGTGTTTGGGTCA  50180        TC  AAA
                                TGACCCAGG  CA  GTTCCA
                                |||||||||  ||  ||||||
                                ACTGGGTTT  GT  TAAGGT
                                      __ GCG
GAM640  FLJ10525  3'  AACTTTGATTTGGGTTGTA   36722   TG      CA
                                TA  ACCCAGGTC  AAAGTT
                                ||  |||||||||  ||||||
                                AT  TGGGTTTAG  TTTCAA
                                 GT       __
GAM640  FLJ12568  5'  TGATTTTTTGGATTTGGGTTA  47142            T  CA
                                TGACCCAGGTCCAAAAG TC
                                |||||||||||||||| ||
                                ATTGGGTTTAGGTTTTT AG
                                          T  T
GAM640  FLJ13840  3'  TGGTGCACCTGGGTTATG    45701          ___
                                TATGACCCAGGT  CCA
                                ||||||||||||  |||
                                GTATTGGGTCCA  GGT
                                       CGT
GAM640  FLJ14594  3'  GGAGCCTGGCTTGGGT     52508       T   AAA
                                ACCCAGG CCA  GTTCC
                                ||||||| |||  |||||
                                TGGGTTC GGT  CGAGG
                                    _  C__
GAM640  FLJ20306  5'  TGGACCCAAGGGCTTGGGTGAT 35402    G       AAAAGT
          G                      TAT ACCCAGGTCC     TCCA
                                ||| ||||||||||     ||||
                                GTA TGGGTTCGGG     AGGT
                                  G        AACCC_
GAM640  FLJ21415  3'  TGGAGCTTTTTCTTTGGGCCAT 45692     A     TCC
          A                      TATG CCCAGG   AAAAGTTCCA
                                |||| ||||||  ||||||||||
                                ATAC GGGTTT   TTTTCGAGGT
                                  C     CT_
GAM640  FLJ21432  3'  TGGGGAAAGGATCTGGTTCATG 44947      C      AAAAG
                                TATGA CCAGGTCC    TTCCA
                                ||||| ||||||||    |||||
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                                GTACT GGTCTAGG    GGGGT
                                  T       AAA__
GAM640  FLJ22215  5'  TGGGGCGGGCAGCTTGGGTC  43400        CCAAAA
                                GACCCAGGT     GTTCCA
                                |||||||||     ||||||
                                CTGGGTTCG     CGGGGT
                                     ACGGG_
GAM640  FLJ22215  3'  TGGGGCGGGCAGCTTGGGTC  43401        CCAAAA
                                GACCCAGGT     GTTCCA
                                |||||||||     ||||||
                                CTGGGTTCG     CGGGGT
                                     ACGGG_
GAM640  FLJ23550  3'  TGGAGTTAGATCTGGGTTATG  47545          C  AAG
                                TATGACCCAGGTC AA   TTCCA
                                |||||||||||| ||   |||||
                                GTATTGGGTCTAG TT   GAGGT
                                       A  ___
GAM640  FRAT1     3'  TGGGATCCTGGGGGCCTGGGTT 19691          AAAA_
                                GACCCAGGTCC    GTTCCA
                                ||||||||||     ||||||
                                TTGGGTCCGGG    TAGGGT
                                     GGTCC
GAM640  GALNT11   3'  TGGGGCTTTAGGAAAGCCTGGG 42246         ___  A
          TT                     GACCCAGGT   CC AAAGTTCCA
                                |||||||||   || |||||||||
                                TTGGGTCCG   GG TTTCGGGGT
                                     AAA  A
GAM640  GALNT8    3'  TGGTGCTGGATCTGGGTCAT   34275          AAA  T
                                ATGACCCAGGTCCA   GT CCA
                                ||||||||||||||   || |||
                                TACTGGGTCTAGGT   CG GGT
                                       ___  T
GAM640  HSA250839 3'  TGGAGCTGGGAAGCCTGGGTT  37856        CCAAA
                                GACCCAGGT    AGTTCCA
                                |||||||||    |||||||
                                TTGGGTCCG    TCGAGGT
                                     AAGGG
GAM640  HTCD37    3'  TGGAATGAGAGGCCTGGGTC   68303        CAAAA
                                GACCCAGGTC    GTTCCA
                                ||||||||||    ||||||
                                CTGGGTCCGG    TAAGGT
                                     AGAG_
GAM640  KIAA0276  3'  TGGAAAAAGGTTTGGGTTAT   71525        T  AAAAG
                                ATGACCCAGG CC    TTCCA
                                |||||||||| ||    |||||
                                TATTGGGTTT GG    AAGGT
                                     _  AAA__
GAM640  KIAA0711  3'  TGGAATTTATGATCTGGGTTA  30155         CAA
                                TGACCCAGGTC   AAGTTCCA
                                ||||||||||    ||||||||
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                                ATTGGGTCTAG  TTTAAGGT
                                      TA_
GAM640  KIAA0773  3'  TGGAGAAGGACCTGGGCTGTG  28730    GA      AAAAG
                                TAT  CCCAGGTCC    TTCCA
                                |||  |||||||||    |||||
                                GTG  GGGTCCAGG    GAGGT
                                  TC       AA___
GAM640  KIAA0982  3'  TGGGACTTTTGGACCCGTC   26712    CCA
                                GAC   GGTCCAAAAGTTCCA
                                |||   ||||||||||||||
                                CTG   CCAGGTTTTCAGGGT
                                  C__
GAM640  KIAA1016  3'  TGGTCCTGGTGCTTGGGTTATG 93390          _   AAA TT
                                TATGACCCAGGT CCA   G  CCA
                                |||||||||||| |||   |  |||
                                GTATTGGGTTCG GGT   C  GGT
                                       T   ___ CT
GAM640  KIAA1582  5'  TGGGACAGAGGCCTGGGGTTGT 65995    TG   _    CAAAA
            G                    TA  ACCC AGGTC    GTTCCA
                                ||  |||| |||||    ||||||
                                GT  TGGG TCCGG    CAGGGT
                                 GT    G    AGA__
GAM640  KIAA1952  5'  GCACTTGGGCCTGGGTTA    73546           AA
                                TGACCCAGGTCCAA  GT
                                ||||||||||||||  ||
                                ATTGGGTCCGGGTT  CG
                                       CA
GAM640  LMOD1    3'  TGGAACTGCCACCTTGGGTC   25107       _   CCAAA
                                GACCCA GGT     AGTTCCA
                                ||||||| |||    |||||||
                                CTGGGT CCA     TCAAGGT
                                   T   CCG__
GAM640  MGC15416  5'  GGTCATGGACTGGGTCGTG   51405         G    AAAGTT
                                TATGACCCAG TCCA     CC
                                |||||||||| ||||     ||
                                GTGCTGGGTC AGGT     GG
                                      _    ACT____
GAM640  MSTP028   3'  AACTTTGGGTCTGGTTTGTG   50060    TG C    GT     A
                                TA  A CCAG  CCAAA GTT
                                ||  | ||||  ||||| |||
                                GT  T GGTC  GGTTT CAA
                                 GT T    TG    _
GAM640  NINJ2     3'  GGGACAGGGGTCTGGGTTTG   33728    T      GT  AAAA     A
                                A GACCCAG  CC    GTTCC
                                | |||||||  ||   |||||
                                G TTGGGTC  GG    CAGGG
                                 T      TG  GA__     G
GAM640  RODH-4    3'  TGGTTGCATGGATTTGGGGTGT 14926     GA       AAA  T_
            G                    TAT  CCCAGGTCCA   GT  CCA
                                |||  ||||||||||   ||  |||
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                                GTG  GGGTTTAGGT   CG  GGT
                                  TG        A__  TT
GAM640  SHAPY    3'  TGGAACTGTGCCTGGGTT    57914         CCAAA
                                GACCCAGGT    AGTTCCA
                                |||||||||    |||||||
                                TTGGGTCCG    TCAAGGT
                                     TG___
GAM640  SPR1     5'  TGGGGTGACGCAGGCTCTGGGT 26814          _  CAAAA_ TT
           CATG                    TATGACCCAG GTC     G  CCA
                                |||||||||| |||     |  |||
                                GTACTGGGTC CGG     T  GGT
                                      T   ACGCAG GG
GAM640  SUPT4H1  3'  TGGGGTGGGAGGGATTTGGGTT 13488          AAAA_ TT
                                GACCCAGGTCC    G  CCA
                                ||||||||||    |  |||
                                TTGGGTTTAGG    T  GGT
                                      GAGGG GG
GAM640  UBN1     3'  TGGGGCTTGCGCTGGGCCGTG  34196     A    _  CCAA
                                TATG CCCAG GT    AAGTTCCA
                                |||| ||||| ||    ||||||||
                                GTGC GGGTC CG    TTCGGGGT
                                  C    G  ____
GAM640  UNC5D    3'  TGGAATCCACATTTGGGTTA   56012         CCAAAA
                                TGACCCAGGT     GTTCCA
                                ||||||||||     ||||||
                                ATTGGGTTTA     TAAGGT
                                      CACC__
GAM640  LOC115399 3'  GGGGCCTGGCCTGGGTGATG   73815    G      T   AAA
                                TAT ACCCAGG CCA   GTTCC
                                ||| ||||||| |||   |||||
                                GTA TGGGTCC GGT   CGGGG
                                  G      _  C__
GAM640  LOC148089 3'  TGGGCAGCCGGGCCGGGGTCAT 79336         A    AAAA  T
           G                     TATGACCC GGTCC    GT CCA
                                |||||||| |||||    || |||
                                GTACTGGG CCGGG    CG GGT
                                     G    CCGA  _
GAM640  LOC148394 5'  GGAGATGGGTTTGGGTTTG    85302   T     GT   AAAG
                                A GACCCAG  CCA    TTCC
                                | |||||||  |||    ||||
                                G TTGGGTT  GGT    GAGG
                                 T      TG   A___
GAM640  LOC148936 5'  TGGAATGATAGGGTTTGGTTGT 85461    TG   C  GT  AAAA
           G                     TA  ACC AG  CC    GTTCCA
                                ||  ||| ||  ||    ||||||
                                GT  TGG TT  GG    TAAGGT
                                 GT   _  TG  ATAG
GAM640  LOC148938 5'  TGGAATGATAGGGTTTGGTTGT 85443    TG   C  GT  AAAA
           G                     TA  ACC AG  CC    GTTCCA
                                ||  ||| ||  ||    ||||||
```

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                                GT  TGG TT  GG    TAAGGT
                                 GT   _  TG  ATAG
GAM640   LOC149668 3'  TGGTGACTTGGGCTTGGGTC   85705          AA    _
                                GACCCAGGTCCA  AGTT CCA
                                ||||||||||||  |||| |||
                                CTGGGTTCGGGT  TCAG GGT
                                      __    T
GAM640   LOC154739 5'  TGGAGTAAGGACTTGGGT    87448         AAAAG
                                ACCCAGGTCC    TTCCA
                                ||||||||||    |||||
                                TGGGTTCAGG    GAGGT
                                      AAT__
GAM640   LOC157663 3'  TGGAACTTTTTTCCTGGGTAGT 82457    G      TCC
           A                     TAT ACCCAGG   AAAAGTTCCA
                                ||| |||||||   ||||||||||
                                ATG TGGGTCC   TTTTCAAGGT
                                  A      TT_
GAM640   LOC201109 3'  TGGGATTTTCTTAATTGGGTC  91329       GTCCA
                                GACCCAG    AAAGTTCCA
                                |||||||    |||||||||
                                CTGGGTT    TTTTAGGGT
                                    AATTC
GAM640   LOC202018 3'  GGGGCAGGCCTGGGTC      90610         CAAAA
                                GACCCAGGTC    GTTCC
                                ||||||||||    |||||
                                CTGGGTCCGG    CGGGG
                                      A____
GAM640   LOC205100 5'  TGGAGTTTTTACAGTGAGGTTG 92392    TG  _  G_  CC   GT
           TG                    TA  ACC CA  GT  AAAA  TCCA
                                ||  ||| ||  ||  ||||  ||||
                                GT  TGG GT  CA  TTTT  AGGT
                                 GT   A  GA  __   TG
GAM640   LOC221692 3'  TGGAGCTTTGAGAGCCTTGGGT 93859      _  _  CA
           T                     GACCCA GG TC  AAAGTTCCA
                                ||||||  ||  ||  |||||||||
                                TTGGGT CC AG  TTTCGAGGT
                                    T  G  AG
GAM640   LOC221749 3'  TGGAAACTGGGTTTGGGTCA  93651       GT   AAAG
                                TGACCCAG  CCA   TTCCA
                                ||||||||  |||   |||||
                                ACTGGGTT  GGT   AAGGT
                                     TG   CA__
GAM640   LOC254196 5'  GGAGATGGGTTTGGGTTTG   99185   T     GT   AAAG
                                A GACCCAG  CCA   TTCC
                                | |||||||  |||   ||||
                                G TTGGGTT  GGT   GAGG
                                 T      TG   A___
GAM640   LOC90355  5'  TGGGATTTAGTCTGGATTGTG  53769    TG C    TCCAA
                                TA  A CCAGG    AAGTTCCA
                                ||  | |||||    ||||||||
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                                GT  T GGTCT    TTTAGGGT
                                 GT A    GA___
GAM640  LOC90631  5'  TGGAGACGTTGTGGGCCTGGGT 64397          AAA_ _
           C                     GACCCAGGTCCA   GT TCCA
                                 ||||||||||||   || ||||
                                 CTGGGTCCGGGT   CA AGGT
                                       GTTG  G
GAM641  ADAMTS13  5'  GCTCCACTCCTCGGGCTGG   58142   C  _  A
                                 CC GCC GAG AGTGGAGC
                                 || ||| ||| ||||||||
                                 GG CGG CTC TCACCTCG
                                  T  G  C
GAM641  ADAMTS13  5'  GCTCCACTCCTCGGGCTGG   58145   C  _  A
                                 CC GCC GAG AGTGGAGC
                                 || ||| ||| ||||||||
                                 GG CGG CTC TCACCTCG
                                  T  G  C
GAM641  ADAMTS13  5'  GCTCCACTCCTCGGGCTGG   58154   C  _  A
                                 CC GCC GAG AGTGGAGC
                                 || ||| ||| ||||||||
                                 GG CGG CTC TCACCTCG
                                  T  G  C
GAM641  CSHL1   3'  GCTCCACTGCTTCAGGAAGGA  8984    C_  GCC  A
                                 TCC  CC  GAG AGTGGAGC
                                 |||  ||  ||| ||||||||
                                 AGG  GG  TTC TCACCTCG
                                   AA  AC_  G
GAM641  CSHL1   3'  GCTCCACTGCTTCAGGAAGGA  42936    C_  GCC  A
                                 TCC  CC  GAG AGTGGAGC
                                 |||  ||  ||| ||||||||
                                 AGG  GG  TTC TCACCTCG
                                   AA  AC_  G
GAM641  FBXL5   5'  GCCCCACACTGGCGGATGA   54317   CC   G  AA   A
                                 TC  CCGCC AG  GTGG GC
                                 ||  ||||| ||  |||| ||
                                 AG  GGCGG TC  CACC CG
                                  TA   _ A_   C
GAM641  GAB2    3'  GCTCCACTTCTGCAAGG    55406   CC  CG
                                 CC  GC  AGAAGTGGAGC
                                 ||  ||  ||||||||||
                                 GG  CG  TCTTCACCTCG
                                  AA  __
GAM641  GAB2    3'  GCTCCACTTCTGCAAGG    25460   CC  CG
                                 CC  GC  AGAAGTGGAGC
                                 ||  ||  ||||||||||
                                 GG  CG  TCTTCACCTCG
                                  AA  __
GAM641  GAN     3'  CCACTTCTCATTGGGGGA   42119      CC
                                 TCCCCCG  GAGAAGTGG
                                 |||||||  |||||||||
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                                AGGGGGT  CTCTTCACC
                                    TA
GAM641  GARP    3'  CTCTAGGTCAGTGGGGGA    19778       CGA  AG
                                TCCCCCGC   GA  TGGAG
                                ||||||||   ||  |||||
                                AGGGGGTG   CT  ATCTC
                                    A__  GG
GAM641  GPR48   5'  GCCCGGGGGCGGCGGGGGA   38095        AGAAG  A
                                TCCCCCGCCG    TGG GC
                                ||||||||||    ||| ||
                                AGGGGGCGGC    GCC CG
                                     GGGG_  _
GAM641  IL2RB   3'  GCCCCACTTCTCAGCCTGG   7940    CC  C       A
                                CC  GC GAGAAGTGG GC
                                ||  || |||||||| ||
                                GG  CG CTCTTCACC CG
                                 TC  A       C
GAM641  ITGA4   5'  GCTCCCGGCTCGGCGGCAGA  7956    CC      AAGT
                                TC  CCGCCGAG   GGAGC
                                ||  ||||||||   |||||
                                AG  GGCGGCTC   CCTCG
                                 AC      GGC_
GAM641  MDM4    5'  CCGGGCTCGGCGGGGGA    11509          AAG
                                TCCCCCGCCGAG   TGG
                                ||||||||||||   |||
                                AGGGGGCGGCTC   GCC
                                     GG_
GAM641  MIC2    5'  GCCCCACCCGGCCCGTGGGGGA 11580       ____   AGAA   A
                                TCCCCC   GCCG   GTGG GC
                                ||||||   ||||   |||| ||
                                AGGGGG   CGGC   CACC CG
                                   TGCC   C___   C
GAM641  NFE2L1  3'  GCTCCACTCGGGTGGAGTGGA  13631    C__    GA  A
                                TCC   CCGCC  GA GTGGAGC
                                |||   |||||  || |||||||
                                AGG   GGTGG  CT CACCTCG
                                  TGA    G_  _
GAM641  NFKBIB  5'  GCCCCTGAGGCGGCGGGGG   11782        AGA_  T  A
                                CCCCCGCCG    AG GG GC
                                |||||||||    || || ||
                                GGGGGCGGC    TC CC CG
                                     GGAG  _  _
GAM641  OTX1    3'  GCTTCCGCCTCGGCGGG    28055        AA    _
                                CCCGCCGAG  GTGGA GC
                                |||||||||  ||||| ||
                                GGGCGGCTC  CGCCT CG
                                     __    T
GAM641  PAX5    5'  CCAGCTCGGCGGGGGA     34124          AAG
                                TCCCCCGCCGAG   TGG
                                ||||||||||||   |||
```

```
                                AGGGGGCGGCTC  ACC
                                      G__
GAM641  PHF1    5'  GCCCTCTCCGCGCGGGGGA  44392       _ A  A T  A
                                TCCCCCGC CG GA G GG GC
                                |||||||| || || | || ||
                                AGGGGGCG GC CT C CC CG
                                     C  _  _ T  _
GAM641  PLA2G10  5'  GCCCAGGTGAGCGGGGGA  14532       _ AGAAG  A
                                TCCCCCGC CG    TGG GC
                                |||||||| ||    ||| ||
                                AGGGGGCG GT    ACC CG
                                     A  GG___  _
GAM641  PYGM    5'  GCTCCACTCCTTGGCTGGAGG  20035   _ C    A
                                CC CC GCCGAG AGTGGAGC
                                || || |||||| ||||||||
                                GG GG CGGTTC TCACCTCG
                                 A  T    C
GAM641  SACM2L  5'  GCTCCACTCCGGGGAACGGA  42884    C__ G  A  A
                                TCC  CC CCG GA GTGGAGC
                                |||  || ||| || |||||||
                                AGG  GG GGC CT CACCTCG
                                  CAA  _  _ _
GAM641  SACM2L  5'  GCTCCACTCCGGGGAACGGA  55456    C__ G  A  A
                                TCC  CC CCG GA GTGGAGC
                                |||  || ||| || |||||||
                                AGG  GG GGC CT CACCTCG
                                  CAA  _  _ _
GAM641  TCF19   3'  GCTCCACTCCACGGGTGGA  99579    _  CCGA  A
                                TCC CCCG   GA GTGGAGC
                                ||| ||||   || |||||||
                                AGG GGGC   CT CACCTCG
                                  T   AC__  _
GAM641  TCF19   3'  GCTCCACTCCACGGGTGGA  99688    _  CCGA  A
                                TCC CCCG   GA GTGGAGC
                                ||| ||||   || |||||||
                                AGG GGGC   CT CACCTCG
                                  T   AC__  _
GAM641  UPF3B   5'  CCGCTTCAGCGGGGGA     55530       CGA
                                TCCCCCGC  GAAGTGG
                                ||||||||  |||||||
                                AGGGGGCG  CTTCGCC
                                     A__
GAM641  UPF3B   5'  CCGCTTCAGCGGGGGA     43730       CGA
                                TCCCCCGC  GAAGTGG
                                ||||||||  |||||||
                                AGGGGGCG  CTTCGCC
                                     A__
GAM641  APCL    3'  GCCTCATCCCCTGGCGGGGGA  20817       AGAA  GA
                                TCCCCCGCCG   GTG  GC
                                ||||||||||   |||  ||
```

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                                AGGGGGCGGT   TAC  CG
                                     CCCC   TC
GAM641  CCR7     3'  GCTCCACTGGGATGGGAGGA  10224    _   _ GAGA
                                TCC CCCG CC   AGTGGAGC
                                ||| |||| ||   ||||||||
                                AGG GGGT GG   TCACCTCG
                                  A   A  G___
GAM641  CDC2L5   5'  GCTCCCGTTTCCGGCGGGGGA 49209        AG  GT
                                TCCCCCGCCG  AA  GGAGC
                                ||||||||||  ||  |||||
                                AGGGGGCGGC  TT  CCTCG
                                     CT  GC
GAM641  CDC2L5   5'  GCTCCCGTTTCCGGCGGGGGA 14940        AG  GT
                                TCCCCCGCCG  AA  GGAGC
                                ||||||||||  ||  |||||
                                AGGGGGCGGC  TT  CCTCG
                                     CT  GC
GAM641  CNNM4    3'  CTCCCTCGGCGGGAGG     39864   _      AAGT
                                CC CCCGCCGAG   GGAG
                                || |||||||||   ||||
                                GG GGGCGGCTC   CCTC
                                 A       _____
GAM641  FLJ10718 3'  GCTCCACTTTGGGTCTGAGGA 37029    CCC_  GA
                                TCC   GCC  GAAGTGGAGC
                                |||   |||  ||||||||||
                                AGG   TGG  TTTCACCTCG
                                  AGTC   G_
GAM641  FLJ10743 3'  GCTCCACTCAGGGGAGG    37085    C  G  GA  A
                                CC CC CC  GA GTGGAGC
                                || || ||  || |||||||
                                GG GG GG  CT CACCTCG
                                 A  _  A_  _
GAM641  FLJ12355 3'  GCTCTCACCGCGGCGGGGGA  47119        AGAA  _
                                TCCCCCGCCG   GTG GAGC
                                ||||||||||   ||| ||||
                                AGGGGGCGGC   CAC CTCG
                                     GC__   T
GAM641  FLJ23447 5'  CTCTCACTCTGCGGGGGA   46131       CG   A  _
                                TCCCCCGC  AGA GTG GAG
                                ||||||||  ||| ||| |||
                                AGGGGGCG  TCT CAC CTC
                                    __   _   T
GAM641  GOLPH3   5'  GCTCGGCGCCTCGGCGGG   42391        AA  G
                                CCCGCCGAG  GT GAGC
                                |||||||||  || ||||
                                GGGCGGCTC  CG CTCG
                                     CG  G
GAM641  HIG2     5'  GCTCTGTTTCTCTGCAGAGGA 26203    CCC  C     TG
                                TCC   GC GAGAAG  GAGC
                                |||   || ||||||  ||||
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                                AGG   CG CTCTTT  CTCG
                                  AGA  T     GT
GAM641  HUMZD58C02 3'  GCTCCTCCCGGCGGGGG     80577         A  AGT
                                CCCCCGCCG GA   GGAGC
                                ||||||||| ||   |||||
                                GGGGGCGGC CT   CCTCG
                                     C  ___
GAM641  KIAA0427  3'  ACTTCTGCCCCGGCGGGGGG   29369         ____
                                TCCCCCGCCG    AGAAGT
                                ||||||||||    ||||||
                                GGGGGGCGGC    TCTTCA
                                      CCCG
GAM641  KIAA0574  3'  GCCCAGCTTGGCGGAGGA    69816     C       AAG   A
                                TCC CCGCCGAG   TGG GC
                                ||| ||||||||   ||| ||
                                AGG GGCGGTTC   ACC CG
                                  A       G__   _
GAM641  KIAA0987  3'  GCTTCTTACTCGGCGGGAGA   25509    C       AAGT
                                TC CCCGCCGAG    GGAGC
                                || |||||||||    |||||
                                AG GGGCGGCTC    CTTCG
                                 A        ATT_
GAM641  KIAA1274  3'  GCTCCACTTGTCTGGG      93011      CC  G
                                CCCG  GA AAGTGGAGC
                                ||||  || |||||||||
                                GGGT  CT TTCACCTCG
                                  __  G
GAM641  KIAA1465  3'  GCCCCTGCTTCGGCGGG     61499         A_  T  A
                                CCCGCCGAG  AG GG GC
                                |||||||||  || || ||
                                GGGCGGCTT  TC CC CG
                                     CG  _  _
GAM641  KIAA1677  3'  GCTCCACTTATCTGGG      67665      CC  G
                                CCCG  GA AAGTGGAGC
                                ||||  || |||||||||
                                GGGT  CT TTCACCTCG
                                  __  A
GAM641  KIAA1940  3'  GCTGGTCCTGGCGGGGGA    80788         A  AGTGG
                                TCCCCCGCCG GA     AGC
                                |||||||||| ||     |||
                                AGGGGGCGGT CT     TCG
                                     C  GG___
GAM641  MGC7036   5'  GCTCCGAGGTCGGCGGGGG   59618         GAAG
                                CCCCCGCCGA    TGGAGC
                                ||||||||||    ||||||
                                GGGGGCGGCT    GCCTCG
                                      GGA_
GAM641  MMP24     3'  GCTCCACTCCTGGCTGG     22920    C   G  A
                                CC GCC AG AGTGGAGC
                                || ||| || ||||||||
```

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                                GG CGG TC TCACCTCG
                                 T  _ C
GAM641  MRPS14   3' GCTCCACTTCTTCTTGTG   42291    C__
                                CGC  GAGAAGTGGAGC
                                |||  ||||||||||||
                                GTG  TTCTTCACCTCG
                                  TTC
GAM641  NMA      5' GCTCCGGAAGCCGGCGGGGG  25627       AGAAG
                                CCCCCGCCG   TGGAGC
                                |||||||||   ||||||
                                GGGGGCGGC   GCCTCG
                                     CGAAG
GAM641  PRO1866  5' GCTCCACTATTGAAAAAGGGA 38148    CCGC_  GA
                                TCCC   CGA  AGTGGAGC
                                ||||   |||  ||||||||
                                AGGG   GTT  TCACCTCG
                                  AAAAA  A_
GAM641  RAI16    3' CATTCCTCCCCGCGGGGGA   43044      C__  A
                                TCCCCCGC   GAG AGTG
                                ||||||||   ||| ||||
                                AGGGGGCG   CTC TTAC
                                     CCC   C
GAM641  RGS7     5' CCGTGACCTTGGCGGAGGA   12863    C      AA_
                                TCC CCGCCGAG   GTGG
                                ||| ||||||||   ||||
                                AGG GGCGGTTC   TGCC
                                  A       CAG
GAM641  SKD3     3' GCTCCACTGGGAGTGGAGGA  48727    C   CGAGA
                                TCC CCGC    AGTGGAGC
                                ||| ||||    ||||||||
                                AGG GGTG    TCACCTCG
                                  A   AGGG_
GAM641  WSB1     3' CTCTGTTTCTGCAGGGGA    56974     C  CG    TG
                                TCCCC GC  AGAAG  GAG
                                ||||| ||  |||||  |||
                                AGGGG CG  TCTTT  CTC
                                   A __    GT
GAM641  WSB1     3' CTCTGTTTCTGCAGGGGA    56991     C  CG    TG
                                TCCCC GC  AGAAG  GAG
                                ||||| ||  |||||  |||
                                AGGGG CG  TCTTT  CTC
                                   A __    GT
GAM641  LOC130026 5' TTCCCTCGGCGGTGGA     57442    C      AAGT
                                TCC CCGCCGAG   GGAG
                                ||| ||||||||   ||||
                                AGG GGCGGCTC   CCTT
                                  T      ____
GAM641  LOC135892 3' GCCCATCCCGGCGGGG     75761       A  AG   A
                                CCCCGCCG GA  TGG GC
                                |||||||| ||  ||| ||
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                                GGGGCGGC CT  ACC CG
                                    C  __  _
GAM641  LOC149351 5'  GCTCCGCTCCCCGGCGGG    80085       AGA
                                CCCGCCG  AGTGGAGC
                                |||||||  ||||||||
                                GGGCGGC  TCGCCTCG
                                   CCC
GAM641  LOC155066 3'  GCTCCGGCCCAGGCGGGGGA  82209        GAGAAG
                                TCCCCCGCC    TGGAGC
                                |||||||||    ||||||
                                AGGGGGCGG    GCCTCG
                                     ACCCG_
GAM641  LOC158314 3'  GCTCCACTTCCGAGGAGGA   88097    C  GC  A
                                TCC CC  CG GAAGTGGAGC
                                ||| ||  || ||||||||||
                                AGG GG  GC CTTCACCTCG
                                  A  A_  _
GAM641  LOC199848 5'  TCCCTTCCCCGGCGGGGGA   91454        A_   T
                                TCCCCCGCCG  GAAG GGA
                                ||||||||||  |||| |||
                                AGGGGGCGGC  CTTC CCT
                                     CC   _
GAM641  LOC201706 3'  GCCCCACTTCTGGCTGGG    91084    C  G      A
                                CCC GCC AGAAGTGG GC
                                ||| ||| |||||||| ||
                                GGG CGG TCTTCACC CG
                                  T  _      C
GAM641  LOC253868 5'  CCAGCACCTCAGTGGGGGA   97318       C  AA _
                                TCCCCCGC GAG  G TGG
                                |||||||| |||  | |||
                                AGGGGGTG CTC  C ACC
                                    A  CA G
GAM641  LOC253955 5'  GCCCACCCCTGCGGGGGA    96074       CG  AA   A
                                TCCCCCGC  AG  GTGG GC
                                ||||||||  ||  |||| ||
                                AGGGGGCG  TC  CACC CG
                                    __  CC   _
GAM641  LOC254826 5'  GCTCTGCGCCTCAGCGGGGGA  99051       C  AA TG
                                TCCCCCGC GAG  G  GAGC
                                |||||||| |||  |  ||||
                                AGGGGGCG CTC  C  CTCG
                                    A  CG GT
GAM641  LOC256686 3'  CTCCACTTGGCTCCAGGGGG   98628     GCC  __
                                CCCCC  GAG  AAGTGGAG
                                |||||  |||  ||||||||
                                GGGGG  CTC  TTCACCTC
                                  AC_  GG
GAM641  LOC91179  3'  GCTCCTCCCGGCGGGGG     65766       A  AGT
                                CCCCCGCCG GA  GGAGC
                                ||||||||| ||  |||||
```

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                                GGGGGCGGC CT   CCTCG
                                     C ___
GAM641  LOC91301  5'  GCCCCAGCTGCTGGCGGGGGA  66148        G  A  _   A
                                TCCCCCGCC AG AG TGG GC
                                ||||||||| || || ||| ||
                                AGGGGGCGG TC TC ACC CG
                                     _ G  G   C
GAM642  ABCC3     3'  TCCAGTGCTCAGAGGGCGGGG  39617        GTT_  CCAG
                                TCTCGCTCT   GC   GCTGGA
                                |||||||||   ||   ||||||
                                GGGGCGGGA   CG   TGACCT
                                     GACT  ____
GAM642  ABCC3     3'  TCCAGTGCTCAGAGGGCGGGG  39618        GTT_  CCAG
                                TCTCGCTCT   GC   GCTGGA
                                |||||||||   ||   ||||||
                                GGGGCGGGA   CG   TGACCT
                                     GACT  ____
GAM642  ACK1      3'  GCCTGGGTGACAGACTGGGA  20515      C    TG    _
                                TCTCG TCTGT  CCCAGG C
                                ||||| |||||  |||||| |
                                AGGGT AGACA  GGGTCC G
                                   C    GT    C
GAM642  ACP5      3'  TCCGGGGTGCAATGGGGGAGG  9658       G       _  AGG
                                TCTC CTCTGTTGC CC   CTGGA
                                |||| ||||||||| ||   |||||
                                GGAG GGGGTAACG GG   GGCCT
                                  _        T  ___
GAM642  ADAM12    3'  TTTAGCTTGGGAAAGGTGG    14428      T  GTTG
                                TCGC CT    CCCAGGCTGGA
                                ||||  ||    ||||||||||
                                GGTG GA    GGGTTCGATTT
                                  _  AA__
GAM642  ADAM17    3'  ACTCCAGCCTGGGTGACAGAGT 41841          TG
          GAGA                    TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      GT          CAC
GAM642  ADAM17    3'  CTCCAGCCTGGGTGACAGAGTG 41845          TG
          AGA                     TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      GT          CA
GAM642  ADAT1     3'  TCCAGCCTGGGTGATAGAGCAA 24919     C      TG
          GA                      TCT GCTCTGT  CCCAGGCTGGA
                                |||  |||||||  ||||||||||
                                AGA CGAGATA  GGGTCCGACCT
                                  A      GT
GAM642  ADCY1     3'  TCTGGGGTGCACATGGGGTGGG 94341          _   _  AGG TG
          A                       TCTCGCTCTGT TGC CC   C  GA
                                ||||||||||| ||| ||   |  ||
```

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                                AGGGTGGGGTA ACG GG   G  CT
                                      C   T  ___ GT
GAM642  ADCY2    3'  ACTCCAGCCTGGGTGACAGAGC 65642          TG
           GAGA                   TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      GT         CAC
GAM642  ADCY6    3'  TCCAGCCTTTGGGAGCAGGGGA 40964      G      G   __
           GG                   TCTC CTCTGTT CCCA  GGCTGGA
                                |||| ||||||| ||||  |||||||
                                GGAG GGGACGA GGGT  CCGACCT
                                  _      _   TT
GAM642  AF5Q31   5'  TCGGGCCTAGCGGAGCCGGG  27779     C       GCCC     G
                                TCT GCTCTGTT    AGGCT GA
                                ||| ||||||||    ||||| ||
                                GGG CGAGGCGA    TCCGG CT
                                  C        ____     G
GAM642  AICDA    3'  TCCAGCCTGGGCGACAAGAGC  40698      _
                                GCTCT GTTGCCCAGGCTGGA
                                ||||| ||||||||||||||||
                                CGAGA CAGCGGGTCCGACCT
                                   A
GAM642  AIRE     3'  TCCAGTCTGGTCGGCAAGAGTG 7246          _   C
           AGA                   TCTCGCTCT GTTG CCAGGCTGGA
                                |||||||||  |||| ||||||||||
                                AGAGTGAGA CGGC GGTCTGACCT
                                      A   T
GAM642  AK1      3'  TCCAGCCTGGGTGACAGAGCAA 6641      C      TG
           GA                    TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM642  AKAP13   3'  TCTGGCCCTTGCTGGGTGAGG  91255         T  TGCCCA   TG
                                TCTCGCTC GT     GGC  GA
                                |||||||| ||     |||  ||
                                GGAGTGGG CG     CCG  CT
                                      T  TTC___   GT
GAM642  ALDH3A2  3'  TTCAGCTTGGGCAACAGAGCAA 69804     C
           GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGAGACAACGGGTTCGACTT
                                  A
GAM642  ALDH3B1  3'  TCCGGCCTGGGTGACAGAAGGA 93162      GC     TG
           GG                    TCTC  TCTGT  CCCAGGCTGGA
                                ||||  |||||  ||||||||||||
                                GGAG  AGACA  GGGTCCGGCCT
                                  GA    GT
GAM642  ALDH8A1  3'  TTCAGCCTGGGGGATACAGTGA 42917         C   G
           GA                    TCTCGCT TGTT CCCAGGCTGGA
                                |||||||  ||||  ||||||||||||
```

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                                AGAGTGA ATAG GGGTCCGACTT
                                    C   G
GAM642  ALPP    3'  ACTGCAGCCTGGGCGACAGAGC 69403                GA
            GAGA                TCTCGCTCTGTTGCCCAGGCTG
                                ||||||||||||||||||||
                                AGAGCGAGACAGCGGGTCCGAC
                                          GTCAC
GAM642  AMN     3'  TCCGGTGAGGGGAGGGTGAGG  48922        GTTG  AG
                                TCTCGCTCT   CCC  GCTGGA
                                |||||||||   |||  ||||||
                                GGAGTGGGA   GGG  TGGCCT
                                    G___   AG
GAM642  ANKH    3'  TCCAGCCTGGGTGACAAGAGC  55074      _  TG
                                GCTCT GT  CCCAGGCTGGA
                                |||||  ||  ||||||||||
                                CGAGA CA  GGGTCCGACCT
                                   A  GT
GAM642  AP1S1   3'  CCTGGCAGCGTGGCGGGA    55105       C     C
                                TCTCGCT TGTTGCC AGG
                                ||||||| ||||||| |||
                                AGGGCGG GCGACGG TCC
                                    T     _
GAM642  APAF1   3'  TCCAGCCTGGGTGACATAGCAA 25984    C  C  TG
            GA                    TCT GCT TGT  CCCAGGCTGGA
                                ||| ||| |||  ||||||||||
                                AGA CGA ACA  GGGTCCGACCT
                                  A  T  GT
GAM642  APOC4   3'  AGACCAGCCTGGGCAACACAGC 9704        C          A
            GAGA                TCTCGCT TGTTGCCCAGGCTGG
                                ||||||| ||||||||||||||
                                AGAGCGA ACAACGGGTCCGACC
                                    C           AGAG
GAM642  APOL1   3'  ACTCCAGCCTGGGTGACAGAGC 14721          TG
            GAGA                TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      GT         CAC
GAM642  ARF4L   3'  ATTTGGTGCCACACTGGGGTGG 70387         ___  T  _    CTGGA
            GG                  TCTCGCTCT   GT GC CCAGG
                                |||||||||   || || |||||
                                GGGGTGGGG   CA CG GGTTT
                                     TCA  C  T       AG
GAM642  ARF4L   3'  GCACACTTGGACAGCAGGGTGG 70388           C    C  GA
            GA                  TCTCGCTCTGTTG CCAGG TG
                                ||||||||||||| ||||| ||
                                AGGGTGGGACGAC GGTTC AC
                                       A    _  ACGT
GAM642  ARHGEF12 3'  TTCGGATAGTGGCAGGGGTGGG 31651         GT   CAGG_
            G                    TCTCGCTCT  TGCC    CTGGA
                                |||||||||  ||||    |||||
```

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                                GGGGTGGGG  ACGG    GGCTT
                                     __    TGATA
GAM642  ARSD    3'  AGACCAGCCTGGGCAACATAGT 9797        C           A
            GAGA                  TCTCGCT TGTTGCCCAGGCTGG
                                  ||||||| ||||||||||||||
                                  AGAGTGA ACAACGGGTCCGACC
                                      T           AGAA
GAM642  ARSD    3'  TCCAGCCTGGGCCACATAGCAA 9800     C  C  T
            GA                    TCT GCT TGT GCCCAGGCTGGA
                                  ||| ||| ||| ||||||||||||
                                  AGA CGA ACA CGGGTCCGACCT
                                    A  T  C
GAM642  ASC     5'  TTTGCTGGAGGGCAACGGACCG 26070      C       A__  TGGA
            GGG                   TCTCG TCTGTTGCCC  GGC
                                  ||||| ||||||||||  |||
                                  GGGGC AGGCAACGGG  TCG
                                     C        AGG  TTT
GAM642  ASIC4   3'  TTCGGCTGAGCTTGGAGGGTGG 38542        GTT_  CCA
            GA                    TCTCGCTCT   GC  GGCTGGA
                                  |||||||||   ||  |||||||
                                  AGGGTGGGA   CG  TCGGCTT
                                       GGTT  AG_
GAM642  ASS     3'  CCGGCTGGCAGCGTAGTGGGG  5281       C     CA    A
                                  TCTCGCT TGTTGCC  GGCTGG
                                  ||||||| |||||||  ||||||
                                  GGGGTGA GCGACGG  TCGGCC
                                      T     __
GAM642  ASS     3'  CCGGCTGGCAGCGTAGTGGGG  5281       C     CA    A
                                  TCTCGCT TGTTGCC  GGCTGG
                                  ||||||| |||||||  ||||||
                                  GGGGTGA GCGACGG  TCGGCC
                                      T     __     C
GAM642  ATM     3'  TCCAGCCTGGGAGACAGAGCGA 5303          TG
            GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GA
GAM642  ATM     3'  TCCAGCCTGGGTGACAAGAGCG 5304       _  TG
            A                      TCGCTCT GT  CCCAGGCTGGA
                                  ||||||| ||  ||||||||||
                                  AGCGAGA CA  GGGTCCGACCT
                                      A  GT
GAM642  ATP1A2  3'  TCCAGCCTGGGCGAAAGGGTGA 7369         G
            GA                    TCTCGCTCT TTGCCCAGGCTGGA
                                  ||||||||| ||||||||||||||
                                  AGAGTGGGA AGCGGGTCCGACCT
                                       A
GAM642  ATP6V0E 5'  TCCGAGTGAGGCGACGGGGTAG 15461    CG       CAG  _
            GG                    TCT  CTCTGTTGCC   GCT GGA
                                  |||  ||||||||||   ||| |||
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                                GGG  GGGGCAGCGG   TGA CCT
                                  AT         AG_   G
GAM642  ATP8B2   3'  TTTGGTCAGTGGGGAGGGG   65851      G   TG   C
                                TCTC CTC  TTG CCAGG
                                |||| |||  ||| |||||
                                GGGG GGG  GAC GGTTT
                                  A   GT   T
GAM642  BAK1     3'  CTGGGCTTGGGGTGTGGGGTGG 93629         TG TG       GGA
           GG                     TCTCGCTC  T  CCCAGGCT
                                |||||||| |  ||||||||
                                GGGGTGGG  G  GGGTTCGG
                                    GT TG       GTCT
GAM642  BAK1     3'  TTCAGCCAAATGCAGGGAGGGG 93636      G     TGCCCA
                                TCTC CTCTGT     GGCTGGA
                                |||| ||||||     |||||||
                                GGGG GGGACG     CCGACTT
                                  A     TAAA__
GAM642  BCAS1    3'  TCCACCCTGGGCGACAGAGCAA 14715     C            C
           GA                     TCT GCTCTGTTGCCCAGG TGGA
                                ||| |||||||||||||| ||||
                                AGA CGAGACAGCGGGTCC ACCT
                                  A            C
GAM642  BCL2     5'  TCGGGGGCCGTGGGGTGGGA   7242          TG T    AGG TG
                                TCTCGCTC  T GCCC   C  GA
                                |||||||| | ||||  |  ||
                                AGGGTGGG  G CGGG   G  CT
                                    GT C   ___ GT
GAM642  BCL7A    3'  CTGGGGGTGGGGTGGGG     40982         TG  G
                                TCTCGCTC  TT CCCAG
                                |||||||| || |||||
                                GGGGTGGG  GG GGGTC
                                    GT  _
GAM642  BCL7A    3'  TTCAGCTTCGAGCCAGGGGGCG 40997         GTT  CC_
           GGG                    TCTCGCTCT   GC   AGGCTGGA
                                |||||||||  ||  ||||||||
                                GGGGCGGGG   CG   TTCGACTT
                                    GAC  AGC
GAM642  BHMT2    3'  CTTCAGCCTGGGTGACAGAGTG 34733          TG
           AGA                    TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACTT
                                    GT         CA
GAM642  BPHL     3'  TCCAACCTGGGCAACAGAGTAA 16336     CG          C
           GA                     TCT  CTCTGTTGCCCAGG TGGA
                                |||  |||||||||||||| ||||
                                AGA  GAGACAACGGGTCC ACCT
                                  AT           A
GAM642  BRCA1    5'  CTCCAGCCTGGGCGACAGAGCG 24555
           AGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||||
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                                AGAGCGAGACAGCGGGTCCGACCT
                                      CA
GAM642  BRCA1    3'  TCCAGCCTGGGTGACAGTGAGA 24577       CT  TG
                                TCTCGCT  GT  CCCAGGCTGGA
                                |||||||  ||  ||||||||||
                                AGAGTGA  CA  GGGTCCGACCT
                                   __  GT
GAM642  BRCA1    3'  TCCAGCCTGGGTGACAGTGAGA 24578       CT  TG
                                TCTCGCT  GT  CCCAGGCTGGA
                                |||||||  ||  ||||||||||
                                AGAGTGA  CA  GGGTCCGACCT
                                   __  GT
GAM642  BRCA1    3'  TCCAGCCTGGGTGACAGTGAGA 24579       CT  TG
                                TCTCGCT  GT  CCCAGGCTGGA
                                |||||||  ||  ||||||||||
                                AGAGTGA  CA  GGGTCCGACCT
                                   __  GT
GAM642  BRCA1    3'  TCCAGCCTGGGTGACAGTGAGA 24580       CT  TG
                                TCTCGCT  GT  CCCAGGCTGGA
                                |||||||  ||  ||||||||||
                                AGAGTGA  CA  GGGTCCGACCT
                                   __  GT
GAM642  C1orf1   3'  TCCAGCCTAGGCGACAGAGTGA 8683             C
           GA                    TCTCGCTCTGTTGCC AGGCTGGA
                                 ||||||||||||||| ||||||||
                                 AGAGTGAGACAGCGG TCCGACCT
                                       A
GAM642  C5R1     3'  TCTAGCCTGGGTGACCGAGGGA 9977      G   T  TG
           GG                    TCTC CTC GT  CCCAGGCTGGA
                                 ||||  ||| ||  ||||||||||
                                 GGAG GAG CA  GGGTCCGATCT
                                   G   C  GT
GAM642  C8orf1   3'  CTGGGGGTGGGGTGAGG     16345         TG  G
                                TCTCGCTC  TT CCCAG
                                ||||||||  || |||||
                                GGAGTGGG  GG GGGTC
                                     GT  _
GAM642  CA12     3'  ACTCTAGCCTGGGTGACAGAGC 8686           TG
           GAGA                    TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   AGAGCGAGACA  GGGTCCGATCT
                                         GT         CAC
GAM642  CACNA1D  3'  TCTGGCCTCAGGTGGGGCGCAG 7404     _     GTT   C_   TG
           G                     TCT CGCTCT   GCC  AGGC  GA
                                 |||  ||||||   |||  ||||  ||
                                 GGA GCGGGG   TGG  TCCG  CT
                                   C     ___   AC   GT
GAM642  CACNA2D2 3'  TCTGGTCTGCGCCTTGGGATGG 21225      CT   TT  C    TG
           GG                    TCTCG  CTG  GC CAGGC  GA
                                 |||||  |||  || |||||  ||
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                                GGGGT  GGT  CG GTCTG  CT
                                  AG   TC  C    GT
GAM642  CAPN11   3'  CTAGCCCAGGAGGGTGGGG   23912        G   CCCA
                                TCTCGCTCT TTG   GGCTGG
                                ||||||||| |||   ||||||
                                GGGGTGGGA GAC   CCGATC
                                    G  ____
GAM642  CARKL    3'  TCCAGCCTGGGTGACAGAGCAA 26109     C      TG
           GA                     TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM642  CASP10   3'  ACTCCAGCTTGGGCAACAGGGC 53195
           GAGA                     TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||||
                                AGAGCGGGACAACGGGTTCGACCT
                                          CAC
GAM642  CASP10   3'  CTCCAGCTTGGGCAACAGGGCG 53257
           AGA                      TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||||
                                AGAGCGGGACAACGGGTTCGACCT
                                          CA
GAM642  CASP3    3'  TTTAGTTTGTATGCCAAGTGAG 53357        C  TT CC
           A                     TCTCGCT TG  G  CAGGCTGGA
                                ||||||| ||  |  |||||||||
                                AGAGTGA AC  T  GTTTGATTT
                                    _  CG AT
GAM642  CASP6    3'  TCCAGCCTGGGCAACGAGTGA  53366       T
                                TCGCTC GTTGCCCAGGCTGGA
                                ||||||| ||||||||||||||
                                AGTGAG CAACGGGTCCGACCT
                                   _
GAM642  CASP8    3'  TCAAGCTTGGGTGACAGAGCAA 54084     C      TG       G
           GA                     TCT GCTCTGT  CCCAGGCT GA
                                ||| |||||||  |||||||| ||
                                AGA CGAGACA  GGGTTCGA CT
                                  A      GT       A
GAM642  CASP8    3'  TCAAGCTTGGGTGACAGAGCAA 8767      C      TG       G
           GA                     TCT GCTCTGT  CCCAGGCT GA
                                ||| |||||||  |||||||| ||
                                AGA CGAGACA  GGGTTCGA CT
                                  A      GT       A
GAM642  CCND1    3'  TCTGTCGTGATGGGGCAAGG   54961     C      TG C_
                                TCT GCTCTGT  C  CAGG
                                ||| |||||||  |  ||||
                                GGA CGGGGTA  G  GTCT
                                  A      GT CT
GAM642  CCNF     3'  GCCACCCTGGGTGGGGTGTGG  10078    T     GTT      C   A
                                TC CGCTCT   GCCCAGG TGG
                                || ||||||   ||||||| |||
```

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                                GG GTGGGG   TGGGTCC ACC
                                 T     ___      C   GG
GAM642   CD28     3'  TCCAGCCTGGGCGACAGAGTGA 21557
                GA                 TCTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGTGAGACAGCGGGTCCGACCT

GAM642   CD68     3'  TCCAGCCTGGGCGACAGAGCCA 60508     C
                GA                 TCT GCTCTGTTGCCCAGGCTGGA
                                   ||| ||||||||||||||||||||
                                   AGA CGAGACAGCGGGTCCGACCT
                                     C
GAM642   CD8A     3'  TTTAGTGGGGGCGGGGTGGGA  10098         GTT    AG
                                   TCTCGCTCT   GCCC  GCTGGA
                                   |||||||||   ||||  ||||||
                                   AGGGTGGGG   CGGG  TGATTT
                                         ___    GG
GAM642   CD97     3'  TCCAGGACACCCAGTGGGGTGG 10124    T    TG   CCCAGG
                A                   TC CGCTC  TTG     CTGGA
                                   || |||||  |||     |||||
                                   AG GTGGG  GAC     GACCT
                                    _    GT   CCACAG
GAM642   CDC23    3'  TTCAGCCTTTATCTAGATGAGG 17410      C    TTGCCC
                                   TCTCG TCTG     AGGCTGGA
                                   ||||| ||||     ||||||||
                                   GGAGT AGAT     TCCGACTT
                                      _    CTATT_
GAM642   CDC42    3'  GCTGGGGGGTAGGGTGGGG    10140         GTT    A_
                                   TCTCGCTCT   GCCC  GGC
                                   |||||||||   ||||  |||
                                   GGGGTGGGA   TGGG  TCG
                                         ___    GG
GAM642   CDC6     5'  TCTGTGAGGCAGCGGAGCTGGG 8829      C         ___
                                   TCT GCTCTGTTGCC   CAGG
                                   ||| ||||||||||   ||||
                                   GGG CGAGGCGACGG   GTCT
                                     T          AGT
GAM642   CDH2     3'  TGGTTTGGGGAGGGAGA     10146      G   TGTTG      TG
                                   TCTC CTC     CCCAGGC  G
                                   |||| |||     |||||||  |
                                   AGAG GAG     GGGTTTG  T
                                     G   _____       GT
GAM642   CDK2     3'  TTCAGGGCTGTGATTGAGTGAG 10155         T   ___    AGGCTGGA
                G                   TCTCGCTC GTT   GCCC
                                   ||||||||| |||   ||||
                                   GGAGTGAG TAG   CGGG
                                        T   TGT    ACTT
GAM642   CDK5R2   3'  GATTTGCTGGGCGTGGAGTGGG 15448         TG T      GCTGGA
                G                   TCTCGCTC  T GCCCAG
                                   ||||||||  | ||||||
```

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                                GGGGTGAG  G CGGGTC
                                    GT _     GTTTAGG
GAM642  CDKN1A   3'  CTAGCTGTGGGGGTGAGG    55267       CTGTTG   _
                                TCTCGCT     CCCA GGCTGG
                                |||||||     |||| ||||||
                                GGAGTGG     GGGT TCGATC
                                    _______   G
GAM642  CDKN2D   3'  TCAGGCATGGGGGGGTGGGG   10160       TGTTG   G _
                                TCTCGCTC    CCCA GC TGG
                                ||||||||    |||| || |||
                                GGGGTGGG    GGGT CG ACT
                                    ______   A  G
GAM642  CEACAM1  3'  TCTAGGGTAGAGGGGTGGGG  9931         G    _
                                TCTCGCTCT TTGCCC AGG
                                ||||||||| |||||| |||
                                GGGGTGGGG GATGGG TCT
                                     A     A
GAM642  CELSR2   3'  GCTGTGATGTGGGTGGGG    9195        _  TG CCA
                                TCTCGCTC TGT  C   GGC
                                |||||||| |||  |   |||
                                GGGGTGGG GTA  G   TCG
                                    T   GT ___
GAM642  CELSR3   3'  CCGAAGGGTAGGGTGGGA    9185        GTT   AGGC
                                TCTCGCTCT   GCCC   TGG
                                |||||||||   ||||   |||
                                AGGGTGGGA   TGGG   GCC
                                    ___   AA__
GAM642  CENTD2   3'  TCCAGTCTGGGCTGAGTGGGG  58275       TGTT
                                TCTCGCTC   GCCCAGGCTGGA
                                ||||||||   ||||||||||||
                                GGGGTGAG   CGGGTCTGACCT
                                    T___
GAM642  CHES1    5'  TTCGGCACGAGCGGCGGCGGGG 19027       CT    CCAG
                                TCTCGCT  GTTGC   GCTGGA
                                |||||||  |||||   ||||||
                                GGGGCGG  CGGCG   CGGCTT
                                    __    AGCA
GAM642  CHRNA4   3'  TCCAGCCAGGGGTGGGGATGGG 7439      _   GTT   A_
          G                      TCTCG CTCT   GCCC  GGCTGGA
                                |||||  ||||   ||||  |||||||
                                GGGGT GGGG   TGGG  CCGACCT
                                   A   ___   GA
GAM642  CHRNB4   3'  CCTGGGTTGTGGGGTGAGA   7448        TG T
                                TCTCGCTC  T GCCCAGG
                                ||||||||  | |||||||
                                AGAGTGGG  G TGGGTCC
                                    GT T
GAM642  CLASP1   3'  TTTGGGGGTGGGGTGGGG    65899       TG  G
                                TCTCGCTC  TT CCCAGG
                                ||||||||  || ||||||
```

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                                GGGGTGGG  GG GGGTTT
                                    GT  _
GAM642  CNGB1    3'  CTGGGCAACATAGCGAGA    8934        C
                                TCTCGCT TGTTGCCCAG
                                ||||||| ||||||||||
                                AGAGCGA ACAACGGGTC
                                    T
GAM642  COL5A1   5'  GCGGGGCGGCGGCGGCGAGG  5409        _       AG
                                TCTCGCT CTGTTGCCC  GC
                                ||||||| |||||||||  ||
                                GGAGCGG GGCGGCGGG  CG
                                    C       G_
GAM642  COPA     3'  TCCAGCCTGGGTGACAGAGCAA 16480     C      TG
            GA                    TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM642  CPM      3'  TCCAGCTTGGGCAACAGAGTAA 60411     CG
            GA                    TCT  CTCTGTTGCCCAGGCTGGA
                                |||  ||||||||||||||||||
                                AGA  GAGACAACGGGTTCGACCT
                                  AT
GAM642  CPO      5'  CCAGGTGATAGTGCGGGA    5415        T    TG  CAGGC
                                TCTCGC CTGT  CC     TGG
                                |||||| ||||  ||     |||
                                AGGGCG GATA  GG     ACC
                                    T    GT  _____
GAM642  CPT2     3'  ACTCCGGCCTGGGCGACAGAGC 5418
            GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGCGAGACAGCGGGTCCGGCCT
                                              CAC
GAM642  CREBBP   3'  ATTTGGTTTTTTTTTGGCGGGG 16494         G    C_____    TG
            GGGTGGGG                TCTCGCTCT TTGCC     AGGC  GA   T
                                ||||||||| |||||     ||||  ||   |
                                GGGGTGGGG GGCGG     TTTG  TT   A
                                      G    TTTTTT    GT
GAM642  CREBL1   3'  TCAGTTGTGGGGTGGGTG    16499       TGTTG   _
                                CGCTC     CCCA GGCTGG
                                |||||     |||| ||||||
                                GTGGG     GGGT TTGACT
                                   TG___    G
GAM642  CRMP1    3'  TTTAGTTGGTGCTGATGGAGGG 8973       G      _ _   G
            AGG                   TCTC CTCTGTT GC CCAG CTGGA
                                |||| ||||||| || |||| |||||
                                GGAG GAGGTAG CG GGTT GATTT
                                  G      T  T   _
GAM642  CROT     3'  AGACCAGCCTGGGCAACAGGGT 41255     CG              A
            AAGG                    TCT  CTCTGTTGCCCAGGCTGG
                                |||  |||||||||||||||||
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                                GGA  GGGACAACGGGTCCGACC
                                  AT               AGAG
GAM642  CRY2     3'  CCAGGAGCAGTAGGTGGGA   72660       T      _  AGGC
                                TCTCGC CTGTTGC CC    TGG
                                |||||| ||||||| ||    |||
                                AGGGTG GATGACG GG    ACC
                                   _       A  ____
GAM642  CSNK1D   5'  TCCATCCGCGGCGGGGAGAGG  58172      G        CCA  C
                                TCTC CTCTGTTGC   GG TGGA
                                |||| |||||||||   || ||||
                                GGAG GGGGCGGCG   CC ACCT
                                  A        ___  T
GAM642  CTSS     3'  TCCAGCCTGGATGACAGAGTGG 15822    T        GC
                A                TC CGCTCTGTT  CCAGGCTGGA
                                || |||||||||  ||||||||||
                                AG GTGAGACAG  GGTCCGACCT
                                 _        TA
GAM642  CUBN     3'  TCCAGCCTGGGCGAGACGGCAA 8425      C   CTG
                GA                 TCT GCT   TTGCCCAGGCTGGA
                                ||| |||   ||||||||||||||
                                AGA CGG   AGCGGGTCCGACCT
                                  A   CAG
GAM642  CYP26A1   5'  TTGGGCCGGGGCAGCGGGTGGG 7600        T        A    G
                A                TCTCGC CTGTTGCCC GGCT GA
                                |||||| ||||||||| |||| ||
                                AGGGTG GGCGACGGG CCGG TT
                                   _        G   G
GAM642  CYP2A6   3'  TCTGGTGGGCGGGGCCAGG   7536      C       GC
                                TCT GCTCTGTT  CCAGG
                                ||| ||||||||  |||||
                                GGA CGGGGCGG  GGTCT
                                  C        GT
GAM642  CYP3A4   3'  TCCAGTCTGGGTGAGAGTGAGA 34366         TG TG
                                TCTCGCTC  T  CCCAGGCTGGA
                                |||||||  |  ||||||||||
                                AGAGTGAG  A  GGGTCTGACCT
                                     __ GT
GAM642  CYP4F3   3'  CCAGCCTGGGGGAGGGGGA   8001       G   GTTG
                                TCTC CTCT    CCCAGGCTGG
                                |||| ||||    ||||||||||
                                AGGG GAGG    GGGTCCGACC
                                  G   ____
GAM642  CYP4F3   3'  TCCAGCCTGGGTGAAAGAGCTA 8015      C     G TG
                GA                 TCT GCTCT T  CCCAGGCTGGA
                                ||| ||||| |  ||||||||||
                                AGA CGAGA A  GGGTCCGACCT
                                  T     A GT
GAM642  CYP4F3   3'  TCTGTGAGTGGAAGAGTGGGG  8016          G TG C__
                                TCTCGCTCT T  C   CAGG
                                |||||||| |  |   ||||
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                                GGGGTGAGA G  G   GTCT
                                     A GT AGT
GAM642  DAPP1    3'  TCTAGCCTGGGTGACAGAGTCA 27683     C      TG
            GA                    TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA TGAGACA  GGGTCCGATCT
                                    C      GT
GAM642  DBN1     5'  TCCGGGCGGGGACGGGGCGGGG 16561           G   AGG
                                  TCTCGCTCTGTT CCC   CTGGA
                                  |||||||||||| |||   |||||
                                  GGGGCGGGGCAG GGG   GGCCT
                                        _   CG_
GAM642  DBT      3'  AGACCAGCCTGGGCAACATAGT 10362        C           A
            GAGA                     TCTCGCT TGTTGCCCAGGCTGG
                                  ||||||| ||||||||||||||||
                                  AGAGTGA ACAACGGGTCCGACC
                                     T             AGAG
GAM642  DBT      3'  TCCAGCCTGGGCGACAGAGCAA 10379     C
            GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM642  DBT      3'  TCCAGCCTGGGTGGCAGAGC   10380        TG
                                  GCTCTGT  CCCAGGCTGGA
                                  |||||||  ||||||||||
                                  CGAGACG  GGGTCCGACCT
                                     GT
GAM642  DBT      3'  TCCAGTATGGGTGACAGAGTGA 10382           TG   G
            GA                    TCTCGCTCTGT  CCCA GCTGGA
                                  ||||||||||  |||| ||||||
                                  AGAGTGAGACA  GGGT TGACCT
                                        GT   A
GAM642  DCLRE1C  3'  TCTAGTCTGGGTGACAGAGCAA 42824     C      TG
            GA                    TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCTGATCT
                                    A      GT
GAM642  DCLRE1C  3'  TCCAGCCTGGGCAACAAGAGC  42822       _
                                  GCTCT GTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||||
                                  CGAGA CAACGGGTCCGACCT
                                     A
GAM642  DCTN1    5'  CCTCAGGCAGCAGAGGGGA   15828      G        C_
                                  TCTC CTCTGTTGCC  AGG
                                  |||| ||||||||||  |||
                                  AGGG GAGACGACGG  TCC
                                    _         AC
GAM642  DDEF1    3'  TCTTGGCAATGAGTGAGA    60307         T     C
                                  TCTCGCTC GTTGCC AGG
                                  |||||||| |||||| |||
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```
                                AGAGTGAG TAACGG TCT
                                   _     T
GAM642  DDOST    3'  TCCAGCCTGGGCAACAGTGT   19066    T
                                GC CTGTTGCCCAGGCTGGA
                                || ||||||||||||||||
                                TG GACAACGGGTCCGACCT
                                 T
GAM642  DEDD     3'  CGGCTTGGGCAAAGGGC     53377      G        TG
                                GCTCT TTGCCCAGGC  G
                                ||||| ||||||||||  |
                                CGGGA AACGGGTTCG  C
                                   _        GT
GAM642  DEFB103  5'  TCCAGTCTCAGCGTGGGGTGA  38491       TG T  CC
                                TCGCTC  T GC  AGGCTGGA
                                ||||||  | ||  ||||||||
                                AGTGGG  G CG  TCTGACCT
                                    GT _  AC
GAM642  DFFA     3'  ACTCCAGCCTGGGCAACAGAGC 16586
            GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGCGAGACAACGGGTCCGACCT
                                                CAC
GAM642  DGCR6    3'  AGGGCCAGGCAGAGAGTGAGG  20244         G    CA   GGA
                                TCTCGCTCT TTGCC  GGCT
                                |||||||| |||||  ||||
                                GGAGTGAGA GACGG  CCGG
                                      _    A_   GAC
GAM642  DGKI     5'  TCCAGCCTGGGCGACAAAGCAA 17529     C   C
            GA                    TCT GCT TGTTGCCCAGGCTGGA
                                ||| ||| ||||||||||||||||
                                AGA CGA ACAGCGGGTCCGACCT
                                  A   A
GAM642  DHFR     5'  TCCGGCGAGACATGGCAGGGCA 7658      C       GCCCAG_
            AGG                   TCT GCTCTGTT      GCTGGA
                                ||| ||||||||      ||||||
                                GGA CGGGACGG      CGGCCT
                                  A       TACAGAG
GAM642  DLEC1    3'  TCCAGTGCCAGCAATAGGGTGG 96281           CCAG
                                TCGCTCTGTTGC   GCTGGA
                                ||||||||||||   ||||||
                                GGTGGGATAACG   TGACCT
                                       ACCG
GAM642  DLEC1    3'  TCCAGTGCCAGCAATAGGGTGG 96282           CCAG
                                TCGCTCTGTTGC   GCTGGA
                                ||||||||||||   ||||||
                                GGTGGGATAACG   TGACCT
                                       ACCG
GAM642  DLG4     3'  TCCAGCCTGTTGGAGGGGGG  9088      G    TTGCC
                                TCTC CTCTG    CAGGCTGGA
                                |||| |||||    |||||||||
```

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                                GGGG GAGGT    GTCCGACCT
                                  G    T____
GAM642  DMC1     3'  TCCAGCCTAGGTGACAGAGTGA 23947          TG  C
                GA                 TCTCGCTCTGT  CC AGGCTGGA
                                   ||||||||||  || ||||||||
                                   AGAGTGAGACA  GG TCCGACCT
                                         GT  A
GAM642  DNASE2   3'  TTCAGCCTGGGTGACAGAATGA 9102       C    TG
                GA                 TCTCG TCTGT  CCCAGGCTGGA
                                   ||||| |||||  ||||||||||
                                   AGAGT AGACA  GGGTCCGACTT
                                     A    GT
GAM642  DPH2L1   5'  CCGGGGCAGCGGAGCAGGG   9110    TC         A
                                   TC  GCTCTGTTGCCC GG
                                   ||  ||||||||||| ||
                                   GG  CGAGGCGACGGG CC
                                    GA          G
GAM642  DPP6     5'  TCTGGAGCGGGGTGGGGAGTGG 56326        G TG   AGG_ TG
                GA                 TCTCGCTCT T  CCC    C  GA
                                   |||||||| |  |||    |  ||
                                   AGGGTGAGG G  GGG    G  CT
                                        _ GT   GCGA GT
GAM642  DPP6     5'  TTTAATCTGGAGCGGGGTGGGG 56327          GC    GC
                                   TCTCGCTCTGTT  CCAG  TGGA
                                   ||||||||||||  ||||  ||||
                                   GGGGTGGGGCGA  GGTC  ATTT
                                         __    TA
GAM642  DRPLA    5'  TTCAGCTGCCCAGGCAGAGGAG 10429      G      GCCCA
                A                   TCTC CTCTGTT     GGCTGGA
                                    |||| |||||||     |||||||
                                    AGAG GAGACGG     TCGACTT
                                      _      ACCCG
GAM642  DSC1     3'  TCCAGCCTGGGCAACAAGAGCG 44606        _
                A                   TCGCTCT GTTGCCCAGGCTGGA
                                    |||||||  ||||||||||||||
                                    AGCGAGA CAACGGGTCCGACCT
                                        A
GAM642  DSC1     3'  TCCAGCCTGGGCAACAAGAGCG 44607        _
                A                   TCGCTCT GTTGCCCAGGCTGGA
                                    |||||||  ||||||||||||||
                                    AGCGAGA CAACGGGTCCGACCT
                                        A
GAM642  DVL3     3'  TCCAGCCTGGGTGACAGAGTGA 16651          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          GT
GAM642  DYRK1A   3'  TGTTTTGGGTGGGAGGGTGGGA 56084         G TG     CTGGA
                                    TCTCGCTCT T  CCCAGG
                                    |||||||| |  ||||||
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                                AGGGTGGGA G  GGGTTT
                                     G GT     TGTT
GAM642  DYRK1A   3'  TTGTTTTGGGTGGGAGGGTGGG 56086        G TG     CTGGA
           A                   TCTCGCTCT T  CCCAGG
                               ||||||||| |  ||||||
                               AGGGTGGGA G  GGGTTT
                                     G GT     TGTTT
GAM642  EDAR     3'  CGGCTGGATTCAGCGAAAGAGT 42525         G  _________  AGGCT
           GGGG                  TCTCGCTCT TTGC       CC    G
                               ||||||||| ||||       ||    |
                               GGGGTGAGA AGCG       GG    C
                                     A   ACTT   A  TCGGA
GAM642  EGFL4    3'  TCCAACCTGGGTGACAGAGCGA 62475         TG     C
           GA                    TCTCGCTCTGT  CCCAGG TGGA
                               ||||||||||  |||||| ||||
                               AGAGCGAGACA  GGGTCC ACCT
                                     GT     A
GAM642  EGFL5    3'  TCCAGCCTGGGCGACAGAGCAA 87921     C
           GA                    TCT GCTCTGTTGCCCAGGCTGGA
                               ||| ||||||||||||||||||||
                               AGA CGAGACAGCGGGTCCGACCT
                                 A
GAM642  EGLN2    5'  TTTGGGCAGAGGGTGGGA    34523         G
                               TCTCGCTCT TTGCCCAGG
                               ||||||||| |||||||||
                               AGGGTGGGA GACGGGTTT
                                        _
GAM642  EGLN2    3'  TCTTGCTGGCAATGGGGTGGGA 54921             CA   T
                               TCTCGCTCTGTTGCC  GGC GGA
                               ||||||||||||||  ||| |||
                               AGGGTGGGGTAACGG  TCG TCT
                                        __   T
GAM642  EGLN2    3'  TCTTGCTGGCAATGGGGTGGGA 54922             CA   T
                               TCTCGCTCTGTTGCC  GGC GGA
                               ||||||||||||||  ||| |||
                               AGGGTGGGGTAACGG  TCG TCT
                                        __   T
GAM642  EHD3     5'  CCGGCCTGGGCTGCTGGA    28201     _  T
                               TCT GT GCCCAGGCTGG
                               ||| || ||||||||||
                               AGG CG CGGGTCCGGCC
                                 T  T
GAM642  EIF2AK3  5'  TCCATGCCTGCGCGCGGGGCGG 17903          T  C    _
           GA                    TCTCGCTCTGT GC CAGGC TGGA
                               |||||||||| || ||||| ||||
                               AGGGCGGGGCG CG GTCCG ACCT
                                     _  C     T
GAM642  EIF2C1   3'  TTCTTTGGGGAATGGGGTGGGG 25201          G     CTGGA
                               TCTCGCTCTGTT CCCAGG
                               |||||||||||| ||||||
```

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                                GGGGTGGGGTAA GGGTTT
                                      G     CTTT
GAM642  EIF2C1   3'  TTTGGCCTTCTAAGCAGATTGG 25202      C     GCCC   TG
            GA                    TCTCG TCTGTT    AGGC  GA
                                  ||||| ||||||    ||||  ||
                                  AGGGT AGACGA    TCCG  TT
                                    T     ATCT    GT
GAM642  ELK1     3'  TGGTGGGGTGGGTGGGA     19091        TGTT   AG  TG
                                  TCTCGCTC    GCCC  GC  G
                                  ||||||||    ||||  ||  |
                                  AGGGTGGG    TGGG  TG  T
                                       _____    G_  GT
GAM642  EMX2     3'  TCTAAAGAGGCAGCTGAGTGAG 88956         T     CAGGC
            A                     TCTCGCTC GTTGCC     TGGA
                                  |||||||| ||||||     ||||
                                  AGAGTGAG CGACGG     ATCT
                                       T     AGAA_
GAM642  ENC1     3'  TTTGGTTGTGCTGATAGGGTAA 14654     CG     _  CCA   TG
            GG                    TCT  CTCTGTT GC   GGC  GA
                                  |||  ||||||| ||   |||  ||
                                  GGA  GGGATAG CG   TTG  TT
                                    AT      T  TG_   GT
GAM642  ENPP3    3'  TCCAGAGCCTGGGTGACAGAGC 73331     C      TG      __
            AAGA                    TCT GCTCTGT  CCCAGGCT  GGA
                                  ||| |||||||  ||||||||  |||
                                  AGA CGAGACA  GGGTCCGA  CCT
                                    A      GT       GA
GAM642  F2R      3'  TCCAGCCTGGGCAACAGAGCAA 10573     C
            GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAACGGGTCCGACCT
                                    A
GAM642  F2RL3    3'  TCCAGCCTGGGCAACAGAGCAA 15527     C
            GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAACGGGTCCGACCT
                                    A
GAM642  F2RL3    3'  TCCAGCCTGGGCGAAAGAGCG  15528       G
                                  CGCTCT TTGCCCAGGCTGGA
                                  ||||||  ||||||||||||||
                                  GCGAGA AGCGGGTCCGACCT
                                     A
GAM642  FANCC    3'  CTCCAGCCTGGGCAACAGAGCG 71039
            AGA                     TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAACGGGTCCGACCT
                                              CA
GAM642  FCAR     3'  CCAGGACAGTGGAGAGAGA   56566      G   TG   C  AGGC
                                  TCTC CTC  TTG CC    TGG
                                  ||||  |||  ||| ||    |||
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                                AGAG GAG  GAC GG    ACC
                                  A  GT   A  ____
GAM642  FCAR    3'  TCCAGCCTGGGTGACAGAACGA 56582       C     TG
                GA                TCTCG TCTGT  CCCAGGCTGGA
                                  ||||| |||||  ||||||||||
                                  AGAGC AGACA  GGGTCCGACCT
                                    A     GT
GAM642  FCAR    3'  TCCAGCCTGGGTGACAGAACGA 56583       C     TG
                GA                TCTCG TCTGT  CCCAGGCTGGA
                                  ||||| |||||  ||||||||||
                                  AGAGC AGACA  GGGTCCGACCT
                                    A     GT
GAM642  FCMD    3'  TTCAGCCTGGGCGATAGAGCAA 23051      C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||
                                  AGA CGAGATAGCGGGTCCGACTT
                                    A
GAM642  FGF2    3'  TCCAGCCTAGGCAACAGAGTGA 10622              C
                GA                TCTCGCTCTGTTGCC AGGCTGGA
                                  |||||||||||||| ||||||||
                                  AGAGTGAGACAACGG TCCGACCT
                                           A
GAM642  FGFR1   3'  TCCAGCCTGGGTGACAGAGTGA 7023           TG
                G                  CTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   GAGTGAGACA  GGGTCCGACCT
                                         GT
GAM642  FGFR2   3'  TCCAGCCTTGGCGACAGAGCGA 5566              C
                GA                TCTCGCTCTGTTGCC AGGCTGGA
                                  |||||||||||||| ||||||||
                                  AGAGCGAGACAGCGG TCCGACCT
                                           T
GAM642  FGFR3   3'  TCCAGCCTGCCCCGGAGCTGGA 5571      C     TTGCC
                                  TCT GCTCTG    CAGGCTGGA
                                  ||| ||||||    |||||||||
                                  AGG CGAGGC    GTCCGACCT
                                    T     CCC__
GAM642  FKRP    3'  TCAGTCTTGCAGAGGAGG    44439      G     TGCCC
                                  TCTC CTCTGT    AGGCTGG
                                  |||| ||||||    |||||||
                                  GGAG GAGACG    TCTGACT
                                    _     T_____
GAM642  FLNA    3'  TTTGGTTCTGGGAGGGGTGAGG 9387          GTTG    _ TG
                                  TCTCGCTCT   CCCAGG C  GA
                                  |||||||||   |||||| |  ||
                                  GGAGTGGGG   GGGTCT G  TT
                                       A___      T GT
GAM642  FLRT2   5'  TCCAGCCTAAGCAACAGAGCAA 26004     C        CC
                GA                TCT GCTCTGTTGC  AGGCTGGA
                                  ||| ||||||||||  ||||||||
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                                AGA CGAGACAACG  TCCGACCT
                                  A         AA
GAM642   FMN2     3'  TTCAGCTGACCTGAGAGTGGGA 80132         GTTGCCCA
                                TCTCGCTCT       GGCTGGA
                                |||||||||       |||||||
                                AGGGTGAGA       TCGACTT
                                    GTCCAG__
GAM642   FOSB     3'  TTTGGGGACAGGGGGTGGGA  23062        __    G
                                TCTCGCT  CTGTT CCCAGG
                                |||||||  ||||| ||||||
                                AGGGTGG  GACAG GGGTTT
                                    GG    _
GAM642   FSTL3    3'  TCTAGCCTGGGTGAGTACGGAG 20739       ___
                                CTCTGT   TGCCCAGGCTGGA
                                ||||||   ||||||||||||
                                GAGGCA   GTGGGTCCGATCT
                                   TGA
GAM642   FSTL3    3'  TCTAGCCTGGGTGAGTACGGAG 20740   G    ___
            GG                    C CTCTGT   TGCCCAGGCTGGA
                                | ||||||   ||||||||||||
                                G GAGGCA   GTGGGTCCGATCT
                                 G     TGA
GAM642   FSTL3    3'  TCTAGCCTGGGTGAGTACGGAG 20741   G    ___
            GG                    C CTCTGT   TGCCCAGGCTGGA
                                | ||||||   ||||||||||||
                                G GAGGCA   GTGGGTCCGATCT
                                 G     TGA
GAM642   FSTL3    3'  TCTAGCCTGGGTGTGTACGGAG 20746       ___
                                CTCTGT   TGCCCAGGCTGGA
                                ||||||   ||||||||||||
                                GAGGCA   GTGGGTCCGATCT
                                   TGT
GAM642   FSTL3    3'  TCTAGCCTGGGTGTGTACGGAG 20747       ___
                                CTCTGT   TGCCCAGGCTGGA
                                ||||||   ||||||||||||
                                GAGGCA   GTGGGTCCGATCT
                                   TGT
GAM642   FSTL3    3'  TCTAGCCTGGGTGTGTATGGAG 20748       ___
                                CTCTGT   TGCCCAGGCTGGA
                                ||||||   ||||||||||||
                                GAGGTA   GTGGGTCCGATCT
                                   TGT
GAM642   FSTL3    3'  TCTAGCCTGGGTGTGTATGGAG 20749       ___
                                CTCTGT   TGCCCAGGCTGGA
                                ||||||   ||||||||||||
                                GAGGTA   GTGGGTCCGATCT
                                   TGT
GAM642   FSTL3    3'  TCTAGCCTGGGTGTGTATGGAG 20750       ___
                                CTCTGT   TGCCCAGGCTGGA
                                ||||||   ||||||||||||
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                                GAGGTA  GTGGGTCCGATCT
                                   TGT
GAM642  FSTL3   3'  TCTAGTCTGGGTGTGTACGGAG 20751      ___
                                CTCTGT  TGCCCAGGCTGGA
                                ||||||  ||||||||||||||
                                GAGGCA  GTGGGTCTGATCT
                                   TGT
GAM642  FUT4    5'  GGGCCACAGTGAGCGAGG    10722       __  T
                                TCTCGCTC  TGT GCCC
                                ||||||||  ||| ||||
                                GGAGCGAG  ACA CGGG
                                     TG  C
GAM642  GABRE   3'  GTTGGGGGGGTGGATAGGGTGGG 18288          _   AGG TG A
           G                     TCTCGCTCTGTT GCCC  C  G
                                ||||||||||||| ||||  |  |
                                GGGGTGGGATAG TGGG  G  T
                                       G   G__ GT GT
GAM642  GABRE   3'  GTTGGGGGGGTGGATAGGGTGGG 18289          _   AGG TG A
           G                     TCTCGCTCTGTT GCCC  C  G
                                ||||||||||||| ||||  |  |
                                GGGGTGGGATAG TGGG  G  T
                                       G   G__ GT GT
GAM642  GADD45B 3'  TCCACTCGGGGGGTGGAGTGAGA 32247       TG  G   AG C
                                TCTCGCTC  TT CCC  G TGGA
                                ||||||||  || |||  | ||||
                                AGAGTGAG  GG GGG  C ACCT
                                     GT  _   CT _
GAM642  GALNT7  3'  TCCAACCTGGGTGACAGAGTGA 34281         TG     C
           GA                      TCTCGCTCTGT  CCCAGG TGGA
                                ||||||||||  |||||| ||||
                                AGAGTGAGACA  GGGTCC ACCT
                                       GT     A
GAM642  GAN     5'  TCCAGCTTCTGCTCAGAGCGCG 42123     _     TT  CC
           GA                      TCT CGCTCTG  GC  AGGCTGGA
                                ||| |||||||  ||  ||||||||
                                AGG GCGAGAC  CG  TTCGACCT
                                  C      T_  TC
GAM642  GAS1    5'  TCTCGGGTGGGAGAGCGGGA  10764        G TG  _
                                TCTCGCTCT T  CCC AGG
                                |||||||| |  ||| |||
                                AGGGCGAGA G  GGG TCT
                                     G GT   C
GAM642  GAS7    3'  TCCAGCTTGGGTGACAGAGCAA 20859     C      TG
           GA                      TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTTCGACCT
                                  A      GT
GAM642  GAS7    3'  TCTGGGGGTGGGGTGAGG    20861        TG  G
                                TCTCGCTC  TT CCCAGG
                                ||||||||  || ||||||
```

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                                GGAGTGGG  GG GGGTCT
                                    GT  _
GAM642  GATA6    5'  CCGGGGCGGAGAGCGGGG    19145        G     A
                                TCTCGCTCT TTGCCC GG
                                ||||||||| |||||| ||
                                GGGGCGAGA GGCGGG CC
                                     _     G
GAM642  GCH1     3'  TTTGGGTTATGATGGGGCAAGA 5681      C       ___
                                TCT GCTCTGTT   GCCCAGG
                                ||| ||||||||   |||||||
                                AGA CGGGGTAG   TGGGTTT
                                  A       TAT
GAM642  GCN5L1   5'  CCAGCTTCCGGAGCCGGA    9436     C     TTGCCC
                                TCT GCTCTG     AGGCTGG
                                ||| ||||||     |||||||
                                AGG CGAGGC     TTCGACC
                                  C     C_____
GAM642  GDF2     5'  TCCAGCCCGGCAGCGGGTGAGA 33021       T       CA
                                TCTCGC CTGTTGCC  GGCTGGA
                                |||||| ||||||||  |||||||
                                AGAGTG GGCGACGG  CCGACCT
                                    _       C_
GAM642  GGCX     3'  CCTGGGCAACAGAGCAAGA   7703      C
                                TCT GCTCTGTTGCCCAGG
                                ||| ||||||||||||||
                                AGA CGAGACAACGGGTCC
                                  A
GAM642  GHR      3'  TTTGGGGGAGTGACAGGATGGG 5707       CT    TG _  AGG TG
           G                     TCTCG  CTGT  C CC   C  GA
                                ||||| ||||  | ||  |  ||
                                GGGGT  GACA  G GG   G  TT
                                   AG    GT A  G__ GT
GAM642  GM2A     3'  TCCAGCCTGGTGACAGAGTGAG 68390          TG  C
           A                     TCTCGCTCTGT  CC AGGCTGGA
                                |||||||||||  || ||||||||
                                AGAGTGAGACA  GG TCCGACCT
                                      GT  _
GAM642  GP2      3'  TCCAGCCTGGGCAACAGAGCAA 9483      C
           GA                      TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||
                                AGA CGAGACAACGGGTCCGACCT
                                  A
GAM642  GP6      3'  AGACCAGCCTGGGCAACATAGT 33468        C            A
           GAGA                      TCTCGCT TGTTGCCCAGGCTGG
                                ||||||| ||||||||||||||
                                AGAGTGA ACAACGGGTCCGACC
                                     T            AGAA
GAM642  GPC4     3'  TTTCTTGGGGGATGGGGTGGGG 9357           G     CTGGA
                                TCTCGCTCTGTT CCCAGG
                                |||||||||||| ||||||
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                                GGGGTGGGGTAG GGGTTC
                                      G     TTTT
GAM642  GPR17   3'  TTCATCTGTGGCAGGGAGAGA  19183     G     TG CC   C
                                TCTC CTCTGT  C  AGG TGGA
                                |||| ||||||  |  ||| |||||
                                AGAG GGGACG  G  TCT ACTT
                                  A     GT __   _
GAM642  GPR44   3'  TCTAGGGCAGTGGAGTCGGA   17702     C    TG     _
                                TCT GCTC  TTGCCC AGG
                                ||| ||||  |||||| |||
                                AGG TGAG  GACGGG TCT
                                  C    GT     A
GAM642  GPR48   5'  TCGGAGGGCAGCGGAGCGAG   38097              AGG
                                CTCGCTCTGTTGCCC   CTGG
                                ||||||||||||||   ||||
                                GAGCGAGGCGACGGG   GGCT
                                         A__
GAM642  GRAF    3'  TCCAGCCTGGGTGACAGAGCCA 31248     C      TG
            GA                    TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  C      GT
GAM642  GRIN2B  3'  TTGGGCCTGGCTGGGTGGGA   7732          TGTTGC      G
                                TCTCGCTC     CCAGGCT GA
                                ||||||||     ||||||| ||
                                AGGGTGGG     GGTCCGG TT
                                     TC____      G
GAM642  GRM3    5'  TCCAGTTTGGAAATGAGAGAGG 7749      G   T   GC
                                TCTC CTC GTT  CCAGGCTGGA
                                |||| ||| |||  ||||||||||
                                GGAG GAG TAA  GGTTTGACCT
                                  A   _   A_
GAM642  GRM6    3'  CTCCAGCCTGGGTGACAGAGCG 7764            TG
            AGA                     TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                       GT          CA
GAM642  GTF2F1  3'  TCCAGCCTGGGTGACAGAATGA 10893     C     TG
                                TCG TCTGT  CCCAGGCTGGA
                                ||| |||||  ||||||||||
                                AGT AGACA  GGGTCCGACCT
                                  A     GT
GAM642  GTF2F1  3'  TCCAGCCTGGGTGACAGTGAGA 10894        CT  TG
                                TCTCGCT  GT  CCCAGGCTGGA
                                |||||||  ||  ||||||||||
                                AGAGTGA  CA  GGGTCCGACCT
                                     __ GT
GAM642  GZMM    3'  TCCAGGGGTGCAGTGGGGTGGG 19215        TG   _  AGG
                                CTCGCTC  TTGC CC   CTGGA
                                |||||||  |||| ||   |||||
```

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                                GGGTGGG  GACG GG   GACCT
                                    GT    T  G__
GAM642  HD      3'  CGGTGGGTGGAGTCAGG     10913     C    GTT    AG  TG
                                TCT GCTCT   GCCC  GC  G
                                ||| |||||   ||||  ||  |
                                GGA TGAGG   TGGG  TG  C
                                  C    ___    __  GT
GAM642  HDAC6    3'  TCCAGCCTGTACCTTGGATGAG 21280      C    TTGCC
            G                    TCTCG TCTG     CAGGCTGGA
                                |||||| ||||    |||||||||
                                GGAGT AGGT     GTCCGACCT
                                   _    TCCAT
GAM642  HEPH     5'  TCAGTGTGGTAGATGAGA    29652      C    TTGC   G
                                TCTCG TCTG    CCA GCTGG
                                ||||| ||||    ||| |||||
                                AGAGT AGAT    GGT TGACT
                                   _    ____   G
GAM642  HIP1     3'  ACTCCGGCCTGGGTGACAGAGT 19245          TG
            GAGA                   TCTCGCTCTGT  CCCAGGCTGGA
                                |||||||||||  ||||||||||||
                                AGAGTGAGACA  GGGTCCGGCCT
                                      GT          CAC
GAM642  HIP1     3'  TCCAGCCTGAGTGACAGAGCGA 19264          TG C
            GA                    TCTCGCTCTGT  C CAGGCTGGA
                                |||||||||||  | |||||||||
                                AGAGCGAGACA  G GTCCGACCT
                                      GT A
GAM642  HIP1     3'  TCCAGCCTGGGCAACAAGAGC  19265      _
                                GCTCT GTTGCCCAGGCTGGA
                                ||||| ||||||||||||||
                                CGAGA CAACGGGTCCGACCT
                                   A
GAM642  HLA-E    3'  TCCAGCCTGGGTGACAGGGTGA 92677          TG
                                TCGCTCTGT  CCCAGGCTGGA
                                |||||||||  ||||||||||
                                AGTGGGACA  GGGTCCGACCT
                                      GT
GAM642  HMGA2    3'  TCTGGGGTGGGGTGGGGTGGGG 14458         TG TG    GG TG
                                TCTCGCTC  T  CCCA  C  GA
                                |||||||  |  ||||  |  ||
                                GGGGTGGG  G  GGGT  G  CT
                                     GT __    GG GT
GAM642  HMGCS1   3'  TGGGGTGGGCATGGGGTGGGG  10941           T    GG
                                TCTCGCTCTGT GCCCA  CTG
                                |||||||||| |||||  |||
                                GGGGTGGGGTA CGGGT  GGT
                                      _    GG
GAM642  HNRPH1   3'  TCCAGTATGAGTGGTGGATGGG 19813      C  TG TG C  G
            G                    TCTCG TC  T  C CA GCTGGA
                                ||||| ||  |  | || ||||||
```

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                                GGGGT AG  G  G GT TGACCT
                                   _  GT GT A  A
GAM642  HNRPK    3'  TTTAGTTCTTACAAACAGGGTT 49197     C       GCCC  _
             GGG                    TCT GCTCTGTT    AGG CTGGA
                                ||| ||||||||    ||| |||||
                                GGG TGGGACAA    TCT GATTT
                                  T       ACAT   T
GAM642  HRH1     3'  TCCAGCCTGGGCAACAGAGCAA 7828      C
             GA                     TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGAGACAACGGGTCCGACCT
                                  A
GAM642  HS3ST4   3'  TTTAGAGATGGCAGAGAGTGAG 73859         G    CAGG
             G                      TCTCGCTCT TTGCC    CTGGA
                                |||||||||| |||||    |||||
                                GGAGTGAGA GACGG    GATTT
                                     _    TAGA
GAM642  HSD17B1  5'  TTTGGCTCAGAACAGGGTGGGG 6431           GCCCA   TG
                                TCTCGCTCTGTT    GGC  GA
                                ||||||||||||    |||  ||
                                GGGGTGGGACAA    TCG  TT
                                       GAC__   GT
GAM642  HSPA1L   5'  TTGCAGGGAGGGACGGGGTGGG 99600          G__   AG  TGGA
             G                      TCTCGCTCTGTT   CCC  GC
                                |||||||||||   |||  ||
                                GGGGTGGGGCAG   GGG  CG
                                       GGA   A_  TTT
GAM642  HSPA5    3'  TCCAGCCTGGCGACAAGAGTGA 19290         _     C
             GA                     TCTCGCTCT GTTGCC AGGCTGGA
                                |||||||| |||||| ||||||||
                                AGAGTGAGA CAGCGG TCCGACCT
                                     A     _
GAM642  HTLF     5'  TCAGCCTGGGAAGTGAGG    10975       CTGTTG
                                TCTCGCT     CCCAGGCTGG
                                |||||||     ||||||||||
                                GGAGTGA     GGGTCCGACT
                                    A_____
GAM642  HTR2A    3'  CCTGGGTAACAAAGTGAGA    7103        C
                                TCTCGCT TGTTGCCCAGG
                                ||||||| ||||||||||
                                AGAGTGA ACAATGGGTCC
                                    A
GAM642  HTR2A    3'  TCCTCCTGGGCAACAGAGTGAG 7107              CT
             A                      TCTCGCTCTGTTGCCCAGG  GGA
                                |||||||||||||||||  |||
                                AGAGTGAGACAACGGGTCC  CCT
                                          T_
GAM642  HUNK     3'  TCCAGCTTAGGTGGCAAAGTGA 28192       C   TG  C
             GA                     TCTCGCT TGT  CC AGGCTGGA
                                ||||||| |||  || ||||||||
```

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                                AGAGTGA ACG  GG TTCGACCT
                                    A   GT  A
GAM642  HYAL3    5'  TCCGAGGTGGCGACTGAGTGAG 14517         T     CAGGC
            A                    TCTCGCTC GTTGCC     TGGA
                                 |||||||| ||||||     ||||
                                 AGAGTGAG CAGCGG     GCCT
                                     T      TGGA_
GAM642  IAPP     3'  ACTCCAGCCTGGGTGGCAGAGT 6433            TG
            GAGA                   TCTCGCTCTGT  CCCAGGCTGGA
                                 ||||||||||  ||||||||||
                                 AGAGTGAGACG  GGGTCCGACCT
                                       GT          CAC
GAM642  ICA1     3'  AGACCAGCCTGGGCAACAAAGT 18308         C             A
            GAGA                   TCTCGCT TGTTGCCCAGGCTGG
                                 |||||||| ||||||||||||||||
                                 AGAGTGA ACAACGGGTCCGACC
                                    A             AGAG
GAM642  ICA1     3'  TCCAGCCTGGGCGACAGAAGT  42519     _
                                 GCT CTGTTGCCCAGGCTGGA
                                 ||| ||||||||||||||||
                                 TGA GACAGCGGGTCCGACCT
                                   A
GAM642  ICAM1    3'  CTAGCCTGATGAGAGGGGA   72036      G    GTTGCC
                                 TCTC CTCT      CAGGCTGG
                                 |||| ||||      ||||||||
                                 AGGG GAGA      GTCCGATC
                                   _    GTA___
GAM642  ICOS     3'  TCTGTGTGTGGGGTGGGG    24925         TG T  C
                                 TCTCGCTC  T GC CAGG
                                 ||||||||  | || ||||
                                 GGGGTGGG  G TG GTCT
                                     GT _  T
GAM642  ID1      3'  TCCAGCCTGGGGCTGAGGCTGA 70574      _ _  T  TG
            GG                     TCTC GC TC GT  CCCAGGCTGGA
                                 |||| || || ||  ||||||||||
                                 GGAG CG AG CG  GGGTCCGACCT
                                   T  G  T  __
GAM642  ID3      3'  TTTGGCGCCAACTGGGTGGGG  79808         T   _ _
                                 TCTCGCTC GTTG C CCAGG
                                 |||||||| |||| | |||||
                                 GGGGTGGG CAAC G GGTTT
                                     T    C C
GAM642  IFIT4    3'  TCCAGCCTGGGCAACAGAGCAA 71497     C
            GA                     TCT GCTCTGTTGCCCAGGCTGGA
                                 ||| ||||||||||||||||||||
                                 AGA CGAGACAACGGGTCCGACCT
                                   A
GAM642  IFNAR1   3'  TCCAGCCTGGTGACAGCGTGAG 7142         T    TG  C
            A                      TCTCGC CTGT  CC AGGCTGGA
                                 |||||| ||||  || ||||||||
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                                AGAGTG GACA  GG TCCGACCT
                                   C    GT  _
GAM642  IFRD1    3'  AGACCAGCCTGGGCAACATAGC 60752        C           A
                GAGA                    TCTCGCT TGTTGCCCAGGCTGG
                                        ||||||| ||||||||||||||||
                                        AGAGCGA ACAACGGGTCCGACC
                                           T            AGAG
GAM642  IGFBP4   3'  TCTGAGCAGTCAGGGTGGGA   9555          _   C
                                        TCTCGCTCTG TTGC CAGG
                                        |||||||||| |||| ||||
                                        AGGGTGGGAC GACG GTCT
                                              T    A
GAM642  IL10     3'  TCCAGCCTGGGTGACAGAGCAA 6929      C      TG
                GA                      TCT GCTCTGT  CCCAGGCTGGA
                                        ||| |||||||  ||||||||||
                                        AGA CGAGACA  GGGTCCGACCT
                                          A      GT
GAM642  IL13RA1  3'  TCTAGCCTGGGTGACAGAGCAA 9576      C      TG
                GA                      TCT GCTCTGT  CCCAGGCTGGA
                                        ||| |||||||  ||||||||||
                                        AGA CGAGACA  GGGTCCGATCT
                                          A      GT
GAM642  IL17R    3'  CTGCAGCCTGGATGACAGAGCG 27553          GC       GA
                AGA                      TCTCGCTCTGTT  CCAGGCTG
                                        ||||||||||||  ||||||||
                                        AGAGCGAGACAG  GGTCCGAC
                                              TA       GTCA
GAM642  IL18     3'  TCTAGCCTGGGCAACAACAGC  9596     C_
                                        GCT  TGTTGCCCAGGCTGGA
                                        |||  ||||||||||||||||
                                        CGA  ACAACGGGTCCGATCT
                                          CA
GAM642  IL1F5    3'  TCTGTGGGGGTGGGGTGGGG   25379        TG  G  _
                                        TCTCGCTC  TT CC CAGG
                                        ||||||||  || || ||||
                                        GGGGTGGG  GG GG GTCT
                                             GT  G  T
GAM642  IL2RA    3'  TCCAGCCTGGGCAACAGAGCAA 6453      C
                GA                      TCT GCTCTGTTGCCCAGGCTGGA
                                        ||| ||||||||||||||||||||
                                        AGA CGAGACAACGGGTCCGACCT
                                          A
GAM642  IMMP2L   5'  TGCCAAATTGGGCGAGG     51708         T   GCCCA   TG
                                        TCTCGCTC GTT    GGC  G
                                        |||||||| |||    |||  |
                                        GGAGCGGG TAA    CCG  T
                                             T  A____   G
GAM642  IPP      3'  TCCACTCTGGGCAACAGAATGA 20907       C          GC
                GA                      TCTCG TCTGTTGCCCAG  TGGA
                                        ||||| ||||||||||||  ||||
```

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                                AGAGT AGACAACGGGTC  ACCT
                                  A          TC
GAM642  IRAK1    3'  TCCAGCCTGGGTGACAGAGCAA 9618      C      TG
             GA                    TCT GCTCTGT  CCCAGGCTGGA
                                |||  |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM642  IRAK4    3'  CTCCAGCCTGGGTGACAGAGTG 61842           TG
             AGA                    TCTCGCTCTGT  CCCAGGCTGGA
                                |||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      GT         CA
GAM642  ITCH     3'  TTTGGGCAGCGTGGTGGGG   49757        C
                                TCTCGCT TGTTGCCCAGG
                                |||||||  ||||||||||
                                GGGGTGG GCGACGGGTTT
                                    T
GAM642  ITGA5    3'  TTAGCCTGCAGTGTGAGG    61936       T   TTGCC
                                TCTCGC CTG    CAGGCTGG
                                ||||||  |||    ||||||||
                                GGAGTG GAC    GTCCGATT
                                   T  ______
GAM642  ITGAL    3'  TCCAGCCTGGGCAACACAGCGA 11050        C
             GA                    TCTCGCT TGTTGCCCAGGCTGGA
                                |||||||  ||||||||||||||||
                                AGAGCGA ACAACGGGTCCGACCT
                                    C
GAM642  ITPKB    3'  GCTGGGGGGTGGAGGGTGGGA   11067         G TG   A_
                                TCTCGCTCT T  CCC  GGC
                                |||||||||  |  |||  |||
                                AGGGTGGGA G  GGG  TCG
                                      _ GT   GG
GAM642  JMJ      3'  TCTCGGTGGGGGGGTGGGG    18325         G TG  C
                                TCTCGCTCT T  CC AGG
                                |||||||||  |  ||  |||
                                GGGGTGGGG G  GG TCT
                                      _ GT  C
GAM642  JPH2     5'  CGGCTGGTGGAGTCGGG     96082      _    GTT   CA   TG
                                CTCG CTCT   GCC  GGC  G
                                ||||  ||||   |||  |||  |
                                GGGC GAGG   TGG  TCG  C
                                  T   ____   __   GT
GAM642  JUP      3'  TCCGTGCAGGCGATGGGGCAAG 11113     C         CAG  _
             A                     TCT GCTCTGTTGCC   GC TGGA
                                |||  ||||||||||   ||  ||||
                                AGA CGGGGTAGCGG   CG GCCT
                                  A          A__  T
GAM642  KCNA7    3'  AGACCAGCCTGGGCAACATGGT 49885        C            A
             GAGA                    TCTCGCT TGTTGCCCAGGCTGG
                                |||||||  |||||||||||||||
```

```
                                AGAGTGG ACAACGGGTCCGACC
                                   T            AGAA
GAM642  KCNA7   3'  TCCAGCCTGGGCAACAGAGGGA 49905     G
                G                   CTC CTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||
                                    GAG GAGACAACGGGTCCGACCT
                                      G
GAM642  KCNA7   3'  TCCAGCCTGGGCAGCAGAGC   49906
                                    GCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||
                                    CGAGACGACGGGTCCGACCT

GAM642  KCNJ5   3'  ACTCCAGCCTGGGCGACAGAGC 7965
                GAGA                TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACAGCGGGTCCGACCT
                                                CAC
GAM642  KCNK3   3'  TCCAGCCTGGGTGACAGGGCAA 11178     C      TG
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGGGACA  GGGTCCGACCT
                                      A      GT
GAM642  KCNK6   3'  TCCAGCCTGCGGGACAGAGTGA 17885           G _
                GA                  TCTCGCTCTGTT CC CAGGCTGGA
                                    |||||||||||| || |||||||||
                                    AGAGTGAGACAG GG GTCCGACCT
                                          _ C
GAM642  KCNN2   5'  TCCGGTGCCCCGGCGGCGGGGG 41495         _     CA  __
                CGGGA                 TCTCGCTCT GTTGCC  GGC  TGGA
                                    ||||||||| ||||||  |||  ||||
                                    AGGGCGGGG CGGCGG  CCG  GCCT
                                         G     CC   TG
GAM642  KIF1B   3'  TCCAGCCTGGGTGACAGAGCAA 31271     C      TG
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGAGACA  GGGTCCGACCT
                                      A      GT
GAM642  KIF3B   3'  TTCCAGCCTGGGTGACAGAGTG 17811           TG
                AGA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          GT         TA
GAM642  KLHL3   3'  TCTGGTCTCACTATGAAGTGGG 88853       CT  TGCCC   TG
                G                   TCTCGCT  GT    AGGC  GA
                                    |||||||  ||    ||||  ||
                                    GGGGTGA  TA    TCTG  CT
                                       AG  TCAC_   GT
GAM642  KLRG1   3'  TCCAGCCTGGGAGATAGAGCAA 20557     C      TG
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
```

```
                                AGA CGAGATA  GGGTCCGACCT
                                  A      GA
GAM642  KNSL1    3'  TCCAGCCTGGGCAACAGAGCAA 16949     C
              GA                   TCT GCTCTGTTGCCCAGGCTGGA
                                   ||| ||||||||||||||||||||
                                   AGA CGAGACAACGGGTCCGACCT
                                     A
GAM642  KNSL2    3'  TCTATGTATCGGGTGAGGGGTG 74289          G TG   AG_ _
              GGA                    TCTCGCTCT T  CCC   GC TGGA
                                   |||||||||| |  |||   || ||||
                                   AGGGTGGGG A  GGG   TG ATCT
                                        _ GT   CTA  T
GAM642  LAMB1    5'  CCCGGAGCAGGGCGAGA     11262           G  CA
                                   TCTCGCTCTGTT CC  GG
                                   ||||||||||||| ||  ||
                                   AGAGCGGGACGA GG  CC
                                         _  C_
GAM642  LAMC2    3'  TCCAGCCTGGGGAACAGAGCAA 19909     C       G
              GA                   TCT GCTCTGTT CCCAGGCTGGA
                                   ||| |||||||| ||||||||||||
                                   AGA CGAGACAA GGGTCCGACCT
                                     A       G
GAM642  LDLR     3'  TCCAGCCTGGGCAACAGATGAA 6744      _  C
              GA                   TCT CG TCTGTTGCCCAGGCTGGA
                                   ||| || ||||||||||||||||||
                                   AGA GT AGACAACGGGTCCGACCT
                                     A  _
GAM642  LDLR     3'  TCCAGCCTGGGCAACATAGTAA 6745      CG  C
              GA                   TCT  CT TGTTGCCCAGGCTGGA
                                   |||  || ||||||||||||||||
                                   AGA  GA ACAACGGGTCCGACCT
                                     AT  T
GAM642  LDLR     3'  TCTGGCCTGGGCGACAGAGCGA 6746                 TG
              GA                   TCTCGCTCTGTTGCCCAGGC  GA
                                   |||||||||||||||||||  ||
                                   AGAGCGAGACAGCGGGTCCG  CT
                                                GT
GAM642  LEF1     5'  TCGGCCTCGGGGCGGGCG    33227     T    TG  _
                                   CGC CTGT  CCC AGGCTGG
                                   ||| ||||  ||| |||||||
                                   GCG GGCG  GGG TCCGGCT
                                     _   __  C
GAM642  LEP      3'  TCCGGCCTGATGACAGAGCGAG 5870             CC
              A                     TCTCGCTCTGTTG  CAGGCTGGA
                                   ||||||||||||  |||||||||
                                   AGAGCGAGACAGT  GTCCGGCCT
                                          A_
GAM642  LEPR     5'  TCTGGCTTGGGCAGGCTGCCCG 11297      CTCT  _       TG
              GG                    CTCG    GT TGCCCAGGC  GA
                                   ||||    || |||||||||  ||
```

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                                GGGC   CG ACGGGTTCG  CT
                                  CCGT  G       GT
GAM642  LFG     3'  ATAGCCAGGATAGGGCGGGA  77229         TGC  A    GA
                                TCTCGCTCTGT   CC GGCTG
                                ||||||||||   || |||||
                                AGGGCGGGATA   GG CCGAT
                                      ___  A    AC
GAM642  LFG     3'  TTTGGCCTGGGTGGGGCTGGG  77244    _    GTT      TG
                                CTC GCTCT   GCCCAGGC  GA
                                ||| |||||   ||||||||  ||
                                GGG CGGGG   TGGGTCCG  TT
                                  T    ___       GT
GAM642  LIF     3'  TCCAGTCTGAGAGCAGGGGAGG 11308     G      GCC
                                TCTC CTCTGTT   CAGGCTGGA
                                |||| |||||||   |||||||||
                                GGAG GGGACGA   GTCTGACCT
                                  _      GA_
GAM642  LILRA3   5'  TCCACAGAGCAGTGCAGTGGGA 23425       C GT   CCAGGC
                                TCTCGCT T  TGC     TGGA
                                ||||||| |  |||     ||||
                                AGGGTGA G  ACG     ACCT
                                    C TG   AGAC__
GAM642  LIMD1    3'  TCCAGCTCAGTGTGGGGCGTGG 27264    T    TG TGCCCA
                                TC CGCTC  T     GGCTGGA
                                || |||||  |     |||||||
                                GG GCGGG  G     TCGACCT
                                 T    GT TGAC__
GAM642  LPIN1    3'  TCCAGCCTGGGTGACAGAGTAA 67992     CG     TG
            GA                    TCT  CTCTGT  CCCAGGCTGGA
                                |||  ||||||  ||||||||||
                                AGA  GAGACA  GGGTCCGACCT
                                  AT     GT
GAM642  LRRC2    3'  ACTCCAGCCTGGGCAACAGAGT 44731
            GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||
                                AGAGTGAGACAACGGGTCCGACCT
                                          CAC
GAM642  LRRC2    3'  TCCAGCCTGGGTGACAGAGCCA 44760     C      TG
            GA                    TCT GCTCTGT  CCCAGGCTGGA
                                |||  |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  C      GT
GAM642  LRRC2    3'  CCTCCAGCCTGGGTGACAGAGT 45721          TG
            GAGA                    TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      GT         CCC
GAM642  LTC4S    5'  TCTGAGCAGCAGACGGGG    8022       C       C
                                TCTCG TCTGTTGC CAGG
                                ||||| |||||||| ||||
```

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                                GGGGC AGACGACG GTCT
                                  _       A
GAM642  LUZP1    3'  TCCAGCCTGGGCAACAAGAGTG 54405        _
              A                   TCGCTCT GTTGCCCAGGCTGGA
                                  ||||||| ||||||||||||||||
                                  AGTGAGA CAACGGGTCCGACCT
                                     A
GAM642  LY64     3'  TCCGCATGTGGAAGAGTGGGA  19949         G TG CCAG  T
                                  TCTCGCTCT T  C    GC GGA
                                  ||||||||| |  |    || |||
                                  AGGGTGAGA G  G    CG CCT
                                       A GT TA__  _
GAM642  LY94     3'  TTGAGCCTGGGCGACAGAGCGA 17898                 G
              GA                    TCTCGCTCTGTTGCCCAGGCT GA
                                  |||||||||||||||||||| ||
                                  AGAGCGAGACAGCGGGTCCGA TT
                                                G  T
GAM642  MADH2    5'  GGCCTGGGGGGCGGGGCGGGA  20916           G
                                  TCTCGCTCTGTT CCCAGGCT
                                  |||||||||||| ||||||||
                                  AGGGCGGGGCGG GGGTCCGG
                                                _
GAM642  MAFF     3'  TCCAGCCTGGGCAACATAGC  25583     C
                                  GCT TGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||
                                  CGA ACAACGGGTCCGACCT
                                    T
GAM642  MAFF     3'  TTTAGCCTTTTTAGATTGAGA  25588       C    TTGCCC
                                  TCTCG TCTG     AGGCTGGA
                                  ||||| ||||     ||||||||
                                  AGAGT AGAT     TCCGATTT
                                     T    TTT____
GAM642  MAP3K14  3'  TCCAGCCTGGGTCAGAAGGGGT 15548         G_  _
              GGG                    CTCGCTCT  TTG CCCAGGCTGGA
                                  ||||||||  ||| ||||||||||
                                  GGGTGGGG  GAC GGGTCCGACCT
                                       AA   T
GAM642  MAPK4    3'  TCTGCAGAAGCGTGGGGTGGGG 12304         TG T  CCAG  T
                                  TCTCGCTC  T GC    GC GGA
                                  ||||||||  | ||    || |||
                                  GGGGTGGG  G CG    CG TCT
                                       GT _  AAGA  _
GAM642  MASP1    3'  TCCATTACTGGGCAATAGAGC  58219            GC_
                                  GCTCTGTTGCCCAG   TGGA
                                  ||||||||||||||   ||||
                                  CGAGATAACGGGTC   ACCT
                                            ATT
GAM642  MATN4    3'  TCCGGCTTGGGCTGTCGGGGCG 48358    T      TT_
              GA                     TC CGCTCTG   GCCCAGGCTGGA
                                  || |||||||   ||||||||||||
```

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                                AG GCGGGGC   CGGGTTCGGCCT
                                 _      TGT
GAM642  MBD4    3'  TCCAGTCTGGATGACAGAGAGA 15389     G     GC
            GA                   TCTC CTCTGTT  CCAGGCTGGA
                                 |||| |||||||  ||||||||||
                                 AGAG GAGACAG  GGTCTGACCT
                                   A      TA
GAM642  MCL1    3'  TTTAGTGAAGATGGTAGGGTGG 41991    T     TT CCCAG
            A                    TC CGCTCTG  G    GCTGGA
                                 || |||||||  |    ||||||
                                 AG GTGGGAT  T    TGATTT
                                  _      GG AGAAG
GAM642  MCM4    3'  TCCAGCCTCAGCAATAGAGTGA 62583           CC
            GA                   TCTCGCTCTGTTGC  AGGCTGGA
                                 ||||||||||||||  ||||||||
                                 AGAGTGAGATAACG  TCCGACCT
                                          AC
GAM642  MDM4    3'  TCCAGCCTGGGTGACAGCGCGA 11514       T   TG
            GA                   TCTCGC CTGT  CCCAGGCTGGA
                                 ||||||  ||||  ||||||||||
                                 AGAGCG GACA  GGGTCCGACCT
                                    C   GT
GAM642  MECP2   3'  TCTAGCCCTGCCCGGATGGAGC 18414          ___  CCA
            GGGG                  TCTCGCTCTGTT   GC   GGCTGGA
                                  ||||||||||||   ||   |||||||
                                  GGGGCGAGGTAG   CG   CCGATCT
                                         GCC  TC_
GAM642  MEN1    5'  TCCAGCCTGGGCGAAAGAG   56360     G
                                 CTCT TTGCCCAGGCTGGA
                                 |||| ||||||||||||||
                                 GAGA AGCGGGTCCGACCT
                                   A
GAM642  MGAT3   3'  CCTGGGTAGCGGGGGAGG    11560     G
                                 TCTC CTCTGTTGCCCAGG
                                 |||| ||||||||||||||
                                 GGAG GGGGCGATGGGTCC
                                   _
GAM642  MGAT5   5'  TCAGTGGGTGTGGGTGGGG   11570       TGTT   AG
                                 TCTCGCTC   GCCC  GCTGG
                                 |||||||   ||||  |||||
                                 GGGGTGGG   TGGG  TGACT
                                     TG__   __
GAM642  MHC2TA  3'  ATAGCCTAGGTGACAGAGTGAG 5968          TG  C     GA
            A                    TCTCGCTCTGT  CC AGGCTG
                                 ||||||||||  || ||||||
                                 AGAGTGAGACA  GG TCCGAT
                                        GT  A     AT
GAM642  MKPX    5'  CCGCGAGGGCGGAGTGGGG   39877        GTT   AG  T
                                 TCTCGCTCT   GCCC  GC GG
                                 |||||||||   ||||  || ||
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                                GGGGTGAGG   CGGG  CG CC
                                    ____    AG  _
GAM642  MLC1     3'  TCTGCTCCTGGGAATGGGGTGG 58294          G     CT_
            GA                    TCTCGCTCTGTT CCCAGG   GGA
                                  |||||||||||| ||||||   |||
                                  AGGGTGGGGTAA GGGTCC   TCT
                                        _     TCG
GAM642  MMP11    3'  TCCTGCAGGGGGATGGGGTGGG 21046          G   AG  T
            G                     TCTCGCTCTGTT CCC  GC GGA
                                  |||||||||||| |||  || |||
                                  GGGGTGGGGTAG GGG  CG CCT
                                        G   A_  T
GAM642  MOG      3'  TCTAGCCGGAGTGACAGAGTAA 11677     CG     TG _  A
            GA                    TCT  CTCTGT  C CC GGCTGGA
                                  |||  ||||||  | || |||||||
                                  AGA  GAGACA  G GG CCGATCT
                                    AT     GT A  _
GAM642  MPDU1    3'  TCTGGACGGCAGAGTGGA    18028    T       C
                                  TC CGCTCTGTTG CCAGG
                                  || ||||||||| |||||
                                  AG GTGAGACGGC GGTCT
                                   _        A
GAM642  MSH3     3'  TCCAGCTTGGGCAACAGAGCAA 11693     C
            GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||
                                  AGA CGAGACAACGGGTTCGACCT
                                    A
GAM642  MTMR8    3'  TCCAGCCTGAGCAACAGAGCGA 31917           C
            GA                    TCTCGCTCTGTTGC CAGGCTGGA
                                  |||||||||||||| |||||||||
                                  AGAGCGAGACAACG GTCCGACCT
                                        A
GAM642  MTMR8    3'  TCCAGCCTGGGCGAAAGGGCAA 31918     C    G
            GA                    TCT GCTCT TTGCCCAGGCTGGA
                                  ||| ||||| ||||||||||||||
                                  AGA CGGGA AGCGGGTCCGACCT
                                    A    A
GAM642  MUC4     5'  CCTGGTGGGGTAGTGGGGTGGG 37875        TG     AG  TG A
            G                     TCTCGCTC  TTGCCC  GC  G
                                  ||||||||  ||||||  ||  |
                                  GGGGTGGG  GATGGG  TG  C
                                       GT     G_  GT CT
GAM642  MUC4     5'  CTGGTGGGGTAGTGGGGTGGGG 37878        TG     AG  TG A
                                  TCTCGCTC  TTGCCC  GC  G
                                  ||||||||  ||||||  ||  |
                                  GGGGTGGG  GATGGG  TG  C
                                       GT     G_  GT C
GAM642  MUCDHL   3'  TCCGGCAGCGGCGATGAGGGCG 88651         _     CAG
            AGG                     TCTCGCTCT GTTGCC   GCTGGA
                                  |||||||| ||||||   ||||||
```

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                                GGAGCGGGA TAGCGG   CGGCCT
                                     G     CGA
GAM642  MYCL1    5'  TCCAGGTGGCGGGCGGCTGGAG 19366         _      AGG__
            CGAGG                  TCTCGCTCT GTTGCCC     CTGGA
                                |||||||||  |||||||     |||||
                                GGAGCGAGG CGGCGGG     GACCT
                                     T      CGGTG
GAM642  MYH11    3'  TCCAGCCTGGGCAACAGAG   43446
                                CTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||
                                GAGACAACGGGTCCGACCT

GAM642  MYH11    3'  TCCAGCCTGGGCAACAGAG   11745
                                CTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||
                                GAGACAACGGGTCCGACCT

GAM642  MYH11    3'  TCCAGCCTGGGCAACGTAGT   11746     C
                                GCT TGTTGCCCAGGCTGGA
                                |||  ||||||||||||||||
                                TGA GCAACGGGTCCGACCT
                                  T
GAM642  MYH11    3'  TCCAGCCTGGGCAACGTAGT   11747     C
                                GCT TGTTGCCCAGGCTGGA
                                |||  ||||||||||||||||
                                TGA GCAACGGGTCCGACCT
                                  T
GAM642  MYL2     5'  TTCAGAAGAACGGCATGGGGTG 61247           T   CAGG__
            GGG                    TCTCGCTCTGT GCC      CTGGA
                                ||||||||||| |||      |||||
                                GGGGTGGGGTA CGG      GACTT
                                      _   CAAGAA
GAM642  MYO10    3'  TCTGAGGGAAGGTGAGGGAGTG 25615          G TG  CAGG  _
            GGA                    TCTCGCTCT T  CC    CT GGA
                                |||||||||  |  ||    || |||
                                AGGGTGAGG A  GG    GA TCT
                                     G GT  AAGG  G
GAM642  MYO15A   3'  TCTGGCCCACTGTGCAGTGGAG 33184     C    TG    C ___   TG
            CAGA                   TCT GCTC  TTGC CA   GGC  GA
                                |||  ||||  ||||  ||   |||  ||
                                AGA CGAG  GACG GT   CCG  CT
                                  _   GT    T  CAC   GT
GAM642  MYO1C    3'  ACTCCAGCCTGGGCAACAGAGC 61850
            GAGA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||||
                                AGAGCGAGACAACGGGTCCGACCT
                                           CAC
GAM642  MYO1C    3'  ATTTGAGGCAGTGCTGGAGTGG 61853          _ __   _   CTGGA
            GG                     TCTCGCTCT GT  TGCC CAGG
                                |||||||||  ||  |||| ||||
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                                GGGGTGAGG CG  ACGG GTTT
                                     T  TG   A      AG
GAM642  NAV2    3'  TCCGTGAGAGTGAGTGACGGAG 60798          TG C  GG  ___
            TGAGA                  TCTCGCTCTGT  C CA  CT   GGA
                                   ||||||||||  | ||  ||   |||
                                   AGAGTGAGGCA  G GT  GA   CCT
                                         GT A  GA  GTG
GAM642  NAV2    3'  TTCATTAGGGGTGGGGTGGGA  60801         GTT    AGGC
                                   TCTCGCTCT   GCCC    TGGA
                                   |||||||||   ||||    ||||
                                   AGGGTGGGG   TGGG    ACTT
                                         ___   GATT
GAM642  NCAM2   3'  CCAGAGGTAATAGAGTGA    17001            CAGG
                                   TCGCTCTGTTGCC    CTGG
                                   ||||||||||||    ||||
                                   AGTGAGATAATGG    GACC
                                          A___
GAM642  NCAM2   5'  TCCGGTCTCTCTCCAGGGCTGG 17004     C     TTGCCC
            A                       TCT GCTCTG     AGGCTGGA
                                    |||  ||||||     ||||||||
                                    AGG CGGGAC     TCTGGCCT
                                      T     CTCTC_
GAM642  NCOA6   5'  TCCAGCCCAGGCAACAGAGCGT 26849    T          CA
            GA                        TC CGCTCTGTTGCC  GGCTGGA
                                      || ||||||||||||  |||||||
                                      AG GCGAGACAACGG  CCGACCT
                                       T          AC
GAM642  NDRG1   3'  TCCAGCCTTCCAGGTGGCGTGA 60312       TCT  TG  C___
            GA                        TCTCGC   GT  CC    AGGCTGGA
                                      ||||||   ||  ||    ||||||||
                                      AGAGTG   CG  GG    TCCGACCT
                                         ___  GT  ACCT
GAM642  NDUFA1  5'  TTTGGCCTAGGTAACGGGGCAG 17006     C          C    TG
            A                         TCT GCTCTGTTGCC AGGC  GA
                                      ||| ||||||||||| ||||  ||
                                      AGA CGGGGCAATGG TCCG  TT
                                       _          A    GT
GAM642  NDUFA5  5'  CCAGGGTGACAGAGTGG     18445          TG   AGGC
                                   TCGCTCTGT  CCC    TGG
                                   |||||||||  |||    |||
                                   GGTGAGACA  GGG    ACC
                                         GT   _____
GAM642  NFKBIL2 3'  TCCAGCCTGGGCGACAGACCGA 26455       C
            GA                        TCTCG TCTGTTGCCCAGGCTGGA
                                      |||||  ||||||||||||||||||
                                      AGAGC AGACAGCGGGTCCGACCT
                                        C
GAM642  NKX3A   3'  TCCAGCCTGGGCAACGAGCAAG 21617     C    T
            A                         TCT GCTC GTTGCCCAGGCTGGA
                                      |||  ||||  ||||||||||||||
```

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                                AGA CGAG CAACGGGTCCGACCT
                                  A   _
GAM642  NP      5'  TCAGCATAGCGGAGCGG     6052           CCCAG
                                TCGCTCTGTTG    GCTGG
                                ||||||||||    |||||
                                GGCGAGGCGAT    CGACT
                                      A____
GAM642  NPHS1    3'  CTCCAGCCTGGGCGACAGAGCG 17370
            AGA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGCGAGACAGCGGGTCCGACCT
                                         CA
GAM642  NPTX1    3'  TTTGGCCTCCCGGAGTGCAGA  11843    _     TTGCCC   TG
                                TCT CGCTCTG     AGGC  GA
                                ||| |||||||     ||||  ||
                                AGA GTGAGGC     TCCG  TT
                                  C      CC____    GT
GAM642  NRG2     5'  TCCAGGTCCTGGCGCACAGGGT 18084          T _    __
            GGGA                  TCTCGCTCTGT GC CCAGG  CTGGA
                                ||||||||||| || |||||  |||||
                                AGGGTGGGACA CG GGTCC  GACCT
                                      _ C    TG
GAM642  NRXN2    3'  TGGTGGGGTTGGGTGGGA    57826        TGTT   AG  TG
                                TCTCGCTC   GCCC  GC  G
                                ||||||||   ||||  ||  |
                                AGGGTGGG   TGGG  TG  T
                                     T___    G_  GT
GAM642  NRXN2    3'  TGTGGGGTTGGGTGGGA     57827        TGTT   AG  TG
                                TCTCGCTC   GCCC  GC  G
                                ||||||||   ||||  ||  |
                                AGGGTGGG   TGGG  TG  T
                                     T___    G_  G
GAM642  NT5C2    3'  TCCAGCCTGGGCAACAAGA   25268    _
                                TCT GTTGCCCAGGCTGGA
                                ||| ||||||||||||||
                                AGA CAACGGGTCCGACCT
                                  A
GAM642  OGG1     5'  TCCAGCCTAGGCGACAGAGTGA 34160            C
            GA                    TCTCGCTCTGTTGCC AGGCTGGA
                                ||||||||||||||| ||||||||
                                AGAGTGAGACAGCGG TCCGACCT
                                        A
GAM642  OPA3     3'  ACCCTAGCCTGGGCAACAGAGC 47837     C             A
            AAGA                   TCT GCTCTGTTGCCCAGGCTGG
                                ||| ||||||||||||||||||
                                AGA CGAGACAACGGGTCCGATC
                                  A               CCAC
GAM642  OPA3     3'  TCCAGCCCGGGTGACAGAGCAA 47848     C      TG   A
            GA                    TCT GCTCTGT  CCC GGCTGGA
                                ||| |||||||  ||| |||||||
```

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                                AGA CGAGACA  GGG CCGACCT
                                  A      GT   C
GAM642  OPRD1    3'  TCTGGTTTGGGGCGAGGCAGAG 8070        __    _   TG
                                CTCTGT  TGCCC AGGC  GA
                                ||||||  ||||| ||||  ||
                                GAGACG  GCGGG TTTG  CT
                                   GA    G   GT
GAM642  OPTN     3'  TCCAGCCTGGGTGACAGAGGGA 42053      G     TG
           GA                     TCTC CTCTGT  CCCAGGCTGGA
                                  |||| ||||||  ||||||||||
                                  AGAG GAGACA  GGGTCCGACCT
                                    G     GT
GAM642  P53AIP1  3'  TCCAGCCTGGGCGACAGAGAGA 42340      G
           GA                     TCTC CTCTGTTGCCCAGGCTGGA
                                  |||| ||||||||||||||||||
                                  AGAG GAGACAGCGGGTCCGACCT
                                    A
GAM642  PA2G4    3'  TCCAGCCTGGGTGACAGAATGA 71831       C    TG
           GA                     TCTCG TCTGT  CCCAGGCTGGA
                                  ||||| |||||  ||||||||||
                                  AGAGT AGACA  GGGTCCGACCT
                                    A    GT
GAM642  PAICS    3'  TCCAACCTGGGCAGCAGAGCAA 22268     C           C
           GA                     TCT GCTCTGTTGCCCAGG TGGA
                                  ||| ||||||||||||| ||||
                                  AGA CGAGACGACGGGTCC ACCT
                                    A            A
GAM642  PAX5     5'  CCGGGCCGGCAGTGTGGGG   34125       T    _  A
                                TCTCGC CTGTTG CCC GG
                                |||||| |||||| ||| ||
                                GGGGTG GACGGC GGG CC
                                   T     C  _
GAM642  PCDH11X  3'  TCCAGCCTGGGTGACAGAGCAA 28017     C      TG
           GA                     TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A      GT
GAM642  PCDH11Y  3'  TCCAGCCTGGGTGACAGAGCAA 53169     C      TG
           GA                     TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A      GT
GAM642  PCDH7    5'  TCTGGCCCCTTCCGACAGAGCG 11993           CCCA_  TG
           GGG                     TCTCGCTCTGTTG    GGC  GA
                                  ||||||||||||    |||  ||
                                  GGGGCGAGACAGC    CCG  CT
                                         CTTCC   GT
GAM642  PCDHB9   3'  TCCAGCCTGGGCAATAAGAGC  39451      _
                                GCTCT GTTGCCCAGGCTGGA
                                ||||| ||||||||||||||
```

```
                                CGAGA TAACGGGTCCGACCT
                                  A
GAM642  PDE4C    3'  TCCAGCCTGGGCAACACAGCAA 8107      C   C
                GA                TCT GCT TGTTGCCCAGGCTGGA
                                  ||| ||| ||||||||||||||||
                                  AGA CGA ACAACGGGTCCGACCT
                                    A   C
GAM642  PDE4C    3'  TCCAGCCTGGGGCTGACAGAGC 8108      C       _   _
                AAGA                TCT GCTCTGTT GCCC AGGCTGGA
                                  ||| |||||||| |||| ||||||||
                                  AGA CGAGACAG CGGG TCCGACCT
                                    A       T   G
GAM642  PHF1     3'  CCAAGAGTGGGGAGTGGGG   44388         TGTTG   GG _
                                  TCTCGCTC    CCCA  CT GG
                                  ||||||||    ||||  || ||
                                  GGGGTGAG    GGGT  GA CC
                                       _____   GA  A
GAM642  PHF1     3'  CCAGAGTGGGGAGTGGGG   44391         TGTTG   GG _
                                  TCTCGCTC    CCCA  CT GG
                                  ||||||||    ||||  || ||
                                  GGGGTGAG    GGGT  GA CC
                                       _____   GA  A
GAM642  PHKB     3'  ACACCAGCCTGGGTGACAGAGC 6092            TG        A
                GAGA                TCTCGCTCTGT  CCCAGGCTGG
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACC
                                        GT         ACAC
GAM642  PHLDA3   3'  TTCGGCCTAAGGTGGTGGGGGT 25696        _ TG TG  C_
                GAGG                TCTCGCT C  T  CC  AGGCTGGA
                                  ||||||| |  |  ||  ||||||||
                                  GGAGTGG G  G  GG  TCCGGCTT
                                     G GT GT  AA
GAM642  PIAS3    3'  CCAGTATGACAGAGGAGG    21444      G      GCCCAG
                                  TCTC CTCTGTT      GCTGG
                                  |||| |||||||      |||||
                                  GGAG GAGACAG      TGACC
                                    _      TA____
GAM642  PIK3CG   3'  TATCAGCCTGGGCAACACAGTG 12123         C            A
                AGA                 TCTCGCT TGTTGCCCAGGCTGG
                                  ||||||| ||||||||||||||||
                                  AGAGTGA ACAACGGGTCCGACT
                                     C             ATT
GAM642  PIK3CG   3'  TCCAGCCTGGATAACAGAGCGA 12125             C
                GA                  TCTCGCTCTGTTG CCAGGCTGGA
                                  |||||||||||| ||||||||||
                                  AGAGCGAGACAAT GGTCCGACCT
                                        A
GAM642  PIM1     3'  CCGGGGGTGGGGGGGTGGGG   92683         G TG   AGG
                                  TCTCGCTCT T  CCC   CTGG
                                  ||||||||| |  |||   ||||
```

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                                GGGGTGGGG G  GGG   GGCC
                                     _ GT   ___
GAM642  PITPNB   3'  TCTGGCCTGCGTGCGGTGAGG  25703       CT  T  C    TG
                                TCTCGCT  GT GC CAGGC  GA
                                |||||||  || || |||||  ||
                                GGAGTGG  CG TG GTCCG  CT
                                   __ _ C    GT
GAM642  PLA2G2D  3'  TCCAGCCTGGGCAACAGAGTGA 25723
                                TCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||
                                AGTGAGACAACGGGTCCGACCT

GAM642  PMM2     3'  TCTAGTTTCTCAGGGATGGAGC 72565          TG  ____
           GAGA                   TCTCGCTCTGT  CCC    AGGCTGGA
                                ||||||||||  |||   ||||||||
                                AGAGCGAGGTA  GGG    TTTGATCT
                                     __  ACTC
GAM642  POLH     3'  CTCCAGCCTGGGCAACAGAGCG 22480
           AGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGCGAGACAACGGGTCCGACCT
                                        CG
GAM642  POLH     3'  TCCAGCCTGGGCAACAGAGCGA 22485
           GA                     TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGCGAGACAACGGGTCCGACCT

GAM642  POLK     3'  CCAGCCTGAAGAGCGAGA    33100         GTTGCC
                                TCTCGCTCT     CAGGCTGG
                                |||||||||     ||||||||
                                AGAGCGAGA     GTCCGACC
                                     A_____
GAM642  POLR2J   5'  TCTGGACGCAACGGCGGCGGGA 21724        _     __
                                TCTCGCT CTGTTGC  CCAGG
                                ||||||| |||||||  |||||
                                AGGGCGG GGCAACG  GGTCT
                                    C      CA
GAM642  POU4F1   3'  TTCGGGGGAGTGGGGAGTGGGG 21768         GTTG_  AGG
                                TCTCGCTCT    CCC   CTGGA
                                |||||||||    |||  |||||
                                GGGGTGAGG    GGG   GGCTT
                                     GGTGA  ___
GAM642  PPP1R12B 3'  TCCAGCCTGGGTGACAGAGCAA 50366     C      TG
           GA                     TCT GCTCTGT  CCCAGGCTGGA
                                |||  |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM642  PPP1R8   3'  TTTGGTCATGGAGAAGGGTGGG 57513         GTTGC  _  TG
           A                      TCTCGCTCT    CCA GGC  GA
                                |||||||||    ||| |||  ||
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                                AGGGTGGGA    GGT CTG  TT
                                     AGA__   A   GT
GAM642  PPP2R4   3'  TCCAGTCTGGTTTTGAGAGCAG 61183     _    GTTGC
           GGG                    TCTC GCTCT    CCAGGCTGGA
                                |||| |||||    ||||||||||
                                GGGG CGAGA    GGTCTGACCT
                                  A    GTTTT
GAM642  PPP5C    3'  CCTCGGGGTGGGGTGGGG    21809        GTT   AGGCT
                                TCTCGCTCT   GCCC    GG
                                |||||||||  ||||    ||
                                GGGGTGGGG   TGGG    CC
                                     ___   GCT__
GAM642  PRKACA   3'  TCCAGCCTTCCCTCAGCTGAGT 12271        T   CCC__
           GGGG                   TCTCGCTC GTTG    AGGCTGGA
                                |||||||| ||||    ||||||||
                                GGGGTGAG CGAC    TCCGACCT
                                     T   TCCCT
GAM642  PRKACA   3'  TGGTCGGGGGGGGTGGGA    12272        GTTG  A  TG
                                TCTCGCTCT   CCC GGC  G
                                |||||||||   ||| |||  |
                                AGGGTGGGG   GGG CTG  T
                                     ____  _  GT
GAM642  PRKCABP  3'  AGCCTGGGAGCGGGGCGGGG  25745          G
                                TCTCGCTCTGTT CCCAGGCT
                                |||||||||||| ||||||||
                                GGGGCGGGGCGA GGGTCCGA
                                          _
GAM642  PRKCI    5'  TCCAGCGTTGAGGCGGGGGAGT 12288         G   _  _
           GAGG                   TCTCGCTCT TTGCC CAG GCTGGA
                                |||||||||  ||||| ||| ||||||
                                GGAGTGAGG GGCGG GTT CGACCT
                                     G    A  G
GAM642  PRKY     3'  AGACTGGCCTGGGCAGCATAGC 12360        C          TG A
           GAGA                   TCTCGCT TGTTGCCCAGGC  G
                                |||||||  ||||||||||||  |
                                AGAGCGA ACGACGGGTCCG  C
                                     T          GT AGAG
GAM642  PRKY     3'  CCTCCAGCCTGGGTGACAGAGT 12371          TG
           GAGA                   TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                       GT         CCC
GAM642  PRKY     3'  TCCAGCCAGGGCGAAGGAGTGA 12383         G     A
           GA                     TCTCGCTCT TTGCCC GGCTGGA
                                |||||||||  ||||||  |||||||
                                AGAGTGAGG AGCGGG CCGACCT
                                     A     A
GAM642  PROC     3'  GCATGGCAATGGATGGGA    6134       C       CAG
                                TCTCG TCTGTTGCC   GC
                                |||||  |||||||||   ||
```

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                                AGGGT AGGTAACGG   CG
                                  _       TA_
GAM642  PSMB2   3'  TCCAGCCTGGCTGACAGAGCAA 12479     C       GC
                GA                TCT GCTCTGTT  CCAGGCTGGA
                                  ||| ||||||||  ||||||||||
                                  AGA CGAGACAG  GGTCCGACCT
                                    A       TC
GAM642  PSMB9   3'  TCCAGCCTGGGAAACAGAGCGA 12509          G
                                  TCGCTCTGTT CCCAGGCTGGA
                                  |||||||||| ||||||||||
                                  AGCGAGACAA GGGTCCGACCT
                                        A
GAM642  PSMB9   3'  TCCAGCCTGGGCGACAAAGCGA 12510        C
                GA                TCTCGCT TGTTGCCCAGGCTGGA
                                  ||||||| ||||||||||||||||
                                  AGAGCGA ACAGCGGGTCCGACCT
                                      A
GAM642  PSMB9   3'  TCCAGTCTGGACGACAGAGTGA 12511            C
                GA                TCTCGCTCTGTTG CCAGGCTGGA
                                  |||||||||||| ||||||||||
                                  AGAGTGAGACAGC GGTCTGACCT
                                        A
GAM642  PTEN    5'  TCCAGAGCCAAGCGGCGGCAGA 6140              CA__   __
                GCGAGG                TCTCGCTCTGTTGCC   GGCT  GGA
                                  ||||||||||||||   ||||  |||
                                  GGAGCGAGACGGCGG   CCGA  CCT
                                        CGAA   GA
GAM642  PTEN    3'  TCGGGTTAGGGCAATGGAGGGG 6141      G        AG   G
                A                  TCTC CTCTGTTGCCC  GCT GA
                                  |||| ||||||||||  ||| ||
                                  AGGG GAGGTAACGGG  TGG CT
                                    _        AT   G
GAM642  PTGES   3'  TCTGGCTCAGGTGTGGGTGGGA 18074        TGTT   CA   TG
                                  TCTCGCTC   GCC  GGC  GA
                                  ||||||||   |||  |||  ||
                                  AGGGTGGG   TGG  TCG  CT
                                      TG__   AC   GT
GAM642  PTGIS   3'  GGAGCTGACAGAGCCAGA    8216     C      _ _
                                  TCT GCTCTGTT GC CC
                                  ||| |||||||| || ||
                                  AGA CGAGACAG CG GG
                                    C       T  A
GAM642  PTGIS   3'  TCCAGCCTGGGCGACAGAGCAA 8229     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM642  PTGIS   3'  TCTAGCTTTAGCTGGAGGGAGA 8230      G   GTT  CC
                                  TCTC CTCT   GC  AGGCTGGA
                                  |||| ||||   ||  ||||||||
```

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                                AGAG GAGG   CG  TTCGATCT
                                  G    T__  AT
GAM642  PTGS1    3'  TCTGTAGGCAGCAGAGAGAGA  55479      G        __
                                TCTC CTCTGTTGCC  CAGG
                                |||| ||||||||||  ||||
                                AGAG GAGACGACGG  GTCT
                                  A         AT
GAM642  PTK2     3'  TCTAGCCTTCCACCAGCAGCGA 20034        _  T  CCC
             GG                   TCTCGCT CTG TG   AGGCTGGA
                                |||||||| ||| ||   ||||||||
                                GGAGCGA GAC AC   TCCGATCT
                                    C   C  CT_
GAM642  PTPN23   5'  CCGGCACGAAGGGGCGGGG   64473         G   CCCAG
                                TCTCGCTCT TTG    GCTGG
                                ||||||||| |||    |||||
                                GGGGCGGGG AGC    CGGCC
                                     A   A____
GAM642  PTPRF    5'  TCCAGCTCGGGTGGCGGTGGCG 56141        _   TG   AG
             GGA                   TCTCGCT CTGT  CCC  GCTGGA
                                ||||||| ||||  |||  ||||||
                                AGGGCGG GGCG  GGG  CGACCT
                                    T    GT   CT
GAM642  PTPRO    3'  TTCAGCTTCAAAGTAGAGTAGA 48415     C       GCCC
                                TCT GCTCTGTT    AGGCTGGA
                                ||| ||||||||    ||||||||
                                AGA TGAGATGA    TTCGACTT
                                  _       AAC_
GAM642  PTPRO    3'  TTCAGCTTCAAAGTAGAGTAGA 48416     C       GCCC
                                TCT GCTCTGTT    AGGCTGGA
                                ||| ||||||||    ||||||||
                                AGA TGAGATGA    TTCGACTT
                                  _       AAC_
GAM642  PTPRS    3'  CCGGGGTGGGGGGGTGGGG    12629         TGTTG    GG
                                TCTCGCTC    CCCA  CTGG
                                ||||||||    ||||  ||||
                                GGGGTGGG    GGGT  GGCC
                                     _____   GG
GAM642  PUM1     3'  TCTAGTCTCAAGTATAGCGAGA 28647        C  _   CCC
                                TCTCGCT TG TTG   AGGCTGGA
                                ||||||| || |||   ||||||||
                                AGAGCGA AT AAC   TCTGATCT
                                    T  G   ___
GAM642  PUNC     3'  TCCAGAGGGTGGACGGAGCGGG 91232          _ TG   AGG
             G                    TCTCGCTCTG T  CCC   CTGGA
                                |||||||||| |  |||   |||||
                                GGGGCGAGGC G  GGG   GACCT
                                      A GT   A__
GAM642  PXF      3'  TCCGTAAGTTGCAGAGTGAGG  12658          T  CCAG  T
                                TCTCGCTCTGT GC    GC GGA
                                |||||||||| ||    || |||
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                                GGAGTGAGACG TG    TG CCT
                                      T  AA__  _
GAM642  PXN      3'  CTGTGGGGTGGGGTGGGG    12672         GTT    AG  T
                                TCTCGCTCT   GCCC  GC GG
                                |||||||||   ||||  || ||
                                GGGGTGGGG   TGGG  TG TC
                                     ___    G_  _
GAM642  PYGM     5'  TTCGGTGGGGGTGGAGTGAGG  20038         GTT    AG
                                TCTCGCTCT   GCCC  GCTGGA
                                |||||||||   ||||  ||||||
                                GGAGTGAGG   TGGG  TGGCTT
                                     ___    GG
GAM642  RAB30    3'  TCCAGTCTGGAGTTGGAGCAAG 27940     C     TT  _
             G                   TCT GCTCTG  GC CCAGGCTGGA
                                ||| ||||||  || ||||||||||
                                GGA CGAGGT  TG GGTCTGACCT
                                  A     __ A
GAM642  RAB5C    3'  TTTGGTTTGGGCGGTGGGGCAG 60528     C    TG        TG
             A                   TCT GCTC  TTGCCCAGGC  GA
                                ||| ||||  ||||||||||  ||
                                AGA CGGG  GGCGGGTTTG  TT
                                  _   GT        GT
GAM642  RAB7L1   3'  TTCAGCCTGGGCAACAAGAGTG 15415        _
             A                   TCGCTCT GTTGCCCAGGCTGGA
                                ||||||| |||||||||||||||
                                AGTGAGA CAACGGGTCCGACTT
                                    A
GAM642  RAB7L1   3'  TTCAGCCTGGGTGACAGAGAAG 15416     CG     TG
             GA                    TCT  CTCTGT  CCCAGGCTGGA
                                |||  ||||||  ||||||||||
                                AGG  GAGACA  GGGTCCGACTT
                                  AA     GT
GAM642  RABIF    3'  TCCAGCCTGGGCAACAGAGTGA 12730
             GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGACAACGGGTCCGACCT

GAM642  RABIF    3'  AGACTAGCCTGGGCAACATAGT 12721         C            A
             GAGA                   TCTCGCT TGTTGCCCAGGCTGG
                                ||||||| |||||||||||||||
                                AGAGTGA ACAACGGGTCCGATC
                                    T            AGAG
GAM642  RAD21    3'  TTCAGTTTCTTCAGAGTGG   21837         TTGCCC
                                TCGCTCTG     AGGCTGGA
                                ||||||||     ||||||||
                                GGTGAGAC     TTTGACTT
                                     TTC___
GAM642  RAD50    3'  ATCCTGGGGGTGGTGGTGGGGT 20404         TG TG  _____    CTGGA
             GGGG                   TCTCGCTC  T  CC    CAGG
                                ||||||||  |  ||    ||||
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                                GGGGTGGG  G  GG    GTCC
                                    GT GT  TGGGG   T  AG
GAM642  RAD50    3'  TCCTGGGGGTGGTGGTGGGGTG 20413       TG TG _____   CTGGA
           GGG                   TCTCGCTC  T  CC    CAGG
                                 ||||||||  |  ||    ||||
                                 GGGGTGGG  G  GG    GTCC
                                    GT GT  TGGGG   T  A
GAM642  RAD50    5'  TTTGGTTGGACCCAATGGGGCG 20414          C__   G TG
           GGA                   TCTCGCTCTGTTG  CCAG C  GA
                                 ||||||||||||||  |||| |  ||
                                 AGGGCGGGGTAAC  GGTT G  TT
                                       CCA   _ GT
GAM642  RANBP2L1 3'  TCCAGCTCGGGGAACAGAGCGA 51052          G  AG
           GA                    TCTCGCTCTGTT CCC  GCTGGA
                                 ||||||||||||| |||  ||||||
                                 AGAGCGAGACAA GGG  CGACCT
                                       G  CT
GAM642  RBBP5    3'  TCCAGCCTAGGTGACAGAATGA 18579      C    TG  C
           GA                    TCTCG TCTGT  CC AGGCTGGA
                                 |||||  |||||  ||  ||||||||
                                 AGAGT AGACA  GG TCCGACCT
                                    A    GT  A
GAM642  RBBP9    3'  TCCATCCTGGGTGATGGAGCGA 70698        TG     C
                                 TCGCTCTGT  CCCAGG TGGA
                                 |||||||||  ||||||  ||||
                                 AGCGAGGTA  GGGTCC ACCT
                                       GT     T
GAM642  RBL1     3'  TCCAGCCTGGGCAACAAGAGT  12789      _
                                 GCTCT GTTGCCCAGGCTGGA
                                 |||||  ||||||||||||||||
                                 TGAGA CAACGGGTCCGACCT
                                    A
GAM642  RBM8A    3'  TTCAGTTAGCATGGTGGGGGAG 18817     G  TGT_  CCA
           A                      TCTC CTC   TGC   GGCTGGA
                                  ||||  |||   |||   |||||||
                                  AGAG GGG   ACG   TTGACTT
                                    G  TGGT  A__
GAM642  RECQL5   3'  TCTGCAGGCGATGGGGCAGGG  16202    TC        __
                                 TC  GCTCTGTTGCC  CAGG
                                 ||  ||||||||||  ||||
                                 GG  CGGGGTAGCGG  GTCT
                                  GA         AC
GAM642  RFC2     3'  TCCAGCCTGGGCGACAGAG    12847
                                 CTCTGTTGCCCAGGCTGGA
                                 ||||||||||||||||||
                                 GAGACAGCGGGTCCGACCT

GAM642  RFX1     3'  TCCAGCCTCAGCCAGGGCAGGG 12852      _     TT  CC
           A                      TCTC GCTCTG  GC  AGGCTGGA
                                  ||||  ||||||  ||  ||||||||
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                                AGGG CGGGAC  CG  TCCGACCT
                                  A     __  AC
GAM642  RGS2    3'  TCAGCCTGGGTGTTCAGG    12862      T_
                                TCTG  TGCCCAGGCTGG
                                ||||  ||||||||||||
                                GGAC  GTGGGTCCGACT
                                  TT
GAM642  RGS3    5'  TCCAGCCTCTCTCCAGAGTGG  56317         TTGCCC
                                TCGCTCTG     AGGCTGGA
                                ||||||||     ||||||||
                                GGTGAGAC     TCCGACCT
                                    CTCTC_
GAM642  RNMT    3'  TTTAGCCTGCATGGCAGGGAGA 15060      G       CC
          GG                    TCTC CTCTGTTG  CAGGCTGGA
                                |||| ||||||||  |||||||||
                                GGAG GGGACGGT  GTCCGATTT
                                  A       AC
GAM642  ROCK2   3'  TCCAGCCTGGGCAGCTGAACAA 66625     CGC  T
          GA                    TCT   TC GTTGCCCAGGCTGGA
                                |||   || ||||||||||||||||
                                AGA   AG CGACGGGTCCGACCT
                                 ACA  T
GAM642  RPH3AL  3'  TCAGCTTGAGGAGCTGGGA   23743      _    GTTGCC
                                TCTC GCTCT     CAGGCTGG
                                |||| |||||     ||||||||
                                AGGG CGAGG     GTTCGACT
                                  T    A_____
GAM642  RREB1   3'  TTTGGCTGTTGAGGAGTGAGA  12913         GTT  CCA   TG
                                TCTCGCTCT   GC   GGC  GA
                                |||||||||   ||   |||  ||
                                AGAGTGAGG   TG   TCG  TT
                                    AGT  ___   GT
GAM642  RXRA    3'  TCTGGTTGAAGGTGGGGTGGGG 12924         GTT   CA_   TG
                                TCTCGCTCT   GCC   GGC  GA
                                |||||||||   |||   |||  ||
                                GGGGTGGGG   TGG   TTG  CT
                                    ___   AAG   GT
GAM642  RXRB    5'  TTTGGTACTGAGCAGAGCGA   42035         GCC   _  TG
                                TCGCTCTGTT   CAG GC  GA
                                ||||||||||   ||| ||  ||
                                AGCGAGACGA   GTC TG  TT
                                    ___   A  GT
GAM642  RYR2    3'  TTTAGTCTTTTCTTTAGTGGGG 8292       G   TG   CCC___
          GAGG                    TCTC CTC  TTG     AGGCTGGA
                                |||| |||  |||     ||||||||
                                GGAG GGG  GAT     TCTGATTT
                                  _   GT   TTCTTT
GAM642  SCA1    3'  TCTGGCCAGAGCAGGGCTGGA  6186      C       GCCCA   TG
                                TCT GCTCTGTT    GGC  GA
                                ||| ||||||||    |||  ||
```

```
                                AGG CGGGACGA    CCG  CT
                                  T      GA___   GT
GAM642  SCAP2    3'  ACTCCAGCCTGGGCGACAGAGT 15419
                GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                        ||||||||||||||||||||||||
                                        AGAGTGAGACAGCGGGTCCGACCT
                                                    CAC
GAM642  SCN4A    3'  TCTGGGCATGGCAGGGCCAGG  6208     C     __
                                        TCT GCTCTGT  TGCCCAGG
                                        ||| |||||||  ||||||||
                                        GGA CGGGACG  ACGGGTCT
                                          C      GT
GAM642  SCN4A    3'  TTTGGCCTGGGGGGAGGTCAGA  6211     C   CTG  G     TG
                                        TCT GCT   TT CCCAGGC  GA
                                        ||| |||   || |||||||  ||
                                        AGA TGG   AG GGGTCCG  TT
                                          C  ___  G      GT
GAM642  SELPLG   3'  TTCAGCCTGTGAGGGCTGGGA  60420     _    GTTGCC
                                        TCTC GCTCT     CAGGCTGGA
                                        |||| |||||     |||||||||
                                        AGGG CGGGA     GTCCGACTT
                                          T    GT____
GAM642  SEPX1    3'  TCCAGGCCAGCCAGAGTGGGG  33380         TT  CCA  _
                                        TCTCGCTCTG  GC   GGC TGGA
                                        ||||||||||  ||   ||| ||||
                                        GGGGTGAGAC  CG   CCG ACCT
                                              __  A__   G
GAM642  SFRP1    3'  CCCGGGGGCAGGGTGGGG    13025          G   A
                                        TCTCGCTCTGTT CCC GG
                                        |||||||||||| ||| ||
                                        GGGGTGGGACGG GGG CC
                                              _   C
GAM642  SFRS2IP  5'  ACTCCAGCCTGGGTGACAGAGT 17534          TG
                GAGA                    TCTCGCTCTGT  CCCAGGCTGGA
                                        ||||||||||  ||||||||||
                                        AGAGTGAGACA  GGGTCCGACCT
                                              GT         CAC
GAM642  SH3BP2   3'  AGAGTGTGTTGGGGTGGGA   13047         TTGCC  G   GGA
                                        TCTCGCTCTG    CA GCT
                                        ||||||||||    || |||
                                        AGGGTGGGGT    GT TGA
                                              T____  G   GAA
GAM642  SH3BP2   3'  TTCAGCCTGCCTGGGGTGAGA  13090        GTTGCC
                                        TCTCGCTCT     CAGGCTGGA
                                        |||||||||     |||||||||
                                        AGAGTGGGG     GTCCGACTT
                                              TCC___
GAM642  SHANK2   3'  CCAGCAGGGTAAAGCGGGA   25524       CTG     AG
                                        TCTCGCT   TTGCCC  GCTGG
                                        |||||||   ||||||  |||||
```

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                                AGGGCGA  AATGGG  CGACC
                                   ___     A_
GAM642  SHC1     3'  TCTGGGAGGGCGGGGTGGGG  13124          G_
                                TCTCGCTCTGTT  CCCAGG
                                ||||||||||||  ||||||
                                GGGGTGGGGCGG  GGGTCT
                                      GA
GAM642  SIGLEC11  3'  ACTCCAGCCTGGGCAACAGAGT 54644
            GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||||
                                AGAGTGAGACAACGGGTCCGACCT
                                         CAC
GAM642  SIGLEC6   3'  TGCCAGCCTGGGCAACAGAGCG 60607                  A
            AGA                     TCTCGCTCTGTTGCCCAGGCTGG
                                ||||||||||||||||||||||||
                                AGAGCGAGACAACGGGTCCGACC
                                         GTA
GAM642  SIM2     3'  ACTCCAGCCTGGGTAACAGAGT 18621
            GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||||
                                AGAGTGAGACAATGGGTCCGACCT
                                         CAC
GAM642  SIP      3'  GCAGCTTGGGTAACAGATTGAG 27733       C            GA
            A                    TCTCG TCTGTTGCCCAGGCTG
                                ||||| ||||||||||||||||
                                AGAGT AGACAATGGGTTCGAC
                                   T            GT
GAM642  SIRT4    3'  TCCAGTTCCCATTCAACAGAGT 25293     CG       CCCA__
            AGGG                    TCT  CTCTGTTG     GGCTGGA
                                |||  ||||||||     |||||||
                                GGG  GAGACAAC     TTGACCT
                                  AT       TTACCC
GAM642  SLC14A2  3'  TCCAGCCTGGGCAACGGATTGA 24128       C
            GA                     TCTCG TCTGTTGCCCAGGCTGGA
                                ||||| ||||||||||||||||||
                                AGAGT AGGCAACGGGTCCGACCT
                                   T
GAM642  SLC17A5  3'  ACTCCAGCCTGGGCGATGGAGC 25822
            GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||||
                                AGAGCGAGGTAGCGGGTCCGACCT
                                         CAC
GAM642  SLC18A3  5'  TTCGGAAGAGCATCGGGGTGGG 13214          T   CCAGG
            G                    TCTCGCTCTG TGC     CTGGA
                                |||||||||| |||     |||||
                                GGGGTGGGGC ACG     GGCTT
                                      T   AGAA_
GAM642  SLC21A2  3'  CCTGGCAGCAGATGAGG     20081       C        C
                                TCTCG TCTGTTGCC AGG
                                ||||| ||||||||| |||
```

```
                                GGAGT AGACGACGG TCC
                                  _     _
GAM642  SLC25A15  3'  TCCAGACTGGGTGACACAGCGA 27296       C  TG    G
            GA                    TCTCGCT TGT  CCCAG CTGGA
                                  ||||||| |||  ||||| |||||
                                  AGAGCGA ACA  GGGTC GACCT
                                     C  GT    A
GAM642  SLC26A4   3'  TCCAGCCTGGGCGACAGAGCAA 6530     C
            GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM642  SLC28A2   3'  CTCCAGCCTGGGTGACAGAGCG 16150          TG
            AGA                    TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GT         CA
GAM642  SLC2A3    3'  TCTAGCCTGGGCCACAGGGCGA 23647          T
            GA                    TCTCGCTCTGT GCCCAGGCTGGA
                                  |||||||||| ||||||||||
                                  AGAGCGGGACA CGGGTCCGATCT
                                        C
GAM642  SLC2A6    3'  TCCAGCCTGGGCAACGAGAGTG 34577       _
            A                      TCGCTCT GTTGCCCAGGCTGGA
                                  ||||||| ||||||||||||||
                                  AGTGAGA CAACGGGTCCGACCT
                                     G
GAM642  SLC31A1   3'  TCCAGCCTGGGTGACAAGAGTG 10279       _  TG
            A                      TCGCTCT GT  CCCAGGCTGGA
                                  ||||||| ||  ||||||||||
                                  AGTGAGA CA  GGGTCCGACCT
                                     A  GT
GAM642  SLC31A1   3'  TTTGGATTCAATGAGTGGGA   10282       T   C__
                                  TCTCGCTC GTTG   CCAGG
                                  |||||||| ||||   |||||
                                  AGGGTGAG TAAC   GGTTT
                                     _    TTA
GAM642  SLC4A10   5'  CCGGCTAAGCAGAGCGAG    42153          GCCCA
                                  CTCGCTCTGTT    GGCTGG
                                  ||||||||||    ||||||
                                  GAGCGAGACGA    TCGGCC
                                        A____
GAM642  SMARCB1   3'  TCGGGTGGGGGTGGAGTGGGG  66188        GTT   AG   G
                                  TCTCGCTCT   GCCC  GCT GA
                                  |||||||||   ||||  ||| ||
                                  GGGGTGAGG   TGGG  TGG CT
                                        ___    GG   G
GAM642  SMCX      5'  TCCGGTTTGTTGTGGTGTGGGG 16090       T TG TGCC
                                  TCTCGC C  T    CAGGCTGGA
                                  |||||| |  |    |||||||||
```

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                                GGGGTG G  G    GTTTGGCCT
                                   T GT TT__
GAM642  SMCX     5'  TTTGGAAGAAACGGAGCGGGA  16091          GC__
                                TCTCGCTCTGTT    CCAGG
                                ||||||||||||    |||||
                                AGGGCGAGGCAA    GGTTT
                                      AGAA
GAM642  SMG1     3'  TCCAGCCTGGGCAACAGAGCTA 31352     C
           GA                     TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGAGACAACGGGTCCGACCT
                                  T
GAM642  SPAG8    3'  TCGGCTTGGGGAGAGTGGGA   25843         GTTG      TG
                                TCTCGCTCT    CCCAGGC  GA
                                |||||||||    |||||||  ||
                                AGGGTGAGA    GGGTTCG  CT
                                     G___       GT
GAM642  SPAG8    3'  TTGGGGGCAGAGCGGGG     25845           G
                                TCTCGCTCTGTT CCCAG
                                |||||||||||| |||||
                                GGGGCGAGACGG GGGTT
                                             _
GAM642  SPK      3'  TCGGGGCTGGGGGACGGGGCGG 17873           G     G  G
           GG                     TCTCGCTCTGTT CCCAG CT GA
                                |||||||||||| ||||| || ||
                                GGGGCGGGGCAG GGGTC GG CT
                                       G     G  G
GAM642  SRGAP1   5'  ACTCCAGCCTGGGCAACAGAGC 72710
           GAGA                     TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||||
                                AGAGCGAGACAACGGGTCCGACCT
                                           CAC
GAM642  SRGAP1   3'  TCCAGCCTGGGCAGCATAGTGT 72722     T    C
           GA                     TC CGCT TGTTGCCCAGGCTGGA
                                || |||| ||||||||||||||||
                                AG GTGA ACGACGGGTCCGACCT
                                 T    T
GAM642  SRGAP1   3'  TTCGGTTCCATGTGGAGCGGGG 72725         TG TGCCCA
                                TCTCGCTC  T     GGCTGGA
                                |||||||  |     |||||||
                                GGGGCGAG  G     TTGGCTT
                                     GT TACC__
GAM642  SSRP1    3'  TTTGGGGAGAGATAGGGTGGGA 13421           G___
                                TCTCGCTCTGTT    CCCAGG
                                ||||||||||||    ||||||
                                AGGGTGGGATAG    GGGTTT
                                      AGAG
GAM642  STAC     3'  GTACTGGCCTGGGTGACAGAGC 13428    TC      TG      TG A
           AGGA                     TC  GCTCTGT  CCCAGGC  G
                                ||  |||||||  |||||||  |
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                                AG  CGAGACA  GGGTCCG  C
                                 GA      GT      GT ATGG
GAM642  STC1     3'  TCTGGCAAATGATGATGGGGTG 13464          GCCCAG_  TG
            GGA                   TCTCGCTCTGTT      GC  GA
                                  ||||||||||||      ||  ||
                                  AGGGTGGGGTAG      CG  CT
                                        TAGTAAA  GT
GAM642  STK38    5'  TCCAGCCTGGGCAACAAGAGCG 24401        _
            A                     TCGCTCT GTTGCCCAGGCTGGA
                                  |||||||  ||||||||||||||||
                                  AGCGAGA CAACGGGTCCGACCT
                                      A
GAM642  SULT2A1  3'  ACTCCAGCCTGGGTGACAGAGC 72222          TG
            GAGA                  TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GT          CAC
GAM642  SUPT6H   3'  TTCAGTTTGGGGCAGGAGGGAG 61033      G    GT    _
            A                     TCTC CTCT  TGCCC AGGCTGGA
                                  ||||  ||||  |||||  ||||||||
                                  AGAG GAGG  ACGGG TTTGACTT
                                    G    __     G
GAM642  SURF5    5'  TTCGGACCGCGGCGCGGCGGGG 56923        C      CCA  _
                                  TCTCGCT TGTTGC   GG CTGGA
                                  |||||||  ||||||   ||  |||||
                                  GGGGCGG GCGGCG   CC GGCTT
                                      C      ____  A
GAM642  SWAP70   3'  CTCCAGCTTGGGCAACAGAGTG 71867
            AGA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAACGGGTTCGACCT
                                                CA
GAM642  SYT5     5'  TTCAGACCCTGCGGAGGGGCGA 13505          G    CCA  _
            GG                    TCTCGCTCT TTGC   GG CTGGA
                                  |||||||||  ||||   ||  |||||
                                  GGAGCGGGG GGCG   CC GACTT
                                        A    TC_  A
GAM642  T        5'  TCGGGGACGGCGGGGAGGGG   13508      G       _  A
                                  TCTC CTCTGTTG CCC GG
                                  ||||  ||||||||  |||  ||
                                  GGGG GGGGCGGC GGG CT
                                    A       A   G
GAM642  TADA2L   3'  TCCAGCCTGGGCAACAAAGTGA 56765        C
            GA                    TCTCGCT TGTTGCCCAGGCTGGA
                                  |||||||  ||||||||||||||||
                                  AGAGTGA ACAACGGGTCCGACCT
                                      A
GAM642  TAF1C    3'  TTGGTGAGGGTGGAGTGAGG   20267          GTT    AG  TG
                                  TCTCGCTCT   GCCC  GC  GA
                                  |||||||||   ||||  ||  ||
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                                GGAGTGAGG  TGGG  TG  TT
                                    ___    AG  GT
GAM642  TBL1X    5'  TCCGGGACTCGGCGGCGGCGGG 20138            C___  G_
           GCGGGG                  TCTCGCTCTGTTGCC   AG  CTGGA
                                |||||||||||||||   ||  |||||
                                GGGGCGGGGCGGCGG   TC  GGCCT
                                      CGGC  AG
GAM642  TBX1     3'  CTCCAGCCTGGGTGACAGAGTG 55540          TG
           AGA                    TCTCGCTCTGT  CCCAGGCTGGA
                                |||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      GT         CA
GAM642  TBX2     3'  TCTGGTCTTCCAGCGAGGTGGG 21144       TC    CCC    TG
           A                     TCTCGC  TGTTG   AGGC  GA
                                ||||||  |||||   ||||  ||
                                AGGGTG  GCGAC   TCTG  CT
                                   GA    CT_    GT
GAM642  TCF7     3'  TCCAGTCTGGGTAACAGGGAGA 13625    G
                                TC CTCTGTTGCCCAGGCTGGA
                                || ||||||||||||||||||
                                AG GGGACAATGGGTCTGACCT
                                 A
GAM642  TCTA     3'  TCCAGCCTGGGCAACAGAGCAA 42503     C
           GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||
                                AGA CGAGACAACGGGTCCGACCT
                                  A
GAM642  TEM7     3'  ACTCCAGCCTGGGTGACAGAGC 40239          TG
           GAGA                    TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      GT         CAC
GAM642  TEM7     3'  CTCCAGCCTGGGTGACAGAGTG 40256          TG
           AGA                    TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      GT         CA
GAM642  TEM8     5'  TCCGGGGAGTTGCGAGGGAGCG 36856        G   CCAGG_
           AGG                    TCTCGCTCT TTGC     CTGGA
                                |||||||| ||||     |||||
                                GGAGCGAGG AGCG     GGCCT
                                    G   TTGAGG
GAM642  TGFB1    3'  AGACCAGCCTGGGTAACATAGT 7250        C           A
           GAGA                    TCTCGCT TGTTGCCCAGGCTGG
                                ||||||| ||||||||||||||
                                AGAGTGA ACAATGGGTCCGACC
                                    T            AGAG
GAM642  TM7SF3   3'  TCCAGCTTGGGTGACAGAG   60395       TG
                                CTCTGT  CCCAGGCTGGA
                                ||||||  ||||||||||
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                                GAGACA  GGGTTCGACCT
                                   GT
GAM642  TMEM2    3'  TCCAGTTTGATACAGAATGGGG 26339      C    TGCC
                                TCTCG TCTGT   CAGGCTGGA
                                ||||| |||||   |||||||||
                                GGGGT AGACA   GTTTGACCT
                                   A    TA__
GAM642  TNFRSF10C 3'  TCCTCAACTGGGTGACAAGGGT 15205        _ TG    GCT_
           GAGG                  TCTCGCTCT GT  CCCAG   GGA
                                ||||||||| ||  |||||   |||
                                GGAGTGGGA CA  GGGTC   CCT
                                     A  GT    AACT
GAM642  TNFRSF1B  3'  ACTCCAGCCTGGGCGACAGAGC 8380
           GAGA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGCGAGACAGCGGGTCCGACCT
                                                CAC
GAM642  TNFRSF1B  3'  TCCAGCCTGAGCAACAGAGTGA 8402            C
           GA                    TCTCGCTCTGTTGC CAGGCTGGA
                                |||||||||||||| |||||||||
                                AGAGTGAGACAACG GTCCGACCT
                                        A
GAM642  TNFSF15   3'  TCCAGCCTGGGTAACAAGAGC  18870      _
                                GCTCT GTTGCCCAGGCTGGA
                                ||||| ||||||||||||||
                                CGAGA CAATGGGTCCGACCT
                                   A
GAM642  TPM4     3'  TCCAGCCTGGTCGACAGAGTGA 13834           C
           GA                    TCTCGCTCTGTTG CCAGGCTGGA
                                |||||||||||| |||||||||
                                AGAGTGAGACAGC GGTCCGACCT
                                        T
GAM642  TPMT     3'  ACGCCAGCCTGGGCAACAGAGC 6299      C             A
           AAGA                  TCT GCTCTGTTGCCCAGGCTGG
                                ||| ||||||||||||||||||
                                AGA CGAGACAACGGGTCCGACC
                                  A               GCAC
GAM642  TRIM14   3'  ACTCCAGCCTGGGCAATAGAGT 29502
           GAGA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGATAACGGGTCCGACCT
                                                CAC
GAM642  TRIM9    5'  TCTAGCCTGGGCAACAAGAGTG 31462       _
           A                     TCGCTCT GTTGCCCAGGCTGGA
                                ||||||| ||||||||||||||
                                AGTGAGA CAACGGGTCCGATCT
                                   A
GAM642  TRPM8    3'  TCCAGCCGGGGTGACAGAGTGA 44208          TG   A
           GA                    TCTCGCTCTGT  CCC GGCTGGA
                                ||||||||||  ||| |||||||
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                                AGAGTGAGACA  GGG CCGACCT
                                      GT   G
GAM642  TSN      3'  AGACCAGCCTGGGCAACAAAGT 17294        C            A
            GAGA                    TCTCGCT TGTTGCCCAGGCTGG
                                    ||||||| ||||||||||||||
                                    AGAGTGA ACAACGGGTCCGACC
                                       A             AGAG
GAM642  TSNAX    3'  TCCAGCCTGGGTAACAGAGCAA 21160     C
            GA                      TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAATGGGTCCGACCT
                                      A
GAM642  UBE2B    3'  TCCAGCCTGGGTGACAGAGC   13938        TG
                                    GCTCTGT  CCCAGGCTGGA
                                    |||||||  ||||||||||
                                    CGAGACA  GGGTCCGACCT
                                       GT
GAM642  UBE2B    5'  TCCGGAGGCGGCGGAGGGAGA  13940      G         CAGG
                                    TCTC CTCTGTTGCC    CTGGA
                                    |||| ||||||||||    |||||
                                    AGAG GAGGCGGCGG    GGCCT
                                      G         A___
GAM642  UBE2G2   3'  ACTCCAGCCTGGGCAACAGAGC 65473
            GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                    |||||||||||||||||||||||||
                                    AGAGCGAGACAACGGGTCCGACCT
                                                 CAC
GAM642  UBE2G2   3'  ACTCCAGCCTGGGCAACAGAGT 65474
            GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                    |||||||||||||||||||||||||
                                    AGAGTGAGACAACGGGTCCGACCT
                                                 CAC
GAM642  UBE2L3   3'  TCTGGTCTGTGCAGAAGTGGGG 13965        CTG    C     TG
                                    TCTCGCT   TTGC CAGGC  GA
                                    |||||||   |||| |||||  ||
                                    GGGGTGA   GACG GTCTG  CT
                                       A__    T     GT
GAM642  UC28     3'  TCCAGCCTGGGCAACAGGAGT  41590      _
                                    GCTC TGTTGCCCAGGCTGGA
                                    |||| ||||||||||||||||
                                    TGAG ACAACGGGTCCGACCT
                                      G
GAM642  USP14    3'  TCCAGCCTGGGTGACAGAGAGA 18940    G     TG
                                    TC CTCTGT  CCCAGGCTGGA
                                    || ||||||  ||||||||||
                                    AG GAGACA  GGGTCCGACCT
                                     A     GT
GAM642  VDR      3'  TTCAGGAAAACTGACAGAGGAG 6348       G      GCCCAGG
            G                       TCTC CTCTGTT      CTGGA
                                    |||| |||||||      |||||
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                                GGAG GAGACAG      GACTT
                                  _      TCAAAAG
GAM642  VEGF    3'  TTTGGGTCCGGAGGGCGAGA  14045         GTT_
                                TCTCGCTCT   GCCCAGG
                                |||||||||   |||||||
                                AGAGCGGGA   TGGGTTT
                                    GGCC
GAM642  VHL     3'  TCCAGCCTGGGAAACAAGAGTG 6875        _  G
          A                      TCGCTCT GTT CCCAGGCTGGA
                                |||||||  ||| ||||||||||
                                AGTGAGA CAA GGGTCCGACCT
                                   A  A
GAM642  VHL     3'  TCCAGCCTGGGGGGACAGAGCAA 6876     C      G
          GA                     TCT GCTCTGTT CCCAGGCTGGA
                                ||| ||||||| ||||||||||
                                AGA CGAGACAG GGGTCCGACCT
                                  A       G
GAM642  VHL     3'  TCTAACCTGGGCGACAGAGTGA 6879               C
          GA                     TCTCGCTCTGTTGCCCAGG TGGA
                                |||||||||||||||||| ||||
                                AGAGTGAGACAGCGGGTCC ATCT
                                           A
GAM642  VPS41   3'  TCCAGCCTGGGCAACAAGAGC  27697      _
                                GCTCT GTTGCCCAGGCTGGA
                                ||||| ||||||||||||||
                                CGAGA CAACGGGTCCGACCT
                                  A
GAM642  WHN     3'  TCCAGCTTTCCCCAGGGTGA  14580        TTGCCC
                                TCGCTCTG    AGGCTGGA
                                ||||||||    ||||||||
                                AGTGGGAC    TTCGACCT
                                    CCCT__
GAM642  WHSC1   3'  CCAGTTCTACAGAGTGAGA   56704         TGCCCA
                                TCTCGCTCTGT    GGCTGG
                                ||||||||||    ||||||
                                AGAGTGAGACA    TTGACC
                                      TC_____
GAM642  WHSC1   3'  CCAGTTCTACAGAGTGAGA   24656         TGCCCA
                                TCTCGCTCTGT    GGCTGG
                                ||||||||||    ||||||
                                AGAGTGAGACA    TTGACC
                                      TC_____
GAM642  WHSC1   3'  CCAGTTCTACAGAGTGAGA   24657         TGCCCA
                                TCTCGCTCTGT    GGCTGG
                                ||||||||||    ||||||
                                AGAGTGAGACA    TTGACC
                                      TC_____
GAM642  WHSC1   3'  CCATTGTAATAGGGTGG    24659          CCAGGC
                                TCGCTCTGTTGC    TGG
                                ||||||||||||    |||
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                                GGTGGGATAATG     ACC
                                      TT____
GAM642  WIG1     3'  ACTCCAGCCTGGGTGACAGAGC 96091          TG
             GAGA                   TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      GT         CAC
GAM642  WNT10B   3'  TCAGCAGGAAGGGTGGGA    14129        GTTGC  AG
                                TCTCGCTCT    CC  GCTGG
                                |||||||||    ||  |||||
                                AGGGTGGGA    GG  CGACT
                                     A____  A_
GAM642  WNT5A    3'  GGCAATAATGGGGGTGGGA    14122         ____
                                TCTCGCTCT    GTTGCC
                                |||||||||    ||||||
                                AGGGTGGGG    TAACGG
                                     GTAA
GAM642  WSX1     3'  TCCAGGCTGGGTAACAGAATGA 17917       C          G
             GA                   TCTCG TCTGTTGCCCAG CTGGA
                                ||||| |||||||||||| |||||
                                AGAGT AGACAATGGGTC GACCT
                                   A          G
GAM642  XT3      3'  TCCAGTCTGGGCGACAGAGCAA 39918     C
             GA                   TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||
                                AGA CGAGACAGCGGGTCTGACCT
                                  A
GAM642  ZNF124   5'  TTCAGGAACTAATAGAGCGAGA 14285           CCCAGG
                                TCTCGCTCTGTTG     CTGGA
                                ||||||||||||     |||||
                                AGAGCGAGATAAT     GACTT
                                      CAAG__
GAM642  ZNF132   5'  TCTTGGCAATGGAGTAGAGG   14288      _        C
                                TCTC GCTCTGTTGCC AGG
                                |||| |||||||||| |||
                                GGAG TGAGGTAACGG TCT
                                   A          T
GAM642  ZNF14    3'  TCCAGCCTGTGCGACAGAATGA 41058       C       C
             GA                   TCTCG TCTGTTGC CAGGCTGGA
                                ||||| |||||||| |||||||||
                                AGAGT AGACAGCG GTCCGACCT
                                   A       T
GAM642  ZNF147   3'  TTTAGCCAGGAAAGGGGTGAGA 18681         GTTG  CA
                                TCTCGCTCT   CC  GGCTGGA
                                |||||||||   ||  |||||||
                                AGAGTGGGG   GG  CCGATTT
                                     AAA_  A_
GAM642  ZNF217   3'  TTGGGTTGGGTGGGGCGGGA  22551         GTT     G TG
                                TCTCGCTCT   GCCCAG C  GA
                                |||||||||   |||||| |  ||
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                                AGGGCGGGG  TGGGTT G  TT
                                     ___     G GT
GAM642  ZNF264   3'  ACTCCAGCCTGGGCAACAGAGC 14186
           GAGA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAACGGGTCCGACCT
                                           CAC
GAM642  ZNF264   3'  ACTCCAGCCTGGGCAGCAGAGC 14187
           GAGA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACGACGGGTCCGACCT
                                           CAC
GAM642  ZNF36    3'  TCCAGCCTGGGTGACTAGC   95587    CT  TG
                                  GCT  GT  CCCAGGCTGGA
                                  |||  ||  ||||||||||
                                  CGA  CA  GGGTCCGACCT
                                    T_  GT
GAM642  ZNF41    5'  TCCAGCTTGGGGAAGAGTGGGG 64648        GTTG
                                  TCTCGCTCT   CCCAGGCTGGA
                                  |||||||||   ||||||||||
                                  GGGGTGAGA   GGGTTCGACCT
                                       AG__
GAM642  ZNF76    3'  TTCAGCCCAGTAGCAGTGGAGC 14271     TG   CCA__
                                  GCTC  TTGC    GGCTGGA
                                  ||||  ||||    |||||||
                                  CGAG  GACG    CCGACTT
                                    GT    ATGAC
GAM642  ZNF91    3'  TCAAGCCTGGGCGACAGAGCGA 14283               G
           GA                     TCTCGCTCTGTTGCCCAGGCT GA
                                  |||||||||||||||||||| ||
                                  AGAGCGAGACAGCGGGTCCGA CT
                                           A
GAM642  ACYP2    5'  TCCGGGACCGGTGACAGGCGCG 57406       _    TG  CA  __
           GGG                      TCTCGC TCTGT  CC  GG  CTGGA
                                  ||||||  |||||  ||  ||  |||||
                                  GGGGCG GGACA  GG  CC  GGCCT
                                     C    GT  __  AG
GAM642  AF020591 3'  TCCAGCCTGGGCAACAGAGCAA 27916    C
           GA                     TCT GCTCTGTTGCCCAGGCTGGA
                                  |||  ||||||||||||||||||||
                                  AGA CGAGACAACGGGTCCGACCT
                                    A
GAM642  AKR1D1   3'  TCCGGCCTGGGTGAAAGAGCGA 21134         G TG
           GA                     TCTCGCTCT T  CCCAGGCTGGA
                                  |||||||||  |  ||||||||||
                                  AGAGCGAGA A  GGGTCCGGCCT
                                       A GT
GAM642  ALS2CR3  3'  CTGGGTAGAGGGTGGGA    31182          G
                                  TCTCGCTCT TTGCCCAG
                                  |||||||||  ||||||||
```

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                                AGGGTGGGA GATGGGTC
                                      _
GAM642  ALTE    3'  TCCAGCCTGGAGGCCAGAGTGA 61006         _  GC
           GA                   TCTCGCTCTG TT  CCAGGCTGGA
                                |||||||||| ||  ||||||||||
                                AGAGTGAGAC GG  GGTCCGACCT
                                     C  A_
GAM642  ALTE    3'  TCCAGCCTGGGCGACAAGAGCG 61007         _
           AGA                   TCTCGCTCT GTTGCCCAGGCTGGA
                                 ||||||||| ||||||||||||||
                                 AGAGCGAGA CAGCGGGTCCGACCT
                                     A
GAM642  AP1G2   5'  TCTCGGGCGGTGGGGTGGG   15357       TG    _
                                 CTCGCTC  TTGCCC AGG
                                 |||||||  |||||| |||
                                 GGGTGGG  GGCGGG TCT
                                    GT     C
GAM642  AP1GBP1  3'  TCCGGTCTGAGCGACAGAGCAA 24355    C       C
           GA                    TCT GCTCTGTTGC CAGGCTGGA
                                 ||| |||||||||| |||||||||
                                 AGA CGAGACAGCG GTCTGGCCT
                                   A         A
GAM642  AP4M1   5'  CCGGGGCCGCAGGGCGGGG   17549          T   A
                                 TCTCGCTCTGT GCCC GG
                                 |||||||||| |||| ||
                                 GGGGCGGGACG CGGG CC
                                      C   G
GAM642  AP4S1   3'  TCCAATCTGGCAACAGAGCGAG 23965            C  GC
           A                     TCTCGCTCTGTTGCC AG  TGGA
                                 |||||||||||||| ||  ||||
                                 AGAGCGAGACAACGG TC  ACCT
                                       _  TA
GAM642  APCL    3'  TCCGGCGGAGCCCAAAAGGGTG 20822         GTT__ _  AG
           GGG                   TCTCGCTCT    GC CC  GCTGGA
                                 |||||||||    || ||  ||||||
                                 GGGGTGGGA    CG GG  CGGCCT
                                    AAACC  A  __
GAM642  APOF    3'  ATTCCAGCCTGGGTGACAGAGC 9689          TG
           GAGA                   TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                      GT         TAC
GAM642  APOL6   3'  TCCAGTCTGGGTGTCAGAATGA 48375      C   T
           GA                    TCTCG TCTG TGCCCAGGCTGGA
                                 |||||| |||| ||||||||||||
                                 AGAGT AGAC GTGGGTCTGACCT
                                   A   T
GAM642  APXL2   3'  TCCAGCCTGGGCGACAGAGCAA 75686    C
           GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                 ||| ||||||||||||||||||||
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                                AGA CGAGACAGCGGGTCCGACCT
                                  A
GAM642  ARNTL2   3'  ACCCCAGCCTGGGCGACAGAGC 39834                    A
           GAGA                   TCTCGCTCTGTTGCCCAGGCTGG
                                  ||||||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCCGACC
                                           CCAC
GAM642  ARNTL2   3'  ACTCCAGTCTGGGCAACAGAGT 39835
           GAGA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAACGGGTCTGACCT
                                           CAC
GAM642  ASAHL    3'  TCTAGCCTGGGCAACAGAGCGA 64321
           GA                     TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAACGGGTCCGATCT

GAM642  ATIP1    3'  TTCAGTCTGACTGTGGGGGTGG 40777          GTTGCC
           GG                     TCTCGCTCT     CAGGCTGGA
                                  |||||||||     |||||||||
                                  GGGGTGGGG     GTCTGACTT
                                       GTGTCA
GAM642  ATP1B4   3'  ATTCCAGCCTGGGTGACAGAGT 24835           TG
           GAGA                   TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                        GT          TAC
GAM642  BA108L7.2 3'  TCTGGCTTCAGTGGTGGGTGGG 49081       T TG TG CC    TG
           G                       TCTCGC C  T  C  AGGC  GA
                                  ||||||  |  |  |  ||||  ||
                                  GGGGTG G  G  G  TTCG  CT
                                     _ GT GT AC    GT
GAM642  BA108L7.2 3'  TTCAGTGGTGGGTGGGGCAGGG 49085    TC    GTT    G_
                                  TC  GCTCT   GCCCA  GCTGGA
                                  ||  |||||   |||||  ||||||
                                  GG  CGGGG   TGGGT  TGACTT
                                   GA    ___     GG
GAM642  BAG4     5'  TCGGCCGTGGGGAGCGGGGCGG 18048           G   _     A
           GA                     TCTCGCTCTGTT CCCA GGCTGG
                                  ||||||||||||  |||| ||||||
                                  AGGGCGGGGCGA GGGT CCGGCT
                                        G   G
GAM642  BANP     3'  TCCAGACTGTGCGACAGAGCGA 66805            C   G
           GA                     TCTCGCTCTGTTGC CAG CTGGA
                                  ||||||||||||||  ||| |||||
                                  AGAGCGAGACAGCG GTC GACCT
                                         T   A
GAM642  BCL2L1   3'  CCAGCCTGGGCAGCCAGGC   57588     CT
                                  GCT  GTTGCCCAGGCTGG
                                  |||  ||||||||||||||
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                                CGG  CGACGGGTCCGACC
                                  AC
GAM642  BFAR     3'  TTCAGCCTGGGTGACAGAGGGA 61427      G     TG
                GA                  TCTC CTCTGT  CCCAGGCTGGA
                                    |||| ||||||  ||||||||||
                                    AGAG GAGACA  GGGTCCGACTT
                                      G     GT
GAM642  BIRC1    3'  TCCAGCCTGGGCAACAGAGCAA 16995     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAACGGGTCCGACCT
                                      A
GAM642  BIVM     3'  TCCAGCCTGGGCAACAGGGCAA 35160     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGGGACAACGGGTCCGACCT
                                      A
GAM642  BLOV1    3'  TCCAGCCTGGGCAACAAGAGCG 76799        _
                A                    TCGCTCT GTTGCCCAGGCTGGA
                                    ||||||| ||||||||||||||||
                                    AGCGAGA CAACGGGTCCGACCT
                                       A
GAM642  BLOV1    3'  TCCAGCCTGGGCGACAGAGCAA 76800     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAGCGGGTCCGACCT
                                      A
GAM642  BTN3A2   3'  TCCAGCCTGGGAGACAGAGCGA 23880          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGCGAGACA  GGGTCCGACCT
                                          GA
GAM642  C12orf2  3'  ACTCCAGCCTGGGTAACAGAGT 83675
                GAGA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAATGGGTCCGACCT
                                                CAC
GAM642  C13orf1  3'  TCCAGCCTAGGCAACAGAGTGA 40372             C
                GA                  TCTCGCTCTGTTGCC AGGCTGGA
                                    |||||||||||||| ||||||||
                                    AGAGTGAGACAACGG TCCGACCT
                                             A
GAM642  C17orf31 3'  TCCAGTGGAGACAGGGCAGGG  34544    TC       GC  AG
                                    TC  GCTCTGTT  CC  GCTGGA
                                    ||  ||||||||  ||  ||||||
                                    GG  CGGGACAG  GG  TGACCT
                                     GA       A_  __
GAM642  C1orf2   5'  TCCAGTGCCCGTGGTGGGGAGG 96268      G   TG TG CCAG
                GA                  TCTC CTC  T  C    GCTGGA
                                    |||| |||  |  |    ||||||
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                                AGGG GGG  G  G    TGACCT
                                  A   GT GT CCCG
GAM642  C1orf22   3'  CGGCTGGATTTAGTAGTGGAGT 48040        TG   _________  AGGCT
           GGGG                    TCTCGCTC  TTGC       CC    G
                                |||||||| ||||       ||    |
                                GGGGTGAG  GATG      GG    C
                                    GT    ATTT   A  TCGGA
GAM642  C1orf24   3'  ACTCCAGCTTGGGCGACGGAGT 54778
           GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||
                                AGAGTGAGGCAGCGGGTTCGACCT
                                              CAC
GAM642  C1orf33   3'  TCCAGCCTGGGCAACAGAGT   32987
                                GCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||
                                TGAGACAACGGGTCCGACCT

GAM642  C1orf34   3'  GCCTTAGCCTGGGCGACAGAGC 61314                    A
           GAGA                    TCTCGCTCTGTTGCCCAGGCTGG
                                |||||||||||||||||||||
                                AGAGCGAGACAGCGGGTCCGATT
                                              CCGA
GAM642  C1QTNF2   3'  ACTCCAGCCTGGGCAACAGAGT 49966
           GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||
                                AGAGTGAGACAACGGGTCCGACCT
                                              CAC
GAM642  C20orf102 5'  CCGGGGACAGCGGGCGAGG    55508       T     _   A
                                TCTCGC CTGTTG CCC GG
                                |||||| |||||| ||| ||
                                GGAGCG GGCGAC GGG CC
                                  _     A   G
GAM642  C20orf106 3'  TCCAGCCCAGGTGACAGAGTGA 55914           TG  CA
           GA                     TCTCGCTCTGT  CC  GGCTGGA
                                |||||||||||  ||  |||||||
                                AGAGTGAGACA  GG  CCGACCT
                                     GT  AC
GAM642  C20orf108 3'  TCCAGCCTGGGCGACAGAGGGA 55883      G
           GA                     TCTC CTCTGTTGCCCAGGCTGGA
                                ||||  ||||||||||||||||||
                                AGAG GAGACAGCGGGTCCGACCT
                                  G
GAM642  C20orf12  3'  TCCAGCCTGGGCAACAAGAGC  36850      _
                                GCTCT GTTGCCCAGGCTGGA
                                |||||  ||||||||||||||
                                CGAGA CAACGGGTCCGACCT
                                  A
GAM642  C20orf124 3'  CCTGGGGCAGGAGGGCGAGA   45839         G    _
                                TCTCGCTCT TTGCCC AGG
                                |||||||| |||||| |||
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                                AGAGCGGGA GACGGG TCC
                                    G     G
GAM642  C20orf142 3'  GACCAGCCTGGGCAACATAGTG 75282       C          A
          AGA                    TCTCGCT TGTTGCCCAGGCTGG
                                 ||||||| ||||||||||||||||
                                 AGAGTGA ACAACGGGTCCGACC
                                    T           AGA
GAM642  C20orf142 3'  TCCAGCCTGAGCGACAGAGTGA 75289           C
          GA                     TCTCGCTCTGTTGC CAGGCTGGA
                                 |||||||||||||| |||||||||
                                 AGAGTGAGACAGCG GTCCGACCT
                                       A
GAM642  C20orf172 3'  TCCAGCCTGAGCGACAGAGTGA 46768           C
          GA                     TCTCGCTCTGTTGC CAGGCTGGA
                                 |||||||||||||| |||||||||
                                 AGAGTGAGACAGCG GTCCGACCT
                                       A
GAM642  C20orf175 3'  TTCAGCCTGGGCGAAAGTAAGA 55931    CG  CTG
                                 TCT  CT   TTGCCCAGGCTGGA
                                 |||  ||   ||||||||||||||
                                 AGA  GA   AGCGGGTCCGACTT
                                   AT  A__
GAM642  C20orf177 3'  TCCAGCCTGGGCAACAAGAGGG 62841    G   _
          A                      TC CTCT GTTGCCCAGGCTGGA
                                 || |||| ||||||||||||||
                                 AG GAGA CAACGGGTCCGACCT
                                  G   A
GAM642  C20orf177 3'  TTGCTTGGGGTGAGGGGCGGGA 62842         GTTG     TGGA
                                 TCTCGCTCT   CCCAGGC
                                 |||||||||   |||||||
                                 AGGGCGGGG   GGGTTCG
                                       AGTG      TTT
GAM642  C20orf183 3'  TCCAGGCTGGGCGACAGAGCGA 48537              G
          GA                     TCTCGCTCTGTTGCCCAG CTGGA
                                 |||||||||||||||| |||||
                                 AGAGCGAGACAGCGGGTC GACCT
                                       G
GAM642  C20orf29  3'  ACTCCAGCCTGGGCAACAGAGT 37704
          GAGA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                 ||||||||||||||||||||||||
                                 AGAGTGAGACAACGGGTCCGACCT
                                        CAC
GAM642  C20orf42  3'  TTTGGTTTGTTAGAGGTGGGA  35065      _   TTGCC    TG
                                 TCTCGC TCTG    CAGGC  GA
                                 |||||| ||||    |||||  ||
                                 AGGGTG AGAT    GTTTG  TT
                                    G   T____    GT
GAM642  C21orf108 3'  TCCAGCCTAGGTGACAGAGCAA 90121    C      TG  C
          GA                     TCT GCTCTGT  CC AGGCTGGA
                                 ||| |||||||  || ||||||||
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                                AGA CGAGACA  GG TCCGACCT
                                  A      GT  A
GAM642  C21orf25  3'  TTTGGCCTGACGCTGGAGTGCG 64309    T     GT  CC    TG
              G                    TC CGCTCT  TG  CAGGC  GA
                                || ||||||  ||  |||||  ||
                                GG GTGAGG  GC  GTCCG  TT
                                 C     TC  A_    GT
GAM642  C21orf57  5'  TTAGTCTCCCAAGCGAGA    75301        CTGT  CCC
                                TCTCGCT    TG   AGGCTGG
                                |||||||    ||   |||||||
                                AGAGCGA    AC   TCTGATT
                                     _____  CC_
GAM642  C22orf19  3'  TCCGGCCTGGGCAACGTAGTGA 14829         C
              GA                    TCTCGCT TGTTGCCCAGGCTGGA
                                |||||||  ||||||||||||||||
                                AGAGTGA GCAACGGGTCCGGCCT
                                     T
GAM642  C22orf19  3'  TCTGGACAACAGAGCAAGA    14831     C       C
                                TCT GCTCTGTTG CCAGG
                                |||  |||||||||  |||||
                                AGA CGAGACAAC GGTCT
                                  A        A
GAM642  C22orf20  3'  TCCAGCCTGGGCAACATGAGTG 48200         _
              A                    TCGCTC TGTTGCCCAGGCTGGA
                                |||||||  ||||||||||||||||
                                AGTGAG ACAACGGGTCCGACCT
                                     T
GAM642  C3orf4    3'  CCAGTTCAGCCGGGCGAGG    39590         T    CCCA
                                TCTCGCTC GTTG    GGCTGG
                                ||||||||  ||||    ||||||
                                GGAGCGGG CGAC    TTGACC
                                     C    _____
GAM642  C5orf4    3'  TCTGGGACCAGAGGGTGGGA   51497          GTTG_
                                TCTCGCTCT    CCCAGG
                                |||||||||    ||||||
                                AGGGTGGGA    GGGTCT
                                     GACCA
GAM642  C5orf4    3'  TCTGGGACCAGAGGGTGGGA   51498          GTTG_
                                TCTCGCTCT    CCCAGG
                                |||||||||    ||||||
                                AGGGTGGGA    GGGTCT
                                     GACCA
GAM642  C5orf5    3'  TCTGGGGGGTGGGGGGTGAGG  33945          G TG   AGG TG
                                TCTCGCTCT T  CCC   C  GA
                                |||||||||  |  |||   |  ||
                                GGAGTGGGG G  GGG   G  CT
                                     _ GT   G__ GT
GAM642  C6.1A     3'  GACCAGCCTGGGCAACATAGTG 44532         C             A
              AGA                    TCTCGCT TGTTGCCCAGGCTGG
                                |||||||  ||||||||||||||||
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                                AGAGTGA ACAACGGGTCCGACC
                                   T            AGA
GAM642  C6.1A    3'  TCCAACCTGTGTAACAGAGTGA 44538            C   C
           GG                    TCTCGCTCTGTTGC CAGG TGGA
                                 ||||||||||||| |||| ||||
                                 GGAGTGAGACAATG GTCC ACCT
                                       T   A
GAM642  C6orf5   3'  ACTCCAGCCTGGGCAATAGAGT 31962
           GAGA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGATAACGGGTCCGACCT
                                              CAC
GAM642  C6orf5   3'  TCTAGCTTGGGAGACAGAGCGA 32006          TG
           GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                 ||||||||||  ||||||||||
                                 AGAGCGAGACA  GGGTTCGATCT
                                       GA
GAM642  C8orf17  3'  GCAGCCTGGGCAACAGAATGAG 39995      C            GA
           A                     TCTCG TCTGTTGCCCAGGCTG
                                 ||||| ||||||||||||||||
                                 AGAGT AGACAACGGGTCCGAC
                                    A            GT
GAM642  C8orf2   3'  TCTAGCTTGGGCAATAGAGCAA 24157    C
           GG                    TCT GCTCTGTTGCCCAGGCTGGA
                                 ||| ||||||||||||||||||
                                 GGA CGAGATAACGGGTTCGATCT
                                   A
GAM642  C9orf5   3'  TCCAGCCTGGGTGAGAGAGTGA 50108         G TG
           GA                    TCTCGCTCT T  CCCAGGCTGGA
                                 ||||||||| |  ||||||||||
                                 AGAGTGAGA A  GGGTCCGACCT
                                      G GT
GAM642  CAMKK2   5'  TCCAGCCTGGGCAACACAGAGA 22630      G  C
           GA                    TCTC CT TGTTGCCCAGGCTGGA
                                 |||| || ||||||||||||||||
                                 AGAG GA ACAACGGGTCCGACCT
                                   A  C
GAM642  CAMKK2   5'  TCCAGCGTGGGCGACAGAGCGA 22631              G
           GA                    TCTCGCTCTGTTGCCCA GCTGGA
                                 |||||||||||||||| ||||||
                                 AGAGCGAGACAGCGGGT CGACCT
                                       G
GAM642  CAMTA1   5'  GCGTGGGCCGCGGGGCGGGG  68505          T    G
                                 TCTCGCTCTGT GCCCA GC
                                 |||||||||| ||||| ||
                                 GGGGCGGGGCG CGGGT CG
                                      C    G
GAM642  CBCIP2   3'  TCCAGCCTGGGCGACAGAGCCA 52661     C
           GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                 ||| ||||||||||||||||||
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                                AGA CGAGACAGCGGGTCCGACCT
                                  C
GAM642  CCR5     3'  TGGGCTGGGGGTGGGGTGGGA  6964          TG  G    G
                                TCTCGCTC  TT CCCAG CTG
                                ||||||||  || ||||| |||
                                AGGGTGGG  GG GGGTC GGT
                                     GT  _    G
GAM642  CCR5     3'  TTTGGTTTGGAAGTGAGGGTCA 6965      C    GTTGC     TG
           GA                     TCT GCTCT    CCAGGC  GA
                                ||| |||||    ||||||  ||
                                AGA TGGGA    GGTTTG  TT
                                  C    GTGAA     GT
GAM642  CCR6     3'  ACTCCAGCCTGGGTGACAGAGC 49395           TG
           GAGA                     TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      GT         CAC
GAM642  CDA08    3'  TCTGGCTTGAAAAAATAGGGGA 48635      G      GCC_    TG
           GA                     TCTC CTCTGTT    CAGGC  GA
                                |||| |||||||    |||||  ||
                                AGAG GGGATAA    GTTCG  CT
                                  _      AAAA     GT
GAM642  CDC14A   3'  ATCTGGACGAGCAGTGGAGAGG 14784      G   TG   ____    CTGGA
           GA                     TCTC CTC  TTGC    CCAGG
                                |||| |||  ||||    |||||
                                AGGG GAG  GACG    GGTCT
                                  A  GT    AGCA       AG
GAM642  CDKL2    5'  TTGGGGACAGAGTGAGG     15472           G
                                TCTCGCTCTGTT CCCAG
                                |||||||||||| |||||
                                GGAGTGAGACAG GGGTT
                                        _
GAM642  CDT1     3'  TCCAGCCTGGGTGACAGAGCGA 78166           TG
           GA                     TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      GT
GAM642  CECR1    5'  TCTGAGAGCAGGGCGAGA    34283           GCC
                                TCTCGCTCTGTT   CAGG
                                ||||||||||||   ||||
                                AGAGCGGGACGA   GTCT
                                      GA_
GAM642  CENTA2   3'  AGAAGAGCCTGGGCAACATAGT 37861        C          GGA
           GAGA                     TCTCGCT TGTTGCCCAGGCT
                                ||||||| ||||||||||||
                                AGAGTGA ACAACGGGTCCGA
                                     T           GAAGAG
GAM642  CENTA2   3'  CTTAGCCTGGGTGACAGAGTGA 37867           TG        A
           GA                     TCTCGCTCTGT  CCCAGGCTGG
                                ||||||||||  ||||||||||
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                                AGAGTGAGACA  GGGTCCGATT
                                      GT         CA
GAM642  CENTA2   3'  TTCCAGCCTGGGTGACAGAGCG 37870          TG
            AGA                    TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      GT         TA
GAM642  CENTG3   3'  TTGAGCTGCAGCAGAGAGGGA  50049      G       CCA    G
                                TCTC CTCTGTTGC   GGCT GA
                                |||| |||||||||   |||| ||
                                AGGG GAGACGACG   TCGA TT
                                  A        ___    G
GAM642  cerk     3'  TCCAGCCTGGGCAACAGAGGGA 43169      G
            GA                     TCTC CTCTGTTGCCCAGGCTGGA
                                |||| ||||||||||||||||||
                                AGAG GAGACAACGGGTCCGACCT
                                  G
GAM642  CG012    3'  TCCAGCCTCGCCGACAAAGCGA 84167        C     CCC
            GA                     TCTCGCT TGTTG   AGGCTGGA
                                ||||||| |||||   ||||||||
                                AGAGCGA ACAGC   TCCGACCT
                                    A     CGC
GAM642  CG012    5'  TCCAGCCTGGGCAACAGAACGA 84168       C
            GA                     TCTCG TCTGTTGCCCAGGCTGGA
                                ||||| ||||||||||||||||||
                                AGAGC AGACAACGGGTCCGACCT
                                   A
GAM642  CG012    3'  CCTGGGCGACAGAGTGAG    84156
                                CTCGCTCTGTTGCCCAGG
                                ||||||||||||||||||
                                GAGTGAGACAGCGGGTCC

GAM642  CG012    5'  TCCAGCCCAGGTGACAGAGGGA 84166      G     TG  CA
            GA                     TCTC CTCTGT  CC  GGCTGGA
                                |||| ||||||  ||  |||||||
                                AGAG GAGACA  GG  CCGACCT
                                  G     GT  AC
GAM642  CGI-203  3'  ACTCCAGCCTGGGTGACAGAGT 40275          TG
            GAGA                   TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      GT         CAA
GAM642  CHFR     5'  TCCGGGTTCGGCGCGGGGCGGG 37189          T   C  G
            G                      TCTCGCTCTGT GCC AG CTGGA
                                ||||||||||| ||| || |||||
                                GGGGCGGGGCG CGG TT GGCCT
                                      _   C  G
GAM642  CHST3    3'  AGACCAGCCTGGGCAACATGGT 16228        C           A
            GAGA                   TCTCGCT TGTTGCCCAGGCTGG
                                |||||||  ||||||||||||||
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                                AGAGTGG ACAACGGGTCCGACC
                                   T            AGAG
GAM642  CHST3    3'  TTGGCCTGGGTGGTAGAGGAGA 16247     G    TT      TG A
                                TCTC CTCTG  GCCCAGGC  G
                                |||| |||||  ||||||||  |
                                AGAG GAGAT  TGGGTCCG  T
                                  _    GG       GT C
GAM642  CIC      3'  TCCAGTTTGGGGCGGAATGAGG 31370      C    TG
                                TCTCG TCTGT  CCCAGGCTGGA
                                ||||| |||||  ||||||||||
                                GGAGT AGGCG  GGGTTTGACCT
                                  A    __
GAM642  CINP     5'  CCGGTGGGGTGGGCGGGG    51925        TGTT   AG
                                TCTCGCTC    GCCC  GCTGG
                                ||||||||    ||||  |||||
                                GGGGCGGG    TGGG  TGGCC
                                    _____   G_
GAM642  CLDN4    3'  TTTGGGCAGTGGTGGGGGAGG  8959      G  __ TG
                                TCTC CT  C  TTGCCCAGG
                                |||| ||  |  |||||||||
                                GGAG GG  G  GACGGGTTT
                                  G  GT GT
GAM642  CLONE24945 3'  TTCAGTCTGGGAGAAACAGAGC 32256     C       G__
           CAGA                   TCT GCTCTGTT   CCCAGGCTGGA
                                ||| ||||||||   ||||||||||
                                AGA CGAGACAA   GGGTCTGACTT
                                  C       AGA
GAM642  CLSP     5'  TCTGAGAGCAGCAGGTTGAGG  34278      CT      C__
                                TCTCG  CTGTTGC   CAGG
                                |||||  |||||||   ||||
                                GGAGT  GACGACG   GTCT
                                   TG      AGA
GAM642  CLSTN1   3'  GCTTGGTGGTAGGGCAGGA   30790    TC     TT   C
                                TC  GCTCTG  GCC AGGC
                                ||  ||||||  ||| ||||
                                AG  CGGGAT  TGG TTCG
                                 GA     GG  _
GAM642  CLSTN2   3'  TTCATGGTGGGTGGAGTGGGG  42403         GTT    GGC
                                TCTCGCTCT   GCCCA   TGGA
                                |||||||||   |||||   ||||
                                GGGGTGAGG   TGGGT   ACTT
                                    ___     GGT
GAM642  CNNM1    3'  TTCATCCTAGGCAACAGAGCGA 40126             C   C
           GA                     TCTCGCTCTGTTGCC AGG TGGA
                                |||||||||||||| ||| ||||
                                AGAGCGAGACAACGG TCC ACTT
                                      A   T
GAM642  CNNM4    3'  TCCAGCCCTGGATAGGGGGGG  39874     G     TGC    _
                                CTC CTCTGT   CCAGG CTGGA
                                ||| ||||||   ||||| |||||
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                                GGG GGGATA   GGTCC GACCT
                                  G     ___     C
GAM642  COE2     3'  TCCAGCCTGGGTGACAGAG    64910        TG
                                CTCTGT  CCCAGGCTGGA
                                ||||||  ||||||||||
                                GAGACA  GGGTCCGACCT
                                   GT
GAM642  CPR2     3'  AGTCCAGCCTGGGCGACAGAGT 48825
              GAGA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGACAGCGGGTCCGACCT
                                            GAC
GAM642  CPR2     3'  TCCAGCCTGGGTAACAGAGCAA 48840     C
              GA                   TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||
                                AGA CGAGACAATGGGTCCGACCT
                                  A
GAM642  CRTAM    3'  TCCAGCCTGGGCGACAGAGGGA 39476      G
              GA                   TCTC CTCTGTTGCCCAGGCTGGA
                                |||| ||||||||||||||||||
                                AGAG GAGACAGCGGGTCCGACCT
                                  G
GAM642  CSEN     3'  TCTGGGCTGGCAGAGGGGA   26462      G     _
                                TCTC CTCTGTT GCCCAGG
                                |||| ||||||| |||||||
                                AGGG GAGACGG CGGGTCT
                                  _      T
GAM642  CSEN     3'  TTCAGTGGGAATGCAGTGGGTG 26463        __   TG_  AG
              GGG                  TCTCGCT  CTGT   CCC  GCTGGA
                                |||||||  ||||  |||  ||||||
                                GGGGTGG  GACG   GGG  TGACTT
                                   GT   TAA  __
GAM642  CXYorf1  3'  CCAGCTCTGCAGGGTGGGG   82907          TTGCC  _
                                TCTCGCTCTG    CAG GCTGG
                                ||||||||||    ||| |||||
                                GGGGTGGGAC    GTC CGACC
                                      _____  T
GAM642  CXYorf1  3'  TCCGGCCTCCCCAGCGCGGGG  82920       T  TTGCCC
                                TCTCGC CTG     AGGCTGGA
                                |||||| |||     ||||||||
                                GGGGCG GAC     TCCGGCCT
                                   C   CCC___
GAM642  CYB5-M   3'  AGACCAGCCTGGGCAACATAGC 96200        C           A
              GAGA                  TCTCGCT TGTTGCCCAGGCTGG
                                |||||||  ||||||||||||||
                                AGAGCGA ACAACGGGTCCGACC
                                   T            AGAA
GAM642  CYB5-M   3'  GACCAGCCTGGGCAACATAGCG 96202        C           A
              AGA                   TCTCGCT TGTTGCCCAGGCTGG
                                |||||||  ||||||||||||||
```

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                                AGAGCGA ACAACGGGTCCGACC
                                   T            AGA
GAM642  CYP2A7   3'  TCTGGTGGGCGGGGCCAGG   7543     C      GC
                                TCT GCTCTGTT  CCAGG
                                ||| ||||||||  |||||
                                GGA CGGGGCGG  GGTCT
                                  C       GT
GAM642  D21S2056E 3'  TCCAGCCTGGGCAACGAGAGGG 14873     G   T
          A                      TCTC CTC GTTGCCCAGGCTGGA
                                 |||| ||| ||||||||||||||
                                 AGGG GAG CAACGGGTCCGACCT
                                   A  _
GAM642  DAPK2    3'  TCCAGTCTGGGTGACAGAGAGA 27516     G     TG
          GA                     TCTC CTCTGT  CCCAGGCTGGA
                                 |||| ||||||  ||||||||||
                                 AGAG GAGACA  GGGTCTGACCT
                                   A     GT
GAM642  DARS     3'  TCCAGTGTGGATGACAGAGCGA 9051           GC   G
          GA                     TCTCGCTCTGTT  CCA GCTGGA
                                 ||||||||||||  ||| ||||||
                                 AGAGCGAGACAG  GGT TGACCT
                                       TA   G
GAM642  DCOHM    3'  TCCAGCCTGGGTGACGGAACGG 50537      C    TG
          GA                     TCTCG TCTGT  CCCAGGCTGGA
                                 |||||| |||||  ||||||||||
                                 AGGGC AGGCA  GGGTCCGACCT
                                   A    GT
GAM642  DDX34    3'  TCCAGCCTGGTTGACAGAGCAA 28678     C      GC
          GA                     TCT GCTCTGTT  CCAGGCTGGA
                                 ||| ||||||||  ||||||||||
                                 AGA CGAGACAG  GGTCCGACCT
                                   A       TT
GAM642  DEGS     3'  TCCACCCTGGGCAACAGAGCAA 14805     C           C
          GA                     TCT GCTCTGTTGCCCAGG TGGA
                                 ||| ||||||||||||||| ||||
                                 AGA CGAGACAACGGGTCC ACCT
                                   A            C
GAM642  DEGS     3'  TCCACCCTGGGCAACAGAGCAA 59270     C           C
          GA                     TCT GCTCTGTTGCCCAGG TGGA
                                 ||| ||||||||||||||| ||||
                                 AGA CGAGACAACGGGTCC ACCT
                                   A            C
GAM642  DGCR6L   3'  TTCAGGACCAGGCAGAGAGTGA 53832         G    CA __
          GG                     TCTCGCTCT TTGCC  GG  CTGGA
                                 ||||||||| |||||  ||  |||||
                                 GGAGTGAGA GACGG  CC  GACTT
                                      _    A_  AG
GAM642  DGKD     3'  TTCAGCTTGGGGTGTGAGTGAG 60115         TGTTG
          A                      TCTCGCTC    CCCAGGCTGGA
                                 ||||||||    ||||||||||
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                                AGAGTGAG    GGGTTCGACTT
                                    TGTG_
GAM642  DIS3     3'  TCCAGCCTGGGTGACAGAACAA 30922     CGC    TG
            GA                    TCT   TCTGT  CCCAGGCTGGA
                                  |||   |||||  ||||||||||
                                  AGA   AGACA  GGGTCCGACCT
                                    ACA     GT
GAM642  DIS3     3'  TTCAGCCTGGATGATGAGAGTG 30928         _   GC
            AGA                     TCTCGCTCT GTT  CCAGGCTGGA
                                  |||||||||  |||  ||||||||||
                                  AGAGTGAGA TAG  GGTCCGACTT
                                      G   TA
GAM642  DJ122O8.2 3'  ACTTCAGCCTGGGTGACAGAGT 40391          TG
            GAGA                    TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACTT
                                        GT          CAC
GAM642  DJ159A19.3 5'  TCGGCGTGGGAGAGCGAGA    32283         GTTG    G
                                  TCTCGCTCT    CCCA GCTGG
                                  |||||||||    |||| |||||
                                  AGAGCGAGA    GGGT CGGCT
                                       ____    G
GAM642  DJ37E16.5 3'  TCCAGTTCTGCACCGGGGTGGG 40099          T   CCA
            G                     TCTCGCTCTG TGC   GGCTGGA
                                  ||||||||||  |||   |||||||
                                  GGGGTGGGGC ACG   TTGACCT
                                       C   TC_
GAM642  dJ383J4.3 3'  TCCAGCCTGGGCAACAAAGTGA 67498        C
            GA                      TCTCGCT TGTTGCCCAGGCTGGA
                                  |||||||  ||||||||||||||||
                                  AGAGTGA ACAACGGGTCCGACCT
                                     A
GAM642  DKFZP434A0131 3'  TCCAGCCTGGGTGACAGAGCAA 39154     C       TG
            GA                      TCT GCTCTGT  CCCAGGCTGGA
                                  |||  |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A       GT
GAM642  DKFZP434B168 3'  TCCAGCCTGGGCGACAGAGCGA 31871
            GA                      TCTCGCTCTGTTGCCCAGGCTGGA
                                  |||||||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCCGACCT
                                              C
GAM642  DKFZP434B172 5'  TCCAGGAGACACAGAGTGAGG  70577           TGCCCAGG
                                  TCTCGCTCTGT       CTGGA
                                  ||||||||||        |||||
                                  GGAGTGAGACA       GACCT
                                       CAGAG___
GAM642  DKFZP434B205 5'  CCGGGTCGCGCAGGGCGGGG   75843           T__    A
                                  TCTCGCTCTGT   GCCC GG
                                  ||||||||||   |||| ||
```

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                                GGGGCGGGACG   TGGG CC
                                      CGC   _
GAM642   DKFZP434C171 3'  TCCAGCCCGGGTGACAGAGCAA 32199     C      TG   A
           GA                   TCT GCTCTGT  CCC GGCTGGA
                                ||| |||||||  ||| |||||||
                                AGA CGAGACA  GGG CCGACCT
                                  A      GT   C
GAM642   DKFZp434E169 3'  ACGCCAGCCTGGGCGACAGAGC 51072                    A
           GAGA                   TCTCGCTCTGTTGCCCAGGCTGG
                                  ||||||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCCGACC
                                        GCAC
GAM642   DKFZp434E2220 5'  ACTCCAGCCTGGGCGACAGGGT 34703
           GAGA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGGGACAGCGGGTCCGACCT
                                        CAC
GAM642   DKFZP434F091 5'  TTCAGCTTGGGGAGAGAGGGG  31899     G    G  G
                                CTC CTCT TT CCCAGGCTGGA
                                ||| |||| || ||||||||||
                                GGG GAGA AG GGGTTCGACTT
                                  _    G  _
GAM642   DKFZP434F1735 3'  TCCAGCCTGGGCAGTATAGCAA 32117     C   C
           GA                   TCT GCT TGTTGCCCAGGCTGGA
                                ||| ||| ||||||||||||||||
                                AGA CGA ATGACGGGTCCGACCT
                                  A   T
GAM642   DKFZp434G171 3'  TCCAGCCTGGGAGACACAGCGA 80247        C   TG
           GA                   TCTCGCT TGT  CCCAGGCTGGA
                                ||||||| |||  ||||||||||
                                AGAGCGA ACA  GGGTCCGACCT
                                    C   GA
GAM642   DKFZp434G171 3'  TCCAGCCTGGGCAACAAGAGGG 80248    G   _
           A                    TC CTCT GTTGCCCAGGCTGGA
                                || |||| ||||||||||||||||
                                AG GAGA CAACGGGTCCGACCT
                                 G    A
GAM642   DKFZP434I0714 5'  CCCGTGGCGTGGGGTGAGA    86991         TG T   CAG  T
                                TCTCGCTC  T GCC   GC GG
                                ||||||||  | |||   || ||
                                AGAGTGGG  G CGG   TG CC
                                     GT _   ___  C
GAM642   DKFZP434I1735 3'  ACTCCAGCCTGGGCGACAGAGT 89162
           GAGA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAGCGGGTCCGACCT
                                        CAC
GAM642   DKFZP434K1421 3'  TCCAACCTGGGCAACAGAATGA 50468      C           C
           GA                   TCTCG TCTGTTGCCCAGG TGGA
                                ||||| |||||||||||| ||||
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                                AGAGT AGACAACGGGTCC ACCT
                                  A           A
GAM642   DKFZp434K1815 3'  TTCAGCTTTGGGCCGATGGGGG 95917          _   _    _
           TGGGG                  TCTCGCTCT GTTG CCCAG GCTGGA
                                  ||||||||| |||| ||||| ||||||
                                  GGGGTGGGG TAGC GGGTT CGACTT
                                     G   C    T
GAM642   DKFZP434N1511 3'  TCCAGCCTGGGCAACAGAGCAA 93063     C
           GA                     TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAACGGGTCCGACCT
                                    A
GAM642   DKFZp434O0320 5'  CCTGGGTGGCGGAAGTGGGA   84697       _   TG
                                  TCTCGCT CTGT  CCCAGG
                                  ||||||| ||||  ||||||
                                  AGGGTGA GGCG  GGGTCC
                                      A   GT
GAM642   DKFZP434P0721 3'  TCCAGAAACATGGCAGAGCAGA 64467     C       GCCCAGG
                                  TCT GCTCTGTT      CTGGA
                                  ||| ||||||||      |||||
                                  AGA CGAGACGG      GACCT
                                    _       TACAAA_
GAM642   DKFZP434P211 3'  TCCAGCCTGGTCGACAGAGTGA 28031           C
                                  TCGCTCTGTTG CCAGGCTGGA
                                  |||||||||| |||||||||
                                  AGTGAGACAGC GGTCCGACCT
                                        T
GAM642   DKFZp547G183 3'  TCCAGCCTGGGCGACAAGAGC  38649      _
                                  GCTCT GTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||
                                  CGAGA CAGCGGGTCCGACCT
                                    A
GAM642   DKFZp547I094 3'  ACTCCAGCCTGGGCGGCAGAGT 50550
           GAGA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACGGCGGGTCCGACCT
                                                CAC
GAM642   DKFZP564A022 3'  ACTCCAGCCTGGGCAACAGAGT 48967
           GAGA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAACGGGTCCGACCT
                                                CAC
GAM642   DKFZP564B1023 3'  TCCAGCCTGGACAACAGATTGA 49368      C      C
           GA                     TCTCG TCTGTTG CCAGGCTGGA
                                  ||||| ||||||| ||||||||||
                                  AGAGT AGACAAC GGTCCGACCT
                                    T      A
GAM642   DKFZP564B1023 3'  TCCAGCCTGGGCAACAAGAGTG 49369       _
           A                       TCGCTCT GTTGCCCAGGCTGGA
                                  ||||||| ||||||||||||||||
```

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                                AGTGAGA CAACGGGTCCGACCT
                                    A
GAM642  DKFZP564C1940 5'  TCTGGCCTGGGAGCTGGCGA   26746      CT   G      TG
                                TCGCT  GTT CCCAGGC  GA
                                |||||  ||| |||||||  ||
                                AGCGG  CGA GGGTCCG  CT
                                   T_  _      GT
GAM642  DKFZP564I0422 3'  CTCCAGCCTGGGCAATGGAGTG 49511
           AGA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||||
                                AGAGTGAGGTAACGGGTCCGACCT
                                              CA
GAM642  DKFZP564I052 3'  TCCAGGCTGGGCAACAGAGTGA 67286              G
           GA                    TCTCGCTCTGTTGCCCAG CTGGA
                                |||||||||||||||||| |||||
                                AGAGTGAGACAACGGGTC GACCT
                                           G
GAM642  DKFZP564I122 3'  TCTAGCCTGGGTGACAGTGTGA 63881       T    TG
           GA                    TCTCGC CTGT  CCCAGGCTGGA
                                ||||||| ||||  ||||||||||
                                AGAGTG GACA  GGGTCCGATCT
                                   T    GT
GAM642  DKFZp564K142 3'  TCCAGCCTGAGTGATAGAGTGA 50436          TG C
           GA                    TCTCGCTCTGT  C CAGGCTGGA
                                ||||||||||  | |||||||||
                                AGAGTGAGATA  G GTCCGACCT
                                      GT A
GAM642  DKFZP564M182 3'  CTGTAGCCTGGGTGACAGTGTG 78627       T    TG       GA
           AGA                    TCTCGC CTGT  CCCAGGCTG
                                ||||||| ||||  |||||||||
                                AGAGTG GACA  GGGTCCGAT
                                   T    GT       GTCG
GAM642  DKFZP564M182 3'  TCCAGCCTGATGACAGAGCAAG 78642     C       CC
           A                     TCT GCTCTGTTG  CAGGCTGGA
                                ||| |||||||||  |||||||||
                                AGA CGAGACAGT  GTCCGACCT
                                  A        A_
GAM642  DKFZP564M182 3'  TCCAGCCTGGGCAACAGAGAGA 78643     G
           GA                    TCTC CTCTGTTGCCCAGGCTGGA
                                |||| ||||||||||||||||||||
                                AGAG GAGACAACGGGTCCGACCT
                                  A
GAM642  DKFZP564M182 3'  TCCAGCCTGGGCGGCAGAGC   78644
                                GCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||
                                CGAGACGGCGGGTCCGACCT

GAM642  DKFZp566H0824 3'  TCCAGCCTGGGCAACAGAGCAA 34492     C
           GG                    TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
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                                GGA CGAGACAACGGGTCCGACCT
                                  A
GAM642   DKFZp566H0824 5'  TCCAGCCTGGGCGACAGAGCGA 34493
            GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCCGACCT

GAM642   DKFZP586C1324 3'  TCAAGTCTGGGCGACAGGGTGA 70361                G
            GA                    TCTCGCTCTGTTGCCCAGGCT GA
                                  |||||||||||||||||||| ||
                                  AGAGTGGGACAGCGGGTCTGA CT
                                              A
GAM642   DKFZP586D2223 3'  AGACTAGCCTGGGCAACATAGC 38284        C          A
            GAGA                    TCTCGCT TGTTGCCCAGGCTGG
                                  ||||||| ||||||||||||||||
                                  AGAGCGA ACAACGGGTCCGATC
                                     T          AGAA
GAM642   DKFZP586D2223 3'  ATTCTAGCCTGGGCAACAGAGT 38285
            GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAACGGGTCCGATCT
                                              TAC
GAM642   DKFZP586D2223 3'  TTCAGCCTGGGTGACAGAGCAA 38300     C      TG
            GA                    TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACTT
                                    A      GT
GAM642   DKFZP586M1120 3'  TCCAGCCTGGGCAACAGAGTGA 49286
                                  TCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||
                                  AGTGAGACAACGGGTCCGACCT

GAM642   DKFZP667O116 3'  AGACCAGCCTGGGCAACATAGC 95938        C          A
            GAGA                    TCTCGCT TGTTGCCCAGGCTGG
                                  ||||||| ||||||||||||||||
                                  AGAGCGA ACAACGGGTCCGACC
                                     T          AGAG
GAM642   DKFZp727G131 3'  TCCAGCCTGGGCAACAGCGTGA 59698       T
            GA                    TCTCGC CTGTTGCCCAGGCTGGA
                                  ||||||| ||||||||||||||||
                                  AGAGTG GACAACGGGTCCGACCT
                                     C
GAM642   DKFZp761B0514 5'  ACCGGCGGCGGCGGGGCGGGA  51141             CAG    A
                                  TCTCGCTCTGTTGCC   GCTGG
                                  ||||||||||||||   |||||
                                  AGGGCGGGGCGGCGG   CGGCC
                                              ___    AG
GAM642   DKFZP761G1913 3'  TCCAGCCTGGGTGAAGGAGTGA 49699         G TG
            GA                    TCTCGCTCT T  CCCAGGCTGGA
                                  |||||||| |  ||||||||||
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                                AGAGTGAGG A  GGGTCCGACCT
                                     A GT
GAM642  DKFZp761J139 5'  TCCAGGTTGGGCTACAGAGTGA 51113          T     G
          GA                      TCTCGCTCTGT GCCCAG CTGGA
                                  |||||||||| |||||| |||||
                                  AGAGTGAGACA CGGGTT GACCT
                                        T     G
GAM642  DKFZp761N0624 3'  TCTAGCCTTGAAAATGGAGTGA 51161          GCCC
                                  TCGCTCTGTT    AGGCTGGA
                                  ||||||||||    ||||||||
                                  AGTGAGGTAA    TCCGATCT
                                        AAGT
GAM642  DKFZp761O17121 3'  TCCAGCCTGTAGGGGAGTGA   51135        G    CC
                                  TCGCTCT TTGC  AGGCTGGA
                                  ||||||| ||||  ||||||||
                                  AGTGAGG GATG  TCCGACCT
                                     G   __
GAM642  DLAT     5'  TCTGGCCTGGGGAGCGGGTGGA 68086    T  T    G      TG
                                  TC CGC CTGTT CCCAGGC  GA
                                  || ||| ||||| |||||||  ||
                                  AG GTG GGCGA GGGTCCG  CT
                                   _  _    G      GT
GAM642  DMRTB1    3'  CCTGGCCAGCAGAGTGGGG    66839            C
                                  TCTCGCTCTGTTG CCAGG
                                  |||||||||||| |||||
                                  GGGGTGAGACGAC GGTCC
                                        C
GAM642  DOC-1R    5'  TCTGAAGCAGCGCGAGTGAGG  20723          _     C_
                                  TCTCGCTC TGTTGC  CAGG
                                  |||||||| ||||||  ||||
                                  GGAGTGAG GCGACG  GTCT
                                     C      AA
GAM642  DRF1      3'  TCCAGCCTGGGCGATAGAGCTA 47757     C
          GA                        TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||
                                  AGA CGAGATAGCGGGTCCGACCT
                                    T
GAM642  DRF1      3'  CTCCAGCCTGGGTGACAGAGCG 47746           TG
          AGA                       TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GT          CA
GAM642  DSCR6     3'  TCCAGCCTGGGCAACAAGAGCG 39076        _
          A                         TCGCTCT GTTGCCCAGGCTGGA
                                  ||||||| ||||||||||||||||
                                  AGCGAGA CAACGGGTCCGACCT
                                     A
GAM642  DXS1357E  5'  TCCGGCCGCGGTATGAGGGGCG 20435         GT_    CA
          GGG                       TCTCGCTCT   TGCC  GGCTGGA
                                  |||||||||   ||||  |||||||
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                                GGGGCGGGG  ATGG  CCGGCCT
                                     AGT   CG
GAM642  DXS9879E  3'  GCCTGGCCTGGGCAAATGGAGC 21180          _      TG A
           GAGG                   TCTCGCTCTGTT GCCCAGGC  G
                                  |||||||||||| ||||||||  |
                                  GGAGCGAGGTAA CGGGTCCG  C
                                         A       GT CGA
GAM642  E1B-AP5  3'  TCTGGTGGGATTCAGTGGGTGA 59233       __  TTG  AG  TG
           GA                     TCTCGCT  CTG  CCC  GC  GA
                                  |||||||  |||  |||  ||  ||
                                  AGAGTGG  GAC  GGG  TG  CT
                                     GT  TTA  __ GT
GAM642  EIF2S1   3'  TCGAGCCTGGGTGACAGGGCAA 15848    C     TG      G
           GA                     TCT GCTCTGT  CCCAGGCT GA
                                  ||| |||||||  |||||||| ||
                                  AGA CGGGACA  GGGTCCGA CT
                                    A      GT       G
GAM642  EIF4B    3'  TTGGGCAGTAGGGGAGG     76498      G
                                  TCTC CTCTGTTGCCCAG
                                  |||| ||||||||||||
                                  GGAG GGGATGACGGGTT
                                   _
GAM642  EMILIN-2  3'  TCCAGCCAGGCTGCAGGGAGTG 50257         __  T   CA
           AGG                     TCTCGCTCT  GT GCC  GGCTGGA
                                  |||||||||  || |||  |||||||
                                  GGAGTGAGG  CG CGG  CCGACCT
                                       GA  T   A_
GAM642  EPN2     3'  CCGAGGGCGTGGGGTGGGG   31039        TG T    A_
                                  TCTCGCTC  T GCCC  GG
                                  ||||||||  | ||||  ||
                                  GGGGTGGG  G CGGG  CC
                                       GT _    AG
GAM642  ESDN     5'  TCCGGCCTGGGGTCTCGGCGCG 56063      T   TTG_
           GG                      CTCGC CTG    CCCAGGCTGGA
                                  ||||| |||    ||||||||||
                                  GGGCG GGC    GGGTCCGGCCT
                                    C   TCTG
GAM642  ET       3'  TCCAGGCTGGGCAACGGAGTGA 44475               G
           GA                      TCTCGCTCTGTTGCCCAG CTGGA
                                  |||||||||||||||| |||||
                                  AGAGTGAGGCAACGGGTC GACCT
                                           G
GAM642  FADS1    3'  TCCAGCCTGGGCGACAGAGCAA 26386     C
           GA                      TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM642  FAM8A1   3'  TTTAGTATTCAAGCTGAGTGAG 33204         T   GCCCAG
           A                       TCTCGCTC GTT      GCTGGA
                                  |||||||| |||      ||||||
```

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                                AGAGTGAG CGA      TGATTT
                                    T   ACTTA_
GAM642   FBXO26   3'  TCCAGCCTGGGTGAGAAAGCAA 46631     C   CTG TG
              GA                  TCT GCT   T  CCCAGGCTGGA
                                  ||| |||   |  ||||||||||
                                  AGA CGA   A  GGGTCCGACCT
                                    A   AAG GT
GAM642   FBXO27   3'  ACTCCAGCCTGGGTGACAGAGC 74998           TG
              GAGA                  TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GT          CAC
GAM642   FBXO27   3'  TCCAGCCTGGGCAACACAGCGA 75014        C
              GA                  TCTCGCT TGTTGCCCAGGCTGGA
                                  |||||||  ||||||||||||||||
                                  AGAGCGA ACAACGGGTCCGACCT
                                      C
GAM642   FBXO6    3'  CTCCAGCCTGGGTGACAGAGCG 37992           TG
              AGA                   TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GT          CA
GAM642   FBXO9    3'  TCCAGCCTGAGCAACACAGTGA 54255        C     C
              GA                  TCTCGCT TGTTGC CAGGCTGGA
                                  |||||||  ||||||  |||||||||
                                  AGAGTGA ACAACG GTCCGACCT
                                      C      A
GAM642   FEM1B    5'  TCCGGCCTGAGGCCCGGGGCGG 31680         TT   _
                                  TCGCTCTG  GCC CAGGCTGGA
                                  ||||||||  ||| |||||||||
                                  GGCGGGGC  CGG GTCCGGCCT
                                       C_   A
GAM642   FHX      5'  TCAGCCTTCTGGAGAGGGG    37923      G    GTTGCCC
                                  TCTC CTCT       AGGCTGG
                                  |||| ||||       |||||||
                                  GGGG GAGG       TCCGACT
                                    A    TCT____
GAM642   FHX      5'  TCCAGTTTGGGGGGGAGGGGA  37924      G    GT G
                                  TCTC CTCT  T CCCAGGCTGGA
                                  |||| ||||  | ||||||||||
                                  AGGG GAGG  G GGGTTTGACCT
                                    _    __ G
GAM642   FKBP14   3'  TCCAGCCTGGGTGACAGAGCAA 36070     C       TG
              GA                  TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A       GT
GAM642   FKSG17   3'  TCCAGCCTGGGTGACAGAGTGA 50159           TG
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
```

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                                AGAGTGAGACA  GGGTCCGACCT
                                      GT
GAM642  FKSG43   5'  TCCAGCCTGGGTGACAGAGCAA 50163     C      TG
           GA                   TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM642  FKSG44   5'  ACTCCAGCCTGGGCGACAGAGC 49960
           GAGA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGCGAGACAGCGGGTCCGACCT
                                          CAC
GAM642  FLJ00007 5'  TTCAGACCTGGCAGCAGAGGGA 71785      G        C  _
           GG                   TCTC CTCTGTTGCC AGG CTGGA
                                |||| |||||||||| ||| |||||
                                GGAG GAGACGACGG TCC GACTT
                                  G        _  A
GAM642  FLJ00007 3'  TCTGGCCTAAGGTAGGGGAG   71783     G    C_   TG
                                CTCT TTGCC  AGGC  GA
                                |||| |||||  ||||  ||
                                GAGG GATGG  TCCG  CT
                                  G    AA   GT
GAM642  FLJ00060 3'  TCCAGCCTGGGCGATAGAGCAA 61755     C
           GA                   TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||
                                AGA CGAGATAGCGGGTCCGACCT
                                  A
GAM642  FLJ10008 3'  TCCAGCCTGGGCGACACAGCAA 36193     C  C
           GA                   TCT GCT TGTTGCCCAGGCTGGA
                                ||| ||| ||||||||||||||||
                                AGA CGA ACAGCGGGTCCGACCT
                                  A  C
GAM642  FLJ10043 3'  ACTCCAGCCTGGGTGACAGAGC 36225          TG
           GAGA                   TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      GT         CAC
GAM642  FLJ10058 3'  TCCAGCCTGGGCAACACAGTGA 36264       C
           GA                   TCTCGCT TGTTGCCCAGGCTGGA
                                ||||||| ||||||||||||||||
                                AGAGTGA ACAACGGGTCCGACCT
                                    C
GAM642  FLJ10097 3'  CCAGACTCACAGAGTGGGG   69035          T CCC  G
                                TCTCGCTCTGT G   AG CTGG
                                |||||||||| |   || ||||
                                GGGGTGAGACA C   TC GACC
                                      _ ___  A
GAM642  FLJ10139 3'  AGACCAGCCTGGGCAACATGGT 36314       C           A
           GAGA                   TCTCGCT TGTTGCCCAGGCTGG
                                ||||||| ||||||||||||||||
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                                AGAGTGG ACAACGGGTCCGACC
                                   T            AGAG
GAM642  FLJ10139  3' TCCAGCCTGGGTGACAAAGTAA 36317    CG  C   TG
             GA                  TCT  CT TGT  CCCAGGCTGGA
                                 |||  || |||  ||||||||||
                                 AGA  GA ACA  GGGTCCGACCT
                                   AT  A   GT
GAM642  FLJ10199  3' TTGGATGGCGGCGGGCGGGG   71757       T      CAGG TG
                                 TCTCGC CTGTTGCC    C  GA
                                 ||||||| ||||||||    |  ||
                                 GGGGCG GGCGGCGG    G  TT
                                    _       TA__ GT
GAM642  FLJ10201  3' TCCAGCCCTGGTGACAGAGGAG 36355     G     TG  CA
             A                   TCTC CTCTGT  CC  GGCTGGA
                                 |||| ||||||  ||  |||||||
                                 AGAG GAGACA  GG  CCGACCT
                                   _     GT  TC
GAM642  FLJ10244  3' TCCAGCCTGGGCAAAAAGAGC  36406      G_
                                 GCTCT  TTGCCCAGGCTGGA
                                 |||||  ||||||||||||||
                                 CGAGA  AACGGGTCCGACCT
                                   AA
GAM642  FLJ10379  3' TCTAGGTAGCAGATGAGA    36568       C       C
                                 TCTCG TCTGTTGCC AGG
                                 ||||| ||||||||| |||
                                 AGAGT AGACGATGG TCT
                                    _        A
GAM642  FLJ10460  3' TCCAACCTGGGTGATGGAGCAA 36623     C      TG     C
             GA                  TCT GCTCTGT  CCCAGG TGGA
                                 ||| |||||||  |||||| ||||
                                 AGA CGAGGTA  GGGTCC ACCT
                                   A      GT     A
GAM642  FLJ10520  3' TCCAGCCTCGGTGACAGAGCAA 36710     C      TG  C
             GA                  TCT GCTCTGT  CC AGGCTGGA
                                 ||| |||||||  || ||||||||
                                 AGA CGAGACA  GG TCCGACCT
                                   A      GT  C
GAM642  FLJ10525  5' TCCGGCCTGTGTGTGGCGCGAG 36724       T TG T  C
             G                   TCTCGC C  T GC CAGGCTGGA
                                 |||||| |  | || |||||||||
                                 GGAGCG G  G TG GTCCGGCCT
                                    C GT _  T
GAM642  FLJ10546  3' TTTGGTCTCTTTTGGTGGGGTG 60186        TG  GCCC_   TG
             GGG                   TCTCGCTC  TT    AGGC  GA
                                   ||||||||  ||    ||||  ||
                                   GGGGTGGG  GG    TCTG  TT
                                      GT  TTTTC    GT
GAM642  FLJ10547  3' TCCAGCCTGGGCTACAGAGCGA 36779          T
             GA                    TCTCGCTCTGT GCCCAGGCTGGA
                                   |||||||||| ||||||||||
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                                AGAGCGAGACA CGGGTCCGACCT
                                      T
GAM642  FLJ10613  3'  TCTAGCCTGGGCAACAACACGA 39341     CTC
                                TCG   TGTTGCCCAGGCTGGA
                                |||   ||||||||||||||||
                                AGC   ACAACGGGTCCGATCT
                                  ACA
GAM642  FLJ10648  3'  TTCAGTCTAGCCCAGACCGGGA 36894      C    TT  CC
                                TCTCG TCTG  GC  AGGCTGGA
                                ||||| ||||  ||  ||||||||
                                AGGGC AGAC  CG  TCTGACTT
                                   C    C_  A_
GAM642  FLJ10650  3'  TCCAGCCTGGGCGACAGAATGA 36903      C
           GA                     TCTCG TCTGTTGCCCAGGCTGGA
                                ||||| ||||||||||||||||||
                                AGAGT AGACAGCGGGTCCGACCT
                                   A
GAM642  FLJ10704  3'  TCCAGCCTGGACGACAGAGTGA 36984           C
           GA                     TCTCGCTCTGTTG CCAGGCTGGA
                                |||||||||||| ||||||||||
                                AGAGTGAGACAGC GGTCCGACCT
                                      A
GAM642  FLJ10709  3'  TCTGGCTCACAGGGGGAGGGTG 36989         GT G   A___   TG
           AGG                    TCTCGCTCT  T CCC    GGC  GA
                                |||||||||  | |||   |||  ||
                                GGAGTGGGA  G GGG    TCG  CT
                                     __ G   ACAC   GT
GAM642  FLJ10761  3'  TCTTGGTGATGGGTGGGG    37133       T    TG  C
                                TCTCGC CTGT  CC AGG
                                ||||||| ||||  || |||
                                GGGGTG GGTA  GG TCT
                                   _    GT  T
GAM642  FLJ10781  3'  TCCAGCCTGGGCAGCAGAGTGA 37176
           GA                     TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGACGACGGGTCCGACCT

GAM642  FLJ10803  3'  TCCAGCCTGGGCAACAGAGCAA 37209     C
           GA                     TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||
                                AGA CGAGACAACGGGTCCGACCT
                                  A
GAM642  FLJ10811  3'  CCTGGGCAATGTAGTGAGA    37222        CT
                                TCTCGCT  GTTGCCCAGG
                                |||||||  ||||||||||
                                AGAGTGA  TAACGGGTCC
                                    TG
GAM642  FLJ10826  3'  TCCAGCCTGGGCAACAAGAGTG 37250         _
           A                      TCGCTCT GTTGCCCAGGCTGGA
                                ||||||| ||||||||||||||||
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                                AGTGAGA CAACGGGTCCGACCT
                                    A
GAM642  FLJ10830  3'  TCCAGCCTGGGCGACAGAACGA 37267      C
            GA                    TCTCG TCTGTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||||||
                                  AGAGC AGACAGCGGGTCCGACCT
                                    A
GAM642  FLJ10936  3'  TCCAGCCTGGGCAACAGAGGGA 37450     G
            GA                    TCTC CTCTGTTGCCCAGGCTGGA
                                  |||| ||||||||||||||||||
                                  AGAG GAGACAACGGGTCCGACCT
                                    G
GAM642  FLJ10986  5'  TCTGGTGGACCAGAGTGGGG  37492         _ GC
                                  TCTCGCTCTG TT  CCAGG
                                  |||||||||| ||  |||||
                                  GGGGTGAGAC AG  GGTCT
                                        C  GT
GAM642  FLJ10989  3'  TCCAGCCTGGGTGACAAAGCAA 37507    C   C   TG
            GA                    TCT GCT TGT  CCCAGGCTGGA
                                  ||| ||| |||  ||||||||||
                                  AGA CGA ACA  GGGTCCGACCT
                                    A   A   GT
GAM642  FLJ10998  3'  TCCAGCCTGGGTGACAGTGA  37523      CT  TG
                                  TCGCT  GT  CCCAGGCTGGA
                                  |||||  ||  ||||||||||
                                  AGTGA  CA  GGGTCCGACCT
                                    __  GT
GAM642  FLJ11000  3'  TCTAGCTTCAGGAGGGTGGGG  37528        G   CCC
                                  TCTCGCTCT TTG   AGGCTGGA
                                  ||||||||| |||   ||||||||
                                  GGGGTGGGA GAC   TTCGATCT
                                        G  ___
GAM642  FLJ11036  3'  CCTGGGCAACATAGTGAGA   37555       C
                                  TCTCGCT TGTTGCCCAGG
                                  ||||||| ||||||||||
                                  AGAGTGA ACAACGGGTCC
                                      T
GAM642  FLJ11036  3'  TCCAGCCTGGGCGACAGAGCAA 37556    C
            GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM642  FLJ11042  3'  TCCAGTTTGGACTACAGAGTGA 37566          TGC
            GA                    TCTCGCTCTGT   CCAGGCTGGA
                                  |||||||||||   ||||||||||
                                  AGAGTGAGACA   GGTTTGACCT
                                        TCA
GAM642  FLJ11106  3'  TCCAGCCTGGGTGACAGATCCA 37626    CGC    TG
            GA                    TCT   TCTGT  CCCAGGCTGGA
                                  |||   |||||  ||||||||||
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                                AGA   AGACA  GGGTCCGACCT
                                  CCT     GT
GAM642  FLJ11116 3' TTTGGCCTCTTACTAGGGGGGA 83476      G    T  CCC    TG
                                TCTC CTCTG TG   AGGC  GA
                                |||| ||||| ||   ||||  ||
                                AGGG GGGAT AT   TCCG  TT
                                  _    C  TC_    GT
GAM642  FLJ11126 3' ACTCCAGCCTGGGTAACAGAGC 37646
            GAGA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||
                                AGAGCGAGACAATGGGTCCGACCT
                                              CAC
GAM642  FLJ11149 3' GACCAGTCTGGGCAACATAGCG 37685        C            A
            AGA                   TCTCGCT TGTTGCCCAGGCTGG
                                ||||||| |||||||||||||||
                                AGAGCGA ACAACGGGTCTGACC
                                    T            AGA
GAM642  FLJ11151 3' TCCAGCCTGGGCAACAGAGCAA 68482     C
            GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGAGACAACGGGTCCGACCT
                                  A
GAM642  FLJ11259 3' ACTCCAGTCTGGGCAACAGAGT 37761
            GAGA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||
                                AGAGTGAGACAACGGGTCTGACCT
                                              CAC
GAM642  FLJ11267 3' GACTTGCCTGGGCGGCATAGTG 39497        C          T  A
            AGA                   TCTCGCT TGTTGCCCAGGC GG
                                ||||||| |||||||||||| ||
                                AGAGTGA ACGGCGGGTCCG TC
                                    T          T  AGA
GAM642  FLJ11301 3' ACTCCAGCCTGGGCGACAGAGT 37801
            GAGA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||
                                AGAGTGAGACAGCGGGTCCGACCT
                                              CAC
GAM642  FLJ11301 3' TTCAGTTAGTGTACAGCGGGG  37813        CC  __
                                CTCTGTTG  CA  GGCTGGA
                                ||||||||  ||  |||||||
                                GGGGCGAC  GT  TTGACTT
                                     AT  GA
GAM642  FLJ11370 3' TTCAGATCTGCAGCAGAGCAAG 46971     C        CC  _
            A                    TCT GCTCTGTTGC  AGG CTGGA
                                ||| ||||||||||  ||| |||||
                                AGA CGAGACGACG  TCT GACTT
                                  A         __  A
GAM642  FLJ11413 3' TCTGGCCTGTGGCAGGGCCGGG 44959       _     TG CC    TG
            A                    TCTCG CTCTGT  C  AGGC  GA
                                ||||| ||||||  |  ||||  ||
```

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                                AGGGC GGGACG  G  TCCG  CT
                                  C     GT __    GT
GAM642  FLJ11577  3'  TCCAGCCTGGGCAACAAGAGTG 47960         _
          AGA                    TCTCGCTCT GTTGCCCAGGCTGGA
                                 ||||||||| ||||||||||||||||
                                 AGAGTGAGA CAACGGGTCCGACCT
                                    A
GAM642  FLJ11700  3'  TCCAGCCTGGGCAACAGAACAA 46567     CGC
          GA                     TCT   TCTGTTGCCCAGGCTGGA
                                 |||   ||||||||||||||||||
                                 AGA   AGACAACGGGTCCGACCT
                                   ACA
GAM642  FLJ11710  5'  AGACCAGCCTGGGCAACACAGT 46239         C             A
          GAGA                     TCTCGCT TGTTGCCCAGGCTGG
                                   ||||||| ||||||||||||||
                                   AGAGTGA ACAACGGGTCCGACC
                                      C             AGAG
GAM642  FLJ11710  5'  TCCAGCCTGGGCAACAGAGCAA 46252     C
          GA                     TCT GCTCTGTTGCCCAGGCTGGA
                                 ||| ||||||||||||||||||||
                                 AGA CGAGACAACGGGTCCGACCT
                                   A
GAM642  FLJ11715  3'  ACTCCAGCCTGGGTGATAGAGT 44973           TG
          GAGA                     TCTCGCTCTGT  CCCAGGCTGGA
                                   |||||||||||  ||||||||||
                                   AGAGTGAGATA  GGGTCCGACCT
                                      GT          CAC
GAM642  FLJ11715  3'  TTTGGGCAACACAGTGAGA    44984         C
                                 TCTCGCT TGTTGCCCAGG
                                 ||||||| ||||||||||
                                 AGAGTGA ACAACGGGTTT
                                    C
GAM642  FLJ11722  3'  TCCAGCCTGGCCACAGAGCGAG 47009           T   C
          A                       TCTCGCTCTGT GCC AGGCTGGA
                                  |||||||||| ||| ||||||||
                                  AGAGCGAGACA CGG TCCGACCT
                                     C   _
GAM642  FLJ11726  3'  TCCAGCCTGGGCGACAGAGCAG 47031    TC
          GA                     TC  GCTCTGTTGCCCAGGCTGGA
                                 ||  ||||||||||||||||||||
                                 AG  CGAGACAGCGGGTCCGACCT
                                   GA
GAM642  FLJ11800  3'  TCCAGCCTGGGCAACAGAG    47042
                                 CTCTGTTGCCCAGGCTGGA
                                 ||||||||||||||||||
                                 GAGACAACGGGTCCGACCT

GAM642  FLJ11827  3'  TTCAGCCTGGGCAACATAGCAA 47683     C   C
          GA                     TCT GCT TGTTGCCCAGGCTGGA
                                 ||| ||| ||||||||||||||||
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                                AGA CGA ACAACGGGTCCGACTT
                                  A   T
GAM642  FLJ11996 3' TCCAACCTGGGCAACAGAGTAA 47069     CG          C
           GA                    TCT  CTCTGTTGCCCAGG TGGA
                                |||  |||||||||||||| ||||
                                AGA  GAGACAACGGGTCC ACCT
                                  AT           A
GAM642  FLJ11996 3' TCCAGCTTGGGTGACAGAGCAA 47070     C      TG
           GA                    TCT GCTCTGT  CCCAGGCTGGA
                                |||  |||||||  ||||||||||
                                AGA CGAGACA  GGGTTCGACCT
                                  A      GT
GAM642  FLJ12056 3' TCCAGCCTGCTTCAGGAGGGAG 46825      G    GTTGCC
           G                     TCTC CTCT     CAGGCTGGA
                                ||||  ||||     |||||||||
                                GGAG GAGG     GTCCGACCT
                                  G    ACTTC_
GAM642  FLJ12056 3' TTCAGCCCGGGCAACAAGAGCG 46827          _      A
           AGA                     TCTCGCTCT GTTGCCC GGCTGGA
                                |||||||||  |||||||  |||||||
                                AGAGCGAGA CAACGGG CCGACTT
                                     A      C
GAM642  FLJ12078 3' TCCAGCCTGGGTGGCAGAGAGA 47086      G     TG
           GA                    TCTC CTCTGT  CCCAGGCTGGA
                                ||||  ||||||  ||||||||||
                                AGAG GAGACG  GGGTCCGACCT
                                  A     GT
GAM642  FLJ12190 3' TCCAGCCTGGGCAACAGAGC   47572
                                GCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||
                                CGAGACAACGGGTCCGACCT

GAM642  FLJ12294 3' TCCAGCCTGGGTGACAGAGAGA 47721      G     TG
           GA                    TCTC CTCTGT  CCCAGGCTGGA
                                ||||  ||||||  ||||||||||
                                AGAG GAGACA  GGGTCCGACCT
                                  A     GT
GAM642  FLJ12298 3' ACTCCAGCCTGGGCAACAGAGC 50592
           GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||||
                                AGAGCGAGACAACGGGTCCGACCT
                                        CAC
GAM642  FLJ12331 3' TCCAGCCTGAGCTACAGAGCAA 47114     C      T  C
           GA                    TCT GCTCTGT GC CAGGCTGGA
                                |||  |||||||  ||  |||||||||
                                AGA CGAGACA CG GTCCGACCT
                                  A      T  A
GAM642  FLJ12363 3' TCCAGCCTGGGCAACAAGAGAG 50643      G  C
           A                     TCTC CT TGTTGCCCAGGCTGGA
                                ||||  ||  ||||||||||||||||
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                                AGAG GA ACAACGGGTCCGACCT
                                  A _
GAM642  FLJ12409  3'  TCTAGCTTTGATGGCGAAGTGA 47773        CTG    C___
                GA                TCTCGCT   TTGCC    AGGCTGGA
                                  |||||||   |||||    ||||||||
                                  AGAGTGA   AGCGG    TTCGATCT
                                     ___    TAGT
GAM642  FLJ12448  3'  TCTAGCCTAAGCAATGGAGCAA 43481     C        CC
                GA                TCT GCTCTGTTGC  AGGCTGGA
                                  ||| ||||||||||  ||||||||
                                  AGA CGAGGTAACG  TCCGATCT
                                    A         AA
GAM642  FLJ12484  3'  TCCGGCTTGGCTGTTCCAGCAG 43177       T     C_____
                GTGGGG                TCTCGC CTGTTG     CCAGGCTGGA
                                  ||||||| ||||||      ||||||||||
                                  GGGGTG GACGAC     GGTTCGGCCT
                                     _     CTTGTC
GAM642  FLJ12586  3'  ACTCCAGCCTGGGTGACAGAGC 45203           TG
                GAGA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                       GT         CAC
GAM642  FLJ12587  5'  TCTGAGGCGGCGGCGGCGGCGG 42785       ____      _   CTGGA
                GG                TCTCGCT    CTGTTGCC CAGG
                                  |||||||    |||||||| ||||
                                  GGGGCGG    GGCGGCGG GTCT
                                     CGGC       A      A
GAM642  FLJ12592  3'  GGACCAGCCTGGGCAACATAGC 50652        C           A
                GAGA                TCTCGCT TGTTGCCCAGGCTGG
                                  ||||||| ||||||||||||||
                                  AGAGCGA ACAACGGGTCCGACC
                                     T            AGGA
GAM642  FLJ12592  3'  TCCAGCCTGGGTGACCGAGTGA 50655         T  TG
                GA                TCTCGCTC GT  CCCAGGCTGGA
                                  |||||||| ||  ||||||||||
                                  AGAGTGAG CA  GGGTCCGACCT
                                     C  GT
GAM642  FLJ12606  3'  ACTTCAGCCTGGGTGACAGAGT 46059           TG
                GAGA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACTT
                                       GT         CAC
GAM642  FLJ12618  3'  TCCAGCCTGGGTGACAGAGCAA 46508     C      TG
                GA                TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A      GT
GAM642  FLJ12643  5'  GCTTGGGCCGCAGGGCGGGA   83672           T
                                  TCTCGCTCTGT GCCCAGGC
                                  |||||||||| ||||||||
```

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                                AGGGCGGGACG CGGGTTCG
                                      C
GAM642  FLJ12650  3'  TTCGGAGGAGTGGGGCGGGGCG 44827          TG   GG___
                GGG                TCTCGCTCTGT  CCCA    CTGGA
                                   |||||||||||  ||||    |||||
                                   GGGGCGGGGCG  GGGT    GGCTT
                                         __   GAGGA
GAM642  FLJ12660  3'  TCCAGCCTGGTCAATGGAGTGC 47900    T       C
                GA                  TC CGCTCTGTTG CCAGGCTGGA
                                    || |||||||||| ||||||||||
                                    AG GTGAGGTAAC GGTCCGACCT
                                     C        T
GAM642  FLJ12666  3'  TCCAGCCTGGGCAACAAAACGA 45072      CTC
                GA                  TCTCG   TGTTGCCCAGGCTGGA
                                    |||||   ||||||||||||||||
                                    AGAGC   ACAACGGGTCCGACCT
                                       AAA
GAM642  FLJ12671  3'  TCCAGCCTGGGTGACAAGAGTG 49112        _ TG
                AGA                 TCTCGCTCT GT  CCCAGGCTGGA
                                    |||||||||  ||  ||||||||||
                                    AGAGTGAGA CA  GGGTCCGACCT
                                         A  GT
GAM642  FLJ12687  3'  CTCCAGCCTGGGTGACAGAGTG 46749          TG
                AGA                 TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          GT         CA
GAM642  FLJ12800  3'  TCCAGGCTGGGCGACAGAGTGA 43534              G
                GA                  TCTCGCTCTGTTGCCCAG CTGGA
                                    |||||||||||||||||| |||||
                                    AGAGTGAGACAGCGGGTC GACCT
                                             G
GAM642  FLJ12847  3'  TCCAGCCTGGGCAACAGAGT   45079
                                    GCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||
                                    TGAGACAACGGGTCCGACCT

GAM642  FLJ12891  3'  TTGGCGGGGGGGTGGAGCGGGG  46934        TG  G   AG  TG
                                    TCTCGCTC  TT CCC  GC  G
                                    ||||||||  || |||  ||  |
                                    GGGGCGAG  GG GGG  CG  T
                                         GT  G   __  GT
GAM642  FLJ12921  3'  ACTCCAGCCTGGGCGACGGAGC 46389
                GAGA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                      ||||||||||||||||||||||||
                                      AGAGCGAGGCAGCGGGTCCGACCT
                                                CAC
GAM642  FLJ12949  3'  TCCAGCCTGGGCAACAAAGCAA 43727     C   C
                GA                  TCT GCT TGTTGCCCAGGCTGGA
                                    ||| ||| ||||||||||||||||
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                                AGA CGA ACAACGGGTCCGACCT
                                  A   A
GAM642  FLJ13117  3'  TCCAGCCTGGGAGACAGAGCAA 43811     C      TG
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGAGACA  GGGTCCGACCT
                                      A      GA
GAM642  FLJ13162  3'  TCCGGCCTGGGCAACAAGAGC  47188       _
                                    GCTCT GTTGCCCAGGCTGGA
                                    ||||| ||||||||||||||
                                    CGAGA CAACGGGTCCGGCCT
                                      A
GAM642  FLJ13194  5'  TCTGGCTGGCGGCAGCGGCGGG 47874        _       CA   TG
                A                    TCTCGCT CTGTTGCC  GGC  GA
                                    ||||||| ||||||||  |||  ||
                                    AGGGCGG GACGGCGG  TCG  CT
                                        C       __   GT
GAM642  FLJ13241  3'  TCCAGCCTGGGTGGCAGAGCCA 47656     C      TG
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGAGACG  GGGTCCGACCT
                                      C      GT
GAM642  FLJ13262  3'  TTAGTCCCGGTGGAGCGG    46697        GTT   CA
                                    TCGCTCT   GCC  GGCTGG
                                    |||||||   |||  ||||||
                                    GGCGAGG   TGG  CTGATT
                                        ____   CC
GAM642  FLJ13265  3'  TCTGTATCTGGTGGTGGATGGG 46413       C  TG TG  C   CT_
                G                    TCTCG TC  T  CC AGG   GGA
                                    ||||| ||  |  || |||   |||
                                    GGGGT AG  G  GG TCT   TCT
                                      _  GT GT  _   ATG
GAM642  FLJ13273  5'  TCCAGCTCGGACTGGGCGGGA  45724         T  TGC  AG
                                    TCTCGCTC GT   CC  GCTGGA
                                    |||||||| ||   ||  ||||||
                                    AGGGCGGG CA   GG  CGACCT
                                        T  ____  CT
GAM642  FLJ13315  3'  TTTAGCCTGGGCAGTATAGTGA 47202       C
                                    TCGCT TGTTGCCCAGGCTGGA
                                    ||||| ||||||||||||||||
                                    AGTGA ATGACGGGTCCGATTT
                                      T
GAM642  FLJ13352  3'  AGCCTGGCCTGGGCAACAGAGC 45047     C             TG A
                AAGA                  TCT GCTCTGTTGCCCAGGC  G
                                    ||| ||||||||||||||||  |
                                    AGA CGAGACAACGGGTCCG  C
                                      A             GT CGAC
GAM642  FLJ13390  3'  TCCATCCTGGGTCACAGAGTGA 42840           T      C
                GA                  TCTCGCTCTGT GCCCAGG TGGA
                                    |||||||||| ||||||| ||||
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                                AGAGTGAGACA TGGGTCC ACCT
                                      C      T
GAM642  FLJ13448  3'  TCCAGCCTGGGCAACAGAGGGA 47885      G
                GA                  TCTC CTCTGTTGCCCAGGCTGGA
                                    |||| ||||||||||||||||||
                                    AGAG GAGACAACGGGTCCGACCT
                                      G
GAM642  FLJ13456  3'  AGACTAGCCTGGGCAACATAGT 66526        C            A
                GAGA                  TCTCGCT TGTTGCCCAGGCTGG
                                    ||||||| |||||||||||||||
                                    AGAGTGA ACAACGGGTCCGATC
                                       T            AGAA
GAM642  FLJ13456  3'  GCACCTGGGAAACAGAGCGAGA 66550           G     C  GA
                                    TCTCGCTCTGTT CCCAGG TG
                                    |||||||||||| |||||| ||
                                    AGAGCGAGACAA GGGTCC AC
                                          A     _  GG
GAM642  FLJ13456  3'  TCCAGCCTGGACAACGGAGTGA 66563           C
                GA                  TCTCGCTCTGTTG CCAGGCTGGA
                                    |||||||||||| ||||||||||
                                    AGAGTGAGGCAAC GGTCCGACCT
                                          A
GAM642  FLJ13456  3'  TCCAGCCTGGGTGACAGAGTAA 66564     CG     TG
                GA                  TCT  CTCTGT  CCCAGGCTGGA
                                    |||  ||||||  ||||||||||
                                    AGA  GAGACA  GGGTCCGACCT
                                      AT     GT
GAM642  FLJ13544  3'  TCCAGCCTGGATGACAGAGTGA 47210          GC
                GA                  TCTCGCTCTGTT  CCAGGCTGGA
                                    ||||||||||||  ||||||||||
                                    AGAGTGAGACAG  GGTCCGACCT
                                          TA
GAM642  FLJ13611  3'  TCTAGCCTGAGCGACAGAGTGA 46868           C
                GA                  TCTCGCTCTGTTGC CAGGCTGGA
                                    |||||||||||||| |||||||||
                                    AGAGTGAGACAGCG GTCCGATCT
                                          A
GAM642  FLJ13615  5'  TCGGCCTTGGCGGAGTTGGGG  47797      _   GTT   C    TG
                                    TCTCG CTCT   GCC AGGC  GA
                                    ||||| ||||   ||| ||||  ||
                                    GGGGT GAGG   CGG TCCG  CT
                                       T    ___   T    GT
GAM642  FLJ13621  3'  ACTCCAGCCTGGGCGACAGAGC 47213
                GAGA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACAGCGGGTCCGACCT
                                                CAC
GAM642  FLJ13659  3'  TCCAGCCTGGGCAACAAGAGTG 48036        _
                G                    TCGCTCT GTTGCCCAGGCTGGA
                                    ||||||| |||||||||||||||
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                                GGTGAGA CAACGGGTCCGACCT
                                    A
GAM642  FLJ13769  3'  ACTCCAGCCTGGGTGACAGAGC 47237          TG
          GAGA                  TCTCGCTCTGT  CCCAGGCTGGA
                                |||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      GT         CAC
GAM642  FLJ13769  3'  TCCAGCAGTCTGGGCGACAGAG 47263              ___
          TGAGA                  TCTCGCTCTGTTGCCCAG   GCTGGA
                                |||||||||||||||||   ||||||
                                AGAGTGAGACAGCGGGTC   CGACCT
                                      TGA
GAM642  FLJ13848  3'  TCCAGCCTAGGCGACAGAGTGA 45831            C
          GA                    TCTCGCTCTGTTGCC AGGCTGGA
                                |||||||||||||| ||||||||
                                AGAGTGAGACAGCGG TCCGACCT
                                      A
GAM642  FLJ13902  3'  AGGCCAACCTGGGCAATAGAGC 45378              C   A
          GAGA                  TCTCGCTCTGTTGCCCAGG TGG
                                |||||||||||||||||| |||
                                AGAGCGAGATAACGGGTCC ACC
                                      A   GGAA
GAM642  FLJ13920  3'  TTTGAGCATGGAGTGAGA    44964          T  C
                                TCTCGCTCTGT GC CAGG
                                |||||||||| || ||||
                                AGAGTGAGGTA CG GTTT
                                      _  A
GAM642  FLJ13952  3'  TCCAGCCTGGGCAACAAGAGTG 46021         _
          A                     TCGCTCT GTTGCCCAGGCTGGA
                                |||||||  ||||||||||||||
                                AGTGAGA CAACGGGTCCGACCT
                                    A
GAM642  FLJ13955  5'  TCCTCGCGGTGCAACAGGGCGG 45750           _  AG  T_
          GG                    TCTCGCTCTGTTGC CC  GC  GGA
                                |||||||||||||  ||  ||  |||
                                GGGGCGGGACAACG GG  CG  CCT
                                      T  __  CT
GAM642  FLJ13984  3'  TCCAAACTGGGTGACATGGTGA 45812        C   TG    GC
          GA                    TCTCGCT TGT  CCCAG  TGGA
                                |||||||  |||  |||||  ||||
                                AGAGTGG ACA  GGGTC  ACCT
                                    T   GT    AA
GAM642  FLJ14011  3'  TCCAGTCTGGGCAACAGAGCAA 42320     C
          GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                |||  ||||||||||||||||||
                                AGA CGAGACAACGGGTCTGACCT
                                  A
GAM642  FLJ14100  3'  TCCAGCCTGGGCGACAAAGCAA 47340     C   C
          GA                    TCT GCT TGTTGCCCAGGCTGGA
                                |||  ||| ||||||||||||||||
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                              AGA CGA ACAGCGGGTCCGACCT
                                A   A
GAM642  FLJ14117  3'  TCCAGCCTGGGCAACAGA    43233
                              TCTGTTGCCCAGGCTGGA
                              ||||||||||||||||||
                              AGACAACGGGTCCGACCT

GAM642  FLJ14117  3'  TCCAGCTTGGGCAACAGAGCAA 43235     C
          GA                    TCT GCTCTGTTGCCCAGGCTGGA
                              ||| ||||||||||||||||||||
                              AGA CGAGACAACGGGTTCGACCT
                                A
GAM642  FLJ14124  3'  TATGCCTGTGGTGGAGCTGGG  46360     C    GTT  _    TGGA
                              TCT GCTCT   GCC CAGGC
                              ||| |||||   ||| |||||
                              GGG CGAGG   TGG GTCCG
                                T    ___   T    TATT
GAM642  FLJ14129  3'  TTTAGCCTGGGCGACAGAGAGA 48817    G
                              TC CTCTGTTGCCCAGGCTGGA
                              || ||||||||||||||||||
                              AG GAGACAGCGGGTCCGATTT
                               A
GAM642  FLJ14154  3'  TCCGATGCAGGGGTGGGGTGGG 46235         GTT   AG  __
          G                    TCTCGCTCT   GCCC  GC  TGGA
                              |||||||||   ||||  ||  ||||
                              GGGGTGGGG   TGGG  CG  GCCT
                                    ___    GA  TA
GAM642  FLJ14166  3'  TTAGTTTGGGGTTGGGGGA   44994    G   TGTTG
                              TC CTC    CCCAGGCTGG
                              || |||    ||||||||||
                              AG GGG    GGGTTTGATT
                               G  TTG__
GAM642  FLJ14166  3'  TTTAGTTTGGGGTTGGGG    44995      TTG
                              CTCTG   CCCAGGCTGGA
                              |||||   ||||||||||
                              GGGGT   GGGTTTGATTT
                                 TG_
GAM642  FLJ14251  3'  CTCCAGCCTGGGTAACAGAGCG 46479
          AGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                              ||||||||||||||||||||||||
                              AGAGCGAGACAATGGGTCCGACCT
                                           CA
GAM642  FLJ14251  3'  TCCAGCCTTGGTGACAGAGTGA 46492          TG  C
          GA                    TCTCGCTCTGT  CC AGGCTGGA
                              ||||||||||  || ||||||||
                              AGAGTGAGACA  GG TCCGACCT
                                    GT  T
GAM642  FLJ14326  3'  TCCAGCTTGGGCAACGAGC    50784      T
                              GCTC GTTGCCCAGGCTGGA
                              |||| ||||||||||||||
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                                CGAG CAACGGGTTCGACCT
                                  _
GAM642  FLJ14326 3' TTAGCTGCTGTGGCAATGGGGT 50789            _  __   A
           GGGG                  TCTCGCTCTGTTGCC CAG  GCTGG
                                 ||||||||||||||| |||  |||||
                                 GGGGTGGGGTAACGG GTC  CGATT
                                       T  GT
GAM642  FLJ14327 3' AGACCAGCTTGGGCAACATAGT 46671       C          A
           GAGA                  TCTCGCT TGTTGCCCAGGCTGG
                                 |||||||  ||||||||||||||||
                                 AGAGTGA ACAACGGGTTCGACC
                                    T            AGAG
GAM642  FLJ14327 3' AGACCAGTTTGGGCAACATAGT 46672       C          A
           GAGA                  TCTCGCT TGTTGCCCAGGCTGG
                                 |||||||  ||||||||||||||||
                                 AGAGTGA ACAACGGGTTTGACC
                                    T            AGAG
GAM642  FLJ14327 3' TCCAGCCTGGACAACAGAGCTA 46688    C       C
           GA                    TCT GCTCTGTTG CCAGGCTGGA
                                 |||  |||||||| ||||||||||
                                 AGA CGAGACAAC GGTCCGACCT
                                   T       A
GAM642  FLJ14327 3' TCCAGCCTGGATAATAGAGTGA 46689          C
           GA                    TCTCGCTCTGTTG CCAGGCTGGA
                                 ||||||||||||  |||||||||
                                 AGAGTGAGATAAT GGTCCGACCT
                                       A
GAM642  FLJ14345 3' TCCAGCCTGGGCAACAAGAGTG 45662       _
           A                     TCGCTCT GTTGCCCAGGCTGGA
                                 |||||||  ||||||||||||||||
                                 AGTGAGA CAACGGGTCCGACCT
                                    A
GAM642  FLJ14346 3' TCCAGCCTGGGCAACAGAGCAA 47372    C
           GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                 |||  ||||||||||||||||||||
                                 AGA CGAGACAACGGGTCCGACCT
                                   A
GAM642  FLJ14346 3' TCCAGCCTGGGGGACAGAGCGA 47373          G
           GA                    TCTCGCTCTGTT CCCAGGCTGGA
                                 ||||||||||||  ||||||||||
                                 AGAGCGAGACAG GGGTCCGACCT
                                       G
GAM642  FLJ14397 3' TCCAGCCTGGGCAACAAGGGC  52333      _
                                 GCTCT GTTGCCCAGGCTGGA
                                 |||||  ||||||||||||||
                                 CGGGA CAACGGGTCCGACCT
                                   A
GAM642  FLJ14397 3' TCCAGCCTGGGTGACAGAGCAA 52335    C      TG
           GA                    TCT GCTCTGT  CCCAGGCTGGA
                                 |||  |||||||  ||||||||||
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                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM642  FLJ14457  3'  TCCAGCCTGGGAGACAGAGTGA 52413          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          GA
GAM642  FLJ14466  3'  TCCAACCTGGGCAACAGAGGGA 52431      G           C
                GA                  TCTC CTCTGTTGCCCAGG TGGA
                                    ||||| ||||||||||||| ||||
                                    AGAG GAGACAACGGGTCC ACCT
                                      G            A
GAM642  FLJ14466  3'  TCCAGCCTGGGCAACAACAGTG 52432       C_
                A                    TCGCT  TGTTGCCCAGGCTGGA
                                    |||||  ||||||||||||||||
                                    AGTGA  ACAACGGGTCCGACCT
                                       CA
GAM642  FLJ14490  3'  TCCAGCCTGGGCAACAGAGCAA 52448     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    |||| ||||||||||||||||||||
                                    AGA CGAGACAACGGGTCCGACCT
                                      A
GAM642  FLJ14621  3'  TCCAGCCTGGGCAACAGAGC   52540
                                    GCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||
                                    CGAGACAACGGGTCCGACCT

GAM642  FLJ14816  3'  TTCAGCTTGTGGGCAACAGAGC 52712     C           __
                CGGA                    TCT GCTCTGTTGCCCA  GGCTGGA
                                    ||| ||||||||||||  |||||||
                                    AGG CGAGACAACGGGT  TCGACTT
                                      C           GT
GAM642  FLJ14840  5'  CCAGTGGGCGTGTGGGGCGGGG 52722          TG _    AG    A
                                    TCTCGCTC  T TGCCC  GCTGG
                                    ||||||||  | |||||  |||||
                                    GGGGCGGG  G GCGGG  TGACC
                                         GT T    __
GAM642  FLJ20004  3'  ACTCCAGCCTGGGTGACAGAGT 34743          TG
                GAGA                    TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          GT          CAC
GAM642  FLJ20004  3'  TCCAGCCTGGGCAACAGAGGGA 34767      G
                GA                  TCTC CTCTGTTGCCCAGGCTGGA
                                    |||| ||||||||||||||||||||
                                    AGAG GAGACAACGGGTCCGACCT
                                      G
GAM642  FLJ20006  3'  AATCCAGCCTGGGCGATAGAGT 34773
                GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
```

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                                AGAGTGAGATAGCGGGTCCGACCT
                                      AAC
GAM642  FLJ20013  3'  AGGCCAGCCTGGGCAACATAGT 34794        C           A
          GAGA                  TCTCGCT TGTTGCCCAGGCTGG
                                ||||||| ||||||||||||||||
                                AGAGTGA ACAACGGGTCCGACC
                                   T            GGAG
GAM642  FLJ20013  3'  TCCAGCCTCGGTGACAGAGCAA 34803     C      TG  C
          GA                    TCT GCTCTGT  CC AGGCTGGA
                                ||| |||||||  || ||||||||
                                AGA CGAGACA  GG TCCGACCT
                                  A      GT  C
GAM642  FLJ20019  3'  TCCAGCCTAGGTGACAGGGCAA 34816     C      TG  C
          GA                    TCT GCTCTGT  CC AGGCTGGA
                                ||| |||||||  || ||||||||
                                AGA CGGGACA  GG TCCGACCT
                                  A      GT  A
GAM642  FLJ20045  3'  TCCAGCCTGGGTGAGAAGAGCG 34893        G_ TG
          A                     TCGCTCT  T  CCCAGGCTGGA
                                |||||||  |  ||||||||||
                                AGCGAGA  A  GGGTCCGACCT
                                   AG GT
GAM642  FLJ20069  3'  TCCAGCCTGGGGGGACAGAGCAA 34957     C       G
          GA                    TCT GCTCTGTT CCCAGGCTGGA
                                ||| |||||||| ||||||||||
                                AGA CGAGACAG GGGTCCGACCT
                                  A       G
GAM642  FLJ20081  3'  CCTGGGTGACAGAATGAGA    34990      C     TG
                                TCTCG TCTGT  CCCAGG
                                ||||| |||||  ||||||
                                AGAGT AGACA  GGGTCC
                                   A     GT
GAM642  FLJ20084  3'  CTCCAGCCTGGGCAACAGAGCG 34996
          AGA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||||
                                AGAGCGAGACAACGGGTCCGACCT
                                      CA
GAM642  FLJ20130  3'  TCCAGTTGAATCATAGGGTGA  35084          TGCCCA
                                TCGCTCTGT     GGCTGGA
                                |||||||||     |||||||
                                AGTGGGATA     TTGACCT
                                   CTAAG_
GAM642  FLJ20139  3'  TCCAGCCTGCGTGACAAAGTGA 35122        C   TG C
          GA                    TCTCGCT TGT  C CAGGCTGGA
                                ||||||| |||  | |||||||||
                                AGAGTGA ACA  G GTCCGACCT
                                   A   GT C
GAM642  FLJ20170  3'  TCCAGCCTGGGTGACAGAGTGA 35166           TG
          GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
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                                AGAGTGAGACA  GGGTCCGACCT
                                      GT
GAM642  FLJ20170  5'  TCCAGTCAGCCACAGGGTGAGA 35168          T  CCA
                                TCTCGCTCTGT GC   GGCTGGA
                                |||||||||||  ||   |||||||
                                AGAGTGGGACA CG   CTGACCT
                                      C  A__
GAM642  FLJ20174  5'  CGGCTGGGTAAGTGGGG     35191        CTGT      G TG
                                TCTCGCT    TGCCCAG C  G
                                |||||||    ||||||| |  |
                                GGGGTGA    ATGGGTC G  C
                                    _____      _ GT
GAM642  FLJ20200  3'  AGACCAGCCTGGGCAACATAGT 35231        C            A
           GAGA                      TCTCGCT TGTTGCCCAGGCTGG
                                |||||||  ||||||||||||||||
                                AGAGTGA ACAACGGGTCCGACC
                                     T            AGAG
GAM642  FLJ20211  3'  ACTCCAGCCTGGGCAACAGAGT 35251
           GAGA                      TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||||
                                AGAGTGAGACAACGGGTCCGACCT
                                                CAC
GAM642  FLJ20211  3'  ACTCCAGCCTGGGCGACAGAGT 35252
           GAGA                      TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||||
                                AGAGTGAGACAGCGGGTCCGACCT
                                                CAC
GAM642  FLJ20241  3'  TCCAGCCTGGACAACAGAGCGA 35291            C
           GA                        TCTCGCTCTGTTG CCAGGCTGGA
                                |||||||||||||  ||||||||||
                                AGAGCGAGACAAC GGTCCGACCT
                                       A
GAM642  FLJ20274  5'  TTCGCGCCGGCGATAGACGAGG 63326       C        CA  _
                                TCTCG TCTGTTGCC  GGC TGGA
                                |||||  |||||||||  |||  ||||
                                GGAGC AGATAGCGG  CCG GCTT
                                   _        __  C
GAM642  FLJ20280  3'  TCCAGCCTGGGTGACAGAGCGA 35333           TG
           GA                        TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      GT          C
GAM642  FLJ20306  3'  TCCAGCCTGGACGACTGAGTGA 35399         T    C
           GA                        TCTCGCTC GTTG CCAGGCTGGA
                                ||||||||  ||||  ||||||||||
                                AGAGTGAG CAGC GGTCCGACCT
                                     T   A
GAM642  FLJ20337  3'  TGGTAGTGGAGGGTGGGG    35444          GTTGC   G_  TG
                                TCTCGCTCT    CCA  GC  G
                                |||||||||    |||  ||  |
```

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                                GGGGTGGGA    GGT  TG  T
                                     _____   GA  GT
GAM642  FLJ20340  3'  TCCAGCCTGGTGACAGAGCGAG 35460          TG  C
          A                   TCTCGCTCTGT  CC AGGCTGGA
                              ||||||||||  || ||||||||
                              AGAGCGAGACA  GG TCCGACCT
                                    GT  _
GAM642  FLJ20401  3'  TTCGGGAAGTAGCGGATGGGA  35584       C       CCAGG
                              TCTCG TCTGTTGC    CTGGA
                              ||||| ||||||||    ||||||
                              AGGGT AGGCGATG    GGCTT
                                _       AAG__
GAM642  FLJ20456  3'  TCCAGCCTGGGTAACAGAGCTA 35666    C
          GA                  TCT GCTCTGTTGCCCAGGCTGGA
                              ||| ||||||||||||||||||||
                              AGA CGAGACAATGGGTCCGACCT
                                T
GAM642  FLJ20464  3'  TCTAGCCTGGGCAACAAGAGC  35700      _
                              GCTCT GTTGCCCAGGCTGGA
                              ||||| ||||||||||||||||
                              CGAGA CAACGGGTCCGATCT
                                 A
GAM642  FLJ20546  3'  TCCAGCCTGGGCAACGAGCGA  35814       T
                              TCGCTC GTTGCCCAGGCTGGA
                              |||||| ||||||||||||||||
                              AGCGAG CAACGGGTCCGACCT
                                   _
GAM642  FLJ20625  3'  TCTGGCCAGGGATGGGGTGGGG 35899          TG   A   TG
                              TCTCGCTCTGT  CCC GGC  GA
                              ||||||||||  ||| |||  ||
                              GGGGTGGGGTA  GGG CCG  CT
                                    __   A   GT
GAM642  FLJ20640  5'  TCCAGCCTGCGCCTGGGGTTGG 35918    C    GTT  C
          A                   TCT GCTCT   GC CAGGCTGGA
                              ||| |||||   || |||||||||
                              AGG TGGGG   CG GTCCGACCT
                                T    TC_  C
GAM642  FLJ20671  3'  ATTCCAGCCTGGGTGACAGAGC 35934          TG
          GAGA                  TCTCGCTCTGT  CCCAGGCTGGA
                              ||||||||||  ||||||||||
                              AGAGCGAGACA  GGGTCCGACCT
                                    GT         TAC
GAM642  FLJ20686  3'  TCCAGCTTGGGTGACAGAGTGA 35957          TG
          GA                    TCTCGCTCTGT  CCCAGGCTGGA
                              ||||||||||  ||||||||||
                              AGAGTGAGACA  GGGTTCGACCT
                                    GT
GAM642  FLJ20700  3'  TCCAGCCTGGGCGACACAGCGA 36020       C
          GA                    TCTCGCT TGTTGCCCAGGCTGGA
                              |||||||  ||||||||||||||||
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                                AGAGCGA ACAGCGGGTCCGACCT
                                    C
GAM642  FLJ20700  5' TTCGGCCTGGGCTGGGTGG   36021      TGTT
                                TCGCTC   GCCCAGGCTGGA
                                ||||||   ||||||||||||
                                GGTGGG   CGGGTCCGGCTT
                                   T___
GAM642  FLJ20783  3' ACTTCAGCCTGGGTGACAGAGT 36093         TG
          GAGA                   TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACTT
                                      GT         CAC
GAM642  FLJ20802  3' CTCCAGCCTGGGCGACAGAGCG 36110
          AGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGCGAGACAGCGGGTCCGACCT
                                              CA
GAM642  FLJ20813  3' TCTAGCCTGGGGAATAGAGTGA 36136          G
          GA                     TCTCGCTCTGTT CCCAGGCTGGA
                                ||||||||||| ||||||||||
                                AGAGTGAGATAA GGGTCCGATCT
                                      G
GAM642  FLJ20825  3' TCCAGCCTGGCCCACAGAGTGA 36148          TGC
          GA                     TCTCGCTCTGT   CCAGGCTGGA
                                ||||||||||   ||||||||||
                                AGAGTGAGACA   GGTCCGACCT
                                      CCC
GAM642  FLJ20825  3' TCCAGCCTGGGCAACAAGAGCG 36149        _
          A                      TCGCTCT GTTGCCCAGGCTGGA
                                |||||||  ||||||||||||||
                                AGCGAGA CAACGGGTCCGACCT
                                    A
GAM642  FLJ20972  3' TCCAGCCTGGGCAACAAGAGAA 47389     CG   _
          GA                     TCT  CTCT GTTGCCCAGGCTGGA
                                |||  ||||  ||||||||||||||
                                AGA  GAGA CAACGGGTCCGACCT
                                  A_   A
GAM642  FLJ21144  3' ACTCCAGCCTGGGCAACAGAGT 43185
          GAGA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGACAACGGGTCCGACCT
                                              CAC
GAM642  FLJ21162  3' TCCAGCCTGGGAAATAGAGTGA 46376          G
          G                      CTCGCTCTGTT CCCAGGCTGGA
                                |||||||||| ||||||||||
                                GAGTGAGATAA GGGTCCGACCT
                                      A
GAM642  FLJ21240  3' TCCAGCCTGGGCAAAAAGAGC  46268       G_
                                GCTCT  TTGCCCAGGCTGGA
                                |||||  ||||||||||||||
```

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                                CGAGA  AACGGGTCCGACCT
                                  AA
GAM642  FLJ21369  3'  TCCAGCCTGGGTGACAGAGCAA 46056     C      TG
            GA                    TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A       GT
GAM642  FLJ21415  3'  CCAGCCTGGGTGAGGAG     45684      G TG
                                  CTCT T  CCCAGGCTGG
                                  |||| |  ||||||||||
                                  GAGG A  GGGTCCGACC
                                    _ GT
GAM642  FLJ21551  3'  GCAACCTGGGTGACAGAGCGAG 46038          TG     C  GA
            A                     TCTCGCTCTGT  CCCAGG TG
                                  ||||||||||  ||||||  ||
                                  AGAGCGAGACA  GGGTCC AC
                                        GT      A  GT
GAM642  FLJ21603  3'  TCCAGTCTGGACCACAGAGTGA 45779          TGC
            GA                    TCTCGCTCTGT   CCAGGCTGGA
                                  ||||||||||   ||||||||||
                                  AGAGTGAGACA   GGTCTGACCT
                                        CCA
GAM642  FLJ21687  3'  ACTCCAGCCTGGGTGACAGAGC 46286          TG
            GAGA                    TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GT          CAC
GAM642  FLJ21802  5'  TTCGGCCCCGGCCGGCCGGGCG 45329        T   _  CA
            GGG                     TCTCGCTC GTTG CC  GGCTGGA
                                  |||||||| |||| ||  |||||||
                                  GGGGCGGG CGGC GG  CCGGCTT
                                       C    C  CC
GAM642  FLJ21870  3'  TCCAGCCTGGGCAACGGAG    43750
                                  CTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||
                                  GAGGCAACGGGTCCGACCT


GAM642  FLJ22009  3'  TTCCAGCTTGGGCGACAGAGCG 60924
            AGA                     TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAGCGGGTTCGACCT
                                                TA
GAM642  FLJ22054  3'  TCCAGCCTGGGCAACAGAGCAA 96053     C
            GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||
                                  AGA CGAGACAACGGGTCCGACCT
                                    A
GAM642  FLJ22056  3'  TCCAGCCCCTGAAGTTGGAGTG 42836          TTGCCCA_
            GGG                     TCTCGCTCTG       GGCTGGA
                                  ||||||||||       |||||||
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                                GGGGTGAGGT       CCGACCT
                                      TGAAGTCC
GAM642  FLJ22167  3'  ACCCTAGCTTGGGTGGCAGAGC 44855     C      TG        A
            AAGA                   TCT GCTCTGT  CCCAGGCTGG
                                   ||| |||||||  ||||||||||
                                   AGA CGAGACG  GGGTTCGATC
                                     A      GT         CCAC
GAM642  FLJ22269  3'  TCTGGTCCACCTGCGGGCGGGG 50899       T    TGCCCA   TG
                                   TCTCGC CTGT      GGC  GA
                                   |||||| ||||      |||  ||
                                   GGGGCG GGCG      CTG  CT
                                      _    TCCAC_   GT
GAM642  FLJ22282  3'  TTTAGCCACAGAAGGCTGCGGA 45967          T   CA____
            GTGAGG                     TCTCGCTCTGT GCC      GGCTGGA
                                   |||||||||||| |||      |||||||
                                   GGAGTGAGGCG CGG      CCGATTT
                                         T   AAGACA
GAM642  FLJ22313  3'  TCCACCCTGGGCGACAGAGTGA 42582                C
            GA                       TCTCGCTCTGTTGCCCAGG TGGA
                                   ||||||||||||||||||| ||||
                                   AGAGTGAGACAGCGGGTCC ACCT
                                                C
GAM642  FLJ22316  3'  TCCAGCCTGGGCAACAGAGCCA 47619     C
            GG                       TCT GCTCTGTTGCCCAGGCTGGA
                                   ||| ||||||||||||||||||
                                   GGA CGAGACAACGGGTCCGACCT
                                     C
GAM642  FLJ22378  3'  CTCAGGGTGGGCAGTGGGGGTG 47594        _ TG      GG    A
            GGG                      TCTCGCT C  TTGCCCA  CTGG
                                   |||||||  |  |||||||  ||||
                                   GGGGTGG G  GACGGGT  GACT
                                        G GT       GG    CT
GAM642  FLJ22415  3'  TCCAGCCTGGGTGACAAAGCAA 93121     C   C   TG
            GA                       TCT GCT TGT  CCCAGGCTGGA
                                   ||| ||| |||  ||||||||||
                                   AGA CGA ACA  GGGTCCGACCT
                                     A   A   GT
GAM642  FLJ22474  3'  ACTCCAGCCTGGGCAACAGAGT 45609
            GAGA                      TCTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGTGAGACAACGGGTCCGACCT
                                                CAC
GAM642  FLJ22644  3'  TCCAGCCTGGGCTACAGAGCGA 47703           T
            GA                       TCTCGCTCTGT GCCCAGGCTGGA
                                   |||||||||||  ||||||||||||
                                   AGAGCGAGACA CGGGTCCGACCT
                                         T
GAM642  FLJ22671  3'  TTCAGTGCCTGGTGGGGCAGGG 46316        GC_     __
                                   CTCTGTT   CCAGGC  TGGA
                                   |||||||   ||||||  ||||
```

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                                GGGACGG  GGTCCG  ACTT
                                   GGT     TG
GAM642  FLJ22692  3'  TTCAGCCTGGGTGACAGAAAGA 47486     GC    TG
           GA                    TCTC  TCTGT  CCCAGGCTGGA
                                 ||||  |||||  ||||||||||
                                 AGAG  AGACA  GGGTCCGACTT
                                   AA    GT
GAM642  FLJ22692  3'  TTGAGCCTGGGCGACACAGCGA 47487       C         G
           GA                    TCTCGCT TGTTGCCCAGGCT GA
                                 |||||||  |||||||||||| ||
                                 AGAGCGA ACAGCGGGTCCGA TT
                                    C          G
GAM642  FLJ22814  3'  TCCAACCTGGGTGACGAGTGAG 46731        T  TG    C
           A                     TCTCGCTC GT  CCCAGG TGGA
                                 ||||||||  ||  ||||||  ||||
                                 AGAGTGAG CA  GGGTCC ACCT
                                     _  GT     A
GAM642  FLJ22814  3'  TCCAGCCTGGGTGACAGAGGGA 46732    G     TG
                                 TC CTCTGT  CCCAGGCTGGA
                                 ||  ||||||  ||||||||||
                                 AG GAGACA  GGGTCCGACCT
                                  G     GT
GAM642  FLJ22865  5'  TCCAGTCTGGCCGGGCGGGG  47786        TGTT  C
                                 TCTCGCTC    GCC AGGCTGGA
                                 ||||||||    ||| ||||||||
                                 GGGGCGGG    CGG TCTGACCT
                                     C___  _
GAM642  FLJ22965  3'  TCTAGCCTGGGCGACAGAGTGA 42301
           GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                 ||||||||||||||||||||||||
                                 AGAGTGAGACAGCGGGTCCGATCT

GAM642  FLJ23022  3'  TCCAGCCTGGGCGACAAGAGC  47499      _
                                 GCTCT GTTGCCCAGGCTGGA
                                 |||||  ||||||||||||||
                                 CGAGA CAGCGGGTCCGACCT
                                    A
GAM642  FLJ23040  3'  TCCAGCCTGGGCAATAGAGCAA 47992     C
           GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                 |||  ||||||||||||||||||
                                 AGA CGAGATAACGGGTCCGACCT
                                   A
GAM642  FLJ23042  3'  TCCAGCCTGGGCAACAAGAGTG 47949        _
           A                      TCGCTCT GTTGCCCAGGCTGGA
                                  |||||||  ||||||||||||||
                                  AGTGAGA CAACGGGTCCGACCT
                                     A
GAM642  FLJ23091  3'  TCATGTGGGGGTGGGGTGGGG  46666         GTT   AG  _
                                 TCTCGCTCT   GCCC  GC TGG
                                 |||||||||   ||||  || |||
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                                GGGGTGGGG  TGGG  TG ACT
                                    ___    GG  T
GAM642  FLJ23120  3'  TCCAGCCTGGGTGACGGAGAAA 86330    CG    TG
          GA                  TCT  CTCTGT  CCCAGGCTGGA
                              |||  ||||||  ||||||||||
                              AGA  GAGGCA  GGGTCCGACCT
                                AA     GT
GAM642  FLJ23185  3'  TCCAGCCTTGGCAACAGAGTGA 47523            C
          GA                  TCTCGCTCTGTTGCC AGGCTGGA
                              |||||||||||||| ||||||||
                              AGAGTGAGACAACGG TCCGACCT
                                       T
GAM642  FLJ23229  3'  TCCAGCCTGGACAACAGAGCAA 47532    C       C
          GA                  TCT GCTCTGTTG CCAGGCTGGA
                              ||| ||||||||| ||||||||||
                              AGA CGAGACAAC GGTCCGACCT
                                A        A
GAM642  FLJ23251  3'  TTGGCCTTTTGGAGTGGGG   46102         TTGCCC   TG
                              TCTCGCTCTG     AGGC  GA
                              ||||||||||     ||||  ||
                              GGGGTGAGGT     TCCG  TT
                                   TT____    GT
GAM642  FLJ23360  3'  CCAGCCTCGTGGCGTGGGA   43827       TCT  TG CC
                              TCTCGC   GT  C  AGGCTGG
                              ||||||   ||  |  |||||||
                              AGGGTG   CG  G  TCCGACC
                                 ___  GT C_
GAM642  FLJ23360  3'  TCCAGCCCGGGTGACAGAGCGA 43835          TG   A
          GA                  TCTCGCTCTGT  CCC GGCTGGA
                              ||||||||||  ||| |||||||
                              AGAGCGAGACA  GGG CCGACCT
                                    GT   C
GAM642  FLJ23420  3'  AGATCAGCCTGGGTAACATAGC 47534        C           A
          GAGA                  TCTCGCT TGTTGCCCAGGCTGG
                              |||||||  ||||||||||||||
                              AGAGCGA ACAATGGGTCCGACT
                                 T            AGAG
GAM642  FLJ23447  3'  TTTAGACTGGGCAACAGAGCAA 46135    C          G
          GA                  TCT GCTCTGTTGCCCAG CTGGA
                              ||| |||||||||||||| |||||
                              AGA CGAGACAACGGGTC GATTT
                                A           A
GAM642  FLJ23462  3'  TCCAAAATTGGTAATAGAGCCA 46222    C        CAGGC
          GA                  TCT GCTCTGTTGCC    TGGA
                              ||| ||||||||||     ||||
                              AGA CGAGATAATGG    ACCT
                                C         TTAAA
GAM642  FLJ23499  3'  CTTTAGCCTGGGTGACAGAGCG 43136          TG
          AGA                   TCTCGCTCTGT  CCCAGGCTGGA
                              ||||||||||  ||||||||||
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                                AGAGCGAGACA  GGGTCCGATTT
                                      GT         CA
GAM642  FLJ23499  3'  TCCAGCCTGGGCGACAAGAGCG 43140       _
            A                  TCGCTCT GTTGCCCAGGCTGGA
                               ||||||| ||||||||||||||||
                               AGCGAGA CAGCGGGTCCGACCT
                                   A
GAM642  FLJ23510  3'  TTCAGCCAGAAAGCAGAGTGG  45628         GCCCA
                               TCGCTCTGTT    GGCTGGA
                               ||||||||||    |||||||
                               GGTGAGACGA    CCGACTT
                                     AAGA_
GAM642  FLJ23537  3'  TCCAGCCTGGGCAACAAGAGGA 88921    G   _
                               TC CTCT GTTGCCCAGGCTGGA
                               || |||| ||||||||||||||||
                               AG GAGA CAACGGGTCCGACCT
                                _   A
GAM642  FLJ23556  3'  TCCAGCCTGGGCGACTGTGAGA 46455       TCT
                               TCTCGC   GTTGCCCAGGCTGGA
                               ||||||   ||||||||||||||||
                               AGAGTG   CAGCGGGTCCGACCT
                                   T__
GAM642  FLJ23878  3'  ATCCAGCCTGGGTGACAGGGCG 59367          TG
            AGA                  TCTCGCTCTGT  CCCAGGCTGGA
                               ||||||||||  ||||||||||
                               AGAGCGGGACA  GGGTCCGACCT
                                     GT         AC
GAM642  FLJ25006  3'  TCCAGCCTGAGCAACAGAGTGA 58789           C
            GA                   TCTCGCTCTGTTGC CAGGCTGGA
                               |||||||||||||| |||||||||
                               AGAGTGAGACAACG GTCCGACCT
                                       A
GAM642  FLJ25012  3'  CTGCAGCCTGGGTGGCAGAGTG 58709          TG       GA
            AGA                  TCTCGCTCTGT  CCCAGGCTG
                               ||||||||||  |||||||||
                               AGAGTGAGACG  GGGTCCGAC
                                     GT        GTCA
GAM642  FLJ30092  3'  AGACCAGCCTGGGCAACATGGC 59338       C           A
            GAGA                 TCTCGCT TGTTGCCCAGGCTGG
                               ||||||| ||||||||||||||||
                               AGAGCGG ACAACGGGTCCGACC
                                   T            AGAG
GAM642  FLJ30092  3'  TCCAGCCTGGGCAACAGAGTGA 59342
            G                   CTCGCTCTGTTGCCCAGGCTGGA
                               ||||||||||||||||||||||||
                               GAGTGAGACAACGGGTCCGACCT

GAM642  FLJ30294  5'  TCTGGTCTCAGGCAAGGTGGGG 58899       CTG    C_   TG
                               TCTCGCT   TTGCC  AGGC  GA
                               |||||||   |||||  ||||  ||
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                                GGGGTGG  AACGG  TCTG  CT
                                   ___    AC   GT
GAM642  FLJ30655  5'  TTCAGTCTCTCACCAGGGCCAG 58956    C     T  CCC
            G                   TCT GCTCTG TG   AGGCTGGA
                                ||| |||||| ||   ||||||||
                                GGA CGGGAC AC   TCTGACTT
                                  C     C  TC_
GAM642  FLJ30681  3'  TCCAGCCTAGGCAACAGAGGGA 93440     G        C
            GA                    TCTC CTCTGTTGCC AGGCTGGA
                                  |||| |||||||||| ||||||||
                                  AGAG GAGACAACGG TCCGACCT
                                    G         A
GAM642  FLJ30681  3'  TTCAGTTAAAAAGGGGTGGGG  93443          GTTGCCCA
                                  TCTCGCTCT       GGCTGGA
                                  |||||||||       |||||||
                                  GGGGTGGGG       TTGACTT
                                       AAAAA___
GAM642  FLJ31168  3'  ACTCCAGCCTGGGCGACAGAGC 59174
            GAGA                     TCTCGCTCTGTTGCCCAGGCTGGA
                                     ||||||||||||||||||||||||
                                     AGAGCGAGACAGCGGGTCCGACCT
                                                 CAC
GAM642  FLJ31168  3'  TTTGGGCTAAGAGAGTGGGG   59188          G  _
                                  TCTCGCTCT TT GCCCAGG
                                  ||||||||| || |||||||
                                  GGGGTGAGA AA CGGGTTT
                                       G  T
GAM642  FLJ31455  3'  TCCAGCCTGGGCGACAGAGCCA 59291     C
            GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    C
GAM642  FLJ31455  3'  TCCAGCCTGGGTGACAGAGCAA 59292     C      TG
            GA                    TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A      GT
GAM642  FLJ31890  5'  TTTGGTCTTACGCCCTAGGGTG 92988          TT  CC_   TG
            GGG                     TCTCGCTCTG  GC   AGGC  GA
                                    |||||||||  ||   ||||  ||
                                    GGGGTGGGAT  CG   TCTG  TT
                                         CC  CAT    GT
GAM642  FLJ31952  3'  CTCCAGCCTGGGCAACAGAGTG 59045
            AGA                     TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAACGGGTCCGACCT
                                                 CA
GAM642  FLJ32499  5'  TCCAGTGACCGACAGAGCAAGA 58782     C        CCCAG
                                  TCT GCTCTGTTG     GCTGGA
                                  ||| |||||||||     ||||||
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                                AGA CGAGACAGC     TGACCT
                                  A        CAG__
GAM642  FLJ32915  5'  TCCAGCCTGGGCGACAAGAGCG 59437          _
            AGA                    TCTCGCTCT GTTGCCCAGGCTGGA
                                   ||||||||| ||||||||||||||||
                                   AGAGCGAGA CAGCGGGTCCGACCT
                                       A
GAM642  FOXO3A   5'  GCGGCTGGGCGGCGGGGGGAGG 9382       G          G   GA
                                   TCTC CTCTGTTGCCCAG CTG
                                   |||| |||||||||||| |||
                                   GGAG GGGGCGGCGGGTC GGC
                                     G           _  GT
GAM642  FREQ     5'  CCGGCCCGGGGGGGGCGGGG   27368          GTTG   A
                                   TCTCGCTCT    CCC GGCTGG
                                   |||||||||    ||| ||||||
                                   GGGGCGGGG    GGG CCGGCC
                                        _____   C
GAM642  FRSB     3'  CCTCCAGCCTGGGTGACAGAGT 20290           TG
            GAGA                     TCTCGCTCTGT  CCCAGGCTGGA
                                     ||||||||||  ||||||||||
                                     AGAGTGAGACA  GGGTCCGACCT
                                           GT          CCC
GAM642  FUSIP1    3'  CTCCAGCCTGGGCAACAGAGTG 55036
            AGA                      TCTCGCTCTGTTGCCCAGGCTGGA
                                     ||||||||||||||||||||||||
                                     AGAGTGAGACAACGGGTCCGACCT
                                                 CA
GAM642  GABARAPL1 3'  TTTGGGATTTTGTGGGGTGGGA 49428          TG TG___
                                   TCTCGCTC  T     CCCAGG
                                   ||||||||  |     ||||||
                                   AGGGTGGG  G     GGGTTT
                                        GT TTTTA
GAM642  GALNT6    3'  TCCAGCCTGGGCAACAGGTAAG 24252      CG T
            A                       TCT  C CTGTTGCCCAGGCTGGA
                                    |||  | ||||||||||||||||
                                    AGA  G GACAACGGGTCCGACCT
                                      AT _
GAM642  GCN2     3'  TCCAGTCTGGGACAACAGAGCA 63440      C        _
            AGA                      TCT GCTCTGTTG CCCAGGCTGGA
                                     ||| ||||||||| ||||||||||
                                     AGA CGAGACAAC GGGTCTGACCT
                                       A        A
GAM642  GGA2     3'  TCCAGCCTGGGCTACATAGTGA 57682         C   T
            GA                       TCTCGCT TGT GCCCAGGCTGGA
                                     ||||||| ||| ||||||||||||
                                     AGAGTGA ACA CGGGTCCGACCT
                                         T   T
GAM642  GGA2     3'  TCCAGCCTGGGCTACATAGTGA 57683         C   T
            GA                       TCTCGCT TGT GCCCAGGCTGGA
                                     ||||||| ||| ||||||||||||
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                                AGAGTGA ACA CGGGTCCGACCT
                                    T   T
GAM642  GIOT-3   5'  TTTGGCCTCCGGTGGGCGAGA  33221        TGTT   C_   TG
                                TCTCGCTC   GCC  AGGC  GA
                                ||||||||   |||  ||||  ||
                                AGAGCGGG   TGG  TCCG  TT
                                    _____  CC   GT
GAM642  GIT1     3'  TCTGGAGTTTTGAGGGGTGAGG 26723         GTT__  _
                                TCTCGCTCT    GC CCAGG
                                |||||||||    || |||||
                                GGAGTGGGG    TG GGTCT
                                     AGTTT  A
GAM642  GK001    3'  TCTGGTGGGAGTGGGGTGG   39883       TG  G   AG  TG
                                TCGCTC  TT CCC  GC  GA
                                ||||||  || |||  ||  ||
                                GGTGGG  GA GGG  TG  CT
                                   GT  _  __  GT
GAM642  GLTP     3'  TCCAGCCTGGGCAACAAGAGCG 33588        _
             A                   TCGCTCT GTTGCCCAGGCTGGA
                                 |||||||  ||||||||||||||
                                 AGCGAGA CAACGGGTCCGACCT
                                    A
GAM642  GNB4     3'  TCCAGCCTAGGCGACAGAGTGA 41570             C
             GA                    TCTCGCTCTGTTGCC AGGCTGGA
                                   ||||||||||||||  ||||||||
                                   AGAGTGAGACAGCGG TCCGACCT
                                         A
GAM642  GOLGA3   3'  TCTGCGGGTGACAGGGAGAGG  20898     G     TG   AG  T
                                TCTC CTCTGT  CCC  GC GGA
                                ||||  ||||||  |||  || |||
                                GGAG GGGACA  GGG  CG TCT
                                  A     GT  __  _
GAM642  GP5      3'  CTCTAGCCTGGGCGACAGAGCG 16874
             AGA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGCGAGACAGCGGGTCCGATCT
                                              CA
GAM642  GPS2     5'  TTCAGACACCGGCAGTGAGGGC 88512          _     CAGG_
             GAGG                  TCTCGCTCT GTTGCC     CTGGA
                                   |||||||| ||||||     |||||
                                   GGAGCGGGA TGACGG     GACTT
                                       G     CCACA
GAM642  GR6      5'  CTGGGTGGCTGGGTGGGG    24745         T  TG
                                TCTCGCTC GT  CCCAG
                                |||||||| ||  |||||
                                GGGGTGGG CG  GGGTC
                                     T  GT
GAM642  GR6      5'  TCTGAGCAGTGGGTGAGG    24752        T TG    C
                                TCTCGC C  TTGC CAGG
                                |||||| |  |||| ||||
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                                GGAGTG G  GACG GTCT
                                   _ GT   A
GAM642  GR6     3'  TTTGGATGATAAGAGTGAGG  24755        _  GC
                                TCTCGCTCT GTT  CCAGG
                                ||||||||| |||  |||||
                                GGAGTGAGA TAG  GGTTT
                                     A   TA
GAM642  GS3955   5'  TTTGGTCTCGGGGTAGGGGGAG 41629     G    TTG  _   TG
          A                      TCTC CTCTG   CCC AGGC  GA
                                |||| |||||   ||| ||||  ||
                                AGAG GGGAT   GGG TCTG  TT
                                  G    G__   C   GT
GAM642  GTF2A1   5'  CCTTGGCGCGGGGTGGGG    32403          T  C
                                TCTCGCTCTGT GCC AGG
                                |||||||||| ||| |||
                                GGGGTGGGGCG CGG TCC
                                     _  T
GAM642  GTPBP5   3'  TCCAGCCTGAGCGACAGAGCAA 65981     C        C
          GA                      TCT GCTCTGTTGC CAGGCTGGA
                                ||| |||||||||| |||||||||
                                AGA CGAGACAGCG GTCCGACCT
                                  A         A
GAM642  GTPBP5   3'  TCCAGCCTGAGTGACAGAGCGA 65982          TG C
          GA                      TCTCGCTCTGT  C CAGGCTGGA
                                |||||||||||  | |||||||||
                                AGAGCGAGACA  G GTCCGACCT
                                     GT A
GAM642  GTSE1    3'  TCCAGCCTGGGCACCAATGTGA 33565       TC  T
          GA                      TCTCGC  TG TGCCCAGGCTGGA
                                ||||||  || ||||||||||||
                                AGAGTG  AC ACGGGTCCGACCT
                                   TA  C
GAM642  HCGIX    3'  TCCAGCCTGGGTGACAGCAAGA 20717     GCT   TG
          GA                      TCTC   CTGT  CCCAGGCTGGA
                                ||||   ||||  ||||||||||
                                AGAG   GACA  GGGTCCGACCT
                                  AAC    GT
GAM642  HDAC11   3'  CCCAGGCAGCAGGTGGGA    46136       T      CA
                                TCTCGC CTGTTGCC  GG
                                |||||| ||||||||  ||
                                AGGGTG GACGACGG  CC
                                   _       AC
GAM642  HEI10    3'  CTCCAGCCTGGGCAACAGAGTG 41295
          AGA                      TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGACAACGGGTCCGACCT
                                                 CA
GAM642  HES2     3'  TCCAGGCTGGGCGACAGAGCGA 39378              G
          GA                      TCTCGCTCTGTTGCCCAG CTGGA
                                |||||||||||||||| |||||
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                                AGAGCGAGACAGCGGGTC GACCT
                                        G
GAM642  HIC      3'  ACTCCAGCCTGGGCAACAGAGC 68042
            GAGA                TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||
                                AGAGCGAGACAACGGGTCCGACCT
                                        CAC
GAM642  HIC2     3'  TCTGGGGTTCCGGGGGGTGGGG 65874        __ TT   _
                                TCTCGCTCT  G  GCCC AGG
                                |||||||||  |  |||| |||
                                GGGGTGGGG  C  TGGG TCT
                                     GG CT    G
GAM642  HN1L     3'  TCTGCGAGGCAGTGGGGTGGGA 58621        TG    CAG  T
                                TCTCGCTC  TTGCC   GC GGA
                                ||||||||  |||||   || |||
                                AGGGTGGG  GACGG   CG TCT
                                     GT    AG_ _
GAM642  HOMER-3  3'  TCCGGCCTGGGATGCGGGCCAG 17907     C  T    TG
            G                    TCT GC CTGT  CCCAGGCTGGA
                                 ||| || ||||  ||||||||||
                                 GGA CG GGCG  GGGTCCGGCCT
                                   C  _    TA
GAM642  HSA250303 3'  TCCAGCCTGGGCTACAGAGTGA 38023          T
            GA                   TCTCGCTCTGT GCCCAGGCTGGA
                                 ||||||||||| ||||||||||||
                                 AGAGTGAGACA CGGGTCCGACCT
                                        T
GAM642  HSC3     3'  TCCAGCTTGGGTGACAAAGTAA 59734     CG  C   TG
            GA                   TCT  CT TGT  CCCAGGCTGGA
                                 |||  || |||  ||||||||||
                                 AGA  GA ACA  GGGTTCGACCT
                                   AT  A   GT
GAM642  HSC3     3'  TTTGCCTGGGCAGTATAGTGAG 59735        C          TGGA
            A                    TCTCGCT TGTTGCCCAGGC
                                 |||||||  ||||||||||||
                                 AGAGTGA ATGACGGGTCCG
                                     T          TTT
GAM642  HSD17B7  3'  TCCAGCCTGGGTGACAGCGAGA 33484        CT  TG
                                 TCTCGCT  GT  CCCAGGCTGGA
                                 |||||||  ||  ||||||||||
                                 AGAGCGA  CA  GGGTCCGACCT
                                     __  GT
GAM642  HSH2     3'  TCCAGCCTGGATGACAGAGTGA 52744           GC
            GA                   TCTCGCTCTGTT  CCAGGCTGGA
                                 ||||||||||||  ||||||||||
                                 AGAGTGAGACAG  GGTCCGACCT
                                        TA
GAM642  HSJ001348 3'  TTCAGTATTGATGGGGAGGGA  62861      G      GCCCAG
                                 TCTC CTCTGTT     GCTGGA
                                 |||| |||||||     ||||||
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                                AGGG GGGGTAG     TGACTT
                                  A      TTA___
GAM642  HSJ1     3'  GGCCTGGGTGGCGGGTGGGG  23083       T   TG
                                TCTCGC CTGT  CCCAGGCT
                                ||||||| ||||  ||||||||
                                GGGGTG GGCG  GGGTCCGG
                                   _   GT
GAM642  HSMPP8   3'  TCCAGCCTGAGTGACAGAATGA 95141      C    TG C
           GA                     TCTCG TCTGT  C CAGGCTGGA
                                ||||| |||||  | |||||||||
                                AGAGT AGACA  G GTCCGACCT
                                  A    GT A
GAM642  HSOBRGRP 5'  TCTGGCTTGGGCAGGCTGCCCG 34464     CTCT _       TG
           GG                     CTCG    GT TGCCCAGGC  GA
                                ||||   || |||||||||  ||
                                GGGC    CG ACGGGTTCG  CT
                                  CCGT  G        GT
GAM642  HSPC043  3'  TCCAGCCTGGGTGACAGTGAG  68353       CT  TG
                                CTCGCT  GT  CCCAGGCTGGA
                                ||||||  ||  ||||||||||
                                GAGTGA  CA  GGGTCCGACCT
                                   __  GT
GAM642  HSPC072  3'  TCTAGCCTGCTGGAGGATGAGA 27173      C   GTTGCC
                                TCTCG TCT      CAGGCTGGA
                                ||||| |||      |||||||||
                                AGAGT AGG      GTCCGATCT
                                  _  AGGTC_
GAM642  HSPC195  5'  TCTGTTGTGGGCAGCAGGGCCA 81870     C          _  T
           GG                     TCT GCTCTGTTGCCCA GGC GGA
                                ||| |||||||||||| ||| |||
                                GGA CGGGACGACGGGT TTG TCT
                                  C          G  _
GAM642  HSU79252 5'  AGTCCAGCCTGGGTGACAGAGT 26141           TG
           GAGA                     TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      GT         GAG
GAM642  HYPK     3'  TCCAGCCTGGGGGAAAGAGTGA 33516        G  G
                                TCGCTCT TT CCCAGGCTGGA
                                ||||||| || ||||||||||
                                AGTGAGA AG GGGTCCGACCT
                                   A  G
GAM642  IL-23R   3'  TCCAGCCTGGGCAACAAGAGC  59132       _
                                GCTCT GTTGCCCAGGCTGGA
                                ||||| ||||||||||||||
                                CGAGA CAACGGGTCCGACCT
                                  A
GAM642  IL10RB   3'  TCCAGCCTGGGTGACAAAGTGA 7129         C   TG
           GA                     TCTCGCT TGT  CCCAGGCTGGA
                                ||||||| |||  ||||||||||
```

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                                AGAGTGA ACA  GGGTCCGACCT
                                   A   GT
GAM642   IMAGE:4907098 3'  TCCAGCCTGGGCGACAGAGCAA 57758     C
            GA                   TCT GCTCTGTTGCCCAGGCTGGA
                                 ||| ||||||||||||||||||||
                                 AGA CGAGACAGCGGGTCCGACCT
                                   A
GAM642   INE1     3'  TCCAGCCTGTGTGATGGAGAGA 14760      G     TG C
            GA                   TCTC CTCTGT  C CAGGCTGGA
                                 |||| ||||||  | |||||||||
                                 AGAG GAGGTA  G GTCCGACCT
                                   A     GT T
GAM642   JDD1     3'  AGACCTGCCTGGGTAACATAGT 63908        C         T  A
            GAGA                   TCTCGCT TGTTGCCCAGGC GG
                                 ||||||| |||||||||||| ||
                                 AGAGTGA ACAATGGGTCCG CC
                                    T          T  AGAA
GAM642   JDD1     5'  CTAGGTGACGGGGCGAGA    63914          TG  C
                                 TCTCGCTCTGT  CC AG
                                 ||||||||||  || ||
                                 AGAGCGGGGCA  GG TC
                                      GT  A
GAM642   JDD1     3'  TCCAGCCTGGGTGATGGAG    63919       TG
                                 CTCTGT  CCCAGGCTGGA
                                 ||||||  ||||||||||
                                 GAGGTA  GGGTCCGACCT
                                    GT
GAM642   jdp2     3'  TCGGGGGTGGCCAGGGCGGGG  56203         _ TG   AGG
                                 TCTCGCTCTG T  CCC   CTGG
                                 |||||||||| |  |||   ||||
                                 GGGGCGGGAC G  GGG   GGCT
                                      C GT  ___
GAM642   KALI     3'  TCCAGTCTGGGTGACAGAGTGA 54697           TG
            GA                   TCTCGCTCTGT  CCCAGGCTGGA
                                 ||||||||||  ||||||||||
                                 AGAGTGAGACA  GGGTCTGACCT
                                      GT
GAM642   KATII    5'  TCCAGGCCACGGCGCGGGGCGG 33169          T   CA  _
            GA                   TCTCGCTCTGT GCC  GGC TGGA
                                 |||||||||| |||  ||| ||||
                                 AGGGCGGGGCG CGG  CCG ACCT
                                      _   CA   G
GAM642   KBRAS2   3'  TCCAGCCTGGTCAACAGAGCAA 34628     C       C
            GA                   TCT GCTCTGTTG CCAGGCTGGA
                                 ||| ||||||||| ||||||||||
                                 AGA CGAGACAAC GGTCCGACCT
                                   A        T
GAM642   KCNH6    3'  ACTCCAGCCTGGGTGACAGAGT 48566          TG
            GAGA                   TCTCGCTCTGT  CCCAGGCTGGA
                                 ||||||||||  ||||||||||
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                                AGAGTGAGACA  GGGTCCGACCT
                                      GT         CAC
GAM642  KCNJ9    3'  GGGAAATGGAGGGTGGGG    18368         __  G
                                TCTCGCTCT  GTT CCC
                                |||||||||  ||| |||
                                GGGGTGGGA  TAA GGG
                                     GG   A
GAM642  KCNJ9    3'  TTCAGGGAAGCAGGCAGAGCGG 18370          _  __  AGG
           GG                     TCTCGCTCTGT TGC  CC   CTGGA
                                |||||||||||  |||  ||   |||||
                                GGGGCGAGACG ACG  GG   GACTT
                                      G   AA  ___
GAM642  KIAA0014 3'  TCCAGCCCTACAGGGCGAGG   28545           TGCCCA
                                TCTCGCTCTGT     GGCTGGA
                                ||||||||||      |||||||
                                GGAGCGGGACA     CCGACCT
                                      TC_____
GAM642  KIAA0042 3'  TCCAGTCTGAGCAACAGAACGA 30239       C       C
           GA                     TCTCG TCTGTTGC CAGGCTGGA
                                |||||  ||||||||  |||||||||
                                AGAGC AGACAACG GTCTGACCT
                                   A       A
GAM642  KIAA0061 3'  TTTGGGGGTGATGAGGTGGGG  68841        CT  TG   AGG TG
                                TCTCGCT  GT  CCC   C  GA
                                |||||||  ||  |||   |  ||
                                GGGGTGG  TA  GGG   G  TT
                                    AG  GT   ___ GT
GAM642  KIAA0125 5'  TTTGGCTAGGGATGGAGCAGA  61130     C      TG   A   TG
                                TCT GCTCTGT  CCC GGC  GA
                                |||  |||||||  ||| |||  ||
                                AGA CGAGGTA  GGG TCG  TT
                                  _      __   A   GT
GAM642  KIAA0159 3'  TCCAGCTTGGGCAACAATAGCG 30143       C_
           A                     TCGCT  TGTTGCCCAGGCTGGA
                                |||||  ||||||||||||||||
                                AGCGA  ACAACGGGTTCGACCT
                                   TA
GAM642  KIAA0184 3'  TCCAGCCTGGGTGACAGCACGA 65815       CT    TG
           GA                     TCTCG  CTGT  CCCAGGCTGGA
                                |||||  ||||  ||||||||||||
                                AGAGC  GACA  GGGTCCGACCT
                                   AC    GT
GAM642  KIAA0186 3'  TCCAGCCTGGGTGACAAAGTGA 41119        C   TG
           GA                     TCTCGCT TGT  CCCAGGCTGGA
                                |||||||  |||  ||||||||||||
                                AGAGTGA ACA  GGGTCCGACCT
                                   A   GT
GAM642  KIAA0215 3'  TCTAGTTTTGGAAAGTGTAGTG 29086        C GT GC    _
           GGA                     TCTCGCT T  T  CCAGG CTGGA
                                |||||||  |  |  |||||  |||||
```

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                                AGGGTGA G  A  GGTTT GATCT
                                    T TG AA    T
GAM642  KIAA0218 3' ATTCAGCTTCTGGGTGGTGGGT 29292       T TG TG   __
            GGGG                 TCTCGC C  T  CCCAG  GCTGGA   T
                                ||||||| |  |  |||||  ||||||   |
                                GGGGTG G  G  GGGTC  CGACTT   A
                                   _ GT GT    TT
GAM642  KIAA0226 3' TCCAGCCTGGGTGACAGAGTGA 64264          TG
            GA                   TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      GT
GAM642  KIAA0247 3' TTTGTGGTGACGGAGGGGA   29080     G     TG _
                                TCTC CTCTGT  CC CAGG
                                |||| ||||||  || ||||
                                AGGG GAGGCA  GG GTTT
                                  _     GT  T
GAM642  KIAA0252 3' ACTCCAGTCTGGGTGACAGAGT 63448          TG
            GAGA                 TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCTGACCT
                                      GT         CAC
GAM642  KIAA0266 3' TCTAGCCTGGGCAATAAGC   41644     C
                                GCT TGTTGCCCAGGCTGGA
                                ||| ||||||||||||||
                                CGA ATAACGGGTCCGATCT
                                 _
GAM642  KIAA0275 5' GCCAGCAGCGGGGTGGGA    29328           CCA
                                TCTCGCTCTGTTGC   GGC
                                ||||||||||||||   |||
                                AGGGTGGGGCGACG   CCG
                                       A__
GAM642  KIAA0317 5' TCTTGGTGGGAGAGTGGGG   29749         G TG  C
                                TCTCGCTCT T  CC AGG
                                ||||||||| |  || |||
                                GGGGTGAGA G  GG TCT
                                     G GT  T
GAM642  KIAA0321 3' CTTGGGCAGTGGGGCCAGG   63051     C    TG
                                TCT GCTC  TTGCCCAGG
                                ||| ||||  |||||||||
                                GGA CGGG  GACGGGTTC
                                  C    GT
GAM642  KIAA0336 3' TCCAGCTCGGGGAACAGAGCGA 28324           G   AG
            GA                   TCTCGCTCTGTT CCC  GCTGGA
                                ||||||||||| |||  ||||||
                                AGAGCGAGACAA GGG  CGACCT
                                       G   CT
GAM642  KIAA0337 3' TCCAGTCATGATCGGGTGGGG  29482        T   CCCA
                                TCTCGCTC GTTG   GGCTGGA
                                |||||||| ||||   |||||||
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                                GGGGTGGG TAGT    CTGACCT
                                    C    A___
GAM642  KIAA0337 3' TTTGGTTTTGTTTGGGGTGGG  29487        TT  CC    TG
                                CTCGCTCTG  GC  AGGC  GA
                                |||||||||  ||  ||||  ||
                                GGGTGGGGT  TG  TTTG  TT
                                     T_  T_    GT
GAM642  KIAA0350 3' CCAGGTGTGTGGGGTGAGG   61826        GTT  C  GG
                                TCTCGCTCT   GC CA  CTGG
                                |||||||||   || ||  ||||
                                GGAGTGGGG   TG GT  GACC
                                     ___  T  G_
GAM642  KIAA0352 3' TCCGGCCTTCTGTGGGGCAGAG 29828      _    TG TGCCC
           A                     TCTC GCTC  T     AGGCTGGA
                                ||||| ||||  |    ||||||||
                                AGAG CGGG  G     TCCGGCCT
                                  A    GT TCT__
GAM642  KIAA0355 3' ACTCCAGCCTGGGTGACAGAGT 28696          TG
           GAGA                    TCTCGCTCTGT  CCCAGGCTGGA
                                |||||||||||  ||||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                     GT          CAC
GAM642  KIAA0391 3' CTCTAGCCTGGGTGACAGAGCG 28609          TG
           AGA                     TCTCGCTCTGT  CCCAGGCTGGA
                                |||||||||||  ||||||||||||
                                AGAGCGAGACA  GGGTCCGATCT
                                     GT          CA
GAM642  KIAA0391 3' TCCAGCCTAGGTGACAGAGTGA 28621          TG  C
           GA                      TCTCGCTCTGT  CC AGGCTGGA
                                |||||||||||  ||  ||||||||
                                AGAGTGAGACA  GG TCCGACCT
                                     GT  A
GAM642  KIAA0408 3' ACTCCAGCCTGGGTGACAGAGT 28791          TG
           GAGA                    TCTCGCTCTGT  CCCAGGCTGGA
                                |||||||||||  ||||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                     GT          CAC
GAM642  KIAA0419 3' TCCAGTCGGGTTAACAGAGCAA 28863     C       _   A
           GA                      TCT GCTCTGTTG CCC GGCTGGA
                                ||| |||||||| ||| |||||||
                                AGA CGAGACAAT GGG CTGACCT
                                  A       T  _
GAM642  KIAA0420 3' AGACCAGCCTGGGCAACATAGT 64081        C           A
           GAGA                    TCTCGCT TGTTGCCCAGGCTGG
                                |||||||  ||||||||||||||||
                                AGAGTGA ACAACGGGTCCGACC
                                     T            AGAA
GAM642  KIAA0420 3' ATTTGGGAGCACCAGCAGAATG 64082       C     _____     CTGGA
           GGG                     TCTCG TCTGTTG    CCCAGG
                                ||||| |||||||    ||||||
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                                GGGGT AGACGAC    GGGTTT
                                  A      CACGA       AG
GAM642  KIAA0427  3'  TCTGAGAGTGGCGAGTGGGG  29392        T  TG C__
                                TCTCGCTC GT  C   CAGG
                                |||||||| ||  |   ||||
                                GGGGTGAG CG  G   GTCT
                                     _  GT AGA
GAM642  KIAA0431  3'  TCCAACCTGGGTAACAGGGCAA 31554     C            C
           GA                     TCT GCTCTGTTGCCCAGG TGGA
                                |||  |||||||||||||| ||||
                                AGA CGGGACAATGGGTCC ACCT
                                  A             A
GAM642  KIAA0441  3'  TCAAGCCTGGCGACAGAGCGAG 29642              C     G
           A                      TCTCGCTCTGTTGCC AGGCT GA
                                |||||||||||||| ||||| ||
                                AGAGCGAGACAGCGG TCCGA CT
                                        _     A
GAM642  KIAA0445  5'  TCCAGCCTGTGTGACAGAGCAA 28642     C       TG C
           GA                     TCT GCTCTGT  C CAGGCTGGA
                                |||  |||||||  | |||||||||
                                AGA CGAGACA  G GTCCGACCT
                                  A       GT T
GAM642  KIAA0446  5'  ACTCCAGCCTGGGCGACAGAGC 69437
           GAGA                     TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||||
                                AGAGCGAGACAGCGGGTCCGACCT
                                          CAC
GAM642  KIAA0447  3'  TCCAGCCTGGGCAACAGGGCAA 72129     C
           GA                     TCT GCTCTGTTGCCCAGGCTGGA
                                |||  ||||||||||||||||||
                                AGA CGGGACAACGGGTCCGACCT
                                  A
GAM642  KIAA0450  3'  TTAGAAGGGTGAAGAGTGAGG  28378          G TG   AGG
                                TCTCGCTCT T  CCC   CTGG
                                |||||||| |  |||   ||||
                                GGAGTGAGA A  GGG   GATT
                                     _ GT   AA_
GAM642  KIAA0451  3'  TTCAGCCTCCCAACAGGGCAGA 29785      _        CCC
           GA                     TCTC GCTCTGTTG   AGGCTGGA
                                |||| |||||||||   ||||||||
                                AGAG CGGGACAAC   TCCGACTT
                                  A        CC_
GAM642  KIAA0451  5'  TTCAGCCTGGGCAACAGAGCAA 29786     C
           GA                     TCT GCTCTGTTGCCCAGGCTGGA
                                |||  ||||||||||||||||||
                                AGA CGAGACAACGGGTCCGACTT
                                  A
GAM642  KIAA0472  3'  ACTCCAGCCTGGGCAACAGAGC 72330
           GAGA                     TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||||
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                                AGAGCGAGACAACGGGTCCGACCT
                                        CAC
GAM642  KIAA0472 3' CTCCAGCCTGGGCGACAGAGTG 72349
           AGA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                 ||||||||||||||||||||||||
                                 AGAGTGAGACAGCGGGTCCGACCT
                                        CA
GAM642  KIAA0472 3' TCCAGCCTGGGCAGCAGAGCAA 72368     C
           GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                 ||| ||||||||||||||||||||
                                 AGA CGAGACGACGGGTCCGACCT
                                   A
GAM642  KIAA0472 3' TCCATATTGTGTCAGAGTGGGA 72370          TT  C   GC
                                 TCTCGCTCTG  GC CAG  TGGA
                                 ||||||||||  || |||  ||||
                                 AGGGTGAGAC  TG GTT  ACCT
                                       __  T   AT
GAM642  KIAA0475 3' TCCAGCCTGGGAGACAGAGCGA 30130          TG
           GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                 ||||||||||  ||||||||||
                                 AGAGCGAGACA  GGGTCCGACCT
                                       GA
GAM642  KIAA0493 5' TCAGAGTGGCAGAGGAGA    64937     G     TG CCAGG
                                 TCTC CTCTGT  C    CTGG
                                 |||| ||||||  |    ||||
                                 AGAG GAGACG  G    GACT
                                   _     GT A____
GAM642  KIAA0493 5' TCTGGTTTTGGAGTAGAGA   64939     _     TT   C
                                 TCTC GCTCTG  GCC AGG
                                 |||| ||||||  ||| |||
                                 AGAG TGAGGT  TGG TCT
                                   A     TT  _
GAM642  KIAA0513 3' TCTAGCCTGCAGAGTGCAGTGA 29052         TGT   C_____
           GTGAGA                TCTCGCTC   TGC     CAGGCTGGA
                                 ||||||||   |||     |||||||||
                                 AGAGTGAG   ACG     GTCCGATCT
                                      TG_   TGAGAC
GAM642  KIAA0513 3' TTTAGAGAAATGTCAGAGCGAG 29058          TTGCCCAGG
           G                     TCTCGCTCTG        CTGGA
                                 ||||||||||        |||||
                                 GGAGCGAGAC        GATTT
                                       TGTAAAGA_
GAM642  KIAA0514 3' TCCAGCCTGGATGACGGAGCCA 28755     C       GC
           GA                    TCT GCTCTGTT  CCAGGCTGGA
                                 ||| ||||||||  ||||||||||
                                 AGA CGAGGCAG  GGTCCGACCT
                                   C       TA
GAM642  KIAA0514 3' TCCAGTTTGAGCAAGAGGAGGG 28757          G ___   C
           TGAGG                 TCTCGCTCT T   TGC CAGGCTGGA
                                 |||||||||  |   ||| |||||||||
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                                GGAGTGGGA G   ACG GTTTGACCT
                                     G AGA   A
GAM642  KIAA0515 5' TCCGGCGCCTCCGGCAAGAGCG 64556        GT   C_   __
           GGA                   TCTCGCTCT  TGCC  AGGC  TGGA
                                 |||||||||  ||||  ||||  ||||
                                 AGGGCGAGA  ACGG  TCCG  GCCT
                                      __   CC   CG
GAM642  KIAA0543 3' CCAGATGGTGGAGCTGGG    69518    C     TTGC   GG
                                 TCT GCTCTG    CCA  CTGG
                                 ||| ||||||    |||  ||||
                                 GGG CGAGGT    GGT  GACC
                                   T     _____   A_
GAM642  KIAA0547 3' TCCTGCCTGGTTGACAGAGTGA 29601          GC     T
           GA                    TCTCGCTCTGTT  CCAGGC GGA
                                 ||||||||||||  |||||| |||
                                 AGAGTGAGACAG  GGTCCG CCT
                                       TT     T
GAM642  KIAA0553 3' TGGCTTGCAGGGGTGGG     70454        GT   CC   TG
                                 CTCGCTCT  TGC  AGGC  G
                                 ||||||||  |||  ||||  |
                                 GGGTGGGG  ACG  TTCG  T
                                      __   __    GT
GAM642  KIAA0557 3' TCCAGCCTGGTGATAGAACGAG 78576      C    TG  C
           A                     TCTCG TCTGT  CC AGGCTGGA
                                 |||||  |||||  ||  ||||||||
                                 AGAGC  AGATA  GG TCCGACCT
                                    A    GT  _
GAM642  KIAA0560 5' TTTAGTTTCCACTGGAGTGGA  62173    T     GT  CCC
                                 TC CGCTCT  TG   AGGCTGGA
                                 || ||||||  ||   ||||||||
                                 AG GTGAGG  AC   TTTGATTT
                                  _     TC  C__
GAM642  KIAA0563 5' CCGGCAGGGCAGGATGGGA   29876      C   GT    AG
                                 TCTCG TCT  TGCCC  GCTGG
                                 |||||  |||  |||||  |||||
                                 AGGGT AGG  ACGGG  CGGCC
                                    _  __     A_
GAM642  KIAA0563 3' TCCAGCCTGGGCGACAGAGCAA 29890     C
           GA                     TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM642  KIAA0565 3' TCCAACCTGGGCGACAGAGCAA 67441     C            C
           GA                     TCT GCTCTGTTGCCCAGG TGGA
                                  ||| |||||||||||||| ||||
                                  AGA CGAGACAGCGGGTCC ACCT
                                    A            A
GAM642  KIAA0607 3' TCTGGCCTGGCTGGAGCCAGG  72955    C    GTT   C    TG
                                  TCT GCTCT   GCC AGGC  GA
                                  ||| |||||   ||| ||||  ||
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                                GGA CGAGG   CGG TCCG  CT
                                  C    T__  _   GT
GAM642  KIAA0618 3' CAGGGGGGTGAGGAGTGGGG  29848        G TG   AGG   GA
                                TCTCGCTCT T  CCC   CTG
                                |||||||||  |  |||   |||
                                GGGGTGAGG A  GGG   GAC
                                     _ GT   GG_   A
GAM642  KIAA0618 5' TTTGGCCTCTAGTGGATGAGA  29862      C  TG   CCC    TG
                                TCTCG TC  TTG   AGGC  GA
                                |||||  ||  |||   ||||  ||
                                AGAGT AG  GAT   TCCG  TT
                                   _ GT   C__    GT
GAM642  KIAA0628 3' TCTAGCCTGGGCAACCAAGAGT 29536        __
           GA                     TCGCTCT  GTTGCCCAGGCTGGA
                                |||||||  ||||||||||||||||
                                AGTGAGA  CAACGGGTCCGATCT
                                    AC
GAM642  KIAA0635 3' TCCAGCCTGGGTGACAGAGT   28421        TG
                                GCTCTGT  CCCAGGCTGGA
                                |||||||  ||||||||||||
                                TGAGACA  GGGTCCGACCT
                                    GT
GAM642  KIAA0643 3' ACTCCAGCCTGGGTGACAGAGT 45969           TG
           GAGA                    TCTCGCTCTGT  CCCAGGCTGGA
                                |||||||||||  ||||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      GT         CAC
GAM642  KIAA0644 5' TCCGGCCGCTGCACGCAGGGCG 29728           _  CCA
           GGA                     TCTCGCTCTGT TGC   GGCTGGA
                                |||||||||||| |||   |||||||
                                AGGGCGGGACG ACG   CCGGCCT
                                      C   TCG
GAM642  KIAA0664 3' TTTAGTTTGGGGCGGGACGGGA 64945      CT    TG
                                TCTCG  CTGT  CCCAGGCTGGA
                                |||||  ||||  ||||||||||||
                                AGGGC  GGCG  GGGTTTGATTT
                                   AG   __
GAM642  KIAA0682 3' TGGGCTGGGGGGGCGGGGCGGGG 30032           G    G
                                TCTCGCTCTGTT CCCAG CTG
                                |||||||||||| ||||| |||
                                GGGGCGGGGCGG GGGTC GGT
                                      G    G
GAM642  KIAA0694 3' CGGCCAGGCATGGTGGGG    72967       CTGT    CA   TG
                                TCTCGCT    TGCC  GGC  G
                                |||||||    ||||  |||  |
                                GGGGTGG    ACGG  CCG  C
                                    T____    A_   GT
GAM642  KIAA0694 3' CTCCAGCCTGGGCAACAGAGTG 72968
           AGA                     TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||||
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                                AGAGTGAGACAACGGGTCCGACCT
                                      CA
GAM642  KIAA0694  3'  GACCAGCCTGGGCAACATAGTG 72969        C           A
          AGA                   TCTCGCT TGTTGCCCAGGCTGG
                                ||||||| ||||||||||||||||
                                AGAGTGA ACAACGGGTCCGACC
                                   T           AGA
GAM642  KIAA0737  3'  TTTGGAGGGTAGCAGTAGAGA  29821     GCT       AGG TG
                                TCTC   CTGTTGCCC   C  GA
                                ||||   |||||||||   |  ||
                                AGAG   GACGATGGG   G  TT
                                  AT_       A__ GT
GAM642  KIAA0738  3'  CCCAGACATGGGCGATGGGGAG 28885     G         GG_   A
          GGA                   TCTC CTCTGTTGCCCA   CTGG
                                |||| ||||||||||||   ||||
                                AGGG GGGGTAGCGGGT   GACC
                                  A          ACA    CT
GAM642  KIAA0738  3'  TCCAGCCTGGGGGACAGAGTGA 28887          G
          GA                    TCTCGCTCTGTT CCCAGGCTGGA
                                |||||||||||| ||||||||||
                                AGAGTGAGACAG GGGTCCGACCT
                                      G
GAM642  KIAA0752  3'  TCCAGCCTGGGCAACGAGCGA  67635       T
                                TCGCTC GTTGCCCAGGCTGGA
                                |||||| ||||||||||||||
                                AGCGAG CAACGGGTCCGACCT
                                  _
GAM642  KIAA0794  3'  TCCAGCCTGGGCGACAAAGCGA 81238       C
                                TCGCT TGTTGCCCAGGCTGGA
                                ||||| ||||||||||||||||
                                AGCGA ACAGCGGGTCCGACCT
                                   A
GAM642  KIAA0795  3'  TCCAGCCTGGTTGACAGAGTGA 47232          GC
          GA                    TCTCGCTCTGTT  CCAGGCTGGA
                                ||||||||||||  ||||||||||
                                AGAGTGAGACAG  GGTCCGACCT
                                      TT
GAM642  KIAA0798  3'  TCCAGCCTGGGCAACAAGAGCG 28455        _
          A                      TCGCTCT GTTGCCCAGGCTGGA
                                 ||||||| ||||||||||||||||
                                 AGCGAGA CAACGGGTCCGACCT
                                    A
GAM642  KIAA0821  3'  TTTAGTTTCCTGGGCAGGGAGG 30613     G   G       ___
          GG                    CTC CTCT TTGCCCAGG   CTGGA
                                ||| |||| |||||||||   |||||
                                GGG GAGG GACGGGTCC   GATTT
                                  _   _        TTT
GAM642  KIAA0830  3'  TTAGACTTGACAGAGGAGA   70273      G     TGCC   _
                                TCTC CTCTGT    CAGG CTGG
                                |||| ||||||    |||| ||||
```

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                                AGAG GAGACA    GTTC GATT
                                  _     ____    A
GAM642  KIAA0831  3'  TCCAGCCTGGGCAACAAGAGCG 30655         _
            AGG                   TCTCGCTCT GTTGCCCAGGCTGGA
                                  ||||||||| ||||||||||||||||
                                  GGAGCGAGA CAACGGGTCCGACCT
                                     A
GAM642  KIAA0872  3'  CTCCAGCCTGGGTGACAGAGTG 30752           TG
            AGA                   TCTCGCTCTGT  CCCAGGCTGGA
                                  |||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                     GT         CA
GAM642  KIAA0876  3'  ACTCCAGCCTGGGCAACAGAGC 65311
            GAGA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                  |||||||||||||||||||||||||
                                  AGAGCGAGACAACGGGTCCGACCT
                                              CAC
GAM642  KIAA0884  3'  TCCAACCTGGGTAACAGAGTGA 70758                C
            GA                    TCTCGCTCTGTTGCCCAGG TGGA
                                  |||||||||||||||||| ||||
                                  AGAGTGAGACAATGGGTCC ACCT
                                           A
GAM642  KIAA0889  3'  ACTCCAGCCTGGGTGACAGAGT 31748           TG
            GAGA                   TCTCGCTCTGT  CCCAGGCTGGA
                                  |||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                     GT         CAC
GAM642  KIAA0889  3'  TCCAGCCTGGGTGACAGACTAA 31785     CGC     TG
            GA                    TCT   TCTGT  CCCAGGCTGGA
                                  |||   |||||  ||||||||||||
                                  AGA   AGACA  GGGTCCGACCT
                                    ATC     GT
GAM642  KIAA0889  5'  TCCAGCCTGGGTGACATATCAA 31787     CGCTC   TG
            GA                    TCT    TGT  CCCAGGCTGGA
                                  |||    |||  ||||||||||||
                                  AGA    ACA  GGGTCCGACCT
                                    ACTAT   GT
GAM642  KIAA0889  3'  TCTGAGCAACATGGTGAGA    31790        C     C
                                  TCTCGCT TGTTGC CAGG
                                  ||||||| |||||| ||||
                                  AGAGTGG ACAACG GTCT
                                     T     A
GAM642  KIAA0892  3'  TCCAGCCTGGGTGACGGTGAGA 71572        CT  TG
                                  TCTCGCT  GT  CCCAGGCTGGA
                                  |||||||  ||  ||||||||||||
                                  AGAGTGG  CA  GGGTCCGACCT
                                     __ GT
GAM642  KIAA0894  3'  ACTCCAGCCTGGGTGACAGAGC 30322           TG
            GAGA                   TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
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                                AGAGCGAGACA  GGGTCCGACCT
                                      GT          CAC
GAM642  KIAA0907  3'  TCCAGCCTGGGCAATAGAGCAA 30882     C
            GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGATAACGGGTCCGACCT
                                    A
GAM642  KIAA0907  3'  TCCAGCCTGGGCACTAGAGTGA 30883          T
            GA                    TCTCGCTCTG TGCCCAGGCTGGA
                                  |||||||||| ||||||||||||
                                  AGAGTGAGAT ACGGGTCCGACCT
                                        C
GAM642  KIAA0912  3'  CTCCAGCCTGGGTGACAGAGTG 65042           TG
            AGG                     TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  GGAGTGAGACA  GGGTCCGACCT
                                        GT          CA
GAM642  KIAA0916  5'  CCGGGGTGGCGGGGTTAGA    31187     C      TG   A
                                  TCT GCTCTGT  CCC GG
                                  ||| |||||||  ||| ||
                                  AGA TGGGGCG  GGG CC
                                    T      GT   G
GAM642  KIAA0924  3'  CTCCAGCCTGGGCAACAGAGCG 30362
            AGA                     TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAACGGGTCCGACCT
                                              CG
GAM642  KIAA0930  3'  TCAGAGGTGAGGGGCGGGA    71075          G TG  CAGG
                                  TCTCGCTCT T  CC    CTGG
                                  |||||||||  |  ||    ||||
                                  AGGGCGGGG A  GG    GACT
                                        _ GT  A___
GAM642  KIAA0930  3'  TCTAGCCTGGGCAACGAGAGCG 71076          _
            A                      TCGCTCT GTTGCCCAGGCTGGA
                                  ||||||| ||||||||||||||||
                                  AGCGAGA CAACGGGTCCGATCT
                                      G
GAM642  KIAA0931  3'  TCCTAAGGGCGGGGAGCGGGG  68018          G      AGGCT
                                  TCTCGCTCT TTGCCC     GGA
                                  |||||||||  ||||||    |||
                                  GGGGCGAGG GGCGGG     CCT
                                        _      AAT__
GAM642  KIAA0937  3'  TTTAGCTCATTCCTAATGGAGT 93229     C        CCCA__
            TGGG                      TCT GCTCTGTTG      GGCTGGA
                                  ||| |||||||||      |||||||
                                  GGG TGAGGTAAT      TCGATTT
                                    T        CCTTAC
GAM642  KIAA0953  3'  TTCAGCCTAGGTGACAGAGTGA 67335           TG  C
            GA                      TCTCGCTCTGT  CC AGGCTGGA
                                  ||||||||||  || ||||||||
```

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                                AGAGTGAGACA  GG TCCGACTT
                                      GT  A
GAM642  KIAA0961  3'  TCCAGCCTGGGCAACAAGAGC  30409      _
                                GCTCT GTTGCCCAGGCTGGA
                                ||||| ||||||||||||||
                                CGAGA CAACGGGTCCGACCT
                                  A
GAM642  KIAA0978  5'  TCCAGCTACAGTGGAGGGAGA  70997     G   TG   CCCA
                                TCTC CTC  TTG    GGCTGGA
                                |||| |||  |||    |||||||
                                AGAG GAG  GAC    TCGACCT
                                  G   GT   A___
GAM642  KIAA0981  3'  TCCAGCCTGGGCAACAGAGCAA 62093     C
            GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||
                                AGA CGAGACAACGGGTCCGACCT
                                  A
GAM642  KIAA1001  3'  TCCAGCCTGGGTGATGGAGCAA 31012     C      TG
            GA                    TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGGTA  GGGTCCGACCT
                                  A      GT
GAM642  KIAA1001  3'  TCTAGCCTGAGGGACAGAGTGA 31014          G  _
            GA                    TCTCGCTCTGTT CC CAGGCTGGA
                                |||||||||||| || |||||||||
                                AGAGTGAGACAG GG GTCCGATCT
                                      _  A
GAM642  KIAA1017  3'  AGACCAGCCTGGGCAACATAGT 24266        C           A
            GAGA                    TCTCGCT TGTTGCCCAGGCTGG
                                ||||||| ||||||||||||||||
                                AGAGTGA ACAACGGGTCCGACC
                                    T            AGAA
GAM642  KIAA1030  3'  TCCAGCCTGGGTGACAGAG   94985       TG
                                CTCTGT  CCCAGGCTGGA
                                ||||||  ||||||||||
                                GAGACA  GGGTCCGACCT
                                   GT
GAM642  KIAA1032  3'  TCCAGCCTGGGCAACAGA    66732
                                TCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||
                                AGACAACGGGTCCGACCT

GAM642  KIAA1045  3'  TCAGACCAGCAGAGTGA     71610          CCCAGG
                                TCGCTCTGTTG     CTGG
                                ||||||||||      ||||
                                AGTGAGACGAC     GACT
                                      CA_____
GAM642  KIAA1056  3'  TCCGGCCTGGGTGACAGAGCCA 30317     C      TG
            GA                    TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
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                                AGA CGAGACA  GGGTCCGGCCT
                                  C       GT
GAM642  KIAA1086 3'  TCCAGCCTGGGCAACAGAAGAA 71289     _ GC
            GA                    TCT C  TCTGTTGCCCAGGCTGGA
                                  ||| |  ||||||||||||||||||
                                  AGA G  AGACAACGGGTCCGACCT
                                    A A_
GAM642  KIAA1086 3'  TCCAGCCTGGGTTACAGAGCGA 71290           T
            GA                    TCTCGCTCTGT GCCCAGGCTGGA
                                  ||||||||||| ||||||||||||
                                  AGAGCGAGACA TGGGTCCGACCT
                                        T
GAM642  KIAA1089 3'  CTAGCTTCCAGGGCAGGGA    69429      _      TTGCCC
                                  TCTC GCTCTG      AGGCTGG
                                  |||| ||||||      |||||||
                                  AGGG CGGGAC      TTCGATC
                                    A     C_____
GAM642  KIAA1130 3'  TCCTGCCTGGGTGACAGAGCGA 63100           TG       T
            GA                    TCTCGCTCTGT  CCCAGGC GGA
                                  ||||||||||  ||||||| |||
                                  AGAGCGAGACA  GGGTCCG CCT
                                        GT       T
GAM642  KIAA1143 3'  TCCAGCCTGGGCAACAGAGTAA 69251     CG
            GA                    TCT  CTCTGTTGCCCAGGCTGGA
                                  |||  ||||||||||||||||||
                                  AGA  GAGACAACGGGTCCGACCT
                                    AT
GAM642  KIAA1164 3'  GCAAGCCTGGGCAATAGAGCGA 70044                  GGA
            GA                    TCTCGCTCTGTTGCCCAGGCT
                                  |||||||||||||||||||||
                                  AGAGCGAGATAACGGGTCCGA
                                              ACGT
GAM642  KIAA1164 3'  TCCAGCCTGGGTGACAGAGGGA 70051      G      TG
            GA                    TCTC CTCTGT  CCCAGGCTGGA
                                  |||| ||||||  ||||||||||
                                  AGAG GAGACA  GGGTCCGACCT
                                    G     GT
GAM642  KIAA1181 3'  TCTGCAGTGGCAGGGAGTGGGG 68915          G     CAG  T
                                  TCTCGCTCT TTGCC   GC GGA
                                  ||||||||| |||||   || |||
                                  GGGGTGAGG GACGG   CG TCT
                                        _     TGA  _
GAM642  KIAA1191 3'  TCCAGCCTGGGCGACAGAACGA 40336       C
            GA                    TCTCG TCTGTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||||||
                                  AGAGC AGACAGCGGGTCCGACCT
                                    A
GAM642  KIAA1202 3'  TCCATCCTGGGCAACAGAGTGA 72492                 C
            GA                    TCTCGCTCTGTTGCCCAGG TGGA
                                  |||||||||||||||||| ||||
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                                AGAGTGAGACAACGGGTCC ACCT
                                          T
GAM642  KIAA1204 3' AGACCAGCCTGGGCAACACAGC 69736       C          A
           GAGA                 TCTCGCT TGTTGCCCAGGCTGG
                                ||||||| ||||||||||||||
                                AGAGCGA ACAACGGGTCCGACC
                                   C            AGAA
GAM642  KIAA1228 3' CTCCAGCCTGGGCAACAGAGTG 65674
           AGA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||
                                AGAGTGAGACAACGGGTCCGACCT
                                          CA
GAM642  KIAA1253 3' TCTAGCCTGGGCAACAGAGTAA 93550    CG
           GA                   TCT  CTCTGTTGCCCAGGCTGGA
                                |||  ||||||||||||||||||
                                AGA  GAGACAACGGGTCCGATCT
                                  AT
GAM642  KIAA1255 3' TCTGGCTTGTGTGCTGGATGAG 67747     C   TT  C    TG
           G                    TCTCG TCTG  GC CAGGC  GA
                                ||||| ||||  || |||||  ||
                                GGAGT AGGT  TG GTTCG  CT
                                  _   CG  T    GT
GAM642  KIAA1257 3' TCCAGCCTGGGCAGCAGAGCAA 63419    C
           GA                   TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||
                                AGA CGAGACGACGGGTCCGACCT
                                  A
GAM642  KIAA1266 3' TTTGGCCTAGAGGTGTGGAGTG 66704       TG T   C__   TG
           AGA                  TCTCGCTC  T GCC   AGGC  GA
                                |||||||| | |||   |||| ||
                                AGAGTGAG  G TGG   TCCG  TT
                                   GT _   AGA    GT
GAM642  KIAA1271 3' TCCAACCTGGGTGAGAGAGCGA 70145        G TG     C
           GA                   TCTCGCTCT T  CCCAGG TGGA
                                ||||||||| |  |||||| ||||
                                AGAGCGAGA A  GGGTCC ACCT
                                     G GT     A
GAM642  KIAA1271 3' TCCAGCCTGGGCGACAGAGTGG 70146
                                TCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||
                                GGTGAGACAGCGGGTCCGACCT

GAM642  KIAA1276 3' AACCAGCCTGGGTGACAGAGGG 67025     G     TG        A
           AGA                  TCTC CTCTGT  CCCAGGCTGG
                                |||| ||||||  ||||||||||
                                AGAG GAGACA  GGGTCCGACC
                                  G     GT         AAC
GAM642  KIAA1277 3' TCCAGCCTGGACAACAGAGCAA 65086    C       C
           GA                   TCT GCTCTGTTG CCAGGCTGGA
                                ||| ||||||||| ||||||||||
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                                AGA CGAGACAAC GGTCCGACCT
                                  A       A
GAM642  KIAA1297 5' TTTGGCTGCCCCATGGAGGAGA 72646     G     TGCCCA  TG
                                TCTC CTCTGT     GGC  GA
                                |||| ||||||     |||  ||
                                AGAG GAGGTA     TCG  TT
                                  _     CCCCG_   GT
GAM642  KIAA1319 3' TCCACTCTGGAGCAGGGTGAGG 40791          GC   GC
                                TCTCGCTCTGTT  CCAG  TGGA
                                ||||||||||||  ||||  ||||
                                GGAGTGGGACGA  GGTC  ACCT
                                       __   TC
GAM642  KIAA1322 3' TCCAGCCTGCACAGTAGAGTGA 73117          CC
           GG                     TCTCGCTCTGTTG  CAGGCTGGA
                                ||||||||||||||  |||||||||
                                GGAGTGAGATGAC  GTCCGACCT
                                       AC
GAM642  KIAA1328 3' TCCAGCCTGGGTGACAGAGCAA 62334     C      TG
           GA                     TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM642  KIAA1340 3' TCCAGCCTGGGCGACAGTGCAA 69699     C  T
           GA                     TCT GC CTGTTGCCCAGGCTGGA
                                ||| || ||||||||||||||||
                                AGA CG GACAGCGGGTCCGACCT
                                  A  T
GAM642  KIAA1348 3' TCCAGCCTGGGCAACAAGAGTG 69129        _
           A                      TCGCTCT GTTGCCCAGGCTGGA
                                ||||||| ||||||||||||||||
                                AGTGAGA CAACGGGTCCGACCT
                                     A
GAM642  KIAA1361 3' CGGCTGGATCCCGCAGCAGAGT 62885           _________ AGGCT
           GAGG                     TCTCGCTCTGTTGC       CC    G
                                ||||||||||||||       ||    |
                                GGAGTGAGACGACG       GG    C
                                       CCCT   A  TCGGA
GAM642  KIAA1364 3' TCCAGCCTGGGAGATGGTGAGA 64358        CT  TG
                                TCTCGCT  GT  CCCAGGCTGGA
                                |||||||  ||  ||||||||||
                                AGAGTGG  TA  GGGTCCGACCT
                                     __  GA
GAM642  KIAA1364 3' TCCAGCCTGTGTGACAGAATGA 64359      C     TG C
           GA                     TCTCG TCTGT  C CAGGCTGGA
                                ||||| |||||  | |||||||||
                                AGAGT AGACA  G GTCCGACCT
                                  A    GT T
GAM642  KIAA1377 3' CCAGCCTGGGTGACAGTGTGAG 67757       T    TG        A
           A                      TCTCGC CTGT  CCCAGGCTGG
                                ||||||| ||||  ||||||||||
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                                AGAGTG GACA  GGGTCCGACC
                                   T   GT        A
GAM642  KIAA1393  5'  TCCGATCGGTACCGGAGCGGGA 72575          T   CA GC
                                TCTCGCTCTG TGCC  G  TGGA
                                |||||||||| ||||  |  ||||
                                AGGGCGAGGC ATGG  C  GCCT
                                     C   __ TA
GAM642  KIAA1404  3'  TCCAGTCTGGGCGACAGGAGC  62693     _
                                GCTC TGTTGCCCAGGCTGGA
                                |||| ||||||||||||||||
                                CGAG ACAGCGGGTCTGACCT
                                  G
GAM642  KIAA1423  3'  TCCAGCCTGGGTGTCAGAGCGA 62398          T
           GA                     TCTCGCTCTG TGCCCAGGCTGGA
                                |||||||||| ||||||||||||
                                AGAGCGAGAC GTGGGTCCGACCT
                                     T
GAM642  KIAA1441  3'  CCGGGGCGGGGGGGGTGGGG   89788         G     A
                                TCTCGCTCT TTGCCC GG
                                ||||||||| ||||||  ||
                                GGGGTGGGG GGCGGG CC
                                     G     G
GAM642  KIAA1456  5'  TCCAGCCTGGGTGACTGAGGGA 67569      G   T  TG
           GA                     TCTC CTC GT  CCCAGGCTGGA
                                |||| ||| ||  ||||||||||
                                AGAG GAG CA  GGGTCCGACCT
                                  G   T  GT
GAM642  KIAA1458  3'  TTTAGTCTTCATGGGGTTGGA  69573     C      T CCC
                                TCT GCTCTGT G   AGGCTGGA
                                ||| |||||||  |   ||||||||
                                AGG TGGGGTA C   TCTGATTT
                                  T      _ T__
GAM642  KIAA1473  3'  TCCGTCCTGGGTGACAAAGTGA 71213        C   TG     C
           GA                     TCTCGCT TGT  CCCAGG TGGA
                                ||||||| |||  |||||| ||||
                                AGAGTGA ACA  GGGTCC GCCT
                                     A   GT     T
GAM642  KIAA1486  3'  ACTCCAGCCTGGGTGACAGAGC 67966           TG
           GAGA                     TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                     GT          CAC
GAM642  KIAA1497  5'  ACTCCAGCCTGGGCGACAGAGC 68106
           GAGA                     TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGCGAGACAGCGGGTCCGACCT
                                          CAC
GAM642  KIAA1503  3'  TCCAGCCTGGGCGACAGAGTGA 68900
                                TCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||
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                                AGTGAGACAGCGGGTCCGACCT

GAM642  KIAA1508  3'  CTCCAGCCTGGGTGACAGAGCG 62548          TG
                AGA                  TCTCGCTCTGT  CCCAGGCTGGA
                                     ||||||||||  ||||||||||
                                     AGAGCGAGACA  GGGTCCGACCT
                                           GT         CA
GAM642  KIAA1522  5'  TCTGGAGAGGCAGGGTGGGA  65611          GC_
                                     TCTCGCTCTGTT  CCAGG
                                     ||||||||||||  |||||
                                     AGGGTGGGACGG  GGTCT
                                           AGA
GAM642  KIAA1554  3'  TCCAACCTGGGTGACAGAGTGA 96862          TG     C
                GA                   TCTCGCTCTGT  CCCAGG TGGA
                                     ||||||||||  |||||| ||||
                                     AGAGTGAGACA  GGGTCC ACCT
                                           GT     A
GAM642  KIAA1559  3'  CTCCAGCCTGGGTGACAGAGTG 73454          TG
                AGA                  TCTCGCTCTGT  CCCAGGCTGGA
                                     ||||||||||  ||||||||||
                                     AGAGTGAGACA  GGGTCCGACCT
                                           GT         CA
GAM642  KIAA1559  3'  TCCAGCCTGGGTAACAGAGCAA 73461     C
                GA                   TCT GCTCTGTTGCCCAGGCTGGA
                                     ||| ||||||||||||||||||
                                     AGA CGAGACAATGGGTCCGACCT
                                       A
GAM642  KIAA1582  5'  TCCAGCCTGGAGTGCAGGAGGG 65993     G   GTT _
                GG                   CTC CTCT   GC CCAGGCTGGA
                                     ||| ||||   || ||||||||||
                                     GGG GAGG   TG GGTCCGACCT
                                       G   ACG  A
GAM642  KIAA1586  5'  ACTCCAGCTTGGGTGACAGAGC 93934          TG
                GAGA                   TCTCGCTCTGT  CCCAGGCTGGA
                                     ||||||||||  ||||||||||
                                     AGAGCGAGACA  GGGTTCGACCT
                                           GT         CAC
GAM642  KIAA1586  5'  TCTACCCTGGGCAACAGAGCAA 93942     C          C
                GA                   TCT GCTCTGTTGCCCAGG TGGA
                                     ||| |||||||||||||| ||||
                                     AGA CGAGACAACGGGTCC ATCT
                                       A            C
GAM642  KIAA1594  3'  ACTGCAGTCTGAGTGACAGAGT 72549          TG C     GA
                GAGA                   TCTCGCTCTGT  C CAGGCTG
                                     ||||||||||  | |||||||
                                     AGAGTGAGACA  G GTCTGAC
                                           GT A      GTCAC
GAM642  KIAA1614  3'  TCCAGCCTGGGCAACAAGAGC  70668      _
                                     GCTCT GTTGCCCAGGCTGGA
                                     ||||| ||||||||||||||
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                                CGAGA CAACGGGTCCGACCT
                                  A
GAM642  KIAA1630  3'  TCCAGCCTGGGTGACAGAGCAA 38657     C      TG
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGAGACA  GGGTCCGACCT
                                      A      GT
GAM642  KIAA1644  3'  CTCCAGCCTGGGCAACAGAGTG 86221
                AGA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                      ||||||||||||||||||||||||
                                      AGAGTGAGACAACGGGTCCGACCT
                                                    CA
GAM642  KIAA1649  5'  ACTTCAGCCTGGGTGACAGAGT 51210          TG
                GAGA                  TCTCGCTCTGT  CCCAGGCTGGA
                                      ||||||||||  ||||||||||
                                      AGAGTGAGACA  GGGTCCGACTT
                                            GT         CAC
GAM642  KIAA1649  3'  CCAGGCTGGCAGAGCTGGA   51225     C     TTGC   G
                                      TCT GCTCTG   CCAG CTGG
                                      ||| ||||||   |||| ||||
                                      AGG CGAGAC   GGTC GACC
                                        T     ____   G
GAM642  KIAA1649  3'  CCAGGCTGGCAGAGCTGGA   51226     C     TTGC   G
                                      TCT GCTCTG   CCAG CTGG
                                      ||| ||||||   |||| ||||
                                      AGG CGAGAC   GGTC GACC
                                        T     ____   G
GAM642  KIAA1649  3'  TCCAGCCTGTGCAACAGAGCGA 51248           C
                GG                    TCTCGCTCTGTTGC CAGGCTGGA
                                      |||||||||||||| |||||||||
                                      GGAGCGAGACAACG GTCCGACCT
                                                T
GAM642  KIAA1649  3'  TCCATCCTGGGCAACACAGTGA 51249       C        C
                GA                    TCTCGCT TGTTGCCCAGG TGGA
                                      ||||||| |||||||||| ||||
                                      AGAGTGA ACAACGGGTCC ACCT
                                         C         T
GAM642  KIAA1649  5'  TTTGAGCAGGGGAGTGAGG   51257        G   C
                                      TCTCGCTCT TTGC CAGG
                                      ||||||||| |||| ||||
                                      GGAGTGAGG GACG GTTT
                                           G   A
GAM642  KIAA1649  5'  TTTGGCTTTTAAGTACAGTGGG 67519       C   GCCC   TG
                A                     TCTCGCT TGTT   AGGC  GA
                                      ||||||| ||||   ||||  ||
                                      AGGGTGA ATGA   TTCG  TT
                                         C   ATT_   GT
GAM642  KIAA1671  5'  TCCAGCGTGACAGGAGTGAGA  66290        _  TG CCAG
                                      TCTCGCTC TGT  C   GCTGGA
                                      |||||||| |||  |   ||||||
```

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                                AGAGTGAG ACA  G    CGACCT
                                     G   GT ____
GAM642  KIAA1674  3'  ACTCCAGCCTGGGCGACAGAGC 69325
                GAGA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                      ||||||||||||||||||||||||
                                      AGAGCGAGACAGCGGGTCCGACCT
                                                 CAC
GAM642  KIAA1679  3'  TCCAGTACAATCTAACAGAGTG 70713    T        CCCAG_
                GA                    TC CGCTCTGTTG     GCTGGA
                                      || ||||||||||      ||||||
                                      AG GTGAGACAAT     TGACCT
                                       _        CTAACA
GAM642  KIAA1715  3'  TCCAGCCTGGGCAACAAGAGTG 68691        _
                A                     TCGCTCT GTTGCCCAGGCTGGA
                                      |||||||| ||||||||||||||
                                      AGTGAGA CAACGGGTCCGACCT
                                           A
GAM642  KIAA1718  3'  TTTGGGGGGTGATGGGGAGGGG 64980      G     TG   AGG TG
                                      TCTC CTCTGT  CCC   C  GA
                                      |||| ||||||  |||   |  ||
                                      GGGG GGGGTA  GGG   G  TT
                                        A     GT   G__ GT
GAM642  KIAA1724  3'  TCCAGCCAGAGTGACAGAGCAA 67622     C      TG CCA
                GA                    TCT GCTCTGT  C   GGCTGGA
                                      ||| |||||||  |   |||||||
                                      AGA CGAGACA  G   CCGACCT
                                        A      GT AGA
GAM642  KIAA1726  3'  TCCAGAAATAATATGGGTGAGG 67834         _    CCCAGG
                                      TCTCGCTC TGTTG     CTGGA
                                      |||||||| |||||     |||||
                                      GGAGTGGG ATAAT     GACCT
                                           T    AAA___
GAM642  KIAA1727  3'  TCCAGCCTGGATGACAGAGTGA 64765          GC
                GA                    TCTCGCTCTGTT  CCAGGCTGGA
                                      ||||||||||||  ||||||||||
                                      AGAGTGAGACAG  GGTCCGACCT
                                             TA
GAM642  KIAA1735  3'  CCAGTTTCCAAAGCGAGA    89001       CTG   CCC
                                      TCTCGCT   TTG   AGGCTGG
                                      |||||||   |||   |||||||
                                      AGAGCGA   AAC   TTTGACC
                                         ___   C__
GAM642  KIAA1786  3'  CCAGCCCGGGTGACAGAGCGAG 66630          TG   A     A
                A                     TCTCGCTCTGT  CCC GGCTGG
                                      ||||||||||||  ||| ||||||
                                      AGAGCGAGACA  GGG CCGACC
                                             GT   C
GAM642  KIAA1795  3'  TTTGGTCTCACCAACAAGTGAG 72619       C    CCC    TG
                G                     TCTCGCT TGTTG   AGGC  GA
                                      ||||||| |||||   ||||  ||
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                                GGAGTGA ACAAC   TCTG  TT
                                   _    CAC    GT
GAM642  KIAA1811  3'  CTGCGGGGTGGGGTGGGG    65419        GTT    AG  T
                                TCTCGCTCT   GCCC  GC GG
                                |||||||||   ||||  || ||
                                GGGGTGGGG   TGGG  CG TC
                                    ___    G_  _
GAM642  KIAA1821  3'  GAGGTGTTTTGGGGGTGGGGCG 72267        TG  G     CTGGA
           AGG                    TCTCGCTC  TT CCCAGG
                                |||||||||  || ||||||
                                GGAGCGGG  GG GGGTTT
                                    GT  _     TGTGGAGA
GAM642  KIAA1821  3'  TTTGGCCTGGGTGTTAGGTCAG 72278     C  T   TT       TG
           A                     TCT GC CTG  GCCCAGGC  GA
                                ||| || |||  |||||||||  ||
                                AGA TG GAT  TGGGTCCG  TT
                                  C  _   TG       GT
GAM642  KIAA1826  5'  TCCAAGGGCTGCGACGTAGCGG 67793        C     CCA    ___
           GA                     TCTCGCT TGTTGC   GGCT   GGA
                                |||||||| ||||||   ||||   |||
                                AGGGCGA GCAGCG   TCGG   CCT
                                    T     ___    GAA
GAM642  KIAA1829  3'  TCCAGCCTGGGCAACAAGAGCG 62656        _
           A                     TCGCTCT GTTGCCCAGGCTGGA
                                |||||||| ||||||||||||||||
                                AGCGAGA CAACGGGTCCGACCT
                                    A
GAM642  KIAA1841  3'  CCTAGCCTGGGTGACAGAGCAA 80850     C      TG         A
           GA                     TCT GCTCTGT  CCCAGGCTGG
                                ||| ||||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGATC
                                  A      GT         CT
GAM642  KIAA1854  3'  CGGCTGGATCTAGCAACAGAGC 72203     C         _________  AGGCT
           CAGA                    TCT GCTCTGTTGC       CC     G
                                ||| ||||||||||       ||     |
                                AGA CGAGACAACG       GG     C
                                  C         ATCT   A  TCGGA
GAM642  KIAA1870  3'  TTCAGCCTGGATGACAGAGTGA 50590           GC
           GA                     TCTCGCTCTGTT  CCAGGCTGGA
                                ||||||||||||  ||||||||||
                                AGAGTGAGACAG  GGTCCGACTT
                                      TA
GAM642  KIAA1871  3'  TCCAGCCTGGGCAACAAGTGCG 61911      T  _
           A                     TCGC CT GTTGCCCAGGCTGGA
                                |||| || ||||||||||||||||
                                AGCG GA CAACGGGTCCGACCT
                                  T  A
GAM642  KIAA1872  3'  TCCAGCCTGGGAGACAGAGCAA 63620     C      TG
           GA                     TCT GCTCTGT  CCCAGGCTGGA
                                ||| ||||||||  ||||||||||
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                                AGA CGAGACA  GGGTCCGACCT
                                  A      GA
GAM642  KIAA1872 3' TCCAGCCTGGGCAACAAGAGC  63621       _
                                GCTCT GTTGCCCAGGCTGGA
                                ||||| ||||||||||||||
                                CGAGA CAACGGGTCCGACCT
                                  A
GAM642  KIAA1872 3' TCCAGCCTGGGCGACAGAGCAA 63623     C
           GA                   TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGAGACAGCGGGTCCGACCT
                                  A
GAM642  KIAA1879 3' TCCAGCCTGGGAGACAGAGCAA 73946     C      TG
           GA                   TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A      GA
GAM642  KIAA1889 5' AGCCGACAGAGTGGGG      73879           GCCCA
                                TCTCGCTCTGTT    GGCT
                                ||||||||||||    ||||
                                GGGGTGAGACAG    CCGA
                                      _____
GAM642  KIAA1904 3' CCAGGCGGCCAGGGCGGGG   73863          TT   CAGG
                                TCTCGCTCTG  GCC    CTGG
                                |||||||||  |||    ||||
                                GGGGCGGGAC  CGG    GACC
                                     __   CG__
GAM642  KIAA1922 5' TCTAGTCTCCTTTTAGAGATGA 74008       _    TTGCCC
           GA                   TCTCG CTCTG     AGGCTGGA
                                ||||| |||||     ||||||||
                                AGAGT GAGAT     TCTGATCT
                                  A    TTTCC_
GAM642  KIAA1938 3' CGGCGGGATAGGGGAGG     93823     G     TG   AG  TG
                                TCTC CTCTGT  CCC  GC  G
                                |||| ||||||  |||  ||  |
                                GGAG GGGATA  GGG  CG  C
                                  _     __   __  GT
GAM642  KIAA1948 5' ACTCCAGCCTGGGTGACAGAGT 83289           TG
           GAGA                   TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                       GT          CAC
GAM642  KIAA1948 3' AGACCAGCCTGGGCAACATGGT 83291        C            A
           GAGA                   TCTCGCT TGTTGCCCAGGCTGG
                                  |||||||  |||||||||||||||
                                  AGAGTGG ACAACGGGTCCGACC
                                       T             AGAG
GAM642  KIAA1948 3' TCCAGCCTGGGTGACAGACCGA 83306       C     TG
           GA                     TCTCG TCTGT  CCCAGGCTGGA
                                  ||||| |||||  ||||||||||
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                                AGAGC AGACA  GGGTCCGACCT
                                  C     GT
GAM642  KIAA1950  3'  CTGGGCAACATGGTGAGA    94180        C
                                TCTCGCT TGTTGCCCAG
                                ||||||| ||||||||||
                                AGAGTGG ACAACGGGTC
                                    T
GAM642  KIAA1951  3'  CTCCAGCCTGGGCGACAGAGTG 74153
            AGA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGACAGCGGGTCCGACCT
                                              CA
GAM642  KIAA1951  3'  TCCAGTCTGGGCAACAGTGCAA 74166     C  T
            GA                    TCT GC CTGTTGCCCAGGCTGGA
                                ||| || ||||||||||||||||
                                AGA CG GACAACGGGTCTGACCT
                                  A  T
GAM642  KIAA1954  3'  TCCAGCCTGAGCAACAGAGCAA 78231     C        C
            GA                    TCT GCTCTGTTGC CAGGCTGGA
                                ||| |||||||||| |||||||||
                                AGA CGAGACAACG GTCCGACCT
                                  A         A
GAM642  KIAA1957  3'  TCCGTGCATGTGGCCAGGGCGG 76219          TT  _  G  _
            GG                    TCTCGCTCTG  GCC CA GC TGGA
                                |||||||||  ||| || || ||||
                                GGGGCGGGAC  CGG GT CG GCCT
                                     __  T  A  T
GAM642  KIAA1958  3'  TCCAGCCTGGGCAACAAAGCTA 82792     C   C
            GA                    TCT GCT TGTTGCCCAGGCTGGA
                                ||| ||| ||||||||||||||||
                                AGA CGA ACAACGGGTCCGACCT
                                  T   A
GAM642  KIAA1979  3'  TCCAGCATGGGTGATGGAGAGA 89655      G     TG    G
            GA                    TCTC CTCTGT  CCCA GCTGGA
                                |||| ||||||  |||| ||||||
                                AGAG GAGGTA  GGGT CGACCT
                                  A     GT    A
GAM642  KLF5     3'  TCAACATGGGTAAGGGGTGGGG 9963          G     GGC   A
                                TCTCGCTCT TTGCCCA   TGG
                                ||||||||| |||||||   |||
                                GGGGTGGGG AATGGGT   ACT
                                     _      ACA   C
GAM642  KLHL6    3'  TCTAGTCCCAAGAAGGGTGAGG 56176         G_   CCCA
                                TCTCGCTCT  TTG    GGCTGGA
                                |||||||||  |||    |||||||
                                GGAGTGGGA  AAC    CTGATCT
                                     AG   C___
GAM642  KR18     3'  TCCAGCCTGGGCAACAAGA    53896     _
                                TCT GTTGCCCAGGCTGGA
                                ||| ||||||||||||||
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                                AGA CAACGGGTCCGACCT
                                  A
GAM642  KREMEN   3'  TCCAGCCTGAGCAGCAGAGCGG 50237            C
                GA                TCTCGCTCTGTTGC CAGGCTGGA
                                  ||||||||||||| |||||||||
                                  AGGGCGAGACGACG GTCCGACCT
                                        A
GAM642  KREMEN   3'  TCCAGTGTAGGCAACAGAGTGA 50238            CAG
                GA                TCTCGCTCTGTTGCC  GCTGGA
                                  ||||||||||||||  ||||||
                                  AGAGTGAGACAACGG  TGACCT
                                        ATG
GAM642  LANO     3'  TCCAGCCCGGGTGACAGAGCGA 47977          TG  A
                GA                TCTCGCTCTGT  CCC GGCTGGA
                                  ||||||||||  ||| |||||||
                                  AGAGCGAGACA  GGG CCGACCT
                                        GT  C
GAM642  LGP2     3'  TTTGGGCTGTAGGGGGCGGGA  44381         GTT__
                                  TCTCGCTCT    GCCCAGG
                                  |||||||||    |||||||
                                  AGGGCGGGG    CGGGTTT
                                       GATGT
GAM642  LIAS     3'  TCCAGCCTGGGTGACAAGAGC  71169      _  TG
                                  GCTCT GT  CCCAGGCTGGA
                                  ||||| ||  ||||||||||
                                  CGAGA CA  GGGTCCGACCT
                                     A  GT
GAM642  LIM      3'  ACTCCAGCCTGGGTGACAGAGT 22310          TG
                GAGA                 TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                        GT         CAC
GAM642  LIM      3'  TCCAGCCTGGTGACAGAGCAAG 22335     C      TG  C
                A                  TCT GCTCTGT  CC AGGCTGGA
                                  ||| |||||||  || ||||||||
                                  AGA CGAGACA  GG TCCGACCT
                                    A      GT  _
GAM642  LIN-28   3'  TCCAGCCTGGTTACAGAGCGAG 45471          TGC
                A                  TCTCGCTCTGT   CCAGGCTGGA
                                  ||||||||||   ||||||||||
                                  AGAGCGAGACA   GGTCCGACCT
                                        TT_
GAM642  LIPG     3'  TTTGGAACCCAGTGGAGTTGGG 21236     C    TG   C___
                                  TCT GCTC  TTG    CCAGG
                                  ||| ||||  |||   |||||
                                  GGG TGAG  GAC    GGTTT
                                    T   GT   CCAA
GAM642  LRG      3'  TCTAGCCTGGGCGACAGAGCAA 54826     C
                GA                 TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
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                                AGA CGAGACAGCGGGTCCGATCT
                                  A
GAM642  LSR68    3'  TCCAGCCTGGGCGACAGAATGA 38559      C
                GA                  TCTCG TCTGTTGCCCAGGCTGGA
                                    ||||| ||||||||||||||||||
                                    AGAGT AGACAGCGGGTCCGACCT
                                      A
GAM642  LUC7A    5'  TTCGGCCTGAGAGCGGGCCGAG 33559      CT    GCC
                G                    TCTCG  CTGTT   CAGGCTGGA
                                    |||||  |||||   |||||||||
                                    GGAGC  GGCGA   GTCCGGCTT
                                      CG    GA_
GAM642  LUC7L    3'  TCTGGTGGGGATGGGGCTGGG  36367    C      G   AG  TG
                                    TCT GCTCTGTT CCC  GC  GA
                                    ||| ||||||| |||  ||  ||
                                    GGG CGGGGTAG GGG  TG  CT
                                      T       _  __  GT
GAM642  LW-1     5'  TCGGCTAGGACAGGGTGGA   60888    T      TGC  A   TG
                                    TC CGCTCTGT   CC GGC  GA
                                    || ||||||||   || |||  ||
                                    AG GTGGGACA   GG TCG  CT
                                     _      ___ A   GT
GAM642  LW-1     5'  TCTGGCTAGGACAGGGTGGA   60889    T      TGC  A   TG
                                    TC CGCTCTGT   CC GGC  GA
                                    || ||||||||   || |||  ||
                                    AG GTGGGACA   GG TCG  CT
                                     _      ___ A   GT
GAM642  MACF1    3'  TCCAGCCTGGGCAACAGACAGA 53435          ____
                GTGAGA                TCTCGCTCTGT    TGCCCAGGCTGGA
                                    ||||||||||    ||||||||||||
                                    AGAGTGAGACA    ACGGGTCCGACCT
                                          GACA
GAM642  MADHIP   3'  TGGGGTGGGGAATAGGGTGGGA 17819          G    GG
                                    TCTCGCTCTGTT CCCA  CTG
                                    |||||||||||| ||||  |||
                                    AGGGTGGGATAA GGGT  GGT
                                          G    GG
GAM642  MADHIP   3'  TGGGGTGGGGAATAGGGTGGGA 17820          G    GG
                                    TCTCGCTCTGTT CCCA  CTG
                                    |||||||||||| ||||  |||
                                    AGGGTGGGATAA GGGT  GGT
                                          G    GG
GAM642  MAPKAPK2 5'  TCGGGGGGCGGCGGGGAGGGG  17664     G        AGG
                                    TCTC CTCTGTTGCCC   CTGG
                                    |||| ||||||||||   ||||
                                    GGGG GGGGCGGCGGG   GGCT
                                      A         G__
GAM642  MAWBP    3'  GACCAGCCTGGGCAACACAGCG 42384       C           A
                AGA                   TCTCGCT TGTTGCCCAGGCTGG
                                    |||||||  |||||||||||||||
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                                AGAGCGA ACAACGGGTCCGACC
                                   C            AGA
GAM642  MAWBP    3'  TCCAGCCTGGGCAACAGAGTAA 42388     CG
           GA                    TCT  CTCTGTTGCCCAGGCTGGA
                                 |||  ||||||||||||||||||
                                 AGA  GAGACAACGGGTCCGACCT
                                   AT
GAM642  MBLL39   3'  TCCAGCTTGACAAGATTGAGA  59262      C   GT  CC
                                 TCTCG TCT  TG  CAGGCTGGA
                                 |||||| |||  ||  |||||||||
                                 AGAGT AGA  AC  GTTCGACCT
                                    T   __  A_
GAM642  MCAM     3'  TCCAGCCTGGGCAACACAGCGA 22466        C
           GA                    TCTCGCT TGTTGCCCAGGCTGGA
                                 |||||||| ||||||||||||||||
                                 AGAGCGA ACAACGGGTCCGACCT
                                    C
GAM642  MCM10    3'  TTCAGTTTATATATAGAGAGAG 38182      G     TGCCC
           A                     TCTC CTCTGT    AGGCTGGA
                                 |||| ||||||    ||||||||
                                 AGAG GAGATA    TTTGACTT
                                   A     TATA_
GAM642  MESDC2   3'  TCCAGCCTGGATGACGGGATGA 72924       CT    GC
           GA                    TCTCG  CTGTT  CCAGGCTGGA
                                 |||||  |||||  ||||||||||
                                 AGAGT  GGCAG  GGTCCGACCT
                                    AG    TA
GAM642  METL     3'  TCCAGCCTGGGCAAAATAGCGA 37841        CTG
           GA                    TCTCGCT   TTGCCCAGGCTGGA
                                 |||||||   ||||||||||||||
                                 AGAGCGA   AACGGGTCCGACCT
                                    TAA
GAM642  MGC10200 3'  ACTCCAGTCTGGGCAACAGAGC 59630
           GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGCGAGACAACGGGTCTGACCT
                                              CAC
GAM642  MGC10765 3'  TCCAGCCTAGGCGACAGAGCGA 44567             C
           GA                    TCTCGCTCTGTTGCC AGGCTGGA
                                 ||||||||||||||| ||||||||
                                 AGAGCGAGACAGCGG TCCGACCT
                                           A
GAM642  MGC10771 3'  TCCAGCCTGGCTGACAGTGAGA 44716        CT   GC
                                 TCTCGCT  GTT  CCAGGCTGGA
                                 |||||||  |||  ||||||||||
                                 AGAGTGA  CAG  GGTCCGACCT
                                    __   TC
GAM642  MGC10814 3'  TCCAGCCTGGGCAACAAGAGC  52025       _
                                 GCTCT GTTGCCCAGGCTGGA
                                 ||||| ||||||||||||||
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                                CGAGA CAACGGGTCCGACCT
                                  A
GAM642  MGC10814  5'  TCCAGCCTGGGCAACAGAGTGA 52027
                GG                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  GGAGTGAGACAACGGGTCCGACCT

GAM642  MGC11266  5'  TCTGGCCTGGGTGAGCTAGA  44491    C   TGTT      TG
                                  TCT GCTC   GCCCAGGC  GA
                                  ||| ||||   ||||||||  ||
                                  AGA CGAG   TGGGTCCG  CT
                                    T  _____      GT
GAM642  MGC11386  3'  ACTCCAGCCTGGGCAACAGAGC 53051
                GAGA                TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACAACGGGTCCGACCT
                                                CAC
GAM642  MGC12921  5'  TTGGAGCTGGGTGGCAGAGGAG 64518     G     TG    G_ TG A
                A                    TCTC CTCTGT  CCCAG  C  G
                                     |||| ||||||  |||||  |  |
                                     AGAG GAGACG  GGGTC  G  T
                                       _     GT    GA GT
GAM642  MGC12945  3'  TCCAGCCTAGGCATGGTGAGA  51269       CTGT   C
                                  TCTCGCT   TGCC AGGCTGGA
                                  |||||||   |||| ||||||||
                                  AGAGTGG   ACGG TCCGACCT
                                      T___   A
GAM642  MGC13007  5'  TCAGAGCAGTAGTGTGAGG   51282      T     CCAGG
                                  TCTCGC CTGTTGC    CTGG
                                  ||||||| |||||||    ||||
                                  GGAGTG GATGACG    GACT
                                     T     A____
GAM642  MGC13008  3'  TCCAGCCTGGGCAACAGAATGA 52059      C
                GA                  TCTCG TCTGTTGCCCAGGCTGGA
                                    ||||| ||||||||||||||||||
                                    AGAGT AGACAACGGGTCCGACCT
                                      A
GAM642  MGC13053  3'  ACTCCAGCCTGGGCGACAGAGT 52091
                GAGA                TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAGCGGGTCCGACCT
                                                CAC
GAM642  MGC13053  3'  TCCAGCCTGGGCGACAGCAAGA 52115    GCT
                                  TC   CTGTTGCCCAGGCTGGA
                                  ||   ||||||||||||||||
                                  AG   GACAGCGGGTCCGACCT
                                   AAC
GAM642  MGC13090  3'  TCTGGCCTTGGAGCAGGTCGGG 52125      CT    G  C    TG
                A                    TCTCG  CTGTT CC AGGC  GA
                                     |||||  ||||| || ||||  ||
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                                AGGGC  GACGA GG TCCG  CT
                                  TG    _ T   GT
GAM642  MGC13090 3' TTTGGATGCGGGGTGAGG    52126          TGC
                                TCTCGCTCTGT   CCAGG
                                ||||||||||   |||||
                                GGAGTGGGGCG   GGTTT
                                     TA_
GAM642  MGC13170 3' TCTGCCCAGGCAGCAGGGTGGG 52133            CA   T
                                CTCGCTCTGTTGCC  GGC GGA
                                ||||||||||||||  ||| |||
                                GGGTGGGACGACGG  CCG TCT
                                      AC  _
GAM642  MGC14126 3' TCCAGCCTGGGCGATGAGC    52942      T
                                GCTC GTTGCCCAGGCTGGA
                                |||| ||||||||||||||
                                CGAG TAGCGGGTCCGACCT

                                  _
GAM642  MGC14407 3' TCCAGCCTGGGTGACAGAGCAA 52977     C      TG
           GA                     TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM642  MGC14436 3' TCCAGCCTGGGTGACAGAACGA 52931       C     TG
           GA                     TCTCG TCTGT  CCCAGGCTGGA
                                ||||| |||||  ||||||||||
                                AGAGC AGACA  GGGTCCGACCT
                                   A    GT
GAM642  MGC14799 3' TCCAGCCTGGGTGACAGTGAGA 51332        CT  TG
                                TCTCGCT  GT  CCCAGGCTGGA
                                |||||||  ||  ||||||||||
                                AGAGTGA  CA  GGGTCCGACCT
                                    __  GT
GAM642  MGC15397 3' ACTCCAGCCTGGGTGATAGAGT 55548           TG
           GAGA                    TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGAGATA  GGGTCCGACCT
                                      GT         CAC
GAM642  MGC15631 3' TCCAGCCTGTGCAACAGAGCCA 52235     C        C
           GA                     TCT GCTCTGTTGC CAGGCTGGA
                                ||| |||||||||| |||||||||
                                AGA CGAGACAACG GTCCGACCT
                                  C         T
GAM642  MGC16037 3' TCCAGCCTGGACAACAGAGTGG 52894            C
           GA                     TCTCGCTCTGTTG CCAGGCTGGA
                                ||||||||||||| ||||||||||
                                AGGGTGAGACAAC GGTCCGACCT
                                      A
GAM642  MGC16142 3' TCCAGTCTGGGCAACAGACGGA 52267      GC
           GA                     TCTC  TCTGTTGCCCAGGCTGGA
                                ||||  ||||||||||||||||||
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                                AGAG  AGACAACGGGTCTGACCT
                                  GC
GAM642  MGC16175  3'  TCCAGCCTGGGCAATAGAGCAA 52279     C
            GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGATAACGGGTCCGACCT
                                    A
GAM642  MGC16332  3'  AGACCAGCCTGGGCAACATAGT 57541         C            A
            GAGA                    TCTCGCT TGTTGCCCAGGCTGG
                                  |||||||| ||||||||||||||
                                  AGAGTGA ACAACGGGTCCGACC
                                      T             AGAA
GAM642  MGC16384  3'  GTAGCCTGGGTGACAAAGTGAG 54937         C   TG        GA
            A                     TCTCGCT TGT  CCCAGGCTG
                                  |||||||| |||  |||||||||
                                  AGAGTGA ACA  GGGTCCGAT
                                      A   GT        GT
GAM642  MGC16703  3'  ACTCCAGCCTGGGCAACAGAGC 73484
            GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||||
                                  AGAGCGAGACAACGGGTCCGACCT
                                                CAC
GAM642  MGC17998  3'  TCCAGCCTGGTGACAGCGTGAG 59388        T    TG  C
            A                     TCTCGC CTGT  CC AGGCTGGA
                                  |||||| ||||  || ||||||||
                                  AGAGTG GACA  GG TCCGACCT
                                     C    GT  _
GAM642  MGC1842   3'  CCAAAGCAACGGGCTGGGG    66251      _  T      CCAGGC
                                  TCTC GC CTGTTGC      TGG
                                  |||| || |||||||      |||
                                  GGGG CG GGCAACG      ACC
                                    T  _       AA_____
GAM642  MGC1842   5'  TTGGGCGAGAGGGTGGGG    66266          G
                                  TCTCGCTCT TTGCCCAG
                                  |||||||| ||||||||
                                  GGGGTGGGA AGCGGGTT
                                        G
GAM642  MGC20235  3'  TCCAGCCTGGGCAAAAGAGC   59562       G
                                  GCTCT TTGCCCAGGCTGGA
                                  ||||| ||||||||||||||
                                  CGAGA AACGGGTCCGACCT
                                     A
GAM642  MGC23244  3'  CTCCAGCCTGGGCGACAGAGTG 58830
            AGA                     TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||||
                                  AGAGTGAGACAGCGGGTCCGACCT
                                                CA
GAM642  MGC2396   3'  TCCAGCCTGGGCAATAAGAGTG 54562         _
            A                     TCGCTCT GTTGCCCAGGCTGGA
                                  ||||||| |||||||||||||||
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                                AGTGAGA TAACGGGTCCGACCT
                                    A
GAM642  MGC2452   5'  TCCAGTTACAGCGGCAGGAGCG 51968        _     CCA
            GGA                    TCTCGCTC TGTTGC   GGCTGGA
                                   |||||||| ||||||   |||||||
                                   AGGGCGAG ACGGCG   TTGACCT
                                      G      ACA
GAM642  MGC24976  5'  TCCGGGTCGCGGCGAGTGGGA  58736         T    CCA   _
                                   TCTCGCTC GTTGC   GGCT GGA
                                   |||||||| |||||   |||| |||
                                   AGGGTGAG CGGCG   CTGG CCT
                                      _    ____   G
GAM642  MGC2562   3'  TCCAGCCTGACGACAAAGCGAG 51449        C    CC
            A                       TCTCGCT TGTTG  CAGGCTGGA
                                   |||||||| |||||  |||||||||
                                   AGAGCGA ACAGC  GTCCGACCT
                                      A    A_
GAM642  MGC2562   3'  TCCAGCCTGGGCGACAGAGC   51451
                                   GCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||
                                   CGAGACAGCGGGTCCGACCT

GAM642  MGC2663   3'  ACTCCAGCCTGGGCGATGGAGT 44327
            GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGTGAGGTAGCGGGTCCGACCT
                                                CAC
GAM642  MGC26641  3'  TCCAGCCTGGGCAATAGGGCAA 59326     C
            GA                      TCT GCTCTGTTGCCCAGGCTGGA
                                   ||| ||||||||||||||||||||
                                   AGA CGGGATAACGGGTCCGACCT
                                     A
GAM642  MGC2668   3'  TCCAGCAGCTGTGGTGGGGGAG 61196      G TG  _   __
                                   CTCT T  CC CAG  GCTGGA
                                   |||| |  || |||  ||||||
                                   GAGG G  GG GTC  CGACCT
                                     G GT  T   GA
GAM642  MGC26877  5'  AACCCAGCCTGGGTGACAGAGC 58888          TG        A
            GAGA                    TCTCGCTCTGT  CCCAGGCTGG
                                   ||||||||||  ||||||||||
                                   AGAGCGAGACA  GGGTCCGACC
                                         GT         CAAC
GAM642  MGC2731   3'  TCCAGCCTGGGCAATAAGAGCG 44164        _
            A                       TCGCTCT GTTGCCCAGGCTGGA
                                   ||||||| ||||||||||||||||
                                   AGCGAGA TAACGGGTCCGACCT
                                      A
GAM642  MGC29643  3'  TTTATTCTGGGTAGGGAGCGGG 58695         G       GC
            A                       TCTCGCTCT TTGCCCAG  TGGA
                                   |||||||| ||||||||  ||||
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                                AGGGCGAGG GATGGGTC  ATTT
                                      _       TT
GAM642  MGC29762  3'  TCCAGCCTGGGCAACAAGAGC  59148       _
                                GCTCT GTTGCCCAGGCTGGA
                                ||||| ||||||||||||||
                                CGAGA CAACGGGTCCGACCT
                                   A
GAM642  MGC29891  3'  TCCAGCCTGGCGACACAGTGAG 58870        C      C
           A                     TCTCGCT TGTTGCC AGGCTGGA
                                ||||||| ||||||| ||||||||
                                AGAGTGA ACAGCGG TCCGACCT
                                   C      _
GAM642  MGC29891  3'  TCCAGCCTGGGCAACAGAGCCA 58871     C
           GA                     TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGAGACAACGGGTCCGACCT
                                  C
GAM642  MGC29937  3'  TCCAGCCTGGGCAACAAGAGTG 58734        _
           A                     TCGCTCT GTTGCCCAGGCTGGA
                                ||||||| ||||||||||||||||
                                AGTGAGA CAACGGGTCCGACCT
                                   A
GAM642  MGC3040   3'  TTTGAGGTAGTAGAGCGA    67386          _
                                TCGCTCTGTTGCC CAGG
                                |||||||||||| ||||
                                AGCGAGATGATGG GTTT
                                      A
GAM642  MGC3047   3'  TTTGGCCTGGGCGTATGCAGAG 51349       ___       TG
                                CTCTGT   TGCCCAGGC  GA
                                ||||||   |||||||||  ||
                                GAGACG   GCGGGTCCG  TT
                                   TAT       GT
GAM642  MGC3101   5'  ACTCCAGCCTGGGTGACAGAGC 44099          TG
           GAGA                    TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      GT         CAC
GAM642  MGC3101   3'  CCAGGAGCAGCAGAGGAGG    44102      G       _  AGGC
                                TCTC CTCTGTTGC CC    TGG
                                |||| ||||||||| ||    |||
                                GGAG GAGACGACG GG    ACC
                                  _       A _____
GAM642  MGC3207   3'  ACTCCAGCCTGGGCAACAGAGC 63229
           GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGCGAGACAACGGGTCCGACCT
                                         CAC
GAM642  MGC3329   3'  ACAGCCTGGGCGACAAAGTGGG 44237        C          GA
           A                     TCTCGCT TGTTGCCCAGGCTG
                                ||||||| |||||||||||||
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                                AGGGTGA ACAGCGGGTCCGAC
                                    A           AT
GAM642  MGC35558  3'  TCTAGTCTGAAAGGAGCGCAGG 59420    _    GTTGCC
                                TCT CGCTCT     CAGGCTGGA
                                ||| ||||||     |||||||||
                                GGA GCGAGG     GTCTGATCT
                                  C     AAA___
GAM642  MGC4248   3'  TCCAGCCTGGGTGACTGAG   51319    T  TG
                                CTC GT  CCCAGGCTGGA
                                ||| ||  ||||||||||
                                GAG CA  GGGTCCGACCT
                                  T  GT
GAM642  MGC4309   3'  TTCAGCTTGAATTGATGGGGAG 44369     G      CC_
          GGA                     TCTC CTCTGTTG   CAGGCTGGA
                                ||||| ||||||||   |||||||||
                                AGGG GGGGTAGT   GTTCGACTT
                                  A       TAA
GAM642  MGC4342   3'  TCCGGCCCCAGTGTGGTGGGCG 44518      T TG TG CCA__
          AGG                     TCTCGC C  T  C    GGCTGGA
                                |||||| |  | |    |||||||
                                GGAGCG G  G  G    CCGGCCT
                                   _ GT GT TGACC
GAM642  MGC4342   3'  TCTGGAGAGAGTGGGGCGGGA  44519       TG  GC__
                                TCTCGCTC  TT    CCAGG
                                ||||||||  ||    |||||
                                AGGGCGGG  GA    GGTCT
                                     GT  GAGA
GAM642  MGC4400   3'  CCTGGGCAACATAGCGAGA   52037       C
                                TCTCGCT TGTTGCCCAGG
                                ||||||| ||||||||||
                                AGAGCGA ACAACGGGTCC
                                    T
GAM642  MGC4562   3'  ATTCCAGCCTGGGCAACAGAGC 56733
          GAGA                      TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGCGAGACAACGGGTCCGACCT
                                                TAC
GAM642  MGC4663   3'  TCCAGCCTGGGCAACAGAGCCA 44791    C
          GA                      TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||
                                AGA CGAGACAACGGGTCCGACCT
                                  C
GAM642  MGC4730   3'  TTCAGTAAGTCCGTGATGGAGC 64916    C      TG CCAG__
          TAGA                      TCT GCTCTGT  C     GCTGGA
                                ||| |||||||  |     ||||||
                                AGA CGAGGTA  G     TGACTT
                                  T      GT CCTGAA
GAM642  MGC4766   5'  TTTGGGCCAGTAGAGACGGGG  49566      _      _
                                TCTCG CTCTGTTG CCCAGG
                                ||||| |||||||| ||||||
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                                GGGGC GAGATGAC GGGTTT
                                   A       C
GAM642  MGC4771  3'  ACTCCAGCCTGGGCAACAGAGT 51997
                GAGA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                      ||||||||||||||||||||||||
                                      AGAGTGAGACAACGGGTCCGACCT
                                            CAC
GAM642  MGC4840  3'  TCCAGCACCCTGGGCGACAGAG 72028                ___
                TGAGA                  TCTCGCTCTGTTGCCCAG   GCTGGA
                                      ||||||||||||||||||   ||||||
                                      AGAGTGAGACAGCGGGTC   CGACCT
                                            CCA
GAM642  MGC4840  3'  TCCAGCCTGGCTGACAGAGCGA 72029           GC
                GA                    TCTCGCTCTGTT  CCAGGCTGGA
                                      ||||||||||||  ||||||||||
                                      AGAGCGAGACAG  GGTCCGACCT
                                            TC
GAM642  MGC5384  3'  CTCCAGCCTGGGCGACAGAGTG 49089
                AGA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                      ||||||||||||||||||||||||
                                      AGAGTGAGACAGCGGGTCCGACCT
                                            CG
GAM642  MGC5457  3'  ACTCCAGCCTGGGTGACAGAGC 51932           TG
                GAGA                  TCTCGCTCTGT  CCCAGGCTGGA
                                      ||||||||||  ||||||||||
                                      AGAGCGAGACA  GGGTCCGACCT
                                            GT         CAC
GAM642  MGC5627  3'  CCAGATGGTGGAGCCAGG    44277    C    TTGC   GG
                                      TCT GCTCTG    CCA  CTGG
                                      ||| ||||||    |||  ||||
                                      GGA CGAGGT    GGT  GACC
                                        C     ____   A_
GAM642  MGC7036  3'  TTTGGCCTGGGCCAGTGAGA   59621        CTGTT       TG
                                      TCTCGCT    GCCCAGGC  GA
                                      |||||||    ||||||||  ||
                                      AGAGTGA    CGGGTCCG  TT
                                         C____       GT
GAM642  MKRN4    3'  CCCAGCCTGGGTGACAGAGCGA 48457          TG        A
                GA                    TCTCGCTCTGT  CCCAGGCTGG
                                      ||||||||||  ||||||||||
                                      AGAGCGAGACA  GGGTCCGACC
                                            GT         CT
GAM642  MLCB     5'  TTAGCGGCTCTCTGGGTAGCAG 88739             ___   GA
                GGTGG                   TCGCTCTGTTGCCCAG   GCTG
                                      ||||||||||||||||   ||||
                                      GGTGGGACGATGGGTC   CGGC
                                            TCT    GATTT
GAM642  MMD      3'  GGCACTTGGGAGTGGGGTGAGA 60512        TG  G     C  GA
                                      TCTCGCTC  TT CCCAGG TG
                                      ||||||||  || |||||| ||
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                                AGAGTGGG  GA GGGTTC AC
                                    GT  _     _  GGT
GAM642  MOST2    5'  TCCAGCCTGGGCACCACAGCAA 40072     C   C  T
            GA                    TCT GCT TG TGCCCAGGCTGGA
                                  ||| ||| || ||||||||||||
                                  AGA CGA AC ACGGGTCCGACCT
                                    A   C  C
GAM642  MRPL3    5'  TCCACGTGGCGGTGGCGTGGGG 24235       T TG     CAG  _
                                  TCTCGC C  TTGCC   GC TGGA
                                  |||||| |  |||||   || ||||
                                  GGGGTG G  GGCGG   TG ACCT
                                     C GT     ___  C
GAM642  MRPL48   5'  TCCAGCCTGCGCAACAGAGCGA 32662             C
            GA                    TCTCGCTCTGTTGC CAGGCTGGA
                                  |||||||||||||| |||||||||
                                  AGAGCGAGACAACG GTCCGACCT
                                            C
GAM642  MRPL56   3'  TTCAGGCTGGGCGAAAGAGTGA 52759          G       G
            GA                    TCTCGCTCT TTGCCCAG CTGGA
                                  ||||||||| ||||||||| |||||
                                  AGAGTGAGA AGCGGGTC GACTT
                                        A       G
GAM642  MRPS18B  3'  TCCAGCCTGGGTGACAGCTAGA 26755    GCT    TG
                                  TC   CTGT  CCCAGGCTGGA
                                  ||   ||||  ||||||||||
                                  AG   GACA  GGGTCCGACCT
                                    ATC    GT
GAM642  MSI2     5'  TTTGGGGGTGGGGGGGCGGGG  58048         G TG   AGG TG
                                  TCTCGCTCT T  CCC   C  GA
                                  ||||||||| |  |||   |  ||
                                  GGGGCGGGG G  GGG   G  TT
                                        G GT   ___ GT
GAM642  MT-ACT48 3'  TCCAGTCTGGGTGACAGCAAGA 25610    GCT    TG
                                  TC   CTGT  CCCAGGCTGGA
                                  ||   ||||  ||||||||||
                                  AG   GACA  GGGTCTGACCT
                                    AAC    GT
GAM642  MY014    5'  TCCGGCTGCCAGGCAGGGCGAG 48881           GCCCA
                                  CTCGCTCTGTT     GGCTGGA
                                  ||||||||||     |||||||
                                  GAGCGGGACGG     TCGGCCT
                                         ACCG_
GAM642  My015    3'  TCCAGCCTGGGAGACAGAGCAA 67235     C       TG
            GA                    TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A       GA
GAM642  N4BP2    3'  TCAGCCTGGGTGACAGAGCAAG 36943     C       TG         A
            A                     TCT GCTCTGT  CCCAGGCTGG
                                  ||| |||||||  |||||||||
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                                AGA CGAGACA  GGGTCCGACT
                                  A      GT
GAM642  NDUFC2   3'  TCCAGCCTGGGTGACAAAGGAG 17038     G  C   TG
                A                  TCTC CT TGT  CCCAGGCTGGA
                                   |||| || |||  ||||||||||
                                   AGAG GA ACA  GGGTCCGACCT
                                     _ A   GT
GAM642  NEIL2    3'  CCGGAAGGCAATGGGGCAAGG  59568     C         CAGG    A
                                   TCT GCTCTGTTGCC    CTGG
                                   ||| ||||||||||    ||||
                                   GGA CGGGGTAACGG    GGCC
                                     A         AA__    C
GAM642  NK4      5'  TCAGGCTGGTGGGGTGGGG    16159          TTGC    G
                                   TCTCGCTCTG    CCAG CTGG
                                   ||||||||||    |||| ||||
                                   GGGGTGGGGT    GGTC GACT
                                         _____    G
GAM642  NKX2C    3'  TCCGGGCCTGGTAGGGACGGGG 59910      _    TTGC     _
                                   TCTCG CTCTG    CCAGGCT GGA
                                   ||||| |||||    ||||||| |||
                                   GGGGC GGGAT    GGTCCGG CCT
                                     A     _____      G
GAM642  NMNAT    3'  ACTCCAGCCTGGGTGACAGAGC 43275           TG
                GAGA                  TCTCGCTCTGT  CCCAGGCTGGA
                                      ||||||||||  ||||||||||
                                      AGAGCGAGACA  GGGTCCGACCT
                                            GT          CAC
GAM642  NMT1     3'  TCCAGTCTGTGTGTAGGGAGAG 41152      G    GTT  C
                A                   TCTC CTCT   GC CAGGCTGGA
                                    |||| ||||   || |||||||||
                                    AGAG GGGA   TG GTCTGACCT
                                      A    TG_  T
GAM642  NMT2     3'  TCCAGCCTGGGTGACAGAGCGT 17859     T       TG
                GA                    TC CGCTCTGT  CCCAGGCTGGA
                                      || ||||||||  ||||||||||
                                      AG GCGAGACA  GGGTCCGACCT
                                       T       GT
GAM642  NPTXR    3'  TCCAGCCTGGGCAACAGAGCAA 27445     C
                GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                      ||| ||||||||||||||||||||
                                      AGA CGAGACAACGGGTCCGACCT
                                        A
GAM642  NR4A3    3'  TAGGCATTGGGGGGATGGGGTGG 23722           G    _  GGA
                GA                    TCTCGCTCTGTT CCCAG GCT
                                      |||||||||||| ||||| |||
                                      AGGGTGGGGTAG GGGTT CGG
                                            G    A  ATT
GAM642  NSE1     5'  TTCGGCTCGGGGTAGAGCGGA  59679    T      TTG   AG
                                   TC CGCTCTG   CCC  GCTGGA
                                   || |||||||   |||  ||||||
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                                AG GCGAGAT   GGG  CGGCTT
                                 _      G__   CT
GAM642  Nup43    3'  TCCAGCCTGGGCAAAAGAGC   45355       G
                                GCTCT TTGCCCAGGCTGGA
                                ||||| ||||||||||||||
                                CGAGA AACGGGTCCGACCT
                                   A
GAM642  NY-BR-1  3'  TCCAGCCTAGGTGACAGAGTGA 54853           TG  C
           GA                     TCTCGCTCTGT  CC AGGCTGGA
                                ||||||||||  || ||||||||
                                AGAGTGAGACA  GG TCCGACCT
                                      GT  A
GAM642  OBTP     3'  TCCAGCCTGCAAACTCAGAGGG 34669     G    TTGCC_
           GG                     CTC CTCTG     CAGGCTGGA
                                ||| |||||     |||||||||
                                GGG GAGAC     GTCCGACCT
                                  G     TCAAAC
GAM642  OR2C3    3'  TCTGTCGCAGTTGGGCGAGA   75977         TG    C_
                                TCTCGCTC  TTGC  CAGG
                                ||||||||  ||||  ||||
                                AGAGCGGG  GACG  GTCT
                                     TT    CT
GAM642  OR51E2   3'  TCCAGCCTGGGCAACGGAGCAA 48521     C
           GA                     TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGAGGCAACGGGTCCGACCT
                                  A
GAM642  ORC6L    3'  CTCCAGCCTGGGTGACAGAGCG 27490           TG
           AGA                     TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      GT         CA
GAM642  ORC6L    3'  TCCAGCCTGGGTGACAGAGCGA 27494           TG
           GA                     TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      GT
GAM642  OS4      3'  TCCAGTTTCACCGTGTGTTAGG 20395          TT  CC____
           GTGAGG                   TCTCGCTCTG  GC     AGGCTGGA
                                ||||||||||  ||     ||||||||
                                GGAGTGGGAT  TG     TTTGACCT
                                      TG  TGCCAC
GAM642  P11      3'  TTTGGTTTTTTCCAGAGTTAGA 21217     C     TTGCCC    TG
                                TCT GCTCTG     AGGC  GA
                                ||| ||||||     ||||  ||
                                AGA TGAGAC     TTTG  TT
                                  T     CTTT__    GT
GAM642  P114-RHO-GEF 3'  TCTAGCTTCAGCCAGGGCGGG  31677         TT  CC
                                CTCGCTCTG  GC  AGGCTGGA
                                |||||||||  ||  ||||||||
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                                GGGCGGGAC  CG  TTCGATCT
                                     __  AC
GAM642  p25     3'  CCGGTCTGTGGGGACGAG    23829     T   G  _
                                CTC GTT CC CAGGCTGG
                                ||| ||| || ||||||||
                                GAG CAG GG GTCTGGCC
                                  _   G  T
GAM642  PAFAH2   3'  ATCTGGGACCTTGATGGAGTGG 6494             ____     CTGGA
          GG                      TCTCGCTCTGTTG    CCCAGG
                                ||||||||||||    ||||||
                                GGGGTGAGGTAGT    GGGTCT
                                       TCCA        AG
GAM642  PAFAH2   3'  CTGCAGCCTGGACAGTAGAGCG 6500             C       GA
          AGA                      TCTCGCTCTGTTG CCAGGCTG
                                ||||||||||||| ||||||||
                                AGAGCGAGATGAC GGTCCGAC
                                       A       GTCG
GAM642  PAFAH2   3'  TCCAGCCTGGGTGACAGAGCAA 6508      C      TG
          GA                      TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM642  PALM    3'  CCGGGCAGTGGAGGGAGG    11963      G   TG     A
                                TCTC CTC  TTGCCC GG
                                |||| |||  |||||| ||
                                GGAG GAG  GACGGG CC
                                  G   GT     _
GAM642  PALM    3'  CTCAGGCAGTTGGGGTGAGG   11964         GT_    CA
                                TCTCGCTCT   TGCC  GG
                                |||||||||   ||||  ||
                                GGAGTGGGG   ACGG  TC
                                     TTG    AC
GAM642  PASK    5'  TTCGGCTTCTATCCAGAGTCAG 31425     C     TTGCCC
          A                      TCT GCTCTG     AGGCTGGA
                                ||| ||||||     ||||||||
                                AGA TGAGAC     TTCGGCTT
                                  C     CTATC_
GAM642  PB1     3'  TCCAGCCTGGGCAACAAGAGCG 36880        _
          A                      TCGCTCT GTTGCCCAGGCTGGA
                                ||||||| ||||||||||||||
                                AGCGAGA CAACGGGTCCGACCT
                                   A
GAM642  PB1     3'  TCCAGCCTGGGCAACAGAGTGA 36881
          G                      CTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||
                                GAGTGAGACAACGGGTCCGACCT

GAM642  PB1     3'  TTAGTTACTGGGGGTGGGG   37584        CTGTTG    __
                                TCTCGCT     CCCAG  GCTGG
                                |||||||     |||||  |||||
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                                GGGGTGG     GGGTC  TGATT
                                   ______    AT
GAM642  PDCD7    3'  TCCAGCCTGGGAGACAGAGCAA 72611     C      TG
             GA                    TCT GCTCTGT  CCCAGGCTGGA
                                   ||| |||||||  ||||||||||
                                   AGA CGAGACA  GGGTCCGACCT
                                     A      GA
GAM642  PDE1C    5'  TCCGGTTCTGTGGCGGGTGCGA 18465       T  GT   _   _
             GA                    TCTCGC CT  TGCC CAGG CTGGA
                                   |||||| ||  |||| |||| |||||
                                   AGAGCG GG  GCGG GTCT GGCCT
                                      T __    T   T
GAM642  PDE2A    5'  TCCAGGCAGCGGGGACAGGGCG 12006           G  CAG  _
             AGG                     TCTCGCTCTGTT CC   GC TGGA
                                   ||||||||||||| ||   || ||||
                                   GGAGCGGGACAG GG   CG ACCT
                                         G  CGA  G
GAM642  PDP      3'  GCAGCAGGGTGGCAGGGCAGA  38031     C      TG   AG    GA
                                   TCT GCTCTGT  CCC  GCTG
                                   ||| |||||||  |||  ||||
                                   AGA CGGGACG  GGG  CGAC
                                     _      GT   A_   GT
GAM642  PGGT1B   3'  TTAGATTGGGAGGGTGGGG   18477         GTTG    G
                                   TCTCGCTCT    CCCAG CTGG
                                   |||||||||    ||||| ||||
                                   GGGGTGGGA    GGGTT GATT
                                        _____    A
GAM642  PGS1     3'  TCCAGTCTGGGTGTCCCAGCGA 44594       CTGT
             G                      CTCGCT    TGCCCAGGCTGGA
                                   ||||||    ||||||||||||||
                                   GAGCGA    GTGGGTCTGACCT
                                      CCCT
GAM642  phorbolin-1 3'  TCCAGCCTGGGCGACAGTACCA 90213     CGCT
             GA                      TCT    CTGTTGCCCAGGCTGGA
                                   |||    ||||||||||||||||
                                   AGA    GACAGCGGGTCCGACCT
                                     CCAT
GAM642  PILR(ALPHA) 3'  TTTGGATAATGGGAGCGAGG   26483          _    C
                                   TCTCGCTCT GTTG CCAGG
                                   ||||||||| |||| |||||
                                   GGAGCGAGG TAAT GGTTT
                                        G    A
GAM642  PIP5K1C   3'  TCCATGGCAGGACAGAGCGGGA 71310           __    CAGGC
                                   TCTCGCTCTGT  TGCC     TGGA
                                   ||||||||||  ||||     ||||
                                   AGGGCGAGACA  ACGG     ACCT
                                         GG    T____
GAM642  PIP5K2B   5'  CCCCGGGGCGGGGCGGGA    57691         GTT    A  CT
                                   TCTCGCTCT   GCCC GG  GG
                                   |||||||||   |||| ||  ||
```

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                                AGGGCGGGG  CGGG CC  CC
                                     ___   G __
GAM642  PM5     5'  TCTGGCGGCGGCGGTGGGGCGG 27384        TG    CAG  TG
            GG                    TCTCGCTC  TTGCC   GC  GA
                                  ||||||||  |||||   ||  ||
                                  GGGGCGGG  GGCGG   CG  CT
                                      GT    CGG  GT
GAM642  POFUT1   3'  ATTCCAGCCTGGGCAACAGAGC 70971
            GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAACGGGTCCGACCT
                                              TAC
GAM642  POLR2J2  5'  TCTGGACGCAACGGCGGCGGGA 60008        _      __
                                  TCTCGCT CTGTTGC  CCAGG
                                  |||||||  |||||||  |||||
                                  AGGGCGG GGCAACG  GGTCT
                                      C      CA
GAM642  POLYDOM  3'  TCCAGCCTGGGCAATGGAGAGA 44692      G
            GG                    TCTC CTCTGTTGCCCAGGCTGGA
                                  ||||  ||||||||||||||||||
                                  GGAG GAGGTAACGGGTCCGACCT
                                    A
GAM642  PP1628   5'  TCTGGCCTGGCCTCTGGGCTGG 48081      _   TGTT   C    TG
            GG                    TCTC GCTC    GCC AGGC  GA
                                  ||||  ||||    |||  ||||  ||
                                  GGGG CGGG    CGG TCCG  CT
                                    T    TCTC   _    GT
GAM642  PP591    5'  TCCAGCCTGGGTGACAGAG    48150       TG
                                  CTCTGT  CCCAGGCTGGA
                                  ||||||  ||||||||||
                                  GAGACA  GGGTCCGACCT
                                     GT
GAM642  PPP1R10  3'  TCCAGTCTGGGGAGGAGAGAGA 12232      G    GTTG
                                  TCTC CTCT    CCCAGGCTGGA
                                  ||||  ||||    ||||||||||
                                  AGAG GAGG    GGGTCTGACCT
                                    A    AG__
GAM642  PPP1R12C  3'  TCCATGTGCAATAGGGAGGGA  34694      G       C  GGC
                                  TCTC CTCTGTTGC CA   TGGA
                                  ||||  |||||||| ||   ||||
                                  AGGG GGGATAACG GT   ACCT
                                    A        T ___
GAM642  PPP1R13B  3'  TTCAGTTCCCTGAATGGAGTCA 31662      C       GCC    ___
            GG                    TCT GCTCTGTT   CAGG   CTGGA
                                  |||  ||||||||   ||||   |||||
                                  GGA TGAGGTAA   GTCC   GACTT
                                    C        ___    CTT
GAM642  PPP1R14C  3'  GGATGGGTAATAGGTGAGA    48929       T        GG
                                  TCTCGC CTGTTGCCCA  CT
                                  ||||||  ||||||||||  ||
```

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                                AGAGTG GATAATGGGT  GG
                                  _        A_
GAM642  PPP1R3B  3'  TCCCGCCTGGGCAGCAGAGCGA 45145                T
           GA                     TCTCGCTCTGTTGCCCAGGC GGA
                                  |||||||||||||||||||| |||
                                  AGAGCGAGACGACGGGTCCG CCT
                                           C
GAM642  PPP1R3B  3'  TTCAGCCTGAGCGACAGAGTGA 45148            C
                                  TCGCTCTGTTGC CAGGCTGGA
                                  |||||||||||| |||||||||
                                  AGTGAGACAGCG GTCCGACTT
                                        A
GAM642  PRIC285  3'  ACTCCAGCCTGGGTGACAGAGC 62105            TG
           GAGA                     TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GT          CAC
GAM642  PRKWNK2  3'  CCAGCCTCCCAGGTGGGG    92193       T   TTGCCC
                                  TCTCGC CTG      AGGCTGG
                                  |||||| |||      |||||||
                                  GGGGTG GAC      TCCGACC
                                     _   CC_____
GAM642  PRO0038  3'  AGACCAGCCTGGGTAACAAAGT 26927         C            A
           GAGA                     TCTCGCT TGTTGCCCAGGCTGG
                                  ||||||| ||||||||||||||
                                  AGAGTGA ACAATGGGTCCGACC
                                       A              AGAA
GAM642  PRO0038  3'  TCCAGCCTGGGTGACAGACCGA 26931       C     TG
           GA                       TCTCG TCTGT  CCCAGGCTGGA
                                  ||||| |||||  ||||||||||
                                  AGAGC AGACA  GGGTCCGACCT
                                     C     GT
GAM642  PRO0478  5'  TCCAGCCTGGACAACAGAGTGA 27036            C
           GA                       TCTCGCTCTGTTG CCAGGCTGGA
                                  |||||||||||| |||||||||
                                  AGAGTGAGACAAC GGTCCGACCT
                                        A
GAM642  PRO0478  3'  TCCAGCCTGGGGGACAGAGCAA 27038     C       G
           GG                       TCT GCTCTGTT CCCAGGCTGGA
                                  ||| |||||||| ||||||||||
                                  GGA CGAGACAG GGGTCCGACCT
                                    A       G
GAM642  PRO0618  3'  TCTAGCCTGGTGGCAGAGTGAG 27055           TG  C
           A                        TCTCGCTCTGT  CC AGGCTGGA
                                  ||||||||||  || ||||||||
                                  AGAGTGAGACG  GG TCCGATCT
                                        GT  _
GAM642  PRO1048  5'  AAACCAGCCTGGGCAATAGAGT 38099                  A
           GAGA                     TCTCGCTCTGTTGCCCAGGCTGG
                                  ||||||||||||||||||||||||
```

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                                AGAGTGAGATAACGGGTCCGACC
                                       AAAC
GAM642  PRO1048  5'  TCCAGCCTGGGTGACAGAGCGA 38119          TG
            GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      GT
GAM642  PRO1048  3'  TCCAGGCCTGGGTGACAGTGCG 38120       T   TG    _
            AGA                   TCTCGC CTGT  CCCAGGC TGGA
                                ||||||  ||||  |||||||  ||||
                                AGAGCG GACA  GGGTCCG ACCT
                                   T   GT      G
GAM642  PRO1386  3'  CTCCAGCCTGGGCAACAGAGTG 49216
            AGA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGACAACGGGTCCGACCT
                                       CA
GAM642  PRO1496  3'  TCCAACCTGGGTGACAGACCGA 38368      C    TG    C
            GA                  TCTCG TCTGT  CCCAGG TGGA
                                |||||  |||||  ||||||  ||||
                                AGAGC AGACA  GGGTCC ACCT
                                   C    GT     A
GAM642  PRO2015  3'  TCCAGCCTGGGCCACACAGTGA 38166       C  T
            GA                  TCTCGCT TGT GCCCAGGCTGGA
                                |||||||  |||  ||||||||||||
                                AGAGTGA ACA CGGGTCCGACCT
                                    C  C
GAM642  PRO2133  3'  TCCAGTCTGGGCAACAGAGCGA 38400
                                TCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||
                                AGCGAGACAACGGGTCTGACCT

GAM642  PRO2389  3'  TCCAGCCCCATATAGGGTGA  64482         TGCCCA
                                TCGCTCTGT     GGCTGGA
                                |||||||||     |||||||
                                AGTGGGATA     CCGACCT
                                      TACC__
GAM642  PRO2730  3'  TCCGGCCTGGGCAACAACAGC  48188    C_
                                GCT  TGTTGCCCAGGCTGGA
                                |||  ||||||||||||||||
                                CGA  ACAACGGGTCCGGCCT
                                  CA
GAM642  PRO2859  3'  TCCAGCCTGGGGAGACAGAGCG 38214          G_
            AGA                   TCTCGCTCTGTT  CCCAGGCTGGA
                                ||||||||||||  ||||||||||
                                AGAGCGAGACAG  GGGTCCGACCT
                                       AG
GAM642  PRO2964  3'  TCCAGCCTGGGCAAAAAGAGC  38265      G_
                                GCTCT  TTGCCCAGGCTGGA
                                |||||  ||||||||||||||
```

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                                CGAGA  AACGGGTCCGACCT
                                   AA
GAM642  PROL2    3'  TCCAGCCTGGGTAACAGACGC  23323    _
                                GC TCTGTTGCCCAGGCTGGA
                                || ||||||||||||||||||
                                CG AGACAATGGGTCCGACCT
                                 C
GAM642  PRPF4    3'  TCTAGCCTGTGTGACAGAGCAA 17470     C      TG C
           GA                     TCT GCTCTGT  C CAGGCTGGA
                                ||| |||||||  | |||||||||
                                AGA CGAGACA  G GTCCGATCT
                                  A      GT T
GAM642  PRRG1    5'  TCCGCGAGTAGCGGAGCGGGA  8153             CCAG  T
                                TCTCGCTCTGTTGC    GC GGA
                                ||||||||||||||   || |||
                                AGGGCGAGGCGATG    CG CCT
                                         AG__  _
GAM642  PSR      3'  GACCAGTCTGGGCAACATAGTG 65785        C           A
           AGA                     TCTCGCT TGTTGCCCAGGCTGG
                                ||||||| ||||||||||||||||
                                AGAGTGA ACAACGGGTCTGACC
                                    T            AGA
GAM642  PSR      3'  TCCAGCCTGGGTGACAGACCGA 65794      C    TG
           GA                     TCTCG TCTGT  CCCAGGCTGGA
                                ||||| |||||  ||||||||||
                                AGAGC AGACA  GGGTCCGACCT
                                   C    GT
GAM642  PTK6     3'  ACTCCAGCCTGGGCGACAGAGC 21065
           GAGA                     TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGCGAGACAGCGGGTCCGACCT
                                         CAC
GAM642  PTPN9    5'  TCCGCCCGGCGGCGGTGGCGGG 12598        _      CA   T
           G                      TCTCGCT CTGTTGCC  GGC GGA
                                ||||||| ||||||||  ||| |||
                                GGGGCGG GGCGGCGG  CCG CCT
                                    T       C_  _
GAM642  PTPRU    3'  TGGTTGGGTGGGTGGGA     20325        TGTT     G TG
                                TCTCGCTC    GCCCAG C  G
                                ||||||||    |||||| |  |
                                AGGGTGGG    TGGGTT G  T
                                     _____     _ GT
GAM642  PTRF     3'  ACTCCAGCCTGGGTGACAGAGT 64229           TG
           GAGA                     TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      GT          CAC
GAM642  PTRF     3'  TCCATCCTAGGCAACAGAGTGA 64246             C   C
           GA                     TCTCGCTCTGTTGCC AGG TGGA
                                ||||||||||||||| ||| ||||
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                                AGAGTGAGACAACGG TCC ACCT
                                       A   T
GAM642  Rab11-FIP3 3'  TCTGTGCAGCGGTGTGGGG   28789       T     C
                                TCTCGC CTGTTGC CAGG
                                |||||| ||||||| ||||
                                GGGGTG GGCGACG GTCT
                                   T      T
GAM642  RAB35   3'  TGGAGCCACGGGATGGGGTGGG 23420          TG  A_   GGA
          G                      TCTCGCTCTGT  CCC  GGCT
                                ||||||||||  |||  ||||
                                GGGGTGGGGTA  GGG  CCGA
                                      __  CA   GGTT
GAM642  RAB4B   5'  TCCAGCCTGGGCAACGAAAAGT 32905      C__
          GA                     TCGCT   TGTTGCCCAGGCTGGA
                                |||||  ||||||||||||||||
                                AGTGA   GCAACGGGTCCGACCT
                                   AAA
GAM642  Rabip4R  3'  TCCAACCTGGGTGACAGAGCAA 36279    C     TG    C
          GA                     TCT GCTCTGT  CCCAGG TGGA
                                ||| |||||||  |||||| ||||
                                AGA CGAGACA  GGGTCC ACCT
                                  A      GT     A
GAM642  RAD51   3'  TCCAGCCAGGGTGACAGAGTGA 56833          TG  A
          GA                     TCTCGCTCTGT  CCC GGCTGGA
                                ||||||||||  ||| |||||||
                                AGAGTGAGACA  GGG CCGACCT
                                      GT   A
GAM642  RERG    3'  TCTAGTTTCTGTTTGAAGTGAG 53003       CT TT  CC
          G                      TCTCGCT  G  GC  AGGCTGGA
                                |||||||  |  ||  ||||||||
                                GGAGTGA  T  TG  TTTGATCT
                                    AG T_  TC
GAM642  RERG    3'  TCTGGCCTCTAATAGGTTGGGA 53004      CT    CCC   TG
                                TCTCG  CTGTTG   AGGC  GA
                                |||||  ||||||   ||||  ||
                                AGGGT  GATAAT   TCCG  CT
                                   TG     C__    GT
GAM642  RFX4    3'  GCCAGCCTGGGCAACATAGTGA 12855       C          A
          GA                     TCTCGCT TGTTGCCCAGGCTGG
                                |||||||  ||||||||||||||||
                                AGAGTGA ACAACGGGTCCGACC
                                    T           GT
GAM642  RFX4    3'  TCTAGCCTTAGTGATACAGTGA 12858       C   TG CC
          GA                     TCTCGCT TGT  C  AGGCTGGA
                                |||||||  |||  |  ||||||||
                                AGAGTGA ATA  G  TCCGATCT
                                    C   GT AT
GAM642  RHOBTB3  3'  TCCAGCCTGGGTGACAAGAGCG 30432       _  TG
          A                      TCGCTCT GT  CCCAGGCTGGA
                                |||||||  ||  ||||||||||
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                                AGCGAGA CA  GGGTCCGACCT
                                   A  GT
GAM642  RIN3     5'  TCCGGGGATGGCGGCAGAGGGG 46163      G        CAGG
           GA                    TCTC CTCTGTTGCC    CTGGA
                                 |||| ||||||||||    |||||
                                 AGGG GAGACGGCGG    GGCCT
                                   G         TAGG
GAM642  RNASE6PL 5'  CCTCGGGCAGCAGGTGGGA    14952       T       _
                                 TCTCGC CTGTTGCCC AGG
                                 |||||| ||||||||| |||
                                 AGGGTG GACGACGGG TCC
                                    _       C
GAM642  RNO2     5'  TCCAGCCTAGACAACAGGGCAA 53941     C        CCC
           GG                    TCT GCTCTGTTG   AGGCTGGA
                                 ||| |||||||||   ||||||||
                                 GGA CGGGACAAC   TCCGACCT
                                   A         AGA
GAM642  RNO2     5'  TCCAGCCTGGGCAACAAGAGCG 53942        _
           A                      TCGCTCT GTTGCCCAGGCTGGA
                                 ||||||| ||||||||||||||||
                                 AGCGAGA CAACGGGTCCGACCT
                                    A
GAM642  RoXaN    3'  TCCAGCCTGAGAGACAGAATGA 47303       C     GCC
           GA                    TCTCG TCTGTT   CAGGCTGGA
                                 ||||| ||||||   ||||||||
                                 AGAGT AGACAG   GTCCGACCT
                                    A      AGA
GAM642  RoXaN    3'  TCCAGCCTGGGCTACAGAGTGA 47304           T
           GA                    TCTCGCTCTGT GCCCAGGCTGGA
                                 |||||||||| ||||||||||||
                                 AGAGTGAGACA CGGGTCCGACCT
                                       T
GAM642  Rpo1-2   3'  TCCAGCCTGGGCGACAGAATGA 39225       C
           GA                    TCTCG TCTGTTGCCCAGGCTGGA
                                 ||||| ||||||||||||||||||
                                 AGAGT AGACAGCGGGTCCGACCT
                                    A
GAM642  Rpo1-2   3'  TCCAGCCTGGGTGACAGAGCAG 39226    TC      TG
           GA                    TC  GCTCTGT  CCCAGGCTGGA
                                 ||  |||||||  ||||||||||
                                 AG  CGAGACA  GGGTCCGACCT
                                   GA      GT
GAM642  RRP4     3'  TCCAGCCTGGGTGACAGAGCGA 27363           TG
           GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                 ||||||||||  ||||||||||
                                 AGAGCGAGACA  GGGTCCGACCT
                                       GT
GAM642  SAC2     3'  TCCAGCCTGGGGGACAGAGCAA 30728     C       G
           GA                    TCT GCTCTGTT CCCAGGCTGGA
                                 ||| |||||||| ||||||||||
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                                AGA CGAGACAG GGGTCCGACCT
                                  A       G
GAM642  SAD1     5'  TCCGGTCGCGTCAAGCGGGAGC 64724          _   GCCCA_
                GAGA                    TCTCGCTCT GTT      GGCTGGA
                                |||||||||  |||      |||||||
                                AGAGCGAGG CGA      CTGGCCT
                                    G   ACTGCG
GAM642  SAMHD1   3'  ACTCCAGCCTGGGTGACAGAGT 61972            TG
                GAGA                    TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      GT          CAC
GAM642  SC65     3'  ACTCCAGCCTGGGCGACAGAGT 22284
                GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGACAGCGGGTCCGACCT
                                            CAC
GAM642  SC65     3'  TCCAGCCTGGGCGACAGAGCGA 22302
                GA                      TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGCGAGACAGCGGGTCCGACCT

GAM642  SCAMP5   3'  TCTGGCCTGGGGTCGGGTGA   58063      T   TTG      TG
                                TCGC CTG   CCCAGGC  GA
                                ||||  |||   |||||||  ||
                                AGTG GGC   GGGTCCG  CT
                                  _   TG_      GT
GAM642  SCAMP5   3'  TTCAGGTTAGGCAGGGTGGGA  58067          GTT   C  G
                                TCTCGCTCT   GCC AG CTGGA
                                |||||||||   ||| || |||||
                                AGGGTGGGA   CGG TT GACTT
                                      ___   A  G
GAM642  SCAND2   3'  ACTCCAGCCTGGGCGACAGAGT 54413
                GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGACAGCGGGTCCGACCT
                                            CAC
GAM642  SCAND2   3'  TTCCAGCCTGGGCGACAGAGTG 54425
                AGA                     TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGACAGCGGGTCCGACCT
                                            TA
GAM642  SCAND2   3'  TTGAGCCTGGGCGACAGAGTGA 54426                 G
                GA                      TCTCGCTCTGTTGCCCAGGCT GA
                                ||||||||||||||||||||  ||
                                AGAGTGAGACAGCGGGTCCGA TT
                                            G
GAM642  SCDGF-B  3'  TTTAGTTTAAGGAGGGTGAGA  53636          G  GCCCA
                                TCTCGCTCT TT     GGCTGGA
                                |||||||||  ||     |||||||
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                                AGAGTGGGA GA     TTGATTT
                                     G  AT___
GAM642  SCIN     3'  TCCAGCCTGGGCAACAGAG    53605
                                CTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||
                                GAGACAACGGGTCCGACCT

GAM642  SCN12A   3'  TCCAGCCTGGTGACAGAGTGAG 27083           TG  C
           A                     TCTCGCTCTGT  CC AGGCTGGA
                                ||||||||||  || ||||||||
                                AGAGTGAGACA  GG TCCGACCT
                                      GT  _
GAM642  SCYA5    3'  ACTCCAGCCTGGGCGACAGAGC 12953
           GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGCGAGACAGCGGGTCCGACCT
                                              CAC
GAM642  SCYA5    3'  TCCAGCCTGGGTGACAAAGTGA 12972         C   TG
           GA                     TCTCGCT TGT  CCCAGGCTGGA
                                ||||||| |||  ||||||||||
                                AGAGTGA ACA  GGGTCCGACCT
                                   A   GT
GAM642  SCYD1    3'  TCTGGCAGCTCAGAGAGGGTGG 92561          G  GCCCAG  TG
           GA                     TCTCGCTCT TT      GC  GA
                                |||||||| ||      ||  ||
                                AGGGTGGGA AG      CG  CT
                                     G  ACTCGA  GT
GAM642  SELM     3'  TCCGGGGGCGCGGCGGAGCTGG 55400     C        _  AGG
           G                      TCT GCTCTGTTGC CC   CTGGA
                                ||| ||||||||| ||   |||||
                                GGG CGAGGCGGCG GG   GGCCT
                                  T         C  G__
GAM642  SEMA3E   3'  TCCGGCCTGGGCGACAGAGCGA 25812
           GA                     TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGCGAGACAGCGGGTCCGGCCT

GAM642  SEMA5A   3'  TCCAGGGTCTTGGCAGGGGGG  15598      G    C    __
                                CTCT TTGCC AGGCT  GGA
                                |||| ||||| |||||  |||
                                GGGG GACGG TCTGG  CCT
                                  G    T    GA
GAM642  SEMA5A   3'  TCCATCCTGGGTGACAGAGAGA 15599      G     TG     C
           GA                     TCTC CTCTGT  CCCAGG TGGA
                                |||| ||||||  |||||| ||||
                                AGAG GAGACA  GGGTCC ACCT
                                  A     GT     T
GAM642  SEPT6    5'  CAAGGGGTGGGCGGTAGAGGGG 31391      G    TT    GG  GGA
           A                      TCTC CTCTG  GCCCA  CT
                                |||| |||||  |||||  ||
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                                AGGG GAGAT  CGGGT  GG
                                  _    GG    GG  AACT
GAM642  SERF2    5'  TTCAGCCGCAGAGGGGCGGGA  20492         G   CCA
                                TCTCGCTCT TTGC   GGCTGGA
                                ||||||||| ||||   |||||||
                                AGGGCGGGG GACG   CCGACTT
                                    A   ___
GAM642  SFXN5    3'  TCTGGCCTGGGAAAAGGGCAGG 58659    TC    GTTG     TG
           A                     TC  GCTCT    CCCAGGC  GA
                                ||  |||||   |||||||  ||
                                AG  CGGGA    GGGTCCG  CT
                                 GA    AAA_     GT
GAM642  SGKL     3'  TTCAGCCTGGGTGCCACAGCGA 26065        C  TT
           GA                     TCTCGCT TG  GCCCAGGCTGGA
                                |||||||  ||  ||||||||||||
                                AGAGCGA AC  TGGGTCCGACTT
                                    C  CG
GAM642  ShrmL    3'  TTTAGTTTTTAACAGGCTGAGG 40856      _  T     CCC
                                TCTC GC CTGTTG   AGGCTGGA
                                |||| || ||||||   ||||||||
                                GGAG CG GACAAT   TTTGATTT
                                  T  _     T__
GAM642  SIAT4A   3'  GACCAGCCTGGGCAACATAGTG 13137        C           A
           AGA                     TCTCGCT TGTTGCCCAGGCTGG
                                |||||||  ||||||||||||||||
                                AGAGTGA ACAACGGGTCCGACC
                                    T            AGA
GAM642  SIAT8C   5'  TCTTGCAGGCGGCGGAGGAGA  32453      G        CAG  T
                                TCTC CTCTGTTGCC   GC GGA
                                ||||  ||||||||||   || |||
                                AGAG GAGGCGGCGG   CG TCT
                                  _        A__  T
GAM642  SLAC2-B  3'  TCTAGTCTGGGCAGTGTCTGC  31194    TC_ GT
                                GC   T  TGCCCAGGCTGGA
                                ||   |  ||||||||||||||
                                CG   G  ACGGGTCTGATCT
                                 TCT TG
GAM642  SLC2A4RG  3'  TTTACTTGGGGTGGGGGGGCGG 39634         G TG  _  C
           GG                     TCTCGCTCT T  CCC AGG TGGA
                                |||||||||  |  ||| ||| ||||
                                GGGGCGGGG G  GGG TTC ATTT
                                     G GT   G   _
GAM642  SLC37A1   5'  CCAGCCTGTGGGAGCGGC    39088     CT   G  _
                                GCT  GTT CC CAGGCTGG
                                |||  ||| || ||||||||
                                CGG  CGA GG GTCCGACC
                                  __   G  T
GAM642  SLC7A11   3'  TCCAGCCTGGGTGACAAAGTCA 27532     C   C   TG
           GA                     TCT GCT TGT  CCCAGGCTGGA
                                ||| ||| |||  ||||||||||
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                                AGA TGA ACA  GGGTCCGACCT
                                  C   A   GT
GAM642  SLK      3'  TTCAGTTTGATTTGAGTGGGA  28893         TGTTGCC
                                TCTCGCTC      CAGGCTGGA
                                ||||||||      |||||||||
                                AGGGTGAG      GTTTGACTT
                                    TTTA___
GAM642  SMA3     3'  TCCAGCCTGGGTGACAGAGC   23262         TG
                                GCTCTGT  CCCAGGCTGGA
                                |||||||  ||||||||||
                                CGAGACA  GGGTCCGACCT
                                    GT
GAM642  SMA3     3'  TCCAGGAGATACAACAGAGGAG 23263      G       CCCAGG
            A                    TCTC CTCTGTTG     CTGGA
                                ||||| ||||||||      |||||
                                AGAG GAGACAAC     GACCT
                                  _       ATAGAG
GAM642  SMAP-5   3'  ATCCAGCCTGGGTGACAGGGTG 48655           TG
            AGA                    TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGGGACA  GGGTCCGACCT
                                      GT          AC
GAM642  SMCR5    3'  CACAGTCTGGGCGACAGAGCAA 59246     C              GA
            GA                    TCT GCTCTGTTGCCCAGGCTG
                                ||| |||||||||||||||
                                AGA CGAGACAGCGGGTCTGAC
                                  A               ACG
GAM642  SMCR5    3'  CCGGTTTCAGGGGTGAGA    59248         GTTGCCC
                                TCTCGCTCT      AGGCTGG
                                |||||||||      |||||||
                                AGAGTGGGG      TTTGGCC
                                    AC_____
GAM642  SMCR7    3'  TTTAGTTTTCTTGCTGAGCGGG 58242         T  TGCCC
            A                    TCTCGCTC GT    AGGCTGGA
                                ||||||| ||    ||||||||
                                AGGGCGAG CG    TTTGATTT
                                    T  TTCT_
GAM642  SNAPC1   3'  ACTCCAGCCTGGGCAACAGAGT 13271
            GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGACAACGGGTCCGACCT
                                          CAC
GAM642  SNPH     3'  TTTGGTGGATGTGACAGGGCTG 28911     C      TG __  AG  TG
            GG                    TCT GCTCTGT  C  CC  GC  GA
                                ||| |||||||  |  ||  ||  ||
                                GGG CGGGACA  G  GG  TG  TT
                                  T      GT TA  __  GT
GAM642  SNRK     3'  TCTGAGGTGACGGACTGAGA   35284      C     TG  _
                                TCTCG TCTGT  CC CAGG
                                ||||| |||||  || ||||
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                                AGAGT AGGCA  GG GTCT
                                  C    GT  A
GAM642  SNX11    5'  TCTGGCTATATGGTGGGGCGCG 26176      T  G TG  CA__   TG
            GG                   CTCGC CT T  CC    GGC  GA
                                |||||  || |  ||    |||  ||
                                GGGCG GG G  GG    TCG  CT
                                  C  _ GT  TATA   GT
GAM642  SPRY4    3'  ACTCCAGCCTGGGTGACAGAGT 48990          TG
            GAGA                  TCTCGCTCTGT  CCCAGGCTGGA
                                |||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      GT         CAC
GAM642  SPRY4    3'  TCCAGCCTGGGTGACAGAGCAA 49032     C      TG
            GA                    TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM642  SPTLC2   3'  ACTCCAGCCTGGGTGACAGAGT 17975          TG
            GAGA                  TCTCGCTCTGT  CCCAGGCTGGA
                                |||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      GT         CAC
GAM642  SPTLC2   3'  TCCAGCCTTGGCGACAGAGGGA 18002      G        C
            GA                    TCTC CTCTGTTGCC AGGCTGGA
                                |||| ||||||||| ||||||||
                                AGAG GAGACAGCGG TCCGACCT
                                  G         T
GAM642  SPTLC2   3'  TCTAGCCTGGGTGACAGAGC   18003        TG
                                GCTCTGT  CCCAGGCTGGA
                                |||||||  ||||||||||
                                CGAGACA  GGGTCCGATCT
                                    GT
GAM642  SRPUL    3'  CTTGGGCAGTGGGTTGGGG   27845      CT TG
                                TCTCG  C  TTGCCCAGG
                                |||||  |  |||||||||
                                GGGGT  G  GACGGGTTC
                                   TG GT
GAM642  SSR3     3'  GCCTGGGTGGCAAGGGTGAGA  24036         _  TG
                                TCTCGCTCT GT  CCCAGGC
                                |||||||| ||  |||||||
                                AGAGTGGGA CG  GGGTCCG
                                     A  GT
GAM642  STI2     3'  TCCTTACTCCTGGGTGGGGAGT 90407         G TG     CT___
            GGGA                  TCTCGCTCT T  CCCAGG    GGA
                                |||||||| |  ||||||    |||
                                AGGGTGAGG G  GGGTCC    CCT
                                     _ GT     TCATT
GAM642  STK38L   5'  CCCGGGGGCGGGGCGAGG    69687          G   A
                                TCTCGCTCTGTT CCC GG
                                |||||||||||| ||| ||
```

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                                GGAGCGGGGCGG GGG CC
                                      _  C
GAM642  STMN4    3'  TCCACCCTGCAGCAGGTGGGA  48652      T     CC  C
                                TCTCGC CTGTTGC  AGG TGGA
                                |||||| |||||||  ||| ||||
                                AGGGTG GACGACG  TCC ACCT
                                   _     __  C
GAM642  SUN1     3'  TTTGGTTTAAAACAGGGTGA  47929         GCCC   TG
                                TCGCTCTGTT   AGGC  GA
                                ||||||||||   ||||  ||
                                AGTGGGACAA   TTTG  TT
                                      AA__   GT
GAM642  SUPT4H1  3'  TTTGGACTACAGGTGGGGTGGG 13489        GTT  CA_ _ TG
           A                    TCTCGCTCT  GCC  GG C  GA
                                |||||||||  |||  || |  ||
                                AGGGTGGGG  TGG  TC G  TT
                                     ___  ACA  A GT
GAM642  SYAP1    3'  ACTCCAGCCTGGGTGATAGAGT 52464          TG
           GAGA                   TCTCGCTCTGT  CCCAGGCTGGA
                                |||||||||||  ||||||||||||
                                AGAGTGAGATA  GGGTCCGACCT
                                      GT         CAC
GAM642  SYNE-2   3'  TTGGCCACGGCGGGGGTGGGG  31477        GT   CA   TG
                                TCTCGCTCT  TGCC  GGC  GA
                                |||||||||  ||||  |||  ||
                                GGGGTGGGG  GCGG  CCG  TT
                                     __   CA   GT
GAM642  SYT13    3'  TTGGGGGGGGGCGGGGCGGGG   95111          G   AGG TG
                                TCTCGCTCTGTT CCC   C  GA
                                |||||||||||| |||   |  ||
                                GGGGCGGGGCGG GGG   G  TT
                                      G   ___ GT
GAM642  SZF1     5'  TCTGGTTCCAGTGGCAGATGGG 32733      C    TG CCA   TG
           G                    TCTCG TCTGT  C   GGC  GA
                                ||||| |||||  |   |||  ||
                                GGGGT AGACG  G   TTG  CT
                                   _    GT ACC   GT
GAM642  TA-LRRP  3'  CACCAGCCTGGGTGACAGAGCA 31709     C      TG        A
           AGA                    TCT GCTCTGT  CCCAGGCTGG
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACC
                                  A      GT         ACA
GAM642  TA-PP2C  3'  TTTGGTAGACGCGGTGGGGGCG 58408       _ TG    CCAG  TG
           GGG                    TCTCGCT C  TTGC    GC  GA
                                |||||||  |  ||||    ||  ||
                                GGGGCGG G  GGCG    TG  TT
                                    G GT    CAGA  GT
GAM642  TADA3L   3'  TCCAGCCTGGGCAACAAGAGTG 22047        _
           A                    TCGCTCT GTTGCCCAGGCTGGA
                                |||||||  |||||||||||||||
```

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                                AGTGAGA CAACGGGTCCGACCT
                                    A
GAM642  TAF5L   5' CCGGAGGCGGCGGCGGCGGGG 27721      _      CAGG   A
                                TCTCGCT CTGTTGCC   CTGG
                                ||||||| ||||||||   ||||
                                GGGGCGG GGCGGCGG   GGCC
                                    C      A___   C
GAM642  TBL1Y   5' TCAGCCTGGAAGGCGAGG   53864      T  GTTGC
                                TCTCGC CT    CCAGGCTGG
                                |||||| ||    ||||||||||
                                GGAGCG GA    GGTCCGACT
                                   _ A_____
GAM642  TBX19   3' TCCAGCCTGGGTGGTAGA    18923     TT
                                TCTG  GCCCAGGCTGGA
                                ||||  ||||||||||||
                                AGAT  TGGGTCCGACCT
                                  GG
GAM642  TGIF2   3' TCTGGCTTTTAGTAGAGACGGG 41760      _      CCC   TG
            G                    TCTCG CTCTGTTG   AGGC  GA
                                ||||| ||||||||   ||||  ||
                                GGGGC GAGATGAT   TTCG  CT
                                  A      T__   GT
GAM642  THEA    3' TCCAGCCCAGGCAATAGAGTAA 66896    CG       CA
            GA                   TCT  CTCTGTTGCC  GGCTGGA
                                ||| ||||||||||  |||||||
                                AGA  GAGATAACGG  CCGACCT
                                  AT         AC
GAM642  THEA    3' TCCAGCCGGGGTAAGAGAGCGA 66897         G     A
            GA                   TCTCGCTCT TTGCCC GGCTGGA
                                ||||||||| |||||| |||||||
                                AGAGCGAGA AATGGG CCGACCT
                                     G     G
GAM642  THEA    3' TCCAGCCTGGGTGACAGAGTGA 66898         TG
                                TCGCTCTGT  CCCAGGCTGGA
                                |||||||||  ||||||||||
                                AGTGAGACA  GGGTCCGACCT
                                     GT
GAM642  TIP47   3' TCCAGCCTGGGGGACAAGAGTG 20608         _  G
            AGA                   TCTCGCTCT GTT CCCAGGCTGGA
                                ||||||||| ||| ||||||||||
                                AGAGTGAGA CAG GGGTCCGACCT
                                     A  G
GAM642  TMG4    5' TCCAGACCCTGCGGAGAGCGAG 44216         G   CCA _
            G                    TCTCGCTCT TTGC   GG CTGGA
                                ||||||||| ||||  || |||||
                                GGAGCGAGA GGCG   CC GACCT
                                     _   TC_  A
GAM642  TMG4    3' TCCAGCCTGGGCGACAGAGCAA 44217     C
            GA                   TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||
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                                AGA CGAGACAGCGGGTCCGACCT
                                  A
GAM642  TNRC4    3'  TTTGGCCTTTGTGAGGGAGCGA 24194          G TG CC    TG
           GG                    TCTCGCTCT T  C  AGGC  GA
                                 ||||||||| |  |  ||||  ||
                                 GGAGCGAGG A  G  TCCG  TT
                                     G GT TT    GT
GAM642  TOM1     3'  TCTGCGCGCAGTGGGCGAGA   19699        __    T  C
                                 TCTCGCT  CTGT GC CAGG
                                 |||||||  |||| || ||||
                                 AGAGCGG  GACG CG GTCT
                                     GT    _  C
GAM642  TOMM40   5'  GGTTGCGCGTGGCGCACGGGGT 21485           T  _   G  TGGA
           GGGA                  TCTCGCTCTGT GC CCA GC
                                 ||||||||||| || ||| ||
                                 AGGGTGGGGCA CG GGT CG
                                       _  C   G  CGTTGGC
GAM642  TOMM70A  3'  TCCAGCCTGGGCAATATAGCAA 29739     C   C
           GA                    TCT GCT TGTTGCCCAGGCTGGA
                                 ||| ||| ||||||||||||||||
                                 AGA CGA ATAACGGGTCCGACCT
                                   A   T
GAM642  TP53INP1  3'  ACTGAATCTGGTGATGGGGTGG 53866          TG  C   CTGGA
           GG                    TCTCGCTCTGT  CC AGG
                                 ||||||||||  || |||
                                 GGGGTGGGGTA  GG TCT
                                       GT  _   AAGTCAT
GAM642  TP53INP1  3'  TCTGGTGATGGGGTGGGG    53872          TG  C
                                 TCTCGCTCTGT  CC AGG
                                 ||||||||||  || |||
                                 GGGGTGGGGTA  GG TCT
                                       GT  _
GAM642  TSGA2    3'  TCCAGCCTGGGTGGCAGAGCGA 55955          TG
           GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                 ||||||||||  ||||||||||
                                 AGAGCGAGACG  GGGTCCGACCT
                                       GT         C
GAM642  TU3A     5'  ATCTGGGACTTCCCGGTGGAGT 24178        TG  ______     CTGGA
           GAGG                  TCTCGCTC  TTG     CCCAGG
                                 ||||||||  |||     ||||||
                                 GGAGTGAG  GGC     GGGTCT
                                     GT   CCTTCA        AG
GAM642  UBCE7IP5  3'  TCCAGCCTGGGAGCCCCTGGAG 30854        ____  G
           TGG                    TCGCTCT    GTT CCCAGGCTGGA
                                 |||||||    ||| ||||||||||
                                 GGTGAGG    CGA GGGTCCGACCT
                                     TCCC  _
GAM642  UBCE7IP5  3'  TCCAGCCTGGGCGACGGAGTGA 30855
           GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                 ||||||||||||||||||||||||
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                                AGAGTGAGGCAGCGGGTCCGACCT
                                                C
GAM642  UBE2E1   5' GCGGGGTGGGGTGGGG     13949        GTT   AG
                                TCTCGCTCT  GCCC  GC
                                |||||||||  ||||  ||
                                GGGGTGGGG  TGGG  CG
                                     ___   G_
GAM642  USP19    3' CGGTGGGAGAGGGTGGGG    90402        GTTG  AG  TG
                                TCTCGCTCT   CCC  GC  G
                                |||||||||   |||  ||  |
                                GGGGTGGGA   GGG  TG  C
                                     GA__  __  GT
GAM642  UST      3' ACTCCAGCCTGGGTGACAGAGT 20347          TG
           GAGA                  TCTCGCTCTGT  CCCAGGCTGGA
                                 ||||||||||  ||||||||||
                                 AGAGTGAGACA  GGGTCCGACCT
                                       GT         CAC
GAM642  VIT1     5' ACTCCAGCCTGGGTGGCAGAGT 38597          TG
           GAGA                  TCTCGCTCTGT  CCCAGGCTGGA
                                 ||||||||||  ||||||||||
                                 AGAGTGAGACG  GGGTCCGACCT
                                       GT         CAC
GAM642  VPS4B    3' TCCAGCCTGGGCGACTGA    18024    T
                                TC GTTGCCCAGGCTGGA
                                || ||||||||||||||
                                AG CAGCGGGTCCGACCT
                                 T
GAM642  WBSCR17  3' TCCAGCCATCAACACGGTGGGA 82219        C    CCCA
                                TCTCGCT TGTTG   GGCTGGA
                                ||||||| |||||   |||||||
                                AGGGTGG ACAAC   CCGACCT
                                    C    TA__
GAM642  WBSCR21  3' TCCAGCCTAGGCAACAGAGCAA 49306     C         C
           GA                     TCT GCTCTGTTGCC AGGCTGGA
                                  ||| |||||||||| ||||||||
                                  AGA CGAGACAACGG TCCGACCT
                                    A         A
GAM642  WBSCR22  3' TCTGCGGAGGTGGGGTGGGA   34471        TG TG  _
                                TCTCGCTC  T  CC CAGG
                                ||||||||  |  || ||||
                                AGGGTGGG  G  GG GTCT
                                     GT GA  C
GAM642  WBSCR23  5' CCTGGGCAATATAGTGAGA   47431        C
                                TCTCGCT TGTTGCCCAGG
                                ||||||| ||||||||||
                                AGAGTGA ATAACGGGTCC
                                    T
GAM642  WBSCR23  3' TCCAGCCTGGGCGACAAAGTGA 47443        C
           GA                     TCTCGCT TGTTGCCCAGGCTGGA
                                  ||||||| ||||||||||||||||
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                                AGAGTGA ACAGCGGGTCCGACCT
                                   A
GAM642  WBSCR23  3'  TCCAGCCTGGGCGACAGAGCAA 47444     C
           GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                 ||| ||||||||||||||||||||
                                 AGA CGAGACAGCGGGTCCGACCT
                                   A
GAM642  WBSCR23  5'  TCCAGCCTGGGCGACAGAGCCA 47445     C
           GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                 ||| ||||||||||||||||||||
                                 AGA CGAGACAGCGGGTCCGACCT
                                   C
GAM642  WBSCR23  3'  TCCAGCCTGGGTGATAGAGCAA 47446     C      TG
           GA                    TCT GCTCTGT  CCCAGGCTGGA
                                 ||| |||||||  ||||||||||
                                 AGA CGAGATA  GGGTCCGACCT
                                   A      GT
GAM642  WIRE     3'  TCCAGCCTGGGCGACAGAGCCA 78907     C
           GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                 ||| ||||||||||||||||||||
                                 AGA CGAGACAGCGGGTCCGACCT
                                   C
GAM642  WSB1     3'  TCCAACCTGGACAACAGAGCGA 56978            C    C
           GA                    TCTCGCTCTGTTG CCAGG TGGA
                                 |||||||||||| ||||| ||||
                                 AGAGCGAGACAAC GGTCC ACCT
                                       A    A
GAM642  WSB1     3'  TCCAACCTGGACAACAGAGCGA 56979            C    C
           GA                    TCTCGCTCTGTTG CCAGG TGGA
                                 |||||||||||| ||||| ||||
                                 AGAGCGAGACAAC GGTCC ACCT
                                       A    A
GAM642  YAP1     3'  TTTAGCTTAGGGGGAGGGTGGG 21468          GT G  _
           A                     TCTCGCTCT  T CCC AGGCTGGA
                                 |||||||||  | ||| ||||||||
                                 AGGGTGGGA  G GGG TTCGATTT
                                      __ G   A
GAM642  YKT6     3'  CTGGGCAGGAGGGTGGGG    22638          G
                                 TCTCGCTCT TTGCCCAG
                                 |||||||| ||||||||
                                 GGGGTGGGA GACGGGTC
                                    G
GAM642  YME1L1   3'  ACTCCAGCCTGGGTGACAGAGT 58418          TG
           GAGA                    TCTCGCTCTGT  CCCAGGCTGGA
                                 ||||||||||  ||||||||||
                                 AGAGTGAGACA  GGGTCCGACCT
                                       GT         CAC
GAM642  YME1L1   3'  TCCAGCCTGGGCAACAGAGCAA 58439     C
           GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                 ||| ||||||||||||||||||||
```

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                                AGA CGAGACAACGGGTCCGACCT
                                  A
GAM642  ZAK     3'  TCCAGCCTGGATGACAGAGTGA 34109          GC
           GA                    TCTCGCTCTGTT  CCAGGCTGGA
                                 ||||||||||||  ||||||||||
                                 AGAGTGAGACAG  GGTCCGACCT
                                       TA
GAM642  ZAK     3'  TCTGGTTAGCAGGGCCAGG   34110    C       C
                                 TCT GCTCTGTTG CCAGG
                                 ||| ||||||||| |||||
                                 GGA CGGGACGAT GGTCT
                                   C       T
GAM642  ZDHHC1  5'  CCAGCCTGCTGGAGCCGGA   78208    C     TTGCC
                                 TCT GCTCTG    CAGGCTGG
                                 ||| ||||||    ||||||||
                                 AGG CGAGGT    GTCCGACC
                                   C     C____
GAM642  ZDHHC3  3'  TTTAGCTTTTGCTTGGGGTGGG 33937          TT  CC
           G                     TCTCGCTCTG  GC  AGGCTGGA
                                 ||||||||||  ||  ||||||||
                                 GGGGTGGGGT  CG  TTCGATTT
                                       T_  TT
GAM642  ZFP106  3'  TCCAGCCTGGGCGACAAGAGTG 42741        _
           A                     TCGCTCT GTTGCCCAGGCTGGA
                                 |||||||  ||||||||||||||
                                 AGTGAGA CAGCGGGTCCGACCT
                                    A
GAM642  ZFP106  3'  TCCAGCCTGGTGACAGAGTGAG 42742          TG  C
           A                     TCTCGCTCTGT  CC AGGCTGGA
                                 ||||||||||  ||  ||||||||
                                 AGAGTGAGACA  GG TCCGACCT
                                       GT  _
GAM642  ZFP91   5'  TTCGGGAGGCGAGGGGGCGGGG 54881          G    CAGG
                                 TCTCGCTCT TTGCC   CTGGA
                                 |||||||| |||||   |||||
                                 GGGGCGGGG AGCGG   GGCTT
                                       G    AG__
GAM642  ZIC4    5'  TCTAGCTCAAGGCGCGGCGGGG 50545          _  A__
                                 CTCTGTTGC CC   GGCTGGA
                                 |||||||| ||   |||||||
                                 GGGGCGGCG GG   TCGATCT
                                       C  AAC
GAM642  ZNF197  3'  TCCAGCCTGGGCAACAAGAGCG 23760        _
           A                     TCGCTCT GTTGCCCAGGCTGGA
                                 |||||||  ||||||||||||||
                                 AGCGAGA CAACGGGTCCGACCT
                                    A
GAM642  ZNF271  3'  ATTCCAGCCTGGGCAACAGAGT 96956
           GAGA                      TCTCGCTCTGTTGCCCAGGCTGGA
                                     ||||||||||||||||||||||||
```

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                                AGAGTGAGACAACGGGTCCGACCT
                                                    TAC
GAM642  ZNF271   3'  TCCAGTCTGGGCAACAGAGCAA 96969     C
            GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAACGGGTCTGACCT
                                    A
GAM642  ZNF282   3'  ATCCAGTTCTCCCAGGGCAGAG 90692          G     A _____
            GGGCGAGG                  TCTCGCTCT TTGCCC GG    CTGGA   T
                                  ||||||||| |||||| ||     |||||   |
                                  GGAGCGGGG GACGGG CC    GACCT   A
                                        A     A  CTCTT
GAM642  ZNF297   5'  TCTGGCCGCCGAGTGAGGGGCG 19573          G TG CCA__   TG
            GGG                     TCTCGCTCT T  C     GGC  GA
                                  ||||||||| |  |     |||  ||
                                  GGGGCGGGG A  G     CCG  CT
                                        _ GT AGCCG   GT
GAM642  ZNF297B  3'  TCCAGCCTGCGCGACAGATCGA 26672       C       C
            GA                    TCTCG TCTGTTGC CAGGCTGGA
                                  ||||| |||||||| |||||||||
                                  AGAGC AGACAGCG GTCCGACCT
                                     T       C
GAM642  ZNF297B  5'  TCCAGCCTGGGCAACAAGAGC  26673       _
                                  GCTCT GTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||
                                  CGAGA CAACGGGTCCGACCT
                                     A
GAM642  ZNF297B  5'  TCCAGCCTGGGCAACAGAGCAA 26675     C
            GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAACGGGTCCGACCT
                                    A
GAM642  ZNF297B  5'  TCCAGCCTGGGTAAAAGAGTGA 26676          G
            GA                    TCTCGCTCT TTGCCCAGGCTGGA
                                  ||||||||| ||||||||||||||
                                  AGAGTGAGA AATGGGTCCGACCT
                                        A
GAM642  ZNF297B  3'  TGGAATGGGTAATGGGGTGAG  26678              GG
                                  CTCGCTCTGTTGCCCA  CTG
                                  |||||||||||||||  |||
                                  GAGTGGGGTAATGGGT  GGT
                                           AA
GAM642  ZNF333   3'  TCCAGCCTGGGCAACAGAGTGA 51595
                                  TCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||
                                  AGTGAGACAACGGGTCCGACCT

GAM642  ZNF339   3'  TCCAGCCTGGGCAACAGAGTGG 41399     T
            A                     TC CGCTCTGTTGCCCAGGCTGGA
                                  || ||||||||||||||||||||
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                                AG GTGAGACAACGGGTCCGACCT
                                  _
GAM642  ZNF33A    3'  CAGCCTGGGTGACAGAATGAGA 92993      C    TG       GA
                                TCTCG TCTGT  CCCAGGCTG
                                ||||| |||||  |||||||||
                                AGAGT AGACA  GGGTCCGAC
                                   A    GT       G
GAM642  LOC112687 3'  ACTCCAGCCTGGGCAACAGAGT 73218
           GGGA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGGGTGAGACAACGGGTCCGACCT
                                              CAC
GAM642  LOC112724 3'  TCTGCACGGCATGGAGTGGGA  57307          T  CAG  T
                                TCTCGCTCTGT GCC   GC GGA
                                |||||||||| |||   || |||
                                AGGGTGAGGTA CGG   CG TCT
                                      _  CA_ _
GAM642  LOC112817 5'  TCTGGCTTCAGAGCTGGGA   57333     _     TT  C
                                TCTC GCTCTG  GCC AGG
                                |||| ||||||  ||| |||
                                AGGG CGAGAC  CGG TCT
                                  T     TT  _
GAM642  LOC112868 3'  TCCAGCCTGACCCCAGAGCAGA 73271     C     TTGCC
                                TCT GCTCTG    CAGGCTGGA
                                ||| ||||||    |||||||||
                                AGA CGAGAC    GTCCGACCT
                                  _     CCCA_
GAM642  LOC112868 3'  TCCAGTTTACAAACAGTGTGGG 73272       T    GCCC
           G                    TCTCGC CTGTT    AGGCTGGA
                                ||||||| |||||    ||||||||
                                GGGGTG GACAA    TTTGACCT
                                   T    ACA_
GAM642  LOC113201 3'  TCCAGCTTGGGCACCAGAGCAA 57357     C     T
           GA                     TCT GCTCTG TGCCCAGGCTGGA
                                ||| |||||| ||||||||||||
                                AGA CGAGAC ACGGGTTCGACCT
                                  A     C
GAM642  LOC113523 3'  TCCAGCCTGGGCGACAGGGCAA 73434     C
           GA                     TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGGGACAGCGGGTCCGACCT
                                  A
GAM642  LOC114987 3'  AAGTGGCAGCAGAGTGGGA   59790            CAG   GGA
                                TCTCGCTCTGTTGCC   GCT
                                ||||||||||||||   |||
                                AGGGTGAGACGACGG   TGA
                                      ___   AA
GAM642  LOC114987 3'  TCCAGCCTGGGCAACAAGAGCG 59800        _
           A                     TCGCTCT GTTGCCCAGGCTGGA
                                ||||||| ||||||||||||||
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                                AGCGAGA CAACGGGTCCGACCT
                                    A
GAM642  LOC114987 3'  TTGGAATGGCCAGAGTGAGG   59802          TT   C GG TG
                                TCTCGCTCTG  GCC A  C  GA
                                ||||||||||  ||| |  |  ||
                                GGAGTGAGAC  CGG T  G  TT
                                      __   _ AA GT
GAM642  LOC115129 3'  TCCAGCCTGAGCGACAGAGTAA 73629     CG        C
           GA                    TCT  CTCTGTTGC CAGGCTGGA
                                |||  ||||||||| |||||||||
                                AGA  GAGACAGCG GTCCGACCT
                                  AT        A
GAM642  LOC115196 3'  TCCAGCCTGGGAGACAGAGCGA 73661           TG
           GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      GA
GAM642  LOC115207 3'  TCCAGTAGTAGCTGGGTGAGA  57399         T    CCAG
                                TCTCGCTC GTTGC    GCTGGA
                                |||||||| |||||    ||||||
                                AGAGTGGG CGATG    TGACCT
                                     T    A___
GAM642  LOC115273 3'  ACTCCAGCCTGGGCAACAGAGT 73744
           GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||
                                AGAGTGAGACAACGGGTCCGACCT
                                           CAC
GAM642  LOC115399 3'  TGGCCTGGGGAGGGAGG     73818      G   TGTTG      TG
                                TCTC CTC     CCCAGGC  G
                                |||| |||     |||||||  |
                                GGAG GAG     GGGTCCG  T
                                  G  ______      GT
GAM642  LOC115648 3'  TCTGGGTTTGTAGTGGAGTGGG 60032         TG ____      CTGGA
           G                     TCTCGCTC  TT    GCCCAGG
                                ||||||||  ||    |||||||
                                GGGGTGAG  GA    TGGGTCT
                                     GT  TGTT         A
GAM642  LOC115708 3'  CCTGGGTGGCCAGAGTGGGA   73914          _ TG
                                TCTCGCTCTG T  CCCAGG
                                ||||||||||  |  ||||||
                                AGGGTGAGAC G  GGGTCC
                                      C GT
GAM642  LOC115757 3'  CCCCATCCTGGGTGACAGAGTG 73953           TG     C   A
           AGA                    TCTCGCTCTGT  CCCAGG TGG
                                ||||||||||  ||||||  |||
                                AGAGTGAGACA  GGGTCC ACC
                                      GT     T   CCA
GAM642  LOC115761 3'  ACTCCAGTCTGGGCAACAGAGT 93393
           GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||
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                                AGAGTGAGACAACGGGTCTGACCT
                                      CAC
GAM642  LOC115861 3'  TCAACCTGGGCAAGAGAGTGAG 57418        G       C  A
          A                    TCTCGCTCT TTGCCCAGG TGG
                               ||||||||| ||||||||| |||
                               AGAGTGAGA AACGGGTCC ACT
                                    G       A
GAM642  LOC115950 5'  TCTGGCTCCTAACAACGGGGGA 57872     G      CCCA_  TG
          GG                   TCTC CTCTGTTG    GGC  GA
                               |||| ||||||||    |||  ||
                               GGAG GGGGCAAC    TCG  CT
                                 _      AATCC   GT
GAM642  LOC116143 3'  TCCAGCCCTGGCGACAGAGTGA 74193            CA
          GA                   TCTCGCTCTGTTGCC  GGCTGGA
                               |||||||||||||||  |||||||
                               AGAGTGAGACAGCGG  CCGACCT
                                      TC
GAM642  LOC116143 3'  TCCAGCCTGGGCAACTGAGCAA 74194     C   T
          GA                   TCT GCTC GTTGCCCAGGCTGGA
                               ||| |||| ||||||||||||||
                               AGA CGAG CAACGGGTCCGACCT
                                 A   T
GAM642  LOC116225 3'  TCCAGCAGAGACAACGGAGGAG 57428     G      CCCAG
          G                    TCTC CTCTGTTG    GCTGGA
                               |||| ||||||||    ||||||
                               GGAG GAGGCAAC    CGACCT
                                 _      AGAGA
GAM642  LOC116228 3'  TCTAGCCTAGGTGACAGAGTGA 74231          TG  C
          GA                   TCTCGCTCTGT  CC AGGCTGGA
                               |||||||||||  || ||||||||
                               AGAGTGAGACA  GG TCCGATCT
                                     GT  A
GAM642  LOC116236 3'  TCCAGCCTGGGCGACAGAGTAA 74248     CG
          GA                   TCT  CTCTGTTGCCCAGGCTGGA
                               |||  ||||||||||||||||||
                               AGA  GAGACAGCGGGTCCGACCT
                                 AT
GAM642  LOC116349 3'  CTCCAGCCTGGGCAACAGAGCG 74276
          AGG                   TCTCGCTCTGTTGCCCAGGCTGGA
                               |||||||||||||||||||||||||
                               GGAGCGAGACAACGGGTCCGACCT
                                      CA
GAM642  LOC116412 5'  TCCGCGCTGCATGCGGGGCGGG 74304          _  CCA  _
          G                    TCTCGCTCTGT TGC   GGC TGGA
                               |||||||||| |||   ||| ||||
                               GGGGCGGGGCG ACG   TCG GCCT
                                     T  ___  C
GAM642  LOC119504 5'  TCCAGCCTGGGCAACAAGAGGG 74449    G   _
          A                    TC CTCT GTTGCCCAGGCTGGA
                               || |||| ||||||||||||||
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                                AG GAGA CAACGGGTCCGACCT
                                 G   A
GAM642   LOC120406 3'  TCCAGCCTGGGTGACAGAGCGA 76066          TG
              GA                   TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   AGAGCGAGACA  GGGTCCGACCT
                                         GT
GAM642   LOC120526 5'  TCTGGCCGACAGCAGGCGAGG  74468       T     CCCA   TG
                                   TCTCGC CTGTTG    GGC  GA
                                   ||||||  ||||||    |||  ||
                                   GGAGCG GACGAC    CCG  CT
                                      _     AG__   GT
GAM642   LOC120856 3'  TTAGTTACAATGGAGTAGA    74475     C       CCCA
                                   TCT GCTCTGTTG    GGCTGG
                                   |||  |||||||||    ||||||
                                   AGA TGAGGTAAC    TTGATT
                                     _       A___
GAM642   LOC121536 5'  TGGGCAGCAGCGGCGGGA     74530        _
                                   TCTCGCT CTGTTGCCCA
                                   |||||||  ||||||||||
                                   AGGGCGG GACGACGGGT
                                       C
GAM642   LOC122553 3'  CCAGCTGAGCAGAGTTGGA    74592     C      TGCCCA
                                   TCT GCTCTGT      GGCTGG
                                   |||  |||||||      ||||||
                                   AGG TGAGACG      TCGACC
                                     T      AG____
GAM642   LOC122704 3'  TCCAACCTGGGCGACAGGGCGA 74611                C
              GA                   TCTCGCTCTGTTGCCCAGG TGGA
                                   ||||||||||||||||||  ||||
                                   AGAGCGGGACAGCGGGTCC ACCT
                                              A
GAM642   LOC123591 3'  TCAGCAGGGTAGAGTGTGG    76133    T     GTT    AG
                                   TC CGCTCT   GCCC  GCTGG
                                   ||  ||||||   ||||  |||||
                                   GG GTGAGA   TGGG  CGACT
                                    T     ____    A_
GAM642   LOC124045 3'  TTCAGTGGCCAGTGGAGCCAGG 76551     C    TG   C  AG
                                   TCT GCTC  TTG CC  GCTGGA
                                   |||  ||||  |||  ||  ||||||
                                   GGA CGAG  GAC GG  TGACTT
                                     C    GT   C  __
GAM642   LOC124602 3'  TCCAGCTGCACAGCGGGCAGGG 74792           _  CCA__
              TGAGA                    TCTCGCTCTGTT GC     GGCTGGA
                                   ||||||||||||  ||     |||||||
                                   AGAGTGGGACGG CG     TCGACCT
                                          G  ACACG
GAM642   LOC124801 3'  GAGCTTTGGGGGTGGGGTGGGG 74813         TG  G  C     GGA
                                   TCTCGCTC  TT CC AGGCT
                                   ||||||||  ||  ||  |||||
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                                GGGGTGGG  GG GG TTCGA
                                    GT  G  T    GA
GAM642   LOC124842 3'  TCCAGCTTGGGGTCAGGTGGG  76160      T   TTG
                                CTCGC CTG   CCCAGGCTGGA
                                ||||| |||   ||||||||||
                                GGGTG GAC   GGGTTCGACCT
                                  _   TG_
GAM642   LOC124976 3'  TCTGGTGCGGGGGGTGGGGTGGG 74844        TG  G   AG  TG
           G                     TCTCGCTC  TT CCC  GC  GA
                                ||||||||  || |||  ||  ||
                                GGGGTGGG  GG GGG  TG  CT
                                    GT  _   CG  GT
GAM642   LOC126031 5'  GCAGAATGTGGGGGGTGGGG   74902         GTTG  _  GG   GA
                                TCTCGCTCT    CC CA  CTG
                                |||||||||    || ||  |||
                                GGGGTGGGG    GG GT  GAC
                                     ____  T  AA   GT
GAM642   LOC126282 3'  GACCAGTCTGGGCAACATGGTG 74957        C            A
           AGA                    TCTCGCT TGTTGCCCAGGCTGG
                                ||||||| ||||||||||||||||
                                AGAGTGG ACAACGGGTCTGACC
                                    T            AGA
GAM642   LOC126282 3'  TCCAGCCTGGGTGACAGAGCAA 74967     C      TG
           GA                     TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM642   LOC126282 3'  TCCAGCTTGGGTGAGAGTGGGA 74968         TG TG
                                TCTCGCTC  T  CCCAGGCTGGA
                                ||||||||  |  ||||||||||
                                AGGGTGAG  A  GGGTTCGACCT
                                    __ GT
GAM642   LOC126282 3'  TTCAGCCTGGTGACAGAGCGAG 74973          TG  C
           A                     TCTCGCTCTGT  CC AGGCTGGA
                                ||||||||||  || ||||||||
                                AGAGCGAGACA  GG TCCGACTT
                                      GT  _
GAM642   LOC126353 3'  CCAGTCTGAGGGAGGAGG    74990      G   TGTTG  _
                                TCTC CTC     CC CAGGCTGG
                                |||| |||     || ||||||||
                                GGAG GAG     GG GTCTGACC
                                  _   _____  A
GAM642   LOC126669 3'  TCCAGCCTGAGTGACAGAGTGA 75951          TG C
           GA                     TCTCGCTCTGT  C CAGGCTGGA
                                ||||||||||  | |||||||||
                                AGAGTGAGACA  G GTCCGACCT
                                      GT A
GAM642   LOC126917 3'  TTCAGAAATGTGGTGGGTGGGG 75101         TGTT  _  GG_
                                TCTCGCTC    GCC CA   CTGGA
                                ||||||||    ||| ||   |||||
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                                GGGGTGGG   TGG GT   GACTT
                                    ____   T  AAA
GAM642   LOC127262 3'  TCCAGCCCGGGCGACAGAGCGA 76605              A
                GA                  TCTCGCTCTGTTGCCC GGCTGGA
                                    ||||||||||||||| |||||||
                                    AGAGCGAGACAGCGGG CCGACCT
                                          C
GAM642   LOC127428 3'  ACTCCAGCCTGGGCAACAGAGT 75152
                GAGA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAACGGGTCCGACCT
                                          CAC
GAM642   LOC129880 3'  TCCAGCTTGGGCAACAGAGCAA 75409     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||
                                    AGA CGAGACAACGGGTTCGACCT
                                      A
GAM642   LOC130026 3'  TCCAGCCTAGGCAACAGAGCAA 57441     C         C
                GA                  TCT GCTCTGTTGCC AGGCTGGA
                                    ||| |||||||||| ||||||||
                                    AGA CGAGACAACGG TCCGACCT
                                      A         A
GAM642   LOC130497 3'  TCCGGGACTAGGAGAGCGGGA  75453         GTTG  C  G_
                                    TCTCGCTCT    CC AG  CTGGA
                                    |||||||||    || ||  |||||
                                    AGGGCGAGA    GG TC  GGCCT
                                          _____  A  AG
GAM642   LOC130535 3'  TCCAGCCTGGGCAACAAGAATG 76655     C  _
                A                    TCG TCT GTTGCCCAGGCTGGA
                                    ||| ||| ||||||||||||||||
                                    AGT AGA CAACGGGTCCGACCT
                                      A   A
GAM642   LOC130535 3'  TCCAGCCTGGGTGACAGAGCAA 76656     C      TG
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGAGACA  GGGTCCGACCT
                                      A       GT
GAM642   LOC130617 5'  TCCGGTAACCCGGGCTGGGCGG 57938         TGTT    A  ___
                GG                  TCTCGCTC    GCCC GG   CTGGA
                                    ||||||||    |||| ||   |||||
                                    GGGGCGGG    CGGG CC   GGCCT
                                         T___    C  AAT
GAM642   LOC131744 3'  TCCAGCCTGGGTGACAGAGTGA 76392          TG
                                    TCGCTCTGT  CCCAGGCTGGA
                                    |||||||||  ||||||||||
                                    AGTGAGACA  GGGTCCGACCT
                                         GT
GAM642   LOC131965 3'  ACTCCAGCCTGGGCGACAGAGT 75516
                GAGA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
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                                AGAGTGAGACAGCGGGTCCGACCT
                                          CAC
GAM642  LOC132625 3'  AGACCAGCCTGGGCAACATAGT 76429       C           A
          GAGA                  TCTCGCT TGTTGCCCAGGCTGG
                                ||||||| ||||||||||||||||
                                AGAGTGA ACAACGGGTCCGACC
                                   T            AGAC
GAM642  LOC133926 3'  CTCCAGCCTGGGCGACAGAGCG 75632
          AGA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||||
                                AGAGCGAGACAGCGGGTCCGACCT
                                          CA
GAM642  LOC134147 3'  CTCTAGCCTGGGCAGCAGAGTG 57958
          AGA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||||
                                AGAGTGAGACGACGGGTCCGATCT
                                          CA
GAM642  LOC134147 3'  TCCAGCCTGGACAACAGAGGGA 57967     G      C
          GA                    TCTC CTCTGTTG CCAGGCTGGA
                                |||| |||||||| ||||||||||
                                AGAG GAGACAAC GGTCCGACCT
                                  G       A
GAM642  LOC135154 3'  TCCAGCCTGGGCAACAAGAGCG 75736       _
          A                     TCGCTCT GTTGCCCAGGCTGGA
                                ||||||| ||||||||||||||||
                                AGCGAGA CAACGGGTCCGACCT
                                   A
GAM642  LOC135818 3'  AGACCAGCCTGGGTAATGTAGC 75743       CT          A
          GAGA                  TCTCGCT  GTTGCCCAGGCTGG
                                |||||||  ||||||||||||||
                                AGAGCGA  TAATGGGTCCGACC
                                   TG           AGAC
GAM642  LOC135818 3'  TCCAGCCTGGGCAATAGGGTAA 75749     CG
          GA                    TCT  CTCTGTTGCCCAGGCTGGA
                                |||  ||||||||||||||||||
                                AGA  GGGATAACGGGTCCGACCT
                                  AT
GAM642  LOC136442 3'  TTTGGTTTTGGCGGGGAGAGG  55261     G   GTT  C   TG
                                TCTC CTCT   GCC AGGC  GA
                                |||| ||||   ||| ||||  ||
                                GGAG GGGG   CGG TTTG  TT
                                  A  ___  T   GT
GAM642  LOC137362 3'  TCCAGCCTGGGCAACAAGAGC  75787      _
                                GCTCT GTTGCCCAGGCTGGA
                                ||||| ||||||||||||||||
                                CGAGA CAACGGGTCCGACCT
                                  A
GAM642  LOC138241 5'  TCCAGCCTACTAGCGGGCGGGG 75838       T     CCC
                                TCTCGC CTGTTG   AGGCTGGA
                                |||||| ||||||   ||||||||
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                                GGGGCG GGCGAT   TCCGACCT
                                   _     CA_
GAM642   LOC138389 3'  TCCAGCCTGGGCAACAAGAGTG 76744       _
           A                    TCGCTCT GTTGCCCAGGCTGGA
                                ||||||| |||||||||||||||
                                AGTGAGA CAACGGGTCCGACCT
                                   A
GAM642   LOC138428 3'  ACTCCAGTCTGGGTGACAGAGT 75852          TG
           GAGA                   TCTCGCTCTGT  CCCAGGCTGGA
                                  |||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCTGACCT
                                        GT         CAC
GAM642   LOC139422 3'  TTCTAGCCTGGGTGACAGAGCG 76357          TG
           AGA                    TCTCGCTCTGT  CCCAGGCTGGA
                                  |||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGATCT
                                        GT         TA
GAM642   LOC139673 3'  TTGGGCAGTAGGGGAGG     76501      G
                                TCTC CTCTGTTGCCCAG
                                |||| ||||||||||||
                                GGAG GGGATGACGGGTT
                                  _
GAM642   LOC142779 3'  GCAGCCTGGTGACAGAGTGAGA 76907          TG  C     GA
                                TCTCGCTCTGT  CC AGGCTG
                                |||||||||||  || ||||||
                                AGAGTGAGACA  GG TCCGAC
                                        GT  _     GT
GAM642   LOC142927 3'  TCTAGCCTGGGTGACAGAACGA 76952       C    TG
           GA                     TCTCG TCTGT  CCCAGGCTGGA
                                  |||||  |||||  ||||||||||
                                  AGAGC AGACA  GGGTCCGATCT
                                     A     GT
GAM642   LOC142937 3'  TCCAGCCTGGGCCACAGAACGA 57447       C    T
           GA                     TCTCG TCTGT GCCCAGGCTGGA
                                  |||||  |||||  ||||||||||||
                                  AGAGC AGACA CGGGTCCGACCT
                                     A     C
GAM642   LOC142948 3'  ACTCCAGCCTGGGTGACAGAGC 83771          TG
           GAGG                   TCTCGCTCTGT  CCCAGGCTGGA
                                  |||||||||||  ||||||||||
                                  GGAGCGAGACA  GGGTCCGACCT
                                        GT         CAC
GAM642   LOC142964 5'  TTCGGCATCAAATGGGGCAGGA 76971     TC       GCCCAG
                                TC  GCTCTGTT      GCTGGA
                                ||  ||||||||      ||||||
                                AG  CGGGGTAA      CGGCTT
                                 GA       ACTA__
GAM642   LOC143310 3'  CCCCAGCCTGGGTGACAGAGCG 77041          TG         A
           AGA                    TCTCGCTCTGT  CCCAGGCTGG
                                  |||||||||||  |||||||||
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                                AGAGCGAGACA  GGGTCCGACC
                                      GT         CCA
GAM642   LOC143465 3'  CTCCAGCCTGGGTGACGGAGTG 83872          TG
                AGA                    TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGAGGCA  GGGTCCGACCT
                                      GT         CA
GAM642   LOC143677 3'  TTTGGTTTTTGTTTTGAGGGGG 83900         G ___ CC    TG
                TGGGG                  TCTCGCTCT TT   GC  AGGC  GA
                                |||||||| ||   ||  ||||  ||
                                GGGGTGGGG AG   TG  TTTG  TT
                                      G  TTT  TT    GT
GAM642   LOC143888 3'  ACTCCAGCCTGGGTGACAGAGT 77164          TG
                GAGA                   TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      GT         CAC
GAM642   LOC143916 5'  TTTGGCACTGGTGGTAGTGGGG 77152     TG    __  _ TG
                                CTC  TTGCC  CAG GC  GA
                                |||  |||||  ||| ||  ||
                                GGG  GATGG  GTC CG  TT
                                  GT    TG   A  GT
GAM642   LOC143943 3'  ACTCCAGCCTGGGTGACAGAGC 83909          TG
                GAGA                   TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      GT         CAC
GAM642   LOC144184 5'  CCAGCTCCCGCGGAGGAGG    77194      G     TGCCCA
                                TCTC CTCTGT     GGCTGG
                                ||||  ||||||     ||||||
                                GGAG GAGGCG     TCGACC
                                  _     CCC___
GAM642   LOC144289 3'  ACTCCAGCCTGGGTGACAGAGT 83945          TG
                GAGA                   TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      GT         CAC
GAM642   LOC144308 5'  TCCAGCCTGGGTGACAGAGC   83985        TG
                                GCTCTGT  CCCAGGCTGGA
                                |||||||  ||||||||||
                                CGAGACA  GGGTCCGACCT
                                    GT
GAM642   LOC144465 3'  TCCAGCCTGGGCAACAAGAGTG 77352         _
                A                     TCGCTCT GTTGCCCAGGCTGGA
                                |||||||  ||||||||||||||
                                AGTGAGA CAACGGGTCCGACCT
                                    A
GAM642   LOC144465 3'  TCCAGCCTGGGCAACAAGAGC  77350       _
                                GCTCT GTTGCCCAGGCTGGA
                                |||||  ||||||||||||||
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                                CGAGA CAACGGGTCCGACCT
                                  A
GAM642  LOC144481 3'  CTTGGGCAACAGAATGAGA   84019      C
                                TCTCG TCTGTTGCCCAGG
                                ||||| ||||||||||||
                                AGAGT AGACAACGGGTTC
                                  A
GAM642  LOC144519 5'  ACTCCAGCCTGGGCGACAGAGT 77364
          GAGA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGACAGCGGGTCCGACCT
                                          CAC
GAM642  LOC144524 3'  CTCCAGCCTGGGTGACAGAGTG 84052          TG
          GGA                   TCTCGCTCTGT  CCCAGGCTGGA
                                |||||||||||  ||||||||||
                                AGGGTGAGACA  GGGTCCGACCT
                                      GT         CA
GAM642  LOC144563 3'  TCCAGCTTGGGCAACAGAGTAA 77405    CG
          GA                    TCT  CTCTGTTGCCCAGGCTGGA
                                |||  ||||||||||||||||||
                                AGA  GAGACAACGGGTTCGACCT
                                  AT
GAM642  LOC144583 3'  TCCAGCCCGAGTGACAGAATGA 77422      C    TG CCA
          GG                    TCTCG TCTGT  C   GGCTGGA
                                ||||| |||||  |   |||||||
                                GGAGT AGACA  G   CCGACCT
                                  A    GT AGC
GAM642  LOC144667 3'  ATCTGGGAAATGCATGGGGTGG 84086         __ TG__     CTGGA
          GA                    TCTCGCTCT  GT    CCCAGG
                                |||||||||  ||    ||||||
                                AGGGTGGGG  CG    GGGTCT
                                     TA  TAAA        AG
GAM642  LOC144845 3'  TCCAGCCCGGGCGACAGAGCAA 57464    C          A
          GA                    TCT GCTCTGTTGCCC GGCTGGA
                                ||| ||||||||||| |||||||
                                AGA CGAGACAGCGGG CCGACCT
                                  A          C
GAM642  LOC145231 3'  TCCAGCCTGGGTGACAGTGTGA 84260      T    TG
                                TCGC CTGT  CCCAGGCTGGA
                                |||| ||||  ||||||||||
                                AGTG GACA  GGGTCCGACCT
                                  T    GT
GAM642  LOC145299 3'  TCCGGCCTGGGCGACAGAGCGA 84279
          GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGCGAGACAGCGGGTCCGGCCT

GAM642  LOC145333 3'  ACTCCAGCCTGGGCGACAGAGC 84284
          GAGA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
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                                AGAGCGAGACAGCGGGTCCGACCT
                                        CAC
GAM642  LOC145387 3'  ACTCCAGCCTGGGTGGCAGAGT 84326          TG
          GAGA                  TCTCGCTCTGT  CCCAGGCTGGA
                                |||||||||||  ||||||||||
                                AGAGTGAGACG  GGGTCCGACCT
                                    GT          CAC
GAM642  LOC145387 3'  TCCAGCCTGGGCGACAGAGAGA 84344      G
          GA                    TCTC CTCTGTTGCCCAGGCTGGA
                                |||| ||||||||||||||||||
                                AGAG GAGACAGCGGGTCCGACCT
                                  A
GAM642  LOC145438 3'  ACTCCAGCCTGGGCGACAGAGC 84305
          GAGA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||||
                                AGAGCGAGACAGCGGGTCCGACCT
                                        CAC
GAM642  LOC145438 3'  TCTAGCCTGGGTGACAGAGTGA 84318          TG
          GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                |||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGATCT
                                    GT
GAM642  LOC145438 3'  TCTGGCTTTTAAAATGGGATGA 84319      CT    GCCC    TG
          GG                    TCTCG  CTGTT    AGGC  GA
                                |||||  |||||    ||||  ||
                                GGAGT  GGTAA    TTCG  CT
                                   AG     AATT    GT
GAM642  LOC145453 3'  CTTCAGCCTGGGCAACAGAGTG 77659
          AGA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||||
                                AGAGTGAGACAACGGGTCCGACTT
                                        CA
GAM642  LOC145482 3'  TCCAGCCTGGGCGACAAGAGTG 77747        _
          A                     TCGCTCT GTTGCCCAGGCTGGA
                                |||||||  ||||||||||||||
                                AGTGAGA CAGCGGGTCCGACCT
                                    A
GAM642  LOC145483 3'  TCCAGCCTGGGCAGCAGAGC   77758
                                GCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||
                                CGAGACGACGGGTCCGACCT

GAM642  LOC145608 5'  TCCAGCCTGGGTGACAGAGCAA 84386     C      TG
          GA                    TCT GCTCTGT  CCCAGGCTGGA
                                |||  |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM642  LOC145609 3'  TCCAGCCTGGGTGACAGAGCAA 84370     C      TG
          GA                    TCT GCTCTGT  CCCAGGCTGGA
                                |||  |||||||  ||||||||||
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                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM642   LOC145662 3'  TCCAGACTGGGCAGCAGAGTGA 77837              G
                                TCGCTCTGTTGCCCAG CTGGA
                                ||||||||||||||| |||||
                                AGTGAGACGACGGGTC GACCT
                                          A
GAM642   LOC145663 3'  TCCAGCCTGGGCGACAGAGCTA 84430     C
            GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGAGACAGCGGGTCCGACCT
                                  T
GAM642   LOC145757 3'  TCCAGCCTAGGTGACAGAGCGA 77942          TG  C
            GA                    TCTCGCTCTGT  CC AGGCTGGA
                                ||||||||||  || ||||||||
                                AGAGCGAGACA  GG TCCGACCT
                                      GT  A
GAM642   LOC145820 3'  TCCAGCCTGGGCGACAGAGCAA 77980     C
            GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGAGACAGCGGGTCCGACCT
                                  A
GAM642   LOC145945 5'  TCCAGCCTGAGCAACAGAGCAA 84571     C        C
            GA                    TCT GCTCTGTTGC CAGGCTGGA
                                ||| |||||||||| |||||||||
                                AGA CGAGACAACG GTCCGACCT
                                  A         A
GAM642   LOC145978 3'  TTTGGTCAAATAGACTGAGA   78054       C     GC_
                                TCTCG TCTGTT   CCAGG
                                ||||| ||||||   |||||
                                AGAGT AGATAA   GGTTT
                                   C      ACT
GAM642   LOC145988 5'  TCCAGCCTGGAAGGCAGAGAGA 78072      G      GC
            GA                    TCTC CTCTGTT  CCAGGCTGGA
                                |||| |||||||  ||||||||||
                                AGAG GAGACGG  GGTCCGACCT
                                  A       AA
GAM642   LOC145989 3'  TCTGCCAGGGTGGTGGTGGCGG 60298        _ TG TG   A   T
            GG                    TCTCGCT C  T  CCC GGC GGA
                                ||||||| |  |  ||| ||| |||
                                GGGGCGG G  G  GGG CCG TCT
                                    T GT GT   A  _
GAM642   LOC146059 3'  ACTCCAGTCTGGGTAACAGAGC 78081
            GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGCGAGACAATGGGTCTGACCT
                                              CAC
GAM642   LOC146092 5'  TTGAGCAGTGGAGTGGGA    84587         TG    C
                                TCTCGCTC  TTGC CAG
                                ||||||||  |||| |||
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                                AGGGTGAG  GACG GTT
                                    GT    A
GAM642   LOC146108 5'  TCTAGTCTGGGCTCTGGCAGAG 78153       ___
                                CTCTGTT   GCCCAGGCTGGA
                                |||||||   ||||||||||||
                                GAGACGG   CGGGTCTGATCT
                                    TCT
GAM642   LOC146174 5'  CCGGGGCTCGGGGGGTGGGG   78198        GTT_   A
                                TCTCGCTCT    GCCC GG
                                |||||||||    |||| ||
                                GGGGTGGGG    CGGG CC
                                     GGCT    G
GAM642   LOC146229 3'  CTCCAGCCTGGGCGACAGAGCG 78277
           AGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||||
                                AGAGCGAGACAGCGGGTCCGACCT
                                              CA
GAM642   LOC146443 5'  TTCAGTTTGTAAGTAGTGAGA  78448       _ GTTGCC
                                TCTCGCT CT     CAGGCTGGA
                                |||||||  ||     |||||||||
                                AGAGTGA GA     GTTTGACTT
                                    T  AT____
GAM642   LOC146445 3'  TCTGGCCTGTCTGTGCTGCAGA 84684          T  C____    TG
           GCGGGG                  TCTCGCTCTGT GC    CAGGC  GA
                                |||||||||||  ||    |||||  ||
                                GGGGCGAGACG CG    GTCCG  CT
                                     T  TGTCT    GT
GAM642   LOC146475 5'  CGGCCTCCGGAGCTGGGA    84689     _    TTGCCC    TG
                                TCTC GCTCTG     AGGC  G
                                ||||  ||||||     ||||  |
                                AGGG CGAGGC     TCCG  C
                                  T     C_____    GT
GAM642   LOC146475 5'  TCAAGCCTGGGCGACAGAGGGA 84693      G            G
           GA                     TCTC CTCTGTTGCCCAGGCT GA
                                |||| ||||||||||||||| ||
                                AGAG GAGACAGCGGGTCCGA CT
                                  G             A
GAM642   LOC146488 5'  CCAAGGTGGCAGAGTCAGG    71355     C      TG  CAGGC
                                TCT GCTCTGT  CC     TGG
                                |||  |||||||  ||     |||
                                GGA TGAGACG  GG     ACC
                                  C      GT  A____
GAM642   LOC146540 3'  TCCAGCCTGGGCTACAAAGCAG 78530    TC   C   T
           GA                     TC  GCT TGT GCCCAGGCTGGA
                                ||  ||| ||| ||||||||||||
                                AG  CGA ACA CGGGTCCGACCT
                                 GA   A   T
GAM642   LOC146656 3'  TCTGAGCAACATAGTGAGA    78669        C     C
                                TCTCGCT TGTTGC CAGG
                                |||||||  ||||||  ||||
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                                AGAGTGA ACAACG GTCT
                                   T     A
GAM642   LOC146713 3'  TCCAGCCTGGGCAACAGAGC   84739
                                GCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||
                                CGAGACAACGGGTCCGACCT

GAM642   LOC146713 3'  TCCAGCCTGGTCAACAGAGCAA 84741     C        C
            GA                    TCT GCTCTGTTG CCAGGCTGGA
                                  ||| ||||||||| ||||||||||
                                  AGA CGAGACAAC GGTCCGACCT
                                    A        T
GAM642   LOC146728 3'  TCCAGCCTGGGAAGCAGAGTGA 84774            G
            GA                    TCTCGCTCTGTT CCCAGGCTGGA
                                  |||||||||||| ||||||||||
                                  AGAGTGAGACGA GGGTCCGACCT
                                        A
GAM642   LOC146756 3'  ACTCCAGCCTGGGCGACAGAGC 84791
            GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACAGCGGGTCCGACCT
                                                CAC
GAM642   LOC146839 5'  TCCAGCCTGGGCAACATAGC   84853     C
                                GCT TGTTGCCCAGGCTGGA
                                ||| ||||||||||||||
                                CGA ACAACGGGTCCGACCT
                                  T
GAM642   LOC146895 3'  TCCAGCCTGGGTGACAAGAGC  84874       _  TG
                                GCTCT GT  CCCAGGCTGGA
                                ||||| ||  ||||||||||
                                CGAGA CA  GGGTCCGACCT
                                   A  GT
GAM642   LOC146901 3'  TCCAGTTTGGGCAACAGAATGA 84913       C
            GG                    TCTCG TCTGTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||||||
                                  GGAGT AGACAACGGGTTTGACCT
                                     A
GAM642   LOC146923 3'  CTCCAGCCTGGGCGACAGAGTG 78800
            AGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGTGAGACAGCGGGTCCGACCT
                                               CA
GAM642   LOC146958 3'  TCCAGCCTGGGTGACACAGCGA 84946        C   TG
            GA                    TCTCGCT TGT  CCCAGGCTGGA
                                  ||||||| |||  ||||||||||
                                  AGAGCGA ACA  GGGTCCGACCT
                                     C   GT
GAM642   LOC146958 3'  TCCAGCCTGGGTGACAGAGCGA 84947           TG
            GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
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                                AGAGCGAGACA  GGGTCCGACCT
                                      GT         C
GAM642   LOC147040 3'  TCACTGGTGGGGGGTGGGG   78836        G TG  CA  C
                                TCTCGCTCT T  CC  GG TGG
                                |||||||||  |  ||  || |||
                                GGGGTGGGG G  GG  TC ACT
                                     _ GT  __  _
GAM642   LOC147040 3'  TCCCCATGGCAATGGGGCTGGA 78837     C         CA  CT
                                TCT GCTCTGTTGCC  GG  GGA
                                |||  ||||||||||  ||  |||
                                AGG CGGGGTAACGG  CC  CCT
                                  T         TA  __
GAM642   LOC147040 3'  TTTGGGACAGTGGGGGAGG   78840     G   TG  _
                                TCTC CTC  TTG CCCAGG
                                ||||  |||  ||| ||||||
                                GGAG GGG  GAC GGGTTT
                                  _  GT  A
GAM642   LOC147043 3'  TTTAGTTTTGCTTACAGAGCAG 88505     C      T_  CC
            A                    TCT GCTCTGT  GC  AGGCTGGA
                                |||  |||||||  ||  ||||||||
                                AGA CGAGACA  CG  TTTGATTT
                                  _      TT  T_
GAM642   LOC147057 3'  CCGCCACTGGGCGACAGAGTGA 84979              __  T  A
            GA                     TCTCGCTCTGTTGCCCA  GGC GG
                                ||||||||||||||||  ||| ||
                                AGAGTGAGACAGCGGGT  CCG CC
                                        CA  _  G
GAM642   LOC147063 5'  AGACCAGCCTGGGCAACAGAGT 85013                  A
            GAGA                    TCTCGCTCTGTTGCCCAGGCTGG
                                ||||||||||||||||||||||
                                AGAGTGAGACAACGGGTCCGACC
                                          AGAG
GAM642   LOC147071 5'  CCGGCAGGGCAGGATGGGA   73358      C  GT    AG
                                TCTCG TCT  TGCCC  GCTGG
                                |||||  |||  |||||  |||||
                                AGGGT AGG  ACGGG  CGGCC
                                  _  __    A_
GAM642   LOC147071 3'  TCCAGCCTGGGCGACAGAGCAA 73373     C
            GA                     TCT GCTCTGTTGCCCAGGCTGGA
                                |||  ||||||||||||||||||
                                AGA CGAGACAGCGGGTCCGACCT
                                  A
GAM642   LOC147077 3'  CGGCTTGCGGCGCGAGG     78847       TCTGTT  _    TG
                                TCTCGC     GCC CAGGC  G
                                ||||||     ||| |||||  |
                                GGAGCG     CGG GTTCG  C
                                   _______  C    GT
GAM642   LOC147080 3'  TCCAGCTTAGGTGACAGAGTGA 85052          TG  C
            GA                     TCTCGCTCTGT  CC AGGCTGGA
                                ||||||||||  ||  ||||||||
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                                AGAGTGAGACA  GG TTCGACCT
                                      GT  A
GAM642   LOC147180 5'  TCCAGCCCGGGTGACAGAGTGA 85105         TG   A
                                TCGCTCTGT  CCC GGCTGGA
                                |||||||||  ||| |||||||
                                AGTGAGACA  GGG CCGACCT
                                     GT   C
GAM642   LOC147184 5'  TCCGGAACTAAACGGGGTGAGG 59871           GCCCAGG
                                TCTCGCTCTGTT      CTGGA
                                ||||||||||||      |||||
                                GGAGTGGGGCAA      GGCCT
                                       ATCAA__
GAM642   LOC147229 5'  TCTAGGAGAGGGACAGAGTGGG 78927          TG   AGG_
            A                    TCTCGCTCTGT  CCC    CTGGA
                                ||||||||||  |||    |||||
                                AGGGTGAGACA  GGG    GATCT
                                      __   AGAG
GAM642   LOC147229 5'  TTTGGTCTGGGACACGGTGGG  78930       C   TG      TG
                                CTCGCT TGT  CCCAGGC  GA
                                |||||| |||  |||||||  ||
                                GGGTGG ACA  GGGTCTG  TT
                                   C   __       GT
GAM642   LOC147599 3'  TCCAGCCTGGGCAACAGAGAGA 85166    G
                                TC CTCTGTTGCCCAGGCTGGA
                                || ||||||||||||||||||
                                AG GAGACAACGGGTCCGACCT
                                 A
GAM642   LOC147622 3'  TCCAGCCTGGGTGACAGAGCTA 85172     C      TG
            GA                    TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  T      GT
GAM642   LOC147649 3'  TCCAGAGCCTGGGCGACAGAGC 79064                  __
            GAGA                    TCTCGCTCTGTTGCCCAGGCT  GGA
                                ||||||||||||||||||||  |||
                                AGAGCGAGACAGCGGGTCCGA  CCT
                                        GA
GAM642   LOC147660 3'  TCCAGGCTGGGCGACAGAGTGA 79032              G
            GA                    TCTCGCTCTGTTGCCCAG CTGGA
                                |||||||||||||||| |||||
                                AGAGTGAGACAGCGGGTC GACCT
                                       G
GAM642   LOC147664 3'  TCCAGCCTGGGCAACGAGAGGG 79050      G   _
            GA                    TCTC CTCT GTTGCCCAGGCTGGA
                                |||| |||| ||||||||||||||
                                AGGG GAGA CAACGGGTCCGACCT
                                  _   G
GAM642   LOC147669 3'  TCCAGCCTGGGTGACAAGGGAA 85186     _ G  C   TG
            GA                    TCT C CT TGT  CCCAGGCTGGA
                                ||| | || |||  ||||||||||
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                                AGA G GA ACA  GGGTCCGACCT
                                  A G  _   GT
GAM642   LOC147727 5'  ACTCCAGCCTGGGCGATAGAGT 79120
                GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                        ||||||||||||||||||||||||
                                        AGAGTGAGATAGCGGGTCCGACCT
                                                CAC
GAM642   LOC147727 5'  ACTCCAGTCTGGGCGACAGAGC 79121
                GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                        ||||||||||||||||||||||||
                                        AGAGCGAGACAGCGGGTCTGACCT
                                                CAC
GAM642   LOC147741 3'  TCCAGCCTGGCGACTGAGCGAG 79144          T     C
                A                        TCTCGCTC GTTGCC AGGCTGGA
                                        |||||||| |||||| ||||||||
                                        AGAGCGAG CAGCGG TCCGACCT
                                             T     _
GAM642   LOC147779 3'  TTTGGTGGCAAAAGCAGGCTGG 79156      _ T   ___    CAG  TG
                GG                       TCTC GC CTGT   TGCC   GC  GA
                                        |||| || ||||   ||||   ||  ||
                                        GGGG CG GACG   ACGG   TG  TT
                                          T  _    AAA    ___ GT
GAM642   LOC147791 5'  CCAGCTGCCAGGGGCGAGG    85189          GTT  CCA
                                        TCTCGCTCT   GC   GGCTGG
                                        |||||||||   ||   ||||||
                                        GGAGCGGGG   CG   TCGACC
                                             AC_  ___
GAM642   LOC147837 3'  ACCCCAGCCTGGGCGACAGAGC 79199     C               A
                CAGA                     TCT GCTCTGTTGCCCAGGCTGG
                                        ||| ||||||||||||||||||
                                        AGA CGAGACAGCGGGTCCGACC
                                          C               CCAC
GAM642   LOC147837 3'  TCCAGCCTGGGCAGCAAGAGC  79209       _
                                        GCTCT GTTGCCCAGGCTGGA
                                        ||||| ||||||||||||||
                                        CGAGA CGACGGGTCCGACCT
                                           A
GAM642   LOC147949 3'  TTCAGTCTTATTTATAGTGTGG 79280        T    TGCCC
                GA                       TCTCGC CTGT     AGGCTGGA
                                        |||||| ||||     ||||||||
                                        AGGGTG GATA     TCTGACTT
                                           T    TTTAT
GAM642   LOC147990 3'  TCCAGCCTGGGCAACAGAGC   85235
                                        GCTCTGTTGCCCAGGCTGGA
                                        ||||||||||||||||||||
                                        CGAGACAACGGGTCCGACCT

GAM642   LOC148089 3'  CCAGGATGGCAGAGCCAGG    79327     C     TTGC   GG
                                        TCT GCTCTG    CCA  CTGG
                                        ||| ||||||    |||  ||||
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                                GGA CGAGAC    GGT  GACC
                                  C      ____   AG
GAM642   LOC148166 3'  AGACCAGCCTGGGCAATATAGT 79409        C            A
                  GAGA                  TCTCGCT TGTTGCCCAGGCTGG
                                        ||||||| ||||||||||||||||
                                        AGAGTGA ATAACGGGTCCGACC
                                           T            AGAA
GAM642   LOC148166 5'  TCAGTTTGGGAAGAGGAGA   79423      G    GTTG
                                        TCTC CTCT    CCCAGGCTGG
                                        |||| ||||    ||||||||||
                                        AGAG GAGA    GGGTTTGACT
                                          _    A___
GAM642   LOC148166 3'  TCCAGCCTAGGCGACGGGGCAA 79424     C         C
                  GA                    TCT GCTCTGTTGCC AGGCTGGA
                                        ||| |||||||||| ||||||||
                                        AGA CGGGGCAGCGG TCCGACCT
                                          A          A
GAM642   LOC148166 3'  TCCGGCCTGGGCAACAGATCG  79425    C
                                        CG TCTGTTGCCCAGGCTGGA
                                        || ||||||||||||||||||
                                        GC AGACAACGGGTCCGGCCT
                                         T
GAM642   LOC148198 3'  TCCATCCTGGGTGACAAAGTGA 71228        C   TG     C
                  GA                    TCTCGCT TGT  CCCAGG TGGA
                                        ||||||| |||  |||||| ||||
                                        AGAGTGA ACA  GGGTCC ACCT
                                           A   GT     T
GAM642   LOC148206 3'  TCCAGCCTGGGCCACAAGGCAA 79466     C  TC   T
                  GA                    TCT GC  TGT GCCCAGGCTGGA
                                        ||| ||  ||| ||||||||||||
                                        AGA CG  ACA CGGGTCCGACCT
                                          A  GA   C
GAM642   LOC148254 3'  CCAGCCTGGGAGACGGGG     79501        TG
                                        CTCTGT  CCCAGGCTGG
                                        ||||||  ||||||||||
                                        GGGGCA  GGGTCCGACC
                                           GA
GAM642   LOC148267 3'  GGACCAGCCTGGGCAACATAGT 79514        C            A
                  GAGA                  TCTCGCT TGTTGCCCAGGCTGG
                                        ||||||| ||||||||||||||||
                                        AGAGTGA ACAACGGGTCCGACC
                                           T            AGGG
GAM642   LOC148343 3'  ACACCAGCCTGGGCGACAGGGT 79533                  A
                  GAGA                  TCTCGCTCTGTTGCCCAGGCTGG
                                        ||||||||||||||||||||||||
                                        AGAGTGGGACAGCGGGTCCGACC
                                                    ACAC
GAM642   LOC148343 3'  GACCAGCCTGGGCAATACAGTG 79544        C            A
                  AGA                   TCTCGCT TGTTGCCCAGGCTGG
                                        ||||||| ||||||||||||||||
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                                AGAGTGA ATAACGGGTCCGACC
                                   C            AGA
GAM642  LOC148534 3'  TCCAGCCTGGGCGACAGAGCAA 79640     C
          GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGAGACAGCGGGTCCGACCT
                                  A
GAM642  LOC148710 3'  TCTGTGGGTGGTGATGGAGGAG 85350      G     ___    GGCTGGA
          G                     TCTC CTCTGTT   GCCCA
                                |||| |||||||   |||||
                                GGAG GAGGTAG   TGGGT
                                  _     TGG    GTCT
GAM642  LOC148758 5'  TCCAGCCTGGGCAACAAGAGC  79726       _
                                GCTCT GTTGCCCAGGCTGGA
                                ||||| ||||||||||||||
                                CGAGA CAACGGGTCCGACCT
                                   A
GAM642  LOC148775 5'  TCCAGGGCCCTGGCGGGGC    85379       TTGC    ___
                                GCTCTG    CCAGG   CTGGA
                                ||||||    |||||   |||||
                                CGGGGC    GGTCC   GACCT
                                   ____     CGG
GAM642  LOC148809 3'  TCCAGCCTGGGCGACAGAGCAA 79762     C
          GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGAGACAGCGGGTCCGACCT
                                  A
GAM642  LOC148809 5'  TCCAGCCTGGGTGACAGAGCAA 79763     C      TG
          GA                    TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM642  LOC148823 3'  TCCAGCTTGGGCAACAGAGTGA 59896
          GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGACAACGGGTTCGACCT

GAM642  LOC148872 3'  TTCGGCCGCGCGCGGGCGGGG  85384       T   T  CCA
                                TCTCGC CTGT GC   GGCTGGA
                                |||||| |||| ||   |||||||
                                GGGGCG GGCG CG   CCGGCTT
                                   _    _ CG_
GAM642  LOC148932 3'  TTGCCAGAGGCTGTGGAGCGAG 79851        TG T   CA_   TGGA
          G                     TCTCGCTC  T GCC   GGC
                                |||||||| | |||   |||
                                GGAGCGAG  G CGG   CCG
                                     GT T   AGA   TTT
GAM642  LOC148936 3'  TCCAGGTTGGGCAACAGAGCAA 85459     C           G
          GA                    TCT GCTCTGTTGCCCAG CTGGA
                                ||| |||||||||||||| |||||
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                                AGA CGAGACAACGGGTT GACCT
                                  A           G
GAM642   LOC149073 3'  TCCAGCCTGGGCAACAGTGTGA 85487       T
                GA                TCTCGC CTGTTGCCCAGGCTGGA
                                  |||||| ||||||||||||||||
                                  AGAGTG GACAACGGGTCCGACCT
                                     T
GAM642   LOC149127 3'  TCTGGGTGCAGAGGGCGAGA  85505        GT_
                                  TCTCGCTCT  TGCCCAGG
                                  |||||||||  ||||||||
                                  AGAGCGGGA  GTGGGTCT
                                       GAC
GAM642   LOC149175 3'  ACTCCAGCCTGGGCGACAGAGC 79944
                GAGA                TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACAGCGGGTCCGACCT
                                                 CAC
GAM642   LOC149194 5'  TCCAGCCTGGGCAACAAGAGC  79990      _
                                  GCTCT GTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||||
                                  CGAGA CAACGGGTCCGACCT
                                    A
GAM642   LOC149271 3'  TCCAGCCTGGGCAACAAGAGTG 80012       _
                A                  TCGCTCT GTTGCCCAGGCTGGA
                                   ||||||| ||||||||||||||
                                   AGTGAGA CAACGGGTCCGACCT
                                       A
GAM642   LOC149297 5'  TCCGGCTACGGGGCGGGGCCGG 85544    C     TG  A_
                G                   TCT GCTCTGT  CCC  GGCTGGA
                                    ||| |||||||  |||  |||||||
                                    GGG CGGGGCG  GGG  TCGGCCT
                                      C      __   CA
GAM642   LOC149373 3'  CCAGTGTAGGAGGGTGGGA   80092        G   CCAG
                                  TCTCGCTCT TTGC   GCTGG
                                  ||||||||| ||||   |||||
                                  AGGGTGGGA GATG   TGACC
                                       G   _____
GAM642   LOC149386 3'  CGGAGCTGGGGAGTGGGA    85555        TGTTG    G_ TG
                                  TCTCGCTC    CCCAG  C  G
                                  ||||||||    |||||  |  |
                                  AGGGTGAG    GGGTC  G  C
                                        _____    GA GT
GAM642   LOC149386 5'  TTTGGCCTGGGCAAAAGTCCCA 85568    CGCT  G       TG
                GG                  TCT   CT TTGCCCAGGC  GA
                                    |||   || ||||||||||  ||
                                    GGA   GA AACGGGTCCG  TT
                                      CCCT  A        GT
GAM642   LOC149426 3'  TCCCCTGGTGATGGGGCAGGA  85575    TC     TG  C   CT
                                  TC  GCTCTGT  CC AGG  GGA
                                  ||  |||||||  || |||  |||
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                                AG  CGGGGTA  GG TCC  CCT
                                 GA      GT  _  __
GAM642   LOC149464 3'  TCCAGCCTGGGCAACAAGAGC  85600      _
                                GCTCT GTTGCCCAGGCTGGA
                                ||||| ||||||||||||||
                                CGAGA CAACGGGTCCGACCT
                                  A
GAM642   LOC149464 5'  TTCAGCTTGGGTGACAGAGCCA 85602     C      TG
            GA                    TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTTCGACTT
                                  C      GT
GAM642   LOC149506 3'  TCTATGGGGGGGTGGGGCGAGG  85650        TG  G    GGC
                                TCTCGCTC  TT CCCA   TGGA
                                ||||||||  || ||||   ||||
                                GGAGCGGG  GG GGGT   ATCT
                                    GT  G   ___
GAM642   LOC149579 5'  TCCAGCCTGTGTGACAGAGCAA 71695     C      TG C
            GA                    TCT GCTCTGT  C CAGGCTGGA
                                ||| |||||||  | |||||||||
                                AGA CGAGACA  G GTCCGACCT
                                  A      GT T
GAM642   LOC149606 3'  GCAGCCTGGGCAACATAGCGAG 80264        C           GA
            A                     TCTCGCT TGTTGCCCAGGCTG
                                ||||||| ||||||||||||||
                                AGAGCGA ACAACGGGTCCGAC
                                    T           GT
GAM642   LOC149628 3'  ACTCCAGCCTGGGTGACAGAGC 80272          TG
            GAGA                    TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      GT         CAC
GAM642   LOC149668 5'  GTCTGCCTGGGTGTGGGGTGAG 85702        TG T       T  A
            G                     TCTCGCTC  T GCCCAGGC GG
                                ||||||||  | ||||||||  ||
                                GGAGTGGG  G TGGGTCCG CT
                                    GT _       T  GT
GAM642   LOC149672 5'  ACTCCAGCCTGGGCAACAGAGT 80333
            GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGACAACGGGTCCGACCT
                                          CAC
GAM642   LOC149705 3'  TCCAGCCTGGGTGACGAGTGA  85787       T  TG
                                TCGCTC GT  CCCAGGCTGGA
                                ||||||  ||  ||||||||||
                                AGTGAG CA  GGGTCCGACCT
                                   _  GT
GAM642   LOC149707 3'  TCTAGCCTGGGTGACAGAATGA 80299      C    TG
            GA                    TCTCG TCTGT  CCCAGGCTGGA
                                ||||| |||||  ||||||||||
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                                AGAGT AGACA  GGGTCCGATCT
                                  A     GT
GAM642   LOC149711 3'  ACTCCAGCCTGGGTGACAGAGT 85834          TG
            GAGA                   TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   AGAGTGAGACA  GGGTCCGACCT
                                         GT          CAC
GAM642   LOC149721 5'  TTCAGGGGATGGCAGAGCTGGG 80322     C       _  AGG
                                   TCT GCTCTGTTG CCC   CTGGA
                                   ||| ||||||||| |||   |||||
                                   GGG CGAGACGGT GGG   GACTT
                                     T       A  ___
GAM642   LOC149830 3'  TTTGGCTTGGGCACGACAGG   85888       __       TG
                                   TCTGT  TGCCCAGGC  GA
                                   |||||  |||||||||  ||
                                   GGACA  ACGGGTTCG  TT
                                      GC        GT
GAM642   LOC149912 3'  TCCAGCCTGGGCGACAGTGA   85882       CT
                                   TCGCT  GTTGCCCAGGCTGGA
                                   |||||  ||||||||||||||||
                                   AGTGA  CAGCGGGTCCGACCT
                                      __
GAM642   LOC149952 3'  TTCCAGCCTGGGCAATAGAGTG 80373
            AGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGTGAGATAACGGGTCCGACCT
                                               TA
GAM642   LOC150095 3'  ACTCCAGCCTGGGCAACAGAGC 85988
            GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGCGAGACAACGGGTCCGACCT
                                               CAC
GAM642   LOC150139 3'  TCCAGCCTGGGTGACAGAGAGA 80413    G     TG
                                   TC CTCTGT  CCCAGGCTGGA
                                   || ||||||  ||||||||||
                                   AG GAGACA  GGGTCCGACCT
                                    A     GT
GAM642   LOC150142 5'  CTCCAGCTTGGGTGACAGAGTG 80406          TG
            AGA                    TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   AGAGTGAGACA  GGGTTCGACCT
                                         GT          CA
GAM642   LOC150174 3'  TCCAGCCTGGTCAACAGAGTGA 80441           C
            GA                     TCTCGCTCTGTTG CCAGGCTGGA
                                   ||||||||||||| |||||||||
                                   AGAGTGAGACAAC GGTCCGACCT
                                            T
GAM642   LOC150185 3'  CTCCAGCCTGGGTGACAGAGCG 86067          TG
            AGA                    TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
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                                AGAGCGAGACA  GGGTCCGACCT
                                      GT         CA
GAM642   LOC150197 3'  TCCAGGCCCTGGCAGGTGGGG  80427       T   TTGC    __
                                TCTCGC CTG    CCAGG  CTGGA
                                ||||||| |||    |||||  |||||
                                GGGGTG GAC    GGTCC  GACCT
                                   _  ____     CG
GAM642   LOC150213 3'  TCCAGCCTGGTCAACAGAGTGA 75360           C
            GA                    TCTCGCTCTGTTG CCAGGCTGGA
                                ||||||||||||| ||||||||||
                                AGAGTGAGACAAC GGTCCGACCT
                                      T
GAM642   LOC150225 3'  TCCAGCCTGGGCGTCAGAGTGA 86206          T
            GA                    TCTCGCTCTG TGCCCAGGCTGGA
                                ||||||||||| ||||||||||||
                                AGAGTGAGAC GCGGGTCCGACCT
                                     T
GAM642   LOC150236 3'  TCCAGCCTGGTCAACAGAGTGA 80503           C
            GA                    TCTCGCTCTGTTG CCAGGCTGGA
                                ||||||||||||| ||||||||||
                                AGAGTGAGACAAC GGTCCGACCT
                                      T
GAM642   LOC150244 3'  TCCAGCCTGGGCGACAGAGCGA 80552
            GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGCGAGACAGCGGGTCCGACCT

GAM642   LOC150245 3'  TCCAGCCTGGGTGACAGAATAA 86119     CGC     TG
            GA                    TCT   TCTGT  CCCAGGCTGGA
                                |||   |||||  ||||||||||
                                AGA   AGACA  GGGTCCGACCT
                                  ATA     GT
GAM642   LOC150319 3'  TCCAGCCTGGGCAACAAGAGCG 80477         _
            A                      TCGCTCT GTTGCCCAGGCTGGA
                                ||||||| ||||||||||||||
                                AGCGAGA CAACGGGTCCGACCT
                                     A
GAM642   LOC150358 3'  TCTAGCCTGGGCAACAAGAGC  86103       _
                                GCTCT GTTGCCCAGGCTGGA
                                ||||| ||||||||||||||
                                CGAGA CAACGGGTCCGATCT
                                   A
GAM642   LOC150358 3'  TTCCAGCCTGGGCGACAGAGCG 86105
            AGA                     TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGCGAGACAGCGGGTCCGACCT
                                        TA
GAM642   LOC150372 3'  TTTGGCCCAAGGGAGGGTGGGG 80626         GTTG   A__   TG
                                TCTCGCTCT    CCC   GGC  GA
                                |||||||||    |||   |||  ||
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                                GGGGTGGGA   GGG  CCG  TT
                                     ____   AAC  GT
GAM642  LOC150481 3'  CCAGCTTGGGCCTGGGG    80696     GTT
                                CTCT  GCCCAGGCTGG
                                ||||  ||||||||||
                                GGGG  CGGGTTCGACC
                                  TC_
GAM642  LOC150481 3'  TCCAGCCTGGTGACAGAGCAAG 80714    C     TG  C
          A                      TCT GCTCTGT  CC AGGCTGGA
                                 ||| |||||||  || ||||||||
                                 AGA CGAGACA  GG TCCGACCT
                                   A      GT  _
GAM642  LOC150577 3'  TCCAGCCTGGATGACAGAGTGA 86260         GC
                                 TCGCTCTGTT  CCAGGCTGGA
                                 ||||||||||  ||||||||||
                                 AGTGAGACAG  GGTCCGACCT
                                       TA
GAM642  LOC150606 3'  TCTAGTTTGATTAGGAGCTAGA 86274    C    GTTGCC
                                 TCT GCTCT     CAGGCTGGA
                                 ||| |||||     |||||||||
                                 AGA CGAGG     GTTTGATCT
                                   T    ATTA__
GAM642  LOC150622 3'  TCCAGCCTGGGCAACAAGAGC  80768      _
                                 GCTCT GTTGCCCAGGCTGGA
                                 ||||| ||||||||||||||
                                 CGAGA CAACGGGTCCGACCT
                                    A
GAM642  LOC150622 3'  TTTGGCCTGGGCAGTGGAGC   80772     TG       TG
                                 GCTC  TTGCCCAGGC  GA
                                 ||||  ||||||||||  ||
                                 CGAG  GACGGGTCCG  TT
                                   GT        GT
GAM642  LOC150630 5'  ACTCCAGCCTGGGCAGCAGAGT 86282
          GAGA                     TCTCGCTCTGTTGCCCAGGCTGGA
                                 |||||||||||||||||||||||||
                                 AGAGTGAGACGACGGGTCCGACCT
                                              CAC
GAM642  LOC150759 3'  TCTGAAGCAGCAGAGTGA    80796          C_
                                 TCGCTCTGTTGC  CAGG
                                 ||||||||||||  ||||
                                 AGTGAGACGACG  GTCT
                                       AA
GAM642  LOC150848 5'  TTTGGCAACAGGCACGGGTGAG 86322       T   T  CAG_  TG
          G                       TCTCGC CTGT GCC   GC  GA
                                  |||||| |||| |||   ||  ||
                                  GGAGTG GGCA CGG   CG  TT
                                     _   _  ACAA  GT
GAM642  LOC150889 3'  TCCAGCCTGCGGGACAGAGTGA 80819          G  _
          GA                      TCTCGCTCTGTT CC CAGGCTGGA
                                  |||||||||||| || |||||||||
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                                AGAGTGAGACAG GG GTCCGACCT
                                       _  C
GAM642   LOC150960 3'  TCCAGCTTGGGCAACAAAGTGA 80879        C
            GA                    TCTCGCT TGTTGCCCAGGCTGGA
                                  ||||||| ||||||||||||||||
                                  AGAGTGA ACAACGGGTTCGACCT
                                     A
GAM642   LOC150984 5'  TTCAGCAGCTAGCGGAGCGG   61013          _  CCAG
                                  TCGCTCTGTT GC    GCTGGA
                                  |||||||||| ||    ||||||
                                  GGCGAGGCGA CG    CGACTT
                                        T  A___
GAM642   LOC150998 3'  GCAGCCTGGGTGACAGAGCAAG 86359     C      TG       GA
            A                     TCT GCTCTGT  CCCAGGCTG
                                  ||| |||||||  |||||||||
                                  AGA CGAGACA  GGGTCCGAC
                                    A      GT       GT
GAM642   LOC151005 5'  CTAGTCTTGTCAGGGCGG    80896        TT  CC
                                  TCGCTCTG  GC  AGGCTGG
                                  ||||||||  ||  |||||||
                                  GGCGGGAC  TG  TCTGATC
                                       __  T_
GAM642   LOC151040 3'  TCCGGGGACTGTTGTGGGGTGG 80908        TG TGCC   G__
            GG                    TCTCGCTC  T    CAG   CTGGA
                                  ||||||||  |    |||   |||||
                                  GGGGTGGG  G    GTC   GGCCT
                                       GT TT__   AGG
GAM642   LOC151057 3'  TCTGAGGCTGGGGCGGGGTGGG 86399          TG    G  _
            G                     TCTCGCTCTGT  CCCAG CT GGA
                                  ||||||||||  ||||| || |||
                                  GGGGTGGGGCG  GGGTC GA TCT
                                        __    G  G
GAM642   LOC151057 3'  TCTGGTTAATGCAAAGGGTGAG 86400         G    CCA   TG
            A                     TCTCGCTCT TTGC   GGC  GA
                                  |||||||| ||||   |||  ||
                                  AGAGTGGGA AACG   TTG  CT
                                       _   TAA   GT
GAM642   LOC151194 5'  TCTGAGCAGAGGGCGGGG    59897         G    C
                                  TCTCGCTCT TTGC CAGG
                                  ||||||||| |||| ||||
                                  GGGGCGGGA GACG GTCT
                                       _   A
GAM642   LOC151196 3'  TCCAGCCTGGGCAACACAGCAA 86456     C   C
            GA                    TCT GCT TGTTGCCCAGGCTGGA
                                  ||| ||| ||||||||||||||||
                                  AGA CGA ACAACGGGTCCGACCT
                                    A   C
GAM642   LOC151248 3'  TCCAGCCCAGGTAACAGAGTGA 80998             CA
            GA                    TCTCGCTCTGTTGCC  GGCTGGA
                                  ||||||||||||||  |||||||
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                                AGAGTGAGACAATGG  CCGACCT
                                      AC
GAM642   LOC151248 3'  TCCAGCCTGGTGACAGAGCGAG 80999          TG  C
           A                    TCTCGCTCTGT  CC AGGCTGGA
                                |||||||||||  || ||||||||
                                AGAGCGAGACA  GG TCCGACCT
                                     GT  _
GAM642   LOC151248 5'  TCCCGCCTGGGCGACAGAGCGA 81000               T
           GA                     TCTCGCTCTGTTGCCCAGGC GGA
                                  ||||||||||||||||||| |||
                                  AGAGCGAGACAGCGGGTCCG CCT
                                        C
GAM642   LOC151323 3'  TCTGAAGCAGCAGAGTGA    81027          C_
                                  TCGCTCTGTTGC  CAGG
                                  ||||||||||||  ||||
                                  AGTGAGACGACG  GTCT
                                        AA
GAM642   LOC151429 5'  CCTGGTGGGCGGGGTGGGG    86533          GC
                                  TCTCGCTCTGTT  CCAGG
                                  ||||||||||||  |||||
                                  GGGGTGGGGCGG  GGTCC
                                        GT
GAM642   LOC151429 3'  TCCAGCCTGGGCGACAGAGCAA 86549     C
           GA                     TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM642   LOC151429 3'  TCCAGCCTGGGTGACAGAGCAA 86550     C      TG
           GA                     TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A      GT
GAM642   LOC151556 3'  TCCAGCCTGAGCAACAGAGCAA 81085     C        C
           GA                     TCT GCTCTGTTGC CAGGCTGGA
                                  ||| |||||||||| |||||||||
                                  AGA CGAGACAACG GTCCGACCT
                                    A         A
GAM642   LOC151556 5'  TCTGGTTGGAGTTGGAGGGTGA 81086          GTT  _   G TG
           GA                     TCTCGCTCT   GC CCAG C  GA
                                  |||||||||   || |||| |  ||
                                  AGAGTGGGA   TG GGTT G  CT
                                       GGT  A    _ GT
GAM642   LOC151602 3'  ACTCCAGCTTGGGTGACAGAGC 81101           TG
           GAGA                     TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||||  ||||||||||
                                    AGAGCGAGACA  GGGTTCGACCT
                                          GT          CAC
GAM642   LOC151632 3'  TCCAGCCTGGGCAACAGAGTAA 86651     CG
           GA                     TCT  CTCTGTTGCCCAGGCTGGA
                                  |||  ||||||||||||||||||
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                                AGA  GAGACAACGGGTCCGACCT
                                  AT
GAM642   LOC151720 3'  CTCCAGCCTGGGCGACAGAGCG 81153
                 AGA                TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACAGCGGGTCCGACCT
                                          CA
GAM642   LOC151871 5'  AGACCAGCCTGGGCAACACAGT 57976        C           A
                 GAGG               TCTCGCT TGTTGCCCAGGCTGG
                                    |||||||  ||||||||||||||
                                    GGAGTGA ACAACGGGTCCGACC
                                       C            AGAA
GAM642   LOC151904 3'  ACTCCAGCCTGGGCAACAGAGC 81197
                 GAGA               TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACAACGGGTCCGACCT
                                          CAC
GAM642   LOC152002 3'  TCCAGCCTGGACGACAGAGTGA 81268           C
                 GA                 TCTCGCTCTGTTG CCAGGCTGGA
                                    ||||||||||||| ||||||||||
                                    AGAGTGAGACAGC GGTCCGACCT
                                          A
GAM642   LOC152106 3'  TCCAGCCTGGTCGACAGAGTGA 70598           C
                 GA                 TCTCGCTCTGTTG CCAGGCTGGA
                                    ||||||||||||| ||||||||||
                                    AGAGTGAGACAGC GGTCCGACCT
                                          T
GAM642   LOC152263 3'  TCCAGCCAGGATGACAGAGCAA 86860     C      GC  A
                 GA                 TCT GCTCTGTT  CC GGCTGGA
                                    ||| ||||||||  || |||||||
                                    AGA CGAGACAG  GG CCGACCT
                                      A       TA  A
GAM642   LOC152271 3'  TCCAGCCTGGGCAACAGAGTAA 81365     CG
                 GA                 TCT  CTCTGTTGCCCAGGCTGGA
                                    |||  ||||||||||||||||||
                                    AGA  GAGACAACGGGTCCGACCT
                                      AT
GAM642   LOC152283 3'  TCCAGCCTGGGCAACAAGAGTG 86875          _
                 AGA                TCTCGCTCT GTTGCCCAGGCTGGA
                                    |||||||||  ||||||||||||||
                                    AGAGTGAGA CAACGGGTCCGACCT
                                         A
GAM642   LOC152313 3'  CTCCAGCCTGGGTGACAGAGCG 86851           TG
                 AGA                TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGCGAGACA  GGGTCCGACCT
                                          GT         CA
GAM642   LOC152316 3'  TCCAGCCTAGGCAACAGAGCGA 86794            C
                 GA                 TCTCGCTCTGTTGCC AGGCTGGA
                                    |||||||||||||| ||||||||
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                                AGAGCGAGACAACGG TCCGACCT
                                      A
GAM642   LOC152426 3'  ACTCCAGCCTGGGCGACAGAGT 86886
                GAGA                TCTCGCTCTGTTGCCCAGGCTGGA
                                    |||||||||||||||||||||||
                                    AGAGTGAGACAGCGGGTCCGACCT
                                          CAC
GAM642   LOC152445 3'  TCCAGTCTGGGTAAGAAGAGTG 86966        G_
                A                    TCGCTCT  TTGCCCAGGCTGGA
                                    |||||||  ||||||||||||||
                                    AGTGAGA  AATGGGTCTGACCT
                                       AG
GAM642   LOC152453 3'  CTCCAGCTTGGGTGACAGAGCG 81472           TG
                AGA                   TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGCGAGACA  GGGTTCGACCT
                                          GT          CA
GAM642   LOC152453 3'  CTCCAGCTTGGGTGACAGAGTG 81473           TG
                AGA                   TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTTCGACCT
                                          GT          CA
GAM642   LOC152453 3'  TCCAGCCTGGGCAACAAGAGCG 81480        _
                A                    TCGCTCT GTTGCCCAGGCTGGA
                                    ||||||| ||||||||||||||
                                    AGCGAGA CAACGGGTCCGACCT
                                       A
GAM642   LOC152627 3'  TCCAGCCTGGGCCACAGAGTGA 81516           T
                GA                    TCTCGCTCTGT GCCCAGGCTGGA
                                    ||||||||||| ||||||||||||
                                    AGAGTGAGACA CGGGTCCGACCT
                                          C
GAM642   LOC152641 3'  TCTAGTTCCCGGTGGAATGAGA 81521       C  TG   CCCA
                                    TCTCG TC  TTG    GGCTGGA
                                    ||||| ||  |||    |||||||
                                    AGAGT AG  GGC    TTGATCT
                                       A  GT   CC__
GAM642   LOC152804 3'  ACTCCAGCCTGGGCAACAGAGC 87064
                GAGG                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    |||||||||||||||||||||||
                                    GGAGCGAGACAACGGGTCCGACCT
                                          CAC
GAM642   LOC152804 3'  TCCGGCCTGGGGACAAGAGCAA 87089     C    _  G
                GA                    TCT GCTCT GTT CCCAGGCTGGA
                                    ||| ||||| ||| ||||||||||
                                    AGA CGAGA CAG GGGTCCGGCCT
                                      A    A  _
GAM642   LOC152829 5'  TCCAGCATGGGCAACACAGTGA 81572        C        G
                GA                    TCTCGCT TGTTGCCCA GCTGGA
                                    ||||||| ||||||||| ||||||
```

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                                AGAGTGA ACAACGGGT CGACCT
                                    C       A
GAM642   LOC152860 3'  TCCAGCCTGGGCAGCAAGAGTG 81582       _
           A                     TCGCTCT GTTGCCCAGGCTGGA
                                 ||||||| |||||||||||||||
                                 AGTGAGA CGACGGGTCCGACCT
                                    A
GAM642   LOC152897 3'  CCTGGGTAATATGGTGGGG   81605       C
                                 TCTCGCT TGTTGCCCAGG
                                 ||||||| ||||||||||
                                 GGGGTGG ATAATGGGTCC
                                    T
GAM642   LOC152897 3'  TCCCAGCCTGGGAGACAGAGTG 81610          TG        A
           AGA                    TCTCGCTCTGT  CCCAGGCTGG
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACC
                                        GA         CTA
GAM642   LOC153077 3'  TCCAGCCTGGGCTACAGAGCAA 87133     C      T
           GA                     TCT GCTCTGT GCCCAGGCTGGA
                                  ||| ||||||| ||||||||||||
                                  AGA CGAGACA CGGGTCCGACCT
                                    A       T
GAM642   LOC153146 3'  TCCAGCCTGGGTGACAGAGGGA 87148      G     TG
           GA                     TCTC CTCTGT  CCCAGGCTGGA
                                  |||| ||||||  ||||||||||
                                  AGAG GAGACA  GGGTCCGACCT
                                    G      GT
GAM642   LOC153146 5'  TTCAGCAGGAGTGGAGTGGG   87150        TG  G  CAG
                                  CTCGCTC  TT CC   GCTGGA
                                  |||||||  || ||   ||||||
                                  GGGTGAG  GA GG   CGACTT
                                     GT  _  A__
GAM642   LOC153338 3'  TCCAGCCTGGGTGACAGAGCAA 87198     C      TG
           GA                     TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A       GT
GAM642   LOC153505 5'  TCTAGTGCTGGGTGTGGAGTGA 81708         TG T     _
           GG                     TCTCGCTC  T GCCCAG GCTGGA
                                  ||||||||  | |||||| ||||||
                                  GGAGTGAG  G TGGGTC TGATCT
                                     GT _      G
GAM642   LOC153561 3'  TTGAGCCTGGGCAACAGAGTGA 81754                 G
           GA                     TCTCGCTCTGTTGCCCAGGCT GA
                                  |||||||||||||||||||| ||
                                  AGAGTGAGACAACGGGTCCGA TT
                                              G
GAM642   LOC153577 5'  TCTGGAGCGGGCAGAGCGGGG  87244           _ _
                                  TCTCGCTCTGTT GC CCAGG
                                  |||||||||||| || |||||
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                                GGGGCGAGACGG CG GGTCT
                                      G  A
GAM642  LOC153579 3'  ACTCCAGCCTGGGCGACAGAGC 81760
          GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCCGACCT
                                        CAC
GAM642  LOC153682 3'  TCCAGCCTGAGCGACAGAGCAA 87276     C        C
          GA                      TCT GCTCTGTTGC CAGGCTGGA
                                  ||| |||||||||| |||||||||
                                  AGA CGAGACAGCG GTCCGACCT
                                    A         A
GAM642  LOC153688 3'  GAAGCCTGGGCAATAAGTGAGA 87313        C          GGA
                                  TCTCGCT TGTTGCCCAGGCT
                                  |||||||| ||||||||||||
                                  AGAGTGA ATAACGGGTCCGA
                                      _           AGT
GAM642  LOC153688 3'  TCCAGCCTGGGCGACAGAGGGA 87333      G
          GA                      TCTC CTCTGTTGCCCAGGCTGGA
                                  |||| ||||||||||||||||||||
                                  AGAG GAGACAGCGGGTCCGACCT
                                    G
GAM642  LOC153688 3'  TCTGAGTGGTGGTGGAGGGTGG 87337          G TG  CAG  _
          GG                      TCTCGCTCT T  CC   GCT GGA
                                  |||||||||  |  ||   ||| |||
                                  GGGGTGGGA G  GG   TGA TCT
                                       _ GT  TGG   G
GAM642  LOC153727 3'  TCTAGCCTGGGTGACAGAGAGA 87364      G      TG
          GA                      TCTC CTCTGT  CCCAGGCTGGA
                                  |||| ||||||  ||||||||||||
                                  AGAG GAGACA  GGGTCCGATCT
                                    A      GT
GAM642  LOC154089 3'  TTTAGTCTGGGTGACAGAGCAA 81949     C      TG
          GA                      TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||||
                                  AGA CGAGACA  GGGTCTGATTT
                                    A      GT
GAM642  LOC154386 3'  TCCAGCAGGGGAGGGGTGGGA  81990          GTTG   AG
                                  TCTCGCTCT    CCC  GCTGGA
                                  |||||||||    |||  ||||||
                                  AGGGTGGGG    GGG  CGACCT
                                       A___    GA
GAM642  LOC154739 5'  TCCAGCCTGGGCAACAGGTGAG 87443        T
          A                        TCTCGC CTGTTGCCCAGGCTGGA
                                   ||||||| |||||||||||||||||
                                   AGAGTG GACAACGGGTCCGACCT
                                        _
GAM642  LOC154739 3'  TCCAGCCTGGGTGACAGAGTGA 87444           TG
          GA                      TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
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                                AGAGTGAGACA  GGGTCCGACCT
                                      GT
GAM642   LOC154791 3'  TCCAGCCTGGGCAACAAGAGC  82055      _
                                GCTCT GTTGCCCAGGCTGGA
                                ||||| ||||||||||||||||
                                CGAGA CAACGGGTCCGACCT
                                  A
GAM642   LOC154834 3'  TCCAGTCTTCTGGGGTGGGG   87497         GTTGCCC
                                TCTCGCTCT      AGGCTGGA
                                |||||||||      ||||||||
                                GGGGTGGGG      TCTGACCT
                                     TCT_____
GAM642   LOC154877 3'  TCCAGCCTAGGTGATAGAGCAA 87576     C      TG  C
            GA                    TCT GCTCTGT  CC AGGCTGGA
                                ||| |||||||  || ||||||||
                                AGA CGAGATA  GG TCCGACCT
                                  A      GT  A
GAM642   LOC154992 3'  TTCAGCCTGGGTGACCAAG    82145    CT  TG
                                CT  GT  CCCAGGCTGGA
                                ||  ||  ||||||||||||
                                GA  CA  GGGTCCGACTT
                                 AC  GT
GAM642   LOC155006 3'  TCCAGCCTGGGCGGCAGAGCAA 82176     C
            GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGAGACGGCGGGTCCGACCT
                                  A
GAM642   LOC155054 3'  TCCAGCCTGGGTGACAGAGCAA 82206     C      TG
            GA                    TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM642   LOC155061 3'  TCTAGCTCTCAGCAGAGCTGGG 82192     C        CCCA
                                TCT GCTCTGTTG    GGCTGGA
                                ||| |||||||||    |||||||
                                GGG CGAGACGAC    TCGATCT
                                  T        TC__
GAM642   LOC155072 3'  TCCAACCTGGGTGACAGAGCGA 87672          TG     C
                                TCGCTCTGT  CCCAGG TGGA
                                |||||||||  |||||| ||||
                                AGCGAGACA  GGGTCC ACCT
                                     GT     A
GAM642   LOC155072 3'  TCCAGCCTGGGTGACTGAGCGA 87673         T  TG
            GA                    TCTCGCTC GT  CCCAGGCTGGA
                                ||||||||| ||  ||||||||||||
                                AGAGCGAG CA  GGGTCCGACCT
                                     T  GT
GAM642   LOC155376 3'  ACTCCAGTCTGGGTGACAGAGT 82236           TG
            GAGA                    TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||||
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                                AGAGTGAGACA  GGGTCTGACCT
                                      GT         CAC
GAM642   LOC155376 3'  TCCAGCCTGGGTGACAAAGCAA 82251     C   C   TG
           GA                   TCT GCT TGT  CCCAGGCTGGA
                                ||| ||| |||  ||||||||||
                                AGA CGA ACA  GGGTCCGACCT
                                  A   A   GT
GAM642   LOC155435 3'  TCCCCGTGGCATGCGGGGTGAG 82274          _   CA  CT
           G                    TCTCGCTCTGT TGCC  GG  GGA
                                |||||||||| ||||  ||  |||
                                GGAGTGGGGCG ACGG  CC  CCT
                                      T   TG  __
GAM642   LOC157254 5'  TCCAGAGGGCGCGGCGGGTGGG 82315       T     _  AGG
           G                    TCTCGC CTGTTGC CC   CTGGA
                                |||||| ||||||| ||   |||||
                                GGGGTG GGCGGCG GG   GACCT
                                   _      C  GA_
GAM642   LOC157313 5'  TCGGTACCGAGGGGCGGGG   82325        G   CCCAG
                                TCTCGCTCT TTG    GCTGG
                                ||||||||| |||    |||||
                                GGGGCGGGG AGC    TGGCT
                                     _  CA___
GAM642   LOC157376 3'  TCGGTGGCTCAACGGGTGGGA  82354      T    C_  AG  TG
                                TCTCGC CTGTTG  CC  GC  GA
                                |||||| ||||||  ||  ||  ||
                                AGGGTG GGCAAC  GG  TG  CT
                                   _     TC  __  GT
GAM642   LOC157464 5'  TCCAGCCTGGGCAACGGGCGAG 87752       T
           A                    TCTCGC CTGTTGCCCAGGCTGGA
                                |||||| ||||||||||||||||
                                AGAGCG GGCAACGGGTCCGACCT
                                   _
GAM642   LOC157562 5'  TCCAGCCTGGGCAACATAGTGA 87776       C
           GA                     TCTCGCT TGTTGCCCAGGCTGGA
                                  ||||||| ||||||||||||||||
                                  AGAGTGA ACAACGGGTCCGACCT
                                     T
GAM642   LOC157567 5'  TCCAGCTGCTCGGCCGGGGCGA 82394         TT  CA__
           GA                     TCTCGCTCTG  GCC    GGCTGGA
                                  |||||||||  |||    |||||||
                                  AGAGCGGGGC  CGG    TCGACCT
                                       __  CTCG
GAM642   LOC157657 3'  TCCAGCCTGGACAACACAGTGA 82437       C    C
           GA                     TCTCGCT TGTTG CCAGGCTGGA
                                  ||||||| ||||| ||||||||||
                                  AGAGTGA ACAAC GGTCCGACCT
                                     C    A
GAM642   LOC157660 3'  TCCAGCGTGGGCAACAGAGTGA 87807             G
           GA                     TCTCGCTCTGTTGCCCA GCTGGA
                                  |||||||||||||||| ||||||
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                                AGAGTGAGACAACGGGT CGACCT
                                        G
GAM642  LOC157663 3'  TGCAGCAGGGTGGCAGGGTCAG 82456     C      TG   AG    GA
          G                      TCT GCTCTGT  CCC  GCTG
                                 ||| |||||||  |||  ||||
                                 GGA TGGGACG  GGG  CGAC
                                   C      GT   A_    GTT
GAM642  LOC157737 3'  TCCAGCCTGGGCAACAGAGAGA 87846      G
          GA                     TCTC CTCTGTTGCCCAGGCTGGA
                                 |||| ||||||||||||||||||
                                 AGAG GAGACAACGGGTCCGACCT
                                   A
GAM642  LOC157848 3'  CCAGCTGTTGGGGCGGGG    82517          TTGCCCA
                                 TCTCGCTCTG      GGCTGG
                                 ||||||||||      ||||||
                                 GGGGCGGGGT      TCGACC
                                       TG_____
GAM642  LOC158156 3'  TTTGGCTCTTAACAGAGTGG   82631          CCCA   TG
                                 TCGCTCTGTTG    GGC  GA
                                 ||||||||||    |||  ||
                                 GGTGAGACAAT    TCG  TT
                                       TC__   GT
GAM642  LOC158160 3'  TCCAGCCTGGGTGACAGCGAGA 73476        CT  TG
                                 TCTCGCT  GT  CCCAGGCTGGA
                                 |||||||  ||  ||||||||||
                                 AGAGCGA  CA  GGGTCCGACCT
                                     __  GT
GAM642  LOC158187 3'  TCCAGCCTGGGTGACAGAGCAA 87998     C      TG
          GA                     TCT GCTCTGT  CCCAGGCTGGA
                                 ||| |||||||  ||||||||||
                                 AGA CGAGACA  GGGTCCGACCT
                                   A      GT
GAM642  LOC158191 3'  CCAGCTTGGGCCTGGGG     82668      GTT
                                 CTCT   GCCCAGGCTGG
                                 ||||   ||||||||||
                                 GGGG   CGGGTTCGACC
                                    TC_
GAM642  LOC158235 3'  TCCAGCCTGGGCAACACAGAGA 88008      G  C
          GA                     TCTC CT TGTTGCCCAGGCTGGA
                                 |||| || ||||||||||||||||
                                 AGAG GA ACAACGGGTCCGACCT
                                   A  C
GAM642  LOC158288 5'  GACCAGCCTGGGCAACATAGTG 88022        C            A
          AGG                     TCTCGCT TGTTGCCCAGGCTGG
                                  ||||||| |||||||||||||||
                                  GGAGTGA ACAACGGGTCCGACC
                                     T             AGA
GAM642  LOC158292 5'  ACTCCAGCCTGGGCGACAGAGC 88034
          GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                  |||||||||||||||||||||||||
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                                AGAGCGAGACAGCGGGTCCGACCT
                                      CAC
GAM642   LOC158292 5'  TCCAGCCTGGGCAACAGAGCAA 88056     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAACGGGTCCGACCT
                                    A
GAM642   LOC158310 3'  AGACCAGCCTGGGCAACATAGT 88073         C             A
                GAGA                TCTCGCT TGTTGCCCAGGCTGG
                                  ||||||| ||||||||||||||||
                                  AGAGTGA ACAACGGGTCCGACC
                                      T             AGAG
GAM642   LOC158310 3'  TCTGCCGACTGGAATGGAGTGA 88093            G  CA__   T
                GA                TCTCGCTCTGTT CC    GGC GGA
                                  |||||||||||| ||    ||| |||
                                  AGAGTGAGGTAA GG    CCG TCT
                                        _  TCAG   _
GAM642   LOC158337 3'  ATTCCAGCCTGGGTGACAGAGC 88107           TG
                GAGA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                      GT          TAC
GAM642   LOC158364 5'  TCCAACATGCAGTAGAATGAGG 82758       C       CCAGGC
                                  TCTCG TCTGTTGC      TGGA
                                  ||||| ||||||||      ||||
                                  GGAGT AGATGACG      ACCT
                                    A       TACA__
GAM642   LOC158382 5'  ACCAGCCTGGGCAACATAGTGA 88121         C             A
                GA                TCTCGCT TGTTGCCCAGGCTGG
                                  ||||||| ||||||||||||||||
                                  AGAGTGA ACAACGGGTCCGACC
                                      T             AT
GAM642   LOC158382 5'  TCCAGAACCCAGCAGAGCAGA  88128     C       CCCAGG
                                  TCT GCTCTGTTG      CTGGA
                                  ||| |||||||||      |||||
                                  AGA CGAGACGAC      GACCT
                                    _        CCAA__
GAM642   LOC158434 3'  TCTAGCCTGGGTGACAAAGTGA 88163         C   TG
                GA                TCTCGCT TGT  CCCAGGCTGGA
                                  ||||||| |||  ||||||||||
                                  AGAGTGA ACA  GGGTCCGATCT
                                      A   GT
GAM642   LOC158677 5'  TCCAGCCTGGGTGACAGAGCAA 88252     C      TG
                GA                TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A       GT
GAM642   LOC158819 3'  ACTCCAGCCTGGGTGACAGAGC 88263           TG
                GAGA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
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                                AGAGCGAGACA  GGGTCCGACCT
                                      GT          CAC
GAM642   LOC158957 3'  TCCAGTTGGACTCCAAAAGAGT 82931         G   C___    G
           GGGG                    TCTCGCTCT TTG    CCAG CTGGA
                                |||||||||  |||    |||| |||||
                                GGGGTGAGA AAC    GGTT GACCT
                                     A   CTCA   _
GAM642   LOC158987 3'  CTCCAGCCTGGGTGACAGAGCG 88323           TG
           AGA                     TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      GT          CA
GAM642   LOC158987 3'  TCCAGCCTGGGCAACAGAGGGA 88334     G
           G                      CTC CTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||
                                GAG GAGACAACGGGTCCGACCT
                                  G
GAM642   LOC158987 3'  TCCAGCCTGGGCAACATAGTGA 88335         C
           GA                      TCTCGCT TGTTGCCCAGGCTGGA
                                |||||||  ||||||||||||||||
                                AGAGTGA ACAACGGGTCCGACCT
                                    T
GAM642   LOC159036 3'  ACTCCAGCCTGGGCGACAGAGT 88339
           GAGG                    TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                GGAGTGAGACAGCGGGTCCGACCT
                                          CAC
GAM642   LOC159053 3'  TCCTGCTTGGGCGACAGAGTGA 88378                 T
           GA                      TCTCGCTCTGTTGCCCAGGC GGA
                                |||||||||||||||||| |||
                                AGAGTGAGACAGCGGGTTCG CCT
                                          T
GAM642   LOC160336 5'  CCGTGTGAATGGGGTGAGA    83086           GCC  G  T
                                TCTCGCTCTGTT   CA GC GG
                                ||||||||||||   || || ||
                                AGAGTGGGGTAA   GT TG CC
                                     ____  G  _
GAM642   LOC161823 3'  TCCAGCCTGGGCAACAGAGTGA 83176
                                TCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||
                                AGTGAGACAACGGGTCCGACCT

GAM642   LOC162333 3'  CCAGGTGGCCAGAGCGGGG    88489          TT   CAGG
                                TCTCGCTCTG  GCC    CTGG
                                ||||||||||  |||    ||||
                                GGGGCGAGAC  CGG    GACC
                                     __   TG__
GAM642   LOC162333 5'  CGGTGGGAGCAGGGCAGA    88491     C       G   AG  TG
                                TCT GCTCTGTT CCC  GC  G
                                ||| ||||||||  |||  ||  |
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                                AGA CGGGACGA GGG  TG  C
                                  _      _  __ GT
GAM642  LOC162962 3'  TCCAGCCTGGGTGACAGCGAGA 83260       CT  TG
                                TCTCGCT  GT  CCCAGGCTGGA
                                |||||||  ||  ||||||||||||
                                AGAGCGA  CA  GGGTCCGACCT
                                   __ GT
GAM642  LOC163412 5'  TGGTGGCCGGGGTGGGG     83020         TT   CAG  TG
                                TCTCGCTCTG  GCC   GC  G
                                ||||||||||  |||   ||  |
                                GGGGTGGGGC  CGG   TG  T
                                      __  ____ GT
GAM642  LOC164395 5'  TCTAGCAGAAACGTGACGGGGC 83404     C      TG CCAG__
           TGGA                    TCT GCTCTGT  C      GCTGGA
                                |||  |||||||  |      ||||||
                                AGG CGGGGCA  G      CGATCT
                                  T      GT CAAAGA
GAM642  LOC164714 3'  CCACCGGCAGCAGGGGGGG    88580     G        CA  C
                                CTC CTCTGTTGCC  GG TGG
                                |||  ||||||||||  || |||
                                GGG GGGACGACGG  CC ACC
                                  G         __ _
GAM642  LOC165283 3'  TCCAGGATGCACAGAGTGAGA  88548          T  CCAGG
                                TCTCGCTCTGT GC     CTGGA
                                ||||||||||| ||     |||||
                                AGAGTGAGACA CG     GACCT
                                      _  TAG__
GAM642  LOC168574 5'  TCCAGGGCGCAGCAGGGGAGG  83594      G        _  AGG
                                TCTC CTCTGTTGC CC   CTGGA
                                ||||  |||||||| ||   |||||
                                GGAG GGGACGACG GG   GACCT
                                  _        C  ____
GAM642  LOC170395 3'  TCAAGCCTGGGCAACAGAGTGA 76876                 G
           GA                     TCTCGCTCTGTTGCCCAGGCT GA
                                |||||||||||||||||||| ||
                                AGAGTGAGACAACGGGTCCGA CT
                                        A
GAM642  LOC170395 3'  TCCAGCCTGGGCAACAAGAGC  76877       _
                                GCTCT GTTGCCCAGGCTGGA
                                |||||  ||||||||||||||||
                                CGAGA CAACGGGTCCGACCT
                                   A
GAM642  LOC196047 5'  ACTCCAGCCTGGGTGACAGAGC 91140           TG
           GAGA                     TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      GT          CAC
GAM642  LOC196529 3'  TCTAGCCTGGGTGACAAGAGC  89141      _  TG
                                GCTCT GT  CCCAGGCTGGA
                                |||||  ||  ||||||||||
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                                CGAGA CA  GGGTCCGATCT
                                  A  GT
GAM642  LOC196540 3'  CTCCAGCCTGGGTGACAGAGTG 91200          TG
                AGA                TCTCGCTCTGT  CCCAGGCTGGA
                                   |||||||||||  ||||||||||
                                   AGAGTGAGACA  GGGTCCGACCT
                                         GT          CG
GAM642  LOC196761 3'  TCCAGCCTGGGCGATAGAGGGA 91121      G
                GA                  TCTC CTCTGTTGCCCAGGCTGGA
                                    |||| ||||||||||||||||||
                                    AGAG GAGATAGCGGGTCCGACCT
                                      G
GAM642  LOC196872 3'  TCTAGGTGAAGGGCGTGGAGTG 89160        TG T    AGG__
                AGA                TCTCGCTC  T GCCC     CTGGA
                                   ||||||||  | ||||     |||||
                                   AGAGTGAG  G CGGG     GATCT
                                       GT _    AAGTG
GAM642  LOC197132 3'  TCCAGCTTGGGAGACAAGAGCG 89230        _ TG
                A                   TCGCTCT GT  CCCAGGCTGGA
                                    |||||||  ||  ||||||||||
                                    AGCGAGA CA  GGGTTCGACCT
                                        A  GA
GAM642  LOC197196 3'  TCCAGCCTGGGCGACAAGAGCG 91306        _
                A                   TCGCTCT GTTGCCCAGGCTGGA
                                    |||||||  ||||||||||||||
                                    AGCGAGA CAGCGGGTCCGACCT
                                        A
GAM642  LOC197201 3'  TCCAGCCTGGGCAACACAGCAA 89288     C   C
                GA                  TCT GCT TGTTGCCCAGGCTGGA
                                    |||  |||  ||||||||||||||||
                                    AGA CGA ACAACGGGTCCGACCT
                                      A   C
GAM642  LOC197201 3'  TCTAGCCTGGGCAACAAGAGTG 89290        _
                A                   TCGCTCT GTTGCCCAGGCTGGA
                                    |||||||  ||||||||||||||
                                    AGTGAGA CAACGGGTCCGATCT
                                        A
GAM642  LOC197259 5'  TCCGGTACAGTCAGCAGAGTGC 89303     _        CCCAG
                AGG                 TCT CGCTCTGTTG     GCTGGA
                                    |||  ||||||||||     ||||||
                                    GGA GTGAGACGAC     TGGCCT
                                      C          TGACA
GAM642  LOC197358 3'  TTTGGTAGGGGTAACAGAGGGG 89452      G         AG  TG
                A                   TCTC CTCTGTTGCCC  GC  GA
                                    ||||  ||||||||||  ||  ||
                                    AGGG GAGACAATGGG  TG  TT
                                      _          GA  GT
GAM642  LOC197362 3'  TTCCAGCCTGGGTGACAGAGTG 91313          TG
                AGA                 TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
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                                AGAGTGAGACA  GGGTCCGACCT
                                      GT          TA
GAM642  LOC199221 3'  CCCGGGTGGCAGAGTCGGA   81166     C      TG   A
                                TCT GCTCTGT  CCC GG
                                ||| |||||||  ||| ||
                                AGG TGAGACG  GGG CC
                                  C      GT   C
GAM642  LOC199676 3'  TCCAGCCTGGGAGACAGAGTTA 91362     C      TG
          GA                      TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA TGAGACA  GGGTCCGACCT
                                  T      GA
GAM642  LOC199729 3'  TCCAGCCAGGGCAACAGAGTGA 73397              A
          GA                      TCTCGCTCTGTTGCCC GGCTGGA
                                |||||||||||||| |||||||
                                AGAGTGAGACAACGGG CCGACCT
                                        A
GAM642  LOC199733 3'  TCCAACCTGGGCAACAGAGCCA 91443     C            C
          GA                      TCT GCTCTGTTGCCCAGG TGGA
                                ||| |||||||||||||| ||||
                                AGA CGAGACAACGGGTCC ACCT
                                  C             A
GAM642  LOC199733 5'  TCCGGTGCCGACGGAGCCGGG  91444     C        CCCAG
                                TCT GCTCTGTTG     GCTGGA
                                ||| |||||||||     ||||||
                                GGG CGAGGCAGC     TGGCCT
                                  C         CG___
GAM642  LOC199745 5'  TTCGTCACGTGACGAGGGCGGG 89721          _  TG CCA   TGGA
          A                       TCTCGCTCT GT  C   GGC
                                ||||||||| ||  |   |||
                                AGGGCGGGA CA  G   CTG
                                      G  GT CA_   CTT
GAM642  LOC199786 3'  TCCAGCCTGGGTGATGGGAGTG 89767          _  TG
          AGA                       TCTCGCTCT GT  CCCAGGCTGGA
                                ||||||||| ||  ||||||||||
                                AGAGTGAGG TA  GGGTCCGACCT
                                      G  GT
GAM642  LOC199858 3'  CTCCAGCCTGGGCGACAGAGCG 89798
          AGA                       TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||||
                                AGAGCGAGACAGCGGGTCCGACCT
                                           CA
GAM642  LOC199923 3'  GACCAGCCTGGGCAATACAGCG 89872         C            A
          AGA                       TCTCGCT TGTTGCCCAGGCTGG
                                |||||||| ||||||||||||||
                                AGAGCGA ATAACGGGTCCGACC
                                   C             AGA
GAM642  LOC199923 3'  TCCAGCCTGGACGACAGAGCAA 89874     C        C
          GA                      TCT GCTCTGTTG CCAGGCTGGA
                                ||| ||||||||| ||||||||||
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                                AGA CGAGACAGC GGTCCGACCT
                                  A       A
GAM642   LOC199923 3'  TCCAGCCTGGGCAACTGAGC   89875     T
                                GCTC GTTGCCCAGGCTGGA
                                |||| ||||||||||||||
                                CGAG CAACGGGTCCGACCT
                                  T
GAM642   LOC199958 3'  AGGCCAGGCTGGGCAACAGAGT 91488              G   A
           GAGG                   TCTCGCTCTGTTGCCCAG CTGG
                                |||||||||||||||| ||||
                                GGAGTGAGACAACGGGTC GACC
                                         G   GGAG
GAM642   LOC200014 3'  TCCAGCCTGGGCGACAGAGCAA 89948     C
           GA                     TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||
                                AGA CGAGACAGCGGGTCCGACCT
                                  A
GAM642   LOC200014 3'  TTTAGTGGGTCACAGAGCGGGA 89949          T   AG
                                TCTCGCTCTGT GCCC  GCTGGA
                                |||||||||| ||||  ||||||
                                AGGGCGAGACA TGGG  TGATTT
                                      C   __
GAM642   LOC200014 3'  TTTGGGGGATAACAGGGCTGGA 89950     C       _  AGG TG
                                TCT GCTCTGTTG CCC   C  GA
                                ||| ||||||||| |||   |  ||
                                AGG CGGGACAAT GGG   G  TT
                                  T       A  ___ GT
GAM642   LOC200058 3'  AGCAGCCTTGGTATGGGGTGGG 89956          T  C     GA
           G                     TCTCGCTCTGT GCC AGGCTG
                                |||||||||| ||| ||||||
                                GGGGTGGGGTA TGG TCCGAC
                                      _  T     GAC
GAM642   LOC200093 3'  CCAGCTCTGCAGGGTGGGG   63764          TTGCC  _
                                TCTCGCTCTG    CAG GCTGG
                                ||||||||||    ||| |||||
                                GGGGTGGGAC    GTC CGACC
                                      _____  T
GAM642   LOC200205 3'  CCAGGAGCGTGGGGTGGGG   90025        TG T  _  AGGC
                                TCTCGCTC  T GC CC   TGG
                                |||||||  | || ||   |||
                                GGGGTGGG  G CG GG   ACC
                                     GT _  A  ____
GAM642   LOC200227 3'  TCTAGCCTGGGTGACAGAATGA 90044      C    TG
           GA                     TCTCG TCTGT  CCCAGGCTGGA
                                ||||| |||||  ||||||||||
                                AGAGT AGACA  GGGTCCGATCT
                                  A    GT
GAM642   LOC200269 3'  TCTGGCCTCCCTGGCGGGGTGG 90077          CCC   TG
                                TCGCTCTGTTG   AGGC  GA
                                ||||||||||   ||||  ||
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                                GGTGGGGCGGT   TCCG  CT
                                      CCC    GT
GAM642   LOC200301 5'  TCTGGAACTAACAGAGTGAGA  90157           C__
                                TCTCGCTCTGTTG   CCAGG
                                ||||||||||||   |||||
                                AGAGTGAGACAAT   GGTCT
                                     CAA
GAM642   LOC200317 3'  TCCAGCCTGGGCAACAAGAGTG 90229        _
           A                     TCGCTCT GTTGCCCAGGCTGGA
                                 ||||||| ||||||||||||||||
                                 AGTGAGA CAACGGGTCCGACCT
                                    A
GAM642   LOC200399 3'  TCTGAAGCAGCAGAGTGA    90243          C_
                                TCGCTCTGTTGC  CAGG
                                ||||||||||||  ||||
                                AGTGAGACGACG  GTCT
                                     AA
GAM642   LOC200728 3'  TCCATCCTGGGTGACAGAGCAA 91687     C      TG     C
           GA                     TCT GCTCTGT  CCCAGG TGGA
                                  ||| |||||||  |||||| ||||
                                  AGA CGAGACA  GGGTCC ACCT
                                    A      GT     T
GAM642   LOC200731 3'  ATCCAGCCCCAGCTGGGTGACA 91691          TG   _____
           GAGTGAGA                TCTCGCTCTGT  CCCA    GGCTGGA   T
                                   ||||||||||  ||||    |||||||  |
                                   AGAGTGAGACA  GGGT    CCGACCT   A
                                         GT    CGACC
GAM642   LOC200734 3'  TCCAGTTTGGAAAAGGAGCAGA 90282      _    G  GC
           GA                     TCTC GCTCT TT  CCAGGCTGGA
                                  |||| ||||| ||  ||||||||||
                                  AGAG CGAGG AA  GGTTTGACCT
                                    A    A  A_
GAM642   LOC200734 3'  TTCACCCGTAATAGACTGAGA  90286      C      CCA  C
                                TCTCG TCTGTTGC   GG TGGA
                                ||||| ||||||||   || ||||
                                AGAGT AGATAATG   CC ACTT
                                   C       ___  C
GAM642   LOC200803 3'  ATTCCACCCTGGGCAACAGGGT 90296               C
           GAGA                    TCTCGCTCTGTTGCCCAGG TGGA
                                   |||||||||||||||||| ||||
                                   AGAGTGGGACAACGGGTCC ACCT
                                            C    TAC
GAM642   LOC200853 3'  TCCAGCCTGGGAGACAGAGCGA 90335         TG
                                TCGCTCTGT  CCCAGGCTGGA
                                |||||||||  ||||||||||
                                AGCGAGACA  GGGTCCGACCT
                                     GA
GAM642   LOC200904 3'  TCTAGCCTGGGCAACAGAGTAA 91785     CG
           GA                     TCT  CTCTGTTGCCCAGGCTGGA
                                  |||  ||||||||||||||||||
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                                AGA  GAGACAACGGGTCCGATCT
                                  AT
GAM642   LOC200918 3'  TCCAGCCTGGGCGACAAGAGTG 90370       _
             A                    TCGCTCT GTTGCCCAGGCTGGA
                                  ||||||| ||||||||||||||
                                  AGTGAGA CAGCGGGTCCGACCT
                                     A
GAM642   LOC200918 3'  TTTGGATTCAATGAGTGGGA   90372        T   C__
                                  TCTCGCTC GTTG   CCAGG
                                  |||||||| ||||   |||||
                                  AGGGTGAG TAAC   GGTTT
                                       _   TTA
GAM642   LOC200939 3'  TCCAGTCTGGGTGAGACCTGAG 91800      CTCTG TG
             G                    TCTCG    T  CCCAGGCTGGA
                                  |||||    |  ||||||||||
                                  GGAGT    A  GGGTCTGACCT
                                     CCAG_ GT
GAM642   LOC200940 3'  CTCCAGCCTGGGCGACAGAGTG 90392
             AGA                     TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAGCGGGTCCGACCT
                                                CA
GAM642   LOC201102 5'  TCCGGGGCCTGGCGGGCCGGGG 89473      CT   TTGC     __
                                  TCTCG  CTG   CCAGGCT  GGA
                                  |||||  |||   |||||||  |||
                                  GGGGC  GGC   GGTCCGG  CCT
                                     CG  ____      GG
GAM642   LOC201109 3'  CCAGGCCTGGGCAATATGGCGA 91326        C         _  A
             GA                      TCTCGCT TGTTGCCCAGGC TGG
                                  ||||||| |||||||||||| |||
                                  AGAGCGG ATAACGGGTCCG ACC
                                     T          G  G
GAM642   LOC201173 5'  CCGGCAGGGCAGGATGGGA   88678      C  GT    AG
                                  TCTCG TCT  TGCCC  GCTGG
                                  ||||| |||  |||||  |||||
                                  AGGGT AGG  ACGGG  CGGCC
                                     _  __     A_
GAM642   LOC201173 3'  TCCAGCCTGGGCGACAGAGCAA 88694     C
             GA                      TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM642   LOC201182 5'  TCCAGCCTGGTCAACAGAGCAA 91338     C        C
             GA                      TCT GCTCTGTTG CCAGGCTGGA
                                  ||| ||||||||| ||||||||||
                                  AGA CGAGACAAC GGTCCGACCT
                                    A        T
GAM642   LOC201220 5'  CCGGCAGGGCAGGATGGGA   88713      C  GT    AG
                                  TCTCG TCT  TGCCC  GCTGG
                                  ||||| |||  |||||  |||||
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                                AGGGT AGG  ACGGG  CGGCC
                                  _  __     A_
GAM642  LOC201220 3'  TCCAGCCTGGGTGACAGAGCAA 88727     C      TG
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGAGACA  GGGTCCGACCT
                                      A       GT
GAM642  LOC201252 3'  TCTAGCCTGAGTGACAGAGCAG 89556     C      TG C
                A                   TCT GCTCTGT  C CAGGCTGGA
                                    ||| |||||||  | |||||||||
                                    AGA CGAGACA  G GTCCGATCT
                                      _       GT A
GAM642  LOC201264 3'  TCTCACTGGGCGACAGAGCCAG 91349     C            GCT
                A                   TCT GCTCTGTTGCCCAG   GGA
                                    ||| ||||||||||||||   |||
                                    AGA CGAGACAGCGGGTC   TCT
                                      C            AC_
GAM642  LOC201562 3'  TTTGGGGGGCAGGGTGGGG     90417            G
                                    TCTCGCTCTGTT CCCAGG
                                    |||||||||||| ||||||
                                    GGGGTGGGACGG GGGTTT
                                                 _
GAM642  LOC201564 3'  TCCAGCCTGGGCAACAAGAGC  81276       _
                                    GCTCT GTTGCCCAGGCTGGA
                                    ||||| ||||||||||||||
                                    CGAGA CAACGGGTCCGACCT
                                       A
GAM642  LOC201627 3'  TCAGTGGCAGCGGAGTGGA    90462    T          CAG
                                    TC CGCTCTGTTGCC   GCTGG
                                    || ||||||||||||   |||||
                                    AG GTGAGGCGACGG   TGACT
                                      _          ____
GAM642  LOC201627 3'  TCCAGCTTGGGTGACACAGTGA 90463         C   TG
                GA                    TCTCGCT TGT  CCCAGGCTGGA
                                      ||||||| |||  ||||||||||
                                      AGAGTGA ACA  GGGTTCGACCT
                                         C   GT
GAM642  LOC201689 3'  ACTCCAGCCTGGGTGACAGGGT 67728           TG
                GAGA                    TCTCGCTCTGT  CCCAGGCTGGA
                                        ||||||||||  ||||||||||
                                        AGAGTGGGACA  GGGTCCGACCT
                                             GT          CAC
GAM642  LOC201689 3'  AGACCAGCCTGGGCAACATAGT 67729         C            A
                GAGA                    TCTCGCT TGTTGCCCAGGCTGG
                                        ||||||| |||||||||||||||
                                        AGAGTGA ACAACGGGTCCGACC
                                           T             AGAA
GAM642  LOC201705 3'  TCCAGCCTGGGTGACAGAGTCA 91856     C      TG
                GA                    TCT GCTCTGT  CCCAGGCTGGA
                                      ||| |||||||  ||||||||||
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                                AGA TGAGACA  GGGTCCGACCT
                                  C      GT
GAM642   LOC201895 3'  TCCAGCCTAAGCAATAGAGCGA 90548            CC
                GA                TCTCGCTCTGTTGC  AGGCTGGA
                                  ||||||||||||||  ||||||||
                                  AGAGCGAGATAACG  TCCGACCT
                                        AA
GAM642   LOC201911 3'  TCCAGCCTGGGCAACAAGAGC  91869      _
                                  GCTCT GTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||||
                                  CGAGA CAACGGGTCCGACCT
                                    A
GAM642   LOC201931 3'  ACTCCAGCCTGGGCGACAGAGC 90558
                GAGA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCCGACCT
                                           CAC
GAM642   LOC202020 3'  TCCAGCCCGGGCGACAGAGTGA 90603              A
                GA                TCTCGCTCTGTTGCCC GGCTGGA
                                  |||||||||||||||| |||||||
                                  AGAGTGAGACAGCGGG CCGACCT
                                           C
GAM642   LOC202781 3'  CTCCAGCCTGGGCGACAGAGCG 91970
                AGA                 TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCCGACCT
                                           CA
GAM642   LOC202868 3'  CTCCAGCCTGGGTGACAGAGCG 92001          TG
                AGA                 TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GT         CA
GAM642   LOC202868 3'  TCCAACCTGGGTGACAGAGCGA 92009         TG     C
                                  TCGCTCTGT  CCCAGG TGGA
                                  |||||||||  |||||| ||||
                                  AGCGAGACA  GGGTCC ACCT
                                        GT     A
GAM642   LOC203025 3'  TCCAGCCTGGGCAACAAGAGC  90749      _
                                  GCTCT GTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||||
                                  CGAGA CAACGGGTCCGACCT
                                    A
GAM642   LOC203052 3'  AGGGCTGCAGCCAGGGTGAGG  92075        _   CCA   GGA
                                  TCTCGCTCTG TTGC   GGCT
                                  |||||||||| ||||   ||||
                                  GGAGTGGGAC GACG   TCGG
                                        C    ___    GAA
GAM642   LOC203083 3'  TCCAGCCTGGGCAACAGAGTAA 92095     CG
                GA                  TCT  CTCTGTTGCCCAGGCTGGA
                                  |||  ||||||||||||||||||
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                                AGA  GAGACAACGGGTCCGACCT
                                  AT
GAM642   LOC203197 5'  TCGGGGTTGGGCGACCGAGCGG 90818        T       G  G
            GG                    TCTCGCTC GTTGCCCAG CT GA
                                  |||||||| ||||||||| || ||
                                  GGGGCGAG CAGCGGGTT GG CT
                                      C       G  G  C
GAM642   LOC203235 5'  TCCAGCCTGGCCTCAGAAAGGA 92100         GT__  C__
            GCGGGG                  TCTCGCTCT   TG   CCAGGCTGGA
                                  |||||||||   ||   ||||||||||
                                  GGGGCGAGG   AC   GGTCCGACCT
                                      AAAG  TCC
GAM642   LOC203246 3'  TCCCGCCTGGGCGACAGAACGA 90838      C          T
            GA                    TCTCG TCTGTTGCCCAGGC GGA
                                  ||||| |||||||||||||| |||
                                  AGAGC AGACAGCGGGTCCG CCT
                                     A           C
GAM642   LOC203260 3'  CCTGGGAGGTGGGGCGGGG   90849        TG TG
                                  TCTCGCTC  T  CCCAGG
                                  |||||||| | ||||||
                                  GGGGCGGG  G  GGGTCC
                                      GT GA
GAM642   LOC203276 3'  ACTCCAGCCTGGGCAACAGAGT 92107
            GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                  |||||||||||||||||||||||
                                  AGAGTGAGACAACGGGTCCGACCT
                                           CAA
GAM642   LOC203276 3'  TCCAGCCTGGGTGACACAGTGA 92131       C   TG
            GA                    TCTCGCT TGT  CCCAGGCTGGA
                                  ||||||| |||  ||||||||||
                                  AGAGTGA ACA  GGGTCCGACCT
                                      C   GT
GAM642   LOC203305 3'  ACTCCAGCCTGGGCAACAGAGT 92160
            GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                  |||||||||||||||||||||||
                                  AGAGTGAGACAACGGGTCCGACCT
                                           CAA
GAM642   LOC203305 3'  TCCAGCCTGGGTGACACAGTGA 92184       C   TG
            GA                    TCTCGCT TGT  CCCAGGCTGGA
                                  ||||||| |||  ||||||||||
                                  AGAGTGA ACA  GGGTCCGACCT
                                      C   GT
GAM642   LOC203350 3'  TCCAGCCTGGATGACAGAGTGA 92250          GC
            GA                    TCTCGCTCTGTT  CCAGGCTGGA
                                  ||||||||||||  ||||||||||
                                  AGAGTGAGACAG  GGTCCGACCT
                                        TA
GAM642   LOC203378 3'  TCCAGCCTGGGCGACAGAACAA 92303     CGC
            GA                    TCT   TCTGTTGCCCAGGCTGGA
                                  |||   ||||||||||||||||||
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                                AGA   AGACAGCGGGTCCGACCT
                                  ACA
GAM642   LOC203378 3'  TCCTGCCTGGGTGACACAGCGA 92305        C   TG      T
                GA                  TCTCGCT TGT  CCCAGGC GGA
                                    ||||||| |||  ||||||| |||
                                    AGAGCGA ACA  GGGTCCG CCT
                                       C   GT      T
GAM642   LOC203397 3'  TCCAGCTGCACAGCGGGCAGGG 90905           _  CCA__
                TGAGA                 TCTCGCTCTGTT GC     GGCTGGA
                                    ||||||||||||| ||     |||||||
                                    AGAGTGGGACGG CG     TCGACCT
                                          G  ACACG
GAM642   LOC203554 5'  TTCAGCGGGAGGCAGCAGAGGG 92329      G         CAG_
                GA                  TCTC CTCTGTTGCC    GCTGGA
                                    |||| ||||||||||    ||||||
                                    AGGG GAGACGACGG    CGACTT
                                      _         AGGG
GAM642   LOC204084 5'  CCGGGCGGTGGATGAGA     90995       C  TG     A
                                    TCTCG TC  TTGCCC GG
                                    ||||| ||  |||||| ||
                                    AGAGT AG  GGCGGG CC
                                       _ GT     _
GAM642   LOC204804 3'  TTTGGTTTCTGCTTATGGTGGG 91058        C  TT  CC    TG
                G                   TCTCGCT TG  GC  AGGC  GA
                                    ||||||| ||  ||  ||||  ||
                                    GGGGTGG AT  CG  TTTG  TT
                                       T  T_  TC    GT
GAM642   LOC205327 3'  TCCAACCTGGGCAACATAGTGG 91072         C         C
                GA                  TCTCGCT TGTTGCCCAGG TGGA
                                    ||||||| |||||||||| ||||
                                    AGGGTGA ACAACGGGTCC ACCT
                                       T         A
GAM642   LOC206389 5'  TCCGGCCGGAGCCGGCGGAGCT 92403     C       _ _  A
                GGA                   TCT GCTCTGTTG C CC GGCTGGA
                                    ||| ||||||||| | || |||||||
                                    AGG CGAGGCGGC G GG CCGGCCT
                                      T        C A  _
GAM642   LOC206962 5'  TCCAAGATGGCGGCGGGGCGGG 91109              CAGG  _
                G                   TCTCGCTCTGTTGCC    CT GGA
                                    ||||||||||||||    || |||
                                    GGGGCGGGGCGGCGG    GA CCT
                                          TA__  A
GAM642   LOC219347 3'  ACTCCAGCCTGGGCAACAGAGT 94570
                GAGA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    |||||||||||||||||||||||
                                    AGAGTGAGACAACGGGTCCGACCT
                                                CAC
GAM642   LOC219513 3'  GCGGGGGCGCCAGGGCGGGG   95986          T    AG
                                    TCTCGCTCTG TGCCC  GC
                                    |||||||||| |||||  ||
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                                GGGGCGGGAC GCGGG  CG
                                      C     GG
GAM642   LOC219540 3'  ACTCCAGCCTGGGCGACAGAGC 95237
            GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACAGCGGGTCCGACCT
                                          CAC
GAM642   LOC219627 3'  TCCAGCCTGGGCAACAAGCGA  93812       C
                                    TCGCT TGTTGCCCAGGCTGGA
                                    ||||| ||||||||||||||||
                                    AGCGA ACAACGGGTCCGACCT
                                      _
GAM642   LOC219649 3'  ACTCCAGCCTGGGCGACAGAGT 94540
            GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAGCGGGTCCGACCT
                                          CAC
GAM642   LOC219672 5'  TCCAGCCTGGGCAACAAGAGTG 92973        _
            A                        TCGCTCT GTTGCCCAGGCTGGA
                                    |||||||| ||||||||||||||
                                    AGTGAGA CAACGGGTCCGACCT
                                       A
GAM642   LOC219722 5'  TTCAGCCTGGACAACAGAGTGA 94691             C
            GA                      TCTCGCTCTGTTG CCAGGCTGGA
                                    |||||||||||| |||||||||
                                    AGAGTGAGACAAC GGTCCGACTT
                                          A
GAM642   LOC219842 5'  TCTGGCTTGGTGAGATGGGGGA 94893      G      GC_     TG
            GG                      TCTC CTCTGTT   CCAGGC  GA
                                    |||| |||||||   ||||||  ||
                                    GGAG GGGGTAG   GGTTCG  CT
                                      _      AGT     GT
GAM642   LOC219919 3'  TCCAGCCTGGGCAACAGAGTAA 94933     CG
            GA                      TCT  CTCTGTTGCCCAGGCTGGA
                                    |||  ||||||||||||||||||
                                    AGA  GAGACAACGGGTCCGACCT
                                      AT
GAM642   LOC219920 5'  CCGGGAACAGAGTGGGG     94943           G   A
                                    TCTCGCTCTGTT CCC GG
                                    |||||||||||| ||| ||
                                    GGGGTGAGACAA GGG CC
                                          _  _
GAM642   LOC219920 5'  TCTGGCCTGGGGGCCAGGGCAG 94964    TC     TTG      TG
            GA                      TC  GCTCTG   CCCAGGC  GA
                                    ||  ||||||   |||||||  ||
                                    AG  CGGGAC   GGGTCCG  CT
                                     GA     CGG      GT
GAM642   LOC220018 5'  CGGTGGGTAGAGCCAGA     95027     C    GTT    AG  TG
                                    TCT GCTCT   GCCC  GC  G
                                    ||| |||||   ||||  ||  |
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                                AGA CGAGA   TGGG  TG  C
                                  C    ____   __  GT
GAM642   LOC220038 3'  TCCAGCCTGGGCGATGGAGTGA 93377
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGGTAGCGGGTCCGACCT

GAM642   LOC220045 5'  TTCAGAGTTGGAGGGGTGGGG  95039         GTTGC    G_
                                    TCTCGCTCT    CCAG  CTGGA
                                    |||||||||    ||||  |||||
                                    GGGGTGGGG    GGTT  GACTT
                                         A____    GA
GAM642   LOC220070 3'  TCCAGCCTGGAAAACGGAGTGA 59942            GC
                GA                  TCTCGCTCTGTT  CCAGGCTGGA
                                    ||||||||||||  ||||||||||
                                    AGAGTGAGGCAA  GGTCCGACCT
                                          AA
GAM642   LOC220431 5'  TCCAGTGTGCATGCCAGAGTGG 95997           TT CC  G
                GG                  TCTCGCTCTG  G  CA GCTGGA
                                    ||||||||||  |  || ||||||
                                    GGGGTGAGAC  T  GT TGACCT
                                         CG AC  G
GAM642   LOC220506 3'  TCCAGCCTGGGCAACAGAACAA 74521      CGC
                GA                  TCT   TCTGTTGCCCAGGCTGGA
                                    |||   ||||||||||||||||||
                                    AGA   AGACAACGGGTCCGACCT
                                      ACA
GAM642   LOC220549 3'  TCCAGCCTGGGTGACAGAATGA 94511       C     TG
                GA                  TCTCG TCTGT  CCCAGGCTGGA
                                    |||||  |||||  ||||||||||
                                    AGAGT AGACA  GGGTCCGACCT
                                       A     GT
GAM642   LOC220575 3'  TCCGGCCTGGGCAACAGAG    76817
                                    CTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||
                                    GAGACAACGGGTCCGGCCT

GAM642   LOC220662 3'  TCCAGCCTGGGCAACACGAGCG 92831        _
                A                    TCGCTC TGTTGCCCAGGCTGGA
                                    ||||||  ||||||||||||||||
                                    AGCGAG ACAACGGGTCCGACCT
                                       C
GAM642   LOC220692 3'  TCCAGCTCGGGGAACAGAGCGA 92866            G   AG
                GA                  TCTCGCTCTGTT CCC  GCTGGA
                                    ||||||||||||  |||  ||||||
                                    AGAGCGAGACAA GGG  CGACCT
                                          G   CT
GAM642   LOC220739 3'  GCTTGTGGCAGGGGTGAGA    94524          GT   _
                                    TCTCGCTCT  TGCC CAGGC
                                    |||||||||  |||| |||||
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                                AGAGTGGGG  ACGG GTTCG
                                     __    T
GAM642   LOC220906 3'  TCCAGCCTGGGCAACAAGCGA  93037       C
                                TCGCT TGTTGCCCAGGCTGGA
                                ||||| ||||||||||||||||
                                AGCGA ACAACGGGTCCGACCT
                                  _
GAM642   LOC220992 3'  TCCAGCCTGGGCAACATAGCAA 93110     C   C
           GA                     TCT GCT TGTTGCCCAGGCTGGA
                                ||| ||| ||||||||||||||||
                                AGA CGA ACAACGGGTCCGACCT
                                  A   T
GAM642   LOC221002 3'  TCTGGTCCTGGGTGGAGCAGGA 93111    TC    GTT      _ TG
                                TC  GCTCT   GCCCAGG C  GA
                                ||  |||||   ||||||| |  ||
                                AG  CGAGG   TGGGTCC G  CT
                                 GA    ___       T GT
GAM642   LOC221042 3'  TCCAGCCTGGGTGACAGAGCAA 94807     C      TG
           GA                     TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A       GT
GAM642   LOC221069 3'  TCCAGCCTGGGCGACAGAGCAA 94821     C
           GA                     TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGAGACAGCGGGTCCGACCT
                                  A
GAM642   LOC221178 3'  TCCAGCCTGGGAGATACAGCGA 95176        C   TG
           GA                     TCTCGCT TGT  CCCAGGCTGGA
                                |||||||  |||  ||||||||||
                                AGAGCGA ATA  GGGTCCGACCT
                                    C   GA
GAM642   LOC221271 3'  ACTCCAGCCTGGGTGACAGAGC 93489           TG
           GAGA                     TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      GT          CAC
GAM642   LOC221271 3'  GACCAGCCTGGGCAATATAGTG 93517        C            A
           AGA                      TCTCGCT TGTTGCCCAGGCTGG
                                ||||||| |||||||||||||||
                                AGAGTGA ATAACGGGTCCGACC
                                    T             AGA
GAM642   LOC221271 3'  TCCAGCCTGGGCAACAGAGGGA 93530      G
           GA                     TCTC CTCTGTTGCCCAGGCTGGA
                                |||| ||||||||||||||||||||
                                AGAG GAGACAACGGGTCCGACCT
                                  G
GAM642   LOC221271 3'  TCCAGCCTGGGCGACATCTAGA 93531    GCTC
                                TC    TGTTGCCCAGGCTGGA
                                ||    ||||||||||||||||
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                                AG    ACAGCGGGTCCGACCT
                                 ATCT
GAM642   LOC221288 3'  TCCAGCCTGGGCGACAGAGTGA 95263
             GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGTGAGACAGCGGGTCCGACCT

GAM642   LOC221303 5'  TCCAGCGCGCGGCAGGCCGGGG 93554       CT      CCAG
                                   TCTCG  CTGTTGC    GCTGGA
                                   |||||  |||||||    ||||||
                                   GGGGC  GACGGCG    CGACCT
                                      CG      CG__
GAM642   LOC221312 5'  TCTGGCTCTGCCGGCGGAGGGG 93560     G       CC   _  TG
             G                     CTC CTCTGTTG  CAG GC  GA
                                   ||| ||||||||  ||| ||  ||
                                   GGG GAGGCGGC  GTC CG  CT
                                     G       C_   T  GT
GAM642   LOC221337 3'  TCCAGCCTGGGCAACAAGAGTG 93738        _
             A                     TCGCTCT GTTGCCCAGGCTGGA
                                   |||||||  ||||||||||||||
                                   AGTGAGA CAACGGGTCCGACCT
                                       A
GAM642   LOC221410 3'  ACTCCAGCCTGGGTGACAGAGC 93685           TG
             GAGA                      TCTCGCTCTGT  CCCAGGCTGGA
                                       ||||||||||  ||||||||||
                                       AGAGCGAGACA  GGGTCCGACCT
                                            GT          CAC
GAM642   LOC221421 3'  TCTGGCCTCAGCCATGGGGCGA 93896           T  CC    TG
             GA                      TCTCGCTCTGT GC  AGGC  GA
                                     ||||||||||| ||  ||||  ||
                                     AGAGCGGGGTA CG  TCCG  CT
                                           C  AC    GT
GAM642   LOC221424 3'  CCTGGCAGTGTGGTGGGA    95270        C GT    C
                                     TCTCGCT T  TGCC AGG
                                     |||||||  |  |||| |||
                                     AGGGTGG G  ACGG TCC
                                        T TG   _
GAM642   LOC221474 3'  ACTCTAGCCTGGGTGACAGAGC 93985           TG
             GAGA                      TCTCGCTCTGT  CCCAGGCTGGA
                                       ||||||||||  ||||||||||
                                       AGAGCGAGACA  GGGTCCGATCT
                                            GT          CAC
GAM642   LOC221474 5'  TGGGCAGCTGGGGTGGGA    94003         _
                                     TCTCGCTCT GTTGCCCA
                                     |||||||| ||||||||
                                     AGGGTGGGG CGACGGGT
                                           T
GAM642   LOC221477 3'  TCCAGCCTGGGCGACAGAGCGA 93776
                                     TCGCTCTGTTGCCCAGGCTGGA
                                     ||||||||||||||||||||||
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                                AGCGAGACAGCGGGTCCGACCT

GAM642  LOC221489 3'  TCCAGCCTGGGTGATAAGAGTG 95290       _ TG
            A                  TCGCTCT GT  CCCAGGCTGGA
                               ||||||| ||  ||||||||||
                               AGTGAGA TA  GGGTCCGACCT
                                   A  GT
GAM642  LOC221491 3'  CCATGGTGATGGGGCCAGA   93655    C     TG  CAGGC
                               TCT GCTCTGT  CC    TGG
                               ||| |||||||  ||    |||
                               AGA CGGGGTA  GG    ACC
                                 C      GT  T____
GAM642  LOC221543 3'  TCCAGCCTGGGCAACAAGAGTA 95386    CG   _
            AG                   CT  CTCT GTTGCCCAGGCTGGA
                               ||  |||| ||||||||||||||||
                               GA  GAGA CAACGGGTCCGACCT
                                AT   A
GAM642  LOC221543 5'  TCCAGCCTGGGCGACAGAGCAA 95388    C
            GA                   TCT GCTCTGTTGCCCAGGCTGGA
                               ||| ||||||||||||||||||||
                               AGA CGAGACAGCGGGTCCGACCT
                                 A
GAM642  LOC221550 3'  TCCAGTCTGGTTGACAGAGTGA 93748          GC
            GA                   TCTCGCTCTGTT  CCAGGCTGGA
                               ||||||||||||  ||||||||||
                               AGAGTGAGACAG  GGTCTGACCT
                                     TT
GAM642  LOC221641 3'  ACACTAGCCTGGGTGACAGAGC 95336    C     TG       A
            AAGA                   TCT GCTCTGT  CCCAGGCTGG
                               ||| |||||||  ||||||||||
                               AGA CGAGACA  GGGTCCGATC
                                 A      GT        ACAC
GAM642  LOC221641 5'  ACTCCAGCCTGGGTGGCAGAGC 95340          TG
            GAGA                   TCTCGCTCTGT  CCCAGGCTGGA
                               ||||||||||  ||||||||||
                               AGAGCGAGACG  GGGTCCGACCT
                                     GT         CAC
GAM642  LOC221787 3'  AGAAGGCTGGGTGACAGAGTGA 94061          TG    G  GGA
            GG                   TCTCGCTCTGT  CCCAG CT
                               ||||||||||  ||||| ||
                               GGAGTGAGACA  GGGTC GA
                                     GT    G  AGAA
GAM642  LOC221787 3'  TTAGCTTGGGCAACACAGTGAG 94063       C          A
            A                   TCTCGCT TGTTGCCCAGGCTGG
                               ||||||| |||||||||||||||
                               AGAGTGA ACAACGGGTTCGATT
                                   C
GAM642  LOC221795 3'  TCCAGCCTGGGCAACAGAGTAA 94081    CG
            GA                   TCT  CTCTGTTGCCCAGGCTGGA
                               |||  ||||||||||||||||||
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                                AGA  GAGACAACGGGTCCGACCT
                                  AT
GAM642   LOC221883 5'  TTCAGCTTGTGCCTGAGCAGAC 95539       C     ___  C
                GGGG                    TCTCG TCTGTT   GC CAGGCTGGA
                                |||||| ||||||   || |||||||||
                                GGGGC AGACGA   CG GTTCGACTT
                                  _     GTC  T
GAM642   LOC221935 3'  CCAGTCTGAAAGGTGAGG    94199       T  GTTGCC
                                TCTCGC CT     CAGGCTGG
                                |||||| ||     ||||||||
                                GGAGTG GA     GTCTGACC
                                  _  AA_____
GAM642   LOC221943 5'  TCCAGCCTGGGCGACAGAGCAA 95625     C
                GA                      TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGAGACAGCGGGTCCGACCT
                                  A
GAM642   LOC221954 5'  CTCCAGCCTGGGCAACAGAGCG 95645
                AGA                      TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||||
                                AGAGCGAGACAACGGGTCCGACCT
                                                  CA
GAM642   LOC221954 5'  TCCAGCCTGGGTGACAGAGTAA 95652     CG     TG
                GA                      TCT  CTCTGT  CCCAGGCTGGA
                                |||  ||||||  ||||||||||
                                AGA  GAGACA  GGGTCCGACCT
                                  AT     GT
GAM642   LOC221954 5'  TCCAGCTTGGGCGACAGAGCAA 95653     C
                GA                      TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGAGACAGCGGGTTCGACCT
                                  A
GAM642   LOC222008 5'  TCCAGCCTGGGCTCCGCAGG   95659       T__
                                TCTGT   GCCCAGGCTGGA
                                |||||   ||||||||||||
                                GGACG   CGGGTCCGACCT
                                   CCT
GAM642   LOC222060 5'  TCCAGCCTGGGCGACAGAGCAA 95758     C
                GA                      TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGAGACAGCGGGTCCGACCT
                                  A
GAM642   LOC222066 3'  CTCCAGCTTGGGTGACAGAGTG 94320           TG
                AGA                      TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTTCGACCT
                                      GT         CA
GAM642   LOC222133 5'  TCTGTTGCGGCGGAGCGAG    95763            C_
                                CTCGCTCTGTTGC  CAGG
                                ||||||||||||  ||||
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                                GAGCGAGGCGGCG  GTCT
                                       TT
GAM642   LOC222160 3'  TCCAGCCTGGGCAGCAGAGGAA 95791     CG
            GA                   TCT  CTCTGTTGCCCAGGCTGGA
                                 |||  ||||||||||||||||||
                                 AGA  GAGACGACGGGTCCGACCT
                                   AG
GAM642   LOC222160 5'  TCCAGCCTGGGCGACAGAGCAA 95792     C
            GA                   TCT GCTCTGTTGCCCAGGCTGGA
                                 ||| ||||||||||||||||||||
                                 AGA CGAGACAGCGGGTCCGACCT
                                   A
GAM642   LOC222182 3'  CTCCAGCCTGGGCAATAGAGTG 95854
            AGA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGATAACGGGTCCGACCT
                                           CA
GAM642   LOC222256 3'  TCTAGCCTGGGTGACAAAGCAA 95912     C   C   TG
            GA                   TCT GCT TGT  CCCAGGCTGGA
                                 ||| ||| |||  ||||||||||
                                 AGA CGA ACA  GGGTCCGATCT
                                   A   A   GT
GAM642   LOC222865 3'  TCCAGCCTGAGTGACAGAGCGA 94450          TG C
            GA                   TCTCGCTCTGT  C CAGGCTGGA
                                 ||||||||||  | |||||||||
                                 AGAGCGAGACA  G GTCCGACCT
                                       GT A
GAM642   LOC245812 3'  TCTGGGGTGGAGGGTGGGG   95571         G TG  _
                                 TCTCGCTCT T  CCC AGG
                                 |||||||| |  ||| |||
                                 GGGGTGGGA G  GGG TCT
                                      _ GT   G
GAM642   LOC253003 3'  TCCAGTCTGGGCGACAGAGCG  98676
                                 CGCTCTGTTGCCCAGGCTGGA
                                 |||||||||||||||||||||
                                 GCGAGACAGCGGGTCTGACCT

GAM642   LOC253039 3'  TCCAGCCTGGGCGACAGAGCAA 97867     C
            GA                   TCT GCTCTGTTGCCCAGGCTGGA
                                 ||| ||||||||||||||||||||
                                 AGA CGAGACAGCGGGTCCGACCT
                                   A
GAM642   LOC253071 5'  TTCAGTGGTCAGTGGGGTGGGA 97420        TG   C  AG
                                 TCTCGCTC  TTG CC  GCTGGA
                                 ||||||||  ||| ||  ||||||
                                 AGGGTGGG  GAC GG  TGACTT
                                      GT   T  __
GAM642   LOC253314 3'  TACTTTGGGGGATGGGGCGGGA 97614           G     CTGGA
                                 TCTCGCTCTGTT CCCAGG
                                 |||||||||||| ||||||
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                                AGGGCGGGGTAG GGGTTT
                                      G      CATT
GAM642  LOC253532 3'  TCCAGCCTGGGTGACAAAGCAA 97740     C   C   TG
          GA                    TCT GCT TGT  CCCAGGCTGGA
                                ||| ||| |||  ||||||||||
                                AGA CGA ACA  GGGTCCGACCT
                                  A   A   GT
GAM642  LOC253532 3'  TCCAGTCTGGGTGACAGCGTGA 97741       T    TG
          GA                    TCTCGC CTGT  CCCAGGCTGGA
                                ||||||| ||||  ||||||||||
                                AGAGTG GACA  GGGTCTGACCT
                                   C    GT
GAM642  LOC253539 3'  TTTGGCCATGGTAGTGGAGTGG 97701    T     TG     CA   TG
          A                     TC CGCTC  TTGCC  GGC  GA
                                || |||||  |||||  |||  ||
                                AG GTGAG  GATGG  CCG  TT
                                 _    GT     TA   GT
GAM642  LOC253612 5'  TCCAGCCTAGGCAACAGAGTGA 98559              C
          GA                    TCTCGCTCTGTTGCC AGGCTGGA
                                |||||||||||||| ||||||||
                                AGAGTGAGACAACGG TCCGACCT
                                          A
GAM642  LOC253613 5'  TCCAACATGCAGTAGAATGAGG 97919       C       CCAGGC
                                TCTCG TCTGTTGC      TGGA
                                ||||| ||||||||      ||||
                                GGAGT AGATGACG      ACCT
                                   A       TACA__
GAM642  LOC253639 3'  ACTCCAGCCTGGGCGACAGAGT 97507
          GAGA                      TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAGCGGGTCCGACCT
                                              CAC
GAM642  LOC253664 3'  AGACCAGCCTGGGCAACATAGT 96453         C             A
          GAGA                      TCTCGCT TGTTGCCCAGGCTGG
                                    ||||||| ||||||||||||||
                                    AGAGTGA ACAACGGGTCCGACC
                                       T             AGAG
GAM642  LOC253681 3'  TCACTGGTGGGGGGTGGGG    96841          G TG  CA  C
                                TCTCGCTCT T  CC  GG TGG
                                ||||||||| |  ||  || |||
                                GGGGTGGGG G  GG  TC ACT
                                     _ GT  __  _
GAM642  LOC253681 3'  TCCCCATGGCAATGGGGCTGGA 96842     C         CA  CT
                                TCT GCTCTGTTGCC  GG  GGA
                                ||| ||||||||||  ||  |||
                                AGG CGGGGTAACGG  CC  CCT
                                  T         TA  __
GAM642  LOC253681 3'  TTTGGGACAGTGGGGGAGG    96845      G   TG   _
                                TCTC CTC  TTG CCCAGG
                                |||| |||  ||| ||||||
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                                GGAG GGG  GAC GGGTTT
                                  _  GT   A
GAM642   LOC253778 5'  ATTCCAGCCTGGGCGACAGAGT 96522
                GAGA                TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAGCGGGTCCGACCT
                                                TAC
GAM642   LOC253786 3'  TCCAGCCTGGGCAATAGAGCAA 98834     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGATAACGGGTCCGACCT
                                      A
GAM642   LOC253832 3'  TCCAGCCTGGGCGACGAGTGA  96593       T
                                    TCGCTC GTTGCCCAGGCTGGA
                                    |||||| ||||||||||||||||
                                    AGTGAG CAGCGGGTCCGACCT

                                      _
GAM642   LOC253840 5'  TCCAGCCTGGGCAACAGAGCAA 97914     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAACGGGTCCGACCT
                                      A
GAM642   LOC253868 3'  TTCAGCTTTGTGAGTGGGGCGA 97330         TG  _  CC
                GG                  TCTCGCTC  TT GC  AGGCTGGA
                                    ||||||||  || ||  ||||||||
                                    GGAGCGGG  GA TG  TTCGACTT
                                        GT  G  T_
GAM642   LOC253906 3'  AGAACAGCCTGGGCAACAAAGT 98296        C           GA
                GAGA                TCTCGCT TGTTGCCCAGGCTG
                                    |||||||  ||||||||||||||
                                    AGAGTGA ACAACGGGTCCGAC
                                        A           AAGAG
GAM642   LOC253906 3'  TTGAGCTTGGGTGACAGAGTAA 98301     CG     TG       G
                GA                  TCT  CTCTGT  CCCAGGCT GA
                                    |||  ||||||  |||||||| ||
                                    AGA  GAGACA  GGGTTCGA TT
                                      AT     GT       G
GAM642   LOC253912 3'  TTTGGTGAAATGGAGCGTGG   99209    T       GC_
                                    TC CGCTCTGTT   CCAGG
                                    || |||||||||   |||||
                                    GG GCGAGGTAA   GGTTT
                                     T        AGT
GAM642   LOC253926 3'  GCAGCCAGTGACAGAGGAGA   96594      G     TG CCA    GA
                                    TCTC CTCTGT  C   GGCTG
                                    |||| ||||||  |  |||||
                                    AGAG GAGACA  G   CCGAC
                                      _     GT A__     GA
GAM642   LOC253980 5'  CCGGGTGGTGCGAGCGAGA    96770         TGTT  _  GG
                                    TCTCGCTC    GC CCA  CTGG
                                    ||||||||    || |||  ||||
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                                AGAGCGAG   CG GGT  GGCC
                                    ____  T  G_
GAM642  LOC254020 5'  TCTCGGAACGGGGCGGGG   97856          G  C
                                TCTCGCTCTGTT CC AGG
                                |||||||||||| || |||
                                GGGGCGGGGCAA GG TCT
                                      _ C
GAM642  LOC254045 3'  CTTGGGCAACAGAATGAGA   98269      C
                                TCTCG TCTGTTGCCCAGG
                                ||||| ||||||||||||
                                AGAGT AGACAACGGGTTC
                                   A
GAM642  LOC254100 3'  CTCCAGCCTGGGCAACAGAGTG 98153
                AGA                 TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGACAACGGGTCCGACCT
                                          CA
GAM642  LOC254176 3'  TCCAGCCTGGGCAACAGAGTAA 99176    CG
                GA                  TCT  CTCTGTTGCCCAGGCTGGA
                                |||  ||||||||||||||||||
                                AGA  GAGACAACGGGTCCGACCT
                                  AT
GAM642  LOC254243 3'  ACTCCAGCCTGGGCAACAGAGT 99247
                GAGA                 TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGACAACGGGTCCGACCT
                                          CAA
GAM642  LOC254243 3'  TCCAGCCTGGGTGACACAGTGA 99270       C   TG
                GA                  TCTCGCT TGT  CCCAGGCTGGA
                                |||||||  |||  ||||||||||
                                AGAGTGA ACA  GGGTCCGACCT
                                    C   GT
GAM642  LOC254423 3'  TCTGGTCTGGCTGAAGAATGGG 99303      C   GTT   C    TG
                A                   TCTCG TCT   GCC AGGC  GA
                                ||||| |||   ||| ||||  ||
                                AGGGT AGA   CGG TCTG  CT
                                   A   AGT   _    GT
GAM642  LOC254531 5'  TCCAGCCTGGGTGACAGAGCAA 96673     C      TG
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM642  LOC254685 3'  TCCAGTTTGGGCAACAAGAGC  98242       _
                                GCTCT GTTGCCCAGGCTGGA
                                ||||| ||||||||||||||
                                CGAGA CAACGGGTTTGACCT
                                   A
GAM642  LOC254756 3'  TCCAGCCTGGGCAATAGAGTAA 99212     CG
                GA                  TCT  CTCTGTTGCCCAGGCTGGA
                                |||  ||||||||||||||||||
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                                AGA  GAGATAACGGGTCCGACCT
                                  AT
GAM642   LOC254808 3'  TCCAGCCTGGGCAACAGAGCAA 98810     C
                  GA                TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAACGGGTCCGACCT
                                      A
GAM642   LOC254875 3'  CTCCAGTCTGGGTGACAGAGTG 97778          TG
                  AGA                TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCTGACCT
                                          GT         CA
GAM642   LOC254875 3'  TCCAGCCTGGGTGACAAAGCAA 97785     C   C   TG
                  GA                TCT GCT TGT  CCCAGGCTGGA
                                    ||| ||| |||  ||||||||||
                                    AGA CGA ACA  GGGTCCGACCT
                                      A   A   GT
GAM642   LOC255030 5'  ACTCCAGCCTGGGTGACAGAGC 99079          TG
                  GAGA                TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGCGAGACA  GGGTCCGACCT
                                          GT         CAC
GAM642   LOC255031 3'  AGACCAGCCTGGGCAACATAGT 99028        C           A
                  GAGA                TCTCGCT TGTTGCCCAGGCTGG
                                    ||||||| ||||||||||||||
                                    AGAGTGA ACAACGGGTCCGACC
                                       T            AGAG
GAM642   LOC255031 3'  TCCAGCCTGGCTACAGAGTGAG 99044          T   C
                  A                 TCTCGCTCTGT GCC AGGCTGGA
                                    |||||||||| ||| ||||||||
                                    AGAGTGAGACA CGG TCCGACCT
                                          T  _
GAM642   LOC255042 3'  ACTCTAGCCTGGGTGACAGAGT 97028          TG
                  GAGA                TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGATCT
                                          GT         CAC
GAM642   LOC255042 3'  TCCAGCCTGGGCAACAAGAGCG 97056        _
                  A                 TCGCTCT GTTGCCCAGGCTGGA
                                    ||||||| ||||||||||||||
                                    AGCGAGA CAACGGGTCCGACCT
                                       A
GAM642   LOC255042 3'  TCCAGCCTGGGCGACGAGC   97057     T
                                    GCTC GTTGCCCAGGCTGGA
                                    |||| ||||||||||||||
                                    CGAG CAGCGGGTCCGACCT
                                      _
GAM642   LOC255177 3'  TCCAGCCTAGGCAACAGAGTGA 98401           C
                  GA                TCTCGCTCTGTTGCC AGGCTGGA
                                    |||||||||||||| ||||||||
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                                AGAGTGAGACAACGG TCCGACCT
                                       A
GAM642  LOC255177 3'  TTTGGTTGTCTCTTGATGGGGG 98405     G     GCCCA__  TG
          AGG                   TCTC CTCTGTT      GGC  GA
                                |||| |||||||      |||  ||
                                GGAG GGGGTAG      TTG  TT
                                  _     TTCTCTG   GT
GAM642  LOC255196 3'  ACAACCTGGGCAACAGAGCCAG 98941    C          C  GA
          A                    TCT GCTCTGTTGCCCAGG TG
                               ||| |||||||||||||| ||
                               AGA CGAGACAACGGGTCC AC
                                 C           A  AT
GAM642  LOC255231 3'  CTCCAGCCTGGGTGACAGAGTG 97120          TG
          AGA                   TCTCGCTCTGT  CCCAGGCTGGA
                                |||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      GT         CA
GAM642  LOC255252 3'  TCCAGCGTGGGTGACAGAGTGA 96710          TG   G
          GA                    TCTCGCTCTGT  CCCA GCTGGA
                                |||||||||||  |||| ||||||
                                AGAGTGAGACA  GGGT CGACCT
                                      GT   G
GAM642  LOC255271 5'  TCCGGTGCGGGCGGAGTCGGA  97244    C    GTT   AG
                               TCT GCTCT   GCCC  GCTGGA
                               ||| |||||   ||||  ||||||
                               AGG TGAGG   CGGG  TGGCCT
                                 C    ___   CG
GAM642  LOC255326 3'  TCCAGCCTGGGTGACAGAGCAA 98124    C     TG
          GA                    TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM642  LOC255328 3'  TCCAGCCTGGGTGATAAGAGC  98347      _  TG
                               GCTCT GT  CCCAGGCTGGA
                               ||||| ||  ||||||||||
                               CGAGA TA  GGGTCCGACCT
                                  A  GT
GAM642  LOC255452 5'  TCTGCAAAGCAGCAGGGCAGA  99402    C       CCAG  T
                               TCT GCTCTGTTGC    GC GGA
                               ||| ||||||||||    || |||
                               AGA CGGGACGACG    CG TCT
                                 _         AAA_  _
GAM642  LOC255463 3'  TCCAGCCTGGACAACATAGTGA 96543       C    C
          GA                    TCTCGCT TGTTG CCAGGCTGGA
                                ||||||| ||||| ||||||||||
                                AGAGTGA ACAAC GGTCCGACCT
                                   T    A
GAM642  LOC255523 3'  TCCAGCCTGGGCAACAGAGCAA 96737    C
          GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
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                                AGA CGAGACAACGGGTCCGACCT
                                  A
GAM642   LOC255671 5'  ACTCCAGCCTGGGTGACAGAGT 99061          TG
                  GAGA                  TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      GT          CAC
GAM642   LOC255671 5'  TCCAGCCTGGGCGACAGAGGGT 99075    _  G
                  GA                  TC TC CTCTGTTGCCCAGGCTGGA
                                || || ||||||||||||||||||
                                AG GG GAGACAGCGGGTCCGACCT
                                 T  _
GAM642   LOC255671 3'  TCCAGCCTGGGTAACAGAGCAA 99076     C
                  GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||
                                AGA CGAGACAATGGGTCCGACCT
                                  A
GAM642   LOC255862 3'  TGGTCTTCATGGACGAGA    96116      C    T CCC    TG
                                TCTCG TCTGT G   AGGC  G
                                ||||| ||||| |   ||||  |
                                AGAGC AGGTA C   TCTG  T
                                   _    _ T__    GT
GAM642   LOC255937 3'  TCCATCCTGGGTGACAGAGCAA 97684     C      TG     C
                  GA                  TCT GCTCTGT  CCCAGG TGGA
                                ||| |||||||  |||||| ||||
                                AGA CGAGACA  GGGTCC ACCT
                                  A      GT     T
GAM642   LOC255971 3'  ACTACAGCCTGGGTGACAGAGC 98304     C      TG       GA
                  AAGA                  TCT GCTCTGT  CCCAGGCTG
                                ||| |||||||  |||||||||
                                AGA CGAGACA  GGGTCCGAC
                                  A      GT        ATCAC
GAM642   LOC256073 3'  TGACCAGCCTGGGCAACATAGC 98490         C            A
                  GAGA                  TCTCGCT TGTTGCCCAGGCTGG
                                |||||||  ||||||||||||||
                                AGAGCGA ACAACGGGTCCGACC
                                     T            AGTA
GAM642   LOC256158 5'  GGGCAGTGGCAGAGGAGG    99509      G    ___
                                TCTC CTCTGT   TGCCC
                                |||| ||||||   |||||
                                GGAG GAGACG   ACGGG
                                   _     GTG
GAM642   LOC256207 3'  TCCAACCTGGGCGACAGAGCAA 96880     C            C
                  GA                  TCT GCTCTGTTGCCCAGG TGGA
                                ||| |||||||||||||| ||||
                                AGA CGAGACAGCGGGTCC ACCT
                                  A            A
GAM642   LOC256218 3'  TCCAGAGCGGCAAGAGCGAGA  96886          GT    CAGG
                                TCTCGCTCT  TGCC    CTGGA
                                |||||||||  ||||    |||||
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                                AGAGCGAGA  ACGG    GACCT
                                     __    CGA_
GAM642   LOC256267 5'  TCCAGCCTGGGAGACAGAGTGA 98613          TG
            GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                        GA
GAM642   LOC256306 5'  CCAGGGCAGCAGAGCTAGG    98509     C         A
                                  TCT GCTCTGTTGCCC GG
                                  ||| ||||||||||| ||
                                  GGA CGAGACGACGGG CC
                                    T          A
GAM642   LOC256494 5'  CTAGGCTGGCAGGGCGA     99094         TTGC    G
                                  TCGCTCTG    CCAG CTGG
                                  ||||||||    |||| ||||
                                  AGCGGGAC    GGTC GATC
                                       ____    G
GAM642   LOC256515 3'  TCCAGCCTGGGCAACAGAGTAA 98218     CG
            GA                    TCT  CTCTGTTGCCCAGGCTGGA
                                  |||  ||||||||||||||||||
                                  AGA  GAGACAACGGGTCCGACCT
                                    AT
GAM642   LOC256520 3'  TCCAGCCTGGGCGACAGAGCCA 97670     C
            GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    C
GAM642   LOC256594 3'  TCCAGCCTGGGCAACAGAGTAA 98868     CG
            GA                    TCT  CTCTGTTGCCCAGGCTGGA
                                  |||  ||||||||||||||||||
                                  AGA  GAGACAACGGGTCCGACCT
                                    AT
GAM642   LOC256790 5'  TCCCCAAGGTGACGGGTTGAGG 96494      CT    TG  CA  CT
                                  TCTCG  CTGT  CC  GG  GGA
                                  |||||  ||||  ||  ||  |||
                                  GGAGT  GGCA  GG  CC  CCT
                                     TG    GT  AA  __
GAM642   LOC256956 5'  TTTGGCAACAATAGGGAGAGG  98017     G      CCCAG  TG
                                  TCTC CTCTGTTG    GC  GA
                                  |||| ||||||||    ||  ||
                                  GGAG GGGATAAC    CG  TT
                                    A       AA___  GT
GAM642   LOC257078 5'  CCGGGGCAGCAGGGCTGGG    98916     C         A
                                  TCT GCTCTGTTGCCC GG
                                  ||| ||||||||||| ||
                                  GGG CGGGACGACGGG CC
                                    T          G
GAM642   LOC257222 5'  TTTGGTCTGTTGCGGGATAGAG 99447     C      __  C_    TG
            TAGA                    TCT GCTCTGTT  GC  CAGGC  GA
                                  ||| ||||||||  ||  |||||  ||
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                                AGA TGAGATAG  CG  GTCTG  TT
                                  _       GG  TT     GT
GAM642   LOC257282 5'  TCAAGCCTGGGCAACAGAGCAA 98136     C              G
                GA                    TCT GCTCTGTTGCCCAGGCT GA
                                      ||| |||||||||||||||| ||
                                      AGA CGAGACAACGGGTCCGA CT
                                        A               A
GAM642   LOC257354 3'  AGACCAGCCTGGGCAACATAGT 96783         C             A
                GAGA                    TCTCGCT TGTTGCCCAGGCTGG
                                        ||||||| ||||||||||||||
                                        AGAGTGA ACAACGGGTCCGACC
                                           T             AGAA
GAM642   LOC257354 3'  ATTTGGGAGCACCAGCAGAATG 96784       C      _____      CTGGA
                GGG                     TCTCG TCTGTTG     CCCAGG
                                        ||||| |||||||     ||||||
                                        GGGGT AGACGAC     GGGTTT
                                           A       CACGA        AG
GAM642   LOC257443 3'  TTTAGTCTTCATGGGGTTGGA  97548     C       T CCC
                                        TCT GCTCTGT G   AGGCTGGA
                                        ||| ||||||| |   ||||||||
                                        AGG TGGGGTA C   TCTGATTT
                                          T       _ T__
GAM642   LOC257479 5'  CCGGTCCGCGCGGCGGGG     97986          CCA
                                        CTCTGTTGC   GGCTGG
                                        |||||||||   ||||||
                                        GGGGCGGCG   CTGGCC
                                             CGC
GAM642   LOC257480 5'  TCCAGGGCGAGGCGGCGGAGCG 78435     T          CAGG_
                TGG                     TC CGCTCTGTTGCC     CTGGA
                                        || ||||||||||||     |||||
                                        GG GCGAGGCGGCGG     GACCT
                                         T           AGCGG
GAM642   LOC257495 3'  TCCAGTCTGGTTGACAGAGTGA 99575            GC
                GA                      TCTCGCTCTGTT  CCAGGCTGGA
                                        ||||||||||||  ||||||||||
                                        AGAGTGAGACAG  GGTCTGACCT
                                              TT
GAM642   LOC257539 3'  TCCAGCCTGGGTGACAGGGTGA 99551          TG
                                        TCGCTCTGT  CCCAGGCTGGA
                                        |||||||||  ||||||||||
                                        AGTGGGACA  GGGTCCGACCT
                                             GT
GAM642   LOC257576 3'  TCCAGTCTGGTTGACAGAGTGA 99712            GC
                GA                      TCTCGCTCTGTT  CCAGGCTGGA
                                        ||||||||||||  ||||||||||
                                        AGAGTGAGACAG  GGTCTGACCT
                                              TT
GAM642   LOC257578 3'  TCCAGCCTGGGTGACAGGGTGA 99663          TG
                                        TCGCTCTGT  CCCAGGCTGGA
                                        |||||||||  ||||||||||
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                                AGTGGGACA  GGGTCCGACCT
                                     GT
GAM642  LOC257596 3'  TCCAGCCTGGGCAACAAGAGTA 99789    CG   _
           AG                    CT  CTCT GTTGCCCAGGCTGGA
                                 ||  |||| ||||||||||||||||
                                 GA  GAGA CAACGGGTCCGACCT
                                  AT    A
GAM642  LOC257596 5'  TCCAGCCTGGGCGACAGAGCAA 99791     C
           GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                 ||| ||||||||||||||||||||
                                 AGA CGAGACAGCGGGTCCGACCT
                                   A
GAM642  LOC257618 5'  TTTGCAGGGAGGGACGGGGTGG 99678          G__   AG  TGGA
           GG                    TCTCGCTCTGTT   CCC  GC
                                 ||||||||||||   |||  ||
                                 GGGGTGGGGCAG   GGG  CG
                                        GGA   A_  TTT
GAM642  LOC51075  3'  TTTGGCTGTGACTGGGTGGGG  32556        T  TG CCA   TG
                                 TCTCGCTC GT  C   GGC  GA
                                 ||||||||  ||  |   |||  ||
                                 GGGGTGGG CA  G   TCG  TT
                                      T  GT ____   GT
GAM642  LOC51145  3'  CCTCCAGCCTGGGCGACAGAGT 32923
           GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                 ||||||||||||||||||||||||||
                                 AGAGTGAGACAGCGGGTCCGACCT
                                           CCC
GAM642  LOC51161  3'  TTCAGTGTTTAGAGAGTGGGG  33047         G   CC AG
                                 TCTCGCTCT TTG  C  GCTGGA
                                 |||||||||  |||  |  ||||||
                                 GGGGTGAGA GAT  G  TGACTT
                                      _   TT __
GAM642  LOC51212  3'  TCCAGCCTGGGTGACAGAGCAA 33501     C      TG
           GA                    TCT GCTCTGT  CCCAGGCTGGA
                                 ||| |||||||  ||||||||||
                                 AGA CGAGACA  GGGTCCGACCT
                                   A      GT
GAM642  LOC51333  3'  TCCGGCCTGGGCAACAGAGGAA 34057     CG
           GA                    TCT  CTCTGTTGCCCAGGCTGGA
                                 |||  ||||||||||||||||||||
                                 AGA  GAGACAACGGGTCCGGCCT
                                   AG
GAM642  LOC51336  3'  TCCAGCCTGGGTGACAGCGTAA 34079     CG T    TG
           GA                    TCT  C CTGT  CCCAGGCTGGA
                                 |||  | ||||  ||||||||||
                                 AGA  G GACA  GGGTCCGACCT
                                   AT C    GT
GAM642  LOC51667  3'  CCAGTTTGGACTGATGGGA   32775       C  T  TGC
                                 TCTCG TC GT   CCAGGCTGG
                                 |||||  || ||   |||||||||
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                                AGGGT AG CA   GGTTTGACC
                                  _ T ___
GAM642  LOC51759  3' TCCAGCCTGGGCAACGAGC   73172     T
                                GCTC GTTGCCCAGGCTGGA
                                |||| ||||||||||||||
                                CGAG CAACGGGTCCGACCT
                                  _
GAM642  LOC54466  3' TCGGTCTGGAGGGGGCAGGG  39177      G __    TG
                                CTCTGTT CC  CAGGC  GA
                                ||||||| ||  |||||  ||
                                GGGACGG GG  GTCTG  CT
                                   G  AG    GT
GAM642  LOC56963  5' CCGCCGGCGGAGCGAGG    71949       GTT   CA   T
                                TCTCGCTCT   GCC  GGC GG
                                |||||||||   |||  ||| ||
                                GGAGCGAGG   CGG  CCG CC
                                    ___   __   C
GAM642  LOC57118  3' TCCAGCCTGGGTGACAGATTGA 40228      C     TG
          GA                    TCTCG TCTGT  CCCAGGCTGGA
                                ||||| |||||  ||||||||||
                                AGAGT AGACA  GGGTCCGACCT
                                  T    GT
GAM642  LOC58504  3' TCCAGCCTTGTATGGAGTTAGA 41407    C      T  CC
                                TCT GCTCTGT GC  AGGCTGGA
                                ||| ||||||| ||  ||||||||
                                AGA TGAGGTA TG  TCCGACCT
                                  T      _ T_
GAM642  LOC58525  3' TCTAGCAGCCAGGCAGGGCGA  79353        GCCCAG
                                TCGCTCTGTT     GCTGGA
                                ||||||||||     ||||||
                                AGCGGGACGG     CGATCT
                                     ACCGA_
GAM642  LOC58525  3' TCTGGGGCCCTGGAGGGTGGGG 79354        GTTGC    ___ TG
                                TCTCGCTCT    CCAGG   C  GA
                                |||||||||    |||||  |  ||
                                GGGGTGGGA    GGTCC   G  CT
                                     _____    CGG GT
GAM642  LOC59346  5' TCCAGAACTGGTAGAGCCGGG  41574     C     TTGC    G_
                                TCT GCTCTG   CCAG  CTGGA
                                ||| ||||||   ||||  |||||
                                GGG CGAGAT   GGTC  GACCT
                                  C     ____   AA
GAM642  LOC63929  3' TCCAGCCTGGGTGACTGAGCAA 42285     C    T  TG
          GA                    TCT GCTC GT  CCCAGGCTGGA
                                ||| |||| ||  ||||||||||
                                AGA CGAG CA  GGGTCCGACCT
                                  A   T  GT
GAM642  LOC64167  3' TCCAGCCTGGGTGACTGAGCGA 42543        T  TG
          GA                    TCTCGCTC GT  CCCAGGCTGGA
                                |||||||| ||  ||||||||||
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                                AGAGCGAG CA  GGGTCCGACCT
                                    T  GT
GAM642  LOC81558  3'  TTCAGCTGCTGGCAGAGGGAGG 48681      G      _  CCA
                                TCTC CTCTGTT GC   GGCTGGA
                                |||| ||||||| ||   |||||||
                                GGAG GAGACGG CG   TCGACTT
                                  G      T  ___
GAM642  LOC85479  5'  TCCAGCCTGGGCGACAGAGCAA 53571     C
            GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGAGACAGCGGGTCCGACCT
                                  A
GAM642  LOC89890  3'  TCCAGCCTGGATGACAGAGTGA 61209            GC
            GA                    TCTCGCTCTGTT  CCAGGCTGGA
                                ||||||||||||  ||||||||||
                                AGAGTGAGACAG  GGTCCGACCT
                                      TA
GAM642  LOC89958  3'  AGACCAGCCTGGGCAACGCAGT 61580         C            A
            GAGA                    TCTCGCT TGTTGCCCAGGCTGG
                                ||||||| ||||||||||||||||
                                AGAGTGA GCAACGGGTCCGACC
                                    C             AGAG
GAM642  LOC90038  3'  CTCCAGCCTGGGCAACAGAGTG 61804
            AGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGACAACGGGTCCGACCT
                                        CA
GAM642  LOC90038  3'  TCCAGCCTGGGTGACACAGTGA 61814        C   TG
            GA                    TCTCGCT TGT  CCCAGGCTGGA
                                ||||||| |||  ||||||||||||
                                AGAGTGA ACA  GGGTCCGACCT
                                    C   GT
GAM642  LOC90049  5'  TCTGACTGCAGCGCGGCGGGG  61877        C     C__
                                TCTCGCT TGTTGC   CAGG
                                ||||||| ||||||   ||||
                                GGGGCGG GCGACG   GTCT
                                    C      TCA
GAM642  LOC90072  3'  TCCAGCCTGGGGAACAGAGCAA 61963     C       G
            GA                    TCT GCTCTGTT CCCAGGCTGGA
                                ||| |||||||| ||||||||||||
                                AGA CGAGACAA GGGTCCGACCT
                                  A       G
GAM642  LOC90072  5'  TCCAGCCTGGGTGACAGAACAA 61964     CGC     TG
            GA                    TCT   TCTGT  CCCAGGCTGGA
                                |||   |||||  ||||||||||||
                                AGA   AGACA  GGGTCCGACCT
                                  ACA     GT
GAM642  LOC90072  5'  TCCAGCCTGGGTGACATATCAA 61965     CGCTC   TG
            GA                    TCT     TGT  CCCAGGCTGGA
                                |||     |||  ||||||||||||
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                                AGA    ACA  GGGTCCGACCT
                                  ACTAT   GT
GAM642  LOC90092  3'  TCCAGCCTGGCGACAAGAGCGA 62075         _     C
                GA                  TCTCGCTCT GTTGCC AGGCTGGA
                                    ||||||||| |||||| ||||||||
                                    AGAGCGAGA CAGCGG TCCGACCT
                                       A     _
GAM642  LOC90110  5'  TCCAGCCTGGGCAACGGAGTGA 62181
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGGCAACGGGTCCGACCT
                                                 C
GAM642  LOC90139  3'  TTTGGTCTGGGCTCAGTGGGAG 56272      G _   TT       TG
                A                    TCTC CT CTG  GCCCAGGC  GA
                                    |||| || |||  ||||||||  ||
                                    AGAG GG GAC  CGGGTCTG  TT
                                      _ T   T_       GT
GAM642  LOC90141  3'  TCCAGCCTGGATGATAGAGCAA 62310     C       GC
                GA                  TCT GCTCTGTT  CCAGGCTGGA
                                    ||| ||||||||  ||||||||||
                                    AGA CGAGATAG  GGTCCGACCT
                                      A       TA
GAM642  LOC90155  5'  TCCAGCCTGGGCAACAAGAGTG 62368         _
                A                    TCGCTCT GTTGCCCAGGCTGGA
                                    ||||||| ||||||||||||||
                                    AGTGAGA CAACGGGTCCGACCT
                                       A
GAM642  LOC90233  3'  TCCAGCCCAGGCAACAGAGTGA 57197              CA
                GA                  TCTCGCTCTGTTGCC  GGCTGGA
                                    ||||||||||||||  |||||||
                                    AGAGTGAGACAACGG  CCGACCT
                                              AC
GAM642  LOC90321  3'  CTCCAGCTTGGGTGACAGAGCG 62933           TG
                AGA                   TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGCGAGACA  GGGTTCGACCT
                                          GT          CA
GAM642  LOC90321  3'  TCCAACCTGGGTGACAGAGCGA 62938           TG     C
                GA                  TCTCGCTCTGT  CCCAGG TGGA
                                    ||||||||||  |||||| ||||
                                    AGAGCGAGACA  GGGTCC ACCT
                                          GT     A
GAM642  LOC90353  3'  TCTGATGCCGCGGGGGTGGGG   59770          T  C_
                                    TCTCGCTCTGT GC  CAGG
                                    ||||||||||| ||  ||||
                                    GGGGTGGGGCG CG  GTCT
                                          C  TA
GAM642  LOC90393  5'  ACTCCAGCCTGGGTGACAGAGT 63302           TG
                GAGA                    TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
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                                AGAGTGAGACA  GGGTCCGACCT
                                      GT         CAC
GAM642  LOC90459  5'  GGGCTCTGCAGAGTGAGA    63557          T__
                                TCTCGCTCTGT   GCCC
                                ||||||||||   ||||
                                AGAGTGAGACG   CGGG
                                      TCT
GAM642  LOC90538  3'  TCCAGTCTGGGTGAAAGAGCGA 63900         G TG
          GA                    TCTCGCTCT T  CCCAGGCTGGA
                                |||||||| |  ||||||||||
                                AGAGCGAGA A  GGGTCTGACCT
                                     A GT
GAM642  LOC90573  5'  GTCCAGCCTGGGCGACAGAGTG 63961
          AGA                     TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGACAGCGGGTCCGACCT
                                            GA
GAM642  LOC90591  3'  TTCAGCCTGGGCAACAAGAGTG 64197        _
          A                      TCGCTCT GTTGCCCAGGCTGGA
                                ||||||| ||||||||||||||
                                AGTGAGA CAACGGGTCCGACTT
                                   A
GAM642  LOC90624  3'  TCCAGCCTGGGGGACAGAGTGA 64373           G
          GA                    TCTCGCTCTGTT CCCAGGCTGGA
                                |||||||||||| ||||||||||
                                AGAGTGAGACAG GGGTCCGACCT
                                      G
GAM642  LOC90631  3'  TCGGCTTCCAGAGTTGGG    64396    C    TTGCCC
                                TCT GCTCTG     AGGCTGG
                                ||| ||||||     |||||||
                                GGG TGAGAC     TTCGGCT
                                  T    C_____
GAM642  LOC90639  3'  TCCAGCCTGAGCAACAGAGCCG 64416    C        C
          GA                    TCT GCTCTGTTGC CAGGCTGGA
                                ||| |||||||||| |||||||||
                                AGG CGAGACAACG GTCCGACCT
                                  C         A
GAM642  LOC90784  5'  CTCCAGCCTGGGCAACAGAGTG 64696
          AGA                     TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGACAACGGGTCCGACCT
                                            CA
GAM642  LOC90784  5'  TCCAGCTCGGGTGACAAGAGTG 64701         _ TG   AG
          AGA                     TCTCGCTCT GT  CCC  GCTGGA
                                ||||||||| ||  |||  ||||||
                                AGAGTGAGA CA  GGG  CGACCT
                                     A  GT   CT
GAM642  LOC90785  3'  ATTCCAGCCTGGGTGACAGAGC 64709           TG
          GAGA                    TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
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                                AGAGCGAGACA  GGGTCCGACCT
                                      GT         TAC
GAM642  LOC90841  5' TCCAGCCTGGGTGATAGAGCTG 64873     C      TG
             GA                   TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGG CGAGATA  GGGTCCGACCT
                                    T      GT
GAM642  LOC90918  5' TCTGGGGACTGTGGTGGGG   65006       CT_  G     CTGGA
                                  TCTCGCT   GTT CCCAGG
                                  |||||||   ||| ||||||
                                  GGGGTGG   CAG GGGTCT
                                      TGT   _       A
GAM642  LOC91040  3' CCAGCTCTGCAGGGTGGGG   65338         TTGCC  _
                                  TCTCGCTCTG    CAG GCTGG
                                  ||||||||||    ||| |||||
                                  GGGGTGGGAC    GTC CGACC
                                        _____   T
GAM642  LOC91056  3' TCCAGCCTGGGCGACAGAGCAA 96410     C
             GG                   TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  GGA CGAGACAGCGGGTCCGACCT
                                    A
GAM642  LOC91064  3' TCCAGCGTGGGCGACAGAGCAA 65391     C          G
             GA                   TCT GCTCTGTTGCCCA GCTGGA
                                  ||| |||||||||||| ||||||
                                  AGA CGAGACAGCGGGT CGACCT
                                    A          G
GAM642  LOC91250  5' CTCCAGCCTGGGCAACAGAGTG 65915
             AGA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGTGAGACAACGGGTCCGACCT
                                              CA
GAM642  LOC91250  5' TCCAGCCTGAGTGACAGAGTGA 65921          TG C
             GA                   TCTCGCTCTGT  C CAGGCTGGA
                                  ||||||||||  | |||||||||
                                  AGAGTGAGACA  G GTCCGACCT
                                        GT A
GAM642  LOC91380  3' ACTCCAGCCTGGGTGACAGAGT 66430          TG
             GAGA                   TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          GT         CAC
GAM642  LOC91442  3' TCCAGCCTGGGCACCAGAGCGA 66648          T
             GA                   TCTCGCTCTG TGCCCAGGCTGGA
                                  |||||||||| ||||||||||||
                                  AGAGCGAGAC ACGGGTCCGACCT
                                        C
GAM642  LOC91450  3' TTTGGGCAGAGGAGTGGGG   66658         G
                                  TCTCGCTCT TTGCCCAGG
                                  ||||||||| |||||||||
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                                GGGGTGAGG GACGGGTTT
                                    A
GAM642  LOC91496  5' TTCAGCCATGGATGAGGAGTGG 66812        G  GC  _
             GA                   TCTCGCTCT TT  CCA GGCTGGA
                                  ||||||||| ||  ||| |||||||
                                  AGGGTGAGG AG  GGT CCGACTT
                                      _ TA   A
GAM642  LOC91547  3' CTCCAGCCTGGGCGACAGAGCG 67001
             AGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACAGCGGGTCCGACCT
                                                CA
GAM642  LOC91565  3' AGACCATCCTGGGCAACAGGGT 67051              C   A
             GAGA                   TCTCGCTCTGTTGCCCAGG TGG
                                    |||||||||||||||||| |||
                                    AGAGTGGGACAACGGGTCC ACC
                                                T   AGAG
GAM642  LOC91660  3' GCAATCTGGGTTACGGAGTGAG 67403          T     GC  GA
             A                      TCTCGCTCTGT GCCCAG  TG
                                    |||||||||| ||||||  ||
                                    AGAGTGAGGCA TGGGTC  AC
                                          T     TA  GT
GAM642  LOC91689  5' CTGGGCGGTGGGGTGCGG    53977    T    TG
                                    TC CGCTC  TTGCCCAG
                                    || |||||  ||||||||
                                    GG GTGGG  GGCGGGTC
                                     C    GT
GAM642  LOC91750  3' ACTCCAGCCTGGGCAACAGAGT 67643
             GAGA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAACGGGTCCGACCT
                                                CAC
GAM642  LOC91796  5' TCCAGCCAGGGGATAGAGCGAG 67788          G   A
             A                      TCTCGCTCTGTT CCC GGCTGGA
                                    |||||||||||| ||| |||||||
                                    AGAGCGAGATAG GGG CCGACCT
                                          _  A
GAM642  LOC91812  3' TCCAGCCTGGGCAACAGAACGA 67821      C
             GA                     TCTCG TCTGTTGCCCAGGCTGGA
                                    ||||| ||||||||||||||||||
                                    AGAGC AGACAACGGGTCCGACCT
                                      A
GAM642  LOC91813  3' TCCAGCCTGGGCAACAGAACGA 67848      C
             GA                     TCTCG TCTGTTGCCCAGGCTGGA
                                    ||||| ||||||||||||||||||
                                    AGAGC AGACAACGGGTCCGACCT
                                      A
GAM642  LOC91862  3' TCCAGCCCAGGTGACAGAGCGA 54574          TG  CA
             GA                     TCTCGCTCTGT  CC  GGCTGGA
                                    ||||||||||  ||  |||||||
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                                AGAGCGAGACA  GG  CCGACCT
                                      GT  AC
GAM642  LOC91960  3'  GACGACTGGCAGTGGAGTGGGG 68285        TG    C  GCTGGA
                                TCTCGCTC  TTGCC AG
                                ||||||||  ||||| ||
                                GGGGTGAG  GACGG TC
                                    GT    _  AGCAGT
GAM642  LOC91963  5'  TCCAGCCTGGGCAACAGAGTGA 68327
                                TCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||
                                AGTGAGACAACGGGTCCGACCT

GAM642  LOC91963  3'  TCTAGCTTGGGTGACAGAGCAA 68329     C      TG
            GA                    TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTTCGATCT
                                  A      GT
GAM642  LOC92078  3'  ACTCCAGCCTGGGTGACAGAGT 68586          TG
            GAGA                    TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      GT         CAC
GAM642  LOC92140  5'  CTGGCGGCGGCGGAGTGAGG   68824            CAG  TG A
                                TCTCGCTCTGTTGCC   GC  G
                                ||||||||||||||   ||  |
                                GGAGTGAGGCGGCGG   CG  C
                                      ___  GT
GAM642  LOC92181  5'  CCGGAGGTGGCGGACGAGG    68944      C    TG  CAGG
                                TCTCG TCTGT  CC    CTGG
                                ||||| |||||  ||    ||||
                                GGAGC AGGCG  GG    GGCC
                                  _    GT  A___
GAM642  LOC92223  3'  TCCAGCCTGGGCAACAAGAGTG 69055        _
            A                    TCGCTCT GTTGCCCAGGCTGGA
                                ||||||| ||||||||||||||
                                AGTGAGA CAACGGGTCCGACCT
                                    A
GAM642  LOC92228  3'  CCCAGCCTGGGCAACGGAGTGA 69074                  A
            GA                    TCTCGCTCTGTTGCCCAGGCTGG
                                ||||||||||||||||||||||
                                AGAGTGAGGCAACGGGTCCGACC
                                          CT
GAM642  LOC92267  3'  TCCAGCCTGGGCAACAAGAGAG 69179      G  C
            A                    TCTC CT TGTTGCCCAGGCTGGA
                                ||||| || ||||||||||||||||
                                AGAG GA ACAACGGGTCCGACCT
                                  A  _
GAM642  LOC92270  5'  TCCAGCTTGGGTGACAGAGTGA 69190          TG
            G                    CTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
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                                GAGTGAGACA  GGGTTCGACCT
                                      GT
GAM642  LOC92299  3'  ACTGCAGCCTAGGTGACAGAGC 69358          TG  C     GA
          GAGA                    TCTCGCTCTGT  CC AGGCTG
                                |||||||||||  || ||||||
                                AGAGCGAGACA  GG TCCGAC
                                      GT  A     GTCAC
GAM642  LOC92299  3'  TCCAGCCTGGCGACAAAGCGAG 69373        C      C
          A                     TCTCGCT TGTTGCC AGGCTGGA
                                ||||||| ||||||| ||||||||
                                AGAGCGA ACAGCGG TCCGACCT
                                   A      _
GAM642  LOC92340  3'  TCCAGCCTAGTAATGGAGCAAG 69568     C         CC
          A                     TCT GCTCTGTTGC  AGGCTGGA
                                ||| ||||||||||  ||||||||
                                AGA CGAGGTAATG  TCCGACCT
                                  A         A_
GAM642  LOC92360  3'  TCCAGCCTGGGTGACAGAGCAA 69626     C      TG
          GG                      TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||||
                                GGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM642  LOC92405  3'  TCTAGCCTGGGCAACAGAGCAA 69718     C
          GG                      TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                GGA CGAGACAACGGGTCCGATCT
                                  A
GAM642  LOC92421  3'  TCCAGACTGGGCAACAGAGGGA 69729      G           G
          GA                      TCTC CTCTGTTGCCCAG CTGGA
                                |||| |||||||||||| |||||
                                AGAG GAGACAACGGGTC GACCT
                                  G           A
GAM642  LOC92421  5'  TCCGGTCTGGGTCCCCGAGA   69730       CTCTGTT
                                TCTCG      GCCCAGGCTGGA
                                |||||      ||||||||||||
                                AGAGC      TGGGTCTGGCCT
                                   CCC____
GAM642  LOC92421  3'  TTTAGTATAGCGGGGGGTGGGG 69733          G    CCAG
                                TCTCGCTCT TTGC    GCTGGA
                                ||||||||| ||||    ||||||
                                GGGGTGGGG GGCG    TGATTT
                                     _    ATA_
GAM642  LOC92465  5'  ACTCCAGCCTGGGCGACAGAGC 69934
          GAGA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGCGAGACAGCGGGTCCGACCT
                                                CAC
GAM642  LOC92465  5'  TCCAGTCTGGGCAACAGAGCAA 69956     C
          GA                      TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
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                                AGA CGAGACAACGGGTCTGACCT
                                  A
GAM642  LOC92466  5'  TCCAGCCTGGGAGACAGAGTGA 69969          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                       GA
GAM642  LOC92482  3'  ACCCCAGCCTGGGCAACAGAGC 70014     C             A
                AAGA                  TCT GCTCTGTTGCCCAGGCTGG
                                    ||| ||||||||||||||||||
                                    AGA CGAGACAACGGGTCCGACC
                                      A               CCAC
GAM642  LOC92492  3'  TCCAGCCTGGATGACAGCGAGA 70083       CT   GC
                                    TCTCGCT  GTT  CCAGGCTGGA
                                    |||||||  |||  ||||||||||
                                    AGAGCGA  CAG  GGTCCGACCT
                                       __  TA
GAM642  LOC92497  5'  CCCAGCGGCAGCAGGGTGAGG  70095            CAG    A
                                    TCTCGCTCTGTTGCC   GCTGG
                                    ||||||||||||||   |||||
                                    GGAGTGGGACGACGG   CGACC
                                             ___    CG
GAM642  LOC92539  3'  TCTAGCTTGGAAGGGGGAGGGA 70224    G    G  GC
                                    TC CTCT TT  CCAGGCTGGA
                                    || |||| ||  ||||||||||
                                    AG GAGG GG  GGTTCGATCT
                                     G    G  AA
GAM642  LOC92568  3'  ACTCCAGCCTGGGTGACAGAGT 70322          TG
                GAGA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          GT         CAC
GAM642  LOC92568  3'  TCTGGGGACTGTTGTGGGGTGG 70333         _______  G     CTGGA
                GA                    TCTCGCTCT     GTT CCCAGG
                                    |||||||||     ||| ||||||
                                    AGGGTGGGG     CAG GGGTCT
                                        TGTTGT  _       A
GAM642  LOC92573  3'  ACTCCAGCCTGGGTGACAGAGC 70365          TG
                GAGA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGCGAGACA  GGGTCCGACCT
                                          GT         CAC
GAM642  LOC92609  3'  TCCAGATGGGGGCATCAGGGTG 73211          T    AGG_
                AGG                   TCTCGCTCTG TGCCC    CTGGA
                                    |||||||||| |||||   |||||
                                    GGAGTGGGAC ACGGG    GACCT
                                          T    GGTA
GAM642  LOC92659  3'  TCCAGCCTGGGCGACAGAG   70610
                                    CTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||
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                                GAGACAGCGGGTCCGACCT

GAM642  LOC92661  5' TCATGATGGGTGGCAGAGCAAG 70635     C      TG    GGC   A
                      A                    TCT GCTCTGT  CCCA   TGG
                                           ||| |||||||  ||||   |||
                                           AGA CGAGACG  GGGT   ACT
                                             A      GT    AGT
GAM642  LOC92710  5' TCTGGTCACCAAGGCTGGGCGG 70870         T   GCCCA   TG
                      GA                     TCTCGCTC GTT     GGC  GA
                                             ||||||||  |||     |||  ||
                                             AGGGCGGG CGG     CTG  CT
                                                 T   AACCA   GT
GAM642  LOC92714  5' GCGGGCGGCGGGCGGGG     70899       T       AG
                                           TCTCGC CTGTTGCCC  GC
                                           ||||||  |||||||||  ||
                                           GGGGCG GGCGGCGGG  CG

                                             _       __
GAM642  LOC92771  3' TCCAGCCTGGGCCACAGAATGA 54215       C    T
                      GA                     TCTCG TCTGT GCCCAGGCTGGA
                                             |||||  |||||  ||||||||||||
                                             AGAGT AGACA CGGGTCCGACCT
                                               A    C
GAM642  LOC92973  5' CTCCAGCCTGGGCAACAGAGTG 71589
                      AGG                     TCTCGCTCTGTTGCCCAGGCTGGA
                                              |||||||||||||||||||||||||
                                              GGAGTGAGACAACGGGTCCGACCT
                                                          CA
GAM642  LOC93070  3' TCCAGCCTGGGCAACAGAGGGA 71815      G
                      GA                     TCTC CTCTGTTGCCCAGGCTGGA
                                             ||||  ||||||||||||||||||
                                             AGAG GAGACAACGGGTCCGACCT
                                               G
GAM642  LOC93109  3' CGGCTGGATTCAGTAACGCAGC 71921        C     _________  AGGCT
                      GGGA                     TCTCGCT TGTTGC       CC    G
                                               |||||||  ||||||       ||    |
                                               AGGGCGA GCAATG       GG    C
                                                  C     ACTT   A  TCGGA
GAM642  LOC93132  5' ACCGTAGCCTGGGTGATAAGAG 71972          _  TG       GA
                      TGAGA                     TCTCGCTCT GT  CCCAGGCTG
                                                |||||||||  ||  |||||||||
                                                AGAGTGAGA TA  GGGTCCGAT
                                                   A  GT        GCCAC
GAM642  LOC93132  3' TCCAGCTCGGGCAACAAAGTGA 72000        C       AG
                      GA                     TCTCGCT TGTTGCCC  GCTGGA
                                             |||||||  ||||||||  ||||||
                                             AGAGTGA ACAACGGG  CGACCT
                                                A       CT
GAM642  LOC93190  3' TCCAGCCTTGGTGACAGAGTGA 72100           TG  C
                      GA                     TCTCGCTCTGT  CC AGGCTGGA
                                             ||||||||||  || ||||||||
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                                AGAGTGAGACA  GG TCCGACCT
                                      GT  T
GAM642  LOC93259  5'  TCCAGCCTGACTGGGGCAGGA  72293    TC    _  TGCC
                                TC  GCTCT GT    CAGGCTGGA
                                ||  ||||| ||    |||||||||
                                AG  CGGGG CA    GTCCGACCT
                                 GA     T _____
GAM642  LOC93259  5'  TCTGGAAAAAGCATGGGGTGGG 72295          T  CCAGG TG
              G                   TCTCGCTCTGT GC     C  GA
                                ||||||||||| ||     |  ||
                                GGGGTGGGGTA CG     G  CT
                                      _  AAAAA GT
GAM642  LOC93589  3'  CTGTGTTGGGGTGGGG      73050          TT  C
                                TCTCGCTCTG  GC CAG
                                ||||||||||  || |||
                                GGGGTGGGGT  TG GTC
                                      __  T
GAM642  LOC93613  3'  TCCAACCTGGGCGGCAGAGTGA 73082                C
              GA                    TCTCGCTCTGTTGCCCAGG TGGA
                                ||||||||||||||||||| ||||
                                AGAGTGAGACGGCGGGTCC ACCT
                                           A
GAM642  LOC96597  5'  TCCAGCCCCTGATGGGGCAGA  67466     C       CCCA
                                TCT GCTCTGTTG    GGCTGGA
                                ||| |||||||||    |||||||
                                AGA CGGGGTAGT    CCGACCT
                                  _        CC__
GAM642  LOC96597  5'  TCCAGCCTGGGCGACAAGAGGG 67467     G   _
              AG                    CTC CTCT GTTGCCCAGGCTGGA
                                ||| |||| ||||||||||||||||
                                GAG GAGA CAGCGGGTCCGACCT
                                  G    A
GAM642  LOC96597  5'  TCCTTCGTCTGGGAGTGGGGTG 67469         TG  G      T__
              GGG                     TCTCGCTC  TT CCCAGGC   GGA
                                ||||||||  || |||||||   |||
                                GGGGTGGG  GA GGGTCTG   CCT
                                     GT  _      CTT
GAM642  LOC96597  5'  TCGGACCCTGATGGGGTGGA   67470    T      TGCC    __ TG
                                TC CGCTCTGT    CAGG  C  GA
                                || ||||||||    ||||  |  ||
                                AG GTGGGGTA    GTCC  G  CT
                                  _       _____    CA GT
GAM643  CDH12     3'  CTTATCATTTAAAGTGGTGTA  15777          CCCAA   GA
                                TACACCACT     GAA  ATAAG
                                |||||||||     |||  |||||
                                ATGTGGTGA     TTT  TATTC
                                      AA___   AC
GAM643  GOCAP1    3'  ATTGTTCTTGGGAGCAGTGTA  43007       CA         G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
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                                ATGTG  GAGGGTTCTT TTA
                                  AC        G
GAM643  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090      T   AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                  _   GTCA_
GAM643  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
          A                      TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                  TACTCCC_
GAM643  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126        CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM643  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
          TA                     TACA   TCC   GAAGAATAAG
                                ||||   |||   ||||||||||
                                ATGT   AGG   TTTCTTATTC
                                  AAA_  ATTG
GAM643  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68742            _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                         G
GAM643  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM643  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748     CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM643  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM643  OSBPL11   3'  CTTAATTTCCCAAGAGTGGTG  43206        CCAA   AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                     AACC   A_
GAM643  YME1L1    3'  TCATTCTTGATGTGGTGTA   58438        TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   |||||| ||
```

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                                ATGTGGTG  GTTCTT CT
                                    TA_    A
GAM643  ZNF262   3' CTTATTTTGTTTGGGAGT   18723       A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                   G
GAM643  LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294      TC_   AAGA
                                TACACCAC  CCAAG   ATA
                                ||||||||  |||||   |||
                                ATGTGGTG  GGTTC   TGT
                                    CAA   GG__
GAM644  BCAT1    3' AGAAAACAAAGAGGCATACT  66782   C      AAT
                                AG ATGCCTCTT  TTTTCT
                                || |||||||||  ||||||
                                TC TACGGAGAA  AAAAGA
                                 A       AC_
GAM644  ETF1     3' AGAAAAATTAAATTGCTGC   17587    T CTC
                                GCA GC  TTAATTTTTCT
                                ||| ||  ||||||||||
                                CGT CG  AATTAAAAAGA
                                  _ TTA
GAM644  EXTL2    5' AGAAGGATAGATGCACGCTA  9325     A  C  TA
                                TAGC TGC TCT  ATTTTTCT
                                |||| ||| |||  ||||||||
                                ATCG ACG AGA  TAGGAAGA
                                  C  T  __
GAM644  FOXE1    3' AGAAAAATTAAGTTAGGGCA  16777     ___
                                TGCCT  CTTAATTTTTCT
                                |||||  ||||||||||||
                                ACGGG  GAATTAAAAAGA
                                   ATT
GAM644  FZD3     3' AGAAAAATGCTGGAACATGCT 34257     CC  TA_
                                AGCATG  TCT  ATTTTTCT
                                ||||||  |||  ||||||||
                                TCGTAC  AGG  TAAAAAGA
                                   A_  TCG
GAM644  RRM2B    3' AAAAATTAAGAGTGTGTT    68429      C
                                AGCATGC TCTTAATTTTT
                                ||||||| ||||||||||
                                TTGTGTG AGAATTAAAAA
                                        _
GAM644  ZNF132   3' AGAAAAATTACCTCCATGCT  14286     CCTCT
                                AGCATG    TAATTTTTCT
                                ||||||    ||||||||||
                                TCGTAC    ATTAAAAAGA
                                   CTCC_
GAM644  BAP29    3' AGAAAAATATAAGCATGTTA  61331      CTCTTA
                                TAGCATGC    ATTTTTCT
                                ||||||||    ||||||||
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                                ATTGTACG     TAAAAAGA
                                     AATA__
GAM644  FAM8A1    3'  AGAAAAATCTGGCATACTG   33197     C    TCTTA
                                TAG ATGCC    ATTTTTCT
                                ||| |||||    ||||||||
                                GTC TACGG    TAAAAAGA
                                  A    TC___
GAM644  FLJ10648  3'  AGAAAAATTAGGTTCCATGC   36888      CCT
                                GCATG   CTTAATTTTTCT
                                |||||   ||||||||||||
                                CGTAC   GGATTAAAAAGA
                                   CTT
GAM644  FLJ10970  3'  AGAAAAATCAAGATAGGCCTG  37476    T   __    A
                                CA GCC  TCTT ATTTTTCT
                                || |||  |||| ||||||||
                                GT CGG  AGAA TAAAAAGA
                                 C   AT    C
GAM644  FLJ14735  3'  AAAAACTGATGAGGCATGC    52663         _   A
                                GCATGCCTC TTA TTTTT
                                ||||||||| ||| |||||
                                CGTACGGAG AGT AAAAA
                                     T   C
GAM644  KIAA0830  3'  AGAAAAATAGCGGAGGCA    70266        TA_
                                TGCCTCT   ATTTTTCT
                                |||||||   ||||||||
                                ACGGAGG   TAAAAAGA
                                    CGA
GAM644  KIAA0907  3'  AGAAAAATTAAGCTGGGCA   30862      __
                                TGCCT  CTTAATTTTTCT
                                |||||  ||||||||||||
                                ACGGG  GAATTAAAAAGA
                                   TC
GAM644  KIAA1348  3'  AGAAACTTTGAGCCATGCTA   69116       CCT    TT
                                TAGCATG   CTTAA  TTTCT
                                |||||||   |||||  |||||
                                ATCGTAC   GAGTT  AAAGA
                                    C__    TC
GAM644  RNF2      3'  AGAAAAATTAAATTGGTAGT   24256    A   TC_
                                GC TGCC   TTAATTTTTCT
                                || ||||   ||||||||||
                                TG ATGG   AATTAAAAAGA
                                 _   TTA
GAM644  LOC143146 3'  AGAAAATGGCCGAGGCATGCTA 60763          TTAAT
                                TAGCATGCCTC    TTTTCT
                                ||||||||||    ||||||
                                ATCGTACGGAG    AAAAGA
                                      CCGGT
GAM644  LOC146059 3'  AGAAAAGTCCAGAGATGC    78082      GC    TA
                                GCAT  CTCT  ATTTTTCT
                                ||||  ||||  ||||||||
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                                CGTA  GAGA  TGAAAAGA
                                  __    CC
GAM644   LOC151391 3'  AGAAAGATCAAAGCATGC    86511       CTC  A
                                GCATGC   TT ATTTTTCT
                                ||||||   || ||||||||
                                CGTACG   AA TAGAAAGA
                                   A__  C
GAM644   LOC157507 5'  AAAGAAGAGGAGGCAACTA   82374     CA      AA
                                TAG  TGCCTCTT  TTTTT
                                |||  ||||||||  |||||
                                ATC  ACGGAGGA  AGAAA
                                 A_       GA
GAM644   LOC158434 3'  AAAAATTACAAGGCATGC    88156        CT
                                GCATGCCT  TAATTTTT
                                ||||||||  ||||||||
                                CGTACGGA  ATTAAAAA
                                     AC
GAM644   LOC220020 5'  AGAAAACAGGTGAAGGCATGC  95043        _ TTAAT
                                GCATGCCT C    TTTTCT
                                |||||||| |    ||||||
                                CGTACGGA G    AAAAGA
                                     A TGGAC
GAM644   LOC221979 3'  AGAGTGCAGAAGGCATGC    94216        _  TA
                                GCATGCCT CT  ATTTT
                                |||||||| ||  |||||
                                CGTACGGA GA  TGAGA
                                     A  CG
GAM644   LOC92078  3'  AGAAATCCGAAGAGGCAGCTA  68588     A       AATT
                                TAGC TGCCTCTT    TTTCT
                                |||| ||||||||    |||||
                                ATCG ACGGAGAA    AAAGA
                                  _       GCCT
GAM644   LOC92080  5'  AGAAAAATCAAGACCATGTTA  68617       CC    A
                                TAGCATG  TCTT ATTTTTCT
                                |||||||  |||| ||||||||
                                ATTGTAC  AGAA TAAAAAGA
                                    C_   C
GAM645   AF5Q31    5'  CCACTGCCGCAGCCAGGAG   27778        GT    _
                                CTCCTGGT  TGGC GTGG
                                ||||||||  |||| ||||
                                GAGGACCG  GCCG CACC
                                     AC    T
GAM645   AGRN      5'  CCACTGGGGACACCAGGA    79583         GG _
                                TCCTGGTGTT  C GTGG
                                ||||||||||  | ||||
                                AGGACCACAG  G CACC
                                      GG T
GAM645   ARVCF     5'  CCACGCTGCGCTCCAGGA    9801        T  _
                                TCCTGG GT TGGCGTGG
                                ||||||  || ||||||||
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                                AGGACC CG GTCGCACC
                                   T  C
GAM645  CAPS    3'  CCACGCCATGCTGACCAGAG  15766    C   __ _
                                CTC TGGT  GT TGGCGTGG
                                ||| ||||  || ||||||||
                                GAG ACCA  CG ACCGCACC
                                  _   GT  T
GAM645  CD244   3'  CCAGTTGGCCACCAGGGG   33503       _ TG  G
                                CTCCTGGTG T  GC TGG
                                ||||||||| |  || |||
                                GGGGACCAC G  TG ACC
                                     C GT  _
GAM645  CD7     3'  CCACGCCGCCACCGGGAG   21542       T
                                CTCCTGGTG TGGCGTGG
                                ||||||||| ||||||||
                                GAGGGCCAC GCCGCACC
                                     C
GAM645  CELL    3'  CCACAGTGACCGACCAGGAG  10168       __   GC
                                CTCCTGGT  GTTG  GTGG
                                ||||||||  ||||  ||||
                                GAGGACCA  CAGT  CACC
                                     GC   GA
GAM645  CRY2    3'  CCACAGTGCTGCCAGTGAG   72659    _   GTT  ___
                                CTC CTGGT  GGC  GTGG
                                ||| |||||  |||  ||||
                                GAG GACCG  TCG  CACC
                                  T   ___  TGA
GAM645  FGA     3'  CCATTCAGTACATCAGGA    6701        __  C
                                TCCTGGTGT  TGG GTGG
                                |||||||||  ||| ||||
                                AGGACTACA  ACT TACC
                                     TG  _
GAM645  FHL2    5'  CCACGCCCGGTGCCAGCGAG  9364    _   TG  _
                                CTC CTGG  TTGG CGTGG
                                ||| ||||  |||| |||||
                                GAG GACC  GGCC GCACC
                                  C   GT   C
GAM645  GTF2H1  3'  CCACGCCAACTCCCAGAG    19209    CT  T
                                CTC  GG GTTGGCGTGG
                                |||  || ||||||||||
                                GAG  CC CAACCGCACC
                                  AC  T
GAM645  IL1F5   5'  CCACAGCTCCCGCCAGGAG   25375       TT  _
                                CTCCTGGTG  GGC GTGG
                                |||||||||  ||| ||||
                                GAGGACCGC  TCG CACC
                                     CC   A
GAM645  LGALS3BP 3'  CCACTAGGGTCCACCAGGAG  69858       TT  ____
                                CTCCTGGTG  GGC   GTGG
                                |||||||||  |||   ||||
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                                GAGGACCAC  CTG   CACC
                                    __  GGAT
GAM645  OVOL1    5'  CCACAGCCCTACCGGGAG    17062        TT  _
                                CTCCTGGTG  GGC GTGG
                                |||||||||  ||| ||||
                                GAGGGCCAT  CCG CACC
                                    C_  A
GAM645  SLC13A4  3'  CCACTAGGACCACCAGGAG   25860        _ GGC
                                CTCCTGGTG TT  GTGG
                                |||||||||  ||  ||||
                                GAGGACCAC AG  CACC
                                    C  GAT
GAM645  TCF2     3'  CCACAGCGATCCACGGAG    6610      _  T   GC
                                CTCC TGG GTTG  GTGG
                                ||||  ||| ||||  ||||
                                GAGG ACC TAGC  CACC
                                  C  _  GA
GAM645  TSG      3'  CCACCTAGAGCACCAGGA    40603        __  C
                                TCCTGGTGT  TGG GTGG
                                |||||||||  ||| ||||
                                AGGACCACG  ATC CACC
                                    AG  _
GAM645  AGS3     5'  CCACGGCGAGCCCCAGGAG   73508       T  G  _
                                CTCCTGG GTT GC GTGG
                                |||||||  ||| ||  ||||
                                GAGGACC CGA CG CACC
                                   C  G  G
GAM645  AMOT     5'  CCACAGCAGCAGCCAGGAG   56538       _   GC
                                CTCCTGG TGTTG  GTGG
                                |||||||  |||||  ||||
                                GAGGACC ACGAC  CACC
                                   G   GA
GAM645  BM-002   3'  CTATGAAAACACCAGGAG    34007         GG
                                CTCCTGGTGTT  CGTGG
                                ||||||||||  |||||
                                GAGGACCACAA  GTATC
                                    AA
GAM645  C11orf9  3'  CCACACCAGGGACCAGGGG   26117       G _  C
                                CTCCTGGT T TGG GTGG
                                ||||||||  | ||| ||||
                                GGGGACCA G ACC CACC
                                   G G  A
GAM645  CENTG2   5'  CCACGCCACGGCCAGGAG    30537       GT
                                CTCCTGGT  TGGCGTGG
                                ||||||||  ||||||||
                                GAGGACCG  ACCGCACC
                                    GC
GAM645  DKFZP586P0123 5'  CCATCTCACAGCACCAGGAG  96495          GC__
                                CTCCTGGTGTTG   GTGG
                                ||||||||||||   ||||
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                                GAGGACCACGAC   TACC
                                      ACTC
GAM645  EAT2     3'  CCAGACATATACCAGGAG    80048        _ GCG
                                CTCCTGGTGT TG   TGG
                                |||||||||| ||   |||
                                GAGGACCATA AC   ACC
                                     T  AG_
GAM645  FLJ11175 3'  CCTTGAGAACAGCCAGGAG   37715       _   GG  T
                                CTCCTGG TGTT  CG GG
                                ||||||| ||||  || ||
                                GAGGACC ACAA  GT CC
                                    G   GA  T
GAM645  FLJ11807 3'  CCACAAGGGCCAACCAGGAG  46943       GT   ____
                                CTCCTGGT  TGGC   GTGG
                                ||||||||  ||||   ||||
                                GAGGACCA  ACCG   CACC
                                    __   GGAA
GAM645  FLJ12436 5'  CCACGCCAGATCTCAGGA    45414      TG_
                                TCCTGG   TTGGCGTGG
                                ||||||   |||||||||
                                AGGACT   GACCGCACC
                                   CTA
GAM645  FLJ14001 5'  CCACTTCACGACACCGGAG   45489     T     GC__
                                CTCC GGTGTTG   GTGG
                                |||| |||||||   ||||
                                GAGG CCACAGC   CACC
                                  _     ACTT
GAM645  FLJ14146 3'  CCACTCTGTCACCAGGAG    45567       T  C
                                CTCCTGGTG TGG GTGG
                                ||||||||| ||| ||||
                                GAGGACCAC GTC CACC
                                     T  T
GAM645  FLJ14824 3'  CCACCTAAAGACCAGGAG    52715       G_  C
                                CTCCTGGT  TTGG GTGG
                                ||||||||  |||| ||||
                                GAGGACCA  AATC CACC
                                     GA  _
GAM645  FLJ22282 5'  CCACGCGGCGCCAGCGAG    45964    _      G
                                CTC CTGGTGTTG CGTGG
                                ||| ||||||||| |||||
                                GAG GACCGCGGC GCACC
                                  C       _
GAM645  KIAA0140 3'  CCACGCAGCAGTCAGGGG    28507      _   G
                                CTCCTGG TGTTG CGTGG
                                ||||||| ||||| |||||
                                GGGGACT ACGAC GCACC
                                    G   _
GAM645  KIAA0720 5'  CCACGCCGACTGCCAGCAG   62978   C   _
                                CT CTGGT GTTGGCGTGG
                                || ||||| ||||||||||
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                                GA GACCG CAGCCGCACC
                                 C    T
GAM645  KIAA0773  3'  CCACGCCAGGCCCAAGAG    28720    C   TG
                                CTC TGG  TTGGCGTGG
                                ||| |||  |||||||||
                                GAG ACC  GACCGCACC
                                  A   CG
GAM645  KIAA1026  3'  CCAGAAATAACCACCAGGAG   71733        _  GCG_
                                CTCCTGGTG TTG    TGG
                                ||||||||| |||    |||
                                GAGGACCAC AAT    ACC
                                     C   AAAG
GAM645  MGC2734   5'  CCACGCCGAGGCCACGAG    53578    C    G
                                CTC TGGT TTGGCGTGG
                                ||| |||| |||||||||
                                GAG ACCG AGCCGCACC
                                  C    G
GAM645  MGC33182  5'  CCACGCCCTGTAACACCGGGA  76093         ____
                                TCCTGGTGTT    GGCGTGG
                                ||||||||||    |||||||
                                AGGGCCACAA    CCGCACC
                                      TGTC
GAM645  MGC3771   5'  CCACACCAAGGACACCAGGAG  49051         ___  C
                                CTCCTGGTGT   TGG GTGG
                                ||||||||||   ||| ||||
                                GAGGACCACA   ACC CACC
                                      GGA   A
GAM645  PRO2900   3'  CCACGCCGGCTGAGGTAG    38438    _  GGT
                                CT CCT   GTTGGCGTGG
                                || |||   ||||||||||
                                GA GGA   CGGCCGCACC
                                 T   GT_
GAM645  PRO2949   5'  CCAGGTCAACACCAGTAG    38220    C        G
                                CT CTGGTGTTGGC TGG
                                || ||||||||||| |||
                                GA GACCACAACTG ACC
                                 T         G
GAM645  RP4-622L5 3'  CCAGCTCTCAGCCAGGAG    39423       _ TT   G
                                CTCCTGG TG  GGC TGG
                                ||||||| ||  ||| |||
                                GAGGACC AC  TCG ACC
                                    G  TC  _
GAM645  SIAT8C    5'  CCACCTAGCCCATCAGGAG   32444        TT  ___
                                CTCCTGGTG  GGC   GTGG
                                |||||||||  |||   ||||
                                GAGGACTAC  CCG   CACC
                                      __  ATC
GAM645  LOC124930 3'  CCACGCCCAGGGCCAGGAG   74823        G   _
                                CTCCTGGT TTGG CGTGG
                                |||||||| |||| |||||
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                                GAGGACCG GACC GCACC
                                     G    C
GAM645   LOC125268 3'  CCACACCGAAGCCAGGGG    76572        G    C
                                CTCCTGGT TTGG GTGG
                                |||||||| |||| ||||
                                GGGGACCG AGCC CACC
                                     A    A
GAM645   LOC143158 5'  CCACGTTCGTGACCGGGAG   76998        GT   _
                                CTCCTGGT  TGG CGTGG
                                |||||||| ||| |||||
                                GAGGGCCA  GCT GCACC
                                     GT   T
GAM645   LOC144395 3'  CCACCTTGGCACCAGGAG    77320        TG C
                                CTCCTGGTGT  G GTGG
                                ||||||||||  | ||||
                                GAGGACCACG  T CACC
                                      GT C
GAM645   LOC148148 5'  CCACAGCTAAGACACCAGGA  79378         __  _
                                TCCTGGTGTT  GGC GTGG
                                ||||||||||  ||| ||||
                                AGGACCACAG  TCG CACC
                                      AA   A
GAM645   LOC148753 3'  CCACGGGTAGGCACCAGGGG  85369         GG__
                                CTCCTGGTGTT    CGTGG
                                ||||||||||    |||||
                                GGGGACCACGG    GCACC
                                      ATGG
GAM645   LOC148764 3'  CCACGCCACTTCACACCAGGG 79734         ____
                                TCCTGGTGT    TGGCGTGG
                                |||||||||    ||||||||
                                GGGACCACA    ACCGCACC
                                     CTTC
GAM645   LOC149832 5'  CCACGGAGGGGCCAGGAG    85862        G  GG
                                CTCCTGGT TT  CGTGG
                                |||||||| ||  |||||
                                GAGGACCG GG  GCACC
                                     G  AG
GAM645   LOC152286 3'  CCACACTAGACAGCCAGGAG   86805        _  _  C
                                CTCCTGG TGT TGG GTGG
                                ||||||| ||| ||| ||||
                                GAGGACC ACA ATC CACC
                                    G  G   A
GAM645   LOC152317 5'  CCACACAGCGAGCCAGGGG   86826        __   GC
                                CTCCTGGT  GTTG  GTGG
                                ||||||||  ||||  ||||
                                GGGGACCG  CGAC  CACC
                                     AG    A_
GAM645   LOC153196 5'  CCACGCCATGGAGCCAGGGG  87165        GT__
                                CTCCTGGT    TGGCGTGG
                                ||||||||    ||||||||
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                                GGGGACCG   ACCGCACC
                                    AGGT
GAM645  LOC157860 3'  CCATCGAGACACCATGGA    87877    _     GG  _
                                TCC TGGTGTT  CG TGG
                                ||| |||||||  || |||
                                AGG ACCACAG  GC ACC
                                  T      A_  T
GAM645  LOC159199 3'  CCACAGCCAACACCAGCAG   83058    C        _
                                CT CTGGTGTTGGC GTGG
                                || |||||||||| ||||
                                GA GACCACAACCG CACC
                                 C          A
GAM645  LOC202404 5'  CCACGCCAAGTCCGCCCAGG  90649      _ ___
                                CCTGG TG   TTGGCGTGG
                                ||||| ||   ||||||||
                                GGACC GC   AACCGCACC
                                   C  CTG
GAM645  LOC203113 3'  CCACAAGTTAACATCAAGA   90793    C       __
                                TC TGGTGTTGGC  GTGG
                                || ||||||||||  ||||
                                AG ACTACAATTG  CACC
                                 A         AA
GAM645  LOC204275 3'  CCATCATTAACACCAAGA    91004    C       C_
                                TC TGGTGTTGG  GTGG
                                || |||||||||  ||||
                                AG ACCACAATT  TACC
                                 A        AC
GAM645  LOC205418 5'  CCACGCATGCTGACCAGGG   92370       __ TG
                                TCCTGGT  GT  GCGTGG
                                |||||||  ||  ||||||
                                GGGACCA  CG  CGCACC
                                    GT  TA
GAM645  LOC253712 5'  CCACACCCTGCAGCGGGAG   98726       G  T_  C
                                CTCCTG TGT  GG GTGG
                                |||||| |||  || ||||
                                GAGGGC ACG  CC CACC
                                   G   TC  A
GAM645  LOC256306 5'  CCACGCCAAGGGGCTAGG    98506       G__
                                CCTGGT   TTGGCGTGG
                                ||||||   |||||||||
                                GGATCG   AACCGCACC
                                   GGG
GAM645  LOC51162  5'  CCACGCCTGGGCTCCAGCAG  33049    C   T  __
                                CT CTGG GTT  GGCGTGG
                                || |||| |||  |||||||
                                GA GACC CGG  CCGCACC
                                 C   T   GT
GAM645  LOC55565  3'  CCACACCCACAGCCACGAG   34473    C  _  T  C
                                CTC TGG TGT GG GTGG
                                ||| ||| ||| || ||||
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                                GAG ACC ACA CC CACC
                                  C   G   C A
GAM645  LOC91145  3'  CCACACCATGCTGAGGTAG   65681    _  _    T  C
                                CT CCT GGTGT GG GTGG
                                || ||| ||||| || ||||
                                GA GGA TCGTA CC CACC
                                 T   G    _ A
GAM646  VAT1      3'  TAACCAAGGCTGCCTCTT    22091     A  C   C
                                AAGA GC GCC TGGTTG
                                |||| || ||| ||||||
                                TTCT CG CGG ACCAAT
                                  C T   A
GAM646  AP3M2     3'  CATGTGCAGAAGTAGCTTCT  23300      CG CCTGG
                                AGAAGC  C    TTGCACATG
                                ||||||  |    |||||||||
                                TCTTCG  G    GACGTGTAC
                                   AT AA___
GAM646  FLJ12505  5'  GTCAACAAGAGCGGCTTC    45717       C  G   C
                                GAAGCCGC CT GTTG AC
                                |||||||| || |||| ||
                                CTTCGGCG GA CAAC TG
                                    A  A   _
GAM646  ITPK1     3'  ATGTGAGAGTGGCTTC      27228       C  GGTTG
                                GAAGCCGC CT    CACAT
                                |||||||| ||    |||||
                                CTTCGGTG GA    GTGTA
                                    A  _____
GAM646  KIAA0275  3'  CATGTGTTCAAAGAACGGTTTC 29324       CC  GGTT
           TT                    AAGAAGCCG  CT   GCACATG
                                |||||||||  ||   |||||||
                                TTCTTTGGC  GA   TGTGTAC
                                    AA  AACT
GAM646  KIAA0830  3'  GCATCCAAACGGCTTCTT    70268       CCC   T
                                AAGAAGCCG   TGG TGC
                                |||||||||   ||| |||
                                TTCTTCGGC   ACC ACG
                                    AA_   T
GAM646  KIAA1399  3'  CATGTGCAATGCCAGCCCCTTC 70790     CC  CC   __
                                GAAG  GC  TGGT  TGCACATG
                                ||||  ||  ||||  ||||||||
                                CTTC  CG  ACCG  ACGTGTAC
                                  CC  __   TA
GAM646  KIAA1643  3'  CATATGCATAGAAACGGCTTCT 65154       CC_  GT   C
                                AGAAGCCG   CTG  TGCA ATG
                                ||||||||   |||  |||| |||
                                TCTTCGGC   GAT  ACGT TAC
                                    AAA   __   A
GAM646  MAGE-E1   3'  GCACCCTAGGCGGCTTCTT   48675         CT  T
                                AAGAAGCCGCC  GG TGC
                                ||||||||||  || |||
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                                TTCTTCGGCGG  CC ACG
                                      AT  C
GAM646  MRPS2    3'  CATGTGCAGAACGGCCCCTT  32631     AA    CCCTGG
                                AAG  GCCG     TTGCACATG
                                |||  ||||     |||||||||
                                TTC  CGGC     GACGTGTAC
                                  CC    AA____
GAM646  SSTK     3'  CATGCGCATCCGCGATTC    50169     GC   CCT  T   A
                                GAA  CGC   GG TGC CATG
                                |||  |||   || ||| ||||
                                CTT  GCG   CC ACG GTAC
                                  A_  ___  T   C
GAM646  LOC148887 3'  CATGCGCATTAAAGCAGGGCGG 85396    A   _     G ____   A
            GCTCCT                  AG AGCC GCCCTG T    TGC CATG
                                || |||| |||||| |    ||| ||||
                                TC TCGG CGGGAC A    ACG GTAC
                                 C   G     G AATT   C
GAM646  LOC150605 5'  TGGGACCAGGGGGCCTC     86263    A  G      G
                                GA GCC CCCTGGTT CA
                                || ||| ||||||||| ||
                                CT CGG GGGACCAG GT
                                 C  _       G
GAM646  LOC152402 5'  GTGCCCAGAGCCGGCTTCT    86884        _ C    TT
                                AGAAGCCG C CTGG  GCAC
                                |||||||| | ||||  ||||
                                TCTTCGGC G GACC  CGTG
                                     C A   __
GAM646  LOC158078 3'  CATGTGTGTTGAGAGCTTCT   82600       CGCC  GGT
                                AGAAGC   CT   TGCACATG
                                ||||||   ||   ||||||||
                                TCTTCG   GA   GTGTGTAC
                                   A___  GTT
GAM646  LOC163882 3'  CATAGGCAACCAGAGCCACTTC 83040      CC  C       AC
                                GAAG  GC CTGGTTGC  ATG
                                ||||  || ||||||||  |||
                                CTTC  CG GACCAACG  TAC
                                  AC  A       GA
GAM646  LOC200138 3'  CATGTGCTTCCAGGGTGGCTTC 91539           TT
                                GAAGCCGCCCTGG  GCACATG
                                ||||||||||||  |||||||
                                CTTCGGTGGGACC  CGTGTAC
                                       TT
GAM646  LOC51099  3'  CAACCAGGCAGCCTTCTT    32600       _ C   C
                                AAGAAG C GCC TGGTTG
                                |||||| | ||| ||||||
                                TTCTTC G CGG ACCAAC
                                   C A  _
GAM647  ADRA1B    5'  GGAGGGCGGACTCTAA      7285         ATCAA    C
                                TTGGAGTC    TGCCC CC
                                ||||||||    ||||| ||
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                                AATCTCAG    GCGGG GG
                                   _____    A
GAM647  F3      3'  GGGGGCTGACTTCAA      67679        TCAAT    C
                                TTGGAGTCA    GCCCC C
                                |||||||||    ||||| |
                                AACTTCAGT    CGGGG G
                                   _____    A
GAM647  GABPA   3'  GGACATTCTGAGACTCCAA   10749       A  __  _
                                TTGGAGTC TCA  ATG CC
                                |||||||| |||  ||| ||
                                AACCTCAG AGT  TAC GG
                                   _  CT   A
GAM647  HIP1    3'  GGGCTGATGGATTCCAA     19260       _   AT
                                TTGGAGTC ATCA  GCCC
                                |||||||| ||||  ||||
                                AACCTTAG TAGT  CGGG
                                   G   __
GAM647  HR      5'  TGGGGGGCACCCCGCCCAA   18919     A  CATCAA
                                TTGG GT     TGCCCCCCA
                                |||| ||     |||||||||
                                AACC CG     ACGGGGGGT
                                  _ CCCC__
GAM647  IGF1    3'  TGGGAAGCATTTGATTTTCAA  7087       _  TC    CC
                                TTGGAG TCA  AATGC  CCCA
                                |||||| |||  |||||  ||||
                                AACTTT AGT  TTACG  GGGT
                                   T  __    AA
GAM647  IL1RN   3'  GGCCACTTGATGACCCCCAA  6958      A_      T__
                                TTGG  GTCATCAA   GCC
                                ||||  ||||||||   |||
                                AACC  CAGTAGTT   CGG
                                  CC       CAC
GAM647  KCNC3   3'  TGGGAGGGGGTGTCCCCAA   18333     AGT   AATG  _
                                TTGG   CATC    CCC CCCA
                                ||||   ||||    ||| ||||
                                AACC   GTGG    GGG GGGT
                                  CCT    _____  A
GAM647  KIFC3   5'  TGGGGGGCACCGACTTGGA   19894    G    ATCAA
                                TT GAGTC    TGCCCCCCA
                                || |||||    |||||||||
                                AG TTCAG    ACGGGGGGT
                                 G    CC___
GAM647  PPP6C   3'  GGGCACGATGGACTCCAA    12253       _  AA
                                TTGGAGTC ATC  TGCCC
                                |||||||| |||  |||||
                                AACCTCAG TAG  ACGGG
                                   G  C_
GAM647  RNGTT   5'  GGGGAGGCGGCTCCAA      15066       ATCAAT  _
                                TTGGAGTC     GCC CCCC
                                ||||||||     ||| ||||
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                                AACCTCGG     CGG GGGG
                                   _______   A
GAM647  SFRS1    3'  GGAGGCAATGGTATGACTCCAA 23623          __ A   C
                                TTGGAGTCAT  CA TGCC CC
                                ||||||||||  || |||| ||
                                AACCTCAGTA  GT ACGG GG
                                      TG  A    A
GAM647  SNCA     3'  GGGGTGTTGAAGACCCCAA   6227      A   A
                                TTGG GTC TCAATGCCCC
                                |||| ||| ||||||||||
                                AACC CAG AGTTGTGGGG
                                  C   A
GAM647  SP110    3'  TGGGGAAGCAAATGACTCTAA  16914         CAA   C_
                                TTGGAGTCAT   TGC  CCCCA
                                ||||||||||   |||  |||||
                                AATCTCAGTA   ACG  GGGGT
                                      A__   AA
GAM647  VIPR1    3'  TGGGAGGACGGTGCAACCCAA  17315     A __    AATG  C
                                TTGG GT  CATC    CC CCCA
                                |||| ||  ||||    || ||||
                                AACC CA  GTGG    GG GGGT
                                  _ AC    CA__  A
GAM647  ZNF83    3'  TGGGAAACCATTATGACTTCAA 37538         C    CCC_
                                TTGGAGTCAT AATG    CCCA
                                |||||||||| ||||    ||||
                                AACTTCAGTA TTAC    GGGT
                                      _    CAAA
GAM647  AMOT     3'  GGAGGCAATGGCTCCAA     56547         CAA    C
                                TTGGAGTCAT   TGCC CC
                                ||||||||||   |||| ||
                                AACCTCGGTA   ACGG GG
                                      ____    A
GAM647  C1orf17  3'  TGGGGGGCCGTGCACACCCCAA 68770      A  CAT  AT
                                TTGG GT   CA  GCCCCCCA
                                |||| ||   ||  ||||||||
                                AACC CA   GT  CGGGGGGT
                                  C  CAC  GC
GAM647  DKFZP434O047 5'  GGGGGGCCAGAACCCAA     32124      A  CA  AAT
                                TTGG GT  TC   GCCCCCC
                                |||| ||  ||   |||||||
                                AACC CA  AG   CGGGGGG
                                  _  __  AC_
GAM647  DKFZp761H039 3'  TGGGGGGCTGGCAGGCCCCAA  77384      A   ATCAAT
                                TTGG GTC     GCCCCCCA
                                |||| |||     ||||||||
                                AACC CGG     CGGGGGGT
                                  C   ACGGT_
GAM647  FKSG28   3'  TGGGAGGCCTATTTGACTCCAA 48911         TCAAT   C
                                TTGGAGTCA    GCC CCCA
                                |||||||||    ||| ||||
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                                AACCTCAGT    CGG GGGT
                                     TTATC   A
GAM647  FLJ20626  5'  GGCCCATCTTGACGATTCCAA  35904       A   T____
                                TTGGAGTC TCAA    GCC
                                |||||||| ||||    |||
                                AACCTTAG AGTT    CGG
                                     C   CTACC
GAM647  FLJ20950  5'  GGGCTGTTGACTCCAA     46941        T  AT
                                TTGGAGTCA CA  GCCC
                                ||||||||| ||  ||||
                                AACCTCAGT GT  CGGG
                                     T  __
GAM647  FLJ22035  3'  GGAGTAAATGTGACTCCAA   44830        CAA   C
                                TTGGAGTCAT   TGC CC
                                ||||||||||   ||| ||
                                AACCTCAGTG   ATG GG
                                      TAA   A
GAM647  FLJ25179  3'  GGGGGTTATGGCTCCAA     59013        CAAT
                                TTGGAGTCAT   GCCCCC
                                ||||||||||   ||||||
                                AACCTCGGTA   TGGGGG
                                     T___
GAM647  FLJ32743  5'  TGGGACCAGCACAATGACTGCA 59464    G    CAA   CC__
          A                      TTG AGTCAT   TGC    CCCA
                                ||| ||||||   |||   ||||
                                AAC TCAGTA   ACG    GGGT
                                  G     AC_   ACCA
GAM647  LHFPL2    3'  TGGGGTTGCAATGACTCC    70501       CAA   C_
                                GGAGTCAT   TGC  CCCCA
                                ||||||||   |||  |||||
                                CCTCAGTA   ACG  GGGGT
                                     ___   TT
GAM647  MGC12945  5'  GGGGAGCACCTGGCTACAA   51268    G    TCAA   C
                                TTG AGTCA    TGC CCCC
                                ||| |||||    ||| ||||
                                AAC TCGGT    ACG GGGG
                                  A    CC__   A
GAM647  MGC16279  3'  GGCTTTGCCCTGAGACTCCAA  52988       A   AT  CCC_
                                TTGGAGTC TCA  GC    CC
                                |||||||| |||  ||    ||
                                AACCTCAG AGT  CG    GG
                                     _   CC  TTTC
GAM647  MGC20253  3'  TGGGAAGGACTTGACTCCAG   58679        TCAATG  C_
                                TTGGAGTCA     CC  CCCA
                                |||||||||     ||  ||||
                                GACCTCAGT     GG  GGGT
                                     TCA___   AA
GAM647  NIR3      5'  GGGAAGGCTTGGACTCCAA   66832        AT   T   C_
                                TTGGAGTC  CAA GCC  CCC
                                ||||||||  ||| |||  |||
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                                AACCTCAG  GTT CGG  GGG
                                   __  _  AA
GAM647  OSMR     3'  GGGGGGCATAGCTCTAA     15672        CATCA
                                TTGGAGT    ATGCCCCCC
                                |||||||    |||||||||
                                AATCTCG    TACGGGGGG
                                   A____
GAM647  TSCOT    3'  TGAGGGGCTTCAGACTCCAG   53512        ATCAAT    C
                                TTGGAGTC     GCCCC CA
                                ||||||||     ||||| ||
                                GACCTCAG     CGGGG GT
                                   ACTT__    A
GAM647  LOC124602 5'  TGAAGGACAGCGGGGACTCCAA 74793         AT AA  C  CC
                                TTGGAGTC  C  TG CC  CA
                                ||||||||  |  || ||  ||
                                AACCTCAG  G  AC GG  GT
                                   GG CG  A  AA
GAM647  LOC143034 5'  GGATGGTGACGACTCCGA    83785        A  AAT   CC
                                TTGGAGTC TC   GCC  CC
                                |||||||| ||   |||  ||
                                AGCCTCAG AG   TGG  GG
                                   C  ___   TA
GAM647  LOC144811 3'  TGGAAAAGTCATTAATGACTCT 84109         C   _ CCC_
          AA                     TTGGAGTCAT AATG C    CCA
                                ||||||||||| |||| |    |||
                                AATCTCAGTA TTAC G    GGT
                                   A    T AAAA
GAM647  LOC149127 3'  TGGAGAAGGAGATGACTTCAA  85506         AATG  CC__
                                TTGGAGTCATC    CC    CCA
                                ||||||||||    ||    |||
                                AACTTCAGTAG    GG    GGT
                                   A___  AAGA
GAM647  LOC149566 3'  GGCTTTGTTGAGACTCCAA    85652        A    ___
                                TTGGAGTC TCAAT   GCC
                                |||||||| |||||   |||
                                AACCTCAG AGTTG   CGG
                                   _     TTT
GAM647  LOC149832 5'  GGAGGGCAGACTCTAA      85865        ATCAA    C
                                TTGGAGTC     TGCCC CC
                                ||||||||     ||||| ||
                                AATCTCAG     ACGGG GG
                                   _____     A
GAM647  LOC150837 3'  TGGAACTTGGAAATGATTCCAA 80806         CAATG  CC___
                                TTGGAGTCAT    CC    CCA
                                ||||||||||    ||    |||
                                AACCTTAGTA    GG    GGT
                                   AA___  TTCAA
GAM647  LOC157450 3'  GGAAGCATTTCTGAGACTCCAA 71532        A   ___   CC
                                TTGGAGTC TCA   ATGC  CC
                                |||||||| |||   ||||  ||
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                                AACCTCAG AGT   TACG  GG
                                     _  CTT    AA
GAM647  LOC200488 5'  GGAGGGGCTATGACTTCAA   91652         CAAT    _
                                TTGGAGTCAT    GCCCC CC
                                ||||||||||    ||||| ||
                                AACTTCAGTA    CGGGG GG
                                      T___     A
GAM647  LOC203286 3'  TGGAGGGCATTGTTTCCCAG   92150      AGTCAT       C
                                TTGG     CAATGCCC CCA
                                ||||     |||||||| |||
                                GACC     GTTACGGG GGT
                                  CTTT__       A
GAM647  LOC203397 5'  TGAAGGACAGCGGGGACTCCAA 90906         AT AA  C  CC
                                TTGGAGTC  C  TG CC  CA
                                ||||||||  |  || ||  ||
                                AACCTCAG  G  AC GG  GT
                                     GG CG  A  AA
GAM647  LOC219793 5'  GGGCATTGAGGACCCCAA    93021      A   A
                                TTGG GTC TCAATGCCC
                                |||| ||| |||||||||
                                AACC CAG AGTTACGGG
                                  C   G
GAM647  LOC221424 3'  TGGGGGGCACTTGAACCCA    95275     A  CA    _
                                TGG GT  TCAA TGCCCCCCA
                                ||| ||  |||| |||||||||
                                ACC CA  AGTT ACGGGGGGT
                                  _ __    C
GAM647  LOC256267 5'  TGGGGGGCGGCGGAACTGCAA  98618     G   CA  AA_
                                TTG AGT  TC   TGCCCCCCA
                                ||| |||  ||   |||||||||
                                AAC TCA  AG   GCGGGGGGT
                                  G   __  GCG
GAM647  LOC256586 3'  GGGGGCATAACTCTAA      96620        CATCA
                                TTGGAGT    ATGCCCCC
                                |||||||    ||||||||
                                AATCTCA    TACGGGGG
                                     A____
GAM647  LOC92360  3'  TGGGGGGCACCTGTAACCCCAG 69628      A  CAT  A_
                                TTGG GT   CA  TGCCCCCCA
                                |||| ||   ||  |||||||||
                                GACC CA   GT  ACGGGGGGT
                                  C  AT_  CC
GAM647  LOC92466  5'  TGGGGGGCGGCGGAACTGCAA  69974     G   CA  AA_
                                TTG AGT  TC   TGCCCCCCA
                                ||| |||  ||   |||||||||
                                AAC TCA  AG   GCGGGGGGT
                                  G   __  GCG
GAM648  AP2A1    5'  TCCTTGGCGCTGCCTGGGGTCC 27219          T   AGACT_
            TT                   AAGGACCCCAGG CAG     GGA
                                ||||||||||| |||     |||
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                                TTCCTGGGGTCC GTC     CCT
                                      _  GCGGTT
GAM648  AP2A1    5'  TCCTTGGCGCTGCCTGGGGTCC 56306          T   AGACT_
            TT                   AAGGACCCCAGG CAG     GGA
                                ||||||||||| |||     |||
                                TTCCTGGGGTCC GTC     CCT
                                      _  GCGGTT
GAM648  BAT4     3'  CTCTGACCTGGGCCCTT     53741      AC
                                AAGG  CCCAGGTCAGAG
                                ||||  ||||||||||||
                                TTCC  GGGTCCAGTCTC
                                  C_
GAM648  BLMH     3'  TCCAGTCTCCACCAGGAACCT  6361      AC  CA   CA
                                AGG  CC  GGT  GAGACTGGA
                                |||  ||  |||  |||||||||
                                TCC  GG  CCA  CTCTGACCT
                                  AA  A_   C_
GAM648  CPNE7    3'  CCAGTCCTCCTGGGATCCT    27791      C     TC  A
                                AGGA CCCAGG  AG GACTGG
                                |||| ||||||  || ||||||
                                TCCT GGGTCC  TC CTGACC
                                  A     __  _
GAM648  CRHR2    3'  CCAGCCTCTCTGGCCAGGGCCT 10300      A   CA       __
            T                    AAGG CCC  GGTCAGAGA  CTGG
                                |||| |||  |||||||||  ||||
                                TTCC GGG  CCGGTCTCT  GACC
                                  _  A_       CC
GAM648  HPCAL1   5'  GGTCAGACCTGGGGTCCT    57011           AGA
                                AGGACCCCAGGTC   GACT
                                ||||||||||||   ||||
                                TCCTGGGGTCCAG   CTGG
                                       A__
GAM648  HTRA3    3'  CCACCTGACCTGAGGCCCC   90577    AC  _      AGAC
                                GG  CC CAGGTCAG    TGG
                                ||  || ||||||||    |||
                                CC  GG GTCCAGTC    ACC
                                 CC  A       C___
GAM648  IL2RB    3'  CCAGCTAACTCTGACCTGGGAG 7934     AC         A___
            CC                    GG  CCCAGGTCAGAG    CTGG
                                ||  ||||||||||||    ||||
                                CC  GGGTCCAGTCTC    GACC
                                 GA          AATC
GAM648  LY95     5'  CCAGTCTTCTCCAGGTGTCC   17895      C  A  TCA
                                GGAC CC GG   GAGACTGG
                                |||| || ||   ||||||||
                                CCTG GG CC   TTCTGACC
                                  T  A  TC_
GAM648  MCM7     3'  ATCCAGCCTGCTTGCAACCCTG 20976          T___  _ _  A    ___
            GGGTCCT                  AGGACCCCAGG    CA G AG CTGGA   T
                                ||||||||||    || | || |||||   |
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                                TCCTGGGGTCC   GT C TC GACCT  A
                                      CAAC  T G  C    ___
GAM648  MOG     3'  TCCAGTCTTCCACCTGGAAGCC 11675    ACC     CA
                                GG  CCAGGT  GAGACTGGA
                                ||  ||||||  |||||||||
                                CC  GGTCCA  TTCTGACCT
                                 GAA     CC
GAM648  NESH    5'  CCAGTCTCCGACCCCATCC   33569    CCCCA   A
                                GGA    GGTC GAGACTGG
                                |||    |||| ||||||||
                                CCT    CCAG CTCTGACC
                                 ACC__   C
GAM648  OCRL    3'  TCACTGACCTGGGATCTTT   9631       C       A
                                AAGGA CCCAGGTCAG GA
                                ||||| |||||||||| ||
                                TTTCT GGGTCCAGTC CT
                                   A        A
GAM648  OCRL    3'  TCACTGACCTGGGATCTTT   6060       C       A
                                AAGGA CCCAGGTCAG GA
                                ||||| |||||||||| ||
                                TTTCT GGGTCCAGTC CT
                                   A        A
GAM648  RANBP3  3'  CCAACTATAGGCCTGGGACCC  24640    AC      AG_  AC
                                GG  CCCAGGTC  AG  TGG
                                ||  ||||||||  ||  |||
                                CC  GGGTCCGG  TC  ACC
                                 CA      ATA  A_
GAM648  RANBP3  3'  CCAACTATAGGCCTGGGACCC  14632    AC      AG_  AC
                                GG  CCCAGGTC  AG  TGG
                                ||  ||||||||  ||  |||
                                CC  GGGTCCGG  TC  ACC
                                 CA      ATA  A_
GAM648  SREBF1  3'  TCCTGACCTGAGGCTCCT   96078     C  _      A
                                AGGA CC CAGGTCAG GA
                                |||| || |||||||| ||
                                TCCT GG GTCCAGTC CT
                                  C  A      _
GAM648  TBX1    3'  CCAGTCCCTGGAGCCACCGCGG 55542        CA  _____  A
          GTCCTT                AAGGACCC  GGT    CAG GACTGG
                                |||||||  |||    ||| ||||||
                                TTCCTGGG  CCA    GTC CTGACC
                                    CG   CCGAG   C
GAM648  TEM5    3'  CCAAGGTCTGACCTAGGGTTC  52296      C      GA  _
                                GGACCC AGGTCAGA  CT GG
                                ||||||  ||||||||  || ||
                                CTTGGG TCCAGTCT  GA CC
                                   A      G_  A
GAM648  WNT1    3'  CCAGTCTCTGTCGTGGAGCC  19476    ACC  _  T
                                GG  CCA GG CAGAGACTGG
                                ||  ||| || ||||||||||
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                                CC   GGT CT GTCTCTGACC
                                 GA_   G  _
GAM648  ATP5D    3'  CCAGCTCCTGGGGTCC      9858          TCAG  A
                                GGACCCCAGG    AG CTGG
                                ||||||||||    || ||||
                                CCTGGGGTCC    TC GACC
                                      _____  _
GAM648  C21orf57  5'  CCGCCCGCCTGGAGTCCTT   75298       C     CAGAGAC
                                AAGGAC CCAGGT      TGG
                                ||||||| ||||||      |||
                                TTCCTG GGTCCG      GCC
                                   A     CCC_____
GAM648  C2orf7   3'  TCCAGCCTCCCCTACCCAGGGT 51273       CA   CA__   A
             CT                   GGACCC  GGT    GAG CTGGA
                                ||||||  |||    ||| |||||
                                TCTGGG  CCA    CTC GACCT
                                   AC   TCCC   C
GAM648  CLIPR-59  5'  CCAGTCTCCACTTTGGTCC   32014      CC    CA
                                GGACC  AGGT  GAGACTGG
                                |||||  ||||  ||||||||
                                CCTGG  TTCA  CTCTGACC
                                   T_    C_
GAM648  CLIPR-59  3'  TCCAGGGCGGACCTGGGGCC   32020    A       AGAGA
                                GG CCCCAGGTC     CTGGA
                                || |||||||||     |||||
                                CC GGGGTCCAG     GACCT
                                 _        GCGG_
GAM648  COL12A1   3'  CCAGTCTCTGACCCTTCC    16469     CCCCA
                                GGA    GGTCAGAGACTGG
                                |||    ||||||||||||
                                CCT    CCAGTCTCTGACC
                                  TC___
GAM648  COL12A1   3'  CCAGTCTCTGACCCTTCC    55533     CCCCA
                                GGA    GGTCAGAGACTGG
                                |||    ||||||||||||
                                CCT    CCAGTCTCTGACC
                                  TC___
GAM648  CYP2A7   5'  TCAGCTGCCCTGGGGTCC    48353          T   AGA
                                GGACCCCAGG CAG   CTGG
                                |||||||||| |||   ||||
                                CCTGGGGTCC GTC   GACT
                                      C  ___
GAM648  CYP2A7   5'  TCAGCTGCCCTGGGGTCC    7541           T   AGA
                                GGACCCCAGG CAG   CTGG
                                |||||||||| |||   ||||
                                CCTGGGGTCC GTC   GACT
                                      C  ___
GAM648  FBXL9    3'  CCAGTCTCCAACCCTGGCCTT  25139     ACC    TCA_
                                AAGG   CCAGG   GAGACTGG
                                ||||   |||||   ||||||||
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                                TTCC   GGTCC    CTCTGACC
                                  ___     CAAC
GAM648  FLJ10874  3'  TCCAGAAAGAGTGACCTGGTGT 37329      C       GAGA__
          CC                      GGAC CCAGGTCA     CTGGA
                                  |||| ||||||||      |||||
                                  CCTG GGTCCAGT     GACCT
                                    T       GAGAAA
GAM648  FLJ10874  3'  TCCAGCCTCTGACATGCTCTT  37331     CCC  G      A
                                  AGGA   CA GTCAGAG CTGGA
                                  ||||   || ||||||| |||||
                                  TTCT   GT CAGTCTC GACCT
                                    C__  A      C
GAM648  FLJ13241  3'  CCAGTCTCTCAGGCCTCC    47648    CCCCA   __
                                  GGA    GGTC  AGAGACTGG
                                  |||     ||||  |||||||||
                                  CCT    CCGG  TCTCTGACC
                                    ______    AC
GAM648  FLJ14549  3'  CCACCTACCCGGGGTCCT    52497        A   C  AGAC
                                  AGGACCCC GGT AG    TGG
                                  |||||||| ||| ||    |||
                                  TCCTGGGG CCA TC    ACC
                                      C   _  C___
GAM648  FLJ22551  5'  CCGTATGACCTGGGACCT    45561     AC       GAGAC
                                  AGG  CCCAGGTCA    TGG
                                  |||  |||||||||    |||
                                  TCC  GGGTCCAGT    GCC
                                    A_       AT___
GAM648  GIT1      3'  CCAACCTGTGTGCTGGGGTCC  26719        GT  G  AC
                                  GGACCCCAG  CA AG  TGG
                                  |||||||||  || ||  |||
                                  CCTGGGGTC  GT TC  ACC
                                       GT  G  CA
GAM648  GNB1L     3'  CCAGCCTTGGCCTGAAACCT   54864     ACCC      G  A
                                  AGG    CAGGTCA AG CTGG
                                  |||    ||||||| || ||||
                                  TCC    GTCCGGT TC GACC
                                    AAA_      _  C
GAM648  GOLPH2    3'  TCCAGCCTCACTTTGAGTCCT  33773      CCC    CA   A
                                  AGGAC   AGGT  GAG CTGGA
                                  |||||   ||||  ||| |||||
                                  TCCTG   TTCA  CTC GACCT
                                    AGT    __   C
GAM648  KIAA0397  3'  CCACGAGTGAACCTGGGGCC   62344    A       _  GAGAC
                                  GG CCCCAGGT CA     TGG
                                  || |||||||| ||     |||
                                  CC GGGGTCCA GT     ACC
                                   _       A  GAGC_
GAM648  KIAA0449  5'  CAGTTCCCTGGGGTCC      34633          TCAGA
                                  GGACCCCAGG     GACTG
                                  ||||||||||     |||||
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                                CCTGGGGTCC    TTGAC
                                      C____
GAM648  KIAA0471  5'  TCCAGTCTACTTTGGGGTTCT  30046         TCAG
                                AGGACCCCAGG   AGACTGGA
                                ||||||||||   ||||||||
                                TCTTGGGGTTT   TCTGACCT
                                      CA__
GAM648  KIAA0493  5'  CCAGCCCGAGACGCCTGGGGTC 64929         CAGAGA__
              C                  GGACCCCAGGT      CTGG
                                ||||||||||       ||||
                                CCTGGGGTCCG      GACC
                                      CAGAGCCC
GAM648  KIAA0674  3'  TCAGACTGACCTGGGAGCC   61243    AC       AGA
                                GG  CCCAGGTCAG   CTGG
                                ||  ||||||||||   ||||
                                CC  GGGTCCAGTC   GACT
                                 GA        A__
GAM648  KIAA1130  5'  CCAGTCCCCCACCTGGGGCGCC 63081    A_      CAGA
                                GG  CCCCAGGT   GACTGG
                                ||  ||||||||   ||||||
                                CC  GGGGTCCA   CTGACC
                                 GC       CCCC
GAM648  KIAA1465  3'  TCCAGCCCGGTGCCTGGGGCGC 61510     A_      CAGAGA
              CT                   AGG  CCCCAGGT     CTGGA
                                |||  ||||||||     |||||
                                TCC  GGGGTCCG     GACCT
                                  GC       TGGCCC
GAM648  KIAA1719  3'  TCTGTCTCCAACCTGGGGTCC  68739         CA    T
                                GGACCCCAGGT  GAGAC GGA
                                ||||||||||  ||||| |||
                                CCTGGGGTCCA  CTCTG TCT
                                      AC    _
GAM648  LGI2      3'  CCAGTCTTCCTGAATCCT    36925     CCC   TCA
                                AGGA   CAGG   GAGACTGG
                                ||||   ||||   ||||||||
                                TCCT   GTCC   TTCTGACC
                                  AA_   ___
GAM648  MGC15906  5'  CCAACGGCCTGGGGCCTT    52884     A       AGAGAC
                                AAGG CCCCAGGTC     TGG
                                |||| |||||||||     |||
                                TTCC GGGGTCCGG     ACC
                                  _       CA____
GAM648  MGC8407   3'  CCAGCCTTACTGGGTCCTT   44111        CA   CA   A
                                AAGGACCC  GGT  GAG CTGG
                                ||||||||  |||  ||| ||||
                                TTCCTGGG  TCA  TTC GACC
                                     __   __   C
GAM648  NOLC1     3'  TCCAGTGGACCTGGGAACC   17636    AC      AGAG
                                GG  CCCAGGTC   ACTGGA
                                ||  ||||||||   ||||||
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                                CC  GGGTCCAG    TGACCT
                                 AA       G___
GAM648  PDE1C    3'  CAGTCTCTGGTTCCTT      18463       C  CAGGTC
                                AAGGA CC     AGAGACTG
                                ||||| ||     ||||||||
                                TTCCT GG     TCTCTGAC
                                  T _______
GAM648  PPP1R16B 3'  CCAGCACCCTGGGGTCTTT    62034           TCAGAGA
                                AAGGACCCCAGG      CTGG
                                ||||||||||||      ||||
                                TTTCTGGGGTCC      GACC
                                      CAC_____
GAM648  PRO2389  3'  CCAGTCAGCTTGGGTCCCT    64475     AC      CAGA
                                AGG  CCCAGGT    GACTGG
                                |||  |||||||    ||||||
                                TCC  GGGTTCG    CTGACC
                                  CT       A___
GAM648  PTPRT    3'  TCTGGGCCAACCAGGGGTCCTT 56511          A   CAGAGA TG
                                AAGGACCCC GGT     C  GA
                                ||||||||| |||     |  ||
                                TTCCTGGGG CCA     G  CT
                                     A   ACCG__ GT
GAM648  RAI17    3'  CCGGCTGCTGCCTGGGGCCCTT 92903      A      T  _  A
                                AAGG CCCCAGG CAG AG CTGG
                                |||| ||||||| ||| || ||||
                                TTCC GGGGTCC GTC TC GGCC
                                  C       _   G  _
GAM648  SHANK3   5'  TCAGCGGCCCGAGCCTGGGGCC 66112     A       CAGAGA__
            CT                    AGG CCCCAGGT       CTGG
                                ||| ||||||||       ||||
                                TCC GGGGTCCG       GACT
                                  C       AGCCCGGC
GAM648  SMARCA4  3'  TCCAGTCTCGACCCCGAGCC   13247    ACCCCA    A
                                GG      GGTC GAGACTGGA
                                ||      |||| |||||||||
                                CC      CCAG CTCTGACCT
                                 GAGCC_    _
GAM648  SMCR5    3'  CCACTTCTGACCTGGGGCCT   59247     A          AC
                                AGG CCCCAGGTCAGAG  TGG
                                ||| ||||||||||||  |||
                                TCC GGGGTCCAGTCTT  ACC
                                  _          C_
GAM648  SPIB     3'  CCACTTGTGCCTGGGGTCC    13354          CA   AC
                                GGACCCCAGGT  GAG  TGG
                                ||||||||||  |||  |||
                                CCTGGGGTCCG  TTC  ACC
                                      TG   __
GAM648  SPIB     3'  CCAGTGAGGCCTGGGACCTT   13356      AC       AGAG
                                AAGG  CCCAGGTC    ACTGG
                                ||||  ||||||||    |||||
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                                TTCC  GGGTCCGG   TGACC
                                  A_      AG__
GAM648  TACR3    5'  TCCAGTCTTATCTGAAGACC  8330    ACCC    CA
                                GG   CAGGT  GAGACTGGA
                                ||   |||||  |||||||||
                                CC   GTCTA  TTCTGACCT
                                 AGAA    __
GAM648  TOMM40   3'  CCAGTGGGCCTGGGGTCC    21481          AGAG
                                GGACCCCAGGTC   ACTGG
                                ||||||||||||   |||||
                                CCTGGGGTCCGG   TGACC
                                       G___
GAM648  TREX2    5'  TCCAACCTCTGACTGGCTGGTC 24233      __   G    AC
           CT                    AGGACC  CCAG TCAGAG  TGGA
                                ||||||  |||| ||||||  ||||
                                TCCTGG  GGTC AGTCTC  ACCT
                                   TC   _     CA
GAM648  LOC115051 3'  TCTGTCCACCCGGGGTCCT   60680       A  ___
                                AGGACCCC GGT   CAGA
                                |||||||| |||   ||||
                                TCCTGGGG CCA   GTCT
                                     C   CCT
GAM648  LOC115704 3'  TAGGGTCCGACCTGGGCTCCT  73911     C      A  GA
                                AGGA CCCAGGTC GA  CTG
                                |||| |||||||| ||  |||
                                TCCT GGGTCCAG CT  GAT
                                  C       C  GG
GAM648  LOC126282 3'  CCAATTCAAGGACTGGGGTCCT 74950          G  AGA  C_
           T                     AAGGACCCCAG TC   GA  TGG
                                ||||||||||| ||   ||  |||
                                TTCCTGGGGTC AG   CT  ACC
                                       _ GAA  TA
GAM648  LOC132001 5'  CCAGTCTCCGACTTCC     57949     CCCCA   A
                                GGA    GGTC GAGACTGG
                                |||    |||| ||||||||
                                CCT    TCAG CTCTGACC
                                  ______   C
GAM648  LOC145757 5'  CCAGTCCCCTCAACGGTCCTT  77925       CC__   TCAGA
                                AAGGACC   AGG    GACTGG
                                |||||||   |||    ||||||
                                TTCCTGG   TCC    CTGACC
                                    CAAC  C_____
GAM648  LOC147136 3'  CCAGTGAGAACTGACCTGAGTC 78861     CC      AG___
           C                     GGAC  CAGGTCAG    ACTGG
                                ||||  ||||||||    |||||
                                CCTG  GTCCAGTC    TGACC
                                  A_      AAGAG
GAM648  LOC147929 5'  TCCAGCAGCCTTGGGGTCC   79272       _  CAGAGA
                                GGACCCCA GGT     CTGGA
                                |||||||| |||     |||||
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                                CCTGGGGT CCG     GACCT
                                     T  AC____
GAM648  LOC149566 3'  TCCAGCCTGGATGACCTGGGAC 85653    AC       G__  A
            CC                    GG  CCCAGGTCA  AG CTGGA
                                  ||  |||||||||  || |||||
                                  CC  GGGTCCAGT  TC GACCT
                                   CA       AGG  C
GAM648  LOC149773 5'  CCAGTCTTCTGAGGCCCT    80291    A  C   GTCA
                                  AGG CC CAG   GAGACTGG
                                  ||| || |||   ||||||||
                                  TCC GG GTC   TTCTGACC
                                    C  A  ____
GAM648  LOC154807 5'  CTCTGCGACCTGGGGCCCT   87463    A       __
                                  AGG CCCCAGGTC  AGAG
                                  ||| |||||||||  ||||
                                  TCC GGGGTCCAG  TCTC
                                    C       CG
GAM648  LOC199958 3'  CCAGTCTCTGGCAACGCCCCT  91490    ACCCCAG
                                  AGG      GTCAGAGACTGG
                                  |||      ||||||||||||
                                  TCC      CGGTCTCTGACC
                                    CCGCAA_
GAM648  LOC220581 3'  TCCAGCCTTCTTGGGGTGCT   76803    G       TCA  A
                                  AG ACCCCAGG   GAG CTGGA
                                  || ||||||||   ||| |||||
                                  TC TGGGGTTC   TTC GACCT
                                   G       ___   C
GAM648  LOC221179 3'  CCAGTCTCTCCTCGGAGGCCCT 95194     A  _  _  TC
            T                      AAGG CC CC AGG  AGAGACTGG
                                  ||||  ||  ||  |||  |||||||||
                                  TTCC GG GG TCC  TCTCTGACC
                                    C  A  C   __
GAM648  LOC253502 3'  CCAGTCCTCCTGGGATCCT   96217     C     TC  A
                                  AGGA CCCAGG  AG GACTGG
                                  |||| ||||||  || ||||||
                                  TCCT GGGTCC  TC CTGACC
                                    A     __  _
GAM648  LOC254105 3'  CCAGTCCAGGGCCTGGGCTCC  96418    C       AGA
                                  GGA CCCAGGTC   GACTGG
                                  ||| ||||||||   ||||||
                                  CCT GGGTCCGG   CTGACC
                                    C       GAC
GAM648  LOC256790 5'  CCAGTCTCATGGCATCCT    96490     CC   GGTCA
                                  AGGA  CCA    GAGACTGG
                                  ||||  |||    ||||||||
                                  TCCT  GGT    CTCTGACC
                                    AC   A____
GAM648  LOC51161  3'  TCCTGACCTGAGGGCCCT    33046    A  _      A
                                  AGG CCC CAGGTCAG GA
                                  ||| ||| |||||||| ||
```

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                                TCC GGG GTCCAGTC CT
                                  C  A      _
GAM648  LOC56912  5'  CCAGCCCTAGGCTGGGGTTCTT 39748          G  _  AGA
                                AAGGACCCCAG TC AG  CTGG
                                |||||||||| || ||  ||||
                                TTCTTGGGGTC GG TC  GACC
                                      _  A  CC_
GAM648  LOC91156  5'  CCAACTAAGGCCTGAGAGTCC  65705     CC_    AG  AC
                                GGAC  CAGGTC  AG  TGG
                                ||||  ||||||  ||  |||
                                CCTG  GTCCGG  TC  ACC
                                  AGA     AA  A_
GAM648  LOC92822  3'  CCAGTCTTCGGACGAGTCCTT  71180      CCCAG  A_
                                AAGGAC    GTC  GAGACTGG
                                ||||||    |||  ||||||||
                                TTCCTG    CAG  TTCTGACC
                                   AG___  GC
GAM649  EPHA8   3'  GAGTCCAACAGGGACATCA   40434   A  C       A
                                C ATG CCCTGTTGGA TTC
                                | ||| |||||||||| |||
                                A TAC GGGACAACCT GAG
                                 C  A       _
GAM649  ICMT    3'  TGCCGAATCAAGGCGGAACAT  25739    CCC    GGA
                                ATG  CTGTT  ATTCGGCA
                                |||  |||||  ||||||||
                                TAC  GGCGG  TAAGCCGT
                                  AA_    AAC
GAM649  ATPAF2   3'  CCAAATTCCGACAAGGC    74856    CC       C
                                GCC  TGTTGGAATT GG
                                |||  |||||||||| ||
                                CGG  ACAGCCTTAA CC
                                  A_       A
GAM649  ODZ2    3'  TGAAGACCTAACAGGGGCACTG 71425    A        AA_
                                CA TGCCCCTGTTGG  TTCG
                                || ||||||||||||  ||||
                                GT ACGGGGACAATC  AAGT
                                 C         CAG
GAM649  TRPV6   3'  CCCTTCCGACAGGAGCACTG  38462   A  C       TTC
                                CA TGC CCTGTTGGAA  GG
                                || ||| ||||||||||  ||
                                GT ACG GGACAGCCTT  CC
                                 C  A       C__
GAM649  UBF-fl  3'  TGAGCCCAGCAGGGGCACTG  52636   A        AA
                                CA TGCCCCTGTTGG  TTCG
                                || ||||||||||||  ||||
                                GT ACGGGGACGACC  GAGT
                                 C         C_
GAM649  LOC145622 5'  GGGTCCCCAACAGGGCCACTG  77820   A  C       A_
                                CA TG CCCTGTTGG  ATTC
                                || || |||||||||  ||||
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                                GT AC GGGACAACC  TGGG
                                 C  C        CC
GAM649  LOC148645 3'  TGCCGAATCTGTCAGGG     85341       T    A
                                CCCTG TGGA TTCGGCA
                                ||||| |||| |||||||
                                GGGAC GTCT AAGCCGT
                                   T    _
GAM649  LOC151996 5'  TGCCTGGTGCCAACAGGGGCAT 86724    A          A  TC
           CC                    C ATGCCCCTGTTGG AT  GGCA
                                | ||||||||||||| ||  ||||
                                C TACGGGGACAACC TG  CCGT
                                 C           G  GT
GAM649  LOC220177 5'  TGCCATGGGCCACAGGGGCATT 95970           T  AATTC
           G                     CAATGCCCCTGT GG     GGCA
                                |||||||||||| ||     ||||
                                GTTACGGGGACA CC     CCGT
                                       _  GGGTA
GAM650  CAPON    3'  CCAGAGCCCCCAGCCTTACC   64657    C   ACA   CT_
                                GG AAG   GCT   GGCTCTGG
                                || |||   |||   ||||||||
                                CC TTC   CGA   CCGAGACC
                                 A   ___   CCC
GAM650  GALGT    5'  GCCAGAGCCCTCCCCGCGCTGC 9420       AGACA  TCT___
           CA                    TGGCA    GC     GGCTCTGGC
                                |||||    ||     |||||||||
                                ACCGT    CG     CCGAGACCG
                                   CG___  CCCCTC
GAM650  GATA2    3'  CCAAAGCCAGAGTGGCCA    10768      AAGACA       C
                                TGGC     GCTCTGGCT TGG
                                ||||     ||||||||| |||
                                ACCG     TGAGACCGA ACC
                                  G_____        A
GAM650  GNA14    3'  CCAGAGCCAGTCCCATGCCA   16283      AGACAGCT
                                TGGCA       CTGGCTCTGG
                                |||||       ||||||||||
                                ACCGT       GACCGAGACC
                                   ACCCT___
GAM650  IGF2R    3'  GCCAGAGCCTCGGCCCTAGC   7914     A  ACA   CT
                                GC AG   GCT  GGCTCTGGC
                                || ||   |||  |||||||||
                                CG TC   CGG  CCGAGACCG
                                 A  C__   CT
GAM650  LRP3     5'  GCCAGAGCCAGAGCCGGAGCC  65714     AAGACA
                                GGC     GCTCTGGCTCTGGC
                                |||     ||||||||||||||
                                CCG     CGAGACCGAGACCG
                                  AGGC__
GAM650  PML      3'  AGGCAGAGCCATCTGCCA    53799       A  CA     G
                                TGGCA GA  GCTCTG CT
                                ||||| ||  |||||| ||
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                                ACCGT CT  CGAGAC GA
                                  _ AC     G
GAM650  PML      3'  AGGCAGAGCCATCTGCCA    53800       A  CA     G
                                TGGCA GA  GCTCTG CT
                                |||||  ||  ||||||  ||
                                ACCGT CT  CGAGAC GA
                                  _ AC     G
GAM650  PRDM16   3'  CCAACGGAGCTGCCTCGC    42343    A  A      GCTC
                                GC AG CAGCTCTG    TGG
                                ||  ||  ||||||||   |||
                                CG TC GTCGAGGC    ACC
                                 C  C       A___
GAM650  SLC1A4   5'  GCCAGAGCCCACGTCCCCTGCC 13173       A__   AGCTCT
           A                     TGGCA   GAC     GGCTCTGGC
                                |||||   |||     |||||||||
                                ACCGT   CTG     CCGAGACCG
                                  CCC   CAC___
GAM650  SMCY     3'  GCTCAGAAGTGTCTTGCCA    17387          GC   _
                                TGGCAAGACA  TCTG GC
                                ||||||||||  ||||  ||
                                ACCGTTCTGT  AGAC CG
                                     GA    T
GAM650  VTN      5'  CCAGAGCCCAGCTTGCCA    7161       AGAC    CT
                                TGGCA   AGCT  GGCTCTGG
                                |||||   ||||  ||||||||
                                ACCGT   TCGA  CCGAGACC
                                  _____   C_
GAM650  ARHGDIG  3'  GCCAGAGTCACCACCTTGCC  8624        ACAGCTC
                                GGCAAG      TGGCTCTGGC
                                ||||||      ||||||||||
                                CCGTTC      ACTGAGACCG
                                   CACC___
GAM650  DKFZp434H2215 3'  CCAGAGCCATGAGACCTACCA  34526     CA  ACAG  _
                                TGG  AG   CTC TGGCTCTGG
                                |||  ||   ||| |||||||||
                                ACC  TC   GAG ACCGAGACC
                                  A_  CA__   T
GAM650  FLJ14154 3'  GCCTCCAGAGCTGCCCAGCCA  46234     AAGA       CTCT
                                TGGC   CAGCTCTGG   GGC
                                ||||   |||||||||   |||
                                ACCG   GTCGAGACC   CCG
                                  ACCC       T___
GAM650  FLJ14249 3'  CCAGTGGAGCTGCCTTCCCA   56091     C   A      GCT
                                TGG AAG CAGCTCTG   CTGG
                                ||| ||| ||||||||   ||||
                                ACC TTC GTCGAGGT   GACC
                                  C   C      ___
GAM650  FLJ14249 3'  CCAGTGGAGCTGCCTTCCCA   42641     C   A      GCT
                                TGG AAG CAGCTCTG   CTGG
                                ||| ||| ||||||||   ||||
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                                ACC TTC GTCGAGGT   GACC
                                  C   C      ___
GAM650  FLJ20297  3'  CCAAGCTTGGGAGCCAGCCTGC 35372      AGACA    __    C
            CA                    TGGCA    GCTCT  GGCT TGG
                                  |||||    |||||  |||| |||
                                  ACCGT    CGAGG  TCGA ACC
                                    CCGAC    GT   _
GAM650  FLJ20297  3'  CCAAGCTTGGGAGCCAGCCTGC 35373      AGACA    __    C
            CA                    TGGCA    GCTCT  GGCT TGG
                                  |||||    |||||  |||| |||
                                  ACCGT    CGAGG  TCGA ACC
                                    CCGAC    GT   _
GAM650  FLJ31762  3'  CCATGACAGGGCTGCCCCGCCA 58761     AAGA      GCTC
                                  TGGC   CAGCTCTG   TGG
                                  ||||   ||||||||   |||
                                  ACCG   GTCGGGAC   ACC
                                    CCCC      AGT_
GAM650  KIAA1870  5'  GCCAGAGTCTCCCGTCCCA   50583    CAA   AGCTCT
                                  TGG   GAC    GGCTCTGGC
                                  |||   |||    |||||||||
                                  ACC   CTG    CTGAGACCG
                                    ___   CCCT__
GAM650  MGC2306  3'  CCAAAGCCAGAGTGGCCA    51952     AAGACA      C
                                  TGGC    GCTCTGGCT TGG
                                  ||||    ||||||||| |||
                                  ACCG    TGAGACCGA ACC
                                    G_____       A
GAM650  MGC2749  3'  CCAGAGCCAGATGTCCCCCA   44167    CAA   GC
                                  TGG   GACA  TCTGGCTCTGG
                                  |||   ||||  ||||||||||
                                  ACC   CTGT  AGACCGAGACC
                                    CC_   __
GAM650  PNMA5    3'  GCCAGAGCCCACCATCCTGGCA 73973    G  A  CAGCTCT
                                  TG CA GA      GGCTCTGGC
                                  || || ||      |||||||||
                                  AC GT CT      CCGAGACCG
                                   G  C  ACCAC__
GAM650  SARM     3'  GCCAGAGTCTGTCTTGGCCA   31294     _     _
                                  TGGC AAGACAG CTCTGGC
                                  |||| ||||||| |||||||
                                  ACCG TTCTGTC GAGACCG
                                    G      T
GAM650  SLC2A11  3'  CCAGAGCCAAAGCCAGCTA   48693     AAGACA   C
                                  TGGC    GCT TGGCTCTGG
                                  ||||    ||| |||||||||
                                  ATCG    CGA ACCGAGACC
                                    AC_____  A
GAM650  TEKT3    3'  CCAGAGCACTGTCTCAGC    49951    A_    CTCTG
                                  GC  AGACAG    GCTCTGG
                                  ||  ||||||    |||||||
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                                CG  TCTGTC    CGAGACC
                                 AC     A____
GAM650   LOC124997 3'  CCAGAGCCACCAAGCCTGCCA  74846      AGACA   C__
                                TGGCA    GCT   TGGCTCTGG
                                |||||    |||   |||||||||
                                ACCGT    CGA   ACCGAGACC
                                   C____   ACC
GAM650   LOC126536 3'  GCCAGAACCAAGAGTCCAGCCA 75040      AAGACA    _ C
                                TGGC     GCTCT GG TCTGGC
                                ||||     ||||| || ||||||
                                ACCG     TGAGA CC AGACCG
                                  ACC___     A  A
GAM650   LOC145581 5'  GCCACCTGGAGCCACCTTGCC  77793       ACA    TG CTC
                                GGCAAG   GCTC  G   TGGC
                                ||||||   ||||  |   ||||
                                CCGTTC   CGAG  C   ACCG
                                   CAC    GT C__
GAM650   LOC148397 3'  CCAGAGCCAGGTGCTGCCA    79564      AGACA  _
                                TGGCA    GC TCTGGCTCTGG
                                |||||    || ||||||||||
                                ACCGT    CG GGACCGAGACC
                                  _____  T
GAM650   LOC148764 5'  CGCCAGAGCCAGGCCGGGGATG 79735      AGACA_  T         ___
            CC                    GGCA     GC CTGGCTCTGGC   G
                                ||||     || ||||||||||   |
                                CCGT     CG GACCGAGACCG   C
                                  AGGGGC  _         ___
GAM650   LOC150685 5'  GCCAGAGCTGTGGCTACCTTGG 88534    G    AC    CT
            CA                    TG CAAG  AGCT  GGCTCTGGC
                                || ||||  ||||  |||||||||
                                AC GTTC  TCGG  TCGAGACCG
                                 G   CA    TG
GAM650   LOC150776 3'  CCAAGCTTGGGAGCCAGCCTGC 63923      AGACA     __    C
            CA                    TGGCA    GCTCT  GGCT TGG
                                |||||    |||||  |||| |||
                                ACCGT    CGAGG  TCGA ACC
                                   CCGAC    GT   _
GAM650   LOC153514 5'  CCAAAAAGTCCTGTCTTGC    81710         CTCT    C__
                                GCAAGACAG    GGCT   TGG
                                |||||||||    ||||   |||
                                CGTTCTGTC    CTGA   ACC
                                     _____    AAA
GAM650   LOC199800 5'  CCAGAGCCAGCGCTTCCCCGCC 91446     AA_  C   T
                                GGC   GA AGC CTGGCTCTGG
                                |||   || ||| ||||||||||
                                CCG   CT TCG GACCGAGACC
                                  CCC  _   C
GAM650   LOC200779 3'  CCACTTTGAGCTGTCCTGCC   90289      A       TGGCTC
                                GGCA GACAGCTC      TGG
                                |||| ||||||||      |||
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                                CCGT CTGTCGAG     ACC
                                  C       TTTC__
GAM650  LOC222602 5'  GCCAAAGCAGTAGGAGAACATC 94433        CAG_   G___  C
           TTGCCA                  TGGCAAGA   CTCT   GCT TGGC
                                |||||||||  ||||  ||| ||||
                                ACCGTTCT   GAGG   CGA ACCG
                                     ACAA   ATGA   A
GAM650  LOC253187 5'  CCAGGAGGCATCTTGCCA    98902        CAGCTC  G  _
                                TGGCAAGA     TG CTC TGG
                                |||||||||     || ||| |||
                                ACCGTTCT     AC GAG ACC
                                     _______ G   G
GAM650  LOC256740 5'  GCCAGAGCCAGAGCTGGATCC  98920    CAAGA
                                GG    CAGCTCTGGCTCTGGC
                                ||    ||||||||||||||||
                                CC    GTCGAGACCGAGACCG
                                 TAG__
GAM650  LOC89890  5'  CCAGAGCCGGGTCCTGC     61205     A   AGCT
                                GCA GAC    CTGGCTCTGG
                                ||| |||    ||||||||||
                                CGT CTG    GGCCGAGACC
                                  C  _____
GAM651  GYG2      3'  AGAAACACCTCGGCTGTGGTC  15360          AC    ACA
                                GATCACAGCT  GGTG   TTTCT
                                ||||||||||  ||||   |||||
                                CTGGTGTCGG  CCAC   AAAGA
                                      CT    ___
GAM651  HPRT1     3'  AGAAATGTCAGTTGCTG     5758       T  GG
                                CAGC AC  TGACATTTCT
                                |||| ||  ||||||||||
                                GTCG TG  ACTGTAAAGA
                                  T  __
GAM651  PLAG1     3'  AGAAATGTATGTGTAGCTGTG  12145          GTG
                                CACAGCTACG   ACATTTCT
                                ||||||||||   ||||||||
                                GTGTCGATGT   TGTAAAGA
                                      GTA
GAM651  C20orf50  5'  AGAAATGTCACCACACAGGTAT 70611     C  AGCTAC
           C                     GAT AC      GGTGACATTTCT
                                ||| ||      ||||||||||||
                                CTA TG      CCACTGTAAAGA
                                  _  GACACA
GAM651  DKFZP564O0423 5'  AAATGATGCCAACTGTGATT   93334        CTAC    A
                                GATCACAG    GGTG CATTT
                                ||||||||    |||| |||||
                                TTAGTGTC    CCGT GTAAA
                                     AA__    A
GAM651  FLJ14735  3'  AAATGTCACCATGGCTTTCATC 52664     CAC     C
                                GAT   AGCTA GGTGACATTT
                                |||   ||||| ||||||||||
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                                CTA   TCGGT CCACTGTAAA
                                  CTT     A
GAM651  LCE      3'  AGAAATGCCAGCTGCTGTAGA  44256    _    TAC   GA_
                                TC ACAGC   GGT   CATTTCT
                                || |||||   |||   |||||||
                                AG TGTCG   TCG   GTAAAGA
                                 A     ___   ACC
GAM651  SPARCL1   3'  AGAAATATATGCAGCTGTGAT  17431         A  GTGAC
                                ATCACAGCT CG    ATTTCT
                                |||||||||| ||    ||||||
                                TAGTGTCGA GT    TAAAGA
                                     C  ATA__
GAM651  STK33     5'  AGAAATACATTTCATACTGTGA 63568        CTAC_   AC
              TC                   GATCACAG    GGTG  ATTTCT
                                |||||||||    ||||  ||||||
                                CTAGTGTC    TTAC  TAAAGA
                                     ATACT    A_
GAM651  TOM1L1    3'  AGAAATCGTCACACAGCTGTGA 19694         ACG    _
              T                    ATCACAGCT   GTGAC ATTTCT
                                |||||||||   ||||| ||||||
                                TAGTGTCGA   CACTG TAAAGA
                                     CA_    C
GAM651  LOC147660 3'  AGAAATGTCACAAGTGTGAT   79024       G  ACG
                                ATCACA CT   GTGACATTTCT
                                |||||| ||   ||||||||||
                                TAGTGT GA   CACTGTAAAGA
                                   _  A__
GAM651  LOC148085 3'  AAATGTCAGGCCTGTGA     85252       _  ACGG
                                TCACAG CT    TGACATTT
                                |||||| ||    ||||||||
                                AGTGTC GG    ACTGTAAA
                                   C  _____
GAM651  LOC221756 3'  AGAAACAAAGGCAGCTGTGG   93756         ACGG_  ACA
                                TCACAGCT    TG   TTTCT
                                ||||||||    ||   |||||
                                GGTGTCGA    AC   AAAGA
                                     CGGAA  ___
GAM651  LOC256021 3'  AGCAGTGAACATAGCTGTGA   98276         CG  GA    T
                                TCACAGCTA  GT  CATT CT
                                |||||||||  ||  |||| ||
                                AGTGTCGAT  CA  GTGA GA
                                     A_  A_   C
GAM651  LOC56899  5'  GAAATGTGGAGCTAGGATC    39712      AC    ACGGTG
                                GATC  AGCT     ACATTTC
                                ||||  ||||     |||||||
                                CTAG  TCGA     TGTAAAG
                                  GA   GG_____
GAM652  AMPD3     3'  CTTGTCTATACTTGTTCCT    6654           __
                                AGGAGCAGGT  GGACAAG
                                |||||||||  |||||||
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                                TCCTTGTTCA  TCTGTTC
                                      TA
GAM652  AMT      3'  TTCAGGACCCTGCTTCTGA   6659          ____
                                TCAGGAGCAGG   TGGA
                                ||||||||||   ||||
                                AGTCTTCGTCC   ACTT
                                      CAGG
GAM652  AP2M1    3'  TCCACCTGTCTGTCCTGG    15800       ___
                                TCAGGA  GCAGGTGGA
                                ||||||  |||||||||
                                GGTCCT  TGTCCACCT
                                   GTC
GAM652  APOB48R  3'  CTTGCTCCAATGCCACTGA   38586     GA  GG  _
                                TCAG  GCA  TGGA CAAG
                                ||||  |||  |||| ||||
                                AGTC  CGT  ACCT GTTC
                                  AC  A_   C
GAM652  CHGA     3'  CTTGTCTCCTACTCCTGA    8880        C  T
                                TCAGGAG AGG GGACAAG
                                ||||||| ||| |||||||
                                AGTCCTC TCC TCTGTTC
                                    A  _
GAM652  CLCN4    3'  CTTATCCATCAGTTTCTGA   10210        A    C
                                TCAGGAGC GGTGGA AAG
                                |||||||| |||||| |||
                                AGTCTTTG CTACCT TTC
                                     A    A
GAM652  CRK      3'  CTTGTGTGTTAGCTTCTGA   60543        A GT G
                                TCAGGAGC G  G ACAAG
                                |||||||| |  | |||||
                                AGTCTTCG T  T TGTTC
                                     A TG G
GAM652  DAAM2    3'  CTTGTCCAGAGTTCCTG     93903        AGG
                                CAGGAGC   TGGACAAG
                                |||||||   ||||||||
                                GTCCTTG   ACCTGTTC
                                    AG_
GAM652  DMP1     3'  CTTGTTTCTTGCTCCTGA    16611          T
                                TCAGGAGCAGG GGACAAG
                                |||||||||||| |||||||
                                AGTCCTCGTTC TTTGTTC
                                          _
GAM652  DVL3     3'  CTTGTCCGACTCTCTTGA    16645        C  G
                                TCAGGAG AG TGGACAAG
                                ||||||| || ||||||||
                                AGTTCTC TC GCCTGTTC
                                    _  A
GAM652  EML1     3'  CTTGTTCACACGCCCTGA    60448       A  AG
                                TCAGG GC  GTGGACAAG
                                ||||| ||  |||||||||
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                                AGTCC CG  CACTTGTTC
                                   _ CA
GAM652  EPM2A    3'  CTTGTCCAAGGTCTCATGA   20235    G  _ AGG
                                TCA GAG C   TGGACAAG
                                ||| ||| |   ||||||||
                                AGT CTC G   ACCTGTTC
                                  A  T GA_
GAM652  FUT4     3'  TCACAGCCTTGGCTCCTGA   10723       __  _ _
                                TCAGGAGC  AGG TG GA
                                ||||||||  ||| || ||
                                AGTCCTCG  TCC AC CT
                                     GT   G  A
GAM652  GNLY     5'  CTTGCAGCCATGCTCCTGG   22230       _  GGA
                                TCAGGAGCA GGT   CAAG
                                ||||||||| |||   ||||
                                GGTCCTCGT CCG   GTTC
                                      A   AC_
GAM652  IFI35    5'  CTTGCGGGCTCTGCTCTGA   63718     G   _ GGA
                                TCAG AGCAG GT   CAAG
                                |||| ||||| ||   ||||
                                AGTC TCGTC CG   GTTC
                                   _    T  GGC
GAM652  MAT2A    3'  TGTCCTCTTTCAGCTCCTGA  20972       ___  T
                                TCAGGAGC   AGG GGACA
                                ||||||||   ||| |||||
                                AGTCCTCG   TTC CCTGT
                                     ACT   T
GAM652  PCDH12   5'  CTTGTCCATCATTTGCTGA   33885     G  CA
                                TCAG AG  GGTGGACAAG
                                |||| ||  ||||||||||
                                AGTC TT  CTACCTGTTC
                                  G  TA
GAM652  PDE4B    3'  CTTGTCCCTTTGTCTGCC    12011   _ _   T
                                GG AG CAGG GGACAAG
                                || || |||| |||||||
                                CC TC GTTT CCTGTTC
                                 G  T   C
GAM652  PPIL1    3'  CTTGTGCATGTCTGCTCTGA  32667     G   __  G
                                TCAG AGCAG  GTG ACAAG
                                |||| |||||  ||| |||||
                                AGTC TCGTC  TAC TGTTC
                                   _    TG  G
GAM652  PPP2R5B  3'  CTTGCCAGAGTGGCTTCTGA  21798       AGG__  A
                                TCAGGAGC    TGG CAAG
                                ||||||||    ||| ||||
                                AGTCTTCG    ACC GTTC
                                     GTGAG  _
GAM652  REV3L    5'  CTTGCCGGGTGCTCCTGA    12821       GG  A
                                TCAGGAGCA  TGG CAAG
                                |||||||||  ||| ||||
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                                AGTCCTCGT  GCC GTTC
                                     GG  _
GAM652  SLC7A9   5'  CTTGTCTGCTGCTGCTGA    27336     G   G TG
                                TCAG AGCA G  GACAAG
                                |||| |||| |  ||||||
                                AGTC TCGT C  CTGTTC
                                  G   _ GT
GAM652  TCF2     3'  CTTGATTGAGTGCTCCTG    6614        GG  A
                                CAGGAGCA  TGG CAAG
                                ||||||||  ||| ||||
                                GTCCTCGT  GTT GTTC
                                     GA  A
GAM652  TYRO3    5'  CTTGTACCGTGCTCCTGA    21936        _  GG
                                TCAGGAGCA GGT  ACAAG
                                |||||||| |||  |||||
                                AGTCCTCGT CCA  TGTTC
                                     G  __
GAM652  WBSCR5   3'  TGCCATGGTTGCTCCTGG    42115         __   A
                                TCAGGAGCAG  GTGG CA
                                ||||||||||  |||| ||
                                GGTCCTCGTT  TACC GT
                                     GG  _
GAM652  ARHGEF4  3'  CTTTTTCCCTGCTCCTGG    53370         T  C
                                TCAGGAGCAGG GGA AAG
                                |||||||||| ||| |||
                                GGTCCTCGTCC CTT TTC
                                     _  T
GAM652  CAPN6    3'  TGACATCCTAGCTCCTGA    27402        _  _ GA
                                TCAGGAGC AGG TG  CA
                                |||||||| ||| ||  ||
                                AGTCCTCG TCC AC  GT
                                     A  T  A_
GAM652  CXYorf1  3'  CTTGCCAGCTGGCCCCTG    82913     A _ G  A
                                CAGG GC AG TGG CAAG
                                |||| || || ||| ||||
                                GTCC CG TC ACC GTTC
                                  C  G  G  _
GAM652  DKFZP564O0423 3'  CTTGTCCACTGGTTGCCC    93348    A  ___
                                GG GCA   GGTGGACAAG
                                || |||   ||||||||||
                                CC CGT   TCACCTGTTC
                                 _   TGG
GAM652  DNAJC6   3'  CTTGTCAGTATCTGCTCTGA   29493     G      __
                                TCAG AGCAGGTG  GACAAG
                                |||| ||||||||  ||||||
                                AGTC TCGTCTAT  CTGTTC
                                  _       GA
GAM652  FER1L4   3'  CTTCAATGCCTGCTCCTGG    48120          GAC
                                TCAGGAGCAGGTG   AAG
                                ||||||||||||   |||
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                                GGTCCTCGTCCGT  TTC
                                      AAC
GAM652  FKBP14   5' CTTGTCCGTAAGCCTTGA   36067     A  AG
                                TCAGG GC  GTGGACAAG
                                ||||| ||  |||||||||
                                AGTTC CG  TGCCTGTTC
                                  _ AA
GAM652  FLJ10815 3' CTTGTCCACACCTTCCTGG   37233      CAG
                                TCAGGAG  GTGGACAAG
                                |||||||  |||||||||
                                GGTCCTT  CACCTGTTC
                                    CCA
GAM652  FLJ11184 5' CTTGTGAGCTGCTGCTCCTG  37720       __ GG
                                CAGGAGCAG  GT  ACAAG
                                |||||||||  ||  |||||
                                GTCCTCGTC  CG  TGTTC
                                     GT  AG
GAM652  FLJ13612 3' TGCCCACCTCTGTCTCCTG   48089      _ __    A
                                CAGGAG CA  GGTGG CA
                                |||||| ||  ||||| ||
                                GTCCTC GT  CCACC GT
                                   T  CT    C
GAM652  FLJ20170 3' CTTGTATTCCTGTTCCTGA   35165        TGG
                                TCAGGAGCAGG  ACAAG
                                ||||||||||  |||||
                                AGTCCTTGTCC  TGTTC
                                      TTA
GAM652  FLJ20232 3' CTTGTTTGCCGCTGCTGA    39185     G  A  TG
                                TCAG AGC GG  GACAAG
                                |||| ||| ||  ||||||
                                AGTC TCG CC  TTGTTC
                                  G  _ GT
GAM652  FLJ23189 3' CTTGCAGAATCCTTGCTCCTGA 47528         T  A____
                                TCAGGAGCAGG GG    CAAG
                                |||||||||| ||    ||||
                                AGTCCTCGTTC CT    GTTC
                                      _ AAGAC
GAM652  GRO2     3' TTGGTGGCTGTTCCTGA     60254        G  GA
                                TCAGGAGCAG TG  CAA
                                |||||||||| ||  |||
                                AGTCCTTGTC GT  GTT
                                     G  G_
GAM652  GTF2F2   5' CTTGTCCTTTGTTCCGGA    15944    A      T
                                TC GGAGCAGG GGACAAG
                                || |||||||| |||||||
                                AG CCTTGTTT CCTGTTC
                                 G      _
GAM652  HSPC128  3' CTTATTTATTTGCCTCTGA   27181     GA       C
                                TCAG  GCAGGTGGA AAG
                                ||||  ||||||||| |||
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                                AGTC  CGTTTATTT TTC
                                  TC        A
GAM652  KIAA0427  3'  CTTGCCACAGCCCTGCTCC   29380        ____  A
                                GGAGCAGG   TGG CAAG
                                ||||||||   ||| ||||
                                CCTCGTCC   ACC GTTC
                                    CGAC  _
GAM652  KIAA0450  3'  TGGGCCACCTGCCCGTGA    28374    _ A      A_
                                TCA GG GCAGGTGG  CA
                                ||| || ||||||||  ||
                                AGT CC CGTCCACC  GT
                                  G _       GG
GAM652  KIAA0561  3'  CTTGTCCAGTCTACCCTGG   66477     AGC  _
                                TCAGG   AGG TGGACAAG
                                |||||   ||| ||||||||
                                GGTCC   TCT ACCTGTTC
                                   CA_  G
GAM652  KIAA0775  5'  TGTCCACGGTTGCTCCTG    28958       __
                                CAGGAGCAG  GTGGACA
                                |||||||||  |||||||
                                GTCCTCGTT  CACCTGT
                                     GG
GAM652  KIAA0961  5'  TGTGGACCCTGCTTCTGA    30416         _ GG
                                TCAGGAGCAGG T  ACA
                                |||||||||||  |  |||
                                AGTCTTCGTCC A  TGT
                                      C GG
GAM652  KIAA1130  3'  TGTATCCCTAGCTCCTGA    63103       _  T  _
                                TCAGGAGC AGG GG ACA
                                |||||||| ||| || |||
                                AGTCCTCG TCC CT TGT
                                     A  _  A
GAM652  KIAA1742  3'  CTTGATCTGTCTGCTCCT    78140       TG  _
                                AGGAGCAGG  GA CAAG
                                |||||||||  || ||||
                                TCCTCGTCT  CT GTTC
                                     GT  A
GAM652  MGC13269  3'  CTTGTGGCTTCTGCTCTGA   52163    G     TGG_
                                TCAG AGCAGG    ACAAG
                                ||||  ||||||    |||||
                                AGTC TCGTCT    TGTTC
                                  _     TCGG
GAM652  MGC2705   5'  CTTGCCCTCACCTGCTCCTG  52082          A__
                                CAGGAGCAGGTGG   CAAG
                                ||||||||||||||  ||||
                                GTCCTCGTCCACT   GTTC
                                       CCC
GAM652  MKRN2     3'  CTTGAATTCTGCTCCTGA    72848         TGGA
                                TCAGGAGCAGG    CAAG
                                ||||||||||    ||||
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                                AGTCCTCGTCT   GTTC
                                      TAA_
GAM652  NIR3     3'  TGCCCACCTGTCTGCCTG    66834     _ _     A
                                CAGG AG CAGGTGG CA
                                |||| || ||||||| ||
                                GTCC TC GTCCACC GT
                                  G T     C
GAM652  RAP140   3'  CTTGAGCCACTGCTCCTGG   31514        G  A_
                                TCAGGAGCAG TGG  CAAG
                                |||||||||| |||  ||||
                                GGTCCTCGTC ACC  GTTC
                                      _  GA
GAM652  YKT6     3'  CTTGGGAGCTCTGCTCTGA   22639     G   _ GGA
                                TCAG AGCAG GT   CAAG
                                |||| ||||| ||   ||||
                                AGTC TCGTC CG   GTTC
                                  _    T  AGG
GAM652  ZF       5'  CTTGTTCGCTGCCCTCTGA   41366     _ A   G
                                TCAG G GCAG TGGACAAG
                                |||| | |||| ||||||||
                                AGTC C CGTC GCTTGTTC
                                  T C   _
GAM652  ZFP67    3'  TGTCCCAGCTGCTCCTGG    32427        G  _
                                TCAGGAGCAG TGG ACA
                                |||||||||| ||| |||
                                GGTCCTCGTC ACC TGT
                                      G   C
GAM652  LOC147645 3'  CTTGAATTTGCCGTTCCTGA   79068       A  TG  __
                                TCAGGAGC GG  GA  CAAG
                                |||||||| ||  ||  ||||
                                AGTCCTTG CC  TT  GTTC
                                     _ GT  AA
GAM652  LOC150407 3'  CTTGTCCATCTTCCTG     80641     GC
                                CAGGA  AGGTGGACAAG
                                |||||  ||||||||||
                                GTCCT  TCTACCTGTTC
                                     __
GAM652  LOC150468 3'  CTTGTCCAAGTGACCTGG    80684     AG  GG
                                TCAGG  CA  TGGACAAG
                                |||||  ||  ||||||||
                                GGTCC  GT  ACCTGTTC
                                  A_  GA
GAM652  LOC150696 5'  CTTGTCTGTTCCCTCCTGA   59158       CA  TG
                                TCAGGAG  GG  GACAAG
                                |||||||  ||  ||||||
                                AGTCCTC  TT  CTGTTC
                                    CC  GT
GAM652  LOC157858 5'  CTTGCCCAGGGGCCTCCTGG  87887       _ AGG  A
                                TCAGGAG C   TGG CAAG
                                ||||||| |   ||| ||||
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                                GGTCCTC G   ACC GTTC
                                    C GGG   C
GAM652   LOC200093 3'  CTTGCCAGCTGGCCCCTG    63773     A _ G   A
                                CAGG GC AG TGG CAAG
                                |||| || || ||| ||||
                                GTCC CG TC ACC GTTC
                                  C  G  G   _
GAM652   LOC220567 3'  CTTGCTCCAATGCCACTGA    92435     GA   GG   _
                                TCAG  GCA  TGGA CAAG
                                ||||  |||  |||| ||||
                                AGTC  CGT  ACCT GTTC
                                  AC   A_    C
GAM652   LOC221143 3'  CTTGCCCAAGGGCTCCTGA    95214       AGG   A
                                TCAGGAGC   TGG CAAG
                                ||||||||   ||| ||||
                                AGTCCTCG   ACC GTTC
                                     GGA   C
GAM652   LOC222936 5'  CTTGCCAAAAGCTCCTGA    96026       AGG   A
                                TCAGGAGC   TGG CAAG
                                ||||||||   ||| ||||
                                AGTCCTCG   ACC GTTC
                                     AAA   _
GAM652   LOC254182 5'  CTTGTCAATCTGCTCCTGA    97748         G
                                TCAGGAGCAGGT GACAAG
                                |||||||||||| ||||||
                                AGTCCTCGTCTA CTGTTC
                                       A
GAM652   LOC257449 3'  CTTGATCTGTCTGCTCCT     63376       TG _
                                AGGAGCAGG  GA CAAG
                                |||||||||  || ||||
                                TCCTCGTCT  CT GTTC
                                     GT  A
GAM652   LOC51195  3'  CTTGTCTACTCTGCCCCTG    33405     A   _
                                CAGG GCAG GTGGACAAG
                                |||| |||| |||||||||
                                GTCC CGTC CATCTGTTC
                                  C    T
GAM652   LOC91040  3'  CTTGCCAGCTGGCCCCTG    65347     A _ G   A
                                CAGG GC AG TGG CAAG
                                |||| || || ||| ||||
                                GTCC CG TC ACC GTTC
                                  C  G  G   _
GAM652   LOC91351  3'  CTTGCATCCAGTGTTCCTGA   66297       GG   __
                                TCAGGAGCA  TGGA  CAAG
                                |||||||||  ||||  ||||
                                AGTCCTTGT  ACCT  GTTC
                                     G_    AC
GAM652   LOC92230  5'  CTTGCCCACCTGCCTCTGG    69086     GA      A
                                TCAG  GCAGGTGG CAAG
                                ||||  |||||||| ||||
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                                GGTC  CGTCCACC GTTC
                                  TC       C
GAM653  CD5     3'  GCTCTGCACATTCACCGC    27221    A      T  A
                                GC GTGAATGT CA AGC
                                || |||||||| || |||
                                CG CACTTACA GT TCG
                                 C       C  C
GAM653  CEBPA   3'  GCTGGAACTCACTGCG      16430        AT   AA
                                CGCAGTGA  GTTC  AGC
                                ||||||||  ||||  |||
                                GCGTCACT  CAAG  TCG
                                     __   G_
GAM653  CHD2    3'  GCTTTCTGTTTCACTGTGG   8869          TGTTC
                                CCGCAGTGAA    AAAGC
                                ||||||||||    |||||
                                GGTGTCACTT    TTTCG
                                      TGTC_
GAM653  DDX11   3'  GCTGTGGCATCCACTGTGG   48390        A   T  A
                                CCGCAGTG ATGT CA AGC
                                |||||||| |||| || |||
                                GGTGTCAC TACG GT TCG
                                     C   _  G
GAM653  DDX11   3'  GCTGTGGCATCCACTGTGG   16577        A   T  A
                                CCGCAGTG ATGT CA AGC
                                |||||||| |||| || |||
                                GGTGTCAC TACG GT TCG
                                     C   _  G
GAM653  DUSP7   3'  GCTTTGGGCGTCCACCAGG   66041    GCA  A
                                CC  GTG ATGTTCAAAGC
                                ||  ||| ||||||||||
                                GG  CAC TGCGGGTTTCG
                                 AC_  C
GAM653  F2R     3'  GCCCTGAACATTTCATGGTG   10568    A   _    AA
                                CGC GTGAA TGTTCA  GC
                                ||| ||||| ||||||  ||
                                GTG TACTT ACAAGT  CG
                                  G    T    CC
GAM653  GCNT2   5'  CTCTGGCTTTCACTGCG     9454         T  T  A
                                CGCAGTGAA GT CA AG
                                ||||||||| || || ||
                                GCGTCACTT CG GT TC
                                     T  _  C
GAM653  IL6R    3'  CTTTGGACACTCACACGG    6910     CA   A
                                CCG  GTGA TGTTCAAAG
                                |||  |||| |||||||||
                                GGC  CACT ACAGGTTTC
                                  A_   C
GAM653  NRGN    3'  GCTTTCCTGCGCGCACTGCGG 21626        AA  TC_
                                CCGCAGTG  TGT  AAAGC
                                ||||||||  |||  |||||
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                                GGCGTCAC  GCG   TTTCG
                                    GC   TCC
GAM653  NTSR1    3'  GCTTTGGGCCTCACGTGC    11860     _   AT
                                GCA GTGA  GTTCAAAGC
                                ||| ||||  |||||||||
                                CGT CACT  CGGGTTTCG
                                  G    C_
GAM653  OPCML    3'  CTTTAATCTACACTGCGG    11898       AAT   C
                                CCGCAGTG   GTT AAAG
                                ||||||||   ||| ||||
                                GGCGTCAC   TAA TTTC
                                    ATC   _
GAM653  PAX5     3'  GCTTGGAGAACTCACTGTGG   34132       ATG   A
                                CCGCAGTGA   TTC AAGC
                                |||||||||   ||| ||||
                                GGTGTCACT   GAG TTCG
                                     CAA   G
GAM653  RAB27A   3'  GCTTTAGTTCACTGTG      17150        GTTC
                                CGCAGTGAAT    AAAGC
                                ||||||||||    |||||
                                GTGTCACTTG    TTTCG
                                     A___
GAM653  RAD51C   3'  CTTCTGCATGTTCATTGC     55241         T  _
                                GCAGTGAATGT CA AAG
                                |||||||||||  || |||
                                CGTTACTTGTA GT TTC
                                      C  C
GAM653  RAG1     3'  GCTTTTTACCACTGTGG      6545        AAT  TC
                                CCGCAGTG   GT  AAAGC
                                ||||||||   ||  |||||
                                GGTGTCAC   CA  TTTCG
                                    ___  TT
GAM653  RTKN     3'  GCTTTGAGGATGGCACTG     53503      A_  G
                                CAGTG  AT TTCAAAGC
                                |||||  || ||||||||
                                GTCAC  TA GAGTTTCG
                                   GG  G
GAM653  SECTM1   3'  GCTTTTGTCTTCGTCACTGCGG 13009         ATGTT_   _
                                CCGCAGTGA     CAAA GC
                                |||||||||     |||| ||
                                GGCGTCACT     GTTT CG
                                     GCTTCT    T
GAM653  SNAI2    3'  GCTTTGAACATTCCTGGCG    13241     _  T
                                CGC AG GAATGTTCAAAGC
                                ||| ||  ||||||||||||
                                GCG TC CTTACAAGTTTCG
                                  G  _
GAM653  TACC1    3'  GCTTTGAAAGCAGTCACTGTGG 21876         A   __
                                CCGCAGTGA TGT  TCAAAGC
                                ||||||||| |||  |||||||
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                                GGTGTCACT ACG  AGTTTCG
                                     G   AA
GAM653  YES1     3'  GCTTCACATTCATTGC      19541          TCA
                                GCAGTGAATGT   AAGC
                                ||||||||||   ||||
                                CGTTACTTACA   TTCG
                                      C__
GAM653  C11orf15 3'  GCTTTGAACTAGGGCTGGGG   40595    G    GAAT
                                CC CAGT    GTTCAAAGC
                                || ||||    |||||||||
                                GG GTCG    CAAGTTTCG
                                 G   GGAT
GAM653  C11orf23 3'  GCTTCTCCATCCCACTGTGG   37568        A_   TTCA
                                CCGCAGTG  ATG    AAGC
                                ||||||||  |||    ||||
                                GGTGTCAC  TAC    TTCG
                                     CC   CTC_
GAM653  C20orf130 5' GCTTTGAGCAGAAGCTGC     62416       GAA
                                GCAGT   TGTTCAAAGC
                                |||||   ||||||||||
                                CGTCG   ACGAGTTTCG
                                   AAG
GAM653  C3orf4    5'  GCCTTGAGTCATTTTACCGCGG 39594      A    _ _    A
                                CCGC GTGAA TG TTCAA GC
                                |||| ||||| || ||||| ||
                                GGCG CATTT AC GAGTT CG
                                  C    T T    C
GAM653  C8orf13   5'  GCCCTGTGCGGCTCACTGCG   82479        A_   T  AA
                                CGCAGTGA  TGT CA  GC
                                ||||||||  ||| ||  ||
                                GCGTCACT  GCG GT  CG
                                     CG   T  CC
GAM653  C9orf14   3'  GCTTTGAATCTCAATACGG    87958     CAG   AT
                                CCG   TGA  GTTCAAAGC
                                |||   |||  |||||||||
                                GGC   ACT  TAAGTTTCG
                                  ATA   C_
GAM653  CARD14    5'  GCTTTGGAGACACTGCGG     44354        AATG
                                CCGCAGTG    TTCAAAGC
                                ||||||||    ||||||||
                                GGCGTCAC    AGGTTTCG
                                     AG__
GAM653  DDX12     3'  GCAGTGGCATCCACTGTGG    60423        A    T  AA
                                CCGCAGTG ATGT CA  GC
                                |||||||| |||| ||  ||
                                GGTGTCAC TACG GT  CG
                                     C    _  GA
GAM653  DDX35     3'  GCTCTGAAGTGGGCTGCGG    41928        GA  G    A
                                CCGCAGT  AT TTCA AGC
                                |||||||  || |||| |||
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                                GGCGTCG  TG AAGT TCG
                                    GG  _   C
GAM653  DKFZP761G1913 3'  GCTTTTTTGAATTCACTGTG  49697         GTTC_
                                CGCAGTGAAT    AAAGC
                                ||||||||||    |||||
                                GTGTCACTTA    TTTCG
                                     AGTTT
GAM653  DKFZp761G2113 5'  GCTTTGAGGTACACCGG    70468    CA  A  G
                                CCG  GTG AT TTCAAAGC
                                |||  ||| || ||||||||
                                GGC  CAC TG GAGTTTCG
                                  __  A  _
GAM653  EIF2C2   3'  GCCTTGAACATTCTGATGT   72414    GT_       A
                                GCA   GAATGTTCAA GC
                                |||   |||||||||| ||
                                TGT   CTTACAAGTT CG
                                  AGT        C
GAM653  FLJ13052  5'  GCCCTGTACTTCACTGTGG   43753         T  T  AA
                                CCGCAGTGAA GT CA  GC
                                |||||||||| || ||  ||
                                GGTGTCACTT CA GT  CG
                                     _  T  CC
GAM653  FLJ22794  5'  GCTTTGAAGATACTGC     93249      GA  G
                                GCAGT  AT TTCAAAGC
                                |||||  || ||||||||
                                CGTCA  TA AAGTTTCG
                                  __  G
GAM653  FLJ23119  3'  GCTAAACATTCACTGC     45376          CAA
                                GCAGTGAATGTT   AGC
                                ||||||||||||   |||
                                CGTCACTTACAA   TCG
                                     A__
GAM653  GPR88    3'  GCTTTGAACATTCTGTACTG  42137     ___
                                CAGT   GAATGTTCAAAGC
                                ||||   ||||||||||||||
                                GTCA   CTTACAAGTTTCG
                                  TGT
GAM653  GRP3     3'  GCCTTGGGACACTGTGG     31739        AATG    A
                                CCGCAGTG    TTCAA GC
                                ||||||||    ||||| ||
                                GGTGTCAC    GGGTT CG
                                     A___     C
GAM653  HM74     5'  GCTGGAGCATTCACTAGG    21201    GC        AA
                                CC  AGTGAATGTTC  AGC
                                ||  ||||||||||  |||
                                GG  TCACTTACGAG  TCG
                                 A_         G_
GAM653  HPCAL4   3'  CTTTAGAGATCACTGTGG    33208         A G TC
                                CCGCAGTGA T T  AAAG
                                |||||||| | |  ||||
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                                GGTGTCACT A A  TTTC
                                     _ G GA
GAM653  HSU24186 3' GCTTTGAACTTTTCGG     26240     CAGT   T
                                CCG    GAA GTTCAAAGC
                                |||    ||| |||||||||
                                GGC    TTT CAAGTTTCG
                                 _____   T
GAM653  KIAA0232 3' GCTTTGAACATTTGGGT     73121    AG
                                GC  TGAATGTTCAAAGC
                                ||  ||||||||||||||
                                TG  GTTTACAAGTTTCG
                                 G_
GAM653  KIAA0254 3' GCTTTGAATCTGCTGC      29282       AAT
                                GCAGTG   GTTCAAAGC
                                ||||||   |||||||||
                                CGTCGT   TAAGTTTCG
                                   C__
GAM653  KIAA0416 5' CTTTTACAGACTCACTGCG   32092        A__   TC
                                CGCAGTGA   TGT  AAAG
                                ||||||||   |||  ||||
                                GCGTCACT   ACA  TTTC
                                     CAG   T_
GAM653  KIAA0551 3' GCTCTGAACATTCCCAGCG   67380     AGT       A
                                CGC   GAATGTTCA AGC
                                |||   ||||||||| |||
                                GCG   CTTACAAGT TCG
                                  ACC        C
GAM653  KIAA0766 3' GCTTTGAATATTCACAGC    29674    A
                                GC GTGAATGTTCAAAGC
                                || ||||||||||||||
                                CG CACTTATAAGTTTCG
                                 A
GAM653  KIAA1474 3' GCTTTGAGGGAAACTGTGG   67477       GAATG
                                CCGCAGT    TTCAAAGC
                                |||||||    ||||||||
                                GGTGTCA    GAGTTTCG
                                    AAGG_
GAM653  KIAA1712 5' GCTTTGAAGGTCTTGCGG    68161      T  A G
                                CCGCAG GA T TTCAAAGC
                                |||||| || | ||||||||
                                GGCGTT CT G AAGTTTCG
                                   _ _ G
GAM653  KIAA1804 5' GCTTCGGGGACCGCTGCGG   70350       AAT   A__
                                CCGCAGTG   GTTC   AAGC
                                ||||||||   ||||   ||||
                                GGCGTCGC   CAGG   TTCG
                                     ___    GGC
GAM653  KIAA1817 3' CTCTGGGCCTCACTGTG     68777       AT    A
                                CGCAGTGA  GTTCA AG
                                ||||||||  ||||| ||
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                                GTGTCACT  CGGGT TC
                                    C_    C
GAM653  KIAA1912  3'  CTTTAAAATATTGCACTGC   73759      _    C_
                                GCAGTG AATGTT  AAAG
                                |||||| ||||||  ||||
                                CGTCAC TTATAA  TTTC
                                   G     AA
GAM653  L3MBTL    3'  GCTTCACCTCACTGTGG    70087       AT  TCA
                                CCGCAGTGA  GT   AAGC
                                |||||||||  ||   ||||
                                GGTGTCACT  CA   TTCG
                                     C_  C__
GAM653  LEAP-2    5'  CTTTGAACTTTCCACAGC   54808    A  _  T
                                GC GTG AA GTTCAAAG
                                || ||| || ||||||||
                                CG CAC TT CAAGTTTC
                                 A   C  T
GAM653  MDS018    3'  GCTTTCCTAGCATTTACTGC  41827         C__
                                GCAGTGAATGTT   AAAGC
                                ||||||||||||   |||||
                                CGTCATTTACGA   TTTCG
                                       TCC
GAM653  MGC12538  3'  GCTTCATTGCGTCACTGCG   52204       A   TCA_
                                CGCAGTGA TGT    AAGC
                                |||||||| |||    ||||
                                GCGTCACT GCG    TTCG
                                    _   TTAC
GAM653  MGC14126  5'  GCTTTGCGTGCACTGCGG    52940       A   TT
                                CCGCAGTG ATG  CAAAGC
                                |||||||| |||  ||||||
                                GGCGTCAC TGC  GTTTCG
                                    G   __
GAM653  MGC15482  3'  GCCTTGAAATCACTGTGG    52855       ATG    A
                                CCGCAGTGA   TTCAA GC
                                |||||||||   ||||| ||
                                GGTGTCACT   AAGTT CG
                                     A__     C
GAM653  MISS      5'  GCTTCTAGACCCTACTGCGG   58640       AAT   CA_
                                CCGCAGTG   GTT   AAGC
                                ||||||||   |||   ||||
                                GGCGTCAT   CAG   TTCG
                                    CC_   ATC
GAM653  PLAGL2    3'  CTCTGAACCTGCTGTGG     70960       AAT    A
                                CCGCAGTG   GTTCA AG
                                ||||||||   ||||| ||
                                GGTGTCGT   CAAGT TC
                                    C__     C
GAM653  PTP4A1    5'  GCTCCGAGCCGCTCACTGCG  14409       AT_   AA
                                CGCAGTGA   GTTC  AGC
                                ||||||||   ||||  |||
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                                GCGTCACT  CGAG  TCG
                                    CGC   CC
GAM653  RABEX5   3'  GCTTCCTCTGGCATTCACTGTG 27962          CA___
          G                  CCGCAGTGAATGTT   AAGC
                             ||||||||||||||   ||||
                             GGTGTCACTTACGG   TTCG
                                   TCTCC
GAM653  REM      3'  GCTCCAGGGACGCCACTGCGG  26687      AA   AA__
                             CCGCAGTG  TGTTC   AGC
                             ||||||||  |||||   |||
                             GGCGTCAC  GCAGG   TCG
                                 C_    GACC
GAM653  RNPS1    5'  GCTTTGAACACCTCAGAAGG  22966   GCAG  A_
                             CC   TGA  TGTTCAAAGC
                             ||   |||  ||||||||||
                             GG   ACT  ACAAGTTTCG
                              AAG_  CC
GAM653  RNPS1    5'  GCTTTGAACACCTCAGAAGG  55487   GCAG  A_
                             CC   TGA  TGTTCAAAGC
                             ||   |||  ||||||||||
                             GG   ACT  ACAAGTTTCG
                              AAG_  CC
GAM653  RPS6KB1  3'  GCTCTGAATCACTGTG     13470       ATG   A
                             CGCAGTGA   TTCA AGC
                             ||||||||   |||| |||
                             GTGTCACT   AAGT TCG
                                ___    C
GAM653  SMCR5    5'  GCTTCCATTTACTACGG    59250    C      TTCA
                             CCG AGTGAATG   AAGC
                             ||| ||||||||   ||||
                             GGC TCATTTAC   TTCG
                               A      C___
GAM653  SSB-3    3'  GCTCCCGGGCTCACTGCG   55960       AT   AA_
                             CGCAGTGA  GTTC  AGC
                             ||||||||  ||||  |||
                             GCGTCACT  CGGG  TCG
                                __    CCC
GAM653  SSB-3    5'  GCTGGGACTGCACTGCGG   55961       AAT   AA
                             CCGCAGTG  GTTC  AGC
                             ||||||||  ||||  |||
                             GGCGTCAC  CAGG  TCG
                                 GT_   G_
GAM653  SV2B     3'  GCTTTGAACATAAACAGGG   29952   GCA  GA
                             CC  GT  ATGTTCAAAGC
                             ||  ||  ||||||||||
                             GG  CA  TACAAGTTTCG
                              GA_  AA
GAM653  LOC121506 3'  GCTTTAAGAGACTCACTGTG  74534       ATG  __
                             CGCAGTGA  TTC  AAAGC
                             ||||||||  |||  |||||
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                                GTGTCACT  GAG  TTTCG
                                    CA_  AA
GAM653  LOC124976 3' GCTTTGAGGCTCACGCG    74843    A   ATG
                                CGC GTGA  TTCAAAGC
                                ||| ||||  ||||||||
                                GCG CACT  GAGTTTCG
                                  _   CG_
GAM653  LOC128989 3' GCCTTGAGGGGCACTGTGG   75319       AATG   A
                                CCGCAGTG   TTCAA GC
                                ||||||||   ||||| ||
                                GGTGTCAC   GAGTT CG
                                    GGG_   C
GAM653  LOC144373 3' GCTGTGGCATCCACTGTGG   77312       A   T  A
                                CCGCAGTG ATGT CA AGC
                                |||||||| |||| || |||
                                GGTGTCAC TACG GT TCG
                                    C   _  G
GAM653  LOC144840 3' GCTCCTGAGTTCACTGC     77527       GT  A_
                                GCAGTGAAT  TCA  AGC
                                |||||||||  |||  |||
                                CGTCACTTG  AGT  TCG
                                    __  CC
GAM653  LOC145255 3' GCTTTGAACAGTCCTGGG    84269    G  T  A
                                CC CAG GA TGTTCAAAGC
                                || ||| || ||||||||||
                                GG GTC CT ACAAGTTTCG
                                 _  _  G
GAM653  LOC146378 3' GCCTTGGTGGCGTTCACGC   78421    A      __   A
                                GC GTGAATGT  TCAA GC
                                || ||||||||  |||| ||
                                CG CACTTGCG  GGTT CG
                                 _      GT   C
GAM653  LOC146957 3' GCTTTAAAAGCATACCACTGTG 78817       A_   C__
          G                      CCGCAGTG  ATGTT   AAAGC
                                |||||||  |||||  |||||
                                GGTGTCAC  TACGA   TTTCG
                                    CA    AAA
GAM653  LOC148181 5' GCTGTTGCTTCACTGCGG    79437       T  TCAA
                                CCGCAGTGAA GT   AGC
                                |||||||||| ||   |||
                                GGCGTCACTT CG   TCG
                                    _ TTG_
GAM653  LOC149108 3' TTTTAGACTTCACTGTGG    85512       T  TC
                                CCGCAGTGAA GT  AAAG
                                |||||||||| ||  ||||
                                GGTGTCACTT CA  TTTT
                                    _ GA
GAM653  LOC149271 5' GCTTTCTGGAATTTCACTGC  80007       TG   __
                                GCAGTGAA  TTCA  AAGC
                                ||||||||  ||||  ||||
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                                CGTCACTT  AGGT  TTCG
                                    TA    CT
GAM653   LOC150095 5'  GCTTCGAAGTTCACTGTGG   85995          G   A
                                CCGCAGTGAAT TTC AAGC
                                |||||||||||  ||| ||||
                                GGTGTCACTTG AAG TTCG
                                      _   C
GAM653   LOC150155 3'  GCTTTGGACTCACCATCGG   71413     CA_   AT
                                CCG   GTGA  GTTCAAAGC
                                |||   ||||  |||||||||
                                GGC   CACT  CAGGTTTCG
                                  TAC   __
GAM653   LOC150418 3'  GCTTGTGTTCACTGTGG     66115         TG TCA
                                CCGCAGTGAA  T   AAGC
                                ||||||||||  |   ||||
                                GGTGTCACTT  G   TTCG
                                      GT ___
GAM653   LOC151446 3'  GCTTTGAACATGATGATGG   86573     _  GTGA
                                CCG CA    ATGTTCAAAGC
                                ||| ||    ||||||||||
                                GGT GT    TACAAGTTTCG
                                  A  AG__
GAM653   LOC153027 5'  GCTTTGAACACCTCAGAAGG  68031    GCAG   A_
                                CC    TGA  TGTTCAAAGC
                                ||    |||  |||||||||
                                GG    ACT  ACAAGTTTCG
                                  AAG_   CC
GAM653   LOC154990 5'  GCTGTTGCTTCACTGCGG    82153         T  TCAA
                                CCGCAGTGAA GT    AGC
                                ||||||||||  ||    |||
                                GGCGTCACTT CG    TCG
                                      _  TTG_
GAM653   LOC157247 5'  GCTTTGGATACTACTGC     82300       AA
                                GCAGTG  TGTTCAAAGC
                                ||||||  ||||||||||
                                CGTCAT  ATAGGTTTCG
                                   C_
GAM653   LOC158674 3'  GCTCCTGAGTTCACTGC     82856         GT   A_
                                GCAGTGAAT  TCA  AGC
                                |||||||||  |||  |||
                                CGTCACTTG  AGT  TCG
                                     __   CC
GAM653   LOC158678 3'  GCTCCTGAGTTCACTGC     61133         GT   A_
                                GCAGTGAAT  TCA  AGC
                                |||||||||  |||  |||
                                CGTCACTTG  AGT  TCG
                                     __   CC
GAM653   LOC199957 3'  GCTTGTGTTCACTGTGG     89889         TG TCA
                                CCGCAGTGAA  T   AAGC
                                ||||||||||  |   ||||
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                                GGTGTCACTT  G   TTCG
                                      GT ___
GAM653   LOC200942 3'  GCTGAGGACACTCACTGTGG   90377         A     AA
                                CCGCAGTGA TGTTC  AGC
                                ||||||||| |||||  |||
                                GGTGTCACT ACAGG  TCG
                                     C     AG
GAM653   LOC206463 3'  GCTTGTGTTCACTGTGG     91103          TG TCA
                                CCGCAGTGAA  T   AAGC
                                |||||||||| |   ||||
                                GGTGTCACTT  G   TTCG
                                      GT ___
GAM653   LOC219914 3'  GCTGTAACACTCACTGTG    94969         A    CAA
                                CGCAGTGA TGTT   AGC
                                |||||||| ||||   |||
                                GTGTCACT ACAA   TCG
                                     C    TG_
GAM653   LOC220980 3'  GCTCTGTGTCAGCCACTGCGG  94769         AA  TT_  A
                                CCGCAGTG  TG   CA AGC
                                |||||||  ||   || |||
                                GGCGTCAC  AC   GT TCG
                                     CG  TGT  C
GAM653   LOC221687 3'  GCTTTAATATTTTATTCACTGT 93869          TTC____
           G                     CGCAGTGAATG      AAAGC
                                ||||||||||       |||||
                                GTGTCACTTAT      TTTCG
                                      TTTATAA
GAM653   LOC221810 3'  GCTTTTATCTTCACTGC     95548         T  TC
                                GCAGTGAA GT  AAAGC
                                |||||||| ||  |||||
                                CGTCACTT TA  TTTCG
                                     C  T_
GAM653   LOC222166 3'  GCTTGTTGTTCACTGGG     95741    G       TTCA
                                CC CAGTGAATG    AAGC
                                || |||||||||    ||||
                                GG GTCACTTGT    TTCG
                                 _       TG__
GAM653   LOC222899 5'  GCTTCTCCATCTCCACTGTGG  96029         A__   TTCA
                                CCGCAGTG   ATG    AAGC
                                ||||||||   |||   ||||
                                GGTGTCAC   TAC    TTCG
                                     CTC   CTC_
GAM653   LOC245757 3'  GCTCCTGAGTTCACTGC     92456         GT   A_
                                GCAGTGAAT  TCA  AGC
                                |||||||||  |||  |||
                                CGTCACTTG  AGT  TCG
                                      __  CC
GAM653   LOC253841 5'  GCTTTGGATCACCTGCGG    98093        _   ATG
                                CCGCAG TGA   TTCAAAGC
                                |||||| |||   ||||||||
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                                GGCGTC ACT   AGGTTTCG
                                   C  ___
GAM653  LOC254778 5'  GCTTCCAAATTCACTGCGG   97833         GTTCA
                                CCGCAGTGAAT    AAGC
                                ||||||||||    ||||
                                GGCGTCACTTA    TTCG
                                     AACC_
GAM653  LOC255870 3'  GCTTTGGGTCACCCACTGGG  96313   G    AA  _
                                CC CAGTG  TG TTCAAAGC
                                || |||||  || ||||||||
                                GG GTCAC  AC GGGTTTCG
                                 _    CC  T
GAM653  LOC51312  3'  GCTTTTCTGCTTCACTGTGG  33993        T  TC_
                                CCGCAGTGAA GT   AAAGC
                                |||||||||| ||   |||||
                                GGTGTCACTT CG   TTTCG
                                     _ TCT
GAM653  LOC56270  3'  CTTTGAACATTCGTTATGG   39506    C
                                CCG AGTGAATGTTCAAAG
                                ||| ||||||||||||||
                                GGT TTGCTTACAAGTTTC
                                  A
GAM653  LOC56961  5'  GCTCCGCGCTCGCTGCGG    63578        A   TCAA
                                CCGCAGTGA TGT    AGC
                                ||||||||| |||    |||
                                GGCGTCGCT GCG    TCG
                                     C   CC__
GAM653  LOC90268  3'  GCTTTGTGTTCTTCACTGTG   62665        TGTT_
                                CGCAGTGAA    CAAAGC
                                |||||||||    ||||||
                                GTGTCACTT    GTTTCG
                                     CTTGT
GAM654  ATP2B4    5'  ACCCGCCCAGCTCTCCTGC   70846    TT  CA       A
                                GCA  GA  AGCTGGGCG GT
                                |||  ||  |||||||||| ||
                                CGT  CT  TCGACCCGC CA
                                  C_  C_       C
GAM654  CCR9      3'  ACTCGCCGGAGCATCAATGCCG 22794        CAA   G_
                                CGGCATTGA   GCT  GGCGAGT
                                |||||||||   |||  |||||||
                                GCCGTAACT   CGA  CCGCTCA
                                     A__   GG
GAM654  CCR9      3'  ACTCGCCGGAGCATCAATGCCG 49122        CAA   G_
                                CGGCATTGA   GCT  GGCGAGT
                                |||||||||   |||  |||||||
                                GCCGTAACT   CGA  CCGCTCA
                                     A__   GG
GAM654  FGFR1     3'  ACCCAGCCCAGCTTGCCAATGG 43883    G    A       GA_
            CG                    CG CATTG CAAGCTGGGC   GT
                                || ||||| ||||||||||   ||
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                                GC GTAAC GTTCGACCCG   CA
                                 G    C        ACC
GAM654  SKI     3'  ACCCCGCCCGCCACGCCG    13167     AT  ACAA  T    A_
                                CGGC  TG   GC GGGCG  GT
                                ||||  ||   || |||||  ||
                                GCCG  AC   CG CCCGC  CA
                                  C_ _____ _    CC
GAM654  SRD5A2   5'  CCCACTCCCTGTCAATGC    60118         ___  C
                                GCATTGACA   AG TGGG
                                |||||||||   || ||||
                                CGTAACTGT   TC ACCC
                                     CCC  _
GAM654  CDH22    3'  ACCCGCCCAGCACACGCCG   41436     AT  ACAA      A
                                CGGC  TG   GCTGGGCG GT
                                ||||  ||   |||||||| ||
                                GCCG  AC   CGACCCGC CA
                                  C_  A___       C
GAM654  KIAA1040  3'  ACTGCGCCCAGCCAATACC   72675    C   ACAA      _
                                GG ATTG   GCTGGGCG AGT
                                || ||||   |||||||| |||
                                CC TAAC   CGACCCGC TCA
                                 A   _____       G
GAM654  LOC115129 3'  ACTCACTTTCTGTCAATGTC   73600         AGCT   C
                                GGCATTGACA   GGG GAGT
                                ||||||||||   ||| ||||
                                CTGTAACTGT   TTC CTCA
                                     CT__   A
GAM654  LOC137362 3'  ACTTCAGCTGTATCAATGCC   75776        CA_    GGC
                                GGCATTGA   AGCTG   GAGT
                                ||||||||   |||||   ||||
                                CCGTAACT   TCGAC   TTCA
                                    ATG    ___
GAM654  LOC203025 3'  ACTTCAGCTGTATCAATGCC   90737        CA_    GGC
                                GGCATTGA   AGCTG   GAGT
                                ||||||||   |||||   ||||
                                CCGTAACT   TCGAC   TTCA
                                    ATG    ___
GAM654  LOC254835 5'  TACTCGCCCAGCCCAGCC    98712    AT  ACAA
                                GGC  TG   GCTGGGCGAGTA
                                |||  ||   ||||||||||||
                                CCG  AC   CGACCCGCTCAT
                                  __  C___
GAM654  LOC58525  3'  ACTGAGCCCACAATGCC     79339       ACAAGC    G_
                                GGCATTG     TGGGC  AGT
                                |||||||     |||||  |||
                                CCGTAAC     ACCCG  TCA
                                   _______    AG
GAM655  AGRP     5'  CTTCATTAGGCCCTGCCATA   24616        A  A
                                TATGGCA GG CCTGATGGAG
                                ||||||| || ||||||||||
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                                ATACCGT CC GGATTACTTC
                                    C  _
GAM655  CGTHBA   3'  CTTCCCTCCAGTCCTTGCCG  24890          C  AT  A
                                TGGCAAGGAC TG  GG GAAG
                                |||||||||| ||  || ||||
                                GCCGTTCCTG AC  CC CTTC
                                     _  CT  _
GAM655  COL5A3   3'  CTCCCCAGGCTCACCTTGCCAT 32318          A___   AT
           G                     TATGGCAAGG   CCTG  GGAG
                                ||||||||||   ||||  ||||
                                GTACCGTTCC   GGAC  CCTC
                                     ACTC   C_
GAM655  FGF23    3'  CTTCTCTGGGGTCCCTTCCA  40557    CAA    GA
                                TGG   GGACCT  TGGAGAAG
                                |||   ||||||  ||||||||
                                ACC   CCTGGG  GTCTCTTC
                                  TTC    __
GAM655  FUT3     3'  CTCCCAGAGACCTTGCCA   5621         AC_   AT
                                TGGCAAGG   CTG  GGAG
                                ||||||||   |||  ||||
                                ACCGTTCC   GAC  CCTC
                                     AGA   __
GAM655  FUT5     3'  CTCCCAGAGACCTTGCCA   10726        AC_   AT
                                TGGCAAGG   CTG  GGAG
                                ||||||||   |||  ||||
                                ACCGTTCC   GAC  CCTC
                                     AGA   __
GAM655  TCF12    3'  TCTCCTATCCTCTTGCCATA  13639          ACCT   _
                                TATGGCAAGG    GAT GGAGA
                                ||||||||||    ||| |||||
                                ATACCGTTCT    CTA CCTCT
                                     C___   T
GAM655  WSX1     3'  CTCCCCCACATCCTTTCCTTGC 17915         CCT   _____
           C                     GGCAAGGA   GAT    GGAG
                                ||||||||   |||    ||||
                                CCGTTCCT   CTA    CCTC
                                     TTC   CACCC
GAM655  ZAP70    3'  CTTCCCCACCCTCAGCCCCACC 71375    CAA  AC   ___   A
           CCA                     TGG   GG  CTGA   TGG GAAG
                                |||   ||  ||||   ||| ||||
                                ACC   CC  GACT   ACC CTTC
                                  CCA  CC    CCC   C
GAM655  C1orf34  3'  CCTCTGGCCATTGCCATA    61303         _  A  T  T
                                TATGGCAA GG CC GA GG
                                |||||||| || || || ||
                                ATACCGTT CC GG CT CC
                                     A  _  T  _
GAM655  CLSTN1   3'  CTCCCCAGAGCACCCCCTGCCA 30787        A  AC____   AT
           T                     ATGGCA GG     CTG  GGAG
                                ||||||  ||     |||  ||||
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                                TACCGT CC     GAC  CCTC
                                   C  CCACGA   C_
GAM655  DKFZP434J193 3'  CTTCTCCACCACTCTCCTTGCC 71562          CC_  A
             ATG                    TATGGCAAGGA   TG TGGAGAAG
                                ||||||||||   || ||||||||
                                GTACCGTTCCT   AC ACCTCTTC
                                      CTC  C
GAM655  DNAJC6   3'  CTCCAAAGTTCCCACCATA   29492      CAA   C  GA
                                TATGG   GGA CT  TGGAG
                                |||||   ||| ||  |||||
                                ATACC   CCT GA  ACCTC
                                   AC_   T  A_
GAM655  FLJ12122  5'  CTGCCAGCTCAGGTCCCTGCCA 47092       A       __   _
                                TGGCA GGACCTGA  TGG AG
                                ||||| ||||||||  ||| ||
                                ACCGT CCTGGACT  ACC TC
                                   C       CG   G
GAM655  FLJ14642  3'  CTTCTCCGTAGTCCCCGCC   52575     AA    CTG
                                GGC  GGAC   ATGGAGAAG
                                |||  ||||   |||||||||
                                CCG  CCTG   TGCCTCTTC
                                  CC    A__
GAM655  FLJ20275  3'  CTGTCAGATCCTTGCCAT    35308          C
                                ATGGCAAGGA CTGATGG
                                |||||||||| |||||||
                                TACCGTTCCT GACTGTC
                                      A
GAM655  FLJ21369  3'  CTTCTCCATCAAGTTTCACCA  46051     CAA    C
                                TGG   GGAC TGATGGAGAAG
                                |||   |||| ||||||||||
                                ACC   TTTG ACTACCTCTTC
                                  AC_    A
GAM655  HSPC016   3'  TCTCTATTCCCTGCCATA    32503        A   CCTG
                                TATGGCA GGA    ATGGAGA
                                ||||||| |||    |||||||
                                ATACCGT CCT    TATCTCT
                                    C  _____
GAM655  HT014    3'  CTTCCTAATAAATCCTTGCCA  40153         CC  A   A
                                TGGCAAGGA  TG TGG GAAG
                                |||||||||  || ||| ||||
                                ACCGTTCCT  AT ATC CTTC
                                     AA  A   _
GAM655  KIAA0773  3'  CTTCTCCACGACCTCACC    28722    CA   ACC  A
                                GG  AGG   TG TGGAGAAG
                                ||  |||   || ||||||||
                                CC  TCC   GC ACCTCTTC
                                 AC   A__  _
GAM655  KIAA1181  3'  CTCCATCAGCTGGTCA      68911      A  GAC
                                TGGC AG   CTGATGGAG
                                ||||  ||   |||||||||
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                                ACTG TC   GACTACCTC
                                  G ___
GAM655  KIAA1321  3'  CTCCTTAGGTCCTCACA     62899    GCA       T
                                TG   AGGACCTGA GGAG
                                ||   ||||||||| ||||
                                AC   TCCTGGATT CCTC
                                 AC_       _
GAM655  KIAA1348  3'  CTTCTTAGGTCTTGCCA     69122       G     T
                                TGGCAAG ACCTGA GGAG
                                ||||||| |||||| ||||
                                ACCGTTC TGGATT CTTC
                                    _     _
GAM655  KIAA1493  3'  CTTCTCCACCTAGTCTGCC   64840     AG   CTGA
                                GGCA  GAC    TGGAGAAG
                                ||||  |||    ||||||||
                                CCGT  CTG    ACCTCTTC
                                  __  ATCC
GAM655  KIAA1535  3'  CTCTGTGGTCCTTGCC      80212         TG
                                GGCAAGGACC  ATGGAG
                                ||||||||||  ||||||
                                CCGTTCCTGG  TGTCTC
                                      __
GAM655  KIAA1819  5'  CTTCTCCACGGCTCCCCCA   70252    CAA   C   A
                                TGG   GGA CTG TGGAGAAG
                                |||   ||| ||| ||||||||
                                ACC   CCT GGC ACCTCTTC
                                  C__   C   _
GAM655  LAT1-3TM  3'  CTCCATCAGTGTCATCACCA   49143    CAAG   _
                                TGG    GAC CTGATGGAG
                                |||    ||| |||||||||
                                ACC    CTG GACTACCTC
                                  ACTA   T
GAM655  LAT1-3TM  5'  CTCCATCAGTGTCATTACCA   49144    CAAG   _
                                TGG    GAC CTGATGGAG
                                |||    ||| |||||||||
                                ACC    CTG GACTACCTC
                                  ATTA   T
GAM655  OS4       3'  CTTCCCCATCATCCCTTCCATT 20389       _   CC___     A
            GCCA                    TGGCAA GGA     TGATGG GAAG
                                |||||| |||     |||||| ||||
                                ACCGTT CCT     ACTACC CTTC
                                   A   TCCCT     C
GAM655  RASSF2    3'  CTTCTCCACCTTCTCTCCA   29097    CA    CCTGA
                                TGG  AGGA    TGGAGAAG
                                |||  ||||    ||||||||
                                ACC  TCTT    ACCTCTTC
                                  TC    CC___
GAM655  SARM      3'  CTCCCCCAGGCCCTGCCAT   31285       A  A    AT
                                ATGGCA GG CCTG  GGAG
                                |||||| || ||||  ||||
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                                TACCGT CC GGAC  CCTC
                                   C  _   CC
GAM655  SELB     3'  CTCCCCCAGGGCCTCCTTGCC  62591        ___   AT
                                GGCAAGGA  CCTG  GGAG
                                ||||||||  ||||  ||||
                                CCGTTCCT  GGAC  CCTC
                                    CCG   CC
GAM655  SERPING1 3'  CTTCTCCATGGCCCTGCCATG  5348        A  A  TG
                                TATGGCA GG CC  ATGGAGAAG
                                ||||||| || ||  |||||||||
                                GTACCGT CC GG  TACCTCTTC
                                   C  _ __
GAM655  SLIT1    3'  TCTCCGGAAGTCCTTGC     13233        C GA
                                GCAAGGAC T  TGGAGA
                                |||||||| |  ||||||
                                CGTTCCTG A  GCCTCT
                                    _ AG
GAM655  ZDHHC8   3'  TCCCCACCAACTTCTCTGCC  64622     _   CC  A   A
                                GGCA AGGA  TG TGG GA
                                |||| ||||  || ||| ||
                                CCGT TCTT  AC ACC CT
                                  C   CA  C   C
GAM655  LOC112868 5'  CTCCCAGCCCTTGCCA     73268        AC   AT
                                TGGCAAGG  CTG  GGAG
                                ||||||||  |||  ||||
                                ACCGTTCC  GAC  CCTC
                                    C_  __
GAM655  LOC142946 3'  CCATGGTCCTTGCCATA     83783           TG
                                TATGGCAAGGACC  ATGG
                                ||||||||||||  ||||
                                ATACCGTTCCTGG  TACC
                                          __
GAM655  LOC150319 3'  CTTCTCCATCCTCCTGCCAT  80471       A   CCT
                                ATGGCA GGA   GATGGAGAAG
                                ||||||  |||  ||||||||||
                                TACCGT CCT   CTACCTCTTC
                                   _  C__
GAM655  LOC197423 5'  CTCCATCAGTGTCATTACCA  78424     CAAG  _
                                TGG   GAC CTGATGGAG
                                |||   ||| |||||||||
                                ACC   CTG GACTACCTC
                                  ATTA  T
GAM655  LOC199923 5'  CTTCTCCACCTCCTGCCA    89871      A   CCTGA
                                TGGCA GGA    TGGAGAAG
                                |||||  |||    ||||||||
                                ACCGT CCT    ACCTCTTC
                                   _  CC___
GAM655  LOC206657 5'  CTTCTCAGTCTTGCCA      91105        AC   T
                                TGGCAAGG  CTGA GGAG
                                ||||||||  |||| ||||
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                                ACCGTTCT  GACT CTTC
                                   __   _
GAM655  LOC220565 5'  CTCCATCAGTGTCATCACCA  92441    CAAG  _
                                TGG   GAC CTGATGGAG
                                |||   ||| |||||||||
                                ACC   CTG GACTACCTC
                                  ACTA  T
GAM655  LOC221975 5'  CTTCTCCATGGAGCCTGCC   94192    A  AC  G
                                GGCA GG  CT ATGGAGAAG
                                |||| ||  || |||||||||
                                CCGT CC  GG TACCTCTTC
                                  _ GA  _
GAM655  LOC222160 5'  TCCCATTAGGCCCCCA     95793    CAA  A      A
                                TGG   GG CCTGATGG GA
                                |||   || |||||||| ||
                                ACC   CC GGATTACC CT
                                  C__  _      _
GAM655  LOC257239 5'  CTTCTCCACCTCAACCACCA  98844    CAA  ACC  __
                                TGG   GG   TGA  TGGAGAAG
                                |||   ||   |||  |||||||||
                                ACC   CC   ACT  ACCTCTTC
                                  A__  A__   CC
GAM655  LOC90499  3'  CTTCTCCATGGCCCCCTCCA  63741    CAA  A  TG
                                TGG   GG CC  ATGGAGAAG
                                |||   || ||  |||||||||
                                ACC   CC GG  TACCTCTTC
                                  TCC  C  __
GAM656  ABCC1    3'  CCTGGTAAACCAAGCCTCC   39603     _     CGGAGA
                                GGAG CTTGGTT     CAGG
                                |||| |||||||     ||||
                                CCTC GAACCAA     GTCC
                                  C      ATG___
GAM656  ADAM10   5'  CTCCGGACCAAGCCCCTT    8477      A
                                AAGG GCTTGGTTCGGAG
                                |||| |||||||||||||
                                TTCC CGAACCAGGCCTC
                                  C
GAM656  APBA1    3'  CCTCTCTGGAAGGCCCCTT   70474     A   GG      CA
                                AAGG GCTT  TTCGGAGA  GG
                                |||| ||||  ||||||||  ||
                                TTCC CGGA  AGGTCTCT  CC
                                  C   __      __
GAM656  APOC3    3'  GCCTATCCATCCTGCGAGCTCC 5265          GTTC  __  C
           TT                    AAGGAGCTTG   GGA  GA AGGC
                                ||||||||||   |||  || ||||
                                TTCCTCGAGC   CCT  CT TCCG
                                      GT__   AC  A
GAM656  AREG     5'  GCCCGCCGCCCCGAGCTCC   9765         TT   AGACA
                                GGAGCTTGG  CGG    GGC
                                |||||||||  |||    |||
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                                CCTCGAGCC  GCC    CCG
                                     CC   GC___
GAM656  EXTL1    5'  GCCTGTCCCTGGCCAAGCCGCC 16737     A_      TC  A
             T                    AGG  GCTTGGT  GG GACAGGC
                                  |||  |||||||  || |||||||
                                  TCC  CGAACCG  CC CTGTCCG
                                    GC      GT  _
GAM656  FBXL11   3'  CCTGCCTCCCAGCCAGGCTCCT 25514           C    A
                                  AGGAGCTTGGTT GGAG CAGG
                                  ||||||||||||| |||| ||||
                                  TCCTCGGACCGA CCTC GTCC
                                         C    C
GAM656  FPGS     3'  GCCTGTCTCCCCCAACACCC   18267    AGC    TTC
                                  GG   TTGG   GGAGACAGGC
                                  ||   ||||   ||||||||||
                                  CC   AACC   CCTCTGTCCG
                                   CAC    C__
GAM656  LIMK1    3'  CCTGTCTGGTCCATAGCTCC   34140       _   TT GG
                                  GGAGCT TGG  C  AGACAGG
                                  |||||| |||  |  |||||||
                                  CCTCGA ACC  G  TCTGTCC
                                     T   TG __
GAM656  LIMK1    3'  CCTGTCTGGTCCATAGCTCC   11329       _   TT GG
                                  GGAGCT TGG  C  AGACAGG
                                  |||||| |||  |  |||||||
                                  CCTCGA ACC  G  TCTGTCC
                                     T   TG __
GAM656  LZTR1    3'  GCCTGTCACCCAAGGCTCCT   23171         GGTTC  A
                                  AGGAGCTT    GG GACAGGC
                                  ||||||||    || |||||||
                                  TCCTCGGA    CC CTGTCCG
                                       AC___  A
GAM656  MEN1     3'  GCCCCTAGAAACCCAAGCTCCT 56350          __   GG  ACA
                                  AGGAGCTTGG  TTC  AG   GGC
                                  ||||||||||  |||  ||   |||
                                  TCCTCGAACC  AAG  TC   CCG
                                        CA   A_  C__
GAM656  NEUD4    3'  CCTGCCTCTCCGAGCTCCT    17377         TTC    A
                                  AGGAGCTTGG   GGAG CAGG
                                  ||||||||||   |||| ||||
                                  TCCTCGAGCC   TCTC GTCC
                                         ___    C
GAM656  SLC9A1   3'  CCTGTCTGTCCAACCCCTC    70924     CTT    C  __
                                  GAG   GGTT GGA  GACAGG
                                  |||   |||| |||  ||||||
                                  CTC   CCAA CCT  CTGTCC
                                    C__    _   GT
GAM656  TGFB1    5'  GCCTGTCTCCTGAGCCCCC    7256     AGCTT    _
                                  GG    GGTTC GGAGACAGGC
                                  ||    ||||| ||||||||||
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                                CC    CCGAG CCTCTGTCCG
                                 C____    T
GAM656  WBSCR5   3'  CCCGTCACCAAGCCCT     42110    A     TCGGA  A
                                AGG GCTTGGT    GAC GG
                                ||| |||||||    ||| ||
                                TCC CGAACCA    CTG CC
                                  _     _____  C
GAM656  DKFZp434J1015 3'  GCCTCCACCTGAAAAGCTCCTT 94210         GG    AGAC
                                AAGGAGCTT  TTCGG   AGGC
                                |||||||||  |||||   ||||
                                TTCCTCGAA  AAGTC   TCCG
                                      __    CACC
GAM656  DKFZP564B1162 3'  CCTGTCTCCCACTCAAACCTCT 49348     C_  _ TC
                                GGAG  TTG GT  GGAGACAGG
                                ||||  ||| ||  |||||||||
                                TCTC  AAC CA  CCTCTGTCC
                                  CA   T  C_
GAM656  FLJ10743  3'  GCCTGTCTCCTTCCACCTCCTT 37084       CT   TTC
                                AAGGAG  TGG   GGAGACAGGC
                                ||||||  |||   ||||||||||
                                TTCCTC  ACC   CCTCTGTCCG
                                   C_   TT_
GAM656  FLJ23093  3'  GCCTGTCCATGGCACCAGACTC 45326      CT   _  GA
           CT                    AGGAG  TGGT TCG  GACAGGC
                                |||||  |||| |||  |||||||
                                TCCTC  ACCA GGT  CTGTCCG
                                   AG   C   AC
GAM656  FLJ30294  5'  CCTGTCTCCGTACCCCTTC   58896     CTT   T
                                GGAG   GGT CGGAGACAGG
                                ||||   ||| ||||||||||
                                CTTC   CCA GCCTCTGTCC
                                  C__   T
GAM656  IL1F10   3'  GCCCCCAAACCAAGCTC     51762         C  AGACA
                                GAGCTTGGTT GG    GGC
                                |||||||||| ||    |||
                                CTCGAACCAA CC    CCG
                                     A  C____
GAM656  KIAA0326  3'  GCCCACCTCCCCAAGCTCCTT  64963          TTC   ACA
                                AAGGAGCTTGG   GGAG   GGC
                                ||||||||||   ||||   |||
                                TTCCTCGAACC   CCTC   CCG
                                      ___    CAC
GAM656  KIAA1554  3'  GCCTCCCTGGACAGTTCC    96858       TG    A  CA
                                GGAGCT  GTTCGG GA  GGC
                                ||||||  |||||| ||  |||
                                CCTTGA  CAGGTC CT  CCG
                                   __     C  __
GAM656  MCF2L    3'  GCCCGTCCCCGCCTGATCTCC  61529     C TG TT   A   A
                                GGAG T  G  CGG GAC GGC
                                |||| |  |  ||| ||| |||
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                                CCTC A  C  GCC CTG CCG
                                  T GT C_  C  C
GAM656  MKRN1    3'  CCTGTCTTCTCAACCCCTC   26494    CTT   C_
                                GAG  GGTT  GGAGACAGG
                                |||  ||||  |||||||||
                                CTC  CCAA  CTTCTGTCC
                                  C__   CT
GAM656  MKRN4    3'  CCTGTCTTGTCAACCCCTC   48460    CTT   CG_
                                GAG  GGTT  GAGACAGG
                                |||  ||||  ||||||||
                                CTC  CCAA  TTCTGTCC
                                  C__   CTG
GAM656  MSTP028  3'  CCTACCTCCCAGGCTCCT   50061        TTCG  AC
                                AGGAGCTTGG   GAG  AGG
                                ||||||||||   |||  |||
                                TCCTCGGACC   CTC  TCC
                                     _____  CA
GAM656  SYT6     3'  GCCCATCTCCGAAACCACCTCC 79521     CT   _    CA
                                GGAG  TGGTT CGGAGA  GGC
                                ||||  ||||| ||||||  |||
                                CCTC  ACCAA GCCTCT  CCG
                                  C_    A     AC
GAM656  TTYH2    3'  CCTGTCTCCCTAACCCTCC   51976    CTT   C_
                                GGAG  GGTT  GGAGACAGG
                                ||||  ||||  |||||||||
                                CCTC  CCAA  CCTCTGTCC
                                   ___   TC
GAM656  UBXD2    3'  GCCTGCCTCCATCAGCTTCTT  68895       T  TC   A
                                AAGGAGCT GGT  GGAG CAGGC
                                |||||||| |||  |||| |||||
                                TTCTTCGA CTA  CCTC GTCCG
                                     _  __   C
GAM656  LOC145601 3'  GCCTGTCCCCGGAGGCATTCCT 84351      __  TGG   A
          T                    AAGGA  GCT   TTCGG GACAGGC
                               |||||  |||   ||||| |||||||
                               TTCCT  CGG   AGGCC CTGTCCG
                                  TA  ___    C
GAM656  LOC148183 3'  CCTGTGCTACAAGCTCCTT   85263        GTTC  AG
                                AAGGAGCTTG   GG  ACAGG
                                ||||||||||   ||  |||||
                                TTCCTCGAAC   TC  TGTCC
                                     A___  G_
GAM656  LOC148354 3'  CCTGTCTCCTCAGCTGCTC   79549     TT   C_
                                GAGC  GGTT  GGAGACAGG
                                ||||  ||||  |||||||||
                                CTCG  TCGA  CCTCTGTCC
                                  __   CT
GAM656  LOC149721 3'  GCCTGTCTCCATGTAGGTTCCT 80318        GTTC
                                AGGAGCTTG   GGAGACAGGC
                                |||||||||   ||||||||||
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                                TCCTTGGAT   CCTCTGTCCG
                                    GTA_
GAM656  LOC150378 5'  GCCTGCCCGGTCTCCAGGCTCC 80559        T__   AGA
          T                  AGGAGCTTGG  TCGG  CAGGC
                             ||||||||||  ||||  |||||
                             TCCTCGGACC  GGCC  GTCCG
                                  TCT   C__
GAM656  LOC157349 5'  GCCCGTCTCCGGCAGCCCCT  82343    A  TG  T    A
                             AGG GCT  GT CGGAGAC GGC
                             ||| |||  || ||||||| |||
                             TCC CGA  CG GCCTCTG CCG
                               C  __ _     C
GAM656  LOC157349 5'  GCCCGTCTCCGGCAGCCCCT  82344    A  TG  T    A
                             AGG GCT  GT CGGAGAC GGC
                             ||| |||  || ||||||| |||
                             TCC CGA  CG GCCTCTG CCG
                               C  __ _     C
GAM656  LOC165693 5'  CCTGCAATACCAGCTCCTT   83486       T  TCGGAGA
                             AAGGAGCT GGT      CAGG
                             |||||||| |||      ||||
                             TTCCTCGA CCA      GTCC
                                  _  TAAC___
GAM656  LOC221424 5'  GCCTATCGCTCCCAGCTCCTT  95274       T  TTC  A  C
                             AAGGAGCT GG   GG GA AGGC
                             |||||||| ||   || || ||||
                             TTCCTCGA CC   TC CT TCCG
                                  C  ___  G  A
GAM656  LOC221495 3'  CCTGCCTGGCCAAATTCC    95494     C    TC  AGA
                             GGAG TTGGT  GG   CAGG
                             |||| |||||  ||   ||||
                             CCTT AACCG  CC   GTCC
                               A    GT  ___
GAM656  LOC254826 5'  GCCTGTCTCCAGCTCTGCGCCT 99050     A  TT   C
                             AGG GC  GGTT GGAGACAGGC
                             ||| ||  |||| ||||||||||
                             TCC CG  TCGA CCTCTGTCCG
                               G  TC   _
GAM657  FLJ22332  5'  GGAAAGAAAACTACATCACA   45637     G  A      _______
                             TGTG AT TAGTTTTC     CC
                             |||| || ||||||||     ||
                             ACAC TA ATCAAAAG     GG
                               _ C       AAA___
GAM658  AMACR    3'  TTGTATGCATGGAAACATGGA  69103      ATC       G
                             TCCAT   TCCATGCATG CGG
                             |||||   |||||||||| |||
                             AGGTA   AGGTACGTAT GTT
                                CAA        _
GAM658  BCL2L11   3'  TCGCCCAGAGATATGGA     57615         CA  CAT   G
                             TCCATATCTC  TG   GGCG A
                             |||||||||  ||   |||| |
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                                AGGTATAGAG  AC   CCGC T
                                   __ ____   G
GAM658  BCL2L11  3' TCGCCCAGAGATATGGA    57616        CA CAT   G
                                TCCATATCTC  TG   GGCG A
                                ||||||||||  ||   |||| |
                                AGGTATAGAG  AC   CCGC T
                                   __ ____   G
GAM658  FGFR2    5' CGTCCACATGGAGATATGGA  43633          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM658  FGFR2    5' CGTCCACATGGAGATATGGA  43638          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM658  FGFR2    5' CGTCCACATGGAGATATGGA  43642          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM658  FGFR2    5' CGTCCACATGGAGATATGGA  43652          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM658  FGFR2    5' CGTCCACATGGAGATATGGA  43665          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM658  FGFR2    5' CGTCCACATGGAGATATGGA  43674          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM658  FGFR2    5' CGTCCACATGGAGATATGGA  43678          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM658  FGFR2    5' CGTCCACATGGAGATATGGA  43763          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM658  FGFR2    5' CGTCCACATGGAGATATGGA  43767          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
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                                AGGTATAGAGGTAC  ACC GC
                                      __   T
GAM658  FGFR2    5'  CGTCCACATGGAGATATGGA   43771          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __   T
GAM658  FGFR2    5'  CGTCCACATGGAGATATGGA   5559           CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __   T
GAM658  MAP3K14  3'  ATCCGCCACGTGAAGAGA    15541     CA  A
                                TCTC  TGC TGGCGGAT
                                ||||  ||| ||||||||
                                AGAG  GTG ACCGCCTA
                                  AA  C
GAM658  KIAA0819 3'  CCCCAGCATCACAGGAGACATG 64330      A   ____   A  C
           GA                     TCCAT TCTCC   ATGC TGG GG
                                |||||  |||||   ||||  ||| ||
                                AGGTA  AGAGG   TACG ACC CC
                                  C    ACAC   _  _
GAM658  PORIMIN  3'  CATACATGGAGTATGGA     54702       T     C
                                TCCATA CTCCATG ATG
                                ||||||  ||||||| |||
                                AGGTAT  GAGGTAC TAC
                                   _     A
GAM658  RDC1     3'  CCGGCACGGGATATGGA     72832        T  A  A
                                TCCATATC CC TGC TGG
                                ||||||||  ||  ||| |||
                                AGGTATAG  GG ACG GCC
                                     _  C  _
GAM658  VEZATIN  3'  ATCCGCCACAACAGACAATG   34656    A_  CCA  CA
                                CAT  TCT   TG  TGGCGGAT
                                |||  |||   ||  ||||||||
                                GTA  AGA   AC  ACCGCCTA
                                  AC   CA_  __
GAM658  LOC147645 5'  ATCCGCTGGTGGCAGAGACACG 79065    ATA   CA  AT__
           G                     CC   TCTC  TGC   GGCGGAT
                                ||   ||||  |||   |||||||
                                GG   AGAG  ACG   TCGCCTA
                                 CAC   __   GTGG
GAM658  LOC199775 3'  TTGCTGCATCAGAGATATG   89726        C_   TG
                                CATATCTC  ATGCA  GCGG
                                ||||||||  |||||  ||||
                                GTATAGAG  TACGT  CGTT
                                     AC    __
GAM658  LOC51279  3'  CCGCTATTAGAGTATGGA    33752       T  CATGC
                                TCCATA CTC    ATGGCGG
                                ||||||  |||    |||||||
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                                AGGTAT GAG    TATCGCC
                                   _  AT___
GAM659  NME4     3'  AGAACCCAAGCCCACATCCAA  18452      CTTCAT  CC
                                TTGGAT    GC  TGGGTTCT
                                ||||||    ||  ||||||||
                                AACCTA    CG  ACCCAAGA
                                   CACC__  A_
GAM659  C1orf2   3'  CAGGCACGAAGAGTCCAA   96265     _   A   C
                                TTGGA TCTTC TGCC TG
                                ||||| ||||| |||| ||
                                AACCT AGAAG ACGG AC
                                  G   C   _
GAM659  NR6A1    3'  ACCCAGGACACAAAGCCCAA  9441     AT  CA  C
                                TTGG  CTT  TG CCTGGGT
                                ||||  |||  || |||||||
                                AACC  GAA  AC GGACCCA
                                  C_  AC  A
GAM659  SIAT8A   3'  AGGAGCAATGAAGATCCAA   13143        _ _
                                TTGGATCTTCAT GC CCT
                                |||||||||||| || |||
                                AACCTAGAAGTA CG GGA
                                      A  A
GAM659  LOC151720 5'  AGAACCCAGAAATAAAGCCAA  81144    AT  C  GCC
                                TTGG  CTT AT   CTGGGTTCT
                                ||||  ||| ||   |||||||||
                                AACC  GAA TA   GACCCAAGA
                                  __  A  AA_
GAM659  LOC90538  3'  AGCTGTGGGAGCACAGAGATCC 63893       CA  _   _
           AA                    TTGGATCTT  TGC CCTG GGTT
                                |||||||||  ||| |||| ||||
                                AACCTAGAG  ACG GGGT TCGA
                                     AC  A   G
GAM659  LOC90957  3'  AGCCCAGGGCATGAAGCCCAA  65089    AT
                                TTGG  CTTCATGCCCTGGGTT
                                ||||  ||||||||||||||||
                                AACC  GAAGTACGGGACCCGA
                                  C_
GAM660  CBFB     3'  CTGCCATGGTTTTGCA     10036        GCG
                                TGCAAAACCA   TGGCGG
                                ||||||||||   ||||||
                                ACGTTTTGGT   ACCGTC
                                     ___
GAM660  CBFB     3'  CTGCCATGGTTTTGCA     43438        GCG
                                TGCAAAACCA   TGGCGG
                                ||||||||||   ||||||
                                ACGTTTTGGT   ACCGTC
                                     ___
GAM660  DNAH9    5'  GTCTGCCATGGTTTTACA   17412   C    GCG   _
                                TG AAAACCA   TGGCGG C
                                || |||||||   |||||| |
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                                AC TTTTGGT   ACCGTC G
                                 A      ___      T
GAM660  DNASE1   5'  CGCCGCGCACGGCGCTGGTGCT 19071      AA       G_______  GGCC
            GCA                   TGCA  ACCAGCGT       GC    G
                                ||||  ||||||||       ||    |
                                ACGT  TGGTCGCG       CG    C
                                  CG       GCAC___G  CCGG
GAM660  DSCAM    5'  GGCCGCTGGCTGCGCA      9134      AAAAC    G
                                TGC     CAGC TGGCGGCC
                                |||     |||| ||||||||
                                ACG     GTCG GTCGCCGG
                                 C____    _
GAM660  HNF3A    5'  CGCGGCCGCCCGTCGCTTCGCA 60458     AAAACCA   T
                                TGC      GCG GGCGGCCGCG
                                |||      ||| ||||||||||
                                ACG      TGC CCGCCGGCGC
                                 CTTCGC_  _
GAM660  JUND     3'  CGCGGCCGCCCCGTGTTGCA   19295      AACCA   T
                                TGCAA    GCG GGCGGCCGCG
                                |||||    ||| ||||||||||
                                ACGTT    TGC CCGCCGGCGC
                                  G____   C
GAM660  PMM2     3'  CGCAGCCTAGGCAGGCTCTGCA 72559      AAA  A  G  GC   C
                                TGCA   CC GC TG  GGC GCG
                                ||||   || || ||  ||| |||
                                ACGT   GG CG AT  CCG CGC
                                  CTC  A  G  __   A
GAM660  ABIN-2   5'  GCAGCTGCCGCGCTCTGCA    44459     AAACC         C
                                TGCA    AGCGTGGCGGC GC
                                ||||    |||||||||| ||
                                ACGT    TCGCGCCGTCG CG
                                  C____          A
GAM660  FLJ13052 3'  GCGGCCTCCAGCTGCCGCA    43754     AAAAC    G   C
                                TGC     CAGC TGG GGCCGC
                                |||     |||| ||| ||||||
                                ACG     GTCG ACC CCGGCG
                                 CC___    _   T
GAM660  FLJ14124 3'  CGCGGCCGCGCCGGGCCTCGC  46355    AAAA_  A  GTG
                                GC     CC GC   GCGGCCGCG
                                ||     || ||   |||||||||
                                CG     GG CG   CGCCGGCGC
                                 CTCCG  C  ___
GAM660  FLJ20255 5'  CGCGGCAGCCGCCGTCCTTGCA 35300       AACCA  _   G
                                TGCAA    GCG TGGC GCCGCG
                                |||||    ||| |||| ||||||
                                ACGTT    TGC GCCG CGGCGC
                                  CC___   C    A
GAM660  KIAA0211 5'  CGCGGCCGAGACTCTGGCCTGC 28284      AAA   C  GG
            A                   TGCA   CCAG GT  CGGCCGCG
                                ||||   |||| ||  ||||||||
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                                ACGT   GGTC CA  GCCGGCGC
                                  CC_    T  GA
GAM660  KIAA0227  5'  CGGCCGCCACGAAGCCTGCG   61347      AAACCAG
                                TGCA      CGTGGCGGCCG
                                ||||      ||||||||||
                                GCGT      GCACCGCCGGC
                                  CCGAA__
GAM660  MAPK13    5'  CGCAGCCGCCACGCCGGGGCCG 12318    AAAA  A        C
          C                      GC    CC GCGTGGCGGC GCG
                                ||    || |||||||||| |||
                                CG    GG CGCACCGCCG CGC
                                 CCGG  C         A
GAM660  OSBPL5    3'  CGCGGCGGCTGCAGGCCCTGCA 73062      AAA  AGC TG  G
                                TGCA   CC   G  GC GCCGCG
                                ||||   ||   |  || ||||||
                                ACGT   GG   C  CG CGGCGC
                                  CCC  A__ GT  G
GAM660  PNMA1     5'  CGCAGCCGCCGCGACTTCGGCA 21219     AAAACCAG        C
                                TGC       CGTGGCGGC GCG
                                |||       ||||||||| |||
                                ACG       GCGCCGCCG CGC
                                  GCTTCA__        A
GAM660  PSIP1     5'  CGCGGCCGCCCCCGCGCCGCCGC 41243     AAAACCA   T
          A                      TGC      GCG GGCGGCCGCG
                                |||      ||| ||||||||||
                                ACG      CGC CCGCCGGCGC
                                  CCGCCG_  C
GAM660  SPRY4     3'  CGCTGTGGCCACGCTGGTT    49010          G  C
                                AACCAGCGTGGC GC GCG
                                |||||||||||| || |||
                                TTGGTCGCACCG TG CGC
                                       G  T
GAM660  LOC148697 3'  GCCACGCTGTGTCTTGCA     79676       A  _
                                TGCAA AC CAGCGTGGC
                                ||||| || |||||||||
                                ACGTT TG GTCGCACCG
                                  C  T
GAM660  LOC245806 5'  CGCGGAGCGCGCTGGCTTTGC  93541       A       G GG
                                GCAAA CCAGCGTG C  CCGCG
                                ||||| |||||||| |  |||||
                                CGTTT GGTCGCGC G  GGCGC
                                  C       _ A_
GAM661  ADAMTS5   3'  GTGACCAGTCATGCTTCAGTGA 23861      A       _______  GTGA
                                TCAC GAAGCATG     GG    C
                                |||| ||||||||     ||    |
                                AGTG CTTCGTAC     CC    G
                                  A       TGA___  AGTG
GAM661  ADH5      3'  CCAGTCTGCTTCTGTGATA    7265            T _______
                                TATCACAGAAGCA G     GG
                                |||||||||||| |     ||
```

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                                ATAGTGTCTTCGT C     CC
                                      _ TGA___
GAM661  APEX    3'  GTGACCAACCAGGCTCCTGTGA 9701        A  A  _______ GTGA
          TA                    TATCACAG AGC TGG     G   C
                                |||||||| ||| |||     |   |
                                ATAGTGTC TCG ACC     C   G
                                    C   G   AA___C AGTG
GAM661  APEX    3'  GTGACCAACCAGGCTCCTGTGA 55544       A  A  _______ GTGA
          TA                    TATCACAG AGC TGG     G   C
                                |||||||| ||| |||     |   |
                                ATAGTGTC TCG ACC     C   G
                                    C   G   AA___C AGTG
GAM661  APEX    3'  GTGACCAACCAGGCTCCTGTGA 55545       A  A  _______ GTGA
          TA                    TATCACAG AGC TGG     G   C
                                |||||||| ||| |||     |   |
                                ATAGTGTC TCG ACC     C   G
                                    C   G   AA___C AGTG
GAM661  AQP6    3'  CACCCTGTGGTCCTGATA    54985     CA  AG
                                TATCA  GA  CATGGGGTG
                                |||||  ||  |||||||||
                                ATAGT  CT  GTGTCCCAC
                                  C_  G_
GAM661  C2      3'  GGCCACCCTTAGACCCTGTGAT 5350       AAGCAT     A
                                ATCACAG     GGGGTG CC
                                |||||||     |||||| ||
                                TAGTGTC     TCCCAC GG
                                    CCAGAT     C
GAM661  C7orf2  3'  CCCCATGCTTCTGCAATG    42636     CA
                                TAT  CAGAAGCATGGGG
                                |||  |||||||||||||
                                GTA  GTCTTCGTACCCC
                                  AC
GAM661  EDAR    3'  GTGACCAATCAAGGCTTTTGTG 42529         A_  _______  GTGA
          ATA                   TATCACAGAAGC  TG     GG   C
                                ||||||||||||  ||     ||   |
                                ATAGTGTTTTCG  AC     CC   G
                                      GA  TAA___  AGTG
GAM661  ENTPD3  3'  GTGACCAGCCAGGCTTCTGTCA 8807      C      A  _______ GTGA
          TA                    TAT ACAGAAGC TGG     G   C
                                ||| |||||||| |||     |   |
                                ATA TGTCTTCG ACC     C   G
                                  C       G   GA___C AGTG
GAM661  FHL2    3'  ACCCTTTAGTGCTTTGTGATA  9363         A   ___
                                TATCACAGA GCAT   GGGGT
                                |||||||||  ||||   |||||
                                ATAGTGTTT CGTG   TCCCA
                                      _   ATT
GAM661  KCND3   3'  CCGACATAGCCCTGTGATA    18353        AA  _  _____
                                TATCACAG  GC ATG    GG
                                ||||||||  || |||    ||
```

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                                ATAGTGTC  CG TAC    CC
                                    C_  A  AG___
GAM661  KRT4    5'  GCCCTGTCACTTCTCTGATA  11227     C    C_
                                TATCA AGAAG  ATGGGGT
                                ||||| |||||  |||||||
                                ATAGT TCTTC  TGTCCCG
                                   C    AC
GAM661  NCOA6   5'  GTGACCGGCATATGCTTCTGGA 26846    CA      G_______  GTGA
           ATA                    TAT  CAGAAGCAT      GG   C
                                ||| |||||||||      ||   |
                                ATA  GTCTTCGTA      CC   G
                                  AG       TACGG___  AGTG
GAM661  P23     3'  TCACCCCAGCCTGTGA     22754      AA  A
                                TCACAG  GC TGGGGTGA
                                ||||||  || ||||||||
                                AGTGTC  CG ACCCCACT
                                  __  _
GAM661  PLEK    3'  ACCTGTCCACTTCTGTGA    12165       CA  ___
                                TCACAGAAG  TGG  GGT
                                |||||||||  |||  |||
                                AGTGTCTTC  ACC  CCA
                                     __  TGT
GAM661  POP4    3'  GGGTGACCAATCAGTTGCATCT 22786        A  __  _______  GTGA
           GTGATA                  TATCACAGA GCA  TG    GG   CC
                                |||||||||  |||  ||    ||   ||
                                ATAGTGTCT CGT  AC    CC   GG
                                     A  TG  TAA___  AGTG
GAM661  PRSS16  3'  GGTCACCTCAGTCCTGGA   20783   A  AA  A
                                TC CAG  GC TGGGGTGACC
                                || |||  || ||||||||||
                                AG GTC  TG ACTCCACTGG
                                 _  C_  _
GAM661  PTPRO   3'  GCCCTGCTTTGTAATA     12627    C    A  TG
                                TAT ACAGA GCA  GGGT
                                ||| ||||| |||  ||||
                                ATA TGTTT CGT  CCCG
                                  A    _  __
GAM661  PTPRO   3'  GCCCTGCTTTGTAATA     48412    C    A  TG
                                TAT ACAGA GCA  GGGT
                                ||| ||||| |||  ||||
                                ATA TGTTT CGT  CCCG
                                  A    _  __
GAM661  PTPRO   3'  GCCCTGCTTTGTAATA     48417    C    A  TG
                                TAT ACAGA GCA  GGGT
                                ||| ||||| |||  ||||
                                ATA TGTTT CGT  CCCG
                                  A    _  __
GAM661  PTPRO   3'  GCCCTGCTTTGTAATA     48418    C    A  TG
                                TAT ACAGA GCA  GGGT
                                ||| ||||| |||  ||||
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                                ATA TGTTT CGT  CCCG
                                  A    _  __
GAM661  PTPRO    3'  GCCCTGCTTTGTAATA     48419     C    A   TG
                                TAT ACAGA GCA  GGGT
                                ||| ||||| |||  ||||
                                ATA TGTTT CGT  CCCG
                                  A    _  __
GAM661  SLC1A3   3'  GGTCACCAGGTCCTGTGA    16063       AA  ATGG
                                TCACAG  GC   GGTGACC
                                ||||||  ||   |||||||
                                AGTGTC  TG   CCACTGG
                                   C_  GA__
GAM661  SNRPC    3'  GTGACCGATCATGCTGCTGTGA 13295        A    _______ GTGA
           TA                     TATCACAG AGCATG     GG   C
                                ||||||||| ||||||     ||   |
                                ATAGTGTC TCGTAC     CC   G
                                     G     TAG___  AGTG
GAM661  TAF4B    3'  GTCACCCTCTGTACGTGA    88513     AGAA   T
                                TCAC    GCA GGGGTGAC
                                ||||    ||| ||||||||
                                AGTG    TGT TCCCACTG
                                  CA__   C
GAM661  TCN2     3'  GGCCACCCCATGGTCTG     6266      AG       A
                                CAGA  CATGGGGTG CC
                                ||||  ||||||||| ||
                                GTCT  GTACCCCAC GG
                                  G_       C
GAM661  AKAP7    3'  GGTCACTTGCCTCCTGTTGA   17911    _  AA_  TGG
                                TCA CAG   GCA   GGTGACC
                                ||| |||   |||   |||||||
                                AGT GTC   CGT   TCACTGG
                                  T   CTC   ___
GAM661  AKAP7    3'  GGTCACTTGCCTCCTGTTGA   33495    _  AA_  TGG
                                TCA CAG   GCA   GGTGACC
                                ||| |||   |||   |||||||
                                AGT GTC   CGT   TCACTGG
                                  T   CTC   ___
GAM661  AKAP7    3'  GGTCACTTGCCTCCTGTTGA   57621    _  AA_  TGG
                                TCA CAG   GCA   GGTGACC
                                ||| |||   |||   |||||||
                                AGT GTC   CGT   TCACTGG
                                  T   CTC   ___
GAM661  BIK      3'  GGTCACACCCCTGTGTGATA   8655       AGAA   T  _
                                TATCAC    GCA GGG GTGACC
                                ||||||    ||| ||| ||||||
                                ATAGTG    TGT CCC CACTGG
                                   _____   C   A
GAM661  CENTG2   3'  GTCACACAGGCTTCTGTG    30543        A  GG
                                CACAGAAGC TG  GTGAC
                                ||||||||| ||  |||||
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                                GTGTCTTCG AC  CACTG
                                     G  A_
GAM661  CGB1     3'  CACCCCTTGACCTGTGATG   54129        AAG  T
                                TATCACAG   CA GGGGTG
                                ||||||||   || ||||||
                                GTAGTGTC   GT CCCCAC
                                     CA_  T
GAM661  CGB2     3'  CACCCCTTGACCTGTGATG   54130        AAG  T
                                TATCACAG   CA GGGGTG
                                ||||||||   || ||||||
                                GTAGTGTC   GT CCCCAC
                                     CA_  T
GAM661  DCLRE1A  5'  GTGACCAGTTGCTACTCCTGTG 69684        A___   TG____ GTGA
           ATA                    TATCACAG   AGCA    GG   C
                                ||||||||   ||||    ||   |
                                ATAGTGTC   TCGT    CC   G
                                     CTCA   TGA___ AGTG
GAM661  DKFZp547G183 3'  CCGGCCAGTTTCTGTGATA   38641          A  _______
                                TATCACAGAAGC TGG     G
                                ||||||||||| |||     |
                                ATAGTGTCTTTG ACC     C
                                       _  GG___C
GAM661  DKFZP564O0423 3'  ACCCTGTGCCTATGTAATA   93337     C   GAA
                                TAT ACA   GCATGGGGT
                                ||| |||   |||||||||
                                ATA TGT   CGTGTCCCA
                                  A   ATC
GAM661  DNAJB5   3'  ATCCCACTTTTGTGATA     25352          CA
                                TATCACAGAAG  TGGGGT
                                ||||||||||  ||||||
                                ATAGTGTTTTC  ACCCTA
                                       __
GAM661  ELF4     3'  CCAGCCTGCCTCTGTGATG   9229         A  T  _______
                                TATCACAGA GCA GG     G
                                ||||||||| ||| ||     |
                                GTAGTGTCT CGT CC     C
                                     C   _  GA___C
GAM661  FLJ10743  3'  GGCCATGTCTGTGCCTCTGTG  37088       A     _  A
                                CACAGA GCATGGG GTG CC
                                |||||| ||||||| ||| ||
                                GTGTCT CGTGTCT TAC GG
                                   C      G   C
GAM661  FLJ11113  5'  GCCATCATGCTCTGTAATA   60100     C    A    _
                                TAT ACAGA GCATGG GGT
                                ||| ||||| |||||| |||
                                ATA TGTCT CGTACT CCG
                                  A    _     A
GAM661  FLJ12331  3'  GTGACCAGTCATGCTTCCTTGA 47113       CA      _______ GTGA
           TA                    TATCA  GAAGCATG     GG   C
                                |||||  ||||||||     ||   |
```

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                                ATAGT  CTTCGTAC     CC   G
                                  TC       TGA___  AGTG
GAM661  FLJ23018  3'  GCCAGTTGCATTCTGTGATA  46079         _  TGG
                                TATCACAGAA GCA   GGT
                                |||||||||| |||   |||
                                ATAGTGTCTT CGT   CCG
                                     A   TGA
GAM661  FLJ23018  3'  GCCTTTGCTTCTGGATA    46080     A      T
                                TATC CAGAAGCA GGGGT
                                |||| |||||||| |||||
                                ATAG GTCTTCGT TTCCG
                                  _       _
GAM661  FUBP1     3'  GTGACCGGTTGATGCTTTGTGA 15333        A   GG________ GTGA
          TA                     TATCACAGA GCAT       G   C
                                |||||||| ||||       |   |
                                ATAGTGTTT CGTA       C   G
                                     _   GTTGG___C AGTG
GAM661  H326      5'  GTCCTTACTTCAGTGATA    32329      A   CATG   T
                                TATCAC GAAG   GGG GAC
                                |||||| ||||   ||| |||
                                ATAGTG CTTC   TTC CTG
                                   A   A___   _
GAM661  KIAA0189  3'  CACCCCATGGGGTCCTGTG   28940     _ AG_
                                CACAG A   CATGGGGTG
                                ||||| |   |||||||||
                                GTGTC T   GTACCCCAC
                                   C GGG
GAM661  KIAA0892  3'  CACCCTGTTATCTATGTATA  71566    _  C   AGC
                                TAT CA AGA   ATGGGGTG
                                ||| || |||   ||||||||
                                ATA GT TCT   TGTCCCAC
                                  T  A   AT_
GAM661  KIAA1029  3'  GTCTTGAAATGCATTCCATGAT 24432     CA   _   GGGGT
          A                     TATCA  GAA GCAT    GAC
                                |||||  ||| ||||    |||
                                ATAGT  CTT CGTA    CTG
                                   AC   A   AAGTT
GAM661  KIAA1110  3'  GGTCACCCAGACGTCACTGTGA 62503       AA  ATG_
          TA                     TATCACAG  GC   GGGTGACC
                                |||||||  ||   ||||||||
                                ATAGTGTC  TG   CCCACTGG
                                    AC  CAGA
GAM661  KIAA1423  3'  CCAACATATTCTGTGATA    62391        GC  _____
                                TATCACAGAA  ATG    GG
                                ||||||||||  |||    ||
                                ATAGTGTCTT  TAC    CC
                                     A_   AA___
GAM661  KIAA1906  3'  GTCACACAGCTCCTGTG     73574      A   A  GG
                                CACAG AGC TG  GTGAC
                                ||||| ||| ||  |||||
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                                GTGTC TCG AC  CACTG
                                  C  _ A_
GAM661  KIAA1975  3'  GTCACACAGGCTTCTGT    74425        A  GG
                                ACAGAAGC TG  GTGAC
                                |||||||| ||  |||||
                                TGTCTTCG AC  CACTG
                                    G  A_
GAM661  MGC12904  3'  GTCACCTACTGTGATA     49164        AAGCATG
                                TATCACAG     GGGTGAC
                                ||||||||     |||||||
                                ATAGTGTC     TCCACTG
                                    A_____
GAM661  MRIP2     3'  GTCACACAGGCTTCTGT     56790        A  GG
                                ACAGAAGC TG  GTGAC
                                |||||||| ||  |||||
                                TGTCTTCG AC  CACTG
                                    G  A_
GAM661  MSTP032   3'  GTGACCGACTCATGCTTCTGGA 48206     A       _______ GTGA
           TA                     TATC CAGAAGCATG      GG   C
                                |||| ||||||||||      ||   |
                                ATAG GTCTTCGTAC      CC   G
                                  _       TCAG___ AGTG
GAM661  PRO2900   5'  GTCACCCCAGCCTATGA    38439    C  AA  A
                                TCA AG  GC TGGGGTGAC
                                ||| ||  || |||||||||
                                AGT TC  CG ACCCCACTG
                                  A  __  _
GAM661  PSTPIP2   3'  GCTAGTGCTTCTGTGATA    44657          GG
                                TATCACAGAAGCAT  GGT
                                ||||||||||||||  |||
                                ATAGTGTCTTCGTG  TCG
                                       A_
GAM661  SEPW1     3'  GTGACCAGCAGACGCTTCATGA 13015      CA    A__ _____ GTGA
           TA                     TATCA  GAAGC   TG    GG   C
                                |||||  |||||  ||    ||   |
                                ATAGT  CTTCG   AC    CC   G
                                  A_    CAG  GA___ AGTG
GAM661  SH3BGRL2  3'  TCCCATGCTTTGTAATA     49679    C    A
                                TAT ACAGA GCATGGGG
                                ||| ||||| ||||||||
                                ATA TGTTT CGTACCCT
                                  A    _
GAM661  SIPL      3'  GTCACCTTCATTTTCTGT    37388        C   _
                                ACAGAAG ATGG GGTGAC
                                ||||||| |||| ||||||
                                TGTCTTT TACT CCACTG
                                    _   T
GAM661  SMCR8     3'  CACCCCATGCTCAGGTTTG   59252      ____
                                CAGA   AGCATGGGGTG
                                ||||   ||||||||||
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                                GTTT    TCGTACCCCAC
                                  GGAC
GAM661   LOC118704 3'  GTCACACAGGCTTCTGT     74360        A  GG
                                ACAGAAGC TG  GTGAC
                                |||||||| ||  |||||
                                TGTCTTCG AC  CACTG
                                     G  A_
GAM661   LOC118706 3'  GTCACACAGGCTTCTGT     74362        A  GG
                                ACAGAAGC TG  GTGAC
                                |||||||| ||  |||||
                                TGTCTTCG AC  CACTG
                                     G  A_
GAM661   LOC124045 3'  GGCCACCCCACCCTGTGA     76542       AAGCA      A
                                TCACAG     TGGGGTG CC
                                ||||||     ||||||| ||
                                AGTGTC     ACCCCAC GG
                                    CC___       C
GAM661   LOC128708 5'  CCAACCAGCTTTGTGATA     76291         A  A  _______
                                TATCACAGA GC TGG      G
                                ||||||||| || |||      |
                                ATAGTGTTT CG ACC      C
                                      _ _   AA___C
GAM661   LOC143158 3'  GTCACACAGGCTTCTGT     77001        A  GG
                                ACAGAAGC TG  GTGAC
                                |||||||| ||  |||||
                                TGTCTTCG AC  CACTG
                                     G  A_
GAM661   LOC143187 3'  GCTTTATGATTCTGTAATA    59761     C     G
                                TAT ACAGAA CATGGGGT
                                ||| |||||| ||||||||
                                ATA TGTCTT GTATTTCG
                                  A     A
GAM661   LOC143452 5'  GTGACCAATCCTGTTCCTGTGA 77072         A    T _______  GTGA
            TA                    TATCACAG AGCA G      GG    C
                                ||||||||| |||| |      ||    |
                                ATAGTGTC TTGT C      CC    G
                                     C    C TAA___  AGTG
GAM661   LOC145134 5'  CCTATGCACTTCCTGATA     84208       CA   __
                                TATCA  GAA  GCATGGG
                                |||||  |||  |||||||
                                ATAGT  CTT  CGTATCC
                                  C_   CA
GAM661   LOC145824 5'  GTGACCAGTTTATACTTCTGTG 77988           C  ________  GTGA
            ATG                   TATCACAGAAG ATG       GG    C
                                |||||||||||| |||       ||    |
                                GTAGTGTCTTC TAT       CC    G
                                      A   TTGA___  AGTG
GAM661   LOC146229 3'  GTCATGTTTTACTTCTGTGAT  78303          CAT  G
                                ATCACAGAAG   GG GTGAC
                                ||||||||||   || |||||
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                                TAGTGTCTTC   TT TACTG
                                     ATT  G
GAM661   LOC146268 3'  GTCACCCCTCCTCCTGCGA   78343    A   A  CAT
                                TC CAG AG   GGGGTGAC
                                || ||| ||   ||||||||
                                AG GTC TC   CCCCACTG
                                 C   C  CT_
GAM661   LOC148438 3'  TCACCTCACTTCCTGCAGTA   85311     CA   _   CA
                                TAT  CAG AAG  TGGGGTGA
                                |||  ||| |||  ||||||||
                                ATG  GTC TTC  ACTCCACT
                                  AC   C   __
GAM661   LOC150998 3'  GCCTTTGCTCTGTGATA     86361         A   T
                                TATCACAGA GCA GGGGT
                                ||||||||| ||| |||||
                                ATAGTGTCT CGT TTCCG
                                      _   _
GAM661   LOC152373 5'  GGTCATAGTTGCCTTTGTGA   81453        A   TGGG
                                TCACAGA GCA    GTGACC
                                ||||||| |||    ||||||
                                AGTGTTT CGT    TACTGG
                                    C   TGA_
GAM661   LOC153514 3'  GGTCACCCCACATGCCCTG    81712     AA   __
                                CAG  GCA  TGGGGTGACC
                                |||  |||  ||||||||||
                                GTC  CGT  ACCCCACTGG
                                  C_   AC
GAM661   LOC157807 3'  GTCACCCCAATGCTCCTG     82514     A    _
                                CAG AGCAT GGGGTGAC
                                ||| ||||| ||||||||
                                GTC TCGTA CCCCACTG
                                  C    A
GAM661   LOC158130 3'  CCAGCTATGCTTCTGTGA     69704           _______
                                TCACAGAAGCATGG      G
                                ||||||||||||||     |
                                AGTGTCTTCGTATC      C
                                        GA___C
GAM661   LOC166793 5'  CACCTGGCATGCCTTGTAATA  59918     C    AA    __
                                TAT ACAG  GCATG  GGGTG
                                ||| ||||  |||||  |||||
                                ATA TGTT  CGTAC  TCCAC
                                  A   C_    GG
GAM661   LOC195979 3'  GTCACACAGGCTTCTGT      88929         A  GG
                                ACAGAAGC TG  GTGAC
                                |||||||| ||  |||||
                                TGTCTTCG AC  CACTG
                                     G  A_
GAM661   LOC203275 3'  GTGACCGACAATGCCTCTGTGA 90857         A    _ _____  GTGA
            T                    ATCACAGA GCAT G     GG    C
                                ||||||||| |||| |     ||    |
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                                TAGTGTCT CGTA C     CC    G
                                    C    A AG___  AGTG
GAM661   LOC203292 3'  TCACCCCAGCCTGTGA      92156       AA  A
                                TCACAG  GC TGGGGTGA
                                |||||||  || ||||||||
                                AGTGTC  CG ACCCCACT
                                  __  _
GAM661   LOC220045 3'  GCCCCTGCTTCTGGATA     95035      A       T
                                TATC CAGAAGCA GGGGT
                                |||| |||||||| |||||
                                ATAG GTCTTCGT CCCCG
                                  _       _
GAM661   LOC220466 3'  GTCACACAGGCTTCTGT     74399         A  GG
                                ACAGAAGC TG  GTGAC
                                |||||||| ||  |||||
                                TGTCTTCG AC  CACTG
                                    G  A_
GAM661   LOC222159 5'  GGTCACCCACAGCCTGTGTATA 95730     _    AA  A  _
                                TAT CACAG  GC TG GGGTGACC
                                ||| |||||  || || ||||||||
                                ATA GTGTC  CG AC CCCACTGG
                                  T    __  _  A
GAM661   LOC255319 3'  GTCACACAGGCTTCTGT     96153         A  GG
                                ACAGAAGC TG  GTGAC
                                |||||||| ||  |||||
                                TGTCTTCG AC  CACTG
                                    G  A_
GAM661   LOC256114 5'  GTCCCGCGCCTGTGATA     98113         AA  AT G  T
                                TATCACAG  GC  G GG GAC
                                ||||||||  ||  | || |||
                                ATAGTGTC  CG  C CC CTG
                                    __  __ G  _
GAM661   LOC256277 5'  GTGACCAGCTATGCTTCTTGTG 96354        _       _______ GTGA
           ATA                    TATCACA GAAGCATGG     G    C
                                |||||||| |||||||||     |   |
                                ATAGTGT CTTCGTATC     C    G
                                    T        GA___C AGTG
GAM661   LOC256764 5'  GGTCATTCAGCTTCGGT     96622     A    ATG
                                AC GAAGC   GGGTGACC
                                || |||||   ||||||||
                                TG CTTCG   CTTACTGG
                                 G    A__
GAM661   LOC51049  3'  CCGGCCTGCTTTGTGATA    32456         A  T  _______
                                TATCACAGA GCA GG      G
                                ||||||||| ||| ||     |
                                ATAGTGTTT CGT CC      C
                                    _  _  GG___C
GAM661   LOC51236  3'  CACCCTCTGCCCCTGTGGTA  33619         AA   T
                                TATCACAG  GCA GGGGTG
                                ||||||||  ||| ||||||
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                                ATGGTGTC  CGT TCCCAC
                                    CC   C
GAM661  LOC56181  3'  GGGTGACCAGTCTCATGCTCCT 97279    CA  A    _________ GTGA
          GGAATA                  TAT  CAG AGCATG      GG   CC
                                |||  ||| ||||||       ||   ||
                                ATA  GTC TCGTAC      CC   GG
                                  AG   C     TCTGA___  AGTG
GAM661  LOC57822  5'  GGGTGACCGATCAAGATCTTCT 79669        CA__ _______ GTGA
          GTGA                    TCACAGAAG   TG    GG   CC
                                |||||||||   ||    ||   ||
                                AGTGTCTTC   AC    CC   GG
                                    TAGA  TAG___  AGTG
GAM661  LOC90520  3'  CTCCATGCTCCTGCAATA   63837    CA  A
                                TAT  CAG AGCATGGGG
                                |||  ||| |||||||||
                                ATA  GTC TCGTACCTC
                                  AC   C
GAM662  GPD1    3'  TCATGCCACCACATTTG    60398      C      C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A      _
GAM662  IL5RA   5'  TCGCATGGCCACCGCATTT   6906          AT__
                                AAATGCGGTGGC   CGA
                                ||||||||||||   |||
                                TTTACGCCACCG   GCT
                                     GTAC
GAM662  MYO1C   3'  TGCCGATGCCAAATATTTG   61873      CGG     A
                                TAAATG   TGGCATCG CA
                                ||||||   |||||||| ||
                                GTTTAT   ACCGTAGC GT
                                   AA_      C
GAM662  C6orf37  3'  TGTCACACTGCATTTA     68097         GCATC
                                TAAATGCGGTG    GACA
                                ||||||||||    ||||
                                ATTTACGTCAC    CTGT
                                     A____
GAM662  DNAJC6   3'  TTGCAGAACCACCGCATT    29498        CA  GA
                                AATGCGGTGG  TC  CAA
                                |||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                     A_  AC
GAM662  FLJ11210 3'  GTCGATGTGCATGCTTTTA   60319     T  GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM662  FLJ12476 3'  TCGATCTTCTGCATTTA     43270        T  C
                                TAAATGCGG GG ATCGA
                                ||||||||| || |||||
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                                ATTTACGTC TC TAGCT
                                     T  _
GAM662  KIAA1034  3'  TCGATGGCATCCGCATTTG   63134        _  G
                                TAAATGCGG TG CATCGA
                                ||||||||| || ||||||
                                GTTTACGCC AC GTAGCT
                                     T  G
GAM662  KIAA1987  3'  TCATGTAACTGCATTTA    89391         G   C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                     A   _
GAM662  MGC16063  3'  TGTCCTGGCCACTGCATT   54929          ATC
                                AATGCGGTGGC  GACA
                                ||||||||||  ||||
                                TTACGTCACCG  CTGT
                                      GTC
GAM662  LOC147949 3'  TGTCAGATGTCCACATTGCA  79279    __  _  _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM662  LOC150577 3'  GTCCTCACCGCATTTG     86258          CATC
                                TAAATGCGGTGG   GAC
                                ||||||||||||   |||
                                GTTTACGCCACT   CTG
                                      C___
GAM662  LOC158219 3'  TGTGTGTCACCACATTT    82694      C      CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                   A       __
GAM662  LOC202020 3'  TGTCTCACCACATTTA     90605      C    CATC
                                TAAATG GGTGG   GACA
                                |||||| |||||   ||||
                                ATTTAC CCACT   CTGT
                                    A   _____
GAM662  LOC90826  5'  TGTCGATGCAGGTTTATTTG  64788      CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                    TTGGA
GAM662  LOC93587  3'  TTGTCTTTACCTGCATTTA   73042       _    CATC
                                TAAATGC GGTGG   GACAA
                                ||||||| |||||   |||||
                                ATTTACG CCATT   CTGTT
                                    T    T___
GAM663  EHF       3'  TCCAAAACCCAAGGTTGGCT  25127     AT   _   C
                                AGT  GCCT GGGT TTGGA
                                |||  |||| |||| |||||
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                                TCG  TGGA CCCA AACCT
                                  GT   A   A
GAM663  EPHA2    3'  CCATCGGCCAAGAATACTTGAA 16675         GC  G   T_
            G                    CTTCAAGTAT  CT GGTC  TGG
                                 ||||||||||  || ||||  |||
                                 GAAGTTCATA  GA CCGG  ACC
                                       A_  A   CT
GAM663  ITGA5    3'  CCCAGAGACATACTTGAAG   61933          C__
                                 CTTCAAGTATG  CTGGG
                                 ||||||||||   |||||
                                 GAAGTTCATAC  GACCC
                                       AGA
GAM663  TREM2    3'  TCCAAGACTGTCATATTT    39098       CCTG
                                 AAGTATG   GGTCTTGGA
                                 |||||||   |||||||||
                                 TTTATAC   TCAGAACCT
                                     TG__
GAM663  UQCRB    3'  CCAACATAGGCATACTTAAG  21939    C        GGTC
                                 CTT AAGTATGCCTG   TTGG
                                 ||| ||||||||||   ||||
                                 GAA TTCATACGGAT   AACC
                                   _         AC__
GAM663  ATP10D   3'  CAGAGACCACTTGAAG      73526        ATGCCTG   _
                                 CTTCAAGT      GGTCT TG
                                 ||||||||      ||||| ||
                                 GAAGTTCA      CCAGA AC
                                       _______    G
GAM663  B3GNT7   3'  CCCTTCCAGGCAACCTGAA   71678     A  A      TCTT
                                 TTCA GT TGCCTGGG   GG
                                 |||| || ||||||||   ||
                                 AAGT CA ACGGACCT   CC
                                   C  _       TC__
GAM663  DKFZp547I224 3'  TCCAAAATTGACCACATACTTG 39963          CCTG  ____
            GA                   TTCAAGTATG   GGTC   TTGGA
                                 ||||||||||   ||||   |||||
                                 AGGTTCATAC   CCAG   AACCT
                                       A___   TTAA
GAM663  FLJ22341 3'  CCAAGCTCAGGCACACCCAAG  45114    CAA  A      T
                                 CTT   GT TGCCTGGG CTTGG
                                 |||   || |||||||| |||||
                                 GAA   CA ACGGACTC GAACC
                                   CC_  C       _
GAM663  KIAA0779 3'  CCGAACAGCATACTTGAAG   86908          C  GGTC
                                 CTTCAAGTATGC TG   TTGG
                                 |||||||||||| ||   ||||
                                 GAAGTTCATACG AC   AGCC
                                       _  A___
GAM663  LOC144233 3'  CCAAGGCACATAATTGAA    77246      G   CCTGG
                                 TTCAA TATG    GTCTTGG
                                 ||||| ||||    |||||||
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```
                                AAGTT ATAC    CGGAACC
                                  A   A____
GAM663  LOC147341 3'  ACCCAGGCATAACTGAAG    85116      AG
                                CTTCA  TATGCCTGGGT
                                |||||  ||||||||||
                                GAAGT  ATACGGACCCA
                                  CA
GAM663  LOC221088 5'  TCCAAGGTGCTGGCCACTCGAA 94888     A   AT   TGGG
          G                      CTTC AGT  GCC    TCTTGGA
                                |||| |||  |||    |||||||
                                GAAG TCA  CGG    GGAACCT
                                  C   C_   TCGT
GAM664  ABCA3    5'  CCCAGTAGTCCTGAAGGGAG   8442       C_   CT
                                CTCCC  CAG  CTGCTGGG
                                |||||  |||  ||||||||
                                GAGGG  GTC  GATGACCC
                                  AA   CT
GAM664  ANGPT2   5'  CCCAGCCTTGAGGGAGGGA   8559         C   CTCT
                                TCCCTCCC CAG    GCTGGG
                                |||||||| |||    ||||||
                                AGGGAGGG GTT    CGACCC
                                    A   C___
GAM664  BLTR2    5'  CAGAGCTGGGGGAGGGAT    39518
                                ATCCCTCCCCCAGCTCTG
                                ||||||||||||||||||
                                TAGGGAGGGGGTCGAGAC

GAM664  CD79B    3'  CCCAGCAGAGCTTGGGAAGGG  41489      C   C
                                CCCT CCC AGCTCTGCTGGG
                                |||| ||| ||||||||||||
                                GGGA GGG TCGAGACGACCC
                                  A   T
GAM664  CD79B    3'  CCCAGCAGAGCTTGGGAAGGG  7119       C   C
                                CCCT CCC AGCTCTGCTGGG
                                |||| ||| ||||||||||||
                                GGGA GGG TCGAGACGACCC
                                  A   T
GAM664  CEBPA    3'  CCGTCGGCAGCTGGGGGAAGGG 16427       C        _   C
          TC                     GATCC TCCCCCAGCT CTG TGG
                                ||||| |||||||||| ||| |||
                                CTGGG AGGGGGTCGA GGC GCC
                                  A        C   T
GAM664  CHRND    3'  CCCTCAGACTGGGGAAGAGTC  7454      CC  C     C    CT
                                GAT  CT CCCCAG TCTG  GGG
                                |||  || |||||| ||||  |||
                                CTG  GA GGGGTC AGAC  CCC
                                  A_  A      _    T_
GAM664  CREBL2   5'  CCGGCTGAGCCGGGGGAGGGCT 8966     T       A    T
          C                      GA CCCTCCCCC GCTC GCTGG
                                || |||||||| |||| |||||
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                                CT GGGAGGGGG CGAG CGGCC
                                 C       C   T
GAM664  LRPAP1   3'  CCCAGCCCGGCAGGGAAGAGG  11366     C_  A  CT
                                CCTC  CCC GCT  GCTGGG
                                |||| ||| |||  ||||||
                                GGAG  GGG CGG  CGACCC
                                  AA  A  CC
GAM664  PTGFRN   3'  CCAGGAGGAGCAGAAGAGGGAT 67767       CCCCA   G_
           C                     GATCCCTC    GCTCT  CTGG
                                ||||||||    |||||  ||||
                                CTAGGGAG    CGAGG  GACC
                                    AAGA_    AG
GAM664  RERE     3'  CCCAGTTCTTGGGGGAG     25015        CTCT
                                CTCCCCCAG   GCTGGG
                                |||||||||   ||||||
                                GAGGGGGTT   TGACCC
                                     CT__
GAM664  SCA1     3'  CCAAGGAGACCCGGGGGAGG  6173        AG__   GC
                                CCTCCCCC   CTCT  TGG
                                ||||||||   ||||  |||
                                GGAGGGGG   GAGG  ACC
                                    CCCA   A_
GAM664  SNAI1    3'  CCCAGCTCCAGCAGGAAGGA  21123    C  CCCA  CT_
                                TCC TCC    GCT   GCTGGG
                                ||| |||    |||   ||||||
                                AGG AGG    CGA   CGACCC
                                  A  A___   CCT
GAM664  SRRM2    3'  CCCAGCAGAGCCGTGGGAGGGT 33384    T     CCA
           C                     GA CCCTCCC   GCTCTGCTGGG
                                || |||||||   ||||||||||
                                CT GGGAGGG   CGAGACGACCC
                                 _      TGC
GAM664  STAT5B   5'  CCGGCCGAGGGAGGGA     25855        CCAGC  T
                                TCCCTCCC    TC GCTGG
                                ||||||||    || |||||
                                AGGGAGGG    AG CGGCC
                                    _____  C
GAM664  TEL2     3'  CCAGCAGAGCAGCAGGATC   32849      CTCCCCCA
                                GATCC       GCTCTGCTGG
                                |||||       ||||||||||
                                CTAGG       CGAGACGACC
                                   ACGA____
GAM664  TNS      3'  CCCAGCAGGAGTGGGAGGGTC  42947    T     CCA   _
                                GA CCCTCCC   GCTC TGCTGGG
                                || |||||||   |||| |||||||
                                CT GGGAGGG   TGAG ACGACCC
                                 _      ___   G
GAM664  FLJ10901 3'  CCCAGCCTGGGCTGGGGGAG  37357          T_
                                CTCCCCCAGCTC  GCTGGG
                                ||||||||||||  ||||||
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                                GAGGGGGTCGGG  CGACCC
                                      TC
GAM664  FLJ12517  3'  CCCAGCAGGGGAGGAGGCATC  43718     C    _  AGCT
                                GAT CCTCC CCC    CTGCTGGG
                                ||| ||||| |||    ||||||||
                                CTA GGAGG GGG    GACGACCC
                                  C    A  _____
GAM664  FLJ14166  3'  CCCAGCAGAACTGGGAGG    44987    _    C
                                CC CCCAG TCTGCTGGG
                                || ||||| |||||||||
                                GG GGGTC AGACGACCC
                                 A    A
GAM664  FLJ22059  5'  CCCAGCAGAGACTGGAGAG   43053     CC   _
                                CTC  CCAG CTCTGCTGGG
                                |||  |||| ||||||||||
                                GAG  GGTC GAGACGACCC
                                  A_   A
GAM664  GPT2     3'  CCCTGGGGCTGAGAAAGGGTC  56768    T   CCCC     GCT
                                GA CCCT   CAGCTCT   GGG
                                || ||||   |||||||   |||
                                CT GGGA   GTCGGGG   CCC
                                 _   AAGA     T__
GAM664  HIC2     3'  CCCTGGGGCTGGGGGAGGGATT 65864              GCT
                                GATCCCTCCCCCAGCTCT   GGG
                                ||||||||||||||||||  |||
                                TTAGGGAGGGGGTCGGGG   CCC
                                      T__
GAM664  HU-K4    3'  CCCAGCAGAGCTGGGGGAGGGA 25358
           TC                   GATCCCTCCCCCAGCTCTGCTGGG
                                ||||||||||||||||||||||||
                                CTAGGGAGGGGGTCGAGACGACCC

GAM664  KIAA0370  3'  CCCAGCAGAGCTGGCTTCTGGG 73582      CTCCC
           TC                   GATCC    CCAGCTCTGCTGGG
                                |||||    ||||||||||||||
                                CTGGG    GGTCGAGACGACCC
                                   TCTTC
GAM664  KIAA0937  3'  TCTGCTGGGGAAAACTGGGGGA 93228    T  C     G_________   TGCT
           AGGCTC                GA CC TCCCCCA       CTC   GG
                                || || |||||||       |||   ||
                                CT GG AGGGGGT       GGG   CT
                                 C  A      CAAAAG___   TCGT
GAM664  MGC2705  3'  CCAGCAGGGAGAGAGGGTC   52080    T    CCCCAG
                                GA CCCTC     CTCTGCTGG
                                || |||||     |||||||||
                                CT GGGAG     GGGACGACC
                                 _    AGA___
GAM664  RABAC1   3'  CCCATCACAAGCCCGGGGAGGG 22221          CA   C_  C
           ATC                   GATCCCTCCCC  GCT  TG TGGG
                                ||||||||||  |||  || ||||
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                                CTAGGGAGGGG  CGA  AC ACCC
                                      CC   AC  T
GAM664  TGFB1I1   3'  CCTTACTGGGGGAGGGTC    32496    T        CTCTGCT
                                GA CCCTCCCCCAG      GG
                                || ||||||||||       ||
                                CT GGGAGGGGGTC      CC
                                 _         ATT_____
GAM664  TTTY11    3'  CCCAGCAGAATCAAAGTGGATC 50024      _ CCCCCAGC
                                GATCC CT       TCTGCTGGG
                                ||||| ||       |||||||||
                                CTAGG GA       AGACGACCC
                                   T  AACTA___
GAM664  ZNF282    3'  CCAGGGTGGGGCAGGGATC   90694       C    G TCTG
                                GATCCCT CCCCA C    CTGG
                                ||||||| ||||| |    ||||
                                CTAGGGA GGGGT G    GACC
                                    C    G ____
GAM664  LOC126917 3'  CCCAGGGCCCTGGGGGGAGGGA 75085          _  CT  G
           TC                     GATCCCTCCCCC AG  CT CTGGG
                                ||||||||||| ||  || |||||
                                CTAGGGAGGGGG TC  GG GACCC
                                      G  CC  _
GAM664  LOC126917 3'  CCCTGGAGCTGGGAGAGAGG   75086    _  C       GCT
                                CC CTC CCCAGCTCT   GGG
                                || ||| |||||||||   |||
                                GG GAG GGGTCGAGG   CCC
                                 A  A        T__
GAM664  LOC132617 5'  CCCAAGGAGCTGGAGGAG    76410     C      GC
                                CTCC CCAGCTCT  TGGG
                                |||| ||||||||  ||||
                                GAGG GGTCGAGG  ACCC
                                  A       A_
GAM664  LOC145608 5'  CCCAAGCGGTGGGGAAGG    84379     C    GCT    _
                                CCT CCCCA   CTGCT GGG
                                ||| |||||   ||||| |||
                                GGA GGGGT   GGCGA CCC
                                  A    ___     A
GAM664  LOC146268 3'  CCCAGTAGTTCTGGAGGAAGG  78333    C   C    CT
                                CC TCC CCAG  CTGCTGGG
                                || ||| ||||  ||||||||
                                GG AGG GGTC  GATGACCC
                                 A  A   TT
GAM664  LOC147299 5'  CCCACGGGCAGCGGGGAAGAAA 78977     CC  C    A   __   C
           TC                     GAT  CT CCCC GCT  CTG TGGG
                                |||  || |||| |||  ||| ||||
                                CTA  GA GGGG CGA  GGC ACCC
                                  AA  A    _   CG   _
GAM664  LOC151568 5'  CCCATGCCTGGGGGAGAGA    57493    C       CTCT  _
                                TC CTCCCCCAG    GC TGGG
                                || |||||||||    || ||||
```

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                                AG GAGGGGGTC   CG ACCC
                                 A       ____  T
GAM664  LOC152503 5'  CCCAGCAGCCGTAGGAGAGGAG 86978   TC   CC  A  T_
            TC                    GA  CCTC  CC GC  CTGCTGGG
                                  ||  ||||  || ||  ||||||||
                                  CT  GGAG  GG TG  GACGACCC
                                   GA   A_  A  CC
GAM664  LOC163682 3'  CCCAGCAGAGCCCACAAGAGAG 88400    CC   CCCCA_
            TC                    GAT  CTC    GCTCTGCTGGG
                                  |||  |||    ||||||||||
                                  CTG  GAG    CGAGACGACCC
                                   A_  AACACC
GAM664  LOC163782 5'  CCCAGCAGGGAGGGAGGAGA  83035   _    CCAG
                                  TC CCTCCC   CTCTGCTGGG
                                  || ||||||   ||||||||||
                                  AG GGAGGG   GGGACGACCC
                                   A    A___
GAM664  LOC201304 3'  CCCAGAGCTGAGAGGGA    89603      CCC      CT
                                  TCCCTC  CAGCTCTG  GG
                                  ||||||  ||||||||  ||
                                  AGGGAG  GTCGAGAC  CC
                                     A__      __
GAM664  LOC245771 5'  CCCAGCCTGGGCTGGGGGAG  94470          T_
                                  CTCCCCCAGCTC  GCTGGG
                                  ||||||||||||  ||||||
                                  GAGGGGGTCGGG  CGACCC
                                        TC
GAM664  LOC255452 5'  CCCAGCAGAGTGAAAGTGGATC 99393     _  CCCCCA
                                  GATCC CT    GCTCTGCTGGG
                                  ||||| ||    ||||||||||
                                  CTAGG GA    TGAGACGACCC
                                     T  AAG___
GAM664  LOC90917  3'  CCCAGCAGAGCTACAGGAGG  64983     CCC
                                  CCTCC  AGCTCTGCTGGG
                                  |||||  ||||||||||||
                                  GGAGG  TCGAGACGACCC
                                     ACA
GAM664  LOC91355  5'  CCCAGCAGCCTCAGAAGGATC  66304     C  CCCC  CT
                                  GATCC TC   AG  CTGCTGGG
                                  ||||| ||   ||  ||||||||
                                  CTAGG AG   TC  GACGACCC
                                     A  AC__  C_
GAM665  CA7     3'  CCAGTCACCAAAGCCACCT   60828    A_     TCGGA  A
                                  AGG  GCTTTGGT   GAC GG
                                  |||  ||||||||   ||| ||
                                  TCC  CGAAACCA   CTG CC
                                   AC       _____  A
GAM665  E2F3    3'  CTGTCTCCATGAACCACTC   10467    CTT    __
                                  GAG  TGGTTC  GGAGACAG
                                  |||  ||||||  ||||||||
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                                CTC   ACCAAG  CCTCTGTC
                                  ___     TA
GAM665  HD      3'  CCTATCCCCAGGACAGGTCCCT 10911     AG   TG   _ A  C
                                AGG  CTT  GTTC GG GA AGG
                                |||  |||  |||| || || |||
                                TCC  GGA  CAGG CC CT TCC
                                  CT   __    A  C  A
GAM665  LZTR1   3'  CTGTCACCCAAGGCTCCT    23170          TTCG A
                                AGGAGCTTTGG    G GACAG
                                ||||||||||    | |||||
                                TCCTCGGAACC    C CTGTC
                                       ____ A
GAM665  MECP2   3'  CCGTCTAACCACAGCTCCTT   18395        T    CGG    A
                                AAGGAGCT TGGTT   AGAC GG
                                |||||||| |||||   |||| ||
                                TTCCTCGA ACCAA   TCTG CC
                                     C     ___    C
GAM665  PLA2G2A  5'  CTGTCTCCAAACAGCCTT    6110     A   TTG   C
                                AGG GCT   GTT GGAGACAG
                                ||| |||   ||| ||||||||
                                TTC CGA   CAA CCTCTGTC
                                  _  ___   A
GAM665  PLOD    3'  CCTGAAAAACCAAGGCCCC    6114     A       CGGAGA
                                GG GCTTTGGTT     CAGG
                                || |||||||||     ||||
                                CC CGGAACCAA     GTCC
                                 C        AAA___
GAM665  POLR2A   3'  CCTGTCCCCAAATTGAAGATCC 8128       G   TG   C  A
           TT                     AAGGA CTT  GTT GG GACAGG
                                |||||| |||  ||| || ||||||
                                TTCCT GAA  TAA CC CTGTCC
                                   A   GT   A  C
GAM665  RAB36   3'  CCTGTCTCCAACACCGCCTCCT 18163      CTT    TC_
                                AGGAG   TGGT   GGAGACAGG
                                |||||   ||||   |||||||||
                                TCCTC   GCCA   CCTCTGTCC
                                   C__    CAA
GAM665  RAP1    3'  CCTGTCCTTTGGCAGAAGCTCC 39111         G  T    _
           TT                     AAGGAGCTTT GT CGGAG ACAGG
                                |||||||||| || ||||| |||||
                                TTCCTCGAAG CG GTTTC TGTCC
                                      A  _    C
GAM665  SFRP5   3'  CCTGCCCCAAGGCCCAGAGCTC 13032          TT __  AGA
           C                      GGAGCTTTGG  C  GG   CAGG
                                ||||||||||  |  ||   ||||
                                CCTCGAGACC  G  CC   GTCC
                                      CG AA  CC_
GAM665  SORCS2   3'  CCTGTCCCCCAGACCCAAAGCT 40800          T  _  A_
           CT                     GGAGCTTTGG TC GG  GACAGG
                                |||||||||| || ||  ||||||
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                                TCTCGAAACC AG CC  CTGTCC
                                     C  A  CC
GAM665  TFR2     3'  CCCGTCCCCCAGTCAAGAGCTC 13698         _ GT C  A   A
           CT                    AGGAGCTTT G  T GG GAC GG
                                ||||||||| |  | || ||| ||
                                TCCTCGAGA C  A CC CTG CC
                                     A TG C  C   C
GAM665  C1orf35  3'  CTGCCTCGGAAGCTCCTT    44480        TTGGT  G   A
                                AAGGAGCT    TC GAG CAG
                                ||||||||    || ||| |||
                                TTCCTCGA    AG CTC GTC
                                     _____  G   C
GAM665  DKFZp434J1015 3'  CCGCCTCCACCTGAAAAGCTCC 94209          ___  TC   ACA
           TT                    AAGGAGCTTT   GGT  GGAG   GG
                                ||||||||||   |||  ||||   ||
                                TTCCTCGAAA   CCA  CCTC   CC
                                     AGT   __   CG_
GAM665  FLJ10350  5'  CCGCCTCCGAGTCGCTACTT   97248    G   TTT GT    ACA
                                AAG AGC   G  TCGGAG   GG
                                ||| |||   |  ||||||   ||
                                TTC TCG   C  AGCCTC   CC
                                  A  ___ TG     CG_
GAM665  HRI      3'  CTGCCCCACAAGCTCCTT    27738         _   TT
                                AAGGAGCTT TGG  CGG
                                ||||||||| |||  |||
                                TTCCTCGAA ACC  GTC
                                     C   CC
GAM665  KIAA0057  3'  CCTGTCTCTTGCAAGCTCC   25409       TG  TC
                                GGAGCTT  GT  GGAGACAGG
                                |||||||  ||  |||||||||
                                CCTCGAA  CG  TCTCTGTCC
                                     __  T_
GAM665  KIAA0189  3'  CCTGTCCCCTTTCCTAAAGCTC 28941          TTC_  A
           CT                    AGGAGCTTTGG    GG GACAGG
                                ||||||||||    || ||||||
                                TCCTCGAAATC    CC CTGTCC
                                      CTTT  C
GAM665  KIAA1203  3'  CCTGCCCTCCCACCAAAGCCTC 72087      _      TC    A_
           CT                    AGGAG CTTTGGT  GGAG  CAGG
                                ||||| |||||||  ||||  ||||
                                TCCTC GAAACCA  CCTC  GTCC
                                   C      C_   CC
GAM665  KIAA1533  5'  CCTGCCCCCAAGCCGGCCCC   74140    A   TT    C  AGA
                                GG GCT  GGTT GG   CAGG
                                || |||  |||| ||   ||||
                                CC CGG  CCGA CC   GTCC
                                 C   __    A  CCC
GAM665  SAMHD1    3'  CCTGCCCCCGTGAAGAGTTCC  61981        GGTT   AGA
                                GGAGCTTT    CGG   CAGG
                                ||||||||    |||   ||||
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                                CCTTGAGA   GCC   GTCC
                                     AGT_   CCC
GAM665  SCGN     3'  CCTGTCTCACTGAAAGCCCCT  23775     A    _   TCG
                                AGG GCTTT GGT   GAGACAGG
                                ||| ||||| |||   ||||||||
                                TCC CGAAA TCA   CTCTGTCC
                                  C    G   ___
GAM665  SYT6     3'  CTCTCCGAAACCACCTC     79519     CTT    _     CA
                                GAG   TGGTT CGGAGA  G
                                |||   ||||| ||||||  |
                                CTC   ACCAA GCCTCT  C
                                  C__     A     A
GAM665  UBXD2    3'  CTGCCTCCATCAGCTTCTT    68892        TT   TC    A
                                AAGGAGCT  GGT  GGAG CAG
                                ||||||||  |||  |||| |||
                                TTCTTCGA  CTA  CCTC GTC
                                     __   __    C
GAM665  LOC113146 3'  CCTAAAATGGAACCAAAGCTTC 73334            GGAGAC
                                GGAGCTTTGGTTC     AGG
                                ||||||||||||      |||
                                CTTCGAAACCAAG     TCC
                                       GTAAAA
GAM665  LOC113521 5'  CCGTCTCCGAGCTGCTCC    73404       TTT         A
                                GGAGC   GGTTCGGAGAC GG
                                |||||   |||||||||| ||
                                CCTCG   TCGAGCCTCTG CC
                                   ___          C
GAM665  LOC115704 3'  CCTGCAGCGGAAACCAAAGTCC 73906    AG      __   GAGA
             C                   GG  CTTTGGT  TCG    CAGG
                                 ||  |||||||  |||    ||||
                                 CC  GAAACCA  GGC    GTCC
                                  CT      AA   GAC_
GAM665  LOC136345 3'  CCTACCCCACCCAAAGCTGCCT 76712     _       TTC  AGAC
                                AGG AGCTTTGG   GG    AGG
                                ||| ||||||||   ||    |||
                                TCC TCGAAACC   CC    TCC
                                  G       CA_  CCA_
GAM665  LOC144231 5'  CCTGTCTTCCTTGACCAAAGCT 83938           C__
             CT                   GGAGCTTTGGTT   GGAGACAGG
                                  ||||||||||||   |||||||||
                                  TCTCGAAACCAG   CTTCTGTCC
                                         TTC
GAM665  LOC146856 5'  CTGTCTCCATGAACCACTC    83700     CTT     __
                                GAG   TGGTTC  GGAGACAG
                                |||   ||||||  ||||||||
                                CTC   ACCAAG  CCTCTGTC
                                  ___      TA
GAM665  LOC147669 5'  CCGCCTCCTGGGCAAGCTCC   85180        TG   _   ACA
                                GGAGCTT  GTTC GGAG   GG
                                |||||||  |||| ||||   ||
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                                CCTCGAA  CGGG CCTC   CC
                                   __   T   CG_
GAM665  LOC148021 5'  CTACCTCCAGAGCTACTT    79316    G      TTC  _
                                AAG AGCTTTGG   GG AG
                                ||| ||||||||   || ||
                                TTC TCGAGACC   CC TC
                                  A       T__  A
GAM665  LOC153688 3'  CCTGCCCCCAAACCAAGGCCT  87307    A       C  AGA
                                GG GCTTTGGTT GG   CAGG
                                || |||||||| ||   ||||
                                TC CGGAACCAA CC   GTCC
                                  _       A  CCC
GAM665  LOC155032 5'  CCTACCCCACCCAAAGCTGCCT 87592     _      TTC  AGAC
                                AGG AGCTTTGG   GG    AGG
                                ||| ||||||||   ||    |||
                                TCC TCGAAACC   CC    TCC
                                  G       CA_  CCA_
GAM665  LOC157349 5'  CCGTCTCCGGCAGCCCCT    82335    A   TTG  T     A
                                AGG GCT   GT CGGAGAC GG
                                ||| |||   || ||||||| ||
                                TCC CGA   CG GCCTCTG CC
                                  C  ___  _      C
GAM665  LOC157349 5'  CCGTCTCCGGCAGCCCCT    82336    A   TTG  T     A
                                AGG GCT   GT CGGAGAC GG
                                ||| |||   || ||||||| ||
                                TCC CGA   CG GCCTCTG CC
                                  C  ___  _      C
GAM665  LOC199991 3'  CCTGTCCACCCTCAAAGCCCT  91515    A     TTC  A_
                                AGG GCTTTGG   GG  GACAGG
                                ||| |||||||   ||  ||||||
                                TCC CGAAACT   CC  CTGTCC
                                  _     C__  AC
GAM666  AGRP     5'  CTTCATTAGGCCCTGCCATA   24616       A  A
                                TATGGCA GG CCTGATGGAG
                                ||||||| || ||||||||||
                                ATACCGT CC GGATTACTTC
                                    C  _
GAM666  CGTHBA   3'  CTTCCCTCCAGTCCTTGCCG   24890         C  AT  A
                                TGGCAAGGAC TG  GG GAAG
                                |||||||||| ||  || ||||
                                GCCGTTCCTG AC  CC CTTC
                                      _  CT  _
GAM666  COL5A3   3'  CTCCCCAGGCTCACCTTGCCAT 32318         A___   AT
          G                   TATGGCAAGG   CCTG  GGAG
                              ||||||||||   ||||  ||||
                              GTACCGTTCC   GGAC  CCTC
                                    ACTC   C_
GAM666  FGF23    3'  CTTCTCTGGGGTCCCTTCCA  40557    CAA    GA
                              TGG   GGACCT  TGGAGAAG
                              |||   ||||||  ||||||||
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                                ACC  CCTGGG  GTCTCTTC
                                 TTC    __
GAM666  FUT3    3'  CTCCCAGAGACCTTGCCA   5621       AC_  AT
                                TGGCAAGG  CTG  GGAG
                                ||||||||  |||  ||||
                                ACCGTTCC  GAC  CCTC
                                    AGA  __
GAM666  FUT5    3'  CTCCCAGAGACCTTGCCA   10726      AC_  AT
                                TGGCAAGG  CTG  GGAG
                                ||||||||  |||  ||||
                                ACCGTTCC  GAC  CCTC
                                    AGA  __
GAM666  TCF12   3'  TCTCCTATCCTCTTGCCATA  13639       ACCT  _
                                TATGGCAAGG   GAT GGAGA
                                ||||||||||   ||| |||||
                                ATACCGTTCT   CTA CCTCT
                                     C___  T
GAM666  WSX1    3'  CTCCCCCACATCCTTTCCTTGC 17915      CCT  _____
           C                     GGCAAGGA  GAT   GGAG
                                ||||||||  |||   ||||
                                CCGTTCCT  CTA   CCTC
                                    TTC  CACCC
GAM666  ZAP70   3'  CTTCCCCACCCTCAGCCCCACC 71375    CAA  AC   ___  A
           CCA                    TGG  GG  CTGA  TGG GAAG
                                |||  ||  ||||  ||| ||||
                                ACC  CC  GACT  ACC CTTC
                                 CCA  CC   CCC  C
GAM666  C1orf34 3'  CCTCTGGCCATTGCCATA   61303       _  A  T  T
                                TATGGCAA GG CC GA GG
                                |||||||| || || || ||
                                ATACCGTT CC GG CT CC
                                    A  _  T  _
GAM666  CLSTN1  3'  CTCCCCAGAGCACCCCCTGCCA 30787      A  AC____  AT
           T                    ATGGCA GG    CTG  GGAG
                                ||||||  ||    |||  ||||
                                TACCGT CC    GAC  CCTC
                                   C  CCACGA  C_
GAM666  DKFZP434J193 3'  CTTCTCCACCACTCTCCTTGCC 71562        CC_  A
           ATG                    TATGGCAAGGA  TG TGGAGAAG
                                ||||||||||  ||  ||||||||
                                GTACCGTTCCT  AC ACCTCTTC
                                     CTC  C
GAM666  DNAJC6  3'  CTCCAAAGTTCCCACCATA   29492     CAA  C  GA
                                TATGG  GGA CT  TGGAG
                                |||||  ||| ||  |||||
                                ATACC  CCT GA  ACCTC
                                   AC_  T  A_
GAM666  FLJ12122 5'  CTGCCAGCTCAGGTCCCTGCCA 47092     A     __  _
                                TGGCA GGACCTGA  TGG AG
                                ||||| ||||||||  ||| ||
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                                ACCGT CCTGGACT  ACC TC
                                  C       CG   G
GAM666  FLJ14642  3'  CTTCTCCGTAGTCCCCGCC   52575    AA   CTG
                                GGC  GGAC   ATGGAGAAG
                                |||  ||||   |||||||||
                                CCG  CCTG   TGCCTCTTC
                                  CC   A__
GAM666  FLJ20275  3'  CTGTCAGATCCTTGCCAT    35308         C
                                ATGGCAAGGA CTGATGG
                                |||||||||| |||||||
                                TACCGTTCCT GACTGTC
                                      A
GAM666  FLJ21369  3'  CTTCTCCATCAAGTTTCACCA  46051    CAA   C
                                TGG   GGAC TGATGGAGAAG
                                |||   |||| ||||||||||
                                ACC   TTTG ACTACCTCTTC
                                  AC_   A
GAM666  HSPC016   3'  TCTCTATTCCCTGCCATA    32503       A  CCTG
                                TATGGCA GGA    ATGGAGA
                                ||||||| |||    |||||||
                                ATACCGT CCT    TATCTCT
                                    C  _____
GAM666  HT014     3'  CTTCCTAATAAATCCTTGCCA  40153        CC  A   A
                                TGGCAAGGA  TG TGG GAAG
                                |||||||||  || ||| ||||
                                ACCGTTCCT  AT ATC CTTC
                                     AA  A  _
GAM666  KIAA0773  3'  CTTCTCCACGACCTCACC    28722    CA   ACC  A
                                GG  AGG   TG TGGAGAAG
                                ||  |||   || ||||||||
                                CC  TCC   GC ACCTCTTC
                                 AC   A__  _
GAM666  KIAA1493  3'  CTTCTCCACCTAGTCTGCC   64840     AG   CTGA
                                GGCA  GAC    TGGAGAAG
                                ||||  |||    ||||||||
                                CCGT  CTG    ACCTCTTC
                                  __   ATCC
GAM666  KIAA1819  5'  CTTCTCCACGGCTCCCCCA   70252    CAA   C   A
                                TGG   GGA CTG TGGAGAAG
                                |||   ||| ||| ||||||||
                                ACC   CCT GGC ACCTCTTC
                                  C__   C   _
GAM666  LAT1-3TM  3'  CTCCATCAGTGTCATCACCA   49143    CAAG  _
                                TGG    GAC CTGATGGAG
                                |||    ||| |||||||||
                                ACC    CTG GACTACCTC
                                  ACTA   T
GAM666  LAT1-3TM  5'  CTCCATCAGTGTCATTACCA   49144    CAAG  _
                                TGG    GAC CTGATGGAG
                                |||    ||| |||||||||
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                                ACC    CTG GACTACCTC
                                  ATTA   T
GAM666  OS4      3'  CTTCCCCATCATCCCTTCCATT 20389       _   CC___     A
             GCCA                    TGGCAA GGA     TGATGG GAAG
                                |||||| |||    |||||| ||||
                                ACCGTT CCT    ACTACC CTTC
                                   A   TCCCT     C
GAM666  RASSF2   3'  CTTCTCCACCTTCTCTCCA   29097     CA    CCTGA
                                TGG  AGGA    TGGAGAAG
                                |||  ||||    ||||||||
                                ACC  TCTT    ACCTCTTC
                                  TC    CC___
GAM666  SARM     3'  CTCCCCCAGGCCCTGCCAT   31285       A  A    AT
                                ATGGCA GG CCTG  GGAG
                                |||||| || ||||  ||||
                                TACCGT CC GGAC  CCTC
                                   C  _    CC
GAM666  SELB     3'  CTCCCCCAGGGCCTCCTTGCC  62591         ___    AT
                                GGCAAGGA   CCTG  GGAG
                                ||||||||   ||||  ||||
                                CCGTTCCT   GGAC  CCTC
                                     CCG    CC
GAM666  SERPING1  3'  CTTCTCCATGGCCCTGCCATG  5348         A  A  TG
                                TATGGCA GG CC  ATGGAGAAG
                                ||||||| || ||  |||||||||
                                GTACCGT CC GG  TACCTCTTC
                                    C  _  __
GAM666  ZDHHC8   3'  TCCCCACCAACTTCTCTGCC   64622     _    CC  A   A
                                GGCA AGGA  TG TGG GA
                                |||| ||||  || ||| ||
                                CCGT TCTT  AC ACC CT
                                  C    CA  C   C
GAM666  LOC150319 3'  CTTCTCCATCCTCCTGCCAT   80471       A   CCT
                                ATGGCA GGA   GATGGAGAAG
                                |||||| |||   ||||||||||
                                TACCGT CCT   CTACCTCTTC
                                   _   C__
GAM666  LOC197423 5'  CTCCATCAGTGTCATTACCA   78424     CAAG   _
                                TGG    GAC CTGATGGAG
                                |||    ||| |||||||||
                                ACC    CTG GACTACCTC
                                  ATTA   T
GAM666  LOC199923 5'  CTTCTCCACCTCCTGCCA    89871      A   CCTGA
                                TGGCA GGA    TGGAGAAG
                                ||||| |||    ||||||||
                                ACCGT CCT    ACCTCTTC
                                   _   CC___
GAM666  LOC220565 5'  CTCCATCAGTGTCATCACCA   92441     CAAG   _
                                TGG    GAC CTGATGGAG
                                |||    ||| |||||||||
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                                ACC    CTG GACTACCTC
                                  ACTA   T
GAM666  LOC221975 5'  CTTCTCCATGGAGCCTGCC   94192      A  AC  G
                                GGCA GG  CT ATGGAGAAG
                                |||| ||  || |||||||||
                                CCGT CC  GG TACCTCTTC
                                  _  GA  _
GAM666  LOC257239 5'  CTTCTCCACCTCAACCACCA   98844     CAA  ACC  __
                                TGG   GG   TGA  TGGAGAAG
                                |||   ||   |||  ||||||||
                                ACC   CC   ACT  ACCTCTTC
                                  A__  A__   CC
GAM666  LOC90499  3'  CTTCTCCATGGCCCCCTCCA   63741    CAA  A  TG
                                TGG   GG CC  ATGGAGAAG
                                |||   || ||  |||||||||
                                ACC   CC GG  TACCTCTTC
                                  TCC  C  __
GAM667  ABCC1     3'  CCTGGTAAACCAAGCCTCC    39603     _     CGGAGA
                                GGAG CTTGGTT     CAGG
                                |||| |||||||     ||||
                                CCTC GAACCAA     GTCC
                                  C      ATG___
GAM667  ADAM10    5'  CTCCGGACCAAGCCCCTT    8477      A
                                AAGG GCTTGGTTCGGAG
                                |||| ||||||||||||
                                TTCC CGAACCAGGCCTC
                                  C
GAM667  APBA1     3'  CCTCTCTGGAAGGCCCCTT   70474     A   GG      CA
                                AAGG GCTT  TTCGGAGA  GG
                                |||| ||||  ||||||||  ||
                                TTCC CGGA  AGGTCTCT  CC
                                  C   __      __
GAM667  APOC3     3'  GCCTATCCATCCTGCGAGCTCC 5265          GTTC  __  C
          TT                      AAGGAGCTTG    GGA  GA AGGC
                                ||||||||||    |||  || ||||
                                TTCCTCGAGC    CCT  CT TCCG
                                      GT__   AC  A
GAM667  AREG      5'  GCCCGCCGCCCCGAGCTCC   9765          TT   AGACA
                                GGAGCTTGG  CGG    GGC
                                |||||||||  |||    |||
                                CCTCGAGCC  GCC    CCG
                                     CC   GC___
GAM667  EXTL1     5'  GCCTGTCCCTGGCCAAGCCGCC 16737     A_      TC  A
          T                       AGG  GCTTGGT  GG GACAGGC
                                |||  |||||||  || |||||||
                                TCC  CGAACCG  CC CTGTCCG
                                  GC      GT  _
GAM667  FBXL11    3'  CCTGCCTCCCAGCCAGGCTCCT 25514           C    A
                                AGGAGCTTGGTT GGAG CAGG
                                |||||||||||| |||| ||||
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                                TCCTCGGACCGA CCTC GTCC
                                      C    C
GAM667  FPGS     3'  GCCTGTCTCCCCCAACACCC  18267    AGC    TTC
                                GG   TTGG   GGAGACAGGC
                                ||   ||||   ||||||||||
                                CC   AACC   CCTCTGTCCG
                                 CAC    C__
GAM667  LIMK1    3'  CCTGTCTGGTCCATAGCTCC  11330      _   TT GG
                                GGAGCT TGG  C  AGACAGG
                                |||||| |||  |  |||||||
                                CCTCGA ACC  G  TCTGTCC
                                   T   TG __
GAM667  LIMK1    3'  CCTGTCTGGTCCATAGCTCC  34139      _   TT GG
                                GGAGCT TGG  C  AGACAGG
                                |||||| |||  |  |||||||
                                CCTCGA ACC  G  TCTGTCC
                                   T   TG __
GAM667  LZTR1    3'  GCCTGTCACCCAAGGCTCCT  23171        GGTTC  A
                                AGGAGCTT    GG GACAGGC
                                ||||||||    || |||||||
                                TCCTCGGA    CC CTGTCCG
                                     AC___  A
GAM667  MEN1     3'  GCCCCTAGAAACCCAAGCTCCT 56350          __   GG  ACA
                                AGGAGCTTGG  TTC  AG   GGC
                                ||||||||||  |||  ||   |||
                                TCCTCGAACC  AAG  TC   CCG
                                      CA   A_  C__
GAM667  NEUD4    3'  CCTGCCTCTCCGAGCTCCT   17377         TTC    A
                                AGGAGCTTGG   GGAG CAGG
                                ||||||||||   |||| ||||
                                TCCTCGAGCC   TCTC GTCC
                                      ___    C
GAM667  SLC9A1   3'  CCTGTCTGTCCAACCCCTC   70924     CTT    C   __
                                GAG   GGTT GGA  GACAGG
                                |||   |||| |||  ||||||
                                CTC   CCAA CCT  CTGTCC
                                  C__    _   GT
GAM667  TGFB1    5'  GCCTGTCTCCTGAGCCCCC   7256     AGCTT    _
                                GG    GGTTC GGAGACAGGC
                                ||    ||||| ||||||||||
                                CC    CCGAG CCTCTGTCCG
                                 C_____    T
GAM667  DKFZp434J1015 3'  GCCTCCACCTGAAAAGCTCCTT 94210          GG    AGAC
                                AAGGAGCTT  TTCGG    AGGC
                                |||||||||  |||||    ||||
                                TTCCTCGAA  AAGTC    TCCG
                                      __    CACC
GAM667  DKFZP564B1162 3'  CCTGTCTCCCACTCAAACCTCT 49348      C_   _  TC
                                GGAG  TTG GT  GGAGACAGG
                                ||||  ||| ||  |||||||||
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                                TCTC  AAC CA  CCTCTGTCC
                                  CA   T  C_
GAM667  FLJ10743  3'  GCCTGTCTCCTTCCACCTCCTT 37084      CT   TTC
                                AAGGAG  TGG   GGAGACAGGC
                                ||||||  |||   ||||||||||
                                TTCCTC  ACC   CCTCTGTCCG
                                   C_   TT_
GAM667  FLJ23093  3'  GCCTGTCCATGGCACCAGACTC 45326      CT   _   GA
          CT                     AGGAG  TGGT TCG  GACAGGC
                                |||||  |||| |||  |||||||
                                TCCTC  ACCA GGT  CTGTCCG
                                  AG   C   AC
GAM667  FLJ30294  5'  CCTGTCTCCGTACCCCTTC   58896     CTT   T
                                GGAG   GGT CGGAGACAGG
                                ||||   ||| ||||||||||
                                CTTC   CCA GCCTCTGTCC
                                  C__   T
GAM667  IL1F10   3'  GCCCCCAAACCAAGCTC     51762         C  AGACA
                                GAGCTTGGTT GG    GGC
                                ||||||||||  ||    |||
                                CTCGAACCAA CC    CCG
                                     A  C____
GAM667  KIAA0326  3'  GCCCACCTCCCCAAGCTCCTT  64963          TTC    ACA
                                AAGGAGCTTGG   GGAG   GGC
                                ||||||||||   ||||   |||
                                TTCCTCGAACC   CCTC   CCG
                                     ___    CAC
GAM667  KIAA1554  3'  GCCTCCCTGGACAGTTCC    96858       TG     A  CA
                                GGAGCT  GTTCGG GA  GGC
                                ||||||  ||||||  ||  |||
                                CCTTGA  CAGGTC CT  CCG
                                   __     C  __
GAM667  MCF2L    3'  GCCCGTCCCCGCCTGATCTCC  61529      C TG TT   A   A
                                GGAG T  G  CGG GAC GGC
                                ||||  |  |  ||| ||| |||
                                CCTC A  C  GCC CTG CCG
                                  T GT C_   C   C
GAM667  MKRN1    3'  CCTGTCTTCTCAACCCCTC    26494     CTT    C_
                                GAG   GGTT  GGAGACAGG
                                |||   ||||  |||||||||
                                CTC   CCAA  CTTCTGTCC
                                  C__    CT
GAM667  MKRN4    3'  CCTGTCTTGTCAACCCCTC    48460     CTT    CG_
                                GAG   GGTT   GAGACAGG
                                |||   ||||   ||||||||
                                CTC   CCAA   TTCTGTCC
                                  C__    CTG
GAM667  MSTP028  3'  CCTACCTCCCAGGCTCCT    50061         TTCG   AC
                                AGGAGCTTGG   GAG  AGG
                                ||||||||||   |||  |||
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                                TCCTCGGACC   CTC  TCC
                                     ____  CA
GAM667  SYT6    3'  GCCCATCTCCGAAACCACCTCC 79521     CT   _    CA
                                GGAG  TGGTT CGGAGA  GGC
                                ||||  ||||| ||||||  |||
                                CCTC  ACCAA GCCTCT  CCG
                                  C_    A     AC
GAM667  TTYH2   3'  CCTGTCTCCCTAACCCTCC   51976     CTT   C_
                                GGAG   GGTT  GGAGACAGG
                                ||||   ||||  |||||||||
                                CCTC   CCAA  CCTCTGTCC
                                  ___   TC
GAM667  UBXD2   3'  GCCTGCCTCCATCAGCTTCTT  68895       T   TC   A
                                AAGGAGCT GGT  GGAG CAGGC
                                |||||||| |||  |||| |||||
                                TTCTTCGA CTA  CCTC GTCCG
                                    _  __   C
GAM667  LOC145601 3'  GCCTGTCCCCGGAGGCATTCCT 84351      __  TGG   A
          T                      AAGGA  GCT   TTCGG GACAGGC
                                 |||||  |||   ||||| |||||||
                                 TTCCT  CGG   AGGCC CTGTCCG
                                   TA  ___    C
GAM667  LOC148183 3'  CCTGTGCTACAAGCTCCTT   85263        GTTC  AG
                                AAGGAGCTTG   GG  ACAGG
                                ||||||||||   ||  |||||
                                TTCCTCGAAC   TC  TGTCC
                                     A___  G_
GAM667  LOC148354 3'  CCTGTCTCCTCAGCTGCTC   79549     TT   C_
                                GAGC  GGTT  GGAGACAGG
                                ||||  ||||  |||||||||
                                CTCG  TCGA  CCTCTGTCC
                                  __   CT
GAM667  LOC149721 3'  GCCTGTCTCCATGTAGGTTCCT 80318        GTTC
                                AGGAGCTTG   GGAGACAGGC
                                |||||||||   ||||||||||
                                TCCTTGGAT   CCTCTGTCCG
                                     GTA_
GAM667  LOC150378 5'  GCCTGCCCGGTCTCCAGGCTCC 80559        T__   AGA
          T                      AGGAGCTTGG   TCGG   CAGGC
                                 ||||||||||   ||||   |||||
                                 TCCTCGGACC   GGCC   GTCCG
                                      TCT   C__
GAM667  LOC157349 5'  GCCCGTCTCCGGCAGCCCCT   82343    A   TG  T     A
                                AGG GCT  GT CGGAGAC GGC
                                ||| |||  || ||||||| |||
                                TCC CGA  CG GCCTCTG CCG
                                  C  __  _     C
GAM667  LOC157349 5'  GCCCGTCTCCGGCAGCCCCT   82344    A   TG  T     A
                                AGG GCT  GT CGGAGAC GGC
                                ||| |||  || ||||||| |||
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                                TCC CGA  CG GCCTCTG CCG
                                  C  __ _     C
GAM667  LOC157355 3'  CCTGTCTCCCCAGCTCC     82352       T  TTC
                                GGAGCT GG   GGAGACAGG
                                |||||| ||   |||||||||
                                CCTCGA CC   CCTCTGTCC
                                  _ ____
GAM667  LOC165693 5'  CCTGCAATACCAGCTCCTT    83486        T   TCGGAGA
                                AAGGAGCT GGT      CAGG
                                |||||||| |||      ||||
                                TTCCTCGA CCA      GTCC
                                    _  TAAC___
GAM667  LOC221424 5'  GCCTATCGCTCCCAGCTCCTT  95274        T  TTC  A  C
                                AAGGAGCT GG   GG GA AGGC
                                |||||||| ||   || || ||||
                                TTCCTCGA CC   TC CT TCCG
                                    C  ___  G  A
GAM667  LOC221495 3'  CCTGCCTGGCCAAATTCC    95494     C    TC  AGA
                                GGAG TTGGT  GG   CAGG
                                |||| |||||  ||   ||||
                                CCTT AACCG  CC   GTCC
                                  A    GT  ___
GAM667  LOC254826 5'  GCCTGTCTCCAGCTCTGCGCCT 99050     A  TT    C
                                AGG GC  GGTT GGAGACAGGC
                                ||| ||  |||| ||||||||||
                                TCC CG  TCGA CCTCTGTCCG
                                  G  TC   _
GAM668  AGRP     5'  CTTCATTAGGCCCTGCCATA   24616       A  A
                                TATGGCA GG CCTGATGGAG
                                ||||||| || ||||||||||
                                ATACCGT CC GGATTACTTC
                                    C  _
GAM668  CGTHBA    3'  CTTCCCTCCAGTCCTTGCCG   24890         C  AT  A
                                TGGCAAGGAC TG  GG GAAG
                                |||||||||| ||  || ||||
                                GCCGTTCCTG AC  CC CTTC
                                    _  CT  _
GAM668  COL5A3    3'  CTCCCCAGGCTCACCTTGCCAT 32318         A___    AT
          G                   TATGGCAAGG    CCTG  GGAG
                              ||||||||||    ||||  ||||
                              GTACCGTTCC    GGAC  CCTC
                                  ACTC    C_
GAM668  FGF23    3'  CTTCTCTGGGGTCCCTTCCA  40557     CAA     GA
                                TGG   GGACCT  TGGAGAAG
                                |||   ||||||  ||||||||
                                ACC   CCTGGG  GTCTCTTC
                                  TTC     __
GAM668  FUT3     3'  CTCCCAGAGACCTTGCCA    5621         AC_   AT
                                TGGCAAGG   CTG  GGAG
                                ||||||||   |||  ||||
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                                ACCGTTCC  GAC  CCTC
                                   AGA  __
GAM668  FUT5     3'  CTCCCAGAGACCTTGCCA   10726       AC_  AT
                                TGGCAAGG  CTG  GGAG
                                ||||||||  |||  ||||
                                ACCGTTCC  GAC  CCTC
                                   AGA  __
GAM668  TCF12    3'  TCTCCTATCCTCTTGCCATA  13639        ACCT  _
                                TATGGCAAGG   GAT GGAGA
                                ||||||||||   ||| |||||
                                ATACCGTTCT   CTA CCTCT
                                     C___  T
GAM668  WSX1     3'  CTCCCCCACATCCTTTCCTTGC 17915       CCT  _____
           C                     GGCAAGGA  GAT   GGAG
                                ||||||||  |||   ||||
                                CCGTTCCT  CTA   CCTC
                                   TTC  CACCC
GAM668  ZAP70    3'  CTTCCCCACCCTCAGCCCCACC 71375    CAA  AC  ___  A
           CCA                    TGG  GG  CTGA  TGG GAAG
                                |||  ||  ||||  ||| ||||
                                ACC  CC  GACT  ACC CTTC
                                 CCA  CC   CCC  C
GAM668  C1orf34  3'  CCTCTGGCCATTGCCATA   61303       _  A  T  T
                                TATGGCAA GG CC GA GG
                                |||||||| || || || ||
                                ATACCGTT CC GG CT CC
                                   A  _  T  _
GAM668  CLSTN1   3'  CTCCCCAGAGCACCCCCTGCCA 30787      A  AC____  AT
           T                    ATGGCA GG    CTG  GGAG
                                ||||||  ||     |||  ||||
                                TACCGT CC     GAC  CCTC
                                   C  CCACGA  C_
GAM668  DKFZP434J193 3'  CTTCTCCACCACTCTCCTTGCC 71562         CC_  A
           ATG                    TATGGCAAGGA  TG TGGAGAAG
                                ||||||||||  ||  ||||||||
                                GTACCGTTCCT  AC ACCTCTTC
                                      CTC  C
GAM668  DNAJC6   3'  CTCCAAAGTTCCCACCATA   29492     CAA  C  GA
                                TATGG  GGA CT  TGGAG
                                |||||  ||| ||  |||||
                                ATACC  CCT GA  ACCTC
                                   AC_  T  A_
GAM668  FLJ12122 5'  CTGCCAGCTCAGGTCCCTGCCA 47092     A     __  _
                                TGGCA GGACCTGA  TGG AG
                                ||||| ||||||||  ||| ||
                                ACCGT CCTGGACT  ACC TC
                                   C      CG  G
GAM668  FLJ14642 3'  CTTCTCCGTAGTCCCCGCC   52575    AA   CTG
                                GGC  GGAC  ATGGAGAAG
                                |||  ||||  |||||||||
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                                CCG  CCTG   TGCCTCTTC
                                  CC    A__
GAM668  FLJ20275  3'  CTGTCAGATCCTTGCCAT    35308          C
                                ATGGCAAGGA CTGATGG
                                |||||||||| |||||||
                                TACCGTTCCT GACTGTC
                                     A
GAM668  FLJ21369  3'  CTTCTCCATCAAGTTTCACCA  46051     CAA    C
                                TGG   GGAC TGATGGAGAAG
                                |||   |||| ||||||||||
                                ACC   TTTG ACTACCTCTTC
                                  AC_    A
GAM668  HSPC016   3'  TCTCTATTCCCTGCCATA    32503       A   CCTG
                                TATGGCA GGA    ATGGAGA
                                ||||||| |||    |||||||
                                ATACCGT CCT    TATCTCT
                                    C  ____
GAM668  HT014     3'  CTTCCTAATAAATCCTTGCCA 40153         CC  A   A
                                TGGCAAGGA  TG TGG GAAG
                                |||||||||  || ||| ||||
                                ACCGTTCCT  AT ATC CTTC
                                     AA  A  _
GAM668  KIAA0773  3'  CTTCTCCACGACCTCACC    28722    CA   ACC  A
                                GG  AGG   TG TGGAGAAG
                                ||  |||   || ||||||||
                                CC  TCC   GC ACCTCTTC
                                 AC   A__  _
GAM668  KIAA1348  3'  CTTCTTAGGTCTTGCCA     69122        G     T
                                TGGCAAG ACCTGA GGAG
                                ||||||| |||||| ||||
                                ACCGTTC TGGATT CTTC
                                    _     _
GAM668  KIAA1493  3'  CTTCTCCACCTAGTCTGCC   64840      AG   CTGA
                                GGCA  GAC    TGGAGAAG
                                ||||  |||    ||||||||
                                CCGT  CTG    ACCTCTTC
                                  __   ATCC
GAM668  KIAA1819  5'  CTTCTCCACGGCTCCCCCA   70252     CAA   C   A
                                TGG   GGA CTG TGGAGAAG
                                |||   ||| ||| ||||||||
                                ACC   CCT GGC ACCTCTTC
                                  C__   C   _
GAM668  LAT1-3TM  5'  CTCCATCAGTGTCATTACCA   69156     CAAG   _
                                TGG    GAC CTGATGGAG
                                |||    ||| |||||||||
                                ACC    CTG GACTACCTC
                                  ATTA   T
GAM668  LAT1-3TM  3'  CTCCATCAGTGTCATCACCA   49143     CAAG   _
                                TGG    GAC CTGATGGAG
                                |||    ||| |||||||||
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                                ACC   CTG GACTACCTC
                                  ACTA  T
GAM668  OS4     3'  CTTCCCCATCATCCCTTCCATT 20389      _  CC___    A
            GCCA                  TGGCAA GGA    TGATGG GAAG
                                |||||| |||    |||||| ||||
                                ACCGTT CCT    ACTACC CTTC
                                   A  TCCCT    C
GAM668  RASSF2  3'  CTTCTCCACCTTCTCTCCA  29097    CA   CCTGA
                                TGG  AGGA    TGGAGAAG
                                |||  ||||    ||||||||
                                ACC  TCTT    ACCTCTTC
                                  TC   CC___
GAM668  SARM    3'  CTCCCCCAGGCCCTGCCAT   31285      A  A   AT
                                ATGGCA GG CCTG  GGAG
                                |||||| || ||||  ||||
                                TACCGT CC GGAC  CCTC
                                   C  _   CC
GAM668  SELB    3'  CTCCCCCAGGGCCTCCTTGCC  62591       ___   AT
                                GGCAAGGA   CCTG  GGAG
                                ||||||||   ||||  ||||
                                CCGTTCCT   GGAC  CCTC
                                     CCG   CC
GAM668  SERPING1  3'  CTTCTCCATGGCCCTGCCATG  5348       A  A  TG
                                TATGGCA GG CC  ATGGAGAAG
                                ||||||| || ||  |||||||||
                                GTACCGT CC GG  TACCTCTTC
                                    C  _  __
GAM668  SLIT1   3'  TCTCCGGAAGTCCTTGC    13233       C GA
                                GCAAGGAC T  TGGAGA
                                |||||||| |  ||||||
                                CGTTCCTG A  GCCTCT
                                     _ AG
GAM668  ZDHHC8   3'  TCCCCACCAACTTCTCTGCC   64622    _   CC  A   A
                                GGCA AGGA  TG TGG GA
                                |||| ||||  || ||| ||
                                CCGT TCTT  AC ACC CT
                                  C   CA  C   C
GAM668  LOC142946 3'  CCATGGTCCTTGCCATA    83783          TG
                                TATGGCAAGGACC  ATGG
                                ||||||||||||  ||||
                                ATACCGTTCCTGG  TACC
                                          __
GAM668  LOC150319 3'  CTTCTCCATCCTCCTGCCAT   80471      A   CCT
                                ATGGCA GGA   GATGGAGAAG
                                ||||||  |||   ||||||||||
                                TACCGT CCT   CTACCTCTTC
                                   _   C__
GAM668  LOC197423 5'  CTCCATCAGTGTCATTACCA   78424    CAAG   _
                                TGG    GAC CTGATGGAG
                                |||    ||| |||||||||
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                                ACC    CTG GACTACCTC
                                  ATTA   T
GAM668  LOC199923 5'  CTTCTCCACCTCCTGCCA    89871      A   CCTGA
                                TGGCA GGA    TGGAGAAG
                                ||||| |||    ||||||||
                                ACCGT CCT    ACCTCTTC
                                  _  CC___
GAM668  LOC206657 5'  CTTCTCAGTCTTGCCA     91105       AC    T
                                TGGCAAGG  CTGA GGAG
                                ||||||||  |||| ||||
                                ACCGTTCT  GACT CTTC
                                    __   _
GAM668  LOC220565 5'  CTCCATCAGTGTCATCACCA  92441     CAAG  _
                                TGG    GAC CTGATGGAG
                                |||    ||| |||||||||
                                ACC    CTG GACTACCTC
                                  ACTA   T
GAM668  LOC221975 5'  CTTCTCCATGGAGCCTGCC   94192     A  AC  G
                                GGCA GG  CT ATGGAGAAG
                                |||| ||  || |||||||||
                                CCGT CC  GG TACCTCTTC
                                  _ GA  _
GAM668  LOC257239 5'  CTTCTCCACCTCAACCACCA  98844     CAA  ACC  __
                                TGG   GG   TGA  TGGAGAAG
                                |||   ||   |||  ||||||||
                                ACC   CC   ACT  ACCTCTTC
                                  A__  A__   CC
GAM668  LOC90499  3'  CTTCTCCATGGCCCCCTCCA  63741    CAA  A  TG
                                TGG   GG CC  ATGGAGAAG
                                |||   || ||  |||||||||
                                ACC   CC GG  TACCTCTTC
                                  TCC  C  __
GAM669  DNA2L     3'  TTGACTTTGAGCTTTA     92951       CTA
                                TAAAGC   CAAAGTTAA
                                ||||||   |||||||||
                                ATTTCG   GTTTCAGTT
                                   A__
GAM669  FZD7      3'  TTTGTTTTGTTGGCTTTA    14507       T     TT
                                TAAAGCC ACAAAG  AA
                                ||||||| ||||||  ||
                                ATTTCGG TGTTTT  TT
                                    T     GT
GAM669  HIVEP2    3'  AGCATTTGTAGGTCCAGA    23072     AAA       _
                                TCT   GCCTACAAA GTT
                                |||   ||||||||| |||
                                AGA   TGGATGTTT CGA
                                  CC_       A
GAM669  MTMR8     3'  TTGAAGTGAAGGCTTTAGA   31920         A  AAG
                                TCTAAAGCCT CA   TTAA
                                |||||||||| ||   ||||
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                                AGATTTCGGA GT   AGTT
                                      A  GA_
GAM669  CAMKK2   5' GTTAACTAGAGGGCTTTG    22627        ACAA
                                TAAAGCCT    AGTTAAC
                                ||||||||    |||||||
                                GTTTCGGG    TCAATTG
                                    AGA_
GAM669  DKFZP434N093 3' GGTACTTGATGTAGGCTCTA   80744    A      __    TA
                                TA AGCCTACA  AAGT  ACC
                                || ||||||||  ||||  |||
                                AT TCGGATGT  TTCA  TGG
                                 C       AG   __
GAM669  FAM8A1   3' GTTAATTTAGGCGTCTAGA   33202     AA_    CAA
                                TCTA   GCCTA   AGTTAAC
                                ||||   |||||   |||||||
                                AGAT   CGGAT   TTAATTG
                                  CTG    ___
GAM669  FLJ20034  3' AACTTTAAAATAGGCTTTTGA  34828    T      C___
                                TC AAAGCCTA    AAAGTT
                                || ||||||||    ||||||
                                AG TTTCGGAT    TTTCAA
                                 T       AAAA
GAM669  FLJ20051  3' GGCATACTTTGTAGACTTTG   39364      C       TAA
                                TAAAG CTACAAAGT   CC
                                ||||| |||||||||   ||
                                GTTTC GATGTTTCA   GG
                                   A        TAC
GAM669  FLJ20086  3' GGTGCTGTTGTAGGTTCAGA   35013     AA       _   TA
                                TCT  AGCCTACAA AGT  ACC
                                |||  ||||||||| |||  |||
                                AGA  TTGGATGTT TCG  TGG
                                  C_       G   __
GAM669  FLJ21240  3' GTTGGGTGCAGGTTTTAGA   46267         A  AAGT
                                TCTAAAGCCT CA    TAAC
                                |||||||||| ||    ||||
                                AGATTTTGGA GT    GTTG
                                      C  GG__
GAM669  KIAA0889  3' GTTAACTTTGCAGAAAGGGA   31784     AAAGC  A
                                TCT    CT CAAAGTTAAC
                                |||    || ||||||||||
                                AGG    GA GTTTCAATTG
                                  GAAA_  C
GAM669  KIAA0982  3' GGTTATAAACAGGTTTTAGA   26711         ACAAAGT
                                TCTAAAGCCT      TAACC
                                ||||||||||      |||||
                                AGATTTTGGA      ATTGG
                                      CAAAT__
GAM669  KIAA1018  3' GACTTTGTGGGCCTCAGA    31057     AAA
                                TCT   GCCTACAAAGTT
                                |||   ||||||||||||
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                                AGA  CGGGTGTTTCAG
                                  CTC
GAM669  KIAA1495  3'  AATTTTGGCTTTAGA      73563        TAC
                                TCTAAAGCC  AAAGTT
                                |||||||||  ||||||
                                AGATTTCGG  TTTTAA
                                     ___
GAM669  KIAA1951  5'  GGTGTGTGTAGGCTTCAGA   74163    A      AAGTTA
                                TCT AAGCCTACA    ACC
                                ||| |||||||||    |||
                                AGA TTCGGATGT    TGG
                                  C       GTG___
GAM669  MGC12837  3'  GGTTGGTATGCTGGCTTTAGA  52172        TA  AAG
                                TCTAAAGCC  CA  TTAACC
                                |||||||||  ||  ||||||
                                AGATTTCGG  GT  GGTTGG
                                     TC  AT_
GAM669  PIP5K2B   3'  TTAACTTTGTAATTTATGGA   57702    A  CC
                                TCTA AG  TACAAAGTTAA
                                ||||  ||  ||||||||||
                                AGGT TT  ATGTTTCAATT
                                  A  TA
GAM669  PRO2000   5'  AGTTTTGCAGGCTTTGGA    26916        A   GT
                                TCTAAAGCCT CAAA  T
                                |||||||||| ||||  |
                                AGGTTTCGGA GTTT  A
                                     C   TG
GAM669  SIPL      3'  GTTAACTTCATGTTTTGGA   37389       CTACA
                                TCTAAAGC    AAGTTAAC
                                ||||||||    ||||||||
                                AGGTTTTG    TTCAATTG
                                    TAC__
GAM669  LOC153205 3'  GACTTTATTAGGCTTTAGA   87158         C_
                                TCTAAAGCCTA  AAAGTT
                                ||||||||||  ||||||
                                AGATTTCGGAT  TTTCAG
                                     TA
GAM669  LOC166741 5'  GACTTTGGAGGCTTCAGA    88615    A    A
                                TCT AAGCCT CAAAGTT
                                ||| |||||| |||||||
                                AGA TTCGGA GTTTCAG
                                  C     G
GAM669  LOC197319 3'  GTTCTGCGTAGGCTTTA     89327        AA  TT
                                TAAAGCCTAC  AG  AAC
                                ||||||||||  ||  |||
                                ATTTCGGATG  TC  TTG
                                     CG  __
GAM669  LOC221560 3'  AATGGTGTGGGCTTCAGA    95411    A      AA
                                TCT AAGCCTACA  GTT
                                ||| |||||||||  |||
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                                AGA TTCGGGTGT  TAA
                                  C        GG
GAM669  LOC253664 3'  GTTACTCTCATGGCTTTAGA   96472         TACAA   T
                                TCTAAAGCC     AGT AAC
                                |||||||||     ||| |||
                                AGATTTCGG     TCA TTG
                                     TACTC  _
GAM669  LOC253782 3'  GGTTAACCTTGTAGGTTGCAGA 97402     AA        A
                                TCT  AGCCTACAA GTTAACC
                                |||  ||||||||| |||||||
                                AGA  TTGGATGTT CAATTGG
                                  CG        C
GAM669  LOC257535 3'  AATGGTGTGGGCTTCAGA    99617     A        AA
                                TCT AAGCCTACA  GTT
                                ||| |||||||||  |||
                                AGA TTCGGGTGT  TAA
                                  C        GG
GAM669  LOC257595 3'  AATGGTGTGGGCTTCAGA    99798     A        AA
                                TCT AAGCCTACA  GTT
                                ||| |||||||||  |||
                                AGA TTCGGGTGT  TAA
                                  C        GG
GAM669  LOC90072  3'  GTTAACTTTGCAGAAAGGGA   61962     AAAGC  A
                                TCT    CT CAAAGTTAAC
                                |||    || ||||||||||
                                AGG    GA GTTTCAATTG
                                  GAAA_  C
GAM669  LOC90750  3'  GGCTTCGCATAGGCTTTAGA   64631          CA__
                                TCTAAAGCCTA    AAGTT
                                ||||||||||    |||||
                                AGATTTCGGAT    TTCGG
                                       ACGC
GAM670  ENTPD5    3'  TCGCATTTCAACCCTTTGA    8810         CC__    A
                                TCAAAGGG    AATG TGA
                                ||||||||    |||| |||
                                AGTTTCCC    TTAC GCT
                                     AACT   _
GAM670  IL4R      3'  AAGGTGATTGGCCCCACTGA   6455      AA_       GATG
                                TCA   GGGCCAAT    ACCTT
                                |||   ||||||||    |||||
                                AGT   CCCGGTTA    TGGAA
                                  CAC       G___
GAM670  MGST2     5'  AAGGTCATTCAGCCGCTTGA   11576     AG   CAAT
                                TCAA  GGC    GATGACCTT
                                ||||  |||    |||||||||
                                AGTT  CCG    TTACTGGAA
                                  CG   AC__
GAM670  SHANK2    3'  AAGGTCACACTTGACCCTTTGA 25520         C   _  A
                                TCAAAGGG CAA TG TGACCTT
                                ||||||| ||| || |||||||
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                                AGTTTCCC GTT AC ACTGGAA
                                     A   C  _
GAM670  TUFT1    3'  AAGGCACTGCAGCCCTTTGG   39662         CAATGA  A
                                TCAAAGGGC     TG CCTT
                                |||||||||     || ||||
                                GGTTTCCCG     AC GGAA
                                     ACGTC_  _
GAM670  VDR      3'  AAGGTCATCATCGATTCT    6333       CCA
                                AGGG   ATGATGACCTT
                                ||||   ||||||||||
                                TCTT   TACTACTGGAA
                                  AGC
GAM670  C16orf5  3'  AAGGAACTTGTCCCTTTGA   26346        C   TGATGA
                                TCAAAGGG CAA     CCTT
                                |||||||| |||     ||||
                                AGTTTCCC GTT     GGAA
                                     T   CAA___
GAM670  CGI-85   3'  AAGGTCATCATATGTTTT    32627      CA
                                AGGGC  ATGATGACCTT
                                |||||  ||||||||||
                                TTTTG  TACTACTGGAA
                                   TA
GAM670  CSMD1    5'  AAGGTCATCAAGCTTGCCTTT  53785       CAA__
                                AAGGGC    TGATGACCTT
                                ||||||    ||||||||||
                                TTTCCG    ACTACTGGAA
                                    TTCGA
GAM670  DKFZP564A1164 3'  GGCAGGTAGGCCCTTTGA    71537         A  GA  A
                                TCAAAGGGCC AT  TG CC
                                |||||||||| ||  || ||
                                AGTTTCCCGG TG  AC GG
                                     A  G_  _
GAM670  DNCH1    3'  AAGGCCAATGGCGTGGCTCCTT 67863        _   ATGA__  A
           TGA                    TCAAAGG GCCA     TG CCTT
                                |||||||| ||||     || ||||
                                AGTTTCC CGGT     AC GGAA
                                     T    GCGGTA  C
GAM670  FLJ10996 5'  AAGGCTTATCACCCTTTGA   39302        CCAA     _
                                TCAAAGGG    TGATGA CCTT
                                ||||||||    |||||| ||||
                                AGTTTCCC    ACTATT GGAA
                                     _____      C
GAM670  FLJ14708 3'  GGGTCATCTTGGCCCTCTGA   52608     A       T
                                TCA AGGGCCAA GATGACCT
                                ||| |||||||| ||||||||
                                AGT TCCCGGTT CTACTGGG
                                  C       _
GAM670  FLJ21432 3'  AAGAACAGTATTAATCCCTTTG 44937         CC_    A  AC
           A                     TCAAAGGG   AATG TG  CTT
                                |||||||||   |||| ||  |||
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                                AGTTTCCC   TTAT AC  GAA
                                     TAA    G  AA
GAM670  MGC11349  3'  AAGACCAGCGTAGCCCTTTTGA 47787      _   CA   A  AC
                                TCAAA GGGC  ATG TG  CTT
                                ||||| ||||  ||| ||  |||
                                AGTTT CCCG  TGC AC  GAA
                                   T   A_  G  CA
GAM670  MGC27044  3'  AAGGCATTAAGTTGGCCTCCTG 59333     AA      __   A
          A                      TCA  GGGCCAAT  GATG CCTT
                                ||| ||||||||  |||| ||||
                                AGT  TCCGGTTG  TTAC GGAA
                                  CC       AA   _
GAM670  PHRET1    3'  AAGAGTTATCAGTCCTTTGA   41349        CAA      _
                                TCAAAGGGC   TGATGAC CTT
                                |||||||||   ||||||| |||
                                AGTTTCCTG   ACTATTG GAA
                                     ___      A
GAM670  PP591     5'  AAGGCTGGGGTGGCCCTTGA   48142     A     ATGA GA
                                TCAA GGGCCA    T  CCTT
                                |||| ||||||    |  ||||
                                AGTT CCCGGT    G  GGAA
                                  _     GGG_ TC
GAM670  PTPRT     3'  AAGGTACAGCTTTGGCCCT    56483        TGA  _
                                AGGGCCAA   TG ACCTT
                                ||||||||   || |||||
                                TCCCGGTT   AC TGGAA
                                     TCG  A
GAM670  LOC143188 5'  AAGGTGTGTAGCCTCTTTGA   83788       _  CAA  ATG
                                TCAAAG GGC   TG   ACCTT
                                |||||| |||   ||   |||||
                                AGTTTC CCG   AT   TGGAA
                                   T   ___  GTG
GAM670  LOC149706 5'  AAGGCACAGAATTGGCCCCTTG 85800     A      GA  A_
                                CAA GGGCCAAT  TG  CCTT
                                ||| ||||||||  ||  ||||
                                GTT CCCGGTTA  AC  GGAA
                                  C       AG  AC
GAM670  LOC151568 5'  AAGGTTGTTTGGGCCCCTGA   57490     AA    AAT  TG
                                TCA  GGGCC   GA  ACCTT
                                |||  |||||   ||  |||||
                                AGT  CCCGG   TT  TGGAA
                                  C_    GT_  GT
GAM670  LOC205095 3'  AAGGTCATCACCAGCCCT    92378      CAA
                                AGGGC   TGATGACCTT
                                |||||   ||||||||||
                                TCCCG   ACTACTGGAA
                                   ACC
GAM670  LOC221486 3'  AAGACTGTCATTGCCCCTCCGA 92653    AA   C       AC
                                TC  AGGG CAATGATG  CTT
                                ||  |||| ||||||||  |||
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                                AG  TCCC GTTACTGT  GAA
                                 CC    C       CA
GAM670   LOC221663 5'  GTCATCATTACTGCTTTGA   95468       _  CC
                                TCAAAG GG  AATGATGAC
                                |||||| ||  |||||||||
                                AGTTTC TC  TTACTACTG
                                   G  A_
GAM670   LOC222070 5'  GTCAAATCAGCCCTTTGG    95820         CA  GA
                                TCAAAGGGC  AT  TGAC
                                |||||||||  ||  ||||
                                GGTTTCCCG  TA  ACTG
                                     AC  A_
GAM670   LOC223055 5'  AAGGTCATCTCTCCTTTG    94460        CCAAT
                                CAAAGGG    GATGACCTT
                                |||||||    |||||||||
                                GTTTCCT    CTACTGGAA
                                   CT___
GAM670   LOC253943 3'  AAGGATTCATTAACTCTTTGA  97843         CC    TGA
                                TCAAAGGG  AATGA   CCTT
                                ||||||||  |||||   ||||
                                AGTTTCTC  TTACT   GGAA
                                     AA    TA_
GAM670   LOC254428 3'  AAGGCCATGTGCCCCTTTGA   97191         C  ATG   A
                                TCAAAGGG CA   ATG CCTT
                                |||||||| ||   ||| ||||
                                AGTTTCCC GT   TAC GGAA
                                     C  G__   C
GAM670   LOC255187 5'  AAGGCCTCCCTTGGCTCTCTGA 98973     A       TGATGA
                                TCA AGGGCCAA      CCTT
                                ||| ||||||||      ||||
                                AGT TCTCGGTT      GGAA
                                  C       CCCTCC
GAM670   LOC51099  3'  AAGGTTATTTGTCCCTCTGA   32599     A    C  AT
                                TCA AGGG CA  GATGACCTT
                                ||| |||| ||  |||||||||
                                AGT TCCC GT  TTATTGGAA
                                  C    T  __
GAM670   LOC51295  3'  AAGGCATGAGATGCCCTTTGA  33889         CAATG   A
                                TCAAAGGGC     ATG CCTT
                                |||||||||     ||| ||||
                                AGTTTCCCG     TAC GGAA
                                     TAGAG   _
GAM671   DMBT1     3'  TCTTGGTGTCATATTCCAACTC 16609    A   CA  C       GGT
            A                    C AGT  GA TATGACAT   GGA
                                | |||  || ||||||||   |||
                                A TCA  CT ATACTGTG   TCT
                                 C   AC  T       GT_
GAM671   GSBS      3'  TCATTTTTGTCATCGTCTGACT 92733          T     T_
            TG                     CAAGTCAGAC ATGACA  GGTGG
                                |||||||||| ||||||  |||||
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                                GTTCAGTCTG TACTGT  TTACT
                                      C     TT
GAM671  SCN4A    3'  TCCACCATGCTCTCTCACCTG  6206     A  C   CTAT  _
                                CA GT AGA    GA CATGGTGGA
                                || || |||    || |||||||||
                                GT CA TCT    CT GTACCACCT
                                 C  C  ____  C
GAM671  TNFRSF11A 3'  CCACCATGTTACCCAGCCTG   15190     A  A__
                                CAG CT   TGACATGGTGG
                                ||| ||   ||||||||||
                                GTC GA   ATTGTACCACC
                                  C  CCC
GAM671  VAPB     3'  TCCACCATATCATGGGATTT   17629      AGA     C
                                AAGTC   CTATGA ATGGTGGA
                                |||||   |||||| ||||||||
                                TTTAG   GGTACT TACCACCT
                                   ___     A
GAM671  ABHD2    3'  CCACCATGCACACCTGTCT    23794    T   ACTA  A
                                AG CAG    TG CATGGTGG
                                || |||    || ||||||||
                                TC GTC    AC GTACCACC
                                 T   CAC_  _
GAM671  C12orf2   5'  TCCACCACACGCACCTACAGTC 83687         A____  ACA_
            TGACT                  AGTCAGACT    TG    TGGTGGA
                                |||||||||    ||   |||||||
                                TCAGTCTGA    AC    ACCACCT
                                     CATCC  GCAC
GAM671  DKFZP586I2223 3'  CTGTGACAGCCTGACTTG    31877        ACTA  A
                                CAAGTCAG    TG CATGG
                                ||||||||    || |||||
                                GTTCAGTC    AC GTGTC
                                     CG__  A
GAM671  FENS-1    3'  GTGCCATAATCTGCACTT    40835     _   C    A
                                AAGT CAGA TATG CAT
                                |||| |||| |||| |||
                                TTCA GTCT ATAC GTG
                                  C    A    C
GAM671  FLJ13912  3'  CCACCATGCCAGCCTGACTTG  43179        ACTA  A
                                CAAGTCAG    TG CATGGTGG
                                ||||||||    || ||||||||
                                GTTCAGTC    AC GTACCACC
                                     CG__  C
GAM671  FLJ14855  3'  CTGCCCCACATTCTGACTTG   53763        CT   ACAT  TG
                                CAAGTCAGA  ATG   GG  G
                                |||||||||  |||   ||  |
                                GTTCAGTCT  TAC    CC  C
                                     __  ACC_  GT
GAM671  FLJ21986  3'  CCACCCCTGCACATAAACCTGA 46691        AC_   A_  T_
            CTTG                  CAAGTCAG   TATG  CA  GGTGG
                                ||||||||   ||||  ||  |||||
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                                GTTCAGTC  ATAC  GT  CCACC
                                    CAA   AC  CC
GAM671  GPR9     3'  TTCGCCCACAGTCTGACTT   9488         A  ACAT
                                AAGTCAGACT TG   GGTGGA
                                |||||||||| ||   ||||||
                                TTCAGTCTGA AC   CCGCTT
                                   C ____
GAM671  ITGA10   3'  CCAGACCAGCAGCCTGACTTG  60087       A  A_  ACA
                                CAAGTCAG CT  TG   TGG
                                |||||||| ||  ||   |||
                                GTTCAGTC GA  AC   ACC
                                    C  CG  CAG
GAM671  KIAA1970 3'  CCACATTGAATAGGCCTGACTT 74779       A_   GA  TG
           G                     CAAGTCAG  CTAT  CA  GTGG
                                |||||||| ||||  ||  ||||
                                GTTCAGTC  GATA  GT  CACC
                                    CG   A_  TA
GAM671  WBSCR16  3'  CCACCACGCTCACTGCCTGGCT 96147       ACTA  CA_
           TG                    CAAGTCAG   TGA  TGGTGG
                                |||||||||   |||  ||||||
                                GTTCGGTC   ACT  ACCACC
                                    CGTC  CGC
GAM671  LOC127602 5'  CCACCATGTGATTTCCAAC   75174    CA  CT  G
                                GT  GA  AT ACATGGTGG
                                ||  ||  || |||||||||
                                CA  CT  TA TGTACCACC
                                 AC  T_  G
GAM671  LOC149483 3'  TCACCACAGTTCTGACTTG   80188        CTA  ACA
                                CAAGTCAGA   TG   TGGTGG
                                |||||||||   ||   ||||||
                                GTTCAGTCT   AC   ACCACT
                                    TG_  ___
GAM671  LOC254295 5'  TCCACTGTGCCAGCCCGACTTG 97898       AGACTA  A
                                CAAGTC     TG CATGGTGGA
                                ||||||     || |||||||||
                                GTTCAG     AC GTGTCACCT
                                   CCCG__  C
GAM671  LOC92391  5'  CCACCATGCCAGTTTGA     69680        AT A
                                TCAGACT  G CATGGTGG
                                |||||||  | ||||||||
                                AGTTTGA  C GTACCACC
                                   __ C
GAM672  ITGB2    3'  ACAAGGCCGTCAGGACCC    5797             C
                                GGGTCCTGACGGCCT GT
                                |||||||||||||| ||
                                CCCAGGACTGCCGGA CA
                                      A
GAM672  MGEA5    5'  ACGAGGACAGGACCCTTGGC  25215           ACGG
                                GCCAAGGGTCCTG   CCTCGT
                                ||||||||||||   ||||||
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                                CGGTTCCCAGGAC   GGAGCA
                                      A___
GAM672  SORCS2   3'  ACGAGGCCATCAGCTGCCATGC 40794    CAAG  C_   C
            A                   TGC   GGT  CTGA GGCCTCGT
                                |||   |||  |||| ||||||||
                                ACG   CCG  GACT CCGGAGCA
                                  TA__  TC   A
GAM672  CDC37    5'  ACGAGGCCGCCACCCGAGC   23922    CAA   CCT A
                                GC   GGGT   G CGGCCTCGT
                                ||   ||||   | |||||||||
                                CG   CCCA   C GCCGGAGCA
                                 AG_   ___ C
GAM672  DKFZP566J091 3'  GCTAATGTCAGGACCCTCAGC  48863    CA        ___
                                GC  AGGGTCCTGAC   GGC
                                ||  ||||||||||   |||
                                CG  TCCCAGGACTG   TCG
                                 AC         TAA
GAM672  KIAA0469  3'  GTCCCAGGACCCCTGACA    29995    C  A      AC
                                TG CA GGGTCCTG  GGC
                                || || ||||||||  |||
                                AC GT CCCAGGAC  CTG
                                 A  C       C_
GAM672  KREMEN   3'  ACGAAGACTCAAGACCCTCAGG 50223    A_     C   CGGCC
                                CC  AGGGTC TGA    TCGT
                                ||  |||||| |||    ||||
                                GG  TCCCAG ACT    AGCA
                                 AC     A   CAGA_
GAM672  LRRFIP1   5'  CGAGGCCGCTCCCCGGC     17611     AA   TCCT  _
                                GCC  GGG    GA CGGCCTCG
                                |||  |||    || ||||||||
                                CGG  CCC    CT GCCGGAGC
                                  __   _____  C
GAM672  MGC4342   3'  CGAGGCCGCCACACCGGC    44514     AAG   CC  A
                                GCC   GGT  TG CGGCCTCG
                                |||   |||  || ||||||||
                                CGG   CCA  AC GCCGGAGC
                                  ____   C_  C
GAM672  PTPRU    3'  AGGCCAAGCCCCTTGGCA    20319         TC  GAC
                                TGCCAAGGG  CT   GGCCT
                                |||||||||  ||   |||||
                                ACGGTTCCC  GA   CCGGA
                                     C_  A__
GAM672  LOC149668 5'  ACGAGGCCGCCTGACGCCTCAG 85689     CA   _   CTGA
            CA                    TGC  AGG GTC    CGGCCTCGT
                                |||  ||| |||    |||||||||
                                ACG  TCC CAG    GCCGGAGCA
                                  AC   G   TCC_
GAM672  LOC154834 3'  AGGCCACCAGGCCCTTGGCA   87491         T    AC
                                TGCCAAGGG CCTG  GGCCT
                                ||||||||| ||||  |||||
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                                ACGGTTCCC GGAC  CCGGA
                                      _   CA
GAM672  LOC256107 5'  CGAGATGGGACCCTCGG    98598    A       ACGGC
                                CC AGGGTCCTG    CTCG
                                || |||||||||    ||||
                                GG TCCCAGGGT    GAGC
                                 C       A____
GAM673  APOL1    3'  ACTACAGGCGCCTACCACCATG 14720     TAT  CCA_
                                CATG   GT   GCCTGTAGT
                                ||||   ||   |||||||||
                                GTAC   CA   CGGACATCA
                                  CAC  TCCG
GAM673  BSN      3'  ACTACAGGCCAGGGGATG    14375    G   A_
                                TAT TCC  GCCTGTAGT
                                ||| |||  |||||||||
                                GTA GGG  CGGACATCA
                                  G   AC
GAM673  CASP10   3'  ACTACAGGCATGAAATACTGTG 53236     T   G  CA
                                CACA GTAT TC  GCCTGTAGT
                                |||| |||| ||  |||||||||
                                GTGT CATA AG  CGGACATCA
                                  _   A  TA
GAM673  CASP10   3'  ACTACAGGCATGAAATACTGTG 53237     T   G  CA
                                CACA GTAT TC  GCCTGTAGT
                                |||| |||| ||  |||||||||
                                GTGT CATA AG  CGGACATCA
                                  _   A  TA
GAM673  CSPG4    3'  GGGCTAAACATGCATGTG    10326         CC
                                CACATGTATGT  AGCCT
                                ||||||||||  |||||
                                GTGTACGTACA  TCGGG
                                      AA
GAM673  IARS     3'  CTATCCCCTACACATACATG   10979        CC  CCT
                                CATGTATGT  AG   GTAG
                                |||||||||  ||   ||||
                                GTACATACA  TC   TATC
                                     CA  CCC
GAM673  NCF4     5'  ACACAGGCTGAGACGAGAC   7144     A_   _      A
                                GT  TGTC CAGCCTGT GT
                                ||  |||| |||||||| ||
                                CA  GCAG GTCGGACA CA
                                 GA   A      C
GAM673  PCDHA9   3'  ACTACAGGCGCCTGCCACCATG 49830     TAT  CCA_
                                CATG   GT   GCCTGTAGT
                                ||||   ||   |||||||||
                                GTAC   CG   CGGACATCA
                                  CAC  TCCG
GAM673  RPP30    3'  ACTACAGGCGCTCGCCATGT   22188      TA  TCCA
                                ACATG  TG   GCCTGTAGT
                                |||||  ||   |||||||||
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                                TGTAC  GC    CGGACATCA
                                  C_  TCG_
GAM673  SLC4A1   3'  ACTGAGGACCAAAGATACATGT 6220         GTCCAG_   G
                                ACATGTAT      CCT TAGT
                                ||||||||      ||| ||||
                                TGTACATA      GGA GTCA
                                    GAAACCA   _
GAM673  UGDH     3'  ACTACAGGCACCCGCCACAGTG 13988     A   ATGTCCA
                                CAC TGT      GCCTGTAGT
                                ||| |||      |||||||||
                                GTG ACA      CGGACATCA
                                  _  CCGCCCA
GAM673  ARHGAP10 3'  ACTACAGCCAGAAGAACATATA 40828         _ CAGC__
           T                     ATGTATGT C     CTGTAGT
                                ||||||||  |     |||||||
                                TATATACA G     GACATCA
                                    A AAGACC
GAM673  BIRC4    3'  ACTATAACTGAACACAATGTG  8600       GTA   C   CC
                                CACAT   TGT CAG  TGTAGT
                                |||||   ||| |||  ||||||
                                GTGTA   ACA GTC  ATATCA
                                  AC_   A   A_
GAM673  C11orf17 3'  ACTACAGGCACCCGCCACCATG 40572      TAT  CCA_
                                CATG   GT    GCCTGTAGT
                                ||||   ||    |||||||||
                                GTAC   CG    CGGACATCA
                                  CAC  CCCA
GAM673  CTCF     3'  CAGTGACGGACATGCACGTG   22677     A       AGC_
                                CAC TGTATGTCC    CTG
                                ||| |||||||||    |||
                                GTG ACGTACAGG    GAC
                                  C        CAGT
GAM673  FLJ00060 5'  ACTACAGGCGCCCACCACCATG 61730      TAT  CCA_
                                CATG   GT    GCCTGTAGT
                                ||||   ||    |||||||||
                                GTAC   CA    CGGACATCA
                                  CAC  CCCG
GAM673  FLJ10846 3'  ACTACAGGCACCTGCCACCATG 37282      TAT  CCA_
                                CATG   GT    GCCTGTAGT
                                ||||   ||    |||||||||
                                GTAC   CG    CGGACATCA
                                  CAC  TCCA
GAM673  FLJ12960 3'  ACTACAGGCGCCCGCCACCATG 45288      TAT  CCA_
                                CATG   GT    GCCTGTAGT
                                ||||   ||    |||||||||
                                GTAC   CG    CGGACATCA
                                  CAC  CCCG
GAM673  FLJ20511 3'  ACTACAGGCGCCCGCCACCATG 35763      TAT  CCA_
                                CATG   GT    GCCTGTAGT
                                ||||   ||    |||||||||
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                                GTAC  CG   CGGACATCA
                                  CAC CCCG
GAM673  FLJ21777  3'  ACTACAGGCCCCGAAGCACGT  50830     ATG  CA_
                                ATGT  TC  GCCTGTAGT
                                ||||  ||  |||||||||
                                TGCA  AG  CGGACATCA
                                  CGA CCC
GAM673  GPR107    3'  ACCACAGGCTGCCATAGCA   40911    _  TC      A
                                TGT ATG  CAGCCTGT GT
                                ||| |||  |||||||| ||
                                ACG TAC  GTCGGACA CA
                                  A  C_      C
GAM673  KIAA1924  3'  ACTACAGGCGCCTGCCAACATG 74038      AT  CCA_
                                CATGT  GT   GCCTGTAGT
                                |||||  ||   |||||||||
                                GTACA  CG   CGGACATCA
                                   AC  TCCG
GAM673  NYD-SP29  3'  ACTGGCATGCTGAACATATAT  75077        C   C  _
                                ATGTATGT CAGC TGT AGT
                                |||||||| |||| ||| |||
                                TATATACA GTCG ACG TCA
                                    A   T   G
GAM673  PRDM8     5'  ACTACAGTTTCCTACATGTG   39971        TGTCCAGC
                                CACATGTA      CTGTAGT
                                ||||||||      |||||||
                                GTGTACAT      GACATCA
                                    CCTTT___
GAM673  LOC125228 3'  ACTATGGGCAAAGATACATGTG 74861         GTCCA
                                CACATGTAT    GCCTGTAGT
                                |||||||||    |||||||||
                                GTGTACATA    CGGGTATCA
                                    GAAA_
GAM673  LOC128989 3'  ACTCACATGGCACACACATACA 75306        CCA_  _  _
                                TGTATGT   GCC TGT AGT
                                |||||||   ||| ||| |||
                                ACATACA   CGG ACA TCA
                                    CACA  T  C
GAM673  LOC130074 3'  ACACAGGCTGTGCCCATG    76619     TAT TC      A
                                CATG  G  CAGCCTGT GT
                                ||||  |  |||||||| ||
                                GTAC  C  GTCGGACA CA
                                  C__ GT      C
GAM673  LOC143153 3'  ACTACAGGCCACGGCCACCATG 76975     TAT  CA_
                                CATG  GTC  GCCTGTAGT
                                ||||  |||  |||||||||
                                GTAC  CGG  CGGACATCA
                                  CAC  CAC
GAM673  LOC143154 3'  ACTACAGGCCACGGCCACCATG 76986     TAT  CA_
                                CATG  GTC  GCCTGTAGT
                                ||||  |||  |||||||||
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                                GTAC  CGG  CGGACATCA
                                  CAC  CAC
GAM673  LOC148147 3'  ACTACAGGCCTCCATCACCATG 79382     T__  TCCA
                                CATG  ATG  GCCTGTAGT
                                |||| ||| |||||||||
                                GTAC  TAC  CGGACATCA
                                  CAC  CTC_
GAM673  LOC150596 3'  ACTACAGGATGGATACTTAT  80747    TA    G
                                ATG  TGTCCA CCTGTAGT
                                |||  |||||| ||||||||
                                TAT  ATAGGT GGACATCA
                                  TC    A
GAM673  LOC199699 3'  ACTACAGGCACCCGCCACCATG 89661     TAT  CCA_
                                CATG  GT   GCCTGTAGT
                                |||| ||  |||||||||
                                GTAC  CG   CGGACATCA
                                  CAC  CCCA
GAM673  LOC200382 3'  GGGCCAGACTTACATGTG   90237       T  CA
                                CACATGTA GTC  GCCT
                                |||||||| |||  ||||
                                GTGTACAT CAG  CGGG
                                    T  AC
GAM673  LOC201952 3'  ACCACAGGCCTGGCACATTGTG 91875     TGT  _  _   A
                                CACA  ATGT CCAG CCTGT GT
                                ||||  |||| |||| ||||| ||
                                GTGT  TACA GGTC GGACA CA
                                  ___  C  C   C
GAM673  LOC202908 5'  ACCACAGGCTGGAGTACAGTG  90703    A   G       A
                                CAC TGTAT TCCAGCCTGT GT
                                ||| ||||| |||||||||| ||
                                GTG ACATG AGGTCGGACA CA
                                  _   _       C
GAM673  LOC202908 5'  ACTACAGGCGCCTGCCACCATG 90704     TAT  CCA_
                                CATG  GT   GCCTGTAGT
                                |||| ||  |||||||||
                                GTAC  CG   CGGACATCA
                                  CAC  TCCG
GAM673  LOC203369 3'  ACTACAGGCGCCCGCCACCATG 90878     TAT  CCA_
                                CATG  GT   GCCTGTAGT
                                |||| ||  |||||||||
                                GTAC  CG   CGGACATCA
                                  CAC  CCCG
GAM673  LOC219294 3'  ACTACAGGCCACGGCCACCATG 94592     TAT  CA_
                                CATG  GTC  GCCTGTAGT
                                |||| |||  |||||||||
                                GTAC  CGG  CGGACATCA
                                  CAC  CAC
GAM673  LOC219295 3'  ACTACAGGCCACGGCCACCATG 94583     TAT  CA_
                                CATG  GTC  GCCTGTAGT
                                |||| |||  |||||||||
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                                GTAC  CGG  CGGACATCA
                                  CAC  CAC
GAM673  LOC219731 5'  ACTACAGGCTTGCACTAC   94694    _  CC
                                GTA TGT  AGCCTGTAGT
                                ||| |||  ||||||||||
                                CAT ACG  TCGGACATCA
                                  C  T_
GAM673  LOC220662 3'  ACTACAGGCCCACACTAC   92800    _  CCA
                                GTA TGT  GCCTGTAGT
                                ||| |||  |||||||||
                                CAT ACA  CGGACATCA
                                  C  CC_
GAM673  LOC256905 3'  ACTGCAATAAACATACATGTG  98657         CCAGCC
                                CACATGTATGT    TGTAGT
                                ||||||||||    ||||||
                                GTGTACATACA    ACGTCA
                                      AATA__
GAM673  LOC91115  3'  ACTACAGGCACCCGCCACCATG 65540     TAT  CCA_
                                CATG  GT   GCCTGTAGT
                                ||||  ||   |||||||||
                                GTAC  CG   CGGACATCA
                                  CAC  CCCA
GAM673  LOC91561  5'  ACTACAGGCGCTGGCCACCACA 67037    A_  T  __
                                TGT  TG CCA  GCCTGTAGT
                                |||  || |||  |||||||||
                                ACA  AC GGT  CGGACATCA
                                  CC  C  CG
GAM674  C7orf2    3'  GTACAGTCTAATAAGCTGTGG  42637        CCCCATT
                                CCACAGCTTA     CTGTAC
                                ||||||||||     ||||||
                                GGTGTCGAAT     GACATG
                                     AATCT__
GAM674  CDC27     3'  TACAGAATGAAAGGCAGTG   8834     A   ACCC
                                CAC GCTT   CATTCTGTA
                                ||| ||||   |||||||||
                                GTG CGGA   GTAAGACAT
                                  A   AA__
GAM674  CML66     3'  TGTGGAATGAAGCTGCAGA   68786   CA    ACCC   TG
                                TC  CAGCTT   CATTC  TA
                                ||  ||||||   |||||  ||
                                AG  GTCGAA   GTAAG  GT
                                 AC     ____    GT
GAM674  GCH1      3'  ACAGAATGAACTGACGGTGGA  5677      AGC  CCC
                                TCCAC  TTA  CATTCTGT
                                |||||  |||  ||||||||
                                AGGTG  AGT  GTAAGACA
                                  GC_  CAA
GAM674  LZTR1     5'  TACAGTGACAAGCTGTGGA   23175        ACCCCATT
                                TCCACAGCTT     CTGTA
                                ||||||||||     |||||
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                                AGGTGTCGAA       GACAT
                                      CAGT____
GAM674  MPP5     3'  GCAGCAGTATAAGCTGTAGA  42747    C      CCCC  _
                                TC ACAGCTTA    ATT CTGT
                                || ||||||||    ||| ||||
                                AG TGTCGAAT    TGA GACG
                                 A       A___   C
GAM674  PCDHA9   5'  TGCAGAATAACTGTG       26628      C  CCCCA
                                CACAG TTA     TTCTGTA
                                ||||| |||     |||||||
                                GTGTC AAT     AAGACGT
                                  _  ______
GAM674  PCDHA9   5'  TGCAGAATAACTGTG       49853      C  CCCCA
                                CACAG TTA     TTCTGTA
                                ||||| |||     |||||||
                                GTGTC AAT     AAGACGT
                                  _  ______
GAM674  RHO      3'  ACAGAATGGGGCACACAGTAGG 6766     _  AGCTTA
                                CC AC      CCCCATTCTGT
                                || ||      ||||||||||||
                                GG TG      GGGGTAAGACA
                                 A  ACACAC
GAM674  SCN8A    3'  GCAGAACAGCTGTGGA      27215         TACCCCA
                                TCCACAGCT      TTCTGT
                                |||||||||      ||||||
                                AGGTGTCGA      AAGACG
                                     C_______
GAM674  UPF3B    3'  GCTGGTGGGGTACACTGCAGA  43731    CA   CT       CT
                                TC  CAG  TACCCCATT  GT
                                ||  |||  |||||||||  ||
                                AG  GTC  ATGGGGTGG  CG
                                 AC   AC       T_
GAM674  UPF3B    3'  GCTGGTGGGGTACACTGCAGA  55531    CA   CT       CT
                                TC  CAG  TACCCCATT  GT
                                ||  |||  |||||||||  ||
                                AG  GTC  ATGGGGTGG  CG
                                 AC   AC       T_
GAM674  ANKT     3'  AGAATAGGGTAAGCTGGGA   33453     A        C
                                TCC CAGCTTACCC ATTCT
                                ||| |||||||||| |||||
                                AGG GTCGAATGGG TAAGA
                                  _        A
GAM674  DKFZp434A1520 3'  GCAGGTTGAGGCAAGTGTAGA  61769    C   G   A  C  TT
                                TC ACA CTT CC CA  CTGT
                                || ||| ||| || ||  ||||
                                AG TGT GAA GG GT  GACG
                                 A  _  C  A  TG
GAM674  FLJ10297 3'  GTACAGAGCCAGACAAAGCTGT 36442         ACCCCA_
           G                     CACAGCTT      TTCTGTAC
                                ||||||||      ||||||||
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                                GTGTCGAA      GAGACATG
                                     ACAGACC
GAM674  FLJ21918  3'  GTACAGAACTGAAGCCTCGGA  46861     ACA    ACCCCA
                                TCC   GCTT     TTCTGTAC
                                |||   ||||     ||||||||
                                AGG   CGAA     AAGACATG
                                  CTC    GTC___
GAM674  GABPB2    3'  TACAGAATGAAAGTGCGTAGT  10752     A  T   CC_
                                AC GC TAC   CATTCTGTA
                                || || |||   |||||||||
                                TG TG GTG   GTAAGACAT
                                 A  C   AAA
GAM674  HRK       3'  ACAGAATGGGACTGGG      15069     A   CTTAC
                                CC CAG     CCCATTCTGT
                                || |||     ||||||||||
                                GG GTC     GGGTAAGACA
                                 _   A_____
GAM674  KIAA0140  3'  GCAGGAAGGGACAAGCTGTGGA 28515          AC   A
                                TCCACAGCTT  CCC TTCTGT
                                ||||||||||  ||| ||||||
                                AGGTGTCGAA  GGG AGGACG
                                      CA   A
GAM674  KIAA1023  3'  GGGTGGGGTGAGCTGTGGA   34682
                                TCCACAGCTTACCCCATTC
                                |||||||||||||||||||
                                AGGTGTCGAGTGGGGTGGG

GAM674  KIAA1483  3'  GTACAACATGACAAGCTGTG   70435        ACCC   TC
                                CACAGCTT    CAT  TGTAC
                                ||||||||    |||  |||||
                                GTGTCGAA    GTA  ACATG
                                     CA__    CA
GAM674  LEC3      3'  ACAGCTGGAATAGCTGTGGA   31529         TACC   TT
                                TCCACAGCT    CCA  CTGT
                                |||||||||    |||  ||||
                                AGGTGTCGA    GGT  GACA
                                      TAA_   C_
GAM674  LGALS8    3'  TACAGAATGGCTTCTGTG    22452       CTTACC
                                CACAG     CCATTCTGTA
                                |||||     ||||||||||
                                GTGTC     GGTAAGACAT
                                   TTC___
GAM674  MRG15     3'  ACAGAGGGATATGCTGTAGA  23282     C    T  C   AT
                                TC ACAGC TA CCC  TCTGT
                                || ||||| || |||  |||||
                                AG TGTCG AT GGG  AGACA
                                 A    T  A   __
GAM674  PRO2730   3'  GCAGGAATAGGCTGTG      48183         CCCCA
                                CACAGCTTA    TTCTGT
                                |||||||||    ||||||
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                                GTGTCGGAT    AGGACG
                                     A____
GAM674  QKI      5'  GCGGGCGGAGTGAGCTGCGGA  66049     A       C  AT
                                TCC CAGCTTAC CC  TCTGT
                                ||| |||||||| ||  |||||
                                AGG GTCGAGTG GG  GGGCG
                                  C       A  C_
GAM674  RP4-622L5 3'  TACAGAATGGAGCCGTG     39430     A   TACC
                                CAC GCT    CCATTCTGTA
                                ||| |||    ||||||||||
                                GTG CGA    GGTAAGACAT
                                  C  _____
GAM674  ZNF271    5'  GAATGGGATAAGTGTGGA    96966       G    C
                                TCCACA CTTA CCCATTC
                                |||||| |||| |||||||
                                AGGTGT GAAT GGGTAAG
                                   _   A
GAM674  LOC147172 3'  ACAGGAGGACAAGTTGTGGA   78900          ACC  A
                                TCCACAGCTT   CC TTCTGT
                                ||||||||||   || ||||||
                                AGGTGTTGAA   GG AGGACA
                                     CA_  _
GAM674  LOC150343 5'  TACAGAATGGAAGGTGTATG   80497    GCT   __
                                CA   TACC  CCATTCTGTA
                                ||   ||||  ||||||||||
                                GT   GTGG  GGTAAGACAT
                                 AT_    AA
GAM674  LOC150606 3'  GTACAGAATTTGGAGCTAAGGA 86271     AC    TA  CC
                                TCC  AGCT  CC  ATTCTGTAC
                                |||  ||||  ||  |||||||||
                                AGG  TCGA  GG  TAAGACATG
                                  AA    __  TT
GAM674  LOC154215 3'  ACAGAAACAGCTGTGGA     81951          TACCCCA
                                TCCACAGCT      TTCTGT
                                |||||||||      ||||||
                                AGGTGTCGA      AAGACA
                                     CA_____
GAM675  DIAPH2    3'  ATCTGAGATAAAGTAAACAAGT 24587         CC  CTTCCAG
             GA                   TCACTTGT  AC      CAGAT
                                ||||||||  ||      |||||
                                AGTGAACA  TG      GTCTA
                                     AA  AAATAGA
GAM675  FMO5     5'  GGAAAGGCGGACAGGCGA    9391     A     A   _
                                TC CTTGTCC CCTT CC
                                || ||||||| |||| ||
                                AG GGACAGG GGAA GG
                                 C      C    A
GAM675  ITGA11    3'  ATCTGCCGGCCCCCAGGACAAG 25212          ACCTT_  A
             TGG                    TCACTTGTCC     CC GCAGAT
                                ||||||||||     || ||||||
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                                GGTGAACAGG     GG CGTCTA
                                      ACCCCC  C
GAM675  MBNL     3'  ATCTGCTGAAAGGACAAATG  41066    C     ACC  C
                                CA TTGTCC   TT CAGCAGAT
                                || ||||||   || ||||||||
                                GT AACAGG   AA GTCGTCTA
                                 A     ___  A
GAM675  MYO1E    3'  CTGGTGAGAGGACAAGTGA   18439          AC  _
                                TCACTTGTCC  CTT CCAG
                                ||||||||||  ||| ||||
                                AGTGAACAGG  GAG GGTC
                                      A_   T
GAM675  PMX1     3'  ATCTGCTGGGGGGGAAAAAGT  23562      GTCCA
                                ACTT    CCTTCCAGCAGAT
                                ||||    ||||||||||||
                                TGAA    GGGGGGTCGTCTA
                                  AAA__
GAM675  PMX1     3'  ATCTGCTGGGGGGGAAAAAGT  23563      GTCCA
                                ACTT    CCTTCCAGCAGAT
                                ||||    ||||||||||||
                                TGAA    GGGGGGTCGTCTA
                                  AAA__
GAM675  CGRP-RCP 5'  ATCTGCTGGAAGGTGGACCCTT 27885     CTT
           GG                     TCA   GTCCACCTTCCAGCAGAT
                                ||| ||||||||||||||||||
                                GGT   CAGGTGGAAGGTCGTCTA
                                  TCC
GAM675  DKFZp547I094 3'  CTGCTGGAAAGGAAAAACAG   50557      CCA_   _
                                TTGT    CCTT CCAGCAG
                                ||||    |||| |||||||
                                GACA    GGAA GGTCGTC
                                  AAAA    A
GAM675  DKFZp566O084 3'  ATCTGCTGGCAGAGGACAA    31947       AC  T
                                TTGTCC  CT CCAGCAGAT
                                ||||||  || |||||||||
                                AACAGG  GA GGTCGTCTA
                                   A_  C
GAM675  DKFZp761K1423 3'  ATCTAAACCTTGTAGACAAGTG 37936          C  CTTCCAGC
           A                     TCACTTGTC AC       AGAT
                                |||||||| ||       ||||
                                AGTGAACAG TG       TCTA
                                     A  TTCCAAA_
GAM675  FLJ00001 3'  ATCTGCTGACGGGAACAAGT   82709       CCA   TC
                                ACTTGT   CCT  CAGCAGAT
                                ||||||   |||  ||||||||
                                TGAACA   GGG  GTCGTCTA
                                   A__   CA
GAM675  FLJ14146 3'  GGAAAAGTGAAACAAGTGA   45571         C_  C_
                                TCACTTGT  CAC  TTCC
                                ||||||||  |||  ||||
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                                AGTGAACA  GTG  AAGG
                                    AA   AA
GAM675  FLJ20005  5'  ATCTGAAATAGGAAACAAGTGA 34771        CCA   TCCAG
                                TCACTTGT   CCT    CAGAT
                                ||||||||   |||    |||||
                                AGTGAACA   GGA    GTCTA
                                    AA_   TAAA_
GAM675  FOXO3A    3'  ATCTGCTCTCAGCAAGTGGACA 9380       T     ___  TCC
           GTGA                   TCACT GTCCAC   CT   AGCAGAT
                                |||||  ||||||   ||   |||||||
                                AGTGA CAGGTG   GA   TCGTCTA
                                   _     AAC  CTC
GAM675  KIAA0352  3'  TCTGCTGATTGAACAGTGA   29829      T  C  CCTTC
                                TCACT GT CA    CAGCAGA
                                |||||  ||  ||    |||||||
                                AGTGA CA GT    GTCGTCT
                                   _  A  TA___
GAM675  KIAA1126  5'  ATCTGCTGGACGTGGTGGACAG 72413    A  T     T__
           CGA                    TC CT GTCCACC   TCCAGCAGAT
                                ||  ||  |||||||   ||||||||||
                                AG GA CAGGTGG   AGGTCGTCTA
                                 C  _      TGC
GAM675  MGC4604   3'  ATCTGCTGGAGTGGGGTGGACA 49795     CT       ___
           CATGA                   TCA  TGTCCACCT   TCCAGCAGAT
                                |||  |||||||||   ||||||||||
                                AGT  ACAGGTGGG   AGGTCGTCTA
                                  AC        GTG
GAM675  SYTL2    3'  ATCTGAGTAGGTGGACAA    53077         TCCAG
                                TTGTCCACCT    CAGAT
                                ||||||||||    |||||
                                AACAGGTGGA    GTCTA
                                     TGA__
GAM675  TANK     3'  ATCTGCTGGAATTCCAAACAG  56824      CCACC_
                                TTGT     TTCCAGCAGAT
                                ||||     ||||||||||
                                GACA     AAGGTCGTCTA
                                  AACCTT
GAM675  LOC170063 3'  ATCTACTTTTAGTGATGGCAAG 88597         __  CTTCC  C
           TGA                    TCACTTGTC  CAC    AG AGAT
                                |||||||||  |||    || ||||
                                AGTGAACGG  GTG    TC TCTA
                                     TA   ATTT_  A
GAM675  LOC220980 3'  ATCTGCTGGAAACTTTCAAATG 94765    C   TCCACC
                                CA TTG     TTCCAGCAGAT
                                ||  |||     ||||||||||
                                GT AAC     AAGGTCGTCTA
                                 A   TTTCA_
GAM675  LOC253951 5'  ATCCACTGGAAGGCTGGATGG  99412   TG   _      CA
                                T  TCCA CCTTCCAG  GAT
                                |  ||||  ||||||||  |||
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                                G  AGGT GGAAGGTC  CTA
                                 GT    C       AC
GAM676  HADHB    5'  CTCGCGGACGTCAGCCAAGATT 5738          _ _   A   A
            CCA                    TGGAATCTTG C GGC TCC CGAG
                                ||||||||||  | ||| ||| ||||
                                ACCTTAGAAC G CTG AGG GCTC
                                     C A   C   C
GAM676  BHLHB2   5'  CTCAAAGCCGAAGATTCCA   14763         G   ATCCAC
                                TGGAATCTT CGGC     GAG
                                |||||||||  ||||     |||
                                ACCTTAGAA GCCG     CTC
                                     _   AAA___
GAM676  CPSF1    3'  CGTGGATGCCGTCACCACCA   65160     AATCTT
                                TGG     GCGGCATCCACG
                                |||     ||||||||||||
                                ACC     TGCCGTAGGTGC
                                  ACCAC_
GAM676  DKFZP434K0427 3'  TCTCACAGATGTGCTGTATCC  50500     ATCT      CCAC__
                                GGA    TGCGGCAT     GAGA
                                |||    ||||||||     ||||
                                CCT    ATGTCGTG     CTCT
                                  _____       TAGACA
GAM676  FLJ14166  3'  TCTCGGTTCCGGAAGATTCCA  44992         G   CATCCA
                                TGGAATCTT CGG     CGAGA
                                |||||||||  |||     |||||
                                ACCTTAGAA GCC     GCTCT
                                     G   TTG___
GAM676  FLJ20618  3'  TCTCACAAGGCTGCACCAGATT 35888         __     ATCCAC
            CCA                    TGGAATCT  TGCGGC     GAGA
                                ||||||||  ||||||     ||||
                                ACCTTAGA  ACGTCG     CTCT
                                    CC     GAACA_
GAM676  LOC125988 5'  TCTCAGAGCCGCAAGACACCA  74900     AA       A  CAC
                                TGG  TCTTGCGGC TC   GAGA
                                |||  |||||||||  ||   ||||
                                ACC  AGAACGCCG AG   CTCT
                                  AC        _  A__
GAM676  LOC148697 3'  TCTCGTGGACACCCACATCTCA 79681    GA  CT  C  CA
                                TG  AT  TG GG  TCCACGAGA
                                ||  ||  || ||  |||||||||
                                AC  TA  AC CC  AGGTGCTCT
                                 TC  C_  _  AC
GAM676  LOC195977 3'  GGATGCCGCCCAAGATTCC    88933         __
                                GGAATCTT  GCGGCATCC
                                ||||||||  |||||||||
                                CCTTAGAA  CGCCGTAGG
                                     CC
GAM677  ALDH3A2   5'  CAGCCCGCTGCCAGAGCCGGGG 69796          ATG_   A
            A                      TCCCTGGCTT    AGC GGCTG
                                ||||||||||    ||| |||||
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                                AGGGGCCGAG   TCG CCGAC
                                     ACCG   C
GAM677  CAPNS1   3'  CAGCCTGCCAGGCCAGG     10013       TA  A
                                CCTGGCT  TG GCAGGCTG
                                |||||||  || ||||||||
                                GGACCGG  AC CGTCCGAC
                                   __  _
GAM677  CASP10   3'  CAGCCTGCTTTCACACTAAGGA 53218     C   CTTAT
                                TCC TGG    GAGCAGGCTG
                                ||| |||    ||||||||||
                                AGG ATC    TTCGTCCGAC
                                  A   ACACT
GAM677  DLEC1    3'  TGGCCCCACAAGCCAGG     24723        A  AGCA
                                CCTGGCTT TG   GGCTG
                                |||||||| ||   |||||
                                GGACCGAA AC   CCGGT
                                     C  C___
GAM677  DLEC1    3'  TGGCCCCACAAGCCAGG     24733        A  AGCA
                                CCTGGCTT TG   GGCTG
                                |||||||| ||   |||||
                                GGACCGAA AC   CCGGT
                                     C  C___
GAM677  DYT1     3'  CAGCCCACTCATCGCAGGG   5477       G TT    CA
                                CCCTG C  ATGAG  GGCTG
                                ||||| |  |||||  |||||
                                GGGAC G  TACTC  CCGAC
                                   _ C_    AC
GAM677  LPIN1    5'  CAGCCTGCTGAGAACTAG    67985      C  ATG
                                CTGG TT   AGCAGGCTG
                                ||||  ||   |||||||||
                                GATC AA   TCGTCCGAC
                                   _  GAG
GAM677  RCV1     5'  CAGCCTGCGGCCAGGGG     12801        TATGA
                                TCCCTGGCT    GCAGGCTG
                                |||||||||    ||||||||
                                GGGGACCGG    CGTCCGAC
                                     _____
GAM677  TNXB     5'  CTCAGCCTTGGGCCAAGCCTGG 51634     CT    TA  A ___
             A                   TCC  GGCT  TG GC   AGGCTGAG
                                 |||  ||||  || ||   ||||||||
                                 AGG  CCGA  AC CG   TCCGACTC
                                   T_   __  _  GGT
GAM677  C20orf150 3'  CAGCCTGCCCTCAAGCCAAGGA 66009     C     ATGA
                                TCC TGGCTT    GCAGGCTG
                                ||| ||||||    ||||||||
                                AGG ACCGAA    CGTCCGAC
                                  A     CTCC
GAM677  C20orf39  5'  CAGCCTGCCGGCCAGGCGA   46571    _      TAT A
                                TC CCTGGCT   G GCAGGCTG
                                || |||||||   | ||||||||
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                                AG GGACCGG   C CGTCCGAC
                                 C      ___ _
GAM677  CBX6     3'  CAGCCTGCCTGAAGCAAAGGA  27407     CTG    ATGA
                                TCC   GCTT    GCAGGCTG
                                |||   ||||    ||||||||
                                AGG   CGAA    CGTCCGAC
                                  AAA    GTC_
GAM677  CD84     3'  CTCAGCCTGTAAGCAAAGCAGG 81570      G   A  A__
                                CCTG CTT TG   GCAGGCTGAG
                                |||| ||| ||   ||||||||||
                                GGAC GAA AC   TGTCCGACTC
                                  _   _  GAA
GAM677  CYP2D6   3'  CAGCCTGCTCCTAGCCCAGAGG 5451     _    C   T
                                CC CTGG TTA GAGCAGGCTG
                                || |||| ||| ||||||||||
                                GG GACC GAT CTCGTCCGAC
                                 A    C   C
GAM677  DKFZP586J0619 3'  CTCAGCCTGCCCAGCAGGGA   82317       G  TAT A
                                TCCCTG CT   G GCAGGCTGAG
                                ||||||| ||   | ||||||||||
                                AGGGAC GA   C CGTCCGACTC
                                   _  ____ C
GAM677  FKHL18   3'  CAGCCCTGGTGAGCCAAGGA   80370     C       G  CA
                                TCC TGGCTTAT AG  GGCTG
                                ||| |||||||| ||  |||||
                                AGG ACCGAGTG TC  CCGAC
                                  A       G  __
GAM677  FLJ14800  3'  CAACCTGCTCAGGCACCACAGA 52684    CC   CTTA       C
                                TC  TGG    TGAGCAGG TG
                                ||  |||    |||||||| ||
                                AG  ACC    ACTCGTCC AC
                                 AC   ACGG       A
GAM677  FLJ14957  3'  CTCAGCCCACTCATACCTAGAG 52816    C    CT     CA
           A                     TC CTGG  TATGAG  GGCTGAG
                                || ||||  ||||||  |||||||
                                AG GATC  ATACTC  CCGACTC
                                 A   C_     AC
GAM677  HIC2     3'  CAGCCTGGAGCCAGG       65861          ATGAG
                                CCTGGCTT     CAGGCTG
                                ||||||||     |||||||
                                GGACCGAG     GTCCGAC
                                             _____
GAM677  KIAA1023  3'  CAGGCTCAGAAGCCAGGGA   34677           A    AGG
                                TCCCTGGCTT TGAGC   CTG
                                |||||||||| |||||   |||
                                AGGGACCGAA ACTCG   GAC
                                      G    ___
GAM677  KIAA1655  5'  CTCAGCCCACTCCCAAACCAG  67183      C  AT   CA
                                CTGG TT  GAG  GGCTGAG
                                |||| ||  |||  |||||||
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                                GACC AA  CTC  CCGACTC
                                  A  CC   AC
GAM677  MGC35521  3'  CTCAGGTGTCAGTAAGCCAG  59666        GA   GG
                                CTGGCTTAT  GCA  CTGAG
                                |||||||||  |||  |||||
                                GACCGAATG  TGT  GACTC
                                     AC   G_
GAM677  MGC5508   3'  CAGCCTGCCTCACCAGGGA   44264       CTTA   _
                                TCCCTGG    TGAG CAGGCTG
                                |||||||    |||| |||||||
                                AGGGACC    ACTC GTCCGAC
                                   ____   C
GAM677  PADI1     3'  CAGCCTGCACTGAGTCA     62700       TGA
                                TGGCTTA   GCAGGCTG
                                |||||||   ||||||||
                                ACTGAGT   CGTCCGAC
                                    CA_
GAM677  RIN3      5'  CTCAGCCTGCCTCCCCAAGGGA 46162      _  CTTAT  _
                                TCCCT GG    GAG CAGGCTGAG
                                ||||| ||    ||| |||||||||
                                AGGGA CC    CTC GTCCGACTC
                                   A  C____   C
GAM677  SOX17     3'  CAGCCTGCAGGCCAG       42630       ATGA
                                CTGGCTT    GCAGGCTG
                                |||||||    ||||||||
                                GACCGGA    CGTCCGAC
                                     ____
GAM677  SP140     3'  AGTATCTCATCAGCCAGGGA   24326        T    CAG
                                TCCCTGGCT ATGAG   GCT
                                ||||||||| |||||   |||
                                AGGGACCGA TACTC   TGA
                                     C    TA_
GAM677  VI        3'  CAGCCGCTAGGCCAGGGA    26486         ATG   A
                                TCCCTGGCTT   AGC GGCTG
                                ||||||||||   ||| |||||
                                AGGGACCGGA   TCG CCGAC
                                    ___   _
GAM677  LOC112817 5'  CAGTGGCCACAAGTCAGGGA   57319         A  A  AG
                                TCCCTGGCTT TG GC  GCTG
                                |||||||||| || ||  ||||
                                AGGGACTGAA AC CG  TGAC
                                     C  _  G_
GAM677  LOC129676 5'  CTCAGCCTGCAGACACAGGGA  76232       GCTTATGA
                                TCCCTG       GCAGGCTGAG
                                ||||||       ||||||||||
                                AGGGAC       CGTCCGACTC
                                   ACAGA___
GAM677  LOC134266 3'  CTCAGCCTACCAAGTAGCCAGG 75644        TATGAGC
                                CCTGGCT      AGGCTGAG
                                |||||||      ||||||||
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                                GGACCGA      TCCGACTC
                                    TGAACCA
GAM677  LOC150248 3'  CCACCTCATCAGCCAGGGA   86126         T    CA
                                TCCCTGGCT ATGAG  GG
                                ||||||||| |||||  ||
                                AGGGACCGA TACTC  CC
                                      C    CA
GAM677  LOC155179 3'  CAGGCTCAGAAGCCAGGGA   82225          A    AGG
                                TCCCTGGCTT TGAGC   CTG
                                |||||||||| |||||  |||
                                AGGGACCGAA ACTCG   GAC
                                       G    ___
GAM677  LOC158056 5'  CTCAGCCCAGGAGAGCCAGGGG 82589          ATGAGCA
                                TCCCTGGCTT      GGCTGAG
                                |||||||||       |||||||
                                GGGGACCGAG      CCGACTC
                                       AGGAC__
GAM677  LOC219405 3'  CAGCCTGCTCTACCCAGAGA   92450    C    CTTAT
                                TC CTGG    GAGCAGGCTG
                                || ||||    ||||||||||
                                AG GACC    CTCGTCCGAC
                                 A   CAT__
GAM677  LOC221496 3'  TCAGCCTGCTCCCTGGGA    93643      T  CTTAT
                                TCCC GG    GAGCAGGCTGA
                                |||| ||    ||||||||||
                                AGGG CC    CTCGTCCGACT
                                  T _____
GAM677  LOC222031 3'  CAGCCTGTCTAACCCAAAGA   95672    CC   C   T  G
                                TC  TGG TTA GA CAGGCTG
                                ||  ||| ||| || |||||||
                                AG  ACC AAT CT GTCCGAC
                                 AA   C   _ _
GAM677  LOC51320  3'  CTGCAACTAATAAGCCAAGGA  34028     C       GA___
                                TCC TGGCTTAT    GCAG
                                ||| ||||||||    ||||
                                AGG ACCGAATA    CGTC
                                  A       ATCAA
GAM678  A1BG      3'  AGACAGGGTCTCACTGTGTTGC 56276           A    CA
            C                    GGCAACATGGTGA ACCC  TCT
                                ||||||||||||| ||||  |||
                                CCGTTGTGTCACT TGGG  AGA
                                      C    AC
GAM678  ACADSB    3'  AGATGGGGTTTTACCATATTGC 9642       C
            C                    GGCAA ATGGTGAAACCCCATCT
                                ||||| ||||||||||||||||
                                CCGTT TACCATTTTGGGGTAGA
                                   A
GAM678  ADAMTS4   3'  AGACAGGGTTTCACCATGTTGG 18745     _           CA
            CC                     GGC AACATGGTGAAACCC  TCT
                                ||| ||||||||||||||  |||
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                                CCG TTGTACCACTTTGGG  AGA
                                  G            AC
GAM678  ADAMTS4  3'  AGACGGGGTTTCACCATGTTGG 18748    _           A
             CC                   GGC AACATGGTGAAACCCC TCT
                                  ||| |||||||||||||| |||
                                  CCG TTGTACCACTTTGGGG AGA
                                    G            C
GAM678  ADCY6    5'  AGACGAGGTTTCACCATCTTGG 31584    AAC_        CCA
             CC                   GGC   ATGGTGAAACC   TCT
                                  |||   ||||||||||   |||
                                  CCG   TACCACTTTGG   AGA
                                    GTTC         AGC
GAM678  AIM1     3'  AGATGGGGTTTCATCACGTTGC 93459       A
             C                    GGCAAC TGGTGAAACCCCATCT
                                  |||||| ||||||||||||||||
                                  CCGTTG ACTACTTTGGGGTAGA
                                     C
GAM678  ALDH1B1  3'  AGATGAGGTTTCACCATTTTGG 7313     AAC_        C
             CC                   GGC   ATGGTGAAACC CATCT
                                  |||   |||||||||||| |||||
                                  CCG   TACCACTTTGG GTAGA
                                    GTTT         A
GAM678  ALOX15   3'  AGACGGGGCCTCACTATGTTGC 8540            AA   A
             C                    GGCAACATGGTGA  CCCC TCT
                                  |||||||||||||  ||||| |||
                                  CCGTTGTATCACT  GGGG AGA
                                         CC   C
GAM678  APAF1    3'  AGACAGAGTCTTGCTTTGTTGC 8576         T  TG A  CCCA
             CA                   TGGCAACA GG  A AC   TCT
                                  |||||||| ||  | ||   |||
                                  ACCGTTGT TC  T TG   AGA
                                      T  GT C  AGAC
GAM678  APAF1    3'  AGACGGGGTTTCACCATGTTGG 8577     _           A
             CC                   GGC AACATGGTGAAACCCC TCT
                                  ||| |||||||||||||| |||
                                  CCG TTGTACCACTTTGGGG AGA
                                    G            C
GAM678  APAF1    3'  AGACAGAGTCTTGCTTTGTTGC 25956        T  TG A  CCCA
             CA                   TGGCAACA GG  A AC   TCT
                                  |||||||| ||  | ||   |||
                                  ACCGTTGT TC  T TG   AGA
                                      T  GT C  AGAC
GAM678  APAF1    3'  AGACGGGGTTTCACCATGTTGG 25958    _           A
             CC                   GGC AACATGGTGAAACCCC TCT
                                  ||| |||||||||||||| |||
                                  CCG TTGTACCACTTTGGGG AGA
                                    G            C
GAM678  APM1     3'  AGACAGGGTTTCACCATATTGG 17755    AAC_        CA
             CC                   GGC   ATGGTGAAACCC  TCT
                                  |||   |||||||||||  |||
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                                CCG   TACCACTTTGGG  AGA
                                  GTTA          AC
GAM678  APM1     3'  AGATGGAGTTTCCCTCTGTTGC 17758        T_  T    C
           CA                     TGGCAACA  GG GAAAC CCATCT
                                  ||||||||  || ||||| ||||||
                                  ACCGTTGT  CC CTTTG GGTAGA
                                      CT  _    A
GAM678  APOL1    3'  AGATGGGGTTTCACCATGTTGG 14725     _
           CC                     GGC AACATGGTGAAACCCCATCT
                                  ||| ||||||||||||||||||||
                                  CCG TTGTACCACTTTGGGGTAGA
                                    G
GAM678  APPBP2   3'  AGACGGAGTTTCGCTCTTGTTG 22115        T_       C  A
           CC                     GGCAACA  GGTGAAAC CC TCT
                                  |||||||  |||||||| || |||
                                  CCGTTGT  TCGCTTTG GG AGA
                                      TC       A  C
GAM678  ARCN1    3'  AGACGGGGTTTCACCGTGTTGC 9744                 A
           C                       GGCAACATGGTGAAACCCC TCT
                                  |||||||||||||||||| |||
                                  CCGTTGTGCCACTTTGGGG AGA
                                                C
GAM678  ATM      3'  GGGTTTCACCATATTGCC    57146       C
                                  GGCAA ATGGTGAAACCC
                                  ||||| ||||||||||
                                  CCGTT TACCACTTTGGG
                                    A
GAM678  ATP1B2   3'  AGATGGAGTTTCGCTCTTGTTG 9825         T_       C
           CC                     GGCAACA  GGTGAAAC CCATCT
                                  |||||||  |||||||| ||||||
                                  CCGTTGT  TCGCTTTG GGTAGA
                                      TC       A
GAM678  AXL      3'  AGACAGGGTTTCACCATGTTGG 9898      _           CA
           CC                     GGC AACATGGTGAAACCC  TCT
                                  ||| ||||||||||||||  |||
                                  CCG TTGTACCACTTTGGG  AGA
                                    G             AC
GAM678  AXL      3'  AGACAGGGTTTCACCATGTTGG 41873     _           CA
           CC                     GGC AACATGGTGAAACCC  TCT
                                  ||| ||||||||||||||  |||
                                  CCG TTGTACCACTTTGGG  AGA
                                    G             AC
GAM678  BRIP1    3'  AGATGGGGTTTCACCATGTTGG 50204     _
           CC                     GGC AACATGGTGAAACCCCATCT
                                  ||| ||||||||||||||||||||
                                  CCG TTGTACCACTTTGGGGTAGA
                                    G
GAM678  C14orf1  3'  AGACGGGGTTTCACTCTGTCAC 24162    CA   T         A
           C                       GG  ACA GGTGAAACCCC TCT
                                  ||  ||| |||||||||| |||
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                                CC  TGT TCACTTTGGGG AGA
                                 AC  C         C
GAM678  CAMLG    3'  AGACAGAGTTTCGCTCTTGTTG 9993        T_      CCCA
            CC                    GGCAACA  GGTGAAAC    TCT
                                  |||||||  ||||||||    |||
                                  CCGTTGT  TCGCTTTG    AGA
                                     TC       AGAC
GAM678  CASP10   3'  AGATGGGGTTTCACTATGTTGC 53214
            C                     GGCAACATGGTGAAACCCCATCT
                                  ||||||||||||||||||||||
                                  CCGTTGTATCACTTTGGGGTAGA

GAM678  CASP10   3'  AGATGGGGTTTCACTATGTTGC 53241
            C                     GGCAACATGGTGAAACCCCATCT
                                  ||||||||||||||||||||||
                                  CCGTTGTATCACTTTGGGGTAGA

GAM678  CASP2    3'  AGACAGGGTTTCACCATGTTAG 53284     _          CA
            CC                    GGC AACATGGTGAAACCC  TCT
                                  ||| ||||||||||||||  |||
                                  CCG TTGTACCACTTTGGG  AGA
                                    A            AC
GAM678  CASP2    3'  AGACAGGGTTTCACCATGTTAG 53300     _          CA
            CC                    GGC AACATGGTGAAACCC  TCT
                                  ||| ||||||||||||||  |||
                                  CCG TTGTACCACTTTGGG  AGA
                                    A            AC
GAM678  CASP2    3'  AGACAGGGTTTCACCATGTTAG 53318     _          CA
            CC                    GGC AACATGGTGAAACCC  TCT
                                  ||| ||||||||||||||  |||
                                  CCG TTGTACCACTTTGGG  AGA
                                    A            AC
GAM678  CASP2    3'  AGACAGGGTTTCACCATGTTAG 8703      _          CA
            CC                    GGC AACATGGTGAAACCC  TCT
                                  ||| ||||||||||||||  |||
                                  CCG TTGTACCACTTTGGG  AGA
                                    A            AC
GAM678  CBFB     3'  AGACAGGGTCTCGCAGTGTTGC 10034        G   A   CA
            C                     GGCAACAT GTGA ACCC  TCT
                                  |||||||| |||| ||||  |||
                                  CCGTTGTG CGCT TGGG  AGA
                                     A   C   AC
GAM678  CBFB     3'  AGACAGGGTCTCGCAGTGTTGC 43436        G   A   CA
            C                     GGCAACAT GTGA ACCC  TCT
                                  |||||||| |||| ||||  |||
                                  CCGTTGTG CGCT TGGG  AGA
                                     A   C   AC
GAM678  CCNB1    3'  TGGCACCATGTGCCA      50077      A      AAACC
                                  TGGCA CATGGTG    CCA
                                  ||||| |||||||    |||
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                                ACCGT GTACCAC    GGT
                                  _    _____
GAM678  CCNF    3'  AGACGGGATTTCACCATGTTGG 10064    _         C   A
            CC                    GGC AACATGGTGAAA CCC TCT
                                  ||| |||||||||||| ||| |||
                                  CCG TTGTACCACTTT GGG AGA
                                    G          A   C
GAM678  CDH1    3'  AGATGGGGTCTTGCTATGTTGC 16399          TG A
            C                     GGCAACATGG  A ACCCCATCT
                                  ||||||||||  | |||||||||
                                  CCGTTGTATC  T TGGGGTAGA
                                        GT C
GAM678  CIAS1   5'  AGATGGAGTCTTGCTGTGTCGC 18092    A     TG A  C
            C                     GGC ACATGG  A AC CCATCT
                                  ||| ||||||  | || ||||||
                                  CCG TGTGTC  T TG GGTAGA
                                    C     GT C  A
GAM678  CLECSF12  3'  AGACAGAGTTTCGCTCTTGTTG 77203        T_      CCCA
            CC                    GGCAACA  GGTGAAAC    TCT
                                  |||||||  ||||||||    |||
                                  CCGTTGT  TCGCTTTG    AGA
                                     TC       AGAC
GAM678  CNGA1   5'  AGATGGGATTTCACCATGTTGG 60231    _         C
            CC                    GGC AACATGGTGAAA CCCATCT
                                  ||| |||||||||||| |||||||
                                  CCG TTGTACCACTTT GGGTAGA
                                    G          A
GAM678  COX15   3'  AGACAGAGTTTCACTCTTGTTG 55276        T_      CCCA
            CC                    GGCAACA  GGTGAAAC    TCT
                                  |||||||  ||||||||    |||
                                  CCGTTGT  TCACTTTG    AGA
                                     TC       AGAC
GAM678  CR1     3'  AGACGGGGTTTCACCATGTTAG 6935     _          A
            CC                    GGC AACATGGTGAAACCCC TCT
                                  ||| ||||||||||||||| |||
                                  CCG TTGTACCACTTTGGGG AGA
                                    A            C
GAM678  CTF1    3'  AGACGAGGTTTCGCCATGTTGC 9006             CCA
            C                     GGCAACATGGTGAAACC   TCT
                                  ||||||||||||||||   |||
                                  CCGTTGTACCGCTTTGG   AGA
                                           AGC
GAM678  CXCL16  3'  AGACGGGGTTTCACCATGTTGA 42159    _          A
            CC                    GG CAACATGGTGAAACCCC TCT
                                  || |||||||||||||||| |||
                                  CC GTTGTACCACTTTGGGG AGA
                                   A            C
GAM678  CYP1A2  3'  AGACAGAGTCTTACTCTGTTGC 7495        T    A  CCCA
            CA                    TGGCAACA GGTGA AC    TCT
                                  |||||||| ||||| ||    |||
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                                ACCGTTGT TCATT TG    AGA
                                    C     C  AGAC
GAM678  CYP1A2   3'  AGATGGGGTTTCACCATGTTGG 7500      _
            CC                    GGC AACATGGTGAAACCCCATCT
                                  ||| ||||||||||||||||||||
                                  CCG TTGTACCACTTTGGGGTAGA
                                    G
GAM678  DFFB     3'  AGACGGGGTTTCACCATGTTG  88755              A
                                  CAACATGGTGAAACCCC TCT
                                  |||||||||||||||| |||
                                  GTTGTACCACTTTGGGG AGA
                                             C
GAM678  DFFB     3'  AGATGGAGTTTCACTTTTGTTG 88758        T_       C
            CC                    GGCAACA  GGTGAAAC CCATCT
                                  |||||||  |||||||| ||||||
                                  CCGTTGT  TCACTTTG GGTAGA
                                      TT       A
GAM678  DFFB     3'  GGGGTTTCACCATGTTGGCC   88775     _
                                  GGC AACATGGTGAAACCCC
                                  ||| ||||||||||||||||
                                  CCG TTGTACCACTTTGGGG
                                    G
GAM678  DHFR     3'  AGATGGGGTTTCACCATGTTG  7639
                                  CAACATGGTGAAACCCCATCT
                                  ||||||||||||||||||||
                                  GTTGTACCACTTTGGGGTAGA

GAM678  DISC1    3'  AGACAGGGCTTCACCATGTTG  38498           A   CA
                                  CAACATGGTGAA CCC  TCT
                                  |||||||||||| |||  |||
                                  GTTGTACCACTT GGG  AGA
                                           C   AC
GAM678  DSCR3    3'  AGACAGGGTCTCCCTATGTTGC 21304          T  A    CA
            C                      GGCAACATGG GA ACCC  TCT
                                  |||||||||| || ||||  |||
                                  CCGTTGTATC CT TGGG  AGA
                                         C  C    AC
GAM678  DSCR3    3'  AGACGGGGCTTCACCATCTTGG 21305     AAC_      A    A
            CC                    GGC    ATGGTGAA CCCC TCT
                                  |||    |||||||| |||| |||
                                  CCG    TACCACTT GGGG AGA
                                    GTTC       C    C
GAM678  EHD2     3'  AGACGGGGTTTCACCATGTTGG 28211     _            A
            CC                    GGC AACATGGTGAAACCCC TCT
                                  ||| ||||||||||||||| |||
                                  CCG TTGTACCACTTTGGGG AGA
                                    G             C
GAM678  EPB72    3'  AGACGGGGTTTCACCATGTTGG 15866     _            A
            CC                    GGC AACATGGTGAAACCCC TCT
                                  ||| ||||||||||||||| |||
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                                CCG TTGTACCACTTTGGGG AGA
                                  G             C
GAM678  EPB72    3'  AGATGGAGTTTCACTCTTGTTG 15869        T_      C
                CC                GGCAACA  GGTGAAAC CCATCT
                                  ||||||| |||||||| ||||||
                                  CCGTTGT  TCACTTTG GGTAGA
                                     TC       A
GAM678  F2RL2    3'  AGACGGGGTTTCACCATGTTGA 15891    _             A
                CC                GG CAACATGGTGAAACCCC TCT
                                  || |||||||||||||||| |||
                                  CC GTTGTACCACTTTGGGG AGA
                                   A             C
GAM678  F2RL3    3'  AGACGGAGTTTCACCATGTTGG 15490    _          C  A
                CC                GGC AACATGGTGAAAC CC TCT
                                  ||| |||||||||||| || |||
                                  CCG TTGTACCACTTTG GG AGA
                                    G           A  C
GAM678  F3       3'  AGATGGGGTTTCACCATCTTGG 67671    AAC_
                CC                GGC   ATGGTGAAACCCCATCT
                                  |||   ||||||||||||||||
                                  CCG   TACCACTTTGGGGTAGA
                                    GTTC
GAM678  FABP2    3'  AGATGGGGTCTTGCTATATTGC 5532       C   TG A
                C                  GGCAA ATGG  A ACCCCATCT
                                   ||||| ||||  | |||||||||
                                   CCGTT TATC  T TGGGGTAGA
                                      A   GT C
GAM678  FANCF    3'  AGACGGGGTTTCACCATGCTGG 42971    AA_          A
                CC                GGC   CATGGTGAAACCCC TCT
                                  |||   |||||||||||||| |||
                                  CCG   GTACCACTTTGGGG AGA
                                    GTC           C
GAM678  FCAR     3'  AGACAGGGTTTCACCATGTTGG 56629    _          CA
                CC                GGC AACATGGTGAAACCC  TCT
                                  ||| ||||||||||||||  |||
                                  CCG TTGTACCACTTTGGG  AGA
                                    G             AC
GAM678  FEZ1     3'  AGATGAAGTTTCATTCTATCGC 42865    AACAT      CC
                C                  GGC    GGTGAAAC  CATCT
                                   |||    ||||||||  |||||
                                   CCG    TTACTTTG  GTAGA
                                     CTATC       AA
GAM678  FGF5     3'  AGACGGGGTTTCACCATGTTG  53648             A
                                  CAACATGGTGAAACCCC TCT
                                  |||||||||||||||| |||
                                  GTTGTACCACTTTGGGG AGA
                                             C
GAM678  FGF5     3'  AGACGGGGTTTCACCATGTTG  16755             A
                                  CAACATGGTGAAACCCC TCT
                                  |||||||||||||||| |||
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                                  GTTGTACCACTTTGGGG AGA
                                        C
GAM678  FUT1     3'  AGACAGGGTTTCACCATGTTGG 5578      _          CA
           CC                    GGC AACATGGTGAAACCC  TCT
                                 ||| ||||||||||||||  |||
                                 CCG TTGTACCACTTTGGG  AGA
                                   G            AC
GAM678  G6PC     3'  AGACAGGGTCTCACTATGTTGC 5650           A   CA
           C                     GGCAACATGGTGA ACCC  TCT
                                 |||||||||||| ||||  |||
                                 CCGTTGTATCACT TGGG  AGA
                                       C   AC
GAM678  GHR      3'  AGACGGGGTTTCACCATGTTGG 5689      _          A
           CC                    GGC AACATGGTGAAACCCC TCT
                                 ||| |||||||||||||| |||
                                 CCG TTGTACCACTTTGGGG AGA
                                   G            C
GAM678  GM2A     3'  AGATGGGGTTTCACCATGTTGG 68372     _
           CC                    GGC AACATGGTGAAACCCCATCT
                                 ||| ||||||||||||||||||
                                 CCG TTGTACCACTTTGGGGTAGA
                                   G
GAM678  GPR4     3'  AGACAGGGTCTCACTGTGTTGC 60574          A   CA
           C                     GGCAACATGGTGA ACCC  TCT
                                 |||||||||||| ||||  |||
                                 CCGTTGTGTCACT TGGG  AGA
                                       C   AC
GAM678  GRINL1A  3'  AGATGGGGTCTTGCTCTGTCGC 70058    A  T  TG A
           C                     GGC ACA GG  A ACCCCATCT
                                 ||| ||| ||  | |||||||||
                                 CCG TGT TC  T TGGGGTAGA
                                   C  C  GT C
GAM678  GRM6     3'  AGACGAGGTCTCACTATGTTGC 7757           A  CCA
           C                     GGCAACATGGTGA ACC   TCT
                                 |||||||||||| |||   |||
                                 CCGTTGTATCACT TGG   AGA
                                       C  AGC
GAM678  HMG20A   3'  AGATGAGGTCTTGCTGTGTTGC 37060        TG A  C
           C                     GGCAACATGG  A ACC CATCT
                                 ||||||||||  | ||| |||||
                                 CCGTTGTGTC  T TGG GTAGA
                                     GT C  A
GAM678  HTR1E    5'  AGACGGGATTTCACCATGTTGG 7855      _        C  A
           CC                    GGC AACATGGTGAAA CCC TCT
                                 ||| |||||||||||| ||| |||
                                 CCG TTGTACCACTTT GGG AGA
                                   G          A  C
GAM678  IL11     3'  AGACAGGGTTTCACCATGTTGG 7175      _          CA
           CC                    GGC AACATGGTGAAACCC  TCT
                                 ||| ||||||||||||||  |||
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                                CCG TTGTACCACTTTGGG  AGA
                                  G             AC
GAM678  IMPA2    5'  AGATGGGGCTTCGCCATGCTGC 96942      A        A
                C                  GGCA CATGGTGAA CCCCATCT
                                   |||| ||||||||| ||||||||
                                   CCGT GTACCGCTT GGGGTAGA
                                     C        C
GAM678  INMT     3'  AGACGGAGTTTCGCTCTGTCGC 23205     A   T       C  A
                C                  GGC ACA GGTGAAAC CC TCT
                                   ||| ||| |||||||| || |||
                                   CCG TGT TCGCTTTG GG AGA
                                     C  C       A  C
GAM678  JAK3     3'  AGATGAGGTTTCACCATGATGG 5824      AA_          C
                CC                 GGC   CATGGTGAAACC CATCT
                                   |||   |||||||||||| |||||
                                   CCG   GTACCACTTTGG GTAGA
                                     GTA           A
GAM678  JRK      3'  AGACAGGGTCTCACTGTGTTGC 87814            A    CA
                C                  GGCAACATGGTGA ACCC  TCT
                                   |||||||||||| ||||  |||
                                   CCGTTGTGTCACT TGGG  AGA
                                          C    AC
GAM678  KLRD1    3'  AGACAAGGTCTTGCTATGTTGC 11211          TG A   CCA
                C                  GGCAACATGG  A ACC   TCT
                                   |||||||||  | |||   |||
                                   CCGTTGTATC  T TGG   AGA
                                        GT C   AAC
GAM678  KLRD1    3'  AGACAAGGTCTTGCTATGTTGC 24705          TG A   CCA
                C                  GGCAACATGG  A ACC   TCT
                                   |||||||||  | |||   |||
                                   CCGTTGTATC  T TGG   AGA
                                        GT C   AAC
GAM678  LLGL1    3'  AGATGGGGTTTCACCATGTTAG 67413     _
                CC                 GGC AACATGGTGAAACCCCATCT
                                   ||| ||||||||||||||||||
                                   CCG TTGTACCACTTTGGGGTAGA
                                     A
GAM678  LNK      3'  AGACAGGGTTTCACCATGTTGG 19629     _           CA
                CC                 GGC AACATGGTGAAACCC  TCT
                                   ||| ||||||||||||||  |||
                                   CCG TTGTACCACTTTGGG  AGA
                                     G             AC
GAM678  LTB4R    5'  AGACGGGGTTTCACCATGTTGG 7457      _           A
                CC                 GGC AACATGGTGAAACCCC TCT
                                   ||| ||||||||||||||| |||
                                   CCG TTGTACCACTTTGGGG AGA
                                     G             C
GAM678  MAK      3'  AGACAGGGTTTCACCATGTTG  20938             CA
                                   CAACATGGTGAAACCC  TCT
                                   |||||||||||||||  |||
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                                GTTGTACCACTTTGGG  AGA
                                      AC
GAM678  MEF2A    5'  AGATGGAGTTTCACCATGTTGG 19989     _          C
            CC                  GGC AACATGGTGAAAC CCATCT
                                ||| |||||||||||| ||||||
                                CCG TTGTACCACTTTG GGTAGA
                                  G           A
GAM678  MFI2     3'  GGGTCTCACCATGTTGCC    53972             A
                                GGCAACATGGTGA ACCC
                                |||||||||||| ||||
                                CCGTTGTACCACT TGGG
                                       C
GAM678  MLANA    3'  AGATGGAGTTTCGCTTTTGTTG 19759        T_       C
            CC                  GGCAACA  GGTGAAAC CCATCT
                                ||||||| |||||||| ||||||
                                CCGTTGT  TCGCTTTG GGTAGA
                                    TT       A
GAM678  MPL      3'  AGACAGGGTTTTGCCATGTTGC 19336          TG     CA
            C                    GGCAACATGG  AAACCC  TCT
                                ||||||||||  ||||||  |||
                                CCGTTGTACC  TTTGGG  AGA
                                      GT     AC
GAM678  MPL      3'  AGACGGAGCCTTGCCTGTTGCC 19338         T  TG AACC  A
            A                    TGGCAACA GG  A    CC TCT
                                |||||||| ||  |    || |||
                                ACCGTTGT CC  T    GG AGA
                                    _  GT CCGA  C
GAM678  MRPL49   3'  AGATGGGGTTTCACCATGTTGG 70158     _
            CC                  GGC AACATGGTGAAACCCCATCT
                                ||| ||||||||||||||||||||
                                CCG TTGTACCACTTTGGGGTAGA
                                  G
GAM678  MYCL2    3'  AGATGGGGTTTCACCACATTGG 19368     AACA_
            CC                  GGC    TGGTGAAACCCCATCT
                                |||    ||||||||||||||||
                                CCG    ACCACTTTGGGGTAGA
                                  GTTAC
GAM678  NCOA6IP  3'  AGACGAGGTCCCACCATGTTGC 46149           AA   CCA
            C                    GGCAACATGGTG  ACC   TCT
                                ||||||||||||  |||   |||
                                CCGTTGTACCAC  TGG   AGA
                                      CC   AGC
GAM678  NDRG3    3'  AGATGGAGTTTCACCATGTTGG 50115     _          C
            CC                  GGC AACATGGTGAAAC CCATCT
                                ||| |||||||||||| ||||||
                                CCG TTGTACCACTTTG GGTAGA
                                  G           A
GAM678  NPR2L    3'  AGACAGGGTTTCCCTATGTTGC 22590          T      CA
            C                    GGCAACATGG GAAACCC  TCT
                                |||||||||| |||||||  |||
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                                CCGTTGTATC CTTTGGG  AGA
                                      C      AC
GAM678  ORC1L    3'  AGACAGGGCTTCACCATGTTGC 15979            A   CA
                CA                TGGCAACATGGTGAA CCC  TCT
                                  |||||||||||||| |||  |||
                                  ACCGTTGTACCACTT GGG  AGA
                                        C   AC
GAM678  PCDHB11  3'  AGACGGGGTTTCACCACGTTGG 38914    _  A         A
                CC                GGC AAC TGGTGAAACCCC TCT
                                  ||| ||| |||||||||||| |||
                                  CCG TTG ACCACTTTGGGG AGA
                                    G  C          C
GAM678  PDE6B    3'  AGATGGGGTTTCACCATATTG  6068     C
                                  CAA ATGGTGAAACCCCATCT
                                  ||| ||||||||||||||||
                                  GTT TACCACTTTGGGGTAGA
                                    A
GAM678  PER2     3'  AGACAGGGTTTCACCATGTTGG 43340     _          CA
                CC                GGC AACATGGTGAAACCC  TCT
                                  ||| ||||||||||||||  |||
                                  CCG TTGTACCACTTTGGG  AGA
                                    G            AC
GAM678  PIGR     3'  AGACAAAGTCTCACTGTGTCAC 72984    CA       A  CCCA
                C                  GG  ACATGGTGA AC    TCT
                                   ||  |||||||| ||    |||
                                   CC  TGTGTCACT TG    AGA
                                    AC        C  AAAC
GAM678  PIK3C2B  3'  AGACGGGGTTTCACCATGTTGG 12088     _           A
                CC                GGC AACATGGTGAAACCCC TCT
                                  ||| |||||||||||||| |||
                                  CCG TTGTACCACTTTGGGG AGA
                                    G            C
GAM678  PIK3CD   3'  AGATGGGGTCTTCCTCTGTTGC 18485       T  T  _
                C                  GGCAACA GG GAA ACCCCATCT
                                   ||||||| || ||| |||||||||
                                   CCGTTGT TC CTT TGGGGTAGA
                                      C  _  C
GAM678  POU2AF1  3'  AGACGGGGTTTCACCATGTTGG 21729     _           A
                CC                GGC AACATGGTGAAACCCC TCT
                                  ||| |||||||||||||| |||
                                  CCG TTGTACCACTTTGGGG AGA
                                    G            C
GAM678  PPID     3'  AGATGGGGTTTCACCATATTG  88818     C
                                  CAA ATGGTGAAACCCCATCT
                                  ||| ||||||||||||||||
                                  GTT TACCACTTTGGGGTAGA
                                    A
GAM678  PPP1R12B 3'  AGATGGGGTTTTGCCATGTTGC 50376          TG
                C                  GGCAACATGG  AAACCCCATCT
                                   ||||||||||  ||||||||||
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                                CCGTTGTACC  TTTGGGGTAGA
                                      GT
GAM678  PRKR     3'  AGACAGGGTTTCACCATGTTGG 12342     _          CA
                CC                  GGC AACATGGTGAAACCC  TCT
                                    ||| ||||||||||||||  |||
                                    CCG TTGTACCACTTTGGG  AGA
                                      G            AC
GAM678  PSMB2    3'  AGACAGGGTCTCACCATGT   12458        A   CA
                                    ACATGGTGA ACCC  TCT
                                    |||||||| ||||  |||
                                    TGTACCACT TGGG  AGA
                                         C   AC
GAM678  PTGES    3'  AGACGGGTTCACCATGTTGCC  18053           AC  A
                                    GGCAACATGGTGAA  CCC TCT
                                    ||||||||||||||  ||| |||
                                    CCGTTGTACCACTT  GGG AGA
                                          __  C
GAM678  RAB36    3'  AGATGGAGTTTCACCCTTGTTG 18152       T_     C
                CC                  GGCAACA  GGTGAAAC CCATCT
                                    |||||||  |||||||| ||||||
                                    CCGTTGT  CCACTTTG GGTAGA
                                       TC       A
GAM678  RABL2A   3'  AGACGGGGTTTCACCATGTTGC 26402              A
                C                    GGCAACATGGTGAAACCCC TCT
                                    |||||||||||||||||| |||
                                    CCGTTGTACCACTTTGGGG AGA
                                              C
GAM678  RABL2B   3'  AGACGGGGTTTCACCATGTTGC 23970              A
                C                    GGCAACATGGTGAAACCCC TCT
                                    |||||||||||||||||| |||
                                    CCGTTGTACCACTTTGGGG AGA
                                              C
GAM678  RAD52    3'  AGACGGGGTCTGGCTGTGTTGC 12756         GAA    A
                C                    GGCAACATGGT   ACCCC TCT
                                    ||||||||||   ||||| |||
                                    CCGTTGTGTCG   TGGGG AGA
                                          GTC    C
GAM678  RAD52    3'  AGACGGGGTCTGGCTGTGTTGC 57022         GAA    A
                C                    GGCAACATGGT   ACCCC TCT
                                    ||||||||||   ||||| |||
                                    CCGTTGTGTCG   TGGGG AGA
                                          GTC    C
GAM678  RAD52    3'  AGACGGGGTCTGGCTGTGTTGC 57042         GAA    A
                C                    GGCAACATGGT   ACCCC TCT
                                    ||||||||||   ||||| |||
                                    CCGTTGTGTCG   TGGGG AGA
                                          GTC    C
GAM678  RAD52    3'  AGACGGGGTCTGGCTGTGTTGC 57049         GAA    A
                C                    GGCAACATGGT   ACCCC TCT
                                    ||||||||||   ||||| |||
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                                CCGTTGTGTCG   TGGGG AGA
                                      GTC    C
GAM678  RBBP9    3'  AGACAGGGTTTCACCATGTTGG 70678    _          CA
             CC                  GGC AACATGGTGAAACCC  TCT
                                 ||| ||||||||||||||  |||
                                 CCG TTGTACCACTTTGGG  AGA
                                   G           AC
GAM678  RBBP9    3'  ATGGGGCAGAGTGTTGCCA   70683        GG  AAA
                                 TGGCAACAT  TG   CCCCAT
                                 |||||||||  ||   ||||||
                                 ACCGTTGTG  AC   GGGGTA
                                      AG  ___
GAM678  RBM8A    3'  AGATAGAGTCTTGCTGTGTTAC 18801    C      TG A  CCC
             C                   GG AACATGG  A AC   ATCT
                                 || |||||||  | ||   ||||
                                 CC TTGTGTC  T TG   TAGA
                                  A      GT C  AGA
GAM678  RBM8A    3'  AGATGGGGTCTTGCTGTGTTAC 18802    C      TG A
             C                   GG AACATGG  A ACCCCATCT
                                 || |||||||  | |||||||||
                                 CC TTGTGTC  T TGGGGTAGA
                                  A      GT C
GAM678  RHD      3'  AGATGGGGTTTCACCATGTTGG 32813    _
             CC                  GGC AACATGGTGAAACCCCATCT
                                 ||| ||||||||||||||||||
                                 CCG TTGTACCACTTTGGGGTAGA
                                   G
GAM678  RHD      3'  AGATGGGGTTTCACCATGTTGG 33133    _
             CC                  GGC AACATGGTGAAACCCCATCT
                                 ||| ||||||||||||||||||
                                 CCG TTGTACCACTTTGGGGTAGA
                                   G
GAM678  RRM2B    3'  GGACTGGGTTTTGCTGTCCA  68434    CAAC   TG    CA
                                 TGG   ATGG  AAACCC  TCT
                                 |||   ||||  ||||||  |||
                                 ACC   TGTC  TTTGGG  AGG
                                   ____   GT     TC
GAM678  SAS      3'  AGACAGGGTTTCACCATGTTAG 21093    _          CA
             TC                  GGC AACATGGTGAAACCC  TCT
                                 ||| ||||||||||||||  |||
                                 CTG TTGTACCACTTTGGG  AGA
                                   A           AC
GAM678  SCML2    3'  AGATGGAGTTTCACTCTTGTGC 21420     A  T_     C
             C                   GGCA CA  GGTGAAAC CCATCT
                                 |||| ||  |||||||| ||||||
                                 CCGT GT  TCACTTTG GGTAGA
                                   _ TC       A
GAM678  SCNN1G   3'  GGATCTCACTATGTTGCC    8300           AAC
                                 GGCAACATGGTGA   CC
                                 ||||||||||||   ||
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                                CCGTTGTATCACT  GG
                                       CTA
GAM678  SEDL    3'  AGACAGGGTTTCACCATATTG  28073    C        CA
                                CAA ATGGTGAAACCC  TCT
                                ||| ||||||||||||  |||
                                GTT TACCACTTTGGG  AGA
                                  A          AC
GAM678  SEDL    3'  AGACAGGGTTTCACCATATTG  28074    C        CA
                                CAA ATGGTGAAACCC  TCT
                                ||| ||||||||||||  |||
                                GTT TACCACTTTGGG  AGA
                                  A          AC
GAM678  SEPN1   3'  AGATGGGGTTTCACCATATTG  66958    C
                                CAA ATGGTGAAACCCCATCT
                                ||| ||||||||||||||||
                                GTT TACCACTTTGGGGTAGA
                                  A
GAM678  SIL     5'  AGACGGGGTTTCACCATGTTG  13150            A
                                CAACATGGTGAAACCCC TCT
                                |||||||||||||||| |||
                                GTTGTACCACTTTGGGG AGA
                                       C
GAM678  SLC14A2  5'  AGACGGGGTTTCACCACATTGG 24107    AACA_        A
           CC                    GGC    TGGTGAAACCCC TCT
                                |||    |||||||||||| |||
                                CCG    ACCACTTTGGGG AGA
                                  GTTAC          C
GAM678  SLC15A1  3'  AGATGGGGTTTCACCATGTT  18634
                                AACATGGTGAAACCCCATCT
                                ||||||||||||||||||||
                                TTGTACCACTTTGGGGTAGA

GAM678  SLC17A5  3'  AGATGGGGTCTCGTTTTGTCGC 25824    A  TG   A
           C                     GGC ACA  GTGA ACCCCATCT
                                ||| |||  |||| |||||||||
                                CCG TGT  TGCT TGGGGTAGA
                                  C  TT   C
GAM678  SLC3A2   5'  AGACGGGGTCTGACTGTGTTAC 11516   C      GAA    A
           C                     GG AACATGGT   ACCCC TCT
                                || ||||||||   ||||| |||
                                CC TTGTGTCA   TGGGG AGA
                                  A       GTC    C
GAM678  SMAC    5'  AGATGGGGTTTCACCATGTTG  58012
                                CAACATGGTGAAACCCCATCT
                                ||||||||||||||||||||
                                GTTGTACCACTTTGGGGTAGA

GAM678  SNAP23   3'  AGACAGGGTTTCACCATGTCAA 56333    A__          CA
           GC                    GC   ACATGGTGAAACCC  TCT
                                ||   ||||||||||||||  |||
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                                CG   TGTACCACTTTGGG  AGA
                                 AAC           AC
GAM678  SNAP23   3'  AGACAGGGTTTCACCATGTCAA 15134    A__          CA
             GC                   GC   ACATGGTGAAACCC  TCT
                                ||   ||||||||||||||  |||
                                CG   TGTACCACTTTGGG  AGA
                                 AAC           AC
GAM678  SPN      3'  AGACAGAGTTTCGCTTTGTCGC 13363     A   T      CCCA
             C                    GGC ACA GGTGAAAC    TCT
                                ||| ||| ||||||||    |||
                                CCG TGT TCGCTTTG    AGA
                                  C   T       AGAC
GAM678  SPN      3'  AGATGGGGTTTCACCATGTTG  13366
                                CAACATGGTGAAACCCCATCT
                                ||||||||||||||||||||
                                GTTGTACCACTTTGGGGTAGA

GAM678  SULT1C1  3'  GGGTCTTGCTATGTTGCC    8320          TG A
                                GGCAACATGG  A ACCC
                                ||||||||||  | ||||
                                CCGTTGTATC  T TGGG
                                      GT C
GAM678  TAF11    3'  AGATGGGGTCTTGCTTTGTTGC 20116        T  TG A
             C                    GGCAACA GG  A ACCCCATCT
                                ||||||| ||  | |||||||||
                                CCGTTGT TC  T TGGGGTAGA
                                    T  GT C
GAM678  TAF7L    3'  ATGGGGTCTTGTTATGTTGCC  46513          TG A
                                GGCAACATGG  A ACCCCAT
                                ||||||||||  | |||||||
                                CCGTTGTATT  T TGGGGTA
                                      GT C
GAM678  TAPBP    3'  AGACGGGGTTTCACCATGTTGG 13544     _           A
             CC                   GGC AACATGGTGAAACCCC TCT
                                ||| ||||||||||||||| |||
                                CCG TTGTACCACTTTGGGG AGA
                                  G             C
GAM678  TAT      3'  AGACAGGGTTTCACCATGTTAG 6248      _          CA
             CC                   GGC AACATGGTGAAACCC  TCT
                                ||| ||||||||||||||  |||
                                CCG TTGTACCACTTTGGG  AGA
                                  A             AC
GAM678  TEM7     3'  AGACAGGGTCTCACTGTGTCGC 40242     A       A   CA
             C                    GGC ACATGGTGA ACCC  TCT
                                ||| |||||||| ||||  |||
                                CCG TGTGTCACT TGGG  AGA
                                  C        C   AC
GAM678  TIM3     3'  AGACAGGGTTTCACCATGTTGG 52348     _          CA
             CC                   GGC AACATGGTGAAACCC  TCT
                                ||| ||||||||||||||  |||
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                                CCG TTGTACCACTTTGGG  AGA
                                  G            AC
GAM678  TMPRSS3  3'  AGACAGGGTTTCACCATGTTGG 44012     _          CA
                CC                GGC AACATGGTGAAACCC  TCT
                                  ||| ||||||||||||||  |||
                                CCG TTGTACCACTTTGGG  AGA
                                  G            AC
GAM678  TMPRSS3  3'  AGACAGGGTTTCACCATGTTGG 51509     _          CA
                CC                GGC AACATGGTGAAACCC  TCT
                                  ||| ||||||||||||||  |||
                                CCG TTGTACCACTTTGGG  AGA
                                  G            AC
GAM678  TMPRSS3  3'  AGACAGGGTTTCACCATGTTGG 51537     _          CA
                CC                GGC AACATGGTGAAACCC  TCT
                                  ||| ||||||||||||||  |||
                                CCG TTGTACCACTTTGGG  AGA
                                  G            AC
GAM678  TNFAIP2  3'  AGACAGGGTCTTGCTGTGTTGC 21917          TG A   CA
                C                 GGCAACATGG  A ACCC  TCT
                                  ||||||||||  | ||||  |||
                                CCGTTGTGTC  T TGGG  AGA
                                      GT C    AC
GAM678  TNFRSF10B 3'  AGACGGGGTTTCACCATGTTG  15212              A
                                CAACATGGTGAAACCCC TCT
                                ||||||||||||||||| |||
                                GTTGTACCACTTTGGGG AGA
                                        C
GAM678  TNFRSF11A 3'  AGACACGGTCCCACCATGTTAC 15185    C       AA   CCA
                C                 GG AACATGGTG  ACC   TCT
                                  || |||||||||  |||   |||
                                CC TTGTACCAC  TGG   AGA
                                  A        CC   CAC
GAM678  TP53     3'  AGATGGGGTCTCACAGTGTTGC 6793          G    A
                C                 GGCAACAT GTGA ACCCCATCT
                                  |||||||| |||| |||||||||
                                CCGTTGTG CACT TGGGGTAGA
                                      A    C
GAM678  TPMT     3'  AGACGGGGTTTCACCATGTTG  6302               A
                                CAACATGGTGAAACCCC TCT
                                ||||||||||||||||| |||
                                GTTGTACCACTTTGGGG AGA
                                        C
GAM678  TPMT     3'  AGATGGAGTTTCGTTCTTGTTG 6304         TGG_     C
                CC                GGCAACA    TGAAAC CCATCT
                                  |||||||    |||||| ||||||
                                CCGTTGT    GCTTTG GGTAGA
                                    TCTT     A
GAM678  TRIM9    5'  AGACGGGGTTTCACCATACTGG 31440     AAC_          A
                CC                GGC    ATGGTGAAACCCC TCT
                                  |||    |||||||||||| |||
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                                CCG    TACCACTTTGGGG AGA
                                  GTCA          C
GAM678  TRPM6    3'  AGATGGGGTTTCACCATGTTGG 35024     _
                CC                GGC AACATGGTGAAACCCCATCT
                                  ||| ||||||||||||||||||||
                                  CCG TTGTACCACTTTGGGGTAGA
                                    G
GAM678  TRPV1    3'  AGACAGAGTTTCACTCTTGTTG 38682        T_      CCCA
                CC                GGCAACA  GGTGAAAC    TCT
                                  |||||||  ||||||||    |||
                                  CCGTTGT  TCACTTTG    AGA
                                     TC       AGAC
GAM678  TRPV1    3'  AGACGGGGTTTCACCATGTTGG 38683     _           A
                CC                GGC AACATGGTGAAACCCC TCT
                                  ||| ||||||||||||||| |||
                                  CCG TTGTACCACTTTGGGG AGA
                                    G             C
GAM678  TRPV1    3'  AGACAGAGTTTCACTCTTGTTG 55650        T_      CCCA
                CC                GGCAACA  GGTGAAAC    TCT
                                  |||||||  ||||||||    |||
                                  CCGTTGT  TCACTTTG    AGA
                                     TC       AGAC
GAM678  TRPV1    3'  AGACGGGGTTTCACCATGTTGG 55653     _           A
                CC                GGC AACATGGTGAAACCCC TCT
                                  ||| ||||||||||||||| |||
                                  CCG TTGTACCACTTTGGGG AGA
                                    G             C
GAM678  TRPV1    3'  AGACAGAGTTTCACTCTTGTTG 55698        T_      CCCA
                CC                GGCAACA  GGTGAAAC    TCT
                                  |||||||  ||||||||    |||
                                  CCGTTGT  TCACTTTG    AGA
                                     TC       AGAC
GAM678  TRPV1    3'  AGACGGGGTTTCACCATGTTGG 55699     _           A
                CC                GGC AACATGGTGAAACCCC TCT
                                  ||| ||||||||||||||| |||
                                  CCG TTGTACCACTTTGGGG AGA
                                    G             C
GAM678  TRPV1    3'  AGACAGAGTTTCACTCTTGTTG 55729        T_      CCCA
                CC                GGCAACA  GGTGAAAC    TCT
                                  |||||||  ||||||||    |||
                                  CCGTTGT  TCACTTTG    AGA
                                     TC       AGAC
GAM678  TRPV1    3'  AGACGGGGTTTCACCATGTTGG 55730     _           A
                CC                GGC AACATGGTGAAACCCC TCT
                                  ||| ||||||||||||||| |||
                                  CCG TTGTACCACTTTGGGG AGA
                                    G             C
GAM678  TUFT1    3'  AGATGGGGTTTCACCATACTGG 39667     AAC_
                CT                GGC    ATGGTGAAACCCCATCT
                                  |||    ||||||||||||||||
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                                TCG    TACCACTTTGGGGTAGA
                                  GTCA
GAM678  UGDH     3'  AGACAGGGTTTCACCATGTGAG 13990     A_          CA
                CC                 GGC  ACATGGTGAAACCC  TCT
                                   |||  ||||||||||||||  |||
                                   CCG  TGTACCACTTTGGG  AGA
                                     AG            AC
GAM678  UMPS     3'  AGATGAGGTCTTGCCATGTTAC 6328     C      TG A   C
                C                   GG AACATGG  A ACC CATCT
                                    ||  |||||||  |  |||  |||||
                                    CC TTGTACC  T TGG GTAGA
                                     A      GT C   A
GAM678  VENTX2   3'  ATGGGGTTTCACCATGTTAGCC 27855     _
                                    GGC AACATGGTGAAACCCCAT
                                    |||  |||||||||||||||||
                                    CCG TTGTACCACTTTGGGGTA
                                     A
GAM678  VHL      3'  AGACGGGGTTTCACCATGTTGT 6827                 A
                C                   GGCAACATGGTGAAACCCC TCT
                                    ||||||||||||||||||  |||
                                    CTGTTGTACCACTTTGGGG AGA
                                                C
GAM678  VIPR2    3'  AGACAGGGTTTCACCATGTTAG 14056     _          CA
                CC                  GGC AACATGGTGAAACCC  TCT
                                    |||  ||||||||||||||  |||
                                    CCG TTGTACCACTTTGGG  AGA
                                     A             AC
GAM678  WBSCR5   5'  AGATGGAATTTCACCGTGTTGC 51627             CC
                C                   GGCAACATGGTGAAA  CCATCT
                                    ||||||||||||||  ||||||
                                    CCGTTGTGCCACTTT  GGTAGA
                                              AA
GAM678  WBSCR5   5'  AGATGGAATTTCACCGTGTTGC 42108             CC
                C                   GGCAACATGGTGAAA  CCATCT
                                    ||||||||||||||  ||||||
                                    CCGTTGTGCCACTTT  GGTAGA
                                              AA
GAM678  XRCC2    3'  AGACGGGGTTTCACCATGTTGG 19489     _           A
                CC                  GGC AACATGGTGAAACCCC TCT
                                    |||  ||||||||||||||  |||
                                    CCG TTGTACCACTTTGGGG AGA
                                     G             C
GAM678  ZNF253   3'  AGATGGAGTTTCACTCTTGTCA 41075       CAT       C
                                    TGGCAA   GGTGAAAC CCATCT
                                    ||||||   ||||||||  ||||||
                                    ACTGTT   TCACTTTG GGTAGA
                                       C__       A
GAM678  ZNF264   3'  AGACGGGGTTTCACCATCTTGG 14188     AAC_          A
                CC                  GGC    ATGGTGAAACCCC TCT
                                    |||    ||||||||||||| |||
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                                CCG    TACCACTTTGGGG AGA
                                  GTTC           C
GAM678  ZNF264    3'  AGACGGGGTTTCACCATGTTGC 14191                 A
              T                    GGCAACATGGTGAAACCCC TCT
                                   |||||||||||||||||| |||
                                   TCGTTGTACCACTTTGGGG AGA
                                              C
GAM678  AAK1      3'  AGACAGAGTTTCACTCTTGTTG 30512         T_       CCCA
              CC                   GGCAACA  GGTGAAAC    TCT
                                   |||||||  ||||||||    |||
                                   CCGTTGT  TCACTTTG    AGA
                                      TC       AGAC
GAM678  ANKT      3'  AGACAGGGTCTCACTGTGTTGC 33455             A    CA
              C                    GGCAACATGGTGA ACCC  TCT
                                   ||||||||||||| ||||  |||
                                   CCGTTGTGTCACT TGGG  AGA
                                            C   AC
GAM678  AP3S2     3'  AGACAGGGTTTCACCATGTTGG 20640      _           CA
              CC                   GGC AACATGGTGAAACCC  TCT
                                   ||| ||||||||||||||  |||
                                   CCG TTGTACCACTTTGGG  AGA
                                     G             AC
GAM678  ARHF      3'  AGACAGGGTTTCACCATGTTGG 39259      _           CA
              CC                   GGC AACATGGTGAAACCC  TCT
                                   ||| ||||||||||||||  |||
                                   CCG TTGTACCACTTTGGG  AGA
                                     G             AC
GAM678  ASE-1     3'  AGATGGGGTTTCACCACGTTAG 24967      _  A
              CC                   GGC AAC TGGTGAAACCCCATCT
                                   ||| ||| ||||||||||||||||
                                   CCG TTG ACCACTTTGGGGTAGA
                                     A  C
GAM678  ATP1B4    3'  AGACAGGGTTTCACCATGTTGG 24831      _           CA
              CC                   GGC AACATGGTGAAACCC  TCT
                                   ||| ||||||||||||||  |||
                                   CCG TTGTACCACTTTGGG  AGA
                                     G             AC
GAM678  ATP1B4    3'  AGATGGAGTTTCGCTGTTGTCA 24833          TG      C
                                   TGGCAACA  GTGAAAC CCATCT
                                   |||||||  ||||||| ||||||
                                   ACTGTTGT  CGCTTTG GGTAGA
                                        __       A
GAM678  BAGE      3'  AGATGGAGTTTCACTGTGTCA  8638     A          C
                                   C ACATGGTGAAAC CCATCT
                                   | ||||||||||| ||||||
                                   A TGTGTCACTTTG GGTAGA
                                    C           A
GAM678  BNIP-S    3'  AGACGGGGTTTCACCATGTTGG 57084      _           A
              CC                   GGC AACATGGTGAAACCCC TCT
                                   ||| ||||||||||||||| |||
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                                CCG TTGTACCACTTTGGGG AGA
                                  G             C
GAM678  BRAG     3'  AGATGGGGTCTCGCCGTGTTGC 30096           A
                                GCAACATGGTGA ACCCCATCT
                                |||||||||||| |||||||||
                                CGTTGTGCCGCT TGGGGTAGA
                                       C
GAM678  BTN3A1   3'  AGATGGAGTCTTACTCTGTTGC 23885        T    A  C
           TA                    TGGCAACA GGTGA AC CCATCT
                                 |||||||| ||||| || ||||||
                                 ATCGTTGT TCATT TG GGTAGA
                                     C    C  A
GAM678  C13orf1  3'  AGATGGGGTTTCACCATGTTGT 40350
           C                     GGCAACATGGTGAAACCCCATCT
                                 |||||||||||||||||||||||
                                 CTGTTGTACCACTTTGGGGTAGA

GAM678  C1QTNF6  3'  AGATGGGGTTTCACCATATTGG 49983     AAC_
           CC                    GGC   ATGGTGAAACCCCATCT
                                 |||   ||||||||||||||||
                                 CCG   TACCACTTTGGGGTAGA
                                   GTTA
GAM678  C21orf25 3'  AGATGGAGTTTCACTCTGTTGC 64280       T      C
           C                     GGCAACA GGTGAAAC CCATCT
                                 ||||||| |||||||| ||||||
                                 CCGTTGT TCACTTTG GGTAGA
                                     C       A
GAM678  C21orf25 3'  ATGGAGTCTCACCATGTTG   64281          A  C
                                 CAACATGGTGA AC CCAT
                                 |||||||||| || ||||
                                 GTTGTACCACT TG GGTA
                                       C  A
GAM678  C3F      3'  GGGATTTCACCACGTTGGCC  20477    _  A      C
                                 GGC AAC TGGTGAAA CCC
                                 ||| ||| |||||||| |||
                                 CCG TTG ACCACTTT GGG
                                   G  C       A
GAM678  C6orf5   3'  AGACAGGGTTTCATATTGGCCA 31966     AACATG       CA
                                 TGGC     GTGAAACCC  TCT
                                 ||||     |||||||||  |||
                                 ACCG     TACTTTGGG  AGA
                                   GTTA__        AC
GAM678  CARD6    3'  AGACAGAGTTTCACTCTTGTTG 51837       T_      CCCA
           CC                    GGCAACA  GGTGAAAC   TCT
                                 |||||||  ||||||||   |||
                                 CCGTTGT  TCACTTTG   AGA
                                     TC       AGAC
GAM678  CDC14B   3'  AGACAGGGTTTCACCATGTTGG 53997     _          CA
           CC                    GGC AACATGGTGAAACCC  TCT
                                 ||| ||||||||||||||  |||
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                                CCG TTGTACCACTTTGGG  AGA
                                  G             AC
GAM678  CENPH    3'  AGACGGGGTTTCACCGTGTTGC 43563                A
              C                   GGCAACATGGTGAAACCCC TCT
                                  |||||||||||||||||| |||
                                  CCGTTGTGCCACTTTGGGG AGA
                                        C
GAM678  CHSY1    3'  AGACGGGGTTTCACCATGCAAG 30560     AA_          A
              CC                    GGC   CATGGTGAAACCCC TCT
                                  |||   |||||||||||||| |||
                                  CCG   GTACCACTTTGGGG AGA
                                    AAC           C
GAM678  CIP29    3'  AGACGGGGTTTCACCATGTTGC 51368                A
              C                   GGCAACATGGTGAAACCCC TCT
                                  |||||||||||||||||| |||
                                  CCGTTGTACCACTTTGGGG AGA
                                        C
GAM678  COLEC12  3'  GGGTCTTGCTATGTTGCC    48614          TG A
                                  GGCAACATGG  A ACCC
                                  ||||||||||  | ||||
                                  CCGTTGTATC  T TGGG
                                       GT C
GAM678  COQ7     3'  GGCGAAGTCTCACTATGTCGCC 32858      A       A  C___
              A                    TGGC ACATGGTGA AC    CC
                                  |||| ||||||||| ||    ||
                                  ACCG TGTATCACT TG    GG
                                    C        C  AAGC
GAM678  CPSF2    3'  AGACAGGGTTTCACCATGTTGG 62257     _           CA
              CC                    GGC AACATGGTGAAACCC  TCT
                                  ||| ||||||||||||||  |||
                                  CCG TTGTACCACTTTGGG  AGA
                                    G             AC
GAM678  DBR1     3'  AGATGGAGTTTCACTCTTGTCA 33060       CAT       C
                                  TGGCAA   GGTGAAAC CCATCT
                                  ||||||   |||||||| ||||||
                                  ACTGTT   TCACTTTG GGTAGA
                                     C__        A
GAM678  DCOHM    3'  AGATGGAGTTTCGCTCTTGTCG 50507     A  T_       C
              CC                    GGC ACA  GGTGAAAC CCATCT
                                  ||| |||  |||||||| ||||||
                                  CCG TGT  TCGCTTTG GGTAGA
                                    C  TC       A
GAM678  DCOHM    3'  AGATGGGGTCTCGTTCTGTCA  50508      AC    TGAA
                                  TGGCA  ATGG    ACCCCATCT
                                  |||||  ||||    |||||||||
                                  ACTGT  TGCT    TGGGGTAGA
                                     CT    C___
GAM678  DKFZP434C212 3'  GGGGTTTCACCATGTTGGCC   69492     _
                                  GGC AACATGGTGAAACCCC
                                  ||| ||||||||||||||||
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                                CCG TTGTACCACTTTGGGG
                                  G
GAM678  DKFZp547H025 3'  AGATGAGGTTTCACCATGTTGG 39768    _          C
           CC                    GGC AACATGGTGAAACC CATCT
                                 ||| |||||||||||||| |||||
                                 CCG TTGTACCACTTTGG GTAGA
                                   G           A
GAM678  DKFZP564G092 5'  AGACAGGATTTCACCATGTTGG 32149    _        C  CA
           CC                    GGC AACATGGTGAAA CC  TCT
                                 ||| |||||||||||| ||  |||
                                 CCG TTGTACCACTTT GG  AGA
                                   G          A  AC
GAM678  DKFZP564G092 5'  AGACGGAGTTTCGCTCTTGTCG 32152    A  T_      C  A
           CC                    GGC ACA  GGTGAAAC CC TCT
                                 ||| |||  |||||||| || |||
                                 CCG TGT  TCGCTTTG GG AGA
                                   C  TC       A  C
GAM678  DKFZP564O0423 3'  AGATGGGGTCTCACTATGTTGC 93341           A
           C                     GGCAACATGGTGA ACCCCATCT
                                 |||||||||||| |||||||||
                                 CCGTTGTATCACT TGGGGTAGA
                                        C
GAM678  DKFZP566C243 3'  AGATGGGGTTTGCAGCTGCCA  31809      ACATG  G
                                 TGGCA    GT AAACCCCATCT
                                 |||||    || ||||||||||
                                 ACCGT    CG TTTGGGGTAGA
                                    CGA__  _
GAM678  DKFZP586A0522 3'  AGACAGGGTCTCACTGTGTTGC 26726           A   CA
           C                     GGCAACATGGTGA ACCC  TCT
                                 |||||||||||| ||||  |||
                                 CCGTTGTGTCACT TGGG  AGA
                                        C   AC
GAM678  DKFZP761E2110 3'  AGATGGGGTCTTGTTATATTGC 48960      C   TG A
           C                     GGCAA ATGG  A ACCCCATCT
                                 ||||| ||||  | |||||||||
                                 CCGTT TATT  T TGGGGTAGA
                                    A   GT C
GAM678  DKFZp761N1114 3'  AGACAGAGTCTCACTCTGTTGC 79772        T    A  CCCA
           CA                    TGGCAACA GGTGA AC    TCT
                                 ||||||| ||||| ||    |||
                                 ACCGTTGT TCACT TG    AGA
                                     C    C  AGAC
GAM678  DKFZp761O0113 5'  AGATGGAGTTTCGCTCTTGTTG 37888       T_      C
           CC                    GGCAACA  GGTGAAAC CCATCT
                                 |||||||  |||||||| ||||||
                                 CCGTTGT  TCGCTTTG GGTAGA
                                    TC       A
GAM678  DKFZp762P2111 3'  AGATGGAGTTTCACTCTTGTTG 87624       T_      C
           CC                    GGCAACA  GGTGAAAC CCATCT
                                 |||||||  |||||||| ||||||
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                                CCGTTGT  TCACTTTG GGTAGA
                                   TC       A
GAM678  ERO1L    3'  AGACAAGGTTTTGCTGTGTTGC 28153          TG    CCA
            C                    GGCAACATGG  AAACC   TCT
                                 ||||||||||  |||||   |||
                                 CCGTTGTGTC  TTTGG   AGA
                                      GT     AAC
GAM678  EVI5     3'  AGATGGGGTTTCACCATGTTG  20196
                                 CAACATGGTGAAACCCCATCT
                                 ||||||||||||||||||||
                                 GTTGTACCACTTTGGGGTAGA

GAM678  FER1L4   3'  AGACAGGGTTTCACCATGTTGT 48108              CA
            C                    GGCAACATGGTGAAACCC  TCT
                                 ||||||||||||||||  |||
                                 CTGTTGTACCACTTTGGG  AGA
                                       AC
GAM678  FLJ00060 5'  AGATGGAATTTCACCATGTTAG 61734    _         CC
            CC                     GGC AACATGGTGAAA  CCATCT
                                   |||  ||||||||||||  ||||||
                                   CCG TTGTACCACTTT  GGTAGA
                                     A          AA
GAM678  FLJ10232 5'  AGATGGGGTTTTGCTATGTTGC 36371          TG
            C                    GGCAACATGG  AAACCCCATCT
                                 ||||||||||  ||||||||||
                                 CCGTTGTATC  TTTGGGGTAGA
                                      GT
GAM678  FLJ10298 3'  AGACGGGGTTTCACCATGTTG  36451              A
                                 CAACATGGTGAAACCCC TCT
                                 ||||||||||||||||| |||
                                 GTTGTACCACTTTGGGG AGA
                                           C
GAM678  FLJ10535 3'  AGATGGGGTTTCACCATGTTGG 36736    _
            CC                     GGC AACATGGTGAAACCCCATCT
                                   |||  ||||||||||||||||||
                                   CCG TTGTACCACTTTGGGGTAGA
                                     G
GAM678  FLJ10713 3'  AGATGGGGTTTCACCATGTTGG 36996    _
            CC                     GGC AACATGGTGAAACCCCATCT
                                   |||  ||||||||||||||||||
                                   CCG TTGTACCACTTTGGGGTAGA
                                     G
GAM678  FLJ10846 3'  AGACAGGGTCTCACCATGTTAG 37284    _        A   CA
            CC                     GGC AACATGGTGA ACCC  TCT
                                   |||  ||||||||||  ||||  |||
                                   CCG TTGTACCACT TGGG  AGA
                                     A         C    AC
GAM678  FLJ10922 3'  AGACGGGGTTTTGTCTCATTGC 37396      CAT  TG      A
            C                      GGCAA   GG  AAACCCC TCT
                                   |||||   ||  |||||||  |||
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                                CCGTT   CT  TTTGGGG AGA
                                  ACT  GT      C
GAM678  FLJ10956  3'  AGACGGGGTTTCACCATGTTGG 37460     _           A
            CC                   GGC AACATGGTGAAACCCC TCT
                                 ||| |||||||||||||| |||
                                 CCG TTGTACCACTTTGGGG AGA
                                   G             C
GAM678  FLJ11193  3'  AGATGGGGTCTCACCATGTTAC 37745    C        A
            C                    GG AACATGGTGA ACCCCATCT
                                 || |||||||||| |||||||||
                                 CC TTGTACCACT TGGGGTAGA
                                  A         C
GAM678  FLJ12610  3'  AGACAAGGCTTTGCCATGTTGC 45855          TG  A  CCA
            C                    GGCAACATGG  AA CC   TCT
                                 ||||||||||  || ||   |||
                                 CCGTTGTACC  TT GG   AGA
                                       GT  C  AAC
GAM678  FLJ12687  3'  AGACAGGGTTTCACCATGTTGG 46741     _           CA
            CC                   GGC AACATGGTGAAACCC  TCT
                                 ||| ||||||||||||||  |||
                                 CCG TTGTACCACTTTGGG  AGA
                                   G             AC
GAM678  FLJ12891  3'  AGACGGGGTCTTGTTGTGTCAC 46916    CA   TG TG A    A
            C                    GG  ACA  G  A ACCCC TCT
                                 ||  |||  |  | ||||| |||
                                 CC  TGT  T  T TGGGG AGA
                                  AC   GT GT C    C
GAM678  FLJ12903  3'  AGACGGAGTTTCGCTGTTGTTG 43063        _       C  A
            CC                   GGCAACA TGGTGAAAC CC TCT
                                 ||||||| ||||||||| || |||
                                 CCGTTGT GTCGCTTTG GG AGA
                                     T        A  C
GAM678  FLJ12960  3'  AGATGGGGTTTCACCGTATGAG 45290     AAC_
            CC                   GGC    ATGGTGAAACCCCATCT
                                 |||    ||||||||||||||||
                                 CCG    TGCCACTTTGGGGTAGA
                                   AGTA
GAM678  FLJ12975  3'  AGACGGGGTTTCGCCTTGTTGC 70183        T         A
            C                    GGCAACA GGTGAAACCCC TCT
                                 ||||||| |||||||||| |||
                                 CCGTTGT CCGCTTTGGGG AGA
                                     T         C
GAM678  FLJ13072  5'  AGACAGGGTTTCACCATGTTG  91383             CA
                                 CAACATGGTGAAACCC  TCT
                                 |||||||||||||||  |||
                                 GTTGTACCACTTTGGG  AGA
                                           AC
GAM678  FLJ13114  3'  AGATGGAGTTTCACCATGTTAC 44893    C          C
            C                    GG AACATGGTGAAAC CCATCT
                                 || |||||||||||| ||||||
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                                CC TTGTACCACTTTG GGTAGA
                                 A           A
GAM678  FLJ13305  5'  AGATGGGGTTTCACCATGTTGG 91704     _
              CC                  GGC AACATGGTGAAACCCCATCT
                                  ||| ||||||||||||||||||||
                                  CCG TTGTACCACTTTGGGGTAGA
                                    G
GAM678  FLJ13456  3'  AGACAGAGTTTCACTCTGTCGC 66525     A   T       CCCA
              C                   GGC ACA GGTGAAAC    TCT
                                  ||| ||| ||||||||    |||
                                  CCG TGT TCACTTTG    AGA
                                    C   C       AGAC
GAM678  FLJ13769  5'  AGATGGGGTTTCACTATGTTGC 47241
              C                   GGCAACATGGTGAAACCCCATCT
                                  ||||||||||||||||||||||||
                                  CCGTTGTATCACTTTGGGGTAGA

GAM678  FLJ14950  3'  AGACAGGGTTTCACCATGTTGG 52779     _           CA
              CC                  GGC AACATGGTGAAACCC  TCT
                                  ||| ||||||||||||||  |||
                                  CCG TTGTACCACTTTGGG  AGA
                                    G             AC
GAM678  FLJ14957  3'  AGACGGGGTTTCACCATGTTG  52806              A
                                  CAACATGGTGAAACCCC TCT
                                  |||||||||||||||| |||
                                  GTTGTACCACTTTGGGG AGA
                                          C
GAM678  FLJ14957  3'  AGATGGAGTTTCATTCTTGTTG 52809        T_      C
              CC                  GGCAACA  GGTGAAAC CCATCT
                                  |||||||  |||||||| ||||||
                                  CCGTTGT  TTACTTTG GGTAGA
                                     TC       A
GAM678  FLJ20147  3'  AGATAGGGTCTTGCTGTGTTGC 35130          TG A    C
              C                   GGCAACATGG  A ACCC ATCT
                                  ||||||||||  | |||| ||||
                                  CCGTTGTGTC  T TGGG TAGA
                                        GT C    A
GAM678  FLJ20344  3'  AGACAGGGTTTCACCATGTTGG 35474     _           CA
              CC                  GGC AACATGGTGAAACCC  TCT
                                  ||| ||||||||||||||  |||
                                  CCG TTGTACCACTTTGGG  AGA
                                    G             AC
GAM678  FLJ20507  3'  AGACAGGGTTTCACCATGTTGG 35728     _           CA
              CC                  GGC AACATGGTGAAACCC  TCT
                                  ||| ||||||||||||||  |||
                                  CCG TTGTACCACTTTGGG  AGA
                                    G             AC
GAM678  FLJ20507  3'  AGACAGGGTTTCACCATGTTGG 60837     _           CA
              CC                  GGC AACATGGTGAAACCC  TCT
                                  ||| ||||||||||||||  |||
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                                CCG TTGTACCACTTTGGG  AGA
                                  G           AC
GAM678  FLJ20958  3'  AGATGGGATCACTATGTTGCC  42308          AAC
                                GGCAACATGGTGA  CCCATCT
                                ||||||||||||  |||||||
                                CCGTTGTATCACT  GGGTAGA
                                      A__
GAM678  FLJ21302  3'  AGACAGGGTTTCACCATGTTGG 43501    _          CA
          CC                    GGC AACATGGTGAAACCC  TCT
                                ||| ||||||||||||||  |||
                                CCG TTGTACCACTTTGGG  AGA
                                  G           AC
GAM678  FLJ21324  5'  AGATGGGGTTTCACCATGTTGG 92840    _
          CC                    GGC AACATGGTGAAACCCCATCT
                                ||| ||||||||||||||||||
                                CCG TTGTACCACTTTGGGGTAGA
                                  G
GAM678  FLJ21657  3'  AGATGGGGCCACTGCACTGC  42794    ACA    AAA
                                GCA  TGGTG  CCCCATCT
                                |||  |||||  ||||||||
                                CGT  GTCAC  GGGGTAGA
                                  CAC    C__
GAM678  FLJ21777  3'  AGACAAGGTCTCTCCATGTTGC 50831        T  A  CCA
          C                     GGCAACATGG GA ACC  TCT
                                |||||||||| || |||  |||
                                CCGTTGTACC CT TGG  AGA
                                      T  C  AAC
GAM678  FLJ22316  5'  AGATGAGGTCTTGCTATGTTGC 47609        TG A  C
          C                     GGCAACATGG  A ACC CATCT
                                ||||||||||  | ||| |||||
                                CCGTTGTATC  T TGG GTAGA
                                      GT C  A
GAM678  FLJ22329  3'  AGACGGGGTTTCACCATGTTGG 45391    _          A
          CC                    GGC AACATGGTGAAACCCC TCT
                                ||| |||||||||||||| |||
                                CCG TTGTACCACTTTGGGG AGA
                                  G           C
GAM678  FLJ22529  3'  AGACAGGGTTTCACCACATTGG 45935    AACA_       CA
          CC                    GGC    TGGTGAAACCC  TCT
                                |||    ||||||||||  |||
                                CCG    ACCACTTTGGG  AGA
                                  GTTAC        AC
GAM678  FLJ22684  3'  AGACAGGGTTTCACCATGTTGG 47463    _          CA
          CC                    GGC AACATGGTGAAACCC  TCT
                                ||| ||||||||||||||  |||
                                CCG TTGTACCACTTTGGG  AGA
                                  G           AC
GAM678  FLJ22794  3'  AGACAGGGTTTCACCATGTTG  93235          CA
                                CAACATGGTGAAACCC  TCT
                                ||||||||||||||  |||
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                                GTTGTACCACTTTGGG  AGA
                                      AC
GAM678  FLJ22969  3'  AGACAGGGTTTCACCATGTTGC 69195              CA
          C                    GGCAACATGGTGAAACCC  TCT
                               |||||||||||||||||  |||
                               CCGTTGTACCACTTTGGG  AGA
                                     AC
GAM678  FLJ23024  3'  AGACGGGGTTTCACCATGTTGG 46835    _          A
          CC                   GGC AACATGGTGAAACCCC TCT
                               ||| |||||||||||||| |||
                               CCG TTGTACCACTTTGGGG AGA
                                 G            C
GAM678  FLJ23392  3'  AGACAGGGTTTCACCATGTTGG 45873    _          CA
          CC                   GGC AACATGGTGAAACCC  TCT
                               ||| ||||||||||||||  |||
                               CCG TTGTACCACTTTGGG  AGA
                                 G            AC
GAM678  FLJ23556  3'  AGATGGAGTTTTGCTCTGTCAC 46427   CA  T  TG   C
          C                    GG  ACA GG  AAAC CCATCT
                               ||  |||  ||  ||||  ||||||
                               CC  TGT TC  TTTG GGTAGA
                                AC  C  GT   A
GAM678  FLJ25416  5'  AGATGGGGTTTCACCATGTTGG 59446    _
          CC                   GGC AACATGGTGAAACCCCATCT
                               ||| ||||||||||||||||||
                               CCG TTGTACCACTTTGGGGTAGA
                                 G
GAM678  FLJ30532  3'  AGATGGAGTTTCGCTCTTGTTG 59214       T_     C
          CC                   GGCAACA  GGTGAAAC CCATCT
                               |||||||  |||||||| ||||||
                               CCGTTGT  TCGCTTTG GGTAGA
                                  TC       A
GAM678  FLJ31153  3'  AGATGGGGTTTCACCATGCTGG 58741    AA_
          CC                   GGC   CATGGTGAAACCCCATCT
                               |||   ||||||||||||||||||
                               CCG   GTACCACTTTGGGGTAGA
                                 GTC
GAM678  FLJ32865  3'  AGACAGAGTTTCGCTCTTGTCA 58797      CAT      CCCA
                               TGGCAA   GGTGAAAC    TCT
                               ||||||   ||||||||    |||
                               ACTGTT   TCGCTTTG    AGA
                                  C__       AGAC
GAM678  GGA2      3'  AGACAGGATTTCACCATGTTGG 57649    _        C  CA
          CC                   GGC AACATGGTGAAA CC  TCT
                               ||| ||||||||||| ||  |||
                               CCG TTGTACCACTTT GG  AGA
                                 G          A  AC
GAM678  GGA2      3'  AGACAGGATTTCACCATGTTGG 31155    _        C  CA
          CC                   GGC AACATGGTGAAA CC  TCT
                               ||| ||||||||||| ||  |||
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                                CCG TTGTACCACTTT GG  AGA
                                  G          A  AC
GAM678  GMPPB    5'  AGACAGGGTTTCACCAGGTTGG 97430     _  A         CA
                CC                  GGC AAC TGGTGAAACCC  TCT
                                    ||| ||| ||||||||||  |||
                                    CCG TTG ACCACTTTGGG  AGA
                                      G  G          AC
GAM678  GNG4     3'  AGACGGGGTTTCACCATGTTG  16840              A
                                    CAACATGGTGAAACCCC TCT
                                    |||||||||||||||| |||
                                    GTTGTACCACTTTGGGG AGA
                                               C
GAM678  GREB1    3'  AGACGGAGTTTCACTCTTGCTG 28551      A  T_      C  A
                CC                  GGCA CA  GGTGAAAC CC TCT
                                    |||| ||  |||||||| || |||
                                    CCGT GT  TCACTTTG GG AGA
                                      C  TC       A  C
GAM678  GREB1    3'  AGACGGGGTTTCACCATGTTAG 28553     _           A
                CC                  GGC AACATGGTGAAACCCC TCT
                                    ||| |||||||||||||| |||
                                    CCG TTGTACCACTTTGGGG AGA
                                      A             C
GAM678  GRWD     3'  AGACGGGGTTTCACCATGTTGG 49772     _           A
                CC                  GGC AACATGGTGAAACCCC TCT
                                    ||| |||||||||||||| |||
                                    CCG TTGTACCACTTTGGGG AGA
                                      G             C
GAM678  GTPBG3   3'  AGACAAGGTTTCACCATGTTGA 51888    _           CCA
                CC                  GG CAACATGGTGAAACC   TCT
                                    || ||||||||||||||   |||
                                    CC GTTGTACCACTTTGG   AGA
                                     A             AAC
GAM678  H-plk    5'  AGATGGAGTCTTGCTGTGTCAC 32376     CA     TG A  C
                CA                  TGG  ACATGG  A AC CCATCT
                                    |||  ||||||  | || ||||||
                                    ACC  TGTGTC  T TG GGTAGA
                                      AC     GT C  A
GAM678  HRH4     3'  AGATGAAGTCTCACTGTGTTGC 41526           A  CC
                C                    GGCAACATGGTGA AC  CATCT
                                    ||||||||||||| ||  |||||
                                    CCGTTGTGTCACT TG  GTAGA
                                            C  AA
GAM678  HSMPP8   3'  AGACGGAGTTTCGCTCTTGTTG 95124       T_      C  A
                CC                  GGCAACA  GGTGAAAC CC TCT
                                    |||||||  |||||||| || |||
                                    CCGTTGT  TCGCTTTG GG AGA
                                       TC       A  C
GAM678  HSNOV1   3'  AGATGGGGTTTCGCCATGTTGC 34425
                C                    GGCAACATGGTGAAACCCCATCT
                                    ||||||||||||||||||||||
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                                CCGTTGTACCGCTTTGGGGTAGA

GAM678  HSNOV1   3' ATGGGGTTTCACCATGTTGCC  34426
                                GGCAACATGGTGAAACCCCAT
                                |||||||||||||||||||
                                CCGTTGTACCACTTTGGGGTA

GAM678  HSPC065  3' AGATGGGGTTTCACCATGTTGG 27135    _
           CC                    GGC AACATGGTGAAACCCCATCT
                                 ||| ||||||||||||||||||
                                 CCG TTGTACCACTTTGGGGTAGA
                                   G
GAM678  HSPC232  3' AGATGGGGTTCACCATGTTGGC 33654     _        A
           CA                    TGGC AACATGGTGAA CCCCATCT
                                 |||| |||||||||| ||||||||
                                 ACCG TTGTACCACTT GGGGTAGA
                                   G        _
GAM678  IMPACT   3' AGATAGGGTCTTTCTATGTTGC 37999          T  A    C
           C                     GGCAACATGG GA ACCC ATCT
                                 |||||||||| || |||| ||||
                                 CCGTTGTATC TT TGGG TAGA
                                       T  C    A
GAM678  JAM1     3' AGACAGGGTTTCACCATGTTG  34210             CA
                                 CAACATGGTGAAACCC  TCT
                                 |||||||||||||||  |||
                                 GTTGTACCACTTTGGG  AGA
                                       AC
GAM678  JAM1     3' AGACAGGGTTTCACCATGTTG  58503             CA
                                 CAACATGGTGAAACCC  TCT
                                 |||||||||||||||  |||
                                 GTTGTACCACTTTGGG  AGA
                                       AC
GAM678  JAM1     3' AGACAGGGTTTCACCATGTTG  58531             CA
                                 CAACATGGTGAAACCC  TCT
                                 |||||||||||||||  |||
                                 GTTGTACCACTTTGGG  AGA
                                       AC
GAM678  JAM1     3' AGACAGGGTTTCACCATGTTG  58558             CA
                                 CAACATGGTGAAACCC  TCT
                                 |||||||||||||||  |||
                                 GTTGTACCACTTTGGG  AGA
                                       AC
GAM678  JM11     3' AGACAAGGTTTCACCATATTGG 54351     AAC_        CCA
           CC                    GGC   ATGGTGAAACC   TCT
                                 |||   ||||||||||   |||
                                 CCG   TACCACTTTGG   AGA
                                   GTTA         AAC
GAM678  KIAA0087 3' AGATGGGGTTTCACCATCTTGG 29337     AAC_
           CC                    GGC   ATGGTGAAACCCCATCT
                                 |||   ||||||||||||||||
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                                CCG    TACCACTTTGGGGTAGA
                                  GTTC
GAM678  KIAA0161  3'  AGACGGGGTTTCACCATGTTGG 29188     _           A
              CC                  GGC AACATGGTGAAACCCC TCT
                                  ||| |||||||||||||| |||
                                  CCG TTGTACCACTTTGGGG AGA
                                    G            C
GAM678  KIAA0186  3'  TAGATGGGGTTTCACCATGTTG 41117     _            ___
              GCCA                  TGGC AACATGGTGAAACCCCATCT   A
                                  |||| ||||||||||||||||||||  |
                                  ACCG TTGTACCACTTTGGGGTAGA   T
                                    G              ___
GAM678  KIAA0205  3'  AGATGGGGTTTCACCATGTTGG 30200     _
              CC                  GGC AACATGGTGAAACCCCATCT
                                  ||| ||||||||||||||||||
                                  CCG TTGTACCACTTTGGGGTAGA
                                    G
GAM678  KIAA0391  3'  AGACGGGTTTTCACCATGTTGC 28597           C   A
              C                    GGCAACATGGTGAAA CCC TCT
                                  |||||||||||||| ||| |||
                                  CCGTTGTACCACTTT GGG AGA
                                           T   C
GAM678  KIAA0423  5'  GACGGGGGCCATTTTGCCA   89181      C    GAAA   A
                                  TGGCAA ATGGT   CCCC TC
                                  |||||| |||||   |||| ||
                                  ACCGTT TACCG   GGGG AG
                                     T    _____   C
GAM678  KIAA0426  3'  AGACGGGGTTTCACCATGTTGG 28916     _           A
              CC                  GGC AACATGGTGAAACCCC TCT
                                  ||| |||||||||||||| |||
                                  CCG TTGTACCACTTTGGGG AGA
                                    G            C
GAM678  KIAA0446  5'  AGACGGAGTCTCCCTATGTTGC 69439         T  A  C  A
              C                    GGCAACATGG GA AC CC TCT
                                  |||||||||| || || || |||
                                  CCGTTGTATC CT TG GG AGA
                                        C  C  A  C
GAM678  KIAA0459  3'  AGACGGGGTTTCACCATGTTAG 61642     _           A
              CC                  GGC AACATGGTGAAACCCC TCT
                                  ||| |||||||||||||| |||
                                  CCG TTGTACCACTTTGGGG AGA
                                    A            C
GAM678  KIAA0469  3'  AGACAGGGTCTTGCTGTGTTAC 29966    C      TG A    CA
              C                    GG AACATGG  A ACCC  TCT
                                  || |||||||  | ||||  |||
                                  CC TTGTGTC  T TGGG  AGA
                                    A      GT C    AC
GAM678  KIAA0478  3'  AGACAGGGTCTCGCCATGTTGC 30170           A    CA
              C                    GGCAACATGGTGA ACCC  TCT
                                  |||||||||||| ||||  |||
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                                CCGTTGTACCGCT TGGG  AGA
                                      C    AC
GAM678  KIAA0495 3' AGATGGGATTTCACCATGTTGG 63257     _         C
             CC                   GGC AACATGGTGAAA CCCATCT
                                  ||| |||||||||||| |||||||
                                  CCG TTGTACCACTTT GGGTAGA
                                    G          A
GAM678  KIAA0513 3' AGATGGGGTTTCACCATGCTGG 29015     AA_
             CC                   GGC   CATGGTGAAACCCCATCT
                                  |||   ||||||||||||||||||
                                  CCG   GTACCACTTTGGGGTAGA
                                    GTC
GAM678  KIAA0527 3' AGATGGAGTTTCACCATGTTGG 97487     _         C
             CC                   GGC AACATGGTGAAAC CCATCT
                                  ||| |||||||||||| ||||||
                                  CCG TTGTACCACTTTG GGTAGA
                                    G          A
GAM678  KIAA0532 3' AGATGAGGTCTCACTATGTTGC 71316           A   C
             C                     GGCAACATGGTGA ACC CATCT
                                  |||||||||||| ||| |||||
                                  CCGTTGTATCACT TGG GTAGA
                                        C   A
GAM678  KIAA0544 3' AGATGGAGTTTCACTCTTGCTG 71456      A  T_      C
             CC                   GGCA CA  GGTGAAAC CCATCT
                                  |||| ||  |||||||| ||||||
                                  CCGT GT  TCACTTTG GGTAGA
                                    C  TC       A
GAM678  KIAA0561 3' AGACGGGGTTTCACCATGTTG  66464              A
                                  CAACATGGTGAAACCCC TCT
                                  |||||||||||||||| |||
                                  GTTGTACCACTTTGGGG AGA
                                           C
GAM678  KIAA0562 3' AGACGGGGTTTCACCATATTGG 28814     AAC_          A
             CC                   GGC    ATGGTGAAACCCC TCT
                                  |||    |||||||||||| |||
                                  CCG    TACCACTTTGGGG AGA
                                    GTTA          C
GAM678  KIAA0682 3' AGACGGGGTTTCACCATGTGGG 30012     A_           A
             CC                   GGC  ACATGGTGAAACCCC TCT
                                  |||  |||||||||||||| |||
                                  CCG  TGTACCACTTTGGGG AGA
                                    GG            C
GAM678  KIAA0737 3' AGACAGGGTTTCACCATGTTGG 29795     _          CA
             CC                   GGC AACATGGTGAAACCC  TCT
                                  ||| ||||||||||||||  |||
                                  CCG TTGTACCACTTTGGG  AGA
                                    G            AC
GAM678  KIAA0737 3' AGATGGGGTCTCACTATGTTGC 29800           A
             C                     GGCAACATGGTGA ACCCCATCT
                                  |||||||||||| |||||||||
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                                CCGTTGTATCACT TGGGGTAGA
                                      C
GAM678  KIAA0828 3' AGACAGGGTTTCACTATGTTGC 82108              CA
            C                   GGCAACATGGTGAAACCC  TCT
                                |||||||||||||||||  |||
                                CCGTTGTATCACTTTGGG  AGA
                                     AC
GAM678  KIAA0918 3' AGATGGGGCTACTGTTGTTA  73519       TG   AAA
                                TGGCAACA  GTG   CCCCATCT
                                ||||||||  |||   ||||||||
                                ATTGTTGT  CAT   GGGGTAGA
                                    __  C__
GAM678  KIAA0924 3' AGACAAGGTCTTGCTATGTTGC 30350         TG A   CCA
            C                   GGCAACATGG  A ACC   TCT
                                ||||||||||  | |||   |||
                                CCGTTGTATC  T TGG   AGA
                                      GT C   AAC
GAM678  KIAA0924 3' AGATGGGGTTTCACCATATTGG 30352     AAC_
            CC                    GGC    ATGGTGAAACCCCATCT
                                  |||    ||||||||||||||||
                                  CCG    TACCACTTTGGGGTAGA
                                    GTTA
GAM678  KIAA0931 3' AGACGGGGTTTCACCATGTTGG 68002     _            A
            CC                    GGC AACATGGTGAAACCCC TCT
                                  ||| ||||||||||||||| |||
                                  CCG TTGTACCACTTTGGGG AGA
                                    G             C
GAM678  KIAA0961 3' AGATGGGGTTTCACCATGTTGG 30387     _
            CC                    GGC AACATGGTGAAACCCCATCT
                                  ||| ||||||||||||||||||||
                                  CCG TTGTACCACTTTGGGGTAGA
                                    G
GAM678  KIAA1010 3' AGATGGGGTCTTGCTATGTTGC 72537          TG A
            C                   GGCAACATGG  A ACCCCATCT
                                ||||||||||  | |||||||||
                                CCGTTGTATC  T TGGGGTAGA
                                      GT C
GAM678  KIAA1026 3' AGATGAGATTTCACCATGTTGG 71728     _        CCC
            CC                    GGC AACATGGTGAAA   CATCT
                                  ||| ||||||||||||   |||||
                                  CCG TTGTACCACTTT   GTAGA
                                    G          AGA
GAM678  KIAA1040 3' AGATGGGGTTTCACCATTTTGG 72677     AAC_
            CC                    GGC    ATGGTGAAACCCCATCT
                                  |||    ||||||||||||||||
                                  CCG    TACCACTTTGGGGTAGA
                                    GTTT
GAM678  KIAA1041 3' AGATGGGGTTTCACCATGTTGC 30817
            C                   GGCAACATGGTGAAACCCCATCT
                                |||||||||||||||||||||||
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                                CCGTTGTACCACTTTGGGGTAGA

GAM678  KIAA1115 5' AGACAGGGTTTCGCCATGTTGC 30685              CA
              C                  GGCAACATGGTGAAACCC  TCT
                                 ||||||||||||||||||  |||
                                 CCGTTGTACCGCTTTGGG  AGA
                                       AC
GAM678  KIAA1161 5' AGATGGGGTTTACCATGTTGGC 82637     _        A
              CA                   TGGC AACATGGTGAA CCCCATCT
                                   |||| |||||||||| ||||||||
                                   ACCG TTGTACCATTT GGGGTAGA
                                    G        _
GAM678  KIAA1170 3' AGACAGAGTTTCGCTCTTGTTG 70409       T_      CCCA
              CC                   GGCAACA  GGTGAAAC    TCT
                                   |||||||  ||||||||    |||
                                   CCGTTGT  TCGCTTTG    AGA
                                      TC       AGAC
GAM678  KIAA1170 3' GGGTTTCACCATGTTAGCC    70418    _
                                   GGC AACATGGTGAAACCC
                                   ||| ||||||||||||||
                                   CCG TTGTACCACTTTGGG
                                    A
GAM678  KIAA1185 3' AGACGGGGTTTCACCATTTTGA 63283    _  C          A
              CC                   GG CAA ATGGTGAAACCCC TCT
                                   || ||| ||||||||||||| |||
                                   CC GTT TACCACTTTGGGG AGA
                                    A  T           C
GAM678  KIAA1193 3' AGATGGGGTTTCTCCTTATTGC 68262       CAT  T
              C                    GGCAA   GG GAAACCCCATCT
                                   |||||   || ||||||||||||
                                   CCGTT   CC CTTTGGGGTAGA
                                      ATT  T
GAM678  KIAA1198 3' AGACGGGGTTTCACCATGTTGG 63988     _           A
              CC                   GGC AACATGGTGAAACCCC TCT
                                   ||| |||||||||||||| |||
                                   CCG TTGTACCACTTTGGGG AGA
                                    G             C
GAM678  KIAA1198 3' AGACGGGGTTTCACCATGTTGG 63989     _           A
              CC                   GGC AACATGGTGAAACCCC TCT
                                   ||| |||||||||||||| |||
                                   CCG TTGTACCACTTTGGGG AGA
                                    G             C
GAM678  KIAA1198 3' AGATGGGGTTTCACCATGTTGA 64000    _
              CC                   GG CAACATGGTGAAACCCCATCT
                                   || ||||||||||||||||||||
                                   CC GTTGTACCACTTTGGGGTAGA
                                    A
GAM678  KIAA1200 3' AGACGGGGTTTCACCATGTTGG 63027     _           A
              CC                   GGC AACATGGTGAAACCCC TCT
                                   ||| |||||||||||||| |||
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                                CCG TTGTACCACTTTGGGG AGA
                                  G            C
GAM678  KIAA1210 3'  AGACGGGGTTTCACCATGTTGG 98062    _           A
                CC                GGC AACATGGTGAAACCCC TCT
                                  ||| |||||||||||||| |||
                                CCG TTGTACCACTTTGGGG AGA
                                  G            C
GAM678  KIAA1254 3'  AGATGGGGTTTCACCATGTTGG 70552    _
                CC                GGC AACATGGTGAAACCCCATCT
                                  ||| ||||||||||||||||||
                                CCG TTGTACCACTTTGGGGTAGA
                                  G
GAM678  KIAA1257 3'  AGACAAGGTCTTGCTATGTTGC 63388         TG A  CCA
                C                  GGCAACATGG  A ACC   TCT
                                  ||||||||||  | |||  |||
                                CCGTTGTATC  T TGG   AGA
                                      GT C   AAC
GAM678  KIAA1465 3'  AGACGGGGTTTCACCATGTTGG 61483    _           A
                CC                GGC AACATGGTGAAACCCC TCT
                                  ||| |||||||||||||| |||
                                CCG TTGTACCACTTTGGGG AGA
                                  G            C
GAM678  KIAA1467 3'  AGACGGGGTTTCACCATGTTGG 72058    _           A
                CC                GGC AACATGGTGAAACCCC TCT
                                  ||| |||||||||||||| |||
                                CCG TTGTACCACTTTGGGG AGA
                                  G            C
GAM678  KIAA1497 5'  AGACAGGGTTTCACCATGTTGG 68109    _           CA
                TCA                TGGC AACATGGTGAAACCC  TCT
                                  |||| ||||||||||||||  |||
                                ACTG TTGTACCACTTTGGG  AGA
                                  G            AC
GAM678  KIAA1530 3'  AGATGAGGTCTCACTGTGTTGC 68546          A  C
                C                  GGCAACATGGTGA ACC CATCT
                                  |||||||||||| ||| |||||
                                CCGTTGTGTCACT TGG GTAGA
                                       C  A
GAM678  KIAA1610 3'  ATGAGGTTTCATAATTCTGCC  67738     ACATG      C
                                GGCA    GTGAAACC CAT
                                ||||    |||||||| |||
                                CCGT    TACTTTGG GTA
                                  CTTAA       A
GAM678  KIAA1617 3'  AGACAGGGTTTCACCATGTTG  93068           CA
                                CAACATGGTGAAACCC  TCT
                                ||||||||||||||||  |||
                                GTTGTACCACTTTGGG  AGA
                                       AC
GAM678  KIAA1649 3'  AGACAAAGTCTCACTCTGTTGC 51212       T    A  CCCA
                CA                 TGGCAACA GGTGA AC    TCT
                                  |||||||| ||||| ||   |||
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                                ACCGTTGT TCACT TG    AGA
                                    C     C  AAAC
GAM678  KIAA1649  3'  AGATGAGGTTTCACCGTGTTGC 51216             C
                                GCAACATGGTGAAACC CATCT
                                |||||||||||||||| |||||
                                CGTTGTGCCACTTTGG GTAGA
                                       A
GAM678  KIAA1712  3'  AGACAGGGTTTCACCATGTTGC 68147              CA
            C                    GGCAACATGGTGAAACCC  TCT
                                |||||||||||||||||  |||
                                CCGTTGTACCACTTTGGG  AGA
                                       AC
GAM678  KIAA1737  3'  AGATGGAGTTTCGCTCTTGTTG 67929        T_       C
            CC                     GGCAACA  GGTGAAAC CCATCT
                                |||||||  |||||||| ||||||
                                CCGTTGT  TCGCTTTG GGTAGA
                                    TC       A
GAM678  KIAA1755  3'  AGATGGGGCCTCACTACATTGC 62004       CA     AA
            C                    GGCAA  TGGTGA  CCCCATCT
                                |||||  ||||||  ||||||||
                                CCGTT  ATCACT  GGGGTAGA
                                   AC     CC
GAM678  KIAA1784  3'  GGGGTTTCACCATGTTGCT   65751
                                GGCAACATGGTGAAACCCC
                                ||||||||||||||||||
                                TCGTTGTACCACTTTGGGG

GAM678  KIAA1821  3'  AGACAGGGTCTCACTGTGTTGC 72256           A   CA
            C                    GGCAACATGGTGA ACCC  TCT
                                ||||||||||||| ||||  |||
                                CCGTTGTGTCACT TGGG  AGA
                                       C   AC
GAM678  KIAA1829  3'  AGATGGGGTTTCGCGAGTTGCC 62629       ATG
                                GGCAAC   GTGAAACCCCATCT
                                ||||||   ||||||||||||||
                                CCGTTG   CGCTTTGGGGTAGA
                                   AG_
GAM678  KIAA1871  3'  AGATGAGGTCTCACTATGTTGC 61892           A  C
            C                    GGCAACATGGTGA ACC CATCT
                                ||||||||||||| ||| |||||
                                CCGTTGTATCACT TGG GTAGA
                                       C   A
GAM678  KIAA1922  5'  AGACAAAGTTTCGCTCTTGTTG 73980        T_       CCCA
            CC                     GGCAACA  GGTGAAAC    TCT
                                |||||||  ||||||||    |||
                                CCGTTGT  TCGCTTTG    AGA
                                    TC       AAAC
GAM678  KIAA1975  5'  AGATGGGGTTTCACCATGTT   74411
                                AACATGGTGAAACCCCATCT
                                ||||||||||||||||||||
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                                TTGTACCACTTTGGGGTAGA

GAM678  KLK7     3'  AGACAGGGTTTCACCATGTTGG 58385     _           CA
                CC                   GGC AACATGGTGAAACCC  TCT
                                     ||| ||||||||||||||  |||
                                     CCG TTGTACCACTTTGGG  AGA
                                       G            AC
GAM678  KLK7     3'  AGACAGGGTTTCACCATGTTGG 18538     _           CA
                CC                   GGC AACATGGTGAAACCC  TCT
                                     ||| ||||||||||||||  |||
                                     CCG TTGTACCACTTTGGG  AGA
                                       G            AC
GAM678  LAMP3    3'  AGACGGAGTTTCACTCTTGTCA 60193       CAT      C  A
                                     TGGCAA   GGTGAAAC CC TCT
                                     ||||||   |||||||| || |||
                                     ACTGTT   TCACTTTG GG AGA
                                        C__       A  C
GAM678  LAMP3    3'  AGACGGGGTTTCACCATGTTGG 60196     _           A
                CC                   GGC AACATGGTGAAACCCC TCT
                                     ||| ||||||||||||||| |||
                                     CCG TTGTACCACTTTGGGG AGA
                                       G            C
GAM678  LY75     3'  AGATGGGGTTTCACCATGTTGG 11386     _
                CC                   GGC AACATGGTGAAACCCCATCT
                                     ||| ||||||||||||||||||
                                     CCG TTGTACCACTTTGGGGTAGA
                                       G
GAM678  MAP-1    3'  AGACGGGGTTTCACCATGTTGG 42432     _           A
                CC                   GGC AACATGGTGAAACCCC TCT
                                     ||| ||||||||||||||| |||
                                     CCG TTGTACCACTTTGGGG AGA
                                       G            C
GAM678  MCLC     3'  AGATGGGGTTTCACCATGTTG  31376
                                     CAACATGGTGAAACCCCATCT
                                     ||||||||||||||||||||
                                     GTTGTACCACTTTGGGGTAGA

GAM678  MGC10200 3'  AGATGGGGTTTCACCATGTTGC 59633
                C                     GGCAACATGGTGAAACCCCATCT
                                      ||||||||||||||||||||||
                                      CCGTTGTACCACTTTGGGGTAGA

GAM678  MGC13159 3'  AGACAGGGTCTTCTATGTTGCC 53034          T  A    CA
                                     GGCAACATGG GA ACCC  TCT
                                     |||||||||| || ||||  |||
                                     CCGTTGTATC TT TGGG  AGA
                                           _ C   AC
GAM678  MGC15563 3'  AGATGGGATCTCACCATGTTGC 52858           AAC
                C                     GGCAACATGGTGA   CCCATCT
                                      ||||||||||||   |||||||
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                                CCGTTGTACCACT  GGGTAGA
                                       CTA
GAM678  MGC21675 3' AGACAGAGTTTCGCTCTTGTTG 54581       T_      CCCA
           CC                   GGCAACA  GGTGAAAC   TCT
                                |||||||  ||||||||   |||
                                CCGTTGT  TCGCTTTG   AGA
                                   TC       AGAC
GAM678  MGC21675 3' AGATGGGGTTTCACCATGTTG  54584
                                CAACATGGTGAAACCCCATCT
                                ||||||||||||||||||||
                                GTTGTACCACTTTGGGGTAGA

GAM678  MGC22014 3' GGGGCCGTGCCCACCATGTTGC 65115          AAA____
           CA                   TGGCAACATGGTG      CCCC
                                ||||||||||||       ||||
                                ACCGTTGTACCAC      GGGG
                                       CCGTGCC
GAM678  MGC2474  3' AGATGGGGTTTCACCATGTTG  43947
                                CAACATGGTGAAACCCCATCT
                                ||||||||||||||||||||
                                GTTGTACCACTTTGGGGTAGA

GAM678  MGC2603  3' AGACGAGGTTTCACCATATTAG 44070     _ C        CCA
           CC                   GGC AA ATGGTGAAACC   TCT
                                ||| || ||||||||||   |||
                                CCG TT TACCACTTTGG   AGA
                                  A  A         AGC
GAM678  MGC3113  3' AGACAGGGTTTCGCCACATTGC 44057      CA        CA
           C                    GGCAA  TGGTGAAACCC  TCT
                                |||||  ||||||||||  |||
                                CCGTT  ACCGCTTTGGG  AGA
                                   AC         AC
GAM678  MGC5149  3' AGATGGGGTTTCACCACATTGG 72751     AACA_
           CC                   GGC    TGGTGAAACCCCATCT
                                |||    ||||||||||||||||
                                CCG    ACCACTTTGGGGTAGA
                                  GTTAC
GAM678  MLZE    5' AGACAGGGTTTCACCATCTTGG 49444     AAC_        CA
           CC                   GGC    ATGGTGAAACCC  TCT
                                |||    ||||||||||||  |||
                                CCG    TACCACTTTGGG  AGA
                                  GTTC          AC
GAM678  MRAS    3' AGACAGGGTCTGGCTTTTGCCA 25235      CAT   GAA   CA
                                TGGCAA   GGT   ACCC  TCT
                                ||||||   |||   ||||  |||
                                ACCGTT   TCG   TGGG  AGA
                                   T__   GTC    AC
GAM678  MRPS27  3' AGATGGGGTTTCACCATGTTG  31318
                                CAACATGGTGAAACCCCATCT
                                ||||||||||||||||||||
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                                GTTGTACCACTTTGGGGTAGA

GAM678  MtFMT    3'  AGATGGGGTTTCACCATGTTG  58328
                                CAACATGGTGAAACCCCATCT
                                ||||||||||||||||||||
                                GTTGTACCACTTTGGGGTAGA

GAM678  NAPG     5'  AGATGGAGTTGCTCCATGTTGC 98533          TGA   C
                                GCAACATGG   AAC CCATCT
                                |||||||||   ||| |||||||
                                CGTTGTACC   TTG GGTAGA
                                      TCG   A
GAM678  NDUFC2   3'  AGACGGGGTTTCACCATGTTGG 17023     _            A
              CC                  GGC AACATGGTGAAACCCC TCT
                                ||| ||||||||||||||| |||
                                CCG TTGTACCACTTTGGGG AGA
                                  G             C
GAM678  NXN      3'  AGATGGGGTTTCACCATGTTG  42664
                                CAACATGGTGAAACCCCATCT
                                ||||||||||||||||||||
                                GTTGTACCACTTTGGGGTAGA

GAM678  OCT11    3'  AGATGGGGTTTCACCATGTTG  27581
                                CAACATGGTGAAACCCCATCT
                                ||||||||||||||||||||
                                GTTGTACCACTTTGGGGTAGA

GAM678  OR51E2   3'  AGACAGAGTTTCACCATGTTGG 48500     _          CCCA
              CC                  GGC AACATGGTGAAAC    TCT
                                ||| ||||||||||||    |||
                                CCG TTGTACCACTTTG    AGA
                                  G           AGAC
GAM678  OR51E2   3'  AGATGGGGTCTCGCTCTGTCAC 48503     CA   T    A
              CA                  TGG  ACA GGTGA ACCCCATCT
                                |||  ||| ||||| |||||||||
                                ACC  TGT TCGCT TGGGGTAGA
                                  AC   C    C
GAM678  OSBPL2   3'  AGACGGAGTTTCACTCTTGTTG 29895        T_      C  A
              CC                  GGCAACA  GGTGAAAC CC TCT
                                |||||||  |||||||| || |||
                                CCGTTGT  TCACTTTG GG AGA
                                   TC       A  C
GAM678  OSBPL2   3'  AGACGGAGTTTCACTCTTGTTG 58478        T_      C  A
              CC                  GGCAACA  GGTGAAAC CC TCT
                                |||||||  |||||||| || |||
                                CCGTTGT  TCACTTTG GG AGA
                                   TC       A  C
GAM678  PELI1    5'  AGACGGGGTTTCACCATGTTGC 40619               A
              C                   GGCAACATGGTGAAACCCC TCT
                                ||||||||||||||||||| |||
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                                CCGTTGTACCACTTTGGGG AGA
                                      C
GAM678  PELI1    5'  AGATGGGGTTTCACCATGTTGG 40623     _
           CC                   GGC AACATGGTGAAACCCCATCT
                                ||| ||||||||||||||||||||
                                CCG TTGTACCACTTTGGGGTAGA
                                  G
GAM678  PIG7     3'  AGATGGGGTCTTACTATGTTGC 17967            A
           C                    GGCAACATGGTGA ACCCCATCT
                                |||||||||||| |||||||||
                                CCGTTGTATCATT TGGGGTAGA
                                       C
GAM678  PRO1992  3'  AGACAGAGTTTCGCTCTTGTCA 26894       CAT       CCCA
                                TGGCAA   GGTGAAAC    TCT
                                ||||||   ||||||||    |||
                                ACTGTT   TCGCTTTG    AGA
                                   C__       AGAC
GAM678  PRO1992  3'  AGATGGGGTTTTACCATGTGGC 26895      A
           CA                   TGGC ACATGGTGAAACCCCATCT
                                |||| ||||||||||||||||||||
                                ACCG TGTACCATTTTGGGGTAGA
                                  G
GAM678  RAB21    3'  AGACGGGGTTTCACCAGGTTAG 31080     _  A         A
           CC                   GGC AAC TGGTGAAACCCC TCT
                                ||| ||| |||||||||||| |||
                                CCG TTG ACCACTTTGGGG AGA
                                  A  G          C
GAM678  RAB33B   3'  AGATGGGGTTTCACCATGTTGG 49317     _
           CC                   GGC AACATGGTGAAACCCCATCT
                                ||| ||||||||||||||||||||
                                CCG TTGTACCACTTTGGGGTAGA
                                  G
GAM678  RNF8     3'  AGACAGGGTTTCACCATGTTGG 15557     _           CA
           CC                   GGC AACATGGTGAAACCC  TCT
                                ||| ||||||||||||||  |||
                                CCG TTGTACCACTTTGGG  AGA
                                  G            AC
GAM678  SAMHD1   3'  AGACAAGGTTTTGCTCTGTTGC 61975       T  TG    CCA
           C                    GGCAACA GG  AAACC   TCT
                                |||||||  ||  |||||   |||
                                CCGTTGT TC  TTTGG   AGA
                                   C  GT     AAC
GAM678  SARM     3'  AGACAAGGTCTTGCTATGTTGC 31276         TG A   CCA
           C                    GGCAACATGG  A ACC   TCT
                                ||||||||||  | |||   |||
                                CCGTTGTATC  T TGG   AGA
                                      GT C   AAC
GAM678  SCAMP-4  3'  AGACAGAGTTTCACTCTGTCGC 55332     A   T      CCCA
           C                    GGC ACA GGTGAAAC    TCT
                                ||| ||| ||||||||    |||
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                                CCG TGT TCACTTTG    AGA
                                  C  C       AGAC
GAM678  SCAMP-4   3'  AGATGGGGTTTCACCATGTTGG 55335    _
              CC                  GGC AACATGGTGAAACCCCATCT
                                  ||| ||||||||||||||||||||
                                  CCG TTGTACCACTTTGGGGTAGA
                                    G
GAM678  SCAND2    3'  AGATGGGGTCACAATGCTGC  54428    A  G   AA
                                  GCA CAT GTGA  CCCCATCT
                                  ||| ||| ||||  ||||||||
                                  CGT GTA CACT  GGGGTAGA
                                    C  A   __
GAM678  SCYA16    3'  AGACGGGATTCTACCATGTTGC 17165          A  C   A
              C                    GGCAACATGGTG AA CCC TCT
                                  ||||||||||||| || ||| |||
                                  CCGTTGTACCAT TT GGG AGA
                                         C  A   C
GAM678  SCYA22    3'  AGACGAGGCTTCACCATGTTGG 92571    _        A  CCA
              CC                  GGC AACATGGTGAA CC   TCT
                                  ||| ||||||||||| ||   |||
                                  CCG TTGTACCACTT GG   AGA
                                    G          C  AGC
GAM678  SCYA22    3'  AGACGGGGTTTTGCCATGTTAC 92574    C      TG      A
              C                    GG AACATGG  AAACCCC TCT
                                  || |||||||  ||||||| |||
                                  CC TTGTACC  TTTGGGG AGA
                                    A      GT      C
GAM678  SCYA22    3'  AGATGGAGTTTCGCTCTTGTCA 92576       CAT      C
                                  TGGCAA   GGTGAAAC CCATCT
                                  ||||||   |||||||| ||||||
                                  ACTGTT   TCGCTTTG GGTAGA
                                     C__       A
GAM678  SERF1B    3'  AGATGGGGTTTCACCATGTTGG 43688    _
              CC                  GGC AACATGGTGAAACCCCATCT
                                  ||| ||||||||||||||||||||
                                  CCG TTGTACCACTTTGGGGTAGA
                                    G
GAM678  SFXN2     3'  AGACGGGGTTTCACCATGCTGG 74370    AA_          A
              CC                  GGC   CATGGTGAAACCCC TCT
                                  |||   |||||||||||||| |||
                                  CCG   GTACCACTTTGGGG AGA
                                    GTC           C
GAM678  SLC12A8   3'  AGACAGGGTTTCACCATGTTGG 45231    _          CA
              CC                  GGC AACATGGTGAAACCC  TCT
                                  ||| ||||||||||||||  |||
                                  CCG TTGTACCACTTTGGG  AGA
                                    G           AC
GAM678  SQV7L     5'  AGATGGGATCTTTCTATGTTGC 71092          TGAAAC
              C                    GGCAACATGG     CCCATCT
                                  ||||||||||     |||||||
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                                CCGTTGTATC     GGGTAGA
                                     TTTCTA
GAM678  SREC     3'  AGACAGGGTTTCACCATGTTAG 14896     _          CA
              CC                   GGC AACATGGTGAAACCC  TCT
                                   ||| ||||||||||||||  |||
                                   CCG TTGTACCACTTTGGG  AGA
                                     A            AC
GAM678  SS-56    3'  AGACGGAGTTTCACCATGTTAG 60343     _         C  A
              CT                   GGC AACATGGTGAAAC CC TCT
                                   ||| |||||||||||| || |||
                                   TCG TTGTACCACTTTG GG AGA
                                     A          A  C
GAM678  SYT13    3'  AGATGGGGTTTCACCATGTTGG 95093     _
              CC                   GGC AACATGGTGAAACCCCATCT
                                   ||| ||||||||||||||||||
                                   CCG TTGTACCACTTTGGGGTAGA
                                     G
GAM678  TCL6     5'  AGACGAGGTTTCACCATGTTGG 40504     _          CCA
              CC                   GGC AACATGGTGAAACC   TCT
                                   ||| ||||||||||||   |||
                                   CCG TTGTACCACTTTGG   AGA
                                     G            AGC
GAM678  TCL6     5'  AGACGAGGTTTCACCATGTTGG 27750     _          CCA
              CC                   GGC AACATGGTGAAACC   TCT
                                   ||| ||||||||||||   |||
                                   CCG TTGTACCACTTTGG   AGA
                                     G            AGC
GAM678  TCL6     5'  AGACGAGGTTTCACCATGTTGG 25898     _          CCA
              CC                   GGC AACATGGTGAAACC   TCT
                                   ||| ||||||||||||   |||
                                   CCG TTGTACCACTTTGG   AGA
                                     G            AGC
GAM678  TCL6     5'  AGACGAGGTTTCACCATGTTGG 40458     _          CCA
              CC                   GGC AACATGGTGAAACC   TCT
                                   ||| ||||||||||||   |||
                                   CCG TTGTACCACTTTGG   AGA
                                     G            AGC
GAM678  TERA     3'  AGACGGGGTTTCACCACGTTGG 41414     _  A        A
              CC                   GGC AAC TGGTGAAACCCC TCT
                                   ||| ||| ||||||||||| |||
                                   CCG TTG ACCACTTTGGGG AGA
                                     G  C          C
GAM678  TGIF2    3'  AGACGGGGTTTCACCATCTTGG 41740     AAC_         A
              CC                   GGC    ATGGTGAAACCCC TCT
                                   |||    |||||||||||| |||
                                   CCG    TACCACTTTGGGG AGA
                                     GTTC          C
GAM678  TRIM16   3'  AGATGGGGTTTCACCATGTTGG 22363     _
              CC                   GGC AACATGGTGAAACCCCATCT
                                   ||| ||||||||||||||||||
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                                CCG TTGTACCACTTTGGGGTAGA
                                  G
GAM678  TU12B1-TY 3'  AGATGGGGTTTCACCATGTTGG 33825     _
           CC                     GGC AACATGGTGAAACCCCATCT
                                  ||| ||||||||||||||||||||
                                  CCG TTGTACCACTTTGGGGTAGA
                                    G
GAM678  TU12B1-TY 3'  AGACGGGGTTTCACCATGTTGG 33820     _           A
           CC                     GGC AACATGGTGAAACCCC TCT
                                  ||| |||||||||||||| |||
                                  CCG TTGTACCACTTTGGGG AGA
                                    G             C
GAM678  TUCAN    3'  AGACAGGGTTTCACCATTTTGG 30962     AAC_         CA
           CC                     GGC    ATGGTGAAACCC  TCT
                                  |||    ||||||||||||  |||
                                  CCG    TACCACTTTGGG  AGA
                                    GTTT          AC
GAM678  UBF-fl   3'  ATGGGGTTTCACCATGCTGGCC 52616      AA_
           A                       TGGC   CATGGTGAAACCCCAT
                                  ||||   ||||||||||||||||
                                  ACCG   GTACCACTTTGGGGTA
                                    GTC
GAM678  VDU1     3'  AGATGGGGTTTCACCATGTTGG 31116     _
           CC                     GGC AACATGGTGAAACCCCATCT
                                  ||| ||||||||||||||||||||
                                  CCG TTGTACCACTTTGGGGTAGA
                                    G
GAM678  WBSCR23   3'  AGACGGGGTTTCACCATGTTGG 47411     _           A
           CC                     GGC AACATGGTGAAACCCC TCT
                                  ||| |||||||||||||| |||
                                  CCG TTGTACCACTTTGGGG AGA
                                    G             C
GAM678  LOC113523 5'  AGACAGGGTTTCACCATGTTAG 73409     _          CA
           CC                     GGC AACATGGTGAAACCC  TCT
                                  ||| ||||||||||||||  |||
                                  CCG TTGTACCACTTTGGG  AGA
                                    A             AC
GAM678  LOC115648 3'  AGACGGGGTTTCACCATGTTG  60015              A
                                  CAACATGGTGAAACCCC TCT
                                  |||||||||||||||| |||
                                  GTTGTACCACTTTGGGG AGA
                                              C
GAM678  LOC120105 5'  GGGTTCACCATACCGCCA    76027      AAC       A
                                  TGGC   ATGGTGAA CCC
                                  ||||   |||||||| |||
                                  ACCG   TACCACTT GGG
                                    CCA       _
GAM678  LOC120114 3'  AGATGGGGTTTCACCATGTTGG 76038     _
           CC                     GGC AACATGGTGAAACCCCATCT
                                  ||| ||||||||||||||||||||
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                                CCG TTGTACCACTTTGGGGTAGA
                                  G
GAM678  LOC120224 5'  AGACAGGGTTTCACCATGTTTG 57880      _          CA
                TC                GGCAA CATGGTGAAACCC  TCT
                                  ||||| |||||||||||||  |||
                                  CTGTT GTACCACTTTGGG  AGA
                                    T           AC
GAM678  LOC120224 5'  AGATGGAGTTTTGCTTTTGTCA 57883       CAT  TG    C
                                  TGGCAA   GG  AAAC CCATCT
                                  ||||||   ||  |||| ||||||
                                  ACTGTT   TC  TTTG GGTAGA
                                     T__  GT    A
GAM678  LOC126661 3'  AGACAGGTTTTCACCATGTTGC 75043             C  CA
                C                  GGCAACATGGTGAAA CC  TCT
                                  |||||||||||||||  ||  |||
                                  CCGTTGTACCACTTT GG  AGA
                                            T  AC
GAM678  LOC126661 3'  AGATGGGGTTTCACCATGTTGG 75047     _
                CC                GGC AACATGGTGAAACCCCATCT
                                  ||| ||||||||||||||||||||
                                  CCG TTGTACCACTTTGGGGTAGA
                                    G
GAM678  LOC126669 3'  AGACGAAGTCTCGCTGTGTTGC 75920           A  CCCA
                C                  GGCAACATGGTGA AC    TCT
                                  ||||||||||||  ||    |||
                                  CCGTTGTGTCGCT TG    AGA
                                          C  AAGC
GAM678  LOC128077 3'  AGACAGGGTTTCACCATGTTGG 75198     _          CA
                CC                GGC AACATGGTGAAACCC  TCT
                                  ||| |||||||||||||  |||
                                  CCG TTGTACCACTTTGGG  AGA
                                    G            AC
GAM678  LOC128077 3'  AGACGGGGTTTCACCATGTTAG 75201     _          A
                CC                GGC AACATGGTGAAACCCC TCT
                                  ||| ||||||||||||||| |||
                                  CCG TTGTACCACTTTGGGG AGA
                                    A            C
GAM678  LOC128989 3'  AGACGGGGTTTCACCATGTTG  75308             A
                                  CAACATGGTGAAACCCC TCT
                                  ||||||||||||||||| |||
                                  GTTGTACCACTTTGGGG AGA
                                             C
GAM678  LOC132625 3'  AGATGGGGTTTCACCATGTTGG 76432     _
                CC                GGC AACATGGTGAAACCCCATCT
                                  ||| ||||||||||||||||||||
                                  CCG TTGTACCACTTTGGGGTAGA
                                    G
GAM678  LOC135154 3'  AGACAAGGTTTCACCATGTTAG 75721     _          CCA
                CC                GGC AACATGGTGAAACC   TCT
                                  ||| ||||||||||||||   |||
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                                CCG TTGTACCACTTTGG   AGA
                                  A           AAC
GAM678  LOC143187 3'  AGATGGAGTTTCACCATGTTGG 59753    _         C
                CC                GGC AACATGGTGAAAC CCATCT
                                  ||| |||||||||||| ||||||
                                  CCG TTGTACCACTTTG GGTAGA
                                    G           A
GAM678  LOC144519 5'  AGACGGGGTTTTGCCATGTTGC 77366        TG      A
                C                 GGCAACATGG  AAACCCC TCT
                                  |||||||||  ||||||| |||
                                  CCGTTGTACC  TTTGGGG AGA
                                        GT      C
GAM678  LOC144667 3'  AGATGGGGTCTCCCTATGTTGC 84085        T  A
                C                 GGCAACATGG GA ACCCCATCT
                                  |||||||||| || |||||||||
                                  CCGTTGTATC CT TGGGGTAGA
                                        C  C
GAM678  LOC145082 5'  AGACGAGGTTTTGCCATGTTGC 84179        TG    CCA
                C                 GGCAACATGG  AAACC   TCT
                                  |||||||||  |||||   |||
                                  CCGTTGTACC  TTTGG   AGA
                                        GT    AGC
GAM678  LOC145268 5'  AGACAGAGTTTCACCATGTTGG 77569    _         CCCA
                CC                GGC AACATGGTGAAAC    TCT
                                  ||| ||||||||||||    |||
                                  CCG TTGTACCACTTTG    AGA
                                    G           AGAC
GAM678  LOC145873 5'  AGACAAGGTCTCGCCATGTTGC 78009          A   CCA
                C                 GGCAACATGGTGA ACC   TCT
                                  |||||||||||| |||   |||
                                  CCGTTGTACCGCT TGG   AGA
                                        C   AAC
GAM678  LOC146050 3'  AGATGGGGTTTCACCATGTTGG 78099    _
                CC                GGC AACATGGTGAAACCCCATCT
                                  ||| ||||||||||||||||||
                                  CCG TTGTACCACTTTGGGGTAGA
                                    G
GAM678  LOC146229 3'  AGACGGGGTTTCACCATGTTGG 78252    _          A
                CC                GGC AACATGGTGAAACCCC TCT
                                  ||| |||||||||||||| |||
                                  CCG TTGTACCACTTTGGGG AGA
                                    G             C
GAM678  LOC146229 3'  AGATGGAGTTTCATTCTTGTTG 78258       T_      C
                CC                GGCAACA  GGTGAAAC CCATCT
                                  |||||||  |||||||| ||||||
                                  CCGTTGT  TTACTTTG GGTAGA
                                     TC       A
GAM678  LOC146429 5'  AGACAGGGTTTCACCATGATAG 84660     AA_         CA
                CC                GGC   CATGGTGAAACCC  TCT
                                  |||   |||||||||||||  |||
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                                CCG   GTACCACTTTGGG  AGA
                                  ATA           AC
GAM678   LOC146784 5'  AGATGGAGTTTCACTCTTGTTG 78702        T_      C
                 CC                GGCAACA  GGTGAAAC CCATCT
                                   ||||||| ||||||| ||||||
                                   CCGTTGT  TCACTTTG GGTAGA
                                      TC       A
GAM678   LOC146784 5'  AGATGGGGTTTCACCATGTTGG 78704     _
                 CC                GGC AACATGGTGAAACCCCATCT
                                   ||| ||||||||||||||||||||
                                   CCG TTGTACCACTTTGGGGTAGA
                                     G
GAM678   LOC146894 3'  AGATGGGGTTTCACCATGTTGG 59851     _
                 CC                GGC AACATGGTGAAACCCCATCT
                                   ||| ||||||||||||||||||||
                                   CCG TTGTACCACTTTGGGGTAGA
                                     G
GAM678   LOC146901 3'  AGACGGGGTTTCACCATGTTGG 84884     _           A
                 CC                GGC AACATGGTGAAACCCC TCT
                                   ||| |||||||||||||| |||
                                   CCG TTGTACCACTTTGGGG AGA
                                     G            C
GAM678   LOC146952 5'  AGACAGGGTTTCACCACATTGG 84921     AACA_       CA
                 CC                GGC    TGGTGAAACCC  TCT
                                   |||    ||||||||||  |||
                                   CCG    ACCACTTTGGG  AGA
                                     GTTAC          AC
GAM678   LOC147071 5'  AGACGGAGTTTCACCATGTTG  73347           C  A
                                   CAACATGGTGAAAC CC TCT
                                   |||||||||||||| || |||
                                   GTTGTACCACTTTG GG AGA
                                            A  C
GAM678   LOC147080 5'  AGACAAGGTTTCACCATGTTAG 85024     _          CCA
                 CC                GGC AACATGGTGAAACC   TCT
                                   ||| ||||||||||||||   |||
                                   CCG TTGTACCACTTTGG   AGA
                                     A           AAC
GAM678   LOC147166 3'  AGATGGGGTTTCACCATGTTGG 78880     _
                 CC                GGC AACATGGTGAAACCCCATCT
                                   ||| ||||||||||||||||||||
                                   CCG TTGTACCACTTTGGGGTAGA
                                     G
GAM678   LOC147276 3'  AGATGGAGTTTCACTCTTGTTG 78951        T_      C
                 CC                GGCAACA  GGTGAAAC CCATCT
                                   ||||||| ||||||| ||||||
                                   CCGTTGT  TCACTTTG GGTAGA
                                      TC       A
GAM678   LOC147429 3'  AGATGGGGTTTCACCATGTTAG 78989     _
                 TC                GGC AACATGGTGAAACCCCATCT
                                   ||| ||||||||||||||||||||
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                                CTG TTGTACCACTTTGGGGTAGA
                                  A
GAM678  LOC147817 3'  AGACAGGGCTTCACCATGTTGG 79165    G         A   CA
          CA                    TG CAACATGGTGAA CCC  TCT
                                || |||||||||||| |||  |||
                                AC GTTGTACCACTT GGG  AGA
                                 G          C   AC
GAM678  LOC147817 3'  AGACGGAGTTTCACCATATTGG 79166    AAC_       C  A
          CT                    GGC   ATGGTGAAAC CC TCT
                                |||   |||||||||| || |||
                                TCG   TACCACTTTG GG AGA
                                  GTTA        A  C
GAM678  LOC147841 3'  AGATGGAGTTTCACCATGGTGG 79222    AA_        C
          TC                    GGC   CATGGTGAAAC CCATCT
                                |||   |||||||||| ||||||
                                CTG   GTACCACTTTG GGTAGA
                                  GTG         A
GAM678  LOC148137 3'  AGATGGAGTTTCACCCTTGTTG 59087       T_      C
          CC                    GGCAACA  GGTGAAAC CCATCT
                                |||||||  |||||||| ||||||
                                CCGTTGT  CCACTTTG GGTAGA
                                   TC       A
GAM678  LOC148189 5'  AGACGGGGTTTCACCATGTTGA 79444    _           A
          CC                    GG CAACATGGTGAAACCCC TCT
                                || |||||||||||||||| |||
                                CC GTTGTACCACTTTGGGG AGA
                                 A             C
GAM678  LOC148443 3'  GGGTCTCACCATGTTGCC    79602           A
                                GGCAACATGGTGA ACCC
                                |||||||||||| ||||
                                CCGTTGTACCACT TGGG
                                        C
GAM678  LOC148645 5'  AGACAGGGCCTCACTCTGTTGC 85327        T    AA   CA
          CA                    TGGCAACA GGTGA  CCC  TCT
                                |||||||| |||||  |||  |||
                                ACCGTTGT TCACT  GGG  AGA
                                   C    CC   AC
GAM678  LOC148887 5'  AGACAGGGTTTCACCATGTTG  85389            CA
                                CAACATGGTGAAACCC  TCT
                                ||||||||||||||||  |||
                                GTTGTACCACTTTGGG  AGA
                                        AC
GAM678  LOC149194 3'  AGATGGGATCTCATTTTGTTGC 79975       TG   AAC
          C                     GGCAACA  GTGA   CCCATCT
                                |||||||  ||||   |||||||
                                CCGTTGT  TACT   GGGTAGA
                                   TT   CTA
GAM678  LOC149692 3'  AGACAGGGTTTCACCATGTTGG 85723    _          CA
          CC                    GGC AACATGGTGAAACCC  TCT
                                ||| ||||||||||||||  |||
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                                CCG TTGTACCACTTTGGG  AGA
                                  G             AC
GAM678  LOC150166 5'  ATGGGGTTTCACCATGTTGTC  86034
                                GGCAACATGGTGAAACCCCAT
                                ||||||||||||||||||||
                                CTGTTGTACCACTTTGGGGTA

GAM678  LOC150290 3'  AGATGAGATTTTACTATGTCGC 80583     A         CCC
          C                      GGC ACATGGTGAAA   CATCT
                                 ||| ||||||||||   |||||
                                 CCG TGTATCATTTT   GTAGA
                                   C          AGA
GAM678  LOC150696 3'  AGACGGGGTTTTGCCATGTTGC 59153          TG       A
          C                      GGCAACATGG  AAACCCC TCT
                                 ||||||||||  ||||||| |||
                                 CCGTTGTACC  TTTGGGG AGA
                                       GT      C
GAM678  LOC151050 5'  AGACAGAGTTTCACCATGTTGG 80913     _          CCCA
          CC                     GGC AACATGGTGAAAC    TCT
                                 ||| ||||||||||||    |||
                                 CCG TTGTACCACTTTG    AGA
                                   G           AGAC
GAM678  LOC151057 3'  AGACGGGGTTTCACCATGTTGG 86381     _            A
          CC                     GGC AACATGGTGAAACCCC TCT
                                 ||| |||||||||||||| |||
                                 CCG TTGTACCACTTTGGGG AGA
                                   G             C
GAM678  LOC151201 3'  AGACGGGGTTTCACCATGTTG  86463              A
                                CAACATGGTGAAACCCC TCT
                                |||||||||||||||| |||
                                GTTGTACCACTTTGGGG AGA
                                            C
GAM678  LOC151475 5'  AGACGAGGTTTCACCATGTTGG 86581     _          CCA
          CC                     GGC AACATGGTGAAACC   TCT
                                 ||| ||||||||||||   |||
                                 CCG TTGTACCACTTTGG   AGA
                                   G           AGC
GAM678  LOC151701 3'  AGACGGGGTTTCACCATGTTGG 86662     _            A
          CC                     GGC AACATGGTGAAACCCC TCT
                                 ||| |||||||||||||| |||
                                 CCG TTGTACCACTTTGGGG AGA
                                   G             C
GAM678  LOC151877 3'  AGATGGGGTCTTGCTGTGTTGC 86690          TG A
          C                      GGCAACATGG  A ACCCCATCT
                                 ||||||||||  | |||||||||
                                 CCGTTGTGTC  T TGGGGTAGA
                                       GT C
GAM678  LOC151979 5'  AGACGGGGTTTCACCATGTTAC 81243     C            A
          C                      GG AACATGGTGAAACCCC TCT
                                 || |||||||||||||| |||
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                                CC TTGTACCACTTTGGGG AGA
                                 A             C
GAM678  LOC152300 3'  AGACAGGGTTTCACCATATTGG 81378    AAC_         CA
          CC                     GGC   ATGGTGAAACCC  TCT
                                 |||   ||||||||||||  |||
                                 CCG   TACCACTTTGGG  AGA
                                   GTTA          AC
GAM678  LOC152343 3'  AGATGGAGTCTTGCTGTGTCAC 81416    CA     TG A  C
          C                      GG  ACATGG  A AC CCATCT
                                 ||  ||||||  | || ||||||
                                 CC  TGTGTC  T TG GGTAGA
                                  AC     GT C  A
GAM678  LOC152343 3'  GGGTTTCACCATGTTGCC    81429
                                 GGCAACATGGTGAAACCC
                                 ||||||||||||||||||
                                 CCGTTGTACCACTTTGGG

GAM678  LOC152445 3'  AGACAGGGTTTCACCATGTTAG 86927    _          CA
          CC                     GGC AACATGGTGAAACCC  TCT
                                 ||| ||||||||||||||  |||
                                 CCG TTGTACCACTTTGGG  AGA
                                   A             AC
GAM678  LOC152719 5'  AGACGGGGTTTCACCATGTTG  87013             A
                                 CAACATGGTGAAACCCC TCT
                                 |||||||||||||||| |||
                                 GTTGTACCACTTTGGGG AGA
                                               C
GAM678  LOC153077 3'  AGATGGGGCTTCACCATGTTGG 87108    _        A
          CC                     GGC AACATGGTGAA CCCCATCT
                                 ||| |||||||||| ||||||||
                                 CCG TTGTACCACTT GGGGTAGA
                                   G         C
GAM678  LOC153606 5'  AGATAGGGTTTCACCATGTTGG 87253    _          C
          CC                     GGC AACATGGTGAAACCC ATCT
                                 ||| |||||||||||||| ||||
                                 CCG TTGTACCACTTTGGG TAGA
                                   G             A
GAM678  LOC153688 3'  AGACAGGATTTCATCGTGTTGC 87287             C  CA
          C                      GGCAACATGGTGAAA CC  TCT
                                 |||||||||||||| ||  |||
                                 CCGTTGTGCTACTTT GG  AGA
                                           A  AC
GAM678  LOC153688 3'  AGACAGGGTTTCACCATGTTGG 87289    _          CA
          CC                     GGC AACATGGTGAAACCC  TCT
                                 ||| |||||||||||||  |||
                                 CCG TTGTACCACTTTGGG  AGA
                                   G             AC
GAM678  LOC153811 3'  GGTTTCACCACGTTGGCC    81842    _  A
                                 GGC AAC TGGTGAAACC
                                 ||| ||| ||||||||||
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                                CCG TTG ACCACTTTGG
                                  G   C
GAM678  LOC154726 5'  AGACAGAGTTTCGCTCTTGTTG 82006       T_      CCCA
          CC                    GGCAACA  GGTGAAAC    TCT
                                |||||||  ||||||||    |||
                                CCGTTGT  TCGCTTTG    AGA
                                   TC       AGAC
GAM678  LOC154877 3'  AGACAGGATCTCACTATGTTGC 87520           AAC  CA
          C                     GGCAACATGGTGA   CC  TCT
                                ||||||||||||   ||  |||
                                CCGTTGTATCACT   GG  AGA
                                       CTA  AC
GAM678  LOC154877 3'  AGACAGGGTCTCACCATGTTG  87521          A   CA
                                CAACATGGTGA ACCC  TCT
                                ||||||||||| ||||  |||
                                GTTGTACCACT TGGG  AGA
                                       C    AC
GAM678  LOC154877 3'  AGTCGGGGTTTCACCATGTTGC 87526              AT
          C                     GGCAACATGGTGAAACCCC  CT
                                ||||||||||||||||||  ||
                                CCGTTGTACCACTTTGGGG  GA
                                          CT
GAM678  LOC155372 3'  AGACGGAATTTCACCATGGTGG 82255     AA_       CC  A
          CC                    GGC   CATGGTGAAA  CC TCT
                                |||   ||||||||||  || |||
                                CCG   GTACCACTTT  GG AGA
                                  GTG         AA  C
GAM678  LOC157247 5'  AGACAGAGTTTCATTCTTGTTG 82282       T_      CCCA
          CC                    GGCAACA  GGTGAAAC    TCT
                                |||||||  ||||||||    |||
                                CCGTTGT  TTACTTTG    AGA
                                   TC       AGAC
GAM678  LOC157506 3'  AGACGGGGTTTCACCATGTTG  82359              A
                                CAACATGGTGAAACCCC TCT
                                |||||||||||||||| |||
                                GTTGTACCACTTTGGGG AGA
                                          C
GAM678  LOC157623 3'  AGATGGAGTTTCACCATATTGC 82408      C        C
          C                     GGCAA ATGGTGAAAC CCATCT
                                ||||| |||||||||| ||||||
                                CCGTT TACCACTTTG GGTAGA
                                  A         A
GAM678  LOC157798 5'  AGACGGAGTCTTGCTGTGTCAC 87849     CA     TG A  C  A
          CA                    TGG  ACATGG  A AC CC TCT
                                |||  ||||||  | || || |||
                                ACC  TGTGTC  T TG GG AGA
                                  AC     GT C  A  C
GAM678  LOC158014 5'  AGACGGAGTTTCACCATGTTAG 82551     _          C  A
          CC                    GGC AACATGGTGAAAC CC TCT
                                ||| ||||||||||||| || |||
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                                CCG TTGTACCACTTTG GG AGA
                                  A           A  C
GAM678  LOC158014 5'  AGATAGAGTTTCACTCTTGTCA 82553       CAT       CCC
                                TGGCAA   GGTGAAAC   ATCT
                                ||||||   ||||||||   ||||
                                ACTGTT   TCACTTTG   TAGA
                                   C__       AGA
GAM678  LOC158476 3'  AGACAGGGTTTCACCATATTGG 88178     AAC_          CA
          CC                      GGC    ATGGTGAAACCC  TCT
                                |||    ||||||||||||  |||
                                CCG    TACCACTTTGGG  AGA
                                  GTTA          AC
GAM678  LOC158476 3'  AGACAGGGTTTCACCATGTTG  88181              CA
                                CAACATGGTGAAACCC  TCT
                                ||||||||||||||||  |||
                                GTTGTACCACTTTGGG  AGA
                                        AC
GAM678  LOC158629 5'  AGACAGGGTTTTGCTATGTTAC 88239    C      TG     CA
          C                      GG AACATGG  AAACCC  TCT
                                || |||||||  ||||||  |||
                                CC TTGTATC  TTTGGG  AGA
                                 A      GT     AC
GAM678  LOC160646 3'  AGATGGGGCTTCACCATGTTGG 83103     _         A
          CC                      GGC AACATGGTGAA CCCCATCT
                                ||| |||||||||| ||||||||
                                CCG TTGTACCACTT GGGGTAGA
                                  G          C
GAM678  LOC161829 3'  AGATGGGGTTTCACCATGTTGG 83181     _
          CC                      GGC AACATGGTGAAACCCCATCT
                                ||| ||||||||||||||||||||
                                CCG TTGTACCACTTTGGGGTAGA
                                  G
GAM678  LOC162427 3'  ATGGGGTTTCACCATGTTGGCC 83222     _
                                GGC AACATGGTGAAACCCCAT
                                ||| |||||||||||||||||
                                CCG TTGTACCACTTTGGGGTA
                                  G
GAM678  LOC169611 3'  AGACAGAGTTTCGCTTTTGTTG 83632        T_      CCCA
          CC                      GGCAACA  GGTGAAAC    TCT
                                |||||||  ||||||||    |||
                                CCGTTGT  TCGCTTTG    AGA
                                   TT       AGAC
GAM678  LOC169611 3'  AGACAGGATTTCACCATGTTGG 83633     _         C  CA
          CC                      GGC AACATGGTGAAA CC  TCT
                                ||| ||||||||||| ||  |||
                                CCG TTGTACCACTTT GG  AGA
                                  G          A  AC
GAM678  LOC170082 5'  AGATGGGGTTTCACCATGTTAG 83438     _
          CC                      GGC AACATGGTGAAACCCCATCT
                                ||| ||||||||||||||||||||
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                                CCG TTGTACCACTTTGGGGTAGA
                                  A
GAM678  LOC196264 3'  AGACGGGGTTTCACCATTTTGG 88978     AAC_          A
          CC                    GGC    ATGGTGAAACCCC TCT
                                |||    |||||||||||||| |||
                                CCG    TACCACTTTGGGG AGA
                                  GTTT           C
GAM678  LOC196529 3'  AGACAGGGTCTCACTGTGTTGC 89119           A    CA
          C                     GGCAACATGGTGA ACCC  TCT
                                |||||||||||| ||||  |||
                                CCGTTGTGTCACT TGGG  AGA
                                       C    AC
GAM678  LOC197358 3'  AGATGGGGTTTCACCATGTTG  89416
                                CAACATGGTGAAACCCCATCT
                                |||||||||||||||||||
                                GTTGTACCACTTTGGGGTAGA

GAM678  LOC199675 3'  GATGGGGCTGCACCTGCCA    89642      ACAT    AAA
                                TGGCA    GGTG   CCCCATC
                                |||||    ||||   |||||||
                                ACCGT    CCAC   GGGGTAG
                                   _____    GTC
GAM678  LOC199699 3'  AGACAGAGTTTCACCATATTAG 89662     _ C         CCCA
          CC                    GGC AA ATGGTGAAAC    TCT
                                ||| || ||||||||||    |||
                                CCG TT TACCACTTTG    AGA
                                  A  A         AGAC
GAM678  LOC199725 5'  AGACGGGATTTCACCATGTTG  91407           C   A
                                CAACATGGTGAAA CCC TCT
                                |||||||||||| ||| |||
                                GTTGTACCACTTT GGG AGA
                                       A   C
GAM678  LOC199786 3'  AGACAAGGTCTCGCTATGCTGC 89734      A       A   CCA
          C                     GGCA CATGGTGA ACC   TCT
                                |||| |||||||| |||   |||
                                CCGT GTATCGCT TGG   AGA
                                  C       C   AAC
GAM678  LOC199786 3'  AGATGGGGTTTCACCATGTTGG 89739     _
          CC                    GGC AACATGGTGAAACCCCATCT
                                ||| ||||||||||||||||||||
                                CCG TTGTACCACTTTGGGGTAGA
                                  G
GAM678  LOC200169 5'  AGACGGAGTTTCACCATGTTGG 91548     _          C  A
          CC                    GGC AACATGGTGAAAC CC TCT
                                ||| |||||||||||| || |||
                                CCG TTGTACCACTTTG GG AGA
                                  G           A  C
GAM678  LOC200268 3'  AGATGGGATTTTGCCATGTTGC 90081          TG   C
          C                     GGCAACATGG  AAA CCCATCT
                                ||||||||||  ||| |||||||
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                                CCGTTGTACC  TTT GGGTAGA
                                      GT   A
GAM678  LOC200310 3'  AGACGGGGTTTCACCATGTTG  66317              A
                                CAACATGGTGAAACCCC TCT
                                |||||||||||||||| |||
                                GTTGTACCACTTTGGGG AGA
                                        C
GAM678  LOC200314 3'  AGATGGAGTCTCCCTCTGTTGC 91586        T_ T  A  C
          CA                      TGGCAACA  GG GA AC CCATCT
                                |||||||| || || || ||||||
                                ACCGTTGT  CC CT TG GGTAGA
                                    CT  _  C  A
GAM678  LOC200314 3'  AGATGGGGTTTCACCACGTTGG 91587     _  A
          CC                      GGC AAC TGGTGAAACCCCATCT
                                ||| ||| ||||||||||||||||
                                CCG TTG ACCACTTTGGGGTAGA
                                  G   C
GAM678  LOC200316 3'  AGACGGAGTTTCACTCTGTCGC 90168     A  T      C  A
          C                       GGC ACA GGTGAAAC CC TCT
                                ||| ||| |||||||| || |||
                                CCG TGT TCACTTTG GG AGA
                                  C   C       A  C
GAM678  LOC200558 3'  AGATGGAATTTTTTGTTGCC   90249       TGGT   CC
                                GGCAACA   GAAA  CCATCT
                                |||||||   ||||  ||||||
                                CCGTTGT   TTTT  GGTAGA
                                    T___   AA
GAM678  LOC201164 3'  AGACAGGGTTTCACCATGTTG  89485             CA
                                CAACATGGTGAAACCC  TCT
                                ||||||||||||||||  |||
                                GTTGTACCACTTTGGG  AGA
                                        AC
GAM678  LOC201173 5'  AGACGGAGTTTCACCATGTTG  88666            C  A
                                CAACATGGTGAAAC CC TCT
                                |||||||||||||| || |||
                                GTTGTACCACTTTG GG AGA
                                        A  C
GAM678  LOC201220 5'  AGATGGAGTTTCACCATGTTG  88702            C
                                CAACATGGTGAAAC CCATCT
                                |||||||||||||| ||||||
                                GTTGTACCACTTTG GGTAGA
                                        A
GAM678  LOC201294 3'  AGACGGGGTTTCACCATGTTGG 89571     _           A
          CC                      GGC AACATGGTGAAACCCC TCT
                                ||| ||||||||||||||| |||
                                CCG TTGTACCACTTTGGGG AGA
                                  G             C
GAM678  LOC201294 3'  AGATGGAGTCTTGCTCTGTTGC 89574        T  TG A  C
          CA                      TGGCAACA GG  A AC CCATCT
                                |||||||| ||  | || ||||||
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                                ACCGTTGT TC  T TG GGTAGA
                                    C  GT C  A
GAM678  LOC201411 3'  AGACAGGGTTTCACCATGTTG  63633            CA
                                CAACATGGTGAAACCC  TCT
                                |||||||||||||||  |||
                                GTTGTACCACTTTGGG  AGA
                                      AC
GAM678  LOC201411 3'  AGATGGAGTTTCGTTCTCGTTG 63636      ATGG_    C
          CC                    GGCAAC    TGAAAC CCATCT
                                ||||||    |||||| ||||||
                                CCGTTG    GCTTTG GGTAGA
                                   CTCTT     A
GAM678  LOC201626 3'  AGATGGAGTTTCACTCTTGTTG 90424       T_      C
          CC                    GGCAACA  GGTGAAAC CCATCT
                                |||||||  |||||||| ||||||
                                CCGTTGT  TCACTTTG GGTAGA
                                    TC       A
GAM678  LOC201696 3'  AGATGGAGTTTCACTCTTGTTG 63811       T_      C
          CC                    GGCAACA  GGTGAAAC CCATCT
                                |||||||  |||||||| ||||||
                                CCGTTGT  TCACTTTG GGTAGA
                                    TC       A
GAM678  LOC202460 5'  AGATGGGGTTTCACCATGTAGG 90662     A_
          CC                    GGC  ACATGGTGAAACCCCATCT
                                |||  ||||||||||||||||||
                                CCG  TGTACCACTTTGGGGTAGA
                                  GA
GAM678  LOC202908 5'  AGATGGGGTCTCACCCTGTCAC 90706    CA  T    A
          C                     GG  ACA GGTGA ACCCCATCT
                                ||  ||| ||||| |||||||||
                                CC  TGT CCACT TGGGGTAGA
                                 AC  C    C
GAM678  LOC202934 3'  AGACAGGGTTTCACCACGTTGG 92024     _  A        CA
          CC                    GGC AAC TGGTGAAACCC  TCT
                                ||| ||| ||||||||||  |||
                                CCG TTG ACCACTTTGGG  AGA
                                  G  C         AC
GAM678  LOC203339 3'  AGATGGGGTTTCACCATGTTTG 92205      _
          CC                    GGCAA CATGGTGAAACCCCATCT
                                |||||| ||||||||||||||||||
                                CCGTT GTACCACTTTGGGGTAGA
                                   T
GAM678  LOC219673 3'  AGACAGGGTCTCACTATGTTGC 94608           A   CA
          C                     GGCAACATGGTGA ACCC  TCT
                                |||||||||||| ||||  |||
                                CCGTTGTATCACT TGGG  AGA
                                      C   AC
GAM678  LOC219731 5'  AGACAGAGTTTCGTCATGTTGC 94696        GT    CCCA
          C                     GGCAACATG  GAAAC    TCT
                                |||||||||  |||||   |||
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                                CCGTTGTAC  CTTTG    AGA
                                     TG     AGAC
GAM678  LOC220074 3'  AGACGGGGTTTCACCATGTTAG 59956     _           A
              CC                  GGC AACATGGTGAAACCCC TCT
                                  ||| |||||||||||||| |||
                                  CCG TTGTACCACTTTGGGG AGA
                                    A             C
GAM678  LOC220776 3'  GATGGGGGAACATATGCCA   68931      AC   GTGAAA
                                  TGGCA  ATG     CCCCATC
                                  |||||  |||     |||||||
                                  ACCGT  TAC     GGGGTAG
                                    A_   AAG___
GAM678  LOC221296 3'  AGACGGGGTTTCACCATGCTGG 93601     AA_          A
              CC                  GGC   CATGGTGAAACCCC TCT
                                  |||   |||||||||||||| |||
                                  CCG   GTACCACTTTGGGG AGA
                                    GTC           C
GAM678  LOC221663 5'  AGACAAGGTTTCACTATGTTGC 95453             CCA
              C                    GGCAACATGGTGAAACC   TCT
                                  |||||||||||||||||   |||
                                  CCGTTGTATCACTTTGG   AGA
                                           AAC
GAM678  LOC221663 5'  AGACAGGGTCTCGCTCTGTTGC 95454        T    A    CA
              CA                  TGGCAACA GGTGA ACCC  TCT
                                  |||||||| ||||| ||||  |||
                                  ACCGTTGT TCGCT TGGG  AGA
                                      C    C    AC
GAM678  LOC222224 5'  AGACAGGGTTTCACCATGTTGG 95867     _          CA
              CC                  GGC AACATGGTGAAACCC  TCT
                                  ||| ||||||||||||||  |||
                                  CCG TTGTACCACTTTGGG  AGA
                                    G             AC
GAM678  LOC253666 3'  AGACGGGGTTTCACCATGTTCG 96758     _           A
              CC                  GGC AACATGGTGAAACCCC TCT
                                  ||| |||||||||||||| |||
                                  CCG TTGTACCACTTTGGGG AGA
                                    C             C
GAM678  LOC254100 3'  AGATGGGGTTTCGTCATGTTGC 98146        GT
              C                    GGCAACATG  GAAACCCCATCT
                                  |||||||||  ||||||||||||
                                  CCGTTGTAC  CTTTGGGGTAGA
                                       TG
GAM678  LOC254205 5'  GGGTTCCACCATGTCACC    98466    CA      A
                                  GG  ACATGGTG AACCC
                                  ||  |||||||| |||||
                                  CC  TGTACCAC TTGGG
                                   AC       C
GAM678  LOC254268 3'  AGATGGGGTTTCACCATGTTGG 97136     _
              CC                  GGC AACATGGTGAAACCCCATCT
                                  ||| ||||||||||||||||||
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                                CCG TTGTACCACTTTGGGGTAGA
                                  G
GAM678  LOC254532 5'  AGACAGGGTTTCTCCATGTTGC 98444          T      CA
                C                  GGCAACATGG GAAACCC  TCT
                                   |||||||||| |||||||  |||
                                   CCGTTGTACC CTTTGGG  AGA
                                         T      AC
GAM678  LOC254655 3'  AGACGGGGTTTCACCATGTTGG 97212     _            A
                CC                   GGC AACATGGTGAAACCCC TCT
                                     ||| ||||||||||||||| |||
                                     CCG TTGTACCACTTTGGGG AGA
                                       G             C
GAM678  LOC254778 3'  AGACAGGATTTTGCTGTGTTGC 97828          TG   C  CA
                C                    GGCAACATGG  AAA CC  TCT
                                     ||||||||||  ||| ||  |||
                                     CCGTTGTGTC  TTT GG  AGA
                                           GT   A  AC
GAM678  LOC255037 3'  AGACGAAGTCTCGCTGTGTCAC 98436    CA       A  CCCA
                C                    GG  ACATGGTGA AC    TCT
                                     ||  ||||||||| ||    |||
                                     CC  TGTGTCGCT TG    AGA
                                      AC        C  AAGC
GAM678  LOC255177 3'  AGACAGAGTTTCACTCTCGTTG 98385       AT_      CCCA
                CC                   GGCAAC   GGTGAAAC    TCT
                                     ||||||   ||||||||    |||
                                     CCGTTG   TCACTTTG    AGA
                                        CTC       AGAC
GAM678  LOC255497 3'  AGACGGGGTTTCACCATGTTGG 98981     _            A
                CC                   GGC AACATGGTGAAACCCC TCT
                                     ||| ||||||||||||||| |||
                                     CCG TTGTACCACTTTGGGG AGA
                                       G             C
GAM678  LOC255714 5'  AGATGGGGCGGTCACATGTCCC 98196     CA    G   AA_
                A                     TGG  ACATG TGA   CCCCATCT
                                      |||  ||||| |||   ||||||||
                                      ACC  TGTAC ACT   GGGGTAGA
                                       C_    _   GGC
GAM678  LOC255919 3'  AGACGGAGTCTCGCTCTGTTGC 96742         T    A  C  A
                CA                    TGGCAACA GGTGA AC CC TCT
                                      |||||||| ||||| || || |||
                                      ACCGTTGT TCGCT TG GG AGA
                                          C     C  A  C
GAM678  LOC255927 5'  AGACGGGGTTTCACCATCTTGG 97708     AAC_          A
                CC                    GGC    ATGGTGAAACCCC TCT
                                      |||    |||||||||||||| |||
                                      CCG    TACCACTTTGGGG AGA
                                       GTTC           C
GAM678  LOC256306 3'  AGACGGGGTTTCACCATGTTGG 98502     _            A
                CC                    GGC AACATGGTGAAACCCC TCT
                                      ||| ||||||||||||||| |||
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                                CCG TTGTACCACTTTGGGG AGA
                                  G             C
GAM678  LOC257486 3'  AGACGGGGTTTCACCATGTTGG 69763    _           A
                CC                GGC AACATGGTGAAACCCC TCT
                                  ||| |||||||||||||| |||
                                CCG TTGTACCACTTTGGGG AGA
                                  G             C
GAM678  LOC51159  5'  AGACGGGATTTCACCATGTTGG 33025    _       C   A
                CC                GGC AACATGGTGAAA CCC TCT
                                  ||| |||||||||||| ||| |||
                                CCG TTGTACCACTTT GGG AGA
                                  G          A  C
GAM678  LOC51193  3'  AGATGAGATCTCGCTATGTTGC 33358          AACCC
                C                  GGCAACATGGTGA    CATCT
                                   ||||||||||||     |||||
                                   CCGTTGTATCGCT    GTAGA
                                         CTAGA
GAM678  LOC57146  3'  AGATGGGGTTTCACCATGTTG  40290
                                   CAACATGGTGAAACCCCATCT
                                   |||||||||||||||||||||
                                   GTTGTACCACTTTGGGGTAGA

GAM678  LOC81034  3'  ATGGGGTTTCACCATGTTAGCC 48583    _
                                   GGC AACATGGTGAAACCCCAT
                                   ||| ||||||||||||||||
                                   CCG TTGTACCACTTTGGGGTA
                                     A
GAM678  LOC89231  3'  AGATGGGGTCTCACTATGTTGC 94293          A
                C                  GGCAACATGGTGA ACCCCATCT
                                   |||||||||||| |||||||||
                                   CCGTTGTATCACT TGGGGTAGA
                                         C
GAM678  LOC89919  3'  AGACGGGGTTTCACCATGTT   61367           A
                                   AACATGGTGAAACCCC TCT
                                   |||||||||||||| |||
                                   TTGTACCACTTTGGGG AGA
                                        C
GAM678  LOC89932  3'  AGACAGAGTTTCACTCTTGTTG 61438       T_     CCCA
                CC                 GGCAACA  GGTGAAAC   TCT
                                   |||||||  ||||||||   |||
                                   CCGTTGT  TCACTTTG   AGA
                                      TC       AGAC
GAM678  LOC89932  3'  AGATGGGGTTTCACCATGTTGG 61443    _
                CC                 GGC AACATGGTGAAACCCCATCT
                                   ||| |||||||||||||||||||
                                   CCG TTGTACCACTTTGGGGTAGA
                                     G
GAM678  LOC90288  3'  AGATGGGGTTTCACCATATTG  62769    C
                                   CAA ATGGTGAAACCCCATCT
                                   ||| ||||||||||||||||
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                                GTT TACCACTTTGGGGTAGA
                                  A
GAM678  LOC91012  5' AGACAAGGTTTTGCCATGTTGC 65241         TG    CCA
                C                  GGCAACATGG  AAACC   TCT
                                   ||||||||||  |||||   |||
                                   CCGTTGTACC  TTTGG   AGA
                                       GT    AAC
GAM678  LOC91115  3' AGATGGAGTTTCACTCTTGTCA 65543       CAT      C
                                   TGGCAA   GGTGAAAC CCATCT
                                   ||||||   |||||||| ||||||
                                   ACTGTT   TCACTTTG GGTAGA
                                      C__       A
GAM678  LOC91115  3' AGATGGGGTTTCATCATGTTTG 65546      _
                CC                   GGCAA CATGGTGAAACCCCATCT
                                     ||||| ||||||||||||||||||
                                     CCGTT GTACTACTTTGGGGTAGA
                                       T
GAM678  LOC91291  5' AGACAAGGTTTCACCCTGTTGG 66084    G    T       CCA
                CA                   TG CAACA GGTGAAACC   TCT
                                     || ||||| |||||||||   |||
                                     AC GTTGT CCACTTTGG   AGA
                                      G    C        AAC
GAM678  LOC91373  3' AGACGGAGTTTCACTCTTGTTG 66403        T_      C  A
                CC                   GGCAACA  GGTGAAAC CC TCT
                                     |||||||  |||||||| || |||
                                     CCGTTGT  TCACTTTG GG AGA
                                        TC       A  C
GAM678  LOC92267  3' AGATGGGGTTTCACCATATTGG 69161     AAC_
                CC                   GGC    ATGGTGAAACCCCATCT
                                     |||    ||||||||||||||||
                                     CCG    TACCACTTTGGGGTAGA
                                       GTTA
GAM678  LOC92689  3' AGACAGGGTTTCACCATGTTGG 70768     _          CA
                CC                   GGC AACATGGTGAAACCC  TCT
                                     ||| ||||||||||||||  |||
                                     CCG TTGTACCACTTTGGG  AGA
                                       G            AC
GAM678  LOC92841  3' AGACAGGGTTTCACCATGTTGG 71241     _          CA
                CC                   GGC AACATGGTGAAACCC  TCT
                                     ||| ||||||||||||||  |||
                                     CCG TTGTACCACTTTGGG  AGA
                                       G            AC
GAM678  LOC92841  3' AGACGGGGTTTCACCATGTTAG 71244     _           A
                CC                   GGC AACATGGTGAAACCCC TCT
                                     ||| |||||||||||||| |||
                                     CCG TTGTACCACTTTGGGG AGA
                                       A            C
GAM678  LOC93129  3' AGACGGGGTTTCGCTGTTCCCA 71952     C   TG       A
                                     TGG AACA  GTGAAACCCC TCT
                                     ||| ||||  |||||||||| |||
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                                ACC TTGT  CGCTTTGGGG AGA
                                  C   __        C
GAM679  CCND2    3'  CATTTCAGGCACAACGATA   10047     T C  C
                                TATC G TG GCCTGAGATG
                                ||||| || ||||||||||
                                ATAG C AC CGGACTTTAC
                                  _ A  A
GAM679  SLC16A2  3'  ACTCATCTCAGGCTGAGC    22521     GC
                                GCT  GCCTGAGATGAGT
                                |||  ||||||||||||
                                CGA  CGGACTCTACTCA
                                  GT
GAM679  SURF5    3'  TACTCATTAACTCAGCAGA    56918       CGCCTGA
                                TCTGCTG      GATGAGTA
                                |||||||      ||||||||
                                AGACGAC      TTACTCAT
                                    TCAA___
GAM679  BANP     5'  TACCCAGATCACACAGCTGATA 66803     T   CGCC   GA  A
                                TATC GCTG    TGA  TG GTA
                                |||| ||||    |||  || |||
                                ATAG CGAC    ACT  AC CAT
                                  T    AC__   AG  C
GAM679  LOXL4    3'  ACTCATCTCTACAGAGATA    50854      G   CGCCT
                                TATCT CTG    GAGATGAGT
                                ||||| |||    |||||||||
                                ATAGA GAC    CTCTACTCA
                                  _   AT___
GAM679  LOC127881 5'  TACTCAAGGCCACACAGCAAGT 75988    TC    C___   GAGA
            A                    TA  TGCTG    GCCT    TGAGTA
                                || |||||    ||||   ||||||
                                AT  ACGAC    CGGA    ACTCAT
                                 GA     ACAC   _____
GAM680  ATF5     5'  ACCCCTTTGTGCCCCCGGCCC  24815      CGAAA
                                GGGCC    GGGCACAAAGGGGT
                                |||||    ||||||||||||||
                                CCCGG    CCCGTGTTTCCCCA
                                  CC___
GAM680  TCF3     3'  ACCAGCAGGGTGTCCCCTCGGG 71269        AA     AAAGG_
            CCC                   GGGCCCGA  GGGCAC     GGT
                                |||||||  ||||||     |||
                                CCCGGGCT  CCTGTG     CCA
                                    CC     GGACGA
GAM680  VWF      3'  TTGTGCCCTTCTGAGCCC    6888       C  A
                                GGGC CG AAGGGCACAA
                                |||| || ||||||||||
                                CCCG GT TTCCCGTGTT
                                  A  C
GAM680  VWF      3'  TTGTGCCCTTCTGAGCCC    6889       C  A
                                GGGC CG AAGGGCACAA
                                |||| || ||||||||||
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                                CCCG GT TTCCCGTGTT
                                  A  C
GAM680  ZFP103   5' CCCACGGCCCCTCGGGCCC   20223        AA   ACAAA
                                GGGCCCGA  GGGC    GGG
                                ||||||||  ||||    |||
                                CCCGGGCT  CCCG    CCC
                                    C_    GCA__
GAM680  ARHGEF15 3' CCTGTGCCCTCTCAAGCC    30952    CC  A      AA
                                GGC  GA AGGGCACA  GG
                                |||  || ||||||||  ||
                                CCG  CT TCCCGTGT  CC
                                 AA  C      __
GAM680  CACNA1H  3' ACCAGGTTGCGTCCTTTCAGGC 41184      C      A   AGG
           CC                     GGGCC GAAAGGGC CAA   GGT
                                |||||  |||||||| |||   |||
                                CCCGG CTTTCCTG GTT   CCA
                                   A       C   GGA
GAM680  FLJ10743 3' ACTTCTCGCTGCCCTTCCAAGC 37076     CCGA     CAA
           CC                     GGGC    AAGGGCA   AGGGGT
                                ||||    |||||||   ||||||
                                CCCG    TTCCCGT   TCTTCA
                                  AACC      CGC
GAM680  FLJ12547 3' CTCATGCCCTTTCAAGTCC   47132     CC       CAAA
                                GGGC  GAAAGGGCA   GGG
                                ||||  |||||||||   |||
                                CCTG  CTTTCCCGT   CTC
                                  AA        A___
GAM680  FLJ20401 5' CCTGCCGCCCCTCGGGCCC   35581        AA   ACAA
                                GGGCCCGA  GGGC    AGG
                                ||||||||  ||||    |||
                                CCCGGGCT  CCCG    TCC
                                    C_    CCG_
GAM680  FLJ20979 5' CCAGGCCCCTTCGGGCCC    44384        A    ACAAAGG
                                GGGCCCGAA GGGC      GG
                                |||||||||| ||||      ||
                                CCCGGGCTT CCCG      CC
                                     C    GA_____
GAM680  GSH-2    5' CCCCTTTGTTCCCAGCCC    56554     CCGAAA   C
                                GGGC     GGG ACAAAGGGG
                                ||||     ||| |||||||||
                                CCCG     CCC TGTTTCCCC
                                  A_____   T
GAM680  HA-1     5' ACCCCCAGCCCGCCCCCTCGGG 66153        AA   ACAAA_
           CTC                    GGGCCCGA  GGGC     GGGGT
                                ||||||||  ||||     |||||
                                CTCGGGCT  CCCG     CCCCA
                                    CC    CCCGAC
GAM680  KIAA0057 3' ACCCCCTTGTGCCTAGAAAAGG 25397      CGAAA_      A
           CCT                    GGGCC     GGGCACAA GGGGT
                                |||||     |||||||| |||||
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                                TCCGG     TCCGTGTT CCCCA
                                  AAAAGA       C
GAM680  PLA2G3    3'  GCTGCCGTGCCCTTCCTGGCCC 32310      CGA       AAA  _
                                GGGCC   AAGGGCAC   GG GGT
                                |||||   ||||||||   || |||
                                CCCGG   TTCCCGTG   CC TCG
                                  TCC       ___  G
GAM680  SMARCF1   3'  ACCCCTTTTCCACCCTGGGCCC 38037      GAA    CAC_
                                GGGCCC   AGGG    AAAGGGGT
                                ||||||   ||||    ||||||||
                                CCCGGG   TCCC    TTTCCCCA
                                  ___    ACCT
GAM680  LOC148046 3'  CCCCTCTGCACCTCGGGCCC   85245       AA  _   CAA
                                GGGCCCGA  GG GCA   AGGGG
                                ||||||||  || |||   |||||
                                CCCGGGCT  CC CGT   TCCCC
                                   __  A   C__
GAM680  LOC164537 5'  ACCCCGACCGCCCCTCGGGCCC 88573        AA    ACAAA
                                GGGCCCGA  GGGC    GGGGT
                                ||||||||  ||||    |||||
                                CCCGGGCT  CCCG    CCCCA
                                   C_    CCAG_
GAM680  LOC253254 3'  CCCTGTTGTCCTTTCAGGCCC  98906      C        CAA
                                GGGCC GAAAGGGCA   AGGG
                                ||||| |||||||||   ||||
                                CCCGG CTTTCCTGT   TCCC
                                  A        TG_
GAM680  LOC92080  3'  CCTGTGCCCTTCCAGGGCC    68628      GA_       AA
                                GGCCC   AAGGGCACA  GG
                                |||||   |||||||||  ||
                                CCGGG   TTCCCGTGT  CC
                                  ACC        __
GAM681  KCNK4     3'  CCGTTGGGGCAGAACCATGGAG 33980         A_  __  G TG  C
          GA                      TTCTCCATG  TC  CC C  GC GG
                                |||||||||  ||  || |  || ||
                                AGGAGGTAC  AG  GG G  TG CC
                                    CA  AC  _ GT  _
GAM681  KRT3      3'  CCCGGCCAAGCCCAGTCACGAG 55102      CA    CCC  _
          AA                      TTCTC  TGAT   GCT GGCCGGG
                                |||||  ||||   ||| |||||||
                                AAGAG  ACTG   CGA CCGGCCC
                                  C_    ACC   A
GAM681  TNFRSF1B  3'  CCCAGCCATTACCATGGAGA   8390        ATCCCGC    C
                                TCTCCATG      TGGC GGG
                                ||||||||      |||| |||
                                AGAGGTAC      ACCG CCC
                                    CATT___    A
GAM681  FLJ10307  3'  CCCAGCCAGCAGAGATGGAGAG 36475        GA  CC     C
                                TTCTCCAT  TC  GCTGGC GGG
                                ||||||||  ||  |||||| |||
```

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                                GAGAGGTA  AG  CGACCG CCC
                                    G_  A_     A
GAM681  FLJ10546  3'  CTAGTACAAGACATGGAGAA  60180        A  CC__
                                TTCTCCATG TC    GCTGG
                                |||||||||  ||    |||||
                                AAGAGGTAC AG    TGATC
                                    _  AACA
GAM681  FLJ12526  3'  CCCGATCAAGAACATGGAGAA  45926        A  CCGC  GC
                                TTCTCCATG TC    TG  CGGG
                                |||||||||  ||    ||  ||||
                                AAGAGGTAC AG    AC  GCCC
                                    A  A___  TA
GAM681  GAPCENA  3'  CCAGGTAGACATGGAGAA    25176        A  CCG
                                TTCTCCATG TC   CTGG
                                |||||||||  ||   ||||
                                AAGAGGTAC AG   GACC
                                    _  ATG
GAM681  GPS2     5'  CCAAGGGGACATGGAGAA    16887        A   GC
                                TTCTCCATG TCCC  TGG
                                |||||||||  ||||  |||
                                AAGAGGTAC AGGG  ACC
                                    _   GA
GAM681  KIAA0256  5'  CCCGAGCGGGGGGCCATGGAGA 65049        AT   G   GC
           A                     TTCTCCATG  CCC CTG  CGGG
                                 |||||||||  ||| |||  ||||
                                 AAGAGGTAC  GGG GGC  GCCC
                                     CG   _   GA
GAM681  KIAA1938  3'  CCCGGCTGCAGATTACGGAGAA 93822       A    CC  T
                                TTCTCC TGATC  GC GGCCGGG
                                ||||||  |||||  ||  |||||||
                                AAGAGG ATTAG  CG TCGGCCC
                                   C    A_  _
GAM681  NDRG4    3'  CCCAAGGAAGACAGAACATGGA 40377        A  CCG  GG  __
           GAA                    TTCTCCATG TC   CT  CC  GGG
                                  |||||||||  ||   ||  ||  |||
                                  AAGAGGTAC AG   GA  GG  CCC
                                      A  ACA  A_  AA
GAM681  NDRG4    3'  CCCAAGGAAGACAGAACATGGA 43576        A  CCG  GG  __
           GAA                    TTCTCCATG TC   CT  CC  GGG
                                  |||||||||  ||   ||  ||  |||
                                  AAGAGGTAC AG   GA  GG  CCC
                                      A  ACA  A_  AA
GAM681  OATPRP4  3'  CGGTTAGCAAAACCATGGGAA  48983     T    ATCCC
                                TTC CCATG    GCTGGCCG
                                |||  |||||    ||||||||
                                AAG GGTAC    CGATTGGC
                                  _    CAAAA
GAM681  LOC164173 3'  CCCAAACTAGCAAAACCTATGG 83051        ATCCC_    CC_
           AGAA                   TTCTCCATG    GCTGG   GGG
                                  |||||||||    |||||  |||
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                                AAGAGGTAT     CGATC   CCC
                                     CCAAAA     AAA
GAM681  LOC257438 3'  CCCAGCCAGCAGAGATGGAGAG 95591         GA  CC     C
                                TTCTCCAT  TC  GCTGGC GGG
                                ||||||||  ||  |||||| |||
                                GAGAGGTA  AG  CGACCG CCC
                                     G_  A_     A
GAM682  KIAA0356  3'  CAAAGCCATGAATTCCC     66770       GTG
                                GGGAG   TGTGGCTTTG
                                |||||   ||||||||||
                                CCCTT   GTACCGAAAC
                                   AA_
GAM682  PRO1728   5'  CAAAACCACACATTGTAAAATC 38134       CGGGA       C
           A                     TGATT     GGTGTGTGG TTTG
                                |||||     ||||||||| ||||
                                ACTAA     TTACACACC AAAC
                                   AATG_       A
GAM683  AF5Q31    3'  TGCCATAACATACCACCT    27780         CATCTATC
                                AGGTGGTG       TATGGCA
                                ||||||||       |||||||
                                TCCACCAT       ATACCGT
                                     ACA_____
GAM683  DMRT2     3'  TGCTAAATGCCACCACCT    22655         _   CTATCTA
                                AGGTGGTG CAT      TGGCA
                                |||||||| |||      |||||
                                TCCACCAC GTA      ATCGT
                                     C   A_______
GAM683  FZD10     5'  GCTCCAGACGCGCCACCT    24216         A   ATCTAT
                                AGGTGGTGC TCT     GGC
                                ||||||||| |||     |||
                                TCCACCGCG AGA     TCG
                                     C   CC____
GAM683  IL11      3'  CTGTGGATAGAACACCACC    7182         CA
                                GGTGGTG  TCTATCTATGG
                                |||||||  ||||||||||
                                CCACCAC  AGATAGGTGTC
                                     A_
GAM683  LDHA      3'  TGCCACCTCTGACGCACCACT  19916         A  TATCTA
                                GGTGGTGC TC     TGGCA
                                |||||||| ||     |||||
                                TCACCACG AG     ACCGT
                                     C  TCTCC_
GAM683  LTBP2     3'  TGCCATGGGATACAGCACC    6468       G  C   TAT
                                GGTG TG ATC   CTATGGCA
                                ||||  ||  |||   ||||||||
                                CCAC AC TAG   GGTACCGT
                                   G  A   ___
GAM683  AKAP8     3'  TTGCCATAGATAGAAGGTATC  20737       A_
                                GGTGC  TCTATCTATGGCAA
                                |||||  ||||||||||||||
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                                CTATG  AGATAGATACCGTT
                                   GA
GAM683  FLJ11722  3'  TAGACAGACACATCACCT    47007        CA   A
                                AGGTGGTG  TCT TCTA
                                ||||||||  ||| ||||
                                TCCACTAC  AGA AGAT
                                    AC   C
GAM683  FLJ22969  3'  CCTTGGAAATGCACCGCCT   69200         CTA    T
                                AGGTGGTGCAT   TCTA GG
                                ||||||||||   |||| ||
                                TCCGCCACGTA   AGGT CC
                                     A__    T
GAM683  KIAA0532  3'  CCACAGGTATGCACCACC    71320        TC     A
                                GGTGGTGCA  TATCT TGG
                                |||||||||  ||||| |||
                                CCACCACGT  ATGGA ACC
                                    __     C
GAM683  KIAA1485  3'  CCAGCATAGACACACACC    90764     _  CA    CTA
                                GGTG GTG  TCTAT   TGG
                                |||| |||  |||||   |||
                                CCAC CAC  AGATA   ACC
                                  A  __    CG_
GAM683  NPEPL1    5'  TGCTCGGGCAGCTGCACCACCT 45426         T  AT  AT
                                AGGTGGTGCA CT  CT  GGCA
                                |||||||||| ||  ||  ||||
                                TCCACCACGT GA  GG  TCGT
                                     C  CG  C_
GAM683  LOC253539 3'  CCAGCAATAGCACCACCT    97699         ATC   CTA
                                AGGTGGTGC   TAT   TGG
                                |||||||||   |||   |||
                                TCCACCACG   ATA   ACC
                                    ___   ACG
GAM684  CDH12     3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM684  GOCAP1    3'  ATTGTTCTTGGGAGCAGTGTA  43007       CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC         G
GAM684  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090       T    AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT     TTATTC
                                  _   GTCA_
GAM684  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
            A                    TACAC       AGAAGAATAAG
                                |||||       ||||||||||
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                              ATGTG      TCTTCTTATTC
                                 TACTCCC_
GAM684  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126        CCCAAGAA
                              TACACCACT      GAATAAG
                              |||||||||      |||||||
                              ATGTGGTGA      TTTATTC
                                   AGACG___
GAM684  HMP19     3'  CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
           TA                   TACA   TCC   GAAGAATAAG
                              ||||   |||   ||||||||||
                              ATGT   AGG   TTTCTTATTC
                                AAA_  ATTG
GAM684  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA  68742             _
                              TACACCACTCCCAAGA AGA
                              |||||||||||||||| |||
                              ATGTGGTGAGGGTTCT TCT
                                        G
GAM684  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                              CAC  CT CCAAGAAGAA
                              |||  || ||||||||||
                              GTG  GA GGTTCTTTTT
                                AC  A
GAM684  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748     CCA__
                              ACTC    AGAAGAATAAG
                              ||||    ||||||||||
                              TGAG    TCTTCTTATTC
                                TACCG
GAM684  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                              CCA    CAAGAAGAATAAG
                              |||    ||||||||||||
                              GGT    GTTCTTCTTATTC
                                TTTCA
GAM684  OSBPL11   3'  CTTAATTTCCCAAGAGTGGTG  43206        CCAA    AA
                              CACCACTC   GAAG  TAAG
                              ||||||||   ||||  ||||
                              GTGGTGAG   CTTT  ATTC
                                   AACC   A_
GAM684  YME1L1    3'  TCATTCTTGATGTGGTGTA   58438        TCC     _
                              TACACCAC   CAAGAA GA
                              ||||||||   |||||| ||
                              ATGTGGTG   GTTCTT CT
                                   TA_     A
GAM684  ZNF262    3'  CTTATTTTGTTTGGGAGT    18723         A
                              ACTCCCAAG AGAATAAG
                              ||||||||| ||||||||
                              TGAGGGTTT TTTTATTC
                                   G
GAM684  LOC91960  3'  TGTGGCTTGGAACGTGGTGTA  68294        TC_    AAGA
                              TACACCAC   CCAAG   ATA
                              ||||||||   |||||   |||
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                                ATGTGGTG  GGTTC   TGT
                                    CAA   GG__
GAM685  CALM1    3'  AAAATCTGCATGTATTGGTT  23535       ATTAGGA
                                AACCAATA     TAGATTTT
                                ||||||||     ||||||||
                                TTGGTTAT     GTCTAAAA
                                    GTAC___
GAM685  APG3     3'  ATAAAATCTATCCTAATTATTG 42827                ___
           GTT                   AACCAATAATTAGGATAGATTTTA  T
                                ||||||||||||||||||||||||  |
                                TTGGTTATTAATCCTATCTAAAAT  A
                                                    ___
GAM685  KIAA0057  3'  AAAAGCCGGTCCTAATTACGG  25393   AA       AGA_
                                CC  TAATTAGGAT   TTTT
                                ||  ||||||||||   ||||
                                GG  ATTAATCCTG   AAAA
                                 C_       GCCG
GAM685  LOC143909 3'  TAAAACCTATCCTGTGTGTTGG 83925       AT      A
           TT                   AACCAATA  TAGGATAG TTTTA
                                ||||||||  |||||||| |||||
                                TTGGTTGT  GTCCTATC AAAAT
                                    GT       C
GAM685  LOC144305 3'  AAGAGTTCCTAATTATTAGG   83966   _       TAGA
                                CC AATAATTAGGA   TTTT
                                || ||||||||||   ||||
                                GG TTATTAATCCT   AGAA
                                 A         TG__
GAM685  LOC147429 3'  TAAAATCTATTTTGTTTATGGT 79000     A  T
                                ACCA TAA TAGGATAGATTTTA
                                |||| ||| ||||||||||||||
                                TGGT ATT GTTTTATCTAAAAT
                                  _  T
GAM685  LOC151249 3'  AAAATCATGGAATTATTGGTT  60688         AGGATA
                                AACCAATAATT     GATTTT
                                ||||||||||     ||||||
                                TTGGTTATTAA     CTAAAA
                                      GGTA__
GAM685  LOC153817 3'  AAAATCATGGAATTATTGGTT  61701         AGGATA
                                AACCAATAATT     GATTTT
                                ||||||||||     ||||||
                                TTGGTTATTAA     CTAAAA
                                      GGTA__
GAM685  LOC157556 5'  AAAATCTATTCTATCTATT   87777     AT
                                AATA  TAGGATAGATTTT
                                ||||  ||||||||||||
                                TTAT  ATCTTATCTAAAA
                                  CT
GAM685  LOC220840 3'  AAAATCATGGAATTATTGGTT  92481         AGGATA
                                AACCAATAATT     GATTTT
                                ||||||||||     ||||||
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                                TTGGTTATTAA     CTAAAA
                                      GGTA__
GAM686  CDH12    3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM686  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM686  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT    98090      T    AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT     TTATTC
                                   _   GTCA_
GAM686  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
             A                   TACAC       AGAAGAATAAG
                                 |||||       ||||||||||
                                 ATGTG       TCTTCTTATTC
                                    TACTCCC_
GAM686  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM686  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
             TA                   TACA   TCC    GAAGAATAAG
                                  ||||   |||    ||||||||||
                                  ATGT   AGG    TTTCTTATTC
                                    AAA_   ATTG
GAM686  KIAA1579  3'  TACTCTTAGTGGTGTA      37154         CCCAAG    A
                                TACACCACT     AAGA TA
                                |||||||||     |||| ||
                                ATGTGGTGA     TTCT AT
                                      _______   C
GAM686  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68742              _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                         G
GAM686  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM686  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748      CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
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                                TGAG    TCTTCTTATTC
                                  TACCG
GAM686  KIAA1906 3'  CTTATTCTTCTTGACTTTTGG  73571    CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM686  OSBPL11  3'  CTTAATTTCCCAAGAGTGGTG  43206       CCAA   AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                     AACC   A_
GAM686  YME1L1   3'  TCATTCTTGATGTGGTGTA   58438       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                     TA_    A
GAM686  YME1L1   3'  TCATTCTTGATGTGGTGTA   27323       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                     TA_    A
GAM686  ZNF262   3'  CTTATTTTGTTTGGGAGT    18723        A
                                ACTCCCAAG AGAATAAG
                                ||||||||| |||||||
                                TGAGGGTTT TTTTATTC
                                     G
GAM686  LOC91960 3'  TGTGGCTTGGAACGTGGTGTA  68294       TC_    AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
                                ATGTGGTG   GGTTC   TGT
                                     CAA    GG__
GAM687  CARD15   3'  GGATGTACAAGGACAGCCCCTC 42472      AC   GCAC_
                                GAGGG  CTG    GTACATCC
                                |||||  |||    ||||||||
                                CTCCC  GAC    CATGTAGG
                                   C_   AGGAA
GAM687  CDKN2B   3'  GGGACTGACGCCAGGTTCC   55312        AC  A  _
                                GGGACCTGGC  GT CA TCCC
                                ||||||||||  || || ||||
                                CCTTGGACCG  CA GT AGGG
                                     __  _  C
GAM687  CERD4    3'  GGATGACCAGGTCCCTGG    24880   G       CACGTA
                                C AGGGACCTGG     CATCC
                                | ||||||||||     |||||
                                G TCCCTGGACC     GTAGG
                                 G        A_____
GAM687  FANCC    3'  TGCAGAGCCAGGTCCCTC    71052          AC_
                                GAGGGACCTGGC   GTA
                                ||||||||||||   |||
```

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                                CTCCCTGGACCG  CGT
                                      AGA
GAM687  GNA11    3'  GGGATGTACATCTCTCCCTC  10814      CCT  CAC
                                GAGGGA  GG  GTACATCCC
                                ||||||  ||  |||||||||
                                CTCCCT  CT  CATGTAGGG
                                   CT_  A__
GAM687  RPS6KA2  3'  GGAACACACGGGTCCTTC   41224        GCAC  ACA
                                GAGGGACCTG   GT  TCC
                                ||||||||||   ||  |||
                                CTTCCTGGGC   CA  AGG
                                      ACA_  ____
GAM687  APELIN   3'  GGGATGGGGACCAGGTCTC   34269        CACGTA
                                GGGACCTGG    CATCCC
                                |||||||||    ||||||
                                CTCTGGACC    GTAGGG
                                      AGGG__
GAM687  BIRC5    3'  GTCCGCCCAGGTCCCCG    8604    A      CA  T
                                CG GGGACCTGG  CG AC
                                || |||||||||  || ||
                                GC CCCTGGACC  GC TG
                                 _       C_  C
GAM687  CGI-01   3'  GTGTGTGCAAGCCCCTC    32507      AC  G
                                GAGGG  CT GCACGTAC
                                |||||  || ||||||||
                                CTCCC  GA CGTGTGTG
                                   C_  A
GAM687  DKFZP434K1772 5'  GGAGTGTGCGTCAGGCCCCCCG 68336    A  A   GC     TC
                                CG GGG CCTG  ACGTACA  CC
                                || ||| ||||  |||||||  ||
                                GC CCC GGAC  TGCGTGT  GG
                                 C  C   __      GA
GAM687  DKFZp547I014 5'  GGATGTTTACCTAGGTCCCTC  39945          CACGT
                                GAGGGACCTGG    ACATCC
                                ||||||||||    ||||||
                                CTCCCTGGATC    TGTAGG
                                      CATT_
GAM687  ELF4     3'  GGGTGTACCAATGCCCCTC   9234      ACCTG  C__
                                GAGGG    GCA  GTACATCC
                                |||||    |||  ||||||||
                                CTCCC    CGT  CATGTGGG
                                   _____  AAC
GAM687  FLJ11117  3'  GGACATGGACACTTCCAGGTCC 37636          CAC_  A  __
          CTC                    GAGGGACCTGG   GT CA  TCC
                                ||||||||||    || ||  |||
                                CTCCCTGGACC   CA GT  AGG
                                      TTCA  G  AC
GAM687  KIAA0323  3'  GGATTCCTGCCAGGTCCCCG  63949    A        CGTAC
                                CG GGGACCTGGCA    ATCC
                                || ||||||||||     ||||
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                                GC CCCTGGACCGT    TAGG
                                 _        CCT__
GAM687  KIAA0924  5'  GATGCTCCCAAGTCCCTTG   30365       C  CACGTA
                                CGAGGGAC TGG     CATC
                                |||||||| |||     ||||
                                GTTCCCTG ACC     GTAG
                                    A  CTC___
GAM687  KIAA1344  5'  GGAACGGCCCAGGTCCCCG   72868   A      CA  ACA
                                CG GGGACCTGG  CGT  TCC
                                || |||||||||  |||  |||
                                GC CCCTGGACC  GCA  AGG
                                 _       CG  ___
GAM687  KIAA1622  3'  GGAATGTACGTTGTGGCCCTC  55245     A  TG  _    _
                                GAGGG CC  GCA CGTACAT CC
                                ||||| ||  ||| ||||||| ||
                                CTCCC GG  TGT GCATGTA GG
                                  _ __  T     A
GAM687  KIAA1924  3'  GGGCGTCTGTGCCAGGCCTCCC 74055     __      T  AT
                                GGGA  CCTGGCACG AC  CC
                                ||||  ||||||||| ||  ||
                                CCCT  GGACCGTGT TG  GG
                                  CC       C  CG
GAM687  XYLT1    5'  GGATGTGTCCAGACCGCCTC  78415     GAC_   C  GT
                                GAGG   CTGG AC  ACATCC
                                ||||   |||| ||  ||||||
                                CTCC   GACC TG  TGTAGG
                                  GCCA   _ __
GAM687  LOC125456 5'  GGAAGTGCTGCCAGGTTCCTC  76168          C   A
                                GAGGGACCTGGCA GTAC TCC
                                |||||||||||| |||| |||
                                CTCCTTGGACCGT CGTG AGG
                                       _   A
GAM687  LOC152580 3'  GATGCACACCAGGTCCC     86985        CAC  A
                                GGGACCTGG   GT CATC
                                |||||||||   || ||||
                                CCCTGGACC   CA GTAG
                                     A__  C
GAM687  LOC219818 3'  GGATACACAGCCTGCAGGTCCC 92538       ___  AC  AC
                                GGGACCT   GGC  GT  ATCC
                                |||||||   |||  ||  ||||
                                CCCTGGA   CCG  CA  TAGG
                                   CGT   A_  CA
GAM687  LOC51035  5'  GTCACACACCAGGTCCCCG   32393   A      CAC  _
                                CG GGGACCTGG   GT AC
                                || |||||||||   || ||
                                GC CCCTGGACC   CA TG
                                 _       ACA  C
GAM688  B4GALT5   3'  ACCAGCTGGCTTCAGTGAT   17680      TT__  GG
                                ATCACT   CC  AGCTGGT
                                ||||||   ||  |||||||
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                                TAGTGA   GG  TCGACCA
                                   CTTC  __
GAM688  HRB      3'  ACCATTGCTACTGGAAAGT   16912        _  __
                                ACTTTCCGG AGC  TGGT
                                |||||||||  |||  ||||
                                TGAAAGGTC TCG  ACCA
                                     A   TT
GAM688  MS4A7    3'  ACTGAGCAGAAGGTGATA    41353        CGGA  _
                                TATCACTTTC   GCT GGT
                                ||||||||||   ||| |||
                                ATAGTGGAAG   CGA TCA
                                     A___   G
GAM688  PPGB     3'  ACCAGCTCCACGGCCTGATG  6123       CTTT  __
                                TATCA   CC  GGAGCTGGT
                                |||||   ||  |||||||||
                                GTAGT   GG  CCTCGACCA
                                   CC__  CA
GAM688  RORC     3'  ACCAGCTCTTTGGAAGTGA   18586       C_
                                TCACTTTC  GGAGCTGGT
                                ||||||||  |||||||||
                                AGTGAAGG  TCTCGACCA
                                     TT
GAM688  SLC25A12 3'  ACCACTGAATAAGTGATA    14918       TC_  AGC
                                TATCACTT   CGG   TGGT
                                ||||||||   |||   ||||
                                ATAGTGAA   GTC   ACCA
                                     TAA  ___
GAM688  UTY      5'  ACCAGCCTATGGAGGTGA    24061       C_  A
                                TCACTTTC  GG GCTGGT
                                ||||||||  || ||||||
                                AGTGGAGG  TC CGACCA
                                     TA  _
GAM688  CASPR3   3'  ACCAAAGGGAAGAGTGATA   46415        _  GGAGC
                                TATCACTTT CC    TGGT
                                |||||||||  ||    ||||
                                ATAGTGAGA GG    ACCA
                                     A  GAA__
GAM688  DKFZP434I092 3'  ACCAGCTTTACAAATTGA    68410    C   CC
                                TCA TTT  GGAGCTGGT
                                |||  |||  |||||||||
                                AGT AAA  TTTCGACCA
                                  T   CA
GAM688  DKFZP564L2423 3'  ACCAGCTCCAGGTTTGAT    63020     CTTT  _
                                ATCA   CC GGAGCTGGT
                                ||||   || |||||||||
                                TAGT   GG CCTCGACCA
                                  TT__  A
GAM688  FLJ20464 5'  ACCAGCTCCGGGAGGCGA    35678    A
                                TC CTTTCCGGAGCTGGT
                                || ||||||||||||||
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                                AG GGAGGGCCTCGACCA
                                 C
GAM688  FLJ23436  3'  ACCAGGGTGGAGGAAGTGA   45461      __   GAG
                                TCACTT  TCCG   CTGGT
                                ||||||  ||||   |||||
                                AGTGAA  AGGT   GACCA
                                   GG    GG_
GAM688  KIAA0323  3'  ACCAATTATCTGGAAAATGA  63944    C      GC__
                                TCA TTTCCGGA    TGGT
                                |||  ||||||||    ||||
                                AGT AAAGGTCT    ACCA
                                  A       ATTA
GAM688  KIAA0711  3'  ACTGTCCCCGGAAAAGGATA  30146    AC     A_  T
                                TATC  TTTCCGG  GC GGT
                                ||||  |||||||  || |||
                                ATAG  AAAGGCC  TG TCA
                                  GA      CC  _
GAM688  KIAA0976  3'  ACCCTCTGACTAAAAGTGATA 30546       C___    CT
                                TATCACTTT   CGGAG  GGT
                                |||||||||   |||||  |||
                                ATAGTGAAA   GTCTC  CCA
                                     ATCA    __
GAM688  KIAA1464  3'  GGGTCCAGAGAAGTGATA    68821      _  C   G
                                TATCACT TTC GGA CT
                                |||||||  ||| ||| ||
                                ATAGTGA GAG CCT GG
                                    A   A   G
GAM688  KIAA1908  5'  ACCAGCTCTCGGGCGATG    73779     ACTT   _
                                TATC    TCCG GAGCTGGT
                                ||||    |||| ||||||||
                                GTAG    GGGC CTCGACCA
                                  C___    T
GAM688  KIAA1912  3'  ACCACTGCCAGAAAGTGATA  73755       C  _  C
                                TATCACTTTC GG AG TGGT
                                ||||||||||  ||  ||  ||||
                                ATAGTGAAAG CC TC ACCA
                                     A  G  _
GAM688  MGC20235  3'  ACCATGTGAAAAAGTGATA   59545       CCGGA  _
                                TATCACTTT    GC TGGT
                                |||||||||    ||  ||||
                                ATAGTGAAA    TG ACCA
                                     AAG__  T
GAM688  MRP63     3'  ACCAGCTTGGCCAAGGTGATA 44040       __  G
                                TATCACTTT  CCG AGCTGGT
                                |||||||||  |||  |||||||
                                ATAGTGGAA  GGT TCGACCA
                                     CC   _
GAM688  TSARG1    3'  ACCAGCCCCAGGAGTTGATA  58190     CT   _  A
                                TATCA  TTCC GG GCTGGT
                                |||||  ||||  ||  ||||||
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                                ATAGT  GAGG CC CGACCA
                                  T_   A  C
GAM688  LOC144698 5'  ACCAGCTCCGCGGGGATG    77430     A   TC
                                TATC CTT  CGGAGCTGGT
                                |||| |||  ||||||||||
                                GTAG GGG  GCCTCGACCA
                                  _   C_
GAM688  LOC152992 5'  ACCAGCTCCGGGGCGGGAT   81641     ACT
                                ATC   TTCCGGAGCTGGT
                                |||   ||||||||||||
                                TAG   GGGGCCTCGACCA
                                  GGC
GAM688  LOC51716  3'  ACCAGCCAGGGCAACAAAGTGA 33257        _____   GGA
           TA                     TATCACTT    TCC   GCTGGT
                                |||||||     |||   ||||||
                                ATAGTGAA    GGG   CGACCA
                                    ACAAC   AC_
GAM689  MARK3    5'  AATTAACCAGACAAATCGCTCC 11458
           AC                     GTGGAGCGATTTGTCTGGTTAATT
                                |||||||||||||||||||||||
                                CACCTCGCTAAACAGACCAATTAA

GAM689  SHMT1    3'  AACCAGGCTTTCCTGCTCCAC  16054        ATTT_
                                GTGGAGCG    GTCTGGTT
                                |||||||     ||||||||
                                CACCTCGT    CGGACCAA
                                    CCTTT
GAM690  ACCN2    5'  GCGCGCGGGCGGGCGGACA   39628       GGG   A
                                TGTCCG   CTGC CGCGCGC
                                ||||||   |||| |||||||
                                ACAGGC   GGCG GCGCGCG
                                   G__   G
GAM690  EDN2     3'  AGCAACCGTGCAGCCACGAACA 10481     C  G       CGC
                                TGT CG GGCTGCACG   GCT
                                ||| || |||||||||   |||
                                ACA GC CCGACGTGC   CGA
                                  A  A       CAA
GAM690  EFNA4    3'  AGCAGTAGACAGCCCTGGACA  19083          CAC  GC
                                TGTCCGGGGCTG   GC  GCT
                                ||||||||||||   ||  |||
                                ACAGGTCCCGAC   TG  CGA
                                      AGA  A_
GAM690  JUN      5'  GCGCGCGCGAGTCGACA     11103     CGG   GCA
                                TGTC   GGCT   CGCGCGC
                                ||||   ||||   |||||||
                                ACAG   CTGA   GCGCGCG
                                  ___    GC_
GAM690  KCNQ4    5'  AGCGCGCCCCCGCCCCGGAC   17476        TGCAC
                                GTCCGGGGC    GCGCGCT
                                |||||||||    |||||||
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                                CAGGCCCCG    CGCGCGA
                                     CCCC_
GAM690  KRTHA2   3' AGCAGGGCCAGCCCCGGTCA  11239   T      CAC  GC_
                                TG CCGGGGCTG  GC  GCT
                                || |||||||||  ||  |||
                                AC GGCCCCGAC  CG  CGA
                                 T       ____ GGA
GAM690  M11S1    5' AGCGCGCGACACTGCCCGGA  20909      G TGCA_
                                TCCGGG C    CGCGCGCT
                                |||||| |    ||||||||
                                AGGCCC G    GCGCGCGA
                                   _ TCACA
GAM690  MARK3    5' AGCGCGCGTGCAGCCCCGGACA 11459
                                TGTCCGGGGCTGCACGCGCGCT
                                |||||||||||||||||||||
                                ACAGGCCCCGACGTGCGCGCGA

GAM690  MEF2C    5' AGCACACGCGTACACCCAGACA 11530     CG  C C    C__
                                TGTC  GGG TG ACGCG  GCT
                                ||||  ||| || |||||  |||
                                ACAG  CCC AC TGCGC  CGA
                                  A_  _ A    ACA
GAM690  PAX2     3' GCGCGGCCCAGCCCCGGGCA  15660         CA_
                                TGTCCGGGGCTG  CGCGC
                                ||||||||||||  |||||
                                ACGGGCCCCGAC  GCGCG
                                      CCG
GAM690  PAX2     3' GCGCGGCCCAGCCCCGGGCA  15667         CA_
                                TGTCCGGGGCTG  CGCGC
                                ||||||||||||  |||||
                                ACGGGCCCCGAC  GCGCG
                                      CCG
GAM690  RNF6     5' AGCACACGTTCTCCGGACA   21084       CTGC  CGC
                                TGTCCGGGG   ACG  GCT
                                |||||||||   |||  |||
                                ACAGGCCTC   TGC  CGA
                                     T___   ACA
GAM690  UMPK     5' AGCGGCCTCAGCCCCGGCA   25935   T      CAC  G
                                TG CCGGGGCTG  GC CGCT
                                || |||||||||  || ||||
                                AC GGCCCCGAC  CG GCGA
                                 _       TC_ _
GAM690  ZNF264   5' AGCGCGCCTGGAAGCCCCGGGC 14195         G_  C
           A                     TGTCCGGGGCT  CA GCGCGCT
                                 ||||||||||  || |||||||
                                 ACGGGCCCCGA  GT CGCGCGA
                                       AG  C
GAM690  CHST3    3' GCTGGCAGCCCCAGCA     16240    CC      A  C
                                TGT  GGGGCTGC CG GC
                                |||  |||||||| || ||
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                                ACG  CCCCGACG GT CG
                                  A_      _ _
GAM690  CRMP5    5' AGCGCGCGTGCAGCCGCCG   39701    _
                                CGG GGCTGCACGCGCGCT
                                ||| ||||||||||||||
                                GCC CCGACGTGCGCGCGA
                                  G
GAM690  FLJ00058 5' AGCGCGCGTGCACCTCCAGAC 79505    C   C
                                GTC GGGG TGCACGCGCGCT
                                ||| |||| ||||||||||||
                                CAG CCTC ACGTGCGCGCGA
                                  A   C
GAM690  FLJ10520 3' AGCGCCTAGCAGCCCCAAGCA 36697    CC      ACGC
                                TGT  GGGGCTGC   GCGCT
                                |||  ||||||||   |||||
                                ACG  CCCCGACG   CGCGA
                                  AA      ATC_
GAM690  FLJ13910 3' AGCTCTGCATGCAGCCCCAGCA 43249    CC      C  C_
                                TGT  GGGGCTGCA GCG  GCT
                                |||  ||||||||| |||  |||
                                ACG  CCCCGACGT CGT  CGA
                                  A_       A  CT
GAM690  FLJ20457 5' AGCGCGCGTGCGCACGACA   35670    C GG  T
                                TGTC G  GC GCACGCGCGCT
                                |||| |  || ||||||||||
                                ACAG C  CG CGTGCGCGCGA
                                  _ A_  _
GAM690  HSU79303 3' GCGCGACGGCCCCGGAC    26151         CA
                                GTCCGGGGCTG  CGCGC
                                ||||||||||  |||||
                                CAGGCCCCGGC  GCGCG
                                      A_
GAM690  KIAA0090 3' AGCTCACTGCAGCCTCGAACA 89809    C       CGCGC
                                TGT CGGGGCTGCA    GCT
                                ||| ||||||||||    |||
                                ACA GCTCCGACGT    CGA
                                  A       CACT_
GAM690  KIAA0218 5' AGCGCTTCGTAGCCCCGGA   29291         ACGC
                                TCCGGGGCTGC   GCGCT
                                ||||||||||   |||||
                                AGGCCCCGATG   CGCGA
                                      CTT_
GAM690  PAK6     5' AGCAGCTGCCAGCCCCGGCA  39807   T      _ C  GC
                                TG CCGGGGCTG CA GC  GCT
                                || |||||||| || ||  |||
                                AC GGCCCCGAC GT CG  CGA
                                  _       C  _  A_
GAM690  PCAF     5' AGCGCGCGGGGCCCGGCCA   15283   T   G  GCA
                                TG CCGGG CT   CGCGCGCT
                                || ||||| ||   ||||||||
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                                AC GGCCC GG   GCGCGCGA
                                 C    G ___
GAM690  PL6      3'  GCTGGCAGCCCCAAGCA     23815     CC       A  C
                                TGT  GGGGCTGC CG GC
                                |||  |||||||| || ||
                                ACG  CCCCGACG GT CG
                                  AA      _ _
GAM690  LOC130367 5'  GCGCGGCCCCGGGCA       75436          TGCA
                                TGTCCGGGGC   CGCGC
                                ||||||||||   |||||
                                ACGGGCCCCG   GCGCG
                                          _____
GAM690  LOC143098 3'  AGCCATGAGCAGCTCCAGACA  76973      C       A  CGC
                                TGTC GGGGCTGC CG   GCT
                                |||| |||||||| ||   |||
                                ACAG CCTCGACG GT   CGA
                                  A       A  AC_
GAM690  LOC150115 5'  CGCGGCGGCCCGGACA      80387        G    A
                                TGTCCGGG CTGC CGCG
                                |||||||| |||| ||||
                                ACAGGCCC GGCG GCGC
                                      _   _
GAM690  LOC153397 5'  AGCGCGCGCGCGCACATACA   87225     CCGGG  T  A
                                TGT    GC GC CGCGCGCT
                                |||    || || ||||||||
                                ACA    CG CG GCGCGCGA
                                  TACA_  _  C
GAM690  LOC195977 3'  GGCTCGCTGCAGCCCAAACA   88934     CCG       C  C
                                TGT   GGGCTGCA GCG GCT
                                |||   |||||||| ||| |||
                                ACA   CCCGACGT CGC CGG
                                  AA_       _  T
GAM690  LOC257458 5'  GCGTCACCAACCCCGGGCA    68402         C  CAC
                                TGTCCGGGG TG   GCGC
                                |||||||| ||   ||||
                                ACGGGCCCC AC   TGCG
                                      A  CAC
GAM691  BSN      3'  CCCAGCATCATGAGCAAG     14380          A  CTTCA  AA
                                CTTGCTCAT GT    GC  GG
                                |||||||| ||    ||  ||
                                GAACGAGTA TA    CG  CC
                                      C  _____  AC
GAM691  CLCA2    3'  CCTTACACTTTGGCTATGAACA 22563     C       TTCAGC_
          A                      TTG TCATAGTC      AAGG
                                |||  ||||||||      ||||
                                AAC AGTATCGG      TTCC
                                  A       TTTCACA
GAM691  CRY2     3'  CCTTGCTCCGTGAGCAA     72661         AGTCTTC
                                TTGCTCAT      AGCAAGG
                                ||||||||      |||||||
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                                AACGAGTG      TCGTTCC
                                    CC_____
GAM691  FADD    3'  TCCTCACTATGACACTGAGCAA 15126        TA   TTC  CA
          G                  CTTGCTCA  GTC   AG  AGGA
                             ||||||||  |||   ||  ||||
                             GAACGAGT  CAG   TC  TCCT
                                 CA   TA_  AC
GAM691  HLCS    5'  TCCATTGAAGACTTGAACAAG  6421      C   T       CAA
                             CTTG TCA AGTCTTCAG   GGA
                             |||| ||| |||||||||   |||
                             GAAC AGT TCAGAAGTT   CCT
                               A   _       A__
GAM691  MEST    3'  CTGAAAGACCTATGAGCAA   70459          _   _
                             TTGCTCATAG TCTT CAG
                             |||||||||| |||| |||
                             AACGAGTATC AGAA GTC
                                   C    A
GAM691  PCDH7   5'  CCCCGCTGCATGAGCAG    51616        A TCTT    AA
                             TTGCTCAT G    CAGC  GG
                             |||||||| |    ||||  ||
                             GACGAGTA C    GTCG  CC
                                 _ _____    CC
GAM691  PCDH7   5'  CCCCGCTGCATGAGCAG    51619        A TCTT    AA
                             TTGCTCAT G    CAGC  GG
                             |||||||| |    ||||  ||
                             GACGAGTA C    GTCG  CC
                                 _ _____    CC
GAM691  PCDH7   5'  CCCCGCTGCATGAGCAG    11987        A TCTT    AA
                             TTGCTCAT G    CAGC  GG
                             |||||||| |    ||||  ||
                             GACGAGTA C    GTCG  CC
                                 _ _____    CC
GAM691  PLP2    5'  TCCTCGAAACCACGAGCAAG   12176       ATA  C   AGCA
                             CTTGCTC   GT TTC    AGGA
                             |||||||   || |||    ||||
                             GAACGAG   CA AAG    TCCT
                                 CAC  _   C___
GAM691  PLXNA2  3'  TCCCTAAAGTTACTATGAGAAG 48003     G       __   C  CAA
                             CTT CTCATAGT  CTT AG   GGA
                             ||| ||||||||  ||| ||   |||
                             GAA GAGTATCA  GAA TC   CCT
                               _       TT   A  ___
GAM691  AP1GBP1 3'  CCTCAGACCAGTGAGCAA    24346        A_    TCAGCA
                             TTGCTCAT  GTCT     AGG
                             ||||||||  ||||     |||
                             AACGAGTG  CAGA     TCC
                                 AC    C_____
GAM691  AP1GBP1 3'  CCTCAGACCAGTGAGCAA    55438        A_    TCAGCA
                             TTGCTCAT  GTCT     AGG
                             ||||||||  ||||     |||
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                                AACGAGTG CAGA    TCC
                                   AC   C_____
GAM691  AP1GBP1  3' CCTCAGACCAGTGAGCAA   55444       A_   TCAGCA
                                TTGCTCAT GTCT    AGG
                                |||||||| ||||    |||
                                AACGAGTG CAGA    TCC
                                   AC   C_____
GAM691  CAP350   3' CCTACTGAAGACTGGGC    29703     TA      CA
                                GCTCA GTCTTCAG AGG
                                ||||| |||||||| |||
                                CGGGT CAGAAGTC TCC
                                  __      A_
GAM691  DDX34    3' TCCCTGCTGGAGACCAACAAG 28679     CTCATA       A
                                CTTG    GTCTTCAGCA GGA
                                ||||    |||||||||| |||
                                GAAC    CAGAGGTCGT CCT
                                  AAC___       C
GAM691  DKFZP586G1122 3' CCGCAAAACTGTGAGCAA   61938         CTTCA AA
                                TTGCTCATAGT   GC GG
                                ||||||||||   || ||
                                AACGAGTGTCA   CG CC
                                     AAA__ __
GAM691  FAM10A6  3' CCTTGCTGAAGGAAAAGCAA  72782     CATAG
                                TTGCT   TCTTCAGCAAGG
                                |||||   ||||||||||||
                                AACGA   GGAAGTCGTTCC
                                  AAA__
GAM691  FLJ10546 5' TGCAAAGACTATGAGCA    60184         CA
                                TGCTCATAGTCTT GCA
                                |||||||||||| |||
                                ACGAGTATCAGAA CGT
                                     A_
GAM691  FLJ10726 3' CTTAACTATGAGCAGG     37042         CTTCAGC
                                CTTGCTCATAGT     AAG
                                ||||||||||     |||
                                GGACGAGTATCA     TTC
                                     A______
GAM691  KIAA0475 5' CCTTAATACATGAGCAAG   30115       A C CAGC
                                CTTGCTCAT GT TT   AAGG
                                |||||||| || ||   ||||
                                GAACGAGTA CA AA   TTCC
                                     _ T ____
GAM691  KIAA1655 5' CCTCACTGTGGATGAGCAA  67179      TAG  T  CA
                                TTGCTCA  TCT CAG AGG
                                |||||||  ||| |||  |||
                                AACGAGT  AGG GTC TCC
                                   ___  T  AC
GAM691  MGC3077  3' TCCTTGTTTTTAGACTAT   44128      TC_
                                ATAGTCT  AGCAAGGA
                                |||||||  ||||||||
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                                TATCAGA   TTGTTCCT
                                    TTT
GAM691   RAB40C    3'  CCTTGTTTGGGATTATGAACAA 41278     C        TC
                                TTG TCATAGTCT  AGCAAGG
                                ||| |||||||||  |||||||
                                AAC AGTATTAGG  TTGTTCC
                                  A        GT
GAM691   SENP2     3'  CTGCTGAAGAGCAGG       76832        ATAGTC      A
                                CTTGCTC     TTCAGCA G
                                |||||||     ||||||| |
                                GGACGAG     AAGTCGT C
                                    _______     C
GAM691   ST13      3'  CCTTGCTGAAGGAAAAGCAA   15431       CATAG
                                TTGCT     TCTTCAGCAAGG
                                |||||     ||||||||||||
                                AACGA     GGAAGTCGTTCC
                                   AAA__
GAM691   LOC118491 5'  TCCTGTTGGAGAACTATGAGCA 74358           _       A
            AG                     CTTGCTCATAGT CTTCAGCA GGA
                                |||||||||||| |||||||| |||
                                GAACGAGTATCA GAGGTTGT CCT
                                       A       _
GAM691   LOC125228 3'  CCTTTGGAAACTATGGGCAA   74863           C    GC
                                TTGCTCATAGT TTCA  AAGG
                                |||||||||| ||||  ||||
                                AACGGGTATCA AGGT  TTCC
                                       A   __
GAM691   LOC126751 3'  CCCTGCTGAGATTGAGCCAG   75072    T     TA    T     A
                                CT GCTCA  GTCT CAGCA GG
                                || |||||  |||| ||||| ||
                                GA CGAGT  TAGA GTCGT CC
                                 C     __   _     C
GAM691   LOC144840 3'  CCTACTGAAGACTGGAG     77526     A         CA
                                CTC TAGTCTTCAG  AGG
                                ||| ||||||||||  |||
                                GAG GTCAGAAGTC  TCC
                                  _         A_
GAM691   LOC149052 3'  CCTTGCTGAAGGAAAAGCAA   79872       CATAG
                                TTGCT     TCTTCAGCAAGG
                                |||||     ||||||||||||
                                AACGA     GGAAGTCGTTCC
                                   AAA__
GAM691   LOC158886 3'  CCTTGCTGAAGGAAAAGCAA   83722       CATAG
                                TTGCT     TCTTCAGCAAGG
                                |||||     ||||||||||||
                                AACGA     GGAAGTCGTTCC
                                   AAA__
GAM691   LOC200197 3'  CCCTGCCGACATGAGCAA     90016         A   TTCA   A
                                TTGCTCAT GTC    GCA GG
                                |||||||| |||    ||| ||
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                                AACGAGTA CAG    CGT CC
                                     _  C___   C
GAM691  LOC219731 5'  CCAGGTTAAAACTATGAGGAAG 94699     G       C  C   AA
                                CTT CTCATAGT TT AGC  GG
                                ||| |||||||| || |||  ||
                                GAA GAGTATCA AA TTG  CC
                                  G       A  _   GA
GAM691  LOC221178 3'  CCCTGCTGATGATGAGCAAG   95168         AGTCT     A
                                CTTGCTCAT     TCAGCA GG
                                |||||||||     |||||| ||
                                GAACGAGTA     AGTCGT CC
                                     GT___      C
GAM691  LOC222407 5'  CCTACACTGAAAACAATGAGCA 95973         A  C     CA_
          A                      TTGCTCAT GT TTCAG   AGG
                                ||||||||| || |||||   |||
                                AACGAGTA CA AAGTC   TCC
                                     A  A     ACA
GAM691  LOC245718 3'  CCTTGCTGAAGGAAAAGCAA   92415      CATAG
                                TTGCT     TCTTCAGCAAGG
                                |||||     ||||||||||||
                                AACGA     GGAAGTCGTTCC
                                   AAA__
GAM691  LOC256228 5'  CCTTGCTGAAGCAGGACAGCAA 97969       CATAGT
          G                     CTTGCT      CTTCAGCAAGG
                                ||||||      ||||||||||
                                GAACGA      GAAGTCGTTCC
                                   CAGGAC
GAM692  CYP4A11   3'  AACTCCTGCCTGCCCTCCA    7584       AA       _
                                TGGA  GCAGGTAG AGTT
                                ||||  |||||||| ||||
                                ACCT  CGTCCGTC TCAA
                                  CC       C
GAM692  EHD2      3'  AAGCCAAGGCTTCTTCCCA    28207     A   C    AGAG
                                TGG AAG AGGT    TTGGCTT
                                ||| ||| ||||    |||||||
                                ACC TTC TTCG    AACCGAA
                                  C   _    G___
GAM692  GALE      3'  AAAGCAGCAGCTGCCTGCTCTC 63858      A        AGTTG
          CA                      TGGA AGCAGGTAG     GCTTT
                                |||| |||||||||     |||||
                                ACCT TCGTCCGTC     CGAAA
                                  C        GACGA
GAM692  LCP1      3'  AAAGCCAACATGTGGCTCCTCC 11280     A_   AGGTAGA
                                GGA  AGC       GTTGGCTTT
                                |||  |||       |||||||||
                                CCT  TCG       CAACCGAAA
                                  CC   GTGTA__
GAM692  NEDD4     3'  CCACTTTCTACTTTCCA     70543        C   TA    T
                                TGGAAAG AGG  GAGT GG
                                ||||||| |||  |||| ||
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                                ACCTTTC TCT  TTCA CC
                                    A  __   _
GAM692  BTBD3    3'  AAAGCCAAACTCTTCTCTCCA  31024      AA C   T     _
                                TGGA  G AGG AGAGTT GGCTTT
                                ||||  | ||| |||||| ||||||
                                ACCT  C TCT TCTCAA CCGAAA
                                  __ _  _     A
GAM692  FLJ20694  3'  AAAGCCAAACTGACCATCTGCT 35966           AG__   _
           TTCCA                  TGGAAAGCAGGT    AGTT GGCTTT
                                ||||||||||||   |||| ||||||
                                ACCTTTCGTCTA    TCAA CCGAAA
                                      CCAG    A
GAM692  HSPC157   5'  GTCCTACTACCTGCTTTCCA   27191            _ TT
                                TGGAAAGCAGGTAG AG  GGC
                                |||||||||||||| ||  |||
                                ACCTTTCGTCCATC TC  CTG
                                      A  __
GAM692  KIAA1522  3'  CCACCCTCCTGCCTTCCA    65604      A    T  A  T
                                TGGAA GCAGG AG GT GG
                                ||||| ||||| || || ||
                                ACCTT CGTCC TC CA CC
                                   C    _ C  _
GAM692  PP1628    5'  AAGCCAGCCCCTCCTCCCA   48069     AA  C   TAGA
                                TGG  AG AGG   GTTGGCTT
                                |||  || |||   ||||||||
                                ACC  TC TCC   CGACCGAA
                                  C_  C   C___
GAM692  TIX1     3'  AGTTGGCTTTAAACCACCTGCT 62405     A      T_________   TTGG
           TCCCA                  TGG AAGCAGG       AGAG    CT
                                ||| |||||||       ||||   ||
                                ACC TTCGTCC       TTTC    GA
                                  C      ACCAAA___    GGTT
GAM692  LOC118987 3'  CCAACCCAAGGATCTGCTTTC  74393         AGA___
                                GAAAGCAGGT     GTTGG
                                ||||||||||     |||||
                                CTTTCGTCTA     CAACC
                                      GGAACC
GAM692  LOC132617 3'  AAAGCCAACTCTACAATGCTCA 76405    A   G_
                                A AGCA  GTAGAGTTGGCTTT
                                | ||||  ||||||||||||||
                                A TCGT  CATCTCAACCGAAA
                                 C   AA
GAM692  LOC152503 3'  CCACTTTCCTGCTTTCCA    86976          T    T
                                TGGAAAGCAGG AGAGT GG
                                |||||||||| ||||| ||
                                ACCTTTCGTCC TTTCA CC
                                          _   _
GAM693  CDH12    3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
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                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM693  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM693  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090      T   AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                   _   GTCA_
GAM693  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
           A                     TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM693  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM693  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
           TA                    TACA   TCC   GAAGAATAAG
                                ||||   |||   ||||||||||
                                ATGT   AGG   TTTCTTATTC
                                  AAA_  ATTG
GAM693  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA  68742              _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                          G
GAM693  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM693  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748     CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM693  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM693  OSBPL11   3'  CTTAATTTCCCAAGAGTGGTG  43206        CCAA    AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
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                                GTGGTGAG   CTTT  ATTC
                                    AACC   A_
GAM693  YME1L1   3'  TCATTCTTGATGTGGTGTA   58438       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   |||||| ||
                                ATGTGGTG   GTTCTT CT
                                    TA_    A
GAM693  ZNF262   3'  CTTATTTTGTTTGGGAGT    18723       A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                     G
GAM693  LOC91960 3'  TGTGGCTTGGAACGTGGTGTA 68294       TC_   AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
                                ATGTGGTG   GGTTC   TGT
                                    CAA    GG__
GAM694  ADCY8    5'  GCTCACAGCGCTGCGGCTCCT  8501     A  AT   CAA
                                AGGA CC  GGC   CTGTGAGC
                                |||| ||  |||   ||||||||
                                TCCT GG  TCG   GACACTCG
                                  C  CG   C__
GAM694  CIT      5'  GCTCACAGAGCTACAGCTCTCC 70304    ACCA__   CAA
                                GGA     TGGC   CTGTGAGC
                                |||     ||||   ||||||||
                                CCT     ATCG   GACACTCG
                                  CTCGAC   A__
GAM694  FAAH     5'  GCGGTCTCCGGCCATGGCCCC  44452    AA      A___
                                GG  CCATGGCC    ACTGT
                                ||  ||||||||    |||||
                                CC  GGTACCGG    TGGCG
                                 CC       CCTC
GAM694  GSTM3    5'  GCTCACAGTTTCCCTAGTCCT  68638     ACCAT  CC
                                AGGA    GG  AACTGTGAGC
                                ||||    ||  ||||||||||
                                TCCT    CC  TTGACACTCG
                                  GAT__  CT
GAM694  HMX1     3'  GCGGTCGGCCATGGCC      38947    AA      A
                                GG  CCATGGCC ACTGT
                                ||  |||||||| |||||
                                CC  GGTACCGG TGGCG
                                 __       C
GAM694  HSD11B2  3'  GCTCCGTGAGCCTTGGTTCCT  5771        T   CA  T T
                                AGGAACCA GGC  AC G GAGC
                                |||||||| |||  || | ||||
                                TCCTTGGT CCG  TG C CTCG
                                    T  AG  _ _
GAM694  HYAL1    5'  CTCCAGTGGCCATGCTCC    24603     AC      A   T
                                GGA  CATGGCCA CTG GAG
                                |||  |||||||| ||| |||
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                                CCT  GTACCGGT GAC CTC
                                  C_       _  _
GAM694  MAT1A    3'  TGGTGGCCATGCTCCT      92507      AC       A
                                AGGA  CATGGCCA CTG
                                ||||  |||||||| |||
                                TCCT  GTACCGGT GGT
                                  C_       _
GAM694  NPTX2    3'  GCTGGAGTGGCCATGTCCCTT  94085      AAC       A  G G
                                AAGG   CATGGCCA CT T AGC
                                ||||   |||||||| || | |||
                                TTCC   GTACCGGT GA G TCG
                                  CT_       _ G _
GAM694  RFX2     3'  GCCCCACCAGACCATGGGTTCC 7158          _    CCAA   _  A_
           TT                     AAGGAACC ATGG    CTG TG  GC
                                ||||||||| ||||    ||| ||  ||
                                TTCCTTGG TACC    GAC AC  CG
                                     G    A___   C  CC
GAM694  SMAP     5'  GCCCCACAGAGCCATGGTCC   22932     A      CAA     A_
                                GGA CCATGGC   CTGTG  GC
                                ||| |||||||   |||||  ||
                                CCT GGTACCG   GACAC  CG
                                  _      A__     CC
GAM694  SMURF1   3'  GCTCACAGCCCTGAGCTCTTT  94049       AC_  T   CAAC
                                AAGGA   CA GGC    TGTGAGC
                                |||||   || |||    |||||||
                                TTTCT   GT CCG    ACACTCG
                                   CGA  C  _____
GAM694  SORCS2   3'  CAGTGCCCATGGTTCCT     40798          CCA
                                AGGAACCATGG   ACTG
                                ||||||||||||  ||||
                                TCCTTGGTACC   TGAC
                                      CG_
GAM694  DC-TM4F2 3'  ACTGTTGGCCAGGGCTCCT   48895      A  A       T
                                AGGA CC TGGCCAAC GT
                                |||| || |||||||| ||
                                TCCT GG ACCGGTTG CA
                                  C  G       T
GAM694  DKFZp566H0824 5'  GCTCACAAACCCCATAGTTGCC 34488      _   C    CCAAC
           T                     AGG AAC ATGG     TGTGAGC
                                ||| ||| ||||     |||||||
                                TCC TTG TACC     ACACTCG
                                  G   A    CCAA_
GAM694  FLJ10292 3'  GCCCACAGTTGTTGGTTGTTCC 36432        C  GGC       A
           T                     AGGAAC AT   CAACTGTG GC
                                ||||||  ||   |||||||| ||
                                TCCTTG TG   GTTGACAC CG
                                   T  GTT       C
GAM694  FLJ20085 3'  GCTCATGGTGCCACAGCCCCT  35009     AACCA    CA
                                AGG    TGGC  ACTGTGAGC
                                |||    ||||  |||||||||
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                                TCC    ACCG  TGGTACTCG
                                  CCGAC   __
GAM694  FLJ22690  3'  GCTCACAGCCGACCTGTGGCCT 45575    AA    CCAA_
                                AGG  CCATGG    CTGTGAGC
                                |||  ||||||    ||||||||
                                TCC  GGTGTC    GACACTCG
                                  __     CAGCC
GAM694  FLJ32449  3'  GCATTTGGCCATGGTTCCTT   59378            C
                                AAGGAACCATGGCCAA TGT
                                |||||||||||||||| |||
                                TTCCTTGGTACCGGTT ACG
                                         T
GAM694  HPIP    3'  GCTCACAGCTGCCTTGGCCCC  40425    AA   T   CAA
                                GG  CCA GGC   CTGTGAGC
                                ||  ||| |||   ||||||||
                                CC  GGT CCG   GACACTCG
                                 CC   T   TC_
GAM694  ILF3    3'  GCTCACAGTCGAACTACAGCTC 16924    ACCA   CCA_
            C                    GGA    TGG    ACTGTGAGC
                                |||    |||    |||||||||
                                CCT    ATC    TGACACTCG
                                  CGAC   AAGC
GAM694  KIAA1190  3'  GCTCACAGAGCACCCCAGTTCC 71651       CAT  CCAA
            T                    AGGAAC   GG    CTGTGAGC
                                ||||||   ||    ||||||||
                                TCCTTG   CC    GACACTCG
                                   ACC  ACGA
GAM694  MGC11266  3'  GCTCACAGTGGTCAGGGCCC   44488    AA  A     A
                                GG  CC TGGCCA CTGTGAGC
                                ||  || |||||| ||||||||
                                CC  GG ACTGGT GACACTCG
                                 CG  _     _
GAM694  MGC11352  5'  ACTGTTGGCCAGGGCTCCT    65424     A  A      T
                                AGGA CC TGGCCAAC GT
                                |||| || |||||||| ||
                                TCCT GG ACCGGTTG CA
                                  C  G       T
GAM694  MGC5590   3'  CACAACTTTGGTTTCTT     44149         T  CCAAC
                                AAGGAACCA GG     TGTG
                                |||||||| ||     ||||
                                TTCTTTGGT TC     ACAC
                                     T  A_____
GAM694  MKP-7    3'  GCTTCTCTTGGCCATGGTCCC  67015    A         CTGT
                                GG ACCATGGCCAA    GAGC
                                || ||||||||||    ||||
                                CC TGGTACCGGTT    TTCG
                                 C         CTC_
GAM694  MSP     3'  GCTCAGGCAGGCCATGGCC    50245    AA       AA  G
                                GG  CCATGGCC  CT TGAGC
                                ||  ||||||||  || |||||
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                                CC  GGTACCGG  GG ACTCG
                                 __       AC  _
GAM694  PGR1     3'  CTCACAGTTGGAGTTCTCC   53905   A    CATGG
                                A GGAAC    CCAACTGTGAG
                                | |||||    ||||||||||
                                C TCTTG    GGTTGACACTC
                                 C    A____
GAM694  PTPRT    3'  GCTTCGTGTTGGCCAAGACTCC 56502      ACCA       TGT
           TT                    AAGGA   TGGCCAAC   GAGC
                                |||||   ||||||||  ||||
                                TTCCT   ACCGGTTG   TTCG
                                  CAGA       TGC
GAM694  TRF4-2   3'  CTCAAACAAGCCATGGTTCCTT 42611           CAACTG
                                AAGGAACCATGGC     TGAG
                                ||||||||||||      ||||
                                TTCCTTGGTACCG     ACTC
                                       AACAA_
GAM694  LOC122786 3'  GCCTTTGGCCATGATTCT    74622      C        CT
                                GGAA CATGGCCAA  GT
                                |||| |||||||||  ||
                                TCTT GTACCGGTT  CG
                                  A        TC
GAM694  LOC138428 3'  TAGTGGCCATGGCTGCCT    75862     AA_       A
                                AGG   CCATGGCCA CTG
                                |||   |||||||| |||
                                TCC   GGTACCGGT GAT
                                  GTC        _
GAM694  LOC145581 3'  GCTCCATTAGACCATGGTTC   77794         CCAAC  T
                                GAACCATGG     TG GAGC
                                |||||||||     || ||||
                                CTTGGTACC     AC CTCG
                                      AGATT  _
GAM694  LOC146268 5'  GCTCACAGTCGGCTTGCTGCCT 78342     AAC  T    A
                                AGG   CA GGCC ACTGTGAGC
                                |||   || |||| |||||||||
                                TCC   GT TCGG TGACACTCG
                                  GTC  _    C
GAM694  LOC147299 3'  GCTGTGAGCCGCCATGGTCCC  78981    A       CAA  GTG
                                GG ACCATGGC   CT   AGC
                                || ||||||||   ||   |||
                                CC TGGTACCG   GA   TCG
                                 C       CC_  GTG
GAM694  LOC159199 3'  GCTCACAGCTGGCGGCCCT    83062     AA  ATG    A
                                AGG  CC   GCCA CTGTGAGC
                                |||  ||   |||| ||||||||
                                TCC  GG   CGGT GACACTCG
                                  C_  ____    C
GAM694  LOC200982 5'  AGTTGGCCATGGCTCTTT     91807      A
                                AAGGA CCATGGCCAACT
                                ||||| ||||||||||||
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                                TTTCT GGTACCGGTTGA
                                   C
GAM694  LOC221495 5'  CCACAGCTTGGTTCCT      95493         T   CAAC    A
                                AGGAACCA GGC    TGTG G
                                |||||||| |||    |||| |
                                TCCTTGGT TCG    ACAC C
                                     _  ____    C
GAM694  LOC253842 3'  GCTCATAGAAGCCTGGTCCCT  99238     A    T   CAA
                                AGG ACCA GGC   CTGTGAGC
                                ||| |||| |||   ||||||||
                                TCC TGGT CCG   GATACTCG
                                  C   _   AA_
GAM694  LOC254778 3'  GCCCTGTGTTGGCCAAGGTTCC 97831        A       TGTGA
                                GGAACC TGGCCAAC     GC
                                |||||| ||||||||     ||
                                CCTTGG ACCGGTTG     CG
                                    A       TGTCC
GAM694  LOC255231 3'  CTCACAGTTAGCCAGCTGACC  97119    AACCA    C
                                GG     TGGC AACTGTGAG
                                ||     |||| |||||||||
                                CC     ACCG TTGACACTC
                                 AGTCG    A
GAM694  LOC257358 5'  GCTCGTGAAGAGCATGGTTCCT 98900           G CAACTG
           T                     AAGGAACCATG C      TGAGC
                                ||||||||||| |      |||||
                                TTCCTTGGTAC G      GCTCG
                                      _ AGAAGT
GAM694  LOC90190  3'  CGCCCACAGAGCAATTGGCCAT 62422     AC       _____     A ___
           GCCTCC                  GGA  CATGGCCAA     CTGTG GC   G
                                |||  |||||||||     ||||| ||   |
                                CCT  GTACCGGTT     GACAC CG   C
                                  CC        AACGA     C ___
GAM694  LOC90495  3'  GCTCACAGTCAACTGCTTTCTT 63737       CCAT   CA___
           T                     AAGGAA    GGC     ACTGTGAGC
                                ||||||    |||     |||||||||
                                TTTCTT    TCG     TGACACTCG
                                     _____  TCAAC
GAM694  LOC90750  3'  GCTCACAGCCCTGCCCTGCCCC 64630    AAC  T   CAA_
           C                     GG   CA GGC    CTGTGAGC
                                ||   || |||    ||||||||
                                CC   GT CCG    GACACTCG
                                 CCC  C   TCCC
GAM695  FLJ21438  5'  CAAAACGCTTCCCCCCATCCCA 62190      GAGATTATC
                                TGGGA        AAGCGTTTTG
                                |||||        ||||||||||
                                ACCCT        TTCGCAAAAC
                                   ACCCCCC__
GAM695  FLJ32334  3'  AAAACGCTATTCCTTCCCA    58605       A  TTATCA
                                TGGGAG GA     AGCGTTTT
                                |||||| ||     ||||||||
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                                ACCCTT CT     TCGCAAAA
                                   C  TA____
GAM695  HHLA2    3'  CAATGTACTTTGTAATCTCCCC 23953      A       C   CG T
              CA                    TGGG GAGATTAT AAG  T TTG
                                ||||| |||||||| |||  | |||
                                ACCC CTCTAATG TTC  G AAC
                                   C       T   AT T
GAM696  ARHA     3'  CTCTGCACTCCCACCTGA    71232    T_   A
                                TC  GTGG GAGTGCAGAG
                                ||  |||| ||||||||||
                                AG  CACC CTCACGTCTC
                                 TC   _
GAM696  ASGR2    5'  CTCCACACCTTTCACAGATC   56032     T       A   CA
                                GAT CTGTGGAG GTG  GAG
                                ||| |||||||| |||  |||
                                CTA GACACTTT CAC  CTC
                                  _       C   AC
GAM696  EPHA1    3'  CTCTGCACCCCAGAA       19098       T  AGA
                                TTCTG GG   GTGCAGAG
                                ||||| ||   ||||||||
                                AAGAC CC   CACGTCTC
                                  _ ___
GAM696  EPHA8    3'  CTCCACGTCACAGAGTC     40431          AGA   C
                                GATTCTGTGG   GTG AG
                                ||||||||||   ||| ||
                                CTGAGACACT   CAC TC
                                     G__   C
GAM696  GZMM     3'  CTCGCTGTCTCCACAGGA    19213          GT  A
                                TTCTGTGGAGA  GC GAG
                                ||||||||||  || |||
                                AGGACACCTCT  CG CTC
                                      GT  _
GAM696  IFNAR2   3'  CTCTGCCACCTCTACAGAATC  7899           A  _
                                GATTCTGTGGAG GTG CAGAG
                                |||||||||||| ||| |||||
                                CTAAGACATCTC CAC GTCTC
                                      _  C
GAM696  KAL1     3'  CTCTGCATAGATACAAAAT   5835      C   GAGA
                                ATT TGTG    GTGCAGAG
                                ||| ||||    ||||||||
                                TAA ACAT    TACGTCTC
                                  A   AGA_
GAM696  KPNB2    3'  CTCTGCACCCAGGGAA      11226      G   AGA
                                TTCT TGG   GTGCAGAG
                                |||| |||   ||||||||
                                AAGG ACC   CACGTCTC
                                  G  ___
GAM696  LIF      3'  CTGCACAGCATCACTGAATC   11303       T   AGA_
                                GATTC GTGG    GTGCAG
                                ||||| ||||    ||||||
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                                CTAAG CACT    CACGTC
                                   T    ACGA
GAM696  MHC2TA   3'  CTGCACTTGCAGACTC      5981     T    GGA
                                GA TCTGT   GAGTGCAG
                                || |||||   ||||||||
                                CT AGACG   TTCACGTC
                                 C    ___
GAM696  MTMR1    5'  CTGGACAGTCCCACAGGATC   70724          A __ G
                                GATTCTGTGG GA  GT CAG
                                |||||||||| ||  || |||
                                CTAGGACACC CT  CA GTC
                                       _ GA  G
GAM696  PKIG     3'  CTCATGGAGCTCCACAGATC   23927     T       AGTG _
                                GAT CTGTGGAG    CA GAG
                                ||| ||||||||    || |||
                                CTA GACACCTC    GT CTC
                                  _       GAG_  A
GAM696  PPP1R3C  3'  CTCTGCAGTGACAGAATT    19423        GGAGAG
                                GATTCTGT     TGCAGAG
                                ||||||||     |||||||
                                TTAAGACA     ACGTCTC
                                     GTG___
GAM696  PTPRH    3'  CTCTGCACCCCACCATC     12616     TCT    AGA
                                GAT   GTGG   GTGCAGAG
                                |||   ||||   ||||||||
                                CTA   CACC   CACGTCTC
                                  C__    C__
GAM696  RFX2     3'  CTCTGCACTCAACTGGAACC   7156    A   _ GGA
                                G TTCT GT   GAGTGCAGAG
                                | |||| ||   ||||||||||
                                C AAGG CA   CTCACGTCTC
                                 C    T  A__
GAM696  SHMT2    3'  CTCCTTATTCCCTACAGAATC  19435          A    CA
                                GATTCTGTGG GAGTG  GAG
                                |||||||||| |||||  |||
                                CTAAGACATC CTTAT  CTC
                                       C     TC
GAM696  STK4     3'  CTCTGTCGTCTCTCCACAG    21864          _ _
                                CTGTGGAGAG TG CAGAG
                                |||||||||| || |||||
                                GACACCTCTC GC GTCTC
                                       T  T
GAM696  TEM8     3'  CTCTAGCTTTCCACAAATC    50826      C        GC
                                GATT TGTGGAGAGT  AGAG
                                |||| ||||||||||  ||||
                                CTAA ACACCTTTCG  TCTC
                                  _        A_
GAM696  USH3A    3'  CTGCACTCTTATTGGATTC    54842    T   GTG
                                GA TCT   GAGAGTGCAG
                                || |||   ||||||||||
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                                CT AGG   TTCTCACGTC
                                 T   TTA
GAM696  ZNF219   5' CTGCACTTCCCAGAACC     33554   A    T   G
                                G TTCTG GGA AGTGCAG
                                | ||||| ||| |||||||
                                C AAGAC CCT TCACGTC
                                 C    _  _
GAM696  ASB13    3' CTGCGCTGTTCTACAGAA    45546         _
                                TTCTGTGGAG AGTGCAG
                                |||||||||| |||||||
                                AAGACATCTT TCGCGTC
                                      G
GAM696  CLIPR-59 3' CTCTGCACCCTCAAGAA     32016     GTG   A
                                TTCT   GAG GTGCAGAG
                                ||||   ||| ||||||||
                                AAGA   CTC CACGTCTC
                                  A__   C
GAM696  Di-Ras2  3' CTCTGGAGTCACAGAATC    34611         AGAGTG
                                GATTCTGTGG     CAGAG
                                ||||||||||     |||||
                                CTAAGACACT     GTCTC
                                      GAG___
GAM696  DKFZP434N014 3' CTCTGCACCCCCAGCCTATC  61229     T__   T  AGA
                                GAT   CTG GG   GTGCAGAG
                                |||   ||| ||   ||||||||
                                CTA   GAC CC   CACGTCTC
                                  TCC   _  C__
GAM696  FLJ10432 3' CTCTGCACTCCATGATGAA   39351     T__    GA
                                TTC   GTGGA  GTGCAGAG
                                |||   |||||  ||||||||
                                AAG   TACCT  CACGTCTC
                                  TAG    __
GAM696  FLJ11181 3' CTCTGCCCTCCACAGA      37718         AGT
                                TCTGTGGAG   GCAGAG
                                |||||||||   ||||||
                                AGACACCTC   CGTCTC
                                      C__
GAM696  FLJ12505 3' CTCTGCACTTTACCCAGCATC 45714     T   T  _
                                GAT CTG GG AGAGTGCAGAG
                                ||| ||| || ||||||||||
                                CTA GAC CC TTTCACGTCTC
                                  C   _  A
GAM696  FLJ22692 3' CTGTCTCCACAAAATT      47483      C      AGT
                                GATT TGTGGAG   GCAG
                                |||| |||||||   ||||
                                TTAA ACACCTC   TGTC
                                  A      ___
GAM696  KIAA0420 3' CTGCACTCTCTGGAATT     64087       GT
                                GATTCT  GGAGAGTGCAG
                                ||||||  ||||||||||
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                                TTAAGG  TCTCTCACGTC
                                  __
GAM696  KIAA1030  3'  CTCTGCACCCTTGGGGA     94978      GTG   A
                                TTCT   GAG GTGCAGAG
                                ||||   ||| ||||||||
                                AGGG   TTC CACGTCTC
                                  G__   C
GAM696  KIAA1643  3'  CTCTGCACCCTCTGGAA     65155      GT    A
                                TTCT  GGAG GTGCAGAG
                                ||||  |||| ||||||||
                                AAGG  TCTC CACGTCTC
                                  __    C
GAM696  KIAA1854  3'  CTCCGACCTCCCTACAGAATC  72205          A   TGCA
                                GATTCTGTGG GAG    GAG
                                |||||||||| |||    |||
                                CTAAGACATC CTC    CTC
                                      C   CAGC
GAM696  KIF13B    3'  CTTTCTCTCCACAAAGTC    83715      C       TGC
                                GATT TGTGGAGAG   AG
                                |||| |||||||||   ||
                                CTGA ACACCTCTC   TC
                                  A        TT_
GAM696  KIF13B    3'  CTTTCTCTCCACAAAGTC    31563      C       TGC
                                GATT TGTGGAGAG   AG
                                |||| |||||||||   ||
                                CTGA ACACCTCTC   TC
                                  A        TT_
GAM696  MAP       3'  CTCTTCAGGTTCACAGAA    43367         GAG  C
                                TTCTGTGGA   TG AGAG
                                |||||||||   || ||||
                                AAGACACTT   AC TCTC
                                     GG_  T
GAM696  MGC4655   3'  CTGTCTCCACAGGATC     53960           AGT
                                GATTCTGTGGAG   GCAG
                                ||||||||||||   ||||
                                CTAGGACACCTC   TGTC
                                  ____
GAM696  PRKRI     5'  CTCTTCCCTCCACAGATC    21828      T      AGTGC
                                GAT CTGTGGAG    AGAG
                                ||| ||||||||    ||||
                                CTA GACACCTC    TCTC
                                  _      CCT__
GAM696  PRO0650   5'  CTGTGACGCTCCACAGAA    27071          A  _
                                TTCTGTGGAG GT GCAG
                                |||||||||| || ||||
                                AAGACACCTC CA TGTC
                                      G  G
GAM696  RASSF2    3'  CTCCACCTTCTCTCCACAGAAT 29096            TGCA__
                                ATTCTGTGGAGAG     GAG
                                ||||||||||||      |||
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                                TAAGACACCTCTC     CTC
                                      TTCCAC
GAM696  TRIM26   3'  CTCTGCACTCTCTGGAAT    14347      GT
                                ATTCT  GGAGAGTGCAGAG
                                |||||  ||||||||||||||
                                TAAGG  TCTCTCACGTCTC
                                  __
GAM696  TTTY11   3'  CTGGACCCAGCAGAATC     50025       _  AGA  G
                                GATTCTG TGG   GT CAG
                                ||||||| |||   || |||
                                CTAAGAC ACC   CA GTC
                                   G   ___  G
GAM696  LOC143326 3'  CTCTGCCAACACAGGATC    77055        GAGAGT
                                GATTCTGTG     GCAGAG
                                |||||||||     ||||||
                                CTAGGACAC     CGTCTC
                                     AAC___
GAM696  LOC144058 5'  CTCTGAGGGCCACAGAATT    77181         AGAGTG
                                GATTCTGTGG     CAGAG
                                ||||||||||     |||||
                                TTAAGACACC     GTCTC
                                     GGGA__
GAM696  LOC146443 3'  CTCTTGGACCCCACAGAAT    78446        AGA  G  _
                                ATTCTGTGG   GT CA GAG
                                |||||||||   || || |||
                                TAAGACACC   CA GT CTC
                                     C__  G  T
GAM696  LOC146756 3'  CTCTGAGAAGCCTCCACAGAAT 84801          A  G___
          C                      GATTCTGTGGAG GT    CAGAG
                                ||||||||||||| ||    |||||
                                CTAAGACACCTC CG    GTCTC
                                      _  AAGA
GAM696  LOC165246 5'  CTCCCACTGCCCACAGAA    83365        AG    CA
                                TTCTGTGG  AGTG  GAG
                                ||||||||  ||||  |||
                                AAGACACC  TCAC  CTC
                                     CG    C_
GAM696  LOC199796 5'  TCTGCACTGGAGAGTC      74925       G GGAG
                                GATTCT T    AGTGCAGA
                                ||||||| |   ||||||||
                                CTGAGA G    TCACGTCT
                                   G ____
GAM696  LOC201304 3'  CTCTGCACTCCAGAA       89604       TGGA
                                TTCTG    GAGTGCAGAG
                                |||||    ||||||||||
                                AAGAC    CTCACGTCTC
                                  _____
GAM696  LOC202052 3'  CTCTGCAGGCATTCCACAGAGT 91898          A  __
          C                      GATTCTGTGGAG GT  GCAGAG
                                ||||||||||| ||  ||||||
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                                CTGAGACACCTT CG  CGTCTC
                                      A  GA
GAM696  LOC206426 3'  CTCCATCCTCTCCACAGCATC  91098     T        TGCA
                                GAT CTGTGGAGAG    GAG
                                ||| ||||||||||    |||
                                CTA GACACCTCTC    CTC
                                  C         CTAC
GAM696  LOC219920 5'  CTCCGCACTCTCCTGGGTC    94949      TGT        A
                                GATTC   GGAGAGTGC GAG
                                |||||   ||||||||| |||
                                CTGGG   CCTCTCACG CTC
                                   T__        C
GAM696  LOC221354 3'  CTCCAGAACCTCACACAGAATC 94012          _   A  GCA_
                                GATTCTGTG GAG GT    GAG
                                ||||||||| ||| ||    |||
                                CTAAGACAC CTC CA    CTC
                                      A   _  AGAC
GAM696  LOC255423 5'  CTCTTACTGCCCACAGAA     99439         AG    C
                                TTCTGTGG  AGTG AGAG
                                ||||||||  |||| ||||
                                AAGACACC  TCAT TCTC
                                     CG    _
GAM696  LOC257354 3'  CTGCACTCTCTGGAATT      96789       GT
                                GATTCT  GGAGAGTGCAG
                                ||||||  ||||||||||
                                TTAAGG  TCTCTCACGTC
                                  __
GAM696  LOC257464 5'  CTCTTGCTTTCCCCAAAATC   91242      C  T       C
                                GATT TG GGAGAGTG AGAG
                                |||| || |||||||| ||||
                                CTAA AC CCTTTCGT TCTC
                                  A  C       _
GAM696  LOC257494 3'  CTCTGCACTCTCTGGAAT     99632       GT
                                ATTCT  GGAGAGTGCAGAG
                                |||||  ||||||||||||
                                TAAGG  TCTCTCACGTCTC
                                  __
GAM696  LOC92840  3'  CTCCCAGGCCTCCACAGAGTC  57246           A  GCA_
                                GATTCTGTGGAG GT    GAG
                                |||||||||||| ||    |||
                                CTGAGACACCTC CG    CTC
                                      _  GACC
GAM697  ADAT1     3'  CCAGCAAAGAATGAAGGC     24914     __         C
                                GTC  CATTCTTTGC GG
                                |||  |||||||||| ||
                                CGG  GTAAGAAACG CC
                                  AA         A
GAM697  M17S2     5'  CCGGTAGCGGACGGTCCTT    20910           ATTCT
                                AAGGACCGTCC    TTGCCGG
                                ||||||||||     |||||||
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                                TTCCTGGCAGG    GATGGCC
                                      C____
GAM697  ST14    5'  CCGGCAGGGACGACGCCT    42042    AC   CAT
                                AGG  CGTC   TCTTTGCCGG
                                |||  ||||   ||||||||||
                                TCC  GCAG   AGGGACGGCC
                                  __    C__
GAM697  HTGN29  5'  GCCAACTGTGTGGCGGTCC   39885       _  TC  T
                                GGACCGTC CAT  TT GC
                                |||||||| |||  || ||
                                CCTGGCGG GTG  AA CG
                                     T   TC  C
GAM697  PMAIP1  3'  GCAAGAATGGAAGACCCTT   41211     ACCG       T
                                AAGG    TCCATTCTT GC
                                ||||    |||||||||| ||
                                TTCC    AGGTAAGAA CG
                                  CAGA        _
GAM697  LOC144278 3'  GCCAGCAAAGACTGCTCGATGG 77274         ___  T      C
            TCCT                    AGGACCGTC   CA TCTTTGC GGC
                                |||||||||   || ||||||| |||
                                TCCTGGTAG   GT AGAAACG CCG
                                     CTC  C      A
GAM697  LOC147976 3'  CCGGTGAATGAAGACCCT    79287     ACC   CA   _  TG
                                AGG   GTC  TTC TT  CCGG
                                |||   |||  ||| ||  ||||
                                TCC   CAG  AAG AA  GGCC
                                  ___   __   T  GT
GAM697  LOC254263 5'  GCCGGCAGCGGACGCGCC    96367    AC    ATTCT
                                GG  CGTCC    TTGCCGGC
                                ||  |||||    ||||||||
                                CC  GCAGG    GACGGCCG
                                 GC    C____
GAM698  ADAM19  3'  TTCCTTGGAAGCCCAGAGGG   53850       C    TG T
                                CCCTCTG GCTTC  A GGGA
                                ||||||| |||||  | ||||
                                GGGAGAC CGAAG  T CCTT
                                    C    GT _
GAM698  AES     3'  TCCCATCGCCCACAAAAGGGG  8526       C___  C  TTCT
                                CCCCT    TG GC    GATGGGA
                                |||||    || ||    |||||||
                                GGGGA    AC CG    CTACCCT
                                   AAAC  C  ____
GAM698  AP2A1   3'  CCCAAGCACAGAGGGG      27218        C   TCTGA
                                CCCCTCTG GCT     TGGG
                                |||||||| |||     ||||
                                GGGGAGAC CGA     ACCC
                                    A  _____
GAM698  AP2A1   3'  CCCAAGCACAGAGGGG      56304        C   TCTGA
                                CCCCTCTG GCT     TGGG
                                |||||||| |||     ||||
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                                GGGGAGAC CGA    ACCC
                                   A  _____
GAM698  CD44    3'  TTTGTCAGAGGCACAAAAGGG  7028     C_ C      GG
                                CCCT  TG GCTTCTGAT  G
                                ||||  || ||||||||| |
                                GGGA  AC CGGAGACTG  T
                                  AA  A       TT
GAM698  CGA     5'  CCTGCAAAAAGCCCAGAG    7425      C   C_  A
                                CTCTG GCTT  TG TGGG
                                ||||| ||||  || ||||
                                GAGAC CGAA  AC GTCC
                                  C   AA  _
GAM698  CYLN2   3'  CCCATCAGTGGACCAGAGGG  14089      CG  T
                                CCCTCTG  CT CTGATGGG
                                |||||||  || ||||||||
                                GGGAGAC  GG GACTACCC
                                   CA  T
GAM698  DACH    3'  TTCCCACCCTTGTCAGAGGG  55826      C  TTCTGA
                                CCCTCTG GC     TGGGAA
                                ||||||| ||     ||||||
                                GGGAGAC TG     ACCCTT
                                   _  TTCCC_
GAM698  ERBB3   3'  TTTCCCATCAGACTGTCAAGA  10539    GC  T_
                                TCT  GC  TCTGATGGGAAA
                                |||  ||  ||||||||||||
                                AGA  TG  AGACTACCCTTT
                                  AC  TC
GAM698  FRAP1   3'  CTGAGCAGATGCACAGAGGGG  18271       C  T   ATG
                                CCCCTCTG GC TCTG   GG
                                |||||||| || ||||   ||
                                GGGGAGAC CG AGAC   TC
                                   A  T   GAG
GAM698  GDF5    3'  TCCTGGAATCACAGAGGGG   6899       CGC   GAT
                                CCCCTCTG   TTCT   GGGA
                                ||||||||   ||||   ||||
                                GGGGAGAC   AAGG   TCCT
                                   ACT   ___
GAM698  GRM7    3'  TTCCCATCACCGGAGG     7793       CGCTTC
                                CCTCTG     TGATGGGAA
                                ||||||     |||||||||
                                GGAGGC     ACTACCCTT
                                  C_____
GAM698  IGF1    3'  TTTCCCATGCCTGCTCAGAAGG 7088     C   C  TTCTG
          G                      CCC TCTG GC    ATGGGAAA
                                ||| |||| ||    ||||||||
                                GGG AGAC CG    TACCCTTT
                                  A   T  TCCG_
GAM698  IGFBP3  3'  TCCTTGAAAACAGAGGGG    7005       CGC   TGAT
                                CCCCTCTG   TTC   GGGA
                                ||||||||   |||   ||||
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                                GGGGAGAC  AAG   TCCT
                                   AA_  T___
GAM698  LENG4   3'  TTCCCATTTCACAAAGGGG  44423     C  CGCTTCT
                                CCCCT TG     GATGGGAA
                                ||||| ||     ||||||||
                                GGGGA AC     TTACCCTT
                                  A  ACT____
GAM698  NPTX2   3'  TCCCCAAAGCAGAGGGG    94086       GCTTC  AT
                                CCCCTCTGC    TG  GGGA
                                |||||||||    ||  ||||
                                GGGGAGACG    AC  CCCT
                                   AA___ __
GAM698  OGG1    3'  CCAGCAAAGCGCAGAAAGG   34150   CC      C  A
                                CC  TCTGCGCTT TG TGG
                                ||  |||||||||| || |||
                                GG  AGACGCGAA AC ACC
                                 AA       _  G
GAM698  PCOLN3  3'  TTCCCATCAGCCAGAGGGG   12418       C   TCT
                                CCCCTCTG GCT   GATGGGAA
                                |||||||| |||   ||||||||
                                GGGGAGAC CGA   CTACCCTT
                                   _   ___
GAM698  PFKFB3  5'  TTCCCCTGGCAGCGCAGG    83755       T  GAT
                                TCTGCGCT CT   GGGAA
                                |||||||| ||   |||||
                                GGACGCGA GG   CCCTT
                                   C  TC_
GAM698  PRKACA  3'  CCCAAAAAGACAGAGGGG    12266       CGCT   GA_
                                CCCCTCTG   TCT   TGGG
                                ||||||||   |||   ||||
                                GGGGAGAC   AGA   ACCC
                                   _____  AAA
GAM698  RAD23B  5'  TCCCCAGAGCGCGAGG     12737     T    T   AT
                                CCTC GCGCT CTG  GGGA
                                |||| ||||| |||  ||||
                                GGAG CGCGA GAC  CCCT
                                  _    _  ___
GAM698  SORT1   3'  TTCCATCAAAGCCAAAAGG   12928    C_  C   C
                                CCT  TG GCTT TGATGGGA
                                |||  || |||| ||||||||
                                GGA  AC CGAA ACTACCTT
                                  AA  _   _
GAM698  SPTB    3'  TCCCCACAGCGCAGAGG     6236         TC  AT
                                CCTCTGCGCT  TG  GGGA
                                ||||||||||  ||  ||||
                                GGAGACGCGA  AC  CCCT
                                   C_  __
GAM698  TLL1    3'  TCTGTCAGAACACAAAGG    25878     C  CGC
                                CCT TG   TTCTGATGGG
                                ||| ||   ||||||||||
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                                GGA AC   AAGACTGTCT
                                  A  AC_
GAM698  TPMT     3'  TCTCTACTGAAAGTGCAGAAGG 6318     C       _ TGAT
                                CC TCTGCGCTT C    GGGA
                                || |||||||| |    ||||
                                GG AGACGTGAA G    CTCT
                                 A        A TCAT
GAM698  C20orf100 3'  TCCCACCAGACTCTGCAGAGG  52880        CT_    A
                                CCTCTGCG   TCTG TGGGA
                                ||||||||   |||| |||||
                                GGAGACGT   AGAC ACCCT
                                     CTC    C
GAM698  C20orf72  3'  TTCCCCAGGGTTCACCCAGAGG 54608        C____   T   AT
           GG                     CCCCTCTG    GCT CTG  GGGAA
                                |||||||     ||| |||  |||||
                                GGGGAGAC    TGG GAC  CCCTT
                                     CCACT  _  __
GAM698  CAMK2G   5'  TTCCCATCACCAGAATGGG   69538    C_   CGCTTC
                                CCC  TCTG     TGATGGGAA
                                |||  ||||     |||||||||
                                GGG  AGAC     ACTACCCTT
                                  TA   C_____
GAM698  CDH22    3'  CCCATCAGAGTTAAGAGG    41438      GC   T
                                CCTCT  GCT CTGATGGG
                                |||||  ||| ||||||||
                                GGAGA  TGA GACTACCC
                                   AT  _
GAM698  CLSTN2   3'  TCCCCCAGGACAGAGGGG    42402        CGC    AT
                                CCCCTCTG   TTCTG  GGGA
                                ||||||||   |||||  ||||
                                GGGGAGAC   AGGAC  CCCT
                                     ___     C_
GAM698  DGKD     3'  CCCAGAACCACAGAGGGG    60102        CGC    GAT
                                CCCCTCTG   TTCT   GGG
                                ||||||||   ||||   |||
                                GGGGAGAC   AAGA   CCC
                                     ACC   ___
GAM698  DKFZP434C171 3'  CCCATCAGTGAAAAGGGG    32189      CTG    TCT
                                CCCCT   CGCT   GATGGG
                                |||||   ||||   ||||||
                                GGGGA   GTGA   CTACCC
                                   AAA   ___
GAM698  DKFZP566J091 3'  TTTCCCATCATGACGGAAGAAG 48866      GCG_  _  _
           AG                     CTCT    CT TC TGATGGGAAA
                                ||||    || || ||||||||||
                                GAGA    GG AG ACTACCCTTT
                                  AGAA  C  T
GAM698  DKFZP586L151 3'  CCCACAAGCAGAAGCACAGAGG 64656        C      A___
           GG                     CCCCTCTG GCTTCTG    TGGG
                                |||||||| |||||||    ||||
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                                GGGGAGAC CGAAGAC   ACCC
                                    A      GAAC
GAM698  FLJ10898  5' TTCCCATCAAGTGCCCAAAGG 60145    CT__    TC
                                CCT   GCGCT  TGATGGGAA
                                |||   |||||  |||||||||
                                GGA   CGTGA  ACTACCCTT
                                  AACC    __
GAM698  FLJ13154  3' TTTCCCAGAGAGGCAGAGGGG 45113        G  T  GA
                                CCCCTCTGC CT CT  TGGGAAA
                                ||||||||| || ||  |||||||
                                GGGGAGACG GA GA  ACCCTTT
                                     _ _ G_
GAM698  FLJ14743  3' TTCCCTTAACCAGAGGGG    68636        CGCTTC   T
                                CCCCTCTG     TGA GGGAA
                                ||||||||     ||| |||||
                                GGGGAGAC     ATT CCCTT
                                    CA_____  _
GAM698  FLJ21135  5' CCTCCAGGCACAGAGGGG    46348        C  TT   AT
                                CCCCTCTG GC  CTG  GG
                                |||||||| ||  |||  ||
                                GGGGAGAC CG  GAC  CC
                                    A  __   CT
GAM698  FLJ21195  5' CTCAGAGAAGGCAGAGGG    42702        G    GA
                                CCCTCTGC CTTCT  TGGG
                                |||||||| |||||  ||||
                                GGGAGACG GAAGA  ACTC
                                    _    G_
GAM698  FLJ23132  3' GTCAAAAGCACAAAGGGG    97840      C  C    C
                                CCCCT TG GCTT TGAT
                                ||||| || |||| ||||
                                GGGGA AC CGAA ACTG
                                   A  A    A
GAM698  KIAA0316  3' TTCCCGGGGAGAAGAACAGAGG 70247        CG    GA_
           GG                     CCCCTCTG  CTTCT   TGGGAA
                                |||||||  |||||   ||||||
                                GGGGAGAC  GAAGA   GCCCTT
                                    AA    GGG
GAM698  KIAA0451  3' CCCATCCAATCTAGACAGAGGG 29769        CG  TCT___
           G                     CCCCTCTG  CT     GATGGG
                                ||||||||  ||     ||||||
                                GGGGAGAC  GA     CTACCC
                                    A_  TCTAAC
GAM698  KIAA0543  3' CCTAGAGGCACAGAGGGG    69521        C      AT
                                CCCCTCTG GCTTCTG  GG
                                |||||||| |||||||  ||
                                GGGGAGAC CGGAGAT  CC
                                    A      __
GAM698  KIAA0552  5' TCCCATTTCGCAGAGG      28998        CTTCT
                                CCTCTGCG    GATGGGA
                                ||||||||    |||||||
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                                GGAGACGC    TTACCCT
                                    T____
GAM698  KIAA1076 3' CCCCAGAAAGCAGAGG     66121       GC    AT
                                CCTCTGC  TTCTG  GGG
                                |||||||  |||||  |||
                                GGAGACG  AAGAC  CCC
                                   A_    __
GAM698  KIAA1277 3' CTCACAGAAACACAAAAGGG  65074     C_  CGC    A
                                CCCT  TG   TTCTG TGGG
                                ||||  ||   ||||| ||||
                                GGGA  AC   AAGAC ACTC
                                  AA  ACA    _
GAM698  MAST205  5' TTCCGTGAGGAGCGCAGAGG  31360           G
                                CCTCTGCGCTTCT ATGGGA
                                |||||||||||| ||||||
                                GGAGACGCGAGGA TGCCTT
                                       G
GAM698  MGC:5244 3' TTTCCTTTTGGAAGCAAGA   49152     GC    TG T
                                TCT  GCTTC  A GGGAAA
                                |||  |||||  | ||||||
                                AGA  CGAAG  T TCCTTT
                                  A_    GT T
GAM698  MGC10955 5' TTCCATGAAAGGCAAAGG    52033     C   G   CTG
                                CCT TGC CTT   ATGGGA
                                ||| ||| |||   ||||||
                                GGA ACG GAA   TACCTT
                                  A  _   AG_
GAM698  MGC13017 3' CCCAGGCAGAAGCACAAAGG  55572     C  C      A_
                                CCT TG GCTTCTG  TGGG
                                ||| || |||||||  ||||
                                GGA AC CGAAGAC  ACCC
                                  A  A      GG
GAM698  MGC20647 5' TCTGGGAGAAAGCGCAGAGGG 97351           _  GA
                                CCCTCTGCGCTT CT  TGGG
                                |||||||||||| ||  ||||
                                GGGAGACGCGAA GA  GTCT
                                       A  GG
GAM698  MGC22014 3' TTCATCAGGACACACAGAGGGG 65121         CGC_
                                CCCCTCTG    TTCTGATGGG
                                ||||||||    ||||||||||
                                GGGGAGAC    AGGACTACTT
                                    ACAC
GAM698  MGC5508  3' CCCATCAGCCAAAGCAAAAGA  44265     GC_   ___
                                TCT   GCTT   CTGATGGG
                                |||   ||||   ||||||||
                                AGA   CGAA   GACTACCC
                                  AAA    ACC
GAM698  PLSCR3   3' CCCATCAACAGCTGCAGGGGG  92447         _   TC
                                CCCTCTGC GCT  TGATGGG
                                |||||||| |||  |||||||
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                                GGGGGACG CGA  ACTACCC
                                    T   CA
GAM698  PLSCR3   3'  CCCATCAACAGCTGCAGGGGG  40152       _  TC
                                CCCTCTGC GCT  TGATGGG
                                |||||||| |||  |||||||
                                GGGGGACG CGA  ACTACCC
                                    T   CA
GAM698  PRO1768  3'  TTTCCCATAAACACAGGGG   26886     C  CGCTTCTG
                                CCCCT TG      ATGGGAAA
                                ||||| ||      ||||||||
                                GGGGA AC      TACCCTTT
                                  C  AAA_____
GAM698  SCYD1    3'  TCCCATCACCCGCTAAGAGGG  92560      __  CTTC
                                CCCTCT  GCG   TGATGGGA
                                ||||||  |||   ||||||||
                                GGGAGA  CGC   ACTACCCT
                                   AT   CC__
GAM698  SDC3     3'  CCCACCGCAGCTGGCAGAGGGG 28465       __  TC  A
                                CCCCTCTGC  GCT  TG TGGG
                                |||||||||  |||  || ||||
                                GGGGAGACG  CGA  GC ACCC
                                     GT   C_  C
GAM698  SEMA6B   3'  CCCACTCTGCAGAGGG     40010       CTTCT  _
                                CCCTCTGCG    GA TGGG
                                |||||||||    || ||||
                                GGGAGACGT    CT ACCC
                                     _____  C
GAM698  SEMA6B   3'  CCCACTCTGCAGAGGG     56660       CTTCT  _
                                CCCTCTGCG    GA TGGG
                                |||||||||    || ||||
                                GGGAGACGT    CT ACCC
                                     _____  C
GAM698  SEMA6B   3'  CCCACTCTGCAGAGGG     50402       CTTCT  _
                                CCCTCTGCG    GA TGGG
                                |||||||||    || ||||
                                GGGAGACGT    CT ACCC
                                     _____  C
GAM698  STMN3    3'  TTCCCACTTGGCACCCAGAGGG 32470       C__  TCTGA
          G                      CCCCTCTG   GCT    TGGGAA
                                 ||||||||   |||    ||||||
                                 GGGGAGAC   CGG    ACCCTT
                                     CCA   TTC__
GAM698  SYNPO2   5'  CAGGCAGAAGACAGAAGGG   72388    C   CG    A_
                                CCC TCTG  CTTCTG  TG
                                ||| ||||  ||||||  ||
                                GGG AGAC  GAAGAC  AC
                                  A   A_     GG
GAM698  ZNF282   3'  TCCCAGGGCAGAGGGG     90696       G  TCTGAT
                                CCCCTCTGC CT     GGGA
                                ||||||||| ||     ||||
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                                GGGGAGACG GA     CCCT
                                     G _______
GAM698  LOC112937 5'  TTCCCCTCCGAGGGCAGAGAGG 93179    _     G    T  T
                                CC CTCTGC CTTC GA GGGAA
                                || |||||| |||| || |||||
                                GG GAGACG GGAG CT CCCTT
                                 A     _    C  C
GAM698  LOC118987 3'  TCTCGTTGAAAAGCCAGAG    74395      C    CT_
                                CTCTG GCTT   GATGGGA
                                ||||| ||||   |||||||
                                GAGAC CGAA   TTGCTCT
                                   _    AAG
GAM698  LOC119146 5'  TCCCCTGCGCAAGCGCAGGAG  76022     _      C  AT_
                                CTC TGCGCTT TG   GGGA
                                ||| ||||||| ||   ||||
                                GAG ACGCGAA GC   CCCT
                                  G      C  GTC
GAM698  LOC127841 5'  TCCCACAGAGACAGAGGGG    75190         CGC     A
                                CCCCTCTG   TTCTG TGGGA
                                ||||||||   ||||| |||||
                                GGGGAGAC   GAGAC ACCCT
                                     A__    _
GAM698  LOC130470 3'  TCCCATCAGGACAGAG      75442       CGC
                                CTCTG   TTCTGATGGGA
                                |||||   ||||||||||
                                GAGAC   AGGACTACCCT
                                   ___
GAM698  LOC130813 3'  CCCATCAGCTGAAGAAGGG    76269     C   G  CTT
                                CCC TCT CG   CTGATGGG
                                ||| ||| ||   ||||||||
                                GGG AGA GT   GACTACCC
                                  A   A  C__
GAM698  LOC144017 5'  TTTCCAGGTATCTGAAGCGCAG 83933           T   ___
           AGG                    CCTCTGCGCTTC GATG   GGAAA
                                |||||||||||| ||||   |||||
                                GGAGACGCGAAG CTAT   CCTTT
                                       T    GGA
GAM698  LOC148114 5'  CCCATCAGAGGGATGGG     79361     C  TGCG
                                CCC TC    CTTCTGATGGG
                                ||| ||    ||||||||||
                                GGG AG    GGAGACTACCC
                                  T _____
GAM698  LOC149837 5'  CCTGTGGTCAGAATCGCAGAGG 85894          C      ___
           GG                     CCCCTCTGCG TTCTGAT   GGG
                                |||||||||| |||||||   |||
                                GGGGAGACGC AAGACTG   TCC
                                      T      GTG
GAM698  LOC149997 5'  CTGAGCAGAAGCACAGGGAGG  76825    _    C      ATG
                                CC CTCTG GCTTCTG   GG
                                || ||||| |||||||   ||
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                                GG GGGAC CGAAGAC   TC
                                 A    A      GAG
GAM698   LOC150207 3'  TTTCCTTTTGGAAGCAAAAAGA 80598     GC__    TG T
                                TCT   GCTTC  A GGGAAA
                                |||   |||||  | ||||||
                                AGA   CGAAG  T TCCTTT
                                  AAAA    GT T
GAM698   LOC151429 3'  TCCCAGGGGAACAGAGGGG   86551       CGC   GA
                                CCCCTCTG   TTCT  TGGGA
                                ||||||||   ||||  |||||
                                GGGGAGAC   AAGG  ACCCT
                                     ___   GG
GAM698   LOC152048 3'  TCCCATCACCCCCAGATGGG   86735    C   CGCTTC
                                CCC TCTG     TGATGGGA
                                ||| ||||     ||||||||
                                GGG AGAC     ACTACCCT
                                  T   CCCC__
GAM698   LOC154449 5'  TCCCGTGTGAGTGCAGAG    81993         CTG
                                CTCTGCGCTT   ATGGGA
                                ||||||||||   ||||||
                                GAGACGTGAG   TGCCCT
                                      TG_
GAM698   LOC159256 5'  CCCAGAGAAGGGCAGAGGG   83071       G    GA
                                CCCTCTGC CTTCT  TGGG
                                |||||||| |||||  ||||
                                GGGAGACG GAAGA  ACCC
                                     G    G_
GAM698   LOC164714 3'  TCCCACCGGCAGCAGGGGGG   88590        GCTT   A
                                CCCCTCTGC    CTG TGGGA
                                |||||||||    ||| |||||
                                GGGGGGACG    GGC ACCCT
                                      AC__   C
GAM698   LOC196453 5'  TCAAGGTGCAGAAAACAGAGGG 92342        CGC    ATGG__
           G                     CCCCTCTG   TTCTG     GA
                                ||||||||   |||||     ||
                                GGGGAGAC   AAGAC     CT
                                     AA_    GTGGAA
GAM698   LOC197342 3'  CCCACCCAGCACAGCAGCAGAG 89356         _   T__   A_
           GGG                    CCCCTCTGC GCT   CTG  TGGG
                                |||||||| |||   |||  ||||
                                GGGGAGACG CGA   GAC  ACCC
                                     A   CAC   CC
GAM698   LOC197358 3'  TTTCCCATCAGAAGTCCGAGG  89451     T C
                                CCTC G GCTTCTGATGGGAAA
                                |||| | |||||||||||||||
                                GGAG C TGAAGACTACCCTTT
                                  _ C
GAM698   LOC201191 3'  CTCAACAGGAGCGCAGAG    91343           A
                                CTCTGCGCTTCTG TGGG
                                |||||||||||| ||||
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                                GAGACGCGAGGAC ACTC
                                      A
GAM698  LOC201245 5'  TCCCTGAGCCAGAGGGG     88736        C   CTGAT
                                CCCCTCTG GCTT    GGGA
                                |||||||| ||||    ||||
                                GGGGAGAC CGAG    CCCT
                                    _   T____
GAM698  LOC204498 5'  CCCAGAGAAGGGCAGAGGG   91024        G   GA
                                CCCTCTGC CTTCT  TGGG
                                |||||||| |||||  ||||
                                GGGAGACG GAAGA  ACCC
                                     G   G_
GAM698  LOC220070 3'  TCCCCCACTGTCAGAGAGG   59943    _   C  TTC  AT
                                CC CTCTG GC   TG  GGGA
                                || ||||| ||   ||  ||||
                                GG GAGAC TG   AC  CCCT
                                 A    _ TC_  C_
GAM698  LOC221760 3'  TTCCCATCCCAGAGAAGGG   95433    __    CGCTTCT
                                CCC  CTCTG     GATGGGAA
                                |||  |||||     ||||||||
                                GGG  GAGAC     CTACCCTT
                                  AA    C_______
GAM698  LOC256286 3'  TTTCCTTTTGGAAGCAAGA   96898    GC    TG T
                                TCT  GCTTC  A GGGAAA
                                |||  |||||  | ||||||
                                AGA  CGAAG  T TCCTTT
                                  A_    GT T
GAM698  LOC256699 3'  TTCCAGGAAAAGCGCAGGAGGG 98568    CT      CTGA
                                CCC  CTGCGCTT   TGGGA
                                |||  ||||||||   |||||
                                GGG  GACGCGAA   ACCTT
                                  AG       AAGG
GAM698  LOC256789 3'  CTCAAAGCAAAGCGCAGA    99306        __  GA
                                TCTGCGCTT  CT  TGGG
                                |||||||||  ||  ||||
                                AGACGCGAA  GA  ACTC
                                     AC  A_
GAM698  LOC91035  5'  TCCCCAAGCTGGCAGAGGGG   65308        __   CTGAT
                                CCCCTCTGC  GCTT    GGGA
                                |||||||||  ||||    ||||
                                GGGGAGACG  CGAA    CCCT
                                     GT   C_____
GAM698  LOC91632  3'  TTTCCTTTTGGAAGCAAGA   67315    GC    TG T
                                TCT  GCTTC  A GGGAAA
                                |||  |||||  | ||||||
                                AGA  CGAAG  T TCCTTT
                                  A_    GT T
GAM698  LOC93166  5'  TTCCGCTGCAGCGCAGAGG   72082         TCTGA
                                CCTCTGCGCT    TGGGA
                                ||||||||||    |||||
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                                GGAGACGCGA    GCCTT
                                     CGTC_
GAM699  CKAP1    5'  AGTCCGATCACAGAGGCAGGG  73897       GATTA
                                CCCTGTTT    TGATCGGACT
                                ||||||||    ||||||||||
                                GGGACGGA    ACTAGCCTGA
                                    GAC__
GAM699  LOC146611 3'  TCTGTTAATCAAACAGAGC   78612    C       TGAT
                                GC CTGTTTGATTA   CGGA
                                || ||||||||||   ||||
                                CG GACAAACTAAT   GTCT
                                 A        T___
GAM699  LOC93082  5'  TGATTACAATAAACAGG     57257       A  A
                                CCTGTTTG TT TGATCG
                                |||||||| || ||||||
                                GGACAAAT AA ATTAGT
                                    _  C
GAM700  HMGA2    3'  CACCTCAAATACCACCC     14450     CGT      A
                                GGGT   GTGTTTGA GTG
                                ||||   |||||||| |||
                                CCCA   CATAAACT CAC
                                  C__       C
GAM700  SLC13A4   3'  CACCAGGAGCACACAACCCCAG 25859    AA   C      GAA
           A                     TC  GGGT GTGTGTTT   GTG
                                ||  |||| ||||||||   |||
                                AG  CCCA CACACGAG   CAC
                                 AC   A      GAC
GAM700  ATP10B   3'  CACTGGTCCACATAACCCTTGA 64104       CG   TTTGA
                                TCAAGGGT  TGTG    AGTG
                                ||||||||  ||||    ||||
                                AGTTCCCA  ACAC    TCAC
                                    AT   CTGG_
GAM700  DKFZP761G1913 3'  CACCCCAAACACAACTC     49693     CG      AA
                                GGGT  TGTGTTTG  GTG
                                ||||  ||||||||  |||
                                CTCA  ACACAAAC  CAC
                                  __       CC
GAM700  FLJ12076  3'  CACATTGCCACATGACCCTT   48021          TTT  A
                                AAGGGTCGTGTG   GA GTG
                                ||||||||||||   || |||
                                TTCCCAGTACAC   TT CAC
                                      CG_  A
GAM700  KIAA0750  5'  CACTGCCGCACACGACTCCTGA 28304     A        TTGA
                                TCA GGGTCGTGTGT    AGTG
                                ||| ||||||||||    ||||
                                AGT CTCAGCACACG    TCAC
                                  C         CCG_
GAM700  KIAA1485  3'  TAGACACACACCCCCTGA    90771     A   TC
                                TCA GGG  GTGTGTTTG
                                ||| |||  |||||||||
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                                AGT CCC  CACACAGAT
                                  C   CA
GAM700  SFXN5    3'  CACTTCAAACATGCCCT     58646      CGT
                                AGGGT   GTGTTTGAAGTG
                                |||||   ||||||||||||
                                TCCCG   TACAAACTTCAC
                                  ____
GAM700  LOC145608 5'  CACCCCAAATTACTGACCCTTG 84374          T  _   AA
          A                     TCAAGGGTCG GTG TTTG  GTG
                                |||||||||| ||| ||||  |||
                                AGTTCCCAGT CAT AAAC  CAC
                                      _  T   CC
GAM701  BACH2    3'  TGGAGTTGGTATTCATACA   41790    GC    GGTCTA
                                TG  ATGAA     CAACTCCA
                                ||  |||||     ||||||||
                                AC  TACTT     GTTGAGGT
                                 A_    ATG___
GAM701  EDAR     3'  GTGGAGCTATAGGAAATGCCA  42530       GAAGG    CAA
                                TGGCAT    TCTA   CTCCAC
                                ||||||    ||||   ||||||
                                ACCGTA    GGAT   GAGGTG
                                   AA___    ATC
GAM701  EGR2     3'  GTGAAGTATAGCCTTTATGCCA 6376           T   CA   C
                                TGGCATGAAGG CTA  ACT CAC
                                |||||||||| |||  ||| |||
                                ACCGTATTTCC GAT  TGA GTG
                                      _  A_   A
GAM701  EIF1A    3'  AGTTGTAGCTTATATGC     90003      A   T
                                GCATG AGG CTACAACT
                                ||||| ||| ||||||||
                                CGTAT TTC GATGTTGA
                                   A  _
GAM701  NOS1     3'  TGGAGCTTGACTTCATGCCA   7100          G  TACAA
                                TGGCATGAAG TC    CTCCA
                                |||||||||| ||    |||||
                                ACCGTACTTC AG    GAGGT
                                      _  TTC__
GAM701  PPP3R1   3'  TTGTATCCAAATTTATGCCA   76829         ___  TC
                                TGGCATGAA   GG  TACAA
                                |||||||||   ||  |||||
                                ACCGTATTT   CC  ATGTT
                                     AAA  T_
GAM701  SAR1     3'  TGAAGTTACAGATTTTAGCCA  39734      ATG      AC   C
                                TGGC   AAGGTCT  AACT CA
                                ||||   |||||||  |||| ||
                                ACCG   TTTTAGA  TTGA GT
                                  A__      CA   A
GAM701  FLJ20701 3'  TGGGAGAGCTTCATGCCA    36026          G   ACAAC
                                TGGCATGAAG TCT    TCCA
                                |||||||||| |||    ||||
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                                ACCGTACTTC AGA    GGGT
                                      G  _____
GAM701  KIAA1026  3'  GTGGAGTTATACCTACAGCCA  71743     A  A   CTAC
                                TGGC TG AGGT   AACTCCAC
                                |||| || ||||   ||||||||
                                ACCG AC TCCA   TTGAGGTG
                                  _ A   TA__
GAM701  KIAA1285  3'  GAGTTGTAGAGATCACAACA  91980    GCA  AGG
                                TG  TGA  TCTACAACTC
                                ||  |||  ||||||||||
                                AC  ACT  AGATGTTGAG
                                 AAC  AG_
GAM701  TRIP-Br2  3'  GAGTTGGAGTGCCTTCATCCA  29266    C      _  A
                                TGG ATGAAGGT CT CAACTC
                                ||| |||||||| || ||||||
                                ACC TACTTCCG GA GTTGAG
                                  _      T  G
GAM701  ZAK     3'  GTTGCAAACTTTCATACCA   34108    C      CTA
                                TGG ATGAAGGT  CAAC
                                ||| ||||||||  ||||
                                ACC TACTTTCA  GTTG
                                  A       AAC
GAM701  LOC121838 5'  GTGGAATTTGGGACTTCATGCC 76517        GT  C  C
                                GGCATGAAG  CTA AA TCCAC
                                |||||||||  ||| || |||||
                                CCGTACTTC  GGT TT AGGTG
                                     AG  _  A
GAM701  LOC128153 5'  GGAGTTGTAAACCCAAGGCCA  57918     ATGAA  C
                                TGGC    GGT TACAACTCC
                                ||||    ||| |||||||||
                                ACCG    CCA ATGTTGAGG
                                  GAAC_  A
GAM701  LOC149386 5'  AGCTGTGTCCTCATGCTA   85553       A  TC   A
                                TGGCATGA GG  TACA CT
                                |||||||| ||  |||| ||
                                ATCGTACT CC  GTGT GA
                                     _ T_   C
GAM701  LOC158450 3'  GAGCCATAGATTTTGCCA   82814     TGA     CAA
                                TGGCA  AGGTCTA  CTC
                                |||||  |||||||  |||
                                ACCGT  TTTAGAT  GAG
                                   ___     ACC
GAM701  LOC158504 3'  GAGCCATAGATTTTGCCA   82828     TGA     CAA
                                TGGCA  AGGTCTA  CTC
                                |||||  |||||||  |||
                                ACCGT  TTTAGAT  GAG
                                   ___     ACC
GAM701  LOC170371 3'  TGGCCAGGAGCCCTCATGCCA  83724       A  T  ACAACT
                                TGGCATGA GG CT    CCA
                                |||||||| || ||    |||
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                                ACCGTACT CC GA     GGT
                                    C  _  GGACC_
GAM701  LOC220827 3'  TGGAGTTTGCCCCTGCCA    92884      TGAA   CTAC
                                TGGCA   GGT    AACTCCA
                                ||||||   |||   |||||||
                                ACCGT   CCG    TTGAGGT
                                   CC__   T___
GAM701  LOC90161  3'  TGGAGTTGTACAGCTATGCCA  62371      GAA   C_
                                TGGCAT   GGT  TACAACTCCA
                                ||||||   |||  ||||||||||
                                ACCGTA   TCG  ATGTTGAGGT
                                    ___   AC
GAM701  LOC90230  3'  TGGAGTTGTGATCATCCCA   62527    CAT  A    T
                                TGG   GA GGTC ACAACTCCA
                                |||   || |||| |||||||||
                                ACC   CT CTAG TGTTGAGGT
                                  ___  A   _
GAM701  LOC91689  3'  TGGGCTAACTAAAGCCTCATGC 53982        A   CTACAAC__
           CA                     TGGCATGA GGT        TCCA
                                |||||||| |||         ||||
                                ACCGTACT CCG        GGGT
                                    _   AAATCAATC
GAM701  LOC91948  3'  GTGAAGCTGCAGACCTTCGC   68244    AT       A  A  C
                                GC  GAAGGTCT CA CT CAC
                                ||  |||||||| || || |||
                                CG  CTTCCAGA GT GA GTG
                                 __       C  C  A
GAM701  LOC92017  5'  GTGGAGTTGTAAACAAGGGAAC 68492     CATGAAG  C
           CA                     TGG      GT TACAACTCCAC
                                |||       || ||||||||||||
                                ACC      CA ATGTTGAGGTG
                                  AAGGGAA  A
GAM701  LOC92340  3'  GAGCTGAGTGAACTTCATGCCA 69562         G  TA_  A
                                TGGCATGAAG TC   CA CTC
                                ||||||||||  ||   || |||
                                ACCGTACTTC AG   GT GAG
                                     A  TGA  C
GAM702  CYLN2     3'  ATGCAGCCCATCGGGGA     14088          CCCA
                                TCCCCGATGG    CTGCGT
                                ||||||||||    ||||||
                                AGGGGCTACC    GACGTA
                                     C___
GAM702  GADD45B   3'  CACGAGGACCATCGGGGG    32246         C  ACTG
                                TCCCCGATGG CC    CGTG
                                ||||||||||  ||    ||||
                                GGGGGCTACC GG    GCAC
                                     A  A___
GAM702  ITGA3     3'  CACGCAGTGCGGATCCGGGA   11028      C   GG  _
                                TCCC GAT  CC CACTGCGTG
                                |||| |||  || |||||||||
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                                AGGG CTA  GG GTGACGCAC
                                  C   __  C
GAM702  LEP      3'  TCACACAGTGGGTGGTGG    5869     G  G       C
                                CC AT GCCCACTG GTGA
                                || || |||||||| ||||
                                GG TG TGGGTGAC CACT
                                 _ G       A
GAM702  LOXL2    5'  ACTGCGTGATCCAGCCATCGGA 11350    C       C________   TGC
             GA                   TC CCGATGGC       CAC   GT
                                || ||||||||       |||   ||
                                AG GGCTACCG       GTG   CA
                                 A       ACCT___A   CGT
GAM702  SFRS7    3'  TCACGCAGCAGGAGCAGGGGA  60151      GATGG  CA
                                TCCCC    CC  CTGCGTGA
                                |||||    ||  ||||||||
                                AGGGG    GG  GACGCACT
                                   ACGA_  AC
GAM702  SIRT7    3'  ACTGCGTGACCTGGCCATCGAG 33735     C       ________   TGC
             GA                   TCC CGATGGCC      CAC   GT
                                ||| ||||||||      |||   ||
                                AGG GCTACCGG      GTG   CA
                                  A       TCC___A   CGT
GAM702  TBL1X    3'  ACTGCGTGACCCAGCCATCGGG 20128          C________   TGC
             GA                   TCCCCGATGGC       CAC   GT
                                ||||||||||       |||   ||
                                AGGGGCTACCG       GTG   CA
                                      ACCC___A   CGT
GAM702  CTRP5    5'  CGAAGGAGGCCATCGGGGA   32230          CA  G
                                TCCCCGATGGCC  CT CG
                                ||||||||||||  || ||
                                AGGGGCTACCGG  GA GC
                                       AG  A
GAM702  CXYorf1  5'  GGTGCAGGCCATTGGAGA    82918    C       __
                                TC CCGATGGCC  CACT
                                || |||||||||  ||||
                                AG GGTTACCGG  GTGG
                                 A        AC
GAM702  DKFZP434J1813 5'  CGCGGCTGGGCCGTCGGAGA   62437    C         _
                                TC CCGATGGCCCA CTGCG
                                || ||||||||||| |||||
                                AG GGCTGCCGGGT GGCGC
                                 A         C
GAM702  DKFZP727M111 5'  ACTGCGTGACCAGGACCATCGG 32051         _ ________   TGC
             G                    CCCGATGG CC       CAC   GT
                                |||||||| ||      |||   ||
                                GGGCTACC GG       GTG   CA
                                    A  ACC___A   CGT
GAM702  FLJ11506 3'  TGTATGGGCCATGGAGA     45437    C  G       C
                                TC CC ATGGCCCA TGCG
                                || || |||||||| ||||
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                                AG GG TACCGGGT ATGT
                                 A  _      _
GAM702  FLJ20552  3'  CACGTCGGCCGTCGGG     35826         CACT
                                CCCGATGGCC   GCGTG
                                ||||||||||   |||||
                                GGGCTGCCGG   TGCAC
                                     C___
GAM702  FLJ22160  3'  CACGAGGGCATCAGGGA    45030     C   G  ACTG
                                TCCC GATG CCC   CGTG
                                |||| |||| |||   ||||
                                AGGG CTAC GGG   GCAC
                                  A   _  A___
GAM702  FLJ22169  5'  CATGTATGCTCATCGGGGA   44230        _ CCAC
                                TCCCCGATG GC   TGCGTG
                                ||||||||| ||   ||||||
                                AGGGGCTAC CG   ATGTAC
                                     T  T___
GAM702  FLJ23598  3'  CACACAAGCACTTCATCGGGGG 45863        CCCAC_ C
                                TCCCCGATGG     TG GTG
                                ||||||||||     || |||
                                GGGGGCTACT     AC CAC
                                     TCACGA  A
GAM702  FOXP1     3'  CACGCAGCAGTATTGGGGG   52043        G CCA
                                TCCCCGATG C  CTGCGTG
                                ||||||||| |  |||||||
                                GGGGGTTAT G  GACGCAC
                                     _ AC_
GAM702  HSBP1     5'  CAAGCTGGGCATCGGGGA    9519         G   CT  G
                                TCCCCGATG CCCA  GC TG
                                ||||||||| ||||  || ||
                                AGGGGCTAC GGGT  CG AC
                                     _   __  A
GAM702  HSH2      3'  TCAGAGCAAGGCCCTCAGGGA  52743     C  T   CAC   G_
                                TCCC GA GGCC   TGC  TGA
                                |||| || ||||   |||  |||
                                AGGG CT CCGG   ACG  ACT
                                  A  C   A__   AG
GAM702  KIAA1904  3'  CGGGGCAAGCCGTCGGGGA   73865         CCA  G
                                TCCCCGATGGC   CT CG
                                ||||||||||   || ||
                                AGGGGCTGCCG   GG GC
                                     AAC  G
GAM702  SIAT4A    5'  CACACAGCCGTGTCTGGGA   13134     C  __  CCAC  C
                                TCCC GAT  GGC   TG GTG
                                |||| |||  |||   || |||
                                AGGG CTG  CCG   AC CAC
                                  T  TG  _____  A
GAM702  STC2      3'  CACACAGTGGGTGCTGGG    14933     ATG      C
                                CCCG   GCCCACTG GTG
                                ||||   |||||||| |||
```

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                                GGGT   TGGGTGAC CAC
                                  CG_       A
GAM702  ZDHHC3    3'  ACTGCGTGATATTGACCATCGG 33927          CC_________  TGC
            GGA                    TCCCCGATGG        CAC   GT
                                   ||||||||||        |||   ||
                                   AGGGGCTACC        GTG   CA
                                        AGTTAT___A   CGT
GAM702  LOC128916 5'  CACACAGTGGTGGGGA      76297       ATGGC     C
                                   TCCCCG    CCACTG GTG
                                   ||||||    |||||| |||
                                   AGGGGT    GGTGAC CAC
                                      _____     A
GAM702  LOC149111 3'  TCACGCAGCAGCTGGGA     79932      CGAT   CCA
                                   TCCC    GGC   CTGCGTGA
                                   ||||    |||   ||||||||
                                   AGGG    TCG   GACGCACT
                                     _____  AC_
GAM702  LOC149837 5'  CAGAGGGGCCATCAGGGA    85890      C       A_
                                   TCCC GATGGCCC  CTG
                                   |||| ||||||||  |||
                                   AGGG CTACCGGG  GAC
                                     A       GA
GAM702  LOC152313 5'  CACACTGGGCCATGAGGGA   86845      CG       CTGC
                                   TCCC  ATGGCCCA    GTG
                                   ||||  ||||||||    |||
                                   AGGG  TACCGGGT    CAC
                                     AG       CA__
GAM702  LOC166983 5'  TGGAGCAGGCCATCGGGGA   88619           CA  G
                                   TCCCCGATGGCC  CT CG
                                   ||||||||||||  || ||
                                   AGGGGCTACCGG  GA GT
                                          AC  G
GAM702  LOC196500 3'  ACTGCGTGATCAAGGCCATCGG 89080          _________  TGC
            G                       CCCGATGGCC       CAC   GT
                                    ||||||||||       |||   ||
                                    GGGCTACCGG       GTG   CA
                                         AACT___A    CGT
GAM702  LOC199958 3'  TCACGTAGGGAGCCCCAGG   91493    GAT   _  A
                                   CC   GGC CC CTGCGTGA
                                   ||   ||| || ||||||||
                                   GG   CCG GG GATGCACT
                                    ACC   A  _
GAM702  LOC200093 5'  GGTGCAGGCCATTGGAGA    63775    C        __
                                   TC CCGATGGCC  CACT
                                   || |||||||||  ||||
                                   AG GGTTACCGG  GTGG
                                    A        AC
GAM702  LOC90342  5'  CACGCAGTGGACAGTAAGGG   63009     GA__  GC
                                   CCC    TG  CCACTGCGTG
                                   |||    ||  ||||||||||
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                                GGG   AC  GGTGACGCAC
                                  AATG  A_
GAM702  LOC91040  5'  GGTGCAGGCCATTGGAGA    65349    C       __
                                TC CCGATGGCC  CACT
                                || |||||||||  ||||
                                AG GGTTACCGG  GTGG
                                  A        AC
GAM702  LOC91828  5'  CGGGGTGGGCCTTCGGGGA   67858       T      G
                                TCCCCGA GGCCCACT CG
                                ||||||| |||||||| ||
                                AGGGGCT CCGGGTGG GC
                                    T       G
GAM703  ABCB8     3'  CCGGCTGCCTCCCTCCCA    24203        _
                                TGGGAGGG GGCAGCTGG
                                |||||||| |||||||||
                                ACCCTCCC CCGTCGGCC
                                     T
GAM703  ABP1      3'  CAGCCCCCAGTTCCTCCCCCA  63797     A    C   __
                                TGGG GGGGG AGCT  GGGCTG
                                |||| ||||| ||||  ||||||
                                ACCC CCTCC TTGA  CCCGAC
                                  _    _   CC
GAM703  ACTN1     5'  CAGCCCAGCCCAGCCCA     8468      AGG   AGC
                                TGGG   GGGC   TGGGCTG
                                ||||   ||||   |||||||
                                ACCC   CCCG   ACCCGAC
                                  GA_   ____
GAM703  ACTN1     5'  CAGCCCAGCCCTACTCCCTCCC 8469         CA__
                                GGGAGGGGG    GCTGGGCTG
                                |||||||||    |||||||||
                                CCCTCCCTC    CGACCCGAC
                                     ATCC
GAM703  ADRBK1    3'  TCAGGGGCTGCCCGCTCCCA  9669       G      GGG
                                TGGGAG GGGCAGCT   CTGA
                                |||||| ||||||||   ||||
                                ACCCTC CCCGTCGG   GACT
                                   G       G__
GAM703  ALDOA     3'  CAGGCCCTGCCCCCTCCCA   5263          CT  G
                                TGGGAGGGGGGCAG  GG CTG
                                ||||||||||||  || |||
                                ACCCTCCCCCGTC  CC GAC
                                       __  G
GAM703  AMH       3'  CAGCTCGCGCCCCTTCCCA   6651          A  T
                                TGGGAGGGGGC GC GGGCTG
                                |||||||||| || ||||||
                                ACCCTTCCCCG CG CTCGAC
                                       _ _
GAM703  AR        5'  CACCCCGCCTCCCCCCA     5271      A     AGCT   C
                                TGGG GGGGGC    GGG TG
                                |||| ||||||    ||| ||
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                                ACCC CCTCCG    CCC AC
                                  C     _____  C
GAM703  AR      5'  TCAGCCAACCCCCCTCACCA  5277     _      CAGCTG
                                TGG GAGGGGG     GGCTGA
                                ||| |||||||     ||||||
                                ACC CTCCCCC     CCGACT
                                  A      CAA___
GAM703  ARF1    3'  CAGCCCAGCTGTTCCCCT    71195    A
                                GG GGGGGCAGCTGGGCTG
                                || ||||||||||||||||
                                TC CCCTTGTCGACCCGAC
                                 _
GAM703  ARHG    3'  CAACCCAGTGCCCCCTCCCA  9791           G    C
                                TGGGAGGGGGCA CTGGG TG
                                |||||||||||| ||||| ||
                                ACCCTCCCCCGT GACCC AC
                                      _    A
GAM703  ARHGDIA 3'  CAGCCCCTCCCCTCCC     16293        CAGCT
                                GGGAGGGGG    GGGCTG
                                |||||||||    ||||||
                                CCCTCCCCT    CCCGAC
                                     C____
GAM703  ARHGDIA 3'  CAGCCCTCCCCCACCCA     16294     A    CAGCT
                                TGGG GGGGG    GGGCTG
                                |||| |||||    ||||||
                                ACCC CCCCC    CCCGAC
                                  A    T____
GAM703  ASGR2   5'  CAGCCCAGCCCAGCCCA     8629      AGG   AGC
                                TGGG  GGGC  TGGGCTG
                                ||||  ||||  |||||||
                                ACCC  CCCG  ACCCGAC
                                  GA_   ___
GAM703  ASGR2   5'  CAGCCCAGCCCAGCTCC     8630      GG  CA
                                GGAG  GG  GCTGGGCTG
                                ||||  ||  |||||||||
                                CCTC  CC  CGACCCGAC
                                  GA  __
GAM703  ASGR2   5'  CAGCCCAGCTCCAGCTCC    8631      GG  C
                                GGAG  GG AGCTGGGCTG
                                ||||  || ||||||||||
                                CCTC  CC TCGACCCGAC
                                  GA  _
GAM703  ASGR2   5'  CAGCCCAGCCCAGCCCA     56029     AGG   AGC
                                TGGG  GGGC  TGGGCTG
                                ||||  ||||  |||||||
                                ACCC  CCCG  ACCCGAC
                                  GA_   ___
GAM703  ASGR2   5'  CAGCCCAGCCCAGCTCC     56030     GG  CA
                                GGAG  GG  GCTGGGCTG
                                ||||  ||  |||||||||
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                                CCTC  CC  CGACCCGAC
                                  GA  __
GAM703  ASGR2   5' CAGCCCAGCTCCAGCTCC   56031    GG  C
                                GGAG  GG AGCTGGGCTG
                                ||||  || ||||||||||
                                CCTC  CC TCGACCCGAC
                                  GA  _
GAM703  ASGR2   5' CAGCCCAGCCCAGCCCA    56034    AGG   AGC
                                TGGG  GGGC  TGGGCTG
                                ||||  ||||  |||||||
                                ACCC  CCCG  ACCCGAC
                                  GA_  ____
GAM703  ASGR2   5' CAGCCCAGCCCAGCTCC    56035    GG  CA
                                GGAG  GG  GCTGGGCTG
                                ||||  ||  |||||||||
                                CCTC  CC  CGACCCGAC
                                  GA  __
GAM703  ASGR2   5' CAGCCCAGCTCCAGCTCC   56036    GG  C
                                GGAG  GG AGCTGGGCTG
                                ||||  || ||||||||||
                                CCTC  CC TCGACCCGAC
                                  GA  _
GAM703  ASGR2   5' CAGCCCAGCCCAGCCCA    56039    AGG   AGC
                                TGGG  GGGC  TGGGCTG
                                ||||  ||||  |||||||
                                ACCC  CCCG  ACCCGAC
                                  GA_  ____
GAM703  ASGR2   5' CAGCCCAGCCCAGCTCC    56040    GG  CA
                                GGAG  GG  GCTGGGCTG
                                ||||  ||  |||||||||
                                CCTC  CC  CGACCCGAC
                                  GA  __
GAM703  ASGR2   5' CAGCCCAGCTCCAGCTCC   56043    GG  C
                                GGAG  GG AGCTGGGCTG
                                ||||  || ||||||||||
                                CCTC  CC TCGACCCGAC
                                  GA  _
GAM703  BACE    5' CATGCCCGCCCCTCCCA    58080       GCAGC   _
                                TGGGAGGGG   TGGGC TG
                                |||||||||   ||||| ||
                                ACCCTCCCC   GCCCG AC
                                    _____   T
GAM703  BACE    5' CATGCCCGCCCCTCCCA    25028       GCAGC   _
                                TGGGAGGGG   TGGGC TG
                                |||||||||   ||||| ||
                                ACCCTCCCC   GCCCG AC
                                    _____   T
GAM703  C18orf2 3' CATCCCGCCCACCCCCCA   49460    A  _   AGCT  C
                                TGGG GG GGGC   GGG TG
                                |||| || ||||   ||| ||
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                                ACCC CC CCCG   CCC AC
                                  C A   ____  T
GAM703  CACNB1   3' CAGCAACCCTGCCCCTCCCCA 7405     AG     CTGG
                                TGGG GGGGCAG   GCTG
                                |||| |||||||   ||||
                                ACCC CCCCGTC   CGAC
                                  CT     CCAA
GAM703  CACNG3   5' CCAGCCGGCCCCCGCCCCA  22564    A_    A_
                                TGGG GGGGGC GCTGG
                                |||| |||||| |||||
                                ACCC CCCCCG CGACC
                                  CG    GC
GAM703  CAMLG    5' CCACTGCCACCCCTCCCA   9996       __   C
                                TGGGAGGGG GCAG TGG
                                ||||||||| |||| |||
                                ACCCTCCCC CGTC ACC
                                     AC  _
GAM703  CAV1     5' CAGCCACCGCCCCCCTCC   10022      CA TG_
                                GGAGGGGG GC  GGCTG
                                |||||||| ||  |||||
                                CCTCCCCC CG  CCGAC
                                    __ CCA
GAM703  CBFA2T3  3' TCAGACGTGCTCCCTCCCA  19019        GC GG
                                TGGGAGGGGGCA TG CTGA
                                |||||||||||| ||  ||||
                                ACCCTCCCTCGT GC GACT
                                     __ A_
GAM703  CD74     3' TCAGCCCCCAGCCCCTCCCC  16381    AG   AGCT
                                GGG GGGGC   GGGCTGA
                                ||| |||||   |||||||
                                CCC CCCCG   CCCGACT
                                 CT   ACC_
GAM703  CKM      5' CAGCCCAGCCAGGTCTCCT   10198      A__
                                AGGGGGC  GCTGGGCTG
                                |||||||  |||||||||
                                TCCTCTG  CGACCCGAC
                                   GAC
GAM703  CNP      3' CAGCCCAGCTGCTCTGCCCA  53616    AG
                                TGGG GGGGCAGCTGGGCTG
                                |||| ||||||||||||||
                                ACCC TCTCGTCGACCCGAC
                                  G_
GAM703  COL1A1   3' CAACCTGGCTCCCTCCCA   5391       GGC  TG C
                                TGGGAGGG  AGC  GG TG
                                ||||||||  |||  || ||
                                ACCCTCCC  TCG  CC AC
                                    ___  GT  A
GAM703  EGFL4    5' TCAGACCTGCCCCCTCCCA  62474         CTGGG
                                TGGGAGGGGGCAG   CTGA
                                ||||||||||||    ||||
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                                ACCCTCCCCCGTC    GACT
                                      CA___
GAM703  EPHA8   3'  CAGCCCTGCCCCCCCTCCC   40429        CA  T
                                GGGAGGGGG  GC GGGCTG
                                |||||||||  || ||||||
                                CCCTCCCCC  CG CCCGAC
                                     C_  T
GAM703  EVX1    5'  CAGCAGCTCCGCGCCCTCCCA  10545       G __   GG
                                TGGGAGGG GC  AGCT  GCTG
                                |||||||| ||  ||||  ||||
                                ACCCTCCC CG  TCGA  CGAC
                                    G  CC   __
GAM703  F3      5'  CAGCCCAACCTCCCCA     67675     A   GCAGC
                                TGGG GGGG    TGGGCTG
                                |||| ||||    |||||||
                                ACCC CTCC    ACCCGAC
                                  _   A____
GAM703  FGFR1   3'  CAGCCACTTCATCCCCTCCCA  43884        CAGCTG
                                TGGGAGGGGG    GGCTG
                                ||||||||||    |||||
                                ACCCTCCCCT    CCGAC
                                      ACTTCA
GAM703  FGFR1   3'  CAGCCACTTCATCCCCTCCCA  32371        CAGCTG
                                TGGGAGGGGG    GGCTG
                                ||||||||||    |||||
                                ACCCTCCCCT    CCGAC
                                      ACTTCA
GAM703  FGFR1   3'  CAGCCACTTCATCCCCTCCCA  7017         CAGCTG
                                TGGGAGGGGG    GGCTG
                                ||||||||||    |||||
                                ACCCTCCCCT    CCGAC
                                      ACTTCA
GAM703  FOSB    3'  AGACCCTGCCCCCTGCCA   23054    G      GCT  _
                                TGG AGGGGGCA  GGG CT
                                ||| ||||||||  ||| ||
                                ACC TCCCCCGT  CCC GA
                                  G       ___  A
GAM703  FOSB    3'  TCTAGCCACTCCCTCCCA   23058        CA
                                TGGGAGGGGG  GCTGGG
                                ||||||||||  ||||||
                                ACCCTCCCTC  CGATCT
                                      AC
GAM703  FOXD2   5'  TCAGTCCCCCGCCCCCTCCC  16793        AGCT
                                GGGAGGGGGC   GGGCTGA
                                ||||||||||   |||||||
                                CCCTCCCCCG   CCTGACT
                                      CCC_
GAM703  FOXG1B  3'  AGCCCCCCCCCTCCCA      19132         CAGCT
                                TGGGAGGGGG    GGGCT
                                ||||||||||    |||||
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                                ACCCTCCCCC    CCCGA
                                      _____
GAM703  GPRK6   3' CAGCCCTGGCCCTTCCCA    10865        G  GCT
                                TGGGAGGGG CA   GGGCTG
                                ||||||||| ||   ||||||
                                ACCCTTCCC GT   CCCGAC
                                     G ___
GAM703  GRLF1   3' TCAGCTGCGCCCCCCTCCCA  79262        CA  TG
                                TGGGAGGGGG  GC  GGCTGA
                                |||||||||  ||  ||||||
                                ACCCTCCCCC  CG  TCGACT
                                     CG __
GAM703  HCFC1   3' GGCCCACCCCTCCCA      71549        GCAGC
                                TGGGAGGGG    TGGGCT
                                |||||||||    ||||||
                                ACCCTCCCC    ACCCGG
                                      _____
GAM703  HEPH    5' CAGCCCTTCCCCCTCCC     29648        CAGCT
                                GGGAGGGGG    GGGCTG
                                |||||||||    ||||||
                                CCCTCCCCC    CCCGAC
                                     TT___
GAM703  HOXC6   3' TCAGCTCTGGACCCCCTCCC  16911        CAGCT
                                GGGAGGGGG    GGGCTGA
                                |||||||||    |||||||
                                CCCTCCCCC    CTCGACT
                                     AGGT_
GAM703  HR      5' CAGCTCTGGCACTGCCCCCTCC 18914          __  TG _
           CA                     TGGGAGGGGGCA  GC  G GCTG
                                ||||||||||||  ||  | ||||
                                ACCCTCCCCCGT  CG  C CGAC
                                      CA  GT T
GAM703  IMMP2L  5' CCAACAACGCGCCCTCTCCCA  51705          A  _____
                                TGGGAGGGGGC GC    TGG
                                |||||||||| ||    |||
                                ACCCTCTCCCG CG    ACC
                                     _  CAACA
GAM703  IMPDH1  3' CAGCCTGGCCCCCACCCCA  7950      AG   CA  TG
                                TGGG  GGGG  GC  GGCTG
                                ||||  ||||  ||  |||||
                                ACCC  CCCC  CG  CCGAC
                                  CA   __  GT
GAM703  INHBC   3' CCTGGCTACCCCCTTCCA    19859        C   TG
                                TGGGAGGGGG AGC  GG
                                |||||||||| |||  ||
                                ACCTTCCCCC TCG  CC
                                     A   GT
GAM703  ITGA3   3' CAGCCCCAGCCCCTTCC     19732        AGCT
                                GGAGGGGGC   GGGCTG
                                |||||||||   ||||||
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                                CCTTCCCCG   CCCGAC
                                     AC__
GAM703  ITGA3   3'  CAGCCCCAGCCCCTTCC     11030         AGCT
                                GGAGGGGGC   GGGCTG
                                |||||||||   ||||||
                                CCTTCCCCG   CCCGAC
                                     AC__
GAM703  KRT2A   3'  CAACCCAGACTCTCCCA     6461         GGCAG    C
                                TGGGAGGG    CTGGG TG
                                ||||||||    ||||| ||
                                ACCCTCTC    GACCC AC
                                     A____    A
GAM703  LTK     3'  CAGCCCAGGCCTCCCA      11375        GGGCAG
                                TGGGAGG     CTGGGCTG
                                |||||||     ||||||||
                                ACCCTCC     GACCCGAC
                                    G_____
GAM703  MAFF    3'  CCACACTGCCCCTCCCCA    25577      AG      C _
                                TGGG  GGGGCAG TG GG
                                ||||  ||||||| || ||
                                ACCC  CCCCGTC AC CC
                                  CT      _ A
GAM703  MSI1    3'  CCTAGGACCGCCCCCTCCC    11698          AG__
                                GGGAGGGGGC   CTGGG
                                ||||||||||   |||||
                                CCCTCCCCCG   GATCC
                                     CCAG
GAM703  MYL1    5'  TCAACCCAACCACCATCCTCTT 55323          CAGC___    C
            CCA                   TGGGAGGGGG      TGGG TGA
                                ||||||||||      |||| |||
                                ACCTTCTCCT      ACCC ACT
                                     ACCACCA    A
GAM703  NFIA    5'  CCGCAGCCGCCCCCTCCC     70884          A   _
                                GGGAGGGGGC GCTG GG
                                |||||||||| |||| ||
                                CCCTCCCCCG CGAC CC
                                     C   G
GAM703  NFIX    3'  CAGCCCAGCCCAGCCCA     11781      AGG   AGC
                                TGGG   GGGC   TGGGCTG
                                ||||   ||||   |||||||
                                ACCC   CCCG   ACCCGAC
                                  GA_   ___
GAM703  NGFR    3'  CAGCCCAGGGTTCCCCC     11789    A     AG
                                GG GGGGGC  CTGGGCTG
                                || ||||||  ||||||||
                                CC CCCTTG  GACCCGAC
                                 _     G_
GAM703  NTF5    5'  CAGGTGGTTGCCCCCTCCC    21630           GGG
                                GGGAGGGGGCAGCT   CTG
                                ||||||||||||||   |||
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                                CCCTCCCCCGTTGG  GAC
                                      TG_
GAM703  NTSR1    3'  GGACCCCCCCCTCCCA     11862        CAGCT  _
                                TGGGAGGGGG    GGG CT
                                ||||||||||    ||| ||
                                ACCCTCCCCC    CCC GG
                                      _____  A
GAM703  PACSIN1  3'  CAGCCCAGCCCTGTTTCCCCTC 93877      __  __
                                GAGGGG  GCA  GCTGGGCTG
                                ||||||  |||  |||||||||
                                CTCCCC  TGT  CGACCCGAC
                                   TT   CC
GAM703  PCDH11X  5'  TCAACCCCTCTCCTCTCCCA  28016       C  CT  C
                                TGGGAGGGGG AG  GGG TGA
                                |||||||||| ||  ||| |||
                                ACCCTCTCCT TC  CCC ACT
                                      C  __  A
GAM703  PCDH11X  5'  TCAACCCCTCTCCTCTCCCA  53137       C  CT  C
                                TGGGAGGGGG AG  GGG TGA
                                |||||||||| ||  ||| |||
                                ACCCTCTCCT TC  CCC ACT
                                      C  __  A
GAM703  PCDH11X  5'  TCAACCCCTCTCCTCTCCCA  53144       C  CT  C
                                TGGGAGGGGG AG  GGG TGA
                                |||||||||| ||  ||| |||
                                ACCCTCTCCT TC  CCC ACT
                                      C  __  A
GAM703  PCDH11Y  5'  TCAACCCCTCTCCTCTCCCA  53185       C  CT  C
                                TGGGAGGGGG AG  GGG TGA
                                |||||||||| ||  ||| |||
                                ACCCTCTCCT TC  CCC ACT
                                      C  __  A
GAM703  PCDH11Y  5'  TCAACCCCTCTCCTCTCCCA  53189       C  CT  C
                                TGGGAGGGGG AG  GGG TGA
                                |||||||||| ||  ||| |||
                                ACCCTCTCCT TC  CCC ACT
                                      C  __  A
GAM703  PCTK3    3'  CAGCCAGCCCCCGCCCA    73324     A    AGCTG
                                TGGG GGGGGC    GGCTG
                                |||| ||||||    |||||
                                ACCC CCCCCG    CCGAC
                                  G     A____
GAM703  PIK3R2   5'  CAACCCAGCGGACCCTCCCA  18509       GGCA    C
                                TGGGAGGG   GCTGGG TG
                                ||||||||   |||||| ||
                                ACCCTCCC   CGACCC AC
                                     AGG_     A
GAM703  PIK4CB   3'  CCAGCTCTACCCCTCCCA    12129       GC_
                                TGGGAGGGG  AGCTGG
                                |||||||||  ||||||
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                                ACCCTCCCC  TCGACC
                                     ATC
GAM703  PIK4CB   3'  CCAGGGACCTACCCCTCCCA  12130       GC ____
                                TGGGAGGGG AG   CTGG
                                ||||||||| ||   ||||
                                ACCCTCCCC TC   GACC
                                     A_ CAGG
GAM703  PK428    5'  TCAGGGACCTCGCCCCCTCCC 14603       AGCT G__
                                GGGAGGGGGC  GG  CTGA
                                |||||||||   ||  ||||
                                CCCTCCCCCG  CC  GACT
                                     CT__ AGG
GAM703  PKP2     3'  CAGCCCAGCCTTGCCCACC   17106   _   __
                                GG GGGCA  GCTGGGCTG
                                || |||||  |||||||||
                                CC CCCGT  CGACCCGAC
                                 A    TC
GAM703  PLA2G4C  5'  CAGCCCGCGACCTCCTCCCA  73806       CA  T
                                TGGGAGGGGG  GC GGGCTG
                                ||||||||||  || ||||||
                                ACCCTCCTCC  CG CCCGAC
                                     AG  _
GAM703  PNUTL1   3'  TCAGCACCACCCCCTCCCA   12193       CAGC  _
                                TGGGAGGGGG   TGG GCTGA
                                ||||||||||   ||| |||||
                                ACCCTCCCCC   ACC CGACT
                                     _____  A
GAM703  PNUTL2   3'  CCATGCCGGCCCCTCCCA    17114       G A_  _
                                TGGGAGGGG C  GC TGG
                                ||||||||| |  || |||
                                ACCCTCCCC G  CG ACC
                                     _ GC  T
GAM703  PNUTL2   3'  CCATGCCGGCCCCTCCCA    55372       G A_  _
                                TGGGAGGGG C  GC TGG
                                ||||||||| |  || |||
                                ACCCTCCCC G  CG ACC
                                     _ GC  T
GAM703  PNUTL2   3'  CCATGCCGGCCCCTCCCA    55378       G A_  _
                                TGGGAGGGG C  GC TGG
                                ||||||||| |  || |||
                                ACCCTCCCC G  CG ACC
                                     _ GC  T
GAM703  PNUTL2   3'  CCATGCCGGCCCCTCCCA    55379       G A_  _
                                TGGGAGGGG C  GC TGG
                                ||||||||| |  || |||
                                ACCCTCCCC G  CG ACC
                                     _ GC  T
GAM703  POU2F2   3'  CAGCCATGCCTCCCCTCCCA  12212       CA  TG
                                TGGGAGGGGG  GC  GGCTG
                                ||||||||||  ||  |||||
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                                ACCCTCCCCT  CG  CCGAC
                                      C_  TA
GAM703  PPGB    3'  CCAGGACTGCCCCCTTCCCA  6125      _     __
                                TGGGA GGGGGGCAG  CTGG
                                ||||| ||||||||  ||||
                                ACCCT CCCCCGTC  GACC
                                   T       AG
GAM703  PPP2R4  3'  CCAGCAGTGGCCCCTCCC    61179       G __
                                GGGAGGGG CA  GCTGG
                                |||||||| ||  |||||
                                CCCTCCCC GT  CGACC
                                     G  GA
GAM703  PRCC    3'  CAGCCCAGCTGGCCTGGCCC  21063    AG  G
                                GGG  GGG CAGCTGGGCTG
                                |||  ||| ||||||||||
                                CCC  TCC GTCGACCCGAC
                                  GG  G
GAM703  PTPRN   3'  CAGCCTCCTCCCACCACCCTCC 12624       _ CAGCT__
            CA                    TGGGAGGG GG      GGGCTG
                                ||||||| ||      ||||||
                                ACCCTCCC CC      TCCGAC
                                     A  ACCCTCC
GAM703  RANBP3  3'  CAGCCCTCTGCCCCTGCCCA  14631    A      CT
                                TGGG GGGGGCAG  GGGCTG
                                |||| ||||||||  ||||||
                                ACCC TCCCCGTC  CCCGAC
                                  G       T_
GAM703  RANBP3  3'  CAGCCCTCTGCCCCTGCCCA  24639    A      CT
                                TGGG GGGGGCAG  GGGCTG
                                |||| ||||||||  ||||||
                                ACCC TCCCCGTC  CCCGAC
                                  G       T_
GAM703  RFX1    3'  CTTGGCCGCCCCCCTCCCA   12849        _ A  TG
                                TGGGAGGGGG C GC  GG
                                |||||||||| | ||  ||
                                ACCCTCCCCC G CG  TC
                                      C C  GT
GAM703  RGR     3'  TCATCCCTCACCCCCTCCCA  12861        CAGCT  C
                                TGGGAGGGGG    GGG TGA
                                ||||||||||    ||| |||
                                ACCCTCCCCC    CCC ACT
                                      ACT__   T
GAM703  RXRA    3'  CCAGCTGGGCCCCTCCCA    12916       G_
                                TGGGAGGGG  CAGCTGG
                                |||||||||  |||||||
                                ACCCTCCCC  GTCGACC
                                      GG
GAM703  RXRB    3'  CAGCTTCCCGCCGCCCCCCCCA 42029     A    A  T  __
                                TGGG GGGGGC GC GG  GCTG
                                |||| |||||| || ||  ||||
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                                ACCC CCCCCG CG CC  CGAC
                                  _     C  C  TT
GAM703  RYR1     5'  CAGCCCGCAGCCCCCTCCC   6771          A  T
                                GGGAGGGGGC GC GGGCTG
                                |||||||||| || ||||||
                                CCCTCCCCCG CG CCCGAC
                                     A  _
GAM703  SLC22A12 3'  AGCCTGCCTCCTCCCA     58681           GCTG
                                TGGGAGGGGGCA   GGCT
                                ||||||||||||   ||||
                                ACCCTCCTCCGT   CCGA
                                      _____
GAM703  SLC7A6   3'  CAGGAATTTGCTGCCCCCCACC 15638    GA       TGGG__
           A                     TGG  GGGGGCAGC     CTG
                                |||  |||||||||     |||
                                ACC  CCCCCGTCG     GAC
                                  AC       TTTAAG
GAM703  SNCB     3'  CAGTGTTGCCTCCTCCCA    13285           TGG
                                TGGGAGGGGGGCAGC   GCTG
                                ||||||||||||||   ||||
                                ACCCTCCTCCGTTG   TGAC
                                      ____
GAM703  SNL      3'  TCTCCCAGCCACCTCCTCCCA  13292          CA     CT
                                TGGGAGGGGGG  GCTGGG  GA
                                ||||||||||  ||||||  ||
                                ACCCTCCTCC  CGACCC  CT
                                     AC     T_
GAM703  SOX12    3'  CAGCAGCCAGCCCCCTCC    23681         A_   GG
                                GGAGGGGGC  GCT  GCTG
                                |||||||||  |||  ||||
                                CCTCCCCCG  CGA  CGAC
                                     AC  __
GAM703  SYNGR1   3'  TCAGCCCAGAAGCCCTTCC   17512         G AG
                                GGAGGGG C  CTGGGCTGA
                                |||||||  |  |||||||||
                                CCTTCCC G  GACCCGACT
                                    _ AA
GAM703  TAGLN    3'  CAGCCCAGCCTGCCCCCT    60376          _
                                AGGGGGCAG CTGGGCTG
                                |||||||||  ||||||||
                                TCCCCCGTC GACCCGAC
                                     C
GAM703  TCF7     3'  CCAGTGTGCACCCCTCCC    13616         _  _
                                GGGAGGGG GCA GCTGG
                                |||||||| ||| |||||
                                CCCTCCCC CGT TGACC
                                     A  G
GAM703  TFEB     3'  CCAGGGGCACCTCCCTCCCA  93750          ___  AG
                                TGGGAGGGG   GC  CTGG
                                |||||||||   ||  ||||
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                                ACCCTCCCT  CG  GACC
                                     CCA  GG
GAM703  THRA     5' CACTCCCTGGCCCCTCCCA  13753        G  CT  GC
                                TGGGAGGGG CAG  GG  TG
                                ||||||||| |||  ||  ||
                                ACCCTCCCC GTC  CC  AC
                                     G  __  TC
GAM703  TMEPAI   3' CCAGCTGCTACCCCCTCCC  39826        ___
                                GGGAGGGG  GCAGCTGG
                                ||||||||  ||||||||
                                CCCTCCCC  CGTCGACC
                                    CAT
GAM703  TNFRSF1B 3' CAGCCTTCCCCCTCCCA    8388         CAGCT
                                TGGGAGGGGG   GGGCTG
                                ||||||||||   ||||||
                                ACCCTCCCCC   TCCGAC
                                     T_____
GAM703  WARS     3' TCAGCCCATGCCCCCTCCCA  67867          GC
                                TGGGAGGGGGCA  TGGGCTGA
                                ||||||||||||  ||||||||
                                ACCCTCCCCCGT  ACCCGACT
                                      __
GAM703  WWP2     3' CCGAGGCCGCCCCTCCCA    61726        G A  G_
                                TGGGAGGGG C GCT  GG
                                ||||||||| | |||  ||
                                ACCCTCCCC G CGG  CC
                                     _ C  AG
GAM703  20D7-FC4 3' TCAGCCCCAACCCCCTCCC   61570        CAGCT
                                GGGAGGGGG   GGGCTGA
                                |||||||||   |||||||
                                CCCTCCCCC   CCCGACT
                                     AAC__
GAM703  AAMP     3' CAGCCCAGGGCCCTCCC    8435    A    AG
                                GG GGGGGC  CTGGGCTG
                                || ||||||  ||||||||
                                CC CTCCCG  GACCCGAC
                                 _    G_
GAM703  ANKRD2   3' CAGCCCAGCCAGCTACCC   72587    _  A_
                                GGG GGC  GCTGGGCTG
                                ||| |||  |||||||||
                                CCC TCG  CGACCCGAC
                                  A  AC
GAM703  Apg4B    3' CCGTGCTGCCTCCCCCCA    26181    A      _
                                TGGG GGGGGCAGC TGG
                                |||| ||||||||| |||
                                ACCC CCTCCGTCG GCC
                                  C       T
GAM703  ARTN     5' CCAGCATCTACCCCCCTCCCA 55112        CA____
                                TGGGAGGGGG    GCTGG
                                ||||||||||    |||||
```

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                                ACCCTCCCCC     CGACC
                                     CATCTA
GAM703  BA108L7.2 3'  CCACTGCACCCCCTCCCA    49068         __   C
                                TGGGAGGGG  GCAG TGG
                                |||||||||  |||| |||
                                ACCCTCCCC  CGTC ACC
                                     CA   _
GAM703  BICD2     3'  CCGTGTTGCCCCCTCCCA    70908          _
                                TGGGAGGGGGCAGC TGG
                                |||||||||||||| |||
                                ACCCTCCCCCGTTG GCC
                                       T
GAM703  C14orf4   3'  CAACCCAACTCGACCCTCCC  67897       GGC  C    C
                                GGGAGGG   AG TGGG TG
                                |||||||   || |||| ||
                                CCCTCCC   TC ACCC AC
                                    AGC  A    A
GAM703  C5orf6    3'  TCAGCCCCACCCCCTCCC    33957         CAGCT
                                GGGAGGGGGG    GGGCTGA
                                |||||||||     |||||||
                                CCCTCCCCC     CCCGACT
                                     AC___
GAM703  CBX6      3'  CCAAAGATGCCCCCTCCCA   27408          GC__
                                TGGGAGGGGGCA   TGG
                                ||||||||||||   |||
                                ACCCTCCCCCGT   ACC
                                       AGAA
GAM703  CNNM2     3'  CAGCCCCTGCTCCTCCTCCCA 34939         C   T_
                                TGGGAGGGGG AGC  GGGCTG
                                |||||||||| |||  ||||||
                                ACCCTCCTCC TCG  CCCGAC
                                      _   TC
GAM703  CSR1      3'  TCAGGCACCACCCCCTCC    33186        CAGC  _ _
                                GGAGGGGG    TGG GC TGA
                                ||||||||    ||| || |||
                                CCTCCCCC    ACC CG ACT
                                     _____  A  G
GAM703  CX46.6    3'  CAGCCCTCCCCTTCCCA     40308          CAGCT
                                TGGGAGGGGG    GGGCTG
                                |||||||||     ||||||
                                ACCCTTCCCC    CCCGAC
                                      T_____
GAM703  DGKZ      3'  CAGCCCCCGCTCCTGCCCCACC 14676      AG      CT____
           CCA                    TGGG  GGGGCAG     GGGCTG
                                ||||  |||||||     ||||||
                                ACCC  CCCCGTC     CCCGAC
                                  CA      CTCGCC
GAM703  DJ37E16.5 3'  CCTTGCAACCCCCCTCCCA    40094          CA  T
                                TGGGAGGGGG  GC GGG
                                ||||||||||  || |||
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                                ACCCTCCCCC  CG TCC
                                      AA  T
GAM703  DKFZP434J193 3'  TCAACCCCAGGCCACCCCCA  71563     A  G   AG    C_
                                TGGG GG GGC  CTGGG  TGA
                                |||| || |||  |||||  |||
                                ACCC CC CCG  GACCC  ACT
                                  _ A   __    CA
GAM703  DKFZP434J193 3'  TCAGCTGAATCCCCTCCCA   71564          __
                                TGGGAGGGGG  CAGCTGG
                                ||||||||||  |||||||
                                ACCCTCCCCT  GTCGACT
                                      AA
GAM703  DKFZP434N1817 3'  CAGCCCAGCCCTGCCTCCC   68719       G  CA
                                GGGAGG GG  GCTGGGCTG
                                ||||||  ||  |||||||||
                                CCCTCC TC  CGACCCGAC
                                   G  C_
GAM703  DKFZp434P2235 3'  CATGCCCAGCCCCTCCCA    51045        GGCA     _
                                TGGGAGGG    GCTGGGC TG
                                ||||||||    ||||||| ||
                                ACCCTCCC    CGACCCG AC
                                     ____       T
GAM703  DKFZp547J036 3'  TCAGCCCAGCCAGGCCCCCTCC 51123          A__
          C                      GGGAGGGGGC   GCTGGGCTGA
                                ||||||||||   ||||||||||
                                CCCTCCCCCG   CGACCCGACT
                                      GAC
GAM703  DKFZp547O146 3'  CAGCCCAGCCCCGCCCTCCC   39965        _  CA
                                GGGAGGG GG  GCTGGGCTG
                                |||||||  ||  |||||||||
                                CCCTCCC CC  CGACCCGAC
                                   G  C_
GAM703  DKFZP586G1122 3'  TCAACCCTGAACCCCTCCCA   61940         GCAGCT   C
                                TGGGAGGGG     GGG TGA
                                |||||||||     ||| |||
                                ACCCTCCCC     CCC ACT
                                     AAGT__   A
GAM703  DKFZP586M1019 3'  CAGCCCTTCGAGCCCCCTCCC  32171          AGCT_
                                GGGAGGGGGC    GGGCTG
                                ||||||||||    ||||||
                                CCCTCCCCCG    CCCGAC
                                      AGCTT
GAM703  DNAJC5    3'  CCAGTCTCCCCCCTCCCA    62133          C  _
                                TGGGAGGGGG AG CTGG
                                |||||||||| || ||||
                                ACCCTCCCCC TC GACC
                                      C  T
GAM703  FBXO2     5'  CCGTAGCCGCCTCCTCCCA   25141           A   _
                                TGGGAGGGGGC GCTG GG
                                |||||||||| |||| ||
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                                ACCCTCCTCCG CGAT CC
                                      C   G
GAM703  FLJ00007  3' CCTTGGGCTGCCCTCCCCCA  71776     A       __
                                TGGG GGGGGGCAGCT  GGG
                                |||| ||||||||||  |||
                                ACCC CTCCCGTCGG  TCC
                                  C        GT
GAM703  FLJ00024  3' TCAGGGGCGCCCCTCCCA   64505       _ AG
                                TGGGAGGGG GC  CTGG
                                ||||||||| ||  ||||
                                ACCCTCCCC CG  GACT
                                     G  GG
GAM703  FLJ10535  3' TCAACCCATTTCCCTCCC   36757       CAGC   C
                                GGGAGGGGG   TGGG TGA
                                |||||||||   |||| |||
                                CCCTCCCTT   ACCC ACT
                                     T___   A
GAM703  FLJ10759  3' CAGCCCAGCCCTGACCTC   37120     __  CA
                                GAGG  GGG  GCTGGGCTG
                                ||||  |||  |||||||||
                                CTCC  TCC  CGACCCGAC
                                  AG  __
GAM703  FLJ12387  3' CCTTATGCACTGCCCCTCCCA 43375       ____  GCT
                                TGGGAGGGG   GCA  GGG
                                |||||||||   |||  |||
                                ACCCTCCCC   CGT  TCC
                                     GTCA  AT_
GAM703  FLJ12650  3' CACTCCACCCCCTTCCA    44818       CAGC  GC
                                TGGGAGGGGG   TGG  TG
                                ||||||||||   |||  ||
                                ACCTTCCCCC   ACC  AC
                                     ____  TC
GAM703  FLJ12681  3' CATCCCACCCTCCTCCCA   43183       CAGC   C
                                TGGGAGGGGG   TGGG TG
                                ||||||||||   |||| ||
                                ACCCTCCTCC   ACCC AC
                                     C___   T
GAM703  FLJ12783  3' CCAGGATTCGCCCTCTCCCA  49484       AG___
                                TGGGAGGGGGC   CTGG
                                ||||||||||    ||||
                                ACCCTCTCCCG   GACC
                                     CTTAG
GAM703  FLJ12788  3' CAACCAGCCCCTCTCCCA   42844       CA   GC
                                TGGGAGGGGG GCTGG  TG
                                |||||||||| |||||  ||
                                ACCCTCTCCC CGACC  AC
                                     __   A_
GAM703  FLJ12875  3' CCTTGTGTTACCCCCTCCCA  44916       CA__ T
                                TGGGAGGGGG   GC GGG
                                ||||||||||   || |||
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                                ACCCTCCCCC   TG TCC
                                     ATTG  T
GAM703  FLJ13153  5' CAGCCCAGCCCCTGCTCCC   45922     G  CA
                                GGGAG GGG  GCTGGGCTG
                                ||||| |||  |||||||||
                                CCCTC TCC  CGACCCGAC
                                   G  C_
GAM703  FLJ14126  3' CAGCCCCCTCTCCTCCCA    46274        CAGCT
                                TGGGAGGGGG    GGGCTG
                                ||||||||||    ||||||
                                ACCCTCCTCT    CCCGAC
                                     CC___
GAM703  FLJ14327  3' CAGCCCTTTCCTCTGCCCCCAC 46676     A      CT____
          CCA                     TGGG GGGGGCAG     GGGCTG
                                |||| ||||||||     ||||||
                                ACCC CCCCCGTC     CCCGAC
                                  A       TCCTTT
GAM703  FLJ14800  3' TCAACCCCTGGCCCCCTCCC   52689        AGCT   C
                                GGGAGGGGGC    GGG TGA
                                ||||||||||    ||| |||
                                CCCTCCCCCG    CCC ACT
                                     GTC_  A
GAM703  FLJ14810  3' CAACCCATCCCCCACCCA    52696     A    CAGC   C
                                TGGG GGGGG    TGGG TG
                                |||| |||||    |||| ||
                                ACCC CCCCC    ACCC AC
                                  A    T___    A
GAM703  FLJ20320  5' CCTACACTGCCTCCTCCCA    35421          C_
                                TGGGAGGGGGGCAG  TGGG
                                ||||||||||||  ||||
                                ACCCTCCTCCGTC  ATCC
                                       AC
GAM703  FLJ20542  3' CACCTCTGCCCTCTCCCA    50743          CT   C
                                TGGGAGGGGGGCAG  GGG TG
                                ||||||||||||  ||| ||
                                ACCCTCTCCCGTC  TCC AC
                                      __  _
GAM703  FLJ20850  3' CAGCCCAGCCCTAACTGCCA   36174    G  GG  CA
                                TGG AG  GG  GCTGGGCTG
                                ||| ||  ||  |||||||||
                                ACC TC  TC  CGACCCGAC
                                  G  AA  C_
GAM703  FLJ23058  5' TCAGCCCAGCTGGGTTCC    45528     GGGG
                                GGAG   CAGCTGGGCTGA
                                ||||   ||||||||||||
                                CCTT   GTCGACCCGACT
                                  GG__
GAM703  FLJ23604  3' CAGCCCATGCACCCCTCCC    47546        _  GC
                                GGGAGGGG GCA  TGGGCTG
                                |||||||| |||  |||||||
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                                CCCTCCCC CGT  ACCCGAC
                                    A  __
GAM703  FLJ32332  3'  CAGCCCGTGGCCCTCCCA    58942       GGCA  T
                                TGGGAGGG   GC GGGCTG
                                ||||||||   || ||||||
                                ACCCTCCC   TG CCCGAC
                                    GG__  _
GAM703  GMEB2     3'  CTGAGCCGGCCCCTCCCA    25661       G A_  G
                                TGGGAGGGG C  GCT GG
                                |||||||||  |  ||| ||
                                ACCCTCCCC G  CGA TC
                                    _ GC   G
GAM703  HA-1      3'  CAGCGGGCGCCTCCTCCCA   66154        A  GG
                                TGGGAGGGGGC GCT  GCTG
                                |||||||||||  |||  ||||
                                ACCCTCCTCCG CGG  CGAC
                                    _  G_
GAM703  HTCD37    3'  CAGCAGAGCACTCCCTCCCA  68297        CA  GG
                                TGGGAGGGGG  GCT  GCTG
                                ||||||||||  |||  ||||
                                ACCCTCCCTC  CGA  CGAC
                                    A_  GA
GAM703  KDELR1    5'  CAGCCCAGCTACCCGTTC    23296    G  C
                                GAG GGG AGCTGGGCTG
                                ||| ||| ||||||||||
                                CTT CCC TCGACCCGAC
                                  G  A
GAM703  KIAA0275  3'  CAGCCCAGCCCTGACCCCT   29323     G  __
                                AGGGG CA  GCTGGGCTG
                                |||||  ||  |||||||||
                                TCCCC GT  CGACCCGAC
                                   A  CC
GAM703  KIAA0285  3'  TCAACCCTCACCCTCCTCCCA 29689        CAGCT  C
                                TGGGAGGGGG    GGG TGA
                                ||||||||||    ||| |||
                                ACCCTCCTCC    CCC ACT
                                    CACT_  A
GAM703  KIAA0321  5'  CAGCCACACCACCCTCTCCCA 63046        CAGCTG
                                TGGGAGGGGG    GGCTG
                                ||||||||||    |||||
                                ACCCTCTCCC    CCGAC
                                    ACCACA
GAM703  KIAA0397  3'  CAGCCCAGCCCTGCCCCC    62342       __
                                GGGGGCA  GCTGGGCTG
                                |||||||  |||||||||
                                CCCCCGT  CGACCCGAC
                                    CC
GAM703  KIAA0542  3'  TCAGCCAGCAGCCCCCTCCC   66668        A   G
                                GGGAGGGGGC GCTGG CTGA
                                |||||||||| ||||| ||||
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                                CCCTCCCCCG CGACC GACT
                                     A    _
GAM703  KIAA0574  3'  TAGCCCGGCCCCCCCCA     69823     A     AGC
                                TGGG GGGGGC  TGGGCTG
                                |||| ||||||  |||||||
                                ACCC CCCCCG  GCCCGAT
                                  _    ____
GAM703  KIAA0792  3'  CAGCCCAGCAGTCCCTCC    28763       G A
                                GGAGGGG C GCTGGGCTG
                                ||||||| | |||||||||
                                CCTCCCT G CGACCCGAC
                                    _ A
GAM703  KIAA1023  3'  CAGCCCAGCCTGTTCTCTCCCA 34675          _
                                TGGGAGGGGGCAG CTGGGCTG
                                |||||||||||| ||||||||
                                ACCCTCTCTTGTC GACCCGAC
                                       C
GAM703  KIAA1029  5'  CCAGCTGACCACCCCTCCCA  24424        __ _
                                TGGGAGGGG  G CAGCTGG
                                |||||||||  | |||||||
                                ACCCTCCCC  C GTCGACC
                                     AC A
GAM703  KIAA1100  3'  TCAGCCTGGTCCCACCCCCA  30443     A _  CA  TG
                                TGGG GG GGG  GC  GGCTGA
                                |||| || |||  ||  ||||||
                                ACCC CC CCC  TG  CCGACT
                                  _ A  __ GT
GAM703  KIAA1130  3'  CACGCCCACCCCCTCCCA    63078         CAGC    _
                                TGGGAGGGGGG   TGGGC TG
                                ||||||||||   ||||| ||
                                ACCCTCCCCC   ACCCG AC
                                     _____    C
GAM703  KIAA1184  3'  CAGCCCAGCCCACTCCC     42923      G   AGC
                                GGGAG GGGC  TGGGCTG
                                ||||| ||||  |||||||
                                CCCTC CCCG  ACCCGAC
                                   A   ___
GAM703  KIAA1317  5'  TCAACCCAACCTCCTCTCA   87214         CAGC   C
                                TGGGAGGGGG   TGGG TGA
                                ||||||||||   |||| |||
                                ACTCTCCTCC   ACCC ACT
                                     A___   A
GAM703  KIAA1388  3'  CAGCCCAACCTTCCCA     95225        GGCAGC
                                TGGGAGGG     TGGGCTG
                                ||||||||     |||||||
                                ACCCTTCC     ACCCGAC
                                     A_____
GAM703  KIAA1514  3'  CAGCCAGCTGCCCCCTTCCA  39325             G
                                TGGGAGGGGGCAGCTGG CTG
                                |||||||||||||||| |||
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                                ACCTTCCCCCGTCGACC GAC
                                                _
GAM703  KIAA1554  3'  CAACCCTGACCTTCCCCCTCCC 96852         C  CT__   C
                A                TGGGAGGGGG AG   GGG TG
                                 |||||||||| ||   ||| ||
                                 ACCCTCCCCC TC   CCC AC
                                       T  CAGT   A
GAM703  KIAA1582  5'  CAACCCAGCTGCCTGGCCT   65984     AGG        C
                                 GGG   GGGCAGCTGGG TG
                                 |||   |||||||||| ||
                                 TCC   TCCGTCGACCC AC
                                   GG_         A
GAM703  KIAA1719  3'  CAGCCCAAGCCCCTCC      68727        G AGC
                                 GGAGGGG C   TGGGCTG
                                 |||||||  |   |||||||
                                 CCTCCCC G   ACCCGAC
                                     _ A__
GAM703  KIAA1762  3'  CAGCAGAGTCCTGCCTCCTCCC 64528           __  GG
                A                TGGGAGGGGGCAG  CT  GCTG
                                 ||||||||||||  ||  ||||
                                 ACCCTCCTCCGTC  GA  CGAC
                                       CT  GA
GAM703  KIAA1831  3'  CCATTGCTCCACGCCCTCCCA  64522        _____    C
                                 TGGGAGGG    GGCAG TGG
                                 ||||||||    ||||| |||
                                 ACCCTCCC    TCGTT ACC
                                     GCACC    _
GAM703  KIAA1862  3'  CAGGCCACCCTCTCCCA     69504         CAGC   G
                                 TGGGAGGGGG    TGG CTG
                                 ||||||||||    ||| |||
                                 ACCCTCTCCC    ACC GAC
                                       ____  G
GAM703  KIAA1879  5'  CCATGCTGGCCACCCCCTCC   73934        ____   _
                                 GGAGGGGG    CAGC TGG
                                 ||||||||    |||| |||
                                 CCTCCCCC    GTCG ACC
                                     ACCG    T
GAM703  KIAA1893  3'  CAGCCCCATCCCCTCTCCCA   73587         CAGCT
                                 TGGGAGGGGG    GGGCTG
                                 ||||||||||    ||||||
                                 ACCCTCTCCC    CCCGAC
                                       CTAC_
GAM703  KIAA1938  3'  CATCCTCCCCCTCCCA      93818         CAGCT   C
                                 TGGGAGGGGG    GGG TG
                                 ||||||||||    ||| ||
                                 ACCCTCCCCC    TCC AC
                                       _____  T
GAM703  KIAA1957  3'  CCGGGACGCCCCCTCCCA    76214          AG  G
                                 TGGGAGGGGGC  CT GG
                                 ||||||||||  || ||
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                                ACCCTCCCCCG  GG CC
                                      CA  G
GAM703  MGC1127  3' CACCCCACACCCCTCCCA    54331        GCAGC   C
                                TGGGAGGGG    TGGG TG
                                |||||||||    |||| ||
                                ACCCTCCCC    ACCC AC
                                     AC___   C
GAM703  MGC13057 5' CAGCAAGCCCCCCTCCCA    51283        CA  GG
                                TGGGAGGGGG  GCT  GCTG
                                ||||||||||  |||  ||||
                                ACCCTCCCCC  CGA  CGAC
                                     __  A_
GAM703  MGC14436 5' TCAGCCGAAAGCCCCCCGCCCA 52930     A   CA  G__
                                TGGG GGGGG  GCT  GGCTGA
                                |||| |||||  |||  ||||||
                                ACCC CCCCC  CGA  CCGACT
                                  G    __  AAG
GAM703  MGC14832 3' CAGCCACCTCATACCCCCTTCC 51339        CAGCTG___
          CA                    TGGGAGGGGG       GGCTG
                                ||||||||||       |||||
                                ACCCTTCCCC       CCGAC
                                     CATACTCCA
GAM703  MGC15416 3' TCAGCCCGACTGCCCTCCTCCC 57347       _    C
          A                     TGGGAGG GGGCAG TGGGCTGA
                                ||||||| |||||| ||||||||
                                ACCCTCC CCCGTC GCCCGACT
                                    T    A
GAM703  MGC15476 3' CCAGCTATGGCCCCCTCTCA  59607         ___
                                TGGGAGGGGGC  AGCTGG
                                ||||||||||  ||||||
                                ACTCTCCCCCG  TCGACC
                                      GTA
GAM703  MGC20235 5' CAGCCCAGCCCAGCCCA    59550     AGG   AGC
                                TGGG  GGGC  TGGGCTG
                                ||||  ||||  |||||||
                                ACCC  CCCG  ACCCGAC
                                  GA_  ___
GAM703  MGC3035  5' CAGCCCCCTCCCCTTCC    44394       C  CT
                                GGAGGGGG AG  GGGCTG
                                |||||||| ||  ||||||
                                CCTTCCCC TC  CCCGAC
                                     _  C_
GAM703  MGC4707  3' TCAGCCCAGCCAGTGGCCCC  44364     G  ___
                                GGGG CA  GCTGGGCTGA
                                |||| ||  ||||||||||
                                CCCC GT  CGACCCGACT
                                  G  GAC
GAM703  MIL1     3' CCAGTGGCACCCCCTCCCA  31725        CA__
                                TGGGAGGGGG  GCTGG
                                |||||||||  |||||
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                                ACCCTCCCCC   TGACC
                                     ACGG
GAM703  MSE55   5' CAGCCCACCTCCCTCCC    23914       CAGC
                                GGGAGGGGG   TGGGCTG
                                |||||||||   |||||||
                                CCCTCCCTC   ACCCGAC
                                     C___
GAM703  NFAT5   5' CAGCCTCCCCCCCTCCCA   57784        CAGCT
                                TGGGAGGGGG   GGGCTG
                                ||||||||||   ||||||
                                ACCCTCCCCC   TCCGAC
                                     CC___
GAM703  NKD1    3' TCAACTCTGCCCCACCCCA   53588    AG     CT  GC
                                TGGG  GGGGCAG  GG  TGA
                                ||||  |||||||  ||  |||
                                ACCC  CCCCGTC  TC  ACT
                                  CA     __  A_
GAM703  NKD1    3' TCAGCCCACACCCTTCCCA   53589       GCAGC
                                TGGGAGGGGG   TGGGCTGA
                                |||||||||    ||||||||
                                ACCCTTCCC    ACCCGACT
                                     AC___
GAM703  OAZ2    5' CCTGCGCCGCCTCCTCCCA   11875         A  _
                                TGGGAGGGGGC GC TGGG
                                |||||||||| || ||||
                                ACCCTCCTCCG CG GTCC
                                      C  C
GAM703  PF1     5' TCAGGAGCGCCCCCTCCC    96834        A  GGG
                                GGGAGGGGGC GCT  CTGA
                                |||||||||| |||  ||||
                                CCCTCCCCCG CGA  GACT
                                     _  G__
GAM703  PIP5K1C  3' TCAGGCTCCCCGCCCCCTCC  71308       AGCT  G
                                GGAGGGGGC   GG CTGA
                                |||||||||   || ||||
                                CCTCCCCCG   TC GACT
                                     CCCC  G
GAM703  PLAGL2   3' CAGCAATGAGCTGTCCCCCTCC 70954        _    GG__
           CA                    TGGGAGGGGG CAGCT   GCTG
                                |||||||||| |||||   ||||
                                ACCCTCCCCC GTCGA   CGAC
                                     T    GTAA
GAM703  PPP1R16B 3' CAGCCCAGCCCATCTCA    62032     GG   AGC
                                TGGGA  GGGC  TGGGCTG
                                |||||  ||||  |||||||
                                ACTCT  CCCG  ACCCGAC
                                  A_   ____
GAM703  PPY2    3' CAGCCCAGCTCTCCCCTCC   41173       C
                                GGAGGGGG AGCTGGGCTG
                                |||||||| ||||||||||
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                                CCTCCCCT TCGACCCGAC
                                     C
GAM703  QKI     5'  CAGCCCAGAGAGACCCCCCG  66042     A  GGCAG
                                TGGG GGG    CTGGGCTG
                                |||| |||    ||||||||
                                GCCC CCC    GACCCGAC
                                  _  AGAGA
GAM703  RPH3A   3'  TCAGCCCACCTCCCTCACCA  30937    _     CAGC
                                TGG GAGGGGG   TGGGCTGA
                                ||| |||||||   ||||||||
                                ACC CTCCCTC   ACCCGACT
                                  A     C___
GAM703  SCAMP-4  3'  CAGCCTCGCCCCCTCCC    55341        AGCT
                                GGGAGGGGGC   GGGCTG
                                ||||||||||   ||||||
                                CCCTCCCCCG   TCCGAC
                                      C___
GAM703  SCGF    5'  CCAGAGGCCACCCCTCCCA   12944        __ AG
                                TGGGAGGGG  GC  CTGG
                                |||||||||  ||  ||||
                                ACCCTCCCC  CG  GACC
                                     AC  GA
GAM703  SEC14L1  3'  CATCCCCTGCCCCCTCCCA   13005         CT  C
                                TGGGAGGGGGCAG  GGG TG
                                ||||||||||||  ||| ||
                                ACCCTCCCCCGTC  CCC AC
                                       __  T
GAM703  SFXN5   3'  AGGCTGCCTGCCCCATCCCA  58645     G     CT  G
                                TGGGA GGGGCAG  GG CT
                                |||||  |||||||  || ||
                                ACCCT CCCCGTC  TC GA
                                   A     CG  G
GAM703  SLC26A10  5'  CCAGATTGCCCCCTCTCA   56840          _
                                TGGGAGGGGGCAG CTGG
                                |||||||||||| ||||
                                ACTCTCCCCCGTT GACC
                                       A
GAM703  SOX17   5'  TCATTCCCCACCCCCTCCC   42631        CAGC  C__
                                GGGAGGGGG   TGGG  TGA
                                |||||||||   ||||  |||
                                CCCTCCCCC   ACCC  ACT
                                     _____  CTT
GAM703  SSH-3   3'  CACCCCCGCCCCCTCCC    35788        AGCT  C
                                GGGAGGGGGC   GGG TG
                                ||||||||||   ||| ||
                                CCCTCCCCCG   CCC AC
                                      C___  C
GAM703  STMN3   3'  CAGCCCCAACACCCTTCCCA  32463       GCAGCT
                                TGGGAGGGG    GGGCTG
                                |||||||||    ||||||
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                                ACCCTTCCC     CCCGAC
                                     ACAAC_
GAM703  TACTILE  3'  TCAGCCCAGACTCCTGCCA   20593    G    GCAG
                                TGG AGGGG   CTGGGCTGA
                                ||| |||||   |||||||||
                                ACC TCCTC   GACCCGACT
                                  G    A___
GAM703  TLN1     3'  CCAAGTGCCTGCCCCTCCCCA  21901     AG     _ ___
                                TGGG  GGGGCAG C   TGG
                                ||||  ||||||| |   |||
                                ACCC  CCCCGTC G   ACC
                                  CT      C TGA
GAM703  TOMM34   3'  CAGCCCAGCTAGCTGATC    23314    GGG  _
                                GA   GGC AGCTGGGCTG
                                ||   ||| ||||||||||
                                CT   TCG TCGACCCGAC
                                 AG_   A
GAM703  VMP1     3'  CAACCCTTCCTCTCCCA     48916         CAGCT   C
                                TGGGAGGGGG    GGG TG
                                ||||||||||    ||| ||
                                ACCCTCTCCT    CCC AC
                                      T_____   A
GAM703  WFDC2    3'  CAGCCCACCTGCCCTCCCC   55779    A      C
                                GGG GGGGGCAG TGGGCTG
                                ||| |||||||| |||||||
                                CCC CTCCCGTC ACCCGAC
                                  _       C
GAM703  WFDC2    3'  CAGCCCACCTGCCCTCCCC   55780    A      C
                                GGG GGGGGCAG TGGGCTG
                                ||| |||||||| |||||||
                                CCC CTCCCGTC ACCCGAC
                                  _       C
GAM703  WFDC2    3'  CAGCCCACCTGCCCTCCCC   55781    A      C
                                GGG GGGGGCAG TGGGCTG
                                ||| |||||||| |||||||
                                CCC CTCCCGTC ACCCGAC
                                  _       C
GAM703  WFDC2    3'  CAGCCCACCTGCCCTCCCC   21450    A      C
                                GGG GGGGGCAG TGGGCTG
                                ||| |||||||| |||||||
                                CCC CTCCCGTC ACCCGAC
                                  _       C
GAM703  YARS     3'  CAGCCCAGCATCTTCCCCCC  14853    A    CA
                                GGG GGGGG  GCTGGGCTG
                                ||| |||||  |||||||||
                                CCC CCTTC  CGACCCGAC
                                  C    TA
GAM703  YKT6     3'  CAGCCCAGCCCCCACCCA    22637     AG    AGC
                                TGGG  GGGGC   TGGGCTG
                                ||||  |||||   |||||||
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                                ACCC  CCCCG   ACCCGAC
                                  A_    ___
GAM703   LOC112476 3'  CCTGGCCGCCTCCTCCCA    59785          A  TG
                                TGGGAGGGGGC GC  GG
                                |||||||||| ||  ||
                                ACCCTCCTCCG CG  CC
                                      C  GT
GAM703   LOC113730 5'  CAGCCCAGACCCTCCCCCA   73499     A    CAG
                                TGGG GGGGG   CTGGGCTG
                                |||| |||||   ||||||||
                                ACCC CCTCC   GACCCGAC
                                  _    CA_
GAM703   LOC115110 5'  CAGCCCAGCCCCGGTTCCTCCC 72173       ____   CA
                                GGGAGG   GGG  GCTGGGCTG
                                ||||||   |||  |||||||||
                                CCCTCC   CCC  CGACCCGAC
                                   TTGG  __
GAM703   LOC116150 3'  TCAGCCCAGCTACTTCCC    57425       GGGC
                                GGGAGG   AGCTGGGCTGA
                                ||||||   ||||||||||
                                CCCTTC   TCGACCCGACT
                                   A___
GAM703   LOC123775 3'  TCATTTCCCACCCACCCCCCA  76143     A  _   CAGC   C__
                                TGGG GG GGG   TGGG  TGA
                                |||| || |||   ||||  |||
                                ACCC CC CCC   ACCC  ACT
                                  C  A  ____   TTT
GAM703   LOC124222 3'  CAGCCCAGAGCCTCCTC     74745        AG
                                GAGGGGGC  CTGGGCTG
                                ||||||||  ||||||||
                                CTCCTCCG  GACCCGAC
                                    A_
GAM703   LOC124930 3'  CACCCCCACCCCTTCCCA     74822         CAGCT   C
                                TGGGAGGGGG    GGG TG
                                ||||||||||    ||| ||
                                ACCCTTCCCC    CCC AC
                                      AC___   C
GAM703   LOC130497 3'  GCGGGGCAGCCCCCTCCCA    75452         A   GG
                                TGGGAGGGGGC GCT  GC
                                |||||||||| |||  ||
                                ACCCTCCCCCG CGG  CG
                                      A   GG
GAM703   LOC134187 5'  CCACTTCTGCCCCCTTCCA    76464          C__
                                TGGGAGGGGGCAG   TGG
                                ||||||||||||   |||
                                ACCTTCCCCCGTC   ACC
                                       TTC
GAM703   LOC138389 5'  CAGCCCAGGCACCCTCC     76728       G  AG
                                GGAGGG GC  CTGGGCTG
                                |||||| ||  ||||||||
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                                CCTCCC CG  GACCCGAC
                                   A  __
GAM703   LOC143677 3'  CACTTGGCGCCCCCTCCCA   83893          A  TG  C
                                TGGGAGGGGGC GC  GG TG
                                |||||||||| ||  || ||
                                ACCCTCCCCCG CG  TC AC
                                      _  GT  _
GAM703   LOC143915 5'  CCATTATCTGCCCCCTCCCA  83904           C___
                                TGGGAGGGGGCAG   TGG
                                ||||||||||||   |||
                                ACCCTCCCCCGTC   ACC
                                     TATT
GAM703   LOC144262 5'  CCAAGTGTAGCCCCTCCCA   77259         __  GC
                                TGGGAGGGG  GCA  TGG
                                |||||||||  |||  |||
                                ACCCTCCCC  TGT  ACC
                                    GA   GA
GAM703   LOC144402 5'  CCAAGGCGCCTCCTCCCA    77323          A  __
                                TGGGAGGGGGC GCT  GG
                                |||||||||| |||  ||
                                ACCCTCCTCCG CGG  CC
                                      _  AA
GAM703   LOC145678 3'  CCAGGGTGACCCCTCCCA    84432         G  G _
                                TGGGAGGGG CA C TGG
                                ||||||||| || | |||
                                ACCCTCCCC GT G ACC
                                    A  G G
GAM703   LOC145757 3'  CAGCCCAGGCACCTCCTCCCA 77919          CAG
                                TGGGAGGGGG  CTGGGCTG
                                ||||||||||  ||||||||
                                ACCCTCCTCC  GACCCGAC
                                    ACG
GAM703   LOC145989 3'  CCCAGCCACCTCCTCCCA    60289         CA
                                TGGGAGGGGG  GCTGGG
                                ||||||||||  ||||||
                                ACCCTCCTCC  CGACCC
                                    AC
GAM703   LOC146562 3'  CAGCCCCCAGGCCCTCTCCCA 58251          AGCT
                                TGGGAGGGGGC   GGGCTG
                                ||||||||||   ||||||
                                ACCCTCTCCCG   CCCGAC
                                    GACC
GAM703   LOC146782 3'  CATGCCCAGCCCCTCCCA    76804        GGCA     _
                                TGGGAGGG   GCTGGGC TG
                                ||||||||   ||||||| ||
                                ACCCTCCC   CGACCCG AC
                                    ____     T
GAM703   LOC147136 5'  CAGCAAGCTGCCCCCTCC    78858          GG
                                GGAGGGGGCAGCT  GCTG
                                ||||||||||||  ||||
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                                CCTCCCCCGTCGA  CGAC
                                      A_
GAM703   LOC147136 3'  CAGCCCAAGCCCCCTC      78859        AGC
                                GAGGGGGC   TGGGCTG
                                ||||||||   |||||||
                                CTCCCCCG   ACCCGAC
                                    A__
GAM703   LOC148181 5'  CAGCCCAGCTCATGCCTCCC   79430       GGGC
                                GGGAGG   AGCTGGGCTG
                                ||||||   ||||||||||
                                CCCTCC   TCGACCCGAC
                                   GTAC
GAM703   LOC148250 5'  TCAGAGCATGCCCCCTCCCA   79495          _   GGG
                                TGGGAGGGGGCA GCT   CTGA
                                ||||||||||| |||   ||||
                                ACCCTCCCCCGT CGA   GACT
                                      A   ___
GAM703   LOC148398 3'  CAGCCCAGCCCAGCCCA     79574     AGG   AGC
                                TGGG   GGGC   TGGGCTG
                                ||||   ||||   |||||||
                                ACCC   CCCG   ACCCGAC
                                  GA_   ___
GAM703   LOC148697 3'  CAACCCAGCTGCCTTACCT    79675     AG         C
                                GGG  GGGGCAGCTGGG TG
                                |||  |||||||||||| ||
                                TCC  TTCCGTCGACCC AC
                                  A_          A
GAM703   LOC149134 5'  TCACATGACTGTCCCCTCCCA  85521           CT GGC
                                TGGGAGGGGGCAG  G   TGA
                                ||||||||||||  |   |||
                                ACCCTCCCCTGTC  T   ACT
                                      AG AC_
GAM703   LOC149448 3'  CAACCCCTCCCTCCCA      85577         CAGCT   C
                                TGGGAGGGGG    GGG TG
                                ||||||||||    ||| ||
                                ACCCTCCCTC    CCC AC
                                     _____  A
GAM703   LOC150368 3'  CCTGACTGCCCCCTCCCA    80514           CT
                                TGGGAGGGGGCAG  GGG
                                ||||||||||||  |||
                                ACCCTCCCCCGTC  TCC
                                      AG
GAM703   LOC150886 3'  TCAGCCCAACACGCTCCCCTCC 86333         _  AGC_
            CA                    TGGGAGGGG GC    TGGGCTGA
                                ||||||||| ||    ||||||||
                                ACCCTCCCC CG    ACCCGACT
                                     T  CACA
GAM703   LOC151470 3'  CCATCTCTACCCCCTCCCA    81055         C  C__
                                TGGGAGGGGG AG   TGG
                                |||||||||| ||   |||
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                                ACCCTCCCCC TC   ACC
                                      A  TCT
GAM703   LOC154222 5'  TCAGCGTCACCTCCTCCCA   87393         CA  TGG
                                TGGGAGGGGG  GC   GCTGA
                                ||||||||||  ||   |||||
                                ACCCTCCTCC  TG   CGACT
                                      AC  ___
GAM703   LOC154990 5'  CAGCCCAGCTCATGCCTCCC   82147       GGGC
                                GGGAGG    AGCTGGGCTG
                                ||||||    ||||||||||
                                CCCTCC    TCGACCCGAC
                                   GTAC
GAM703   LOC155179 3'  CAGCCCAGCCTGTTCTCTCCCA 82223           _
                                TGGGAGGGGGCAG CTGGGCTG
                                |||||||||||| ||||||||
                                ACCCTCTCTTGTC GACCCGAC
                                        C
GAM703   LOC157349 5'  CCAGCGGGCACCACCCTCCCA  82330        _  CA___
                                TGGGAGGG GG     GCTGG
                                |||||||| ||     |||||
                                ACCCTCCC CC     CGACC
                                     A  ACGGG
GAM703   LOC163682 3'  CAGCCCTTCCCACCCCCA     88398      A  _   CAGCT
                                TGGG GG GGG     GGGCTG
                                |||| || |||     ||||||
                                ACCC CC CCC     CCCGAC
                                  _  A   TT___
GAM703   LOC163682 3'  CAGCCTCACCCACCCCCTCC   88399        CAGC  _
                                GGAGGGGG    TG GGCTG
                                ||||||||    || |||||
                                CCTCCCCC    AC CCGAC
                                     ACCC  T
GAM703   LOC170393 3'  CAGCCCCTGCTTGGCCCCTCCC 83733         G  _  T_
           A                     TGGGAGGGG CA GC  GGGCTG
                                 |||||||||  || ||  ||||||
                                 ACCCTCCCC GT CG  CCCGAC
                                       G  T  TC
GAM703   LOC196337 5'  TCAGCCCAGCTATGGCCC     89026      ___
                                GGGC   AGCTGGGCTGA
                                ||||   ||||||||||
                                CCCG   TCGACCCGACT
                                  GTA
GAM703   LOC200301 5'  TCAGAAATGCCCCCTCCCA    90153          GCTGGG
                                TGGGAGGGGGCA     CTGA
                                ||||||||||||     ||||
                                ACCCTCCCCCGT     GACT
                                       AAA___
GAM703   LOC203954 5'  GGCCCCGCCCCTTCCCA      92339          AGCT
                                TGGGAGGGGGC    GGGCT
                                ||||||||||    |||||
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                                ACCCTTCCCCG   CCCGG
                                      C___
GAM703  LOC205095 3'  CCAGTGCACCCCGTCCCA   92381     _   _  G
                                TGGGA GGGG GCA CTGG
                                ||||| |||| ||| ||||
                                ACCCT CCCC CGT GACC
                                   G   A  _
GAM703  LOC219562 3'  CATGCCCAGCCCCTCCCA   92448       GGCA     _
                                TGGGAGGG   GCTGGGC TG
                                ||||||||   ||||||| ||
                                ACCCTCCC   CGACCCG AC
                                     ____     T
GAM703  LOC220018 5'  TCAACCCAAGGGACCCCTCCC 95030       GCAGC   C
                                GGGAGGGG    TGGG TGA
                                ||||||||    |||| |||
                                CCCTCCCC    ACCC ACT
                                     AGGGA   A
GAM703  LOC220739 3'  TCAGCCCAGCTCTGCCTCGCA 94528   G   G  C
                                TG GAGG GG AGCTGGGCTGA
                                || |||| || ||||||||||
                                AC CTCC TC TCGACCCGACT
                                 G   G  _
GAM703  LOC221486 3'  TCAGCCCAGCACCTGCTCCCA 92659     G   CA
                                TGGGAG GGG  GCTGGGCTGA
                                |||||| |||  ||||||||||
                                ACCCTC TCC  CGACCCGACT
                                   G   A_
GAM703  LOC253609 5'  CAGCCCACCAGCCCTCC    98563      __ CAGC
                                GGAGGG  GG   TGGGCTG
                                ||||||  ||   |||||||
                                CCTCCC  CC   ACCCGAC
                                   GA  ____
GAM703  LOC254295 5'  TCAGCCCAGCTGCTTGGCCT  97897    AGG
                                GGG  GGGCAGCTGGGCTGA
                                |||  ||||||||||||||
                                TCC  TTCGTCGACCCGACT
                                  GG_
GAM703  LOC255612 5'  CAGCCCCTGTCCCCCCCCA   99365    A      CT
                                TGGG GGGGGCAG  GGGCTG
                                |||| ||||||||  ||||||
                                ACCC CCCCTGTC  CCCGAC
                                  C      __
GAM703  LOC255975 3'  CAGCCCAGCTCATGCCTCCC  97572      GGGC
                                GGGAGG   AGCTGGGCTG
                                ||||||   ||||||||||
                                CCCTCC   TCGACCCGAC
                                   GTAC
GAM703  LOC256867 5'  CACGTCCTGCCCCCCGCCA   96511    GA     GCT   _
                                TGG  GGGGGCA   GGGC TG
                                |||  |||||||   |||| ||
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                                ACC  CCCCCGT   CCTG AC
                                  GC      ___    C
GAM703  LOC257016 3'  TCAGCCCAGCCCACCCTC    96753      _  CA
                                GAGGG GG  GCTGGGCTGA
                                |||||  ||  ||||||||||
                                CTCCC CC  CGACCCGACT
                                   A  __
GAM703  LOC257181 3'  CATGCCCAGCCCCTCCCA    96229        GGCA     _
                                TGGGAGGG    GCTGGGC TG
                                ||||||||    ||||||| ||
                                ACCCTCCC    CGACCCG AC
                                     _____      T
GAM703  LOC257200 3'  CAACCCCCCACCTCCCA     97367       _  CAGCT   C
                                TGGGAGG GGG     GGG TG
                                |||||||  |||     ||| ||
                                ACCCTCC CCC     CCC AC
                                   A   ______   A
GAM703  LOC257457 5'  CCAAGCCTGCCCCCTTCCA    63315           _  _
                                TGGGAGGGGGCAG CT GG
                                ||||||||||||| || ||
                                ACCTTCCCCCGTC GA CC
                                      C  A
GAM703  LOC257482 3'  AGCCAGCCCCTCCCA       95895        GGCA    G
                                TGGGAGGG    GCTGG CT
                                ||||||||    ||||| ||
                                ACCCTCCC    CGACC GA
                                     _____    _
GAM703  LOC51107  5'  CAGCTGGCGCGCCCCTCCCA   32607         _  A  TG G
                                TGGGAGGGG GC GC  G CTG
                                |||||||||  || ||  | |||
                                ACCCTCCCC CG CG  C GAC
                                     G  _  GT _
GAM703  LOC51308  3'  CAGCAGTCGCCTCCTCCCA    33960          A   GG
                                TGGGAGGGGGC GCT  GCTG
                                ||||||||||| |||  ||||
                                ACCCTCCTCCG TGA  CGAC
                                      C   __
GAM703  LOC51713  3'  CCGGGCGCGGCCCCCTCCCA   33228          A__   G
                                TGGGAGGGGGC   GCT GG
                                ||||||||||   ||| ||
                                ACCCTCCCCCG   CGG CC
                                      GCG   G
GAM703  LOC90917  3'  CGCACTGCCCCTCCCA      64984         G   CTGG  T
                                TGGGAGGGG CAG    GC G
                                |||||||| |||    || |
                                ACCCTCCCC GTC    CG C
                                     _   A___   T
GAM703  LOC91252  3'  CCAGAGCTGCCCACCTCCCA   65937        _      G_
                                TGGGAGG GGGCAGCT  GG
                                |||||||  ||||||||  ||
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                                ACCCTCC CCCGTCGA  CC
                                   A       GA
GAM703  LOC91300  5'  CAGCCCCTGCTCAGCCCCTCCC 57861         ____   CT
            A                   TGGGAGGGG   GCAG  GGGCTG
                                |||||||||   ||||  ||||||
                                ACCCTCCCC   CGTC  CCCGAC
                                    GACT   __
GAM703  LOC91300  5'  CAGCCCCTGCTCAGCCCCTCCC 96233         ____   CT
            A                   TGGGAGGGG   GCAG  GGGCTG
                                |||||||||   ||||  ||||||
                                ACCCTCCCC   CGTC  CCCGAC
                                    GACT   __
GAM703  LOC91409  3'  TCAGCCCAGCCCTAACCCTC  66574      GGCA_
                                GAGGG    GCTGGGCTGA
                                |||||    ||||||||||
                                CTCCC    CGACCCGACT
                                   AATCC
GAM703  LOC92080  5'  CACCCCACCCCTCCCA     68621        GCAGC   C
                                TGGGAGGGG    TGGG TG
                                |||||||||    |||| ||
                                ACCCTCCCC    ACCC AC
                                    _____   C
GAM703  LOC92223  5'  CAACCCGCCGCTGCCCCCTCCC 69044          __   C
                                GGGAGGGGGCAGC  TGGG TG
                                ||||||||||||  |||| ||
                                CCCTCCCCCGTCG  GCCC AC
                                      CC   A
GAM704  ANXA8     3'  TGGGCACAGGTTATACAGACCC 73466    AGCC   ___
            CA                    TGG   TCTGT   ACCTGTGCCCA
                                  |||   |||||  ||||||||||
                                  ACC   AGACA   TGGACACGGGT
                                    CC__    TAT
GAM704  ANXA8     3'  TGGGCACAGGTTATACAGACCC 73467    AGCC   ___
            CA                    TGG   TCTGT   ACCTGTGCCCA
                                  |||   |||||  ||||||||||
                                  ACC   AGACA   TGGACACGGGT
                                    CC__    TAT
GAM704  ATP8A2    3'  CACAGGTACCTATCAG     95153     _ CCTCT
                                CTGG AG    GTACCTGTG
                                |||| ||    |||||||||
                                GACT TC    CATGGACAC
                                  A _____
GAM704  CASP3     3'  TGGGCATGGTCAAAGGCTC   53356      C  T   T
                                GAGCCT TG ACC GTGCCCA
                                |||||| || ||| |||||||
                                CTCGGA AC TGG TACGGGT
                                   A  _   _
GAM704  CCND2     3'  TGGACACAGGTGATTGGCTCC  10057      TCTG      C
                                GGAGCC   TACCTGTG CCA
                                ||||||   |||||||| |||
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                                CCTCGG   GTGGACAC GGT
                                   TTA_      A
GAM704  DPEP1    5'  GGCCAGCACAGAGGCACCAG  16620     A      AC  T
                                CTGG GCCTCTGT  CTG GCC
                                |||| ||||||||  ||| |||
                                GACC CGGAGACA  GAC CGG
                                  A      C_  _
GAM704  EPHB4    3'  TGGGGACTCACAGAGGCCCC  16710    A      ACCT  G
                                GG GCCTCTGT   GT CCCA
                                || |||||||   || ||||
                                CC CGGAGACA   CA GGGT
                                 C      CT__  G
GAM704  EVA1     5'  GGCACAGGTGAGGAACTC    20532    __    TGT
                                GAG  CCTC   ACCTGTGCC
                                |||  ||||   |||||||||
                                CTC  GGAG   TGGACACGG
                                  AA   ___
GAM704  FANCC    3'  TGGGCACAGGGGCAGCCGC   71053    CT   TA
                                GC  CTG  CCTGTGCCCA
                                ||  |||  ||||||||||
                                CG  GAC  GGACACGGGT
                                 CC   GG
GAM704  ITGA5    3'  CAGGGACAGAGGCCCCAG    61932     A      A
                                CTGG GCCTCTGT CCTG
                                |||| |||||||| ||||
                                GACC CGGAGACA GGAC
                                  C      G
GAM704  LDB3     3'  TGGGCAATTGCCAGGGCTCCAG 76928        T   TACCTG
                                CTGGAGCC CTG     TGCCCA
                                |||||||| |||     ||||||
                                GACCTCGG GAC     ACGGGT
                                    _  CGTTA_
GAM704  LZTS1    3'  TGGGCACAGTCCAGACCCA   41042    AGCC   TAC
                                TGG   TCTG   CTGTGCCCA
                                |||   ||||   |||||||||
                                ACC   AGAC   GACACGGGT
                                  C___   CT_
GAM704  MDM1     3'  TGAGCACATAAGCAGAGGCTGC 39684    G      ACC    C
           AG                    CTG AGCCTCTGT   TGTGC CA
                                ||| |||||||||   ||||| ||
                                GAC TCGGAGACG   ACACG GT
                                  G       AAT    A
GAM704  NEURL    3'  GGACAGGCTGCAGAGGGCTCCA 16130        _    _    G
           G                     CTGGAGCC TCTGTA CCTGT CC
                                |||||||| |||||| ||||| ||
                                GACCTCGG AGACGT GGACA GG
                                    G     C    _
GAM704  ONECUT2  3'  GGGCACAAGTCACCTCCA    17943      CCTC  T  C
                                TGGAG   TG AC TGTGCCC
                                |||||   || || |||||||
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                                ACCTC   AC TG ACACGGG
                                  C___  _  A
GAM704  PLOD    3'  GGCACAGGTGTTGCACCAG   6116      A  CTCTG
                                CTGG GC    TACCTGTGCC
                                |||| ||    ||||||||||
                                GACC CG    GTGGACACGG
                                  A  TT___
GAM704  SCN4A   3'  TGGCACCACCAGGGCTCCAG  6210        T  TACCT   C
                                CTGGAGCC CTG    GTGC CA
                                |||||||| |||    |||| ||
                                GACCTCGG GAC    CACG GT
                                    _  CAC__   A
GAM704  SYNGR3  3'  GGAGAGAGGCCCAGAGGCTCCA 16120          TA  GTG_
          G                      CTGGAGCCTCTG  CCT   CC
                                ||||||||||||  |||   ||
                                GACCTCGGAGAC  GGA   GG
                                      CC   GAGA
GAM704  SYNGR3  3'  GGCACAGACCAGGGCTCCA   16121       T  TAC
                                TGGAGCC CTG   CTGTGCC
                                ||||||| |||   |||||||
                                ACCTCGG GAC   GACACGG
                                   _  CA_
GAM704  BG1     3'  TGGGCACAGGCATTTCTGCCA  88655     AGCCTCT  A
                                TGG      GT CCTGTGCCCA
                                |||      || ||||||||||
                                ACC      TA GGACACGGGT
                                  GTCTT__  C
GAM704  CALN1   3'  TGAGCACAAGTAAAACTAAGGC 49671        CT  ___  C    C
          TTCAG                   CTGGAGCCT  GT   AC TGTGC CA
                                |||||||||  ||   || ||||| ||
                                GACTTCGGA  CA   TG ACACG GT
                                     AT  AAA  A    A
GAM704  DGKD    3'  GGGCACAGACACTGACCAG   60111     AGCC  T  AC
                                CTGG   TC GT  CTGTGCCC
                                ||||   || ||  ||||||||
                                GACC   AG CA  GACACGGG
                                  _____  T  CA
GAM704  DKFZP566G1424 3'  GGGAGGGGCACAGGGCTCCAG  85944       T   A  GTG
                                CTGGAGCC CTGT CCT   CCC
                                ||||||| |||| |||   |||
                                GACCTCGG GACA GGG   GGG
                                   _   C   GA_
GAM704  EMILIN-2  3'  TGGCTTGCCACAGAGGCTCC   50259         ACCTGT  C
                                GGAGCCTCTGT     GC CA
                                ||||||||||     || ||
                                CCTCGGAGACA     CG GT
                                     CCGTT_  A
GAM704  FKSG28  3'  CAGAGGTGCAGGCACCAG    48906     A   CT    G
                                CTGG GCCT  GTACCT TG
                                |||| ||||  |||||| ||
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                                GACC CGGA  CGTGGA AC
                                  A   __     G
GAM704  FLJ11286  3'  TGGGCACAGGCATGGTACCACC 37796     AGCCT   A
          AG                      CTGG    CTGT CCTGTGCCCA
                                  ||||    |||| ||||||||||
                                  GACC    GGTA GGACACGGGT
                                    ACCAT   C
GAM704  FLJ12056  3'  GGGCACAGGCACGGGCACAG   46822    GA   CT  A
                                  CTG  GCCT  GT CCTGTGCCC
                                  |||  ||||  || |||||||||
                                  GAC  CGGG  CA GGACACGGG
                                    A_   __ C
GAM704  FLJ13052  3'  GGGCACAGGGGAAGCCCAG   43756     A  C   GTA
                                  CTGG GC TCT   CCTGTGCCC
                                  |||| || |||   |||||||||
                                  GACC CG AGG   GGACACGGG
                                    _ A   ___
GAM704  FLJ14103  5'  GGACAGCCAGAGGCTGCAG   97938    G      TAC   G
                                  CTG AGCCTCTG   CTGT CC
                                  ||| ||||||||   |||| ||
                                  GAC TCGGAGAC   GACA GG
                                    G       C__   _
GAM704  KIAA0321  5'  GCAGCCCAGAAAGCTCCAG   63054       C_   TAC
                                  CTGGAGC  TCTG   CTGT
                                  |||||||  ||||   ||||
                                  GACCTCG  AGAC   GACG
                                      AA   CC_
GAM704  KIAA0476  3'  GCCCAGTCAAAGGCTCCA    30040       C  TAC   T
                                  TGGAGCCT TG   CTG GC
                                  |||||||| ||   ||| ||
                                  ACCTCGGA AC   GAC CG
                                       A  T__   C
GAM704  KIAA0819  5'  GGGAACCAGAGGCTCCAG    64334         TACCT  G
                                  CTGGAGCCTCTG    GT CCC
                                  ||||||||||||    || |||
                                  GACCTCGGAGAC    CA GGG
                                        _____  A
GAM704  KIAA1001  3'  GGCACAGGTGCCAGCTCCAG   31010       CTCT
                                  CTGGAGC   GTACCTGTGCC
                                  |||||||   ||||||||||
                                  GACCTCG   CGTGGACACGG
                                      AC__
GAM704  KIAA1076  3'  TGGGCACAGTGAGGAGACCCCA 66129    AGC   G   C
                                  TGG   CTCT TAC TGTGCCCA
                                  |||   |||| ||| ||||||||
                                  ACC   GAGG GTG ACACGGGT
                                    CCA   A  _
GAM704  MYH7B     3'  CAGGCCACAGAGGCCCAG    71055     A      A_
                                  CTGG GCCTCTGT  CCTG
                                  |||| ||||||||  ||||
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                                GACC CGGAGACA  GGAC
                                  _      CC
GAM704  NYD-SP25  3'  TGGGCAAGTCAGTGGCTCCAG  54306       T   T  CTG
                                CTGGAGCC CTG AC   TGCCCA
                                |||||||| ||| ||   ||||||
                                GACCTCGG GAC TG   ACGGGT
                                    T   _  A__
GAM704  PDE2A    3'  TGGGGGATACAGGGGCCCCAG  12007     A       _  TGTG
                                CTGG GCCTCTGTA CC    CCCA
                                |||| ||||||||| ||    ||||
                                GACC CGGGGACAT GG    GGGT
                                  C       A  _____
GAM704  RoXaN    3'  CACAAGTAAATGCAGGCTGCAG 47275     G    CTG__   C
                                CTG AGCCT    TAC TGTG
                                ||| |||||    ||| ||||
                                GAC TCGGA    ATG ACAC
                                  G    CGTAA   A
GAM704  SPIB     3'  TGGCACACCCGAGGCTCC    13359        TGTACC    C
                                GGAGCCTC     TGTGC CA
                                ||||||||     ||||| ||
                                CCTCGGAG     ACACG GT
                                    CCC___     A
GAM704  TREX1    5'  GGGACACAATGGCTCCAG    50611        TC   ACCT  GC
                                CTGGAGCC  TGT   GT  CC
                                |||||||  |||   ||  ||
                                GACCTCGG  ACA   CA  GG
                                    TA  _____  GA
GAM704  TREX1    5'  GGGACACAATGGCTCCAG    50612        TC   ACCT  GC
                                CTGGAGCC  TGT   GT  CC
                                |||||||  |||   ||  ||
                                GACCTCGG  ACA   CA  GG
                                    TA  _____  GA
GAM704  YKT6     3'  TGAGCCCACCACAGAGGCCACA 22645     GA       ACC  T  C
            G                    CTG  GCCTCTGT   TG GC CA
                                |||  ||||||||   || || ||
                                GAC  CGGAGACA   AC CG GT
                                  AC       CC_  C  A
GAM704  LOC121629 5'  GGGTCACAAGAGGCTCCAG    76085          GTACC   _
                                CTGGAGCCTCT    TGTG CCC
                                ||||||||||     |||| |||
                                GACCTCGGAGA    ACAC GGG
                                      _____   T
GAM704  LOC127702 3'  GGGCAGCACAGAGGCCCC    75986    A       ACCTG
                                GG GCCTCTGT    TGCCC
                                || ||||||||    |||||
                                CC CGGAGACA    ACGGG
                                  C       CG___
GAM704  LOC142972 3'  TGGGCACAGGTTATACAGACCC 65722     AGCC    ___
            CA                    TGG   TCTGT   ACCTGTGCCCA
                                |||   |||||  ||||||||||
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                                ACC    AGACA   TGGACACGGGT
                                  CC__     TAT
GAM704   LOC145317 3'  GCACAGACACAGAGGCCCAG   84280      A       AC
                                CTGG GCCTCTGT  CTGTGC
                                |||| ||||||||  ||||||
                                GACC CGGAGACA  GACACG
                                   _       CA
GAM704   LOC147160 5'  GGCACAGGGTCAGGCCCAG    85079      A    CTGTA
                                CTGG GCCT    CCTGTGCC
                                |||| ||||    ||||||||
                                GACC CGGA    GGACACGG
                                   _   CTG__
GAM704   LOC148114 5'  GGGCACAGACCAGCCCCA     79362     A  CTC  TAC
                                TGG GC   TG   CTGTGCCC
                                ||| ||   ||   ||||||||
                                ACC CG   AC   GACACGGG
                                  C  ___  CA_
GAM704   LOC153205 3'  ATATATACTAGAAGCTCCA    87152       C   _   CC
                                TGGAGC TCT GTA  TGT
                                |||||| ||| |||  |||
                                ACCTCG AGA CAT  ATA
                                   A   T   AT
GAM704   LOC153561 3'  TGAGCACAGGAGTTGGAGGCTG 81753     G       TA_      C
            CAG                    CTG AGCCTCTG   CCTGTGC CA
                                ||| ||||||||   ||||||| ||
                                GAC TCGGAGGT   GGACACG GT
                                  G       TGA      A
GAM704   LOC158263 5'  GGGCACCACTCAGAGGCTCCAG 82730           TACCT
                                CTGGAGCCTCTG     GTGCCC
                                ||||||||||||     ||||||
                                GACCTCGGAGAC     CACGGG
                                       TCAC_
GAM704   LOC167410 3'  CAGAGGTCCTCAGAGGCTCCAG 83563           T__    G
                                CTGGAGCCTCTG   ACCT TG
                                ||||||||||||   |||| ||
                                GACCTCGGAGAC   TGGA AC
                                       TCC    G
GAM704   LOC170127 3'  TGGGCACAGATTCCGATTCCAG 83462       CC  TGTAC
                                CTGGAG  TC     CTGTGCCCA
                                ||||||  ||     |||||||||
                                GACCTT  AG     GACACGGGT
                                   __  CCTTA
GAM704   LOC197336 3'  TGGACACAGGCTTGGCAGAGGC 59925      A       A___      C
            GCCAG                    CTGG GCCTCTGT    CCTGTG CCA
                                |||| ||||||||    ||||||| |||
                                GACC CGGAGACG    GGACAC GGT
                                  G       GTTC      A
GAM704   LOC200282 3'  TGCTGGAACAGAGGCTCCA    90102           A  T
                                TGGAGCCTCTGT CC GTG
                                |||||||||||| || |||
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                                ACCTCGGAGACA GG CGT
                                      A  T
GAM704  LOC201100 3'  GCCCAGCACAGAGGCTCCA   91324          AC   T
                                TGGAGCCTCTGT  CTG GC
                                |||||||||||  ||| ||
                                ACCTCGGAGACA  GAC CG
                                      C_   C
GAM704  LOC203286 5'  ACAGGACAGCAGAGGCTCCAG  92139          A__
                                CTGGAGCCTCTGT   CCTGT
                                ||||||||||||   |||||
                                GACCTCGGAGACG   GGACA
                                       ACA
GAM704  LOC203636 3'  CAGGTCTTCACAGAGGCCCCGG 90975     A      ____
                                CTGG GCCTCTGT    ACCTG
                                |||| ||||||||    |||||
                                GGCC CGGAGACA    TGGAC
                                  C       CTTC
GAM704  LOC219513 3'  GGACACAGAGTGCAGAGACCCC 95987     AGC      _    C
          GG                      CTGG   CTCTGTAC CTGTG CC
                                |||||   |||||||| ||||| ||
                                GGCC   GAGACGTG GACAC GG
                                  CCA       A     A
GAM704  LOC221822 5'  GGACTGGACAGAGGCACCAG   94451     A      A  T  G
                                CTGG GCCTCTGT CC GT CC
                                |||| |||||||| || || ||
                                GACC CGGAGACA GG CA GG
                                  A       _  T  _
GAM704  LOC253027 3'  GGCACAGGTGCCCTGCCCA    98770     A  CTCT
                                TGG GC    GTACCTGTGCC
                                |||  ||    ||||||||||
                                ACC CG    CGTGGACACGG
                                  _  TCC_
GAM704  LOC255104 3'  GCACAGGTTAGAGTCCCAG    97128      AG C    T
                                CTGG  C TCTG ACCTGTGC
                                ||||  | |||| ||||||||
                                GACC  G AGAT TGGACACG
                                  CT _   _
GAM704  LOC90092  5'  TGGGCACAGACACTCACAGCCC 62078     A  CTCT_  AC
          CA                      TGG GC     GT  CTGTGCCCA
                                |||  ||     ||  |||||||||
                                ACC CG     CA  GACACGGGT
                                  C  ACACT  CA
GAM704  LOC90917  3'  GGCACAGGCCTCAGAGCCCAG  64987     A  C    TA_
                                CTGG GC TCTG   CCTGTGCC
                                |||| || ||||   ||||||||
                                GACC CG AGAC   GGACACGG
                                  _  _    TCC
GAM704  LOC91516  5'  GCAGCTCAGAGGCTCCAG     66908          TAC
                                CTGGAGCCTCTG   CTGT
                                ||||||||||||   ||||
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                                GACCTCGGAGAC  GACG
                                      TC_
GAM704  LOC91661  3'  GGTGCACAGAGGCCCCGG   57215     A      ACCT TG
                                CTGG GCCTCTGT   G  CC
                                |||| ||||||||   |  ||
                                GGCC CGGAGACA   C  GG
                                  C       ____ GT
GAM704  LOC92340  3'  TGGGCACAGGGCTAAGTCCAG  69569      GC  CT  A
                                CTGGA  CT  GT CCTGTGCCCA
                                |||||  ||  || ||||||||||
                                GACCT  GA  CG GGACACGGGT
                                   __  AT  _
GAM705  ABCC11   3'  GGGTAAATGTAGGGGGGGTG  53686          A  GAA   TT
                                CATTCCTTCTA CA   TTAT  C
                                |||||||||| ||   ||||  |
                                GTGGGGGGGAT GT   AATG  G
                                      _  A__    GG
GAM705  ACCN2    3'  GAGGTGGGTTTGGGAGGAA   39627         CAGAA
                                TTCCTTCTAA    TTATTTC
                                ||||||||||    |||||||
                                AAGGAGGGTT    GGTGGAG
                                      TG___
GAM705  ADCY7    3'  GGGTGGCGGTGGAGGGAA    8492         A AGAA   TT
                                TTCCTTCTA C    TTAT  C
                                |||||||| |    ||||  |
                                AAGGGAGGT G    GGTG  G
                                      _ GC__    GG
GAM705  ALS2     5'  GGAATGATTTGGTGATGGAGTG 40882       T  TA  A
                                CATTCC TC  AC GAATTATTTC
                                ||||||  ||  || ||||||||||
                                GTGAGG AG  TG TTTAGTAAGG
                                   T  __  G
GAM705  APP      3'  GAAGTAATTTTGGGTGGGGA   6661       TCTAA
                                TTCCT    CAGAATTATTTC
                                |||||    ||||||||||||
                                AGGGG    GTTTTAATGAAG
                                   TGG__
GAM705  ATP1A2   3'  GGATGGTGATGGAGAGGGA   7365        AA  GA    TT
                                TCCTTCT  CA  ATTAT  C
                                |||||||  ||  |||||  |
                                AGGGAGA  GT  TGGTA  G
                                    G_  AG    GG
GAM705  ATP7A    3'  GAGGTGATTATGGAGGGAAT   5323          ACAG
                                ATTCCTTCTA    AATTATTTC
                                ||||||||||    |||||||||
                                TAAGGGAGGT    TTAGTGGAG
                                      A___
GAM705  B29      3'  GAAATGGTTCTGTATGAGTG   50038       CTTCTA
                                CATTC     ACAGAATTATTTC
                                |||||     ||||||||||||
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                                GTGAG     TGTCTTGGTAAAG
                                  TA____
GAM705  CALD1    3'  GAGATTAGAACTGTTAGAAGGA 53698           AATT_
           GT                    ATTCCTTCTAACAG     ATTTC
                                 ||||||||||||||     |||||
                                 TGAGGAAGATTGTC     TAGAG
                                       AAGAT
GAM705  CASP8    5'  GAAGTGAGGCCATGGAGGGAG  54074         ACAGAA
                                 TTCCTTCTA     TTATTTC
                                 |||||||||     |||||||
                                 GAGGGAGGT     AGTGAAG
                                       ACCGG_
GAM705  CASP8    5'  GAAGTGAGGCCATGGAGGGAG  8751          ACAGAA
                                 TTCCTTCTA     TTATTTC
                                 |||||||||     |||||||
                                 GAGGGAGGT     AGTGAAG
                                       ACCGG_
GAM705  CENPF    3'  GGAATAGTTTTGTATCGGGAAT 33416        TCTA
                                 ATTCCT    ACAGAATTATTTC
                                 ||||||    ||||||||||||||
                                 TAAGGG    TGTTTTGATAAGG
                                    CTA_
GAM705  CLCN3    5'  GGAATAATGAGCAAGGAGGGTG 10205     T     AACAGA
           TG                    CAT CCTTCT     ATTATTTC
                                 ||| ||||||     ||||||||
                                 GTG GGGAGG     TAATAAGG
                                   T     AACGAG
GAM705  CNTN3    3'  ATTTTGTTGGAGAGGAGTG    67269        _
                                 CATTCCT TCTAACAGAAT
                                 |||||||| ||||||||||
                                 GTGAGGA AGGTTGTTTTA
                                     G
GAM705  CSRP1    3'  GGAATAGTGGTGGGAGGAA    15814         ACAGA
                                 TTCCTTCTA    ATTATTTC
                                 |||||||||    ||||||||
                                 AAGGAGGGT    TGATAAGG
                                       GG___
GAM705  CYBB     3'  GAGATAATTCCTACGGGGAAT  76847       TC  ACA
                                 ATTCCT  TA   GAATTATTTC
                                 ||||||  ||   ||||||||||
                                 TAAGGG  AT   CTTAATAGAG
                                    GC  C__
GAM705  EGFL5    3'  GAGATGATGTTCTGGAGGGAGT 87912         ACAGA
                                 ATTCCTTCTA    ATTATTTC
                                 ||||||||||    ||||||||
                                 TGAGGGAGGT    TAGTAGAG
                                       CTTG_
GAM705  EIF2C1   3'  GAGGTGGGGTAGGGAGGAGTG  25195         A  AGAAT
                                 CATTCCTTCT AC    TATTTC
                                 |||||||||| ||    ||||||
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                                GTGAGGAGGG TG    GTGGAG
                                     A  GG___
GAM705  EYA2    3'  GATGCTGGGAAGGAATG     19125          AA   A
                                CATTCCTTCT  CAG ATT
                                ||||||||||  ||| |||
                                GTAAGGAAGG  GTC TAG
                                     __   G
GAM705  FUT7    3'  GAGGTGAGAGTGGGAGGGAG   16804        A  AGAA
                                TTCCTTCT AC    TTATTTC
                                ||||||||| ||    |||||||
                                GAGGGAGG TG    AGTGGAG
                                     G  AG__
GAM705  GAB2    3'  GAGGTAGGCCTTAGAAGGGG   25459        AC  AA
                                TTCCTTCTA  AG  TTATTTC
                                |||||||||  ||  |||||||
                                GGGGAAGAT  TC  GATGGAG
                                     __ CG
GAM705  GAB2    3'  GGGGTGGGGAATATGGGAGGGA 25463         AACAGAA_   TT
           GTG                    CATTCCTTCT       TTAT  C
                                ||||||||||       ||||  |
                                GTGAGGGAGG       GGTG  G
                                     GTATAAGG    GG
GAM705  GDF3    3'  GAAATGGGAATAGAAGGAGTG  40553          ACAGAA
                                CATTCCTTCTA     TTATTTC
                                ||||||||||     |||||||
                                GTGAGGAAGAT     GGTAAAG
                                     AAG___
GAM705  GJA1    3'  GAAATAATTCTGGCCAGGAAT  5714        TCTAA
                                ATTCCT    CAGAATTATTTC
                                ||||||    ||||||||||||
                                TAAGGA    GTCTTAATAAAG
                                   CCG__
GAM705  GPT     3'  GTGGGGTGGGGGGGGGTG     19189          ACAGAA
                                CATTCCTTCTA     TTAT
                                ||||||||||     ||||
                                GTGGGGGGGGT     GGTG
                                     GG____
GAM705  GYS1    3'  GAAGTGGGGCTCTGGGAGGGAT 89782          AC  AA
           G                     CATTCCTTCTA  AG  TTATTTC
                                ||||||||||  ||  |||||||
                                GTAGGGAGGGT  TC  GGTGAAG
                                     C_  GG
GAM705  HKE4    3'  GGAGTGATTGGGGGGGATGGGGT 23710       _   AA  GA
           G                     CATTCC TTCT  CA  ATTATTTC
                                ||||||  ||||  ||  ||||||||
                                GTGGGG AGGG  GT  TAGTGAGG
                                   T   GG  __
GAM705  HOXA7   3'  GAGTAATTGCTGAGGGATG   23556        TCTAA  _
                                CATTCCT    CAG AATTATTT
                                |||||||    ||| ||||||||
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                                GTAGGGA    GTC TTAATGAG
                                   _____  G
GAM705  IL16    3'  GAAGTAATCCTAGGGAAGGG  16916       AAC  A
                                TCCTTCT   AG ATTATTTC
                                |||||||   || ||||||||
                                GGGAAGG   TC TAATGAAG
                                   GA_  C
GAM705  IL6R    5'  GGAGTGGTAGCCGAGGAGGAA 6913        AACAGA
                                TTCCTTCT     ATTATTTC
                                ||||||||     ||||||||
                                AAGGAGGA     TGGTGAGG
                                   GCCGA_
GAM705  KCNJ3   3'  GAGGTAATTCTCCCTAAGGAAT 11149       CTAAC
                                ATTCCTT    AGAATTATTTC
                                |||||||    ||||||||||
                                TAAGGAA    TCTTAATGGAG
                                   TCCC_
GAM705  KIF3C   3'  GAAATGGGGGGTGTGGGAGGTG 11206    TC    A  GAA_
           GTG                    CAT  CTTCT ACA    TTATTTC
                                ||| ||||| |||    |||||||
                                GTG  GGAGG TGT    GGTAAAG
                                  GT    G  GGGG
GAM705  LEP     3'  GGTTCTTTGGAAGGAGTG    5868          C
                                CATTCCTTCTAA AGAATT
                                |||||||||||| ||||||
                                GTGAGGAAGGTT TCTTGG
                                   _
GAM705  LGR6    3'  GAAGTAAAGACAGTGAAGGGGT 85355        TAACAGAA
           G                     CATTCCTTC       TTATTTC
                                |||||||||       |||||||
                                GTGGGGAAG       AATGAAG
                                   TGACAGA_
GAM705  MAN2A2  3'  GGGATGGAGCAGTAGAAGGAAT 21515         ACAGAA   TT
                                ATTCCTTCTA     TTAT  C
                                ||||||||||     ||||  |
                                TAAGGAAGAT     GGTA  G
                                   GACGA_   GG
GAM705  MAP1A   3'  GAGATGGGAGCTAGGGGGAGG  11439      AAC  AA_
                                CCTTCT   AG   TTATTTC
                                ||||||   ||   |||||||
                                GGAGGG   TC   GGTAGAG
                                   GGA  GAG
GAM705  MECP2   3'  GGAATGGTTAGAAGTGAGGGAG 18407       TAACAG
           T                     ATTCCTTC     AATTATTTC
                                ||||||||     |||||||||
                                TGAGGGAG     TTGGTAAGG
                                   TGAAGA
GAM705  MGAT3   5'  GAAGTGGGGGTGGGGGGAGG   11563      AA  GAA
                                CCTTCT  CA   TTATTTC
                                ||||||  ||   |||||||
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                                GGAGGG GT  GGTGAAG
                                   GG GGG
GAM705  MGEA5   3' GGAGTGATTCCAAGTGGGATG 25221     TT AACA
                                CATTCC CT   GAATTATTTC
                                |||||| ||   ||||||||||
                                GTAGGG GA   CTTAGTGAGG
                                   T_ AC__
GAM705  MLF2    5' GAGGTGGCAGCTGTGGGAGGAG 19556      A AA_
                                TTCCTTCTA CAG  TTATTTC
                                ||||||||| |||  |||||||
                                GAGGAGGGT GTC  GGTGGAG
                                      _ GAC
GAM705  NFE2L1  3' AAATGGGGGGTGGGGGGAA   13627      A AGAA
                                TTCCTTCTA C   TTATTT
                                ||||||||| |   ||||||
                                AAGGGGGGT G   GGTAAA
                                     _ GG__
GAM705  NGFR    3' GGATGGTACTAGGGGGAA   11800      AAC A   TT
                                TTCCTTCT  AG ATTAT  C
                                |||||||  || |||||  |
                                AAGGGGGA  TC TGGTA  G
                                    ___ A   GG
GAM705  NR1I2   5' GAGGTGGTTTCAACAAAGGAGG 15301      AACA__
           AA                    TTCCTTCT    GAATTATTTC
                                 ||||||||    ||||||||||
                                 AAGGAGGA    TTTGGTGGAG
                                     AACAAC
GAM705  NRXN2   3' GGGTGGGGGGGTGGGAGGGAG  57824      A AGAA   TT
                                TTCCTTCT AC   TTAT  C
                                |||||||| ||   ||||  |
                                GAGGGAGG TG   GGTG  G
                                    G  GGG_   GG
GAM705  NRXN2   3' GGTGGGGGGGTGGGAGGGAG   57825      A AGAA   TT
                                TTCCTTCT AC   TTAT  C
                                |||||||| ||   ||||  |
                                GAGGGAGG TG   GGTG  G
                                    G  GGG_   G
GAM705  OGT     3' GGGATGGTTAGTGTGGAGGGGA 14594      ACAG    TT
                                TTCCTTCTA   AATTAT  C
                                |||||||||   ||||||  |
                                AGGGGAGGT   TTGGTA  G
                                    GTGA    GG
GAM705  PAX5    3' GGAGTGATTTTGACATGGGGGT 34133      TCTAA
           G                     CATTCCT   CAGAATTATTTC
                                 |||||||   ||||||||||||
                                 GTGGGGG   GTTTTAGTGAGG
                                    TACA_
GAM705  PFKFB2  3' GGATGATCTGGAGGAGGAG   21700      AA  A   TT
                                TTCCTTCT  CAGA TTAT  C
                                ||||||||  |||| ||||  |
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                                GAGGAGGA  GTCT AGTA  G
                                    G_   _   GG
GAM705  PIG8     3'  AGATGAGATAGGAGGAA     18077         ACAGAA
                                TTCCTTCTA     TTATTT
                                |||||||||     ||||||
                                AAGGAGGAT     AGTAGA
                                    AG____
GAM705  POU4F1   3'  GGAGTGGGGAGTGGGGGGAA  21763         ACAGAA
                                TTCCTTCTA     TTATTTC
                                |||||||||     |||||||
                                AAGGGGGGT     GGTGAGG
                                    GAGG__
GAM705  PRKCM    3'  GAAGTAGTTCTGTTTGGTGTG  12289     T  TTCT
                                CAT CC    AACAGAATTATTTC
                                ||| ||    ||||||||||||||
                                GTG GG    TTGTCTTGATGAAG
                                  T  T___
GAM705  PTPRS    3'  GGGTGGGGGGGTGGGGGGATG  12631         TA  AGAA   TT
                                CATTCCTTC  AC    TTAT  C
                                |||||||||  ||    ||||  |
                                GTAGGGGGG  TG    GGTG  G
                                    __ GGG_    GG
GAM705  PTPRS    3'  GGTGGGGGGGTGGGGGGATG   12632         TA  AGAA   TT
                                CATTCCTTC  AC    TTAT  C
                                |||||||||  ||    ||||  |
                                GTAGGGGGG  TG    GGTG  G
                                    __ GGG_    G
GAM705  SAR1     3'  GAGATGAAAAGTTGGGAGGA  39732         AGAA
                                TCCTTCTAAC    TTATTTC
                                ||||||||||    |||||||
                                AGGAGGGTTG    AGTAGAG
                                    AAA_
GAM705  SEMA3F   3'  GGGGTGATTGGAAGGGAGGGAG 16084         AACAG     TT
                                TTCCTTCT    AATTAT  C
                                ||||||||    ||||||  |
                                GAGGGAGG    TTAGTG  G
                                    GAAGG     GG
GAM705  SLC6A6   3'  GGAGTGGTGGGGAGGTGAGTG  13185      _    AACAGA
                                CATTC CTTCT     ATTATTTC
                                ||||| |||||     ||||||||
                                GTGAG GGAGG     TGGTGAGG
                                   T    GG____
GAM705  SMCX     3'  GGGGTGGGCGGGTAGGGGGGGT 16088         ACAGAA   TT
                G                   CATTCCTTCTA     TTAT  C
                                ||||||||||     ||||  |
                                GTGGGGGGGAT     GGTG  G
                                      GGGCG_   GG
GAM705  SORCS1   3'  GAGTGTGTAGGGAGGGATG   54682         A   GAAT
                                CATTCCTTCT ACA    TATTT
                                |||||||||| |||    |||||
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                                GTAGGGAGGG TGT   GTGAG
                                     A  ____
GAM705  SRRM2    3'  GGGGTTTGGGGTGGGAGGGAAT 33386         A  AGAATT  TT
           G                    CATTCCTTCT AC     AT  C
                                |||||||||| ||     ||  |
                                GTAAGGGAGG TG     TG  G
                                     G  GGGTT_  GG
GAM705  THBD     3'  GGGGTGATTAGAGGGAGGAGAA 6278       _    AACAG     TT
           TG                    CATTC CTTCT    AATTAT  C
                                ||||| |||||    ||||||  |
                                GTAAG GGAGG    TTAGTG  G
                                   A    GAGA_     GG
GAM705  TRIM9    3'  GGGGTGCAGAGTTGGCAGGAGT 31458       T    AGAAT   TT
           G                    CATTCCT CTAAC    TAT  C
                                ||||||| |||||    |||  |
                                GTGAGGA GGTTG    GTG  G
                                   C    AGAC_   GG
GAM705  XT3      3'  GAATAGTGAAGGAGGGAG    39912        AACAGA
                                TTCCTTCT     ATTATTT
                                ||||||||     |||||||
                                GAGGGAGG     TGATAAG
                                   AAG___
GAM705  ZNF10    3'  GAAATGGTTTTCATTAAGGGAG 31818       CTAAC
           T                    ATTCCTT    AGAATTATTTC
                                |||||||    ||||||||||
                                TGAGGGA    TTTTGGTAAAG
                                   ATTAC
GAM705  ZNF137   3'  GAGATAATTCTGAGCCTTGAGA 14310       TC  ____
           GGAATG                  CATTCCT  TAA   CAGAATTATTTC
                                ||||||| |||   ||||||||||||
                                GTAAGGA  GTT   GTCTTAATAGAG
                                   GA   CCGA
GAM705  AP1G2    5'  GGGTACCAGGTTAGGGGGAG   15354         AGAAT   TT
                                TTCCTTCTAAC    TAT  C
                                ||||||||||    |||  |
                                GAGGGGGATTG    ATG  G
                                     GACC_   GG
GAM705  C20orf108 3'  GAAGTAATTCTGTCCTGCGGGG 55880      TTCTA
           T                    ATTCC    ACAGAATTATTTC
                                |||||    ||||||||||||
                                TGGGG    TGTCTTAATGAAG
                                  CGTCC
GAM705  C6.1A    3'  GGATAGGGACTGGAGGGGGTG  44536         ACAGAA   TT
                                CATTCCTTCTA     TTAT  C
                                ||||||||||     ||||  |
                                GTGGGGGAGGT     GATA  G
                                     CAGG__   GG
GAM705  CBX6     3'  GAGGTGGACAGAGTTGGGGGGA 27415         AGAA_
                                TCCTTCTAAC    TTATTTC
                                |||||||||     |||||||
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                                AGGGGGGTTG    GGTGGAG
                                      AGACA
GAM705  CCR6     5'  GGAGTGAGGCTGAAGGGAGTG  16446        CTAA   AA
                                CATTCCTT    CAG  TTATTTC
                                ||||||||    |||  |||||||
                                GTGAGGGA    GTC  AGTGAGG
                                     A___   GG
GAM705  CCR6     5'  GGAGTGAGGCTGAAGGGAGTG  49407        CTAA   AA
                                CATTCCTT    CAG  TTATTTC
                                ||||||||    |||  |||||||
                                GTGAGGGA    GTC  AGTGAGG
                                     A___   GG
GAM705  CDH26    3'  GAAATAATTCATGGAAGGGA   41765        ACA
                                TTCCTTCTA   GAATTATTTC
                                |||||||||   ||||||||||
                                AGGGAAGGT   CTTAATAAAG
                                     A__
GAM705  CDKL1    3'  GAGATGATTTTAAAAAAGGAAT 16095        CTAAC
                                ATTCCTT     AGAATTATTTC
                                |||||||     ||||||||||||
                                TAAGGAA     TTTTAGTAGAG
                                    AAAA_
GAM705  CGI-57   3'  GGGGTGGTGGGGCAGAAGGACT 74307     T      AACAGA     TT
           G                     CA TCCTTCT      ATTAT  C
                                 || |||||||      |||||  |
                                 GT AGGAAGA      TGGTG  G
                                  C      CGGGG_     GG
GAM705  DKFZP434B195 3'  GGGTAATTTTTCTGAGGAAGG  49249        AA   ___    TT
                                CCTTCT  CAGA   ATTAT  C
                                ||||||  ||||   |||||  |
                                GGAAGG  GTCT   TAATG  G
                                   A_   TTT    GG
GAM705  DKFZP434C171 3'  AGGTGAGGCTAGGGGAGTG   32181        T  AAC  AA
                                CATTCCT CT   AG  TTATTT
                                ||||||| ||   ||  ||||||
                                GTGAGGG GA   TC  AGTGGA
                                   _ ___  GG
GAM705  DKFZP586F1524 3'  GGGGTTCTTTTTGTGGGGAGGG 32107          A     TT_  TT
           GTG                    CATTCCTTCT ACAGAA   AT  C
                                  |||||||||| ||||||   ||  |
                                  GTGGGGAGGG TGTTTT   TG  G
                                       G     TCT  GG
GAM705  DKFZp761K1423 5'  GAGGTGATGAACAGAGGGGGTG 37938          AACAGA
                                CATTCCTTCT     ATTATTTC
                                ||||||||||     ||||||||
                                GTGGGGGAGA     TAGTGGAG
                                      CAAG__
GAM705  DNAJA4   5'  GAAATGATTCCCATGAGGAGG  38360       AACA_
                                CCTTCT    GAATTATTTC
                                ||||||    ||||||||||
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                                GGAGGA    CTTAGTAAAG
                                   GTACC
GAM705  FLJ10415  3'  GAGATGATTTGGAAGATGGGGG 36587       _  AA   A
              TG                  CATTCCT TCT  CAGA TTATTTC
                                  ||||||| |||  |||| |||||||
                                  GTGGGGG AGA  GTTT AGTAGAG
                                     T  AG   _
GAM705  FLJ10482  3'  GAGGTAGGAGGATGGAGGGAG  36648        ACAGAA
                                  TTCCTTCTA     TTATTTC
                                  |||||||||     |||||||
                                  GAGGGAGGT     GATGGAG
                                       AGGAG_
GAM705  FLJ10759  3'  GAGGTGGGAACTGGAGGAGTG  37123        TAACAGAA
                                  CATTCCTTC       TTATTTC
                                  |||||||||       |||||||
                                  GTGAGGAGG       GGTGGAG
                                       TCAAG___
GAM705  FLJ11016  3'  GAAATAATGCAAAAGAAGGAAT 37541         AACAGA
              G                    CATTCCTTCT     ATTATTTC
                                  ||||||||||     ||||||||
                                  GTAAGGAAGA     TAATAAAG
                                       AAACG_
GAM705  FLJ11703  3'  GAGATGGAGGTAGAAGGAAT   46984         A AGAA
                                  ATTCCTTCTA C    TTATTTC
                                  |||||||||| |    |||||||
                                  TAAGGAAGAT G    GGTAGAG
                                       _ GA__
GAM705  FLJ11996  3'  GAAGTGAAGGCTTGAGGGGATG 47062        TAAC  AA_
                                  CATTCCTTC    AG   TTATTTC
                                  |||||||||    ||   |||||||
                                  GTAGGGGAG    TC   AGTGAAG
                                       T___  GGA
GAM705  FLJ12526  3'  GGAGTAAGGTTAGAAGGGA    45928         AGAA
                                  TTCCTTCTAAC    TTATTTC
                                  ||||||||||    |||||||
                                  AGGGAAGATTG    AATGAGG
                                       G___
GAM705  FLJ13114  3'  GGGATAATCTTATTTGGGGAGG 44906         AAC___   A    TT
              AATG                   CATTCCTTCT     AGA TTAT  C
                                  ||||||||||     ||| ||||  |
                                  GTAAGGAGGG     TCT AATA  G
                                       GTTTAT   _    GG
GAM705  FLJ14054  3'  GAGATGATTCATAGGGGAG    44968       T   ACA
                                  TTCCT CTA   GAATTATTTC
                                  ||||| |||   ||||||||||
                                  GAGGG GAT   CTTAGTAGAG
                                     _   A__
GAM705  FLJ20097  3'  GGAATGGTGGTGGTGGGGAATG 35047        CTAA  GA
                                  CATTCCTT    CA  ATTATTTC
                                  ||||||||    ||  ||||||||
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                                GTAAGGGG   GT  TGGTAAGG
                                    TG__  GG
GAM705  FLJ20320  5'  GATGTGTTAGGGTGAATG    35427      C      GA
                                CATTC TTCTAACA  ATT
                                ||||| ||||||||  |||
                                GTAAG GGGATTGT  TAG
                                   T      G_
GAM705  FLJ20378  3'  GGAATGGTTTCTGGGGAGGCGT 35556    T     AA    _
          G                      CAT CCTTCT  CAGAA TTATTTC
                                 ||| ||||||  ||||| |||||||
                                 GTG GGAGGG  GTCTT GGTAAGG
                                   C     __    T
GAM705  FLJ21276  3'  GGGGTGGGCAGGGTGGGAGGGA 45262          ACAGAA   TT
          TG                     CATTCCTTCTA     TTAT  C
                                 ||||||||||      ||||  |
                                 GTAGGGAGGGT     GGTG  G
                                       GGGACG    GG
GAM705  FLJ21438  3'  GAGATAGCCATCTTAGGGGGGG 62193          CAGAA
          TG                     CATTCCTTCTAA    TTATTTC
                                 ||||||||||||    |||||||
                                 GTGGGGGGGATT    GATAGAG
                                       CTACC
GAM705  FLJ23277  3'  GGGTGGTGGGTGGGAGGGG   50917       A  AGA    TT
                                 TCCTTCT AC   ATTAT  C
                                 ||||||| ||   |||||  |
                                 GGGGAGG TG   TGGTG  G
                                     G  GG_    GG
GAM705  FOXP1     3'  GGGGTGGTTCGGGGGAGGGGTG 52047         AACA      TT
                                 CATTCCTTCT    GAATTAT  C
                                 ||||||||||    |||||||  |
                                 GTGGGGAGGG    CTTGGTG  G
                                       GG__      GG
GAM705  GPR107    3'  GGGTAGTTTGGAGAAGGAG   40912        AACA      TT
                                 TTCCTTCT    GAATTAT  C
                                 ||||||||    |||||||  |
                                 GAGGAAGA    TTTGATG  G
                                     GG__      GG
GAM705  HML2      3'  AAATGGCGGTGGGAGGAG    22021         A AGAA
                                 TTCCTTCTA C    TTATTT
                                 |||||||||  |    ||||||
                                 GAGGAGGGT G    GGTAAA
                                      _ GC__
GAM705  HSPC216   3'  ATGGTTCTGTTAAAGGAGTG   33635         C
                                 CATTCCTT TAACAGAATTAT
                                 |||||||| ||||||||||||
                                 GTGAGGAA ATTGTCTTGGTA
                                      _
GAM705  HTATIP    5'  GAAGTGGCAGTGGAGGGAG    22137         ACAGAA
                                 TTCCTTCTA     TTATTTC
                                 |||||||||     |||||||
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                                GAGGGAGGT     GGTGAAG
                                    GAC___
GAM705  HYPH     3' GGGGTGGGAGATGTGGGGGAAT 96569        TA  GAA_   TT
           G                    CATTCCTTC  ACA    TTAT  C
                                |||||||||  |||   ||||  |
                                GTAAGGGGG  TGT    GGTG  G
                                    __   AGAG    GG
GAM705  KCNJ9    3' GAGGTGGTGGAGGAGGAGGAG  18365        AACAGA
                                TTCCTTCT     ATTATTTC
                                ||||||||     ||||||||
                                GAGGAGGA     TGGTGGAG
                                    GGAGG_
GAM705  KCNMB2   3' GAGATGATACTTACAAGGAGTG 20686        C  AC  A
                                CATTCCTT TA  AG ATTATTTC
                                |||||||| ||  || ||||||||
                                GTGAGGAA AT  TC TAGTAGAG
                                    C  __  A
GAM705  KIAA0040 5' AAGTAACGTGGAAGGAG     28486         ACAGAA
                                TTCCTTCTA     TTATTT
                                |||||||||     ||||||
                                GAGGAAGGT     AATGAA
                                    GC_____
GAM705  KIAA0057 3' GGGATGGTTCTGGGTGAGAGGG 25421        AA__       TT
           GA                     TTCCTTCT   CAGAATTAT  C
                                  ||||||||   |||||||||  |
                                  AGGGGAGA   GTCTTGGTA  G
                                      GTGG       GG
GAM705  KIAA0255 3' GAGATTCTCTTTTTAGGGGGAA 29133          C___     ATTTC
           TG                       CATTCCTTCTAA    AGAATT
                                    ||||||||||||    ||||||
                                    GTAAGGGGGATT    TCTTAG
                                        TTTC     AG
GAM705  KIAA0321 3' GGGTGGTGGGGGGGAGCGGGTG  63060      _    AA  GAA    TT
                                CATTC CTTCT  CA   TTAT  C
                                ||||| |||||  ||   ||||  |
                                GTGGG GAGGG  GT   GGTG  G
                                  C    GG  ___    GG
GAM705  KIAA0426 3' TGCTGAATTTTGTTGGGGGGAA 28937              ATTTC
           TG                     CATTCCTTCTAACAGAATT
                                  ||||||||||||||||||
                                  GTAAGGGGGGTTGTTTTAA
                                        GTCGTA
GAM705  KIAA0638 3' GAGATGATGCAGCAGAGGGGA  72829        AACAGA
                                TTCCTTCT     ATTATTTC
                                ||||||||     ||||||||
                                AGGGGAGA     TAGTAGAG
                                    CGACG_
GAM705  KIAA0831 3' CCTTTGATTTTGTTTGGGAGGG 30632          _       TTTC
           GTG                      CATTCCTTCTAA CAGAATTA
                                    |||||||||||| ||||||||
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                                GTGGGGAGGGTT GTTTTAGT
                                      T       TTCCT
GAM705  KIAA0924  3'  GAAATGATTTGCAGGGGATG  30363        CTAACA
                                CATTCCTT     GAATTATTTC
                                ||||||||     ||||||||||
                                GTAGGGGA     TTTAGTAAAG
                                   CG____
GAM705  KIAA1012  3'  GAGATGATTCTGAGAAAGGAA  30730      _  AA
                                TTCCTT CT  CAGAATTATTTC
                                ||||||  ||  ||||||||||||
                                AAGGAA GA  GTCTTAGTAGAG
                                   A  __
GAM705  KIAA1183  3'  GAGATGATTCCAGAAAGGAA   63193      _  AACA
                                TTCCTT CT    GAATTATTTC
                                ||||||  ||    ||||||||||
                                AAGGAA GA    CTTAGTAGAG
                                   A  C___
GAM705  KIAA1300  3'  GAGGTGAGTGGCTTGTTGGGAG 63524          _ AA__
            GAA                    TTCCTTCTAACA G    TTATTTC
                                ||||||||||||  |    |||||||
                                AAGGAGGGTTGT C    AGTGGAG
                                      T GGTG
GAM705  KIAA1348  3'  GAGGTGGTGGGCAGGAGGGAG  69123        AACAGA
                                TTCCTTCT     ATTATTTC
                                ||||||||     ||||||||
                                GAGGGAGG     TGGTGGAG
                                   ACGGG_
GAM705  KIAA1432  5'  GGAATGACAAATGGAAGGAA   67306        ACAGAA
                                TTCCTTCTA     TTATTTC
                                |||||||||     |||||||
                                AAGGAAGGT     AGTAAGG
                                   AAAC__
GAM705  KIAA1485  3'  GGGTGGGGGTAGGGGGATTG   90769    T      A AGAA    TT
                                CA TCCTTCTA C    TTAT  C
                                || ||||||||  |    ||||  |
                                GT AGGGGGAT G    GGTG  G
                                 T       _ GG__    GG
GAM705  KIAA1577  3'  GGTGGGGATGGGAGGGATG    65102         ACAGAA    TT
                                CATTCCTTCTA     TTAT  C
                                ||||||||||     ||||  |
                                GTAGGGAGGGT     GGTG  G
                                      AGG___    G
GAM705  KIAA1822  3'  GGAGTGTGTGTTGGGGGCGGTG 68191     TC       GAAT
                                CAT  CTTCTAACA    TATTTC
                                |||  |||||||||   ||||||
                                GTG  GGGGGTTGT    GTGAGG
                                  GC       GT__
GAM705  LCHN     3'  GAGGTGGGAGTGGGAGGTAGTG 87472      _      ACAGAA
                                CATT CCTTCTA     TTATTTC
                                ||||  |||||||     |||||||
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                                GTGA GGAGGGT     GGTGGAG
                                  T      GAG___
GAM705  LY6G5B   5' GGAATAGGTCTTTGGAGGGTAT 41403     T      C   A
            G                    CAT CCTTCTAA AGA TTATTTC
                                ||| |||||||| ||| |||||||
                                GTA GGGAGGTT TCT GATAAGG
                                  T      _   G
GAM705  MGC11242 3' GAGGTGGGCATGGCAGGGAATG 44483        CTAA  GAA
                                CATTCCTT   CA   TTATTTC
                                ||||||||   ||   |||||||
                                GTAAGGGA   GT   GGTGGAG
                                     CG__  ACG
GAM705  MGC14156 3' GAAATAATTCCAAAGGAGTG  52958        CTAACA
                                CATTCCTT     GAATTATTTC
                                ||||||||     ||||||||||
                                GTGAGGAA     CTTAATAAAG
                                     AC____
GAM705  MGC23918 3' GATGGTCTTGGGCAGGGATG  59191       T  AAC   A   TT
                                CATTCCT CT   AGA TTAT  C
                                ||||||| ||   ||| ||||  |
                                GTAGGGA GG   TCT GGTA  G
                                     C  GT_  _   G
GAM705  MGC2477  3' GGATGTCTTTGGGAGGGAA   44306       AA   AT   TT
                                TTCCTTCT  CAGA  TAT  C
                                ||||||||  ||||  |||  |
                                AAGGGAGG  GTTT  GTA  G
                                     __   CT   GG
GAM705  MMPL1    3' GGGATATGGCTTGAGGAGGGAT 15965        AAC  AAT   TT
            G                    CATTCCTTCT   AG   TAT  C
                                ||||||||||   ||   |||  |
                                GTAGGGAGGA   TC   ATA  G
                                     GT_  GGT   GG
GAM705  MOST2    5' GGGATGGCGTGGGTTGGAGGGG 40069        AGAA_   TT
                                TCCTTCTAAC    TTAT  C
                                ||||||||||    ||||  |
                                GGGGAGGTTG    GGTA  G
                                     GGTGC   GG
GAM705  MRG15    5' GGGTGGTGGGAGAAGGAG    23285       AA  GAA   TT
                                TTCCTTCT  CA   TTAT  C
                                ||||||||  ||   ||||  |
                                GAGGAAGA  GT   GGTG  G
                                     GG  ___   GG
GAM705  MRPS24   3' GGAATGGTATGTGGGGGAA   50131       TA  GA
                                TTCCTTC  ACA  ATTATTTC
                                |||||||  |||  ||||||||
                                AAGGGGG  TGT  TGGTAAGG
                                     __  A_
GAM705  MY038    5' GAAGTGATTCTGAGTATCGGGG 51924      TAA___
            G                    CCTTC     CAGAATTATTTC
                                |||||     ||||||||||||
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                              GGGGG    GTCTTAGTGAAG
                                 CTATGA
GAM705  P2RXL1   3' GGAGTGATGGGGGAGGGGG  19562       AA  GAA
                              TTCCTTCT  CA   TTATTTC
                              ||||||||  ||   |||||||
                              GGGGGAGG  GT   AGTGAGG
                                   GG  ___
GAM705  PDE3A    3' GGATGGTTTGAGAGGGG    76071       AACA     TT
                              TCCTTCT   GAATTAT  C
                              |||||||   ||||||| |
                              GGGGAGA   TTTGGTA  G
                                   G___     GG
GAM705  PIP3-E   3' GAAATGGACTGTGGAAGGGG  67351        A   AA
                              TTCCTTCTA CAG  TTATTTC
                              ||||||||| |||  |||||||
                              GGGGAAGGT GTC  GGTAAAG
                                   _  A_
GAM705  POPX1    3' GAAGTAATTGGAATGAAGGAG  30474       TAACAG
                              TTCCTTC    AATTATTTC
                              |||||||    |||||||||
                              GAGGAAG    TTAATGAAG
                                   TAAGG_
GAM705  PRO2730  3' GGAATGATTGTTAAGAGAGAGT 48185     _ TC    GA
           G                   CATTC CT  TAACA  ATTATTTC
                              |||||  ||  |||||  ||||||||
                              GTGAG GA  ATTGT  TAGTAAGG
                                 A  GA   __
GAM705  PTD002   3' GAAATAATATAGGAAGGAA   32864       AACAGA
                              TTCCTTCT    ATTATTTC
                              ||||||||    ||||||||
                              AAGGAAGG    TAATAAAG
                                   ATA___
GAM705  PTK6     3' GGGGTGGTTCCGGGCTGGGGGG 21080    TT     ACA__     TT
           GCTG                   CA  CCTTCTA    GAATTAT  C
                              ||  |||||||   |||||||  |
                              GT  GGGGGGT    CTTGGTG  G
                                CG     CGGGC     GG
GAM705  RA-GEF-2 3' GGAGTAGTTTGGGGAGGAGGG 33413      AACA
                              TCCTTCT   GAATTATTTC
                              |||||||   ||||||||||
                              GGGAGGA   TTTGATGAGG
                                   GGGG
GAM705  SCYD1    3' GGGATGATTGGAGGGGGGAG  92559       AA  GA    TT
                              TTCCTTCT  CA  ATTAT  C
                              ||||||||  ||  |||||  |
                              GAGGGGGG  GT  TAGTA  G
                                   AG  __    GG
GAM705  SFRS5    3' GGTGGGATTTGGAAGGGGG   23625      AA   A_   TT
                              CCTTCT  CAGA  TTAT  C
                              ||||||  ||||  ||||  |
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                                GGGGGA  GTTT  GGTG  G
                                   AG   AG   G
GAM705  SLC6A13  3'  GGATGGCTGTGGAGGGAA   34003        A  AA   TT
                                TTCCTTCTA CAG  TTAT  C
                                ||||||||| |||  ||||  |
                                AAGGGAGGT GTC  GGTA  G
                                     _  __   GG
GAM705  STAT5A   3'  GAGATGATTCAGAAGGGGAGGG 13442       AACA__
           GA                    TTCCTTCT     GAATTATTTC
                                 ||||||||     ||||||||||
                                 AGGGGAGG     CTTAGTAGAG
                                     GGAAGA
GAM705  STK22B   3'  GGGTCGGGGTTGGGGGGCATG  54868    T       AGAATT  TT
                                 CAT CCTTCTAAC     AT  C
                                 ||| |||||||||     ||  |
                                 GTA GGGGGGTTG     TG  G
                                   C       GGGC__  GG
GAM705  THEA     3'  GGAGTGGTTTGAGATTAGGGAG 66891       CTAACA
           TG                    CATTCCTT     GAATTATTTC
                                 ||||||||     ||||||||||
                                 GTGAGGGA     TTTGGTGAGG
                                     TTAGAG
GAM705  ZFP91    3'  GGAATAAAGATAGAAGGGATG  54877         ACAGAA
                                 CATTCCTTCTA     TTATTTC
                                 ||||||||||     |||||||
                                 GTAGGGAAGAT     AATAAGG
                                       AGA___
GAM705  ZNF304   3'  AGATAATGGAGTGGGGATG   40679       T  AACAGA
                                 CATTCCT CT     ATTATTT
                                 ||||||| ||     |||||||
                                 GTAGGGG GA     TAATAGA
                                    T  GG____
GAM705  LOC126964 3'  GGAGTGAGAAGTGTGGAGGGGA 75117         ACAGAA
                                 TTCCTTCTA     TTATTTC
                                 |||||||||     |||||||
                                 AGGGGAGGT     AGTGAGG
                                      GTGAAG
GAM705  LOC129526 3'  GGAGTGATGAATGGAAGGGGG  75387      AA  GA_
                                 CCTTCT  CA   ATTATTTC
                                 ||||||  ||   ||||||||
                                 GGGGGA  GT   TAGTGAGG
                                    AG  AAG
GAM705  LOC130612 3'  AGATGGGGGTGGGGGGGTG   75463        TA  AGAA
                                 CATTCCTTC  AC    TTATTT
                                 |||||||||  ||    ||||||
                                 GTGGGGGGG  TG    GGTAGA
                                      __  GG__
GAM705  LOC130612 3'  GGGGTGGGCAGGCTTGGAGGGG 75469         CAGAA_   TT
           A                      TTCCTTCTAA     TTAT  C
                                  ||||||||||     ||||  |
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                                AGGGGAGGTT     GGTG  G
                                      CGGACG    GG
GAM705   LOC132228 3'  GGATAGTAGATGGGGAGGGA   75546        AA  GA_    TT
                                TCCTTCT  CA   ATTAT  C
                                |||||||  ||   |||||  |
                                AGGGAGG  GT   TGATA  G
                                    G_  AGA    GG
GAM705   LOC132948 3'  GAGTAATTGTTGTGAGGAGTG  59846        C    GA
                                CATTCCTT TAACA  ATTATTT
                                |||||||| |||||  |||||||
                                GTGAGGAG GTTGT  TAATGAG
                                     T    __
GAM705   LOC143146 3'  ATTTTGTTGGAGGTGGTG    60764     TC
                                CAT  CTTCTAACAGAAT
                                |||  ||||||||||||
                                GTG  GGAGGTTGTTTTA
                                  GT
GAM705   LOC143286 5'  AAATGGCTGGGGGGGGGG     83841       AA   AA
                                CCTTCT  CAG  TTATTT
                                ||||||  |||  ||||||
                                GGGGGG  GTC  GGTAAA
                                   GG   __
GAM705   LOC143286 3'  GAGACTCAATTGTTAGAATGAA 83844       C        AATTA
           TG                     CATTC TTCTAACAG     TTTC
                                |||||| |||||||||     ||||
                                GTAAG AAGATTGTT     AGAG
                                   T        AACTC
GAM705   LOC144319 5'  GGAATGGGCCCTGGGAGGAGTG 83989           ACAGAA
                                CATTCCTTCTA      TTATTTC
                                ||||||||||      |||||||
                                GTGAGGAGGGT     GGTAAGG
                                      CCCG__
GAM705   LOC144473 5'  GGTATTGTGGGGAGGGATG    83996          A    A
                                CATTCCTTCT ACAG ATT
                                |||||||||| |||| |||
                                GTAGGGAGGG TGTT TGG
                                      G    A
GAM705   LOC145134 5'  GGGATGATTTTACACGTGAGGG 84210        TAAC__       TT
           AG                     TTCCTTC     AGAATTAT  C
                                |||||||      ||||||||  |
                                GAGGGAG     TTTTAGTA  G
                                    TGCACA       GG
GAM705   LOC146050 3'  GAAGTGGTCAAAGGAGGGAA   78115        AACA  A
                                TTCCTTCT    GA TTATTTC
                                ||||||||    || |||||||
                                AAGGGAGG    CT GGTGAAG
                                     AAA_  _
GAM705   LOC146455 5'  GAAGTCCAGGTTAGAGGGAA   78459          AGAATT
                                TTCCTTCTAAC     ATTTC
                                ||||||||||      |||||
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                                AAGGGAGATTG      TGAAG
                                      GACC__
GAM705   LOC146714 5'  GAGATGGTTCTGAACTCAGGAG 84745       TCTAA
                                TTCCT     CAGAATTATTTC
                                |||||     ||||||||||||
                                GAGGA     GTCTTGGTAGAG
                                   CTCAA
GAM705   LOC146714 5'  GGAGTGATTCGCAGAGGGGGAG 84748         AACA
                                TTCCTTCT    GAATTATTTC
                                ||||||||    ||||||||||
                                GAGGGGGA    CTTAGTGAGG
                                     GACG
GAM705   LOC146880 5'  GAAAGGCCCTGTTGGGGGAGGT 78749     TC         AATTA
            G                    CAT  CTTCTAACAG     TTTC
                                |||  ||||||||||     ||||
                                GTG  GGGGGTTGTC     AAAG
                                  GA         CCGG_
GAM705   LOC149127 3'  GAGGTGGCTGTTTGGAGGGAA  85500          _   AA
                                TTCCTTCTAA CAG  TTATTTC
                                ||||||||||| |||  |||||||
                                AAGGGAGGTT GTC  GGTGGAG
                                      T   __
GAM705   LOC149149 3'  GAAATGGTGAGGAGGGGGAA   85523         AACAGA
                                TTCCTTCT      ATTATTTC
                                ||||||||      ||||||||
                                AAGGGGGA      TGGTAAAG
                                     GGAG__
GAM705   LOC150291 3'  AGGTGATGAGGAGGAAT      86128          AACAGA
                                ATTCCTTCT     ATTATTT
                                |||||||||     |||||||
                                TAAGGAGGA     TAGTGGA
                                      G_____
GAM705   LOC152373 5'  GGAATAGTTTCAGTAGGAATG  81451         T  AACA
                                CATTCCT CT    GAATTATTTC
                                ||||||| ||    ||||||||||
                                GTAAGGA GA    TTTGATAAGG
                                     T  C___
GAM705   LOC152373 5'  GGAGTGGTTTTGGTATCAGGA  81452      TCTAA
                                TCCT     CAGAATTATTTC
                                ||||     ||||||||||||
                                AGGA     GTTTTGGTGAGG
                                   CTATG
GAM705   LOC153592 3'  GGAGTAATTCTGTGGTTGAATG 87247       CTT   A
                                CATTC   CTA CAGAATTATTTC
                                |||||   ||| ||||||||||||
                                GTAAG   GGT GTCTTAATGAGG
                                   TT_  _
GAM705   LOC157273 3'  GAGGTAAAGCCATTGGGAGGTA 87721      _       CAGAA
            ATG                    CATT CCTTCTAA     TTATTTC
                                |||| ||||||||     |||||||
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                                GTAA GGAGGGTT    AATGGAG
                                  T       ACCGA
GAM705  LOC157273 3'  GGATGATATCTGGATGGGATG  87724       T  TAA   _    TT
                                CATTCC TC   CAGA ATTAT  C
                                |||||| ||   |||| |||||  |
                                GTAGGG AG   GTCT TAGTA  G
                                   T ___    A    GG
GAM705  LOC157556 3'  GAAGTACCACAGCTGGAAGGGG 87782          ACAGAAT
          TG                     CATTCCTTCTA      TATTTC
                                ||||||||||       ||||||
                                GTGGGGAAGGT      ATGAAG
                                      CGACACC
GAM705  LOC157621 3'  GGAGTGGATGTGGAGGGAAT   87791         A  GAAT
                                ATTCCTTCTA CA    TATTTC
                                |||||||||| ||    ||||||
                                TAAGGGAGGT GT    GTGAGG
                                      _  AG__
GAM705  LOC157622 3'  GGAGTGGATGTGGAGGGAAT   87796         A  GAAT
                                ATTCCTTCTA CA    TATTTC
                                |||||||||| ||    ||||||
                                TAAGGGAGGT GT    GTGAGG
                                      _  AG__
GAM705  LOC158191 3'  AAATGGTTTGGAGAGGAA    82658       T  AACA
                                TTCCT CT    GAATTATTT
                                ||||| ||    |||||||||
                                AAGGA GA    TTTGGTAAA
                                   _  GG__
GAM705  LOC158263 3'  GATTCTGTTGGGAGGAATG    82729
                                CATTCCTTCTAACAGAATT
                                |||||||||||||||||||
                                GTAAGGAGGGTTGTCTTAG

GAM705  LOC159110 5'  GGAGTGGTTGTCCGAGGGTGTG 82992     T    TA   GA
                                CAT CCTTC  ACA  ATTATTTC
                                ||| |||||  |||  ||||||||
                                GTG GGGAG  TGT  TGGTGAGG
                                  T    CC   __
GAM705  LOC159116 5'  GGAGTGGTTGTCCGAGGGTGTG 82975     T    TA   GA
                                CAT CCTTC  ACA  ATTATTTC
                                ||| |||||  |||  ||||||||
                                GTG GGGAG  TGT  TGGTGAGG
                                  T    CC   __
GAM705  LOC168667 3'  AAATGATGGAGAAGGGA     94334         AACAGA
                                TTCCTTCT     ATTATTT
                                ||||||||     |||||||
                                AGGGAAGA     TAGTAAA
                                     GG____
GAM705  LOC196205 3'  GAGGTGATAGGAATTGGAAGGA 88975          CAGA_
          G                      TTCCTTCTAA    ATTATTTC
                                ||||||||||    ||||||||
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                                GAGGAAGGTT    TAGTGGAG
                                      AAGGA
GAM705  LOC196540 5'  GGAATGGTGGTTGGAGGTGGTG 91204    TC      AGA
                                CAT  CTTCTAAC   ATTATTTC
                                |||  ||||||||   ||||||||
                                GTG  GGAGGTTG   TGGTAAGG
                                  GT       G__
GAM705  LOC196761 3'  GAAGTGACCTTGTGAGGAGTG  91119       CTA   AA
                                CATTCCTT   ACAG  TTATTTC
                                ||||||||   ||||  |||||||
                                GTGAGGAG   TGTT  AGTGAAG
                                     ___    CC
GAM705  LOC197117 3'  GGTGTTGTTGGGAGCAGTG   91284     C       A
                                CATT CTTCTAACAG ATT
                                |||| |||||||||| |||
                                GTGA GAGGGTTGTT TGG
                                   C        G
GAM705  LOC200830 3'  GAGGTGATTGGATCATGGGGGA 91728        TAACAG_
          ATG                     CATTCCTTC      AATTATTTC
                                |||||||||      |||||||||
                                GTAAGGGGG      TTAGTGGAG
                                     TACTAGG
GAM705  LOC201283 3'  GGGTGATTTTGTTTTTAGAAG  61051       ___       TT
                                CTTCTA   ACAGAATTAT  C
                                ||||||   ||||||||||  |
                                GAAGAT   TGTTTTAGTG  G
                                    TTT        GG
GAM705  LOC203378 5'  GAAATAATTGTTAGGGAAGGA  92288       AACAG
                                TCCTTCT    AATTATTTC
                                |||||||    |||||||||
                                AGGAAGG    TTAATAAAG
                                    GATTG
GAM705  LOC221468 3'  GAATGATTCTCGGGAG     60005      AAC
                                CTTCT   AGAATTATTT
                                |||||   ||||||||||
                                GAGGG   TCTTAGTAAG
                                   C__
GAM705  LOC221683 5'  GAAATGGGGGTAGGGGGAG   95327        A AGAA
                                TTCCTTCTA C    TTATTTC
                                |||||||| |    |||||||
                                GAGGGGGAT G    GGTAAAG
                                     _ GG__
GAM705  LOC221747 3'  GAGGTGATTTAATTATGGGGGT 93964       TC   CA
          G                      CATTCCT  TAA  GAATTATTTC
                                |||||||  |||  ||||||||||
                                GTGGGGG  ATT  TTTAGTGGAG
                                    T_   AA
GAM705  LOC221865 3'  GGAGTGGTTGAAGGAAGGCAGT 94088     _     AA  GA
          G                      CATT CCTTCT  CA  ATTATTTC
                                |||| ||||||  ||  ||||||||
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                                GTGA GGAAGG  GT  TGGTGAGG
                                  C     AA  __
GAM705  LOC221914 3'  GAAGTTGGAAGTGGGGAGGGGT 95564          A  AGAATT
          G                        CATTCCTTCT AC      ATTTC
                                   |||||||||| ||      |||||
                                   GTGGGGAGGG TG      TGAAG
                                        G  AAGGT_
GAM705  LOC255486 5'  GAAAGGCCCTGTTGGGGGAGGT 96900     TC         AATTA
          G                        CAT  CTTCTAACAG     TTTC
                                   |||  ||||||||||     ||||
                                   GTG  GGGGGTTGTC     AAAG
                                     GA         CCGG_
GAM705  LOC256176 5'  GGAATAGTTTCAGAAGGAATG  98281          AACA
                                   CATTCCTTCT    GAATTATTTC
                                   ||||||||||    ||||||||||
                                   GTAAGGAAGA    TTTGATAAGG
                                        C___
GAM705  LOC51102  3'  GAGTGACATGGGAGGGGA    64605        AA  GAA
                                   TTCCTTCT  CA   TTATTT
                                   ||||||||  ||   ||||||
                                   AGGGGAGG  GT   AGTGAG
                                        __  AC_
GAM705  LOC51644  3'  GAATAGTTCATAGGGAAGG    32665       AACA
                                   CCTTCT    GAATTATTT
                                   ||||||    |||||||||
                                   GGAAGG    CTTGATAAG
                                      GATA
GAM705  LOC90495  3'  GGAATAATAGGTAGAGGGAA   63738         A AGA
                                   TTCCTTCTA C   ATTATTTC
                                   |||||||||| |   ||||||||
                                   AAGGGAGAT G   TAATAAGG
                                        _ GA_
GAM705  LOC90750  3'  GAGGTAATTTAAGGAGGGAA   64629        AACA
                                   TTCCTTCT    GAATTATTTC
                                   ||||||||    ||||||||||
                                   AAGGGAGG    TTTAATGGAG
                                        AA__
GAM705  LOC92267  3'  GGAGTGTTATTTGGAAGGAGTG 69172           CAG   T
                                   CATTCCTTCTAA   AAT ATTTC
                                   ||||||||||||   ||| |||||
                                   GTGAGGAAGGTT   TTG TGAGG
                                          TA_   _
GAM705  LOC93132  5'  GAAGTGGGCCTTTGGGAGGGAT 71988          C  AA
                                   ATTCCTTCTAA AG  TTATTTC
                                   |||||||||||| ||  |||||||
                                   TAGGGAGGGTT TC  GGTGAAG
                                          _  CG
GAM706  APPBP2    3'  GGCAATTTCAATGGCATA     22119        C    ACTTAG
                                   TATGCCA TGAAA     GTC
                                   ||||||| |||||     |||
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                                ATACGGT ACTTT     CGG
                                    A    AA____
GAM706  ATF6    3'  AGAACAATGTTTCTTCAGTGGC 64651         __   TTAG  C
            A                    TGCCACTGAA  AAC   GT CT
                                 ||||||||||  |||   || ||
                                 ACGGTGACTT  TTG   CA GA
                                      CT   TAA_  A
GAM706  HSPA8   3'  AGGACCTAAATTCGTAGCA   22736    C  T   AAC
                                 TGC AC GAA   TTAGGTCCT
                                 ||| || |||   |||||||||
                                 ACG TG CTT   AATCCAGGA
                                   A  _   A__
GAM706  LPIN2   3'  ACACAGTTCTCAGTGGCA    28426        A    TAG
                                 TGCCACTGA AACT   GT
                                 |||||||| ||||   ||
                                 ACGGTGACT TTGA   CA
                                      C    CA_
GAM706  MANBA   3'  AGGTTGTATTTTCAGTGGACA  20956    _       CT   GT
                                 TG CCACTGAAAA  TAG  CCT
                                 || ||||||||||  |||  |||
                                 AC GGTGACTTTT  GTT  GGA
                                   A        AT   __
GAM706  SCO1    3'  CCAGGTTTTCAGTGACATA    17161     C         A
                                 TATG CACTGAAAACTT GG
                                 |||| ||||||||||| ||
                                 ATAC GTGACTTTTGGA CC
                                   A         _
GAM706  SURF6   3'  AGGTGAATTTTAGTGGCATA   23131          ___
                                 TATGCCACTGAAA   ACTT
                                 ||||||||||||   ||||
                                 ATACGGTGATTTT   TGGA
                                        AAG
GAM706  CSMD1   3'  GCTGGGAGTTTTCAGTGGCA   73516           A_
                                 TGCCACTGAAAACTT  GGT
                                 ||||||||||||||  |||
                                 ACGGTGACTTTTGAG  TCG
                                        GG
GAM706  HBXAP   5'  GAATTAGGTTTTTCAGTAGCA  33881    C      _    G
                                 TGC ACTGAAAA CTTAG TC
                                 ||| |||||||| ||||| ||
                                 ACG TGACTTTT GGATT AG
                                   A       T    A
GAM706  KIAA1922 5' AGGACCTGGCCCAGCAGCA   73984    CA   AAAAC
                                 TGC  CTG    TTAGGTCCT
                                 |||  |||    |||||||||
                                 ACG  GAC    GGTCCAGGA
                                   AC   CC___
GAM706  KIAA1958 3' AGGGCGAATCTTCAGTGGCAT  82774         AAC  AG
                                 ATGCCACTGAA   TT  GTCCT
                                 ||||||||||   ||  |||||
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                                TACGGTGACTT  AA  CGGGA
                                     CT_  G_
GAM706  MGC2488   3'  GAGTAGATTTCAGTGGCA    44089          ___
                                TGCCACTGAAA  ACTT
                                ||||||||||  ||||
                                ACGGTGACTTT  TGAG
                                     AGA
GAM706  PDZD2     3'  GGTCGTCTTCAGTGGCA     81729         A  TTA  T
                                TGCCACTGAA AC  GG CC
                                |||||||||| ||  || ||
                                ACGGTGACTT TG  CT GG
                                     C  ___  _
GAM706  POLR3F    3'  AGGACATATTTTCAGTACATA  60615     CC       CTTAG
                                TATG  ACTGAAAA    GTCCT
                                ||||  ||||||||    |||||
                                ATAC  TGACTTTT    CAGGA
                                  A_      ATA__
GAM706  SCLY      3'  AGGAGTCATTTTCAGTGG    33669         CTTA  _
                                CCACTGAAAA   GG TCCT
                                ||||||||||   || ||||
                                GGTGACTTTT   CT AGGA
                                     A___  G
GAM706  SLC12A5   3'  ACCCAAGTTTTCTGTGC     40766    C  T      A
                                GC AC GAAAACTT GGT
                                || || |||||||| |||
                                CG TG CTTTTGAA CCA
                                 _  T      C
GAM706  SLC26A7   3'  AGGACCTAATAGAGTGACATA  54510     C   GAAAAC
                                TATG CACT     TTAGGTCCT
                                |||| ||||     |||||||||
                                ATAC GTGA     AATCCAGGA
                                  A   GAT___
GAM706  LOC148022 5'  AGGACCCCAGGACCCAGTGGCG 79317        AAAA  TA
                                TGCCACTG   CT  GGTCCT
                                ||||||||   ||  ||||||
                                GCGGTGAC   GA  CCAGGA
                                     CCAG  CC
GAM706  LOC149103 5'  AGGACCTAAACAAAGTTTTGCA 79937      C__   GAAAAC
           TA                    TATGC   ACT     TTAGGTCCT
                                |||||   |||     |||||||||
                                ATACG   TGA     AATCCAGGA
                                   TTT   AACA__
GAM706  LOC158714 3'  AGGACCTAAATTTGTAGCA   82868     C  TGA   C
                                TGC AC   AAA TTAGGTCCT
                                ||| ||   ||| |||||||||
                                ACG TG   TTT AATCCAGGA
                                  A  ___   A
GAM706  LOC159199 5'  AGGACCTGGTGTTCATGGCA  83056      C   A   T
                                TGCCA TGAA ACT AGGTCCT
                                ||||| |||| ||| |||||||
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                                ACGGT ACTT TGG TCCAGGA
                                  _   G  _
GAM706  LOC197317 5'  GACCTGAGCTCAGAGCA    91310    CA   AAA
                                TGC  CTGA   CTTAGGTC
                                |||  ||||   ||||||||
                                ACG  GACT   GAGTCCAG
                                  A_   C__
GAM706  LOC201910 3'  AGTTTTCTTCAGTGGCATG   90551          ___
                                TATGCCACTGAA   AACT
                                ||||||||||||   ||||
                                GTACGGTGACTT   TTGA
                                       CTT
GAM706  LOC221979 3'  AGGACCTAAATTTGTAGCA   94217    C  TGA   C
                                TGC AC   AAA TTAGGTCCT
                                ||| ||   ||| |||||||||
                                ACG TG   TTT AATCCAGGA
                                  A ___  A
GAM706  LOC91549  3'  AGGACCTAAATCAGAATCATA  67022     CCA   AAAC
                                TATG   CTGA   TTAGGTCCT
                                ||||   ||||   |||||||||
                                ATAC   GACT   AATCCAGGA
                                  TAA   A___
GAM707  CDH12     3'  CTTATCATTTAAAGTGGTGTA  15777        CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM707  GOCAP1    3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM707  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090      T   AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                   _   GTCA_
GAM707  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
          A                      TACAC       AGAAGAATAAG
                                 |||||       ||||||||||
                                 ATGTG       TCTTCTTATTC
                                    TACTCCC_
GAM707  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126        CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM707  HMP19     3'  CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
          TA                     TACA   TCC   GAAGAATAAG
                                 ||||   |||   ||||||||||
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                              ATGT   AGG   TTTCTTATTC
                                AAA_  ATTG
GAM707  KIAA1719 3' TCTGTCTTGGGAGTGGTGTA  68742           _
                              TACACCACTCCCAAGA AGA
                              |||||||||||||||| |||
                              ATGTGGTGAGGGTTCT TCT
                                       G
GAM707  KIAA1853 3' TTTTTCTTGGAAGCAGTG    69929    CA  C
                              CAC  CT CCAAGAAGAA
                              |||  || ||||||||||
                              GTG  GA GGTTCTTTTT
                                AC  A
GAM707  KIAA1877 3' CTTATTCTTCTGCCATGAGT  66748     CCA__
                              ACTC    AGAAGAATAAG
                              ||||    ||||||||||
                              TGAG    TCTTCTTATTC
                                TACCG
GAM707  KIAA1906 3' CTTATTCTTCTTGACTTTTGG 73571    CTCC_
                              CCA    CAAGAAGAATAAG
                              |||    ||||||||||||
                              GGT    GTTCTTCTTATTC
                                TTTCA
GAM707  OSBPL11  3' CTTAATTTCCCAAGAGTGGTG 43206       CCAA   AA
                              CACCACTC   GAAG  TAAG
                              ||||||||   ||||  ||||
                              GTGGTGAG   CTTT  ATTC
                                   AACC   A_
GAM707  YME1L1   3' TCATTCTTGATGTGGTGTA   58438       TCC    _
                              TACACCAC   CAAGAA GA
                              ||||||||   ||||||  ||
                              ATGTGGTG   GTTCTT CT
                                   TA_    A
GAM707  ZNF262   3' CTTATTTTGTTTGGGAGT    18723        A
                              ACTCCCAAG AGAATAAG
                              ||||||||| ||||||||
                              TGAGGGTTT TTTTATTC
                                   G
GAM707  LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_   AAGA
                              TACACCAC   CCAAG   ATA
                              ||||||||   |||||   |||
                              ATGTGGTG   GGTTC   TGT
                                   CAA    GG__
GAM708  BCL2     3' GAAGTCCGCAGAACCTGC    7235        T  T  G
                              GCAGGTTCT CG GA TTC
                              ||||||||| || || |||
                              CGTCCAAGA GC CT AAG
                                   C  _  G
GAM708  C6.1A    3' CGAGGAGAAAAAAGAACCTCT  44530    C      CGTGAG
                              AG AGGTTCTT     TTCCTCG
                              || ||||||||     |||||||
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                                TC TCCAAGAA     GAGGAGC
                                 _      AAAA__
GAM708  CBX6    3' AGGTGCTACGAGAACCTGC   27405        T  G  T
                                GCAGGTTCT CGT AGT CCT
                                ||||||||| ||| ||| |||
                                CGTCCAAGA GCA TCG GGA
                                     _  _  T
GAM708  LOXL4   3' AGGGGCACCAAGAACCTGCT  50855         C  GA
                                AGCAGGTTCTT GT  GTTCCT
                                |||||||||||  ||  ||||||
                                TCGTCCAAGAA CA  CGGGGA
                                      C  __
GAM708  MGC10646 3' AGGAACTTTGAGACCTGC   52077       CT  T
                                GCAGGTT  TCG GAGTTCCT
                                |||||||  ||| ||||||||
                                CGTCCAG  AGT TTCAAGGA
                                   __  _
GAM708  PSKH1   5' CGAGACGCCGAAGAGCCCGC  68794   A       TGA  TC
                                GC GGTTCTTCG  GT  CTCG
                                || |||||||||  ||  ||||
                                CG CCGAGAAGC  CA  GAGC
                                 C       CG_ __
GAM709  AKAP1   3' ACTATGGGTTCTCTTCGCAAA 14472     A  CTT      C
                                TTTGT GA  GGAACCCA AGT
                                ||||| ||  |||||||| |||
                                AAACG CT  TCTTGGGT TCA
                                   _ TC_      A
GAM709  AKAP1   3' ACTATGGGTTCTCTTCGCAAA 58373     A  CTT      C
                                TTTGT GA  GGAACCCA AGT
                                ||||| ||  |||||||| |||
                                AAACG CT  TCTTGGGT TCA
                                   _ TC_      A
GAM709  EGF     3' ACTATAGGTTTTGGTTCCACAA 10488     A  C TG    CAC
                                TTGT GA T  GAACC   AGT
                                |||| || |  |||||   |||
                                AACA CT G  TTTGG   TCA
                                  C  T GT    ATA
GAM709  EZH1    3' GACTGTGGGTTCCAAATTAC  10551     AC
                                GTAG  TTGGAACCCACAGTC
                                ||||  ||||||||||||||
                                CATT  AACCTTGGGTGTCAG
                                  A_
GAM709  STAC    3' GACTGTGGAGTAATAGCCACAA 13427     AGA  TGGA  _
           A                     TTTGT   CT    AC CCACAGTC
                                |||||   ||    || ||||||||
                                AAACA   GA    TG GGTGTCAG
                                  CC_  TAA_  A
GAM709  CCR1    3' GACTGTGGGCTCCATTC    8927    CT   A
                                GA  TGGA CCCACAGTC
                                ||  |||| |||||||||
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                                CT  ACCT GGGTGTCAG
                                 T_    C
GAM709  FLJ10483  3'  GACTGTGGAAGAGATTACAAA  36652        A   GGAAC
                                TTTGTAG CTT    CCACAGTC
                                ||||||| |||    ||||||||
                                AAACATT GAG    GGTGTCAG
                                   A   AA___
GAM709  KIAA1871  3'  ACTGTAAGAGTCTACAAA    61890          GGAACCC
                                TTTGTAGACTT      ACAGT
                                ||||||||||       |||||
                                AAACATCTGAG      TGTCA
                                      AA_____
GAM709  LOC150821 3'  GGGTTCCACATCCACAAA    60944       A  CT
                                TTTGT GA  TGGAACCC
                                ||||| ||  ||||||||
                                AAACA CT  ACCTTGGG
                                   C  AC
GAM709  LOC151057 3'  ACTGTGGGTACACCTATAAA  86379        ACT  GA
                                TTTGTAG   TG  ACCCACAGT
                                |||||||   ||  |||||||||
                                AAATATC   AC  TGGGTGTCA
                                   C__  A_
GAM709  LOC157507 5'  ACTGTAAAAGTCTGCAAA    82377          GGAACCC
                                TTTGTAGACTT      ACAGT
                                ||||||||||       |||||
                                AAACGTCTGAA      TGTCA
                                      AA_____
GAM709  LOC203339 5'  GGATTCCCAGTCTACAAA    92214          T    C
                                TTTGTAGACT GGAA CC
                                |||||||||| |||| ||
                                AAACATCTGA CCTT GG
                                      C    A
GAM709  LOC51030  3'  ACTGTAAATTAAACCAATCTAC 32695        C    AACCC___
          AAA                     TTTGTAGA TTGG       ACAGT
                                |||||||| ||||       |||||
                                AAACATCT AACC       TGTCA
                                   _   AAATTAAA
GAM709  LOC90906  3'  GACTGTGGATCCCAAACTTTGC 64951       C_    AAC
          A                      TGTAGA  TTGG   CCACAGTC
                                ||||||  ||||   ||||||||
                                ACGTTT  AACC   GGTGTCAG
                                   CA    CTA
GAM710  FGF13    3'  ACCAAGAAAATGTAAAAGACC  54441       CAGG  ___
                                GGTCTT    GC   TTCTTGGT
                                ||||||    ||   ||||||||
                                CCAGAA    TG   AAGAACCA
                                   AA__  TAA
GAM710  INSRR    3'  ACCCGTGGCCCTGAAGACGGTG 68987       G         TCTT
                                CACCG TCTTCAGGGCT    GGT
                                ||||| ||||||||||    |||
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                                GTGGC AGAAGTCCCGG   CCA
                                  _        TGC_
GAM710  LOXL3    3'  ACCAAGAAACCCATGTCAGC  51865   CTT _  C
                                GT  CA GGG TTCTTGGT
                                ||  || ||| ||||||||
                                CG  GT CCC AAGAACCA
                                 ACT A  A
GAM710  RAP1GA1  3'  ACCTCTGCCCTGAAGACC   12767         TTCTT
                                GGTCTTCAGGGC   GGT
                                ||||||||||||   |||
                                CCAGAAGTCCCG   CCA
                                       TCT__
GAM710  XRCC5    5'  ACCAAAGCGCCTGAGGACCGG 41239          _   CT
                                CCGGTCTTCAGG GCTT  TGGT
                                |||||||||||| ||||  ||||
                                GGCCAGGAGTCC CGAA  ACCA
                                       G   __
GAM710  EDG1     5'  CCACCCCTGAAGCCAGTG   60049    C  T     CTTCT
                                CAC GG CTTCAGGG   TGG
                                ||| || ||||||||   |||
                                GTG CC GAAGTCCC   ACC
                                 A  _      C____
GAM710  KIAA0323 3'  CCAAGAAGGGAAACGGTG   63947     GTC  AGGG
                                CACCG  TTC  CTTCTTGG
                                |||||  |||  ||||||||
                                GTGGC  AGG  GAAGAACC
                                  AA_  ____
GAM710  MGC15875 5'  ACCAGCGCCCGAAGGCCG   53011       A   TTC
                                CGGTCTTC GGGC  TTGGT
                                |||||||| ||||  |||||
                                GCCGGAAG CCCG  GACCA
                                     _   C__
GAM710  LOC199786 3' ACCAAGTTGCGGAGACCGGT  89730        AGG  TT
                                ACCGGTCTTC  GC  CTTGGT
                                ||||||||||  ||  ||||||
                                TGGCCAGAGG  CG  GAACCA
                                      ___  TT
GAM710  LOC200030 3' ACCAAGAAGTGGAAGAAGACC  80123       AGG_
                                GGTCTTC   GCTTCTTGGT
                                |||||||   ||||||||||
                                CCAGAAG   TGAAGAACCA
                                   AAGG
GAM710  LOC200030 3' ACCAAGAAGAGGAAGAAGACC  80119       AGGG_
                                GGTCTTC   CTTCTTGGT
                                |||||||   |||||||||
                                CCAGAAG   GAAGAACCA
                                   AAGGA
GAM710  LOC200030 3' ACCAAGAAGAGGAAGAAGACC  80120       AGGG_
                                GGTCTTC   CTTCTTGGT
                                |||||||   |||||||||
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                                CCAGAAG    GAAGAACCA
                                   AAGGA
GAM710  LOC200030 3'  ACCAAGAAGTGGAAGAAGACC  80121       AGG_
                                GGTCTTC    GCTTCTTGGT
                                |||||||    ||||||||||
                                CCAGAAG    TGAAGAACCA
                                   AAGG
GAM710  LOC200030 3'  ACCAAGAAGTGGAAGAAGACC  80122       AGG_
                                GGTCTTC    GCTTCTTGGT
                                |||||||    ||||||||||
                                CCAGAAG    TGAAGAACCA
                                   AAGG
GAM710  LOC204285 3'  ACCAAGAAGCTTCCAAACGAC  91009     TTCA__
                                GTC     GGGCTTCTTGGT
                                |||     ||||||||||||
                                CAG     TTCGAAGAACCA
                                  CAAACC
GAM710  LOC51629  3'  ACCAAGAAGCCCTCAGCCTGGT 32604       T  TC
           G                     CACCGG CT  AGGGCTTCTTGGT
                                |||||| ||  ||||||||||||
                                GTGGTC GA  TCCCGAAGAACCA
                                   C  C_
GAM711  ADH1B    3'  ATGGGGGCTTTCCAAAG     73039     C    CTGCT
                                CTT TGGA    GCCCCCAT
                                ||| ||||    ||||||||
                                GAA ACCT    CGGGGGTA
                                  _   TT___
GAM711  CAPN10   3'  ATGGAGGCCTCACACCCAGAGG 41445        AC_  CT   C
           GT                     ACCTTCTGG   TG  GCC CCAT
                                |||||||||   ||  ||| ||||
                                TGGGAGACC   AC  CGG GGTA
                                     CAC  TC   A
GAM711  CAPN10   3'  ATGGAGGCCTCACACCCAGAGG 43857        AC_  CT   C
           GT                     ACCTTCTGG   TG  GCC CCAT
                                |||||||||   ||  ||| ||||
                                TGGGAGACC   AC  CGG GGTA
                                     CAC  TC   A
GAM711  CAPN10   3'  ATGGAGGCCTCACACCCAGAGG 43859        AC_  CT   C
           GT                     ACCTTCTGG   TG  GCC CCAT
                                |||||||||   ||  ||| ||||
                                TGGGAGACC   AC  CGG GGTA
                                     CAC  TC   A
GAM711  CAPN10   3'  ATGGAGGCCTCACACCCAGAGG 43862        AC_  CT   C
           GT                     ACCTTCTGG   TG  GCC CCAT
                                |||||||||   ||  ||| ||||
                                TGGGAGACC   AC  CGG GGTA
                                     CAC  TC   A
GAM711  CAPN10   3'  ATGGAGGCCTCACACCCAGAGG 43865        AC_  CT   C
           GT                     ACCTTCTGG   TG  GCC CCAT
                                |||||||||   ||  ||| ||||
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                                TGGGAGACC   AC  CGG GGTA
                                     CAC  TC   A
GAM711  CAPN10   3'  ATGGAGGCCTCACACCCAGAGG 43868        AC_  CT   C
           GT                    ACCTTCTGG   TG  GCC CCAT
                                |||||||||   ||  ||| ||||
                                TGGGAGACC   AC  CGG GGTA
                                     CAC  TC   A
GAM711  CSNK1E   3'  ATGGAGACTGCTTCCAGAAGG  97355        CT  TGCCC
                                CCTTCTGGA  GC    CCAT
                                |||||||||  ||    ||||
                                GGAAGACCT  CG    GGTA
                                     T_  TCAGA
GAM711  DTNBP1   5'  GGCAGCAGCAGCCCGAGG    50439     T  A     CC
                                CTTC GG CTGCTGC  CC
                                |||| || |||||||  ||
                                GGAG CC GACGACG  GG
                                  C  _      AC
GAM711  IPP      3'  GGGCTATACAGTCCAGCAGG   20906     T      CT__
                                CCT CTGGACTG    GCCC
                                |||  ||||||||    ||||
                                GGA GACCTGAC    CGGG
                                  C       ATAT
GAM711  LILRB4   3'  ATGGAGACTCAGGACCCCAGAA 23384        ACTG   CCC__
           GG                    CCTTCTGG    CTG    CCAT
                                |||||||    |||    ||||
                                GGAAGACC    GAC    GGTA
                                     CCAG   TCAGA
GAM711  MECP2    3'  ATGGAGGCAGTAGGACAAGGTG 18384      TC  GA      C
                                CACCT  TG  CTGCTGCC CCAT
                                |||||  ||  |||||||| ||||
                                GTGGA  AC  GATGACGG GGTA
                                   __  AG       A
GAM711  MEL      3'  GGAAGCGAGGTCCCAGAAGG   19330        _   GC   CC
                                CCTTCTGG ACT  TGC  CC
                                |||||||| |||  |||  ||
                                GGAAGACC TGG  GCG  GG
                                     C   A_   AA
GAM711  PPP2R2C  3'  ATGAGGACAGCTGCAGAGGTG  62417      T   GACT   C  C
                                CACCT CTG    GCTG CC CAT
                                |||||  |||    |||| || |||
                                GTGGA GAC    CGAC GG GTA
                                   _   GT__    A  A
GAM711  RXRB     3'  ATGGGGAACTCCCCCAGAGGTG 42028      T    ACTGCTGC
                                CACCT CTGG       CCCCAT
                                |||||  ||||       ||||||
                                GTGGA GACC       GGGGTA
                                   _    CCCTCAA_
GAM711  SP3      5'  ATGGGGGTATAAATCAAGAA   83381      G  CTGC
                                TTCT GA    TGCCCCCAT
                                ||||  ||    |||||||||
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                                AAGA CT    ATGGGGGTA
                                  A  AAAT
GAM711  TCF1     3'  ATGAGGGCAGCAGCCAG     6782       A       C
                                CTGG CTGCTGCCC CAT
                                |||| ||||||||| |||
                                GACC GACGACGGG GTA
                                  _       A
GAM711  TRAF1    3'  GGCAAAGGGTCCAGAAGG    20176          GC_
                                CCTTCTGGACT   TGCC
                                ||||||||||   ||||
                                GGAAGACCTGG   ACGG
                                      GAA
GAM711  WNT5A    3'  GGTACACATCCAGAAGGT    14124          C_  C
                                ACCTTCTGGA  TG TGCC
                                |||||||||  || ||||
                                TGGAAGACCT  AC ATGG
                                     AC  _
GAM711  ATF3     3'  ATGGGAGGACTCCAGAAG    15730        CTGCTG  _
                                CTTCTGGA     CC CCCAT
                                ||||||||     || |||||
                                GAAGACCT     GG GGGTA
                                     CA____  A
GAM711  C20orf16 5'  GGAGCGGTTCCTAGAAGGTG  39241         _  _    G
                                CACCTTCT GGA CTGCT CC
                                |||||||| ||| ||||| ||
                                GTGGAAGA CCT GGCGA GG
                                     T  T    _
GAM711  C21orf41 3'  ATGGAGCGTGAAACCCAGAAGG 57170        ACTGC_  CC
                                CCTTCTGG     TGC  CCAT
                                ||||||||     |||  ||||
                                GGAAGACC     GCG  GGTA
                                     CAAAGT   A_
GAM711  FBX30    5'  GGAGGGTGTCCAGAAG      53747        TGCT   _
                                CTTCTGGAC    GCCC CC
                                |||||||||    |||| ||
                                GAAGACCTG    TGGG GG
                                     ____    A
GAM711  FLJ10468 3'  GGGTAGGTCCAGAAGGTG    36633          TG
                                CACCTTCTGGAC  CTGCCC
                                ||||||||||||  ||||||
                                GTGGAAGACCTG  GATGGG
                                      __
GAM711  FLJ14442 3'  GGGGGGAGTACAGAAGGT    52387        GAC    G
                                ACCTTCTG   TGCT CCCCC
                                ||||||||   |||| |||||
                                TGGAAGAC   ATGA GGGGG
                                     ___    G
GAM711  FLJ20651 3'  GGGCACCTGCACCCCAGAAGGT 35922         AC  ___
           G                     CACCTTCTGG  TGC   TGCCC
                                ||||||||||  |||   |||||
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                                GTGGAAGACC ACG  ACGGG
                                     CC  TCC
GAM711  FLJ21195 3' CAGCAGGCCCAGAAGGTG   42701       A_
                                CACCTTCTGG CTGCTG
                                |||||||||| ||||||
                                GTGGAAGACC GACGAC
                                     CG
GAM711  FLJ22169 3' TGGGGGCTTCCAGAGG    44235      CTGCT
                                CTTCTGGA   GCCCCCA
                                ||||||||   |||||||
                                GGAGACCT   CGGGGGT
                                    T____
GAM711  FLJ30663 3' ATGGAGGAAACAATCTAGAAG 79356      C CTG C
                                CTTCTGGA TG  CC CCAT
                                |||||||| ||  || ||||
                                GAAGATCT AC  GG GGTA
                                    A AAA A
GAM711  GIT2    3' ATGAAGGCGCACCAGAAGG   58286      AC  T  CC
                                CCTTCTGG TGC GCC CAT
                                |||||||| ||| ||| |||
                                GGAAGACC ACG CGG GTA
                                    __  _  AA
GAM711  H11     5' GGCTTGCAGCCCAGAAGG    27636      A  T_
                                CCTTCTGG CTGC GCC
                                |||||||| |||| |||
                                GGAAGACC GACG CGG
                                    C   TT
GAM711  HM74    3' GGGGATTAGCCCCAGAAGG   21202      ACT  C_
                                CCTTCTGG  GCTG CCCC
                                |||||||| |||| ||||
                                GGAAGACC  CGAT GGGG
                                    C__   TA
GAM711  KIAA0280 3' ATGAGGATGAGGCCCAGGAG  93289      ACT  GCC_ _
                                CTTCTGG  GCT   CC CAT
                                |||||||  |||   || |||
                                GAGGACC  CGG   GG GTA
                                   ___  AGTA  A
GAM711  KIAA0547 3' ATGGGGGCAAAAAGAAGAGTG 29588    _   GGACTGC
                                CAC CTTCT     TGCCCCCAT
                                ||| |||||     |||||||||
                                GTG GAAGA     ACGGGGGTA
                                  A   AAA____
GAM711  KIAA0945 3' ATGAAGGCCCTCCTCCCAGGAG 30898       ACTGCT_  CC
           GT                   ACCTTCTGG     GCC  CAT
                                |||||||||     |||  |||
                                TGGAGGACC     CGG  GTA
                                    CTCCTCC   AA
GAM711  KIAA1364 3' GGAGGGCAGCACAGAA     64353     GAC     _
                                TTCTG  TGCTGCCC CC
                                |||||  |||||||| ||
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                                AAGAC   ACGACGGG GG
                                  ___       A
GAM711  KIAA1505  5'  GGCTGTTGCACCCAGAGGTG   95848      T   AC   T  CC
                                CACCT CTGG  TGC GC  CC
                                ||||| ||||  ||| ||  ||
                                GTGGA GACC  ACG TG  GG
                                  _   C_   T  TC
GAM711  MGC10715  3'  GGGGACAACTCCAGAAGGT   44500         CTGC  C
                                ACCTTCTGGA    TG CCCC
                                ||||||||||    || ||||
                                TGGAAGACCT    AC GGGG
                                     CA__  A
GAM711  RASSF2    3'  ATGGAGTGGAAGCCCAGAAGG  29090        A  G TG CC
                                CCTTCTGG CT C  C  CCAT
                                |||||||| || |  |  ||||
                                GGAAGACC GA G  G  GGTA
                                     C  A GT A_
GAM711  RDH-E2    3'  GGGGCAGCAGTCTCAGGGGGTG 58071         _
                                CACCTTCTG GACTGCTGCCCC
                                ||||||||| ||||||||||||
                                GTGGGGGAC CTGACGACGGGG
                                     T
GAM711  SNRK      3'  GGGCCTAGTACAGAAGGTG    35279        G    CT
                                CACCTTCTG ACTG  GCCC
                                ||||||||| ||||  ||||
                                GTGGAAGAC TGAT  CGGG
                                     A    C_
GAM711  SRCAP     5'  GGGGTGTGGCCCGGAAGGTG   22846         ACT  TG _
                                CACCTTCTGG   GC  C CCCC
                                ||||||||||   ||  | ||||
                                GTGGAAGGCC   CG  G GGGG
                                     ___  GT T
GAM711  LOC134265 3'  ATGGGTTAGAAATCCAGGAGG  75652         CTG   CC
                                CCTTCTGGA   CTG  CCCAT
                                |||||||||   |||  |||||
                                GGAGGACCT   GAT  GGGTA
                                     AAA   T_
GAM711  LOC148293 3'  GCAGAGAGCAGAATGGTG     79529      _    GA  G
                                CACC TTCTG  CT CTGC
                                |||| |||||  || ||||
                                GTGG AAGAC  GA GACG
                                  T    GA  _
GAM711  LOC150397 3'  ATGAAAGCCACAGATCCAGAAG 80653         _   CT  CCC
                                CTTCTGGA CTG  GC   CAT
                                |||||||| |||  ||   |||
                                GAAGACCT GAC  CG   GTA
                                     A   AC  AAA
GAM711  LOC151657 5'  ATGAAAGCAGAGGACAGAAGGT 86653         GA  G    CCC
          G                    CACCTTCTG  CT CTGC   CAT
                               |||||||||  || ||||   |||
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                                GTGGAAGAC  GA GACG   GTA
                                     AG  _    AAA
GAM711   LOC153057 5'  ATGGGAACAGCTCTGGAAG   87097     TG  CT   CC
                                CTTC  GA  GCTG  CCCAT
                                ||||  ||  ||||  |||||
                                GAAG  CT  CGAC  GGGTA
                                  GT  __    AA
GAM711   LOC158263 5'  ATGGAAGAGTTGGTCCAGGA   82725         _  GCCC
                                TTCTGGACTG CT    CCAT
                                ||||||||||  ||    ||||
                                AGGACCTGGT GA    GGTA
                                      T  GAA_
GAM711   LOC204823 5'  TATGGAGACAGCAACCCAAAGA 91059       _____  AC    CCC    ___
            GAAGG                  CCTTCT   GG  TGCTG   CCAT   A
                                ||||||   ||  |||||   ||||   |
                                GGAAGA   CC  ACGAC   GGTA   T
                                   GAAA  CA    AGA   ___
GAM711   LOC220021 3'  ATGGAAGCAGCAGTTCCTGAA  95017     T  _     CC
                                TTC GGA CTGCTGC  CCAT
                                |||  |||  |||||||  ||||
                                AAG CCT GACGACG  GGTA
                                  T   T      AA
GAM711   LOC221474 5'  GGTGAGGTCCAAAGGTG     93999       C     GC
                                CACCTT TGGACT  TGCC
                                ||||||  ||||||  ||||
                                GTGGAA ACCTGG  GTGG
                                   _     A_
GAM711   LOC255294 5'  GGAAGTAGACAATCCAGAAG   96108        C  _   CC
                                CTTCTGGA TG CTGC  CC
                                ||||||||  ||  ||||  ||
                                GAAGACCT AC GATG  GG
                                     A  A    AA
GAM711   LOC257471 5'  ATGGGGGTATAAATCAAGAA   97387      G  CTGC
                                TTCT GA    TGCCCCCAT
                                ||||  ||    |||||||||
                                AAGA CT    ATGGGGGTA
                                  A  AAAT
GAM711   LOC92497  5'  GGCAGCAGTGACAAGGAG    70096       _ G_
                                CTTCT G  ACTGCTGCC
                                |||||  |  |||||||||
                                GAGGA C  TGACGACGG
                                   A AG
GAM712   GABRR2    3'  AACAATGCAGCAGCTACTGGAC 10753          CGAACAGT
                                GTCCAGTAGC       TTGTT
                                ||||||||||       |||||
                                CAGGTCATCG       AACAA
                                      ACGACGT_
GAM712   KLHL1     3'  AACAAACTGTCCTACT      40867       CCGA
                                AGTAG    ACAGTTTGTT
                                |||||    ||||||||||
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                                TCATC    TGTCAAACAA
                                  C___
GAM712  MS4A2    5'  AACAAACTGCACCCACTGAAC  41974    C    AGCCGAA
                                GT CAGT      CAGTTTGTT
                                || ||||      |||||||||
                                CA GTCA      GTCAAACAA
                                 A   CCCAC__
GAM712  SPK      5'  AACAAAGACCCACACTACTGGA 17872          CCGAACAG
           CA                     TGTCCAGTAG       TTTGTT
                                  ||||||||||       ||||||
                                  ACAGGTCATC       AAACAA
                                       ACACCCAG
GAM712  VAPA     3'  AACAAACTGTTCGGCTACTGGA 14544
           CA                     TGTCCAGTAGCCGAACAGTTTGTT
                                  ||||||||||||||||||||||||
                                  ACAGGTCATCGGCTTGTCAAACAA

GAM712  VAPA     3'  AACTGTTCGGCTACTGGACA   14545
                                TGTCCAGTAGCCGAACAGTT
                                ||||||||||||||||||||
                                ACAGGTCATCGGCTTGTCAA

GAM712  FLJ13315  3'  AACAAATAAAGGGCTACTG    47196        GAACA
                                CAGTAGCC    GTTTGTT
                                ||||||||    |||||||
                                GTCATCGG    TAAACAA
                                     GAAA_
GAM712  SYT13    3'  AACAAACTCTGAGGCCACCAGC 95089     CCA  A   GAAC
           A                     TGT   GT GCC    AGTTTGTT
                                 |||   || |||    ||||||||
                                 ACG   CA CGG    TCAAACAA
                                   AC_  C   AGTC
GAM712  LOC150372 5'  AACAAACTGCCACCCTGGAC   80600       TAGCCGAA
                                GTCCAG       CAGTTTGTT
                                ||||||       |||||||||
                                CAGGTC       GTCAAACAA
                                    CCACC___
GAM712  LOC253367 3'  GGACTCGGCCAGCTGGACA    99437        A_    ACA
                                TGTCCAGT  GCCGA   GTTT
                                ||||||||  |||||   ||||
                                ACAGGTCG  CGGCT   CAGG
                                     AC    ___
GAM712  LOC51622  5'  AACAAACTGAGTTCCACTG    32203     AGCC   __
                                CAGT    GAAC  AGTTTGTT
                                ||||    ||||  ||||||||
                                GTCA    CTTG  TCAAACAA
                                  C___    AG
GAM713  SCAMP1    3'  GCTAAATAAATATTCTCC    54500     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
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                                CCT TTATAA TAAATCG
                                  C     A
GAM713  SCAMP1   3'  GCTAAATAAATATTCTCC    54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM713  NX-17    3'  TGAATATCAGCCCCTAATA   40706        ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                     CGAC
GAM713  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
              TA                  TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM714  HADHB    5'  CTCGCGGACGTCAGCCAAGATT 5738          _ _  A  A
              CCA                   TGGAATCTTG C GGC TCC CGAG
                                ||||||||||  | ||| ||| ||||
                                ACCTTAGAAC G CTG AGG GCTC
                                      C A   C   C
GAM714  BHLHB2   5'  CTCAAAGCCGAAGATTCCA   14763         G   ATCCAC
                                TGGAATCTT CGGC     GAG
                                |||||||| ||||     |||
                                ACCTTAGAA GCCG     CTC
                                     _   AAA___
GAM714  CPSF1    3'  CGTGGATGCCGTCACCACCA  65160     AATCTT
                                TGG     GCGGCATCCACG
                                |||     ||||||||||||
                                ACC     TGCCGTAGGTGC
                                  ACCAC_
GAM714  DKFZP434K0427 3'  TCTCACAGATGTGCTGTATCC  50500     ATCT      CCAC__
                                GGA   TGCGGCAT     GAGA
                                |||   ||||||||     ||||
                                CCT   ATGTCGTG     CTCT
                                  _____       TAGACA
GAM714  FLJ14166  3'  TCTCGGTTCCGGAAGATTCCA  44992         G   CATCCA
                                TGGAATCTT CGG     CGAGA
                                |||||||| |||     |||||
                                ACCTTAGAA GCC     GCTCT
                                     G   TTG___
GAM714  FLJ20618  3'  TCTCACAAGGCTGCACCAGATT 35888         __     ATCCAC
              CCA                   TGGAATCT  TGCGGC     GAGA
                                ||||||||  ||||||     ||||
                                ACCTTAGA  ACGTCG     CTCT
                                     CC     GAACA_
GAM714  LOC125988 5'  TCTCAGAGCCGCAAGACACCA  74900     AA        A  CAC
                                TGG  TCTTGCGGC TC   GAGA
                                |||  |||||||| ||   ||||
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                                ACC  AGAACGCCG AG   CTCT
                                  AC        _ A__
GAM714  LOC148697 3'  TCTCGTGGACACCCACATCTCA 79681    GA  CT  C  CA
                                TG  AT  TG GG  TCCACGAGA
                                ||  ||  || ||  |||||||||
                                AC  TA  AC CC  AGGTGCTCT
                                 TC  C_  _  AC
GAM714  LOC195977 3'  GGATGCCGCCCAAGATTCC   88933        __
                                GGAATCTT  GCGGCATCC
                                ||||||||  |||||||||
                                CCTTAGAA  CGCCGTAGG
                                     CC
GAM715  MXI1     3'  CCACAGCAGCATTTTTATTTCA 56124        ACTACACC__
              GAT                   ATCTGAAA        GCTGTGG
                                ||||||||        |||||||
                                TAGACTTT        CGACACC
                                     ATTTTTACGA
GAM715  MXI1     3'  CCACAGCAGCATTTTTATTTCA 56125        ACTACACC__
              GAT                   ATCTGAAA        GCTGTGG
                                ||||||||        |||||||
                                TAGACTTT        CGACACC
                                     ATTTTTACGA
GAM715  TSN      3'  CCACACGCCCCAATTTTCAGGT 17296         CTACAC  C
              A                   TATCTGAAAA     CG TGTGG
                                ||||||||||     || |||||
                                ATGGACTTTT     GC ACACC
                                     AACCCC  _
GAM715  DKFZP547N043 3'  GTCGTGTATAATTTTTAGATA  50137         C__    C
                                TATCTGAAAA   TACAC GC
                                ||||||||||   ||||| ||
                                ATAGATTTTT   ATGTG TG
                                     AAT    C
GAM715  FLJ10326  3'  CAGCGGAGTCTTCAGATA    36500        A   ACA
                                TATCTGAA ACT   CCGCTG
                                ||||||||| |||   ||||||
                                ATAGACTT TGA   GGCGAC
                                     C  ____
GAM715  KIAA1046  3'  CCAATATGTTATTTTCAGATA  30660         CT   CCGCTG
                                TATCTGAAAA  ACA     TGG
                                ||||||||||  |||     |||
                                ATAGACTTTT  TGT     ACC
                                     AT   ATA____
GAM715  KIAA1726  3'  CCACAAATAGTGTAGTTTTAGA 67828         A     CGC_
              TA                   TATCTGAAA CTACAC    TGTGG
                                |||||||||| ||||||    |||||
                                ATAGATTTT GATGTG    ACACC
                                     _     ATAA
GAM715  TACTILE   3'  CAGTCAAGTCTTCAGATA    20583        A   ACACC
                                TATCTGAA ACT    GCTG
                                ||||||||| |||    ||||
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                                ATAGACTT TGA    TGAC
                                    C  AC___
GAM715  LOC145980 3'  CCACAGCAGGTGGAGTTTTCAG 84580        A  _
                                CTGAAAACT CACC GCTGTGG
                                ||||||||| |||| |||||||
                                GACTTTTGA GTGG CGACACC
                                    G   A
GAM715  LOC146988 3'  CGGTGAGTTTTCAAATA    84957    C      A
                                TAT TGAAAACT CACCG
                                ||| |||||||| |||||
                                ATA ACTTTTGA GTGGC
                                  A      _
GAM716  ATP1A2   3'  CCATCCCGATGAACCTGCA   7361       A    A  TTC
                                TGCAGG TCATC GG   GG
                                |||||| ||||| ||   ||
                                ACGTCC AGTAG CC   CC
                                   A    C  TA_
GAM716  B3GALT5  3'  TCATCCGAGGAAATGTCCCCGC 21340    A  AT   CAGG
           A                     TGC GG  CAT   TTCGGATGA
                                ||| ||  |||   |||||||||
                                ACG CC  GTA   GAGCCTACT
                                  C  CT   AAG_
GAM716  B3GALT5  3'  TCATCCGAGGAAATGTCCCCGC 53723    A  AT   CAGG
           A                     TGC GG  CAT   TTCGGATGA
                                ||| ||  |||   |||||||||
                                ACG CC  GTA   GAGCCTACT
                                  C  CT   AAG_
GAM716  B3GALT5  3'  TCATCCGAGGAAATGTCCCCGC 53727    A  AT   CAGG
           A                     TGC GG  CAT   TTCGGATGA
                                ||| ||  |||   |||||||||
                                ACG CC  GTA   GAGCCTACT
                                  C  CT   AAG_
GAM716  B3GALT5  3'  TCATCCGAGGAAATGTCCCCGC 53731    A  AT   CAGG
           A                     TGC GG  CAT   TTCGGATGA
                                ||| ||  |||   |||||||||
                                ACG CC  GTA   GAGCCTACT
                                  C  CT   AAG_
GAM716  B3GALT5  3'  TCATCCGAGGAAATGTCCCCGC 53737    A  AT   CAGG
           A                     TGC GG  CAT   TTCGGATGA
                                ||| ||  |||   |||||||||
                                ACG CC  GTA   GAGCCTACT
                                  C  CT   AAG_
GAM716  LAMC1    3'  CATTGCAGTCCTGATGATCCT  11264          TTCG_
                                AGGATCATCAGG    GATG
                                ||||||||||||    ||||
                                TCCTAGTAGTCC    TTAC
                                      TGACG
GAM716  TCFL4    3'  TCACTCTTCTGACATCCTGCA  64214        CA    TTC  _
                                TGCAGGAT  TCAGG   GGA TGA
                                ||||||||  |||||   ||| |||
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                                ACGTCCTA  AGTCT   TCT ACT
                                    C_    ___   C
GAM716  XYLB     3'  TCACCCAGAGTGACAAAATCCT 18830       CA__  GG  C  A
            GCA                   TGCAGGAT    TCA  TT GG TGA
                                ||||||||   |||  || || |||
                                ACGTCCTA    AGT  GA CC ACT
                                    AAAC   GA  C  _
GAM716  CHL1     3'  TCATCCAGAAGTCAACATCCTG 22767       CATCAGG  _
            CA                   TGCAGGAT      TTC GGATGA
                                ||||||||      ||| ||||||
                                ACGTCCTA      AAG CCTACT
                                    CAACTG_   A
GAM716  PC326    5'  CATCTTAATAATAAGTCCTGCA 38025       CATCAG   C
                                TGCAGGAT     GTT GGATG
                                ||||||||     ||| |||||
                                ACGTCCTG     TAA TCTAC
                                    AATAA_   T
GAM716  LOC133688 3'  CCACCTGCCACTGATCCTGCA  75605        T___    TC
                                TGCAGGATCA   CAGGT  GG
                                ||||||||||   |||||  ||
                                ACGTCCTAGT   GTCCA  CC
                                     CACC    __
GAM716  LOC145547 5'  TCGCTACCCACCGATCCTGCA  77784        ATCA   T_
                                TGCAGGATC    GGT  CGG
                                |||||||||   |||  |||
                                ACGTCCTAG    CCA  GCT
                                     CCAC   TC
GAM716  LOC145624 5'  TCATCTCCTAAAGATCCTGCA  84403        ATC   TTC
                                TGCAGGATC   AGG   GGATGA
                                |||||||||  |||   ||||||
                                ACGTCCTAG   TCC   TCTACT
                                     AAA   ___
GAM716  LOC148696 5'  CATCCGAACAGATCCTCA    85345    C     ATCAG
                                TG AGGATC    GTTCGGATG
                                || ||||||    |||||||||
                                AC TCCTAG    CAAGCCTAC
                                 _     A____
GAM716  LOC219988 3'  CACCCAGGATGATCCTCA    93259    C       AGGTTC  A
                                TG AGGATCATC     GG TG
                                || |||||||||     || ||
                                AC TCCTAGTAG     CC AC
                                 _       GA____  C
GAM717  PRO0650   5'  AATCCAAACTCTCAGGCACA   27070    _  __  A
                                TG GTC  GGA TTTGGATT
                                || |||  ||| ||||||||
                                AC CGG  TCT AAACCTAA
                                 A  AC   C
GAM717  LOC219333 3'  CCCTTCCGATCATGGTA     95184           TTT
                                TACCATGGTCGGAA   GG
                                ||||||||||||||   ||
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                                ATGGTACTAGCCTT  CC
                                      C__
GAM718  CNGA1   5' ACCAGTGACGTCCACTTCTA  60229    C      _ A_
                                TAG AGTGGACG CG  GGT
                                ||| |||||||| ||  |||
                                ATC TCACCTGC GT  CCA
                                  T       A  GA
GAM718  MADD    3' CGTTATAACTGTCCACTGC   56207        CGAGG  C
                                GCAGTGGACG    TA AACG
                                ||||||||||    || ||||
                                CGTCACCTGT    AT TTGC
                                      CA___  A
GAM718  MADD    3' CGTTATAACTGTCCACTGC   56221        CGAGG  C
                                GCAGTGGACG    TA AACG
                                ||||||||||    || ||||
                                CGTCACCTGT    AT TTGC
                                      CA___  A
GAM718  MADD    3' CGTTATAACTGTCCACTGC   56225        CGAGG  C
                                GCAGTGGACG    TA AACG
                                ||||||||||    || ||||
                                CGTCACCTGT    AT TTGC
                                      CA___  A
GAM718  MADD    3' CGTTATAACTGTCCACTGC   56229        CGAGG  C
                                GCAGTGGACG    TA AACG
                                ||||||||||    || ||||
                                CGTCACCTGT    AT TTGC
                                      CA___  A
GAM718  MADD    3' CGTTATAACTGTCCACTGC   56233        CGAGG  C
                                GCAGTGGACG    TA AACG
                                ||||||||||    || ||||
                                CGTCACCTGT    AT TTGC
                                      CA___  A
GAM718  MADD    3' CGTTATAACTGTCCACTGC   14856        CGAGG  C
                                GCAGTGGACG    TA AACG
                                ||||||||||    || ||||
                                CGTCACCTGT    AT TTGC
                                      CA___  A
GAM718  MBD3    3' TGCCAGAATGCTCCACTGC   15395        C  A___
                                GCAGTGGA GCG   GGTA
                                |||||||| |||   ||||
                                CGTCACCT CGT   CCGT
                                     _  AAGA
GAM718  WBP2    3' GTCTGGCACCCACTGCTA    73390        AC  G
                                TAGCAGTGG  GC AGGT
                                |||||||||  || ||||
                                ATCGTCACC  CG TCTG
                                      CA  G
GAM718  HAN11   3' TGCTTTGCACCCACTGTTA   20635         AC
                                TAGCAGTGG  GCGAGGTA
                                |||||||||  ||||||||
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                                ATTGTCACC  CGTTTCGT
                                     CA
GAM718  MGC16384  5'  CGTTGCACTTTCTCTCACTGCT 54933        _ CGC    A
            A                    TAGCAGTG GA   GAGGT CAACG
                                 |||||||| ||   ||||| |||||
                                 ATCGTCAC CT   TTTCA GTTGC
                                      T  C__    C
GAM718  MGC3101   3'  TTGTCCTGCACCCACTGCTA   44108        AC  G   T
                                 TAGCAGTGG  GC AGG ACAA
                                 |||||||||  || ||| ||||
                                 ATCGTCACC  CG TCC TGTT
                                      CA  _  _
GAM718  ST13      3'  TTGTACCTGACATTGCTA    15437        GACGCG
                                 TAGCAGTG     AGGTACAA
                                 ||||||||     ||||||||
                                 ATCGTTAC     TCCATGTT
                                      AG____
GAM718  LOC145873 3'  TGTCCTCCACTGCTA       78016         CGCGA  T
                                 TAGCAGTGGA    GG ACA
                                 ||||||||||    || |||
                                 ATCGTCACCT    CC TGT
                                       _____ _
GAM718  LOC148188 5'  ACTATCCCATCTACTGCTA    79455         CGC  _
                                 TAGCAGTGGA   GA GGT
                                 ||||||||||   || |||
                                 ATCGTCATCT   CT TCA
                                       ACC  A
GAM718  LOC158735 3'  GTCTTCCACATCACTGCTA    88254        ACGC   T
                                 TAGCAGTGG    GAGG AC
                                 |||||||||    |||| ||
                                 ATCGTCACT    CTTC TG
                                      ACAC   _
GAM718  LOC91272  5'  CGTTTCTGCCGCGTCCAC     66033        GA   C_
                                 GTGGACGC  GGTA  AACG
                                 ||||||||  ||||  ||||
                                 CACCTGCG  CCGT  TTGC
                                      __   CT
GAM719  MYLK      3'  CCAAAATCAGTAGGAAATCT   98794        C  CA  GTG
                                 GGATTTCC AC  GA   TGG
                                 |||||||| ||  ||   |||
                                 TCTAAAGG TG  CT   ACC
                                      A  A_  AAA
GAM719  KIAA0444  3'  CCACACTCCAGTCTGGATCCAG 62995    _     CCC  CA
            G                    CC GGATTT   AC  GAGTGTGG
                                 || ||||||   ||  ||||||||
                                 GG CCTAGG   TG  CTCACACC
                                  A     TC_  AC
GAM719  MGC14836  5'  CCGGCGCTGATGGGAAATCC   54173         C   A  G
                                 GGATTTCCCA CAG GT TGG
                                 |||||||||| ||| || |||
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                                CCTAAAGGGT GTC CG GCC
                                     A   G  _
GAM720  CCNF     3'  TCTTTGTGCTGAATTTCTG   10089       CC      TGTGT
                                CGGAAA  CAGCACG    AGA
                                ||||||  |||||||    |||
                                GTCTTT  GTCGTGT    TCT
                                   AA      T____
GAM720  CKAP1    5'  CACACGTGCTGGCTCCCCG   73898     AAAC
                                CGG    CCAGCACGTGTG
                                |||    ||||||||||||
                                GCC    GGTCGTGCACAC
                                  CCTC
GAM720  PPOX     5'  CTACCTATTGTGGGTTTCCG   6128          G  C   T
                                CGGAAACCCA CA GTG GTAG
                                |||||||||| || ||| ||||
                                GCCTTTGGGT GT TAT CATC
                                     _  _   C
GAM720  PPP3CA   5'  CTCCATTCCGCGGTGCTGGGTC 8136       A       _   T_  A
           TCCG                    CGGA ACCCAGCAC GTG  GT GAG
                                |||| |||||||| |||  || |||
                                GCCT TGGGTCGTG CGC  TA CTC
                                  C       G   CT  C
GAM720  SLC7A5   3'  CTGCTGTGCTGGAATTCC    14464      AC       TGT
                                GGAA  CCAGCACG   GTAG
                                ||||  ||||||||   ||||
                                CCTT  GGTCGTGT   CGTC
                                  AA       ___
GAM720  SLC7A5   3'  TTCTGGCCGGTGCTGGGTTCCC 14469    A        G  TG
                                GG AACCCAGCAC TG  TAGAG
                                || ||||||||| ||  |||||
                                CC TTGGGTCGTG GC  GTCTT
                                 C        _  CG
GAM720  UPF3A    3'  CTGCACGCACCTGGCCTCC   43732     AAC    CAC
                                GGA   CCAG   GTGTGTAG
                                |||   ||||   ||||||||
                                CCT   GGTC   CGCACGTC
                                  CC_   CA_
GAM720  ZNF157   5'  CTCTACACACAGACAGCTGTCC 14331     AACC    AC___
                                GGA    CAGC    GTGTGTAGAG
                                |||    ||||    ||||||||||
                                CCT    GTCG    CACACATCTC
                                  _____   ACAGA
GAM720  APCL     3'  CACGTTTCTGTACCGGGTTTCT 20812         A__  _____
           G                     CGGAAACCC   GC   ACGTG
                                |||||||||   ||   |||||
                                GTCTTTGGG   TG   TGCAC
                                     CCA  TCTT
GAM720  BRAG     3'  TGCACGTGCTGGGCCCGCC   30102    AAA_
                                GG    CCCAGCACGTGTG
                                ||    ||||||||||||
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                                CC   GGGTCGTGCACGT
                                 GCCC
GAM720  C20orf150 3'  CTCCACCATGCTGGGTCCC   66011   AA      CG  T  A
                                GG  ACCCAGCA  TG GT GAG
                                ||  ||||||||  || || |||
                                CC  TGGGTCGT  AC CA CTC
                                 C_      __  _  C
GAM720  DKFZp434N0650 3'  CTCCCACCGGTGCTGGGCCCCG 51054    AAA      GT   TA
                                CGG  CCCAGCAC  GTG  GAG
                                |||  ||||||||  |||  |||
                                GCC  GGGTCGTG  CAC  CTC
                                 CC_      GC  C_
GAM720  EAT2    3'  CTCTGTACCTGCTGGACCCCC  80050   AAAC    CGT
                                GG   CCAGCA   GTGTAGAG
                                ||   ||||||   ||||||||
                                CC   GGTCGT   CATGTCTC
                                 CCCA    C__
GAM720  FLJ13590  5'  CTAAAGTGCTGGGATTCC    46205    A      GTGTG
                                GGAA CCCAGCAC    TAG
                                |||| ||||||||    |||
                                CCTT GGGTCGTG    ATC
                                  A       AA___
GAM720  FLJ14251  5'  CTCTGTGCGCTGGGCTCCCG   46480    AAA    ACGT TG
                                CGG  CCCAGC   G  TAGAG
                                |||  ||||||   |  |||||
                                GCC  GGGTCG   C  GTCTC
                                 CTC     _____ GT
GAM720  FLJ20729  5'  CTCCACACGTGGGCCGCCG   36082    AAA  AGC     T
                                CGG  CCC  ACGTGTG AG
                                |||  |||  ||||||| ||
                                GCC  GGG  TGCACAC TC
                                 GCC  ___      C
GAM720  FLJ23153  3'  CTCTACACACTTGTGATTCC  45268    ACCCA  C
                                GGAA    GCA GTGTGTAGAG
                                ||||    ||| ||||||||||
                                CCTT    TGT CACACATCTC
                                  AG___   T
GAM720  KIAA0215  3'  CTATTTATGCACTAGGTTTCTG 29082       C  CA   T
                                CGGAAACC AG  CGTG GTAG
                                |||||||| ||  |||| ||||
                                GTCTTTGG TC  GTAT TATC
                                    A  AC   T
GAM720  MMPL1   3'  CTCCAAAAGTGCTGGGTTT   15963        GTG  T
                                AAACCCAGCAC   TG AG
                                ||||||||||   || ||
                                TTTGGGTCGTG   AC TC
                                      AAA  C
GAM720  PIG11   3'  TTGCGGAGTGCTGGGCTCC   62293    AA      GTG
                                GGA  CCCAGCAC   TGTAG
                                |||  ||||||||   |||||
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                                CCT  GGGTCGTG   GCGTT
                                  C_       AG_
GAM720  QSCN6    3'  TTACACATGCTTGATTCC    12571     ACCC    CG
                                GGAA   AGCA  TGTGTAG
                                ||||   ||||  |||||||
                                CCTT   TCGT  ACACATT
                                  AGT_   __
GAM720  TTY7     5'  CTCAGCTGGTGCTGGGCTTCC  50018     A      GTGT  A
                                GGAA CCCAGCAC    GT GAG
                                |||| ||||||||    || |||
                                CCTT GGGTCGTG    CG CTC
                                  C       GT__  A
GAM720  LOC149577 5'  CTCTGTACTGCGTACTGGGTCA 85674    AA     C   _
           CC                     GG  ACCCAG ACGT GTGTAGAG
                                ||  |||||| |||| ||||||||
                                CC  TGGGTC TGCG CATGTCTC
                                 AC     A    T
GAM720  LOC151534 3'  CTACACACGCTGCGCCTCC    57483     AACCCA  _
                                GGA     GCA CGTGTGTAG
                                |||     ||| |||||||||
                                CCT     CGT GCACACATC
                                  CCG___   C
GAM720  LOC153196 5'  CTACTCTGTGCCAGGTTCC    87168     A  CA    TGT
                                GGAA CC  GCACG   GTAG
                                |||| ||  |||||   ||||
                                CCTT GG  CGTGT   CATC
                                  _ AC    CT_
GAM720  LOC157273 5'  CTGCAGCACGTGCTGATCTCC  87720     AACC       _
                                GGA    CAGCACGTG TGTAG
                                |||    ||||||||| |||||
                                CCT    GTCGTGCAC ACGTC
                                  CTA_       G
GAM720  LOC157739 3'  CTCAAGCACGTGCCGGAATTCC 82485      AC  A      GTA
                                GGAA  CC GCACGTGT   GAG
                                ||||  || ||||||||   |||
                                CCTT  GG CGTGCACG   CTC
                                  AA  C       AA_
GAM720  LOC202284 5'  CTGCACACACTGAGTCCCC    91933    AA  C   CAC
                                GG  AC CAG   GTGTGTAG
                                ||  || |||   ||||||||
                                CC  TG GTC   CACACGTC
                                 CC  A   A__
GAM720  LOC253254 3'  CTCCCGGCACCTAGGTCTCC   98907     A   C  CAC    GTA
                                GGA ACC AG   GTGT   GAG
                                ||| ||| ||   ||||   |||
                                CCT TGG TC   CACG   CTC
                                  C   A ____    GCC
GAM720  LOC57118  5'  CTCTGCGCCCGCGCCGCGCCCC 40220     AAACCCA  A  T
           CG                     CGG      GC CG GTGTAGAG
                                |||      || || ||||||||
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                              GCC      CG GC CGCGTCTC
                                CCCGCGC  C  C
GAM720  LOC91516  5' CTCTACACTATTCTGGAGCTCC 66905     AAC   CACGT
                              GGA  CCAG    GTGTAGAG
                              |||  ||||    ||||||||
                              CCT  GGTC    CACATCTC
                                CGA   TTAT_
GAM720  LOC91526  5' CTCTGCATGCTGCAGCCTCC  66938     AACCCA  C
                              GGA     GCA GTGTGTAGAG
                              |||     ||| ||||||||||
                              CCT     CGT CGTACGTCTC
                                CCGA__  _
GAM721  CUL5     3'  CCTTACAAAAACAACTAT    14430         CTC
                              ATAGTTGTTT  TGGGG
                              ||||||||||  |||||
                              TATCAACAAA  ATTCC
                                    AAC
GAM721  FCGR2A   3'  CCCCAAAAAACAATTATGT   80026          CTC
                              ACATAGTTGTTT  TGGGG
                              ||||||||||||  |||||
                              TGTATTAACAAA  ACCCC
                                     AA_
GAM721  HSD11B1  3'  GTCCCCAGAGACATGCAA    19828     T__
                              TTGT  TCTCTGGGGAC
                              ||||  ||||||||||
                              AACG  AGAGACCCCTG
                                TAC
GAM721  PON1     3'  TCCCCAAAGACTACACTG    6541      T  T_  C
                              TAGT GT  TCT TGGGGA
                              |||| ||  ||| ||||||
                              GTCA CA  AGA ACCCCT
                                _  TC  A
GAM721  FLJ12910 3'  TCCCCAGAAAAGGAGCACGTG  45006     A  T   ___
                              CAT GT GTTTC  TCTGGGGA
                              ||| || |||||  ||||||||
                              GTG CA CGAGG  AGACCCCT
                                _  _    AAA
GAM721  FLJ13848 3'  GTCCCCAAAGAGGAACACACTG 45829      _      __
                              TAGT TGTTTCTCT  GGGGAC
                              |||| |||||||||  ||||||
                              GTCA ACAAGGAGA  CCCCTG
                                C       AA
GAM721  NYD-SP22 3'  GTCCCCAGAGAAACAACTATGT 51859
           TA                   TAACATAGTTGTTTCTCTGGGGAC
                              ||||||||||||||||||||||||
                              ATTGTATCAACAAAGAGACCCCTG

GAM721  p25      3'  GTCCCCAGAGCAGGGACTCTGT 23836     T   G  T
                              ACA AGTT TT CTCTGGGGAC
                              ||| |||| || ||||||||||
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                                TGT TCAG GA GAGACCCCTG
                                  C   G  C
GAM721  PRO1575  3'  TTCCAGAAAAATCAACTA    26874       _  C
                                TAGTTG TTT TCTGGGG
                                |||||| ||| |||||||
                                ATCAAC AAA AGACCTT
                                   T   A
GAM721  LOC197003 3'  GTCCCCAGTTAAACTTTGCTA  89215     T__   CT
                                TAGT   GTTT  CTGGGGAC
                                ||||   ||||  ||||||||
                                ATCG   CAAA  GACCCCTG
                                  TTT    TT
GAM721  LOC254945 5'  GTCCCCAGAGGCAAGGAACTAT 98678        G  __
           GT                     ACATAGTT TT  TCTCTGGGGAC
                                |||||||| ||  ||||||||||
                                TGTATCAA GA  GGAGACCCCTG
                                     G  AC
GAM721  LOC90246  3'  GTCCCCAGAAAAATTTGC    62589    T_   C
                                GT  GTTT TCTGGGGAC
                                ||  |||| |||||||||
                                CG  TAAA AGACCCCTG
                                 TT    A
GAM722  ASNS     5'  ACTCATCAAGTGACTTGCTGA  9808         _ GGAGTA   C
                                TCAGCAAG CA     TGA GAGT
                                |||||||| ||     ||| ||||
                                AGTCGTTC GT     ACT CTCA
                                     A  GA____   A
GAM722  CCND2    3'  ACTCAAGAGACACCCCTTCCTG 10044       AGC   A  ATGAC__
           CTGA                    TCAGCA   AGG GT      GAGT
                                ||||||   ||| ||      ||||
                                AGTCGT   TCC CA      CTCA
                                   CCT   C  CAGAGAA
GAM722  FRAP1    3'  ACTCATCATAAGTACTTGCTGA 18269        CAGGAG    C
                                TCAGCAAG     TATGA GAGT
                                ||||||||     ||||| ||||
                                AGTCGTTC     ATACT CTCA
                                     ATGA__     A
GAM722  SMT3H1   3'  TCATCTCTTGCTTGCTTGA   60631     _        T
                                TCA GCAAGCAGGAG ATGA
                                ||| ||||||||||| ||||
                                AGT CGTTCGTTCTC TACT
                                  T        _
GAM722  TPD52L2  3'  ACTCCAACCCTCCTGCTTGCTG 13828           TATGAC
                                CAGCAAGCAGGAG     GAGT
                                ||||||||||||||     ||||
                                GTCGTTCGTCCTC     CTCA
                                        CCAAC_
GAM722  DKFZp586I021 3'  ACTCGTCACACCCAAGCTGCTG 51080       A  A_  A  A
           G                     TCAGCA GC  GG GT TGACGAGT
                                |||||| ||  || || ||||||||
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                                GGTCGT CG  CC CA ACTGCTCA
                                   _ AA  _  C
GAM722  EHM2     3'  TCACCTCCTGCTCGCTGA    39419       A       TA
                                TCAGC AGCAGGAG  TGA
                                ||||| ||||||||  |||
                                AGTCG TCGTCCTC  ACT
                                   C       C_
GAM722  FLJ23017  3'  ACTCACATAAGCCACCGCTTGC 43414         A__  AG    AC
           TGA                    TCAGCAAGC   GG  TATG  GAGT
                                |||||||||   ||  ||||  ||||
                                AGTCGTTCG   CC  ATAC  CTCA
                                     CCA  GA   A_
GAM722  FLJ32670  3'  ACTCATCTTAGCATCTGCTTGC 58790         GA  AT_  C
           T                     AGCAAGCAG  GT   GA GAGT
                                |||||||||  ||   || ||||
                                TCGTTCGTC  CG   CT CTCA
                                     TA  ATT  A
GAM722  GFR      3'  CTCACCAACTGCTTGCTGA   25445          GA_  ATGAC
                                TCAGCAAGCAG   GT    GAG
                                ||||||||||   ||    |||
                                AGTCGTTCGTC   CA    CTC
                                      AAC  _____
GAM722  MGC4604   3'  ACTCGCCACTGGCTGCTTGTT  49794         GAGTA  A
                                AGCAAGCAG    TG CGAGT
                                |||||||||    || |||||
                                TTGTTCGTC    AC GCTCA
                                     GGTC_  C
GAM722  LOC129607 3'  ACTCGTCATGATGGGCTCGCTG 75396      A   AGGAG
                                CAGC AGC    TATGACGAGT
                                ||||| |||    ||||||||||
                                GTCG TCG    GTACTGCTCA
                                  C  GGTA_
GAM722  LOC146780 5'  ACTCATCAGTTTCTGCTTACTG 84815      C       GTA   C
           G                     TCAG AAGCAGGA   TGA GAGT
                                |||| ||||||||   ||| ||||
                                GGTC TTCGTCTT   ACT CTCA
                                  A       TG_   A
GAM722  LOC153886 3'  ACTCACCAATCATCTCCTTCCT 60265      AGC    T    C____
           GCT                     AGCA   AGGAG ATGA    GAGT
                                ||||   ||||| ||||    ||||
                                TCGT   TCCTC TACT    CTCA
                                  CCT    _    AACCA
GAM722  LOC51008  3'  ACCGTCATACTACCAGCTGA   32523       AAGCA  _       A
                                TCAGC    GG AGTATGACG GT
                                |||||    || |||||||| ||
                                AGTCG    CC TCATACTGC CA
                                  A____  A       C
GAM723  AP1B1    3'  ACATGGTCAAGACCAGGCAG   8514          CGGCACC
                                CTGTCTGG      ACCATGT
                                ||||||||      |||||||
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                                GACGGACC      TGGTACA
                                    AGAAC__
GAM723  CDH1    3'  ACATGGTGGTGATGTCCA    16397     _  G
                                TGG CG CACCACCATGT
                                ||| || ||||||||||
                                ACC GT GTGGTGGTACA
                                  T  A
GAM723  CLC     3'  ACATGGTGGCAATTCTACACA  26024     C   CGGCA
                                TGT TGG    CCACCATGT
                                ||| |||    |||||||||
                                ACA ATC    GGTGGTACA
                                  C   TTAAC
GAM723  DSC1    3'  ACATAGTTGGTGCCAGATA    18239        G  CC  C
                                TGTCTGGCG CA  AC ATGT
                                ||||||||| ||  || ||||
                                ATAGACCGT GT  TG TACA
                                     G  __  A
GAM723  DSC1    3'  ACATAGTTGGTGCCAGATA    44598        G  CC  C
                                TGTCTGGCG CA  AC ATGT
                                ||||||||| ||  || ||||
                                ATAGACCGT GT  TG TACA
                                     G  __  A
GAM723  GABRE   3'  ACATGATAGGGCTAGACAG    42069        GGCA  AC_
                                CTGTCTGGC   CC   CATGT
                                |||||||||   ||   |||||
                                GACAGATCG   GG   GTACA
                                     ____  ATA
GAM723  GABRE   3'  ACATGATAGGGCTAGACAG    18279        GGCA  AC_
                                CTGTCTGGC   CC   CATGT
                                |||||||||   ||   |||||
                                GACAGATCG   GG   GTACA
                                     ____  ATA
GAM723  GABRE   3'  ACATGATAGGGCTAGACAG    42055        GGCA  AC_
                                CTGTCTGGC   CC   CATGT
                                |||||||||   ||   |||||
                                GACAGATCG   GG   GTACA
                                     ____  ATA
GAM723  GABRE   3'  ACATGATAGGGCTAGACAG    42059        GGCA  AC_
                                CTGTCTGGC   CC   CATGT
                                |||||||||   ||   |||||
                                GACAGATCG   GG   GTACA
                                     ____  ATA
GAM723  GAS7    3'  ACATGGTGGCAGGGACAG    20837      GGCGGCA
                                CTGTCT     CCACCATGT
                                ||||||     |||||||||
                                GACAGG     GGTGGTACA
                                   GAC____
GAM723  MTMR6   3'  ACATGGTGGCATGAAGTACA  95197     _  GG  GCA
                                TGT CT  CG   CCACCATGT
                                ||| ||  ||   |||||||||
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                                ACA GA  GT   GGTGGTACA
                                  T  A_  AC_
GAM723  PRKG1    3'  ACATGGTGGTCCTGAAGCA   21818    T  GG   C
                                TG CT  CGG ACCACCATGT
                                || ||  ||| ||||||||||
                                AC GA  GTC TGGTGGTACA
                                 _ A_   C
GAM723  AK5      3'  ACATGGTGATGCATTTCAGCA  24927    T   CG_   C
                                TG CTGG   GCA CACCATGT
                                || ||||   ||| ||||||||
                                AC GACT   CGT GTGGTACA
                                 _   TTA   A
GAM723  DKFZP564K0822 3'  ACATGGTAGTGTGGTGACAG   95695      TG  G   C
                                CTGTC  GC GCAC ACCATGT
                                |||||  || |||| |||||||
                                GACAG  TG TGTG TGGTACA
                                  __  G   A
GAM723  DOCK3    3'  ACATGGTGATGCTGGGTGACGG 67089      TGG    C
                                CTGTC   CGGCA CACCATGT
                                |||||   ||||| ||||||||
                                GGCAG   GTCGT GTGGTACA
                                   TGG    A
GAM723  FLJ10040  5'  ACAAGGACACCTCCAGACAG   36217        C  CACCA  A
                                CTGTCTGG GG    CC TGT
                                |||||||| ||    || |||
                                GACAGACC CC    GG ACA
                                     T  ACA__  A
GAM723  FLJ22477  5'  ATGTCGGCGCCGCCAGCAG    45667    T      A  AC
                                CTG CTGGCGGC CC  CAT
                                ||| |||||||| ||  |||
                                GAC GACCGCCG GG  GTA
                                  _      C  CT
GAM723  HUMAGCGB  3'  ACATGGTGATAGTCATCGTCAG 26130        C_  ___
                                CTGGCGG  AC   CACCATGT
                                |||||||  ||   ||||||||
                                GACTGCT  TG   GTGGTACA
                                    AC  ATA
GAM723  KIAA1458  3'  ACATGTCACCACCACCAGATAG 69571        C  CACCAC
                                CTGTCTGG GG     CATGT
                                |||||||| ||     |||||
                                GATAGACC CC     GTACA
                                     A  ACCACT
GAM723  KIAA1985  5'  ACATGGTGGTACCCAAGATA   45016      GGC  C
                                TGTCT   GG ACCACCATGT
                                |||||   || ||||||||||
                                ATAGA   CC TGGTGGTACA
                                   AC_  A
GAM723  ZNF297B   5'  ACATGGTGGCATGTACATACAG 26633      C  _   GCA
                                CTGT TG GCG   CCACCATGT
                                |||| || |||   |||||||||
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                                GACA AC TGT   GGTGGTACA
                                  T A   AC_
GAM723   LOC123242 3'  GGCAGTGCCGCCAGCAG     76118     T        CA
                                CTG CTGGCGGCAC  CC
                                ||| ||||||||||  ||
                                GAC GACCGCCGTG  GG
                                  _         AC
GAM723   LOC143310 3'  ACATGGTGACCTGAGCAAACA  77029     C  G_   CAC
                                TGT TG  CGG   CACCATGT
                                ||| ||  |||   ||||||||
                                ACA AC  GTC   GTGGTACA
                                  A  GA   CA_
GAM723   LOC148166 5'  GCATGGTCCAACCAGACAG    79417        C_  CACC
                                CTGTCTGG  GG    ACCATGT
                                ||||||||  ||    |||||||
                                GACAGACC  CC    TGGTACG
                                     AA  ____
GAM723   LOC150159 3'  ACATGATGGTGCTGCAAGA    58258     G        C
                                TCT GCGGCACCA CATGT
                                ||| ||||||||| |||||
                                AGA CGTCGTGGT GTACA
                                  A        A
GAM723   LOC151571 5'  ACACGGCAGGCTTTGCCAGA   86626         CA  A_  A
                                TCTGGCGG  CC  CC TGT
                                ||||||||  ||  || |||
                                AGACCGTT  GG  GG ACA
                                     TC  AC  C
GAM723   LOC196549 5'  GCATGGTGCCAGACA       59921         GGCACC
                                TGTCTGGC     ACCATGT
                                ||||||||     |||||||
                                ACAGACCG     TGGTACG
                                     _______
GAM723   LOC253001 3'  GGCAGTGCCGCCAGCAG     97996     T        CA
                                CTG CTGGCGGCAC  CC
                                ||| ||||||||||  ||
                                GAC GACCGCCGTG  GG
                                  _         AC
GAM723   LOC253974 3'  ACATGGTGGTGAAGACGCCAG  99280       G___
                                CTGGCG    CACCACCATGT
                                ||||||    ||||||||||
                                GACCGC    GTGGTGGTACA
                                   AGAA
GAM723   LOC257443 3'  ACATGTCACCACCACCAGATAG 97547         C  CACCAC
                                CTGTCTGG GG     CATGT
                                |||||||| ||     |||||
                                GATAGACC CC     GTACA
                                     A  ACCACT
GAM723   LOC91308  5'  ACATGGTGGTGGTTGAACA    66161     CT   GG
                                TGT  GGC  CACCACCATGT
                                |||  |||  ||||||||||
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                                ACA  TTG  GTGGTGGTACA
                                  AG  __
GAM724  HAL      5'  GCCACTCCTGCATAAAGCTC   10903          TGAAAA
                                GAGCTTTATGC     GGTGGC
                                ||||||||||     ||||||
                                CTCGAAATACG     TCACCG
                                      TCC___
GAM724  HMGN2    3'  GGCCACCTTGGCACAAAAGC   19809      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _ GG
GAM724  NMI      5'  GGCCACCTCCTCAGGAAG    17436     ATG   AA
                                CTTT   CTGA  AGGTGGCC
                                ||||   ||||  ||||||||
                                GAAG   GACT  TCCACCGG
                                  ___    CC
GAM724  PACE     3'  GGCCACCTCTCCAAGGGCTT   11944       A  CT  AAA
                                GAGCTTT TG  GA   GGTGGCC
                                |||||||  ||  ||   |||||||
                                TTCGGGA AC  CT   CCACCGG
                                   _  CT  ___
GAM724  PYCR1    3'  CCACCTTCCTCTAGAGCTC    70639        TGCT  A_
                                GAGCTTTA    GA  AAGGTGG
                                ||||||||    ||  |||||||
                                CTCGAGAT    CT  TTCCACC
                                     _____  CC
GAM724  SDC1     3'  GGCCACCTCCCCAGCATTCCAG 12991     TT_     AAA
          C                      GCT   ATGCTG   AGGTGGCC
                                 |||   ||||||   ||||||||
                                 CGA   TACGAC   TCCACCGG
                                   CCT     CCC
GAM724  FLJ11560 5'  GCCCAGGCCCAGCATAAAG   48008         AAAA  ___
                                CTTTATGCTG    GGT   GGC
                                ||||||||||    |||   |||
                                GAAATACGAC    CCG   CCG
                                      _____   GAC
GAM724  KIAA0446 5'  CCACCTTTTGAAGAGCTC    69446       ATGCTG
                                GAGCTTT     AAAAGGTGG
                                |||||||     |||||||||
                                CTCGAGA     TTTTCCACC
                                   AG_____
GAM724  KIAA0971 3'  GTTGTTCTCAGCATAAAGT   30677          AAA  TG
                                GCTTTATGCTGA   GG  GC
                                ||||||||||||   ||  ||
                                TGAAATACGACT   TT  TG
                                      C__  GT
GAM724  KIAA1393 3'  GGCCACCTTGGCACAAAAGC   72574      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
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                                CGAAA AC AC  TTCCACCGG
                                   _ _ GG
GAM724  KIAA1656 3' GGCCACCTCCTCCTAGAAGCC 66377   A    ATGCT  AA
                                G GCTTT    GA  AGGTGGCC
                                | |||||    ||  ||||||||
                                C CGAAG    CT  TCCACCGG
                                _    ATC__  CC
GAM724  KIAA1884 3' GCCACCTTCATCTACCAAGGCT 73728       ATGCT  A_
          C                      GAGCTTT    GA  AAGGTGGC
                                |||||||    ||  ||||||||
                                CTCGGAA    CT  TTCCACCG
                                    CCAT_  AC
GAM724  PP3501   3' GGCCACCGTTGACAGCATAAAG 41683         AAAA_
                                CTTTATGCTG    GGTGGCC
                                ||||||||||    |||||||
                                GAAATACGAC    CCACCGG
                                      AGTTG
GAM724  SDCCAG3  3' GGTGTTCTCAGCATGAAGCTC  22803           AAA  TG
                                GAGCTTTATGCTGA   GG  GCC
                                ||||||||||||||   ||  |||
                                CTCGAAGTACGACT   CT  TGG
                                       ___  TG
GAM724  SP140    3' GGCCACCTCCATGCAGAAGC  24327      A   TGAAA
                                GCTTT TGC    AGGTGGCC
                                ||||| |||    ||||||||
                                CGAAG ACG    TCCACCGG
                                   _  TACC_
GAM724  LOC148760 3' GGCCACCTTCTCCAACAAGCTC 85364      TA  CT  A
                                GAGCTT  TG  GA AAGGTGGCC
                                ||||||  ||  || |||||||||
                                CTCGAA  AC  CT TTCCACCGG
                                   CA  __  C
GAM724  LOC150170 5' ACCTGTTTCACATAAAGC    80414        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                     _    G
GAM724  LOC150175 5' ACCTGTTTCACATAAAGC    80453        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                     _    G
GAM724  LOC150215 5' ACCTGTTTCACATAAAGC    80456        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                     _    G
GAM724  LOC150218 5' ACCTGTTTCACATAAAGC    80525        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
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                                CGAAATAC ACTTT TCCA
                                   _    G
GAM724  LOC152065 3'  GGCCACCTTCTCCTTGGCAGGC 86737      TTA   ___  A
          TC                    GAGCT  TGCT  GA AAGGTGGCC
                                ||||||  ||||  || |||||||||
                                CTCGG  ACGG  CT TTCCACCGG
                                  ____  TTC  C
GAM724  LOC152267 3'  GGCCACCTTGGCACAAAAGC  61036      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _ GG
GAM724  LOC158292 5'  CCTCTGGACCCAGCATAAGGCT 88046           AAAA_  T
          C                     GAGCTTTATGCTG    GG GG
                                ||||||||||||    || ||
                                CTCGGAATACGAC    TC CC
                                       CCAGG  T
GAM724  LOC219997 3'  GCCACCTCTTCAGCCTC    93256    CTTTAT    A
                                GAG    GCTGAA AGGTGGC
                                |||    |||||| |||||||
                                CTC    CGACTT TCCACCG
                                 _______    C
GAM724  LOC256269 3'  GGCCACCTTGGCACAAAAGC  96608      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _ GG
GAM724  LOC91963  5'  GGCCACCTCCTCTGAGAAGC  68321      ATGCT  AA
                                GCTTT    GA  AGGTGGCC
                                |||||    ||  ||||||||
                                CGAAG    CT  TCCACCGG
                                  AGT__  CC
GAM725  CCND2     3'  TCCCCAGCAAATCATCGGGCCA 10056          CCACA  _  A
                                TGGCCTGATGAT    GC GG GA
                                ||||||||||||    || || ||
                                ACCGGGCTACTA    CG CC CT
                                       AA___  A  C
GAM725  GCN5L2    5'  CTCCGCTGCGGGGGAGGCC   60529      GATGA  A
                                GGCCT    TCC CAGCGGAG
                                |||||    ||| ||||||||
                                CCGGA    GGG GTCGCCTC
                                  GG___  C
GAM725  GJA5      3'  CTGACCAGATCATCAGCCA   19164      C      CACAG
                                TGGC TGATGATC    CGG
                                |||| ||||||||    |||
                                ACCG ACTACTAG    GTC
                                  _      ACCA_
GAM725  HIVEP3    3'  TCCCCGCTGTGGTTGGCAGCCA 44702      C  ATGAT       A
                                TGGC TG    CCACAGCGG GA
                                |||| ||    ||||||||| ||
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                                ACCG AC    GGTGTCGCC CT
                                  _ GGTT_       C
GAM725  HOXD1    5' CCGCCGGTATATTAGGCCA   44696         AT  ACA
                                TGGCCTGATG  CC   GCGG
                                ||||||||||  ||   ||||
                                ACCGGATTAT  GG   CGCC
                                      AT  C__
GAM725  SUFU     3' CCTTGTGACCCATCAGGCCA  32934         ATC    C
                                TGGCCTGATG   CACAG GG
                                ||||||||||   ||||| ||
                                ACCGGACTAC   GTGTT CC
                                      CCA    _
GAM725  ARHGEF15 3' CTGTGGACCACAGGCCA     30953        A  A
                                TGGCCTG TG TCCACAG
                                ||||||| || |||||||
                                ACCGGAC AC AGGTGTC
                                    _ C
GAM725  DKFZP586J1624 3'  CTCCGCCCAGTCACCATCAGGC 32043          ATCCACA_
            CA                    TGGCCTGATG       GCGGAG
                                ||||||||||       ||||||
                                ACCGGACTAC       CGCCTC
                                      CACTGACC
GAM725  KIAA1671  3'  CTTTGCTTATGAATCATCAGAC 66282    C       C  C_
            C                     GG CTGATGAT CA  AGCGGAG
                                || |||||||| ||  |||||||
                                CC GACTACTA GT  TCGTTTC
                                 A       A  AT
GAM725  MGC18079  3'  CCGCGGACCTCAGGCCA     59033        TGA   ACA
                                TGGCCTGA   TCC   GCGG
                                ||||||||   |||   ||||
                                ACCGGACT   AGG   CGCC
                                    CC_   ___
GAM725  LOC115110 3'  TGCAGACATCAGGCCA      72186         A  CACA
                                TGGCCTGATG TC    GCG
                                |||||||||| ||    |||
                                ACCGGACTAC AG    CGT
                                      _  A___
GAM725  LOC159110 5'  TCTCCGCTGCCCCGGTCAACCA 82995     CCTGA    CA__
                                TGG    TGATC    CAGCGGAGA
                                |||    |||||   |||||||||
                                ACC    ACTGG    GTCGCCTCT
                                  A_____    CCCC
GAM725  LOC159116 5'  TCTCCGCTGCCCCGGTCAACCA 82978     CCTGA    CA__
                                TGG    TGATC    CAGCGGAGA
                                |||    |||||   |||||||||
                                ACC    ACTGG    GTCGCCTCT
                                  A_____    CCCC
GAM725  LOC165476 5'  CTCCGCTGCCTGCTCAGCCA   88550     C   TGATCCA
                                TGGC TGA      CAGCGGAG
                                |||| |||      ||||||||
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                                ACCG ACT      GTCGCCTC
                                  _  CGTCC__
GAM725  LOC200032 5'  CTGACCAGATCATCAGCCA   85475     C      CACAG
                                TGGC TGATGATC    CGG
                                |||| ||||||||    |||
                                ACCG ACTACTAG    GTC
                                  _      ACCA_
GAM725  LOC219654 5'  CTCCGCTGCGGAGGGGGGCC   92932      GATGA   A
                                GGCCT    TCC CAGCGGAG
                                |||||    ||| ||||||||
                                CCGGG    AGG GTCGCCTC
                                   GGG__   C
GAM725  LOC255862 3'  TCAAATGTAGACTATCAGGCCA 96115          A  C   GCG
                                TGGCCTGATG TC ACA   GA
                                |||||||||| || |||   ||
                                ACCGGACTAT AG TGT   CT
                                      C  A   AAA
GAM726  ADCY1    3'  CCACCGAGCAGGCACAGCACA  94339     AA       GCCT
                                TGT  TGTGCCTGT   GTGG
                                |||  |||||||||   ||||
                                ACA  ACACGGACG   CACC
                                  CG       AGC_
GAM726  CDH1     3'  CCACAGGCATGCACCACTAC   16400     AT_   CT
                                GTA   GTGC  GTGCCTGTGG
                                |||   ||||  ||||||||||
                                CAT   CACG  TACGGACACC
                                  CAC   __
GAM726  COL4A4   3'  GTTAGCATAAACACATCACA   5406     A    CC    CTG
                                TGT ATGTG  TGTGC   TGGC
                                ||| |||||  |||||   ||||
                                ACA TACAC  ATACG   ATTG
                                  C    AA    ___
GAM726  IGF1R    3'  GGCCACAGGCACACAGGT    7909      __
                                GCC  TGTGCCTGTGGCC
                                |||  |||||||||||||
                                TGG  ACACGGACACCGG
                                  AC
GAM726  NFE2L1   3'  GCCACAGGCAGCTTCTCCACA  13630      CCT__ _
                                TGTG    G TGCCTGTGGC
                                ||||    | ||||||||||
                                ACAC    C ACGGACACCG
                                   CTCTT G
GAM726  PER2     3'  CCACAGGCGACTGCCACCACA  43345     AA  T  CTG
                                TGT  TG GC   TGCCTGTGG
                                |||  || ||   |||||||||
                                ACA  AC CG   GCGGACACC
                                  CC  _  TCA
GAM726  TAL1     3'  CCACAGGTGTGAGCCACCACA  13524     AA  T  CT TG
                                TGT  TG GC  G  CCTGTGG
                                |||  || ||  |  |||||||
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                                ACA  AC CG  T  GGACACC
                                  CC  _  AG GT
GAM726  TMPRSS3  3'  CCACAGGTGCCCGCCACCACA  44019     AA  T  CT TG
                                TGT  TG GC  G  CCTGTGG
                                |||  || ||  |  |||||||
                                ACA  AC CG  C  GGACACC
                                  CC  _  CC GT
GAM726  ASB16    3'  CCACAGGTGGGCAGCACCACA  55976     AA  _    GT
                                TGT  TG TGCCT  GCCTGTGG
                                |||  || |||||  ||||||||
                                ACA  AC ACGGG  TGGACACC
                                  CC  G    __
GAM726  C(27)-3BETA-HSD 3'  CCACAGGTGCACGCCACCACA  48050     AA  T  C  TG
                                TGT  TG GC TG  CCTGTGG
                                |||  || || ||  |||||||
                                ACA  AC CG AC  GGACACC
                                  CC  _  C  GT
GAM726  FLJ10718  3'  CCACAGGCACGTGCCACCACA  37026     AA  T  C
                                TGT  TG GC TGTGCCTGTGG
                                |||  || || ||||||||||
                                ACA  AC CG GCACGGACACC
                                  CC  _  T
GAM726  FLJ20147  3'  CCACAGGTGTGTGCCACCACA  35132     AA  T  C  TG
                                TGT  TG GC TG  CCTGTGG
                                |||  || || ||  |||||||
                                ACA  AC CG GT  GGACACC
                                  CC  _  T  GT
GAM726  HIF3A    3'  GCCACACAGGCACATGCACA  42655      C       __
                                TGTGC TGTGCCTGT  GGC
                                |||||  |||||||||  |||
                                ACACG ACACGGACA  CCG
                                   T       CA
GAM726  HRH4     3'  CCGTGGCCAGGCACAAGACA  41534     AA     GT__  TGT
                                TGT  TGTGCCT   GCC  GG
                                |||  |||||||   |||  ||
                                ACA  ACACGGA   CGG  CC
                                  GA      ___C  TGT
GAM726  HSPC065  3'  GGCCACGGCTTACAGACCACTA 27155     AT  C_   __  T
            CA                    TGTA  GTG  CTGT  GCC GTGGCC
                                ||||  |||  ||||  ||| ||||||
                                ACAT  CAC  GACA  CGG CACCGG
                                  __   CA   TT  _
GAM726  IGF2AS   3'  GGCCACAGGCACAGCAGCTCA  33530    T __
                                TG GC  CTGTGCCTGTGGCC
                                ||  ||  ||||||||||||||
                                AC CG  GACACGGACACCGG
                                 T  AC
GAM726  KIAA0089  3'  GCAAGTCCCAAACACATTACA  70508        CC  T_  C
                                TGTAATGTG  TG  GC TGT
                                |||||||||  ||  || |||
```

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                                ACATTACAC  AC  TG ACG
                                     AA  CC  A
GAM726  KIAA1924  3'  GGCCACAGGCGTGTGCCACCAC 74052     AA  T  C GT
            A                    TGT  TG GC T  GCCTGTGGCC
                                 ||| || || | ||||||||||
                                 ACA  AC CG G  CGGACACCGG
                                   CC  _  T TG
GAM726  KIAA1981  3'  GGCCACAGACACAGAGACCAC  89716     C___    C
                                 GTG    CTGTG CTGTGGCC
                                 |||    ||||| ||||||||
                                 CAC    GACAC GACACCGG
                                   CAGA    A
GAM726  SBBI31    3'  GGCCACAGACACACACTGC    26730     AT   CC    C
                                 GTA  GTG  TGTG CTGTGGCC
                                 |||  |||  |||| ||||||||
                                 CGT  CAC  ACAC GACACCGG
                                   __  __    A
GAM726  SIMRP7    3'  GCCACAGGGGCCACCTACA    93975      AT   CCT  G
                                 TGTA  GTG   GT CCTGTGGC
                                 ||||  |||   || ||||||||
                                 ACAT  CAC   CG GGACACCG
                                   C_   ___  G
GAM726  LOC124222 3'  GGCCACAGGCACAAGGGCTGCA 74753     _   __
                                 TGT GCCT  GTGCCTGTGGCC
                                 ||| ||||  ||||||||||||
                                 ACG CGGG  CACGGACACCGG
                                   T   AA
GAM726  LOC126133 3'  GGCCACAGACATGCACCACCAC 74912      CCT   ____
            A                    TGTG   GTGC    CTGTGGCC
                                 ||||   ||||    ||||||||
                                 ACAC   CACG    GACACCGG
                                   CAC    TACA
GAM726  LOC127841 5'  GGCCTCTTTCCCAGGCACATCA 75189     A       TGCCTGT
            CA                     TGT ATGTGCCTG      GGCC
                                 ||| |||||||||      ||||
                                 ACA TACACGGAC      CCGG
                                   C        CCTTTCT
GAM726  LOC151521 3'  GGCCACACTTGAAACACATTAT 86623         CCTGTGCC
            A                    TGTAATGTG       TGTGGCC
                                 |||||||||       |||||||
                                 ATATTACAC       ACACCGG
                                      AAAGTTC_
GAM726  LOC152220 3'  CCACAGGCACCCGCCACCACA  86761     AA  T  CT
                                 TGT  TG GC  GTGCCTGTGG
                                 |||  || ||  ||||||||||
                                 ACA  AC CG  CACGGACACC
                                   CC  _  CC
GAM726  LOC154449 5'  CCCACACAGGCACATTCCA    81992    T         CC  T
                                 TG AATGTGCCTGTG  TG GG
                                 || ||||||||||||  || ||
```

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                                AC TTACACGGACAC  AC CC
                                 C          __ _
GAM726  LOC91308  3'  CCACAGGTGCGTGCCACCACA  66163     AA  T  C  TG
                                TGT  TG GC TG  CCTGTGG
                                |||  || || ||  |||||||
                                ACA  AC CG GC  GGACACC
                                  CC  _  T  GT
GAM727  DKFZp547I224 3'  AAAATCATGCCAAAATGTAAAG 39946      G         TA_
          A                      TCTT TACATTTTGGC   GTTTT
                                |||| ||||||||||   |||||
                                AGAA ATGTAAAACCG   TAAAA
                                  _         TAC
GAM727  FLJ14708  3'  AAAAGCCCCAAAATGTCAAGA  52602       T        CTA
                                TCTTG ACATTTTGG   GTTTTT
                                ||||| |||||||||   ||||||
                                AGAAC TGTAAAACC   CGAAAA
                                  _       C__
GAM727  TAF9L     3'  AAAAACAGGTAAAATGTATAA  32559           G  A
                                TTGTACATTTTG CT GTTTTT
                                |||||||||||| || ||||||
                                AATATGTAAAAT GA CAAAAA
                                       G  _
GAM727  USP16     3'  AAAAATACCTAAAAATGTACAA 22246           GGCTA
                                TTGTACATTTT    GTTTTT
                                ||||||||||    ||||||
                                AACATGTAAAA    TAAAAA
                                      ATCCA
GAM727  LOC222681 5'  AAAAACTACAAAAAACATACAA 94417        CA   GGC
          GA                    TCTTGTA  TTTT   TAGTTTTT
                                |||||||  ||||   ||||||||
                                AGAACAT  AAAA   ATCAAAAA
                                   AC    AAC
GAM727  LOC257507 5'  AAAAACTACAAAAAACATACAA 99604        CA   GGC
          GA                    TCTTGTA  TTTT   TAGTTTTT
                                |||||||  ||||   ||||||||
                                AGAACAT  AAAA   ATCAAAAA
                                   AC    AAC
GAM727  LOC257625 5'  AAAAACTACAAAAAACATACAA 99724        CA   GGC
          GA                    TCTTGTA  TTTT   TAGTTTTT
                                |||||||  ||||   ||||||||
                                AGAACAT  AAAA   ATCAAAAA
                                   AC    AAC
GAM728  SCAMP1    3'  GCTAAATAAATATTCTCC    54500     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM728  SCAMP1    3'  GCTAAATAAATATTCTCC    54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
```

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                                CCT TTATAA TAAATCG
                                  C     A
GAM728  NX-17    3'  TGAATATCAGCCCCTAATA   40706        ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM728  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
          TA                     TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM729  AXIN1    3'  GCCGAGGCCACCCGCAGGGCCC 61538    C      CC_
                                GG CCCTGCG   GGCCTCGGC
                                || |||||||   |||||||||
                                CC GGGACGC   CCGGAGCCG
                                 C      CCA
GAM729  BCAR1    3'  CCGAAGCCCAGGGGCCGG    64663         CGCC   C
                                TCGGCCCCTG    GGC TCGG
                                ||||||||||    ||| ||||
                                GGCCGGGGAC    CCG AGCC
                                      _____   A
GAM729  CHAT     5'  CCGAGGCAGCAGAGCCGA    40966      CC    GCCG
                                TCGGC  CTGC    GCCTCGG
                                |||||  ||||    |||||||
                                AGCCG  GACG    CGGAGCC
                                   A_    A___
GAM729  DUX4     5'  GCACGCGGCGCGAGGCCGA   73196      CC     _______
                                TCGGCC  TGCGCCG     GC
                                ||||||  |||||||     ||
                                AGCCGG  GCGCGGC     CG
                                   A_      GCAIII
GAM729  ELAVL1   5'  CCGAGGCCGAGCGGAGCCG   9222      CC    GC
                                CGGC  CTGC  CGGCCTCGG
                                ||||  ||||  |||||||||
                                GCCG  GGCG  GCCGGAGCC
                                   A_    A_
GAM729  FZD10    5'  GCCGAGGCCGGCGCAGGG    24215
                                CCCTGCGCCGGCCTCGGC
                                ||||||||||||||||||
                                GGGACGCGGCCGGAGCCG

GAM729  GLDC     5'  CCGAGGCCAGGAGAGGGGCC   64894       GCG  _
                                GGCCCCT   CC GGCCTCGG
                                |||||||   || ||||||||
                                CCGGGGA   GG CCGGAGCC
                                    GA_  A
GAM729  GNA11    5'  CCGAGGCCGGAGGGCCG     10811       CTGCG
                                CGGCCC    CCGGCCTCGG
                                ||||||    ||||||||||
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                                GCCGGG    GGCCGGAGCC
                                  A____
GAM729  H1F0     5'  GCCGAGACCAAGCGACAGACCG 19217     CCC  _  C_  C
                G                  TCGG   CTG CGC  GG CTCGGC
                                   ||||   ||| |||  || |||||||
                                   GGCC   GAC GCG  CC GAGCCG
                                     A__   A   AA  A
GAM729  IL6R     5'  GCCGAGCGCGGCGCGGGGCCGA 6912         T    _  C
                                   TCGGCCCC GCGCCG GC TCGGC
                                   |||||||| |||||| || |||||
                                   AGCCGGGG CGCGGC CG AGCCG
                                       _     G  _
GAM729  JUND     5'  CTCGGCGCGCGGCGCAGGAGCC 19297     C       _______  CTCG
                G                   CGGC CCTGCGCCG     GC   G
                                    |||| |||||||||     ||   |
                                    GCCG GGACGCGGC     CG   C
                                      A        GCGIII  GCTC
GAM729  LHX5     5'  GCCGAGGCCAGCAGCCACCCGA 42562     CCC_   GCC
                                   TCGG   CTGC   GGCCTCGGC
                                   ||||   ||||   |||||||||
                                   AGCC   GACG   CCGGAGCCG
                                     CACC   A__
GAM729  LIMD1    3'  GCCGGGGACACAGGAGCCGG   27263      C   CGCCGG
                                   TCGGC CCTG     CCTCGGC
                                   ||||| ||||     |||||||
                                   GGCCG GGAC     GGGGCCG
                                     A   ACA___
GAM729  MYO3A    3'  GCCTGCGGGGCAGCAGGGGCC  60770         _  GG  T _
                                   GGCCCCTGC GCC  CC C GGC
                                   ||||||||| |||  || | |||
                                   CCGGGGACG CGG  GG G CCG
                                        A   __  C T
GAM729  PAX7     5'  GCCGAGGCCAGCCGGCAGAGGC 26528    G   C   __  C
                GGA                   TC GCC CTGC  GC GGCCTCGGC
                                   || ||| ||||  || |||||||||
                                   AG CGG GACG  CG CCGGAGCCG
                                    G   A   GC  A
GAM729  PAX7     5'  GCCGAGGCCAGCCGGCAGAGGC 11973    G   C   __  C
                GGA                   TC GCC CTGC  GC GGCCTCGGC
                                   || ||| ||||  || |||||||||
                                   AG CGG GACG  CG CCGGAGCCG
                                    G   A   GC  A
GAM729  RARA     3'  CCGAGGCCAGGAACTGA     8251       CC   GCGCC
                                   TCGG  CCT    GGCCTCGG
                                   ||||  |||    ||||||||
                                   AGTC  GGA    CCGGAGCC
                                     AA  _____
GAM729  SLC38A2  5'  CCGAGGCCGACTCGCGGGCCG  39113       CT   C__
                                   CGGCCC  GCG   CGGCCTCGG
                                   ||||||  |||   |||||||||
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                                GCCGGG  CGC   GCCGGAGCC
                                   __   TCA
GAM729  TLR9     5'  GCTGTGGTGCAGGAGCC     34308     C       GCCT
                                GGC CCTGCGCCG    CGGC
                                ||| |||||||||    ||||
                                CCG GGACGTGGT    GTCG
                                  A       _____
GAM729  AHCYL1   5'  CTCGGCGCTCGACGCAGGGGCC 22772           C _______ CTCG
           GG                     TCGGCCCCTGCG CG     GC    G
                                ||||||||||||| ||     ||    |
                                GGCCGGGGACGC GC     CG    C
                                      A  TCGIII  GCTC
GAM729  ATP9B    3'  GCCCAGGGCACAGAGGCCGG   78976       C   C   GGC  C
                                TCGGCC CTG GCC   CT GGC
                                |||||| ||| |||   || |||
                                GGCCGG GAC CGG   GA CCG
                                   A   A   ___  C
GAM729  C1orf17  5'  GCCGAGGCCAGTGTGTGAGCCG 68765      CCC     C
           G                      TCGGC   TGCGC GGCCTCGGC
                                |||||   ||||| |||||||||
                                GGCCG   GTGTG CCGGAGCCG
                                   AGT    A
GAM729  DKFZp667O2416 5'  CCGCGGGGCGCGGAGCCGA   70934      CC      GG  T
                                TCGGC  CTGCGCC  CC CGG
                                |||||  |||||||  || |||
                                AGCCG  GGCGCGG  GG GCC
                                   A_      __  C
GAM729  DKK2     5'  GCCGAGATCCCGGCGGGACC   27775    C   TGC    C__
                                GG CCC   GCCGG   CTCGGC
                                || |||   |||||   ||||||
                                CC GGG   CGGCC   GAGCCG
                                 A  ____    CTA
GAM729  DMWD     3'  GCTCCCCGGCCAGGGGCC    61552        C    CCTC
                                GGCCCCTG GCCGG    GGC
                                |||||||| |||||    |||
                                CCGGGGAC CGGCC    TCG
                                     _    CC__
GAM729  FLJ10211  5'  CCGAGGCCAGAGCCGGGACC   36364    C   T  GCC
                                GG CCC GC   GGCCTCGG
                                || ||| ||   ||||||||
                                CC GGG CG   CCGGAGCC
                                 A   C  AGA
GAM729  FLJ10350  5'  GCCGAGGCCGGGACTGGGCCGG 97252        CTGCG
                                TCGGCCC    CCGGCCTCGGC
                                |||||||    ||||||||||
                                GGCCGGG    GGCCGGAGCCG
                                    TCAG_
GAM729  FLJ11856  5'  CCGGGAGGCGCAGGGACCGG   44850      C       GG  T
                                TCGG CCCTGCGCC  CC CGG
                                |||| |||||||||  || |||
```

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                                GGCC GGGACGCGG  GG GCC
                                  A       A_ _
GAM729  FLJ20257  5'  CCGCGGCACAGGGGCC     39483        C   GCCT
                                GGCCCCTG GCCG   CGG
                                |||||||| ||||   |||
                                CCGGGGAC CGGC   GCC
                                    A  _____
GAM729  FLJ20356  3'  CTCGGCGCACGAACGCAGGGGC 39139         C_ _______ CTCG
              C                  GGCCCCTGCG  CG    GC   G
                                |||||||||| ||    ||   |
                                CCGGGGACGC  GC    CG   C
                                      AA  ACGIII  GCTC
GAM729  FLJ31762  5'  CCGAGGCCTGGAACAGCC   58764    CCC  CG  _
                                GGC   TG  CC GGCCTCGG
                                |||   ||  || ||||||||
                                CCG   AC  GG CCGGAGCC
                                  ___  AA  T
GAM729  FLJ32762  5'  GCCCGGGGGCGCAGAGGCCGG  59484      C     GG   C
                                TCGGCC CTGCGCC  CCT GGC
                                ||||||  |||||||  |||  |||
                                GGCCGG GACGCGG  GGG CCG
                                   A      __   C
GAM729  GPS2      5'  GCCGGATGTGACGCAGGGGCC  16890         _______
                                GGCCCCTGCG     CCGGC
                                ||||||||||     |||||
                                CCGGGGACGC     GGCCG
                                      AGTGTA
GAM729  KIAA0441  5'  GGCGGCGCAGGAGCAGA     29637    G  C       G
                                TC GC CCTGCGCCG CC
                                || || |||||||||  ||
                                AG CG GGACGCGGC GG
                                 A  A       _
GAM729  KIAA0494  5'  GCCGAAGCCGGAGCAGGGGCCG 29402          G    C
              G                  TCGGCCCCTGC CCGGC TCGGC
                                ||||||||||| ||||| |||||
                                GGCCGGGGACG GGCCG AGCCG
                                      A    A
GAM729  KIAA0995  5'  CCGAGGCCGAGCTGGGGCCGG  73251        T  GC
                                TCGGCCCC GC  CGGCCTCGG
                                ||||||||  ||  |||||||||
                                GGCCGGGG CG  GCCGGAGCC
                                    T  A_
GAM729  KIAA1280  5'  GCCGAGGCTGACAGGGACCGG  70284     C    CGC
                                TCGG CCCTG   CGGCCTCGGC
                                ||||  |||||   ||||||||||
                                GGCC GGGAC   GTCGGAGCCG
                                  A    A__
GAM729  KIAA1940  3'  CCAAGGCTCCAAAGGCTGA   80779       CC  CGCC    C
                                TCGGCC  TG   GGCCT GG
                                ||||||  ||   ||||| ||
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                                AGTCGG  AC    TCGGA CC
                                   AA  C___    A
GAM729  KIAA1981  3'  GCCGAGGCCACGGGAGCTGA   89715      C    CGCC
                                TCGGC CCTG    GGCCTCGGC
                                ||||| ||||    |||||||||
                                AGTCG GGGC    CCGGAGCCG
                                   A    A___
GAM729  MGC10520  5'  GCTCGGCGGCGCTGAGGCC    48337      CCT     G  TC
                                GGCC   GCGCCG CC  GGC
                                ||||   |||||| ||  |||
                                CCGG   CGCGGC GG  TCG
                                  AGT      _  C_
GAM729  PDCD7     5'  GCCCGGGAACGCGAGGCCGA   72607       CC    CCGG   C
                                TCGGCC  TGCG    CCT GGC
                                ||||||  ||||    ||| |||
                                AGCCGG  GCGC    GGG CCG
                                   A_    AA__   C
GAM729  PGLYRP    5'  GCCGAGGTTCTCTGCCGAGGCC 54670      CCT   CC_
                                GGCC   GCG   GGCCTCGGC
                                ||||   |||   |||||||||
                                CCGG   CGT   TTGGAGCCG
                                  AGC   CTC
GAM729  LOC113523 5'  GCCGGCTCGGCGCGGGGGCC   73426           _   TC
                                GGCCCCTGCGCCG GCC  GGC
                                |||||||||||| |||  |||
                                CCGGGGGCGCGGC CGG  CCG
                                      T   __
GAM729  LOC131583 5'  GCCGAGCCTGGCAGGGGCCGG  76382         GC    C
                                TCGGCCCCT  GCCGG CTCGGC
                                |||||||||  ||||| ||||||
                                GGCCGGGGA  CGGTC GAGCCG
                                     __     C
GAM729  LOC196214 5'  CCGAGGCCAGCGCCCTGA    91175      CCCCT    C
                                TCGG     GCGC GGCCTCGG
                                ||||     |||| ||||||||
                                AGTC     CGCG CCGGAGCC
                                  C____    A
GAM729  LOC200186 5'  GCCGAGGCCGCGGCGGAGGCCG 91567       C    GC
                                CGGCC CTGC  CGGCCTCGGC
                                ||||| ||||  ||||||||||
                                GCCGG GGCG  GCCGGAGCCG
                                   A    GC
GAM729  LOC201324 5'  GCCCAGGGCACAGAGGCCGG   69097       C   C   GGC  C
                                TCGGCC CTG GCC   CT GGC
                                |||||| ||| |||   || |||
                                GGCCGG GAC CGG   GA CCG
                                   A  A   ___  C
GAM729  LOC206836 5'  CCGAGGCCAGCGCCCCGG    91106      CCCCT    C
                                TCGG     GCGC GGCCTCGG
                                ||||     |||| ||||||||
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                                GGCC    CGCG CCGGAGCC
                                  C____   A
GAM729  LOC219686 5'  GCCGAGGCGCCGGAGGAGGCCG 92509      _  G  C  G
            A                      TCGGCC CCT CG CG CCTCGGC
                                   |||||| ||| || || |||||||
                                   AGCCGG GGA GC GC GGAGCCG
                                      A  G  C  _
GAM729  LOC220001 5'  CTCGGCGCGCGGCGCAGGAGCC 93276      C       _______ CTCG
            GA                     TCGGC CCTGCGCCG     GC   G
                                   ||||| |||||||||     ||   |
                                   AGCCG GGACGCGGC     CG   C
                                     A       GCGIII  GCTC
GAM729  LOC220758 5'  CCGAGGCCAGGAGAGGGGCCGA 92463        GCG  _
                                   TCGGCCCCT   CC GGCCTCGG
                                   |||||||||   || ||||||||
                                   AGCCGGGGA   GG CCGGAGCC
                                        GA_  A
GAM729  LOC245744 3'  GCAGCGCGCAGGGGCCGA    92785          CG_
                                   TCGGCCCCTGCGC   GC
                                   ||||||||||||   ||
                                   AGCCGGGGACGCG   CG
                                          CGA
GAM730  ACCN2    5'  GCGCGCGGGCGGGCGGACA    39628       GGG   A
                                   TGTCCG   CTGC CGCGCGC
                                   ||||||   |||| |||||||
                                   ACAGGC   GGCG GCGCGCG
                                      G__   G
GAM730  EDN2     3'  AGCAACCGTGCAGCCACGAACA 10481     C  G       CGC
                                   TGT CG GGCTGCACG   GCT
                                   ||| || |||||||||   |||
                                   ACA GC CCGACGTGC   CGA
                                     A  A       CAA
GAM730  EFNA4    3'  AGCAGTAGACAGCCCTGGACA  19083          CAC  GC
                                   TGTCCGGGGCTG   GC  GCT
                                   ||||||||||||   ||  |||
                                   ACAGGTCCCGAC   TG  CGA
                                          AGA  A_
GAM730  JUN      5'  GCGCGCGCGAGTCGACA     11103      CGG   GCA
                                   TGTC   GGCT   CGCGCGC
                                   ||||   ||||   |||||||
                                   ACAG   CTGA   GCGCGCG
                                     ___    GC_
GAM730  KCNQ4    5'  AGCGCGCCCCCGCCCCGGAC   17476         TGCAC
                                   GTCCGGGGC    GCGCGCT
                                   |||||||||    |||||||
                                   CAGGCCCCG    CGCGCGA
                                        CCCC_
GAM730  KRTHA2   3'  AGCAGGGCCAGCCCCGGTCA   11239    T       CAC  GC_
                                   TG CCGGGGCTG   GC   GCT
                                   || |||||||||   ||   |||
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                                AC GGCCCCGAC   CG   CGA
                                 T        ___  GGA
GAM730  M11S1   5'  AGCGCGCGACACTGCCCGGA  20909       G TGCA_
                                TCCGGG C    CGCGCGCT
                                |||||| |    ||||||||
                                AGGCCC G    GCGCGCGA
                                   _ TCACA
GAM730  MARK3   5'  AGCGCGCGTGCAGCCCCGGACA 11459
                                TGTCCGGGGCTGCACGCGCGCT
                                ||||||||||||||||||||||
                                ACAGGCCCCGACGTGCGCGCGA

GAM730  MEF2C   5'  AGCACACGCGTACACCCAGACA 11530     CG   C  C    C__
                                TGTC  GGG TG ACGCG   GCT
                                ||||  ||| || |||||   |||
                                ACAG  CCC AC TGCGC   CGA
                                  A_  _ A    ACA
GAM730  PAX2    3'  GCGCGGCCCAGCCCCGGGCA  15660          CA_
                                TGTCCGGGGCTG   CGCGC
                                ||||||||||||   |||||
                                ACGGGCCCCGAC   GCGCG
                                      CCG
GAM730  PAX2    3'  GCGCGGCCCAGCCCCGGGCA  15667          CA_
                                TGTCCGGGGCTG   CGCGC
                                ||||||||||||   |||||
                                ACGGGCCCCGAC   GCGCG
                                      CCG
GAM730  RNF6    5'  AGCACACGTTCTCCGGACA   21084        CTGC   CGC
                                TGTCCGGGG    ACG   GCT
                                |||||||||    |||   |||
                                ACAGGCCTC    TGC   CGA
                                     T____   ACA
GAM730  UMPK    5'  AGCGGCCTCAGCCCCGGCA   25935    T       CAC  G
                                TG CCGGGGCTG   GC CGCT
                                || |||||||||   || ||||
                                AC GGCCCCGAC   CG GCGA
                                 _        TC_  _
GAM730  ZNF264  5'  AGCGCGCCTGGAAGCCCCGGGC 14195          G_  C
            A                    TGTCCGGGGCT  CA GCGCGCT
                                |||||||||||  || |||||||
                                ACGGGCCCCGA  GT CGCGCGA
                                      AG  C
GAM730  CHST3   3'  GCTGGCAGCCCCAGCA      16240     CC       A  C
                                TGT  GGGGCTGC CG GC
                                |||  |||||||| || ||
                                ACG  CCCCGACG GT CG
                                  A_       _ _
GAM730  CRMP5   5'  AGCGCGCGTGCAGCCGCCG   39701     _
                                CGG GGCTGCACGCGCGCT
                                ||| ||||||||||||||
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                                GCC CCGACGTGCGCGCGA
                                  G
GAM730  FLJ00058  5'  AGCGCGCGTGCACCTCCAGAC  79505     C   C
                                GTC GGGG TGCACGCGCGCT
                                ||| |||| ||||||||||||
                                CAG CCTC ACGTGCGCGCGA
                                  A   C
GAM730  FLJ10520  3'  AGCGCCTAGCAGCCCCAAGCA  36697     CC      ACGC
                                TGT  GGGGCTGC   GCGCT
                                |||  ||||||||   |||||
                                ACG  CCCCGACG   CGCGA
                                  AA      ATC_
GAM730  FLJ13910  3'  AGCTCTGCATGCAGCCCCAGCA 43249     CC      C  C_
                                TGT  GGGGCTGCA GCG  GCT
                                |||  ||||||||| |||  |||
                                ACG  CCCCGACGT CGT  CGA
                                  A_       A  CT
GAM730  FLJ20457  5'  AGCGCGCGTGCGCACGACA   35670     C GG  T
                                TGTC G  GC GCACGCGCGCT
                                |||| |  || ||||||||||
                                ACAG C  CG CGTGCGCGCGA
                                  _ A_ _
GAM730  HSU79303  3'  GCGCGACGGCCCCGGAC     26151         CA
                                GTCCGGGGCTG  CGCGC
                                ||||||||||  |||||
                                CAGGCCCCGGC  GCGCG
                                      A_
GAM730  KIAA0090  3'  AGCTCACTGCAGCCTCGAACA  89809     C       CGCGC
                                TGT CGGGGCTGCA    GCT
                                ||| ||||||||||    |||
                                ACA GCTCCGACGT    CGA
                                  A       CACT_
GAM730  KIAA0218  5'  AGCGCTTCGTAGCCCCGGA   29291         ACGC
                                TCCGGGGCTGC   GCGCT
                                ||||||||||   |||||
                                AGGCCCCGATG   CGCGA
                                      CTT_
GAM730  PAK6      5'  AGCAGCTGCCAGCCCCGGCA  39807    T      _  C  GC
                                TG CCGGGGCTG CA GC  GCT
                                || |||||||| || ||  |||
                                AC GGCCCCGAC GT CG  CGA
                                  _       C  _  A_
GAM730  PCAF      5'  AGCGCGCGGGGCCCGGCCA   15283    T    G  GCA
                                TG CCGGG CT   CGCGCGCT
                                || ||||| ||   ||||||||
                                AC GGCCC GG   GCGCGCGA
                                  C    G  ____
GAM730  PL6       3'  GCTGGCAGCCCCAAGCA     23815     CC      A  C
                                TGT  GGGGCTGC CG GC
                                |||  |||||||| || ||
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                                ACG  CCCCGACG GT CG
                                  AA       _ _
GAM730  LOC130367 5'  GCGCGGCCCCGGGCA       75436          TGCA
                                TGTCCGGGGC    CGCGC
                                ||||||||||    |||||
                                ACGGGCCCCG    GCGCG
                                      ____
GAM730  LOC143098 3'  AGCCATGAGCAGCTCCAGACA  76973      C       A  CGC
                                TGTC GGGGCTGC CG   GCT
                                |||| |||||||| ||   |||
                                ACAG CCTCGACG GT   CGA
                                  A       A  AC_
GAM730  LOC150115 5'  CGCGGCGGCCCGGACA      80387        G    A
                                TGTCCGGG CTGC CGCG
                                |||||||| |||| ||||
                                ACAGGCCC GGCG GCGC
                                      _    _
GAM730  LOC153397 5'  AGCGCGCGCGCGCACATACA   87225     CCGGG  T  A
                                TGT     GC GC CGCGCGCT
                                |||     || || ||||||||
                                ACA     CG CG GCGCGCGA
                                  TACA_  _  C
GAM730  LOC195977 3'  GGCTCGCTGCAGCCCAAACA   88934     CCG       C   C
                                TGT   GGGCTGCA GCG GCT
                                |||   |||||||| ||| |||
                                ACA   CCCGACGT CGC CGG
                                  AA_       _   T
GAM730  LOC257458 5'  GCGTCACCAACCCCGGGCA    68402          C  CAC
                                TGTCCGGGG TG   GCGC
                                |||||||||  ||   ||||
                                ACGGGCCCC AC   TGCG
                                      A  CAC
GAM731  ABCB1     3'  AGTCAAGTTCAGAGTCTTC    8111         GGTC
                                GAAGAC    GAACTTGACT
                                ||||||    ||||||||||
                                CTTCTG    CTTGAACTGA
                                   AGA_
GAM731  AOC3      3'  AGTCAAGTTCCGTCTCCTC    14958     A     TCG
                                GAG AGACGG   AACTTGACT
                                |||  ||||||   |||||||||
                                CTC TCTGCC   TTGAACTGA
                                  C     ___
GAM731  MARK3     5'  TAGTCAAGTTCGACCGTCTTCT 11463
              CA                  TGAGAAGACGGTCGAACTTGACTA
                                ||||||||||||||||||||||||||
                                ACTCTTCTGCCAGCTTGAACTGAT

GAM731  SYBL1     3'  AGTCTCTTCAACCCTCTTCTCA 20109          C   C   CTT
                                TGAGAAGA GGT GAA   GACT
                                ||||||||  ||| |||   ||||
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                                ACTCTTCT CCA CTT   CTGA
                                    C   A   CT_
GAM731   C20orf36  3'  TAGTCAAGCTTCAGTCTTTCA  37336      A   GGTC  _
                                TGAGA GAC    GAA CTTGACTA
                                ||||| |||    ||| ||||||||
                                ACTTT CTG    CTT GAACTGAT
                                  _   A___   C
GAM731   CAPS2     3'  CAAGTTTCCTGTCCTTTCA   71126      A    TC
                                TGAGA GACGG  GAACTTG
                                ||||| |||||  |||||||
                                ACTTT CTGTC  TTTGAAC
                                  C    C_
GAM731   FLJ20085  3'  AGTCTTTGACTGCCTTCCCA  35003    A   A      CTT
                                TG GAAG CGGTCGAA   GACT
                                || |||| ||||||||   ||||
                                AC CTTC GTCAGTTT   CTGA
                                 C   C       ___
GAM731   RERG      3'  AGTTCAAGCATCTTCTCA    52999        CG  C_
                                TGAGAAGA  GT  GAACT
                                ||||||||  ||  |||||
                                ACTCTTCT  CG  CTTGA
                                    A_  AA
GAM731   LOC157421 5'  TAGTCAAGCGGGGGTCGTCTCA 87740      A   GG   AA
                                TGAGA GAC  TCG  CTTGACTA
                                ||||| |||  |||  ||||||||
                                ACTCT CTG  GGC  GAACTGAT
                                  G   GG  __
GAM731   LOC221300 3'  CAAATTCCTTCCTTTTCTCA  93574        C  TC_   C
                                TGAGAAGA GG   GAA TTG
                                |||||||| ||   ||| |||
                                ACTCTTTT CC   CTT AAC
                                    _  TTC   A
GAM731   LOC254828 3'  AAGCTCCGACCGTCCTCTC   98413      A       AA_
                                GAGA GACGGTCG   CTT
                                |||| ||||||||   |||
                                CTCT CTGCCAGC   GAA
                                  C       CTC
GAM731   LOC256663 5'  TAGTCAAGCTCTACTCCCTTC  98748      AC   C  A
                                GAAG  GGT GA CTTGACTA
                                ||||  ||| || ||||||||
                                CTTC  TCA CT GAACTGAT
                                  CC   T  C
GAM732   ARNT2     3'  TCTGAGCCCATGATCCCTGGCT 30091    G  TT        C
                                AG CA  GATCATGGGC CAGA
                                || ||  |||||||||| ||||
                                TC GT  CTAGTACCCG GTCT
                                 G  CC         A
GAM732   DLG5      5'  GGCCTGTCCCAGTGCCT     83819         ATC
                                AGGCATTG   ATGGGCC
                                ||||||||   |||||||
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                                TCCGTGAC  TGTCCGG
                                    CC_
GAM732  HK1     3'  TTCTGGGCCTCCAAAGCC   5750     A  ATCAT
                                GGC TTG   GGGCCCAGAA
                                ||| |||   ||||||||||
                                CCG AAC   TCCGGGTCTT
                                  A  C____
GAM732  KL      3'  CTGCCATAATAATGCCT    17743       ATC   GCC
                                AGGCATTG  ATGG  CAG
                                ||||||||  ||||  |||
                                TCCGTAAT  TACC  GTC
                                    AA_   ___
GAM732  LOX     3'  CCCAATGGATAAATCAGTGCCT 11344        _____  _
                                AGGCATTGAT    CAT GGG
                                ||||||||||    ||| |||
                                TCCGTGACTA    GTA CCC
                                     AATAG  A
GAM732  NTSR1   3'  TCCCGGGCCTGTCCCCAACTCC 11865    CA  ATC     A_
          T                      AGG  TTG  ATGGGCCC  GA
                                ||| |||  ||||||||  ||
                                TCC  AAC  TGTCCGGG  CT
                                  TC  CCC      CC
GAM732  OGDH    3'  CTGGGCCCAGGCAGCACCT   92749    CA  A  A
                                AGG  TTG TC TGGGCCCAG
                                |||  ||| || |||||||||
                                TCC  GAC GG ACCCGGGTC
                                  AC  _ _
GAM732  PEA15   3'  CTGGGCTTGTGAACACCT    15008    CAT  A  TG
                                AGG   TG TCA  GGCCCAG
                                |||   || |||  |||||||
                                TCC   AC AGT  TCGGGTC
                                  ___  A  GT
GAM732  SELPLG  5'  CTTCTGGGCCCACGAGGCAGCT 60419    AT  A_  A
                                GGC  TG  TC TGGGCCCAGAAG
                                |||  ||  || ||||||||||||
                                TCG  AC  AG ACCCGGGTCTTC
                                  __  GG  C
GAM732  SIP     3'  CTGAAGTCAGGACCAGTGCCT  27732       A  ATG  C_
                                AGGCATTG TC   GGC  CAG
                                |||||||| ||   |||  |||
                                TCCGTGAC AG   CTG  GTC
                                    C  GA_   AA
GAM732  TLL1    3'  CTTCTAATTTTGATCAATCC   25876    C      TG GCCC
                                GG ATTGATCA  G    AGAAG
                                || ||||||||  |    |||||
                                CC TAACTAGT  T    TCTTC
                                 _      TT AA__
GAM732  C1orf26 3'  CTTCTGGAGTTCACAATGCCT  35066       ATCA   _
                                AGGCATTG   TGGGC CCAGAAG
                                ||||||||   ||||| |||||||
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                                TCCGTAAC   ACTTG GGTCTTC
                                     ____    A
GAM732  DKFZp434I099 3'  TCTATCCAGCCAATGCCT    51079       ATCA   CCC
                                AGGCATTG   TGGG  AGA
                                ||||||||   ||||  |||
                                TCCGTAAC   ACCT  TCT
                                    CG__   A__
GAM732  FLJ10375  3'  CTGAACCCAGACCCAATGCTT  36557       A_ A   CC
                                AGGCATTG  TC TGGG  CAG
                                ||||||||  || ||||  |||
                                TTCGTAAC  AG ACCC  GTC
                                    CC  _   AA
GAM732  FLJ12649  3'  CTGGGCCCATCAGTCCT     45089    C    TCA
                                AGG ATTGA   TGGGCCCAG
                                ||| |||||   |||||||||
                                TCC TGACT   ACCCGGGTC
                                  _    ___
GAM732  FLJ20507  3'  CTTCCAAGCCCATGGTAGTCCC 35737    C  G       CCA
           T                     AGG ATT ATCATGGGC   GAAG
                                ||| ||| |||||||||   ||||
                                TCC TGA TGGTACCCG   CTTC
                                  C  _       AAC
GAM732  FLJ20626  3'  CTTCTATGGCTGACCAGTGCCT 35903       A  TGG  C_
                                AGGCATTG TCA   GCC  AGAAG
                                |||||||| |||   |||  |||||
                                TCCGTGAC AGT   CGG  TCTTC
                                    C   ___   TA
GAM732  FLJ23519  3'  CTGTGACTGATCAGTGCCT   50948         TG GCC
                                AGGCATTGATCA  G   CAG
                                ||||||||||||  |   |||
                                TCCGTGACTAGT  C   GTC
                                      __ AGT
GAM732  KIAA0014  3'  CTTCTGGGCACACCTCAAGCCT 28541     A   TCA  G
                                AGGC TTGA   TG GCCCAGAAG
                                |||| ||||   || |||||||||
                                TCCG AACT   AC CGGGTCTTC
                                  _   CC_  A
GAM732  MAPKAPK2  3'  CCCAGGAGGAGATGACCAGTGC 17661       A  _________
           CT                    AGGCATTG TCA       TGGG
                                |||||||| |||       ||||
                                TCCGTGAC AGT       ACCC
                                    C   AGAGGAGG
GAM732  MGC13251  3'  CTCATGACAATCTAATGCCT   52136       _ ___
                                AGGCATT GA   TCATGGG
                                ||||||| ||   |||||||
                                TCCGTAA CT   AGTACTC
                                    T  AAC
GAM732  P2RX1    3'  CTGGGCCCACCCCCAGACCT   67750     CA   ATCA
                                AGG  TTG   TGGGCCCAG
                                |||  |||   |||||||||
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                                TCC  GAC    ACCCGGGTC
                                  A_   CCCC
GAM732  PRO0899   5' CTGGGCCCAAGAGATCCT    38308     C   GA  A
                                AGG ATT  TC TGGGCCCAG
                                ||| |||  || |||||||||
                                TCC TAG  AG ACCCGGGTC
                                  _   __  A
GAM732  PRO0899   5' CTGGGCCCAAGCAATCCT    38309     C    ATCA
                                AGG ATTG    TGGGCCCAG
                                ||| ||||    |||||||||
                                TCC TAAC    ACCCGGGTC
                                  _    GA__
GAM732  TESK2     3' TTCTGGGCTCCCAGTGCC     63888       ATCAT
                                GGCATTG     GGGCCCAGAA
                                |||||||     ||||||||||
                                CCGTGAC     CTCGGGTCTT
                                    C_____
GAM732  LOC124044 3' TCTGGGCCCACAACTCCCT    76534     CA_   ATCA
                                AGG   TTG   TGGGCCCAGA
                                |||   |||   ||||||||||
                                TCC   AAC   ACCCGGGTCT
                                  CTC   _____
GAM732  LOC124997 3' TCTGGGCCCTGAACCCCT    74849     CATTGA   T
                                AGG     TCA GGGCCCAGA
                                |||     ||| |||||||||
                                TCC     AGT CCCGGGTCT
                                  CCA___   _
GAM732  LOC125268 3' CTTCTGAAGAACTGCCAATGCC 76577         AT  TGGGCC
           T                     AGGCATTG  CA     CAGAAG
                                ||||||||  ||     ||||||
                                TCCGTAAC  GT     GTCTTC
                                    C_  CAAGAA
GAM732  LOC134266 3' CTGGGCCCAAGCAATCCT    75645     C   ATCA
                                AGG ATTG    TGGGCCCAG
                                ||| ||||    |||||||||
                                TCC TAAC    ACCCGGGTC
                                  _    GA__
GAM732  LOC146229 3' TCCCGGGCCCTAATGCTT    78318       ATCAT    A_
                                AGGCATTG    GGGCCC  GA
                                ||||||||    ||||||  ||
                                TTCGTAAT    CCCGGG  CT
                                    _____     CC
GAM732  LOC158377 5' CTGGGCCCACGAGGCC      88132     A   ATCA
                                GGC TTG    TGGGCCCAG
                                ||| |||    |||||||||
                                CCG AGC    ACCCGGGTC
                                  G   _____
GAM732  LOC197136 3' TCTGGGCCCACAACTCCCT    91288     CA_   ATCA
                                AGG   TTG   TGGGCCCAGA
                                |||   |||   ||||||||||
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                                TCC  AAC   ACCCGGGTCT
                                  CTC  ____
GAM732  LOC202460 5'  CTTATGATAATCTAATGCCT  90670       ____
                                AGGCATTG   ATCATGGG
                                ||||||||   ||||||||
                                TCCGTAAT   TAGTATTC
                                    CTAA
GAM732  LOC254105 3'  CTGGGCCTGCACTGCCT    96420     T  ATCA
                                AGGCA TG   TGGGCCCAG
                                ||||| ||   |||||||||
                                TCCGT AC   GTCCGGGTC
                                  C ____
GAM733  DXYS155E  3'  GCAGCCCGTCCTGGACATCCTG 18689     _  CGTTTC
          CA                    TGCAG ATG    GACGGGCTGC
                                ||||| |||    ||||||||||
                                ACGTC TAC    CTGCCCGACG
                                  C  AGGTC_
GAM733  DKFZp434N0650 3'  GCAGCCCGCCGCTGCCCGCACC 51055     A   TTT__  A
          TGC                   GCAG TGCG    CG CGGGCTGC
                                |||| ||||    || ||||||||
                                CGTC ACGC    GC GCCCGACG
                                  C   CCGTC  C
GAM733  QKI     5'  GCAGCCCGCGCCCCGCGCCCGC 66048    AGA   TTT  A
          A                     TGC  TGCG   CG CGGGCTGC
                                |||  ||||   || ||||||||
                                ACG  GCGC   GC GCCCGACG
                                  CCC   CCC  _
GAM733  LOC147160 5'  GCAGCCCGGGTGCACGCCCTGC 85077     AT   TTCGA
          A                     TGCAG  GCGT    CGGGCTGC
                                |||||  ||||    ||||||||
                                ACGTC  CGCA    GCCCGACG
                                  C_   CGTGG
GAM733  LOC157531 5'  GCAGCCCGTCAAGCGATCCCAT 87767     ____    C
          C                     GATG   CGTTT GACGGGCTGC
                                ||||   ||||| ||||||||||
                                CTAC   GCGAA CTGCCCGACG
                                  CCTA   _
GAM733  LOC158956 5'  GCAGCCCGCAGGCACCCGGCA  67214    AGA_  GTTT GA
                                TGC   TGC   C  CGGGCTGC
                                |||   |||   |  ||||||||
                                ACG   ACG   G  GCCCGACG
                                  GCCC  ____ AC
GAM733  LOC196484 5'  CAGTTTGAGAAAAGCATCTGCA 63538       G   GA
                                TGCAGATGC TTTC  CGGGCTG
                                ||||||||| ||||  |||||||
                                ACGTCTACG AAAG  GTTTGAC
                                    A   A_
GAM733  LOC220073 5'  CAGGAGAAAAGCATCTGCA   95073       G   GACGGG
                                TGCAGATGC TTTC    CTG
                                ||||||||| ||||    |||
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                                ACGTCTACG AAAG     GAC
                                     A   AG____
GAM734  APOL1   3' ACTACAGGCGCCTACCACCATG 14720     TAT  CCA_
                                CATG  GT   GCCTGTAGT
                                ||||  ||   |||||||||
                                GTAC  CA   CGGACATCA
                                  CAC  TCCG
GAM734  BSN     3' ACTACAGGCCAGGGGATG    14375    G   A_
                                TAT TCC  GCCTGTAGT
                                ||| |||  |||||||||
                                GTA GGG  CGGACATCA
                                  G  AC
GAM734  CASP10  3' ACTACAGGCATGAAATACTGTG 53236     T   G  CA
                                CACA GTAT TC  GCCTGTAGT
                                |||| |||| ||  |||||||||
                                GTGT CATA AG  CGGACATCA
                                  _   A  TA
GAM734  CASP10  3' ACTACAGGCATGAAATACTGTG 53237     T   G  CA
                                CACA GTAT TC  GCCTGTAGT
                                |||| |||| ||  |||||||||
                                GTGT CATA AG  CGGACATCA
                                  _   A  TA
GAM734  CSPG4   3' GGGCTAAACATGCATGTG    10326         CC
                                CACATGTATGT  AGCCT
                                ||||||||||  |||||
                                GTGTACGTACA  TCGGG
                                      AA
GAM734  IARS    3' CTATCCCCTACACATACATG   10979        CC  CCT
                                CATGTATGT  AG   GTAG
                                |||||||||  ||   ||||
                                GTACATACA  TC   TATC
                                     CA  CCC
GAM734  NCF4    5' ACCACAGGCTGAGACGAGAC   7145    A_   _     A
                                GT  TGTC CAGCCTGT GT
                                ||  |||| |||||||| ||
                                CA  GCAG GTCGGACA CA
                                 GA   A      C
GAM734  PCDHA9  3' ACTACAGGCGCCTGCCACCATG 49830     TAT  CCA_
                                CATG  GT   GCCTGTAGT
                                ||||  ||   |||||||||
                                GTAC  CG   CGGACATCA
                                  CAC  TCCG
GAM734  RPP30   3' ACTACAGGCGCTCGCCATGT   22188     TA  TCCA
                                ACATG  TG   GCCTGTAGT
                                |||||  ||   |||||||||
                                TGTAC  GC   CGGACATCA
                                  C_  TCG_
GAM734  SLC4A1  3' ACTGAGGACCAAAGATACATGT 6220        GTCCAG_  G
                                ACATGTAT     CCT TAGT
                                ||||||||     ||| ||||
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                                TGTACATA      GGA GTCA
                                    GAAACCA  _
GAM734  UGDH     3'  ACTACAGGCACCCGCCACAGTG 13988     A   ATGTCCA
                                CAC TGT      GCCTGTAGT
                                ||| |||      |||||||||
                                GTG ACA      CGGACATCA
                                  _  CCGCCCA
GAM734  ARHGAP10  3'  ACTACAGCCAGAAGAACATATA 40828        _ CAGC__
          T                      ATGTATGT C     CTGTAGT
                                ||||||||  |     |||||||
                                TATATACA G     GACATCA
                                    A AAGACC
GAM734  BIRC4    3'  ACTATAACTGAACACAATGTG  8600       GTA   C   CC
                                CACAT   TGT CAG  TGTAGT
                                |||||   ||| |||  ||||||
                                GTGTA   ACA GTC  ATATCA
                                   AC_   A   A_
GAM734  C11orf17  3'  ACTACAGGCACCCGCCACCATG 40572     TAT  CCA_
                                CATG   GT    GCCTGTAGT
                                ||||   ||    |||||||||
                                GTAC   CG    CGGACATCA
                                  CAC  CCCA
GAM734  CTCF     3'  CAGTGACGGACATGCACGTG   22677     A       AGC_
                                CAC TGTATGTCC    CTG
                                ||| |||||||||    |||
                                GTG ACGTACAGG    GAC
                                  C        CAGT
GAM734  FLJ00060  5'  ACTACAGGCGCCCACCACCATG 61730     TAT  CCA_
                                CATG   GT    GCCTGTAGT
                                ||||   ||    |||||||||
                                GTAC   CA    CGGACATCA
                                  CAC  CCCG
GAM734  FLJ10846  3'  ACTACAGGCACCTGCCACCATG 37282     TAT  CCA_
                                CATG   GT    GCCTGTAGT
                                ||||   ||    |||||||||
                                GTAC   CG    CGGACATCA
                                  CAC  TCCA
GAM734  FLJ12960  3'  ACTACAGGCGCCCGCCACCATG 45288     TAT  CCA_
                                CATG   GT    GCCTGTAGT
                                ||||   ||    |||||||||
                                GTAC   CG    CGGACATCA
                                  CAC  CCCG
GAM734  FLJ20511  3'  ACTACAGGCGCCCGCCACCATG 35763     TAT  CCA_
                                CATG   GT    GCCTGTAGT
                                ||||   ||    |||||||||
                                GTAC   CG    CGGACATCA
                                  CAC  CCCG
GAM734  FLJ21777  3'  ACTACAGGCCCCGAAGCACGT  50830     ATG  CA_
                                ATGT   TC   GCCTGTAGT
                                ||||   ||   |||||||||
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                                TGCA  AG  CGGACATCA
                                  CGA CCC
GAM734  GPR107   3' ACCACAGGCTGCCATAGCA   40911    _  TC      A
                                TGT ATG  CAGCCTGT GT
                                ||| |||  |||||||| ||
                                ACG TAC  GTCGGACA CA
                                  A  C_      C
GAM734  KIAA1924 3' ACTACAGGCGCCTGCCAACATG 74038      AT  CCA_
                                CATGT  GT   GCCTGTAGT
                                |||||  ||   |||||||||
                                GTACA  CG   CGGACATCA
                                   AC  TCCG
GAM734  NYD-SP29 3' ACTGGCATGCTGAACATATAT  75077        C   C  _
                                ATGTATGT CAGC TGT AGT
                                |||||||| |||| ||| |||
                                TATATACA GTCG ACG TCA
                                     A   T  G
GAM734  PRDM8    5' ACTACAGTTTCCTACATGTG   39971        TGTCCAGC
                                CACATGTA      CTGTAGT
                                ||||||||      |||||||
                                GTGTACAT      GACATCA
                                     CCTTT___
GAM734  SS18L1   3' ACAGCTGGACACACATG     65943      A      C
                                CATGT TGTCCAGC TGT
                                ||||| |||||||| |||
                                GTACA ACAGGTCG ACA
                                   C      _
GAM734  LOC125228 3' ACTATGGGCAAAGATACATGTG 74861         GTCCA
                                CACATGTAT    GCCTGTAGT
                                |||||||||    |||||||||
                                GTGTACATA    CGGGTATCA
                                     GAAA_
GAM734  LOC128989 3' ACTCACATGGCACACACATACA 75306        CCA_  _  _
                                TGTATGT   GCC TGT AGT
                                |||||||   ||| ||| |||
                                ACATACA   CGG ACA TCA
                                     CACA  T  C
GAM734  LOC130074 3' ACCACAGGCTGTGCCCATG   76620      TAT TC      A
                                CATG  G  CAGCCTGT GT
                                ||||  |  |||||||| ||
                                GTAC  C  GTCGGACA CA
                                  C__ GT       C
GAM734  LOC143153 3' ACTACAGGCCACGGCCACCATG 76975      TAT  CA_
                                CATG  GTC  GCCTGTAGT
                                ||||  |||  |||||||||
                                GTAC  CGG  CGGACATCA
                                  CAC  CAC
GAM734  LOC143154 3' ACTACAGGCCACGGCCACCATG 76986      TAT  CA_
                                CATG  GTC  GCCTGTAGT
                                ||||  |||  |||||||||
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                                GTAC  CGG  CGGACATCA
                                  CAC  CAC
GAM734  LOC148147 3' ACTACAGGCCTCCATCACCATG 79382     T__  TCCA
                                CATG  ATG  GCCTGTAGT
                                ||||  |||  |||||||||
                                GTAC  TAC  CGGACATCA
                                  CAC  CTC_
GAM734  LOC150596 3' ACTACAGGATGGATACTTAT  80747    TA    G
                                ATG  TGTCCA CCTGTAGT
                                |||  |||||| ||||||||
                                TAT  ATAGGT GGACATCA
                                  TC    A
GAM734  LOC199699 3' ACTACAGGCACCCGCCACCATG 89661     TAT  CCA_
                                CATG  GT   GCCTGTAGT
                                ||||  ||   |||||||||
                                GTAC  CG   CGGACATCA
                                  CAC  CCCA
GAM734  LOC200382 3' GGGCCAGACTTACATGTG    90237       T  CA
                                CACATGTA GTC  GCCT
                                |||||||| |||  ||||
                                GTGTACAT CAG  CGGG
                                    T  AC
GAM734  LOC201952 3' ACCACAGGCCTGGCACATTGTG 91875     TGT  _  _   A
                                CACA  ATGT CCAG CCTGT GT
                                ||||  |||| |||| ||||| ||
                                GTGT  TACA GGTC GGACA CA
                                  ___  C  C   C
GAM734  LOC202908 5' ACCACAGGCTGGAGTACAGTG  90703    A   G       A
                                CAC TGTAT TCCAGCCTGT GT
                                ||| ||||| |||||||||| ||
                                GTG ACATG AGGTCGGACA CA
                                  _   _       C
GAM734  LOC202908 5' ACTACAGGCGCCTGCCACCATG 90704     TAT  CCA_
                                CATG  GT   GCCTGTAGT
                                ||||  ||   |||||||||
                                GTAC  CG   CGGACATCA
                                  CAC  TCCG
GAM734  LOC203369 3' ACTACAGGCGCCCGCCACCATG 90878     TAT  CCA_
                                CATG  GT   GCCTGTAGT
                                ||||  ||   |||||||||
                                GTAC  CG   CGGACATCA
                                  CAC  CCCG
GAM734  LOC219294 3' ACTACAGGCCACGGCCACCATG 94592     TAT  CA_
                                CATG  GTC  GCCTGTAGT
                                ||||  |||  |||||||||
                                GTAC  CGG  CGGACATCA
                                  CAC  CAC
GAM734  LOC219295 3' ACTACAGGCCACGGCCACCATG 94583     TAT  CA_
                                CATG  GTC  GCCTGTAGT
                                ||||  |||  |||||||||
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                                GTAC  CGG  CGGACATCA
                                  CAC  CAC
GAM734  LOC219731 5'  ACTACAGGCTTGCACTAC   94694    _  CC
                                GTA TGT  AGCCTGTAGT
                                ||| |||  ||||||||||
                                CAT ACG  TCGGACATCA
                                  C  T_
GAM734  LOC220662 3'  ACTACAGGCCCACACTAC   92800    _  CCA
                                GTA TGT  GCCTGTAGT
                                ||| |||  |||||||||
                                CAT ACA  CGGACATCA
                                  C  CC_
GAM734  LOC256905 3'  ACTGCAATAAACATACATGTG  98657         CCAGCC
                                CACATGTATGT    TGTAGT
                                ||||||||||    ||||||
                                GTGTACATACA    ACGTCA
                                      AATA__
GAM734  LOC91115  3'  ACTACAGGCACCCGCCACCATG 65540     TAT  CCA_
                                CATG  GT   GCCTGTAGT
                                ||||  ||   |||||||||
                                GTAC  CG   CGGACATCA
                                  CAC  CCCA
GAM734  LOC91561  5'  ACTACAGGCGCTGGCCACCACA 67037    A_  T  __
                                TGT  TG CCA  GCCTGTAGT
                                |||  || |||  |||||||||
                                ACA  AC GGT  CGGACATCA
                                  CC  C  CG
GAM735  C7orf2    3'  GTACAGTCTAATAAGCTGTGG  42637        CCCCATT
                                CCACAGCTTA     CTGTAC
                                ||||||||||     ||||||
                                GGTGTCGAAT     GACATG
                                     AATCT__
GAM735  CDC27     3'  TACAGAATGAAAGGCAGTG   8834     A   ACCC
                                CAC GCTT   CATTCTGTA
                                ||| ||||   |||||||||
                                GTG CGGA   GTAAGACAT
                                  A   AA__
GAM735  CML66     3'  TGTGGAATGAAGCTGCAGA   68786   CA    ACCC   TG
                                TC  CAGCTT   CATTC  TA
                                ||  ||||||   |||||  ||
                                AG  GTCGAA   GTAAG  GT
                                 AC     ____    GT
GAM735  GCH1      3'  ACAGAATGAACTGACGGTGGA  5677      AGC  CCC
                                TCCAC  TTA  CATTCTGT
                                |||||  |||  ||||||||
                                AGGTG  AGT  GTAAGACA
                                  GC_  CAA
GAM735  LZTR1     5'  TACAGTGACAAGCTGTGGA   23175        ACCCCATT
                                TCCACAGCTT     CTGTA
                                ||||||||||     |||||
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                                AGGTGTCGAA       GACAT
                                     CAGT____
GAM735  MPP5     3'  GCAGCAGTATAAGCTGTAGA  42747    C      CCCC  _
                                TC ACAGCTTA    ATT CTGT
                                || ||||||||    ||| ||||
                                AG TGTCGAAT    TGA GACG
                                 A       A___   C
GAM735  PCDHA9   5'  TGCAGAATAACTGTG       49853      C  CCCCA
                                CACAG TTA     TTCTGTA
                                ||||| |||     |||||||
                                GTGTC AAT     AAGACGT
                                  _  ______
GAM735  PCDHA9   5'  TGCAGAATAACTGTG       26628      C  CCCCA
                                CACAG TTA     TTCTGTA
                                ||||| |||     |||||||
                                GTGTC AAT     AAGACGT
                                  _  ______
GAM735  RHO      3'  ACAGAATGGGGCACACAGTAGG 6766     _  AGCTTA
                                CC AC      CCCCATTCTGT
                                || ||      ||||||||||||
                                GG TG      GGGGTAAGACA
                                 A  ACACAC
GAM735  SCN8A    3'  GCAGAACAGCTGTGGA      27215         TACCCCA
                                TCCACAGCT      TTCTGT
                                |||||||||      ||||||
                                AGGTGTCGA      AAGACG
                                     C_______
GAM735  UPF3B    3'  GCTGGTGGGGTACACTGCAGA  55531    CA   CT       CT
                                TC  CAG  TACCCCATT  GT
                                ||  |||  |||||||||  ||
                                AG  GTC  ATGGGGTGG  CG
                                 AC   AC       T_
GAM735  UPF3B    3'  GCTGGTGGGGTACACTGCAGA  43731    CA   CT       CT
                                TC  CAG  TACCCCATT  GT
                                ||  |||  |||||||||  ||
                                AG  GTC  ATGGGGTGG  CG
                                 AC   AC       T_
GAM735  ANKT     3'  AGAATAGGGTAAGCTGGGA   33453     A        C
                                TCC CAGCTTACCC ATTCT
                                ||| |||||||||| |||||
                                AGG GTCGAATGGG TAAGA
                                  _        A
GAM735  DKFZp434A1520 3'  GCAGGTTGAGGCAAGTGTAGA  61769    C   G   A  C  TT
                                TC ACA CTT CC CA  CTGT
                                || ||| ||| || ||  ||||
                                AG TGT GAA GG GT  GACG
                                 A  _  C  A  TG
GAM735  FLJ10297 3'  GTACAGAGCCAGACAAAGCTGT 36442         ACCCCA_
             G                   CACAGCTT      TTCTGTAC
                                 ||||||||      ||||||||
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                                GTGTCGAA      GAGACATG
                                     ACAGACC
GAM735  FLJ21918  3'  GTACAGAACTGAAGCCTCGGA  46861     ACA    ACCCCA
                                TCC   GCTT     TTCTGTAC
                                |||   ||||     ||||||||
                                AGG   CGAA     AAGACATG
                                  CTC    GTC___
GAM735  GABPB2    3'  TACAGAATGAAAGTGCGTAGT  10752     A  T   CC_
                                AC GC TAC   CATTCTGTA
                                || || |||   |||||||||
                                TG TG GTG   GTAAGACAT
                                 A  C   AAA
GAM735  HRK       3'  ACAGAATGGGACTGGG      15069     A   CTTAC
                                CC CAG     CCCATTCTGT
                                || |||     ||||||||||
                                GG GTC     GGGTAAGACA
                                 _   A_____
GAM735  KIAA0140  3'  GCAGGAAGGGACAAGCTGTGGA 28515          AC   A
                                TCCACAGCTT  CCC TTCTGT
                                ||||||||||  ||| ||||||
                                AGGTGTCGAA  GGG AGGACG
                                      CA   A
GAM735  KIAA1023  3'  GGGTGGGGTGAGCTGTGGA   34682
                                TCCACAGCTTACCCCATTC
                                |||||||||||||||||||
                                AGGTGTCGAGTGGGGTGGG

GAM735  KIAA1483  3'  GTACAACATGACAAGCTGTG   70435        ACCC   TC
                                CACAGCTT    CAT  TGTAC
                                ||||||||    |||  |||||
                                GTGTCGAA    GTA  ACATG
                                     CA__    CA
GAM735  LEC3      3'  ACAGCTGGAATAGCTGTGGA   31529         TACC   TT
                                TCCACAGCT    CCA  CTGT
                                |||||||||    |||  ||||
                                AGGTGTCGA    GGT  GACA
                                      TAA_   C_
GAM735  LGALS8    3'  TACAGAATGGCTTCTGTG    22452       CTTACC
                                CACAG     CCATTCTGTA
                                |||||     ||||||||||
                                GTGTC     GGTAAGACAT
                                   TTC___
GAM735  MRG15     3'  ACAGAGGGATATGCTGTAGA  23282     C    T  C   AT
                                TC ACAGC TA CCC  TCTGT
                                || ||||| || |||  |||||
                                AG TGTCG AT GGG  AGACA
                                 A    T  A   __
GAM735  PRO2730   3'  GCAGGAATAGGCTGTG      48183         CCCCA
                                CACAGCTTA    TTCTGT
                                |||||||||    ||||||
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                                GTGTCGGAT    AGGACG
                                     A____
GAM735  QKI      5'  GCGGGCGGAGTGAGCTGCGGA  66049    A      C  AT
                                TCC CAGCTTAC CC  TCTGT
                                ||| |||||||| ||  |||||
                                AGG GTCGAGTG GG  GGGCG
                                  C       A  C_
GAM735  RP4-622L5 3'  TACAGAATGGAGCCGTG     39430    A   TACC
                                CAC GCT    CCATTCTGTA
                                ||| |||    ||||||||||
                                GTG CGA    GGTAAGACAT
                                  C  _____
GAM735  ZNF271    5'  GAATGGGATAAGTGTGGA    96966      G    C
                                TCCACA CTTA CCCATTC
                                |||||| |||| |||||||
                                AGGTGT GAAT GGGTAAG
                                   _   A
GAM735  LOC147172 3'  ACAGGAGGACAAGTTGTGGA   78900         ACC  A
                                TCCACAGCTT   CC TTCTGT
                                ||||||||||   || ||||||
                                AGGTGTTGAA   GG AGGACA
                                     CA_  _
GAM735  LOC150343 5'  TACAGAATGGAAGGTGTATG   80497    GCT   __
                                CA   TACC  CCATTCTGTA
                                ||   ||||  ||||||||||
                                GT   GTGG  GGTAAGACAT
                                 AT_    AA
GAM735  LOC150606 3'  GTACAGAATTTGGAGCTAAGGA 86271     AC    TA  CC
                                TCC  AGCT  CC  ATTCTGTAC
                                |||  ||||  ||  |||||||||
                                AGG  TCGA  GG  TAAGACATG
                                  AA    __  TT
GAM735  LOC154215 3'  ACAGAAACAGCTGTGGA     81951         TACCCCA
                                TCCACAGCT      TTCTGT
                                |||||||||      ||||||
                                AGGTGTCGA      AAGACA
                                     CA_____
GAM736  ADD1     3'  GAGGAGGGGGCCGCCGCGG    27209     C   G   G
                                CCGC GCGG CTC TCCTC
                                |||| |||| ||| |||||
                                GGCG CGCC GGG AGGAG
                                  C   G   G
GAM736  AQP5     5'  GAGCGGCGGGCCCGCAGCGG   9719      C        _
                                CCGC GCGGGCTCGTC CTC
                                |||| |||||||||| |||
                                GGCG CGCCCGGGCGG GAG
                                  A         C
GAM736  ATBF1    5'  GAGGAGGCGGCGGCGGCGG    23528       GG  T  T
                                CCGCCGC  GC CG CCTCCTC
                                |||||||  || || |||||||
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                                GGCGGCG  CG GC GGAGGAG
                                   G_  _  _
GAM736  BCL11B   5'  GAGGAGGAGGTGCGGCGGCGG  57576       _ G   CG
                                CCGCCGC G GCT  TCCTCCTC
                                ||||||| | |||  ||||||||
                                GGCGGCG C TGG  AGGAGGAG
                                   G G   __
GAM736  BDP1     5'  GAGGAGGAGGCGGCGGCGG   37967       GG   CG
                                CCGCCGC  GCT  TCCTCCTC
                                |||||||  |||  ||||||||
                                GGCGGCG  CGG  AGGAGGAG
                                   G_   __
GAM736  CASP7    5'  GAACACCAGCTGCGGTGG    54032        G  C  CC
                                CCGCCGCGG CT GT  TC
                                ||||||||| || ||  ||
                                GGTGGCGTC GA CA  AG
                                     _  C  CA
GAM736  CD63     5'  GAGCCCCGGAGCCGCGGCGG   10116        G   GTC__
                                CCGCCGCGG CTC    CTC
                                ||||||||| |||    |||
                                GGCGGCGCC GAG    GAG
                                     _  GCCCC
GAM736  CDC2L2   5'  GAGGAGGAGACCGGCAGC    43994    C  G  C  G
                                GC GC GG TC TCCTCCTC
                                || || || || ||||||||
                                CG CG CC AG AGGAGGAG
                                 A  G  _  _
GAM736  CREBL2   5'  GAGGAGGAGGCGGCGGCGG   8969       GG   CG
                                CCGCCGC  GCT  TCCTCCTC
                                |||||||  |||  ||||||||
                                GGCGGCG  CGG  AGGAGGAG
                                   G_   __
GAM736  CRIM1    5'  GAGGAGGAGGCGGCGGCGG   33602       GG   CG
                                CCGCCGC  GCT  TCCTCCTC
                                |||||||  |||  ||||||||
                                GGCGGCG  CGG  AGGAGGAG
                                   G_   __
GAM736  CRYAA    3'  GAGAGCGCAGCCCGCGGC    6365         _  TC
                                GCCGCGGGCT CG  CTC
                                |||||||||| ||  |||
                                CGGCGCCCGA GC  GAG
                                     C  GA
GAM736  DHFR     5'  GAGGAGCGCGAACCCGCGGC  7649         C   C
                                GCCGCGGG TCGT CTCCTC
                                |||||||| |||| ||||||
                                CGGCGCCC AGCG GAGGAG
                                   A   C
GAM736  EGFL6    5'  AGGAGGACCCGTGCG      31937     C    CTCG
                                CGC GCGGG   TCCTCCT
                                ||| |||||   |||||||
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                                GCG TGCCC    AGGAGGA
                                  _    _____
GAM736  EP300    5'  GAGGAGGACAGCGCCGAGG    9284     G   _   C
                                CC CGG GCT GTCCTCCTC
                                || ||| ||| |||||||||
                                GG GCC CGA CAGGAGGAG
                                 A   G   _
GAM736  ETS1     5'  GAGGAGCGGGCGCGCGGCGG   19114         G     TC
                                CCGCCGCG GCTCG  CTCCTC
                                |||||||| |||||  ||||||
                                GGCGGCGC CGGGC  GAGGAG
                                     G    __
GAM736  FGF18    5'  GAGGAGGGAGCAGCAGC     15260    C  GG    GT
                                GC GC  GCTC  CCTCCTC
                                || ||  ||||  |||||||
                                CG CG  CGAG  GGAGGAG
                                 A  A_   __
GAM736  FKRP     3'  GAGGAGAGCACCAGGACG    44435    _  GC  _    G
                                CG CC  GG GCTC TCCTC
                                || ||  || |||| |||||
                                GC GG  CC CGAG AGGAG
                                 A  A_  A    _
GAM736  FRAT2    3'  GAGAAGTTACCAGCCGCGGCG  24901         G  C  C_  C
                                CGCCGCGG CT GT  CT CTC
                                |||||||| || ||  || |||
                                GCGGCGCC GA CA  GA GAG
                                     _  C  TT  A
GAM736  GABRB2   5'  GAAGAGGACGAGGTGGCG    7695        GGG        C
                                CGCCGC   CTCGTCCTC TC
                                ||||||   ||||||||| ||
                                GCGGTG   GAGCAGGAG AG
                                   ___         A
GAM736  GPC6     5'  GAGCCGAGCCCGCAGCG     20332     C         TC
                                CGC GCGGGCTCG  CTC
                                ||| |||||||||  |||
                                GCG CGCCCGAGC  GAG
                                  A        C_
GAM736  GPR48    5'  AGGGGCCGAGCCCGCGCGG    38092     C         T  T
                                CCGC GCGGGCTCG CC CCT
                                |||| ||||||||| || |||
                                GGCG CGCCCGAGC GG GGA
                                   _        C  _
GAM736  GYG2     5'  GAGGACCCGCGCCCGCGGGGG  15363    G        T __
                                CC CCGCGGGC C  GTCCTC
                                || |||||||| |  ||||||
                                GG GGCGCCCG G  CAGGAG
                                 G       C CC
GAM736  HOXB3    3'  GAGGAAGACGAGACAGGACGAG 10954     G  GG____     C
              GC                   GCC CG     CTCGTC TCCTC
                                ||| ||     |||||| |||||
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                                CGG GC     GAGCAG AGGAG
                                  A  AGGACA     A
GAM736  ID2     3'  AGGAGGACAAGTTGAATGG   70057    CG_   C
                                CCG   GGCT GTCCTCCT
                                |||   |||| ||||||||
                                GGT   TTGA CAGGAGGA
                                  AAG    A
GAM736  IGF2R   3'  GAGGAGGGAGGCCAGGCGG   7912      GC  G   GT
                                CCGCC  GG CTC  CCTCCTC
                                |||||  || |||  |||||||
                                GGCGG  CC GAG  GGAGGAG
                                  A_  G  __
GAM736  IGF2R   3'  GAGGAGGGAGGCCGGGCGG   7913      G   G   GT
                                CCGCC CGG CTC  CCTCCTC
                                ||||| ||| |||  |||||||
                                GGCGG GCC GAG  GGAGGAG
                                  _  G  __
GAM736  ING1L   5'  GAGCTGAGGGCCCGCGGCGG  9600          GTC_
                                CCGCCGCGGGCTC   CTC
                                ||||||||||||   |||
                                GGCGGCGCCCGGG   GAG
                                       AGTC
GAM736  KCNA7   5'  AGGGGACCCCGGGACGG    49887    _ G   CTC   T
                                CCG CC CGGG   GTCC CCT
                                ||| || ||||   |||| |||
                                GGC GG GCCC   CAGG GGA
                                  A _   ____   _
GAM736  KIFC3   3'  AGGAGGGTTCCCGCAGCTGG  19888   _ C   CTCG
                                CC GC GCGGG   TCCTCCT
                                || || |||||   |||||||
                                GG CG CGCCC   GGGAGGA
                                 T  A    TT__
GAM736  LNK     5'  GAGGACGCGCCCAGGGCGG   19646     GC   T
                                CCGCC  GGGC CGTCCTC
                                |||||  |||| |||||||
                                GGCGG  CCCG GCAGGAG
                                   GA   C
GAM736  MAML1   3'  GAAGAGGGTGACCTCAGCGG  29277     _  C  GT   C
                                CCGC GGG TC  CCTC TC
                                |||| ||| ||  |||| ||
                                GGCG CTC AG  GGAG AG
                                  A  C  TG   A
GAM736  MAML1   5'  GAGGAAAACCCGCCGCCGCGCG 29278    _   __ TC  CC
          CG                    CGC CGCGG  GC  GT  TCCTC
                                ||| |||||  ||  ||  |||||
                                GCG GCGCC  CG  CA  AGGAG
                                  C    GC  CC  AA
GAM736  MAP3K1  5'  GAGCCGCGAGCCGCGGCGG   68427        G    C_
                                CCGCCGCGG CTCGT  CTC
                                ||||||||| |||||  |||
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                                GGCGGCGCC GAGCG  GAG
                                      _    CC
GAM736  MAPK8IP1  3'  GAGGAGGAGCTGCCGCAAGG  19579   GCC   __   G
                                CC  GCGG  GCTC TCCTC
                                ||  ||||  |||| |||||
                                GG  CGCC  CGAG AGGAG
                                 AA_   GT   G
GAM736  MRPL23   3'  GAGCAGCGACCCGCGGCGG   41219        C   C_
                                CCGCCGCGGG TCGT  CTC
                                |||||||||| ||||  |||
                                GGCGGCGCCC AGCG  GAG
                                      _   AC
GAM736  NPAS2    5'  GAGACCCGCAGCCGCGGCGG   11821        G  _  TC_
                                CCGCCGCGG CT CG   CTC
                                ||||||||| || ||   |||
                                GGCGGCGCC GA GC   GAG
                                      _ C  CCA
GAM736  NPDC1    5'  GAGCCCGGAGCCCGCGCCG   31814   C       _ TC
                                CG CGCGGGCTC G  CTC
                                || |||||||| |  |||
                                GC GCGCCCGAG C  GAG
                                 C       G CC
GAM736  NRIP1    5'  GAGGCTGGGAGCCGCGGCGG  60623        G_   T
                                CCGCCGCGG  CTCG CCTC
                                |||||||||  |||| ||||
                                GGCGGCGCC  GGGT GGAG
                                      GA   C
GAM736  NTSR1    5'  GAGGCACCTGGAACCCGTGGC  11855        C  ___  _
                                GCCGCGGG TC   GT CCTC
                                |||||||| ||   || ||||
                                CGGTGCCC AG   CA GGAG
                                     A  GTC  C
GAM736  PAX8     5'  GAGGAAGCCCCGAGCCCTCGGC 14412       C     _____
           GG                     CCGCCG GGGCTCG    TCCTC
                                |||||| |||||||    |||||
                                GGCGGC CCCGAGC    AGGAG
                                   T      CCCGA
GAM736  PCDH7    5'  GAGCGCCGAACCCGCGGCG   11989        C  TC_
                                CGCCGCGGG TCG   CTC
                                |||||||||  |||  |||
                                GCGGCGCCC AGC   GAG
                                      A   CGC
GAM736  PLA2G5   5'  GAGACGGGGAGCCCGCG    8114         G  TC
                                CGCGGGCTC TCC  CTC
                                |||||||||  |||  |||
                                GCGCCCGAG GGG  GAG
                                      _  CA
GAM736  POLI     5'  GAGGAGGAAGGCGGCGGCG   24211       GG  CG
                                CGCCGC  GCT  TCCTCCTC
                                ||||||  |||  ||||||||
```

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                                GCGGCG  CGG  AGGAGGAG
                                   G_   A_
GAM736  PPP1R12B  5'  GAGAAGCATGAGCCCTCAGC   50355    CGC      C  C
                                GC   GGGCTCGT CT CTC
                                ||   |||||||| || |||
                                CG   CCCGAGTA GA GAG
                                 ACT       C  A
GAM736  PSEN1     5'  GAGCTACGAGCCGCGGCGG   24620         G    C_
                                CCGCCGCGG CTCGT  CTC
                                ||||||||| |||||  |||
                                GGCGGCGCC GAGCA  GAG
                                      _    TC
GAM736  PTS       5'  GAGGAGGCACCGGCCGCGCGGC 6144         _   C  _
              GG                   CCGCCGCG GGCT GT CCTCCTC
                                ||||||||| |||| || |||||||
                                GGCGGCGC CCGG CA GGAGGAG
                                     G   C  C
GAM736  RENT1     3'  GAGGAGGGGCCGGCCCGCGG   12813         C   _
                                CCGCGGGCT GTCC TCCTC
                                ||||||||| |||| |||||
                                GGCGCCCGG CGGG AGGAG
                                     C   G
GAM736  SBF1      3'  AGGTACAGCCCGCAATGG    66067     CC      C  _
                                CCG  GCGGGCT GT CCT
                                |||  ||||||| || |||
                                GGT  CGCCCGA CA GGA
                                  AA       _  T
GAM736  SDC2      5'  GAGGAGGAGGGGCGCAGC    67715    C  GG   G
                                GC GC  GCTC TCCTCCTC
                                || ||  |||| ||||||||
                                CG CG  CGGG AGGAGGAG
                                 A  __   G
GAM736  SFRP2     5'  GAAGAGAGCGGGCCCGGG    72531    G      TC   C
                                CC CGGGCTCG  CTC TC
                                || ||||||||  ||| ||
                                GG GCCCGGGC  GAG AG
                                 _       GA   A
GAM736  SMAC      5'  GAGGAGGAGGGACACGGC    58002     CGGG   G
                                GCCG    CTC TCCTCCTC
                                ||||    ||| ||||||||
                                CGGC    GGG AGGAGGAG
                                  ACA_   _
GAM736  SMARCD1   5'  GAAGATGGCGGCCCGGGCGG   58186     G    T    C  C
                                CCGCC CGGGC CGTC TC TC
                                ||||| ||||| |||| || ||
                                GGCGG GCCCG GCGG AG AG
                                   _    _   T  A
GAM736  SNX3      5'  GAGGAGGGAGCCCGCGGCGG   15042          GT
                                CCGCCGCGGGCTC  CCTCCTC
                                ||||||||||||  |||||||
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                                GGCGGCGCCCGAG  GGAGGAG
                                           __
GAM736  STIP1    3'  GAGGAGCTGGGACCGCGGCG  23334       G   TC
                                CGCCGCGG CTCG  CTCCTC
                                |||||||| ||||  ||||||
                                GCGGCGCC GGGT  GAGGAG
                                     A   C_
GAM736  SURF5    5'  GAAGAGAGACTGCGGCGG   56913       G  G  C
                                CCGCCGCGG CTC TC TC
                                ||||||||| ||| || ||
                                GGCGGCGTC GAG AG AG
                                     A  _  A
GAM736  TACC1    5'  GAGGAGGACGCGGCGCCG   21874    _  _
                                CGG GCT CGTCCTCCTC
                                ||| ||| ||||||||||
                                GCC CGG GCAGGAGGAG
                                  G  C
GAM736  TBL1X    5'  GAGGAGGGCCGGCGGCGG   20134      G   G
                                CCGCCGC GGCTC TCCTC
                                ||||||| ||||| |||||
                                GGCGGCG CCGGG AGGAG
                                    G   _
GAM736  TLE1     5'  GAGGGCCGGAGCCCGCACCG  18667   CC      __
                                CG  GCGGGCTC  GTCCTC
                                ||  ||||||||  ||||||
                                GC  CGCCCGAG  CGGGAG
                                 CA       GC
GAM736  UBQLN3   5'  GAGAAGGACGGGACCACAGC  34372   CGCG _     C
                                GC   GG CTCGTCCT CTC
                                ||   || |||||||| |||
                                CG   CC GGGCAGGA GAG
                                 ACA_ A       A
GAM736  YWHAG    3'  GAGGAAGACGATTTGGGGGGG  25942   G  G   C   C
                                CC CC CGGG TCGTC TCCTC
                                || || |||| ||||| |||||
                                GG GG GTTT AGCAG AGGAG
                                 G  G   _    A
GAM736  YY1      5'  GAGGAGGCGCGGCCAGGGCGG  14152     GCG  T  _
                                CCGCC   GGC CGT CCTCCTC
                                |||||   ||| ||| |||||||
                                GGCGG   CCG GCG GGAGGAG
                                   GA_  _  C
GAM736  ZIC3     5'  GAGGAGGGGTGCCCGGG    14171   G    TCG
                                CC CGGGC   TCCTCCTC
                                || |||||   ||||||||
                                GG GCCCG   GGGAGGAG
                                 _    TG_
GAM736  ZNF216   5'  AGGAAGACCCCGCGGCGG   21170       CTC  C
                                CCGCCGCGGG   GTC TCCT
                                ||||||||||   ||| ||||
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                                GGCGGCGCCC   CAG AGGA
                                     ___   A
GAM736  ARF6     5'  GAGGAGCGGGAACCGCGGCGG  9789         G_   TC
                                CCGCCGCGG  CTCG  CTCCTC
                                |||||||||  ||||  ||||||
                                GGCGGCGCC  GGGC  GAGGAG
                                     AA   __
GAM736  C1orf21  5'  GAGGAGGACAGGGGCGGGGG  48690    G   GGG  _
                                CC CCGC   CTC GTCCTCCTC
                                || ||||   ||| |||||||||
                                GG GGCG   GGG CAGGAGGAG
                                 G   ___   A
GAM736  C20orf178 5'  GAGGAGAGGCCTGCGGCGG   75293          CG
                                CCGCCGCGGGCT  TCCTC
                                ||||||||||||  |||||
                                GGCGGCGTCCGG  AGGAG
                                      AG
GAM736  C21orf67  5'  GAGGACGCGAGCCCCGCGGC  55230        _    CC
                                GCCGCGGG CTCGT  TCCTC
                                |||||||| |||||  |||||
                                CGGCGCCC GAGCG  AGGAG
                                     C    C_
GAM736  CECR2    3'  GAGGAAATGAGCCCCAAGC   49432    CGC      CC
                                GC   GGGCTCGT  TCCTC
                                ||   ||||||||  |||||
                                CG   CCCGAGTA  AGGAG
                                 AAC       A_
GAM736  CHSY1    5'  AGGCGCAGGCCGCGGCGG    30562        G  _  T
                                CCGCCGCGG CT CG CCT
                                ||||||||| || || |||
                                GGCGGCGCC GA GC GGA
                                     G  C  _
GAM736  CXYorf1  3'  GAGGAGGACGAGGACGACTGG  82915     CCG  GG
                                CCG   CG  CTCGTCCTCCTC
                                |||   ||  ||||||||||||
                                GGT   GC  GAGCAGGAGGAG
                                  CA_  AG
GAM736  D13S106E  5'  AGGGGAGTGCCCGCGGC     20536         TCG   T
                                GCCGCGGGC   TCC CCT
                                |||||||||   ||| |||
                                CGGCGCCCG   AGG GGA
                                     TG_   _
GAM736  DDR1     3'  GAGGAGGACAAGAAGGAGAGG  26559    G__  GCGGG  C
                                CC   CC    CT GTCCTCCTC
                                ||   ||    || |||||||||
                                GG   GG    GA CAGGAGGAG
                                 AGA  AA___  A
GAM736  DKFZP564K0322 5'  GAGGAGGACTCCACGGTGG    50186       C   CTC
                                CCGCCG GGG   GTCCTCCTC
                                |||||| |||   |||||||||
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                                GGTGGC CCT   CAGGAGGAG
                                   A  ___
GAM736  DKFZp586I021 3'  GAGGAGGACACGGCCGCCG   51082    CC    G  C_
                                CG  GCGG CT  GTCCTCCTC
                                ||  |||| ||  |||||||||
                                GC  CGCC GG  CAGGAGGAG
                                 __   _ CA
GAM736  DKFZp761B0514 5'  GAGGCCGGACCCGCGGCGG   51146          CT  T
                                CCGCCGCGGG  CG CCTC
                                ||||||||||  || ||||
                                GGCGGCGCCC  GC GGAG
                                      AG  C
GAM736  Dlc2     5'  GAGCCGGAGACCGCGGCGG   55628          G   GTC
                                CCGCCGCGG CTC   CTC
                                ||||||||| |||   |||
                                GGCGGCGCC GAG   GAG
                                      A   GCC
GAM736  EDR1     5'  GAGGGGAGCCCGCCGCGG    16660      C       G
                                CCGC GCGGGCTC TCCTC
                                |||| |||||||| |||||
                                GGCG CGCCCGAG GGGAG
                                  C      _
GAM736  ELL2     5'  GAGACGAGCCCGGGGCGG    24894       G        C
                                CCGCC CGGGCTCGTC TC
                                ||||| |||||||||| ||
                                GGCGG GCCCGAGCAG AG
                                   G         _
GAM736  FBXO9    5'  GAGGGGGCAGCTCCGCGGCGG  54247          _  C    T
                                CCGCCGCGG GCT GTCC CCTC
                                ||||||||| ||| |||| ||||
                                GGCGGCGCC CGA CGGG GGAG
                                      T  _   _
GAM736  FLJ10140 3'  GAGAAGGACAGCGTCAAGG    36318    GC  _  C    C
                                CC  GG GCT GTCCT CTC
                                ||  || ||| ||||| |||
                                GG  CT CGA CAGGA GAG
                                 AA  G   _    A
GAM736  FLJ10378 5'  GAAGAGGACGAGGCAGAGG    36566    GCC  GGG       C
                                CC   GC   CTCGTCCTC TC
                                ||   ||   |||||||||| ||
                                GG   CG   GAGCAGGAG AG
                                 AGA  ___        A
GAM736  FLJ10483 5'  GAGGAGGACGAGGAGCTGG    36654    _  GGG
                                CC GC   CTCGTCCTCCTC
                                || ||   ||||||||||||
                                GG CG   GAGCAGGAGGAG
                                 T  AG_
GAM736  FLJ10521 3'  GAGGAGGACAAGCCAGACGG   36719     CG_   C
                                CCG   GGCT GTCCTCCTC
                                |||   |||| |||||||||
```

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                                GGC   CCGA CAGGAGGAG
                                  AGA    A
GAM736  FLJ10648  5' GAGGAGAGGGCGGCGGCGG   36891       GG    GTC
                                CCGCCGC  GCTC   CTCCTC
                                |||||||  ||||   ||||||
                                GGCGGCG  CGGG   GAGGAG
                                    G_    A__
GAM736  FLJ10852  5' GAAGAGGCGACCCAAGGCGG   39252      GC   C   T    C
                                CCGCC  GGG TCG CCTC TC
                                |||||  ||| ||| |||| ||
                                GGCGG  CCC AGC GGAG AG
                                   AA   _   _    A
GAM736  FLJ12229  5' GAGGAGGACATTCGCAGG    46406    _    CTC
                                CC GCGGG   GTCCTCCTC
                                || |||||   |||||||||
                                GG CGCTT   CAGGAGGAG
                                 A    A__
GAM736  FLJ12505  5' GAGGAGGACAAAGACGGCGG   45715       CGGGCTC
                                CCGCCG      GTCCTCCTC
                                ||||||      |||||||||
                                GGCGGC      CAGGAGGAG
                                   AGAAA__
GAM736  FLJ12529  3' AGGAGGAGGCAGCAGCG     46081     C  GG   CG
                                CGC GC  GCT  TCCTCCT
                                ||| ||  |||  |||||||
                                GCG CG  CGG  AGGAGGA
                                  A  A_   __
GAM736  FLJ12552  3' GAAGAGAAGCTGTCCGTGGCGG 43395          TCGTC   C
                                CCGCCGCGGGC     CTC TC
                                ||||||||||     ||| ||
                                GGCGGTGCCTG     GAG AG
                                      TCGAA   A
GAM736  FLJ20277  5' GAGGAGGCGGAGGCCGCGGCG  35314        G   GT
                                CGCCGCGG CTC  CCTCCTC
                                ||||||||  |||  |||||||
                                GCGGCGCC GAG  GGAGGAG
                                    G   GC
GAM736  FLJ21144  5' GAGCAGCTCCGAGGCCGCGGCG 43193        G    TC_  C
                                CGCCGCGG CTCG   CT CTC
                                ||||||||  ||||   || |||
                                GCGGCGCC GAGC   GA GAG
                                    G    CTC  C
GAM736  FLJ22037  5' GAGGAAGAGGGCATGGCGG    95534      GCGG    G  C
                                CCGCC    GCTC TC TCCTC
                                |||||    ||||  || |||||
                                GGCGG    CGGG AG AGGAG
                                   TA__    _  A
GAM736  FLJ22301  5' GAGGAGGACATCCCATGCGG   46178      CGC   CTC
                                CCGC   GGG   GTCCTCCTC
                                ||||   |||   |||||||||
```

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                                GGCG  CCC  CAGGAGGAG
                                  TA_  TA_
GAM736  FLJ22559  3'  GAGGAGGACAAAGATAAGGTGG 46805     GCGGG  C_
                                CCGCC   CT  GTCCTCCTC
                                |||||    ||  |||||||||
                                GGTGG   GA  CAGGAGGAG
                                   AATA_  AA
GAM736  FOXD4   3'  GAGGAGGACTGCGCCAACGG  25162    CG  T _
                                CCG  GGC C GTCCTCCTC
                                |||  ||| | |||||||||
                                GGC  CCG G CAGGAGGAG
                                 AA  C T
GAM736  GADD45A  5'  GAGGAGGAGCCCGGGCGG   10404     G     G
                                CCGCC CGGGCTC TCCTC
                                ||||| ||||||| |||||
                                GGCGG GCCCGAG AGGAG
                                   _     G
GAM736  GPR     5'  GAGGAGAGGCTCCGCGCGG   24291     C   _  CG
                                CCGC GCGG GCT  TCCTC
                                |||| |||| |||  |||||
                                GGCG CGCC CGG  AGGAG
                                  _   T  AG
GAM736  GPS2    5'  GAGGAGGATGGCACGAGG   88509   G  G  T
                                CC CG GC CGTCCTCCTC
                                || || || ||||||||||
                                GG GC CG GTAGGAGGAG
                                 A  A  _
GAM736  HYA22   5'  GAGCGGGCAGAGCCCGCGGCGG 20554          _   TC
                                CCGCCGCGGGCTC GTCC  CTC
                                |||||||||||| ||||  |||
                                GGCGGCGCCCGAG CGGG  GAG
                                       A   C_
GAM736  ITPK1   5'  GAGGAGGAAGTGGCGGCGGCGG 27231       GG  CG_
                                CCGCCGC  GCT   TCCTCCTC
                                |||||||  |||  ||||||||
                                GGCGGCG  CGG   AGGAGGAG
                                   G_  TGA
GAM736  JIK     5'  GAGGAAGCGGCGGCGGCGG   33264       GG  T  CC
                                CCGCCGC  GC CGT  TCCTC
                                |||||||  || |||  |||||
                                GGCGGCG  CG GCG  AGGAG
                                   G_  _  A_
GAM736  KCNT1   3'  GAGGAGGACTACATGGCGG   62491      CGGGCTC
                                CCGCCG     GTCCTCCTC
                                ||||||     |||||||||
                                GGCGGT     CAGGAGGAG
                                   ACAT___
GAM736  KIAA0258 3'  GAGGAGGAGCTCAGGCGG   29469     GC    G
                                CCGCC  GGGCTC TCCTC
                                |||||  |||||| |||||
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                                GGCGG  CTCGAG AGGAG
                                  A_     G
GAM736  KIAA0354  5'  GAGGAAGTCCCGTAACGG    30190     CC    _ CG
                                CCG  GCGGG CT  TCCTC
                                |||  ||||| ||  |||||
                                GGC  TGCCC GA  AGGAG
                                 AA    T __
GAM736  KIAA0415  3'  GAGGAGGCAAGGCCCACGGTGG 94162       C    CGT
                                CCGCCG GGGCT   CCTCCTC
                                |||||| |||||   |||||||
                                GGTGGC CCCGG   GGAGGAG
                                   A    AAC
GAM736  KIAA0419  5'  GAGGAGAAGGCGGCGGCGG   28860       GG   CGTC
                                CCGCCGC  GCT   CTCCTC
                                |||||||  |||   ||||||
                                GGCGGCG  CGG   GAGGAG
                                    G_   AA__
GAM736  KIAA0447  5'  GAGGAGCGGCGCCCGCGGGG   72123    G      TC  _
                                CC CCGCGGGC  GTC CTCCTC
                                || ||||||||  ||| ||||||
                                GG GGCGCCCG  CGG GAGGAG
                                 _      __  C
GAM736  KIAA0537  5'  GGGGCGCCCAGGCCCGCGGCGG 29930           ____
                                CCGCCGCGGGCT   CGTCCT
                                ||||||||||||   ||||||
                                GGCGGCGCCCGG   GCGGGG
                                       ACCC
GAM736  KIAA0565  3'  GAGGAAGACTGGTAGCGGGG   67437    G   GG   C   C
                                CC CCGC  GCT GTC TCCTC
                                || ||||  ||| ||| |||||
                                GG GGCG  TGG CAG AGGAG
                                 _   A_  T   A
GAM736  KIAA0711  5'  GAAGAGGAGCCGCGGCG     30149        G   G  C
                                CGCCGCGG CTC TC TC
                                |||||||| ||| || ||
                                GCGGCGCC GAG AG AG
                                    _  G  A
GAM736  KIAA0923  5'  AGGCGGGAGCCCGCAGCGG   26705     C      GT  T
                                CCGC GCGGGCTC  CC CCT
                                |||| ||||||||  || |||
                                GGCG CGCCCGAG  GG GGA
                                  A       __ C
GAM736  KIAA0923  5'  GAGGAGGGGCCGCGGGCGG   26707      G _    G
                                CCGCC CG GGCTC TCCTC
                                ||||| || ||||| |||||
                                GGCGG GC CCGGG AGGAG
                                  _ G    G
GAM736  KIAA1016  5'  GAGGAACCGGCGCCCCCGGCGG 93384       C   _  __
                                CCGCCG GGGC TCG  TCCTC
                                |||||| |||| |||  |||||
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                                GGCGGC CCCG GGC  AGGAG
                                   C   C   CA
GAM736  KIAA1194  5'  GAGGAGGCGGCAGCGGCGG   97635       GG  T  T
                                CCGCCGC  GC CG CCTCCTC
                                |||||||  || || |||||||
                                GGCGGCG  CG GC GGAGGAG
                                   A_  _ _
GAM736  KIAA1198  3'  AGAAGGACTTGGGCCCCAGC   63983    CGC    __    C
                                GC   GGGCTC  GTCCT CT
                                ||   ||||||  ||||| ||
                                CG   CCCGGG  CAGGA GA
                                 AC_     TT    A
GAM736  KIAA1373  5'  GAGGAGAACGACGCACGG    71507    CC   GGC   C
                                CCG  GCG   TCGT CTCCTC
                                |||  |||   |||| ||||||
                                GGC  CGC   AGCA GAGGAG
                                  A_  ____   A
GAM736  KIAA1545  5'  GAGGAGGAGGTCATCGACGG   61335    C  CG   CG
                                CCG CG  GGCT  TCCTCCTC
                                ||| ||  ||||  ||||||||
                                GGC GC  CTGG  AGGAGGAG
                                  A  TA   __
GAM736  MGC15730  5'  GAGCCGAGAACCGCGGCG    52865       G_   TC
                                CGCCGCGG  CTCG  CTC
                                ||||||||  ||||  |||
                                GCGGCGCC  GAGC  GAG
                                     AA   C_
GAM736  MGC15875  5'  GAGGCCCAGCCCGCGCGG    53015     C     CGT
                                CCGC GCGGGCT   CCTC
                                ||||| |||||||   ||||
                                GGCG CGCCCGA   GGAG
                                  _      CCC
GAM736  MGC3035   5'  GAGGAGGCGGCCACGGC     44402     CG   T  T
                                GCCG  GGC CG CCTCCTC
                                ||||  ||| || |||||||
                                CGGC  CCG GC GGAGGAG
                                  A_  _ _
GAM736  NTKL      5'  AGGCGCCGAACCCGCGGCG    40719        C   T__
                                CGCCGCGGG TCG   CCT
                                |||||||||  |||   |||
                                GCGGCGCCC AGC   GGA
                                     A   CGC
GAM736  OATPRP4   5'  GAGGGTGCCGCGAGCCCAGGCG 48985      GC      CC__
          G                      CCGCC  GGGCTCGT   TCCTC
                                |||||  ||||||||   |||||
                                GGCGG  CCCGAGCG   GGGAG
                                  A_      CCGT
GAM736  OBSCN     3'  GAAGAAGATGGGCCCGCAGG   71187    _        C  C
                                CC GCGGGCTCGTC TC TC
                                || ||||||||||| || ||
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                                GG CGCCCGGGTAG AG AG
                                 A         A  A
GAM736  OBSCN    3'  GAGATCGGGGAGCCCACGGTGG 71188       C     G   TC_
                                CCGCCG GGGCTC TCC   CTC
                                |||||| |||||| |||   |||
                                GGTGGC CCCGAG GGG   GAG
                                   A     _   CTA
GAM736  PCDH16   5'  GAGGAGGAGCTCCGTGGC    73184        _   G
                                GCCGCGG GCTC TCCTC
                                ||||||| |||| |||||
                                CGGTGCC CGAG AGGAG
                                   T   G
GAM736  POU2F1   5'  GAGAGTTCAGCCGCGGCGG   12210         _____   G
                                CCGCCGCGG   GCTC TC
                                |||||||||   |||| ||
                                GGCGGCGCC   TGAG AG
                                     GACT   _
GAM736  PSMD8    5'  GAGCTCCGGGCCCGCGGC    12520          TC_
                                GCCGCGGGCTCG   CTC
                                ||||||||||||   |||
                                CGGCGCCCGGGC   GAG
                                       CTC
GAM736  PTRF     5'  GAGGAGGACGCAGCGGCG    64240       GG  TC
                                CGCCGC  GC  GTCCTCCTC
                                ||||||  ||  |||||||||
                                GCGGCG  CG  CAGGAGGAG
                                   A_  __
GAM736  QKI      5'  GAGACCCCCCGAGCCCGCGGC  66046          TCCTC_
                                GCCGCGGGCTCG     CTC
                                ||||||||||||     |||
                                CGGCGCCCGAGC     GAG
                                       CCCCCA
GAM736  QKI      5'  GAGGAGGAGCGCAGTCGG    66047     _ C  GG    G
                                CCG C GC  GCTC TCCTC
                                ||| | ||  |||| |||||
                                GGC G CG  CGAG AGGAG
                                  T A  __    G
GAM736  RAB11B   3'  GAGGAGGACGGGCGGACGGCG  74336       CGG
                                CGCCG   GCTCGTCCTCCTC
                                |||||   |||||||||||||
                                GCGGC   CGGGCAGGAGGAG
                                   AGG
GAM736  RAB2     5'  GAGGAGGAGCAGCAGCGG    12695      C  GG    G
                                CCGC GC  GCTC TCCTC
                                |||| ||  |||| |||||
                                GGCG CG  CGAG AGGAG
                                  A  A_    G
GAM736  RNF24    5'  GAGGAGACCGCGGGCCCGCGC  24280    C         C__
                                GC GCGGGCTCGT   CTCCTC
                                || ||||||||||   ||||||
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                                CG CGCCCGGGCG   GAGGAG
                                 _        CCA
GAM736  SEC10L1  5'  GAGCTGGGGAGCCCGCAGCGG  22587     C      G   TC
                                CCGC GCGGGCTC TCC  CTC
                                |||| |||||||| |||  |||
                                GGCG CGCCCGAG GGG  GAG
                                  A       _   TC
GAM736  SHARP    5'  GAGGGGGAGCCAGCAGCGG   31102     C  G    G
                                CCGC GC GGCTC TCCTC
                                |||| || ||||| |||||
                                GGCG CG CCGAG GGGAG
                                  A  A    G
GAM736  TOB2     5'  GAGAAGCCGCCCCGCGGC    33237        CT  TC  C
                                GCCGCGGG  CG  CT CTC
                                ||||||||  ||  || |||
                                CGGCGCCC  GC  GA GAG
                                     C_  C_  A
GAM736  YEA      5'  GAGAAGGGGAGACCGCGGCGG  52601         G   G    C
                                CCGCCGCGG CTC TCCT CTC
                                ||||||||| ||| |||| |||
                                GGCGGCGCC GAG GGGA GAG
                                     A   _    A
GAM736  ZF       5'  GAGGAGGAGACGGCGGCGG    41368        GGG   G
                                CCGCCGC   CTC TCCTC
                                |||||||   ||| |||||
                                GGCGGCG   GAG AGGAG
                                    GCA   G
GAM736  ZF       5'  GAGGGGGAGCCGCGGCGG    41369         G   G
                                CCGCCGCGG CTC TCCTC
                                ||||||||| ||| |||||
                                GGCGGCGCC GAG GGGAG
                                     _  G
GAM736  ZNF339   5'  GAGGAGGGGGCCGCAGTCGG   41394     _ C    G   G
                                CCG C GCGG CTC TCCTC
                                ||| | |||| ||| |||||
                                GGC G CGCC GGG AGGAG
                                  T A   G   G
GAM736  LOC113675 3'  GAGGAGGACTCAGTGCTGGC   57380     _  GG   C_
                                GCC GC  GCT  GTCCTCCTC
                                ||| ||  |||  |||||||||
                                CGG CG  TGA  CAGGAGGAG
                                  T  __   CT
GAM736  LOC121536 5'  GAGGAGGACGACGAGGAGG    74526    G  G  GGC
                                CC CC CG   TCGTCCTCCTC
                                || || ||   ||||||||||
                                GG GG GC   AGCAGGAGGAG
                                 A  A  ____
GAM736  LOC126432 5'  AGAAGGACGAGGATCCAGG    75019    GC  __      C
                                CC  GGG  CTCGTCCT CT
                                ||  |||  |||||||| ||
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                                GG  CCT  GAGCAGGA GA
                                 A_   AG       A
GAM736   LOC128344 3'  GAGGAGGACTCCCCAGGGC   75245     GC   CTC
                                GCC  GGG   GTCCTCCTC
                                |||  |||   |||||||||
                                CGG  CCC   CAGGAGGAG
                                  GA   CT_
GAM736   LOC144524 3'  GAGGAGGAGGTCGCAGTG    84056     C    G   G
                                CGC GCGG CTC TCCTC
                                ||| |||| ||| |||||
                                GTG CGCT GAG AGGAG
                                  A    G   G
GAM736   LOC146337 3'  GAGGAGGACGCCGCAGAGG    84640    GCC    GCT
                                CC   GCGG   CGTCCTCCTC
                                ||   ||||   ||||||||||
                                GG   CGCC   GCAGGAGGAG
                                 AGA    ____
GAM736   LOC146512 3'  GAGAAAGAACGAACGTGGC    78499       GGC    C  C_
                                GCCGCG   TCGT CT  CTC
                                ||||||   |||| ||  |||
                                CGGTGC   AGCA GA  GAG
                                   A__    A  AA
GAM736   LOC146774 3'  GAGGACAGCTCGCGACGG     78695     C       C
                                CCG CGCGGGCT GTCCTC
                                ||| |||||||| ||||||
                                GGC GCGCTCGA CAGGAG
                                  A       _
GAM736   LOC146990 5'  AGGATACCCAAACCCGCGGTGG 84953          CTC_____
                                CCGCCGCGGG      GTCCT
                                ||||||||||      |||||
                                GGTGGCGCCC      TAGGA
                                     AAACCCA
GAM736   LOC147650 5'  GAGGAGGACAGAGATGAGGC   79018     G  GG   _
                                GCC CG  CTC GTCCTCCTC
                                ||| ||  ||| |||||||||
                                CGG GT  GAG CAGGAGGAG
                                  A  A_   A
GAM736   LOC147965 5'  GAGGAGGACTTTCTGCGGC    79300        CTC
                                GCCGCGGG   GTCCTCCTC
                                |||||||   |||||||||
                                CGGCGTCT   CAGGAGGAG
                                    TT_
GAM736   LOC149606 3'  GAGGAGCAGTAGCCCGCGG    80263        CGTC
                                CCGCGGGCT    CTCCTC
                                |||||||||    ||||||
                                GGCGCCCGA    GAGGAG
                                     TGAC
GAM736   LOC151429 3'  GAGGAGAGTCCCTGCGGC     86538      _   _   G
                                GCCGC GGG CTC TCCTC
                                ||||| ||| ||| |||||
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                                CGGCG CCC GAG AGGAG
                                  T  T  _
GAM736  LOC155340 5' GAGGAGGACAACTCGGACG   73769   _  C  GCTC
                                CG CCG GG   GTCCTCCTC
                                || ||| ||   |||||||||
                                GC GGC TC   CAGGAGGAG
                                 A  _  AA__
GAM736  LOC158668 5' GAGGAGGACGAGGGCCTAGTGG 69900     _   __
                                CCGC GGGC  TCGTCCTCCTC
                                |||| ||||  ||||||||||
                                GGTG TCCG  AGCAGGAGGAG
                                  A   GG
GAM736  LOC158856 5' AGGAAAGCTGGGCCGCGGCGG  88288        G  C  CC
                                CCGCCGCGG CT GT  TCCT
                                ||||||||| || ||  ||||
                                GGCGGCGCC GG CG  AGGA
                                     G  T  AA
GAM736  LOC159090 5' GAAGAGGAGGCACCGCGGCGG  82962        _  CG   C
                                CCGCCGCGG GCT  TCCTC TC
                                ||||||||| |||  ||||| ||
                                GGCGGCGCC CGG  AGGAG AG
                                     A  __   A
GAM736  LOC161734 3' GAGGAGGATGCTGCACTGC   88466    _ T_
                                GCGG GC  CGTCCTCCTC
                                |||| ||  ||||||||||
                                CGTC CG  GTAGGAGGAG
                                  A  TC
GAM736  LOC164584 5' AGGAGGACGCCGTCCAGG   83417   GC   T_
                                CC  GGGC  CGTCCTCCT
                                ||  ||||  |||||||||
                                GG  CCTG  GCAGGAGGA
                                 A_   CC
GAM736  LOC164584 5' AGGAGGACGCCGTCCAGG   83418   GC   T_
                                CC  GGGC  CGTCCTCCT
                                ||  ||||  |||||||||
                                GG  CCTG  GCAGGAGGA
                                 A_   CC
GAM736  LOC165253 5' GACCGCAGGCCCGCGGCGG   88543        TC  CC
                                CCGCCGCGGGC  GT  TC
                                ||||||||||  ||  ||
                                GGCGGCGCCCG  CG  AG
                                     GA  CC
GAM736  LOC169008 5' AGGAATGACTCCTGCGGCG   83596       CTC  C_
                                CGCCGCGGG   GTC  TCCT
                                |||||||||   |||  ||||
                                GCGGCGTCC   CAG  AGGA
                                     T__   TA
GAM736  LOC170394 5' GAGAACGGCGAGCCCACGGC  83737     C       CTC
                                GCCG GGGCTCGTC   CTC
                                |||| |||||||||   |||
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                                CGGC CCCGAGCGG   GAG
                                  A        CAA
GAM736   LOC170394 5'  GAGGAGGACAGGGCCCCGGC   83738      C     _
                                GCCG GGGCTC GTCCTCCTC
                                |||| |||||| |||||||||
                                CGGC CCCGGG CAGGAGGAG
                                  _     A
GAM736   LOC199993 5'  GAGGAGCGGCGCCCGCGGGG   72141    G      TC  _
                                CC CCGCGGGC  GTC CTCCTC
                                || ||||||||  ||| ||||||
                                GG GGCGCCCG  CGG GAGGAG
                                 _      __  C
GAM736   LOC200093 3'  GAGGAGGACGAGGACGACTGG  63774     CCG  GG
                                CCG   CG  CTCGTCCTCCTC
                                |||   ||  ||||||||||||
                                GGT   GC  GAGCAGGAGGAG
                                  CA_  AG
GAM736   LOC200186 5'  GAGGAGCCGGGCCGAGGCCGCG 91565          G   _  ___
           GCGG                    CCGCCGCGG CTCG TCC   TCCTC
                                |||||||||  |||| |||   |||||
                                GGCGGCGCC GAGC GGG   AGGAG
                                     G   C   CCG
GAM736   LOC203221 5'  GAGAGGACGAGGATGAGG    91107    G  GG       C
                                CC CG  CTCGTCCTC TC
                                || ||  |||||||||  ||
                                GG GT  GAGCAGGAG AG
                                 A  AG        A
GAM736   LOC203338 3'  GAGGAGGACTGCGCCAACGG   88883     CG   T _
                                CCG  GGC C GTCCTCCTC
                                |||  ||| | |||||||||
                                GGC  CCG G CAGGAGGAG
                                  AA   C T
GAM736   LOC205418 3'  GAGGAGAACGAGCTCCTGCAGG 92372    _ _ _     C
                                CC GC GG GCTCGT CTCCTC
                                || || || |||||| ||||||
                                GG CG CC CGAGCA GAGGAG
                                 A  T  T     A
GAM736   LOC219397 3'  AGGAGCCCGGGCCCCGCGGCGG 95118           _   TC
                                CCGCCGCGGG CTCG  CTCCT
                                |||||||||  ||||  |||||
                                GGCGGCGCCC GGGC  GAGGA
                                     C    CC
GAM736   LOC219649 3'  GAGAATGGTGTGAACCCGGGCG 94553      G    C   TC  C__
           G                     CCGCC CGGG TCG  CT   CTC
                                |||||  |||| |||  ||   |||
                                GGCGG GCCC AGT  GG   GAG
                                  _   A  GT  TAA
GAM736   LOC220537 3'  GAAGAGGGAGACTCCGCGGC   92424        GC  GT    C
                                GCCGCGG  TC  CCTC TC
                                |||||||  ||  |||| ||
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                                CGGCGCC  AG  GGAG AG
                                    TC  AG    A
GAM736   LOC221535 5'  AGGAGGACCCTGAGGGC     95442     G_    CTC
                                GCC  CGGG   GTCCTCCT
                                |||  ||||   ||||||||
                                CGG  GTCC   CAGGAGGA
                                  GA   ___
GAM736   LOC221766 3'  GAGGAGGTGGAACCCGCGGC   95419         C  GT
                                GCCGCGGG TC  CCTCCTC
                                |||||||| ||  |||||||
                                CGGCGCCC AG  GGAGGAG
                                    A  GT
GAM736   LOC221766 3'  GAGGAGGTGGAACCCGCGGCG  95420          C  GT
                                CGCCGCGGG TC  CCTCCTC
                                ||||||||| ||  |||||||
                                GCGGCGCCC AG  GGAGGAG
                                     A  GT
GAM736   LOC222488 3'  GAGGAGGAGGCCGAGCGG    96009      CG   G   G
                                CCGC  CGG CTC TCCTC
                                ||||  ||| ||| |||||
                                GGCG  GCC GAG AGGAG
                                  A_   G   G
GAM736   LOC253018 5'  AGGAGGACCCTGAGGGC     97705     G_    CTC
                                GCC  CGGG   GTCCTCCT
                                |||  ||||   ||||||||
                                CGG  GTCC   CAGGAGGA
                                  GA   ___
GAM736   LOC253267 5'  GAGCCCGGCCCGCGGCGG    99455          T  TC
                                CCGCCGCGGGC CG  CTC
                                |||||||||| ||  |||
                                GGCGGCGCCCG GC  GAG
                                      _ CC
GAM736   LOC253272 5'  GAGGAGGACGAGGAGGAGCG  97107     GGG__
                                CGC    CTCGTCCTCCTC
                                |||    ||||||||||||
                                GCG    GAGCAGGAGGAG
                                  AGGAG
GAM736   LOC255251 5'  GAGGCCCAGCCCGCGCGG    97620      C      CGT
                                CCGC GCGGGCT   CCTC
                                |||| |||||||   ||||
                                GGCG CGCCCGA   GGAG
                                  _      CCC
GAM736   LOC255533 5'  GAGGAGGACGAGGAGGAGG   98753    G  GCGGG
                                CC CC    CTCGTCCTCCTC
                                || ||    ||||||||||||
                                GG GG    GAGCAGGAGGAG
                                 A  AG___
GAM736   LOC255620 5'  GAGGAGGACAACTCGGACG   98874    _   C  GCTC
                                CG CCG GG    GTCCTCCTC
                                || ||| ||    |||||||||
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                                GC GGC TC    CAGGAGGAG
                                 A   _  AA__
GAM736   LOC255737 5'  AGGAGGGTCCACGGCGG     98005       C     G
                                CCGCCG GGGCTC TCCT
                                |||||| |||||| ||||
                                GGCGGC CCTGGG AGGA
                                   A     _
GAM736   LOC256158 5'  GAGGAGGAGGCCCGGGGCGG   99494      G     CG
                                CCGCC CGGGCT  TCCTCCTC
                                ||||| ||||||  ||||||||
                                GGCGG GCCCGG  AGGAGGAG
                                  G     __
GAM736   LOC256207 3'  GAGGAAGACTGGTAGCGGGG   96876    G   GG   C   C
                                CC CCGC  GCT GTC TCCTC
                                || ||||  ||| ||| |||||
                                GG GGCG  TGG CAG AGGAG
                                 _   A_  T   A
GAM736   LOC256227 5'  AGGAGGCGGGGCCTGCAGC    97761    C       GT
                                GC GCGGGCTC  CCTCCT
                                || ||||||||  ||||||
                                CG CGTCCGGG  GGAGGA
                                 A       GC
GAM736   LOC256273 3'  GAGGAGAACCTGGCAGG     98140    _   C  GC  G
                                CC GCCG GG  TC TCCTC
                                || |||| ||  || |||||
                                GG CGGT CC  AG AGGAG
                                 A   _  A_  _
GAM736   LOC256310 3'  GAGGAGGACAAGCGGCGGCGG  98100        GG   C
                                CCGCCGC  GCT GTCCTCCTC
                                |||||||  ||| |||||||||
                                GGCGGCG  CGA CAGGAGGAG
                                    G_  A
GAM736   LOC256598 5'  GAGGAGGACAACTCGGACG    98106    _  C  GCTC
                                CG CCG GG    GTCCTCCTC
                                || ||| ||    |||||||||
                                GC GGC TC    CAGGAGGAG
                                 A   _  AA__
GAM736   LOC256740 5'  GAGCCAGAGTCCGCGGCGG    98919           GTC
                                CCGCCGCGGGCTC   CTC
                                ||||||||||||   |||
                                GGCGGCGCCTGAG   GAG
                                       ACC
GAM736   LOC256880 5'  GAGAAGAAGGGCACCGCGG    98889       _   GTC  C
                                CCGCGG GCTC   CT CTC
                                |||||| ||||   || |||
                                GGCGCC CGGG   GA GAG
                                   A   AA_  A
GAM736   LOC256950 3'  GAGACATGAGCCCGCAGCG    97155     C        C_
                                CGC GCGGGCTCGT  CTC
                                ||| ||||||||||  |||
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                                GCG CGCCCGAGTA  GAG
                                  A         CA
GAM736  LOC257426 3'  GAGGAGGACTGACACGGAGG  67219    G   CGGGC  _
                                CC CCG     TC GTCCTCCTC
                                || |||     || |||||||||
                                GG GGC     AG CAGGAGGAG
                                 A  AC___  T
GAM736  LOC257548 5'  AGGAGGACCCTGAGGGC     99581     G_   CTC
                                GCC  CGGG   GTCCTCCT
                                |||  ||||   ||||||||
                                CGG  GTCC   CAGGAGGA
                                  GA   ___
GAM736  LOC257549 5'  AGGAGGACCCTGAGGGC     99588     G_   CTC
                                GCC  CGGG   GTCCTCCT
                                |||  ||||   ||||||||
                                CGG  GTCC   CAGGAGGA
                                  GA   ___
GAM736  LOC257610 5'  AGGAGGACCCTGAGGGC     99681     G_   CTC
                                GCC  CGGG   GTCCTCCT
                                |||  ||||   ||||||||
                                CGG  GTCC   CAGGAGGA
                                  GA   ___
GAM736  LOC257611 5'  AGGAGGACCCTGAGGGC     99690     G_   CTC
                                GCC  CGGG   GTCCTCCT
                                |||  ||||   ||||||||
                                CGG  GTCC   CAGGAGGA
                                  GA   ___
GAM736  LOC51308  3'  GAAGAAGACCTCTGGCGG    33966       C   C  G  C
                                CCGCCG GGG TC TC TC
                                |||||| ||| || || ||
                                GGCGGT TCC AG AG AG
                                   C   _  A  A
GAM736  LOC58509  5'  GAGGAGGACCTGATCCAGC   89717    G  C  __
                                GC GG TC  GTCCTCCTC
                                || || ||  |||||||||
                                CG CC AG  CAGGAGGAG
                                 A  T  TC
GAM736  LOC90643  3'  GAGGAGGAAGCCCAAGC     64439    CGC    CG
                                GC   GGGCT  TCCTCCTC
                                ||   |||||  ||||||||
                                CG   CCCGA  AGGAGGAG
                                 AA_    __
GAM736  LOC91040  3'  GAGGAGGACGAGGATGACTGG  65348     CCG  GG
                                CCG   CG  CTCGTCCTCCTC
                                |||   ||  ||||||||||||
                                GGT   GT  GAGCAGGAGGAG
                                  CA_  AG
GAM736  LOC91516  5'  GAGAAGGACGAGGCCAAGG   66907    GC  G      C
                                CC  GG CTCGTCCT CTC
                                ||  || |||||||| |||
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                                GG  CC GAGCAGGA GAG
                                 AA  G       A
GAM736  LOC91978  5'  GAGGAGGACTTCCTGCGGC   68403        CTC
                                GCCGCGGG   GTCCTCCTC
                                ||||||||   |||||||||
                                CGGCGTCC   CAGGAGGAG
                                    TT_
GAM737  EIF2B5   3'  GTGACCACCATCCAGGCT    62206          CAGACAG
                                AGCCTGGATGGTG      CAC
                                ||||||||||||      |||
                                TCGGACCTACCAC      GTG
                                       CA_____
GAM737  MAFF     3'  AGCGCCGCCTCTGTGCCCAGGT 25571       ATG TG    CA__  A
                                GCCTGG   G  CAGA    GC CT
                                ||||||   |  ||||    || ||
                                TGGACC   C  GTCT    CG GA
                                   ___ GT    CCGC  C
GAM737  RRM1     5'  GTGCTGTCTGGCTCCAACT    8283     A   T  _
                                GG TGG GC AGACAGCAC
                                || ||| || |||||||||
                                TC ACC CG TCTGTCGTG
                                 A   T  G
GAM737  SAG      5'  GCGCTGCCCCTTCAGGCT    6773         T  T    ACA
                                AGCCTGGA GG GCAG   GC
                                |||||||| || ||||   ||
                                TCGGACTT CC CGTC   CG
                                     C  _    G__
GAM737  TBL2     3'  AGTGCTGTCTACCATC      53351       GC
                                GATGGT  AGACAGCACT
                                ||||||  ||||||||||
                                CTACCA  TCTGTCGTGA
                                   __
GAM737  C6orf26  3'  GTTCCTGCACCACCCAGG    48272       A       AC
                                CCTGG TGGTGCAG  AGC
                                ||||| ||||||||  |||
                                GGACC ACCACGTC  TTG
                                   C       C_
GAM737  DKFZP564O0823 3'  GCCTTGCACCAGCCAGGC    60259       A       ACA
                                GCCTGG TGGTGCAG   GC
                                |||||| ||||||||   ||
                                CGGACC ACCACGTT   CG
                                   G       C__
GAM737  KIAA1297  5'  AGTGCTGTTAACACCCATGGC  72628     TGGAT    CA
                                GCC    GGTG  GACAGCACT
                                |||    ||||  |||||||||
                                CGG    CCAC  TTGTCGTGA
                                  TAC__    AA
GAM737  KIAA1881  3'  AGTGCTGTGGCATCCCAGGCT  97080        AT    AG
                                AGCCTGG  GGTGC  ACAGCACT
                                |||||||  |||||  ||||||||
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                                TCGGACC  CTACG  TGTCGTGA
                                   __    G_
GAM737  LEPROTL1  3'  AGTGCTGTCTCTGATTTCTAGG 31700       TGGTGC
          CT                     AGCCTGGA    AGACAGCACT
                                 ||||||||    ||||||||||
                                 TCGGATCT    TCTGTCGTGA
                                    TTAGTC
GAM737  USP24     3'  GTGCCGTATCATCAGACT    92794    C  G     AGACA
                                 AG CTG ATGGTGC    GCAC
                                 || ||| |||||||    ||||
                                 TC GAC TACTATG    CGTG
                                  A  _     C____
GAM737  LOC123905 5'  AGCGCGGGGCCACCATCCAG   74721        _ AGACA  A
                                 CTGGATGGTG C    GC CT
                                 |||||||||| |    || ||
                                 GACCTACCAC G    CG GA
                                       C GGG__  C
GAM737  LOC147166 5'  TGCCATCTCCAGGCTCCAGGCT 78897       TGG  C   CA
                                 AGCCTGGA   TG AGA  GCA
                                 ||||||||   || |||  |||
                                 TCGGACCT   AC TCT  CGT
                                      CGG  C   AC
GAM737  LOC148709 5'  GCAAGGTACACAGCCATCCAGG 79691         GCAG_  A__
          CT                     AGCCTGGATGGT    AC   GC
                                 ||||||||||||    ||   ||
                                 TCGGACCTACCG    TG   CG
                                       ACACA  GAA
GAM737  LOC150378 3'  TTGTCTGCACCCCCCAAGC   80562    C   AT
                                 GC TGG  GGTGCAGACAG
                                 || |||  ||||||||||
                                 CG ACC  CCACGTCTGTT
                                  A  CC
GAM737  LOC152897 3'  TGCTGTCTGCAAAGTAGAGCT  81612    _   GATGG
                                 AGC CTG    TGCAGACAGCA
                                 ||| |||    ||||||||||
                                 TCG GAT    ACGTCTGTCGT
                                   A  GAA__
GAM737  LOC200918 3'  AGTGCTGCACATCATCCAGGT  90364         CAGA
                                 GCCTGGATGGTG   CAGCACT
                                 ||||||||||||   |||||||
                                 TGGACCTACTAC   GTCGTGA
                                       AC__
GAM737  LOC255189 5'  AGTGCTATCTGTTTGCCAAGGC 98375      GGA   __    C
          T                      AGCCT   TGGT  GCAGA AGCACT
                                 |||||   ||||  ||||| ||||||
                                 TCGGA   ACCG  TGTCT TCGTGA
                                    ___    TT    A
GAM737  LOC256948 3'  GTGACCACCATCCAAGCT    96118     C       CAGACAG
                                 AGC TGGATGGTG      CAC
                                 ||| |||||||||      |||
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                                TCG ACCTACCAC      GTG
                                  A        CA_____
GAM737  LOC54466  5'  GCTCTACTGCACCACCCCAG  39175      A_       AC_
                                CTGG  TGGTGCAG   AGC
                                ||||  ||||||||   |||
                                GACC  ACCACGTC   TCG
                                  CC       ATC
GAM737  LOC90826  5'  CTGTCTGGGCGTCCAGG     64785        G G
                                CCTGGATG T CAGACAG
                                |||||||| | |||||||
                                GGACCTGC G GTCTGTC
                                     _ G
GAM738  BCL11B    3'  AAACTGATCTTCCTATTTGA   57574        A   __
                                TCAAATGG AAGA  AGTTT
                                |||||||| ||||  |||||
                                AGTTTATC TTCT  TCAAA
                                     C    AG
GAM738  CENPB     3'  GAATCCTCTTTCCTCCCCATTT 70114        AA __   TTT
              GG                  TCAAATGG  AG  AAG   GATTC
                                |||||||  ||  |||   |||||
                                GGTTTACC  TC  TTC   CTAAG
                                     CC  CT   TC_
GAM738  PPP3CA    3'  GAATGCCCTTCTTTCCAT    8137          TT G
                                ATGGAAAGAAG  T ATTC
                                ||||||||||  | ||||
                                TACCTTTCTTC  G TAAG
                                       CC _
GAM738  PTN       3'  AAATTATTTTTCCATCTGA   83591     A       _
                                TCA ATGGAAAGA AGTTT
                                ||| ||||||||| |||||
                                AGT TACCTTTTT TTAAA
                                  C        A
GAM738  RAD50     3'  GAACAGGCCTCTCCATTTG   20408        AA  A    A
                                CAAATGGA  GA GTTTG TTC
                                ||||||||  || ||||| |||
                                GTTTACCT  CT CGGAC AAG
                                     __  C    _
GAM738  TOX       3'  GAACACCTCTTCTTTCCACTGA 28962     AA        TT_  A
                                TCA  TGGAAAGAAG   TG TTC
                                |||  ||||||||||   || |||
                                AGT  ACCTTTCTTC   AC AAG
                                  C_         TCC  _
GAM738  ZNF131    3'  AATCAAACTTAAATCATTAGA  70722    A    AAAG
                                TC AATGG    AAGTTTGATT
                                || |||||    ||||||||||
                                AG TTACT    TTCAAACTAA
                                  A    AAA_
GAM738  C1orf25   3'  AATCATACTTCTCTCCACATTG 72938     A_   A     T
              A                   TCAA  TGGA AGAAGT TGATT
                                ||||  |||| |||||| |||||
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                                AGTT  ACCT TCTTCA ACTAA
                                  AC   C     T
GAM738  COVA1    3'  AATCAAGGGAAACTTTCCATTT 73637         AAG__
                                AAATGGAAAG    TTTGATT
                                ||||||||||    |||||||
                                TTTACCTTTC    GAACTAA
                                     AAAGG
GAM738  CXYorf1  3'  GGAATCAGGGTTTCCCACCA  82917    AAA_  G
                                TGG   GAA TTTGATTCC
                                |||   ||| |||||||||
                                ACC   TTT GGACTAAGG
                                  ACCC  G
GAM738  FLJ10716 3'  GAACTCATTTCCATTTGA    37016          GA
                                TCAAATGGAAA  AGTTT
                                ||||||||||  |||||
                                AGTTTACCTTT  TCAAG
                                      AC
GAM738  FLJ12529 3'  GAATTTTTTTCTCCCCATTTG  46084       AA    TTT
                                CAAATGG  AGAAG   GATTC
                                |||||||  |||||   |||||
                                GTTTACC  TCTTT   TTAAG
                                    CC    TT_
GAM738  FLJ20051 3'  GGAACTAGTTTTTTTTCCATTT 39363          T   A
                                AAATGGAAAGAAG TTG TTCC
                                |||||||||||||| ||| ||||
                                TTTACCTTTTTTT GAT AAGG
                                       T   C
GAM738  FLJ21272 3'  AATCAAACTTCTGTTACTA   47391    AA__
                                TGG   AGAAGTTTGATT
                                |||   ||||||||||||
                                ATC   TCTTCAAACTAA
                                  ATTG
GAM738  FLJ21415 3'  GAATCAGCCTCTCCTTTGA   45686     T   AA  A   T
                                TCAAA GGA  GA GTT GATTC
                                ||||| |||  ||  ||| |||||
                                AGTTT CCT  CT CGA CTAAG
                                   _  __  C   _
GAM738  FLJ21918 3'  GAATCAAGGGTCCATCTGA   46858    A    AAGAAG
                                TCA ATGGA     TTTGATTC
                                ||| |||||     ||||||||
                                AGT TACCT     GAACTAAG
                                  C    GG____
GAM738  FLJ32468 5'  AGAGTTGCTTCCATTTGA    59706         AG  G
                                TCAAATGGAA  AA TTT
                                ||||||||||  ||  |||
                                AGTTTACCTT  TT AGA
                                      CG  G
GAM738  KIAA0828 3'  GATTTAACCTCTTCCATTTGA  82116          A  A   T
                                TCAAATGGAA GA GTT GATT
                                |||||||||| ||  ||| ||||
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                                AGTTTACCTT CT CAA TTAG
                                      _ C   T
GAM738  PP13     3'  GGAATCCCTCTTTCTACCTGA  26091     AA       A TTT
                                TCA  TGGAAAGA G   GATTCC
                                |||  |||||||| |   ||||||
                                AGT  ATCTTTCT C   CTAAGG
                                  CC       _ C__
GAM738  PRO1496  3'  AATCAGGATCCCCATTTGA   38365        AAA  AG
                                TCAAATGG   GA  TTTGATT
                                ||||||||   ||  |||||||
                                AGTTTACC   CT  GGACTAA
                                     C__  A_
GAM738  TP53TG1  3'  AATCAAACTTCAGTTTCA    24320      A_
                                TGGAA  GAAGTTTGATT
                                |||||  ||||||||||
                                ACTTT  CTTCAAACTAA
                                   GA
GAM738  LOC133121 3'  AATCCTAGCTTTCCATTTG   75588          AAGTTT
                                CAAATGGAAAG     GATT
                                ||||||||||     ||||
                                GTTTACCTTTC     CTAA
                                      GATC__
GAM738  LOC150378 3'  GGAATCAAACTCAAGCCCAT   80560      AAAGA
                                ATGG    AGTTTGATTCC
                                ||||    ||||||||||
                                TACC    TCAAACTAAGG
                                  CGAAC
GAM738  LOC150406 3'  AGATTTCTTTCTTCCATTT    80670        ___
                                AAATGGAA   AGAAGTTT
                                ||||||||   ||||||||
                                TTTACCTT   TCTTTAGA
                                     CTT
GAM738  LOC153577 3'  GAACCATACTCTTTCCACTGA  87238     AA       A  T  A
                                TCA  TGGAAAGA GT TG TTC
                                |||  |||||||| || || |||
                                AGT  ACCTTTCT CA AC AAG
                                  C_       _  T  C
GAM738  LOC154881 3'  GGAAGTGACTTTTCCCCATTTG 82071        AA      TGA
           A                     TCAAATGG  AGAAGTT   TTCC
                                |||||||  |||||||   ||||
                                AGTTTACC  TTTTCAG   AAGG
                                     CC      TG_
GAM738  LOC199725 3'  GGAATCCCTCTTTCCATGTGA  91421     A       A TTT
                                TCA ATGGAAAGA G   GATTCC
                                ||| |||||||| |   ||||||
                                AGT TACCTTTCT C   CTAAGG
                                  G        _ C__
GAM738  LOC253786 5'  GAATCAAACCCCCCTCTCCA   98833     A  AA__
                                TGGA AG    GTTTGATTC
                                ||||  ||    |||||||||
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                                ACCT TC    CAAACTAAG
                                  C  CCCC
GAM738  LOC56891  3'  GGAATCCCTCTTTCTACCTGA  39688     AA       A TTT
                                TCA  TGGAAAGA G   GATTCC
                                |||  |||||||| |   ||||||
                                AGT  ATCTTTCT C   CTAAGG
                                  CC       _ C__
GAM738  LOC90297  5'  AGTCCAGCCTCTCCCCATTTGA 62848         AA   A   T
                                TCAAATGG  AGA GTT GATT
                                ||||||||  ||| ||| ||||
                                AGTTTACC  TCT CGA CTGA
                                     CC   C   C
GAM738  LOC90906  5'  GAACTTGCCCACTCCATTTGA  64950         AAG___
                                TCAAATGGA     AAGTTT
                                |||||||||     ||||||
                                AGTTTACCT     TTCAAG
                                      CACCCG
GAM738  LOC93380  3'  GAAACAAGCTCCTTCCATCAGA 72653     AA     A A    A
                                TC  ATGGAA GA GTTTG TTC
                                ||  |||||| || ||||| |||
                                AG  TACCTT CT CGAAC AAG
                                 AC     C _    A
GAM739  DTR       3'  CAAACAGAGTATGTCCG     10453       ACAGAC
                                TGGACA     CTCTGTTTG
                                ||||||     |||||||||
                                GCCTGT     GAGACAAAC
                                   AT_____
GAM739  HLA-DMA   3'  CAAACAGAGGATGCTCAG    21501     GA  ACAGA
                                CTG  CA    CCTCTGTTTG
                                |||  ||    ||||||||||
                                GAC  GT    GGAGACAAAC
                                  TC  A_____
GAM739  ICOS      3'  CCACCTGGCCTGGTTGTCCA   24924        _  A  TCTGTT
                                TGGACAAC AG CC     TGG
                                |||||||| || ||     |||
                                ACCTGTTG TC GG     ACC
                                     G  C  TCC___
GAM739  KHK       3'  CCATCCAGCCTGGCGTCCAGG  22416       AA   ACCT   TT
                                CCTGGAC  CAG   CTG  TGG
                                |||||||  |||   |||  |||
                                GGACCTG  GTC   GAC  ACC
                                   CG   C___   CT
GAM739  KHK       3'  CCATCCAGCCTGGCGTCCAGG  5845        AA   ACCT   TT
                                CCTGGAC  CAG   CTG  TGG
                                |||||||  |||   |||  |||
                                GGACCTG  GTC   GAC  ACC
                                   CG   C___   CT
GAM739  PTGFRN    5'  CCAGCACAGATGCCACTGTCCA 67766        ACAGACC    _
          GG                    CCTGGACA      TCTGT TTGG
                                ||||||||      ||||| ||||
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                                GGACCTGT      AGACA GACC
                                    CACCGT_    C
GAM739  RAF1     3'  CCAAACAGCCCAGGACTGCCGA 81371    _ ACAA  A  ___
           G                     CT GG   CAG CCT  CTGTTTGG
                                || ||   ||| |||  ||||||||
                                GA CC   GTC GGA  GACAAACC
                                 G ____  A  CCC
GAM739  STAT6    3'  CAAATTCCTGTTAGCCAGG   13449      AC    ACCTCT
                                CCTGG  AACAG     GTTTG
                                |||||  |||||     |||||
                                GGACC  TTGTC     TAAAC
                                   GA    CT____
GAM739  DDX35    3'  CCAATGAGGTCTGCTGCCAGG  41927      A  A      TGT
                                CCTGG CA CAGACCTC   TTGG
                                ||||| || ||||||||   ||||
                                GGACC GT GTCTGGAG   AACC
                                   _ C       T__
GAM739  FLJ13576 3'  CCAAACAGTAGGTTTCATCCA  42807     CAAC    _
                                TGGA   AGACCT CTGTTTGG
                                ||||   |||||| ||||||||
                                ACCT   TTTGGA GACAAACC
                                  AC__     T
GAM739  FLJ14146 3'  AGAAGTTTGCTGTCCAGG    45565       A    C
                                CCTGGACA CAGAC TCT
                                |||||||| ||||| |||
                                GGACCTGT GTTTG AGA
                                     C    A
GAM739  KIAA0350 3'  CCAAACAGAGACAGCTTCCAG  61825      CAAC  AC__
                                CTGGA   AG   CTCTGTTTGG
                                |||||   ||   ||||||||||
                                GACCT   TC   GAGACAAACC
                                   _____ GACA
GAM739  KIAA0847 3'  AGAAGTCTGTTGCCAGG     78073      A      C
                                CCTGG CAACAGAC TCT
                                ||||| |||||||| |||
                                GGACC GTTGTCTG AGA
                                   _       A
GAM739  KRTHB4   3'  CAGACAGCTGCTGCCCAG    53499     A  A   ACCT
                                CTGG CA CAG   CTGTTTG
                                |||| || |||   |||||||
                                GACC GT GTC   GACAGAC
                                  C  C  _____
GAM739  p25      3'  CCAAACAGGGTGGCTCCCCAGG 23825      ACAACAG   T
                                CCTGG      ACC CTGTTTGG
                                |||||      ||| ||||||||
                                GGACC      TGG GACAAACC
                                   CCTCGG_  _
GAM739  RAI16    3'  CCAAACAGATGGCTTTCCAGG  43045      CAAC  A  _
                                CCTGGA   AG CC TCTGTTTGG
                                ||||||   || || |||||||||
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                                GGACCT    TC GG AGACAAACC
                                   T___  _  T
GAM739  RoXaN     3'  CAAACAGATGTCACCAG     47274      ACAACA   C
                                CTGG      GAC TCTGTTTG
                                ||||      ||| ||||||||
                                GACC      CTG AGACAAAC
                                  A_____   T
GAM739  SLC1A7    3'  CCAAAGGCCTGTGCGTCCA    22880       A_    A   CTGT
                                TGGAC  ACAG CCT    TTGG
                                |||||  |||| |||    ||||
                                ACCTG  TGTC GGA    AACC
                                   CG    C  ____
GAM739  SLC26A8   3'  CCAAAAAGGGGTCAATTGTCCA 54768         CA      G
           G                     CTGGACAA  GACCTCT TTTGG
                                ||||||||  ||||||| |||||
                                GACCTGTT  CTGGGGA AAACC
                                     AA       A
GAM739  SLC26A8   3'  CCAAAAAGGGGTCAATTGTCCA 57802         CA      G
           G                     CTGGACAA  GACCTCT TTTGG
                                ||||||||  ||||||| |||||
                                GACCTGTT  CTGGGGA AAACC
                                     AA       A
GAM739  LOC144699 3'  CAGAGGCTGCTGCCCAGG     77435       A  A   A
                                CCTGG CA CAG CCTCTG
                                ||||| || ||| ||||||
                                GGACC GT GTC GGAGAC
                                   C  C   _
GAM739  LOC163255 5'  CAGCTGGTTTGTTATCCAGG   83342        C       T_
                                CCTGGA AACAGACC  CTG
                                |||||| ||||||||  |||
                                GGACCT TTGTTTGG  GAC
                                   A       TC
GAM739  LOC255452 5'  CAAACGGCTGCTGCTCAG     99388     GA  A   ACCT
                                CTG  CA CAG    CTGTTTG
                                |||  || |||    |||||||
                                GAC  GT GTC    GGCAAAC
                                  TC  C  _____
GAM739  LOC257464 5'  CCAAACAGCATATTGGCCAGG  91241       A   CAGACCT
                                CCTGG CAA      CTGTTTGG
                                |||||  |||      ||||||||
                                GGACC GTT      GACAAACC
                                   G   ATAC___
GAM739  LOC51246  3'  CCAAGTAGGGCCTGTCACACCA 33638       ACA_    A  T
           GG                    CCTGG    ACAG CC CTGTTTGG
                                |||||    |||| || ||||||||
                                GGACC    TGTC GG GATGAACC
                                   ACAC    C  _
GAM739  LOC90494  5'  CGGAGGTCTGTTGTACAG     63732      G
                                CTG ACAACAGACCTCTG
                                ||| ||||||||||||||
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                                GAC TGTTGTCTGGAGGC
                                  A
GAM740  ATP11A   3'  ACATATACACACATGTG     77550    T    T
                                CA CATGT GTGTATATGT
                                || ||||| ||||||||||
                                GT GTACA CACATATACA
                                 _    _
GAM740  HOXC9    3'  ACACACACACATACATGATAAT 61926     C      _     ATA
           G                     TAT ATCATGT TGTGT   TGT
                                ||| ||||||| |||||   |||
                                GTA TAGTACA ACACA   ACA
                                  A      T    CAC
GAM740  LRAT     3'  ACATATACACAGACTGAGA    60728    A   TG
                                TC TCA  TTGTGTATATGT
                                || |||  ||||||||||||
                                AG AGT  GACACATATACA
                                 _  CA
GAM740  MGAT5    5'  ACATATACATTGTGAAATGAT  11566      __     TT
                                ATCA  TCATG  GTGTATATGT
                                ||||  |||||  ||||||||||
                                TAGT  AGTGT  TACATATACA
                                  AA    __
GAM740  PMP22    3'  ACAATTTTACAACATAAGATAG 6118        ATC       TATA
           A                     TCTATC   ATGTTGTG    TGT
                                ||||||   ||||||||    |||
                                AGATAG   TACAACAT    ACA
                                   AA_       TTTA
GAM740  PTGFR    3'  ACATATACACACAGACATCAGA 8176      ATCA  A   T
                                TCT    TC TGT GTGTATATGT
                                |||    || ||| ||||||||||
                                AGA    AG ACA CACATATACA
                                  CTAC  _  _
GAM740  FLJ12716 3'  ACACATACACAACAACATAGG  41942       CATCA         A
                                TCTAT     TGTTGTGTAT TGT
                                |||||     |||||||||| |||
                                GGATA     ACAACACATA ACA
                                   CA___         C
GAM740  GRID1    3'  ACATATGTGTAAATAATGACAG 69019     A    CATG   TG
           A                     TCT TCAT    TTG  TATATGT
                                ||| ||||    |||  |||||||
                                AGA AGTA    AAT  GTATACA
                                  C    ATA_   GT
GAM740  KIAA0971 3'  ACACACACATAAATATGATAGA 30666         C___    _
                                TCTATCAT    ATGT TGTGT
                                ||||||||    |||| |||||
                                AGATAGTA    TACA ACACA
                                     TAAA    C
GAM740  KIAA1357 3'  ACATATACACAAACAACATGTA 72431     ATCAT     ____
           CAGA                    TCT    CATGT    TGTGTATATGT
                                |||    |||||   ||||||||||
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                                AGA    GTACA   ACACATATACA
                                  CAT__    ACAA
GAM740  KIAA1975  5'  ACATTAACATGATGATTGA   74409    T        _
                                TC ATCATCATGTTG TGT
                                || |||||||||||| |||
                                AG TAGTAGTACAAT ACA
                                  T          T
GAM740  LOC123624 3'  ACATATACACAGACGTGTAGA  76136     TCAT    _
                                TCTA   CATGT TGTGTATATGT
                                ||||   ||||| ||||||||||
                                AGAT   GTGCA ACACATATACA
                                  ____    G
GAM740  LOC152345 3'  ACACAGTTTATCATGATGACAG 81444    A      _____
            A                    TCT TCATCATG    TTGTGT
                                ||| ||||||||    ||||||
                                AGA AGTAGTAC    GACACA
                                  C       TATTT
GAM740  LOC154215 3'  ACATATACATTTGAAAATGATA 81952       CATGTT
            GA                   TCTATCAT    GTGTATATGT
                                ||||||||    ||||||||||
                                AGATAGTA    TACATATACA
                                     AAAGTT
GAM740  LOC255981 3'  ACACTTGAAACATGATGAAAGA 98918    A       ____
                                TCT TCATCATGTT   GTGT
                                ||| ||||||||||   ||||
                                AGA AGTAGTACAA   CACA
                                  A        AGTT
GAM741  PTEN    3'  TCTTGTTTTACCCTATACATCC 6142         ATA  TT
            A                    TGGATGTATA  GT  AGCAAGA
                                ||||||||||  ||  |||||||
                                ACCTACATAT  CA  TTGTTCT
                                     CC_  TT
GAM741  TCTA    3'  TCCTGTTGGATATCATACTTCC 42504     T   A  G     A
            A                    TGGA GTAT ATA TTTAGCA GA
                                |||| |||| ||| ||||||| ||
                                ACCT CATA TAT AGGTTGT CT
                                  T   C  _      C
GAM741  AP4E1   3'  TGCTAAATTTTACTCCA    24739     T   TAAT
                                TGGA GTA   AGTTTAGCA
                                |||| |||   |||||||||
                                ACCT CAT   TTAAATCGT
                                  _   T___
GAM741  C20orf38  3'  CTTGCTAGAGACCTAGACATCC 37630       ATAATAG
            A                    TGGATGT      TTTAGCAAG
                                |||||||      |||||||||
                                ACCTACA      AGATCGTTC
                                    GATCCAG
GAM741  FLJ13114  3'  TGCTGTTGTTTACATCCA   44913       T    TT
                                TGGATGTA AATAG  TAGCA
                                |||||||| |||||  |||||
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                                ACCTACAT TTGTT  GTCGT
                                      _    __
GAM741  MGC16075 3'  TTGCACCGTACATCCA     52255        AATA  TTA
                                TGGATGTAT   GT   GCAA
                                |||||||||   ||   ||||
                                ACCTACATG   CA   CGTT
                                    C___  ___
GAM741  SCYB11   3'  CTTGTTGCATTATACATTCA  88835          A  TT
                                TGGATGTATAAT GT  AGCAAG
                                ||||||||||||| ||  ||||||
                                ACTTACATATTA CG  TTGTTC
                                      _ __
GAM742  VMD2     3'  CACAGCCATACAGCTGTCCAC  16079        ACT  GTA
                                GTGGACAGC   TA   GCTGTG
                                |||||||||   ||   ||||||
                                CACCTGTCG   AT   CGACAC
                                    AC_  AC_
GAM742  DKFZP434C171 5'  CACAGCTATAACTGTCCA    32183       CACTTA
                                TGGACAG     GTAGCTGTG
                                |||||||     |||||||||
                                ACCTGTC     TATCGACAC
                                   AA____
GAM742  FLJ31164  3'  CACAGCTGCCTGCTGTCC    59393        CTTA
                                GGACAGCA    GTAGCTGTG
                                ||||||||    |||||||||
                                CCTGTCGT    CGTCGACAC
                                    C___
GAM742  HRIHFB2072 3'  CACAGCTTTATGTACCCTGTCC 51694        C__  T   T
           AC                     GTGGACAG   AC TAG AGCTGTG
                                |||||||||   || ||| |||||||
                                CACCTGTC   TG ATT TCGACAC
                                    CCA  T   _
GAM742  KIAA0298  3'  ACAGCCAAAGACTGTCACT    77073      G    CA   AGTA
                                AGTG ACAG  CTT    GCTGT
                                |||| ||||  |||    |||||
                                TCAC TGTC  GAA    CGACA
                                  _    A_   AC__
GAM742  KIAA0553  3'  CAGTAAGTGCTACCCAC     70443      AC      AGTA
                                GTGG  AGCACTT    GCTG
                                ||||  |||||||    ||||
                                CACC  TCGTGAA    TGAC
                                  CA      _____
GAM742  MGC12921  3'  CACAGCCCGAGGAAAGTGCTGG 64510      A       AGTA___
           CCAC                    GTGG CAGCACTT      GCTGTG
                                |||| ||||||||      ||||||
                                CACC GTCGTGAA      CGACAC
                                  G       AGGAGCC
GAM742  POLR2D   3'  CACAACCAGGTGTGCACTGTTC 17839         ____     A  AGC
           ACT                     AGTGGACAG    CACTT GT   TGTG
                                |||||||||    ||||| ||   ||||
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                                TCACTTGTC   GTGGA CA   ACAC
                                     ACGT    C  ___
GAM742  LOC116028 3'  ACAGCCTCTGCTGCCCCT   74093    T  A    CTTA TA
                                AG GG CAGCA   G  GCTGT
                                || || |||||   |  |||||
                                TC CC GTCGT   C  CGACA
                                 _  C    _____ TC
GAM742  LOC152286 3'  ACAGCTGTTGGCATCCACT   86801       CA  ACT
                                AGTGGA  GC   TAGTAGCTGT
                                ||||||  ||   ||||||||||
                                TCACCT  CG   GTTGTCGACA
                                   A_  ___
GAM742  LOC163231 5'  CACAGGGACAACATGTCCACT  83329        GCACTTA  AG
                                AGTGGACA      GT  CTGTG
                                ||||||||      ||  |||||
                                TCACCTGT      CA  GACAC
                                     ACAA___  GG
GAM742  LOC163231 3'  CACAGTGGGAAACTGTCCACT  83330        CAC  AGTA
                                AGTGGACAG   TT   GCTGTG
                                |||||||||   ||   ||||||
                                TCACCTGTC   AG   TGACAC
                                     AA_  GG__
GAM742  LOC253805 3'  CACAGTAAAATGCTGTCCA    98169         C  AGTA
                                TGGACAGCA TT   GCTGTG
                                ||||||||| ||   ||||||
                                ACCTGTCGT AA   TGACAC
                                     A  A___
GAM743  CDH12    3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM743  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM743  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090      T   AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                   _   GTCA_
GAM743  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
          A                      TACAC       AGAAGAATAAG
                                 |||||       ||||||||||
                                 ATGTG       TCTTCTTATTC
                                    TACTCCC_
GAM743  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT      GAATAAG
                                |||||||||      |||||||
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                                ATGTGGTGA      TTTATTC
                                     AGACG___
GAM743  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
            TA                    TACA   TCC   GAAGAATAAG
                                  ||||   |||   ||||||||||
                                  ATGT   AGG   TTTCTTATTC
                                    AAA_   ATTG
GAM743  KIAA1719 3'  TCTGTCTTGGGAGTGGTGTA  68742           _
                                  TACACCACTCCCAAGA AGA
                                  |||||||||||||||| |||
                                  ATGTGGTGAGGGTTCT TCT
                                           G
GAM743  KIAA1853 3'  TTTTTCTTGGAAGCAGTG    69929    CA  C
                                  CAC  CT CCAAGAAGAA
                                  |||  || ||||||||||
                                  GTG  GA GGTTCTTTTT
                                    AC  A
GAM743  KIAA1877 3'  CTTATTCTTCTGCCATGAGT   66748    CCA__
                                  ACTC    AGAAGAATAAG
                                  ||||    ||||||||||
                                  TGAG    TCTTCTTATTC
                                    TACCG
GAM743  KIAA1906 3'  CTTATTCTTCTTGACTTTTGG  73571    CTCC_
                                  CCA    CAAGAAGAATAAG
                                  |||    ||||||||||||
                                  GGT    GTTCTTCTTATTC
                                    TTTCA
GAM743  OSBPL11  3'  CTTAATTTCCCAAGAGTGGTG  43206       CCAA   AA
                                  CACCACTC   GAAG  TAAG
                                  ||||||||   ||||  ||||
                                  GTGGTGAG   CTTT  ATTC
                                       AACC   A_
GAM743  YME1L1   3'  TCATTCTTGATGTGGTGTA   58438       TCC    _
                                  TACACCAC   CAAGAA GA
                                  ||||||||   |||||| ||
                                  ATGTGGTG   GTTCTT CT
                                       TA_     A
GAM743  ZNF262   3'  CTTATTTTGTTTGGGAGT    18723        A
                                  ACTCCCAAG AGAATAAG
                                  |||||||||  ||||||||
                                  TGAGGGTTT TTTTATTC
                                       G
GAM743  LOC91960 3'  TGTGGCTTGGAACGTGGTGTA  68294       TC_   AAGA
                                  TACACCAC   CCAAG   ATA
                                  ||||||||   |||||   |||
                                  ATGTGGTG   GGTTC   TGT
                                       CAA    GG__
GAM744  CHAT     5'  GAGGAGAGCAGGTCCACACC   40969    CC  A      ATG
                                  GG  TG ACCTGCTTT   CTC
                                  ||  || |||||||||   |||
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                                CC  AC TGGACGAGA   GAG
                                 AC  C        G__
GAM744  PNN      5'  TGTAAAGCAGTCTCAAGCC   71665     C   AC
                                GGC TGA  CTGCTTTATG
                                ||| |||  ||||||||||
                                CCG ACT  GACGAAATGT
                                  A   CT
GAM744  C16orf5  3'  GGTACAGGTTCAGTCC      26356    C       CTTTA
                                GG CTGAACCTG     TGCT
                                || |||||||||     ||||
                                CC GACTTGGAC     ATGG
                                 T       _____
GAM744  C19orf7  3'  GCGTGGAAGCAGGTCCAGGC   61781      A       _
                                GCCTG ACCTGCTTT ATGC
                                ||||| ||||||||| ||||
                                CGGAC TGGACGAAG TGCG
                                   C        G
GAM744  FLJ20085 5'  CTGAGCCGGGAGCAGGTCCAAC 35006    CC  A       AT
            C                    GG  TG ACCTGCTTT  GCTCAG
                                ||  || |||||||||  ||||||
                                CC  AC TGGACGAGG  CGAGTC
                                 A_  C        GC
GAM744  FLJ23499 3'  CTGAGCATGGTGGCTCACGCC  43135     C   A  T   TT
                                GGC TGA CC GCT  ATGCTCAG
                                ||| ||| || |||  ||||||||
                                CCG ACT GG TGG  TACGAGTC
                                  C   C  _  __
GAM744  KIAA0089 3'  CTGAACTTTTACAGTTCAGGCC 70507        C   CTTTATGC
                                GGCCTGAA CTG       TCAG
                                |||||||| |||       ||||
                                CCGGACTT GAC       AGTC
                                     _  ATTTTCA_
GAM744  KIAA0257 3'  AGCAGGGCAGGCTCAGACC    71370    C    A      TA
                                GG CTGA CCTGCTT  TGCT
                                || |||| |||||||  ||||
                                CC GACT GGACGGG  ACGA
                                 A   C      __
GAM744  KIAA1389 3'  CTGAGCTTGCACAGATCAGACC 70318    C    ACC_   TTTAT
                                GG CTGA    TGC     GCTCAG
                                || ||||    |||     ||||||
                                CC GACT    ACG     CGAGTC
                                 A    AGAC   TT___
GAM744  KIAA1456 3'  CTGAGCATGGTGGCTCATGCC  67552     C   A  T   TT
                                GGC TGA CC GCT  ATGCTCAG
                                ||| ||| || |||  ||||||||
                                CCG ACT GG TGG  TACGAGTC
                                  T   C  _  __
GAM744  LSM10    3'  GAGAAGAAAGCAGGGCCAGGCC 52869       AA       ATG
                                GGCCTG  CCTGCTTT   CTC
                                ||||||  ||||||||   |||
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                                CCGGAC  GGACGAAA   GAG
                                   CG       GAA
GAM744  MGC26954  3'  AGACAGAGCAATTCAGGCC   59490        CC     ATG
                                GGCCTGAA  TGCTTT   CT
                                ||||||||  ||||||   ||
                                CCGGACTT  ACGAGA   GA
                                    A_     CA_
GAM744  OAZ2      3'  GAGTAAGCAGGTCCGACC    11876    CC  A      TTA
                                GG  TG ACCTGCT   TGCTC
                                ||  || |||||||   |||||
                                CC  GC TGGACGA   ATGAG
                                 A_  C      ___
GAM744  REM       3'  CTGAGCATCCCCCAGATCCAAG 26686     C  AAC   CTTT
             CC                   GGC TG   CTG    ATGCTCAG
                                ||| ||   |||    ||||||||
                                CCG AC   GAC    TACGAGTC
                                  A  CTA   CCCC
GAM744  TGOLN2    3'  GAGCATAAAACAGAACTTGGGC 64743     TG AC_   C
                                GCC  A   CTG TTTATGCTC
                                |||  |   ||| |||||||||
                                CGG  T   GAC AAATACGAG
                                  GT CAA   A
GAM744  TRIAD3    3'  TGAGCATCAGCTCAGCC     96141     C   ACCT   TT
                                GGC TGA    GCT  ATGCTCA
                                ||| |||    |||  |||||||
                                CCG ACT    CGA  TACGAGT
                                  _  _____   C_
GAM744  LOC123242 5'  CTGGAGGAGGCAGGCCCAAGCC 76115     C  AA       ATG T
                                GGC TG  CCTGCTTT   C CAG
                                ||| ||  ||||||||   | |||
                                CCG AC  GGACGGAG   G GTC
                                  A  CC       GA_ _
GAM744  LOC131405 5'  CTGAGCATCGAGCAGGCCCAG  76377     AA      T
                                CTG  CCTGCTT ATGCTCAG
                                |||  ||||||| ||||||||
                                GAC  GGACGAG TACGAGTC
                                  CC      C
GAM744  LOC146159 5'  GAGCGGGGCAGGTTCTGGCC   78176     T        TA
                                GGCC GAACCTGCTT  TGCTC
                                |||| ||||||||||  |||||
                                CCGG CTTGGACGGG  GCGAG
                                   T        __
GAM744  LOC158117 3'  CTGAGCATGTGCAGCCCTGGCC 82612      TGAAC    TT
                                GGCC    CTGC  TATGCTCAG
                                ||||    ||||  |||||||||
                                CCGG    GACG  GTACGAGTC
                                  TCCC_    T_
GAM744  LOC203275 3'  CTGAGCATGTGCAGCCCTGGCC 90854      TGAAC    TT
                                GGCC    CTGC  TATGCTCAG
                                ||||    ||||  |||||||||
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                                CCGG    GACG  GTACGAGTC
                                  TCCC_   T_
GAM744  LOC253001 5'  CTGGAGGAGGCAGGCCCAAGCC 97994     C  AA       ATG T
                                GGC TG  CCTGCTTT   C CAG
                                ||| ||  ||||||||   | |||
                                CCG AC  GGACGGAG   G GTC
                                  A  CC       GA_ _
GAM744  LOC257464 3'  CTGAACATAAAGCAAGTTCAGC 91243     C    C       C
           T                     GGC TGAAC TGCTTTATG TCAG
                                ||| ||||| ||||||||| ||||
                                TCG ACTTG ACGAAATAC AGTC
                                  _    A       A
GAM745  DDX11   3'  GGCCCATCTGCCTCTGCCC   16579      T  AGAT  CA
                                GGGCA GA   CA  ATGGGCC
                                ||||| ||   ||  |||||||
                                CCCGT CT   GT  TACCCGG
                                  _ CC__  C_
GAM745  DDX11   3'  GGCCCATCTGCCTCTGCCC   48392      T  AGAT  CA
                                GGGCA GA   CA  ATGGGCC
                                ||||| ||   ||  |||||||
                                CCCGT CT   GT  TACCCGG
                                  _ CC__  C_
GAM745  PCDHGA1  3'  AGGCCCATCCATCCCATGCCT  38834       AA   CACA
                                GGGCATG  GAT   ATGGGCCT
                                |||||||  |||   ||||||||
                                TCCGTAC  CTA   TACCCGGA
                                   C_   CC__
GAM745  PCDHGA10 3'  AGGCCCATCCATCCCATGCCT  38839       AA   CACA
                                GGGCATG  GAT   ATGGGCCT
                                |||||||  |||   ||||||||
                                TCCGTAC  CTA   TACCCGGA
                                   C_   CC__
GAM745  PCDHGA11 3'  AGGCCCATCCATCCCATGCCT  38841       AA   CACA
                                GGGCATG  GAT   ATGGGCCT
                                |||||||  |||   ||||||||
                                TCCGTAC  CTA   TACCCGGA
                                   C_   CC__
GAM745  PCDHGA11 3'  AGGCCCATCCATCCCATGCCT  50315       AA   CACA
                                GGGCATG  GAT   ATGGGCCT
                                |||||||  |||   ||||||||
                                TCCGTAC  CTA   TACCCGGA
                                   C_   CC__
GAM745  PCDHGA12 3'  AGGCCCATCCATCCCATGCCT  14963       AA   CACA
                                GGGCATG  GAT   ATGGGCCT
                                |||||||  |||   ||||||||
                                TCCGTAC  CTA   TACCCGGA
                                   C_   CC__
GAM745  PCDHGA2  3'  AGGCCCATCCATCCCATGCCT  38848       AA   CACA
                                GGGCATG  GAT   ATGGGCCT
                                |||||||  |||   ||||||||
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                              TCCGTAC CTA  TACCCGGA
                                 C_  CC__
GAM745  PCDHGA3  3' AGGCCCATCCATCCCATGCCT 38854     AA  CACA
                              GGGCATG GAT  ATGGGCCT
                              ||||||| |||  ||||||||
                              TCCGTAC CTA  TACCCGGA
                                 C_  CC__
GAM745  PCDHGA4  3' AGGCCCATCCATCCCATGCCT 38856     AA  CACA
                              GGGCATG GAT  ATGGGCCT
                              ||||||| |||  ||||||||
                              TCCGTAC CTA  TACCCGGA
                                 C_  CC__
GAM745  PCDHGA5  3' AGGCCCATCCATCCCATGCCT 38862     AA  CACA
                              GGGCATG GAT  ATGGGCCT
                              ||||||| |||  ||||||||
                              TCCGTAC CTA  TACCCGGA
                                 C_  CC__
GAM745  PCDHGA6  3' AGGCCCATCCATCCCATGCCT 38864     AA  CACA
                              GGGCATG GAT  ATGGGCCT
                              ||||||| |||  ||||||||
                              TCCGTAC CTA  TACCCGGA
                                 C_  CC__
GAM745  PCDHGA7  3' AGGCCCATCCATCCCATGCCT 38869     AA  CACA
                              GGGCATG GAT  ATGGGCCT
                              ||||||| |||  ||||||||
                              TCCGTAC CTA  TACCCGGA
                                 C_  CC__
GAM745  PCDHGA8  3' AGGCCCATCCATCCCATGCCT 50303     AA  CACA
                              GGGCATG GAT  ATGGGCCT
                              ||||||| |||  ||||||||
                              TCCGTAC CTA  TACCCGGA
                                 C_  CC__
GAM745  PCDHGA9  3' AGGCCCATCCATCCCATGCCT 38870     AA  CACA
                              GGGCATG GAT  ATGGGCCT
                              ||||||| |||  ||||||||
                              TCCGTAC CTA  TACCCGGA
                                 C_  CC__
GAM745  PCDHGB1  3' AGGCCCATCCATCCCATGCCT 38873     AA  CACA
                              GGGCATG GAT  ATGGGCCT
                              ||||||| |||  ||||||||
                              TCCGTAC CTA  TACCCGGA
                                 C_  CC__
GAM745  PCDHGB2  3' AGGCCCATCCATCCCATGCCT 38879     AA  CACA
                              GGGCATG GAT  ATGGGCCT
                              ||||||| |||  ||||||||
                              TCCGTAC CTA  TACCCGGA
                                 C_  CC__
GAM745  PCDHGB3  3' AGGCCCATCCATCCCATGCCT 38881     AA  CACA
                              GGGCATG GAT  ATGGGCCT
                              ||||||| |||  ||||||||
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                                TCCGTAC CTA  TACCCGGA
                                   C_  CC__
GAM745  PCDHGB4  3' AGGCCCATCCATCCCATGCCT 14965      AA  CACA
                                GGGCATG GAT  ATGGGCCT
                                ||||||| |||  ||||||||
                                TCCGTAC CTA  TACCCGGA
                                   C_  CC__
GAM745  PCDHGB5  3' AGGCCCATCCATCCCATGCCT 38888      AA  CACA
                                GGGCATG GAT  ATGGGCCT
                                ||||||| |||  ||||||||
                                TCCGTAC CTA  TACCCGGA
                                   C_  CC__
GAM745  PCDHGB6  3' AGGCCCATCCATCCCATGCCT 38894      AA  CACA
                                GGGCATG GAT  ATGGGCCT
                                ||||||| |||  ||||||||
                                TCCGTAC CTA  TACCCGGA
                                   C_  CC__
GAM745  PCDHGB7  3' AGGCCCATCCATCCCATGCCT 38897      AA  CACA
                                GGGCATG GAT  ATGGGCCT
                                ||||||| |||  ||||||||
                                TCCGTAC CTA  TACCCGGA
                                   C_  CC__
GAM745  PCDHGC3  3' AGGCCCATCCATCCCATGCCT 11985      AA  CACA
                                GGGCATG GAT  ATGGGCCT
                                ||||||| |||  ||||||||
                                TCCGTAC CTA  TACCCGGA
                                   C_  CC__
GAM745  PCDHGC3  3' AGGCCCATCCATCCCATGCCT 51532      AA  CACA
                                GGGCATG GAT  ATGGGCCT
                                ||||||| |||  ||||||||
                                TCCGTAC CTA  TACCCGGA
                                   C_  CC__
GAM745  PCDHGC4  3' AGGCCCATCCATCCCATGCCT 38903      AA  CACA
                                GGGCATG GAT  ATGGGCCT
                                ||||||| |||  ||||||||
                                TCCGTAC CTA  TACCCGGA
                                   C_  CC__
GAM745  PCDHGC5  3' AGGCCCATCCATCCCATGCCT 38909      AA  CACA
                                GGGCATG GAT  ATGGGCCT
                                ||||||| |||  ||||||||
                                TCCGTAC CTA  TACCCGGA
                                   C_  CC__
GAM745  DKFZP434B044 3' AGGCCCTTCATCTTCATGGCC 49710    G       CACAAT
                                GG CATGAAGAT     GGGCCT
                                || |||||||||     ||||||
                                CC GTACTTCTA     CCCGGA
                                 G       CTT___
GAM745  PSKH1    3' AGACCCACTTGGGCCTTCATGC 68787        AT A  _   C
            C                    GGCATGAAG  C CAA TGGG CT
                                |||||||||  | ||| |||| ||
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                                CCGTACTTC  G GTT ACCC GA
                                     CG _  C   A
GAM745  LOC144373 3'  GGCCCATCTGCCTCTGCCC   77313      T  AGAT  CA
                                GGGCA GA   CA  ATGGGCC
                                ||||| ||   ||  |||||||
                                CCCGT CT   GT  TACCCGG
                                  _ CC__  C_
GAM745  LOC147664 3'  AGACCCACGACGTCCTTATGCC 79038        A   CACAA   C
          C                      GGGCATGA GAT    TGGG CT
                                ||||||||| |||    |||| ||
                                CCCGTATT CTG    ACCC GA
                                     C  CAGC_   A
GAM745  LOC220776 3'  AGGCCCATCGTGACAATGGTGC 68917      GAAGA   A
          C                      GGCAT    TCAC ATGGGCCT
                                |||||    |||| ||||||||
                                CCGTG    AGTG TACCCGGA
                                   GTAAC   C
GAM746  ACLY    5'  AGAAGCGCCGCGCACGGACTT  65683    CT   A  CATC
                                AAG  CGT GC   GCGCTTCT
                                |||  ||| ||   ||||||||
                                TTC  GCA CG   CGCGAAGA
                                  AG   _  CGC_
GAM746  FANCA   3'  AGAAGGTGCGAGGCCACAGC   5539     C  A   A    _
                                GCT GT GCC TCGCGC TTCT
                                ||| || ||| |||||| ||||
                                CGA CA CGG AGCGTG AAGA
                                  _ C  _     G
GAM746  GGT1    5'  AGAAGATTCTGTGGCTACAGGC 19157     TC      CGCG_
          TT                     AAGC  GTAGCCAT    CTTCT
                                ||||  ||||||||    |||||
                                TTCG  CATCGGTG    GAAGA
                                  GA       TCTTA
GAM746  GGT1    5'  AGAAGATTCTGTGGCTACAGGC 26418     TC      CGCG_
          TT                     AAGC  GTAGCCAT    CTTCT
                                ||||  ||||||||    |||||
                                TTCG  CATCGGTG    GAAGA
                                  GA       TCTTA
GAM746  GGT1    5'  AGAAGATTCTGTGGCTACAGGC 26435     TC      CGCG_
          TT                     AAGC  GTAGCCAT    CTTCT
                                ||||  ||||||||    |||||
                                TTCG  CATCGGTG    GAAGA
                                  GA       TCTTA
GAM746  GGT2    5'  AGAAGATTCTGTGGCTACAGGC 74081     TC      CGCG_
          TT                     AAGC  GTAGCCAT    CTTCT
                                ||||  ||||||||    |||||
                                TTCG  CATCGGTG    GAAGA
                                  GA       TCTTA
GAM746  CAMK1G  3'  GAGAAGCGGTGCCCACCAGCTT 40317      C  AGC   CG
                                AAGCT GT   CAT  CGCTTCTC
                                ||||| ||   |||  ||||||||
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                                TTCGA CA   GTG  GCGAAGAG
                                  C  CCC   __
GAM746  DREV1    5'  GCCGCGATGGCTCGAGCT    32619       T        _
                                AGCTCG AGCCATCGCG C
                                |||||| |||||||||| |
                                TCGAGC TCGGTAGCGC G
                                  _        C
GAM746  FLJ23320  5'  GAGTGTCTGCTACGAGCT    45466          CATC
                                AGCTCGTAGC    GCGCTT
                                ||||||||||    ||||||
                                TCGAGCATCG    TGTGAG
                                     TC__
GAM746  KIAA1814  5'  GAGAAGCTCAACAACTACGAGC 70878         CCATCGC
                                GCTCGTAG      GCTTCTC
                                ||||||||      |||||||
                                CGAGCATC      CGAAGAG
                                    AACAACT
GAM746  SDC3     3'  AAGTGTGGGGCCACAGC     28460     C  A   A
                                GCT GT GCC TCGCGCTT
                                ||| || ||| ||||||||
                                CGA CA CGG GGTGTGAA
                                  _ C  _
GAM746  LOC220522 5'  AGAAGATTCTGTGGCTACAGGC 61137      TC       CGCG_
           TT                    AAGC  GTAGCCAT     CTTCT
                                ||||  ||||||||     |||||
                                TTCG  CATCGGTG     GAAGA
                                  GA       TCTTA
GAM746  LOC92710  5'  AAGCCACTGATGGCTGCGAGCT 70862              C__
           T                     AAGCTCGTAGCCATCG   GCTT
                                ||||||||||||||||   ||||
                                TTCGAGCGTCGGTAGT   CGAA
                                        CAC
GAM747  CCND1    3'  GGAATCCTTTGGTGCCA     54959     T        AGAGTG
                                TGG CACCAAAGGA     CC
                                ||| ||||||||||     ||
                                ACC GTGGTTTCCT     GG
                                  _        AA____
GAM747  CD2AP    3'  TACTTTCTTTTAATGACCA    25081       CC     A
                                TGGTCA  AAAGGA GAGTG
                                ||||||  |||||| |||||
                                ACCAGT  TTTTCT TTCAT
                                    AA     _
GAM747  CENTD1    5'  TTTTCTTTTAATGACCAG    58279        CC
                                CTGGTCA  AAAGGAAGA
                                |||||||  |||||||||
                                GACCAGT  TTTTCTTTT
                                    AA
GAM747  EZH1     3'  CACCCTTCCTTCAGTGAGCAG  10549     G   CA      A
                                CTG TCAC  AAGGAAG GTG
                                ||| ||||  ||||||| |||
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                                GAC AGTG  TTCCTTC CAC
                                  G   AC      C
GAM747  HMG20A   3'  GCACTGCTTTTGTGACCAG   37067        C    AAG
                                CTGGTCAC AAAGG   AGTGC
                                |||||||| |||||   |||||
                                GACCAGTG TTTTC   TCACG
                                     _    G__
GAM747  RAD52    3'  TGACACATTAGCCTTGAACAAC 57038      CACCA   AA  _   C
           CAG                    CTGGT    AAGG  GA GTG CA
                                |||||    ||||  || ||| ||
                                GACCA    TTCC  TT CAC GT
                                   ACAAG   GA  A   A
GAM747  RAD52    3'  TGACACATTAGCCTTGAACAAC 57039      CACCA   AA  _   C
           CAG                    CTGGT    AAGG  GA GTG CA
                                |||||    ||||  || ||| ||
                                GACCA    TTCC  TT CAC GT
                                   ACAAG   GA  A   A
GAM747  RAD52    3'  TGACACATTAGCCTTGAACAAC 12760      CACCA   AA  _   C
           CAG                    CTGGT    AAGG  GA GTG CA
                                |||||    ||||  || ||| ||
                                GACCA    TTCC  TT CAC GT
                                   ACAAG   GA  A   A
GAM747  ARHGDIG  3'  GCACCCCCCGTGAGTGACCAG  8621         _  AA  AAGA
                                CTGGTCAC CA  GG   GTGC
                                |||||||| ||  ||   ||||
                                GACCAGTG GT  CC   CACG
                                     A  GC  CC__
GAM747  CGI-57   3'  GGAGAGCTTCCGCTTGGTGACC 74306          A_    AGTG
           AG                     CTGGTCACCAA  GGAAG   CC
                                ||||||||||  |||||   ||
                                GACCAGTGGTT  CCTTC   GG
                                      CG    GAGA
GAM747  DKFZP434O125 3'  GTTTTCCCCTTTGGTAATCA   65589     C       AA   T
                                TGGT ACCAAAGG  GAG GC
                                |||| ||||||||  ||| ||
                                ACTA TGGTTTCC  CTT TG
                                  A       C_   T
GAM747  FLJ12768  3'  TGGCACTCTTCTCCCTGAGACC 47965      ACCAAA
           A                     TGGTC     GGAAGAGTGCCA
                                |||||     ||||||||||||
                                ACCAG     TCTTCTCACGGT
                                   AGTCCC
GAM747  FLJ13063  5'  TACTCCCTTTGGTGACCA    72302           AA
                                TGGTCACCAAAGG  GAGTG
                                ||||||||||||  |||||
                                ACCAGTGGTTTCC  CTCAT
                                              __
GAM747  FLJ13593  3'  ACTCTTTTGGTAACCAG     45852       C   AAG
                                CTGGT ACCA   GAAGAGT
                                ||||| ||||   |||||||
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                                GACCA TGGT   TTTCTCA
                                  A   ___
GAM747  HMT-1    3'  GCACCTCCCAGTGGCCAG    39410       CAAA  A  A
                                CTGGTCAC    GG AG GTGC
                                ||||||||    || || ||||
                                GACCGGTG    CC TC CACG
                                   A___  C  _
GAM747  INSM2    3'  TGGCTACCCTTTGGTAGCCA  51857     TC      AAGA  _
                                TGG  ACCAAAGG    GT GCCA
                                |||  ||||||||    || ||||
                                ACC  TGGTTTCC    CA CGGT
                                  GA       _____ T
GAM747  KIAA0848 3'  TGACACTTCATCCTGATGCCA  30659    T  CCAA   A_    C
                                TGG CA    AGGA  GAGTG CA
                                ||| ||    ||||  ||||| ||
                                ACC GT    TCCT  TTCAC GT
                                  _ AG__    AC    A
GAM747  MAD4     3'  GCAGAATCCACCCGGTGACCAG 22274        AAA_  AGAG
                                CTGGTCACC    GGA    TGC
                                |||||||||    |||    |||
                                GACCAGTGG    CCT    ACG
                                     CCCA   AAG_
GAM747  MGC16384 5'  GGAAGCTCCTTTGGTGCCAG   54936     T        A AGTG
                                CTGG CACCAAAGGA G    CC
                                |||| ||||||||||  |    ||
                                GACC GTGGTTTCCT C    GG
                                  _        _ GAA_
GAM747  MGC22014 3'  TGTTCTTCCCTTGGTGGCCA   65120         A     GT
                                TGGTCACCAA GGAAGA  G
                                ||||||||||  ||||||  |
                                ACCGGTGGTT CCTTCT  T
                                     C     TG
GAM747  MGC29898 3'  CACTTTTTTGGCAATCAG    59584      CA   AAG
                                CTGGT  CCA   GAAGAGTG
                                |||||  |||   ||||||||
                                GACTA  GGT   TTTTTCAC
                                  AC   ___
GAM747  NUDT11   3'  TGACACTCTTCCTCATGATACC 60660      CACCAA        C
           AG                     CTGGT     AGGAAGAGTG CA
                                |||||     |||||||||| ||
                                GACCA     TCCTTCTCAC GT
                                   TAGTAC         A
GAM747  PRO0365  3'  GGCACTCCCAAGTGACTAG   26988       CAAA  AA
                                CTGGTCAC    GG  GAGTGCC
                                ||||||||    ||  |||||||
                                GATCAGTG    CC  CTCACGG
                                     AA__  __
GAM747  PRO1575  3'  TGGCACTCTGTAGGTAATGACC 26873       CCAAAGGA
           A                     TGGTCA       AGAGTGCCA
                                ||||||       |||||||||
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                                ACCAGT       TCTCACGGT
                                   AATGGATG
GAM747  RP4-622L5 3'  GGCACTCCTCGATGCCCAG   39429      T  CCAAAG  A
                                CTGG CA     GA GAGTGCC
                                |||| ||     || |||||||
                                GACC GT     CT CTCACGG
                                  C  AG____  C
GAM747  SARM      3'  CACTCTTCCTCCAGAGATCA  31279      ACCAA
                                TGGTC    AGGAAGAGTG
                                ||||||    ||||||||||
                                ACTAG    TCCTTCTCAC
                                   AGACC
GAM747  SNX11     3'  TCTCCTCAGGTGACCAG     26174        AA   A
                                CTGGTCACC  AGGA GA
                                |||||||||  |||| ||
                                GACCAGTGG  TCCT CT
                                     AC   _
GAM747  LOC122481 5'  TGGCGCTTTCACCTTAGCAACC 76099      CACCA   A_
           AG                     CTGGT    AAGG  AGAGTGCCA
                                |||||    ||||  |||||||||
                                GACCA    TTCC  TTTCGCGGT
                                   ACGA_   AC
GAM747  LOC146958 5'  GCACCCCTGTGTGACTAG    84943       CAA   AAGA
                                CTGGTCAC   AGG   GTGC
                                ||||||||   |||   ||||
                                GATCAGTG   TCC   CACG
                                     TG_   C___
GAM747  LOC147660 3'  TGGCAAAGCCTTTAGTGACCAG 79035       C    AAGAG
                                CTGGTCAC AAAGG    TGCCA
                                |||||||| |||||    |||||
                                GACCAGTG TTTCC    ACGGT
                                     A    GAA__
GAM747  LOC148789 3'  TGGCACTTTCACCCAGAACCA  79742     CACCAAA  A_
                                TGGT      GG  AGAGTGCCA
                                ||||      ||  |||||||||
                                ACCA      CC  TTTCACGGT
                                  AGAC___  AC
GAM747  LOC151443 5'  TGGACATCTCTCCGATGACCAG 81044       CCAAA   A  _ _
                                CTGGTCA    GGA GAG TG CCA
                                |||||||    ||| ||| || |||
                                GACCAGT    CCT CTC AC GGT
                                     AG___   _   T  A
GAM747  LOC153688 3'  GCAGAGTCCTGGGTGACCAG   87318        AA   AGAG
                                CTGGTCACC  AGGA   TGC
                                |||||||||  ||||   |||
                                GACCAGTGG  TCCT   ACG
                                     G_   GAG_
GAM747  LOC158230 5'  ACCCGCCTTTAGTGACCAG   82697        C    AAGA
                                CTGGTCAC AAAGG   GT
                                |||||||| |||||   ||
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                                GACCAGTG TTTCC    CA
                                    A    GCC_
GAM747  LOC221399 5'  GCCCCTCCCTAGTGACCAG   95485       CAA   AA   T_
                                CTGGTCAC   AGG  GAG  GC
                                ||||||||   |||  |||  ||
                                GACCAGTG   TCC  CTC  CG
                                    A__   __   CC
GAM748  ANKRA2   5'  TATCCAGATTCCAAGAACACA  43792    GA       G
                                TG  TTCTTGGGA CTGGATA
                                ||  ||||||||| |||||||
                                AC  AAGAACCTT GACCTAT
                                 AC        A
GAM748  FLJ22457  3'  TCAGCTCCCAAAATCCA     46611       C
                                TGGATT TTGGGAGCTGG
                                |||||| ||||||||||
                                ACCTAA AACCCTCGACT
                                    _
GAM748  KALI     3'  GAGTATCCAAATCCAAAAATCC 54692       C    AGC
           A                     TGGATT TTGGG   TGGATACTC
                                |||||| |||||   |||||||||
                                ACCTAA AACCT   ACCTATGAG
                                   A    AA_
GAM748  KIAA1243  5'  AGCCATCCCAAGAATCCA    74020          __
                                TGGATTCTTGGGA  GCT
                                ||||||||||||  |||
                                ACCTAAGAACCCT  CGA
                                      AC
GAM748  PRO2012   5'  AGTATCCAAACAGATCCA    38387       CT  GGAGC
                                TGGATT  TG    TGGATACT
                                ||||||  ||    ||||||||
                                ACCTAG  AC    ACCTATGA
                                   __  AA___
GAM748  LOC115294 3'  ATCAATCCCAAGAATCCA    73380          GCTG
                                TGGATTCTTGGGA   GAT
                                ||||||||||||   |||
                                ACCTAAGAACCCT   CTA
                                      AA__
GAM748  LOC121838 5'  ATCCCCCAAAAATTCA      76511       C    AGCT
                                TGGATT TTGGG   GGAT
                                |||||| |||||   ||||
                                ACTTAA AACCC   CCTA
                                   A   _____
GAM748  LOC145231 3'  GAGTAATGGTCCCCCAAGATAT 84250      _     A_   GA
           CCA                    TGGAT TCTTGGG  GCTG  TACTC
                                |||||  |||||||  ||||  |||||
                                ACCTA AGAACCC  TGGT  ATGAG
                                   T      CC   A_
GAM748  LOC151414 3'  CAGCCTCCCCAGAATCCA    81033        T    _
                                TGGATTCT GGGAG CTG
                                |||||||| ||||| |||
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                                ACCTAAGA CCCTC GAC
                                    C    C
GAM748  LOC200325 5'  AGTACACAGCCCAGGAATCCA  91577          GA   GA
                                TGGATTCTTGG  GCTG  TACT
                                ||||||||||  ||||  ||||
                                ACCTAAGGACC  CGAC  ATGA
                                      __    AC
GAM748  LOC200407 3'  GAGCATGTGGCTCCCAGAACCC 91628    A   T     G  A
          A                    TGG TTCT GGGAGCTG AT CTC
                               ||| |||| |||||||| || |||
                               ACC AAGA CCCTCGGT TA GAG
                                 C   _      G  C
GAM749  EN2     5'  GCTCTGTTGAATCTCTCAT   9259         CCA   CCA
                               ATGAGAGAT   AACA   AGC
                               |||||||||   ||||   |||
                               TACTCTCTA   TTGT   TCG
                                    AG_   C__
GAM749  LOXL2   5'  GCTTGGTGCTTGCTTTCTC   11352       TC   A
                               GAGAGA  CAA CACCAAGC
                               ||||||  ||| ||||||||
                               CTCTTT  GTT GTGGTTCG
                                  C_   C
GAM749  PTMS    3'  GCCTGATCCCTGGATCTCCCTC 12564    __      AACAC  A
          A                    TGA  GAGATCCA    CA GC
                               |||  ||||||||    || ||
                               ACT  CTCTAGGT    GT CG
                                 CC       CCCTA  C
GAM749  TCFL4   3'  CTTGGTGTTTGGTTTTTC    64211       T
                               GAGAGA CCAAACACCAAG
                               |||||| ||||||||||||
                               CTTTTT GGTTTGTGGTTC
                                  _
GAM749  AD-020  3'  GCTTGGTGTTTAGAGCTGCTTC 60092   T  _  A  C
          A                    A GAG AG TC AAACACCAAGC
                               | ||| || || ||||||||||
                               A TTC TC AG TTTGTGGTTCG
                                C  G  G  A
GAM749  COVA1   3'  GCTCACTGATGCATCTCTCAT  73642        C  AA  CCA
                               ATGAGAGAT CA  CA   AGC
                               |||||||| ||  ||   |||
                               TACTCTCTA GT  GT   TCG
                                    C  A_  CAC
GAM749  CXYorf1  3'  CTTGATGTCGGATCTCTTCA  82912   T      AA   C
                               A GAGAGATCC  ACA CAAG
                               | |||||||||  ||| ||||
                               A TTCTCTAGG  TGT GTTC
                                C       C_   A
GAM749  DKFZp434E0519 3'  GCTTGGTGCACACTCTCATT   50994        ATCCAAA
                               AATGAGAG      CACCAAGC
                               ||||||||      ||||||||
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                                TTACTCTC      GTGGTTCG
                                    ACAC___
GAM749  FLJ14054  3'  GTTTGTTCAAATTTCTCATTA  44970          C____
                                TAATGAGAGAT    CAAAC
                                ||||||||||    |||||
                                ATTACTCTTTA    GTTTG
                                      AACTT
GAM749  FLJ23416  3'  GCCTGGTGTTTGGCAAACTCA  50933     AGAT       A
                                TGAG   CCAAACACCA GC
                                ||||   |||||||||| ||
                                ACTC   GGTTTGTGGT CG
                                  AAAC        C
GAM749  KIAA0628  3'  CTTGGCATTGTCAGTCTCTTA  29529       C__  ACA
                                TGAGAGAT  CAA  CCAAG
                                ||||||||  |||  |||||
                                ATTCTCTG  GTT  GGTTC
                                    ACT  AC_
GAM749  KIAA1726  3'  CTTGGTGTTTGTCTATCA    67831    G  TC
                                TGA AGA  CAAACACCAAG
                                ||| |||  ||||||||||
                                ACT TCT  GTTTGTGGTTC
                                  A  __
GAM749  P2RX1     3'  GCTTCTCTCTCCGGACTCTCAT 67751        A  AAACACC_
          TA                    TAATGAGAG TCC      AAGC
                                |||||||| |||      ||||
                                ATTACTCTC AGG      TTCG
                                    _  CCTCTCTC
GAM749  PDZD2     3'  GCTTGTCTGAGTCCAGATTTCT 81727        CAAA__ C_
          CAT                   ATGAGAGATC     CA  CAAGC
                                ||||||||||     ||  |||||
                                TACTCTTTAG     GT  GTTCG
                                    ACCTGA  CT
GAM749  LOC149773 5'  CGCTTGGTACTTAAATGAAACA 80292       GA__  CAAAC___     ___
          TCTTATTA              TAATGAGA   TC      ACCAAGC  G
                                ||||||||   ||      |||||||  |
                                ATTATTCT   AG      TGGTTCG  C
                                    ACAA  TAAATTCA     __
GAM749  LOC152920 5'  GCTTCATTTGGATTTCTCAT  81624          CACC
                                ATGAGAGATCCAAA   AAGC
                                ||||||||||||||   ||||
                                TACTCTTTAGGTTT   TTCG
                                      AC__
GAM749  LOC158983 3'  CTCAGTGACTTATTTCTCATTA 82949        CCAAA  CA
                                TAATGAGAGAT    CAC  AG
                                ||||||||||    |||  ||
                                ATTACTCTTTA    GTG  TC
                                    TTCA_  AC
GAM749  LOC199993 3'  GCTTGGTCACTGTCTCTCA   72142       CCAAAC
                                TGAGAGAT     ACCAAGC
                                ||||||||     |||||||
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                                ACTCTCTG     TGGTTCG
                                     TCAC__
GAM749  LOC200093 3'  CTTGATGTCGGATCTCTTCA  63772   T       AA   C
                                A GAGAGATCC  ACA CAAG
                                | |||||||||  ||| ||||
                                A TTCTCTAGG  TGT GTTC
                                 C       C_   A
GAM749  LOC91040  3'  CTTGATGTCGGATCTCTTCA  65346   T       AA   C
                                A GAGAGATCC  ACA CAAG
                                | |||||||||  ||| ||||
                                A TTCTCTAGG  TGT GTTC
                                 C       C_   A
GAM750  DPYSL2    3'  TGTACCGGGTCATGGTA     9118          AG   C
                                TACCATGGC  GGT ACA
                                |||||||||  ||| |||
                                ATGGTACTG  CCA TGT
                                     GG  _
GAM750  DTR       3'  TGTGACCCATCTGTAGTA    10459     C   CA
                                TAC ATGG  GGGTCACA
                                |||  ||||  ||||||||
                                ATG TGTC  CCCAGTGT
                                  A   TA
GAM750  HSPA4     3'  TTGGATATAGCCATGGTA    90656         AGG  A
                                TACCATGGC   GTC CAA
                                |||||||||   ||| |||
                                ATGGTACCG   TAG GTT
                                     ATA  _
GAM750  PUM2      3'  TTGTGACCATATGTGTA     31666     _   GCAG
                                TAC CATG    GGTCACAA
                                |||  ||||    ||||||||
                                ATG GTAT    CCAGTGTT
                                  T   A___
GAM750  RTKN      3'  TTGTGGTTGCCATGGTA     53504         GG
                                TACCATGGCAG  TCACAA
                                ||||||||||  ||||||
                                ATGGTACCGTT  GGTGTT
                                          __
GAM750  SLC7A8    3'  TTGTGACCCCTTCAGAGTA   25307    CA   CA
                                TAC  TGG  GGGTCACAA
                                |||  |||  |||||||||
                                ATG  ACT  CCCAGTGTT
                                  AG   TC
GAM750  TARDBP    3'  TGTAAATATTCTGCCATAGG  24790    _       C___
                                CC ATGGCAGGGT    ACA
                                || ||||||||||    |||
                                GG TACCGTCTTA    TGT
                                 A         TAAA
GAM750  TGFBI     3'  TTGTGACAGAGCCATGGTG   6271          AGG
                                TACCATGGC   GTCACAA
                                |||||||||   |||||||
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                                GTGGTACCG   CAGTGTT
                                      AGA
GAM750  D4ST-1    3'  TTGTGACTGTGGCTGGTA    56199      TGG  G
                                TACCA   CA GGTCACAA
                                |||||   || ||||||||
                                ATGGT   GT TCAGTGTT
                                   CG_  G
GAM750  DKFZP434G156 3'  TTGTGGAAGCCTATGGTA    70340      _   AGGG
                                TACCAT GGC    TCACAA
                                |||||| |||    ||||||
                                ATGGTA CCG    GGTGTT
                                    T   AA__
GAM750  DKFZP434I1735 3'  TGTGACTCTTCAAAGTA    89175     CA   C
                                TAC  TGG AGGGTCACA
                                |||  ||| |||||||||
                                ATG  ACT TCTCAGTGT
                                  AA   _
GAM750  DKFZP564M182 3'  TGTAACCCTGTTAGGGTG    78649      A       C
                                TACC TGGCAGGGT ACA
                                |||| ||||||||| |||
                                GTGG ATTGTCCCA TGT
                                   G        A
GAM750  ENAH      3'  TTGTGACTTTAATTGGTA    37159      TGGC
                                TACCA    AGGGTCACAA
                                |||||    ||||||||||
                                ATGGT    TTTCAGTGTT
                                   TAA_
GAM750  FLJ10718  3'  TTGTACAGAGCCATGGTA    37034        AGG  C
                                TACCATGGC   GT ACAA
                                |||||||||   || ||||
                                ATGGTACCG   CA TGTT
                                      AGA  _
GAM750  FLJ12891  3'  TTGTGGAGTTACCATGGTG   46935        C  GG
                                TACCATGG AG  TCACAA
                                |||||||| ||  ||||||
                                GTGGTACC TT  GGTGTT
                                     A  GA
GAM750  GOLGA3    3'  TGTGTTTTTCCATGGTA     20900        C    T
                                TACCATGG AGGG CACA
                                |||||||| |||| ||||
                                ATGGTACC TTTT GTGT
                                     T   _
GAM750  HXCP2     3'  TTGTGACCATGACAGTA     51806     CA  G  G
                                TAC  TG CA GGTCACAA
                                |||  || || ||||||||
                                ATG  AC GT CCAGTGTT
                                  __  A  A
GAM750  KIAA0102  5'  TGTTTCTTTGCCATAGTG    29249     C       TC
                                TAC ATGGCAGGG  ACA
                                ||| |||||||||  |||
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                                GTG TACCGTTTC  TGT
                                  A        TT
GAM750  KIAA0186  3'  TGTGAGTTCTCATGGTG     41127        CA  G
                                TACCATGG  GG TCACA
                                ||||||||  || |||||
                                GTGGTACT  TT AGTGT
                                     C_  G
GAM750  KIAA0447  3'  TTGTGAAAAATTACCATGGTG  72139        C  GG__
                                TACCATGG AG    TCACAA
                                ||||||||  ||    ||||||
                                GTGGTACC TT    AGTGTT
                                     A  AAAA
GAM750  KIAA1041  3'  TGGGAAGCCAGCCATGGTA    30834        A  G_  A
                                TACCATGGC GG  TC CA
                                |||||||||  ||  || ||
                                ATGGTACCG CC  AG GT
                                      A  GA  G
GAM750  MGC26651  3'  TTGTAACCTTCTATGGTG     58952        C    C
                                TACCATGG AGGGT ACAA
                                ||||||||  |||||  ||||
                                GTGGTATC TTCCA TGTT
                                     _    A
GAM750  PTGES2    3'  TTGTGGCGCCTGTCATGG     47581         _
                                CCATGGCAGG GTCACAA
                                ||||||||||  |||||||
                                GGTACTGTCC CGGTGTT
                                      G
GAM750  PTPNS1    3'  TGTGACCCCGCTGTGGTA     55845        A
                                TACCATGGC GGGTCACA
                                |||||||||  ||||||||
                                ATGGTGTCG CCCAGTGT
                                     C
GAM750  TSGA14    3'  TTGTGCTCTTTGTCATGG     38669         T_
                                CCATGGCAGGG  CACAA
                                ||||||||||  |||||
                                GGTACTGTTTC  GTGTT
                                      TC
GAM750  LOC120196 3'  TGTACTTCCCATGGTG      76061        CA   C
                                TACCATGG  GGGT ACA
                                ||||||||  ||||  |||
                                GTGGTACC  TTCA TGT
                                     C_   _
GAM750  LOC126520 5'  TGCGACCCCGCAACATCGTG   75027     C  __  A    A
                                TAC ATG  GC GGGTC CA
                                |||  |||  ||  |||||  ||
                                GTG TAC  CG CCCAG GT
                                  C  AA  C    C
GAM750  LOC144559 3'  TTGTGACTTTTTCACGTA     77387     CA  C
                                TAC  TGG AGGGTCACAA
                                |||  ||| ||||||||||
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                                ATG  ACT TTTCAGTGTT
                                  C_   T
GAM750   LOC144848 3'  GTGACCCAGGGCCATGGTG   73960         A__
                                TACCATGGC   GGGTCAC
                                |||||||||   |||||||
                                GTGGTACCG   CCCAGTG
                                     GGA
GAM750   LOC145387 3'  TTGTGAAGCACCTGCCATG   84347          _ __
                                CATGGCAGG GT  CACAA
                                ||||||||| ||  |||||
                                GTACCGTCC CG  GTGTT
                                      A  AA
GAM750   LOC154726 3'  GTGAAGTTTTGCCAGGTA    82011      A       __
                                TACC TGGCAGGG  TCAC
                                |||| ||||||||  ||||
                                ATGG ACCGTTTT  AGTG
                                  _       GA
GAM750   LOC154761 3'  TTGTGTCTTTCTGCCAGG    82022    A     __  T
                                CC TGGCAG  GG CACAA
                                || ||||||  || |||||
                                GG ACCGTC  TC GTGTT
                                  _     TT  T
GAM750   LOC170409 3'  TGTGGCTTTACACGGTA     83748      A  GC
                                TACC TG  AGGGTCACA
                                |||| ||  |||||||||
                                ATGG AC  TTTCGGTGT
                                  C  A_
GAM750   LOC202865 5'  TGTGACCTTACTTATGGTG   59935        _ C
                                TACCATG G AGGGTCACA
                                ||||||| | |||||||||
                                GTGGTAT C TTCCAGTGT
                                     T A
GAM750   LOC255320 5'  TGTTTCTTTGCCATAGTG    96702     C        TC
                                TAC ATGGCAGGG  ACA
                                ||| |||||||||  |||
                                GTG TACCGTTTC  TGT
                                  A        TT
GAM750   LOC255743 5'  TTGTAATTTTGACCATGG    97607       _     C
                                CCATGG CAGGGT ACAA
                                |||||| |||||| ||||
                                GGTACC GTTTTA TGTT
                                    A     A
GAM750   LOC255870 3'  TTGTATTCTTGCCAAGTA    96314     CA       TC
                                TAC  TGGCAGGG  ACAA
                                |||  ||||||||  ||||
                                ATG  ACCGTTCT  TGTT
                                  A_       TA
GAM750   LOC90120  3'  TTGTGACCCTACCCTGTCAGG  62219    A    _____
                                CC TGGCA    GGGTCACAA
                                || |||||    |||||||||
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                                GG ACTGT    CCCAGTGTT
                                 _    CCCAT
GAM751  B3GALT2  3'  GTGTCTCAGGCTCAA      15032     A  AG
                                TTGA GCC  TGGGGCAC
                                |||| |||  ||||||||
                                AACT CGG  ACTCTGTG
                                  _  __
GAM751  DRG2     3'  TGGTTAGTGGCTTCAA     9131         G  GGGC
                                TTGAAGCCA TG   ACCA
                                ||||||||| ||   ||||
                                AACTTCGGT AT   TGGT
                                     G _____
GAM751  HPS4     3'  GAATTGGTGCCACAAGCTTC  42227     CAG  G
                                GAAGC  TG GGCACCAATTC
                                |||||  || ||||||||||
                                CTTCG  AC CCGTGGTTAAG
                                   A__  A
GAM751  KCNMB2   3'  AATTGGTGGACTGGTTTCAA  20682        GGGG
                                TTGAAGCCAGT   CACCAATT
                                ||||||||||   ||||||||
                                AACTTTGGTCA   GTGGTTAA
                                     G___
GAM751  LOC124871 3'  TGCTGCCCCACCAGCTTCAG  74818      CA      C
                                TTGAAGC  GTGGGGCA CA
                                |||||||  |||||||| ||
                                GACTTCG  CACCCCGT GT
                                    AC       C
GAM751  LOC149705 3'  GAATTGGTACCTAAAAGCTTC  85780     CAG   GC
                                GAAGC  TGGG  ACCAATTC
                                |||||  ||||  ||||||||
                                CTTCG  ATCC  TGGTTAAG
                                   AAA   A_
GAM752  SCAMP1   3'  GCTAAATAAATATTCTCC   18013    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM752  SCAMP1   3'  GCTAAATAAATATTCTCC   54501    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM752  NX-17    3'  TGAATATCAGCCCCTAATA   40706       ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM752  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
            TA                  TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
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                                ATAATCCCTATTATAAGTAAATCG

GAM753  RUNX1    5'  CAGCAGGCAGGACGAATCA   10027    CA       ATCA
                                TGA  TCGTCCTGCTT   CTG
                                |||  ||||||||||   |||
                                ACT  AGCAGGACGGA   GAC
                                  A_       C___
GAM753  DKFZP434A0225 3'  TCAGTGATAAACCACTGAC   95526    C_  C_
                                GTC  TG  TTATCACTGA
                                |||  ||  ||||||||||
                                CAG  AC  AATAGTGACT
                                  TC  CA
GAM753  KIAA0450  3'  CAGCAGGCAGGAGACATCA   28342    CA  G      ATCA
                                TGA  TC TCCTGCTT   CTG
                                |||  || ||||||||   |||
                                ACT  AG AGGACGGA   GAC
                                  AC  _      C___
GAM754  DXYS155E  3'  GCAGCCCGTCCTGGACATCCTG 18689      _  CGTTTC
          CA                    TGCAG ATG     GACGGGCTGC
                                |||||  |||     ||||||||||
                                ACGTC TAC     CTGCCCGACG
                                   C   AGGTC_
GAM754  DKFZp434N0650 3'  GCAGCCCGCCGCTGCCCGCACC 51055      A   TTT__  A
          TGC                    GCAG TGCG     CG CGGGCTGC
                                ||||  ||||     ||  ||||||||
                                CGTC ACGC     GC GCCCGACG
                                  C    CCGTC  C
GAM754  QKI      5'  GCAGCCCGCGCCCCGCGCCCGC 66048     AGA    TTT  A
          A                     TGC   TGCG   CG CGGGCTGC
                                |||   ||||   ||  ||||||||
                                ACG   GCGC   GC GCCCGACG
                                  CCC    CCC  _
GAM754  LOC147160 5'  GCAGCCCGGGTGCACGCCCTGC 85077      AT    TTCGA
          A                     TGCAG  GCGT    CGGGCTGC
                                |||||  ||||    ||||||||
                                ACGTC  CGCA    GCCCGACG
                                   C_    CGTGG
GAM754  LOC157531 5'  GCAGCCCGTCAAGCGATCCCAT 87767      _____    C
          C                     GATG    CGTTT GACGGGCTGC
                                ||||    ||||| ||||||||||
                                CTAC    GCGAA CTGCCCGACG
                                   CCTA    _
GAM754  LOC158956 5'  GCAGCCCGCAGGCACCCGGCA  67214     AGA_   GTTT GA
                                TGC    TGC    C  CGGGCTGC
                                |||    |||    |  ||||||||
                                ACG    ACG    G  GCCCGACG
                                  GCCC   _____ AC
GAM754  LOC196484 5'  CAGTTTGAGAAAAGCATCTGCA 63538         G    GA
                                TGCAGATGC TTTC  CGGGCTG
                                |||||||| ||||  |||||||
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                                ACGTCTACG AAAG  GTTTGAC
                                     A    A_
GAM754  LOC219848 3'  TCCAAAACACATCTGCA     93127        C    CGAC
                                TGCAGATG GTTT    GGG
                                |||||||| ||||    |||
                                ACGTCTAC CAAA    CCT
                                     A    A___
GAM754  LOC220073 5'  CAGGAGAAAAGCATCTGCA    95073         G    GACGGG
                                TGCAGATGC TTTC     CTG
                                ||||||||| ||||     |||
                                ACGTCTACG AAAG     GAC
                                     A    AG____
GAM755  FLJ21438  5'  CAAAACGCTTCCCCCCATCCCA 62190       GAGATTATC
                                TGGGA        AAGCGTTTTG
                                |||||        ||||||||||
                                ACCCT        TTCGCAAAAC
                                   ACCCCCC__
GAM755  FLJ32334  3'  AAAACGCTATTCCTTCCCA    58605       A  TTATCA
                                TGGGAG GA     AGCGTTTT
                                |||||| ||     ||||||||
                                ACCCTT CT     TCGCAAAA
                                   C  TA____
GAM755  HHLA2     3'  CAATGTACTTTGTAATCTCCCC 23953      A       C   CG T
             CA                   TGGG GAGATTAT AAG  T TTG
                                |||| |||||||| |||  | |||
                                ACCC CTCTAATG TTC  G AAC
                                  C       T   AT T
GAM756  ADAT1     3'  CCAGCAAAGAATGAAGGC    24914     __         C
                                GTC  CATTCTTTGC GG
                                |||  |||||||||| ||
                                CGG  GTAAGAAACG CC
                                  AA         A
GAM756  M17S2     5'  CCGGTAGCGGACGGTCCTT    20910          ATTCT
                                AAGGACCGTCC    TTGCCGG
                                ||||||||||     |||||||
                                TTCCTGGCAGG    GATGGCC
                                      C_____
GAM756  ST14      5'  CCGGCAGGGACGACGCCT    42042     AC    CAT
                                AGG  CGTC   TCTTTGCCGG
                                |||  ||||   ||||||||||
                                TCC  GCAG   AGGGACGGCC
                                  __    C__
GAM756  HTGN29    5'  GCCAACTGTGTGGCGGTCC    39885        _  TC  T
                                GGACCGTC CAT  TT GC
                                |||||||| |||  || ||
                                CCTGGCGG GTG  AA CG
                                     T   TC  C
GAM756  PMAIP1    3'  GCAAGAATGGAAGACCCTT    41211      ACCG        T
                                AAGG    TCCATTCTT GC
                                ||||    ||||||||| ||
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                                TTCC    AGGTAAGAA CG
                                  CAGA       _
GAM756  LOC144278 3'  GCCAGCAAAGACTGCTCGATGG 77274          ___ T      C
           TCCT                    AGGACCGTC   CA TCTTTGC GGC
                                |||||||||   || ||||||| |||
                                TCCTGGTAG   GT AGAAACG CCG
                                     CTC  C      A
GAM756  LOC147976 3'  CCGGTGAATGAAGACCCT    79287     ACC   CA   _  TG
                                AGG   GTC  TTC TT  CCGG
                                |||   |||  ||| ||  ||||
                                TCC   CAG  AAG AA  GGCC
                                  ___   __   T  GT
GAM756  LOC254263 5'  GCCGGCAGCGGACGCGCC    96367    AC    ATTCT
                                GG  CGTCC    TTGCCGGC
                                ||  |||||    ||||||||
                                CC  GCAGG    GACGGCCG
                                 GC    C____
GAM757  ARHA     3'  CTCTGCACTCCCACCTGA    71232    T_   A
                                TC  GTGG GAGTGCAGAG
                                ||  |||| ||||||||||
                                AG  CACC CTCACGTCTC
                                 TC   _
GAM757  ASGR2    5'  CTCCACACCTTTCACAGATC   56046     T       A   CA
                                GAT CTGTGGAG GTG  GAG
                                ||| |||||||| |||  |||
                                CTA GACACTTT CAC  CTC
                                  _       C   AC
GAM757  GZMM     3'  CTCGCTGTCTCCACAGGA    19213           GT  A
                                TTCTGTGGAGA  GC GAG
                                ||||||||||  || |||
                                AGGACACCTCT  CG CTC
                                       GT  _
GAM757  IFNAR2   3'  CTCTGCCACCTCTACAGAATC  7899            A  _
                                GATTCTGTGGAG GTG CAGAG
                                |||||||||||| ||| |||||
                                CTAAGACATCTC CAC GTCTC
                                       _  C
GAM757  KAL1     3'  CTCTGCATAGATACAAAAT   5835      C   GAGA
                                ATT TGTG    GTGCAGAG
                                |||| ||||    ||||||||
                                TAA ACAT    TACGTCTC
                                  A    AGA_
GAM757  LIF      3'  CTGCACAGCATCACTGAATC   11303      T   AGA_
                                GATTC GTGG    GTGCAG
                                ||||| ||||    ||||||
                                CTAAG CACT    CACGTC
                                   T    ACGA
GAM757  MTMR1    5'  CTGGACAGTCCCACAGGATC   70724          A  __  G
                                GATTCTGTGG GA  GT CAG
                                |||||||||| ||  || |||
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                                CTAGGACACC CT  CA GTC
                                      _ GA  G
GAM757  PKIG     3'  CTCATGGAGCTCCACAGATC  23927     T       AGTG  _
                                GAT CTGTGGAG   CA GAG
                                ||| ||||||||   || |||
                                CTA GACACCTC   GT CTC
                                  _      GAG_  A
GAM757  PPP1R3C  3'  CTCTGCAGTGACAGAATT    19423        GGAGAG
                                GATTCTGT     TGCAGAG
                                ||||||||     |||||||
                                TTAAGACA     ACGTCTC
                                     GTG___
GAM757  RFX2     3'  CTCTGCACTCAACTGGAACC  7156    A   _  GGA
                                G TTCT GT   GAGTGCAGAG
                                | |||| ||   ||||||||||
                                C AAGG CA   CTCACGTCTC
                                 C    T  A__
GAM757  SHMT2    3'  CTCCTTATTCCCTACAGAATC  19435         A    CA
                                GATTCTGTGG GAGTG  GAG
                                |||||||||| |||||  |||
                                CTAAGACATC CTTAT  CTC
                                      C     TC
GAM757  STK4     3'  CTCTGTCGTCTCTCCACAG   21864          _ _
                                CTGTGGAGAG TG CAGAG
                                |||||||||| || |||||
                                GACACCTCTC GC GTCTC
                                      T  T
GAM757  TEM8     3'  CTCTAGCTTTCCACAAATC   50826      C        GC
                                GATT TGTGGAGAGT  AGAG
                                |||| ||||||||||  ||||
                                CTAA ACACCTTTCG  TCTC
                                  _        A_
GAM757  USH3A    3'  CTGCACTCTTATTGGATTC   54842    T   GTG
                                GA TCT   GAGAGTGCAG
                                || |||   ||||||||||
                                CT AGG   TTCTCACGTC
                                 T   TTA
GAM757  ASB13    3'  CTGCGCTGTTCTACAGAA    45546          _
                                TTCTGTGGAG AGTGCAG
                                |||||||||| |||||||
                                AAGACATCTT TCGCGTC
                                      G
GAM757  Di-Ras2  3'  CTCTGGAGTCACAGAATC    34611          AGAGTG
                                GATTCTGTGG     CAGAG
                                ||||||||||     |||||
                                CTAAGACACT     GTCTC
                                      GAG___
GAM757  DKFZP434N014 3'  CTCTGCACCCCCAGCCTATC  61229     T__   T  AGA
                                GAT   CTG GG   GTGCAGAG
                                |||   ||| ||   ||||||||
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                                CTA   GAC CC   CACGTCTC
                                  TCC   _ C__
GAM757  FLJ10432  3'  CTCTGCACTCCATGATGAA   39351     T__    GA
                                TTC   GTGGA  GTGCAGAG
                                |||   |||||  ||||||||
                                AAG   TACCT  CACGTCTC
                                  TAG    __
GAM757  FLJ12505  3'  CTCTGCACTTTACCCAGCATC  45714     T  T  _
                                GAT CTG GG AGAGTGCAGAG
                                ||| ||| || ||||||||||
                                CTA GAC CC TTTCACGTCTC
                                  C   _  A
GAM757  KIAA1854  3'  CTCCGACCTCCCTACAGAATC  72205          A   TGCA
                                GATTCTGTGG GAG    GAG
                                |||||||||| |||    |||
                                CTAAGACATC CTC    CTC
                                      C   CAGC
GAM757  KIF13B    3'  CTTTCTCTCCACAAAGTC    31562      C       TGC
                                GATT TGTGGAGAG   AG
                                |||| |||||||||   ||
                                CTGA ACACCTCTC   TC
                                  A        TT_
GAM757  KIF13B    3'  CTTTCTCTCCACAAAGTC    31563      C       TGC
                                GATT TGTGGAGAG   AG
                                |||| |||||||||   ||
                                CTGA ACACCTCTC   TC
                                  A        TT_
GAM757  MAP       3'  CTCTTCAGGTTCACAGAA    43367         GAG  C
                                TTCTGTGGA   TG AGAG
                                |||||||||   || ||||
                                AAGACACTT   AC TCTC
                                     GG_  T
GAM757  PRKRI     5'  CTCTTCCCTCCACAGATC    21828     T      AGTGC
                                GAT CTGTGGAG    AGAG
                                ||| ||||||||    ||||
                                CTA GACACCTC    TCTC
                                  _       CCT__
GAM757  PRO0650   5'  CTGTGACGCTCCACAGAA    27071          A  _
                                TTCTGTGGAG GT GCAG
                                |||||||||| || ||||
                                AAGACACCTC CA TGTC
                                      G  G
GAM757  RASSF2    3'  CTCCACCTTCTCTCCACAGAAT 29096            TGCA__
                                ATTCTGTGGAGAG     GAG
                                ||||||||||||      |||
                                TAAGACACCTCTC     CTC
                                      TTCCAC
GAM757  TRIM26    3'  CTCTGCACTCTCTGGAAT    14347      GT
                                ATTCT  GGAGAGTGCAGAG
                                |||||  ||||||||||||
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                                TAAGG  TCTCTCACGTCTC
                                  __
GAM757   LOC143326 3'  CTCTGCCAACACAGGATC    77055        GAGAGT
                                GATTCTGTG     GCAGAG
                                |||||||||     ||||||
                                CTAGGACAC     CGTCTC
                                   AAC___
GAM757   LOC144058 5'  CTCTGAGGGCCACAGAATT   77181         AGAGTG
                                GATTCTGTGG     CAGAG
                                ||||||||||     |||||
                                TTAAGACACC     GTCTC
                                   GGGA__
GAM757   LOC146443 3'  CTCTTGGACCCCACAGAAT   78446        AGA  G  _
                                ATTCTGTGG   GT CA GAG
                                |||||||||   || || |||
                                TAAGACACC   CA GT CTC
                                   C__  G  T
GAM757   LOC146756 3'  CTCTGAGAAGCCTCCACAGAAT 84801          A  G___
           C                     GATTCTGTGGAG GT    CAGAG
                                |||||||||||| ||    |||||
                                CTAAGACACCTC CG    GTCTC
                                   _  AAGA
GAM757   LOC165246 5'  CTCCCACTGCCCACAGAA    83365        AG    CA
                                TTCTGTGG  AGTG  GAG
                                ||||||||  ||||  |||
                                AAGACACC  TCAC  CTC
                                   CG    C_
GAM757   LOC202052 3'  CTCTGCAGGCATTCCACAGAGT 91898          A  __
           C                     GATTCTGTGGAG GT  GCAGAG
                                |||||||||||| ||  ||||||
                                CTGAGACACCTT CG  CGTCTC
                                   A  GA
GAM757   LOC206426 3'  CTCCATCCTCTCCACAGCATC  91098     T        TGCA
                                GAT CTGTGGAGAG    GAG
                                ||| ||||||||||    |||
                                CTA GACACCTCTC    CTC
                                  C         CTAC
GAM757   LOC219920 5'  CTCCGCACTCTCCTGGGTC    94949      TGT       A
                                GATTC   GGAGAGTGC GAG
                                |||||   ||||||||| |||
                                CTGGG   CCTCTCACG CTC
                                   T__        C
GAM757   LOC221354 3'  CTCCAGAACCTCACACAGAATC 94012         _  A  GCA_
                                GATTCTGTG GAG GT    GAG
                                ||||||||| ||| ||    |||
                                CTAAGACAC CTC CA    CTC
                                   A   _  AGAC
GAM757   LOC255423 5'  CTCTTACTGCCCACAGAA    99439        AG    C
                                TTCTGTGG  AGTG AGAG
                                ||||||||  |||| ||||
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                                AAGACACC  TCAT TCTC
                                    CG   _
GAM757  LOC257464 5'  CTCTTGCTTTCCCCAAAATC   91242     C  T      C
                                GATT TG GGAGAGTG AGAG
                                |||| || |||||||| ||||
                                CTAA AC CCTTTCGT TCTC
                                  A  C      _
GAM757  LOC257494 3'  CTCTGCACTCTCTGGAAT    99632      GT
                                ATTCT  GGAGAGTGCAGAG
                                |||||  ||||||||||||||
                                TAAGG  TCTCTCACGTCTC
                                  __
GAM757  LOC92840  3'  CTCCCAGGCCTCCACAGAGTC  57246          A  GCA_
                                GATTCTGTGGAG GT   GAG
                                ||||||||||||| ||   |||
                                CTGAGACACCTC CG   CTC
                                      _ GACC
GAM758  HRH1      3'  CTCAAACATGTTTAGAGTGGA  7819      A    TGG
                                TCCA TCTGA   GCATGTTTGAG
                                |||| |||||   ||||||||||||
                                AGGT AGATT   TGTACAAACTC
                                  G    ___
GAM758  TRIM37    3'  CTCAAATTTGTCATCAG     31625       G  T
                                CTGATGG CA GTTTGAG
                                ||||||| || |||||||
                                GACTACT GT TAAACTC
                                    _ T
GAM758  HTMP10    3'  CTCAAAAAAGCCATCAGATCTG 53758    CA       G ATG
          A                      TC  ATCTGATGG C   TTTGAG
                                ||  |||||||||  |   ||||||
                                AG  TAGACTACC G   AAACTC
                                 TC       _ AAA
GAM758  PAK2      5'  CTCAAATATCACCAAACTAGA  67140     A__  GC
                                TCTG   TGG  ATGTTTGAG
                                ||||   |||  |||||||||
                                AGAT   ACC  TATAAACTC
                                  CAA   AC
GAM758  SEMA6A    3'  CTCGAGTACCCACCAGA     40818     A   CA
                                TCTG TGGG  TGTTTGAG
                                |||| ||||  ||||||||
                                AGAC ACCC  ATGAGCTC
                                  C   __
GAM758  TTY7      3'  TCAAACATGCAGGCTGGA    50019     AT  GATGG
                                TCCA  CT    GCATGTTTGA
                                ||||  ||    ||||||||||
                                AGGT  GA    CGTACAAACT
                                  CG  _____
GAM758  LOC144766 3'  CTCAAACATGAGAAGACTGGG  77481     A   GATGGG
                                TCCA TCT     CATGTTTGAG
                                |||| |||     ||||||||||
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                                GGGT AGA     GTACAAACTC
                                  C   AGA___
GAM758  LOC201685 5'  TAAACACCCATCAGATGGA   91845     A       CA
                                TCCA TCTGATGGG  TGTTTG
                                |||| |||||||||  ||||||
                                AGGT AGACTACCC  ACAAAT
                                  _       __
GAM758  LOC221596 5'  CTCAAACAAAACTCAGATT   93623       TG GCA
                                AATCTGA  G   TGTTTGAG
                                |||||||  |   ||||||||
                                TTAGACT  C   ACAAACTC
                                   __ AAA
GAM758  LOC93622  3'  CTCTGCAGACCATCAGAT    57729        GCA   TT
                                ATCTGATGG   TGT  GAG
                                |||||||||   |||  |||
                                TAGACTACC   ACG  CTC
                                     AG_   T_
GAM759  ADH7      3'  GAGATTTTTAAGAGTTTTA   7270         A    CCCA
                                TAAAACTC TAGA    GGTCTC
                                |||||||| ||||    ||||||
                                ATTTTGAG ATTT    TTAGAG
                                     A   _____
GAM759  ATP8B2    3'  GGAGGCTTTTATGTGACTTTTA 65839      C     GACCC
                                TAAAA TCATA     AGGTCTCC
                                ||||| |||||     ||||||||
                                ATTTT AGTGT     TTCGGAGG
                                   C     ATT__
GAM759  BCL7A     3'  TGGGGTGGGGTCATGGGTTTTG 40995          A     AGGT
                                TAAAACTCAT GACCC    CTCC
                                |||||||||| |||||    ||||
                                GTTTTGGGTA CTGGG    GGGG
                                     _    GT__    TG
GAM759  CTSB      3'  GAGACCTGTGCTAGTTTTA   65363        CAT  ACC
                                TAAAACT   AG   CAGGTCTC
                                |||||||   ||   ||||||||
                                ATTTTGA   TC   GTCCAGAG
                                   ___  GT_
GAM759  DPYSL2    3'  GGGGATCTGGTTGGGGTTTTG  9116         ATAGAC
                                TAAAACTC     CCAGGTCTCC
                                ||||||||     ||||||||||
                                GTTTTGGG     GGTCTAGGGG
                                     GTT___
GAM759  SNRPC     3'  GGAGGCCTTATTGTATCGGTTT 13294        C   GACCC
          TA                      TAAAACT ATA     AGGTCTCC
                                ||||||| |||     ||||||||
                                ATTTTGG TAT     TCCGGAGG
                                   C   GTTAT
GAM759  ZNF10     3'  GGAGATTTTGACTGAGTTTTA  31819         TAGACCC
                                TAAAACTCA      AGGTCTCC
                                |||||||||      ||||||||
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                                ATTTTGAGT      TTTAGAGG
                                     CAGT___
GAM759  CALN1    3'  GGGGAAAAGATGTTTATGAGTT 49668          CCAGG_
           T                     AAACTCATAGAC     TCTCC
                                 ||||||||||||     |||||
                                 TTTGAGTATTTG     AGGGG
                                      TAGAAA
GAM759  CBX6     3'  GGAGACTTCTTTTTGTTGGTTT 27418       C    CCC
           TA                     TAAAACT ATAGA   AGGTCTCC
                                  ||||||| |||||   ||||||||
                                  ATTTTGG TGTTT   TTCAGAGG
                                      T    TTC
GAM759  CLDN1    3'  GGAGACCTGGATTTGAGTCTTG 41187     A    TAGAC
                                  TAA ACTCA    CCAGGTCTCC
                                  ||| |||||    ||||||||||
                                  GTT TGAGT    GGTCCAGAGG
                                    C    TTA__
GAM759  DGS-A    3'  GGAGGTCTGGGATCTCTGGTTT 86053       T  T  _    GT
           TA                     TAAAAC CA AGA CCCAG  CTCC
                                  |||||| || ||| |||||  ||||
                                  ATTTTG GT TCT GGGTC  GAGG
                                     _ C   A    TG
GAM759  FLJ10936 3'  GGAGATTGGTTCCTAGTGAGTT 37447          A__  C   G
           TTG                     TAAAACTCAT   GA CCAG TCTCC
                                   ||||||||||   || |||| |||||
                                   GTTTTGAGTG   CT GGTT AGAGG
                                        ATC  T   _
GAM759  FLJ12892 3'  GGGAAATTTGTGGGTTTT    68454          CCCAGG
                                  AAAACTCATAGA     TCTC
                                  ||||||||||||     ||||
                                  TTTTGGGTGTTT     AGGG
                                        AA_____
GAM759  GIT1     3'  GGAGGCCTGGTCCATCTGGAGT 26722         A   C___
           TTTG                     TAAAACTC TAGA    CCAGGTCTCC
                                   |||||||| ||||    ||||||||||
                                   GTTTTGAG GTCT    GGTCCGGAGG
                                      _    ACCT
GAM759  KIAA1005 3'  GGAGACCTGGGTTTGAAGTGTT 72745     A   CA
           G                      TAA ACT  TAGACCCAGGTCTCC
                                  ||| |||  ||||||||||||||||
                                  GTT TGA  GTTTGGGTCCAGAGG
                                    G   A_
GAM759  KIAA1157 3'  GGGGATCTATTTTGTGTGTTTT 72704       T     CCC
           G                      TAAAAC CATAGA   AGGTCTCC
                                  |||||| ||||||   ||||||||
                                  GTTTTG GTGTTT   TCTAGGGG
                                     T     TA_
GAM759  KIAA1240 3'  TCTATTTTGGGTTTGTAGTTTT 67293        C         TCTCC
           A                      TAAAACT ATAGACCCAGG
                                  |||||||  ||||||||||
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                                ATTTTGA TGTTTGGGTTT
                                   _        TATCTG
GAM759  KIAA1853  3'  GGAGGCTTGTGGGTGAGTTT  69923       AGA  _
                                AAACTCAT  CC CAGGTCTCC
                                ||||||||  || |||||||||
                                TTTGAGTG  GG GTTCGGAGG
                                   ___  T
GAM759  MGC5391  3'  CCGGGGGTTTTATAATGATGTT 52196      _  ____    AGGTCTCC
          TTA                    TAAAAC TCAT   AGACCC
                                ||||||| ||||   ||||||
                                ATTTTG AGTA   TTTGGG
                                   T   ATAT    GG  CCT
GAM759  MKP-7   3'  GGAGGTTTGGGGGACTTGGTTT 67016      CATAGA   GT
          TA                     TAAAACT    CCCAG  CTCC
                                |||||||     |||||  ||||
                                ATTTTGG     GGGTT  GAGG
                                   TTCAGG    TG
GAM759  NMT1    3'  GGAGGCCTGAGGCTTCAGTTTT 41149      CAT  A  _
          A                      TAAAACT   AG CC CAGGTCTCC
                                |||||||   || || |||||||||
                                ATTTTGA   TC GG GTCCGGAGG
                                   CT_  _  A
GAM759  PIP5K2B  3'  GGAGGCTTGATGTGGGTTTTG  57697        GACC
                                TAAAACTCATA   CAGGTCTCC
                                ||||||||||   |||||||||
                                GTTTTGGGTGT   GTTCGGAGG
                                   A___
GAM759  SEPT3   3'  GGAGATCTGGGGGAGGTTT   39404     CATAGA
                                AAACT    CCCAGGTCTCC
                                |||||    ||||||||||
                                TTTGG    GGGTCTAGAGG
                                  AGG___
GAM759  SLC19A3  3'  GGAGGCCAAGGTGGGAGTTTTG 48246       ATAG  CA
                                TAAAACTC   ACC  GGTCTCC
                                ||||||||   |||  |||||||
                                GTTTTGAG   TGG  CCGGAGG
                                   GG__   AA
GAM759  SLC34A2  3'  GGGGATGGTCCTTGAGTTTTG  22223       TA   CAG
                                TAAAACTCA  GACC   GTCTCC
                                |||||||||  ||||   ||||||
                                GTTTTGAGT  CTGG   TAGGGG
                                   TC   ___
GAM759  SMC1L1   3'  GGGGACAGACAGTTATGGGTT  72421       ACCCAG
                                AACTCATAG     GTCTCC
                                |||||||||     ||||||
                                TTGGGTATT     CAGGGG
                                   GACAGA
GAM759  ZNF220   3'  GGAGATCACGGTGTGAGTTT  23158       AG  CA
                                AAACTCAT  ACC  GGTCTCC
                                ||||||||  |||  |||||||
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                                TTTGAGTG  TGG  CTAGAGG
                                   __  CA
GAM759  LOC115286 3'  GGAGACTTGGGGAAGAGTT   73764      ATAGA
                                AACTC    CCCAGGTCTCC
                                |||||    ||||||||||
                                TTGAG    GGGTTCAGAGG
                                  AAG__
GAM759  LOC126282 3'  GGGTGGGGTTTGTGGGTTTT   74965           AGGT
                                AAAACTCATAGACCC   CTC
                                ||||||||||||||   |||
                                TTTTGGGTGTTTGGG   GGG
                                       GT__
GAM759  LOC143310 3'  GGAGGCCTGGGATGGAGTT   77048      ATAGA
                                AACTC    CCCAGGTCTCC
                                |||||    ||||||||||
                                TTGAG    GGGTCCGGAGG
                                  GTA__
GAM759  LOC146272 5'  GGAGATTTGAGGTGGGTTT   78329      ATAG  _
                                AAACTC   ACC CAGGTCTCC
                                ||||||   ||| |||||||||
                                TTTGGG   TGG GTTTAGAGG
                                   ____  A
GAM759  LOC146756 3'  GGGGGCTTGGGTCTGAGT    84810      TA
                                ACTCA  GACCCAGGTCTCC
                                |||||  ||||||||||||
                                TGAGT  CTGGGTTCGGGGG
                                   __
GAM759  LOC154860 5'  GGAGGCTTGTTCTGTGTTTGTG 87508       _____     CC
          GTTTTG                 TAAAACT    CATAGA  CAGGTCTCC
                                |||||||    ||||||  |||||||||
                                GTTTTGG    GTGTCT  GTTCGGAGG
                                   TGTTT     T_
GAM759  LOC199714 5'  GGAGGCCTGCACGCCTGGGTT  89702       TAGACC
                                AACTCA     CAGGTCTCC
                                ||||||     |||||||||
                                TTGGGT     GTCCGGAGG
                                  CCGCAC
GAM759  LOC222255 5'  GGGGGCCCTAACTTTTGAGTTT 95951         TAGACCCA
          TG                    TAAAACTCA       GGTCTCC
                                |||||||||       |||||||
                                GTTTTGAGT       CCGGGGG
                                   TTTCAATC
GAM759  LOC253115 3'  GGGGGCCTGGGTCAGATTTTTA 96124      C  ATA
                                TAAAA TC   GACCCAGGTCTCC
                                ||||| ||   ||||||||||||
                                ATTTT AG   CTGGGTCCGGGGG
                                  T  A__
GAM759  LOC257556 3'  GGGGGCCTGGGTCAGATTTTTA 99552      C  ATA
                                TAAAA TC   GACCCAGGTCTCC
                                ||||| ||   ||||||||||||
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                                ATTTT AG   CTGGGTCCGGGGG
                                   T  A__
GAM759  LOC257617 3'  GGGGGCCTGGGTCAGATTTTTA 99646      C  ATA
                                TAAAA TC   GACCCAGGTCTCC
                                ||||| ||   ||||||||||||
                                ATTTT AG   CTGGGTCCGGGGG
                                   T  A__
GAM759  LOC51031  3'  GGAGGCTTGGGTAGTGCAGATT 32709      A  _   AG
           TG                     TAAA CT CAT  ACCCAGGTCTCC
                                |||| || |||  ||||||||||||
                                GTTT GA GTG  TGGGTTCGGAGG
                                   A  C   A_
GAM759  LOC91355  5'  GGGACCTGGCTGAGTTTT     66309         TAGAC
                                AAAACTCA     CCAGGTCTC
                                ||||||||     |||||||||
                                TTTTGAGT     GGTCCAGGG
                                     C_____
GAM759  LOC92305  3'  GGGGGCCTGACACTTGGGATTT 57236      A    T  ACC
           G                     TAAA CTCA AG   CAGGTCTCC
                                |||| |||| ||   |||||||||
                                GTTT GGGT TC   GTCCGGGGG
                                   A    _  ACA
GAM759  LOC93070  3'  GGAGATTGGTTCCTAGTGAGTT 71812          A__  C    G
           TTG                     TAAAACTCAT   GA CCAG TCTCC
                                ||||||||||   || |||| |||||
                                GTTTTGAGTG   CT GGTT AGAGG
                                     ATC  T   _
GAM760  CDH12     3'  CTTATCATTTAAAGTGGTGTA  15777          CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA____   AC
GAM760  GOCAP1    3'  ATTGTTCTTGGGAGCAGTGTA  43007       CA         G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC         G
GAM760  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT    98090       T    AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||     ||||||
                                TGGTG GGGT     TTATTC
                                   _    GTCA_
GAM760  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
           A                     TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM760  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126          CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
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                                ATGTGGTGA      TTTATTC
                                     AGACG___
GAM760  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
            TA                    TACA   TCC   GAAGAATAAG
                                  ||||   |||   ||||||||||
                                  ATGT   AGG   TTTCTTATTC
                                    AAA_   ATTG
GAM760  KIAA1719 3'  TCTGTCTTGGGAGTGGTGTA  68742           _
                                  TACACCACTCCCAAGA AGA
                                  |||||||||||||||| |||
                                  ATGTGGTGAGGGTTCT TCT
                                           G
GAM760  KIAA1853 3'  TTTTTCTTGGAAGCAGTG    69929    CA  C
                                  CAC  CT CCAAGAAGAA
                                  |||  || ||||||||||
                                  GTG  GA GGTTCTTTTT
                                    AC  A
GAM760  KIAA1877 3'  CTTATTCTTCTGCCATGAGT   66748     CCA__
                                  ACTC    AGAAGAATAAG
                                  ||||    ||||||||||
                                  TGAG    TCTTCTTATTC
                                    TACCG
GAM760  KIAA1906 3'  CTTATTCTTCTTGACTTTTGG  73571    CTCC_
                                  CCA    CAAGAAGAATAAG
                                  |||    ||||||||||||
                                  GGT    GTTCTTCTTATTC
                                    TTTCA
GAM760  OSBPL11   3'  CTTAATTTCCCAAGAGTGGTG  43206       CCAA    AA
                                  CACCACTC    GAAG  TAAG
                                  ||||||||    ||||  ||||
                                  GTGGTGAG    CTTT  ATTC
                                       AACC    A_
GAM760  YME1L1    3'  TCATTCTTGATGTGGTGTA   58438       TCC     _
                                  TACACCAC   CAAGAA GA
                                  ||||||||   |||||| ||
                                  ATGTGGTG   GTTCTT CT
                                       TA_     A
GAM760  ZNF262    3'  CTTATTTTGTTTGGGAGT    18723        A
                                  ACTCCCAAG AGAATAAG
                                  |||||||||  ||||||||
                                  TGAGGGTTT TTTTATTC
                                       G
GAM760  LOC91960 3'  TGTGGCTTGGAACGTGGTGTA  68294       TC_    AAGA
                                  TACACCAC   CCAAG    ATA
                                  ||||||||   |||||    |||
                                  ATGTGGTG   GGTTC    TGT
                                       CAA    GG__
GAM761  LENG4     5'  GAACATCTCCCTAGCAACCGTG 44420      C  GGAC
                                  CACGGT GT    GAGATGTTC
                                  |||||| ||    |||||||||
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                                GTGCCA CG   CTCTACAAG
                                   A  ATCC
GAM761  ODF2     5'  GAACACCCCTGTCCACGTCC  11886    T      AGA_
                                GG CGTGGACG   TGTTC
                                || ||||||||   |||||
                                CC GCACCTGT   ACAAG
                                 T       CCCC
GAM761  FLJ10300 5'  AACATCTCTGGGCCATAC    36466    C    A_ _
                                GT GTGG  C GAGATGTT
                                || ||||  | ||||||||
                                CA TACC  G CTCTACAA
                                 _   GG T
GAM761  KIAA0014 3'  AACATCTCGTGGCCGCGCT   28535    T    __
                                GG CGTGG  ACGAGATGTT
                                || |||||  ||||||||||
                                TC GCGCC  TGCTCTACAA
                                 _    GG
GAM761  LOC158263 3'  GAACATCTCACCCAGCATCC  82728    TC _   AC
                                GG  G TGG  GAGATGTTC
                                ||  | |||  |||||||||
                                CC  C ACC  CTCTACAAG
                                 TA G   CA
GAM762  FNTB     3'  TGACCCTCTAGTTCAA      10714          TGCAAT  A
                                TTGAATTAGA     GG TCA
                                ||||||||||     || |||
                                AACTTGATCT     CC AGT
                                       _______ C
GAM762  SLC25A15 3'  CCTTATGCACCTAATTCAA   27293         A    AT_
                                TTGAATTAG TGCA   GG
                                ||||||||| ||||   ||
                                AACTTAATC ACGT   CC
                                      C    ATT
GAM762  KIAA0682 3'  TGGTTTCAACATCTAATTCAA 30034           CAAT
                                TTGAATTAGATG   GGATCA
                                ||||||||||||   ||||||
                                AACTTAATCTAC   TTTGGT
                                       AAC_
GAM762  UNC5D    3'  GTCTTTGCTACATGTAATTCAA 56007        G ____   T
                                TTGAATTA AT   GCAA GGAT
                                |||||||| ||   |||| ||||
                                AACTTAAT TA   CGTT TCTG
                                     G  CAT   _
GAM762  LOC149386 3'  GTGATCCATACAATTTAA    85561       GCA
                                TTAGAT   ATGGATCAC
                                ||||||   |||||||||
                                AATTTA   TACCTAGTG
                                   ACA
GAM762  LOC253782 3'  CCATTCACATTTAATTCAA   97397           C_
                                TTGAATTAGATG  AATGG
                                ||||||||||||  |||||
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                                AACTTAATTTAC  TTACC
                                      AC
GAM763  CD8A    3'  ATCTCCTGTTAATATGGTGTA  10095       __    A
                                TACACCAT  TGGCA GGAGAT
                                ||||||||  ||||| ||||||
                                ATGTGGTA  ATTGT CCTCTA
                                    TA   _
GAM763  HEPH    5'  GATCTCCTCATCACAAAAGTAA 29649    C   ACCAT   CA
          TG                     CA TAC    TGG  AGGAGATC
                                || |||    |||  ||||||||
                                GT ATG    ACT  TCCTCTAG
                                 A  AAAAC   AC
GAM763  MLLT2   3'  CTTTCTGCCAATGAACAGTG  21029     ACAC      AG
                                CACT   CATTGGCA  GAG
                                ||||   ||||||||  |||
                                GTGA   GTAACCGT  TTC
                                  CAA_      CT
GAM763  NCOA6   3'  ATCTCCTAATGATGTATTG   26826    C   C   GGCA
                                CA TACA CATT   AGGAGAT
                                || |||| ||||   |||||||
                                GT ATGT GTAA   TCCTCTA
                                 T   A   ____
GAM763  NDUFS5  3'  CTCCTTGTCAAAGTGTG     17045      CA
                                TACAC  TTGGCAAGGAG
                                |||||  ||||||||||
                                GTGTG  AACTGTTCCTC
                                  A_
GAM763  PKIA    3'  ATCTCCTTGCAATCATGTG   23342     CC   G
                                TACA  ATTG CAAGGAGAT
                                ||||  |||| |||||||||
                                GTGT  TAAC GTTCCTCTA
                                  AC   _
GAM763  RAD21   3'  GATCTCCTTTTCCAGTGCTG  21836    C     C_
                                CA CATTGG  AAGGAGATC
                                || ||||||  |||||||||
                                GT GTGACC  TTCCTCTAG
                                 C     TT
GAM763  SDHC    3'  GATCTCCTTGGAGCAGTAG   69912     ACCA  GG
                                CTAC   TT  CAAGGAGATC
                                ||||   ||  ||||||||||
                                GATG   AG  GTTCCTCTAG
                                  ACG_ __
GAM763  TRIM37  3'  ATCTCCTTTTTGGAGTATGT  31622   _  A  TTGGC
                                AC TAC CCA    AAGGAGAT
                                || ||| |||    ||||||||
                                TG ATG GGT    TTCCTCTA
                                 T  A  TT___
GAM763  FLJ21140 3' GATCTCCTTTAGAGGGCACAGT 45837     ACA  A  GGC
          G                     CACT   CC TT   AAGGAGATC
                                ||||   || ||   |||||||||
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                                GTGA  GG AG  TTCCTCTAG
                                  CAC  G  AT_
GAM763  KIAA0159  3'  ATCTCCTTGTTTTCTAATG   30138      ____
                                CATTGG   CAAGGAGAT
                                ||||||   |||||||||
                                GTAATC   GTTCCTCTA
                                   TTTT
GAM763  KIAA1975  5'  CCACCAATAGTGATAGTG    74417      _  C    CAA
                                CACTA CAC ATTGG  GG
                                ||||| ||| |||||  ||
                                GTGAT GTG TAACC  CC
                                  A  A    A__
GAM763  MDS031    3'  GATCTCCTCTCACAGTGGT   38066       GCA_
                                ACCATTG   AGGAGATC
                                |||||||   ||||||||
                                TGGTGAC   TCCTCTAG
                                    ACTC
GAM763  PER3      3'  ATCTCCTTTCAAAGTAGTG   34173      ACCA   C
                                CACTAC   TTGG AAGGAGAT
                                ||||||   |||| ||||||||
                                GTGATG   AACT TTCCTCTA
                                  A___   _
GAM763  LOC145453 3'  CTTGCCAATGGTGGAGTG    77661     A
                                CACT CACCATTGGCAAG
                                |||| ||||||||||||
                                GTGA GTGGTAACCGTTC
                                  G
GAM763  LOC148824 3'  TTTTGCCAATAATGTGTA    85382      C__
                                TACAC  ATTGGCAAGG
                                |||||  ||||||||||
                                ATGTG  TAACCGTTTT
                                  TAA
GAM763  LOC219920 5'  ATCTCCTGCAGTGTAG      94939      CATTG  A
                                CTACAC    GCA GGAGAT
                                ||||||    ||| ||||||
                                GATGTG    CGT CCTCTA
                                  A____  _
GAM763  LOC220662 3'  ATCTCCTTTACCAATAGGTAGT 92806     ACC    C_
                                ACTAC  ATTGG  AAGGAGAT
                                |||||  |||||  ||||||||
                                TGATG  TAACC  TTCCTCTA
                                  GA_    AT
GAM763  LOC253827 3'  GATCTCCTCTGCAGTGTAG   96573      CATTG  _
                                CTACAC    GCA AGGAGATC
                                ||||||    ||| ||||||||
                                GATGTG    CGT TCCTCTAG
                                  A____  C
GAM764  AKAP1     3'  ACTATGGGTTCTCTTCGCAAA  14472     A  CTT     C
                                TTTGT GA  GGAACCCA AGT
                                ||||| ||  |||||||| |||
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                                AAACG CT   TCTTGGGT TCA
                                  _ TC_       A
GAM764  AKAP1    3'  ACTATGGGTTCTCTTCGCAAA  58373      A  CTT       C
                                TTTGT GA   GGAACCCA AGT
                                ||||| ||   |||||||| |||
                                AAACG CT   TCTTGGGT TCA
                                  _ TC_       A
GAM764  EGF      3'  ACTATAGGTTTTGGTTCCACAA 10488      A  C TG     CAC
                                TTGT GA T  GAACC   AGT
                                |||| || |  |||||   |||
                                AACA CT G  TTTGG   TCA
                                  C  T GT    ATA
GAM764  EZH1     3'  GACTGTGGGTTCCAAATTAC   10551      AC
                                GTAG  TTGGAACCCACAGTC
                                ||||  ||||||||||||||||
                                CATT  AACCTTGGGTGTCAG
                                  A_
GAM764  STAC     3'  GACTGTGGAGTAATAGCCACAA 13427      AGA  TGGA  _
          A                      TTTGT   CT    AC CCACAGTC
                                |||||   ||    || ||||||||
                                AAACA   GA    TG GGTGTCAG
                                  CC_  TAA_  A
GAM764  CCR1     3'  GACTGTGGGCTCCATTC     8927     CT    A
                                GA  TGGA CCCACAGTC
                                ||  |||| |||||||||
                                CT  ACCT GGGTGTCAG
                                 T_   C
GAM764  FLJ10483 3'  GACTGTGGAAGAGATTACAAA  36652       A   GGAAC
                                TTTGTAG CTT    CCACAGTC
                                ||||||| |||    ||||||||
                                AAACATT GAG    GGTGTCAG
                                   A  AA___
GAM764  KIAA1871 3'  ACTGTAAGAGTCTACAAA    61890         GGAACCC
                                TTTGTAGACTT      ACAGT
                                ||||||||||      |||||
                                AAACATCTGAG      TGTCA
                                      AA_____
GAM764  LOC150821 3'  GGGTTCCACATCCACAAA    60944      A  CT
                                TTTGT GA  TGGAACCC
                                ||||| ||  ||||||||
                                AAACA CT  ACCTTGGG
                                  C  AC
GAM764  LOC151057 3'  ACTGTGGGTACACCTATAAA  86379       ACT  GA
                                TTTGTAG   TG  ACCCACAGT
                                |||||||   ||  |||||||||
                                AAATATC   AC  TGGGTGTCA
                                   C__  A_
GAM764  LOC157507 5'  ACTGTAAAAGTCTGCAAA    82377         GGAACCC
                                TTTGTAGACTT      ACAGT
                                ||||||||||      |||||
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                                AAACGTCTGAA      TGTCA
                                      AA_____
GAM764  LOC203339 5'  GGATTCCCAGTCTACAAA    92214          T   C
                                TTTGTAGACT GGAA CC
                                |||||||||| |||| ||
                                AAACATCTGA CCTT GG
                                     C   A
GAM764  LOC51030  3'  ACTGTAAATTAAACCAATCTAC 32695        C   AACCC___
          AAA                    TTTGTAGA TTGG       ACAGT
                                |||||||| ||||       |||||
                                AAACATCT AACC       TGTCA
                                   _   AAATTAAA
GAM764  LOC90906  3'  GACTGTGGATCCCAAACTTTGC 64951       C_   AAC
          A                     TGTAGA  TTGG   CCACAGTC
                                ||||||  ||||   ||||||||
                                ACGTTT  AACC   GGTGTCAG
                                   CA    CTA
GAM765  FGF13    3'  ACCAAGAAAATGTAAAAGACC  54441      CAGG  ___
                                GGTCTT    GC   TTCTTGGT
                                ||||||    ||   ||||||||
                                CCAGAA    TG   AAGAACCA
                                   AA__  TAA
GAM765  INSRR    3'  ACCCGTGGCCCTGAAGACGGTG 68987      G         TCTT
                                CACCG TCTTCAGGGCT    GGT
                                ||||| ||||||||||    |||
                                GTGGC AGAAGTCCCGG    CCA
                                   _          TGC_
GAM765  LOXL3    3'  ACCAAGAAACCCATGTCAGC   51865    CTT  _   C
                                GT   CA GGG TTCTTGGT
                                ||   || ||| ||||||||
                                CG   GT CCC AAGAACCA
                                 ACT  A   A
GAM765  RAP1GA1   3'  ACCTCTGCCCTGAAGACC    12767           TTCTT
                                GGTCTTCAGGGC     GGT
                                ||||||||||||     |||
                                CCAGAAGTCCCG     CCA
                                      TCT__
GAM765  XRCC5     5'  ACCAAAGCGCCTGAGGACCGG  41239           _   CT
                                CCGGTCTTCAGG GCTT  TGGT
                                |||||||||||| ||||  ||||
                                GGCCAGGAGTCC CGAA  ACCA
                                      G   __
GAM765  EDG1     5'  CCACCCCTGAAGCCAGTG    60049     C  T      CTTCT
                                CAC GG CTTCAGGG     TGG
                                ||| || ||||||||     |||
                                GTG CC GAAGTCCC     ACC
                                  A  _       C_____
GAM765  KIAA0323  3'  CCAAGAAGGGAAACGGTG    63947      GTC   AGGG
                                CACCG   TTC    CTTCTTGG
                                |||||   |||    ||||||||
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                                GTGGC  AGG   GAAGAACC
                                  AA_  ____
GAM765  MGC15875  5' ACCAGCGCCCGAAGGCCG   53011       A   TTC
                                CGGTCTTC GGGC  TTGGT
                                |||||||| ||||  |||||
                                GCCGGAAG CCCG  GACCA
                                    _   C__
GAM765  NYD-SP21  3' ACCAAGAAGTCCAAACC    51860    CTTCA
                                GGT   GGGCTTCTTGGT
                                |||   ||||||||||||
                                CCA   CCTGAAGAACCA
                                 AA___
GAM765  TTC2      3' CCAATGCCGAAGACCG     13876       AG  TTC
                                CGGTCTTC  GGC  TTGG
                                ||||||||  |||  ||||
                                GCCAGAAG  CCG  AACC
                                    __  T__
GAM765  LOC199786 3' ACCAAGTTGCGGAGACCGGT  89730        AGG  TT
                                ACCGGTCTTC  GC  CTTGGT
                                ||||||||||  ||  ||||||
                                TGGCCAGAGG  CG  GAACCA
                                    ___  TT
GAM765  LOC200030 3' ACCAAGAAGAGGAAGAAGACC  80119      AGGG_
                                GGTCTTC   CTTCTTGGT
                                |||||||   |||||||||
                                CCAGAAG   GAAGAACCA
                                   AAGGA
GAM765  LOC200030 3' ACCAAGAAGAGGAAGAAGACC  80120      AGGG_
                                GGTCTTC   CTTCTTGGT
                                |||||||   |||||||||
                                CCAGAAG   GAAGAACCA
                                   AAGGA
GAM765  LOC200030 3' ACCAAGAAGTGGAAGAAGACC  80121      AGG_
                                GGTCTTC   GCTTCTTGGT
                                |||||||   ||||||||||
                                CCAGAAG   TGAAGAACCA
                                   AAGG
GAM765  LOC200030 3' ACCAAGAAGTGGAAGAAGACC  80122      AGG_
                                GGTCTTC   GCTTCTTGGT
                                |||||||   ||||||||||
                                CCAGAAG   TGAAGAACCA
                                   AAGG
GAM765  LOC200030 3' ACCAAGAAGTGGAAGAAGACC  80123      AGG_
                                GGTCTTC   GCTTCTTGGT
                                |||||||   ||||||||||
                                CCAGAAG   TGAAGAACCA
                                   AAGG
GAM765  LOC204285 3' ACCAAGAAGCTTCCAAACGAC  91009    TTCA__
                                GTC    GGGCTTCTTGGT
                                |||    ||||||||||||
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                                CAG     TTCGAAGAACCA
                                  CAAACC
GAM765  LOC51629  3'  ACCAAGAAGCCCTCAGCCTGGT 32604       T  TC
            G                    CACCGG CT  AGGGCTTCTTGGT
                                 |||||| ||  ||||||||||||
                                 GTGGTC GA  TCCCGAAGAACCA
                                    C  C_
GAM766  COL9A2    3'  CATGCACCCATCCCCAGTCCAG 10253         T  A__  A
            G                    CCTGGGCTGG GA   GT CATG
                                 |||||||||| ||   || ||||
                                 GGACCTGACC CT   CA GTAC
                                       C  ACC  C
GAM766  ETV6      3'  GCGGGCCAGCAGCCCAGGGAA  10543          G  AA__
                                 TTCCCTGGGCTG TG    GT
                                 |||||||||||| ||    ||
                                 AAGGGACCCGAC AC    CG
                                        G  CGGG
GAM766  FLJ11618  3'  CATGTACCACACACCAAAGAA  42622     CC   GCTG   AA
                                 TTC  TGG    GTG  GTACATG
                                 |||  |||    |||  |||||||
                                 AAG  ACC    CAC  CATGTAC
                                   AA   ACA_  __
GAM766  KIAA0323  3'  ACTTCCCCAGCCCAGAGAA   63945     C       T
                                 TTC CTGGGCTGG GAAGT
                                 ||| |||||||| |||||
                                 AAG GACCCGACC CTTCA
                                   A        C
GAM766  KIAA1453  3'  CATGTCTCCTCCACCAGCC   47657        A  T__
                                 GGCTGGTG AG   ACATG
                                 |||||||| ||   |||||
                                 CCGACCAC TC   TGTAC
                                      C  CTC
GAM766  LOC125893 5'  CATATACTTCACACTGGAGAG  76172     C TG GCTG       C
                                 TTC C  G    GTGAAGTA ATG
                                 ||| |  |    |||||||| |||
                                 GAG G  C    CACTTCAT TAC
                                   A GT A___       A
GAM766  LOC158696 3'  ACTCAACACCAGCCCATGAA   82858     CC        A__
                                 TTC  TGGGCTGGTG   AGT
                                 |||  ||||||||||   |||
                                 AAG  ACCCGACCAC   TCA
                                   T_         AAC
GAM766  LOC255623 5'  CATATACTTCACACTGGAGAG  96498     C TG GCTG       C
                                 TTC C  G    GTGAAGTA ATG
                                 ||| |  |    |||||||| |||
                                 GAG G  C    CACTTCAT TAC
                                   A GT A___       A
GAM766  LOC90092  5'  GCCCCACCTAGCCCAAGGAA   62064     C     _    AA
                                 TTCC TGGGCT GGTG  GT
                                 |||| |||||| ||||  ||
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                                AAGG ACCCGA CCAC  CG
                                  A     T    CC
GAM767  FLJ21438  5'  CAAAACGCTTCCCCCCATCCCA 62190       GAGATTATC
                                TGGGA        AAGCGTTTTG
                                |||||        ||||||||||
                                ACCCT        TTCGCAAAAC
                                   ACCCCCC__
GAM767  FLJ32334  3'  AAAACGCTATTCCTTCCCA   58605       A  TTATCA
                                TGGGAG GA     AGCGTTTT
                                |||||| ||     ||||||||
                                ACCCTT CT     TCGCAAAA
                                   C  TA____
GAM767  HHLA2     3'  CAATGTACTTTGTAATCTCCCC 23953      A       C   CG T
            CA                    TGGG GAGATTAT AAG  T TTG
                                |||| |||||||| |||  | |||
                                ACCC CTCTAATG TTC  G AAC
                                  C       T   AT T
GAM768  ADAT1     3'  CCAGCAAAGAATGAAGGC    24914     __        C
                                GTC  CATTCTTTGC GG
                                |||  ||||||||||| ||
                                CGG  GTAAGAAACG CC
                                  AA         A
GAM768  M17S2     5'  CCGGTAGCGGACGGTCCTT    20910          ATTCT
                                AAGGACCGTCC    TTGCCGG
                                ||||||||||     |||||||
                                TTCCTGGCAGG    GATGGCC
                                      C_____
GAM768  ST14      5'  CCGGCAGGGACGACGCCT    42042     AC    CAT
                                AGG  CGTC   TCTTTGCCGG
                                |||  ||||   ||||||||||
                                TCC  GCAG   AGGGACGGCC
                                  __    C__
GAM768  HTGN29    5'  GCCAACTGTGTGGCGGTCC    39885         _   TC  T
                                GGACCGTC CAT  TT GC
                                |||||||| |||  || ||
                                CCTGGCGG GTG  AA CG
                                     T   TC  C
GAM768  PMAIP1    3'  GCAAGAATGGAAGACCCTT    41211      ACCG        T
                                AAGG    TCCATTCTT GC
                                ||||    ||||||||| ||
                                TTCC    AGGTAAGAA CG
                                  CAGA        _
GAM768  LOC144278 3'  GCCAGCAAAGACTGCTCGATGG 77274          ___ T      C
            TCCT                    AGGACCGTC   CA TCTTTGC GGC
                                |||||||||   || ||||||| |||
                                TCCTGGTAG   GT AGAAACG CCG
                                     CTC  C      A
GAM768  LOC147976 3'  CCGGTGAATGAAGACCCT    79287     ACC   CA   _  TG
                                AGG   GTC  TTC TT  CCGG
                                |||   |||  ||| ||  ||||
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                                TCC   CAG  AAG AA  GGCC
                                 ___   __   T  GT
GAM768  LOC254263 5'  GCCGGCAGCGGACGCGCC    96367    AC     ATTCT
                                GG  CGTCC    TTGCCGGC
                                ||  |||||    ||||||||
                                CC  GCAGG    GACGGCCG
                                 GC    C____
GAM769  GRIK5     3'  ATGATCCCACCAGCC      10877     C      CGAG
                                GGC TGGTGGG    ATCAT
                                |||  |||||||    |||||
                                CCG ACCACCC    TAGTA
                                  _     _____
GAM769  MEF2D     3'  TTGACAATCTCACCGCCCGCC  20991     CT     GC     CA
                                GGC  GGTGG  GAGAT  TCAA
                                |||  |||||  |||||  ||||
                                CCG  CCGCC  CTCTA  AGTT
                                  C_    A_    AC
GAM769  PCLO      3'  TGATAATCTGCCTCCACCAGCC 95890     C     __ G    C
                                GGC TGGTGG  GC AGAT ATCA
                                |||  ||||||  ||  |||| ||||
                                CCG ACCACC  CG TCTA TAGT
                                  _     TC  _    A
GAM769  PFKL      5'  TGACAAGCCCACCAGGCC    12061           GAGA
                                GGCCTGGTGGGC    TCA
                                ||||||||||||    |||
                                CCGGACCACCCG    AGT
                                       AAC_
GAM769  PTMA      3'  ATGATCTCGGATGACCAAACC  12557    CC    _ GG
                                GG  TGGT G  CGAGATCAT
                                ||  ||||  |  |||||||||
                                CC  ACCA T  GCTCTAGTA
                                 AA    G AG
GAM769  SRM       3'  TGGCTCTCGCCCACCAACC    13402    CC          _
                                GG  TGGTGGGCGAGA TCA
                                ||  ||||||||||| |||
                                CC  ACCACCCGCTCT GGT
                                 A_           C
GAM769  FLJ10916  3'  TGATTTTGGCCCCCAAACC    37393    CC   T    _
                                GG  TGG GGGC GAGATCA
                                ||  |||  ||||  |||||||
                                CC  ACC CCCG TTTTAGT
                                 AA   _    G
GAM769  FLJ12750  3'  ATGTGTCTCACCCACCGGCC   45439      T     C    _
                                GGCC GGTGGG GAGAT CAT
                                ||||  ||||||  |||||  |||
                                CCGG CCACCC CTCTG GTA
                                  _     A    T
GAM769  GFR       3'  GATATGCCCACCAAGCC     25447     C       AG
                                GGC TGGTGGGCG  ATC
                                |||  |||||||||  |||
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                                CCG ACCACCCGT  TAG
                                  A       A_
GAM769  KIAA0436  3'  ATGATTGTTCACCAAGC    60684   C      GA
                                GC TGGTGGGC  GATCAT
                                || ||||||||  ||||||
                                CG ACCACTTG  TTAGTA
                                 A      __
GAM769  SCYA14    5'  TGAAGCTCCCACCAGGCC    53108         CG  A_
                                GGCCTGGTGGG  AG  TCA
                                ||||||||||  ||  |||
                                CCGGACCACCC  TC  AGT
                                      __ GA
GAM769  SCYA14    5'  TGAAGCTCCCACCAGGCC    16053         CG  A_
                                GGCCTGGTGGG  AG  TCA
                                ||||||||||  ||  |||
                                CCGGACCACCC  TC  AGT
                                      __ GA
GAM769  LOC122786 3'  TGAGTCTCCCACCAGACCG   74623    C      C  GA
                                CGG CTGGTGGG GA  TCA
                                ||| ||||||| ||  |||
                                GCC GACCACCC CT  AGT
                                  A       T  G_
GAM769  LOC145123 3'  ATGATCTCGGATGACCAAACC  68135   CC   _ GG
                                GG  TGGT G  CGAGATCAT
                                ||  |||| |  |||||||||
                                CC  ACCA T  GCTCTAGTA
                                 AA   G AG
GAM769  LOC150928 3'  ATGATCTCCGATGACCAAACC  74580   CC   GGG  _
                                GG  TGGT   CG AGATCAT
                                ||  ||||   || |||||||
                                CC  ACCA   GC TCTAGTA
                                 AA   GTA  C
GAM769  LOC254182 5'  TGATGTCCCCACCAGCC    97751    C      C  G
                                GGC TGGTGGG GA ATCA
                                ||| ||||||| || ||||
                                CCG ACCACCC CT TAGT
                                  _      _  G
GAM769  LOC51337  3'  TCGCCGCCCACCAGGGCC    34088    _       A_
                                GGCC TGGTGGGCG  GA
                                |||| |||||||||  ||
                                CCGG ACCACCCGC  CT
                                  G       CG
GAM770  AXIN1     3'  ACCAGAAAATCATGCAGTG   61532         CC__
                                CACTGCGTGA   TTGGT
                                ||||||||||   |||||
                                GTGACGTACT   GACCA
                                     AAAA
GAM770  B4GALT4   5'  GCCACGGAACTCACGCAGTG  15028          ___  T
                                CACTGCGTGA   CC TGGT
                                ||||||||||   || ||||
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                                GTGACGCACT  GG ACCG
                                     CAA  C
GAM770  CMAR     3'  GCTGGTCTAGTCACGCA    19033       CT  TT
                                TGCGTGAC  TGG  CAGC
                                ||||||||  |||  ||||
                                ACGCACTG  ATC  GTCG
                                   __  TG
GAM770  COL17A1  3'  CTGAACCAGGCCAGAGCA   6685     G_  A  T
                                TGC  TG CCT GGTTCAG
                                |||  || ||| |||||||
                                ACG  AC GGA CCAAGTC
                                  AG  C  _
GAM770  COL17A1  3'  CTGAACCAGGCCAGAGCA   56256    G_  A  T
                                TGC  TG CCT GGTTCAG
                                |||  || ||| |||||||
                                ACG  AC GGA CCAAGTC
                                  AG  C  _
GAM770  CRY2     3'  GCCAGTGGAGTCAGGCAGTG  72664      G  _ __
                                CACTGC TGAC CT  TGGT
                                |||||| |||| ||  ||||
                                GTGACG ACTG GG  ACCG
                                   G   A  TG
GAM770  CSPG2    5'  GCCGAACCCAGTCGCGCAG   16514       CTT   A
                                CTGCGTGAC   GGTTC GC
                                |||||||||   ||||| ||
                                GACGCGCTG   CCAAG CG
                                     AC_    C
GAM770  EMS1     3'  GCCAAATTGACTGTCACGCGG  19094       C_ TG  CA
                                CTGCGTGAC  T  GTT  GC
                                |||||||||  |  |||  ||
                                GGCGCACTG  A  TAA  CG
                                     TC GT   AC
GAM770  EMS1     3'  GCCAAATTGACTGTCACGCGG  57519       C_ TG  CA
                                CTGCGTGAC  T  GTT  GC
                                |||||||||  |  |||  ||
                                GGCGCACTG  A  TAA  CG
                                     TC GT   AC
GAM770  FBXL7    3'  CTGAATCAGAGGCCACACAG   25495    C  A  _
                                CTG GTG CCT TGGTTCAG
                                |||  ||| ||| ||||||||
                                GAC CAC GGA ACTAAGTC
                                  A   C   G
GAM770  FGF18    3'  CTGAACCAAAACTCTTGGGG   15258    G  T  CC_
                                CT CG GA   TTGGTTCAG
                                ||  ||  ||  |||||||||
                                GG GT CT   AACCAAGTC
                                 G  T  CAA
GAM770  GARP     3'  CTGACTCAAGGTCACACAGTG  19779      C       GT
                                CACTG GTGACCTTG  TCAG
                                |||||  |||||||||  ||||
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                                GTGAC CACTGGAAC  AGTC
                                   A        TC
GAM770  HDLBP    3'  CTAAACCAAGGTCATGAG    68508    G          C
                                CT CGTGACCTTGGTT AG
                                || |||||||||||| ||
                                GA GTACTGGAACCAA TC
                                 _          A
GAM770  KCNJ16   5'  GCTGGTCAGTCACGCAGT    38486          CTTGGT
                                ACTGCGTGAC     TCAGC
                                ||||||||||     |||||
                                TGACGCACTG     GGTCG
                                      ACT___
GAM770  MHC2TA   3'  CTGAAGTCACACAGTG      5980       C    CTTGG
                                CACTG GTGAC    TTCAG
                                ||||| |||||    |||||
                                GTGAC CACTG    AAGTC
                                   A    _____
GAM770  PCDH7    5'  GCCGAACCCGCGGCGCGCAGTG 11990         A  TT_    A
                                CACTGCGTG CC   GGTTC GC
                                ||||||||| ||   ||||| ||
                                GTGACGCGC GG   CCAAG CG
                                      _ CGC    C
GAM770  PCDH7    5'  GCCGAACCCGCGGCGCGCAGTG 51617         A  TT_    A
                                CACTGCGTG CC   GGTTC GC
                                ||||||||| ||   ||||| ||
                                GTGACGCGC GG   CCAAG CG
                                      _ CGC    C
GAM770  PCDH7    5'  GCCGAACCCGCGGCGCGCAGTG 51621         A  TT_    A
                                CACTGCGTG CC   GGTTC GC
                                ||||||||| ||   ||||| ||
                                GTGACGCGC GG   CCAAG CG
                                      _ CGC    C
GAM770  SPG7     3'  GCTGGTCTAGTCACGCA     13347         CT   TT
                                TGCGTGAC  TGG  CAGC
                                ||||||||  |||  ||||
                                ACGCACTG  ATC  GTCG
                                     __   TG
GAM770  TESK1    3'  CTGAACCAGACACAGCA     21886     _   ACC
                                TGC GTG   TTGGTTCAG
                                ||| |||   |||||||||
                                ACG CAC   GACCAAGTC
                                  A  A__
GAM770  TOP3A    3'  GCTGAAAAGTCACGCAG     17260          CTTGG
                                CTGCGTGAC     TTCAGC
                                |||||||||     ||||||
                                GACGCACTG     AAGTCG
                                      AA___
GAM770  AP1GBP1  3'  GCTGGGGATAAAAGCCACTGCA 24351        _   AC   GG___
            GTG                    CACTGC GTG  CTT     TTCAGC
                                ||||||| |||  |||     ||||||
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                                GTGACG CAC  GAA    GGGTCG
                                   T  C_  AATAG
GAM770  AP1GBP1  3'  GCTGGGGATAAAAGCCACTGCA 55440      _  AC  GG___
            GTG                   CACTGC GTG  CTT    TTCAGC
                                |||||| |||  |||    ||||||
                                GTGACG CAC  GAA    GGGTCG
                                   T  C_  AATAG
GAM770  C16orf7  3'  TGAGCCGGCCAGCAGTG    18146      G  A  TT
                                CACTGC TG CC  GGTTCA
                                |||||| || ||  ||||||
                                GTGACG AC GG  CCGAGT
                                   _ C  __
GAM770  CEACAM7  3'  GCTGTCTGAGTCAGCACAGT  23542     C _   C TG TT
                                ACTG G TGAC T  G  CAGC
                                |||| | |||| |  |  ||||
                                TGAC C ACTG A  C  GTCG
                                  A G   _ GT T_
GAM770  CENTG2   3'  GCCGAGGAGGTAGTCACGCGG  30539       _______
                                CTGCGTGA    CCTTGGT
                                ||||||||    |||||||
                                GGCGCACT    GGAGCCG
                                     GATGGA
GAM770  DCOHM    3'  GCTGCTTAGGTCACGCAG    50529          T  TT
                                CTGCGTGACCT GG  CAGC
                                |||||||||| ||  ||||
                                GACGCACTGGA TC  GTCG
                                      T  __
GAM770  DGKD     3'  GCCGAACCAAGAACATGATGTG 60109    TG   AC      A
                                CAC  CGTG  CTTGGTTC GC
                                |||  ||||  |||||||| ||
                                GTG  GTAC  GAACCAAG CG
                                  TA   AA      C
GAM770  DKFZP434K2235 5'  GCTGAGAGGGACACGCAGTG  84496         A   GG
                                CACTGCGTG CCTT  TTCAGC
                                ||||||||| ||||  ||||||
                                GTGACGCAC GGGA  GAGTCG
                                     A   __
GAM770  DKFZp566D234 5'  GCTGAACCTGAGACGCG    62520      GAC  _
                                TGCGT   CTT GGTTCAGC
                                |||||   ||| ||||||||
                                GCGCA   GAG CCAAGTCG
                                   ___   T
GAM770  FLJ11457  3'  GCTTCTATGAGGTCACCAG   45727    C       GTTC
                                CTG GTGACCTTG   AGC
                                ||| |||||||||   |||
                                GAC CACTGGAGT   TCG
                                  _       ATCT
GAM770  FLJ11806  5'  GCCAAGCGCCGCGCAGTG   46127         AC_
                                CACTGCGTG  CTTGGT
                                |||||||||  ||||||
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                                GTGACGCGC  GAACCG
                                     CGC
GAM770  FLJ21588  5' GCCGAGGAGGGTCACGCAG   50804          GG  A
                                CTGCGTGACCTT  TTC GC
                                ||||||||||||  ||| ||
                                GACGCACTGGGA  GAG CG
                                      G_  C
GAM770  FLJ22639  5' GCCAAACCCAGCCACGCAGT  45996        AC  T   CA
                                ACTGCGTG  CT GGTT  GC
                                ||||||||  || ||||  ||
                                TGACGCAC  GA CCAA  CG
                                     C_ C   AC
GAM770  FLJ30681  3' GCTGAACCAATATACAGTG   93436      CG  ACC
                                CACTG  TG   TTGGTTCAGC
                                |||||  ||   ||||||||||
                                GTGAC  AT   AACCAAGTCG
                                   AT  ___
GAM770  KIAA0415  3' GCTATTCGAGGTCACCCAGTG  94165      C        TTC
                                CACTG GTGACCTTGG   AGC
                                ||||| ||||||||||   |||
                                GTGAC CACTGGAGCT   TCG
                                   C        TA_
GAM770  KIAA0472  3' GCCAAAGAAGGGTCACAAAGTG 72357      GC      _____
                                CACT  GTGACCT     TGGT
                                ||||  |||||||     ||||
                                GTGA  CACTGGG     ACCG
                                  AA      AAGAA
GAM770  KIAA0513  3' GCCAGAGTCACAGCAGTG    29035       _    C
                                CACTGC GTGAC TTGGT
                                |||||| ||||| |||||
                                GTGACG CACTG GACCG
                                   A    A
GAM770  KIAA0545  3' GCTCCAGGAGGTCACACAG   63846     C      __  TTC
                                CTG GTGACCT  TGG   AGC
                                ||| |||||||  |||   |||
                                GAC CACTGGA  ACC   TCG
                                  A      GG  ___
GAM770  KIAA0877  3' GCTGAACCAAGATTTCTGC   62483     T  C__
                                GCG GA   CTTGGTTCAGC
                                ||| ||   ||||||||||
                                CGT CT   GAACCAAGTCG
                                  _  TTA
GAM770  KIAA0976  3' GCTTCCAGAGGTCACCCA    30552    C      _  TTC
                                TG GTGACCT TGG   AGC
                                || ||||||| |||   |||
                                AC CACTGGA ACC   TCG
                                 C      G  T__
GAM770  KIAA1136  3' ACCGACATGATCATGCAGTG  92954         CC___
                                CACTGCGTGA    TTGGT
                                ||||||||||    |||||
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                                GTGACGTACT    AGCCA
                                     AGTAC
GAM770  KIAA1243 3' GCTCTCCAAAAATACACAGTG  74028      C  ACC   TTC
                                CACTG GTG   TTGG   AGC
                                ||||| |||   ||||   |||
                                GTGAC CAT   AACC   TCG
                                   A   AAA   TC_
GAM770  KIAA1957 3' GCTGGGAGCGACACGCAGTG  76216        ACC  G_
                                CACTGCGTG   TTG  TTCAGC
                                |||||||||   |||  ||||||
                                GTGACGCAC   AGC  GGGTCG
                                     ___  GA
GAM770  MEGF10   3' CTGAACCAAATCCATCAG    51607    C  ACC
                                CTG GTG   TTGGTTCAG
                                ||| |||   |||||||||
                                GAC TAC   AACCAAGTC
                                  _  CTA
GAM770  MGC20255 3' CTGAATTGTCCCAGCAGTG   54537      GT_  CTT
                                CACTGC   GAC   GGTTCAG
                                ||||||   |||   |||||||
                                GTGACG   CTG   TTAAGTC
                                   ACC   ___
GAM770  MGC33547 3' GCCAAGTATACCATGCAGTG  58986        AC___
                                CACTGCGTG    CTTGGT
                                |||||||||    ||||||
                                GTGACGTAC    GAACCG
                                     CATAT
GAM770  ORMDL3   3' GCTGAACATGGACCACGCAGT  74797        A_  TTG
                                ACTGCGTG  CC   GTTCAGC
                                ||||||||  ||   |||||||
                                TGACGCAC  GG   CAAGTCG
                                     CA  TA_
GAM770  RGS11    3' GCTGAACCCAGCACCAGTG   15164      C  AC  T
                                CACTG GTG  CT GGTTCAGC
                                ||||| |||  || ||||||||
                                GTGAC CAC  GA CCAAGTCG
                                  _  __  C
GAM770  TCL6     5' GCCAAGTCCAAGGTCACACAG  25909    C        _  CA
                                CTG GTGACCTTGG TT  GC
                                ||| ||||||||| ||  ||
                                GAC CACTGGAACC GA  CG
                                  A         T  AC
GAM770  TCL6     5' GCCAAGTCCAAGGTCACACAG  27761    C        _  CA
                                CTG GTGACCTTGG TT  GC
                                ||| ||||||||| ||  ||
                                GAC CACTGGAACC GA  CG
                                  A         T  AC
GAM770  TCL6     5' GCCAAGTCCAAGGTCACACAG  40480    C        _  CA
                                CTG GTGACCTTGG TT  GC
                                ||| ||||||||| ||  ||
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                                GAC CACTGGAACC GA  CG
                                  A        T  AC
GAM770  TCL6     5'  GCCAAGTCCAAGGTCACACAG  40512     C        _  CA
                                CTG GTGACCTTGG TT  GC
                                ||| |||||||||| ||  ||
                                GAC CACTGGAACC GA  CG
                                  A        T  AC
GAM770  TLN2     3'  GCTGAACTGGACAGACAGTG   62356      CG  A  TT
                                CACTG  TG CC  GGTTCAGC
                                |||||  || ||  ||||||||
                                GTGAC  AC GG  TCAAGTCG
                                   AG  A  __
GAM770  LOC144893 5'  GCTGAAGGAGCCAGGCAG    84111      G  AC   GG
                                CTGC TG  CTT  TTCAGC
                                |||| ||  |||  ||||||
                                GACG AC  GAG  AAGTCG
                                  G  C_   G_
GAM770  LOC146756 3'  GCTACGTGGATACGCAGTG   84807         A  TTG  TC
                                CACTGCGTG CC   GT  AGC
                                ||||||||| ||   ||  |||
                                GTGACGCAT GG   CA  TCG
                                     A  TG_  __
GAM770  LOC147057 3'  GCTGAACCAGTGCCGCAG    84986      TG  CT
                                CTGCG  AC  TGGTTCAGC
                                |||||  ||  |||||||||
                                GACGC  TG  ACCAAGTCG
                                   CG  __
GAM770  LOC148147 3'  GCTAAACCCTGGAAAGCCACAA 79401      GC   A____  TT   C
          GTG                     CACT  GTG    CC  GGTT AGC
                                ||||  |||    ||  |||| |||
                                GTGA  CAC    GG  CCAA TCG
                                  A_   CGAAA  TC   A
GAM770  LOC149478 5'  GCTGAACCTTTTTCCGCAG   80172      T  CCTT
                                CTGCG GA    GGTTCAGC
                                ||||| ||   ||||||||
                                GACGC CT    CCAAGTCG
                                   _  TTTT
GAM770  LOC149734 3'  GCTGAACCAGTTCCACAAG   85796    GC   ACC
                                CT  GTG   TTGGTTCAGC
                                ||  |||   ||||||||||
                                GA  CAC   GACCAAGTCG
                                 A_   CTT
GAM770  LOC149951 3'  GCTGAACCAGCTGGGCGCGCA  85951       A  ___
                                TGCGTG CCT   TGGTTCAGC
                                |||||| |||   |||||||||
                                ACGCGC GGG   ACCAAGTCG
                                   _   TCG
GAM770  LOC150538 3'  CTAAACCAAGGTCAAGGGG   80737    GCG        C
                                CT   TGACCTTGGTT AG
                                ||   |||||||||| ||
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                                GG   ACTGGAACCAA TC
                                 GGA         A
GAM770   LOC164714 5'  GCTGAACCACTACGCA     88585       ACCT
                                TGCGTG    TGGTTCAGC
                                ||||||    |||||||||
                                ACGCAT    ACCAAGTCG
                                   C___
GAM770   LOC219920 3'  CTAGAGCCACACAGCAG     94946     _   ACCT     _
                                CTGC GTG    TGGTTC AG
                                |||| |||    |||||| ||
                                GACG CAC    ACCGAG TC
                                  A  ____     A
GAM770   LOC220824 5'  GCCAAACCCAGCCACGCAGT   92480        AC  T    CA
                                ACTGCGTG  CT GGTT  GC
                                ||||||||  || ||||  ||
                                TGACGCAC  GA CCAA  CG
                                     C_  C    AC
GAM770   LOC254659 5'  GCTGAACCAAACAGCCCACG   96821      AC  ___
                                CGTG  CT   TGGTTCAGC
                                ||||  ||   |||||||||
                                GCAC  GA   ACCAAGTCG
                                  CC  CAA
GAM770   LOC257007 5'  GCTGCCCGGGTCACGCGTG    99444     T       T  TT
                                CAC GCGTGACCT GG  CAGC
                                ||| |||||||| ||  ||||
                                GTG CGCACTGGG CC  GTCG
                                  _        C  __
GAM771   BAP1     3'  ACAGCCCCATGGCCTCTGC    17392       A    G   A
                                GCAGA GTTG TGG GCTGT
                                ||||| |||| ||| |||||
                                CGTCT CGGT ACC CGACA
                                   C    _   C
GAM771   C14orf1   3'  ACAGCTCTCCTTCTATCT    24159     _  TT  T
                                AGA AG  GG GGAGCTGT
                                ||| ||  || ||||||||
                                TCT TC  CC TCTCGACA
                                  A  TT  _
GAM771   RB1      5'  ACAGCTCGCTGGCTCCCGCCGC 92552    A  AGA   TG   G
                                GC GC   AGT  GTG AGCTGT
                                || ||   |||  ||| ||||||
                                CG CG   TCG  CGC TCGACA
                                 C  CCC   GT   _
GAM771   SLC9A1    3'  CAGCTCCTCCCCTGCCGC    70919    A    AAGTT  T
                                GC GCAG     GG GGAGCTG
                                || ||||     || |||||||
                                CG CGTC     CC CCTCGAC
                                 C    C_____  T
GAM771   SNAP23    3'  ACAGTTTTGCAACCTCTGCTCC 56332    C      A   G TG
            A                    TG AGCAGA GTT G  GAGCTGT
                                || |||||| ||| |  |||||||
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                                AC TCGTCT CAA C  TTTGACA
                                 C     C  _ GT
GAM771  SNAP23   3' ACAGTTTTGCAACCTCTGCTCC 15132    C     A  G TG
           A                     TG AGCAGA GTT G  GAGCTGT
                                 || |||||| ||| |  |||||||
                                AC TCGTCT CAA C  TTTGACA
                                 C     C  _ GT
GAM771  CDC14A   3' ACAGGGTACAACCCCCTGCTGC 14780        AA_   GTGGAG
           A                     TGCAGCAG  GTTG     CTGT
                                 ||||||||  ||||     ||||
                                ACGTCGTC  CAAC     GACA
                                     CCC   ATGG__
GAM771  FLJ10604 5' ACAGCCCCTGCCCCTGCTGC  36857       AAGTT  _ A
                                GCAGCAG    GGT GG GCTGT
                                |||||||    ||| || |||||
                                CGTCGTC    CCG CC CGACA
                                     C_____  T  C
GAM771  FLJ13154 3' ACAGCCCGGGTTCTCCTGCTGC 45101       A  TTGG  A
                                GCAGCAG AG   TGG GCTGT
                                ||||||| ||   ||| |||||
                                CGTCGTC TC   GCC CGACA
                                     C  TTGG  _
GAM771  FLJ20171 3' ACATTTCCAGCTCCTGCTGCA  35172       A  TGG   C
                                TGCAGCAG AGT  TGGAG TGT
                                |||||||| |||  ||||| |||
                                ACGTCGTC TCG  ACCTT ACA
                                     C  ___    T
GAM771  FLJ23047 3' AGAAAAACCAATTTCCACTGCA 44930      CA       GGAG
                                TGCAG  GAAGTTGGT   CT
                                |||||  |||||||||   ||
                                ACGTC  CTTTAACCA   GA
                                   AC       AAAA
GAM771  HPCAL4   3' CAAGCAACTTTCTGCTACA   33205    C     _   G_
                                TG AGCAGAA GTTG  TG
                                || ||||||| ||||  ||
                                AC TCGTCTT CAAC  AC
                                 A      T   GA
GAM771  KIAA1045 3' CCACCAACCTCTGGCA     71600     AG   A
                                TGC  CAGA GTTGGTGG
                                |||  |||| ||||||||
                                ACG  GTCT CAACCACC
                                  __   C
GAM771  KIAA1061 3' ACAGAGTCAACTTCTGCAGCA  71714     A        TGGAG
                                TGC GCAGAAGTTGG    CTGT
                                ||| ||||||||||    ||||
                                ACG CGTCTTCAACT    GACA
                                  A        GA___
GAM771  MGC5601  5' ACAGCTGGGAATCCCTGCTGCA 48258        AA  GGTGG
                                TGCAGCAG  GTT    AGCTGT
                                ||||||||  |||    ||||||
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                                ACGTCGTC  TAA    TCGACA
                                    CC   GGG__
GAM771  MRPL35   3'  TTCACCAACTTCTCTACA    34025    C  C
                                TG AG AGAAGTTGGTGGA
                                || || ||||||||||||
                                AC TC TCTTCAACCACTT
                                 A  _
GAM771  RGS4     5'  CAGCTCCTCCTGCCGCA     20044     A   GAAGTT  T
                                TGC GCA     GG GGAGCTG
                                ||| |||     || |||||||
                                ACG CGT     CC CCTCGAC
                                  C  _______ T
GAM771  LOC144110 3'  ACAACTCCATCTTCTGCTGC   77187          TTG     C
                                GCAGCAGAAG   GTGGAG TGT
                                ||||||||||   |||||| |||
                                CGTCGTCTTC   TACCTC ACA
                                      ___     A
GAM771  LOC170127 3'  CAGGCAAGCTTCCACTGCA    83454      CA     G  GGAG
                                TGCAG  GAAGTT GT    CTG
                                |||||  |||||| ||    |||
                                ACGTC  CTTCGA CG    GAC
                                   AC     A  ____
GAM771  LOC196955 3'  CAGCTGGATCCTGCTGCA     77863        AAGTT   GG
                                TGCAGCAG    GGT  AGCTG
                                ||||||||    |||  |||||
                                ACGTCGTC    CTA  TCGAC
                                     _____  GG
GAM771  LOC220776 3'  CAGCCCTCTTCTGCCGC     68918    A      TTGGT  A
                                GC GCAGAAG    GG GCTG
                                || |||||||    || ||||
                                CG CGTCTTC    CC CGAC
                                 C      T____  _
GAM771  LOC84549  3'  ACAGACACACCCTCTGCCACA  51677    CA    AGTT    GAG
                                TG  GCAGA   GGTG   CTGT
                                ||  |||||   ||||   ||||
                                AC  CGTCT   CCAC   GACA
                                 AC    C___   ACA
GAM772  CD8A     3'  TTTTCTACACATACATGTA    10099          ATCT
                                TACATGTGTG   GAAAA
                                ||||||||||   |||||
                                ATGTACATAC   CTTTT
                                      ACAT
GAM772  EXT2     3'  GTTTTCAGTTCCATGTA     6383        TGT  T
                                TACATG   GA CTGAAAAC
                                ||||||   || ||||||||
                                ATGTAC   CT GACTTTTG
                                   ___  T
GAM772  ING1     3'  GTTTTCATTGGTACACGTGTA  19857          ATC_
                                TACATGTGTG   TGAAAAC
                                ||||||||||   |||||||
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                                ATGTGCACAT    ACTTTTG
                                      GGTT
GAM772  MGMT     3'  TTTGAGCGACACACACGTGTA  11575          AT___  G
                                TACATGTGTG    CT AAA
                                ||||||||||    || |||
                                ATGTGCACAC    GA TTT
                                      ACAGC  G
GAM772  RUNX1    3'  TTTTACACACATGCAGTAG    10032      A       ATC
                                TTACT CATGTGTG   TGAAA
                                ||||| ||||||||   |||||
                                GATGA GTACACAC   ATTTT
                                   C      ___
GAM772  SFRS2    3'  TTCAGATCTAAATGGTAA     65799       CATG  T
                                TTACTA    TG GATCTGAA
                                ||||||    || ||||||||
                                AATGGT    AT CTAGACTT
                                    AA__  _
GAM772  TACC1    3'  TTTTCAGATGGACATGTA     21882        G G
                                TACATGT T ATCTGAAAA
                                ||||||| | |||||||||
                                ATGTACA G TAGACTTTT
                                    G _
GAM772  DKFZp434N2435 5'  TCAAATCAACTGACTGTAGTAA 98091         TGTG__    C
                                TTACTACA     TGAT TGA
                                ||||||||     |||| |||
                                AATGATGT     ACTA ACT
                                      CAGTCA    A
GAM772  FLJ12387 3'  TTTTCAGATGTTGCTGTAG    43378       T   TG
                                CTACA GTG  ATCTGAAAA
                                ||||| |||  |||||||||
                                GATGT CGT  TAGACTTTT
                                   _  TG
GAM772  FLJ30927 3'  TTTTCTAACCACAGTGTAGTAA 59082          G    ATCT
                                TTACTACAT TGTG    GAAAA
                                ||||||||| ||||    |||||
                                AATGATGTG ACAC    CTTTT
                                      _   CAAT
GAM772  KIAA0186 3'  TTTTCAAATCACATGCAAGTGA 41132       ACA       C
                                TTACT   TGTGTGAT TGAAAA
                                |||||   |||||||| ||||||
                                AGTGA   GTACACTA ACTTTT
                                   AC_       A
GAM772  KIAA0227 3'  TTCAGATCTTTACATGTA    61357         T_
                                TACATGTG  GATCTGAA
                                ||||||||  ||||||||
                                ATGTACAT  CTAGACTT
                                      TT
GAM772  KIAA1765 3'  TTTTCAGATCACGAGGGAG   71138    ACATG
                                CT    TGTGATCTGAAAA
                                ||    ||||||||||||
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                                GA    GCACTAGACTTTT
                                 GGGA_
GAM772  LOC144017 3'  CATTTTAACATGTAGTA    83928         G   TC
                                TACTACATGT TGA  TG
                                |||||||||| |||  ||
                                ATGATGTACA ATT  AC
                                      _  TT
GAM772  LOC151742 5'  TTTTCAACACATGTA      58349        GATC
                                TACATGTGT   TGAAAA
                                |||||||||   ||||||
                                ATGTACACA   ACTTTT
                                     ____
GAM772  LOC220469 5'  GTTTTCCTGACACATGTA    76894        GATCT
                                TACATGTGT    GAAAAC
                                |||||||||    ||||||
                                ATGTACACA    CTTTTG
                                     GTC__
GAM772  LOC256366 3'  TTTTCAGATCAGCATCAAG   97648    AC   G
                                CT  ATGT TGATCTGAAAA
                                ||  |||| ||||||||||
                                GA  TACG ACTAGACTTTT
                                 AC   _
GAM772  LOC51018  3'  TTTTCAGAAATACAGTA     32650     A    GA
                                TAC TGTGT  TCTGAAAA
                                ||| |||||  ||||||||
                                ATG ACATA  AGACTTTT
                                  _    A_
GAM773  ARHGEF12  3'  TTTGGTTTTCCTTGTGCA    31653       ATTTTAA
                                TGTACAG      AAAACCAAA
                                |||||||      |||||||||
                                ACGTGTT      TTTTGGTTT
                                    CC_____
GAM773  ARPC2     3'  TTTGGTTCCATTTTGTACA   20402       TTTTAAAA
                                TGTACAGA      AACCAAA
                                ||||||||      |||||||
                                ACATGTTT      TTGGTTT
                                     TACC____
GAM773  C1D       3'  TTTGGTTTTGATGTACA     22014       GATTTTAA
                                TGTACA       AAAACCAAA
                                ||||||       |||||||||
                                ACATGT       TTTTGGTTT
                                   AG______
GAM773  C7        3'  TTGGTTTTTTAAAATCTGTA  6991
                                TACAGATTTTAAAAAACCAA
                                ||||||||||||||||||||
                                ATGTCTAAAATTTTTTGGTT

GAM773  CBFB      3'  TTGGTTTTTTACTTCTGCAC  10040    A   TTT
                                GT CAGA   TAAAAAACCAA
                                || ||||   ||||||||||
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                                CA GTCT   ATTTTTTGGTT
                                 C    TC_
GAM773  CBFB     3'  TTGGTTTTTTACTTCTGCAC  43444    A    TTT
                                GT CAGA   TAAAAAACCAA
                                || ||||   ||||||||||
                                CA GTCT   ATTTTTTGGTT
                                 C    TC_
GAM773  CDH13    3'  GGTTTTTTATTTTCTTTACA  8839      C   TTT
                                TGTA AGA   TAAAAAACC
                                |||| |||   |||||||||
                                ACAT TCT   ATTTTTTGG
                                  T   TTT
GAM773  CXCL6    3'  TTGGTTTTTTAAATAAAAGCA  12981     ACAGAT
                                TGT     TTTAAAAAACCAA
                                |||     ||||||||||||
                                ACG     AAATTTTTTGGTT
                                  AAAAT_
GAM773  DACH     3'  TTTTGTTGTACAAAATCTGTAC 55828           AAAA   C
                A                TGTACAGATTTT    AAC AAAA
                                ||||||||||||    ||| ||||
                                ACATGTCTAAAA    TTG TTTT
                                       CATG   _
GAM773  DGKG     3'  TGGTTCCAGAGAATTTGCACA  9044      A       AAAA
                                TGT CAGATTTT    AACCA
                                ||| ||||||||    |||||
                                ACA GTTTAAGA    TTGGT
                                  C       GACC
GAM773  EMS1     3'  TGGTTTTTTTCCTGTGC     57520       ATTTT
                                GTACAG     AAAAAACCA
                                ||||||     |||||||||
                                CGTGTC     TTTTTTGGT
                                   CT___
GAM773  EMS1     3'  TGGTTTTTTTCCTGTGC     19096       ATTTT
                                GTACAG     AAAAAACCA
                                ||||||     |||||||||
                                CGTGTC     TTTTTTGGT
                                   CT___
GAM773  GALNT3   3'  TTTGGGTAAAATCTGTA     16831          AAAAA
                                TACAGATTTTA     CCAAA
                                ||||||||||     |||||
                                ATGTCTAAAAT     GGTTT
                                       G____
GAM773  HIVEP2   3'  TGGTACTTTTAAAATTGTACA  23077       A       A_
                                TGTACAG TTTTAAAA  ACCA
                                ||||||| ||||||||  ||||
                                ACATGTT AAAATTTT  TGGT
                                   _       CA
GAM773  NT5C2    3'  TTTTGGTTTTGTGTATCTGTAC 25275         TTTAA
                                GTACAGAT     AAAACCAAAA
                                ||||||||     ||||||||||
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                                CATGTCTA    TTTTGGTTTT
                                    TGTG_
GAM773  RNF4    3'  TGGTTGCAGAATCTGCACA   12888    A      AAAA
                                TGT CAGATTTT   AACCA
                                ||| ||||||||   |||||
                                ACA GTCTAAGA   TTGGT
                                  C      CG__
GAM773  SHOC2   3'  TTTTTTAAATTCTGTACA    24785       T
                                TGTACAGA TTTAAAAAA
                                |||||||| |||||||||
                                ACATGTCT AAATTTTTT
                                    T
GAM773  SNL     3'  TTGGTCTTTTATTTTTTGTA  13293      TTT    A
                                TACAGA   TAAAA ACCAA
                                ||||||   ||||| |||||
                                ATGTTT   ATTTT TGGTT
                                   TTT    C
GAM773  SRRM2   3'  TTTTGGTTTTTTAAAATCTGTA 33388
            CA                    TGTACAGATTTTAAAAAACCAAAA
                                ||||||||||||||||||||||||
                                ACATGTCTAAAATTTTTTGGTTTT

GAM773  UCHL1   3'  TTTGGTTTCTGTCTGTA     16078       TTTAAA
                                TACAGAT     AAACCAAA
                                |||||||     ||||||||
                                ATGTCTG     TTTGGTTT
                                    TC_____
GAM773  VSX1    3'  TTTTGGCCTTTCAAAATTTGTG 28199          A   AA
                                TACAGATTTT AAA  CCAAAA
                                |||||||||| |||  ||||||
                                GTGTTTAAAA TTT  GGTTTT
                                      C   CC
GAM773  DKFZP434J1813 3'  TTTTGGTTTTTCACTCCTGTCC 62438    T    ATTTTA
            A                    TG ACAG     AAAAACCAAAA
                                || ||||     ||||||||||
                                AC TGTC     TTTTTGGTTTT
                                 C    CTCAC_
GAM773  DKFZP564K2062 3'  TTGGTTTTCACATCTGTA    31855       TTTAA
                                TACAGAT    AAAACCAA
                                |||||||    ||||||||
                                ATGTCTA    TTTTGGTT
                                    CAC__
GAM773  DKFZP586N0721 5'  TTGGCTTCCTAGAGTTTGGACA 31828    A       AA  A
                                TGT CAGATTTTA  AA CCAA
                                ||| |||||||||  || ||||
                                ACA GTTTGAGAT  TT GGTT
                                  G       CC  C
GAM773  EDR1    3'  TTTTTTAAAATCTTTACA    16661     C
                                TGTA AGATTTTAAAAAA
                                |||| ||||||||||||
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                                ACAT TCTAAAATTTTTT
                                  T
GAM773  KIAA0157  3'  TTTGAACTAGTTAAAATCTGTA 50753          AAAAC_
                                TACAGATTTTAA     CAAA
                                ||||||||||||     ||||
                                ATGTCTAAAATT     GTTT
                                      GATCAA
GAM773  KIAA0924  3'  GGTTTCTTAAAATCTTTGC   30370    C       A
                                GTA AGATTTTAA AAACC
                                ||| ||||||||| |||||
                                CGT TCTAAAATT TTTGG
                                  T       C
GAM773  KLHL8     3'  TGGTTTTTCTGACTGTACA   63522       A  TTA
                                TGTACAG TT   AAAAACCA
                                ||||||| ||   ||||||||
                                ACATGTC AG   TTTTTGGT
                                   _  TC_
GAM773  MGC4342   3'  TTTTGGCCTTAGAATCTG    44521         AAAA
                                CAGATTTTAA   CCAAAA
                                ||||||||||   ||||||
                                GTCTAAGATT   GGTTTT
                                     CC__
GAM773  MKRN1     3'  TGGTGAAATCTGCACA      26497    A      AAAAA
                                TGT CAGATTTT    ACCA
                                ||| ||||||||    ||||
                                ACA GTCTAAAG    TGGT
                                  C      _____
GAM773  MKRN4     3'  TGGTTAAATCTGCACA      48478    A     TAAAA
                                TGT CAGATTT    AACCA
                                ||| |||||||    |||||
                                ACA GTCTAAA    TTGGT
                                  C     _____
GAM773  OSAP      3'  TTTGGTTTTTTTTTCTAGACA  51915    AC   TTTT
                                TGT  AGA   AAAAAACCAAA
                                |||  |||   ||||||||||
                                ACA  TCT   TTTTTTGGTTT
                                  GA  TT__
GAM773  OSGEP     3'  TTTTGGTTTTTTGGTTTTGTA  35585      TT
                                TACAGA  TTAAAAAACCAAAA
                                ||||||  ||||||||||||||
                                ATGTTT  GGTTTTTTGGTTTT
                                   T_
GAM773  SPTLC2    3'  TTGGTTCTGTTTGTACA     18007        TTTAAAA
                                TGTACAGAT      AACCAA
                                |||||||||      ||||||
                                ACATGTTTG      TTGGTT
                                     TC_____
GAM773  LOC144747 3'  TGGTTTTTCAGCCTGTACG   77475       ATTTTA
                                TGTACAG     AAAAACCA
                                |||||||     ||||||||
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                                GCATGTC     TTTTTGGT
                                    CGAC__
GAM773  LOC146506 3'  TTTAGTTTTTTAAGATATGTA  78496     G         C
                                TACA ATTTTAAAAAAC AAA
                                |||| |||||||||||| |||
                                ATGT TAGAATTTTTTG TTT
                                  A          A
GAM773  LOC153397 3'  TTGGCCTGAGTATCTGTGCA  87227         _   AAAAA
                                TGTACAGAT TTTA    CCAA
                                ||||||||| ||||    ||||
                                ACGTGTCTA GAGT    GGTT
                                     T   CC___
GAM773  LOC158527 5'  TTTTTTACTTCTGTGCA    82842        TTT
                                TGTACAGA   TAAAAAA
                                ||||||||   |||||||
                                ACGTGTCT   ATTTTTT
                                     TC_
GAM773  LOC159250 5'  TTTTGGTTTTGGTGTCTGTAC  88429        TTTAA
                                GTACAGAT    AAAACCAAAA
                                ||||||||    ||||||||||
                                CATGTCTG    TTTTGGTTTT
                                     TGG__
GAM773  LOC221140 3'  TGGTTTTTTTGCGTGTGCA   95147       GATTTT
                                TGTACA     AAAAAACCA
                                ||||||     |||||||||
                                ACGTGT     TTTTTTGGT
                                   GCGT__
GAM774  FLJ22332  5'  GGAAAGAAAACTACATCACA  45637     G  A      _______
                                TGTG AT TAGTTTTC     CC
                                |||| || ||||||||     ||
                                ACAC TA ATCAAAAG     GG
                                  _ C       AAA___
GAM775  GSTA4     3'  GTTTAATAACAACCGAATGTCT 9498         TACCA
                                AGGCATTCG    GTTATTAAAC
                                |||||||||    ||||||||||
                                TCTGTAAGC    CAATAATTTG
                                     CAA__
GAM775  MLLT2     3'  GTTTAATAACTTCTAATGGCC  21031     ATTCG  CC
                                GGC    TA  AGTTATTAAAC
                                |||    ||  ||||||||||
                                CCG    AT  TCAATAATTTG
                                  GTA__  CT
GAM775  NT5C2     3'  TTTAATAGCACAAATGCTT    25274       C  ACCA
                                AGGCATT GT    GTTATTAAA
                                ||||||| ||    |||||||||
                                TTCGTAA CA    CGATAATTT
                                   A ____
GAM775  LOC121504 3'  GTTCAATAACTGAACAGAATAT 74552    GC    GTAC      A
            CT                    AG  ATTC    CAGTTATT AAC
                                ||  ||||    |||||||| |||
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                                TC  TAAG    GTCAATAA TTG
                                 TA    ACAA       C
GAM776  FLRT2     3'  ACGTACTTATACATTTTA    25990           AA_
                                TAAGATGTATAAG   GT
                                ||||||||||||   ||
                                ATTTTACATATTC   CA
                                       ATG
GAM776  DKFZP564A2416 3'  AAGACTTTGCAGCATTTTA    32038         ATAA
                                TAAGATGT    GAAGTCTT
                                ||||||||    ||||||||
                                ATTTTACG    TTTCAGAA
                                     ACG_
GAM776  EMR2      3'  CGTTAAGACCTCTTTCACAGCC 26500    A_   AT    A
           T                     AG  TGT  AAGA GTCTTAACG
                                ||  |||  |||| |||||||||
                                TC  ACA  TTCT CAGAATTGC
                                 CG   CT    C
GAM777  CLCN3     5'  AGCGCAAAAAACAGCCACCGA  10202        _    CC  G
                                TCGGTGG TGTTT  TG GCT
                                |||||||  |||||  ||  |||
                                AGCCACC ACAAA  AC CGA
                                     G     AA  G
GAM777  GRM6      3'  CATGGTGGGAAACAGCCACCGA 7761         _      GG
                                TCGGTGG TGTTTCCT  GCTATG
                                |||||||  ||||||||  ||||||
                                AGCCACC ACAAAGGG  TGGTAC
                                     G       __
GAM777  PCOLN3    3'  CATAGCCCAAGGAGGCACCAC  12409           _
                                GTGGTGTTTCCT GGGCTATG
                                ||||||||||||  ||||||||
                                CACCACGGAGGA CCCGATAC
                                       A
GAM777  DKFZP434N1511 3'  CTCAGGAACCACCGA       93059         GTT
                                TCGGTGGT   TCCTGGG
                                ||||||||   |||||||
                                AGCCACCA   AGGACTC
                                          ___
GAM777  FLJ20972  3'  ATAACCAAACACCACAGA    47380    G       TCC   GC
                                TC GTGGTGTT   TGG  TAT
                                ||  ||||||||   |||  |||
                                AG CACCACAA   ACC  ATA
                                 A       ___   A_
GAM777  FLJ23186  3'  AGCCTTAGGAACACCACC    61039          CT
                                GGTGGTGTTTC  GGGCT
                                ||||||||||  |||||
                                CCACCACAAGG  TCCGA
                                       AT
GAM777  LOC150358 5'  AGCCCAGGGCACTCGA      86086     GT    TT
                                TCG  GGTGT  CCTGGGCT
                                |||  |||||  ||||||||
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                                AGC  TCACG  GGACCCGA
                                  __    __
GAM777  LOC91464  3'  AGCCCAGGAAGCTACCCTGA  66710     T  _
                                TCGG GGT GTTTCCTGGGCT
                                |||| ||| ||||||||||||
                                AGTC CCA CGAAGGACCCGA
                                  _  T
GAM778  BBS4     3'  ATTTGCCCAAAGGGAATCCAGA 53447        G_ G_   A
            ACA                   TGTTCTGGA  CT  TTGG CAAAT
                                |||||||||  ||  |||| |||||
                                ACAAGACCT  GG  AACC GTTTA
                                     AA  GA   C
GAM778  CENTD2   3'  CCAACAAACTCCAGAACA    58270         C_
                                TGTTCTGGAG  TGTTGG
                                ||||||||||  ||||||
                                ACAAGACCTC  ACAACC
                                      AA
GAM778  HAMP     3'  TCCTGCTGCCCCAGAACA    41289        A  T  T
                                TGTTCTGG GC GT GGA
                                |||||||| || || |||
                                ACAAGACC CG CG CCT
                                     C  T  T
GAM778  ITGA11   3'  TCTGCCGGCCCCCAGGACA   25213        A_   TT
                                TGTTCTGG  GCTG  GGA
                                ||||||||  ||||  |||
                                ACAGGACC  CGGC  TCT
                                     CC    CG
GAM778  KITLG    3'  ATTTGCATGGCTCCAGAA    15671          TGGA
                                TTCTGGAGCTGT   CAAAT
                                ||||||||||||   |||||
                                AAGACCTCGGTA   GTTTA
                                       C___
GAM778  MAPK4    5'  CCTGGGCAGCTCCAGATCA   12300    T         __
                                TG TCTGGAGCTGTT  GG
                                || ||||||||||||  ||
                                AC AGACCTCGACGG  CC
                                 T          GT
GAM778  MGAT2    3'  ATTTGTCCAAACAGGACA    11557       GAGCTG
                                TGTTCTG     TTGGACAAAT
                                |||||||     ||||||||||
                                ACAGGAC     AACCTGTTTA
                                    A_____
GAM778  PSPHL    5'  TTGTCATACAGCTCCAAACA  94499     C       TG
                                TGTT TGGAGCTGT  GACAA
                                |||| |||||||||  |||||
                                ACAA ACCTCGACA  CTGTT
                                  _       TA
GAM778  TTC3     3'  TATTTGTCCAACAACTGTCAGA 13885        _  C
            ATA                   TGTTCTGG AG TGTTGGACAAATA
                                |||||||| || ||||||||||||
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                                ATAAGACT TC ACAACCTGTTTAT
                                    G  A
GAM778  H2BFQ    3'  TTTAAGAGAACTCCAGGACA  60079          __ G
                                TGTTCTGGAG  CT TTGGA
                                ||||||||||  || |||||
                                ACAGGACCTC  GA AATTT
                                     AA  G
GAM778  LRG      3'  TCCATCCATGCTTCCTAGAACA 54825       _  _ _ T_
                                TGTTCT GGA GC TG  TGGA
                                |||||| ||| || ||  ||||
                                ACAAGA CCT CG AC  ACCT
                                   T  T T  CT
GAM778  NMT2     3'  ATTTGTCCATGTAACAGAACA  17852        GA  TGT
                                TGTTCTG  GC   TGGACAAAT
                                |||||||  ||   |||||||||
                                ACAAGAC  TG   ACCTGTTTA
                                     AA  T__
GAM778  NYD-SP21  3'  TATTTGTCCAATCTAGATTCAG 51863         G  __
              AACA                  TGTTCTGGA CT  GTTGGACAAATA
                                ||||||||| ||  ||||||||||||
                                ACAAGACTT GA  TAACCTGTTTAT
                                     A  TC
GAM778  PSPH     3'  TTGTCGTACAGCTCCAAACA   17143      C        TG
                                TGTT TGGAGCTGT  GACAA
                                |||| |||||||||  |||||
                                ACAA ACCTCGACA  CTGTT
                                   _        TG
GAM778  LOC122258 3'  CCACCAGCCTCCGGAACA    59820          _  T
                                TGTTCTGGAG CTG TGG
                                |||||||||| ||| |||
                                ACAAGGCCTC GAC ACC
                                     C  C
GAM778  LOC151826 3'  ATTTGTCCAACCTAGCACA   81176     T    AGCT
                                TGT CTGG   GTTGGACAAAT
                                ||| ||||   ||||||||||||
                                ACA GATC   CAACCTGTTTA
                                  C  ____
GAM778  LOC169611 3'  TCCAGTGGCAGCTCCAGAA   83663           ___
                                TTCTGGAGCTGT  TGGA
                                ||||||||||||  ||||
                                AAGACCTCGACG  ACCT
                                      GTG
GAM778  LOC196746 3'  TCAGAGCAGCTCCAAGACA   88903     TC        G_
                                TGT  TGGAGCTGTT  GA
                                |||  ||||||||||  ||
                                ACA  ACCTCGACGA  CT
                                  GA        GA
GAM778  LOC253142 5'  TTGCTAGGATGCCCCAGAATA  99230         A  TG_   A
                                TGTTCTGG GC   TTGG CAA
                                |||||||| ||   |||| |||
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                                ATAAGACC CG   GATC GTT
                                    C  TAG   _
GAM779  BMP1    3'  GGTCATCACCTCCCAGT    21523    C       CCCC
                                AC GGGAGGTGA   TGACC
                                || |||||||||   |||||
                                TG CCCTCCACT   ACTGG
                                 A       _____
GAM779  BMP1    3'  GGTCATCACCTCCCAGT    21535    C       CCCC
                                AC GGGAGGTGA   TGACC
                                || |||||||||   |||||
                                TG CCCTCCACT   ACTGG
                                 A       _____
GAM779  CRYAA   3'  GGCCAGGTGCCTCCTG     6366          ACC    A
                                CGGGAGGTG   CCTG CC
                                |||||||||   |||| ||
                                GTCCTCCGT   GGAC GG
                                    ___    C
GAM779  GALNT2  3'  CTGGCCAGAGTCTGTCCTGGTG 16815        GGT   CC   A
                                CACCGGGA   GAC  CTG CCAG
                                ||||||||   |||  ||| ||||
                                GTGGTCCT   CTG  GAC GGTC
                                    GT_   A_   C
GAM779  IL6     3'  CTGGTCAGAAACCTGTCC    7007     _    GACCC
                                GGG AGGT    CTGACCAG
                                ||| ||||    ||||||||
                                CCT TCCA    GACTGGTC
                                  G    AA___
GAM779  MYO1D   3'  AGCTGGACCACCTCCCGCTG   72240    C       AC _____
                                CA CGGGAGGTG  CC    CT
                                || |||||||||  ||    ||
                                GT GCCCTCCAC  GG    GA
                                 C        CA  TC___
GAM779  OTX1    3'  GGCCAGAGCCTCCCGGCG    28056   A       GACCC   A
                                C CCGGGAGGT    CTG CC
                                | |||||||||    ||| ||
                                G GGCCCTCCG    GAC GG
                                 C        A____   C
GAM779  PNUTL1  3'  CTGGGCGGTGAGCCACCTCCTG 12190         ACCC_   A
            G                    CCGGGAGGTG    CTG CCAG
                                ||||||||||    ||| ||||
                                GGTCCTCCAC    GGC GGTC
                                     CGAGT   G
GAM779  PTPN14  3'  CTGGAGGAGAGTCACCTCC   19428        C__   GA
                                GGAGGTGAC   CCT  CCAG
                                |||||||||   |||  ||||
                                CCTCCACTG   GGA  GGTC
                                     AGA   __
GAM779  RASD1   3'  CTGGCGTCTCCCCTCCCGG   32727        T  CCCC  A
                                CCGGGAGG GA    TG CCAG
                                |||||||| ||    || ||||
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                                GGCCCTCC CT    GC GGTC
                                    C  CT__  _
GAM779  SFTPA2    3'  TGGTCAGGCTCTCCAGGTG   23631      G     TGACC
                                CACC GGAGG     CCTGACCA
                                |||| |||||     ||||||||
                                GTGG CCTCT     GGACTGGT
                                  A     C____
GAM779  TAZ       5'  GTCAGGGGCCAGTGTCTCG    5485       G _  A
                                CGGGA G TG CCCCTGAC
                                ||||| | || ||||||||
                                GCTCT T AC GGGGACTG
                                   G G  C
GAM779  CST8      5'  CTGGTCAGGTCAGCTCCC     19713      G     CC
                                GGGAG TGACC  TGACCAG
                                ||||| |||||  |||||||
                                CCCTC ACTGG  ACTGGTC
                                   G     __
GAM779  DKFZp434J0226 3'  GTCACCGGCCACCTCCCAGG   72794    _       A  CC
                                CC GGGAGGTG CC  TGAC
                                || ||||||||  ||  ||||
                                GG CCCTCCAC GG  ACTG
                                 A       C  CC
GAM779  FKSG28    3'  CTGGCCAGTAGGACCTCC     48908       GA  C_   A
                                GGAGGT  CC  CTG CCAG
                                ||||||  ||  ||| ||||
                                CCTCCA  GG  GAC GGTC
                                    __  AT   C
GAM779  GAB3      3'  GTCAGGGGTCGTCCAGTG     55522     CG   GG
                                CAC  GGA  TGACCCCTGAC
                                |||  |||  ||||||||||
                                GTG  CCT  GCTGGGGACTG
                                  A_  __
GAM779  KIAA0415  3'  TCGGGATCACTTCCCAGTG    94170     C       CC
                                CAC GGGAGGTGA  CCTGA
                                ||| |||||||||  |||||
                                GTG CCCTTCACT  GGGCT
                                  A       A_
GAM779  KIAA0420  3'  GTCAGGGGTCACCAACTTG    64093     A_
                                CGGG  GGTGACCCCTGAC
                                ||||  ||||||||||||
                                GTTC  CCACTGGGGACTG
                                   AA
GAM779  KIAA0495  5'  CTGGCCTCGGTCACCTCCCGG  63265           CCTGA
                                CCGGGAGGTGACC    CCAG
                                ||||||||||||     ||||
                                GGCCCTCCACTGG    GGTC
                                       CTCC_
GAM779  KIAA0616  3'  GGTTGTCCACCTCCCG      47316         _  CCCT
                                CGGGAGGTG AC    GACC
                                |||||||| ||    ||||
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                                GCCCTCCAC TG    TTGG
                                     C _____
GAM779  KIAA0652  3'  CGGGGGCAAAGTCACCTCCCAG 29122     C       _____
              TG                   CAC GGGAGGTGA     CCCCTG
                                   ||| |||||||||     ||||||
                                   GTG CCCTCCACT     GGGGGC
                                     A        GAAAC
GAM779  KIAA0876  3'  CTGGCCAGGGGAAGCCCGG   65316      AGGTGA     A
                                   CCGGG     CCCCTG CCAG
                                   |||||     |||||| ||||
                                   GGCCC     GGGGAC GGTC
                                      GAA___     C
GAM779  KIAA1396  3'  CTGACGGGGAGACACCTCCC   63669        AC_    AC
                                   GGGAGGTG   CCCTG  CAG
                                   ||||||||   |||||  |||
                                   CCCTCCAC   GGGGC  GTC
                                        AGA    A_
GAM779  KIAA1755  3'  CTGGCCAGAGTGGCCCCTG   62013     A   G  CC   A
                                   CGGG GGT AC  CTG CCAG
                                   |||| ||| ||  ||| ||||
                                   GTCC CCG TG  GAC GGTC
                                     _   G  A_   C
GAM779  KIAA1958  3'  CTGACCAGGTGTGACCTCCCGG 82782          G  C    AC
              T                     ACCGGGAGGT AC CCTG  CAG
                                   |||||||||| || ||||  |||
                                   TGGCCCTCCA TG GGAC  GTC
                                        G  T    CA
GAM779  KIF13B    3'  CTGACCAGCAGACTCACCTCCC 83714         CCC__   AC
                                   GGGAGGTGA     CTG  CAG
                                   |||||||||     |||  |||
                                   CCCTCCACT     GAC  GTC
                                        CAGAC   CA
GAM779  KIF13B    3'  CTGACCAGCAGACTCACCTCCC 31561         CCC__   AC
                                   GGGAGGTGA     CTG  CAG
                                   |||||||||     |||  |||
                                   CCCTCCACT     GAC  GTC
                                        CAGAC   CA
GAM779  KRT6      3'  GTCAGGAGCTCTCTCAGTG   83096     C    _  GACC
                                   CAC GGGAG GT    CCTGAC
                                   ||| ||||| ||    ||||||
                                   GTG CTCTC CG    GGACTG
                                     A    T  A___
GAM779  MGC5442   3'  TCGGGGCCACCTCCCGG     49507          A    T
                                   CCGGGAGGTG CCCC GA
                                   |||||||||| |||| ||
                                   GGCCCTCCAC GGGG CT
                                        C    _
GAM779  MGC7036   3'  CTGGCAAAACCACCTCCCTGTG 59617     C       ACCCC  A
                                   CAC GGGAGGTG     TG CCAG
                                   ||| ||||||||     || ||||
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                                GTG CCCTCCAC    AC GGTC
                                  T       CAAA_ _
GAM779  NCOR1    5'  TTAGCCAGCTCCCGGTG    21957        G  ACCC
                                CACCGGGAG TG   CTGA
                                ||||||||| ||   ||||
                                GTGGCCCTC AC   GATT
                                     G  C___
GAM779  PANX2    3'  GGCCAGCCTCCCGGTG     54519         TGACCC   A
                                CACCGGGAGG     CTG CC
                                ||||||||||     ||| ||
                                GTGGCCCTCC     GAC GG
                                     _______  C
GAM779  PLSCR2   5'  TCAAATTCACCTCCCAGTG   40150     C       CCCC
                                CAC GGGAGGTGA   TGA
                                ||| |||||||||   |||
                                GTG CCCTCCACT   ACT
                                  A       TAA_
GAM779  SYNGR4   5'  TGGCTCCCACCTCCCAGTG   25865     C       ACCCCT _
                                CAC GGGAGGTG     GA CCA
                                ||| ||||||||     || |||
                                GTG CCCTCCAC     CT GGT
                                  A       C_____  C
GAM779  LOC115399 3'  CTGGTCCCTTCACCTCCC    73814         CCCCT
                                GGGAGGTGA    GACCAG
                                |||||||||    ||||||
                                CCCTCCACT    CTGGTC
                                     TCC__
GAM779  LOC129450 5'  CGGGCAGCACCTCCCGGT    75380          ACC
                                ACCGGGAGGTG   CCTG
                                ||||||||||   ||||
                                TGGCCCTCCAC   GGGC
                                      GAC
GAM779  LOC146332 3'  CTGGGGAGGGGGGTCACCTCC  78356           GA__
                                GGAGGTGACCCCT   CCAG
                                ||||||||||||   ||||
                                CCTCCACTGGGGG   GGTC
                                      GAGG
GAM779  LOC147160 5'  CTGGCCAGAAATCCCCACTTCC 85076        ACCC___  A
          C                     GGGAGGTG      CTG CCAG
                                ||||||||      ||| ||||
                                CCCTTCAC      GAC GGTC
                                     CCCTAAA   C
GAM779  LOC151009 3'  CTGGTCAACCTGCAACCTCCTG 86369        GACCCC_
                                CGGGAGGT      TGACCAG
                                ||||||||      |||||||
                                GTCCTCCA      ACTGGTC
                                     ACGTCCA
GAM779  LOC160646 3'  AGTGGTCACCTCCCCGTG    83105     C         C
                                CAC GGGAGGTGACC CT
                                ||| ||||||||||| ||
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                                GTG CCCTCCACTGG GA
                                  C         T
GAM779  LOC257354 3'  GTCAGGGGTCACCAACTTG   96795     A_
                                CGGG  GGTGACCCCTGAC
                                ||||  ||||||||||||
                                GTTC  CCACTGGGGACTG
                                  AA
GAM779  LOC57406  5'  CTGGTCAGGAGTCAGCCAGCC  40716    GA _   C
                                GG  GG TGAC CCTGACCAG
                                ||  || |||| |||||||||
                                CC  CC ACTG GGACTGGTC
                                 GA  G   A
GAM780  SLC12A6   3'  GAATCTCAGAAGTCATGGTTC  18892        GC  CC
                                GAACCATGA  TC  AGATTC
                                |||||||||  ||  ||||||
                                CTTGGTACT  AG  TCTAAG
                                     GA  AC
GAM780  SORCS1    3'  GAATCTGGGAAATGGGCTAGG  54681    GAA_   GAGC
                                CC   CCAT   TCCCAGATTC
                                ||   ||||   ||||||||||
                                GG   GGTA   AGGGTCTAAG
                                 ATCG   A___
GAM780  DKFZp762K222 5'  GAATCTGGAAGCTATAAGCCGG 71668     AACCATG   C
                                CCG      AGCT CCAGATTC
                                |||      |||| ||||||||
                                GGC      TCGA GGTCTAAG
                                  CGAATA_   A
GAM780  GDF10     3'  GAATCTGGGAATTAGCCCTGG  18299     AACCA   GC
                                CCG    TGA  TCCCAGATTC
                                |||    |||  ||||||||||
                                GGT    ATT  AGGGTCTAAG
                                  CCCG_  A_
GAM780  KIAA0674  5'  GAACTTTGAGCTAATGGTTCGG 61241        G    CC  A
                                CCGAACCAT AGCTC  AG TTC
                                ||||||||| |||||  || |||
                                GGCTTGGTA TCGAG  TC AAG
                                     A    TT  _
GAM780  KIAA1576  3'  AATCTGGGTTTGGTTTGGT   66487        TGAGCT
                                ACCGAACCA     CCCAGATT
                                |||||||||     ||||||||
                                TGGTTTGGT     GGGTCTAA
                                     TT_____
GAM780  KLF12     3'  GAATCCCTTTTCATGGTCTG   24362    A      CTCCCA
                                CG ACCATGAG     GATTC
                                || |||||||||    |||||
                                GT TGGTACTT     CTAAG
                                 C       TTCC__
GAM780  SEC22C    3'  AATCTGGGAATGGCTGGATTCG 16112      _  TGAGC
           G                     CCGAA CCA     TCCCAGATT
                                |||||  |||    |||||||||
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                                GGCTT GGT    AGGGTCTAA
                                  A  CGGTA
GAM780  LOC134121 3'  GAATCTGGAGACCGATTC    75638    CCA  AG   C
                                GAA  TG  CTCC AGATTC
                                |||  ||  |||| ||||||
                                CTT  GC  GAGG TCTAAG
                                 A__  CA   _
GAM780  LOC145453 3'  AATCTAGGGGTTTGGCTGGGT  77650    GAA  TG    C
                                ACC  CCA  AGCTCC AGATT
                                |||  |||  |||||| |||||
                                TGG  GGT  TTGGGG TCTAA
                                 GTC  __     A
GAM780  LOC150519 3'  AATTTGGAGCTCATAACTC   80727    ACC       C
                                GA  ATGAGCTCC AGATT
                                ||  ||||||||| |||||
                                CT  TACTCGAGG TTTAA
                                 CAA       _
GAM780  LOC201175 5'  GAATCTGGGTGGCCAGATTC  89512    CCA  A  _
                                GAA  TG GCT CCCAGATTC
                                |||  || ||| |||||||||
                                CTT  AC CGG GGGTCTAAG
                                 AG_  _  T
GAM780  LOC253805 3'  GAATCAGGGAGCTCATGCTC  98175    AC        A
                                GA  CATGAGCTCCC GATTC
                                ||  |||||||||| |||||
                                CT  GTACTCGAGGG CTAAG
                                 C_         A
GAM781  AGTPBP1   3'  GGGTTTGCCTTGAAACCA    31537    CTC  C
                                TGG  CA AGGCAAACCC
                                |||  || ||||||||||
                                ACC  GT TCCGTTTGGG
                                 AAA  _
GAM781  BACH2     3'  CCCTTGGATCTGCCTTTGTCC  41780    CTC  C    AAC
                                GG  CA AGGCA  CCAAGGG
                                ||  || |||||  |||||||
                                CC  GT TCCGT  GGTTCCC
                                 T__  T    CTA
GAM781  BCLG      3'  CAAGGGCTGTCTGCCTCGTGGA 57805        _    AA_______  CAAG
           GCCA                  TGGCTCCAC AGGCA      CC   G
                                |||||||| |||||       ||   |
                                ACCGAGGTG TCCGT       GG   C
                                     C    CTGTC___  GAAC
GAM781  BRCA1     5'  CAAGGGCAAACTTGCATGTGGA 24541         G   AC________ CAAG
           GCCA                  TGGCTCCACA GCAA       C   G
                                |||||||||| ||||       |   |
                                ACCGAGGTGT CGTT       G   C
                                     A   CAAAC___G GAAC
GAM781  BRCA1     3'  CAAGGGCAAACTTGCATGTGGA 24542         G   AC________ CAAG
           GCCA                  TGGCTCCACA GCAA       C   G
                                |||||||||| ||||       |   |
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                                ACCGAGGTGT CGTT       G   C
                                     A   CAAAC___G GAAC
GAM781  CAPN10   3'  CCCAGGTTGCCTGGGCCA   41446     CCA     A  CAA
                                TGGCT   CAGGCAA CC   GG
                                |||||   ||||||| ||   ||
                                ACCGG   GTCCGTT GG   CC
                                  ___     _ AC_
GAM781  COLQ     3'  CCCTTGGGTTTTTGTACGAAGC 20254      _ C_   GC
          TA                     TGGCT C  ACAG  AAACCCAAGGG
                                |||||  |  ||||  ||||||||||
                                ATCGA G  TGTT  TTTGGGTTCCC
                                  A CA   __
GAM781  COLQ     3'  CCCTTGGGTTTTTGTACGAAGC 20255      _ C_   GC
          TA                     TGGCT C  ACAG  AAACCCAAGGG
                                |||||  |  ||||  ||||||||||
                                ATCGA G  TGTT  TTTGGGTTCCC
                                  A CA   __
GAM781  DIAPH2   3'  CCCTTGGGCTTATCTACAGAGC 24590     CAC  GC  A
                                GCTC   AG  AA CCCAAGGG
                                ||||   ||  || ||||||||
                                CGAG   TC  TT GGGTTCCC
                                  ACA  TA  C
GAM781  FUT6     5'  CCCTGGTGTCCCTGTGGAACC  5634     C      CAA   CA
                                GG TCCACAGG   ACC  AGGG
                                || ||||||||   |||  ||||
                                CC AGGTGTCC   TGG  TCCC
                                 A       CTG  __
GAM781  HPS1     3'  CCCTTGGCGGCCGTGGAGCC   5762         A   AAAC
                                GGCTCCAC GGC    CCAAGGG
                                |||||||| |||    |||||||
                                CCGAGGTG CCG    GGTTCCC
                                     _   GC__
GAM781  MSX1     3'  CCCAGGTCCCCACCTGTGGGCC 11709      T      CAA__   CAA
          A                      TGGC CCACAGG    ACC   GGG
                                |||| |||||||    |||   |||
                                ACCG GGTGTCC    TGG   CCC
                                  _      ACCCC   A__
GAM781  POLH     3'  CCCTCAGGCTTGCCTGTAGGA  22479     _      A  CA
                                TCC ACAGGCAA CC  AGGG
                                ||| |||||||| ||  ||||
                                AGG TGTCCGTT GG  TCCC
                                  A       C  AC
GAM781  PRKACA   3'  CCCTTGGGCTTTGAAAGCCA   12267      CCACAGG   _
                                TGGCT      CAAA CCCAAGGG
                                |||||      |||| ||||||||
                                ACCGA      GTTT GGGTTCCC
                                  AA_____   C
GAM781  SIM1     3'  GGGTTTGCTTGTAAAACCA   18619     CTCC
                                TGG    ACAGGCAAACCC
                                |||    ||||||||||||
```

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                                ACC   TGTTCGTTTGGG
                                  AAAA
GAM781  SMARCC1  3'  CCCTCAGGTTTGCCTCTAACCA 13250    CTCCAC       CA
                                TGG     AGGCAAACC  AGGG
                                |||     |||||||||  ||||
                                ACC     TCCGTTTGG  TCCC
                                  AATC__       AC
GAM781  TNFRSF8  3'  CCCAGTGGGCATGGAGCCA   8797       CAGGCAAA   A_
                                TGGCTCCA      CCCA  GGG
                                ||||||||      ||||  |||
                                ACCGAGGT      GGGT  CCC
                                    AC______   GA
GAM781  BPES     3'  CCCTCTGGGCCCGCCTCTGGAG 43795       C   AAA   _
           CCA                    TGGCTCCA AGGC   CCCA AGGG
                                ||||||||| ||||   |||| ||||
                                ACCGAGGT TCCG   GGGT TCCC
                                    C   CCC   C
GAM781  CLDN6    3'  CCTTGGATGATGGAGCCA    41335       CAGG  AAC
                                TGGCTCCA   CA   CCAAGG
                                ||||||||   ||   ||||||
                                ACCGAGGT   GT   GGTTCC
                                    A___  A__
GAM781  DKFZp761A132 3'  CCCTGGGTTTGCAGAGC     51165     CACAG       A
                                GCTC    GCAAACCCA GG
                                ||||    ||||||||| ||
                                CGAG    CGTTTGGGT CC
                                  A____       C
GAM781  DKFZp762P2111 3'  CCCTTGGGTTTGGGAAGAGGCA 87627    G   CACAGG
                                TG CTC     CAAACCCAAGGG
                                || |||     ||||||||||||
                                AC GAG     GTTTGGGTTCCC
                                 G  AAGG__
GAM781  EBF2     3'  CCCTTGGGTCTGCAAGGAGCCA 42957       ACAG   A
                                TGGCTCC   GCA ACCCAAGGG
                                |||||||   ||| |||||||||
                                ACCGAGG   CGT TGGGTTCCC
                                    AA__  C
GAM781  FLJ20123  5'  CCCCCGGGCCCCCTGGAGTCA  35069       CA  CAAA   AA
                                TGGCTCCA  GG   CCC  GGG
                                ||||||||  ||   |||  |||
                                ACTGAGGT  CC   GGG  CCC
                                    CC  C___   CC
GAM781  HSPC111  3'  CCCCCGGACCAGTGAAGCTGGA 33508       CAGG  AAC__  AA
           GCCA                   TGGCTCCA   CA    CC  GGG
                                ||||||||   ||    ||  |||
                                ACCGAGGT   GT    GG  CCC
                                    CGAA  GACCA  CC
GAM781  KIAA0073  5'  GGCCTTTACCTGTGGAGGCA   68408    G       C  A_____
                                TG CTCCACAGG AA     CC
                                || |||||||| ||     ||
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                                AC GAGGTGTCC TT     GG
                                 G       A  TCC___
GAM781  KIAA0418  3'  CCCTTGGGTCAGACTGGAGCCA 28293        CAGGCAA
                                TGGCTCCA      ACCCAAGGG
                                ||||||||      |||||||||
                                ACCGAGGT      TGGGTTCCC
                                    CAGAC__
GAM781  KIAA0553  3'  CCTTGGGGGTGTTGAGCCA   70447       CACA   AA
                                TGGCTC   GGCA  CCCAAGG
                                ||||||   ||||  |||||||
                                ACCGAG   TTGT  GGGTTCC
                                   ____   GG
GAM781  KIAA1128  3'  CCTTAGGCTTGTGGATCCA   69002     C       AAACCC
                                TGG TCCACAGGC     AAGG
                                ||| |||||||||      ||||
                                ACC AGGTGTTCG     TTCC
                                  T       GA____
GAM781  KIAA1404  3'  CCCCTGGGCCCTGAATGGAGCT 62687         __   CAAA   A
            A                    TGGCTCCA  CAGG   CCCA GGG
                                ||||||||  ||||   |||| |||
                                ATCGAGGT  GTCC   GGGT CCC
                                    AA   C___   C
GAM781  PSTPIP1   3'  CCTGCCCTGCCAGTGGAGCCA  15616         A   AACCCA
                                TGGCTCCAC GGCA     AGG
                                |||||||||  ||||     |||
                                ACCGAGGTG CCGT     TCC
                                    A   CCCG__
GAM781  RHO6     3'  CCTTGGGGTGCAGAGGCA    27875    G   CACAG   AA
                                TG CTC    GCA  CCCAAGG
                                || |||     |||  |||||||
                                AC GAG    CGT  GGGTTCC
                                 G   A_____   G_
GAM781  TNKS1BP1  3'  CCCTTGGGTTTTCTTTTGATAC 54148     CTC  C   C
            CA                    TGG   CA AGG AAACCCAAGGG
                                |||   || ||| ||||||||||
                                ACC   GT TTC TTTGGGTTCCC
                                  ATA  T   T
GAM781  TOB2     3'  CAAGGGCTACCTGCCCGTGGGG 33233         A   AA_______  CAAG
            CCA                    TGGCTCCAC GGCA       CC    G
                                |||||||||  ||||       ||    |
                                ACCGGGGTG CCGT       GG    C
                                    C    CCATC___  GAAC
GAM781  TUB      3'  CCTGCCTGCCTGTGGAGACA   13893    G        AACCCA
                                TG CTCCACAGGCA     AGG
                                || ||||||||||      |||
                                AC GAGGTGTCCGT     TCC
                                 A          CCG___
GAM781  LOC124626 3'  CCCAAGGGCCGTCCTTACCTAT 74800         C   CAAA_________  CAAG
            GGAGCTA                   TGGCTCCA AGG          CC    GG
                                |||||||| |||          ||    ||
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                                ATCGAGGT TCC          GG    CC
                                    A   ATTCCTGCC___  GAAC
GAM781   LOC138639 3'  CCCTTGGGTTGCTGCTGAGCCA 75879       CACA     A
                                TGGCTC    GGCAA CCCAAGGG
                                ||||||    ||||| ||||||||
                                ACCGAG    TCGTT GGGTTCCC
                                   TCG_     _
GAM781   LOC150886 3'  CCCACACCGGCTGTGGAGCCA  86331           G AAACCCAA
                                TGGCTCCACAG C       GGG
                                |||||||||||| |       |||
                                ACCGAGGTGTC G       CCC
                                      _ GCCACA__
GAM781   LOC151534 3'  CCCTAGAAGCCGTGGAGTCA   57482         A   AAACCCA
                                TGGCTCCAC GGC      AGGG
                                ||||||||| |||      ||||
                                ACTGAGGTG CCG      TCCC
                                    _   AAGA___
GAM781   LOC152359 3'  CCTTGAGCACATGGGGCCA    86882        CAG  AAACC
                                TGGCTCCA   GC     CAAGG
                                ||||||||   ||     |||||
                                ACCGGGGT   CG     GTTCC
                                    ACA  A____
GAM781   LOC164397 5'  CCTTCATCCGCCTGTGGAACC  83408     C        AAACCC
                                GG TCCACAGGC      AAGG
                                || |||||||||      ||||
                                CC AGGTGTCCG      TTCC
                                  A        CCTAC_
GAM781   LOC253027 3'  CTTTGCTCACCCCATGGAGCCA 98768         CA  CAAACC
                                TGGCTCCA  GG      CAAGG
                                ||||||||  ||      |||||
                                ACCGAGGT  CC      GTTTC
                                    AC  CACTC_
GAM781   LOC56996  3'  CCTTGGGACGTGGAGCC     40038         AGGCAAA
                                GGCTCCAC       CCCAAGG
                                ||||||||       |||||||
                                CCGAGGTG       GGGTTCC
                                    CA_____
GAM781   LOC90268  3'  CCCTTGGGCCCCTGGGAGCCA  62662        A    CAAA
                                TGGCTCC CAGG    CCCAAGGG
                                ||||||| ||||    ||||||||
                                ACCGAGG GTCC    GGGTTCCC
                                   _    CC__
GAM781   LOC92578  5'  CAAGGGCCATTTGCCTGCAAAG 70393       CCA      A_______  CAAG
            CCA                    TGGCT   CAGGCAA      CC    G
                                |||||   |||||||      ||    |
                                ACCGA   GTCCGTT      GG    C
                                  AAC      TACC___  GAAC
GAM781   LOC93259  5'  CCTCTTGCCTTGGAGCCA    72281         C      ACCCA
                                TGGCTCCA AGGCAA     AGG
                                |||||||| ||||||     |||
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                                ACCGAGGT TCCGTT    TCC
                                    _     C____
GAM782  BBS4    3'  ATTTGCCCAAAGGGAATCCAGA 53447        G_ G_   A
            ACA                   TGTTCTGGA  CT  TTGG CAAAT
                                  |||||||||  ||  |||| |||||
                                  ACAAGACCT  GG  AACC GTTTA
                                       AA  GA   C
GAM782  CENTD2  3'  CCAACAAACTCCAGAACA    31539         C_
                                  TGTTCTGGAG  TGTTGG
                                  ||||||||||  ||||||
                                  ACAAGACCTC  ACAACC
                                       AA
GAM782  HAMP    3'  TCCTGCTGCCCCAGAACA    41289        A  T  T
                                  TGTTCTGG GC GT GGA
                                  |||||||| || || |||
                                  ACAAGACC CG CG CCT
                                       C  T  T
GAM782  ITGA11  3'  TCTGCCGGCCCCCAGGACA   25213        A_   TT
                                  TGTTCTGG  GCTG  GGA
                                  ||||||||  ||||  |||
                                  ACAGGACC  CGGC  TCT
                                       CC    CG
GAM782  KITLG   3'  ATTTGCATGGCTCCAGAA    8023           TGGA
                                  TTCTGGAGCTGT    CAAAT
                                  ||||||||||||    |||||
                                  AAGACCTCGGTA    GTTTA
                                        C___
GAM782  MAPK4   5'  CCTGGGCAGCTCCAGATCA   12300    T         __
                                  TG TCTGGAGCTGTT  GG
                                  || ||||||||||||  ||
                                  AC AGACCTCGACGG  CC
                                   T          GT
GAM782  MGAT2   3'  ATTTGTCCAAACAGGACA    11557        GAGCTG
                                  TGTTCTG     TTGGACAAAT
                                  |||||||     ||||||||||
                                  ACAGGAC     AACCTGTTTA
                                      A_____
GAM782  PSPHL   5'  TTGTCATACAGCTCCAAACA   94499      C        TG
                                  TGTT TGGAGCTGT  GACAA
                                  |||| |||||||||  |||||
                                  ACAA ACCTCGACA  CTGTT
                                    _        TA
GAM782  TTC3    3'  TATTTGTCCAACAACTGTCAGA 13885         _ C
            ATA                   TGTTCTGG AG TGTTGGACAAATA
                                  |||||||| || ||||||||||||
                                  ATAAGACT TC ACAACCTGTTTAT
                                       G  A
GAM782  H2BFQ   3'  TTTAAGAGAACTCCAGGACA  60079          __ G
                                  TGTTCTGGAG  CT TTGGA
                                  ||||||||||  || |||||
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                                ACAGGACCTC  GA AATTT
                                      AA  G
GAM782  LRG      3'  TCCATCCATGCTTCCTAGAACA 54825       _  _ _ T_
                                TGTTCT GGA GC TG  TGGA
                                |||||| ||| || ||  ||||
                                ACAAGA CCT CG AC  ACCT
                                   T   T  T  CT
GAM782  NMT2     3'  ATTTGTCCATGTAACAGAACA  17852       GA  TGT
                                TGTTCTG  GC   TGGACAAAT
                                |||||||  ||   |||||||||
                                ACAAGAC  TG   ACCTGTTTA
                                   AA  T__
GAM782  NYD-SP21  3'  TATTTGTCCAATCTAGATTCAG 51863         G  __
           AACA                    TGTTCTGGA CT  GTTGGACAAATA
                                |||||||||  ||  ||||||||||||
                                ACAAGACTT GA  TAACCTGTTTAT
                                      A  TC
GAM782  PSPH     3'  TTGTCGTACAGCTCCAAACA   17143     C       TG
                                TGTT TGGAGCTGT  GACAA
                                ||||  |||||||||  |||||
                                ACAA ACCTCGACA  CTGTT
                                  _       TG
GAM782  LOC122258 3'  CCACCAGCCTCCGGAACA    59820          _  T
                                TGTTCTGGAG CTG TGG
                                |||||||||| ||| |||
                                ACAAGGCCTC GAC ACC
                                      C   C
GAM782  LOC151826 3'  ATTTGTCCAACCTAGCACA   81176     T   AGCT
                                TGT CTGG   GTTGGACAAAT
                                |||  ||||   ||||||||||
                                ACA GATC   CAACCTGTTTA
                                  C   ____
GAM782  LOC169611 3'  TCCAGTGGCAGCTCCAGAA   83663          ___
                                TTCTGGAGCTGT   TGGA
                                ||||||||||||   ||||
                                AAGACCTCGACG   ACCT
                                       GTG
GAM782  LOC196746 3'  TCAGAGCAGCTCCAAGACA   88903     TC       G_
                                TGT  TGGAGCTGTT  GA
                                |||  ||||||||||  ||
                                ACA  ACCTCGACGA  CT
                                  GA        GA
GAM782  LOC253142 5'  TTGCTAGGATGCCCCAGAATA  99230        A  TG_   A
                                TGTTCTGG GC   TTGG CAA
                                |||||||| ||   |||| |||
                                ATAAGACC CG   GATC GTT
                                     C  TAG   _
GAM783  GALNT2   3'  CTGGCCAGAGTCTGTCCTGGTG 16815        GGT   CC   A
                                CACCGGGA   GAC  CTG CCAG
                                ||||||||   |||  ||| ||||
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                                GTGGTCCT  CTG  GAC GGTC
                                    GT_  A_  C
GAM783  IL6     3'  CTGGTCAGAAACCTGTCC    7007     _   GACCC
                                GGG AGGT    CTGACCAG
                                ||| ||||    ||||||||
                                CCT TCCA    GACTGGTC
                                  G   AA___
GAM783  MYO1D   3'  AGCTGGACCACCTCCCGCTG  72240   C      AC _____
                                CA CGGGAGGTG  CC    CT
                                || |||||||||  ||    ||
                                GT GCCCTCCAC  GG    GA
                                 C       CA  TC___
GAM783  OTX1    3'  GGCCAGAGCCTCCCGGCG    28056   A      GACCC  A
                                C CCGGGAGGT    CTG CC
                                | |||||||||    ||| ||
                                G GGCCCTCCG    GAC GG
                                 C       A____  C
GAM783  PNUTL1  3'  CTGGGCGGTGAGCCACCTCCTG 12190        ACCC_  A
            G                    CCGGGAGGTG    CTG CCAG
                                ||||||||||    ||| ||||
                                GGTCCTCCAC    GGC GGTC
                                     CGAGT  G
GAM783  PTPN14  3'  CTGGAGGAGAGTCACCTCC   19428       C__  GA
                                GGAGGTGAC  CCT  CCAG
                                |||||||||  |||  ||||
                                CCTCCACTG  GGA  GGTC
                                     AGA  __
GAM783  RASD1   3'  CTGGCGTCTCCCCTCCCGG   32727       T  CCCC  A
                                CCGGGAGG GA   TG CCAG
                                |||||||| ||   || ||||
                                GGCCCTCC CT   GC GGTC
                                    C  CT__  _
GAM783  SFTPA2  3'  TGGTCAGGCTCTCCAGGTG   23631     G    TGACC
                                CACC GGAGG    CCTGACCA
                                |||| |||||    ||||||||
                                GTGG CCTCT    GGACTGGT
                                  A    C____
GAM783  TAZ     5'  GTCAGGGGCCAGTGTCTCG   5485      G _  A
                                CGGGA G TG CCCCTGAC
                                ||||| | || ||||||||
                                GCTCT T AC GGGGACTG
                                   G G  C
GAM783  CST8    5'  CTGGTCAGGTCAGCTCCC    19713     G    CC
                                GGGAG TGACC  TGACCAG
                                ||||| |||||  |||||||
                                CCCTC ACTGG  ACTGGTC
                                   G    __
GAM783  DKFZp434J0226 3'  GTCACCGGCCACCTCCCAGG  72794   _      A  CC
                                CC GGGAGGTG CC  TGAC
                                || |||||||| ||  ||||
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                                GG CCCTCCAC GG  ACTG
                                 A       C  CC
GAM783  FKSG28   3' CTGGCCAGTAGGACCTCC    48908       GA  C_   A
                                GGAGGT  CC  CTG CCAG
                                ||||||  ||  ||| ||||
                                CCTCCA  GG  GAC GGTC
                                   __ AT   C
GAM783  GAB3     3' GTCAGGGGTCGTCCAGTG    55522     CG   GG
                                CAC  GGA  TGACCCCTGAC
                                |||  |||  ||||||||||
                                GTG  CCT  GCTGGGGACTG
                                 A_  __
GAM783  KIAA0415 3' TCGGGATCACTTCCCAGTG   94170     C       CC
                                CAC GGGAGGTGA  CCTGA
                                ||| |||||||||  |||||
                                GTG CCCTTCACT  GGGCT
                                 A       A_
GAM783  KIAA0420 3' GTCAGGGGTCACCAACTTG   64093     A_
                                CGGG  GGTGACCCCTGAC
                                ||||  ||||||||||||
                                GTTC  CCACTGGGGACTG
                                  AA
GAM783  KIAA0495 5' CTGGCCTCGGTCACCTCCCGG  63265           CCTGA
                                CCGGGAGGTGACC    CCAG
                                ||||||||||||    ||||
                                GGCCCTCCACTGG    GGTC
                                      CTCC_
GAM783  KIAA0652 3' CGGGGGCAAAGTCACCTCCCAG 29122     C       _____
           TG                   CAC GGGAGGTGA    CCCCTG
                                ||| |||||||||    ||||||
                                GTG CCCTCCACT    GGGGGC
                                 A       GAAAC
GAM783  KIAA0876 3' CTGGCCAGGGGAAGCCCGG   65316      AGGTGA     A
                                CCGGG     CCCCTG CCAG
                                |||||     |||||| ||||
                                GGCCC     GGGGAC GGTC
                                   GAA___     C
GAM783  KIAA1396 3' CTGACGGGGAGACACCTCCC   63669       AC_    AC
                                GGGAGGTG   CCCTG  CAG
                                ||||||||   |||||  |||
                                CCCTCCAC   GGGGC  GTC
                                    AGA    A_
GAM783  KIAA1755 3' CTGGCCAGAGTGGCCCCTG   62013     A   G  CC   A
                                CGGG GGT AC  CTG CCAG
                                |||| ||| ||  ||| ||||
                                GTCC CCG TG  GAC GGTC
                                  _  G  A_   C
GAM783  KIAA1958 3' CTGACCAGGTGTGACCTCCCGG 82782         G  C    AC
           T                     ACCGGGAGGT AC CCTG  CAG
                                ||||||||| || ||||  |||
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                                TGGCCCTCCA TG GGAC  GTC
                                      G  T    CA
GAM783  KIF13B   3'  CTGACCAGCAGACTCACCTCCC 83714         CCC__   AC
                                GGGAGGTGA    CTG  CAG
                                |||||||||    |||  |||
                                CCCTCCACT    GAC  GTC
                                     CAGAC   CA
GAM783  KIF13B   3'  CTGACCAGCAGACTCACCTCCC 31561         CCC__   AC
                                GGGAGGTGA    CTG  CAG
                                |||||||||    |||  |||
                                CCCTCCACT    GAC  GTC
                                     CAGAC   CA
GAM783  KRT6     3'  GTCAGGAGCTCTCTCAGTG   83096    C    _  GACC
                                CAC GGGAG GT    CCTGAC
                                |||  ||||| ||    ||||||
                                GTG CTCTC CG    GGACTG
                                  A     T  A___
GAM783  MGC7036  3'  CTGGCAAAACCACCTCCCTGTG 59617    C       ACCCC  A
                                CAC GGGAGGTG    TG CCAG
                                |||  ||||||||    || ||||
                                GTG CCCTCCAC    AC GGTC
                                  T       CAAA_  _
GAM783  PLSCR2   5'  TCAAATTCACCTCCCAGTG   40150    C       CCCC
                                CAC GGGAGGTGA   TGA
                                |||  |||||||||   |||
                                GTG CCCTCCACT   ACT
                                  A       TAA_
GAM783  SYNGR4   5'  TGGCTCCCACCTCCCAGTG   25865    C       ACCCCT  _
                                CAC GGGAGGTG     GA CCA
                                |||  ||||||||     || |||
                                GTG CCCTCCAC     CT GGT
                                  A       C_____  C
GAM783  LOC115399 3' CTGGTCCCTTCACCTCCC    73814        CCCCT
                                GGGAGGTGA    GACCAG
                                |||||||||    ||||||
                                CCCTCCACT    CTGGTC
                                     TCC__
GAM783  LOC129450 5' CGGGCAGCACCTCCCGGT    75380         ACC
                                ACCGGGAGGTG  CCTG
                                ||||||||||   ||||
                                TGGCCCTCCAC  GGGC
                                      GAC
GAM783  LOC146332 3' CTGGGGAGGGGGGGTCACCTCC  78356          GA__
                                GGAGGTGACCCCT   CCAG
                                ||||||||||||   ||||
                                CCTCCACTGGGGG   GGTC
                                       GAGG
GAM783  LOC147160 5' CTGGCCAGAAATCCCCACTTCC 85076        ACCC___  A
          C                     GGGAGGTG      CTG CCAG
                                ||||||||      ||| ||||
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                                CCCTTCAC      GAC GGTC
                                     CCCTAAA   C
GAM783  LOC151009 3'  CTGGTCAACCTGCAACCTCCTG 86369         GACCCC_
                                CGGGAGGT      TGACCAG
                                ||||||||      |||||||
                                GTCCTCCA      ACTGGTC
                                     ACGTCCA
GAM783  LOC160646 3'  AGTGGTCACCTCCCCGTG    83105     C         C
                                CAC GGGAGGTGACC CT
                                ||| |||||||||| ||
                                GTG CCCTCCACTGG GA
                                  C         T
GAM783  LOC257354 3'  GTCAGGGGTCACCAACTTG   96795      A_
                                CGGG  GGTGACCCCTGAC
                                ||||  ||||||||||||
                                GTTC  CCACTGGGGACTG
                                   AA
GAM783  LOC57406  5'  CTGGTCAGGAGTCAGCCAGCC  40716    GA _   C
                                GG  GG TGAC CCTGACCAG
                                ||  || |||| |||||||||
                                CC  CC ACTG GGACTGGTC
                                 GA  G    A
GAM784  ADAMTS13  3'  CCCCAAAACGTGCATGGA    58151    G       CC   A
                                TC GTGTACGT  TGG GG
                                || ||||||||  ||| ||
                                AG TACGTGCA  ACC CC
                                 G       AA  _
GAM784  PAX5      3'  CCTCCAGGACCCCAGCAAGTG  34127      CG  GTAC
                                CACT  GT    GTCCTGGAGG
                                ||||  ||    ||||||||||
                                GTGA  CG    CAGGACCTCC
                                  A_  ACCC
GAM784  RBP3      3'  CCTCTGGGACACACACCAAG   12795    C     AC    TG
                                CT GGTGT  GTCC  GAGG
                                || |||||  ||||  ||||
                                GA CCACA  CAGG  CTCC
                                 A    CA    GT
GAM784  TCF19     3'  CCTCCAGGAAATTGCCAGTG   99578      C    TACG
                                CACT GGTG    TCCTGGAGG
                                |||| ||||    |||||||||
                                GTGA CCGT    AGGACCTCC
                                   _    TAA_
GAM784  TEM8      3'  CCTGGAGTTACGCACACTGAGT 50825          A _____   T
          G                      CACTCGGTGT CG    TCC GG
                                ||||||||||  ||    ||| ||
                                GTGAGTCACA GC    AGG CC
                                     C  ATTG   T
GAM784  UBASH3A   3'  CCTGCAGCATGTACACCGAGTG 39049             C   G
                                CACTCGGTGTACGT CTG AGG
                                |||||||||||||| ||| |||
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                                GTGAGCCACATGTA GAC TCC
                                      C   G
GAM784  DOCK3    3'  CCTCCAGGGTAGAGATGCACCG 67092    C      CG____
            AATG                  CA TCGGTGTA     TCCTGGAGG
                                || ||||||||     |||||||||
                                GT AGCCACGT     GGGACCTCC
                                 A       AGAGAT
GAM784  FLJ13782 3'  CCTCCAGGGTTCCCAGCAAGTG 46700     CG  GTACG_
                                CACT  GT     TCCTGGAGG
                                ||||  ||     |||||||||
                                GTGA  CG     GGGACCTCC
                                  A_  ACCCTT
GAM784  FLJ21034 3'  CCTCCCTGCAACACCGAGTG   46864         AC  CCT
                                CACTCGGTGT  GT   GGAGG
                                ||||||||||  ||   |||||
                                GTGAGCCACA  CG   CCTCC
                                      A_  TC_
GAM784  KIAA0792 3'  CCTCCAGGGGGCACCAAG    28765    C    ACG
                                CT GGTGT   TCCTGGAGG
                                || |||||   |||||||||
                                GA CCACG   GGGACCTCC
                                 A    G__
GAM784  KIAA1028 3'  CCTCCAGGACATAGCCAG    93589    C   GTAC
                                CT GGT    GTCCTGGAGG
                                || |||    ||||||||||
                                GA CCG    CAGGACCTCC
                                 _   ATA_
GAM784  MGC9753   5'  CCTCCAGGAAGGTCACAAAGTG 54187     CG   T  G_
                                CACT  GTG AC  TCCTGGAGG
                                ||||  ||| ||  |||||||||
                                GTGA  CAC TG  AGGACCTCC
                                  AA   _  GA
GAM784  RARRES2   3'  CCTCCAGGACCGCTGCGGGTG  12778       GT  AC
                                CACTCG  GT  GTCCTGGAGG
                                ||||||  ||  ||||||||||
                                GTGGGC  CG  CAGGACCTCC
                                    GT  C_
GAM784  RDH-E2    3'  CCTGGATACGCAGACCGAGTG  58070         __  AC    T
                                CACTCGGT  GT  GTCC GG
                                ||||||||  ||  |||| ||
                                GTGAGCCA  CG  TAGG CC
                                     GA  CA    T
GAM784  ZNF340    5'  CCTCCAGGACCTGCCCGTGTG  85711     T   T   C
                                CAC CGG GTA GTCCTGGAGG
                                ||| ||| ||| ||||||||||
                                GTG GCC CGT CAGGACCTCC
                                  T   _   C
GAM784  LOC124411 3'  CCCCAGAGGCCCACACCGGG   74772         AC   _    A
                                CTCGGTGT  GTC CTGG GG
                                ||||||||  ||| |||| ||
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                                GGGCCACA  CGG GACC CC
                                    CC   A   _
GAM784   LOC149076 3'  CCTCCAGGAACCACCAAG    79877    C    TACG
                                CT GGTG    TCCTGGAGG
                                || ||||    |||||||||
                                GA CCAC    AGGACCTCC
                                 A    CA__
GAM784   LOC165283 3'  CCTCCAGGATGCACAGAGTG   88545      G    AC
                                CACTC GTGT  GTCCTGGAGG
                                ||||| ||||  ||||||||||
                                GTGAG CACG  TAGGACCTCC
                                   A    __
GAM784   LOC197416 3'  CCCCAGAGGCCCACACCGGG   91322        AC   _    A
                                CTCGGTGT  GTC CTGG GG
                                ||||||||  ||| |||| ||
                                GGGCCACA  CGG GACC CC
                                    CC   A   _
GAM784   LOC200058 3'  CCTCCAGGTCCACGGAGTG    89959      G   TACGT
                                CACTC GTG     CCTGGAGG
                                ||||| |||     ||||||||
                                GTGAG CAC     GGACCTCC
                                   G   CT___
GAM784   LOC255652 3'  CCTCCAGGACTGCCACAGAG   98530     G   _  C
                                CTC GTG TA GTCCTGGAGG
                                ||| ||| || ||||||||||
                                GAG CAC GT CAGGACCTCC
                                  A   C  _
GAM784   LOC256581 5'  CCTCCAGGAGGCACGGAATG   99432    C  G    ACG
                                CA TC GTGT   TCCTGGAGG
                                || || ||||   |||||||||
                                GT AG CACG   AGGACCTCC
                                 A  G    G__
GAM785   CDH12     3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM785   GOCAP1    3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC         G
GAM785   DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT    98090      T    AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||     ||||||
                                TGGTG GGGT     TTATTC
                                   _    GTCA_
GAM785   DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
            A                    TACAC       AGAAGAATAAG
                                |||||       ||||||||||
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                              ATGTG      TCTTCTTATTC
                                 TACTCCC_
GAM785  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126        CCCAAGAA
                              TACACCACT      GAATAAG
                              |||||||||      |||||||
                              ATGTGGTGA      TTTATTC
                                   AGACG___
GAM785  HMP19     3'  CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
           TA                   TACA   TCC   GAAGAATAAG
                              ||||   |||   ||||||||||
                              ATGT   AGG   TTTCTTATTC
                                AAA_  ATTG
GAM785  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA  68742             _
                              TACACCACTCCCAAGA AGA
                              |||||||||||||||| |||
                              ATGTGGTGAGGGTTCT TCT
                                        G
GAM785  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                              CAC  CT CCAAGAAGAA
                              |||  || ||||||||||
                              GTG  GA GGTTCTTTTT
                                AC  A
GAM785  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748     CCA__
                              ACTC    AGAAGAATAAG
                              ||||    ||||||||||
                              TGAG    TCTTCTTATTC
                                TACCG
GAM785  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                              CCA    CAAGAAGAATAAG
                              |||    ||||||||||||
                              GGT    GTTCTTCTTATTC
                                TTTCA
GAM785  OSBPL11   3'  CTTAATTTCCCAAGAGTGGTG  43206        CCAA    AA
                              CACCACTC   GAAG  TAAG
                              ||||||||   ||||  ||||
                              GTGGTGAG   CTTT  ATTC
                                   AACC   A_
GAM785  YME1L1    3'  TCATTCTTGATGTGGTGTA   58438        TCC     _
                              TACACCAC   CAAGAA GA
                              ||||||||   |||||| ||
                              ATGTGGTG   GTTCTT CT
                                   TA_     A
GAM785  ZNF262    3'  CTTATTTTGTTTGGGAGT    18723         A
                              ACTCCCAAG AGAATAAG
                              ||||||||| ||||||||
                              TGAGGGTTT TTTTATTC
                                   G
GAM785  LOC91960  3'  TGTGGCTTGGAACGTGGTGTA  68294        TC_    AAGA
                              TACACCAC   CCAAG   ATA
                              ||||||||   |||||   |||
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                                ATGTGGTG  GGTTC   TGT
                                    CAA   GG__
GAM786  A1BG    3'  GACAGGGTCTCACTGTGTT  56291        A   CA
                                AACACAGTGA ACCC  TC
                                |||||||||| ||||  ||
                                TTGTGTCACT TGGG  AG
                                     C   AC
GAM786  A1BG    3'  GAGATGGGGTTTCACCTTGTT 56292     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  TC
GAM786  ADAMTS4  3'  GAGACAGGGTTTCACCATGTT 18762     CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC       AC
GAM786  ADAMTS4  3'  GAGACGGGGTTTCACCATGTT 18763     CA       A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC       C
GAM786  AIM1    3'  GAGATGGGGTTTCATCACGTT  93465    ACA
                                AAC   GTGAAACCCCATCTC
                                |||   ||||||||||||||
                                TTG   TACTTTGGGGTAGAG
                                 CAC
GAM786  APAF1   3'  GAGACGGGGTTTCACCATGTT  25973     CA       A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC       C
GAM786  APM1    3'  ATGGGGTTTCGTCATGTT    17759     CA
                                AACA  GTGAAACCCCAT
                                ||||  ||||||||||||
                                TTGT  TGCTTTGGGGTA
                                  AC
GAM786  APOL1   3'  GAGATGGGGTTTCACCATGTT  14740     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  |||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  APPBP2  3'  AGACGGTTCTTCATTGTGT   22116        ACC  A
                                ACACAGTGAA   CC TCT
                                ||||||||||   || |||
                                TGTGTTACTT   GG AGA
                                     CTT  C
GAM786  APPL    3'  GAGACGGGGTTTCACCGTGTT  24948      A        A
                                AACAC GTGAAACCCC TCTC
                                ||||| |||||||||| ||||
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                                TTGTG CACTTTGGGG AGAG
                                  C         C
GAM786  ARCN1    3'  GAGACGGGGTTTCACCGTGTT  9754       A         A
                                AACAC GTGAAACCCC TCTC
                                ||||| |||||||||| ||||
                                TTGTG CACTTTGGGG AGAG
                                  C         C
GAM786  ATP1B2   3'  GAGATGGAGTTTCGCTCTTGT  9835      C_       C
                                ACA  AGTGAAAC CCATCTC
                                |||  |||||||| |||||||
                                TGT  TCGCTTTG GGTAGAG
                                  TC       A
GAM786  ATP7A    3'  GAGACGGGGTTTCGCCATGTT  5322       CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CGCTTTGGGG AGAG
                                  AC         C
GAM786  AXL      3'  GAGACAGGGTTTCACCATGTT  41886      CA        CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC         AC
GAM786  BRIP1    3'  GAGATGGGGTTTCACCATGTT  50209      CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  C14orf1  3'  GAGACGGGGTTTCACTCTGT   24169     C         A
                                ACA AGTGAAACCCC TCTC
                                ||| |||||||||| ||||
                                TGT TCACTTTGGGG AGAG
                                  C         C
GAM786  C14orf1  3'  GAGATGGGGTCTTACTATGTT  24170      C     A
                                AACA AGTGA ACCCCATCTC
                                |||| ||||| ||||||||||
                                TTGT TCATT TGGGGTAGAG
                                  A    C
GAM786  C7       3'  GAGATGGGTTTCACCATGTT   6986       CA        C
                                AACA  GTGAAACCC ATCTC
                                ||||  |||||||| |||||
                                TTGT  CACTTTGGG TAGAG
                                  AC        _
GAM786  CA14     3'  ATGAGGAAATCGCTGTGTT    25057          AAC  _
                                AACACAGTGA   CC CAT
                                ||||||||||   || |||
                                TTGTGTCGCT   GG GTA
                                      AAA  A
GAM786  CASP10   3'  GAGATGGGGTTTCACTATGTT  53258      C
                                AACA AGTGAAACCCCATCTC
                                |||| ||||||||||||||||
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                                TTGT TCACTTTGGGGTAGAG
                                  A
GAM786  CASP10   3'  GAGATGGGGTTTCACTATGTT  53259     C
                                AACA AGTGAAACCCCATCTC
                                |||| ||||||||||||||||
                                TTGT TCACTTTGGGGTAGAG
                                  A
GAM786  CASP2    3'  GAGACAGGGTTTCACCATGTT  53332     CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  CASP2    3'  GAGACAGGGTTTCACCATGTT  53333     CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  CASP2    3'  GAGACAGGGTTTCACCATGTT  8709      CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  CASP8    3'  GAGACAGGGTTTCACTGTGTT  54076           CA
                                AACACAGTGAAACCC  TCTC
                                ||||||||||||||  ||||
                                TTGTGTCACTTTGGG  AGAG
                                      AC
GAM786  CASP8    3'  GAGACAGGGTTTCACTGTGTT  54077           CA
                                AACACAGTGAAACCC  TCTC
                                ||||||||||||||  ||||
                                TTGTGTCACTTTGGG  AGAG
                                      AC
GAM786  CBFA2T2  3'  GAGACGGGGTTTCTCCTTGTT  18711     CAGT      A
                                AACA   GAAACCCC TCTC
                                ||||   |||||||| ||||
                                TTGT   CTTTGGGG AGAG
                                  TCCT       C
GAM786  CDC6     3'  GAGACAGGGTTTTACCATGTT  8821      CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CATTTTGGG  AGAG
                                  AC        AC
GAM786  CIAS1    5'  GAGATGGAGTCTTGCTGTGT   18097      TG A  C
                                ACACAG  A AC CCATCTC
                                ||||||  | || |||||||
                                TGTGTC  T TG GGTAGAG
                                   GT C  A
GAM786  CLECSF11 5'  GAGATGGGGTTTCACTATGTT  56149     C
                                AACA AGTGAAACCCCATCTC
                                |||| ||||||||||||||||
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                                TTGT TCACTTTGGGGTAGAG
                                  A
GAM786  CNGA1    5'  GAGATGGGATTTCACCATGTT  60240     CA     C
                                AACA  GTGAAA CCCATCTC
                                ||||  |||||| ||||||||
                                TTGT  CACTTT GGGTAGAG
                                  AC     A
GAM786  CNN2     3'  GAGATGGGGTTTCCCCATGTT  16461     CAGT
                                AACA    GAAACCCCATCTC
                                ||||    ||||||||||||
                                TTGT    CTTTGGGGTAGAG
                                  ACCC
GAM786  CR1      3'  GAGACGGGGTTTCACCATGTT  6944      CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  CRTAP    3'  GAGACGGGGTTTTGCCATGTT  22080     CA TG      A
                                AACA  G  AAACCCC TCTC
                                ||||  |  ||||||| ||||
                                TTGT  C  TTTGGGG AGAG
                                  AC GT      C
GAM786  CTF1     3'  GAGACGAGGTTTCGCCATGTT  9016      CA       CCA
                                AACA  GTGAAACC   TCTC
                                ||||  ||||||||   ||||
                                TTGT  CGCTTTGG   AGAG
                                  AC       AGC
GAM786  CXCL16   3'  GAGACGGGGTTTCACCATGTT  42169     CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  CYP1A2   3'  GAGACGAGGTTTCACTGTGTT  7515            CCA
                                AACACAGTGAAACC   TCTC
                                ||||||||||||||   ||||
                                TTGTGTCACTTTGG   AGAG
                                        AGC
GAM786  CYP1A2   3'  GAGACGGGTTTCACCATGTT   7516      CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        C_
GAM786  CYP1A2   3'  GAGATGGGGTTTCACCATGTT  7517      CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  CYP1B1   3'  GAGATGAGGTCAGTTGTGTT   5446        _  AA  C
                                AACACAG TGA  CC CATCTC
                                |||||||  |||  ||  ||||||
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                                TTGTGTT ACT  GG GTAGAG
                                   G  __  A
GAM786  CYP2B6   3'  GAGATGGGGTTTCACTGTGT   7562
                                ACACAGTGAAACCCCATCTC
                                ||||||||||||||||||||
                                TGTGTCACTTTGGGGTAGAG

GAM786  CYP4F3   3'  GAGGCGGGGTTTCGCCATGTT  8008      CA        AT
                                AACA  GTGAAACCCC  CTC
                                ||||  ||||||||||  |||
                                TTGT  CGCTTTGGGG  GAG
                                  AC         CG
GAM786  CYP51    3'  GAGACGGGGGTTTCACTATGTT 7616      C         A_
                                AACA AGTGAAACCCC  TCTC
                                |||| ||||||||||  ||||
                                TTGT TCACTTTGGGG  AGAG
                                  A          GC
GAM786  DAP      3'  GAGATGGGGGATCCTGTG    72946      T  AA
                                CACAG GA  CCCCATCTC
                                |||||| ||  |||||||||
                                GTGTC CT  GGGGTAGAG
                                  _  AG
GAM786  DFFB     3'  GAGACGGGGTTTCACCATGTT  88771     CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  DHFR     3'  GAGATGGGGTTTCACCATGTT  7648      CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  DSC3     3'  GAGACGGGGTTTCACTGTGTT  44622             A
                                AACACAGTGAAACCCC TCTC
                                |||||||||||||| ||||
                                TTGTGTCACTTTGGGG AGAG
                                        C
GAM786  DSC3     3'  GAGACGGGGTTTCACTGTGTT  44623             A
                                AACACAGTGAAACCCC TCTC
                                |||||||||||||| ||||
                                TTGTGTCACTTTGGGG AGAG
                                        C
GAM786  EHD2     3'  GAGACGGGGTTTCACCATGTT  28222     CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  EIF2S3   3'  GAGACGGGGTTTCAGCATGTT  9208      CAG       A
                                AACA   TGAAACCCC TCTC
                                ||||   ||||||||| ||||
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                                TTGT  ACTTTGGGG AGAG
                                  ACG       C
GAM786  EPB72   3' GAGACGGGGTTTCACCATGTT 15876     CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC        C
GAM786  EPB72   3' GAGATGGAGTTTCACTCTTGT 15877     C_      C
                                ACA  AGTGAAAC CCATCTC
                                |||  |||||||| |||||||
                                TGT  TCACTTTG GGTAGAG
                                  TC       A
GAM786  F2RL2   3' GAGACGGGGTTTCACCATGTT 15897     CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC        C
GAM786  FANCF    3' GAGACGGGGTTTCACCATG   42980    CA        A
                                CA  GTGAAACCCC TCTC
                                ||  |||||||||| ||||
                                GT  CACTTTGGGG AGAG
                                 AC        C
GAM786  FCAR    3' GAGATGGGGTTTCACTGTGTT 56574
                                AACACAGTGAAACCCCATCTC
                                |||||||||||||||||||||
                                TTGTGTCACTTTGGGGTAGAG

GAM786  FCAR    3' GACAGGGTTTCACCATGTT   10588     CA       CA
                                AACA  GTGAAACCC  TC
                                ||||  |||||||||  ||
                                TTGT  CACTTTGGG  AG
                                  AC        AC
GAM786  FCGR2A   3' GAGACAGGGTTTCGCAATGTT 80029     CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CGCTTTGGG  AGAG
                                  AA        AC
GAM786  FEZ1    3' GAGATGGGAGTTTCACCATGT  42869    CA     _
                                ACA  GTGAAAC CCCATCTC
                                |||  ||||||| ||||||||
                                TGT  CACTTTG GGGTAGAG
                                  AC      A
GAM786  FGF5    3' GAGACGGGGTTTCACCATGTT 53659     CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC        C
GAM786  FGF5    3' GAGACGGGGTTTCACCATGTT 53660     CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
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                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  FSHPRH1  5'  GAGACATTGGTCTCACTGTGTT 23067          A   CCA_
                                AACACAGTGA ACC    TCTC
                                |||||||||| |||    ||||
                                TTGTGTCACT TGG    AGAG
                                     C   TTAC
GAM786  FUT1     3'  GAGACGGGGTTTCATCGTGTT  5594        A        A
                                AACAC GTGAAACCCC TCTC
                                ||||| |||||||||| ||||
                                TTGTG TACTTTGGGG AGAG
                                  C         C
GAM786  FUT1     3'  GAGACAGGGTTTCACCATGTT  5592       CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  G6PC     3'  GAGATGGGATTTCATCATGTT  5661       CA     C
                                AACA  GTGAAA CCCATCTC
                                ||||  ||||||  ||||||||
                                TTGT  TACTTT GGGTAGAG
                                  AC     A
GAM786  GHR      3'  GAGACGGGGTTTCACCATGTT  5700       CA       A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  GM2A     3'  GAGATGGGGTTTCACCATGTT  68382      CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  GNE      3'  GACAGGGTTTCACCATGTT   19670      CA       CA
                                AACA  GTGAAACCC  TC
                                ||||  |||||||||  ||
                                TTGT  CACTTTGGG  AG
                                  AC        AC
GAM786  GPR4     3'  GAGACAGGGTCTCACTGTGTT  60578          A   CA
                                AACACAGTGA ACCC  TCTC
                                |||||||||| ||||  ||||
                                TTGTGTCACT TGGG  AGAG
                                     C    AC
GAM786  GPR81    3'  GACGGGGTTTCATTGTGTT   51749             A
                                AACACAGTGAAACCCC TC
                                |||||||||||||||| ||
                                TTGTGTTACTTTGGGG AG
                                        C
GAM786  GPR81    3'  GAGACAGGGTTTTGCCATGTT  51750      CA TG     CA
                                AACA  G  AAACCC  TCTC
                                ||||  |  ||||||  ||||
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                                TTGT  C  TTTGGG  AGAG
                                  AC GT     AC
GAM786  GRAF     3'  GAGATGGGGTTTTGCCATGTT  31237      CA TG
                                AACA  G  AAACCCCATCTC
                                ||||  |  ||||||||||||
                                TTGT  C  TTTGGGGTAGAG
                                  AC GT
GAM786  GRINL1A  3'  GAGATGGGGTCTTGCTCTGT   70062     C  TG A
                                ACA AG  A ACCCCATCTC
                                ||| ||  | ||||||||||
                                TGT TC  T TGGGGTAGAG
                                 C  GT C
GAM786  GRM7     5'  GAGATTGGGTTTCACCATGTT  7787       CA        C
                                AACA  GTGAAACCC ATCTC
                                ||||  ||||||||| |||||
                                TTGT  CACTTTGGG TAGAG
                                  AC        T
GAM786  HTR1D    3'  AGACGGGGTTTCATCATGTT   7834       CA        A
                                AACA  GTGAAACCCC TCT
                                ||||  |||||||||| |||
                                TTGT  TACTTTGGGG AGA
                                  AC         C
GAM786  HUNK     3'  ATGGGGTTTCGCCATGTT    28176      CA
                                AACA  GTGAAACCCCAT
                                ||||  ||||||||||||
                                TTGT  CGCTTTGGGGTA
                                  AC
GAM786  HUS1     3'  GAGACAGGGTCTCACTGTGTT  92739          A    CA
                                AACACAGTGA ACCC  TCTC
                                |||||||||| ||||  ||||
                                TTGTGTCACT TGGG  AGAG
                                     C    AC
GAM786  HYAL4    5'  GAGATGGGGTTTCACCGTGTT  25369       A
                                AACAC GTGAAACCCCATCTC
                                ||||| ||||||||||||||||
                                TTGTG CACTTTGGGGTAGAG
                                  C
GAM786  IGF1     3'  GAGACGGGGTTTTACCATGTT  7074       CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CATTTTGGGG AGAG
                                  AC         C
GAM786  IGF1     3'  GAGATGGGGTCTCGCACTGT   7075        AA__
                                ACAGTG    ACCCCATCTC
                                ||||||    ||||||||||
                                TGTCAC    TGGGGTAGAG
                                   GCTC
GAM786  IL11     3'  GAGACAGGGTTTCACCATGTT  7185       CA        CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
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                                TTGT  CACTTTGGG  AGAG
                                  AC         AC
GAM786  IMPA2    5'  GAGATGGGGCTTCGCCATG   96947    CA     A
                                CA  GTGAA CCCCATCTC
                                ||  ||||| |||||||||
                                GT  CGCTT GGGGTAGAG
                                 AC     C
GAM786  INMT     3'  GAGACGGAGTTTCGCTCTGT   23216     C       C  A
                                ACA AGTGAAAC CC TCTC
                                ||| |||||||| || ||||
                                TGT TCGCTTTG GG AGAG
                                  C       A  C
GAM786  INMT     3'  GATATGGGGTTTCACCGTGTT  23217       A          C
                                AACAC GTGAAACCCCAT TC
                                ||||| |||||||||||| ||
                                TTGTG CACTTTGGGGTA AG
                                   C          T
GAM786  JAK3     3'  GAGATGAGGTTTCACCATG    5831     CA       C
                                CA  GTGAAACC CATCTC
                                ||  |||||||| ||||||
                                GT  CACTTTGG GTAGAG
                                 AC       A
GAM786  JRK      3'  GAGACAGGGTCTCACTGTGTT  87827          A    CA
                                AACACAGTGA ACCC  TCTC
                                |||||||||| ||||  ||||
                                TTGTGTCACT TGGG  AGAG
                                      C   AC
GAM786  LLGL1    3'  GAGATGGGGTTTCACCATGTT  67419      CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  LNK      3'  GAGACAGGGTTTCACCATGTT  19645      CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  LTB4R    5'  GAGACGGGGTTTCACCATGTT  7464       CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  LYZ      3'  GAGACAGGGTTTCACCGTGTT  5895       A       CA
                                AACAC GTGAAACCC  TCTC
                                ||||| |||||||||  ||||
                                TTGTG CACTTTGGG  AGAG
                                  C        AC
GAM786  MAK      3'  GAGACAGGGTTTCACCATGTT  20947      CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
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                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  MDM2    3'  GAGACAGGGTTTCACCGTGTT  23497      A        CA
                                AACAC GTGAAACCC  TCTC
                                ||||| |||||||||  ||||
                                TTGTG CACTTTGGG  AGAG
                                   C        AC
GAM786  MEFV    3'  GAGACGGGGGTTTCACCATGTT 5938       CA        A_
                                AACA  GTGAAACCCC  TCTC
                                ||||  ||||||||||  ||||
                                TTGT  CACTTTGGGG  AGAG
                                  AC         GC
GAM786  MEN1    5'  AGATGGGGCACTGCTGTGT   56341        AAA
                                ACACAGTG   CCCCATCT
                                ||||||||   ||||||||
                                TGTGTCGT   GGGGTAGA
                                     CAC
GAM786  MHC2TA  3'  GAGACAGGGTTTTGCCGTGTT  5985       A TG     CA
                                AACAC G  AAACCC  TCTC
                                ||||| |  ||||||  ||||
                                TTGTG C  TTTGGG  AGAG
                                   C GT     AC
GAM786  MICB    3'  GAGACGGGGTTTCGCCAAGTT  21023     ACA        A
                                AAC   GTGAAACCCC TCTC
                                |||   |||||||||| ||||
                                TTG   CGCTTTGGGG AGAG
                                  AAC         C
GAM786  MLANA   3'  GAGACGGGGTTTCTCCATGTT  19763     CAGT       A
                                AACA    GAAACCCC TCTC
                                ||||    |||||||| ||||
                                TTGT    CTTTGGGG AGAG
                                  ACCT       C
GAM786  MLANA   3'  GAGATGGAGTTTCGCTTTTGTT 19764      C_       C
                                AACA  AGTGAAAC CCATCTC
                                ||||  |||||||| |||||||
                                TTGT  TCGCTTTG GGTAGAG
                                  TT       A
GAM786  MPL     3'  GAGACAGGGTTTTGCCATGTT  19355      CA TG     CA
                                AACA  G  AAACCC  TCTC
                                ||||  |  ||||||  ||||
                                TTGT  C  TTTGGG  AGAG
                                  AC GT     AC
GAM786  MRPL49  3'  GAGATGGGGTTTCACCATGTT  70169      CA
                                AACA  GTGAAACCCCATCTC
                                ||||  |||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  MTR     3'  GAGACAGGATTTCACTGTGTT  6018           C  CA
                                AACACAGTGAAA CC  TCTC
                                |||||||||||| ||  ||||
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                                TTGTGTCACTTT GG  AGAG
                                      A  AC
GAM786  NCOA6    5'  GAGGCGGGGTTTCGCCATGTT  26836     CA        AT
                                AACA  GTGAAACCCC  CTC
                                ||||  ||||||||||  |||
                                TTGT  CGCTTTGGGG  GAG
                                  AC         CG
GAM786  NCOA6    5'  GATGGGGTTTCATCATGTT   26837     CA
                                AACA  GTGAAACCCCATC
                                ||||  ||||||||||||
                                TTGT  TACTTTGGGGTAG
                                  AC
GAM786  NDUFS2   5'  GAGGGCGGCTTCACTGTG    17042         A  _  A
                                CACAGTGAA CC CC TC
                                ||||||||| || || ||
                                GTGTCACTT GG GG AG
                                      C  C  G
GAM786  PCDHA9   3'  GAGATGGGGTTTCACCGTGTT  49845       A
                                AACAC GTGAAACCCCATCTC
                                ||||| ||||||||||||||
                                TTGTG CACTTTGGGGTAGAG
                                   C
GAM786  PCDHA9   3'  GAGATGGGGTTTCATCATGTT  49846      CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  TACTTTGGGGTAGAG
                                  AC
GAM786  PCDHB11  3'  GAGACGGGGTTTCACCACGTT  38924     ACA        A
                                AAC   GTGAAACCCC TCTC
                                |||   |||||||||| ||||
                                TTG   CACTTTGGGG AGAG
                                  CAC         C
GAM786  PDGFB    3'  GAGATGGAGTTTGCTGTTG   12025   C    G   C
                                A ACAGT AAAC CCATCTC
                                | ||||| |||| |||||||
                                G TGTCG TTTG GGTAGAG
                                 T    _   A
GAM786  PER2     3'  GAGACAGGGTTTCACCATGTT  43352      CA        CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC         AC
GAM786  PEX14    3'  GAGATGGGGGCTCACTCC    64402   C    AA
                                A AGTGA  CCCCATCTC
                                | |||||  |||||||||
                                C TCACT  GGGGTAGAG
                                 C    CG
GAM786  PIGR     3'  GAGACAAAGTCTCACTGTGT   72998         A  CCCA
                                ACACAGTGA AC    TCTC
                                ||||||||| ||    ||||
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                                TGTGTCACT TG    AGAG
                                     C  AAAC
GAM786  PIGR     3'  GAGACAGGGTTTCACCGTGTT  72999       A        CA
                                AACAC GTGAAACCC  TCTC
                                ||||| |||||||||  ||||
                                TTGTG CACTTTGGG  AGAG
                                   C        AC
GAM786  PIGR     3'  GAGACAGGGTTTCGCCATGTT  73000      CA        CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CGCTTTGGG  AGAG
                                  AC        AC
GAM786  PIK3C2B  3'  GAGACGGGGTTTCACCATGTT  12101      CA         A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  PIK3CD   3'  GAGACGGGGGTTTCACCATGTT 18492      CA         A_
                                AACA  GTGAAACCCC  TCTC
                                ||||  ||||||||||  ||||
                                TTGT  CACTTTGGGG  AGAG
                                  AC         GC
GAM786  PIK3CD   3'  GAGATGGGGTCTTCCTCTGT   18493      T_  _
                                ACAG  GAA ACCCCATCTC
                                ||||  ||| ||||||||||
                                TGTC  CTT TGGGGTAGAG
                                  TC   C
GAM786  POU2AF1  3'  GAGACGGGGTTTCACCATGTT  21743      CA         A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  PPP1R12B 3'  GAGATGGGGTTTTGCCATGTT  50356      CA TG
                                AACA  G  AAACCCCATCTC
                                ||||  |  ||||||||||||
                                TTGT  C  TTTGGGGTAGAG
                                  AC GT
GAM786  PRKR     3'  AGACAGGGTTTCACCATGTT   12339      CA        CA
                                AACA  GTGAAACCC  TCT
                                ||||  |||||||||  |||
                                TTGT  CACTTTGGG  AGA
                                  AC        AC
GAM786  PRKWNK3  3'  GATGGGGTTTCACTATGTT    62233      C
                                AACA AGTGAAACCCCATC
                                |||| ||||||||||||||
                                TTGT TCACTTTGGGGTAG
                                  A
GAM786  PTGIS    3'  GAGACGGGGTTTCCCCATGTT  8209       CAGT       A
                                AACA    GAAACCCC TCTC
                                ||||    |||||||| ||||
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                                TTGT   CTTTGGGG AGAG
                                  ACCC      C
GAM786  PTGIS    3' GAGATGGGATTTCACCGT   8210    A    C
                                AC GTGAAA CCCATCTC
                                || |||||| ||||||||
                                TG CACTTT GGGTAGAG
                                 C     A
GAM786  RAB36    3' GAGAGAGGTTTCACCATGTT  18169    CA     CCA
                                AACA  GTGAAACC  TCTC
                                ||||  ||||||||  ||||
                                TTGT  CACTTTGG  AGAG
                                  AC      AG_
GAM786  RAB36    3' GAGATGGGGTTTCTCCATGTT  18171    CAGT
                                AACA   GAAACCCCATCTC
                                ||||   ||||||||||||
                                TTGT   CTTTGGGGTAGAG
                                  ACCT
GAM786  RABL2A   3' GAGACGGGGTTTCACCATGTT  23996    CA       A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC        C
GAM786  RABL2B   3' GAGACGGGGTTTCACCATGTT  23978    CA       A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC        C
GAM786  RAD52    3' GAGACGGGGTCTGGCTGTGTT  57032      GAA    A
                                AACACAGT   ACCCC TCTC
                                ||||||||   ||||| ||||
                                TTGTGTCG   TGGGG AGAG
                                    GTC    C
GAM786  RAD52    3' GAGACGGGGTCTGGCTGTGTT  57033      GAA    A
                                AACACAGT   ACCCC TCTC
                                ||||||||   ||||| ||||
                                TTGTGTCG   TGGGG AGAG
                                    GTC    C
GAM786  RAD52    3' GAGACGGGGTCTGGCTGTGTT  57034      GAA    A
                                AACACAGT   ACCCC TCTC
                                ||||||||   ||||| ||||
                                TTGTGTCG   TGGGG AGAG
                                    GTC    C
GAM786  RAD52    3' GAGACGGGGTCTGGCTGTGTT  57035      GAA    A
                                AACACAGT   ACCCC TCTC
                                ||||||||   ||||| ||||
                                TTGTGTCG   TGGGG AGAG
                                    GTC    C
GAM786  RBBP9    3' GAGACAGGGTTTCACCATGTT  70691    CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
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                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  RBM8A    3'  GAGATAGAGTCTTGCTGTGTT  18806        TG A  CCC
                                AACACAG  A AC   ATCTC
                                |||||||  | ||   |||||
                                TTGTGTC  T TG   TAGAG
                                   GT C  AGA
GAM786  RBM8A    3'  GAGATGGGGTCTTGCTGTGTT  18807        TG A
                                AACACAG  A ACCCCATCTC
                                |||||||  | ||||||||||
                                TTGTGTC  T TGGGGTAGAG
                                   GT C
GAM786  RGR      3'  GAGATAAGGTCTCATTGTG   12860         A   CC
                                CACAGTGA ACC  ATCTC
                                ||||||||| |||  |||||
                                GTGTTACT TGG  TAGAG
                                     C   AA
GAM786  RGS9     5'  AGACGGGGTTTTGTCATGTT  15169      CA TG      A
                                AACA  G  AAACCCC TCT
                                ||||  |  ||||||| |||
                                TTGT  T  TTTGGGG AGA
                                  AC GT      C
GAM786  RHD      3'  AGATGGGGTTTCACCATGTT  32807      CA
                                AACA  GTGAAACCCCATCT
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGA
                                  AC
GAM786  RHD      3'  GACAGGGTTTCACCATGTT   32828      CA       CA
                                AACA  GTGAAACCC  TC
                                ||||  |||||||||  ||
                                TTGT  CACTTTGGG  AG
                                  AC        AC
GAM786  RHD      3'  GACAGGGTTTCACCATGTT   32829      CA       CA
                                AACA  GTGAAACCC  TC
                                ||||  |||||||||  ||
                                TTGT  CACTTTGGG  AG
                                  AC        AC
GAM786  RHD      3'  AGATGGGGTTTCACCATGTT  33132      CA
                                AACA  GTGAAACCCCATCT
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGA
                                  AC
GAM786  RP2      3'  GAGATGGGGTTTTTCCAC    23603      ___
                                GTG   AAACCCCATCTC
                                |||   ||||||||||||
                                CAC   TTTGGGGTAGAG
                                  CTT
GAM786  RPH3AL   3'  GAGATGGGGTTTCTCCATGTT  23734      CAGT
                                AACA   GAAACCCCATCTC
                                ||||   ||||||||||||
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                                TTGT   CTTTGGGGTAGAG
                                  ACCT
GAM786  RPP30    3'  GAGACGGGGTTTCACCGTGTT  22199      A        A
                                AACAC GTGAAACCCC TCTC
                                ||||| |||||||||| ||||
                                TTGTG CACTTTGGGG AGAG
                                  C         C
GAM786  SAS      3'  GAGACAGGGTTTCACCATGTT  21101      CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  SCML2    3'  GAGATGGAGTTTCACTCTTGT  21425      C_       C
                                ACA  AGTGAAAC CCATCTC
                                |||  |||||||| |||||||
                                TGT  TCACTTTG GGTAGAG
                                  TC       A
GAM786  SCML2    3'  GAGATGGGGTTTCTCCATGTT  21426      CAGT
                                AACA   GAAACCCCATCTC
                                ||||   ||||||||||||
                                TTGT   CTTTGGGGTAGAG
                                  ACCT
GAM786  SEDL     3'  GAGATGGAGTTTCGCTCTGTT  28099      C        C
                                AACA AGTGAAAC CCATCTC
                                |||| |||||||| |||||||
                                TTGT TCGCTTTG GGTAGAG
                                  C       A
GAM786  SERPINB9 3'  GAGACGGGGTTTCACCGTGTT  16021      A        A
                                AACAC GTGAAACCCC TCTC
                                ||||| |||||||||| ||||
                                TTGTG CACTTTGGGG AGAG
                                  C         C
GAM786  SH3GL3   5'  GAGATGGGTTTCACCATGTT   13108      CA       C
                                AACA  GTGAAACCC ATCTC
                                ||||  ||||||||| |||||
                                TTGT  CACTTTGGG TAGAG
                                  AC        _
GAM786  SHOX     3'  GAGATGGGGTTTGACCATGTT  6576       CA  G
                                AACA  GT AAACCCCATCTC
                                ||||  || ||||||||||||
                                TTGT  CA TTTGGGGTAGAG
                                  AC  G
GAM786  SIGLEC11 3'  GAGACAGGGTTTTGCCATGTT  54654      CA TG    CA
                                AACA  G  AAACCC  TCTC
                                ||||  |  ||||||  ||||
                                TTGT  C  TTTGGG  AGAG
                                  AC GT     AC
GAM786  SIL      5'  GAGACGGGGTTTCACCATGTT  13155      CA       A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
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                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  SLC15A1  3'  GAGATGGGGTTTCACCATGTT  18642      CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  SLC17A5  3'  GAGATGGGGTCTCGTTTTGT  25833     C     A
                                ACA AGTGA ACCCCATCTC
                                ||| ||||| ||||||||||
                                TGT TTGCT TGGGGTAGAG
                                  T    C
GAM786  SLC3A2   5'  GAGACGGGGTCTGACTGTGTT  11522         GAA     A
                                AACACAGT   ACCCC TCTC
                                ||||||||   ||||| ||||
                                TTGTGTCA   TGGGG AGAG
                                     GTC    C
GAM786  SLC3A2   5'  GAGTTGGGGTCTCACTGTGTT  11523          A      T
                                AACACAGTGA ACCCCA CTC
                                |||||||||| |||||| |||
                                TTGTGTCACT TGGGGT GAG
                                      C     T
GAM786  SMAC     5'  GAGATGGGGTTTCACCATGTT  58001      CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  SNAP23   3'  GAGACAGGGTTTCACCATGT   15139     CA        CA
                                ACA  GTGAAACCC  TCTC
                                |||  |||||||||  ||||
                                TGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  SNX15    3'  GAGTTGGAGTCTCGCTGTGT   74122         A  C   T
                                ACACAGTGA AC CCA CTC
                                ||||||||| || ||| |||
                                TGTGTCGCT TG GGT GAG
                                      C  A   T
GAM786  SPN      3'  GAGACAGAGTTTCGCTTTGT   13375     C       CCCA
                                ACA AGTGAAAC    TCTC
                                ||| ||||||||    ||||
                                TGT TCGCTTTG    AGAG
                                  T       AGAC
GAM786  SPN      3'  GAGATGGGGTTTCACCATGTT  13376      CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  STARD4   3'  GAGATGTGGTCACACTGTGTT  58247         AA   C
                                AACACAGTG  ACC CATCTC
                                |||||||||  ||| ||||||
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                                TTGTGTCAC  TGG GTAGAG
                                     AC   T
GAM786  TAF11    3'  GAGATGGGGTCTTGCTTTGTT  20121     C  TG A
                                AACA AG  A ACCCCATCTC
                                |||| ||  | ||||||||||
                                TTGT TC  T TGGGGTAGAG
                                  T  GT C
GAM786  TAPBP    3'  GAGACGGGGTTTCACCATGTT  13562     CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  TAPBP    3'  GAGACGGGGTTTCACCGTGTT  13563      A        A
                                AACAC GTGAAACCCC TCTC
                                ||||| |||||||||| ||||
                                TTGTG CACTTTGGGG AGAG
                                   C         C
GAM786  TAPBP    3'  GAGACGGGGTTTCACCGTGTT  13564      A        A
                                AACAC GTGAAACCCC TCTC
                                ||||| |||||||||| ||||
                                TTGTG CACTTTGGGG AGAG
                                   C         C
GAM786  TAT      3'  GAGACAGGGTTTCACCATGTT  6255       CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  TBXA2R   3'  GAGACGGGGTTTCACCGTGTT  8358       A        A
                                AACAC GTGAAACCCC TCTC
                                ||||| |||||||||| ||||
                                TTGTG CACTTTGGGG AGAG
                                   C         C
GAM786  TEM7     3'  GAGACAGGGTCTCACTGTGT   40261        A   CA
                                ACACAGTGA ACCC  TCTC
                                ||||||||| ||||  ||||
                                TGTGTCACT TGGG  AGAG
                                     C    AC
GAM786  TERF1    3'  GAGGCGGGGTTTCACCATG   34394    CA        AT
                                CA  GTGAAACCCC  CTC
                                ||  ||||||||||  |||
                                GT  CACTTTGGGG  GAG
                                  AC         CG
GAM786  TERF2    3'  GAGACGGGGTTTCACCGTGTT  20152      A        A
                                AACAC GTGAAACCCC TCTC
                                ||||| |||||||||| ||||
                                TTGTG CACTTTGGGG AGAG
                                   C         C
GAM786  TIM3     3'  GAGACAGGGTTTCACCATGTT  52356     CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
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                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  TMPRSS3  3'  GAGACAGGGTTTCACCATGTT  44025      CA        CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  TNFAIP2  3'  GAGACAGGGTCTTGCTGTGTT  21921        TG A    CA
                                AACACAG  A ACCC  TCTC
                                |||||||  | ||||  ||||
                                TTGTGTC  T TGGG  AGAG
                                   GT C    AC
GAM786  TNFRSF10B 3'  GAGACGGGGTTTCACCATGTT  15227      CA         A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  TOP3B    5'  GAGATGGGCCCGCCATGTG   15442      __   AAAC
                                CACA  GTG    CCCATCTC
                                ||||  |||    ||||||||
                                GTGT  CGC    GGGTAGAG
                                  AC   CC__
GAM786  TP53     3'  GAGATGGGGTCTCACAGTGTT  6801       A    A
                                AACAC GTGA ACCCCATCTC
                                ||||| |||| ||||||||||
                                TTGTG CACT TGGGGTAGAG
                                   A    C
GAM786  TPMT     3'  GAGACGGGGTTTCACCATGTT  6310       CA         A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  TPMT     3'  GAGATGGAGTTTCGTTCTTGT  6311       ___      C
                                ACAG   TGAAAC CCATCTC
                                ||||   |||||| |||||||
                                TGTT   GCTTTG GGTAGAG
                                  CTT      A
GAM786  TRIM9    5'  GAGACGGAGTTTCGCTCTTGT  31453     C_       C  A
                                ACA  AGTGAAAC CC TCTC
                                |||  |||||||| || ||||
                                TGT  TCGCTTTG GG AGAG
                                  TC       A  C
GAM786  TRPM6    3'  GAGATGGGGTTTCACCATGTT  35033      CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  TRPV1    3'  GAGACGGGGTTTCACCATGTT  55675      CA         A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
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                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  TRPV1    3'  GAGACGGGGTTTCACCATGTT  55676     CA         A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  TRPV1    3'  GATATGGGGTTTCGCCATGTT  55677     CA          C
                                AACA  GTGAAACCCCAT TC
                                ||||  |||||||||||| ||
                                TTGT  CGCTTTGGGGTA AG
                                  AC          T
GAM786  UGDH     3'  GAGACAGGGTTTCACCATGTG  13998     __         CA
                                CACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                GTGT  CACTTTGGG  AGAG
                                  AC         AC
GAM786  VENTX2   3'  ATGGGGTTTCACCATGTT    27853     CA
                                AACA  GTGAAACCCCAT
                                ||||  ||||||||||||
                                TTGT  CACTTTGGGGTA
                                  AC
GAM786  VHL      3'  GAGACGGGGTTTCACCATGTT  6858      CA         A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  VIPR2    3'  GAGACAGGGTTTCACCATGTT  14063     CA         CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC         AC
GAM786  XRCC2    3'  GAGACGGGGTTTCACCATGTT  19501     CA         A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  ZNF157   3'  AGACGGGTTTCACCATGTT    14323     CA         CA
                                AACA  GTGAAACCC  TCT
                                ||||  |||||||||  |||
                                TTGT  CACTTTGGG  AGA
                                  AC         C_
GAM786  ZNF253   3'  GAGATGGAGTTTCACTCTTGT  41079     C_         C
                                ACA  AGTGAAAC CCATCTC
                                |||  |||||||| |||||||
                                TGT  TCACTTTG GGTAGAG
                                  TC         A
GAM786  ZNF264   3'  GAGACGGGGTTTCACCATGTT  14215     CA         A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
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                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  ZNF74    5'  GAGACGGGGTTTTGCCATGTT  14261      CA TG      A
                                AACA  G  AAACCCC TCTC
                                ||||  |  ||||||| ||||
                                TTGT  C  TTTGGGG AGAG
                                  AC GT      C
GAM786  AAK1     3'  GAGATGGGGTTTCTCCATGTT  30524      CAGT
                                AACA   GAAACCCCATCTC
                                ||||   ||||||||||||
                                TTGT   CTTTGGGGTAGAG
                                  ACCT
GAM786  ANKT     3'  GAGACAGGGTCTCACTGTGTT  33457          A   CA
                                AACACAGTGA ACCC  TCTC
                                |||||||||| ||||  ||||
                                TTGTGTCACT TGGG  AGAG
                                      C   AC
GAM786  AP1S3    3'  GGGATGGGATCTCACTCTGT   75428     C    AAC
                                ACA AGTGA   CCCATCTC
                                ||| |||||   ||||||||
                                TGT TCACT   GGGTAGGG
                                  C    CTA
GAM786  AP3S2    3'  GAGACAGGGTTTCACCATGTT  20652      CA        CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  APOL2    3'  GAGACGGGGTTTCACTGTGTT  48789             A
                                AACACAGTGAAACCCC TCTC
                                |||||||||||||||| ||||
                                TTGTGTCACTTTGGGG AGAG
                                          C
GAM786  ARHF     3'  GAGACAGGGTTTCACCATGTT  39269      CA        CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  ARHGAP11A 3' GAGACGGTTTCACCGTGTT   29448       A       CCA
                                AACAC GTGAAACC   TCTC
                                ||||| ||||||||   ||||
                                TTGTG CACTTTGG   AGAG
                                  C       C__
GAM786  ARHGAP5  5'  GAGATGGGGTTTCTCCATGTT  77602      CAGT
                                AACA   GAAACCCCATCTC
                                ||||   ||||||||||||
                                TTGT   CTTTGGGGTAGAG
                                  ACCT
GAM786  ASE-1    3'  GAGATGGGGTTTCACCACGTT  24980     ACA
                                AAC   GTGAAACCCCATCTC
                                |||   ||||||||||||||
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                                TTG  CACTTTGGGGTAGAG
                                  CAC
GAM786  ATP1B4   3'  GAGACAGGGTTTCACCATGTT  24844     CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  ATP1B4   3'  GAGATGGAGTTTCGCTGTTGT  24845    _       C
                                ACA CAGTGAAAC CCATCTC
                                ||| ||||||||| |||||||
                                TGT GTCGCTTTG GGTAGAG
                                  T        A
GAM786  BA108L7.2 3'  GAGATGGGGGTTTCACCATGTT 49075     CA       _
                                AACA  GTGAAACCCC ATCTC
                                ||||  |||||||||| |||||
                                TTGT  CACTTTGGGG TAGAG
                                  AC         G
GAM786  BAGE     3'  GAGATGGAGTTTCACTGTGT   8639          C
                                ACACAGTGAAAC CCATCTC
                                |||||||||||| |||||||
                                TGTGTCACTTTG GGTAGAG
                                      A
GAM786  BLCAP    3'  GAGGGGGCCTCATTGTGT    22944         AA   A
                                ACACAGTGA  CCCC TC
                                |||||||||  |||| ||
                                TGTGTTACT  GGGG AG
                                     CC    G
GAM786  BNIP-S   3'  GAGACGGGGTTTCACCATGTT  57102     CA       A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  BRAG     3'  GAGATGGGGTCTCGCCGTGTT  30101      A   A
                                AACAC GTGA ACCCCATCTC
                                ||||| |||| ||||||||||
                                TTGTG CGCT TGGGGTAGAG
                                  C    C
GAM786  C13orf1  3'  GAGATGGGGTTTCACCATGTT  40362     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  C1orf24  3'  GAGATGGGTTTTCACCATGTT  54790     CA    C
                                AACA  GTGAAA CCCATCTC
                                ||||  |||||| ||||||||
                                TTGT  CACTTT GGGTAGAG
                                  AC     T
GAM786  C1QR1    3'  GAGATGATGCACTGTGTT    24870         AAACCC
                                AACACAGTG     CATCTC
                                |||||||||     ||||||
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                                TTGTGTCAC     GTAGAG
                                     GTA___
GAM786  C20orf142 3'  GAGATGGGGTTTCTCCATGTT  75283      CAGT
                                AACA    GAAACCCCATCTC
                                ||||    ||||||||||||||
                                TTGT    CTTTGGGGTAGAG
                                  ACCT
GAM786  C21orf25  3'  GAGATGGAGTTTCACTCTGTT  64295      C       C
                                AACA AGTGAAAC CCATCTC
                                |||| |||||||| |||||||
                                TTGT TCACTTTG GGTAGAG
                                  C       A
GAM786  C6orf5    3'  GAGACAGGGTTTCATATTG    31991    CA       CA
                                CA  GTGAAACCC  TCTC
                                ||  |||||||||  ||||
                                GT  TACTTTGGG  AGAG
                                 TA        AC
GAM786  C6orf5    3'  GAGACAGGGTTTTGCCATGTT  31992      CA TG     CA
                                AACA  G  AAACCC  TCTC
                                ||||  |  ||||||  ||||
                                TTGT  C  TTTGGG  AGAG
                                  AC GT     AC
GAM786  C9orf9    3'  GAGATGGAGTTTCACTCTGT   39022     C       C
                                ACA AGTGAAAC CCATCTC
                                ||| |||||||| |||||||
                                TGT TCACTTTG GGTAGAG
                                  C       A
GAM786  CCRN4L    3'  GAGACGGGGTTTCACCGTGTT  25068       A        A
                                AACAC GTGAAACCCC TCTC
                                ||||| |||||||||| ||||
                                TTGTG CACTTTGGGG AGAG
                                   C         C
GAM786  CDC14B    3'  GAGACAGGGTTTCACCATGTT  14777      CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  CEACAM8   3'  GAGACGGGGTTTCACTGTG    10181            A
                                CACAGTGAAACCCC TCTC
                                |||||||||||||| ||||
                                GTGTCACTTTGGGG AGAG
                                         C
GAM786  CENPH     3'  GAGACGGGGTTTCACCGTGTT  43566       A        A
                                AACAC GTGAAACCCC TCTC
                                ||||| |||||||||| ||||
                                TTGTG CACTTTGGGG AGAG
                                   C         C
GAM786  CHSY1     3'  GAGACGGGGTTTCACCATG    30569     CA        A
                                CA  GTGAAACCCC TCTC
                                ||  |||||||||| ||||
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                                GT  CACTTTGGGG AGAG
                                 AC         C
GAM786  CIP29    3'  GAGACGGGGTTTCACCATGTT  51377      CA         A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  COLEC12  3'  GAGAGGGGTTTCACAGTGTT   56103       A         A
                                AACAC GTGAAACCCC TCTC
                                ||||| |||||||||| ||||
                                TTGTG CACTTTGGGG AGAG
                                  A         _
GAM786  CPSF2    3'  GAGACAGGGTTTCACCATGTT  62270      CA        CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC         AC
GAM786  CPSF2    3'  GAGACGGGGTTTCTCCATGTT  62271      CAGT       A
                                AACA    GAAACCCC TCTC
                                ||||    |||||||| ||||
                                TTGT    CTTTGGGG AGAG
                                  ACCT       C
GAM786  DBR1     3'  GACAGGGTTTCACCGTGTT   33065       A         CA
                                AACAC GTGAAACCC  TC
                                ||||| |||||||||  ||
                                TTGTG CACTTTGGG  AG
                                  C         AC
GAM786  DBR1     3'  GAGATGGAGTTTCACTCTTGT  33066     C_       C
                                ACA  AGTGAAAC CCATCTC
                                |||  |||||||| |||||||
                                TGT  TCACTTTG GGTAGAG
                                  TC       A
GAM786  DCOHM    3'  GAGATGGAGTTTCGCTCTTGT  50523     C_       C
                                ACA  AGTGAAAC CCATCTC
                                |||  |||||||| |||||||
                                TGT  TCGCTTTG GGTAGAG
                                  TC       A
GAM786  DCOHM    3'  GAGATGGGGGTCTCACTATG   50524     C     AA_
                                CA AGTGA   CCCCATCTC
                                || |||||   |||||||||
                                GT TCACT   GGGGTAGAG
                                 A    CTG
GAM786  DCOHM    3'  GAGATGGGGTCTCGTTCTGT   50525      __   A
                                ACAG  TGA ACCCCATCTC
                                ||||  ||| ||||||||||
                                TGTC  GCT TGGGGTAGAG
                                  TT   C
GAM786  DCOHM    3'  GAGATGGGGTTTCGCCATGTT  50526      CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
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                                TTGT  CGCTTTGGGGTAGAG
                                  AC
GAM786  DKFZp434A2417 3'  GAGACGGGGTTTCTCCATGTT  66679      CAGT       A
                                AACA    GAAACCCC TCTC
                                ||||    |||||||| ||||
                                TTGT    CTTTGGGG AGAG
                                  ACCT       C
GAM786  DKFZP434B044 3'  GAGATGGGGTTTCATTATGTT  49718      C
                                AACA AGTGAAACCCCATCTC
                                |||| ||||||||||||||||
                                TTGT TTACTTTGGGGTAGAG
                                  A
GAM786  DKFZP434D146 3'  GAGACAGGGTTTCATCATGTT  32135      CA        CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  TACTTTGGG  AGAG
                                  AC        AC
GAM786  DKFZP434F0318 3'  GAGACAGGGTTTCGCCATGTT  48758      CA        CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CGCTTTGGG  AGAG
                                  AC        AC
GAM786  DKFZp434F1719 3'  GAGATGGGATTTCGCCATGTT  51015      CA     C
                                AACA  GTGAAA CCCATCTC
                                ||||  ||||||  ||||||||
                                TTGT  CGCTTT GGGTAGAG
                                  AC     A
GAM786  DKFZp547G183 3'  GAGATGGGGCAACTGAGT    38643    A   GAAA
                                AC CAGT    CCCCATCTC
                                || ||||    |||||||||
                                TG GTCA    GGGGTAGAG
                                 A    AC__
GAM786  DKFZp547H025 3'  GAGATGAGGTTTCACCATGTT  39773      CA       C
                                AACA  GTGAAACC CATCTC
                                ||||  ||||||||  ||||||
                                TTGT  CACTTTGG GTAGAG
                                  AC       A
GAM786  DKFZP564G092 5'  GAGACGGAGTTTCGCTCTTGT  32160     C_       C  A
                                ACA  AGTGAAAC CC TCTC
                                |||  ||||||||  ||  ||||
                                TGT  TCGCTTTG GG AGAG
                                  TC       A  C
GAM786  DKFZP564O0423 3'  GAGATGGGGTCTCACTATGTT  93350      C     A
                                AACA AGTGA ACCCCATCTC
                                |||| |||||  ||||||||||
                                TTGT TCACT TGGGGTAGAG
                                  A     C
GAM786  DKFZP586A0522 3'  GAGACAGGGTCTCACTGTGTT  26727          A    CA
                                AACACAGTGA ACCC  TCTC
                                ||||||||||  ||||  ||||
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                                TTGTGTCACT TGGG  AGAG
                                      C    AC
GAM786  DKFZp761J139 5'  GAGATGGGGTTTGACCATGTT  51106      CA  G
                                AACA  GT AAACCCCATCTC
                                ||||  || ||||||||||||
                                TTGT  CA TTTGGGGTAGAG
                                  AC  G
GAM786  DKFZp761O0113 5'  GAGACGGGGTTTCTCCATGTT  37893      CAGT       A
                                AACA    GAAACCCC TCTC
                                ||||    |||||||| ||||
                                TTGT    CTTTGGGG AGAG
                                  ACCT       C
GAM786  DKFZp761O0113 5'  GAGATGGAGTTTCGCTCTTGT  37894     C_       C
                                ACA  AGTGAAAC CCATCTC
                                |||  |||||||| |||||||
                                TGT  TCGCTTTG GGTAGAG
                                  TC       A
GAM786  DKFZp762P2111 3'  AGATGGAGTTTCACTCTTGT   87623     C_       C
                                ACA  AGTGAAAC CCATCT
                                |||  |||||||| ||||||
                                TGT  TCACTTTG GGTAGA
                                  TC       A
GAM786  DKFZp762P2111 3'  GAGACAGGGTTTCATCATGTT  87635      CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  TACTTTGGG  AGAG
                                  AC        AC
GAM786  DSCR6    3'  GAGACTCGGTTTCACCATGTT  39068      CA       CCA
                                AACA  GTGAAACC   TCTC
                                ||||  ||||||||   ||||
                                TTGT  CACTTTGG   AGAG
                                  AC       CTC
GAM786  EREG     3'  GAGGCGGGGTTTCACCATGTT  9307       CA        AT
                                AACA  GTGAAACCCC  CTC
                                ||||  ||||||||||  |||
                                TTGT  CACTTTGGGG  GAG
                                  AC         CG
GAM786  ERO1L    3'  GAGACAAGGTTTTGCTGTGTT  28159        TG    CCA
                                AACACAG  AAACC   TCTC
                                |||||||  |||||   ||||
                                TTGTGTC  TTTGG   AGAG
                                    GT     AAC
GAM786  EVI5     3'  GAGACAGGTGTCTCACTGTGTT 20209          A  _  CA
                                AACACAGTGA AC CC  TCTC
                                |||||||||| || ||  ||||
                                TTGTGTCACT TG GG  AGAG
                                      C  T  AC
GAM786  EVI5     3'  GAGATGGGGTTTCACCATGTT  20211      CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
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                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  EVI5     3'  GAGATGGGGTTTCGCTATGTT  20212      C
                                AACA AGTGAAACCCCATCTC
                                |||| ||||||||||||||||
                                TTGT TCGCTTTGGGGTAGAG
                                  A
GAM786  FBP17    3'  GAGACAGGGTTTCACCGTGTT  73150      A        CA
                                AACAC GTGAAACCC  TCTC
                                ||||| |||||||||  ||||
                                TTGTG CACTTTGGG  AGAG
                                  C        AC
GAM786  FER1L4   3'  GAGACAGGGTTTCACCATGTT  48122      CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  FKBP9    3'  GAGACGGGGTTTCACCGTGTT  95716      A        A
                                AACAC GTGAAACCCC TCTC
                                ||||| |||||||||| ||||
                                TTGTG CACTTTGGGG AGAG
                                  C         C
GAM786  FLJ10101 3'  GAGATAAGGTCTTGCTGTGT   45600      TG A   CC
                                ACACAG  A ACC  ATCTC
                                ||||||  | |||  |||||
                                TGTGTC  T TGG  TAGAG
                                   GT C   AA
GAM786  FLJ10232 5'  GAGATGGGGTTTTGCTATGTT  36380      C  TG
                                AACA AG  AAACCCCATCTC
                                |||| ||  ||||||||||||
                                TTGT TC  TTTGGGGTAGAG
                                  A  GT
GAM786  FLJ10298 3'  GAGACGGGGTTTCACCATGTT  36458      CA       A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  FLJ10346 5'  GAGGCAGGGTTTCACCATGTT  36524      CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  GGAG
                                  AC        AC
GAM786  FLJ10535 3'  GAGACGGGGTTTCATTATGTT  36747      C        A
                                AACA AGTGAAACCCC TCTC
                                |||| |||||||||| ||||
                                TTGT TTACTTTGGGG AGAG
                                  A         C
GAM786  FLJ10535 3'  GAGATGGGGTTTCACCATGTT  36748      CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
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                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  FLJ10560 3' GAGACGGGGTTTCACCGTGTT  36795      A        A
                                AACAC GTGAAACCCC TCTC
                                ||||| |||||||||| ||||
                                TTGTG CACTTTGGGG AGAG
                                  C         C
GAM786  FLJ10713 3' GAGATGGGGTTTCACCATGTT  37003      CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  FLJ10901 3' GAGATGGGGTTTCATCATGTT  37363      CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  TACTTTGGGGTAGAG
                                  AC
GAM786  FLJ10956 3' GAGACGGGGTTTCACCATGTT  37467      CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  FLJ11186 3' GAGATGGGGTTTCGTCATGTT  37726      CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  TGCTTTGGGGTAGAG
                                  AC
GAM786  FLJ11193 3' GAGATGGGGTCTCACCATGTT  37750      CA   A
                                AACA  GTGA ACCCCATCTC
                                ||||  |||| ||||||||||
                                TTGT  CACT TGGGGTAGAG
                                  AC   C
GAM786  FLJ12363 3' GATGGGGTTTCACCATGTT    50636      CA
                                AACA  GTGAAACCCCATC
                                ||||  |||||||||||||
                                TTGT  CACTTTGGGGTAG
                                  AC
GAM786  FLJ12581 3' GAGACAGGGTTTCACTGTGTT  46335            CA
                                AACACAGTGAAACCC  TCTC
                                ||||||||||||||  ||||
                                TTGTGTCACTTTGGG  AGAG
                                       AC
GAM786  FLJ12649 3' GAGATAGGGTTTTACCATGTT  45091      CA        C
                                AACA  GTGAAACCC ATCTC
                                ||||  ||||||||| |||||
                                TTGT  CATTTTGGG TAGAG
                                  AC        A
GAM786  FLJ12668 3' GAGATGAGGTTTCACCTTGTT  47159      CA       C
                                AACA  GTGAAACC CATCTC
                                ||||  |||||||| ||||||
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                                TTGT  CACTTTGG GTAGAG
                                  TC       A
GAM786  FLJ12687  3'  GAGACAGGGTTTCACCATGTT  46751     CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  FLJ12876  3'  GAGACGGGGTTTCACTGTG   43092           A
                                CACAGTGAAACCCC TCTC
                                |||||||||||||| ||||
                                GTGTCACTTTGGGG AGAG
                                         C
GAM786  FLJ12891  3'  GAGACGGGGTCTTGTTGTGT   46924       TG A    A
                                ACACAG  A ACCCC TCTC
                                ||||||  | ||||| ||||
                                TGTGTT  T TGGGG AGAG
                                   GT C    C
GAM786  FLJ12903  3'  GAGACGGAGTTTCGCTGTTGT  43071    _       C  A
                                ACA CAGTGAAAC CC TCTC
                                ||| ||||||||| || ||||
                                TGT GTCGCTTTG GG AGAG
                                  T        A  C
GAM786  FLJ12960  3'  GAGATGGGGTTTCACCGT    45298    A
                                AC GTGAAACCCCATCTC
                                || ||||||||||||||
                                TG CACTTTGGGGTAGAG
                                 C
GAM786  FLJ12973  3'  GAGATGGGGTTTCATCATGTT  46642     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  TACTTTGGGGTAGAG
                                  AC
GAM786  FLJ12975  3'  AGACGGGGTTTCGCCTTGTT   70180     CA       A
                                AACA  GTGAAACCCC TCT
                                ||||  |||||||||| |||
                                TTGT  CGCTTTGGGG AGA
                                  TC        C
GAM786  FLJ13072  5'  GAGACAGGGTTTCACCATGTT  91391     CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  FLJ13188  3'  GAGACAGAGTTTTGCTGTGTT  42190       TG   CCCA
                                AACACAG  AAAC   TCTC
                                |||||||  ||||   ||||
                                TTGTGTC  TTTG   AGAG
                                   GT   AGAC
GAM786  FLJ13305  5'  GAGATGGGGTTTCACCATGTT  91711     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
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                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  FLJ13456 3' GAGACAGAGTTTCACTCTGT  66547    C      CCCA
                                ACA AGTGAAAC   TCTC
                                ||| ||||||||   ||||
                                TGT TCACTTTG   AGAG
                                  C       AGAC
GAM786  FLJ13769 5' GAGATGGGGTTTCACTATGTT  47250    C
                                AACA AGTGAAACCCCATCTC
                                |||| ||||||||||||||||
                                TTGT TCACTTTGGGGTAGAG
                                  A
GAM786  FLJ13952 3' GAGACGGGTTTCACCACGTT  46014    ACA       CA
                                AAC   GTGAAACCC  TCTC
                                |||   |||||||||  ||||
                                TTG   CACTTTGGG  AGAG
                                  CAC       C_
GAM786  FLJ14442 3' GAGATGGGGTTTTACCATGTT  52384    CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||||
                                TTGT  CATTTTGGGGTAGAG
                                  AC
GAM786  FLJ14950 3' GAGACAGGGTTTCACCATGTT  52789    CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  FLJ14957 3' GAGACGGGGTTTCACCATGTT  52820    CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC        C
GAM786  FLJ14957 3' GAGATGGAGTTTCATTCTTGT  52821    C_      C
                                ACA  AGTGAAAC CCATCTC
                                |||  |||||||| |||||||
                                TGT  TTACTTTG GGTAGAG
                                  TC       A
GAM786  FLJ20033 3' GAGATGGGATTCCTTTCTTGT  34819    T   C____
                                ACAG GAAA    CCCATCTC
                                |||| ||||    ||||||||
                                TGTT CTTT    GGGTAGAG
                                  _   CCTTA
GAM786  FLJ20034 3' GAGATGGGGTCTCTCCATGTT  34847    CAGT  A
                                AACA   GA ACCCCATCTC
                                ||||   || ||||||||||
                                TTGT   CT TGGGGTAGAG
                                  ACCT  C
GAM786  FLJ20147 3' GAGATAGGGTCTTGCTGTGTT  35134      TG A   C
                                AACACAG  A ACCC ATCTC
                                |||||||  | |||| |||||
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                                TTGTGTC  T TGGG TAGAG
                                   GT C    A
GAM786  FLJ20294  3' GAGACGGTCTTCACTGTCC   35355   C      AC  CA
                                A ACAGTGAA  CC  TCTC
                                | ||||||||  ||  ||||
                                C TGTCACTT  GG  AGAG
                                 C       CT  C_
GAM786  FLJ20344  3' GAGACAGGGTTTCACCATGTT  35482     CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  FLJ20507  3' GAGACAGGGTTTCACCATGTT  60845     CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  FLJ20671  3' GAGATGGGGGAATGTGTT    35940      GTGAAA
                                AACACA     CCCCATCTC
                                ||||||     |||||||||
                                TTGTGT     GGGGTAGAG
                                   AAG___
GAM786  FLJ20729  3' GAGATGGGGTCTTGGAGTG   36083     AG   A
                                CAC  TGA ACCCCATCTC
                                |||  ||| ||||||||||
                                GTG  GTT TGGGGTAGAG
                                  AG   C
GAM786  FLJ20813  3' GAGATGGGCTTTCACTACGTT  36132     AC      C
                                AAC  AGTGAAA CCCATCTC
                                |||  ||||||| ||||||||
                                TTG  TCACTTT GGGTAGAG
                                  CA      C
GAM786  FLJ20897  5' GAGACGGGGTTTCAACGTGTT  51475      AG       A
                                AACAC  TGAAACCCC TCTC
                                |||||  ||||||||| ||||
                                TTGTG  ACTTTGGGG AGAG
                                   CA        C
GAM786  FLJ20958  3' GAGATGGGATCACTATGTT    42309     C    AAC
                                AACA AGTGA   CCCATCTC
                                |||| |||||   ||||||||
                                TTGT TCACT   GGGTAGAG
                                  A    A__
GAM786  FLJ21302  3' GAGACAGGGTTTCACCATGTT  43509     CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  FLJ21324  5' GAGATGGGGTTTCACCATGTT  92855     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
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                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  FLJ21603  3'  GAGATGGGGTTTCACCCTGTT  45772     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  CC
GAM786  FLJ22002  3'  GAGATGAGGTTTCGCCATGTT  46198     CA      C
                                AACA  GTGAAACC CATCTC
                                ||||  |||||||| ||||||
                                TTGT  CGCTTTGG GTAGAG
                                  AC       A
GAM786  FLJ22167  5'  GAGATGGGGTCTCACTGTGTT  44872         A
                                AACACAGTGA ACCCCATCTC
                                |||||||||| ||||||||||
                                TTGTGTCACT TGGGGTAGAG
                                      C
GAM786  FLJ22329  3'  GAGACGGGGTTTCACCATGTT  45401     CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  FLJ22479  3'  GAGATGGGAAAATTTCTTGT  46606     T   C___
                                ACAG GAAA   CCCATCTC
                                |||| ||||   ||||||||
                                TGTT CTTT   GGGTAGAG
                                  _   AAAA
GAM786  FLJ22529  3'  GAGACAGGGTTTCATCATGTT  45944     CA      CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  TACTTTGGG  AGAG
                                  AC        AC
GAM786  FLJ22684  3'  GAGACAGGGTTTCACCATGTT  47469     CA      CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  FLJ22794  3'  GAGACAGGGTTTCACCATGTT  93247     CA      CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  FLJ22969  3'  GAGACAGGGTTTCACCATGTT  69205     CA      CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  FLJ23024  3'  GAGACGGGGTTTCACCATGTT  46842     CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
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                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  FLJ23392 3' GAGACAGGGTTTCACCATGTT 45892      CA        CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC         AC
GAM786  FLJ23392 3' GAGACAGGGTTTCACCGTGTT 45893      A         CA
                                AACAC GTGAAACCC  TCTC
                                ||||| |||||||||  ||||
                                TTGTG CACTTTGGG  AGAG
                                   C         AC
GAM786  FLJ23392 3' GAGACGGGGTTTCACCGTGTT 45894      A         A
                                AACAC GTGAAACCCC TCTC
                                ||||| |||||||||| ||||
                                TTGTG CACTTTGGGG AGAG
                                   C         C
GAM786  FLJ23519 3' GAGATGGGGTTTCACCGTGTT 50951      A
                                AACAC GTGAAACCCCATCTC
                                ||||| ||||||||||||||
                                TTGTG CACTTTGGGGTAGAG
                                   C
GAM786  FLJ23556 3' GAGACGGGGTTTCACCGTGTT 46442      A         A
                                AACAC GTGAAACCCC TCTC
                                ||||| |||||||||| ||||
                                TTGTG CACTTTGGGG AGAG
                                   C         C
GAM786  FLJ23556 3' GAGATGGAGTTTTGCTCTGT  46443    C  TG    C
                                ACA AG  AAAC CCATCTC
                                ||| ||  |||| |||||||
                                TGT TC  TTTG GGTAGAG
                                  C  GT    A
GAM786  FLJ25416 3' ATGGGGGTCCCTTACTGTGTT 59448          AA___
                                AACACAGTGA    CCCCAT
                                ||||||||||    ||||||
                                TTGTGTCATT    GGGGTA
                                      CCCTG
GAM786  FLJ25416 5' GAGATGGGGTTTCACCATGTT 59455      CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  FLJ30532 3' GAGATGGAGTTTCGCTCTTGT 59220     C_       C
                                ACA  AGTGAAAC CCATCTC
                                |||  |||||||| |||||||
                                TGT  TCGCTTTG GGTAGAG
                                  TC       A
GAM786  FLJ31153 3' GAGATGGGGTTTCACCATG   58748    CA
                                CA  GTGAAACCCCATCTC
                                ||  ||||||||||||||
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                                GT  CACTTTGGGGTAGAG
                                 AC
GAM786  FLJ32865  3'  GAGACGGGGTTTCTCCGTGTT  58812      AGT       A
                                AACAC   GAAACCCC TCTC
                                |||||   |||||||| ||||
                                TTGTG   CTTTGGGG AGAG
                                   CCT       C
GAM786  FLJ32894  3'  GAGATGGGATTTCACTGTGTT  58998           C
                                AACACAGTGAAA CCCATCTC
                                |||||||||||| ||||||||
                                TTGTGTCACTTT GGGTAGAG
                                       A
GAM786  GMPPB     5'  GAGACAGGGTTTCACCAGGTT  26221     ACA       CA
                                AAC   GTGAAACCC  TCTC
                                |||   |||||||||  ||||
                                TTG   CACTTTGGG  AGAG
                                  GAC       AC
GAM786  GNG4      3'  AGACGGGGTTTCACCATGTT   16837      CA        A
                                AACA  GTGAAACCCC TCT
                                ||||  |||||||||| |||
                                TTGT  CACTTTGGGG AGA
                                   AC        C
GAM786  GOLGA3    3'  ATGGGGTTTCACCATGTT    20880      CA
                                AACA  GTGAAACCCCAT
                                ||||  ||||||||||||
                                TTGT  CACTTTGGGGTA
                                   AC
GAM786  GREB1     3'  GAGACGGGGTTTCACCATGTT  28568      CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                   AC        C
GAM786  GREB1     3'  GAGATGGGGTTTCGCCAGGTT  28569     ACA
                                AAC   GTGAAACCCCATCTC
                                |||   ||||||||||||||
                                TTG   CGCTTTGGGGTAGAG
                                  GAC
GAM786  GRWD      3'  GAGACGGGGTTTCACCATGTT  49783      CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                   AC        C
GAM786  GT650     3'  GAGATGGGATCCTATGTGTT   54552       GT_  AAC
                                AACACA   GA   CCCATCTC
                                ||||||   ||   ||||||||
                                TTGTGT   CT   GGGTAGAG
                                   ATC  A__
GAM786  GTF2E1    3'  GAGGCAGGGTTTCACCATGTT  19799      CA        CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
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                                TTGT  CACTTTGGG  GGAG
                                  AC        AC
GAM786  GTPBG3   3'  GAGACAAGGTTTCACCATGTT  51897     CA       CCA
                                AACA  GTGAAACC   TCTC
                                ||||  ||||||||   ||||
                                TTGT  CACTTTGG   AGAG
                                  AC       AAC
GAM786  H-plk    5'  GAGATGGAGTCTTGCTGTGT   32383       TG A  C
                                ACACAG  A AC CCATCTC
                                ||||||  | || |||||||
                                TGTGTC  T TG GGTAGAG
                                   GT C  A
GAM786  H-plk    5'  GAGATGGTATCTCACTGTG   32384        AACC
                                CACAGTGA   CCATCTC
                                ||||||||   |||||||
                                GTGTCACT   GGTAGAG
                                     CTAT
GAM786  H2AV     3'  GACGTGGGGTTTCACCATGTT  57630      CA          C
                                AACA  GTGAAACCCCAT TC
                                ||||  ||||||||||||  ||
                                TTGT  CACTTTGGGGTG AG
                                  AC          C
GAM786  HARS2    3'  GAGACGGGGTTTTACCATGTT  55865      CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  ||||||||||  ||||
                                TTGT  CATTTTGGGG AGAG
                                  AC         C
GAM786  HCA4     3'  GAGACGGGGTTTTGCCATGTT  57743      CA TG      A
                                AACA  G  AAACCCC TCTC
                                ||||  |  |||||||  ||||
                                TTGT  C  TTTGGGG AGAG
                                  AC GT      C
GAM786  HCGIV.9  3'  GAGACAGGGTTTTTTGTTGTT  39131     _  T      CA
                                AACA CAG GAAACCC  TCTC
                                ||||  |||  |||||||  ||||
                                TTGT GTT TTTTGGG  AGAG
                                  T  _      AC
GAM786  HRH4     3'  GAGATGAAGTCTCACTGTGTT  41540          A  CC
                                AACACAGTGA AC  CATCTC
                                ||||||||||  ||  ||||||
                                TTGTGTCACT TG  GTAGAG
                                     C  AA
GAM786  HSA277841 3'  GAGATGGGGTCCTGTTGTT   38268      _  T  AA
                                AACA CAG GA  CCCCATCTC
                                ||||  |||  ||  |||||||||
                                TTGT GTC CT  GGGGTAGAG
                                  T  _  __
GAM786  HSMPP8   3'  GAGACGGAGTTTCGCTCTTGT  95134     C_       C  A
                                ACA  AGTGAAAC CC TCTC
                                |||  ||||||||  ||  ||||
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                                TGT  TCGCTTTG GG AGAG
                                  TC       A  C
GAM786  HSMPP8   3' GAGATGGGGTTTATCCATGTT 95135     CAGTG
                                AACA    AAACCCCATCTC
                                ||||    ||||||||||||
                                TTGT    TTTGGGGTAGAG
                                  ACCTA
GAM786  HSNOV1   3' GACATGGGGTTTCACCATGTT 34435     CA          C
                                AACA  GTGAAACCCCAT TC
                                ||||  |||||||||||| ||
                                TTGT  CACTTTGGGGTA AG
                                  AC          C
GAM786  HSNOV1   3' GAGATGGGGTTTCGCCATGTT 34436     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CGCTTTGGGGTAGAG
                                  AC
GAM786  HSPC065  3' GAGATGGGGTTTCACCATGTT 27152     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  HSPC065  3' GAGATGGGGTTTCACGATGTT 27153     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AG
GAM786  HSPC232  3' GAGATGGGGTTCACCATGTT  33657     CA    A
                                AACA  GTGAA CCCCATCTC
                                ||||  ||||| |||||||||
                                TTGT  CACTT GGGGTAGAG
                                  AC    _
GAM786  ICK      3' GAGACGGGGTTTCACTGTGTT 33688           A
                                AACACAGTGAAACCCC TCTC
                                |||||||||||||||| ||||
                                TTGTGTCACTTTGGGG AGAG
                                        C
GAM786  JAM1     3' GAGACAGGGTTTCACCATGTT 34228     CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  JAM1     3' GAGACAGGGTTTCACCATGTT 58572     CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  KIAA0063 3' GAGATGGGGTTTCTCCATGTT 30258     CAGT
                                AACA   GAAACCCCATCTC
                                ||||   ||||||||||||
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                                TTGT   CTTTGGGGTAGAG
                                  ACCT
GAM786  KIAA0161 3' GAGACGGAGTTTCGCTTTTGT 29201    C_      C  A
                                ACA  AGTGAAAC CC TCTC
                                |||  |||||||| || ||||
                                TGT  TCGCTTTG GG AGAG
                                  TT       A  C
GAM786  KIAA0161 3' GAGACGGGGTTTCACCATGTT 29202     CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  KIAA0186 3' CGAGATGGGGTTTCACCATGTT 41106     CA           ___
                                AACA  GTGAAACCCCATCTC   G
                                ||||  ||||||||||||||   |
                                TTGT  CACTTTGGGGTAGAG   C
                                  AC           __
GAM786  KIAA0205 3' GAGATGGGGTTTCACCATGTT  30214     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  KIAA0408 3' GAGATGGAGACAATCCTGGTT  28798    A   T  AACC__
                                AAC CAG GA     CCATCTC
                                ||| ||| ||     |||||||
                                TTG GTC CT     GGTAGAG
                                  _   _  AACAGA
GAM786  KIAA0426 3' GAGACGGGGTTTCACCATGTT  28927     CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  KIAA0459 3' GAGACGGGGTTTCACCATGTT  61653     CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  KIAA0469 3' GAGACAGGGTCTTGCTGTGTT  29981       TG A    CA
                                AACACAG  A ACCC  TCTC
                                |||||||  | ||||  ||||
                                TTGTGTC  T TGGG  AGAG
                                    GT C    AC
GAM786  KIAA0469 3' GAGACGGGATTTCACTGTGTT  29982          C   A
                                AACACAGTGAAA CCC TCTC
                                ||||||||||||| ||| ||||
                                TTGTGTCACTTT GGG AGAG
                                       A   C
GAM786  KIAA0495 3' GAGATGGGATTTCACCATGTT  63268     CA     C
                                AACA  GTGAAA CCCATCTC
                                ||||  ||||||  ||||||||
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                                TTGT  CACTTT GGGTAGAG
                                  AC     A
GAM786  KIAA0513 5' GAGACAGGGTTTCGCCATGTT  29031     CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CGCTTTGGG  AGAG
                                  AC        AC
GAM786  KIAA0513 3' GAGATGGGGTTTCACCATG   29032    CA
                                CA  GTGAAACCCCATCTC
                                ||  ||||||||||||||
                                GT  CACTTTGGGGTAGAG
                                 AC
GAM786  KIAA0555 3' GAGACAGGGTTTCACTATG   60742    C        CA
                                CA AGTGAAACCC  TCTC
                                || ||||||||||  ||||
                                GT TCACTTTGGG  AGAG
                                 A         AC
GAM786  KIAA0557 3' GAGACGGGGCCTTGCTGTGT  78563       TG AA    A
                                ACACAG  A  CCCC TCTC
                                ||||||  |  |||| ||||
                                TGTGTC  T  GGGG AGAG
                                   GT CC    C
GAM786  KIAA0557 3' GAGATGGGGTTTCTCCATGTT 78564     CAGT
                                AACA    GAAACCCCATCTC
                                ||||    ||||||||||||
                                TTGT    CTTTGGGGTAGAG
                                  ACCT
GAM786  KIAA0561 3' GACGGGGTTTCACCATGTT   66478     CA       A
                                AACA  GTGAAACCCC TC
                                ||||  ||||||||||  ||
                                TTGT  CACTTTGGGG AG
                                  AC        C
GAM786  KIAA0599 3' GAGACGGGGTTTCGCCGTGTT 77693      A        A
                                AACAC GTGAAACCCC TCTC
                                |||||  |||||||||| ||||
                                TTGTG CGCTTTGGGG AGAG
                                   C        C
GAM786  KIAA0682 3' GAGACTGGGTTTCACCATGT  30024    CA       CA
                                ACA  GTGAAACCC  TCTC
                                |||  |||||||||  ||||
                                TGT  CACTTTGGG  AGAG
                                  AC        TC
GAM786  KIAA0682 3' GACGGGGTTTCACCATGTG   33009     __       A
                                CACA  GTGAAACCCC TC
                                ||||  ||||||||||  ||
                                GTGT  CACTTTGGGG AG
                                  AC        C
GAM786  KIAA0737 3' GAGACAGGGTTTCACCATGTT 29809     CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
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                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  KIAA0737 3' GAGATGGGGTCTCACTATGTT  29810      C     A
                                AACA AGTGA ACCCCATCTC
                                |||| ||||| ||||||||||
                                TTGT TCACT TGGGGTAGAG
                                  A    C
GAM786  KIAA0759 3' ATGGGGTTTTAAATTGTT    67882      CAG
                                AACA   TGAAACCCCAT
                                ||||   ||||||||||
                                TTGT   ATTTTGGGGTA
                                  TAA
GAM786  KIAA0798 3' GAGACGGGGTTTCACTGTGTT  28447              A
                                AACACAGTGAAACCCC TCTC
                                |||||||||||||||| ||||
                                TTGTGTCACTTTGGGG AGAG
                                          C
GAM786  KIAA0828 3' GAGACAGGGTTTCACTATGTT  82115      C        CA
                                AACA AGTGAAACCC  TCTC
                                |||| ||||||||||  ||||
                                TTGT TCACTTTGGG  AGAG
                                  A         AC
GAM786  KIAA0831 3' GAGACGGGGGTTTTCACCATGT 30637     CA     _    A_
                                ACA  GTGAAA CCCC  TCTC
                                |||  |||||| ||||  ||||
                                TGT  CACTTT GGGG  AGAG
                                  AC      T    GC
GAM786  KIAA0841 3' GACGGGGTTTCATCATGTT    71896      CA        A
                                AACA  GTGAAACCCC TC
                                ||||  |||||||||| ||
                                TTGT  TACTTTGGGG AG
                                  AC         C
GAM786  KIAA0861 3' GAGACGGGGTTTCCCCGTGTT  90349       AGT       A
                                AACAC   GAAACCCC TCTC
                                |||||   |||||||| ||||
                                TTGTG   CTTTGGGG AGAG
                                   CCC       C
GAM786  KIAA0884 3' GAGGTGAGGTTTCACCATGTT  70753      CA       C
                                AACA  GTGAAACC CATCTC
                                ||||  |||||||| ||||||
                                TTGT  CACTTTGG GTGGAG
                                  AC       A
GAM786  KIAA0889 3' GAGACGGGGTTTCACCGTGTT  31777       A        A
                                AACAC GTGAAACCCC TCTC
                                ||||| |||||||||| ||||
                                TTGTG CACTTTGGGG AGAG
                                  C         C
GAM786  KIAA0918 3' AGATGGGGCTACTGTTGTT    73518      _     AAA
                                AACA CAGTG   CCCCATCT
                                |||| |||||   ||||||||
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                                TTGT GTCAT   GGGGTAGA
                                  T    C__
GAM786  KIAA0931  3' GAGACGGGGTTTCACCATGTT  68012     CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  KIAA0961  3' GAGATGGGGTTTCACCATGTT  30400     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  KIAA1010  3' GAGATGGGGTCTTGCTATGTT  72542     C  TG A
                                AACA AG  A ACCCCATCTC
                                ||||  ||  | ||||||||||
                                TTGT TC  T TGGGGTAGAG
                                  A  GT C
GAM786  KIAA1041  3' GAGATGGGGTTTCACCATGTT  30823     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  KIAA1054  3' GAGGTGGGGTTTCACCGTGTT  68965      A
                                AACAC GTGAAACCCCATCTC
                                |||||  |||||||||||||||
                                TTGTG CACTTTGGGGTGGAG
                                  C
GAM786  KIAA1069  3' AGATGTCCTTTACTGTGT    68524         ACCC
                                ACACAGTGAA    CATCT
                                ||||||||||    |||||
                                TGTGTCATTT    GTAGA
                                     CCT_
GAM786  KIAA1115  5' GAGACAGGGTTTCGCCATGTT  30691     CA        CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CGCTTTGGG  AGAG
                                  AC        AC
GAM786  KIAA1143  3' GAGACGGGGTTTCACTTTGTT  69242     C         A
                                AACA AGTGAAACCCC TCTC
                                |||| ||||||||||| ||||
                                TTGT TCACTTTGGGG AGAG
                                  T         C
GAM786  KIAA1161  5' GAGATGGGGTTTACCATGTT   82646     CA    A
                                AACA  GTGAA CCCCATCTC
                                ||||  |||||  |||||||||
                                TTGT  CATTT GGGGTAGAG
                                  AC    _
GAM786  KIAA1198  3' GAGACGGGGTTTCACCATGTT  64037     CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
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                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  KIAA1198 3' GAGACGGGGTTTCACCATGTT  64038     CA         A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  KIAA1198 3' GAGACGGGGTTTCACCGTGTT  64039      A         A
                                AACAC GTGAAACCCC TCTC
                                ||||| |||||||||| ||||
                                TTGTG CACTTTGGGG AGAG
                                   C         C
GAM786  KIAA1198 3' GAGATGGGGTTTCACCATGTT  64040     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  KIAA1198 3' GAGATGGGGTTTCTCCATGTT  64041     CAGT
                                AACA   GAAACCCCATCTC
                                ||||   ||||||||||||
                                TTGT   CTTTGGGGTAGAG
                                  ACCT
GAM786  KIAA1200 3' GAGACGGGGTTTCACCATGTT  63038     CA         A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  KIAA1210 3' GAGACGGGGTTTCACCATGTT  98070     CA         A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  KIAA1210 3' GAGTAGTTATCACTGTGT    98071        _  CCCAT
                                ACACAGTGA AAC    CTC
                                ||||||||| |||    |||
                                TGTGTCACT TTG    GAG
                                     A  AT___
GAM786  KIAA1254 3' GAGATGGGGTTTCACCATGTT  70561     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  KIAA1373 3' GAGATGGGGTTTTACCCTGTT  71506     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CATTTTGGGGTAGAG
                                  CC
GAM786  KIAA1443 3' GAGACGGGTTTCATCATGTT   64571     CA         CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
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                                TTGT  TACTTTGGG  AGAG
                                  AC        C_
GAM786  KIAA1456 3' GAGACGGGGTTTCACCGTGTT 67555      A         A
                                AACAC GTGAAACCCC TCTC
                                ||||| |||||||||| ||||
                                TTGTG CACTTTGGGG AGAG
                                  C         C
GAM786  KIAA1465 3' GAGACGGGGTTTCACCATGTT 61496      CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC        C
GAM786  KIAA1467 3' GAGACGGGGTTTCACCATGTT 72068      CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC        C
GAM786  KIAA1493 3' GAGATGGGGTTTCACCTTGTT 64841      CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  TC
GAM786  KIAA1497 5' GAGACAGGGTTTCACCATGTT 68123      CA        CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  KIAA1530 3' GAGACGGGATTTCACTGTGTT 68561           C   A
                                AACACAGTGAAA CCC TCTC
                                |||||||||||| ||| ||||
                                TTGTGTCACTTT GGG AGAG
                                      A   C
GAM786  KIAA1530 3' GAGATGAGGTCTCACTGTGTT 68562         A   C
                                AACACAGTGA ACC CATCTC
                                |||||||||| ||| ||||||
                                TTGTGTCACT TGG GTAGAG
                                    C   A
GAM786  KIAA1617 3' GAGACAGGGTTTCACCATGTT 93078      CA        CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  KIAA1649 3' GAGATGAGGTTTCACCGTGTT 51238      A       C
                                AACAC GTGAAACC CATCTC
                                ||||| |||||||| ||||||
                                TTGTG CACTTTGG GTAGAG
                                  C       A
GAM786  KIAA1655 3' GAGACAGGTTTCACCATGTT  67187      CA        CCA
                                AACA  GTGAAACC   TCTC
                                ||||  ||||||||   ||||
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                                TTGT  CACTTTGG   AGAG
                                  AC       AC_
GAM786  KIAA1668 3' GAGACGGGGTTTCACCGTGTT  67069      A        A
                                AACAC GTGAAACCCC TCTC
                                ||||| |||||||||| ||||
                                TTGTG CACTTTGGGG AGAG
                                   C         C
GAM786  KIAA1712 3' GAGACAGGGTTTCACCATGTT  68158     CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  KIAA1727 3' GAGATGGGATCTCACTATGTT  64761     C    AAC
                                AACA AGTGA   CCCATCTC
                                |||| |||||   ||||||||
                                TTGT TCACT   GGGTAGAG
                                  A    CTA
GAM786  KIAA1737 3' ATGGGGTTTTACCGTGTT    67931      A
                                AACAC GTGAAACCCCAT
                                ||||| ||||||||||||
                                TTGTG CATTTTGGGGTA
                                   C
GAM786  KIAA1737 3' GAGATGGAGTTTCGCTCTTGT  67942     C_       C
                                ACA  AGTGAAAC CCATCTC
                                |||  |||||||| |||||||
                                TGT  TCGCTTTG GGTAGAG
                                  TC       A
GAM786  KIAA1821 3' GAGACAGGGTCTCACTGTGTT  72265         A   CA
                                AACACAGTGA ACCC  TCTC
                                |||||||||| ||||  ||||
                                TTGTGTCACT TGGG  AGAG
                                     C    AC
GAM786  KIAA1829 3' GAGATGGGGTTTCGCGAGTT   62644     ACA
                                AAC   GTGAAACCCCATCTC
                                |||   ||||||||||||||||
                                TTG   CGCTTTGGGGTAGAG
                                  AG_
GAM786  KIAA1877 3' GAGACAGGGTTTCACCGTGTT  66749      A       CA
                                AACAC GTGAAACCC  TCTC
                                ||||| |||||||||  ||||
                                TTGTG CACTTTGGG  AGAG
                                   C        AC
GAM786  KIAA1971 3' GAGACAAGGTTTCGCTATGTT  74680     C       CCA
                                AACA AGTGAAACC   TCTC
                                |||| |||||||||   ||||
                                TTGT TCGCTTTGG   AGAG
                                  A        AAC
GAM786  KIAA1971 3' GAGACGAGGTTTCACCGTGTT  74681      A      CCA
                                AACAC GTGAAACC   TCTC
                                ||||| ||||||||   ||||
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                                TTGTG CACTTTGG  AGAG
                                  C      AGC
GAM786  KIAA1975 5' GAGATGGGGTTTCACCATGTT 74422     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  KLK7     3' GAGACAGGGTTTCACCATGTT 18544     CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC       AC
GAM786  LAMP3    3' GACGGGGTTTCACCATGTT   60204     CA       A
                                AACA  GTGAAACCCC TC
                                ||||  |||||||||| ||
                                TTGT  CACTTTGGGG AG
                                  AC        C
GAM786  LAMP3    3' GAGACGGAGTTTCACTCTTGT 60205     C_      C  A
                                ACA  AGTGAAAC CC TCTC
                                |||  |||||||| || ||||
                                TGT  TCACTTTG GG AGAG
                                  TC       A  C
GAM786  LIECG3   3' GAGGGGGGTCTCACTGTGTT  88799         A    A
                                AACACAGTGA ACCCC TCTC
                                |||||||||| ||||| ||||
                                TTGTGTCACT TGGGG GGAG
                                      C    _
GAM786  LY75     3' GAGATGGGGTTTCACCATGTT 11394     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  MAP-1    3' GAGACGGGGTTTCACCATGTT  42441     CA       A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC        C
GAM786  MAP4K3   3' AGATGGGGAAAATTTTGTT   14626     C  GAAA
                                AACA AGT   CCCCATCT
                                |||| |||   ||||||||
                                TTGT TTA   GGGGTAGA
                                  T  AAA_
GAM786  MCLC     3' GAGATGGGGTTTCACCATGTT 31382     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  MCM10    3' GAGATGGGGTTTTGCCATGTT 38177     CA TG
                                AACA  G  AAACCCCATCTC
                                ||||  |  ||||||||||||
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                                TTGT  C  TTTGGGGTAGAG
                                  AC GT
GAM786  MEF-2    3' GAGACTGGGTTTCACCATGTT  65022     CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC       TC
GAM786  MGC10200 3' GAGATGGGGTTTCACCATGTT  59644     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  MGC11386 3' GAGATGGGGATCTCACTGTGTT 53065         AA_
                                AACACAGTGA   CCCCATCTC
                                ||||||||||   |||||||||
                                TTGTGTCACT   GGGGTAGAG
                                     CTA
GAM786  MGC12466 3' GAGATGGGATCTCGCTGT    79797       AAC
                                ACAGTGA   CCCATCTC
                                |||||||   ||||||||
                                TGTCGCT   GGGTAGAG
                                   CTA
GAM786  MGC12518 3' GAGTGAGGGTTTCACCATGTT  64777     CA       _  T
                                AACA  GTGAAACCC CA CTC
                                ||||  ||||||||| || |||
                                TTGT  CACTTTGGG GT GAG
                                  AC       A  _
GAM786  MGC13007 5' GAATTGGTTCCACTGTGTT   51279        A   CCA
                                AACACAGTG AACC   TC
                                |||||||||| ||||   ||
                                TTGTGTCAC TTGG   AG
                                     C   TTA
GAM786  MGC13061 3' GAGATGGGATCTCACTAGGTT  51289    AC    AAC
                                AAC  AGTGA   CCCATCTC
                                |||  |||||   ||||||||
                                TTG  TCACT   GGGTAGAG
                                  GA    CTA
GAM786  MGC15563 3' GAGATGGGATCTCACCATGTT  52861     CA   AAC
                                AACA  GTGA   CCCATCTC
                                ||||  ||||   ||||||||
                                TTGT  CACT   GGGTAGAG
                                  AC    CTA
GAM786  MGC21675 3' GAGATGGGGTTTCACCATGTT  54593     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  MGC2474  3' GAGATGGGGTTCCCACTATGT  43958    C   A_
                                ACA AGTG  AACCCCATCTC
                                ||| ||||  ||||||||||
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                                TGT TCAC  TTGGGGTAGAG
                                  A   CC
GAM786  MGC2474  3' GAGATGGGGTTTCACCATGTT  43959     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  MGC29898 3' GAGATGGGATCTCACTCTGTT  59586     C    AAC
                                AACA AGTGA   CCCATCTC
                                |||| |||||   ||||||||
                                TTGT TCACT   GGGTAGAG
                                  C    CTA
GAM786  MGC4766  5' GAGACGGGGTTTCACCGTGTT  49558     A        A
                                AACAC GTGAAACCCC TCTC
                                ||||| |||||||||| ||||
                                TTGTG CACTTTGGGG AGAG
                                   C         C
GAM786  moblak   3' GAGACAGGGTTTCACCGTGTT  56400     A       CA
                                AACAC GTGAAACCC  TCTC
                                ||||| |||||||||  ||||
                                TTGTG CACTTTGGG  AGAG
                                   C        AC
GAM786  MOCS3    3' GAGGGGGTTTCACCATGTT   27932     CA        A
                                AACA  GTGAAACCCC TC
                                ||||  |||||||||| ||
                                TTGT  CACTTTGGGG AG
                                  AC         G
GAM786  MRPL44   3' GAGATGGGGTTTCACCAAGTT  43598    ACA
                                AAC   GTGAAACCCCATCTC
                                |||   ||||||||||||||
                                TTG   CACTTTGGGGTAGAG
                                  AAC
GAM786  MRPS27   3' GAGATGGGGTTTCACCATGTT  31330     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  MSP      3' GAGATGAGGATTCACTGT    50243       A  C
                                ACAGTGAA CC CATCTC
                                |||||||| || ||||||
                                TGTCACTT GG GTAGAG
                                    A  A
GAM786  MtFMT    3' GAGATGGGGTTTCACCATGTT  58336     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  MYO5C    3' GAGACAGGTTTCACCATGTT  38719     CA       CCA
                                AACA  GTGAAACC   TCTC
                                ||||  ||||||||   ||||
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                                TTGT  CACTTTGG   AGAG
                                  AC       AC_
GAM786  NDP52    3'  GAGACAGGGTTTCACTATGTT  20671     C        CA
                                AACA AGTGAAACCC  TCTC
                                |||| ||||||||||  ||||
                                TTGT TCACTTTGGG  AGAG
                                  A         AC
GAM786  NDUFC2   3'  GAGACGGGGTTTCACCATGTT  17031     CA         A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  NFAT5    3'  GAGATGGGGTTTTGCCATGTT  57771     CA TG
                                AACA  G  AAACCCCATCTC
                                ||||  |  ||||||||||||
                                TTGT  C  TTTGGGGTAGAG
                                  AC GT
GAM786  NINJ2    3'  GAGACGGGGTTTCTCCATGTT  33725     CAGT       A
                                AACA    GAAACCCC TCTC
                                ||||    |||||||| ||||
                                TTGT    CTTTGGGG AGAG
                                  ACCT       C
GAM786  Nup43    3'  GAGACGACAGGGTTTCACCATG 45347     CA        CA___
          TT                      AACA  GTGAAACCC     TCTC
                                ||||  |||||||||     ||||
                                TTGT  CACTTTGGG     AGAG
                                  AC         ACAGC
GAM786  Nup43    3'  GAGATGGGGTTTCACTGTGTT  45348
                                AACACAGTGAAACCCCATCTC
                                ||||||||||||||||||||
                                TTGTGTCACTTTGGGGTAGAG

GAM786  NXN      3'  GAGATGGGGTTTCACCATGTT  42675     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  OCT11    3'  GAGATGGGGTTTCACCATGTT  27590     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  OR51E2   3'  GAGATGGGGTCTCGCTCTGT   48510     C     A
                                ACA AGTGA ACCCCATCTC
                                ||| ||||| ||||||||||
                                TGT TCGCT TGGGGTAGAG
                                  C     C
GAM786  OSBPL2   3'  GAGACGGAGTTTCACTCTTGT  58486     C_       C  A
                                ACA  AGTGAAAC CC TCTC
                                |||  |||||||| || ||||
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                                TGT  TCACTTTG GG AGAG
                                  TC       A  C
GAM786  PASK     5'  GAGACGGGGTTTCTCCATGTT  31412      CAGT       A
                                AACA    GAAACCCC TCTC
                                ||||    |||||||| ||||
                                TTGT    CTTTGGGG AGAG
                                  ACCT       C
GAM786  PELI1    5'  GAGACGGGGTTTCACCATGTT  40641      CA         A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  PELI1    5'  GAGATGGGGTTTCACCATGTT  40642      CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  PIG7     3'  GAGATGGGGTCTTACTATGTT  17970      C    A
                                AACA AGTGA ACCCCATCTC
                                |||| ||||| ||||||||||
                                TTGT TCATT TGGGGTAGAG
                                  A    C
GAM786  PIP5K1C  3'  GAGACGAGGGTGCTGTGT    71301       GAA   CA_
                                ACACAGT   ACCC   TCTC
                                |||||||   ||||   ||||
                                TGTGTCG   TGGG   AGAG
                                    ___    AGC
GAM786  PRO0365  5'  GAGACGGGGTTTCACTATGTT  26982      C         A
                                AACA AGTGAAACCCC TCTC
                                |||| |||||||||| ||||
                                TTGT TCACTTTGGGG AGAG
                                  A          C
GAM786  PRO1992  3'  GAGATGGGGTTTTACCATGTG  26907      __
                                CACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                GTGT  CATTTTGGGGTAGAG
                                  AC
GAM786  PRO2955  3'  GAGACAGGGTTTTACCATGTT  38239      CA        CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CATTTTGGG  AGAG
                                  AC         AC
GAM786  PSTPIP2  3'  GAGACAGGGTTTTACCATGTT  44655      CA        CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CATTTTGGG  AGAG
                                  AC         AC
GAM786  RAB21    3'  GAGACGGGGTTTCACCAGGTT  31089      ACA       A
                                AAC   GTGAAACCCC TCTC
                                |||   |||||||||| ||||
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                                TTG  CACTTTGGGG AGAG
                                  GAC        C
GAM786  RAB33B   3'  GATGGGGTTTCACCATGTT   49328     CA
                                AACA  GTGAAACCCCATC
                                ||||  ||||||||||||
                                TTGT  CACTTTGGGGTAG
                                  AC
GAM786  RAP140   3'  GAGACAGGGTTTCACTGTGTT  31515           CA
                                AACACAGTGAAACCC  TCTC
                                ||||||||||||||  ||||
                                TTGTGTCACTTTGGG  AGAG
                                        AC
GAM786  RES4-25  3'  GAGACGGGGTTTCTCCATGTT  65267     CAGT      A
                                AACA   GAAACCCC TCTC
                                ||||   |||||||| ||||
                                TTGT   CTTTGGGG AGAG
                                  ACCT      C
GAM786  RNF8     3'  GAGACAGGGTTTCACCATGTT  15568     CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  RNO2     5'  GAGATGGGGTGTCACCATGTT  53937     CA   A
                                AACA  GTGA ACCCCATCTC
                                ||||  |||| ||||||||||
                                TTGT  CACT TGGGGTAGAG
                                  AC   G
GAM786  SAMHD1   3'  GAGACAAGGTTTTGCTCTGTT  61985     C  TG    CCA
                                AACA AG  AAACC   TCTC
                                |||| ||  |||||   ||||
                                TTGT TC  TTTGG   AGAG
                                  C  GT    AAC
GAM786  SC4MOL   3'  GAGATGGGGTTTCTCGATGTT  23105     CAGT
                                AACA   GAAACCCCATCTC
                                ||||   ||||||||||||
                                TTGT   CTTTGGGGTAGAG
                                  AGCT
GAM786  SCAMP-4  3'  GAGACAGAGTTTCACTCTGT   55348    C      CCCA
                                ACA AGTGAAAC   TCTC
                                ||| ||||||||   ||||
                                TGT TCACTTTG   AGAG
                                  C       AGAC
GAM786  SCAMP-4  3'  GATGGGGTTTCACCATGTT   55350     CA
                                AACA  GTGAAACCCCATC
                                ||||  ||||||||||||
                                TTGT  CACTTTGGGGTAG
                                  AC
GAM786  SCYA22   3'  GAGACGGGGTTTTGCCATGTT  92595     CA TG      A
                                AACA  G  AAACCCC TCTC
                                ||||  |  ||||||| ||||
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                                TTGT  C  TTTGGGG AGAG
                                  AC GT      C
GAM786  SCYA22   3'  GAGATGGAGTTTCGCTCTTGT  92596     C_       C
                                ACA  AGTGAAAC CCATCTC
                                |||  |||||||| |||||||
                                TGT  TCGCTTTG GGTAGAG
                                  TC       A
GAM786  SCYA28   3'  GACGGGGTTTCACCGTGTT   39543      A        A
                                AACAC GTGAAACCCC TC
                                ||||| |||||||||| ||
                                TTGTG CACTTTGGGG AG
                                   C         C
GAM786  SERF1B   3'  GAGATGGGGTTTCACCATGTT  43697      CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  SFXN2    3'  GAGACGGGGTTTCACCATG   74376    CA        A
                                CA  GTGAAACCCC TCTC
                                ||  |||||||||| ||||
                                GT  CACTTTGGGG AGAG
                                 AC         C
GAM786  SIRPB1   3'  GAGATGGGGTTTCTCCATGTT  21367     CAGT
                                AACA    GAAACCCCATCTC
                                ||||    ||||||||||||
                                TTGT    CTTTGGGGTAGAG
                                  ACCT
GAM786  SLC12A8  3'  GAGACAGGGTTTCACCATGTT  45237     CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  SLC16A4  3'  GAGGCGGGGTTTCACCATGTT  17451     CA        AT
                                AACA  GTGAAACCCC  CTC
                                ||||  ||||||||||  |||
                                TTGT  CACTTTGGGG  GAG
                                  AC         CG
GAM786  SLC19A3  3'  GAGATGGGGTTTCACAATGTT  48243     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AA
GAM786  SLC19A3  3'  GAGATGGGTGGCATATGTT   48244     CA   AA   C
                                AACA  GTG  ACCC ATCTC
                                ||||  |||  |||| |||||
                                TTGT  TAC  TGGG TAGAG
                                  A_   GG   _
GAM786  SLC2A10  3'  GAGATGGGGTTTCACTGTGTT  48552
                                AACACAGTGAAACCCCATCTC
                                |||||||||||||||||||
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                                  TTGTGTCACTTTGGGGTAGAG

GAM786  SREC     3'  GAGACAGGGTTTCACCATGTT  14903      CA        CA
                                  AACA  GTGAAACCC  TCTC
                                  ||||  |||||||||  ||||
                                  TTGT  CACTTTGGG  AGAG
                                    AC         AC
GAM786  STAF65(gamma) 3'  GAGATGAGGTTTCACCGTGTT  30069       A       C
                                  AACAC GTGAAACC CATCTC
                                  ||||| |||||||| ||||||
                                  TTGTG CACTTTGG GTAGAG
                                    C       A
GAM786  STARD7   3'  GAGATGGAGTTTCACTCTGTT  39741      C       C
                                  AACA AGTGAAAC CCATCTC
                                  |||| |||||||| |||||||
                                  TTGT TCACTTTG GGTAGAG
                                    C       A
GAM786  STRBP    5'  GAGACGGGGTTTTGCCATGTT  37819      CA TG      A
                                  AACA  G  AAACCCC TCTC
                                  ||||  |  ||||||| ||||
                                  TTGT  C  TTTGGGG AGAG
                                    AC GT      C
GAM786  SULT1C2  3'  GAGACGAGGTTTCACCGTGTT  22713       A       CCA
                                  AACAC GTGAAACC   TCTC
                                  ||||| ||||||||   ||||
                                  TTGTG CACTTTGG   AGAG
                                    C       AGC
GAM786  SUN1     3'  GAGACAGGGTTTCACTGTGTT  47914             CA
                                  AACACAGTGAAACCC  TCTC
                                  ||||||||||||||  ||||
                                  TTGTGTCACTTTGGG  AGAG
                                          AC
GAM786  SYT13    3'  GAGATGGGGTTTCACCATGTT  95101      CA
                                  AACA  GTGAAACCCCATCTC
                                  ||||  ||||||||||||||
                                  TTGT  CACTTTGGGGTAGAG
                                    AC
GAM786  TADA3L   3'  GAGACGGGGTTTCACCGTGTT  22040       A        A
                                  AACAC GTGAAACCCC TCTC
                                  ||||| |||||||||| ||||
                                  TTGTG CACTTTGGGG AGAG
                                    C         C
GAM786  TBCC     3'  GAGACGGGGTTTCGCCATGTT  13604      CA        A
                                  AACA  GTGAAACCCC TCTC
                                  ||||  |||||||||| ||||
                                  TTGT  CGCTTTGGGG AGAG
                                    AC         C
GAM786  TCL6     3'  GAGACAGGGTTTCACCGTGTT  40477       A        CA
                                  AACAC GTGAAACCC  TCTC
                                  ||||| |||||||||  ||||
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                                TTGTG CACTTTGGG  AGAG
                                  C        AC
GAM786  TCL6     5'  GAGACGAGGTTTCACCATGTT  40478      CA       CCA
                                AACA  GTGAAACC   TCTC
                                ||||  ||||||||   ||||
                                TTGT  CACTTTGG   AGAG
                                  AC       AGC
GAM786  TERA     3'  GAGACGGGGTTTCACCACGTT  41418     ACA        A
                                AAC   GTGAAACCCC TCTC
                                |||   |||||||||| ||||
                                TTG   CACTTTGGGG AGAG
                                  CAC        C
GAM786  THEA     3'  GAGACACTTTCACTGTGTT   66889          CCCCA
                                AACACAGTGAAA    TCTC
                                ||||||||||||    ||||
                                TTGTGTCACTTT    AGAG
                                       CAC__
GAM786  THEA     3'  GAGATGGGGTTTCACTGTGTT  66890
                                AACACAGTGAAACCCCATCTC
                                |||||||||||||||||||||
                                TTGTGTCACTTTGGGGTAGAG

GAM786  TIX1     3'  AGATGGGGTTCTCATCAGTT   62404     ACA   _
                                AAC   GTGA AACCCCATCT
                                |||   |||| ||||||||||
                                TTG   TACT TTGGGGTAGA
                                  AC_   C
GAM786  TRIM16   3'  GAGATGGGGTTTCACCATGTT  22372      CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  TRIM5    3'  GAGACGGGGTTTCCCCATGTT  53470      CAGT       A
                                AACA    GAAACCCC TCTC
                                ||||    |||||||| ||||
                                TTGT    CTTTGGGG AGAG
                                  ACCC       C
GAM786  TRIM5    3'  GAGACGGGGTTTCCCCATGTT  53471      CAGT       A
                                AACA    GAAACCCC TCTC
                                ||||    |||||||| ||||
                                TTGT    CTTTGGGG AGAG
                                  ACCC       C
GAM786  TRIM6    3'  GAGATAGGGTTTCACCGTGTT  55181       A        C
                                AACAC GTGAAACCC ATCTC
                                ||||| ||||||||| |||||
                                TTGTG CACTTTGGG TAGAG
                                  C        A
GAM786  TU12B1-TY 3'  GAGACGGGGTTTCACCATGTT  33849      CA         A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
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                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  TU12B1-TY 3'  GAGATGGGGTTTCACCATGTT  33850      CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  TU12B1-TY 3'  GAGATGGGGTTTCTCCATG   33851    GT__
                                CA   GAAACCCCATCTC
                                ||   ||||||||||||
                                GT   CTTTGGGGTAGAG
                                 ACCT
GAM786  TUSP      3'  GAGATGGGGTTTTGCCATGTT  40028      CA TG
                                AACA  G  AAACCCCATCTC
                                ||||  |  ||||||||||||
                                TTGT  C  TTTGGGGTAGAG
                                  AC GT
GAM786  UBF-fl    3'  GATGGGGTTTTACCATGTT   52625      CA
                                AACA  GTGAAACCCCATC
                                ||||  |||||||||||||
                                TTGT  CATTTTGGGGTAG
                                  AC
GAM786  VDU1      3'  GAGATGGGGTTTCACCATGTT  31125      CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  WBSCR23   3'  GAGACGGGGTTTCACCATGTT  47435      CA         A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  LOC112687 3'  GAGATGGGGTTTGCCATGT   73235      CA  G
                                ACA  GT AAACCCCATCTC
                                |||  || ||||||||||||
                                TGT  CG TTTGGGGTAGAG
                                  AC  _
GAM786  LOC112817 3'  GAGACAGAGTTTCACTCTGT   57326     C       CCCA
                                ACA AGTGAAAC    TCTC
                                ||| ||||||||    ||||
                                TGT TCACTTTG    AGAG
                                  C       AGAC
GAM786  LOC112817 3'  GAGATGGGGTTTCACCGTGTT  57327       A
                                AACAC GTGAAACCCCATCTC
                                ||||| |||||||||||||||
                                TTGTG CACTTTGGGGTAGAG
                                   C
GAM786  LOC113523 5'  GAGACAGGGTTTCACCATGTT  73423      CA         CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
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                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  LOC115219 5'  GAGACGGGGTTTCATCATGTT  73695     CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  TACTTTGGGG AGAG
                                  AC         C
GAM786  LOC115648 3'  GAGACGGGGTTTCACCATGTT  60022     CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  LOC116411 5'  GAGACGGGGTTTCGCTGTGTT  74300               A
                                AACACAGTGAAACCCC TCTC
                                |||||||||||||||| ||||
                                TTGTGTCGCTTTGGGG AGAG
                                        C
GAM786  LOC119392 3'  GAGACTGGGTTTCACCACGTT  59814     ACA       CA
                                AAC   GTGAAACCC  TCTC
                                |||   |||||||||  ||||
                                TTG   CACTTTGGG  AGAG
                                  CAC        TC
GAM786  LOC120114 3'  GAGATGGGGTTTCACCATGTT  76045     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  LOC120224 5'  GAGACAGGGTTTCACCATGTT  57888     CA        CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  LOC120448 5'  GAGATTGGCTTCTCTGTGT    76068       T   A  CC
                                ACACAG GAA CC  ATCTC
                                |||||| ||| ||  |||||
                                TGTGTC CTT GG  TAGAG
                                   T   C  T_
GAM786  LOC120939 3'  GAGAGGGGGTTTCACCATGTT  76762     CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         G
GAM786  LOC126364 3'  GAGATGGGGTTTCGCCATGTT  76192     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CGCTTTGGGGTAGAG
                                  AC
GAM786  LOC126661 3'  GAGATGGGGTTTCACCATGTT  75057     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
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                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786   LOC126669 3'  GAGACGAAGTCTCGCTGTGTT  75935         A  CCCA
                                AACACAGTGA AC    TCTC
                                |||||||||| ||    ||||
                                TTGTGTCGCT TG    AGAG
                                     C  AAGC
GAM786   LOC126669 3'  GAGATGGGGTTTCGCCGT    75936    A
                                AC GTGAAACCCCATCTC
                                || ||||||||||||||
                                TG CGCTTTGGGGTAGAG
                                 C
GAM786   LOC128077 3'  GAGACAGGGTTTCACCATGTT  75215     CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786   LOC128077 3'  GAGACGGGGTTTCACCATGTT  75217     CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786   LOC128989 3'  GAGACGGGGTTTCACCATGTT  75317     CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786   LOC129880 3'  GAGACGGGGTTTCGCTGTGTT  75406             A
                                AACACAGTGAAACCCC TCTC
                                |||||||||||||||| ||||
                                TTGTGTCGCTTTGGGG AGAG
                                        C
GAM786   LOC130813 3'  GAGATGGGGTTTCTCCATGTT  76275     CAGT
                                AACA   GAAACCCCATCTC
                                ||||   ||||||||||||
                                TTGT   CTTTGGGGTAGAG
                                  ACCT
GAM786   LOC132241 5'  GAGAGTGGGTTTCACTATGTT  75562     C        CA
                                AACA AGTGAAACCC  TCTC
                                |||| ||||||||||  ||||
                                TTGT TCACTTTGGG  AGAG
                                  A         TG
GAM786   LOC132625 3'  GAGATGGGGTTTCACCATGTT  76440     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786   LOC135154 3'  AGACAAGGTTTCACCATGTT   75718     CA       CCA
                                AACA  GTGAAACC   TCT
                                ||||  ||||||||   |||
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                                TTGT  CACTTTGG   AGA
                                  AC       AAC
GAM786   LOC143916 3'  GAGATGGGGTTTCACCTTGTT  77141     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  TC
GAM786   LOC144317 5'  GAGACTGGGGTTTCTCCATGTT 77295     CAGT       _
                                AACA    GAAACCCCA TCTC
                                ||||    ||||||||| ||||
                                TTGT    CTTTGGGGT AGAG
                                  ACCT        C
GAM786   LOC144519 5'  GAGACGGGGTTTTGCCATGTT  77374     CA TG      A
                                AACA  G  AAACCCC TCTC
                                ||||  |  ||||||| ||||
                                TTGT  C  TTTGGGG AGAG
                                  AC GT      C
GAM786   LOC144667 3'  GAGATGGGGTCTCCCTATGTT  84087     C  T  A
                                AACA AG GA ACCCCATCTC
                                |||| || || ||||||||||
                                TTGT TC CT TGGGGTAGAG
                                  A  C  C
GAM786   LOC144871 3'  ATGGGGTTTCACTGTGTT    84118
                                AACACAGTGAAACCCCAT
                                ||||||||||||||||||
                                TTGTGTCACTTTGGGGTA

GAM786   LOC145453 5'  GAGACAGGGTCTCACTGTGT   77663        A    CA
                                ACACAGTGA ACCC  TCTC
                                ||||||||| ||||  ||||
                                TGTGTCACT TGGG  AGAG
                                     C    AC
GAM786   LOC145453 5'  GAGATGGGGTTTTGTCATGTT  77664     CA TG
                                AACA  G  AAACCCCATCTC
                                ||||  |  ||||||||||||
                                TTGT  T  TTTGGGGTAGAG
                                  AC GT
GAM786   LOC145622 3'  GAGAGGGGGTTTCACCACGTT  77816     ACA        A
                                AAC   GTGAAACCCC TCTC
                                |||   ||||||||| ||||
                                TTG   CACTTTGGGG AGAG
                                  CAC         G
GAM786   LOC146050 3'  GAGATGGGGTTTCACCATGTT  78117     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786   LOC146050 3'  GAGATGGGGTTTCTCCATGTT  78118     CAGT
                                AACA    GAAACCCCATCTC
                                ||||    ||||||||||||
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                                TTGT    CTTTGGGGTAGAG
                                  ACCT
GAM786   LOC146229 3'  GACGGGGTTTCACCATGTT    78279      CA         A
                                AACA  GTGAAACCCC TC
                                ||||  |||||||||| ||
                                TTGT  CACTTTGGGG AG
                                  AC          C
GAM786   LOC146229 3'  GAGACGGGGTTTCACCATGTT  78282      CA         A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC          C
GAM786   LOC146229 3'  GAGACGGGGTTTTACCGTGTT  78283       A         A
                                AACAC GTGAAACCCC TCTC
                                |||||  |||||||||| ||||
                                TTGTG CATTTTGGGG AGAG
                                   C          C
GAM786   LOC146229 3'  GAGATGGAGTTTCATTCTTGT  78284      C_        C
                                ACA  AGTGAAAC CCATCTC
                                |||  |||||||| |||||||
                                TGT  TTACTTTG GGTAGAG
                                  TC        A
GAM786   LOC146229 3'  GAGGCTGCACTTCGCTGTGTT  78285                ACCC  _
                                AACACAGTGAA    CA TCTC
                                ||||||||||    || ||||
                                TTGTGTCGCTT    GT GGAG
                                      CAC_  C
GAM786   LOC146346 5'  GAGACGGGGTTTCACCGTGTT  78397       A         A
                                AACAC GTGAAACCCC TCTC
                                |||||  |||||||||| ||||
                                TTGTG CACTTTGGGG AGAG
                                   C          C
GAM786   LOC146603 5'  GAGACGGGGTTTCACCGTGTT  78595       A         A
                                AACAC GTGAAACCCC TCTC
                                |||||  |||||||||| ||||
                                TTGTG CACTTTGGGG AGAG
                                   C          C
GAM786   LOC146784 5'  GAGATGGAGTTTCACTCTTGT  78712      C_        C
                                ACA  AGTGAAAC CCATCTC
                                |||  |||||||| |||||||
                                TGT  TCACTTTG GGTAGAG
                                  TC        A
GAM786   LOC146784 5'  GAGATGGGGTTTCACCATGTT  78713      CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786   LOC146839 3'  GAGACGGGGTTTCACCGTGTT  84842       A         A
                                AACAC GTGAAACCCC TCTC
                                |||||  |||||||||| ||||
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                                TTGTG CACTTTGGGG AGAG
                                  C         C
GAM786  LOC146894 3'  GAGATGGGGTTTCACCATGTT  59862      CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  LOC146901 3'  GAGACGGGGTTTCACCATGTT  84901      CA         A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  LOC146909 3'  GAGATGGGGTTTCACCGTGTT  78772       A
                                AACAC GTGAAACCCCATCTC
                                |||||| ||||||||||||||
                                TTGTG CACTTTGGGGTAGAG
                                  C
GAM786  LOC147054 3'  GATGGGGTTTCTCCATGTT    85007      CAGT
                                AACA    GAAACCCCATC
                                ||||    ||||||||||
                                TTGT    CTTTGGGGTAG
                                  ACCT
GAM786  LOC147080 5'  GAGACAAGGTTTCACCATGTT  85037      CA       CCA
                                AACA  GTGAAACC   TCTC
                                ||||  ||||||||   ||||
                                TTGT  CACTTTGG   AGAG
                                  AC       AAC
GAM786  LOC147166 3'  GAGATGGGGTTTCACCATGTT  78889      CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  LOC147276 3'  GAGATGGAGTTTCACTCTTGT  78963      C_       C
                                ACA  AGTGAAAC CCATCTC
                                |||  |||||||| |||||||
                                TGT  TCACTTTG GGTAGAG
                                  TC       A
GAM786  LOC147429 3'  GAGATGGGGTTTCACCATGTT  78996      CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  LOC147694 3'  GAGACGGGGTTTCACCGTGTT  79097       A         A
                                AACAC GTGAAACCCC TCTC
                                |||||| |||||||||| ||||
                                TTGTG CACTTTGGGG AGAG
                                  C         C
GAM786  LOC148137 3'  GAGACGGTGTTTCACTGTGTT  59099             C  A
                                AACACAGTGAAAC CC TCTC
                                |||||||||||| || ||||
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                                TTGTGTCACTTTG GG AGAG
                                      T  C
GAM786  LOC148147 3'  GAGATGAGGTTTCACCTTGTT  79399     CA       C
                                AACA  GTGAAACC CATCTC
                                ||||  |||||||| ||||||
                                TTGT  CACTTTGG GTAGAG
                                  TC       A
GAM786  LOC148189 5'  GAGACGGGGTTTCACCATGTT  79448     CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  LOC148887 5'  GAGACAGGGTTTCACCATGTT  85401     CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  LOC149171 5'  GAGATGGGGTTTCTCCATGTT  79968     CAGT
                                AACA   GAAACCCCATCTC
                                ||||   ||||||||||||
                                TTGT   CTTTGGGGTAGAG
                                  ACCT
GAM786  LOC149478 3'  GAGACGGGGGTTTCACCATGTT 80170     CA        A_
                                AACA  GTGAAACCCC  TCTC
                                ||||  ||||||||||  ||||
                                TTGT  CACTTTGGGG  AGAG
                                  AC         GC
GAM786  LOC149506 3'  GAGATCCCCTTCACTGTGT   85635         ACCCC
                                ACACAGTGAA    ATCTC
                                ||||||||||    |||||
                                TGTGTCACTT    TAGAG
                                     CCCC_
GAM786  LOC149577 3'  GAGACAGGCTTTCGCTGTGTT  85676          C  CA
                                AACACAGTGAAA CC  TCTC
                                ||||||||||| ||  ||||
                                TTGTGTCGCTTT GG  AGAG
                                       C  AC
GAM786  LOC149577 3'  GAGATGGGGTTTTGCCATGTT  85677     CA TG
                                AACA  G  AAACCCCATCTC
                                ||||  |  ||||||||||||
                                TTGT  C  TTTGGGGTAGAG
                                  AC GT
GAM786  LOC149684 5'  GAGATGGGGGCTCCCTATGTT  85764     C  T  AA
                                AACA AG GA  CCCCATCTC
                                |||| || ||  |||||||||
                                TTGT TC CT  GGGGTAGAG
                                  A  C  CG
GAM786  LOC149692 3'  GAGACAGGGTTTCACCATGTT  85735     CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
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                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786   LOC149703 5'  GAGACGGGGTTTTGCCATGTT  85820     CA TG      A
                                AACA  G  AAACCCC TCTC
                                ||||  |  ||||||| ||||
                                TTGT  C  TTTGGGG AGAG
                                  AC GT      C
GAM786   LOC149711 3'  GAGATGGGGTTTTACCATGTT  85852     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CATTTTGGGGTAGAG
                                  AC
GAM786   LOC150166 5'  ATGGGGTTTCACCATGTT    86032     CA
                                AACA  GTGAAACCCCAT
                                ||||  ||||||||||||
                                TTGT  CACTTTGGGGTA
                                  AC
GAM786   LOC150225 3'  GAGACGGTTTCACCATGT    86193     CA       CCA
                                ACA  GTGAAACC   TCTC
                                |||  ||||||||   ||||
                                TGT  CACTTTGG   AGAG
                                  AC       C__
GAM786   LOC150587 3'  GAGATGGGGGTCTCACTATGT  86243     C     AA_
                                ACA AGTGA   CCCCATCTC
                                ||| |||||   |||||||||
                                TGT TCACT   GGGGTAGAG
                                  A     CTG
GAM786   LOC150630 5'  GAGAGGGGGTTTCACCGTG    86301     A         A
                                CAC GTGAAACCCC TCTC
                                ||| ||||||||||| ||||
                                GTG CACTTTGGGG AGAG
                                  C         G
GAM786   LOC150696 3'  GAGACGGGGTTTTGCCATGTT  59159     CA TG      A
                                AACA  G  AAACCCC TCTC
                                ||||  |  ||||||| ||||
                                TTGT  C  TTTGGGG AGAG
                                  AC GT      C
GAM786   LOC150960 3'  GAGATGGGGTCTCACCCTGTT  80875     CA    A
                                AACA  GTGA ACCCCATCTC
                                ||||  |||| ||||||||||
                                TTGT  CACT TGGGGTAGAG
                                  CC    C
GAM786   LOC151057 3'  GAGACGGGGTTTCACCATGTT  86388     CA         A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786   LOC151201 3'  GAGACGGGGTTTCACCATGTT  86477     CA         A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
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                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786   LOC151475 5'  GAGACGAGGTTTCACCATGTT  86593     CA       CCA
                                AACA  GTGAAACC   TCTC
                                ||||  ||||||||   ||||
                                TTGT  CACTTTGG   AGAG
                                  AC       AGC
GAM786   LOC151701 3'  GAGACGGGGTTTCACCATGTT  86672     CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786   LOC151826 3'  GAGACAGGGTTTCACCGTGTT  81182      A       CA
                                AACAC GTGAAACCC  TCTC
                                |||||  |||||||||  ||||
                                TTGTG CACTTTGGG  AGAG
                                   C        AC
GAM786   LOC151877 3'  GAGATGGGGTCTTGCTGTGTT  86698       TG A
                                AACACAG  A ACCCCATCTC
                                |||||||  | ||||||||||
                                TTGTGTC  T TGGGGTAGAG
                                    GT C
GAM786   LOC151979 5'  GAGACGGGGTTTCACCATGTT  81249     CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786   LOC152137 3'  AGAGCGGGTTTCACCATGTT   81305     CA       CA
                                AACA  GTGAAACCC  TCT
                                ||||  |||||||||  |||
                                TTGT  CACTTTGGG  AGA
                                  AC       CG
GAM786   LOC152343 3'  GACTGGGTTTCACCATGTT    81427     CA       CA
                                AACA  GTGAAACCC  TC
                                ||||  |||||||||  ||
                                TTGT  CACTTTGGG  AG
                                  AC       TC
GAM786   LOC152343 3'  GAGATGGAGTCTTGCTGTGT   81428       TG A  C
                                ACACAG  A AC CCATCTC
                                ||||||  | || |||||||
                                TGTGTC  T TG GGTAGAG
                                   GT C  A
GAM786   LOC152445 3'  GAGACAGGGTTTCACCATGTT  86948     CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC       AC
GAM786   LOC152719 5'  GAGACGGGGTTTCACCATGTT  87029     CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
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                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786   LOC152794 5'  GAGATGGGGTTTCATCATGTT  81559      CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  TACTTTGGGGTAGAG
                                  AC
GAM786   LOC152804 3'  GAGACTGGGTCTCGCTGTGTT  87080          A    CA
                                AACACAGTGA ACCC  TCTC
                                |||||||||| ||||  ||||
                                TTGTGTCGCT TGGG  AGAG
                                      C    TC
GAM786   LOC153077 3'  GAGATGGGGCTTCACCATGTT  87126      CA     A
                                AACA  GTGAA CCCCATCTC
                                ||||  ||||| |||||||||
                                TTGT  CACTT GGGGTAGAG
                                  AC    C
GAM786   LOC153606 5'  GAGATAGGGTTTCACCATGTT  87257      CA        C
                                AACA  GTGAAACCC ATCTC
                                ||||  ||||||||| |||||
                                TTGT  CACTTTGGG TAGAG
                                  AC        A
GAM786   LOC153688 3'  GAGACAGGGTTTCACCATGTT  87316      CA        CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786   LOC153883 5'  ATGGGGTTTTACCATGTT    81887      CA
                                AACA  GTGAAACCCCAT
                                ||||  ||||||||||||
                                TTGT  CATTTTGGGGTA
                                  AC
GAM786   LOC153910 5'  GAGACAGGGTTTTGCCATGTT  81907      CA TG     CA
                                AACA  G  AAACCC  TCTC
                                ||||  |  ||||||  ||||
                                TTGT  C  TTTGGG  AGAG
                                  AC GT     AC
GAM786   LOC154877 5'  GAGACAGGGTTTCACCCTGTT  87550      CA        CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  CC        AC
GAM786   LOC154877 3'  GAGATGGGGTCTTGCTATGT   87551     C  TG A
                                ACA AG  A ACCCCATCTC
                                ||| ||  | ||||||||||
                                TGT TC  T TGGGGTAGAG
                                  A  GT C
GAM786   LOC154877 5'  GAGATGGGGTTTTGCCATGTT  87552      CA TG
                                AACA  G  AAACCCCATCTC
                                ||||  |  ||||||||||||
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                                TTGT  C  TTTGGGGTAGAG
                                  AC GT
GAM786  LOC154877 3'  GAGTCGGGGTTTCACCATGTT  87553     CA        AT
                                AACA  GTGAAACCCC  CTC
                                ||||  ||||||||||  |||
                                TTGT  CACTTTGGGG  GAG
                                  AC         CT
GAM786  LOC154930 3'  GAGACAGGATTTTACTGTGTT  82092           C  CA
                                AACACAGTGAAA CC  TCTC
                                ||||||||||||  ||  ||||
                                TTGTGTCATTTT GG  AGAG
                                       A  AC
GAM786  LOC157247 5'  GAGACGGGGTTTCACCAGTGT  82298     A_        A
                                ACAC  GTGAAACCCC TCTC
                                ||||  ||||||||||  ||||
                                TGTG  CACTTTGGGG AGAG
                                  AC         C
GAM786  LOC157506 3'  GAGACGGGGTTTCACCATGTT  82367     CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  ||||||||||  ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  LOC157798 5'  GAGACGGAGTCTTGCTGTGT   87858      TG A  C  A
                                ACACAG  A AC CC TCTC
                                ||||||  | || || ||||
                                TGTGTC  T TG GG AGAG
                                   GT C  A  C
GAM786  LOC157798 5'  GAGACGGGGTTTCACCTTGTT  87859     CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  ||||||||||  ||||
                                TTGT  CACTTTGGGG AGAG
                                  TC         C
GAM786  LOC157858 5'  GAGACAGGGTTTCACTATGT   87888     C         CA
                                ACA AGTGAAACCC  TCTC
                                |||  ||||||||||  ||||
                                TGT TCACTTTGGG  AGAG
                                  A         AC
GAM786  LOC158014 5'  GAGATAGAGTTTCACTCTTGT  82560     C_       CCC
                                ACA  AGTGAAAC   ATCTC
                                |||  ||||||||   |||||
                                TGT  TCACTTTG   TAGAG
                                  TC       AGA
GAM786  LOC158014 5'  GAGATGGGGTCTCGCTATGTT  82561     C     A
                                AACA AGTGA ACCCCATCTC
                                |||| ||||| ||||||||||
                                TTGT TCGCT TGGGGTAGAG
                                  A    C
GAM786  LOC158310 5'  GAGACAGGGTTTCACAATGTT  88082     CA        CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
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                                TTGT  CACTTTGGG  AGAG
                                  AA        AC
GAM786   LOC158402 5'  GAGGGGGGTTTCACCGTGTT   88148      A        A
                                AACAC GTGAAACCCC TCTC
                                ||||| |||||||||| ||||
                                TTGTG CACTTTGGGG GGAG
                                  C        _
GAM786   LOC158476 3'  GAGACAGGGTTTCACCATGTT  88194      CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786   LOC158549 5'  GAGATAGGGGTTTCACCGTGTT 88224       A        _
                                AACAC GTGAAACCCC ATCTC
                                ||||| |||||||||| |||||
                                TTGTG CACTTTGGGG TAGAG
                                  C         A
GAM786   LOC158629 5'  AGACAGGGTTTTGCTATGTT   88236      C  TG     CA
                                AACA AG  AAACCC  TCT
                                |||| ||  ||||||  |||
                                TTGT TC  TTTGGG  AGA
                                  A  GT     AC
GAM786   LOC158668 3'  GAGGTGGGGTTTCACCATG    69901    CA
                                CA  GTGAAACCCCATCTC
                                ||  ||||||||||||||
                                GT  CACTTTGGGGTGGAG
                                 AC
GAM786   LOC158865 5'  GAGATGGGGACTTCACCGTGT  88308      A    A_
                                ACAC GTGAA  CCCCATCTC
                                |||| |||||  |||||||||
                                TGTG CACTT  GGGGTAGAG
                                  C    CA
GAM786   LOC160646 3'  GAGATGGGGCTTCACCATGTT  83113      CA    A
                                AACA  GTGAA CCCCATCTC
                                ||||  ||||| |||||||||
                                TTGT  CACTT GGGGTAGAG
                                  AC    C
GAM786   LOC161829 3'  GAGATGGGGTTTCACCATGTT  83190      CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786   LOC162427 3'  ATGGGGTTTCACCATGTT    83220      CA
                                AACA  GTGAAACCCCAT
                                ||||  ||||||||||||
                                TTGT  CACTTTGGGGTA
                                  AC
GAM786   LOC169611 3'  GAGACAGAGTTTCGCTTTTGTT 83649      C_       CCCA
                                AACA  AGTGAAAC    TCTC
                                ||||  ||||||||    ||||
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                                TTGT  TCGCTTTG    AGAG
                                  TT       AGAC
GAM786   LOC169611 3'  GAGACAGGGGTTTCACCACGTT 83650     ACA        A_
                                AAC   GTGAAACCCC  TCTC
                                |||   ||||||||||  ||||
                                TTG   CACTTTGGGG  AGAG
                                  CAC         AC
GAM786   LOC170082 5'  GAGATGGGGTTTCACCATGTT  83443     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786   LOC196047 5'  GAGCCAGGGTTTCACCATGT   91154     CA       CAT
                                ACA  GTGAAACCC   CTC
                                |||  |||||||||   |||
                                TGT  CACTTTGGG   GAG
                                  AC        ACC
GAM786   LOC196411 3'  GAGATGGGGTTTCACTATGTT  89047     C
                                AACA AGTGAAACCCCATCTC
                                |||| ||||||||||||||||
                                TTGT TCACTTTGGGGTAGAG
                                  A
GAM786   LOC196529 3'  GAGACAGGGTCTCACTGTGTT  89133          A    CA
                                AACACAGTGA ACCC  TCTC
                                |||||||||| ||||  ||||
                                TTGTGTCACT TGGG  AGAG
                                      C    AC
GAM786   LOC196529 3'  GAGACAGGGTTTCACTACGTT  89134     AC        CA
                                AAC  AGTGAAACCC  TCTC
                                |||  ||||||||||  ||||
                                TTG  TCACTTTGGG  AGAG
                                  CA         AC
GAM786   LOC196792 5'  GAGATGGGAAGCTGCAGTT    88914     A_   GAAAC
                                AAC  CAGT    CCCATCTC
                                |||  ||||    ||||||||
                                TTG  GTCG    GGGTAGAG
                                  AC    AA___
GAM786   LOC197358 3'  GAGACGGGGTTTCATCATGTT  89432     CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  TACTTTGGGG AGAG
                                  AC         C
GAM786   LOC197358 3'  GAGATGGGGTTTCACCATGTT  89433     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786   LOC199699 3'  AGACAGGGTTTCACCGTGTT   89664      A       CA
                                AACAC GTGAAACCC  TCT
                                |||||  |||||||||  |||
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                                TTGTG CACTTTGGG  AGA
                                  C        AC
GAM786  LOC199786 3'  GAGACGGTGGTTTCACCATGTT 89753      CA       _  A
                                AACA  GTGAAACC CC TCTC
                                ||||  |||||||| || ||||
                                TTGT  CACTTTGG GG AGAG
                                  AC       T  C
GAM786  LOC199786 3'  GAGATGGGGTTTCACCATGTT  89754      CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  LOC199906 3'  AGACAGGGTTTCATCATGTT   89842      CA        CA
                                AACA  GTGAAACCC  TCT
                                ||||  |||||||||  |||
                                TTGT  TACTTTGGG  AGA
                                  AC        AC
GAM786  LOC199906 3'  GAGAGGGAGTCTCGCTGTGTT  89853          A  _  A
                                AACACAGTGA AC CCC TCTC
                                |||||||||| || ||| ||||
                                TTGTGTCGCT TG GGG AGAG
                                     C  A  _
GAM786  LOC200107 5'  GATCCGGTTTCATCGTGTT    89987       A       CC
                                AACAC GTGAAACC  ATC
                                |||||| ||||||||  |||
                                TTGTG TACTTTGG  TAG
                                  C       CC
GAM786  LOC200268 3'  GAGATGGGATTTTGCCATGTT  90086      CA TG   C
                                AACA  G  AAA CCCATCTC
                                ||||  |  ||| ||||||||
                                TTGT  C  TTT GGGTAGAG
                                  AC GT   A
GAM786  LOC200301 5'  GAGACGGGGTTTCACCGTGTT  90140       A         A
                                AACAC GTGAAACCCC TCTC
                                ||||| |||||||||| ||||
                                TTGTG CACTTTGGGG AGAG
                                  C         C
GAM786  LOC200310 3'  GAGACGGGGTTTCACCATGTT  66327      CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  LOC200314 3'  GAGATGGGGTTTCACCACGTT  91600     ACA
                                AAC   GTGAAACCCCATCTC
                                |||   ||||||||||||||||
                                TTG   CACTTTGGGGTAGAG
                                  CAC
GAM786  LOC200316 3'  GACTGGGTTTCACCATGTT    90181      CA        CA
                                AACA  GTGAAACCC  TC
                                ||||  |||||||||  ||
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                                TTGT  CACTTTGGG  AG
                                  AC        TC
GAM786  LOC200316 3'  GAGACGGAGTTTCACTCTGT  90182    C      C  A
                                ACA AGTGAAAC CC TCTC
                                ||| |||||||| || ||||
                                TGT TCACTTTG GG AGAG
                                  C       A  C
GAM786  LOC200316 5'  GAGACGGGGTTTCTCCATGTT  90183     CAGT      A
                                AACA   GAAACCCC TCTC
                                ||||   |||||||| ||||
                                TTGT   CTTTGGGG AGAG
                                  ACCT      C
GAM786  LOC200339 3'  GAGATGGGATTTTCCCTTGTT  91616     C  T   C_
                                AACA AG GAAA  CCCATCTC
                                |||| || ||||  ||||||||
                                TTGT TC CTTT  GGGTAGAG
                                  _  C    TA
GAM786  LOC200407 3'  GAGACAGGGTTTTGCCATGTT  91627     CA TG     CA
                                AACA  G  AAACCC  TCTC
                                ||||  |  ||||||  ||||
                                TTGT  C  TTTGGG  AGAG
                                  AC GT     AC
GAM786  LOC200845 5'  GAGATGGGGTTTCACTATGTT  90317     C
                                AACA AGTGAAACCCCATCTC
                                |||| ||||||||||||||||
                                TTGT TCACTTTGGGGTAGAG
                                  A
GAM786  LOC200860 3'  GAGACGGGGTTTCGCTCTTGT  91748     C_        A
                                ACA  AGTGAAACCCC TCTC
                                |||  |||||||||| ||||
                                TGT  TCGCTTTGGGG AGAG
                                  TC         C
GAM786  LOC200860 3'  GAGACGGGGTTTCTCCATGTT  91749     CAGT      A
                                AACA   GAAACCCC TCTC
                                ||||   |||||||| ||||
                                TTGT   CTTTGGGG AGAG
                                  ACCT      C
GAM786  LOC201164 3'  GAGACAGGGTTTCACCATGTT  89494     CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  LOC201294 3'  GAGACGGGGTTTCACCATGTT  89584     CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC        C
GAM786  LOC201411 3'  GAGACAGGGTTTCACCATGTT  63642     CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
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                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786   LOC201626 3'  ATGGGGTTTCGCCACGTT    90425     ACA
                                AAC   GTGAAACCCCAT
                                |||   ||||||||||||
                                TTG   CGCTTTGGGGTA
                                  CAC
GAM786   LOC201626 3'  GAGATGGAGTTTCACTCTTGT  90433     C_       C
                                ACA  AGTGAAAC CCATCTC
                                |||  |||||||| |||||||
                                TGT  TCACTTTG GGTAGAG
                                  TC       A
GAM786   LOC201627 3'  GAGATGGGGTTTCTCCATGTT  90455      CAGT
                                AACA    GAAACCCCATCTC
                                ||||    ||||||||||||||
                                TTGT    CTTTGGGGTAGAG
                                  ACCT
GAM786   LOC201696 3'  GAGATGGAGTTTCACTCTTGT  63820     C_       C
                                ACA  AGTGAAAC CCATCTC
                                |||  |||||||| |||||||
                                TGT  TCACTTTG GGTAGAG
                                  TC       A
GAM786   LOC202020 5'  CGAGACAGCCCTTGGCCACCAC 90598         AAACC  ________   ___
           TGTGT                  ACACAGTG    CCA      TCTC   G
                                |||||||     |||      ||||   |
                                TGTGTCAC    GGT      AGAG   C
                                    CACC_   TCCCGAC    __
GAM786   LOC202347 3'  GAGATGACTTAAATCACTGTGT 91945         AACCC__
           T                    AACACAGTGA      CATCTC
                                ||||||||||      ||||||
                                TTGTGTCACT      GTAGAG
                                     AAATTCA
GAM786   LOC202460 5'  GAGATGGGGTTTCACCATGT   90671     CA
                                ACA  GTGAAACCCCATCTC
                                |||  ||||||||||||||||
                                TGT  CACTTTGGGGTAGAG
                                  AC
GAM786   LOC202868 5'  AGATGGCTTCTCGCTGTGT    91985         AACC
                                ACACAGTGA    CCATCT
                                |||||||||    ||||||
                                TGTGTCGCT    GGTAGA
                                     CTTC
GAM786   LOC202908 5'  GAGATGAGGTTTCACTCTGTT  90724      C       C
                                AACA AGTGAAACC CATCTC
                                |||| ||||||||| ||||||
                                TTGT TCACTTTGG GTAGAG
                                  C        A
GAM786   LOC202908 5'  GAGATGGGGTCTCACCCTGT   90725     CA    A
                                ACA  GTGA ACCCCATCTC
                                |||  |||| ||||||||||
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                                TGT  CACT TGGGGTAGAG
                                  CC    C
GAM786   LOC202934 3'  GAGACAGGGTTTCACCACGTT  92039     ACA        CA
                                AAC   GTGAAACCC  TCTC
                                |||   |||||||||  ||||
                                TTG   CACTTTGGG  AGAG
                                  CAC        AC
GAM786   LOC203197 3'  GAGATGGGGTTTCGCCATGTT  90812      CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CGCTTTGGGGTAGAG
                                  AC
GAM786   LOC203339 3'  GAGATGGGGTTTCACCATGTT  92211      CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786   LOC203350 3'  GAGACGGGGTTTCACCGTGTT  92240       A         A
                                AACAC GTGAAACCCC TCTC
                                |||||  |||||||||| ||||
                                TTGTG CACTTTGGGG AGAG
                                   C         C
GAM786   LOC203369 3'  GATGGGGTTTCACTGTGTT   90889
                                AACACAGTGAAACCCCATC
                                |||||||||||||||||||
                                TTGTGTCACTTTGGGGTAG

GAM786   LOC204804 3'  GAGACAGGGTCTCACTGTGT   91043          A    CA
                                ACACAGTGA ACCC  TCTC
                                |||||||||  ||||  ||||
                                TGTGTCACT TGGG  AGAG
                                     C    AC
GAM786   LOC204804 3'  GAGATGAGGTTTCACCTTGTT  91044      CA        C
                                AACA  GTGAAACC CATCTC
                                ||||  ||||||||  ||||||
                                TTGT  CACTTTGG GTAGAG
                                  TC        A
GAM786   LOC205251 5'  GACAGGGTTTCACCATGTT   92357      CA        CA
                                AACA  GTGAAACCC  TC
                                ||||  |||||||||  ||
                                TTGT  CACTTTGGG  AG
                                  AC         AC
GAM786   LOC219445 5'  GACGGGGTTTCACCGTGTT   93204       A         A
                                AACAC GTGAAACCCC TC
                                |||||  |||||||||| ||
                                TTGTG CACTTTGGGG AG
                                   C         C
GAM786   LOC219735 3'  GAGACGGGGTTTCACCGTGTT  94728       A         A
                                AACAC GTGAAACCCC TCTC
                                |||||  |||||||||| ||||
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                                TTGTG CACTTTGGGG AGAG
                                   C         C
GAM786   LOC219736 3'  GAGATGGGGTTTTGCCATGTT  94741      CA TG
                                AACA  G  AAACCCCATCTC
                                ||||  |  ||||||||||||
                                TTGT  C  TTTGGGGTAGAG
                                  AC GT
GAM786   LOC219894 3'  GAGATGGGGTTTCACCGTGTT  94905       A
                                AACAC GTGAAACCCCATCTC
                                |||||| ||||||||||||||||
                                TTGTG CACTTTGGGGTAGAG
                                   C
GAM786   LOC220064 3'  GAGATGGGGTTTTGCCTTGTT  95066      CA TG
                                AACA  G  AAACCCCATCTC
                                ||||  |  ||||||||||||
                                TTGT  C  TTTGGGGTAGAG
                                  TC GT
GAM786   LOC220074 3'  GAGACAAGGTTTCGCCATGTT  59978      CA       CCA
                                AACA  GTGAAACC   TCTC
                                ||||  ||||||||   ||||
                                TTGT  CGCTTTGG   AGAG
                                  AC       AAC
GAM786   LOC220074 3'  GAGACGGGGTTTCACCATGTT  59981      CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786   LOC220074 3'  GAGATGGGGTTTCGCCATGTT  59982      CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||||
                                TTGT  CGCTTTGGGGTAGAG
                                  AC
GAM786   LOC221042 3'  GAGACGGGGTTTGCTGTGTT   94802        G      A
                                AACACAGT AAACCCC TCTC
                                |||||||| ||||||| ||||
                                TTGTGTCG TTTGGGG AGAG
                                     _      C
GAM786   LOC221271 3'  GAGGGGGTTTCATCATGTT    93518      CA        A
                                AACA  GTGAAACCCC TC
                                ||||  |||||||||| ||
                                TTGT  TACTTTGGGG AG
                                  AC         G
GAM786   LOC221296 3'  GAGACGGGGTTTCACCATG    93609     CA        A
                                CA  GTGAAACCCC TCTC
                                ||  |||||||||| ||||
                                GT  CACTTTGGGG AGAG
                                 AC         C
GAM786   LOC221663 5'  GAGACAAGGTTTCACTATGTT  95461      C        CCA
                                AACA AGTGAAACC   TCTC
                                |||| |||||||||   ||||
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                                TTGT TCACTTTGG   AGAG
                                  A        AAC
GAM786   LOC221814 3'  GAGATGAAGGGGTTTCCAGGT  95555    AGT      ___
                                AC   GAAACCCC   ATCTC
                                ||   ||||||||   |||||
                                TG   CTTTGGGG   TAGAG
                                 GAC        AAG
GAM786   LOC221964 3'  GAGACAGGGTTTTGCCGTGTT  95606     A TG     CA
                                AACAC G  AAACCC  TCTC
                                ||||| |  ||||||  ||||
                                TTGTG C  TTTGGG  AGAG
                                   C GT     AC
GAM786   LOC221968 3'  GAGATGGAAATGTTTTACT   94153       C___
                                AGTGAAAC   CCATCTC
                                ||||||||   |||||||
                                TCATTTTG   GGTAGAG
                                     TAAA
GAM786   LOC222068 3'  GAGATGGGGTTTTACCATGTT  94276     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CATTTTGGGGTAGAG
                                  AC
GAM786   LOC222224 5'  GAGACAGGGTTTCACCATGTT  95872     CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786   LOC245771 5'  GAGATGGGGTTTCATCATGTT  94477     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  TACTTTGGGGTAGAG
                                  AC
GAM786   LOC253664 3'  GAGATGGGGTTTCCCCATGTT  96466     CAGT
                                AACA   GAAACCCCATCTC
                                ||||   ||||||||||||
                                TTGT   CTTTGGGGTAGAG
                                  ACCC
GAM786   LOC253666 3'  GAGACGGGGTTTCACCATGTT  96761     CA       A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786   LOC253805 3'  GAGATAGGGTTTCACAATGTT  98176     CA       C
                                AACA  GTGAAACCC ATCTC
                                ||||  ||||||||| |||||
                                TTGT  CACTTTGGG TAGAG
                                  AA        A
GAM786   LOC254018 5'  GAGATGGGGTTTCGCCATGTT  98740     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
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                                TTGT  CGCTTTGGGGTAGAG
                                  AC
GAM786   LOC254100 3'  GAGATGGGGTTTCGTCATGTT  98155     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  TGCTTTGGGGTAGAG
                                  AC
GAM786   LOC254268 3'  GAGATGGGGTTTCACCATGTT  97143     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786   LOC254295 5'  GAGACGGGGTTTCACCGTGTT  97891      A        A
                                AACAC GTGAAACCCC TCTC
                                ||||| |||||||||| ||||
                                TTGTG CACTTTGGGG AGAG
                                   C         C
GAM786   LOC254351 5'  GACGGGGTTTCTCCGTGTT   96688      AGT      A
                                AACAC   GAAACCCC TC
                                |||||   |||||||| ||
                                TTGTG   CTTTGGGG AG
                                   CCT       C
GAM786   LOC254413 5'  GAGACAGGGAGAGCTGTGTT   98913       GAAA   CA
                                AACACAGT    CCC  TCTC
                                ||||||||    |||  ||||
                                TTGTGTCG    GGG  AGAG
                                     AGA_   AC
GAM786   LOC254655 3'  GAGACGGGGTTTCACCATGTT  97220     CA       A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786   LOC254778 3'  AGACAGGATTTTGCTGTGTT   97826       TG   C  CA
                                AACACAG  AAA CC  TCT
                                |||||||  ||| ||  |||
                                TTGTGTC  TTT GG  AGA
                                     GT   A  AC
GAM786   LOC254806 5'  GAGACGGCGCGTGCACTGTGTT 97480         AAACC_  A
                                AACACAGTG     CC TCTC
                                |||||||||     || ||||
                                TTGTGTCAC     GG AGAG
                                     GTGCGC  C
GAM786   LOC255002 3'  GAGATGCAGATACTGTGTT    98579        AAACCC
                                AACACAGTG     CATCTC
                                |||||||||     ||||||
                                TTGTGTCAT     GTAGAG
                                     AGAC__
GAM786   LOC255037 3'  GAGACGAAGTCTCGCTGTGT   98439         A  CCCA
                                ACACAGTGA AC    TCTC
                                |||||||||  ||    ||||
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                                TGTGTCGCT TG    AGAG
                                     C  AAGC
GAM786  LOC255308 3'  GAGACGGGGTTTCGGCATGTT  96176     CAG        A
                                AACA   TGAAACCCC TCTC
                                ||||   ||||||||| ||||
                                TTGT   GCTTTGGGG AGAG
                                  ACG        C
GAM786  LOC255338 5'  GAGACAGGGCATCACTGTGTT  97632          AA   CA
                                AACACAGTGA  CCC  TCTC
                                ||||||||||  |||  ||||
                                TTGTGTCACT  GGG  AGAG
                                     AC   AC
GAM786  LOC255465 3'  GAGACGGGTTTCACCATGTT   99114     CA        CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        C_
GAM786  LOC255497 3'  GAGACGGGGTTTCACCATGTT  98985     CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  LOC255645 3'  GAGATGTGATCACTGGTT    98475     A     AACCC
                                AAC CAGTGA     CATCTC
                                ||| ||||||     ||||||
                                TTG GTCACT     GTAGAG
                                  _     AGT__
GAM786  LOC256221 3'  GAGACGGGGTTTCACCGTGTT  96910      A        A
                                AACAC GTGAAACCCC TCTC
                                ||||| |||||||||| ||||
                                TTGTG CACTTTGGGG AGAG
                                   C         C
GAM786  LOC256306 3'  GAGACGGGGTTTCACCATGTT  98515     CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  LOC256453 5'  GAGATGGGGAAATGGTGTG    98324     G  AAA
                                CACA TG   CCCCATCTC
                                |||| ||   |||||||||
                                GTGT GT   GGGGTAGAG
                                  G  AAA
GAM786  LOC257486 3'  GAGACGGGGTTTCACCATGTT  69771     CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC         C
GAM786  LOC257486 3'  GAGTAGTTATCACTGTGT    69772          _  CCCAT
                                ACACAGTGA AAC     CTC
                                ||||||||| |||     |||
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                                TGTGTCACT TTG    GAG
                                     A  AT___
GAM786  LOC51008  5' GAGATGGGGTTTCTCCATGTT  32533     CAGT
                                AACA   GAAACCCCATCTC
                                ||||   ||||||||||||
                                TTGT   CTTTGGGGTAGAG
                                  ACCT
GAM786  LOC51193  5' GAGACGGGGTTTCCCCATGTT  33367     CAGT      A
                                AACA   GAAACCCC TCTC
                                ||||   |||||||| ||||
                                TTGT   CTTTGGGG AGAG
                                  ACCC      C
GAM786  LOC51219  5' GAGACGGGGTTTCTCCATGT   33545    GT__      A
                                ACA   GAAACCCC TCTC
                                |||   |||||||| ||||
                                TGT   CTTTGGGG AGAG
                                  ACCT      C
GAM786  LOC56181  5' GAGACAGGGCTTCACTGTGTT  97273          A  CA
                                AACACAGTGAA CCC  TCTC
                                |||||||||| |||  ||||
                                TTGTGTCACTT GGG  AGAG
                                      C  AC
GAM786  LOC57107  3' GAGATGGGGTTTCACTATGTT  40188     C
                                AACA AGTGAAACCCCATCTC
                                |||| ||||||||||||||||
                                TTGT TCACTTTGGGGTAGAG
                                  A
GAM786  LOC57146  3' GATGGGGTTTCACCATGTT   40296     CA
                                AACA  GTGAAACCCCATC
                                ||||  ||||||||||||
                                TTGT  CACTTTGGGGTAG
                                  AC
GAM786  LOC81034  3' ATGGGGTTTCACCATGTT    48581     CA
                                AACA  GTGAAACCCCAT
                                ||||  ||||||||||||
                                TTGT  CACTTTGGGGTA
                                  AC
GAM786  LOC89231  3' GAGATGGGGTCTCACTATGTT  94299     C    A
                                AACA AGTGA ACCCCATCTC
                                |||| ||||| ||||||||||
                                TTGT TCACT TGGGGTAGAG
                                  A    C
GAM786  LOC89919  3' GAGACGGGGTTTCACCATGTT  61374     CA       A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC        C
GAM786  LOC89932  3' GAGACGGGGTTTCTCCATGTT  61462     CAGT      A
                                AACA   GAAACCCC TCTC
                                ||||   |||||||| ||||
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                                TTGT   CTTTGGGG AGAG
                                  ACCT       C
GAM786  LOC89932  3' GAGATGGGGTTTCACCATGTT  61463     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGAG
                                  AC
GAM786  LOC90288  3' GAGACGGGGTTTCACAGTGTT  62789      A        A
                                AACAC GTGAAACCCC TCTC
                                ||||| |||||||||| ||||
                                TTGTG CACTTTGGGG AGAG
                                  A         C
GAM786  LOC90333  3' GAGACTGGGTTTCACCGTGTT  62959      A       CA
                                AACAC GTGAAACCC  TCTC
                                ||||| |||||||||  ||||
                                TTGTG CACTTTGGG  AGAG
                                  C         TC
GAM786  LOC90459  3' GAGGCGGGGTTTCACCATGTT  63556     CA        AT
                                AACA  GTGAAACCCC  CTC
                                ||||  ||||||||||  |||
                                TTGT  CACTTTGGGG  GAG
                                  AC         CG
GAM786  LOC90485  3' GAGGCAGGGTTTCACCATGTT  63700     CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  GGAG
                                  AC         AC
GAM786  LOC90485  3' GAGGCGGGGTTTCACCATGTT  63701     CA        AT
                                AACA  GTGAAACCCC  CTC
                                ||||  ||||||||||  |||
                                TTGT  CACTTTGGGG  GAG
                                  AC         CG
GAM786  LOC90670  3' GATATGGTTTGACTGTGTT   64484        G    CC
                                AACACAGT AAACC  ATC
                                |||||||| |||||  |||
                                TTGTGTCA TTTGG  TAG
                                     G    TA
GAM786  LOC91115  3' GAGATGGAGTTTCACTCTTGT  65565    C_      C
                                ACA  AGTGAAAC CCATCTC
                                |||  |||||||| |||||||
                                TGT  TCACTTTG GGTAGAG
                                  TC       A
GAM786  LOC91115  3' GAGATGGGGTTTCACTGTGTT  65566
                                AACACAGTGAAACCCCATCTC
                                |||||||||||||||||||||
                                TTGTGTCACTTTGGGGTAGAG

GAM786  LOC91115  3' GAGATGGGGTTTCATCATGTT  65567     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
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                                TTGT  TACTTTGGGGTAGAG
                                  AC
GAM786  LOC91250  5' GAGATGGGGTTTCATCATGTT  65916     CA
                                AACA  GTGAAACCCCATCTC
                                ||||  ||||||||||||||
                                TTGT  TACTTTGGGGTAGAG
                                  AC
GAM786  LOC91291  5' GAGACAAGGTTTCACCCTGTT  66089     CA      CCA
                                AACA  GTGAAACC   TCTC
                                ||||  ||||||||   ||||
                                TTGT  CACTTTGG   AGAG
                                  CC       AAC
GAM786  LOC91373  3' GAGATGGGGTTTGACCGTGTT  66414      A  G
                                AACAC GT AAACCCCATCTC
                                |||||  || ||||||||||||
                                TTGTG CA TTTGGGGTAGAG
                                  C  G
GAM786  LOC91893  3' GAGACGAGGTTTCACCGTGTT  68072      A      CCA
                                AACAC GTGAAACC   TCTC
                                |||||  ||||||||   ||||
                                TTGTG CACTTTGG   AGAG
                                  C       AGC
GAM786  LOC92148  5' GAGACGGGGTTTCACCGTGTT  68879      A        A
                                AACAC GTGAAACCCC TCTC
                                |||||  |||||||||| ||||
                                TTGTG CACTTTGGGG AGAG
                                  C         C
GAM786  LOC92303  3' GAGATGGGTTTCACCATGTT   69392     CA       C
                                AACA  GTGAAACCC ATCTC
                                ||||  ||||||||| |||||
                                TTGT  CACTTTGGG TAGAG
                                  AC        _
GAM786  LOC92482  3' GAGATGAGGTCTTGCTTTGTT  70021     C  TG A   C
                                AACA AG  A ACC CATCTC
                                |||| ||  | ||| ||||||
                                TTGT TC  T TGG GTAGAG
                                  T  GT C   A
GAM786  LOC92661  5' GAGGCGGGGTTTCACTGTGTT  70630            AT
                                AACACAGTGAAACCCC  CTC
                                ||||||||||||||||  |||
                                TTGTGTCACTTTGGGG  GAG
                                        CG
GAM786  LOC92689  3' GAGACAGGGTTTCACCATGTT  70775     CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  LOC92697  5' GAGACGGGGTTTCGCTGTGTT  70811            A
                                AACACAGTGAAACCCC TCTC
                                |||||||||||||||| ||||
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                                TTGTGTCGCTTTGGGG AGAG
                                        C
GAM786  LOC92841  3' GAGACAGGGTTTCACCATGTT  71253     CA       CA
                                AACA  GTGAAACCC  TCTC
                                ||||  |||||||||  ||||
                                TTGT  CACTTTGGG  AGAG
                                  AC        AC
GAM786  LOC92841  3' GAGACGGGGTTTCACCATGTT  71254     CA        A
                                AACA  GTGAAACCCC TCTC
                                ||||  |||||||||| ||||
                                TTGT  CACTTTGGGG AGAG
                                  AC        C
GAM786  LOC93129  3' GAGACGGGGTTTCGCTGT    71957           A
                                ACAGTGAAACCCC TCTC
                                |||||||||||| ||||
                                TGTCGCTTTGGGG AGAG
                                        C
GAM786  LOC93349  3' GAGACGGGGTTTCACTATGTT  57268     C        A
                                AACA AGTGAAACCCC TCTC
                                |||| |||||||||| ||||
                                TTGT TCACTTTGGGG AGAG
                                  A         C
GAM787  VAT1      3' TAACCAAGGCTGCCTCTT    22091     A  C   C
                                AAGA GC GCC TGGTTG
                                |||| || ||| ||||||
                                TTCT CG CGG ACCAAT
                                  C  T   A
GAM787  AP3M2     3' CATGTGCAGAAGTAGCTTCT   23300      CG CCTGG
                                AGAAGC  C    TTGCACATG
                                ||||||  |    |||||||||
                                TCTTCG  G    GACGTGTAC
                                   AT AA___
GAM787  FLJ12505  5' GTCAACAAGAGCGGCTTC    45717       C  G    C
                                GAAGCCGC CT GTTG AC
                                |||||||| || |||| ||
                                CTTCGGCG GA CAAC TG
                                     A  A   _
GAM787  KIAA0275  3' CATGTGTTCAAAGAACGGTTTC 29324        CC  GGTT
           TT                    AAGAAGCCG  CT   GCACATG
                                |||||||||  ||   |||||||
                                TTCTTTGGC  GA   TGTGTAC
                                     AA  AACT
GAM787  KIAA0830  3' GCATCCAAACGGCTTCTT    70268        CCC   T
                                AAGAAGCCG   TGG TGC
                                |||||||||   ||| |||
                                TTCTTCGGC   ACC ACG
                                     AA_   T
GAM787  KIAA1399  3' CATGTGCAATGCCAGCCCCTTC 70790     CC  CC   __
                                GAAG  GC  TGGT  TGCACATG
                                ||||  ||  ||||  ||||||||
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                                CTTC  CG  ACCG  ACGTGTAC
                                  CC  __   TA
GAM787  KIAA1643  3'  CATATGCATAGAAACGGCTTCT 65154       CC_  GT   C
                                AGAAGCCG   CTG  TGCA ATG
                                ||||||||   |||  |||| |||
                                TCTTCGGC   GAT  ACGT TAC
                                    AAA   __   A
GAM787  MAGE-E1   3'  GCACCCTAGGCGGCTTCTT   48675         CT  T
                                AAGAAGCCGCC  GG TGC
                                ||||||||||  || |||
                                TTCTTCGGCGG  CC ACG
                                      AT  C
GAM787  MRPS2    3'  CATGTGCAGAACGGCCCCTT   32631    AA   CCCTGG
                                AAG  GCCG    TTGCACATG
                                |||  ||||    |||||||||
                                TTC  CGGC    GACGTGTAC
                                  CC   AA____
GAM787  SSTK     3'  CATGCGCATCCGCGATTC    50169    GC   CCT  T   A
                                GAA  CGC   GG TGC CATG
                                |||  |||   || ||| ||||
                                CTT  GCG   CC ACG GTAC
                                  A_   ___  T   C
GAM787  LOC148887 3'  CATGCGCATTAAAGCAGGGCGG 85396    A   _     G ____   A
          GCTCCT                 AG AGCC GCCCTG T    TGC CATG
                                || |||| |||||| |    ||| ||||
                                TC TCGG CGGGAC A    ACG GTAC
                                 C   G     G AATT   C
GAM787  LOC152402 5'  GTGCCCAGAGCCGGCTTCT   86884        _ C    TT
                                AGAAGCCG C CTGG  GCAC
                                |||||||| | ||||  ||||
                                TCTTCGGC G GACC  CGTG
                                    C A   __
GAM787  LOC158078 3'  CATGTGTGTTGAGAGCTTCT   82600       CGCC  GGT
                                AGAAGC   CT   TGCACATG
                                ||||||   ||   ||||||||
                                TCTTCG   GA   GTGTGTAC
                                   A___  GTT
GAM787  LOC163882 3'  CATAGGCAACCAGAGCCACTTC 83040      CC  C       AC
                                GAAG  GC CTGGTTGC  ATG
                                ||||  || ||||||||  |||
                                CTTC  CG GACCAACG  TAC
                                  AC  A       GA
GAM787  LOC200138 3'  CATGTGCTTCCAGGGTGGCTTC 91539           TT
                                GAAGCCGCCCTGG  GCACATG
                                ||||||||||||  |||||||
                                CTTCGGTGGGACC  CGTGTAC
                                       TT
GAM787  LOC51099  3'  CAACCAGGCAGCCTTCTT    32600       _ C   C
                                AAGAAG C GCC TGGTTG
                                |||||| | ||| ||||||
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                                TTCTTC G CGG ACCAAC
                                   C A  _
GAM788  FSTL1    3'  TTGAAAGAGGAACAGACCC   24008       CT  GC
                                GGGTCTGT  CTT  TTCAA
                                ||||||||  |||  |||||
                                CCCAGACA  GAG  AAGTT
                                    AG   A_
GAM788  MTMR6    5'  GGCAGACAGACCCGCGG    95199          CTT
                                CCGCGGGTCTGTCT   GCT
                                ||||||||||||||   |||
                                GGCGCCCAGACAGA   CGG
                                      ___
GAM788  MYO3A    3'  GAAACAAGAGACCTGGG    60769    G    TGTC    C
                                CC CGGGTC    TCTTG TTC
                                || ||||||    ||||| |||
                                GG GTCCAG    AGAAC AAG
                                _    _____    A
GAM788  SLC6A6   3'  TTGTACAAAAAGAAAACCCACG 13187    C   CTG   C  GCTT
           G                     CCG GGGT   TCT TT    CAA
                                ||| ||||   ||| ||    |||
                                GGC CCCA   AGA AA    GTT
                                  A    AA_   A  ACAT
GAM788  BANP     5'  AAGCAAGAAACTTGAGG     66797    G    CTGTC
                                CC CGGGT    TCTTGCTT
                                || |||||    ||||||||
                                GG GTTCA    AGAACGAA
                                 A    A_____
GAM788  GBA2     5'  TGAAGCAAGAGCTCCCCGG   71579    C   TCTGT
                                CCG GGG    CTCTTGCTTCA
                                ||| |||    ||||||||||
                                GGC CCC    GAGAACGAAGT
                                  _  TC___
GAM788  KIAA1318 5'  GAGTCAGACAGACCCG     67876         CTT
                                CGGGTCTGTCT   GCTT
                                ||||||||||   ||||
                                GCCCAGACAGA   TGAG
                                      C__
GAM788  KIAA1817 3'  TGAAGCAAGCGGACCC     68783       TCT
                                GGGTCTG   CTTGCTTCA
                                |||||||   |||||||||
                                CCCAGGC   GAACGAAGT
                                     ___
GAM788  MST4     3'  AAGCAAGATCATTTACCCAAGG 33741    GC   CT  C_
                                CC  GGGT  GT  TCTTGCTT
                                ||  ||||  ||  ||||||||
                                GG  CCCA  TA  AGAACGAA
                                 AA   TT  CT
GAM788  ZIC5     3'  GAGCCTGAGACAAACCCGTG   53614       C     TT
                                CGCGGGT TGTCTC  GCTT
                                ||||||| ||||||  ||||
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                                GTGCCCA ACAGAG  CGAG
                                    A     TC
GAM788  LOC150174 3'  TGAAACACAGACCCAGG     80442    GC       CTCTT C
                                CC  GGGTCTGT    G TTCA
                                ||  ||||||||    | ||||
                                GG  CCCAGACA    C AAGT
                                 A_       _____ A
GAM788  LOC150213 3'  TGAAACACAGACCCAGG     75361    GC       CTCTT C
                                CC  GGGTCTGT    G TTCA
                                ||  ||||||||    | ||||
                                GG  CCCAGACA    C AAGT
                                 A_       _____ A
GAM788  LOC152762 5'  GAGAAGAAAACAGACCCAGG  81534    GC       C_   G
                                CC  GGGTCTGT  TCTT CTT
                                ||  ||||||||  |||| |||
                                GG  CCCAGACA  AGAA GAG
                                 A_       AA   _
GAM788  LOC220021 5'  GAAGCAAGTCACAACCCAGC  95022    _    C   CT
                                GC GGGT TGT  CTTGCTTC
                                || |||| |||  ||||||||
                                CG CCCA ACA  GAACGAAG
                                 A    _   CT
GAM788  LOC254835 3'  TTGAAGCAAGAGACAGACCC  98713
                                GGGTCTGTCTCTTGCTTCAA
                                ||||||||||||||||||||
                                CCCAGACAGAGAACGAAGTT

GAM788  LOC257364 3'  GAAGCAGGTCCAAACCCAGG  96644    GC    C  TCT
                                CC  GGGT TG   CTTGCTTC
                                ||  |||| ||   ||||||||
                                GG  CCCA AC   GGACGAAG
                                 A_    A  CT_
GAM789  ABCC11    3'  GCTGAGCTCAGAGGTTC     53684       T     C
                                GAGCCT CTGAGC CAGC
                                |||||| |||||| ||||
                                CTTGGA GACTCG GTCG
                                    _      A
GAM789  BCS1L     3'  GCTGGGCTCAGCTCAGCTCT   16328      CTT_
                                AGAGC    CTGAGCCCAGC
                                |||||    ||||||||||||
                                TCTCG    GACTCGGGTCG
                                   ACTC
GAM789  CAMLG     3'  GCTGAGCTAGTGCTTTTA    10001        _ TCTG   C
                                TAAGAGC CT    AGC CAGC
                                ||||||| ||    ||| ||||
                                ATTTTCG GA    TCG GTCG
                                    T _____   A
GAM789  CD97      3'  GCCGGGCAGGAGGTTCT     10123          GA    A
                                AGAGCCTTCT  GCCC GC
                                ||||||||||  |||| ||
```

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                                TCTTGGAGGA  CGGG CG
                                      __    C
GAM789  CD97    3'  GCCGGGCAGGAGGTTCT     55306         GA    A
                                AGAGCCTTCT  GCCC GC
                                ||||||||||  |||| ||
                                TCTTGGAGGA  CGGG CG
                                      __    C
GAM789  CERD4   3'  GCTGAGCTCTGAGAAGGCTC   24879         __    C
                                GAGCCTTCT  GAGC CAGC
                                |||||||||  |||| ||||
                                CTCGGAAGA  CTCG GTCG
                                     GT    A
GAM789  CETP    5'  GCTGAACGGCTCGGGCCACTTA 5374      A_    TCT     ___
                                TAAG  GCCT   GAGCC   CAGC
                                ||||  ||||   |||||   ||||
                                ATTC  CGGG   CTCGG   GTCG
                                  AC    ___     CAA
GAM789  CHD2    5'  GCTGGGAAGGAGGCTCT     8868          GAG
                                AGAGCCTTCT   CCCAGC
                                ||||||||||   ||||||
                                TCTCGGAGGA   GGGTCG
                                     A__
GAM789  CLN6    3'  CTGGGCCCAGAGGCTTT     35836        T   A
                                AGAGCCT CTG GCCCAG
                                ||||||| ||| ||||||
                                TTTCGGA GAC CGGGTC
                                    _  C
GAM789  CNTN2   5'  GCTGAGCTGAGGCTCTT     18662         CTG   C
                                AAGAGCCTT   AGC CAGC
                                |||||||||   ||| ||||
                                TTCTCGGAG   TCG GTCG
                                     ___   A
GAM789  CTSB    5'  GCTGGGCTGCAGGCTCT     65366        TCTG
                                AGAGCCT    AGCCCAGC
                                |||||||    ||||||||
                                TCTCGGA    TCGGGTCG
                                    CG__
GAM789  DGSI    3'  GCTGGGCTCATAGACGCTTCA  42964    A    CTTC_
                                A GAGC     TGAGCCCAGC
                                | ||||     ||||||||||
                                A TTCG     ACTCGGGTCG
                                 C    CAGAT
GAM789  DLG4    5'  GCTGGGCTCAGCTTCTT     9082       CCTT
                                AAGAG    CTGAGCCCAGC
                                |||||    ||||||||||
                                TTCTT    GACTCGGGTCG
                                  C___
GAM789  FOLR2   3'  GCTGGGCTCAGCTCAGCTC   7687       CTT_
                                GAGC    CTGAGCCCAGC
                                ||||    ||||||||||
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                                CTCG   GACTCGGGTCG
                                  ACTC
GAM789  GGA3    3' GCTGGACACAGGAGGCCTC  57610    _     AGC
                                GAG CCTTCTG  CCAGC
                                ||| |||||||  |||||
                                CTC GGAGGAC  GGTCG
                                  C      ACA
GAM789  GGA3    3' GCTGGACACAGGAGGCCTC  26589    _     AGC
                                GAG CCTTCTG  CCAGC
                                ||| |||||||  |||||
                                CTC GGAGGAC  GGTCG
                                  C      ACA
GAM789  GGT1    3' GCCAGGCTCAGGTGGCCTC  26426    _ T      CA
                                GAG CC TCTGAGCC  GC
                                ||| || ||||||||  ||
                                CTC GG GGACTCGG  CG
                                  C  T       AC
GAM789  GNB3    5' GCTGAGGGAGTAAGGAGGCTC 10842        GAG_  __
                                GAGCCTTCT   CCC  AGC
                                |||||||||   |||  |||
                                CTCGGAGGA   GGG  TCG
                                     ATGA   AG
GAM789  GRM1    3' GCTGGGCTGACAGACTCCTC  7740     CCT   __
                                GAG   TCTG  AGCCCAGC
                                |||   ||||  ||||||||
                                CTC   AGAC  TCGGGTCG
                                  CTC    AG
GAM789  HEM1    5' CTGGGTCCTAAGGCTCTT   19236        CT  G
                                AAGAGCCTT  GA CCCAG
                                |||||||||  || |||||
                                TTCTCGGAA  CT GGGTC
                                     TC  _
GAM789  HIS1    3' CTGGAAGAGGCTCTTG     22338        T  GAGC
                                TAAGAGCCT CT    CCAG
                                ||||||||| ||    ||||
                                GTTCTCGGA GA    GGTC
                                     _  A___
GAM789  IMPDH1  3' GCTGCAGTCGAAGGCTTT   7952         T  GCC
                                AGAGCCTTC GA   CAGC
                                ||||||||| ||   ||||
                                TTTCGGAAG CT   GTCG
                                     _  GAC
GAM789  INSRR   3' CTGGGCCAGGGCTCTT     68988       TT   A
                                AAGAGCC  CTG GCCCAG
                                |||||||  ||| ||||||
                                TTCTCGG  GAC CGGGTC
                                     __   _
GAM789  LZTR1   3' GCTGAGCCGGGAGGCCCTTG  23172     A      A  C
                                TAAG GCCTTCTG GC CAGC
                                |||| |||||||| || ||||
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                                GTTC CGGAGGGC CG GTCG
                                  C       _ A
GAM789  MKI67    3'  CTGGGGCAGGTTCTTA      11594         TCT AG
                                TAAGAGCCT   G  CCCAG
                                |||||||||   |  |||||
                                ATTCTTGGA   C  GGGTC
                                     ___ G_
GAM789  MYO1C    3'  GCTGGGCTCTGGTGCCCTCT   61866      CCT_  T
                                AGAG    TC GAGCCCAGC
                                ||||    || |||||||||
                                TCTC    GG CTCGGGTCG
                                  CCGT  T
GAM789  RENT1    3'  GCTGGACTCAGAAGCCAAGCT  12817      ____       C
                                AGC    CTTCTGAG CCAGC
                                |||    |||||||| |||||
                                TCG    GAAGACTC GGTCG
                                  AACC       A
GAM789  RFC1     3'  GCTGGGTCAGGCTCTTA      12828         TCT  G
                                TAAGAGCCT   GA CCCAGC
                                |||||||||   || ||||||
                                ATTCTCGGA   CT GGGTCG
                                     ___ _
GAM789  RGS6     3'  GCTGGGCCCGGTGGAGGCTC   16279        __  A
                                GAGCCTT  CTG GCCCAGC
                                |||||||  ||| |||||||
                                CTCGGAG  GGC CGGGTCG
                                    GT   C
GAM789  SIM2     3'  GCCGGGCTCAGTGGCTC      24801       TT       A
                                GAGCC  CTGAGCCC GC
                                |||||  |||||||| ||
                                CTCGG  GACTCGGG CG
                                   T_       C
GAM789  SLC28A2  3'  GCCGGGCTCAGTGGCTC      16151       TT       A
                                GAGCC  CTGAGCCC GC
                                |||||  |||||||| ||
                                CTCGG  GACTCGGG CG
                                   T_       C
GAM789  SNRPN    5'  GCTGAGCTCAGAGCCTTCT    43320       CC       C
                                AGAG  TTCTGAGC CAGC
                                ||||  |||||||| ||||
                                TCTT  GAGACTCG GTCG
                                  CC       A
GAM789  SNRPN    5'  GCTGAGCTCAGAGCCTTCT    43327       CC       C
                                AGAG  TTCTGAGC CAGC
                                ||||  |||||||| ||||
                                TCTT  GAGACTCG GTCG
                                  CC       A
GAM789  SNRPN    5'  GCTGAGCTCAGAGCCTTCT    43329       CC       C
                                AGAG  TTCTGAGC CAGC
                                ||||  |||||||| ||||
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                                TCTT  GAGACTCG GTCG
                                  CC       A
GAM789  SNRPN    5'  GCTGAGCTCAGAGCCTTCT   43331     CC       C
                                AGAG  TTCTGAGC CAGC
                                ||||  |||||||| ||||
                                TCTT  GAGACTCG GTCG
                                  CC       A
GAM789  UNG      5'  GGGCCCAGCCCTGGGCTCTTA  14013       T___   A
                                TAAGAGCCT    CTG GCCC
                                |||||||||    ||| ||||
                                ATTCTCGGG    GAC CGGG
                                     TCCC   C
GAM789  WHSC1    3'  GCTCCTGAGAAGGCTCTTG   56697          ___
                                TAAGAGCCTTCT   GAGC
                                ||||||||||||   ||||
                                GTTCTCGGAAGA   CTCG
                                       GTC
GAM789  A4GALT   3'  GCTGGGTGGGGAGGCTCTT   34300         GA
                                AAGAGCCTTCT  GCCCAGC
                                ||||||||||  |||||||
                                TTCTCGGAGGG  TGGGTCG
                                      G_
GAM789  ACAS2L   3'  GCTGGGCTGAGAGCCCTTT   68647     CC   G
                                AGAG  TTCT AGCCCAGC
                                ||||  |||| ||||||||
                                TTTC  GAGA TCGGGTCG
                                  CC   G
GAM789  AF311304 3'  CTGGTCATAGAAGGCTTT    49153         AGC
                                AGAGCCTTCTG   CCAG
                                ||||||||||   ||||
                                TTTCGGAAGAT   GGTC
                                      ACT
GAM789  C20orf162 3' GCTGGGCTGGGAGGCTT     55501        G
                                GAGCCTTCT AGCCCAGC
                                ||||||||| ||||||||
                                TTCGGAGGG TCGGGTCG
                                          _
GAM789  C6orf5   3'  GCCGGGCTCAGGTGACCCTTA  31994     AGCCT       A
                                TAAG    TCTGAGCCC GC
                                ||||    ||||||||| ||
                                ATTC    GGACTCGGG CG
                                  CCAGT       C
GAM789  CASP9    3'  GCCAGTGACAGACAGGCTCTTA 8773        _   A_  CCA
                                TAAGAGCCT TCTG  GC   GC
                                ||||||||| ||||  ||   ||
                                ATTCTCGGA AGAC  TG   CG
                                     C   AG  AC_
GAM789  CNOT8    3'  GCTGAGCTGTGAGGGCTT    17708       TG   C
                                GAGCCTTC  AGC CAGC
                                ||||||||  ||| ||||
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                                TTCGGGAG  TCG GTCG
                                     TG   A
GAM789  CRMP5    3'  GCTGGGCTCACAGGCCTCT   39703     _  TC
                                AGAG CCT  TGAGCCCAGC
                                |||| |||  ||||||||||
                                TCTC GGA  ACTCGGGTCG
                                  C   C_
GAM789  DDM36    3'  GCTGTTTTAACAGTAGGCTCTT 40926        T  __  CC
           A                     TAAGAGCCT CTG  AG  CAGC
                                |||||||||  |||  ||  ||||
                                ATTCTCGGA GAC  TT  GTCG
                                      T   AA  TT
GAM789  FASTK    3'  GCTGGGCTCGAGGGCCCT    47687    A     T
                                AG GCCTTC GAGCCCAGC
                                || ||||||  |||||||||
                                TC CGGGAG CTCGGGTCG
                                 C     _
GAM789  FLJ11560 5'  GCTGAGCTCAGGAGCTGC    48010    __       C
                                GC  CTTCTGAGC CAGC
                                ||  |||||||||  ||||
                                CG  GAGGACTCG GTCG
                                 TC        A
GAM789  FLJ13220 3'  GCCATCGAAAGGTTCTTA    41922          C  __
                                TAAGAGCCTT TGA  GC
                                ||||||||||  |||  ||
                                ATTCTTGGAA GCT  CG
                                      A   AC
GAM789  FLJ14490 3'  GCTGGGCTCAGGCAGCTCTTG  52445        CT
                                TAAGAGC  TCTGAGCCCAGC
                                |||||||  ||||||||||||
                                GTTCTCG  GGACTCGGGTCG
                                    AC
GAM789  FLJ20330 3'  GCTGGGCAAGAGCTTTTA    39143       CT   GA
                                TAAGAGC  TCT  GCCCAGC
                                |||||||  |||  |||||||
                                ATTTTCG  AGA  CGGGTCG
                                   __   A_
GAM789  FLJ20886 5'  CTAAGCCAGGAGGCTTT     96811          A  CC
                                AGAGCCTTCTG GC  AG
                                ||||||||||| ||  ||
                                TTTCGGAGGAC CG  TC
                                      _  AA
GAM789  FLJ21687 5'  GCCGGAAGGAGGCTGTTA    46299     G       GAGC  A
                                TAA AGCCTTCT    CC GC
                                ||| ||||||||    || ||
                                ATT TCGGAGGA    GG CG
                                  G       A___  C
GAM789  FLJ21841 5'  CTGGCTCAGGAAAGCCCT    45154    A  C_       C
                                AG GC  TTCTGAGCC AG
                                || ||  ||||||||| ||
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                                TC CG  AGGACTCGG TC
                                 C  AA       _
GAM789  FLJ21977  3'  GCTGAGCTGCAGGGGCTTT   50870       T  _  C
                                AGAGCCT CTG AGC CAGC
                                ||||||| ||| ||| ||||
                                TTTCGGG GAC TCG GTCG
                                    _  G   A
GAM789  FLJ21977  5'  GCTGAGGCTTCGAAGACCTC  50871    C_   T   _
                                GAG  CTTC GAGCC CAGC
                                |||  |||| ||||| ||||
                                CTC  GAAG TTCGG GTCG
                                  CA   C    A
GAM789  FLJ22029  3'  GCCAGCATCAAGGCTTTTA   46911         ____  A
                                TAAGAGCCTT   CTG GC
                                ||||||||||   ||| ||
                                ATTTTCGGAA   GAC CG
                                      CTAC  _
GAM789  FLJ22246  3'  GCTGGGCCCAGGGTTCT    48214      TT  A
                                AGAGCC  CTG GCCCAGC
                                ||||||  ||| |||||||
                                TCTTGG  GAC CGGGTCG
                                   __  C
GAM789  FLJ23584  3'  GCTGGCAGAGAGGGCTC    45038       GA  C
                                GAGCCTTCT  GCC AGC
                                |||||||||  ||| |||
                                CTCGGGAGA  CGG TCG
                                     GA  _
GAM789  HERPUD1   3'  CTGTACGTAGAAGGCCTTA   28693    A     AGCC
                                TAAG GCCTTCTG   CAG
                                |||| ||||||||   |||
                                ATTC CGGAAGAT   GTC
                                  _      GCAT
GAM789  HIC2      3'  GCTGGGCTGGCAGCCTTT    65870    C  T  G
                                AGAG CT CT AGCCCAGC
                                |||| || || ||||||||
                                TTTC GA GG TCGGGTCG
                                  C  C  _
GAM789  HRIHFB2436 5'  GCCGGGCCCGGCCGGCTTCA  27570   A   TT  A   A
                                A GAGCC  CTG GCCC GC
                                | |||||  ||| |||| ||
                                A TTCGG  GGC CGGG CG
                                 C    CC  C   C
GAM789  HS3ST1    3'  GCTAAGCTCAGAAACTTT    18854    CC      CC
                                AGAG  TTCTGAGC  AGC
                                ||||  ||||||||  |||
                                TTTC  AAGACTCG  TCG
                                  A_      AA
GAM789  HSH2      3'  GCCGGGCTCAGTGGCTC     52741     TT      A
                                GAGCC  CTGAGCCC GC
                                |||||  |||||||| ||
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                                CTCGG  GACTCGGG CG
                                   T_       C
GAM789  HSPC121   5' GCCGGGTTGCAGGCGCTC    60469     CT   _    A
                                GAGC  TCTG AGCCC GC
                                ||||  |||| ||||| ||
                                CTCG  GGAC TTGGG CG
                                  C_   G    C
GAM789  KBRAS2    3' GCTGGGCTCAGTGGCTC     34623      TT
                                GAGCC  CTGAGCCCAGC
                                |||||  ||||||||||
                                CTCGG  GACTCGGGTCG
                                   T_
GAM789  KIAA0161  3' GCTGGGCTTGAGCCCTC     29203     CC   T
                                GAG  TTC GAGCCCAGC
                                |||  ||| |||||||||
                                CTC  GAG TTCGGGTCG
                                  CC   _
GAM789  KIAA0323  3' GCTAAACTTAGAGGCTGCT    63948    _    T    CCC
                                AG AGCCT CTGAG   AGC
                                || ||||| |||||   |||
                                TC TCGGA GATTC   TCG
                                 G    _    AAA
GAM789  KIAA0514  3' GCTGGGCTCAGCCAAGCTC    28749     CTT_
                                GAGC    CTGAGCCCAGC
                                ||||    ||||||||||
                                CTCG    GACTCGGGTCG
                                  AACC
GAM789  KIAA0800  3' GCTGGGCTCAGAAGCACT     28806    A  C
                                AG GC TTCTGAGCCCAGC
                                || || |||||||||||||
                                TC CG AAGACTCGGGTCG
                                 A  _
GAM789  KIAA1030  3' GCTGTAGGGAAAGGGTCTTA   94982      G   _  GAGCC
                                TAAGA CCTT CT     CAGC
                                ||||| |||| ||     ||||
                                ATTCT GGAA GG     GTCG
                                   G    A  GAT__
GAM789  KIAA1042  5' GCTGAGCTCTCATGGAGGCTCT 31051        T___    C
                                AGAGCCTTC    GAGC CAGC
                                |||||||||    |||| ||||
                                TCTCGGAGG    CTCG GTCG
                                     TACT    A
GAM789  KIAA1155  3' CTGGGCCCAGAAGGTCTTG    62912      G      A
                                TAAGA CCTTCTG GCCCAG
                                ||||| ||||||| ||||||
                                GTTCT GGAAGAC CGGGTC
                                   _      C
GAM789  KIAA1432  5' GCTGGGGTGCAGAAGGCT     67305        AG_
                                AGCCTTCTG   CCCAGC
                                |||||||||   ||||||
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                                TCGGAAGAC  GGGTCG
                                     GTG
GAM789  KIAA1719  3'  GCTGGGCTCTGCCCCTTG   68733     A_  CTTCT
                                TAAG  GC    GAGCCCAGC
                                ||||  ||    |||||||||
                                GTTC  CG    CTCGGGTCG
                                  CC  T____
GAM789  KIAA1808  5'  GCTGGACTACCAGAGGCTCT  87049       T  __  C
                                AGAGCCT CTG  AG CCAGC
                                ||||||| |||  || |||||
                                TCTCGGA GAC  TC GGTCG
                                    _  CA  A
GAM789  KIAA1862  3'  GCTGGGCTCATGGCCCT    69511    A  TTC
                                AG GCC   TGAGCCCAGC
                                || |||   ||||||||||
                                TC CGG   ACTCGGGTCG
                                 C  T__
GAM789  KIAA1871  3'  GCTGGACTTGAACTCTTG    61906      CC  T  C
                                TAAGAG  TTC GAG CCAGC
                                ||||||  ||| ||| |||||
                                GTTCTC  AAG TTC GGTCG
                                   __  _  A
GAM789  KIAA1893  3'  GCTGGGCTCACAGAAGCTCTT  73589      C  __
                                AAGAGC TTCT  GAGCCCAGC
                                |||||| ||||  |||||||||
                                TTCTCG AAGA  CTCGGGTCG
                                   _  CA
GAM789  KIAA1904  3'  GCTGGGCTCAGGCCCTGGGCTC 73873       ____
           T                     AGAGCCT   TCTGAGCCCAGC
                                |||||||   ||||||||||||
                                TCTCGGG   GGACTCGGGTCG
                                    TCCC
GAM789  LGI2    3'  GCCAGGCTCAGAGCTCT    36927     CT     CA
                                AGAGC  TCTGAGCC  GC
                                |||||  ||||||||  ||
                                TCTCG  AGACTCGG  CG
                                  __       AC
GAM789  MADP-1   5'  GCTGAGCCGAGGGCTC     53577       T A  C
                                GAGCCTTC G GC CAGC
                                |||||||| | || ||||
                                CTCGGGAG C CG GTCG
                                   _ _  A
GAM789  MGC22014  3'  GCTGGAGTGCGAGGTTCTTA  65114         CTGA  _
                                TAAGAGCCTT   GC CCAGC
                                ||||||||||   || |||||
                                ATTCTTGGAG   TG GGTCG
                                     CG__  A
GAM789  MGC2454  3'  GCCGGGTTCAGGCCCTTG   48284    A   TCT    A
                                TAAG GCCT  GAGCCC GC
                                |||| ||||  |||||| ||
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                                GTTC CGGA   CTTGGG CG
                                  C   ___     C
GAM789  MGC2474  3' GCTGGGCTCAAGGAATCCTC  43962    CC   __
                                GAG  TTCT  GAGCCCAGC
                                |||  ||||  |||||||||
                                CTC  AAGG  CTCGGGTCG
                                  CT    AA
GAM789  MGC3123  3' GCTGGGCCCTAGGCTCTTG   44345        TCTGA
                                TAAGAGCCT    GCCCAGC
                                |||||||||    |||||||
                                GTTCTCGGA    CGGGTCG
                                     TCC__
GAM789  MRPS21   5' CTGAGCGCGCGAGGCTCT    49959        C  A  C
                                AGAGCCTT TG GC CAG
                                |||||||| || || |||
                                TCTCGGAG GC CG GTC
                                     C  G  A
GAM789  NETO2    3' GCCAGGCTCAGGCTGCCTCTT 36595      _ CT       CA
                                AAGAG C  TCTGAGCC  GC
                                |||||  |  ||||||||  ||
                                TTCTC G  GGACTCGG  CG
                                   C TC       AC
GAM789  NPEPL1   3' GCTGACAGCCAGGCTCTTA   45424        T_   AGCC
                                TAAGAGCCT  CTG    CAGC
                                |||||||||  |||    ||||
                                ATTCTCGGA  GAC    GTCG
                                     CC   A___
GAM789  PILR(ALPHA) 5' CTGGTTTGGGGAAGGCTC    26481         __    C
                                GAGCCTTCT  GAGCC AG
                                |||||||||  |||||  ||
                                CTCGGAAGG  TTTGG TC
                                     GG    _
GAM789  PTPRT    3' CTGGGCTCAGGAGCTCT     56492      C
                                AGAGC TTCTGAGCCCAG
                                |||||  ||||||||||||
                                TCTCG AGGACTCGGGTC
                                  _
GAM789  PTPRT    3' GCTGGGGTCTGGAAGGCTC   56501        _  G
                                GAGCCTTCT GA CCCAGC
                                |||||||||  ||  ||||||
                                CTCGGAAGG CT GGGTCG
                                     T  G
GAM789  SCAND2   5' GCTGGGACAGGAAGGCTCT   42143        GAG
                                AGAGCCTTCT   CCCAGC
                                ||||||||||   ||||||
                                TCTCGGAAGG   GGGTCG
                                      ACA
GAM789  SCAND2   5' GCTGGGACAGGAAGGCTCT   54418        GAG
                                AGAGCCTTCT   CCCAGC
                                ||||||||||   ||||||
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                                TCTCGGAAGG  GGGTCG
                                     ACA
GAM789  SCAND2   5' GCTGGGACAGGAAGGCTCT  54429       GAG
                                AGAGCCTTCT  CCCAGC
                                ||||||||||  ||||||
                                TCTCGGAAGG  GGGTCG
                                     ACA
GAM789  SCAND2   5' GCTGGGACAGGAAGGCTCT  54430       GAG
                                AGAGCCTTCT  CCCAGC
                                ||||||||||  ||||||
                                TCTCGGAAGG  GGGTCG
                                     ACA
GAM789  SCAND2   5' GCTGGGACAGGAAGGCTCT  54431       GAG
                                AGAGCCTTCT  CCCAGC
                                ||||||||||  ||||||
                                TCTCGGAAGG  GGGTCG
                                     ACA
GAM789  SCAND2   5' GCTGGGACAGGAAGGCTCT  54433       GAG
                                AGAGCCTTCT  CCCAGC
                                ||||||||||  ||||||
                                TCTCGGAAGG  GGGTCG
                                     ACA
GAM789  SNTG1    3' GCTGGGAAATTTGAAAGCCTTA 39100     A  C   TGAG__
                                TAAG GC TTC     CCCAGC
                                |||| || |||     ||||||
                                ATTC CG AAG     GGGTCG
                                  _ A   TTTAAA
GAM789  TESK2    3' CGCCAGGCTCAACTTCTGGGCT 63883     TC____     CA ___
          C                      GAGCCT     TGAGCC  GC   G
                                ||||||     ||||||  ||   |
                                CTCGGG     ACTCGG  CG   C
                                   TCTTCA     AC  ___
GAM789  TIAF1    3' GCCGGGTCCAGGTTCTTA    55295       TCT AG   A
                                TAAGAGCCT   G  CCC GC
                                |||||||||   |  ||| ||
                                ATTCTTGGA   C  GGG CG
                                     ___ CT   C
GAM789  TNFRSF21 3' CTGGATTGTGAGGCTCTTA   27825       CT  GC
                                TAAGAGCCTT  GA  CCAG
                                ||||||||||  ||  ||||
                                ATTCTCGGAG  TT  GGTC
                                     TG  A_
GAM789  ZNF286   3' GCTGGGTTCAAAGTCCTTA   40668     AG C  C
                                TAAG  C TT TGAGCCCAGC
                                ||||  | || ||||||||||
                                ATTC  G AA ACTTGGGTCG
                                  CT _  _
GAM789  LOC112817 5' GCTGGGCTTCTGGCTTCA   57330   A    TTCT
                                A GAGCC   GAGCCCAGC
                                | |||||   |||||||||
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                                A TTCGG    TTCGGGTCG
                                 C     TC__
GAM789   LOC113730 5'  GCTGACGGGTCAAAGCCTC    73500     C   C   G __
                                GAG CTT TGA CC  CAGC
                                ||| ||| ||| ||  ||||
                                CTC GAA ACT GG  GTCG
                                  C   _   G  CA
GAM789   LOC116437 3'  GCTGGACCTGTCTTGAAGGCTC 74327          T  _ ____
           TT                     AAGAGCCTTC GAG C    CCAGC
                                ||||||||||| ||| |    |||||
                                TTCTCGGAAG TTC G    GGTCG
                                      _   T TCCA
GAM789   LOC130813 5'  CTGGGCTCAAATGCTCT     76274       C  C
                                AGAGC TT TGAGCCCAG
                                ||||| || |||||||||
                                TCTCG AA ACTCGGGTC
                                   T  _
GAM789   LOC138389 5'  CTGGACTGGGCTCTTG      76737         TCTG  C
                                TAAGAGCCT    AG CCAG
                                |||||||||    || ||||
                                GTTCTCGGG    TC GGTC
                                     ____  A
GAM789   LOC144473 5'  CTGGGGAAAAGGTTCTTA     83994          CTGAG
                                TAAGAGCCTT     CCCAG
                                ||||||||||     |||||
                                ATTCTTGGAA     GGGTC
                                     AAG__
GAM789   LOC145719 5'  GCTGAGCCTGGGGGCTCTTA   84467          TGA  C
                                TAAGAGCCTTC   GC CAGC
                                ||||||||||   || ||||
                                ATTCTCGGGGG   CG GTCG
                                     TC_  A
GAM789   LOC145720 5'  GCTGAGCCTGGGGGCTCTTA   84453          TGA  C
                                TAAGAGCCTTC   GC CAGC
                                ||||||||||   || ||||
                                ATTCTCGGGGG   CG GTCG
                                     TC_  A
GAM789   LOC145783 5'  GCTGGGCCCAGAGGCTC     77951       T   A
                                GAGCCT CTG GCCCAGC
                                |||||| ||| |||||||
                                CTCGGA GAC CGGGTCG
                                   _   C
GAM789   LOC146287 5'  GCTGGGCTCAGGACTTTC     84633     CC
                                GAG  TTCTGAGCCCAGC
                                |||  ||||||||||||
                                CTT  AGGACTCGGGTCG
                                  TC
GAM789   LOC149175 3'  GCTGGGCTGGCTATGGCTTT   79954       TT__  G
                                AGAGCC    CT AGCCCAGC
                                ||||||    || ||||||||
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                                TTTCGG   GG TCGGGTCG
                                   TATC  _
GAM789  LOC149464 5'  GCTGGACGTGGCGGCTCTTG  85593       T  TGAGC
                                TAAGAGCC TC    CCAGC
                                |||||||| ||    |||||
                                GTTCTCGG GG    GGTCG
                                     C  TGCA_
GAM789  LOC149535 3'  GCCAGGAACTTAGGCTTTTA  80219        _____   A
                                TAAGAGCCT    TCTG GC
                                |||||||||    |||| ||
                                ATTTTCGGA    GGAC CG
                                     TTCAA   _
GAM789  LOC152641 3'  GCTGGGCAGGGGCTCT     81519       CTGA
                                AGAGCCTT   GCCCAGC
                                ||||||||   |||||||
                                TCTCGGGG   CGGGTCG
                                     A___
GAM789  LOC160646 3'  GCTGGGTGTGGAGGCTC    83117       TGA
                                GAGCCTTC   GCCCAGC
                                ||||||||   |||||||
                                CTCGGAGG   TGGGTCG
                                     TG_
GAM789  LOC162083 5'  GCTGGGCTCCATAGACCCTC  83207    CCT  ___
                                GAG   TCT   GAGCCCAGC
                                |||   |||   |||||||||
                                CTC   AGA   CTCGGGTCG
                                  CC_   TAC
GAM789  LOC169008 5'  GCTGGACTCTGGGTTCT    83597      TCT   C
                                AGAGCCT   GAG CCAGC
                                |||||||   ||| |||||
                                TCTTGGG   CTC GGTCG
                                     T__   A
GAM789  LOC196214 5'  GCTGGGCTCCTGGATGCTC   91180    C   T_
                                GAGC TTC  GAGCCCAGC
                                |||| |||  |||||||||
                                CTCG AGG  CTCGGGTCG
                                   T   TC
GAM789  LOC197114 5'  GCTGAGCCTGGGGGCTCTTA  91273         TGA  C
                                TAAGAGCCTTC   GC CAGC
                                ||||||||||   || ||||
                                ATTCTCGGGGG   CG GTCG
                                      TC_  A
GAM789  LOC197117 5'  GCTGAGCCTGGGGGCTCTTA  91283         TGA  C
                                TAAGAGCCTTC   GC CAGC
                                ||||||||||   || ||||
                                ATTCTCGGGGG   CG GTCG
                                      TC_  A
GAM789  LOC200772 5'  CTGGGCCTGGAGGGCCTT    91721    A     GA
                                AAG GCCTTCT  GCCCAG
                                ||| |||||||  ||||||
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                                TTC CGGGAGG  CGGGTC
                                  _      TC
GAM789   LOC201182 5'  GCTGGGCTCAGTGGCTC     91337      TT
                                GAGCC  CTGAGCCCAGC
                                |||||  ||||||||||
                                CTCGG  GACTCGGGTCG
                                   T_
GAM789   LOC201229 5'  GCTGGACAGAGGGTCTC     89520     _      AGC
                                GAG CCTTCTG   CCAGC
                                ||| |||||||   |||||
                                CTC GGGAGAC   GGTCG
                                  T      A__
GAM789   LOC203197 3'  CTGAGCAGTCAGGAAGGCTTCA 90810    A       _  __  C
                                A GAGCCTTC TGA  GC CAG
                                | ||||||||| |||  || |||
                                A TTCGGAAG ACT  CG GTC
                                 C       G   GA  A
GAM789   LOC203274 5'  CTGGACTGGGCTCTTG      92101         TCTG  C
                                TAAGAGCCT    AG CCAG
                                |||||||||    || ||||
                                GTTCTCGGG    TC GGTC
                                      ____  A
GAM789   LOC221583 3'  GCTGAGTTGGAGGCTC      93759         TG   C
                                GAGCCTTC  AGC CAGC
                                ||||||||  ||| ||||
                                CTCGGAGG  TTG GTCG
                                     __   A
GAM789   LOC221876 5'  GCTGGGCCACCGGCTCTT    95542        TTC  A
                                AAGAGCC   TG GCCCAGC
                                |||||||   || |||||||
                                TTCTCGG   AC CGGGTCG
                                    CC_  _
GAM789   LOC253027 3'  CTGGGCCTGGAGGGCCTT    98767     A      GA
                                AAG GCCTTCT  GCCCAG
                                ||| |||||||  ||||||
                                TTC CGGGAGG  CGGGTC
                                  _      TC
GAM789   LOC254835 5'  GCTGGGCTCATAAGGCTCTTA  98710          C
                                TAAGAGCCTT TGAGCCCAGC
                                |||||||||| ||||||||||
                                ATTCTCGGAA ACTCGGGTCG
                                      T
GAM789   LOC255974 5'  GCTGGACTCAGAAGACAGGC   99342      ____      C
                                GCCT    TCTGAG CCAGC
                                ||||    |||||| |||||
                                CGGA    AGACTC GGTCG
                                  CAGA      A
GAM789   LOC51030  5'  GCCGGGCTGAGGCTCTTA    32696          CTG     A
                                TAAGAGCCTT   AGCCC GC
                                ||||||||||   ||||| ||
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                                ATTCTCGGAG   TCGGG CG
                                     ___     C
GAM789  LOC85479  5'  GCTAAGCTCAGAACAGGACTT  53568     _  __      CC
                                GAG CCT  TCTGAGC  AGC
                                ||| |||  |||||||  |||
                                TTC GGA  AGACTCG  TCG
                                  A   CA      AA
GAM789  LOC90841  5'  GCTGGGCTAGAAAATCTCT    64870     CC_   G
                                AGAG   TTCT AGCCCAGC
                                ||||   |||| ||||||||
                                TCTC   AAGA TCGGGTCG
                                  TAA   _
GAM790  EHF       3'  TCCAAAACCCAAGGTTGGCT   25127     AT   _   C
                                AGT  GCCT GGGT TTGGA
                                |||  |||| |||| |||||
                                TCG  TGGA CCCA AACCT
                                  GT    A    A
GAM790  EPHA2     3'  CCATCGGCCAAGAATACTTGAA 16675         GC  G    T_
          G                      CTTCAAGTAT  CT GGTC  TGG
                                ||||||||||  || ||||  |||
                                GAAGTTCATA  GA CCGG  ACC
                                     A_  A    CT
GAM790  ITGA5     3'  CCCAGAGACATACTTGAAG    61933          C__
                                CTTCAAGTATG   CTGGG
                                ||||||||||   |||||
                                GAAGTTCATAC   GACCC
                                     AGA
GAM790  TREM2     3'  TCCAAGACTGTCATATTT     39098       CCTG
                                AAGTATG    GGTCTTGGA
                                |||||||    |||||||||
                                TTTATAC    TCAGAACCT
                                   TG__
GAM790  UQCRB     3'  CCAACATAGGCATACTTAAG   21939     C        GGTC
                                CTT AAGTATGCCTG    TTGG
                                ||| ||||||||||    ||||
                                GAA TTCATACGGAT    AACC
                                  _         AC__
GAM790  ATP10D    3'  CAGAGACCACTTGAAG       73526        ATGCCTG    _
                                CTTCAAGT      GGTCT TG
                                ||||||||      ||||| ||
                                GAAGTTCA      CCAGA AC
                                     _______    G
GAM790  B3GNT7    3'  CCCTTCCAGGCAACCTGAA    71678      A  A      TCTT
                                TTCA GT TGCCTGGG    GG
                                |||| || ||||||||    ||
                                AAGT CA ACGGACCT    CC
                                  C  _       TC__
GAM790  DKFZp547I224 3'  TCCAAAATTGACCACATACTTG 39963          CCTG   _____
          GA                     TTCAAGTATG    GGTC    TTGGA
                                ||||||||||    ||||    |||||
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                                AGGTTCATAC   CCAG   AACCT
                                     A___    TTAA
GAM790  FLJ22341  3'  CCAAGCTCAGGCACACCCAAG  45114    CAA  A      T
                                CTT   GT TGCCTGGG CTTGG
                                |||   || |||||||| |||||
                                GAA   CA ACGGACTC GAACC
                                  CC_  C       _
GAM790  KIAA0779  3'  CCGAACAGCATACTTGAAG   86908          C  GGTC
                                CTTCAAGTATGC TG   TTGG
                                |||||||||||| ||   ||||
                                GAAGTTCATACG AC   AGCC
                                       _ A___
GAM790  LOC144233 3'  CCAAGGCACATAATTGAA    77246      G   CCTGG
                                TTCAA TATG    GTCTTGG
                                ||||| ||||    |||||||
                                AAGTT ATAC    CGGAACC
                                   A   A____
GAM790  LOC147341 3'  ACCCAGGCATAACTGAAG    85116      AG
                                CTTCA  TATGCCTGGGT
                                |||||  ||||||||||
                                GAAGT  ATACGGACCCA
                                   CA
GAM790  LOC221088 5'  TCCAAGGTGCTGGCCACTCGAA 94888     A   AT   TGGG
           G                     CTTC AGT  GCC   TCTTGGA
                                 |||| |||  |||   |||||||
                                 GAAG TCA  CGG   GGAACCT
                                   C   C_   TCGT
GAM791  ACHE     3'  CTCGACGAGGCGGAGCGCCAGT 32332        A__   AGAACAC
           GGA                    TCCATTGGC   CCG      CGAG
                                  |||||||||   |||      ||||
                                  AGGTGACCG   GGC      GCTC
                                       CGA   GGAGCA_
GAM791  FUT5     3'  CTCGGTGTGAGCGCCAGCGGA  10727     A    ACC AGA
                                TCC TTGGC   G   ACACCGAG
                                ||| |||||   |   ||||||||
                                AGG GACCG   C   TGTGGCTC
                                  C    ___ GAG
GAM791  FLJ20626  3'  CTCGGTGTTCTCGGGGCCTGGA 35901     TT   A
                                TCCA  GGC CCGAGAACACCGAG
                                ||||  ||| ||||||||||||||
                                AGGT  CCG GGCTCTTGTGGCTC
                                  __   G
GAM791  LOC158401 5'  TCAGTCTTGGACCAATGGA   82805        CA     ACACC
                                TCCATTGG  CCGAGA    GA
                                ||||||||  ||||||    ||
                                AGGTAACC  GGTTCT    CT
                                     A_     GA___
GAM791  LOC219920 5'  TCGGCCTGGTGCCAAGGA    94963     A       G  AACA
                                TCC TTGGCACC AG    CCGA
                                ||| |||||||| ||    ||||
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                                AGG AACCGTGG TC    GGCT
                                  _       _ C___
GAM791  LOC221463 3'  TGGTCCTCAGTAACCAATGGA  93711        C_  C   AAC
                                TCCATTGG  AC GAG   ACCG
                                ||||||||  || |||   ||||
                                AGGTAACC  TG CTC   TGGT
                                    AA  A   C__
GAM791  LOC91355  5'  CGGTAGACGGACCAATGGA   66306        CA   AGAAC
                                TCCATTGG  CCG    ACCG
                                ||||||||  |||    ||||
                                AGGTAACC  GGC    TGGC
                                    A_   AGA__
GAM792  ABCD3     3'  CCCTATTTAAAACTGGGTC   12663        C  TG_  C
                                GATCCAGTT TA   AG GG
                                ||||||||| ||   || ||
                                CTGGGTCAA AT   TC CC
                                     A  TTA  _
GAM792  BAP1      3'  AGCCCCTGTAAATACTGGATC  17394        TC_   G  C
                                GATCCAGT   TAT AG GGCT
                                ||||||||   ||| || ||||
                                CTAGGTCA   ATG TC CCGA
                                     TAA   _  C
GAM792  FANCC     3'  AGCCACCCTGGAAGGAACTGGA 71030         ATG_  C__
                                TCCAGTTCT    AG   GGCT
                                |||||||||    ||   ||||
                                AGGTCAAGG    TC   CCGA
                                     AAGG  CCA
GAM792  GNB1      5'  AGCCGCCGCGGCGGGACTGGA  10833        A_  A_
                                TCCAGTTCT  TG  GCGGCT
                                |||||||||  ||  ||||||
                                AGGTCAGGG  GC  CGCCGA
                                     CG  GC
GAM792  MAPK4     3'  AGCGGGTTTGAACTGGA     12299        TAT   G_
                                TCCAGTTC   GAGC  GCT
                                ||||||||   ||||  |||
                                AGGTCAAG   TTTG  CGA
                                    ____   GG
GAM792  MRPS12    3'  AGCCACTCATGGATTCAAGTC  41195     CCAGT      C
                                GAT    TCTATGAG GGCT
                                |||    |||||||| ||||
                                CTG    AGGTACTC CCGA
                                  AACTT       A
GAM792  MRPS12    3'  AGCCACTCATGGATTCAAGTC  54126     CCAGT      C
                                GAT    TCTATGAG GGCT
                                |||    |||||||| ||||
                                CTG    AGGTACTC CCGA
                                  AACTT       A
GAM792  MRPS12    3'  AGCCACTCATGGATTCAAGTC  54127     CCAGT      C
                                GAT    TCTATGAG GGCT
                                |||    |||||||| ||||
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                                CTG    AGGTACTC CCGA
                                  AACTT      A
GAM792  RAD9    3' AGCCAGTGGCAGAACTGGGTC 17156        ATGA _
                                GATCCAGTTCT   GC GGCT
                                ||||||||||   || ||||
                                CTGGGTCAAGA   TG CCGA
                                     CGG_ A
GAM792  WIG1    3' AGCCGCTCATAGCATGTGA  96094   _ GTT
                                TC CA  CTATGAGCGGCT
                                || ||  ||||||||||||
                                AG GT  GATACTCGCCGA
                                 T AC_
GAM792  C7orf13 3' CCAACTTAGACTGGATC    51921       CTA   C_
                                GATCCAGTT  TGAG GG
                                |||||||||  |||| ||
                                CTAGGTCAG  ATTC CC
                                     ___   AA
GAM792  FBXO22  5' AGCCGCCGTAGGACTGGTTC 25144   T       A
                                GA CCAGTTCTATG GCGGCT
                                || ||||||||||| ||||||
                                CT GGTCAGGATGC CGCCGA
                                 T        _
GAM792  FLJ11181 3' AGCCATCCAGAACTGGA    37717       AT GC
                                TCCAGTTCT GA GGCT
                                |||||||||  ||  ||||
                                AGGTCAAGA CT CCGA
                                     C_ A_
GAM792  FLJ22693 5' AGCCGCTCAGCTGCGGACC  43047  A  A TCTA
                                G TCC GT   TGAGCGGCT
                                | ||| ||   |||||||||
                                C AGG CG   ACTCGCCGA
                                 C  _ TCG_
GAM792  G0S2    3' CCGCTGACATCTAGAACTG   32306       __ __
                                CAGTTCTA TG AGCGG
                                ||||||||  ||  |||||
                                GTCAAGAT AC TCGCC
                                     CT AG
GAM792  HBXIP   3' AGCCTGTCATAGGAACTGGATC 22152        _   GC
                                GATCCAGTTC TATGA GGCT
                                |||||||||| |||||  ||||
                                CTAGGTCAAG ATACT CCGA
                                     G    GT
GAM792  KIAA0173 5' AGCCGGGGCGAAGCTGGATC  28381       CTA AG_
                                GATCCAGTT  TG  CGGCT
                                |||||||||  ||  |||||
                                CTAGGTCGA  GC  GCCGA
                                     A__ GGG
GAM792  KIAA1908 5' AGCCACATCTCACTGGATC   73780       TCT  AGC
                                GATCCAGT  ATG  GGCT
                                ||||||||  |||  ||||
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                                CTAGGTCA  TAC  CCGA
                                    CTC  A__
GAM792  L3MBTL2  5' AGCCGGGTGTACTGGATC   90158      TCT  AG
                                GATCCAGT  ATG CGGCT
                                ||||||||  ||| |||||
                                CTAGGTCA  TGT GCCGA
                                    ____  GG
GAM792  LOC119504 5' AGCCACTCAGGCTGGTC    74439   T    CTA   C
                                GA CCAGTT  TGAG GGCT
                                || ||||||  |||| ||||
                                CT GGTCGG  ACTC CCGA
                                 _    ____  A
GAM792  LOC146057 5' CCCTTGGGAACTGGAT     78132       A   C
                                ATCCAGTTCT TGAG GG
                                |||||||||| |||| ||
                                TAGGTCAAGG GTTC CC
                                    _  _
GAM792  LOC146728 5' AGCCCTGGGAAAACTGGATC  84758       CTATG  C
                                GATCCAGTT   AG GGCT
                                |||||||||   || ||||
                                CTAGGTCAA   TC CCGA
                                    AAGGG  _
GAM792  LOC146728 5' AGCCCTGGGAAAACTGGGTC  84759       CTATG  C
                                GATCCAGTT   AG GGCT
                                |||||||||   || ||||
                                CTGGGTCAA   TC CCGA
                                    AAGGG  _
GAM792  LOC149414 5' AGCCGCTCGGCTGACTGGA   85569      CTA
                                TCCAGTT  TGAGCGGCT
                                |||||||  |||||||||
                                AGGTCAG  GCTCGCCGA
                                   TCG
GAM792  LOC150113 5' AGCCGCCATGTAACCAGAT   88563    CA  C   A
                                ATC  GTT TATG GCGGCT
                                |||  ||| |||| ||||||
                                TAG  CAA GTAC CGCCGA
                                  AC  T   _
GAM792  LOC151278 5' AGCCGCTTCTCAAACTGGGTC 81008       CTAT
                                GATCCAGTT   GAGCGGCT
                                |||||||||   ||||||||
                                CTGGGTCAA   TTCGCCGA
                                    ACTC
GAM792  LOC164312 3' CGTCTCATCGAACTGGATC   83392        T   _
                                GATCCAGTTC ATGAG CG
                                |||||||||| ||||| ||
                                CTAGGTCAAG TACTC GC
                                    C    T
GAM792  LOC202546 5' AGCTGGGCACAGCAACTGGATC 91959       _ A  AG
                                GATCCAGTT CT TG  CGGCT
                                ||||||||| || ||  |||||
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                                CTAGGTCAA GA AC  GTCGA
                                     C  C  GG
GAM792  LOC221477 5'  AGCCGCTCAGTTGTGATC    93764      _  GTTCTA
                                GATC CA     TGAGCGGCT
                                |||| ||     |||||||||
                                CTAG GT     ACTCGCCGA
                                  T  TG____
GAM792  LOC254826 5'  AGCCACGTGGAACTGG      99047          AGC
                                CCAGTTCTATG   GGCT
                                ||||||||||   ||||
                                GGTCAAGGTGC   CCGA
                                      A__
GAM793  CASP8    3'  ATCTATCAACTATAAGCCC   8745     C  A   AAG
                                GG CT GTGG   TGATAGAT
                                || || ||||   ||||||||
                                CC GA TATC   ACTATCTA
                                 C  A   A__
GAM793  CASP8    3'  ATCTATCAACTATAAGCCC   54069    C  A   AAG
                                GG CT GTGG   TGATAGAT
                                || || ||||   ||||||||
                                CC GA TATC   ACTATCTA
                                 C  A   A__
GAM793  CASP8    3'  ATCTATCAACTATAAGCCC   54094    C  A   AAG
                                GG CT GTGG   TGATAGAT
                                || || ||||   ||||||||
                                CC GA TATC   ACTATCTA
                                 C  A   A__
GAM793  CASP8    3'  ATCTATCAACTATAAGCCC   54110    C  A   AAG
                                GG CT GTGG   TGATAGAT
                                || || ||||   ||||||||
                                CC GA TATC   ACTATCTA
                                 C  A   A__
GAM793  CLK2     3'  CTATCACTTCAACCCCT     61021     CCTA  G
                                AGG   GT GAAGTGATAG
                                |||   || ||||||||||
                                TCC   CA CTTCACTATC
                                  C___  A
GAM793  CLK2     3'  CTATCACTTCAACCCCT     8918      CCTA  G
                                AGG   GT GAAGTGATAG
                                |||   || ||||||||||
                                TCC   CA CTTCACTATC
                                  C___  A
GAM793  CLK2     3'  CTATCACTTCAACCCCT     15670     CCTA  G
                                AGG   GT GAAGTGATAG
                                |||   || ||||||||||
                                TCC   CA CTTCACTATC
                                  C___  A
GAM793  GPR44    3'  CTATCACTTCCACTGCACC   17696    CC
                                GG  TAGTGGAAGTGATAG
                                ||  ||||||||||||||
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                                CC  GTCACCTTCACTATC
                                 AC
GAM793  TRADD    3'  CTGAAACTCCACTTGGCCTAT  15038       T     A  GA
                                ATAGGCC AGTGGA GT  TAG
                                ||||||| ||||||  ||  |||
                                TATCCGG TCACCT CA  GTC
                                    T     _  AA
GAM793  C12orf3  5'  TCTATCATGACCAGCCTA    40167      CTAG   AA
                                TAGGC   TGG  GTGATAGA
                                ||||||   |||  ||||||||
                                ATCCG   ACC  TACTATCT
                                   _____  AG
GAM793  ENDO180  3'  ATCCATCACTCCTGTGCCTG  21264      CTAGT  A    A
                                TAGGC    GGA GTGAT GAT
                                |||||    ||| ||||| |||
                                GTCCG    CCT CACTA CTA
                                   TGT__  _    C
GAM793  KIAA1189 3'  ATCTATCACATAACAGGACC  72505   _  A  GGAA
                                GG CCT GT   GTGATAGAT
                                || ||| ||   |||||||||
                                CC GGA CA   CACTATCTA
                                 A  _  ATA_
GAM793  LOC124222 3'  CTGTTCCTCCCACCAGGCCTGT 74749        A   A  TG
                                ATAGGCCT GTGG AG  ATAG
                                |||||||| |||| ||  ||||
                                TGTCCGGA CACC TC  TGTC
                                     C   C  CT
GAM794  EN2      3'  TCACCAGCAGCCGCCCAGGC  9272     CATCGT
                                GCT     GTGGCTGCTGGTGA
                                |||     ||||||||||||||
                                CGG     CGCCGACGACCACT
                                  ACC___
GAM794  ENG      3'  CACCAGCAGCATGGCATAGC  5491     CATC   G__
                                GCT   GTGT   GCTGCTGGTG
                                |||   ||||   ||||||||||
                                CGA   TACG   CGACGACCAC
                                  _____   GTA
GAM794  TEM5     3'  TCACCAGCAAAGCAGAGATGAG 52304      G_  GGC
                                CTCATC  TGT   TGCTGGTGA
                                ||||||  |||   |||||||||
                                GAGTAG  ACG   ACGACCACT
                                   AG   AA_
GAM794  TRAF5    3'  TCACCAGCAGTTTGCAAGC   17285    CATCG  TG _
                                GCT    TG  G CTGCTGGTGA
                                |||    ||  | ||||||||||
                                CGA    AC  T GACGACCACT
                                  ______ GT T
GAM794  PP1628   3'  CACCAGCAGCCATGGCTGGC  48073    CA  GT
                                GCT  TC  GTGGCTGCTGGTG
                                |||  ||  |||||||||||||
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                                CGG  GG  TACCGACGACCAC
                                  TC  __
GAM794   LOC116411 5'  CACCAGCAGGTGGACCATATGA 74293        _____
                                TCGTGTGG    CTGCTGGTG
                                ||||||||    |||||||||
                                AGTATACC    GACGACCAC
                                     AGGTG
GAM794   LOC151056 3'  CCACAGCCACACCATGAGC   80924       C       C
                                GCTCAT GTGTGGCTG TGG
                                |||||| ||||||||| |||
                                CGAGTA CACACCGAC ACC
                                   C       _
GAM794   LOC152282 3'  CACCAGCAGCCCCAGTAGC   81395     C  CG  T
                                GCT AT  TG GGCTGCTGGTG
                                ||| ||  || ||||||||||
                                CGA TG  AC CCGACGACCAC
                                  _ __  C
GAM794   LOC219612 5'  TCACCTGCCAGCACGACAAGC  95936     CA    _    TGCT
                                GCT  TCGTG TGGC   GGTGA
                                |||  ||||| ||||   |||||
                                CGA  AGCAC ACCG   CCACT
                                  AC    G   T___
GAM794   LOC221935 3'  TCACCAGCAGCAGCGTGA    94206       G
                                TCGTGT GCTGCTGGTGA
                                |||||| ||||||||||
                                AGTGCG CGACGACCACT
                                   A
GAM794   LOC256364 5'  CCAGGGCCACACTGATGAGC   96443        _      G
                                GCTCATC GTGTGGCT CTGG
                                ||||||| |||||||| ||||
                                CGAGTAG CACACCGG GACC
                                    T       _
GAM794   LOC96597  3'  CCTGCAACCACACGACGGGC   67454      A      C   T
                                GCTC TCGTGTGG TGC GG
                                |||| |||||||| ||| ||
                                CGGG AGCACACC ACG CC
                                  C       A   T
GAM795   AR        3'  TCATATGGCCCAGTGTCAA    5278          TACAAT  C
                                TTGACACTG     CC TATGA
                                |||||||||     || |||||
                                AACTGTGAC     GG ATACT
                                     CC_____  T
GAM795   EIF4E     3'  TCATAGGAGACTGCGTCAA    10506       ACT   CAA  _
                                TTGAC   GTA   TC CCTATGA
                                |||||   |||   || |||||||
                                AACTG   CGT   AG GGATACT
                                   ____  C__  A
GAM795   C1QTNF3   3'  CTCATAGAGGTACAGTGCCAA  48925     A       AATCC
                                TTG CACTGTAC    CTATGAG
                                ||| ||||||||    |||||||
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                                AAC GTGACATG    GATACTC
                                  C       GA___
GAM795  LOC143872 3'  GGAAGATTGTAAAGTGTCAA  77155        G     __
                                TTGACACT TACAATC  CC
                                |||||||| |||||||  ||
                                AACTGTGA ATGTTAG  GG
                                     A      AA
GAM795  LOC150082 5'  CTCATAAATACTACAGTGTGAA 80386    G      CAATCCC
                                TT ACACTGTA      TATGAG
                                || ||||||||      |||||||
                                AA TGTGACAT      ATACTC
                                 G       CATAA__
GAM796  DMD     3'  ACTTTCCACTGACAACGAA   5461    G  CAA  A
                                TT GTT   CGG TGGAAAGT
                                || |||   ||| ||||||||
                                AA CAA   GTC ACCTTTCA
                                 G  CA_  _
GAM796  DMD     3'  ACTTTCCACTGACAACGAA   15678   G  CAA  A
                                TT GTT   CGG TGGAAAGT
                                || |||   ||| ||||||||
                                AA CAA   GTC ACCTTTCA
                                 G  CA_  _
GAM796  DMD     3'  ACTTTCCACTGACAACGAA   15681   G  CAA  A
                                TT GTT   CGG TGGAAAGT
                                || |||   ||| ||||||||
                                AA CAA   GTC ACCTTTCA
                                 G  CA_  _
GAM796  DMD     3'  ACTTTCCACTGACAACGAA   15684   G  CAA  A
                                TT GTT   CGG TGGAAAGT
                                || |||   ||| ||||||||
                                AA CAA   GTC ACCTTTCA
                                 G  CA_  _
GAM796  DMD     3'  ACTTTCCACTGACAACGAA   15688   G  CAA  A
                                TT GTT   CGG TGGAAAGT
                                || |||   ||| ||||||||
                                AA CAA   GTC ACCTTTCA
                                 G  CA_  _
GAM796  DMD     3'  ACTTTCCACTGACAACGAA   15693   G  CAA  A
                                TT GTT   CGG TGGAAAGT
                                || |||   ||| ||||||||
                                AA CAA   GTC ACCTTTCA
                                 G  CA_  _
GAM796  DMD     3'  ACTTTCCACTGACAACGAA   15696   G  CAA  A
                                TT GTT   CGG TGGAAAGT
                                || |||   ||| ||||||||
                                AA CAA   GTC ACCTTTCA
                                 G  CA_  _
GAM796  DMD     3'  ACTTTCCACTGACAACGAA   15701   G  CAA  A
                                TT GTT   CGG TGGAAAGT
                                || |||   ||| ||||||||
```

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                                AA CAA   GTC ACCTTTCA
                                 G   CA_  _
GAM796  DMD     3'  ACTTTCCACTGACAACGAA   15705    G   CAA   A
                                TT GTT   CGG TGGAAAGT
                                || |||   ||| ||||||||
                                AA CAA   GTC ACCTTTCA
                                 G   CA_  _
GAM796  DMD     3'  ACTTTCCACTGACAACGAA   15708    G   CAA   A
                                TT GTT   CGG TGGAAAGT
                                || |||   ||| ||||||||
                                AA CAA   GTC ACCTTTCA
                                 G   CA_  _
GAM796  DMD     3'  ACTTTCCACTGACAACGAA   15711    G   CAA   A
                                TT GTT   CGG TGGAAAGT
                                || |||   ||| ||||||||
                                AA CAA   GTC ACCTTTCA
                                 G   CA_  _
GAM796  DMD     3'  ACTTTCCACTGACAACGAA   15715    G   CAA   A
                                TT GTT   CGG TGGAAAGT
                                || |||   ||| ||||||||
                                AA CAA   GTC ACCTTTCA
                                 G   CA_  _
GAM796  DMD     3'  ACTTTCCACTGACAACGAA   15720    G   CAA   A
                                TT GTT   CGG TGGAAAGT
                                || |||   ||| ||||||||
                                AA CAA   GTC ACCTTTCA
                                 G   CA_  _
GAM796  AKAP6    3'  TGACTTTCAGGTTTGTTGAAC  16254          G_
                                GTTCAACGGAT  GAAAGTCA
                                ||||||||||  ||||||||
                                CAAGTTGTTTG  CTTTCAGT
                                      GA
GAM796  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA  37205       CAACG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM796  KIAA0882  3'  TGACCATCTTTCCATCAAATCA 83537       CAACG      _____
            A                    TTGGTT    GATGGAAA   GTCA
                                ||||||    ||||||||   ||||
                                AACTAA    CTACCTTT   CAGT
                                   A____       CTAC
GAM796  MSTP028  3'  TGACCCCTGTCGTTGAAC    50068         AT  AAA
                                GTTCAACGG  GG   GTCA
                                |||||||||  ||   ||||
                                CAAGTTGCT  CC   CAGT
                                     GT  C__
GAM797  APLP2    3'  CTTCAGCCTCATTCACTGTCCT 92543     T  _____
                                AGG CA    TGAGGCTGAAG
                                ||| ||    ||||||||||
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                                TCC GT    ACTCCGACTTC
                                  T  CACTT
GAM797  BACE    3'  CTTCAGCCCTGAACCTTTG   58085       _  TGA
                                TAAAGGT CA   GGCTGAAG
                                ||||||| ||   ||||||||
                                GTTTCCA GT   CCGACTTC
                                    A  C__
GAM797  COX8    3'  CTTCTGCAATCATGACCT    15806        G_  T
                                AGGTCATGA  GC GAAG
                                |||||||||  || ||||
                                TCCAGTACT  CG CTTC
                                     AA  T
GAM797  CTF1    3'  CTTCAGCCCCTCTGCCCT    9014     T  T  __
                                AGG CA GA  GGCTGAAG
                                ||| || ||  ||||||||
                                TCC GT CT  CCGACTTC
                                  C  _  CC
GAM797  CYP8B1  5'  CAGGTGCTCAGACCTTTA    16531        A   G__
                                TAAAGGTC TGAG   CTG
                                |||||||| ||||   |||
                                ATTTCCAG ACTC   GAC
                                     _   GTG
GAM797  GOT2    3'  CTTCAGCCTCTGCTATTG    94496     A  T  T
                                TAA GG CA GAGGCTGAAG
                                ||| || || ||||||||||
                                GTT TC GT CTCCGACTTC
                                  A  _  _
GAM797  IL13    3'  CTTCAGCCTAGCCGACCTCA   10994   A    ATG_
                                A AGGTC    AGGCTGAAG
                                | |||||    |||||||||
                                A TCCAG    TCCGACTTC
                                 C    CCGA
GAM797  MCL1    3'  TCGGAACATGACCTTTA     41989          AGG
                                TAAAGGTCATG   CTGA
                                ||||||||||   ||||
                                ATTTCCAGTAC   GGCT
                                      AA_
GAM797  PCDHB7  3'  CTTCAGAACATATGACTTT   38943        AGG_
                                AAGGTCATG    CTGAAG
                                |||||||||    ||||||
                                TTTCAGTAT    GACTTC
                                     ACAA
GAM797  PLA2G4C 3'  CTTCAGCCACACGCTTCA    73807   A   CA  A
                                A AGGT  TG GGCTGAAG
                                | ||||  || ||||||||
                                A TTCG  AC CCGACTTC
                                 C   C_  A
GAM797  SELL    3'  CTTCAGCCTCCCCACCTT    7228       CAT
                                AAGGT   GAGGCTGAAG
                                |||||   ||||||||||
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                                TTCCA   CTCCGACTTC
                                   CCC
GAM797  VMD2     3'  CTTCAGCCTTTAATGCCTTT   16080       CAT_
                                AAAGGT    GAGGCTGAAG
                                ||||||    ||||||||||
                                TTTCCG    TTCCGACTTC
                                    TAAT
GAM797  ZNF141   3'  CTTCAGACCATCCACAAACCTT 14314        CAT__ _ _
           TA                     TAAAGGT    GA GG CTGAAG
                                ||||||||    || || ||||||
                                ATTTCCA     CT CC GACTTC
                                    AACAC  A  A
GAM797  C20orf38 3'  CTTCAGCCCTAGACTTT     37629        A  A
                                AAGGTC TG GGCTGAAG
                                |||||| || ||||||||
                                TTTCAG AT CCGACTTC
                                    _  C
GAM797  CGI-57   3'  CTTCAACCCTGATCTTT     74305        TGA  C
                                AAAGGTCA   GG TGAAG
                                ||||||||   || |||||
                                TTTCTAGT   CC ACTTC
                                     C__  A
GAM797  DKFZP434H132 5'  CTTCAGCCCCAGGGGACTCC   31931    A    A__  A
                                A GGTC   TG GGCTGAAG
                                | ||||   || ||||||||
                                C TCAG   AC CCGACTTC
                                 C    GGG  C
GAM797  FLJ10724 3'  CTTCAGTTGAATGCCCTCA   37040    A   T   GA
                                A AGG CAT  GGCTGAAG
                                | ||| |||  ||||||||
                                A TCC GTA  TTGACTTC
                                 C   C   AG
GAM797  FLJ20419 3'  TCCTTTTTATGGACCTTTA   35609         _     CT
                                TAAAGGTC ATGAGG  GA
                                |||||||| ||||||  ||
                                ATTTCCAG TATTTT  CT
                                     G     TC
GAM797  IMP-2    3'  CTTCAGCCATCCACTTCA    22608    A   CAT  _
                                A AGGT   GA GGCTGAAG
                                | ||||   || ||||||||
                                A TTCA   CT CCGACTTC
                                 C   C__  A
GAM797  JWA      3'  CTACAGCCATGATCTTTA    22159          GA    A
                                TAAAGGTCAT  GGCTG AG
                                ||||||||||  ||||| ||
                                ATTTCTAGTA  CCGAC TC
                                       __    A
GAM797  KIAA0185 3'  TCAGCCTCACTGGTACCT    63655      __ _
                                AGGT  CA TGAGGCTGA
                                ||||  || |||||||||
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                                TCCA  GT ACTCCGACT
                                  TG  C
GAM797  KIAA0205  3'  CTTCAGCTTGTTGACCTTT   30212        TG
                                AAAGGTCA  AGGCTGAAG
                                ||||||||  |||||||||
                                TTTCCAGT  TTCGACTTC
                                    TG
GAM797  KIAA0265  3'  CTTTGCTGCATGACTTCA    70441   A      A   T
                                A AGGTCATG GGC GAAG
                                | |||||||| ||| ||||
                                A TTCAGTAC TCG TTTC
                                 C       G  _
GAM797  KIAA0322  3'  CTTCAGCCCCCATTGTCTT   94330     TC   A_
                                AAGG  ATG  GGCTGAAG
                                ||||  |||  ||||||||
                                TTCT  TAC  CCGACTTC
                                  GT   CC
GAM797  KIAA0825  3'  TCAGCCTCATAAAGACCTTTA  61690        ___
                                TAAAGGTC   ATGAGGCTGA
                                ||||||||   ||||||||||
                                ATTTCCAG   TACTCCGACT
                                    AAA
GAM797  KIAA1037  3'  TCAGCCTCACTGTGACCTTT   31137        ___
                                AAAGGTCA   TGAGGCTGA
                                ||||||||   |||||||||
                                TTTCCAGT   ACTCCGACT
                                    GTC
GAM797  KIAA1254  3'  CTTCAGCCACAGCCTT      70559      CA  A
                                AAGGT  TG GGCTGAAG
                                |||||  || ||||||||
                                TTCCG  AC CCGACTTC
                                  __  A
GAM797  L3MBTL    3'  TTTCAGCCACAAACTTCA    70091    A   CA  A
                                A AGGT  TG GGCTGAAG
                                | ||||  || ||||||||
                                A TTCA  AC CCGACTTT
                                 C   A_  A
GAM797  LEPROTL1  3'  CTTAAGCCATGACTTTTA    31702         GA   G
                                TAAAGGTCAT  GGCT AAG
                                |||||||||  |||| |||
                                ATTTTCAGTA  CCGA TTC
                                    __    A
GAM797  LGALS9    3'  TCAGCCCCTCCTCTCTGACCTT 11299         T ________
          TA                    TAAAGGTCA GA      GGCTGA
                                |||||||||  ||      ||||||
                                ATTTCCAGT CT      CCGACT
                                    _  CTCCTCC
GAM797  MGC12945  5'  CTTCAGCCTCCGCCGCCTCC   51266    A    CAT_
                                A AGGT    GAGGCTGAAG
                                | ||||    ||||||||||
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                                C TCCG   CTCCGACTTC
                                 C   CCGC
GAM797  MMP28   3' CAACCTCAGAGGCCCTTTG   44442      _ A_   C
                                TAAAGG TC  TGAGG TG
                                |||||| ||  ||||| ||
                                GTTTCC GG  ACTCC AC
                                   C  AG    A
GAM797  MMP28   3' CAACCTCAGAGGCCCTTTG   44443      _ A_   C
                                TAAAGG TC  TGAGG TG
                                |||||| ||  ||||| ||
                                GTTTCC GG  ACTCC AC
                                   C  AG    A
GAM797  MRPS10  3' CTTGTGCCCCATGACCTT   36818        A  TG
                                AAGGTCATG GGC  AAG
                                ||||||||| |||  |||
                                TTCCAGTAC CCG  TTC
                                     C   TG
GAM797  MRVI1   3' CTTCAGCCTCCCATTCTTT   56095     TCAT
                                AAAGG   GAGGCTGAAG
                                |||||   ||||||||||
                                TTTCT   CTCCGACTTC
                                  TACC
GAM797  PAPOLG  3' CTTCAGTCTAATAACCTT   43471     C  G
                                AAGGT AT AGGCTGAAG
                                ||||| || |||||||||
                                TTCCA TA TCTGACTTC
                                  A  A
GAM797  PCCX2   3' CTTCAGCCTTTGCACTCA   66585   A  _  T
                                A GGT CA GAGGCTGAAG
                                | ||| || ||||||||||
                                A TCA GT TTCCGACTTC
                                 C   C  _
GAM797  PRO0902 3' TCAGTTTCTCCACCTTTA   54971      CAT
                                TAAAGGT   GAGGCTGA
                                |||||||   ||||||||
                                ATTTCCA   CTTTGACT
                                    CCT
GAM797  RAB25   3' CTTCAGCCCCAGGACCTTT   73256      A  A
                                AAAGGTC TG GGCTGAAG
                                ||||||| || ||||||||
                                TTTCCAG AC CCGACTTC
                                   G  C
GAM797  RENT2   3' CTTCAGAAATCTGACCTTTG  32066       T  GG_
                                TAAAGGTCA GA   CTGAAG
                                ||||||||| ||   ||||||
                                GTTTCCAGT CT   GACTTC
                                     _  AAA
GAM797  SEC22C  3' TTAGTACATATGACCTTTA   16115        AG_
                                TAAAGGTCATG   GCTGA
                                ||||||||||   |||||
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                                ATTTCCAGTAT   TGATT
                                      ACA
GAM797   LOC116150 3'  CTTCAGCCCAGCTACTTCC    57424    A    CA_  A
                                A AGGT   TG GGCTGAAG
                                | ||||   || ||||||||
                                C TTCA   AC CCGACTTC
                                 C    TCG  _
GAM797   LOC126364 3'  CTTCAGAGGACAATGACTTTTA 76190          GAGG__
                                TAAAGGTCAT     CTGAAG
                                ||||||||||     ||||||
                                ATTTTCAGTA     GACTTC
                                      ACAGGA
GAM797   LOC129607 3'  CTTCAGCCATCGTACCCT     75397     TC    _
                                AGG  ATGA GGCTGAAG
                                |||  |||| ||||||||
                                TCC  TGCT CCGACTTC
                                  CA    A
GAM797   LOC139322 3'  CTTGCATTTGATGACCTTTA   75897          G   C  _
                                TAAAGGTCAT AGG TG AAG
                                |||||||||| ||| || |||
                                ATTTCCAGTA TTT AC TTC
                                      G   _  G
GAM797   LOC145739 3'  CTTCAGCCCCTATGTGCCT    77905      _    A_
                                AGGT CATG  GGCTGAAG
                                |||| ||||  ||||||||
                                TCCG GTAT  CCGACTTC
                                  T    CC
GAM797   LOC147124 3'  TCAGCCCCTCCTCTCTGACCTT 76807          T  ________
            TA                    TAAAGGTCA GA      GGCTGA
                                |||||||||  ||       ||||||
                                ATTTCCAGT CT      CCGACT
                                      _  CTCCTCC
GAM797   LOC152559 3'  CTTCAGATATTATATCCTTTA  81493       TC    GG_
                                TAAAGG  ATGA   CTGAAG
                                ||||||  ||||   ||||||
                                ATTTCC  TATT   GACTTC
                                    TA    ATA
GAM797   LOC153196 5'  CTTCAGCCTGCATCTCCT     87170     TC   _
                                AGG  ATG AGGCTGAAG
                                |||  ||| |||||||||
                                TCC  TAC TCCGACTTC
                                  TC   G
GAM797   LOC157773 5'  CTTCAGAGAGAGATGCCTTTA  82508       T   GAGG__
                                TAAAGG CAT     CTGAAG
                                |||||| |||     ||||||
                                ATTTCC GTA     GACTTC
                                    _   GAGAGA
GAM797   LOC196872 5'  TAGTTTTCCACGGACCTTTA   89159         AT___
                                TAAAGGTC    GAGGCTG
                                ||||||||    |||||||
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                                ATTTCCAG    TTTTGAT
                                    GCACC
GAM797  LOC201952 5'  CTTCAGCCTCCTGTCTCT    91876   _ T  T
                                AG G CA GAGGCTGAAG
                                || | || ||||||||||
                                TC C GT CTCCGACTTC
                                 T T  C
GAM797  LOC203078 3'  CTTCAACTGCCTTATGCCCTT  90789     T      ___
                                AAGG CATGAGGC   TGAAG
                                |||| ||||||||   |||||
                                TTCC GTATTCCG   ACTTC
                                   C       TCA
GAM797  LOC219743 3'  CTTCAGCCCCATGGATCCTT   94746     __    A
                                AAGG  TCATG GGCTGAAG
                                ||||  ||||| ||||||||
                                TTCC  GGTAC CCGACTTC
                                   TA    C
GAM797  LOC253955 3'  CTTCAGCCTCAGTTTCCTCG   96073   A   TCA_
                                A AGG    TGAGGCTGAAG
                                | |||    ||||||||||
                                G TCC    ACTCCGACTTC
                                 C   TTTG
GAM797  LOC254198 5'  TCAGCTTTTAGATCTTTA    98323       AT
                                TAAAGGTC  GAGGCTGA
                                ||||||||  ||||||||
                                ATTTCTAG  TTTCGACT
                                     AT
GAM797  LOC51024  3'  CTTCAGCCCCATCATGTGCT   32681    _    ___
                                GGT CATGA   GGCTGAAG
                                ||| |||||   ||||||||
                                TCG GTACT   CCGACTTC
                                  T    ACC
GAM797  LOC90313  5'  CTTCAGCCTCACGCAGGATC   62897     A____
                                GGTC    TGAGGCTGAAG
                                ||||    ||||||||||
                                CTAG    ACTCCGACTTC
                                   GACGC
GAM797  LOC93132  5'  CTTCAGCCTTCAAATCTT    71987      CAT
                                AAGGT   GAGGCTGAAG
                                |||||   ||||||||||
                                TTCTA   TTCCGACTTC
                                   AAC
GAM798  AP1M1    3'  TCGGGGCTCCTGGTGGCAG   51654         A  A  G
                                CTGCCACCAG AG CT TGG
                                |||||||||| || || |||
                                GACGGTGGTC TC GG GCT
                                     C  _  G
GAM798  KIR2DL1   3'  CAGTCTTCTGTCAGCAGT    27239      CAC
                                ACTGC   CAGAAGACTG
                                |||||   ||||||||||
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                                TGACG  GTCTTCTGAC
                                  ACT
GAM798  KIR2DL2  3'  CAGTCTTCTGTCAGCAGT   27240     CAC
                                ACTGC  CAGAAGACTG
                                |||||  ||||||||||
                                TGACG  GTCTTCTGAC
                                  ACT
GAM798  LZTFL1   3'  TCCACAGTTATGTAAGGCAGTG 40112       ACCAGAA
          A                    TCACTGCC     GACTGTGGA
                               ||||||||     |||||||||
                               AGTGACGG     TTGACACCT
                                   AATGTA_
GAM798  MHC2TA   3'  CCCAGCGAGCCCCTGGTGGCAG 5974           AAGA___  T
          TGG                    TCACTGCCACCAG     CTG GG
                                 ||||||||||||      ||| ||
                                 GGTGACGGTGGTC     GAC CC
                                       CCCGAGC  _
GAM798  SLC25A15 3'  CCACAGTCCCCTGCTCAGTG  27291     CCAC  AA
                                CACTG   CAG  GACTGTGG
                                |||||   |||  ||||||||
                                GTGAC   GTC  CTGACACC
                                  TC__  CC
GAM798  ZNF264   3'  CCACAGTCTTCTGAGTTGTGC  14204   _ _ _
                                GC CA C CAGAAGACTGTGG
                                || || | ||||||||||||
                                CG GT G GTCTTCTGACACC
                                 T  T A
GAM798  FLJ10074 3'  CAGACCTTCTGACTGGCAGTGA 36283       C_    A_
                                TCACTGCCA  CAGAAG  CTG
                                |||||||||  ||||||  |||
                                AGTGACGGT  GTCTTC  GAC
                                     CA     CA
GAM798  FLJ10094 3'  TCCACAGTCATAATGATGGCA  36298     C  GAA_
                                TGCCA CA   GACTGTGGA
                                ||||| ||   |||||||||
                                ACGGT GT   CTGACACCT
                                  A  AATA
GAM798  FLJ11068 3'  TCCACAGTCTCCAACAACAGT  37588    CCACCA  A
                                ACTG     GA GACTGTGGA
                                ||||     || |||||||||
                                TGAC     CT CTGACACCT
                                  AACAAC  _
GAM798  FLJ12387 3'  CGGTCCCCTGGTGGCAGGA   43376   A       AA
                                TC CTGCCACCAG  GACTG
                                || ||||||||||  |||||
                                AG GACGGTGGTC  CTGGC
                                 _        CC
GAM798  FLJ23514 3'  TAGTTTCTGATGGCAGTGA   41832       C   A
                                TCACTGCCA CAGA GACTG
                                ||||||||| |||| |||||
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                                AGTGACGGT GTCT TTGAT
                                      A   _
GAM798  FLJ32762  5' CCACAGTCTCAGCAGGGA   59482   A   CACCA  A
                                TC CTGC    GA GACTGTGG
                                || ||||    || ||||||||
                                AG GACG    CT CTGACACC
                                 G   A____  _
GAM798  IDN3    3' CCAGGTAATCTGGTGGAGCGA  56758   A  G      AG   G
                                TC CT CCACCAGA  ACT TGG
                                || || ||||||||  ||| |||
                                AG GA GGTGGTCT  TGG ACC
                                 C  _       AA  _
GAM798  KIAA0140  3' CCATTCAGGCCTGGTGGCAGGA 28509    A        AAGA  __
                                TC CTGCCACCAG    CTG  TGG
                                || ||||||||||    |||  |||
                                AG GACGGTGGTC    GAC  ACC
                                 _        CG__   TT
GAM798  KIAA0552  5' TCCGGGAAGTCTTCCTGGTGGC 28999          _     GT__
            AGTGA                   TCACTGCCACCAG AAGACT    GGA
                                ||||||||||||| ||||||    |||
                                AGTGACGGTGGTC TTCTGA    CCT
                                       C     AGGG
GAM798  KIAA1025  3' CCACAGTCCTGCACTGTGA   64673     TGCCAC   AA
                                TCAC     CAG  GACTGTGG
                                ||||     |||  ||||||||
                                AGTG     GTC  CTGACACC
                                  TCAC__   __
GAM798  KIAA1161  3' CCATACTGTTCTGGTGGTAGTG 82645            GAC
            A                    TCACTGCCACCAGAA   TGTGG
                                ||||||||||||||   |||||
                                AGTGATGGTGGTCTT   ATACC
                                       GTC
GAM798  KIAA1377  3' CCACAAAATGGCCCTTGGTGGC 67756         AAGAC____
            AG                    CTGCCACCAG        TGTGG
                                ||||||||||        |||||
                                GACGGTGGTT        ACACC
                                      CCCGGTAAA
GAM798  KIAA1404  5' CCAGCACTCGCCGGCGGCAGTG 62685        A  AGAA  C  _
            A                    TCACTGCC CC    GA TG TGG
                                ||||||| ||    || || |||
                                AGTGACGG GG    CT AC ACC
                                     C  CCG_  C  G
GAM798  KIAA1855  3' CCACAGTCTTCTGGGAGC    93948    CA
                                GC  CCAGAAGACTGTGG
                                ||  ||||||||||||||
                                CG  GGTCTTCTGACACC
                                 AG
GAM798  KIAA1908  3' CCACAGCCTTTTGGTAGTGA   73782         CCA    A
                                TCACTGCCA   GAAG CTGTGG
                                |||||||||   |||| ||||||
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                                AGTGATGGT   TTTC GACACC
                                    ___    C
GAM798  KIAA1950  3'  CGCACTCCACGGCGGCAGTGA  94179        A  AGAA  C  TG
                                TCACTGCC CC    GA TG  G
                                |||||||| ||    || ||  |
                                AGTGACGG GG    CT AC  C
                                    C  CAC_  C  GT
GAM798  Kv6.3     3'  TCCACAGTAAGGATGCCAATGA 56856     C  C  _  AGAAG
                                TCA TG CA CC     ACTGTGGA
                                ||| || || ||     ||||||||
                                AGT AC GT GG     TGACACCT
                                  A  C  A  AA___
GAM798  LYPLA3    3'  CCTTTCTCTGTGGCAGTGA   25560          C   A  CTGT
                                TCACTGCCAC AGA GA    GG
                                |||||||||| ||| ||    ||
                                AGTGACGGTG TCT CT    CC
                                    _   _  TT__
GAM798  MRPL43    3'  CCTGCTTCTGGGGGGCAGTGA   50409        A      ACTGT
                                TCACTGCC CCAGAAG     GG
                                |||||||| |||||||     ||
                                AGTGACGG GGTCTTC     CC
                                    G      GT___
GAM798  PDZD2     3'  CCTCCTCTGGTGGCATGA    81719     C        A  CTGT
                                TCA TGCCACCAGA GA    GG
                                ||| |||||||||| ||    ||
                                AGT ACGGTGGTCT CT    CC
                                  _         C  _____
GAM798  PRO1866   5'  CCATGCTGTTCTGGTGATAGTG 38147       C       GAC
            A                    TCACTG CACCAGAA   TGTGG
                                |||||| ||||||||   |||||
                                AGTGAT GTGGTCTT   GTACC
                                   A       GTC
GAM798  PSR       3'  CCACAAATGCATTCAGTGGCAG 65782          CA   GAC___
            TGA                    TCACTGCCAC  GAA     TGTGG
                                |||||||||  |||     |||||
                                AGTGACGGTG  CTT     ACACC
                                    A_   ACGTAA
GAM798  SCRG1     5'  CCACAGTCCTGGCTGGAGCAG  24415     CA   AA__
                                CTGC  CCAG    GACTGTGG
                                ||||  ||||    ||||||||
                                GACG  GGTC    CTGACACC
                                  A_    GGTC
GAM798  TIX1      3'  CCACACTAGCCCAGTGGCAGTG 62406          CAGAAGAC
            G                    TCACTGCCAC       TGTGG
                                ||||||||||       |||||
                                GGTGACGGTG       ACACC
                                    ACCCGATC
GAM798  LOC131873 3'  CCACAGTTGGTAGCAATGG   76395     C   C    GAAG
                                TCA TGC ACCA    ACTGTGG
                                ||| ||| ||||    |||||||
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                                GGT ACG TGGT    TGACACC
                                  A   A   ____
GAM798   LOC147632 5'  TCCACGTGTTCTGGTGGAATGA 57471     CTG       G  T
                                TCA   CCACCAGAA AC GTGGA
                                |||   ||||||||| || |||||
                                AGT   GGTGGTCTT TG CACCT
                                  AA_       G  _
GAM798   LOC149386 5'  TCCACAAATAACATGTTGGCAG 85563         C  GAAGAC_
           TGA                    TCACTGCCA CA      TGTGGA
                                |||||||||| ||      ||||||
                                AGTGACGGT GT      ACACCT
                                     T  ACAATAA
GAM798   LOC149386 5'  TCCACAGTCTTCTGGGTGGCAG 85564     A       _
           CGA                    TC CTGCCACC AGAAGACTGTGGA
                                || |||||||| ||||||||||||
                                AG GACGGTGG TCTTCTGACACCT
                                 C       G
GAM798   LOC199958 3'  TCTGCCTGGTGGCAGTGA    91494            A_
                                TCACTGCCACCAG  AGA
                                ||||||||||||  |||
                                AGTGACGGTGGTC  TCT
                                       CG
GAM798   LOC221938 3'  TCCAAGGTGACTTCTGGTGACA 94224     C        __  G
           G                     CTG CACCAGAAG  ACT TGGA
                                ||| |||||||||  ||| ||||
                                GAC GTGGTCTTC  TGG ACCT
                                  A        AG   A
GAM798   LOC254228 3'  CCACACAGTTGGTGGCAAGGA  97649    AC        AAGAC
                                TC  TGCCACCAG    TGTGG
                                ||  |||||||||    |||||
                                AG  ACGGTGGTT    ACACC
                                 GA        GAC__
GAM798   LOC51246  3'  TCCACGGTGTTCTGGCAGCAGG 33642    A   CA     G
           GA                     TC CTGC  CCAGAA ACTGTGGA
                                || ||||  |||||| ||||||||
                                AG GACG  GGTCTT TGGCACCT
                                 G   AC     G
GAM798   LOC90520  3'  CCACAGTCCTCCAGGCGCCAGT 63835      CCA  A_  A
           G                      CACTG   CC  GA GACTGTGG
                                |||||   ||  || ||||||||
                                GTGAC   GG  CT CTGACACC
                                   CGC  AC  C
GAM798   LOC90520  5'  CCACAGTCCTCCAGGTGG    63836      A_  A
                                CCACC  GA GACTGTGG
                                |||||  || ||||||||
                                GGTGG  CT CTGACACC
                                   AC  C
GAM798   LOC92249  3'  TCGCTGACTCCTGGTGGCAAGG 69112    AC       A  ACT
           A                      TC  TGCCACCAG AG   GTGG
                                ||  ||||||||| ||   ||||
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                                AG  ACGGTGGTC TC   CGCT
                                 GA        C  AGT
GAM799  ARSD     3'  CACTTTTAAACAACCAGATCTC 9798           C  _____
              GT                   ACGAGATTTGGT GT     AGTG
                                ||||||||||| ||     |||||
                                TGCTCTAGACCA CA     TCAC
                                       A  AATTT
GAM799  ABCA9    3'  TGTGCCAGCAACCAAATC    55366        C  AG   G
                                GATTTGGT GT  TGG GCG
                                |||||||| ||  ||| |||
                                CTAAACCA CG  ACC TGT
                                     A  __   G
GAM799  C21orf108 3'  CGTCACGACACAAATCTC    90112         _    AG
                                GAGATTTG GTCGT  TG
                                |||||||| |||||  ||
                                CTCTAAAC CAGCA  GC
                                     A    CT
GAM799  FLJ21135  3'  GCCCCACCACCACCCAGT    46350     T   C  A
                                ATT GGT GT GTGGGGC
                                ||| ||| || |||||||
                                TGA CCA CA CACCCCG
                                  C   C  C
GAM799  LOC127534 3'  CCCCACTGGCACCAAATC    75967         CG
                                GATTTGGT  TAGTGGGG
                                ||||||||  ||||||||
                                CTAAACCA  GTCACCCC
                                     CG
GAM799  LOC221747 5'  CCCCACTATTCTTAATGTC    93962    G   T  TC
                                GA ATT GG  GTAGTGGGG
                                || ||| ||  |||||||||
                                CT TAA TC  TATCACCCC
                                 G   T  T_
GAM799  LOC253974 3'  CGCCTAATACGACCAAATCCGT 99281     A          GTG
                                ACG GATTTGGTCGTA   GGGCG
                                ||| ||||||||||||   |||||
                                TGC CTAAACCAGCAT   TCCGC
                                  _          AA_
GAM800  ACCN2    3'  GGGGGCCCCCAGCTGCCTCCTC 39630      A  A
              A                    TGAG GA GCAGCTGGGGGCCCTC
                                |||| || ||||||||||||||||
                                ACTC CT CGTCGACCCCCGGGGG
                                  _ C
GAM800  CCND2    3'  GCCCTCAAGAGGCTGCTTCTCT 10051           T________  GGCC
                                AGAGAAGCAGC       GGG   C
                                ||||||||||       |||   |
                                TCTCTTCGTCG       CTC   G
                                      GAGAA___   CCG
GAM800  CHRM1    5'  GAGGACCCTACAGACCCCTCTT 96432       AAGCAG  _   C
                                GAGAG     CTG GGGG CCTC
                                |||||     ||| |||| ||||
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                                TTCTC     GAC TCCC GGAG
                                   CCCA__   A   A
GAM800  CKTSF1B1  3'  AGAACCCCCAGCTGCCTCCT   26291    A  A        CC
                                AG GA GCAGCTGGGGG  CT
                                || || ||||||||||  ||
                                TC CT CGTCGACCCCC  GA
                                 _ C         AA
GAM800  EPB49    3'  CCCCCAGCTGCTTTCCTCA   10525     AG
                                TGAG  AAGCAGCTGGGGG
                                ||||  ||||||||||||
                                ACTC  TTCGTCGACCCCC
                                  CT
GAM800  FGFR2    3'  GAGGGCCCTTCACTTCCATCA  5561     GA   CAGCT
                                TGA  GAAG    GGGGGCCCTC
                                |||  ||||    ||||||||||
                                ACT  CTTC    TTCCCGGGAG
                                  AC   AC___
GAM800  IL7R     3'  AGAGCATCCTGCTTCTACCA   10988    AG     GCT  GG  C
                                TG  AGAAGCA   GG  GC CT
                                ||  |||||||   ||  || ||
                                AC  TCTTCGT   CC  CG GA
                                 CA      ___  TA  A
GAM800  KCNQ1    3'  GAGGGCCTGGGCCTGGCTCCCT 5842     AAGC   TG  ____
           C                     GAG    AGC  GG    GGCCCTC
                                |||    |||  ||    |||||||
                                CTC    TCG  CC    CCGGGAG
                                  CC__   GT  GGGT
GAM800  LARGE    3'  GGGCCCTCGAAAATCAGCTGCC 56929    AG   A     G_________  GCCC
           TCTACCA                  TG  AGA GCAGCTG       GG    TC
                                ||  ||| |||||||       ||    ||
                                AC  TCT CGTCGAC       CT    GG
                                 CA   C      TAAAAG___  CCCG
GAM800  MAPRE3   3'  GGCCCCCAGCCACTCCCTC   25599     A  A CA
                                GAG GA G  GCTGGGGGCC
                                ||| || |  ||||||||||
                                CTC CT C  CGACCCCCGG
                                  C  _ AC
GAM800  MAPT     3'  GCCCCCAGCTGCTCCTCGCA   34177    A   A
                                TG GAG AGCAGCTGGGGGC
                                || ||| ||||||||||||
                                AC CTC TCGTCGACCCCCG
                                 G   C
GAM800  MMP15    3'  AGGGCCCTGGGCCTGCCTC    11612     AA   _  G
                                GAG  GCAG CT GGGGCCCT
                                |||  |||| || ||||||||
                                CTC  CGTC GG TCCCGGGA
                                  __    C  G
GAM800  MUCDHL   3'  AGGATGCAGCTGCCCCTTCTCA 88635       AA_      GGGGC
                                TGAGAG   GCAGCTG    CCT
                                ||||||   |||||||    |||
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                                ACTCTT  CGTCGAC   GGA
                                   CCC     GTA__
GAM800  NMI     5'  GAGAACCCGGGCCTTCCCCTC  17435    A_   CA  G  GCC
                                GAG  GAAG  GCT GGG  CTC
                                |||  ||||  ||| |||  |||
                                CTC  CTTC  CGG CCC  GAG
                                  CC   __  G  AA_
GAM800  PKIA    5'  GCCCCCCTGGCTCTTCTCTC  23344       C   __
                                GAGAGAAG AGCT  GGGGGC
                                |||||||| ||||  ||||||
                                CTCTCTTC TCGG  CCCCCG
                                     _   TC
GAM800  SHOX    3'  AGGCGTTACCTCTTCTCCCA  6563    A    CAGCT  GG  _
                                TG GAGAAG    GG  GC CCT
                                || ||||||    ||  || |||
                                AC CTCTTC    CC  TG GGA
                                 C     T____  AT  C
GAM800  SNL     3'  GCCTCTCCCAGCCACCTCCTCC 13290    A  A  CA_    ___
           CA                    TG GAG AG   GCTGGG   GGC
                                || ||| ||   ||||||   |||
                                AC CTC TC   CGACCC   CCG
                                 C   C  CAC     TCT
GAM800  TAZ     3'  AGGACCTCAGCTGCTTCTCCCA 5483    A          GC
                                TG GAGAAGCAGCTGGGG  CCT
                                || ||||||||||||||  |||
                                AC CTCTTCGTCGACTCC  GGA
                                 C           A_
GAM800  TCFL4   3'  AGGCTCCTGCCCTCTCA    64206      AA  GCTG   C
                                TGAGAG  GCA   GGGGC CT
                                ||||||  |||   ||||| ||
                                ACTCTC  CGT   CCTCG GA
                                   C_  ____    A
GAM800  TYRO3   5'  AGGGCCCCGCCCTCCTC    21935    A  CA  TG
                                GAG AG  GC  GGGGCCCT
                                ||| ||  ||  ||||||||
                                CTC TC  CG  CCCCGGGA
                                  C  C_ __
GAM800  ZNF42   5'  GCCCTCACTGCTCTCTCA    14243       A   C
                                TGAGAGA GCAG TGGGGGC
                                ||||||| |||| |||||||
                                ACTCTCT CGTC ACTCCCG
                                     _   _
GAM800  BTN2A1  3'  GAGAACATCTTCCAGCTGCCTC 55300       A       CC___
           TTTCA                   TGAGAGA GCAGCTGGGGG    CTC
                                ||||||| ||||||||||    |||
                                ACTTTCT CGTCGACCTTC    GAG
                                   C         TACAA
GAM800  C12orf22 3'  GGCCCTCGAAGCAGCTGCTGCT 48709    A  A     ________  GGCCC
           CCCA                    TG GAG AGCAGCTG     GG    T
                                || ||| ||||||||     ||    |
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                                AC CTC TCGTCGAC      CT    G
                                 C  G       GAAG___  CCCGG
GAM800  C21orf59  5'  TCGAATCAGCTGTCCTCTCA  35705       AA     G_______
                                TGAGAG  GCAGCTG      GG
                                ||||||  |||||||      ||
                                ACTCTC  TGTCGAC      CT
                                   C_       TAAG___
GAM800  C5orf7    3'  GAGAACCCACTGCTTTTCCCA  64598    A       C   GGCC
                                TG GAGAAGCAG TGGG    CTC
                                || |||||||| ||||    |||
                                AC CTTTTCGTC ACCC    GAG
                                 C        _   AA__
GAM800  CALN1     3'  CTCCCAGCCCCTTCTCCCA   49663    A     CA
                                TG GAGAAG  GCTGGGGG
                                || ||||||  ||||||||
                                AC CTCTTC  CGACCCTC
                                 C     CC
GAM800  CNOT8     3'  CTCGAGACTAGTTCTCTCA   17706        GC  _  G
                                TGAGAGAA  AG CT GGG
                                ||||||||  || || |||
                                ACTCTCTT  TC GA CTC
                                     GA  A  G
GAM800  DJ37E16.5 3'  GAGGGCCCTTGCAACCCCCTCC 40096    A   AAGCA_  T
           CA                     TG GAG     GC GGGGGCCCTC
                                || |||     || ||||||||||
                                AC CTC     CG TTCCCGGGAG
                                 C  CCCCAA  _
GAM800  DOC-1R    3'  GCCCTTCCCAGCACTTCTCCCA 20722    A     CA     ___
                                TG GAGAAG  GCTGGG   GGC
                                || ||||||  ||||||   |||
                                AC CTCTTC  CGACCC   CCG
                                 C     A_     TTC
GAM800  FLJ10483  3'  GAGAACCCTCAGCTTCTCTC   36653       AGC       CC
                                GAGAGA   AGCTGGGGG  CTC
                                ||||||   |||||||||  |||
                                CTCTCT   TCGACTCCC  GAG
                                   ___         AA
GAM800  FLJ10815  3'  GAGGACCCCTCCTCCTCTC    37234      A  CAGCT    C
                                GAGAG AG    GGGGG CCTC
                                ||||| ||    ||||| ||||
                                CTCTC TC    TCCCC GGAG
                                   C  C____    A
GAM800  FLJ10856  3'  AGAGCCCTTTCAGCACTTTCTC 37322       CA   __    C
                                GAGAAG  GCTG  GGGGC CT
                                ||||||  ||||  ||||| ||
                                CTCTTT  CGAC  TCCCG GA
                                   CA   TT    A
GAM800  FLJ11320  3'  GCCCTCAAGGAGCTGCTTCTCT 37829          T________  GGCC
           C                    GAGAGAAGCAGC       GGG   C
                                ||||||||||||       |||   |
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                                CTCTCTTCGTCG      CTC   G
                                      AGGAA___  CCG
GAM800  FLJ13848  3'  GCCTTCCTCTTCTCTCA    45823        C  CT
                                TGAGAGAAG AG  GGGGGC
                                ||||||||| ||  ||||||
                                ACTCTCTTC TC  CTTCCG
                                      _  __
GAM800  FLJ14957  3'  TTCCCTGCTGCTTCTCCCA   52829    A       T
                                TG GAGAAGCAGC GGGGG
                                || |||||||||| |||||
                                AC CTCTTCGTCG CCCTT
                                 C        T
GAM800  FLJ20320  5'  GAGGGCCTACACTGCCTCCTC  35425    A  A   C  GG
                                GAG GA GCAG TG  GGCCCTC
                                ||| || |||| ||  |||||||
                                CTC CT CGTC AC  CCGGGAG
                                  _  C   _  AT
GAM800  FLJ20397  5'  GAGGGCCTGTCTGCAGCCCTCC 35580    A   AA  A  T  _
           CA                     TG GAG  GC GC GG GGGCCCTC
                                || |||  || || || ||||||||
                                AC CTC  CG CG CT TCCGGGAG
                                 C   C_  A  T  G
GAM800  GABARAPL1 3'  GGGCCCTCGATGGCCAGCTGCT 49419     A         _________  GCCC
           TCCCTC                  GAG GAAGCAGCTGG       GG    TC
                                ||| ||||||||||       ||    ||
                                CTC CTTCGTCGACC       CT    GG
                                  C         GGTAG___  CCCG
GAM800  HSA243396 3'  AGGGCCCCATCGCTTCCCTT   37843     A    AGCTG
                                GAG GAAGC    GGGGCCCT
                                ||| |||||    ||||||||
                                TTC CTTCG    CCCCGGGA
                                  C    CTA__
GAM800  HSRNAFEV  3'  GAGGGCCCGGGAGCCTCCGTCA 34449     GA  A  AG  GG
                                TGA  GA GC  CT  GGGCCCTC
                                |||  || ||  ||  ||||||||
                                ACT  CT CG  GG  CCCGGGAG
                                  GC  C  AG  __
GAM800  HUMGT198A 3'  GAGGGCCCACGGCTTCACTCA  33790     A    AGCTGG
                                TGAG GAAGC     GGGCCCTC
                                |||| |||||     ||||||||
                                ACTC CTTCG     CCCGGGAG
                                   A    GCA___
GAM800  HUMGT198A 3'  GAGGGCCCACGGCTTCACTCA  33791     A    AGCTGG
                                TGAG GAAGC     GGGCCCTC
                                |||| |||||     ||||||||
                                ACTC CTTCG     CCCGGGAG
                                   A    GCA___
GAM800  IGF2AS    3'  GAGGGCCGTTGTTGCCTCTC   33528      AA    T  G
                                GAGAG  GCAGC GG GGCCCTC
                                |||||  ||||| || |||||||
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                                CTCTC  CGTTG TT CCGGGAG
                                  __    _ G
GAM800  KIAA0125 3' GAGAACTTCCCTGCCTCCTC  29566    A A   CT    CC
                                GAG GA GCAG  GGGGG  CTC
                                ||| || ||||  |||||  |||
                                CTC CT CGTC  CCTTC  GAG
                                  _ C   __    AA
GAM800  KIAA0258 3' GAGGGCCCCCAGGTGGTC   29470   AG  G
                                GA  CA CTGGGGGCCCTC
                                ||  || ||||||||||||
                                CT  GT GACCCCCGGGAG
                                 G_  G
GAM800  KIAA0342 3' GAGCATTCCCAGCTGCCTCTCC 71140   A   A        CC
           A                     TG GAGA GCAGCTGGGGG  CTC
                                || |||| ||||||||||  |||
                                AC CTCT CGTCGACCCTT  GAG
                                 _   C         AC
GAM800  KIAA0354 5' GAGGGGTCACCGCCTCCTTC  30191    C  C  _  G
                                GAAG AG TGG GG CCCTC
                                |||| || ||| || |||||
                                CTTC TC GCC CT GGGAG
                                  C  C   A  G
GAM800  KIAA0970 3' GTTTCTGCTGCTTCTCCCA   30618   A       T  GG
                                TG GAGAAGCAGC GG  GC
                                || ||||||||| ||  ||
                                AC CTCTTCGTCG TC  TG
                                 C        _ TT
GAM800  KIAA1045 3' GGGGCTCTGCTTCCTCA    71607    A     CTGGG
                                TGAG GAAGCAG    GGCCCT
                                |||| |||||||    ||||||
                                ACTC CTTCGTC    TCGGGG
                                  _     _____
GAM800  KIAA1183 3' GAGGGCCCCAGGTGTGCTTCTC 63194   A      _  G
           CCG                    TG GAGAAGCA GCT GGGGCCCTC
                                || |||||||| ||| |||||||||
                                GC CTCTTCGT TGG CCCCGGGAG
                                 C      G  A
GAM800  KIAA1271 3' AGTGGCCACTGCTTCTCCCA  70127   A      CTGGG  _
                                TG GAGAAGCAG    GGCC CT
                                || |||||||||    |||| ||
                                AC CTCTTCGTC    CCGG GA
                                 C       A____   T
GAM800  KIAA1853 3' AGGGTTCAGCTGCTGCTCCCA 69918   A  A      GG
                                TG GAG AGCAGCTGG  GCCCT
                                || ||| |||||||||  |||||
                                AC CTC TCGTCGACT  TGGGA
                                 C  G       __
GAM800  MGC11257 3' AGGGCCCCTTCCCTCCTCCA  51352   A  A  CAGCT
                                TG GAG AG    GGGGGCCCT
                                || ||| ||    |||||||||
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                                AC CTC TC    TCCCCGGGA
                                 _  C  CCT__
GAM800  MGC14386 3'  AGGGCCCCATATTTGCCCCTC  54324    AA   CTG_
                                GAG  GCAG   GGGGCCCT
                                |||  ||||   ||||||||
                                CTC  CGTT   CCCCGGGA
                                  CC   TATA
GAM800  MGC14859 3'  GAAGGCTGGCTGCTGCCCTCA  62601     AGA     GGG   C
                                TGAG  AGCAGCT  GGCC TC
                                ||||  |||||||  |||| ||
                                ACTC  TCGTCGG  TCGG AG
                                  CCG     ___   A
GAM800  MGC15827 3'  GAGGGCCCCGGGGCCTCCTCTC 52874      A  CAG  G
                                GAGAG AG  CT GGGGCCCTC
                                ||||| ||  || |||||||||
                                CTCTC TC  GG CCCCGGGAG
                                   C  CG_  G
GAM800  MGC16179 3'  GCCCTCAAGACCACCTGCCCCT 52282   A  AA   C  ________ GCCC
           CCCA                  TG GAG  GCAG TGG     GG   T
                                || |||  |||| |||      ||   |
                                AC CTC  CGTC ACC     CT   G
                                 C  CC   C  AGAA___  CCCG
GAM800  MGC2835  3'  AGGACACAGCTGCTCCCCTCT  44174     A__      GGGGC
                                AGAG  AGCAGCTG   CCT
                                ||||  ||||||||   |||
                                TCTC  TCGTCGAC   GGA
                                  CCC      ACA__
GAM800  MGC5508  3'  GCTGCCAGCTGCCCCTCTC   44267      AA      G
                                GAGAG  GCAGCTGG GGC
                                |||||  |||||||| |||
                                CTCTC  CGTCGACC TCG
                                   CC      G
GAM800  NPTXR    3'  GAGGGAAATTGCTGCTTCTCCA 27435    A        TGGGGG
                                TG GAGAAGCAGC    CCCTC
                                || ||||||||||    |||||
                                AC CTCTTCGTCG    GGGAG
                                 _       TTAAA_
GAM800  OATPRP4  3'  GAGAGCCTTTCCCCGCTTCTCT 48984         AGCT  ___  C
           C                   GAGAGAAGC   GGG  GGC CTC
                               |||||||||   |||  ||| |||
                               CTCTCTTCG   CCC  CCG GAG
                                    C___   TTT  A
GAM800  PV1     3'  GCCTCCCAGCCACTTCCTCA  49375    A   CA    _
                                TGAG GAAG  GCTGGG GGC
                                |||| ||||  |||||| |||
                                ACTC CTTC  CGACCC CCG
                                  _   AC    T
GAM800  STATI2   5'  AGAGCCCCATCCCTTCTCTC  96188       CAGCTG    C
                                GAGAGAAG    GGGGC CT
                                ||||||||    ||||| ||
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                                CTCTCTTC     CCCCG GA
                                     CCTA__     A
GAM800  STATI2   5'  AGAGCCCCATCCCTTCTCTC  96189        CAGCTG    C
                                GAGAGAAG     GGGGC CT
                                ||||||||     ||||| ||
                                CTCTCTTC     CCCCG GA
                                     CCTA__     A
GAM800  SYNPO2   3'  TCGACAACTGCTTCTCCCA   72391    A       C _____
                                TG GAGAAGCAG TG     GG
                                || |||||||| ||     ||
                                AC CTCTTCGTC AC     CT
                                 C        A  AG___
GAM800  TAGAP    5'  GAGAGTTATGCTGTTTCTCCCA 55100    A        TGGG   C
                                TG GAGAAGCAGC    GGC CTC
                                || ||||||||||    ||| |||
                                AC CTCTTTGTCG    TTG GAG
                                 C         TA__   A
GAM800  TAGAP    5'  GAGAGTTGTGCTGTTTCTCCCA 55101    A        TGGG   C
                                TG GAGAAGCAGC    GGC CTC
                                || ||||||||||    ||| |||
                                AC CTCTTTGTCG    TTG GAG
                                 C         TG__   A
GAM800  TBX21    3'  AGGCCCCCGCTCCCTCT     26246      AAGC   T      C
                                AGAG    AGC GGGGGCC T
                                ||||    ||| ||||||| |
                                TCTC    TCG CCCCCGG A
                                  CC__   _      A
GAM800  TOLLIP   3'  GGCCCTCGAGAGCAGCTGCTTC 39197    AG         _________ GGCCC
           TGCCA                   TG  AGAAGCAGCTG       GG     T
                                ||  ||||||||||       ||     |
                                AC  TCTTCGTCGAC       CT     G
                                 CG         GAGAG___  CCCGG
GAM800  ZWINT    3'  GGCCTCTGACTTCCCTCA    23908      A   _  CTGG
                                TGAG GAAG CAG    GGGCC
                                |||| |||| |||    |||||
                                ACTC CTTC GTC    TCCGG
                                  C    A  ____
GAM800  LOC124222 3'  AGGGCTGCAGCTGCTTCTTCCA 74743    AG         G  G
                                TG  AGAAGCAGCTG GG CCCT
                                ||  |||||||||| || ||||
                                AC  TCTTCGTCGAC TC GGGA
                                 CT         G  _
GAM800  LOC130644 3'  AGGGCCCCGTTTGCCTCTCCA  76249    A    A    CTG
                                TG GAGA GCAG   GGGGCCCT
                                || |||| ||||   ||||||||
                                AC CTCT CGTT   CCCCGGGA
                                 _   C    TG_
GAM800  LOC144017 3'  GGCCCTCAAGAAGCTGCTTTTC 83931    A        T________  GGCC
           CCA                    TG GAGAAGCAGC       GGG    C
                                || ||||||||||       |||    |
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                                AC CTTTTCGTCG       CTC    G
                                 C         AAGAA___   CCGG
GAM800   LOC145098 5'  GAGGGTAGGGAACTGCTTCTC  77536          CTGGGG
                                GAGAAGCAG     GCCCTC
                                |||||||||     ||||||
                                CTCTTCGTC     TGGGAG
                                     AAGGGA
GAM800   LOC145989 3'  CTCCCAGCCACCTCCTCCCA   60292    A   A  CA_
                                TG GAG AG   GCTGGGGG
                                || ||| ||   ||||||||
                                AC CTC TC   CGACCCTC
                                 C   C  CAC
GAM800   LOC147229 5'  GAGGACCCCCAGCCTCTGGCCT 78920      AGA  CA       C
            CA                    TGAG   AG  GCTGGGGG CCTC
                                ||||   ||  |||||||| ||||
                                ACTC   TC  CGACCCCC GGAG
                                   CGG  TC       A
GAM800   LOC149401 5'  GGACCGGGTCTGCTTCTGTCA  80114     G       _  G  GG
                                TGA AGAAGCAG CT GG  CC
                                ||| |||||||| || ||  ||
                                ACT TCTTCGTC GG CC  GG
                                  G       T  G  A_
GAM800   LOC151171 5'  GAGGGCCCCCCCACGCCTCCCA 80948    A   AA  AGCT
                                TG GAG  GC    GGGGGCCCTC
                                || |||  ||    ||||||||||
                                AC CTC  CG    CCCCCGGGAG
                                 C   __  CACC
GAM800   LOC151174 5'  GAGGGTCTGAGCACCTCCCTCA 86437      A  A CA   G   G
                                TGAG GA G  GCT GGG CCCTC
                                |||| || |  ||| ||| |||||
                                ACTC CT C  CGA TCT GGGAG
                                  C  _ CA   G   _
GAM800   LOC151475 5'  GGCCACACTGCCCTCCCA    86597    A   AA    C  GG
                                TG GAG  GCAG TG  GGCC
                                || |||  |||| ||  ||||
                                AC CTC  CGTC AC  CCGG
                                 C   C_   _  A_
GAM800   LOC158490 5'  GAGAACCCGGCAGCCTTCTCTC 82822          _ A     GGCC
            A                     TGAGAGAAG C GCTGGG    CTC
                                |||||||| | ||||||    |||
                                ACTCTCTTC G CGGCCC    GAG
                                     C A      AA__
GAM800   LOC169436 5'  TCGACCAGCTGCTCCTTCA    83621      A  A      _____
                                TGAG GA GCAGCTGG     GG
                                |||| || ||||||||     ||
                                ACTT CT CGTCGACC     CT
                                  C  _       AG___
GAM800   LOC196738 3'  AGGTGCTCCAGCTGCTTCTATC 88885     G           GC
            A                     TGA AGAAGCAGCTGGGG  CCT
                                ||| ||||||||||||||  |||
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                                ACT TCTTCGTCGACCTC  GGA
                                  A           GT
GAM800  LOC196860 3'  AGAGCCACATGCTTCTCTC   91213         GC  GG   C
                                GAGAGAAGCA  TG  GGC CT
                                ||||||||||  ||  ||| ||
                                CTCTCTTCGT  AC  CCG GA
                                      __ A_   A
GAM800  LOC196878 5'  GAAGGCTTGCTGCTGCTTCTCC 89177    A        TGG    C
            A                    TG GAGAAGCAGC   GGGCC TC
                                || ||||||||||   ||||| ||
                                AC CTCTTCGTCG   TTCGG AG
                                 _        TCG    A
GAM800  LOC221092 5'  AGGGCAGCCACTTTTCTCA   94864         CAGC   GG
                                TGAGAGAAG   TGG  GCCCT
                                |||||||||   |||  |||||
                                ACTCTTTTC   ACC  CGGGA
                                      ____  GA
GAM800  LOC221299 5'  GGCCCTCAAAAGGCTGCTTCTC 93480    A        T________  GGCC
            GCA                    TG GAGAAGCAGC       GGG    C
                                || ||||||||||       |||   |
                                AC CTCTTCGTCG       CTC    G
                                 G        GAAAA___   CCGG
GAM800  LOC222060 5'  GAGACTCGCTCCAACTGCCCGC 95754     AGAA_   CTG    C___
            CCTCA                  TGAG    GCAG   GGGGC    CTC
                                ||||    ||||  |||||   |||
                                ACTC    CGTC   CCTCG    GAG
                                  CCGCC    AA_    CTCA
GAM800  LOC255045 5'  GAGGGCCCCAGAAGGCTCCTTC 97958    AG  A   AG_     G
            CA                    TG  AG AGC   CTGGGG CCCTC
                                ||  || |||   |||||| |||||
                                AC  TC TCG   GACCCC GGGAG
                                 CT  C   GAA     _
GAM800  LOC255645 3'  GAGACTTTCAGTTGCTCCTCTC 98474       A      GG  CC
            A                    TGAGAG AGCAGCTG  GG  CTC
                                ||||||| ||||||||  ||  |||
                                ACTCTC TCGTTGAC  TC  GAG
                                   C       TT  A_
GAM800  LOC256848 3'  AGGGCCTCACTTACCTCA    99376     AG   CAGCTG
                                TGAG  AAG     GGGGCCCT
                                ||||  |||     ||||||||
                                ACTC  TTC     CTCCGGGA
                                  CA   A_____
GAM800  LOC257081 3'  TCCCCAGCTGCTCTCCCA    98593    A    A
                                TG GAGA GCAGCTGGGGG
                                || |||| ||||||||||
                                AC CTCT CGTCGACCCCT
                                 C   _
GAM800  LOC51762  3'  GAGGGCCCTTTCCTGCTTCTCT 33706          CT
                                AGAGAAGCAG  GGGGGCCCTC
                                ||||||||||  ||||||||||
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                                TCTCTTCGTC  TTCCCGGGAG
                                      CT
GAM800  LOC58525  5'  AGAGCCCCCAGCTGTCCCT   79340    AA        C
                                AG  GCAGCTGGGGGC CT
                                ||  |||||||||||| ||
                                TC  TGTCGACCCCCG GA
                                 CC          A
GAM800  LOC90785  3'  GAGAAGTCCAGCCGGCTTCTCT 64715         A_    GGCC
           CA                    TGAGAGAAGC  GCTGGG   CTC
                                ||||||||||  ||||||   |||
                                ACTCTCTTCG  CGACCT   GAG
                                      GC     GAA_
GAM800  LOC92335  3'  GAGGACCGCCACCTCTTC    69544     C  C   G  C
                                GAAG AG TGG GG CCTC
                                |||| || ||| || ||||
                                CTTC TC ACC CC GGAG
                                  _ C   G  A
GAM801  PROK1    3'  CACCAACCTGCTGGCTTTAGAA 51567     TCAC  G    AGC
                                TTCT    GG CAGCA   TGGTG
                                ||||    || |||||   |||||
                                AAGA    TC GTCGT   ACCAC
                                  TT__  G    CCA
GAM801  HSA404617 5'  CACCAGCTCGCCCTTCTGAGAA 73089      CAC_   AGCA
                                TTCTT    GGGC    AGCTGGTG
                                |||||    ||||    ||||||||
                                AAGAG    CCCG    TCGACCAC
                                   TCTT    C___
GAM801  KIAA0431  3'  CACCAGCTTGGGCAACATAAGA 31546      CACGG  AG
           A                     TTCTT    GC  CAAGCTGGTG
                                |||||     ||  ||||||||||
                                AAGAA    CG  GTTCGACCAC
                                   TACAA  G_
GAM801  PAK6     5'  ACCAGCCTGCAGTGGAGAA    39806        GG    CAA
                                TTCTTCAC  GCAG   GCTGGT
                                ||||||||  ||||   ||||||
                                AAGAGGTG  CGTC   CGACCA
                                     A_    ___
GAM801  LOC90670  3'  TTTGCTGCCCTGAAGAA     64486        C
                                TTCTTCA GGGCAGCAAG
                                |||||||  ||||||||||
                                AAGAAGT CCCGTCGTTT
                                      _
GAM802  SCAMP1    3'  GCTAAATAAATATTCTCC    54500     T     C
                                GGA AATATT ATTTAGC
                                |||  ||||||  |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM802  SCAMP1    3'  GCTAAATAAATATTCTCC    54501     T     C
                                GGA AATATT ATTTAGC
                                |||  ||||||  |||||||
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                                CCT TTATAA TAAATCG
                                  C     A
GAM802  NX-17    3'  TGAATATCAGCCCCTAATA   40706        ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM802  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
           TA                    TATTAGGGATAATATTCATTTAGC
                                 ||||||||||||||||||||||||
                                 ATAATCCCTATTATAAGTAAATCG

GAM803  SCAMP1   3'  GCTAAATAAATATTCTCC    54500     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM803  SCAMP1   3'  GCTAAATAAATATTCTCC    54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM803  NX-17    3'  TGAATATCAGCCCCTAATA   40706        ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM803  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
           TA                    TATTAGGGATAATATTCATTTAGC
                                 ||||||||||||||||||||||||
                                 ATAATCCCTATTATAAGTAAATCG

GAM804  DLEC1    3'  CATCTGGCCCTCCCTTG     24717      A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                  C    G  _
GAM804  DLEC1    3'  CATCTGGCCCTCCCTTG     96278      A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                  C    G  _
GAM804  PIP5K1A  3'  TATCCCACCCTGCCTTGATA  14520        A   CA  C
                                TATCAAGG AGGG  GG GTG
                                |||||||| ||||  || |||
                                ATAGTTCC TCCC  CC TAT
                                    G   A_  C
GAM804  SOX11    3'  ACCCACCCCCCCTTGGTA    13308        AA   CA  C
                                TATCAAGG  GGG  GG GT
                                ||||||||  |||  || ||
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                                ATGGTTCC  CCC  CC CA
                                    CC   A_ _
GAM804  CHL1     3'  TGTTACCTTTCCTCAATA    22768     CA      CA
                                TAT  AGGAAGGG  GGCG
                                |||  ||||||||  ||||
                                ATA  TCCTTTCC  TTGT
                                  AC       A_
GAM804  EPB41L1  3'  CATTCTGCCCTTCCCTGA    71104     A        C
                                TCA GGAAGGGCAGG GTG
                                ||| ||||||||||| |||
                                AGT CCTTCCCGTCT TAC
                                  C        _
GAM804  FLJ00060 3'  CATACCCCCTGCCCTCCTCTGA 61741     _   A      CGTG
                                TCA AGGA GGGCAGG    ATG
                                ||| |||| |||||||    |||
                                AGT TCCT CCCGTCC    TAC
                                  C   _      CCCA
GAM804  FLJ10898 5'  CACCACAGCCCTTTCTCAATA  60126     CA       AGGC
                                TAT  AGGAAGGGC    GTG
                                |||  |||||||||    |||
                                ATA  TCTTTCCCG    CAC
                                  AC        ACAC
GAM804  FLJ22557 3'  ATCATCCCATCCTTAATA    45581     C    A   CAGGC
                                TAT AAGGA GGG     GTGAT
                                ||| ||||| |||     |||||
                                ATA TTCCT CCC     TACTA
                                  A    A  _____
GAM804  KIAA0574 3'  CATCCCCTGCCCTCCCCTGA   69808     A  A      CGT
                                TCA GG AGGGCAGG   GATG
                                ||| || ||||||||   ||||
                                AGT CC TCCCGTCC   CTAC
                                  C  C       C__
GAM804  KIAA0632 3'  CACCTCAGAAACCCTTCCTTGA 32071          CA___  C
                                TCAAGGAAGGG     GG GTG
                                ||||||||||     || |||
                                AGTTCCTTCCC     CT CAC
                                       AAAGA  C
GAM804  KIAA1045 3'  CATCACATGTCCTTCC      71599         GGC
                                GGAAGGGCA   GTGATG
                                |||||||||   ||||||
                                CCTTCCTGT   CACTAC
                                     A__
GAM804  KIAA1354 5'  CAGTGACTGCCTTCCCTTGATA 61572        A      G  _
                                TATCAAGG AGGGCAG CG TG
                                |||||||| ||||||| || ||
                                ATAGTTCC TTCCGTC GT AC
                                     C      A  G
GAM804  MGC20460 5'  CACCGCCTCCTACCCTTCTT   54901        C___    _
                                AGGAAGGG    AGGCG TG
                                ||||||||    ||||| ||
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                                TTCTTCCC   TCCGC AC
                                    ATCC    C
GAM804  LOC158476 3'  CACGCCCGCCCCCCCCATTGA  88186     _ AA_   A
                                TCAA GG   GGGC GGCGTG
                                |||| ||   |||| ||||||
                                AGTT CC   CCCG CCGCAC
                                  A  CCC    C
GAM804  LOC90459  3'  CACACCCGCCTAATTTTTG   63550      A_   A  C
                                CAAGGA  GGGC GG GTG
                                ||||||  |||| || |||
                                GTTTTT  TCCG CC CAC
                                   AA    C  A
GAM805  BACH2    3'  CTGTCAAGCAATGGATAAACAG 41782        C    GGGA__
          CTCT                   AGAGTTGTT ATCCA     GACAG
                                |||||||||| |||||     |||||
                                TCTCGACAA TAGGT     CTGTC
                                    A     AACGAA
GAM805  CHRNA1   3'  CTGTCTCCCTGAAGAGTGAAC  5375       C___
                                GTTCAT   CAGGGAGACAG
                                ||||||   ||||||||||||
                                CAAGTG   GTCCCTCTGTC
                                   AGAA
GAM805  HHIP     5'  CTGTCCCACCTAAACAACTC   42753       CATCCAG  A
                                GAGTTGTT      GG GACAG
                                ||||||||      || |||||
                                CTCAACAA      CC CTGTC
                                    ATCCA__  _
GAM805  MME      3'  TCCCTATGGAGGAACAACTCT  8034         A   __
                                AGAGTTGTTC TCCA  GGGA
                                |||||||||| ||||  ||||
                                TCTCAACAAG AGGT  CCCT
                                     G    AT
GAM805  MTCP1    5'  CTACATGGATAACAACTCT   27242        C    GGG
                                AGAGTTGTT ATCCA   AG
                                |||||||||| |||||   ||
                                TCTCAACAA TAGGT   TC
                                    _    ACA
GAM805  NR1D1    3'  TGTCTCCCCCACAACCCT    41672    A    TCATCCA
                                AG GTTGT      GGGAGACA
                                || |||||      ||||||||
                                TC CAACA      CCCTCTGT
                                 C    CC_____
GAM805  NR1I2    3'  TGTCTCCCTAGGGAATTC    15304      GTTCA  _
                                GAGTT    TCC AGGGAGACA
                                |||||    ||| |||||||||
                                CTTAA    GGG TCCCTCTGT
                                   _____  A
GAM805  NR1I2    3'  TGTCTCCCTAGGGAATTC    42088      GTTCA  _
                                GAGTT    TCC AGGGAGACA
                                |||||    ||| |||||||||
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                                CTTAA    GGG TCCCTCTGT
                                  _____  A
GAM805  PCOLN3   3'  CTGCCCTGTTGCCAAACAACTC 12411       ___ TC   _
                                GAGTTGTT  CA  CAGGG AG
                                ||||||||  ||  ||||| ||
                                CTCAACAA  GT  GTCCC TC
                                    ACC  T_   G
GAM805  PFN2     3'  TGTCTTCATCAACAACCCT   54889    A    CATCCAG
                                AG GTTGTT     GGAGACA
                                || ||||||     |||||||
                                TC CAACAA     CTTCTGT
                                 C     CTA____
GAM805  PFN2     3'  TGTCTTCATCAACAACCCT   54890    A    CATCCAG
                                AG GTTGTT     GGAGACA
                                || ||||||     |||||||
                                TC CAACAA     CTTCTGT
                                 C     CTA____
GAM805  TNS      3'  CTGTCTCCCTAACTCAACTGCT 42950    _   TTCATCC
                                AG AGTTG      AGGGAGACAG
                                || |||||      ||||||||||
                                TC TCAAC      TCCCTCTGTC
                                 G    TCAA___
GAM805  FLJ10511 3'  CCCTAGAAAAACAACTCT    36686       CA  C
                                AGAGTTGTT  TC AGGG
                                |||||||||  || ||||
                                TCTCAACAA  AG TCCC
                                    AA  A
GAM805  FLJ20195 3'  CCCGATGAACACCTCT     35216     T     CA
                                AGAG TGTTCATC  GGG
                                |||| ||||||||  |||
                                TCTC ACAAGTAG  CCC
                                  C      __
GAM805  HAAO     3'  TCCCTGCCAAACAACTCT    60173       CATC
                                AGAGTTGTT   CAGGGA
                                |||||||||   ||||||
                                TCTCAACAA   GTCCCT
                                    ACC_
GAM805  KIAA0843 3'  CTGAACAACCAGACAGACAACT 30801       CA  CA  GAGA_
          CT                    AGAGTTGTT  TC  GG   CAG
                                |||||||||  ||  ||   |||
                                TCTCAACAG  AG  CC   GTC
                                    AC  A_  AACAA
GAM805  KIAA1497 5'  CTGTCCTTGTATGAGCAAC   68121       C    GA
                                GTTGTTCAT CAGGGA  CAG
                                ||||||||| ||||||  |||
                                CAACGAGTA GTTCCT  GTC
                                    T     __
GAM805  KIAA1710 3'  TCTCCATACATGAACAATCT  63181    G     CCAG
                                AGA TTGTTCAT   GGAGA
                                ||| ||||||||   |||||
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                                TCT AACAAGTA    CCTCT
                                  _       CATA
GAM805  PDE7B    3'  CTGCCGAAATGAGCAACTC    38949          CCA  G
                                GAGTTGTTCAT   GG AG
                                ||||||||||   || ||
                                CTCAACGAGTA   CC TC
                                      AAG  G
GAM805  SEC24B   3'  CTGCATTGTTGGATGACAACTC 21984        T      G  GA
           T                     AGAGTTGT CATCCAG GA  CAG
                                ||||||||| ||||||| ||  |||
                                TCTCAACA GTAGGTT TT  GTC
                                     _      G  AC
GAM805  LOC124753 5'  CTGCCTCCCTGGCTTCCATCTC 74803     T  TTCAT       A
                                GAG TG     CCAGGGAG CAG
                                ||| ||     |||||||| |||
                                CTC AC     GGTCCCTC GTC
                                  T  CTTC_       C
GAM805  LOC142948 3'  CTACCGGGAGGAATGAATAACT 83777          ____   A  G
           C                     GAGTTGTTCA    TCC GG AG
                                ||||||||||    ||| || ||
                                CTCAATAAGT    AGG CC TC
                                      AAGG   G  A
GAM805  LOC153914 5'  CCACTAAAGTGAACAACTC    81898          CC_  _
                                GAGTTGTTCAT   AG GG
                                ||||||||||   || ||
                                CTCAACAAGTG   TC CC
                                      AAA  A
GAM805  LOC219445 5'  CTCCCTGGTTCAAACAATTC   93202        CAT_
                                GAGTTGTT    CCAGGGAG
                                ||||||||    ||||||||
                                CTTAACAA    GGTCCCTC
                                     ACTT
GAM805  LOC219914 5'  CCACTGGGAGGAACGAACAACT 94967         A_____    _
           C                     GAGTTGTTC     TCCAG GG
                                |||||||||     ||||| ||
                                CTCAACAAG     GGGTC CC
                                      CAAGGA     A
GAM806  ATP2B2   5'  CAGCCATCACCCGGCAGC    9846      A      __
                                GCT CTGGGTGA  GCTG
                                ||| ||||||||  ||||
                                CGA GGCCCACT  CGAC
                                  C       AC
GAM806  BSCL2    5'  GGCTACCGGCTTTACCCTCCCA 51995          T_____   T___  ACTA
           GTAGCT                  AGCTACTGGG     GAGC    GG    CC
                                ||||||||||     ||||   ||   ||
                                TCGATGACCC     TTCG    CC    GG
                                      TCCCAT    G___  ATCA
GAM806  IMPA2    5'  AGTGTGTGCTCACCCACAGC   96944     AC       _  G
                                GCT  TGGGTGAGC TG ACT
                                |||  ||||||||| || |||
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                                CGA  ACCCACTCG GT TGA
                                  C_       T  G
GAM806  KCNE1L   3'  AGTCCAGCTTCCAGTTGC    25388    T    GT
                                GC ACTGG  GAGCTGGACT
                                || |||||  ||||||||||
                                CG TGACC  TTCGACCTGA
                                 T    __
GAM806  KRTHA1   3'  GGCAGCCAAGAAACTCACCCAA 11237     AC      C____   A  A
            AGC                   GCT  TGGGTGAG    TGG CT CC
                                |||  ||||||||    ||| || ||
                                CGA  ACCCACTC    ACC GA GG
                                  A_       AAAGA   _  C
GAM806  MADH7    3'  AGTATTGCTCACCCAGTGC    20922    T        TGG
                                GC ACTGGGTGAGC   ACT
                                || ||||||||||   |||
                                CG TGACCCACTCG   TGA
                                 _         TTA
GAM806  SQSTM1   3'  GTACCAGCAGCCCAGCACATAG 15329      _____     GA  T___  ACTA
            CT                    AGCTA   CTGGGT  GC    GG    C
                                |||||   ||||||  ||    ||    |
                                TCGAT   GACCCG  CG    CC    G
                                  ACAC     A_  A___  ATC
GAM806  TPI1     3'  AGCCCAGAAGCCCAGTAACT   6294     C      GAG    A
                                AG TACTGGGT   CTGG CT
                                || ||||||||   |||| ||
                                TC ATGACCCG   GACC GA
                                 A       AA_   C
GAM806  TRHDE    3'  GGTATTCTCACCCAGTAG    26316          CTGG
                                CTACTGGGTGAG    ACT
                                ||||||||||||    |||
                                GATGACCCACTC    TGG
                                       TTA_
GAM806  CAPN6    3'  CAGCATTTCACCCAGCAGC    27398     A      ___
                                GCT CTGGGTGA   GCTG
                                ||| ||||||||   ||||
                                CGA GACCCACT   CGAC
                                  C       TTA
GAM806  DT1P1A10  3'  AGTTTCTGGGCCCACCCTAGCA 62246     A  _    A  ___
            GC                    GCT CT GGGTG GCT   GGACT
                                ||| || ||||| |||   |||||
                                CGA GA CCCAC CGG   TTTGA
                                  C  T    C   GTC
GAM806  FLJ12700  3'  GGCAGTCCACAGGCCTACAGCT 46657     AC     GAGC     A
                                AGCT  TGGGT    TGGACT CC
                                ||||  |||||    |||||| ||
                                TCGA  ATCCG    ACCTGA GG
                                  C_     GAC_     C
GAM806  FLJ32780  3'  AGTCCTCTGGTCCCACAGCT   59297      AC    _ G  CT
                                AGCT  TGGG T AG  GGACT
                                ||||  |||| | ||  |||||
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                                TCGA  ACCC G TC  CCTGA
                                  C_   T G  T_
GAM806  HRD1     3'  CCTGTCTCACCCAGCAGC    70148     A       _ T
                                GCT CTGGGTGAG C GG
                                ||| ||||||||| | ||
                                CGA GACCCACTC G CC
                                  C        T T
GAM806  KIAA0356 3'  GGTCTATGGGCCCACCCAGTGC 66779    T       A  ___
                                GC ACTGGGTG GCT   GGACT
                                || |||||||| |||   |||||
                                CG TGACCCAC CGG   TCTGG
                                 _       C   GTA
GAM806  KIAA0984 3'  AGCTCACTCACCCACCAGCT   66137     AC       C  GA
                                AGCT  TGGGTGAG TG  CT
                                ||||  |||||||| ||  ||
                                TCGA  ACCCACTC AC  GA
                                  CC        _ TC
GAM806  KIAA1598 5'  GTAGTCCAACTGGGATATTAGC 37639     _____ G   GAGC
                                GCTA    CT GGT    TGGACTAC
                                ||||    || |||    ||||||||
                                CGAT    GG TCA    ACCTGATG
                                  TATA  G   _____
GAM806  KIAA1681 3'  AGTCCAAGTCCAGTAACT    61714    C     GTGA  _
                                AG TACTGG    GCT GGACT
                                || ||||||    ||| |||||
                                TC ATGACC    TGA CCTGA
                                 A     _____   A
GAM806  MGC17303 3'  GGCAGTCAGATCCACCCAGTGC 58233     T       AG_   G   A
           T                     AGC ACTGGGTG   CTG ACT CC
                                ||| ||||||||   ||| ||| ||
                                TCG TGACCCAC   GAC TGA GG
                                  _       CTA   _   C
GAM806  PDE4DIP  5'  CCAGTGGTCACCCAGTAGC   97175          __  T___
                                GCTACTGGGTGA  GC    GG
                                ||||||||||||  ||    ||
                                CGATGACCCACT  TG    CC
                                       GG  A___
GAM806  SLC26A10 5'  CCGGTAACCCAACAGTGGCT   56842        ___    GA  T___
                                AGCTACT   GGGT  GC    GG
                                |||||||   ||||  ||    ||
                                TCGGTGA   CCCA  TG    CC
                                    CAA    A_  G___
GAM806  USP2     5'  AGCCGGGACTCACCCGCAGCT  16108     AC       __   A
                                AGCT  TGGGTGAG  CTGG CT
                                ||||  ||||||||  |||| ||
                                TCGA  GCCCACTC  GGCC GA
                                  C_       AG   _
GAM806  LOC151174 5'  GGCCCGGCTCACCCCACAGCT  86438      ACT         A
                                AGCT   GGGTGAGCTGG CT
                                ||||   ||||||||||| ||
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                                TCGA   CCCACTCGGCC GG
                                  CAC          C
GAM806  LOC158055 3'  AGGCCTCCACCCAGTGCT    82576     T       AGCT  A
                                AGC ACTGGGTG    GG CT
                                ||| ||||||||    || ||
                                TCG TGACCCAC    CC GA
                                  _       CT__  G
GAM806  LOC158696 3'  GTAGATCCACCAATAGCT    82861      C   GTGAGC   _
                                AGCTA TGG     TGGA CTAC
                                ||||| |||     |||| ||||
                                TCGAT ACC     ACCT GATG
                                  A  _______   A
GAM806  LOC196027 3'  GGTTTTCACCCAGTAGTT    88940           CTG
                                AGCTACTGGGTGAG   GACT
                                ||||||||||||||   ||||
                                TTGATGACCCACTT   TTGG
                                                 ___
GAM806  LOC200812 5'  CAGCCCATCCAGTATGCT    90301     _       A
                                AGC TACTGGGTG GCTG
                                ||| ||||||||| ||||
                                TCG ATGACCTAC CGAC
                                  T        C
GAM806  LOC253836 5'  CAGCGCTTCACCCAGTGC    99465    T       ___
                                GC ACTGGGTGA   GCTG
                                || |||||||||   ||||
                                CG TGACCCACT   CGAC
                                  _        TCG
GAM806  LOC256436 3'  AGCCCAGAAGCCCAGTAACT   96247    C       GAG    A
                                AG TACTGGGT   CTGG CT
                                || ||||||||   |||| ||
                                TC ATGACCCG   GACC GA
                                  A       AA_   C
GAM806  LOC256492 5'  TCCAGCTCAGTACAGCAGC    99434     A   GG_
                                GCT CTG   TGAGCTGGA
                                ||| |||   |||||||||
                                CGA GAC   ACTCGACCT
                                  C   ATG
GAM806  LOC56181  3'  GTCACTCACTCAGCAGCT    97284      A       CTG
                                AGCT CTGGGTGAG   GAC
                                |||| |||||||||   |||
                                TCGA GACTCACTC   CTG
                                  C        A__
GAM806  LOC92148  5'  TCTACACACCCAGTACT     68888    C       AGC
                                AG TACTGGGTG   TGGA
                                || |||||||||   ||||
                                TC ATGACCCAC   ATCT
                                  _        AC_
GAM807  CNTN3     3'  TGACCCATGCAAAATATTAGC  67271    C  C   GAA_
                                GC AA TGT    CATGGGTCA
                                || || |||    |||||||||
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                                CG TT ATA    GTACCCAGT
                                 A  _   AAAC
GAM807   FE65L2   3'  ACCCTGGACAGTTGGCT     56514          GAA  T
                                AGCCAACTGT   CA GGGT
                                ||||||||||   || ||||
                                TCGGTTGACA   GT CCCA
                                     G__  _
GAM807   FE65L2   3'  ACCCTGGACAGTTGGCT     56515          GAA  T
                                AGCCAACTGT   CA GGGT
                                ||||||||||   || ||||
                                TCGGTTGACA   GT CCCA
                                     G__  _
GAM807   FE65L2   3'  ACCCTGGACAGTTGGCT     56517          GAA  T
                                AGCCAACTGT   CA GGGT
                                ||||||||||   || ||||
                                TCGGTTGACA   GT CCCA
                                     G__  _
GAM807   FE65L2   3'  ACCCTGGACAGTTGGCT     21290          GAA  T
                                AGCCAACTGT   CA GGGT
                                ||||||||||   || ||||
                                TCGGTTGACA   GT CCCA
                                     G__  _
GAM807   GATA6    3'  ACCCACAGGCAGGTTGGTTT   19143          G  AACA
                                AAGCCAACT TG    TGGGT
                                ||||||||| ||    |||||
                                TTTGGTTGG AC    ACCCA
                                     _  GGAC
GAM807   GHR      3'  GAATCTGTTCACACCCAACTTG 5699       CCAAC       T GG
                                CAAG     TGTGAACA G  TC
                                ||||     |||||||| |  ||
                                GTTC     ACACTTGT C  AG
                                  AACCC        _ TA
GAM807   GPI      3'  TGACCCATGTTCACGTTG     5728       T
                                CAAC GTGAACATGGGTCA
                                |||| ||||||||||||||
                                GTTG CACTTGTACCCAGT
                                  _
GAM807   INPP5A   3'  ACCCATGTCATAACCTTG     19862      CCAAC     A
                                CAAG     TGTGA CATGGGT
                                ||||     ||||| |||||||
                                GTTC     ATACT GTACCCA
                                  CA___     _
GAM807   NPC1     3'  ATGCACAGTTGACTTG       6053       C       AA
                                CAAG CAACTGTG  CAT
                                |||| ||||||||  |||
                                GTTC GTTGACAC  GTA
                                  A       __
GAM807   PLGL     3'  CCATCCACAGTTGGTT       12170          AAC
                                AGCCAACTGTG   ATGG
                                ||||||||||   ||||
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                                TTGGTTGACAC   TACC
                                      C__
GAM807  PTGES    5'  TGATCACACCCACAGTTGAGCT 18075     _      AACATG
                                AGC CAACTGTG     GGTCA
                                ||| ||||||||     |||||
                                TCG GTTGACAC     CTAGT
                                  A       CCACA_
GAM807  PTGS1    3'  TGACTCATCCCCACAGCTGGCT 8244       A    AAC
                                AGCCA CTGTG   ATGGGTCA
                                ||||| |||||   ||||||||
                                TCGGT GACAC   TACTCAGT
                                   C    CCC
GAM807  PTGS1    3'  TGACTCATCCCCACAGCTGGCT 55480      A    AAC
                                AGCCA CTGTG   ATGGGTCA
                                ||||| |||||   ||||||||
                                TCGGT GACAC   TACTCAGT
                                   C    CCC
GAM807  RP2      3'  ACCCATTTTAATAAGCTTG   23596      CAACTG   C
                                CAAGC     TGAA ATGGGT
                                |||||     |||| ||||||
                                GTTCG     ATTT TACCCA
                                   AATA__   _
GAM807  TEM8     3'  ATTCTGTTGACAGCCAGCTCA  50824   A  CAA   G   T
                                C AGC   CTGT AACA GGGT
                                | |||   |||| |||| ||||
                                A TCG   GACA TTGT CTTA
                                 C   ACC   G   _
GAM807  C7orf13  3'  ACCCATGTCCTGGTGACGT   51919    CA_   T  A
                                GC   ACTG GA CATGGGT
                                ||   |||| || |||||||
                                TG   TGGT CT GTACCCA
                                 CAG   C  _
GAM807  CLGN     3'  TGACCCACATTTACCTAGTTTG 16416      CAACT    CA
                                CAAGC    GTGAA  TGGGTCA
                                |||||    |||||  |||||||
                                GTTTG    CATTT  ACCCAGT
                                   ATC__    AC
GAM807  FLJ32499 3'  TGACCATACAAAGCTGGCTT   58784       A  G  AACATG
                                AAGCCA CT TG     GGTCA
                                |||||| || ||     |||||
                                TTCGGT GA AC     CCAGT
                                   C  A  ATA___
GAM807  KIAA0229 3'  ACCCATGTGGTTGGC      94023       GTGA
                                GCCAACT    ACATGGGT
                                |||||||    ||||||||
                                CGGTTGG    TGTACCCA
                                     _____
GAM807  KIAA0447 5'  TGACCCATGCTGCCCAGCCTGG 72133     A_   TGAA_
                                CCA  CTG    CATGGGTCA
                                |||  |||    |||||||||
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                                GGT  GAC    GTACCCAGT
                                  CC   CCGTC
GAM807  KIAA0453  3'  TGACCCAGCACAGTTGGC    69611         AACA
                                GCCAACTGTG   TGGGTCA
                                ||||||||||   |||||||
                                CGGTTGACAC   ACCCAGT
                                     G___
GAM807  KIAA1297  3'  TGACCCACCTGCCAGTTGGC  72645        TGAACA
                                GCCAACTG     TGGGTCA
                                ||||||||     |||||||
                                CGGTTGAC     ACCCAGT
                                    CGTCC_
GAM807  MGC3169   3'  GACCAGGCACAGTGGCTCA   44185   A    A    AACATG
                                C AGCCA CTGTG     GGTC
                                | ||||| |||||     ||||
                                A TCGGT GACAC     CCAG
                                 C    _    GGA___
GAM807  PADI3     3'  ACCCATGTGGTTCTCAGACTTG 33172     CCAA   T ___
                                CAAG   CTG GA   ACATGGGT
                                ||||   ||| ||   ||||||||
                                GTTC   GAC CT   TGTACCCA
                                  A___   T  TGG
GAM807  YAP1      3'  TGACCTCTTTCACAGTTGGCT  21467          CAT
                                AGCCAACTGTGAA   GGGTCA
                                ||||||||||||   ||||||
                                TCGGTTGACACTT   TCCAGT
                                      TC_
GAM807  ZNF306    3'  ATCCTCCACAGTTGGTCA    93865   A       AACAT
                                A GCCAACTGTG    GGGT
                                | ||||||||||    ||||
                                A TGGTTGACAC    CCTA
                                 C        CT___
GAM807  LOC158345 5'  TGAACTTTGTTCACACCAACTT 64914     CCAAC       T  G
           G                     CAAG    TGTGAACA GG TCA
                                ||||    |||||||| || |||
                                GTTC    ACACTTGT TC AGT
                                  AACC_       T  A
GAM807  LOC199837 5'  TGATGGTATTCAAGTTGGCTCA 89787   A      G   C  GG
                                C AGCCAACT TGAA AT  GTCA
                                | |||||||| |||| ||  ||||
                                A TCGGTTGA ACTT TG  TAGT
                                 C       _   A  G_
GAM807  LOC199993 5'  TGACCCATGCTGCCCAGCCTGG 72143    A_   TGAA_
                                CCA  CTG    CATGGGTCA
                                |||  |||    |||||||||
                                GGT  GAC    GTACCCAGT
                                  CC   CCGTC
GAM807  LOC255388 5'  ATTCACACAGCTGGCT     98975      A    AACA
                                AGCCA CTGTG   TGGGT
                                ||||| |||||   |||||
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                                TCGGT GACAC    ACTTA
                                  C    ____
GAM807  LOC257078 5'  TGACATCACCCACAGTTGACT  98917    C       AACA  _
                                AG CAACTGTG    TGG GTCA
                                || ||||||||    ||| ||||
                                TC GTTGACAC    ACT CAGT
                                 A       CC__   A
GAM808  AQP6     3'  GGCCCCAGGCCCCAGC      55008      A       CTC
                                GCTG GGCCTGGG   GCC
                                |||| ||||||||   |||
                                CGAC CCGGACCC   CGG
                                  C       ___
GAM808  GCK      5'  CCCAAGCGCCCAGCAATG    5682          A  _ _
                                CATTGCTG GGC CT GGG
                                |||||||| ||| || |||
                                GTAACGAC CCG GA CCC
                                     _  C  A
GAM808  GGT1     5'  TGTCCCCAGGCCTCAGCAA   26439             CT
                                TTGCTGAGGCCTGGG  CG
                                ||||||||||||||  ||
                                AACGACTCCGGACCC  GT
                                         CT
GAM808  GNAT1    3'  GACGCACAGACTCAGCAAT   5721          GC   G  _
                                ATTGCTGAG  CTG GC TC
                                |||||||||  ||| || ||
                                TAACGACTC  GAC CG AG
                                     A_   A  C
GAM808  HAS3     3'  AGGCAAGCGTGTTCTCAGCA  19231         CCT G   C
                                TGCTGAGG   G GCT GCCT
                                ||||||||   | ||| ||||
                                ACGACTCT   T CGA CGGA
                                     TG_ G   A
GAM808  P23      3'  AGGCGAGCCCTCCCCAGCA   22751       A  CCT
                                TGCTG GG   GGGCTCGCCT
                                ||||| ||   ||||||||||
                                ACGAC CC   CCCGAGCGGA
                                   _  CT_
GAM808  SF1      3'  AGGCAGACAGCCTCAGCAA   17339          C  GG  C
                                TTGCTGAGGC TG  CT GCCT
                                |||||||||| ||  || ||||
                                AACGACTCCG AC  GA CGGA
                                      _  A_  _
GAM808  SYN3     3'  GTCGCCTAGTCAGACCTCAGCA 14482          C  ________  CTCG
          AT                   ATTGCTGAGG CTG      GG    C
                               |||||||||| |||      ||    |
                               TAACGACTCC GAC      CC    G
                                     A   TGA___T  GCTC
GAM808  SYN3     3'  GTCGCCTAGTCAGACCTCAGCA 56904          C  ________  CTCG
          AT                   ATTGCTGAGG CTG      GG    C
                               |||||||||| |||      ||    |
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                                TAACGACTCC GAC      CC    G
                                     A   TGA___T  GCTC
GAM808  SYN3     3'  GTCGCCTAGTCAGACCTCAGCA 56906          C  ________  CTCG
              AT                   ATTGCTGAGG CTG      GG    C
                                ||||||||||  |||       ||    |
                                TAACGACTCC GAC      CC    G
                                     A   TGA___T  GCTC
GAM808  WNT5A    3'  CTCAGAAGCATCAGCAATG   14120         G  __
                                CATTGCTGA GC  CTGGG
                                |||||||||  ||  |||||
                                GTAACGACT CG  GACTC
                                     A  AA
GAM808  ARGBP2   5'  AGGCAAGCTTTCCCTGCAAT   14589      TG   CCT    C
                                ATTGC  AGG   GGGCT GCCT
                                |||||  |||   ||||| ||||
                                TAACG  TCC   TTCGA CGGA
                                   __   CT_    A
GAM808  ATP9B    3'  AGGCAAGCCCAGGGCACAG   78971     AG   _     C
                                CTG  GCC TGGGCT GCCT
                                |||  ||| ||||||| ||||
                                GAC  CGG ACCCGA CGGA
                                  A_   G     A
GAM808  ATP9B    3'  AGGCAAGCCCAGGGCACAG   78972     AG   _     C
                                CTG  GCC TGGGCT GCCT
                                |||  ||| ||||||| ||||
                                GAC  CGG ACCCGA CGGA
                                  A_   G     A
GAM808  ATP9B    3'  AGGCAAGCCCAGGGCACAG   78973     AG   _     C
                                CTG  GCC TGGGCT GCCT
                                |||  ||| ||||||| ||||
                                GAC  CGG ACCCGA CGGA
                                  A_   G     A
GAM808  ATP9B    3'  AGGCGAGCCCAGGGCACAG   78974     AG   _
                                CTG  GCC TGGGCTCGCCT
                                |||  ||| ||||||||||||
                                GAC  CGG ACCCGAGCGGA
                                  A_   G
GAM808  CALN1    3'  AGGCAAACCCAGTGGTTTCAGA 49659      G      __    CTC
              AATG                   CATT CTGAGGCC  TGGG   GCCT
                                |||| ||||||||  ||||   ||||
                                GTAA GACTTTGG  ACCC   CGGA
                                   A       TG    AAA
GAM808  CNR2     3'  GCGAGCCTCCAGGCCCAGCAAT 10234         A      __
              G                    CATTGCTG GGCCTGG  GCTCGC
                                |||||||| |||||||  ||||||
                                GTAACGAC CCGGACC  CGAGCG
                                     _      TC
GAM808  DKFZp434A171 3'  GGCTCGCCTAAACATAACCTCA 71342          CCT_________  CTCG
              GCAAT                  ATTGCTGAGG         GGG    CC
                                ||||||||||         |||    ||
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                                TAACGACTCC         TCC    GG
                                     AATACAAA___   GCTC
GAM808  DKFZp762L0311 3'  GTCGCCTAGACGGGCTTCAACA 38672      C       ________  CTCG
          ATG                   CATTG TGAGGCCTG      GG    C
                                ||||| |||||||||      ||    |
                                GTAAC ACTTCGGGC      CC    G
                                   A        AGA___T  GCTC
GAM808  FLJ12076  3'  AGCACCTGTGCCCTCAGCAATG 48020          _ CT_ _
                                CATTGCTGAGG C   GG GCT
                                |||||||||||  |   || |||
                                GTAACGACTCC G   CC CGA
                                      C TGT  A
GAM808  FLJ20297  3'  AGGCAGGTGGGCCCCAGCAA  35369       A    GG  TC
                                TTGCTG GGCCT  GC  GCCT
                                ||||||  |||||  ||  ||||
                                AACGAC CCGGG  TG  CGGA
                                   C     __  GA
GAM808  FLJ20297  3'  AGGCAGGTGGGCCCCAGCAA  36076       A    GG  TC
                                TTGCTG GGCCT  GC  GCCT
                                ||||||  |||||  ||  ||||
                                AACGAC CCGGG  TG  CGGA
                                   C     __  GA
GAM808  KIAA1069  3'  AGTTCCAAACCCCAGCAATG  68525        A  CC   _
                                CATTGCTG GG  TGGG CT
                                ||||||||  ||  |||| ||
                                GTAACGAC CC  ACCT GA
                                     C  AA   T
GAM808  KIAA1272  3'  AGGCCTCACACAGGCCTCAGAA 70731     G        GGCTC_
          ATG                   CATT CTGAGGCCTG     GCCT
                                ||||  ||||||||||     ||||
                                GTAA GACTCCGGAC     CGGA
                                  A        ACACTC
GAM808  MGC:5244  3'  GGCCGGACCTCAGCAAT     49151         _ TG
                                ATTGCTGAGG CC  GGCT
                                ||||||||||  ||  ||||
                                TAACGACTCC GG  CCGG
                                     A  __
GAM808  LOC149194 3'  GCAAGCCCAGGTTGCCAGT   79984      A_       C
                                GCTG  GGCCTGGGCT GC
                                ||||  ||||||||||  ||
                                TGAC  TTGGACCCGA CG
                                  CG        A
GAM808  LOC150207 3'  GGCCGGACCTCAGCAAT     80596         _ TG
                                ATTGCTGAGG CC  GGCT
                                ||||||||||  ||  ||||
                                TAACGACTCC GG  CCGG
                                     A  __
GAM808  LOC158281 3'  AGGCGAGCCCTCCCCAGCA   82734      A  CCT
                                TGCTG GG   GGGCTCGCCT
                                |||||  ||   ||||||||||
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                                ACGAC CC   CCCGAGCGGA
                                  _ CT_
GAM808  LOC163479 5'  AGGCATATTCAAAACTCAGCAA 83021        GCC    CTC
                                TTGCTGAG   TGGG   GCCT
                                ||||||||   ||||   ||||
                                AACGACTC   ACTT   CGGA
                                     AAA    ATA
GAM808  LOC220020 5'  GATCCAGACCTCACCAATG    95045      C    C    C
                                CATTG TGAGG CTGGG TC
                                ||||| ||||| ||||| ||
                                GTAAC ACTCC GACCT AG
                                  C    A    _
GAM808  LOC256286 3'  GGCCGGACCTCAGCAAT     96895          _ TG
                                ATTGCTGAGG CC  GGCT
                                |||||||||| ||  ||||
                                TAACGACTCC GG  CCGG
                                     A  __
GAM808  LOC91632  3'  AGCCGGACCTCAGCAAT     67314          _ TG
                                ATTGCTGAGG CC  GGCT
                                |||||||||| ||  ||||
                                TAACGACTCC GG  CCGA
                                     A  __
GAM808  LOC93538  5'  AGACGAGAACCTGCCTCAGCAA 72952         CT  G_   C
                                TTGCTGAGGC  GG  CTCG CT
                                |||||||||  ||  |||| ||
                                AACGACTCCG  CC  GAGC GA
                                     T_  AA   A
GAM809  CHI3L1    3'  TTTTGGCAAGCTCTATCACCAA 8884           C   G
                                TTGGTGATGGAGC TGT GAAA
                                |||||||||||| ||| ||||
                                AACCACTATCTCG ACG TTTT
                                      A   G
GAM809  IL2RB     3'  CCACAGGCTCTGACCAG     7933       GA
                                TTGGT  TGGAGCCTGTGG
                                |||||  ||||||||||||
                                GACCA  GTCTCGGACACC
                                  __
GAM809  NPR1      3'  CCACAGCAGCCCCATCGCCAA  88740         A  __
                                TTGGTGATGG GC  CTGTGG
                                |||||||||| ||  ||||||
                                AACCGCTACC CG  GACACC
                                     C  AC
GAM809  SORCS3    3'  CCACAGCAGAATCACCAA    31071        GGA  C
                                TTGGTGAT   GC TGTGG
                                ||||||||   || |||||
                                AACCACTA   CG ACACC
                                     AGA  _
GAM809  TEM5      3'  CACTCTGGCCTCATCACCAA  52294         GA   T__
                                TTGGTGATG  GCC   GTG
                                |||||||||  |||   |||
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                                AACCACTAC  CGG   CAC
                                     TC   TCT
GAM809  D6S2654E  3'  TTTCTAGGCCCCATCACCAG  25111         A    T
                                TTGGTGATGG GCCTG GGAA
                                |||||||||| ||||| ||||
                                GACCACTACC CGGAT CTTT
                                      C    _
GAM809  FBXO30    3'  CATAGGCTTCACCACCAA    50488       A
                                TTGGTG TGGAGCCTGTG
                                |||||| ||||||||||
                                AACCAC ACTTCGGATAC
                                   C
GAM809  FLJ13710  5'  TTCTGGACGCTCCATCATCAA  46099           CTG
                                TTGGTGATGGAGC   TGGAA
                                ||||||||||||   |||||
                                AACTACTACCTCG   GTCTT
                                        CAG
GAM809  FLJ22037  5'  TCCGTGAAGACTCCATCACCAA 95538           C  GT__
                                TTGGTGATGGAG CT    GGA
                                |||||||||||| ||    |||
                                AACCACTACCTC GA    CCT
                                       A  AGTG
GAM809  FLJ23168  3'  TTCCTGCTCCATTACCAA    47506           CTGT
                                TTGGTGATGGAGC    GGAA
                                ||||||||||||    ||||
                                AACCATTACCTCG    CCTT
                                       T___
GAM809  RAI17     3'  TCCCTGAGGCTCCACCTCCAA  92909     TGA      GT_
                                TTGG   TGGAGCCT   GGA
                                ||||   ||||||||   |||
                                AACC   ACCTCGGA   CCT
                                  TCC       GTC
GAM809  SPINT1    3'  TTCCGCAGCCCCCACC      63335     AT  A  C
                                GGTG  GG GC TGTGGAA
                                ||||  || || |||||||
                                CCAC  CC CG ACGCCTT
                                  C_  _  _
GAM809  LOC162022 5'  CCTGGGCTTCATCACCAA    83198             T
                                TTGGTGATGGAGCCTG GG
                                |||||||||||||||| ||
                                AACCACTACTTCGGGT CC
                                                 _
GAM809  LOC205888 5'  CGTTTCCACAGACCCTTTGC   91085    TG T  AGC
                                G  A GG   CTGTGGAAACG
                                |  | ||   ||||||||||
                                C  T CC   GACACCTTTGC
                                 GT T  CA_
GAM809  LOC219988 3'  CTGCACTGCTGCCATCACCAA  93263          _   C_  TG
                                TTGGTGATGG AGC  TG  G
                                |||||||||| |||  ||  |
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                                AACCACTACC TCG  AC  C
                                     G   TC  GT
GAM809  LOC91408  3'  TTTCCTGGCCCATCATCAA   66521         A   TGT
                                TTGGTGATGG GCC   GGAAA
                                |||||||||| |||   |||||
                                AACTACTACC CGG   CCTTT
                                     _   T__
GAM810  KIAA1393  3'  ATTGACATTACCAGACAA    72568       T     TG
                                TTGTCT GGTAAT  CAAT
                                |||||| ||||||  ||||
                                AACAGA CCATTA  GTTA
                                   _     CA
GAM810  SEMA3E    3'  AATTGCAATAACACAGACAAGT 25801        TG  A
                                ACTTGTCT  GT ATTGCAATT
                                ||||||||  || |||||||||
                                TGAACAGA  CA TAACGTTAA
                                     CA  A
GAM810  TU12B1-TY 3'  TTGATTTACCAAGACAAG    33866          TTG
                                CTTGTCTTGGTAA   CAA
                                ||||||||||||   |||
                                GAACAGAACCATT   GTT
                                       TA_
GAM810  LOC150279 3'  TGCAGTCCAAAACAAGTTA   80485        C    TA
                                TAACTTGT TTGG  ATTGCA
                                |||||||| ||||  ||||||
                                ATTGAACA AACC  TGACGT
                                     A   __
GAM810  LOC152220 3'  ATTGCAAAAAGACAAGT     86759         GGTAA
                                ACTTGTCTT    TTGCAAT
                                |||||||||    |||||||
                                TGAACAGAA    AACGTTA
                                     A____
GAM811  GABPA     3'  CCAAAAATAGCCAGTAGTA   10748         A   CTGAC
                                TACTACTGG TAT    TGG
                                ||||||||| |||    |||
                                ATGATGACC ATA    ACC
                                     G   AAA__
GAM811  SLC13A4   3'  CCAGTATCCAGCAGTA      25861      A     ATCTG
                                TACT CTGGAT    ACTGG
                                |||| ||||||    |||||
                                ATGA GACCTA    TGACC
                                  C     _____
GAM811  TMEM1     3'  GCTCCAGCCAGACCTTCAGTG  13803        TA   A
                                TACTGGA  TCTG CTGGAGC
                                |||||||  |||| |||||||
                                GTGACTT  AGAC GACCTCG
                                     CC   C
GAM811  CCRK      3'  GCTCCAGTTGGGGATCCAGCAG 25076    A     AT TG
                                CT CTGGAT  C  ACTGGAGC
                                || ||||||  |  ||||||||
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                                GA GACCTA  G  TGACCTCG
                                 C     GG GT
GAM811  FLJ20727  5'  GCTCCAGTCATAGCAGTG    36046      GA  TC
                                TACTG  TA  TGACTGGAGC
                                |||||  ||  ||||||||||
                                GTGAC  AT  ACTGACCTCG
                                   G_  __
GAM811  HPA2      3'  CTCCTCCACTCCAGTAGTA   41833        TATC  ACT
                                TACTACTGGA   TG   GGAG
                                ||||||||||   ||   ||||
                                ATGATGACCT   AC   CCTC
                                      C___  CT_
GAM811  KIAA0205  3'  CTCCAGTCTGTTGCAGTA    30209      _   TCT
                                TACTG GATA   GACTGGAG
                                ||||| ||||   ||||||||
                                ATGAC TTGT   CTGACCTC
                                   G   ___
GAM811  KIAA0205  3'  CTCCAGTCTGTTGCAGTA    30210      _   TCT
                                TACTG GATA   GACTGGAG
                                ||||| ||||   ||||||||
                                ATGAC TTGT   CTGACCTC
                                   G   ___
GAM811  KIAA1110  3'  GCTCCAGTCCTGTGCCAGTAG  62502       A   CT
                                CTACTGG TAT  GACTGGAGC
                                ||||||| |||  |||||||||
                                GATGACC GTG  CTGACCTCG
                                    _  TC
GAM811  MIDORI    3'  GCCCCAGCCCAGTCCAGCAG   74215    A    TAT   A_   A
                                CT CTGGA   CTG  CTGG GC
                                || |||||   |||  |||| ||
                                GA GACCT   GAC  GACC CG
                                 C    ___   CC   C
GAM811  OR7C1     3'  GCTCTCTGATATCCAACAGT   34418     AC      TGACT
                                ACT  TGGATATC    GGAGC
                                |||  ||||||||    |||||
                                TGA  ACCTATAG    TCTCG
                                  CA       TC___
GAM811  SIMRP7    3'  GCTCCAGCCAGATATTAGG    93977    G      A
                                CT GATATCTG CTGGAGC
                                || |||||||| |||||||
                                GG TTATAGAC GACCTCG
                                 A       C
GAM811  YAP       5'  CTCCAGCAGCAGATGCAGCAG  58204    A   G  AT_   A
                                CT CTG AT   CTG CTGGAG
                                || ||| ||   ||| ||||||
                                GA GAC TA   GAC GACCTC
                                 C   G  GAC   _
GAM811  LOC152282 3'  GCCCCAGCAGCAGCAACTCCAG 81404         TAT____   A   A
            TAG                   CTACTGGA      CTG CTGG GC
                                ||||||||      ||| |||| ||
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                                GATGACCT      GAC GACC CG
                                    CAACGAC  _   C
GAM812  ATP6V1G2 3'  TTTTCCTGTGACACTTATA   57118      T  GAT
                                TATAG GTG  CAGGAAAA
                                ||||| |||  ||||||||
                                ATATT CAC  GTCCTTTT
                                  _  AGT
GAM812  CDC42    3'  TTTTCTAGGACGCACTATA   10143        GA  A
                                TATAGTGTG  TC GGAAAA
                                |||||||||  || ||||||
                                ATATCACGC  GG TCTTTT
                                    A_  A
GAM812  CDH10    3'  TTTTCCTGCCAGTCAGCAC   22997     G  ___
                                GTGT GAT   CAGGAAAA
                                |||| |||   ||||||||
                                CACG CTG   GTCCTTTT
                                  A   ACC
GAM812  CEP2     5'  TTCGTGCCCCCACACTGTA   23251        AT_  G
                                TATAGTGTGG   CA GAA
                                ||||||||||   || |||
                                ATGTCACACC   GT CTT
                                     CCC  G
GAM812  CYP24    3'  TTTTCCTAAATGCATACTGTA  7597         G  C_
                                TATAGTGTG AT  AGGAAAA
                                |||||||||  ||  |||||||
                                ATGTCATAC TA  TCCTTTT
                                     G  AA
GAM812  EPHA3    3'  TTTTCCTGTTCATACACTA    19102       _  T
                                TAGTGTG GA CAGGAAAA
                                ||||||| || ||||||||
                                ATCACAT CT GTCCTTTT
                                    A  T
GAM812  FGF7     3'  TTTTCCTGTGGTTGACCTA    10634     T  G  __
                                TAG GT GAT  CAGGAAAA
                                ||| || |||  ||||||||
                                ATC CA TTG  GTCCTTTT
                                  _  G   GT
GAM812  HMGA2    3'  TTTTCCTCAATCACACTA     14461        ATC
                                TAGTGTGG   AGGAAAA
                                ||||||||   |||||||
                                ATCACACT   TCCTTTT
                                     AAC
GAM812  MSL3L1   5'  TTTTCCTGATCTAACTTCTA   23295     TG__
                                TAG    TGGATCAGGAAAA
                                |||    ||||||||||||
                                ATC    ATCTAGTCCTTTT
                                  TTCA
GAM812  PKHD1    3'  TTTTCCTGAGCTCTATAC     57722        __
                                GTGTGGA  TCAGGAAAA
                                |||||||  |||||||||
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                                CATATCT  AGTCCTTTT
                                    CG
GAM812  PLA2G5   3'  TTTCCTGAGATGCACTTA    8115    T     GA
                                A AGTGTG  TCAGGAAA
                                | ||||||  ||||||||
                                A TCACGT  AGTCCTTT
                                 T     AG
GAM812  PSEN1    3'  TTCCTGACCACCTTGCACTAT  24626        _____  A
                                ATAGTGT    GG TCAGGAA
                                |||||||    || |||||||
                                TATCACG    CC AGTCCTT
                                    TTCCA  _
GAM812  RNF18    5'  TTTTCCTGATGGACTGTA    40146       G GG
                                TATAGT T  ATCAGGAAAA
                                ||||||  |  ||||||||||
                                ATGTCA G  TAGTCCTTTT
                                    G __
GAM812  RP42     3'  TTTTCCTGGCAAATCACAT   40569       A___
                                GTGTGG   TCAGGAAAA
                                ||||||   |||||||||
                                TACACT   GGTCCTTTT
                                    AAAC
GAM812  RPP30    3'  TTTTCCTGATAGCTGTATTA  22213       TG __
                                TAGTG  G  ATCAGGAAAA
                                |||||  |  ||||||||||
                                ATTAT  C  TAGTCCTTTT
                                   GT GA
GAM812  SOX11    3'  TTTTCCTTGATTCCTACCATA 13326     A  T     _
                                TAT GTG GGATCA GGAAAA
                                ||| ||| |||||| ||||||
                                ATA CAT CTTAGT CCTTTT
                                  C  C     T
GAM812  C1orf8   5'  TTTCCTGACCCTGGGCTA    18030     G _  A
                                TAGT T GG TCAGGAAA
                                |||| | || ||||||||
                                ATCG G CC AGTCCTTT
                                   G T  C
GAM812  DNAJC6   3'  TTTTCCGGATACATTATA    29499        GG   A
                                TATAGTGT  ATC GGAAAA
                                ||||||||  ||| ||||||
                                ATATTACA  TAG CCTTTT
                                     __  G
GAM812  FLJ10726 3'  TTTTCCTGGTTGTCACTTA   37045   T   TG
                                A AGTG  GATCAGGAAAA
                                | ||||  ||||||||||
                                A TCAC  TTGGTCCTTTT
                                 T   TG
GAM812  FLJ13305 5'  TTTCCTGATATTCACCACT   91719     _   __
                                AGTG TGGA  TCAGGAAA
                                |||| ||||  ||||||||
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                                TCAC ACTT  AGTCCTTT
                                  C    AT
GAM812  FLJ13315  3'  TTCCTTGTTCACCACTATA   47201       _    C
                                TATAGTG TGGAT AGGAA
                                ||||||| ||||| |||||
                                ATATCAC ACTTG TCCTT
                                    C    T
GAM812  FLJ14596  3'  TCCTGGGTTTCCACACTCA   52522   T      ___
                                A AGTGTGGA   TCAGGA
                                | ||||||||   ||||||
                                A TCACACCT   GGTCCT
                                 C       TTG
GAM812  GMPPA     5'  CCTATGATCCAACACCATA   72647    A   _     __
                                TAT GTGT GGATCA  GG
                                ||| |||| ||||||  ||
                                ATA CACA CCTAGT  CC
                                  C    A     AT
GAM812  HNRPA3    3'  TTTCCTGTTTGTACTGTA    20455       TG  T
                                TATAGTG  GA CAGGAAA
                                |||||||  || |||||||
                                ATGTCAT  TT GTCCTTT
                                    GT  _
GAM812  HRI       3'  TTTTCCTGAATTTCCTAC    27740     T  ___
                                GTG GGA   TCAGGAAAA
                                ||| |||   |||||||||
                                CAT CCT   AGTCCTTTT
                                  _   TTA
GAM812  KIAA0186  3'  TCCTGAATGCCAATACCATA  41120     A   _ A__
                                TAT GTGT GG   TCAGGA
                                ||| |||| ||   ||||||
                                ATA CATA CC   AGTCCT
                                  C    A  GTA
GAM812  KIAA0426  3'  TTTCCTGATTTCTTTTAT    28939      TGT
                                ATAG   GGATCAGGAAA
                                ||||   ||||||||||
                                TATT   TTTAGTCCTTT
                                   TTC
GAM812  KIAA0831  3'  TCCTGCCATCCACACTATG   30656          __
                                TATAGTGTGGAT  CAGGA
                                ||||||||||||  |||||
                                GTATCACACCTA  GTCCT
                                      CC
GAM812  KIAA1163  3'  TTTCCCTTTGACTACACTG   79657        A  ___
                                TAGTGTGG TCA   GGAAA
                                |||||||| |||   |||||
                                GTCACATC AGT   CCTTT
                                    _   TTC
GAM812  KIAA1223  3'  TTTTCATATCCATACTATA   71700          CAG
                                TATAGTGTGGAT   GAAAA
                                ||||||||||||   |||||
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                                ATATCATACCTA  CTTTT
                                      TA_
GAM812  KIAA1361 3' TTTTCCTGAATGCGTCATA  62887    AG   GA
                                TAT  TGTG  TCAGGAAAA
                                |||  ||||  |||||||||
                                ATA  GCGT  AGTCCTTTT
                                  CT   A_
GAM812  KLF12    3' TTTTCCTGTAATTACTGTA  33284      TGGAT
                                TATAGTG    CAGGAAAA
                                |||||||    ||||||||
                                ATGTCAT    GTCCTTTT
                                    TAAT_
GAM812  KRT6IRS  3' TCTGGATCCCACACTGTA   54230        _  A
                                TATAGTGTGG ATC GGA
                                |||||||||| ||| |||
                                ATGTCACACC TAG TCT
                                      C  G
GAM812  LANCL2   3' TTTGATGGCCACACTGTA   38624        __
                                TATAGTGTGG  ATCAGG
                                ||||||||||  ||||||
                                ATGTCACACC  TAGTTT
                                      GG
GAM812  LATS1    3' TTTCCTGCCAGTAACTATA  60913      G__  AT
                                TATAGT   TGG  CAGGAAA
                                ||||||   |||  |||||||
                                ATATCA   ACC  GTCCTTT
                                   ATG  __
GAM812  MGC12837 3' TTTTCCTTTGTGTACTCTATA 52173     T  G  C_
                                TATAG GTG AT  AGGAAAA
                                ||||| ||| ||  |||||||
                                ATATC CAT TG  TCCTTTT
                                   T  G  TT
GAM812  MGC15873 3' TTCCCGATGGCACCCTGTA  53010     T  G_  A
                                TATAG GTG  ATC GGAA
                                ||||| |||  ||| ||||
                                ATGTC CAC  TAG CCTT
                                   C  GG  C
GAM812  MGC26641 3' TTTTCCTGATGTGTCACT   59328     _ G
                                AGTG TG ATCAGGAAAA
                                |||| || ||||||||||
                                TCAC GT TAGTCCTTTT
                                  T  G
GAM812  OBSCN    3' CCGTGGTGCCCACACTGTA  71185        __  _
                                TATAGTGTGG  ATCA GG
                                ||||||||||  |||| ||
                                ATGTCACACC  TGGT CC
                                      CG   G
GAM812  PDE2A    3' CCTGAGGACCACTACTATA  12004      _  A__
                                TATAGT GTGG  TCAGG
                                ||||||  ||||  |||||
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                                ATATCA CACC   AGTCC
                                   T    AGG
GAM812  PMX2B    3'  TTTTCCTGTTGGACTATG    15385       G GGAT
                                TATAGT T    CAGGAAAA
                                ||||||| |   ||||||||
                                GTATCA G    GTCCTTTT
                                   G TT__
GAM812  PRO2266  3'  TTTTCCTTTTTTCACAGTATA  38187      G     TC_
                                TATA TGTGGA   AGGAAAA
                                |||| ||||||   |||||||
                                ATAT ACACTT   TCCTTTT
                                  G     TTT
GAM812  SDF1     3'  TTTCCCAATTCACATCTA    92523     _     CA
                                TAG TGTGGAT  GGAAA
                                ||| |||||||  |||||
                                ATC ACACTTA  CCTTT
                                  T      AC
GAM812  SLC2A10  3'  TTCCTGATTCCCCACTCA    48561    T   T  _
                                A AGTG GGA TCAGGAA
                                | |||| ||| |||||||
                                A TCAC CCT AGTCCTT
                                 C   C   T
GAM812  STRAIT11499 3'  TTTTCCTGTTTGCACTAT    41433       TG  T
                                ATAGTG  GA CAGGAAAA
                                ||||||  || ||||||||
                                TATCAC  TT GTCCTTTT
                                   GT  _
GAM812  TIGD4    3'  TTTTCCTGATACATTTTA    90496     T   G
                                TAG GTG ATCAGGAAAA
                                ||| ||| ||||||||||
                                ATT TAC TAGTCCTTTT
                                  T   A
GAM812  TRAF6    3'  TTTTCCTGGGAATCCACA    17289       ___
                                TGTGGAT   CAGGAAAA
                                |||||||   ||||||||
                                ACACCTA   GTCCTTTT
                                    AGG
GAM812  TRIM36   3'  TTTTCCTGATTTATATTTA   38630   T
                                A AGTGTGGATCAGGAAAA
                                | ||||||||||||||||
                                A TTATATTTAGTCCTTTT
                                 T
GAM812  LOC121441 3'  TTTTCCTGACAGATTATG    74506       G  GA
                                TATAGT TG  TCAGGAAAA
                                |||||| ||  |||||||||
                                GTATTA AC  AGTCCTTTT
                                   G  __
GAM812  LOC123096 3'  CCTCATGCCCACACTGTA    74651          __  C
                                TATAGTGTGG  AT AGG
                                ||||||||||  || |||
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                                ATGTCACACC  TA TCC
                                      CG  C
GAM812  LOC131583 5'  TTTTCCTGACATTTTCCACTCT 76384     T    _____
              A                    TAG GTGGA    TCAGGAAAA
                                   ||| |||||    |||||||||
                                   ATC CACCT    AGTCCTTTT
                                     T    TTTAC
GAM812  LOC144144 5'  TTTTCCTGATGGACTGTA    60803       G GG
                                   TATAGT T  ATCAGGAAAA
                                   |||||| |  ||||||||||
                                   ATGTCA G  TAGTCCTTTT
                                      G __
GAM812  LOC146176 5'  TTTTCCTGGTGAACACTATA   78197        GG
                                   TATAGTGT  ATCAGGAAAA
                                   ||||||||  ||||||||||
                                   ATATCACA  TGGTCCTTTT
                                         AG
GAM812  LOC150185 3'  TTCAGTATCCCACACTGTA    86072         _ CAG
                                   TATAGTGTGG AT   GAA
                                   |||||||||| ||   |||
                                   ATGTCACACC TA   CTT
                                         C  TGA
GAM812  LOC151658 3'  TTCTAACATCCACACCATA    86657     A       CA_
                                   TAT GTGTGGAT   GGAA
                                   ||| ||||||||   ||||
                                   ATA CACACCTA   TCTT
                                     C       CAA
GAM812  LOC158116 3'  TTTTCCTGTGGTTGACCTA    60951     T  G   __
                                   TAG GT GAT  CAGGAAAA
                                   ||| || |||  ||||||||
                                   ATC CA TTG  GTCCTTTT
                                     _  G   GT
GAM812  LOC160484 5'  TTCCTGATGGACAACTAT     83093      _  GG
                                   ATAGT GT  ATCAGGAA
                                   ||||| ||  ||||||||
                                   TATCA CA  TAGTCCTT
                                      A  GG
GAM812  LOC199704 3'  TTTTCCTGTTTTACCTTA     89699    T  T    T
                                   A AG GTGGA CAGGAAAA
                                   | || ||||| ||||||||
                                   A TC CATTT GTCCTTTT
                                    T  _     T
GAM812  LOC200609 5'  TTTTCCTGAATATCATAT     91673       A__
                                   GTGTGG   TCAGGAAAA
                                   ||||||   |||||||||
                                   TATACT   AGTCCTTTT
                                      ATA
GAM812  LOC203080 5'  TTTTCCTGGGAAGACTGTA    90776       GTGGA
                                   TATAGT     TCAGGAAAA
                                   ||||||     |||||||||
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                                ATGTCA    GGTCCTTTT
                                   GAAG_
GAM812  LOC220073 5'  TTTCCCGAGCCTACTGTA    95078       T  A  A
                                TATAGTG GG TC GGAAA
                                ||||||| || || |||||
                                ATGTCAT CC AG CCTTT
                                   _ G  C
GAM812  LOC220486 5'  TTTTCCTGGTGGACTGTA    92414       G GG
                                TATAGT T  ATCAGGAAAA
                                |||||| |  ||||||||||
                                ATGTCA G  TGGTCCTTTT
                                   G __
GAM812  LOC253233 5'  TTTCCCCAATACCACATTA    97356        _  CA_
                                TAGTGTGG AT   GGAAA
                                |||||||| ||   |||||
                                ATTACACC TA   CCTTT
                                     A  ACC
GAM812  LOC256809 3'  TTTTCCTGATTAGAACTA    98131     GTG
                                TAGT   GATCAGGAAAA
                                ||||   ||||||||||||
                                ATCA   TTAGTCCTTTT
                                  AGA
GAM812  LOC90309  5'  TTCACCAATCTACACTATA    62877          CAG_
                                TATAGTGTGGAT    GAA
                                ||||||||||||    |||
                                ATATCACATCTA    CTT
                                       ACCA
GAM812  LOC91796  3'  TCCTGGCTCCACACTATA    67789          _
                                TATAGTGTGGA TCAGGA
                                |||||||||||| ||||||
                                ATATCACACCT GGTCCT
                                       C
GAM813  ANK3      3'  AAAGATTTTATCTGTAAAC    8561         C    GG
                                GTTTACAGA AAGA  TTT
                                ||||||||| ||||  |||
                                CAAATGTCT TTTT  AAA
                                     A    AG
GAM813  CRYZ      3'  AAACCTCTATTCTAAACT    10308      AC   CA
                                AGTTT  AGA  AGAGGTTT
                                |||||  |||  ||||||||
                                TCAAA  TCT  TCTCCAAA
                                   __   TA
GAM813  RRM2B     3'  AAACCTCTTGTTTTAAAACT   68430      AC
                                AGTTT  AGACAAGAGGTTT
                                |||||  ||||||||||||
                                TCAAA  TTTGTTCTCCAAA
                                   AT
GAM813  SLC2A6    3'  CTCCTATCTGCAAACTGTG    34570        A    CAA
                                TACAGTTT CAGA   GAG
                                |||||||| ||||   |||
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                                GTGTCAAA GTCT   CTC
                                    C    ATC
GAM813  TEM8     3'  AAACTTCTATAAGACTGTA    50817        ACAGACA
                                TACAGTTT      AGAGGTTT
                                ||||||||      ||||||||
                                ATGTCAGA      TCTTCAAA
                                    ATA____
GAM813  UBL3     3'  GAACAGTCTGCCTGTAAAC    24023        ACA   G_
                                GTTTACAG   AGA  GTTT
                                ||||||||   |||  ||||
                                CAAATGTC   TCT  CAAG
                                    CG_   GA
GAM813  DKFZp547I014 5'  GACCATTTTGTTTGCAAACT   39943       A       _
                                AGTTT CAGACAAGA GGTT
                                ||||| ||||||||| ||||
                                TCAAA GTTTGTTTT CCAG
                                   C        A
GAM813  FLJ10971  3'  AAACCTCTCACCTGAATTTTGT 37480       TTTA   ACA
            G                    TACAG    CAG   AGAGGTTT
                                |||||    |||   ||||||||
                                GTGTT    GTC   TCTCCAAA
                                   TTAA   CAC
GAM813  HTEX4    5'  GAAACATATCTGTAAACT    93724         CAAGAG
                                AGTTTACAGA     GTTTC
                                ||||||||||     |||||
                                TCAAATGTCT     CAAAG
                                     ATA___
GAM813  KIAA0945  3'  GAAACCTCTTGCAGAACT    30902       ACAGA
                                AGTTT    CAAGAGGTTTC
                                |||||    ||||||||||||
                                TCAAG    GTTCTCCAAAG
                                   AC___
GAM813  KIAA1024  3'  GACATTCTATCTGTAAAC    69617         CA   _
                                GTTTACAGA  AGAG GTT
                                |||||||||  |||| |||
                                CAAATGTCT  TCTT CAG
                                     A_    A
GAM813  KIAA1163  3'  GAAACCTCCCGTGAAGACT    79648       A  GACAA
                                AGTTT CA    GAGGTTTC
                                ||||| ||    ||||||||
                                TCAGA GT    CTCCAAAG
                                   A  GCC__
GAM813  KIAA1203  3'  AAATGTCAGTGTCTATAAACTG 72085         C    A_  G
            TA                    TACAGTTTA AGACA  GA GTTT
                                |||||||||| |||||  || ||||
                                ATGTCAAAT TCTGT  CT TAAA
                                     A    GA  G
GAM813  KIAA1718  3'  AAACCTTTCGAAACTGTA    64970         ACAGACA
                                TACAGTTT      AGAGGTTT
                                ||||||||      ||||||||
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                                ATGTCAAA      TTTCCAAA
                                    GC_____
GAM813  KIAA1854  3'  GAAACCTCTTGACAAGACTGTA 72208        ACAGA
                                TACAGTTT    CAAGAGGTTTC
                                ||||||||    ||||||||||
                                ATGTCAGA    GTTCTCCAAAG
                                    ACA__
GAM813  KIAA1962  3'  GAAACCCTGGGATGTAAACTTA 82800   C       GACA  A
                                A AGTTTACA    AG GGTTTC
                                | ||||||||    || ||||||
                                A TCAAATGT    TC CCAAAG
                                 T       AGGG  _
GAM813  KLHL8     3'  AAACCTTTTTGTAGACTGTA   63501           CAA
                                TACAGTTTACAGA   GAGGTTT
                                ||||||||||||   |||||||
                                ATGTCAGATGTTT   TTCCAAA

                                    ___
GAM813  MGC33182  5'  AAACCCTCGCAAACTGTG    76091        ACA  CAA A
                                TACAGTTT   GA   G GGTTT
                                ||||||||   ||   | |||||
                                GTGTCAAA   CT   C CCAAA
                                    CG_  ___ _
GAM813  PTPRU     3'  AATTTCCCCATCTGTAAACTGT 20317           CAA_
            A                    TACAGTTTACAGA    GAGGTT
                                ||||||||||||    ||||||
                                ATGTCAAATGTCT    CTTTAA
                                      ACCC
GAM813  PTPRU     3'  AATTTCCCCATCTGTAAACTGT 20318           CAA_
            A                    TACAGTTTACAGA    GAGGTT
                                ||||||||||||    ||||||
                                ATGTCAAATGTCT    CTTTAA
                                      ACCC
GAM813  RIT       3'  GAAGTGTTTATCTGTGAACTG  23583          CA   GG
                                CAGTTTACAGA  AGA  TTTC
                                ||||||||||  |||  ||||
                                GTCAAGTGTCT  TTT  GAAG
                                      A_   GT
GAM813  LOC148438 3'  AAACCTCTTGCCTGAAGC    85308      A   A
                                GTTT CAG CAAGAGGTTT
                                |||| ||| ||||||||||
                                CGAA GTC GTTCTCCAAA
                                  _   C
GAM813  LOC166713 5'  GAACCTCCCGTCTGTAACCTG  88612     T       AA
                                CAG TTACAGAC  GAGGTTT
                                ||| ||||||||  |||||||
                                GTC AATGTCTG  CTCCAAG
                                  C       CC
GAM814  CYP11B1   3'  CTGGCCAGGGCCCCTGCGCA   62865       TGAGA
                                TGCGCA    CCCTGGCTAG
                                ||||||    ||||||||||
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                                ACGCGT    GGGACCGGTC
                                   CCCC_
GAM814  C21orf80  3'  CTTTAGTTCTCATGCACA    31527    C      CCCTG
                                TG GCATGAGA    GCTAGAG
                                || ||||||||    |||||||
                                AC CGTACTCT    TGATTTC
                                 A      _____
GAM814  C2orf7    3'  CTACCCAGGGTCTCTGCACA   51271    C   T       C
                                TG GCA GAGACCCTGG TAG
                                || ||| |||||||||| |||
                                AC CGT CTCTGGGACC ATC
                                 A   _        C
GAM814  DJ971N18.2 3'  TCTCTAGTCATTTGGTCTCATG 41264     G       C__
           GCA                    TGC CATGAGACC   TGGCTAGAGA
                                ||| |||||||||   ||||||||||
                                ACG GTACTCTGG   ACTGATCTCT
                                  _       TTT
GAM814  FLJ10346  5'  TCTCTAGCCCACCCTCGCACA  36532    C  AT   ACCCT
                                TG GC  GAG    GGCTAGAGA
                                || ||  |||    |||||||||
                                AC CG  CTC    CCGATCTCT
                                 A  __   CCAC_
GAM814  KCNT1     3'  AGACCAGGACCTCATGCG    62485        AC    _
                                CGCATGAG  CCTGG CT
                                ||||||||  ||||| ||
                                GCGTACTC  GGACC GA
                                     CA    A
GAM814  KIAA0232  3'  TCTCCATTCAGCAAAATCTCAT 73124    CG     CC___    CTA
           GTACA                  TG  CATGAGA    CTGG   GAGA
                                ||  |||||||    ||||   ||||
                                AC  GTACTCT    GACT   CTCT
                                 AT      AAAAC    TAC
GAM814  KIAA0984  3'  AGCTGAAGATCTTATGCACA   66138    C      CC  __
                                TG GCATGAGA  CT  GGCT
                                || ||||||||  ||  ||||
                                AC CGTATTCT  GA  TCGA
                                 A       A_  AG
GAM814  KIAA1904  3'  CTCTAACTCTCATGCTCA    73868    C      CCCTG C
                                TG GCATGAGA    G TAGAG
                                || ||||||||    | |||||
                                AC CGTACTCT    C ATCTC
                                 T       _____ A
GAM814  LOC152373 5'  CTCTAGCCTCTAATCATGGGCA 81449     G    GACCCT
                                TGC CATGA     GGCTAGAG
                                ||| |||||     ||||||||
                                ACG GTACT     CCGATCTC
                                  G    AATCT_
GAM814  LOC152503 3'  TCTCTAGCTTATCCCTGCACA  86981    C   TGA  CCCT
                                TG GCA   GA    GGCTAGAGA
                                || |||   ||    |||||||||
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                                AC CGT   CT    TCGATCTCT
                                 A   CC_  AT__
GAM814  LOC157927 5'  TCTCCAGCCAGGGCTGAGTGGC 87949     G   G_  A       A
              A                   TGC CAT  AG CCCTGGCT GAGA
                                  ||| |||  || |||||||| ||||
                                  ACG GTG  TC GGGACCGA CTCT
                                    _   AG  _       C
GAM814  LOC202915 3'  CTCCAGCCAGGGGGTCAGGGC  92017    A_   GA      A
                                  GC  TGA  CCCTGGCT GAG
                                  ||  |||  |||||||| |||
                                  CG  ACT  GGGACCGA CTC
                                   GG   GG       C
GAM814  LOC256790 5'  AGCCCCAGTCTCATGGCA    96488     G       CCT
                                  TGC CATGAGAC   GGCT
                                  ||| ||||||||   ||||
                                  ACG GTACTCTG   CCGA
                                    _       ACC
GAM815  CALCR    3'  GAGGTCACAAAGAATCTA    9984       CATTAG  CA
                                  TAGAT     CT  GTGACCTC
                                  |||||     ||  ||||||||
                                  ATCTA     GA  CACTGGAG
                                     A_____  AA
GAM815  LARGE    3'  GGAGGGCAAACCGATGATCTA  56928         AGCTCAG  A
                                  TAGATCATT      TG CCTCC
                                  |||||||||      || |||||
                                  ATCTAGTAG      AC GGAGG
                                        CCAA___  G
GAM815  MTMR8    3'  TCACTGAGACAACAATCTA   31916      CA  AG
                                  TAGAT  TT  CTCAGTGA
                                  |||||  ||  ||||||||
                                  ATCTA  AA  GAGTCACT
                                     AC  CA
GAM815  RAP1GA1   3'  GAGGTCACTGAAGACTGTGATT 12772       TAG  _
                                  GATCAT   CT CAGTGACCTC
                                  ||||||   || ||||||||||
                                  TTAGTG   GA GTCACTGGAG
                                      TCA  A
GAM815  TPX1     3'  GAAATCACTTTCAGGCAATGAT 13843         A   C___    CC
              TTA                   TAGATCATT GCT    AGTGA  TC
                                  ||||||||| |||    |||||  ||
                                  ATTTAGTAA CGG    TCACT  AG
                                        _  ACTT    AA
GAM815  CDC37    3'  GAGGTCACCAGGCTGGTCTA   23923       TTA   CA
                                  TAGATCA   GCT  GTGACCTC
                                  |||||||   |||  ||||||||
                                  ATCTGGT   CGG  CACTGGAG
                                      ___   AC
GAM815  COL21A1   3'  GGAAATAAAGCTAATGCTCTA  48773     T       CA  GA
                                  TAGA CATTAGCT  GT  CC
                                  |||| ||||||||  ||  ||
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                                ATCT GTAATCGA  TA  GG
                                  C       AA  AA
GAM815  FLJ11116  3'  GAGGCAGTGTTAATGATCTA   83474          TC G  A
                                TAGATCATTAGC  A TG CCTC
                                |||||||||||  | || ||||
                                ATCTAGTAATTG  T AC GGAG
                                      __ G  _
GAM815  FLJ11142  3'  GGAGGTCACTGAATTGATC    37683      TTAGC
                                GATCA    TCAGTGACCTCC
                                |||||    ||||||||||||
                                CTAGT    AGTCACTGGAGG
                                   TA___
GAM815  MGC30052  3'  GGAAATCACTGAGGCCATATCT 59207      CATTAG       CC
                                AGAT     CTCAGTGA  TCC
                                ||||     ||||||||  |||
                                TCTA     GAGTCACT  AGG
                                  TACCG_       AA
GAM815  OBSCN     3'  GGAAGTCACTGAGCAAGAGACT 71190     A  A  A        C
            A                    TAG TC TT GCTCAGTGAC TCC
                                |||  ||  ||  |||||||||| |||
                                ATC AG GA CGAGTCACTG AGG
                                  _  A  A        A
GAM815  OSRF      3'  GGAGCTTATAAGTAATGATCTA 60269          G  CA    C
                                TAGATCATTA CT  GTGA CTCC
                                ||||||||||  ||  |||| ||||
                                ATCTAGTAAT GA  TATT GAGG
                                      _  A_   C
GAM815  PTDSS2    3'  GAGATCACTGAGCTGCCCCTC  48625    TCAT         C
                                GA    TAGCTCAGTGA CTC
                                ||    |||||||||||  |||
                                CT    GTCGAGTCACT GAG
                                 CCCC          A
GAM815  LOC133088 5'  GGAGGCCAAAGTAATGATT    75586        G  CAG  A
                                GATCATTA CT   TG CCTCC
                                ||||||||  ||   ||  |||||
                                TTAGTAAT GA   AC GGAGG
                                     _  A__  C
GAM815  LOC199718 5'  AGGCCCTGCAGCTAAGTGATCT 89703          _    _   TGA
            A                    TAGATCATT AGCT CAG   CCT
                                |||||||||  ||||  |||   |||
                                ATCTAGTGA TCGA GTC   GGA
                                      A    C   CC_
GAM815  LOC200125 5'  GGAAGTAACTACAACTAATGAT 91536         CTC_   G  C
            C                    GATCATTAG    AGT AC TCC
                                |||||||||    |||  ||  |||
                                CTAGTAATC    TCA TG AGG
                                      AACA   A  A
GAM815  LOC201689 5'  GAGGTCACTGTGGATGTCTA   67734      T    AGCT
                                TAGA CATT    CAGTGACCTC
                                ||||  ||||    ||||||||||
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                                ATCT GTAG   GTCACTGGAG
                                  _   GT__
GAM816  BMP1     3'  CTGAATACCCCAATGGCT    21530          __  C
                                AGCCATTGGG  AT CAG
                                ||||||||||  || |||
                                TCGGTAACCC  TA GTC
                                     CA  A
GAM816  NR5A2    5'  TCTGATGTGTCCTTCCCAAGGC 15118     A     TCCAG
                                GCC TTGGGA    ACATCAGA
                                ||| ||||||    ||||||||
                                CGG AACCCT    TGTAGTCT
                                  _     TCCTG
GAM816  PKD2     3'  TCTGATGTCTGTGGGACTAA   33616     GA  _
                                TTGG  TC CAGACATCAGA
                                ||||  || ||||||||||
                                AATC  GG GTCTGTAGTCT
                                  AG  T
GAM816  SLA      3'  CTGATGTCTGCAGCCATGGCT  23112       TG  ATC
                                AGCCAT  GG   CAGACATCAG
                                ||||||  ||   ||||||||||
                                TCGGTA  CC   GTCTGTAGTC
                                   __ GAC
GAM816  SPINT2   5'  CTGATCGCGAGACCCCAACGGC 63849      A    A  CAGAC
           T                     AGCC TTGGG TC     ATCAG
                                ||||| ||||| ||    |||||
                                TCGG AACCC AG     TAGTC
                                  C    C  AGCGC
GAM816  DKFZP434G1411 3'  CTGATGTCTAAATTGCAGTG   93731       G   CC
                                CATTG GAT  AGACATCAG
                                ||||| |||  |||||||||
                                GTGAC TTA  TCTGTAGTC
                                   G   AA
GAM816  DKFZp434G179 3'  TCTGATGTCTTCAAACAAACAG 80893     CA_   GGATCC
           CT                    AGC   TTG     AGACATCAGA
                                |||   |||     ||||||||||
                                TCG   AAC     TCTGTAGTCT
                                  ACA   AAACT_
GAM816  DUSP9    3'  TCGTTGCACTGGATCCCAGTGG 9158             A_  TCA
           CT                    AGCCATTGGGATCCAG  CA   GA
                                ||||||||||||||||  ||   ||
                                TCGGTGACCCTAGGTC  GT   CT
                                         AC  TG_
GAM816  FLJ21135 5'  ATGGCCCGGATCCCGACGGC   46347     A       AGA_
                                GCC TTGGGATCC    CAT
                                ||| |||||||||    |||
                                CGG AGCCCTAGG    GTA
                                  C        CCCG
GAM816  KIAA0644 3'  CTAATGCCTGGATCTGTG    29725     TG       A   C
                                CAT  GGATCCAG CAT AG
                                |||  |||||||| ||| ||
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                                GTG  TCTAGGTC GTA TC
                                  __       C   A
GAM816  LOC126767 3'  CTGATGTCCAGAGGACGTGGT  75959       T GGA  CA
                                GCCAT G   TC  GACATCAG
                                |||||  |   ||  ||||||||
                                TGGTG C   AG  CTGTAGTC
                                  _ AGG  AC
GAM816  LOC146562 5'  TCTGATGCCCGCGGTAGCCAAT 58256     _     GAT  AGA__
          GAGCT                   AGC CATTGG   CC     CATCAGA
                                ||| ||||||   ||    |||||||
                                TCG GTAACC   GG    GTAGTCT
                                  A     GAT  CGCCC
GAM816  LOC146957 3'  CTGATTTTGACCCCAGTGGC   78814         ATC    C
                                GCCATTGGG   CAGA ATCAG
                                |||||||||   |||| |||||
                                CGGTGACCC   GTTT TAGTC
                                     CA_   _
GAM816  LOC220980 5'  TCTGATGTCTATTGTGAATTGG 94774       __  G   CC
          CT                    AGCCA  TTG GAT  AGACATCAGA
                                |||||  ||| |||  ||||||||||
                                TCGGT  AGT TTA  TCTGTAGTCT
                                  TA   G   __
GAM816  LOC221486 3'  TCTGATGTCCATTTGTCCCAAT 92662     C       CCA__
          AGCT                   AGC ATTGGGAT    GACATCAGA
                                ||| ||||||||    |||||||||
                                TCG TAACCCTG    CTGTAGTCT
                                  A       TTTAC
GAM816  LOC221496 3'  TCTGATGTCTGGATGATCGGC  93644     _  GGG
                                GCC ATT   ATCCAGACATCAGA
                                ||| |||   ||||||||||||||
                                CGG TAG   TAGGTCTGTAGTCT
                                  C  ___
GAM816  LOC91050  3'  CTGAGACTAGATCCCAAAGCT  65374     CA       C  ACA
                                AGC  TTGGGATC AG   TCAG
                                |||  |||||||| ||   ||||
                                TCG  AACCCTAG TC   AGTC
                                  A_       A  AG_
GAM817  AGER      3'  TCCCATCCATCAGCTCC     8533           A  AA
                                GGAGTTGATG GA  GGA
                                |||||||||| ||  |||
                                CCTCGACTAC CT  CCT
                                     _  AC
GAM817  ARF3      3'  GGTCCTTTCTACATTCC     9778       TGATG
                                GGAGT    AGAAAGGACC
                                |||||    ||||||||||
                                CCTTA    TCTTTCCTGG
                                  CA___
GAM817  B3GALT5   3'  GTCCCCTCCACCTCAGCTCC   21339        __  A  AA
                                GGAGTTGA  TG GA  GGAC
                                ||||||||  || ||  ||||
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                                CCTCGACT  AC CT  CCTG
                                    CC  _  CC
GAM817  B3GALT5  3'  GTCCCCTCCACCTCAGCTCC   53722        __  A  AA
                                GGAGTTGA  TG GA  GGAC
                                ||||||||  || ||  ||||
                                CCTCGACT  AC CT  CCTG
                                    CC  _  CC
GAM817  B3GALT5  3'  GTCCCCTCCACCTCAGCTCC   53726        __  A  AA
                                GGAGTTGA  TG GA  GGAC
                                ||||||||  || ||  ||||
                                CCTCGACT  AC CT  CCTG
                                    CC  _  CC
GAM817  B3GALT5  3'  GTCCCCTCCACCTCAGCTCC   53730        __  A  AA
                                GGAGTTGA  TG GA  GGAC
                                ||||||||  || ||  ||||
                                CCTCGACT  AC CT  CCTG
                                    CC  _  CC
GAM817  B3GALT5  3'  GTCCCCTCCACCTCAGCTCC   53735        __  A  AA
                                GGAGTTGA  TG GA  GGAC
                                ||||||||  || ||  ||||
                                CCTCGACT  AC CT  CCTG
                                    CC  _  CC
GAM817  CALCRL   3'  GTCCTTTTTGTAACTACC    20529   _    ATGA
                                GG AGTTG   GAAAGGAC
                                || |||||   ||||||||
                                CC TCAAT   TTTTCCTG
                                 A    GT__
GAM817  CLCN5    5'  TCCTTTCCCATTGCACATC    5386    _ _    A
                                GA GT TGATG GAAAGGA
                                || || ||||| |||||||
                                CT CA GTTAC CTTTCCT
                                 A  C    C
GAM817  CNTN2    5'  GGTCCTTTCTCAGCCTCC    18663     TTGA
                                GGAG   TGAGAAAGGACC
                                ||||   ||||||||||||
                                CCTC   ACTCTTTCCTGG
                                  CG__
GAM817  EFNA1    3'  GTCCTTTCCCACCATTCC    16665     T A  A
                                GGAGT G TG GAAAGGAC
                                ||||| | || ||||||||
                                CCTTA C AC CTTTCCTG
                                  _ C  C
GAM817  FCGR3A   3'  TCCCTTATCCAACTCT      6918       _    AAA
                                GGAGTTG ATGAG   GGA
                                ||||||| |||||   |||
                                TCTCAAC TATTC   CCT
                                    C    ___
GAM817  FNTA     3'  TCCCTTAGCATCAGCTCC    10710         AG  A
                                GGAGTTGATG  AA GGA
                                ||||||||||  || |||
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                                CCTCGACTAC  TT CCT
                                     GA  C
GAM817  FOXO1A   3'  GTCTTTCACCAACTCC      10652        A    AAA
                                GGAGTTG TGAG   GGAC
                                ||||||| ||||   ||||
                                CCTCAAC ACTT   TCTG
                                   C   ___
GAM817  FUT1     3'  GGCTGTTCTTCAACTCC     5602         TG   A  A
                                GGAGTTGA  AGAA GG CC
                                ||||||||  |||| || ||
                                CCTCAACT  TCTT TC GG
                                     __   G  _
GAM817  GALNT2   3'  GGTCCTTTCTTATGTCC     16820     GTTG
                                GGA   ATGAGAAAGGACC
                                |||   ||||||||||||
                                CCT   TATTCTTTCCTGG
                                  G___
GAM817  GNB3     5'  GTCCTTTCTAATCTCAGCTCC  10843        TG__
                                GGAGTTGA   AGAAAGGAC
                                ||||||||   |||||||||
                                CCTCGACT   TCTTTCCTG
                                     CTAA
GAM817  GPM6A    3'  TCCTTTCTCAGTGTAACT    19177       A__
                                AGTTG   TGAGAAAGGA
                                |||||   ||||||||||
                                TCAAT   ACTCTTTCCT
                                   GTG
GAM817  ILF1     5'  GGCCCCCTCCCTCAGCTCC   16922        T_   AAA  A
                                GGAGTTGA  GAG   GG CC
                                ||||||||  |||   || ||
                                CCTCGACT  CTC   CC GG
                                     CC   CC_  _
GAM817  ITGA1    3'  TCCTTTCAGTATCAACTCT   64276         A_
                                GGAGTTGATG  GAAAGGA
                                ||||||||||  |||||||
                                TCTCAACTAT  CTTTCCT
                                     GA
GAM817  KIT      3'  GTCCTTTCCAAGGCTTC     5850        GA  A
                                GGAGTT  TG GAAAGGAC
                                ||||||  || ||||||||
                                CTTCGG  AC CTTTCCTG
                                   A_  _
GAM817  MAPK8IP1 3'  GTCCCTGTTCTCAGCTCC    19582        T   AAA
                                GGAGTTGA GAG   GGAC
                                |||||||| |||   ||||
                                CCTCGACT CTT   CCTG
                                     _  GTC
GAM817  MSN      3'  TCCCCTTCTCATCACTCC    60883       T      A_
                                GGAGT GATGAGAA  GGA
                                ||||| ||||||||  |||
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                                CCTCA CTACTCTT  CCT
                                  _       CC
GAM817  POLS     3'  GGTCCTTTCCCGAGCTGC    23780   G   GA  A
                                G AGTT  TG GAAAGGACC
                                | ||||  || |||||||||
                                C TCGA  GC CTTTCCTGG
                                 G    __ C
GAM817  PPP1R12B 3'  TCCTCTCACCTCAGCTCC    50397        __    AA
                                GGAGTTGA  TGAGA  GGA
                                ||||||||  |||||  |||
                                CCTCGACT  ACTCT  CCT
                                     CC    __
GAM817  PRX      3'  CCCTTCCAGAGGTTCGACTCC  40892        _____  A   A
                                GGAGTTGA    TG GAA GG
                                ||||||||    || ||| ||
                                CCTCAGCT    AC CTT CC
                                     TGGAG  _   C
GAM817  PYGO2    3'  GGTCCTTTCTCAGCCTCTCT   64686     TTGA
                                GGAG   TGAGAAAGGACC
                                ||||   ||||||||||||
                                TCTC   ACTCTTTCCTGG
                                  TCCG
GAM817  RBP5     3'  GTCCTTTCTCACACTCC     49801      T A
                                GGAGT G TGAGAAAGGAC
                                ||||| | ||||||||||
                                CCTCA C ACTCTTTCCTG
                                  _ _
GAM817  SLC16A2  3'  GTCCAGCTCTTATCAACTCC  22527          AA_
                                GGAGTTGATGAGA  GGAC
                                ||||||||||||  ||||
                                CCTCAACTATTCT  CCTG
                                       CGA
GAM817  SLC9A5   3'  GGCCTTTCTCACCACCTCC   60478     T  A       A
                                GGAG TG TGAGAAAGG CC
                                |||| || ||||||||| ||
                                CCTC AC ACTCTTTCC GG
                                  C  C       _
GAM817  SLC9A5   3'  GGCCTTTCTCACCACCTCC   17183     T  A       A
                                GGAG TG TGAGAAAGG CC
                                |||| || ||||||||| ||
                                CCTC AC ACTCTTTCC GG
                                  C  C       _
GAM817  SPAG8    3'  GGTCCTTTCCGCTCTCC     25842     TTGA  A
                                GGAG   TG GAAAGGACC
                                ||||   || |||||||||
                                CCTC   GC CTTTCCTGG
                                  TC__  _
GAM817  SULT1C1  5'  GTCCTTTCCGTGCCC      8322     A  TG   A
                                GG GT  ATG GAAAGGAC
                                || ||  ||| ||||||||
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                                CC CG  TGC CTTTCCTG
                                 _ __  _
GAM817  TLR5     5'  GTCCTTTCTCCTGATTC     13790      GAT
                                GAGTT  GAGAAAGGAC
                                |||||  ||||||||||
                                CTTAG  CTCTTTCCTG
                                   TC_
GAM817  TRIM14   3'  TCCTTTCATCAGCCC      29518    A      GA
                                GG GTTGATGA  AAGGA
                                || ||||||||  |||||
                                CC CGACTACT  TTCCT
                                 _      __
GAM817  C1orf17  3'  GTCCTTTCTGCTTTCTTC    68769     TT  TG
                                GGAG  GA  AGAAAGGAC
                                ||||  ||  |||||||||
                                CTTC  TT  TCTTTCCTG
                                  T_  CG
GAM817  C20orf102 3'  GTCCTTCCTGTTCAGCTCC    55511        TG  A
                                GGAGTTGA  AG AAGGAC
                                ||||||||  || ||||||
                                CCTCGACT  TC TTCCTG
                                     TG  C
GAM817  CEACAM7  3'  GTCCTTTCTGCTTTAACTCT   23543        TG_
                                GGAGTTGA   AGAAAGGAC
                                ||||||||   |||||||||
                                TCTCAATT   TCTTTCCTG
                                     TCG
GAM817  CREG     3'  GTTTTGTCCCATCAATTCC    15247         A  A
                                GGAGTTGATG GA AGGAC
                                |||||||||| || |||||
                                CCTTAACTAC CT TTTTG
                                      C  G
GAM817  DKFZp434F142 3'  GGTCCTTTCTCATACTGGCC   51034    AGTTG
                                GG    ATGAGAAAGGACC
                                ||    ||||||||||||||
                                CC    TACTCTTTCCTGG
                                 GGTCA
GAM817  FBP17    3'  GGTCCCCTCAAGCATCC     73154     _   GA    AAA
                                GGA GTT  TGAG   GGACC
                                ||| |||  ||||   |||||
                                CCT CGA  ACTC   CCTGG
                                  A  __   C__
GAM817  FEM-2    3'  TCCTTTCTCCAGCCC      28321    A   AT
                                GG GTTG  GAGAAAGGA
                                || ||||  |||||||||
                                CC CGAC  CTCTTTCCT
                                 _   __
GAM817  FKSG28   3'  GGTCCCTTCATCGACTGC    48910   G       AAA
                                G AGTTGATGAG   GGACC
                                | ||||||||||   |||||
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                                C TCAGCTACTT   CCTGG
                                 G        C__
GAM817  FLJ12688  3'  CCTCTCTGTTGTCAACACC   73552    A     __  A
                                GG GTTGATG  AGA AGG
                                || |||||||  ||| |||
                                CC CAACTGT  TCT TCC
                                 A      TG  C
GAM817  FLJ14564  3'  GTCCTTTCTGCATGGCCC    77015    A  G  _
                                GG GTT ATG AGAAAGGAC
                                || ||| ||| |||||||||
                                CC CGG TAC TCTTTCCTG
                                 _  _  G
GAM817  FLJ20249  3'  GTCCTTTCTGCAGCTTC     80222       ATG
                                GGAGTTG   AGAAAGGAC
                                |||||||   |||||||||
                                CTTCGAC   TCTTTCCTG
                                    G__
GAM817  FLJ20509  3'  GGCCCTTTCTCTAATGCC    35760    A   AT      A
                                GG GTTG  GAGAAAGG CC
                                || ||||  |||||||| ||
                                CC TAAT  CTCTTTCC GG
                                 G   __      C
GAM817  FLJ21168  3'  GGTTCACTCATCAACTC     47583         AAA
                                GAGTTGATGAG   GGACC
                                ||||||||||   |||||
                                CTCAACTACTC   CTTGG
                                      A__
GAM817  GP5       5'  GGTCCTTTCCTGACCT      16878    A   ATGA
                                GG GTTG    GAAAGGACC
                                || ||||    |||||||||
                                TC CAGT    CTTTCCTGG
                                 _    C___
GAM817  KCNT1     3'  GGTCCTGTGTGTCAGCTCC   62495         AGAA
                                GGAGTTGATG    AGGACC
                                ||||||||||    ||||||
                                CCTCGACTGT    TCCTGG
                                      GTG_
GAM817  KIAA0022  3'  TCCTACCTTCCACTCAACTCC  30288        _ A  ___
                                GGAGTTGA TG GAA   AGGA
                                |||||||| || |||   ||||
                                CCTCAACT AC CTT   TCCT
                                     C  _   CCA
GAM817  KIAA0227  3'  CCTTTTTTTATCATCAATCC   61343     G     ____
                                GGA TTGATGA    GAAAGG
                                ||| |||||||    ||||||
                                CCT AACTACT    TTTTCC
                                  _      ATTT
GAM817  KIAA0275  3'  GGTCCTTCCTCAGCTCC     29330        T  GAA
                                GGAGTTGA GA   AGGACC
                                |||||||| ||   ||||||
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                                CCTCGACT CT   TCCTGG
                                    C  ___
GAM817  KIAA1026 3' GGCTGGTCTTCAACTCC    71741       TG   AA  A
                                GGAGTTGA  AGA  GG CC
                                |||||||| |||  || ||
                                CCTCAACT  TCT  TC GG
                                   __  GG  _
GAM817  KIAA1138 3' GGCCCCTCGTTAGCCC     62821    A      AAA  A
                                GG GTTGATGAG   GG CC
                                || |||||||||   || ||
                                CC CGATTGCTC   CC GG
                                 _       C__  _
GAM817  KIAA1171 3' GGTCTTGCTGCATCAACTCC  89346        AGAA
                                GGAGTTGATG    AGGACC
                                ||||||||||    ||||||
                                CCTCAACTAC    TTCTGG
                                     GTCG
GAM817  KIAA1762 3' TCCTCCTCCTCAGCTCC     64533       T   AA
                                GGAGTTGA GAG  AGGA
                                |||||||| |||  ||||
                                CCTCGACT CTC  TCCT
                                    C   C_
GAM817  KIAA1949 5' GGTCCTTTCAGGGATTCC    93719      GA   GA
                                GGAGTT  TGA  AAGGACC
                                ||||||  |||  |||||||
                                CCTTAG  ACT  TTCCTGG
                                   GG  __
GAM817  KIAA1949 5' GGTCCTTTCAGGGATTCC    99592      GA   GA
                                GGAGTT  TGA  AAGGACC
                                ||||||  |||  |||||||
                                CCTTAG  ACT  TTCCTGG
                                   GG  __
GAM817  KIAA1949 5' GGTCCTTTCAGGGATTCC    99701      GA   GA
                                GGAGTT  TGA  AAGGACC
                                ||||||  |||  |||||||
                                CCTTAG  ACT  TTCCTGG
                                   GG  __
GAM817  MGC16025 3' GGCCTGCCATCAGCTCC     53025        AGAA  A
                                GGAGTTGATG    AGG CC
                                ||||||||||    ||| ||
                                CCTCGACTAC    TCC GG
                                     CG__  _
GAM817  MRPS25   5' GTCCTTTCTCGTCGCTGC    42860   G  T
                                G AGT GATGAGAAAGGAC
                                | ||| ||||||||||||
                                C TCG CTGCTCTTTCCTG
                                 G  _
GAM817  PKNOX2   3' GTCCCTTCTGGGTTGACTCC  92531     TG  G_   A
                                GGAGT  AT  AGAA GGAC
                                |||||  ||  |||| ||||
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                                CCTCA  TG  TCTT CCTG
                                   GT  GG   C
GAM817  RAB3D    3'  CCTTCCCTCCTGTCAACTGC  16260   G     __  A_
                                G AGTTGAT  GAG  AAGG
                                | |||||||  |||  ||||
                                C TCAACTG  CTC  TTCC
                                 G      TC   CC
GAM817  SCYA3    5'  GTCCTTTCTTGGCTCT     60532      GAT
                                GGAGTT   GAGAAAGGAC
                                ||||||   ||||||||||
                                TCTCGG   TTCTTTCCTG
                                    ___
GAM817  SPRY4    3'  GGTCCTTTGGTACGCACCC   49028    A  _  A  AG
                                GG GT TG TG  AAAGGACC
                                || || || ||  ||||||||
                                CC CA GC AT  TTTCCTGG
                                 _  C  _  GG
GAM817  SYT13    3'  GGCTGGTCTTCAACTCC     95103       TG   AA  A
                                GGAGTTGA  AGA  GG CC
                                ||||||||  |||  || ||
                                CCTCAACT  TCT  TC GG
                                    __   GG  _
GAM817  SYT6     3'  GGTCTTCCCACCAACCCC    79522    A    A  A  AA
                                GG GTTG TG GA  GGACC
                                || |||| || ||  |||||
                                CC CAAC AC CT  TCTGG
                                 C    C  C  __
GAM817  TOR1B    3'  GTCCTTTCTCAGATACTCT   27978      TGA
                                GGAGT   TGAGAAAGGAC
                                |||||   ||||||||||||
                                TCTCA   ACTCTTTCCTG
                                   TAG
GAM817  VAV3     3'  CCTGCCCTCTCATCAATCC   21477     G       A___
                                GGA TTGATGAGA   AGG
                                ||| |||||||||   |||
                                CCT AACTACTCT   TCC
                                  _       CCCG
GAM817  LOC127281 3'  GGCTCCCTCCCCATCAGCTCC  75138         A_  AA  _
                                GGAGTTGATG  GA  GGA CC
                                ||||||||||  ||  ||| ||
                                CCTCGACTAC  CT  CCT GG
                                      CC  C_   C
GAM817  LOC132617 3'  TCCATTTCTCATCCACCC    76421    A  T       _
                                GG GT GATGAGAAA GGA
                                || || ||||||||| |||
                                CC CA CTACTCTTT CCT
                                 _ C       A
GAM817  LOC138046 5'  GGCCCTCGCACGCTCAACTCC  75809        _  AGAA   A
                                GGAGTTGA TG    AGG CC
                                |||||||| ||    ||| ||
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                                CCTCAACT GC    TCC GG
                                    C  ACGC   C
GAM817   LOC142927 3'  GGTCCTTTAATAGCTCC     76949        ATGAG
                                GGAGTTG     AAAGGACC
                                |||||||     ||||||||
                                CCTCGAT     TTTCCTGG
                                   AA___
GAM817   LOC144308 3'  GGCCCGTCTCATCACCCC     83982     A  T      AA  A
                                GG GT GATGAGA  GG CC
                                || || |||||||  || ||
                                CC CA CTACTCT  CC GG
                                 C  _      GC  _
GAM817   LOC149086 5'  GGTCCTTTATTCACCAACTC   85495       A   _
                                GAGTTG TGAG AAAGGACC
                                |||||| |||| ||||||||
                                CTCAAC ACTT TTTCCTGG
                                   C    A
GAM817   LOC149606 3'  GGTCCTTTCTCCCTCC      80266      TTGAT
                                GGAG     GAGAAAGGACC
                                ||||     ||||||||||
                                CCTC     CTCTTTCCTGG
                                  C_____
GAM817   LOC149606 3'  GTCCTTTCCACACACACC     80267     A  _  A  A
                                GG GT TG TG GAAAGGAC
                                || || || || ||||||||
                                CC CA AC AC CTTTCCTG
                                 A  C  _  _
GAM817   LOC150067 3'  GTCCTTCCTTAATTTCAACTC  60963        ___    A
                                GAGTTGA   TGAG AAGGAC
                                |||||||   |||| ||||||
                                CTCAACT   ATTC TTCCTG
                                    TTA    C
GAM817   LOC154094 3'  GTCCTTCCTTAATTTCAACTC  61062        ___    A
                                GAGTTGA   TGAG AAGGAC
                                |||||||   |||| ||||||
                                CTCAACT   ATTC TTCCTG
                                    TTA    C
GAM817   LOC196485 3'  GGTCCCCTCAGTCAACTCT    89075        _    AAA
                                GGAGTTGA TGAG   GGACC
                                |||||||| ||||   |||||
                                TCTCAACT ACTC   CCTGG
                                    G    C__
GAM817   LOC199745 3'  GTCTCTCATCAGCCC       89720     A        AAG
                                GG GTTGATGAGA   GAC
                                || ||||||||||   |||
                                CC CGACTACTCT   CTG
                                 _       ____
GAM817   LOC202986 3'  GGTCCCCTCAGTCAACTCT    92069        _    AAA
                                GGAGTTGA TGAG   GGACC
                                |||||||| ||||   |||||
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                                TCTCAACT ACTC   CCTGG
                                    G    C__
GAM817   LOC219994 3'  TCCTTTCCATTGCTCT      95007       T    A
                                GGAGT GATG GAAAGGA
                                ||||| |||| |||||||
                                TCTCG TTAC CTTTCCT
                                  _    _
GAM817   LOC253776 5'  GGTCCTTTCTTATCCCCCC    99294     AGTT
                                GG    GATGAGAAAGGACC
                                ||    ||||||||||||||
                                CC    CTATTCTTTCCTGG
                                 CCC_
GAM817   LOC254173 3'  GGCCACAATCATCAGCTCC    98644           GAAA  A
                                GGAGTTGATGA    GG CC
                                ||||||||||    || ||
                                CCTCGACTACT    CC GG
                                      AACA  _
GAM817   LOC254826 3'  GGTCCCTTCCACCCAAGCTCC  99053        GA__  A   A
                                GGAGTT    TG GAA GGACC
                                ||||||    || ||| |||||
                                CCTCGA    AC CTT CCTGG
                                   ACCC  _   C
GAM817   LOC256614 3'  GTCCTTTCCCGTCCTCC     98200      TT    A
                                GGAG  GATG GAAAGGAC
                                ||||  |||| ||||||||
                                CCTC  CTGC CTTTCCTG
                                  __    C
GAM817   LOC257451 3'  GGTCCTTTCTCAGCCTCTCT   97298      TTGA
                                GGAG    TGAGAAAGGACC
                                ||||    ||||||||||||
                                TCTC    ACTCTTTCCTGG
                                  TCCG
GAM817   LOC51072  3'  GTCCTTCCTTAATTTCAACTC  32548        ___    A
                                GAGTTGA   TGAG AAGGAC
                                |||||||   |||| ||||||
                                CTCAACT   ATTC TTCCTG
                                    TTA    C
GAM817   LOC63904  5'  GGTCCTCTTTCTCCAACACC   42212    A    AT    A
                                GG GTTG  GAGA AGGACC
                                || ||||  |||| ||||||
                                CC CAAC  CTTT TCCTGG
                                 A    CT    C
GAM817   LOC92095  5'  GGTCCTTTCCAACACCTCC    68654      T  A  A
                                GGAG TG TG GAAAGGACC
                                |||| || || |||||||||
                                CCTC AC AC CTTTCCTGG
                                  C  A  _
GAM817   LOC92096  5'  GGTCCTTTCCAACACCTCC    68656      T  A  A
                                GGAG TG TG GAAAGGACC
                                |||| || || |||||||||
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                                CCTC AC AC CTTTCCTGG
                                  C  A  _
GAM818  ASL     3'  GTTTGACACAGCCTGGGCAACA 72396     GA    A       C
                                TGT  CCCA GCTGTGTC AAT
                                |||  |||| |||||||| |||
                                ACA  GGGT CGACACAG TTG
                                  AC    C       T
GAM818  DHFR    3'  GACCAGCTTGGGCAACA     7647      GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM818  MMP19   3'  GACCAGCTTGGGCAACA     11630     GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM818  MMP19   3'  GACCAGCTTGGGCAACA     43304     GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM818  NR1I2   5'  AGATCAAAGTGGTGGGGTCACA 15294         AA  TG GTCCA
                                TGTGACCC  GC  T    ATCT
                                ||||||||  ||  |    ||||
                                ACACTGGG  TG  G    TAGA
                                     G_  GT AAAC_
GAM818  PRKY    3'  GACCAGCTTGGGCAACA     12375     GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM818  RAD54B  3'  AGATTGTCAGCTTGGTCCACA  57062      AC       TGTC
                                TGTG  CCAAGCTG    CAATCT
                                ||||  ||||||||    ||||||
                                ACAC  GGTTCGAC    GTTAGA
                                  CT       T___
GAM818  RCE1    3'  GATTTAACTTGGGTAACA     18890     G      C  T
                                TGT ACCCAAG TG GTC
                                ||| ||||||| || |||
                                ACA TGGGTTC AT TAG
                                  A      A  T
GAM818  SFRS2IP 5'  GACCAGCTTGGGCAACA     17540     GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM818  TEM7    3'  GACCAGCTTGGGCAACA     40259     GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
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                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM818  FLJ13263  3'  AGATTGCTCCTTCAGCTCAGGG 47809     A  A_    TGTC__
            CCACA                  TGTG CCC  AGCTG     CAATCT
                                |||| |||  |||||     ||||||
                                ACAC GGG  TCGAC     GTTAGA
                                  C   AC    TTCCTC
GAM818  FLJ14327  3'  GACCAGCTTGGGCAACA     46679     GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM818  KIAA0172  3'  GACTGCTAGCCTGGGCACA   65596     A   A  _ _
                                TGTG CCCA GCT GT GTC
                                |||| |||| ||| || |||
                                ACAC GGGT CGA CG CAG
                                  _   C   T  T
GAM818  KIAA1833  3'  GGACCACAGCCTGGGCACA   90753     A   A    _
                                TGTG CCCA GCTGTG TCC
                                |||| |||| ||||||| |||
                                ACAC GGGT CGACAC AGG
                                  _   C     C
GAM818  KIAA1870  3'  GACCAGCTTGGGCAACA     52901     GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM818  MEGF11    3'  ATTGGACAAATGTGGATACA   51599     AC   AGCTG
                                TGTG  CCA    TGTCCAAT
                                ||||  |||    ||||||||
                                ACAT  GGT    ACAGGTTA
                                  A_   GTAA_
GAM818  MGC15631  3'  GACCAGCCTGGGTGACA     52230     G    A   T
                                TGT ACCCA GCTG GTC
                                ||| ||||| |||| |||
                                ACA TGGGT CGAC CAG
                                  G    C   _
GAM818  MGC32043  3'  GACCAGGTCTTGGGCACA    58665     A     __   T
                                TGTG CCCAAG  CTG GTC
                                |||| ||||||  ||| |||
                                ACAC GGGTTC  GAC CAG
                                  _     TG   _
GAM818  PLP1      3'  ATTGGACATTAAGCATCACA   6755      CCCAA   __
                                TGTGA    GCT  GTGTCCAAT
                                |||||    |||  |||||||||
                                ACACT    CGA  TACAGGTTA
                                   A_____   AT
GAM818  PTD012    3'  GACCAGCTTGGGCAACA     26738     GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
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                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM818  STAF42   3'  ATTGAATGTTTTTTGGGTCCA  54942    T      CT TG C
                                TG GACCCAAG  G  T CAAT
                                || ||||||||  |  | ||||
                                AC CTGGGTTT  T  A GTTA
                                 _       TT GT A
GAM818  TRIM31   3'  ACGCCAGCCTGGGTCACA    92649         A   _
                                TGTGACCCA GCTG TGT
                                ||||||||| |||| |||
                                ACACTGGGT CGAC GCA
                                      C   C
GAM818  LOC142893 5'  ATTGGAACATTTTTGGGTCCA  83757    T      CT   _
                                TG GACCCAAG  GTGT CCAAT
                                || ||||||||  |||| |||||
                                AC CTGGGTTT  TACA GGTTA
                                 _       T_   A
GAM818  LOC143503 5'  AGACTGGACAAAGGGGGTCACA 83882         AAGCTG     A
                                TGTGACCC     TGTCCA TCT
                                ||||||||     |||||| |||
                                ACACTGGG     ACAGGT AGA
                                     GGAA__     C
GAM818  LOC145824 5'  GACTTGCAGCTTGGATACACA  77986      AC_       __
                                TGTG   CCAAGCTGT  GTC
                                ||||   |||||||||  |||
                                ACAC   GGTTCGACG  CAG
                                  ATA        TT
GAM818  LOC157603 3'  GACCAGCTTGGGCAACA     87786     GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM818  LOC221300 3'  GACCAGCTTGGGTAACA     93576     G        T
                                TGT ACCCAAGCTG GTC
                                ||| |||||||||| |||
                                ACA TGGGTTCGAC CAG
                                  A        _
GAM818  LOC257608 3'  ACGCCAGCCTGGGTCACA    99664         A   _
                                TGTGACCCA GCTG TGT
                                ||||||||| |||| |||
                                ACACTGGGT CGAC GCA
                                      C   C
GAM818  LOC51337  3'  GACCAGAGCATCCTGGGTACA  34081      A   A___   G  _
                                TGTG CCCA    GCT TG TC
                                |||| ||||    ||| || ||
                                ACAT GGGT    CGA AC AG
                                  _    CCTA   G  C
GAM819  ADCY1    5'  ACGACAATGTGAGCATC     94336          AG
                                GATGCTCACAT  GTTGT
                                ||||||||||  |||||
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                                CTACGAGTGTA  CAGCA
                                      A_
GAM819  C8orf1   3'  ATAGCATGATGTGAGCATC   16343          AG_
                                GATGCTCACAT   GTTGT
                                ||||||||||   |||||
                                CTACGAGTGTA   CGATA
                                      GTA
GAM819  CDH12    3'  ATAGCTATGTGGCATCA     15776       T      G
                                TGATGC CACATAG TTGT
                                |||||| ||||||| ||||
                                ACTACG GTGTATC GATA
                                  _      _
GAM819  HIP1     3'  ACAAACTTGTGAGCATCA     19242          T  G
                                TGATGCTCACA AG TTGT
                                |||||||||| || ||||
                                ACTACGAGTGT TC AACA
                                      _ A
GAM819  DKFZp547I224 5'  ATGGCCTATGTGAGATCA     39948      G         TG
                                TGAT CTCACATAGGT  T
                                |||| ||||||||||  |
                                ACTA GAGTGTATCCG  A
                                  _         GT
GAM819  DKFZp761P1010 3'  GGCACAAATAAGCTCA      37943     T   CACA  GG
                                TGA GCT    TA  TTGTGCC
                                ||| |||    ||  |||||||
                                ACT CGA    AT  AACACGG
                                  _  _____  A_
GAM819  FLJ13114  3'  ACAGGCCAGGTGAGCATCA    44889          ATA  _
                                TGATGCTCAC   GGT TGT
                                ||||||||||   ||| |||
                                ACTACGAGTG   CCG ACA
                                      GA_   G
GAM819  FLJ23024  3'  TGGCACAACCTCAGCTCA     46851     T   CACAT
                                TGA GCT     AGGTTGTGCCA
                                ||| |||     ||||||||||
                                ACT CGA     TCCAACACGGT
                                  _  C_____
GAM819  HNK-1ST   5'  ACAGCAAGGAAATGTGAGCCCC 17946    AT       AG_____
              A                  TG  GCTCACAT     GTTGT
                                 ||  ||||||||     |||||
                                 AC  CGAGTGTA     CGACA
                                  CC       AAGGAA
GAM819  KIAA0459  3'  ACAATCATGTGAGCTCA     61639     T      A
                                TGA GCTCACAT GGTTGT
                                ||| |||||||| ||||||
                                ACT CGAGTGTA CTAACA
                                  _      _
GAM819  KIAA1466  3'  ATAACCTATGAAACATCA     72405       CTCA
                                TGATG   CATAGGTTGT
                                |||||   ||||||||||
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                                ACTAC   GTATCCAATA
                                  AAA_
GAM819  KIAA1954  5'  ACAGCTTACTGAGCATCA    78220        CA
                                TGATGCTCA  TAGGTTGT
                                |||||||||  ||||||||
                                ACTACGAGT  ATTCGACA
                                    C_
GAM819  PACSIN2   3'  ATGGCACAGATTGATGCGCACC 24296   A  T  _  TAGG
          A                      TG TGC CA CA   TTGTGCCAT
                                 || ||| || ||   |||||||||
                                 AC ACG GT GT   GACACGGTA
                                  C  C  A  TA__
GAM819  PARVA     3'  GGCCCATGTGAGCATCA     37183          A  TTGT
                                TGATGCTCACAT GG   GCC
                                ||||||||||||| ||   |||
                                ACTACGAGTGTA CC   CGG
                                      _ _____
GAM819  RoXaN     3'  GCACACATGTGAGCACA     47292    A      AGGT
                                TG TGCTCACAT   TGTGC
                                || |||||||||   |||||
                                AC ACGAGTGTA   ACACG
                                 _       C___
GAM819  LOC148638 3'  ATGGCCATGTGAGCACA     79665    A      A  TG
                                TG TGCTCACAT GGT  T
                                || ||||||||| |||  |
                                AC ACGAGTGTA CCG  A
                                 _       _  GT
GAM819  LOC148696 5'  GGCCAGCATTGAGCATCA    85348        CATAG   T
                                TGATGCTCA    GTTG GCC
                                |||||||||    |||| |||
                                ACTACGAGT    CGAC CGG
                                     TA___   _
GAM819  LOC200609 5'  ATAACACTGTGCAATCATCA  91658      CTCA    _
                                TGATG   CATAG GTTGT
                                |||||   ||||| |||||
                                ACTAC   GTGTC CAATA
                                   TAAC    A
GAM819  LOC203235 3'  ATGACACAACCTGAGAGGCACC 92097   A   CACA      C
          A                     TG TGCT   TAGGTTGTG CAT
                                || ||||   ||||||||| |||
                                AC ACGG   GTCCAACAC GTA
                                 C   AGA_      A
GAM819  LOC219667 3'  GCCAGCCTATGCAACATCA   92948      CTCA       T
                                TGATG   CATAGGTTG GC
                                |||||   ||||||||| ||
                                ACTAC   GTATCCGAC CG
                                   AAC_       _
GAM819  LOC220514 3'  ATGGCACAGATTGATGCGCACC 61072   A  T  _  TAGG
          A                     TG TGC CA CA   TTGTGCCAT
                                || ||| || ||   |||||||||
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                                AC ACG GT GT   GACACGGTA
                                 C  C A  TA__
GAM819  LOC221463 3'  GGCATGGCACGTGAGCAGCA  93706   A     ATAG  TG
                                TG TGCTCAC   GT  TGCC
                                || |||||||   ||  ||||
                                AC ACGAGTG   CG  ACGG
                                 G     CA__  GT
GAM820  CD4     3'  AGGCTCTGCGCCTGCCCCAC  7044        AC   AT
                                GTGGGGCAG  CGCA  GCCT
                                |||||||||  ||||  ||||
                                CACCCCGTC  GCGT  CGGA
                                     C_   CT
GAM820  DNAJB1   3'  CATTCCAGTCTGCCCCAC   21565         CGC
                                GTGGGGCAGAC   AATG
                                ||||||||||   ||||
                                CACCCCGTCTG   TTAC
                                      ACC
GAM820  HPCA    3'  AGGCTGGGTTGGTCTGCCCC  10951         _ AAT
                                GGGGCAGACCG C   GCCT
                                |||||||||| |   ||||
                                CCCCGTCTGGT G   CGGA
                                      T GGT
GAM820  NCOA6   5'  CATAGGTCAAATCTGGCCCAC  26831     G   CCGCAAT
                                GTGGG CAGA     GCCTATG
                                ||||| ||||     |||||||
                                CACCC GTCT     TGGATAC
                                   G   AAAC___
GAM820  SDF2    3'  AGACATCTGTTGCTGCCTCAC  23622       ACC  _  C
                                GTGGGGCAG   GCA ATG CT
                                |||||||||   ||| ||| ||
                                CACTCCGTC   TGT TAC GA
                                     GT_   C   A
GAM820  FLJ14106 3'  GCTGGGATCTGCCCCAC    47548        _  G  AT
                                GTGGGGCAGA CC CA  GC
                                |||||||||| || ||  ||
                                CACCCCGTCT GG GT  CG
                                     A  _  __
GAM820  KIAA0210 3'  CAGTGCCCAGTCCTGCCCCAC  29151       _  C__   A
                                GTGGGGCAG AC   GCA TG
                                |||||||| ||   ||| ||
                                CACCCCGTC TG   CGT AC
                                     C  ACC   G
GAM820  KIAA0376 3'  CGTGGGTCAGCTGCCCCAC   66213       ACCGCAAT
                                GTGGGGCAG      GCCTATG
                                |||||||||      |||||||
                                CACCCCGTC      TGGGTGC
                                     GAC_____
GAM820  KIAA1862 3'  CATAGGCCACGTGTGCCCCAC  69505       G  CGCAAT
                                GTGGGGCA AC    GCCTATG
                                |||||||| ||    |||||||
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                                CACCCCGT TG     CGGATAC
                                     G  CAC___
GAM820  LOC158107 5'  AGGCCGCCGCCTGCCCCAC   87980        ACC  AAT
                                GTGGGGCAG   GC   GCCT
                                |||||||||   ||   ||||
                                CACCCCGTC   CG   CGGA
                                     CGC  C__
GAM820  LOC162083 3'  AGACATTGAAGTGAGTCTGCCC 83205        _  ___   C
                                GGGCAGAC CGC   AATG CT
                                |||||||| |||   |||| ||
                                CCCGTCTG GTG   TTAC GA
                                     A   AAG    A
GAM820  LOC92305  3'  AGACACAGCGTCTGCCCC    57230        C  AA  C
                                GGGGCAGAC GC  TG CT
                                ||||||||| ||  || ||
                                CCCCGTCTG CG  AC GA
                                     _  AC  A
GAM821  ABCE1     5'  GGGGATCGTTTTCTCCAGA   60261        C  CTG
                                TCTGGAGAAA TG   CCTC
                                |||||||||| ||   ||||
                                AGACCTCTTT GC   GGGG
                                      T  TA_
GAM821  AKAP13    3'  TGAGGCAGCTGCCTCCTGA   59238    T   AAACT
                                TC GGAG     GCTGCCTCA
                                || ||||     |||||||||
                                AG CCTC     CGACGGAGT
                                 T    CGT__
GAM821  AKAP13    3'  TGAGGCAGCTGCCTCCTGA   24220    T   AAACT
                                TC GGAG     GCTGCCTCA
                                || ||||     |||||||||
                                AG CCTC     CGACGGAGT
                                 T    CGT__
GAM821  AKAP13    3'  TGAGGCAGCTGCCTCCTGA   23090    T   AAACT
                                TC GGAG     GCTGCCTCA
                                || ||||     |||||||||
                                AG CCTC     CGACGGAGT
                                 T    CGT__
GAM821  ALOX12B   5'  GGGCAGCAGCTTTTCCAGA   8537         A
                                TCTGGAGAA CTGCTGCCT
                                ||||||||| |||||||||
                                AGACCTTTT GACGACGGG
                                      C
GAM821  BCL7A     3'  GAGGCGGCGTTACCTCCAGA   40984       A_  T
                                TCTGGAG  AAC GCTGCCTC
                                |||||||  ||| ||||||||
                                AGACCTC  TTG CGGCGGAG
                                     CA  _
GAM821  CEACAM1   3'  GAGGCTTTCTCCAGG       9930         CTGCT
                                TCTGGAGAAA    GCCTC
                                ||||||||||    |||||
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                                GGACCTCTTT    CGGAG
                                      _____
GAM821  CLDN3    3'  TGGGGCAGCTTCCCCAG     8961      A  ACT
                                CTGG GAA   GCTGCCTCA
                                |||| |||   |||||||||
                                GACC CTT   CGACGGGGT
                                  C  ___
GAM821  COL10A1  5'  AGGCACCATCTCCAGG      6682        AAC  C
                                TCTGGAGA   TG TGCCT
                                ||||||||   || |||||
                                GGACCTCT   AC ACGGA
                                     ___  C
GAM821  CUTL1    3'  GAGCCCCAGTCTCTTCAGA   10348       A   CT  C
                                TCTGGAGA ACTG  GC TC
                                |||||||| ||||  || ||
                                AGACTTCT TGAC  CG AG
                                     C    CC  _
GAM821  CYBB     3'  GAGAGTGTTTCTCCA       76846        T   GC
                                TGGAGAAAC GCT  CTC
                                ||||||||| |||  |||
                                ACCTCTTTG TGA  GAG
                                      _  ___
GAM821  DNASE1   5'  GAAGTGCTTCTTCAGA      19072        ACT  T  C
                                TCTGGAGAA   GC GC TC
                                |||||||||   || || ||
                                AGACTTCTT   CG TG AG
                                     ___  _  A
GAM821  DXYS155E 3'  GAGGATGGCTCTCCAGA     18688        AACT   _
                                TCTGGAGA    GCTG CCTC
                                ||||||||    |||| ||||
                                AGACCTCT    CGGT GGAG
                                     _____    A
GAM821  EFNA1    3'  TGGGGCAGCACTCCCCAGA   16666      A  AAC
                                TCTGG GA   TGCTGCCTCA
                                ||||| ||   ||||||||||
                                AGACC CT   ACGACGGGGT
                                   C  C__
GAM821  EGR1     3'  TGAGCTTCGGTTCTCCAGA   10493        A   CT  C
                                TCTGGAGAA CTG  GC TCA
                                ||||||||| |||  || |||
                                AGACCTCTT GGC  CG AGT
                                      _   TT  _
GAM821  FLT1     3'  TGAGGAGAGTTTTCTCCA    10664        _  G  G
                                TGGAGAAA CT CT CCTCA
                                |||||||| || || |||||
                                ACCTCTTT GA GA GGAGT
                                     T  _  _
GAM821  FRK      5'  AGCCGGTAAGTCTCTCCAGG  10715        A  _    C
                                TCTGGAGA ACT GCTG CT
                                |||||||| ||| |||| ||
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                                GGACCTCT TGA TGGC GA
                                     C  A   C
GAM821  GAB2    3'  GAGGCAGCATCTCCAGA    25458       AAC
                                TCTGGAGA  TGCTGCCTC
                                ||||||||  |||||||||
                                AGACCTCT  ACGACGGAG
                                    ___
GAM821  GAB2    3'  GAGGCAGCATCTCCAGA    55405       AAC
                                TCTGGAGA  TGCTGCCTC
                                ||||||||  |||||||||
                                AGACCTCT  ACGACGGAG
                                    ___
GAM821  GP9     3'  TGAGGCAGGTCCCCAGA    5725      A  AACTG
                                TCTGG GA    CTGCCTCA
                                ||||| ||    ||||||||
                                AGACC CT    GACGGAGT
                                   C  G____
GAM821  GPC6    5'  AGGCAGCAGCCTTCCCAG    20329     A   A_
                                CTGG GAA  CTGCTGCCT
                                ||||  |||  |||||||||
                                GACC CTT  GACGACGGA
                                  _   CC
GAM821  GUCA2B  3'  TGAGGCAGCCCAGCTCCTGA  24020    T    AAACT
                                TC GGAG    GCTGCCTCA
                                || ||||    |||||||||
                                AG CCTC    CGACGGAGT
                                 T   GACC_
GAM821  GUCY1A3 5'  GAGTCAGTTTTCCAGA     64226       AACT   C
                                TCTGGAGA   GCTG CTC
                                ||||||||   |||| |||
                                AGACCTTT   TGAC GAG
                                    ____   T
GAM821  IL8RA   3'  TGAGGCAGGCACTGCCA    7153     _  AAAC  _
                                TGG AG   TGC TGCCTCA
                                ||| ||   ||| |||||||
                                ACC TC   ACG ACGGAGT
                                  G ____  G
GAM821  MADH6   5'  AGGCAGGGCTTTCCAGA    19972       AA TG
                                TCTGGAGA  C  CTGCCT
                                ||||||||  |  ||||||
                                AGACCTTT  G  GACGGA
                                    CG __
GAM821  MGAM    3'  GGGGCAGTTTCTCCAGG    72812           G
                                TCTGGAGAAACTGCT CC
                                |||||||||||||| ||
                                GGACCTCTTTGACGG GG
                                          _
GAM821  MYO7A   3'  GAGGCAGCAGTGGGTTCAGG  6032       GAA
                                TCTGGA   ACTGCTGCCTC
                                ||||||   ||||||||||
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                                GGACTT   TGACGACGGAG
                                   GGG
GAM821  NEUROD2  3'  AGGAGTGCTTCTCCAGG    21592        ACT   G
                                TCTGGAGAA   GCT CCT
                                |||||||||   ||| |||
                                GGACCTCTT   TGA GGA
                                    CG_  _
GAM821  NPY2R    3'  TGAACAGAAATTTCTCCAGG  8067         CTG   CC
                                TCTGGAGAAA   CTG  TCA
                                ||||||||||   |||  |||
                                GGACCTCTTT   GAC  AGT
                                     AAA   A_
GAM821  OXTR     3'  TGAATAGACATTTCTCCA    8083         C  _   CC
                                TGGAGAAA TG CTG  TCA
                                |||||||| || |||  |||
                                ACCTCTTT AC GAT  AGT
                                    _  A   A_
GAM821  PARK2    3'  GAGGAGCCTTTCCAGA      17078        AACT   G
                                TCTGGAGA    GCT CCTC
                                ||||||||    ||| ||||
                                AGACCTTT    CGA GGAG
                                    C___   _
GAM821  PARK2    3'  GAGGAGCCTTTCCAGA      26542        AACT   G
                                TCTGGAGA    GCT CCTC
                                ||||||||    ||| ||||
                                AGACCTTT    CGA GGAG
                                    C___   _
GAM821  PARK2    3'  GAGGAGCCTTTCCAGA      26546        AACT   G
                                TCTGGAGA    GCT CCTC
                                ||||||||    ||| ||||
                                AGACCTTT    CGA GGAG
                                    C___   _
GAM821  PMCHL1   3'  GAGGTGTTCTCCAGA       49917         ACTGC
                                TCTGGAGAA    TGCCTC
                                |||||||||    ||||||
                                AGACCTCTT    GTGGAG
                                     _____
GAM821  PPP2R4   3'  TGAGGCATGTCTTTCCAGA   61184         A  TGC
                                TCTGGAGA AC   TGCCTCA
                                |||||||| ||   |||||||
                                AGACCTTT TG   ACGGAGT
                                    C  T__
GAM821  PRX      3'  GAGGCAGCCCTTCCAGA     40896        AAACT
                                TCTGGAG    GCTGCCTC
                                |||||||    ||||||||
                                AGACCTT    CGACGGAG
                                    CC___
GAM821  REV3L    5'  TGAGGAAGATTTCTCTCA    12825    _    CTG  G
                                TG GAGAAA   CT CCTCA
                                || ||||||   || |||||
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                                AC CTCTTT   GA GGAGT
                                 T     A__  A
GAM821   RXRA     3'  TGAGGCAGCAGCCTTC      12925      AAA
                                GGAG   CTGCTGCCTCA
                                ||||   ||||||||||
                                CTTC   GACGACGGAGT
                                  C__
GAM821   SIRPB2   3'  GAGAAGCTTCTCTAGA      55858         ACT   GC
                                TCTGGAGAA   GCT  CTC
                                |||||||||   |||  |||
                                AGATCTCTT   CGA  GAG
                                      ___   A_
GAM821   SIRPB2   3'  GAGAAGCTTCTCTAGA      38272         ACT   GC
                                TCTGGAGAA   GCT  CTC
                                |||||||||   |||  |||
                                AGATCTCTT   CGA  GAG
                                      ___   A_
GAM821   SURF5    3'  TGAGGCAGCATTTCCTCCA   23130       A  C
                                TGGAG AA TGCTGCCTCA
                                |||||  ||  ||||||||||
                                ACCTC TT ACGACGGAGT
                                   C  T
GAM821   TAF1C    5'  GAGGCCCATTTTCCAGA     20265         AC  CT
                                TCTGGAGAA  TG  GCCTC
                                |||||||||  ||  |||||
                                AGACCTTTT  AC  CGGAG
                                      __  C_
GAM821   VANGL2   3'  TGAGACATCGGACTCTCCGGA  72095         AA   C  C
                                TCTGGAGA  CTG TG CTCA
                                ||||||||  ||| || ||||
                                AGGCCTCT  GGC AC GAGT
                                     CA   T  A
GAM821   WARS     3'  GAGGCAGCAGCCCTCGAGG   67865     G   AAA
                                TCT GAG   CTGCTGCCTC
                                ||| |||   ||||||||||
                                GGA CTC   GACGACGGAG
                                  G   CC_
GAM821   ZNF45    5'  GACTTGGCACTTCTCCAGA   14250         AC    CC
                                TCTGGAGAA  TGCTG  TC
                                |||||||||  |||||  ||
                                AGACCTCTT  ACGGT  AG
                                     C_    TC
GAM821   ARHF     3'  GGGACAGTTTCTCAGA      39272      G      CTG
                                TCTG AGAAACTG   CCT
                                ||||  ||||||||   |||
                                AGAC TCTTTGAC   GGG
                                  _       A__
GAM821   BLR1     3'  TGAGGCAGGGAAGTCCCCAGG  53119      A  AA_  G
                                TCTGG GA   CT CTGCCTCA
                                |||||  ||   ||  ||||||||
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                                GGACC CT   GG GACGGAGT
                                   C  GAA  _
GAM821   BLR1     3'  TGAGGCAGGGAAGTCCCCAGG  9940       A  AA_  G
                                TCTGG GA   CT CTGCCTCA
                                ||||| ||   || ||||||||
                                GGACC CT   GG GACGGAGT
                                   C  GAA  _
GAM821   C20orf150 3'  TGAAGCCGAGCTCCTCCAGA   66017        AAACT   __  C
                                TCTGGAG    GCT  GC TCA
                                |||||||    |||  || |||
                                AGACCTC    CGA  CG AGT
                                    CT___   GC  A
GAM821   C20orf4   3'  GGGCAGCAATCTCTCCAGG   31948        AAC
                                TCTGGAGA   TGCTGCCT
                                ||||||||   ||||||||
                                GGACCTCT   ACGACGGG
                                    CTA
GAM821   C20orf7   3'  TGAATATGCACCTTCTCCAGA  44383        AC   TGCC
                                TCTGGAGAA  TGC    TCA
                                |||||||||  |||    |||
                                AGACCTCTT  ACG    AGT
                                     CC   TATA
GAM821   C6orf26   3'  AGAAAGCAGCTTTCTCCA    48268        _    GC
                                TGGAGAAA CTGCT  CT
                                |||||||| |||||  ||
                                ACCTCTTT GACGA  GA
                                    C     AA
GAM821   CASKIN1   3'  TGAGGCGGATTTCCCCAGA   40784      A    CTG
                                TCTGG GAAA   CTGCCTCA
                                ||||| ||||   ||||||||
                                AGACC CTTT   GGCGGAGT
                                   C    A__
GAM821   CCR8      3'  TGAGGCAGATGCCTCTAGA   19041       AAACTG
                                TCTGGAG     CTGCCTCA
                                |||||||     ||||||||
                                AGATCTC     GACGGAGT
                                    CGTA__
GAM821   CPGL2     5'  GAAGCCGCTTTGTTCTCCAGA  74884        ACT_  T  C
                                TCTGGAGAA    GC GC TC
                                |||||||||    || || ||
                                AGACCTCTT    CG CG AG
                                     GTTT  C  A
GAM821   CSRP2BP   5'  TGAAGCAGCAGTGGGACCAG   70657      AGAA       C
                                CTGG    ACTGCTGC TCA
                                ||||    |||||||| |||
                                GACC    TGACGACG AGT
                                  AGGG       A
GAM821   DGKD      3'  TGAAACAACACTTTCTCCAG   60113        C  C  CC
                                CTGGAGAAA TG TG  TCA
                                ||||||||| || ||  |||
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                                GACCTCTTT AC AC  AGT
                                     C  A  AA
GAM821  DKFZP434A043 3'  TGAGGTAGTAATTTCCTCAGA  31823     GA    C
                                TCTG  GAAA TGCTGCCTCA
                                ||||  |||| ||||||||||
                                AGAC  CTTT ATGATGGAGT
                                  TC    A
GAM821  DKFZP434P0111 3'  TGAGGGTGTCTTTCCAGA    67963        A  T  TG
                                TCTGGAGA AC GC  CCTCA
                                |||||||| || ||  |||||
                                AGACCTTT TG TG  GGAGT
                                     C  _  __
GAM821  DKFZP586M1120 3'  TGAGGCAGCAGCTCCCAG    49287     A  AA
                                CTGG GA  CTGCTGCCTCA
                                |||| ||  ||||||||||
                                GACC CT  GACGACGGAGT
                                  _  C_
GAM821  ERG-1    3'  TGAGACATGTTTCTCCAGG   42102          TGC  C
                                TCTGGAGAAAC   TG CTCA
                                ||||||||||   || ||||
                                GGACCTCTTTG   AC GAGT
                                      T__  A
GAM821  FASTK    3'  TGAGGCAGAAGCTCCAGG    47690       AAACTG
                                TCTGGAG     CTGCCTCA
                                |||||||     ||||||||
                                GGACCTC     GACGGAGT
                                    GAA___
GAM821  FLJ14855  5'  GGTTCCCAGTTTTCCAGA    53766        A   CT_
                                TCTGGAGAA CTG   GCC
                                ||||||||| |||   |||
                                AGACCTTTT GAC   TGG
                                      _  CCT
GAM821  FLJ20249  3'  TGAGGAGTCCCTCCCAGA    80223      A  AACT   G
                                TCTGG GA    GCT CCTCA
                                ||||| ||    ||| |||||
                                AGACC CT    TGA GGAGT
                                  _  CCC_  _
GAM821  FLJ20730  3'  TGAAGAAGCAGTTTCTCAGA   36053     G        GCC
                                TCTG AGAAACTGCT   TCA
                                |||| ||||||||||   |||
                                AGAC TCTTTGACGA   AGT
                                  _        AGA
GAM821  FLJ21007  5'  TGAAGCTTGCACAAGCTCTCCA 48648        AAC__   T_  C
           GA                   TCTGGAGA    TGC  GC TCA
                                ||||||||    |||  || |||
                                AGACCTCT    ACG  CG AGT
                                     CGAAC   TT  A
GAM821  FLJ22938  5'  GAGGAGTTTTTCCAGA      45486          GCTG
                                TCTGGAGAAACT    CCTC
                                ||||||||||||   ||||
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                                AGACCTTTTTGA  GGAG
                                      _____
GAM821  GPT2     3' TGAGGCAGCAGCCTCTA    56772     AAA
                                TGGAG  CTGCTGCCTCA
                                |||||  ||||||||||
                                ATCTC  GACGACGGAGT
                                   C__
GAM821  KIAA0515 5' GAGGAGCTTCTCCAG      64550       ACT  G
                                CTGGAGAA  GCT CCTC
                                ||||||||  ||| ||||
                                GACCTCTT  CGA GGAG
                                    ___  _
GAM821  KIAA0542 3' GGGGCAGCTCCTCCAGG    66665       AAACT
                                TCTGGAG   GCTGCCTC
                                |||||||   ||||||||
                                GGACCTC   CGACGGGG
                                    CT___
GAM821  KIAA0561 3' GAGGGAGCTTTCCAGA     66479       AACT  G
                                TCTGGAGA   GCT CCTC
                                ||||||||   ||| ||||
                                AGACCTTT   CGA GGAG
                                     _____  G
GAM821  KIAA0652 3' TGAGGCAGCAATCTTTGG   29125   TG   AAC
                                C  GAGA  TGCTGCCTCA
                                |  ||||  ||||||||||
                                G  TTCT  ACGACGGAGT
                                 GT   A__
GAM821  KIAA1026 3' GAGACGGCTTTTTCCA     71738       CT   C
                                TGGAGAAA  GCTG CTC
                                ||||||||  |||| |||
                                ACCTTTTT  CGGC GAG
                                    __   A
GAM821  KIAA1030 3' GAGGCAGCAGTGAGCCGAGA  94981    _  AGAA
                                TCT GG   ACTGCTGCCTC
                                ||| ||   ||||||||||
                                AGA CC   TGACGACGGAG
                                  G  GAG_
GAM821  KIAA1086 3' TGAGGCAGGGGGTCCCCA   71291    A  AA  G
                                TGG GA  CT CTGCCTCA
                                ||| ||  || ||||||||
                                ACC CT  GG GACGGAGT
                                  C  GG  _
GAM821  KIAA1277 3' GAGGCAGGTTCTCAGA     65077    G   ACTG
                                TCTG AGAA   CTGCCTC
                                |||| ||||   |||||||
                                AGAC TCTT   GACGGAG
                                  _   G___
GAM821  KIAA1322 3' TGAGATAGTTTTTCCAGA   73118         CTGC
                                TCTGGAGAAACTG   CTCA
                                ||||||||||||   ||||
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                                AGACCTTTTTGAT   GAGT
                                      A___
GAM821  KIAA1634  3'  GCATCAGTCTCTTCTCCAGA  64124        ___   C
                                TCTGGAGAA  ACTG TGC
                                |||||||||  |||| |||
                                AGACCTCTT  TGAC ACG
                                    CTC   T
GAM821  KIAA1638  3'  TGAAACAACGGTGACCTCTCCA 47824       A___   C  CC
          GG                    TCTGGAGA   ACTG TG  TCA
                                ||||||||   |||| ||  |||
                                GGACCTCT   TGGC AC  AGT
                                    CCAG   A  AA
GAM821  KIAA1742  3'  AGGTATTTCTCCAGA      78137         CTGC
                                TCTGGAGAAA   TGCCT
                                ||||||||||   |||||
                                AGACCTCTTT   ATGGA

                                     _____
GAM821  KIAA1771  5'  GGGTTACCAGACCTCTCCAGA  79866       AA_  CT_
                                TCTGGAGA  CTG  GCCT
                                ||||||||  |||  ||||
                                AGACCTCT  GAC  TGGG
                                    CCA  CAT
GAM821  KIAA1831  5'  GGAGCAGTCTCTCCGGA    64525       A    G
                                TCTGGAGA ACTGCT CC
                                |||||||| |||||| ||
                                AGGCCTCT TGACGA GG
                                    C    _
GAM821  KIAA1894  3'  GAGGCAACCTTTGCCTTCTTCA 74285       ACT _______
          GA                    TCTGGAGAA  GC    TGCCTC
                                |||||||||  ||    ||||||
                                AGACTTCTT  CG    ACGGAG
                                    C__  TTTCCA
GAM821  KIAA1937  3'  GAGGCAGTGTCCCCCAGG   74071     AGAA  T
                                TCTGG   AC GCTGCCTC
                                |||||   || ||||||||
                                GGACC   TG TGACGGAG
                                  CCC_  _
GAM821  KIAA1985  3'  TGAAAAGCACTTTCTCCA   45018       C   GCC
                                TGGAGAAA TGCT  TCA
                                |||||||| ||||  |||
                                ACCTCTTT ACGA  AGT
                                    C   AA_
GAM821  LCHN      3'  TGAGATGCTTTCTCCAGA   87480        CT  TGC
                                TCTGGAGAAA  GC  CTCA
                                ||||||||||  ||  ||||
                                AGACCTCTTT  CG  GAGT
                                     __  TA_
GAM821  MGC13007  3'  CAGTTCAGTTATCTCCAGA   51277       _   __
                                TCTGGAGA AACTG  CTG
                                |||||||| |||||  |||
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                                AGACCTCT TTGAC  GAC
                                     A    TT
GAM821  MGC16385  5'  TGAAGCAGCAGCTGGGCTAGG  59543      AGAAA     C
                                TCTGG    CTGCTGC TCA
                                |||||    ||||||| |||
                                GGATC    GACGACG AGT
                                   GGGTC      A
GAM821  MGC26914  3'  TGAATAGACATTTCTCCA    59332       C  _  CC
                                TGGAGAAA TG CTG  TCA
                                |||||||| || |||  |||
                                ACCTCTTT AC GAT  AGT
                                     _ A  A_
GAM821  MRPL20    3'  AGGCATTTTTTCCAGA      36199        CTGC
                                TCTGGAGAAA    TGCCT
                                ||||||||||    |||||
                                AGACCTTTTT    ACGGA
                                      T___
GAM821  NCX       5'  GAGGCCACTCTCCGGA      32944       AAC  CT
                                TCTGGAGA   TG  GCCTC
                                ||||||||   ||  |||||
                                AGGCCTCT   AC  CGGAG
                                     C__  __
GAM821  PPP1R13B  3'  TGAGGCCCTTTCTCCAG     31660       CTGCT
                                CTGGAGAAA    GCCTCA
                                |||||||||    ||||||
                                GACCTCTTT    CGGAGT
                                     CC___
GAM821  PSKH1     3'  AGGCTCCAGCCTCTCCAGA   68791       AA   CT
                                TCTGGAGA  CTG  GCCT
                                ||||||||  |||  ||||
                                AGACCTCT  GAC  CGGA
                                     CC   CT
GAM821  PTPLA     3'  AGGTGCTTTTTCCAGA      27266        CT  T
                                TCTGGAGAAA  GC GCCT
                                ||||||||||  || ||||
                                AGACCTTTTT  CG TGGA
                                      __  _
GAM821  SEMA4G    5'  GGGCAGCTGTCTCCAGA     96330       AACT
                                TCTGGAGA    GCTGCCT
                                ||||||||    |||||||
                                AGACCTCT    CGACGGG
                                     GT__
GAM821  SPAF      3'  TGAAGCGATTTCTTTTTCCAGA 83521        CTGC_  C
                                TCTGGAGAAA    TGC TCA
                                ||||||||||    ||| |||
                                AGACCTTTTT    GCG AGT
                                      CTTTA   A
GAM821  SUN1      3'  TGAGTTTCCCAGTTTCTACAGA 47926     G      CTGC_
                                TCTG AGAAACTG    CTCA
                                |||| ||||||||    ||||
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                                AGAC TCTTTGAC    GAGT
                                  A      CCTTT
GAM821  TSPAN-2  3'  GGGTCAGTTTCTCAGA     20375     G      CT
                                TCTG AGAAACTG  GCCT
                                |||| ||||||||  ||||
                                AGAC TCTTTGAC  TGGG
                                  _      __
GAM821  USP24    3'  TGAAAATGCTGTGTTCTCCAGA 92795        _  T  TGCC
                                TCTGGAGAA AC GC   TCA
                                ||||||||| || ||   |||
                                AGACCTCTT TG CG   AGT
                                     G  T  TAAA
GAM821  LOC123096 3'  TGAGGCAGACACTCCAG    74654       AAAC  _
                                CTGGAG   TG CTGCCTCA
                                ||||||   || ||||||||
                                GACCTC   AC GACGGAGT
                                   ____  A
GAM821  LOC129831 5'  TGAGACAGCAGCGGTGGCAGA  75398     GAGAA     ___
                                TCTG    ACTGCTGC  CTCA
                                ||||    ||||||||  ||||
                                AGAC    TGGCGACG  GAGT
                                  GG___      ACA
GAM821  LOC134637 3'  TGAGAACACCTTCTCCAGG   75693        AC  CTGC
                                TCTGGAGAA  TG   CTCA
                                |||||||||  ||   ||||
                                GGACCTCTT  AC   GAGT
                                     CC  AA__
GAM821  LOC146420 3'  TGAACTTCCAGATTCTCCAGA  84653        A   CTGCC
                                TCTGGAGAA CTG    TCA
                                ||||||||| |||    |||
                                AGACCTCTT GAC    AGT
                                     A   CTTCA
GAM821  LOC147711 5'  TGAGCAGGCAAGTCTCTTCAGA 79117        A  _  GC
                                TCTGGAGA ACT GCT  CTCA
                                |||||||| ||| |||  ||||
                                AGACTTCT TGA CGG  GAGT
                                     C   A   AC
GAM821  LOC148753 3'  TGAGACTCCATTTTCTCCAGG  85373        C  CTGC
                                TCTGGAGAAA TG   CTCA
                                |||||||||| ||   ||||
                                GGACCTCTTT AC   GAGT
                                      T  CTCA
GAM821  LOC150290 3'  TGAGGCAGATGGTGCCCAGA   80592     AGAA   _
                                TCTGG   ACTG CTGCCTCA
                                |||||   |||| ||||||||
                                AGACC   TGGT GACGGAGT
                                  CG__   A
GAM821  LOC153218 5'  TGAAATAGAACTTTTCCAGA   81658        ACTG   CC
                                TCTGGAGAA   CTG  TCA
                                |||||||||   |||  |||
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                                AGACCTTTT   GAT  AGT
                                     CAA_   AA
GAM821   LOC153769 3'  AGGCAGCATTTCAGA      81805       AAAC
                                TCTGGAG    TGCTGCCT
                                |||||||    ||||||||
                                AGACTTT    ACGACGGA
                                    ____
GAM821   LOC157570 5'  TGAGGCTTTTTCTTCAGA    82397        CTGCT
                                TCTGGAGAAA    GCCTCA
                                ||||||||||    ||||||
                                AGACTTCTTT    CGGAGT
                                      TT___
GAM821   LOC197259 5'  TGAGGCAGTGGCCTCCGGA   89304       AAA TG
                                TCTGGAG   C  CTGCCTCA
                                |||||||   |  ||||||||
                                AGGCCTC   G  GACGGAGT
                                    C__ GT
GAM821   LOC199923 3'  TGAGTTAGCCAGTTTCTTCAGA 89879          _  C
                                TCTGGAGAAACTG CTG CTCA
                                |||||||||||| ||| ||||
                                AGACTTCTTTGAC GAT GAGT
                                       C   T
GAM821   LOC200940 3'  TGAGGCAGGCGGATCTCCTGA  90398    T    AA   _
                                TC GGAGA  CTGC TGCCTCA
                                || |||||  |||| |||||||
                                AG CCTCT  GGCG ACGGAGT
                                 T    A_   G
GAM821   LOC201685 3'  AGGAGCTATTTTCCAGA     91834        ACT   G
                                TCTGGAGAA   GCT CCT
                                |||||||||   ||| |||
                                AGACCTTTT   CGA GGA
                                     AT_  _
GAM821   LOC205327 3'  AGTCAATGTTTCTCCAGA    91067         TGC  C
                                TCTGGAGAAAC   TG CT
                                ||||||||||   || ||
                                AGACCTCTTTG   AC GA
                                      TA_  T
GAM821   LOC221288 3'  TGAAGCAGCAGTATCTAGA   95264       GAA       C
                                TCTGGA   ACTGCTGC TCA
                                ||||||   |||||||| |||
                                AGATCT   TGACGACG AGT
                                   A__       A
GAM821   LOC222057 3'  AGGTCAGCCTCTCCAGG     94345        AACT   _
                                TCTGGAGA    GCTG CCT
                                ||||||||    |||| |||
                                GGACCTCT    CGAC GGA
                                     C___    T
GAM821   LOC222057 3'  GAGTCAGCCTCTCCAGG     94354        AACT    C
                                TCTGGAGA    GCTG CTC
                                ||||||||    |||| |||
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                                GGACCTCT   CGAC GAG
                                    C___   T
GAM821  LOC253254 5'  TGAGAAGAACTTCTTCAGA   98908       ACTG  GC
                                TCTGGAGAA   CT  CTCA
                                |||||||||   ||  ||||
                                AGACTTCTT   GA  GAGT
                                    CAA_  A_
GAM821  LOC254672 3'  GAGGTGTTCTCCAGA      96295       ACTGC
                                TCTGGAGAA   TGCCTC
                                |||||||||   ||||||
                                AGACCTCTT   GTGGAG
                                    _____
GAM821  LOC255975 3'  GAGTCAGCCTCTCCAGG    97582       AACT   C
                                TCTGGAGA   GCTG CTC
                                ||||||||   |||| |||
                                GGACCTCT   CGAC GAG
                                    C___   T
GAM821  LOC256789 3'  TGAGGCTGTACTCTCTAGA  99312       AAC  T
                                TCTGGAGA  TGC GCCTCA
                                ||||||||  ||| ||||||
                                AGATCTCT  ATG CGGAGT
                                    C__   T
GAM821  LOC257336 5'  GGGCCCTAGTCCTCCAGA   97900       AA   CT
                                TCTGGAG  ACTG  GCCT
                                |||||||  ||||  ||||
                                AGACCTC  TGAT  CGGG
                                   C_   CC
GAM821  LOC257449 3'  AGGTATTTCTCCAGA      63373       CTGC
                                TCTGGAGAAA   TGCCT
                                ||||||||||   |||||
                                AGACCTCTTT   ATGGA
                                    _____
GAM821  LOC91923  5'  AGAGTTCCAGTTTCTCCA   68169        CT  _
                                TGGAGAAACTG  GC CT
                                ||||||||||  ||  ||
                                ACCTCTTTGAC  TG GA
                                      CT  A
GAM821  LOC92876  5'  AGAGTTCCAGTTTCTCCA   71346        CT  _
                                TGGAGAAACTG  GC CT
                                ||||||||||  ||  ||
                                ACCTCTTTGAC  TG GA
                                      CT  A
GAM821  LOC93496  3'  TGAAACAGACTTACACTTCTTC 72863       ACTG____  CC
          AGA                    TCTGGAGAA      CTG  TCA
                                |||||||||      |||  |||
                                AGACTTCTT      GAC  AGT
                                    CACATTCA   AA
GAM822  CYP4F3    3'  CTGTATTCACAGCTGCTT    8004        CGTAAAAC
                                GAGCAGCTG      ATACAG
                                |||||||||      ||||||
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                                TTCGTCGAC      TATGTC
                                     ACT_____
GAM822  EN2     5'  CTGCATGCGCGCAGCTCTC   9258     C      AAAA  A
                                GAG AGCTGCGT   CAT CAG
                                ||| ||||||||   ||| |||
                                CTC TCGACGCG   GTA GTC
                                  _      C___  C
GAM822  GPR44   3'  CTGTATGCAACAGGCACTC   17697    CA  GC  AAAA
                                GAG  GCT  GT   CATACAG
                                |||  |||  ||   |||||||
                                CTC  CGG  CA   GTATGTC
                                  A_   A_  AC__
GAM822  NUCB1   3'  CCTGTATGCCCACAGCTACT  21639    C   CGTAAAA
                                AG AGCTG      CATACAGG
                                || |||||      ||||||||
                                TC TCGAC      GTATGTCC
                                 A    ACCC___
GAM822  SYNGR3  3'  CCTAGTACTCCACAAGCTGCTC 16118       GC  AAAACA  _
                                GAGCAGCT  GT     TAC AGG
                                ||||||||  ||     ||| |||
                                CTCGTCGA  CA     ATG TCC
                                     A_  CCTC__   A
GAM822  WBSCR14 3'  CCTGCTGCTCACTCAGCTGC  53094       C  AAAA  TA
                                GCAGCTG GT    CA  CAGG
                                ||||||| ||    ||  ||||
                                CGTCGAC CA    GT  GTCC
                                     T  CTC_  C_
GAM822  WBSCR14 3'  CCTGCTGCTCACTCAGCTGC  53096       C  AAAA  TA
                                GCAGCTG GT    CA  CAGG
                                ||||||| ||    ||  ||||
                                CGTCGAC CA    GT  GTCC
                                     T  CTC_  C_
GAM822  DKFZP434F1735 3'  ATGCTTTAGCAGCTGCTC    32114         G    A
                                GAGCAGCTGC TAAA CAT
                                |||||||||| |||| |||
                                CTCGTCGACG ATTT GTA
                                     _    C
GAM822  ELL2    3'  CTGCATTTCGAAGCTGCTC   24893        G  T   ACATA
                                GAGCAGCT CG AAA    CAG
                                |||||||| || |||    |||
                                CTCGTCGA GC TTT    GTC
                                     A  _   AC___
GAM822  FLJ20730 3'  CCTGTATGTTTACAGACT    36049    _  CGTA
                                AG CTG    AAACATACAGG
                                || |||    ||||||||||
                                TC GAC    TTTGTATGTCC
                                 A  A___
GAM822  HSPB7   3'  CCAGGGTGTCAACAGCTGCTC  27783        CGTAAA   ACA
                                GAGCAGCTG     ACAT   GG
                                |||||||||     ||||   ||
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                                CTCGTCGAC     TGTG   CC
                                     AAC___    GGA
GAM822  KIAA0984  3'  TATGCTTTACGCAGTTGCTC   66143             A
                                GAGCAGCTGCGTAAA CATA
                                |||||||||||||| ||||
                                CTCGTTGACGCATTT GTAT
                                       C
GAM822  LOC201627 3'  CCTACATGTTTCACAGTTCAGC 90451        C___  A     AC
          TGCT                    AGCAGCTG   GT AAACAT  AGG
                                |||||||   || ||||||  |||
                                TCGTCGAC   CA TTTGTA  TCC
                                     TTGA  C     CA
GAM823  ADAR     3'  CTGCAGGGCGGGCAAGG     32361    A    CAG  T
                                CC TGCCC   GC CCTGCAG
                                || |||||   || |||||||
                                GG ACGGG   CG GGACGTC
                                 A    ___ _
GAM823  AIRE     3'  TGGGAGCCTGAGGCATGAGAA  7247     C     C
                                TTC CATGCC CAGGCTCCTG
                                ||| |||||| ||||||||||
                                AAG GTACGG GTCCGAGGGT
                                  A     A
GAM823  ANG      5'  GCAGGAGCCTGTGTTGG     8557     T  CC
                                CCA GC  CAGGCTCCTGC
                                ||| ||  ||||||||||
                                GGT TG  GTCCGAGGACG
                                  _  T_
GAM823  BCAS1    3'  CTCGGGAGCCCAACGCACGAGA 14711    CCA   CCCA      C
          A                      TTC   TGC    GGCTCCTG AG
                                |||   |||   |||||||| ||
                                AAG   ACG    CCGAGGGC TC
                                  AGC   CAAC       _
GAM823  DAG1     3'  CTGCAGGATGTAACATGG    16553      CCCCAG  _
                                CCATG     GC TCCTGCAG
                                |||||     || ||||||||
                                GGTAC     TG AGGACGTC
                                   AA____  T
GAM823  GPRK7    3'  CGGGAGCCTGAGGCAGGAGAA  58313     _  A   C
                                TTC CC TGCC CAGGCTCCTG
                                ||| || |||| ||||||||||
                                AAG GG ACGG GTCCGAGGGC
                                  A  _   A
GAM823  KIF1B    3'  TGGGAGCCTGAGGCAGGAGAA  31273     _  A   C
                                TTC CC TGCC CAGGCTCCTG
                                ||| || |||| ||||||||||
                                AAG GG ACGG GTCCGAGGGT
                                  A  _   A
GAM823  NCAM1    5'  CTGCAGGGGGGGGGGCACAGAA 7040     CCA     AGG
                                TTC   TGCCCC   CTCCTGCAG
                                |||   ||||||   |||||||||
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                                AAG  ACGGGG  GGGGACGTC
                                  AC_    GG_
GAM823  NOS1    3'  CTGCAGGGTCCCCAAGGATGG  7095      G  CCA_  CT
                                CCAT CC   GG  CCTGCAG
                                |||| ||   ||  |||||||
                                GGTA GG   CC  GGACGTC
                                  _ AACC  TG
GAM823  PDGFRB  3'  TGCCCCAGGGACATGGGAA   66584       _  CA  CTCCT
                                TTCCCATG CCC  GG   GCA
                                |||||||| |||  ||   |||
                                AAGGGTAC GGG  CC   CGT
                                    A  AC  _____
GAM823  RAB31   3'  CTGCAGGGGGCGGGGCAGGAA  23440     CA    AGG
                                TTCC  TGCCCC  CTCCTGCAG
                                ||||  ||||||  |||||||||
                                AAGG  ACGGGG  GGGGACGTC
                                  __    CG_
GAM823  SCN4A   3'  CTGCGTTCCCAGACCATGGGAA 6200        CCCCA  CTCC
                                TTCCCATG   GG   TGCAG
                                ||||||||   ||   |||||
                                AAGGGTAC   CC   GCGTC
                                    CAGAC  TT__
GAM823  WHSC1   3'  CTGCAATGACTGCAGGGCTGGG 24667      T   __  GCTCC
          AA                  TTCCCA GCCC  CAG   TGCAG
                              |||||| ||||  |||   |||||
                              AAGGGT CGGG  GTC   ACGTC
                                _   AC   AGTA_
GAM823  WHSC1   3'  CTGCAATGACTGCAGGGCTGGG 24668      T   __  GCTCC
          AA                  TTCCCA GCCC  CAG   TGCAG
                              |||||| ||||  |||   |||||
                              AAGGGT CGGG  GTC   ACGTC
                                _   AC   AGTA_
GAM823  WHSC1   3'  CTGCAATGACTGCAGGGCTGGG 24669      T   __  GCTCC
          AA                  TTCCCA GCCC  CAG   TGCAG
                              |||||| ||||  |||   |||||
                              AAGGGT CGGG  GTC   ACGTC
                                _   AC   AGTA_
GAM823  ZFP36L1 3'  CTGCAGGAAGGAAGGCTG   18201   T  __  AGGC
                              CA GCC  CC   TCCTGCAG
                              || |||  ||   ||||||||
                              GT CGG  GG   AGGACGTC
                                _  AA  A___
GAM823  C20orf64 5' CAAGAGCCCTTCCTGCAGGGAA 54334     A  CCCA__   C
                              TTCCC TGC    GGCTC TG
                              ||||| |||    ||||| ||
                              AAGGG ACG    CCGAG AC
                                _  TCCTTC   A
GAM823  DRIL2   3'  CTGCAGGGTGTGGGCAGAGAA  22350    CCA   C G  T
                              TTC  TGCCC A GC CCTGCAG
                              |||  ||||| | || |||||||
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                                AAG   ACGGG T TG GGACGTC
                                  AG_     _ G  _
GAM823  FEM-2    3'  CTGCAGGGCCAAGCCACAGGAA 28312      CAT_  CCCA   T
                                TTCC    GC    GGC CCTGCAG
                                ||||    ||    ||| |||||||
                                AAGG    CG    CCG GGACGTC
                                  ACAC  AA__   _
GAM823  FLJ10737 3'  CTGCAGTCCAAGCTGAACATGG 37054        CCCCA    C___
           GAA                    TTCCCATG    GGCT    CTGCAG
                                ||||||||    ||||    ||||||
                                AAGGGTAC    TCGA    GACGTC
                                    AAG__    ACCT
GAM823  FLJ10898 5'  CTGCCAAACCTGCAACATGGGA 60133        CCC    CTCCT
           A                     TTCCCATG   CAGG    GCAG
                                ||||||||   ||||    ||||
                                AAGGGTAC   GTCC    CGTC
                                    AAC    AAAC_
GAM823  FLJ11618 3'  CTGCAGGGGGAAGAGCCGGGAA 42624      AT  CCCAGG
                                TTCCC  GC     CTCCTGCAG
                                |||||  ||     |||||||||
                                AAGGG  CG     GGGGACGTC
                                  C_  AGAAG_
GAM823  FLJ12287 5'  TGCCTCTGGGGCCTGGGAA   42564       T       CTCCT
                                TTCCCA GCCCCAGG    GCA
                                |||||| ||||||||    |||
                                AAGGGT CGGGGTCT    CGT
                                   C       C_____
GAM823  FLJ14129 3'  TGGGAGCCTGGGGCAGGAGAA  48814     _  A
                                TTC CC TGCCCCAGGCTCCTG
                                ||| || ||||||||||||||
                                AAG GG ACGGGGTCCGAGGGT
                                  A  _
GAM823  KIAA0187 3'  CTGCAGGAGGAGGAACAGAGAA 29250     CCA  CC  AGG
                                TTC   TG  CC   CTCCTGCAG
                                |||   ||  ||   |||||||||
                                AAG   AC  GG   GAGGACGTC
                                  AG_  AA  AG_
GAM823  KIAA0416 5'  GGAAAGCCTGGGACACAGAA   32093     CCA  C      __
                                TTC   TG CCCAGGC  TCC
                                |||   || |||||||  |||
                                AAG   AC GGGTCCG  AGG
                                  AC_  A      AA
GAM823  KIAA1266 3'  CTGCAAGGGCGAGCATGGGA   66695        CCCAG    C
                                TCCCATGC    GCTC TGCAG
                                ||||||||    |||| |||||
                                AGGGTACG    CGGG ACGTC
                                    AG____    A
GAM823  KIAA1483 3'  CTGCAGGGAAAAGGATATAGGA 70434      C   C  CAGG T
           A                     TTCC ATG CC    C CCTGCAG
                                |||| ||| ||    | |||||||
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                                AAGG TAT GG    G GGACGTC
                                  A  A  AAAA _
GAM823  KIAA1706  3'  TGCAGTGAGAGCATGGGA    94372        CCCAGG  _
                                TCCCATGC     CTC CTGCA
                                ||||||||     ||| |||||
                                AGGGTACG     GAG GACGT
                                    A_____   T
GAM823  KIAA1715  3'  CTCAGGAGCCTGAGGCAGGAGA 68684     _ A   C       C
          A                      TTC CC TGCC CAGGCTCCTG AG
                                 ||| || |||| |||||||||| ||
                                 AAG GG ACGG GTCCGAGGAC TC
                                   A _   A        _
GAM823  KIAA1981  3'  CAGGAGCCAAGGTCACAGAA   89710    CCA  C  CA
                                 TTC   TG CC  GGCTCCTG
                                 |||   || ||  ||||||||
                                 AAG   AC GG  CCGAGGAC
                                   AC_  T  AA
GAM823  MCAM      3'  CAGGAACCTGGGGGCCTGTGAA 22457     C  T    _  C
                                 TTC CA GCCCC AGG TCCTG
                                 ||| || ||||| ||| |||||
                                 AAG GT CGGGG TCC AGGAC
                                   T  C    G   A
GAM823  MRPS24    3'  CTGCAGAGAATGGAAACGTGGG 50130        CC_  GG   C
          AA                     TTCCCATG   CCA  CTC TGCAG
                                 ||||||||   |||  ||| |||||
                                 AAGGGTGC   GGT  GAG ACGTC
                                     AAA   AA  _
GAM823  MSE55     3'  TGCAGGACAGACATGGGAG   23916        CCCCAGGC
                                 TTCCCATG       TCCTGCA
                                 ||||||||       |||||||
                                 GAGGGTAC       AGGACGT
                                     AGAC____
GAM823  OS4       3'  CTGCTTTGTGCTAAAAGCATGG 20388        CCCA   TCCT_
          GAA                      TTCCCATGC   GGC    GCAG
                                   |||||||||   |||    ||||
                                   AAGGGTACG   TCG    CGTC
                                       AAAA   TGTTT
GAM823  PASK      5'  CAGGGTCTCGCCTGGGGCATTA 31405     CC        ____
          GAA                      TTC  ATGCCCCAGGC   TCCTG
                                   |||  ||||||||||   |||||
                                   AAG  TACGGGGTCCG   GGGAC
                                     AT         CTCT
GAM823  PRO1163   3'  CTGAATGAGCCTGGGGCA    38323          CTG
                                   TGCCCCAGGCTC   CAG
                                   ||||||||||||   |||
                                   ACGGGGTCCGAG   GTC
                                          TAA
GAM823  THEA      3'  CTCAGGAAGCTGAGGCACAAGA 66887     CCA   C   GC    C
          A                        TTC   TGCC CAG  TCCTG AG
                                   |||   |||| |||  ||||| ||
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                                AAG   ACGG GTC  AGGAC TC
                                  AAC    A   GA    _
GAM823  WFDC3    3'  GCTGACCAGAGCATGGGAA   98702        CCCA  C  CT
                                TTCCCATGC    GG TC  GC
                                |||||||||    || ||  ||
                                AAGGGTACG    CC AG  CG
                                     AGA_  _  T_
GAM823  LOC122726 5'  CTGCAGGAAACACTGAGGCTTG 76103       T   C   GC__
          GGAA                    TTCCCA GCC CAG    TCCTGCAG
                                |||||| ||| |||    ||||||||
                                AAGGGT CGG GTC    AGGACGTC
                                   T   A   ACAA
GAM823  LOC129303 3'  CTGCAGGAATTGGGGGCTGGGA 75373       T     AG C
          A                      TTCCCA GCCCC  G TCCTGCAG
                                |||||| |||||  | ||||||||
                                AAGGGT CGGGG  T AGGACGTC
                                   _    GT A
GAM823  LOC132617 5'  CTGCAGATCGAGGCATGGGA   76415        CCA  CTC
                                TCCCATGCC   GG   CTGCAG
                                |||||||||   ||   ||||||
                                AGGGTACGG   CT   GACGTC
                                     AG_  A__
GAM823  LOC145945 5'  AGGGCCTGGACCATAGAA    84563     CC   CC     T
                                TTC  ATG  CCAGGC CCT
                                |||  |||  |||||| |||
                                AAG  TAC  GGTCCG GGA
                                  A_   CA     _
GAM823  LOC146332 3'  CAGGAGCCTGGGGCCTGTGGA  78353     _  T
                                TCC CA GCCCCAGGCTCCTG
                                ||| || ||||||||||||||
                                AGG GT CGGGGTCCGAGGAC
                                  T  C
GAM823  LOC146714 5'  TGCAGGGCAGGCACAGGGA   84754      A_    CCAG  T
                                TCCC  TGCC    GC CCTGCA
                                ||||  ||||    || ||||||
                                AGGG  ACGG    CG GGACGT
                                   AC    A___  _
GAM823  LOC147958 3'  CTGCAGGGCAGGCAGCAGAA   88523     CCA    CCAG  T
                                TTC   TGCC    GC CCTGCAG
                                |||   ||||    || |||||||
                                AAG   ACGG    CG GGACGTC
                                   ACG    A___  _
GAM823  LOC149501 3'  CTGCAAGAGCCTGGCTGGGAA  75800       T   CC     C
                                TTCCCA GCC  AGGCTC TGCAG
                                |||||| |||  |||||| |||||
                                AAGGGT CGG  TCCGAG ACGTC
                                   _   __     A
GAM823  LOC150397 3'  CAGGAGCCTGAGTGAAGGA   80655     CA   CC
                                TCC  TGC  CAGGCTCCTG
                                |||  |||  ||||||||||
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                                AGG  GTG  GTCCGAGGAC
                                  AA   A_
GAM823   LOC150397 3'  GCAGGAGCCTGCAGGAGA    80664    _  A   CCC
                                TC CC TGC   AGGCTCCTGC
                                || || |||   ||||||||||
                                AG GG ACG   TCCGAGGACG
                                 A  _  ___
GAM823   LOC150517 5'  CTGCAGGTAGGAGCACAGAA   80725    CCA   C  AGGCT
                                TTC   TGC CC    CCTGCAG
                                |||   ||| ||    |||||||
                                AAG   ACG GG    GGACGTC
                                  AC_   A  AT___
GAM823   LOC153688 3'  TGGGAGGCTGGGGCATGAGAA  87341     C        G
                                TTC CATGCCCCAG CTCCTG
                                ||| |||||||||| ||||||
                                AAG GTACGGGGTC GAGGGT
                                  A         G
GAM823   LOC154849 3'  CTGCAGGAGGTGGAAGATG   60941    GCC   GG
                                CAT   CCA  CTCCTGCAG
                                |||   |||  |||||||||
                                GTA   GGT  GAGGACGTC
                                  GAA   G_
GAM823   LOC162137 3'  GCAGGAGCTTCCCATAAAGAA  88480    CC_   CCCC
                                TTC   ATG    AGGCTCCTGC
                                |||   |||    ||||||||||
                                AAG   TAC    TTCGAGGACG
                                  AAA   CC__
GAM823   LOC219654 3'  CAGGAGCCCAGGGGATGGGAA  92925        G   CA
                                TTCCCAT CCC  GGCTCCTG
                                ||||||| |||  ||||||||
                                AAGGGTA GGG  CCGAGGAC
                                    G   AC
GAM823   LOC254552 5'  CAGGAGCCCGGGGCTGG     96422     T    A
                                CCA GCCCC GGCTCCTG
                                ||| ||||| ||||||||
                                GGT CGGGG CCGAGGAC
                                  _     C
GAM823   LOC255042 3'  CTCGGGAGCCTGAGGCAGGAGA 97042     _  A   C        C
            A                    TTC CC TGCC CAGGCTCCTG AG
                                ||| || |||| |||||||||| ||
                                AAG GG ACGG GTCCGAGGGC TC
                                  A  _    A        _
GAM823   LOC257000 3'  CTGCAGGACTCAGAGCATGG   98587       CCCA  C
                                CCATGC    GG TCCTGCAG
                                ||||||    || ||||||||
                                GGTACG    TC AGGACGTC
                                   AGAC  _
GAM823   LOC91750  3'  TGGGGGCCTGAGGCACGAGAA  67659     CCA    C
                                TTC   TGCC CAGGCTCCTG
                                |||   |||| ||||||||||
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                                AAG   ACGG GTCCGGGGGT
                                  AGC    A
GAM824  GNPI     3'  AATCAGAAAAAAAATATCTG   19617       GC  C
                                TAGATG  TT TTTCTGATT
                                ||||||  || |||||||||
                                GTCTAT  AA AAAGACTAA
                                   AA  A
GAM824  HEPH     5'  AAGAAGACCATCTATAAA    29646          _
                                TTTATAGATGG CTTCTT
                                |||||||||||| ||||||
                                AAATATCTACC GAAGAA
                                      A
GAM824  PAX6     5'  CAGAAAGGATGCCTCATAAA   6064       A  T  _
                                TTTAT GA GGC TTCTTTCTG
                                ||||| || ||| |||||||||
                                AAATA CT CCG AGGAAAGAC
                                  _ _   T
GAM824  PAX6     5'  CAGAAAGGATGCCTCATAAA   9632       A  T  _
                                TTTAT GA GGC TTCTTTCTG
                                ||||| || ||| |||||||||
                                AAATA CT CCG AGGAAAGAC
                                  _ _   T
GAM824  LOC157507 5'  AAAGAAGCCATCCATGAA    82375       A
                                TTTAT GATGGCTTCTTT
                                ||||| ||||||||||||
                                AAGTA CTACCGAAGAAA
                                   C
GAM824  LOC91380  5'  AAAGAAGCCATTTATAAA    66429
                                TTTATAGATGGCTTCTTT
                                ||||||||||||||||||
                                AAATATTTACCGAAGAAA

GAM825  LIMK1    3'  CACCGAGACCTCAACTCCCACA 34137      C    ATCAA_
          AC                      GTTG GGGA     GTTTTGGTG
                                ||||| ||||     |||||||||
                                CAAC CCCT     CAGAGCCAC
                                  A    CAACTC
GAM825  C8orf2   3'  CAGAGCTTGATCACCACAACT  24147       C  GA
                                AGTTG GG  ATCAAGTTTTG
                                |||||| ||  ||||||||||||
                                TCAAC CC  TAGTTCGAGAC
                                   A  AC
GAM825  C8orf2   3'  CAGAGCTTGATCACCACAACT  24148       C  GA
                                AGTTG GG  ATCAAGTTTTG
                                |||||| ||  ||||||||||||
                                TCAAC CC  TAGTTCGAGAC
                                   A  AC
GAM825  SAST     5'  CAGAACTTGATCCTCCGCAAC  63659        _ A
                                GTTGCGG G ATCAAGTTTTG
                                ||||||| | ||||||||||||
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                                CAACGCC C TAGTTCAAGAC
                                    T C
GAM825  LOC201911 5'  GCCCGCTTCCCGCAAC     91866        ATCA   TTT
                                GTTGCGGGA   AGT   GGT
                                |||||||||   |||   |||
                                CAACGCCCT   TCG   CCG
                                     _____  C__
GAM826  CD28    3'  AGGTGCCCTGGTGAGAGCTC  21550      A      TT_
                                GAGCTC TCACCAGG   CCT
                                ||||||| ||||||||  |||
                                CTCGAG AGTGGTCC   GGA
                                    _      CGT
GAM826  CYP2B6  3'  AGGCTGGTGGTGAGCTC     7551           GTT
                                GAGCTCATCACCAG   CCT
                                ||||||||||||||   |||
                                CTCGAGTGGTGGTC   GGA
                                         ____
GAM826  DSCAM   5'  GAGTGCCCGGGATGAGCTC   9133        A  A   TC
                                GAGCTCATC CC GGT  CTC
                                ||||||||| || |||  |||
                                CTCGAGTAG GG CCG  GAG
                                     _ C   T_
GAM826  FLT3    3'  GGAGGAGCTGATAATGAACTT  15935    C   CACCA
                                GAG TCAT    GGTTCCTCC
                                ||| ||||    |||||||||
                                TTC AGTA    TCGAGGAGG
                                  A   ATAG_
GAM826  IFRD1   3'  GGGAGGATGGCATGAGC     60754      CA   GGT
                                GCTCAT  CCA   TCCTCCC
                                ||||||  |||   |||||||
                                CGAGTA  GGT   AGGAGGG
                                   C_   ____
GAM826  SF3A1   3'  GAGGAACCTGCTGTCAAGT   20807     CAT  C
                                GCT   CA CAGGTTCCTC
                                |||   || ||||||||||
                                TGA   GT GTCCAAGGAG
                                  ACT  C
GAM826  SUFU    3'  GGAGGAAGTGGGTGAGCTC   32938       CA   GG
                                GAGCTCAT  CCA  TTCCTCC
                                |||||||  |||  |||||||
                                CTCGAGTG  GGT  AAGGAGG
                                     __   G_
GAM826  APOARGC  3'  GGAAGAACCTGCCAAGCTT   44677      CATCAC      C
                                GAGCT     CAGGTTC TCC
                                |||||     ||||||| |||
                                TTCGA     GTCCAAG AGG
                                   ACC____      A
GAM826  C16orf5  3'  AGGGGGCTGGCAATGAGCTT  26347       CA   G
                                GAGCTCAT  CCAG TTCCT
                                ||||||||  |||| |||||
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                                TTCGAGTA  GGTC GGGGA
                                    AC    G
GAM826  DKFZP586D2223 5'  GAGGCGCGCCCTGGTGACAGCT 38292      CA      TT___
          C                   GAGCT  TCACCAGG    CCTC
                              |||||  ||||||||    ||||
                              CTCGA  AGTGGTCC    GGAG
                                C_      CGCGC
GAM826  FHOD2    3'  GGAAGAATTTTAAAATGAGCTC 74262       CACC    C
                              GAGCTCAT   AGGTTC TCC
                              ||||||||   |||||| |||
                              CTCGAGTA   TTTAAG AGG
                                   AAAT    A
GAM826  FLJ10826  5'  AGGAACTGATGAACTT     37240    C    CCAG
                              GAG TCATCA   GTTCCT
                              ||| ||||||   ||||||
                              TTC AGTAGT   CAAGGA
                                A    _____
GAM826  GALNT12   5'  GAGAGGGCCTGGTGCGAGC   45319     AT       _
                              GCTC  CACCAGGTTC CTC
                              ||||  |||||||||| |||
                              CGAG  GTGGTCCGGG GAG
                                C_       A
GAM826  KIAA1404  3'  AGGAACAGAGTATGAGCTC   62680       C  CAG
                              GAGCTCAT AC   GTTCCT
                              |||||||| ||   ||||||
                              CTCGAGTA TG   CAAGGA
                                   _ AGA
GAM826  MGC13186  3'  GAGGAGCCTGATGGAGC    51297     AT  C
                              GCTC  CA CAGGTTCCTC
                              ||||  || ||||||||||
                              CGAG  GT GTCCGAGGAG
                                 __ A
GAM826  MGC15476  3'  CGAGAGGAATGGGGAGGAGC   59608     A  A  AG     C
                              GCTC TC CC  GTTCCTC CG
                              |||| || ||  ||||||| ||
                              CGAG AG GG  TAAGGAG GC
                                G _ G_      A
GAM826  PSMD12    3'  AGGAGAGGTGATGAGCC     12534    A       AGG
                              G GCTCATCACC   TTCCT
                              | ||||||||||   |||||
                              C CGAGTAGTGG   GAGGA
                              _        A__
GAM826  RNF30     3'  CGGGAGGATCTCAATAAAGAAC 51693     C  ATCACCA  T
          TC                    GAG TC      GG TCCTCCCG
                              ||| ||      || ||||||||
                              CTC AG      TC AGGAGGGC
                                A  AAATAAC  T
GAM826  LOC124369 5'  GGGAACCTAGTAACAGACTC   74763     _  CATC  C
                              GAG CT    AC AGGTTCCT
                              ||| ||    || ||||||||
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                                CTC GA   TG TCCAAGGG
                                  A  CAA_  A
GAM826  LOC144347 3'  CGGGAGGATGGACACGATGAGC 77305        A___   GGT
           TC                     GAGCTCATC   CCA  TCCTCCCG
                                  |||||||||   |||  ||||||||
                                  CTCGAGTAG   GGT  AGGAGGGC
                                      CACA  ___
GAM826  LOC150157 5'  GAGGCTGCACGTGAGCTC   86025       CAC  GTT
                                  GAGCTCAT  CAG  CCTC
                                  ||||||||  |||  ||||
                                  CTCGAGTG  GTC  GGAG
                                      CAC  ___
GAM826  LOC163682 3'  CGGGAGGAAGGACAAGAGCTC 88402      ATCA  AGG
                                  GAGCTC   CC  TTCCTCCCG
                                  ||||||   ||  |||||||||
                                  CTCGAG   GG  AAGGAGGGC
                                     AACA  ___
GAM826  LOC196890 5'  GAGGCTGCACGTGAGCTC   91226       CAC  GTT
                                  GAGCTCAT  CAG  CCTC
                                  ||||||||  |||  ||||
                                  CTCGAGTG  GTC  GGAG
                                      CAC  ___
GAM826  LOC200782 5'  GGAAGAACCCGGAGGGGCCC  91076   A   ATCA  A    C
                                  G GCTC   CC GGTTC TCC
                                  | ||||   || ||||| |||
                                  C CGGG   GG CCAAG AGG
                                   C   GA__ C    A
GAM826  LOC220549 5'  GGAGATGGACGGTGATGAGCTC 94509          AG   __
                                  GAGCTCATCACC  GTTC  CTCC
                                  ||||||||||||  ||||  ||||
                                  CTCGAGTAGTGG  CAGG  GAGG
                                        __   TA
GAM826  LOC255374 5'  GGGAGGATCACATGAGC    97792      CACCA   T
                                  GCTCAT    GGT CCTCCC
                                  ||||||    ||| ||||||
                                  CGAGTA    CTA GGAGGG
                                     CA___  _
GAM826  LOC93589  3'  GGGAAGCCAGCGTGAGCTC  73053       CACCA   CC
                                  GAGCTCAT   GGTT  TCCC
                                  ||||||||   ||||  ||||
                                  CTCGAGTG   CCGA  AGGG
                                      CGA__   __
GAM827  ATP2B4   3'  TGTTTTTCAATTTTTCC    70850          TGT
                                  GGAAAAATTGAA  GACA
                                  ||||||||||||  ||||
                                  CCTTTTTAACTT  TTGT
                                        T__
GAM827  CCNT2    3'  TGTTTAGGTCAATTTTTCCT  55249          ATGT
                                  AGGAAAAATTGA   GACA
                                  ||||||||||||   ||||
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                                TCCTTTTTAACT   TTGT
                                     GGAT
GAM827  CSF2RB   3'  CACACATTTTTCCTGT     6369          TGAA
                                ACAGGAAAAAT   TGTG
                                ||||||||||   ||||
                                TGTCCTTTTTA   ACAC
                                   C___
GAM827  DBCCR1   3'  CATGGACTTTTCCTGTTG    28239         A  GA
                                TAACAGGAAAA TT  ATG
                                |||||||||| ||  |||
                                GTTGTCCTTTT AG  TAC
                                   C  G_
GAM827  PRDM2    3'  TCACAGTTTTCCTGTT      25280         ATTGAA
                                AACAGGAAAA     TGTGA
                                |||||||||     |||||
                                TTGTCCTTTT     ACACT
                                   G_____
GAM827  RAD21    3'  CACTGGCAATCTTCCTGTTA  21835        AA   AAT
                                TAACAGGAA  ATTG   GTG
                                |||||||||  ||||   |||
                                ATTGTCCTT  TAAC   CAC
                                   C_   GGT
GAM827  SNAP25   3'  GTCACTTTTTTCCTGT     56424         TTGAAT
                                ACAGGAAAAA     GTGAC
                                |||||||||     |||||
                                TGTCCTTTTT     CACTG
                                   T_____
GAM827  SNAP25   3'  GTCACTTTTTTCCTGT     13270         TTGAAT
                                ACAGGAAAAA     GTGAC
                                |||||||||     |||||
                                TGTCCTTTTT     CACTG
                                   T_____
GAM827  SP100    3'  TGTTTCCAATCTGTCCTGTTA  13339        AAA   AATGT
                                TAACAGGA   ATTG    GACA
                                ||||||||   ||||    ||||
                                ATTGTCCT   TAAC    TTGT
                                   GTC   CT___
GAM827  SRRM1    3'  GCACAATCTTTCCTGTTG    20695         AATT  A   A
                                TAACAGGAAA   GA TGTG C
                                ||||||||||   || |||| |
                                GTTGTCCTTT   CT ACAC G
                                   ____ A   C
GAM827  STC1     3'  TGTCACATCCAACTGGAAATTC 13465      AAA____  A
          C                      GGAA      TTG ATGTGACA
                                ||||      ||| ||||||||
                                CCTT      AAC TACACTGT
                                  AAAGGTC   C
GAM827  WHSC1    3'  CACACCTGATTCCTGTTG    24652         AAA   AA
                                TAACAGGA   ATTG  TGTG
                                ||||||||   ||||  ||||
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                                GTTGTCCT  TAGT  ACAC
                                   ___    CC
GAM827  ARL8     3'  CACTCAATCTTTCCTGT     94811        A     AT
                                ACAGGAAA ATTGA  GTG
                                |||||||| |||||  |||
                                TGTCCTTT TAACT  CAC
                                   C    __
GAM827  CITED2   3'  GCACTTTTTTTCCTGTT     21402         TTGAAT   A
                                AACAGGAAAAA     GTG C
                                ||||||||||      ||| |
                                TTGTCCTTTTT     CAC G
                                      TT____   C
GAM827  KIAA0721 3'  TCACATTGGTTTTCCTGT    41657         ATTG
                                ACAGGAAAA    AATGTGA
                                |||||||||    |||||||
                                TGTCCTTTT    TTACACT
                                   GG__
GAM827  KIAA0721 3'  TCACATTGGTTTTCCTGT    97658         ATTG
                                ACAGGAAAA    AATGTGA
                                |||||||||    |||||||
                                TGTCCTTTT    TTACACT
                                   GG__
GAM827  KIAA1210 3'  TCACATATATCCTGTTA     98083         AAAAT  A
                                TAACAGGA     TG ATGTGA
                                ||||||||     || ||||||
                                ATTGTCCT     AT TACACT
                                   _____  A
GAM827  KIAA1320 5'  TGCCACATTTTGTAATTTCTTG 69853         AATT_      A
           T                     ACAGGAAA     GAATGTG CA
                                ||||||||     ||||||| ||
                                TGTTCTTT     TTTACAC GT
                                   AATGT      C
GAM827  KIAA1336 3'  TGTCACATACGCTTTCCCCT   72790     AA   T  A
                                AGG  AAA TG ATGTGACA
                                |||  ||| || ||||||||
                                TCC  TTT GC TACACTGT
                                  CC   C  A
GAM827  KIAA1936 5'  TGTCACATTCAAGGCCT     73842     AAAAA
                                AGG     TTGAATGTGACA
                                |||     ||||||||||||
                                TCC     AACTTACACTGT
                                  GG___
GAM827  TCF-3    3'  TGTGACATTTCCTGTTA     49243         AAATTGA    G
                                TAACAGGAA      ATGT ACA
                                |||||||||      |||| |||
                                ATTGTCCTT      TACA TGT
                                   _______    G
GAM827  LOC146784 5'  TCACACCATTTCCTGTT     78719         AAT  AA
                                AACAGGAAA   TG  TGTGA
                                |||||||||   ||  |||||
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                                TTGTCCTTT  AC  ACACT
                                    ___ C_
GAM827  LOC151201 5'  TACACAATTTTTCTTG     86485          AA
                                CAGGAAAAATTG  TGTG
                                ||||||||||||  ||||
                                GTTCTTTTTAAC  ACAT
                                    __
GAM827  LOC151610 3'  GTCACAACTTTTCCTGT     81098        ATTGAA
                                ACAGGAAAA     TGTGAC
                                |||||||||     ||||||
                                TGTCCTTTT     ACACTG
                                    CA____
GAM827  LOC153682 3'  TCACATTCAATTTTATGTCT  87275     ___
                                GGA  AAAATTGAATGTGA
                                |||  ||||||||||||||
                                TCT  TTTTAACTTACACT
                                  GTA
GAM827  LOC203107 3'  CACATTCAATTAACTTTGCT  90794    G  ___
                                AG AAA  AATTGAATGTG
                                || |||  ||||||||||
                                TC TTT  TTAACTTACAC
                                 G  CAA
GAM827  LOC219988 5'  TCATTGGCAGTCCTCCTGTTA  93267       AAA   AAT
                                TAACAGGA  ATTG  GTGA
                                ||||||||  ||||  ||||
                                ATTGTCCT  TGAC  TACT
                                    CC_   GGT
GAM827  LOC257081 3'  GCACGTGTTTCCTGTTA     98592        AATTGA    A
                                TAACAGGAAA     ATGTG C
                                ||||||||||     ||||| |
                                ATTGTCCTTT     TGCAC G
                                    G_____     C
GAM827  LOC56930  3'  GCACGTGTTTCCTGTTA     62744        AATTGA    A
                                TAACAGGAAA     ATGTG C
                                ||||||||||     ||||| |
                                ATTGTCCTTT     TGCAC G
                                    G_____     C
GAM827  LOC90594  5'  CACAGCCTCCACTTTCTCCTGT 64215       A  T  AA___
          TA                    TAACAGGA AAA TG    TGTG
                                ||||||| ||| ||    ||||
                                ATTGTCCT TTT AC    ACAC
                                    C  C  CTCCG
GAM827  LOC91408  3'  CGTTCATTTTTCCTGTTA    66515          T
                                TAACAGGAAAAAT GAATG
                                |||||||||||| |||||
                                ATTGTCCTTTTTA CTTGC
                                    _
GAM828  AGT     3'  GAGGCAAAGGCCAGCAGC    5256     CA     _
                                GC  CTGGCCTT GCCTT
                                ||  |||||||| |||||
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                                CG  GACCGGAA CGGAG
                                 AC       A
GAM828  DLG5    5'  GCTGAACAAGGCCACGGC    83817     AC      CC  TG
                                GCC  TGGCCTTG  TT  GC
                                |||  ||||||||  ||  ||
                                CGG  ACCGGAAC  AA  CG
                                  C_       __  GT
GAM828  EZH1    3'  TAGAGGCAAGGCCCAATGGC   10556     CT_
                                GCCA   GGCCTTGCCTTTG
                                ||||   ||||||||||||
                                CGGT   CCGGAACGGAGAT
                                  AAC
GAM828  GRB14   5'  GCGGGAGCAATGCCAGTGGC   16893         C   C   G
                                GCCACTGGC TTGC TTT GC
                                |||||||| |||| ||| ||
                                CGGTGACCG AACG AGG CG
                                     T   _   G
GAM828  IGFBP3  3'  TGCCAAGGACATGACCAGCAGC 7006     CA   CCT  C
                                GC  CTGG   TG CTTTGGCA
                                ||  ||||   || ||||||||
                                CG  GACC   AC GGAACCGT
                                 AC    AGT  A
GAM828  KCNS2   3'  TGCTAGCAAGGGCAGTAGC   68854    C   G     CTT
                                GC ACTG CCTTGC   TGGCA
                                || |||| ||||||   |||||
                                CG TGAC GGAACG   ATCGT
                                 A   G     ___
GAM828  MBNL    3'  TGTGCCAAGCAAAACCA     41074     CC    CT
                                TGG  TTGC  TTGGCACA
                                |||  ||||  ||||||||
                                ACC  AACG  AACCGTGT
                                  AA   __
GAM828  MTMR3   3'  TGCAGTCAAGGCCAAAGC    41171    CAC      C  TTG
                                GC   TGGCCTTG CT   GCA
                                ||   |||||||| ||   |||
                                CG   ACCGGAAC GA   CGT
                                 AA_       T  ___
GAM828  NDUFS8  5'  TGCTTGGCAAGGCAAGTAGC  11768    C   G      TTT
                                GC ACT GCCTTGCC   GGCA
                                || ||| ||||||||   ||||
                                CG TGA CGGAACGG   TCGT
                                 A  A       T__
GAM828  PFKL    5'  GCGGGCAAGGCCATCGGC    12060     AC        TTG
                                GCC  TGGCCTTGCCT   GC
                                |||  ||||||||||   ||
                                CGG  ACCGGAACGGG   CG
                                  CT         ___
GAM828  PRKY    5'  GCCCCGCGAGGCCAGCGGC   12377     A        CTTT
                                GCC CTGGCCTTGC    GGC
                                ||| ||||||||||    |||
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                                CGG GACCGGAGCG   CCG
                                  C        CC__
GAM828  SIT     3'  TGGAGGAGGCAAAGACAGTAGC 27823   C   GCC      GG
                                GC ACTG  TTGCCTTT  CA
                                || ||||  ||||||||  ||
                                CG TGAC  AACGGAGG  GT
                                 A   AGA      AG
GAM828  SMURF1  3'  TGATGAGCAAGGCCAGAAGC  94053   CA       C  TGG
                                GC  CTGGCCTTGC TT  CA
                                ||  ||||||||||  ||  ||
                                CG  GACCGGAACG AG  GT
                                 AA        _  TA_
GAM828  SNRPN   5'  TGCAGTGGCAAGGCCAGCCGC  43325   CA       TTTG
                                GC  CTGGCCTTGCC   GCA
                                ||  ||||||||||   |||
                                CG  GACCGGAACGG   CGT
                                 CC         TGA_
GAM828  ARHGEF9  3'  TCAAAGCAGACCAGTGGC   31493       CC   C
                                GCCACTGG  TTGC TTTGG
                                ||||||||  |||| |||||
                                CGGTGACC  GACG AAACT
                                     A_   _
GAM828  BMF     3'  TGCTGGGGCAAGGCCATCAGC  54290   CAC       T TG
                                GC   TGGCCTTGCC T  GCA
                                ||   ||||||||||  |  |||
                                CG   ACCGGAACGG G  CGT
                                 ACT        _ GT
GAM828  BOLL    5'  TGCGCACGAGGCCAGCGGC   53451    A       CCTT  _
                                GCC CTGGCCTTG   TG GCA
                                ||| |||||||||   || |||
                                CGG GACCGGAGC   AC CGT
                                  C       ____  G
GAM828  C5orf4  3'  TCAAAGGCAAAACCACAGC   51495   CAC   CC
                                GC   TGG  TTGCCTTTGG
                                ||   |||  ||||||||||
                                CG   ACC  AACGGAAACT
                                 AC_   AA
GAM828  C5orf4  3'  TCAAAGGCAAAACCACAGC   33428   CAC   CC
                                GC   TGG  TTGCCTTTGG
                                ||   |||  ||||||||||
                                CG   ACC  AACGGAAACT
                                 AC_   AA
GAM828  CTDP1   3'  TGTGCCAAAGAGCTCAGCAG   17518    G CTT  _
                                CTG C   GC CTTTGGCACA
                                ||| |   || ||||||||||
                                GAC G   CG GAAACCGTGT
                                  _ ACT  A
GAM828  D15Wsu75e 3'  CCAAGCAAGGCCAGTG      67223          CT
                                CACTGGCCTTGC  TTGG
                                ||||||||||||  ||||
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                                GTGACCGGAACG  AACC
                                      __
GAM828  FLJ00024  3'  GTGCCACCCCGAAAGGCAGTAG 64504    C   G   GCCTT_
             C                   GC ACTG CCTT     TGGCAC
                                 || |||| ||||     ||||||
                                 CG TGAC GGAA     ACCGTG
                                  A   _   AGCCCC
GAM828  FLJ11700  3'  TGCGGCGGGGCAAGGCCAGT   46569           TG_
                                 ACTGGCCTTGCCTT   GCA
                                 ||||||||||||||   |||
                                 TGACCGGAACGGGG   CGT
                                          CGG
GAM828  FLJ20085  3'  TGCGCATGGGCAAGGCCAGCGC 35010    CA         T  _
                                 GC  CTGGCCTTGCCT TG GCA
                                 ||  |||||||||||| || |||
                                 CG  GACCGGAACGGG AC CGT
                                  C_          T  G
GAM828  FLJ20174  3'  TGCCCAGAAAGGCCAGCAGC   35195    CA      GC  TT
                                 GC  CTGGCCTT  CT  GGCA
                                 ||  ||||||||  ||  ||||
                                 CG  GACCGGAA  GA  CCGT
                                  AC       A_  C_
GAM828  FLJ31978  3'  GAAGGCAAAGCCAGGGC     59009     A    C
                                 GCC CTGGC TTGCCTTT
                                 ||| ||||| ||||||||
                                 CGG GACCG AACGGAAG
                                   _     A
GAM828  KIAA0125  3'  TGCAAGTGCAAGGCCAGTGG   29580           _  TG
                                 CCACTGGCCTTGC CTT  GCA
                                 ||||||||||||| |||  |||
                                 GGTGACCGGAACG GAA  CGT
                                          T  __
GAM828  KIAA0513  3'  GTGCAGGGCAAGCCAGTGGC   29047         C      TG
                                 GCCACTGGC TTGCCTT  GCAC
                                 |||||||| |||||||  ||||
                                 CGGTGACCG AACGGGA  CGTG
                                       _     __
GAM828  KIAA0841  3'  TGTGCTGTGTCAAGAGCAGCGG 71908     A  GC   CCTT
             C                   GCC CTG  CTTG    TGGCACA
                                 ||| |||  ||||    |||||||
                                 CGG GAC  GAAC    GTCGTGT
                                   C   GA    TGT_
GAM828  KIAA0864  5'  GAAGACAAGGCCAGCGC     63940    CA       C
                                 GC  CTGGCCTTG CTTT
                                 ||  |||||||| ||||
                                 CG  GACCGGAAC GAAG
                                  C_        A
GAM828  MYT1      5'  CGGAGGCAAGGCCAGCAGC   16977    CA
                                 GC  CTGGCCTTGCCTTTG
                                 ||  ||||||||||||||
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                                CG  GACCGGAACGGAGGC
                                 AC
GAM828  PKNOX2   3'  CAAAGCATAACCAGTGGC    92525        CCT   C
                                GCCACTGG   TGC TTTG
                                ||||||||   ||| ||||
                                CGGTGACC   ACG AAAC
                                    AAT  _
GAM828  POLR2D   3'  GTGCCAAAGAGGTCCA      17845     _  TGC
                                TGG CCT   CTTTGGCAC
                                ||| |||   |||||||||
                                ACC GGA   GAAACCGTG
                                  T  ___
GAM828  PP3501   3'  TGTGGGTGGGCAAGGCCAGGGC 41689     A          TTGG
                                GCC CTGGCCTTGCCT    CACA
                                ||| ||||||||||||    ||||
                                CGG GACCGGAACGGG    GTGT
                                  _          TGG_
GAM828  SELB     3'  TGTGCCAAATCCCAACCAGCCA 62596     C__   CC_
                                TGGC   TTG   TTTGGCACA
                                ||||   |||   |||||||||
                                ACCG   AAC   AAACCGTGT
                                   ACC   CCT
GAM828  SEMA4G   5'  GTGCGGGAGAGCAAGGCCAGTG 96332           _   G
                                CACTGGCCTTGC CTTT GCAC
                                |||||||||||| |||| ||||
                                GTGACCGGAACG GAGG CGTG
                                       A   G
GAM828  TRIP-Br2 3'  CCAAAGGGTGAGCAGTGGC   29262        GC  TG  _
                                GCCACTG  CT  CC TTTGG
                                |||||||  ||  || |||||
                                CGGTGAC  GA  GG AAACC
                                    __  GT  G
GAM828  LOC148188 5'  TGTGGAAAAACAAGGCCA    79458        CC   GG
                                TGGCCTTG  TTT  CACA
                                ||||||||  |||  ||||
                                ACCGGAAC  AAA  GTGT
                                     A_   AG
GAM828  LOC152926 5'  CAGCAGGCAAGGCAGTGGC   81629        G      _
                                GCCACTG CCTTGCCT TTG
                                ||||||| |||||||| |||
                                CGGTGAC GGAACGGA GAC
                                    _       C
GAM828  LOC158886 5'  TGCCAAGAGGGCCAGTG     83723          GCC
                                CACTGGCCTT   TTTGGCA
                                ||||||||||   |||||||
                                GTGACCGGGA   GAACCGT
                                              ___
GAM828  LOC158887 5'  TGCCAAGAGGGCCAGTG     88312          GCC
                                CACTGGCCTT   TTTGGCA
                                ||||||||||   |||||||
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                                GTGACCGGGA  GAACCGT
                                    ___
GAM828  LOC162083 5'  TGTACCAAAACTCATCAGTGGC 83209       CCT  CC_    C
                                GCCACTGG  TG  TTTGG ACA
                                ||||||||  ||  ||||| |||
                                CGGTGACT  AC  AAACC TGT
                                    ___ TCA    A
GAM828  LOC202134 3'  GCTACAAGGCCACTGGC    91922     C      CCTT
                                GCCA TGGCCTTG   TGGC
                                |||| ||||||||   ||||
                                CGGT ACCGGAAC   ATCG
                                  C      ____
GAM828  LOC203871 3'  GTACCTGGGCCAGGCCAGTGGC 90988         T   TT  C
                                GCCACTGGCCT GCCT  GG AC
                                |||||||||| ||||  || ||
                                CGGTGACCGGA CGGG  CC TG
                                      C   T_  A
GAM828  LOC220469 3'  TGCCCACACAAAGCCAGTGGC  76895       C   CCTTT
                                GCCACTGGC TTG    GGCA
                                ||||||||| |||    ||||
                                CGGTGACCG AAC    CCGT
                                     A  ACAC_
GAM828  LOC253992 3'  AAAGACAAGACCAGGGC    98421    A   C   C
                                GCC CTGG CTTG CTTT
                                ||| |||| |||| ||||
                                CGG GACC GAAC GAAA
                                  _   A   A
GAM828  LOC254057 5'  GCGGGAGGCAGACCAGCAGC  98783   CA   CC     G
                                GC  CTGG  TTGCCTTT GC
                                ||  ||||  |||||||| ||
                                CG  GACC  GACGGAGG CG
                                 AC   A_      G
GAM828  LOC91056  3'  GCCAGGCAGGCCAGTGG    96407        T   TT
                                CCACTGGCCT GCCT  GGC
                                |||||||||| ||||  |||
                                GGTGACCGGA CGGA  CCG
                                    _   __
GAM828  LOC93349  3'  TGCGAGGGAAAGGCCAGTGGC  57278         G    G
                                GCCACTGGCCTT CCTTTG CA
                                |||||||||||| ||||||  ||
                                CGGTGACCGGAA GGGAGC GT
                                      A    _
GAM829  ATP4A    3'  CCAAGAGTCCCAGCCCCA    7372        CAGCCT   _
                                TGGGGCTG     GGGC CTTGG
                                ||||||||     |||| |||||
                                ACCCCGAC     CCTG GAACC
                                    _______   A
GAM829  FCER2    3'  ACCCTCTCCAGATGCAGCCCCA 10599         GC    CCTT
                                TGGGGCTGCA  CTGGG   GGT
                                |||||||||  |||||   |||
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                                ACCCCGACGT  GACCT   CCA
                                     A_    CTC_
GAM829  FOXO1A   3'  CCAATAACCCCAGCCCCA   10649       CAGCCT  CC_
                                TGGGGCTG    GGG  TTGG
                                ||||||||    |||  ||||
                                ACCCCGAC    CCC  AACC
                                     _______  AAT
GAM829  INPPL1   3'  ACCAAGGCCCAGCTATGGCCCC 9602       GC  C
           A                     TGGGGCT  AGC TGGGCCTTGGT
                                |||||||  ||| ||||||||||
                                ACCCCGG  TCG ACCCGGAACCA
                                   TA  _
GAM829  LRP1     3'  CCAAACCCCAGCCCCA     11358       CAGCCT  CC
                                TGGGGCTG    GGG  TTGG
                                ||||||||    |||  ||||
                                ACCCCGAC    CCC  AACC
                                     _______  A_
GAM829  PIM1     5'  GCCACAGCCACAGCCCCA   92686       CA  C  _
                                TGGGGCTG  GC TG GGC
                                ||||||||  || || |||
                                ACCCCGAC  CG AC CCG
                                     AC  _  A
GAM829  PRX2     3'  GTACCAGAGACTGCAGCCC   33308       C__   ____
                                GGGCTGCAG  CTGG   GC
                                |||||||||  ||||   ||
                                CCCGACGTC  GACC   TG
                                     AGA   A___
GAM829  RET      3'  GGCCAAGCCTCAGCCCCA   40549       C  C  G
                                TGGGGCTG AG CT GGCC
                                |||||||| || || ||||
                                ACCCCGAC TC GA CCGG
                                     _  C  A
GAM829  SLC5A2   3'  CTTGGTACCATAAGCCACAGCC 13180       CA  C__  ____ CTTG
           TCA                    TGGGGCTG  GC  TGG   GC   G
                                |||||||| ||  |||   ||   |
                                ACTCCGAC  CG  ACC   TG   C
                                     AC  AAT   A___  GTTC
GAM829  ADAMTS10 5'  ACCAAGGCCCAGAGAGGGAGGC 48979      GCAGC__
           CC                     GGGCT     CTGGGCCTTGGT
                                |||||      ||||||||||||
                                CCCGG     GACCCGGAACCA
                                   AGGGAGA
GAM829  DC-TM4F2 3'  CCGTGCCTAGCCACAACCCCA  48898      C  CA  C    CT
                                TGGGG TG  GC TGGGC  TGG
                                ||||| ||  || |||||  |||
                                ACCCC AC  CG ATCCG  GCC
                                   A  AC  _    T_
GAM829  FBXO27   3'  ACCAAAACCCTCCGATCCAGCC 74994       CAGCCT_  CC
           CCA                    TGGGGCTG     GGG  TTGGT
                                ||||||||     |||  |||||
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                              ACCCCGAC     CCC  AACCA
                                   CTAGCCT   AA
GAM829  FLJ14249  3'  GTACCAGAAGCCCAGCCCCA  42644       CA __   ____
                              TGGGGCTG  GC  CTGG   GC
                              ||||||||  ||  ||||   ||
                              ACCCCGAC  CG  GACC   TG
                                   C_  AA   A___
GAM829  GDF10     5'  CCCTGTCAGCTGCAGCCCCA  18298         CT___
                              TGGGGCTGCAGC    GGG
                              ||||||||||||    |||
                              ACCCCGACGTCG    CCC
                                     ACTGT
GAM829  KIAA0140  3'  CTTGGTACCAGCAAGCCCAGCC 28514       CA ___   ____ CTTG
           CCA                   TGGGGCTG  GC   CTGG   GC   G
                              ||||||||  ||   ||||   ||   |
                              ACCCCGAC  CG   GACC   TG   C
                                   C_  AAC   A___  GTTC
GAM829  KIAA0444  3'  CCTTTCCCCAGGCACAGCCCCA 62998       CA     CCTT
                              TGGGGCTG  GCCTGGG   GG
                              ||||||||  |||||||   ||
                              ACCCCGAC  CGGACCC   CC
                                   A_     CTTT
GAM829  KIAA0450  5'  GCCCAGGCCGCACCCCA    28357     C   A
                              TGGGG TGC GCCTGGGC
                              |||||  ||| ||||||||
                              ACCCC ACG CGGACCCG
                                 _   C
GAM829  KIAA1077  3'  AGCCCCAGGCTGCAGCCC    73285          C
                              GGGCTGCAGCCTGGG CT
                              |||||||||||||| ||
                              CCCGACGTCGGACCC GA
                                       C
GAM829  MGC10986  3'  GCCTTGGTACTCGCCAGGCTGC 48325          _________ CTTG
           AGCCTCA                 TGGGGCTGCAGCCTGG      GC   GT
                              ||||||||||||||||      ||   ||
                              ACTCCGACGTCGGACC      TG   CG
                                       GCTCA___  GTTC
GAM829  MGC11352  5'  CCGTGCCTAGCCACAACCCCA  65430     C  CA  C    CT
                              TGGGG TG  GC TGGGC  TGG
                              |||||  ||  ||  |||||  |||
                              ACCCC AC  CG ATCCG  GCC
                                 A  AC  _    T_
GAM829  PPP1R16B  5'  CCATGAGGCCCCAGCCCCA   62035       CAGCCT    __
                              TGGGGCTG    GGGCCT  TGG
                              ||||||||    ||||||  |||
                              ACCCCGAC    CCCGGA  ACC
                                   _______    GT
GAM829  TM4SF11   3'  CTTGGTACTCCAGACCTGCAGC 32587         C_   _______ CTTG
           CCCA                  TGGGGCTGCAG  CTGG    GC   G
                              ||||||||||  ||||    ||   |
```

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                                ACCCCGACGTC  GACC     TG   C
                                      CA   TCA___  GTTC
GAM829  LOC154834 5'  GTACACCAGGCTCAGCCCCA  87496       C     _______
                                TGGGGCTG AGCCTGG     GC
                                |||||||| |||||||     ||
                                ACCCCGAC TCGGACC     TG
                                   _      ACA___
GAM829  LOC200030 3'  ACCAAGACCCATCATGCCCCA  80124      TGCAGCC   C
                                TGGGGC      TGGG CTTGGT
                                ||||||      |||| ||||||
                                ACCCCG      ACCC GAACCA
                                   TACT___   A
GAM829  LOC200030 3'  ACCAAGACCCATCATGCCCCA  80125      TGCAGCC   C
                                TGGGGC      TGGG CTTGGT
                                ||||||      |||| ||||||
                                ACCCCG      ACCC GAACCA
                                   TACT___   A
GAM829  LOC200030 3'  ACCAAGACCCATCATGCCCCA  80126      TGCAGCC   C
                                TGGGGC      TGGG CTTGGT
                                ||||||      |||| ||||||
                                ACCCCG      ACCC GAACCA
                                   TACT___   A
GAM829  LOC200030 3'  ACCAAGGCCCACCATGCCCCA  80127      TGCAGCC
                                TGGGGC      TGGGCCTTGGT
                                ||||||      ||||||||||
                                ACCCCG      ACCCGGAACCA
                                   TACC___
GAM829  LOC200030 3'  ACCAAGGCCCACCATGCCCCA  80128      TGCAGCC
                                TGGGGC      TGGGCCTTGGT
                                ||||||      ||||||||||
                                ACCCCG      ACCCGGAACCA
                                   TACC___
GAM829  LOC221431 3'  CCAAGACTCTGCAGCCC     93728        CCT  GC
                                GGGCTGCAG   GG  CTTGG
                                |||||||||   ||  |||||
                                CCCGACGTC   TC  GAACC
                                      ___  A_
GAM830  BLAME    3'  GCCTCAATCCAGTCTTGATA   39653      _    A    _
                                TATCA GACTG GATTG GGC
                                ||||| ||||| ||||| |||
                                ATAGT CTGAC CTAAC CCG
                                   T    _    T
GAM830  KCNJ16   5'  GCCCAATCTCTGCTGGT     38485      ACT
                                ATCAG   GAGATTGGGC
                                |||||   ||||||||||
                                TGGTC   CTCTAACCCG
                                   GT_
GAM830  LRPAP1   3'  GCTGTCAGGTCTGATA      11367        GA  TG
                                TATCAGACT  GAT  GGC
                                |||||||||  |||  |||
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                                ATAGTCTGG  CTG  TCG
                                     A_  __
GAM830  MHC2TA   3'  GCCCACAGGATCAGTCTGAT  5987         GAT__
                                ATCAGACTGA    TGGGC
                                ||||||||||    |||||
                                TAGTCTGACT    ACCCG
                                     AGGAC
GAM830  NPHP1    3'  CTTAATTCAGTCTGATA     63142          A
                                TATCAGACTGAG TTGGG
                                |||||||||||| |||||
                                ATAGTCTGACTT AATTC
                                      _
GAM830  PROCR    3'  GCTGAATTAGTCTGATA     22157        GA   G
                                TATCAGACT  GATT GGC
                                |||||||||  |||| |||
                                ATAGTCTGA  TTAA TCG
                                     __   G
GAM830  PROK1    3'  GTTCAATCTAATCTGATA    51569       CTG
                                TATCAGA   AGATTGGGC
                                |||||||   |||||||||
                                ATAGTCT   TCTAACTTG
                                    AA_
GAM830  RUNX1    3'  CCCAAGGTCATCTGATA     10029       C   GA
                                TATCAGA TGA  TTGGG
                                ||||||| |||  |||||
                                ATAGTCT ACT  AACCC
                                    _  GG
GAM830  TMEM2    3'  CCATTTTCCAGTTTGATA    26335         _  T
                                TATCAGACTG AGA TGG
                                |||||||||| ||| |||
                                ATAGTTTGAC TTT ACC
                                      C   T
GAM830  UBE4A    3'  CCCAATCTAGTAGGATG     17731      AG   G
                                TATC  ACT AGATTGGG
                                ||||  ||| ||||||||
                                GTAG  TGA TCTAACCC
                                  GA  _
GAM830  FLJ10330 3'  CCCAATTGTTAAGTTTGATA  36504         GA__
                                TATCAGACT    GATTGGG
                                |||||||||    |||||||
                                ATAGTTTGA    TTAACCC
                                     ATTG
GAM830  FLJ10852 3'  CCCAAAACTCTCAATCTGAT  39251       C    ___
                                ATCAGA TGAGA   TTGGG
                                |||||| |||||   |||||
                                TAGTCT ACTCT   AACCC
                                   A    CAA
GAM830  FLJ20511 3'  GCCCAATCTCTGATG       35776       CTGA
                                TATCAGA    GATTGGGC
                                |||||||    ||||||||
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                                GTAGTCT   CTAACCCG
                                      ____
GAM830  KIAA0194  3'  GCCCCCTCAGTCTGATG    66591          ATT
                                TATCAGACTGAG  GGGC
                                ||||||||||||  ||||
                                GTAGTCTGACTC  CCCG
                                      C__
GAM830  KIAA0326  3'  GCCCAATCTCAGCCTTGA    64962     A_
                                TCAG  CTGAGATTGGGC
                                ||||  ||||||||||||
                                AGTT  GACTCTAACCCG
                                  CC
GAM830  KIAA0844  5'  GCCCGGCTCAGTCTGAT     30894          A
                                ATCAGACTGAG TTGGGC
                                |||||||||| ||||||
                                TAGTCTGACTC GGCCCG
                                      _
GAM830  KIAA1878  3'  GCCCAAATCGCAGTTTGA    93368        A   _
                                TCAGACTG GATT GGGC
                                |||||||| |||| ||||
                                AGTTTGAC CTAA CCCG
                                     G   A
GAM830  KIAA1906  3'  CCCAAATTATTAGTCTTGATA  73570      _    GA__
                                TATCA GACTGA   TTGGG
                                ||||| ||||||   |||||
                                ATAGT CTGATT   AACCC
                                   T     ATTA
GAM830  NICE-3    3'  GCCCAATGCACTGGTCTGA   31885       G ___
                                TCAGACT AG   ATTGGGC
                                ||||||| ||   |||||||
                                AGTCTGG TC   TAACCCG
                                     _ ACG
GAM830  OGFR      3'  GCTTTTCTTAGTCTGATA    62000          TT
                                TATCAGACTGAGA  GGGC
                                ||||||||||||  ||||
                                ATAGTCTGATTCT  TTCG
                                      T_
GAM830  PRO0902   3'  GCCTAATTCAATTGATA     54967       AC   A
                                TATCAG  TGAG TTGGGC
                                ||||||  |||| ||||||
                                ATAGTT  ACTT AATCCG
                                   A_   _
GAM830  PRPF4     3'  GCCCAATCCCTAGGTGATG   17467      GA  A_
                                TATCA  CTG  GATTGGGC
                                |||||  |||  ||||||||
                                GTAGT  GAT  CTAACCCG
                                   G_   CC
GAM830  SS18L1    3'  GCCCAATTCTAAGTTGATA   65956       A G  _
                                TATCAG CT AGA TTGGGC
                                |||||| || ||| ||||||
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                                ATAGTT GA TCT AACCCG
                                   _ A   T
GAM830  TRIM7    3'  GCTCAGTCACTCTGATA     54042        CTGA
                                TATCAGA    GATTGGGC
                                |||||||    ||||||||
                                ATAGTCT    CTGACTCG
                                    CA__
GAM830  LOC145828 3'  GCCCAATCCAGTATTTGAT    84538       __    A
                                ATCAG  ACTG GATTGGGC
                                |||||  |||| ||||||||
                                TAGTT  TGAC CTAACCCG
                                  TA   _
GAM830  LOC146481 5'  GCCTTCTACAGTTTGATA     78487          _   TT
                                TATCAGACTG AGA  GGGC
                                |||||||||| |||  ||||
                                ATAGTTTGAC TCT  TCCG
                                     A   __
GAM830  LOC147343 3'  GCCCTCAATTTCTATCTAATA  85129     C   CT     __
                                TAT AGA  GAGATT  GGGC
                                ||| |||  ||||||  ||||
                                ATA TCT  CTTTAA  CCCG
                                  A   AT     CT
GAM830  LOC204804 3'  GCCCTCTCAGCCTGAT      91045       A     TT
                                ATCAG CTGAGA  GGGC
                                |||||  ||||||  ||||
                                TAGTC GACTCT  CCCG
                                   C     __
GAM830  LOC257194 3'  GCTGGATCCAATCTGGTA     97242        C  A    G
                                TATCAGA TG GATT GGC
                                ||||||| || |||| |||
                                ATGGTCT AC CTAG TCG
                                    A  _    G
GAM831  ABCC12    5'  CCCAGGCCAAAAGCCCAGGGCT 53790         A  ACCT  A  C
                                AGCCCTGG CT    GC CT GG
                                |||||||| ||    || || ||
                                TCGGGACC GA    CG GA CC
                                     C  AAAC  _  C
GAM831  HMX1      5'  TCCGGGTAGCAGCTCCAGGGC  38948         CTAC    _
                                GCCCTGGA    CTGC ACTCGGA
                                ||||||||    |||| |||||||
                                CGGGACCT    GACG TGGGCCT
                                     C___    A
GAM831  MEN1      3'  TCCAGCTCAGAACCCAGGGCT  56362         ACTAC   CA  C
                                AGCCCTGG     CTG  CT GGA
                                ||||||||     |||  || |||
                                TCGGGACC     GAC  GA CCT
                                     CAA__   TC  _
GAM831  MEN1      3'  TCCAGCTCAGAACCCAGGGCT  56366         ACTAC   CA  C
                                AGCCCTGG     CTG  CT GGA
                                ||||||||     |||  || |||
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                              TCGGGACC    GAC  GA CCT
                                  CAA__   TC  _
GAM831   MEN1    3'  TCCAGCTCAGAACCCAGGGCT  56367       ACTAC   CA  C
                              AGCCCTGG    CTG  CT GGA
                              ||||||||    |||  || |||
                              TCGGGACC    GAC  GA CCT
                                  CAA__   TC  _
GAM831   MEN1    3'  TCCAGCTCAGAACCCAGGGCT  56368       ACTAC   CA  C
                              AGCCCTGG    CTG  CT GGA
                              ||||||||    |||  || |||
                              TCGGGACC    GAC  GA CCT
                                  CAA__   TC  _
GAM831   MEN1    3'  TCCAGCTCAGAACCCAGGGCT  56370       ACTAC   CA  C
                              AGCCCTGG    CTG  CT GGA
                              ||||||||    |||  || |||
                              TCGGGACC    GAC  GA CCT
                                  CAA__   TC  _
GAM831   MEN1    3'  TCCAGCTCAGAACCCAGGGCT  56372       ACTAC   CA  C
                              AGCCCTGG    CTG  CT GGA
                              ||||||||    |||  || |||
                              TCGGGACC    GAC  GA CCT
                                  CAA__   TC  _
GAM831   MEN1    3'  TCCAGCTCAGAACCCAGGGCT  5961        ACTAC   CA  C
                              AGCCCTGG    CTG  CT GGA
                              ||||||||    |||  || |||
                              TCGGGACC    GAC  GA CCT
                                  CAA__   TC  _
GAM831   OGG1    5'  CCGAGTGCAGACAATCCCGG   11890    T   CTAC
                              CC GGA    CTGCACTCGG
                              || |||    ||||||||||
                              GG CCT    GACGTGAGCC
                                C   AACA
GAM831   OGG1    5'  CCGAGTGCAGACAATCCCGG   34152    T   CTAC
                              CC GGA    CTGCACTCGG
                              || |||    ||||||||||
                              GG CCT    GACGTGAGCC
                                C   AACA
GAM831   OGG1    5'  CCGAGTGCAGACAATCCCGG   34164    T   CTAC
                              CC GGA    CTGCACTCGG
                              || |||    ||||||||||
                              GG CCT    GACGTGAGCC
                                C   AACA
GAM831   PLAT    5'  CCTACAGGAGTCCAGGGCT   8116          A    CACTC
                              AGCCCTGGACT CCTG     GG
                              |||||||||| ||||     ||
                              TCGGGACCTGA GGAC     CC
                                    _    AT___
GAM831   PLAT    5'  CCTACAGGAGTCCAGGGCT   53394         A    CACTC
                              AGCCCTGGACT CCTG     GG
                              |||||||||| ||||     ||
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                                TCGGGACCTGA GGAC    CC
                                      _   AT___
GAM831  D21S2056E 3'  TGACAGTAGCCCAGGGCT   14874       A   C  _
                                AGCCCTGG CTAC TG CA
                                |||||||| |||| || ||
                                TCGGGACC GATG AC GT
                                     C   _  A
GAM831  DDX8      3'  TCCAGCAGCAGTAGCCAGGGCT 18232       A   C  A_  C
                                AGCCCTGG CTAC TGC  CT GGA
                                |||||||| |||| |||  || |||
                                TCGGGACC GATG ACG  GA CCT
                                     _   _  AC  _
GAM831  DKFZp434J0226 3'  CCATGAGCCGTCCAGGGC    72792        TAC  G  CTC
                                GCCCTGGAC   CT CA   GG
                                |||||||||   || ||   ||
                                CGGGACCTG   GA GT   CC
                                     CC_  _  A__
GAM831  FLJ10315  5'  CCGAGCTGCCAGTCCAGG    36493       ACCT   _
                                CCTGGACT    GCA CTCGG
                                ||||||||    ||| |||||
                                GGACCTGA    CGT GAGCC
                                     C___   C
GAM831  FLJ13612  3'  CCAAGTGACAGATCCAGGGC   48086       CTAC   _   C
                                GCCCTGGA    CTG CACT GG
                                ||||||||    ||| |||| ||
                                CGGGACCT    GAC GTGA CC
                                     A___   A   A
GAM831  FLJ20487  3'  CCGCCCTCAGTGGCCCAGGGCT 35709       A   C  CACT
                                AGCCCTGG CTAC TG    CGG
                                |||||||| |||| ||    |||
                                TCGGGACC GGTG AC    GCC
                                     C   _  TCCC
GAM831  FLJ30791  5'  CCGAGTGCAGATTCCCCGAGC  59115    CC   ACTAC
                                GC  TGG    CTGCACTCGG
                                ||  |||    ||||||||||
                                CG  GCC    GACGTGAGCC
                                 A_  CCTTA
GAM831  G4        3'  CCGAGTACGAGGGTGCAGGGC  92635      G   ACC  C
                                GCCCTG ACT   TG ACTCGG
                                ||||||  |||   || ||||||
                                CGGGAC TGG   GC TGAGCC
                                   G   GA_  A
GAM831  KIAA0562  3'  CCTGGTGCCCAGGGCT     28821        ACTACCT    C
                                AGCCCTGG      GCACT GG
                                ||||||||      ||||| ||
                                TCGGGACC      CGTGG CC
                                     _______    T
GAM831  KIAA0853  3'  CCAAATGCAGGTGTGTAGG   31213     G  T      CTC
                                CCTG AC ACCTGCA   GG
                                ||||  || |||||||   ||
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                                GGAT TG TGGACGT   CC
                                  G _      AAA
GAM831  KIAA1987  3'  CCATTGTTGTTAGTCCAGGACT 89380    C       CCT   CTC
                                AG CCTGGACTA   GCA   GG
                                || |||||||||   |||   ||
                                TC GGACCTGAT   TGT   CC
                                 A       TGT   TA_
GAM831  MGC21688  3'  CCAAGTGTGGGCTCAAGGCT   58914     C   ACTA  TG    C
                                AGCC TGG    CC  CACT GG
                                |||| |||    ||  |||| ||
                                TCGG ACT    GG  GTGA CC
                                  A  C___  GT    A
GAM831  MGC4737   3'  CCTGGGCTGGCAGCCCAGGGCT 49639        A  A  T  A  C
                                AGCCCTGG CT CC GC CT GG
                                |||||||| || || || || ||
                                TCGGGACC GA GG CG GG CC
                                     C  C  T  _  T
GAM831  NFX1     3'  ATCCAAGTAGTATATGGACAGT 11783          A_  ___   _   C   ___
            CCAGGGCT                AGCCCTGGACT  CC   TGC ACT GGA   T
                                ||||||||||  ||   ||| ||| |||   |
                                TCGGGACCTGA  GG   ATG TGA CCT   A
                                      CA  TAT   A   A   ___
GAM831  PPP1R16B  3'  CCAAGTCTGCGAATCCAGGGT  62033        CTACC   __   C
                                GCCCTGGA    TGC  ACT GG
                                ||||||||    |||  ||| ||
                                TGGGACCT    GCG  TGA CC
                                     AA___   TC   A
GAM831  SARM     3'  TCCACCAGGCAGCTCAGGGCT  31305       GA  A    CACTC
                                AGCCCTG  CT CCTG    GGA
                                |||||||  || ||||    |||
                                TCGGGAC  GA GGAC    CCT
                                    TC  C    CA___
GAM831  SEC24D   5'  CCGAGCGTGAGTCCAGGCT   29752     C     ACC   A
                                AGCC TGGACT   TGC CTCGG
                                |||| ||||||   ||| |||||
                                TCGG ACCTGA   GTG GAGCC
                                  _     ___   C
GAM831  TETRAN   3'  TCCGAGCTGCAGCACTCCAAGG 8510      C   CTAC    _
            CT                    AGCC TGGA    CTGCA CTCGGA
                                |||| ||||    ||||| ||||||
                                TCGG ACCT    GACGT GAGCCT
                                  A   CAC_    C
GAM831  TIAF1    3'  TCCAACTACAGCAGTTCAGGGC 55296          AC   CACTC
            T                    AGCCCTGGACT  CTG    GGA
                                ||||||||||  |||    |||
                                TCGGGACTTGA  GAC    CCT
                                      C_  ATCAA
GAM831  TIGD5    5'  CCGAGTGCACCTTCAAGGC   52767     C   CTACC
                                GCC TGGA    TGCACTCGG
                                ||| ||||    |||||||||
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                                CGG ACTT    ACGTGAGCC
                                  A   CC___
GAM831  TREX1    5'  CCGAGCAAGCGGGCCCGGGGCT 54381       ACTA    A__
                                AGCCCTGG   CCTGC  CTCGG
                                ||||||||   |||||  |||||
                                TCGGGGCC   GGGCG  GAGCC
                                    C___    AAC
GAM831  LOC116113 3'  CCGAGCCTCAAGGCAAGTCCAG 93834    C      A_  GCA__
          GACT                    AG CCTGGACT  CCT    CTCGG
                                || ||||||||  |||    |||||
                                TC GGACCTGA  GGA    GAGCC
                                 A      AC  ACTCC
GAM831  LOC146243 3'  TCTTTGGCAGGAACCCAGGGCT 84623       ACTA    ACTC
                                AGCCCTGG   CCTGC   GGA
                                ||||||||   |||||   |||
                                TCGGGACC   GGACG   TCT
                                    CAA_    GTT_
GAM831  LOC146337 3'  CCGACTTGAAGTGTCCAGGGC  84638       T  CTG  C_
                                GCCCTGGAC AC   CA  TCGG
                                ||||||||| ||   ||  ||||
                                CGGGACCTG TG   GT  AGCC
                                     _  AA_  TC
GAM831  LOC148710 3'  CCAATAGCGGGGCAACCTCAGG 85349       ACTA__    ACTC
          GCT                    AGCCCTGG    CCTGC   GG
                                ||||||||    |||||   ||
                                TCGGGACT    GGGCG   CC
                                    CCAACG    ATAA
GAM831  LOC150622 5'  CCAGGCACCAGGCATCCAGGGC 80758       CTA   CA_ TC
                                GCCCTGGA   CCTG   C  GG
                                ||||||||   ||||   |  ||
                                CGGGACCT   GGAC   G  CC
                                    AC_    CAC GA
GAM831  LOC151568 3'  CCGAGTGTTAGCCCTAGGCT   57494     CT  A   CCT
                                AGCC  GG CTA   GCACTCGG
                                ||||  || |||   ||||||||
                                TCGG  CC GAT   TGTGAGCC
                                  AT  C   ___
GAM831  LOC158055 3'  CCAAGAGCCAGGAGCCCAGGGC 82579       A  A   _ A  C
          T                     AGCCCTGG CT CCTG C CT GG
                                ||||||| || |||| | || ||
                                TCGGGACC GA GGAC G GA CC
                                    C  _   C A  A
GAM831  LOC197329 5'  CCAAGTGCAGGCAGAGC    91311    C   GACTA      C
                                GC CTG    CCTGCACT GG
                                || |||    |||||||| ||
                                CG GAC    GGACGTGA CC
                                 A  _____       A
GAM831  LOC221178 3'  TCCAAACACAGCATCCAGGGCT 95175       CTAC   CACTC
                                AGCCCTGGA   CTG    GGA
                                |||||||||   |||    |||
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                                TCGGGACCT   GAC    CCT
                                     AC__   ACAAA
GAM831  LOC255518 5'  CCGGGGCTGCCCAGGGCT   98652       ACTACCT  A
                                AGCCCTGG     GC CTCGG
                                ||||||||     || |||||
                                TCGGGACC     CG GGGCC
                                     CGT____ _
GAM831  LOC256158 5'  TCCAATGTGGCAGGTAGCACAG 99514    C   GA      _  TC_
           AGCT                    AGC CTG  CTACCTGC AC   GGA
                                ||| |||  |||||||| ||   |||
                                TCG GAC  GATGGACG TG   CCT
                                  A   AC       G  TAA
GAM831  LOC257554 3'  CCGAGTACGAGGGTGCAGGGC  99531      G   ACC  C
                                GCCCTG ACT   TG ACTCGG
                                |||||| |||   || ||||||
                                CGGGAC TGG   GC TGAGCC
                                    G   GA_  A
GAM831  LOC90494  5'  AGCACAGATAGATCCAGGGCT  63730        _   C   CA
                                AGCCCTGGA CTA CTG  CT
                                ||||||||| ||| |||  ||
                                TCGGGACCT GAT GAC  GA
                                     A   A   AC
GAM832  MFAP4    3'  AGAACACAGCTACCGCACACCA 69786    A      C  C  CCC
                                TG TGTGCGGT GC TG   TTCT
                                || |||||||| || ||   ||||
                                AC ACACGCCA CG AC   AAGA
                                 C       T  _  AC_
GAM832  SLC22A7   3'  AGAAGGGCAGGCCCTGCAACTC 22883     TG    TC
           A                     TGA  TGCGG  GCCTGCCCTTCT
                                |||  |||||  ||||||||||||
                                ACT  ACGTC  CGGACGGGAAGA
                                  CA    C_
GAM832  SLC22A7   3'  AGAAGGGCAGGCCCTTCAACTC 22884     TG  C  TC
           A                     TGA  TG GG  GCCTGCCCTTCT
                                |||  || ||  ||||||||||||
                                ACT  AC TC  CGGACGGGAAGA
                                  CA  T  C_
GAM832  KIAA0295  3'  AGAAGAGCAGGTGAAAGCCACC 68657    A  T  GG      C
           A                     TG TG GC  TCGCCTGC CTTCT
                                || || ||  |||||||| |||||
                                AC AC CG  AGTGGACG GAAGA
                                 C  _  AA       A
GAM833  ANPEP    3'  GCTCCAGGGCCAGATGAGC   8565         _ AGGGG
                                GCTCATTTG C     GGAGC
                                |||||||||  |     |||||
                                CGAGTAGAC G     CCTCG
                                     C GGA__
GAM833  CLU      3'  GCTCCCCCCAAGATGAGC    10213        GCA
                                GCTCATTT   GGGGGGAGC
                                ||||||||   |||||||||
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                                CGAGTAGA  CCCCCCTCG
                                   A__
GAM833  F13A1   3'  CTCAGCCTTGCAAATAGC   92710    C       GG
                                GCT ATTTGCAGGG  GAG
                                ||| ||||||||||  |||
                                CGA TAAACGTTCC  CTC
                                  _       GA
GAM833  HRH2    3'  GCTCCCTTTTAAAAGGAGC   42510    A  GC
                                GCTC TTT  AGGGGGGAGC
                                |||| |||  ||||||||||
                                CGAG AAA  TTTTCCCTCG
                                  G  A_
GAM833  IFNGR2  3'  CTTGACTTTGGCAAATGAGC  19848        _  GG
                                GCTCATTTGC AGGG  GAG
                                |||||||||| ||||  |||
                                CGAGTAAACG TTTC  TTC
                                      G   AG
GAM833  MAP4    3'  TGGTCCCACAAATGGGC    48801       CAGGG  G
                                GCTCATTTG   GGGA CCA
                                |||||||||   |||| |||
                                CGGGTAAAC   CCCT GGT
                                   A____   _
GAM833  MAP4    3'  TGGTCCCACAAATGGGC    11454       CAGGG  G
                                GCTCATTTG   GGGA CCA
                                |||||||||   |||| |||
                                CGGGTAAAC   CCCT GGT
                                   A____   _
GAM833  PAK4    3'  TCCAGCCCCTGCAGCAAATGA  20829     ___     __
                                TCATT  TGCAGGGG  GGA
                                |||||  ||||||||  |||
                                AGTAA  ACGTCCCC  CCT
                                   ACG      GA
GAM833  PIM2    3'  CCCAATCCTACAAAGGAGC   60651    A  C  __
                                GCTC TTTG AGGG  GGG
                                |||| |||| ||||  |||
                                CGAG AAAC TCCT  CCC
                                  G   A   AA
GAM833  PKHD1   5'  TTTGGCTGGGACACAAACGAGT 57721    A  CAGGGGGG
                                GCTC TTTG      AGCCAAA
                                |||| ||||      |||||||
                                TGAG AAAC      TCGGTTT
                                  C   ACAGGG__
GAM833  PLAT    3'  CTCCTCAAAAGCAAATGAG   53395       AGG_
                                CTCATTTGC   GGGGAG
                                |||||||||   ||||||
                                GAGTAAACG   CTCCTC
                                     AAAA
GAM833  PLAT    3'  CTCCTCAAAAGCAAATGAG   8117        AGG_
                                CTCATTTGC   GGGGAG
                                |||||||||   ||||||
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                                GAGTAAACG   CTCCTC
                                     AAAA
GAM833  RAI2     3'  TTTGACTTTTCACAAATGAGT  41717        CAGG GG   C
                                GCTCATTTG   G  GAG CAAA
                                |||||||||   |  ||| ||||
                                TGAGTAAAC   C  TTC GTTT
                                     A___ TT   A
GAM833  TGFB3    3'  GGCTCCGGGCAAATGGC    13719    T     AGGGG
                                GC CATTTGC    GGAGCC
                                || |||||||    ||||||
                                CG GTAAACG    CCTCGG
                                 _     GG___
GAM833  BTN2A2   3'  TCCAGCCTACAGATGAGC    23771        C   GG
                                GCTCATTTG AGG  GGA
                                ||||||||| |||  |||
                                CGAGTAGAC TCC  CCT
                                     A   GA
GAM833  C20orf72 5'  TTCGACCGTTGCAAATAG    54609    C      G  G_
                                CT ATTTGCAG GG  GAG
                                || ||||||||  ||  |||
                                GA TAAACGTT CC  CTT
                                 _      G  AG
GAM833  C6orf37  3'  CTAACTCTTGACAAATGAGT   68092        _     GG
                                GCTCATTTG CAGGGG  AG
                                ||||||||| ||||||  ||
                                TGAGTAAAC GTTCTC  TC
                                     A     AA
GAM833  DOC2A    3'  GCTAGTCCCTGCAAATATGC   14563    TC        GG
                                GC  ATTTGCAGGGG  AGC
                                ||  ||||||||||  |||
                                CG  TAAACGTCCCT  TCG
                                 TA         GA
GAM833  FADS1    3'  GCTCCATAAGCAAGTGAGC   26382         AGGGG
                                GCTCATTTGC    GGAGC
                                ||||||||||    |||||
                                CGAGTGAACG    CCTCG
                                     AATA_
GAM833  FLJ20413 3'  CTCAATCCCTGCAAATGA    35595          G_
                                TCATTTGCAGGGG  GAG
                                ||||||||||||  |||
                                AGTAAACGTCCCT  CTC
                                      AA
GAM833  HTATIP2  3'  CTTATGACCGTGCAAATGAGC  22167         G  GG__
                                GCTCATTTGCA GG   GAG
                                |||||||||||  ||   |||
                                CGAGTAAACGT CC   TTC
                                     G  AGTA
GAM833  KIAA1423 3'  CCCAACCCACTAAATGAGC   62392        CA  __
                                GCTCATTTG  GGG  GGG
                                |||||||||  |||  |||
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                                CGAGTAAAT  CCC  CCC
                                     CA   AA
GAM833  MFN1     3'  TTCAACTTGAAAATGAGC    35965        G    GG
                                GCTCATTT CAGG  GGA
                                |||||||| ||||  |||
                                CGAGTAAA GTTC  CTT
                                     A    AA
GAM833  MGC15619 3'  GCCTTAATTGAAAATGAGC   51402        G   GG   A
                                GCTCATTT CAG  GGG GC
                                |||||||| |||  ||| ||
                                CGAGTAAA GTT  TTC CG
                                     A   AA  _
GAM833  MGEA6    5'  GCTCCCCCCCGCAGCCGGC    21013     CAT    A
                                GCT   TTGC GGGGGGAGC
                                |||   |||| |||||||||
                                CGG   GACG CCCCCCTCG
                                  CC_   _
GAM833  NFASC    3'  GCTCCCCCCCCTGCAAGC     70859     CATT        _
                                GCT    TGCAGGGGGG AGC
                                |||    |||||||||| |||
                                CGA    ACGTCCCCCC TCG
                                  _____         C
GAM833  NMT1     3'  GCTCCCCTTCTGAATCAGC    41147     C   TG   _
                                GCT ATT  CAGG GGGGAGC
                                ||| |||  |||| |||||||
                                CGA TAA  GTCT CCCCTCG
                                  C  __   T
GAM833  P114-RHO-GEF 3'  CTCAGCCCCCGGGAAATGAGC  31669        GCA    __
                                GCTCATTT   GGGGG  GAG
                                ||||||||   |||||  |||
                                CGAGTAAA   CCCCC  CTC
                                     GGG    GA
GAM833  TRPV5    5'  CTCAGCTCTGCAAAGAGC    39522      A       GG
                                GCTC TTTGCAGGG  GAG
                                |||| |||||||||  |||
                                CGAG AAACGTCTC  CTC
                                  _       GA
GAM833  LOC126961 3'  GGCTCCCCCCCGCGCGTGA    75121      T   A
                                TCAT TGC GGGGGGAGCC
                                |||| ||| ||||||||||
                                AGTG GCG CCCCCCTCGG
                                  C  _
GAM833  LOC143915 3'  CTCCCCTCGGGCAACAAGC    83906     CAT    A_
                                GCT   TTGC  GGGGGGAG
                                |||   ||||  ||||||||
                                CGA   AACG  CTCCCCTC
                                  AC_   GG
GAM833  LOC145623 5'  TTGGCAGCTCCAGCAAATGAGC 84398          AG    GA
                                GCTCATTTGC  GGGG  GCCAA
                                ||||||||||  ||||  |||||
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                                CGAGTAAACG  CCTC  CGGTT
                                     A_    GA
GAM833   LOC146268 3'  CCCGGGAATCTGCAAATGAGC  78335          _____
                                GCTCATTTGCAGG    GGG
                                ||||||||||||    |||
                                CGAGTAAACGTCT    CCC
                                      AAGGG
GAM833   LOC148479 3'  GGCTTTCTCTGAAATGA    79615      G    GG A
                                TCATTT CAGGG  G GCC
                                |||||| |||||  | |||
                                AGTAAA GTCTC  T CGG
                                   _    TT _
GAM833   LOC148887 3'  GGCTCCCCCGCATGCGC    85405    T  TT   AG
                                GC CA  TGC  GGGGGAGCC
                                || ||  |||  |||||||||
                                CG GT  ACG  CCCCCTCGG
                                 C  __  __
GAM833   LOC196403 3'  GGCCCCTCCAAATGGGC    91191       GCA    A
                                GCTCATTT   GGGGGG GCC
                                ||||||||   |||||| |||
                                CGGGTAAA   CCTCCC CGG
                                     ___    _
GAM833   LOC205100 5'  TGGTCCCTGCAATGAGC    92393       T    GGGA
                                GCTCATT GCAGGG   GCCA
                                ||||||| ||||||   ||||
                                CGAGTAA CGTCCC   TGGT
                                     _    ____
GAM833   LOC207043 3'  GCTCCCCCCGGGTATCAGC   91078    CATT   A_
                                GCT   TGC  GGGGGGAGC
                                |||   |||  |||||||||
                                CGA   ATG  CCCCCCTCG
                                  CT__   GG
GAM833   LOC253786 5'  TTAACTTTTGCAAATGAGC   98836           GG
                                GCTCATTTGCAGGGG  AG
                                ||||||||||||||  ||
                                CGAGTAAACGTTTTC  TT
                                      AA
GAM833   LOC253974 3'  TTTGGCTCCCCCCTGCAAATGA 99286
            GC                   GCTCATTTGCAGGGGGGAGCCAAA
                                ||||||||||||||||||||||||
                                CGAGTAAACGTCCCCCCTCGGTTT

GAM833   LOC256905 3'  TCCATGTCCCTGCAAATGA   98663          ___
                                TCATTTGCAGGGG   GGA
                                ||||||||||||   |||
                                AGTAAACGTCCCT   CCT
                                      GTA
GAM833   LOC257395 3'  GGCTCCCCCCCGCGCGTGA    97149     T   A
                                TCAT TGC GGGGGGAGCC
                                |||| ||| ||||||||||
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                                AGTG GCG CCCCCCTCGG
                                  C  _
GAM833  LOC90233  3'  CCCAGGTCCTGCAAAGGAGC   57193      A       ___
                                GCTC TTTGCAGGG   GGG
                                |||| |||||||||   |||
                                CGAG AAACGTCCT   CCC
                                  G        GGA
GAM834  HADHB    5'  CTCGCGGACGTCAGCCAAGATT 5738          _ _  A   A
           CCA                    TGGAATCTTG C GGC TCC CGAG
                                |||||||||| | ||| ||| ||||
                                ACCTTAGAAC G CTG AGG GCTC
                                     C A   C   C
GAM834  BHLHB2   5'  CTCAAAGCCGAAGATTCCA   14763         G   ATCCAC
                                TGGAATCTT CGGC     GAG
                                ||||||||| ||||     |||
                                ACCTTAGAA GCCG     CTC
                                     _   AAA___
GAM834  CPSF1    3'  CGTGGATGCCGTCACCACCA   65160     AATCTT
                                TGG     GCGGCATCCACG
                                |||     ||||||||||||
                                ACC     TGCCGTAGGTGC
                                  ACCAC_
GAM834  DKFZP434K0427 3'  TCTCACAGATGTGCTGTATCC  50500     ATCT      CCAC__
                                GGA   TGCGGCAT     GAGA
                                |||   ||||||||     ||||
                                CCT   ATGTCGTG     CTCT
                                  _____       TAGACA
GAM834  FLJ14166  3'  TCTCGGTTCCGGAAGATTCCA  44992         G   CATCCA
                                TGGAATCTT CGG     CGAGA
                                ||||||||| |||     |||||
                                ACCTTAGAA GCC     GCTCT
                                     G   TTG___
GAM834  FLJ20618  3'  TCTCACAAGGCTGCACCAGATT 35888         __     ATCCAC
           CCA                    TGGAATCT  TGCGGC     GAGA
                                ||||||||  ||||||     ||||
                                ACCTTAGA  ACGTCG     CTCT
                                     CC     GAACA_
GAM834  LOC125988 5'  TCTCAGAGCCGCAAGACACCA  74900     AA       A  CAC
                                TGG  TCTTGCGGC TC   GAGA
                                |||  ||||||||| ||   ||||
                                ACC  AGAACGCCG AG   CTCT
                                  AC        _  A__
GAM834  LOC148697 3'  TCTCGTGGACACCCACATCTCA 79681    GA  CT  C  CA
                                TG  AT  TG GG  TCCACGAGA
                                ||  ||  || ||  |||||||||
                                AC  TA  AC CC  AGGTGCTCT
                                  TC  C_  _  AC
GAM834  LOC195977 3'  GGATGCCGCCCAAGATTCC   88933         __
                                GGAATCTT  GCGGCATCC
                                ||||||||  |||||||||
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                                CCTTAGAA  CGCCGTAGG
                                     CC
GAM835  GPD1     3'  TCATGCCACCACATTTG     60398       C       C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A      _
GAM835  IL5RA    5'  TCGCATGGCCACCGCATTT   6906           AT__
                                AAATGCGGTGGC   CGA
                                ||||||||||||   |||
                                TTTACGCCACCG   GCT
                                      GTAC
GAM835  MYO1C    3'  TGCCGATGCCAAATATTTG   61873       CGG      A
                                TAAATG   TGGCATCG CA
                                ||||||   |||||||| ||
                                GTTTAT   ACCGTAGC GT
                                   AA_      C
GAM835  C6orf37  3'  TGTCACACTGCATTTA      68097         GCATC
                                TAAATGCGGTG    GACA
                                ||||||||||     ||||
                                ATTTACGTCAC    CTGT
                                      A____
GAM835  DNAJC6   3'  TTGCAGAACCACCGCATT    29498         CA  GA
                                AATGCGGTGG  TC  CAA
                                |||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                      A_  AC
GAM835  FLJ11210 3'  GTCGATGTGCATGCTTTTA   60319     T   GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM835  FLJ12476 3'  TCGATCTTCTGCATTTA     43270        T  C
                                TAAATGCGG GG ATCGA
                                ||||||||| || |||||
                                ATTTACGTC TC TAGCT
                                      T  _
GAM835  KIAA1034 3'  TCGATGGCATCCGCATTTG   63134         _  G
                                TAAATGCGG TG CATCGA
                                ||||||||| || ||||||
                                GTTTACGCC AC GTAGCT
                                      T  G
GAM835  KIAA1987 3'  TCATGTAACTGCATTTA     89391         G   C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                      A   _
GAM835  MGC16063 3'  TGTCCTGGCCACTGCATT    54929          ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
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                                TTACGTCACCG  CTGT
                                      GTC
GAM835  LOC147949 3'  TGTCAGATGTCCACATTGCA  79279     __  _  _
                                TGCG  GTGG CATC GACA
                                |||| |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM835  LOC150577 3'  GTCCTCACCGCATTTG     86258          CATC
                                TAAATGCGGTGG   GAC
                                ||||||||||||   |||
                                GTTTACGCCACT   CTG
                                       C___
GAM835  LOC158219 3'  TGTGTGTCACCACATTT     82694      C      CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                   A       __
GAM835  LOC202020 3'  TGTCTCACCACATTTA      90605      C    CATC
                                TAAATG GGTGG   GACA
                                |||||| |||||   ||||
                                ATTTAC CCACT   CTGT
                                   A    ____
GAM835  LOC90826  5'  TGTCGATGCAGGTTTATTTG  64788      CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                    TTGGA
GAM835  LOC93587  3'  TTGTCTTTACCTGCATTTA   73042       _    CATC
                                TAAATGC GGTGG   GACAA
                                ||||||| |||||   |||||
                                ATTTACG CCATT   CTGTT
                                    T    T___
GAM836  ELF3      3'  TGACCTTGACCTTGACCAA   16685     T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||  ||  ||||
                                AACCA GTTCC   TC   CAGT
                                  _    AGT  ___
GAM836  JAK2      3'  TGACCTTCATTCTGAGACCAA 18318      CAA      AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||  ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_      C_
GAM836  SLC10A2   5'  ACTCTCTGTCTTGACCAA    6590       CAA      A
                                TTGGTT   GGGATGGA AGT
                                ||||||  |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM836  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA 37205      CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
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                                AACCGA    TTG CTTTCAGTG
                                   AA___  A
GAM836  KIAA1958  5'  GTGACTTTGAACCCCAAACC  82788     CAA  ATGG
                                GGTT  GGG   AAAGTCAC
                                ||||  |||   ||||||||
                                CCAA  CCC   TTTCAGTG
                                  A__  CAAG
GAM836  MARCKS   3'  ACTTTCCACCCTGCCCA    11411    TTCA   A
                                TGG   AGGG TGGAAAGT
                                |||   |||| ||||||||
                                ACC   TCCC ACCTTTCA
                                 CG__  _
GAM836  TUB      5'  GTGGGACCATCCCTTAAACC  13898     C       AAAG
                                GGTT AAGGGATGG   TCAC
                                |||| |||||||||   ||||
                                CCAA TTCCCTACC   GGTG
                                  A       AG__
GAM836  LOC80298  3'  ACTTTTACCTTGAACCA    48062         GATG
                                TGGTTCAAGG   GAAAGT
                                ||||||||||   ||||||
                                ACCAAGTTCC   TTTTCA
                                     A___
GAM837  KIT      3'  CTCCCCTTCCTCACTGCCCAAT 5848       A  AATTT  T_
           A                     TATTGG CA    GG  GGGGAG
                                ||||||  ||    ||  ||||||
                                ATAACC GT    CC  CCCCTC
                                   C  CACT_  TT
GAM837  DKFZP434G2226 3'  GCTTTTCAAAGTTTATCCAATA 49155       C     GG  GG
                                TATTGGA AAATTT  TG  GAGC
                                |||||||  ||||||  ||  ||||
                                ATAACCT TTTGAA  AC  TTCG
                                    A     __  TT
GAM837  MIDORI   3'  GCTCCCCACTCCCTGCCCACCA 74216       ACAAATTT_
           ATA                    TATTGG       GGTGGGGAGC
                                ||||||       ||||||||||
                                ATAACC       TCACCCCTCG
                                   ACCCGTCCC
GAM837  LOC132720 3'  CTCCCCACCAAATAATCTCATA 75576     T   CAA
                                TAT GGA   ATTTGGTGGGGAG
                                ||| |||   ||||||||||||||
                                ATA TCT   TAAACCACCCCTC
                                  C   AA_
GAM837  LOC146909 3'  CTCCCCGCCACCCATCCAA   78768      CAAATT
                                TTGGA     TGGTGGGGAG
                                |||||     ||||||||||
                                AACCT     ACCGCCCCTC
                                   ACCC__
GAM837  LOC152273 3'  CTCCCCTGCCCTTGCCAA    81373     A  ATTT  _
                                TTGG CAA    GGT GGGGAG
                                |||| |||    ||| ||||||
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                                AACC GTT   CCG CCCCTC
                                  _  C___  T
GAM838  ELF3     3'  TGACCTTGACCTTGACCAA   16685     T   GAT  AAA
                                TTGGT CAAGG  GG  GTCA
                                ||||| |||||  ||  ||||
                                AACCA GTTCC  TC  CAGT
                                  _    AGT  ___
GAM838  JAK2     3'  TGACCTTCATTCTGAGACCAA  18318      CAA      AA
                                TTGGTT  GGGATGGA  GTCA
                                ||||||  ||||||||  ||||
                                AACCAG  TCTTACTT  CAGT
                                   AG_      C_
GAM838  SLC10A2  5'  ACTCTCTGTCTTGACCAA    6590       CAA      A
                                TTGGTT  GGGATGGA AGT
                                ||||||  |||||||| |||
                                AACCAG  TTCTGTCT TCA
                                  ___       C
GAM838  FLJ10803 3'  GTGACTTTCAGTTAAAGCCAA  37205      CAAGG  G
                                TTGGTT   GAT GAAAGTCAC
                                ||||||   ||| |||||||||
                                AACCGA   TTG CTTTCAGTG
                                   AA___  A
GAM838  KIAA1958 5'  GTGACTTTGAACCCCAAACC  82788     CAA  ATGG
                                GGTT  GGG   AAAGTCAC
                                ||||  |||   ||||||||
                                CCAA  CCC   TTTCAGTG
                                  A__  CAAG
GAM838  MARCKS   3'  ACTTTCCACCCTGCCCA     11411     TTCA  A
                                TGG   AGGG TGGAAAGT
                                |||   |||| ||||||||
                                ACC   TCCC ACCTTTCA
                                 CG__  _
GAM838  TUB      5'  GTGGGACCATCCCTTAAACC   13898     C       AAAG
                                GGTT AAGGGATGG   TCAC
                                |||| |||||||||   ||||
                                CCAA TTCCCTACC   GGTG
                                  A       AG__
GAM838  LOC80298 3'  ACTTTTACCTTGAACCA     48062        GATG
                                TGGTTCAAGG   GAAAGT
                                ||||||||||   ||||||
                                ACCAAGTTCC   TTTTCA
                                     A___
GAM839  GPD1     3'  TCATGCCACCACATTTG     60398       C       C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A       _
GAM839  IL5RA    5'  TCGCATGGCCACCGCATTT   6906          AT__
                                AAATGCGGTGGC   CGA
                                ||||||||||||   |||
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                                TTTACGCCACCG   GCT
                                      GTAC
GAM839  MYO1C    3'  TGCCGATGCCAAATATTTG   61873      CGG      A
                                TAAATG  TGGCATCG CA
                                ||||||  |||||||| ||
                                GTTTAT  ACCGTAGC GT
                                   AA_      C
GAM839  C6orf37  3'  TGTCACACTGCATTTA     68097         GCATC
                                TAAATGCGGTG    GACA
                                ||||||||||    ||||
                                ATTTACGTCAC    CTGT
                                      A____
GAM839  DNAJC6   3'  TTGCAGAACCACCGCATT    29498        CA  GA
                                AATGCGGTGG  TC  CAA
                                |||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                      A_  AC
GAM839  FLJ11210 3'  GTCGATGTGCATGCTTTTA   60319     T  GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM839  FLJ12476 3'  TCGATCTTCTGCATTTA     43270        T  C
                                TAAATGCGG GG ATCGA
                                |||||||| || |||||
                                ATTTACGTC TC TAGCT
                                      T  _
GAM839  KIAA1034 3'  TCGATGGCATCCGCATTTG   63134        _  G
                                TAAATGCGG TG CATCGA
                                |||||||| || ||||||
                                GTTTACGCC AC GTAGCT
                                      T  G
GAM839  KIAA1987 3'  TCATGTAACTGCATTTA     89391        G   C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                      A   _
GAM839  MGC16063 3'  TGTCCTGGCCACTGCATT    54929         ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                      GTC
GAM839  LOC147949 3'  TGTCAGATGTCCACATTGCA  79279     __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM839  LOC150577 3'  GTCCTCACCGCATTTG     86258         CATC
                                TAAATGCGGTGG   GAC
                                ||||||||||||   |||
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                                GTTTACGCCACT   CTG
                                      C___
GAM839  LOC158219 3'  TGTGTGTCACCACATTT    82694      C      CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                   A      __
GAM839  LOC202020 3'  TGTCTCACCACATTTA     90605      C    CATC
                                TAAATG GGTGG   GACA
                                |||||| |||||   ||||
                                ATTTAC CCACT   CTGT
                                   A    ____
GAM839  LOC90826  5'  TGTCGATGCAGGTTTATTTG  64788      CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                   TTGGA
GAM839  LOC93587  3'  TTGTCTTTACCTGCATTTA   73042      _    CATC
                                TAAATGC GGTGG   GACAA
                                ||||||| |||||   |||||
                                ATTTACG CCATT   CTGTT
                                    T    T___
GAM840  ELF3      3'  TGACCTTGACCTTGACCAA   16685     T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                   _    AGT  ___
GAM840  JAK2      3'  TGACCTTCATTCTGAGACCAA 18318      CAA      AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_      C_
GAM840  SLC10A2   5'  ACTCTCTGTCTTGACCAA    6590       CAA      A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM840  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA 37205      CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM840  KIAA1958  5'  GTGACTTTGAACCCCAAACC  82788     CAA   ATGG
                                GGTT   GGG   AAAGTCAC
                                ||||   |||   ||||||||
                                CCAA   CCC   TTTCAGTG
                                  A__   CAAG
GAM840  MARCKS    3'  ACTTTCCACCCTGCCCA    11411     TTCA   A
                                TGG   AGGG TGGAAAGT
                                |||   |||| ||||||||
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                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM840  TUB      5'  GTGGGACCATCCCTTAAACC   13898      C        AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A        AG__
GAM840  LOC80298 3'  ACTTTTACCTTGAACCA     48062          GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                      A___
GAM841  EHF      3'  TCCAAAACCCAAGGTTGGCT   25127     AT   _    C
                                AGT  GCCT GGGT TTGGA
                                |||  |||| |||| |||||
                                TCG  TGGA CCCA AACCT
                                  GT    A    A
GAM841  EPHA2    3'  CCATCGGCCAAGAATACTTGAA 16675          GC  G    T_
           G                     CTTCAAGTAT  CT GGTC  TGG
                                |||||||||  || ||||  |||
                                GAAGTTCATA  GA CCGG  ACC
                                      A_  A    CT
GAM841  ITGA5    3'  CCCAGAGACATACTTGAAG    61933          C__
                                CTTCAAGTATG   CTGGG
                                ||||||||||   |||||
                                GAAGTTCATAC   GACCC
                                      AGA
GAM841  TREM2    3'  TCCAAGACTGTCATATTT     39098        CCTG
                                AAGTATG    GGTCTTGGA
                                |||||||    |||||||||
                                TTTATAC    TCAGAACCT
                                    TG__
GAM841  UQCRB    3'  CCAACATAGGCATACTTAAG   21939     C         GGTC
                                CTT AAGTATGCCTG    TTGG
                                ||| ||||||||||    ||||
                                GAA TTCATACGGAT    AACC
                                  _         AC__
GAM841  ATP10D   3'  CAGAGACCACTTGAAG      73526         ATGCCTG    _
                                CTTCAAGT      GGTCT TG
                                ||||||||      ||||| ||
                                GAAGTTCA      CCAGA AC
                                    _______     G
GAM841  B3GNT7   3'  CCCTTCCAGGCAACCTGAA   71678      A  A       TCTT
                                TTCA GT TGCCTGGG    GG
                                |||| || ||||||||    ||
                                AAGT CA ACGGACCT    CC
                                  C  _       TC__
GAM841  DKFZp547I224 3'  TCCAAAATTGACCACATACTTG 39963          CCTG   _____
           GA                     TTCAAGTATG    GGTC    TTGGA
                                |||||||||    ||||    |||||
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                                AGGTTCATAC   CCAG   AACCT
                                     A___   TTAA
GAM841  FLJ22341  3'  CCAAGCTCAGGCACACCCAAG  45114    CAA  A     T
                                CTT   GT TGCCTGGG CTTGG
                                |||   || |||||||| |||||
                                GAA   CA ACGGACTC GAACC
                                  CC_  C      _
GAM841  KIAA0779  3'  CCGAACAGCATACTTGAAG   86908         C  GGTC
                                CTTCAAGTATGC TG   TTGG
                                |||||||||||| ||   ||||
                                GAAGTTCATACG AC   AGCC
                                      _ A___
GAM841  LOC144233 3'  CCAAGGCACATAATTGAA   77246     G   CCTGG
                                TTCAA TATG    GTCTTGG
                                ||||| ||||    |||||||
                                AAGTT ATAC    CGGAACC
                                   A   A____
GAM841  LOC147341 3'  ACCCAGGCATAACTGAAG   85116     AG
                                CTTCA  TATGCCTGGGT
                                |||||  ||||||||||
                                GAAGT  ATACGGACCCA
                                   CA
GAM841  LOC221088 5'  TCCAAGGTGCTGGCCACTCGAA 94888    A   AT   TGGG
          G                     CTTC AGT  GCC   TCTTGGA
                                |||| |||  |||   |||||||
                                GAAG TCA  CGG   GGAACCT
                                  C   C_   TCGT
GAM842  TERF1    3'  CCCAAATCCTGTTCCAATGA   34391       C   TA   C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                     _   C_   A
GAM842  FLJ10159  3'  CCATGTCACGCCATCCAATGAC 36334       CA_   A   TC
                                GTCATTGGA   CGT GAT  GG
                                |||||||||   ||| |||  ||
                                CAGTAACCT   GCA CTG  CC
                                     ACC   _   TA
GAM842  FLJ14213  3'  CCGATGCTCCCAATGACG    46216       ACAC   GAT
                                CGTCATTGG   GTA   TCGG
                                |||||||||   |||   ||||
                                GCAGTAACC   CGT   AGCC
                                     CT__   ___
GAM842  MGC10715  3'  ATTTACCAGACATCCAATGAC  44495       CAC___
                                GTCATTGGA     GTAGAT
                                |||||||||     ||||||
                                CAGTAACCT     CATTTA
                                     ACAGAC
GAM842  MOST2    5'  CCAGGACTGCCCAATGAC    40059       ACAC   A   _
                                GTCATTGG   GTAG TTC GG
                                ||||||||   |||| ||| ||
```

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                                CAGTAACC   CGTC AGG CC
                                    ____   _  A
GAM842  LOC150370 3'  CCGGGTCTACGTGCCCATGAC  86123      T  A
                                GTCAT GG CACGTAGATTCGG
                                |||||| || ||||||||||||
                                CAGTA CC GTGCATCTGGGCC
                                   C  _
GAM842  LOC152620 3'  CCCAAATCCTGTTCCAATGA   60707       C   TA   C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                     _  C_   A
GAM842  LOC158668 3'  CCCAAATCCTGTTCCAATGA   69896       C   TA   C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                     _  C_   A
GAM843  ELF3    3'  TGACCTTGACCTTGACCAA   16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                   _    AGT  ___
GAM843  JAK2    3'  TGACCTTCATTCTGAGACCAA  18318       CAA      AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_      C_
GAM843  SLC10A2  5'  ACTCTCTGTCTTGACCAA    6590       CAA      A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM843  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM843  KIAA1958  5'  GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||   ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM843  MARCKS   3'  ACTTTCCACCCTGCCCA     11411     TTCA   A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM843  TUB     5'  GTGGGACCATCCCTTAAACC   13898      C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
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                                CCAA TTCCCTACC   GGTG
                                  A       AG__
GAM843  LOC80298  3'  ACTTTTACCTTGAACCA    48062        GATG
                                TGGTTCAAGG   GAAAGT
                                ||||||||||   ||||||
                                ACCAAGTTCC   TTTTCA
                                     A___
GAM844  ELF3      3'  TGACCTTGACCTTGACCAA   16685     T   GAT  AAA
                                TTGGT CAAGG  GG  GTCA
                                ||||| |||||  ||  ||||
                                AACCA GTTCC  TC  CAGT
                                  _    AGT  ___
GAM844  JAK2      3'  TGACCTTCATTCTGAGACCAA 18318     CAA      AA
                                TTGGTT  GGGATGGA GTCA
                                ||||||  |||||||| ||||
                                AACCAG  TCTTACTT CAGT
                                   AG_      C_
GAM844  SLC10A2   5'  ACTCTCTGTCTTGACCAA   6590      CAA      A
                                TTGGTT  GGGATGGA AGT
                                ||||||  |||||||| |||
                                AACCAG  TTCTGTCT TCA
                                   ___      C
GAM844  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA 37205     CAAGG  G
                                TTGGTT   GAT GAAAGTCAC
                                ||||||   ||| |||||||||
                                AACCGA   TTG CTTTCAGTG
                                   AA___  A
GAM844  KIAA1958  5'  GTGACTTTGAACCCCAAACC  82788    CAA  ATGG
                                GGTT  GGG   AAAGTCAC
                                ||||  |||   ||||||||
                                CCAA  CCC   TTTCAGTG
                                  A__  CAAG
GAM844  MARCKS    3'  ACTTTCCACCCTGCCCA    11411    TTCA   A
                                TGG   AGGG TGGAAAGT
                                |||   |||| ||||||||
                                ACC   TCCC ACCTTTCA
                                  CG__   _
GAM844  TUB       5'  GTGGGACCATCCCTTAAACC  13898    C      AAAG
                                GGTT AAGGGATGG   TCAC
                                |||| |||||||||   ||||
                                CCAA TTCCCTACC   GGTG
                                  A       AG__
GAM844  LOC80298  3'  ACTTTTACCTTGAACCA    48062        GATG
                                TGGTTCAAGG   GAAAGT
                                ||||||||||   ||||||
                                ACCAAGTTCC   TTTTCA
                                     A___
GAM845  GPD1      3'  TCATGCCACCACATTTG     60398      C      C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
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                                GTTTAC CCACCGTA CT
                                   A      _
GAM845  IL5RA    5'  TCGCATGGCCACCGCATTT   6906          AT__
                                AAATGCGGTGGC   CGA
                                ||||||||||||   |||
                                TTTACGCCACCG   GCT
                                     GTAC
GAM845  MYO1C    3'  TGCCGATGCCAAATATTTG   61873      CGG      A
                                TAAATG   TGGCATCG CA
                                ||||||   |||||||| ||
                                GTTTAT   ACCGTAGC GT
                                   AA_      C
GAM845  C6orf37  3'  TGTCACACTGCATTTA     68097         GCATC
                                TAAATGCGGTG    GACA
                                ||||||||||     ||||
                                ATTTACGTCAC    CTGT
                                     A____
GAM845  DNAJC6   3'  TTGCAGAACCACCGCATT    29498         CA  GA
                                AATGCGGTGG  TC  CAA
                                ||||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                     A_  AC
GAM845  FLJ11210 3'  GTCGATGTGCATGCTTTTA   60319     T   GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM845  FLJ12476 3'  TCGATCTTCTGCATTTA     43270         T  C
                                TAAATGCGG GG ATCGA
                                |||||||||  || |||||
                                ATTTACGTC TC TAGCT
                                     T  _
GAM845  KIAA1034 3'  TCGATGGCATCCGCATTTG   63134         _  G
                                TAAATGCGG TG CATCGA
                                |||||||||  || ||||||
                                GTTTACGCC AC GTAGCT
                                     T  G
GAM845  KIAA1987 3'  TCATGTAACTGCATTTA     89391         G   C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                     A   _
GAM845  MGC16063 3'  TGTCCTGGCCACTGCATT    54929          ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                     GTC
GAM845  LOC147949 3'  TGTCAGATGTCCACATTGCA  79279      __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
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                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM845  LOC150577 3'  GTCCTCACCGCATTTG     86258          CATC
                                TAAATGCGGTGG   GAC
                                ||||||||||||   |||
                                GTTTACGCCACT   CTG
                                       C___
GAM845  LOC158219 3'  TGTGTGTCACCACATTT     82694      C      CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                  A       __
GAM845  LOC202020 3'  TGTCTCACCACATTTA      90605      C    CATC
                                TAAATG GGTGG   GACA
                                |||||| |||||   ||||
                                ATTTAC CCACT   CTGT
                                   A    _____
GAM845  LOC90826  5'  TGTCGATGCAGGTTTATTTG  64788      CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                   TTGGA
GAM845  LOC93587  3'  TTGTCTTTACCTGCATTTA   73042      _    CATC
                                TAAATGC GGTGG   GACAA
                                ||||||| |||||   |||||
                                ATTTACG CCATT   CTGTT
                                    T    T___
GAM846  AGL     3'  GTTCACAATTTTTTTAATGTA  5254           GT_
                                TACATTAAGAAAATTG  AC
                                ||||||||||||||||  ||
                                ATGTAATTTTTTTAAC  TG
                                          ACT
GAM846  AGL     3'  GTTCACAATTTTTTTAATGTA  7199           GT_
                                TACATTAAGAAAATTG  AC
                                ||||||||||||||||  ||
                                ATGTAATTTTTTTAAC  TG
                                          ACT
GAM846  AGL     3'  GTTCACAATTTTTTTAATGTA  7202           GT_
                                TACATTAAGAAAATTG  AC
                                ||||||||||||||||  ||
                                ATGTAATTTTTTTAAC  TG
                                          ACT
GAM846  AGL     3'  GTTCACAATTTTTTTAATGTA  7205           GT_
                                TACATTAAGAAAATTG  AC
                                ||||||||||||||||  ||
                                ATGTAATTTTTTTAAC  TG
                                          ACT
GAM846  AGL     3'  GTTCACAATTTTTTTAATGTA  7208           GT_
                                TACATTAAGAAAATTG  AC
                                ||||||||||||||||  ||
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                                ATGTAATTTTTTTAAC  TG
                                      ACT
GAM846  AGL     3'  GTTCACAATTTTTTTAATGTA  7217            GT_
                                TACATTAAGAAAATTG  AC
                                ||||||||||||||||  ||
                                ATGTAATTTTTTTAAC  TG
                                      ACT
GAM846  APPL    3'  GTTGTTAGAAGATTTTTTAATG 24955         A  GGT_
           TA                    TACATTAAGAAA TT   ACAAC
                                ||||||||||| ||   |||||
                                ATGTAATTTTTT GA   TGTTG
                                      A  AGAT
GAM846  ARHGEF7  3'  GGTTGTGTGGACTCCTTAATG  15324       AAAA  GG
                                CATTAAG   TT  TACAACC
                                |||||||   ||  |||||||
                                GTAATTC   AG  GTGTTGG
                                    CTC_  GT
GAM846  C18orf1  3'  GTTGCACTATCTTAATGT    60870        AAAT   A
                                ACATTAAGA   TGGT CAAC
                                |||||||||   |||| ||||
                                TGTAATTCT   ATCA GTTG
                                     ____   C
GAM846  CLECSF12 3'  TTGTACCAATTTTACTAA    77222    AG
                                TTA  AAAATTGGTACAA
                                |||  ||||||||||||
                                AAT  TTTTAACCATGTT
                                  CA
GAM846  CYP26A1  3'  GTTTAGTATTTTCTTAGTGTA  7599          TGGT_
                                TACATTAAGAAAAT    AC
                                ||||||||||||||   ||
                                ATGTGATTCTTTTA    TG
                                      TGATT
GAM846  CYP26A1  3'  GTTTAGTATTTTCTTAGTGTA  55124         TGGT_
                                TACATTAAGAAAAT    AC
                                ||||||||||||||   ||
                                ATGTGATTCTTTTA    TG
                                      TGATT
GAM846  DMD     5'  GCCTATTTCCTTAATGTA    15697        A   T
                                TACATTAAG AAAT GGT
                                ||||||||| |||| |||
                                ATGTAATTC TTTA CCG
                                     C   T
GAM846  GHR     3'  GCTATGTTTTTAATGTA     5702          AAT
                                TACATTAAGAA  TGGT
                                ||||||||||  ||||
                                ATGTAATTTTT  ATCG
                                      GT_
GAM846  HIVEP2   3'  TTGTACATTTTTTCTTAATGT  23078         TTG
                                ACATTAAGAAAA  GTACAA
                                ||||||||||||  ||||||
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                                TGTAATTCTTTT  CATGTT
                                      TTA
GAM846  M17S2   3' TGCCTTTTTTCTTAATGT   20914         TT
                                ACATTAAGAAAA  GGTA
                                ||||||||||||  ||||
                                TGTAATTCTTTT  CCGT
                                      TT
GAM846  M17S2   3' TGCCTTTTTTCTTAATGT   49856         TT
                                ACATTAAGAAAA  GGTA
                                ||||||||||||  ||||
                                TGTAATTCTTTT  CCGT
                                      TT
GAM846  M17S2   3' TGCCTTTTTTCTTAATGT   49864         TT
                                ACATTAAGAAAA  GGTA
                                ||||||||||||  ||||
                                TGTAATTCTTTT  CCGT
                                      TT
GAM846  NPPB    3' ACTCATTTTTTTAATGTA   11825          T
                                TACATTAAGAAAAT GGT
                                |||||||||||||| |||
                                ATGTAATTTTTTTA TCA
                                       C
GAM846  STAM    3' TACCATGTTTCTTAATGT   14421         AT
                                ACATTAAGAAA  TGGTA
                                ||||||||||  |||||
                                TGTAATTCTTT  ACCAT
                                      GT
GAM846  TMEM1   3' TTGTCATTTTTTTCTTAATGT 13808         TTGGT
                                ACATTAAGAAAA    ACAA
                                ||||||||||||    ||||
                                TGTAATTCTTTT    TGTT
                                      TTTAC
GAM846  ATP10D  3' TGTACTTTGCTTAATGTA   73531        AAAATT
                                TACATTAAG     GGTACA
                                |||||||||     ||||||
                                ATGTAATTC     TCATGT
                                     GTT___
GAM846  CDW92   3' GCTATTTTTGTTAATGTA   55430        G   T
                                TACATTAA AAAA TGGT
                                |||||||| |||| ||||
                                ATGTAATT TTTT ATCG
                                     G   T
GAM846  DC2     3' GGCTGTACCAATCCTCTAATAT 64920    TA_  AA       A
           G                     CAT   AGA  ATTGGTACA CC
                                 |||   |||  |||||||||| ||
                                 GTA   TCT  TAACCATGT GG
                                   TAA   CC       C
GAM846  DKFZP564A2416 3' GGTTGTGTCATCCTCTCTTAAT 32040   C     AAAT_  GT
           CA                     A ATTAAGA    TG  ACAACC
                                  | |||||||    ||  ||||||
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                                A TAATTCT    AC  TGTTGG
                                 C      CTCCT  TG
GAM846  FER1L4   3'  ATCAGTATCTTCTTAATG    48112        A__
                                CATTAAGAA   ATTGGT
                                |||||||||   ||||||
                                GTAATTCTT   TGACTA
                                     CTA
GAM846  FLJ14624 3'  GTTTTCCATTTTGCTTAATGTA 71845        A   T   TAC
                                TACATTAAG AAA TGG   AAC
                                ||||||||| ||| |||   |||
                                ATGTAATTC TTT ACC   TTG
                                     G   T   TT_
GAM846  KIAA0553 3'  TATAGGATTTTTTTAATGTA   70451           G_
                                TACATTAAGAAAATT  GTA
                                ||||||||||||||  |||
                                ATGTAATTTTTTTAG  TAT
                                          GA
GAM846  KIAA0711 3'  ACCCATTTTCTTACTGTA    30145     T       T
                                TACA TAAGAAAAT GGT
                                |||| |||||||| |||
                                ATGT ATTCTTTTA CCA
                                  C       C
GAM846  KIAA0855 3'  GGTTGGCATTCTTCTTAATGTA 31109          AATTG  A
                                TACATTAAGAA    GT CAACC
                                ||||||||||    || |||||
                                ATGTAATTCTT    CG GTTGG
                                     CTTA_  _
GAM846  KIAA1017 3'  GTTGTACTCAGCATTTCTTAA  24269        A_  _
                                TTAAGAAA  TTG GTACAAC
                                ||||||||  ||| |||||||
                                AATTCTTT  GAC CATGTTG
                                    AC   T
GAM846  LZIC     3'  ATCACATTCTTAATGTA     51397          AAT
                                TACATTAAGAA   TGGT
                                ||||||||||   ||||
                                ATGTAATTCTT   ACTA
                                     AC_
GAM846  NSG-X    3'  ATCAATTTGTTTTTCTTAATGT 27726          _____
                                ACATTAAGAAA    ATTGGT
                                ||||||||||    ||||||
                                TGTAATTCTTT    TAACTA
                                     TTGTT
GAM846  SCDGF-B  3'  ACCAATTAATTTAATGTA    48153        AA
                                TACATTAAG  AATTGGT
                                |||||||||  |||||||
                                ATGTAATTT  TTAACCA
                                     AA
GAM846  SCDGF-B  3'  ACCAATTAATTTAATGTA    53630        AA
                                TACATTAAG  AATTGGT
                                |||||||||  |||||||
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                                ATGTAATTT  TTAACCA
                                     AA
GAM846  TDPGD    3'  TGTCAATATCTTAATGTA    60447        AA   GT
                                TACATTAAGA  ATTG  A
                                ||||||||||  ||||  |
                                ATGTAATTCT  TAAC  T
                                     A_   TG
GAM846  TP53INP1 3'  TGTGCCTTCTTAATGTG    53874         AATT
                                TACATTAAGAA   GGTACA
                                ||||||||||    ||||||
                                GTGTAATTCTT   CCGTGT
                                      ____
GAM846  TP53INP1 3'  TGTGCCTTCTTAATGTG    73323         AATT
                                TACATTAAGAA   GGTACA
                                ||||||||||    ||||||
                                GTGTAATTCTT   CCGTGT
                                      ____
GAM846  LOC121536 3'  GTTGTTTTTTCTTAATGTA   74528          TTGGT
                                TACATTAAGAAAA    ACAAC
                                ||||||||||||     |||||
                                ATGTAATTCTTTT    TGTTG
                                       T____
GAM846  LOC145676 5'  TGCCTGCTTTTCTTAATGT   77849          TT_
                                ACATTAAGAAAA   GGTA
                                ||||||||||||   ||||
                                TGTAATTCTTTT   CCGT
                                       CGT
GAM846  LOC145900 3'  GGTTGGCATTCTTCTTAATGTA 78023         AATTG  A
                                TACATTAAGAA    GT CAACC
                                ||||||||||     || |||||
                                ATGTAATTCTT    CG GTTGG
                                       CTTA_  _
GAM846  LOC145988 3'  GGTTGGCATTCTTCTTAATGTA 78070         AATTG  A
                                TACATTAAGAA    GT CAACC
                                ||||||||||     || |||||
                                ATGTAATTCTT    CG GTTGG
                                       CTTA_  _
GAM846  LOC151438 5'  ATTGATTTTCTTAAGTA    86554     A       TG
                                TAC TTAAGAAAAT  GT
                                |||  ||||||||||  ||
                                ATG AATTCTTTTA  TA
                                  _        GT
GAM846  LOC254428 3'  TTGTACCAACTGCATGTA    97203      TA  AAAA
                                TACAT  AG    TTGGTACAA
                                |||||  ||    |||||||||
                                ATGTA  TC    AACCATGTT
                                   CG  _____
GAM846  LOC254936 3'  GGTTGGCATTCTTCTTAATGTA 96652         AATTG  A
                                TACATTAAGAA    GT CAACC
                                ||||||||||     || |||||
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                                ATGTAATTCTT    CG GTTGG
                                      CTTA_ _
GAM846  LOC50999  3'  ACCGATTTCCATAATGTA    32636       AGA
                                TACATTA   AAATTGGT
                                |||||||   ||||||||
                                ATGTAAT   TTTAGCCA
                                   ACC
GAM847  ABR     3'  AGAACTGGAATGCGTACGTCTT 8450      ACCA  G  C
                                AAGAC   ACG GT CCAGTTCT
                                |||||   ||| || ||||||||
                                TTCTG   TGC TA GGTCAAGA
                                  CA__  G  A
GAM847  ABR     3'  AGAACTGGAATGCGTACGTCTT 41992     ACCA  G  C
                                AAGAC   ACG GT CCAGTTCT
                                |||||   ||| || ||||||||
                                TTCTG   TGC TA GGTCAAGA
                                  CA__  G  A
GAM847  ARF1    3'  AGAACTGGTCTATTTGGTGTC  71194       CG  TC
                                GACACCAA  GG  CCAGTTCT
                                ||||||||  ||  ||||||||
                                CTGTGGTT  TC  GGTCAAGA
                                    TA  T_
GAM847  HERC2   3'  AGAAGGCCATTTGGTGTC    17426       CG   CCAG
                                GACACCAA  GGTC   TTCT
                                ||||||||  ||||   ||||
                                CTGTGGTT  CCGG   AAGA
                                    TA  ____
GAM847  MAP1B   3'  AGAACTGGGAAAACAGTGAATC 20959     __  CAACGGG
          TT                    AAGA  CAC     TCCCAGTTCT
                                ||||  |||     ||||||||||
                                TTCT  GTG     AGGGTCAAGA
                                  AA  ACAAA__
GAM847  MAP1B   3'  AGAACTGGGAAAACAGTGAATC 50089     __  CAACGGG
          TT                    AAGA  CAC     TCCCAGTTCT
                                ||||  |||     ||||||||||
                                TTCT  GTG     AGGGTCAAGA
                                  AA  ACAAA__
GAM847  PRNP    3'  GAACTGGGGTGATGTTTT    6132       C  ACGGG
                                AAGACA CA    TCCCAGTTC
                                ||||||  ||   |||||||||
                                TTTTGT GT    GGGGTCAAG
                                  A  _____
GAM847  RAI14   3'  AGAACTTTCAGCCATGGTGTCT 32098       ACG  CCC_
          T                     AAGACACCA  GGT   AGTTCT
                                |||||||||  |||   ||||||
                                TTCTGTGGT  CCG   TCAAGA
                                    A__  ACTT
GAM847  SLC21A2 3'  AGAACTGGGGGGCTGAGTCTT  20078     ACCAA  G  _
                                AAGAC   CGG TCCC AGTTCT
                                |||||   ||| |||| ||||||
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                                TTCTG    GTC GGGG TCAAGA
                                  A____  G   G
GAM847  CHL1     3'  GAACTGGCTTGGTGACTT   22765    A    CGGGTC
                                AAG CACCAA    CCAGTTC
                                ||| ||||||    |||||||
                                TTC GTGGTT    GGTCAAG
                                  A    C_____
GAM847  CNOT3    5'  GAACTGGGGCTGGTCTCTT   27985    C   ACGG
                                AAGA ACCA   GTCCCAGTTC
                                |||| ||||   ||||||||||
                                TTCT TGGT   CGGGGTCAAG
                                  C   _____
GAM847  ELKS     3'  AGAACTGTGGGAGCTGGTGG  31188    A  G   __
                                CCA CGG TCCCA  GTTCT
                                ||| ||| |||||  |||||
                                GGT GTC AGGGT  CAAGA
                                  G  G    GT
GAM847  PEGASUS  3'  AGAACAGTTAGACACATTGGTG 42688        CGG  CCA__
           TCT                    AGACACCAA  GTC    GTTCT
                                |||||||||  |||    |||||
                                TCTGTGGTT  CAG    CAAGA
                                     ACA  ATTGA
GAM847  PRO2266  5'  AGAACTGGGAACAGGGGTC   38183    A  AACGGG
                                GAC CC     TCCCAGTTCT
                                ||| ||     ||||||||||
                                CTG GG     AGGGTCAAGA
                                  _  GACA__
GAM847  ZNF317   3'  AACTGGGAAGACGAGGCGTT  72469    A  AA  GG_
                                GAC CC  CG   TCCCAGTT
                                ||| ||  ||   ||||||||
                                TTG GG  GC   AGGGTCAA
                                  C  A_  AGA
GAM847  ZNF384   3'  AACTGGGGGTCGGTGCT    56795    A   AAC  G
                                AG CACC   GG TCCCAGTT
                                || ||||   || ||||||||
                                TC GTGG   CT GGGGTCAA
                                  _   ___  G
GAM847  LOC143381 3'  AGAACTGGCCTATTGGCATC  77059    CA   CG  TC
                                GA  CCAA  GG  CCAGTTCT
                                ||  ||||  ||  ||||||||
                                CT  GGTT  CC  GGTCAAGA
                                  AC    AT  __
GAM847  LOC148930 3'  AGGCCTGAGACCCTTGGTGTCT 79839          C    C   TT
           T                     AAGACACCAA GGGTC CAG  CT
                                |||||||||| ||||| |||  ||
                                TTCTGTGGTT CCCAG GTC  GA
                                      _    A   CG
GAM847  LOC165614 5'  AGAACTGAAGGGACACTGGTGT 83482        ACGG   ___
           CT                     AGACACCA   GTCCC   AGTTCT
                                ||||||||   |||||  ||||||
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                                TCTGTGGT   CAGGG  TCAAGA
                                    CA__    AAG
GAM847  LOC200634 3'  GAACTGGGTCTAGGTCTT   90264      ACCAACG  T
                                AAGAC      GG CCCAGTTC
                                |||||      || ||||||||
                                TTCTG      TC GGGTCAAG
                                   GA_____  T
GAM847  LOC253181 5'  GAACTGGGAATGTTGTCT   99416      CCA  GG
                                AGACA  ACG  TCCCAGTTC
                                |||||  |||  |||||||||
                                TCTGT  TGT  AGGGTCAAG
                                   ___  A_
GAM847  LOC253782 3'  AGAACTGGGAACACTTGGGGTC 97395     A   CGGG
          T                      AGAC CCAA   TCCCAGTTCT
                                |||| ||||   ||||||||||
                                TCTG GGTT   AGGGTCAAGA
                                  G   CACA
GAM847  LOC51055  3'  GAACTGGGCCTAGTGTCT   32476      CAAC  T
                                AGACAC   GGG CCCAGTTC
                                ||||||   ||| ||||||||
                                TCTGTG   TCC GGGTCAAG
                                   A___  _
GAM847  LOC56920  3'  AGAACTGGGACCTGAAATAGTC 39793    ACCAA
                                GAC    CGGGTCCCAGTTCT
                                |||    ||||||||||||||
                                CTG    GTCCAGGGTCAAGA
                                  ATAAA
GAM848  ANK3     3'  AAAGATTTTATCTGTAAAC   40973       C   GG
                                GTTTACAGA AAGA  TTT
                                ||||||||| ||||  |||
                                CAAATGTCT TTTT  AAA
                                     A   AG
GAM848  CRYZ     3'  AAACCTCTATTCTAAACT    10308     AC  CA
                                AGTTT  AGA  AGAGGTTT
                                |||||  |||  ||||||||
                                TCAAA  TCT  TCTCCAAA
                                   __  TA
GAM848  DHCR7    3'  CCTCATCTGTAAACTG      9065         CAA
                                CAGTTTACAGA   GAGG
                                ||||||||||   ||||
                                GTCAAATGTCT   CTCC
                                      A__
GAM848  RRM2B    3'  AAACCTCTTGTTTTAAAACT  68430      AC
                                AGTTT  AGACAAGAGGTTT
                                |||||  |||||||||||||
                                TCAAA  TTTGTTCTCCAAA
                                   AT
GAM848  SLC2A6   3'  CTCCTATCTGCAAACTGTG   34570       A   CAA
                                TACAGTTT CAGA   GAG
                                |||||||| ||||   |||
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                                GTGTCAAA GTCT   CTC
                                    C    ATC
GAM848  SPP1     3'  AAACTCCCTGTAAACT      6968          ACAA   G
                                AGTTTACAG    GAG TTT
                                |||||||||    ||| |||
                                TCAAATGTC    CTC AAA
                                    C___   _
GAM848  TEM8     3'  AAACTTCTATAAGACTGTA    50817         ACAGACA
                                TACAGTTT      AGAGGTTT
                                ||||||||      ||||||||
                                ATGTCAGA      TCTTCAAA
                                    ATA____
GAM848  UBL3     3'  GAACAGTCTGCCTGTAAAC    24023         ACA   G_
                                GTTTACAG   AGA  GTTT
                                ||||||||   |||  ||||
                                CAAATGTC   TCT  CAAG
                                    CG_   GA
GAM848  DKFZp547I014 5'  GACCATTTTGTTTGCAAACT   39943       A       _
                                AGTTT CAGACAAGA GGTT
                                ||||| |||||||||| ||||
                                TCAAA GTTTGTTTT CCAG
                                   C        A
GAM848  FLJ10971  3'  AAACCTCTCACCTGAATTTTGT 37480       TTTA   ACA
          G                      TACAG    CAG   AGAGGTTT
                                |||||    |||   ||||||||
                                GTGTT    GTC   TCTCCAAA
                                   TTAA   CAC
GAM848  HTEX4    5'  GAAACATATCTGTAAACT    99565         CAAGAG
                                AGTTTACAGA     GTTTC
                                ||||||||||     |||||
                                TCAAATGTCT     CAAAG
                                    ATA___
GAM848  KIAA0701  3'  AAACCTCTTGTGTTCAC     70092    TT  AG
                                GT  AC  ACAAGAGGTTT
                                ||  ||  ||||||||||||
                                CA  TG  TGTTCTCCAAA
                                 CT  __
GAM848  KIAA0945  3'  GAAACCTCTTGCAGAACT    30902       ACAGA
                                AGTTT    CAAGAGGTTTC
                                |||||    ||||||||||||
                                TCAAG    GTTCTCCAAAG
                                   AC___
GAM848  KIAA1024  3'  GACATTCTATCTGTAAAC    69617         CA   _
                                GTTTACAGA  AGAG GTT
                                |||||||||  |||| |||
                                CAAATGTCT  TCTT CAG
                                    A_    A
GAM848  KIAA1163  3'  GAAACCTCCCGTGAAGACT   79648       A  GACAA
                                AGTTT CA    GAGGTTTC
                                ||||| ||    ||||||||
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                                TCAGA GT    CTCCAAAG
                                  A  GCC__
GAM848  KIAA1203  3'  AAATGTCAGTGTCTATAAACTG 72085        C    A_  G
            TA                    TACAGTTTA AGACA  GA GTTT
                                  ||||||||| |||||  || ||||
                                  ATGTCAAAT TCTGT  CT TAAA
                                       A    GA  G
GAM848  KIAA1718  3'  AAACCTTTCGAAACTGTA    64970        ACAGACA
                                  TACAGTTT      AGAGGTTT
                                  ||||||||      ||||||||
                                  ATGTCAAA      TTTCCAAA
                                       GC_____
GAM848  KIAA1854  3'  GAAACCTCTTGACAAGACTGTA 72208        ACAGA
                                  TACAGTTT    CAAGAGGTTTC
                                  ||||||||    ||||||||||
                                  ATGTCAGA    GTTCTCCAAAG
                                       ACA__
GAM848  KIAA1962  3'  GAAACCCTGGGATGTAAACTTA 82800   C       GACA  A
                                  A AGTTTACA    AG GGTTTC
                                  | ||||||||    || ||||||
                                  A TCAAATGT    TC CCAAAG
                                   T       AGGG  _
GAM848  KLHL8     3'  AAACCTTTTTGTAGACTGTA   63501          CAA
                                  TACAGTTTACAGA   GAGGTTT
                                  ||||||||||||   |||||||
                                  ATGTCAGATGTTT   TTCCAAA
                                                  ___
GAM848  MGC33182  5'  AAACCCTCGCAAACTGTG    76091        ACA  CAA A
                                  TACAGTTT   GA   G GGTTT
                                  ||||||||   ||   | |||||
                                  GTGTCAAA   CT   C CCAAA
                                       CG_  ___ _
GAM848  PTPRU     3'  AATTTCCCCATCTGTAAACTGT 56521          CAA_
            A                     TACAGTTTACAGA    GAGGTT
                                  ||||||||||||    ||||||
                                  ATGTCAAATGTCT    CTTTAA
                                         ACCC
GAM848  PTPRU     3'  AATTTCCCCATCTGTAAACTGT 56525          CAA_
            A                     TACAGTTTACAGA    GAGGTT
                                  ||||||||||||    ||||||
                                  ATGTCAAATGTCT    CTTTAA
                                         ACCC
GAM848  PTPRU     3'  AATTTCCCCATCTGTAAACTGT 20318          CAA_
            A                     TACAGTTTACAGA    GAGGTT
                                  ||||||||||||    ||||||
                                  ATGTCAAATGTCT    CTTTAA
                                         ACCC
GAM848  RIT       3'  GAAGTGTTTATCTGTGAACTG  23583         CA   GG
                                  CAGTTTACAGA  AGA  TTTC
                                  ||||||||||  |||  ||||
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                                GTCAAGTGTCT  TTT  GAAG
                                      A_   GT
GAM848  LOC148438 3'  AAACCTCTTGCCTGAAGC    85308     A   A
                                GTTT CAG CAAGAGGTTT
                                |||| ||| ||||||||||
                                CGAA GTC GTTCTCCAAA
                                  _   C
GAM848  LOC166713 5'  GAACCTCCCGTCTGTAACCTG  88612     T       AA
                                CAG TTACAGAC  GAGGTTT
                                ||| ||||||||  |||||||
                                GTC AATGTCTG  CTCCAAG
                                  C       CC
GAM849  ELF3    3'  TGACCTTGACCTTGACCAA   16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                   _    AGT  ____
GAM849  JAK2    3'  TGACCTTCATTCTGAGACCAA  18318       CAA      AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_       C_
GAM849  SLC10A2   5'  ACTCTCTGTCTTGACCAA    6590       CAA      A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ____       C
GAM849  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA____   A
GAM849  KIAA1958  5'  GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM849  MARCKS    3'  ACTTTCCACCCTGCCCA     11411     TTCA    A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM849  TUB     5'  GTGGGACCATCCCTTAAACC   13898      C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A       AG__
GAM849  LOC80298  3'  ACTTTTACCTTGAACCA     48062          GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
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                                ACCAAGTTCC    TTTTCA
                                      A___
GAM850  PEA15    3'  CCTTTTTGTCTCTCATGGGC   15006       T  AAAATT
                                GCCCAT GA     TGAGAAGG
                                ||||||| ||     ||||||||
                                CGGGTA CT     GTTTTTCC
                                   _ CTCT__
GAM850  RNGTT    3'  CCTTCTCAGCTCACTTCAAT   15064       AAAT_
                                ATTGAA    TTGAGAAGG
                                ||||||    |||||||||
                                TAACTT    GACTCTTCC
                                   CACTC
GAM850  BART1    3'  CTCTTTTTCACATGGGC     25038       _      TTT
                                GCCCAT TGAAAAA   GAG
                                |||||| |||||||   |||
                                CGGGTA ACTTTTT   CTC
                                   C      ___
GAM850  DKFZp434K114 3'  CCTTCTCAAACTCAGCAGC   61384    CCA    AAAA
                                GC   TTGA    TTTGAGAAGG
                                ||   ||||    ||||||||||
                                CG   GACT    AAACTCTTCC
                                 AC_   C___
GAM850  FLJ10287  3'  CTTCTCAAATTTAGGC      39356     CATTGAA
                                GCC      AAATTTGAGAAG
                                |||      ||||||||||||
                                CGG      TTTAAACTCTTC
                                  A_______
GAM850  FLJ11753  3'  CCTTCTTGTGTCCTCAAAGGGC 45413      A    AAAATT
                                GCCC TTGA     TGAGAAGG
                                |||| ||||     ||||||||
                                CGGG AACT     GTTCTTCC
                                  A   CCTGT_
GAM850  FLJ22002  3'  CCTCCTCAAATTCCATTTTGGA 46195    C   TTGAAA      A
           CT                     AG CCA     AATTTGAG AGG
                                || |||     |||||||| |||
                                TC GGT     TTAAACTC TCC
                                 A   TTTACC       C
GAM850  KIAA0427  3'  CTCTGTTTTCTCAAAGGGCT   29378      A   _    TT
                                AGCCC TTGA AAAAT  GAG
                                ||||| |||| |||||  |||
                                TCGGG AACT TTTTG  CTC
                                   A   C    T_
GAM850  KIAA1328  3'  CTTCTCAAACTTCTGCT     62323     CCATT   AAA
                                AGC    GAA   TTTGAGAAG
                                |||    |||   |||||||||
                                TCG    CTT   AAACTCTTC
                                  T_____   C__
GAM850  MGC9753   5'  CTCGTTTCTCAATGGCCT    54189    C      A    TT
                                AG CCATTGA AAAT  GAG
                                || ||||||| ||||  |||
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                                TC GGTAACT TTTG  CTC
                                 C      C   __
GAM850  NFAT5    3'  CCTTTGTTCTTTGAATGGGCT  57785        G   AATTTGA
                                AGCCCATT AAA      GAAGG
                                |||||||| |||      |||||
                                TCGGGTAA TTT      TTTCC
                                    G   CTTG___
GAM850  PXMP4    3'  CTTCTCAAGATCATAGGC    24332     CAT   AAAA
                                GCC   TGA   TTTGAGAAG
                                |||   |||   |||||||||
                                CGG   ACT   GAACTCTTC
                                  AT_   A___
GAM850  RGS19    3'  CCTCCCCAGGCAGCCAATGGGC 20799         AAAAA    AGA
                                GCCCATTG    TTTG   AGG
                                ||||||||    ||||   |||
                                CGGGTAAC    GGAC   TCC
                                    CGAC_    CCC
GAM850  LOC128400 5'  CCTTCTCGCCACTCTTCTCAAG 76285       A    AAAATT___
            GGCT                    AGCCC TTGA        TGAGAAGG
                                ||||| ||||        ||||||||
                                TCGGG AACT        GCTCTTCC
                                  _   CTTCTCACC
GAM850  LOC145622 5'  CTTTGTCTTTCAGTGAGCT   77814     C       AATTTGA
                                AGC CATTGAAA      GAAG
                                ||| ||||||||      ||||
                                TCG GTGACTTT      TTTC
                                  A       CTG____
GAM850  LOC90844  3'  CCTTCTCAAACTCAATAGC   64879    CC    AAAA
                                GC  ATTGA   TTTGAGAAGG
                                ||  |||||   ||||||||||
                                CG  TAACT   AAACTCTTCC
                                 A_    C___
GAM851  AP2B1    3'  CATATGCCCCTGGAGCCCCA   8890     AAG       CCC
                                TGG   TCCAGGGGC   ATG
                                |||   |||||||||   |||
                                ACC   AGGTCCCCG   TAC
                                  CCG       TA_
GAM851  CELSR2   3'  TCAGCGCCCCTGGACCCCCA   9199     AA        CCCA
                                TGG  GTCCAGGGGC    TGA
                                |||  ||||||||||    |||
                                ACC  CAGGTCCCCG    ACT
                                  CC        CG__
GAM851  MAN2A2   3'  TCACTGCCCTGTGACTTCCA   21517        CA    CCCA
                                TGGAAGTC  GGGGC    TGA
                                ||||||||  |||||    |||
                                ACCTTCAG  TCCCG    ACT
                                    TG    TC__
GAM851  MAPK3    3'  CACGGGGCCTCGGGACCTC    73773    A   A       A
                                GA GTCC GGGGCCCC TG
                                || |||| |||||||| ||
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                                CT CAGG CTCCGGGG AC
                                 C   G       C
GAM851  TMEFF2   5' TCGTCTGCCCCTGGACTCCC  32999    A        CCC
                                GG AGTCCAGGGGC  ATGA
                                || |||||||||||  ||||
                                CC TCAGGTCCCCG  TGCT
                                 C         TC_
GAM851  APBA3    3' CATGGCCCCGGAGCCCCA   18086    AAG  A    CC
                                TGG  TCC GGGGCC  ATG
                                |||  ||| ||||||  |||
                                ACC  AGG CCCCGG  TAC
                                 CCG  _    __
GAM851  CRA      3' CTTCATGGTTCCTGGACCCCC 22935    AA       CC
                                GG  GTCCAGGGGCC  ATGAAG
                                ||  ||||||||||  ||||||
                                CC  CAGGTCCTTGG  TACTTC
                                 CC         __
GAM851  FLJ32334 3' CGTGGAGGCCACCTGGACTTCC 58606          _   _
           A                     TGGAAGTCCAGG GGCC CCATG
                                 |||||||||||| |||| |||||
                                 ACCTTCAGGTCC CCGG GGTGC
                                        A   A
GAM851  KIAA0265 3' CTTCATAGAGTTCTAGGACTTC 70440        A    CCC
           C                     GGAAGTCC GGGGC  ATGAAG
                                 |||||||| |||||  ||||||
                                 CCTTCAGG TCTTG  TACTTC
                                      A    AGA
GAM851  KIAA1115 3' TTCTCTCCTCTGGACCCCCA  30698    AA       CCCCAT
                                TGG  GTCCAGGGG     GAA
                                |||  |||||||||     |||
                                ACC  CAGGTCTCC     CTT
                                 CC        TCT___
GAM851  KIAA1272 3' TCACAAACCTTGGACTTCCA  70734          GCCCCA
                                TGGAAGTCCAGGG     TGA
                                ||||||||||||     |||
                                ACCTTCAGGTTCC     ACT
                                       AAAC__
GAM851  KIAA1828 5' CTTCACAGGGCCCCTGCACACC 74204    AA  C       CA
                                GG  GT CAGGGGCCC  TGAAG
                                ||  || |||||||||  |||||
                                CC  CA GTCCCCGGG  ACTTC
                                 A_  C        AC
GAM851  LATS1    3' CTTCATGGGAACCAAACTCTCA 60910    GA   CCAG  GC
                                TG  AGT    GG  CCCATGAAG
                                ||  |||    ||  |||||||||
                                AC  TCA    CC  GGGTACTTC
                                 TC   AA__  AA
GAM851  NGEF     3' CATGCCCCTGGCCCCCA     69681     AA T       CCC
                                TGG  G CCAGGGGC   ATG
                                |||  | ||||||||   |||
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                                ACC  C GGTCCCCG   TAC
                                  CC _      ___
GAM851  PSMA4    3'  CTTCATGGACGTCTTAATCTTC 12453       TCCA    C_
           CA                     TGGAAG   GGGGC  CCATGAAG
                                |||||||   |||||  ||||||||
                                ACCTTC    TTCTG  GGTACTTC
                                   TAA_    CA
GAM851  SEMA5A   3'  CTTCATAAAGCCGCTCTTCC   15593      TCC  G   CCC
                                GGAAG   AG GGC   ATGAAG
                                |||||   || |||   ||||||
                                CCTTC   TC CCG   TACTTC
                                   ___  G   AAA
GAM851  LOC148137 3'  CTTTTGGGCCCCCAGCTCCCA  59097     A   CCA      CAT
                                TGG AGT   GGGGCCC   GAAG
                                ||| |||   |||||||   ||||
                                ACC TCG   CCCCGGG   TTTC
                                  C   AC_     T__
GAM851  LOC149876 5'  TTAGGAGCCCCCTGACTTCCA  80353        CA    C  A
                                TGGAAGTC  GGGGC CC TGA
                                ||||||||  ||||| || |||
                                ACCTTCAG  CCCCG GG ATT
                                     TC    A  _
GAM851  LOC163412 5'  TCAGCTCCTGGACCCCCA    83019     AA        CCCA
                                TGG  GTCCAGGGGC    TGA
                                |||  ||||||||||    |||
                                ACC  CAGGTCCTCG    ACT
                                  CC         _____
GAM851  LOC199986 5'  TCAGGGGCCCCTAGCTCCCA   91512     A   CC       A
                                TGG AGT  AGGGGCCCC TGA
                                ||| |||  ||||||||| |||
                                ACC TCG  TCCCCGGGG ACT
                                  C   A_       _
GAM851  LOC205272 5'  CATCCGCCCCGACTTCCA    91064        CA    CCC
                                TGGAAGTC  GGGGC   ATG
                                ||||||||  |||||   |||
                                ACCTTCAG  CCCCG   TAC
                                     __     CC_
GAM851  LOC220758 3'  CATGGGGCTCCAGTTCCA    92461      GTCCA
                                TGGAA    GGGGCCCCATG
                                |||||    ||||||||||
                                ACCTT    CCTCGGGGTAC
                                   GA___
GAM851  LOC221410 3'  TTCATGGAGCCTGCTTC     93701       CCAG    C
                                GAAGT    GGGC CCATGAA
                                |||||    |||| |||||||
                                CTTCG    TCCG GGTACTT
                                   _____     A
GAM851  LOC54550  5'  TCAGTTCCCCCTGGATCCCA   78188     AA       CCCCA
                                TGG  GTCCAGGGG    TGA
                                |||  |||||||||    |||
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                                ACC  TAGGTCCCC    ACT
                                  C_       CTTG_
GAM851  LOC90632  5' CATGGAACCCTGGACCCA    64403     AA      GCC
                                TGG  GTCCAGGG   CCATG
                                |||  ||||||||   |||||
                                ACC  CAGGTCCC   GGTAC
                                  __       AA_
GAM852  ATRX      5' AAAGATGGGCTTCATGGGATT  57074        ATT  TT
                                GATCCCAT   GT  CCATCTTT
                                ||||||||   ||  ||||||||
                                TTAGGGTA   CG  GGTAGAAA
                                     CTT  __
GAM852  BACE      3' AAAGACAGGGAATAGTGGGATC 58076        AT      A_
                                GATCCCAT  TGTTTCC  TCTTT
                                ||||||||  |||||||  |||||
                                CTAGGGTG  ATAAGGG  AGAAA
                                     __       AC
GAM852  BACE      3' AAAGACAGGGAATAGTGGGATC 25025        AT      A_
                                GATCCCAT  TGTTTCC  TCTTT
                                ||||||||  |||||||  |||||
                                CTAGGGTG  ATAAGGG  AGAAA
                                     __       AC
GAM852  ELMO1     5' AAAGATGGACTTACGGGA     56151      A  TTGTT
                                TCCC TA     TCCATCTTT
                                |||| ||     |||||||||
                                AGGG AT     AGGTAGAAA
                                  C  TC___
GAM852  GFRA2     5' AAAGACAAAAAAACGGTGGGAT 9460         AT    CCA__
           T                     GATCCCAT  TGTTT    TCTTT
                                ||||||||  |||||    |||||
                                TTAGGGTG  GCAAA    AGAAA
                                     __    AAAAC
GAM852  GSBS      3' AAAGATGGAAAAGATACAAGA  92730     CCA    G
                                TC   TATT TTTCCATCTTT
                                ||   |||| ||||||||||
                                AG   ATAG AAAGGTAGAAA
                                  AAC    A
GAM852  ARFGAP1   3' AAAGATGGAAATGCTGG     37135     TAT
                                CCA   TGTTTCCATCTTT
                                |||   ||||||||||||
                                GGT   GTAAAGGTAGAAA
                                  C__
GAM852  DKFZP566F2124 3'  AAATAATTCTTTAATGGGATC  32213        _______
                                GATCCCAT     ATTGTTT
                                ||||||||     |||||||
                                CTAGGGTA     TAATAAA
                                     ATTTCT
GAM852  FBH1      5' AAAGATGGACAAACAGAGATC  52504      CCATA    __
                                GATC    TTGTT  TCCATCTTT
                                ||||    |||||  |||||||||
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                                CTAG    GACAA  AGGTAGAAA
                                  A____    AC
GAM852  KIAA1136  3'  AAAGATGGAGAAACAGGATC  92952      CATATTG
                                GATCC      TTTCCATCTTT
                                |||||      ||||||||||
                                CTAGG      AGAGGTAGAAA
                                   ACAA___
GAM852  PFTK1     3'  AAAGATGAAAAAGGGAATGGG  25684      A  G   C_
                                CCCAT TT TTT  CATCTTT
                                ||||| || |||  |||||||
                                GGGTA GG AAA  GTAGAAA
                                   A  G   AA
GAM852  PLA2G12   3'  AAAGATGGATTTAATGAGAT   48775    CCA    TT
                                ATC   TATTG  TCCATCTTT
                                |||   |||||  |||||||||
                                TAG   GTAAT  AGGTAGAAA
                                  A__    TT
GAM852  LOC150166 5'  ATGGCAACAATATGGATTC    86031    TC        T
                                GA  CCATATTGTT CCAT
                                ||  |||||||||| ||||
                                CT  GGTATAACAA GGTA
                                 TA        C
GAM852  LOC219894 3'  AAAGATGGAAACTAGGGA    94894     ATATT
                                TCCC    GTTTCCATCTTT
                                ||||    ||||||||||||
                                AGGG    CAAAGGTAGAAA
                                  AT___
GAM852  LOC257327 5'  AAAGATGGACTCCGATGGATC  99337      CAT    TT_
                                GATCC   ATTG   TCCATCTTT
                                |||||   ||||   |||||||||
                                CTAGG   TAGC   AGGTAGAAA
                                   ___   CTC
GAM852  LOC90925  3'  AGAGAACAACATGGGA      65054       A     CCA
                                TCCCAT TTGTTT   TCT
                                |||||| ||||||   |||
                                AGGGTA AACAAG   AGA
                                   C     ___
GAM853  DGKB      3'  TTATGTTTTCAAACATGC     94111         _
                                GCATGTTT AAAATGTGG
                                |||||||| |||||||||
                                CGTACAAA TTTTGTATT
                                     C
GAM853  PNN       3'  TCTAACTTAAACATGCTGAT   71664     _       AAT  G
                                ATC GCATGTTTAA   GT GGA
                                ||| ||||||||||   || |||
                                TAG CGTACAAATT   CA TCT
                                  T         ___  A
GAM853  RABL2B    3'  TCCCACATTCTAGGCCCGTGAT 23988      AT    A
                                ATCGC  GTTTA AATGTGGGA
                                |||||  ||||| |||||||||
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                                TAGTG  CGGAT TTACACCCT
                                  CC     C
GAM853  TLX1     3'  CCCACATTTGTGCCGA      19816     _  GTTTA
                                TCG CAT     AAATGTGGG
                                ||| |||     |||||||||
                                AGC GTG     TTTACACCC
                                  C  _____
GAM853  TRPC6    3'  CCCACACTTAGCCATTGA    17290     C  T   AA
                                TCG ATG TTAA  TGTGGG
                                ||| ||| ||||  ||||||
                                AGT TAC GATT  ACACCC
                                  _  C   C_
GAM853  XPNPEP2  3'  TCCCACATTTCTTGGATG    14145     G  TGTTTA
                                CATC CA     AAATGTGGGA
                                |||| ||     ||||||||||
                                GTAG GT     TTTACACCCT
                                  _ TC____
GAM853  ZNF3     3'  TTCCCACACTTGGTGCACACG  35274    CA   TTA  A
                                CG  TGT   AA TGTGGGAA
                                ||  |||   || ||||||||
                                GC  ACG   TT ACACCCTT
                                 AC   TGG  C
GAM853  AWP1     3'  TTCCAGTATTAAACATGC     39181          A  G
                                GCATGTTTAA AT TGGGA
                                |||||||||| || |||||
                                CGTACAAATT TG ACCTT
                                       A  _
GAM853  BCMP1    3'  TATATTATTAAACATGCAATG  49538     C        _
                                CAT GCATGTTTAA AATGTG
                                ||| |||||||||| ||||||
                                GTA CGTACAAATT TTATAT
                                  A         A
GAM853  CRIPT    3'  CTCATGTTCTAAACAGC      74234     A     A
                                GC TGTTTA AATGTGGG
                                || |||||| ||||||||
                                CG ACAAAT TTGTACTC
                                 _     C
GAM853  CST9L    3'  TCCCACATTCCGTGGACATCA  55513    C      A__
                                G ATGTTTA   AATGTGGGA
                                | |||||||   |||||||||
                                A TACAGGT   TTACACCCT
                                 C      GCC
GAM853  DKFZP566K0524 3'  TTCCCACATTTTCCAGTGA    69879      A  TTT
                                TCGC TG   AAAATGTGGGAA
                                |||| ||   ||||||||||||
                                AGTG AC   TTTTACACCCTT
                                  _ C__
GAM853  EAT2     3'  TTCCCATGCATAAACATGC    80057          AAA
                                GCATGTTTA   TGTGGGAA
                                |||||||||   ||||||||
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                                CGTACAAAT  GTACCCTT
                                     AC_
GAM853  FLJ10661  3'  TCCCACACTTGGTGCGCTG   36919   T   GTT  AA
                                CA CGCAT  TAA  TGTGGGA
                                || |||||  |||  |||||||
                                GT GCGTG  GTT  ACACCCT
                                 C    ___  C_
GAM853  FLJ14297  3'  TTCAATAGTTTAAACATGC   46616        A  GG
                                GCATGTTTAAA TGT  GAA
                                |||||||||||| |||  |||
                                CGTACAAATTT ATA  CTT
                                      G  A_
GAM853  FLJ22690  3'  TTCCCATTGAACTGAACATGC  45577       AAAT_
                                GCATGTTTA   GTGGGAA
                                |||||||||   |||||||
                                CGTACAAGT   TACCCTT
                                     CAAGT
GAM853  KIAA0820  3'  TTCCCACATTCTGTTTAGGATG 69592    GCA  TT  A
                                CATC  TG  TA AATGTGGGAA
                                ||||  ||  || ||||||||||
                                GTAG  AT  GT TTACACCCTT
                                  G__  TT  C
GAM853  PCDH20   3'  CCCTATTTAAACATATGAT   43420    C       ATGT
                                ATCG ATGTTTAAA   GGG
                                |||| |||||||||   |||
                                TAGT TACAAATTT   CCC
                                  A       AT__
GAM853  PDZD2    3'  TTCCCACACTTTCTGAAGTGA  81736    ATGTTT  A
                                TCGC    AAA TGTGGGAA
                                ||||    ||| ||||||||
                                AGTG    TTT ACACCCTT
                                  AAGTC_  C
GAM853  PRO1635  3'  CTCAGTTATTTAAACATGC   38343        ATG_
                                GCATGTTTAAA   TGGG
                                ||||||||||   ||||
                                CGTACAAATTT   ACTC
                                      ATTG
GAM853  LOC116228 3'  TTCCCACACTTGTGTGG    74233      GTTTA  A
                                TCGCAT    AA TGTGGGAA
                                ||||||    || ||||||||
                                GGTGTG    TT ACACCCTT
                                    _____  C
GAM853  LOC151414 5'  TCCCACATTCCAGGCATG   81039      AA
                                CATGTTT  AATGTGGGA
                                |||||||  |||||||||
                                GTACGGA  TTACACCCT
                                    CC
GAM853  LOC157567 5'  TTCCCACACCTTCCGCGGCGA  82396    A  TT  AA
                                TCGC TGT  AA  TGTGGGAA
                                |||| |||  ||  ||||||||
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                                AGCG GCG  TT  ACACCCTT
                                  _  CC  CC
GAM853  LOC202126 3'  TTCCCACATTTTAATTTTGC  91910    TGT
                                GCA  TTAAAATGTGGGAA
                                |||  ||||||||||||||
                                CGT  AATTTTACACCCTT
                                 TTT
GAM853  LOC220073 5'  TCCCACACTTGGTGCGCTG  95076   T   GTT  AA
                                CA CGCAT  TAA  TGTGGGA
                                || |||||  |||  |||||||
                                GT GCGTG  GTT  ACACCCT
                                 C    ____  C_
GAM853  LOC91069  3'  TCCCACACTTGGTGCGCTG  65406   T   GTT  AA
                                CA CGCAT  TAA  TGTGGGA
                                || |||||  |||  |||||||
                                GT GCGTG  GTT  ACACCCT
                                 C    ____  C_
GAM854  ABCE1    5'  GGGGATCGTTTTCTCCAGA  60261       C  CTG
                                TCTGGAGAAA TG  CCTC
                                |||||||||| ||  ||||
                                AGACCTCTTT GC  GGGG
                                      T  TA_
GAM854  AKAP13   3'  TGAGGCAGCTGCCTCCTGA  24220   T   AAACT
                                TC GGAG    GCTGCCTCA
                                || ||||    |||||||||
                                AG CCTC    CGACGGAGT
                                 T   CGT__
GAM854  AKAP13   3'  TGAGGCAGCTGCCTCCTGA  23090   T   AAACT
                                TC GGAG    GCTGCCTCA
                                || ||||    |||||||||
                                AG CCTC    CGACGGAGT
                                 T   CGT__
GAM854  AKAP13   3'  TGAGGCAGCTGCCTCCTGA  59238   T   AAACT
                                TC GGAG    GCTGCCTCA
                                || ||||    |||||||||
                                AG CCTC    CGACGGAGT
                                 T   CGT__
GAM854  ALOX12B  5'  GGGCAGCAGCTTTTCCAGA  8537       A
                                TCTGGAGAA CTGCTGCCT
                                ||||||||| |||||||||
                                AGACCTTTT GACGACGGG
                                      C
GAM854  BCL7A    3'  GAGGCGGCGTTACCTCCAGA  40984     A_  T
                                TCTGGAG  AAC GCTGCCTC
                                |||||||  ||| ||||||||
                                AGACCTC  TTG CGGCGGAG
                                    CA  _
GAM854  CEACAM1  3'  GAGGCTTTCTCCAGG      9930        CTGCT
                                TCTGGAGAAA    GCCTC
                                ||||||||||    |||||
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                                GGACCTCTTT    CGGAG
                                      _____
GAM854  CLDN3    3'  TGGGGCAGCTTCCCCAG     8961      A   ACT
                                CTGG GAA   GCTGCCTCA
                                |||| |||   |||||||||
                                GACC CTT   CGACGGGGT
                                  C  ___
GAM854  COL10A1  5'  AGGCACCATCTCCAGG      6682        AAC  C
                                TCTGGAGA   TG TGCCT
                                ||||||||   || |||||
                                GGACCTCT   AC ACGGA
                                     ___  C
GAM854  CUTL1    3'  GAGCCCCAGTCTCTTCAGA   10348       A    CT  C
                                TCTGGAGA ACTG  GC TC
                                |||||||| ||||  || ||
                                AGACTTCT TGAC  CG AG
                                     C    CC  _
GAM854  CYBB     3'  GAGAGTGTTTCTCCA       76846        T   GC
                                TGGAGAAAC GCT  CTC
                                ||||||||| |||  |||
                                ACCTCTTTG TGA  GAG
                                      _  ___
GAM854  DNASE1   5'  GAAGTGCTTCTTCAGA      19072        ACT  T  C
                                TCTGGAGAA   GC GC TC
                                |||||||||   || || ||
                                AGACTTCTT   CG TG AG
                                     ___  _  A
GAM854  DXYS155E 3'  GAGGATGGCTCTCCAGA     18688        AACT   _
                                TCTGGAGA    GCTG CCTC
                                ||||||||    |||| ||||
                                AGACCTCT    CGGT GGAG
                                     _____    A
GAM854  EFNA1    3'  TGGGGCAGCACTCCCCAGA   16666      A  AAC
                                TCTGG GA   TGCTGCCTCA
                                ||||| ||   ||||||||||
                                AGACC CT   ACGACGGGGT
                                   C  C__
GAM854  EGR1     3'  TGAGCTTCGGTTCTCCAGA   10493        A   CT  C
                                TCTGGAGAA CTG  GC TCA
                                ||||||||| |||  || |||
                                AGACCTCTT GGC  CG AGT
                                      _   TT  _
GAM854  FLT1     3'  TGAGGAGAGTTTTCTCCA    10664        _  G  G
                                TGGAGAAA CT CT CCTCA
                                |||||||| || || |||||
                                ACCTCTTT GA GA GGAGT
                                     T  _  _
GAM854  FRK      5'  AGCCGGTAAGTCTCTCCAGG  10715        A  _    C
                                TCTGGAGA ACT GCTG CT
                                |||||||| ||| |||| ||
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                                GGACCTCT TGA TGGC GA
                                     C  A   C
GAM854  GAB2    3'  GAGGCAGCATCTCCAGA    55405       AAC
                                TCTGGAGA  TGCTGCCTC
                                ||||||||  |||||||||
                                AGACCTCT  ACGACGGAG
                                    ___
GAM854  GAB2    3'  GAGGCAGCATCTCCAGA    25458       AAC
                                TCTGGAGA  TGCTGCCTC
                                ||||||||  |||||||||
                                AGACCTCT  ACGACGGAG
                                    ___
GAM854  GP9     3'  TGAGGCAGGTCCCCAGA    5725      A  AACTG
                                TCTGG GA    CTGCCTCA
                                ||||| ||    ||||||||
                                AGACC CT    GACGGAGT
                                   C  G____
GAM854  GPC6    5'  AGGCAGCAGCCTTCCCAG    20329     A   A_
                                CTGG GAA  CTGCTGCCT
                                |||| |||  |||||||||
                                GACC CTT  GACGACGGA
                                  _  CC
GAM854  GUCA2B  3'  TGAGGCAGCCCAGCTCCTGA  24020    T    AAACT
                                TC GGAG    GCTGCCTCA
                                || ||||    |||||||||
                                AG CCTC    CGACGGAGT
                                 T   GACC_
GAM854  GUCY1A3 5'  GAGTCAGTTTTCCAGA     64226       AACT   C
                                TCTGGAGA   GCTG CTC
                                ||||||||   |||| |||
                                AGACCTTT   TGAC GAG
                                    ____   T
GAM854  IL8RA   3'  TGAGGCAGGCACTGCCA    7153     _  AAAC  _
                                TGG AG   TGC TGCCTCA
                                ||| ||   ||| |||||||
                                ACC TC   ACG ACGGAGT
                                 G  ____  G
GAM854  MADH6   5'  AGGCAGGGCTTTCCAGA    19972       AA TG
                                TCTGGAGA  C  CTGCCT
                                ||||||||  |  ||||||
                                AGACCTTT  G  GACGGA
                                    CG __
GAM854  MGAM    3'  GGGGCAGTTTCTCCAGG    72812           G
                                TCTGGAGAAACTGCT CC
                                |||||||||||||| ||
                                GGACCTCTTTGACGG GG
                                          _
GAM854  MYO7A   3'  GAGGCAGCAGTGGGTTCAGG  6032       GAA
                                TCTGGA   ACTGCTGCCTC
                                ||||||   ||||||||||
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                                GGACTT   TGACGACGGAG
                                   GGG
GAM854  NEUROD2  3'  AGGAGTGCTTCTCCAGG    21592        ACT   G
                                TCTGGAGAA   GCT CCT
                                |||||||||   ||| |||
                                GGACCTCTT   TGA GGA
                                    CG_  _
GAM854  NPY2R    3'  TGAACAGAAATTTCTCCAGG  8067         CTG   CC
                                TCTGGAGAAA   CTG  TCA
                                ||||||||||   |||  |||
                                GGACCTCTTT   GAC  AGT
                                     AAA   A_
GAM854  OXTR     3'  TGAATAGACATTTCTCCA    8083        C  _   CC
                                TGGAGAAA TG CTG  TCA
                                |||||||| || |||  |||
                                ACCTCTTT AC GAT  AGT
                                    _  A   A_
GAM854  PARK2    3'  GAGGAGCCTTTCCAGA      26542       AACT   G
                                TCTGGAGA    GCT CCTC
                                ||||||||    ||| ||||
                                AGACCTTT    CGA GGAG
                                    C___   _
GAM854  PARK2    3'  GAGGAGCCTTTCCAGA      26546       AACT   G
                                TCTGGAGA    GCT CCTC
                                ||||||||    ||| ||||
                                AGACCTTT    CGA GGAG
                                    C___   _
GAM854  PARK2    3'  GAGGAGCCTTTCCAGA      17078       AACT   G
                                TCTGGAGA    GCT CCTC
                                ||||||||    ||| ||||
                                AGACCTTT    CGA GGAG
                                    C___   _
GAM854  PMCHL1   3'  GAGGTGTTCTCCAGA       49917        ACTGC
                                TCTGGAGAA    TGCCTC
                                |||||||||    ||||||
                                AGACCTCTT    GTGGAG
                                     _____
GAM854  PPP2R4   3'  TGAGGCATGTCTTTCCAGA   61184        A  TGC
                                TCTGGAGA AC   TGCCTCA
                                |||||||| ||   |||||||
                                AGACCTTT TG   ACGGAGT
                                    C  T__
GAM854  PRX      3'  GAGGCAGCCCTTCCAGA     40896       AAACT
                                TCTGGAG    GCTGCCTC
                                |||||||    ||||||||
                                AGACCTT    CGACGGAG
                                    CC___
GAM854  REV3L    5'  TGAGGAAGATTTCTCTCA    12825   _    CTG  G
                                TG GAGAAA   CT CCTCA
                                || ||||||   || |||||
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                                AC CTCTTT   GA GGAGT
                                 T     A__  A
GAM854  RXRA     3'  TGAGGCAGCAGCCTTC      12925      AAA
                                GGAG   CTGCTGCCTCA
                                ||||   ||||||||||
                                CTTC   GACGACGGAGT
                                  C__
GAM854  SIRPB2   3'  GAGAAGCTTCTCTAGA      38272         ACT   GC
                                TCTGGAGAA   GCT  CTC
                                |||||||||   |||  |||
                                AGATCTCTT   CGA  GAG
                                     ___   A_
GAM854  SIRPB2   3'  GAGAAGCTTCTCTAGA      55858         ACT   GC
                                TCTGGAGAA   GCT  CTC
                                |||||||||   |||  |||
                                AGATCTCTT   CGA  GAG
                                     ___   A_
GAM854  SURF5    3'  TGAGGCAGCATTTCCTCCA    23130       A  C
                                TGGAG AA TGCTGCCTCA
                                |||||  ||  ||||||||||
                                ACCTC TT ACGACGGAGT
                                   C  T
GAM854  TAF1C    5'  GAGGCCCATTTTCCAGA      20265         AC  CT
                                TCTGGAGAA  TG  GCCTC
                                |||||||||  ||  |||||
                                AGACCTTTT  AC  CGGAG
                                     __  C_
GAM854  VANGL2   3'  TGAGACATCGGACTCTCCGGA  72095         AA   C  C
                                TCTGGAGA  CTG TG CTCA
                                ||||||||  ||| || ||||
                                AGGCCTCT  GGC AC GAGT
                                     CA   T  A
GAM854  WARS     3'  GAGGCAGCAGCCCTCGAGG    67865     G   AAA
                                TCT GAG   CTGCTGCCTC
                                ||| |||   ||||||||||
                                GGA CTC   GACGACGGAG
                                  G   CC_
GAM854  ZNF45    5'  GACTTGGCACTTCTCCAGA    14250         AC    CC
                                TCTGGAGAA  TGCTG  TC
                                |||||||||  |||||  ||
                                AGACCTCTT  ACGGT  AG
                                     C_    TC
GAM854  ARHF     3'  GGGACAGTTTCTCAGA      39272      G      CTG
                                TCTG AGAAACTG   CCT
                                ||||  ||||||||   |||
                                AGAC TCTTTGAC   GGG
                                  _       A__
GAM854  BLR1     3'  TGAGGCAGGGAAGTCCCCAGG  9940       A  AA_  G
                                TCTGG GA   CT CTGCCTCA
                                |||||  ||   ||  ||||||||
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                                GGACC CT   GG GACGGAGT
                                   C  GAA  _
GAM854  BLR1     3'  TGAGGCAGGGAAGTCCCCAGG  53119      A  AA_  G
                                TCTGG GA   CT CTGCCTCA
                                ||||| ||   || ||||||||
                                GGACC CT   GG GACGGAGT
                                   C  GAA  _
GAM854  C20orf150 3'  TGAAGCCGAGCTCCTCCAGA   66017       AAACT   __  C
                                TCTGGAG    GCT  GC TCA
                                |||||||    |||  || |||
                                AGACCTC    CGA  CG AGT
                                    CT___   GC  A
GAM854  C20orf4   3'  GGGCAGCAATCTCTCCAGG   31948       AAC
                                TCTGGAGA   TGCTGCCT
                                ||||||||   ||||||||
                                GGACCTCT   ACGACGGG
                                    CTA
GAM854  C20orf7   3'  TGAATATGCACCTTCTCCAGA  44383       AC   TGCC
                                TCTGGAGAA  TGC    TCA
                                |||||||||  |||    |||
                                AGACCTCTT  ACG    AGT
                                    CC   TATA
GAM854  C6orf26   3'  AGAAAGCAGCTTTCTCCA    48268       _    GC
                                TGGAGAAA CTGCT  CT
                                |||||||| |||||  ||
                                ACCTCTTT GACGA  GA
                                    C    AA
GAM854  CASKIN1   3'  TGAGGCGGATTTCCCCAGA   40784     A    CTG
                                TCTGG GAAA   CTGCCTCA
                                ||||| ||||   ||||||||
                                AGACC CTTT   GGCGGAGT
                                   C   A__
GAM854  CCR8      3'  TGAGGCAGATGCCTCTAGA   19041       AAACTG
                                TCTGGAG     CTGCCTCA
                                |||||||     ||||||||
                                AGATCTC     GACGGAGT
                                    CGTA__
GAM854  CPGL2     5'  GAAGCCGCTTTGTTCTCCAGA  74884       ACT_  T  C
                                TCTGGAGAA    GC GC TC
                                |||||||||    || || ||
                                AGACCTCTT    CG CG AG
                                    GTTT  C  A
GAM854  CSRP2BP   5'  TGAAGCAGCAGTGGGACCAG   70657     AGAA      C
                                CTGG    ACTGCTGC TCA
                                ||||    |||||||| |||
                                GACC    TGACGACG AGT
                                  AGGG       A
GAM854  DGKD      3'  TGAAACAACACTTTCTCCAG   60113       C  C  CC
                                CTGGAGAAA TG TG  TCA
                                ||||||||| || ||  |||
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                                GACCTCTTT AC AC  AGT
                                     C  A  AA
GAM854  DKFZP434A043 3'  TGAGGTAGTAATTTCCTCAGA  31823     GA    C
                                TCTG  GAAA TGCTGCCTCA
                                ||||  |||| ||||||||||
                                AGAC  CTTT ATGATGGAGT
                                  TC    A
GAM854  DKFZP434P0111 3'  TGAGGGTGTCTTTCCAGA    67963        A  T  TG
                                TCTGGAGA AC GC  CCTCA
                                |||||||| || ||  |||||
                                AGACCTTT TG TG  GGAGT
                                     C  _  __
GAM854  DKFZP586M1120 3'  TGAGGCAGCAGCTCCCAG    49287      A  AA
                                CTGG GA  CTGCTGCCTCA
                                |||| ||  ||||||||||
                                GACC CT  GACGACGGAGT
                                  _  C_
GAM854  ERG-1    3'  TGAGACATGTTTCTCCAGG   42102          TGC  C
                                TCTGGAGAAAC   TG CTCA
                                ||||||||||   || ||||
                                GGACCTCTTTG   AC GAGT
                                      T__  A
GAM854  FASTK    3'  TGAGGCAGAAGCTCCAGG    47690        AAACTG
                                TCTGGAG     CTGCCTCA
                                |||||||     ||||||||
                                GGACCTC     GACGGAGT
                                    GAA___
GAM854  FLJ14855  5'  GGTTCCCAGTTTTCCAGA    53766         A  CT_
                                TCTGGAGAA CTG   GCC
                                ||||||||| |||   |||
                                AGACCTTTT GAC   TGG
                                      _  CCT
GAM854  FLJ20249  3'  TGAGGAGTCCCTCCCAGA    80223       A  AACT   G
                                TCTGG GA    GCT CCTCA
                                ||||| ||    ||| |||||
                                AGACC CT    TGA GGAGT
                                  _  CCC_  _
GAM854  FLJ20730  3'  TGAAGAAGCAGTTTCTCAGA   36053      G        GCC
                                TCTG AGAAACTGCT   TCA
                                |||| ||||||||||   |||
                                AGAC TCTTTGACGA   AGT
                                  _         AGA
GAM854  FLJ21007  5'  TGAAGCTTGCACAAGCTCTCCA 48648         AAC__   T_  C
          GA                    TCTGGAGA    TGC  GC TCA
                                ||||||||    |||  || |||
                                AGACCTCT    ACG  CG AGT
                                     CGAAC   TT  A
GAM854  FLJ22938  5'  GAGGAGTTTTTCCAGA      45486           GCTG
                                TCTGGAGAAACT    CCTC
                                ||||||||||||    ||||
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                                AGACCTTTTTGA  GGAG
                                      _____
GAM854  GPT2     3' TGAGGCAGCAGCCTCTA    56772     AAA
                                TGGAG  CTGCTGCCTCA
                                |||||  ||||||||||
                                ATCTC  GACGACGGAGT
                                   C__
GAM854  KIAA0515 5' GAGGAGCTTCTCCAG      64550       ACT  G
                                CTGGAGAA  GCT CCTC
                                ||||||||  ||| ||||
                                GACCTCTT  CGA GGAG
                                    ___  _
GAM854  KIAA0542 3' GGGGCAGCTCCTCCAGG    66665       AAACT
                                TCTGGAG   GCTGCCTC
                                |||||||   ||||||||
                                GGACCTC   CGACGGGG
                                    CT___
GAM854  KIAA0561 3' GAGGGAGCTTTCCAGA     66479       AACT  G
                                TCTGGAGA   GCT CCTC
                                ||||||||   ||| ||||
                                AGACCTTT   CGA GGAG
                                     _____  G
GAM854  KIAA0652 3' TGAGGCAGCAATCTTTGG   29125   TG   AAC
                                C  GAGA  TGCTGCCTCA
                                |  ||||  ||||||||||
                                G  TTCT  ACGACGGAGT
                                 GT   A__
GAM854  KIAA1026 3' GAGACGGCTTTTTCCA     71738       CT   C
                                TGGAGAAA  GCTG CTC
                                ||||||||  |||| |||
                                ACCTTTTT  CGGC GAG
                                     __   A
GAM854  KIAA1030 3' GAGGCAGCAGTGAGCCGAGA  94981    _  AGAA
                                TCT GG   ACTGCTGCCTC
                                ||| ||   ||||||||||
                                AGA CC   TGACGACGGAG
                                  G  GAG_
GAM854  KIAA1086 3' TGAGGCAGGGGGTCCCCA   71291    A  AA  G
                                TGG GA  CT CTGCCTCA
                                ||| ||  || ||||||||
                                ACC CT  GG GACGGAGT
                                  C  GG  _
GAM854  KIAA1277 3' GAGGCAGGTTCTCAGA     65077    G   ACTG
                                TCTG AGAA   CTGCCTC
                                |||| ||||   |||||||
                                AGAC TCTT   GACGGAG
                                  _   G___
GAM854  KIAA1322 3' TGAGATAGTTTTTCCAGA   73118          CTGC
                                TCTGGAGAAACTG   CTCA
                                ||||||||||||   ||||
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                                AGACCTTTTTGAT   GAGT
                                      A___
GAM854  KIAA1634  3'  GCATCAGTCTCTTCTCCAGA  64124        ___   C
                                TCTGGAGAA  ACTG TGC
                                |||||||||  |||| |||
                                AGACCTCTT  TGAC ACG
                                    CTC   T
GAM854  KIAA1638  3'  TGAAACAACGGTGACCTCTCCA 47824       A___   C  CC
          GG                    TCTGGAGA   ACTG TG  TCA
                                ||||||||   |||| ||  |||
                                GGACCTCT   TGGC AC  AGT
                                    CCAG   A  AA
GAM854  KIAA1742  3'  AGGTATTTCTCCAGA      78137         CTGC
                                TCTGGAGAAA   TGCCT
                                ||||||||||   |||||
                                AGACCTCTTT   ATGGA

                                     _____
GAM854  KIAA1771  5'  GGGTTACCAGACCTCTCCAGA  79866       AA_  CT_
                                TCTGGAGA  CTG  GCCT
                                ||||||||  |||  ||||
                                AGACCTCT  GAC  TGGG
                                    CCA  CAT
GAM854  KIAA1831  5'  GGAGCAGTCTCTCCGGA    64525       A    G
                                TCTGGAGA ACTGCT CC
                                |||||||| |||||| ||
                                AGGCCTCT TGACGA GG
                                    C    _
GAM854  KIAA1894  3'  GAGGCAACCTTTGCCTTCTTCA 74285       ACT _______
          GA                    TCTGGAGAA  GC    TGCCTC
                                |||||||||  ||    ||||||
                                AGACTTCTT  CG    ACGGAG
                                    C__  TTTCCA
GAM854  KIAA1937  3'  GAGGCAGTGTCCCCCAGG   74071     AGAA  T
                                TCTGG   AC GCTGCCTC
                                |||||   || ||||||||
                                GGACC   TG TGACGGAG
                                  CCC_  _
GAM854  KIAA1985  3'  TGAAAAGCACTTTCTCCA   45018       C   GCC
                                TGGAGAAA TGCT  TCA
                                |||||||| ||||  |||
                                ACCTCTTT ACGA  AGT
                                    C   AA_
GAM854  LCHN      3'  TGAGATGCTTTCTCCAGA   87480        CT  TGC
                                TCTGGAGAAA  GC  CTCA
                                ||||||||||  ||  ||||
                                AGACCTCTTT  CG  GAGT
                                     __  TA_
GAM854  MGC13007  3'  CAGTTCAGTTATCTCCAGA  51277       _   __
                                TCTGGAGA AACTG  CTG
                                |||||||| |||||  |||
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                                AGACCTCT TTGAC  GAC
                                     A    TT
GAM854  MGC16385  5'  TGAAGCAGCAGCTGGGCTAGG  59543      AGAAA     C
                                TCTGG    CTGCTGC TCA
                                |||||    ||||||| |||
                                GGATC    GACGACG AGT
                                   GGGTC      A
GAM854  MGC26914  3'  TGAATAGACATTTCTCCA    59332       C  _  CC
                                TGGAGAAA TG CTG  TCA
                                |||||||| || |||  |||
                                ACCTCTTT AC GAT  AGT
                                     _ A  A_
GAM854  MRPL20    3'  AGGCATTTTTTCCAGA      36199        CTGC
                                TCTGGAGAAA    TGCCT
                                ||||||||||    |||||
                                AGACCTTTTT    ACGGA
                                      T___
GAM854  NCX       5'  GAGGCCACTCTCCGGA      32944       AAC  CT
                                TCTGGAGA   TG  GCCTC
                                ||||||||   ||  |||||
                                AGGCCTCT   AC  CGGAG
                                     C__  __
GAM854  PPP1R13B  3'  TGAGGCCCTTTCTCCAG     31660        CTGCT
                                CTGGAGAAA    GCCTCA
                                |||||||||    ||||||
                                GACCTCTTT    CGGAGT
                                     CC___
GAM854  PSKH1     3'  AGGCTCCAGCCTCTCCAGA   68791       AA   CT
                                TCTGGAGA  CTG  GCCT
                                ||||||||  |||  ||||
                                AGACCTCT  GAC  CGGA
                                     CC   CT
GAM854  PTPLA     3'  AGGTGCTTTTTCCAGA      27266        CT  T
                                TCTGGAGAAA  GC GCCT
                                ||||||||||  || ||||
                                AGACCTTTTT  CG TGGA
                                      __  _
GAM854  SEMA4G    5'  GGGCAGCTGTCTCCAGA     96330       AACT
                                TCTGGAGA    GCTGCCT
                                ||||||||    |||||||
                                AGACCTCT    CGACGGG
                                     GT__
GAM854  SPAF      3'  TGAAGCGATTTCTTTTTCCAGA 83521         CTGC_  C
                                TCTGGAGAAA    TGC TCA
                                ||||||||||    ||| |||
                                AGACCTTTTT    GCG AGT
                                      CTTTA   A
GAM854  SUN1      3'  TGAGTTTCCCAGTTTCTACAGA 47926      G      CTGC_
                                TCTG AGAAACTG    CTCA
                                |||| ||||||||    ||||
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                                AGAC TCTTTGAC    GAGT
                                  A      CCTTT
GAM854  TSPAN-2  3'  GGGTCAGTTTCTCAGA     20375     G      CT
                                TCTG AGAAACTG  GCCT
                                |||| ||||||||  ||||
                                AGAC TCTTTGAC  TGGG
                                  _      __
GAM854  USP24    3'  TGAAAATGCTGTGTTCTCCAGA 92795        _  T  TGCC
                                TCTGGAGAA AC GC   TCA
                                ||||||||| || ||   |||
                                AGACCTCTT TG CG   AGT
                                     G  T  TAAA
GAM854  LOC123096 3'  TGAGGCAGACACTCCAG    74654      AAAC  _
                                CTGGAG   TG CTGCCTCA
                                ||||||   || ||||||||
                                GACCTC   AC GACGGAGT
                                   ____  A
GAM854  LOC129831 5'  TGAGACAGCAGCGGTGGCAGA  75398     GAGAA     ___
                                TCTG    ACTGCTGC  CTCA
                                ||||    ||||||||  ||||
                                AGAC    TGGCGACG  GAGT
                                  GG___      ACA
GAM854  LOC134637 3'  TGAGAACACCTTCTCCAGG   75693       AC  CTGC
                                TCTGGAGAA  TG   CTCA
                                |||||||||  ||   ||||
                                GGACCTCTT  AC   GAGT
                                     CC  AA__
GAM854  LOC146420 3'  TGAACTTCCAGATTCTCCAGA  84653       A   CTGCC
                                TCTGGAGAA CTG    TCA
                                ||||||||| |||    |||
                                AGACCTCTT GAC    AGT
                                     A   CTTCA
GAM854  LOC147711 5'  TGAGCAGGCAAGTCTCTTCAGA 79117       A  _  GC
                                TCTGGAGA ACT GCT  CTCA
                                |||||||| ||| |||  ||||
                                AGACTTCT TGA CGG  GAGT
                                     C   A   AC
GAM854  LOC148753 3'  TGAGACTCCATTTTCTCCAGG  85373       C  CTGC
                                TCTGGAGAAA TG   CTCA
                                |||||||||| ||   ||||
                                GGACCTCTTT AC   GAGT
                                      T  CTCA
GAM854  LOC150290 3'  TGAGGCAGATGGTGCCCAGA   80592     AGAA   _
                                TCTGG   ACTG CTGCCTCA
                                |||||   |||| ||||||||
                                AGACC   TGGT GACGGAGT
                                  CG__   A
GAM854  LOC153218 5'  TGAAATAGAACTTTTCCAGA   81658       ACTG   CC
                                TCTGGAGAA   CTG  TCA
                                |||||||||   |||  |||
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                                AGACCTTTT   GAT  AGT
                                     CAA_   AA
GAM854   LOC153769 3'  AGGCAGCATTTCAGA      81805       AAAC
                                TCTGGAG    TGCTGCCT
                                |||||||    ||||||||
                                AGACTTT    ACGACGGA
                                    ____
GAM854   LOC157570 5'  TGAGGCTTTTTCTTCAGA    82397         CTGCT
                                TCTGGAGAAA    GCCTCA
                                ||||||||||    ||||||
                                AGACTTCTTT    CGGAGT
                                      TT___
GAM854   LOC197259 5'  TGAGGCAGTGGCCTCCGGA   89304       AAA TG
                                TCTGGAG   C  CTGCCTCA
                                |||||||   |  ||||||||
                                AGGCCTC   G  GACGGAGT
                                    C__ GT
GAM854   LOC199923 3'  TGAGTTAGCCAGTTTCTTCAGA 89879           _  C
                                TCTGGAGAAACTG CTG CTCA
                                |||||||||||| ||| ||||
                                AGACTTCTTTGAC GAT GAGT
                                       C   T
GAM854   LOC200940 3'  TGAGGCAGGCGGATCTCCTGA  90398    T    AA   _
                                TC GGAGA  CTGC TGCCTCA
                                || |||||  |||| |||||||
                                AG CCTCT  GGCG ACGGAGT
                                 T    A_   G
GAM854   LOC201685 3'  AGGAGCTATTTTCCAGA     91834        ACT   G
                                TCTGGAGAA   GCT CCT
                                |||||||||   ||| |||
                                AGACCTTTT   CGA GGA
                                     AT_  _
GAM854   LOC205327 3'  AGTCAATGTTTCTCCAGA    91067         TGC  C
                                TCTGGAGAAAC   TG CT
                                ||||||||||   || ||
                                AGACCTCTTTG   AC GA
                                      TA_  T
GAM854   LOC221288 3'  TGAAGCAGCAGTATCTAGA   95264       GAA       C
                                TCTGGA   ACTGCTGC TCA
                                ||||||   |||||||| |||
                                AGATCT   TGACGACG AGT
                                   A__       A
GAM854   LOC222057 3'  AGGTCAGCCTCTCCAGG     94345        AACT   _
                                TCTGGAGA    GCTG CCT
                                ||||||||    |||| |||
                                GGACCTCT    CGAC GGA
                                     C___    T
GAM854   LOC222057 3'  GAGTCAGCCTCTCCAGG     94354        AACT    C
                                TCTGGAGA    GCTG CTC
                                ||||||||    |||| |||
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                                GGACCTCT   CGAC GAG
                                    C___   T
GAM854  LOC253254 5'  TGAGAAGAACTTCTTCAGA   98908       ACTG  GC
                                TCTGGAGAA   CT  CTCA
                                |||||||||   ||  ||||
                                AGACTTCTT   GA  GAGT
                                    CAA_  A_
GAM854  LOC254672 3'  GAGGTGTTCTCCAGA      96295       ACTGC
                                TCTGGAGAA   TGCCTC
                                |||||||||   ||||||
                                AGACCTCTT   GTGGAG
                                    _____
GAM854  LOC255975 3'  GAGTCAGCCTCTCCAGG    97582       AACT   C
                                TCTGGAGA   GCTG CTC
                                ||||||||   |||| |||
                                GGACCTCT   CGAC GAG
                                    C___   T
GAM854  LOC256789 3'  TGAGGCTGTACTCTCTAGA  99312       AAC   T
                                TCTGGAGA   TGC GCCTCA
                                ||||||||   ||| ||||||
                                AGATCTCT   ATG CGGAGT
                                    C__   T
GAM854  LOC257336 5'  GGGCCCTAGTCCTCCAGA   97900       AA   CT
                                TCTGGAG  ACTG  GCCT
                                |||||||  ||||  ||||
                                AGACCTC  TGAT  CGGG
                                   C_   CC
GAM854  LOC257449 3'  AGGTATTTCTCCAGA      63373       CTGC
                                TCTGGAGAAA   TGCCT
                                ||||||||||   |||||
                                AGACCTCTTT   ATGGA
                                    _____
GAM854  LOC91923  5'  AGAGTTCCAGTTTCTCCA   68169        CT  _
                                TGGAGAAACTG  GC CT
                                ||||||||||  ||  ||
                                ACCTCTTTGAC  TG GA
                                     CT  A
GAM854  LOC92876  5'  AGAGTTCCAGTTTCTCCA   71346        CT  _
                                TGGAGAAACTG  GC CT
                                ||||||||||  ||  ||
                                ACCTCTTTGAC  TG GA
                                     CT  A
GAM854  LOC93496  3'  TGAAACAGACTTACACTTCTTC 72863       ACTG____  CC
          AGA                    TCTGGAGAA      CTG  TCA
                                 |||||||||      |||  |||
                                 AGACTTCTT      GAC  AGT
                                     CACATTCA   AA
GAM855  BACH2     3'  CTGTCAAGCAATGGATAAACAG 41782       C    GGGA__
          CTCT                    AGAGTTGTT ATCCA     GACAG
                                  ||||||||| |||||     |||||
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                                TCTCGACAA TAGGT     CTGTC
                                     A    AACGAA
GAM855  CHRNA1   3'  CTGTCTCCCTGAAGAGTGAAC  5375       C___
                                GTTCAT   CAGGGAGACAG
                                ||||||   ||||||||||
                                CAAGTG   GTCCCTCTGTC
                                   AGAA
GAM855  FZD8     3'  CCATGGATAACAACTCT     49873        C    G
                                AGAGTTGTT ATCCA GG
                                ||||||||| ||||| ||
                                TCTCAACAA TAGGT CC
                                     _    A
GAM855  HHIP     5'  CTGTCCCACCTAAACAACTC   42753       CATCCAG  A
                                GAGTTGTT      GG GACAG
                                ||||||||      || |||||
                                CTCAACAA      CC CTGTC
                                     ATCCA__  _
GAM855  MME      3'  TCCCTATGGAGGAACAACTCT  24437        A   __
                                AGAGTTGTTC TCCA  GGGA
                                |||||||||| ||||  ||||
                                TCTCAACAAG AGGT  CCCT
                                     G    AT
GAM855  MME      3'  TCCCTATGGAGGAACAACTCT  24439        A   __
                                AGAGTTGTTC TCCA  GGGA
                                |||||||||| ||||  ||||
                                TCTCAACAAG AGGT  CCCT
                                     G    AT
GAM855  MME      3'  TCCCTATGGAGGAACAACTCT  24441        A   __
                                AGAGTTGTTC TCCA  GGGA
                                |||||||||| ||||  ||||
                                TCTCAACAAG AGGT  CCCT
                                     G    AT
GAM855  MME      3'  TCCCTATGGAGGAACAACTCT  8034         A   __
                                AGAGTTGTTC TCCA  GGGA
                                |||||||||| ||||  ||||
                                TCTCAACAAG AGGT  CCCT
                                     G    AT
GAM855  MTCP1    5'  CTACATGGATAACAACTCT   27242        C    GGG
                                AGAGTTGTT ATCCA   AG
                                ||||||||| |||||   ||
                                TCTCAACAA TAGGT   TC
                                     _    ACA
GAM855  NR1D1    3'  TGTCTCCCCCACAACCCT    41672    A    TCATCCA
                                AG GTTGT      GGGAGACA
                                || |||||      ||||||||
                                TC CAACA      CCCTCTGT
                                 C    CC_____
GAM855  NR1I2    3'  TGTCTCCCTAGGGAATTC    42088      GTTCA  _
                                GAGTT    TCC AGGGAGACA
                                |||||    ||| |||||||||
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                                CTTAA    GGG TCCCTCTGT
                                  _____  A
GAM855  NR1I2    3'  TGTCTCCCTAGGGAATTC    15304      GTTCA  _
                                GAGTT    TCC AGGGAGACA
                                |||||    ||| |||||||||
                                CTTAA    GGG TCCCTCTGT
                                  _____  A
GAM855  PCOLN3   3'  CTGCCCTGTTGCCAAACAACTC 12411        ___  TC    _
                                GAGTTGTT   CA  CAGGG AG
                                ||||||||   ||  ||||| ||
                                CTCAACAA   GT  GTCCC TC
                                     ACC  T_    G
GAM855  PFN2     3'  TGTCTTCATCAACAACCCT   12063    A     CATCCAG
                                AG GTTGTT      GGAGACA
                                || ||||||      |||||||
                                TC CAACAA      CTTCTGT
                                 C     CTA____
GAM855  PFN2     3'  TGTCTTCATCAACAACCCT   54890    A     CATCCAG
                                AG GTTGTT      GGAGACA
                                || ||||||      |||||||
                                TC CAACAA      CTTCTGT
                                 C     CTA____
GAM855  TNS      3'  CTGTCTCCCTAACTCAACTGCT 42950    _    TTCATCC
                                AG AGTTG      AGGGAGACAG
                                || |||||      ||||||||||
                                TC TCAAC      TCCCTCTGTC
                                 G    TCAA___
GAM855  FLJ10511 3'  CCCTAGAAAAACAACTCT    36686        CA  C
                                AGAGTTGTT  TC AGGG
                                |||||||||  || ||||
                                TCTCAACAA  AG TCCC
                                     AA  A
GAM855  FLJ20195 3'  CCCGATGAACACCTCT      35216      T      CA
                                AGAG TGTTCATC  GGG
                                |||| ||||||||  |||
                                TCTC ACAAGTAG  CCC
                                  C       __
GAM855  HAAO     3'  TCCCTGCCAAACAACTCT    60173        CATC
                                AGAGTTGTT   CAGGGA
                                |||||||||   ||||||
                                TCTCAACAA   GTCCCT
                                     ACC_
GAM855  KIAA0843 3'  CTGAACAACCAGACAGACAACT 30801        CA  CA  GAGA_
           CT                    AGAGTTGTT  TC  GG    CAG
                                |||||||||  ||  ||    |||
                                TCTCAACAG  AG  CC    GTC
                                     AC  A_  AACAA
GAM855  KIAA1497 5'  CTGTCCTTGTATGAGCAAC   68121        C     GA
                                GTTGTTCAT CAGGGA  CAG
                                ||||||||| ||||||  |||
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                                CAACGAGTA GTTCCT  GTC
                                     T    __
GAM855  KIAA1710  3'  TCTCCATACATGAACAATCT  63181    G      CCAG
                                AGA TTGTTCAT   GGAGA
                                ||| ||||||||   |||||
                                TCT AACAAGTA   CCTCT
                                  _      CATA
GAM855  PDE7B    3'  CTGCCGAAATGAGCAACTC   38949         CCA  G
                                GAGTTGTTCAT   GG AG
                                ||||||||||   || ||
                                CTCAACGAGTA   CC TC
                                      AAG  G
GAM855  SEC24B   3'  CTGCATTGTTGGATGACAACTC 21984        T     G  GA
           T                     AGAGTTGT CATCCAG GA  CAG
                                ||||||||| ||||||| ||  |||
                                TCTCAACA GTAGGTT TT  GTC
                                     _     G  AC
GAM855  LOC124753 5'  CTGCCTCCCTGGCTTCCATCTC 74803    T  TTCAT      A
                                GAG TG    CCAGGGAG CAG
                                ||| ||    |||||||| |||
                                CTC AC    GGTCCCTC GTC
                                  T  CTTC_      C
GAM855  LOC142948 3'  CTACCGGGAGGAATGAATAACT 83777         ____  A  G
           C                     GAGTTGTTCA   TCC GG AG
                                ||||||||||   ||| || ||
                                CTCAATAAGT   AGG CC TC
                                      AAGG   G  A
GAM855  LOC153914 5'  CCACTAAAGTGAACAACTC   81898         CC_  _
                                GAGTTGTTCAT   AG GG
                                ||||||||||   || ||
                                CTCAACAAGTG   TC CC
                                      AAA  A
GAM855  LOC219445 5'  CTCCCTGGTTCAAACAATTC   93202       CAT_
                                GAGTTGTT   CCAGGGAG
                                ||||||||   ||||||||
                                CTTAACAA   GGTCCCTC
                                     ACTT
GAM855  LOC219914 5'  CCACTGGGAGGAACGAACAACT 94967        A_____   _
           C                     GAGTTGTTC     TCCAG GG
                                |||||||||     ||||| ||
                                CTCAACAAG     GGGTC CC
                                     CAAGGA    A
GAM856  BBS4     3'  ATTTGCCCAAAGGGAATCCAGA 53447        G_  G_   A
           ACA                    TGTTCTGGA  CT  TTGG CAAAT
                                |||||||||  ||  |||| |||||
                                ACAAGACCT  GG  AACC GTTTA
                                     AA  GA   C
GAM856  CENTD2   3'  CCAACAAACTCCAGAACA    31539         C_
                                TGTTCTGGAG  TGTTGG
                                ||||||||||  ||||||
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                                ACAAGACCTC  ACAACC
                                      AA
GAM856  HAMP     3'  TCCTGCTGCCCCAGAACA    41289        A  T  T
                                TGTTCTGG GC GT GGA
                                |||||||| || || |||
                                ACAAGACC CG CG CCT
                                     C  T  T
GAM856  ITGA11   3'  TCTGCCGGCCCCCAGGACA   25213        A_   TT
                                TGTTCTGG  GCTG  GGA
                                |||||||| ||||  |||
                                ACAGGACC  CGGC  TCT
                                     CC    CG
GAM856  KITLG    3'  ATTTGCATGGCTCCAGAA    8023           TGGA
                                TTCTGGAGCTGT    CAAAT
                                ||||||||||||    |||||
                                AAGACCTCGGTA    GTTTA
                                      C___
GAM856  MAPK4    5'  CCTGGGCAGCTCCAGATCA   12300    T         __
                                TG TCTGGAGCTGTT  GG
                                || ||||||||||||  ||
                                AC AGACCTCGACGG  CC
                                 T          GT
GAM856  MGAT2    3'  ATTTGTCCAAACAGGACA    11557        GAGCTG
                                TGTTCTG     TTGGACAAAT
                                |||||||     ||||||||||
                                ACAGGAC     AACCTGTTTA
                                    A_____
GAM856  PSPHL    5'  TTGTCATACAGCTCCAAACA   94499     C        TG
                                TGTT TGGAGCTGT  GACAA
                                |||| |||||||||  |||||
                                ACAA ACCTCGACA  CTGTT
                                  _       TA
GAM856  TTC3     3'  TATTTGTCCAACAACTGTCAGA 13885        _  C
           ATA                    TGTTCTGG AG TGTTGGACAAATA
                                |||||||| || ||||||||||||
                                ATAAGACT TC ACAACCTGTTTAT
                                     G  A
GAM856  H2BFQ    3'  TTTAAGAGAACTCCAGGACA   60079          __  G
                                TGTTCTGGAG  CT TTGGA
                                ||||||||||  || |||||
                                ACAGGACCTC  GA AATTT
                                      AA  G
GAM856  LRG      3'  TCCATCCATGCTTCCTAGAACA 54825       _  _ _  T_
                                TGTTCT GGA GC TG  TGGA
                                |||||| ||| || ||  ||||
                                ACAAGA CCT CG AC  ACCT
                                   T  T  T  CT
GAM856  NMT2     3'  ATTTGTCCATGTAACAGAACA  17852        GA  TGT
                                TGTTCTG  GC   TGGACAAAT
                                |||||||  ||   |||||||||
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                                ACAAGAC  TG   ACCTGTTTA
                                    AA  T__
GAM856  NYD-SP21  3'  TATTTGTCCAATCTAGATTCAG 51863         G  __
            AACA                    TGTTCTGGA CT  GTTGGACAAATA
                                ||||||||| ||  ||||||||||||
                                ACAAGACTT GA  TAACCTGTTTAT
                                    A  TC
GAM856  PSPH     3'  TTGTCGTACAGCTCCAAACA   17143      C        TG
                                TGTT TGGAGCTGT  GACAA
                                |||| |||||||||  |||||
                                ACAA ACCTCGACA  CTGTT
                                  _       TG
GAM856  LOC122258 3'  CCACCAGCCTCCGGAACA    59820          _  T
                                TGTTCTGGAG CTG TGG
                                |||||||||| ||| |||
                                ACAAGGCCTC GAC ACC
                                    C   C
GAM856  LOC151826 3'  ATTTGTCCAACCTAGCACA   81176     T    AGCT
                                TGT CTGG    GTTGGACAAAT
                                ||| ||||    ||||||||||||
                                ACA GATC    CAACCTGTTTA
                                  C   ____
GAM856  LOC169611 3'  TCCAGTGGCAGCTCCAGAA   83663           ___
                                TTCTGGAGCTGT   TGGA
                                ||||||||||||   ||||
                                AAGACCTCGACG   ACCT
                                    GTG
GAM856  LOC196746 3'  TCAGAGCAGCTCCAAGACA   88903     TC        G_
                                TGT  TGGAGCTGTT  GA
                                |||  ||||||||||  ||
                                ACA  ACCTCGACGA  CT
                                  GA        GA
GAM856  LOC253142 5'  TTGCTAGGATGCCCCAGAATA  99230         A  TG_   A
                                TGTTCTGG GC   TTGG CAA
                                |||||||| ||   |||| |||
                                ATAAGACC CG   GATC GTT
                                    C  TAG   _
GAM857  GRM3     3'  ACGTGCAGCTCCAGAATA    7743       A       G
                                TATT TGGAGCTG GCGT
                                |||| |||||||| ||||
                                ATAA ACCTCGAC TGCA
                                  G       G
GAM857  RORA     5'  ACCTTGGACTCCATAGTA    56957          _ TG  C
                                TATTATGGAG C  GG GT
                                |||||||||| |  || ||
                                ATGATACCTC G  TC CA
                                    A GT  _
GAM857  IRX4     3'  ACACTCGACTCCATAATA    33450          C    C
                                TATTATGGAG TGGG GT
                                |||||||||| |||| ||
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                                ATAATACCTC GCTC CA
                                    A   A
GAM857  KIAA1536  3'  ACACTGGGCTCCATGATA    40874          G  C
                                TATTATGGAGCT GG GT
                                |||||||||||| || ||
                                ATAGTACCTCGG TC CA
                                     G  A
GAM857  KIAA1944  5'  TACACCCAATGTCTGCTCCATA 76082        _______   C ___
                                TATGGAGC     TGGG GT   A
                                ||||||||     |||| ||   |
                                ATACCTCG     ACCC CA   T
                                    TCTGTA   A __
GAM857  LOC135154 3'  ACGCCCAGCCTAGAAATG    75715      A_  A
                                TATT  TGG GCTGGGCGT
                                ||||  ||| |||||||||
                                GTAA  ATC CGACCCGCA
                                  AG  _
GAM857  LOC220565 3'  ACACCTGTGTGCCATGATA    92438        A _   C
                                TATTATGG GC TGGG GT
                                |||||||| || |||| ||
                                ATAGTACC TG GTCC CA
                                    G  T   A
GAM857  LOC64150  5'  ACACCTCGGGACTCCATAATA  67864          __  _ C
                                TATTATGGAG  CTG GG GT
                                ||||||||||  ||| || ||
                                ATAATACCTC  GGC CC CA
                                    AG   T  A
GAM858  C18orf1   3'  CAGCCAAGTGAAGGACCT    60861      T       GTGCGT
                                AGGT CCTTCACT     GCTG
                                |||| ||||||||     ||||
                                TCCA GGAAGTGA     CGAC
                                  _       AC_____
GAM858  CNR1      3'  GGGGTTTACAGTGAAGAAAGCC 32720      C_        CG G
                                GGTT  CTTCACTGTG  T CT
                                ||||  ||||||||||  | ||
                                CCGA  GAAGTGACAT  G GG
                                  AA         TT G
GAM858  FACL2     3'  CAAAAACAATGAAGGAAACC   41208     _     C   GCG
                                GGTT CCTTCA TGT   TG
                                |||| |||||| |||   ||
                                CCAA GGAAGT ACA   AC
                                  A     A   AAA
GAM858  FADD      3'  AGCACAGAAGGAATCT      15122          ACTGTGC
                                AGGTTCCTTC      GTGCT
                                ||||||||||      |||||
                                TCTAAGGAAG      CACGA
                                    A_______
GAM858  HIS1      3'  CAGCTGAATGAGGAACC     22337        T  CTGTG  T
                                GGTTCCT CA    CG GCTG
                                ||||||| ||    || ||||
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                                CCAAGGA GT    GT CGAC
                                   _ AA___ _
GAM858  KMO      3'  TATCACAATGGAAGGAACCT  14847         AC_   C
                                AGGTTCCTTC  TGTG GTG
                                ||||||||||  |||| |||
                                TCCAAGGAAG  ACAC TAT
                                     GTA   _
GAM858  OGN      3'  TCAACAATGAGTAAAGGAACTT 26769         C  GTGCG  C
                                AGGTTCCTT ACT    TG TGA
                                ||||||||| |||    || |||
                                TTCAAGGAA TGA    AC ACT
                                     A  GTA__  A
GAM858  OGN      3'  TCAACAATGTGTAAAGGAACTT 44591         CAC  TG  GC_
                                AGGTTCCTT  TG  CGT  TGA
                                |||||||||  ||  |||  |||
                                TTCAAGGAA  AT  GTA  ACT
                                     ___  GT  ACA
GAM858  OGN      3'  TCAACAATGTGTAAAGGAACTT 53401         CAC  TG  GC_
                                AGGTTCCTT  TG  CGT  TGA
                                |||||||||  ||  |||  |||
                                TTCAAGGAA  AT  GTA  ACT
                                     ___  GT  ACA
GAM858  DKFZP564M182 3'  TACTACAGTGAAGAAACCT   78641      C        C
                                AGGTT CTTCACTGTG GTG
                                |||||  |||||||||| |||
                                TCCAA GAAGTGACAT CAT
                                   A        _
GAM858  FLJ12660  3'  TCAGCAATGTGGTGATGGAACC 47899        T    TG GCG
           T                     AGGTTCC TCAC  T   TGCTGA
                                 |||||||  ||||  |   ||||||
                                 TCCAAGG AGTG  G   ACGACT
                                     T   GT TA_
GAM858  IMAGE3451454 5'  TCAGCACGGGTCGAAGGACCCT 54939     T     _  GTG
                                AGG TCCTTC ACT   CGTGCTGA
                                ||| |||||| |||   ||||||||
                                TCC AGGAAG TGG   GCACGACT
                                  C     C  ___
GAM858  KIAA0930  3'  CAACACGCACACCTCCAACCT  71065      CCTTCAC       C
                                AGGTT      TGTGCGTG TG
                                |||||      |||||||| ||
                                TCCAA      ACACGCAC AC
                                   CCTCC__       A
GAM858  KIAA0930  3'  CAGCACACAGGCACCAAGGAAC 71066        CACT   _____
           T                     GGTTCCTT   GTGC   GTGCTG
                                 ||||||||   ||||   ||||||
                                 TCAAGGAA   CACG   CACGAC
                                     C___    GACA
GAM858  KIAA1247  3'  CAGCAGTTGGTATGAAGAACCT 62506       C   CTGT_  G
                                AGGTTC TTCA    GC TGCTG
                                |||||| ||||    || |||||
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                                TCCAAG AAGT    TG ACGAC
                                   _   ATGGT  _
GAM858  KIAA1737  3'  CAGCAAATGGAGGAACCT    67935          CTGTGCG
                                AGGTTCCTTCA      TGCTG
                                ||||||||||       |||||
                                TCCAAGGAGGT      ACGAC
                                     AA_____
GAM858  MGC10955  3'  TTGGCCAAAATAAAGGAACCT  52034         CAC   GCGT  TG
                                AGGTTCCTT   TGT   GC  A
                                |||||||||   |||   ||  |
                                TCCAAGGAA   ATA   CG  T
                                     ___   AAAC  GT
GAM858  POLR3F    5'  CAACTCAGAATGAAGGAACC   60616          __   TGCG
                                GGTTCCTTCA  CTG   TG
                                ||||||||||  |||   ||
                                CCAAGGAAGT  GAC   AC
                                     AA   TCA_
GAM858  LOC127534 3'  CAACACACACAGTGTGTGCC   75965     TCCTT      C   C
                                GGT    CACTGTG GTG TG
                                |||    ||||||| ||| ||
                                CCG    GTGACAC CAC AC
                                  TGT__      A   A
GAM858  LOC144600 3'  CAACACGCACACCTCCAACCT  84083      CCTTCAC       C
                                AGGTT      TGTGCGTG TG
                                |||||      |||||||| ||
                                TCCAA      ACACGCAC AC
                                   CCTCC__       A
GAM858  LOC150282 3'  CAGCACACACAGTGGGTACTT  80538     T  TT      C
                                AGGT CC  CACTGTG GTGCTG
                                |||| ||  ||||||| ||||||
                                TTCA GG  GTGACAC CACGAC
                                  T  __      A
GAM858  LOC255231 3'  CAGCGGCTGAGCAGAGGAACC  97118        CA  GT  G
                                GGTTCCTT  CT  GC TGCTG
                                ||||||||  ||  || |||||
                                CCAAGGAG  GA  CG GCGAC
                                     AC  GT  _
GAM858  LOC91748  5'  CAGCACGCAGGTGCCAGAACC  67636      CTT   G
                                GGTTC   CACT TGCGTGCTG
                                |||||   |||| |||||||||
                                CCAAG   GTGG ACGCACGAC
                                   ACC    _
GAM859  ADAT1     3'  CTCCAGCCTGGGTGATAGA   24915    CC      TTTAT
                                TC  ATCACCC    TTGGAG
                                ||  |||||||    ||||||
                                AG  TAGTGGG    GACCTC
                                  A_      TCC__
GAM859  ASH1      3'  CCAAAATGGAATCATGGGATA  38085        CAC_  TTTA
                                TATCCCAT   CC    TTTGG
                                ||||||||   ||    |||||
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                                ATAGGGTA   GG   AAACC
                                    CTAA  TA__
GAM859  KCNK3    3' CTCCAGCCTGGGTGACAGGG  11174    A_    TTTAT
                                CCC  TCACCC    TTGGAG
                                |||  ||||||    ||||||
                                GGG  AGTGGG    GACCTC
                                  AC     TCC__
GAM859  MS4A1    3' CCAAGATTAAAAGGTGACAGG 5546    CA    C   __
                                CC  TCACC TTTA  TTTGG
                                ||  ||||| ||||  |||||
                                GG  AGTGG AAAT  GAACC
                                 AC    A   TA
GAM859  PART1    3' CTCCATTCCAGGTGACATGGAT 33900     CA_    CTTTATT
           A                     TATCC   TCACC     TGGAG
                                |||||   |||||     |||||
                                ATAGG   AGTGG     ACCTC
                                   TAC    ACCTT__
GAM859  SNX5     3' CTAAGAAAGGGTGTAGGA    27787    CAT      A
                                TCC   CACCCTTT TTTGG
                                |||   |||||||| |||||
                                AGG   GTGGGAAA GAATC
                                  AT_      _
GAM859  FADS1    3' CTCCAGCCTGGGGTGATAGA   26378    CC      TTAT
                                TC  ATCACCCT    TTGGAG
                                ||  ||||||||    ||||||
                                AG  TAGTGGGG    GACCTC
                                 A_      TCC_
GAM859  FLJ10460 3' CTCCAACCTGGGTGATGG    36615       TTTAT
                                CCATCACCC    TTGGAG
                                |||||||||    ||||||
                                GGTAGTGGG    AACCTC
                                     TCC__
GAM859  FLJ20220 3' TCTTAAAAGCAATGGGATG   35277       CACC   ATTT
                                TATCCCAT    CTTT    GGA
                                ||||||||    ||||    |||
                                GTAGGGTA    GAAA    TCT
                                     AC__    AT__
GAM859  FLJ20312 3' CTCCAAATAAATCAAGATGAAG 35409    CC    ACCC
           TA                     TAT  CATC    TTTATTTGGAG
                                |||  ||||    ||||||||||
                                ATG  GTAG    AAATAAACCTC
                                  AA    AACT
GAM859  FRAG1    3' CTCCTTTGCAAAGGTATGGGAT 27944       CAC    ATTT_
           A                     TATCCCAT   CCTTT    GGAG
                                |||||||   |||||    ||||
                                ATAGGGTA   GGAAA    CCTC
                                     T__    CGTTT
GAM859  KIAA1001 3' CTCCAGCCTGGGTGATGG    31005       TTTAT
                                CCATCACCC    TTGGAG
                                |||||||||    ||||||
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                                GGTAGTGGG    GACCTC
                                     TCC__
GAM859  MESDC2   3' CTCCAGCCTGGATGACGGGATG 72913      A  C  TTTAT
                                TATCCC TCA CC    TTGGAG
                                |||||| ||| ||    ||||||
                                GTAGGG AGT GG    GACCTC
                                   C  A  TCC__
GAM859  MGC10612 3' CCAGTGAGAAGGAAAATGGGAT 49521       CAC    AT_
          A                     TATCCCAT  CCTTT  TTGG
                                ||||||||  |||||  ||||
                                ATAGGGTA  GGAAG  GACC
                                     AAA    AGT
GAM859  RNF8     3' CCAAACAATGTACCAGTGATGG 15561       CCT____ A
          G                     CCCATCAC     TT TTTGG
                                ||||||||     || |||||
                                GGGTAGTG     AA AAACC
                                     ACCATGT  C
GAM859  SEMA3C   3' CTCCAAATAAAAATTAGATGG  22106     ACCC_
                                CCATC    TTTATTTGGAG
                                |||||    ||||||||||
                                GGTAG    AAATAAACCTC
                                   ATTAA
GAM859  WBSCR23  3' CTCCAGCCTGGGTGATAGA   47432    CC     TTTAT
                                TC  ATCACCC    TTGGAG
                                ||  |||||||    ||||||
                                AG  TAGTGGG    GACCTC
                                 A_     TCC__
GAM859  LOC124145 3' GATAAAAAGTGATGGGGTA   74723         CC
                                TATCCCATCAC  TTTATT
                                ||||||||||  ||||||
                                ATGGGGTAGTG  AAATAG
                                      AA
GAM859  LOC146280 5' CTCCTGGGAGGGTGATG     78348         ATTT
                                CATCACCCTTT    GGAG
                                ||||||||||    ||||
                                GTAGTGGGAGG    CCTC
                                      GT__
GAM859  LOC147740 3' CCAAATAAAGAGCACAGGATA  79153      CATCACC
                                TATCC      CTTTATTTGG
                                |||||      ||||||||||
                                ATAGG      GAAATAAACC
                                   ACACGA_
GAM859  LOC159110 5' CCAGGCGCGCGGCGATGGGATA 82987        A  CTTTA
                                TATCCCATC CC    TTTGG
                                ||||||||| ||    |||||
                                ATAGGGTAG GG    GGACC
                                      C  CGCGC
GAM859  LOC159116 5' CCAGGCGCGCGGCGATGGGATA 82970        A  CTTTA
                                TATCCCATC CC    TTTGG
                                ||||||||| ||    |||||
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                                ATAGGGTAG GG    GGACC
                                     C  CGCGC
GAM859  LOC255328 3'  CTCCAGCCTGGGTGATAAGA  98339   CC     TTTAT
                                TC  ATCACCC    TTGGAG
                                ||  |||||||    ||||||
                                AG  TAGTGGG    GACCTC
                                 AA      TCC__
GAM859  LOC256980 3'  CTCCACAAAGGTGAGGGGA  96928     A    C   ATT
                                TCCC TCACC TTT   TGGAG
                                |||| ||||| |||   |||||
                                AGGG AGTGG AAA   ACCTC
                                  G    _   C__
GAM859  LOC90573  3'  CTCCAGGCTGGGTGACAGAT  63957    CCA    TTTA
                                ATC   TCACCC   TTTGGAG
                                |||   ||||||   |||||||
                                TAG   AGTGGG   GGACCTC
                                  AC_     TC__
GAM860  CHAD    3'  GGAAGGCTGAGCCTCTC    8855      TA   CTGC
                                GAGAG  CTC   GTCTTCC
                                |||||  |||   |||||||
                                CTCTC  GAG   CGGAAGG
                                   C_   T____
GAM860  DSG1    5'  AGGAAGGCAGAAACACCTC   10449    A  ACTC   GT
                                GAG GT   CTGC  CTTCCT
                                ||| ||   ||||  ||||||
                                CTC CA   GACG  GAAGGA
                                  _  CAAA   __
GAM860  MID1    3'  AAGATGTAGAAGTCCCTC    6351     T_   C
                                GAG  ACT CTGCGTCTT
                                |||  ||| |||||||||
                                CTC  TGA GATGTAGAA
                                  CC   A
GAM860  OTOF    3'  AGGAAGACTCCTGAAACCCTC  17828    A  AC  CTGC
                                GAG GT  TC   GTCTTCCT
                                ||| ||  ||   ||||||||
                                CTC CA  AG   CAGAAGGA
                                  C  A_  TCCT
GAM860  RNMT    3'  AGGACATCCAAGGGTACTCTC  15047       T   GCGTCT
                                GAGAGTAC CCT     TCCT
                                |||||||| |||     ||||
                                CTCTCATG GGA     AGGA
                                     _  ACCTAC
GAM860  SCN3A   5'  AGGAAGACACGTTATACCCT  23612    A   CTCC  C
                                AG GTA   TG GTCTTCCT
                                || |||   || ||||||||
                                TC CAT   GC CAGAAGGA
                                 C  ATT_  A
GAM860  SFRS7   3'  GGAAGGCGATACTCTC     60148       CTCCTG
                                GAGAGTA    CGTCTTCC
                                |||||||    ||||||||
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                                CTCTCAT     GCGGAAGG
                                   A_____
GAM860  SLC13A4  5'  AAGACGAAGGAGGACTCTC   25857       A    G
                                GAGAGT CTCCT CGTCTT
                                |||||| ||||| ||||||
                                CTCTCA GAGGA GCAGAA
                                   G    A
GAM860  SSX2     3'  AGGAAGATGACGAGTAACTC  97962     _   CTG
                                GAGT ACTC  CGTCTTCCT
                                |||| ||||  |||||||||
                                CTCA TGAG  GTAGAAGGA
                                  A   CA_
GAM860  TGFBR2   3'  AAGATTCAAGAGTATTCTC   13725         C  C
                                GAGAGTACTC TG GTCTT
                                |||||||||| || |||||
                                CTCTTATGAG AC TAGAA
                                      A  T
GAM860  TNFRSF11A 3'  AGGAAGACCACCCGGCATTCTC 15187       A  CC_  C
                                GAGAGT CT   TG GTCTTCCT
                                |||||| ||   || ||||||||
                                CTCTTA GG   AC CAGAAGGA
                                   C  CCC  _
GAM860  AP3M2    3'  AGGAAGACCCGTACTCTC    23299        TCCT C
                                GAGAGTAC    G GTCTTCCT
                                ||||||||    | ||||||||
                                CTCTCATG    C CAGAAGGA
                                     _____ C
GAM860  CALN1    3'  AGGAAGACACAGAATTCTTTC  49658      TACTC   C
                                GAGAG     CTG GTCTTCCT
                                |||||     ||| ||||||||
                                CTTTC     GAC CAGAAGGA
                                   TTAA_   A
GAM860  DAMS     5'  AGGAAATTCAAGTACTCT    42084        CC  C  C
                                AGAGTACT  TG GT TTCCT
                                ||||||||  || || |||||
                                TCTCATGA  AC TA AAGGA
                                     __  T  _
GAM860  DKFZP727M111 5'  AGGCCAGGAGGACCCTC     32055     A  A     C
                                GAG GT CTCCTG GTCT
                                ||| || |||||| ||||
                                CTC CA GAGGAC CGGA
                                  C  G     _
GAM860  FLJ14486 5'  AGGAAGGTTCAAGTCTCTC   52434      T   CC  CG
                                GAGAG ACT  TG  TCTTCCT
                                ||||| |||  ||  |||||||
                                CTCTC TGA  AC  GGAAGGA
                                   _  __  TT
GAM860  FUSIP1   3'  AGGAAGACAGCCATAGTCTC  22780     T   CCT  _
                                GAG ACT   GC GTCTTCCT
                                ||| |||   || ||||||||
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                                CTC TGA   CG CAGAAGGA
                                  _   TAC  A
GAM860  HIC      3'  GAAGATTGAGTACTCT      68048         CTGC
                                AGAGTACTC    GTCTTC
                                |||||||||    ||||||
                                TCTCATGAG    TAGAAG
                                     T___
GAM860  IL22R    3'  AGGAAATGCAGGGAAACTC    41467      AC       C
                                GAGT  TCCTGCGT TTCCT
                                ||||  |||||||| |||||
                                CTCA  GGGACGTA AAGGA
                                  AA       _
GAM860  KIAA0472 3'  AGGAGGGGTAAGTACTCTC    72334         CC   G
                                GAGAGTACT  TGC TCTTCCT
                                |||||||||  ||| |||||||
                                CTCTCATGA  ATG GGGAGGA
                                     __   _
GAM860  KIAA1229 3'  AGGATGTAAAAGTTCTCTC    62750       T   CC
                                GAGAG ACT  TGCGTCTT
                                ||||| |||  ||||||||
                                CTCTC TGA  ATGTAGGA
                                   T   AA
GAM860  LAK-4P   3'  AGGAAGACAGTTTCGCCTCTC  24394       TACTCCT  _
                                GAGAG      GC GTCTTCCT
                                |||||      || ||||||||
                                CTCTC      TG CAGAAGGA
                                   CGCTT__  A
GAM860  MRPS35   3'  AGGTCCTCAGGAGTATTCTC   41819           CGTCTT
                                GAGAGTACTCCTG     CCT
                                ||||||||||||      |||
                                CTCTTATGAGGAC     GGA
                                       TCCT__
GAM860  OBTP     5'  AGGATCTGCAAGGAGGACCCTC 34663     A  A    _   TCT
                                GAG GT CTCCT GCG   TCCT
                                ||| || ||||| |||   ||||
                                CTC CA GAGGA CGT   AGGA
                                  C  G    A   CT_
GAM860  RI58     3'  AGATCAGGAATACTCTT     25774        C    C
                                GAGAGTA TCCTG GTCT
                                ||||||| ||||| ||||
                                TTCTCAT AGGAC TAGA
                                    A    _
GAM860  SMBP     3'  AAGACAGAAGTGTACTCTC    72620        TC  GC_
                                GAGAGTAC  CT   GTCTT
                                ||||||||  ||   |||||
                                CTCTCATG  GA   CAGAA
                                     T_  AGA
GAM860  SNTG1    5'  AGGACTCTGAGGAGTACTCTT  39099          G  TCT
                                GAGAGTACTCCT CG   TCCT
                                ||||||||||| ||   ||||
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                                TTCTCATGAGGA GT   AGGA
                                      _ CTC
GAM860  SNX11    3'  AGGACCAGGAGTATCTC     26169      G       C
                                GAGA TACTCCTG GTCTT
                                |||| |||||||| |||||
                                CTCT ATGAGGAC CAGGA
                                  _       _
GAM860  TTY7     3'  AGGAAGACACAGGTAGCT    50015     ACT    C
                                AGT   CCTG GTCTTCCT
                                |||   |||| ||||||||
                                TCG   GGAC CAGAAGGA
                                  AT_    A
GAM860  LOC123872 5' GGAAAGAGGGTACTCTC     74710          _ GCGTC
                                GAGAGTACTC CT     TTCC
                                |||||||||| ||     ||||
                                CTCTCATGGG GA     AAGG
                                      A ______
GAM860  LOC138389 3' AGGAAGACTTGCAAGTCTCTC 76725      T   CC   __
                                GAGAG ACT  TGC  GTCTTCCT
                                ||||| |||  |||  ||||||||
                                CTCTC TGA  ACG  CAGAAGGA
                                   _  __  TT
GAM860  LOC143943 3' AGGAAGATCAGCAGCCTCTC   83911      TA  C   C
                                GAGAG  CT CTG GTCTTCCT
                                |||||  || ||| ||||||||
                                CTCTC  GA GAC TAGAAGGA
                                   C_  C   _
GAM860  LOC145009 5' AAGAAACAAAGGAGTACTTTC  60965           GCG__
                                GAGAGTACTCCT     TCTT
                                ||||||||||||     ||||
                                CTTTCATGAGGA     AGAA
                                      AACAA
GAM860  LOC147976 5' AGGAAGACTGGGGTACCCTC   79285     A      TGC
                                GAG GTACTCC   GTCTTCCT
                                ||| |||||||   ||||||||
                                CTC CATGGGG   CAGAAGGA
                                  C      T__
GAM860  LOC151512 3' AGGAAGACAATGCTTGTACCTC 86611     A   TCCT  ___
                                GAG GTAC    GC   GTCTTCCT
                                ||| ||||    ||   ||||||||
                                CTC CATG    CG   CAGAAGGA
                                  _    TT__  TAA
GAM860  LOC158801 3' GAAAACACAAGAAGTATTCT   88255        _ C  C  C
                                AGAGTACT C TG GT TTC
                                |||||||| | || || |||
                                TCTTATGA G AC CA AAG
                                     A A  A  A
GAM860  LOC206426 3' GAAGCGAGGTGCACTCTC    91099       ACT   G  T
                                GAGAGT   CCT CG CTTC
                                ||||||   ||| || ||||
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                                CTCTCA   GGA GC GAAG
                                   CGT   _ _
GAM860   LOC254337 5'  GGAAAGGGGAGTATCTC     98012      G      GCGTC
                                GAGA TACTCCT     TTCC
                                |||| |||||||     ||||
                                CTCT ATGAGGG     AAGG
                                  _      GA___
GAM860   LOC256790 5'  AGTGCAGGAGTGCCCTC     96489     A         T
                                GAG GTACTCCTGCG CT
                                ||| |||||||||| ||
                                CTC CGTGAGGACGT GA
                                  C         _
GAM860   LOC256946 3'  AGGAAGACAGCCATAGTCTC   96182     T   CCT  _
                                GAG ACT   GC GTCTTCCT
                                ||| |||   || ||||||||
                                CTC TGA   CG CAGAAGGA
                                  _   TAC  A
GAM860   LOC257396 5'  GAAATGTAGGAGCATCTC     98922      GTA       C
                                GAGA   CTCCTGCGT TTC
                                ||||   ||||||||| |||
                                CTCT   GAGGATGTA AAG
                                   AC_       _
GAM860   LOC257408 3'  AGGGCACCAGGAGTACCTC    97797     A       C  CT
                                GAG GTACTCCTG GT  TCCT
                                ||| |||||||| ||  ||||
                                CTC CATGAGGAC CA  GGGA
                                  _       _ C_
GAM860   LOC257453 3'  AGGAAGATGACGAGTAACTC   82927      _   CTG
                                GAGT ACTC   CGTCTTCCT
                                |||| ||||   |||||||||
                                CTCA TGAG   GTAGAAGGA
                                  A    CA_
GAM860   LOC51066  3'  AGGAAGATGGCCGACACTCTC  32500       AC  CTG
                                GAGAGT  TC   CGTCTTCCT
                                ||||||  ||   |||||||||
                                CTCTCA  AG   GTAGAAGGA
                                   C_  CCG
GAM861   ATP6V0C   3'  CCCCAGTAGTTGGTCTTGTA   88658         CTG   _   A
                                TACAAGATCA   ACT CTG GG
                                ||||||||||   ||| ||| ||
                                ATGTTCTGGT   TGA GAC CC
                                      ___   T   C
GAM861   DLX4      3'  GTCCCCAGAACCCTTGGTCTTG 57114         CTGAC    A
                                CAAGATCA     TCTG GGAC
                                ||||||||     |||| ||||
                                GTTCTGGT     AGAC CCTG
                                     TCCCA    C
GAM861   DLX4      3'  GTCCCCAGAACCCTTGGTCTTG 10421         CTGAC    A
                                CAAGATCA     TCTG GGAC
                                ||||||||     |||| ||||
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                                GTTCTGGT    AGAC CCTG
                                    TCCCA   C
GAM861  MNT     3'  TCCTCAGAGGCTGAGCCTGTA 40089     AGA  CTGA
                                TACA  TCA   CTCTGAGGA
                                ||||  |||   |||||||||
                                ATGT  AGT   GAGACTCCT
                                  CCG  CG__
GAM861  SIAH2   3'  TCTCATCAGTGATCTT     18616         CTC
                                AAGATCACTGA  TGAGG
                                ||||||||||  |||||
                                TTCTAGTGACT  ACTCT
                                      ___
GAM861  TCF2    3'  GTCCCCAGAACCAGCTGCAGAT 22411    AGAT _  AC   A
          G                      CA   CA CTG  TCTG GGAC
                                ||   || |||  |||| ||||
                                GT   GT GAC  AGAC CCTG
                                 AGAC  C   CA   C
GAM861  TCL1A   3'  CCTGGACCAGTGGTCT     42017        AC  G
                                AGATCACTG  TCT AGG
                                |||||||||  ||| |||
                                TCTGGTGAC  AGG TCC
                                    C_  _
GAM861  TOB1    3'  TTTTGAGTCAGTGTCTT    20437     T      T
                                AAGA CACTGACTC GAG
                                |||| ||||||||| |||
                                TTCT GTGACTGAG TTT
                                  _       T
GAM861  VNN1    3'  TCCTCAGAGCAATTCTCTGTA  17423     _  TCAC  A
                                TACA AGA   TG CTCTGAGGA
                                |||| |||   || |||||||||
                                ATGT TCT   AC GAGACTCCT
                                  C  TA__  _
GAM861  BMF     5'  CCTCAGAGTCAAACTTTGTG  54280      ATCAC
                                TACAAG    TGACTCTGAGG
                                ||||||    ||||||||||
                                GTGTTT    ACTGAGACTCC
                                   CAA__
GAM861  DDX33   3'  GTCCTCAGTGCGTGACCCTGT  39786    AGA   T ACT
                                ACA   TCAC G   CTGAGGAC
                                |||   |||| |   ||||||||
                                TGT   AGTG C   GACTCCTG
                                  CCC   _ GT_
GAM861  FLJ20364 3'  CCTCAGAGCCATGTATTTG   35528     AT  C  A
                                CAAG  CA TG CTCTGAGG
                                ||||  || || ||||||||
                                GTTT  GT AC GAGACTCC
                                  AT  _  C
GAM861  HMGN4   3'  TCCTTTCCCCAGTGATTTGTA  22034     A      ACTCT
                                TACA GATCACTG    GAGGA
                                |||| ||||||||    |||||
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                                ATGT TTAGTGAC    TTCCT
                                  _      CCCT_
GAM861  KIAA0377  3'  CCTCAGAGCCAGTCTCT    28501    TC   A
                                AGA  ACTG CTCTGAGG
                                |||  |||| ||||||||
                                TCT  TGAC GAGACTCC
                                  C_   C
GAM861  KIAA0449  3'  TCCCCAGCACTCATGATCTTG  34639       C  CT_  A
                                CAAGATCA TGA   CTG GGA
                                |||||||| |||   ||| |||
                                GTTCTAGT ACT   GAC CCT
                                     _  CAC   C
GAM861  KIAA1061  3'  GTCCTCAGAGTGCATTTCCTG  71723    A  TCAC  _
                                CA GA    TG ACTCTGAGGAC
                                || ||    || ||||||||||
                                GT CT    AC TGAGACTCCTG
                                 C  TT__  G
GAM861  KIAA1535  3'  GTCCTCAGCTCAAGAATCCTGT 80214     A  CAC  CT
           A                     TACA GAT   TGA  CTGAGGAC
                                |||| |||   |||  ||||||||
                                ATGT CTA   ACT  GACTCCTG
                                  C   AGA   C_
GAM861  LCHN     3'  TCCTCAGAGTATGTCTTG    87478       CACTG
                                CAAGAT    ACTCTGAGGA
                                ||||||    ||||||||||
                                GTTCTG    TGAGACTCCT
                                   TA___
GAM861  MAGEH1   3'  TCATAATCTATGATCTTGTA  26772        CT  CTC
                                TACAAGATCA  GA   TGA
                                ||||||||||  ||   |||
                                ATGTTCTAGT  CT   ACT
                                      AT  AAT
GAM861  LOC154789 5'  TCCTCAGAGCTCTCCTGTG   82034     A  TCACT  _
                                TACA GA    GA CTCTGAGGA
                                |||| ||    || |||||||||
                                GTGT CT    CT GAGACTCCT
                                  C  _____  C
GAM861  LOC197201 3'  TCCTCAGAAGGTATTTGTA   89289      ATC   GAC
                                TACAAG   ACT   TCTGAGGA
                                ||||||   |||   ||||||||
                                ATGTTT   TGG   AGACTCCT
                                   A__   A__
GAM861  LOC200178 3'  CCTCAGATGCCTTGTA     89998      AT  CTGAC
                                TACAAG  CA    TCTGAGG
                                ||||||  ||    |||||||
                                ATGTTC  GT    AGACTCC
                                   C_  _____
GAM861  LOC255193 3'  CCTCAGAGTCAGGCCTGTA   97103     AGATCA
                                TACA     CTGACTCTGAGG
                                ||||     ||||||||||||
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                                ATGT     GACTGAGACTCC
                                  CCG___
GAM861  LOC96597  5'  TCCCCAGAATTCTCTTGT    67468       TCACT  C_   A
                                ACAAGA    GA  TCTG GGA
                                ||||||    ||  |||| |||
                                TGTTCT    CT  AGAC CCT
                                   _____  TA   C
GAM862  IRS1      3'  CCATAGATGGTTCTCAATTGTA 19874      C        TGAAC
                                TACA ATTGAGAACC    ATGG
                                |||| ||||||||||    ||||
                                ATGT TAACTCTTGG    TACC
                                  _        TAGA_
GAM862  SERPINF1  3'  CCTGTAAGGTTTCAATG     12038        A   GA   T
                                CATTGAGA CCT  ACA GG
                                |||||||| |||  ||| ||
                                GTAACTTT GGA  TGT CC
                                    _   A_   _
GAM862  HSA243396 3'  CCATGTTCAGCAATGTCAATG  37844       GAAC_
                                CATTGA    CTGAACATGG
                                ||||||    ||||||||||
                                GTAACT    GACTTGTACC
                                   GTAAC
GAM862  KIAA1387  3'  CAGGAATTTTCAATATGTA    71444      C      __
                                TACA ATTGAGAA  CCTG
                                |||| ||||||||  ||||
                                ATGT TAACTTTT  GGAC
                                  A       AA
GAM862  MGC16063  3'  TTCAAATTCCAATGTGTA     54930         A   CC
                                TACACATTG GAA  TGAA
                                ||||||||| |||  ||||
                                ATGTGTAAC CTT  ACTT
                                    _  AA
GAM862  SMCR8     3'  CCATGCTCAGGTTTGACTATGT 59253      TGA_      A
                                ACAT    GAACCTGA CATGG
                                ||||    |||||||| |||||
                                TGTA    TTTGGACT GTACC
                                  TCAG       C
GAM862  UPLC1     3'  CCATGCTAGGCCCCAATGT    35227       AGAA    AA
                                ACATTG    CCTG  CATGG
                                ||||||    ||||  |||||
                                TGTAAC    GGAT  GTACC
                                   CCC_    C_
GAM862  ZNF334    3'  CCATAAGTCAACCCTCAATGT  36637        AACC   AC_
                                ACATTGAG    TGA   ATGG
                                ||||||||    |||   ||||
                                TGTAACTC    ACT   TACC
                                    CCA_   GAA
GAM862  LOC145082 3'  TATGGAATGCCCTTAATGTGTA 84196           AACCTGAA
                                TACACATTGAG       CATG
                                ||||||||||        ||||
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                                ATGTGTAATTC       GTAT
                                      CCGTAAG_
GAM862  LOC157723 3'  CCAAGTAAGGTTCTCAAATGT  82465       _       GA  A
                                ACATT GAGAACCT  AC TGG
                                ||||| ||||||||  || |||
                                TGTAA CTCTTGGA  TG ACC
                                   A       A_  A
GAM862  LOC219988 5'  CCATGTTCGGCCCCCAATG    93262       AGAAC
                                CATTG    CTGAACATGG
                                |||||    ||||||||||
                                GTAAC    GGCTTGTACC
                                   CCCC_
GAM863  CDH12     3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                      AA___   AC
GAM863  GOCAP1    3'  ATTGTTCTTGGGAGCAGTGTA  43007       CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM863  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT    98090       T    AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                   _   GTCA_
GAM863  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
           A                     TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM863  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                      AGACG___
GAM863  HMP19     3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
           TA                    TACA    TCC    GAAGAATAAG
                                ||||    |||    ||||||||||
                                ATGT    AGG    TTTCTTATTC
                                   AAA_   ATTG
GAM863  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68742             _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                         G
GAM863  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
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                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM863  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748     CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM863  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571    CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM863  OSBPL11   3'  CTTAATTTCCCAAGAGTGGTG  43206       CCAA   AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                     AACC   A_
GAM863  YME1L1    3'  TCATTCTTGATGTGGTGTA   58438       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                     TA_    A
GAM863  ZNF262    3'  CTTATTTTGTTTGGGAGT    18723       A
                                ACTCCCAAG AGAATAAG
                                |||||||||  ||||||||
                                TGAGGGTTT TTTTATTC
                                     G
GAM863  LOC91960  3'  TGTGGCTTGGAACGTGGTGTA  68294       TC_    AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
                                ATGTGGTG   GGTTC   TGT
                                     CAA    GG__
GAM864  ANKTM1    5'  GCGGACCCCAGCGCCTGGCA   24700     TGA  TCGA
                                TGCC   GC   TGGGGTCCGC
                                ||||   ||   ||||||||||
                                ACGG   CG   ACCCCAGGCG
                                  TC_  CG__
GAM864  APBA1     5'  GCGGACCCAGCTGTCAGGCA   70475       __   CGATG
                                TGCCTGA  GCT    GGGTCCGC
                                |||||||  |||    ||||||||
                                ACGGACT  CGA    CCCAGGCG
                                   GT  _____
GAM864  ARCN1     3'  GCGAACTCCTGAGCTCAGGCA  9755          AT    C
                                TGCCTGAGCTCG  GGGGT CGC
                                ||||||||||||  |||||  |||
                                ACGGACTCGAGT  CCTCA GCG
                                      __    A
GAM864  HMGCL     3'  CGGACCCTGGCCCAGG      5754      A   CGAT
                                CCTG GCT    GGGGTCCG
                                ||||  |||    ||||||||
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                                GGAC CGG   TCCCAGGC
                                  C  ____
GAM864  OXT     5'  CGGACCCTGGACCCAGCGCA  8075     _  AG_  CGAT
                                TGC CTG  CT   GGGGTCCG
                                ||| |||  ||   ||||||||
                                ACG GAC  GG   TCCCAGGC
                                  C  CCA  ____
GAM864  PPP1R2  5'  GCGGACCCCACGCCAAGCA  21785    C  A  TCGA
                                TGC TG GC   TGGGGTCCGC
                                ||| || ||   ||||||||||
                                ACG AC CG   ACCCCAGGCG
                                  A  _  C___
GAM864  RGS6    3'  GCGGACCCCACAGGCAGGC  16278     AG  CGA
                                GCCTG  CT   TGGGGTCCGC
                                |||||  ||   ||||||||||
                                CGGAC  GA   ACCCCAGGCG
                                   G_  C__
GAM864  FLJ12488 3'  GCTCCATCAAATTCAGACA  49158   C    CTC
                                TG CTGAG   GATGGGGT
                                || |||||   ||||||||
                                AC GACTT   CTACCTCG
                                 A    AAA
GAM864  FN5     3'  TGCGGACCCCATCGGCAGGG  39819    GA  T
                                CCT  GC CGATGGGGTCCGCA
                                |||  || ||||||||||||||
                                GGG  CG GCTACCCCAGGCGT
                                  A_  _
GAM864  FREQ    3'  GCGGACCGCAGCCCAGCA   27374    C  A  CGAT G
                                TGC TG GCT   G GGTCCGC
                                ||| || |||   | |||||||
                                ACG AC CGA   C CCAGGCG
                                  _  C   ____ G
GAM864  KIAA1259  5'  GACCCCCTTTAGATGCTCAGGC 50798        _  GAT__
           A                     TGCCTGAGC TC    GGGGTC
                                |||||||||  ||    ||||||
                                ACGGACTCG AG    CCCCAG
                                      T  ATTTC
GAM864  KIAA1784  3'  ACTCCAGAGCTCAGGCA    65741         GA
                                TGCCTGAGCTC  TGGGGT
                                ||||||||||  ||||||
                                ACGGACTCGAG  ACCTCA
                                           __
GAM864  LAP1B   5'  GCTGACCCAGCTCAGGCA    65195        CGATG   C
                                TGCCTGAGCT    GGGTC GC
                                ||||||||||    ||||| ||
                                ACGGACTCGA    CCCAG CG
                                      _____    T
GAM864  NDRG4   3'  GCGGGGCCAGCTCAGGCA    40383         CGATG  G
                                TGCCTGAGCT    GG TCCGC
                                ||||||||||    || |||||
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                                ACGGACTCGA    CC GGGCG
                                      _____ G
GAM864  NDRG4    3' GCGGGGCCAGCTCAGGCA    43579         CGATG  G
                                TGCCTGAGCT    GG TCCGC
                                ||||||||||    || |||||
                                ACGGACTCGA    CC GGGCG
                                      _____ G
GAM864  RAI17    3' ACCTCCAAGCTCAGACA     92897    C     CGA  _
                                TG CTGAGCT   TGG GGT
                                || |||||||   ||| |||
                                AC GACTCGA   ACC CCA
                                 A      ___  T
GAM864  SLC12A8  3' GTGGACCCAAGCCCAGG     45245     A  CGATG
                                CCTG GCT    GGGTCCGC
                                |||| |||    ||||||||
                                GGAC CGA    CCCAGGTG
                                  C  A____
GAM864  LOC144742 3' TGCAAACCCCACCAACCTCAGC 77470    C   CTCGA    CC
                                GC TGAG    TGGGGT  GCA
                                || ||||    ||||||  |||
                                CG ACTC    ACCCCA  CGT
                                 _   CAACC     AA
GAM864  LOC148645 3' GCAGACCCCATGCAGGG     85335    GA  TCG      C
                                CCT  GC   ATGGGGTC GC
                                |||  ||   |||||||| ||
                                GGG  CG   TACCCCAG CG
                                  A_ ___       A
GAM865  COLQ     3' TCATATGGAGACCTGCAATGCA 55428        _  _  G  GGAC
           C                     GTGCATTG AGG CT CA    ATGA
                                ||||||||| ||| || ||    ||||
                                CACGTAAC TCC GA GT    TACT
                                    G  A  G  A___
GAM865  TCP1     3' TCCCACCCCCAATGCAC     48435        A  C  CA
                                GTGCATTG GG TG  GGA
                                |||||||| || ||  |||
                                CACGTAAC CC AC  CCT
                                    C  C  __
GAM865  FLJ13195  3' CATGTCATCCTCAATGCAT   43549         CTGCAG
                                GTGCATTGAGG     GACATG
                                ||||||||||      ||||||
                                TACGTAACTCC     CTGTAC
                                      TA_____
GAM865  FLJ25193  5' CATGGGGTAGCCTCAACGCAT  59354      A       AGGA
                                GTGC TTGAGGCTGC    CATG
                                |||| ||||||||||    ||||
                                TACG AACTCCGATG    GTAC
                                  C        GG__
GAM865  KIAA1010  3' CATACCGCAACCTCAATG    72539        C  A  AC
                                CATTGAGG TGC GG  ATG
                                |||||||| ||| ||  |||
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                                GTAACTCC ACG CC  TAC
                                     A   _ A_
GAM865  KIAA1814  5'  CATATCCTGCAGCAGGTCTAC  70874     C  TGAG        C
                                GTG AT    GCTGCAGGA ATG
                                ||| ||    ||||||||| |||
                                CAT TG    CGACGTCCT TAC
                                  C  GA__        A
GAM865  MRPS26    3'  GTGTGTACAGCCTCAGCGCAC  48725      A        CAGG
                                GTGC TTGAGGCTG    ACAT
                                |||| |||||||||    ||||
                                CACG GACTCCGAC    TGTG
                                  C        ATG_
GAM865  RCD-8     3'  CATATCCTGCAGCTGCTGCA   27519      TTGA        C
                                TGCA    GGCTGCAGGA ATG
                                ||||    |||||||||| |||
                                ACGT    TCGACGTCCT TAC
                                  CG__         A
GAM865  SDC3      3'  CCTGCAGCCTCAACAC      28471     CA
                                GTG  TTGAGGCTGCAGG
                                |||  |||||||||||||
                                CAC  AACTCCGACGTCC
                                  __
GAM865  TAF5L     3'  CACGTCCTGCACTGCAAT    27719      A  C       A
                                ATTG GG TGCAGGAC TG
                                |||| || |||||||| ||
                                TAAC TC ACGTCCTG AC
                                  G  _       C
GAM865  LOC143162 5'  CCTGCAGCCTCAAGCAC     77004      A
                                GTGC TTGAGGCTGCAGG
                                |||| |||||||||||||
                                CACG AACTCCGACGTCC
                                  _
GAM865  LOC144563 5'  TCATTTCCACAGCCTCAACCAC 77404     CA        CA   C
                                GTG  TTGAGGCTG  GGA ATGA
                                |||  |||||||||  ||| ||||
                                CAC  AACTCCGAC  CCT TACT
                                  C_        A_   T
GAM865  LOC145053 5'  CCTGCAGTCTCAATGCAC    84176
                                GTGCATTGAGGCTGCAGG
                                ||||||||||||||||||
                                CACGTAACTCTGACGTCC

GAM865  LOC149703 5'  CATGTCCCTGACCCACCAATGC 85817         A_  CTG   _
          AC                      GTGCATTG  GG   CAGG ACATG
                                ||||||||  ||   |||| |||||
                                CACGTAAC  CC   GTCC TGTAC
                                     CA  CA_    C
GAM865  LOC151632 5'  TCATTTCCACAGCCTCAACCAC 86650     CA        CA   C
                                GTG  TTGAGGCTG  GGA ATGA
                                |||  |||||||||  ||| ||||
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                                CAC  AACTCCGAC  CCT TACT
                                  C_       A_   T
GAM865  LOC196738 5'  CCTGCAGCCTCAAGCAC     88889      A
                                GTGC TTGAGGCTGCAGG
                                |||| ||||||||||||
                                CACG AACTCCGACGTCC
                                  _
GAM865  LOC200904 5'  TCATTTCCACAGCCTCAACCAC 91784     CA       CA   C
                                GTG  TTGAGGCTG  GGA ATGA
                                |||  |||||||||  ||| ||||
                                CAC  AACTCCGAC  CCT TACT
                                  C_       A_   T
GAM865  LOC219919 5'  TCATTTCCACAGCCTCAACCAC 94932     CA       CA   C
                                GTG  TTGAGGCTG  GGA ATGA
                                |||  |||||||||  ||| ||||
                                CAC  AACTCCGAC  CCT TACT
                                  C_       A_   T
GAM865  LOC220980 3'  CATGTCCTGCAACACTGTCC   94766   TG  T  AGGC
                                G  CA TG    TGCAGGACATG
                                |  || ||    ||||||||||
                                C  GT AC    ACGTCCTGTAC
                                 CT  C  A___
GAM865  LOC221795 5'  TCATTTCCACAGCCTCAACCAC 94080     CA       CA   C
                                GTG  TTGAGGCTG  GGA ATGA
                                |||  |||||||||  ||| ||||
                                CAC  AACTCCGAC  CCT TACT
                                  C_       A_   T
GAM865  LOC256515 5'  TCATTTCCACAGCCTCAACCAC 98217     CA       CA   C
                                GTG  TTGAGGCTG  GGA ATGA
                                |||  |||||||||  ||| ||||
                                CAC  AACTCCGAC  CCT TACT
                                  C_       A_   T
GAM865  LOC92822  3'  CCCACAACCTCAATGTAC    71181          C  CA
                                GTGCATTGAGG TG  GG
                                |||||||||| ||  ||
                                CATGTAACTCC AC  CC
                                       A  AC
GAM866  SLC13A4   3'  CACCAGGAGCACACAACCCCAG 25859    AA   C      GAA
          A                      TC  GGGT GTGTGTTT   GTG
                                ||  |||| ||||||||   |||
                                AG  CCCA CACACGAG   CAC
                                 AC    A       GAC
GAM866  ATP10B    3'  CACTGGTCCACATAACCCTTGA 64104        CG    TTTGA
                                TCAAGGGT  TGTG    AGTG
                                ||||||||  ||||    ||||
                                AGTTCCCA  ACAC    TCAC
                                     AT    CTGG_
GAM866  FLJ12076  3'  CACATTGCCACATGACCCTT   48021          TTT  A
                                AAGGGTCGTGTG   GA GTG
                                ||||||||||||   || |||
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                                TTCCCAGTACAC   TT CAC
                                      CG_  A
GAM866  KIAA0750  5'  CACTGCCGCACACGACTCCTGA 28304     A         TTGA
                                TCA GGGTCGTGTGT    AGTG
                                ||| ||||||||||    ||||
                                AGT CTCAGCACACG    TCAC
                                  C         CCG_
GAM866  KIAA1485  3'  TAGACACACACCCCCTGA    90771     A   TC
                                TCA GGG  GTGTGTTTG
                                ||| |||  |||||||||
                                AGT CCC  CACACAGAT
                                  C   CA
GAM866  LOC145608 5'  CACCCCAAATTACTGACCCTTG 84374          T   _    AA
              A                  TCAAGGGTCG GTG TTTG  GTG
                                ||||||||||  ||| ||||  |||
                                AGTTCCCAGT CAT AAAC  CAC
                                      _  T    CC
GAM867  MRPL11    3'  ATCAGGCCTGAATAAACATCC  32649     CGG__
                                GGA    GTTCAGGCCTGAT
                                |||    ||||||||||||||
                                CCT    TAAGTCCGGACTA
                                  ACAAA
GAM867  MYOZ2     5'  ATCAGGCCCAAGTGCCATCCAT 33938      CG   TCA__
                                ATGGA  GGT    GGCCTGAT
                                |||||  |||    ||||||||
                                TACCT  CCG    CCGGACTA
                                   A_   TGAAC
GAM867  LOC145226 3'  TCAGGCCCAATCCATGCCA   77561     AC_    CA
                                TGG   GGGTT  GGCCTGA
                                |||   |||||  |||||||
                                ACC   CCTAA  CCGGACT
                                  GTA    C_
GAM867  LOC146108 5'  ATCAGACCCAAGGGCCCGTTCA 78146          A__  C
                                TGGACGGGTTC   GG CTGAT
                                ||||||||||   || |||||
                                ACTTGCCCGGG   CC GACTA
                                      AAC  A
GAM868  DLEC1     3'  CATCTGGCCCTCCCTTG     96278      A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                   C    G  _
GAM868  DLEC1     3'  CATCTGGCCCTCCCTTG     96279      A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                   C    G  _
GAM868  PIP5K1A   3'  TATCCCACCCTGCCTTGATA   14520        A   CA  C
                                TATCAAGG AGGG  GG GTG
                                ||||||||  ||||  || |||
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                                ATAGTTCC TCCC  CC TAT
                                    G   A_  C
GAM868  SOX11    3'  ACCCACCCCCCCTTGGTA    13308        AA   CA  C
                                TATCAAGG  GGG  GG GT
                                ||||||||  |||  || ||
                                ATGGTTCC  CCC  CC CA
                                    CC   A_  _
GAM868  CHL1     3'  TGTTACCTTTCCTCAATA    22768     CA      CA
                                TAT  AGGAAGGG  GGCG
                                |||  ||||||||  ||||
                                ATA  TCCTTTCC  TTGT
                                  AC       A_
GAM868  EPB41L1  3'  CATTCTGCCCTTCCCTGA    71104     A         C
                                TCA GGAAGGGCAGG GTG
                                ||| ||||||||||| |||
                                AGT CCTTCCCGTCT TAC
                                  C         _
GAM868  FLJ00060 3'  CATACCCCCTGCCCTCCTCTGA 61741     _    A      CGTG
                                TCA AGGA GGGCAGG    ATG
                                ||| |||| |||||||    |||
                                AGT TCCT CCCGTCC    TAC
                                  C    _      CCCA
GAM868  FLJ10898 5'  CACCACAGCCCTTTCTCAATA  60126     CA        AGGC
                                TAT  AGGAAGGGC    GTG
                                |||  |||||||||    |||
                                ATA  TCTTTCCCG    CAC
                                  AC        ACAC
GAM868  FLJ22557 3'  ATCATCCCATCCTTAATA    45581     C    A   CAGGC
                                TAT AAGGA GGG     GTGAT
                                ||| ||||| |||     |||||
                                ATA TTCCT CCC     TACTA
                                  A    A  _____
GAM868  KIAA0574 3'  CATCCCCTGCCCTCCCCTGA   69808     A  A      CGT
                                TCA GG AGGGCAGG   GATG
                                ||| ||  ||||||||   ||||
                                AGT CC TCCCGTCC   CTAC
                                  C  C       C__
GAM868  KIAA0632 3'  CACCTCAGAAACCCTTCCTTGA 32071          CA___  C
                                TCAAGGAAGGG     GG GTG
                                ||||||||||     || |||
                                AGTTCCTTCCC     CT CAC
                                      AAAGA  C
GAM868  KIAA1045 3'  CATCACATGTCCTTCC      71599         GGC
                                GGAAGGGCA   GTGATG
                                |||||||||   ||||||
                                CCTTCCTGT   CACTAC
                                     A__
GAM868  KIAA1354 5'  CAGTGACTGCCTTCCCTTGATA 61572         A      G  _
                                TATCAAGG AGGGCAG CG TG
                                |||||||| ||||||| || ||
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                                ATAGTTCC TTCCGTC GT AC
                                    C      A  G
GAM868  MGC20460  5'  CACCGCCTCCTACCCTTCTT   54901        C___    _
                                AGGAAGGG    AGGCG TG
                                ||||||||    ||||| ||
                                TTCTTCCC    TCCGC AC
                                    ATCC     C
GAM868  LOC158476 3'  CACGCCCGCCCCCCCCATTGA  88186     _ AA_   A
                                TCAA GG   GGGC GGCGTG
                                |||| ||   |||| ||||||
                                AGTT CC   CCCG CCGCAC
                                  A  CCC    C
GAM868  LOC90459  3'  CACACCCGCCTAATTTTTG    63550       A_   A  C
                                CAAGGA  GGGC GG GTG
                                ||||||  |||| || |||
                                GTTTTT  TCCG CC CAC
                                    AA    C  A
GAM869  CDH12     3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM869  GOCAP1    3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC         G
GAM869  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT    98090      T    AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||     ||||||
                                TGGTG GGGT     TTATTC
                                   _    GTCA_
GAM869  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
            A                    TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM869  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM869  HMP19     3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
            TA                    TACA    TCC    GAAGAATAAG
                                ||||    |||    ||||||||||
                                ATGT    AGG    TTTCTTATTC
                                  AAA_   ATTG
GAM869  KIAA1579  3'  TACTCTTAGTGGTGTA      37154         CCCAAG    A
                                TACACCACT     AAGA TA
                                |||||||||     |||| ||
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                                ATGTGGTGA     TTCT AT
                                      _______   C
GAM869  KIAA1719 3'  TCTGTCTTGGGAGTGGTGTA  68742            _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                       G
GAM869  KIAA1853 3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM869  KIAA1877 3'  CTTATTCTTCTGCCATGAGT   66748     CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM869  KIAA1906 3'  CTTATTCTTCTTGACTTTTGG  73571    CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM869  OSBPL11  3'  CTTAATTTCCCAAGAGTGGTG 43206       CCAA    AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                     AACC   A_
GAM869  YME1L1   3'  TCATTCTTGATGTGGTGTA   58438       TCC     _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                     TA_     A
GAM869  YME1L1   3'  TCATTCTTGATGTGGTGTA   27323       TCC     _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                     TA_     A
GAM869  ZNF262   3'  CTTATTTTGTTTGGGAGT    18723        A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                      G
GAM869  LOC91960 3'  TGTGGCTTGGAACGTGGTGTA 68294       TC_    AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
                                ATGTGGTG   GGTTC   TGT
                                     CAA    GG__
GAM870  ITGAL    3'  GATGCCTCCACCCCCCAGAAC  11045     AA   A   AA_
                                GTTC  GGGG TGGA   GTC
                                ||||  |||| ||||   |||
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                                CAAG  CCCC ACCT   TAG
                                  AC    C    CCG
GAM870  MUC3B    3'  CGGTAACTCTGAGCCCTGAA   95921      A   GA    AA  C
                                TTCA GGG  TGGA  GT ACCG
                                |||| |||  ||||  || ||||
                                AAGT CCC  GTCT  CA TGGC
                                  _   GA    __  A
GAM870  MUC3B    5'  CGGTGACTCCCACACCTGTAAC 95922     CAA   GA   AA
                                GTT   GGG  TGG  AGTCACCG
                                |||   |||  |||  ||||||||
                                CAA   TCC  ACC  TCAGTGGC
                                  TG_   AC   C_
GAM870  BMF      3'  GACCTCCACCCCCTCAGAC    54283     CA    A    AA
                                GTT  AGGGG TGGA  GTC
                                |||  ||||| ||||  |||
                                CAG  TCCCC ACCT  CAG
                                  AC    C   C_
GAM870  PDE8B    5'  GACGCCATCCCCCCGAGC    68202      AA      AAA
                                GTTC  GGGGATGG   GTC
                                ||||  ||||||||   |||
                                CGAG  CCCCTACC   CAG
                                  CC       G__
GAM870  SRPK2    3'  CGGTGACTCTCATTCTTT    13411          AA
                                AGGGGATGG  AGTCACCG
                                |||||||||  ||||||||
                                TTTCTTACT  TCAGTGGC
                                     C_
GAM870  TLK1     5'  CGGTTTCCTCCCCCATCCCCTT 25434           AA_  TC_
            GA                    TCAAGGGGATGG   AG   ACCG
                                ||||||||||||   ||   ||||
                                AGTTCCCCTACC   TC   TGGC
                                       CCC  CTT
GAM870  LOC152018 3'  TGACCTCCACCCCCTTGAAC   86731          A    AA
                                GTTCAAGGGG TGGA  GTCA
                                |||||||||| ||||  ||||
                                CAAGTTCCCC ACCT  CAGT
                                       C    C_
GAM870  LOC221103 3'  GTGACCTCATACATCCCCTGAG 94871       A      GAAA__
            C                    GTTCA GGGGATG     GTCAC
                                |||||  |||||||      |||||
                                CGAGT CCCCTAC     CAGTG
                                  _      ATACTC
GAM870  LOC91960  3'  GCTTTGAACCCGTCCCCTTAAA 68288     C        ____
            C                    GTT AAGGGGATGG    AAAGT
                                |||  ||||||||||    |||||
                                CAA TTCCCCTGCC    TTTCG
                                  A         CAAG
GAM871  SCAMP1   3'  GCTAAATAAATATTCTCC    54500     T     C
                                GGA AATATT ATTTAGC
                                |||  ||||||  |||||||
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                                CCT TTATAA TAAATCG
                                  C     A
GAM871  SCAMP1   3'  GCTAAATAAATATTCTCC    54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM871  NX-17    3'  TGAATATCAGCCCCTAATA   40706        ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM871  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
           TA                    TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM872  AP3B1    5'  CCCCGGCAGGACCAACCCC   14750    T    C     T
                                GGG GTTGG CCTGCC GGG
                                ||| ||||| |||||| |||
                                CCC CAACC GGACGG CCC
                                  _    A     C
GAM872  CDH5     3'  CTCCCCAGCCCAGCACCC    10149        CCCT  C    A
                                GGGTGTTGG   GC TGGG AG
                                |||||||||   || |||| ||
                                CCCACGACC   CG ACCC TC
                                     _____ _   C
GAM872  PIAS3    3'  CCTGACAAGGCCAGCACCC   21445          C  CC
                                GGGTGTTGGCC TG  TGGG
                                |||||||||| ||  ||||
                                CCCACGACCGG AC  GTCC
                                      A  A_
GAM872  PIK3C2B  3'  CCCAGCAGAGCCACCACCC   12093      T   C   C
                                GGGTG TGGC CTGC TGGG
                                ||||| |||| |||| ||||
                                CCCAC ACCG GACG ACCC
                                  C   A   _
GAM872  SLC39A4  5'  CCCCAGGGCCAACTCCC    35433    T       CCT
                                GGG GTTGGCCCTG   GGG
                                ||| ||||||||||   |||
                                CCC CAACCGGGAC   CCC
                                  T       ____
GAM872  TIMM44   3'  TCCCCCGCAGGGCCAACCCC  71925    T        CT
                                GGG GTTGGCCCTGC  GGGA
                                ||| ||||||||||  ||||
                                CCC CAACCGGGACG  CCCT
                                  _        CC
GAM872  ZNF265   3'  CCCTGAGCCCAGGGCCAACCCC 19575    T       CCT___
                                GGG GTTGGCCCTG     GGG
                                ||| ||||||||||     |||
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                                CCC CAACCGGGAC     CCC
                                  _        CCGAGT
GAM872  AGPAT1   3'  CCCTGAAGCAGGGCCAAACCC  52199     G        CT__
                                GGGT TTGGCCCTGC   GGG
                                |||| ||||||||||   |||
                                CCCA AACCGGGACG   CCC
                                  _        AAGT
GAM872  AGPAT1   3'  CCCTGAAGCAGGGCCAAACCC  22171     G        CT__
                                GGGT TTGGCCCTGC   GGG
                                |||| ||||||||||   |||
                                CCCA AACCGGGACG   CCC
                                  _        AAGT
GAM872  C14orf4  5'  CTTCCCCAAACCAACACC    67916        CCC  CCT
                                GGTGTTGG   TG   GGGAAG
                                ||||||||   ||   ||||||
                                CCACAACC   AC   CCCTTC
                                     AA_  ___
GAM872  C1QTNF7  3'  CTTCCCAGACAGAGGGGCGGCC 50003    G   GG  _   C
                                GG TGTT  CC CTG CTGGGAAG
                                || ||||  || ||| ||||||||
                                CC GCGG  GG GAC GACCCTTC
                                 G   __ A   A
GAM872  C22orf20 3'  CCCCCAGGCAGGAGCCA     48195     _        AA
                                TGGC CCTGCCTGGG  G
                                |||| ||||||||||  |
                                ACCG GGACGGACCC  C
                                  A        CC
GAM872  FLJ10748 5'  CCTCAGAGCCAACACCC     37099         C   CCT
                                GGGTGTTGGC CTG   GGG
                                |||||||||| |||   |||
                                CCCACAACCG GAC   TCC
                                     A   ___
GAM872  FLJ12132 3'  CAGACAGAGCAACACCC     47097        G C   C
                                GGGTGTTG C CTG CTG
                                |||||||| | ||| |||
                                CCCACAAC G GAC GAC
                                     _ A   A
GAM872  GIT1     3'  CCTCTGCAAGGCCAGCACCC   26721         C   CT
                                GGGTGTTGGCC TGC  GGG
                                |||||||||| |||  |||
                                CCCACGACCGG ACG  TCC
                                     A   TC
GAM872  KIAA0556 3'  CTTCAGCGGCCAACACCC    69648         CT  CTGG
                                GGGTGTTGGCC  GC   GAAG
                                |||||||||| ||   ||||
                                CCCACAACCGG  CG   CTTC
                                     __ A___
GAM872  KIAA0720 3'  CCACCAGACCAACACCC     62976        CC   CC
                                GGGTGTTGG  CTG  TGG
                                |||||||| |||  |||
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                                CCCACAACC  GAC  ACC
                                     A_   C_
GAM872  KIAA1405  3'  CCACAGAGCCCACACCC     61695       T   C   CC
                                GGGTGT GGC CTG  TGG
                                |||||| ||| |||  |||
                                CCCACA CCG GAC  ACC
                                   C   A   __
GAM872  SEC14L2   3'  GCCCCCCAGGCAGGAGGCCGCC 25796      GTT   __       AA
          C                      GGGT   GGCC  CTGCCTGGG  GC
                                ||||   ||||  |||||||||  ||
                                CCCG   CCGG  GACGGACCC  CG
                                  ___    AG       CC
GAM872  TRIP-Br2  3'  CCCTGGCACCAACACCC     29263         CCC    T
                                GGGTGTTGG   TGCC GGG
                                |||||||||   |||| |||
                                CCCACAACC   ACGG CCC
                                     ___    T
GAM872  LOC145333 3'  GCCTCCTATCCAAAGGCCAACA 84298           C_  CC     A
          CCT                     GGGTGTTGGCC  TG  TGGGA GC
                                ||||||||||  ||  ||||| ||
                                TCCACAACCGG  AC  ATCCT CG
                                      AA  CT    C
GAM872  LOC158230 3'  GCCCCCCAAACAGGATGGCGCC 82700        GC    CC    AA
          C                      GGGTGTTG  CCTG  TGGG  GC
                                ||||||||  ||||  ||||  ||
                                CCCGCGGT  GGAC  ACCC  CG
                                     A_    AA    CC
GAM872  LOC197342 3'  CCCAGGCAAGGCCACCACCC   89357      T    C
                                GGGTG TGGCC TGCCTGGG
                                ||||| ||||| ||||||||
                                CCCAC ACCGG ACGGACCC
                                   C    A
GAM872  LOC199906 3'  GCTTCCCAGATTTGCAAACCC  89855     GTTG  CCTGC
                                GGGT    GC     CTGGGAAGC
                                ||||    ||     |||||||||
                                CCCA    CG     GACCCTTCG
                                  AA__  TTTA_
GAM872  LOC220739 3'  GCCCCCCAGGCAGGAGCACCC  94522       GGC        AA
                                GGGTGTT   CCTGCCTGGG  GC
                                |||||||   ||||||||||  ||
                                CCCACGA   GGACGGACCC  CG
                                     ___         CC
GAM872  LOC51287  3'  CCCTGCCAAGACCAGCACCC   33803        CC  __  CT
                                GGGTGTTGG  CT  GC  GGG
                                |||||||||  ||  ||  |||
                                CCCACGACC  GA  CG  CCC
                                     A_  AC  T_
GAM872  LOC51308  3'  GCTCCCAAGAGGGCCAAACCC  33969     G      GCC    A
                                GGGT TTGGCCCT   TGGGA GC
                                |||| ||||||||   ||||| ||
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                                CCCA AACCGGGA   ACCCT CG
                                  _      GA_    _
GAM872  LOC54550  3'  CTTCCTGGAGCCAGCACCC    78185          _ TGCCT
                                GGGTGTTGGC CC    GGGAAG
                                |||||||||| ||    ||||||
                                CCCACGACCG GG    TCCTTC
                                     A _____
GAM873  EHD3      5'  CCGGCCTGGGCTGCTGGATG   28202         A  __
                                CATCCAGCA GTC  GGCCGG
                                ||||||||| |||  ||||||
                                GTAGGTCGT CGG  CCGGCC
                                     _  GT
GAM873  GGA3      3'  CCAGCCACTCTAGCTGCTGGAT 57608          _____  C   C
             GTGAT                 ATCACATCCAGCA    AGT GGC GG
                                ||||||||||||    ||| ||| ||
                                TAGTGTAGGTCGT    TCA CCG CC
                                     CGATC  _  A
GAM873  GGA3      3'  CCAGCCACTCTAGCTGCTGGAT 26583          _____  C   C
             GTGAT                 ATCACATCCAGCA    AGT GGC GG
                                ||||||||||||    ||| ||| ||
                                TAGTGTAGGTCGT    TCA CCG CC
                                     CGATC  _  A
GAM873  KPNA1     3'  TTGACTCCTAAATGTGATA   81134        CC  CA
                                TATCACAT  AG  AGTCGG
                                ||||||||  ||  ||||||
                                ATAGTGTA  TC  TCAGTT
                                     AA  C_
GAM873  SDS       3'  CCAACTTGCTGGCGTGA     23378      AT       C
                                TCAC  CCAGCAAGT GG
                                ||||  ||||||||| ||
                                AGTG  GGTCGTTCA CC
                                  C_       A
GAM873  SLC25A1   3'  CCAGCCATGGCTGGATGTG    21116          AAGTC   C
                                CACATCCAGC     GGC GG
                                ||||||||||     ||| ||
                                GTGTAGGTCG     CCG CC
                                     GTA__   A
GAM873  C1QR1     3'  CCAGCACAAGTCTTGCTAAATG 24868        CC     TCG___  C
             TGATA                 TATCACAT  AGCAAG     GC GG
                                ||||||||  ||||||     || ||
                                ATAGTGTA  TCGTTC     CG CC
                                     AA     TGAACA  A
GAM873  C20orf13  3'  CCAACTGTCGCTGATGTGATA  35271         C   A__   C
                                TATCACATC AGC   AGT GG
                                ||||||||| |||   ||| ||
                                ATAGTGTAG TCG   TCA CC
                                     _  CTG   A
GAM873  CG012     5'  GCCTGCTGGATGTGGTA     84161           AGTC
                                TATCACATCCAGCA    GGC
                                ||||||||||||||    |||
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                                ATGGTGTAGGTCGT   CCG
                                     ____
GAM873  CHRFAM7A 3'  CGCCTGACCAATGTGATA   96718       CCAGCAA  _  C
                                TATCACAT     GTC GGC G
                                ||||||||     ||| ||| |
                                ATAGTGTA     CAG CCG C
                                    AC_____  T  A
GAM873  GPS2     5'  CGGCCGCCGGATGTGA     16888       A  AAGTC  _
                                TCACATCC GC    GGCC G
                                |||||||| ||    |||| |
                                AGTGTAGG CG    CCGG C
                                    C _____   G
GAM873  MGC16025 3'  CCAGCCAACCTTGGGTGTG   53020       CAA  C  C
                                CACATCCAG   GT GGC GG
                                |||||||||   || ||| ||
                                GTGTGGGTT   CA CCG CC
                                    C__  A  A
GAM873  PRDM8    5'  CCACCCGCTGGATGTGA     39973         AA  C
                                TCACATCCAGC  GT GG
                                ||||||||||  || ||
                                AGTGTAGGTCG  CA CC
                                     CC  _
GAM873  LOC93589 3'  CCGGAGAATGCTGGATGGA   73049    A      AG  GG
                                TC CATCCAGCA  TC  CCGG
                                || |||||||||  ||  ||||
                                AG GTAGGTCGT  AG  GGCC
                                 _      A_  A_
GAM874  KCNK1    3'  ACAAAGAAGCTGTGACCCCAGC 11161    CAT  C  CTT
           A                     TGC   GG CAT   TTTCTTTGT
                                |||   || |||   |||||||||
                                ACG   CC GTG   GAAGAAACA
                                  ACC  A  TC_
GAM874  NCAM1    3'  ACAAAAAAAAAAAAAAACCATG 7039        CCATC_   C
           GTA                    TGCCATGG     TTTTT TTTGT
                                |||||||      ||||| |||||
                                ATGGTACC     AAAAA AAACA
                                    AAAAAA    A
GAM874  RAB13    3'  ACAAAAAAAAAAAAAAACCATG 12719       CCATC_   C
           GTA                    TGCCATGG     TTTTT TTTGT
                                |||||||      ||||| |||||
                                ATGGTACC     AAAAA AAACA
                                    AAAAAA    A
GAM874  DKFZp434F1819 3'  ACAGGGAAGACGGCCATGG   51022       A  TTT
                                CCATGGCC TCT   TCTTTGT
                                |||||||| |||   |||||||
                                GGTACCGG AGA   AGGGACA
                                    C  ___
GAM874  FLJ11286 3'  ACAAAGAAGGTGTGGCCAGAAC 37790    CCA     CT
           A                     TG   TGGCCAT  TTTTCTTTGT
                                ||   |||||||  ||||||||||
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                                AC   ACCGGTG  GGAAGAAACA
                                 AAG      T_
GAM874  KIAA1948  5'  ACAAAGAAAAAGTTACCCATAG 83285    C    CCAT
            C                    GC ATGG    CTTTTTCTTTGT
                                 || ||||    ||||||||||||
                                 CG TACC    GAAAAAGAAACA
                                  A    CATT
GAM874  MGC11349  3'  ACAAAGAAAAAGACTTCTGCA  47788     CAT  CCA
                                 TGC   GG   TCTTTTTCTTTGT
                                 |||   ||   ||||||||||||
                                 ACG   TC   AGAAAAAGAAACA
                                   TCT  ___
GAM874  PELI2     3'  ACAAAAAAAAAAGATTCAGAGTG 41453      GGCC_       C
            G                    CCAT     ATCTTTTT TTTGT
                                 ||||     |||||||| |||||
                                 GGTG     TAGAAAAA AAACA
                                    AGACT        A
GAM874  LOC200220 3'  CAAAGACATAGCCATGGC     90033         C  CTTTT
                                 GCCATGGC AT     TCTTTG
                                 |||||||| ||     ||||||
                                 CGGTACCG TA     AGAAAC
                                      A  C_____
GAM874  LOC254266 5'  ACAAAGAGACGATGACCACAGC 99188     CA   C    TT
            A                    TGC  TGG CATC  TTTCTTTGT
                                 |||  ||| ||||  |||||||||
                                 ACG  ACC GTAG  AGAGAAACA
                                   AC   A    C_
GAM875  CDH12     3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                 TACACCACT     GAA  ATAAG
                                 |||||||||     |||  |||||
                                 ATGTGGTGA     TTT  TATTC
                                       AA___   AC
GAM875  GOCAP1    3'  ATTGTTCTTGGGAGCAGTGTA  43007       CA         G
                                 TACAC  CTCCCAAGAA AAT
                                 |||||  |||||||||| |||
                                 ATGTG  GAGGGTTCTT TTA
                                    AC         G
GAM875  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT    98090       T    AGAAG
                                 ACCAC CCCA     AATAAG
                                 ||||| ||||     ||||||
                                 TGGTG GGGT     TTATTC
                                    _    GTCA_
GAM875  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
            A                    TACAC        AGAAGAATAAG
                                 |||||        ||||||||||||
                                 ATGTG        TCTTCTTATTC
                                    TACTCCC_
GAM875  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                 TACACCACT       GAATAAG
                                 |||||||||       |||||||
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                                ATGTGGTGA      TTTATTC
                                     AGACG___
GAM875  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
             TA                   TACA   TCC   GAAGAATAAG
                                  ||||   |||   ||||||||||
                                  ATGT   AGG   TTTCTTATTC
                                    AAA_   ATTG
GAM875  KIAA1719 3'  TCTGTCTTGGGAGTGGTGTA  68742           _
                                  TACACCACTCCCAAGA AGA
                                  |||||||||||||||| |||
                                  ATGTGGTGAGGGTTCT TCT
                                           G
GAM875  KIAA1853 3'  TTTTTCTTGGAAGCAGTG    69929    CA  C
                                  CAC  CT CCAAGAAGAA
                                  |||  || ||||||||||
                                  GTG  GA GGTTCTTTTT
                                    AC  A
GAM875  KIAA1877 3'  CTTATTCTTCTGCCATGAGT   66748     CCA__
                                  ACTC    AGAAGAATAAG
                                  ||||    ||||||||||
                                  TGAG    TCTTCTTATTC
                                    TACCG
GAM875  KIAA1906 3'  CTTATTCTTCTTGACTTTTGG  73571    CTCC_
                                  CCA    CAAGAAGAATAAG
                                  |||    ||||||||||||
                                  GGT    GTTCTTCTTATTC
                                    TTTCA
GAM875  OSBPL11   3'  CTTAATTTCCCAAGAGTGGTG 43206       CCAA    AA
                                  CACCACTC    GAAG  TAAG
                                  ||||||||    ||||  ||||
                                  GTGGTGAG    CTTT  ATTC
                                       AACC    A_
GAM875  YME1L1    3'  TCATTCTTGATGTGGTGTA   58438       TCC     _
                                  TACACCAC   CAAGAA GA
                                  ||||||||   |||||| ||
                                  ATGTGGTG   GTTCTT CT
                                       TA_     A
GAM875  ZNF262    3'  CTTATTTTGTTTGGGAGT    18723        A
                                  ACTCCCAAG AGAATAAG
                                  |||||||||  ||||||||
                                  TGAGGGTTT TTTTATTC
                                       G
GAM875  LOC91960 3'  TGTGGCTTGGAACGTGGTGTA 68294       TC_    AAGA
                                  TACACCAC   CCAAG    ATA
                                  ||||||||   |||||    |||
                                  ATGTGGTG   GGTTC    TGT
                                       CAA    GG__
GAM876  ABCA9     3'  AAAGGATGAGTTCATATTCTTC 55362        CG_   C
             ACA                    TGTGAAGAG   GAGC CATCCTTT
                                  |||||||||   |||| ||||||||
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                                ACACTTCTT   CTTG GTAGGAAA
                                     ATA    A
GAM876  AP1S2    3'  GTGTTGCTCTCTTCACA     15350        GCG    C_
                                TGTGAAGA   GAGC  CAT
                                ||||||||   ||||  |||
                                ACACTTCT   CTCG  GTG
                                     ____    TT
GAM876  DKFZP434F1735 5'  AAAGGATGGACTCTGTTACCCA 32109      AAG      C
            CA                    TGTG   AGCGGAG CCATCCTTT
                                ||||   ||||||| |||||||||
                                ACAC   TTGTCTC GGTAGGAAA
                                  CCA      A
GAM876  DNAJA2   3'  ATGGGCTTTGCACACA      60487      AAGA
                                TGTG    GCGGAGCCCAT
                                ||||    ||||||||||
                                ACAC    CGTTTCGGGTA
                                  A___
GAM876  DRIL2    3'  AAAGGATGGACTCTTCCCAC   22344     AA  GC    C
                                GTG  GA  GGAG CCATCCTTT
                                |||  ||  |||| |||||||||
                                CAC  CT  TCTC GGTAGGAAA
                                  C_  __    A
GAM876  SLC26A9  3'  AAAGGATGAGCCTGGGGTCACA 54708       AGAG   A  C
                                TGTGA    CGG GC CATCCTTT
                                |||||    ||| || ||||||||
                                ACACT    GTC CG GTAGGAAA
                                   GGG_   _  A
GAM876  LOC150837 3'  ATGAGGCTTCGCTCTCCACA   80800      A         _
                                TGTG AGAGCGGAGCC CAT
                                |||| |||||||||| |||
                                ACAC TCTCGCTTCGG GTA
                                  C          A
GAM877  ABL1     3'  GCCCCCACCCAGGTCCC     18954      A       AA
                                GGGA CCTGGGTG  GGC
                                |||| ||||||||  |||
                                CCCT GGACCCAC  CCG
                                  _       CC
GAM877  ABL1     3'  GCCCCCACCCAGGTCCC     24607      A       AA
                                GGGA CCTGGGTG  GGC
                                |||| ||||||||  |||
                                CCCT GGACCCAC  CCG
                                  _       CC
GAM877  LRP1     3'  AGGGCCCCCACCGAGGTTCCC  11357        G    AA   A
                                GGGAACCT GGTG  GGC CCT
                                |||||||| ||||  ||| |||
                                CCCTTGGA CCAC  CCG GGA
                                     G    CC   _
GAM877  GMPPB    3'  AGGGCTCCCCCACCCAGGCCCC 97434     AA       AA  CA
            C                    GGG  CCTGGGTG  GG  CCTT
                                |||  ||||||||  ||  ||||
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                                CCC  GGACCCAC  CC  GGGA
                                  CC       CC  TC
GAM877  KIAA1949  5'  GCCTGCACCCAGGTTCCC    99591          A
                                GGGAACCTGGGTG AGGC
                                |||||||||||| ||||
                                CCCTTGGACCCAC TCCG
                                       G
GAM877  KIAA1949  5'  GCCTGCACCCAGGTTCCC    99697          A
                                GGGAACCTGGGTG AGGC
                                |||||||||||| ||||
                                CCCTTGGACCCAC TCCG
                                       G
GAM877  KIAA1949  5'  GCCTGCACCCAGGTTCCC    93718          A
                                GGGAACCTGGGTG AGGC
                                |||||||||||| ||||
                                CCCTTGGACCCAC TCCG
                                       G
GAM877  KIAA1977  5'  TGCCTTCACACATTGCC     74769    G  CC  G
                                GG AA  TG GTGAAGGCA
                                || ||  || |||||||||
                                CC TT  AC CACTTCCGT
                                 G  __  A
GAM877  RNPC1     3'  AAAGACGCAATCCCAGGTTCCT 34407          TGAAG  AC
                                GGGAACCTGGG    GC  CTTT
                                ||||||||||    ||  ||||
                                TCCTTGGACCC    CG  GAAA
                                      TAA__  CA
GAM877  LOC120526 3'  GAGGTAGTCATCCAGGTTCCC  74465           AGGC
                                GGGAACCTGGGTGA   ACCTT
                                ||||||||||||||   |||||
                                CCCTTGGACCTACT   TGGAG
                                       GA__
GAM877  LOC146909 3'  AAGGTGCTGCCATGTTCCC   78754      CTG   GAA
                                GGGAAC   GGT   GGCACCTT
                                ||||||   |||   ||||||||
                                CCCTTG   CCG   TCGTGGAA
                                   TA_   ____
GAM877  LOC150622 3'  AAAGGAGTTCACTCAAGTTCCC 80750      C      AG  A
                                GGGAAC TGGGTGA  GC CCTTT
                                |||||| |||||||  || |||||
                                CCCTTG ACTCACT  TG GGAAA
                                   A      __  A
GAM877  LOC90750  3'  AAGGACATCCAGGTTCCC    64624          AAGGCA
                                GGGAACCTGGGTG     CCTT
                                ||||||||||||      ||||
                                CCCTTGGACCTAC     GGAA
                                       A_____
GAM877  LOC92017  3'  CCACTCACCCAGGCTTCC    68489      A       A_
                                GGGA CCTGGGTGA  GG
                                |||| |||||||||  ||
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                                CCTT GGACCCACT  CC
                                  C       CA
GAM877  LOC92912  5'  AAAGGAAGCGCCACCCAGGCC  71403    AA      AAG  A_
                                GG  CCTGGGTG   GC  CCTTT
                                ||  ||||||||   ||  |||||
                                CC  GGACCCAC   CG  GGAAA
                                 __       CG_  AA
GAM878  CBFA2T2   3'  CCACACCTGGCCTTGGCTG   18705     A___    A
                                CAGC   GCCGG GTGTGG
                                ||||   ||||| ||||||
                                GTCG   CGGTC CACACC
                                  GTTC   _
GAM878  CD97    3'  CCACTGGTCCTGCTGCTG    55303       C   G _
                                CAGCAGC GGA T GTGG
                                ||||||| ||| | ||||
                                GTCGTCG CCT G CACC
                                    T   G T
GAM878  COLQ    3'  CCACACCTGGGCAGGCTGTTG  20251        _____  A
                                CAGCAGCC    GG GTGTGG
                                ||||||||    || ||||||
                                GTTGTCGG    TC CACACC
                                    ACGGG  _
GAM878  COLQ    3'  CCACACCTGGGCAGGCTGTTG  20252        _____  A
                                CAGCAGCC    GG GTGTGG
                                ||||||||    || ||||||
                                GTTGTCGG    TC CACACC
                                    ACGGG  _
GAM878  LETM1   3'  CCACACAGAGCTGGCTGCTG   25550         A___
                                CAGCAGCCGG   GTGTGG
                                ||||||||||   ||||||
                                GTCGTCGGTC   CACACC
                                     GAGA
GAM878  MASP1   3'  CCACACTGTGTCCTGCTG    58211       C_  G
                                CAGCAG  CG AGTGTGG
                                ||||||  || |||||||
                                GTCGTC  GT TCACACC
                                   CT  G
GAM878  MAT1A   3'  CCAGACGCCTGGCTGCTG    92497         A_  G
                                CAGCAGCCGG  GT TGG
                                ||||||||||  || |||
                                GTCGTCGGTC  CA ACC
                                     CG  G
GAM878  PKD1    3'  CCACTGCTAAGGCTGCTG    98431        GG  _
                                CAGCAGCC  AGT GTGG
                                ||||||||  ||| ||||
                                GTCGTCGG  TCG CACC
                                    AA   T
GAM878  RNMT    3'  CCACACCTGCAGGCGCTG    15050     A  ___  A
                                CAGC GCC   GG GTGTGG
                                |||| |||   || ||||||
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                                GTCG CGG   TC CACACC
                                  _   ACG  _
GAM878  RPL30    5'  CCATCTTAGCGGCTGCTG    8271          __  T
                                CAGCAGCCG  GAG GTGG
                                |||||||||  ||| ||||
                                GTCGTCGGC  TTC TACC
                                     GA   _
GAM878  TEM5     3'  CCACATATGCTGGCTGCTG   52298          A__
                                CAGCAGCCGG  GTGTGG
                                ||||||||||  ||||||
                                GTCGTCGGTC  TACACC
                                     GTA
GAM878  XT3      3'  CCAGCTACTCTGGCTGCTG   39906           __
                                CAGCAGCCGGAGTG  TGG
                                ||||||||||||||  |||
                                GTCGTCGGTCTCAT  ACC
                                       CG
GAM878  AD034    3'  CCACAGTTCAGCTGGCTG    49747     _  C  G
                                CAGC AGC GGA TGTGG
                                |||| ||| ||| |||||
                                GTCG TCG CTT ACACC
                                  G  A  G
GAM878  ALLC     5'  CCTAATTTCAGGCTGCTG    37980       _    GT
                                CAGCAGCC GGAGT  GG
                                |||||||| |||||  ||
                                GTCGTCGG CTTTA  CC
                                     A    AT
GAM878  COLEC12  3'  CCACAGTTTTGGCCTCTG    48607     CA     _
                                CAG  GCCGGAG TGTGG
                                |||  ||||||| |||||
                                GTC  CGGTTTT ACACC
                                  TC      G
GAM878  DKFZP564C186 3'  CCACAACTGTGGGCTGCTG   72841        _ G  _
                                CAGCAGCC G AGT GTGG
                                |||||||| | ||| ||||
                                GTCGTCGG T TCA CACC
                                     G G   A
GAM878  FBXO26   5'  CCAGGACTCTGGCTACTG    46624     C       G_
                                CAG AGCCGGAGT  TGG
                                ||| |||||||||  |||
                                GTC TCGGTCTCA  ACC
                                  A        GG
GAM878  FLJ21736 3'  CCACACTCTGTATCTGGCT   46780     _ C__
                                AGC AG   CGGAGTGTGG
                                ||| ||   ||||||||||
                                TCG TC   GTCTCACACC
                                  G  TAT
GAM878  ITGB5    3'  CCATGTCACCTGGCTGCT    60215         A  ___
                                AGCAGCCGG GTG   TGG
                                ||||||||| |||   |||
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                                TCGTCGGTC CAC   ACC
                                     _  TGT
GAM878  KIAA0084  5'  CCACCGCTCCAGCGGCTG    68706     A  C    _
                                CAGC GC GGAGTG TGG
                                |||| || |||||| |||
                                GTCG CG CCTCGC ACC
                                  G A     C
GAM878  KIAA1582  5'  CCACAGGCTCCAGCTCTG    65987    C  C   __
                                CAG AGC GGAGT  GTGG
                                ||| ||| |||||  ||||
                                GTC TCG CCTCG  CACC
                                  _  A    GA
GAM878  KIAA1879  5'  CCACAGTGCTGCGGCTGCT   73933       G  ___
                                AGCAGCCG AGT   GTGG
                                |||||||| |||   ||||
                                TCGTCGGC TCG   CACC
                                     G   TGA
GAM878  LGI2      3'  GCCACACTCCAGGTCTGT    36926    _ _      ____
                                GCAG CC GGAGTGTGG   C
                                |||| || |||||||||   |
                                TGTC GG CCTCACACC   G
                                  T  A       __
GAM878  MAP-1     3'  CCACCTGCTTCGGCCTCTG   42437    CA      __
                                CAG  GCCGGAGT  GTGG
                                |||  ||||||||  ||||
                                GTC  CGGCTTCG  CACC
                                  TC       TC
GAM878  MGC2647   3'  CCACAGGCTGTGGCTGCT    74076       G  __
                                AGCAGCCG AGT  GTGG
                                |||||||| |||  ||||
                                TCGTCGGT TCG  CACC
                                     G   GA
GAM878  SCAM-1    3'  CCAGCACCCCAGCTTGCTG   20501     _  C  A  _
                                CAGCA GC GG GTG TGG
                                ||||| || || ||| |||
                                GTCGT CG CC CAC ACC
                                   T  A  C   G
GAM878  XYLT1     5'  CCACAAGTTAGGGCTGCTG   78412       G_  G_
                                CAGCAGCC  GA  TGTGG
                                ||||||||  ||  |||||
                                GTCGTCGG  TT  ACACC
                                     GA  GA
GAM878  LOC136120 3'  CCATCAACCTGGCTGCTG    76706        AG  _
                                CAGCAGCCGG  TG TGG
                                ||||||||||  || |||
                                GTCGTCGGTC  AC ACC
                                       CA  T
GAM878  LOC144486 5'  CCACCGACGCCGGTTGCTG   84002         A  __
                                CAGCAGCCGG GT  GTGG
                                |||||||||| ||  ||||
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                                GTCGTTGGCC CA  CACC
                                      G  GC
GAM878  LOC200471 5'  CCAGGCTGCTGGCTGCTG    91634          _  G
                                CAGCAGCCGG AGT TGG
                                |||||||||| ||| |||
                                GTCGTCGGTC TCG ACC
                                      G  G
GAM878  LOC256905 5'  CCACAGCTCTGGCTCCTG    98658     C      _
                                CAG AGCCGGAG TGTGG
                                ||| |||||||| |||||
                                GTC TCGGTCTC ACACC
                                  C       G
GAM879  CDH12    3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                      AA___   AC
GAM879  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM879  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT    98090      T    AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                   _   GTCA_
GAM879  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
            A                    TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM879  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                      AGACG___
GAM879  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
            TA                    TACA   TCC   GAAGAATAAG
                                ||||   |||   ||||||||||
                                ATGT   AGG   TTTCTTATTC
                                  AAA_   ATTG
GAM879  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA  68742            _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                         G
GAM879  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
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                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM879  KIAA1877 3' CTTATTCTTCTGCCATGAGT  66748     CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM879  KIAA1906 3' CTTATTCTTCTTGACTTTTGG 73571    CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM879  OSBPL11  3' CTTAATTTCCCAAGAGTGGTG 43206       CCAA   AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                     AACC   A_
GAM879  YME1L1   3' TCATTCTTGATGTGGTGTA   58438       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                     TA_    A
GAM879  ZNF262   3' CTTATTTTGTTTGGGAGT    18723       A
                                ACTCCCAAG AGAATAAG
                                |||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                     G
GAM879  LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_    AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
                                ATGTGGTG   GGTTC   TGT
                                     CAA    GG__
GAM880  BCL6     3' AGCAGCTCCCCCTCCCCCACTG 9917       ATTCTT_
          C                      GCAGTG     GGGAGCTGCT
                                ||||||     ||||||||||
                                CGTCAC     CCCTCGACGA
                                   CCCCTCC
GAM880  BCL6     3' AGCAGCTCCCCCTCCCCCACTG 58033      ATTCTT_
          C                      GCAGTG     GGGAGCTGCT
                                ||||||     ||||||||||
                                CGTCAC     CCCTCGACGA
                                   CCCCTCC
GAM880  DAP      3' AGCAGCTGCCAACCACCAGC   72945    A_  ATTC   G
                                GC  GTG    TTGG AGCTGCT
                                ||  |||    |||| |||||||
                                CG  CAC    AACC TCGACGA
                                 AC   C___    G
GAM880  ETV6     3' AGCAGCCCAGGGAACCCCTGC  10541     TGA   TG  A
                                GCAG   TTCT  GG GCTGCT
                                ||||   ||||  || ||||||
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                                CGTC   AAGG  CC CGACGA
                                  CCC    GA  _
GAM880  GSTM5    3' AGCAGCTCCCAGGCAGACTGC  7797       GATT
                                GCAGT    CTTGGGAGCTGCT
                                |||||    ||||||||||||||
                                CGTCA    GGACCCTCGACGA
                                   GAC_
GAM880  MMP15    3' AGCAGCCCCCAGCTCCCACCTC 11611     CA   ATTC    A
                                GAG  GTG    TTGGG GCTGCT
                                |||  |||    ||||| ||||||
                                CTC  CAC    GACCC CGACGA
                                  __   CCTC    C
GAM880  FLJ11151 3' AGCAGCTTCTGACCACTGCTC  68466        ATTC TG
                                GAGCAGTG    T  GGAGCTGCT
                                ||||||||    |  |||||||||
                                CTCGTCAC    A  CTTCGACGA
                                     C___ GT
GAM880  FLJ21709 3' AGCAGGAAGTAAAATCACTGC  78474         C   GGAG
                                GCAGTGATT TTG    CTGCT
                                ||||||||| |||    |||||
                                CGTCACTAA AAT    GACGA
                                     _  GAAG
GAM880  FLJ31528 3' AGCAACAAGCCACTGCTC    59034        ATT    GGA
                                GAGCAGTG   CTTG   GCT
                                ||||||||   ||||   |||
                                CTCGTCAC   GAAC   CGA
                                     C__    AA_
GAM880  KIAA0515 3' GCAGCTCCCCTCCTGC      64551      T  TTCTT
                                GCAG GA     GGGAGCTGC
                                ||||  ||    |||||||||
                                CGTC CT     CCCTCGACG
                                  _  C_____
GAM880  KIAA0852 3' AGCAGCTCCCCTGCCCACCTGC 30764      _  ATTCTT
                                GCAG TG      GGGAGCTGCT
                                ||||  ||     ||||||||||
                                CGTC AC      CCCTCGACGA
                                  C  CCGTC_
GAM880  KIAA0982 3' AGCAACTCTTTTTCAACCACTG 26710         ATTCTT_    C
           CTC                    GAGCAGTG      GGGAG TGCT
                                ||||||||       ||||| ||||
                                CTCGTCAC       TTCTC ACGA
                                     CAACTTT    A
GAM880  KIAA1266 3' AGCAGCCCCTCCTCACCATTC  66691     CA    TTCTT   A
                                GAG  GTGA    GGG GCTGCT
                                |||  ||||    ||| ||||||
                                CTT  CACT    CCC CGACGA
                                  AC    CCT__   _
GAM880  RoXaN    3' GCAGGGAGAATCACCGCTT   47293      A       GGGAG
                                GAGC GTGATTCTT    CTGC
                                |||| |||||||||    ||||
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                                TTCG CACTAAGAG    GACG
                                  C       G____
GAM880  LOC126353 3'  AGGATCCAAGAACCACAGCTC  74988     A  A      AG
                                GAGC GTG TTCTTGGG  CT
                                |||| ||| ||||||||  ||
                                CTCG CAC AAGAACCT  GA
                                  A  C       AG
GAM880  LOC144742 5'  GTTTCCAAAAACCACACTC   77466     CA  A  C
                                GAG  GTG TT TTGGGAGC
                                |||  ||| || ||||||||
                                CTC  CAC AA AACCTTTG
                                 A_  C  A
GAM880  LOC160404 5'  AGCATCTGACAAAACCACTGCT 83088        A  C  GG  C
           C                     GAGCAGTG TT TTG  AG TGCT
                                |||||||| || |||  || ||||
                                CTCGTCAC AA AAC  TC ACGA
                                    C  _  AG  T
GAM880  LOC164714 3'  AGCAGCTCTGCAACCTCCGCTC 88578     AGT  TTC  _
                                GAGC  GA  TTG GGAGCTGCT
                                ||||  ||  ||| |||||||||
                                CTCG  CT  AAC TCTCGACGA
                                  C__  CC_  G
GAM880  LOC202126 3'  AGCAGCTCCACTCTCCTGC   91906     T  TTCTTG
                                GCAG GA     GGAGCTGCT
                                |||| ||     |||||||||
                                CGTC CT     CCTCGACGA
                                  _ CTCA__
GAM880  LOC65243  5'  AGCAGCTCCTGATCACCCTGC  43798     __     CTT
                                GCA  GTGATT  GGGAGCTGCT
                                |||  ||||||  ||||||||||
                                CGT  CACTAG  TCCTCGACGA
                                 CC    ____
GAM881  C5      3'  CAAACCTACCACTCAGGAA   9968         CAGCG   G
                                TTCCTGAG    AGGT TTG
                                ||||||||    |||| |||
                                AAGGACTC    TCCA AAC
                                    ACCA_   _
GAM881  DBT     3'  CACCTATAGTCCCAGCTACTCA 10363        C  GA  __  T
           GGAA                   TTCCTGAG AGC  GG  TGT GGTG
                                |||||||| |||  ||  ||| ||||
                                AAGGACTC TCG  CC  ATA CCAC
                                    A  AC  TG  T
GAM881  DNCI1    5'  CACCAACGCTGCCGCCGCCCAG 92711      A  A  A_
           GA                    TCCTG GC GCG  GGTGTTGGTG
                                ||||| || |||  ||||||||||
                                AGGAC CG CGC  TCGCAACCAC
                                  C  C  CG
GAM881  FLNA    5'  CACCGGTCGCTCTCAGGAA   9384         C    __
                                TTCCTGAG AGCGA  GGTG
                                |||||||| |||||  ||||
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                                AAGGACTC TCGCT  CCAC
                                   _    GG
GAM881  FPGS    3'  CCAACATCATCAGGAA     18265       GCAGCGA
                                TTCCTGA     GGTGTTGG
                                |||||||     ||||||||
                                AAGGACT     CTACAACC
                                   A_______
GAM881  NHLH1   3'  ACCGCTCACTGCTTAG     20015       C   GTGT
                                CTGAGCAG GAG   TGGT
                                |||||||| |||   ||||
                                GATTCGTC CTC   GCCA
                                   A  ____
GAM881  RXRA    3'  ACCAGCGCCACCCAGGAA    12915      AGCAGCGA
                                TTCCTG      GGTGTTGGT
                                ||||||      |||||||||
                                AAGGAC      CCGCGACCA
                                   CCA_____
GAM881  SIGLEC7  3'  CACCAACAATGAGTACTCAGAG 33744   _    CA  GAGG
          A                     TC CTGAG  GC   TGTTGGTG
                                || |||||  ||   ||||||||
                                AG GACTC  TG   ACAACCAC
                                 A    A_  AGTA
GAM881  TMPRSS3  3'  CACCAACAGCCACTCAG    44016     CA  GAGG
                                CTGAG  GC   TGTTGGTG
                                |||||  ||   ||||||||
                                GACTC  CG   ACAACCAC
                                   AC  ____
GAM881  TMPRSS3  3'  CACCAACAGCCACTCAG    51513     CA  GAGG
                                CTGAG  GC   TGTTGGTG
                                |||||  ||   ||||||||
                                GACTC  CG   ACAACCAC
                                   AC  ____
GAM881  TMPRSS3  3'  CACCAACAGCCACTCAG    51541     CA  GAGG
                                CTGAG  GC   TGTTGGTG
                                |||||  ||   ||||||||
                                GACTC  CG   ACAACCAC
                                   AC  ____
GAM881  WBSCR1   3'  CACCAACACTTAACTTCAG   50084     GC  CG
                                CTGA  AG  AGGTGTTGGTG
                                ||||  ||  ||||||||||
                                GACT  TC  TTCACAACCAC
                                   __ AA
GAM881  WBSCR1   3'  CACCAACACTTAACTTCAG   42479     GC  CG
                                CTGA  AG  AGGTGTTGGTG
                                ||||  ||  ||||||||||
                                GACT  TC  TTCACAACCAC
                                   __ AA
GAM881  DKFZP564O0423 5'  CACCAACAGTGCACTCAAGAG  93343    C   CA  AGG
                                TTC TGAG  GCG   TGTTGGTG
                                ||| ||||  |||   ||||||||
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                                GAG ACTC  CGT   ACAACCAC
                                  A   A_  G__
GAM881  DPP8     5'  CACCGGCGCCGCCGCCGAGGAA 56117      GA  A  GA
                                TTCCT  GC GC  GGTGTTGGTG
                                |||||  || ||  ||||||||||
                                AAGGA  CG CG  CCGCGGCCAC
                                   GC  C  __
GAM881  IL18BP   3'  CACTGCTCTACTGCTCAG    20308        CG   T  T
                                CTGAGCAG  AGG GT GGTG
                                ||||||||  ||| || ||||
                                GACTCGTC  TCT CG TCAC
                                    A_  _ _
GAM881  LOXL4    3'  CACCAAGAACCTGCTCAGGAA  50856         GCGA   G_
                                TTCCTGAGCA   GGT  TTGGTG
                                ||||||||||   |||  ||||||
                                AAGGACTCGT   CCA  AACCAC
                                     ____  AG
GAM881  MGC17303 3'  ACCAACACTGCCCAGGA     58231      A   GCGAG
                                TCCTG GCA    GTGTTGGT
                                ||||| |||    ||||||||
                                AGGAC CGT    CACAACCA
                                   C  _____
GAM881  PRAM-1   3'  CACCACAAGACCCAGCGCTCAG 69910         A  GA   G __
           GAA                    TTCCTGAGC GC  GGT T  TGGTG
                                ||||||||| ||  ||| |  |||||
                                AAGGACTCG CG  CCA A  ACCAC
                                    _  AC   G AC
GAM881  PRDM8    5'  CACCAACACCTCTTGACATGGA 39972      TGAG   C
           A                     TTCC   CAG GAGGTGTTGGTG
                                ||||   ||| ||||||||||||
                                AAGG   GTT CTCCACAACCAC
                                  TACA  _
GAM881  RHOBTB3  3'  CACCTGTAATCCCAGCTACTCA 30420        C   GA  TGTT__
           GGAA                   TTCCTGAG AGC  GG     GGTG
                                |||||||| |||  ||     ||||
                                AAGGACTC TCG  CC     CCAC
                                    A   AC  TAATGT
GAM881  LOC125206 3'  CAGCAGCTCGGTGCCCAAGAA  76166     C  A   G   G
                                TTC TG GCA CGAG TGTTG
                                ||| || ||| |||| |||||
                                AAG AC CGT GCTC ACGAC
                                  A  C   G   G
GAM881  LOC147791 3'  CATGACCTCGATGCTCAG    85188        G     GT
                                CTGAGCA CGAGGT  TG
                                ||||||| ||||||  ||
                                GACTCGT GCTCCA  AC
                                    A     GT
GAM881  LOC149372 5'  ACCACAGCACTCTCAGGAA    80096         CAGCGA    __
                                TTCCTGAG     GGTGT  TGGT
                                ||||||||     |||||  ||||
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                                AAGGACTC     TCACG  ACCA
                                   _______     AC
GAM881  LOC150287 3'  GCTGGCCCACTCCTCAGGAA   80599        C  CGA  T  TG
                                TTCCTGAG AG   GG GT  GT
                                |||||||| ||   || ||  ||
                                AAGGACTC TC   CC CG  CG
                                     C  A__  _  GT
GAM881  LOC199725 5'  CACCAAAGCTACTCAGGAA   91411        C   GA_
                                TTCCTGAG AGC   GGTG
                                |||||||| |||   ||||
                                AAGGACTC TCG   CCAC
                                     A   AAA
GAM881  LOC221271 3'  CACCTGTAATCCCAGCTACTCA 93496        C   GA  TGTT__
           GGAA                    TTCCTGAG AGC  GG     GGTG
                                |||||||| |||  ||     ||||
                                AAGGACTC TCG  CC     CCAC
                                     A   AC  TAATGT
GAM882  CHAD    3'  GGAAGGCTGAGCCTCTC     8855       TA   CTGC
                                GAGAG  CTC    GTCTTCC
                                |||||  |||    |||||||
                                CTCTC  GAG    CGGAAGG
                                   C_   T___
GAM882  DSG1    5'  AGGAAGGCAGAAACACCTC   10449     A  ACTC   GT
                                GAG GT    CTGC  CTTCCT
                                ||| ||    ||||  ||||||
                                CTC CA    GACG  GAAGGA
                                  _  CAAA   __
GAM882  MID1    3'  AAGATGTAGAAGTCCCTC    6351      T_   C
                                GAG  ACT CTGCGTCTT
                                |||  ||| |||||||||
                                CTC  TGA GATGTAGAA
                                  CC   A
GAM882  OTOF    3'  AGGAAGACTCCTGAAACCCTC  17828     A  AC  CTGC
                                GAG GT  TC    GTCTTCCT
                                ||| ||  ||    ||||||||
                                CTC CA  AG    CAGAAGGA
                                  C  A_  TCCT
GAM882  RNMT    3'  AGGACATCCAAGGGTACTCTC  15047        T   GCGTCT
                                GAGAGTAC CCT     TCCT
                                |||||||| |||     ||||
                                CTCTCATG GGA     AGGA
                                     _  ACCTAC
GAM882  SCN3A   5'  AGGAAGACACGTTATACCCT   23612    A   CTCC  C
                                AG GTA    TG GTCTTCCT
                                || |||    || ||||||||
                                TC CAT    GC CAGAAGGA
                                 C   ATT_  A
GAM882  SFRS7   3'  GGAAGGCGATACTCTC      60148        CTCCTG
                                GAGAGTA     CGTCTTCC
                                |||||||     ||||||||
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                                CTCTCAT     GCGGAAGG
                                   A_____
GAM882  SLC13A4  5'  AAGACGAAGGAGGACTCTC   25857       A    G
                                GAGAGT CTCCT CGTCTT
                                |||||| ||||| ||||||
                                CTCTCA GAGGA GCAGAA
                                   G    A
GAM882  SSX2     3'  AGGAAGATGACGAGTAACTC  97962     _   CTG
                                GAGT ACTC   CGTCTTCCT
                                |||| ||||   |||||||||
                                CTCA TGAG   GTAGAAGGA
                                  A   CA_
GAM882  TGFBR2   3'  AAGATTCAAGAGTATTCTC   13725         C  C
                                GAGAGTACTC TG GTCTT
                                |||||||||| || |||||
                                CTCTTATGAG AC TAGAA
                                      A  T
GAM882  TNFRSF11A 3'  AGGAAGACCACCCGGCATTCTC 15187       A  CC_  C
                                GAGAGT CT   TG GTCTTCCT
                                |||||| ||   || ||||||||
                                CTCTTA GG   AC CAGAAGGA
                                   C  CCC  _
GAM882  AP3M2    3'  AGGAAGACCCGTACTCTC    23299        TCCT C
                                GAGAGTAC    G GTCTTCCT
                                ||||||||    | ||||||||
                                CTCTCATG    C CAGAAGGA
                                     _____ C
GAM882  CALN1    3'  AGGAAGACACAGAATTCTTTC  49658      TACTC   C
                                GAGAG     CTG GTCTTCCT
                                |||||     ||| ||||||||
                                CTTTC     GAC CAGAAGGA
                                   TTAA_   A
GAM882  DAMS     5'  AGGAAATTCAAGTACTCT    42084        CC  C  C
                                AGAGTACT  TG GT TTCCT
                                ||||||||  || || |||||
                                TCTCATGA  AC TA AAGGA
                                     __  T  _
GAM882  DKFZP727M111 5'  AGGCCAGGAGGACCCTC     32055     A  A     C
                                GAG GT CTCCTG GTCT
                                ||| || |||||| ||||
                                CTC CA GAGGAC CGGA
                                  C  G     _
GAM882  FLJ14486 5'  AGGAAGGTTCAAGTCTCTC   52434      T   CC  CG
                                GAGAG ACT  TG  TCTTCCT
                                ||||| |||  ||  |||||||
                                CTCTC TGA  AC  GGAAGGA
                                   _  __  TT
GAM882  FUSIP1   3'  AGGAAGACAGCCATAGTCTC  22780     T   CCT  _
                                GAG ACT   GC GTCTTCCT
                                ||| |||   || ||||||||
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                                CTC TGA   CG CAGAAGGA
                                  _   TAC  A
GAM882  HIC      3'  GAAGATTGAGTACTCT      68048         CTGC
                                AGAGTACTC    GTCTTC
                                |||||||||    ||||||
                                TCTCATGAG    TAGAAG
                                     T___
GAM882  IL22R    3'  AGGAAATGCAGGGAAACTC    41467      AC       C
                                GAGT  TCCTGCGT TTCCT
                                ||||  |||||||| |||||
                                CTCA  GGGACGTA AAGGA
                                  AA       _
GAM882  KIAA0472 3'  AGGAGGGGTAAGTACTCTC    72334         CC   G
                                GAGAGTACT  TGC TCTTCCT
                                |||||||||  ||| |||||||
                                CTCTCATGA  ATG GGGAGGA
                                       __   _
GAM882  KIAA1229 3'  AGGATGTAAAAGTTCTCTC    62750       T   CC
                                GAGAG ACT  TGCGTCTT
                                ||||| |||  ||||||||
                                CTCTC TGA  ATGTAGGA
                                   T   AA
GAM882  LAK-4P   3'  AGGAAGACAGTTTCGCCTCTC  24394       TACTCCT  _
                                GAGAG      GC GTCTTCCT
                                |||||      || ||||||||
                                CTCTC      TG CAGAAGGA
                                   CGCTT__  A
GAM882  MRPS35   3'  AGGTCCTCAGGAGTATTCTC   41819           CGTCTT
                                GAGAGTACTCCTG     CCT
                                ||||||||||||      |||
                                CTCTTATGAGGAC     GGA
                                       TCCT__
GAM882  OBTP     5'  AGGATCTGCAAGGAGGACCCTC 34663     A  A    _   TCT
                                GAG GT CTCCT GCG   TCCT
                                ||| || ||||| |||   ||||
                                CTC CA GAGGA CGT   AGGA
                                  C  G    A   CT_
GAM882  RI58     3'  AGATCAGGAATACTCTT     25774        C    C
                                GAGAGTA TCCTG GTCT
                                ||||||| ||||| ||||
                                TTCTCAT AGGAC TAGA
                                    A    _
GAM882  SMBP     3'  AAGACAGAAGTGTACTCTC    72620        TC  GC_
                                GAGAGTAC  CT   GTCTT
                                ||||||||  ||   |||||
                                CTCTCATG  GA   CAGAA
                                     T_  AGA
GAM882  SNTG1    5'  AGGACTCTGAGGAGTACTCTT  39099          G  TCT
                                GAGAGTACTCCT CG   TCCT
                                ||||||||||| ||   ||||
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                                TTCTCATGAGGA GT   AGGA
                                      _ CTC
GAM882  SNX11    3'  AGGACCAGGAGTATCTC     26169      G       C
                                GAGA TACTCCTG GTCTT
                                |||| |||||||| |||||
                                CTCT ATGAGGAC CAGGA
                                  _       _
GAM882  TTY7     3'  AGGAAGACACAGGTAGCT    50015     ACT    C
                                AGT   CCTG GTCTTCCT
                                |||   |||| ||||||||
                                TCG   GGAC CAGAAGGA
                                  AT_    A
GAM882  LOC123872 5' GGAAAGAGGGTACTCTC     74710          _ GCGTC
                                GAGAGTACTC CT     TTCC
                                |||||||||| ||     ||||
                                CTCTCATGGG GA     AAGG
                                      A _____
GAM882  LOC138389 3' AGGAAGACTTGCAAGTCTCTC 76725      T   CC   __
                                GAGAG ACT  TGC  GTCTTCCT
                                ||||| |||  |||  ||||||||
                                CTCTC TGA  ACG  CAGAAGGA
                                   _  __  TT
GAM882  LOC143943 3' AGGAAGATCAGCAGCCTCTC   83911      TA  C   C
                                GAGAG  CT CTG GTCTTCCT
                                |||||  || ||| ||||||||
                                CTCTC  GA GAC TAGAAGGA
                                   C_  C   _
GAM882  LOC145009 5' AAGAAACAAAGGAGTACTTTC  60965           GCG__
                                GAGAGTACTCCT     TCTT
                                ||||||||||||     ||||
                                CTTTCATGAGGA     AGAA
                                      AACAA
GAM882  LOC147976 5' AGGAAGACTGGGGTACCCTC   79285     A       TGC
                                GAG GTACTCC   GTCTTCCT
                                ||| |||||||   ||||||||
                                CTC CATGGGG   CAGAAGGA
                                  C      T__
GAM882  LOC151512 3' AGGAAGACAATGCTTGTACCTC 86611     A    TCCT  ___
                                GAG GTAC    GC   GTCTTCCT
                                ||| ||||    ||   ||||||||
                                CTC CATG    CG   CAGAAGGA
                                  _    TT__  TAA
GAM882  LOC158801 3' GAAAACACAAGAAGTATTCT   88255        _ C  C  C
                                AGAGTACT C TG GT TTC
                                |||||||| | || || |||
                                TCTTATGA G AC CA AAG
                                     A A  A  A
GAM882  LOC206426 3' GAAGCGAGGTGCACTCTC    91099       ACT   G  T
                                GAGAGT   CCT CG CTTC
                                ||||||   ||| || ||||
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                                CTCTCA   GGA GC GAAG
                                   CGT   _ _
GAM882  LOC254337 5'  GGAAAGGGGAGTATCTC     98012      G      GCGTC
                                GAGA TACTCCT     TTCC
                                |||| |||||||     ||||
                                CTCT ATGAGGG     AAGG
                                  _      GA___
GAM882  LOC256790 5'  AGTGCAGGAGTGCCCTC     96489     A         T
                                GAG GTACTCCTGCG CT
                                ||| |||||||||| ||
                                CTC CGTGAGGACGT GA
                                  C         _
GAM882  LOC256946 3'  AGGAAGACAGCCATAGTCTC   96182     T   CCT  _
                                GAG ACT   GC GTCTTCCT
                                ||| |||   || ||||||||
                                CTC TGA   CG CAGAAGGA
                                  _   TAC  A
GAM882  LOC257396 5'  GAAATGTAGGAGCATCTC     98922      GTA       C
                                GAGA   CTCCTGCGT TTC
                                ||||   ||||||||| |||
                                CTCT   GAGGATGTA AAG
                                   AC_       _
GAM882  LOC257408 3'  AGGGCACCAGGAGTACCTC    97797     A       C  CT
                                GAG GTACTCCTG GT  TCCT
                                ||| |||||||| ||  ||||
                                CTC CATGAGGAC CA  GGGA
                                  _       _ C_
GAM882  LOC257453 3'  AGGAAGATGACGAGTAACTC   82927      _   CTG
                                GAGT ACTC   CGTCTTCCT
                                |||| ||||   |||||||||
                                CTCA TGAG   GTAGAAGGA
                                  A    CA_
GAM882  LOC51066  3'  AGGAAGATGGCCGACACTCTC  32500       AC  CTG
                                GAGAGT  TC   CGTCTTCCT
                                ||||||  ||   |||||||||
                                CTCTCA  AG   GTAGAAGGA
                                   C_  CCG
GAM883  ATP6V0C   3'  CCCCAGTAGTTGGTCTTGTA   88658         CTG   _   A
                                TACAAGATCA   ACT CTG GG
                                ||||||||||   ||| ||| ||
                                ATGTTCTGGT   TGA GAC CC
                                      ___   T   C
GAM883  DLX4      3'  GTCCCCAGAACCCTTGGTCTTG 10421        CTGAC    A
                                CAAGATCA     TCTG GGAC
                                ||||||||     |||| ||||
                                GTTCTGGT     AGAC CCTG
                                     TCCCA    C
GAM883  MNT       3'  TCCTCAGAGGCTGAGCCTGTA  40089      AGA   CTGA
                                TACA   TCA    CTCTGAGGA
                                ||||   |||    |||||||||
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                                ATGT   AGT    GAGACTCCT
                                  CCG   CG__
GAM883  TCF2     3'  GTCCCCAGAACCAGCTGCAGAT 6617     AGAT  _   AC    A
           G                     CA    CA CTG  TCTG GGAC
                                ||    || |||  |||| ||||
                                GT    GT GAC  AGAC CCTG
                                 AGAC  C   CA    C
GAM883  VNN1     3'  TCCTCAGAGCAATTCTCTGTA  17423      _   TCAC  A
                                TACA AGA    TG CTCTGAGGA
                                |||| |||    || |||||||||
                                ATGT TCT    AC GAGACTCCT
                                  C   TA__  _
GAM883  BMF      5'  CCTCAGAGTCAAACTTTGTG   54280       ATCAC
                                TACAAG     TGACTCTGAGG
                                ||||||     ||||||||||
                                GTGTTT     ACTGAGACTCC
                                   CAA__
GAM883  DDX33    3'  GTCCTCAGTGCGTGACCCTGT  39786     AGA    T ACT
                                ACA   TCAC G   CTGAGGAC
                                |||   |||| |   ||||||||
                                TGT   AGTG C   GACTCCTG
                                 CCC    _ GT_
GAM883  FLJ20364 3'  CCTCAGAGCCATGTATTTG    35528      AT  C  A
                                CAAG  CA TG CTCTGAGG
                                ||||  || || ||||||||
                                GTTT  GT AC GAGACTCC
                                  AT  _  C
GAM883  HMGN4    3'  TCCTTTCCCCAGTGATTTGTA  22034      A       ACTCT
                                TACA GATCACTG     GAGGA
                                |||| ||||||||     |||||
                                ATGT TTAGTGAC     TTCCT
                                  _       CCCT_
GAM883  KIAA0449 3'  TCCCCAGCACTCATGATCTTG  34639        C   CT_   A
                                CAAGATCA TGA   CTG GGA
                                |||||||| |||   ||| |||
                                GTTCTAGT ACT   GAC CCT
                                     _   CAC   C
GAM883  KIAA1061 3'  GTCCTCAGAGTGCATTTCCTG  71723     A  TCAC  _
                                CA GA    TG ACTCTGAGGAC
                                || ||    || ||||||||||
                                GT CT    AC TGAGACTCCTG
                                 C  TT__  G
GAM883  KIAA1535 3'  GTCCTCAGCTCAAGAATCCTGT 80214      A   CAC   CT
           A                     TACA GAT   TGA  CTGAGGAC
                                |||| |||   |||  ||||||||
                                ATGT CTA   ACT  GACTCCTG
                                  C   AGA   C_
GAM883  LCHN     3'  TCCTCAGAGTATGTCTTG    87478       CACTG
                                CAAGAT     ACTCTGAGGA
                                ||||||     ||||||||||
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                                GTTCTG    TGAGACTCCT
                                   TA___
GAM883  MAGEH1   3'  TCATAATCTATGATCTTGTA  26772        CT  CTC
                                TACAAGATCA  GA   TGA
                                ||||||||||  ||   |||
                                ATGTTCTAGT  CT   ACT
                                      AT  AAT
GAM883  LOC154789 5'  TCCTCAGAGCTCTCCTGTG   82034     A  TCACT  _
                                TACA GA    GA CTCTGAGGA
                                |||| ||    || |||||||||
                                GTGT CT    CT GAGACTCCT
                                  C _____ C
GAM883  LOC197201 3'  TCCTCAGAAGGTATTTGTA   89289      ATC   GAC
                                TACAAG   ACT   TCTGAGGA
                                ||||||   |||   ||||||||
                                ATGTTT   TGG   AGACTCCT
                                   A__   A__
GAM883  LOC255193 3'  CCTCAGAGTCAGGCCTGTA   97103     AGATCA
                                TACA     CTGACTCTGAGG
                                ||||     ||||||||||||
                                ATGT     GACTGAGACTCC
                                  CCG___
GAM883  LOC96597  5'  TCCCCAGAATTCTCTTGT    67468      TCACT  C_   A
                                ACAAGA    GA  TCTG GGA
                                ||||||    ||  |||| |||
                                TGTTCT    CT  AGAC CCT
                                   _____  TA   C
GAM884  IRO039700 3'  CAGGCCTGCCCCTCCA     38529     C   TT
                                TGGA GGG  CAGGCCTG
                                |||| |||  ||||||||
                                ACCT CCC  GTCCGGAC
                                  _   C_
GAM884  MRPL11   3'  ATCAGGCCTGAATAAACATCC  32649    CGG__
                                GGA    GTTCAGGCCTGAT
                                |||    ||||||||||||
                                CCT    TAAGTCCGGACTA
                                  ACAAA
GAM884  MYOZ2    5'  ATCAGGCCCAAGTGCCATCCAT 33938      CG   TCA__
                                ATGGA  GGT    GGCCTGAT
                                |||||  |||    ||||||||
                                TACCT  CCG    CCGGACTA
                                   A_   TGAAC
GAM884  LOC145226 3'  TCAGGCCCAATCCATGCCA   77561    AC_    CA
                                TGG   GGGTT  GGCCTGA
                                |||   |||||  |||||||
                                ACC   CCTAA  CCGGACT
                                  GTA    C_
GAM884  LOC146108 5'  ATCAGACCCAAGGGCCCGTTCA 78146          A__  C
                                TGGACGGGTTC   GG CTGAT
                                ||||||||||   || |||||
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                                ACTTGCCCGGG   CC GACTA
                                      AAC  A
GAM885  HRH1     3'  CTCAAACATGTTTAGAGTGGA  7819       A     TGG
                                TCCA TCTGA   GCATGTTTGAG
                                |||| |||||   ||||||||||
                                AGGT AGATT   TGTACAAACTC
                                  G    ___
GAM885  TRIM37   3'  CTCAAATTTGTCATCAG     31625        G  T
                                CTGATGG CA GTTTGAG
                                ||||||| || |||||||
                                GACTACT GT TAAACTC
                                    _ T
GAM885  HTMP10   3'  CTCAAAAAAGCCATCAGATCTG 53758    CA       G ATG
           A                     TC  ATCTGATGG C   TTTGAG
                                ||  |||||||||  |   ||||||
                                AG  TAGACTACC G   AAACTC
                                 TC        _ AAA
GAM885  PAK2     5'  CTCAAATATCACCAAACTAGA  67140     A__   GC
                                TCTG   TGG  ATGTTTGAG
                                ||||   |||  |||||||||
                                AGAT   ACC  TATAAACTC
                                  CAA   AC
GAM885  SEMA6A   3'  CTCGAGTACCCACCAGA     40818     A    CA
                                TCTG TGGG  TGTTTGAG
                                |||| ||||  ||||||||
                                AGAC ACCC  ATGAGCTC
                                  C   __
GAM885  TTY7     3'  TCAAACATGCAGGCTGGA    50019     AT  GATGG
                                TCCA  CT    GCATGTTTGA
                                ||||  ||    ||||||||||
                                AGGT  GA    CGTACAAACT
                                  CG  _____
GAM885  LOC144766 3'  CTCAAACATGAGAAGACTGGG  77481     A   GATGGG
                                TCCA TCT     CATGTTTGAG
                                |||| |||     ||||||||||
                                GGGT AGA     GTACAAACTC
                                  C   AGA___
GAM885  LOC201685 5'  TAAACACCCATCAGATGGA   91845     A       CA
                                TCCA TCTGATGGG  TGTTTG
                                |||| |||||||||  ||||||
                                AGGT AGACTACCC  ACAAAT
                                    _       __
GAM885  LOC221596 5'  CTCAAACAAAACTCAGATT   93623        TG GCA
                                AATCTGA  G   TGTTTGAG
                                |||||||  |   ||||||||
                                TTAGACT  C   ACAAACTC
                                    __ AAA
GAM885  LOC93622  3'  CTCTGCAGACCATCAGAT    57729         GCA   TT
                                ATCTGATGG   TGT  GAG
                                |||||||||   |||  |||
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                                TAGACTACC   ACG  CTC
                                     AG_   T_
GAM886  CBFA2T3   3'  CCCCTCACCCCAGCTCCGA    19014      CAA        A
                                TTGG   CTGGGGTGA GGG
                                ||||   ||||||||| |||
                                AGCC   GACCCCACT CCC
                                  TC_        C
GAM886  CFL1      3'  TCCCTTCACCCCAGTTGCCAAA 19747
            CA                    TGTTTGGCAACTGGGGTGAAGGGA
                                ||||||||||||||||||||||||
                                ACAAACCGTTGACCCCACTTCCCT

GAM886  CHRM1     3'  CCCTCCACCCCAGTCCCC     96430    CA        A
                                GG  ACTGGGGTG AGGG
                                ||  ||||||||| ||||
                                CC  TGACCCCAC TCCC
                                 CC        C
GAM886  CHST1     3'  CCCCCCACCCCATTCAGACA   14695        CAAC      AA
                                TGTTTGG    TGGGGTG  GGG
                                |||||||    |||||||  |||
                                ACAGACT    ACCCCAC  CCC
                                    T___       CC
GAM886  GYS1      3'  CCCCCACCCAGTCCGCCAAACA 89780         A_     G  AA
                                TGTTTGGC  ACTGGG TG  GGG
                                ||||||||  |||||| ||  |||
                                ACAAACCG  TGACCC AC  CCC
                                     CC     _  C_
GAM886  HIP12     3'  TCCCCCCACCCCAGCCCTAGCC 66820     AA___       AA
                                GGC    CTGGGGTG  GGGA
                                |||    ||||||||  ||||
                                CCG    GACCCCAC  CCCT
                                  ATCCC       CC
GAM886  MFAP2     3'  TCCCCCCACCCCAGCTGGTCTG 34362    TT   AA_       AA
            C                    GT  GGC   CTGGGGTG  GGGA
                                ||  |||   ||||||||  ||||
                                CG  CTG   GACCCCAC  CCCT
                                 T_   GTC       CC
GAM886  MYO1C     3'  CCCTTCCCAGTTACCAAA     61861       C       TGA
                                TTTGG AACTGGGGG   AGGG
                                ||||| ||||||||   ||||
                                AAACC TTGACCCT   TCCC
                                   A       ___
GAM886  DKFZp547C176 3'  TCCCCTCACCCCAGTTGC     67807            A
                                GCAACTGGGGTGA GGGA
                                |||||||||||||| ||||
                                CGTTGACCCCACT CCCT
                                         C
GAM886  FLJ12387  3'  CCCCTCACCCCAGCCCTGCGCA 43374     _   A__        A
                                TG GCA   CTGGGGTGA GGG
                                || |||   ||||||||| |||
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                                AC CGT   GACCCCACT CCC
                                 G  CCC       C
GAM886  FLJ20294  3'  CCCCTCGAACCGCCAAGCA   35349       AACT  GG   A
                                TGTTTGGC   GG  TGA GGG
                                ||||||||   ||  ||| |||
                                ACGAACCG   CC  GCT CCC
                                    ____  AA   C
GAM886  FLJ22127  3'  CCCCCCACCCGTCTGCCAAGCA 43198        ACTG    AA
                                TGTTTGGCA   GGGTG  GGG
                                |||||||||   |||||  |||
                                ACGAACCGT   CCCAC  CCC
                                     CTG_    CC
GAM886  FLJ32389  3'  CCCCCCACCCCCCAAAC    58841      CAACT    AA
                                GTTTGG    GGGGTG  GGG
                                ||||||    ||||||  |||
                                CAAACC    CCCCAC  CCC
                                   _____     CC
GAM886  IRF7      3'  CCCTCCACCCCAGCCTGCC   15735     A_      A
                                GGCA  CTGGGGTG AGGG
                                ||||  |||||||| ||||
                                CCGT  GACCCCAC TCCC
                                  CC       C
GAM886  KIAA1274  3'  TCCCCCAGTTGCCAAACA    93015            T
                                TGTTTGGCAACTGGGG GA
                                |||||||||||||| ||
                                ACAAACCGTTGACCCC CT
                                                _
GAM886  KIAA1389  3'  CCCTTTGAAGTCACAAACA   70317      GCA   GGGGT
                                TGTTTG   ACT    GAAGGG
                                ||||||   |||    ||||||
                                ACAAAC   TGA    TTTCCC
                                   AC_   AG___
GAM886  SDC3      3'  CCCCTCACCTATTTGGCCAAAC 28466       AACTG     A
          A                      TGTTTGGC    GGGTGA GGG
                                 ||||||||    |||||| |||
                                 ACAAACCG    TCCACT CCC
                                      GTTTA     C
GAM886  LOC123232 3'  TACCCCAGTTCCCAAACA    74658       C
                                TGTTTGG AACTGGGGTG
                                ||||||| ||||||||||
                                ACAAACC TTGACCCCAT
                                    C
GAM886  LOC135138 5'  TCCCTTCACCTAGGAGCTGCCA 75711         A__  G
          AACA                    TGTTTGGCA   CT GGGTGAAGGGA
                                  |||||||||   || ||||||||||
                                  ACAAACCGT   GG TCCACTTCCCT
                                       CGA  A
GAM886  LOC169611 3'  TCCTGGCCACAGCCGCCAAACA 83666        AA   G   GA
                                TGTTTGGC  CTG GGT  AGGG
                                ||||||||  ||| |||  ||||
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                                ACAAACCG  GAC CCG  TCCT
                                    CC   A   G_
GAM886  LOC90719  3'  TCACCCCCAGCTGCCAAGCA   64610         A     _
                                TGTTTGGCA CTGGGG TGA
                                ||||||||| |||||| |||
                                ACGAACCGT GACCCC ACT
                                    C     C
GAM886  LOC91252  3'  CACCTCCAGCTGCCAAACA   65936         A   _
                                TGTTTGGCA CTGG GGTG
                                ||||||||| |||| ||||
                                ACAAACCGT GACC CCAC
                                    C    T
GAM887  HRH1      3'  AAATGTGCCCTTTTGGCCGG  7812      A       A   TCA
                                CC GGCCAAAA GGC   ACATTT
                                || |||||||| |||   ||||||
                                GG CCGGTTTT CCG   TGTAAA
                                 _       C  ____
GAM887  POLD2     5'  TTGAACCTCCTTGGCCTGG   21721         AA   C
                                CCAGGCCAA  AGG TCAA
                                |||||||||  ||| ||||
                                GGTCCGGTT  TCC AGTT
                                    CC   A
GAM887  SCN7A     3'  AAATGTTGAAAGCCTAAGCC  12947     CAAAA   __
                                GGC    AGGC  TCAACATTT
                                |||    ||||  |||||||||
                                CCG    TCCG  AGTTGTAAA
                                  AA___    AA
GAM887  SHANK2    3'  GTTGAACTTCTTCTTTGGCCTC 25531   C       _   C__
          A                      C AGGCCAAA AAGG   TCAAC
                                | |||||||| ||||   |||||
                                A TCCGGTTT TTCT   AGTTG
                                 C       C    TCA
GAM887  SIAT8E    3'  TGAGCCTCCTGGCCTGG     60552         AAA
                                CCAGGCCA   AGGCTCA
                                ||||||||   |||||||
                                GGTCCGGT   TCCGAGT
                                    CC_
GAM887  SLC7A8    3'  GAGCCCTTCCTGGCCTGG    25304         AA   _
                                CCAGGCCA  AAGG CTC
                                ||||||||  |||| |||
                                GGTCCGGT  TTCC GAG
                                    CC    C
GAM887  TFAP2C    3'  TGGGAACCCCTCCTGGCCTGG 13687         AAA  ____
                                CCAGGCCA   AGG    CTCA
                                ||||||||   |||    ||||
                                GGTCCGGT   TCC    GGGT
                                    CC_   CCAA
GAM887  TRPM2     3'  GAGCCTTGCCTGGCCTGG    13864         AA_
                                CCAGGCCA   AAGGCTC
                                ||||||||   |||||||
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                                GGTCCGGT   TTCCGAG
                                     CCG
GAM887  FLJ13189 3' TTGAACCTTTTTTGCCTGG   46498      C     C
                                CCAGGC AAAAAGG TCAA
                                |||||| ||||||| ||||
                                GGTCCG TTTTTCC AGTT
                                   T      A
GAM887  FLJ20208 3' AAATGCAGGCTTTTTAGCC   35240    C     G  CAA
                                GGC AAAAAG CT   CATTT
                                ||| |||||| ||   |||||
                                CCG TTTTTC GA   GTAAA
                                  A     G  C__
GAM887  FLJ22944 3' AAATGTTGGGATTTGAACCC  47866    CCAA   GG
                                GG    AAA  CTCAACATTT
                                ||    |||  ||||||||||
                                CC    TTT  GGGTTGTAAA
                                 CAAG   A_
GAM887  HPRP8BP  3' AAATGTTGGATGTCCAGGCT  60060     AAAAA   __
                                GGCC    GGC  TCAACATTT
                                ||||    |||  |||||||||
                                TCGG    CTG  GGTTGTAAA
                                  AC___   TA
GAM887  KIAA0872 3' AAATGTTAAGCCTTTTGTTATT 30731    GCCA      C
           G                     CAG    AAAAGGCT AACATTT
                                |||    |||||||| |||||||
                                GTT    TTTTCCGA TTGTAAA
                                  ATTG       A
GAM887  KIAA1843 3' AAATGTTGACTGAACCTGACCT 62880     C  AAAA_  C
           G                     CAGG CA     GG TCAACATTT
                                |||| ||     || |||||||||
                                GTCC GT     TC AGTTGTAAA
                                  A  CCAAG  _
GAM887  KIAA1975 3' AAATGTTGATTTTTCTGACC   74407    C  A    C
                                GG CA AAAGG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM887  MRIP2    3' AAATGTTGATTTTTCTGACC   56789    C  A    C
                                GG CA AAAGG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM887  SLC26A10 5' TTGAACCCCTTTGGCCTG    56851         AA  C
                                CAGGCCAAA  GG TCAA
                                |||||||||  || ||||
                                GTCCGGTTT  CC AGTT
                                      CC  A
GAM887  THEG     3' TGAGCTTTTTGGCCTGG     33892            G
                                CCAGGCCAAAAAG CTCA
                                |||||||||||| ||||
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                                GGTCCGGTTTTTC GAGT
                                      _
GAM887  LOC118704 3' AAATGTTGATTTTTCTGACC  74359   C A   C
                                GG CA AAAGG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A C   _
GAM887  LOC118706 3' AAATGTTGATTTTTCTGACC  74361   C A   C
                                GG CA AAAGG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A C   _
GAM887  LOC123036 3' AAATGTTTGCAGTTTTGGCT  74645       AG  TC
                                GGCCAAAA  GC  AACATTT
                                ||||||||  ||  |||||||
                                TCGGTTTT  CG  TTGTAAA
                                     GA  T_
GAM887  LOC123624 3' AAATGTTGGGCTTCTGTGCCT  76134    _ AAA
                                AGGC CA   AGGCTCAACATTT
                                |||| ||   ||||||||||||
                                TCCG GT   TTCGGGTTGTAAA
                                  T  C__
GAM887  LOC128338 3' AAATATTGAGCCTTTTTAATAG 75250   AGGCC         C
          G                      CC    AAAAAGGCTCAA ATTT
                                ||    |||||||||||| ||||
                                GG    TTTTTCCGAGTT TAAA
                                 ATAA_          A
GAM887  LOC143158 3' AAATGTTGATTTTTCTGACC  76997   C A   C
                                GG CA AAAGG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A C   _
GAM887  LOC195979 3' AAATGTTGATTTTTCTGACC  88928   C A   C
                                GG CA AAAGG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A C   _
GAM887  LOC219672 5' AATGGTGCTTTTTGGCTGG   92963    G      G TCAA
                                CCAG CCAAAAAG C   CATT
                                |||| |||||||| |   ||||
                                GGTC GGTTTTTC G   GTAA
                                  _      _ TG__
GAM887  LOC220466 3' AAATGTTGATTTTTCTGACC  74398   C A   C
                                GG CA AAAGG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A C   _
GAM887  LOC254105 3' AGGTGTGGCCCCCTTGGCCTGG 96416        AAA   CA
                                CCAGGCCAA  GGCT  ACATTT
                                |||||||||  ||||  ||||||
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                                GGTCCGGTT  CCGG  TGTGGA
                                     CCC   __
GAM887  LOC255319 3'  AAATGTTGATTTTTCTGACC  96152    C  A    C
                                GG CA AAAGG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM887  LOC91300  5'  GTTGAGCTTTTCTGGCCCGG  96238    A    A
                                CC GGCCA AAAGGCTCAAC
                                || ||||| ||||||||||
                                GG CCGGT TTTTCGAGTTG
                                 C    C
GAM887  LOC91300  5'  GTTGAGCTTTTCTGGCCCGG  96239    A    A
                                CC GGCCA AAAGGCTCAAC
                                || ||||| ||||||||||
                                GG CCGGT TTTTCGAGTTG
                                 C    C
GAM887  LOC91660  5'  AAATGTTTATCTTCTTTTTGGC 67399          CTC__
           TT                    AGGCCAAAAAGG    AACATTT
                                ||||||||||||    |||||||
                                TTCGGTTTTTCT    TTGTAAA
                                      TCTAT
GAM888  BBS4     3'  ATTTGCCCAAAGGGAATCCAGA 53447        G_ G_   A
           ACA                   TGTTCTGGA  CT  TTGG CAAAT
                                |||||||||  ||  |||| |||||
                                ACAAGACCT  GG  AACC GTTTA
                                     AA  GA   C
GAM888  CENTD2   3'  CCAACAAACTCCAGAACA    31539        C_
                                TGTTCTGGAG  TGTTGG
                                ||||||||||  ||||||
                                ACAAGACCTC  ACAACC
                                      AA
GAM888  HAMP     3'  TCCTGCTGCCCCAGAACA    41289        A  T  T
                                TGTTCTGG GC GT GGA
                                |||||||| || || |||
                                ACAAGACC CG CG CCT
                                     C  T  T
GAM888  ITGA11   3'  TCTGCCGGCCCCCAGGACA   25213        A_   TT
                                TGTTCTGG  GCTG  GGA
                                ||||||||  ||||  |||
                                ACAGGACC  CGGC  TCT
                                     CC    CG
GAM888  KITLG    3'  ATTTGCATGGCTCCAGAA    8023           TGGA
                                TTCTGGAGCTGT   CAAAT
                                ||||||||||||   |||||
                                AAGACCTCGGTA   GTTTA
                                       C___
GAM888  MAPK4    5'  CCTGGGCAGCTCCAGATCA   12300    T         __
                                TG TCTGGAGCTGTT  GG
                                || ||||||||||||  ||
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                                AC AGACCTCGACGG  CC
                                 T          GT
GAM888  MGAT2    3'  ATTTGTCCAAACAGGACA    11557        GAGCTG
                                TGTTCTG     TTGGACAAAT
                                |||||||     ||||||||||
                                ACAGGAC     AACCTGTTTA
                                   A_____
GAM888  PSPHL    5'  TTGTCATACAGCTCCAAACA   94499      C        TG
                                TGTT TGGAGCTGT  GACAA
                                |||| |||||||||  |||||
                                ACAA ACCTCGACA  CTGTT
                                  _        TA
GAM888  TTC3     3'  TATTTGTCCAACAACTGTCAGA 13885         _  C
            ATA                    TGTTCTGG AG TGTTGGACAAATA
                                |||||||| || ||||||||||||
                                ATAAGACT TC ACAACCTGTTTAT
                                     G  A
GAM888  H2BFQ    3'  TTTAAGAGAACTCCAGGACA   60079          __  G
                                TGTTCTGGAG  CT TTGGA
                                ||||||||||  || |||||
                                ACAGGACCTC  GA AATTT
                                      AA  G
GAM888  LRG      3'  TCCATCCATGCTTCCTAGAACA 54825        _  _ _  T_
                                TGTTCT GGA GC TG  TGGA
                                |||||| ||| || ||  ||||
                                ACAAGA CCT CG AC  ACCT
                                   T   T  T  CT
GAM888  NMT2     3'  ATTTGTCCATGTAACAGAACA  17852        GA  TGT
                                TGTTCTG  GC   TGGACAAAT
                                |||||||  ||   |||||||||
                                ACAAGAC  TG   ACCTGTTTA
                                   AA  T__
GAM888  NYD-SP21  3'  TATTTGTCCAATCTAGATTCAG 51863         G  __
            AACA                    TGTTCTGGA CT  GTTGGACAAATA
                                |||||||||  ||  ||||||||||||
                                ACAAGACTT GA  TAACCTGTTTAT
                                      A  TC
GAM888  PSPH     3'  TTGTCGTACAGCTCCAAACA   17143      C        TG
                                TGTT TGGAGCTGT  GACAA
                                |||| |||||||||  |||||
                                ACAA ACCTCGACA  CTGTT
                                  _        TG
GAM888  LOC122258 3'  CCACCAGCCTCCGGAACA    59820          _  T
                                TGTTCTGGAG CTG TGG
                                |||||||||| ||| |||
                                ACAAGGCCTC GAC ACC
                                      C  C
GAM888  LOC151826 3'  ATTTGTCCAACCTAGCACA   81176     T   AGCT
                                TGT CTGG   GTTGGACAAAT
                                ||| ||||   ||||||||||
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                                ACA GATC    CAACCTGTTTA
                                  C   ____
GAM888  LOC169611 3'  TCCAGTGGCAGCTCCAGAA    83663          ___
                                TTCTGGAGCTGT   TGGA
                                ||||||||||||  ||||
                                AAGACCTCGACG   ACCT
                                      GTG
GAM888  LOC196746 3'  TCAGAGCAGCTCCAAGACA    88903     TC       G_
                                TGT  TGGAGCTGTT  GA
                                |||  ||||||||||  ||
                                ACA  ACCTCGACGA  CT
                                  GA        GA
GAM888  LOC253142 5'  TTGCTAGGATGCCCCAGAATA  99230        A  TG_   A
                                TGTTCTGG GC   TTGG CAA
                                ||||||||  ||   |||| |||
                                ATAAGACC CG   GATC GTT
                                     C  TAG   _
GAM889  SCAMP1    3'  GCTAAATAAATATTCTCC     54500     T     C
                                GGA AATATT ATTTAGC
                                |||  ||||||  |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM889  SCAMP1    3'  GCTAAATAAATATTCTCC     54501     T     C
                                GGA AATATT ATTTAGC
                                |||  ||||||  |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM889  NX-17     3'  TGAATATCAGCCCCTAATA    40706         ATA_
                                TATTAGGG    ATATTCA
                                ||||||||    |||||||
                                ATAATCCC    TATAAGT
                                     CGAC
GAM889  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
            TA                    TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM890  CNR1      3'  TAGTTACTGTCCTGTTG      32722       T   AAA
                                TAACA GGA   CAGTAACTA
                                |||||  |||   |||||||||
                                GTTGT CCT   GTCATTGAT
                                     _   ____
GAM890  DAZL      3'  TAGTTACTGTGAGCCATATTAC 68699      C    AAA
                                GTAA ATGG   ACAGTAACTA
                                ||||  ||||   ||||||||||
                                CATT TACC   TGTCATTGAT
                                  A    GAG
GAM890  SLC6A3    3'  GCTGCTTTCCATGGCACA     8313      AA       A
                                TGT  CATGGAAA CAGT
                                |||  ||||||||  ||||
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                                ACA  GTACCTTT GTCG
                                  CG       C
GAM890  TACC1    3'  TATTTTTTCCATGTTTCAT   21879     T         C
                                ATG AACATGGAAAA AGTA
                                ||| |||||||||| ||||
                                TAC TTGTACCTTTT TTAT
                                  T         _
GAM890  TNFSF12  3'  ACGTGTTTTCCATCCCACAT   15082      AAC         _
                                ATGT   ATGGAAAACA GT
                                ||||   |||||||||| ||
                                TACA   TACCTTTTGT CA
                                  CCC         G
GAM890  YWHAZ    3'  TACTGTTTCCATGTCCCAT    14156     TA        A
                                ATG  ACATGGAAA CAGTA
                                |||  ||||||||| |||||
                                TAC  TGTACCTTT GTCAT
                                  CC        _
GAM890  ASAH     3'  TAGTTACTAAAATTATGTTAC  16305          AAAAC
                                GTAACATGG     AGTAACTA
                                |||||||||     ||||||||
                                CATTGTATT     TCATTGAT
                                     AAAA_
GAM890  C20orf121 3'  AGTTACTGAATGTTAGAT    44522    G     GGAAAA
                                AT TAACAT     CAGTAACT
                                || ||||||     ||||||||
                                TA ATTGTA     GTCATTGA
                                 G     A_____
GAM890  C5orf5   3'  AGTTACTGTTTCCTGAGTTAC  33942       AT_    A
                                GTAAC   GGAAA CAGTAACT
                                |||||   ||||| ||||||||
                                CATTG   CCTTT GTCATTGA
                                   AGT    _
GAM890  ESDN     3'  AGTTACTGCTCGCCTGTTA    56056       T  AAAA
                                TAACA GG    CAGTAACT
                                ||||| ||    ||||||||
                                ATTGT CC    GTCATTGA
                                   _  GCTC
GAM890  KIAA0125 3'  TTACTTTCCATGTAACA     29582     A       AAC
                                TGT ACATGGAA   AGTAA
                                ||| ||||||||   |||||
                                ACA TGTACCTT   TCATT
                                  A       ___
GAM890  KIAA1155 3'  TAGTTACTGTTGTCCTGTTCAT 62920     T    T   A
                                ATG AACA GGA AACAGTAACTA
                                ||| |||| ||| ||||||||||
                                TAC TTGT CCT TTGTCATTGAT
                                  _   _  G
GAM890  MSTP032  3'  AGCTACTGTTTGTGTTA     48204       GGA       A
                                TAACAT   AAACAGTA CT
                                ||||||   |||||||| ||
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                                ATTGTG   TTTGTCAT GA
                                   ___       C
GAM890  OR51E2    3'  AGTTACTTAATGACCATGTTAT 48504          AAAAC_
              AT                  ATGTAACATGG     AGTAACT
                                  ||||||||||      |||||||
                                  TATATTGTACC     TCATTGA
                                        AGTAAT
GAM890  STX12     3'  AGTTACTGGAGTACATGTTAC  66949        GAAAA
                                  GTAACATG    CAGTAACT
                                  ||||||||    ||||||||
                                  CATTGTAC    GTCATTGA
                                       ATGAG
GAM890  LOC132617 3'  AGTTACTGTTCTTGATGT    76408      G  A
                                  ACAT GA AACAGTAACT
                                  |||| || ||||||||||
                                  TGTA TT TTGTCATTGA
                                    G  C
GAM890  LOC145676 5'  GCTCTTCTCCTTGTTACAT    77847        T   A  C
                                  ATGTAACA GGA AA AGT
                                  |||||||| ||| || |||
                                  TACATTGT CCT TT TCG
                                       T   C  C
GAM890  LOC150311 5'  GCTGAGTTCTTTTCCATGTTAC 80565            _____
                                  GTAACATGGAAAA    CAGT
                                  ||||||||||||     ||||
                                  CATTGTACCTTTT    GTCG
                                        CTTGA
GAM890  LOC152794 5'  TACTGACTTTCCATGTTGCAT  81563             A_
                                  ATGTAACATGGAAA  CAGTA
                                  ||||||||||||||  |||||
                                  TACGTTGTACCTTT  GTCAT
                                           CA
GAM890  LOC221405 3'  ATTGCTTTCCATGCACAT    95506      AA       A
                                  ATGT  CATGGAAA CAGT
                                  ||||  |||||||| ||||
                                  TACA  GTACCTTT GTTA
                                    C_       C
GAM891  COL19A1   3'  ATTCCTTTAATAAAAAGAAACT 10260     A_       C
                                  AGT  TTTTTTAT AAAGGAAT
                                  |||  |||||||| ||||||||
                                  TCA  GAAAAATA TTTCCTTA
                                    AA       A
GAM891  FLJ14735  3'  ATTCCTTTAATAAATTGTATT  52665       TT     C
                                  AGTAT  TTTAT AAAGGAAT
                                  |||||  ||||| ||||||||
                                  TTATG  AAATA TTTCCTTA
                                     TT    A
GAM891  FLJ23516  3'  ATTCCTTACAAAAATACTGT   44885           TATCA
                                  ACAGTATTTTT    AAGGAAT
                                  ||||||||||     |||||||
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                                TGTCATAAAAA    TTCCTTA
                                      CA___
GAM891  KIAA0121  3'  ATTCCTCTGACTTTATACTGTT 73045       TTTTTA  A
                                GACAGTAT     TCA AGGAAT
                                ||||||||     ||| |||||||
                                TTGTCATA     AGT TCCTTA
                                    TTTC__   C
GAM891  PRO2435   3'  TCCAAAGCCAAAGAATACTGTC 38189          ATCAAA
                                GACAGTATTTTTT     GGA
                                ||||||||||||     |||
                                CTGTCATAAGAAA     CCT
                                      CCGAAA
GAM891  LOC202908 5'  ATTCCCTTGAGAACAAGTACTG 90711        T  A   A
           TC                   GACAGTATTT TT TCAA GGAAT
                                ||||||||||| || |||| |||||
                                CTGTCATGAA AA AGTT CCTTA
                                      C  G   C
GAM891  LOC222057 5'  ATTCCCTTGAGAACAAGTACTG 94346        T  A   A
           TC                   GACAGTATTT TT TCAA GGAAT
                                ||||||||||| || |||| |||||
                                CTGTCATGAA AA AGTT CCTTA
                                      C  G   C
GAM891  LOC255975 5'  ATTCCCTTGAGAACAAGTACTG 97571        T  A   A
           TC                   GACAGTATTT TT TCAA GGAAT
                                ||||||||||| || |||| |||||
                                CTGTCATGAA AA AGTT CCTTA
                                      C  G   C
GAM891  LOC256878 5'  ATTCCCTTGAGAACAAGTACTG 98683        T  A   A
           TC                   GACAGTATTT TT TCAA GGAAT
                                ||||||||||| || |||| |||||
                                CTGTCATGAA AA AGTT CCTTA
                                      C  G   C
GAM892  ACVRL1    5'  TTTATTAGGAGGGAGTGGTG   5240          AAGAAG
                                CACCACTCCC     AATAAG
                                ||||||||||     ||||||
                                GTGGTGAGGG     TTATTT
                                      AGGA__
GAM892  BCL11B    3'  TTTGTTTTTGGGGTGGGGGGTG 57582       A_ __      G  TAAG
           TG                   TACACC  CT  CCCAAGAA AA
                                ||||||  ||  |||||||| ||
                                GTGTGG  GG  GGGTTTTT TT
                                   GG  TG       G  T
GAM892  C18orf1   3'  CTTCGTGTGGGAGTGGTGTG   60865          A__
                                TACACCACTCCCA   GAAG
                                ||||||||||||   ||||
                                GTGTGGTGAGGGT   CTTC
                                      GTG
GAM892  ITPR3     3'  CTTGTTTTTCTCCTTTTGGTGT 11085        CTCCCA
           A                    TACACCA     AGAAGAATAAG
                                |||||||     ||||||||||
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                                ATGTGGT     TCTTTTTGTTC
                                    TTTCC_
GAM892  KCNAB1   3'  GTTTGTTTTTTTTTGAAGGGGG 61585          ____
            TGGTGTG                 TACACCACTCCC    AAGAAGAATAAG   T
                                ||||||||||||   ||||||||||||  |
                                GTGTGGTGGGGG    TTTTTTTTGTTT   G
                                      AAGT
GAM892  KRAS2    3'  CTTATTTTTCTTACCAAGTGTG 54123     C   CCC_
                                CAC ACT    AAGAAGAATAAG
                                ||| |||    ||||||||||||
                                GTG TGA    TTCTTTTTATTC
                                  _   ACCA
GAM892  KRAS2    3'  CTTATTTTTCTTACCAAGTGTG 54124     C   CCC_
                                CAC ACT    AAGAAGAATAAG
                                ||| |||    ||||||||||||
                                GTG TGA    TTCTTTTTATTC
                                  _   ACCA
GAM892  LIFR     3'  TTTGTTTTTTTTGGTTGGTTG  11315    C    CTC
                                A ACCA   CCAAGAAGAATAAG
                                | ||||   ||||||||||||||
                                G TGGT   GGTTTTTTTTGTTT
                                 T    T__
GAM892  MEN1     5'  CTTGTTTTTTTCCTTTTGGTG  56348       CTCCCA
                                CACCA     AGAAGAATAAG
                                |||||     ||||||||||
                                GTGGT     TTTTTTTGTTC
                                   TTTCC_
GAM892  MLLT7    3'  TTGTGCCTGGGAGTGTGTG    21043     _       AGAAGA
                                CAC CACTCCCA     ATAA
                                ||| ||||||||     ||||
                                GTG GTGAGGGT     TGTT
                                  T       CCG___
GAM892  SIAH1    3'  TTTGTTTTTGCCGTGGGAGTGT 13128     _       AG__
              GTG                   CAC CACTCCCA    AAGAATAAG
                                ||| ||||||||   |||||||||
                                GTG GTGAGGGT    TTTTTGTTT
                                  T       GCCG
GAM892  SLC7A6   3'  TTTGTTTTTGTGGTGGGTGCTG 15646      C     _   AG
              TG                    TACA CACTC CCA  AAGAATAAG
                                |||| ||||| |||  |||||||||
                                GTGT GTGGG GGT  TTTTTGTTT
                                  C    T   G_
GAM892  STAT6    5'  ATTTTTCTTTTTGGTGGTGGTG 13448       TC        TAAG
                                CACCAC  CCAAGAAGAA
                                ||||||  ||||||||||
                                GTGGTG  GGTTTTTCTT
                                   GT        TTTAT
GAM892  TCF8     3'  CTTGTTTTTTTAAGAGTGTGTG 48429     _    CCA
                                CAC CACTC   AGAAGAATAAG
                                ||| |||||   ||||||||||
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                                GTG GTGAG   TTTTTTTGTTC
                                  T    AA_
GAM892  B3GNT7   3'  TTGTTCTTGGCTGGTGGGTG  71685    A    C_     G
                                TAC CCACT  CCAAGAA AA
                                ||| |||||  ||||||| ||
                                GTG GGTGG  GGTTCTT TT
                                  _    TC      G
GAM892  BCDO     3'  TTATTCTTTCTGTGGGTG    34287      C  AG
                                CACTC CA  AAGAATAA
                                ||||| ||  ||||||||
                                GTGGG GT  TTCTTATT
                                   T  CT
GAM892  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
            A                    TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM892  EPN2     3'  TTTATTTTTCTTTGACTCGTGT 31046       CAC  CC
            G                    TACAC   TC  AAGAAGAATAAG
                                |||||   ||  ||||||||||||
                                GTGTG   AG  TTCTTTTTATTT
                                   CTC  T_
GAM892  FLJ13855  3'  GGGTATTTTTCTTGGGGGTGGA 43853     A              AG
            GTA                   TAC CCACTCCCAAGAAGAATA
                                ||| ||||||||||||||||||
                                ATG GGTGGGGGTTCTTTTTAT
                                  A              GGGA
GAM892  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM892  FLJ32865  3'  TTTGTTGGGGGTGGGGTG    58824     A        G
                                TAC CCACTCCCAA AAG
                                ||| |||||||||| |||
                                GTG GGTGGGGGTT TTT
                                  G        G
GAM892  GRP3     3'  TTGTTCTTCTTGGTGTG     31742     TC
                                CAC  CCAAGAAGAATAA
                                |||  ||||||||||||
                                GTG  GGTTCTTCTTGTT
                                  T_
GAM892  HAND1    3'  TTTGTTCTTCGAATCGTGGTG  17880       TCCCAA
                                CACCAC     GAAGAATAAG
                                ||||||     ||||||||||
                                GTGGTG     CTTCTTGTTT
                                   CTAAG_
GAM892  KIAA0562  3'  TTTGTTTTGCGGGGGTGGTG  28834          AAGA
                                CACCACTCCC    AGAATAAG
                                |||||||||    ||||||||
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                                GTGGTGGGGG   TTTTGTTT
                                     CG__
GAM892  KIAA0871  5'  TTTATTTTTTTGGTGTGTGTGT 31023      _  TC       ATAAG
            G                    TACAC CAC  CCAAGAAGA
                                 ||||| |||  |||||||||
                                 GTGTG GTG  GGTTTTTTT
                                    T  T_       ATTT
GAM892  KIAA0970  3'  TTTGTTTTTTTTGTTAGGGTG  30622     A  CC
                                 CACC CT  CAAGAAGAATAAG
                                 |||| ||  ||||||||||||
                                 GTGG GA  GTTTTTTTTGTTT
                                   _ TT
GAM892  KIAA1240  3'  TTTATTTTTAGGGAGTGGGTA  67297     A       AAG
                                 TAC CCACTCCC   AAGAATAAG
                                 ||| ||||||||   |||||||||
                                 ATG GGTGAGGG   TTTTTATTT
                                   _      A__
GAM892  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68742             _
                                 TACACCACTCCCAAGA AGA
                                 |||||||||||||||| |||
                                 ATGTGGTGAGGGTTCT TCT
                                          G
GAM892  KIAA1750  3'  TTTATTTTTTTGTTCTAGGTGT 68815       ACTCCCA
            G                    TACACC      AGAAGAATAAG
                                 ||||||      ||||||||||
                                 GTGTGG      TTTTTTTATTT
                                     ATCTTG_
GAM892  MAP2K3    3'  CTTGTTTTTCTTGCATGGT    59686     CTCC
                                 ACCA    CAAGAAGAATAAG
                                 ||||    ||||||||||||
                                 TGGT    GTTCTTTTTGTTC
                                   AC__
GAM892  MLN64     3'  CTTGTTGGGGAGTGGGTG    96062     A       _ G
                                 TAC CCACTCCC AA AAG
                                 ||| |||||||| || |||
                                 GTG GGTGAGGG TT TTC
                                   _       G  G
GAM892  NY-REN-41 3'  TTTGTTTTTCTATCCTGGTGG  55564       CCCA_
                                 CCACT     AGAAGAATAAG
                                 |||||     ||||||||||
                                 GGTGG     TCTTTTTGTTT
                                    TCCTA
GAM892  PRO1489   5'  TTTGTTTTTCGTGTGTGTGTG  38334      _  TCCCAA
                                 TACAC CAC      GAAGAATAAG
                                 ||||| |||      ||||||||||
                                 GTGTG GTG      CTTTTTGTTT
                                    T  TG____
GAM892  SEC15L    3'  TTTGTTCTACTTGGGTGGT    72731      CT     A
                                 ACCA  CCCAAG AGAATAAG
                                 ||||  |||||| ||||||||
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                                TGGT  GGGTTC TCTTGTTT
                                  __     A
GAM892  SHAPY    3'  TTTGTTCTTTTTGGAACTGTG  57915    TC__
                                CAC    CCAAGAAGAATAAG
                                |||    ||||||||||||||
                                GTG    GGTTTTTCTTGTTT
                                  TCAA
GAM892  STAM2    3'  TGTTTTTCTTCCTGCAATGTGG 20709        TCC_ A     TAAG
           TGTG                   TACACCAC   CA GAAGAA
                                |||||||||    || ||||||
                                GTGTGGTG    GT CTTCTT
                                     TAAC  C     TTTGTT
GAM892  TUBGCP3  3'  TTTATTTTTTTTTTAGTGTTGTA 21982     C    CCC
                                TACA CACT   AAGAAGAATAAG
                                |||| ||||   ||||||||||||
                                ATGT GTGA   TTTTTTTTTATTT
                                  T    T__
GAM892  ZNF220   3'  CTTGTTTTTTTTACCACCTGGTG 23157      CTCCCA
                                CACCA     AGAAGAATAAG
                                |||||     ||||||||||
                                GTGGT     TTTTTTTGTTC
                                   CCACCA
GAM892  LOC121219 5'  TTGTTCTATGGGTGGGTG    74493     ACT    AGA
                                CACC   CCCA   AGAATAA
                                ||||   ||||   |||||||
                                GTGG   GGGT   TCTTGTT
                                  GT_    A__
GAM892  LOC143146 3'  TTTGTTGGAGGTGGTGTA    60767        TC    G
                                TACACCAC  CCAA AAG
                                ||||||||  |||| |||
                                ATGTGGTG  GGTT TTT
                                     GA    G
GAM892  LOC146445 3'  TTGTTCTTTGTGTGGTTG    84687    C    TCCCAA
                                A ACCAC     GAAGAATAA
                                | |||||     |||||||||
                                G TGGTG     TTTCTTGTT
                                 T     TG____
GAM892  LOC150174 3'  TTTATTTTTTTTTACAATGGTG 80444      CTCCC
                                CACCA     AAGAAGAATAAG
                                |||||     ||||||||||||
                                GTGGT     TTTTTTTTATTT
                                   AACAT
GAM892  LOC150213 3'  TTTATTTTTTTTACAATGGTG  75363      CTCCC
                                CACCA     AAGAAGAATAAG
                                |||||     ||||||||||||
                                GTGGT     TTTTTTTTATTT
                                   AACA_
GAM892  LOC150236 3'  TTTATTTTTTTTACAATGGTG  80505      CTCCC
                                CACCA     AAGAAGAATAAG
                                |||||     ||||||||||||
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                                GTGGT    TTTTTTTTATTT
                                   AACA_
GAM892  LOC154084 3'  CTTGTTTTTTTTAGTAGGTGTG  87378       _  CCCA
                                TACACC ACT    AGAAGAATAAG
                                ||||||| |||   ||||||||||
                                GTGTGG TGA    TTTTTTTGTTC
                                   A  ____
GAM892  LOC170261 3'  TTTATTCTTTGTGAAAGTGGT  83472       CC  A
                                ACCACT  CA GAAGAATAAG
                                ||||||  || ||||||||||
                                TGGTGA  GT TTTCTTATTT
                                   AA  G
GAM892  LOC199692 3'  CTTGTTCTTCTGCTGTAGTGTG 59926       C  TCCCA
                                TACAC AC    AGAAGAATAAG
                                ||||| ||    ||||||||||
                                GTGTG TG    TCTTCTTGTTC
                                   A  TCG__
GAM892  LOC203414 3'  CTTGTCAACTGGGGGTGATGTG 90913      C       A AA  A
                                TACA CACTCCCA G  GA TAAG
                                |||| |||||||| |  || ||||
                                GTGT GTGGGGGT C  CT GTTC
                                   A       _ AA  _
GAM892  LOC222256 3'  TTTTTCTTGTGGTGT       95915        TCCC
                                ACACCAC    AAGAAGAA
                                |||||||    ||||||||
                                TGTGGTG    TTCTTTTT
                                           ____
GAM892  LOC257051 3'  TTTATTCTTTGTGAAAGTGGT  98054       CC  A
                                ACCACT  CA GAAGAATAAG
                                ||||||  || ||||||||||
                                TGGTGA  GT TTTCTTATTT
                                   AA  G
GAM892  LOC92303  3'  TTATTTTTTTTGAGGTGG    69400       CC
                                CCACT  CAAGAAGAATAA
                                |||||  ||||||||||||
                                GGTGG  GTTTTTTTTATT
                                   A_
GAM893  AQP5     5'  CAGCCAGGCCCCCGCCC     9718     A  A  T
                                GG GC GG GCCTGGCTG
                                || || || |||||||||
                                CC CG CC CGGACCGAC
                                 _  C  C
GAM893  ARNT2    3'  CAGAGACACAGAGGCACCTGCC 30083    A        GGC    C
          C                      GG GCAGGTGCCT   TGTC CTG
                                || ||||||||||   |||| |||
                                CC CGTCCACGGA   ACAG GAC
                                 _        GAC    A
GAM893  CARD15   3'  GGACAGCCCCTCCTCC      42471      C   TGCCT
                                GGAG AGG    GGCTGTCC
                                |||| |||    ||||||||
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                                CCTC TCC    CCGACAGG
                                  C  _____
GAM893  COLQ    3'  GGACAGCCTTGGCTGGCTCC  55425     AGGT  T_
                                GGAGC   GCC  GGCTGTCC
                                |||||   |||  ||||||||
                                CCTCG   CGG  CCGACAGG
                                   GT__  TT
GAM893  EYA1    5'  GCGGCCAGGCGCCTGCCC   6697    A
                                GG GCAGGTGCCTGGCTGT
                                || ||||||||||||||||
                                CC CGTCCGCGGACCGGCG
                                 _
GAM893  G6PD    5'  CAGCCCAGGCGCCCGCCC   6385    A  A      _
                                GG GC GGTGCCTGG CTG
                                || || ||||||||| |||
                                CC CG CCGCGGACC GAC
                                 _ C       C
GAM893  HD      3'  CAGAGACATGGGCCTCCCACTC 10907    CA  T_   GC   C
          C                      GGAG  GG  GCCTG  TGTC CTG
                                ||||  ||  |||||  |||| |||
                                CCTC  CC  CGGGT  ACAG GAC
                                  AC  TC    __   A
GAM893  KIF5A   5'  AGAGACTGAGCACCTGTCC   18373    G     CTGGCT  C
                                GGA CAGGTGC     GTC CT
                                ||| |||||||     ||| ||
                                CCT GTCCACG     CAG GA
                                  _      AGT___  A
GAM893  LYN     5'  CAGAGACAGCCAGTTCCTCTCC 11402    C  TGC       C
                                GGAG AGG   CTGGCTGTC CTG
                                |||| |||   ||||||||| |||
                                CCTC TCC   GACCGACAG GAC
                                  _  TT_       A
GAM893  MAPRE3  3'  CAGCCAGCCACCTGCTCC   25596         C
                                GGAGCAGGTG CTGGCTG
                                |||||||||| |||||||
                                CCTCGTCCAC GACCGAC
                                      C
GAM893  NEUROD2 3'  CAGGGACACCCCCATCCTACC  21593   _  CA   CCT  C
                                GG AG  GGTG   GG TGTCCCTG
                                || ||  ||||   || ||||||||
                                CC TC  CTAC   CC ACAGGGAC
                                 A  __   C__  C
GAM893  PACSIN1 3'  CAGGCTGCCGGCACCTGCCC  93878   A       T  TGTC
                                GG GCAGGTGCC GGC    CCTG
                                || |||||||| |||    ||||
                                CC CGTCCACGG CCG    GGAC
                                 _       _  TC__
GAM893  PCDH9   5'  CAGGGACAATGGGACCCCTCC  83691     CA  G   GC
                                GGAG  GGT CCTG  TGTCCCTG
                                ||||  ||| ||||  ||||||||
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                                CCTC  CCA GGGT  ACAGGGAC
                                  C_  _   A_
GAM893  PTPN1    3'  AGGGACACCCCCCGCCC    12573    A  A  TGCCT  C
                                GG GC GG    GG TGTCCCT
                                || || ||    || |||||||
                                CC CG CC    CC ACAGGGA
                                 _ C _____  C
GAM893  RAX      3'  AGGGACAACCCCCCTCC    26465     CA  TGCCT  C
                                GGAG  GG    GG TGTCCCT
                                ||||  ||    || |||||||
                                CCTC  CC    CC ACAGGGA
                                  C_ _____  A
GAM893  ROBO1    5'  CAGGGGTGCAGGCAGCTGCCC  56899    A   G     GC GT
                                GG GCAG TGCCTG  T  CCCTG
                                || |||| ||||||  |  |||||
                                CC CGTC ACGGAC  G  GGGAC
                                 _   G     __ TG
GAM893  SPOCK    5'  CAGCCGCAAGCACCTGCTCC   63471          C__
                                GGAGCAGGTGC   TGGCTG
                                ||||||||||   ||||||
                                CCTCGTCCACG   GCCGAC
                                      AAC
GAM893  VDR      3'  CAGGGACAGAGACACCTGCACC 6338     A      C  GG
                                GG GCAGGTG CT  CTGTCCCTG
                                || ||||||| ||  |||||||||
                                CC CGTCCAC GA  GACAGGGAC
                                 A      A __
GAM893  C20orf110 3'  CAGAGAGGCCAAACCCTGCTCC 80361        TGCC    G  C
                                GGAGCAGG    TGGCT TC CTG
                                ||||||||    ||||| || |||
                                CCTCGTCC    ACCGG AG GAC
                                     CAA_    _  A
GAM893  C20orf151 3'  CAGCCCAGCACCTGCTCC    90092          CT
                                GGAGCAGGTGC  GGCTG
                                ||||||||||  |||||
                                CCTCGTCCACG  CCGAC
                                      AC
GAM893  CCNE1    3'  GACAGTTGCGCGCCTGCTCC   55164          C
                                GGAGCAGGTGC TGGCTGTC
                                |||||||||| ||||||||
                                CCTCGTCCGCG GTTGACAG
                                      C
GAM893  CCNE1    3'  GACAGTTGCGCGCCTGCTCC   8790           C
                                GGAGCAGGTGC TGGCTGTC
                                |||||||||| ||||||||
                                CCTCGTCCGCG GTTGACAG
                                      C
GAM893  CLIPR-59  3'  GGACAGCTCACGACTGCCC   32018    A   __   CCT
                                GG GCAG  GTG   GGCTGTCC
                                || ||||  |||   ||||||||
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                                CC CGTC  CAC   TCGACAGG
                                 _    AG  ___
GAM893  DKFZp434C0923 3'  CAGCCAGGCCCCTGCTCC    34645        T
                                GGAGCAGG GCCTGGCTG
                                |||||||| |||||||||
                                CCTCGTCC CGGACCGAC
                                    C
GAM893  DKFZp547J036 3'  AGAGAGGGGGCACCTCC     51118     GCA     TGG  G  C
                                GGA   GGTGCC   CT TC CT
                                |||   ||||||   || || ||
                                CCT   CCACGG   GG AG GA
                                  ____    ____ G  A
GAM893  FLJ10813  3'  CAGAGATTCAGGCAGCCACTCC 37229      CA  _      CT   C
                                GGAG  GG TGCCTGG  GTC CTG
                                ||||  || |||||||  ||| |||
                                CCTC  CC ACGGACT  TAG GAC
                                  A_  G      __   A
GAM893  FLJ10898  5'  AGGAGAAAGCACCTTCTCC    60123      C     CTGGCTG  _
                                GGAG AGGTGC      TC CCT
                                |||| ||||||      || |||
                                CCTC TCCACG      AG GGA
                                  T     AA_____  A
GAM893  FLJ20200  5'  AGAGACAGCCAGACCCCC    35232    AGCA   GC       C
                                GG    GGT  CTGGCTGTC CT
                                ||    |||  |||||||||  ||
                                CC    CCA  GACCGACAG GA
                                 C___   __        A
GAM893  FLJ20464  3'  CAGGGACAGCAGCACCTGTCC  35691     G      CTG
                                GGA CAGGTGC   GCTGTCCCTG
                                ||| |||||||   ||||||||||
                                CCT GTCCACG   CGACAGGGAC
                                  _      A__
GAM893  FLJ21865  3'  AGGAAGCAGCACCTGCCC    43109    A      CTG   GTC
                                GG GCAGGTGC   GCT   CCT
                                || ||||||||   |||   |||
                                CC CGTCCACG   CGA   GGA
                                 _       A__   A__
GAM893  FLJ22477  3'  CAGCCCATGCACCTGCCC    45669    A      CT_
                                GG GCAGGTGC   GGCTG
                                || ||||||||   |||||
                                CC CGTCCACG   CCGAC
                                 _       TAC
GAM893  FLJ22578  3'  CAGGGACGGCCGCACCTGCCTC 46322      _      CT
          C                      GGAG CAGGTGC  GGCTGTCCCTG
                                |||| |||||||  ||||||||||
                                CCTC GTCCACG  CCGGCAGGGAC
                                  C      __
GAM893  HCNGP    3'  CAGGCAAGCCCTGCTCC     26071        T  C  G
                                GGAGCAGG GC TG CTG
                                |||||||| || || |||
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                                CCTCGTCC CG AC GAC
                                     _ A  G
GAM893  HSA243666 3'  CAACCAGCACCTGCCC     34555    A      C   C
                                GG GCAGGTGC TGG TG
                                || |||||||| ||| ||
                                CC CGTCCACG ACC AC
                                 _      _  A
GAM893  ISL2    3'  GACTGCAGACCCCTGCTCC   71399        TGC   G T
                                GGAGCAGG   CTG C GTC
                                ||||||||   ||| | |||
                                CCTCGTCC   GAC G CAG
                                     CCA   _ T
GAM893  KIAA0682  3'  CAGGGAGCTAGAACCCCTGCTC 33007        TGC_    TG
           C                     GGAGCAGG   CTGGC  TCCCTG
                                ||||||||   |||||  ||||||
                                CCTCGTCC   GATCG  AGGGAC
                                     CCAA   __
GAM893  KIAA1553  3'  GACAGCTGTGGCCCTCTCC   93566     C   T  _
                                GGAG AGG GCC TGGCTGTC
                                |||| ||| ||| ||||||||
                                CCTC TCC CGG GTCGACAG
                                  _  _  T
GAM893  KIAA1691  3'  CAGGGACACGTGCCACCTGCTC 94125         CCTG  _
                                GAGCAGGTG   GC TGTCCCTG
                                |||||||||   || ||||||||
                                CTCGTCCAC   TG ACAGGGAC
                                     CG__  C
GAM893  KIAA1866  3'  GACAGCCAGCGTGCTC     61588      G TGC
                                GAGCA G   CTGGCTGTC
                                ||||| |   |||||||||
                                CTCGT C   GACCGACAG
                                   G ___
GAM893  MGC21621  3'  AGGAATGGGCACCTGCTTC   59439           GCTGTC
                                GGAGCAGGTGCCTG     CCT
                                ||||||||||||||     |||
                                CTTCGTCCACGGGT     GGA
                                       AA____
GAM893  MY050    3'  AGGAAAAGAGGCCCTGCTCC   51916        T   GG  GTC
                                GGAGCAGG GCCT  CT   CCT
                                |||||||| ||||  ||   |||
                                CCTCGTCC CGGA  GA   GGA
                                     _   __ AAA
GAM893  MYT1L    5'  CAGCCCCAGGAACCTGCTCC   67363         G  __
                                GGAGCAGGT CCT  GGCTG
                                ||||||||| |||  |||||
                                CCTCGTCCA GGA  CCGAC
                                     A   CC
GAM893  OS4     3'  AGGGACACCACCCACTCA    20380   A   CC   C
                                C GGTG  TGG TGTCCCT
                                | ||||  ||| |||||||
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                                A TCAC  ACC ACAGGGA
                                 C    CC  _
GAM893  RAB40C   3'  GACACTGGCCTCCTGCTCC   41282        T_  T  C
                                GGAGCAGG  GCC GG TGTC
                                ||||||||  ||| || ||||
                                CCTCGTCC  CGG TC ACAG
                                     TC  _ _
GAM893  RSP3     5'  GGACAGCCACCGTTGCCCC   50013    A  __  GCCT
                                GG GCA  GGT   GGCTGTCC
                                || |||  |||   ||||||||
                                CC CGT  CCA   CCGACAGG
                                 C  TG  ____
GAM893  SIAT4B   5'  CAGGGACAGGACAGCCACTCC  23633   A   C   G_
                                C GGTG CTG  CTGTCCCTG
                                | |||| |||  |||||||||
                                C TCAC GAC  GACAGGGAC
                                 C   C   AG
GAM893  SPR1     3'  CAGGCATCTCCAGGCACCCACG 26811    AGCA       CT  C
           CC                     GG   GGTGCCTGG  GT CCTG
                                ||   |||||||||  || ||||
                                CC   CCACGGACC  TA GGAC
                                 GCAC       TC  C
GAM893  LOC121036 3'  CAGGAACAGCCAGGGGACCTCA 74480   C   G  _     C
                                G AGGT CC TGGCTGT CCTG
                                | |||| || ||||||| ||||
                                A TCCA GG ACCGACA GGAC
                                 C   G  G      A
GAM893  LOC123242 3'  CAGAGCCAGCAGGCACCGACCC 76110    AGCA      G   TCC
                                GG   GGTGCCTG CTG   CTG
                                ||   |||||||| |||   |||
                                CC   CCACGGAC GAC   GAC
                                 CAG_       _  CGA
GAM893  LOC127841 5'  CAGAACCCAGGCACTGCTCC   75185        G     ___
                                GGAGCAG TGCCTGG   CTG
                                ||||||| |||||||   |||
                                CCTCGTC ACGGACC   GAC
                                     _      CAA
GAM893  LOC142927 3'  AGAGAAGAAGCACCTGTCC   76941     G     CTGG  G  C
                                GGA CAGGTGC   CT TC CT
                                ||| |||||||   || || ||
                                CCT GTCCACG   GA AG GA
                                  _      AA__  _  A
GAM893  LOC145757 3'  CAGCCCAGGCACCTCCTCC   77918      C        _
                                GGAG AGGTGCCTGG CTG
                                |||| |||||||||| |||
                                CCTC TCCACGGACC GAC
                                  C        C
GAM893  LOC147669 5'  CAGAGGTTCAGGCACCTGCCC  85176    A         CTGT  _
                                GG GCAGGTGCCTGG   CC CTG
                                || ||||||||||||   || |||
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                                CC CGTCCACGGACT    GG GAC
                                 _          T___  A
GAM893   LOC149653 3'  CAGGGAGCGAGACAGCTGCCC  85708    A   G  C  G  TG
                                GG GCAG TG CT GC  TCCCTG
                                || |||| || || ||  ||||||
                                CC CGTC AC GA CG  AGGGAC
                                 _   G  A  G  __
GAM893   LOC200078 3'  CAGCTCCAGGACCTGCCC    89979    A     G   __
                                GG GCAGGT CCTG  GCTG
                                || |||||| ||||  ||||
                                CC CGTCCA GGAC  CGAC
                                 _     _   CT
GAM893   LOC200081 3'  CAGGGACAGCCAGGCACCTGCT 89972
                   CC                  GGAGCAGGTGCCTGGCTGTCCCTG
                                ||||||||||||||||||||||||
                                CCTCGTCCACGGACCGACAGGGAC

GAM893   LOC200609 3'  AGCTGAATGCCAGGCACCCACA 91657    AGCA       TG  C_
                   CC                  GG   GGTGCCTGGC  TC  CT
                                ||   ||||||||||  ||  ||
                                CC   CCACGGACCG  AG  GA
                                 ACAC        TA  TC
GAM893   LOC221178 3'  GACAGCCAAAGCAGTCCTGCTT 95171        __  C_
                   C                   GGAGCAGG  TGC  TGGCTGTC
                                ||||||||  |||  ||||||||
                                CTTCGTCC  ACG  ACCGACAG
                                     TG   AA
GAM893   LOC221486 3'  CAGCCCAGCACCTGCTCC    92655          CT
                                GGAGCAGGTGC  GGCTG
                                ||||||||||  |||||
                                CCTCGTCCACG  CCGAC
                                       AC
GAM893   LOC253001 3'  CAGAGCCAGCAGGCACCGACCC 97989    AGCA      G   TCC
                                GG   GGTGCCTG CTG   CTG
                                ||   |||||||| |||   |||
                                CC   CCACGGAC GAC   GAC
                                 CAG_       _   CGA
GAM893   LOC254115 5'  CAGGGACAGCCACCGGCACT   96371       __
                                GGTGCC  TGGCTGTCCCTG
                                ||||||  ||||||||||||
                                TCACGG  ACCGACAGGGAC
                                   CC
GAM893   LOC254848 5'  CAGAGAAGGCACCTGGTCC    98879     G       GG_
                                GGA CAGGTGCCT   CTG
                                ||| |||||||||   |||
                                CCT GTCCACGGA   GAC
                                  G        AGA
GAM893   LOC255480 3'  CAGGGACCCCAGACACCTTGCT 98285       _   C    CT
                   CC                  GGAGCA GGTG CTGG  GTCCCTG
                                ||||||| |||| ||||  |||||||
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                                CCTCGT CCAC GACC  CAGGGAC
                                   T   A   C_
GAM893  LOC256158 5'  GGACAGCCAGGCCCTCTCC   99500     C   T
                                GGAG AGG GCCTGGCTGTCC
                                |||| ||| ||||||||||||
                                CCTC TCC CGGACCGACAGG
                                  _  _
GAM893  LOC256158 5'  GGACGGGGCCCTGCTCC    99501       T  TGG
                                GGAGCAGG GCC  CTGTCC
                                |||||||| |||  ||||||
                                CCTCGTCC CGG  GGCAGG
                                   _  ___
GAM893  LOC257458 5'  CAGCCCAAGCACCTGCTGC   68399   G      CT_
                                G AGCAGGTGC  GGCTG
                                | |||||||||  |||||
                                C TCGTCCACG  CCGAC
                                 G       AAC
GAM894  CUBN    3'  TACACTCCAGCCTGGGCGA   8423      GATCAA   CA__
                                TCGCCCA    GGCT   TGTA
                                |||||||    ||||   ||||
                                AGCGGGT    CCGA   ACAT
                                   _______  CCTC
GAM894  DPT     3'  ACATACCAAATCTGGGTGA   60073       CAA  CTC
                                TCGCCCAGAT  GG  ATGT
                                ||||||||||  ||  ||||
                                AGTGGGTCTA  CC  TACA
                                     AA_  A__
GAM894  NAV2    3'  CAGAAGCCCCGTCTGGACGA  60790    C    CAA   CA
                                TCG CCAGAT  GGCT  TG
                                ||| ||||||  ||||  ||
                                AGC GGTCTG  CCGA  AC
                                  A    CC_   AG
GAM894  VHL     3'  CTGCACTCTAACCTGGGCGA  6854       ATCA  CTCA
                                TCGCCCAG   AGG   TGTAG
                                ||||||||   |||   |||||
                                AGCGGGTC   TCT   ACGTC
                                    CAA_  C___
GAM894  ZNF91   3'  CTGCACTCAAGCCTGGGCGA  14281     GATCAA   CA__
                                TCGCCCA    GGCT   TGTAG
                                |||||||    ||||   |||||
                                AGCGGGT    CCGA   ACGTC
                                   _______  ACTC
GAM894  ARNTL2  3'  CTGCACCCCAGCCTGGGCGA  39847     GATCAA   CA__
                                TCGCCCA    GGCT   TGTAG
                                |||||||    ||||   |||||
                                AGCGGGT    CCGA   ACGTC
                                   _______  CCCC
GAM894  C20orf175 3'  TACATTTCAGCCTGGGCGA  55929     GATCAA   C__
                                TCGCCCA    GGCT   ATGTA
                                |||||||    ||||   |||||
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                                AGCGGGT    CCGA  TACAT
                                   _____   CTT
GAM894  DKFZP586C1324 3' CTGCACTCAAGTCTGGGCGA  70357        CAA  CTCA
                                TCGCCCAGAT  GG   TGTAG
                                ||||||||||  ||   |||||
                                AGCGGGTCTG  TC   ACGTC
                                     AAC ____
GAM894  FLJ14768  3' GACCTTGATCTGGAGA    52675   GC       C
                                TC  CCAGATCAAGG TC
                                ||  |||||||||| ||
                                AG  GGTCTAGTTCC AG
                                 A_       _
GAM894  FLJ22692  3' CTGCACTTGAGCCTGGGCGA  47482      GATCAA    __
                                TCGCCCA    GGCTCA  TGTAG
                                |||||||    ||||||  |||||
                                AGCGGGT    CCGAGT  ACGTC
                                   _____    TC
GAM894  KIAA1503  3' TACACTCCAGCCTGGGCGA  68899      GATCAA   CA__
                                TCGCCCA    GGCT   TGTA
                                |||||||    ||||   ||||
                                AGCGGGT    CCGA   ACAT
                                   _____   CCTC
GAM894  MSC     3' CTACAGCTGCGCCGGATCTGGG 76839         AA  T __
           CGA                  TCGCCCAGATC  GGC CA  TGTAG
                                ||||||||||  ||| ||  |||||
                                AGCGGGTCTAG  CCG GT  ACATC
                                     G_  C  CG
GAM894  LOC122704 3'  CATTGCACTCCAACCTGGGCGA 74603       ATCA_ _  TC
                                TCGCCCAG    AG GC  ATG
                                ||||||||    || ||  |||
                                AGCGGGTC    TC CG  TAC
                                    CAACC  A  T_
GAM894  LOC146229 3'  TACACTCCAGCCTGGGCGA   78308      GATCAA   CA__
                                TCGCCCA    GGCT   TGTA
                                |||||||    ||||   ||||
                                AGCGGGT    CCGA   ACAT
                                   _____   CCTC
GAM894  LOC146475 5'  CTGCACTCAAGCCTGGGCGA  84690      GATCAA   CA__
                                TCGCCCA    GGCT   TGTAG
                                |||||||    ||||   |||||
                                AGCGGGT    CCGA   ACGTC
                                   _____   ACTC
GAM894  LOC147837 3'  TGCACCCCAGCCTGGGCGA   79212      GATCAA   CA__
                                TCGCCCA    GGCT   TGTA
                                |||||||    ||||   ||||
                                AGCGGGT    CCGA   ACGT
                                   _____   CCCC
GAM894  LOC154739 5'  CGTAGCCATCAATCTGGGC   87437       CAA_   C
                                GCCCAGAT   GGCT ATG
                                ||||||||   |||| |||
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                                CGGGTCTA   CCGA TGC
                                    ACTA   _
GAM894  LOC203276 3'  CATAGCCATCGATCTGGGC   92113        AA_   C
                                GCCCAGATC   GGCT ATG
                                |||||||||   |||| |||
                                CGGGTCTAG   CCGA TAC
                                    CTA   _
GAM894  LOC203305 3'  CATAGCCATCGATCTGGGC   92166        AA_   C
                                GCCCAGATC   GGCT ATG
                                |||||||||   |||| |||
                                CGGGTCTAG   CCGA TAC
                                    CTA   _
GAM894  LOC254243 3'  CATAGCCATCGATCTGGGC   99252        AA_   C
                                GCCCAGATC   GGCT ATG
                                |||||||||   |||| |||
                                CGGGTCTAG   CCGA TAC
                                    CTA   _
GAM894  LOC90038  3'  CATAGCCATCGATCTGGGC   61795        AA_   C
                                GCCCAGATC   GGCT ATG
                                |||||||||   |||| |||
                                CGGGTCTAG   CCGA TAC
                                    CTA   _
GAM895  FLRT2     3'  GGATGCTTCACTTGATCTCCGG 26002      A      CGT  _
                                CCGGA GATCAAGT   GC TCC
                                ||||| ||||||||   || |||
                                GGCCT CTAGTTCA   CG AGG
                                  _      CTT  T
GAM895  NEDD4L    3'  GAGACTTGACTTGATCCTCTGA 31604    C   A       TG_
          GC                      GC CGGA GATCAAGTCG   CTC
                                || |||| ||||||||||   |||
                                CG GTCT CTAGTTCAGT   GAG
                                 A   C        TCA
GAM895  NUP98     3'  GGAGGGATTGATCTTCAGGGC  33326     G       G  GTG
                                GCCC GAAGATCAA TC   CTCC
                                |||| ||||||||| ||   ||||
                                CGGG CTTCTAGTT AG   GAGG
                                  A       _ G__
GAM895  PTGIS     3'  ATGGTCTTGATCTCCTGAGC   8194     C   A      _
                                GC CGG AGATCAAG TCGT
                                || ||| |||||||| ||||
                                CG GTC TCTAGTTC GGTA
                                 A   C       T
GAM895  B7-H1     3'  GAACTTCTGATCTTCAAGC    27096    CCG      A TC  GC
                                GC   GAAGATCA G  GT  TC
                                ||   |||||||| |  ||  ||
                                CG   CTTCTAGT C  CA  AG
                                 AA_       _ TT  __
GAM895  CIC       3'  GGAGCGTGTGACCTTCAGAGC  31369    CCG   A   AGT
                                GC   GAAG TCA   CGTGCTCC
                                ||   |||| |||   ||||||||
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                                CG   CTTC AGT   GTGCGAGG
                                 AGA    C  ___
GAM895  DKFZP434C1715 3'  GGAGCACGACTGTGTCCC    87354    AA   CA
                                GG  GAT  AGTCGTGCTCC
                                ||  |||  ||||||||||
                                CC  CTG  TCAGCACGAGG
                                 __   TG
GAM895  FLJ10094  5'  GAACACATTTGTCTTCTGAGC  36295    C      T    C  C
                                GC CGGAAGA CAAGT GTG TC
                                || ||||||| ||||| ||| ||
                                CG GTCTTCT GTTTA CAC AG
                                 A      _    _  A
GAM895  ICAM4    3'  GAGCACGACCCTGTCTCC    9541      A   CAA
                                GGA GAT   GTCGTGCTC
                                ||| |||   |||||||||
                                CCT CTG   CAGCACGAG
                                  _   TCC
GAM895  ICAM4    3'  GAGCACGACCCTGTCTCC    9542      A   CAA
                                GGA GAT   GTCGTGCTC
                                ||| |||   |||||||||
                                CCT CTG   CAGCACGAG
                                  _   TCC
GAM895  KIAA0913  5'  GGAGCACGACCTGTTTGCTGGG 69533        A   T  A
            C                    GCCCGG AGA CA GTCGTGCTCC
                                ||||||| ||| || ||||||||||
                                CGGGTC TTT GT CAGCACGAGG
                                   G   _  C
GAM895  KIAA1274  5'  GGAGCACGGATGCCCCCCGGAG 93012    _    AAGATCAAG
            C                    GC CCGG        TCGTGCTCC
                                || ||||        |||||||||
                                CG GGCC        GGCACGAGG
                                 A   CCCCGTA__
GAM895  KIAA1656  3'  GGAGCAAGGCATGATCCCCAAG 66373     C_  AA     A   G
            GC                     GCC  GG  GATCA GTC TGCTCC
                                ||| ||  ||||| ||| ||||||
                                CGG  CC  CTAGT CGG ACGAGG
                                  AA  C_    A   A
GAM895  SLC26A1   3'  GGAACAAGGGGTCTTCCGAGC  57054    C       AAGTCG  C
                                GC CGGAAGATC      TG TCC
                                || |||||||||      || |||
                                CG GCCTTCTGG      AC AGG
                                 A        GGA___  A
GAM895  SRPK1    3'  GATCTTGATCTTCCAGGT    13407     C        _
                                GCC GGAAGATCAAG TC
                                ||| ||||||||||| ||
                                TGG CCTTCTAGTTC AG
                                  A          T
GAM895  LOC158856 5'  GCGACTTGACTTTCCAGGC    88290     C    A
                                GCC GGAAG TCAAGTCGT
                                ||| ||||| |||||||||
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                                CGG CCTTT AGTTCAGCG
                                  A    C
GAM896  AP2A1    3'  TCCTCCCCTCCCACCCCA    56305          CA  A
                                TGGGGTGGGAG  GA GGA
                                ||||||||||  || |||
                                ACCCCACCCTC  CT CCT
                                     CC  _
GAM896  AQP6     5'  GCCCCCACATCCCACCCCA   55006          GCAGAA  AA
                                TGGGGTGGGA     GG  GGC
                                ||||||||||     ||  |||
                                ACCCCACCCT     CC  CCG
                                     ACA___  C_
GAM896  AQP6     5'  GCCCCCACATCCCACCCCA   55007          GCAGAA  AA
                                TGGGGTGGGA     GG  GGC
                                ||||||||||     ||  |||
                                ACCCCACCCT     CC  CCG
                                     ACA___  C_
GAM896  ATRN     3'  GCCCCCTGCCCCCACCCC    24857         A   AA  AA
                                GGGGTGGG GCAG  GG  GGC
                                |||||||| ||||  ||  |||
                                CCCCACCC CGTC  CC  CCG
                                    C   __  __
GAM896  BAIAP3   3'  AGCCCCGGCCCTGGCCCCCACC 15438          A  AGAA  AA__
           CCA                    TGGGGTGGG GC   GG   GGCT
                                ||||||||| ||   ||   ||||
                                ACCCCACCC CG   CC   CCGA
                                     C  GTC_  GGCC
GAM896  CLN6     3'  TCCCCCTGCTCCCACTCCA   35839           AA
                                TGGGGTGGGAGCAG  GGA
                                ||||||||||||||  |||
                                ACCTCACCCTCGTC  CCT
                                       CC
GAM896  COX10    3'  AGCCGGATACCTCTGGCCCCCA 8944          A  _  A  AA___
           CCCCA                    TGGGGTGGG GC AGA GG    GGCT
                                ||||||||| || ||| ||    ||||
                                ACCCCACCC CG TCT CC    CCGA
                                     C  G  _  ATAGG
GAM896  CST2     3'  CCTCCTACTCCCACCCC     8996          CAGA   A
                                GGGGTGGGAG   AGGA GG
                                ||||||||||   |||| ||
                                CCCCACCCTC   TCCT CC
                                     A___   _
GAM896  DAAM2    3'  AGCCTCTCCCTACTCCCATCCC 93899          C  AA  _
           A                     TGGGGTGGGAG AG  GGA AGGCT
                                ||||||||||| ||  ||| |||||
                                ACCCTACCCTC TC  CCT TCCGA
                                      A  __  C
GAM896  DCTN1    5'  AGCCCCCATCACTGCCCCCACC 43757         A   AA__  AA
           CC                     GGGGTGGG GCAG   GG  GGCT
                                |||||||| ||||   ||  ||||
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                                CCCCACCC CGTC    CC  CCGA
                                     C    ACTA  C_
GAM896  DVL3     3'  AGCTCCATTCCGCTCCCACCCC 16636          A  _  AG
              A                   TGGGGTGGGAGC GAA GGA  GCT
                                  |||||||||||| ||| |||  |||
                                  ACCCCACCCTCG CTT CCT  CGA
                                        C   A  __
GAM896  DXF68S1E 3'  GTCTTCCGCCCCCAGCCCA   60664     G    A  AGAA
                                  TGGG TGGG GC    GGAAGGC
                                  |||| |||| ||    |||||||
                                  ACCC ACCC CG    CCTTCTG
                                    G    C ____
GAM896  ELAVL3   3'  TCCTCCTGCCCCCACCCCA   9228          A    A
                                  TGGGGTGGG GCAG AGGA
                                  |||||||| |||| ||||
                                  ACCCCACCC CGTC TCCT
                                       C    C
GAM896  FBLN1    3'  AGCTGTACCTGCCCCACCCCA  22413         A    AAGGAA
                                  TGGGGTGGG GCAG     GGCT
                                  |||||||| ||||     ||||
                                  ACCCCACCC CGTC     TCGA
                                       _    CATG__
GAM896  FGFR1    5'  AGCCCTCCCCCCCGCCCCGCCTC 7013         A  AGAA   A
                                  GGGGTGGG GC    GGA GGCT
                                  |||||||| ||    ||| ||||
                                  CTCCGCCC CG    CCT CCGA
                                       _ CCCC   C
GAM896  FGFR1    5'  AGCCCTCCCCCCCGCCCCGCCTC 7014         A  AGAA   A
                                  GGGGTGGG GC    GGA GGCT
                                  |||||||| ||    ||| ||||
                                  CTCCGCCC CG    CCT CCGA
                                       _ CCCC   C
GAM896  FLOT1    3'  AGCCTTCTGATGATCCCACTCC 20542          G  GAA
              A                   TGGGGTGGGA CA   GGAAGGCT
                                  |||||||||| ||   ||||||||
                                  ACCTCACCCT GT   TCTTCCGA
                                        A  AG_
GAM896  GAS      3'  AGCCTAGCCACCTCCCACCCCA 7689          CAGAA  A_
                                  TGGGGTGGGAG    GG  AGGCT
                                  ||||||||||     ||  |||||
                                  ACCCCACCCTC    CC  TCCGA
                                        CA___  GA
GAM896  GLI2     5'  AGCCTTCACCTTCCCCCACCCC 48289         AGCA    __
              A                   TGGGGTGGG   GAAGG  AAGGCT
                                  |||||||||   |||||  ||||||
                                  ACCCCACCC   CTTCC  TTCCGA
                                       C___    AC
GAM896  HCFC1    3'  TTTTCTGCCCCCCACCCCA   71551         A_
                                  TGGGGTGGG  GCAGAAGG
                                  |||||||||  ||||||||
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                                ACCCCACCC  CGTCTTTT
                                     CC
GAM896  HOXC4    3'  CCCCTGCCCCCACCCCA     28244         A    AA
                                TGGGGTGGG GCAG  GG
                                ||||||||| ||||  ||
                                ACCCCACCC CGTC  CC
                                     C   C_
GAM896  KCNC3    3'  AGCCTCCCTCCCCCCCCACCCC 18328         AGCA  A   A
                                GGGGTGGG   GA GGA GGCT
                                ||||||||   || ||| ||||
                                CCCCACCC   CT CCT CCGA
                                    CCCC  C  _
GAM896  KPNB1    5'  CCCCCGCCCCCCCACCCCA    11218         A_  AGAA  AA
                                TGGGGTGGG  GC   GG  GG
                                |||||||||  ||   ||  ||
                                ACCCCACCC  CG   CC  CC
                                     CC  _____  C_
GAM896  LRP4     3'  TCCTCCTCCTCCCACCCCA   65065          C  A
                                TGGGGTGGGAG AG AGGA
                                |||||||||||  || ||||
                                ACCCCACCCTC TC TCCT
                                      C  C
GAM896  MAP3K10  5'  GCCGCCCCACTCCCACCCC   68583          CAGAA  AA
                                GGGGTGGGAG    GG  GGC
                                ||||||||||    ||  |||
                                CCCCACCCTC    CC  CCG
                                     AC___  CG
GAM896  MAP3K12  3'  AGCCCCTTCCTGCCCCACCCCA 21942         A   _   AA
                                TGGGGTGGG GCAG AAGG  GGCT
                                ||||||||| |||| ||||  ||||
                                ACCCCACCC CGTC TTCC  CCGA
                                     _   C   __
GAM896  MSN      3'  GCCCCTTAGCCCCCACCC    60882        A  AG   AA
                                GGGTGGG GC  AAGG  GGC
                                ||||||| ||  ||||  |||
                                CCCACCC CG  TTCC  CCG
                                    C  A_   __
GAM896  NGB      3'  GGCCCCCGCCCTCACCCCA   41465         A  AGAA  AA
                                TGGGGTGGG GC   GG  GGCT
                                ||||||||| ||   ||  ||||
                                ACCCCACTC CG   CC  CCGG
                                     C  _____  C_
GAM896  NGFR     3'  AGCCCCTCTTGCCCCCCACCCC 11787         A_  GA  AA
           A                     TGGGGTGGG  GCA  AGG  GGCT
                                 |||||||||  |||  |||  ||||
                                 ACCCCACCC  CGT  TCC  CCGA
                                      CC   TC  __
GAM896  NRGN     3'  CCTTCCACTCCACCCCA     21623         G  CA
                                TGGGGTGG AG  GAAGG
                                |||||||| ||  |||||
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                                ACCCCACC TC  CTTCC
                                     _ AC
GAM896  NRXN2    3'  AGCCCTCCAATCCCCATCCCA  57818        AGCAGAA  A
                                TGGGGTGGG     GGA GGCT
                                |||||||||     ||| ||||
                                ACCCTACCC     CCT CCGA
                                     CTAA___  C
GAM896  PABPN1   3'  AGCCAGGTCTACCACCCACCCC 17354        AGC_  AGGAA
                                GGGGTGGG   AGA   GGCT
                                ||||||||   |||   ||||
                                CCCCACCC   TCT   CCGA
                                     ACCA  GGA__
GAM896  PAK4     3'  AGCCCCCCGGGTCACCCCCGCC 20825        A___  AGAA  AA
           CCA                    TGGGGTGGG   GC   GG  GGCT
                                |||||||||   ||   ||  ||||
                                ACCCCGCCC   TG   CC  CCGA
                                     CCAC  GG__  CC
GAM896  PHB      3'  AGCCTTCCTTCTGCTCCCACCC 12068
           CA                     TGGGGTGGGAGCAGAAGGAAGGCT
                                |||||||||||||||||||||||
                                ACCCCACCCTCGTCTTCCTTCCGA

GAM896  PML      3'  AGCCTTCCATGCCCCGACCCCC 53795        A______  GAA
           ACCCCA                 TGGGGTGGG     GCA  GGAAGGCT
                                |||||||||     |||  ||||||||
                                ACCCCACCC     CGT  CCTTCCGA
                                     CCAGCCC  A__
GAM896  PML      3'  AGCCTTCCATGCCCCGACCCCC 53796        A______  GAA
           ACCCCA                 TGGGGTGGG     GCA  GGAAGGCT
                                |||||||||     |||  ||||||||
                                ACCCCACCC     CGT  CCTTCCGA
                                     CCAGCCC  A__
GAM896  PML      3'  AGCCTTCCATGCCCCGACCCCC 53797        A______  GAA
           ACCCCA                 TGGGGTGGG     GCA  GGAAGGCT
                                |||||||||     |||  ||||||||
                                ACCCCACCC     CGT  CCTTCCGA
                                     CCAGCCC  A__
GAM896  PML      3'  AGCCTTCCATGCCCCGACCCCC 53798        A______  GAA
           ACCCCA                 TGGGGTGGG     GCA  GGAAGGCT
                                |||||||||     |||  ||||||||
                                ACCCCACCC     CGT  CCTTCCGA
                                     CCAGCCC  A__
GAM896  RANBP3   3'  GCCCACCCGCCCCCACCCCA  24633        A  AGAA  AA
                                TGGGGTGGG GC   GG  GGC
                                ||||||||| ||   ||  |||
                                ACCCCACCC CG   CC  CCG
                                     C  C___  AC
GAM896  RPS6KA1  3'  GCCTCCAGCCCCCACCCCA   60043        A  AGAA  A
                                TGGGGTGGG GC   GGA GGC
                                ||||||||| ||   ||| |||
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                                ACCCCACCC CG   CCT CCG
                                    _ A___  _
GAM896  RYR1    3'  AGCTGGCCCTCCACCCCCACCT 6770        AGCA  A  AA
          CA                    TGGGGTGGG   GA GG  GGCT
                                |||||||||   || ||  ||||
                                ACTCCACCC   CT CC  TCGA
                                    CCAC  C  GG
GAM896  SEPN1   3'  GCCGCCCACTCCCACCCCA   66974         CAGAA  AA
                                TGGGGTGGGAG   GG  GGC
                                ||||||||||    ||  |||
                                ACCCCACCCTC   CC  CCG
                                     A____  CG
GAM896  SLC21A3  3'  CCCCCCTTCCCCCACCCCA   18653        AGCA    AA
                                TGGGGTGGG   GAAGG  GG
                                |||||||||   |||||  ||
                                ACCCCACCC   CTTCC  CC
                                    C___    CC
GAM896  SMARCB1  3'  AGCCCCAGTCCTGCCCCCCACC 66186        A_   AA__  AA
          CCA                   TGGGGTGGG  GCAG   GG  GGCT
                                |||||||||  ||||   ||  ||||
                                ACCCCACCC  CGTC   CC  CCGA
                                    CC   CTGA  __
GAM896  SPTBN2   3'  AGCCCTCCCTCCCCACCCC   23690       AGCA  A   A
                                GGGGTGGG   GA GGA GGCT
                                ||||||||   || ||| ||||
                                CCCCACCC   CT CCT CCGA
                                    _____  C   C
GAM896  TNFRSF7  3'  AGCCCTGGCCTCCACCCCCACC 8793        AGCA  A  AA__
          CC                    GGGGTGGG   GA GG   GGCT
                                ||||||||   || ||   ||||
                                CCCCACCC   CT CC   CCGA
                                    CCAC  _  GGTC
GAM896  TNFSF4   3'  CCCTCCCGCCCCCACCCC   13911       A  AGAA   A
                                GGGGTGGG GC   GGA GG
                                |||||||| ||   ||| ||
                                CCCCACCC CG   CCT CC
                                    C  C___   C
GAM896  WDR1    3'  GCCCCCATGCCCCCCACCCCA  18848        A   GAA  AA
                                TGGGGTGGG GCA   GG  GGC
                                ||||||||| |||   ||  |||
                                ACCCCACCC CGT   CC  CCG
                                    C   AC_  __
GAM896  ABT1    3'  AGCCCCCCTCCCCCTGCCACCC 26298      G  CAGA   AA
                                GGGTGG AG   AGG  GGCT
                                ||||||  ||   |||  ||||
                                CCCACC TC   TCC  CCGA
                                   G  CCCC   CC
GAM896  AF9Q34   3'  AGCAGAGGCCCTGCCCCCACCC 51711        A   AA  AAG__
          C                     GGGGTGGG GCAG  GG    GCT
                                ||||||||  ||||  ||    |||
```

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                                CCCCACCC CGTC  CC    CGA
                                     C   __ GGAGA
GAM896  AKAP6    3'  GCCTCAATCTCCCACCCCA   16250          CAGAAG  A
                                TGGGGTGGGAG     GA GGC
                                ||||||||||      || |||
                                ACCCCACCCTC     CT CCG
                                     TAA___  _
GAM896  APCL     3'  GCCTCCCACCCCCACCCCG   20818         AGCAGAA   A
                                TGGGGTGGG      GGA GGC
                                |||||||||      ||| |||
                                GCCCCACCC      CCT CCG
                                     CCAC___   _
GAM896  APEG1    3'  GCCTCCCCTCCCCACCCCA   72595         AGCA  A  A
                                TGGGGTGGG    GA GG AGGC
                                |||||||||    || || ||||
                                ACCCCACCC    CT CC TCCG
                                     ____  C  C
GAM896  C11orf25 5'  TCTTCTGCTCCCACTCCCA   49468      _
                                TGGG GTGGGAGCAGAAGG
                                |||| ||||||||||||||
                                ACCC CACCCTCGTCTTCT
                                  T
GAM896  C19orf7  3'  AGGCTCCTATCCCACCCCA   61775         GCAGA    A G
                                TGGGGTGGGA     AGGA G CT
                                ||||||||||     |||| | ||
                                ACCCCACCCT     TCCT C GA
                                     A____    _ G
GAM896  C20orf59 3'  AGCCTCCCCAATCCCAGCCCA  42230      G    GCAGAA   A
                                TGGG TGGGA     GGA GGCT
                                |||| |||||     ||| ||||
                                ACCC ACCCT     CCT CCGA
                                  G    AACC__  _
GAM896  CAPN6    3'  AGCCTTCCCTAATTCCACCCCA 27389          GC  AA
                                TGGGGTGGGA  AG  GGAAGGCT
                                ||||||||||  ||  ||||||||
                                ACCCCACCTT  TC  CCTTCCGA
                                     AA  __
GAM896  CD109    3'  AGCCCTACTGCCCACCCCACCC 56860         A___    A  AAG
           CA                     TGGGGTGGG   GCAG AGG   GCT
                                ||||||||||   |||| |||   |||
                                ACCCCACCC   CGTC TCC   CGA
                                     CACC   A  ___
GAM896  COL4A3BP 5'  CCCTCCTCCTGCTCCCCCCCA  20340      T      A   A
                                TGGGG GGGAGCAG AGGA GG
                                ||||| |||||||| |||| ||
                                ACCCC CCCTCGTC TCCT CC
                                  _      C   C
GAM896  CORO1B   3'  GCCCTCTGCTCCCTCCCCA   40319      T       AGGAA
                                TGGGG GGGAGCAGA    GGC
                                ||||| |||||||||    |||
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                                ACCCC CCCTCGTCT    CCG
                                  T       C____
GAM896  DGKZ     3'  AGCCCCCGCTCCTGCCCCACCC 14674        A   AA__  AA
            CA                    TGGGGTGGG GCAG   GG  GGCT
                                  ||||||||| ||||   ||  ||||
                                  ACCCCACCC CGTC   CC  CCGA
                                      _   CTCG  C_
GAM896  DIO2     5'  CCTTCCCCCTTACCTCCCCCAC 26552      __    C__  AA
            CCC                   GGGGT  GGGAG  AG  GGAAGG
                                  |||||  |||||  ||  ||||||
                                  CCCCA  CCCTC  TC  CCTTCC
                                    CC    CAT  CC
GAM896  DKFZp547J036 3'  AGCCCTCGCACCGCTCCCCACC 51120         _  AGAAG  A
            CCA                   TGGGGTGGG AGC    GA GGCT
                                  ||||||||| |||    || ||||
                                  ACCCCACCC TCG    CT CCGA
                                      C   CCACG  C
GAM896  DKFZP564C1940 3'  AGCCTCCCCTCCACCACTTC   26742       GAGCA  A  A
                                  GGGGTGG    GA GG AGGCT
                                  |||||||    || || |||||
                                  CTTCACC    CT CC TCCGA
                                     AC___  C  C
GAM896  DMWD     3'  AGCCCTCGCCCGGCCCCCACCC 61548         A  AGAAG  A
            CA                    TGGGGTGGG GC    GA GGCT
                                  ||||||||| ||    || ||||
                                  ACCCCACCC CG    CT CCGA
                                      C  GCCCG  C
GAM896  DNAJA3   3'  TCCTTGCTCCCACCCCA    61100           GA
                                  TGGGGTGGGAGCA  AGGA
                                  ||||||||||||  ||||
                                  ACCCCACCCTCGT  TCCT
                                                __
GAM896  DNAJC8   3'  TCCTCCCACTTCCACCCCA   27348          CAGA
                                  TGGGGTGGGAG   AGGA
                                  ||||||||||   ||||
                                  ACCCCACCTTC   TCCT
                                      ACCC
GAM896  DOCK3    3'  AGCAAGTCCCCCAGCCCCACCC 67090        A  AGAA   AG_
            CA                    TGGGGTGGG GC   GGA   GCT
                                  ||||||||| ||   |||   |||
                                  ACCCCACCC CG   CCT   CGA
                                      _ ACCC   GAA
GAM896  FEM-2    3'  AGCCACCCCCCTGCCCCCACTC 28307        A   AA  AA
            CA                    TGGGGTGGG GCAG  GG  GGCT
                                  ||||||||| ||||  ||  ||||
                                  ACCTCACCC CGTC  CC  CCGA
                                      C   CC  CA
GAM896  FLJ10211 5'  AGCCTCCCCTAGCCCACCCC  36362        AGC  AA   A
                                  GGGGTGGG   AG  GGA GGCT
                                  ||||||||   ||  ||| ||||
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                                CCCCACCC   TC  CCT CCGA
                                    GA_  C_  _
GAM896  FLJ10842  3'  CCCTCTGCCCCCACTCCA    37271         A    A
                                TGGGGTGGG GCAGA GG
                                ||||||||| ||||| ||
                                ACCTCACCC CGTCT CC
                                    C    C
GAM896  FLJ12998  3'  AGCCTCCCCTCTTCCCCTCCCC 43147      T_   GC   A  A
          A                      TGGGG  GGGA  AGA GG AGGCT
                                |||||  ||||  ||| || |||||
                                ACCCC  CCCT  TCT CC TCCGA
                                   TC   __   C  C
GAM896  FLJ20273  3'  AGCCTTAAACATGCCCCCACTC 39244     _    A   GAAGG
          CCA                     TGGG GTGGG GCA    AAGGCT
                                |||| ||||| |||    ||||||
                                ACCC CACCC CGT    TTCCGA
                                  T    C   ACAAA
GAM896  FLJ21916  3'  TTCTCTACCCTCACCCCA    43900         AGC   A
                                TGGGGTGGG   AGA GGA
                                |||||||||   ||| |||
                                ACCCCACTC   TCT CTT
                                    CCA  _
GAM896  FLJ23058  3'  GCCCCCCCGCTCCCACCCC    45524          AGAA  AA
                                GGGGTGGGAGC   GG  GGC
                                ||||||||||   ||  |||
                                CCCCACCCTCG   CC  CCG
                                     ____  CC
GAM896  FLJ23462  3'  CCTTCTGCTCCCTCCCCA    46221      T
                                TGGGG GGGAGCAGAAGG
                                ||||| ||||||||||||
                                ACCCC CCCTCGTCTTCC
                                   T
GAM896  FOXH1    3'  CCCTCCCGCTCCCACCCC    15377          AGAA   A
                                GGGGTGGGAGC   GGA GG
                                ||||||||||   ||| ||
                                CCCCACCCTCG   CCT CC
                                     C___   C
GAM896  GTPBP1   3'  AGCCTCCGCATTGCCCCCACCC 16262        A   AA_  A
          C                      GGGGTGGG GCAG   GGA GGCT
                                |||||||| ||||   ||| ||||
                                CCCCACCC CGTT   CCT CCGA
                                    C   ACG   _
GAM896  HIC2     3'  GCCCCCTAACCCCACCCCA   65869         AGCAGA   AA
                                TGGGGTGGG     AGG  GGC
                                |||||||||     |||  |||
                                ACCCCACCC     TCC  CCG
                                    CAA___   C_
GAM896  HYPC     5'  GCCTCCTGGCCCCACCCCA   65219         A  AGA   A
                                TGGGGTGGG GC   AGGA GGC
                                |||||||| ||   |||| |||
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                                ACCCCACCC CG   TCCT CCG
                                    _ G__   _
GAM896  KIAA0284 3' AGCCCCATGGCCACCCCCACCC 63801       A___  AGAA  AA
            C                    GGGGTGGG   GC   GG  GGCT
                                 ||||||||   ||   ||  ||||
                                 CCCCACCC   CG   CC  CCGA
                                     CCAC  GTA_  __
GAM896  KIAA0339 3' GCCCTCCGCCCCCACCCC   71964       A  AGAA   A
                                 GGGGTGGG GC   GGA GGC
                                 ||||||||  ||   ||| |||
                                 CCCCACCC CG   CCT CCG
                                     C  ____  C
GAM896  KIAA0346 5' AGCCCCGTAGCACTGCCCACCC 68902       _  CAGAA_  AA
            CA                    TGGGGTGGG AG     GG  GGCT
                                  |||||||||  ||     ||  ||||
                                  ACCCCACCC TC     CC  CCGA
                                      G  ACGATG  __
GAM896  KIAA0545 3' AGCGCTGCCCCTGCCCCCACCC 63841       A   AA  A  _
            T                     GGGGTGGG GCAG  GG AG GCT
                                  ||||||||  ||||  || || |||
                                  TCCCACCC CGTC  CC TC CGA
                                      C   C_  G  G
GAM896  KIAA0669 5' CCCTCCCACTCCCACCCC   29431         CAGAA   A
                                 GGGGTGGGAG    GGA GG
                                 ||||||||||    ||| ||
                                 CCCCACCCTC    CCT CC
                                      AC___   C
GAM896  KIAA0682 3' CCTGCTCCCCCTGTCCCCACCC 30020       AG   AA   __
            CA                    TGGGGTGGG  CAG  GGA  AGG
                                  |||||||||  |||  |||  |||
                                  ACCCCACCC  GTC  CCT  TCC
                                      CT   CC   CG
GAM896  KIAA1089 3' AGCTCTGCTGCCCCCACCCCA  69428       A   A  GAA
                                 TGGGGTGGG GCAG AG   GGCT
                                 |||||||||  |||| ||   ||||
                                 ACCCCACCC CGTC TC   TCGA
                                      C   G  ___
GAM896  KIAA1171 3' AGCAGTCCTGCCCCCCACCCC   89337       A  GAA   AG
                                 GGGGTGGG GCA   GGA  GCT
                                 ||||||||  |||   |||  |||
                                 CCCCACCC CGT   CCT  CGA
                                      C   ____   GA
GAM896  KIAA1205 3' AGCCCCCCTCCACTCCCTCCCCA 70579      T    CA  A  AA
                                 TGGGG GGGAG  GA GG  GGCT
                                 |||||  |||||  ||  ||  ||||
                                 ACCCC CCCTC  CT CC  CCGA
                                    T    AC  C  __
GAM896  KIAA1372 5' AGCCCCCTGGGCTGCCCTCACCC 93316       A   A__   AA
            CA                    TGGGGTGGG GCAG   AGG  GGCT
                                  |||||||||  ||||   |||  ||||
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                                ACCCCACTC CGTC   TCC  CCGA
                                     C   GGG  __
GAM896  KIAA1453  3'  CCCCCCTTCAGCCCCCACCCCA 47662        A  A    AA
                                TGGGGTGGG GC GAAGG  GG
                                ||||||||| || |||||  ||
                                ACCCCACCC CG CTTCC  CC
                                     C  A    CC
GAM896  KIAA1484  3'  GCCTCCCACCCCACCCCA    70523        AGCAGAA   A
                                TGGGGTGGG      GGA GGC
                                |||||||||      ||| |||
                                ACCCCACCC      CCT CCG
                                     CAC____   _
GAM896  KIAA1817  3'  CCCTCCCCCCCACGCCCCCCACC 68775        A_  AGAA__   A
            CC                    GGGGTGGG  GC     GGA GG
                                |||||||| ||     ||| ||
                                CCCCACCC  CG     CCT CC
                                     CC  CACCCC   C
GAM896  KIAA1924  3'  GCCCCTGACCCCACCCCA    74051        AG   AAGGAA
                                TGGGGTGGG  CAG     GGC
                                |||||||||  |||     |||
                                ACCCCACCC  GTC     CCG
                                     CA   C_____
GAM896  LIECG3    3'  GCCCCACTACCCCACCCCA    88800        AGC  AA  AA
                                TGGGGTGGG   AG  GG  GGC
                                |||||||||   ||  ||  |||
                                ACCCCACCC   TC  CC  CCG
                                     CA_  A_  __
GAM896  MGC10986  3'  AGCCTCCCTCCCCACCTCACCC 48323        AGCAGA   A
            CA                    TGGGGTGGG     AGG AGGCT
                                |||||||||      ||| |||||
                                ACCCCACTC      TCC TCCGA
                                     CACCCC   C
GAM896  MGC14128  3'  AGCAGAATCCCCCACTCCCACC 52945         CAGAA   AG__
            CCA                    TGGGGTGGGAG    GGA   GCT
                                ||||||||||     |||   |||
                                ACCCCACCCTC    CCT   CGA
                                      ACCC_   AAGA
GAM896  MGC15619  3'  AGCTGCCCATCCACTCCCACCC 51401         CA  A  AA
            CA                    TGGGGTGGGAG  GA GG  GGCT
                                |||||||||||  || ||  ||||
                                ACCCCACCCTC  CT CC  TCGA
                                      AC  A  CG
GAM896  MGC4643   3'  CCTTCCTTCTGCTTCTCCC    52138     T
                                GGG GGGAGCAGAAGGAAGG
                                ||| ||||||||||||||||
                                CCC TCTTCGTCTTCCTTCC
                                  _
GAM896  MMP24     3'  AGATGTCCCCCTACCCCCACCC 22915        AGC  AA   AGG
            CA                    TGGGGTGGG   AG  GGA   CT
                                |||||||||   ||  |||   ||
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                                ACCCCACCC  TC  CCT  GA
                                    CCA  CC  GTA
GAM896  MRPS18A  3'  CTATACTCCTGTCCCACCCCA  36781        G  A  GA_
                                TGGGGTGGGA CAG AG  AG
                                |||||||||| ||| ||  ||
                                ACCCCACCCT GTC TC  TC
                                    _  C  ATA
GAM896  N4BP3    3'  AGCCTTCCCTGCAGCCCCTCCC 66843     T  A__  AA
          CA                  TGGGG GGG  GCAG  GGAAGGCT
                              ||||| |||  ||||  ||||||||
                              ACCCC CCC  CGTC  CCTTCCGA
                                T  CGA  __
GAM896  NIR3     3'  AGCCTTAGTCCCACTCCCACC  66821       CA_  AGG
                                GGTGGGAG  GA  AAGGCT
                                ||||||||  ||  ||||||
                                CCACCCTC  CT  TTCCGA
                                    ACC  GA_
GAM896  NKD1     3'  AGCCTCAACTCTGCCCCACCCC 53587        A   AG_  A
          A                   TGGGGTGGG GCAGA  GA GGCT
                              ||||||||| |||||  || ||||
                              ACCCCACCC CGTCT  CT CCGA
                                    _   CAA  _
GAM896  PEG10    3'  AGCCCTCCTCCTACCACTGAAC 31198      __  GAGC  A   A
          CCCA                  TGGGGT  GG   AG AGGA GGCT
                              ||||||  ||   || |||| ||||
                              ACCCCA  TC   TC TCCT CCGA
                                AG  ACCA  C   C
GAM896  PIP5K1C  3'  GCCCTCAGTCCCCACCCCA  71304       AGCA  AG  A
                                TGGGGTGGG   GA  GA GGC
                                |||||||||   ||  || |||
                                ACCCCACCC   CT  CT CCG
                                    _____  GA  C
GAM896  RGS19    5'  GGCCCCTCCTGCCCCCACCCC  20801       A   A   AA
                                GGGGTGGG GCAG AGG  GGCT
                                |||||||| |||| |||  ||||
                                CCCCACCC CGTC TCC  CCGG
                                    C   C  __
GAM896  RNF40    3'  AGCCCATTTACCCCCACCTCA  29362       AGCAG  GAA
                                TGGGGTGGG   AAG  GGCT
                                |||||||||   |||  ||||
                                ACTCCACCC   TTT  CCGA
                                    CCA__  AC_
GAM896  SELB     3'  AGCCCCTGCACACTCCCACCC  62590       CAGA_  AA
                                GGGTGGGAG   AGG  GGCT
                                |||||||||   |||  ||||
                                CCCACCCTC   TCC  CCGA
                                    ACACG  __
GAM896  SEMA4G   3'  CCTCTCCCACCTCCACCCCA  35858       G  CAGAA  _
                                TGGGGTGG AG   GGA AGG
                                |||||||| ||   ||| |||
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                                ACCCCACC TC    CCT TCC
                                    _ CAC__   C
GAM896  SEMA4G   3'  CCTCTCCCACCTCCACCCCA  96325       G  CAGAA  _
                                TGGGGTGG AG    GGA AGG
                                |||||||| ||    ||| |||
                                ACCCCACC TC    CCT TCC
                                    _ CAC__   C
GAM896  SLC26A9  3'  AGCCTCCTGCTCACTCCACCCC 54709       ___    GAA  A
           A                     TGGGGTGG  GAGCA  GGA GGCT
                                |||||||| |||||  ||| ||||
                                ACCCCACC  CTCGT  CCT CCGA
                                    TCA   ___  _
GAM896  SRF      3'  AGCCTCCCCTTCTTCCCGCCCC 13392        GC    A_
           A                     TGGGGTGGGA  AGAAGG  AGGCT
                                |||||||||| ||||||  |||||
                                ACCCCGCCCT  TCTTCC  TCCGA
                                    __     CC
GAM896  TEB4     3'  AGCCCCCCCGCCCGCCCCCACC 61282        A  AGAA  AA_
           CCA                    TGGGGTGGG GC   GG  GGCT
                                |||||||| ||   ||  ||||
                                ACCCCACCC CG   CC  CCGA
                                    C  CCCG  CCC
GAM896  TIAF1    3'  CCTCCAGCCCCCACCCCA    55294        A  AGAA  A
                                TGGGGTGGG GC   GGA GG
                                |||||||| ||   ||| ||
                                ACCCCACCC CG   CCT CC
                                    C  A___  _
GAM896  WIRE     3'  CCCTCTGGGACCCCTCACCCCA 78905        AG____   A
                                TGGGGTGGG     CAGA GG
                                |||||||||     |||| ||
                                ACCCCACTC     GTCT CC
                                    CCCAGG   C
GAM896  LOC116113 3'  AGCCAGGCCTCCACCCCCACCC 93831       AGCA  A  AA_
           C                     GGGGTGGG   GA GG  GGCT
                                |||||||   || ||  ||||
                                CCCCACCC   CT CC  CCGA
                                    CCAC  _  GGA
GAM896  LOC124402 3'  AGCCCCCTGCCCGCCGCCCCCT 59828     T  A  AGA____  AA
           CCCCA                  TGGGG GGG GC     AGG  GGCT
                                ||||| ||| ||     |||  ||||
                                ACCCC CCC CG     TCC  CCGA
                                   T  C  CCGCCCG  C_
GAM896  LOC124976 3'  GCCTCCACCCCCACTCCA   74842        AGCAGAA  A
                                TGGGGTGGG     GGA GGC
                                |||||||||     ||| |||
                                ACCTCACCC     CCT CCG
                                    CCA____  _
GAM896  LOC129566 5'  CCGCATCCTGCCCCACCCCA  76223        A   AAGGAA
                                TGGGGTGGG GCAG    GG
                                |||||||| ||||    ||
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                                ACCCCACCC CGTC     CC
                                     _   CTACG_
GAM896  LOC132422 5'  GCCCCGCCGCCCCCACCCCA  76403        A  AGAA  AA
                                TGGGGTGGG GC    GG  GGC
                                ||||||||| ||    ||  |||
                                ACCCCACCC CG    CC  CCG
                                     C  CCG_  __
GAM896  LOC143916 5'  CCTCCCCACTGCCCCCACCCCA 77140        A    AA  A
                                TGGGGTGGG GCAG  GG AGG
                                ||||||||| ||||  || |||
                                ACCCCACCC CGTC  CC TCC
                                     C    AC  C
GAM896  LOC145978 3'  CCTCCCACCTCCACCCCA    78049        G  CAGAA   A
                                TGGGGTGG AG     GGA GG
                                |||||||| ||     ||| ||
                                ACCCCACC TC     CCT CC
                                     _  CAC__   _
GAM896  LOC147071 5'  AGCTCTGCCGCGCCCCCACCCC 73350        A  AGAA  A  _
          A                      TGGGGTGGG GC    GG AG GCT
                                 ||||||||| ||    || || |||
                                 ACCCCACCC CG    CC TC CGA
                                      C  CG__  G  T
GAM896  LOC147160 3'  CCTTGCTTCCACCCCA      85071           GA
                                TGGGGTGGGAGCA  AGG
                                ||||||||||||  |||
                                ACCCCACCTTCGT  TCC
                                          __
GAM896  LOC149077 3'  GCCCTCCAGCCTCACCCCA   79889        A  AGAA   A
                                TGGGGTGGG GC    GGA GGC
                                ||||||||| ||    ||| |||
                                ACCCCACTC CG    CCT CCG
                                     _  A___    C
GAM896  LOC149461 3'  GCCCCTGCCCCCGACCCCA   80202       _  A   AAGGAA
                                TGGGGT GGG GCAG     GGC
                                |||||| ||| ||||     |||
                                ACCCCA CCC CGTC     CCG
                                   G   C    C_____
GAM896  LOC158177 3'  GCCCTCCCTCCCAGCCCCA   82689       _    CAGAA   A
                                TGGGG TGGGAG    GGA GGC
                                ||||| ||||||    ||| |||
                                ACCCC ACCCTC    CCT CCG
                                   G      _____   C
GAM896  LOC201173 5'  AGCTCTGCCGCGCCCCCACCCC 88669        A  AGAA  A  _
          A                      TGGGGTGGG GC    GG AG GCT
                                 ||||||||| ||    || || |||
                                 ACCCCACCC CG    CC TC CGA
                                      C  CG__  G  T
GAM896  LOC219700 5'  CCCTCCTCTCACCCACCCC   94649        AGC   A   A
                                GGGGTGGG   AGA GGA GG
                                ||||||||   ||| ||| ||
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                                CCCCACCC   TCT CCT CC
                                     AC_  _  C
GAM896  LOC221495 3'  GCCCTCCCTACCCACCCC    95495       _ CAGAA  A
                                GGGGTGGG AG    GGA GGC
                                |||||||| ||    ||| |||
                                CCCCACCC TC    CCT CCG
                                     A _____  C
GAM896  LOC51195  3'  GCCTTCCTCCTGACCCC     33407      GGGAG  A
                                GGGGT    CAG AGGAAGGC
                                |||||    ||| ||||||||
                                CCCCA    GTC TCCTTCCG
                                   _____  C
GAM896  LOC91191  3'  TTTTCTTCCACCCCCACCCCA  65801        AGCA
                                TGGGGTGGG   GAAGGAAG
                                |||||||||   ||||||||
                                ACCCCACCC   CTTCTTTT
                                     CCAC
GAM897  ARHI     5'  TGTGGGAGAACTTGTGCAC   17429         __
                                GTGCACAAGT  TCCCATA
                                ||||||||||  |||||||
                                CACGTGTTCA  AGGGTGT
                                     AG
GAM897  CDK5RAP3  5'  AGGCTTATAGGAGGCAC    48058     ACAAG   C
                                GTGC    TTCC ATAAGCCT
                                ||||    |||| ||||||||
                                CACG    GAGG TATTCGGA
                                  _____   A
GAM897  KIAA1530  3'  ATGCGGAAGCTTGTGCAC   68547          _ _
                                GTGCACAAGTT CC CAT
                                |||||||||||  || |||
                                CACGTGTTCGA GG GTA
                                     A  C
GAM897  KLF12    3'  GGTTGGGAACTTATACAC    33279     CAC       TAA
                                GTG   AAGTTCCCA   GCC
                                |||   |||||||||   |||
                                CAC   TTCAAGGGT   TGG
                                  ATA       ___
GAM897  RoXaN    3'  GGGCCAAGACACTTGTGCAC   47302         _ CCATAA
                                GTGCACAAGT TC     GCCT
                                ||||||||||  ||     ||||
                                CACGTGTTCA AG     CGGG
                                     C  AAC___
GAM897  LOC202025 5'  CTAGGCTCACGGAACTTGCA   91887     CA     CATA
                                TGCA  AGTTCC    AGCCTAG
                                ||||  ||||||    |||||||
                                ACGT  TCAAGG    TCGGATC
                                   __     CAC_
GAM897  LOC253216 3'  AGGCTTATGGGACCTGCA    96628     CAA T
                                TGCA   G TCCCATAAGCCT
                                ||||   | ||||||||||||
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                                ACGT   C AGGGTATTCGGA
                                  ___ C
GAM897  LOC92017  5'  AGGCTTATGACCTGCAC     68485      CAA  TCC
                                GTGCA   GT   CATAAGCCT
                                |||||   ||   |||||||||
                                CACGT   CA   GTATTCGGA
                                  C__  ___
GAM898  CLCA3     3'  AGAAGATTTTGATAAAGCTGCT 18194        C_  G  C
          T                      AAGCAGTT  AT GA ATCTTCT
                                 ||||||||  || || |||||||
                                 TTCGTCGA  TA TT TAGAAGA
                                      AA  G  T
GAM898  OTX1      3'  AAGATGTCCATTGCCTGC    28054      TTC
                                GCAG   ATGGACATCTT
                                ||||   ||||||||||
                                CGTC   TACCTGTAGAA
                                  CGT
GAM898  FXYD3     3'  GAAATGTTCTCATGAACT    21060        _  _  C
                                AGTTCATG GA CAT TTC
                                |||||||| || ||| |||
                                TCAAGTAC CT GTA AAG
                                     T  T  _
GAM898  FXYD3     3'  GAAATGTTCTCATGAACT    41865        _  _  C
                                AGTTCATG GA CAT TTC
                                |||||||| || ||| |||
                                TCAAGTAC CT GTA AAG
                                     T  T  _
GAM898  HGC6.1.1  3'  CGAGAAGAAGAATGAAACGC  27610    AG    GGACA
                                GC  TTCAT    TCTTCTCG
                                ||  |||||    ||||||||
                                CG  AAGTA    AGAAGAGC
                                 CA    AGA__
GAM898  LOC123792 3'  AGGTGGTGCCCATGAACTGCT  74702          A   T
                                AGCAGTTCATGG CATC TCT
                                |||||||||||| |||| |||
                                TCGTCAAGTACC GTGG GGA
                                       C   T
GAM898  LOC146486 5'  AGAAGATGGTTCTAACTCCT   78490    C   CAT   _
                                AG AGTT   GGAC ATCTTCT
                                || ||||   |||| |||||||
                                TC TCAA   CTTG TAGAAGA
                                 C   T__   G
GAM898  LOC152464 5'  AAGACCAAAACTGCTT      60645        CA   ACA
                                AAGCAGTT  TGG   TCTT
                                ||||||||  |||   ||||
                                TTCGTCAA  ACC   AGAA
                                     A_  ___
GAM898  LOC170347 5'  CGAGAAGACACAGCTGACGCT  83480     A   CA_  GACA
                                AGC GTT   TG    TCTTCTCG
                                ||| |||   ||    ||||||||
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                                TCG CAG   AC    AGAAGAGC
                                  _   TCG  AC__
GAM898  LOC170353 5'  CGAGAAGACACAGCTGACGCT  83479     A   CA_  GACA
                                AGC GTT   TG    TCTTCTCG
                                ||| |||   ||    ||||||||
                                TCG CAG   AC    AGAAGAGC
                                  _   TCG  AC__
GAM898  LOC56959  5'  AAGATGTCTGGCTGGTT     82808    G    CAT
                                AA CAGTT   GGACATCTT
                                || |||||   |||||||||
                                TT GTCGG   TCTGTAGAA
                                 G    ____
GAM899  ALDH3B2   3'  GCAGCTCCATCCACTGGG    7343          TAT
                                TCCAGTGGATG   GGCTGC
                                ||||||||||   ||||||
                                GGGTCACCTAC   TCGACG
                                       C__
GAM899  DGSI      3'  CAGCTGTACACCCAGCAGAG  42963     CAG   A
                                CTC   TGG TGTATGGCTG
                                |||   ||| ||||||||||
                                GAG   ACC ACATGTCGAC
                                  ACG   C
GAM899  DSCR3     3'  CGCAAAGTGCTAGCCACTGGA 21310        AT_   GGC
                                TCCAGTGG   GTAT   TGCG
                                ||||||||   ||||   ||||
                                AGGTCACC   CGTG   ACGC
                                     GAT    AA_
GAM899  ENG       5'  CGCAGCCCTGCCACTGGA    5494         ATGTAT
                                TCCAGTGG     GGCTGCG
                                ||||||||     |||||||
                                AGGTCACC     CCGACGC
                                     GTC___
GAM899  FBXL7     5'  CGCAGCACCCCCTCCCACTGGA 25491         ATGTATG_
           G                     CTCCAGTGG      GCTGCG
                                |||||||||       ||||||
                                GAGGTCACC       CGACGC
                                     CTCCCCCA
GAM899  GRIN2A    5'  CGCAGCCATCAGCCCTGGAG   7722        T  A  T
                                CTCCAG GG TG ATGGCTGCG
                                |||||| || || |||||||||
                                GAGGTC CC AC TACCGACGC
                                   _  G  _
GAM899  IGFBP4    3'  CAGCCATGAAGTCACCGGG   9551     A   ATG
                                TCC GTGG   TATGGCTG
                                ||| ||||   ||||||||
                                GGG CACT   GTACCGAC
                                  C    GAA
GAM899  INSR      5'  CGCAGCCATGGGCACCGGGG  71538     A   GATG
                                CTCC GTG    TATGGCTGCG
                                |||| |||    ||||||||||
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                                GGGG CAC    GTACCGACGC
                                  C   GG__
GAM899  MGAT3    5'  CGCAGCCGCTGCCGCCGGAG  11561      A    ATGTA
                                CTCC GTGG    TGGCTGCG
                                |||| ||||    ||||||||
                                GAGG CGCC    GCCGACGC
                                  C    GTC__
GAM899  MYLK2    3'  CGCAGCCACACAGTGGCCGGGG 53583      A  GGA   A
                                CTCC GT   TGT TGGCTGCG
                                |||| ||   ||| ||||||||
                                GGGG CG   ACA ACCGACGC
                                  C  GTG   C
GAM899  NYX      3'  CACACGGGCATCCATTGGA   42904          A  GC
                                TCCAGTGGATGT TG  TG
                                ||||||||||| ||  ||
                                AGGTTACCTACG GC  AC
                                       G  AC
GAM899  RPS6KA1  5'  CGCAGCCGGGGCCGCCGGAG  60042      A    ATGTA
                                CTCC GTGG    TGGCTGCG
                                |||| ||||    ||||||||
                                GAGG CGCC    GCCGACGC
                                  C    GGG__
GAM899  SLC13A3  3'  CAGTTACAACCCACTGGGG   61089        A_    TG
                                CTCCAGTGG  TGTA  GCTG
                                |||||||||  ||||  ||||
                                GGGGTCACC  ACAT  TGAC
                                     CA    __
GAM899  SLC6A5   5'  CGCAGCCCCCTCCCGCTGGAG  16140         ATGTAT
                                CTCCAGTGG     GGCTGCG
                                |||||||||     |||||||
                                GAGGTCGCC     CCGACGC
                                     CTCCC_
GAM899  USP9Y    5'  CAGATACTTCCACTGGAG    64736         T    GG
                                CTCCAGTGGA GTAT  CTG
                                |||||||||| ||||  |||
                                GAGGTCACCT CATA  GAC
                                     T    __
GAM899  VBP1     5'  CGCAGCCAATCAGCACCTAGAG 14029     CA_   GA  TA
                                CTC   GTG  TG  TGGCTGCG
                                |||   |||  ||  ||||||||
                                GAG   CAC  AC  ACCGACGC
                                  ATC   G_  TA
GAM899  C20orf130 3'  CGCAGCCATCAGGACTAGG   62414    _   GGA  T
                                CC AGT   TG ATGGCTGCG
                                || |||   || |||||||||
                                GG TCA   AC TACCGACGC
                                 A  GG_  _
GAM899  CAMK2G   3'  CGCAGCCAGTGGCTCTGGAG   69536       T  ATGTA
                                CTCCAG GG    TGGCTGCG
                                |||||| ||    ||||||||
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                                GAGGTC TC    ACCGACGC
                                   _ GGTG_
GAM899  CST7     3' CAGCCATGACAAACACCAGG  14682    A_  GA  _
                                CC  GTG  TGT ATGGCTG
                                ||  |||  ||| |||||||
                                GG  CAC  ACA TACCGAC
                                 AC   AA   G
GAM899  FLJ10432 3' AGATCTACATCCACCGAG    39347    CA       T  _
                                CTC  GTGGATGTA GG CT
                                |||  ||||||||| || ||
                                GAG  CACCTACAT CT GA
                                  C_        _ A
GAM899  FLJ20127 5' CAGCTGCACATCCTACTGGAG 35078       _     AT
                                CTCCAGT GGATGT  GGCTG
                                ||||||| ||||||  |||||
                                GAGGTCA CCTACA  TCGAC
                                    T     CG
GAM899  FLJ23584 3' CAGACCACGCCCACTGGAG   45037        AT TA  _
                                CTCCAGTGG  G  TGG CTG
                                |||||||||  |  ||| |||
                                GAGGTCACC  C  ACC GAC
                                     __ GC   A
GAM899  FLJ25422 5' CAGCCATACTGCTAGGA     59391    _   GAT
                                TCC AGTG   GTATGGCTG
                                ||| ||||   |||||||||
                                AGG TCGT   CATACCGAC
                                  A   ____
GAM899  KIAA0420 3' CTGTATACCCCACTGGAG    64088        A_
                                CTCCAGTGG  TGTATGG
                                |||||||||  |||||||
                                GAGGTCACC  ATATGTC
                                     CC
GAM899  KIAA1576 5' CGCAGCCACCGCAGCCAC    66492     A  A_
                                GTGG TGT  TGGCTGCG
                                |||| |||  ||||||||
                                CACC ACG  ACCGACGC
                                  G   CC
GAM899  KIAA1855 3' CGCAGCCGGCCACACTGGAG  93950       GA  TA
                                CTCCAGTG  TG  TGGCTGCG
                                ||||||||  ||  ||||||||
                                GAGGTCAC  AC  GCCGACGC
                                     __  CG
GAM899  KIAA1913 5' CGCAGCCACGCCCCTGGA    74316      T  AT TA
                                TCCAG GG  G  TGGCTGCG
                                ||||| ||  |  ||||||||
                                AGGTC CC  C  ACCGACGC
                                   _ __ GC
GAM899  MGC12760 5' CGCAGCCATAGACAACTAGAG 52158     C   GGATG
                                CTC AGT    TATGGCTGCG
                                ||| |||    ||||||||||
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                                GAG TCA    ATACCGACGC
                                  A  ACAG_
GAM899  PTPRT    3'  CATCTTCACATCCACTGG    56489          AT  C
                                CCAGTGGATGT  GG TG
                                ||||||||||  || ||
                                GGTCACCTACA  TC AC
                                      CT  T
GAM899  SIAT8C   5'  CATTGTCCATCCACTGGA    32443          T TG C
                                TCCAGTGGATG A  G TG
                                |||||||||| |  | ||
                                AGGTCACCTAC T  T AC
                                      C GT _
GAM899  SMCR7    3'  CAGCTGGGGCATCTCACTGGAG 58236         _    A_
                                CTCCAGTG GATGT  TGGCTG
                                |||||||| |||||  ||||||
                                GAGGTCAC CTACG  GTCGAC
                                     T    GG
GAM899  SULT1C2  5'  CGCAGCCATATGCTGACTG   22712     _ A
                                CAGT GG TGTATGGCTGCG
                                |||| || ||||||||||||
                                GTCA TC GTATACCGACGC
                                  G  _
GAM899  ZNF339   3'  CGCAGTTGCTCACATTCAC   41391       A__
                                GTGGATGT   TGGCTGCG
                                ||||||||   ||||||||
                                CACTTACA   GTTGACGC
                                     CTC
GAM899  LOC123855 3'  CGCTTGGAATACCCACTGGA   76144        AT   GGCT_
                                TCCAGTGG  GTAT    GCG
                                ||||||||  ||||    |||
                                AGGTCACC  CATA    CGC
                                     __   AGGTT
GAM899  LOC149992 5'  CGCAGCCATTTTCTCCCTGGAG 80374       T   TGT_
                                CTCCAG GGA   ATGGCTGCG
                                ||||||  |||   |||||||||
                                GAGGTC CCT   TACCGACGC
                                   _  CTTT
GAM899  LOC150185 3'  CAGACCACATCCACTAGG    86064    _       AT  _
                                CC AGTGGATGT  GG CTG
                                || |||||||||  || |||
                                GG TCACCTACA  CC GAC
                                 A       __  A
GAM899  LOC200958 3'  GCTCACATCCACCGGAG     66506     A       AT
                                CTCC GTGGATGT  GGC
                                |||| ||||||||  |||
                                GAGG CACCTACA  TCG
                                  C       C_
GAM899  LOC222031 3'  CGCAGCTCTGTCTCACTGGA   95677       _   TAT
                                TCCAGTG GATG   GGCTGCG
                                |||||||  ||||  |||||||
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                                AGGTCAC CTGT   TCGACGC
                                    T   C__
GAM899  LOC253626 5'  CAGCTCCACATCACTGGA    99013       G    AT
                                TCCAGTG ATGT  GGCTG
                                ||||||| ||||  |||||
                                AGGTCAC TACA  TCGAC
                                    _   CC
GAM899  LOC253805 5'  CGCAGCCACACGGCCCGGC   98171    _ A_  A
                                GT GG  TGT TGGCTGCG
                                || ||  ||| ||||||||
                                CG CC  GCA ACCGACGC
                                 G  CG   C
GAM899  LOC257354 3'  CTGTATACCCCACTGGAG    96790        A_
                                CTCCAGTGG  TGTATGG
                                |||||||||  |||||||
                                GAGGTCACC  ATATGTC
                                     CC
GAM899  LOC91300  5'  CGCAGCCGCATCCCCATGGA   96235     GT_    AT
                                TCCA   GGATGT  GGCTGCG
                                ||||   ||||||  |||||||
                                AGGT   CCTACG  CCGACGC
                                  ACC     __
GAM899  LOC91300  5'  CGCAGCCGCATCCCCATGGA   96236     GT_    AT
                                TCCA   GGATGT  GGCTGCG
                                ||||   ||||||  |||||||
                                AGGT   CCTACG  CCGACGC
                                  ACC     __
GAM900  SCAMP1    3'  GCTAAATAAATATTCTCC     18013     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM900  SCAMP1    3'  GCTAAATAAATATTCTCC     54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM900  NX-17     3'  TGAATATCAGCCCCTAATA    40706        ATA_
                                TATTAGGG    ATATTCA
                                ||||||||    |||||||
                                ATAATCCC    TATAAGT
                                     CGAC
GAM900  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
          TA                    TATTAGGGATAATATTCATTTAGC
                                |||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM901  BCL2L10   3'  CAAGAATGCAAATGGCTCTT   40211        GC   CTAG
                                AAGAGCCAT  TGT    TCTTG
                                |||||||||  |||    |||||
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                                TTCTCGGTA  ACG    AGAAC
                                     A_   TA__
GAM901  CLC      3'  GCTAACAGCATGATCTTT    10201      GC       C
                                AAAGA  CATGCTGT TAGT
                                |||||  |||||||| ||||
                                TTTCT  GTACGACA ATCG
                                   A_       _
GAM901  DGKI     3'  CAAGACTATTTAGTGACTCTCT 17523     CCA    TC
                                AGAG   TGCTG  TAGTCTTG
                                ||||   |||||  ||||||||
                                TCTC   GTGAT  ATCAGAAC
                                  TCA     TT
GAM901  FOXI1    3'  GGAGAGACAGCATTGCTC    25169     C       AG
                                GAGC ATGCTGTCT  TCT
                                |||| |||||||||  |||
                                CTCG TACGACAGA  AGG
                                  T        G_
GAM901  MEN1     3'  CAGGACACAACATGGCTCT    95011        C   CTA
                                AGAGCCATG TGT   GTCTTG
                                |||||||||  |||   ||||||
                                TCTCGGTAC ACA   CAGGAC
                                     A  ____
GAM901  MLH3     3'  AGCTTAGACAGCAGGGCTCT   27659       A        T
                                AGAGCC TGCTGTCTAG CT
                                ||||||  |||||||||| ||
                                TCTCGG ACGACAGATT GA
                                   G         C
GAM901  OAS3     3'  TTAGACAGCCTGACTCTCC    21660    A   C  T
                                A AGAG CA GCTGTCTAG
                                | |||| || |||||||||
                                C TCTC GT CGACAGATT
                                 C    A  C
GAM901  WNT15    3'  CAAGCTGCCCAGCCGGCCCT   14137    A   AT    TC   T
                                AG GCC  GCTG  TAG CTTG
                                || |||  ||||  ||| ||||
                                TC CGG  CGAC  GTC GAAC
                                 C   C_    CC   _
GAM901  ARHGEF16 3'  AGGACCCAGCATGGTTC     27817          TCTA
                                GAGCCATGCTG    GTCTT
                                ||||||||||    |||||
                                CTTGGTACGAC    CAGGA
                                       C____
GAM901  C1orf34  3'  AGGACAGAAACATGGCTC    61296        CTG   A
                                GAGCCATG   TCT GTCTT
                                ||||||||   ||| |||||
                                CTCGGTAC   AGA CAGGA
                                     AA_   _
GAM901  DKFZp434O0320 5'  CAAGACGGCGGCCTGGCCCTCC 84696    A  A    T     TA
                                A AG GCCA GCTGTC  GTCTTG
                                | || |||| ||||||  ||||||
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                                C TC CGGT CGGCGG  CAGAAC
                                 C C   C     __
GAM901  FLJ14775  3'  GGAACAGCATGAGCCTTT    52680      A _      _
                                AAAG GC CATGCTGT CT
                                |||| || |||||||| ||
                                TTTC CG GTACGACA GG
                                  _ A       A
GAM901  LOC147057 3'  GGAAGAAACAGCATGATCTTT  84987      GC       CTAG
                                AAAGA  CATGCTGT   TCT
                                |||||  ||||||||   |||
                                TTTCT  GTACGACA   AGG
                                  A_       AAGA
GAM901  LOC155006 3'  CAAAACTGCTCAGTGGCTCTTT 82163        AT   TC   C
                                AAAGAGCC  GCTG  TAGT TTG
                                ||||||||  ||||  |||| |||
                                TTTCTCGG  TGAC  GTCA AAC
                                    __   TC   A
GAM901  LOC221975 3'  AAGTGGTCCAAGATGGCTCTTT 94186         G  GTCTAGT
                                AAAGAGCCAT CT      CTT
                                |||||||||| ||      |||
                                TTTCTCGGTA GA      GAA
                                     _ ACCTGGT
GAM902  AMPH     3'  GGTTTTTAAACCTTCATGA   9687     C__
                                TCA   AGGTTTAAAAACC
                                |||   ||||||||||||
                                AGT   TCCAAATTTTTGG
                                  ACT
GAM902  MPZ      3'  GGTTTTTAAACAACCAAACAA  6752      CACAG_
                                TTGT     GTTTAAAAACC
                                ||||     ||||||||||
                                AACA     CAAATTTTTGG
                                  AACCAA
GAM902  PITX2    3'  TTTTTCGCTTGCGAGCAAGGGA 6162        _ A    TT
                                TCCCTTG TC CAGGT  AAAA
                                ||||||| || |||||  ||||
                                AGGGAAC AG GTTCG  TTTT
                                    G C    CT
GAM902  PLXNA1   3'  GTTTGACATGACAAGG      72773        CAG   TAA
                                CCTTGTCA   GTT   AAAC
                                ||||||||   |||   ||||
                                GGAACAGT   CAG   TTTG
                                    A__   ___
GAM902  PPP1R12B  3'  GTTTTCCTTGTGACAAG     50394          TTTA
                                CTTGTCACAGG    AAAAC
                                ||||||||||    |||||
                                GAACAGTGTTC    TTTTG
                                     C___
GAM902  AND-1    3'  GGTTTTTGTCATGTGCAAGG   24009      T   GGTT
                                CCTTG CACA    TAAAAACC
                                ||||| ||||    ||||||||
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                                GGAAC GTGT   GTTTTTGG
                                  _   ACT_
GAM902  CECR7    5' GTTTCTGTCCCATGACAAGG  80450       CA  TT  A
                                CCTTGTCA  GG  TA AAAC
                                ||||||||  ||  || ||||
                                GGAACAGT  CC  GT TTTG
                                    A_  CT  C
GAM902  DKFZp761P1010 3' TGGACCTGTGCAAAGGA    37945    C   T
                                TCC TTG CACAGGTTTA
                                ||| ||| ||||||||||
                                AGG AAC GTGTCCAGGT
                                  A  _
GAM902  FLJ11301  3' GGTTCCTCCGACTCTAAACAAG 37809       CACA   TAAA_
           GGA                    TCCCTTGT   GGTT    AACC
                                ||||||||   ||||    ||||
                                AGGGAACA   TCAG    TTGG
                                    AATC   CCTCC
GAM902  FLJ11320  3' TTTTGAACACAAGGGA     37832       CACAG
                                TCCCTTGT    GTTTAAAA
                                ||||||||    ||||||||
                                AGGGAACA    CAAGTTTT
                                      _____
GAM902  FLJ13385  3' GTTTTTAAAACCTTAAAAAAGG 46284     GTCAC    _
                                CCTT    AGGTTT AAAAAC
                                ||||    |||||| ||||||
                                GGAA    TCCAAA TTTTTG
                                  AAAAT     A
GAM902  KIAA0227  5' GGCTTTTAAACCCGGGAAGG  61351     G  ACA      A
                                CCTT TC   GGTTTAAAA CC
                                |||| ||   ||||||||| ||
                                GGAA GG   CCAAATTTT GG
                                  G  C__       C
GAM902  KIAA0546  3' AGCTTGTTTTCCACGGCAAGGG 71837       _______
           A                    TCCCTTGTC      ACAGGTT
                                |||||||||      |||||||
                                AGGGAACGG      TGTTCGA
                                     CACCTTT
GAM902  KIAA1078  3' TTTTTAAACATGTACAAAGGG  65719      _  C   G
                                CCCTT GT ACA GTTTAAAAA
                                ||||| || ||| |||||||||
                                GGGAA CA TGT CAAATTTTT
                                  A  _   A
GAM902  KIAA1233  3' GGTTTAGTCTGTGAAAAAG   63758    G_    GT TAA
                                CTT  TCACAG  T   AAACC
                                |||  ||||||  |  |||||
                                GAA  AGTGTC  A   TTTGG
                                  AA     TG ___
GAM902  KIAA1724  3' GGTTTCATGCCCTGTGACTAAG 67621    _      TTTAA
                                CTT GTCACAGG    AAACC
                                ||| ||||||||    |||||
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                                GAA CAGTGTCC    TTTGG
                                  T      CGTAC
GAM902  KIAA1795  3'  GGCTTTTAAAATTATAATAAGG 72617        CACAGG     A
            GA                    TCCCTTGT     TTTAAAA CC
                                  ||||||||     ||||||| ||
                                  AGGGAATA     AAATTTT GG
                                      ATATTA      C
GAM902  MAP       3'  GGTTCAACCTGTGATAAAAGA  43368    CC         TAAA
                                  TC  TTGTCACAGGTT    AACC
                                  ||  ||||||||||||    ||||
                                  AG  AATAGTGTCCAA    TTGG
                                   AA          C___
GAM902  MGC2454   3'  TTTTTGAGCCTGTAACAA     48286      C
                                  TTGT ACAGGTTTAAAAA
                                  |||| ||||||||||||
                                  AACA TGTCCGAGTTTTT
                                    A
GAM902  SLC17A3   5'  TTGAGTCCCACAGCAAGGGA   22792        CACA  _
                                  TCCCTTGT    GG TTTAA
                                  ||||||||    || |||||
                                  AGGGAACG    CC GAGTT
                                      ACAC  T
GAM902  TLK2      3'  GGTTTTTGCCATTGGACAA    23396       A   GTT
                                  TTGTC CAG   TAAAAACC
                                  ||||| |||   ||||||||
                                  AACAG GTT   GTTTTTGG
                                     _   ACC
GAM902  TLK2      3'  GGTTTTTGCCATTGGACAA    78809       A   GTT
                                  TTGTC CAG   TAAAAACC
                                  ||||| |||   ||||||||
                                  AACAG GTT   GTTTTTGG
                                     _   ACC
GAM902  LOC146237 3'  GACCTGCCAGACAAGGGA     84611         A__
                                  TCCCTTGTC   CAGGTT
                                  |||||||||   ||||||
                                  AGGGAACAG   GTCCAG
                                       ACC
GAM902  LOC147976 5'  GGTCTTTTGAATCACAAGGGA  79291         CACA       _
                                  TCCCTTGT    GGTTTAAAA ACC
                                  ||||||||    ||||||||| |||
                                  AGGGAACA    CTAAGTTTT TGG
                                       _____         C
GAM902  LOC150208 5'  GGTTTTTATGATAGTGCAAGG  86078       T   AGGTT
                                  CCTTG CAC     TAAAAACC
                                  ||||| |||     ||||||||
                                  GGAAC GTG     ATTTTTGG
                                     _   ATAGT
GAM902  LOC151103 3'  GGTTTTTGAATGTAACAAG    86412       C   GG
                                  CTTGT ACA  TTTAAAAACC
                                  ||||| |||  ||||||||||
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                                GAACA TGT  AAGTTTTTGG
                                  A  __
GAM902  LOC200186 3'  TGAATTCTGCGCAAGGGA    91568        CA   _
                                TCCCTTGT  CAGG TTTA
                                ||||||||  |||| ||||
                                AGGGAACG  GTCT AAGT
                                    C_   T
GAM902  LOC205011 5'  GGTCCTTAAACCTCGAAGACA  92331     AC__      AA
                                TGTC   AGGTTTAA  ACC
                                ||||   ||||||||  |||
                                ACAG   TCCAAATT  TGG
                                  AAGC       CC
GAM902  LOC220164 3'  GGCTTTTAAAGTTCTGACAGGG 93445        C  G      A
                                CCTTGTCA AG TTTAAAA CC
                                |||||||| || ||||||| ||
                                GGGACAGT TT AAATTTT GG
                                    C  G      C
GAM902  LOC253263 3'  TTTAAACTATGTACAAGGGA   98819        C   _
                                TCCCTTGT ACA GGTTTAAA
                                |||||||| ||| ||||||||
                                AGGGAACA TGT TCAAATTT
                                    _  A
GAM902  LOC83693  3'  GGTTTTTAAATGTGCATCAAG  49606      TCA  G
                                CTTG   CA GTTTAAAAACC
                                ||||   || ||||||||||
                                GAAC   GT TAAATTTTTGG
                                  TAC  G
GAM902  LOC92335  3'  GTTTTGAGACACAAGGGA    69546        CACAGG      A
                                TCCCTTGT     TTTAAAA C
                                ||||||||     ||||||| |
                                AGGGAACA     GAGTTTT G
                                    CA____      C
GAM903  ADORA3    5'  AAGAGCAGCAGCACTTTC    7282       AGA
                                GAAAG   TGCTGCTCTT
                                |||||   ||||||||||
                                CTTTC   ACGACGAGAA
                                  ACG
GAM903  CACNG7    3'  GGTCCCATTCTTTCTCA     49944          A  CT
                                TGAGAAAGAG TG  GCT
                                |||||||||| ||  |||
                                ACTCTTTCTT AC  TGG
                                    _  CC
GAM903  CLOCK     3'  AGCGTTATCTCTTCCTTA    18110      A       C
                                TGAG AAGAGATG TGCT
                                |||| |||||||| ||||
                                ATTC TTCTCTAT GCGA
                                  C       T
GAM903  COLQ      3'  AAGAGGCTCCTCTTCTCA    20250       A   AT  TG
                                TGAGAA GAG  GC  CTCTT
                                |||||| |||  ||  |||||
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                                ACTCTT CTC  CG  GAGAA
                                   _  CT  __
GAM903  COLQ    3' AAGAGGCTCCTCTTCTCA   55409      A  AT  TG
                                TGAGAA GAG  GC  CTCTT
                                |||||| |||  ||  |||||
                                ACTCTT CTC  CG  GAGAA
                                   _  CT  __
GAM903  COLQ    3' AAGAGGCTCCTCTTCTCA   55411      A  AT  TG
                                TGAGAA GAG  GC  CTCTT
                                |||||| |||  ||  |||||
                                ACTCTT CTC  CG  GAGAA
                                   _  CT  __
GAM903  COLQ    3' AAGAGGCTCCTCTTCTCA   55413      A  AT  TG
                                TGAGAA GAG  GC  CTCTT
                                |||||| |||  ||  |||||
                                ACTCTT CTC  CG  GAGAA
                                   _  CT  __
GAM903  COLQ    3' AAGAGGCTCCTCTTCTCA   55415      A  AT  TG
                                TGAGAA GAG  GC  CTCTT
                                |||||| |||  ||  |||||
                                ACTCTT CTC  CG  GAGAA
                                   _  CT  __
GAM903  COLQ    3' AAGAGGCTCCTCTTCTCA   55417      A  AT  TG
                                TGAGAA GAG  GC  CTCTT
                                |||||| |||  ||  |||||
                                ACTCTT CTC  CG  GAGAA
                                   _  CT  __
GAM903  CRHR1   5' AGCCGGGCATCTCCTCA    16500     AAA     __
                                TGAG  GAGATGCT  GCT
                                ||||  ||||||||  |||
                                ACTC  CTCTACGG  CGA
                                  ___      GC
GAM903  DAPK1   3' AGCTAGTGTACCTCCTCTCA 18225     A_  AG   _
                                TGAGA  AG  ATGCT GCT
                                |||||  ||  ||||| |||
                                ACTCT  TC  TGTGA CGA
                                   CC  CA    T
GAM903  FGF7    5' AAGAGCAACTACTCTTTCTTA 10626        ATGC
                                TGAGAAAGAG   TGCTCTT
                                ||||||||||   |||||||
                                ATTCTTTCTC   ACGAGAA
                                     ATCA
GAM903  GAS7    3' AGTCTGGCATCTTTCCCTCA  20840     AA       CT
                                TGAG  AGAGATGCTG  CT
                                ||||  ||||||||||  ||
                                ACTC  TTTCTACGGT  GA
                                  CC        CT
GAM903  KCNAB1  3' AGCAGTATCTTCACTCA     61583     AAA
                                TGAG  GAGATGCTGCT
                                ||||  ||||||||||
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                                ACTC   TTCTATGACGA
                                  AC_
GAM903  MMP15    3'  AAGAGCAGCACCTCCTCA    11609     AAA  A
                                TGAG   GAG TGCTGCTCTT
                                ||||   ||| ||||||||||
                                ACTC   CTC ACGACGAGAA
                                  ____  C
GAM903  NOTCH2   3'  AAGATGGATAATCACTTTCTCA 44572        A   GCTGC_
                                TGAGAAAG GAT     TCTT
                                |||||||| |||     ||||
                                ACTCTTTC CTA     AGAA
                                    A   ATAGGT
GAM903  OPHN1    3'  AAGAGCAGCTCCTTCCT    11902    A   A  T
                                AG AAG GA GCTGCTCTT
                                || ||| || |||||||||
                                TC TTC CT CGACGAGAA
                                 C  _ _
GAM903  POR      5'  AGAAGTATCTCTTTTCA     95839       A      G
                                TGAGAA GAGATGCT CT
                                |||||| |||||||| ||
                                ACTTTT CTCTATGA GA
                                   _       A
GAM903  PPP1R12B 3'  AAGATGATACTTCTTTCTCA   50373         A  CT C
                                TGAGAAAGAG TG  G TCTT
                                |||||||||| ||  | ||||
                                ACTCTTTCTT AT  T AGAA
                                     C  AG _
GAM903  PTGER2   5'  AGGGCGCATCTCTTTTCCA   8171     AG        T
                                TG  AAAGAGATGC GCTCT
                                ||  |||||||||| |||||
                                AC  TTTCTCTACG CGGGA
                                 CT        _
GAM903  PXN      3'  AGCCATCTCTTCCTCA      12665      A       CT
                                TGAG AAGAGATG  GCT
                                |||| ||||||||  |||
                                ACTC TTCTCTAC  CGA
                                  C       __
GAM903  RBBP5    3'  AGTTCTTCATTCTTTCTCA    18576          A  CT__
                                TGAGAAAGAG TG    GCT
                                |||||||||| ||    |||
                                ACTCTTTCTT AC    TGA
                                     _ TTCT
GAM903  SMOH     3'  AAGATGCATCATCTCTTCCTCA 20091      A       C  _
                                TGAG AAGAGATG TGC TCTT
                                |||| |||||||| ||| ||||
                                ACTC TTCTCTAC ACG AGAA
                                  C       T  T
GAM903  THY1     3'  AAGGGCAGCCCTCCTTA     21892      AAA   AT
                                TGAG   GAG  GCTGCTCTT
                                ||||   |||  |||||||||
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                                ATTC   CTC  CGACGGGAA
                                  ___   C_
GAM903  TRHDE    5'  AAGAGCAGCTCACCCTTCGCA  26311    A   AGA_  T
                                TG GAA    GA GCTGCTCTT
                                || |||    || |||||||||
                                AC CTT    CT CGACGAGAA
                                 G   CCCA  _
GAM903  XT3      3'  AAGAGCAGAACATTTCTCA    39898       GAGATG
                                TGAGAAA     CTGCTCTT
                                |||||||     |||||||||
                                ACTCTTT     GACGAGAA
                                    ACAA__
GAM903  C1orf17  3'  GGCGGACACCCTTTCTCA    68768        AGA  _
                                TGAGAAAG   TG CTGCT
                                ||||||||   || |||||
                                ACTCTTTC   AC GGCGG
                                     CC_  A
GAM903  C21orf51 3'  AAGAGTTCTTTGCCTTTCTCA  55223        A_  TGCT
                                TGAGAAAG  GA    GCTCTT
                                ||||||||  ||    ||||||
                                ACTCTTTC  TT    TGAGAA
                                     CG  TCT_
GAM903  C9orf14  5'  AGAGCATCTCTTCCA      87953    A   A      G
                                TG GAA GAGATGCT CT
                                || ||| ||||||||  ||
                                AC CTT CTCTACGA GA
                                 _   _       _
GAM903  CEPT1    3'  AGCCAACTTTTTCTCA      21437          A  CT
                                TGAGAAAGAG TG  GCT
                                ||||||||||  ||  |||
                                ACTCTTTTTC AC  CGA
                                      A  __
GAM903  DKFZP564A2416 3'  AAGAGCAGTTTTCACTCA    32039      AAA    T
                                TGAG   GAGA GCTGCTCTT
                                ||||   ||||  |||||||||
                                ACTC   CTTT TGACGAGAA
                                  A__    _
GAM903  FLJ10252  3'  AAGAGCAGCTCGTTTCTC    36412       GA  T
                                GAGAAA  GA GCTGCTCTT
                                ||||||  ||  |||||||||
                                CTCTTT  CT CGACGAGAA
                                   G_  _
GAM903  FLJ11181  3'  AAGATGCAATCTTTTTCCCA  37716    A       GC   _
                                TG GAAAGAGAT  TGC TCTT
                                || |||||||||  |||  ||||
                                AC CTTTTTCTA  ACG AGAA
                                 C        __   T
GAM903  FLJ11259  3'  AAGAGCAGGAATTCTCTCTTTC 37760      A    TG__
            A                    TGAGA AGAGA    CTGCTCTT
                                |||||  |||||    ||||||||
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                                ACTTT TCTCT    GACGAGAA
                                   C     TAAG
GAM903   FLJ12078  3'  AAGAGTATGCCTCTTTCT    47074        AT  _
                                AGAAAGAG  GC TGCTCTT
                                ||||||||  || |||||||
                                TCTTTCTC  CG ATGAGAA
                                    __  T
GAM903   FLJ13659  3'  AAGAGTGGCACTCCATCTCA  48024      AA   A   TG
                                TGAGA  GAG TGC  CTCTT
                                |||||  ||| |||  |||||
                                ACTCT  CTC ACG  GAGAA
                                   AC   _  GT
GAM903   FLJ20079  3'  GGTGTGCATTCTCTTTCTCA  34973          _   _
                                TGAGAAAGAGA TGC TGCT
                                |||||||||||| ||| ||||
                                ACTCTTTCTCT ACG GTGG
                                      T   T
GAM903   FLJ22679  3'  AGTCAGCAATCTCTTTCTC   35175          _   _
                                GAGAAAGAGAT GCTG CT
                                |||||||||||| |||| ||
                                CTCTTTCTCTA CGAC GA
                                      A   T
GAM903   FUSIP1    3'  GAGGGCCCATCTCTTCTCA   22781       A     CT
                                TGAGAA GAGATG  GCTCTT
                                |||||| ||||||  ||||||
                                ACTCTT CTCTAC  CGGGAG
                                   _     C_
GAM903   H2BFQ     3'  AAGAGCCTTTTCCTTCTC    60074      A    TGCT
                                GAGAA GAGA    GCTCTT
                                ||||| ||||    ||||||
                                CTCTT CTTT    CGAGAA
                                   C    TC__
GAM903   KIAA0471  5'  AAGAGATCCATCTTTCTCA   30044       AA     CTG
                                TGAGA  GAGATG   CTCTT
                                |||||  ||||||   |||||
                                ACTCT  TTCTAC   GAGAA
                                   __     CTA
GAM903   KIAA0789  5'  AGCTCCATCCTTTCTCA     64425        A    CT
                                TGAGAAAG GATG  GCT
                                |||||||| ||||  |||
                                ACTCTTTC CTAC  CGA
                                    _   CT
GAM903   KIAA1128  3'  AAGAGCAGCCTTTTTCATCA  68994     _      AT
                                TGA GAAAGAG  GCTGCTCTT
                                |||  |||||||  |||||||||
                                ACT CTTTTTC  CGACGAGAA
                                  A      __
GAM903   LNIR      3'  AGCAGGTATTTTCTCA      48869        AGA    _
                                TGAGAA   GATGC TGCT
                                ||||||   ||||| ||||
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                                ACTCTT   TTATG ACGA
                                   ___    G
GAM903  LZK1     3'  AGCCATCTCTTTTCA      46174       A     CT
                                TGAGAA GAGATG  GCT
                                |||||| ||||||  |||
                                ACTTTT CTCTAC  CGA
                                   _     __
GAM903  MGC12981 3'  AAGAGGCTGGGCCTCTCTTC   51359     A    T  __ _
                                GAA GAGA GCT  GC TCTT
                                ||| |||| |||  || ||||
                                CTT CTCT CGG  CG AGAA
                                  _   C   GT  G
GAM903  MGC27382 5'  AGAGCCTGTTTCTTTCTCA    59123           GCT
                                TGAGAAAGAGAT   GCTCT
                                ||||||||||||   |||||
                                ACTCTTTCTTTG   CGAGA
                                       TC_
GAM903  MGC5149  3'  AAGAGCAGTGGAGACTTCTC   72748       AGAGA
                                GAGAA    TGCTGCTCTT
                                |||||    ||||||||||
                                CTCTT    GTGACGAGAA
                                   CAGAG
GAM903  MYT1     3'  AAGAGCAGCTCAAAGTCTC    16973      AAGA  T
                                GAGA   GA GCTGCTCTT
                                ||||   || |||||||||
                                CTCT   CT CGACGAGAA
                                  GAAA  _
GAM903  NTSR2    3'  AAGAACAGCACCCATCTCTT   25630       ____    C
                                AAGAGA   TGCTG TCTT
                                ||||||   ||||| ||||
                                TTCTCT   ACGAC AGAA
                                   ACCC    A
GAM903  UNC5D    3'  AGCATCTCGCTTTTCTCA     56002       ___
                                TGAGAAA   GAGATGCT
                                |||||||   ||||||||
                                ACTCTTT   CTCTACGA
                                    TCG
GAM903  YWHAQ    3'  GGGCCATCTCTTCCTCA     23351      A      CT
                                TGAG AAGAGATG  GCTC
                                |||| ||||||||  ||||
                                ACTC TTCTCTAC  CGGG
                                  C      __
GAM903  LOC144233 3'  AAGAATCAGTATCTGTTC    77245     AG      C_
                                GAA  AGATGCTG  TCTT
                                |||  ||||||||  ||||
                                CTT  TCTATGAC  AGAA
                                  G_       TA
GAM903  LOC149386 5'  AAGAGGGATTTTCTTTTTC   85552          TG  G
                                GAGAAAGAGA  CT CTCTT
                                ||||||||||  || |||||
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                                CTTTTTCTTT  GG GAGAA
                                      TA  _
GAM903   LOC149401 5'  AAGAGCAGCCTGGTCCTT    80110     A  ___
                                AAG GAT   GCTGCTCTT
                                ||| |||   |||||||||
                                TTC CTG   CGACGAGAA
                                  _  GTC
GAM903   LOC150282 3'  AAGACCAATCTCTTTCT     80529         GC  C
                                AGAAAGAGAT  TG TCTT
                                ||||||||||  || ||||
                                TCTTTCTCTA  AC AGAA
                                      __  C
GAM903   LOC150538 3'  AAGAGTCTCTCTCTTTCT    80735         TGCT
                                AGAAAGAGA   GCTCTT
                                |||||||||   ||||||
                                TCTTTCTCT   TGAGAA
                                     CTC_
GAM903   LOC154860 5'  AGAGCATTTCTTTCTTA     87499            G
                                TGAGAAAGAGATGCT CT
                                |||||||||||||| ||
                                ATTCTTTCTTTACGA GA
                                                _
GAM903   LOC157450 3'  AAGAGCAGAGCTTACCTCA   71528     AAA  ATG
                                TGAG  GAG  CTGCTCTT
                                ||||  |||  ||||||||
                                ACTC  TTC  GACGAGAA
                                  CA_  GA_
GAM903   LOC157503 3'  AAGAGCAAAATCATCCTTC   87761     A  _  GC
                                GAA GA GAT  TGCTCTT
                                ||| || |||  |||||||
                                CTT CT CTA  ACGAGAA
                                  C  A  AA
GAM903   LOC158490 3'  AAGAGCAGAGCTTACCTCA   82818     AAA  ATG
                                TGAG  GAG  CTGCTCTT
                                ||||  |||  ||||||||
                                ACTC  TTC  GACGAGAA
                                  CA_  GA_
GAM903   LOC196484 5'  AAGAGCAGAGCTTACCTCA   63534     AAA  ATG
                                TGAG  GAG  CTGCTCTT
                                ||||  |||  ||||||||
                                ACTC  TTC  GACGAGAA
                                  CA_  GA_
GAM903   LOC220370 3'  AAGAGCAGCAGTTTTCTC    94389      GAGA
                                GAGAAA   TGCTGCTCTT
                                ||||||   ||||||||||
                                CTCTTT   ACGACGAGAA
                                   TG__
GAM903   LOC221477 3'  AGCCTGCATCTCATCTCTCA  93765      AA_     T_
                                TGAGA  GAGATGC  GCT
                                |||||  |||||||  |||
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                                ACTCT  CTCTACG  CGA
                                  CTA     TC
GAM903  LOC222681 5'  AGCACATCTTTTCCA      94418   A  A    C
                                TG GAA GAGATG TGCT
                                || ||| |||||| ||||
                                AC CTT TTCTAC ACGA
                                 _  _    _
GAM903  LOC254661 3'  AGGAGGCCATCTTTTCCTCA  97763     A      CTG
                                TGAG AAGAGATG  CTCTT
                                |||| ||||||||  |||||
                                ACTC TTTTCTAC  GAGGA
                                  C      CG_
GAM903  LOC256946 3'  GAGGGCCCATCTCTTCTCA   96183      A    CT
                                TGAGAA GAGATG  GCTCTT
                                |||||| ||||||  ||||||
                                ACTCTT CTCTAC  CGGGAG
                                   _     C_
GAM903  LOC257358 5'  AAGAGCATGGTTCCTTTTCTCA 98897       A  TGC_
                                TGAGAAAG GA   TGCTCTT
                                |||||||| ||   |||||||
                                ACTCTTTT CT   ACGAGAA
                                     C  TGGT
GAM903  LOC257407 5'  AAGAGCCTCTTTCTTTCTCA  98758         TGCT
                                TGAGAAAGAGA   GCTCTT
                                ||||||||||   ||||||
                                ACTCTTTCTTT   CGAGAA
                                      CTC_
GAM903  LOC257507 5'  AGCACATCTTTTCCA      99605    A  A    C
                                TG GAA GAGATG TGCT
                                || ||| |||||| ||||
                                AC CTT TTCTAC ACGA
                                 _  _    _
GAM903  LOC257625 5'  AGCACATCTTTTCCA      99725    A  A    C
                                TG GAA GAGATG TGCT
                                || ||| |||||| ||||
                                AC CTT TTCTAC ACGA
                                 _  _    _
GAM903  LOC51762  3'  AAGAACAGACTCCCTTTTTCA  33703       A  TG  C
                                TGAGAAAG GA  CTG TCTT
                                |||||||| ||  ||| ||||
                                ACTTTTTC CT  GAC AGAA
                                     C  CA   A
GAM903  LOC56920  3'  AAGAGTGGGCTGTCTTTCCCA  39792    A    GAT _ TG
                                TG GAAAGA   G C  CTCTT
                                || ||||||   | |  |||||
                                AC CTTTCT   C G  GAGAA
                                 C     GT_ G GT
GAM903  LOC90499  3'  GGAGCAGCACCTCACCCTCA  63743     AAA  A
                                TGAG   GAG TGCTGCTCT
                                ||||   ||| |||||||||
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                                ACTC   CTC ACGACGAGG
                                  CCA   C
GAM903  LOC91010  3'  AAGAGCAGAGGTCTTCTC    65221     AAG   G_
                                GAGA   AGAT  CTGCTCTT
                                ||||   ||||  ||||||||
                                CTCT   TCTG  GACGAGAA
                                  ___    GA
GAM903  LOC91069  3'  AAGAGCAGAGCTTACCTCA   65395     AAA   ATG
                                TGAG   GAG   CTGCTCTT
                                ||||   |||   ||||||||
                                ACTC   TTC   GACGAGAA
                                  CA_   GA_
GAM903  LOC91252  3'  AAGAGCAGCACTGGTCCCA   65935    A  AAG  A
                                TG GA   AG TGCTGCTCTT
                                || ||   || ||||||||||
                                AC CT   TC ACGACGAGAA
                                 C  GG_  _
GAM904  CDH12     3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM904  GOCAP1    3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC         G
GAM904  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090      T    AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||     ||||||
                                TGGTG GGGT     TTATTC
                                  _    GTCA_
GAM904  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
          A                      TACAC       AGAAGAATAAG
                                 |||||       ||||||||||
                                 ATGTG       TCTTCTTATTC
                                    TACTCCC_
GAM904  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM904  HMP19     3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
          TA                     TACA    TCC    GAAGAATAAG
                                 ||||    |||    ||||||||||
                                 ATGT    AGG    TTTCTTATTC
                                   AAA_   ATTG
GAM904  KIAA1579  3'  TACTCTTAGTGGTGTA      37154         CCCAAG    A
                                TACACCACT     AAGA TA
                                |||||||||     |||| ||
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                                ATGTGGTGA     TTCT AT
                                      _______   C
GAM904  KIAA1719 3'  TCTGTCTTGGGAGTGGTGTA  68742            _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                       G
GAM904  KIAA1853 3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM904  KIAA1877 3'  CTTATTCTTCTGCCATGAGT   66748     CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM904  KIAA1906 3'  CTTATTCTTCTTGACTTTTGG  73571    CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM904  OSBPL11  3'  CTTAATTTCCCAAGAGTGGTG  43206        CCAA    AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                     AACC   A_
GAM904  YME1L1   3'  TCATTCTTGATGTGGTGTA   58438        TCC     _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                     TA_     A
GAM904  YME1L1   3'  TCATTCTTGATGTGGTGTA   27323        TCC     _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                     TA_     A
GAM904  ZNF262   3'  CTTATTTTGTTTGGGAGT    18723         A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                      G
GAM904  LOC91960 3'  TGTGGCTTGGAACGTGGTGTA  68294        TC_    AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
                                ATGTGGTG   GGTTC   TGT
                                     CAA    GG__
GAM905  B4GALT6  3'  CAATGCTGGATCATAAACTT   60555     CTG      A  A
                                AAG   ATGATCCA CA TG
                                |||   |||||||| || ||
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                                TTC   TACTAGGT GT AC
                                  AAA       C  A
GAM905  FANCC    3'  CCCGGCCAGACCGTCAGCTT   71035         A  CAACAA
                                AAGCTGATG TC     TGGG
                                |||||||||  ||     ||||
                                TTCGACTGC AG     GCCC
                                     C  ACCG__
GAM905  INHA     3'  CCCCACCATCATCAGCT     10998          CCAACAA
                                AGCTGATGAT      TGGGG
                                ||||||||||      |||||
                                TCGACTACTA      ACCCC
                                     CC_____
GAM905  LOXL2    5'  CCCCTTCGTGGGATCATCAGC  11351          A  AAT
                                GCTGATGATCC AC   GGGG
                                ||||||||||| ||   ||||
                                CGACTACTAGG TG   CCCC
                                      G  CTT
GAM905  SLA2     3'  CCCCCATTGAGGACAACAGC   50886      A  A   AA
                                GCTG TG TCC  CAATGGGGG
                                |||| || |||  |||||||||
                                CGAC AC AGG  GTTACCCCC
                                  A  _   A_
GAM905  ZNF198   5'  CCCCCATTGTTAGATGAGGTCT 14362     _  GATG   C
           T                     AAG CT    ATC AACAATGGGGG
                                |||  ||    |||  ||||||||||
                                TTC GG    TAG TTGTTACCCCC
                                  T  AG__   A
GAM905  CLYBL    3'  CCTCATTAAATCATGAGCTT   57110       G    CCAAC
                                AAGCT ATGAT     AATGGGG
                                |||||  |||||    |||||||
                                TTCGA TACTA     TTACTCC
                                   G     AA___
GAM905  COAS3    3'  CCCCTTTGCAGTTCATCAGC   58138         TCCAA   T
                                GCTGATGA     CAA GGGG
                                ||||||||     |||  ||||
                                CGACTACT     GTT CCCC
                                     TGAC_   T
GAM905  DKFZP434L1435 5'  TGTACCGGAACCATCAGCTT   93790         A_   A__
                                AAGCTGATG  TCC   ACA
                                |||||||||  |||   |||
                                TTCGACTAC  AGG   TGT
                                     CA   CCA
GAM905  KIAA0410 3'  CCCATAATTATGACCATCAGCT 29424         A  CAACA_
                                AGCTGATG TC      ATGGG
                                ||||||||  ||     |||||
                                TCGACTAC AG      TACCC
                                     C  TATTAA
GAM905  KIAA1115 3'  CCCCCATTGCCCTCATCA    30688        TCCAA
                                TGATGA     CAATGGGGG
                                ||||||     |||||||||
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                                ACTACT    GTTACCCCC
                                   CCC__
GAM905  KIAA1854  3'  CCCCCAGTATCGAATCTATCAG 72201        _  CCAACAA
            CTT                   AAGCTGAT GAT      TGGGGG
                                ||||||||| |||      ||||||
                                TTCGACTA CTA      ACCCCC
                                   T   AGCTATG
GAM905  QKI     3'  CCCCCACCATCTTGTCTCACTT 66044     C   T   CCAACAA
                                AAG TGA GAT      TGGGGG
                                ||| ||| |||      ||||||
                                TTC ACT CTG      ACCCCC
                                  _  _  TTCTACC
GAM905  SZF1    3'  CAATGCTGCATCATCAGC    32730         C  A  A
                                GCTGATGAT CA CA TG
                                |||||||||| || || ||
                                CGACTACTA GT GT AC
                                      C  C  A
GAM905  LOC145501 3'  CCTTTCTGTTGGACACCAACTT 77767     C  A  A      AT
                                AAG TG TG TCCAACA  GGGG
                                ||| || || |||||||  ||||
                                TTC AC AC AGGTTGT  TTCC
                                  A  C  _      CT
GAM905  LOC200197 3'  GTTGGTTTCAAATCATCAGCT  90021          ______
                                AGCTGATGAT     CCAAC
                                ||||||||||     |||||
                                TCGACTACTA     GGTTG
                                      AACTTT
GAM905  LOC257258 5'  CCCTAAAACTAGAACATCAGCT 98018         A  CAACAA
                                AGCTGATG TC     TGGGG
                                |||||||| ||     |||||
                                TCGACTAC AG     ATCCC
                                     A  ATCAAA
GAM905  LOC257444 3'  CCCCATTGCAATGAGCTT    82015       G  GATCCAA
                                AAGCT AT      CAATGGGG
                                ||||| ||      ||||||||
                                TTCGA TA      GTTACCCC
                                   G  AC_____
GAM906  ARHGEF12  3'  CAGAAGGCTCGCTTACTTTGGG 31645       T  C    T  ATC
            C                    GCCCA AG AAGCG GGC   CTG
                                ||||| || ||||| |||   |||
                                CGGGT TC TTCGC TCG   GAC
                                   T  A    _   GAA
GAM906  EFNB2    3'  CAGGATGCCACGCCTGGAAGGG 15840      ATAG  A
            C                    GCCC    CA GCGTGGCATCCTG
                                ||||    || ||||||||||||
                                CGGG    GT CGCACCGTAGGAC
                                  AAG_  C
GAM906  GPR86    5'  CAGGATGTTAATATGCTAT    43902        AGCG
                                ATAGCA    TGGCATCCTG
                                ||||||    ||||||||||
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                                TATCGT   ATTGTAGGAC
                                   ATA_
GAM906  PMP2     3' AGGATGTTCACTATGG     12185      GCAAGC   _
                                CCATA    GTGG CATCCT
                                |||||    |||| ||||||
                                GGTAT    CACT GTAGGA
                                   _____   T
GAM906  PPP1R12B 5' CAGTTCCCACCTGCTATGG   50347       A C   CATC
                                CCATAGCA G GTGG   CTG
                                |||||||| | ||||   |||
                                GGTATCGT C CACC   GAC
                                   _ _   CTT_
GAM906  PPP1R12B 5' CAGTTCCCACCTGCTATGG   50370       A C   CATC
                                CCATAGCA G GTGG   CTG
                                |||||||| | ||||   |||
                                GGTATCGT C CACC   GAC
                                   _ _   CTT_
GAM906  RAB6A    3' GATACCACTTGCTGTAGGC   12717    C     GC   C
                                GCC ATAGCAA  GTGG ATC
                                ||| |||||||  |||| |||
                                CGG TGTCGTT  CACC TAG
                                  A      __   A
GAM906  TRPC5    5' CAGGATTTCTGCATTGCTATG  25926       _  T  C
                                CATAGCAA GCG GG ATCCTG
                                |||||||| ||| || ||||||
                                GTATCGTT CGT CT TAGGAC
                                   A  _ T
GAM906  FLJ21945 3' CAGGCGAAGCGCTTGCCATGG  48092     A      GGCAT
                                CCAT GCAAGCGT    CCTG
                                |||| ||||||||    ||||
                                GGTA CGTTCGCG    GGAC
                                  C       AAGC_
GAM906  FLJ23584 3' AGGAAGCGCTTGCTAGG     45036    A       GGCA
                                CC TAGCAAGCGT   TCCT
                                || ||||||||||   ||||
                                GG ATCGTTCGCG   AGGA
                                 _        A___
GAM906  MGC1842  3' AGGATGCCCTGGCCCAGGC   66247    CATA  A  CGT
                                GCC   GC AG   GGCATCCT
                                |||   || ||   ||||||||
                                CGG   CG TC   CCGTAGGA
                                  ACC_  G  ___
GAM906  PPI5PIV  3' CAGGATGCCACCACCTTG    39582     C__
                                CAAG   GTGGCATCCTG
                                ||||   ||||||||||
                                GTTC   CACCGTAGGAC
                                  CAC
GAM906  PRO0246  5' ATGACCACTTGCTATGG     26958        GC   _
                                CCATAGCAA  GTGG CAT
                                |||||||||  |||| |||
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                                GGTATCGTT  CACC GTA
                                     __    A
GAM906  RAB6C    3'  GATACCACTTGCTGTAGGC   50486    C     GC   C
                                GCC ATAGCAA  GTGG ATC
                                ||| |||||||  |||| |||
                                CGG TGTCGTT  CACC TAG
                                  A      __    A
GAM906  LOC159184 3'  CAGTTCCCACCTGCTATGG   60681        A C   CATC
                                CCATAGCA G GTGG   CTG
                                |||||||| | ||||   |||
                                GGTATCGT C CACC   GAC
                                     _ _   CTT_
GAM906  LOC204084 5'  CAGAATACAGCACTGCTATGGG 90991          A_  G  GC  C
           T                     GCCCATAGCA  GC TG  AT CTG
                                ||||||||||  || ||  || |||
                                TGGGTATCGT  CG AC  TA GAC
                                      CA  _  A_  A
GAM907  FLJ10759  3'  CCACGGTCCGTGCCAGCCAAT  37121          CTT_
                                ATTGGCTGGT   ACCGTGG
                                ||||||||||   |||||||
                                TAACCGACCG   TGGCACC
                                      TGCC
GAM907  PMX2B    3'  CACGGTTCAGACAATGGTA   15381        G   TCTT
                                TACCATTG CTGG   ACCGTG
                                |||||||| ||||   ||||||
                                ATGGTAAC GACT   TGGCAC
                                     A   _____
GAM907  LOC155438 3'  CACAGAACAGCCAATG     87681         G  TACC
                                CATTGGCTG TCT   GTG
                                ||||||||| |||   |||
                                GTAACCGAC AGA   CAC
                                     A  _____
GAM907  LOC200014 5'  CAGGAACCAGCCAACAGG   89924    A_       CTTA  G
                                CC  TTGGCTGGT   CC TG
                                ||  |||||||||   || ||
                                GG  AACCGACCA   GG AC
                                 AC       A___  _
GAM907  LOC56267  3'  CCACAATAAGACCATTTAAGTG 39500     GGC_      CC
                                CATT   TGGTCTTA  GTGG
                                ||||   ||||||||  ||||
                                GTGA   ACCAGAAT  CACC
                                  ATTT       AA
GAM908  SCAMP1   3'  GCTAAATAAATATTCTCC    18013     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM908  SCAMP1   3'  GCTAAATAAATATTCTCC    54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
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                                CCT TTATAA TAAATCG
                                  C     A
GAM908  NX-17    3'  TGAATATCAGCCCCTAATA   40706        ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM908  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
            TA                    TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM909  AKAP1    3'  ACTATGGGTTCTCTTCGCAAA  14472      A  CTT      C
                                TTTGT GA   GGAACCCA AGT
                                ||||| ||   |||||||| |||
                                AAACG CT   TCTTGGGT TCA
                                  _ TC_       A
GAM909  AKAP1    3'  ACTATGGGTTCTCTTCGCAAA  58373      A  CTT      C
                                TTTGT GA   GGAACCCA AGT
                                ||||| ||   |||||||| |||
                                AAACG CT   TCTTGGGT TCA
                                  _ TC_       A
GAM909  EGF      3'  ACTATAGGTTTTGGTTCCACAA 10488      A  C TG    CAC
                                TTGT GA T  GAACC   AGT
                                |||| || |  |||||   |||
                                AACA CT G  TTTGG   TCA
                                  C  T GT    ATA
GAM909  EZH1     3'  GACTGTGGGTTCCAAATTAC   10551      AC
                                GTAG  TTGGAACCCACAGTC
                                ||||  ||||||||||||||
                                CATT  AACCTTGGGTGTCAG
                                  A_
GAM909  STAC     3'  GACTGTGGAGTAATAGCCACAA 13427      AGA  TGGA  _
            A                    TTTGT   CT    AC CCACAGTC
                                |||||   ||    || ||||||||
                                AAACA   GA    TG GGTGTCAG
                                  CC_  TAA_  A
GAM909  CCR1     3'  GACTGTGGGCTCCATTC     8927     CT    A
                                GA  TGGA CCCACAGTC
                                ||  |||| |||||||||
                                CT  ACCT GGGTGTCAG
                                 T_    C
GAM909  FLJ10483  3'  GACTGTGGAAGAGATTACAAA  36652       A   GGAAC
                                TTTGTAG CTT    CCACAGTC
                                ||||||| |||    ||||||||
                                AAACATT GAG    GGTGTCAG
                                   A  AA___
GAM909  KIAA1871  3'  ACTGTAAGAGTCTACAAA    61890          GGAACCC
                                TTTGTAGACTT      ACAGT
                                ||||||||||       |||||
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                                AAACATCTGAG      TGTCA
                                      AA_____
GAM909  LOC150821 3'  GGGTTCCACATCCACAAA    60944      A  CT
                                TTTGT GA  TGGAACCC
                                ||||| ||  ||||||||
                                AAACA CT  ACCTTGGG
                                   C  AC
GAM909  LOC151057 3'  ACTGTGGGTACACCTATAAA  86379       ACT  GA
                                TTTGTAG   TG  ACCCACAGT
                                |||||||   ||  |||||||||
                                AAATATC   AC  TGGGTGTCA
                                    C__  A_
GAM909  LOC157507 5'  ACTGTAAAAGTCTGCAAA    82377          GGAACCC
                                TTTGTAGACTT      ACAGT
                                ||||||||||       |||||
                                AAACGTCTGAA      TGTCA
                                      AA_____
GAM909  LOC203339 5'  GGATTCCCAGTCTACAAA    92214          T    C
                                TTTGTAGACT GGAA CC
                                |||||||||| |||| ||
                                AAACATCTGA CCTT GG
                                      C    A
GAM909  LOC51030  3'  ACTGTAAATTAAACCAATCTAC 32695         C    AACCC___
           AAA                    TTTGTAGA TTGG       ACAGT
                                ||||||| ||||       |||||
                                AAACATCT AACC       TGTCA
                                    _   AAATTAAA
GAM909  LOC90906  3'  GACTGTGGATCCCAAACTTTGC 64951       C_   AAC
           A                     TGTAGA  TTGG   CCACAGTC
                                ||||||  ||||   ||||||||
                                ACGTTT  AACC   GGTGTCAG
                                   CA    CTA
GAM910  FGF13    3'  ACCAAGAAAATGTAAAAGACC  54441       CAGG  ___
                                GGTCTT    GC   TTCTTGGT
                                ||||||    ||   ||||||||
                                CCAGAA    TG   AAGAACCA
                                   AA__  TAA
GAM910  INSRR    3'  ACCCGTGGCCCTGAAGACGGTG 68987      G         TCTT
                                CACCG TCTTCAGGGCT    GGT
                                ||||| ||||||||||    |||
                                GTGGC AGAAGTCCCGG    CCA
                                   _         TGC_
GAM910  LOXL3    3'  ACCAAGAAACCCATGTCAGC   51865    CTT  _  C
                                GT   CA GGG TTCTTGGT
                                ||   || ||| ||||||||
                                CG   GT CCC AAGAACCA
                                 ACT  A   A
GAM910  RAP1GA1  3'  ACCTCTGCCCTGAAGACC    12767          TTCTT
                                GGTCTTCAGGGC     GGT
                                ||||||||||||     |||
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                                CCAGAAGTCCCG    CCA
                                      TCT__
GAM910  XRCC5    5' ACCAAAGCGCCTGAGGACCGG 41239          _   CT
                                CCGGTCTTCAGG GCTT  TGGT
                                |||||||||||| ||||  ||||
                                GGCCAGGAGTCC CGAA  ACCA
                                      G   __
GAM910  EDG1     5' CCACCCCTGAAGCCAGTG    60049    C T      CTTCT
                                CAC GG CTTCAGGG    TGG
                                ||| || ||||||||    |||
                                GTG CC GAAGTCCC    ACC
                                  A _      C____
GAM910  KIAA0323 3' CCAAGAAGGGAAACGGTG    63947     GTC  AGGG
                                CACCG  TTC   CTTCTTGG
                                |||||  |||   ||||||||
                                GTGGC  AGG   GAAGAACC
                                   AA_  ____
GAM910  MGC15875 5' ACCAGCGCCCGAAGGCCG    53011       A   TTC
                                CGGTCTTC GGGC  TTGGT
                                |||||||| ||||  |||||
                                GCCGGAAG CCCG  GACCA
                                     _   C__
GAM910  NYD-SP21 3' ACCAAGAAGTCCAAACC     51860    CTTCA
                                GGT    GGGCTTCTTGGT
                                |||    ||||||||||||
                                CCA    CCTGAAGAACCA
                                  AA___
GAM910  TTC2     3' CCAATGCCGAAGACCG      13876       AG  TTC
                                CGGTCTTC  GGC  TTGG
                                ||||||||  |||  ||||
                                GCCAGAAG  CCG  AACC
                                     __  T__
GAM910  LOC199786 3' ACCAAGTTGCGGAGACCGGT  89730        AGG  TT
                                ACCGGTCTTC  GC  CTTGGT
                                ||||||||||  ||  ||||||
                                TGGCCAGAGG  CG  GAACCA
                                      ___  TT
GAM910  LOC200030 3' ACCAAGAAGAGGAAGAAGACC 80119       AGGG_
                                GGTCTTC    CTTCTTGGT
                                |||||||    |||||||||
                                CCAGAAG    GAAGAACCA
                                    AAGGA
GAM910  LOC200030 3' ACCAAGAAGAGGAAGAAGACC 80120       AGGG_
                                GGTCTTC    CTTCTTGGT
                                |||||||    |||||||||
                                CCAGAAG    GAAGAACCA
                                    AAGGA
GAM910  LOC200030 3' ACCAAGAAGTGGAAGAAGACC 80121       AGG_
                                GGTCTTC    GCTTCTTGGT
                                |||||||    ||||||||||
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                                CCAGAAG   TGAAGAACCA
                                    AAGG
GAM910  LOC200030 3'  ACCAAGAAGTGGAAGAAGACC  80122       AGG_
                                GGTCTTC   GCTTCTTGGT
                                |||||||   ||||||||||
                                CCAGAAG   TGAAGAACCA
                                    AAGG
GAM910  LOC200030 3'  ACCAAGAAGTGGAAGAAGACC  80123       AGG_
                                GGTCTTC   GCTTCTTGGT
                                |||||||   ||||||||||
                                CCAGAAG   TGAAGAACCA
                                    AAGG
GAM910  LOC204285 3'  ACCAAGAAGCTTCCAAACGAC  91009     TTCA__
                                GTC     GGGCTTCTTGGT
                                |||     ||||||||||||
                                CAG     TTCGAAGAACCA
                                  CAAACC
GAM910  LOC51629  3'  ACCAAGAAGCCCTCAGCCTGGT 32604       T  TC
          G                      CACCGG CT  AGGGCTTCTTGGT
                                 ||||||  ||  ||||||||||||
                                 GTGGTC GA  TCCCGAAGAACCA
                                    C  C_
GAM911  JRKL      3'  ATACAGGCACAAAATGTATCTG 15019       T  TTA___   C
          A                      TCAGAT GC     TGCC GTAT
                                 ||||||  ||     ||||  ||||
                                 AGTCTA TG     ACGG CATA
                                    _  TAAAAC   A
GAM911  SNCA      3'  ATGCTTATAAGCAACATGA   24583     GA       CC
                                TCA  TTGCTTATG  CGT
                                |||  |||||||||  |||
                                AGT  AACGAATAT  GTA
                                  AC        TC
GAM911  SNCA      3'  ATGCTTATAAGCAACATGA   6226      GA       CC
                                TCA  TTGCTTATG  CGT
                                |||  |||||||||  |||
                                AGT  AACGAATAT  GTA
                                  AC        TC
GAM911  C1orf24   3'  ATACAGGGCATGAGCAACTGA  54781      A         _
                                TCAG TTGCTTATGCCC GTAT
                                ||||  ||||||||||||  ||||
                                AGTC AACGAGTACGGG CATA
                                  _          A
GAM911  C22orf4   3'  ATACAGGCATAAGTGATGTG   61269    G  TG       C
                                CA AT  CTTATGCC GTAT
                                ||  ||  ||||||||  ||||
                                GT TA  GAATACGG CATA
                                 G  GT       A
GAM911  FLJ13231  3'  ATACAATGTGTAGCAATC    43814        T   CC_
                                GATTGCT ATGC   GTAT
                                |||||||  ||||   ||||
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                                CTAACGA TGTG   CATA
                                   _   TAA
GAM911  KIAA0493  3'  ATACTCTTAAGCAATCTGG   64926          TGCCC
                                TCAGATTGCTTA    GTAT
                                ||||||||||||   ||||
                                GGTCTAACGAAT    CATA
                                     TCT__
GAM911  MSTP032   3'  ACTGGAGACAAGCAATCTGA  48202          ATG_ C
                                TCAGATTGCTT   CC GT
                                ||||||||||   || ||
                                AGTCTAACGAA   GG CA
                                     CAGA  T
GAM911  NIBAN     3'  ATACAGGGCATGAGCAACTGA  42238     A         _
                                TCAG TTGCTTATGCCC GTAT
                                |||| ||||||||||| ||||
                                AGTC AACGAGTACGGG CATA
                                  _         A
GAM911  PRO2831   5'  ATATTTGCATACAATCTGA   38197       CT    CC
                                TCAGATTG  TATGC  GTAT
                                ||||||||  |||||  ||||
                                AGTCTAAC  ATACG  TATA
                                   __    TT
GAM911  PSMD12    3'  ATACAGTACTGAAGTAATCTGA 12535         A__   CC
                                TCAGATTGCTT   TGC  GTAT
                                ||||||||||   |||  ||||
                                AGTCTAATGAA   ATG  CATA
                                     GTC   A_
GAM911  TA-KRP    3'  ATACGGGTAACAATCTGA    51671       CTTA
                                TCAGATTG   TGCCCGTAT
                                ||||||||   |||||||||
                                AGTCTAAC   ATGGGCATA
                                   A___
GAM911  LOC148529 5'  ACGCCCCCATAGCAATCTGA  85318         T   CC__
                                TCAGATTGCT ATG   CGT
                                |||||||||| |||   |||
                                AGTCTAACGA TAC   GCA
                                     _  CCCC
GAM911  LOC170372 3'  TACAGTAGCAGTCTGA     76858         TAT  CC
                                TCAGATTGCT   GC  GTA
                                ||||||||||   ||  |||
                                AGTCTGACGA   TG  CAT
                                     ___  A_
GAM911  LOC202460 5'  ATACGATGGTAATGAACAATCT 90665        C   _  __
          GA                     TCAGATTG TTAT GCC  CGTAT
                                ||||||||| |||| |||  |||||
                                AGTCTAAC AGTA TGG  GCATA
                                   A   A   TA
GAM911  LOC254413 5'  ACAGTATGTACAATCTGG    98909        CT    CC
                                TCAGATTG  TATGC  GT
                                ||||||||  |||||  ||
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                                GGTCTAAC  GTATG  CA
                                    AT    A_
GAM911  LOC255809 3'  ACAGGCATGGGCCTGG     98580     ATT       C
                                TCAG   GCTTATGCC GT
                                ||||   ||||||||| ||
                                GGTC   CGGGTACGG CA
                                  ___       A
GAM912  EMR1    3'  GAACACCTGGCTACCA     10517     C       CC
                                TGGT AGCCAGGTG  TTC
                                |||| |||||||||  |||
                                ACCA TCGGTCCAC  AAG
                                  _       __
GAM912  POLS    3'  TGAATTGGCCTGGCTACCA   23783     C      GCC
                                TGGT AGCCAGGT   TTCA
                                |||| ||||||||   ||||
                                ACCA TCGGTCCG   AAGT
                                  _       GTT
GAM912  SLC22A3  3'  AGGGACTAAGCTCCTAGCTGAC 42038       C   T  CT__  A
            CA                    TGGTCAGC AGG GC    TC CCT
                                |||||||| ||| ||    || |||
                                ACCAGTCG TCC CG    AG GGA
                                    A   T  AATC  _
GAM912  ARTN    3'  CAGGTGAAGGGACAACTGACTA 15610       CCAG  G
                                TGGTCAG    GT CCTTCACCTG
                                |||||||    || ||||||||||
                                ATCAGTC    CA GGAAGTGGAC
                                    AA__  G
GAM912  ARTN    3'  CAGGTGAAGGGACAACTGACTA 55108       CCAG  G
                                TGGTCAG    GT CCTTCACCTG
                                |||||||    || ||||||||||
                                ATCAGTC    CA GGAAGTGGAC
                                    AA__  G
GAM912  ARTN    3'  CAGGTGAAGGGACAACTGACTA 55111       CCAG  G
                                TGGTCAG    GT CCTTCACCTG
                                |||||||    || ||||||||||
                                ATCAGTC    CA GGAAGTGGAC
                                    AA__  G
GAM912  ARTN    3'  CAGGTGAAGGGACAACTGACTA 55136       CCAG  G
                                TGGTCAG    GT CCTTCACCTG
                                |||||||    || ||||||||||
                                ATCAGTC    CA GGAAGTGGAC
                                    AA__  G
GAM912  FLJ10211  5'  CAGACAAAGGCACCGAGGCCA  36363      AGCCA      CAC
                                TGGTC    GGTGCCTT   CTG
                                |||||    ||||||||   |||
                                ACCGG    CCACGGAA   GAC
                                  AG___       ACA
GAM912  FLJ13089  3'  CAGGCAAAAGCAACATCTGGTT 71427           C__   CA_
            GACCA                 TGGTCAGCCAGGTG   CTT   CCTG
                                |||||||||||||   |||   ||||
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                                ACCAGTTGGTCTAC  GAA  GGAC
                                      AAC  AAC
GAM912  KIAA1280  5'  GATTAACCTGGCTGACTA   70280          GCCT
                                TGGTCAGCCAGGT   TC
                                ||||||||||||   ||
                                ATCAGTCGGTCCA   AG
                                      ATT_
GAM912  LRG       3'  CAGGTGAAACTCGGGGCTGTCC 54816    T    A_ _  GCC
          A                      TGG CAGCC  G GT  TTCACCTG
                                ||| |||||  | ||  ||||||||
                                ACC GTCGG  C CA  AAGTGGAC
                                  T    GG T  ___
GAM912  LOC155434 3'  GGAGGCACCCGACTACCA    87691     C  CCA
                                TGGT AG  GGTGCCTTC
                                |||| ||  |||||||||
                                ACCA TC  CCACGGAGG
                                  _  AGC
GAM912  LOC196484 5'  CAGGTCACCACCTGGCTGACC  63537          CCTTC
                                GGTCAGCCAGGTG    ACCTG
                                ||||||||||||    |||||
                                CCAGTCGGTCCAC    TGGAC
                                      CAC__
GAM912  LOC256158 5'  AGGCATCCCCCGGCCGACCA  99478     A  A___
                                TGGTC GCC   GGTGCCT
                                ||||| |||   |||||||
                                ACCAG CGG   CTACGGA
                                   C  CCCC
GAM912  LOC91069  3'  CAGGTCACCACCTGGCTGACC  65400          CCTTC
                                GGTCAGCCAGGTG    ACCTG
                                ||||||||||||    |||||
                                CCAGTCGGTCCAC    TGGAC
                                      CAC__
GAM912  LOC93624  3'  CAGGCAAGAGCCGTCTGACC  73099     CCA  GC  CA
                                GGTCAG  GGT  CTT  CCTG
                                ||||||  |||  |||  ||||
                                CCAGTC  CCG  GAA  GGAC
                                   TG_  A_  C_
GAM913  SCAMP1    3'  GCTAAATAAATATTCTCC    54500    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C    A
GAM913  SCAMP1    3'  GCTAAATAAATATTCTCC    54501    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C    A
GAM913  NX-17     3'  TGAATATCAGCCCCTAATA   40706       ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
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                                ATAATCCC    TATAAGT
                                    CGAC
GAM913   LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
           TA                    TATTAGGGATAATATTCATTTAGC
                                 ||||||||||||||||||||||||
                                 ATAATCCCTATTATAAGTAAATCG

GAM914   BCAT1    3'  AGAAAACAAAGAGGCATACT   66782    C       AAT
                                 AG ATGCCTCTT   TTTTCT
                                 || |||||||||   ||||||
                                 TC TACGGAGAA   AAAAGA
                                  A        AC_
GAM914   ETF1     3'  AGAAAAATTAAATTGCTGC    17587     T  CTC
                                 GCA GC   TTAATTTTTCT
                                 ||| ||   ||||||||||
                                 CGT CG   AATTAAAAAGA
                                   _  TTA
GAM914   EXTL2    5'  AGAAGGATAGATGCACGCTA   9325      A   C   TA
                                 TAGC TGC TCT  ATTTTTCT
                                 |||| ||| |||  ||||||||
                                 ATCG ACG AGA  TAGGAAGA
                                   C   T   __
GAM914   FOXE1    3'  AGAAAAATTAAGTTAGGGCA   16777      ___
                                 TGCCT   CTTAATTTTTCT
                                 |||||   ||||||||||||
                                 ACGGG   GAATTAAAAAGA
                                    ATT
GAM914   FZD3     3'  AGAAAAATGCTGGAACATGCT  34257      CC   TA_
                                 AGCATG  TCT   ATTTTTCT
                                 ||||||  |||   ||||||||
                                 TCGTAC  AGG   TAAAAAGA
                                    A_   TCG
GAM914   RRM2B    3'  AAAAATTAAGAGTGTGTT    68429       C
                                 AGCATGC TCTTAATTTTT
                                 ||||||| ||||||||||
                                 TTGTGTG AGAATTAAAAA
                                        _
GAM914   ZNF132   3'  AGAAAAATTACCTCCATGCT   14286      CCTCT
                                 AGCATG    TAATTTTTCT
                                 ||||||    ||||||||||
                                 TCGTAC    ATTAAAAAGA
                                    CTCC_
GAM914   BAP29    3'  AGAAAAATATAAGCATGTTA  61331       CTCTTA
                                 TAGCATGC     ATTTTTCT
                                 ||||||||     ||||||||
                                 ATTGTACG     TAAAAAGA
                                      AATA__
GAM914   FAM8A1   3'  AGAAAAATCTGGCATACTG   33197     C    TCTTA
                                 TAG ATGCC    ATTTTTCT
                                 ||| |||||    ||||||||
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                                GTC TACGG    TAAAAAGA
                                  A    TC___
GAM914  FLJ10648  3'  AGAAAAATTAGGTTCCATGC  36888     CCT
                                GCATG  CTTAATTTTTCT
                                |||||  ||||||||||||
                                CGTAC  GGATTAAAAAGA
                                   CTT
GAM914  FLJ10970  3'  AGAAAAATCAAGATAGGCCTG 37476   T  __   A
                                CA GCC  TCTT ATTTTTCT
                                || |||  |||| ||||||||
                                GT CGG  AGAA TAAAAAGA
                                 C  AT   C
GAM914  FLJ14735  3'  AAAAACTGATGAGGCATGC   52663       _  A
                                GCATGCCTC TTA TTTTT
                                ||||||||| ||| |||||
                                CGTACGGAG AGT AAAAA
                                      T  C
GAM914  KIAA0830  3'  AGAAAAATAGCGGAGGCA    70266      TA_
                                TGCCTCT  ATTTTTCT
                                |||||||  ||||||||
                                ACGGAGG  TAAAAAGA
                                    CGA
GAM914  KIAA0907  3'  AGAAAAATTAAGCTGGGCA   30862     __
                                TGCCT  CTTAATTTTTCT
                                |||||  ||||||||||||
                                ACGGG  GAATTAAAAAGA
                                   TC
GAM914  KIAA1348  3'  AGAAACTTTGAGCCATGCTA  69116      CCT   TT
                                TAGCATG  CTTAA  TTTCT
                                |||||||  |||||  |||||
                                ATCGTAC  GAGTT  AAAGA
                                    C__    TC
GAM914  PLAGL2    3'  AGAAATGAAAGGCATGC    70952      C  ATT
                                GCATGCCT TTA  TTTCT
                                |||||||| |||  |||||
                                CGTACGGA AGT  AAAGA
                                    A  ___
GAM914  RNF2      3'  AGAAAAATTAAATTGGTAGT  24256    A  TC_
                                GC TGCC  TTAATTTTTCT
                                || ||||  ||||||||||
                                TG ATGG  AATTAAAAAGA
                                 _   TTA
GAM914  LOC143146 3'  AGAAAATGGCCGAGGCATGCTA 60763        TTAAT
                                TAGCATGCCTC    TTTTCT
                                ||||||||||    ||||||
                                ATCGTACGGAG    AAAAGA
                                      CCGGT
GAM914  LOC146059 3'  AGAAAAGTCCAGAGATGC    78082     GC   TA
                                GCAT  CTCT  ATTTTTCT
                                ||||  ||||  ||||||||
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                                CGTA  GAGA  TGAAAAGA
                                  __    CC
GAM914   LOC151391 3'  AGAAAGATCAAAGCATGC    86511       CTC  A
                                GCATGC   TT ATTTTTCT
                                ||||||   || ||||||||
                                CGTACG   AA TAGAAAGA
                                   A__  C
GAM914   LOC157507 5'  AAAGAAGAGGAGGCAACTA   82374     CA      AA
                                TAG  TGCCTCTT  TTTTT
                                |||  ||||||||  |||||
                                ATC  ACGGAGGA  AGAAA
                                  A_       GA
GAM914   LOC158434 3'  AAAAATTACAAGGCATGC    88156        CT
                                GCATGCCT  TAATTTTT
                                ||||||||  ||||||||
                                CGTACGGA  ATTAAAAA
                                     AC
GAM914   LOC220020 5'  AGAAAACAGGTGAAGGCATGC  95043        _ TTAAT
                                GCATGCCT C     TTTTCT
                                |||||||| |     ||||||
                                CGTACGGA G     AAAAGA
                                     A TGGAC
GAM914   LOC221979 3'  AGAGTGCAGAAGGCATGC    94216        _  TA
                                GCATGCCT CT  ATTTT
                                |||||||| ||  |||||
                                CGTACGGA GA  TGAGA
                                     A  CG
GAM914   LOC92078  3'  AGAAATCCGAAGAGGCAGCTA  68588      A       AATT
                                TAGC TGCCTCTT    TTTCT
                                |||| ||||||||    |||||
                                ATCG ACGGAGAA    AAAGA
                                   _       GCCT
GAM914   LOC92080  5'  AGAAAAATCAAGACCATGTTA  68617        CC    A
                                TAGCATG  TCTT ATTTTTCT
                                |||||||  |||| ||||||||
                                ATTGTAC  AGAA TAAAAAGA
                                     C_   C
GAM915   BBS4      3'  ATTTGCCCAAAGGGAATCCAGA 53447         G_ G_   A
            ACA                    TGTTCTGGA  CT  TTGG CAAAT
                                |||||||||  ||  |||| |||||
                                ACAAGACCT  GG  AACC GTTTA
                                     AA  GA    C
GAM915   CENTD2    3'  CCAACAAACTCCAGAACA    58270         C_
                                TGTTCTGGAG  TGTTGG
                                ||||||||||  ||||||
                                ACAAGACCTC  ACAACC
                                     AA
GAM915   CENTD2    3'  CCAACAAACTCCAGAACA    31539         C_
                                TGTTCTGGAG  TGTTGG
                                ||||||||||  ||||||
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                                ACAAGACCTC  ACAACC
                                      AA
GAM915  HAMP     3'  TCCTGCTGCCCCAGAACA    41289        A  T  T
                                TGTTCTGG GC GT GGA
                                |||||||| || || |||
                                ACAAGACC CG CG CCT
                                     C  T  T
GAM915  ITGA11   3'  TCTGCCGGCCCCCAGGACA   25213        A_   TT
                                TGTTCTGG  GCTG  GGA
                                ||||||||  ||||  |||
                                ACAGGACC  CGGC  TCT
                                     CC    CG
GAM915  KITLG    3'  ATTTGCATGGCTCCAGAA    8023           TGGA
                                TTCTGGAGCTGT   CAAAT
                                ||||||||||||   |||||
                                AAGACCTCGGTA   GTTTA
                                       C___
GAM915  KITLG    3'  ATTTGCATGGCTCCAGAA    15671          TGGA
                                TTCTGGAGCTGT   CAAAT
                                ||||||||||||   |||||
                                AAGACCTCGGTA   GTTTA
                                       C___
GAM915  MAPK4    5'  CCTGGGCAGCTCCAGATCA   12300    T         __
                                TG TCTGGAGCTGTT  GG
                                || ||||||||||||  ||
                                AC AGACCTCGACGG  CC
                                 T          GT
GAM915  MGAT2    3'  ATTTGTCCAAACAGGACA    11557       GAGCTG
                                TGTTCTG     TTGGACAAAT
                                |||||||     ||||||||||
                                ACAGGAC     AACCTGTTTA
                                    A_____
GAM915  PSPHL    5'  TTGTCATACAGCTCCAAACA   94499      C       TG
                                TGTT TGGAGCTGT  GACAA
                                |||| |||||||||  |||||
                                ACAA ACCTCGACA  CTGTT
                                   _        TA
GAM915  TTC3     3'  TATTTGTCCAACAACTGTCAGA 13885        _ C
             ATA                   TGTTCTGG AG TGTTGGACAAATA
                                |||||||| || ||||||||||||||
                                ATAAGACT TC ACAACCTGTTTAT
                                     G  A
GAM915  FLJ14213 3'  TGATAACAGCTCCAGAA     46218           GA
                                TTCTGGAGCTGTTG  CA
                                ||||||||||||||  ||
                                AAGACCTCGACAAT  GT
                                       A_
GAM915  H2BFQ    3'  TTTAAGAGAACTCCAGGACA   60079          __ G
                                TGTTCTGGAG  CT TTGGA
                                ||||||||||  || |||||
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```
                                ACAGGACCTC  GA AATTT
                                     AA  G
GAM915  LRG      3'  TCCATCCATGCTTCCTAGAACA 54825       _  _ _ T_
                                TGTTCT GGA GC TG  TGGA
                                |||||| ||| || ||  ||||
                                ACAAGA CCT CG AC  ACCT
                                   T   T  T  CT
GAM915  NMT2     3'  ATTTGTCCATGTAACAGAACA  17852       GA  TGT
                                TGTTCTG  GC   TGGACAAAT
                                |||||||  ||   |||||||||
                                ACAAGAC  TG   ACCTGTTTA
                                   AA  T__
GAM915  NYD-SP21  3'  TATTTGTCCAATCTAGATTCAG 51863         G  __
            AACA                   TGTTCTGGA CT  GTTGGACAAATA
                                |||||||||  ||  ||||||||||||
                                ACAAGACTT GA  TAACCTGTTTAT
                                     A  TC
GAM915  PSPH     3'  TTGTCGTACAGCTCCAAACA   17143     C       TG
                                TGTT TGGAGCTGT  GACAA
                                ||||  |||||||||  |||||
                                ACAA ACCTCGACA  CTGTT
                                  _       TG
GAM915  LOC122258 3'  CCACCAGCCTCCGGAACA    59820          _  T
                                TGTTCTGGAG CTG TGG
                                |||||||||| ||| |||
                                ACAAGGCCTC GAC ACC
                                     C   C
GAM915  LOC151826 3'  ATTTGTCCAACCTAGCACA   81176     T   AGCT
                                TGT CTGG   GTTGGACAAAT
                                |||  ||||   ||||||||||
                                ACA GATC   CAACCTGTTTA
                                  C   ____
GAM915  LOC169611 3'  TCCAGTGGCAGCTCCAGAA   83663          ___
                                TTCTGGAGCTGT   TGGA
                                ||||||||||||   ||||
                                AAGACCTCGACG   ACCT
                                       GTG
GAM915  LOC196746 3'  TCAGAGCAGCTCCAAGACA   88903     TC       G_
                                TGT  TGGAGCTGTT  GA
                                |||  ||||||||||  ||
                                ACA  ACCTCGACGA  CT
                                  GA        GA
GAM915  LOC204119 5'  TGCCACAACTCAGAACA     92343       G  C   T  A
                                TGTTCTG AG TGT GG CA
                                ||||||| || ||| || ||
                                ACAAGAC TC ACA CC GT
                                   _  A   _  _
GAM915  LOC253142 5'  TTGCTAGGATGCCCCAGAATA  99230        A  TG_   A
                                TGTTCTGG GC   TTGG CAA
                                |||||||| ||   |||| |||
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                                ATAAGACC CG   GATC GTT
                                    C  TAG   _
GAM916  CDH12    3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM916  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM916  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090      T    AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                   _   GTCA_
GAM916  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
            A                    TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM916  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM916  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
            TA                    TACA   TCC   GAAGAATAAG
                                ||||   |||   ||||||||||
                                ATGT   AGG   TTTCTTATTC
                                  AAA_   ATTG
GAM916  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68742             _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                          G
GAM916  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM916  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748      CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM916  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
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                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM916  OSBPL11   3' CTTAATTTCCCAAGAGTGGTG 43206       CCAA    AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                    AACC   A_
GAM916  YME1L1    3' TCATTCTTGATGTGGTGTA   58438       TCC     _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                    TA_    A
GAM916  ZNF262    3' CTTATTTTGTTTGGGAGT    18723        A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                    G
GAM916  LOC91960  3' TGTGGCTTGGAACGTGGTGTA  68294       TC_    AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
                                ATGTGGTG   GGTTC   TGT
                                    CAA    GG__
GAM917  STAF65(gamma) 3' AACAGGAAATAGCTAAACAC   30054    GAGC   C
                                GTG   GGC ATTTCCTGTT
                                |||   ||| ||||||||||
                                CAC   TCG TAAAGGACAA
                                  AAA_  A
GAM917  TReP-132  5' AACAGGAACACCTGGCTCCAGC 37914    AG     __ CCAT
          CA                    TG  TGGAGC  GG   TTCCTGTT
                                ||  ||||||  ||   ||||||||
                                AC  ACCTCG  CC   AAGGACAA
                                 CG     GT  AC__
GAM917  TReP-132  5' AACAGGAACACCTGGCTCCAGC 54271    AG     __ CCAT
          CA                    TG  TGGAGC  GG   TTCCTGTT
                                ||  ||||||  ||   ||||||||
                                AC  ACCTCG  CC   AAGGACAA
                                 CG     GT  AC__
GAM917  TReP-132  5' AACAGGAACACCTGGCTCCAGC 54275    AG     __ CCAT
          CA                    TG  TGGAGC  GG   TTCCTGTT
                                ||  ||||||  ||   ||||||||
                                AC  ACCTCG  CC   AAGGACAA
                                 CG     GT  AC__
GAM918  BPI       3' AAGTGCATGGTGTGTA      9951        A   A
                                TACACA CCA TGCATTT
                                ||||||  ||| |||||||
                                ATGTGT GGT ACGTGAA
                                    _   _
GAM918  CLN5      3' AGATGTAAGTTGTGTA      22427        CAA
                                TACACAAC   TGCATTT
                                ||||||||   |||||||
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                                ATGTGTTG  ATGTAGA
                                    A__
GAM918  IGF1    3' AAATGCATGGGTGTTGTA   7055     CA  A
                                TACA  ACC ATGCATTT
                                ||||  ||| ||||||||
                                ATGT  TGG TACGTAAA
                                  TG  G
GAM918  MADD    3' AAATGTACAGTTGTGTG    56205      CAA
                                TACACAAC  TGCATTT
                                ||||||||  |||||||
                                GTGTGTTG  ATGTAAA
                                    AC_
GAM918  MADD    3' AAATGTACAGTTGTGTG    56219      CAA
                                TACACAAC  TGCATTT
                                ||||||||  |||||||
                                GTGTGTTG  ATGTAAA
                                    AC_
GAM918  MADD    3' AAATGTACAGTTGTGTG    56223      CAA
                                TACACAAC  TGCATTT
                                ||||||||  |||||||
                                GTGTGTTG  ATGTAAA
                                    AC_
GAM918  MADD    3' AAATGTACAGTTGTGTG    56227      CAA
                                TACACAAC  TGCATTT
                                ||||||||  |||||||
                                GTGTGTTG  ATGTAAA
                                    AC_
GAM918  MADD    3' AAATGTACAGTTGTGTG    56231      CAA
                                TACACAAC  TGCATTT
                                ||||||||  |||||||
                                GTGTGTTG  ATGTAAA
                                    AC_
GAM918  MADD    3' AAATGTACAGTTGTGTG    14854      CAA
                                TACACAAC  TGCATTT
                                ||||||||  |||||||
                                GTGTGTTG  ATGTAAA
                                    AC_
GAM918  PKNOX1  3' AAATGTACAGCGTTGTGTG  17096      CAA_
                                TACACAAC  TGCATTT
                                ||||||||  |||||||
                                GTGTGTTG  ATGTAAA
                                    CGAC
GAM918  PON2    3' AAATGTATGGCATGTGTA    6122     A_  A
                                TACACA  CCA TGCATTT
                                ||||||  ||| |||||||
                                ATGTGT  GGT ATGTAAA
                                   AC  _
GAM918  ABCA5   3' AAATGCTGTGGTTGTGTG    38532       AT
                                TACACAACCA  GCATTT
                                ||||||||||  ||||||
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                                GTGTGTTGGT  CGTAAA
                                      GT
GAM918  CHRAC1   3'  AAATGCATGGTTTTGTA    34324     C    A
                                TACA AACCA TGCATTT
                                |||| ||||| |||||||
                                ATGT TTGGT ACGTAAA
                                  T    _
GAM918  COE2     3'  AAATGTTTGTTGGATGTGTA  64900      A    __
                                TACACA CCAAT  GCATTT
                                |||||| |||||  ||||||
                                ATGTGT GGTTG  TGTAAA
                                   A    TT
GAM918  FLJ11155 3'  AAATGCATAGTTGGTA     37691     A    CA
                                TAC CAAC  ATGCATTT
                                ||| ||||  ||||||||
                                ATG GTTG  TACGTAAA
                                  _   A_
GAM918  FLJ11896 3'  AAATGTGTTGGCTATGTG    60930     A__
                                CACA   CCAATGCATTT
                                ||||   ||||||||||||
                                GTGT   GGTTGTGTAAA
                                  ATC
GAM918  KCNH8    3'  AAATGCACTACTGTTGTGTA   58901       CAA__
                                TACACAAC    TGCATTT
                                ||||||||    |||||||
                                ATGTGTTG    ACGTAAA
                                     TCATC
GAM918  PER3     3'  TAAATGCCACCTACAGGTTGTG 34175        AAT_____     ___
           TA                    TACACAACC      GCATTT   A
                                |||||||||       ||||||  |
                                ATGTGTTGG      CGTAAA   T
                                     ACATCCAC    ___
GAM918  TTY7     3'  AGGTGCAGGTGTGTA      50016      A  AA
                                TACACA CC  TGCATTT
                                |||||| ||  |||||||
                                ATGTGT GG  ACGTGGA
                                   _ __
GAM918  LOC129607 3'  AAATGCAATGTTTGTTGTGTA  75395       ___  A
                                TACACAAC   CA TGCATTT
                                ||||||||   || |||||||
                                ATGTGTTG   GT ACGTAAA
                                     TTT  A
GAM918  LOC155434 3'  AAATGTACTGTTGTGTG     87687       CAA
                                TACACAAC   TGCATTT
                                ||||||||   |||||||
                                GTGTGTTG   ATGTAAA
                                     TC_
GAM919  ACVRL1   5'  TTTATTAGGAGGGAGTGGTG   5240         AAGAAG
                                CACCACTCCC     AATAAG
                                ||||||||||     ||||||
```

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                                GTGGTGAGGG     TTATTT
                                     AGGA__
GAM919  BCL11B   3'  TTTGTTTTTGGGGTGGGGGGTG 57582       A_ __      G  TAAG
            TG                    TACACC  CT  CCCAAGAA AA
                                  ||||||  ||  |||||||| ||
                                  GTGTGG  GG  GGGTTTTT TT
                                     GG  TG       G  T
GAM919  C18orf1  3'  CTTCGTGTGGGAGTGGTGTG   60865           A__
                                  TACACCACTCCCA   GAAG
                                  ||||||||||||   ||||
                                  GTGTGGTGAGGGT   CTTC
                                        GTG
GAM919  ITPR3    3'  CTTGTTTTTCTCCTTTTGGTGT 11085       CTCCCA
            A                     TACACCA     AGAAGAATAAG
                                  |||||||     ||||||||||
                                  ATGTGGT     TCTTTTTGTTC
                                      TTTCC_
GAM919  KCNAB1   3'  GTTTGTTTTTTTTTGAAGGGGG 61585          ____
            TGGTGTG                 TACACCACTCCC    AAGAAGAATAAG   T
                                  ||||||||||||   ||||||||||||  |
                                  GTGTGGTGGGGG    TTTTTTTTGTTT   G
                                        AAGT
GAM919  KRAS2    3'  CTTATTTTTCTTACCAAGTGTG 54123     C   CCC_
                                  CAC ACT    AAGAAGAATAAG
                                  ||| |||    ||||||||||||
                                  GTG TGA    TTCTTTTTATTC
                                    _   ACCA
GAM919  KRAS2    3'  CTTATTTTTCTTACCAAGTGTG 54124     C   CCC_
                                  CAC ACT    AAGAAGAATAAG
                                  ||| |||    ||||||||||||
                                  GTG TGA    TTCTTTTTATTC
                                    _   ACCA
GAM919  LIFR     3'  TTTGTTTTTTTTGGTTGGTTG  11315    C    CTC
                                  A ACCA   CCAAGAAGAATAAG
                                  | ||||   ||||||||||||||
                                  G TGGT   GGTTTTTTTTGTTT
                                   T    T__
GAM919  MEN1     5'  CTTGTTTTTTTCCTTTTGGTG  56348       CTCCCA
                                  CACCA     AGAAGAATAAG
                                  |||||     ||||||||||
                                  GTGGT     TTTTTTTGTTC
                                     TTTCC_
GAM919  MLLT7    3'  TTGTGCCTGGGAGTGTGTG    21043     _       AGAAGA
                                  CAC CACTCCCA     ATAA
                                  ||| ||||||||     ||||
                                  GTG GTGAGGGT     TGTT
                                    T       CCG___
GAM919  SIAH1    3'  TTTGTTTTTGCCGTGGGAGTGT 13128     _       AG__
            GTG                     CAC CACTCCCA    AAGAATAAG
                                  ||| ||||||||    |||||||||
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                                GTG GTGAGGGT    TTTTTGTTT
                                  T       GCCG
GAM919  SLC7A6   3'  TTTGTTTTTGTGGTGGGTGCTG 15646      C     _   AG
              TG                  TACA CACTC CCA  AAGAATAAG
                                  |||| ||||| |||  |||||||||
                                  GTGT GTGGG GGT  TTTTTGTTT
                                    C    T   G_
GAM919  STAT6    5'  ATTTTTCTTTTTGGTGGTGGTG 13448       TC         TAAG
                                  CACCAC  CCAAGAAGAA
                                  ||||||  ||||||||||
                                  GTGGTG  GGTTTTTCTT
                                     GT         TTTAT
GAM919  TCF8     3'  CTTGTTTTTTTAAGAGTGTGTG 48429     _     CCA
                                  CAC CACTC   AGAAGAATAAG
                                  ||| |||||   ||||||||||
                                  GTG GTGAG   TTTTTTTGTTC
                                    T    AA_
GAM919  B3GNT7   3'  TTGTTCTTGGCTGGTGGGTG   71685     A    C_      G
                                  TAC CCACT  CCAAGAA AA
                                  ||| |||||  ||||||| ||
                                  GTG GGTGG  GGTTCTT TT
                                    _    TC      G
GAM919  BCDO     3'  TTATTCTTTCTGTGGGTG    34287       C  AG
                                  CACTC CA  AAGAATAA
                                  ||||| ||  ||||||||
                                  GTGGG GT  TTCTTATT
                                     T  CT
GAM919  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
              A                    TACAC       AGAAGAATAAG
                                  |||||       ||||||||||||
                                  ATGTG       TCTTCTTATTC
                                     TACTCCC_
GAM919  EPN2     3'  TTTATTTTTCTTTGACTCGTGT 31046       CAC  CC
              G                    TACAC   TC  AAGAAGAATAAG
                                  |||||   ||  ||||||||||||
                                  GTGTG   AG  TTCTTTTTATTT
                                     CTC  T_
GAM919  FLJ13855  3'  GGGTATTTTTCTTGGGGGTGGA 43853     A              AG
              GTA                  TAC CCACTCCCAAGAAGAATA
                                  ||| ||||||||||||||||||
                                  ATG GGTGGGGGTTCTTTTTAT
                                    A              GGGA
GAM919  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126          CCCAAGAA
                                  TACACCACT       GAATAAG
                                  |||||||||       |||||||
                                  ATGTGGTGA       TTTATTC
                                        AGACG___
GAM919  FLJ32865  3'  TTTGTTGGGGGTGGGGTG    58824     A         G
                                  TAC CCACTCCCAA AAG
                                  ||| |||||||||| |||
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                                GTG GGTGGGGGTT TTT
                                  G       G
GAM919  GRP3     3'  TTGTTCTTCTTGGTGTG    31742    TC
                                CAC  CCAAGAAGAATAA
                                |||  ||||||||||||
                                GTG  GGTTCTTCTTGTT
                                  T_
GAM919  HAND1    3'  TTTGTTCTTCGAATCGTGGTG  17880      TCCCAA
                                CACCAC     GAAGAATAAG
                                ||||||     ||||||||||
                                GTGGTG     CTTCTTGTTT
                                   CTAAG_
GAM919  KIAA0562 3'  TTTGTTTTGCGGGGGTGGTG   28834        AAGA
                                CACCACTCCC    AGAATAAG
                                ||||||||||    ||||||||
                                GTGGTGGGGG    TTTTGTTT
                                      CG__
GAM919  KIAA0871 5'  TTTATTTTTTTGGTGTGTGTGT 31023      _  TC       ATAAG
           G                     TACAC CAC  CCAAGAAGA
                                |||||  |||  |||||||||
                                GTGTG GTG  GGTTTTTTT
                                   T  T_       ATTT
GAM919  KIAA0970 3'  TTTGTTTTTTTTGTTAGGGTG  30622     A  CC
                                CACC CT  CAAGAAGAATAAG
                                ||||  ||  ||||||||||||
                                GTGG GA  GTTTTTTTTGTTT
                                  _ TT
GAM919  KIAA1240 3'  TTTATTTTTAGGGAGTGGGTA  67297     A       AAG
                                TAC CCACTCCC   AAGAATAAG
                                |||  ||||||||   |||||||||
                                ATG GGTGAGGG   TTTTTATTT
                                  _       A__
GAM919  KIAA1719 3'  TCTGTCTTGGGAGTGGTGTA   68742             _
                                TACACCACTCCCAAGA AGA
                                ||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                          G
GAM919  KIAA1750 3'  TTTATTTTTTTGTTCTAGGTGT 68815       ACTCCCA
           G                     TACACC      AGAAGAATAAG
                                ||||||      ||||||||||||
                                GTGTGG      TTTTTTTATTT
                                   ATCTTG_
GAM919  MAP2K3   3'  CTTGTTTTTCTTGCATGGT    59686     CTCC
                                ACCA    CAAGAAGAATAAG
                                ||||    ||||||||||||||
                                TGGT    GTTCTTTTTGTTC
                                  AC__
GAM919  MLN64    3'  CTTGTTGGGGAGTGGGTG    96062     A       _  G
                                TAC CCACTCCC AA AAG
                                ||| |||||||| || |||
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                                GTG GGTGAGGG TT TTC
                                  _      G  G
GAM919  NY-REN-41 3'  TTTGTTTTTCTATCCTGGTGG  55564      CCCA_
                                CCACT     AGAAGAATAAG
                                |||||     ||||||||||
                                GGTGG     TCTTTTTGTTT
                                   TCCTA
GAM919  PRO1489   5'  TTTGTTTTTCGTGTGTGTGTG  38334      _  TCCCAA
                                TACAC CAC     GAAGAATAAG
                                ||||| |||     ||||||||||
                                GTGTG GTG     CTTTTTGTTT
                                   T  TG____
GAM919  SEC15L    3'  TTTGTTCTACTTGGGTGGT    72731     CT     A
                                ACCA  CCCAAG AGAATAAG
                                ||||  |||||| ||||||||
                                TGGT  GGGTTC TCTTGTTT
                                  __     A
GAM919  SHAPY     3'  TTTGTTCTTTTTGGAACTGTG  57915     TC__
                                CAC    CCAAGAAGAATAAG
                                |||    ||||||||||||||
                                GTG    GGTTTTTCTTGTTT
                                  TCAA
GAM919  STAM2     3'  TGTTTTTCTTCCTGCAATGTGG 20709        TCC_  A     TAAG
           TGTG                   TACACCAC    CA GAAGAA
                                |||||||    || ||||||
                                GTGTGGTG    GT CTTCTT
                                     TAAC  C     TTTGTT
GAM919  TUBGCP3   3'  TTTATTTTTTTTTAGTGTTGTA 21982     C    CCC
                                TACA CACT   AAGAAGAATAAG
                                |||| ||||   ||||||||||||
                                ATGT GTGA   TTTTTTTTATTT
                                  T    T__
GAM919  ZNF220    3'  CTTGTTTTTTTACCACCTGGTG 23157      CTCCCA
                                CACCA     AGAAGAATAAG
                                |||||     ||||||||||
                                GTGGT     TTTTTTTGTTC
                                   CCACCA
GAM919  LOC121219 5'  TTGTTCTATGGGTGGGTG    74493     ACT    AGA
                                CACC   CCCA   AGAATAA
                                ||||   ||||   |||||||
                                GTGG   GGGT   TCTTGTT
                                  GT_    A__
GAM919  LOC143146 3'  TTTGTTGGAGGTGGTGTA    60767       TC    G
                                TACACCAC  CCAA AAG
                                ||||||||  |||| |||
                                ATGTGGTG  GGTT TTT
                                     GA    G
GAM919  LOC146445 3'  TTGTTCTTTGTGTGGTTG    84687    C    TCCCAA
                                A ACCAC     GAAGAATAA
                                | |||||     |||||||||
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```
                                G TGGTG     TTTCTTGTT
                                 T    TG____
GAM919   LOC150174 3'  TTTATTTTTTTTTACAATGGTG 80444      CTCCC
                                CACCA    AAGAAGAATAAG
                                ||||||    ||||||||||||
                                GTGGT    TTTTTTTTATTT
                                   AACAT
GAM919   LOC150213 3'  TTTATTTTTTTTACAATGGTG  75363      CTCCC
                                CACCA    AAGAAGAATAAG
                                ||||||    ||||||||||||
                                GTGGT    TTTTTTTTATTT
                                   AACA_
GAM919   LOC150236 3'  TTTATTTTTTTTACAATGGTG  80505      CTCCC
                                CACCA    AAGAAGAATAAG
                                ||||||    ||||||||||||
                                GTGGT    TTTTTTTTATTT
                                   AACA_
GAM919   LOC154084 3'  CTTGTTTTTTTTAGTAGGTGTG  87378      _  CCCA
                                TACACC ACT    AGAAGAATAAG
                                |||||| |||    ||||||||||
                                GTGTGG TGA    TTTTTTTGTTC
                                   A  ____
GAM919   LOC170261 3'  TTTATTCTTTGTGAAAGTGGT  83472      CC  A
                                ACCACT  CA GAAGAATAAG
                                ||||||  ||  ||||||||||
                                TGGTGA  GT TTTCTTATTT
                                   AA  G
GAM919   LOC199692 3'  CTTGTTCTTCTGCTGTAGTGTG 59926      C  TCCCA
                                TACAC AC     AGAAGAATAAG
                                ||||| ||     ||||||||||
                                GTGTG TG     TCTTCTTGTTC
                                   A  TCG__
GAM919   LOC203414 3'  CTTGTCAACTGGGGGTGATGTG 90913      C       A AA  A
                                TACA CACTCCCA G  GA TAAG
                                |||| |||||||| |  || ||||
                                GTGT GTGGGGGT C  CT GTTC
                                   A       _ AA  _
GAM919   LOC222256 3'  TTTTTCTTGTGGTGT       95915        TCCC
                                ACACCAC    AAGAAGAA
                                |||||||    ||||||||
                                TGTGGTG    TTCTTTTT
                                             ____
GAM919   LOC257051 3'  TTTATTCTTTGTGAAAGTGGT  98054      CC  A
                                ACCACT  CA GAAGAATAAG
                                ||||||  ||  ||||||||||
                                TGGTGA  GT TTTCTTATTT
                                   AA  G
GAM919   LOC92303  3'  TTATTTTTTTTGAGGTGG    69400      CC
                                CCACT  CAAGAAGAATAA
                                |||||  ||||||||||||
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                                GGTGG  GTTTTTTTTATT
                                  A_
GAM920  DLEC1    3'  CATCTGGCCCTCCCTTG    24716      A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                  C    G  _
GAM920  DLEC1    3'  CATCTGGCCCTCCCTTG    96279      A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                  C    G  _
GAM920  PIP5K1A  3'  TATCCCACCCTGCCTTGATA  14520        A   CA  C
                                TATCAAGG AGGG  GG GTG
                                |||||||| ||||  || |||
                                ATAGTTCC TCCC  CC TAT
                                    G   A_  C
GAM920  SOX11    3'  ACCCACCCCCCCTTGGTA    13308        AA   CA  C
                                TATCAAGG  GGG  GG GT
                                ||||||||  |||  || ||
                                ATGGTTCC  CCC  CC CA
                                    CC   A_  _
GAM920  CHL1     3'  TGTTACCTTTCCTCAATA    22768     CA      CA
                                TAT  AGGAAGGG  GGCG
                                |||  ||||||||  ||||
                                ATA  TCCTTTCC  TTGT
                                  AC       A_
GAM920  EPB41L1  3'  CATTCTGCCCTTCCCTGA    71104     A        C
                                TCA GGAAGGGCAGG GTG
                                ||| |||||||||| |||
                                AGT CCTTCCCGTCT TAC
                                  C         _
GAM920  FLJ00060 3'  CATACCCCCTGCCCTCCTCTGA 61741     _   A      CGTG
                                TCA AGGA GGGCAGG    ATG
                                ||| |||| |||||||    |||
                                AGT TCCT CCCGTCC    TAC
                                  C   _      CCCA
GAM920  FLJ10898 5'  CACCACAGCCCTTTCTCAATA  60126     CA       AGGC
                                TAT  AGGAAGGGC    GTG
                                |||  |||||||||    |||
                                ATA  TCTTTCCCG    CAC
                                  AC        ACAC
GAM920  FLJ22557 3'  ATCATCCCATCCTTAATA    45581     C    A   CAGGC
                                TAT AAGGA GGG     GTGAT
                                ||| ||||| |||     |||||
                                ATA TTCCT CCC     TACTA
                                  A    A  _____
GAM920  KIAA0574 3'  CATCCCCTGCCCTCCCCTGA   69808     A  A      CGT
                                TCA GG AGGGCAGG   GATG
                                ||| || ||||||||   ||||
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                                AGT CC TCCCGTCC   CTAC
                                  C  C       C__
GAM920  KIAA0632  3'  CACCTCAGAAACCCTTCCTTGA 32071          CA___  C
                                TCAAGGAAGGG     GG GTG
                                ||||||||||     || |||
                                AGTTCCTTCCC     CT CAC
                                      AAAGA  C
GAM920  KIAA1045  3'  CATCACATGTCCTTCC      71599         GGC
                                GGAAGGGCA   GTGATG
                                |||||||||   ||||||
                                CCTTCCTGT   CACTAC
                                      A__
GAM920  KIAA1354  5'  CAGTGACTGCCTTCCCTTGATA 61572        A      G  _
                                TATCAAGG AGGGCAG CG TG
                                |||||||| ||||||| || ||
                                ATAGTTCC TTCCGTC GT AC
                                     C      A  G
GAM920  MGC20460  5'  CACCGCCTCCTACCCTTCTT   54901        C___    _
                                AGGAAGGG    AGGCG TG
                                ||||||||    ||||| ||
                                TTCTTCCC    TCCGC AC
                                     ATCC     C
GAM920  LOC158476 3'  CACGCCCGCCCCCCCCATTGA  88186      _  AA_    A
                                TCAA GG   GGGC GGCGTG
                                |||| ||   |||| ||||||
                                AGTT CC   CCCG CCGCAC
                                  A  CCC    C
GAM920  LOC90459  3'  CACACCCGCCTAATTTTTG    63550       A_    A  C
                                CAAGGA  GGGC GG GTG
                                ||||||  |||| || |||
                                GTTTTT  TCCG CC CAC
                                   AA    C  A
GAM921  AAAS      3'  TAAGTTTTCCTTTTGTTTTCCA 32243          TA   TT
                                TGGAAAGCAGG  GAG  GGCTTG
                                ||||||||||  |||  ||||||
                                ACCTTTTGTTT  CTT  TTGAAT
                                      TC   __
GAM921  ABCG2     3'  CAAGTTTTTTTGTTGTTTTCT  17892        GGTA   TT
                                GGAAAGCA    GAG  GGCTTG
                                ||||||||    |||  ||||||
                                TCTTTTGT    TTT  TTGAAC
                                     TG__    TT
GAM921  ABR       3'  GTTCCTTCTACTGCTTTTCA   42009          G     TT
                                TGGAAAGCAG TAGAG  GGC
                                |||||||||| |||||  |||
                                ACTTTTCGTC ATCTT  TTG
                                      _     CC
GAM921  ACTB      3'  GGCATGGCTTTATTTGTTTTTT 8465                _   TG
                                GGAAAGCAGGTAGAGTTG GCT
                                |||||||||||||||||| |||
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                                TTTTTTGTTTATTTCGGT CGG
                                          A   T
GAM921  ADAM22   3'  CAAATCTATCTGCTCTTCA   41665     A       G
                                TGGA AGCAGGTAGA TTG
                                |||| |||||||||| |||
                                ACTT TCGTCTATCT AAC
                                  C        A
GAM921  ADAM22   3'  TAGGCTAACTTTAAACATGTAT 41666      _  GG__
           TTTTA                  TGGAAA GCA   TAGAGTTGGCTTG
                                |||||| |||   ||||||||||||
                                ATTTTT TGT   ATTTCAATCGGAT
                                   A   ACAA
GAM921  ADAM22   3'  TAGGCTAACTTTAAACATGTAT 41667      _  GG__
           TTTTA                  TGGAAA GCA   TAGAGTTGGCTTG
                                |||||| |||   ||||||||||||
                                ATTTTT TGT   ATTTCAATCGGAT
                                   A   ACAA
GAM921  AGL      5'  GACTCTGCCTGCTTCTCA    7214     GA
                                TG  AAGCAGGTAGAGTT
                                ||  ||||||||||||||
                                AC  TTCGTCCGTCTCAG
                                 TC
GAM921  AIM1     3'  GCAAGCCCAGCCAAATTTTGTT 93466          TAGA_    _
           TTTT                   GGAAAGCAGG    GTTGG CTTG   C
                                ||||||||||    ||||| ||||   |
                                TTTTTTGTTT    CGACC GAAC   G
                                     TAAAC    C
GAM921  AKAP13   3'  TAGGCCGGGTGCCCCTGTTCTC 91253     A     TAGAG
           C                    GGA AGCAGG    TTGGCTTG
                                ||| ||||||    ||||||||
                                CCT TTGTCC    GGCCGGAT
                                  C     CCGTG
GAM921  ALEX1    5'  TGGGCCAGAGCGAGCCTGTTTT 33976         AGAG_
                                AAAGCAGGT    TTGGCTTG
                                |||||||||    ||||||||
                                TTTTGTCCG    GACCGGGT
                                     AGCGA
GAM921  ALP      3'  CAAGTTGATTTTGCAATTGT   27879      __      TG
                                GCAG  GTAGAGT  GCTTG
                                ||||  |||||||  |||||
                                TGTT  CGTTTTA  TGAAC
                                  AA      GT
GAM921  ALX4     3'  TGGGCCACGCCCATGTTTTCCA 41920         _  TAGA  T
                                TGGAAAGCA GG    GT GGCTTG
                                ||||||||| ||    || ||||||
                                ACCTTTTGT CC    CA CCGGGT
                                     A  CG__  _
GAM921  APG5L    3'  GAGCTAGCTGGCTGTCCA    17939      A   AGGTAG
                                TGGA AGC     AGTTGGCTT
                                |||| |||     |||||||||
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                                ACCT TCG     TCGATCGAG
                                  G  G_____
GAM921  APM1    3'  TGAGTTGTGTGCCTGTTTCT  17795      G     GAGT
                                GGAAA CAGGTA   TGGCTTG
                                ||||| ||||||   |||||||
                                TCTTT GTCCGT   GTTGAGT
                                  _     GT__
GAM921  APPL    3'  TAAGCTTTATATTTGCTT    24956        GAGTT
                                AAGCAGGTA    GGCTTG
                                |||||||||    ||||||
                                TTCGTTTAT    TCGAAT
                                     ATT__
GAM921  APPL    3'  TGAGTTAATTTTGCATTATATC 24960      AAGCAG
           TA                     TGGA     GTAGAGTTGGCTTG
                                ||||     ||||||||||||||
                                ATCT     CGTTTTAATTGAGT
                                  ATATTA
GAM921  AREG    3'  GAGTCGGTCCTCTTTCCA    9763        C   TAGA TT
                                TGGAAAG AGG    G  GGCTT
                                ||||||| |||    |  |||||
                                ACCTTTC TCC    T  CTGAG
                                   _  _____ GG
GAM921  ARHGAP6  5'  TGAGCTGGGCTTTGCTCTCCA  26432     A    GGTA  _ TG
                                TGGA AGCA    GAG T  GCTTG
                                |||| ||||    ||| |  |||||
                                ACCT TCGT    TTC G  CGAGT
                                  C    _____   G GT
GAM921  ARHGEF6  3'  GGGCTGTTGTCTGCTTGCT    68759         GT_
                                AGCAGGTAGA   TGGCTT
                                ||||||||||   ||||||
                                TCGTTCGTCT   GTCGGG
                                     GTT
GAM921  ASH2L    3'  CGGGAGACTGCCTGCCTTTCA  72012      A     AG    GG
                                TGGAA GCAGGT  AGTT  CTTG
                                ||||| ||||||  ||||  ||||
                                ACTTT CGTCCG  TCAG  GGGC
                                  C      __    A_
GAM921  ATF6    3'  TGAGCAAAATGCTGCTTTCT   64652        G  GAGTTG
                                GGAAAGCAG TA     GCTTG
                                ||||||||| ||     |||||
                                TCTTTCGTC GT     CGAGT
                                     _  AAAA__
GAM921  ATP11A   3'  CAATTTCATCTGCTTTCTA   77552          AG
                                TGGAAAGCAGGT  AGTTG
                                ||||||||||||  |||||
                                ATCTTTCGTCTA  TTAAC
                                      CT
GAM921  ATP1B1   3'  GCAAGCCATGTTTTATTGTATC 9819           G  _______
           TGTTTTCTA               TGGAAAGCAGGTA AGT     TGGCTTG  C
                                |||||||||||| |||     |||||||  |
```

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                                ATCTTTTGTCTAT TTA     ACCGAAC   G
                                       G   TTTTGT
GAM921  ATP6V1C1  3'  AGTATCCTTTGCTTGCTTCT   9889      A        TTG   TG
                                GGAA GCAGGTAGAG   GCT
                                |||| ||||||||||   |||
                                TCTT CGTTCGTTTC   TGA
                                  _        CTA   T
GAM921  ATRN      3'  GGCTCGGAGCCTGTTTCCA   24860       G    A__
                                TGGAAA CAGGT   GAGTT
                                |||||| |||||   |||||
                                ACCTTT GTCCG   CTCGG
                                   _    AGG
GAM921  ATSV      3'  CAGGTCGATTTGGTCTCTTTTT 16308        C   TA
              A                  TGGAAAG AGG  GAGTTGGCTTG
                                |||||||| |||  ||||||||||
                                ATTTTTC TCT  TTTAGCTGGAC
                                   _  GG
GAM921  B4GALT5   3'  CAGGCCTTGTTTTGTTTGTTT  17683      GG    TT_
                                AAGCA  TAGAG   GGCTTG
                                |||||  |||||   ||||||
                                TTTGT  GTTTT   CCGGAC
                                  TT    GTT
GAM921  B4GALT5   3'  TAAGCTATAGCATATGTTTTTT 17692         GGTAGAGT
              A                  TGGAAAGCA       TGGCTTG
                                |||||||||       |||||||
                                ATTTTTTGT       ATCGAAT
                                     ATACGAT_
GAM921  BAT4      5'  CAGGCTGATTTTTTTTTCC    53740       CAGGT    TG
                                GGAAAG    AGAGT  GCTTG
                                ||||||    |||||  |||||
                                CCTTTT    TTTTA  CGGAC
                                   T____    GT
GAM921  BCL10     3'  ATTACAATTTTATCTGTTTCC  15366       G         GCTTG
                                GGAAA CAGGTAGAGTTG
                                ||||| ||||||||||||
                                CCTTT GTCTATTTTAAC
                                  _          ATTAA
GAM921  BCL2A1    5'  TGAGCCAGCTCAAGACTTTGCT 15752      A    _ A__
              CTCCA                TGGA AGCAG GT   GAGTTGGCTTG
                                |||| ||||| ||   ||||||||||
                                ACCT TCGTT CA   CTCGACCGAGT
                                  C    T  GAA
GAM921  BCRP2     3'  TAAGCTGAGAGTCTCTTGTTTG 63070     _      T   G  __
              TCT                  GGA AAGCAGG AGA TT  GGCTTG
                                ||| ||||||| ||| ||  ||||||
                                TCT TTTGTTC TCT AG  TCGAAT
                                  G      _  G  AG
GAM921  BGN       3'  TGAGCTGGGACTGCTTTCT    9926          GTAGAG TG
                                GGAAAGCAG     T  GCTTG
                                |||||||||     |  |||||
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                                TCTTTCGTC     G  CGAGT
                                     AG____ GT
GAM921  BTG2     3'  CCTGCCAGCTCTGCCTCCTTTT 23144        C          TTG
              CA                    TGGAAAG AGGTAGAGTTGGC
                                    ||||||| ||||||||||||
                                    ACTTTTC TCCGTCTCGACCG
                                        C           TCCT
GAM921  BUB3     3'  GGAAAGCTTTGTTTGCTTCC   17552      A   GG      GG  TG
                                    GGAA GCA  TAGAGTT  CT
                                    |||| |||  |||||||  ||
                                    CCTT CGT  GTTTCGA  GG
                                      _  TT       AA  T
GAM921  C18orf1  3'  TGAGTCAGAAAAATGTTGTTTT 60874          GTAGAG_
              TCA                    TGGAAAGCAG      TTGGCTTG
                                    ||||||||||      ||||||||
                                    ACTTTTTGTT      GACTGAGT
                                         GTAAAAA
GAM921  C7       3'  ACTCTTTTGCCTCCTTTTTA   6976         C   ___
                                    TGGAAAG AGGT   AGAGT
                                    ||||||| ||||   |||||
                                    ATTTTTC TCCG   TCTCA
                                        C    TTT
GAM921  CALCR    3'  TAAGTCCATTAACTGCTTTCCA 9985           GTAG   T
                                    TGGAAAGCAG    AGT GGCTTG
                                    ||||||||||    ||| ||||||
                                    ACCTTTCGTC    TTA CTGAAT
                                         AA__   C
GAM921  CALM2    3'  CAAGTTGTATATTTGTTTTCCA 9986            GAGT
                                    TGGAAAGCAGGTA    TGGCTTG
                                    ||||||||||||||    |||||||
                                    ACCTTTTGTTTAT    GTTGAAC
                                           AT__
GAM921  CAPN10   3'  TGAGCCGGCTCTGCCTCCTGCC 41447    AA  C
                                    GG  AG AGGTAGAGTTGGCTTG
                                    ||  || ||||||||||||||||
                                    CC  TC TCCGTCTCGGCCGAGT
                                     G_  C
GAM921  CAPN10   3'  TGAGCCGGCTCTGCCTCCTGCC 41448    AA  C
                                    GG  AG AGGTAGAGTTGGCTTG
                                    ||  || ||||||||||||||||
                                    CC  TC TCCGTCTCGGCCGAGT
                                     G_  C
GAM921  CAPN10   3'  TGAGCCGGCTCTGCCTCCTGCC 43871    AA  C
                                    GG  AG AGGTAGAGTTGGCTTG
                                    ||  || ||||||||||||||||
                                    CC  TC TCCGTCTCGGCCGAGT
                                     G_  C
GAM921  CARD4    3'  CGAGTTGGTCACCGCTCTTTTC 21440        CA_   A  G TG
              A                     TGGAAAG   GGT GA T  GCTTG
                                    |||||||   ||| || |  |||||
```

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                              ACTTTTC  CCA CT G  TGAGC
                                  TCG  _  _ GT
GAM921  CASP2   3' AGGCCAGCTCCTTTTCTGT   53320     TA__
                              GCAGG   GAGTTGGCTT
                              |||||   ||||||||||
                              TGTCT   CTCGACCGGA
                                 TTTC
GAM921  CASP2   3' AGGCCAGCTCCTTTTCTGT   53321     TA__
                              GCAGG   GAGTTGGCTT
                              |||||   ||||||||||
                              TGTCT   CTCGACCGGA
                                 TTTC
GAM921  CASP2   3' AGGCCAGCTCCTTTTCTGT   53322     TA__
                              GCAGG   GAGTTGGCTT
                              |||||   ||||||||||
                              TGTCT   CTCGACCGGA
                                 TTTC
GAM921  CASP8   3' TTGGCTAACTATATTTGCTTTT 54086         G     TG
          T                    GGAAAGCAGGTA AGTTGGCT
                              ||||||||||| ||||||||
                              TTTTTCGTTTAT TCAATCGG
                                    A      TTC
GAM921  CASP8   3' TTGGCTAACTATATTTGCTTTT 54087         G     TG
          T                    GGAAAGCAGGTA AGTTGGCT
                              ||||||||||| ||||||||
                              TTTTTCGTTTAT TCAATCGG
                                    A      TTC
GAM921  CASQ1   3' CAGGCCAGCTCTCTCTTATCT  8777    AAGC  GT
                              GGA   AG  AGAGTTGGCTTG
                              |||   ||  ||||||||||||
                              TCT   TC  TCTCGACCGGAC
                                AT__  TC
GAM921  CBFA2T3  3' TGGGTTGATTCTCGACTGCTTT 19021       GT_   TG
          TC                   GGAAAGCAG   AGAGT  GCTTG
                              |||||||||   |||||  |||||
                              CTTTTCGTC   TCTTA  TGGGT
                                   AGC    GT
GAM921  CBFB    3' CAGGCTGGCTTCTGTTTT    43437      GTA   TG
                              AAAGCAG   GAGT  GCTTG
                              |||||||   ||||  |||||
                              TTTTGTC   TTCG  CGGAC
                                  ___    GT
GAM921  CBFB    3' CAGGCTGGCTTCTGTTTT    10035      GTA   TG
                              AAAGCAG   GAGT  GCTTG
                              |||||||   ||||  |||||
                              TTTTGTC   TTCG  CGGAC
                                  ___    GT
GAM921  CBR1    5' GAGCCAGGTCTGTTCTCCA   10042     A   GGTA  G
                              TGGA AGCA    GA TTGGCTT
                              |||| ||||    || |||||||
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                                ACCT TTGT    CT GACCGAG
                                  C    ____  G
GAM921  CCNDBP1  3'  CAGGCTCTGATACCTGCTTTT  25117          GAGTT
                                GAAAGCAGGTA    GGCTTG
                                ||||||||||    ||||||
                                TTTTCGTCCAT    TCGGAC
                                     AGTC_
GAM921  CD83     3'  CAAGTTGATTTAGTGTTTTT  16169       GGTA   TG
                                GAAAGCA   GAGT  GCTTG
                                |||||||   ||||  |||||
                                TTTTTGT   TTTA  TGAAC
                                   GA__   GT
GAM921  CDC25C   5'  TGAGCTAGGTTTTGTTTTTC  10136        GTA  G
                                GGAAAGCAG   GA TTGGCTTG
                                |||||||||   || ||||||||
                                CTTTTTGTT   TT GATCGAGT
                                     ___  G
GAM921  CDH20    3'  ACTCTCGTATCTGTTTTTTA  49939          ___
                                TGGAAAGCAGGT   AGAGT
                                ||||||||||||   |||||
                                ATTTTTTGTCTA   TCTCA
                                      TGC
GAM921  CDKN2C   3'  CAAGTTGAAGACTTTGTTTTT  55316        _  AGAG TG
                                GAAAGCAG GT    T  GCTTG
                                |||||||| ||    |  |||||
                                TTTTTGTT CA    A  TGAAC
                                     T  GA__ GT
GAM921  CELSR2   3'  GTTTTATTTATTTGCTTTTT  9197            GTT
                                GGAAAGCAGGTAGA   GGC
                                ||||||||||||||   |||
                                TTTTTCGTTTATTT   TTG
                                      ATT
GAM921  CELSR3   3'  GCTATTTTGTCTGCTGTCCA  9187      A    GT    T
                                TGGA AGCAG  AGAGT GGC
                                |||| |||||  ||||| |||
                                ACCT TCGTC  TTTTA TCG
                                  G    TG    _
GAM921  CENPB    3'  TGAGCCTGCTTCTGCCTGCTTT 70120            _  T
           CCA                    TGGAAAGCAGGTAGA GT GGCTTG
                                ||||||||||||||| || ||||||
                                ACCTTTCGTCCGTCT CG CCGAGT
                                      T  T
GAM921  CENTD1   3'  CAAGCATTTTGTCTTTTTTC  58276      C  GT    TG
                                GAAAG AG  AGAGT  GCTTG
                                |||||  ||  |||||  |||||
                                CTTTT TC  TTTTA  CGAAC
                                  T  TG    __
GAM921  CHN2     3'  CCACTTGATTTGTTTTCCA   15795          A   T
                                TGGAAAGCAGGT GAGT GG
                                ||||||||||| |||| ||
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                                ACCTTTTGTTTA TTCA CC
                                      G   _
GAM921  CHRM1    3'  AAGTGTGCCTGCTATCCA    96429      A       GAGTTG
                                TGGA AGCAGGTA     GCTT
                                |||| ||||||||      ||||
                                ACCT TCGTCCGT     TGAA
                                  A       G_____
GAM921  CHST6    3'  TGAGCTGACGCCTCTGCTTTCC 41505          TAGA  TG
                                GGAAAGCAGG    GT  GCTTG
                                ||||||||||    ||  |||||
                                CCTTTCGTCT    CA  CGAGT
                                      CCG_  GT
GAM921  CLASP2   3'  CAAATCATCTGCCTGTTTTTT  65201            GT  GC
                                GGAAAGCAGGTAGA  TG  TTG
                                ||||||||||||||  ||  |||
                                TTTTTTGTCCGTCT  AC  AAC
                                      __  TA
GAM921  CLCN3    5'  CAGGTTGACTCTAGGGATCTCC 10204      AAGCAGG     TG
          A                      TGGA      TAGAGT  GCTTG
                                ||||      ||||||  |||||
                                ACCT      ATCTCA  TGGAC
                                  CTAGGG_     GT
GAM921  CLCN4    3'  CAGGTATCATGTCTGCTTTCTA 10208          GT GAGTTG
                                TGGAAAGCAG  A     GCTTG
                                ||||||||||  |     |||||
                                ATCTTTCGTC  T     TGGAC
                                      TG ACTA__
GAM921  CLCN5    3'  GGTTTAATTATATTTGCTTTTT 5385           G     _  TG
          A                      TGGAAAGCAGGTA AGTTGG CT
                                ||||||||||||| |||||| ||
                                ATTTTTCGTTTAT TTAATT GG
                                      A     T  T
GAM921  CLECSF12 3'  CAGGCTAATTTTTGGTGTTTTT 77204         GGT
          T                      GGAAAGCA   AGAGTTGGCTTG
                                ||||||||   ||||||||||||
                                TTTTTTGT   TTTTAATCGGAC
                                     GGT
GAM921  CLECSF12 3'  TAGGAAAGTTTTCTGCTTTTTA 77221           T   G  GG
                                TGGAAAGCAGG AGA TT  CTTG
                                |||||||||| ||| ||  ||||
                                ATTTTTCGTCT TTT AA  GGAT
                                      _  G  A_
GAM921  COL4A2   3'  TGGGCCTGGCCCTGCTTTCTA  10245          TAGA  _
                                TGGAAAGCAGG    GTT GGCTTG
                                ||||||||||    ||| ||||||
                                ATCTTTCGTCC    CGG CCGGGT
                                      ____  T
GAM921  COL4A4   3'  TAAGCCAATTTCAATCTTATTT 5407      GC    A_
                                AAA  AGGT  GAGTTGGCTTG
                                |||  ||||  ||||||||||
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                                TTT  TCTA  TTTAACCGAAT
                                  AT    AC
GAM921  COX10    3'  TGAGCCAGGGCCTGCATTTTT  8949       _     AGAGT
                                GGAAA GCAGGT     TGGCTTG
                                |||||| ||||||     |||||||
                                TTTTT CGTCCG     ACCGAGT
                                   A     GG___
GAM921  COX15    3'  TAAGTCAGCAAATCTTCTGTTT 16491           T  ___
           TTTA                    TGGAAAGCAGG AGA   GTTGGCTTG
                                |||||||||||| |||   |||||||||
                                ATTTTTTGTCT TCT   CGACTGAAT
                                      _  AAA
GAM921  CPNE3    3'  CAGGCTGAGAGGGGACCTGCTT 15343    A       AGAG__ TG
           GCT                     GG AAGCAGGT     T  GCTTG
                                || ||||||||     |  |||||
                                TC TTCGTCCA     A  CGGAC
                                 G       GGGGAG GT
GAM921  CPNE3    3'  CATTTTTATTTGCCTTTCTA   15344        _       T
                                TGGAAAG CAGGTAGAG TG
                                ||||||| ||||||||| ||
                                ATCTTTC GTTTATTTT AC
                                    C        T
GAM921  CPSF6    3'  AAGTAAATGCTTGTTTTT    23788           GAGTTG
                                GAAAGCAGGTA     GCTT
                                ||||||||||     ||||
                                TTTTTGTTCGT     TGAA
                                      AAA___
GAM921  CREBL2   3'  GCTGCTCTCCTTGCTTTCT   8970          T    T
                                GGAAAGCAGG AGAGT GGC
                                |||||||||| ||||| |||
                                TCTTTCGTTC TCTCG TCG
                                      C    _
GAM921  CRMP1    3'  CAAGCCAGCTCTAGGCTTC   8971      A  AGG
                                GAA GC   TAGAGTTGGCTTG
                                ||| ||   ||||||||||||||
                                CTT CG   ATCTCGACCGAAC
                                  _  G__
GAM921  CRSP6    3'  GGGTTTCTATGTGCTTTTTA   16221         G     TTG   G
                                TGGAAAGCA GTAGAG   GCTT
                                |||||||| ||||||   ||||
                                ATTTTTCGT TATCTT   TGGG
                                     G     ___
GAM921  CRSP6    5'  TGGGCCAGCTCCTTTGTTTCCA 16224       G    TA
                                TGGAAA CAGG  GAGTTGGCTTG
                                |||||| ||||  ||||||||||||
                                ACCTTT GTTT  CTCGACCGGGT
                                   _   C_
GAM921  CSK      5'  CAGGTTGGCTTTACTGTGACTC 16504    AA_   G     TG
                                GA   GCAG TAGAGT  GCTTG
                                ||   |||| ||||||  |||||
```

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                                CT   TGTC ATTTCG  TGGAC
                                 CAG   _     GT
GAM921  CSNK2A1  3'  TAGGCTGATTTTCTTTTTTCT  10318       C   T    TG
                                GGAAAG AGG AGAGT  GCTTG
                                ||||||| ||| |||||  |||||
                                TCTTTT TTC TTTTA  CGGAT
                                   _  _    GT
GAM921  CTNNA1   3'  TAAGTTGATTAAAAATGCTTTT 66503        GGTAG   TG
                                GAAAGCA    AGT  GCTTG
                                |||||||    |||  |||||
                                TTTTCGT    TTA  TGAAT
                                    AAAAA   GT
GAM921  CTSD     3'  CAAGCCCGACTTGCTGTTTT   10341        GTA     _
                                AAAGCAG   GAGTTGG CTTG
                                |||||||   ||||||| ||||
                                TTTTGTC   TTCAGCC GAAC
                                    G__      C
GAM921  CYP27B1  3'  AAGCCTTATTTGTTTTTTA   7603             AGTT
                                TGGAAAGCAGGTAG   GGCTT
                                ||||||||||||||   |||||
                                ATTTTTTGTTTATT   CCGAA
                                                 ____
GAM921  CYP4A11  3'  TGAGTTAAAAGAACCTGCTCTC 7592       A      AGAG
           CA                    TGGA AGCAGGT    TTGGCTTG
                                ||||| |||||||   ||||||||
                                ACCT TCGTCCA    AATTGAGT
                                  C      AGAA
GAM921  D12S2489E 5'  GAAGAACTCTGATCTGCTTTCT 24761           _     GGCTTG
           A                     TGGAAAGCAGGT AGAGTT
                                ||||||||||||| ||||||
                                ATCTTTCGTCTA TCTCAA
                                       G     GAAGC
GAM921  DACH     3'  TAAGACCTAGCTTTGTTTTTTT 55825        C GG     _ _
           CTA                    TGGAAAG A  TAGAGTT GG CTTG
                                ||||||| |  ||||||| || ||||
                                ATCTTTT T  GTTTCGA CC GAAT
                                   _ TT      T  A
GAM921  DIAPH2   3'  TGAGTTAAAAGGTTTGTTTCCC 24597     A    GG AGAG
           A                     TGG AAGCA  T    TTGGCTTG
                                ||| |||||  |   ||||||||
                                ACC TTTGT  G    AATTGAGT
                                  C    TT GAA_
GAM921  DIRC1    3'  TGAGTCAATTAAGCCTTTTT   54752      C    AG
                                AAAG AGGT  AGTTGGCTTG
                                |||| ||||  ||||||||||
                                TTTT TCCG  TTAACTGAGT
                                  _    AA
GAM921  DMD      3'  GCCATTTTATTTCTTTTT    15721        C        T
                                GGAAAG AGGTAGAGT GGC
                                |||||| ||||||||| |||
```

```
                                TTTTTC TTTATTTTA CCG
                                     _      _
GAM921  DMD     3'  GCCATTTTATTTCTTTTT    15722       C       T
                                GGAAAG AGGTAGAGT GGC
                                |||||| ||||||||| |||
                                TTTTTC TTTATTTTA CCG
                                     _      _
GAM921  DRD1    3'  GAGCCCTCTGCTGCTTTCCA  7670          G    TT    G
                                TGGAAAGCAG TAGAG  GGCTT
                                |||||||||| |||||  |||||
                                ACCTTTCGTC GTCTC  CCGAG
                                     _    __    A
GAM921  DUOX2   3'  TAAGTCCACCTGTTTATCA   26869     A      A  G
                                TGG AAGCAGGT GA TTG
                                ||| |||||||| || |||
                                ACT TTTGTCCA CT AAT
                                  A       C  G
GAM921  DUSP7   3'  CAGTTTGGCTGTTTTTTA    66040         G   G
                                TGGAAAGCAG TAGA TTG
                                |||||||||| ||||| |||
                                ATTTTTTGTC GTTT GAC
                                     G   _
GAM921  DXS1283E 3'  TGAGTCAATTTTATGGTTCTC  71389    A   AG
                                GA AGC  GTAGAGTTGGCTTG
                                || |||  ||||||||||||||
                                CT TTG  TATTTTAACTGAGT
                                 C   G_
GAM921  DXYS155E 3'  CAGGCTGCAAACTTGTTTT   18686        AGA  T
                                AAAGCAGGT   GT GGCTTG
                                |||||||||   || ||||||
                                TTTTGTTCA   CG TCGGAC
                                     AA_  _
GAM921  DYRK1A  3'  AGGTCAATTTTTTTTCTG    56072     T__
                                CAGG   AGAGTTGGCTT
                                ||||   ||||||||||
                                GTCT   TTTTAACTGGA
                                  TTT
GAM921  DYRK1A  3'  AGGTCAATTTTTTTTCTG    56073     T__
                                CAGG   AGAGTTGGCTT
                                ||||   ||||||||||
                                GTCT   TTTTAACTGGA
                                  TTT
GAM921  EBI3    3'  TGGGCTGGAGTCCTTGCTTTGC 20441    _      TAGAG TG
          T                      GG AAAGCAGG    T  GCTTG
                                || ||||||||    |  |||||
                                TC TTTCGTTC    G  CGGGT
                                 G       CTGA_ GT
GAM921  EDN2    3'  GGACTCTCTGCCTGCTTCC    10484     A        TTGG
                                GGAA GCAGGTAGAG    CT
                                |||| ||||||||||    ||
```

```
                                CCTT CGTCCGTCTC    GG
                                  _        TCA_
GAM921  EDN3     3'  TAGGTTGAATATTTGCTTTC   5482          GAG TG
                                GAAAGCAGGTA   T  GCTTG
                                ||||||||||   |  |||||
                                CTTTCGTTTAT   A  TGGAT
                                      A__ GT
GAM921  EDNRA    3'  AAGTTCAATCTGTTTTTCA    64796          A  GTTG
                                TGGAAAGCAGGT GA    GCTT
                                ||||||||||||  ||    ||||
                                ACTTTTTGTCTA CT    TGAA
                                      A  ____
GAM921  EFNB1    3'  CAACTCATTTTCATCTGTTTTT 16667          A_____     GCTTG
           T                     GGAAAGCAGGT     GAGTTG
                                ||||||||||      ||||||
                                TTTTTTGTCTA     CTCAAC
                                      CTTTTA        G
GAM921  EGFL4    5'  CGGGCCGGTGGTTCCTGCTTTC 62463         TAGA TT
                                GAAAGCAGG    G  GGCTTG
                                |||||||||    |  ||||||
                                CTTTCGTCC    T  CCGGGC
                                     TTGG GG
GAM921  EIF4EBP2 3'  AACTTTGTTCTGTTTTCT    15853          TA_
                                GGAAAGCAGG   GAGTT
                                ||||||||||   |||||
                                TCTTTTGTCT   TTCAA
                                      TGT
GAM921  EMX2     3'  AAGACAGGTTCTGTGTGCTTTT 88951         GG    GT GG_   G
           TA                    TGGAAAGCA  TAGA  T   CTT
                                |||||||||  ||||  |   |||
                                ATTTTTCGT  GTCT  G   GAA
                                     GT    TG ACA   A
GAM921  EMX2     3'  CAGGCACAGGACTTTTTTGTTT 88953          T    __  _
           TTT                     GGAAAGCAGG AGAGT  TG GCTTG
                                ||||||||||  |||||  ||  |||||
                                TTTTTTGTTT TTTCA  AC CGGAC
                                     _    GG  A
GAM921  EPB41L2  3'  CAAGCTGGTAAGGTGCTGTTCA 9291       A    GGTAGA TT
                                TGGA AGCA     G  GGCTTG
                                ||||  ||||     |  ||||||
                                ACTT TCGT     T  TCGAAC
                                  G    GGAA__ GG
GAM921  ERBB2IP  3'  CAGACCATTAATTTTATTTGTT 38612            ___   _  TG
           TTT                     GAAAGCAGGTAGAGT   TGG CT
                                ||||||||||||||   |||  ||
                                TTTTTGTTTATTTTA   ACC GA
                                       ATT   A  C
GAM921  ESRRBL1  3'  CAATTTCTACCTTTTTCT    36322       C       _
                                GGAAAG AGGTAGAG TTG
                                ||||||  ||||||||  |||
```

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                                TCTTTT TCCATCTT AAC
                                   _       T
GAM921  ESRRG    3'  TAAGCCAATATATGTGCTTTTC 66990          G   GA
              A                   TGGAAAGCA GTA  GTTGGCTTG
                                  ||||||||| |||  |||||||||
                                  ACTTTTCGT TAT  TAACCGAAT
                                     G   A_
GAM921  EVA1     3'  TAGGTTGATTTCTTTCTTCAGC 59236        ___   T    _ TG
              TTTCT                 GGAAAGC   AGG AGAG T  GCTTG
                                  |||||||   ||| |||| |  |||||
                                  TCTTTCG   TCT TCTT A  TGGAT
                                     ACT   T    T GT
GAM921  F11      5'  TAAGCCAACAAGGTCTTTTCA  39460        _ AGGTAGA
                                  TGGAAAG C      GTTGGCTTG
                                  ||||||| |      |||||||||
                                  ACTTTTC G      CAACCGAAT
                                     T GAA____
GAM921  F2RL3    3'  AGGCTGATCCTTCTTTTCA    15496        C   TAGA  TG
                                  TGGAAAG AGG    GT  GCTT
                                  ||||||| |||    ||  ||||
                                  ACTTTTC TCC    TA  CGGA
                                     T   _____  GT
GAM921  F3       3'  CAAGCTAATTTTTGTATTTTTT 67674         CAGGT
              A                   TGGAAAG     AGAGTTGGCTTG
                                  |||||||     ||||||||||||
                                  ATTTTTT     TTTTAATCGAAC
                                     ATGT_
GAM921  FADD     3'  TGAGCCACAGACCACCTGCTTC 15127      A     AGAGT_
              T                   GGAA GCAGGT     TGGCTTG
                                  |||| ||||||     |||||||
                                  TCTT CGTCCA     ACCGAGT
                                    _     CCAGAC
GAM921  FANCC    3'  GAGTCAAGACTTGCTTTT    71042          AGAG
                                  GAAAGCAGGT    TTGGCTT
                                  ||||||||||    |||||||
                                  TTTTCGTTCA    AACTGAG
                                        G___
GAM921  FANCG    5'  CAGGCCAGCTTCACCCTTCC   17335      AGCA   AG
                                  GGAA    GGT  AGTTGGCTTG
                                  ||||    |||  ||||||||||
                                  CCTT    CCA  TCGACCGGAC
                                    C___   CT
GAM921  FAT      5'  CGGGCCAACTTTGCGATTCC   19129      AGCAG
                                  GGAA     GTAGAGTTGGCTTG
                                  ||||     ||||||||||||||
                                  CCTT     CGTTTCAACCGGGC
                                    AG___
GAM921  FAT      3'  GGGTTTCATTCTGTCTTTTTCC 19131        C  GT    T_    G
              A                   TGGAAAG AG  AGAGT  GGCTT
                                  ||||||| ||  |||||  |||||
```

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                                ACCTTTT TC  TCTTA  TTGGG
                                    _ TG    CT    A
GAM921  FBLN5    3'  GAGTAGCTAGTTTGCTTTTT  21996        TAG    G  G
                                GGAAAGCAGG  AGTTG CTT
                                ||||||||||  ||||| |||
                                TTTTTCGTTT  TCGAT GAG
                                    GA_    _
GAM921  FBXW1B   3'  GTGAGTTGGCTTTGCTTTTTTA 25478       _____       TG
          GTTTTTC               GGAAAGC    AGGTAGAGT  GCTTG   T
                                |||||||    |||||||||  |||||   |
                                CTTTTTG    TTCGTTTCG  TGAGT   G
                                   ATTTT       GT
GAM921  FCMD     3'  TGAGTCAGCTAGGATGCTGTTT 23048     A   GGTAG
          A                     TGGA AGCA    AGTTGGCTTG
                                |||| ||||    ||||||||||
                                ATTT TCGT    TCGACTGAGT
                                  G   AGGA_
GAM921  FKBP10   3'  GGCTGTAGTTAGCTTTTCA   41938        _ G  G
                                TGGAAAGC AG TA AGTT
                                |||||||| || || ||||
                                ACTTTTCG TT AT TCGG
                                    A  G  G
GAM921  FKBP1A   3'  CAGCATCTCCTGTTTTTT    55030         T  _
                                GGAAAGCAGG AGA GTTG
                                |||||||||| ||| ||||
                                TTTTTTGTCC TCT CGAC
                                    _  A
GAM921  FKBP6    3'  CAGGTGCTGTTTTCTGTTTTCC 76837         TAG_  TG
                                GGAAAGCAGG   AGT  GCTTG
                                ||||||||||   |||  |||||
                                CCTTTTGTCT   TCG  TGGAC
                                    TTTG  __
GAM921  FLRT2    5'  GCCTCTTCCTGTTTTCTA    26000         T  GTT
                                TGGAAAGCAGG AGA   GGC
                                |||||||||| |||   |||
                                ATCTTTTGTCC TCT   CCG
                                    T  ___
GAM921  FLT1     3'  TAAGCTGGCTCTGTTTGATGCT 10661    AAAG  GG    TG
          A                     TGG   CA  TAGAGT  GCTTG
                                |||   ||  ||||||  |||||
                                ATC   GT  GTCTCG  CGAAT
                                  GTA_  TT     GT
GAM921  FLT1     3'  TAAGCTGGCTCTGTTTGATGCT 10662    AAAG  GG    TG
          A                     TGG   CA  TAGAGT  GCTTG
                                |||   ||  ||||||  |||||
                                ATC   GT  GTCTCG  CGAAT
                                  GTA_  TT     GT
GAM921  FMR2     3'  TAGGTTTTCTGTTTTCTA    10699         T  G
                                TGGAAAGCAGG AGA TTG
                                |||||||||| ||| |||
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                                ATCTTTTGTCT TTT GAT
                                      _  G
GAM921  FOXO1A   3'  CAGGTCTTTTCTATTTTTTTTT 10648      C       TT
                                GAAAG AGGTAGAG  GGCTTG
                                ||||| ||||||||  ||||||
                                TTTTT TTTATCTT  CTGGAC
                                   T       TT
GAM921  FOXO1A   3'  GTTTGTACTACCTGTTTTCT   10654           AG TG
                                GGAAAGCAGGTAG  T  GC
                                ||||||||||||  |  ||
                                TCTTTTGTCCATC  G  TG
                                        AT TT
GAM921  FOXP2    5'  TGAGCTAGCTTCTGAGTTTTCC 27947        A_  TA
                                GGAAAGC  GG  GAGTTGGCTTG
                                |||||||  ||  ||||||||||
                                CCTTTTG  TC  TTCGATCGAGT
                                    AG  __
GAM921  FS       5'  CAGGCCAGCTGAGTCCGTTTTC 42080        A  TAG_
           C                     GGAAAGC GG    AGTTGGCTTG
                                |||||||  ||    ||||||||||
                                CCTTTTG CC    TCGACCGGAC
                                    _  TGAG
GAM921  FSTL1    3'  CAAGTTGACTTTATTCTTC    24005     AGCA       TG
                                GAA    GGTAGAGT  GCTTG
                                |||    ||||||||  |||||
                                CTT    TTATTTCA  TGAAC
                                  C___       GT
GAM921  FVT1     3'  TAGCATCTACTTGTTTTTC    10737             _
                                GGAAAGCAGGTAGA GTTG
                                |||||||||||||| ||||
                                CTTTTTGTTCATCT CGAT
                                        A
GAM921  FZD10    3'  TGAGTTGGCTTTGCTACCCA   24218     AA    GGTA    TG
                                TGG  AGCA    GAGT  GCTTG
                                |||  ||||    ||||  |||||
                                ACC  TCGT    TTCG  TGAGT
                                  CA   _____    GT
GAM921  G6PC     3'  CAGGCTAATTTTTATATTTTTA 5654         GCAGGT
                                TGGAAA      AGAGTTGGCTTG
                                ||||||      ||||||||||||
                                ATTTTT      TTTTAATCGGAC
                                    ATAT__
GAM921  G6PC     3'  CGGGCCCTCCTTGCCTGTTTTT 5658             __   TT
           CA                     TGGAAAGCAGGTA  GAG  GGCTTG
                                ||||||||||||  |||  ||||||
                                ACTTTTTGTCCGT  CTC  CCGGGC
                                        TC  __
GAM921  GADD45G  3'  CGGGCAATGCTTCGTTTTCTA  22954         _    GAGTTG
                                TGGAAAGC AGGTA      GCTTG
                                |||||||| |||||      |||||
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                                ATCTTTTG TTCGT     CGGGC
                                    C    AA____
GAM921  GALC    3'  TAGGTTAGTTTTCTTTGTTCCA 5671      AA    T  GT
                                TGGA  GCAGG AGA  TGGCTTG
                                ||||  ||||| |||  |||||||
                                ACCT  TGTTT TTT  ATTGGAT
                                  __    C   TG
GAM921  GAS2    3'  TAAGTCAACAGAAAGTGCCTGC 19142    G       GA____
           TTTACA                 TG AAAGCAGGTA     GTTGGCTTG
                                || ||||||||||     |||||||||
                                AC TTTCGTCCGT     CAACTGAAT
                                 A        GAAAGA
GAM921  GAS7    3'  GCTTGTTTGATCTGTTTTCT   20853          A   TT
                                GGAAAGCAGGT GAG  GGC
                                |||||||||||| |||  |||
                                TCTTTTGTCTA TTT  TCG
                                       G   GT
GAM921  GGT1    5'  GAGCCCTCTAGCTGCTTTCT   26425        G    TT    G
                                GGAAAGCAG TAGAG  GGCTT
                                |||||||||| |||||  |||||
                                TCTTTCGTC ATCTC  CCGAG
                                    G    __
GAM921  GGT2    5'  GAGCCCTCTAGCTGCTTTCT   74088        G    TT    G
                                GGAAAGCAG TAGAG  GGCTT
                                |||||||||| |||||  |||||
                                TCTTTCGTC ATCTC  CCGAG
                                    G    __
GAM921  GHR     3'  CAGGCTAATTTTTTTGTATTTT 5693       A    T
           A                     TGGAA GCAGG AGAGTTGGCTTG
                                ||||| ||||| ||||||||||||
                                ATTTT TGTTT TTTTAATCGGAC
                                   A    _
GAM921  GLUL    3'  CAGGCCAGCTGTGGTTTTCT   10807       AGG  G
                                GGAAAGC   TA AGTTGGCTTG
                                |||||||   || ||||||||||
                                TCTTTTG   GT TCGACCGGAC
                                    ___  G
GAM921  GNAL    5'  CAACTCTCTATTGCTTTTT    10823        GT_
                                GGAAAGCAG   AGAGTTG
                                |||||||||   |||||||
                                TTTTTCGTT   TCTCAAC
                                     ATC
GAM921  GNAT2    3'  CAGGTTCCAGTACTGGTTTTCC 19169        A   GAG   __
           A                     TGGAAAGC GGTA   TTGG  CTTG
                                |||||||| ||||   ||||  ||||
                                ACCTTTTG TCAT   GACC  GGAC
                                    G    ___    TT
GAM921  GNS     3'  TGGGCTGGCTTTAAGTCCTGTT 10845        ___     TG
           T                     AAGCAGG   TAGAGT  GCTTG
                                |||||||   ||||||  |||||
```

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                                TTTGTCC  ATTTCG  CGGGT
                                   TGA     GT
GAM921  GOCAP1   3'  CAGGCTCTCTGTCAGCTTTTCA 43008        A GT   TT
                                TGGAAAGC G  AGAG  GGCTTG
                                |||||||| |  ||||  ||||||
                                ACTTTTCG C  TCTC  TCGGAC
                                    A TG   __
GAM921  GPR4     3'  TAAGTCAAACATTTGGTTTCCA 60582       G    AGAG
                                TGGAAA CAGGT   TTGGCTTG
                                |||||| |||||   ||||||||
                                ACCTTT GTTTA   AACTGAAT
                                   G    CA__
GAM921  GPR44    3'  GGTGCATTTTGCTTGTTT    17700           TG  TG
                                AAGCAGGTAGAGT  GCT
                                ||||||||||||  |||
                                TTTGTTCGTTTTA  TGG
                                       CG   T
GAM921  GPR65    5'  CAAGACTTCTCTGTTTACTTTC 60459       C GG    TT  _
           TA                    TGGAAAG A  TAGAG  GG CTTG
                                |||||||  |  |||||  || ||||
                                ATCTTTC T  GTCTC  TC GAAC
                                    A TT    T_  A
GAM921  GPR81    3'  CAGGCCAACTCTAGCTCCTTTC 51739       C  G
           T                     GGAAAG AG TAGAGTTGGCTTG
                                |||||| || ||||||||||||
                                TCTTTC TC ATCTCAACCGGAC
                                   C  G
GAM921  GRAF     3'  TGAGTCAGTTGCTGTGCTCTTT 31252     A   _    AG
           A                     TGGA AGCA GGTAG  TTGGCTTG
                                ||||  |||| |||||  ||||||||
                                ATTT TCGT TCGTT  GACTGAGT
                                  C   G    __
GAM921  GRB10    3'  CAGACCACACTCTAGTTGTTTT 19193         G    _  _  TG
           CCA                     TGGAAAGCAG TAGAGT TGG CT
                                ||||||||||  ||||||  |||  ||
                                ACCTTTTGTT ATCTCA ACC GA
                                      G     C   A  C
GAM921  GRINL1A  3'  TAGGCCAATTTCTGGGCCTTCT 70070     A  A_  TA
                                GGAA GC  GG  GAGTTGGCTTG
                                ||||  ||  ||  ||||||||||
                                TCTT CG  TC  TTTAACCGGAT
                                  C  GG  __
GAM921  GRM8     3'  CAAGCTAAAGTATTGCTTATTC 7794      _     GTAGAG
           A                     TGGA AAGCAG     TTGGCTTG
                                ||||  ||||||     ||||||||
                                ACTT TTCGTT     AATCGAAC
                                  A     ATGA__
GAM921  HK3      3'  CGGGTCGGGGTCTGCCTGTTTC 10925     A         G  _
           CCA                     TGG AAGCAGGTAGA TT GGCTTG
                                ||| ||||||||||| || ||||||
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                                ACC TTTGTCCGTCT GG CTGGGC
                                  C         G  G
GAM921  HNRPK    3'  TAAGCTGGGGATTTTTTGTTTG 49193        GG    _____ TG
              TTTTT                 GAAAGCA  TAGAG    T  GCTTG
                                ||||||| |||||    | |||||
                                TTTTTGT  GTTTT    G  CGAAT
                                    TT    TTAGG GT
GAM921  HNRPK    3'  TAAGCTGGGGATTTTTTGTTTG 49194        GG    _____ TG
              TTTTT                 GAAAGCA  TAGAG    T  GCTTG
                                ||||||| |||||    | |||||
                                TTTTTGT  GTTTT    G  CGAAT
                                    TT    TTAGG GT
GAM921  HPRT1    3'  AATTTTATCTGTTTTGTA    5757     G
                                TG AAAGCAGGTAGAGTT
                                || ||||||||||||||
                                AT TTTTGTCTATTTTAA
                                 G
GAM921  HRH1     3'  CAAGCTGATGTTTTGTATTTT  7814       A    TAGA  TG
                                GGAA GCAGG    GT  GCTTG
                                |||| |||||    ||  |||||
                                TTTT TGTTT    TA  CGAAC
                                  A    TG__  GT
GAM921  HSPA5    3'  TAAGCGGCTGTTTACTGCTTTT 19289          GTAG_    G
              CA                  TGGAAAGCAG    AGTTG CTTG
                                |||||||||    ||||| ||||
                                ACTTTTCGTC    TCGGC GAAT
                                     ATTTG    _
GAM921  HTRA3    3'  TGAGCCGGCTTCCCCTTCC   90584    AAGC   TA
                                GGA   AGG  GAGTTGGCTTG
                                |||   |||  ||||||||||
                                CCT   TCC  TTCGGCCGAGT
                                  _____  CC
GAM921  IGF1     3'  GCCCTCTGCCTGTTTTCCA   7076             TT
                                TGGAAAGCAGGTAGAG  GGC
                                |||||||||||||||  |||
                                ACCTTTTGTCCGTCTC  CCG
                                                 __
GAM921  IL11     3'  GGGCCGTTTGTTTGTTTTTT  7191         GG   GT    G
                                GGAAAGCA  TAGA  TGGCTT
                                |||||||  ||||  ||||||
                                TTTTTTGT  GTTT  GCCGGG
                                     TT   __
GAM921  IL18R1   3'  AGTTACTTGCTTGTTTTTTA  15251           G   T
                                TGGAAAGCAGGTA AGT GGCT
                                |||||||||||| ||| ||||
                                ATTTTTTGTTCGT TCA TTGA
                                                _  _
GAM921  IL1RAP   3'  AAGTTGTTTTGTTTGTTTTC  57066        GG    TTG   G
                                GAAAGCA  TAGAG   GCTT
                                |||||||  |||||  ||||
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                                CTTTTGT  GTTTT   TGAA
                                   TT    GT_   A
GAM921  IL22RA2  3'  TAAGCTTTTCTTTTCTGTTTGT 54774       GG    TT____
            TTTT                  GAAAGCA  TAGAG     GGCTTG
                                |||||||  |||||     ||||||
                                TTTTTGT  GTCTT     TCGAAT
                                   TT    TTCTTT
GAM921  IL7R    3'  TGAGTCAAGAGCATCCTGCTTC 10989      A    TAGAG_
            TA                   TGGAA GCAGG     TTGGCTTG
                                ||||| |||||     ||||||||
                                ATCTT CGTCC     AACTGAGT
                                  _    TACGAG
GAM921  IMPA1   3'  TAGGCCAACTTTTTTTTCTTT  19853     C   T
                                AAAG AGG AGAGTTGGCTTG
                                |||| ||| ||||||||||||
                                TTTC TTT TTTCAACCGGAT
                                  T   T
GAM921  IMPA2   3'  CAGGTTAGTACGTGTTCTTCT  96945     _   G   GAG
                                GGAA AGCA GTA   TTGGCTTG
                                |||| |||| |||   ||||||||
                                TCTT TTGT CAT   GATTGGAC
                                  C   G   ___
GAM921  IMPG1   3'  AAGCCAGGTTTGCTTCCA    9598      AAGCA     G
                                TGGA    GGTAGA TTGGCTT
                                ||||    |||||| |||||||
                                ACCT    TCGTTT GACCGAA
                                  _____     G
GAM921  ING1    3'  AGTGATTCTGTTTGCCTTTT   19854     A   GG      G
                                GGAA GCA  TAGAGTTG CT
                                |||| |||  |||||||| ||
                                TTTT CGT  GTCTTAGT GA
                                  C   TT      _
GAM921  IRS2    3'  AGAATGTTCTGCCGTTTTCT   60437       A     TTGG
                                GGAAAGC GGTAGAG    CT
                                |||||||  |||||||    ||
                                TCTTTTG CCGTCTT    GA
                                   _      GTAA
GAM921  ITGA4   5'  CGAGTCTTTTTGTTTGGTTTTT 7954       G  GG    TT
                                GGAAA CA  TAGAG  GGCTTG
                                |||||  ||  |||||  ||||||
                                TTTTT GT  GTTTT  CTGAGC
                                   G  TT    T_
GAM921  KCNE1L  3'  CGGGCCAGTTTCTCCCTCTTC  25389     A C   T   GT_
                                GAA G AGG AGA   TGGCTTG
                                |||  |  ||| |||   |||||||
                                CTT C TCC TCT   ACCGGGC
                                  _ _   C   TTG
GAM921  KCNK2   3'  TGAGCCAGCACTTTCTTTCT   27238       C    AGA
                                GGAAAG AGGT   GTTGGCTTG
                                ||||||  ||||   |||||||||
```

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                                TCTTTC TTCA   CGACCGAGT
                                   T   ___
GAM921  KLF8    3'  CAATTTTTCTCTTGTTTTCTA  24371          T__
                                TGGAAAGCAGG   AGAGTTG
                                ||||||||||   |||||||
                                ATCTTTTGTTC   TTTTAAC
                                     TCT
GAM921  KMO     3'  TGAGCTGATTTAAGTTGTTTTT 14849         GTA   TG
           T                     GGAAAGCAG   GAGT  GCTTG
                                |||||||||   ||||  |||||
                                TTTTTTGTT   TTTA  CGAGT
                                     GAA   GT
GAM921  KRAS2   3'  AGGTTTTGTCTCCTTTCCA   54121       C  GT   GTTG
                                TGGAAAG AG  AGA   GCTT
                                |||||||  ||  |||   ||||
                                ACCTTTC TC  TTT   TGGA
                                    C  TG  ____
GAM921  KRAS2   3'  AGGTTTTGTCTCCTTTCCA   54122       C  GT   GTTG
                                TGGAAAG AG  AGA   GCTT
                                |||||||  ||  |||   ||||
                                ACCTTTC TC  TTT   TGGA
                                    C  TG  ____
GAM921  KRT16   3'  TGGGCTAATAAAGCTGACTTTC 96893       CA   AGA
           T                     GGAAAG  GGT   GTTGGCTTG
                                ||||||  |||   |||||||||
                                TCTTTC  TCG   TAATCGGGT
                                   AG   AAA
GAM921  LDB2    3'  TGAGTTGACCATCCTTTCTTTT 8917        C_   TAGA  TG
           TA                     TGGAAAG  AGG   GT  GCTTG
                                |||||||  |||   ||  |||||
                                ATTTTTC  TCC   CA  TGAGT
                                    TT   TAC_  GT
GAM921  LIFR    3'  GTCTTTTTTGTTTGTTTTTT   11313        GG    TT
                                GGAAAGCA  TAGAG  GGC
                                ||||||||  |||||  |||
                                TTTTTTGT  GTTTT  CTG
                                     TT    TT
GAM921  LMO4    3'  CAACATTCTATTTGCTCTTT   23179     A        __
                                GGA AGCAGGTAGA  GTTG
                                |||  ||||||||||  ||||
                                TTT TCGTTTATCT  CAAC
                                  C         TA
GAM921  LMO7    3'  GTCTTTTTTGCTTTTTTTTTA  19305        C       TT
                                TGGAAAG AGGTAGAG  GGC
                                |||||||  ||||||||  |||
                                ATTTTTT TTCGTTTT  CTG
                                    T       TT
GAM921  LMO7    3'  GTCTTTTTTGCTTTTTTTTTA  32368        C       TT
                                TGGAAAG AGGTAGAG  GGC
                                |||||||  ||||||||  |||
```

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                                ATTTTTT TTCGTTTT  CTG
                                    T       TT
GAM921  LPIN2    3'  TAAGTCTCGTATTTGCTTTGCT 28434    _       _  TTG
                                GG AAAGCAGGTA GAG   GCTTG
                                || |||||||||| |||   |||||
                                TC TTTCGTTTAT CTC   TGAAT
                                 G        G  ___
GAM921  M6PR     3'  CAGGCTCACTGGCCGTTTGTTT 11409        ___  AG   T
           TTTA                   TGGAAAGCA   GGT  AGT GGCTTG
                                |||||||||   |||  ||| ||||||
                                ATTTTTTGT   CCG  TCA TCGGAC
                                      TTG   G_   C
GAM921  MAP3K9   5'  GGGAAGGTCTATCGTGCTTTCT 61363        _     G  GG  TG
                                GGAAAGCA GGTAGA TT  CT
                                |||||||| |||||| ||  ||
                                TCTTTCGT CTATCT GA  GG
                                     G     G  AG  T
GAM921  MAT2A    3'  TAAGTTGGGCTTGCTATTCT   20970     _      AGAG TG
                                GGAA AGCAGGT    T  GCTTG
                                |||| |||||||    |  |||||
                                TCTT TCGTTCG    G  TGAAT
                                  A       ____ GT
GAM921  MBL2     3'  AACTCTGTTTTCTTTCTA    5908         C GG
                                TGGAAAG A  TAGAGTT
                                ||||||| |  |||||||
                                ATCTTTC T  GTCTCAA
                                     T TT
GAM921  MECP2    3'  TGGGCTTTTGTTTTGCTTTTTA 18415           TAGAGTT
                                TGGAAAGCAGG      GGCTTG
                                ||||||||||       ||||||
                                ATTTTTCGTTT      TCGGGT
                                       TGTTT__
GAM921  MEFV     3'  CAGGCTGGTTTTCTTGTATTTT 5930        _    T    TT
           TA                     TGGAAA GCAGG AGAG  GGCTTG
                                |||||| ||||| ||||  ||||||
                                ATTTTT TGTTC TTTT  TCGGAC
                                   A    _   GG
GAM921  MEN1     5'  CCCCTTTGCTTTGCTTTTTA   5959          _     TT
                                TGGAAAGCAG GTAGAG  GG
                                |||||||||| ||||||  ||
                                ATTTTTCGTT CGTTTC  CC
                                      T     C_
GAM921  MEN1     3'  GCTTTCTTTAATTGTTTTTTA  56353          G     TT
                                TGGAAAGCAG TAGAG  GGC
                                |||||||||| |||||  |||
                                ATTTTTTGTT ATTTC  TCG
                                      A     TT
GAM921  MEOX2    3'  GGGCAGGTATTTGCTTTT    20995          GAG   G
                                GAAAGCAGGTA   TTG CT
                                ||||||||||   ||| ||
```

```
                                TTTTCGTTTAT  GAC GG
                                      G__  G
GAM921  MFGE8   3' CAGGTCTTCCTGCTTTCCA  21005        T  G
                                TGGAAAGCAGG AGA TTG
                                |||||||||| ||| |||
                                ACCTTTCGTCC TCT GAC
                                      T  G
GAM921  MGAT5   5' ATTTTTTATTGCTTTTCA   11567        GT_
                                TGGAAAGCAG  AGAGT
                                |||||||||  |||||
                                ACTTTTCGTT  TTTTA
                                      ATT
GAM921  MGEA5   3' TGGGGCAGTTATTCTGCTTTTT 25228        TAG GT  G
                                GGAAAGCAGG  A  TG CTTG
                                |||||||||  |  || ||||
                                TTTTTCGTCT  T  AC GGGT
                                      TA_ TG  G
GAM921  MNDA    3' TGAGTTATAGATTAGTTTGCTT 11663        TA  GT__
           TCT                   GGAAAGCAGG  GA   TGGCTTG
                                |||||||||  ||   |||||||
                                TCTTTCGTTT  TT   ATTGAGT
                                      GA  AGAT
GAM921  MSL3L1  3' GTCATGCTGCCTGCTTTCT   23291         AGT
                                GGAAAGCAGGTAG  TGGC
                                ||||||||||||  ||||
                                TCTTTCGTCCGTC  ACTG
                                      GT_
GAM921  MTM1    3' AATGCACAGTTCTATTTGCTAT 6003     A       GT  _  TTG
           CT                    GGA AGCAGGTAGA  TG GC
                                ||| ||||||||||  || ||
                                TCT TCGTTTATCT  AC CG
                                  A        TG  A  TAAA
GAM921  MYBL1   3' TAAGTATGTTGATTGCTTTCTA 64770        G  AGTTG
                                TGGAAAGCAG TAG    GCTTG
                                |||||||||| |||    |||||
                                ATCTTTCGTT GTT    TGAAT
                                      A  GTA__
GAM921  MYCL1   3' CAAGTCAGCTCCAGCTTTCT  19364       AGGTA
                                GGAAAGC    GAGTTGGCTTG
                                |||||||    ||||||||||
                                TCTTTCG    CTCGACTGAAC
                                   AC___
GAM921  MYLK    3' CATTCTATTTTTATCTGCTTTT 54893          T  CT
           T                     GGAAAGCAGGTAGAG TGG  TG
                                |||||||||||||| |||  ||
                                TTTTTCGTCTATTTT ATC  AC
                                      T  TT
GAM921  MYO1E   3' AAGATGTGCTCTGCTTTTTTCC 18437       C       TGG_  G
           A                     TGGAAAG AGGTAGAGT   CTT
                                |||||||  |||||||||   |||
```

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                                ACCTTTT TTCGTCTCG   GAA
                                   _       TGTA   A
GAM921  MYOC    3'  AGGCAGCTTTGACTGCTTTCCA 6033          G      G  TG
                                TGGAAAGCAG TAGAGTTG CT
                                |||||||||| ||||||| ||
                                ACCTTTCGTC GTTTCGAC GA
                                      A      G  C
GAM921  NAGA    5'  TAAGCCAGTGGCTGCCTTTTTC 6039       C     AG_
          T                     GGAAAG AGGTAG   TTGGCTTG
                                |||||| ||||||   ||||||||
                                TCTTTT TCCGTC   GACCGAAT
                                   _     GGT
GAM921  NCOA3   3'  CAGGTCAGTCTGTCTCTTTTTC 22561       C  GT   G
          A                     TGGAAAG AG  AGA TTGGCTTG
                                ||||||| ||  ||| ||||||||
                                ACTTTTT TC  TCT GACTGGAC
                                    C  TG  _
GAM921  NCOA4   3'  TAAGATATCTTTGCTGCTTTCC 19552         G    TTGG
          A                     TGGAAAGCAG TAGAG    CTTG
                                |||||||||| |||||    ||||
                                ACCTTTCGTC GTTTC    GAAT
                                      _    TATA
GAM921  NFIB    3'  TAAGCTAGTTTTATTGGTTT   20009     AG    GT
                                AAGC  GTAGA  TGGCTTG
                                ||||  |||||  |||||||
                                TTTG  TATTT  ATCGAAT
                                  GT    TG
GAM921  NGB     3'  CAAGATGGCTTGCTTTTCA   41460          AGAG
                                TGGAAAGCAGGT    TTG
                                ||||||||||||    |||
                                ACTTTTCGTTCG    AAC
                                      GTAG
GAM921  NRIP1   3'  TAGGGTACTTTATTTTGCTTTT 60625          _     T G
          CA                      TGGAAAGCAGG TAGAGT G CTTG
                                |||||||||| |||||| | ||||
                                ACTTTTCGTTT ATTTCA T GGAT
                                      T     _ G
GAM921  NRXN1   3'  CATCTCTGTGTGCTTTCT    17824        GG    T
                                GGAAAGCA  TAGAG TG
                                ||||||||  ||||| ||
                                TCTTTCGT  GTCTC AC
                                    GT    T
GAM921  NUMB    3'  CAGGATCCCTAGCTTGTTTTCT 14978          AG  TTGG
                                GGAAAGCAGGT  AG    CTTG
                                ||||||||||  ||   ||||
                                TCTTTTGTTCG  TC    GGAC
                                      A_  CCTA
GAM921  OLIG2   3'  TAAGCCGGCTTTCCTCTATTTT 20549      GC_   T
                                GAAA   AGG AGAGTTGGCTTG
                                ||||   ||| ||||||||||||
```

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                                TTTT   TCC TTTCGGCCGAAT
                                  ATC  _
GAM921  OSR1     3'  TGGGCCAGAGAGGCCTGCCTTC 18840      A     AGAG
           T                     GGAA GCAGGT    TTGGCTTG
                                 |||| ||||||    ||||||||
                                 TCTT CGTCCG    GACCGGGT
                                   C     GAGA
GAM921  OTC      5'  CAGGGCACTTCTATTTGTTTTT 6753             T  G
                                 GAAAGCAGGTAGAG TG CTTG
                                 |||||||||||||| || ||||
                                 TTTTTGTTTATCTT AC GGAC
                                          C  G
GAM921  OXCT     3'  CAGGCTGCGTGTTTTTCA    6485          G    AG
                                 TGGAAAGCA GTAG  TTG
                                 |||||||| ||||  |||
                                 ACTTTTTGT CGTC  GAC
                                       G   G_
GAM921  P23      3'  TTTTCAACCTGTTTGTTTTTTA 22756         GG   A    CTTG
                                 TGGAAAGCA  TAG GTTGG
                                 |||||||||  ||| |||||
                                 ATTTTTTGT  GTC CAACT
                                       TT   _    TTTT
GAM921  P2RY1    3'  GACTTTGTTTGTGTTCCA    11931       A   GG
                                 TGGAA GCA  TAGAGTT
                                 ||||| |||  |||||||
                                 ACCTT TGT  GTTTCAG
                                    G   TT
GAM921  P2RY2    5'  CAGGCCTGGGGACCTGTTTTTC 11934           AGAGTT
                                 GGAAAGCAGGT     GGCTTG
                                 ||||||||||      ||||||
                                 CTTTTTGTCCA     CCGGAC
                                       GGGGT_
GAM921  PACE     3'  CAGGCTGACATCTGTGTTTCA  11941       A     AGA  TG
                                 TGGAA GCAGGT   GT  GCTTG
                                 ||||| ||||||   ||  |||||
                                 ACTTT TGTCTA   CA  CGGAC
                                    G     ___  GT
GAM921  PAFAH1B1 3'  GTTTTCTCTGTCTGCTGTCTA  6477       A    GT    TT
                                 TGGA AGCAG  AGAG  GGC
                                 |||| |||||  ||||  |||
                                 ATCT TCGTC  TCTC  TTG
                                   G    TG   TT
GAM921  PAICS    3'  CGAGCTAATTTTATTTTTTGT  22260      ___
                                 GCAG   GTAGAGTTGGCTTG
                                 ||||   ||||||||||||||
                                 TGTT   TATTTTAATCGAGC
                                   TTT
GAM921  PAM      3'  AAGTTGGCTTCTGTTTCTA   57840       G  GTA   TG
                                 TGGAAA CAG   GAGT  GCTT
                                 |||||| |||   ||||  ||||
```

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                                ATCTTT GTC   TTCG  TGAA
                                  _  ___    GT
GAM921  PCDH11X  3' AACTTTACCTGTGTTTTA    28004      A
                                TGGAA GCAGGTAGAGTT
                                ||||| ||||||||||||
                                ATTTT TGTCCATTTCAA
                                   G
GAM921  PCDH11Y  3' AACTTTACCTGTGTTTTA    53148      A
                                TGGAA GCAGGTAGAGTT
                                ||||| ||||||||||||
                                ATTTT TGTCCATTTCAA
                                   G
GAM921  PCDHA9   3' CAAGCTATTTGTTTGTTTTCTA 49833        GG   GT
                                TGGAAAGCA  TAGA  TGGCTTG
                                |||||||||  ||||  |||||||
                                ATCTTTTGT  GTTT  ATCGAAC
                                     TT   __
GAM921  PCDHB12  3' TGAGTTGATTAGAATGCTGTTC 38934    A   GGTAG   TG
                                GGA AGCA    AGT  GCTTG
                                ||| ||||    |||  |||||
                                CTT TCGT    TTA  TGAGT
                                  G   AAGA_  GT
GAM921  PCDHB15  3' TCTTGAATTCTACTTTTTTTTA 38938       C        GGCTTG
                                TGGAAAG AGGTAGAGTT
                                ||||||| ||||||||||
                                ATTTTTT TTCATCTTAA
                                   _        GTTCTA
GAM921  PCDHB9   3' CAAGTTAACTTTTTCTTATTTT 39439     GC   T
                                GAAA  AGG AGAGTTGGCTTG
                                ||||  ||| ||||||||||||
                                TTTT  TCT TTTCAATTGAAC
                                  AT   T
GAM921  PCDHGA1  3' AGTCTTCTGTTTTGTTTTTCA  38835       _ GG    TT
                                TGGAAAGC A  TAGAG  GGCT
                                |||||||| |  |||||  ||||
                                ACTTTTTG T  GTCTT  CTGA
                                     T TT    __
GAM921  PCDHGA10 3' AGTCTTCTGTTTTGTTTTTCA  50310       _ GG    TT
                                TGGAAAGC A  TAGAG  GGCT
                                |||||||| |  |||||  ||||
                                ACTTTTTG T  GTCTT  CTGA
                                     T TT    __
GAM921  PCDHGA11 3' AGTCTTCTGTTTTGTTTTTCA  38842       _ GG    TT
                                TGGAAAGC A  TAGAG  GGCT
                                |||||||| |  |||||  ||||
                                ACTTTTTG T  GTCTT  CTGA
                                     T TT    __
GAM921  PCDHGA12 3' AGTCTTCTGTTTTGTTTTTCA  50317       _ GG    TT
                                TGGAAAGC A  TAGAG  GGCT
                                |||||||| |  |||||  ||||
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                                ACTTTTTG T  GTCTT  CTGA
                                    T TT    __
GAM921  PCDHGA2  3' AGTCTTCTGTTTTGTTTTTCA 38849      _ GG    TT
                                TGGAAAGC A  TAGAG  GGCT
                                |||||||| |  |||||  ||||
                                ACTTTTTG T  GTCTT  CTGA
                                    T TT    __
GAM921  PCDHGA3  3' AGTCTTCTGTTTTGTTTTTCA 50093      _ GG    TT
                                TGGAAAGC A  TAGAG  GGCT
                                |||||||| |  |||||  ||||
                                ACTTTTTG T  GTCTT  CTGA
                                    T TT    __
GAM921  PCDHGA4  3' AGTCTTCTGTTTTGTTTTTCA 38857      _ GG    TT
                                TGGAAAGC A  TAGAG  GGCT
                                |||||||| |  |||||  ||||
                                ACTTTTTG T  GTCTT  CTGA
                                    T TT    __
GAM921  PCDHGA5  3' AGTCTTCTGTTTTGTTTTTCA 50291      _ GG    TT
                                TGGAAAGC A  TAGAG  GGCT
                                |||||||| |  |||||  ||||
                                ACTTTTTG T  GTCTT  CTGA
                                    T TT    __
GAM921  PCDHGA6  3' AGTCTTCTGTTTTGTTTTTCA 38865      _ GG    TT
                                TGGAAAGC A  TAGAG  GGCT
                                |||||||| |  |||||  ||||
                                ACTTTTTG T  GTCTT  CTGA
                                    T TT    __
GAM921  PCDHGA7  3' AGTCTTCTGTTTTGTTTTTCA 50298      _ GG    TT
                                TGGAAAGC A  TAGAG  GGCT
                                |||||||| |  |||||  ||||
                                ACTTTTTG T  GTCTT  CTGA
                                    T TT    __
GAM921  PCDHGA8  3' AGTCTTCTGTTTTGTTTTTCA 26599      _ GG    TT
                                TGGAAAGC A  TAGAG  GGCT
                                |||||||| |  |||||  ||||
                                ACTTTTTG T  GTCTT  CTGA
                                    T TT    __
GAM921  PCDHGA9  3' AGTCTTCTGTTTTGTTTTTCA 50305      _ GG    TT
                                TGGAAAGC A  TAGAG  GGCT
                                |||||||| |  |||||  ||||
                                ACTTTTTG T  GTCTT  CTGA
                                    T TT    __
GAM921  PCDHGB1  3' AGTCTTCTGTTTTGTTTTTCA 38874      _ GG    TT
                                TGGAAAGC A  TAGAG  GGCT
                                |||||||| |  |||||  ||||
                                ACTTTTTG T  GTCTT  CTGA
                                    T TT    __
GAM921  PCDHGB2  3' AGTCTTCTGTTTTGTTTTTCA 50323      _ GG    TT
                                TGGAAAGC A  TAGAG  GGCT
                                |||||||| |  |||||  ||||
```

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                                ACTTTTTG T  GTCTT  CTGA
                                    T TT    __
GAM921  PCDHGB3  3' AGTCTTCTGTTTTGTTTTTCA 38882       _ GG    TT
                                TGGAAAGC A  TAGAG  GGCT
                                |||||||| |  |||||  ||||
                                ACTTTTTG T  GTCTT  CTGA
                                    T TT    __
GAM921  PCDHGB4  3' AGTCTTCTGTTTTGTTTTTCA 50328       _ GG    TT
                                TGGAAAGC A  TAGAG  GGCT
                                |||||||| |  |||||  ||||
                                ACTTTTTG T  GTCTT  CTGA
                                    T TT    __
GAM921  PCDHGB5  3' AGTCTTCTGTTTTGTTTTTCA 38889       _ GG    TT
                                TGGAAAGC A  TAGAG  GGCT
                                |||||||| |  |||||  ||||
                                ACTTTTTG T  GTCTT  CTGA
                                    T TT    __
GAM921  PCDHGB6  3' AGTCTTCTGTTTTGTTTTTCA 50334       _ GG    TT
                                TGGAAAGC A  TAGAG  GGCT
                                |||||||| |  |||||  ||||
                                ACTTTTTG T  GTCTT  CTGA
                                    T TT    __
GAM921  PCDHGB7  3' AGTCTTCTGTTTTGTTTTTCA 38898       _ GG    TT
                                TGGAAAGC A  TAGAG  GGCT
                                |||||||| |  |||||  ||||
                                ACTTTTTG T  GTCTT  CTGA
                                    T TT    __
GAM921  PCDHGC3  3' AGTCTTCTGTTTTGTTTTTCA 51527       _ GG    TT
                                TGGAAAGC A  TAGAG  GGCT
                                |||||||| |  |||||  ||||
                                ACTTTTTG T  GTCTT  CTGA
                                    T TT    __
GAM921  PCDHGC4  3' AGTCTTCTGTTTTGTTTTTCA 38904       _ GG    TT
                                TGGAAAGC A  TAGAG  GGCT
                                |||||||| |  |||||  ||||
                                ACTTTTTG T  GTCTT  CTGA
                                    T TT    __
GAM921  PCDHGC5  3' AGTCTTCTGTTTTGTTTTTCA 51554       _ GG    TT
                                TGGAAAGC A  TAGAG  GGCT
                                |||||||| |  |||||  ||||
                                ACTTTTTG T  GTCTT  CTGA
                                    T TT    __
GAM921  PCLO     3' CAAGTGGCTGCCAGTTTTCCA 95886        A    AGTTG
                                TGGAAAGC GGTAG    GCTTG
                                |||||||| |||||    |||||
                                ACCTTTTG CCGTC    TGAAC
                                    A    GG___
GAM921  PCTK1    3' AGGCATCCTCTGCCTGCTTTCC 53413            TTG   G
                                GGAAAGCAGGTAGAG   GCTT
                                ||||||||||||||   ||||
```

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                                CCTTTCGTCCGTCTC  CGGA
                                       CTA   G
GAM921  PDZK1   3'  TGAGTTGTGACCTGTTTACT  12036   A     AGAGT
                                GG AAGCAGGT    TGGCTTG
                                || ||||||||    |||||||
                                TC TTTGTCCA    GTTGAGT
                                 A      GT___
GAM921  PGK1    3'  TAAGTCAACTTAGCATTTTCT  6087      GCAG  A
                                GGAAA   GT GAGTTGGCTTG
                                |||||   || ||||||||||
                                TCTTT   CG TTCAACTGAAT
                                   TA__  A
GAM921  PIG3    5'  CGGGTCGGCTGGGGGCTTCCA  18079     A  AGGTAG
                                TGGAA GC     AGTTGGCTTG
                                ||||| ||     ||||||||||
                                ACCTT CG     TCGGCTGGGC
                                   _  GGGG__
GAM921  PIGH    3'  TAAGCCATAGGGGCTGGTTTTC 17093      A   AGAGT
           C                    GGAAAGC GGT    TGGCTTG
                                ||||||| |||    |||||||
                                CCTTTTG TCG    ACCGAAT
                                    G   GGGAT
GAM921  PIK3R3  3'  GGGCAATTCCTGTTTTCTA   61708         TAG    G
                                TGGAAAGCAGG   AGTTG CT
                                ||||||||||   ||||| ||
                                ATCTTTTGTCC   TTAAC GG
                                      ___    G
GAM921  PIM2    5'  CGGGCCACCAGTTTCTCTGCTT 60654        GT   GT__
           TCCA                  TGGAAAGCAG  AGA   TGGCTTG
                                ||||||||||  |||   |||||||
                                ACCTTTCGTC  TTT   ACCGGGC
                                      TC   GACC
GAM921  PITPNB  3'  CAGGCCAGTTTTTACTTGTTT  25700         GT_
                                AAGCAGGTAGA   TGGCTTG
                                ||||||||||   |||||||
                                TTTGTTCATTT   ACCGGAC
                                      TTG
GAM921  PITX1   3'  CGGGTTGGTTTTGTGTTTGCTT 12137        __    TT
           TTC                   GGAAAGCAGG  TAGAG  GGCTTG
                                ||||||||||  |||||  ||||||
                                CTTTTCGTTT  GTTTT  TTGGGC
                                      GT    GG
GAM921  PKD2    3'  TGAGTTAGCAACACTGTTTTCT 33617        _  AGA
                                GGAAAGCAG GT   GTTGGCTTG
                                |||||||||  ||   |||||||||
                                TCTTTTGTC CA   CGATTGAGT
                                      A  A__
GAM921  PKHD1   3'  TAGGCCAACTCTAAATTTATTC 57717     AGCAGG
                                GAA     TAGAGTTGGCTTG
                                |||     ||||||||||||
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```
                                CTT     ATCTCAACCGGAT
                                  ATTTAA
GAM921  PKNOX1   3'  TGGGCTGGGTTCTGTTTTCT   17104        GTA  G TG
                                GGAAAGCAG   GA T  GCTTG
                                |||||||||   || |  |||||
                                TCTTTTGTC   TT G  CGGGT
                                     ___  G GT
GAM921  PMM1     3'  CAGGCCACAGCTGCTGCTTGTA 12182      A      _  __
          TTTC                    GGAA GCAGGTAG AGT  TGGCTTG
                                |||| |||||||| |||  |||||||
                                CTTT TGTTCGTC TCG  ACCGGAC
                                  A       G   AC
GAM921  PNUTL1   3'  CAGGTCATTGTGTCTGTTTCC  12187      G   GT G   T
                                GGAAA CAG  A AGT GGCTTG
                                ||||| |||  | ||| ||||||
                                CCTTT GTC  T TTA CTGGAC
                                  _  TG G  _
GAM921  POLG     3'  CAGGCTTTCAGCTGTGCTTTTT 12202        _  A   TT
                                GGAAAGCA GGT GAG  GGCTTG
                                |||||||| ||| |||  ||||||
                                TTTTTCGT TCG CTT  TCGGAC
                                    G   A  __
GAM921  POLR2A   3'  GCCTTTTGTCTGTTATTTTA   8129       _    GT    TT
                                TGGAA AGCAG  AGAG  GGC
                                ||||| |||||  ||||  |||
                                ATTTT TTGTC  TTTT  CCG
                                  A    TG   __
GAM921  POU4F1   3'  AGGTAAAATGCCTGCTTT    21758        GAG   G
                                AAAGCAGGTA   TTG CT
                                ||||||||||   ||| ||
                                TTTCGTCCGT   AAT GA
                                     AA_   G
GAM921  PPP1R2   3'  CAATGTCTGCTCTGTTTTTT   21782        _    _
                                GGAAAGCAG GTAGA GTTG
                                ||||||||| ||||| ||||
                                TTTTTTGTC CGTCT TAAC
                                     T    G
GAM921  PPP1R2   3'  GGGTTTTTTTTGTTTGTTTTTT 21786        GG    TT    G
                                GGAAAGCA  TAGAG  GGCTT
                                ||||||||  |||||  |||||
                                TTTTTTGT  GTTTT  TTGGG
                                    TT    TT    A
GAM921  PPP1R3C  3'  TAAGTTGGTTTTACAATTCTTT 19426      CAG_     TT
          CC                    GGAAAG   GTAGAG  GGCTTG
                                ||||||   ||||||  ||||||
                                CCTTTC   CATTTT  TTGAAT
                                  TTAA     GG
GAM921  PPP2R5B  5'  GAGCCATCCTCCTTTCTA    21799       C   TAGAGT
                                TGGAAAG AGG     TGGCTT
                                ||||||| |||     ||||||
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                                ATCTTTC TCC     ACCGAG
                                    C   T_____
GAM921  PPP2R5C  3' AGTTCTTTTGTTTGTTTTTCA 12247        GG    TT
                                TGGAAAGCA  TAGAG  GGCT
                                |||||||||  |||||  ||||
                                ACTTTTTGT  GTTTT  TTGA
                                     TT    C_
GAM921  PPP4R1   3' ACTTTTGATTGTTTTCTA    18891         GT_
                                TGGAAAGCAG   AGAGT
                                ||||||||||   |||||
                                ATCTTTTGTT   TTTCA
                                      AGT
GAM921  PRKAR2B  3' CAAGCATATATCTGCTTTTT   12285          GAGTTG
                                GGAAAGCAGGTA     GCTTG
                                ||||||||||||     |||||
                                TTTTTCGTCTAT     CGAAC
                                       ATA___
GAM921  PRKG1    3' CAAGCTGATTTACTTTATTC   21819     AGC      G TG
                                GAA   AGGTAGA T  GCTTG
                                |||   ||||||| |  |||||
                                CTT   TTCATTT A  CGAAC
                                  AT_      _ GT
GAM921  PRKG1    3' TGCTCTTTACATGTTTTCT    21821        G     TT   TTG
                                GGAAAGCA GTAGAG  GGC
                                |||||||| ||||||  |||
                                TCTTTTGT CATTTC  TCG
                                     A     __   TG
GAM921  PRPF18   3' CAAGCTGATTTTTCTTTCTTGC 14795         T_  ___  TG
           TTTC                   GAAAGCAGG  AGA   GT  GCTTG
                                |||||||||  |||   ||  |||||
                                CTTTCGTTC  TCT   TA  CGAAC
                                      TT   TTT  GT
GAM921  PSMB2    3' TGGGCTCCTTTATTTTTTTCTA 12482        C       TT
                                TGGAAAG AGGTAGAG  GGCTTG
                                ||||||| ||||||||  ||||||
                                ATCTTTT TTTATTTC  TCGGGT
                                     _       C_
GAM921  PTBP1    5' TGGGTCGGTTCCTGCTATTCC  12542      _     TAG  TT
                                GGAA AGCAGG   AG  GGCTTG
                                |||| ||||||   ||  ||||||
                                CCTT TCGTCC   TT  CTGGGT
                                  A     ___  GG
GAM921  PTEN     5' CGGGCCGGTTTTAAACCTCCC  6139     AAAGC   __    TT
                                GG    AGGT  AGAG  GGCTTG
                                ||    ||||  ||||  ||||||
                                CC    TCCA  TTTT  CCGGGC
                                 C_____    AA    GG
GAM921  PTPRZ1   3' GGTCTTACTCTACCAGTTTTCT 12634        A       T_   TG
                                GGAAAGC GGTAGAGT  GGCT
                                ||||||| ||||||||  ||||
```

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                                TCTTTTG CCATCTCA  CTGG
                                    A       TT   T
GAM921  PUM2    3'  AGATAGCTCTTTTTGCTTTCTA 31664          T      G  TG
                                TGGAAAGCAGG AGAGTTG CT
                                |||||||||||| ||||||| ||
                                ATCTTTCGTTT TCTCGAT GA
                                      T      A  C
GAM921  PXF     3'  CAGGTTTTTTGTTTTCCA    12652          T   G
                                TGGAAAGCAGG AGA TTG
                                |||||||||||| ||| |||
                                ACCTTTTGTTT TTT GAC
                                      _  G
GAM921  PXF     3'  TAAGCTGACGTGGCTTTTTTTC 12657       C    AGA  TG
           T                     GGAAAG AGGT   GT  GCTTG
                                |||||| ||||   ||  |||||
                                TCTTTT TTCG   CA  CGAAT
                                   T   GTG  GT
GAM921  PXN     3'  CAAGCTGGCTTTTCCCATTTC  12667     GCA  T    TG
                                GAAA   GG AGAGT  GCTTG
                                ||||   || |||||  |||||
                                CTTT   CC TTTCG  CGAAC
                                  AC_  T    GT
GAM921  PYGO2   3'  TGGGCTTTATTTGTCTTTTT   64689       _        GGCTTG
                                GGAAAG CAGGTAGAGTT
                                |||||| ||||||||||
                                TTTTTC GTTTATTTCGG
                                   T         GT
GAM921  RAB36   3'  CAGGCTAATTTTTTATATTTTT 18157       GCAGGT
           A                     TGGAAA     AGAGTTGGCTTG
                                ||||||     ||||||||||||
                                ATTTTT     TTTTAATCGGAC
                                   ATATT_
GAM921  RAB4A   3'  GGCATCACTGCCTGTTTTTCA  17146           AGTTG
                                TGGAAAGCAGGTAG    GCT
                                ||||||||||||||    |||
                                ACTTTTTGTCCGTC    CGG
                                      ACTA_
GAM921  RAD23B  3'  TGAGTCAAACTGCTGCCT    12738       _   _
                                AGGTAG AGTT GGCTTG
                                |||||| |||| ||||||
                                TCCGTC TCAA CTGAGT
                                   G   A
GAM921  RAG1    3'  AGCAGTTTTCCTTGCTTTTTA  6543          T   TTG
                                TGGAAAGCAGG AGAG   GCT
                                |||||||||| ||||   |||
                                ATTTTTCGTTC TTTT   CGA
                                      C   GA_
GAM921  RARG    3'  CAGGCTGGGCCCTGCATTTCT  8261       _    TAGAG TG
                                GGAAA GCAGG    T  GCTTG
                                ||||| |||||    |  |||||
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                                TCTTT CGTCC    G  CGGAC
                                  A    CG___ GT
GAM921  RASA1   5'  AAGTTAAGACTGCTGTTCA   42954     A    GTAGAG
                                TGGA AGCAG     TTGGCTT
                                |||| |||||     |||||||
                                ACTT TCGTC     AATTGAA
                                  G    AG____
GAM921  RB1CC1  5'  TAAGCCAGTTTTAATCTACTTT 29437       C   _   GT
           TT                    GGAAAG AGGT AGA  TGGCTTG
                                |||||| |||| |||  |||||||
                                TTTTTC TCTA TTT  ACCGAAT
                                  A   A   TG
GAM921  RBBP2   3'  TGAGCCACAGTGATGCATGCTT 18571        G   GAGT__
           TTC                    GGAAAGCA GTA     TGGCTTG
                                |||||||| |||     |||||||
                                CTTTTCGT CGT     ACCGAGT
                                    A   AGTGAC
GAM921  RBL2    3'  CAAGTTCAATCCTACCTGTTTT 20039          AG   _
                                AAAGCAGGTAG  TTGG CTTG
                                ||||||||||  |||| ||||
                                TTTTGTCCATC  AACT GAAC
                                      CT   T
GAM921  REGL    3'  CAGGTGTTTCTGTCTCTTTCT  22498       C  GT   TTG
                                GGAAAG AG  AGAG   GCTTG
                                |||||| ||  ||||   |||||
                                TCTTTC TC  TCTT   TGGAC
                                   _ TG    TG_
GAM921  REQ     3'  TAATGTGCCTGTTTTTTA    21842           GA
                                TGGAAAGCAGGTA  GTTG
                                ||||||||||||  ||||
                                ATTTTTTGTCCGT  TAAT
                                      G_
GAM921  RFP     3'  GGGCTAGGGCTCCTTTCTA   22510      AGC   T  AG
                                TGGAA   AGG AG  TTGGCTT
                                |||||   ||| ||  |||||||
                                ATCTT   TCC TC  GATCGGG
                                   ___   _ GG
GAM921  RFXAP   3'  CAAAAATTTGTTACTTGTTTTT 6764            __    GGCTTG
           TA                    TGGAAAGCAGGTA  GAGTT
                                ||||||||||||  |||||
                                ATTTTTTGTTCAT  TTTAA
                                      TG    AAAC
GAM921  RGS3    5'  AGGCTGACTTGCATTTCT    56312      _  GGTAG   TG
                                GGAAA GCA    AGT  GCTT
                                ||||| |||    |||  ||||
                                TCTTT CGT    TCA  CGGA
                                  A  _____   GT
GAM921  RNASE6  5'  TAAGTTGGTTTAGCCTTCC   20049    AAGC   A   TT
                                GGA   AGGT GAG  GGCTTG
                                |||   |||| |||  ||||||
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                                CCT   TCCG TTT  TTGAAT
                                 ____   A  GG
GAM921  RNF14   3'  GTGTCATTTTGATCTGCTTTTC 16274          A  T   TTG
           A                     TGGAAAGCAGGT GAG TGGC
                                 |||||||||||| ||| ||||
                                 ACTTTTCGTCTA TTT ACTG
                                        G  T   TGA
GAM921  RNH     5'  CAAGTGGTTGCTTGCTTTCCA  60367           AGTTG
                                 TGGAAAGCAGGTAG   GCTTG
                                 ||||||||||||||   |||||
                                 ACCTTTCGTTCGTT   TGAAC
                                        GG___
GAM921  RORB    3'  GGGCTCTTTTATTTGTTT   23591          TT   G
                                 AAGCAGGTAGAG  GGCTT
                                 ||||||||||||  |||||
                                 TTTGTTTATTTT  TCGGG
                                        C_   G
GAM921  RPN2    3'  TAGTTATACTTTTGCTTGTTTT 12908           _ _   TG
           TCA                    TGGAAAGCAGGTAGA GT TGGCT
                                 |||||||||||||||| || |||||
                                 ACTTTTTGTTCGTTT CA ATTGA
                                          T T   T
GAM921  RRAD    3'  GAGAGGACTCTGCCTTTTTTC  16047      C       GG  G
                                 GAAAG AGGTAGAGTT  CTT
                                 ||||| ||||||||||  |||
                                 CTTTT TCCGTCTCAG  GAG
                                    T        GA  G
GAM921  RUNX1   3'  CAGGTCAACTCTGAAGAGTATT 10028    A  AGG_
           T                     GAA GC   TAGAGTTGGCTTG
                                 ||| ||   ||||||||||||||
                                 TTT TG   GTCTCAACTGGAC
                                   A  AGAA
GAM921  S100B   3'  CGAGCCAGCTCTGGGGGCTCCA 21848     AA  AGG
                                 TGGA  GC   TAGAGTTGGCTTG
                                 ||||  ||   ||||||||||||||
                                 ACCT  CG   GTCTCGACCGAGC
                                   __ GGG
GAM921  SAR1    5'  CGAGCCAGCCGCTGTTTTGCC  39731    _     GTAGA
                                 GG AAAGCAG    GTTGGCTTG
                                 || |||||||    |||||||||
                                 CC TTTTGTC    CGACCGAGC
                                  G      GC___
GAM921  SAT     3'  CAACTTCTCTTGCTTTCTA   12939          TA
                                 TGGAAAGCAGG  GAGTTG
                                 ||||||||||  ||||||
                                 ATCTTTCGTTC  TTCAAC
                                        TC
GAM921  SAT     5'  CGGGCCGACTGGTGTTTATCC  12940    _    GGTAG
                                 GGA AAGCA    AGTTGGCTTG
                                 ||| |||||    ||||||||||
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                                CCT TTTGT    TCAGCCGGGC
                                  A    GG___
GAM921  SCA1    5'  CAAGCTGCAGATTTGTTTGTCA 6172    GA      AGA  T
                                TG  AAGCAGGT   GT GGCTTG
                                ||  ||||||||   || ||||||
                                AC  TTTGTTTA   CG TCGAAC
                                 TG       GA_  _
GAM921  SCA1    3'  TGGGTTGGTTTCCTCTCTTTTC 6188        C   TA   TT
           CA                    TGGAAAG AGG  GAG  GGCTTG
                                ||||||| |||  |||  ||||||
                                ACCTTTT TCT  TTT  TTGGGT
                                    C   CC   GG
GAM921  SF1     3'  CAAGCTGGTTGTGGGTTTTTCA 17340         AGG  G  TT
                                TGGAAAGC   TA AG  GGCTTG
                                ||||||||   || ||  ||||||
                                ACTTTTTG   GT TT  TCGAAC
                                     G__  G  GG
GAM921  SLC10A2  5'  CATCCTAGCTTTATTGTTTTTT 6592          G       CT
           A                     TGGAAAGCAG TAGAGTTGG  TG
                                ||||||||||| |||||||||  ||
                                ATTTTTTGTT ATTTCGATC  AC
                                      _       CT
GAM921  SLC2A2   3'  AACATTTGCTTTGTTTTCTA   6216          _    _
                                TGGAAAGCAG GTAGA GTT
                                |||||||||| ||||| |||
                                ATCTTTTGTT CGTTT CAA
                                     T    A
GAM921  SLC2A2   3'  TGAGTTATAGTTTGCTTTGCTT 6218          _    GT_
           TTTA                    TGGAAAGCAG GTAGA   TGGCTTG
                                |||||||||| |||||   |||||||
                                ATTTTTCGTT CGTTT   ATTGAGT
                                     T    GAT
GAM921  SLC4A4   3'  TGAGTCTATATTATCTAGCTTT 14998        _    A  T
           CTA                     TGGAAAGC AGGTAG GT GGCTTG
                                |||||||| |||||| || ||||||
                                ATCTTTCG TCTATT TA CTGAGT
                                     A    A  T
GAM921  SLC4A7   3'  GGGCTTCTCTATTTGTGTTTCA 14618      A       TT    G
                                TGGAA GCAGGTAGAG  GGCTT
                                ||||| ||||||||||  |||||
                                ACTTT TGTTTATCTC  TCGGG
                                   G        T_
GAM921  SLC7A8   5'  CAGGTTCACAGTTTGTTTTTC  25300        GG AGA  TG
                                GGAAAGCA  T   GT  GCTTG
                                ||||||||  |   ||  |||||
                                CTTTTTGT  G   CA  TGGAC
                                     TT A__  CT
GAM921  SMAC     5'  CGGGCTAATTTTTGTGTTTT   57998       GGT
                                AAAGCA   AGAGTTGGCTTG
                                ||||||   ||||||||||||
```

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                                TTTTGT  TTTTAATCGGGC
                                   GT_
GAM921  SMOH    3'  GGGCTGGCTGCCGTTTTCT  20092      A  AG  TG   G
                                GGAAAGC GGT  AGT  GCTT
                                ||||||| |||  |||  ||||
                                TCTTTTG CCG  TCG  CGGG
                                   _  __  GT
GAM921  SORBS1  3'  CAAGCAGATAGGTTATGTCTGT 31803       GT GA____  G
           TTTCT                GGAAAGCAG  A    GTT GCTTG
                                |||||||||  |    ||| |||||
                                TCTTTTGTC  T    TAG CGAAC
                                     TG ATTGGA  A
GAM921  SORCS1  3'  AATTCTACCTGCATTTCA   54674      A
                                TGGAA GCAGGTAGAGTT
                                ||||| ||||||||||||
                                ACTTT CGTCCATCTTAA
                                   A
GAM921  SORCS1  3'  AGGTTTGCTTTGCTTTTTTTTC 54677       C       TG   G
           A                    TGGAAAG AGGTAGAGT  GCTT
                                ||||||| |||||||||  ||||
                                ACTTTTT TTCGTTTCG  TGGA
                                     T       TT   G
GAM921  SORCS1  3'  CAGGCTTGAGGTTTTTGGCTGT 54680        G    TT____
           TTTTTA                TGGAAAGCAG TAGAG    GGCTTG
                                |||||||||| |||||    ||||||
                                ATTTTTTGTC GTTTT    TCGGAC
                                     G    TGGAGT
GAM921  SOX11   3'  AGGCTGATTTCTTTTTCC   13309      C  GTA   TG
                                GGAAAG AG   GAGT  GCTT
                                |||||| ||   ||||  ||||
                                CCTTTT TC   TTTA  CGGA
                                   _ ___   GT
GAM921  SOX13   3'  GGGGGATTTTTTTGTTTTCT  20282        T    GG
                                GGAAAGCAGG AGAGTT  CT
                                |||||||||| ||||||  ||
                                TCTTTTGTTT TTTTAG  GG
                                     _     GG
GAM921  SPF30   3'  GCTTTTTTCCTGTTTTTT   20796        T   TT
                                GGAAAGCAGG AGAG  GGC
                                |||||||||| ||||  |||
                                TTTTTTGTCC TTTT  TCG
                                     _   T_
GAM921  SPG4    3'  AGTTCCTTCTGCTTGCTTT   30809          TT   TG
                                AAAGCAGGTAGAG  GGCT
                                ||||||||||||  ||||
                                TTTCGTTCGTCTT  TTGA
                                      CC   T
GAM921  SS18    3'  AGGTTTATTCTATCTGTTTTT  20101           TG   G
                                GAAAGCAGGTAGAGT  GCTT
                                ||||||||||||||  ||||
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                                TTTTTGTCTATCTTA  TGGA
                                        TT   G
GAM921  ST5     3'  TAAGCTTTCTTAACTGTTTTTT 58228        GTA   TT
                                GGAAAGCAG   GAG  GGCTTG
                                |||||||||   |||  ||||||
                                TTTTTTGTC   TTC  TCGAAT
                                     AA_   TT
GAM921  STAT3   3'  AGGCGCCTACCTGCATTCT   13432     A      A  TG
                                GGAA GCAGGTAG GT  GCTT
                                |||| |||||||| ||  ||||
                                TCTT CGTCCATC CG  CGGA
                                  A      _ __
GAM921  STAT3   3'  GGCATCCTTCTGCCTGTTTCT  13439      G       TTG_   TG
                                GGAAA CAGGTAGAG    GCT
                                ||||| |||||||||    |||
                                TCTTT GTCCGTCTT    CGG
                                  _       CCTA   C
GAM921  STAU    3'  GAGTTAAGTACTGCTTCCA   17199      A    GTAGAG
                                TGGAA GCAG     TTGGCTT
                                ||||| ||||     |||||||
                                ACCTT CGTC     AATTGAG
                                  _    ATG___
GAM921  STK10   3'  CGGGCTGGAATTCTTGGTTTTT 21135        AGGT     __
           CA                     TGGAAAGC    AGAGTT  GGCTTG
                                |||||||    ||||||  ||||||
                                ACTTTTTG    TCTTAA  TCGGGC
                                     GT__     GG
GAM921  STK38   3'  TGAGCCAATTTGATAGGTGTTT 24402      A  AG  A
           TA                      TGGAA GC  GT GAGTTGGCTTG
                                ||||| ||  || ||||||||||
                                ATTTT TG  TA TTTAACCGAGT
                                   G  GA  G
GAM921  SULT1C1  3'  CAGGCTGGTCTTAACTGACTGC 8318          ___  A  _ TG
           TTTTTA                  TGGAAAGCAG   GT GAG T  GCTTG
                                ||||||||||   || ||| |  |||||
                                ATTTTTCGTC   CA TTC G  CGGAC
                                     AGT  A   T GT
GAM921  SUV39H2  3'  ATACTGAATTTTATACTGTTTT 45452          _      GGCTTG
           CTA                     TGGAAAGCAG GTAGAGTT
                                |||||||||| ||||||||
                                ATCTTTTGTC TATTTTAA
                                     A       GTCATAG
GAM921  TAF4    3'  TGGGCCGACTTTACAGACGTCC 13517      AAGCAG
           A                      TGGA     GTAGAGTTGGCTTG
                                ||||     ||||||||||||||
                                ACCT     CATTTCAGCCGGGT
                                  GCAGA_
GAM921  TAGLN2   5'  TGAGTCAGTGCGCTGCTCTCCA 14538      A    _   GAG
                                TGGA AGCAG GTA   TTGGCTTG
                                |||| ||||| |||   ||||||||
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                                ACCT TCGTC CGT   GACTGAGT
                                  C    G  ___
GAM921  TAP2    3'  AGTCGTTTATCTGTTGTTT   6775     A       GT
                                GGA AGCAGGTAGA  TGGCT
                                ||| ||||||||||  |||||
                                TTT TTGTCTATTT  GCTGA
                                  G        __
GAM921  TCERG1  3'  TGAGCCAATTTTCAGGTTTTT  22960       AGGT
                                GAAAGC   AGAGTTGGCTTG
                                ||||||   ||||||||||||
                                TTTTTG   TTTTAACCGAGT
                                   GAC_
GAM921  TCF8    3'  AGGCGTGTTTTACTTGTTTTTT 48426           TTG   G
                                GGAAAGCAGGTAGAG  GCTT
                                ||||||||||||||  ||||
                                TTTTTTGTTCATTTT  CGGA
                                        GTG   A
GAM921  TEGT    3'  GGTCTGTTACCTGTTTTCCA  65228           AGTT
                                TGGAAAGCAGGTAG   GGCT
                                ||||||||||||||  ||||
                                ACCTTTTGTCCATT   CTGG
                                        GT__
GAM921  TEM5    3'  TAAGTCACAAGGTGCTGCTTTT 52303         GTAGAGT
          CA                    TGGAAAGCAG      TGGCTTG
                                ||||||||||      |||||||
                                ACTTTTCGTC      ACTGAAT
                                     GTGGAAC
GAM921  TEM8    3'  AAGTTTATCCTGTTTTCCA   50820          _   G
                                TGGAAAGCAGG TAGA TT
                                |||||||||| |||| ||
                                ACCTTTTGTCC ATTT AA
                                       T   G
GAM921  TES     3'  CAAGCCACCCATTTGCTTTT  72461         AGA  T
                                GAAAGCAGGT  GT GGCTTG
                                ||||||||||  || ||||||
                                TTTTCGTTTA  CA CCGAAC
                                     CC_  _
GAM921  TFF3    3'  CAAGCCAATAAAACTGTCTTCC 64322      AG   GTAGA
          A                     TGGAA  CAG    GTTGGCTTG
                                |||||  |||    |||||||||
                                ACCTT  GTC    TAACCGAAC
                                  CT   AAAA_
GAM921  TIMP4   3'  TCTTCTGGCTTAGTCTGTTTTC 13758         TA    TG CTTG
          TA                    TGGAAAGCAGG  GAGT  G
                                ||||||||||  ||||  |
                                ATCTTTTGTCT  TTCG  C
                                      GA   GT TTCTT
GAM921  TLE1    5'  GCTTCTGCTTGGCTTTCC    18668       _     GTT
                                GGAAAGC AGGTAGA   GGC
                                ||||||| |||||||   |||
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                                CCTTTCG TTCGTCT   TCG
                                   G     ___
GAM921  TMC1     3'  AAGTCAGAAACTGTTTCT    57706      G   GTAGAG
                                GGAAA CAG     TTGGCTT
                                ||||| |||     |||||||
                                TCTTT GTC     GACTGAA
                                  _   AAA___
GAM921  TNFRSF9  3'  CTAACTTTTTTGTTTTTT    9582          T
                                GGAAAGCAGG AGAGTTGG
                                |||||||||| ||||||||
                                TTTTTTGTTT TTTCAATC
                                          _
GAM921  TNR      3'  CAAGCCAACCAATATTTTCT   13822    C    GA_
                                AG AGGTA   GTTGGCTTG
                                || |||||   |||||||||
                                TC TTTAT   CAACCGAAC
                                 T    AAC
GAM921  TNS      3'  CAAGCTGGGAGAATCTTTTTCT 42946       C    AGAG TG
                                GGAAAG AGGT    T  GCTTG
                                |||||| ||||    |  |||||
                                TCTTTT TCTA    G  CGAAC
                                   _    AGAG GT
GAM921  TOX      3'  CAAGCTGCATGCTTTTCA    28961         G    AG
                                TGGAAAGCA GTAG  TTG
                                ||||||||| ||||  |||
                                ACTTTTCGT CGTC  AAC
                                     A    G_
GAM921  TP53     5'  CGGGCTGGGAGCGTGCTTTCCA 6799          G  AGAG TG
                                TGGAAAGCA GT    T  GCTTG
                                ||||||||| ||    |  |||||
                                ACCTTTCGT CG    G  CGGGC
                                     G  AG__ GT
GAM921  TP63     3'  TAAGCTTCAGTTGCTTGTCTTC 14944      AG      AGTT
           T                     GGAA  CAGGTAG    GGCTTG
                                ||||  |||||||    ||||||
                                TCTT  GTTCGTT    TCGAAT
                                  CT      GACT
GAM921  TRIP11   5'  CAGGCCAGGCCTCTGCGTTTCT 16181       _    GT  AG
           A                      TGGAAA GCAG  AG  TTGGCTTG
                                ||||||| ||||  ||  ||||||||
                                ATCTTT CGTC  TC  GACCGGAC
                                   G    __  CG
GAM921  TRO      3'  GCTTTATTGTTTGCTTTCT   32914         ___
                                GGAAAGCAG   GTAGAGT
                                |||||||||   |||||||
                                TCTTTCGTT   TATTTCG
                                     TGT
GAM921  TSG      3'  AGTTCAACTCTGCTGTTTTTCA 40601          G       _  TG
                                TGGAAAGCAG TAGAGTTGG CT
                                |||||||||| ||||||||| ||
```

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                                ACTTTTTGTC GTCTCAACT GA
                                      _       T  C
GAM921  UBE2L6   3'  CAGGCCAGTTCTCCAGCTCTCC 16160     A  A  T  GT
            A                    TGGA AGC GG AGA  TGGCTTG
                                 |||| ||| || |||  |||||||
                                 ACCT TCG CC TCT  ACCGGAC
                                   C  A  _  TG
GAM921  UBQLN1   3'  GCCAGTTTATTTGCTTTTTA  26475           G   _
                                 TGGAAAGCAGGTAGA TTGG C
                                 |||||||||||||| |||| |
                                 ATTTTTCGTTTATTT GACC G
                                       _   T
GAM921  USP1     3'  AGTCTTTTGTGTTTGCTTTTTA 14018        GG  G  TT   TG
                                 TGGAAAGCA  TA AG  GGCT
                                 |||||||||  || ||  ||||
                                 ATTTTTCGT  GT TT  CTGA
                                       TT  G  TT   C
GAM921  UVRAG    3'  AGCTATTTGTCTGCTTTTTA  14023         GT  GT
                                 TGGAAAGCAG  AGA  TGGCT
                                 ||||||||||  |||  |||||
                                 ATTTTTCGTC  TTT  ATCGA
                                       TG  __
GAM921  VCL      3'  TGAGCTGAAATGCTGCATTTTA 14034      A   G  GAG TG
                                 TGGAA GCAG TA   T  GCTTG
                                 ||||| |||| ||   |  |||||
                                 ATTTT CGTC GT   A  CGAGT
                                    A   _  AA_ GT
GAM921  VDAC1    3'  CCACTCAATTTGTTTTTTA   14035          A   T
                                 TGGAAAGCAGGT GAGT GG
                                 ||||||||||||| |||| ||
                                 ATTTTTTGTTTA CTCA CC
                                       A   _
GAM921  VPS26    3'  ATTTGTAATTTTGCTTTCTTTC 18105       C        GCTTG
            T                     GGAAAG AGGTAGAGTTG
                                  |||||| ||||||||||
                                  TCTTTC TTCGTTTTAAT
                                     T         GTTTAT
GAM921  WNT5A    3'  GGGCTGCTAGCTTGCTTTCT   14123          AG  T   G
                                 GGAAAGCAGGT  AGT GGCTT
                                 ||||||||||  |||  |||||
                                 TCTTTCGTTCG  TCG TCGGG
                                       A_  _
GAM921  WWOX     3'  TAGGCATAGGTCTCTTTGCTTT 33492         T  G  _
            CT                     GGAAAGCAGG AGA TTG GCTTG
                                   |||||||||| ||| ||| |||||
                                   TCTTTCGTTT TCT GAT CGGAT
                                       C  G  A
GAM921  YWHAG    3'  CAGCTTTGGCTCTGGCTGCTTT 25938         G     __   TG
            TTA                     TGGAAAGCAG TAGAGTT  GGCT
                                    |||||||||| |||||||  ||||
```

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                                ATTTTTCGTC GTCTCGG  TCGA
                                      G      TT   C
GAM921  YWHAG    3'  CAGGTTGGTTTTGCTGTTGATC 25939    A_    G    TT
                                GA  AGCAG TAGAG  GGCTTG
                                ||  ||||| |||||  ||||||
                                CT  TTGTC GTTTT  TTGGAC
                                 AG    _    GG
GAM921  YWHAG    3'  TCTCGGCTCTGCATGTTTTCCA 25945         G        CTTG
                                TGGAAAGCA GTAGAGTTGG
                                ||||||||| ||||||||||
                                ACCTTTTGT CGTCTCGGCT
                                      A         CTG
GAM921  ZFP93    3'  TGAAAATTCTAGTCTGTTTTCT 16174           _      GGCTTG
           A                     TGGAAAGCAGG TAGAGTT
                                ||||||||||| |||||||
                                ATCTTTTGTCT ATCTTAA
                                      G      AAGT
GAM921  ZNF157   3'  TGGGCTGTTCATCTCTTGCTTT 14340          T   GT__
           TT                     GGAAAGCAGG AGA    TGGCTTG
                                ||||||||||  |||    |||||||
                                TTTTTCGTTC TCT    GTCGGGT
                                      _   ACTT
GAM921  ZNF189   3'  GAGTGCCTTTTTTGTTTTTCA  14360          T    TTG    G
                                TGGAAAGCAGG AGAG   GCTT
                                ||||||||||| ||||   ||||
                                ACTTTTTGTTT TTTC   TGAG
                                      _    CG_
GAM921  ZNF217   3'  TAAGTTGTAAACCTGCTTGTTC 22546      _       AGAGT
           A                     TGGA AAGCAGGT     TGGCTTG
                                ||||| ||||||||     |||||||
                                ACTT TTCGTCCA     GTTGAAT
                                  G       AAT__
GAM921  ZNF255   5'  CAACATCTATTGTTTTTC     20496          G    _
                                GGAAAGCAG TAGA GTTG
                                ||||||||| |||| ||||
                                CTTTTTGTT ATCT CAAC
                                      _    A
GAM921  ZNF265   3'  AGCTTTAGTTTGTTTTCT     19574           _
                                GGAAAGCAGG TAGAGTT
                                ||||||||| |||||||
                                TCTTTTGTTT ATTTCGA
                                      G
GAM921  ZNF36    3'  TGATTTTTGTTGCTTTTCA    95590          GT
                                TGGAAAGCAG  AGAGTTG
                                ||||||||||  |||||||
                                ACTTTTCGTT  TTTTAGT
                                      GT
GAM921  ZNFN2A1  3'  CAAGCCCACCATCTGCTTCT   61391      A     AGA  T
                                GGAA GCAGGT   GT GGCTTG
                                |||| ||||||   || ||||||
```

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                                TCTT CGTCTA   CA CCGAAC
                                  _     C__  C
GAM921  13CDNA73 3' GATCTTGGCTGCTTTTTA    43787          G  GA
                                TGGAAAGCAG TA  GTT
                                |||||||||| ||  |||
                                ATTTTTCGTC GT  TAG
                                      G  TC
GAM921  20D7-FC4 3' GTTTGTTCTCTCTGTTTTTT  61569         GT    TT
                                GGAAAGCAG  AGAG  GGC
                                |||||||||  ||||  |||
                                TTTTTTGTC  TCTT  TTG
                                      TC    GT
GAM921  AAK1     3' AAGTGTTTTCCTTGCTTTTC  30509         TA   TTG   G
                                GGAAAGCAGG  GAG   GCTT
                                ||||||||||  |||   ||||
                                CTTTTCGTTC  CTT   TGAA
                                      __   TTG
GAM921  ABCA5    5' CGGGTTTGTTTGTTTGTTTTTC 38534        GG    GTT
                                GGAAAGCA  TAGA   GGCTTG
                                ||||||||  ||||   ||||||
                                CTTTTTGT  GTTT   TTGGGC
                                     TT   GT_
GAM921  AKAP11   3' TAACTCTTTTTTGCTTTTCA  58466          T_
                                TGGAAAGCAGG  AGAGTTG
                                ||||||||||  |||||||
                                ACTTTTCGTTT  TCTCAAT
                                      TT
GAM921  ANKRD6   3' CAAGTTGATTTTCATGTGTTT  30770      G  _    TG
                                AAGCA GT AGAGT  GCTTG
                                ||||| || |||||  |||||
                                TTTGT TA TTTTA  TGAAC
                                   G  C    GT
GAM921  AP3M1    3' AGGACCAGTTTGTTTTCCA    24934          TAGAG   _
                                TGGAAAGCAGG    TTGG CTT
                                ||||||||||     |||| |||
                                ACCTTTTGTTT    GACC GGA
                                      _____   A
GAM921  AP3M1    3' TGAGAACATTTGCTTTGCTTTC 24938          _    _  GGCTTG
           T                     GGAAAGCAG GTAGA GTT
                                 |||||||| ||||| |||
                                 TCTTTCGTT CGTTT CAA
                                      T    A   GAGT
GAM921  AP3S2    3' AGGCCCACCTGCTTCCCA    20644     A      AGAGTT
                                TGG AAGCAGGT     GGCTT
                                ||| ||||||||     |||||
                                ACC TTCGTCCA     CCGGA
                                  C       C_____
GAM921  APEG1    3' CAGGCCTGTCTATCTGTTTGTC 72594     _         GTT
           T                     GGA AAGCAGGTAGA   GGCTTG
                                 ||| ||||||||||   ||||||
```

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                                TCT TTTGTCTATCT   CCGGAC
                                  G         GT_
GAM921  APH2     3'  CCTCTTCTACTTGCTGTCT   51301     A        TT
                                GGA AGCAGGTAGAG  GG
                                ||| ||||||||||  ||
                                TCT TCGTTCATCTT  CC
                                  G         CT
GAM921  APOL6    3'  TGAGCTAACTTTATGGCT    48376     AG
                                AGC  GTAGAGTTGGCTTG
                                |||  ||||||||||||||
                                TCG  TATTTCAATCGAGT
                                  G_
GAM921  ARFD1    3'  GCTCTTTACTGTTTTTCA    53791          GT_
                                TGGAAAGCAG   AGAGT
                                ||||||||||   |||||
                                ACTTTTTGTC   TCTCG
                                      ATT
GAM921  ARHGAP5  3'  GGCATTTACCGTTTTTCA    77603        A     GTTG
                                TGGAAAGC GGTAGA    GCT
                                |||||||| ||||||    |||
                                ACTTTTTG CCATTT    CGG
                                     _     A___
GAM921  ARHGAP5  3'  TGCTTTTCAGCCTGCTTTCT   77608          A   TT   TTG
                                GGAAAGCAGGT GAG  GGC
                                |||||||||| |||  |||
                                TCTTTCGTCCG CTT  TCG
                                      A   T_   TA
GAM921  ARHGEF15 3'  CAAGCCAGTTCTTCTCTTCCA  30950      A C   T   GT
                                TGGAA G AGG AGA  TGGCTTG
                                ||||| | ||| |||  |||||||
                                ACCTT C TCT TCT  ACCGAAC
                                   _ _  _   TG
GAM921  ATP10B   3'  CGAGTTGGTTCTGCTTTTTGCC 64106    A   C       TT
                                GG AAG AGGTAGAG  GGCTTG
                                || ||| ||||||||  ||||||
                                CC TTT TTCGTCTT  TTGAGC
                                 G   _       GG
GAM921  B3GNT5   3'  TAAGCTGATTTTAATGACGTTT 50251       AGG__     TG
           TC                    GAAAGC    TAGAGT  GCTTG
                                ||||||    ||||||  |||||
                                CTTTTG    ATTTTA  CGAAT
                                   CAGTA     GT
GAM921  B7-H1    3'  CAATGCCTCAATTTGTTTTCT  27095          A  GTT  _
                                GGAAAGCAGGT GA   GGC TTG
                                |||||||||| ||   ||| |||
                                TCTTTTGTTTA CT   CCG AAC
                                      A ___   T
GAM921  BA526D8.4 5'  GAGCCTCTATTTGTTTTCT   70906           GTT    G
                                GGAAAGCAGGTAGA   GGCTT
                                ||||||||||||||   |||||
```

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                                TCTTTTGTTTATCT  CCGAG
                                      ___    A
GAM921  BART1    3'  CAAGCTACAAGCTCTGTGTTTC 25035      G  GG    ___
           T                   GGAAA CA  TAGAGT  TGGCTTG
                               ||||| ||  ||||||  |||||||
                               TCTTT GT  GTCTCG  ATCGAAC
                                 _ __     AAC
GAM921  BPESC1   3'  CAAGCTGATTTTAAGTGATATT 41769     AAG  GG    TG
           CA                   TGGA  CA  TAGAGT  GCTTG
                               ||||  ||  ||||||  |||||
                               ACTT  GT  ATTTTA  CGAAC
                                 ATA  GA    GT
GAM921  BRPF3    3'  GAGTGACTTTATTTGCTTTCTA 93931              G  G
                               TGGAAAGCAGGTAGAGTTG CTT
                               |||||||||||||||||| |||
                               ATCTTTCGTTTATTTCAGT GAG
                                      _  A
GAM921  C11orf17 3'  CAGGTTTTACTGCTTGCTTTCC 40577           AGTT
           A                    TGGAAAGCAGGTAG   GGCTTG
                               ||||||||||||||   ||||||
                               ACCTTTCGTTCGTC   TTGGAC
                                       ATT_
GAM921  C13orf1  3'  GCATTTTGTCTGGCTTTCTA  40364       _ GT    TG
                               TGGAAAGC AG  AGAGT  GC
                               |||||||| ||  |||||  ||
                               ATCTTTCG TC  TTTTA  CG
                                    G  TG   __
GAM921  C1orf26  3'  TAAGTTGGAAGTCCTTGTTTAC 35067    A     TAGAG TG
           T                    GG AAGCAGG    T  GCTTG
                               || |||||||    |  |||||
                               TC TTTGTTC    G  TGAAT
                                A      CTGAA GT
GAM921  C1QTNF3  3'  CAGGTTGGAAATATTTTTTTCT 48924       C    GAG TG
           A                    TGGAAAG AGGTA   T  GCTTG
                               ||||||| |||||   |  |||||
                               ATCTTTT TTTAT   G  TGGAC
                                   _    AAA GT
GAM921  C20orf11 3'  GAGTTTGATTTGTTTTCC    35866          AGAGTT
                               GGAAAGCAGGT     GGCTT
                               ||||||||||      |||||
                               CCTTTTGTTTA     TTGAG
                                      GT____
GAM921  C20orf139 3' CAGGCTAGCTCAGGCTTATTCA 85915     _   AGGTA
                               TGGA AAGC    GAGTTGGCTTG
                               |||| ||||    ||||||||||
                               ACTT TTCG    CTCGATCGGAC
                                 A   GA___
GAM921  C20orf142 3' CAGGCTAATTTTGTATTTTTA  75277       GCAGG
                               TGGAAA    TAGAGTTGGCTTG
                               ||||||    ||||||||||||
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                                ATTTTT    GTTTTAATCGGAC
                                   AT___
GAM921  C20orf152 5'  AGGAAATCTATTTGTTTCTA  55938       G      GTTGG
                                TGGAAA CAGGTAGA    CTT
                                |||||| ||||||||    |||
                                ATCTTT GTTTATCT    GGA
                                   _       AAA__
GAM921  C20orf27  3'  CAGGTCTGTGTTACTTGGTTTT 35822       G      AGTT
           TA                    TGGAAA CAGGTAG    GGCTTG
                                |||||| |||||||    ||||||
                                ATTTTT GTTCATT    CTGGAC
                                   G      GTGT
GAM921  C20orf42  3'  ATGTCAGATTTTACCTGTTTGC 35062    A          _    TTG
           T                     GG AAGCAGGTAGAGT TGGC
                                || ||||||||||||| ||||
                                TC TTTGTCCATTTTA ACTG
                                 G           G    TAG
GAM921  C20orf50  3'  TGGGCTGATTTTGTTGCTT    70614       G     TG
                                AAGCAG TAGAGT  GCTTG
                                |||||| ||||||  |||||
                                TTCGTT GTTTTA  CGGGT
                                   _     GT
GAM921  C20orf98  3'  GTGTCTTCTACCTGCATTTT   72009      A        TT   TTG
                                GGAA GCAGGTAGAG  GGC
                                |||| ||||||||||  |||
                                TTTT CGTCCATCTT  CTG
                                  A         __   TGT
GAM921  C22orf19  3'  TGAGCACTGGGCTTCTGCTTTC 14833          T  AGTTG_
           T                     GGAAAGCAGG AG      GCTTG
                                |||||||||| ||      |||||
                                TCTTTCGTCT TC      CGAGT
                                      _  GGGTCA
GAM921  C3orf4    3'  CAAGAAACTGCCTGCTTTACA  39588    G         AGTTGG
                                TG AAAGCAGGTAG     CTTG
                                || ||||||||||      ||||
                                AC TTTCGTCCGTC     GAAC
                                 A          AAA___
GAM921  C4S-2     3'  CAGGCCGCACCTGTCTGTTTTT 38447         GT  A  _
                                GAAAGCAG  AG GT TGGCTTG
                                |||||||  || || |||||||
                                TTTTTGTC  TC CA GCCGGAC
                                     TG  _  C
GAM921  C9orf14   5'  CAGGCGCTCACCTTTGCCTGCT 87954     A         T  ___
           CTCT                    GGA AGCAGGTAGAG TG   GCTTG
                                ||| |||||||||| ||   |||||
                                TCT TCGTCCGTTTC AC   CGGAC
                                  C          C  TCG
GAM921  CABIN1    3'  TGAGCCGGCTCTGCCTGTGTCA 25455    GAAA
           CA                      TG    GCAGGTAGAGTTGGCTTG
                                ||    ||||||||||||||||||
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                                AC   TGTCCGTCTCGGCCGAGT
                                 ACTG
GAM921  CABYR    3'  CAGGCCAAAAAGCCCTGTTTTC 25171          TAGAG
              C                   GGAAAGCAGG    TTGGCTTG
                                  ||||||||||    ||||||||
                                  CCTTTTGTCC    AACCGGAC
                                       CGAAA
GAM921  CASPR3   3'  CAAGATTGTCTGCCTGTTTTTC 54455            GTTGG
                                  GGAAAGCAGGTAGA    CTTG
                                  ||||||||||||||    ||||
                                  CTTTTTGTCCGTCT    GAAC
                                         GTTA_
GAM921  CCNG2    3'  CCTTCTATTTGTTATTCA    16377     A        TT
                                  TGGA AGCAGGTAGAG  GG
                                  |||| ||||||||||  ||
                                  ACTT TTGTTTATCTT  CC
                                    A        __
GAM921  CD109    3'  AGTACATTTACTGTGCTTTTCA 56861        _    GTTG  TG
                                  TGGAAAGCA GGTAGA   GCT
                                  |||||||| ||||||   |||
                                  ACTTTTCGT TCATTT   TGA
                                       G     ACA_  C
GAM921  CDC14B   3'  CAAGCTGCTTGTCTTCCA    53986     AG     AG
                                  TGGAA  CAGGTAG  TTG
                                  |||||  |||||||  |||
                                  ACCTT  GTTCGTC  AAC
                                     CT     G_
GAM921  CDCA7    3'  TAAGCTGATTTGAATTTTCA   50045     GCAGGTA   TG
                                  TGGAAA     GAGT  GCTTG
                                  ||||||     ||||  |||||
                                  ACTTTT     TTTA  CGAAT
                                     AAG____   GT
GAM921  CG012    5'  GGGTTTTTGTTTGTTTTCC   84164       GG    TTG
                                  GGAAAGCA  TAGAG   GCTT
                                  ||||||||  |||||   ||||
                                  CCTTTTGT  GTTTT   TGGG
                                       TT    ___
GAM921  CGI-01   3'  TGGGTTGGTTTGTCTTTGCTTC 32510     A    TA_  TT
              C                   GGAA GCAGG   GAG  GGCTTG
                                  |||| |||||   |||  ||||||
                                  CCTT CGTTT   TTT  TTGGGT
                                    _    CTG   GG
GAM921  ChGn     5'  CAAGCTGATTTTTTATTTCT   37776      GCAGGT    TG
                                  GGAAA     AGAGT  GCTTG
                                  |||||     |||||  |||||
                                  TCTTT     TTTTA  CGAAC
                                     ATT___     GT
GAM921  CLDN1    3'  TAAGCCCTTATTTGTTTT    41190          AGTT
                                  AAAGCAGGTAG    GGCTTG
                                  ||||||||||    ||||||
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                                TTTTGTTTATT   CCGAAT
                                      C___
GAM921  CLDN8   3'  TGTGTTCTATTTGCTTT    25096          TTG  TTG
                                AAAGCAGGTAGAG  GC
                                |||||||||||||  ||
                                TTTCGTTTATCTT  TG
                                      G__  TA
GAM921  COPS4   3'  TAAGCTAACTCAGATGTTTT  32847      GGTA
                                AAAGCA   GAGTTGGCTTG
                                ||||||   ||||||||||
                                TTTTGT   CTCAATCGAAT
                                   AGA_
GAM921  COVA1   3'  CAGGTTAATTTTACACTAGCTT 73639     _ _
                                AAGC AG GTAGAGTTGGCTTG
                                |||| || ||||||||||||||
                                TTCG TC CATTTTAATTGGAC
                                  A  A
GAM921  CPSF2   3'  CAGGCAGGATGTCTGTTTTCT  62266        GT GAGTTG
                                GGAAAGCAG  A    GCTTG
                                |||||||||  |    |||||
                                TCTTTTGTC  T    CGGAC
                                     TG AGGA__
GAM921  CREG    3'  GGTTTGTTTGCTTGCTT    15246          GTT   TG
                                AAGCAGGTAGA  GGCT
                                ||||||||||  ||||
                                TTCGTTCGTTT  TTGG
                                      GT_   T
GAM921  Cyt19   3'  CAAGAGTGATCTGCATGTTTTT 73310         G    GTTGG
           TA                    TGGAAAGCA GTAGA    CTTG
                                |||||||||  |||||    ||||
                                ATTTTTTGT  CGTCT    GAAC
                                     A    AGTGA
GAM921  DATF1   3'  CAAGTTAGTGTTGCATCTGATT 55846      G  __   AG
           TTCA                    TGGAAA CAG  GTAG  TTGGCTTG
                                |||||| |||  ||||  ||||||||
                                ACTTTT GTC  CGTT  GATTGAAC
                                   A  TA   GT
GAM921  DATF1   3'  CAAGTTAGTGTTGCATCTGATT 55847      G  __   AG
           TTCA                    TGGAAA CAG  GTAG  TTGGCTTG
                                |||||| |||  ||||  ||||||||
                                ACTTTT GTC  CGTT  GATTGAAC
                                   A  TA   GT
GAM921  DCTN4   3'  TAAGTTAATTTGGATTTGTT  68397       A_
                                AGCAGGT  GAGTTGGCTTG
                                |||||||  ||||||||||
                                TTGTTTA  TTTAATTGAAT
                                   GG
GAM921  DDM36   3'  CAATGTCATTTATTTGGTTTTT 40915       _     GT   _
           CA                    TGGAAAGC AGGTAGA  TGGC TTG
                                |||||||| |||||||  |||| |||
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                                ACTTTTTG TTTATTT  ACTG AAC
                                    G      __   T
GAM921  DDX33    3'  CAATCTGGCTTTGCTGCTTTCT 39781         G     TG C
          A                      TGGAAAGCAG TAGAGT  G TTG
                                 |||||||||| ||||||  | |||
                                 ATCTTTCGTC GTTTCG  C AAC
                                       _     GT T   A
GAM921  DDX35    3'  TGGGCTGGCTTTGCTTTCC    41931        GGTA   TG
                                 GGAAAGCA    GAGT  GCTTG
                                 ||||||||    ||||  |||||
                                 CCTTTCGT    TTCG  CGGGT
                                       ____   GT
GAM921  DKFZP434A0225 3'  AAGTTAATTTTATAATGT    95520     G_
                                 GCA  GTAGAGTTGGCTT
                                 |||  ||||||||||||
                                 TGT  TATTTTAATTGAA
                                   AA
GAM921  DKFZp434E0519 3'  TATCTGTTTTATCTGTTTTACC 50999    _          TT  CTTG
                                 GG AAAGCAGGTAGAG  GG
                                 || ||||||||||||  ||
                                 CC TTTTGTCTATTTT  CT
                                  A          GT  AT
GAM921  DKFZp434E2220 3'  GGTTTTTATCTGTCTTTT    34715      _       TTG
                                 GAAAG CAGGTAGAG   GCT
                                 ||||| |||||||||   |||
                                 TTTTC GTCTATTTT   TGG
                                    T       ___
GAM921  DKFZp434F142 5'  CAAGCCAAGCGCCTGCCTTTCA 51030       A     AGAG
                                 TGGAA GCAGGT    TTGGCTTG
                                 ||||| ||||||    ||||||||
                                 ACTTT CGTCCG    AACCGAAC
                                    C     CG__
GAM921  DKFZp434I1610 3'  CATCCTTTTACTTCTTTTCA   64200        C       TT  CT
                                 TGGAAAG AGGTAGAG  GG  TG
                                 ||||||| ||||||||  ||  ||
                                 ACTTTTC TTCATTTT  CC  AC
                                       _      __ TT
GAM921  DKFZP434L0117 3'  TGAGCTGGCTTTCTGGGTTTTC 43245        A_  T    TG
          T                      GGAAAGC  GG AGAGT  GCTTG
                                 |||||||  || |||||  |||||
                                 TCTTTTG  TC TTTCG  CGAGT
                                      GG  _    GT
GAM921  DKFZp434N074 5'  GCCTCCTCTGCCTGCTTCT    63330      A        TT
                                 GGAA GCAGGTAGAG  GGC
                                 |||| ||||||||||  |||
                                 TCTT CGTCCGTCTC  CCG
                                    _         CT
GAM921  DKFZP434P0721 3'  AAGTAGTCTTACTTGTTTTTTA 64450           A   TTG   G
                                 TGGAAAGCAGGT GAG   GCTT
                                 |||||||||||| |||   ||||
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                                ATTTTTTGTTCA TTC   TGAA
                                      _  TGA
GAM921  DKFZP434P0721 3'  CAAGTTAGTTCTGTCACGCTTC 64458     A  A_ GT   GT
          T                    GGAA GC  G  AGA  TGGCTTG
                               |||| ||  |  |||  |||||||
                               TCTT CG  C  TCT  ATTGAAC
                                 _  CA TG   TG
GAM921  DKFZP434P0721 3'  GATTTTTCTTGCTTTTCA    64461          T
                               TGGAAAGCAGG AGAGTT
                               |||||||||||| ||||||
                               ACTTTTCGTTC TTTTAG
                                      T
GAM921  DKFZP434P0721 3'  TAAGTTAATTTCTTCTCTTTCC 64465       C   TA
          A                    TGGAAAG AGG  GAGTTGGCTTG
                               ||||||| |||  ||||||||||
                               ACCTTTC TCT  TTTAATTGAAT
                                  _  TC
GAM921  DKFZp547C176 3'  GTGCTGACTAGTTTGTTTTCTA 67804          TAG   TG  TTG
                               TGGAAAGCAGG   AGT  GC
                               ||||||||||   |||  ||
                               ATCTTTTGTTT   TCA  CG
                                     GA_   GT  TGA
GAM921  DKFZP564C186 3'  CGGGCTGGTGGCCAGTGTTTCC 72843       _  A   AGAG TG
          A                    TGGAAA GC GGT    T  GCTTG
                               |||||| || |||   |  |||||
                               ACCTTT TG CCG    G  CGGGC
                                  G  A   GT__ GT
GAM921  DKFZP564D0462 3'  GAGTAATGCTTGCTTGCT    71021        G   TG_
                               AGCAGGTA AGT   GCTT
                               |||||||| |||   ||||
                               TCGTTCGT TCG   TGAG
                                    _  TAA
GAM921  DKFZP564F013 3'  CAGGTCAACAAGTGCTCTTT   95879      CA   GA_
                               AAAG  GGTA   GTTGGCTTG
                               ||||  ||||   |||||||||
                               TTTC  TCGT   CAACTGGAC
                                 __   GAA
GAM921  DKFZP564I0422 3'  GACATCAGCTTGCTTTTTA   49515          A  _
                               TGGAAAGCAGGT GA GTT
                               |||||||||||| || |||
                               ATTTTTCGTTCG CT CAG
                                      A  A
GAM921  DKFZP564K0822 3'  CAGGTCATTTGTTTTGCA    95697    G       A  G
                               TG AAAGCAGGT GA TTG
                               || |||||||| || |||
                               AC TTTTGTTTA CT GAC
                                G       _  G
GAM921  DKFZP564M182 3'  TGAGTATACTGTTGGCTTTCCA 78648        AG   AGTTG
                               TGGAAAGC  GTAG    GCTTG
                               ||||||||  ||||    |||||
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                                ACCTTTCG  TGTC    TGAGT
                                     GT   ATA__
GAM921  DKFZP564O0523 3'  AAGTCATTTCTTTGTTTTTT  50414        GT   T    G
                                GGAAAGCAG  AGAG TGGCTT
                                |||||||||  |||| ||||||
                                TTTTTTGTT  TCTT ACTGAA
                                     __   T
GAM921  DKFZP564O1664 5'  AGCTGTCTGTTTGCATTCT   48665     A  GG   GT
                                GGAA GCA  TAGA  TGGCT
                                |||| |||  ||||  |||||
                                TCTT CGT  GTCT  GTCGA
                                  A  TT   __
GAM921  DKFZp566H0824 5'  CAGGTATGCGTATCTGCTATTT 34480      _      GA  TG
          TA                     TGGAA AGCAGGTA  GT  GCTTG
                                |||||  ||||||||  ||  |||||
                                ATTTT TCGTCTAT  CG  TGGAC
                                   A       G_  TA
GAM921  DKFZp566H0824 5'  CCTTTTTCTTGTTTTTCA    34483          T   TT
                                TGGAAAGCAGG AGAG  GG
                                ||||||||||| ||||  ||
                                ACTTTTTGTTC TTTT  CC
                                      _   T_
GAM921  DKFZP566N034 3'  AAGACCTTTACCTGTTTTGTA  80940    G         TTGG  G
                                TG AAAGCAGGTAGAG   CTT
                                || ||||||||||||   |||
                                AT TTTTGTCCATTTC   GAA
                                 G          CA__  A
GAM921  DKFZP586A011 3'  TGGGCTAACCACTTCTTTTTCA 31842       C   AGA
                                TGGAAAG AGGT   GTTGGCTTG
                                |||||||  ||||  |||||||||
                                ACTTTTT TTCA   CAATCGGGT
                                    C   C__
GAM921  DKFZp586I021 3'  TGAGCCAGGCACCTCTGTTTCC 51084      G   TAGAG
                                GGAAA CAGG    TTGGCTTG
                                |||||  ||||   ||||||||
                                CCTTT GTCT    GACCGAGT
                                   _   CCACG
GAM921  DKFZP761L0424 3'  CCCCTTCTTTTGTTTTCT    92978         T   TT
                                GGAAAGCAGG AGAG  GG
                                |||||||||  ||||  ||
                                TCTTTTGTTT TCTT  CC
                                      _   CC
GAM921  DKFZp762E1312 3'  GCTCTCTGTTTGTATTTT    37903     A  GG    TT
                                GGAA GCA  TAGAG  GGC
                                |||| |||  |||||  |||
                                TTTT TGT  GTCTC  TCG
                                  A  TT    __
GAM921  DKFZp762P2111 3'  TGGGCCTCCAGGCCTGCTTTTC 87644          AGAGTT
          A                     TGGAAAGCAGGT     GGCTTG
                                ||||||||||||     ||||||
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                                ACTTTTCGTCCG     CCGGGT
                                      GACCT_
GAM921  DMRTC2   3' CGGGCTTTTTTGTTTGTTT   62480      GG    TT
                                AAGCA  TAGAG  GGCTTG
                                |||||  |||||  ||||||
                                TTTGT  GTTTT  TCGGGC
                                   TT    T_
GAM921  DNAL4    5' CGAGTTGGCAGGGCCTGCTTCC 20421     A     AGA  TG
                                GGAA GCAGGT   GT  GCTTG
                                ||||  ||||||   ||  |||||
                                CCTT CGTCCG   CG  TGAGC
                                   _     GGA  GT
GAM921  DNCLI1   3' AAGCCATTTATTCTGTTTTCT  60224          _   GT     G
                                GGAAAGCAGG TAGA  TGGCTT
                                ||||||||||  ||||  ||||||
                                TCTTTTGTCT ATTT  ACCGAA
                                      T   __
GAM921  DT1P1A10 3' TGGGCCCTTATTTGCTGTTCTA 62248       _       AGTT
                                TGGAA AGCAGGTAG    GGCTTG
                                |||||  |||||||||    ||||||
                                ATCTT TCGTTTATT    CCGGGT
                                   G        C___
GAM921  EAT2     3' CCTGTTGATTCTATTGTGTTTT 80049          _      TG  TTG
           CTA                    TGGAAAGCA GGTAGAGT  GC
                                |||||||||  ||||||||  ||
                                ATCTTTTGT TTATCTTA  TG
                                     G       GT  TCCA
GAM921  EIF4ENIF1 3' CGGGTTGGTTTATGGGCTTTT  39528       AG    G TG
                                GAAAGC  GTAGA T  GCTTG
                                ||||||  |||||  |  |||||
                                TTTTCG  TATTT G  TGGGC
                                   GG    _ GT
GAM921  ELKS     3' GTCTCTTCTGCTTACTTTCCA  31193        C       TT
                                TGGAAAG AGGTAGAG  GGC
                                |||||||  ||||||||  |||
                                ACCTTTC TTCGTCTT  CTG
                                     A       CT
GAM921  ENAH     3' AATTCACTTTCATCTGCTTTCT 37155           _    TGGCTTG
           A                     TGGAAAGCAGGT AGAGT
                                ||||||||||||  |||||
                                ATCTTTCGTCTA TTTCA
                                      C    CTTAAT
GAM921  ENPP4    3' CTTCCTCTGCTTGTATTTT   30715      A        TT
                                GGAA GCAGGTAGAG  GG
                                ||||  ||||||||||  ||
                                TTTT TGTTCGTCTC  TC
                                   A        CT
GAM921  EPB41L1  3' TGAGCCAGCTTTATATTTC   71120      GCAG
                                GAAA   GTAGAGTTGGCTTG
                                ||||   ||||||||||||||
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                                CTTT    TATTTCGACCGAGT
                                  A___
GAM921  EREG     3'  TAGGTCAATAACACTGTATTTT 9319       A   _ AGA
                 A                TGGAA GCAG GT   GTTGGCTTG
                                  ||||| |||| ||   |||||||||
                                  ATTTT TGTC CA   TAACTGGAT
                                    A   A  A__
GAM921  ERO1L    3'  CAAGCTGATATGTGCCTGTTTC 28157      G     GA_  TG
                 T                GGAAA CAGGTA   GT  GCTTG
                                  ||||| ||||||   ||  |||||
                                  TCTTT GTCCGT   TA  CGAAC
                                    _     GTA  GT
GAM921  ETAA16   3'  TAAGTTAGTAGAGACTGTTTTT 39171        GTAGAG
                                  GAAAGCAG     TTGGCTTG
                                  ||||||||     ||||||||
                                  TTTTTGTC     GATTGAAT
                                       AGAGAT
GAM921  FAM8A1   3'  TAAGGTAGTCTCCTGCTTTCCA 33203          T   G   G
                                  TGGAAAGCAGG AGA TTG CTTG
                                  |||||||||||| ||| ||| ||||
                                  ACCTTTCGTCC TCT GAT GAAT
                                        _  _  G
GAM921  FBXO3    3'  GATTCAACTTGTTTTTCA    25154           A
                                  TGGAAAGCAGGT GAGTT
                                  |||||||||||| |||||
                                  ACTTTTTGTTCA CTTAG
                                        A
GAM921  FGD3     3'  TGAGCTGAATCGTGACTTGCTT 73282     A      A__  G TG
                 CCCA                TGG AAGCAGGT   GA T  GCTTG
                                  ||| ||||||||   || |  |||||
                                  ACC TTCGTTCA   CT A  CGAGT
                                    C       GTG  A GT
GAM921  FJX1     3'  TGAGCTAATTCTGCAATTTTCT 27567       CAG
                 A                TGGAAAG   GTAGAGTTGGCTTG
                                  |||||||   ||||||||||||||
                                  ATCTTTT   CGTCTTAATCGAGT
                                       AA_
GAM921  FKSG28   5'  GCCTCTGCTTTCTTTCCA    48909       C     GTT
                                  TGGAAAG AGGTAGA   GGC
                                  ||||||| |||||||   |||
                                  ACCTTTC TTCGTCT   CCG
                                       T     ___
GAM921  FLJ00026 5'  CAAGTCAATTCCAGGCTTGCT  65618       A__
                                  AGCAGGT   GAGTTGGCTTG
                                  |||||||   ||||||||||
                                  TCGTTCG   CTTAACTGAAC
                                       GAC
GAM921  FLJ10044 3'  TGAGCCAGCAAGTCCTGCTGTC 36245     A     TAGA
                 CA                  TGGA AGCAGG   GTTGGCTTG
                                  |||| ||||||   |||||||||
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                                ACCT TCGTCC   CGACCGAGT
                                  G     TGAA
GAM921  FLJ10060 5' CGGGCCAGCTTTCTGCCTGT  36270        __
                                GCAGGTAGA  GTTGGCTTG
                                |||||||||  |||||||||
                                TGTCCGTCT  CGACCGGGC
                                     TT
GAM921  FLJ10199 3' CAAGTTTTGTGTTTGCTGTCTA 71752     A   GG  G  TT
                                TGGA AGCA  TA AG  GGCTTG
                                |||| ||||  || ||  ||||||
                                ATCT TCGT  GT TT  TTGAAC
                                  G   TT  G  __
GAM921  FLJ10232 3' TGAGCCAGTGGAATGTTTTTT  36386       GGTAGA
                                GGAAAGCA    GTTGGCTTG
                                ||||||||    |||||||||
                                TTTTTTGT    TGACCGAGT
                                     AAGG__
GAM921  FLJ10326 3' TGAGTCAACTTTACTGGCT   36503    A
                                AGC GGTAGAGTTGGCTTG
                                ||| ||||||||||||||
                                TCG TCATTTCAACTGAGT
                                  G
GAM921  FLJ10546 3' GTTGTCTTGTCTTTATTTGCTT 60182           TT__  TTG
           TCCA                   TGGAAAGCAGGTAGAG   GGC
                                ||||||||||||||||   |||
                                ACCTTTCGTTTATTTC   CTG
                                        TGTT  TTGA
GAM921  FLJ10579 3' AATTCTACCTGTATTCCA    36826     A
                                TGGAA GCAGGTAGAGTT
                                ||||| ||||||||||||
                                ACCTT TGTCCATCTTAA
                                   A
GAM921  FLJ10713 3' TGGGTTGGATCATTTGTTTTT  37012        A  G TG
                                GAAAGCAGGT GA T  GCTTG
                                |||||||||| || |  |||||
                                TTTTTGTTTA CT G  TGGGT
                                      _  A GT
GAM921  FLJ10719 3' CAGGCTGGCTTCGTTTTTCCA  63206      CAG TA   TG
                                TGGAAAG   G  GAGT  GCTTG
                                |||||||   |  ||||  |||||
                                ACCTTTT   T  TTCG  CGGAC
                                    ___ GC   GT
GAM921  FLJ10726 3' CAAGTTAGCAGGCTTGTTCTTT 37041     _     AGA
           T                    GGAA AGCAGGT   GTTGGCTTG
                                |||| |||||||   |||||||||
                                TTTT TTGTTCG   CGATTGAAC
                                  C      GA_
GAM921  FLJ10781 3' AGGTTAACTTGTTTTTGT    37168      TA_
                                GCAGG   GAGTTGGCTT
                                |||||   ||||||||||
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                                TGTTT  TTCAATTGGA
                                  TTG
GAM921  FLJ10856 3' AAGTTCCTCCTGTTTTCT   37321        TA  GTTG
                                GGAAAGCAGG  GA   GCTT
                                ||||||||||  ||   ||||
                                TCTTTTGTCC  CT   TGAA
                                     TC  ____
GAM921  FLJ10856 3' GAGTTTTATCTGTTTTACA   37324    G        GTTG
                                TG AAAGCAGGTAGA   GCTT
                                || ||||||||||||   ||||
                                AC TTTTGTCTATTT   TGAG
                                 A        ____
GAM921  FLJ10900 3' TGAGCTAAACGTGTCTGTGCTT 66207        _  TAGAG_
          TCTA                    TGGAAAGCA GG     TTGGCTTG
                                |||||||||  ||     ||||||||
                                ATCTTTCGT TC     AATCGAGT
                                     G  TGTGCA
GAM921  FLJ10932 3' ATTTAACTTATTTGCTTTTTA  37424          A     CTTG
                                TGGAAAGCAGGT GAGTTGG
                                ||||||||||| |||||||
                                ATTTTTCGTTTA TTCAATT
                                       _      TAA
GAM921  FLJ10936 5' CGGGTTGCGCTCTGCTTTTGC  37441    __      _
                                GCA  GGTAGAGT TGGCTTG
                                |||  |||||||| |||||||
                                CGT  TCGTCTCG GTTGGGC
                                  TT       C
GAM921  FLJ10956 3' TAGGTCAAAGCTGTTTTT    37472        GTAGAG
                                GAAAGCAG     TTGGCTTG
                                ||||||||     ||||||||
                                TTTTTGTC     AACTGGAT
                                    GA____
GAM921  FLJ11101 3' CGGGTTAGCTCTGTGACTGC  37613     G__
                                GCAG   TAGAGTTGGCTTG
                                ||||   ||||||||||||
                                CGTC   GTCTCGATTGGGC
                                  AGT
GAM921  FLJ11164 3' AGGCCAACATGTGTTCCA    37696     AA   G  AGA
                                TGGA  GCA GT   GTTGGCTT
                                ||||  ||| ||   ||||||||
                                ACCT  TGT TA   CAACCGGA
                                  __   G  ___
GAM921  FLJ11210 3' TAAGTTGACATTTCTGCTTACT 60320    A      TAGA  TG
                                GG AAGCAGG    GT  GCTTG
                                || |||||||    ||  |||||
                                TC TTCGTCT    CA  TGAAT
                                 A      TTA_  GT
GAM921  FLJ11235 3' TGAGTTGACTATTCTACTGCTT 39254       G   ___  TG
                                AAGCAG TAGA   GT  GCTTG
                                |||||| ||||   ||  |||||
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                                TTCGTC ATCT   CA  TGAGT
                                   _    TAT  GT
GAM921  FLJ11269 3' TAAGTTAATTGTAGGTGTGTTC 73028      A   GG  G
              T                  GGAA GCA  TA AGTTGGCTTG
                                 |||| |||  || ||||||||||
                                 TCTT TGT  AT TTAATTGAAT
                                   G   GG  G
GAM921  FLJ11710 3' TAAGTTGGCACCAGCACCTGTT 46251    GA      AGA___  TG
              TCTCA                 TG  AAGCAGGT     GT  GCTTG
                                 ||  ||||||||     ||  |||||
                                 AC  TTTGTCCA     CG  TGAAT
                                  TC       CGACCA  GT
GAM921  FLJ11783 3' TGAGTTGATTTTGCTTTTTT   46551     C       TG
                                 AAAG AGGTAGAGT  GCTTG
                                 |||| |||||||||  |||||
                                 TTTT TTCGTTTTA  TGAGT
                                   _       GT
GAM921  FLJ11850 5' CAGGTTGAGAATTACCTGTTTT 43021           AG_ TG
              CCA                   TGGAAAGCAGGTAG   T  GCTTG
                                 ||||||||||||||   |  |||||
                                 ACCTTTTGTCCATT   A  TGGAC
                                         AAG GT
GAM921  FLJ12190 3' AGGCTGGTTCCTGTTTTCT   47562         TAG  TT
                                 GGAAAGCAGG   AG  GGCTT
                                 ||||||||||   ||  |||||
                                 TCTTTTGTCC   TT  TCGGA
                                      ___  GG
GAM921  FLJ12355 3' TGAGCCGGAGAGCTGCTTGCT  47120        AG__
                                 AGCAGGTAG    TTGGCTTG
                                 |||||||||    ||||||||
                                 TCGTTCGTC    GGCCGAGT
                                      GAGA
GAM921  FLJ12443 3' AATCACCTCGACTTGTTTTTTA 46142          A   T   CTTG
                                 TGGAAAGCAGGT GAG TGG
                                 |||||||||||| ||| |||
                                 ATTTTTTGTTCA CTC ACT
                                        G   C   AAC
GAM921  FLJ12587 3' GCTTTTATCAGTTTTCTA    42782        A     GTT
                                 TGGAAAGC GGTAGA   GGC
                                 |||||||| ||||||   |||
                                 ATCTTTTG CTATTT   TCG
                                      A     ___
GAM921  FLJ12604 3' AAGCCATGTTGTTTTTTA    65058         GTAGAGT
                                 TGGAAAGCAG      TGGCTT
                                 ||||||||||      ||||||
                                 ATTTTTTGTT      ACCGAA
                                      GT_____
GAM921  FLJ12619 5' AAGCCAAATGTGTTTTCCA   48917         G  AGAG
                                 TGGAAAGCA GT    TTGGCTT
                                 |||||||| ||    |||||||
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                                ACCTTTTGT TA    AACCGAA
                                     G _____
GAM921  FLJ12747 3' AAGCTGGCTTTAACTCTCA   50660   A  C  G     TG
                                A AG AG TAGAGT  GCTT
                                | || || ||||||  ||||
                                A TC TC ATTTCG  CGAA
                                 C _  A     GT
GAM921  FLJ12891 3' AGTGCGTCTACACTGCTTTTCA 46918          _    _ TG   TG
                                TGGAAAGCAG GTAGA GT  GCT
                                |||||||||| ||||| ||  |||
                                ACTTTTCGTC CATCT CG  TGA
                                      A    G __  C
GAM921  FLJ12892 3' GGGCACTTTTATTTGTTTTT  68455            T  G
                                GAAAGCAGGTAGAG TG CT
                                |||||||||||||| || ||
                                TTTTTGTTTATTTT AC GG
                                         C  G
GAM921  FLJ12892 3' TAGGTTGGTCTCTCTGCTTCTC 68457     _     GT   _ TG
           TA                     TGGA AAGCAG  AGAG T  GCTTG
                                |||| ||||||  |||| |  |||||
                                ATCT TTCGTC  TCTC G  TGGAT
                                  C     __    T GT
GAM921  FLJ12899 3' CAAGTCTTCCATTTGCTTCT  45060     A     A  TT
                                GGAA GCAGGT GAG  GGCTTG
                                |||| |||||| |||  ||||||
                                TCTT CGTTTA CTT  CTGAAC
                                  _     C  __
GAM921  FLJ12910 3' TAAGTTAATTCTAACTTTT   45004      CAGG
                                GAAAG   TAGAGTTGGCTTG
                                |||||   ||||||||||||||
                                TTTTC   ATCTTAATTGAAT
                                   A___
GAM921  FLJ12960 3' GGCGTCTGCTTGGTTTCT    45302      G      GTTG
                                GGAAA CAGGTAGA   GCT
                                ||||| ||||||||   |||
                                TCTTT GTTCGTCT   CGG
                                   G      G___
GAM921  FLJ12969 5' TGAGCTTCCTCTGCATGTTTTC 43412         G     TT
           TA                     TGGAAAGCA GTAGAG  GGCTTG
                                |||||||| ||||||  ||||||
                                ATCTTTTGT CGTCTC  TCGAGT
                                      A     CT
GAM921  FLJ12998 3' TGAGTCGGTTTCTGTTTCTC  43151   GA    GTA   TT
                                G  AAGCAG   GAG  GGCTTG
                                |  ||||||   |||  ||||||
                                C  TTTGTC   TTT  CTGAGT
                                 TC     ___   GG
GAM921  FLJ13166 3' CAGGTCAGTTTTAGATGTTTTT 47189        GG   GT
                                GAAAGCA  TAGA  TGGCTTG
                                |||||||  ||||  |||||||
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                                TTTTTGT  ATTT  ACTGGAC
                                   AG    TG
GAM921  FLJ13193  3'  TAAGTTTGTTTGCTTTTT    50735        GG    G
                                GGAAAGCA  TAGA TTG
                                ||||||||  |||| |||
                                TTTTTCGT  GTTT AAT
                                   TT    G
GAM921  FLJ13263  3'  AGGACTGCCTGCTTGCTTTCT  47810           A  TGG   G
                                GGAAAGCAGGTAG GT   CTT
                                |||||||||||||| ||   |||
                                TCTTTCGTTCGTC CG   GGA
                                      _ TCA   G
GAM921  FLJ13273  5'  TAAGCTGGCTGTCGTTTTTC   45723       A  TAG   TG
                                GGAAAGC GG   AGT  GCTTG
                                ||||||| ||   |||  |||||
                                CTTTTTG CT   TCG  CGAAT
                                   _ G__   GT
GAM921  FLJ13441  3'  AGGTGTCTGCTGCTTTTT    43908        G    GTTG
                                GGAAAGCAG TAGA    GCTT
                                ||||||||| ||||    ||||
                                TTTTTCGTC GTCT    TGGA
                                   _    G___
GAM921  FLJ13782  3'  TGGGCTGAAGCACTAGCTTTTT 46705        A   AGAG TG
                                GGAAAGC GGT    T  GCTTG
                                ||||||| |||    |  |||||
                                TTTTTCG TCA    A  CGGGT
                                   A   CGA_ GT
GAM921  FLJ13855  3'  CAGGCCAGCATAATTTTGTTTT 43846          TAGA_
          TC                  GGAAAGCAGG    GTTGGCTTG
                              ||||||||||    |||||||||
                              CTTTTTGTTT    CGACCGGAC
                                    TAATA
GAM921  FLJ14007  3'  GTCCTTTTTTTGTTTTCT    45535         T    TT
                                GGAAAGCAGG AGAG  GGC
                                |||||||||| ||||  |||
                                TCTTTTGTTT TTTC  CTG
                                      T   __
GAM921  FLJ14082  3'  TGAGTCAGCTGCTCGTTTCT   47324      G AG  AG
                                GGAAA C  GT  AGTTGGCTTG
                                ||||| |  ||  ||||||||||
                                TCTTT G  CG  TCGACTGAGT
                                   _ CT  __
GAM921  FLJ14084  3'  TGAGCCTCAAACTCTACCTGTT 41598     A          ___
          CTCT                   GGA AGCAGGTAGAGTT   GGCTTG
                                 ||| ||||||||||||   ||||||
                                 TCT TTGTCCATCTCAA   CCGAGT
                                   C           ACT
GAM921  FLJ14326  3'  TAAGTCAGCTTTGCCTGTGGTT 50783     AA
          T                     GGA  GCAGGTAGAGTTGGCTTG
                                |||  ||||||||||||||||||
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                                TTT  TGTCCGTTTCGACTGAAT
                                  GG
GAM921  FLJ14564  3'  TAAGTTAAAGACTTCTTTCCA  77017       C    AGAG
                                TGGAAAG AGGT    TTGGCTTG
                                ||||||| ||||    ||||||||
                                ACCTTTC TTCA    AATTGAAT
                                    _   GA__
GAM921  FLJ14624  3'  TGAGTTGTTCCTGCTGTTTTTT 71846         G   AGT
          A                      TGGAAAGCAG TAG   TGGCTTG
                                ||||||||||  |||   |||||||
                                ATTTTTTGTC GTC   GTTGAGT
                                      _  CTT
GAM921  FLJ14641  3'  CAAGTCAGCATCTCTGCCTTTC 52552      A   GT   _
          A                      TGGAA GCAG  AGA GTTGGCTTG
                                ||||| ||||  |||  |||||||||
                                ACTTT CGTC  TCT CGACTGAAC
                                   C    __  A
GAM921  FLJ20033  5'  GGGCAGTTGCTTGTTTTGCA  34820    G        AG   G
                                TG AAAGCAGGTAG  TTG CT
                                || ||||||||||  |||  ||
                                AC TTTTGTTCGTT  GAC GG
                                 G         __  G
GAM921  FLJ20034  5'  CAGGCCAGGCACTGCTGCTTCC 34837     A     G   A  _
          CA                     TGG AAGCAG TAG GT TGGCTTG
                                ||| |||||| ||| || |||||||
                                ACC TTCGTC GTC CG ACCGGAC
                                  C     _  A  G
GAM921  FLJ20079  3'  GGCTCTGGCTTGTTATCT    34971     A     _
                                GGA AGCAGGT AGAGTT
                                ||| ||||||| ||||||
                                TCT TTGTTCG TCTCGG
                                  A      G
GAM921  FLJ20097  3'  TGAGCTGCTGGCTGCTTGTTTT 35050          AGTT_
          T                      GAAAGCAGGTAG    GGCTTG
                                ||||||||||||    ||||||
                                TTTTTGTTCGTC    TCGAGT
                                      GGTCG
GAM921  FLJ20126  3'  TAAGCTGGTTCTACTGTCTGTT 35077         ___    TT
          TTCC                    GGAAAGCAG   GTAGAG  GGCTTG
                                |||||||||   ||||||  ||||||
                                CCTTTTGTC   CATCTT  TCGAAT
                                     TGT     GG
GAM921  FLJ20154  5'  ACTTTGTCTGCTTTGCTA    73301    _     GT
                                TGG AAAGCAG  AGAGT
                                ||| |||||||  |||||
                                ATC TTTCGTC  TTTCA
                                  G      TG
GAM921  FLJ20275  3'  CAAGCTACTGTTTGTTTTTC  35307       GG   AGT
                                GGAAAGCA  TAG   TGGCTTG
                                ||||||||  |||   |||||||
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                                CTTTTTGT  GTC   ATCGAAC
                                    TT  ___
GAM921  FLJ20297  3' CAAGCCAGCTCTCGGGGCCT  35370     ____
                                AGGT   AGAGTTGGCTTG
                                ||||   ||||||||||||
                                TCCG   TCTCGACCGAAC
                                  GGGC
GAM921  FLJ20297  3' CAAGCCAGCTCTCGGGGCCT  35371     ____
                                AGGT   AGAGTTGGCTTG
                                ||||   ||||||||||||
                                TCCG   TCTCGACCGAAC
                                  GGGC
GAM921  FLJ20337  3' CAGGTTGGTTCTGGGTGTCC  35440   AAA  GG   TT
                                GG  GCA  TAGAG  GGCTTG
                                ||  |||  |||||  ||||||
                                CC  TGT  GTCTT  TTGGAC
                                 ___  GG   GG
GAM921  FLJ20519  3' AGCCTCTGGCTTGTTTTCTA  35796         AG  TT
                                TGGAAAGCAGGT  AG  GGCT
                                ||||||||||||  ||  ||||
                                ATCTTTTGTTCG  TC  CCGA
                                      G_  T_
GAM921  FLJ20558  5' CAGGTTACACTGTTTTCCA   35830        _   AG
                                TGGAAAGCAG GTAG  TTG
                                |||||||||| ||||  |||
                                ACCTTTTGTC CATT  GAC
                                      A   G_
GAM921  FLJ20580  3' TGAGTTAGTTTTCCAAACCTTT 35850      CA__  T   GT
          CC                    GGAAAG   GG AGA  TGGCTTG
                                ||||||   || |||  |||||||
                                CCTTTC   CC TTT  ATTGAGT
                                   CAAA  _   TG
GAM921  FLJ21162  5' GTTTTTCTTTCTGCTTTCCA  46375         T   TT
                                TGGAAAGCAGG AGAG  GGC
                                |||||||||| ||||  |||
                                ACCTTTCGTCT TCTT  TTG
                                      T   T_
GAM921  FLJ21162  5' TGAGTTAACGGTGATGTGTGTT 46379        GG  GA___
          TTTTA                   TGGAAAGCA  TA   GTTGGCTTG
                                |||||||||  ||   |||||||||
                                ATTTTTTGT  GT   CAATTGAGT
                                    GT  AGTGG
GAM921  FLJ21174  5' TGGGCTGACAAACTTTTTCCA  46320      CA   AGA  TG
                                TGGAAAG  GGT   GT  GCTTG
                                |||||||  |||   ||  |||||
                                ACCTTTT  TCA   CA  CGGGT
                                   __  AA_  GT
GAM921  FLJ21415  3' GCAGTTATTTTTGTTTGTATTT 45688    A  GG   T   TG
          C                     GGAA GCA  TAGAG TGGCT
                                |||| |||  ||||| |||||
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                                CTTT TGT  GTTTT ATTGA
                                  A  TT    T    CGG
GAM921  FLJ21816 3' TAGGTTGATTTTTGTAATTTCC 45476      GCAGGT    TG
                                GGAAA     AGAGT  GCTTG
                                |||||     |||||  |||||
                                CCTTT     TTTTA  TGGAT
                                   AATGT_    GT
GAM921  FLJ22002 3' TGGGCCAGTGTTTTTTGTTTGT 46200        GG    ____
           TTTTT                 GGAAAGCA  TAGAG   TTGGCTTG
                                |||||||| |||||   ||||||||
                                TTTTTTGT  GTTTT   GACCGGGT
                                     TT    TTGT
GAM921  FLJ22054 3' GTATATTTGCTTGCTTTTTA  96052            GTTG
                                TGGAAAGCAGGTAGA   GC
                                ||||||||||||||   ||
                                ATTTTTCGTTCGTTT   TG
                                        ATA_
GAM921  FLJ22104 3' TAGGTTTATGATGTTTGTTTTC 43627       GG  GA  TG
                                GAAAGCA  TA  GT  GCTTG
                                |||||||  ||  ||  |||||
                                CTTTTGT  GT  TA  TGGAT
                                    TT  AG  TT
GAM921  FLJ22378 3' GGGTCCTGCTTAGCTTTTT   47600       _     AGTT    G
                                GGAAAGC AGGTAG   GGCTT
                                ||||||| ||||||   |||||
                                TTTTTCG TTCGTC   CTGGG
                                    A    ____
GAM921  FLJ22408 5' GTGGTGCGCTCTGGCTGTTTTC 45987        G     TG   TG
           T                   GGAAAGCAG TAGAGT  GCT
                               |||||||| ||||||  |||
                               TCTTTTGTC GTCTCG  TGG
                                    G     CG   TGA
GAM921  FLJ22477 3' TGGGCTGGCTGGTGGTTTTCT  45679       AGGTAG   TG
                                GGAAAGC     AGT  GCTTG
                                |||||||     |||  |||||
                                TCTTTTG     TCG  CGGGT
                                    GTGG__   GT
GAM921  FLJ22558 5' AAGTATTTGTGCTGCTTTTT   43033        G  G  TTG   G
                                GGAAAGCAG TA AG   GCTT
                                |||||||| || ||   ||||
                                TTTTTCGTC GT TT   TGAA
                                     _ G  TA_
GAM921  FLJ22596 5' AGGCTAGCTCTTGATTCCA   47641      AG  GGT
                                TGGAA  CA   AGAGTTGGCTT
                                |||||  ||   ||||||||||
                                ACCTT  GT   TCTCGATCGGA
                                  A_  ___
GAM921  FLJ23017 3' GCAAGCACTTTCTGGTTTTGCT 43417            TT _______
           TGTTTTTC               GGAAAGCAGGTAGAG  G     GCTTG   C
                                |||||||||||||| |     |||||  |
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                                CTTTTTGTTCGTTTT T    CGAAC  G
                                      GG CTTTCA
GAM921  FLJ23042 3' CAGTACTTTTATTACTTGCTTT 47939          ____   TG  TG
           TT                  GGAAAGCAGGTA   GAGT  GCT
                               ||||||||||||   ||||  |||
                               TTTTTCGTTCAT   TTCA  TGA
                                     TATT   __  C
GAM921  FLJ23047 3' AGTTGCCTTTGCTTTTTTTT  44931      C      TT
                               GAAAG AGGTAGAG  GGCT
                               |||||  ||||||||  ||||
                               TTTTT TTCGTTTC  TTGA
                                  T      CG
GAM921  FLJ23053 3' TGAGCCGATTTTTTTTTTTTTT 43557      C   T
           T                   GGAAAG AGG AGAGTTGGCTTG
                               ||||||  |||  ||||||||||||
                               TTTTTT TTT TTTTAGCCGAGT
                                  T   T
GAM921  FLJ23132 3' CAGGCTGGCTCTGAATTTCTA  97839      GCAGG    TG
                               TGGAAA    TAGAGT  GCTTG
                               ||||||    ||||||  |||||
                               ATCTTT    GTCTCG  CGGAC
                                  AA___     GT
GAM921  FLJ23186 3' GGTATTCTGTTTGTTTTT    61044       GG     TG
                               GAAAGCA  TAGAGT  GCT
                               |||||||  ||||||  |||
                               TTTTTGT  GTCTTA  TGG
                                  TT     __
GAM921  FLJ23309 3' TGGGCCTATCTTTTTGTTTTCC 46593          T   GTT
           A                    TGGAAAGCAGG AGA   GGCTTG
                               ||||||||||| |||   ||||||
                               ACCTTTTGTTT TCT   CCGGGT
                                     T  AT_
GAM921  FLJ23342 3' TGGGTCAGCTATTTCTTTTTT  45252      C   TAG
                               GAAAG AGG   AGTTGGCTTG
                               |||||  |||   ||||||||||
                               TTTTT TCT   TCGACTGGGT
                                  _  TTA
GAM921  FLJ23462 3' AAGCAGTTTCTGTTTTCTA   46219          TAGAGTTG
                               TGGAAAGCAGG       GCTT
                               ||||||||||        ||||
                               ATCTTTTGTCT       CGAA
                                     TTGA____
GAM921  FLJ31812 3' CAAGCCAATTTTTTTTGTTTCT 59309      _      T
           TCA                    TGGA AAGCAGG AGAGTTGGCTTG
                               ||||  |||||||  ||||||||||||
                               ACTT TTTGTTT TTTTAACCGAAC
                                  C      T
GAM921  FYCO1    3' AAGCTGCACTCTCTTTCT    44765       CAGGT    _
                               GGAAAG    AGAGT TGGCTT
                               ||||||    |||||  ||||||
```

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                                TCTTTC    TCTCA GTCGAA
                                ______    C
GAM921  GCN2    3'  AAGTTGAGCTTTGTTAGTTTTT 63433       AG    _ TG   G
            CA                   TGGAAAGC  GTAGAG T  GCTT
                                |||||||| ||||||  |  ||||
                                ACTTTTTG  TGTTTC A  TGAA
                                    AT    G GT   A
GAM921  GFRA4   3'  CAAGCCGGCCCTGGTGCTTTC  42418      GG   A
                                GAAAGCA  TAG GTTGGCTTG
                                |||||||  ||| |||||||||
                                CTTTCGT  GTC CGGCCGAAC
                                   G_   C
GAM921  GGA2    3'  GTCATTTGGCCTGTTTTCTA   57677         A   T
                                TGGAAAGCAGGT GAGT GGC
                                |||||||||||| |||| |||
                                ATCTTTTGTCCG TTTA CTG
                                      G   _
GAM921  GGA2    3'  GTCATTTGGCCTGTTTTCTA   57678         A   T
                                TGGAAAGCAGGT GAGT GGC
                                |||||||||||| |||| |||
                                ATCTTTTGTCCG TTTA CTG
                                      G   _
GAM921  GGTLA4  5'  TAGGCCAGCTCTGGGGTCTC   56051   AA  AGG
                                GA  GC   TAGAGTTGGCTTG
                                ||  ||   ||||||||||||
                                CT  TG   GTCTCGACCGGAT
                                 C_  GG_
GAM921  GIT2    3'  GAGAAAGGACTTTGCCGCTTTT 29411       A      GG__   G
            TA                   TGGAAAGC GGTAGAGTT    CTT
                                |||||||| |||||||||    |||
                                ATTTTTCG CCGTTTCAG    GAG
                                   _       GAAA   A
GAM921  GOLGA3  3'  CAGGCCGGCTGCAGTTTCTCA  20884    GA   AG  AG
                                TG  AAGC  GT  AGTTGGCTTG
                                ||  ||||  ||  ||||||||||
                                AC  TTTG  CG  TCGGCCGGAC
                                 TC   A_  __
GAM921  GOLGA3  3'  GGCTTTTTACTTGTTTTTT   20891          TT
                                GGAAAGCAGGTAGAG  GGCT
                                ||||||||||||||  ||||
                                TTTTTTGTTCATTTT  TCGG
                                                __
GAM921  GP5     3'  TGAGTTTCCACTTGCTTTACA  16884    G      A   TTG
                                TG AAAGCAGGT GAG   GCTTG
                                || |||||||| |||   |||||
                                AC TTTCGTTCA CTT   TGAGT
                                 A       C   ___
GAM921  GRSF1   3'  AGTCTCCTCATTTGCTTTTTA  10878         A   TT
                                TGGAAAGCAGGT GAG  GGCT
                                |||||||||||| |||  ||||
```

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                                ATTTTTCGTTTA CTC  CTGA
                                      _  CT
GAM921  H2AFL    5'  TTCTTGATTTTGTTTGTTTTCT 14511       GG     TG CTTG
                                GGAAAGCA  TAGAGT  G
                                ||||||||  ||||||  |
                                TCTTTTGT  GTTTTA  T
                                    TT     GT CTTT
GAM921  H2AV     3'  GGCCCTGTTTGTTTTTCA    25759        GG   AGTT
                                TGGAAAGCA  TAG   GGCT
                                |||||||||  |||   ||||
                                ACTTTTTGT  GTC   CCGG
                                     TT  _____
GAM921  HGRG8    3'  GTCTTTTTACTATGTTTTTC   33214       _     TT
                                GGAAAGCA GGTAGAG  GGC
                                |||||||| |||||||  |||
                                CTTTTTGT TCATTTT  CTG
                                    A      T_
GAM921  HIC      5'  CAGGCCGGCTCTGGCCTCCT   68045    C   _
                                AG AGGT AGAGTTGGCTTG
                                || |||| ||||||||||||
                                TC TCCG TCTCGGCCGGAC
                                 C   G
GAM921  HNRPU    3'  TAGGCTAACTTTTTAAACATTC 49816      AGCAGGT
           CA                     TGGAA      AGAGTTGGCTTG
                                |||||      ||||||||||||
                                ACCTT      TTTCAATCGGAT
                                   ACAAATT
GAM921  HRH4     3'  AAATCCAGTTTTGTTTTCTTTC 41517       C GG   GT   C  G
           TA                      TGGAAAG A  TAGA  TGG TT
                                ||||||| |  ||||  ||| ||
                                ATCTTTC T  GTTT  ACC AA
                                    T TT   TG   T  AA
GAM921  HS3ST1   3'  AGGGCATTTTGTATTGTTTTTC 18853         GTA   T  G   G
           A                       TGGAAAGCAG   GAG TG CTT
                                ||||||||||   ||| || |||
                                ACTTTTTGTT   TTT AC GGA
                                      ATG   T  G   G
GAM921  HSA011916 3'  CAAGTCAGCTTTGTTGTGATTT 60904     AA   G
                                GGA  GCAG TAGAGTTGGCTTG
                                |||  |||| ||||||||||||||
                                TTT  TGTT GTTTCGACTGAAC
                                  AG   _
GAM921  HSA277841 3'  GAGTTCAGCTTGTTTTTT    38269          A  GTTG
                                GGAAAGCAGGT GA   GCTT
                                |||||||||||  ||   ||||
                                TTTTTTGTTCG CT   TGAG
                                      A  _____
GAM921  HSNOV1   3'  CAGGCCTGTTTTGTTTGTTTTT 34432       GG    TT
                                GAAAGCA  TAGAG  GGCTTG
                                |||||||  |||||  ||||||
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                                TTTTTGT  GTTTT  CCGGAC
                                    TT    GT
GAM921  HSPC157  5'  GTCCTACTACCTGCTTTCCA  27192          _ TT
                                TGGAAAGCAGGTAG AG  GGC
                                |||||||||||||| ||  |||
                                ACCTTTCGTCCATC TC  CTG
                                        A  __
GAM921  HTMP10   5'  CAGGCCAGCTGTGGCTTCTTT  53757     C  G  G
                                AAAG AG TA AGTTGGCTTG
                                |||| || || ||||||||||
                                TTTC TC GT TCGACCGGAC
                                  T  G  G
GAM921  IAN4L1   3'  CGGGTCTCTTCTACCTGCATTC 37799      A        TT
           TA                     TGGAA GCAGGTAGAG  GGCTTG
                                |||||| ||||||||||  ||||||
                                ATCTT CGTCCATCTT  CTGGGC
                                   A         CT
GAM921  IMAGE145052 3'  TGAGTTAGCTCTACTCTTTT  27331      CA
                                GAAAG  GGTAGAGTTGGCTTG
                                |||||  ||||||||||||||||
                                TTTTC  TCATCTCGATTGAGT
                                       __
GAM921  IRF5     3'  TGAGCCAAATAAACCTTTTTCT 51961       C    AGAG
                                GGAAAG AGGT    TTGGCTTG
                                |||||| ||||    ||||||||
                                TCTTTT TCCA    AACCGAGT
                                   _   AATA
GAM921  ITPK1    3'  ATCTGATTCTTCTGTTTTTTA  27227          T    TG CTTG
                                TGGAAAGCAGG AGAGT  G
                                |||||||||||| |||||  |
                                ATTTTTTGTCT TCTTA  C
                                       _    GT TAG
GAM921  KCNB2    5'  CGGGCTGGCGCGGCTCGCTTTC 97815        AG  AGA  TG
           T                     GGAAAGC  GT   GT  GCTTG
                                |||||||  ||   ||  |||||
                                TCTTTCG  CG   CG  CGGGC
                                    CT  GCG  GT
GAM921  KCNN1    5'  TGAGCTGGAGCCACGCTTTCT  11182       A_   AGAG TG
                                GGAAAGC  GGT    T  GCTTG
                                |||||||  |||    |  |||||
                                TCTTTCG  CCG    G  CGAGT
                                    CA   A___ GT
GAM921  KIAA0036 3'  GGTTTCTTCTGTTTTCCA    28391          T    TTG
                                TGGAAAGCAGG AGAG   GCT
                                |||||||||||| ||||   |||
                                ACCTTTTGTCT TCTT   TGG
                                       _   ___
GAM921  KIAA0061 3'  TAAGCCGGCAAGCTGCCTTTC  68838     AGC     A__
                                GAA   AGGTAG   GTTGGCTTG
                                |||   ||||||   |||||||||
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                                CTT   TCCGTC   CGGCCGAAT
                                  ___     GAA
GAM921  KIAA0087 3' TAAGTATATTCATTTGCTTTCT 29348          A    TG
              A                   TGGAAAGCAGGT GAGT  GCTTG
                                  |||||||||||| ||||  |||||
                                  ATCTTTCGTTTA CTTA  TGAAT
                                        _    TA
GAM921  KIAA0089 3' TGGGCTGACCTTTGTTTTTT   70512        GT  A  TG
                                  GGAAAGCAG  AG GT  GCTTG
                                  |||||||||  || ||  |||||
                                  TTTTTTGTT  TC CA  CGGGT
                                       __ _  GT
GAM921  KIAA0092 3' TAAGTGCACTTGTATTGCTTTT 28651         GTA    TG
              TA                    TGGAAAGCAG   GAGT  GCTTG
                                  ||||||||||   ||||  |||||
                                  ATTTTTCGTT   TTCA  TGAAT
                                        ATG    CG
GAM921  KIAA0159 3' CAATCTCCTTGTTTTCTA    30139          T   G
                                  TGGAAAGCAGG AGA TTG
                                  |||||||||||| ||| |||
                                  ATCTTTTGTTC TCT AAC
                                        C   _
GAM921  KIAA0169 3' CGGGTTTCAAACCTGTTTTCCA 73180           AGAGTT
                                  TGGAAAGCAGGT     GGCTTG
                                  ||||||||||||     ||||||
                                  ACCTTTTGTCCA     TTGGGC
                                         AACT__
GAM921  KIAA0182 3' TGAGCTGAACCCCTCCTTTTT  72504       C   TAGAG TG
                                  GGAAAG AGG    T  GCTTG
                                  |||||| |||    |  |||||
                                  TTTTTC TCC    A  CGAGT
                                     C   CCA__ GT
GAM921  KIAA0237 3' GGTCTCTGCTTTGTTTTCT    29230         _     TTG
                                  GGAAAGCAG GTAGAG   GCT
                                  |||||||| ||||||   |||
                                  TCTTTTGTT CGTCTC   TGG
                                        T     ___
GAM921  KIAA0280 3' CAGGCCAGCTTCAACATTCCA  93292       AGCAGGTA
                                  TGGAA       GAGTTGGCTTG
                                  |||||       ||||||||||||
                                  ACCTT       TTCGACCGGAC
                                     ACAAC___
GAM921  KIAA0286 3' TGAGTTGATTCTAGATGGTTAC 68861     A  G  GG     TG
              TA                    TGG AA CA  TAGAGT  GCTTG
                                  ||| || ||  ||||||  |||||
                                  ATC TT GT  ATCTTA  TGAGT
                                    A  G  AG     GT
GAM921  KIAA0298 5' GGCTCCTGCTGTTTTTTA    77079          G   _
                                  TGGAAAGCAG TAG AGTT
                                  |||||||||| ||| ||||
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                                ATTTTTTGTC GTC TCGG
                                      _  C
GAM921  KIAA0332 3' TAGGTCAGTTTTGGGTGCTT  63366     GG   GT
                                AAGCA  TAGA  TGGCTTG
                                |||||  ||||  |||||||
                                TTCGT  GTTT  ACTGGAT
                                   GG   TG
GAM921  KIAA0332 3' TTATTTTGATTTAGCTTGCTTT 63368          A   TG CTTG
           TTA                    TGGAAAGCAGGT GAGT  G
                                ||||||||||||| ||||  |
                                ATTTTTCGTTCG TTTA  T
                                      A   GT TTATTA
GAM921  KIAA0427 3' CAAGTCCCAGTCTGTTTTCT  29373         TAGAGTT
                                GGAAAGCAGG     GGCTTG
                                ||||||||||     ||||||
                                TCTTTTGTCT     CTGAAC
                                     GACC___
GAM921  KIAA0438 3' AAACTAATCTTTGCTTGTTTTC 29729            _   CTTG
           TA                     TGGAAAGCAGGTAGAG TTGG
                                |||||||||||||||| ||||
                                ATCTTTTGTTCGTTTC AATC
                                      T   AAAT
GAM921  KIAA0441 3' AGTTATGTTTTTTTGTTTTCTA 29624         T  GT   TG
                                TGGAAAGCAGG AGA  TGGCT
                                |||||||||| |||  |||||
                                ATCTTTTGTTT TTT  ATTGA
                                      T  GT   C
GAM921  KIAA0447 3' CAGGCCAACAAGACAGCTTTTT 72105       AG  AGA
           A                     TGGAAAGC  GT   GTTGGCTTG
                                ||||||||  ||  |||||||||
                                ATTTTTCG  CA   CAACCGGAC
                                    A_  GAA
GAM921  KIAA0447 5' CAGGCTCTCGCGTCTGCTTCTA 72106     A   TA_  TT
                                TGGAA GCAGG   GAG  GGCTTG
                                ||||| |||||   |||  ||||||
                                ATCTT CGTCT   CTC  TCGGAC
                                   _    GCG  __
GAM921  KIAA0449 5' GCCTCCTCTGTTTGCTTTGCA  34636   G    GG   TT
                                TG AAAGCA  TAGAG  GGC
                                || ||||||  |||||  |||
                                AC TTTCGT  GTCTC  CCG
                                 G     TT    CT
GAM921  KIAA0451 3' CAAATCTTTCTGCTTTTTA   29762         T  G
                                TGGAAAGCAGG AGA TTG
                                |||||||||| ||| |||
                                ATTTTTCGTCT TCT AAC
                                      T  A
GAM921  KIAA0455 3' TGTTGATTCTACCTGTGTTCT  72886     A        TG  TTG
                                GGAA GCAGGTAGAGT  GC
                                |||| ||||||||||  ||
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                                TCTT TGTCCATCTTA  TG
                                  G         GT  TA
GAM921  KIAA0461 3' CAGGTGGGGTATTTGGTTTCTA 71393       G     GAG  G
                                TGGAAA CAGGTA   TT GCTTG
                                |||||| ||||||   || |||||
                                ATCTTT GTTTAT   GG TGGAC
                                   G     G__  G
GAM921  KIAA0470 3' AACCATTCTATTTGCTTCT   29716     A        T  CTTG
                                GGAA GCAGGTAGAGT GG
                                |||| |||||||||||| ||
                                TCTT CGTTTATCTTA CC
                                  _         _ AAA
GAM921  KIAA0495 3' TGAGTCCAGCTTAGCTTTCCA  63276        AGGTA     _
                                TGGAAAGC    GAGTTGG CTTG
                                ||||||||    ||||||| ||||
                                ACCTTTCG    TTCGACC GAGT
                                    A____      T
GAM921  KIAA0495 3' TGGGTTGATTCTGCAGGTT   63278    AG     TG
                                AGC  GTAGAGT  GCTTG
                                |||  |||||||  |||||
                                TTG  CGTCTTA  TGGGT
                                  GA      GT
GAM921  KIAA0495 3' TGGGTTGATTCTGCGGGTT   63279    AG     TG
                                AGC  GTAGAGT  GCTTG
                                |||  |||||||  |||||
                                TTG  CGTCTTA  TGGGT
                                  GG      GT
GAM921  KIAA0513 3' GCCTCTGTTGGCTTTTTA    29038       AG    GTT
                                TGGAAAGC  GTAGA   GGC
                                ||||||||  |||||   |||
                                ATTTTTCG  TGTCT   CCG
                                    GT    ___
GAM921  KIAA0513 3' GGGTTTTCTTTGTTTGTTT   29046     GG    TT    G
                                AAGCA  TAGAG  GGCTT
                                |||||  |||||  |||||
                                TTTGT  GTTTC  TTGGG
                                   TT    TT    G
GAM921  KIAA0515 3' TGAGCTTCTTGTCTGCTTTTC  64557       GTA   TT
                                GGAAAGCAG   GAG  GGCTTG
                                |||||||||   |||  ||||||
                                CTTTTCGTC   TTC  TCGAGT
                                    TG_   T_
GAM921  KIAA0532 3' CAAGTTGCATCTGTTTTT    71318        A_  G
                                GAAAGCAGGT  GA TTG
                                ||||||||||  || |||
                                TTTTTGTCTA  TT AAC
                                     CG  G
GAM921  KIAA0626 3' AGCTTTTTTTGTTTGTTTCCA  41647      G  GG    TT
                                TGGAAA CA  TAGAG  GGCT
                                |||||| ||  |||||  ||||
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                                ACCTTT GT  GTTTT  TCGA
                                   _ TT    TT
GAM921  KIAA0635 3' TGGGCTGGTTTGCTTTTC    28424         TAGAG TG
                                GGAAAGCAGG    T  GCTTG
                                ||||||||||    |  |||||
                                CTTTTCGTTT    G  CGGGT
                                      _____ GT
GAM921  KIAA0660 3' AGGGCATTTTATCTGCTTGCT  25468    A         T G   G
                                GG AAGCAGGTAGAGT G CTT
                                || ||||||||||||| | |||
                                TC TTCGTCTATTTTA C GGA
                                 G          _ G
GAM921  KIAA0673 3' GGTATTATATCTGTTTTTTA   62947           GAGTTG
                                TGGAAAGCAGGTA     GCT
                                ||||||||||||      |||
                                ATTTTTTGTCTAT     TGG
                                       ATTA__
GAM921  KIAA0729 3' TAAGTTTTGCTTATTTGTTTTT 97413         A    T_
                                GAAAGCAGGT GAGT  GGCTTG
                                |||||||||| ||||  ||||||
                                TTTTTGTTTA TTCG  TTGAAT
                                      _   TT
GAM921  KIAA0766 3' TGAGTTGAATTTGCAGTCTGTT 29676         ___    G TG
           TTTTA                TGGAAAGCAG   GTAGA T  GCTTG
                                |||||||||   ||||| |  |||||
                                ATTTTTTGTC   CGTTT A  TGAGT
                                      TGA    A GT
GAM921  KIAA0767 3' CAAGCTGGTTTTCTTATTTTT  61252      C   T    TT
                                GAAAG AGG AGAG  GGCTTG
                                ||||| ||| ||||  ||||||
                                TTTTT TTC TTTT  TCGAAC
                                   A   _    GG
GAM921  KIAA0779 3' AAGTATGCTTTGCCTGTTTCCA 86905       G        TG    G
                                TGGAAA CAGGTAGAGT  GCTT
                                |||||| ||||||||||  ||||
                                ACCTTT GTCCGTTTCG  TGAA
                                   _        TA
GAM921  KIAA0802 3' TAAGTTAATTTTATTTTGTC   63250    AAGC
                                GA    AGGTAGAGTTGGCTTG
                                ||    ||||||||||||||||
                                CT    TTTATTTTAATTGAAT
                                 GT__
GAM921  KIAA0806 3' CGATGTTCTACTTTGCTTTCCA 29719         _    __
                                TGGAAAGCAG GTAGA  GTTG
                                |||||||||| |||||  ||||
                                ACCTTTCGTT CATCT  TAGC
                                      T    TG
GAM921  KIAA0825 3' TGGGCTTACTTTTGTTTTCT   61692         GTA    T
                                GGAAAGCAG   GAGT GGCTTG
                                |||||||||   |||| ||||||
```

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                                TCTTTTGTT   TTCA TCGGGT
                                    ___    T
GAM921  KIAA0828 3' CAGGTTTGTTTGTTTCCCA   82110     A    GG   G
                                TGG AAGCA  TAGA TTG
                                ||| |||||  |||| |||
                                ACC TTTGT  GTTT GAC
                                  C    TT   G
GAM921  KIAA0864 3' CCATTCCTATTTTTGTTTGTTT 63939         GG    TT_  CT
           TTTA                   TGGAAAGCA  TAGAG   GG  TG
                                |||||||||  |||||   ||  ||
                                ATTTTTTGT  GTTTT   CC  AC
                                     TT    TAT  TT  CA
GAM921  KIAA0894 3' AGCTGTGCTTTGTTTTCT    30324         _   G
                                GGAAAGCAG GTA AGTT
                                ||||||||| ||| ||||
                                TCTTTTGTT CGT TCGA
                                     T   G
GAM921  KIAA0924 3' GTTCTCTATTGGCTTTTT    30371        AG     TT
                                GGAAAGC  GTAGAG  GGC
                                |||||||  ||||||  |||
                                TTTTTCG  TATCTC  TTG
                                   GT     __
GAM921  KIAA0940 3' CAAGCTATAGTTTGTTTTC   30531        GG AGAGT
                                GAAAGCA  T    TGGCTTG
                                |||||||  |    |||||||
                                CTTTTGT  G    ATCGAAC
                                   TT AT___
GAM921  KIAA0940 3' CAGGTGTGGTTTTGTTTGTTTT 30532         GG    TT _
           TT                    GGAAAGCA  TAGAG  G GCTTG
                                |||||||  |||||  | |||||
                                TTTTTTGT  GTTTT  T TGGAC
                                   TT    GG G
GAM921  KIAA0940 3' TAAGTTAGTGTTGCTTGTTTTT 30534           AG
                                GAAAGCAGGTAG  TTGGCTTG
                                ||||||||||||  ||||||||
                                TTTTTGTTCGTT  GATTGAAT
                                      GT
GAM921  KIAA0970 3' TAGGCTAATTTTGAAGAACTCC 30620     AAGCAGG
                                GGA      TAGAGTTGGCTTG
                                |||      ||||||||||||
                                CCT      GTTTTAATCGGAT
                                  CAAGAA_
GAM921  KIAA0972 3' TGAGTCTATTTGTTTCTA    30682       G      G
                                TGGAAA CAGGTAGA TTG
                                |||||| |||||||| |||
                                ATCTTT GTTTATCT AGT
                                   _       G
GAM921  KIAA0976 3' TAGGCTAGCTTTGCTTTGTTGT 30555      A    _
           TCA                    TGGA AGCAG GTAGAGTTGGCTTG
                                |||| ||||| ||||||||||||||
```

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                                ACTT TTGTT CGTTTCGATCGGAT
                                  G    T
GAM921  KIAA1013 3' GGGTTTTGTTTGTTTGTTTTTT 90307        GG   GTT    G
           A                     TGGAAAGCA  TAGA   GGCTT
                                 |||||||||  ||||   |||||
                                 ATTTTTTGT  GTTT   TTGGG
                                      TT   GTT    A
GAM921  KIAA1040 3' AAGTCTGTCTGTTTTTTA    72674         GT   G
                                 TGGAAAGCAG  AGA TT
                                 ||||||||||  ||| ||
                                 ATTTTTTGTC  TCT AA
                                       TG   G
GAM921  KIAA1077 3' TGGGTTGGCTTGGTTTTGATTT 73294       _   TA_   TG
           TTT                    GGAAAG CAGG   GAGT  GCTTG
                                 ||||||| ||||   ||||  |||||
                                 TTTTTT GTTT   TTCG  TGGGT
                                    A   TGG   GT
GAM921  KIAA1084 3' GTGAGCTAAAACAGTTTTGTTT 30504      G   TAGAG_
           CC                     GGAAA CAGG     TTGGCTTG   T
                                 |||||| ||||     |||||||||  |
                                 CCTTT GTTT     AATCGAGT   G
                                    _   TGACAA
GAM921  KIAA1102 3' CAGGCTGGTTTTTTGTTTTTT  69581        GT   TT
                                 GGAAAGCAG  AGAG  GGCTTG
                                 |||||||||  ||||  ||||||
                                 TTTTTTGTT  TTTT  TCGGAC
                                       __   GG
GAM921  KIAA1136 3' CAAGTTGAGTTACTTGTTTTGC 92957    G        AG TG
           A                      TG AAAGCAGGTAG  T  GCTTG
                                 || ||||||||||  |  |||||
                                 AC TTTTGTTCATT  A  TGAAC
                                  G         G_ GT
GAM921  KIAA1145 3' CAAGCCACCATGCCTGGCTGTT 66232         G   A ____
           TTTT                    GGAAAGCAG TAG GT    TGGCTTG
                                 |||||||||  ||| ||    |||||||
                                 TTTTTTGTC GTC CG    ACCGAAC
                                       G   _  TACC
GAM921  KIAA1165 3' GGTATATGTGCTTGTTTTCT   67995          GAGTTG
                                 GGAAAGCAGGTA     GCT
                                 ||||||||||||     |||
                                 TCTTTTGTTCGT     TGG
                                       GTATA_
GAM921  KIAA1198 3' AACTTGCTTTCCCTGTTTTCT  63972         T    T  CTTG
                                 GGAAAGCAGG AGAGT GG
                                 |||||||||| ||||| ||
                                 TCTTTTGTCC TTTCG TC
                                       C    T  AAT
GAM921  KIAA1203 3' GTAATGTTTGTTTGCTTTTTA  72088        GG   GTTG
                                 TGGAAAGCA  TAGA   GC
                                 |||||||||  ||||   ||
```

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                                ATTTTTCGT  GTTT   TG
                                     TT   GTAA
GAM921  KIAA1240 3' CAAGTTGCTTTTGTTTGTTT  67288     GG   TT
                                AAGCA  TAGAG  GGCTTG
                                |||||  |||||  ||||||
                                TTTGT  GTTTT  TTGAAC
                                   TT   CG
GAM921  KIAA1243 3' CGGGTCCCTTTATTGCTTTTTA 74024        G   TT
                                TGGAAAGCAG TAGAG  GGCTTG
                                |||||||||| |||||  ||||||
                                ATTTTTCGTT ATTTC  CTGGGC
                                      _   C_
GAM921  KIAA1319 3' AGGATGCTCTTCTTGCTTTTTA 40787         T   TGG  G
                                TGGAAAGCAGG AGAGT  CTT
                                |||||||||| |||||  |||
                                ATTTTTCGTTC TCTCG  GGA
                                       T   TA_
GAM921  KIAA1321 3' GCTGTTTTCCTTGTTTTTCA  62902        TA  T_
                                TGGAAAGCAGG  GAG  TGGC
                                |||||||||| |||  ||||
                                ACTTTTTGTTC  CTT  GTCG
                                      __  TT
GAM921  KIAA1321 3' GGGAAATACTTTATTTCTTTCC 62903      C      TGG_  G
           A                     TGGAAAG AGGTAGAGT   CTT
                                |||||| |||||||||   |||
                                ACCTTTC TTTATTTCA   GGG
                                   _       TAAA  G
GAM921  KIAA1321 3' TGAGTCTCCTGCCTGCTTGCCA 62904    A       AGTT
                                TGG AAGCAGGTAG   GGCTTG
                                ||| ||||||||||   ||||||
                                ACC TTCGTCCGTC   CTGAGT
                                  G       CT__
GAM921  KIAA1323 3' CATTTCTCTTGTTTTCTA   63723         T  T
                                TGGAAAGCAGG AGAG TG
                                |||||||||| |||| ||
                                ATCTTTTGTTC TCTT AC
                                      _  T
GAM921  KIAA1348 3' TAGGTTTGGTTTCCTGTTTTTT 69128        T  GTT
                                GGAAAGCAGG AGA  GGCTTG
                                ||||||||| |||  ||||||
                                TTTTTTGTCC TTT  TTGGAT
                                      _  GGT
GAM921  KIAA1431 3' CAAGTTAGTTTTGTGGCTTTCC 63678       AGG  GT
           A                     TGGAAAGC  TAGA  TGGCTTG
                                |||||||  ||||  |||||||
                                ACCTTTCG  GTTT  ATTGAAC
                                     GT_   TG
GAM921  KIAA1432 3' GGTCCTCTCTCCTTGCTTTTTA 67307        T  TT  TG
                                TGGAAAGCAGG AGAG  GGCT
                                |||||||||| ||||  ||||
```

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                                ATTTTTCGTTC TCTC  CTGG
                                      C   TC   T
GAM921  KIAA1450 3' CAGGTCACAGTTTGCTTTTTA 66399       GG AGA  T
                                TGGAAAGCA  T   GT GGCTTG
                                |||||||||  |   || |||||||
                                ATTTTTCGT  G   CA CTGGAC
                                     TT A__  _
GAM921  KIAA1463 3' TAATTTATTTTTTGCTTTCT  72742        TA__
                                GGAAAGCAGG   GAGTTG
                                ||||||||||   ||||||
                                TCTTTCGTTT   TTTAAT
                                     TTTA
GAM921  KIAA1465 3' GGGCCAATTTCGTTGTCC   61502    A  AGGTA
                                GGA AGC    GAGTTGGCTT
                                ||| |||    ||||||||||
                                CCT TTG    TTTAACCGGG
                                  G  C____
GAM921  KIAA1500 3' TAGGCTACACACAGCTTGCTTT 64812        AGA  _
           T                     GAAAGCAGGT   GT TGGCTTG
                                ||||||||||   || |||||||
                                TTTTCGTTCG   CA ATCGGAT
                                     ACA  C
GAM921  KIAA1545 3' AGGGTGATCTTTTGTTTTCC  61333        T  G  G  G
                                GGAAAGCAGG AGA TTG CTT
                                |||||||||| ||| ||| |||
                                CCTTTTGTTT TCT AGT GGA
                                     _  _  G
GAM921  KIAA1546 3' TAAGCTGGCTTTTGTCTTTTTA 68500       _  GTA   TG
                                TGGAAAG CAG   GAGT  GCTTG
                                ||||||| |||   ||||  |||||
                                ATTTTTC GTT   TTCG  CGAAT
                                    T  ___   GT
GAM921  KIAA1553 3' CAAGCCATGAATTGCCCTGCTT 93562         TA  GT__
           TCTA                  TGGAAAGCAGG  GA   TGGCTTG
                                ||||||||||  ||   |||||||
                                ATCTTTCGTCC  TT   ACCGAAC
                                     CG  AAGT
GAM921  KIAA1553 3' CAGGCCAGCTGCATGCTCTCCA 93563     A   G  AG
                                TGGA AGCA GT  AGTTGGCTTG
                                |||| |||| ||  ||||||||||
                                ACCT TCGT CG  TCGACCGGAC
                                  C   A  __
GAM921  KIAA1560 3' TGGGCTGTAAACCTGTTTTTTA 64855          AGAGT
                                TGGAAAGCAGGT    TGGCTTG
                                ||||||||||||    |||||||
                                ATTTTTTGTCCA    GTCGGGT
                                     AAT__
GAM921  KIAA1598 3' TGAGTTAATTATGTTTTCC   37642        GGTAGA
                                GGAAAGCA    GTTGGCTTG
                                ||||||||    |||||||||
```

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                                CCTTTTGT     TAATTGAGT
                                    AT____
GAM921  KIAA1600 3' AAGCTATTGTTTGTTTTT    71938       GG   AGT
                                GAAAGCA  TAG   TGGCTT
                                |||||||  |||   ||||||
                                TTTTTGT  GTT   ATCGAA
                                   TT  ___
GAM921  KIAA1623 3' CAGGCGATTATTTATTTGTTTT 72536          GTTG_
           T                     GAAAGCAGGTAGA    GCTTG
                                 ||||||||||||     |||||
                                 TTTTTGTTTATTT    CGGAC
                                       ATTAG
GAM921  KIAA1677 3' AAGTTAATTCTAAGTGCT    67661     GG
                                AGCA  TAGAGTTGGCTT
                                ||||  ||||||||||||
                                TCGT  ATCTTAATTGAA
                                  GA
GAM921  KIAA1678 3' TGAGTTAGCTTCAAGCTTCC   72768     A  AGGTA
                                GGAA GC    GAGTTGGCTTG
                                |||| ||    ||||||||||
                                CCTT CG    TTCGATTGAGT
                                  _ AAC__
GAM921  KIAA1710 3' TGAACACTTTGTGCCTGTTTTC 63182          __   TGGCTTG
           TA                    TGGAAAGCAGGTA  GAGT
                                 ||||||||||||  ||||
                                 ATCTTTTGTCCGT  TTCA
                                       GT    CAAGT
GAM921  KIAA1726 3' CAGGTTAGAGCTTTGTTATCCA 67827     A    GT  AG
                                TGGA AGCAG  AG  TTGGCTTG
                                |||| |||||  ||  ||||||||
                                ACCT TTGTT  TC  GATTGGAC
                                  A    __ GA
GAM921  KIAA1737 3' TAAGTTAACTCTGCTGCCATCT 67946     AA   G
                                GGA  GCAG TAGAGTTGGCTTG
                                |||  |||| ||||||||||||
                                TCT  CGTC GTCTCAATTGAAT
                                  AC   _
GAM921  KIAA1750 3' CAAGTCTGCTTTTTTGTTTTTT 68806         T    T
                                GGAAAGCAGG AGAGT GGCTTG
                                |||||||||| ||||| ||||||
                                TTTTTTGTTT TTTCG CTGAAC
                                      _    T
GAM921  KIAA1819 5' TAAGTTAATCAGGGTTTGTTTC 70255       G  GG AGA_
           CA                    TGGAAA CA  T   GTTGGCTTG
                                 ||||||  ||  |   |||||||||
                                 ACCTTT GT  G    TAATTGAAT
                                    _ TT GGAC
GAM921  KIAA1866 3' GCTTCTCTACTTTTTTTT    61590      C      TT
                                GAAAG AGGTAGAG  GGC
                                ||||| ||||||||  |||
```

```
                                TTTTT TTCATCTC  TCG
                                  T       T_
GAM921  KIAA1870  3'  TGGACCTGGGCTCTGCTTGCTT 50589            __ _ TG
            T                    AAAGCAGGTAGAGTT  GG CT
                                 ||||||||||||||  || ||
                                 TTTCGTTCGTCTCGG  CC GG
                                        GT  A  T
GAM921  KIAA1879  5'  GTCCTCTGTCTGCCTTTCA   73943      A   GT   TT
                                 TGGAA GCAG  AGAG  GGC
                                 ||||| ||||  ||||  |||
                                 ACTTT CGTC  TCTC  CTG
                                   C   TG   __
GAM921  KIAA1889  3'  TGGGCTGGAACCGGATCTGTTT 73884       G    AGAG__ TG
            CCA                    TGGAAA CAGGT     T  GCTTG
                                 ||||||| |||||     |  |||||
                                 ACCTTT GTCTA     G  CGGGT
                                    _    GGCCAA GT
GAM921  KIAA1906  3'  CATCTCTTTACTGTTTTCTA   73568         GT_   T
                                 TGGAAAGCAG   AGAG TG
                                 ||||||||||   |||| ||
                                 ATCTTTTGTC   TCTC AC
                                       ATT   T
GAM921  KIAA1906  3'  TGGGTTATAGCACCTTGTTTTC 73576         _  AGAGT
            CA                   TGGAAAGCA GGT    TGGCTTG
                                 |||||||| |||    |||||||
                                 ACCTTTTGT CCA    ATTGGGT
                                      T  CGAT_
GAM921  KIAA1918  3'  CAATTCTACCTTTTTCTA    73535       C
                                 TGGAAAG AGGTAGAGTTG
                                 ||||||| ||||||||||
                                 ATCTTTT TCCATCTTAAC
                                    _
GAM921  KLF12     3'  AAGCTGGGTTTTTTTCCA    24358       CAGGT   G TG
                                 TGGAAAG    AGA T  GCTT
                                 |||||||    ||| |  ||||
                                 ACCTTTT    TTT G  CGAA
                                     _____  G GT
GAM921  KLF12     3'  TGACTCTGCCTGCATTTTA   33282      A
                                 TGGAA GCAGGTAGAGTTG
                                 ||||| ||||||||||||
                                 ATTTT CGTCCGTCTCAGT
                                   A
GAM921  KLF5      3'  TGAGTTGCCTATATTTGCTATT 9964      A      G  TT
            CA                   TGGA AGCAGGTA AG  GGCTTG
                                 |||| |||||||| ||  ||||||
                                 ACTT TCGTTTAT TC  TTGAGT
                                   A       A  CG
GAM921  KLHL6     3'  CACTTCTACTTGGTTTTT    56167      G       T
                                 GGAAA CAGGTAGAG TG
                                 ||||| |||||||| ||
```

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                                TTTTT GTTCATCTT AC
                                  G       C
GAM921  KOC1    5'  CAAGCCTCGGATCTGATTTTTC 92715       _    AGAGTT
           A                     TGGAAAG CAGGT     GGCTTG
                                 ||||||| |||||     ||||||
                                 ACTTTTT GTCTA     CCGAAC
                                    A    GGCT__
GAM921  KRTHA3B  3'  TGGGCCAGTTCTGCCTCT    11241    C     GT
                                 AG AGGTAGA  TGGCTTG
                                 || |||||||  |||||||
                                 TC TCCGTCT  ACCGGGT
                                  _      TG
GAM921  LANO    3'  CAAGTCCTAAAGTATTTGTTTT 47968          GAGTT  _
           T                     GAAAGCAGGTA    GG CTTG
                                 ||||||||||     || ||||
                                 TTTTTGTTTAT    CC GAAC
                                       GAAAT  T
GAM921  LENG5   3'  TGGGTTTGATTCATCTGTTTTC 44192          A    TG _
           TA                     TGGAAAGCAGGT GAGT  G CTTG
                                 |||||||||||| ||||  | ||||
                                 ATCTTTTGTCTA CTTA  T GGGT
                                       _   GT T
GAM921  LHFPL2   3'  TGGGTTGGAGTTCTTGTTTTCC 70502          T  AG TG
                                 GGAAAGCAGG AG  T  GCTTG
                                 |||||||||| ||  |  |||||
                                 CCTTTTGTTC TT  G  TGGGT
                                       _  GA GT
GAM921  LRRN3   5'  TGGGCTAGCACTGAAACTGCTT 69979         G__   A
           TTCA                    TGGAAAGCAG   TAG GTTGGCTTG
                                 ||||||||||   ||| |||||||||
                                 ACTTTTCGTC   GTC CGATCGGGT
                                       AAA   A
GAM921  LY75    3'  GGCCTCTGCTTACTTTTTA   11396       C     GTT
                                 TGGAAAG AGGTAGA   GGCT
                                 ||||||| |||||||   ||||
                                 ATTTTTC TTCGTCT   CCGG
                                    A      ___
GAM921  MAP2K3   3'  GGGTTTGGCTTGTTTTTC    59689          AGAGTT
                                 GGAAAGCAGGT     GGCTT
                                 ||||||||||      |||||
                                 CTTTTTGTTCG     TTGGG
                                       GT____
GAM921  MAP3K3   3'  CAGGTTGGCTCTGCCAGTCC   11536    AAGCA      TG
                                 GGA    GGTAGAGT  GCTTG
                                 |||    ||||||||  |||||
                                 CCT    CCGTCTCG  TGGAC
                                   GA___       GT
GAM921  MAWBP    5'  TAAGTTAATGGTAGTTGTTGTC 42387     A    G  GA
           CA                     TGGA AGCAG TA  GTTGGCTTG
                                 |||| ||||| ||  |||||||||
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                                ACCT TTGTT AT  TAATTGAAT
                                  G    G  GG
GAM921  MDS018   3'  CAGGCCTCTTGCCTGCTTCT  41824     A     G  TT
                                GGAA GCAGGTA AG  GGCTTG
                                |||| ||||||| ||  ||||||
                                TCTT CGTCCGT TC  CCGGAC
                                  _      _ T_
GAM921  MED8     3'  AGTAGCTTTGCCTGCTTTT   54625             G
                                GAAAGCAGGTAGAGTTG CT
                                |||||||||||||||| ||
                                TTTTCGTCCGTTTCGAT GA
                                                 _
GAM921  MED8     5'  GGACAGCTTTGCCTTGCTTTCT 54627        _       G  TG
                                GGAAAGCA GGTAGAGTTG CT
                                |||||||| |||||||||| ||
                                TCTTTCGT CCGTTTCGAC GG
                                     T        A  T
GAM921  MEF-2    3'  AGCTTATTTGTTGCTTTTCA  65017        GGTA   T
                                TGGAAAGCA   GAGT GGCT
                                |||||||||   |||| ||||
                                ACTTTTCGT   TTTA TCGA
                                     TG__   T
GAM921  MEF-2    3'  TAAGTTAGTCCTCTGCTGTTT  65030      G   __
                                AAGCAG TAGAG  TTGGCTTG
                                |||||| |||||  ||||||||
                                TTTGTC GTCTC  GATTGAAT
                                   _    CT
GAM921  MGC10765 3'  CAAGCCAACTCTGTCACCATTC 44554    AGCA GT
                                GAA   G  AGAGTTGGCTTG
                                |||   |  ||||||||||||
                                CTT   C  TCTCAACCGAAC
                                  ACCA TG
GAM921  MGC10871 3'  AAGTTGACTTTTCTTTCC    96427      CAGGT    TG
                                GGAAAG    AGAGT  GCTT
                                ||||||    |||||  ||||
                                CCTTTC    TTTCA  TGAA
                                   T____    GT
GAM921  MGC11386 3'  TGGGCTGGCTCTGCTCGCCTC  53073   AA  AG     TG
                                GA  GC  GTAGAGT  GCTTG
                                ||  ||  |||||||  |||||
                                CT  CG  CGTCTCG  CGGGT
                                 C_  CT      GT
GAM921  MGC1223  3'  TGATTTTATCTCTTTCT     49048      C       TG
                                GGAAAG AGGTAGAGT  G
                                |||||| |||||||||  |
                                TCTTTC TCTATTTTA  T
                                   _       GT
GAM921  MGC14801 3'  TGGGCTGACCCTTTTGATTTCC 52086      G   T  A  TG
          A                     TGGAAA CAGG AG GT  GCTTG
                                |||||| |||| || ||  |||||
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                                ACCTTT GTTT TC CA  CGGGT
                                   A   _ C  GT
GAM921  MGC15437 3' GTCGTTTTGTTTGTTTTTC   52849       GG   AGT
                                GGAAAGCA  TAG   TGGC
                                |||||||| |||  ||||
                                CTTTTTGT  GTT   GCTG
                                    TT   TT_
GAM921  MGC15827 3' TAGGCCAGGGGCTGCTTGTTTT 52875         AG_
           T                    GAAAGCAGGTAG   TTGGCTTG
                                |||||||||||  ||||||||
                                TTTTTGTTCGTC   GACCGGAT
                                      GGG
GAM921  MGC15875 3' CAAGTCAGTCAATTTCCTTTCT 53012      C   A  G
                                GGAAAG AGGT GA TTGGCTTG
                                |||||| |||| || ||||||||
                                TCTTTC TTTA CT GACTGAAC
                                   C   A  _
GAM921  MGC16142 3' CAAGCTAATTTACAAAATTTCC 52260      GCAG    G
           A                    TGGAAA   GTAGA TTGGCTTG
                                ||||||   ||||| ||||||||
                                ACCTTT   CATTT AATCGAAC
                                   AAAA    _
GAM921  MGC20255 3' TGGGCTTCTTTCTGTCTCTTTC 54546      C  GT   TT_
           T                    GGAAAG AG  AGAG   GGCTTG
                                |||||| ||  ||||   ||||||
                                TCTTTC TC  TCTT   TCGGGT
                                   _ TG   TCT
GAM921  MGC23937 3' AGGCCATTATGTTTTTCA    59598        GGTAGAGT
                                TGGAAAGCA       TGGCTT
                                |||||||||       ||||||
                                ACTTTTTGT       ACCGGA
                                     ATT_____
GAM921  MGC2477  5' GTTTTCTTTTTTGCTTTTT   44311         T   TT
                                GGAAAGCAGG AGAG  GGC
                                |||||||||| ||||  |||
                                TTTTTCGTTT TTTC  TTG
                                      _   TT
GAM921  MGC2477  5' TGGGCGTGGTTTTGTTTGTTTT 44313      GG    TT _
           T                    GAAAGCA  TAGAG  G GCTTG
                                |||||||  |||||  | |||||
                                TTTTTGT  GTTTT  T CGGGT
                                    TT    GG G
GAM921  MGC26651 3' CAAGCTGAGCATCTGTATTTCC 58948      _    AGAG TG
           A                    TGGAAA GCAGGT   T  GCTTG
                                |||||| ||||||   |  |||||
                                ACCTTT TGTCTA   A  CGAAC
                                   A    CG__ GT
GAM921  MGC26778 3' GGTTATTTGCCTGTTTTCCA   59406          GT
                                TGGAAAGCAGGTAGA  TGGCT
                                |||||||||||||||  |||||
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                                ACCTTTTGTCCGTTT  ATTGG
                                                 __
GAM921  MGC26914 3'  AAGTCTTCAGTTTGCTTTCT   59329         TA   TT    G
                                GGAAAGCAGG  GAG  GGCTT
                                ||||||||||  |||  |||||
                                TCTTTCGTTT  CTT  CTGAA
                                      GA   __    A
GAM921  MGC26954 3'  TAGGCTAGTTTTGCATGGTTTT 59493        AG_    GT
           TT                    GGAAAGC   GTAGA  TGGCTTG
                                |||||||   |||||  |||||||
                                TTTTTTG   CGTTT  ATCGGAT
                                    GTA    TG
GAM921  MGC2865  3'  TGGGTCAACTCCTTTGTTTTCC 51464         TA
                                GGAAAGCAGG  GAGTTGGCTTG
                                ||||||||||  ||||||||||
                                CCTTTTGTTT  CTCAACTGGGT
                                      C_
GAM921  MGC3123  3'  AAGCACTTTGCTTGCATTTTA  44340      A        TG    G
                                TGGAA GCAGGTAGAGT  GCTT
                                |||||  ||||||||||  ||||
                                ATTTT CGTTCGTTTCA  CGAA
                                   A         __
GAM921  MGC34923 3'  CAAGTTGTGTTTCTGTTTTCC  59193         TAGAGT
                                GGAAAGCAGG     TGGCTTG
                                ||||||||||     |||||||
                                CCTTTTGTCT     GTTGAAC
                                      TTGT__
GAM921  MGC4734  3'  CAGGCCATGTGTTTGCTTCT   59596     A   GG  GAGT
                                GGAA GCA  TA    TGGCTTG
                                ||||  |||  ||    |||||||
                                TCTT CGT  GT    ACCGGAC
                                  _   TT  GT__
GAM921  MGC4832  3'  CAGGTTGACCTGCTTATCA    59656     A      A  G
                                TGG AAGCAGGT GA TTG
                                |||  ||||||||  ||  |||
                                ACT TTCGTCCA TT GAC
                                  A       G  G
GAM921  MGC5139  5'  CAAGCTGAAGGGTCTGCTTT   74567         AGAG TG
                                AAAGCAGGT    T  GCTTG
                                |||||||||    |  |||||
                                TTTCGTCTG    A  CGAAC
                                     GGA_ GT
GAM921  MGC5384  3'  TGAGCCACTTTTCTCAGCCTGT 49095          A   T____
           TTTTT                   GGAAAGCAGGT GAG     TGGCTTG
                                |||||||||||  |||     |||||||
                                TTTTTTGTCCG CTC     ACCGAGT
                                      A   TTTTC
GAM921  MIG      3'  CAGGCTGACCACTTTATTTCTT 11584        C      ___  TG
           TTT                     GGAAAG AGGTAGA   GT  GCTTG
                                ||||||  |||||||   ||  |||||
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                                TTTTTC TTTATTT  CA  CGGAC
                                   _     CAC  GT
GAM921  MRPL4    3'  CATCCCTCTTTTTGTTTTTTA  32551          T   TT  CT
                                TGGAAAGCAGG AGAG  GG  TG
                                |||||||||| ||||  ||  ||
                                ATTTTTTGTTT TCTC  CC  AC
                                      T   __  TT
GAM921  NCKX3    5'  TGAGCCAGCTCTGCTTCCTGGC 40729    AA  C
           C                     GG  AG AGGTAGAGTTGGCTTG
                                ||  || ||||||||||||||||
                                CC  TC TTCGTCTCGACCGAGT
                                 GG  C
GAM921  NDUFA4   5'  TAGGTCGGTTCTCTCCTTTCCA 11761       C  GT   TT
                                TGGAAAG AG  AGAG  GGCTTG
                                |||||||  ||  ||||  ||||||
                                ACCTTTC TC  TCTT  CTGGAT
                                    C  __   GG
GAM921  NFAT5    5'  GCTTTTTACCTGTTTTTC    57775           TT
                                GGAAAGCAGGTAGAG  GGC
                                ||||||||||||||  |||
                                CTTTTTGTCCATTTT  TCG
                                                __
GAM921  NIR3     3'  AGGCCAGTGTTGTTTCCA    66822       GCAGG  AG
                                TGGAAA    TAG  TTGGCTT
                                ||||||    |||  |||||||
                                ACCTTT    GTT  GACCGGA
                                   _____  GT
GAM921  NME7     3'  GGGTACTGCATTGCTTTTTA  26192         _   AGTTG
                                TGGAAAGCAG GTAG    GCTT
                                ||||||||||  ||||    ||||
                                ATTTTTCGTT CGTC    TGGG
                                      A   A____
GAM921  NMU2R    3'  CAAGACTGCCTGATTTTTA   39805       G     AG
                                TGGAAA CAGGTAG  TTG
                                ||||||  |||||||  |||
                                ATTTTT GTCCGTC  AAC
                                   A     AG
GAM921  NTN4     3'  TAGTCATTATATTTACCTGTTT 63583           GT___    TG
           TTTA                   TGGAAAGCAGGTAGA    TGGCT
                                ||||||||||||||    |||||
                                ATTTTTTGTCCATTT    ACTGA
                                         ATATT    T
GAM921  NUDT12   3'  TGAGTTAGCTGGCATTGATTTT 49529       _  _  AG
           TTA                    TGGAAAG CAG GT  AGTTGGCTTG
                                |||||||  |||  ||  ||||||||||
                                ATTTTTT GTT CG  TCGATTGAGT
                                   A  A  G_
GAM921  NUDT4    3'  CAATTTGCATGTTTTTCA    39382         G    G
                                TGGAAAGCA GTAGA TTG
                                |||||||||  |||||  |||
```

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                                ACTTTTTGT CGTTT AAC
                                     A    _
GAM921  NUP107   5' CGGGTCGAAGGGCTTGCTTCC 40235     A     AGAG
                                GGAA GCAGGT   TTGGCTTG
                                |||| ||||||   ||||||||
                                CCTT CGTTCG   AGCTGGGC
                                  _    GGA_
GAM921  NUP54    3' TGAGCCTGTACTCTGCTTTCCA 60727         _  G GTT
                                TGGAAAGCAG GTA A  GGCTTG
                                |||||||||| ||| |  ||||||
                                ACCTTTCGTC CAT T  CCGAGT
                                      T  G ___
GAM921  NY-REN-41 3' TAAGCTAATTTTACCATGC   55561    _
                                GCA GGTAGAGTTGGCTTG
                                ||| ||||||||||||||
                                CGT CCATTTTAATCGAAT
                                  A
GAM921  NYD-SP25 3' GGTTTGTTTGTTTGTTTTCC  54303       GG   GTT
                                GGAAAGCA  TAGA  GGCT
                                ||||||||  ||||  ||||
                                CCTTTTGT  GTTT  TTGG
                                     TT   GT_
GAM921  OAZ2     3' TAAGCTGGCTTAATCTTGTTT  11881      TA_  TG
                                AAGCAGG  GAGT  GCTTG
                                |||||||  ||||  |||||
                                TTTGTTC  TTCG  CGAAT
                                    TAA   GT
GAM921  OLFM3    3' TGAGTTGACTCTACTCATTT  83028    CA     TG
                                AAG  GGTAGAGT  GCTTG
                                |||  ||||||||  |||||
                                TTT  TCATCTCA  TGAGT
                                  AC      GT
GAM921  OSBPL10  3' GCCTTTTGTCTGCTTTCT    35523       GT   TT
                                GGAAAGCAG  AGAG  GGC
                                |||||||||  ||||  |||
                                TCTTTCGTC  TTTT  CCG
                                     TG   __
GAM921  OSBPL8   3' AGATATTTTATTTGTATTTCA  40846     A       TGG
                                TGGAA GCAGGTAGAGT  CT
                                ||||| ||||||||||  ||
                                ACTTT TGTTTATTTTA  GA
                                   A        TA_
GAM921  OVGP1    3' AGGCCAATCTCTTTTCCA    11918      GCAGGT  _
                                TGGAAA     AGAG TTGGCTT
                                ||||||     |||| |||||||
                                ACCTTT     TCTC AACCGGA
                                   _______   T
GAM921  P450RAI-2 3' GATTTTTCCTTGCTTTCT    39573       _ T
                                GGAAAGCA GG AGAGTT
                                |||||||| || ||||||
```

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                                TCTTTCGT CC TTTTAG
                                     T  T
GAM921  PARVA    3'  CAGGTCCTGGGCCTGGTTTTC  37180      G    AG  TT
                                GGAAA CAGGT  AG  GGCTTG
                                ||||| |||||  ||  ||||||
                                CTTTT GTCCG  TC  CTGGAC
                                   G    GG  __
GAM921  PCDH20   3'  GCTTTCTGTTTGCTTTACCA  43422    _    GG    TT
                                TGG AAAGCA  TAGAG  GGC
                                ||| ||||||  |||||  |||
                                ACC TTTCGT  GTCTT  TCG
                                  A     TT    __
GAM921  PDCD6    3'  TAAGCTGATTAATGGTTTTGCA 60275    G    AGGTAG   TG
                                TG AAAGC     AGT  GCTTG
                                || |||||     |||  |||||
                                AC TTTTG     TTA  CGAAT
                                 G    GTAA__   GT
GAM921  PDE1C    3'  TGAGTCAGGAACATTTGTTTTC 18466          AGAG
             T                   GGAAAGCAGGT    TTGGCTTG
                                 ||||||||||    ||||||||
                                 TCTTTTGTTTA    GACTGAGT
                                       CAAG
GAM921  PFDN1    3'  GAGCCCCATTTGCTTCCCA   12049     A      AGAGTT
                                TGG AAGCAGGT     GGCTT
                                ||| ||||||||     |||||
                                ACC TTCGTTTA     CCGAG
                                  C       CC____
GAM921  PFTK1    3'  CAGGTTGACAAGGACTTTTTCT 25685       C  GTAGA  TG
                                GGAAAG AG    GT  GCTTG
                                |||||| ||    ||  |||||
                                TCTTTT TC    CA  TGGAC
                                   _  AGGAA  GT
GAM921  PKNOX2   3'  CAGGTCACACGTGTGTTTTCCA 92526         GGTAGA  _
                                TGGAAAGCA     GT TGGCTTG
                                |||||||||     || |||||||
                                ACCTTTTGT     CA ACTGGAC
                                      GTG___  C
GAM921  PMF1     3'  CAGGTCAGCTCTGCCCCTCC   24284     AAGCA
                                GGA    GGTAGAGTTGGCTTG
                                |||    ||||||||||||||||
                                CCT    CCGTCTCGACTGGAC
                                  CC___
GAM921  POF1B    3'  CAGTCTGTATTTGCTTTTCA   46771           G  _
                                TGGAAAGCAGGTA AG TTG
                                |||||||||||| || |||
                                ACTTTTCGTTTAT TC GAC
                                         G  T
GAM921  POFUT1   3'  TGGGTCTTTTGGCTGCTTTTCA 70986          G    TT
                                TGGAAAGCAG TAGAG  GGCTTG
                                ||||||||| |||||  ||||||
```

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                                ACTTTTCGTC GTTTT  CTGGGT
                                      G    __
GAM921  POT1    3'  TGGCTATGGATTTTGTTTTGCT 31888       _ GG     ___   TG
           TTCT                  GGAAAGC A  TAGAGTT   GGCT
                                |||||||  |  |||||||   ||||
                                TCTTTCG T  GTTTTAG   TCGG
                                   T TT      GTA    T
GAM921  PPAP2A  3'  CAGGTGAAGCTGGCCTGTTTTC 68441          AG   G_
           TA                   TGGAAAGCAGGT  AGTT  GCTTG
                                ||||||||||||  ||||  |||||
                                ATCTTTTGTCCG  TCGA  TGGAC
                                      G_   AG
GAM921  PPP1R3B  3'  TGGGATTGGCTCTTGTTTTCT  45147       GGT    TG _
                                GGAAAGCA   AGAGT  G CTTG
                                ||||||||   |||||  | ||||
                                TCTTTTGT   TCTCG  T GGGT
                                   ___     GT A
GAM921  PRO0082  3'  CATAGCATGGTTTTGTTTGTTT 38344       GG    TT _   TG
           TT                    GAAAGCA  TAGAG  G GCT
                                ||||||||  |||||  | |||
                                TTTTTGT  GTTTT  T CGA
                                   TT    GG A   TACG
GAM921  PRO0082  3'  TAAGTTACAGCTTGTTTTTT   38346          AGA  T
                                GGAAAGCAGGT   GT GGCTTG
                                ||||||||||   || ||||||
                                TTTTTTGTTCG   CA TTGAAT
                                      A__  _
GAM921  PRO0082  3'  TGAGTTAGTTCTACCTGGTGCC 38347     AAAG       GT
           CA                    TGG    CAGGTAGA  TGGCTTG
                                |||    ||||||||  |||||||
                                ACC    GTCCATCT  ATTGAGT
                                  CGTG       TG
GAM921  PRO0132  3'  CAATTTTTATTTGCTTTT    26937            _
                                GAAAGCAGGTAGAG TTG
                                |||||||||||||| |||
                                TTTTCGTTTATTTT AAC
                                      T
GAM921  PRO0246  5'  TAAGTCAGGTGCTCTGTTTTT  26960         _  GAG
                                GAAAGCAG GTA   TTGGCTTG
                                |||||||| |||   ||||||||
                                TTTTTGTC CGT   GACTGAAT
                                   T   G__
GAM921  PRO0386  5'  CAGGTTAGCTTTACAAAGGTCC 38302     AAGCAG
                                GGA     GTAGAGTTGGCTTG
                                |||     ||||||||||||||
                                CCT     CATTTCGATTGGAC
                                  GGAAA_
GAM921  PRO0641  3'  GGTTCTTTACTTCTTTTCA   27066        C       TT
                                TGGAAAG AGGTAGAG  GGCT
                                |||||||  ||||||||  ||||
```

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                                ACTTTTC TTCATTTC  TTGG
                                    _     __
GAM921  PRO0800  3' TAAGCCAATTTCACATTTCTA 38350      GCAG  AG
                                TGGAAA   GT  AGTTGGCTTG
                                ||||||   ||  ||||||||||
                                ATCTTT   CA  TTAACCGAAT
                                   A___  CT
GAM921  PRO1489  5' CAAGCATTTTTTTCTTTGTTTT 38332        T   TTG_
           TC                    GGAAAGCAGG AGAG   GCTTG
                                ||||||||||  ||||   |||||
                                CTTTTTGTTT TTTT   CGAAC
                                      C   TTTA
GAM921  PRO1596  5' CCTTTCAGTGCTGTTTGCTTTT 49220       GG   AG   CTTG
           TA                    TGGAAAGCA  TAG  TTGG
                                |||||||||  |||  ||||
                                ATTTTTCGT  GTC  GACT
                                     TT   GT   TTCCA
GAM921  PRO1777  3' AAGCATGCTGGCTTTCTA   38370       A   GAGTTG
                                TGGAAAGC GGTA    GCTT
                                ||||||||  ||||     ||||
                                ATCTTTCG TCGT    CGAA
                                    G   A_____
GAM921  PRO1777  3' GTAGGTTGACAATTGGTCTGTT 38374       GG   ______  TG
           TGCTTTT               GAAAGCA  TAGA    GT  GCTTG   T
                                |||||||  ||||    ||  |||||   |
                                TTTTCGT  GTCT    CA  TGGAT   G
                                    TT   GGTTAA  GT
GAM921  PRO2037  3' CAGGTTGGTTTTTTTTTTCCA  38395       CAGGT   TT
                                TGGAAAG    AGAG  GGCTTG
                                |||||||    ||||  ||||||
                                ACCTTTT    TTTT  TTGGAC
                                    TT___   GG
GAM921  PRO2730  3' GGTATGTCTGCTTGCTTGCT   48187    A       GTTG
                                GG AAGCAGGTAGA   GCT
                                || ||||||||||   |||
                                TC TTCGTTCGTCT   TGG
                                 G        GTA_
GAM921  PRPF4    3' TGAAGTGTTTAGTTCTATCATG 17471       _    GT  ___   G
           TTTTCT                GGAAAGCA GGTAGA  TG   GCTT
                                |||||||| ||||||  ||   ||||
                                TCTTTTGT CTATCT  AT   TGAA
                                    A     TG  TTG   GT
GAM921  PTD011   3' AATTTTAACTGTTTTCTA    26758         G
                                TGGAAAGCAG TAGAGTT
                                ||||||||||  |||||||
                                ATCTTTTGTC ATTTTAA
                                      A
GAM921  Rab11-FIP2 3' TAAGCTAATATAGCTTGTTTT  30458        AGA
                                AAAGCAGGT   GTTGGCTTG
                                |||||||||   |||||||||
```

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                                TTTTGTTCG   TAATCGAAT
                                     ATA
GAM921   RAB14    3'  TAGCTTTATCTTTTTTTA    33336        C
                                TGGAAAG AGGTAGAGTTG
                                ||||||| ||||||||||
                                ATTTTTT TCTATTTCGAT
                                     _
GAM921   RAB3-GAP150 3'  TAAGTTAAGATTTGCTTTTT   25765          AGAG
                                GGAAAGCAGGT    TTGGCTTG
                                ||||||||||    ||||||||
                                TTTTTCGTTTA    AATTGAAT
                                     G___
GAM921   RAB33B   3'  AGAGTAACTTTATTTCTTTTT  49314       C         G   G
                                GGAAAG AGGTAGAGTTG CTT
                                |||||| |||||||||| |||
                                TTTTTC TTTATTTCAAT GAG
                                _         _  AA
GAM921   RASD2    3'  CAGGCCAGGACTGCTTTTTTTT 27460        C     AG
              A                  TGGAAAG AGGTAG  TTGGCTTG
                                ||||||| ||||||  ||||||||
                                ATTTTTT TTCGTC  GACCGGAC
                                _     AG
GAM921   RBSK     3'  TGATTCTTTTGCTTTCCA    42369          T
                                TGGAAAGCAGG AGAGTTG
                                |||||||||| |||||||
                                ACCTTTCGTTT TCTTAGT
                                     _
GAM921   RC3      3'  AGGCAATTCTGCTTTCTA    31580          TAGA    G
                                TGGAAAGCAGG    GTTG CT
                                ||||||||||    |||| ||
                                ATCTTTCGTCT    TAAC GA
                                     ____    G
GAM921   RENT2    3'  AGCTGTCTTTGGTTTGCTTTCC 32065         GG _    T    TG
              A                  TGGAAAGCA  T AGAG TGGCT
                                |||||||||  | |||| |||||
                                ACCTTTCGT  G TTTC GTCGA
                                     TT G    T    C
GAM921   RERG     5'  CGGGCCACTGGCACTTGCTTCT 53000      A     AG_   T
                                GGAA GCAGGT   AGT GGCTTG
                                |||| ||||||   ||| ||||||
                                TCTT CGTTCA   TCA CCGGGC
                                  _     CGG   _
GAM921   RNF40    3'  TGGGCCAACTTCCAATCATTCC 29367       AGCA_  TA
              A                  TGGAA    GG  GAGTTGGCTTG
                                |||||    ||  ||||||||||
                                ACCTT    CC  TTCAACCGGGT
                                   ACTAA  __
GAM921   RNF8     5'  TGCTTCTGTCTGTTATTTA   15578      A    GT   GTT   TTG
                                TGGA AGCAG  AGA   GGC
                                |||| |||||  |||   |||
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                                ATTT TTGTC  TCT   TCG
                                  A    TG  ___   TT
GAM921  SCAMP5   3'  CAGGTCAGTTCTGGGGTCCCA  58054     AAA  AGG   GT
                                TGG   GC   TAGA  TGGCTTG
                                |||   ||   ||||  |||||||
                                ACC   TG   GTCT  ACTGGAC
                                  C__  GG_    TG
GAM921  SCAMP5   3'  TGGCTTTAGTTTTGTTTTGTTT 58066        _ GG    TT__    TG
           TCCA                   TGGAAAGC A  TAGAG   GGCT
                                |||||||| |  |||||   ||||
                                ACCTTTTG T  GTTTT    TCGG
                                     T TT    GATT    T
GAM921  SCN12A   3'  AAGCTTTCTGTTTGTGTTCCA  27076      A   GG    TT    G
                                TGGAA GCA  TAGAG  GGCTT
                                ||||| |||  |||||  |||||
                                ACCTT TGT  GTCTT  TCGAA
                                   G   TT    __
GAM921  SCYA4    3'  ACATTTGATTCTGTGTGTTTTC 12952         GG     TG CTTG
           CA                     TGGAAAGCA  TAGAGT  G
                                |||||||||  ||||||  |
                                ACCTTTTGT  GTCTTA  T
                                     GT     GT TACAC
GAM921  SE70-2   3'  AACTCTACCTGTGTTTCA    42344       A
                                TGGAA GCAGGTAGAGTT
                                ||||| ||||||||||||
                                ACTTT TGTCCATCTCAA
                                   G
GAM921  SEC15B   3'  CAAGTCAATTCCCAGTGTTTT  67261       __  TA
                                AAAGCA  GG  GAGTTGGCTTG
                                ||||||  ||  ||||||||||||
                                TTTTGT  CC  CTTAACTGAAC
                                   GA  __
GAM921  SEC15B   3'  TGAGAAATCTCCTTGCTTTTCA 67267          T   GTTGG
                                TGGAAAGCAGG AGA    CTTG
                                |||||||||||| |||    ||||
                                ACTTTTCGTTC TCT    GAGT
                                      C   AAA__
GAM921  SEC31B-1  5'  AGGGCCATGTCAGTTTTCT   31926        A GT GAGT     G
                                GGAAAGC G  A    TGGCTT
                                |||||||  |  |   ||||||
                                TCTTTTG C  T    ACCGGG
                                    A TG ____      AG
GAM921  SEC61A1   3'  TGGGCTTAGAGTCTGCCTGTTT 26231      G       G __
           CT                     GGAAA CAGGTAGA TT  GGCTTG
                                |||||  ||||||||  ||  ||||||
                                TCTTT GTCCGTCT AG  TCGGGT
                                   _       G  AT
GAM921  SEF      3'  GTGAGCTCTGCAAACTTTGCCT 69998     A          _____
           GTTTGCTA                 TGG AAGCAGGTAGAGTT    GGCTTG   T
                                ||| ||||||||||||||    ||||||  |
```

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                                ATC TTTGTCCGTTTCAA    TCGAGT   G
                                  G           ACGTC
GAM921  SEMA5A   3'  CAAGTCCATTGGTTTGTTTTTT 15591        GG AG   T
                                GGAAAGCA  T  AGT GGCTTG
                                ||||||||  |  ||| ||||||
                                TTTTTTGT  G  TTA CTGAAC
                                     TT G_   C
GAM921  SEP15    3'  ATTTAGTTTTGCTTGCTTCCA  16203      A       GT   CTTG
                                TGGAA GCAGGTAGA  TGG
                                ||||| |||||||||  |||
                                ACCTT CGTTCGTTT  ATT
                                   _       TG   TAA
GAM921  SFRS12   3'  GTTTTTTTTGTTTGTTTTTC   58250        GG    TT
                                GGAAAGCA  TAGAG  GGC
                                ||||||||  |||||  |||
                                CTTTTTGT  GTTTT  TTG
                                     TT    TT
GAM921  SFRS9    3'  TAGGTTAACTGAGCTGCTTT   15016       G AG
                                AAAGCAG T  AGTTGGCTTG
                                |||||||  |  ||||||||||
                                TTTCGTC G  TCAATTGGAT
                                    _ AG
GAM921  SH3BGRL2  3'  CAGGCTGGTGGCCATGTTCTCT 49676     A   _   AGAG TG
                                GGA AGCA GGT    T  GCTTG
                                ||| |||| |||    |  |||||
                                TCT TTGT CCG    G  CGGAC
                                  C    A   GT__ GT
GAM921  SH3BGRL2  3'  GGGTCCTTACTTGTATTCT    49678      A       AGTT
                                GGAA GCAGGTAG    GGCTT
                                |||| ||||||||    |||||
                                TCTT TGTTCATT    CTGGG
                                  A       C___
GAM921  SIPL     3'  AAGTTAACTTCATGTTTT    37387       GGTA
                                AAAGCA    GAGTTGGCTT
                                ||||||    ||||||||||
                                TTTTGT    TTCAATTGAA
                                   AC__
GAM921  SLC16A6   3'  TAAGCTTTTTTTTTTTGCTTGT 17443            TT____
            TTTT                  GAAAGCAGGTAGAG     GGCTTG
                                ||||||||||||||     ||||||
                                TTTTTGTTCGTTTT     TCGAAT
                                      TTTTTT
GAM921  SLC17A6   5'  CGGGAATTTACATTGTTTTTCA 40109          _    GTTGG
                                TGGAAAGCAG GTAGA    CTTG
                                |||||||||| |||||    ||||
                                ACTTTTTGTT CATTT    GGGC
                                      A    AA___
GAM921  SLC5A7   3'  TGGGCTAATTTGTATGTTTCCA 41806       G  GGTA
                                TGGAAA CA    GAGTTGGCTTG
                                |||||| ||    ||||||||||
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                                ACCTTT GT    TTTAATCGGGT
                                   _ ATG_
GAM921  SMC4L1   3'  TAAGTTGGCAACCACTTGGTTT 19721      G    AGA_  TG
           TT                    GGAAA CAGGT    GT  GCTTG
                                |||||  |||||    ||  |||||
                                TTTTT GTTCA    CG  TGAAT
                                   G    CCAA  GT
GAM921  SMCR7    3'  CGGGTGGTTGCCATGTTTTCTA 58239         _    AGTTG
                                TGGAAAGCA GGTAG    GCTTG
                                |||||||||  |||||    |||||
                                ATCTTTTGT CCGTT    TGGGC
                                      A    GG___
GAM921  SMOC2    3'  CGAGCTGGCTAACAGGCTTGTC 72820     _   AG  AG   TG
           T                     GGA AAGC  GT  AGT  GCTTG
                                |||  ||||  ||  |||  |||||
                                TCT TTCG  CA  TCG  CGAGC
                                  G   GA  A_  GT
GAM921  SMT3H2   3'  CAAGTCAAGCGTCTTGTTGTTT 23657       GT  _  _
                                AAGCAG  AGA GTT GGCTTG
                                ||||||  |||  |||  ||||||
                                TTTGTT  TCT CGA CTGAAC
                                   GT   G   A
GAM921  SMUG1    3'  CAAGTCAGAAGACCTGGCTTTT 27468         _   AGAG
           CA                     TGGAAAGC AGGT    TTGGCTTG
                                |||||||| ||||    ||||||||
                                ACTTTTCG TCCA    GACTGAAC
                                     G   GAA_
GAM921  SNPH     3'  AGGTGGCTGCTTGCTGTCT    28899     A       AGTTG
                                GGA AGCAGGTAG    GCTT
                                |||  |||||||||    ||||
                                TCT TCGTTCGTC    TGGA
                                  G       GG___
GAM921  Spir-1   3'  CGGGCTGGCTCTCCTTTCT    65329     AGC   T    TG
                                GGAA   AGG AGAGT  GCTTG
                                ||||   ||| |||||  |||||
                                TCTT   TCC TCTCG  CGGGC
                                  ___  _    GT
GAM921  Spir-1   3'  TAAGGGACTTTTTGCCTGCATT 65330       A     __    GG
           CTA                     TGGAA GCAGGTA  GAGTT  CTTG
                                |||||  |||||||  |||||  ||||
                                ATCTT CGTCCGT  TTCAG  GAAT
                                   A      TT    G_
GAM921  SQV7L    5'  TGGGTTGATTCCATGTTTTT   71100       GGTA   TG
                                GAAAGCA   GAGT  GCTTG
                                |||||||   ||||  |||||
                                TTTTTGT   CTTA  TGGGT
                                   AC__   GT
GAM921  SRPK1    3'  AGGGCATTGTCTGTTTTCT   13404        GT  AGT  G
                                GGAAAGCAG  AG   TG CTT
                                |||||||||  ||   || |||
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                                TCTTTTGTC  TT   AC GGA
                                     TG  ___  G
GAM921  SSFA2    3'  TAAGCTGGTGTTTGTTTTTT  74170        GG  GAG TG
                                GGAAAGCA  TA   T  GCTTG
                                ||||||||  ||   |  |||||
                                TTTTTTGT  GT   G  CGAAT
                                     TT  ___ GT
GAM921  ST13     3'  CAAATCTGTGTTTGCTTTCT  15428        GG  G  __
                                GGAAAGCA  TA AG  TTG
                                ||||||||  || ||  |||
                                TCTTTCGT  GT TC  AAC
                                     TT  G  TA
GAM921  ST13     3'  CACCTCTGCTTGCTTTCT    15429             T
                                GGAAAGCAGGTAGAG TG
                                |||||||||||||| ||
                                TCTTTCGTTCGTCTC AC
                                          C
GAM921  STAF65(gamma) 5'  GGCTCCGTGCCTGTTCTTC    30071     A       __
                                GGA AGCAGGTA  GAGTT
                                ||| ||||||||  |||||
                                CTT TTGTCCGT  CTCGG
                                  C       GC
GAM921  STARD7   3'  CGAGCTGGTTTTGCTTATGGTC 39740    AAGC       TT
                                GA   AGGTAGAG  GGCTTG
                                ||   ||||||||  ||||||
                                CT   TTCGTTTT  TCGAGC
                                 GGTA       GG
GAM921  STATI2   3'  GGGATACCTGCCTGTTTTTCA  96192            A  TGG   G
                                TGGAAAGCAGGTAG GT   CTT
                                |||||||||||||| ||   |||
                                ACTTTTTGTCCGTC CA   GGG
                                          _  TA_   G
GAM921  STIP-1   3'  CAGGTTATAGACTGGTTTTTCA 70238         A   AGAGT
                                TGGAAAGC GGT    TGGCTTG
                                |||||||| |||    |||||||
                                ACTTTTTG TCA    ATTGGAC
                                     G   GAT__
GAM921  STRIN    3'  AGGAAAATACTTTATTTGCTTT 33229             TGG__   G
           T                     GAAAGCAGGTAGAGT    CTT
                                 ||||||||||||||    |||
                                 TTTTCGTTTATTTCA    GGA
                                           TAAAA   A
GAM921  SYTL4    3'  CGGGCTGTAACTTGCTCTTTT  55785     _      AGAGT
                                GGAA AGCAGGT    TGGCTTG
                                |||| |||||||    |||||||
                                TTTT TCGTTCA    GTCGGGC
                                  C      AT____
GAM921  TAF2     3'  TAAGTTTTTTTGTTTTGTTTTC 13512          TA   TT
           CA                     TGGAAAGCAGG  GAG  GGCTTG
                                  ||||||||||  |||  ||||||
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                                ACCTTTTGTTT  TTT  TTGAAT
                                      TG   TT
GAM921  TAF9L    3'  GAACACCTTTCCCTGTTTTCCA 32561          T   T  GCTTG
                                TGGAAAGCAGG AGAG TG
                                |||||||||||  |||| ||
                                ACCTTTTGTCC TTTC AC
                                      C   C  AAGT
GAM921  TBLR1    3'  TGTTTGTTTTGCTTTGTTTTTT 45432          _     TT   TTG
          A                      TGGAAAGCAG GTAGAG  GGC
                                |||||||||| ||||||  |||
                                ATTTTTTGTT CGTTTT  TTG
                                      T     GT   T
GAM921  TCF6L1   3'  AGCCTGCTGCCTGCTTTTTA  13610            AGTT
                                TGGAAAGCAGGTAG   GGCT
                                ||||||||||||||   ||||
                                ATTTTTCGTCCGTC   CCGA
                                       GT__
GAM921  TCL6     3'  GGTCACCTTTGTCCTGTTTTCT 40484          _    T    TG
          A                      TGGAAAGCAGG TAGAG TGGCT
                                |||||||||||  ||||| |||||
                                ATCTTTTGTCC GTTTC ACTGG
                                      T    C    C
GAM921  TESK2    3'  TAGGCCCTAGGGCCTGCTTCTA 63886      A     AG_  TT
                                TGGAA GCAGGT   AG  GGCTTG
                                |||||  ||||||   ||  ||||||
                                ATCTT CGTCCG   TC  CCGGAT
                                   _     GGA  __
GAM921  TETRAN   3'  GGGCTTCTGTTTGTTTTTTA  8509         GG   GTT
                                TGGAAAGCA  TAGA   GGCTT
                                |||||||||  ||||   |||||
                                ATTTTTTGT  GTCT   TCGGG
                                      TT   ____
GAM921  TLOC1    5'  AAGTCAGTTCTTATCTCT    13773    C    _  GT
                                AG AGGTA GA  TGGCTT
                                || ||||| ||  ||||||
                                TC TCTAT CT  ACTGAA
                                 _    T  TG
GAM921  TLR10    5'  CAGGAATAATTCTATTTGTTTC 48976      G         G_
          C                      GGAAA CAGGTAGAGTTG  CTTG
                                |||||  ||||||||||||  ||||
                                CCTTT GTTTATCTTAAT  GGAC
                                   _          AA
GAM921  TOB2     3'  CAGGTCGGCTTGTTTCTCA   33234    GA      A  G
                                TG  AAGCAGGT GA TTG
                                ||  |||||||| || |||
                                AC  TTTGTTCG CT GAC
                                 TC       G  G
GAM921  TP53INP1 5'  TGACTCTTCTTGCTTTTCA   53873          T
                                TGGAAAGCAGG AGAGTTG
                                ||||||||||| |||||||
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                                ACTTTTCGTTC TCTCAGT
                                      T
GAM921  TP53TG3   3'  GAGATGGCTACTGCCTGCTTTT 31730          _   GG  G
          TA                    TGGAAAGCAGGTAG AGTT  CTT
                                |||||||||||||| ||||  |||
                                ATTTTTCGTCCGTC TCGG  GAG
                                      A   TA  G
GAM921  TRABID    5'  TAGGTTGAAGGACTTGCTTTTT 69042         AGAG TG
                                GGAAAGCAGGT   T  GCTTG
                                ||||||||||    |  |||||
                                TTTTTCGTTCA   A  TGGAT
                                      GGA_ GT
GAM921  TRIM38    3'  TGGGTCAGGGCTTTGATTTCCA 22058      G  GT  AG
                                TGGAAA CAG  AG  TTGGCTTG
                                ||||||| |||  ||  ||||||||
                                ACCTTT GTT  TC  GACTGGGT
                                   A  __  GG
GAM921  TTTY2     5'  CAAGCCAGCTCTGCCTGTACCA 88390    AAA
                                TGG  GCAGGTAGAGTTGGCTTG
                                |||  ||||||||||||||||||
                                ACC  TGTCCGTCTCGACCGAAC
                                 A__
GAM921  TU12B1-TY 3'  AGTGCCTGTCTGTTTTTTA   33827        GT  A  TG
                                TGGAAAGCAG  AG GT  GCT
                                |||||||||  || ||  |||
                                ATTTTTTGTC  TC CG  TGA
                                      TG  _  __
GAM921  U5-100K   3'  TGAGTGAAATCTCTGTTTTCTA 60415        GT  G  G
                                TGGAAAGCAG  AGA TT GCTTG
                                |||||||||  ||| || |||||
                                ATCTTTTGTC  TCT AA TGAGT
                                      __  A  G
GAM921  UCH37     3'  TGAGTCTGACAACTGTTAGTTT 32569      AG   A_  TG _
          TCT                   GGAAAGC  GTAG  GT  G CTTG
                                |||||||  ||||  ||  | ||||
                                TCTTTTG  TGTC  CA  C GAGT
                                   AT   AA  GT T
GAM921  UMP-CMPK  3'  CAAGTTAATGGATGTTTTT   33310      GGTAGA
                                GAAAGCA    GTTGGCTTG
                                |||||||    |||||||||
                                TTTTTGT    TAATTGAAC
                                   AGG___
GAM921  UST       3'  GAGTTGGCTGTGTTTTCT    20353       GGTAG  TG
                                GGAAAGCA    AGT  GCTT
                                ||||||||    |||  ||||
                                TCTTTTGT    TCG  TGAG
                                   G____  GT
GAM921  WBSCR22   3'  CTACCTCTGCTTGTTTTCT   34467           T
                                GGAAAGCAGGTAGAG TGG
                                ||||||||||||||| |||
```

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                                TCTTTTGTTCGTCTC ATC
                                        C
GAM921  YAP1    3'  TAAGCCAGTTGCAGTTTTC   21464      AG   AG
                                GAAAGC  GTAG  TTGGCTTG
                                ||||||  ||||  ||||||||
                                CTTTTG  CGTT  GACCGAAT
                                   A_   __
GAM921  YAP1    3'  TAGGTTTCCCTGCTTTCCA   21465         T  G
                                TGGAAAGCAGG AGA TTG
                                |||||||||||| ||| |||
                                ACCTTTCGTCC TTT GAT
                                      C  G
GAM921  YF13H12  5'  TGGGCTGGGGTTTCTGCTTCT  27456     A    T  AG TG
                                GGAA GCAGG AG  T  GCTTG
                                |||| ||||| ||  |  |||||
                                TCTT CGTCT TT  G  CGGGT
                                  _    _ GG GT
GAM921  ZDHHC7   3'  CAAGTATACTTGACTTTTCA  35317       _    GAG
                                TGGAAAG CAGGTA   TTG
                                |||||||  ||||||   |||
                                ACTTTTC GTTCAT   AAC
                                    A     ATG
GAM921  ZDHHC9   5'  CAGGCCGGCTCCCCCTTCC   62352    AAGC   TA
                                GGA   AGG  GAGTTGGCTTG
                                |||   |||  ||||||||||
                                CCT   TCC  CTCGGCCGGAC
                                  _____  CC
GAM921  ZF      3'  GGGCTTCTGCTGTTTTTTA   41370         G   GTT
                                TGGAAAGCAG TAGA   GGCTT
                                ||||||||||  ||||   |||||
                                ATTTTTTGTC GTCT   TCGGG
                                      _   ___
GAM921  ZFP100   3'  GGGCCTTACACTGTTTTTCA  70588         _   AGTT
                                TGGAAAGCAG GTAG   GGCTT
                                ||||||||||  ||||   |||||
                                ACTTTTTGTC CATT   CCGGG
                                     A   _____
GAM921  ZFR     3'  AGGTTTTGTTTGCTTTTT   32754        GG   GTTG
                                GGAAAGCA  TAGA   GCTT
                                ||||||||  ||||   ||||
                                TTTTTCGT  GTTT   TGGA
                                    TT   _____
GAM921  ZIC4    3'  TGGGCTAACTTTGTACGTATTT 50546     A  AG
          T                      GGAA GC  GTAGAGTTGGCTTG
                                ||||  ||  ||||||||||||||
                                TTTT TG  TGTTTCAATCGGGT
                                  A  CA
GAM921  ZIM2    5'  TGGGTCCAGATACCTGTGTTTT 31722     A     GAGT  _
                                GGAA GCAGGTA   TGG CTTG
                                ||||  |||||||   ||| ||||
```

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                                TTTT TGTCCAT    ACC GGGT
                                  G      AG__   T
GAM921  ZIN      3'  GGCCTCTGTCTGTTTGCCA   26394     A     GT   GTT
                                TGG AAGCAG  AGA   GGCT
                                ||| ||||||  |||   ||||
                                ACC TTTGTC  TCT   CCGG
                                  G     TG  ___
GAM921  ZNF-U69274 3'  TAGGTTGGTGCAATTGCTTTT  27743        GTAGA TT
                                GAAAGCAG    G  GGCTTG
                                ||||||||    |  ||||||
                                TTTTCGTT    T  TTGGAT
                                     AACG_ GG
GAM921  ZNF185   3'  CCTTTTTGCTTCTTTTCA    24093        C       TT
                                TGGAAAG AGGTAGAG  GG
                                ||||||| ||||||||  ||
                                ACTTTTC TTCGTTTT  CC
                                   _      T_
GAM921  ZNF286   3'  TAAGTTGGTTTTATCACTGT   40669      __     TT
                                GCAG  GTAGAG  GGCTTG
                                ||||  ||||||  ||||||
                                TGTC  TATTTT  TTGAAT
                                  AC     GG
GAM921  ZNF297B  3'  GGTTTTTACCTTTTTTTCA   26669        C       TTG
                                TGGAAAG AGGTAGAG   GCT
                                ||||||| ||||||||   |||
                                ACTTTTT TCCATTTT   TGG
                                     T      ___
GAM921  ZNF384   5'  GGGTCTGCCTGCCTTCCA    56796      A       G
                                TGGAA GCAGGTAGA TT
                                ||||| ||||||||| ||
                                ACCTT CGTCCGTCT GG
                                  C       G
GAM921  ZWINT    3'  GGATCTTTATTTGTTTTCT   23906            TTGG
                                GGAAAGCAGGTAGAG    CT
                                ||||||||||||||    ||
                                TCTTTTGTTTATTTC    GG
                                        TA__
GAM921  ZWINT    3'  GGATCTTTATTTGTTTTCT   23907            TTGG
                                GGAAAGCAGGTAGAG    CT
                                ||||||||||||||    ||
                                TCTTTTGTTTATTTC    GG
                                        TA__
GAM921  LOC115294 3'  TGAGCCTACATTTGCTTTT   73385         AGA  T
                                GAAAGCAGGT   GT GGCTTG
                                ||||||||||   || ||||||
                                TTTTCGTTTA   CA CCGAGT
                                      ___  T
GAM921  LOC115557 3'  TAATTTTGTTTTTCCTGTTTTC 56823          _____       GCTTG
          T                    GGAAAGCAGG    TAGAGTTG
                               ||||||||||    ||||||||
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                                TCTTTTGTCC    GTTTTAAT
                                     TTTTT        G
GAM921   LOC120939 5'  CAAGAATATTACCAGTTTTCT  76757       A    A  GG
                                GGAAAGC GGTAG GTT  CTTG
                                ||||||| ||||| |||  ||||
                                TCTTTTG CCATT TAA  GAAC
                                   A    A  __
GAM921   LOC121536 3'  TGAGCTAGCTTTATAACTTGT  74529      ___
                                GCAGGT   AGAGTTGGCTTG
                                ||||||   ||||||||||||
                                TGTTCA   TTTCGATCGAGT
                                   ATA
GAM921   LOC121642 5'  TAACATCTTCTGTTTCC     74564      G   T  _   GCTTG
                                GGAAA CAGG AGA GTTG
                                ||||| |||| ||| ||||
                                CCTTT GTCT TCT CAAT
                                  _   _  A      G
GAM921   LOC123096 3'  TGAGTCGATTGCCCTGCTTCC  74655     A    TAG
                                GGAA GCAGG   AGTTGGCTTG
                                |||| |||||   ||||||||||
                                CCTT CGTCC   TTAGCTGAGT
                                  _    CG_
GAM921   LOC124302 3'  GGGTAAGTTTGCTTGTTTTCC  74761          G  G  TG
                                GGAAAGCAGGTAGA TTG CT
                                |||||||||||||| ||| ||
                                CCTTTTGTTCGTTT AAT GG
                                       G  G  T
GAM921   LOC124460 5'  CAGGTCACACAGCCTGTTTCC  76558      G    AGA  _
                                GGAAA CAGGT   GT TGGCTTG
                                ||||| |||||   || |||||||
                                CCTTT GTCCG   CA ACTGGAC
                                  _    A__  C
GAM921   LOC125079 3'  TGGGCTAATAAAGCTGACTTTC 74851       CA   AGA
           T                     GGAAAG  GGT   GTTGGCTTG
                                ||||||  |||   |||||||||
                                TCTTTC  TCG   TAATCGGGT
                                   AG   AAA
GAM921   LOC125704 3'  CAATTTCTTTGACTGTTTTTCA 74875         GT__   _
                                TGGAAAGCAG    AGAG TTG
                                ||||||||||    |||| |||
                                ACTTTTTGTC    TCTT AAC
                                      AGTT    T
GAM921   LOC126364 3'  CGAGCTAATTTTTGTATTT    76188     A   GTA
                                GAA GCAG   GAGTTGGCTTG
                                |||  ||||   ||||||||||
                                TTT TGTT   TTTAATCGAGC
                                  A   ___
GAM921   LOC126528 3'  GAGCTGTCTACCTGCTGTCCA  75029     A        GT     G
                                TGGA AGCAGGTAGA  TGGCTT
                                |||| ||||||||||  ||||||
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                                ACCT TCGTCCATCT  GTCGAG
                                  G        __
GAM921  LOC129644 3'  CAAATCTGCTTGTTATCTA   75394      A        G
                                TGGA AGCAGGTAGA TTG
                                |||| |||||||||| |||
                                ATCT TTGTTCGTCT AAC
                                  A        A
GAM921  LOC129892 5'  GGCCTTTGCCGCTTTCCA    75413        A     GTT
                                TGGAAAGC GGTAGA   GGCT
                                |||||||| ||||||   ||||
                                ACCTTTCG CCGTTT   CCGG
                                     _    ____
GAM921  LOC131308 3'  ACGTATATTCTACTTGTATTTT 75492      A         TG  TTG
                                GGAA GCAGGTAGAGT  GC
                                |||| ||||||||||  ||
                                TTTT TGTTCATCTTA  TG
                                  A         TA  CAG
GAM921  LOC131873 3'  TAAGATGTATTTGTCTGTTTTT 76396         GT   GTTGG
          C                      GGAAAGCAG  AGA    CTTG
                                |||||||||  |||    ||||
                                CTTTTTGTC  TTT    GAAT
                                     TG   ATGTA
GAM921  LOC132671 3'  CAGGTAGCTCAGTTTATTTGCT 59837            ____     G  TG
          TTCTA                    TGGAAAGCAGGTA   GAGTTG CT
                                |||||||||||||   |||||| ||
                                ATCTTTCGTTTAT   CTCGAT GA
                                     TTGA     G  C
GAM921  LOC132671 3'  GTTCTTTCTGCCTTTTTTTCA  59842        C       TT
                                TGGAAAG AGGTAGAG  GGC
                                ||||||| ||||||||  |||
                                ACTTTTT TCCGTCTT  TTG
                                     T       TC
GAM921  LOC132864 3'  TAAGTGCATTCTTCTGCTTTTC 75579          T     TG
          A                      TGGAAAGCAGG AGAGT  GCTTG
                                |||||||||| |||||  |||||
                                ACTTTTCGTCT TCTTA  TGAAT
                                     _    CG
GAM921  LOC136345 5'  TATCTTCTGCTGTTTGTTTTCC 76717          ___      TTGGCTTG
          A                      TGGAAAGCA   GGTAGAG
                                |||||||||   |||||||
                                ACCTTTTGT   TCGTCTT
                                     TTG      CTAT
GAM921  LOC139202 3'  GAGTCTGGCCTCCTTTCT    76750       C    AGAGTT
                                GGAAAG AGGT     GGCTT
                                |||||| ||||     |||||
                                TCTTTC TCCG     CTGAG
                                   C    GT____
GAM921  LOC139231 3'  AGTTTTAGTTCTGTCTGTTTTC 75895         GT    TT__    TG
                                GAAAGCAG  AGAG    GGCT
                                |||||||| ||||    ||||
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                                CTTTTGTC  TCTT   TTGA
                                    TG   GATT   T
GAM921   LOC143173 5'  TGAGCCAACTTTATAGGC   61019   AG
                                GC  GTAGAGTTGGCTTG
                                ||  ||||||||||||||
                                CG  TATTTCAACCGAGT
                                 GA
GAM921   LOC143188 5'  AAGACCTCTCTGCTTTTCA   83787        GT   TTGG
                                TGGAAAGCAG  AGAG   CTT
                                ||||||||||  ||||   |||
                                ACTTTTCGTC  TCTC   GAA
                                      __   CA__
GAM921   LOC143310 5'  AGTCGCCTTTATTGCTTTCT   77034       G    T
                                GGAAAGCAG TAGAG TGGCT
                                |||||||||| ||||| |||||
                                TCTTTCGTT ATTTC GCTGA
                                    _    C
GAM921   LOC143310 3'  CAGGCCAATTTGTGATTTGTTT 77038       A__
                                AAGCAGGT   GAGTTGGCTTG
                                ||||||||   ||||||||||||
                                TTTGTTTA   TTTAACCGGAC
                                    GTG
GAM921   LOC143451 5'  GGCACCTTTACCTGTGTTTT   77070     A       TTG
                                GGAA GCAGGTAGAG   GCT
                                |||| ||||||||||   |||
                                TTTT TGTCCATTTC   CGG
                                  G        CA_
GAM921   LOC143872 3'  ATATAACTTTATTTGTTTTCCA 77154             GCTTG
                                TGGAAAGCAGGTAGAGTTG
                                |||||||||||||||||||
                                ACCTTTTGTTTATTTCAAT
                                          ATAA
GAM921   LOC144455 3'  CAGGTCAGCTGCCGTCTTTC   77331     CA   AG
                                GAAAG  GGT  AGTTGGCTTG
                                |||||  |||  ||||||||||
                                CTTTC  CCG  TCGACTGGAC
                                  TG   __
GAM921   LOC144512 5'  GGAGTTATCTGTTATCCA    84038     A       AG
                                TGGA AGCAGGTAG  TT
                                |||| |||||||||  ||
                                ACCT TTGTCTATT  GG
                                  A       GA
GAM921   LOC145125 5'  GGCACCTTTACCTGTGTTTT   77547     A       TTG
                                GGAA GCAGGTAGAG   GCT
                                |||| ||||||||||   |||
                                TTTT TGTCCATTTC   CGG
                                  G        CA_
GAM921   LOC145135 5'  CCTTCTTTTTGCTTTCTA    84203         T   TT
                                TGGAAAGCAGG AGAG  GG
                                |||||||||| ||||  ||
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                                ATCTTTCGTTT TCTT  CC
                                      T   __
GAM921  LOC145135 5'  TGGGTTCTCGCTGTTTGTTTTC 84206       GG   AGTT
                                GAAAGCA  TAG   GGCTTG
                                |||||||  |||   ||||||
                                CTTTTGT  GTC   TTGGGT
                                    TT   GCTC
GAM921  LOC145268 5'  CAAGTCACTGTCTGCTTTTC   77573        GT  AGT
                                GGAAAGCAG  AG   TGGCTTG
                                |||||||||  ||   |||||||
                                CTTTTCGTC  TC   ACTGAAC
                                     TG  ___
GAM921  LOC145463 3'  TGAGTTAGCTCTATTCTTTT   71485      CA
                                GAAAG  GGTAGAGTTGGCTTG
                                |||||  ||||||||||||||
                                TTTTC  TTATCTCGATTGAGT
                                  __
GAM921  LOC145501 3'  GGCGCGCTTCTGCCTGCGTTCC 77771      A       T _   TG
          A                      TGGAA GCAGGTAGAG TG GCT
                                 |||||  ||||||||||  ||  |||
                                 ACCTT CGTCCGTCTT GC CGG
                                    G        C G   C
GAM921  LOC145739 3'  AAGAAGCTCTGCCTTTTTTT   77903      C       GG   G
                                GAAAG AGGTAGAGTT  CTT
                                |||||  ||||||||||  |||
                                TTTTT TCCGTCTCGA  GAA
                                   T        A_
GAM921  LOC145820 3'  TAAGCAATCACTGATTTGCTTT 77979         AG   TG__
          CT                     GGAAAGCAGGT  AGT   GCTTG
                                 ||||||||||  |||   |||||
                                 TCTTTCGTTTA  TCA   CGAAT
                                      G_   CTAA
GAM921  LOC145899 5'  CAAGGACACCATACCTGCTTTT 84556          GA  T G_
          TA                     TGGAAAGCAGGTA  GT G  CTTG
                                 ||||||||||||  || |  ||||
                                 ATTTTTCGTCCAT  CA C  GAAC
                                       AC  _ AG
GAM921  LOC145945 5'  GATGCTGGTTGCTTTCCA    84567         G   A
                                TGGAAAGCAG TAG GTT
                                |||||||||| ||| |||
                                ACCTTTCGTT GTC TAG
                                     G   G
GAM921  LOC146050 3'  CAGGCTAAATTTTGCATTTTTA 78105       _    TAGAG
                                TGGAAA GCAGG    TTGGCTTG
                                ||||||  |||||    ||||||||
                                ATTTTT CGTTT    AATCGGAC
                                   A    TA___
GAM921  LOC146056 5'  CAAGTTGATTTTTATACTGCTT 78076        GT__    TG
          TCT                    GGAAAGCAG   AGAGT  GCTTG
                                 |||||||||   |||||  |||||
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                                TCTTTCGTC   TTTTA  TGAAC
                                     ATAT    GT
GAM921   LOC146184 3'  AGCTATTTTGCTTGTGTTCCA  84595      A        T
                                TGGAA GCAGGTAGAGT GGCT
                                ||||| |||||||||||| ||||
                                ACCTT TGTTCGTTTTA TCGA
                                   G         _
GAM921   LOC146315 3'  CAGGTCAGCTGGGAGCTTCT   61558     A  AGGTAG
                                GGAA GC     AGTTGGCTTG
                                |||| ||     ||||||||||
                                TCTT CG     TCGACTGGAC
                                  _ AGGG__
GAM921   LOC146346 5'  GGTATATTTACTTGTATTTCA  78401      A       GTTG
                                TGGAA GCAGGTAGA    GCT
                                ||||| |||||||||    |||
                                ACTTT TGTTCATTT    TGG
                                   A        ATA_
GAM921   LOC146520 5'  CAAGCTGTTGGCTTGTTTGCTA 78514      _    GTA    ___
            TTTCA                   TGGAA AGCAG   GAGTT   GGCTTG
                                |||||| |||||   |||||   ||||||
                                ACTTT TCGTT   TTCGG   TCGAAC
                                   A    TG_    TTG
GAM921   LOC146603 5'  CACTTTTTTTTCTGCTTTTT   78591         T   TT  CTTG
                                GGAAAGCAGG AGAG  GG
                                |||||||||| ||||  ||
                                TTTTTCGTCT TTTT  TC
                                      _   TT  ACA
GAM921   LOC146845 3'  TGAGTCAATTTTTCTCTTTTTC 59604       C   T
                                GGAAAG AGG AGAGTTGGCTTG
                                |||||| ||| ||||||||||||
                                CTTTTT TCT TTTTAACTGAGT
                                   C  _
GAM921   LOC147178 3'  CAAGCCAGCCCACTTTGGTTTT 61995       __   AGA
            T                    GAAAGC  AGGT   GTTGGCTTG
                                ||||||  ||||   |||||||||
                                TTTTTG  TTCA   CGACCGAAC
                                   GT    CC_
GAM921   LOC147219 5'  AAGCTAATGCTGTTTACC    85109    A     GTAGA
                                GG AAGCAG    GTTGGCTT
                                || ||||||    ||||||||
                                CC TTTGTC    TAATCGAA
                                 A     G____
GAM921   LOC147219 3'  CAAGTCAGTGGCTGTTGTTCT  85111     _    G  GAG
                                GGAA AGCAG TA   TTGGCTTG
                                |||| ||||| ||   ||||||||
                                TCTT TTGTC GT   GACTGAAC
                                  G    G ___
GAM921   LOC147639 3'  TGTCCCTAACTTCATTTGTTTT 79013          AG     CTTG
            CTA                    TGGAAAGCAGGT  AGTTGG
                                ||||||||||||  ||||||
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                                ATCTTTTGTTTA  TCAATC
                                      CT     CCTGTA
GAM921  LOC147660 3'  TGAGCCAGTTTTCCCAGCCTGT 79033        ____  GT
            TT                   AAGCAGGT    AGA  TGGCTTG
                                 ||||||||    |||  |||||||
                                 TTTGTCCG    TTT  ACCGAGT
                                     ACCC   TG
GAM921  LOC147669 5'  CAGGTCAGGAACCTGCTTTTTA 85178          AGAG
                                 TGGAAAGCAGGT    TTGGCTTG
                                 ||||||||||||    ||||||||
                                 ATTTTTCGTCCA    GACTGGAC
                                       AG__
GAM921  LOC147671 3'  CAGGTCTGCTTGTTTCTCA    79113    GA        G
                                 TG  AAGCAGGTAGA TTG
                                 ||  ||||||||||| |||
                                 AC  TTTGTTCGTCT GAC
                                  TC         G
GAM921  LOC147935 3'  CAGGCTAATTTTTTTATTTTTT 85203       C   T
            A                    TGGAAAG AGG AGAGTTGGCTTG
                                 |||||||  ||| ||||||||||||
                                 ATTTTTT TTT TTTTAATCGGAC
                                     A  _
GAM921  LOC148397 3'  TGGGTTGAGGGTCTGTTGTCCA 79573     A      AGAG TG
                                 TGGA AGCAGGT    T  GCTTG
                                 |||| |||||||    |  |||||
                                 ACCT TTGTCTG    A  TGGGT
                                   G      GG__ GT
GAM921  LOC148418 3'  TGGGTTAAGTACTTGTTTTT   79595         GAG
                                 GAAAGCAGGTA   TTGGCTTG
                                 ||||||||||   ||||||||
                                 TTTTTGTTCAT   AATTGGGT
                                       G__
GAM921  LOC148697 5'  TAAGCCAAAGTGTTTGCTCTTC 79679     A   GG  GAG
            A                    TGGA AGCA  TA   TTGGCTTG
                                 |||| ||||  ||   ||||||||
                                 ACTT TCGT  GT   AACCGAAT
                                   C    TT  GA_
GAM921  LOC148894 5'  CAAGCTGACTTCATTGTTTCCA 85417       G   GTA    TG
                                 TGGAAA CAG   GAGT  GCTTG
                                 ||||||  |||   ||||  |||||
                                 ACCTTT GTT   TTCA  CGAAC
                                    _   AC_    GT
GAM921  LOC148932 3'  TGGGTTGGCTGGGGTTGTTTCC 79850      G   GTAG   TG
                                 GGAAA CAG    AGT  GCTTG
                                 |||||  |||    |||  |||||
                                 CCTTT GTT    TCG  TGGGT
                                    _  GGGG   GT
GAM921  LOC148936 3'  CATCCTATATCTGTTTGTTTTC 85448        GG    GT   CT
            T                    GGAAAGCA  TAGA  TGG  TG
                                 ||||||||  ||||  |||  ||
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                                TCTTTTGT  GTCT  ATC  AC
                                    TT   AT   CT
GAM921   LOC148938 3'  CATCCTATATCTGTTTGTTTTC 85431       GG   GT   CT
           T                     GGAAAGCA  TAGA  TGG  TG
                                 ||||||||  ||||  |||  ||
                                TCTTTTGT  GTCT  ATC  AC
                                    TT   AT   CT
GAM921   LOC149175 3'  TGGGCTGGCTATGGCTTTACCA 79958    _   AGGTAG   TG
                                TGG AAAGC     AGT  GCTTG
                                ||| |||||     |||  |||||
                                ACC TTTCG     TCG  CGGGT
                                  A    GTA___   GT
GAM921   LOC149267 3'  AAGCCAGCTCAGCCTTCCA   57473     AAGC   A
                                TGGA   AGGT GAGTTGGCTT
                                ||||   |||| ||||||||||
                                ACCT   TCCG CTCGACCGAA
                                  ____   A
GAM921   LOC149332 5'  GAGATGTCTCTCTGCTTTTCA  85549        GT   TTGG   G
                                TGGAAAGCAG  AGAG   CTT
                                ||||||||||  ||||   |||
                                ACTTTTCGTC  TCTC   GAG
                                     __   TGTA
GAM921   LOC149372 3'  TGAGCCGGTAGCTGTGTTTGTT 80108     GG  G  ___
                                AGCA  TA AGT   TGGCTTG
                                ||||  || |||  |||||||
                                TTGT  GT TCG   GCCGAGT
                                  TT  G   ATG
GAM921   LOC149386 3'  TAAGTCAATTAGGGGTTGTCT  85562     A   AGGTAG
                                GGA AGC     AGTTGGCTTG
                                ||| |||     ||||||||||
                                TCT TTG     TTAACTGAAT
                                  G   GGGA__
GAM921   LOC149711 3'  CAACTTTTCTACTGGCTTTCTA 85842        A    ___
                                TGGAAAGC GGTAGA   GTTG
                                |||||||| ||||||   ||||
                                ATCTTTCG TCATCT   CAAC
                                     G     TTT
GAM921   LOC149721 5'  CAGGCCAGCTCTGTCACTGGTC 80316    AA  CA GT
                                GG  AG  G  AGAGTTGGCTTG
                                ||  ||  |  ||||||||||||
                                CT  TC  C  TCTCGACCGGAC
                                  GG  A_ TG
GAM921   LOC150005 3'  CACCTTTCTTTGCTTTCCA   85959          T   T
                                TGGAAAGCAGG AGAG TG
                                |||||||||||| |||| ||
                                ACCTTTCGTTT TTTC AC
                                       C   C
GAM921   LOC150197 3'  ATAGCAGCTTTGCTGCTTTCTA 80417         G      G  TG
                                TGGAAAGCAG TAGAGTTG CT
                                |||||||||| |||||||| ||
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                                ATCTTTCGTC GTTTCGAC GA
                                      _       _ TAT
GAM921  LOC150290 3'  AGGCCACCTCTGCTTCCA    80584      AAGCA      T
                                TGGA    GGTAGAG TGGCTT
                                ||||    ||||||| ||||||
                                ACCT    TCGTCTC ACCGGA
                                  _____       C
GAM921  LOC150295 5'  TGAGTCAACAGAGCCCTGTTTG 86157     A      TAGA_
          CCA                     TGG AAGCAGG    GTTGGCTTG
                                ||| |||||||    |||||||||
                                ACC TTTGTCC    CAACTGAGT
                                  G      CGAGA
GAM921  LOC150299 3'  CAGGCCAGGCATCCTGATTTTT 86163       G    TAGAG
          A                      TGGAAA CAGG    TTGGCTTG
                                |||||| ||||    ||||||||
                                ATTTTT GTCC    GACCGGAC
                                   A   TACG_
GAM921  LOC150776 3'  CAAGCCAGCTCTCGGGGCCT   63922      _____
                                AGGT   AGAGTTGGCTTG
                                ||||   ||||||||||||
                                TCCG   TCTCGACCGAAC
                                  GGGC
GAM921  LOC151009 5'  GGGCCGGCGCTGCTTACC    86371    A     GTAGA
                                GG AAGCAG    GTTGGCTT
                                || ||||||    ||||||||
                                CC TTCGTC    CGGCCGGG
                                 A     G_____
GAM921  LOC151150 3'  TAGGTCAGTCCCTTCCATTTGC 80939          A  _____
          TTTCC                    GGAAAGCAGGT GAG   TTGGCTTG
                                |||||||||||| |||   ||||||||
                                CCTTTCGTTTA CTT   GACTGGAT
                                       C   CCCT
GAM921  LOC151190 3'  TGGGCCATGACCTGCTTTTTA  80964          AGAGT
                                TGGAAAGCAGGT    TGGCTTG
                                ||||||||||||    |||||||
                                ATTTTTCGTCCA    ACCGGGT
                                       GT___
GAM921  LOC151512 5'  CAAGTTGGTGAGCTGTTCTTCC 86613      _    GTAGA TT
          A                      TGGAA AGCAG    G  GGCTTG
                                ||||| |||||    |  ||||||
                                ACCTT TTGTC    T  TTGAAC
                                  C    GAG__ GG
GAM921  LOC151534 3'  GGCCCCACTCCATTTGTTTTTT 57486          A   T_   TG
          A                      TGGAAAGCAGGT GAGT  GGCT
                                |||||||||||| ||||  ||||
                                ATTTTTTGTTTA CTCA  CCGG
                                       C   CC   T
GAM921  LOC151643 3'  GACTTATTTTACTTGTTTTT   81139            T  CTTG
                                GAAAGCAGGTAGAGT GG
                                |||||||||||||| ||
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                                TTTTTGTTCATTTTA TC
                                      T  AGT
GAM921   LOC151736 5'  GGCTGTATCTGTTTTTCA    83499          G
                                TGGAAAGCAGGTA AGTT
                                |||||||||||| ||||
                                ACTTTTTGTCTAT TCGG
                                      G
GAM921   LOC151877 3'  TGAGCTACCACACCTGGCTTTT 86700       _   AGA  T
           CA                     TGGAAAGC AGGT   GT GGCTTG
                                |||||||| ||||   || ||||||
                                ACTTTTCG TCCA   CA TCGAGT
                                    G   CAC  _
GAM921   LOC151907 3'  TAAGCTGTGAGACCAGTTTTTT 81212       A   AGAGT
                                GGAAAGC GGT    TGGCTTG
                                ||||||| |||    |||||||
                                TTTTTTG CCA    GTCGAAT
                                    A   GAGT_
GAM921   LOC151963 3'  TGCTATCTTTCTGTTTTTTA   81216         T   GT   TTG
                                TGGAAAGCAGG AGA  TGGC
                                |||||||||| |||  ||||
                                ATTTTTTGTCT TCT  ATCG
                                      T   __   TA
GAM921   LOC152195 3'  CATTTTCTTTATCTGTTTATCT 86747    _        TT  CTTG
                                GGA AAGCAGGTAGAG  GG
                                ||| ||||||||||||  ||
                                TCT TTTGTCTATTTC  TT
                                  A          TT  AC
GAM921   LOC152274 3'  TGGGCTAGTTCTGGACTTTCC  81348      CAGG   GT
                                GGAAAG   TAGA  TGGCTTG
                                ||||||   ||||  |||||||
                                CCTTTC   GTCT  ATCGGGT
                                   AG__   TG
GAM921   LOC152348 3'  GAGCGCTCACCTGTTTTCCA   86879          A   TG   G
                                TGGAAAGCAGGT GAGT  GCTT
                                |||||||||||| ||||  ||||
                                ACCTTTTGTCCA CTCG  CGAG
                                      _   __
GAM921   LOC152445 5'  AGGCCAGCACTGTATTCTA    86933      A   GTAGA
                                TGGAA GCAG    GTTGGCTT
                                ||||| ||||    ||||||||
                                ATCTT TGTC    CGACCGGA
                                   A   A____
GAM921   LOC152503 3'  AAACCACTTTCCTGCTTTCCA  86974          T   T  CTTG
                                TGGAAAGCAGG AGAGT GG
                                |||||||||| ||||| ||
                                ACCTTTCGTCC TTTCA CC
                                      _   _ AAAA
GAM921   LOC152580 3'  TGGGCTGGTCGTTGCTGTTTTT 86986       GTA_  G TG
                                GAAAGCAG   GA T  GCTTG
                                ||||||||   || |  |||||
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                                TTTTTGTC   CT G  CGGGT
                                    GTTG  _ GT
GAM921   LOC152667 3'  TAGGCTTCATTGCTTTCTGTTT 81526          T  AGTT__
            TTTA                   TGGAAAGCAGG AG     GGCTTG
                                   ||||||||||| ||     ||||||
                                   ATTTTTTGTCT TC     TCGGAT
                                      T  GTTACT
GAM921   LOC152762 3'  AGGCAGCGTCTGTTTTCT    81530         TAGA   G
                                   GGAAAGCAGG   GTTG CT
                                   ||||||||||   |||| ||
                                   TCTTTTGTCT   CGAC GA
                                      G___   G
GAM921   LOC152924 3'  TTTTCAACCTGTTTGTTTTTTA 81623         GG   A    CTTG
                                   TGGAAAGCA  TAG GTTGG
                                   |||||||||  ||| |||||
                                   ATTTTTTGT  GTC CAACT
                                      TT  _    TTTT
GAM921   LOC153196 5'  TGAGCTGATTCCCTTTTCTCCA 87173      A  C   TA   TG
                                   TGGA AG AGG  GAGT  GCTTG
                                   |||| || |||  ||||  |||||
                                   ACCT TT TCC  CTTA  CGAGT
                                     C  T   __   GT
GAM921   LOC153811 3'  TGAGCCGCACCAGCCTGTTTTT 81855           AGA  _
            TA                     TGGAAAGCAGGT   GT TGGCTTG
                                   ||||||||||||   || |||||||
                                   ATTTTTTGTCCG   CA GCCGAGT
                                      AC_  C
GAM921   LOC154084 3'  TAGGTCAGTTTTAGAACTGCT  87382      G__   GT
                                   AGCAG   TAGA  TGGCTTG
                                   |||||   ||||  |||||||
                                   TCGTC   ATTT  ACTGGAT
                                     AAG   TG
GAM921   LOC154428 5'  CAGGCCAGCGAGATGCTCTTCA 87417      A   GGTAGA
                                   TGGA AGCA     GTTGGCTTG
                                   |||| ||||     |||||||||
                                   ACTT TCGT     CGACCGGAC
                                     C   AGAG__
GAM921   LOC154547 3'  CAAGTCAAGCGTCTTGTTGTTT 76568       GT  _  _
                                   AAGCAG  AGA GTT GGCTTG
                                   ||||||  ||| ||| ||||||
                                   TTTGTT  TCT CGA CTGAAC
                                     GT   G   A
GAM921   LOC154562 3'  GCCTCTATCTTGTTTTTT    81996        _    GTT
                                   GGAAAGCA GGTAGA   GGC
                                   |||||||| ||||||   |||
                                   TTTTTTGT CTATCT   CCG
                                      T    ___
GAM921   LOC154792 5'  AAGTCAGGAATGCTTTTCA   87461         GGTAGAG
                                   TGGAAAGCA      TTGGCTT
                                   |||||||||      |||||||
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                                ACTTTTCGT      GACTGAA
                                     AAG____
GAM921   LOC154849 3'  TAGGTTCCTGCCCTGTTTTTT  60943          _  AGTT
                                GGAAAGCAGG TAG   GGCTTG
                                |||||||||| |||   ||||||
                                TTTTTTGTCC GTC   TTGGAT
                                     C  C___
GAM921   LOC154865 5'  TTGCCAGCTTTATTTGCCTTCT 82063      A          TTG
           A                     TGGAA GCAGGTAGAGTTGGC
                                |||||| ||||||||||||||
                                ATCTT CGTTTATTTCGACCG
                                   C           TTG
GAM921   LOC155434 3'  TGAGCTGATTCTGTTTGCTCCA 87693     AA  GG    TG
                                TGGA  GCA  TAGAGT  GCTTG
                                ||||  |||  ||||||  |||||
                                ACCT  CGT  GTCTTA  CGAGT
                                  __  TT     GT
GAM921   LOC157550 5'  GGCTTTTTGTTTGTTTTTC   82387       GG    TT
                                GGAAAGCA  TAGAG  GGCT
                                ||||||||  |||||  ||||
                                CTTTTTGT  GTTTT  TCGG
                                     TT    __
GAM921   LOC157653 5'  CAGGCTAATCTTTCTCTTTCCA 82441       C  T  G
                                TGGAAAG AGG AGA TTGGCTTG
                                ||||||| ||| ||| ||||||||
                                ACCTTTC TCT TCT AATCGGAC
                                   _  T  _
GAM921   LOC157663 3'  TAAGTCAGCTTGGAACTTTTTT 82455      C  GTA_
           C                    GAAAG AG   GAGTTGGCTTG
                                ||||| ||   ||||||||||
                                CTTTT TC   TTCGACTGAAT
                                   T  AAGG
GAM921   LOC157918 3'  TACTTGAATTCTGTCTTGTTTT 87933         _     GGCTTG
           CC                     GGAAAGCAGG TAGAGTT
                                |||||||||| |||||||
                                CCTTTTGTTC GTCTTAA
                                     T      GTTCATG
GAM921   LOC157919 5'  TACTTGAATTCTGTCTTGTTTT 82523         _     GGCTTG
           CC                     GGAAAGCAGG TAGAGTT
                                |||||||||| |||||||
                                CCTTTTGTTC GTCTTAA
                                     T      GTTCATG
GAM921   LOC158014 5'  TGGGTCAATTCTCATATTTTCA 82572       GCAGGT
                                TGGAAA     AGAGTTGGCTTG
                                ||||||     ||||||||||||
                                ACTTTT     TCTTAACTGGGT
                                   ATAC__
GAM921   LOC158219 3'  TGAGCCAATTTTGGATTTGTT  82692       __
                                AGCAGGT  AGAGTTGGCTTG
                                |||||||  ||||||||||||
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                                TTGTTTA  TTTTAACCGAGT
                                    GG
GAM921   LOC158293 3'  ACACAGCACTGCCTGCTTTTT  82743           A    GCTTG
                                GGAAAGCAGGTAG GTTG
                                |||||||||||| ||||
                                TTTTTCGTCCGTC CGAC
                                       A    ACAA
GAM921   LOC158295 5'  CAGGTATGGCATTCTGCCTGTT 88060      G       TG___
           TCT                    GGAAA CAGGTAGAGT    GCTTG
                                |||||| ||||||||||    ||||||
                                TCTTT GTCCGTCTTA    TGGAC
                                   _        CGGTA
GAM921   LOC158376 3'  TGGGCCGGCTCTGCTGATCTA  88138     AAGCA
                                TGGA    GGTAGAGTTGGCTTG
                                ||||    ||||||||||||||
                                ATCT    TCGTCTCGGCCGGGT
                                  AG___
GAM921   LOC158828 3'  TGAGCTGGCCTTGGTTTTTTA  82897       AGGT  A  TG
                                TGGAAAGC    AG GT  GCTTG
                                ||||||||    || ||  ||||||
                                ATTTTTTG    TC CG  CGAGT
                                     GT__  _  GT
GAM921   LOC158969 5'  GGGAAAGTCTTGCCTGTTTTCC 82937           AG  GG   G
           A                     TGGAAAGCAGGTAG  TT  CTT
                                ||||||||||||||  ||  |||
                                ACCTTTTGTCCGTT  GA  GGG
                                       CT  AA   G
GAM921   LOC159148 5'  CAAGCCAGCTCTGCCTGTACCA 88392     AAA
                                TGG   GCAGGTAGAGTTGGCTTG
                                |||   ||||||||||||||||||
                                ACC   TGTCCGTCTCGACCGAAC
                                  A__
GAM921   LOC161003 5'  TGAGTTGCTGCCTGTTCTTCA  59914      A       AGTTG
                                TGGA AGCAGGTAG     GCTTG
                                |||| |||||||||     ||||||
                                ACTT TTGTCCGTC     TGAGT
                                   C        GT___
GAM921   LOC161742 3'  AAGTTTTTTAGTTGTTTTTT   83167         G    TT    G
                                GGAAAGCAG TAGAG  GGCTT
                                |||||||| |||||  |||||
                                TTTTTTGTT ATTTT  TTGAA
                                     G    __
GAM921   LOC163882 3'  TGGGTCATAGAAGTTGCTTTCC 83043         GTAGAGT
                                GGAAAGCAG      TGGCTTG
                                |||||||||      |||||||
                                CCTTTCGTT      ACTGGGT
                                     GAAGAT_
GAM921   LOC166316 5'  CGGCATCACTTGTTTTTCA    88611           A  _
                                TGGAAAGCAGGT GA GTTG
                                |||||||||||| || ||||
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                                ACTTTTTGTTCA CT CGGC
                                      _ A
GAM921   LOC166765 3'  CAATTTTTACCTGTCTTTT   83547      _       _
                                GAAAG CAGGTAGAG TTG
                                ||||| ||||||||| |||
                                TTTTC GTCCATTTT AAC
                                   T       T
GAM921   LOC167040 5'  TGAGTCAGCCTGTGGTCAGCTT 88622       A ___  A
            TCT                   GGAAAGC GG   TAG GTTGGCTTG
                                ||||||| ||   ||| |||||||||
                                TCTTTCG CT   GTC CGACTGAGT
                                   A  GGT   _
GAM921   LOC168448 3'  CAAGCTGCTTGTCTTCTA    83581      AG      AG
                                TGGAA  CAGGTAG  TTG
                                |||||  |||||||  |||
                                ATCTT  GTTCGTC  AAC
                                   CT      G_
GAM921   LOC169026 3'  CAGGTCAACTTTACCACCAGCC 83600    AAAGCA
                                GG     GGTAGAGTTGGCTTG
                                ||     ||||||||||||||
                                CC     CCATTTCAACTGGAC
                                 GACCA_
GAM921   LOC169436 5'  TGGGCCAAGGCCTGCCTTTT   83622     A     AGAG
                                GGAA GCAGGT    TTGGCTTG
                                |||| ||||||    ||||||||
                                TTTT CGTCCG    AACCGGGT
                                  C     G___
GAM921   LOC169611 3'  GGGTAATACTTGCTTCCA    83656      A     AGA    G
                                TGGAA GCAGGT   GTTG CT
                                ||||| ||||||   |||| ||
                                ACCTT CGTTCA   TAAT GG
                                  _     ___    G
GAM921   LOC169611 3'  GTTGCTGAGATATCTGTTTTGC 83659    G        GAG TG  TTG
            A                    TG AAAGCAGGTA   T  GC
                                || ||||||||||   |  ||
                                AC TTTTGTCTAT   A  CG
                                 G         AG_ GT  TTGA
GAM921   LOC170384 3'  TGAGTTGTATTCTGGTTTTCC  83728        AGG     _
                                GGAAAGC   TAGAGT TGGCTTG
                                |||||||   ||||||| |||||||
                                CCTTTTG   GTCTTA GTTGAGT
                                   ___      T
GAM921   LOC170394 5'  TGGGCTGGCGGACTTGTCTTCT 83740      AG    AGA  TG
                                GGAA  CAGGT   GT  GCTTG
                                ||||  |||||   ||  |||||
                                TCTT  GTTCA   CG  CGGGT
                                  CT    GG_  GT
GAM921   LOC196411 3'  CAAGGCTGCTTGTTTTTT    89042            AG
                                GGAAAGCAGGTAG  TTG
                                ||||||||||||  |||
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                                TTTTTTGTTCGTC  AAC
                                      GG
GAM921   LOC196985 3'  CAAGTGGATTCTTTGCTTTTTA 91234         GT     G
                                TGGAAAGCAG  AGAGTT GCTTG
                                |||||||||  |||||| |||||
                                ATTTTTCGTT  TCTTAG TGAAC
                                      __     G
GAM921   LOC196986 3'  CAAGTGGATTCTTTGCTTTTTA 91233         GT     G
                                TGGAAAGCAG  AGAGTT GCTTG
                                |||||||||  |||||| |||||
                                ATTTTTCGTT  TCTTAG TGAAC
                                      __     G
GAM921   LOC197125 3'  GGGTCAATTTTAGCCTCT    89244    C   _
                                AG AGGT AGAGTTGGCTT
                                || |||| ||||||||||
                                TC TCCG TTTTAACTGGG
                                 _   A
GAM921   LOC197358 3'  GCCTTTTTTGTTTGTTTTT    89435       GG    TT
                                GAAAGCA  TAGAG  GGC
                                |||||||  |||||  |||
                                TTTTTGT  GTTTT  CCG
                                    TT    TT
GAM921   LOC199796 5'  CAGGCCGACTTCAGTGTTCTCC 74922      A    GGTA
           A                     TGGA AGCA    GAGTTGGCTTG
                                |||| ||||    ||||||||||
                                ACCT TTGT    TTCAGCCGGAC
                                  C   GAC_
GAM921   LOC199982 3'  TAAGCTAATTTAGGTTTTTC   89901        AGGTA
                                GGAAAGC    GAGTTGGCTTG
                                |||||||    ||||||||||
                                CTTTTTG    TTTAATCGAAT
                                    GA___
GAM921   LOC199993 5'  CAGGCTCTCGCGTCTGCTTCTA 72140      A    TA_   TT
                                TGGAA GCAGG   GAG  GGCTTG
                                ||||| |||||   |||  ||||||
                                ATCTT CGTCT   CTC  TCGGAC
                                   _    GCG   __
GAM921   LOC200059 3'  AAGTTAATTGGGTTTTCC    89954       AGGTAG
                                GGAAAGC     AGTTGGCTT
                                |||||||     |||||||||
                                CCTTTTG     TTAATTGAA
                                    GG____
GAM921   LOC200081 3'  AGGCCAATGATGCTTCTCA    89970    GA    GGTAGA
                                TG  AAGCA     GTTGGCTT
                                ||  |||||     ||||||||
                                AC  TTCGT     TAACCGGA
                                 TC    AG____
GAM921   LOC200227 3'  AAGGTATATTTGTTTTCTA    90041          GAGT  G
                                TGGAAAGCAGGTA    TG CTT
                                ||||||||||||    || |||
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                                ATCTTTTGTTTAT    AT GAA
                                      ____ G
GAM921   LOC200269 3'  CGGGCCCTGCGGGTCTGCTTTC 90073          AGA  T_
           C                    GGAAAGCAGGT   GT  GGCTTG
                                ||||||||||   ||  ||||||
                                CCTTTCGTCTG   CG  CCGGGC
                                     GG_  TC
GAM921   LOC200982 5'  TGAGTTGGCCATGGCTCTTTTC 91815       C  G  GA  TG
           CA                    TGGAAAG AG TA  GT  GCTTG
                                ||||||| || ||  ||  |||||
                                ACCTTTT TC GT  CG  TGAGT
                                    C  G  AC  GT
GAM921   LOC201158 3'  TGGGCCAGCCAGTCCCTGTTTT 61088    _       TAGA_
           ACT                   GG AAAGCAGG    GTTGGCTTG
                                || ||||||||    |||||||||
                                TC TTTTGTCC    CGACCGGGT
                                 A       CTGAC
GAM921   LOC201771 5'  GCTGCTCTCCTGTTTTTCA   70518          T    T
                                TGGAAAGCAGG AGAGT GGC
                                |||||||||| ||||| |||
                                ACTTTTTGTCC TCTCG TCG
                                      _    _
GAM921   LOC202284 5'  CAGGTCACCTCTGCTTTCCA   91931         GGTA   T
                                TGGAAAGCA   GAG TGGCTTG
                                |||||||||   ||| |||||||
                                ACCTTTCGT   CTC ACTGGAC
                                     _____  C
GAM921   LOC202460 5'  TGAGTTTGTTTTTTGTTTGCTT 90680        GG    TT__
           TTC                   GGAAAGCA  TAGAG   GGCTTG
                                ||||||||  |||||   ||||||
                                CTTTTCGT  GTTTT   TTGAGT
                                     TT    TTGT
GAM921   LOC202934 3'  CAGGCTGATCTCTAGTTTTCCA 92029        AGG    _ TG
                                TGGAAAGC   TAGAG T  GCTTG
                                ||||||||   ||||| |  |||||
                                ACCTTTTG   ATCTC A  CGGAC
                                     ___    T GT
GAM921   LOC202934 3'  GCTTCTTCTTGCTTTCCA    92043          T   GTT
                                TGGAAAGCAGG AGA   GGC
                                |||||||||| |||   |||
                                ACCTTTCGTTC TCT   TCG
                                      T  ___
GAM921   LOC202934 5'  TGGGTCAGTTCAGGTTTTCT   92057       AGGTA  GT
                                GGAAAGC    GA  TGGCTTG
                                |||||||    ||  |||||||
                                TCTTTTG    CT  ACTGGGT
                                    GA___  TG
GAM921   LOC203068 3'  GCCTCTATCTTGTTTTTT    90757         _     GTT
                                GGAAAGCA GGTAGA   GGC
                                |||||||| ||||||   |||
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                                TTTTTTGT CTATCT   CCG
                                     T     ___
GAM921   LOC203080 5'  TACTAATGTCCTGTTTTTTA   90774          TAGA    CTTG
                                TGGAAAGCAGG    GTTGG
                                ||||||||||    |||||
                                ATTTTTTGTCC    TAATC
                                      TG__     ATG
GAM921   LOC203286 5'  AGGTTTTGTGCCTGCTTTTT   92141           G  TT    G
                                GGAAAGCAGGTA AG  GGCTT
                                ||||||||||| ||  |||||
                                TTTTTCGTCCGT TT  TTGGA
                                      G  __
GAM921   LOC203522 3'  TGAGTCAAGGGAATTGCTTTCC 90939          GTAGAG
            A                    TGGAAAGCAG     TTGGCTTG
                                ||||||||||     ||||||||
                                ACCTTTCGTT     AACTGAGT
                                      AAGGG_
GAM921   LOC203547 3'  CAGGCCAGCTTTGTGCTTTGCA 90946    G     GG
                                TG AAAGCA  TAGAGTTGGCTTG
                                || ||||||  ||||||||||||
                                AC TTTCGT  GTTTCGACCGGAC
                                 G     __
GAM921   LOC204275 3'  CACTCTTTGCTTGGTTTTT    91003      G       T_
                                GGAAA CAGGTAGAG  TG
                                ||||| |||||||||  ||
                                TTTTT GTTCGTTTC  AC
                                   G        TC
GAM921   LOC206280 5'  TAATTTATCTTGCTTTCCA    92400          TA
                                TGGAAAGCAGG  GAGTTG
                                ||||||||||  ||||||
                                ACCTTTCGTTC  TTTAAT
                                      TA
GAM921   LOC206372 3'  CGAACCATCTACCTGCTTTTC  91095           GT   C
                                GGAAAGCAGGTAGA  TGG TTG
                                ||||||||||||||  ||| |||
                                CTTTTCGTCCATCT  ACC AGC
                                      __   A
GAM921   LOC206426 3'  AAGTGTCTCTATTTGCTTCTA  91096      A       TTG   G
                                TGGAA GCAGGTAGAG   GCTT
                                ||||| ||||||||||   ||||
                                ATCTT CGTTTATCTC   TGAA
                                   _        TG_
GAM921   LOC219654 3'  GGTTGGTTTTTGTTTGTTTTTT 92939         GG   _ TT    TG
            A                    TGGAAAGCA  TAGA G  GGCT
                                |||||||||  |||| |  ||||
                                ATTTTTTGT  GTTT T  TTGG
                                      TT    T GG    T
GAM921   LOC219673 3'  TAGGCTGGTTTTGCACTCC    94634     AAGCAG     TT
                                GGA     GTAGAG  GGCTTG
                                |||     ||||||  ||||||
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                                CCT     CGTTTT  TCGGAT
                                  CA____     GG
GAM921   LOC219793 5'  GAGTCAACTGTCTTTTCC    93020      GC   TAG
                                GGAAA  AGG   AGTTGGCTT
                                |||||  |||   |||||||||
                                CCTTT  TCT   TCAACTGAG
                                   __  G__
GAM921   LOC219988 3'  TAAGTTTGGCCTGCTTTGCTTT 93266          _   A  TG _
            TTA                   TGGAAAGCAG GTAG GT  G CTTG
                                ||||||||||| |||| ||  | ||||
                                ATTTTTCGTT CGTC CG  T GAAT
                                      T   _ GT T
GAM921   LOC220534 3'  CAGGCTGCCATGCTTTTTA   92416          _    AG
                                TGGAAAGCA GGTAG  TTG
                                ||||||||| |||||  |||
                                ATTTTTCGT CCGTC  GAC
                                      A    G_
GAM921   LOC220662 5'  CAAGCTGACTTGTTCTTTTTT  92807      C   TA    TG
                                GAAAG AGG  GAGT  GCTTG
                                ||||| |||  ||||  |||||
                                TTTTT TCT  TTCA  CGAAC
                                   _  TG    GT
GAM921   LOC220766 3'  AACCATTCTATTTGCTTCT    92472      A        T  CTTG
                                GGAA GCAGGTAGAGT GG
                                |||| |||||||||| ||
                                TCTT CGTTTATCTTA CC
                                  _         _ AAA
GAM921   LOC220824 3'  CAAGTTTTCTTTGTGCTGTTTT 92479          _     TT
            CT                    GGAAAGCAG GTAGAG  GGCTTG
                                ||||||||| ||||||  ||||||
                                TCTTTTGTC TGTTTC  TTGAAC
                                      G     TT
GAM921   LOC220963 3'  AGTGCTAATTTTACCTGTTTCC 93097       G           TTG
            A                     TGGAAA CAGGTAGAGTTGGC
                                ||||||| ||||||||||||||
                                ACCTTT GTCCATTTTAATCG
                                   _            TGAA
GAM921   LOC220963 3'  GGCGTTATCTGTTGTCTA    93100      A       A
                                TGGA AGCAGGTAG GTT
                                |||| ||||||||| |||
                                ATCT TTGTCTATT CGG
                                   G        G
GAM921   LOC221122 3'  TGGGCCAGGGCCTGGTTTTTCA 95088          _   AGAGT
                                TGGAAAGC AGGT     TGGCTTG
                                |||||||| ||||     |||||||
                                ACTTTTTG TCCG     ACCGGGT
                                     G   GG___
GAM921   LOC221154 3'  TAAGCATGTCTTGTACTTGCTT 95192           _  TTG_
            TCT                   GGAAAGCAGGTA GAG    GCTTG
                                |||||||||||| |||    |||||
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                                TCTTTCGTTCAT TTC   CGAAT
                                      G  TGTA
GAM921  LOC221398 3'  CAGGCTGCACAGCATTTGCTTT 92665         AGA  _
          CC                    GGAAAGCAGGT  GT TGGCTTG
                                ||||||||||  || |||||||
                                CCTTTCGTTTA  CA GTCGGAC
                                      CGA  C
GAM921  LOC221474 5'  TGGGCTGGCTCTCCCTGCTTCT 94004     A    T    TG
                                GGAA GCAGG AGAGT  GCTTG
                                |||| ||||| |||||  |||||
                                TCTT CGTCC TCTCG  CGGGT
                                  _    C    GT
GAM921  LOC221495 3'  TGGGTCAATATGACTGCTTCTC 95497    GA    GTAGA
          A                     TG  AAGCAG    GTTGGCTTG
                                ||  ||||||    |||||||||
                                AC  TTCGTC    TAACTGGGT
                                 TC     AGTA_
GAM921  LOC221543 3'  GCAATTTCTGTTTGTTTTCTA  95379        GG    TTG
                                TGGAAAGCA  TAGAG   GC
                                |||||||||  |||||  ||
                                ATCTTTTGT  GTCTT   CG
                                     TT    TAA
GAM921  LOC221543 3'  TAAATCTACTCTGCCTGTGTTT 95385      A        T GC
          TA                    TGGAA GCAGGTAGAGT G  TTG
                                ||||| ||||||||||| |  |||
                                ATTTT TGTCCGTCTCA C  AAT
                                   G         T TA
GAM921  LOC221561 3'  CAAGTCAAGCGTCTTGTTGTTT 93752       GT  _  _
                                AAGCAG  AGA GTT GGCTTG
                                ||||||  ||| ||| ||||||
                                TTTGTT  TCT CGA CTGAAC
                                   GT   G   A
GAM921  LOC221584 5'  TGAGCTGATTCTGGGAACTTTG 95472    _   CAGG     TG
          CCA                   TGG AAAG   TAGAGT  GCTTG
                                ||| ||||   ||||||  |||||
                                ACC TTTC   GTCTTA  CGAGT
                                  G   AAGG     GT
GAM921  LOC221641 5'  GCAGGCATCTGGGATTTTACCT 95345            G_____
          GTTTTTC               GGAAAGCAGGTAGAGTT    GCTTG  C
                                |||||||||||||||||    |||||  |
                                CTTTTTGTCCATTTTAG    CGGAC  G
                                     GGTCTA
GAM921  LOC221656 3'  CAAGTATTTACTTTTATCTTTT 93848       C     _  TG__
          TTTTA                 TGGAAAG AGGTAGA GT   GCTTG
                                ||||||| ||||||| ||   |||||
                                ATTTTTT TCTATTT CA   TGAAC
                                   T     T  TTTA
GAM921  LOC221683 3'  TAGGTTTTTGTTTGTTTTCCA  95331        GG    TTG
                                TGGAAAGCA  TAGAG   GCTTG
                                |||||||||  |||||  |||||
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                                ACCTTTTGT  GTTTT   TGGAT
                                     TT    ___
GAM921   LOC221687 3'  TGAGTTAATGAACTTCTTTTCA 93874       C    AGA
                                TGGAAAG AGGT   GTTGGCTTG
                                ||||||| ||||   |||||||||
                                ACTTTTC TTCA   TAATTGAGT
                                   _    AG_
GAM921   LOC221710 5'  CGGGCTGACTCTGCTTGTGTTC 94018     A          TG
                                GAA GCAGGTAGAGT  GCTTG
                                ||| ||||||||||  |||||
                                CTT TGTTCGTCTCA  CGGGC
                                  G          GT
GAM921   LOC221760 3'  TGAGCTGGTCAGCTGCTCTTCA 95431      A    GTA  G TG
                                TGGA AGCAG   GA T  GCTTG
                                |||| |||||   || |  |||||
                                ACTT TCGTC   CT G  CGAGT
                                  C     GA_  _ GT
GAM921   LOC221763 5'  TAAGTTTCTTCTTGCTTTTCA  95439          T    TTG
                                TGGAAAGCAGG AGAG   GCTTG
                                |||||||||||| ||||   |||||
                                ACTTTTCGTTC TCTT   TGAAT
                                      T    ___
GAM921   LOC221922 5'  AGGCCTGGGTCTGCTTCT    94246    C      G  _
                                AG AGGTAGA TT GGCTT
                                || ||||||| || |||||
                                TC TTCGTCT GG CCGGA
                                 _      G  T
GAM921   LOC221981 3'  AAGTCCATTTTATCTGTTTT   95627            T    G
                                AAAGCAGGTAGAGT GGCTT
                                |||||||||||||| |||||
                                TTTTGTCTATTTTA CTGAA
                                        C    A
GAM921   LOC253539 3'  AGGTTAAGCTTCCTTTCT    97697       C    AGAG
                                GGAAAG AGGT    TTGGCTT
                                |||||| ||||    |||||||
                                TCTTTC TTCG    AATTGGA
                                   C    _____
GAM921   LOC253609 3'  GGGTTTATCTGTTTGTTTTTT  98567        GG    GTT    G
                                GGAAAGCA  TAGA   GGCTT
                                ||||||||  ||||   |||||
                                TTTTTTGT  GTCT   TTGGG
                                     TT    AT_
GAM921   LOC253715 5'  GGCTCAGTCTGCTTCCCA    98706     A      TA
                                TGG AAGCAGG  GAGTT
                                ||| |||||||  |||||
                                ACC TTCGTCT  CTCGG
                                  C      GA
GAM921   LOC253782 3'  TAGTCAGAATGCTGTTTTTC   97403         G  GAG     TG
                                GGAAAGCAG TA   TTGGCT
                                |||||||||  ||   ||||||
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                                CTTTTTGTC GT   GACTGA
                                     _ AA_     TT
GAM921   LOC253786 5'  AGGCACTATTTGTTTTCT    98828           AGTTG
                                GGAAAGCAGGTAG    GCTT
                                ||||||||||||    ||||
                                TCTTTTGTTTATC    CGGA
                                      A____
GAM921   LOC254143 5'  AGGAGTTATCTGTTATCCA   98251     A       AGTTGG
                                TGGA AGCAGGTAG     CTT
                                |||| |||||||||     |||
                                ACCT TTGTCTATT     GGA
                                  A       GA____
GAM921   LOC254249 3'  TAAGTTAATAGCTCTGTCTTTT 97187       _  _ AGA
           T                     GGAAAG CAG GT   GTTGGCTTG
                                ||||||| ||| ||   |||||||||
                                TTTTTC GTC CG   TAATTGAAT
                                   T   T  A__
GAM921   LOC254394 3'  CAAGCTAATTTTTGAGTTACCA 97672     _ AG   GTA
                                TGG AA  CAG   GAGTTGGCTTG
                                ||| ||  |||   ||||||||||
                                ACC TT  GTT   TTTAATCGAAC
                                  A  GA  ___
GAM921   LOC254440 5'  GGCACCTTTACCTGTGTTTT   98849     A       TTG
                                GGAA GCAGGTAGAG   GCT
                                |||| ||||||||||   |||
                                TTTT TGTCCATTTC   CGG
                                  G        CA_
GAM921   LOC254531 3'  TAAGTTGATTTTAATTTTTTGT 96672       ____     TG
           TT                    AAGCAGG    TAGAGT  GCTTG
                                |||||||    ||||||  |||||
                                TTTGTTT    ATTTTA  TGAAT
                                    TTTA     GT
GAM921   LOC254734 3'  CAGGTCAATTCTGATTATTC   96623     AGCAGG
                                GAA     TAGAGTTGGCTTG
                                |||     ||||||||||||||
                                CTT     GTCTTAACTGGAC
                                  ATTA__
GAM921   LOC255144 3'  TGAGCCAATAAATTGCTTTC   96768       GTAGA
                                GAAAGCAG    GTTGGCTTG
                                ||||||||    |||||||||
                                CTTTCGTT    TAACCGAGT
                                     AAA__
GAM921   LOC255189 5'  AGTGCTATCTGTTTGCCA    98374     A       AG
                                TGG AAGCAGGTAG  TT
                                ||| ||||||||||  ||
                                ACC TTTGTCTATC  GA
                                  G        GT
GAM921   LOC255465 5'  TGGGTCAGTTCACGTTTTCT   99131       AG  A  GT
                                GGAAAGC  GT GA  TGGCTTG
                                |||||||  || ||  |||||||
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                                TCTTTTG  CA CT  ACTGGGT
                                   __ _  TG
GAM921  LOC255520 3'  TGGCTGTTTTTAATTTTGTCTG 97554      G  GT    _____   TG
                ATTTTTA                 TGGAAA CAG  AGAGTT     GGCT
                                |||||| |||  ||||||     ||||
                                ATTTTT GTC  TTTTAA     TCGG
                                   A  TG     TTTTTG    T
GAM921  LOC255545 3'  TAAGCTGTGAGACCAGTTTTTT 97415       A  AGAGT
                                GGAAAGC GGT    TGGCTTG
                                ||||||| |||    |||||||
                                TTTTTTG CCA    GTCGAAT
                                   A  GAGT_
GAM921  LOC255811 3'  CGGGAGACTGCCTGCCTTTCA  96308      A    AG   GG
                                TGGAA GCAGGT  AGTT  CTTG
                                ||||| ||||||  ||||  ||||
                                ACTTT CGTCCG  TCAG  GGGC
                                   C     __   A_
GAM921  LOC255849 3'  GTCATGTCTGTTTGTTTTTCA  98191        GG   GT
                                TGGAAAGCA  TAGA  TGGC
                                |||||||||  ||||  ||||
                                ACTTTTTGT  GTCT  ACTG
                                     TT   GT
GAM921  LOC256116 5'  GGAAGGTTTGTTTGCGTTCCA  99375     A  GG   G  GG
                                TGGAA GCA  TAGA TT  CT
                                ||||| |||  |||| ||  ||
                                ACCTT CGT  GTTT GA  GG
                                   G  TT   G  A_
GAM921  LOC256401 3'  CAAGCTGCTTGTCTTCCA    97718      AG     AG
                                TGGAA  CAGGTAG  TTG
                                |||||  |||||||  |||
                                ACCTT  GTTCGTC  AAC
                                   CT     G_
GAM921  LOC256980 3'  AGATCTTGATCTGCTTTCT   96924         A  TTGG
                                GGAAAGCAGGT GAG   CT
                                |||||||||||| |||   ||
                                TCTTTCGTCTA TTC   GA
                                      G  TA__
GAM921  LOC257054 3'  TGGTGGTTCTGCCTGCTTGCT  97379    A        TT G  TG
                                GG AAGCAGGTAGAG  G CT
                                || ||||||||||||  | ||
                                TC TTCGTCCGTCTT  T GG
                                 G         GG _  TG
GAM921  LOC257153 5'  TGGGCTGAGAGTGGTGTTTGCT 97468       GG  GA ___ TG
                TTCT                    GGAAAGCA  TA  G   T  GCTTG
                                ||||||||  ||  |   |  |||||
                                TCTTTCGT  GT  T   A  CGGGT
                                     TT  GG GAG GT
GAM921  LOC257364 3'  AAGTTAGGTACGCTTTCCA   96639       AG   GAG
                                TGGAAAGC  GTA   TTGGCTT
                                ||||||||  |||   |||||||
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                                ACCTTTCG  CAT   GATTGAA
                                    __   G__
GAM921   LOC257451 3'  TGGGCTTTATTTGTCTTTTT   97301       _        GGCTTG
                                GGAAAG CAGGTAGAGTT
                                ||||||| ||||||||||
                                TTTTTC GTTTATTTCGG
                                   T         GT
GAM921   LOC257464 3'  TAAGCCAACAAGCATCTTTTCA 91245       CAG  AGA
                                TGGAAAG   GT   GTTGGCTTG
                                |||||||   ||   |||||||||
                                ACTTTTC   CG   CAACCGAAT
                                    TA_  AA_
GAM921   LOC257465 3'  TGAGTTCCTTTCTGCTTGTTAT 82503     A         TT_
            CT                    GGA AGCAGGTAGAG   GGCTTG
                                ||| ||||||||||   ||||||
                                TCT TTGTTCGTCTT   TTGAGT
                                  A         TCC
GAM921   LOC257591 3'  CAAGTCAAGCGTCTTGTTGTTT 99672       GT   _   _
                                AAGCAG  AGA GTT GGCTTG
                                ||||||  ||| ||| ||||||
                                TTTGTT  TCT CGA CTGAAC
                                   GT   G   A
GAM921   LOC257596 3'  GCAATTTCTGTTTGTTTTCTA  99782         GG     TTG
                                TGGAAAGCA  TAGAG   GC
                                |||||||||  |||||   ||
                                ATCTTTTGT  GTCTT   CG
                                     TT     TAA
GAM921   LOC257596 3'  TAAATCTACTCTGCCTGTGTTT 99788       A         T GC
            TA                    TGGAA GCAGGTAGAGT G  TTG
                                ||||| |||||||||||  |  |||
                                ATTTT TGTCCGTCTCA C  AAT
                                   G         T TA
GAM921   LOC51026  3'  GGCTTATTATTTGTTTTTCA   32687            AGTT
                                TGGAAAGCAGGTAG    GGCT
                                ||||||||||||||    ||||
                                ACTTTTTGTTTATT    TCGG
                                        AT__
GAM921   LOC51580  3'  AGGTTGGCCTTGCTTGCT    32428         A  TG
                                AGCAGGTAG GT  GCTT
                                |||||||||  ||  ||||
                                TCGTTCGTT CG  TGGA
                                     C  GT
GAM921   LOC51690  3'  TAGGTTGAATTTTTGTTTTCT  33012          TAGAG TG
                                GGAAAGCAGG     T  GCTTG
                                ||||||||||     |  |||||
                                TCTTTTGTTT     A  TGGAT
                                      TTA__ GT
GAM921   LOC54103  5'  CAGGCTGATTCTTCTTCCTTCT 95884       A C   T     TG
            A                     TGGAA G AGG AGAGT  GCTTG
                                ||||| | ||| |||||  |||||
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                                ATCTT C TTC TCTTA  CGGAC
                                  _ C   T    GT
GAM921  LOC54505  5' CGGGCCGCCGTGTCTGCTTCCA 68446      A   GT GA  T
                                TGGAA GCAG  A  GT GGCTTG
                                ||||| ||||  |  || ||||||
                                ACCTT CGTC  T  CG CCGGGC
                                  _   TG GC  _
GAM921  LOC55885  3' GGATTTTTTTGCTTGCTATTC  38442     A        TTGG  TG
                                GGA AGCAGGTAGAG   CT
                                ||| ||||||||||   ||
                                CTT TCGTTCGTTTT   GG
                                  A         TTTA  T
GAM921  LOC55885  3' TAGGCTGAAATTTGTCTTTCCA 38445       _    AGAG TG
                                TGGAAAG CAGGT   T  GCTTG
                                ||||||| |||||   |  |||||
                                ACCTTTC GTTTA   A  CGGAT
                                   T    A___ GT
GAM921  LOC55893  5' AGGCCGGCGCTGCTTTTC    38488        GTAGA
                                GGAAAGCAG    GTTGGCTT
                                |||||||||    ||||||||
                                CTTTTCGTC    CGGCCGGA
                                     G____
GAM921  LOC56906  3' AAGTTTGCTTGCTTGCCA    39722     A        G
                                TGG AAGCAGGTAGA TT
                                ||| ||||||||||| ||
                                ACC TTCGTTCGTTT AA
                                  G         G
GAM921  LOC81569  3' TGAGCTGGCTTTGGAATTCTA  62676      AGCAGG     TG
                                TGGAA     TAGAGT  GCTTG
                                |||||     ||||||  |||||
                                ATCTT     GTTTCG  CGAGT
                                   AAG___     GT
GAM921  LOC89944  3' TGAGCTGACTTTGTTCTTCC   93175     _   GGTA   TG
                                GGAA AGCA   GAGT  GCTTG
                                |||| ||||   ||||  |||||
                                CCTT TTGT   TTCA  CGAGT
                                  C   _____   GT
GAM921  LOC90170  3' CGGGATGAATTCATCTGCTTTT 62376         A    GG_
          T                      GGAAAGCAGGT GAGTT   CTTG
                                ||||||||||| |||||   ||||
                                TTTTTCGTCTA CTTAA   GGGC
                                      _    GTA
GAM921  LOC90233  3' TGAGTTGTGCTGTCAGCTTTCT 57199        A GT  AGT
          A                     TGGAAAGC G  AG   TGGCTTG
                                |||||||| |  ||   |||||||
                                ATCTTTCG C  TC   GTTGAGT
                                     A TG  GT_
GAM921  LOC90333  3' TGAGCCACTGTGCCTGGCCTGT 62967          _ A  _____
          TTTTT                    GGAAAGCAGGT AG GT    TGGCTTG
                                ||||||||||| || ||    |||||||
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                                TTTTTTGTCCG TC CG    ACCGAGT
                                      G  _  TGTC
GAM921  LOC90342  3'  TGGGCTGGCTACCAGTTCT   63018     AGCA  AG  TG
                                GGAA   GGT  AGT  GCTTG
                                ||||   |||  |||  |||||
                                TCTT   CCA  TCG  CGGGT
                                  GA__   __   GT
GAM921  LOC90459  3'  TAAGCCAATGAATTTCTGCTTT 63563          TAGA_
          TCA                     TGGAAAGCAGG    GTTGGCTTG
                                ||||||||||    |||||||||
                                ACTTTTCGTCT    TAACCGAAT
                                      TTAAG
GAM921  LOC90538  3'  GGGCCGAGTTTGTTTTTC    63898        GGTA  G
                                GGAAAGCA   GA TTGGCTT
                                ||||||||   || |||||||
                                CTTTTTGT   TT AGCCGGG
                                     _____  G
GAM921  LOC90538  3'  TAGGAGACTGGTTGCTTTCTA  63899         G AG   GG
                                TGGAAAGCAG T  AGTT  CTTG
                                |||||||||| |  ||||  ||||
                                ATCTTTCGTT G  TCAG  GGAT
                                      G __   A_
GAM921  LOC90550  3'  ACTCGACTCTATTTGTTTTT   73478             CTTG
                                GAAAGCAGGTAGAGTTGG
                                ||||||||||||||||||
                                TTTTTGTTTATCTCAGCT
                                          CAC
GAM921  LOC90693  5'  CAAGTCTGTTTGTTTGCTTCTT 57857     _    GG   GTT
          CA                     TGGA AAGCA  TAGA   GGCTTG
                                ||||  |||||  ||||   ||||||
                                ACTT TTCGT  GTTT   CTGAAC
                                  C    TT   GT_
GAM921  LOC90693  3'  AAGTTATTTGTTTGCTTTC   57856       GG   GT    G
                                GAAAGCA  TAGA  TGGCTT
                                |||||||  ||||  ||||||
                                CTTTCGT  GTTT  ATTGAA
                                    TT   __
GAM921  LOC90719  5'  GGGCCAACTCCGGCTTCT    64609     A  AGGTA
                                GGAA GC    GAGTTGGCTT
                                |||| ||    ||||||||||
                                TCTT CG    CTCAACCGGG
                                  _  GC___
GAM921  LOC90777  3'  CAAGCCAATATATATTTGTTTT 64664         GA_
                                AAAGCAGGTA   GTTGGCTTG
                                ||||||||||   |||||||||
                                TTTTGTTTAT   TAACCGAAC
                                      ATA
GAM921  LOC90777  3'  TAGGCTAGAATCTCCTGTTTTT 64669         T   G_
                                GAAAGCAGG AGA  TTGGCTTG
                                ||||||||| |||  ||||||||
```

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                                TTTTTGTCC TCT  GATCGGAT
                                      _  AA
GAM921  LOC90982  5' AGGCTTATGTCTCTTTCCA   65145       C  GT GAGTT
                                TGGAAAG AG  A    GGCTT
                                ||||||| ||  |    |||||
                                ACCTTTC TC  T    TCGGA
                                   _  TG AT___
GAM921  LOC91056  3' TGGGCCAGCTTTACGCCTCC  96412    AA  AG
                                GGA  GC  GTAGAGTTGGCTTG
                                |||  ||  ||||||||||||||
                                CCT  CG  CATTTCGACCGGGT
                                  C_  __
GAM921  LOC91115  3' CCTGTCAACTCTTTTTGTTTTT 65561         T       TTG
           T                     GGAAAGCAGG AGAGTTGGC
                                ||||||||||  |||||||||
                                TTTTTTGTTT TCTCAACTG
                                      T        TCCA
GAM921  LOC91147  3' CAGGTTAGTTTGCCATATTTTT 65688       CA_     G
           TA                    TGGAAAG   GGTAGA TTGGCTTG
                                |||||||   ||||||  ||||||||
                                ATTTTTT   CCGTTT GATTGGAC
                                    ATA     _
GAM921  LOC91170  5' CAGGTTAGCTTGCTTTCT    65731          A  G
                                GGAAAGCAGGT GA TTG
                                ||||||||||  || |||
                                TCTTTCGTTCG TT GAC
                                      A  G
GAM921  LOC91750  3' AATGTATATCTGTTTTTTA   67641           GA_
                                TGGAAAGCAGGTA   GTT
                                ||||||||||||   |||
                                ATTTTTTGTCTAT   TAA
                                      ATG
GAM921  LOC91947  3' TAGGCAAATGTATGCTTTTCA  68223        GGTAGA   G
                                TGGAAAGCA     GTT GCTTG
                                |||||||||     ||| |||||
                                ACTTTTCGT     TAA CGGAT
                                     ATG___   A
GAM921  LOC92231  3' TAGGTTAATTTATAGCTGTTT  69094       G  _
                                AAGCAG TA GAGTTGGCTTG
                                ||||||  ||  ||||||||||
                                TTTGTC AT TTTAATTGGAT
                                   G  A
GAM921  LOC92340  3' GTGGGCTCCTGGGTGTTTGCTT 69567     A    GG  _____    GGCTTG
           CCCA                    TGG AAGCA  TA    GAGTT
                                ||| |||||  ||    |||||
                                ACC TTCGT  GT    CTCGG
                                  C    TT  GGGTC    GT   GT
GAM921  LOC92391  3' AGGTCTGTTTTTTTGTTTTTC  69679         T   TT    G
                                GGAAAGCAGG AGAG  GGCTT
                                |||||||||  ||||  |||||
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                                CTTTTTGTTT TTTT  CTGGA
                                      _   GT
GAM921  LOC92497  3'  TAAGCTGCAAAACCTGTTTTCT 70098          AGA  T
          A                    TGGAAAGCAGGT   GT GGCTTG
                               ||||||||||||   || ||||||
                               ATCTTTTGTCCA   CG TCGAAT
                                     AAA  _
GAM921  LOC92597  3'  TAGGCTGATTTTGCAGGTCTTC 70513     AG AG      TG
                               GAA  C  GTAGAGT  GCTTG
                               |||  |  |||||||  |||||
                               CTT  G  CGTTTTA  CGGAT
                                 CT GA      GT
GAM921  LOC92755  3'  GCCTCTATCTTGTTTTTT    71024        _     GTT
                               GGAAAGCA GGTAGA   GGC
                               ||||||||| ||||||   |||
                               TTTTTTGT CTATCT   CCG
                                    T     ___
GAM921  LOC92935  3'  AGTGGCTTGTAGTTTTCTGCTT 71516          TA_________   TTGG
          TCTA                   TGGAAAGCAGG        GAG    CT
                               ||||||||||         |||    ||
                               ATCTTTCGTCT        TTC    GA
                                     TTTGAT   G   GGTT
GAM921  LOC93070  5'  CGGGTTGCGCTCTGCTTTTGC  71805     __      _
                               GCA  GGTAGAGT TGGCTTG
                               |||  |||||||| |||||||
                               CGT  TCGTCTCG GTTGGGC
                                 TT       C
GAM921  LOC93496  3'  CAAGCTAGTACTTGACTTTTTT 72861       C    A   __
          TCT                    GGAAAG AGGT GAGT  TGGCTTG
                               ||||||| |||| ||||  |||||||
                               TCTTTT TTCA TTCA  ATCGAAC
                                  T   G   TG
GAM922  BCAT1    3'  AGAAAACAAAGAGGCATACT   66782    C       AAT
                               AG ATGCCTCTT   TTTTCT
                               || |||||||||   ||||||
                               TC TACGGAGAA   AAAAGA
                                A        AC_
GAM922  ETF1     3'  AGAAAAATTAAATTGCTGC    17587     T  CTC
                               GCA GC   TTAATTTTTCT
                               ||| ||   ||||||||||||
                               CGT CG   AATTAAAAAGA
                                 _  TTA
GAM922  EXTL2    5'  AGAAGGATAGATGCACGCTA   9325      A   C   TA
                               TAGC TGC TCT  ATTTTTCT
                               |||| ||| |||  ||||||||
                               ATCG ACG AGA  TAGGAAGA
                                 C   T   __
GAM922  FOXE1    3'  AGAAAAATTAAGTTAGGGCA   16777      ___
                               TGCCT   CTTAATTTTTCT
                               |||||   ||||||||||||
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                                ACGGG  GAATTAAAAAGA
                                   ATT
GAM922  FZD3     3'  AGAAAAATGCTGGAACATGCT  34257      CC  TA_
                                AGCATG  TCT  ATTTTTCT
                                ||||||  |||  ||||||||
                                TCGTAC  AGG  TAAAAAGA
                                   A_  TCG
GAM922  RRM2B    3'  AAAAATTAAGAGTGTGTT    68429       C
                                AGCATGC TCTTAATTTTT
                                ||||||| ||||||||||
                                TTGTGTG AGAATTAAAAA
                                  _
GAM922  SYT4     3'  AAAGATTAAGATGCTA      63106      TGCC
                                TAGCA   TCTTAATTTTT
                                |||||   ||||||||||
                                ATCGT   AGAATTAGAAA
                                  ____
GAM922  ZNF132   3'  AGAAAAATTACCTCCATGCT  14286      CCTCT
                                AGCATG    TAATTTTTCT
                                ||||||    ||||||||||
                                TCGTAC    ATTAAAAAGA
                                   CTCC_
GAM922  BAP29    3'  AGAAAAATATAAGCATGTTA  61331       CTCTTA
                                TAGCATGC    ATTTTTCT
                                ||||||||    ||||||||
                                ATTGTACG    TAAAAAGA
                                     AATA__
GAM922  FAM8A1   3'  AGAAAAATCTGGCATACTG   33197    C    TCTTA
                                TAG ATGCC    ATTTTTCT
                                ||| |||||    ||||||||
                                GTC TACGG    TAAAAAGA
                                  A    TC___
GAM922  FLJ10648 3'  AGAAAAATTAGGTTCCATGC  36888     CCT
                                GCATG  CTTAATTTTTCT
                                |||||  ||||||||||||
                                CGTAC  GGATTAAAAAGA
                                   CTT
GAM922  FLJ10970 3'  AGAAAAATCAAGATAGGCCTG 37476   T  __   A
                                CA GCC  TCTT ATTTTTCT
                                || |||  |||| ||||||||
                                GT CGG  AGAA TAAAAAGA
                                 C  AT   C
GAM922  FLJ14735 3'  AAAAACTGATGAGGCATGC   52663       _  A
                                GCATGCCTC TTA TTTTT
                                ||||||||| ||| |||||
                                CGTACGGAG AGT AAAAA
                                     T  C
GAM922  KIAA0830 3'  AGAAAAATAGCGGAGGCA   70266       TA_
                                TGCCTCT  ATTTTTCT
                                |||||||  ||||||||
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                                ACGGAGG  TAAAAAGA
                                   CGA
GAM922  KIAA0907  3'  AGAAAAATTAAGCTGGGCA  30862     __
                                TGCCT  CTTAATTTTTCT
                                |||||  ||||||||||||
                                ACGGG  GAATTAAAAAGA
                                  TC
GAM922  KIAA1348  3'  AGAAACTTTGAGCCATGCTA  69116      CCT   TT
                                TAGCATG  CTTAA  TTTCT
                                |||||||  |||||  |||||
                                ATCGTAC  GAGTT  AAAGA
                                   C__   TC
GAM922  PIP3-E    3'  AAAAATGGGGCATGC     67336       TTA
                                GCATGCCTC  ATTTTT
                                |||||||||  ||||||
                                CGTACGGGG  TAAAAA
                                     ___
GAM922  PLAGL2    3'  AGAAATGAAAGGCATGC    70952       C  ATT
                                GCATGCCT TTA  TTTCT
                                |||||||| |||  |||||
                                CGTACGGA AGT  AAAGA
                                    A  ___
GAM922  RNF2      3'  AGAAAAATTAAATTGGTAGT  24256    A  TC_
                                GC TGCC  TTAATTTTTCT
                                || ||||  ||||||||||
                                TG ATGG  AATTAAAAAGA
                                 _  TTA
GAM922  LOC143146 3'  AGAAAATGGCCGAGGCATGCTA 60763         TTAAT
                                TAGCATGCCTC    TTTTCT
                                ||||||||||    ||||||
                                ATCGTACGGAG    AAAAGA
                                      CCGGT
GAM922  LOC146059 3'  AGAAAAGTCCAGAGATGC    78082     GC   TA
                                GCAT  CTCT  ATTTTTCT
                                ||||  ||||  ||||||||
                                CGTA  GAGA  TGAAAAGA
                                  __   CC
GAM922  LOC151391 3'  AGAAAGATCAAAGCATGC    86511      CTC  A
                                GCATGC  TT ATTTTTCT
                                ||||||  || ||||||||
                                CGTACG  AA TAGAAAGA
                                   A__  C
GAM922  LOC157507 5'  AAAGAAGAGGAGGCAACTA   82374    CA     AA
                                TAG  TGCCTCTT  TTTTT
                                |||  ||||||||  |||||
                                ATC  ACGGAGGA  AGAAA
                                 A_      GA
GAM922  LOC158434 3'  AAAAATTACAAGGCATGC    88156       CT
                                GCATGCCT  TAATTTTT
                                ||||||||  ||||||||
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                                CGTACGGA  ATTAAAAA
                                     AC
GAM922  LOC220020 5'  AGAAAACAGGTGAAGGCATGC  95043        _ TTAAT
                                GCATGCCT C     TTTTCT
                                |||||||| |     ||||||
                                CGTACGGA G     AAAAGA
                                     A TGGAC
GAM922  LOC221979 3'  AGAGTGCAGAAGGCATGC    94216        _ TA
                                GCATGCCT CT  ATTTT
                                |||||||| ||  |||||
                                CGTACGGA GA  TGAGA
                                     A  CG
GAM922  LOC92078  3'  AGAAATCCGAAGAGGCAGCTA  68588     A       AATT
                                TAGC TGCCTCTT    TTTCT
                                |||| ||||||||    |||||
                                ATCG ACGGAGAA    AAAGA
                                  _       GCCT
GAM922  LOC92080  5'  AGAAAAATCAAGACCATGTTA  68617       CC    A
                                TAGCATG  TCTT ATTTTTCT
                                |||||||  |||| ||||||||
                                ATTGTAC  AGAA TAAAAAGA
                                     C_   C
GAM923  SCAMP1    3'  GCTAAATAAATATTCTCC    54500     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM923  SCAMP1    3'  GCTAAATAAATATTCTCC    54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM923  NX-17     3'  TGAATATCAGCCCCTAATA   40706        ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                     CGAC
GAM923  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
           TA                    TATTAGGGATAATATTCATTTAGC
                                |||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM924  SCAMP1    3'  GCTAAATAAATATTCTCC    18013     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM924  SCAMP1    3'  GCTAAATAAATATTCTCC    54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
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                                CCT TTATAA TAAATCG
                                  C     A
GAM924  NX-17    3'  TGAATATCAGCCCCTAATA   40706        ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM924  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
          TA                     TATTAGGGATAATATTCATTTAGC
                                 ||||||||||||||||||||||||
                                 ATAATCCCTATTATAAGTAAATCG

GAM925  APAF1    3'  GAGACTGCAGGCACGAGCC   8588       __
                                GGTTC  GCCTGCAGTCTC
                                |||||  ||||||||||||
                                CCGAG  CGGACGTCAGAG
                                   CA
GAM925  APAF1    3'  GAGACTGCAGGCACGAGCC   25974      __
                                GGTTC  GCCTGCAGTCTC
                                |||||  ||||||||||||
                                CCGAG  CGGACGTCAGAG
                                   CA
GAM925  DSCR3    3'  GAGACTACAGGTGAGTGCC   21315    __     C
                                GGT  TCGCCTG AGTCTC
                                |||  ||||||| ||||||
                                CCG  AGTGGAC TCAGAG
                                  TG      A
GAM925  GP1BB    3'  GAGGGAGGCGAACCCGCAC   6394     AA       GCAG
                                GTG  GGTTCGCCT   TCTC
                                |||  |||||||||   ||||
                                CAC  CCAAGCGGA   GGAG
                                  GC       G___
GAM925  HTR1E    5'  ATTACAGGCGAACCTTCAC   7858            C
                                GTGAAGGTTCGCCTG AGT
                                |||||||||||||| |||
                                CACTTCCAAGCGGAC TTA
                                          A
GAM925  LIG3     3'  GAGACTGCAGGGACTCAC    11316     AGGT  G
                                GTGA   TC CCTGCAGTCTC
                                ||||   || ||||||||||||
                                CACT   AG GGACGTCAGAG
                                  C___  _
GAM925  OAS2     3'  AGACTGCAAACCCTTTCAT   34148       TTCGCC
                                GTGAAGG    TGCAGTCT
                                |||||||    ||||||||
                                TACTTTC    ACGTCAGA
                                    CCAA__
GAM925  PIAS3    3'  GGGCCAGACAGACCTTCAC   21447        CGC   CA
                                GTGAAGGTT   CTG  GTCT
                                |||||||||   |||  ||||
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                                CACTTCCAG   GAC  CGGG
                                     ACA  __
GAM925  PTPRE    5' AGACTATAGCCTTCAC     22486       TTCGC   C
                                GTGAAGG    CTG AGTCT
                                |||||||    ||| |||||
                                CACTTCC    GAT TCAGA
                                   _____  A
GAM925  SLC1A4   3' GAGACTGCAGGTGCCGCAC   13171    AA   TC
                                GTG  GGT  GCCTGCAGTCTC
                                |||  |||  ||||||||||||
                                CAC  CCG  TGGACGTCAGAG
                                  G_  __
GAM925  SYNGR1   3' AGAGGCAGGCGATCCCTCAC  17494     A  T      AG
                                GTGA GG TCGCCTGC  TCT
                                |||| || ||||||||  |||
                                CACT CC AGCGGACG  AGA
                                  C  T      G_
GAM925  ARSDR1   3' AGACTGCAGCAGACTACAC   32622    AA   TC  C
                                GTG  GGT  GC TGCAGTCT
                                |||  |||  || ||||||||
                                CAC  TCA  CG ACGTCAGA
                                  A_   GA  _
GAM925  C21orf41 3' GAGACTGCAGCAGCCCCAGC  57171    GAA    C  C
                                GT   GGTT GC TGCAGTCTC
                                ||   |||| || |||||||||
                                CG   CCGA CG ACGTCAGAG
                                 ACC   _ _
GAM925  DKFZP727M111 5' AGACTGCAGGCCATGGCTCC  32053   A    C__
                                A GGTT   GCCTGCAGTCT
                                | ||||   ||||||||||
                                C TCGG   CGGACGTCAGA
                                 C    TAC
GAM925  FLJ10486 3' ACTGATTTGAAACTTTCAC   36660         _  CCTG
                                GTGAAGGTT CG    CAGT
                                ||||||||| ||    ||||
                                CACTTTCAA GT    GTCA
                                     A  TTA_
GAM925  FLJ10619 3' GAATGGAGCAACCTTCAC    36862         C  C G  G
                                GTGAAGGTT GC T CA TC
                                ||||||||| || | || ||
                                CACTTCCAA CG A GT AG
                                     _ _ G  A
GAM925  FLJ12587 3' ACTGCAGGGGGGCCTCA     42772     A     G
                                TGA GGTTC CCTGCAGT
                                ||| ||||| ||||||||
                                ACT CCGGG GGACGTCA
                                  _    G
GAM925  FLJ13263 3' GAGACTGCAGAGTGCCTTC   47813       TC  _
                                GAAGGT  GC CTGCAGTCTC
                                ||||||  || ||||||||||
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                                CTTCCG  TG GACGTCAGAG
                                   __ A
GAM925  GPA33    3'  AGACCAGGCTGCAGCCTCCAC  20567     A    _ _    CA
                                GTG AGGTT C GCCTG  GTCT
                                ||| ||||| | |||||  ||||
                                CAC TCCGA G CGGAC  CAGA
                                  C    C T    __
GAM925  KIAA1190  3'  GAGACTGCAGACCAGTGCTTCA 71648      GTT  ____
                                TGAAG   CGC   CTGCAGTCTC
                                ||||||  |||   ||||||||||
                                ACTTC   GTG   GACGTCAGAG
                                   ___  ACCA
GAM925  KIAA1416  3'  AGACTGCAGAGTCCTCCCTC   87755    A  TTC  _
                                GA GG   GC CTGCAGTCT
                                || ||   || |||||||||
                                CT CC   TG GACGTCAGA
                                 C  TCC  A
GAM925  KIAA1853  3'  GAGACTGCCATGCAACCACCAC 69922     AA    C  CT_
                                GTG  GGTT GC   GCAGTCTC
                                |||  |||| ||   ||||||||
                                CAC  CCAA CG   CGTCAGAG
                                  CA   _  TAC
GAM925  MGC13138  3'  GAGACTACAGGCGGGCAACAC  54158     AAG       C
                                GTG   GTTCGCCTG AGTCTC
                                |||   ||||||||| ||||||
                                CAC   CGGGCGGAC TCAGAG
                                  AA_       A
GAM925  PPP2R3A   3'  GAGCCTAGAAGAAACCTTCAC  12243         _ GC  GC  T
                                GTGAAGGTT C  CT  AG CTC
                                ||||||||| |  ||  || |||
                                CACTTCCAA G  GA  TC GAG
                                     A AA  __  C
GAM925  RHOBTB2   3'  GAGACTGCAGGCTCCCTTC   61600      TTC
                                GAAGG   GCCTGCAGTCTC
                                |||||   ||||||||||||
                                CTTCC   CGGACGTCAGAG
                                   CT_
GAM925  ZNF304    5'  AGACTGCAGGACCTTCCTTCGC 40678       TTCG_
                                GTGAAGG    CCTGCAGTCT
                                |||||||    ||||||||||
                                CGCTTCC    GGACGTCAGA
                                    TTCCA
GAM925  LOC152245 3'  ACTGCAGGATCTCAT      86774     A   TCG
                                GTGA GGT   CCTGCAGT
                                |||| |||   ||||||||
                                TACT CTA   GGACGTCA
                                  _  ___
GAM925  LOC158177 5'  AGACTGGAAACCTTCA     82688        CG  TGC
                                TGAAGGTT  CC   AGTCT
                                ||||||||  ||   |||||
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                                ACTTCCAA  GG   TCAGA
                                    A_ ___
GAM925  LOC159765 5'  GAGACCTCGGAACCTTCA    83075        GCC  CA
                                TGAAGGTTC   TG  GTCTC
                                |||||||||   ||  |||||
                                ACTTCCAAG   GC  CAGAG
                                    ___  TC
GAM925  LOC201771 5'  AGGCTGCAAAGAACCTTCAC   70516         GCC
                                GTGAAGGTTC   TGCAGTCT
                                ||||||||||   ||||||||
                                CACTTCCAAG   ACGTCGGA
                                     AA_
GAM925  LOC219401 3'  AGGCTCAGAAACCTTCAC    94383        CGC   C
                                GTGAAGGTT   CTG AGTCT
                                |||||||||   ||| |||||
                                CACTTCCAA   GAC TCGGA
                                    A__  _
GAM925  LOC219401 3'  GAATGTGAGAAAACCTTCAC   94386        CGC  _   G
                                GTGAAGGTT   CT GCA TC
                                |||||||||   || ||| ||
                                CACTTCCAA   GA TGT AG
                                    AA_  G   A
GAM925  LOC245726 3'  AGACTGCAGTTTCTTCAC    74584       TTCGC
                                GTGAAGG    CTGCAGTCT
                                |||||||    |||||||||
                                CACTTCT    GACGTCAGA
                                   TT___
GAM925  LOC90591  3'  GAATGTGGCAAAGCCTTCAC   64168        C_   T   G
                                GTGAAGGTT  GCC GCA TC
                                |||||||||  ||| ||| ||
                                CACTTCCGA  CGG TGT AG
                                    AA   _   A
GAM926  HRH1      3'  TCCCTTCTCAGAAAACTTCT   7829     C   C       C
                                AG AGTT TCTGAGGAG GA
                                || |||| ||||||||| ||
                                TC TCAA AGACTCTTC CT
                                 T   A       C
GAM926  MEA       3'  CTTCTCAGAGACCCACTTT   28275     CAGT
                                AAAG   TCTCTGAGGAG
                                ||||   ||||||||||
                                TTTC   AGAGACTCTTC
                                  ACCC
GAM926  NEDD4     3'  CTCACAGAAAAACTGTTT    70545        C_   AG
                                AAGCAGTT  TCTG  GAG
                                ||||||||  ||||  |||
                                TTTGTCAA  AGAC  CTC
                                    AA   A_
GAM926  PCDH9     5'  TTCCAGAGAATGCTCC     83698   A   G     A
                                A AGCA TTCTCTG GGA
                                | |||| ||||||| |||
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                                C TCGT AAGAGAC CTT
                                 C   _     _
GAM926  UBE4A    3'  CTAAATTAGAGAACTGCT    17732          GG_
                                AGCAGTTCTCTGA  AG
                                |||||||||||||  ||
                                TCGTCAAGAGATT  TC
                                       AAA
GAM926  BRD2     5'  GCCCCAAAGAGACTGCTTT   18794       T   GA  A
                                AAAGCAGT CTCT  GG GC
                                |||||||| ||||  || ||
                                TTTCGTCA GAGA  CC CG
                                     _   AA  C
GAM926  BRI3     3'  CTCAATAAAGCACTGCTTT   31794       T  C  AG
                                AAAGCAGT CT TG  GAG
                                |||||||| || ||  |||
                                TTTCGTCA GA AT  CTC
                                     C  A  AA
GAM926  FLJ20151 3'  TCACTCCTTGGACTTGCTCC  35147   A    TTC  TG    C
                                A AGCAG   TC  AGGAG GA
                                | |||||   ||  ||||| ||
                                C TCGTT   AG  TCCTC CT
                                 C    C__  GT    A
GAM926  FLJ20507 3'  CGCCCCCAGGCCACCTGCTCC  35736   A    TTC_   A  A
                                A AGCAG    TCTG GG GCG
                                | |||||    |||| || |||
                                C TCGTC    GGAC CC CGC
                                 C    CACC   _  C
GAM926  FLJ20507 3'  CGCCCCCAGGCCACCTGCTCC  60842   A    TTC_   A  A
                                A AGCAG    TCTG GG GCG
                                | |||||    |||| || |||
                                C TCGTC    GGAC CC CGC
                                 C    CACC   _  C
GAM926  HDAC11   3'  CGCCCCTTAGTGCTTT     46137      GTTCT     A
                                AAAGCA    CTGAGG GCG
                                ||||||    |||||| |||
                                TTTCGT    GATTCC CGC
                                    _____     C
GAM926  HSRNAFEV 3'  TTCCCCAAGGAACTGCTCC   34455   A      TC  A
                                A AGCAGTTC  TG GGAG
                                | ||||||||  || ||||
                                C TCGTCAAG  AC CCTT
                                 C       GA  C
GAM926  KIAA0022 3'  TCCAGAATGTAGAAACTGCTTT 30287         C   A_____
                                AAAGCAGTT TCTG     GGA
                                ||||||||| ||||     |||
                                TTTCGTCAA AGAT     CCT
                                     _   GTAAGA
GAM926  KIAA1054 3'  TTCAGGGAAAGAAAGCTGCTT  68975       _______
                                AAGCAGT     TCTCTGAG
                                |||||||     ||||||||
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                                TTCGTCG     AGGGACTT
                                    AAAGAA
GAM926  KIAA1536  3'  ATTCTGTTCCCTAAGAACTGCT 40875          C  A    _
            T                    AAGCAGTTCT TG GGAGC GAAT
                                 |||||||||| || ||||| ||||
                                 TTCGTCAAGA AT CCTTG CTTA
                                       _ C    T
GAM926  KIAA1615  3'  TCCAAATGAAGAGAACTCTTT  69287     C      GA____
                                 AAAG AGTTCTCT     GGA
                                 |||| ||||||||     |||
                                 TTTC TCAAGAGA     CCT
                                   _      AGTAAA
GAM926  KIAA1813  5'  ATTCACTCCTCAGCCCTGTT   70822      TTCT      C
                                 AGCAG    CTGAGGAG GAAT
                                 |||||    |||||||| ||||
                                 TTGTC    GACTCCTC CTTA
                                    CC__       A
GAM926  RHOBTB2   3'  GCAGCCCAGAGAACTCTCC    61602    A  C       A  A_
                                 A AG AGTTCTCTG GG  GC
                                 | || |||||||||  ||  ||
                                 C TC TCAAGAGAC CC  CG
                                  C  _        _  GA
GAM926  SERHL     3'  CCTCAAAGAGGACTACTT    97350     C       __
                                 AAG AGTTCTCT  GAGG
                                 ||| ||||||||  ||||
                                 TTC TCAGGAGA  CTCC
                                   A       AA
GAM926  LOC151318 3'  TGCCCTGAAAACTGCTTT    81031          C  TG   A
                                 AAAGCAGTT TC  AGG GCG
                                 |||||||||  ||  ||| |||
                                 TTTCGTCAA AG  TCC CGT
                                       A  __   _
GAM926  LOC158014 5'  TCTCAGAGCAACTGCTTT    82569          _
                                 AAAGCAGTT CTCTGAGG
                                 |||||||||  ||||||||
                                 TTTCGTCAA GAGACTCT
                                       C
GAM926  LOC158376 3'  ATTCTGAAACCAAAGAGCTGCT 88134          C  AGGAGC
            T                    AAGCAGTTCT TG      GAAT
                                 ||||||||||  ||      ||||
                                 TTCGTCGAGA AC      CTTA
                                       A  CAAAGT
GAM926  LOC158428 3'  ATTCTTTGCCCAGAGAGCTGC  71081          A  AGC_
                                 GCAGTTCTCTG GG    GAAT
                                 ||||||||||| ||    ||||
                                 CGTCGAGAGAC CC    CTTA
                                       _  GTTT
GAM926  LOC220431 5'  ATTCACCTCTTCAGAGACCACT 95993     CA  T        C_
            T                    AAG  GT CTCTGAGGAG  GAAT
                                 |||  || ||||||||||  ||||
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                                TTC  CA GAGACTTCTC  CTTA
                                  AC  _        CA
GAM927  ABL2     5'  TGTGAGTCGCCTGGAGGCAG  24611           A_
                                CTGCCTCCAGGTGAC  GCA
                                |||||||||||||||  |||
                                GACGGAGGTCCGCTG  TGT
                                       AG
GAM927  DYRK1B   3'  TGATTGGGGCCTGGGGCAG   17517      T    GACAG
                                CTGCC CCAGGT    CAATCA
                                ||||| ||||||    ||||||
                                GACGG GGTCCG    GTTAGT
                                   _    GG___
GAM927  GNAZ     3'  CTGCACCCCTGTCACCTGGAGG 10827           CAAT_
                                CCTCCAGGTGACAG    CAG
                                ||||||||||||||    |||
                                GGAGGTCCACTGTC    GTC
                                       CCCAC
GAM927  GYPC     3'  GATAGCCACCTGGAAACA    10900    CC      ACA  A
                                TG  TCCAGGTG   GC ATC
                                ||  ||||||||   || |||
                                AC  AGGTCCAC   CG TAG
                                 AA       ___  A
GAM927  GYPC     3'  GATAGCCACCTGGAAACA    34143    CC      ACA  A
                                TG  TCCAGGTG   GC ATC
                                ||  ||||||||   || |||
                                AC  AGGTCCAC   CG TAG
                                 AA       ___  A
GAM927  IL1R1    3'  TGAGGTCACCTGGAATCAG   7928     CC       AG
                                CTG  TCCAGGTGAC  CA
                                |||  ||||||||||  ||
                                GAC  AGGTCCACTG  GT
                                  TA        GA
GAM927  SLC21A9  3'  TGTGTCACCTGGGGCAG     24384      T       G
                                CTGCC CCAGGTGACA CA
                                ||||| |||||||||| ||
                                GACGG GGTCCACTGT GT
                                   _       _
GAM927  ZNF138   5'  CTGATTACCTGTCTGGA     82099     GGT    C_
                                TCCA   GACAG  AATCAG
                                ||||   |||||  ||||||
                                AGGT   CTGTC  TTAGTC
                                   ___     CA
GAM927  C8orf13  3'  GTGGGTCTCCCGGAGGCAG   82482        A  T   A_
                                CTGCCTCC GG GAC  GC
                                |||||||| || |||  ||
                                GACGGAGG CC CTG  TG
                                     C  T   GG
GAM927  CHST3    3'  TGTGGTCCCTGGAGGCA     16246          T   A
                                TGCCTCCAGG GAC GCA
                                |||||||||| ||| |||
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                                ACGGAGGTCC CTG TGT
                                      _  G
GAM927  CMG1     5'  TGCAATGCCACCTGGGACAG  47728     C T      A __
                                CTG C CCAGGTG CA  GCA
                                ||| | ||||||| ||  |||
                                GAC G GGTCCAC GT  CGT
                                  A _      C  AA
GAM927  DKFZP434H132 3'  GATGGGCCCTGGAGGCAG    31932          TGACA  A_
                                CTGCCTCCAGG    GC  ATC
                                ||||||||||    ||  |||
                                GACGGAGGTCC    CG  TAG
                                      _____ GG
GAM927  FLJ10036  3'  CTGATTGCCCTTATGGAG    96627      GG   CA
                                CTCCA  TGA  GCAATCAG
                                |||||  |||  ||||||||
                                GAGGT  ATT  CGTTAGTC
                                  __  CC
GAM927  FLJ11053  3'  CTGACTATCTACCTGGAGATAG 90123     C       _  C  CAA
                                CTG CTCCAGGT GA AG   TCAG
                                ||| ||||||| || ||   ||||
                                GAT GAGGTCCA CT TC   AGTC
                                  A       T  A  ___
GAM927  FLJ11767  3'  CTGATTGTAAGCACCTGAAGGC 45059       C      ACA
          A                      TGCCT CAGGTG   GCAATCAG
                                |||||  ||||||   ||||||||
                                ACGGA GTCCAC   TGTTAGTC
                                  A     GAA
GAM927  FLJ12691  3'  CTGATTGGTATCTGGAGACAG  45001     C        ACAG
                                CTG CTCCAGGTG    CAATCAG
                                ||| |||||||||    |||||||
                                GAC GAGGTCTAT    GTTAGTC
                                  A       G___
GAM927  GALNT6    3'  CTGATCACCAGCTTCTCTGGAG 24247          T  C   A____
          GC                      GCCTCCAGG GA AGC     ATCAG
                                |||||||||  ||  |||     |||||
                                CGGAGGTCT CT TCG     TAGTC
                                      _  _   ACCAC
GAM927  H-plk     5'  CTGATTACCTGTCTGGAGCA   32381     C    GGT     C_
                                TGC TCCA   GACAG  AATCAG
                                |||  ||||   |||||  ||||||
                                ACG AGGT   CTGTC  TTAGTC
                                  _    ___     CA
GAM927  KIAA0781  3'  GCCACCGTGGAGGCAG      68058          _    ACA
                                CTGCCTCCA GGTG   GC
                                |||||||||  ||||   ||
                                GACGGAGGT CCAC   CG
                                      G   ___
GAM927  KIAA0971  3'  CTGATTACTGTCATTACTAGAG 30670     C  __      C
                                CTC AG  GTGACAG AATCAG
                                |||  ||  |||||||  ||||||
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                                GAG TC  TACTGTC TTAGTC
                                  A AT      A
GAM927  KIAA1344  3' CTGATTATTACCTGGATACA  72866    CC       CAGC
                                TG  TCCAGGTGA   AATCAG
                                ||  |||||||||   ||||||
                                AC  AGGTCCATT   TTAGTC
                                 AT       A___
GAM927  MADCAM1   3' CTGATTGCCTCTTTGGAG   56238       T  CA
                                CTCCAGG GA  GCAATCAG
                                |||||||  ||  ||||||||
                                GAGGTTT CT  CGTTAGTC
                                    _  C_
GAM927  MADCAM1   3' CTGATTGCCTCTTTGGAG   56241       T  CA
                                CTCCAGG GA  GCAATCAG
                                |||||||  ||  ||||||||
                                GAGGTTT CT  CGTTAGTC
                                    _  C_
GAM927  MADCAM1   3' CTGATTGCCTCTTTGGAG   56244       T  CA
                                CTCCAGG GA  GCAATCAG
                                |||||||  ||  ||||||||
                                GAGGTTT CT  CGTTAGTC
                                    _  C_
GAM927  MGC10870  5' CTGACCATGTCACCTGGAGGC  51178           GCAA
                                GCCTCCAGGTGACA   TCAG
                                ||||||||||||||   ||||
                                CGGAGGTCCACTGT   AGTC
                                       ACC_
GAM927  MGC10924  3' CTGTATGAACACCTGGAAGCA  48311    C      _____
                                TGC TCCAGGTG    ACAG
                                |||  ||||||||    ||||
                                ACG AGGTCCAC    TGTC
                                  A       AAGTA
GAM927  MGC14436  5' CTGACCACCTGGAGACAG   52926    C       A_
                                CTG CTCCAGGTG  CAG
                                |||  |||||||||  |||
                                GAC GAGGTCCAC  GTC
                                  A       CA
GAM927  SYT12     3' TGATCGCTGTGGGGGCAG   96390       AGGTG    A
                                CTGCCTCC    ACAGC ATCA
                                ||||||||    ||||| ||||
                                GACGGGGG    TGTCG TAGT
                                    _____    C
GAM927  TReP-132  3' TGTGTGTCACTTAGAGACAG  54274    C  C     _
                                CTG CTC AGGTGACA GCA
                                |||  |||  |||||||| |||
                                GAC GAG TTCACTGT TGT
                                  A  A       G
GAM927  TReP-132  3' TGTGTGTCACTTAGAGACAG  54276    C  C     _
                                CTG CTC AGGTGACA GCA
                                |||  |||  |||||||| |||
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                                GAC GAG TTCACTGT TGT
                                  A  A      G
GAM927  TReP-132  3'  TGTGTGTCACTTAGAGACAG  37915    C  C     _
                                CTG CTC AGGTGACA GCA
                                ||| ||| |||||||| |||
                                GAC GAG TTCACTGT TGT
                                  A  A      G
GAM927  ZFD25     5'  CTGATCACCTGTCTGGAGCA  33109    C   GGT   CA_
                                TGC TCCA  GACAG  ATCAG
                                ||| ||||  |||||  |||||
                                ACG AGGT  CTGTC  TAGTC
                                  _  ___    CAC
GAM927  ZNF177    3'  CTGTTATGGTCACCTGGAAACA 14356    CC       AGCAAT
           G                     CTG  TCCAGGTGAC    CAG
                                ||| ||||||||||     |||
                                GAC  AGGTCCACTG    GTC
                                  AA        GTATT_
GAM927  ZNF90     5'  CTGATCACCTGTCTGGAGCA  79467    C   GGT   CA_
                                TGC TCCA  GACAG  ATCAG
                                ||| ||||  |||||  |||||
                                ACG AGGT  CTGTC  TAGTC
                                  _  ___    CAC
GAM927  LOC149606 3'  CTGAAGCACCACTGGAGGCA  80261        G  ACA  AA
                                TGCCTCCAG TG  GC  TCAG
                                ||||||||| ||  ||  ||||
                                ACGGAGGTC AC  CG  AGTC
                                     _ CA_ A_
GAM927  LOC157663 3'  CTGAAAGTACTGTCATCTAAAA 82450    CTCC      CAA__
           GCA                   TGC   AGGTGACAG   TCAG
                                |||   |||||||||   ||||
                                ACG   TCTACTGTC   AGTC
                                  AAAA       ATGAA
GAM927  LOC196527 3'  TGATTGTACTAGAGACAG   89102    C  CA  GACA
                                CTG CTC  GGT   GCAATCA
                                ||| |||  |||   |||||||
                                GAC GAG  TCA   TGTTAGT
                                  A  A_  _____
GAM927  LOC221025 5'  CTGGCCACCTGGAGACAG   94785    C      A_
                                CTG CTCCAGGTG  CAG
                                ||| |||||||||  |||
                                GAC GAGGTCCAC  GTC
                                  A       CG
GAM927  LOC253943 3'  CTGATTGCTATCATGAAGTA  97845    C  CAG   C
                                TGC TC  GTGA AGCAATCAG
                                ||| ||  |||| |||||||||
                                ATG AG  TACT TCGTTAGTC
                                  A  ___   A
GAM927  LOC255180 3'  GATCACTGTCATCTAAAAGCAG 96732     CTCC      CA
                                CTGC   AGGTGACAG  ATC
                                ||||   |||||||||  |||
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                                GACG   TCTACTGTC  TAG
                                  AAAA       AC
GAM927  LOC256416 3'  CTGTCCACCTGGGGACAG    96059     C       _
                                CTG CTCCAGGTG ACAG
                                ||| ||||||||| ||||
                                GAC GGGGTCCAC TGTC
                                  A       C
GAM927  LOC51673  3'  CTGTCCACCTGGGGACAG    96207     C       _
                                CTG CTCCAGGTG ACAG
                                ||| ||||||||| ||||
                                GAC GGGGTCCAC TGTC
                                  A       C
GAM928  B3GALT1   3'  GTCTTTGCAGTTCCAC      40942       C  CC
                                GTGGA AT  GCAAAGAC
                                ||||| ||  ||||||||
                                CACCT TG  CGTTTCTG
                                  _ A_
GAM928  D2S448    3'  CGGCCCTGGTTGCGTCCACGTC 73889         ATCC   __ A_
                                GACGTGGAC   GCAA  AG  CCG
                                |||||||||   ||||  ||  |||
                                CTGCACCTG   CGTT  TC  GGC
                                     ____   GG  CC
GAM928  HSA250839 3'  TCCTTGGGGCTGTCCATGTCA  37854          T  G   A
                                TGACGTGGACA CC CAA GA
                                |||||||||||| || ||| ||
                                ACTGTACCTGT GG GTT CT
                                      C  G   C
GAM928  MGC4504   5'  CGGTCTTTCCGTGCCCACGCCG 44356    A    A  TC  C
                                TG CGTGG CA  CG AAAGACCG
                                || ||||| ||  || ||||||||
                                GC GCACC GT  GC TTTCTGGC
                                 C    C  __  C
GAM928  TRAF3     5'  CGGCCTTCGGTCTCCATGTCA  60452         CAT   CA   A
                                TGACGTGGA   CCG  AAG CCG
                                |||||||||   |||  ||| |||
                                ACTGTACCT   GGC  TTC GGC
                                     CT_   __   C
GAM928  LOC127540 5'  GTCTCTCCTGTCCACGTTA   75173          TCCGCAA
                                TGACGTGGACA      AGAC
                                ||||||||||       ||||
                                ATTGCACCTGT      TCTG
                                      CCTC___
GAM928  LOC220776 3'  CTTTGCTTTCTGTCCATGTCA  68929          TCC_
                                TGACGTGGACA    GCAAAG
                                ||||||||||    ||||||
                                ACTGTACCTGT    CGTTTC
                                      CTTT
GAM928  LOC221715 5'  GTCTTTGCGGATGACCATG    95395       A
                                CGTGG CATCCGCAAAGAC
                                ||||| ||||||||||||
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                                GTACC GTAGGCGTTTCTG
                                   A
GAM929  DLEC1    3'  CATCTGGCCCTCCCTTG     24716      A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                   C    G  _
GAM929  DLEC1    3'  CATCTGGCCCTCCCTTG     24728      A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                   C    G  _
GAM929  PIP5K1A  3'  TATCCCACCCTGCCTTGATA  14520        A   CA  C
                                TATCAAGG AGGG  GG GTG
                                |||||||| ||||  || |||
                                ATAGTTCC TCCC  CC TAT
                                     G   A_  C
GAM929  SOX11    3'  ACCCACCCCCCCTTGGTA    13308        AA   CA  C
                                TATCAAGG  GGG  GG GT
                                ||||||||  |||  || ||
                                ATGGTTCC  CCC  CC CA
                                     CC   A_  _
GAM929  CHL1     3'  TGTTACCTTTCCTCAATA    22768     CA      CA
                                TAT  AGGAAGGG  GGCG
                                |||  ||||||||  ||||
                                ATA  TCCTTTCC  TTGT
                                  AC       A_
GAM929  EPB41L1  3'  CATTCTGCCCTTCCCTGA    71104     A        C
                                TCA GGAAGGGCAGG GTG
                                ||| |||||||||| |||
                                AGT CCTTCCCGTCT TAC
                                  C         _
GAM929  FLJ00060 3'  CATACCCCCTGCCCTCCTCTGA 61741     _   A      CGTG
                                TCA AGGA GGGCAGG    ATG
                                ||| |||| |||||||    |||
                                AGT TCCT CCCGTCC    TAC
                                  C    _      CCCA
GAM929  FLJ10898 5'  CACCACAGCCCTTTCTCAATA  60126     CA       AGGC
                                TAT  AGGAAGGGC    GTG
                                |||  |||||||||    |||
                                ATA  TCTTTCCCG    CAC
                                  AC        ACAC
GAM929  FLJ22557 3'  ATCATCCCATCCTTAATA    45581     C    A   CAGGC
                                TAT AAGGA GGG     GTGAT
                                ||| ||||| |||     |||||
                                ATA TTCCT CCC     TACTA
                                  A    A  _____
GAM929  KIAA0574 3'  CATCCCCTGCCCTCCCCTGA   69808     A  A      CGT
                                TCA GG AGGGCAGG   GATG
                                ||| || ||||||||   ||||
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                                AGT CC TCCCGTCC   CTAC
                                  C  C       C__
GAM929  KIAA0632  3'  CACCTCAGAAACCCTTCCTTGA 32071          CA___  C
                                TCAAGGAAGGG    GG GTG
                                ||||||||||    || |||
                                AGTTCCTTCCC    CT CAC
                                     AAAGA  C
GAM929  KIAA1045  3'  CATCACATGTCCTTCC      71599         GGC
                                GGAAGGGCA   GTGATG
                                |||||||||   ||||||
                                CCTTCCTGT   CACTAC
                                     A__
GAM929  KIAA1354  5'  CAGTGACTGCCTTCCCTTGATA 61572        A      G  _
                                TATCAAGG AGGGCAG CG TG
                                |||||||| ||||||| || ||
                                ATAGTTCC TTCCGTC GT AC
                                     C      A  G
GAM929  MGC20460  5'  CACCGCCTCCTACCCTTCTT   54901        C___    _
                                AGGAAGGG    AGGCG TG
                                ||||||||    ||||| ||
                                TTCTTCCC    TCCGC AC
                                     ATCC     C
GAM929  LOC158476 3'  CACGCCCGCCCCCCCCATTGA  88186      _  AA_    A
                                TCAA GG   GGGC GGCGTG
                                |||| ||   |||| ||||||
                                AGTT CC   CCCG CCGCAC
                                  A  CCC    C
GAM929  LOC90459  3'  CACACCCGCCTAATTTTTG    63550       A_    A  C
                                CAAGGA  GGGC GG GTG
                                ||||||  |||| || |||
                                GTTTTT  TCCG CC CAC
                                   AA    C  A
GAM930  BCL7A     3'  GAGCCGCTGCCCCCCACCCA   40983      ATA  AT
                                TGGG   GG  TGGCGGCTC
                                ||||   ||  |||||||||
                                ACCC   CC  GTCGCCGAG
                                  ACC  CC
GAM930  DDX11     3'  GAGCCGCCTTGCCATCCC     48388      A  ATT
                                GGGAT GG   GGCGGCTC
                                |||||| ||   ||||||||
                                CCCTA CC   CCGCCGAG
                                  _  GTT
GAM930  ENG       3'  GAGCCACCTGGATCTATCCC   5497         ATT_  C
                                GGGATAGG    GG GGCTC
                                ||||||||    || |||||
                                CCCTATCT    CC CCGAG
                                     AGGT  A
GAM930  FACL6     3'  GAGCCTTTTCCTGTCCCA     31578          TTGGC
                                TGGGATAGGA    GGCTC
                                ||||||||||    |||||
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                                ACCCTGTCCT    CCGAG
                                      TTT__
GAM930  FOXG1B   3'  GAGCCGCCAGATTTCCA    19133     TAGGA
                                TGGGA    TTGGCGGCTC
                                |||||    ||||||||||
                                ACCTT    GACCGCCGAG
                                   TA___
GAM930  GAGED2   5'  GAACCACACAGCCAGTCCCA  56755      A  A   GC_  C
                                TGGGAT GG TTG   GG TC
                                |||||| || |||   || ||
                                ACCCTG CC GAC   CC AG
                                   A  _   ACA  A
GAM930  HD       3'  GAGCCGCCACTCCTATCCC   10916       T
                                GGGATAGGA TGGCGGCTC
                                ||||||||| |||||||||
                                CCCTATCCT ACCGCCGAG
                                      C
GAM930  LMO4     5'  GAGCCGCCGCTGCCATCCC   23183     A  AT_
                                GGGAT GG   TGGCGGCTC
                                ||||| ||   |||||||||
                                CCCTA CC   GCCGCCGAG
                                   _  GTC
GAM930  MAP1A    3'  GAGCCGCCCTCCCTTCCC    11440     TA   TT
                                GGGA  GGA  GGCGGCTC
                                ||||  |||  ||||||||
                                CCCT  CCT  CCGCCGAG
                                  TC   C_
GAM930  PLD2     3'  GAACCCCCTCCCTGTCCCA   12162       ATT  C  C
                                TGGGATAGG   GG GG TC
                                |||||||||   || || ||
                                ACCCTGTCC   CC CC AG
                                      CT_  C  A
GAM930  PLTP     5'  GAGCTGCCCGCCATCCCA    21717      A  ATT
                                TGGGAT GG   GGCGGCTC
                                |||||| ||   ||||||||
                                ACCCTA CC   CCGTCGAG
                                   _  GC_
GAM930  PLXNA2   3'  AGCCGCCCTGTTAATCCC    48001     AG   T_
                                GGGAT  GAT  GGCGGCT
                                |||||  |||  |||||||
                                CCCTA  TTG  CCGCCGA
                                   A_   TC
GAM930  PRV1     3'  AGCTGCCCCTGTCCCA      73895       ATT
                                TGGGATAGG   GGCGGCT
                                |||||||||   |||||||
                                ACCCTGTCC   CCGTCGA
                                      ____
GAM930  PTP4A2   3'  GAGCCATAAGCCTCCCA     14440     TA  A   GC
                                TGGGA  GG TTG  GGCTC
                                |||||  || |||  |||||
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                                ACCCT  CC AAT  CCGAG
                                  __ G  A_
GAM930  RPH3AL   3' GAGCCGTCTGCCTCCCCA   23735     AT  ATT
                                TGGG  AGG  GGCGGCTC
                                ||||  |||  ||||||||
                                ACCC  TCC  CTGCCGAG
                                  C_  GT_
GAM930  SLC10A1  3' AGCCTCACCTATCCC      13200       AT  C
                                GGGATAGG  TGG GGCT
                                ||||||||  ||| ||||
                                CCCTATCC  ACT CCGA
                                    __  _
GAM930  SLC9A5   3' GCCCCAATCCTCCCCA     17182     AT      C
                                TGGG  AGGATTGG GGC
                                ||||  |||||||| |||
                                ACCC  TCCTAACC CCG
                                  C_      _
GAM930  TGFBR2   5' GAGCCCTTGCTTTCCATCCCA 13731      A  TT  ___
                                TGGGAT GGA  GGC  GGCTC
                                ||||||| |||  |||  |||||
                                ACCCTA CCT  TCG  CCGAG
                                   _  T_  TTC
GAM930  TLX1     5' GAGCCGCTGTTGCCTCCCA   19823     TA  AT_
                                TGGGA  GG  TGGCGGCTC
                                |||||  ||  |||||||||
                                ACCCT  CC  GTCGCCGAG
                                  __ GTT
GAM930  ZFP36    3' AGCCGTTGCCAAACCCCACCCA 14158     ATA  A   ___
                                TGGG  GG TTGGC  GGCT
                                ||||  || |||||  ||||
                                ACCC  CC AACCG  CCGA
                                  ACC  A   TTG
GAM930  CENTG1   3' GAGCCTGGGTCCCTCCCA   29353     TA   GGC
                                TGGGA  GGATT  GGCTC
                                |||||  |||||  |||||
                                ACCCT  CCTGG  CCGAG
                                  C_   GT_
GAM930  CG1I     3' GAGCCGCTCATTCACCCA   22025     ATA  T
                                TGGG  GGAT GGCGGCTC
                                ||||  |||| ||||||||
                                ACCC  CTTA TCGCCGAG
                                  A__   C
GAM930  EPB41L1  3' AGCCCTCCCCTGTCCCA    71101       ATT  C
                                TGGGATAGG  GG GGCT
                                |||||||||  || ||||
                                ACCCTGTCC  TC CCGA
                                     CC_ _
GAM930  FLJ12816 3' AGCCCGTCCCTGTCCCA    42183       ATT   _
                                TGGGATAGG  GGCGG CT
                                |||||||||  ||||| ||
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                                ACCCTGTCC  CTGCC GA
                                    ___    C
GAM930  FLJ14950  3' GAGCTGGGCTCTATCCCA   52790       GA  GG
                                TGGGATAG  TT  CGGCTC
                                ||||||||  ||  ||||||
                                ACCCTATC  GG  GTCGAG
                                    TC  __
GAM930  FLJ20457  3' AGCCTAGTCCTAGCCCA    35669     A      GC
                                TGGG TAGGATTG  GGCT
                                |||| ||||||||  ||||
                                ACCC ATCCTGAT  CCGA
                                  G       __
GAM930  FLJ22615  5' GAGCCGTCCTCCAGCCCCA   69040     ATA   TT
                                TGGG   GGA  GGCGGCTC
                                ||||   |||  ||||||||
                                ACCC   CCT  CTGCCGAG
                                  CGA   C_
GAM930  FLJ30567  3' GAACCACATGCCTGTCCCA   59474        AT  GC  C
                                TGGGATAGG  TG  GG TC
                                |||||||||  ||  || ||
                                ACCCTGTCC  AC  CC AG
                                    GT  A_  A
GAM930  KIAA0295  3' GTCCCCATCCTATCCCA     68671         T  C
                                TGGGATAGGAT GG GGC
                                |||||||||| || |||
                                ACCCTATCCTA CC CTG
                                    C  _
GAM930  KIAA0616  3' GAGCCGGGCCGTCCACCCA   47315     ATA   T  __
                                TGGG   GGAT GGC  GGCTC
                                ||||   |||| |||  |||||
                                ACCC   CCTG CCG  CCGAG
                                  A__    _   GG
GAM930  KIAA0882  3' GAGGGTAAATCCTATACCA   83535     G      G  GG
                                TGG ATAGGATT GC  CTC
                                ||| ||||||| ||  |||
                                ACC TATCCTAA TG  GAG
                                  A       A  G_
GAM930  KIAA1091  3' GAGCTGCTCACATCCCA     70263       AG  TTG
                                TGGGAT  GA   GCGGCTC
                                ||||||  ||   |||||||
                                ACCCTA  CT   CGTCGAG
                                   CA  ___
GAM930  KIAA1432  5' GAGCCATGCTGCTATCTCA   67303        GAT   __
                                TGGGATAG   TGGC  GGCTC
                                ||||||||   ||||  |||||
                                ACTCTATC   GTCG  CCGAG
                                    ___    TA
GAM930  KIAA1576  3' AGTGCCAATCCCATGCCA    66489     G  A       G
                                TGG AT GGATTGGCG CT
                                ||| || |||||||| ||
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                                ACC TA CCTAACCGT GA
                                  G  C       _
GAM930  KIAA1858  3'  GAGCCGCCTGGTCCCCCA   67720     ATA    _
                                TGGG  GGATT GGCGGCTC
                                ||||  ||||| ||||||||
                                ACCC  CCTGG CCGCCGAG
                                  ___    T
GAM930  MGC3184  5'  GAGCCGCCTCCGCCCCA    49042     ATA  TT
                                TGGG  GGA  GGCGGCTC
                                ||||  |||  ||||||||
                                ACCC  CCT  CCGCCGAG
                                  CG_  __
GAM930  MGC4549  3'  GAGCCGCCCCCCTCCCCA   51470     AT  ATT
                                TGGG  AGG  GGCGGCTC
                                ||||  |||  ||||||||
                                ACCC  TCC  CCGCCGAG
                                  C_  CC_
GAM930  PLAGL2   3'  GAGCTGTCCCCCTCCCA    70961     TA  ATT
                                TGGGA  GG  GGCGGCTC
                                |||||  ||  ||||||||
                                ACCCT  CC  CTGTCGAG
                                   CC  ___
GAM930  SARM     3'  GAACTGACTCCTGTCCCA   31291       TTGG  C
                                TGGGATAGGA   CGG TC
                                ||||||||||   ||| ||
                                ACCCTGTCCT   GTC AG
                                     CA__  A
GAM930  SCYA2    3'  GAACCACAGTTCTACCCC   12951    A     GC  C
                                GGG TAGGATTG  GG TC
                                ||| ||||||||  || ||
                                CCC ATCTTGAC  CC AG
                                  C      A_ A
GAM930  SLC38A5  5'  GAGCCTATCCCTACCCA    54310    A   AT  GC
                                TGGG TAGG  TG  GGCTC
                                |||| ||||  ||  |||||
                                ACCC ATCC  AT  CCGAG
                                  _   CT  __
GAM930  SOX7     3'  GAGCCGTCCAGCCACACCA   49530    GATA  A   _
                                TGG   GG TTGG CGGCTC
                                |||   || |||| ||||||
                                ACC   CC GACC GCCGAG
                                  ACA_ _   T
GAM930  TCL6     5'  GAGCCGCTGCACCCAGCCCA  40531     ATA  AT
                                TGGG  GG  TGGCGGCTC
                                ||||  ||  |||||||||
                                ACCC  CC  GTCGCCGAG
                                  GAC  AC
GAM930  TCL6     5'  GAGCCGCTGCACCCAGCCCA  40538     ATA  AT
                                TGGG  GG  TGGCGGCTC
                                ||||  ||  |||||||||
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                                ACCC   CC  GTCGCCGAG
                                  GAC  AC
GAM930   TED      3'  GAGCCTCCCCTATCCC      32268        ATT  C
                                GGGATAGG   GG GGCTC
                                ||||||||   || |||||
                                CCCTATCC   CC CCGAG
                                    ____  T
GAM930   LOC124895 5'  GAGCCGCCACATCCCCC     74820     ATA   _
                                GGG   GGAT TGGCGGCTC
                                |||   |||| |||||||||
                                CCC   CCTA ACCGCCGAG
                                  ____   C
GAM930   LOC124930 3'  GAGCGCTGTCCCTATCCC    74826        AT    G
                                GGGATAGG  TGGCG CTC
                                ||||||||  ||||| |||
                                CCCTATCC  GTCGC GAG
                                    CT    _
GAM930   LOC144308 5'  GAGCAAAACCCTATCTCA    83980        A  GGCG
                                TGGGATAGG TT    GCTC
                                |||||||||  ||    ||||
                                ACTCTATCC AA    CGAG
                                     C  AA__
GAM930   LOC145989 3'  GAGCCGCCAGGGCCCCC     60293     ATA  A_
                                GGG   GG  TTGGCGGCTC
                                |||   ||  ||||||||||
                                CCC   CC  GACCGCCGAG
                                  ____  GG
GAM930   LOC146059 3'  AGCCTCATTTGCTATCCCA    78083        _ T   C
                                TGGGATAG GA TGG GGCT
                                |||||||| || ||| ||||
                                ACCCTATC TT ACT CCGA
                                     G  T   _
GAM930   LOC148250 5'  GAGCATGCCCCCTCCCA     79493      TA  ATT    _
                                TGGGA  GG   GGCG GCTC
                                |||||  ||   |||| ||||
                                ACCCT  CC   CCGT CGAG
                                   __  C__    A
GAM930   LOC149149 5'  GAGCTTGTCCTATCTCA     85524          TGGC
                                TGGGATAGGAT    GGCTC
                                ||||||||||    |||||
                                ACTCTATCCTG    TCGAG
                                       T____
GAM930   LOC151318 5'  GAGCCGCCACGTCTTCC     81030     TA   _
                                GGA  GGAT TGGCGGCTC
                                |||  |||| |||||||||
                                CCT  TCTG ACCGCCGAG
                                  __    C
GAM930   LOC151760 5'  GAATCTCCAATCTCTATCCCA  86683         _     C GC
                                TGGGATAG GATTGG G  TC
                                |||||||| |||||| |  ||
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                                ACCCTATC CTAACC C  AG
                                     T     T TA
GAM930  LOC170425 3'  GCTTCCCAATCTATCCCA    76889        G    C_
                                TGGGATAG ATTGG  GGC
                                |||||||| |||||  |||
                                ACCCTATC TAACC  TCG
                                     _    CT
GAM930  LOC222159 5'  CTACCAATCCTGATCCCA    95729       _      CG
                                TGGGAT AGGATTGG  G
                                |||||| ||||||||  |
                                ACCCTA TCCTAACC  C
                                   G       AT
GAM930  LOC257048 3'  GAGCCGCCACGATGTCCC    97956       GGAT
                                GGGATA   TGGCGGCTC
                                ||||||   |||||||||
                                CCCTGT   ACCGCCGAG
                                   AGC_
GAM930  LOC90010  3'  GGGTTATCACTATCCCA     61723        GAT   CG
                                TGGGATAG   TGG  GCTC
                                ||||||||   |||  ||||
                                ACCCTATC   ACT  TGGG
                                     ___   AT
GAM931  DGCR2     5'  CCTCGCCCAGGTTCAGCC    18899       AC    A_  TCA
                                GGCTGA  GCCTG  CG   AGG
                                ||||||  |||||  ||   |||
                                CCGACT  TGGAC  GC   TCC
                                   __    CC  ___
GAM931  FREB      3'  GCCTTGATCTTGAACTTCCAGC 52192       AACGCCT  C
           CT                     AGGCTG      GA GTCAAGGC
                                ||||||      || ||||||||
                                TCCGAC      TT TAGTTCCG
                                   CTTCAAG  C
GAM931  RPS6      5'  CCTCGGAGGCGTTCAGCT    8276          GA  TCA
                                GGCTGAACGCCT  CG   AGG
                                ||||||||||||  ||   |||
                                TCGACTTGCGGA  GC   TCC
                                      G_  ___
GAM931  BART1     3'  GCCCTATGTCAGGCACTCCACC 25039     CT  AC       CAA
           T                      AGG  GA  GCCTGACGT   GGC
                                |||  ||  |||||||||   |||
                                TCC  CT  CGGACTGTA   CCG
                                  AC  CA       TC_
GAM931  FLJ14816  3'  CCCTGACACCAAGTCACTGTTC 52708         CC   _____   A
           AGCTT                    AGGCTGAACG  TGAC    GTCA GG
                                ||||||||||  ||||    |||| ||
                                TTCGACTTGT  ACTG    CAGT CC
                                      C_   AACCA   C
GAM931  GAB3      3'  GCCTTGATGTCCAGCACACAGC 55520       AAC  CT
           CT                     AGGCTG   GC  GACGTCAAGGC
                                ||||||   ||  ||||||||||
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                                TCCGAC  CG  CTGTAGTTCCG
                                   ACA  AC
GAM931  KIAA0125  3'  GCCTCCTCCAAAGTTCAGCCT  61127        GCCT  CGTCA
                                AGGCTGAAC   GA    AGGC
                                |||||||||   ||    ||||
                                TCCGACTTG   CT    TCCG
                                     AAAC  CC___
GAM931  KIAA0125  5'  GCCTCCTCCAAAGTTCAGCCT  29568        GCCT  CGTCA
                                AGGCTGAAC   GA    AGGC
                                |||||||||   ||    ||||
                                TCCGACTTG   CT    TCCG
                                     AAAC  CC___
GAM931  KIAA0280  3'  GCCCTGTGTCATCCAGACTTCA 93303        CGCC___    T  A
           GCCT                   AGGCTGAA      TGACG CA GGC
                                |||||||||      ||||| || |||
                                TCCGACTT      ACTGT GT CCG
                                     CAGACCT    _  C
GAM931  KIAA1274  3'  GGCCGGCGTTCAGCCT     93013          TGAC
                                AGGCTGAACGCC   GTC
                                ||||||||||||   |||
                                TCCGACTTGCGG   CGG
                                       C___
GAM931  ZFP36L2   3'  GCCTTGATAGTTAGCCCTCAGC 23532       AC  C   _
           C                    GGCTGA  GC TGAC GTCAAGGC
                                ||||||  || |||| ||||||||
                                CCGACT  CG ATTG TAGTTCCG
                                   CC  _   A
GAM931  LOC147077 3'  GCCTTGACCAGAGCACCTCAGC 78851       AC_  _   AC
           C                    GGCTGA   GC CTG  GTCAAGGC
                                ||||||   || |||  ||||||||
                                CCGACT   CG GAC  CAGTTCCG
                                   CCA  A   __
GAM931  LOC147165 3'  CCCGGAGTCCAAACGTCAGCC  85082       A  CCT_   G  AA
                                GGCTGA CG    GAC TC  GG
                                ||||||  ||   ||| ||  ||
                                CCGACT GC    CTG AG  CC
                                   _  AAAC   _  GC
GAM931  LOC152457 3'  CCTTGACGGCCCCAGCCT    81487       AAC   TGAC
                                AGGCTG   GCC    GTCAAGG
                                ||||||   |||    |||||||
                                TCCGAC   CGG    CAGTTCC
                                   CC_   _____
GAM931  LOC153811 5'  GCCTTGACCTCGCCTCAGCCT  81837       AC  CT  C
                                AGGCTGA  GC  GA GTCAAGGC
                                |||||||  ||  || ||||||||
                                TCCGACT  CG  CT CAGTTCCG
                                    C_  __  C
GAM931  LOC155036 5'  TGGCCAAGTGTTCAGCC     87617          C  AC
                                GGCTGAACGC TG  GTCA
                                |||||||||| ||  ||||
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                                CCGACTTGTG AC  CGGT
                                     A  __
GAM931  LOC219942 3'  GCCTTGATCTTGGACTTCCAGC 94994       AACGC TG C
           CT                    AGGCTG    C  A GTCAAGGC
                                 ||||||    |  | ||||||||
                                 TCCGAC    G  T TAGTTCCG
                                    CTTCA GT C
GAM931  LOC253386 5'  GCCCTAGTGGGCGTTTAGCCT  96614           G  GTCAA
                                 AGGCTGAACGCCT AC    GGC
                                 ||||||||||||| ||    |||
                                 TCCGATTTGCGGG TG    CCG
                                        _ ATC__
GAM931  LOC93512  3'  CCCGGAGTCCAAACGTCAGCC  72874      A  CCT_  G  AA
                                 GGCTGA CG   GAC TC  GG
                                 |||||| ||   ||| ||  ||
                                 CCGACT GC   CTG AG  CC
                                    _ AAAC   _ GC
GAM932  HAL      5'  GCCACTCCTGCATAAAGCTC   10903          TGAAAA
                                 GAGCTTTATGC     GGTGGC
                                 ||||||||||      ||||||
                                 CTCGAAATACG     TCACCG
                                       TCC___
GAM932  HMGN2    3'  GGCCACCTTGGCACAAAAGC   19809      A  C  AA
                                 GCTTT TG TG  AAGGTGGCC
                                 ||||| || ||  |||||||||
                                 CGAAA AC AC  TTCCACCGG
                                    _ _  GG
GAM932  NMI      5'  GGCCACCTCCTCAGGAAG    17436     ATG   AA
                                 CTTT   CTGA  AGGTGGCC
                                 ||||   ||||  ||||||||
                                 GAAG   GACT  TCCACCGG
                                    ___    CC
GAM932  PACE     3'  GGCCACCTCTCCAAGGGCTT   11944       A  CT  AAA
                                 GAGCTTT TG  GA   GGTGGCC
                                 |||||||  ||  ||   |||||||
                                 TTCGGGA AC  CT   CCACCGG
                                    _ CT  ___
GAM932  PYCR1    3'  CCACCTTCCTCTAGAGCTC    70639        TGCT  A_
                                 GAGCTTTA    GA  AAGGTGG
                                 ||||||||    ||  |||||||
                                 CTCGAGAT    CT  TTCCACC
                                       _____  CC
GAM932  SDC1     3'  GGCCACCTCCCCAGCATTCCAG 12991     TT_     AAA
           C                      GCT   ATGCTG   AGGTGGCC
                                  |||   ||||||   ||||||||
                                  CGA   TACGAC   TCCACCGG
                                    CCT     CCC
GAM932  FLJ11560  5'  GCCCAGGCCCAGCATAAAG   48008          AAAA  ___
                                 CTTTATGCTG    GGT   GGC
                                 ||||||||||    |||   |||
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                                GAAATACGAC   CCG  CCG
                                     ____  GAC
GAM932  KIAA0446 5' CCACCTTTTGAAGAGCTC   69446      ATGCTG
                                GAGCTTT    AAAAGGTGG
                                |||||||    |||||||||
                                CTCGAGA    TTTTCCACC
                                   AG____
GAM932  KIAA0971 3' GTTGTTCTCAGCATAAAGT  30677        AAA  TG
                                GCTTTATGCTGA  GG  GC
                                ||||||||||||  ||  ||
                                TGAAATACGACT  TT  TG
                                      C__  GT
GAM932  KIAA1393 3' GGCCACCTTGGCACAAAAGC  72574     A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _  GG
GAM932  KIAA1656 3' GGCCACCTCCTCCTAGAAGCC 66377   A    ATGCT  AA
                                G GCTTT    GA  AGGTGGCC
                                | |||||    ||  ||||||||
                                C CGAAG    CT  TCCACCGG
                                _    ATC__  CC
GAM932  KIAA1884 3' GCCACCTTCATCTACCAAGGCT 73728      ATGCT  A_
          C                      GAGCTTT    GA  AAGGTGGC
                                |||||||    ||  ||||||||
                                CTCGGAA    CT  TTCCACCG
                                   CCAT_  AC
GAM932  PP3501   3' GGCCACCGTTGACAGCATAAAG 41683       AAAA_
                                CTTTATGCTG    GGTGGCC
                                ||||||||||    |||||||
                                GAAATACGAC    CCACCGG
                                     AGTTG
GAM932  SDCCAG3  3' GGTGTTCTCAGCATGAAGCTC  22803          AAA  TG
                                GAGCTTTATGCTGA  GG  GCC
                                ||||||||||||||  ||  |||
                                CTCGAAGTACGACT  CT  TGG
                                      ___  TG
GAM932  SP140    3' GGCCACCTCCATGCAGAAGC  24327     A  TGAAA
                                GCTTT TGC    AGGTGGCC
                                ||||| |||    ||||||||
                                CGAAG ACG    TCCACCGG
                                  _  TACC_
GAM932  LOC148760 3' GGCCACCTTCTCCAACAAGCTC 85364      TA  CT  A
                                GAGCTT  TG  GA AAGGTGGCC
                                ||||||  ||  || |||||||||
                                CTCGAA  AC  CT TTCCACCGG
                                   CA  __  C
GAM932  LOC150170 5' ACCTGTTTCACATAAAGC   80414       C   _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
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                                CGAAATAC ACTTT TCCA
                                   _    G
GAM932  LOC150175 5'  ACCTGTTTCACATAAAGC    80453        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                   _    G
GAM932  LOC150215 5'  ACCTGTTTCACATAAAGC    80456        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                   _    G
GAM932  LOC150218 5'  ACCTGTTTCACATAAAGC    80525        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                   _    G
GAM932  LOC152065 3'  GGCCACCTTCTCCTTGGCAGGC 86737       TTA   ___  A
          TC                     GAGCT   TGCT   GA AAGGTGGCC
                                |||||   ||||   || |||||||||
                                CTCGG   ACGG   CT TTCCACCGG
                                   ___    TTC  C
GAM932  LOC152267 3'  GGCCACCTTGGCACAAAAGC   61036      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                   _ _  GG
GAM932  LOC158292 5'  CCTCTGGACCCAGCATAAGGCT 88046           AAAA_  T
          C                     GAGCTTTATGCTG     GG GG
                                ||||||||||||     || ||
                                CTCGGAATACGAC     TC CC
                                      CCAGG  T
GAM932  LOC219997 3'  GCCACCTCTTCAGCCTC     93256     CTTTAT     A
                                GAG     GCTGAA AGGTGGC
                                |||     |||||| |||||||
                                CTC     CGACTT TCCACCG
                                  _______     C
GAM932  LOC256269 3'  GGCCACCTTGGCACAAAAGC   96608      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                   _ _  GG
GAM932  LOC91963  5'  GGCCACCTCCTCTGAGAAGC   68321      ATGCT  AA
                                GCTTT    GA  AGGTGGCC
                                |||||    ||  ||||||||
                                CGAAG    CT  TCCACCGG
                                   AGT__  CC
GAM933  ATP1A1    3'  CGCCGTGGAGCATCAGGCCA   7352          A    A
                                TGGCCTGATG TCCAC GCG
                                |||||||||| ||||| |||
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                                ACCGGACTAC AGGTG CGC
                                      G    C
GAM933  AVPR1A   5'  CCGCTGTGAATACAGGC     7378       ATG  C
                                GCCTG   AT CACAGCGG
                                |||||   || ||||||||
                                CGGAC   TA GTGTCGCC
                                   A__  A
GAM933  CCND2    3'  CCAGCAAATCATCGGGCCA   10048          CCACA  _
                                TGGCCTGATGAT    GC GG
                                ||||||||||||    || ||
                                ACCGGGCTACTA    CG CC
                                      AA___  A
GAM933  GCN5L2   5'  TCCGCTGCGGGGGAGGCC    60530      GATGA   A
                                GGCCT    TCC CAGCGGA
                                |||||    ||| |||||||
                                CCGGA    GGG GTCGCCT
                                   GG___  C
GAM933  GJA5     3'  CCCTGACCAGATCATCAGCCA  19163     C       CA__  C
                                TGGC TGATGATC   CAG GG
                                |||| ||||||||   ||| ||
                                ACCG ACTACTAG   GTC CC
                                  _       ACCA  _
GAM933  HIVEP3   3'  CCGCTGTGGTTGGCAGCCA   44701     C  ATGAT
                                TGGC TG    CCACAGCGG
                                |||| ||    |||||||||
                                ACCG AC    GGTGTCGCC
                                  _ GGTT_
GAM933  HOXD1    5'  CCGCCGGTATATTAGGCCA   44697         AT  ACA
                                TGGCCTGATG  CC   GCGG
                                ||||||||||  ||   ||||
                                ACCGGATTAT  GG   CGCC
                                      AT  C__
GAM933  NGFR     3'  CCGTCACCATCTCAGGCCA   11790        T   CCACA
                                TGGCCTGA GAT    GCGG
                                |||||||| |||    ||||
                                ACCGGACT CTA    TGCC
                                     _  CCAC_
GAM933  SUFU     3'  TTGTGACCCATCAGGCCA    32942         ATC
                                TGGCCTGATG   CACAG
                                ||||||||||   |||||
                                ACCGGACTAC   GTGTT
                                      CCA
GAM933  ARHGEF15 3'  CTGTGGACCACAGGCCA     30953        A  A
                                TGGCCTG TG TCCACAG
                                ||||||| || |||||||
                                ACCGGAC AC AGGTGTC
                                     _  C
GAM933  DKFZP586J1624 3'  CTCCGCCCAGTCACCATCAGGC 32044          ATCCACA_
            CA                    TGGCCTGATG       GCGGAG
                                ||||||||||       ||||||
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                                ACCGGACTAC      CGCCTC
                                     CACTGACC
GAM933  FBXO9    5' CTCCGCTGCAGAGACAGGC   54245     ATGA  CA
                                GCCTG   TC  CAGCGGAG
                                |||||   ||  ||||||||
                                CGGAC   AG  GTCGCCTC
                                  AG__  AC
GAM933  MGC18079 3' CCGCGGACCTCAGGCCA    59033       TGA   ACA
                                TGGCCTGA  TCC  GCGG
                                ||||||||  |||  ||||
                                ACCGGACT  AGG  CGCC
                                    CC_  ___
GAM933  SLC26A9  3' CCCTTAGGACCTCAGGCCA  54711       TGA   AC  C
                                TGGCCTGA  TCC  AG GG
                                ||||||||  |||  || ||
                                ACCGGACT  AGG  TC CC
                                    CC_  AT  _
GAM933  SLC26A9  3' CCCTTAGGACCTCAGGCCA  57006       TGA   AC  C
                                TGGCCTGA  TCC  AG GG
                                ||||||||  |||  || ||
                                ACCGGACT  AGG  TC CC
                                    CC_  AT  _
GAM933  LOC115110 3' TGCAGACATCAGGCCA     72187         A  CACA
                                TGGCCTGATG TC   GCG
                                |||||||||| ||   |||
                                ACCGGACTAC AG   CGT
                                     _  A___
GAM933  LOC130074 3' CTGGGCCAGATCTCAGGCCA  76625        T   CACAG
                                TGGCCTGA GATC    CGG
                                |||||||| ||||    |||
                                ACCGGACT CTAG    GTC
                                    _   ACCGG
GAM933  LOC159110 5' CTCCGCTGCCCCGGTCAACCA 82989    CCTGA   CA__
                                TGG    TGATC   CAGCGGAG
                                |||    |||||   ||||||||
                                ACC    ACTGG   GTCGCCTC
                                  A____    CCCC
GAM933  LOC159116 5' CTCCGCTGCCCCGGTCAACCA 82972    CCTGA   CA__
                                TGG    TGATC   CAGCGGAG
                                |||    |||||   ||||||||
                                ACC    ACTGG   GTCGCCTC
                                  A____    CCCC
GAM933  LOC165476 5' CTCCGCTGCCTGCTCAGCCA  88551    C   TGATCCA
                                TGGC TGA     CAGCGGAG
                                |||| |||     ||||||||
                                ACCG ACT     GTCGCCTC
                                  _  CGTCC__
GAM933  LOC200032 5' CCCTGACCAGATCATCAGCCA 85474     C      CA__  C
                                TGGC TGATGATC   CAG GG
                                |||| ||||||||   ||| ||
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                                ACCG ACTACTAG    GTC CC
                                  _       ACCA  _
GAM933  LOC219654 5'  CTCCGCTGCGGAGGGGGGCC  92933      GATGA  A
                                GGCCT     TCC CAGCGGAG
                                |||||     ||| ||||||||
                                CCGGG     AGG GTCGCCTC
                                   GGG__   C
GAM933  LOC220002 3'  CTCCTGGCAACATCAGGCCA  93271         AT_  CAGC
                                TGGCCTGATG  CCA   GGAG
                                ||||||||||  |||   ||||
                                ACCGGACTAC  GGT   CCTC
                                      AAC  ____
GAM934  ACAD8     3'  CTTGATTAGTCTGCATTTTAC  27665      GTC  _
                                GTAAGG  CAG CTGATCAAG
                                ||||||  ||| |||||||||
                                CATTTT  GTC GATTAGTTC
                                    AC_  T
GAM934  AHR       3'  TTTGAGCTACTGGATTCTTATT 9676    T        CTGA
              A                  G GTAAGGGTCCAG   TCAAG
                                 | ||||||||||||   |||||
                                 A TATTCTTAGGTC   AGTTT
                                  T         ATCG
GAM934  ALOX12B   5'  CTTGCCTGCCTTGGGCCTTCGT 8536    TG A      __  TGAT
              GT                   G  T AGGGTCCA  GC   CAAG
                                   |  | ||||||||  ||   ||||
                                   T  G TTCCGGGT  CG   GTTC
                                   GT C       TC  TCC_
GAM934  ATP11B    3'  TTTATCATTGGATCTTTTGCAT 81129       _     C   CAAG
                                GTGTAAG GGTCCAG TGAT
                                ||||||| ||||||| ||||
                                TACGTTT CTAGGTT ACTA
                                    T      _    TTT
GAM934  ATP2C1    3'  CTTGATTTAAATTGGCTTTTG  27661      T   CT__
                                TAAGGG CCAG   GATCAAG
                                |||||| ||||   |||||||
                                GTTTTC GGTT   TTAGTTC
                                   _   AAAT
GAM934  ATP5J     5'  TCCCTGCACCTTTATACA    9857          C   CT
                                TGTGTAAGGGT CAG  GA
                                |||||||||| |||  ||
                                ACATATTTCCA GTC  CT
                                      C   C_
GAM934  ATRN      3'  TTTGACATACCCTGGACTCCTG 24861   TG  A      C___  A
              TGT                  G  TA GGGTCCAG   TG TCAAG
                                   |  || ||||||||   || |||||
                                   T  GT CTCAGGTC   AC AGTTT
                                   GT  C      CCAT  _
GAM934  BSN       3'  TCCTGGCCCTTGCAT       14390         T   CT
                                GTGTAAGGG CCAG  GA
                                ||||||||| ||||  ||
```

```
                                TACGTTCCC GGTC  CT
                                      _   __
GAM934  C14orf1   3'  CCCCCAGCTGGACCCTCATACA 24166       A          ATCAAG
                                TGTGT AGGGTCCAGCTG
                                ||||| ||||||||||||
                                ACATA TCCCAGGTCGAC
                                   C          CCCCT
GAM934  CACNG2    5'  AGAAGTCGGTTGGGTGTTTATA 21398        GG        CAAG
           TA                    TGTGTAAG  TCCAGCTGAT
                                ||||||||  ||||||||||
                                ATATATTT  GGGTTGGCTG
                                    GT        AAGAC
GAM934  CBFB      3'  TTTGGTTGGTTTTGGTGTTGTA 10041      AGGGT  __  TG
           CA                    TGTA    CCA  GC  ATCAAG
                                ||||    |||  ||  ||||||
                                ACAT    GGT  TG  TGGTTT
                                  GTTGT   TT  GT
GAM934  CBFB      3'  TTTGGTTGGTTTTGGTGTTGTA 43445      AGGGT  __  TG
           CA                    TGTA    CCA  GC  ATCAAG
                                ||||    |||  ||  ||||||
                                ACAT    GGT  TG  TGGTTT
                                  GTTGT   TT  GT
GAM934  CCRL1     3'  CTTGGTTGCAGTGGTGCTTATA 33793        G T   G  __
           CA                    TGTGTAAG G CCA CTG  ATCAAG
                                |||||||| | ||| |||  ||||||
                                ACATATTC T GGT GAC  TGGTTC
                                    G _  _  GT
GAM934  COG6      3'  TTTGATTAGTATGTGTTACATA 73255        GGGTCCA
                                TGTGTAA      GCTGATCAAG
                                |||||||      ||||||||||
                                ATACATT      TGATTAGTTT
                                   GTGTA__
GAM934  COL4A4    3'  CTTGATTTGTAATGAGCTCTTA 5404          TC  __  T
           TAT                   GTGTAAGGG  CA  GC GATCAAG
                                |||||||||  ||  || |||||||
                                TATATTCTC  GT  TG TTAGTTC
                                     GA  AA  T
GAM934  CPSF6     3'  CTTGATTAGGTGTTTTTAT    23790        TC  G
                                GTAAGGG  CA CTGATCAAG
                                |||||||  || |||||||||
                                TATTTTT  GT GATTAGTTC
                                   __ G
GAM934  CRH       3'  CTTGGTCAGTTTGGTTGTGTA  7480     TG   GGGT   _
                                TG  TAA    CCAG CTGATCAAG
                                ||  |||    |||| |||||||||
                                AT  GTT    GGTT GACTGGTTC
                                 GT  _____   T
GAM934  CTNS      3'  CGGTTGGGCCCTGGCACA     18219       A
                                TGTGT AGGGTCCAGCTG
                                ||||| ||||||||||||
```

```
                                ACACG TCCCGGGTTGGC
                                  G
GAM934  CXCR6    3'  CTTGGGGCTTGACTTTTGTATA 22674          C    GA
                                TGTGTAAGGGTC AGCT  TCAAG
                                |||||||||||| ||||  |||||
                                ATATGTTTTCAG TCGG  GGTTC
                                       T   __
GAM934  CYP4F3   3'  CATCTGGATTCTTCACA     7999      T       C
                                TGTG AAGGGTCCAG TG
                                |||| |||||||||| ||
                                ACAC TTCTTAGGTC AC
                                  _       T
GAM934  DDB1     3'  TCTCCCTGGATTTTTACCA   10399    T        CT_
                                TG GTAAGGGTCCAG   GA
                                || ||||||||||||   ||
                                AC CATTTTTAGGTC   CT
                                 _         CCT
GAM934  DIO1     3'  TTAACTCTGTGTCTTTACATA  7663         TC   C__
                                TGTGTAAGGG  CAG   TGA
                                ||||||||||  |||   |||
                                ATACATTTCT  GTC   ATT
                                      GT   TCA
GAM934  DYRK1A   3'  TTTGGTTACAGGACTTCTGTGC 9167    TG  AG    AGC
          A                      TG  TA  GGTCC   TGATCAAG
                                 ||  ||  |||||   ||||||||
                                 AC  GT  TCAGG   ATTGGTTT
                                  GT  CT    AC_
GAM934  DYRK1A   3'  TTTGGTTACAGGACTTCTGTGC 56090    TG  AG    AGC
          A                      TG  TA  GGTCC   TGATCAAG
                                 ||  ||  |||||   ||||||||
                                 AC  GT  TCAGG   ATTGGTTT
                                  GT  CT    AC_
GAM934  EDNRA    3'  TTTGATCATTCCCTTTTCCATA 64803     T__    TCCAGC
                                TGTG   AAGGG     TGATCAAG
                                ||||   |||||     ||||||||
                                ATAC   TTCCC     ACTAGTTT
                                  CTT    TT____
GAM934  EGFL5    3'  TTGGTCATCCCTTTATA     87924        TCCAGC
                                TGTAAGGG     TGATCAA
                                ||||||||     |||||||
                                ATATTTCC     ACTGGTT
                                     CT____
GAM934  EGFL6    3'  TTAGCTGGGTCTTTCATA    31940     T   GT
                                TGTG AAGG  CCAGCTGA
                                |||| ||||  ||||||||
                                ATAC TTTC  GGTCGATT
                                  _   TG
GAM934  EGR2     3'  TTTGGTCATTAGCTCTTA    6378        CCAGC
                                TAAGGGT    TGATCAAG
                                |||||||    ||||||||
```

```
                                ATTCTCG    ACTGGTTT
                                   ATT__
GAM934  EPHA2   3'  CTTGGTTGTGTTGAGGTTTTTA 16676    G    GT _   _
          AATA                   TGT TAAGG  C CAGC TGATCAAG
                                 ||| |||||  | |||| ||||||||
                                 ATA ATTTT  G GTTG GTTGGTTC
                                   A    TG A   T
GAM934  ERBB3   3'  CTTGGAACTAGGCTCTTATGT  10537   TG      C  CTGA
                                 G  TAAGGGTC AG   TCAAG
                                 |  |||||||| ||   |||||
                                 T  ATTCTCGG TC   GGTTC
                                  GT       A  AA__
GAM934  ESRRBL1  3'  TCTGATTAGTTGGGTTTTTTAT 36326     T   GT        AG
          A                      TGTG AAGG  CCAGCTGATCA
                                 |||| ||||  ||||||||||
                                 ATAT TTTT  GGTTGATTAGT
                                   _   TG         CTT
GAM934  ESRRG   3'  CTTGTGGTGTTTGGATTCTTG  66988          _ TGAT
                                 TAAGGGTCCAG C    CAAG
                                 |||||||||| |    ||||
                                 GTTCTTAGGTT G    GTTC
                                        T TGGT
GAM934  FACL4   3'  GGAATTAGAACCCTTGCACA   16745          CCAG    CAAG
                                 TGTGTAAGGGT    CTGAT
                                 ||||||||||    |||||
                                 ACACGTTCCCA    GATTA
                                        A___     AGGT
GAM934  FACL4   3'  TTGATCAGTAGTTTGCAT    16749        GGTCCA
                                 GTGTAAG     GCTGATCAA
                                 |||||||     |||||||||
                                 TACGTTT     TGACTAGTT
                                    GA____
GAM934  FASN    3'  GAGGAGCTGGGCCCCTGCACA  15911        A        GA
                                 TGTGTA GGGTCCAGCT  TC
                                 |||||| ||||||||||  ||
                                 ACACGT CCCGGGTCGA  AG
                                    C         GG
GAM934  FECH    3'  CTTGAGGATTGGACTCTTG    5554           _  GA
                                 TAAGGGTCCAG CT  TCAAG
                                 |||||||||| ||  |||||
                                 GTTCTCAGGTT GG  AGTTC
                                        A  __
GAM934  FGF5    3'  TTTGGTTTTTGGTCCTTGCA   16769        T   CT
                                 TGTAAGGG CCAG  GATCAAG
                                 |||||||| ||||  |||||||
                                 ACGTTCCT GGTT  TTGGTTT
                                    _    T_
GAM934  FGF5    3'  TTTGGTTTTTGGTCCTTGCA   53677        T   CT
                                 TGTAAGGG CCAG  GATCAAG
                                 |||||||| ||||  |||||||
```

```
                                ACGTTCCT GGTT  TTGGTTT
                                     _   T_
GAM934  FGF8    3'  TTTGCTGTTGGGTTTTTGC   21498      GT    TGAT
                                GTAAGG  CCAGC    CAAG
                                ||||||  |||||    ||||
                                CGTTTT  GGTTG    GTTT
                                   TG    TC__
GAM934  GEM     3'  TTGGTTGACCCTTGTAT     19152         C   TG
                                GTGTAAGGGTC AGC  A
                                |||||||||||  |||  |
                                TATGTTCCCAG TTG  T
                                      _  GT
GAM934  GEM     3'  TTGGTTGACCCTTGTAT     19153         C   TG
                                GTGTAAGGGTC AGC  A
                                |||||||||||  |||  |
                                TATGTTCCCAG TTG  T
                                      _  GT
GAM934  GOLGA5  3'  CTTGATTGGTGTAAATCTTTTT 18852     T     CCA_  TG
           ATA                    TGTG AAGGGT    GC  ATCAAG
                                ||||  ||||||    ||  ||||||
                                ATAT TTTCTA    TG  TAGTTC
                                  T     AATG  GT
GAM934  GPR56   3'  CTGTCCATCTGGGCCTTTGTAT 20273           C  AT  AG
                                GTGTAAGGGTCCAG TG  CA
                                ||||||||||||||  ||  ||
                                TATGTTTCCGGGTC AC  GT
                                      T  CT  C
GAM934  GRIN2C  3'  TGAGGGCTGGGCTTTTGC    7734            GA
                                GTAAGGGTCCAGCT  TCA
                                ||||||||||||||  |||
                                CGTTTTCGGGTCGG  AGT
                                      G_
GAM934  HADHSC  3'  TTTGGTCAGACATTCCCTCACA 19227      A    TCCAG
           CA                     TGTGT AGGG    CTGATCAAG
                                |||||  ||||    |||||||||
                                ACACA TCCC    GACTGGTTT
                                  C    TTACA
GAM934  HCN4    3'  TTTGGTCACTTGCTTTTATA   19687        CC  C
                                TGTAAGGGT  AG TGATCAAG
                                |||||||||  ||  ||||||||
                                ATATTTTCG  TC ACTGGTTT
                                     T_  _
GAM934  HTR4    3'  TTGGTTGGCCCCCTTGTCA   7888    _     TCCA  TG
                                TG TAAGGG   GC  ATCAA
                                ||  ||||||   ||  |||||
                                AC GTTCCC   CG  TGGTT
                                 T     C___  GT
GAM934  INPP5A  3'  ATTAGCTGGGTGTTTGTGT   19864   TG   GG
                                G  TAAG  TCCAGCTGAT
                                |  ||||  ||||||||||
```

```
                                T  GTTT  GGGTCGATTA
                                 GT    GT
GAM934  ITGAM    3'  CATGCTGGGTTCTGCACA    72305       A GG     _
                                TGTGTA G  TCCAGC TG
                                |||||| |  |||||| ||
                                ACACGT C  GGGTCG AC
                                   _ TT     T
GAM934  ITGB1    3'  CTTGATTTAGCACTATTTACAT 54463        _  CCA    _
           A                     TGTGTAAG GGT   GCTGA TCAAG
                                |||||||| |||   ||||| |||||
                                ATACATTT TCA   CGATT AGTTC
                                     A  ___    T
GAM934  ITM2B    3'  TTATCTGGATTTTTATGT    42083    TG        C
                                G  TAAGGGTCCAG TGA
                                |  ||||||||||| |||
                                T  ATTTTTAGGTC ATT
                                 GT         T
GAM934  JUN      3'  CTTGGTCGCGCCCTCCCTTGGC 11102    G     TCCA  _
                                GT TAAGGG    GC TGATCAAG
                                || ||||||    || ||||||||
                                CG GTTCCC    CG GCTGGTTC
                                  _     TCC_  C
GAM934  KCNS2    3'  CTTGCCCAACTGGACCTTTACT 68848    T         C  AT
           CA                     TG GTAAGGGTCCAG TG  CAAG
                                || ||||||||||| ||  ||||
                                AC CATTTCCAGGTC AC  GTTC
                                 T          A  CC
GAM934  KIT      3'  GCCATCTTAGTTTGGATTCTTA 5849     TG        _   TCAAG
           TGTA                    TG  TAAGGGTCCAG CTGA
                                ||  |||||||||| ||||
                                AT  ATTCTTAGGTT GATT
                                 GT         T    CTACCGT
GAM934  KRT12    3'  TTTGGTCATGTTGGTCTTTG   5853        T    _
                                TAAGGG CCAGC TGATCAAG
                                |||||| ||||| ||||||||
                                GTTTCT GGTTG ACTGGTTT
                                   _    T
GAM934  MADD     3'  CTTGGTTGGTTACCGGTTATGT 56209   TG   G_   CC   TG
                                G  TAA  GGT  AGC  ATCAAG
                                |  |||  |||  |||  ||||||
                                T  ATT  CCA  TTG  TGGTTC
                                 GT   GG   __   GT
GAM934  MADD     3'  CTTGGTTGGTTACCGGTTATGT 56210   TG   G_   CC   TG
                                G  TAA  GGT  AGC  ATCAAG
                                |  |||  |||  |||  ||||||
                                T  ATT  CCA  TTG  TGGTTC
                                 GT   GG   __   GT
GAM934  MAT1A    3'  TGGAGGTTGGATCTTGATGTA  92506    TG A         GA
                                TG  T AGGGTCCAGCT  TCA
                                ||  | ||||||||||  |||
```

```
                                AT  A TTCTAGGTTGG  GGT
                                 GT G          A_
GAM934  MATN2    3'  AGTTGGATTTTTTATACA    11468          _
                                TGTGTAAGGG TCCAGCT
                                |||||||||| |||||||
                                ACATATTTTT AGGTTGA
                                      T
GAM934  MECP2    3'  ATTTTGGTCAGTTGGGTTTTTA 18386    TG    GT
           TGTA                    TG  TAAGG  CCAGCTGATCAAG
                                || |||||  ||||||||||||||
                                AT  ATTTT  GGTTGACTGGTTT
                                 GT    TG          TAT
GAM934  MECP2    3'  CAAAGCAGTTGAATTTTTATAT 18387          C     ATCAAG
           A                     TGTGTAAGGGT CAGCTG
                                |||||||||| ||||||
                                ATATATTTTTA GTTGAC
                                      A     GAAAC
GAM934  MINPP1   3'  CTTGATTACAGGAAGCTTTTAT 18108          __ AGC
           AT                     GTGTAAGGGT  CC   TGATCAAG
                                |||||||||  ||  ||||||||
                                TATATTTTCG  GG   ATTAGTTC
                                      AA  AC_
GAM934  MITF     3'  CTTGATTTGAGATTTTTATGC  6001          _ GCT
                                GTGTAAGGGTC CA   GATCAAG
                                |||||||||| ||  |||||||
                                CGTATTTTTAG GT   TTAGTTC
                                      A ____
GAM934  MS4A6A   3'  CTTGGTAAAGGGCATTTACACA 42535        G   AGCTG
                                TGTGTAAG GTCC     ATCAAG
                                |||||||| ||||     ||||||
                                ACACATTT CGGG     TGGTTC
                                     A    AAA__
GAM934  MTMR8    3'  TGAAAGCTGGTTTTTATACA   31919         T     GA
                                TGTGTAAGGG CCAGCT  TCA
                                |||||||||| ||||||  |||
                                ACATATTTTT GGTCGA  AGT
                                      _     A_
GAM934  NDN      3'  CTTGGTTGGTGCTTTCGCTTTT 11759    TG     CCA___  TG
           GTGC                    G  TAAGGGT     GC  ATCAAG
                                | |||||||     ||  ||||||
                                C  GTTTTCG     TG  TGGTTC
                                 GT      CTTTCG  GT
GAM934  NEURL    3'  TCAGGCTGGGCCTTTGTGC    16136    TG         _
                                G  TAAGGGTCCAGC TGA
                                |  ||||||||||||  |||
                                C  GTTTCCGGGTCG ACT
                                 GT          G
GAM934  NQO1     3'  CTTGGTCAGCTTTTGTTGTTTA 8047          GGTCC__
           TATA                    TGTGTAAG      AGCTGATCAAG
                                ||||||||      ||||||||||
```

```
                                ATATATTT      TCGACTGGTTC
                                     GTTGTTT
GAM934  NR1I2    5' CTTGATCGATCCTTTGCAC   15299         TCCAGC
                                GTGTAAGGG     TGATCAAG
                                |||||||||     ||||||||
                                CACGTTTCC     GCTAGTTC
                                     TA____
GAM934  NRG1     5' TTTGGTTGGGGGGGCCTCTGCG 16905      AG    AG TG
                                TGTA  GGTCC  C  ATCAAG
                                ||||  |||||  |  ||||||
                                GCGT  CCGGG  G  TGGTTT
                                  CT    GG GT
GAM934  NUP98    3' CACCTGGGTCTTTATGCA    33324         GT    C
                                TGTGTAAGG  CCAG TG
                                |||||||||  |||| ||
                                ACGTATTTC  GGTC AC
                                     TG    C
GAM934  OPA1     3' CTTGATCAAAGGTCATTTGTGT 56428    TG    GGT  AGC
           A                     TG  TAAG   CC   TGATCAAG
                                 ||  ||||   ||   ||||||||
                                 AT  GTTT   GG   ACTAGTTC
                                  GT    ACT  AA_
GAM934  PACE4    3' CTTGATCAATTCCCTTGAATA  11949     G     TCCAGC
                                TGT TAAGGG     TGATCAAG
                                ||| ||||||     ||||||||
                                ATA GTTCCC     ACTAGTTC
                                  A     TTA___
GAM934  PAFAH1B1 3' TCTGACTGGATTTTTCTACA   6479      T        CT_
                                TGTG AAGGGTCCAG   GA
                                ||||  ||||||||||   ||
                                ACAT TTTTTAGGTC   CT
                                  C         AGT
GAM934  PFN2     3' TTTGCAGCTTGAGTTTTTATAT 54891         _  C    ATCAAG
                                GTGTAAGGG TC AGCTG
                                ||||||||| || |||||
                                TATATTTTT AG TCGAC
                                     G  T    GTTT
GAM934  PFN2     3' TTTGCAGCTTGAGTTTTTATAT 54892         _  C    ATCAAG
                                GTGTAAGGG TC AGCTG
                                ||||||||| || |||||
                                TATATTTTT AG TCGAC
                                     G  T    GTTT
GAM934  PIGA     3' TTACTGGGATTTTTATGCA    12075          _  C
                                TGTGTAAGGGTCC AG TGA
                                |||||||||||| || |||
                                ACGTATTTTTAGG TC ATT
                                       G  _
GAM934  PIGA     3' TTACTGGGATTTTTATGCA    12076          _  C
                                TGTGTAAGGGTCC AG TGA
                                |||||||||||| || |||
```

```
                                ACGTATTTTTAGG TC ATT
                                      G  _
GAM934  PIGA     3'  TTACTGGGATTTTTATGCA   12077           _  C
                                TGTGTAAGGGTCC AG TGA
                                |||||||||||| || |||
                                ACGTATTTTTAGG TC ATT
                                      G  _
GAM934  PTTG1IP  3'  TTTGGGGTTTGGGCTTTTTTAT 16351     T       _  GA
          A                      TGTG AAGGGTCCAG CT  TCAAG
                                |||| |||||||||| ||  |||||
                                ATAT TTTTCGGGTT GG  GGTTT
                                  T        T __
GAM934  RBBP6    3'  CTTGATTATTTGATTTTTACAT 73860          C  C
                                GTGTAAGGGTC AG TGATCAAG
                                |||||||||| || ||||||||
                                TACATTTTTAG TT ATTAGTTC
                                      _ T
GAM934  RPE      3'  TAGCTGGACCTTTAACA     62878     G
                                TGT TAAGGGTCCAGCTG
                                ||| ||||||||||||||
                                ACA ATTTCCAGGTCGAT
                                  _
GAM934  RPH3AL   5'  TTTGTGTAGTGGACACTTGTAC 23746       G    G   AT
                                GTGTAAG GTCCA CTG  CAAG
                                ||||||| ||||| |||  ||||
                                CATGTTC CAGGT GAT  GTTT
                                    A    _  GT
GAM934  RRM2B    3'  TTTGATCCATTGCTTTTAGACA 68439     G      CCAGCT
                                TGT TAAGGGT     GATCAAG
                                ||| |||||||     |||||||
                                ACA ATTTTCG     CTAGTTT
                                  G      TTAC__
GAM934  SCN3A    3'  CTTGATCTGACATTTGTATACA 23616       AGG__   CAGCT
                                TGTGTA    GTC    GATCAAG
                                ||||||    |||    |||||||
                                ACATAT    CAG    CTAGTTC
                                    GTTTA   T____
GAM934  SEPX1    5'  TTTGGTCAGTTGGCAGCGGCA  33382     AAGG T
                                TGT    G CCAGCTGATCAAG
                                |||    | ||||||||||||||
                                ACG    C GGTTGACTGGTTT
                                  GCGA _
GAM934  SFPQ     3'  TTTGATTAAATGGATCTTTTAT 18613     T       GC
                                GTG AAGGGTCCA  TGATCAAG
                                ||| |||||||||  ||||||||
                                TAT TTTCTAGGT  ATTAGTTT
                                  _        AA
GAM934  SHMT2    3'  CTTGCAGGTTGGACTCTTCACA 19437      T          GAT
                                TGTG AAGGGTCCAGCT   CAAG
                                |||| ||||||||||||   ||||
```

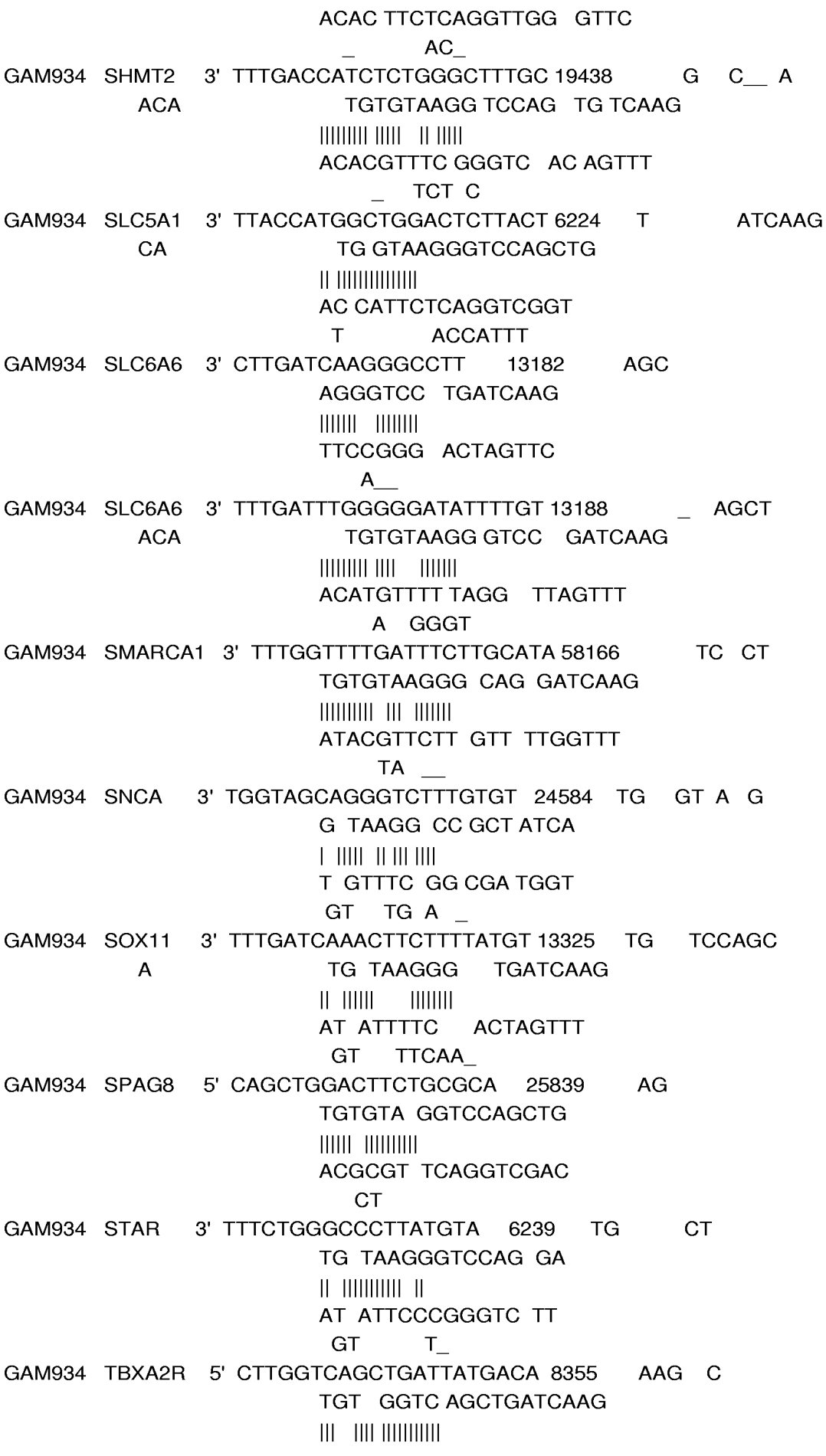
ACAC TTCTCAGGTTGG GTTC
_ AC_
GAM934 SHMT2 3' TTTGACCATCTCTGGGCTTTGC 19438 G C__ A
ACA TGTGTAAGG TCCAG TG TCAAG
ACACGTTTC GGGTC AC AGTTT
_ TCT C
GAM934 SLC5A1 3' TTACCATGGCTGGACTCTTACT 6224 T ATCAAG
CA TG GTAAGGGTCCAGCTG
AC CATTCTCAGGTCGGT
T ACCATTT
GAM934 SLC6A6 3' CTTGATCAAGGGCCTT 13182 AGC
AGGGTCC TGATCAAG
TTCCGGG ACTAGTTC
A__
GAM934 SLC6A6 3' TTTGATTTGGGGGATATTTTGT 13188 _ AGCT
ACA TGTGTAAGG GTCC GATCAAG
ACATGTTTT TAGG TTAGTTT
A GGGT
GAM934 SMARCA1 3' TTTGGTTTTGATTTCTTGCATA 58166 TC CT
TGTGTAAGGG CAG GATCAAG
ATACGTTCTT GTT TTGGTTT
TA __
GAM934 SNCA 3' TGGTAGCAGGGTCTTTGTGT 24584 TG GT A G
G TAAGG CC GCT ATCA
T GTTTC GG CGA TGGT
GT TG A _
GAM934 SOX11 3' TTTGATCAAACTTCTTTTATGT 13325 TG TCCAGC
A TG TAAGGG TGATCAAG
AT ATTTTC ACTAGTTT
GT TTCAA_
GAM934 SPAG8 5' CAGCTGGACTTCTGCGCA 25839 AG
TGTGTA GGTCCAGCTG
ACGCGT TCAGGTCGAC
CT
GAM934 STAR 3' TTTCTGGGCCCTTATGTA 6239 TG CT
TG TAAGGGTCCAG GA
AT ATTCCCGGGTC TT
GT T_
GAM934 TBXA2R 5' CTTGGTCAGCTGATTATGACA 8355 AAG C
TGT GGTC AGCTGATCAAG

```
                                ACA   TTAG TCGACTGGTTC
                                  GTA   _
GAM934  TRIM8    3'  TTGCCTGGATTTTGACACA   48858      A       CTGAT
                                TGTGT AGGGTCCAG    CAA
                                ||||| |||||||||    |||
                                ACACA TTTTAGGTC    GTT
                                   G       C____
GAM934  TSNAX    3'  TTATTGTGGCTTTTACATA   21162          _  C
                                TGTGTAAGGGTC CAG TGA
                                |||||||||||| ||| |||
                                ATACATTTTCGG GTT ATT
                                       T  _
GAM934  TTID     3'  ATCCTTTGACTCTTGCACA   23281          C  CT
                                TGTGTAAGGGTC AG  GAT
                                |||||||||||| ||  |||
                                ACACGTTCTCAG TT  CTA
                                       _  TC
GAM934  VHL      3'  TTGGTTGGTTTTTACATA    6884          T    TG
                                TGTGTAAGGG CCAGC  A
                                |||||||||| |||||  |
                                ATACATTTTT GGTTG  T
                                      _    GT
GAM934  VHL      3'  TTGGTTGGTTTTTACATA    6885          T    TG
                                TGTGTAAGGG CCAGC  A
                                |||||||||| |||||  |
                                ATACATTTTT GGTTG  T
                                      _    GT
GAM934  WHSC1L1  3'  TTTGGTTGGTTTGGGATTCTT  35508        __  TG
                                AAGGGTCC  AGC  ATCAAG
                                ||||||||  |||  ||||||
                                TTCTTAGG  TTG  TGGTTT
                                     GT   GT
GAM934  XCL1     3'  CTTGTAATGGTTCTTTACACA  12984         GT   GCTGAT
                                TGTGTAAGG  CCA     CAAG
                                |||||||||  |||     ||||
                                ACACATTTC  GGT     GTTC
                                      TT   AAT___
GAM934  ZFP37    3'  TTTGAAAATGGATCTTCATATA 14162       A      GCTGA
                                TGTGT AGGGTCCA    TCAAG
                                ||||| ||||||||    |||||
                                ATATA TTCTAGGT    AGTTT
                                   C       AAA__
GAM934  AB026190 3'  TTTGACCTTGGAGCTTTGTACA 27832         G    CTGA
                                TGTGTAAGG TCCAG   TCAAG
                                ||||||||| |||||   |||||
                                ACATGTTTC AGGTT   AGTTT
                                      G    CC__
GAM934  ALS2CR2  5'  TGGAATAGATGGATTTTTGTCA 38322    _       G   A  AAG
                                TG TAAGGGTCCA CTG TC
                                || ||||||||| ||| ||
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                                AC GTTTTTAGGT GAT AG
                                 T        A  A  GTT
GAM934  AMOTL1   3'  TCTCTTGGCCCCTTGTACA   74013         T   CT
                                TGTGTAAGGG CCAG  GA
                                |||||||||| ||||  ||
                                ACATGTTCCC GGTT  CT
                                      C   CT
GAM934  ARTN     3'  CAGACTGGACCCTTACCG    15609    T        _
                                TG GTAAGGGTCCAG CTG
                                || ||||||||||| |||
                                GC CATTCCCAGGTC GAC
                                 _         A
GAM934  ATIP1    3'  TTGATCTACCCTTGCA      40778         CCAGCT
                                TGTAAGGGT     GATCAA
                                |||||||||     ||||||
                                ACGTTCCCA     CTAGTT
                                      T_____
GAM934  BIRC3    3'  TTGATCAGTGTCCTATACA   67778     A   TCCA
                                TGTA GGG    GCTGATCAA
                                |||| |||    |||||||||
                                ACAT TCC    TGACTAGTT
                                  A  TG__
GAM934  BOLL     3'  CTTGTCCAATGATCCTTGCG   53450         CAGC  AT
                                TGTAAGGGTC    TG  CAAG
                                ||||||||||    ||  ||||
                                GCGTTCCTAG    AC  GTTC
                                      TA__  CT
GAM934  BOP      5'  TTTGAATCTGGATTCTTGTACA 86234            CTGA
                                TGTGTAAGGGTCCAG    TCAAG
                                ||||||||||||||    |||||
                                ACATGTTCTTAGGTC    AGTTT
                                         TA__
GAM934  C1orf9   3'  CTTGCCAACTGGATCTTTG    33160          C  AT
                                TAAGGGTCCAG TG  CAAG
                                |||||||||| ||  ||||
                                GTTTCTAGGTC AC  GTTC
                                      A  C_
GAM934  C20orf100 3'  TTTGGGTTTGGGTTCTTGAC   52881    G   GG    CTGA
                                GT TAAG  TCCAG    TCAAG
                                || ||||  |||||    |||||
                                CA GTTC  GGGTT    GGTTT
                                 _    TT     TG__
GAM934  C20orf130 3'  CTTGATCAGTGTCCGTATGTA  62415    TG  AG  TCCA
                                TG  TA  GG    GCTGATCAAG
                                ||  ||  ||    ||||||||||
                                AT  AT  CC    TGACTAGTTC
                                 GT  G_  TG__
GAM934  C20orf177 3'  TTTCTCTGCTAGATTTTTATGC 62843           C   T  TCAAG
           A                     TGTGTAAGGGTC AGC GA
                                ||||||||||| ||| ||
```

```
                                ACGTATTTTTAG TCG CT
                                      A   T  CTTT
GAM934  C20orf21  3'  TTTGATGTCCAGTGGATTTTTG 35574          G  ___
                                TAAGGGTCCA CTG   ATCAAG
                                |||||||||| |||   ||||||
                                GTTTTTAGGT GAC   TAGTTT
                                      _  CTG
GAM934  C6orf32   3'  TCCCTCTGGATTCTTCTGCA  32407     GT        CT_
                                TGT  AAGGGTCCAG   GA
                                |||  ||||||||||   ||
                                ACG  TTCTTAGGTC   CT
                                  TC         TCC
GAM934  CAT56     3'  TTTGGTGCTGTTTCTTGTGCA  48281    TG     TC    TG
                                TG  TAAGGG  CAGC  ATCAAG
                                ||  ||||||  ||||  ||||||
                                AC  GTTCTT  GTCG  TGGTTT
                                  GT     T_   __
GAM934  CDCA7     3'  TTTGATCTGTAATGCTTTTATA 50046          CCA  T
              CA                  TGTGTAAGGGT   GC GATCAAG
                                ||||||||||   || |||||||
                                ACATATTTTCG   TG CTAGTTT
                                      TAA  T
GAM934  CDW92     3'  CTTGATTGTGTGCCATTTTATA 55429         __   CCA  T
              TA                  TGTGTAAG  GGT   GC GATCAAG
                                ||||||||  |||   || |||||||
                                ATATATTT  CCG   TG TTAGTTC
                                     TA   TG_  _
GAM934  CGI-57    3'  TCGCTGGGTCCTTGGCA     74311     G    GT    T
                                TGT TAAGG  CCAGC GA
                                ||| |||||  ||||| ||
                                ACG GTTCC  GGTCG CT
                                  _     TG    _
GAM934  CILP      3'  CTTGATCATAGTTCATACATA  14614        A GG CCAGC
                                TGTGTA G  T    TGATCAAG
                                |||||| |  |    ||||||||
                                ATACAT C  G    ACTAGTTC
                                    A TT AT___
GAM934  CLDN6     3'  TTTGAGATTCTGGATCTTGACA 41338      A        CTGA
              T                   GTGT AGGGTCCAG    TCAAG
                                |||| |||||||||    |||||
                                TACA TTCTAGGTC    AGTTT
                                  G        TTAG
GAM934  COQ7      3'  ATCGTTGTACTTTTGTACA    32853          C    T
                                TGTGTAAGGGT CAGC GAT
                                |||||||||||| |||| |||
                                ACATGTTTTCA GTTG CTA
                                      T   _
GAM934  CPSF2     3'  TGGTTGGATTTTATACA     62287          G
                                TGTGTAAGG TCCAGCTG
                                ||||||||| ||||||||
```

```
                                ACATATTTT AGGTTGGT
                                        _
GAM934  CPVL     5'  CGGCTGGGGTCCTTGCGC    49378        GT  _
                                GTGTAAGG  CC AGCTG
                                ||||||||  || |||||
                                CGCGTTCC  GG TCGGC
                                    TG  G
GAM934  CYP-M    3'  TTTGTAAATTTGGATTTTTATA 40708            CTGAT
           TA                    TGTGTAAGGGTCCAG    CAAG
                                ||||||||||||||    ||||
                                ATATATTTTTAGGTT    GTTT
                                       TAAAT
GAM934  DDX18    3'  CTTGATTTAACAGGATTTTTG  23196         AGCT_
                                TAAGGGTCC    GATCAAG
                                |||||||||    |||||||
                                GTTTTTAGG    TTAGTTC
                                    ACAAT
GAM934  DKFZP434A043 3'  TGGTTGGCATTTTTAACACA   31825      _    _    TG
                                TGTGT AAGGGT CCAGC  A
                                ||||| |||||| |||||  |
                                ACACA TTTTTA GGTTG  T
                                   A     C    GT
GAM934  DKFZp434K114 5'  CTTGGTCTTTCCGGGTCCTTGC 61385        GT  AGCT_
           AC                    GTGTAAGG  CC    GATCAAG
                                ||||||||  ||    |||||||
                                CACGTTCC  GG    CTGGTTC
                                    TG  CCTTT
GAM934  DKFZP434O125 3'  CTTGTTCCCTGATTTTTACACA 65585          C  CT  T
                                TGTGTAAGGGTC AG  GA CAAG
                                |||||||||||| ||  || ||||
                                ACACATTTTTAG TC  CT GTTC
                                       _  C_  T
GAM934  DKFZP434P0721 3'  TTTGATTTTAAATATCTTTACA 64469         CCAGCT
           T                     GTGTAAGGGT     GATCAAG
                                ||||||||||     |||||||
                                TACATTTCTA     TTAGTTT
                                    TAAATT
GAM934  DKFZp547M072 3'  TTTCCTGGACTCTTCAT     61719     T       CT
                                GTG AAGGGTCCAG  GA
                                ||| ||||||||||  ||
                                TAC TTCTCAGGTC  TT
                                  _        CT
GAM934  DKFZP564F013 3'  TTTGAAACACTGGGCTGTTTGC 95882        _     C  A_
           ACA                    TGTGTAAG GGTCCAG TG  TCAAG
                                ||||||||| ||||||| ||  |||||
                                ACACGTTT TCGGGTC AC  AGTTT
                                    G      _ AA
GAM934  DKFZP564F0522 3'  TCTTGCTGGGTTTTTGTACA  69141         GT    T_
                                TGTGTAAGG  CCAGC  GA
                                |||||||||  |||||  ||
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                                ACATGTTTT  GGTCG  CT
                                     TG    TT
GAM934  DKFZp761G0313 3'  CTTGATTATTAGTTGGGCTCTT 66392     T        ___
          CATA                   TGTG AAGGGTCCAGCT   GATCAAG
                                |||| ||||||||||||   |||||||
                                ATAC TTCTCGGGTTGA   TTAGTTC
                                  _         TTA
GAM934  DKFZp761G0313 3'  TTTGATTAGTTGGAGCTTT    66395     G
                                AAGG TCCAGCTGATCAAG
                                |||| ||||||||||||||
                                TTTC AGGTTGATTAGTTT
                                  G
GAM934  DNAM-1    3'  TCATGCATGGATCTTTATGCA  22687           _ _
                                TGTGTAAGGGTCCA GC TGA
                                |||||||||||||| || |||
                                ACGTATTTCTAGGT CG ACT
                                         A  T
GAM934  DUSP10    3'  TCACTGGCTTCTTGTGCA    24234    TG    T   C
                                TG  TAAGGG CCAG TGA
                                ||  |||||| |||| |||
                                AC  GTTCTT GGTC ACT
                                 GT     C   _
GAM934  FHOD2     3'  TTTGATTAGGTATCTTTTTACA 74265         TCCAG
          C                      GTGTAAGGG    CTGATCAAG
                                |||||||||    |||||||||
                                CACATTTTT    GATTAGTTT
                                     CTATG
GAM934  FLJ10375  3'  TTGGCTCGGGATCCTTGGCA  36562     G       __  TG
                                TGT TAAGGGTCC  AGC  A
                                ||| |||||||||  |||  |
                                ACG GTTCCTAGG  TCG  T
                                  _       GC   GT
GAM934  FLJ10388  3'  TTTGGTCAGCCTGGCTTTTG   36572       T   _
                                TAAGGG CCAG CTGATCAAG
                                |||||| |||| |||||||||
                                GTTTTC GGTC GACTGGTTT
                                   _   C
GAM934  FLJ10539  3'  TTTGGTCAGGCATATTTTACTC 36764    T     GTCCAG
          A                     TG GTAAGG     CTGATCAAG
                                || ||||||     |||||||||
                                AC CATTTT     GACTGGTTT
                                 T     ATACG_
GAM934  FLJ10583  3'  TTGGTTGCATTCTTGGACA    36833     G     C    TG
                                TGT TAAGGGT CAGC  A
                                ||| ||||||| ||||  |
                                ACA GTTCTTA GTTG  T
                                  G      C   GT
GAM934  FLJ10898  3'  TTGACCAGTTGGGTTTTTTGC  60146    T   GT     A
                                GTG AAGG  CCAGCTG TCAA
                                ||| ||||  ||||||| ||||
```

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                              CGT TTTT  GGTTGAC AGTT
                                _   TG      C
GAM934  FLJ10970  3'  TTTGGTCAGGAACTTTATA   37479       G   AGC
                              TGTAAGG TCC   TGATCAAG
                              ||||||| |||   ||||||||
                              ATATTTC AGG   ACTGGTTT
                                  A  ___
GAM934  FLJ11053  3'  TTTGGTTTCCTGGTGGACATTT 90125        _    G ____
          TGTACA                TGTGTAAGG GTCCA CT    GATCAAG
                              ||||||||| ||||| ||    |||||||
                              ACATGTTTT CAGGT GG    TTGGTTT
                                  A    _ TCCT
GAM934  FLJ12484  3'  TTTGAATTCTGGGGCCTTTGTG 70232    TG       AGCTGA
          TA                   TG  TAAGGGTCC     TCAAG
                              ||  |||||||||     |||||
                              AT  GTTTCCGGG     AGTTT
                               GT       GTCTTA
GAM934  FLJ12542  3'  TTAATTGGAATTTTACACA   46603        G    C
                              TGTGTAAGG TCCAG TGA
                              ||||||||| ||||| |||
                              ACACATTTT AGGTT ATT
                                  A    A
GAM934  FLJ12592  3'  TTTGATCAGTGGGTTTT    50658    GT   G
                              AGG  CCA CTGATCAAG
                              |||  ||| |||||||||
                              TTT  GGT GACTAGTTT
                                TG  _
GAM934  FLJ12688  3'  CTTGATCAGTCCTCAGCTTTGC 73554       GTCCA_
          A                   TGTAAGG     GCTGATCAAG
                              |||||||     ||||||||||
                              ACGTTTC     TGACTAGTTC
                                  GACTCC
GAM934  FLJ12787  3'  TGGGATTTCTGGGCCCTTGC   50699          CT    AAG
                              GTAAGGGTCCAG  GATC
                              ||||||||||||  ||||
                              CGTTCCCGGGTC  TTAG
                                     T_    GGTT
GAM934  FLJ12891  3'  TTTGACTTGGGGTCTTATATA  46937        G    CTGA
                              TGTGTAAGG TCCAG    TCAAG
                              ||||||||| |||||    |||||
                              ATATATTCT GGGTT    AGTTT
                                  G    C___
GAM934  FLJ12934  3'  CTTGGTATAAAAGACTCTTACA 43490         CAGCTG
                              TGTAAGGGTC     ATCAAG
                              ||||||||||     ||||||
                              ACATTCTCAG     TGGTTC
                                   AAAATA
GAM934  FLJ13081  3'  TTTGATTCTATTGGATTTTTGG 46172     G        CT  _
          CA                   TGT TAAGGGTCCAG  GA TCAAG
                              ||| ||||||||||  || |||||
```

```
                                ACG GTTTTTAGGTT  CT AGTTT
                                  _         AT  T
GAM934  FLJ13614  3'  CTTGAGATATGCAGGATCCTTG 58198           A  TGA__
            TAT                   GTGTAAGGGTCC GC     TCAAG
                                  ||||||||||| ||     |||||
                                  TATGTTCCTAGG CG     AGTTC
                                        A  TATAG
GAM934  FLJ13657  3'  TTATTTGGGGTCTTATAT    46141         G    C
                                  GTGTAAGG TCCAG TGA
                                  |||||||| ||||| |||
                                  TATATTCT GGGTT ATT
                                      G    T
GAM934  FLJ13955  3'  CTTGACTGGTGGGCTTTTTAC  45748     T       G  GA
                                  GTG AAGGGTCCA CT  TCAAG
                                  ||| |||||||| ||  |||||
                                  CAT TTTTCGGGT GG  AGTTC
                                    _       _ TC
GAM934  FLJ20015  3'  CTTGATCAGGAAACTTGTGCA  39160    TG   GG   AGC
                                  TG  TAAG  TCC   TGATCAAG
                                  ||  ||||  |||   ||||||||
                                  AC  GTTC  AGG   ACTAGTTC
                                   GT    AA  ___
GAM934  FLJ20034  3'  TGTGGGGTGGCTGGACCCTGCA 34858       A         A_   AG
            T                     GTGTA GGGTCCAGCTG  TCA
                                  ||||| ||||||||||  |||
                                  TACGT CCCAGGTCGGT  GGT
                                    _         GG   GTT
GAM934  FLJ20195  3'  TTATTGGACCTTTGGCA     35225     G         C
                                  TGT TAAGGGTCCAG TGA
                                  ||| ||||||||||| |||
                                  ACG GTTTCCAGGTT ATT
                                    _         _
GAM934  FLJ20445  3'  CTTGGTCCAAGCTCTTACA    35631          CCAGCT
                                  TGTAAGGGT     GATCAAG
                                  |||||||||     |||||||
                                  ACATTCTCG     CTGGTTC
                                        AAC___
GAM934  FLJ20485  3'  TTTGGTTGCGGTGGCTTTTGCA 39296           CA_  T
            T                     GTGTAAGGGTC   GC GATCAAG
                                  ||||||||||   || |||||||
                                  TACGTTTTCGG   CG TTGGTTT
                                        TGG  _
GAM934  FLJ22679  3'  TTTGTCAGGCTGGTTCTTGCG  50911        T     GAT
                                  TGTAAGGG CCAGCT   CAAG
                                  |||||||| ||||||   ||||
                                  GCGTTCTT GGTCGG   GTTT
                                      _     ACT
GAM934  FLJ22679  3'  TTTGTCAGGCTGGTTCTTGCG  35186        T     GAT
                                  TGTAAGGG CCAGCT   CAAG
                                  |||||||| ||||||   ||||
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                                GCGTTCTT GGTCGG   GTTT
                                   _     ACT
GAM934  FLJ22746  5'  CTTGAACAGTGGGCCTTCTACA 45918       _      G   A
          CA                     TGTGTA AGGGTCCA CTG TCAAG
                                 |||||| |||||||| ||| |||||
                                 ACACAT TTCCGGGT GAC AGTTC
                                    C       _   A
GAM934  FLJ23045  3'  TTTGAATCAGAACTTTTATATA 45552          CCAG    _
                                 TGTGTAAGGGT    CTGAT CAAG
                                 ||||||||||    ||||| ||||
                                 ATATATTTTCA    GACTA GTTT
                                       A___     A
GAM934  FLJ23185  5'  TTTGTTTATGGGCTTTTGCCAC 47524      _        GCT  T
          A                      TGTG TAAGGGTCCA   GA CAAG
                                 |||| ||||||||||   || ||||
                                 ACAC GTTTTCGGGT   TT GTTT
                                   C        AT_ _
GAM934  FLJ31709  3'  TTGGAGTGGACCTTTTGCA    58920      T       G_ TG
                                 TGTG AAGGGTCCA  C  A
                                 |||| |||||||||  |  |
                                 ACGT TTTCCAGGT  G  T
                                   _       GA GT
GAM934  H2AFY2    3'  TTTATAGCATTGACTTTTACAC 38467          CA_   ATCAAG
          A                      TGTGTAAGGGTC   GCTG
                                 ||||||||||||   ||||
                                 ACACATTTTCAG   CGAT
                                       TTA    ATTT
GAM934  HDAC9-PENDING 3'  TTTGGTTAGTATATTCCTTCAT 28844      T    TCCA
          A                      TGTG AAGGG    GCTGATCAAG
                                 |||| |||||    ||||||||||
                                 ATAC TTCCT    TGATTGGTTT
                                   _    TATA
GAM934  HSBP1     3'  TTGGCGGTTCTTGCATA     9520          T  A  TG
                                 TGTGTAAGGG CC GC  A
                                 |||||||||| || ||  |
                                 ATACGTTCTT GG CG  T
                                       _ _  GT
GAM934  HTCD37    3'  CTTGATTGTCTGTATTTCTGTG 68300    TG  AG   C   C
          T                      G  TA  GGT CAG TGATCAAG
                                 |  ||  ||| ||| ||||||||
                                 T  GT  TTA GTC GTTAGTTC
                                  GT  CT   T   T
GAM934  IDI1      3'  CTTGATCAATGTACTTTTTATA 67602      T     C  GC
                                 TGTG AAGGGT CA  TGATCAAG
                                 |||| |||||| ||  ||||||||
                                 ATAT TTTTCA GT  ACTAGTTC
                                   _     T  A_
GAM934  ITGA8     5'  TTAGTCTGGATTTTTATA    94846           _
                                 TGTAAGGGTCCAG CTGA
                                 |||||||||||| ||||
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```
                                ATATTTTTAGGTC GATT
                                      T
GAM934  KIAA0084 3' CTGACAGTGTTGGTTTTTGCAC 68708         T __   A  AG
           A                   TGTGTAAGGG CCA  GCTG TCA
                               |||||||||| |||  |||| |||
                               ACACGTTTTT GGT  TGAC AGT
                                     _  TG   _  C
GAM934  KIAA0089 3' TGAGGAGTTGGAACTTTGCG  70511       G     GA
                               TGTAAGG TCCAGCT  TCA
                               ||||||| |||||||  |||
                               GCGTTTC AGGTTGA  AGT
                                   A     GG
GAM934  KIAA0179 3' TTGGTTGAATCTTTTGCTACA  65461    _     TC_   TG
                               TGT GTAAGGG   CAGC  A
                               ||| |||||||   ||||  |
                               ACA CGTTTTC   GTTG  T
                                 T      TAA   GT
GAM934  KIAA0191 3' TTTGGTTGCTTCAGACTTTATA 66513         GTCC_  T
           TA                   TGTGTAAGG    AGC GATCAAG
                               |||||||||    ||| |||||||
                               ATATATTTC    TCG TTGGTTT
                                    AGACT  _
GAM934  KIAA0212 3' TTTGGTCAGTGCAGTTGTGCA  28633   TG  GG  CCA
                               TG  TAA  GT   GCTGATCAAG
                               ||  |||  ||   ||||||||||
                               AC  GTT  CG   TGACTGGTTT
                                GT   GA  ___
GAM934  KIAA0276 3' CTTGATTGTCTTGATTTTATAT 71521         G  C  C
           A                   TGTGTAAGG TC AG TGATCAAG
                               ||||||||| || || ||||||||
                               ATATATTTT AG TC GTTAGTTC
                                     _ T  T
GAM934  KIAA0323 3' TTGATTGGTTTCTTGCCA   63951   T    GTCC  TG
                               TG GTAAGG   AGC  ATCAA
                               || ||||||   |||  |||||
                               AC CGTTCT   TTG  TAGTT
                                _    ____  GT
GAM934  KIAA0373 5' TTGATTATTCCTTATAC    28691        TCCAGC
                               GTGTAAGGG    TGATCAA
                               |||||||||    |||||||
                               CATATTCCT    ATTAGTT
                                    T_____
GAM934  KIAA0433 3' TGATGAGCTGGCCTTTGTGCA  31501   TG    T    G
                               TG  TAAGGG CCAGCT ATCA
                               ||  |||||| |||||| ||||
                               AC  GTTTCC GGTCGA TAGT
                                GT    _    G
GAM934  KIAA0446 3' TTTGATGAAATGGACTCTTG  69463         GCTG
                               TAAGGGTCCA   ATCAAG
                               ||||||||||   ||||||
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                                GTTCTCAGGT   TAGTTT
                                     AAAG
GAM934  KIAA0494 3' TTGATTTGAGCTTTGCATA   29407        G  CAGCT
                                TGTGTAAGG TC    GATCAA
                                ||||||||| ||    ||||||
                                ATACGTTTC AG    TTAGTT
                                     G  T____
GAM934  KIAA0514 3' TGGGGGCTGGGTTCATACAC  28762      A GG     GA
                                GTGTA G  TCCAGCT  TCA
                                ||||| |  |||||||  |||
                                CACAT C  GGGTCGG  GGT
                                   A TT      G_
GAM934  KIAA0711 3' TTGATTGGCCTTTTATA     30158        TCCA  TG
                                TGTAAGGG   GC  ATCAA
                                ||||||||   ||  |||||
                                ATATTTTC   CG  TAGTT
                                     ____  GT
GAM934  KIAA0746 3' CAGATCTGGATTCTTATACA  69985           __
                                TGTGTAAGGGTCCAG  CTG
                                ||||||||||||||  |||
                                ACATATTCTTAGGTC  GAC
                                          TA
GAM934  KIAA0844 3' CTTGGCATCTGGGCTTCTATGC 30893       AG     C  A
           A                     TGTGTA  GGTCCAG TG TCAAG
                                ||||||  ||||||| || |||||
                                ACGTAT  TCGGGTC AC GGTTC
                                   CT      T  _
GAM934  KIAA0854 3' TCAGTGGGTCCTTGTACA    30780        GT   G
                                TGTGTAAGG  CCA CTGA
                                |||||||||  ||| ||||
                                ACATGTTCC  GGT GACT
                                     TG  _
GAM934  KIAA0888 3' CTTGATCTTGATCCTTATGCA 63926          CAGCT
                                TGTGTAAGGGTC    GATCAAG
                                ||||||||||||    |||||||
                                ACGTATTCCTAG    CTAGTTC
                                      TT___
GAM934  KIAA1000 3' TTTGATCAGCAGCTATTTTATA 65881       GTCCA
           C                     GTGTAAGG    GCTGATCAAG
                                ||||||||    ||||||||||
                                CATATTTT    CGACTAGTTT
                                     ATCGA
GAM934  KIAA1030 3' CATGCTGCACCTTTGCAT    94974        C   _
                                GTGTAAGGGT CAGC TG
                                |||||||||| |||| ||
                                TACGTTTCCA GTCG AC
                                      C   T
GAM934  KIAA1041 3' TTGGACGGCTTTTTGCATA   30836        GTCC    A
                                TGTGTAAGG   AGCTG TCAA
                                |||||||||   ||||| ||||
```

```
                                ATACGTTTT   TCGGC GGTT
                                     ____    A
GAM934  KIAA1074  3'  TTTATTACTGGGCTGTTTATGT 30545   TG  _     C   CAAG
                                G  TAAG GGTCCAG TGAT
                                |  |||| ||||||| ||||
                                T  ATTT TCGGGTC ATTA
                                 GT   G     _   TTT
GAM934  KIAA1143  3'  CTTGGTCAGGTTTCTTTTATAT 69240        TCCAG
                                GTGTAAGGG    CTGATCAAG
                                |||||||||    |||||||||
                                TATATTTTC    GACTGGTTC
                                     TTTG_
GAM934  KIAA1181  3'  TTGGATGGATTTTTTTACA   68916     T       G TG
                                TGTG AAGGGTCCA C  A
                                |||| |||||||||  |  |
                                ACAT TTTTTAGGT G  T
                                   T       A GT
GAM934  KIAA1238  3'  TTTGATCATGCTTACTTGTACA 71637     AG   CC  _
                                TGTA  GGT  AGC TGATCAAG
                                ||||  |||  ||| ||||||||
                                ACAT  TCA  TCG ACTAGTTT
                                  GT   T_   T
GAM934  KIAA1257  3'  TGAACTGGACTTTATACA    63421        G    CTGA
                                TGTGTAAGG TCCAG    TCA
                                |||||||||  |||||    |||
                                ACATATTTC AGGTC    AGT
                                     _    A___
GAM934  KIAA1265  3'  TTGATTAAGACTTTTCACA   71339     T     CAGC
                                TGTG AAGGGTC    TGATCAA
                                |||| |||||||    |||||||
                                ACAC TTTTCAG    ATTAGTT
                                  _      A___
GAM934  KIAA1317  5'  CTTCACCTGTGGACTCTTATAC 87212           __ C   TCAAG
          A                      TGTGTAAGGGTCCA  G TGA
                                |||||||||||||  | |||
                                ACATATTCTCAGGT  C ACT
                                         GT C   TC
GAM934  KIAA1322  3'  CTTGGTTAGTCATGCGTACAT  73111      AGGGTCCA
                                GTGTA       GCTGATCAAG
                                |||||       ||||||||||
                                TACAT       TGATTGGTTC
                                  GCGTAC__
GAM934  KIAA1336  3'  TAGTTGAATTTTTGCACA    72787          C
                                TGTGTAAGGGT CAGCTG
                                |||||||||||  ||||||
                                ACACGTTTTTA GTTGAT
                                       A
GAM934  KIAA1530  3'  CTTGATCAGTGCTGCTTT    68559      CCA
                                AGGGT   GCTGATCAAG
                                |||||   ||||||||||
```

```
                                TTTCG   TGACTAGTTC
                                   TCG
GAM934  KIAA1580 5' CTTGTGAGCCCTGGATCTTAAC 69981       A       __   G T
             ACA                    TGTGT AGGGTCCA  GCT A CAAG
                                |||||| ||||||||  ||| | ||||
                                ACACA TTCTAGGT  CGA T GTTC
                                   A       CC   G _
GAM934  KIAA1598 3' TTTGGTTTTTTGATCTTTATA  37643          C  CT
                                TGTAAGGGTC AG  GATCAAG
                                |||||||||| ||  |||||||
                                ATATTTCTAG TT  TTGGTTT
                                      _ TT
GAM934  KIAA1656 3' TGGAAGCGGCTGGGCCCTTACC 66389    T           A_  AAG
             CA                   TG GTAAGGGTCCAGCTG  TC
                                || ||||||||||||||  ||
                                AC CATTCCCGGGTCGGC  AG
                                 C            GA  GT
GAM934  KIAA1679 3' CAGCTGGGTCCTTGGCA     70709     G     GT
                                TGT TAAGG  CCAGCTG
                                ||| |||||  |||||||
                                ACG GTTCC  GGTCGAC
                                  _    TG
GAM934  KIAA1727 3' CTTGGTACAGTGGTTTTTAAAT 64760     G     T   G   _
             A                   TGT TAAGGG CCA CTG ATCAAG
                                ||| |||||| ||| ||| ||||||
                                ATA ATTTTT GGT GAC TGGTTC
                                  A     _  _   A
GAM934  KIAA1728 3' CTTGGTTTAAAGGTATTTTTAT 68951          _  AGCT
             AT                   GTGTAAGGGT CC    GATCAAG
                                ||||||||||  ||    |||||||
                                TATATTTTTA GG    TTGGTTC
                                      T  AAAT
GAM934  KIAA1796 3' TCAGTTTGGCTTTTATGT    93101    TG       C
                                G  TAAGGGTC AGCTGA
                                |  |||||||| ||||||
                                T  ATTTTCGG TTGACT
                                 GT       T
GAM934  KIAA1804 3' CTTGCATTCTGGATTCTTGCA  70349           CT   _
                                TGTAAGGGTCCAG  GAT CAAG
                                ||||||||||||  ||| ||||
                                ACGTTCTTAGGTC  TTA GTTC
                                      __   C
GAM934  KIAA1813 5' CTTGGGCCTGGGTCTTTGC    70824       GT    CTGA
                                GTAAGG  CCAG    TCAAG
                                ||||||  ||||    |||||
                                CGTTTC  GGTC    GGTTC
                                   TG    CG__
GAM934  KIAA1956 3' CTTGATCAGAGGGTTCTTAC   79078      GG   AG
                                GTAAG  TCC  CTGATCAAG
                                |||||  |||  |||||||||
```

```
                                CATTC  GGG  GACTAGTTC
                                   TT  A_
GAM934  KIAA1971  3'  TGATGCTGGAGCTTTTATGT  74699  TG    _    TG
                                G  TAAGGG TCCAGC  ATCA
                                |  |||||| ||||||  ||||
                                T  ATTTTC AGGTCG  TAGT
                                 GT     G    __
GAM934  LNX       5'  CTTGGCTGGTTTGGGCCCTTG  51911          _  AT
                                TAAGGGTCCAG CTG  CAAG
                                |||||||||||  |||  ||||
                                GTTCCCGGGTT GGT  GTTC
                                       T  CG
GAM934  LRBA      3'  TTTGATTAGCAATTTGTAC  22995    AG  CCA
                                GTA  GGT  GCTGATCAAG
                                |||  |||  ||||||||||
                                CAT  TTA  CGATTAGTTT
                                  GT  A__
GAM934  MAN1      3'  TGGCTGTACTTTTGCATA  27483          C
                                TGTGTAAGGGT CAGCTG
                                ||||||||||| ||||||
                                ATACGTTTTCA GTCGGT
                                       T
GAM934  MEP50     3'  TTGGTACGGTTTTACACA  44320        GGTCCA  _
                                TGTGTAAG     GCTG ATCAA
                                ||||||||     |||| |||||
                                ACACATTT     TGGC TGGTT
                                     _______  A
GAM934  MGC10818  3'  TTTGGTGAGTGGCCTTTGCCCA 48305    T     T  G  G
                                TG GTAAGGG CCA CT ATCAAG
                                || ||||||| ||| || ||||||
                                AC CGTTTCC GGT GA TGGTTT
                                 C      _  _  G
GAM934  MGC13016  3'  TCCTGCTGGGCCCCTGCATA  51344       A       T_
                                TGTGTA GGGTCCAGC  GA
                                |||||| |||||||||  ||
                                ATACGT CCCGGGTCG  CT
                                   C        TC
GAM934  MGC15606  3'  TTTGATTCAGCTAAATTTTATG 59529   TG    GTCC    _
          T                      G  TAAGG    AGCTGA TCAAG
                                |  |||||    |||||| |||||
                                T  ATTTT    TCGACT AGTTT
                                 GT     AAA_     T
GAM934  MGC16491  3'  CTTGGTTACAGGGCTCTCACAT 54738     A      AGC
                                GTGT AGGGTCC   TGATCAAG
                                |||| |||||||   ||||||||
                                TACA TCTCGGG   ATTGGTTC
                                  C      AC_
GAM934  MGC26655  3'  TTGTTCAGCTGATTTTTATATA 57126          C     T
                                TGTGTAAGGGTC AGCTGA CAA
                                ||||||||||| |||||| |||
```

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                                ATATATTTTTAG TCGACT GTT
                                       _     T
GAM934  MGC2865  5' TGCCGTGTTGGATCTTTGCCA  51463    T         TGAT
                                TG GTAAGGGTCCAGC    CA
                                || ||||||||||||    ||
                                AC CGTTTCTAGGTTG    GT
                                 _          TGCC
GAM934  MGC4607  3' GTCGGCTGGGCCCTTGGAC   49543    G
                                GT TAAGGGTCCAGCTGAT
                                || ||||||||||||||||
                                CA GTTCCCGGGTCGGCTG
                                 G
GAM934  MGC4767  3' TTGGTCTGTATCTTTGCTCA  51260    T      C  _ TG
                                TG GTAAGGGT CAG C  A
                                || |||||||| ||| |  |
                                AC CGTTTCTA GTC G  T
                                 T       T   T GT
GAM934  MGC4827  3' CTTGGAATTGGGCTTTTG    44365          CTGA
                                TAAGGGTCCAG    TCAAG
                                ||||||||||    |||||
                                GTTTTCGGGTT    GGTTC
                                      AA__
GAM934  MRPS6    3' TTTGCAAGTTTGGCCTTTATAT 51646           C    GAT
          A                      TGTGTAAGGGTC AGCT   CAAG
                                ||||||||||| ||||   ||||
                                ATATATTTCCGG TTGA   GTTT
                                      T    AC_
GAM934  MST4     3' CTGCACAGTTTGGTTTTTGCAC 33742         GT C    AT  AG
          A                      TGTGTAAGG  C AGCTG  CA
                                |||||||||  | |||||  ||
                                ACACGTTTT  G TTGAC  GT
                                     TG T    AC  C
GAM934  NCBP2    3' TTGATCAGTGTCTTTAC     24770        TCCA
                                GTAAGGG    GCTGATCAA
                                |||||||    |||||||||
                                CATTTCT    TGACTAGTT
                                    G___
GAM934  NDRG4    3' TTTGGTCAAGGTGAACTTTTA  40388        C  G  _
                                TAAGGGT CA CT GATCAAG
                                ||||||| || || |||||||
                                ATTTTCA GT GA CTGGTTT
                                    A  G  A
GAM934  NDRG4    3' TTTGGTCAAGGTGAACTTTTA  40389        C  G  _
                                TAAGGGT CA CT GATCAAG
                                ||||||| || || |||||||
                                ATTTTCA GT GA CTGGTTT
                                    A  G  A
GAM934  NFAT5    3' CTTGATCATGTTACCTTTAT   57768        CC  _
                                GTAAGGGT  AGC TGATCAAG
                                ||||||||  ||| ||||||||
```

```
                                TATTTCCA  TTG ACTAGTTC
                                    __   T
GAM934  NY-REN-41 3'  TCTGTTGTGATTTTTACATA  55562          _   T
                                TGTGTAAGGGTC CAGC GA
                                |||||||||||| |||| ||
                                ATACATTTTTAG GTTG CT
                                      T   T
GAM934  NY-REN-60 3'  CTCAGTGAGTGGATTTTTGTGT 51814   TG       ___    TCAAG
                                G  TAAGGGTCCA   GCTGA
                                |  ||||||||||   |||||
                                T  GTTTTTAGGT   TGACT
                                 GT        GAG    C   G
GAM934  OSBPL3   3'  TTTGGAAATGGGACTTTGTGCA 32080    TG    GT   GCTGA
                                TG  TAAGG  CCA    TCAAG
                                ||  |||||  |||    |||||
                                AC  GTTTC  GGT    GGTTT
                                 GT    AG   AAA__
GAM934  PARVA    3'  TTGATCCATTTCTTACACA   37187         TCCAGCT
                                TGTGTAAGGG      GATCAA
                                ||||||||||      ||||||
                                ACACATTCTT      CTAGTT
                                      TAC_____
GAM934  PB1      3'  CTTGGTTTTGGGTTTTTTTATA 36876     T   GT    CT
                                TGTG AAGG  CCAG  GATCAAG
                                |||| ||||  ||||  |||||||
                                ATAT TTTT  GGTT  TTGGTTC
                                  T   TG   __
GAM934  PCDH20   3'  TTAGTTGGGCCTTTTATAT   43426       _
                                GTGTAAG GGTCCAGCTGA
                                ||||||| ||||||||||
                                TATATTT CCGGGTTGATT
                                    T
GAM934  PEG10    3'  TCAGATGGACTCTTGCAT    31206           G
                                GTGTAAGGGTCCA CTGA
                                |||||||||||| ||||
                                TACGTTCTCAGGT GACT
                                       A
GAM934  PIP5K2B  3'  CGGCTGGGCTCTTGGACA    57695     G
                                TGT TAAGGGTCCAGCTG
                                ||| ||||||||||||||
                                ACA GTTCTCGGGTCGGC
                                  G
GAM934  PLSCR4   3'  CTTGGTCACAGATGCCTTATAT 40132         _  CAGC
          A                      TGTGTAAGG GTC    TGATCAAG
                                |||||||| |||    ||||||||
                                ATATATTCC TAG    ACTGGTTC
                                      G   AC__
GAM934  PPP1R1A  3'  TTTGGTGTTAGGTCCTTGGCA  23097     G    GT C   TG
                                TGT TAAGG  C AGC  ATCAAG
                                ||| |||||  | |||  ||||||
```

```
                                ACG GTTCC  G TTG  TGGTTT
                                  _    TG A  __
GAM934  PRO1617  5'  TTGATAGGGACTCTTTGCA   38340       _   AGCTG
                                TGTAAGG GTCC    ATCAA
                                ||||||| ||||    |||||
                                ACGTTTC CAGG    TAGTT
                                    T   GA___
GAM934  PRO1728  5'  CTTGGTTGGGGCTTGGACCTTT 38136    T       _  __
           GCCA                   TG GTAAGGGTCCA GCT  GATCAAG
                                || ||||||||||| |||  |||||||
                                AC CGTTTCCAGGT CGG  TTGGTTC
                                 _        T  GG
GAM934  PRRG1    3'  TTATTGGACTCTTACCG     8155     T        C
                                TG GTAAGGGTCCAG TGA
                                || ||||||||||| |||
                                GC CATTCTCAGGTT ATT
                                 _        _
GAM934  PTD012   5'  CTTGGTGCGCTGTGGACTCTTG 26737         __ TG
                                TAAGGGTCCA  GC  ATCAAG
                                ||||||||||  ||  ||||||
                                GTTCTCAGGT  CG  TGGTTC
                                     GT  CG
GAM934  PTPRT    3'  CAGGGATGGGCTTTTGCAT   56488          G__
                                GTGTAAGGGTCCA   CTG
                                ||||||||||||   |||
                                TACGTTTTCGGGT   GAC
                                      AGG
GAM934  QKI      3'  TTTGGGTTTTAGTTGGGATTTT 66052        GT     ___
           ACATA                  TGTGTAAGG  CCAGCTGA   TCAAG
                                |||||||||  ||||||||   |||||
                                ATACATTTT  GGTTGATT   GGTTT
                                     AG      TTG
GAM934  QKI      3'  TTTGGTTGGTTGAATAAATTTG 66053      GGTC__   TG
           C                    GTAAG     CAGC  ATCAAG
                                |||||     ||||  ||||||
                                CGTTT     GTTG  TGGTTT
                                   AAATAA   GT
GAM934  RAP2B    3'  TGCAAAGTTGGATTCTTG    97524          GAT  AG
                                TAAGGGTCCAGCT   CA
                                ||||||||||||   ||
                                GTTCTTAGGTTGA   GT
                                      AAC  A
GAM934  RGPR     3'  CTTGATTATTGCTGCCCTTTAT 53595        TC   __
           A                    TGTAAGGG  CAGC  TGATCAAG
                                ||||||||  ||||  ||||||||
                                ATATTTCC  GTCG  ATTAGTTC
                                     C_    TT
GAM934  RNF8     3'  TTGCTCAGCTGGGCTTTGGTGT 15579    TG A         T  G
           A                    TG  T AGGGTCCAGCTGA CAA
                                ||  | ||||||||||||| |||
```

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                                AT  G TTTCGGGTCGACT GTT
                                 GT G           C
GAM934  RNPC2    3'  TTTGGTTAGCATCTCATCTTGC 18133        GTCCA_
                AT                GTGTAAGG     GCTGATCAAG
                                  ||||||||     ||||||||||
                                  TACGTTCT     CGATTGGTTT
                                     ACTCTA
GAM934  Rpo1-2   3'  TTGATGAGGATTTTTACA    39227          AGC G
                                  TGTAAGGGTCC   T ATCAA
                                  ||||||||||   | |||||
                                  ACATTTTTAGG   A TAGTT
                                        ___ G
GAM934  SCLY     3'  TTTGATCATGGCCTCTACAT   33671      AG  T   GC
                                  GTGTA  GG CCA  TGATCAAG
                                  |||||  || |||  ||||||||
                                  TACAT  CC GGT  ACTAGTTT
                                     CT  _   __
GAM934  SDS3     3'  TTTGATCAAGAACCTGTATAT  69755      A    CCAGC
                                  GTGTA GGGT    TGATCAAG
                                  ||||| ||||    ||||||||
                                  TATAT TCCA    ACTAGTTT
                                     G    AGA__
GAM934  SH3BGRL  3'  TAGATTAGTTGGGTTTTCACAT 62622      A   GT        AAG
                                  GTGT AGG  CCAGCTGATC
                                  |||| |||  ||||||||||
                                  TACA TTT  GGTTGATTAG
                                    C   TG         AT
GAM934  SMBP     3'  TTGGGTGGGCTTTTACAT    72622           G TG
                                  GTGTAAGGGTCCA C  A
                                  |||||||||||||  |  |
                                  TACATTTTCGGGT G  T
                                         G GT
GAM934  SMOC1    3'  TTTGGAGACTGACCCTTGTGTA 42416    TG       C  _  GA
                                  TG  TAAGGGTC AG CT  TCAAG
                                  ||  |||||||| || ||  |||||
                                  AT  GTTCCCAG TC GA  GGTTT
                                   GT       _  A  __
GAM934  SNRPD1   3'  TTTGGTTGGCTGAAACTTA   23664      GG  C   TG
                                  TAAG  TC AGC  ATCAAG
                                  ||||  || |||  ||||||
                                  ATTC  AG TCG  TGGTTT
                                    AA  _   GT
GAM934  SPRY1    3'  CAGTGGGCTTTTGTGTA     65631    TG        G
                                  TG  TAAGGGTCCA CTG
                                  ||  |||||||||| |||
                                  AT  GTTTTCGGGT GAC
                                   GT         _
GAM934  SSH2     3'  TGTGATTCCTGGATATTTGTGT 62894    TG   G     CT    AG
                                  G  TAAG GTCCAG  GATCA
                                  |  |||| ||||||  |||||
```

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                                T  GTTT TAGGTC  TTAGT
                                 GT    A     C_     GTT
GAM934  TFIP11   3'  TTTGATTTAAATGCTTTTGCAC 25120          CCAGCT
           A                     TGTGTAAGGGT     GATCAAG
                                 ||||||||||      |||||||
                                 ACACGTTTTCG     TTAGTTT
                                       TAAAT_
GAM934  TOB2     3'  TTTGGTTGGTTTGGGTTTTATA 33244        G  C   TG
           T                     GTGTAAGG TC AGC  ATCAAG
                                 ||||||||  ||  |||  ||||||
                                 TATATTTT GG TTG  TGGTTT
                                      G  T   GT
GAM934  TRIM4    3'  TTTGGTATCTGCCCTTTGTGT  53411    TG     TC   CTG
                                 G  TAAGGG  CAG   ATCAAG
                                 |  ||||||  |||   ||||||
                                 T  GTTTCC  GTC   TGGTTT
                                  GT     C_   TA_
GAM934  TRIP-Br2 3'  CTTGGTTCTCTGACTCTTATGT 29264     TG      C  CT
           A                     TG  TAAGGGTC AG  GATCAAG
                                 ||  ||||||||  ||  |||||||
                                 AT  ATTCTCAG TC  TTGGTTC
                                  GT       _  TC
GAM934  TSC22    3'  CTGAGGAGGTGTGGACTTTTAT 21212            _   GA_   AG
           ATA                     TGTGTAAGGGTCCA GCT   TCA
                                 ||||||||||||||  |||   |||
                                 ATATATTTTCAGGT TGG   AGT
                                        G   AGG   C
GAM934  UBE2C    3'  AAGCCTCGGTTGAGCCCTTGTA 23803          TC      TCAAG
           TA                      TGTGTAAGGG  CAGCTGA
                                 ||||||||||  |||||||
                                 ATATGTTCCC  GTTGGCT
                                       GA      CCGAAT
GAM934  UBE2D3   5'  TTGGCCGGACCTTTGAGCA   13945     G       A  TG
                                 TGT TAAGGGTCC GC  A
                                 |||  |||||||||  ||  |
                                 ACG GTTTCCAGG CG  T
                                   A       C  GT
GAM934  UBE4B    3'  TTTGAGGCAGGGTCATTTGTGT 21289    TG    _ GT  A   GA
                                 G  TAAG G  CC GCT  TCAAG
                                 |  ||||  |  ||  |||  |||||
                                 T  GTTT C  GG CGG  AGTTT
                                  GT    A TG  A   __
GAM934  VDAC3    3'  TGCCAAGCTGGATCTTGATGC  20183      A         GAT  AG
                                 GTGT AGGGTCCAGCT   CA
                                 ||||  ||||||||||   ||
                                 CGTA TTCTAGGTCGA   GT
                                   G          ACC  C
GAM934  ZNF294   5'  TTTGGTTTCCTGGTGGACATTT 71384          _     G  ____
           TGTACA                  TGTGTAAGG GTCCA CT    GATCAAG
                                 |||||||||  |||||  ||    |||||||
```

```
                                ACATGTTTT CAGGT GG    TTGGTTT
                                     A    _ TCCT
GAM934   LOC124402 3'  CTGGGGCAGCTGGACTTTGCAT 59830        G       A_   AG
                                GTGTAAGG TCCAGCTG  TCA
                                |||||||| ||||||||  |||
                                TACGTTTC AGGTCGAC  GGT
                                     _       GG   C
GAM934   LOC124801 3'  CTTGGTGCAAGAGATTCTTGC  74812         CAGC  _
                                GTAAGGGTC    TG ATCAAG
                                |||||||||    || ||||||
                                CGTTCTTAG    AC TGGTTC
                                     AGA_  G
GAM934   LOC125228 3'  TTTGGTTAGTTGCCGAAATATA 74864       AG__  TC
           C                     GTGTA    GG  CAGCTGATCAAG
                                |||||    ||  ||||||||||||
                                CATAT    CC  GTTGATTGGTTT
                                   AAAG  __
GAM934   LOC126917 3'  CTTGGAGCCTGGGCCTTTGCG  75093            _  GA
                                TGTAAGGGTCCAG CT  TCAAG
                                |||||||||||| ||  |||||
                                GCGTTTCCGGGTC GA  GGTTC
                                      C  __
GAM934   LOC127428 3'  TTACCTGGATCTTTATATA    75165             C
                                TGTGTAAGGGTCCAG TGA
                                |||||||||||||| |||
                                ATATATTTCTAGGTC ATT
                                      C
GAM934   LOC127602 3'  TGGTTGGGCTCTAGTACA    75175      TA
                                TGTG  AGGGTCCAGCTG
                                ||||  ||||||||||||
                                ACAT  TCTCGGGTTGGT
                                  GA
GAM934   LOC129450 3'  CAGTTGGAGCCTTGTGCA    75378    TG    G
                                TG  TAAGG TCCAGCTG
                                ||  ||||| ||||||||
                                AC  GTTCC AGGTTGAC
                                 GT    G
GAM934   LOC130250 5'  TCACCCTGGACCCTAATAT    75422      A       C_
                                GTGT AGGGTCCAG  TGA
                                |||| |||||||||  |||
                                TATA TCCCAGGTC  ACT
                                  A        CC
GAM934   LOC130470 5'  CTTGGTCGCCGGGTCCTTGCG  75441        GT  A  T
                                TGTAAGG  CC GC GATCAAG
                                |||||||  || || |||||||
                                GCGTTCC  GG CG CTGGTTC
                                     TG  C  _
GAM934   LOC131377 3'  TTAGTCCTGGACTTTTGGGCA  76782     G         __
                                TGT TAAGGGTCCAG  CTGA
                                ||| ||||||||||  ||||
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```
                                ACG GTTTTCAGGTC  GATT
                                  G         CT
GAM934   LOC132228 3'  TTGGTGAGATTTTTGTACA   75548          CA  TG
                                TGTGTAAGGGTC  GC  A
                                ||||||||||||  ||  |
                                ACATGTTTTTAG  TG  T
                                      AG  GT
GAM934   LOC132347 5'  GAGATAGTTGTGCTTTTACAT  76400         TC     A  AAG
                                GTGTAAGGG  CAGCTG TC
                                |||||||||  ||||||  ||
                                TACATTTTC  GTTGAT AG
                                     GT     _  AGG
GAM934   LOC133686 3'  TTTGATTAGTGCATATTTTTTA 75625         TCCA__
            TA                    TGTAAGGG     GCTGATCAAG
                                |||||||||     ||||||||||
                                ATATTTTT     TGATTAGTTT
                                     TATACG
GAM934   LOC134266 3'  TTTGGTTGGTTGGTTGTTTTTT 75648         T___     TG
            ACA                    TGTAAGGG    CCAGC  ATCAAG
                                |||||||||    |||||  ||||||
                                ACATTTTT    GGTTG  TGGTTT
                                     TGTT     GT
GAM934   LOC137492 3'  CTTGATTAAATGCCTATGCAT  75793       A   TC  GC
                                GTGTA GGG  CA  TGATCAAG
                                |||||  |||  ||  ||||||||
                                TACGT TCC  GT  ATTAGTTC
                                   A   __  AA
GAM934   LOC139331 5'  TTGGTTGGTTCTTACCCA    76335    T      T     TG
                                TG GTAAGGG CCAGC  A
                                ||  |||||||  |||||  |
                                AC CATTCTT GGTTG  T
                                  C       _     GT
GAM934   LOC143720 3'  CTTGGAATTGGGCCTTTG    61065          CTGA
                                TAAGGGTCCAG    TCAAG
                                ||||||||||||    |||||
                                GTTTCCGGGTT    GGTTC
                                       AA__
GAM934   LOC144266 5'  TTGATCTCGCCCTTACTCA    77271    T       CCAGCT
                                TG GTAAGGGT     GATCAA
                                ||  |||||||      ||||||
                                AC CATTCCCG     CTAGTT
                                  T       CT_____
GAM934   LOC145748 3'  TTTGATTGGGACCACCTGTGTA 84477       A    CCAG TG
            CA                    TGTGTA GGGT    C  ATCAAG
                                ||||||  ||||   |  ||||||
                                ACATGT TCCA    G  TAGTTT
                                   G    CCAG GT
GAM934   LOC146176 3'  TTGGTTGTCACCGTTATATA   78195       G   C_    TG
                                TGTGTAA GGT  CAGC  A
                                |||||||  |||  ||||  |
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                                ATATATT CCA  GTTG  T
                                    G   CT    GT
GAM934   LOC146515 3'  TTTGGTTGGTTTTGGCTTTGGC 78522     A     C_   TG
           A                     TGT AGGGTC  AGC  ATCAAG
                                 ||| ||||||  |||  ||||||
                                 ACG TTTCGG  TTG  TGGTTT
                                   G     TT   GT
GAM934   LOC148195 3'  TTTGGTTGGTTAAATCTATATG 85300    TG  A    CC   TG
           TA                     TG  TA GGGT  AGC  ATCAAG
                                 ||  || ||||  |||  ||||||
                                 AT  AT TCTA  TTG  TGGTTT
                                  GT  A    AA   GT
GAM934   LOC148604 5'  TTGGGAGGCCCTTTACATA    79663          TCCA   GA
                                 TGTGTAAGGG    GCT  TCAA
                                 ||||||||||    |||  ||||
                                 ATACATTTCC    CGG  GGTT
                                       _____   AG
GAM934   LOC150372 3'  TTTCAGGGATGGATTTTTATGT 80625    TG        G__    TCAAG
           A                     TG  TAAGGGTCCA   CTGA
                                 ||  ||||||||||   ||||
                                 AT  ATTTTTAGGT   GACT
                                  GT         AGG    TT
GAM934   LOC151201 3'  TCATATTGGACTTTTTACA    86489      T        C_
                                 TGTG AAGGGTCCAG  TGA
                                 |||| ||||||||||  |||
                                 ACAT TTTTCAGGTT  ACT
                                   _         AT
GAM934   LOC151451 3'  TTTGGTCTACCAGGCCCTTGTC 81049    _       CAGCT
           A                     TG TAAGGGTC     GATCAAG
                                 || ||||||||     |||||||
                                 AC GTTCCCGG     CTGGTTT
                                  T       ACCAT
GAM934   LOC151610 3'  CTTGGTCAGAGGCCTCCTTGC  81093       _ T  AG
                                 GTAAGG G CC  CTGATCAAG
                                 |||||| | ||  |||||||||
                                 CGTTCC C GG  GACTGGTTC
                                     T C  A_
GAM934   LOC151877 3'  TTATTTGGTCTTTTGTACA    86702          T    C
                                 TGTGTAAGGG CCAG TGA
                                 |||||||||| |||| |||
                                 ACATGTTTTC GGTT ATT
                                       T    T
GAM934   LOC152313 3'  TTGTGATGGACTTTGCATA    86855         G    GCTGAT
                                 TGTGTAAGG TCCA      CAA
                                 ||||||||| ||||      |||
                                 ATACGTTTC AGGT      GTT
                                       _    AGT___
GAM934   LOC152313 5'  TTTGGTCTAGGAAATCTTTACC 86856    T      __   AGCT
           CA                      TG GTAAGGG  TCC    GATCAAG
                                 || |||||||  |||    |||||||
```

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                                AC CATTTCT  AGG    CTGGTTT
                                 C      AA   AT__
GAM934   LOC152426 3'  CTTGGTTAGAGTCTTCCTTGAC 86897     G     TCCAG
                   A                TGT TAAGGG    CTGATCAAG
                                ||| ||||||    |||||||||
                                ACA GTTCCT    GATTGGTTC
                                  _     TCTGA
GAM934   LOC152790 5'  TTTGAAAATGGGCTCTGCACA  87061       A      GCTGA
                                TGTGTA GGGTCCA    TCAAG
                                |||||| |||||||    |||||
                                ACACGT CTCGGGT    AGTTT
                                   _      AAA__
GAM934   LOC153688 3'  CTTGATTAGAGACCTAGCACA  87310      AA    CAG
                                TGTGT  GGGTC   CTGATCAAG
                                |||||  |||||   |||||||||
                                ACACG  TCCAG   GATTAGTTC
                                   A_    A__
GAM934   LOC153711 3'  TTGGTTCCGGTCTTTAC     87345        T  AGCT
                                GTAAGGG CC    GATCAA
                                ||||||| ||    ||||||
                                CATTTCT GG    TTGGTT
                                   _ CC__
GAM934   LOC154743 3'  TTGATTTGGGCCTTGGTGT    82018    TG A      GCT     G
                                G  T AGGGTCCA   GATCAA
                                |  | ||||||||   ||||||
                                T  G TTCCGGGT   TTAGTT
                                 GT G       ___      G
GAM934   LOC154877 3'  CAGCTGGGCCCATATGCA    87533       A
                                TGTGTA GGGTCCAGCTG
                                |||||| ||||||||||
                                ACGTAT CCCGGGTCGAC
                                   A
GAM934   LOC157663 3'  TTTGATATTCACCTGGATTTTA 82458       A       C  ___
                   ATACA                TGTGT AGGGTCCAG TGA   TCAAG
                                ||||| |||||||| |||   |||||
                                ACATA TTTTAGGTC ACT   AGTTT
                                   A       C   TAT
GAM934   LOC158235 5'  CTTGGTCACACCCCTGACACA  88004      A   TCCAGC
                                TGTGT AGGG     TGATCAAG
                                ||||| ||||     ||||||||
                                ACACA TCCC     ACTGGTTC
                                   G    CAC___
GAM934   LOC158490 3'  TGACCTGGACCTTTAC      82826           CTGA
                                GTAAGGGTCCAG    TCA
                                ||||||||||||    |||
                                CATTTCCAGGTC    AGT
                                        C___
GAM934   LOC158819 3'  CTTGATCATGGTTCTCTTTGTA 88276        _ T_   GC
                   C                 GTGTAAGG G  CCA  TGATCAAG
                                |||||||| |  |||  ||||||||
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                                CATGTTTC C  GGT  ACTAGTTC
                                     T TT  __
GAM934  LOC159090 3'  TTTGATCAGAAATTCTCTTGC  82964       TCCAG
                                GTAAGGG    CTGATCAAG
                                |||||||    |||||||||
                                CGTTCTC    GACTAGTTT
                                    TTAAA
GAM934  LOC160897 3'  CTTGATTAGCAAAGGTTTTTGA 83131     G     T  A__
          CA                      TGT TAAGGG CC   GCTGATCAAG
                                ||| |||||| ||   ||||||||||
                                ACA GTTTTT GG   CGATTAGTTC
                                  _     _  AAA
GAM934  LOC196424 3'  CTTGATCGGAATTTCTTG    89056       TCCAG
                                TAAGGG    CTGATCAAG
                                ||||||    |||||||||
                                GTTCTT    GGCTAGTTC
                                    TAA__
GAM934  LOC196484 5'  TGACCTGGACCTTTAC      63539          CTGA
                                GTAAGGGTCCAG   TCA
                                ||||||||||||   |||
                                CATTTCCAGGTC   AGT
                                       C___
GAM934  LOC196528 3'  TTTGATTGGTTATCCTTTG   89112       TCC   TG
                                TAAGGG   AGC  ATCAAG
                                ||||||   |||  ||||||
                                GTTTCC   TTG  TAGTTT
                                    TA_   GT
GAM934  LOC197287 3'  CTTGATATGCAGGTCCTTGCAT 61546         T  A  TG
                                GTGTAAGGG CC GC  ATCAAG
                                ||||||||| || ||  ||||||
                                TACGTTCCT GG CG  TAGTTC
                                      _ A  TA
GAM934  LOC199775 3'  TATATTAGTTGTGCTTTTATGT 89724    TG     TC      CAAG
          A                      TG  TAAGGG  CAGCTGAT
                                ||  ||||||  ||||||||
                                AT  ATTTTC  GTTGATTA
                                 GT     GT       TATT
GAM934  LOC199899 3'  TTTGGTTACAGCTACTTTTAGA 91473     G      CC    __
          CA                      TGT TAAGGGT  AGCTG  ATCAAG
                                ||| |||||||  |||||  ||||||
                                ACA ATTTTCA  TCGAC  TGGTTT
                                  G      __     AT
GAM934  LOC200312 3'  TGCCCAGCTGGACTCTGCACA  91581       A         AT
                                TGTGTA GGGTCCAGCTG  CA
                                ||||||| ||||||||||  ||
                                ACACGT CTCAGGTCGAC  GT
                                   _         CC
GAM934  LOC200609 5'  CTTGGTTGGTTGGTTGATTTG  91664     GGT_    TG
                                TAAG   CCAGC  ATCAAG
                                ||||   |||||  ||||||
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                                GTTT   GGTTG  TGGTTC
                                  AGTT    GT
GAM934   LOC200803 5'  CTTGACAAAGCTGTACCTTTGT 90298         C    GA_
            AT                    GTGTAAGGGT CAGCT   TCAAG
                                  |||||||||| |||||  |||||
                                  TATGTTTCCA GTCGA   AGTTC
                                       T    AAC
GAM934   LOC200830 3'  TTTGGGGGTGGTTTCTTATGCA 91734         T  G  GA
                                  TGTGTAAGGG CCA CT  TCAAG
                                  |||||||||| ||| ||  |||||
                                  ACGTATTCTT GGT GG  GGTTT
                                       T  G  __
GAM934   LOC201799 3'  TTTGAACACCTGGGCCTTTACA 90495           C  A
            T                     GTGTAAGGGTCCAG TG TCAAG
                                  |||||||||||||| || |||||
                                  TACATTTCCGGGTC AC AGTTT
                                       C  A
GAM934   LOC202299 3'  TTGACGAGGGCCTTTGTCA   91939   _       AGC  A
                                  TG TAAGGGTCC   TG TCAA
                                  || |||||||||   || ||||
                                  AC GTTTCCGGG   GC AGTT
                                   T       A__  _
GAM934   LOC202451 5'  CTTGGGATTGGATTCTATACA  91955       A       CTGA
                                  TGTGTA GGGTCCAG    TCAAG
                                  |||||| ||||||||    |||||
                                  ACATAT CTTAGGTT    GGTTC
                                     _       AG__
GAM934   LOC202754 3'  ATTGATCAGTTGGACTTTTCAC 83586     T             G
                                  GTG AAGGGTCCAGCTGATCAA
                                  ||| ||||||||||||||||||
                                  CAC TTTTCAGGTTGACTAGTT
                                    _              AT
GAM934   LOC219988 3'  TTTGGCAGTGTGGCTTTTTGCA 93268         T  _   A
            CA                    TGTGTAAGGG CCA GCTG TCAAG
                                  |||||||||| ||| |||| |||||
                                  ACACGTTTTT GGT TGAC GGTTT
                                       C  G   _
GAM934   LOC220073 5'  TGACCTGGACCTTTAC      95077           CTGA
                                  GTAAGGGTCCAG    TCA
                                  ||||||||||||    |||
                                  CATTTCCAGGTC    AGT
                                       C___
GAM934   LOC221133 3'  TTTATTACTGGGCTATTTACAC 95211        _     C   CAAG
            A                     TGTGTAAG GGTCCAG TGAT
                                  |||||||| ||||||| ||||
                                  ACACATTT TCGGGTC ATTA
                                       A      _   TTT
GAM934   LOC221543 5'  TTTGATCAGGTGTTTGTTTACA 95393        GGTC  G
            TA                    TGTGTAAG    CA CTGATCAAG
                                  ||||||||    || |||||||||
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                                ATACATTT    GT GACTAGTTT
                                     GTTT  G
GAM934   LOC222031 3'  CTTGGTCAGGTTACCTTAGCA  95679     A     CCAG
                                TGT AGGGT    CTGATCAAG
                                ||| |||||    |||||||||
                                ACG TTCCA    GACTGGTTC
                                  A    TTG_
GAM934   LOC222936 5'  TTGGTTGGGATCATCTTGCCA  96028    T    __    _  TG
                                TG GTAAG  GGTCC AGC  A
                                || |||||  ||||| |||  |
                                AC CGTTC  CTAGG TTG  T
                                 _    TA    G   GT
GAM934   LOC253612 5'  TTGATGTGGTCTTTGCA     98562        T   GCTG
                                TGTAAGGG CCA    ATCAA
                                |||||||| |||    |||||
                                ACGTTTCT GGT    TAGTT
                                     _   G___
GAM934   LOC254050 3'  AAGACAGCTGGATTCTTACA   96560             A  AAG
                                TGTAAGGGTCCAGCTG TC
                                |||||||||||||||| ||
                                ACATTCTTAGGTCGAC AG
                                          _ AAG
GAM934   LOC255144 3'  TCCTCTGGACTTTTCAT     96767     T        CT
                                GTG AAGGGTCCAG  GA
                                ||| ||||||||||  ||
                                TAC TTTTCAGGTC  CT
                                  _         TC
GAM934   LOC255328 3'  TGTGACCAGCTGGGCCTTTGCT 98352    T           A   AG
            CA                    TG GTAAGGGTCCAGCTG TCA
                                || ||||||||||||||| |||
                                AC CGTTTCCGGGTCGAC AGT
                                 T            C   GTC
GAM934   LOC255520 5'  CTGGGCCGGCGGGTCTTTGTGC 97551    TG    GT  A    A_   AG
                                G  TAAGG  CC GCTG  TCA
                                |  |||||  || ||||  |||
                                C  GTTTC  GG CGGC  GGT
                                 GT    TG  _    CG   C
GAM934   LOC255520 3'  GACATATGTAGTTGGAATTTTA 97552         G       ATCAAG
            CATA                    TGTGTAAGG TCCAGCTG
                                |||||||| ||||||||
                                ATACATTTT AGGTTGAT
                                      A       GTATACAGT
GAM934   LOC256096 3'  CTTGGGCCTGGGTTTTTAGGCA 98993     G    GT    CTGA
                                TGT TAAGG  CCAG    TCAAG
                                ||| |||||  ||||    |||||
                                ACG ATTTT  GGTC    GGTTC
                                  G    TG    CG__
GAM934   LOC256435 3'  TTTGATCAGTTTTTGTTTTATT 97168    T     GTCC
            CA                    TG GTAAGG    AGCTGATCAAG
                                || ||||||    ||||||||||
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                                AC TATTTT   TTGACTAGTTT
                                 T    GTTT
GAM934  LOC256733 5'  TCTGGCCTGGCTTTTACG    98838       T   _ _
                                TGTAAGGG CCAG CT GA
                                |||||||| |||| || ||
                                GCATTTTC GGTC GG CT
                                     _   C  T
GAM934  LOC257115 3'  CTTGGTCACACCTCATGCACA  98293      A_   CCAGC
                                TGTGTA  GGGT   TGATCAAG
                                ||||||  ||||   ||||||||
                                ACACGT  TCCA   ACTGGTTC
                                   AC   C____
GAM934  LOC257444 3'  TTTGATGCAGATATTTGCACA  82016       G   CA  TG
                                TGTGTAAG GTC  GC  ATCAAG
                                |||||||| |||  ||  ||||||
                                ACACGTTT TAG  CG  TAGTTT
                                     A   A_  __
GAM934  LOC257467 5'  CTTGGAAGTGGGCCTTGTGCA  90505    TG    G    G  GA
                                TG  TAAGG TCCA CT  TCAAG
                                ||  ||||| |||| ||  |||||
                                AC  GTTCC GGGT GA  GGTTC
                                 GT    _   _ A_
GAM934  LOC257483 3'  TTTGATTGATTGCTTTTATATA 90258         TC   CT
                                TGTGTAAGGG  CAG  GATCAAG
                                ||||||||||  |||  |||||||
                                ATATATTTTC  GTT  TTAGTTT
                                     __  AG
GAM934  LOC257596 5'  TTTGATCAGGTGTTTGTTTACA 99796        GGTC  G
           TA                   TGTGTAAG   CA CTGATCAAG
                                ||||||||   || |||||||||
                                ATACATTT   GT GACTAGTTT
                                     GTTT  G
GAM934  LOC51634  3'  TTTGCCTATTCTGGATCTTTCA 32615      T        CTGAT_
           TA                   TGTG AAGGGTCCAG     CAAG
                                |||| ||||||||||     ||||
                                ATAC TTTCTAGGTC     GTTT
                                  _        TTATCC
GAM934  LOC57086  3'  TTTGGTTTTCTGTCTTTGCG  40131        TC   CT
                                TGTAAGGG  CAG  GATCAAG
                                ||||||||  |||  |||||||
                                GCGTTTCT  GTC  TTGGTTT
                                     __   TT
GAM934  LOC63928  3'  CTTGAAGTCTGGACTCTTA   42271          _ GA
                                TAAGGGTCCAG CT  TCAAG
                                ||||||||||| ||  |||||
                                ATTCTCAGGTC GA  AGTTC
                                       T  __
GAM934  LOC90470  3'  TAGCTGGACCTTTAACA     63654     G
                                TGT TAAGGGTCCAGCTG
                                ||| ||||||||||||||
```

```
                                ACA ATTTCCAGGTCGAT
                                  _
GAM934  LOC91947  3'  TTTGATCAGGGAATTTTCTACA 68230       AG __  AG
            CA                    TGTGTA  GG  TCC  CTGATCAAG
                                  ||||||  ||  |||  |||||||||
                                  ACACAT  TT  AGG  GACTAGTTT
                                     CT  TA  __
GAM934  LOC92935  3'  TTTGGTCAATCAGGATCTTTA  71519         AGC_
                                  TAAGGGTCC   TGATCAAG
                                  |||||||||   ||||||||
                                  ATTTCTAGG   ACTGGTTT
                                        ACTA
GAM935  MSL3L1    3'  GAGTTGGGCAACCATCACTG   55321    A  C     TG A
                                  CA TGA GGTTGCT  A CTT
                                  || ||| |||||||  | |||
                                  GT ACT CCAACGG  T GAG
                                   C  A     GT _
GAM935  ZNF148    5'  TTCAAGCACGTGATCTGG    42016    _  G  GT
                                  CCA AT ACG  TGCTTGAA
                                  ||| || |||  ||||||||
                                  GGT TA TGC  ACGAACTT
                                    C  G  __
GAM935  FLJ11191  3'  AAGTTCAAGCATTCATTG    37739      CGGT
                                  CAATGA   TGCTTGAACTT
                                  ||||||   ||||||||||
                                  GTTACT   ACGAACTTGAA
                                     T___
GAM935  FLJ31890  3'  AAGTTATCAGGCAACATCATT  92983     CG      __
                                  AATGA  GTTGCTTGA  ACTT
                                  |||||  |||||||||  ||||
                                  TTACT  CAACGGACT  TGAA
                                     A_       AT
GAM935  KIAA1755  3'  AAGCTCAAGTGATCCTCTGG   62003    AT  C   TG    A
                                  CCA  GA GGT  CTTGA CTT
                                  |||  || |||  ||||| |||
                                  GGT  CT CTA  GAACT GAA
                                    __  C   GT    C
GAM935  KIAA1884  3'  AAGTTCAAAGATGATCACTGGG 73719     A   CG   GC
                                  CCCA TGA  GTT  TTGAACTT
                                  |||| |||  |||  ||||||||
                                  GGGT ACT  TAG  AACTTGAA
                                    C   AG   A_
GAM935  OSBPL8    3'  TTCAAGCACTACCACTGG    40849    A  AC   T
                                  CCA TG  GGT GCTTGAA
                                  ||| ||  ||| |||||||
                                  GGT AC  TCA CGAACTT
                                    C  CA  _
GAM935  LOC200268 3'  AAGTTGTAACAACCAACCATTG 90080    C    AC_    C  _
            AGT                     AC CAATG   GGTTG TTG AACTT
                                  || |||||   ||||| ||| |||||
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                                TG GTTAC   CCAAC AAT TTGAA
                                 A    CAA    _  G
GAM935  LOC253142 3'  TTCAAGTGTTTTCCTGGGT   99229      AT  CGGT
                                ACCCA  GA   TGCTTGAA
                                |||||  ||   ||||||||
                                TGGGT  CT   GTGAACTT
                                  C_  TTT_
GAM935  LOC96597  5'  TTCACCAGTCGTCTCTGGGT   67473      AT   GT  CT
                                ACCCA  GACG  TG  TGAA
                                |||||  ||||  ||  ||||
                                TGGGT  CTGC  AC  ACTT
                                  CT   TG  C_
GAM936  FBXL7     3'  TTGTCCCTAATCCTTGGCCCTG 25504     A       CA__
                                CAGG CCAAGGAT   GACAA
                                ||||  ||||||||   |||||
                                GTCC GGTTCCTA   CTGTT
                                  C       ATCC
GAM936  GYPC      3'  ACCTTTGTCTGCCATTGATCC  10899     C  _  AT
                                GGA CAA GG  CAGACAAAGGT
                                |||  |||  ||  ||||||||||
                                CCT GTT CC  GTCTGTTTCCA
                                 A   A  __
GAM936  PAFAH1B1  3'  ACCTCCATGTCCTTAGTCCTG  6470       C    T  GACAA
                                CAGGAC AAGGA CA    AGGT
                                ||||||  |||||  ||    ||||
                                GTCCTG TTCCT GT    TCCA
                                   A    _  ACC__
GAM936  PRODH     3'  ACCCCCATGTCCTTGGACCT   33394     A      T  GACAAA
                                AGG CCAAGGA CA     GGT
                                |||  |||||||  ||     |||
                                TCC GGTTCCT GT     CCA
                                 A      _  ACCC__
GAM936  PRPS1     3'  ACCTTCATCTATCTTGATCCT  12400     C    ATC   CA
                                AGGA CAAGG   AGA  AAGGT
                                ||||  |||||   |||  |||||
                                TCCT GTTCT   TCT  TTCCA
                                  A    A__   AC
GAM936  SCNN1B    3'  ACCCTCGTCCCTACCTGTCCTG 6212       CA   ATCA   AAA
                                CAGGAC  AGG   GAC   GGT
                                ||||||  |||   |||   |||
                                GTCCTG  TCC   CTG   CCA
                                   __   ATCC   CTC
GAM936  SCNN1B    3'  ACCTGTCCTGATCCTGGTCCTG 6213        A      ACAA
                                CAGGACCA GGATCAG    AGGT
                                ||||||||  |||||||   ||||
                                GTCCTGGT CCTAGTC    TCCA
                                    _      CTG_
GAM936  SLC7A8    3'  CCTCCCTGCCTTGGTCC     25302         AT   ACAA
                                GGACCAAGG  CAG    AGG
                                |||||||||  |||   |||
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                                CCTGGTTCC  GTC   TCC
                                    __  CC__
GAM936  SURF4   3'  ACCGATTTGATCTTAATCCTG  53706     CCA      CAAA
                                CAGGA  AGGATCAGA   GGT
                                |||||  |||||||||   |||
                                GTCCT  TTCTAGTTT   CCA
                                  AA_      AG__
GAM936  TGFA    3'  CTGCCCTCTAGTTGGTTCTG  13707       __  T__
                                CAGGACCAA  GGA  CAG
                                |||||||||  |||  |||
                                GTCTTGGTT  TCT  GTC
                                     GA  CCC
GAM936  UNG     3'  CCTCCATCCTTGATCTTG   56024     C     CAGACAA
                                CAGGA CAAGGAT     AGG
                                ||||| |||||||     |||
                                GTTCT GTTCCTA     TCC
                                  A     CC_____
GAM936  ZNF264  5'  ACCTTTGTACGAGCCTGACCCC 14183    ACCA  A  AG
          T                      AGG   AGG TC  ACAAAGGT
                                |||   ||| ||  ||||||||
                                TCC   TCC AG  TGTTTCCA
                                 CCAG  G  CA
GAM936  ARHGEF3  3'  CCTTTGTCCCTAGTACTG   39459    G  CA  ATCA
                                CAG AC  AGG   GACAAAGG
                                ||| ||  |||   ||||||||
                                GTC TG  TCC   CTGTTTCC
                                 A  A_  ____
GAM936  DKFZp761D112 3'  CCTTCATCCTTTGGTCT    51166       ATCA  CA
                                GGACCAAGG   GA  AAGG
                                |||||||||   ||  ||||
                                TCTGGTTTC   CT  TTCC
                                     ____  AC
GAM936  FLJ13449  3'  ACCTTCAGTCTCCTTGGTCT  44926       TCA  A_
                                GGACCAAGGA  GAC  AAGGT
                                ||||||||||  |||  |||||
                                TCTGGTTCCT  CTG  TTCCA
                                     ___  AC
GAM936  FLJ20725  3'  CCTCGTATGCTTGATCCTG   36043     C   G  CAG  AA
                                CAGGA CAAG AT   AC  AGG
                                ||||| |||| ||   ||  |||
                                GTCCT GTTC TA   TG  TCC
                                  A   G  ___  C_
GAM936  HMT-1   3'  ACCTCTGCAGAACTCCTCATCC 39408     CCA   __  AGA  A
          TG                     CAGGA   AGGA  TC   CA AGGT
                                |||||   ||||  ||   || ||||
                                GTCCT   TCCT  AG   GT TCCA
                                  AC_   CA  AC_  C
GAM936  KCND1   3'  CCTCACCTCTGATCTGGCCT   18340    A  AG     CAA_
                                AGG CCA  GATCAGA   AGG
                                ||| |||  |||||||   |||
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                                TCC GGT  CTAGTCT    TCC
                                  _  __      CCAC
GAM936  KIAA0449  3'  ACCTTTGTTCTGTCCCCTGCCC 34632    AC  A  AT   _
              C                    GG  CA GG  CAGA CAAAGGT
                                  ||  || ||  |||| |||||||
                                  CC  GT CC  GTCT GTTTCCA
                                   CC  C  CT    T
GAM936  KIAA1084  3'  CCTTTGTCCCTGTAACCTG   30500     ACCA   ATCA
                                  CAGG   AGG   GACAAAGG
                                  ||||   |||   ||||||||
                                  GTCC   TCC   CTGTTTCC
                                    AATG  ____
GAM936  KIAA1209  3'  ACCAACTTGATCCTGGCCCTG  61398     A   A      ACAAA
                                  CAGG CCA GGATCAG     GGT
                                  |||| ||| |||||||     |||
                                  GTCC GGT CCTAGTT     CCA
                                    C  _      CAA__
GAM936  KIAA1237  3'  TCTTACATAATCCTTGGCCCTG 81302      A       CAGACA
                                  CAGG CCAAGGAT     AAGG
                                  |||| ||||||||     ||||
                                  GTCC GGTTCCTA     TTCT
                                    C       ATACA_
GAM936  MGC10702  3'  ACCTTTGTCTAATCAACGTTTC 51989     CCAAG_  C
              C                    GGA     GAT AGACAAAGGT
                                  |||     ||| ||||||||||
                                  CCT     CTA TCTGTTTCCA
                                    TTGCAA   A
GAM936  PCDH19    3'  ACCTTTGTTCTGCCTTGGTCTT 64441          AT   _
                                  AGGACCAAGG  CAGA CAAAGGT
                                  ||||||||||  |||| |||||||
                                  TTCTGGTTCC  GTCT GTTTCCA
                                        __    T
GAM936  PI4KII    3'  ACCTTGCTTCCTGAGTCCTTGG 37946          _   ACA__
              TCC                    GGACCAAGGA TCAG     AAGGT
                                  |||||||||| ||||     |||||
                                  CCTGGTTCCT AGTC     TTCCA
                                       G    CTTCG
GAM936  SPEC1     5'  CCTCTCTCTCTGGTCCTG    40003        AG  TC   CAAA
                                  CAGGACCA  GA  AGA    GG
                                  ||||||||  ||  |||    ||
                                  GTCCTGGT  CT  TCT    CC
                                      CT  C_   ____
GAM936  UQCRH     5'  CCTTACAAGTCCTTCTTGATCC 75147      C     TCA   A___
              TG                    CAGGA CAAGGA   GAC    AAGG
                                  |||||  ||||||   |||    ||||
                                  GTCCT GTTCTT   CTG    TTCC
                                    A     C__   AACA
GAM936  LOC124460 3'  ACCCTCGGCATCCTCAGTTCTG 76553       CA    CA_  CAAA
                                  CAGGAC  AGGAT   GA    GGT
                                  ||||||  |||||   ||    |||
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                                GTCTTG  TCCTA   CT    CCA
                                   AC    CGG  C___
GAM936  LOC128272 3'  CCTCCATGCCTGGCTCCTG   75241      _   A  AT  GACAA
                                CAGGA CCA GG  CA    AGG
                                ||||| ||| ||  ||    |||
                                GTCCT GGT CC  GT    TCC
                                   C   _  __  ACC__
GAM936  LOC146272 5'  ACCTTTGTGGCTCCTGTCCTG  78322       CA    TCAG
                                CAGGAC  AGGA    ACAAAGGT
                                ||||||  ||||    ||||||||
                                GTCCTG  TCCT    TGTTTCCA
                                   __    CGG_
GAM936  LOC151610 3'  ACCCCTGTCTGGTTGGCACTCC 81088     ___   AGG       AA
                                GGA   CCA   ATCAGACA  GGT
                                |||   |||   ||||||||  |||
                                CCT   GGT   TGGTCTGT  CCA
                                  CAC   ___       CC
GAM936  LOC151619 3'  ACCTCTGCAGTACTCCTTAGCC 69308      ACC     TCAGA_  A
          TG                      CAGG   AAGGA     CA AGGT
                                ||||   |||||     || ||||
                                GTCC   TTCCT     GT TCCA
                                  GA_    CATGAC  C
GAM936  LOC154789 5'  ACCTTTGTCCTCTTCAACCT   82023     ACCA    TCA
                                AGG    AGGA   GACAAAGGT
                                |||    ||||   |||||||||
                                TCC    TTCT   CTGTTTCCA
                                  AAC_   C__
GAM936  LOC202279 3'  ACCCTGTCTTTGTCCCCAGCCC 90637      ACCAA    C_     AA
          TG                      CAGG    GGAT  AGACA  GGT
                                ||||    ||||  |||||  |||
                                GTCC    CCTG  TCTGT  CCA
                                  CGACC    TT    C_
GAM936  LOC220549 5'  ACCTTCGTCCCCTTTGATCC   94503     C     ATCA   A
                                GGA CAAGG    GAC AAGGT
                                ||| |||||    ||| |||||
                                CCT GTTTC    CTG TTCCA
                                  A    CC__   C
GAM936  LOC257048 3'  ACCTTTCCCTCCCTGGTCCTG  97955        A   TCA  CA
                                CAGGACCA GGA   GA  AAGGT
                                |||||||| |||   ||  |||||
                                GTCCTGGT CCT   CT  TTCCA
                                    C   CC_  __
GAM936  LOC90538  3'  ACCTTTGCAGATCCTTGATCC  63892     C       AGA
                                GGA CAAGGATC   CAAAGGT
                                ||| ||||||||   |||||||
                                CCT GTTCCTAG   GTTTCCA
                                  A       AC_
GAM937  CHRNA2    5'  GCTCTATTCTGTACCTGCCA   7429       TGAAGAA
                                TGGCA      GGAATAGAGC
                                |||||      ||||||||||
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                                ACCGT     TCTTATCTCG
                                  CCATG__
GAM937  CRY2    3'  GCTCCATGGTGGCTTCATGCC  72665        AAGGA  A
                                GGCATGAAG    AT GAGC
                                |||||||||    || ||||
                                CCGTACTTC    TA CTCG
                                     GGTGG  C
GAM937  DMD     3'  GCTTTACTCTTTCATGCCA   15723        GAA   A
                                TGGCATGAA   GGA TAGAGC
                                |||||||||   ||| ||||||
                                ACCGTACTT   TCT ATTTCG
                                     ___  C
GAM937  DMD     3'  GCTTTACTCTTTCATGCCA   5464         GAA   A
                                TGGCATGAA   GGA TAGAGC
                                |||||||||   ||| ||||||
                                ACCGTACTT   TCT ATTTCG
                                     ___  C
GAM937  EXTL2   3'  CTGTATTTCTTACACGCCA   9326      A _    GA
                                TGGC TG AAGAAG  ATAG
                                |||| || ||||||  ||||
                                ACCG AC TTCTTT  TGTC
                                  C A     A_
GAM937  FAT2    3'  CTCTGGGTTCTTCATCCCA   9349     C      GGAA
                                TGG ATGAAGAA    TAGAG
                                ||| ||||||||    |||||
                                ACC TACTTCTT    GTCTC
                                  C       GG__
GAM937  KRT15   3'  GCTCTATTCCCCCTCTGCC   11233     T  A AA
                                GGCA GA G  GGAATAGAGC
                                |||| || |  ||||||||||
                                CCGT CT C  CCTTATCTCG
                                  _ _ CC
GAM937  MAK     5'  GCCGATTCCTTCATGCTA    20948       AGA    AGA
                                TGGCATGA   AGGAAT   GC
                                ||||||||   ||||||   ||
                                ATCGTACT   TCCTTA   CG
                                     ___     GCC
GAM937  OGG1    5'  GCTCCCTGCTTTTTCATGCCA  34157          GAATA
                                TGGCATGAAGAAG    GAGC
                                ||||||||||||     ||||
                                ACCGTACTTTTTC    CTCG
                                       GTCC_
GAM937  OPCML   3'  GCTCTACTCATTCCTTCCACCA 11899    CA  AA     ____
                                TGG  TG  GAAGGAA    TAGAGC
                                |||  ||  |||||||   ||||||
                                ACC  AC  CTTCCTT    ATCTCG
                                  __ __      ACTC
GAM937  PDCL    5'  GCTCCATTCCTTCCGGCGCC  19398    A_  AA      A
                                GGC  TG  GAAGGAAT GAGC
                                |||  ||  |||||||| ||||
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                                CCG  GC  CTTCCTTA CTCG
                                  CG  __       C
GAM937  RRM2B    3'  GCTCCATTCTTTCCATAACA   68433    GC   AA       A
                                TG  ATG  GAAGGAAT GAGC
                                ||  |||  |||||||| ||||
                                AC  TAC  CTTTCTTA CTCG
                                 AA  __       C
GAM937  TLL2     3'  CTATGCTTCTTCATACCA    25881     C       GA
                                TGG ATGAAGAAG  ATAG
                                |||  |||||||||  ||||
                                ACC TACTTCTTC  TATC
                                  A        G_
GAM937  TNFSF4   3'  GCTTACATCTTCCTCAGCCA   13913      A   A    AATA
                                TGGC TGA GAAGG    GAGC
                                ||||  ||| |||||    ||||
                                ACCG ACT CTTCT    TTCG
                                  _   C     ACA_
GAM937  ZNF289   3'  CTTTATTCCCTCTCACACCA   65930     CA   A  A
                                TGG  TGA GA GGAATAGAG
                                |||  |||  ||  |||||||||
                                ACC  ACT CT CCTTATTTC
                                  AC   _  C
GAM937  ZXDA     3'  CTCTATTCATTCCTTGCCA    67163       TGAA   G
                                TGGCA    GAA GAATAGAG
                                |||||    |||  ||||||||
                                ACCGT    CTT CTTATCTC
                                   TC__   A
GAM937  ARHGEF4  3'  CTATTCCTTCTCCAAGCCA    53369      A  A
                                TGGC TG AGAAGGAATAG
                                ||||  ||  ||||||||||
                                ACCG AC TCTTCCTTATC
                                  A  C
GAM937  ASTN2    3'  CTCTGCTTTCTTCCTGCCA    73557       T       AA
                                TGGCA GAAGAAGG  TAGAG
                                |||||  ||||||||  |||||
                                ACCGT CTTCTTTC  GTCTC
                                   C       __
GAM937  ASTN2    3'  GCTCTTCTTCCTTCTTCCTGCC 73560       T        T_
          A                      TGGCA GAAGAAGGAA  AGAGC
                                 |||||  ||||||||||  |||||
                                 ACCGT CTTCTTCCTT  TCTCG
                                    C         CT
GAM937  BLP1     3'  CTCTACTCCTTCTTCCTG     55298    T       A
                                CA GAAGAAGGA TAGAG
                                ||  |||||||| |||||
                                GT CTTCTTCCT ATCTC
                                 C        C
GAM937  C8orf13  5'  GCTCTGGGCCTTCTTCCTGCCA 82480       T       AA
                                TGGCA GAAGAAGG  TAGAGC
                                |||||  ||||||||  ||||||
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                                ACCGT CTTCTTCC  GTCTCG
                                  C       GG
GAM937  CAPNS2   5'  CTCCATTTCATCTTTTTTCATA 51305     C         ____  A
           CCA                    TGG ATGAAGAAGGA    AT GAG
                                ||| ||||||||||    || |||
                                ACC TACTTTTTTCT    TA CTC
                                  A          ACTT  C
GAM937  DDX17    5'  GCCTATACCTTCTTCACCCCA  22125     CA       A    A
                                TGG  TGAAGAAGG ATAG GC
                                |||  ||||||||| |||| ||
                                ACC  ACTTCTTCC TATC CG
                                  CC        A   _
GAM937  FBXO24   3'  CTAATCCCCCTCATGCTA    25149        A AA   A
                                TGGCATGA G  GGA TAG
                                ||||||||  |  ||| |||
                                ATCGTACT C  CCT ATC
                                     _ CC   A
GAM937  FLJ11259 3'  GCTCCTTCTCTTCATGCC    37769          A   ATA
                                GGCATGAAGA GGA   GAGC
                                ||||||||||  |||   ||||
                                CCGTACTTCT CTT   CTCG
                                      _   C__
GAM937  FLJ12788 3'  CTCTGTTTCTCCACCCCA    42848     CA  AAGA
                                TGG  TG    AGGAATAGAG
                                |||  ||    ||||||||||
                                ACC  AC    TCTTTGTCTC
                                  CC  C___
GAM937  FLJ13204 3'  GCTCCCCACTCCTCTGCCA   45759      T  A  A_  AATA
                                TGGCA GA GA  GG    GAGC
                                |||||  ||  ||  ||    ||||
                                ACCGT CT CT  CC    CTCG
                                   _  C  CA  C___
GAM937  FLJ23516 5'  CTCCATTCCTTCCCCACC    44886    CA  AA       A
                                GG  TG  GAAGGAAT GAG
                                ||  ||  |||||||| |||
                                CC  AC  CTTCCTTA CTC
                                 __  CC       C
GAM937  HARSL    3'  GCTCTATTCCATACCGTGCCA  25210        AAGAA
                                TGGCATG    GGAATAGAGC
                                |||||||    ||||||||||
                                ACCGTGC    CCTTATCTCG
                                    CATA_
GAM937  KCNH8    3'  GCTCCATCTAGGCTCTGCCA   58907      T  A AA_   ATA
                                TGGCA GA G   GGA   GAGC
                                |||||  || |   |||   ||||
                                ACCGT CT C   TCT   CTCG
                                   _  _ GGA   AC_
GAM937  KIAA0280 3'  CTCTCTCCTCCTCATGCCA   93297        A  A   AT
                                TGGCATGA GA GGA  AGAG
                                ||||||||  || |||  ||||
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                                ACCGTACT CT CCT  TCTC
                                    C  _  C_
GAM937  KIAA0286 3' GCTCCAGGTTATCTTCATGCC 68858        AG AATA
                                GGCATGAAGA  G   GAGC
                                ||||||||||  |   ||||
                                CCGTACTTCT  T   CTCG
                                    AT GGAC
GAM937  KIAA0290 3' GCTCCTCCCCCTCATGCCA   66717       A AA  ATA
                                TGGCATGA G  GGA  GAGC
                                ||||||||  |  |||  ||||
                                ACCGTACT C  CCT  CTCG
                                   _ CC  C__
GAM937  KIAA0542 3' CTCTTTCCTCCTTCATGCC   66662       A    T
                                GGCATGAAG AGGAA AGAG
                                |||||||| ||||| ||||
                                CCGTACTTC TCCTT TCTC
                                    C   _
GAM937  LASP1    3' CTGAAGCCTTCTTCTGCCA   21577      T     AA_
                                TGGCA GAAGAAGG  TAG
                                ||||| ||||||||  |||
                                ACCGT CTTCTTCC  GTC
                                  _      GAA
GAM937  MAP3K3   3' GCTCTGTTCTTCCTCAGCCA  11541     A  A   G
                                TGGC TGA GAAG AATAGAGC
                                |||| ||| |||| ||||||||
                                ACCG ACT CTTC TTGTCTCG
                                  _  C   _
GAM937  MGC16943 3' CTTGAACCTCTTCATGTCA   55603        A  AATA
                                TGGCATGAAGA GG   GAG
                                ||||||||||| ||   |||
                                ACTGTACTTCT CC   TTC
                                    _ AAG_
GAM937  MRPL48   3' CTTAGACCCTTTCATGCCA   32659        AA  AA  G
                                TGGCATGAAG  GG  TA AG
                                |||||||||  ||  || ||
                                ACCGTACTTT  CC  AT TC
                                    C_  AG  G
GAM937  NRM      3' GCCTGGCTGCTTCATGCCA   99717        AAGGAA  A
                                TGGCATGAAG     TAG GC
                                |||||||||      ||| ||
                                ACCGTACTTC     GTC CG
                                    GTCG__
GAM937  PHF3     3' GCTCATCATCCCTTCTTCATAC 31432    C       A  A__
          CA                    TGG ATGAAGAAGG AT   GAGC
                                ||| ||||||||| ||   ||||
                                ACC TACTTCTTCC TA   CTCG
                                  A        C  CTA
GAM937  PRO1880  5' CTCTATATACTTCATGTCA   26888        AAGGA
                                TGGCATGAAG    ATAGAG
                                |||||||||     ||||||
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                                ACTGTACTTC    TATCTC
                                     ATA__
GAM937  RP4-622L5 3'  GCCTGGACCTTCATGCTA    39426       AGA  AA  A
                                TGGCATGA  AGG  TAG GC
                                ||||||||  |||  ||| ||
                                ATCGTACT  TCC  GTC CG
                                    ___  AG
GAM937  UPLC1     3'  GCTGGCCTTCTTCCTGCCA   35228     T      AATAG
                                TGGCA GAAGAAGG    AGC
                                ||||| ||||||||    |||
                                ACCGT CTTCTTCC    TCG
                                   C      GG___
GAM937  LOC143158 5'  CTATTCCTCCTCCATTCCA   76999    C  A  A
                                TGG ATG AG AGGAATAG
                                ||| ||| || ||||||||
                                ACC TAC TC TCCTTATC
                                  T  C  C
GAM937  LOC149386 5'  CTCTGAGATCTTCATGGCA   85556    G      AGGAA
                                TG CATGAAGA    TAGAG
                                || ||||||||    |||||
                                AC GTACTTCT    GTCTC
                                 G      AGA__
GAM937  LOC151405 5'  CTCATCACTTCTTCATGACA  86514    G       GA  A
                                TG CATGAAGAAG  AT GAG
                                || ||||||||||  || |||
                                AC GTACTTCTTC  TA CTC
                                 A        AC  _
GAM937  LOC151835 3'  CTCTCTGCCTTCATGCCA    81194        AA  ATA
                                TGGCATGAAG  GGA  GAG
                                ||||||||||  |||  |||
                                ACCGTACTTC  TCT  CTC
                                     CG  ___
GAM937  LOC196264 3'  GCTCCATTCCTTTGACTCCA  88987    CATGAA     A
                                TGG     GAAGGAAT GAGC
                                |||     |||||||| ||||
                                ACC     TTTCCTTA CTCG
                                  TCAG__      C
GAM937  LOC256222 5'  GCCCTTTTACTCTTTCATGCCA 99015       GA  GAAT  A
                                TGGCATGAA  AG   AG GC
                                |||||||||  ||   || ||
                                ACCGTACTT  TC   TC CG
                                     TC  ATTT  C
GAM937  LOC256310 5'  CTGCACCTTCTTCACCCA    98097    CA      AA
                                TGG  TGAAGAAGG  TAG
                                |||  |||||||||  |||
                                ACC  ACTTCTTCC  GTC
                                  C_       AC
GAM938  HRH1      3'  CTCAAACATGTTTAGAGTGGA  7819     A    TGG
                                TCCA TCTGA   GCATGTTTGAG
                                |||| |||||   ||||||||||
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                                AGGT AGATT   TGTACAAACTC
                                  G    ___
GAM938  TRIM37   3'  CTCAAATTTGTCATCAG     31625        G  T
                                CTGATGG CA GTTTGAG
                                ||||||| || |||||||
                                GACTACT GT TAAACTC
                                   _  T
GAM938  HTMP10   3'  CTCAAAAAAGCCATCAGATCTG 53758    CA       G ATG
           A                     TC  ATCTGATGG C   TTTGAG
                                ||  |||||||||| |   ||||||
                                AG  TAGACTACC G   AAACTC
                                 TC        _ AAA
GAM938  PAK2     5'  CTCAAATATCACCAAACTAGA  67140     A__   GC
                                TCTG   TGG  ATGTTTGAG
                                ||||   |||  |||||||||
                                AGAT   ACC  TATAAACTC
                                  CAA   AC
GAM938  SEMA6A   3'  CTCGAGTACCCACCAGA     40818     A   CA
                                TCTG TGGG  TGTTTGAG
                                |||| ||||  ||||||||
                                AGAC ACCC  ATGAGCTC
                                  C   __
GAM938  TTY7     3'  TCAAACATGCAGGCTGGA    50019     AT  GATGG
                                TCCA  CT    GCATGTTTGA
                                ||||  ||    ||||||||||
                                AGGT  GA    CGTACAAACT
                                  CG  _____
GAM938  LOC144766 3'  CTCAAACATGAGAAGACTGGG  77481     A   GATGGG
                                TCCA TCT     CATGTTTGAG
                                |||| |||     ||||||||||
                                GGGT AGA     GTACAAACTC
                                  C   AGA___
GAM938  LOC201685 5'  TAAACACCCATCAGATGGA   91845     A       CA
                                TCCA TCTGATGGG  TGTTTG
                                |||| |||||||||  ||||||
                                AGGT AGACTACCC  ACAAAT
                                   _       __
GAM938  LOC221596 5'  CTCAAACAAAACTCAGATT   93623        TG GCA
                                AATCTGA  G   TGTTTGAG
                                |||||||  |   ||||||||
                                TTAGACT  C   ACAAACTC
                                   __ AAA
GAM938  LOC93622  3'  CTCTGCAGACCATCAGAT    57729         GCA   TT
                                ATCTGATGG   TGT  GAG
                                |||||||||   |||  |||
                                TAGACTACC   ACG  CTC
                                     AG_   T_
GAM939  CACNG2   3'  GAGGAACAAAGAAGCA     21400         CA   A
                                TGCTTCTT  TGT TCTT
                                ||||||||  ||| ||||
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                                ACGAAGAA  ACA GGAG
                                   __   A
GAM939  NUMB     3'  ACAACAGGAAGCAAAGCAA   14976      C       CA
                                TTGCT TGCTTCTT  TGT
                                ||||| ||||||||  |||
                                AACGA ACGAAGGA  ACA
                                   A       CA
GAM939  RNMT     3'  CAAGAATGAAGCAGAGCAA   15049          _  A
                                TTGCTCTGCTTC TTC TG
                                |||||||||||| ||| ||
                                AACGAGACGAAG AAG AC
                                      T   A
GAM939  TPK1     3'  AAGATACATGCTAAGAAAGCA  42607      _  __
                                TGCTT CTT  CATGTATCTT
                                ||||| |||  ||||||||||
                                ACGAA GAA  GTACATAGAA
                                   A   TC
GAM939  CNOT8    3'  AAGAATATGAAAAAGCAGAGCG 17705          C      A
          A                      TTGCTCTGCTT TTCATGT TCTT
                                ||||||||||| ||||||| ||||
                                AGCGAGACGAA AAGTATA AGAA
                                      A     _
GAM939  DKFZp547I224 5'  ATGGGGAAAAAACAGAGCAG   39949        C___
                                TTGCTCTG    TTCTTCAT
                                ||||||||    ||||||||
                                GACGAGAC    AAGGGGTA
                                     AAAA
GAM939  FLJ20435  3'  AAGACTCTATGAAGAAACAGAG 35621      C       TA_
                                CTCTG TTCTTCATG   TCTT
                                ||||| |||||||||   ||||
                                GAGAC AAGAAGTAT   AGAA
                                   A        CTC
GAM939  FLJ30567  3'  AAGACACATGGAGCAGAGC   59471         CTT    A
                                GCTCTGCTT   CATGT TCTT
                                |||||||||   ||||| ||||
                                CGAGACGAG   GTACA AGAA
                                     ___    C
GAM939  KIAA0447  3'  CATTCAGAAACAGAGCAA    72108        C   TC
                                TTGCTCTG TTCT  ATG
                                |||||||| ||||  |||
                                AACGAGAC AAGA  TAC
                                     A   CT
GAM939  KIAA1560  3'  ATGCATGAAAAACAAAGGCAA  64848      T  GC_  C
                                TTGC CT   TT TTCATGTAT
                                |||| ||   || |||||||||
                                AACG GA   AA AAGTACGTA
                                   _  AAC  A
GAM939  KIAA1577  3'  ATACACAGCCAGAGCAG     65098        _  TCTTCA
                                TTGCTCTG CT     TGTAT
                                |||||||| ||     |||||
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                                GACGAGAC GA      ACATA
                                    C  C_____
GAM939  SERF2     5'  AAGAATATGAAAAAGCAGAGCG 20485          C      A
              A                  TTGCTCTGCTT TTCATGT TCTT
                                 |||||||||||  |||||||  ||||
                                 AGCGAGACGAA AAGTATA AGAA
                                       A      _
GAM939  SS18L1    3'  AAGGCCAGTGAAGAAGCAAAGG 65942    G  C        GTA
              AA                   TT CT TGCTTCTTCAT   TCTT
                                 || || ||||||||||   ||||
                                 AA GA ACGAAGAAGTG   GGAA
                                  G  A         ACC
GAM939  LOC130507 3'  ATATGGAAAGCAGAGCAG    75454          C
                                 TTGCTCTGCTT TTCATGT
                                 ||||||||||| |||||||
                                 GACGAGACGAA AGGTATA
                                       _
GAM939  LOC142955 5'  ACAAGAGAAGCAGGCAA     76957      T       CA
                                 TTGC CTGCTTCTT  TGT
                                 |||| |||||||||  |||
                                 AACG GACGAAGAG  ACA
                                   _       A_
GAM939  LOC161734 3'  ATGGGGAAAAAACAGAGCAG   88459        C___
                                 TTGCTCTG    TTCTTCAT
                                 ||||||||    ||||||||
                                 GACGAGAC    AAGGGGTA
                                      AAAA
GAM939  LOC51031  3'  ACATGATGCAGAGCAA      32705         TTCT
                                 TTGCTCTGC    TCATGT
                                 |||||||||    ||||||
                                 AACGAGACG    AGTACA
                                       T___
GAM940  ITSN1     3'  CAATGAAAACACACTGGTGT   13091    TG    ACA
                                 GC  TAGT   TGTTTTCATTG
                                 ||  ||||   ||||||||||
                                 TG  GTCA   ACAAAAGTAAC
                                  TG    C__
GAM940  TMEFF2    3'  CAATGAAAACATGTACTACAGC 32996
              TA                   TAGCTGTAGTACATGTTTTCATTG
                                 |||||||||||||||||||||||
                                 ATCGACATCATGTACAAAAGTAAC

GAM940  DKFZp564I1922 3'  GAGTTACATACATACAGCTA   31850        GTAC    T_
                                 TAGCTGTA    ATGT  TTC
                                 ||||||||    ||||  |||
                                 ATCGACAT    TACA  GAG
                                      ACA_    TT
GAM941  CXCL16    3'  TCGAACTCCTGACCTGGTGAT  42180       TG  A   A  AC
                                 ATCAT  GG TCA GA  TCGA
                                 |||||  || ||| ||  ||||
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                                TAGTG  CC AGT CT  AGCT
                                   GT  _   C  CA
GAM941  FEZ1     3'  TCGAACTCCTGACCTGGTGAT  42872      TG  A   A  AC
                                ATCAT  GG TCA GA  TCGA
                                |||||  || ||| ||  ||||
                                TAGTG  CC AGT CT  AGCT
                                   GT  _   C  CA
GAM941  GRWD     3'  TTCTTGATCTCAAGTGAT    49791       _
                                ATCATT GGGATCAAGAA
                                |||||| ||||||||||
                                TAGTGA CTCTAGTTCTT
                                   A
GAM941  KIAA1209 3'  TCGAACTCCTGATCTCATGAT  61410      T      A  AC
                                ATCAT GGGATCA GA  TCGA
                                ||||| |||||| ||  ||||
                                TAGTA CTCTAGT CT  AGCT
                                   _      C  CA
GAM941  KIAA1373 3'  TCGAATTCCTGACCTCTGATGA 71514      TG _ A   A   C
           T                     ATCAT  G G TCA GAA TCGA
                                 |||||  | | ||| ||| ||||
                                 TAGTA  C C AGT CTT AGCT
                                    GT T C   C   A
GAM941  NFAT5    3'  TCGAACTCCTAACCTCCAGTGA 57792         ATCAA_  AC
           T                     ATCATTGGG     GA  TCGA
                                 |||||||||     ||  ||||
                                 TAGTGACCT     CT  AGCT
                                      CCAATC  CA
GAM941  LOC139274 5'  CGAGCAGCAGGACCCCAGTGAT 76334          A  AAGAA_
           A                     TATCATTGGG TC     CTCG
                                 |||||||||| ||     ||||
                                 ATAGTGACCC AG     GAGC
                                      C  GACGAC
GAM941  LOC147054 3'  TCGAACTCCCGATCTCAGGTGA 85010      _      AA  AC
           T                     ATCAT TGGGATC  GA  TCGA
                                 ||||| |||||||  ||  ||||
                                 TAGTG ACTCTAG  CT  AGCT
                                    G      CC  CA
GAM941  LOC152851 3'  TCGAACTCCTGATCTCAGGTGA 81596      _      A  AC
           T                     ATCAT TGGGATCA GA  TCGA
                                 ||||| |||||||| ||  ||||
                                 TAGTG ACTCTAGT CT  AGCT
                                    G       C  CA
GAM941  LOC90826  5'  CGAGTTCCTGGAGGATA     64784      A  G  ATCAA
                                 TATC TT GG    GAACTCG
                                 |||| || ||    |||||||
                                 ATAG AG TC    CTTGAGC
                                   G  G  _____
GAM942  ABCC5    3'  GCCTTAGCATGTTTGCTGA    20296        G   AC_
                                 TCAGCAGA ATG   AGGC
                                 |||||||| |||   ||||
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                                AGTCGTTT TAC   TCCG
                                     G  GAT
GAM942  B4GALT1  3'  GCCTGGACAGGGTCTCTGCTG  9470          GA____
                                CAGCAGAGAT     CAGGC
                                ||||||||||     |||||
                                GTCGTCTCTG     GTCCG
                                     GGACAG
GAM942  BCL2     3'  GCCTGTTTTGTCTTCTGTTG   7237        _  __
                                CAGCAGA GAT  GACAGGC
                                |||||||  |||  |||||||
                                GTTGTCT CTG  TTGTCCG
                                     T   TT
GAM942  CA12     3'  GCCTCAGGGATCCTCTGCTGG  8691         _ GAC__
                                TCAGCAGAG AT    AGGC
                                |||||||||  ||    ||||
                                GGTCGTCTC TA    TCCG
                                     C  GGGAC
GAM942  CACNA1C  3'  GTTTGACACTTTTGTTGA    7402          A  A
                                TCAGCAGAG TG CAGGC
                                |||||||||  ||  |||||
                                AGTTGTTTT AC GTTTG
                                     C  A
GAM942  CD80     3'  GCCTCCGTCATCTCTTCTGG   19025     C       __
                                TCAG AGAGATGAC  AGGC
                                ||||  |||||||||  ||||
                                GGTC TCTCTACTG  TCCG
                                   T        CC
GAM942  CHD2     3'  CGCCTGAAGGACTTTTTCTGCT 8865          TGA_____
           GG                     TCAGCAGAGA       CAGGC  G
                                ||||||||||       |||||  |
                                GGTCGTCTTT       GTCCG  C
                                     TTCAGGAA
GAM942  CLASP2   3'  GTTTGTTTATATCTTTGTTG   65204         ___
                                CAGCAGAGAT   GACAGGC
                                ||||||||||   |||||||
                                GTTGTTTCTA   TTGTTTG
                                     TAT
GAM942  COL4A1   3'  GCTTGAAAAACAGCTCTGTTGA 10243         A  A____
                                TCAGCAGAG TG    CAGGC
                                |||||||||  ||    |||||
                                AGTTGTCTC AC    GTTCG
                                     G  AAAAA
GAM942  CRI1     3'  GCTTGTTATTTGTCATGC    27538     _ __
                                GCA GA  GATGACAGGC
                                |||  ||  ||||||||||
                                CGT CT  TTATTGTTCG
                                  A  GT
GAM942  CROT     3'  GCCTGTTATGTTTGATGG    41258     G   G
                                TCA CAGA ATGACAGGC
                                |||  ||||  |||||||||
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                                GGT GTTT TATTGTCCG
                                  A   G
GAM942  DLK1    3'  GTCTGTCCTAATCTTTGT    15178       ___
                                GCAGAGAT  GACAGGC
                                ||||||||  |||||||
                                TGTTTCTA  CTGTCTG
                                    ATC
GAM942  DTR     3'  GTCTGTCTACATTTCTGC    10458       ___
                                GCAGAGAT  GACAGGC
                                ||||||||  |||||||
                                CGTCTTTA  CTGTCTG
                                    CAT
GAM942  DUOX2   3'  GTTTGTTTATTCTTCTGTTGA 26868       _ T__
                                TCAGCAGA GA  GACAGGC
                                |||||||| ||  |||||||
                                AGTTGTCT CT  TTGTTTG
                                    T  TAT
GAM942  EGFL5   3'  GCCTATGCATTTCTGATGG   87914    G      AC_
                                TCA CAGAGATG  AGGC
                                ||| ||||||||  ||||
                                GGT GTCTTTAC  TCCG
                                  A       GTA
GAM942  EPS8    3'  GTTTGTCATGGCTCTGTTGA   16715       __
                                TCAGCAGAG  ATGACAGGC
                                |||||||||  |||||||||
                                AGTTGTCTC  TACTGTTTG
                                    GG
GAM942  FBXL4   3'  GTTTGGTTATTTCTCTGG    25134    C      _
                                TCAG AGAGATGAC AGGC
                                |||| ||||||||| ||||
                                GGTC TCTTTATTG TTTG
                                  _       G
GAM942  FGF7    3'  GTTTTTTATTTCTGTTGA    10632          C
                                TCAGCAGAGATGA AGGC
                                |||||||||||| ||||
                                AGTTGTCTTTATT TTTG
                                      T
GAM942  GARP    3'  GTTTGTCACGTCTTCTGA    19786    C  GA
                                TCAG AGA  TGACAGGC
                                |||| |||  ||||||||
                                AGTC TCT  ACTGTTTG
                                  T  GC
GAM942  GPR85   3'  GCCTGTTAATTTTCTTGA    39104    C  A
                                TCAG AGAG TGACAGGC
                                |||| |||| ||||||||
                                AGTT TTTT ATTGTCCG
                                  C   A
GAM942  H1F0    3'  GCTTGTGTGTTTTGTTGG    19218       ATG
                                TCAGCAGAG  ACAGGC
                                |||||||||  ||||||
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                              GGTTGTTTT  TGTTCG
                                   GTG
GAM942  HSPA5   3' GTTTGTTATTTACACTGG   19288    CAG
                              TCAG  AGATGACAGGC
                              ||||  ||||||||||
                              GGTC  TTTATTGTTTG
                                ACA
GAM942  HTR2C   3' GCCTGTTAGGTCTGTTGA   7871       GA
                              TCAGCAGA TGACAGGC
                              ||||||||  ||||||||
                              AGTTGTCT  ATTGTCCG
                                   GG
GAM942  KIF3C   3' GCCTGTTACCCCTGTTTCTGA 11207    ___  AGA
                              TCAG  CAG  TGACAGGC
                              ||||  |||  ||||||||
                              AGTC  GTC  ATTGTCCG
                                TTT  CCC
GAM942  LZTFL1  3' CGTTTGTCATTTTTGTTG   40111
                              CAGCAGAGATGACAGGC  G
                              ||||||||||||||||  |
                              GTTGTTTTTACTGTTTG  C

GAM942  MPP5    3' GCTTAGTTGTATCTCTGT   42748      __  _
                              GCAGAGAT  GAC AGGC
                              ||||||||  ||| ||||
                              TGTCTCTA  TTG TTCG
                                   TG  A
GAM942  MRPS12  3' CGCCTGAAGGACCTTTTCTGCT 41196       TGA_____
           GG                   TCAGCAGAGA      CAGGC  G
                              ||||||||||      |||||  |
                              GGTCGTCTTT      GTCCG  C
                                   TCCAGGAA
GAM942  NUP62   3' GTCTTTATACTTTGCTGA   25651       _  C
                              TCAGCAGAG ATGA AGGC
                              |||||||| |||| ||||
                              AGTCGTTTC TATT TCTG
                                   A  _
GAM942  NXF1    3' GTCTGTCATCTCCTCCTG   22065    CA_
                              CAG  GAGATGACAGGC
                              |||  ||||||||||||
                              GTC  CTCTACTGTCTG
                                CTC
GAM942  OTOF    3' CGCCTGTGTCTGGGTTTCTGTT 17830        G_____
           GG                   TCAGCAGAGAT    ACAGGC  G
                              ||||||||||    ||||||  |
                              GGTTGTCTTTG    TGTCCG  C
                                   GGTCTG
GAM942  PIK3R1  3' CTTCTGTTTTGTTTTGCTGA  69134       AT_    C
                              TCAGCAGAG  GACAGG
                              ||||||||  ||||||
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                                AGTCGTTTT  TTGTCT
                                     GTT    TCG
GAM942  POR     3'  GCTCTTTCTCTCTGCTGA   95842        T  C  _
                                TCAGCAGAGA GA AG GC
                                |||||||||| || || ||
                                AGTCGTCTCT CT TC CG
                                     _  T  T
GAM942  POU4F1  3'  GTCTATGTATGTCTGCTGA   21766       G  AC_
                                TCAGCAGA ATG  AGGC
                                |||||||| |||  ||||
                                AGTCGTCT TAT  TCTG
                                    G  GTA
GAM942  PPP1CB  3'  GCTTGTTTTGTTTTTGTT    12226        __
                                AGCAGAGAT  GACAGGC
                                |||||||||  |||||||
                                TTGTTTTTG  TTGTTCG
                                     TT
GAM942  PTGES   3'  GCTTTGGATGTCTTTGCTG   18064        GA_  _
                                CAGCAGAGAT  CAG GC
                                ||||||||||  ||| ||
                                GTCGTTTCTG  GTT CG
                                     TAG  T
GAM942  PTTG1IP 3'  GCCTGTTGGGCTGTCTGG    16349     _  AGA
                                TCAG CAG  TGACAGGC
                                |||| |||  ||||||||
                                GGTC GTC  GTTGTCCG
                                  T  GG_
GAM942  PYGO2   3'  GTTTGTTGCTTCTCTTTGCT  64687       ____
                                AGCAGAGA   TGACAGGC
                                ||||||||   ||||||||
                                TCGTTTCT   GTTGTTTG
                                    CTTC
GAM942  RBBP2   3'  GCCAAAGTTATTTCTGTT    18570         A__
                                AGCAGAGATGAC  GGC
                                ||||||||||||  |||
                                TTGTCTTTATTG  CCG
                                      AAA
GAM942  RDX     3'  GCTTTTTTGATTTTGCTGA   12806        AT_  C
                                TCAGCAGAG  GA AGGC
                                |||||||||  || ||||
                                AGTCGTTTT  TT TTCG
                                     AGT  T
GAM942  REGL    3'  TTCCTCTTTATTTTTGCTGA  22504          C_  C
                                TCAGCAGAGATGA  AGG
                                ||||||||||||  |||
                                AGTCGTTTTTTATT  TCC
                                      TC  TTT
GAM942  RENT1   3'  GCCTGCCGGCAACTTTGCTGA  12815        A  A___
                                TCAGCAGAG TG   CAGGC
                                |||||||||  ||   |||||
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                                AGTCGTTTC AC   GTCCG
                                     A  GGCC
GAM942  RERE     3'  GCTTGTTTTGTCTGTTGA    25016       GAT
                                TCAGCAGA  GACAGGC
                                ||||||||  |||||||
                                AGTTGTCT  TTGTTCG
                                     GTT
GAM942  RPH3AL   3'  GTCTGTTTAGTTTCTTTGG   23738     C    __
                                TCAG AGAGAT  GACAGGC
                                |||| ||||||  |||||||
                                GGTT TCTTTG  TTGTCTG
                                  _     AT
GAM942  RPS6KA5  3'  GTTTGGAAATTTTTCTGTTGA  17651         TGA___
                                TCAGCAGAGA     CAGGC
                                ||||||||||     |||||
                                AGTTGTCTTT     GTTTG
                                      TTAAAG
GAM942  SERPINE2 3'  GCCTCTTTGTGTTTTTGTTG   75431         AC___
                                CAGCAGAGATG    AGGC
                                ||||||||||    ||||
                                GTTGTTTTTGT    TCCG
                                      GTTTC
GAM942  SLC19A1  3'  GCTTCTCTGTCTCTGTGGA   13217    A      _ C
                                TC GCAGAGAT GA AGGC
                                || |||||||| || ||||
                                AG TGTCTCTG CT TTCG
                                 G       T  C
GAM942  SORCS1   3'  GTTTGTCATCCATGTGTGA   54683    _   GA
                                TCA GCA  GATGACAGGC
                                ||| |||  ||||||||||
                                AGT TGT  CTACTGTTTG
                                  G   AC
GAM942  SPARC    3'  GTTTGTTGTTCTGCCTGG    13346     _   G TG
                                TCAG CAGA A  ACAGGC
                                |||| |||| |  ||||||
                                GGTC GTCT T  TGTTTG
                                  C   _ GT
GAM942  SQSTM1   3'  TTCTGACACTTTCTGCTGG   15331         _ A   C
                                TCAGCAGAGA TG CAGG
                                |||||||||| || ||||
                                GGTCGTCTTT AC GTCT
                                      C  A   TG
GAM942  SRRM1    3'  GCCTGTGGAGTCTCTGCTGA  20696         G__
                                TCAGCAGAGAT   ACAGGC
                                ||||||||||   ||||||
                                AGTCGTCTCTG   TGTCCG
                                      AGG
GAM942  STX7     3'  GTCTTTCATTTTTTTGTTGG  14542        __    C
                                TCAGCAGA  GATGA AGGC
                                ||||||||  ||||| ||||
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                                GGTTGTTT  TTACT TCTG
                                    TT    T
GAM942  TCF3    3'  GTCTCTCGCTATTTCTGCTG  71275        ___  C
                                CAGCAGAGAT  GA AGGC
                                ||||||||||  || ||||
                                GTCGTCTTTA  CT TCTG
                                     TCG  C
GAM942  TPM4    3'  GCCATCTTCGCTTTGCTGG   13833        A  CA__
                                TCAGCAGAG TGA   GGC
                                ||||||||| |||   |||
                                GGTCGTTTC GCT   CCG
                                    _  TCTA
GAM942  UBE2A   3'  GCTTCAGTTTTTCTGTTG   13929        T  __
                                CAGCAGAGA GAC  AGGC
                                ||||||||| |||  ||||
                                GTTGTCTTT TTG  TTCG
                                    _  AC
GAM942  VCP     3'  GCCTATGCCATTTCTGTTG   75889        A  __
                                CAGCAGAGATG CA  GGC
                                |||||||||| ||  |||
                                GTTGTCTTTAC GT  CCG
                                     C  AT
GAM942  ZNF265  3'  GTTTATCTTTTCTCTGCTGA  19576        T__  C
                                TCAGCAGAGA  GA AGGC
                                ||||||||||  || ||||
                                AGTCGTCTCT  CT TTTG
                                     TTT  A
GAM942  ZNF42   5'  GCCTGCACCCTCTTTCTGTTGG 14244        _____  A
                                TCAGCAGAGA   TG CAGGC
                                ||||||||||   || |||||
                                GGTTGTCTTT   AC GTCCG
                                    CTCCC  _
GAM942  ABT1    3'  GCCTTTTTATTTTTGTTGG   26302        C_
                                TCAGCAGAGATGA  AGGC
                                ||||||||||||  ||||
                                GGTTGTTTTTATT  TCCG
                                      TT
GAM942  ADG-90  5'  GTTTGTTTCTTTCTGCTG   53525        T_
                                CAGCAGAGA  GACAGGC
                                |||||||||  |||||||
                                GTCGTCTTT  TTGTTTG
                                    CT
GAM942  ARHGEF9 3'  GTCTGGACATGCTCTGTTG  31491        _  A_
                                CAGCAGAG ATG  CAGGC
                                |||||||| |||  |||||
                                GTTGTCTC TAC  GTCTG
                                    G  AG
GAM942  ATPAF1  3'  GTTTGTCATCTTTATGA    61428    GC
                                TCA  AGAGATGACAGGC
                                |||  ||||||||||||
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                                AGT  TTTCTACTGTTTG
                                  A_
GAM942  C14orf3   3'  GTTTGTGCATGTTTTCTGCTGG 25051          ___  _
                                TCAGCAGAGA   TG ACAGGC
                                ||||||||||   || ||||||
                                GGTCGTCTTT   AC TGTTTG
                                     TGT  G
GAM942  C20orf81  5'  GCCTGTCGTTGCTGGTGG    43118     G   AG
                                TCA CAG  ATGACAGGC
                                ||| |||  |||||||||
                                GGT GTC  TGCTGTCCG
                                  G   GT
GAM942  caspr5    5'  GCCTGTCGTTCTAATTGG    58115     CAG  _
                                TCAG   AGA TGACAGGC
                                ||||   ||| ||||||||
                                GGTT   TCT GCTGTCCG
                                  AA_   T
GAM942  CGRP-RCP  3'  GCCCCTTTTCTCTGCTGG    27891          T  CA
                                TCAGCAGAGA GA  GGC
                                |||||||||| ||  |||
                                GGTCGTCTCT TT  CCG
                                     T  CC
GAM942  CL25084   3'  GCTTTTTTTCATTTTTGTTG   32287           C___
                                CAGCAGAGATGA    AGGC
                                ||||||||||||    ||||
                                GTTGTTTTTACT    TTCG
                                     TTTT
GAM942  CRK7      3'  TCTCTTTCCTTTTTTGCTGA   33667          T_  C   C
                                TCAGCAGAGA  GA AGG
                                ||||||||||  || |||
                                AGTCGTTTTT  CT TCT
                                     TC  T   CTG
GAM942  DDR1      3'  GCCTATACGTTTCTGTGGA    10476    A       AC_
                                TC GCAGAGATG   AGGC
                                || |||||||||   ||||
                                AG TGTCTTTGC   TCCG
                                  G        ATA
GAM942  DKFZP434B172 3'  GCTTGTTAATTTGTTGG     70576         GA
                                TCAGCAGA  TGACAGGC
                                ||||||||  ||||||||
                                GGTTGTTT  ATTGTTCG
                                     A_
GAM942  DKFZP434C1715 3'  GCTTGTTGGTTTAGTTGG    87353       A   AT
                                TCAGC GAG  GACAGGC
                                |||||| |||  |||||||
                                GGTTG TTT  TTGTTCG
                                   A   GG
GAM942  DKFZp434F054 5'  GCCTGTCAGGCTGATTGG    51047      _   AGA
                                TCAG CAG   TGACAGGC
                                |||| |||   ||||||||
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                                GGTT GTC   ACTGTCCG
                                  A  GG_
GAM942   DKFZP434F1735 3'  CGCTTGTTAAGAATTCTCTGCT 32115        _____
                                AGCAGAGA    TGACAGGC   G
                                ||||||||    ||||||||  |
                                TCGTCTCT    ATTGTTCG   C
                                    TAAGA
GAM942   DKFZp434M0331 5'  GCTTGCTATGCTCTCTGTTG   34659        ___  A
                                CAGCAGAGA   TG CAGGC
                                |||||||||   || |||||
                                GTTGTCTCT   AT GTTCG
                                    CGT  C
GAM942   DKFZP434N1235 3'  GTTTGTATATTTTGTTGA    49267         ATG
                                TCAGCAGAG   ACAGGC
                                |||||||||   ||||||
                                AGTTGTTTT   TGTTTG
                                    ATA
GAM942   DKFZP586M1120 3'  GTTTGTCATCATCTGCGTGA   49285    _    _
                                TCA GCAGA GATGACAGGC
                                ||| ||||| ||||||||||
                                AGT CGTCT CTACTGTTTG
                                  G    A
GAM942   DKFZp762E1511 5'  CGTTTGTTGTGATTCTTTTTGT 60250        ______ TG
           TGA                   TCAGCAGAG     A  ACAGGC   G
                                |||||||||     |  ||||||  |
                                AGTTGTTTT     T  TGTTTG   C
                                    TCTTAG GT
GAM942   DNAJC6    3'  GCTTTTCCATCTCTGCTG    29495          AC_
                                CAGCAGAGATG   AGGC
                                ||||||||||   ||||
                                GTCGTCTCTAC   TTCG
                                    CTT
GAM942   ESDN      3'  GTTTGAGTATTTCTGATGA   56061     G      A_
                                TCA CAGAGATG  CAGGC
                                ||| ||||||||  |||||
                                AGT GTCTTTAT  GTTTG
                                  A       GA
GAM942   FBXO30    3'  GCCTTTTAAAGTTTTGCTGA   50490         A__   C
                                TCAGCAGAG   TGA AGGC
                                |||||||||   ||| ||||
                                AGTCGTTTT   ATT TCCG
                                    GAA   T
GAM942   FLJ10260  5'  GTTTGTCCAGTTCTTTGTT   36414        T___
                                AGCAGAGA    GACAGGC
                                ||||||||    |||||||
                                TTGTTTCT    CTGTTTG
                                    TGAC
GAM942   FLJ10276  3'  GCCTGTGTTTTTCTGCTGA   36424         TG_
                                TCAGCAGAGA   ACAGGC
                                ||||||||||   ||||||
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                                AGTCGTCTTT  TGTCCG
                                      TTG
GAM942  FLJ10493  3'  TTCTTTCTAATCTTTGTTGG  36674        __ C  C
                                TCAGCAGAGAT  GA AGG
                                ||||||||||  || |||
                                GGTTGTTTCTA  CT TCT
                                      AT  T   TG
GAM942  FLJ10979  3'  GCCTGGCAGCTTTTGTTG   37487       A_  A
                                CAGCAGAG  TG CAGGC
                                ||||||||  || |||||
                                GTTGTTTT  AC GTCCG
                                     CG  G
GAM942  FLJ11149  3'  GTTTGTTGTTGTTGTTGA   37688       A  TG
                                TCAGCAG GA  ACAGGC
                                |||||||  ||  ||||||
                                AGTTGTT TT  TGTTTG
                                    G  GT
GAM942  FLJ11193  3'  GTCTGTTGAGCTGTATGA   37751    _   AGA
                                TCA GCAG   TGACAGGC
                                |||  ||||   ||||||||
                                AGT TGTC   GTTGTCTG
                                  A   GA_
GAM942  FLJ11342  3'  GTCTTTTTTCCTTTGCTGA   37836       AT_  C
                                TCAGCAGAG   GA AGGC
                                |||||||||   || ||||
                                AGTCGTTTC   TT TCTG
                                      CTT  T
GAM942  FLJ12619  3'  GTCTTCCCATTTGTGCTGG   48918      G    AC_
                                TCAGCA AGATG   AGGC
                                ||||||  |||||   ||||
                                GGTCGT TTTAC   TCTG
                                   G    CCT
GAM942  FLJ13114  3'  GCCTCTCCTGCCTCTGCTGA  44904        AT__  C
                                TCAGCAGAG    GA AGGC
                                |||||||||    || ||||
                                AGTCGTCTC    CT TCCG
                                      CGTC  C
GAM942  FLJ13305  5'  GCCTGGCCAATTCTGTTGA   91713       A  A_
                                TCAGCAGAG TG  CAGGC
                                |||||||||  ||  |||||
                                AGTTGTCTT AC  GTCCG
                                      A  CG
GAM942  FLJ20345  3'  GCCTCTTCGTCTTTCTGA    35494     C      C_
                                TCAG AGAGATGA  AGGC
                                ||||  ||||||||  ||||
                                AGTC TTTCTGCT  TCCG
                                  _       TC
GAM942  FLJ20371  3'  GCTTATCTCACCTCTGCTGG  35537       A  C__
                                TCAGCAGAG TGA   AGGC
                                |||||||||  |||   ||||
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                                GGTCGTCTC ACT   TTCG
                                      C   CTA
GAM942   FLJ20392  5' GCCTGTACTTCTCTGCTGG   35577        TG_
                                TCAGCAGAGA   ACAGGC
                                ||||||||||   ||||||
                                GGTCGTCTCT   TGTCCG
                                      TCA
GAM942   FLJ20442  3' GCTTGTACTGCTTTGTTGA   35630       ATG_
                                TCAGCAGAG    ACAGGC
                                |||||||||    ||||||
                                AGTTGTTTC    TGTTCG
                                      GTCA
GAM942   FLJ20511  5' GCTTGTGCGTTTTCTGTT    35777       _ _
                                AGCAGAGA TG ACAGGC
                                |||||||| || ||||||
                                TTGTCTTT GC TGTTCG
                                      T  G
GAM942   FLJ21032  3' GTCTTTTTTGATCTTTGTTGG 46619         ___ C
                                TCAGCAGAGAT   GA AGGC
                                ||||||||||   || ||||
                                GGTTGTTTCTA   TT TCTG
                                      GTT  T
GAM942   FLJ21865  3' GCCTGTGCCCCTCTGCTGG   43113       ATG_
                                TCAGCAGAG    ACAGGC
                                |||||||||    ||||||
                                GGTCGTCTC    TGTCCG
                                      CCCG
GAM942   FLJ22316  3' GTCTGTCACTTGTTTTGTTG  47618       A___
                                CAGCAGAG    TGACAGGC
                                ||||||||    ||||||||
                                GTTGTTTT    ACTGTCTG
                                     GTTC
GAM942   FLJ22679  3' GCTTGTTGCTCTCGTCTG    35180    CA   _
                                CAG  GAGA TGACAGGC
                                |||  |||| ||||||||
                                GTC  CTCT GTTGTTCG
                                  TG   C
GAM942   FLJ22679  3' GCTTGTTGCTCTCGTCTG    35181    CA   _
                                CAG  GAGA TGACAGGC
                                |||  |||| ||||||||
                                GTC  CTCT GTTGTTCG
                                  TG   C
GAM942   HBOA      3' GTCTGTCATTTCTCTGTTG   23933       __
                                CAGCAGAGA  TGACAGGC
                                |||||||||  ||||||||
                                GTTGTCTCT  ACTGTCTG
                                      TT
GAM942   HCC-4     5' GCTCTTTATTTTTGCCGG    57599    A       CA
                                TC GCAGAGATGA  GGC
                                || ||||||||||  |||
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                                GG CGTTTTTATT  TCG
                                 C         TC
GAM942  HRIHFB2436 3'  GTTTGTTATCTCATCTGG    27573      CA
                                TCAG  GAGATGACAGGC
                                ||||  ||||||||||||
                                GGTC  CTCTATTGTTTG
                                  TA
GAM942  HXCP2    3'  GCTTATGTCATCTCTGTT    51803           __
                                AGCAGAGATGACA  GGC
                                ||||||||||||  |||
                                TTGTCTCTACTGT  TCG
                                       AT
GAM942  KIAA0152 3'  GTTTGTTAGTTTGCCTGG    28980      _   GA
                                TCAG CAGA  TGACAGGC
                                |||| ||||  ||||||||
                                GGTC GTTT  ATTGTTTG
                                  C   G_
GAM942  KIAA0212 3'  GTCTCTTCACTTTGCTGG    28627         A  C_
                                TCAGCAGAG TGA  AGGC
                                |||||||||  |||  ||||
                                GGTCGTTTC ACT  TCTG
                                     _  TC
GAM942  KIAA0295 3'  GCTGGTTATTTCTCCTGG    68667      C        A
                                TCAG AGAGATGAC GGC
                                |||| |||||||||  |||
                                GGTC TCTTTATTG TCG
                                  C        G
GAM942  KIAA0326 3'  GCTATTCATCTTTGTTGG    64964           CA
                                TCAGCAGAGATGA  GGC
                                ||||||||||||  |||
                                GGTTGTTTCTACT  TCG
                                       TA
GAM942  KIAA0354 3'  GTTTGTCTTTGTTCTGCTG    30194        AT__
                                CAGCAGAG    GACAGGC
                                ||||||||    |||||||
                                GTCGTCTT    CTGTTTG
                                     GTTT
GAM942  KIAA0377 3'  GCCAGCAACCTTTTCTGTTGG  28503          ____  ACA
                                TCAGCAGAGA    TG   GGC
                                ||||||||||    ||   |||
                                GGTTGTCTTT    AC   CCG
                                      TCCA  GA_
GAM942  KIAA0478 3'  GCCTGGCCAGGTTTCTGTTGG  30180          GA___
                                TCAGCAGAGAT     CAGGC
                                ||||||||||     |||||
                                GGTTGTCTTTG     GTCCG
                                       GACCG
GAM942  KIAA0532 3'  GCTTAGAGCATGTTTGCTGA   71322         G   AC__
                                TCAGCAGA ATG    AGGC
                                ||||||||  |||   ||||
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                                AGTCGTTT TAC    TTCG
                                    G   GAGA
GAM942  KIAA0555 3' GCTTGTTTTTTCTTTTTGCT   60744      ____    T
                                AGCA    GAGA GACAGGC
                                ||||    |||| |||||||
                                TCGT    CTTT TTGTTCG
                                  TTTT    T
GAM942  KIAA0674 5' GCTGACAACCTCTCTGCTGA   61242          ___  A   GC
                                TCAGCAGAGA   TG CAG
                                ||||||||||   || |||
                                AGTCGTCTCT   AC GTC
                                     CCA  A   G
GAM942  KIAA0953 3' GTCTGTCGTTTACACTGG    67331      CAG
                                TCAG   AGATGACAGGC
                                ||||   ||||||||||
                                GGTC   TTTGCTGTCTG
                                  ACA
GAM942  KIAA1077 3' TCTTGGTTGTCTCTGCTGA    73293          TG  _   C
                                TCAGCAGAGA  AC AGG
                                ||||||||||  || |||
                                AGTCGTCTCT  TG TTC
                                     GT  G   TT
GAM942  KIAA1117 3' GTCTTTCACAAATTCTGTTGG  61773          A___   C
                                TCAGCAGAG    TGA AGGC
                                |||||||||    ||| ||||
                                GGTTGTCTT    ACT TCTG
                                     AAAC   T
GAM942  KIAA1157 3' GCTCTAAATCTCTTTGCTGG   72703          T  C__  _
                                TCAGCAGAGA GA   AG GC
                                |||||||||| ||   || ||
                                GGTCGTTTCT CT   TC CG
                                     _  AAA  T
GAM942  KIAA1223 3' GCCTGTTGATTTGCTGA      71698         GAT
                                TCAGCAGA   GACAGGC
                                ||||||||   |||||||
                                AGTCGTTT   TTGTCCG
                                    AG_
GAM942  KIAA1431 3' CGTCTGTAAATAAAGTTTTGTT 63681          ATG_____
          GG                    TCAGCAGAG       ACAGGC   G
                                |||||||||       ||||||   |
                                GGTTGTTTT       TGTCTG   C
                                     GAAATAAA
GAM942  KIAA1718 3' GCATTTTCATTTCTGCTGA    64976          CAG_
                                TCAGCAGAGATGA    GC
                                ||||||||||||    ||
                                AGTCGTCTTTACT    CG
                                       TTTA
GAM942  KIAA1957 3' GTCTGGCCATTTCTGCTG     76218          A_
                                CAGCAGAGATG  CAGGC
                                ||||||||||  |||||
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                                GTCGTCTTTAC  GTCTG
                                      CG
GAM942  KOC1     3'  GCTGCATTTATATCTGCTGG   92717        ____   A   GC
                                TCAGCAGA   GATG CAG
                                ||||||||   |||| |||
                                GGTCGTCT   TTAC GTC
                                     ATAT   _  G
GAM942  LRP1B    5'  GCTTTCTGTTTCTGCTGA    38278          AC
                                TCAGCAGAGATG  AGGC
                                ||||||||||||  ||||
                                AGTCGTCTTTGT  TTCG
                                      CT
GAM942  MARK2    5'  GCCTGACAGGTTCTGCTG    66221        A_  A
                                CAGCAGAG  TG CAGGC
                                ||||||||  || |||||
                                GTCGTCTT  AC GTCCG
                                     GG  A
GAM942  MESDC2   3'  CGTCTGTGGGCTTTTTCTGTTG 72912         TG____
                                CAGCAGAGA     ACAGGC   G
                                |||||||||     ||||||  |
                                GTTGTCTTT     TGTCTG   C
                                      TTCGGG
GAM942  MGC20255 3'  CGTCTGTCTCCCCCTCTCTGTT 54536        T_____
                                AGCAGAGA     GACAGGC   G
                                ||||||||     |||||||  |
                                TTGTCTCT     CTGTCTG   C
                                     CCCCCT
GAM942  MGC2747  3'  GCTTGTTGAGTTTTTTGTTG   44325         ___
                                CAGCAGAGA   TGACAGGC
                                |||||||||   ||||||||
                                GTTGTTTTT   GTTGTTCG
                                      TGA
GAM942  MGC34923 3'  GCTCCTTTTTTCTGTTGG    59197          T  CA
                                TCAGCAGAGA GA  GGC
                                |||||||||| ||  |||
                                GGTTGTCTTT TT  TCG
                                      T  CC
GAM942  MYO3B    5'  GCCTGAAGTGTTCTGCTGG    58112         _  GA
                                TCAGCAGAG AT  CAGGC
                                |||||||||  ||  |||||
                                GGTCGTCTT TG  GTCCG
                                      G  AA
GAM942  NEK1     3'  CGCCTGTTGAACTTCTTTCTGT 97562        _______
           T                     AGCAGAGA     TGACAGGC   G
                                 ||||||||     ||||||||   |
                                 TTGTCTTT     GTTGTCCG   C
                                      CTTCAA
GAM942  NMU      3'  GCTAAATGTACTCTGTTGA    22908         ATG  ___
                                TCAGCAGAG   ACA   GGC
                                |||||||||   |||   |||
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                                AGTTGTCTC  TGT  TCG
                                    A__  AAA
GAM942  NPD009   5' GCTGTAGCATCTCTGCTGG  96750        __  GC
                                TCAGCAGAGATG ACAG
                                |||||||||||  ||||
                                GGTCGTCTCTAC TGTC
                                   GA  G
GAM942  NPTXR    3' GCTTGATGTGTTTCTGTT   27437        A__
                                AGCAGAGATG  CAGGC
                                |||||||||  |||||
                                TTGTCTTTGT  GTTCG
                                   GTA
GAM942  OAZIN    5' GCCTTGGGTATTTCTGCT   32438        A_ _
                                AGCAGAGATG CA GGC
                                |||||||||  || |||
                                TCGTCTTTAT GT CCG
                                   GG  T
GAM942  PIGM     5' GTCTGCAGTCGTTTCGGTTGG 59718     A     ___
                                TCAGC GAGATGAC  AGGC
                                ||||| ||||||||  ||||
                                GGTTG CTTTGCTG  TCTG
                                  G      ACG
GAM942  PIK3R4   5' GCTTCTTCTCTCTGCTGA   62870        T  C
                                TCAGCAGAGA GA AGGC
                                |||||||||| || ||||
                                AGTCGTCTCT TT TTCG
                                   C  C
GAM942  PPFIBP1  3' CGTTTGTTGTTCTAACTTCTGC 14629      _______ TG
          TG                  CAGCAGA    GA  ACAGGC  G
                                |||||||    ||  ||||||  |
                                GTCGTCT    TT  TGTTTG  C
                                   TCAATC  GT
GAM942  PPP2R3A  3' GCCTTCCAACTTTGCTGG   12244        A  AC
                                TCAGCAGAG TG  AGGC
                                |||||||||  ||  ||||
                                GGTCGTTTC AC  TCCG
                                   A  CT
GAM942  PTP4A1   5' GCACTTCTTTTCTGTTGG   14406        T  C  _
                                TCAGCAGAGA GA AG GC
                                |||||||||| || || ||
                                GGTTGTCTTT CT TC CG
                                   T  _  A
GAM942  RES4-25  3' CGCCTGCGGTTTTGTTTCTGTT 65265      TG _____
                                AGCAGAGA  A    CAGGC  G
                                ||||||||  |    |||||  |
                                TTGTCTTT  T    GTCCG  C
                                   GT TTGGC
GAM942  RHOBTB1  3' GTCTGTTGTATTTTGTTGA  93094        _ TG
                                TCAGCAGAG A  ACAGGC
                                |||||||||  |  ||||||
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                                AGTTGTTTT T  TGTCTG
                                     A GT
GAM942  RI58     3'  GTTTGTCATCTCTAGTGA    25777     GC
                                TCA  AGAGATGACAGGC
                                |||  ||||||||||||
                                AGT  TCTCTACTGTTTG
                                  GA
GAM942  RPS6KC1  3'  GCTTTGTACTCTTTGTTGA   25780         TG   _
                                TCAGCAGAGA  ACAG GC
                                ||||||||||  |||| ||
                                AGTTGTTTCT  TGTT CG
                                     CA    T
GAM942  RTTN     3'  GCCTTTTCCTTTCTGTTGA   93447         T  C_
                                TCAGCAGAGA GA  AGGC
                                ||||||||||  ||  ||||
                                AGTTGTCTTT CT  TCCG
                                     C  TT
GAM942  SARM     3'  GTTTGTTTCAGTTTGCTGA   31304        GAT_
                                TCAGCAGA    GACAGGC
                                ||||||||    |||||||
                                AGTCGTTT    TTGTTTG
                                     GACT
GAM942  SLC26A10 5'  GTTTCCCGTACTTTGCTGG   56847         _  AC
                                TCAGCAGAG ATG  AGGC
                                |||||||||  |||  ||||
                                GGTCGTTTC TGC  TTTG
                                     A   CC
GAM942  SLC2A10  3'  GCTTGATTTATTGTTTGTTGA 48555         _    __
                                TCAGCAGA GATGA  CAGGC
                                ||||||||  |||||  |||||
                                AGTTGTTT TTATT  GTTCG
                                     G     TA
GAM942  SLC39A3  3'  GTTTGTCAGTGTCTGTTGG   58604        G _
                                TCAGCAGA A TGACAGGC
                                ||||||||  |  ||||||||
                                GGTTGTCT T ACTGTTTG
                                     G G
GAM942  SMCR7    3'  GCTTCACATTTCTGCTGA    58240          AC
                                TCAGCAGAGATG  AGGC
                                ||||||||||||  ||||
                                AGTCGTCTTTAC  TTCG
                                       AC
GAM942  SNPH     3'  GTCTACTCTGTCTCTGCTG   28907         _  C_
                                CAGCAGAGAT GA  AGGC
                                ||||||||||  ||  ||||
                                GTCGTCTCTG CT  TCTG
                                     T  CA
GAM942  SRCRB4D  3'  GCCTGTCATCGACTGTTG    55796       A_
                                CAGCAG  GATGACAGGC
                                ||||||  ||||||||||
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                                GTTGTC  CTACTGTCCG
                                   AG
GAM942  STAB2    3'  GCCATACCTCATCTCTCTGG  34528     C      CA___
                                TCAG AGAGATGA    GGC
                                |||| ||||||||    |||
                                GGTC TCTCTACT    CCG
                                  _      CCATA
GAM942  STAF65(gamma) 3'  GCCTTTGTTATTTCTGCT    30070          __
                                AGCAGAGATGACA  GGC
                                ||||||||||||  |||
                                TCGTCTTTATTGT  CCG
                                       TT
GAM942  SURB7    3'  GCGCCTGTTATTTTTGTTG   16212
                                CAGCAGAGATGACAGGC   GC
                                ||||||||||||||||   ||
                                GTTGTTTTTATTGTCCG   CG

GAM942  SV2B     3'  GCCATTTAACTTTCTGTTGG  29951        __  CA
                                TCAGCAGAGA  TGA  GGC
                                |||||||||  |||  |||
                                GGTTGTCTTT  ATT  CCG
                                      CA   TA
GAM942  TJP4     3'  GCCTGTCAGCTGCGTTGA    55506      AG  A
                                TCAGC  AG TGACAGGC
                                |||||  || ||||||||
                                AGTTG  TC ACTGTCCG
                                   CG  G
GAM942  ZDHHC4   3'  GTTTGTTTTGATTTCTGCTG  36645        ___
                                CAGCAGAGAT   GACAGGC
                                ||||||||||   |||||||
                                GTCGTCTTTA   TTGTTTG
                                      GTT
GAM942  LOC114932 3'  GCTTGTCATTTTCTCTGTT   73092       ___
                                AGCAGAGA   TGACAGGC
                                ||||||||   ||||||||
                                TTGTCTCT   ACTGTTCG
                                     TTT
GAM942  LOC123036 5'  GTTTGTGTCTTTTGCTGG    74648       _  G
                                TCAGCAGA GAT ACAGGC
                                |||||||| ||| ||||||
                                GGTCGTTT CTG TGTTTG
                                     T  _
GAM942  LOC126669 3'  GTCTGTTATTGGCTGTTG    75946      A_
                                CAGCAG  GATGACAGGC
                                ||||||  ||||||||||
                                GTTGTC  TTATTGTCTG
                                   GG
GAM942  LOC127703 3'  GTTTGGTTCATTTCTCTGA   75181     C      __
                                TCAG AGAGATGA  CAGGC
                                |||| ||||||||  |||||
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                                AGTC TCTTTACT  GTTTG
                                  _      TG
GAM942   LOC128344 3'  GTCTGTGGGTTTCTGTTGG   75247         G_
                                TCAGCAGAGAT  ACAGGC
                                ||||||||||  ||||||
                                GGTTGTCTTTG  TGTCTG
                                      GG
GAM942   LOC144305 3'  GCTTGGTGTATTTTTGTTG   83973         A__
                                CAGCAGAGATG   CAGGC
                                ||||||||||   |||||
                                GTTGTTTTTAT   GTTCG
                                      GTG
GAM942   LOC144524 5'  GCCTGTTATCCTTCTCGA    84057   _ C  A
                                TC AG AG GATGACAGGC
                                || || || ||||||||||
                                AG TC TC CTATTGTCCG
                                 C  T  _
GAM942   LOC144577 3'  GTTTATCACTTTTCTGCTGA   77426         __  C
                                TCAGCAGAGA  TGA AGGC
                                ||||||||||  ||| ||||
                                AGTCGTCTTT  ACT TTTG
                                      TC   A
GAM942   LOC144809 3'  GCTTTGTGCATATTTGTTGA   84104        G  _   _
                                TCAGCAGA ATG ACAG GC
                                ||||||||| ||| |||| ||
                                AGTTGTTT TAC TGTT CG
                                     A   G   T
GAM942   LOC145652 3'  GTTTGTTCACCTCTGCTG    84406        A  _
                                CAGCAGAG TGA CAGGC
                                |||||||| ||| |||||
                                GTCGTCTC ACT GTTTG
                                     C   T
GAM942   LOC145978 3'  GCCTGTACATTTTTTGCT    78050        _ _
                                AGCAGAGA TG ACAGGC
                                |||||||| || ||||||
                                TCGTTTTT AC TGTCCG
                                     T  A
GAM942   LOC146268 3'  GCCCTCGTGCTTTGCTGG    78341         _   CA
                                TCAGCAGAG ATGA  GGC
                                ||||||||| ||||  |||
                                GGTCGTTTC TGCT  CCG
                                      G   C_
GAM942   LOC146819 3'  GTCTTTTTTTCTTTGTTGA   78743         T_  C
                                TCAGCAGAGA  GA AGGC
                                ||||||||||  || ||||
                                AGTTGTTTCT  TT TCTG
                                      TT  T
GAM942   LOC146821 3'  GTCTTTTTTTCTTTGTTGA   78733         T_  C
                                TCAGCAGAGA  GA AGGC
                                ||||||||||  || ||||
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                                AGTTGTTTCT  TT TCTG
                                      TT  T
GAM942   LOC147694 3'  GCTTTTTCGCTCTGTTGA    79099         A   C_
                                TCAGCAGAG TGA  AGGC
                                ||||||||| |||  ||||
                                AGTTGTCTC GCT  TTCG
                                     _   TT
GAM942   LOC148418 3'  GCTTGCTACATCTCTGTT    79592          A__
                                AGCAGAGATG   CAGGC
                                ||||||||||   |||||
                                TTGTCTCTAC   GTTCG
                                      ATC
GAM942   LOC149465 3'  GCCAAAATTATCTTTGCTG   80193           CA__
                                CAGCAGAGATGA    GGC
                                ||||||||||||    |||
                                GTCGTTTCTATT    CCG
                                       AAAA
GAM942   LOC150054 5'  CGCCCTCATCTTAATCTCTGCT 85970           GACA_____
           GA                     TCAGCAGAGAT       GGC   G
                                ||||||||||         |||  |
                                AGTCGTCTCTA       CCG   C
                                      ATTCTACTC
GAM942   LOC150685 5'  GCTCTCCTCATTTCTCTGA    88536      C       CA__
                                TCAG AGAGATGA    GGC
                                |||| ||||||||    |||
                                AGTC TCTTTACT    TCG
                                  _       CCTC
GAM942   LOC150696 3'  GCTTGTTACTCATCTGTTGA   59161         _ _
                                TCAGCAGA GA TGACAGGC
                                |||||||| || ||||||||
                                AGTTGTCT CT ATTGTTCG
                                     A  C
GAM942   LOC151512 5'  GCTTGGCAGGTTCTCTGCTG   86618          ___  A
                                CAGCAGAGA   TG CAGGC
                                |||||||||   || |||||
                                GTCGTCTCT   AC GTTCG
                                      TGG  G
GAM942   LOC151534 3'  GTCTGTTCCTGTCTGTTGG    57488         GAT_
                                TCAGCAGA    GACAGGC
                                ||||||||    |||||||
                                GGTTGTCT    TTGTCTG
                                     GTCC
GAM942   LOC152106 3'  GCCATCTTCGCTTTGCTGG    70596          A   CA__
                                TCAGCAGAG TGA    GGC
                                ||||||||| |||    |||
                                GGTCGTTTC GCT    CCG
                                      _  TCTA
GAM942   LOC152719 5'  GCCTGTTTTTTTTTTGTTGG   87032          T__
                                TCAGCAGAGA   GACAGGC
                                ||||||||||   |||||||
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                                GGTTGTTTTT  TTGTCCG
                                     TTT
GAM942  LOC154860 3'  GCTTGTGGCTTTTTGTTGA  87506       TG_
                                TCAGCAGAGA  ACAGGC
                                ||||||||||  ||||||
                                AGTTGTTTTT  TGTTCG
                                     CGG
GAM942  LOC157421 5'  GTCTGCAGGGTCTCTGCTG  87739       GA__
                                CAGCAGAGAT  CAGGC
                                ||||||||||  |||||
                                GTCGTCTCTG  GTCTG
                                     GGAC
GAM942  LOC157627 3'  GCCTGCCAGGTTTCTGCTG  82418       __ A
                                CAGCAGAGA TG CAGGC
                                |||||||||  || |||||
                                GTCGTCTTT AC GTCCG
                                     GG  C
GAM942  LOC161742 3'  GTCTGTTTTTGTTTTGTTG  83169      AT__
                                CAGCAGAG  GACAGGC
                                ||||||||  |||||||
                                GTTGTTTT  TTGTCTG
                                    GTTT
GAM942  LOC199923 3'  GCTTTAGAGAGTTTCTGTTGG 89873       GAC___
                                TCAGCAGAGAT    AGGC
                                ||||||||||    ||||
                                GGTTGTCTTTG    TTCG
                                     AGAGAT
GAM942  LOC200781 3'  GCTTTTTTCAGCTTCTGCTGG 91722       A_  C__
                                TCAGCAGAG TGA  AGGC
                                |||||||||  |||  ||||
                                GGTCGTCTT ACT  TTCG
                                     CG  TTT
GAM942  LOC201952 3'  GCCTTGGCTATCTTTGTT   91877       A_ _
                                AGCAGAGATG CA GGC
                                ||||||||||  || |||
                                TTGTTTCTAT GT CCG
                                     CG  T
GAM942  LOC203246 3'  GCCTCTTGGCTCTGCTGA   90834       AT  C
                                TCAGCAGAG  GA AGGC
                                |||||||||  || ||||
                                AGTCGTCTC  TT TCCG
                                     GG  C
GAM942  LOC203504 3'  GCCTGTCAGCCTGCTGG    92325      AGA
                                TCAGCAG   TGACAGGC
                                |||||||   ||||||||
                                GGTCGTC   ACTGTCCG
                                    CG_
GAM942  LOC219529 3'  GTCTGCTCAGTCTTTGCTG  94567       _  _
                                CAGCAGAGA TGA CAGGC
                                ||||||||| ||| |||||
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                                GTCGTTTCT ACT GTCTG
                                     G   C
GAM942   LOC219994 5'  GCCAGATCACACTCTGTTGG  95006        A_  CA_
                                TCAGCAGAG  TGA  GGC
                                |||||||||  |||  |||
                                GGTTGTCTC  ACT  CCG
                                     AC  AGA
GAM942   LOC220074 3'  GCTCTAGTCTTATTTTGCTGA  59984        AT_  _ _
                                TCAGCAGAG  GAC AG GC
                                |||||||||  ||| || ||
                                AGTCGTTTT  CTG TC CG
                                     ATT  A  T
GAM942   LOC220763 5'  GCTTGGGAGTCTTCTGCTGG  73735        _  GA_
                                TCAGCAGA GAT  CAGGC
                                ||||||||| |||  |||||
                                GGTCGTCT CTG  GTTCG
                                     T  AGG
GAM942   LOC220776 3'  GTTTGTTTGGTTTTGTTG   68936        AT_
                                CAGCAGAG  GACAGGC
                                ||||||||  |||||||
                                GTTGTTTT  TTGTTTG
                                     GGT
GAM942   LOC221354 3'  GCTACATTCCTTTTTTGCTGA  94015        T_  CA__
                                TCAGCAGAGA  GA   GGC
                                ||||||||||  ||   |||
                                AGTCGTTTTT  CT   TCG
                                      TC  TACA
GAM942   LOC221416 3'  GTCCTGGAAGGTCTCTGCTGG  95408         GA__   C
                                TCAGCAGAGAT   CAGG
                                ||||||||||    ||||
                                GGTCGTCTCTG   GTCC
                                      GAAG   TG
GAM942   LOC221486 3'  CGCCCCAGGATCACTCTCTGCT 92656         _  CA____
            GG                   TCAGCAGAGA TGA    GGC  G
                                |||||||||| |||    |||  |
                                GGTCGTCTCT ACT    CCG  C
                                     C  AGGACC
GAM942   LOC221543 3'  GTTTGTTATCTATTGCTG   95384       _
                                CAGCAG AGATGACAGGC
                                |||||| ||||||||||
                                GTCGTT TCTATTGTTTG
                                   A
GAM942   LOC222070 5'  GCTTCTTTGGTCTTTGCT   95817        __  C
                                AGCAGAGAT  GA AGGC
                                |||||||||  || ||||
                                TCGTTTCTG  TT TTCG
                                     GT  C
GAM942   LOC254822 5'  GCCTTGTCATCTTTGTTG   99008           _
                                CAGCAGAGATGACA GGC
                                |||||||||||||| |||
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                                GTTGTTTCTACTGT CCG
                                       T
GAM942   LOC255105 3'  GCCTGTCAGTTGTTTGCTGA  97794        GA__
                                TCAGCAGA   TGACAGGC
                                ||||||||   ||||||||
                                AGTCGTTT   ACTGTCCG
                                    GTTG
GAM942   LOC255465 3'  GCCAGTAAGGTTTCTGCTGA  99116         G__  A
                                TCAGCAGAGAT  AC GGC
                                ||||||||||  || |||
                                AGTCGTCTTTG  TG CCG
                                      GAA  A
GAM942   LOC255533 5'  GTTTGTTTTGTTTTGTTG    98754        AT_
                                CAGCAGAG  GACAGGC
                                ||||||||  |||||||
                                GTTGTTTT  TTGTTTG
                                    GTT
GAM942   LOC257451 3'  GTTTGTTGCTTCTCTTTGCT  97299        ____
                                AGCAGAGA   TGACAGGC
                                ||||||||   ||||||||
                                TCGTTTCT   GTTGTTTG
                                    CTTC
GAM942   LOC257596 3'  GTTTGTTATCTATTGCTG    99787       _
                                CAGCAG AGATGACAGGC
                                ||||||| ||||||||||
                                GTCGTT TCTATTGTTTG
                                   A
GAM942   LOC51246  3'  GCCTGTCATGCCTGTTGG    33640        AG
                                TCAGCAG  ATGACAGGC
                                |||||||  |||||||||
                                GGTTGTC  TACTGTCCG
                                    CG
GAM942   LOC85414  3'  GCCTGTTGGTCCTTCTGTTG  53552        __  _
                                CAGCAGA  GAT GACAGGC
                                |||||||  ||| |||||||
                                GTTGTCT  CTG TTGTCCG
                                    TC  G
GAM942   LOC90408  5'  GTTTGATATTTCTGTCGG    63347    A       A
                                TC GCAGAGATG CAGGC
                                || |||||||| |||||
                                GG TGTCTTTAT GTTTG
                                 C       A
GAM942   LOC90841  3'  GTCTGTTACTAATTTTTGTT  64872        ____
                                AGCAGAGAT   GACAGGC
                                |||||||||   |||||||
                                TTGTTTTTA   TTGTCTG
                                     ATCA
GAM942   LOC91351  3'  CGCTTGTTCTCCAATCTCTGCT 66296        _____
                                AGCAGAGAT    GACAGGC  G
                                |||||||||    |||||||  |
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                                TCGTCTCTA    TTGTTCG  C
                                     ACCTC
GAM942  LOC91351  3'  GTCTGTGGTTTTCTGTTGA   66301         _ G
                                TCAGCAGAGA T ACAGGC
                                |||||||||| | ||||||
                                AGTTGTCTTT G TGTCTG
                                      T G
GAM942  LOC91380  5'  GCCTGTTGATTTTGATGA    66448    G    A
                                TCA CAGAG TGACAGGC
                                ||| ||||| ||||||||
                                AGT GTTTT GTTGTCCG
                                  A    A
GAM942  LOC91464  3'  GTCTTTAGTTATCTTGCTGG  66712      G     ___
                                TCAGCA AGATGAC   AGGC
                                |||||| |||||||   ||||
                                GGTCGT TCTATTG   TCTG
                                   _      ATT
GAM942  LOC91923  5'  GCCTTCTCACTCTGTTGA    68172        A  C_
                                TCAGCAGAG TGA  AGGC
                                ||||||||| |||  ||||
                                AGTTGTCTC ACT  TCCG
                                      _  CT
GAM942  LOC92492  5'  GCCTGAGTGGTTTTCTGCTGA  70082         TGA___
                                TCAGCAGAGA     CAGGC
                                ||||||||||     |||||
                                AGTCGTCTTT     GTCCG
                                      TGGTGA
GAM943  ADCY2     3'  CGGTCCCAGTGCCATTGGCTTC 65648          G ____  AATCC
            AA                    TTGAAGCCAGTGG GC   ACC
                                |||||||||||| ||   |||
                                AACTTCGGTTACC TG   TGG
                                       G  ACCC     CC
GAM943  ADD3      3'  GGAGTCCCATTGTTTCAG    34168       C      A
                                TTGAAGC AGTGGGGC CC
                                ||||||| |||||||| ||
                                GACTTTG TTACCCTG GG
                                   _       A
GAM943  ARF1      3'  GGAACCTCTTACTGCTTTCAA  71196       C   __   CA
                                TTGAAG CAGT  GGGG  CC
                                |||||| ||||  ||||  ||
                                AACTTT GTCA  CTCC  GG
                                   C    TT    AA
GAM943  ARNTL     5'  GGGCCTTCATTGGTTCCGA   8627     A      _  A
                                TTG AGCCAGTGG GGC CC
                                ||| ||||||||| ||| ||
                                AGC TTGGTTACT CCG GG
                                  C       T  _
GAM943  ATP8B2    3'  GGATTCCTTAGTCCTGCTGGCC 65841   TG A    TG   ACC__
            TTGG                   T  A GCCAG  GGGC    AATCC
                                |  | |||||  ||||    |||||
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                                G  T CGGTC  CCTG    TTAGG
                                 GT C    GT   ATTCC
GAM943  BCL2    3'  GGGTTTTGTTACCTGGTTTTAA 7239         TGG   CC
                                TTGAAGCCAG  GGCA  AATCC
                                ||||||||||  ||||  |||||
                                AATTTTGGTC  TTGT  TTGGG
                                     CA_   T_
GAM943  BCL7A   3'  GGGTCATGGGTTTTGTTGTTTT 40989   TG  C  TG   A  __
          TGG                     T  AAG CAG  GGGC CCA  ATCC
                                |  ||| |||  |||| |||  ||||
                                G  TTT GTT  TTTG GGT  TGGG
                                 GT  T  GT   _  AC
GAM943  BRCA1   3'  GGAAAGTTCTGCTGTTTTTAG  24568      C  TG   A__
                                TTGAAG CAG  GGGC   CC
                                ||||||  |||  ||||   ||
                                GATTTT GTC  CTTG   GG
                                   T  GT   AAA
GAM943  CDYL    3'  AATTGTGTTTTATTGGTTTTGG 17886   TG          C  CC
                                T  AAGCCAGTGGGGCAC AAT
                                |  ||||||||||||||| |||
                                G  TTTGGTTATTTTGTG TTA
                                 GT          _  AG
GAM943  COLQ    3'  GGCGGCTCTTGTGGTTTCAA  20259       GT   A_
                                TTGAAGCCA  GGGGC  CC
                                |||||||||  |||||  ||
                                AACTTTGGT  TCTCG  GG
                                     GT    GC
GAM943  COLQ    3'  GGCGGCTCTTGTGGTTTCAA  55427       GT   A_
                                TTGAAGCCA  GGGGC  CC
                                |||||||||  |||||  ||
                                AACTTTGGT  TCTCG  GG
                                     GT    GC
GAM943  CSH2    3'  GGCTGCTCTACTGCTTCAG   42945      C      _
                                TTGAAGC AGTGGGGCA CC
                                |||||||  |||||||| ||
                                GACTTCG TCATCTCGT GG
                                    _       C
GAM943  CSH2    3'  GGCTGCTCTACTGCTTCAG   40976      C      _
                                TTGAAGC AGTGGGGCA CC
                                |||||||  |||||||| ||
                                GACTTCG TCATCTCGT GG
                                    _       C
GAM943  CSHL1   3'  GGCTGCTCCACTGCTTCAG   42937      C      _
                                TTGAAGC AGTGGGGCA CC
                                |||||||  |||||||| ||
                                GACTTCG TCACCTCGT GG
                                    _       C
GAM943  CSHL1   3'  GGCTGCTCCACTGCTTCAG   8986       C      _
                                TTGAAGC AGTGGGGCA CC
                                |||||||  |||||||| ||
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                                GACTTCG TCACCTCGT GG
                                   _       C
GAM943  CYBB    3'  GGAGCTCTATGGTTTTGA    76849   TG     G     A
                                T  AAGCCA TGGGGC CC
                                |  |||||| |||||| ||
                                A  TTTGGT ATCTCG GG
                                 GT     _     A
GAM943  CYP1A1  3'  GGTGCTGACTGGCTTCAG    6693           G  G
                                TTGAAGCCAGT GG CACC
                                |||||||||||  || ||||
                                GACTTCGGTCA TC GTGG
                                      G  _
GAM943  DAF     3'  GGATGCTTTCATTGTCTTTAA  6955        C      _  _
                                TTGAAG CAGTGGG GCA CC
                                ||||||  ||||||| ||| ||
                                AATTTC GTTACTT CGT GG
                                    T      T   A
GAM943  DKK1    3'  GGATATACAAGTTCTGTGGTTT 25296          G     ACCA__
           CAG                     TTGAAGCCA TGGGGC      ATCC
                                |||||||||  ||||||      ||||
                                GACTTTGGT GTCTTG      TAGG
                                      _     AACATA
GAM943  DPYD    3'  GGGCTCTGACTGGTTTTAA   61071           _    A
                                TTGAAGCCAGT GGGGC CC
                                ||||||||||  ||||| ||
                                AATTTTGGTCA TCTCG GG
                                      G    _
GAM943  ELMO3   5'  GGCGCCTTGTTCCGCTGGCCTC 45580     A      _____   A  AATCC
           G                     TGA GCCAGTGG     GGC CC
                                |||  ||||||||     ||| ||
                                GCT CGGTCGCC     CCG GG
                                  C       TTGTT   C     C
GAM943  EPB41L2 3'  CTGTGGTGGTGTTCTGTTGGTT 9292      A     TG       ATCC
           ACAA                    TTG AGCCAG  GGGCACCA
                                |||  ||||||  ||||||||
                                AAC TTGGTT  CTTGTGGT
                                  A     GT       GGTGTCG
GAM943  FOXF2   3'  GGATCTTCGTTGCCTTCAG   9374        C       CA
                                TTGAAG CAGTGGGG  CC
                                ||||||  |||||||  ||
                                GACTTC GTTGCTTC  GG
                                    C       TA
GAM943  FZD7    3'  GGATTTTTGTTTTGTTGGCTTT 14505          TG     CC
           AA                     TTGAAGCCAG  GGGCA  AATCC
                                ||||||||||  |||||  |||||
                                AATTTCGGTT  TTTGT  TTAGG
                                      GT     TT
GAM943  GARP    3'  GGCAGGCCCCGCTGGTTT    19784           A__
                                AAGCCAGTGGGGC   CC
                                ||||||||||||   ||
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                                TTTGGTCGCCCCG  GG
                                      GAC
GAM943  GH1     3'  GGCTGCTCTACTGCTTCAG   6707       C      _
                                TTGAAGC AGTGGGGCA CC
                                ||||||| ||||||||| ||
                                GACTTCG TCATCTCGT GG
                                   _       C
GAM943  GH2     3'  GGCTGCTCTACTGCTTCAG   10790      C      _
                                TTGAAGC AGTGGGGCA CC
                                ||||||| ||||||||| ||
                                GACTTCG TCATCTCGT GG
                                   _       C
GAM943  GRM1    3'  GGATTTTTTCTTGCTGTTTTGA 7741    TG   C  TG   CACC
                                T  AAGC AG  GGG   AATCC
                                |  |||| ||  |||   |||||
                                A  TTTG TC  TCT   TTAGG
                                 GT   _  GT   TTT_
GAM943  IL10RA  3'  GGGTCCCTGCCTTGTTGGTGTT 60382     _    TG    CCA
            CAG                   TTGAA GCCAG  GGGCA   ATCC
                                ||||| |||||  |||||   ||||
                                GACTT TGGTT  TCCGT   TGGG
                                   G    GT    CCC
GAM943  INPP5A  3'  GGAGTCCGCCCCGCGGGTTTCA 19867       A      ACCAA
            G                    TTGAAGCC GTGGGGC    TCC
                                |||||||| |||||||    |||
                                GACTTTGG CGCCCCG    AGG
                                     G      CCTG_
GAM943  KCNK5   3'  GGAATCTGTTGTTGGCTTCAG  14969         TG _  CA_
                                TTGAAGCCAG  G GG   CC
                                ||||||||||  | ||   ||
                                GACTTCGGTT  T TC   GG
                                      GT G  TAA
GAM943  LAMP2   3'  CGGTAACGCTCTATCTGGTTTT 26571   TG     _    ___   AATCC
            GG                    T  AAGCCAG TGGGGC   ACC
                                |  ||||||| ||||||   |||
                                G  TTTGGTC ATCTCG   TGG
                                 GT      T     CAA     CC
GAM943  LILRB1  5'  GGGCACTCCATTGGTTTTA   22876           CA_
                                TGAAGCCAGTGGGG   CC
                                ||||||||||||||   ||
                                ATTTTGGTTACCTC   GG
                                      ACG
GAM943  MAN2A1  3'  GGATTGAGAATCATTGGCTTT  11436          GGCAC
                                GAAGCCAGTGG    CAATCC
                                ||||||||||    ||||||
                                TTTCGGTTACT    GTTAGG
                                      AAGA_
GAM943  MBNL    5'  GGGTTGGGTTTGTTGGTTTCA  41069         TG  G A
                                TGAAGCCAG  GG C CCAATCC
                                |||||||||  || | |||||||
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                                ACTTTGGTT  TT G GGTTGGG
                                     GT  _ _
GAM943  MYO1E    3'  GGGCTGGTCCTGCTGGCTTTGA 18440   TG     TG  GC   AT
                                T  AAGCCAG  GG  ACCA  CC
                                |  |||||||  ||  ||||  ||
                                A  TTCGGTC  CC  TGGT  GG
                                 GT      GT  __    CG
GAM943  NCKAP1   3'  TGGTGCCCTGTTGGCATTAG   26470     A    TG
                                TTGA GCCAG  GGGCACCA
                                |||| |||||  ||||||||
                                GATT CGGTT  CCCGTGGT
                                  A     GT
GAM943  NEB      5'  GGGCATCTCCTGCTGCCTTCAG 17010       C   TG  _____  A
                                TTGAAG CAG  GG    GC CC
                                ||||||| |||  ||    || ||
                                GACTTC GTC  CC    CG GG
                                    C   GT  TCTA  _
GAM943  NOX5     5'  GGGTTCTTGGTCTCACTGACTT 44708       C        ACC_
            CAA                    TTGAAG CAGTGGGGC    AATCC
                                |||||| |||||||||    |||||
                                AACTTC GTCACTCTG    TTGGG
                                    A        GTTC
GAM943  OFD1     5'  GGTCCTGCCTCGCTGCCTTCAG 14609       C        ___
                                TTGAAG CAGTGGGGC   ACC
                                |||||| |||||||||   |||
                                GACTTC GTCGCTCCG   TGG
                                    C        TCC
GAM943  OGG1     3'  GGATTCTCATTGCCTTCG    34158      C       CA
                                TGAAG CAGTGGGG  CC
                                |||||  ||||||||  ||
                                GCTTC GTTACTCT  GG
                                   C       TA
GAM943  PFKL     3'  AGGCTGCTGCCCCCTGGCTTTG 12052    TG      T     C  AT C
            G                    T  AAGCCAG GGGGCA CA  C
                                |  ||||||| |||||| ||  |
                                G  TTCGGTC CCCCGT GT  G
                                 GT      _     C  CG AG
GAM943  PKNOX1   3'  GGGTTCTGTTTTCTTTGGTTTC 17100          T_     CC
            GA                    TTGAAGCCAG  GGGGCA  AATCC
                                |||||||||  ||||||  |||||
                                AGCTTTGGTT  TTTTGT  TTGGG
                                      TC     C_
GAM943  PSPHL    5'  GGATGCTTTCATTGGATTTGG  94498    TG  G      _  _
                                T  AA CCAGTGGG GCA CC
                                |  || |||||||| ||| ||
                                G  TT GGTTACTT CGT GG
                                 GT  A       T   A
GAM943  RENT1    3'  GGAGTTTTGTTGTTGGTTTTAG 12818          TG ___   A
                                TTGAAGCCAG  G   GGC CC
                                ||||||||||  |   ||| ||
```

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                                GATTTTGGTT  T   TTG GG
                                      GT GTT   A
GAM943  RNF14    3'  CCGGTGTATATGGTCCACTGGT 16273            _______    AATCC
           TTCAG                   TTGAAGCCAGTGGG     GCACC
                                   ||||||||||||||     |||||
                                   GACTTTGGTCACCT     TGTGG
                                         GGTATA       CCT
GAM943  RPL10    3'  TTCCCGGTGTTTGCTGGTTTCA 21179          TG  G    AATCC
           G                    TTGAAGCCAG  GG CACC
                                ||||||||||  || ||||
                                GACTTTGGTC  TT GTGG
                                      GT _    CCCTTT
GAM943  RRM1     3'  GGAGATTTAGTTTTACTGCTTT 8281     TG    C       ACCAA_
           GA                     T  AAGC AGTGGGGC     TCC
                                  |  |||| ||||||||     |||
                                  A  TTCG TCATTTTG     AGG
                                   GT    _       ATTTAG
GAM943  SCAMP1   3'  GGATTTCATCCCTTACTGGTCT 54502      AG       CACC_
           CAA                     TTGA  CCAGTGGGG    AATCC
                                   ||||  |||||||||    |||||
                                   AACT  GGTCATTCC    TTAGG
                                     CT        CTACT
GAM943  SEPP1    3'  GTGTTCTATTTGCTTTAA    60732        C
                                   TTGAAGC AGTGGGGCAC
                                   |||||||  ||||||||||
                                   AATTTCG TTATCTTGTG
                                        T
GAM943  SH3BP2   3'  GGAAAAGGGCCCCAGTGGCTTT 13077    TG     G     A  AA_
           GG                      T  AAGCCA TGGGGC CC   TCC
                                   |  ||||||  ||||||  ||   |||
                                   G  TTCGGT ACCCCG GG   AGG
                                    GT     G     _ AAA
GAM943  SIAH2    3'  GTGTCCCATCTGGCTTCGA    18614          _
                                   TTGAAGCCAG TGGGGCAC
                                   ||||||||||  ||||||||
                                   AGCTTCGGTC ACCCTGTG
                                         T
GAM943  SLC21A2  3'  GGTTGGCTTTCCTGGTTTCAG  20087          TG   __
                                   TTGAAGCCAG  GGGC  ACC
                                   ||||||||||  ||||  |||
                                   GACTTTGGTC  TTCG  TGG
                                         CT    GT
GAM943  STK18    5'  GGAGAACTTTCCGTGGTTTCAG 27326         G    CACCAA
                                   TTGAAGCCA TGGGG     TCC
                                   |||||||||  |||||     |||
                                   GACTTTGGT GCCTT     AGG
                                         _    TCAAG_
GAM943  SURF4    3'  GGATTGGTGCCAAGTGTTTTA  53710       CAGTGG
                                   TGAAGC     GGCACCAATCC
                                   ||||||     ||||||||||||
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                                ATTTTG     CCGTGGTTAGG
                                   TGAA__
GAM943  TCF21    5'  GGAGGCCTCTTGGTTTCAG   13644          T    A_
                                TTGAAGCCAG GGGGC  CC
                                |||||||||| |||||  ||
                                GACTTTGGTT CTCCG  GG
                                      _    GA
GAM943  TFAP2C   3'  GGGGCCTTCTGGTTTTAG    13685          T    A
                                TTGAAGCCAG GGGGC CC
                                |||||||||| ||||| ||
                                GATTTTGGTC TTCCG GG
                                      _    G
GAM943  TLL2     3'  GGAATTCCATGGGCTTCAA   25884          A     CA
                                TTGAAGCC GTGGGG  CC
                                |||||||| ||||||  ||
                                AACTTCGG TACCTT  GG
                                     G     AA
GAM943  TRIM37   3'  GGCATTGGTGCTCTACTGTCTT 31626   TG   C          _
           TGG                     T  AAG CAGTGGGGCACCAAT CC
                                |  ||| ||||||||||||||| ||
                                G  TTC GTCATCTCGTGGTTA GG
                                 GT   T           C
GAM943  TRIM8    3'  GATTTTGTTTTGGTTTTGG   48855   TG     TGG   CC
                                T  AAGCCAG   GGCA  AATC
                                |  |||||||   ||||  ||||
                                G  TTTGGTT   TTGT  TTAG
                                 GT      ___    T_
GAM943  UC28     3'  GGGTCTCAATGGCTTCAG    41589         G     A
                                TTGAAGCCA TGGGGC CC
                                ||||||||| |||||| ||
                                GACTTCGGT ACTCTG GG
                                     A     _
GAM943  USP7     3'  GATTCGCTGCTGGTGTTAA   14417     A     GG   ACC
                                TTGA GCCAGT  GGC   AATC
                                |||| ||||||  |||   ||||
                                AATT TGGTCG  TCG   TTAG
                                  G     __   C__
GAM943  VCAM1    5'  ATCGGGCCTCACTGGCTTCAG  55635             A  AATCC
                                TTGAAGCCAGTGGGGC CC
                                |||||||||||||||| ||
                                GACTTCGGTCACTCCG GG
                                          _  CTAC
GAM943  VCAM1    5'  CATCGGGCCTCACTGGCTTCAG 55636             A  AATCC
                                TTGAAGCCAGTGGGGC CC
                                |||||||||||||||| ||
                                GACTTCGGTCACTCCG GG
                                          _  CTACG
GAM943  VPS41    3'  GTGCTCTGCTGGCTACGA    27696     A     TG
                                TTG AGCCAG  GGGCAC
                                |||  ||||||  ||||||
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                                AGC TCGGTC  CTCGTG
                                  A     GT
GAM943  XRCC3    5'  GGGCCTCCCACAGGCTTTGA  19520   TG    A    __ A
                                T  AAGCC GTGGG  GC CC
                                |  ||||| |||||  || ||
                                A  TTCGG CACCC  CG GG
                                 GT    A    TC  _
GAM943  ZNF261   3'  GCTCTGGTGATCCTGTTGGCTT 18733   TG     TG  _    ATCC
           TGG                    T  AAGCCAG  GGG CACCA
                                |  |||||||  ||| |||||
                                G  TTCGGTT  CCT GTGGT
                                 GT      GT   A    CTCG
GAM943  AD034    3'  GGAAGATGGCTTATTGGTTTTA 49748            G  CCAA
           A                     TTGAAGCCAGTGGG CA    TCC
                                ||||||||||||||  ||    |||
                                AATTTTGGTTATTC GT    AGG
                                        G  AGA_
GAM943  BTN2A2   3'  GGGTTCTCAGGCCTTTGGCTTT 23770   TG     TG    ACC__
           GG                     T  AAGCCAG  GGGC    AATCC
                                |  |||||||  ||||    |||||
                                G  TTCGGTT  TCCG    TTGGG
                                 GT      __    GACTC
GAM943  C20orf55 3'  GGGTTTTGTTCTTGGCTTTGG  49478   TG     GT     CC
                                T  AAGCCA  GGGGCA  AATCC
                                |  ||||||  ||||||  |||||
                                G  TTCGGT  TCTTGT  TTGGG
                                 GT     __      T_
GAM943  C21orf25 3'  GGAACTGGGTGCTCATGTTGGT 64298          TG_      AA__
           TTTAA                  TTGAAGCCAG   GGGCACC    TCC
                                ||||||||||   |||||||    |||
                                AATTTTGGTT   CTCGTGG    AGG
                                       GTA      GTCA
GAM943  CBX6     3'  GGAGACTTCTTTTTGTTGGTTT 27419          TG   CACCAA_
           TAA                    TTGAAGCCAG  GGG      TCC
                                ||||||||||  |||      |||
                                AATTTTGGTT  TTT      AGG
                                       GT   TCTTCAG
GAM943  CXorf12  5'  GGGCTTCTTTCTGCTGGCTCAG 14488      A     _____    A
                                TTGA GCCAGT    GGGGC CC
                                ||||  ||||||    ||||| ||
                                GACT CGGTCG    CTTCG GG
                                  _     TCTTT    _
GAM943  CYorf14  5'  GGAGGTTTTTTGGTTTCAG   38204          T    A_
                                TTGAAGCCAG GGGGC  CC
                                ||||||||||  |||||  ||
                                GACTTTGGTT TTTTG  GG
                                       _    GA
GAM943  DCTN3    3'  GGAAGCTTTGTATTTATTGGCT 24321            _  CCAA_
           TCAA                   TTGAAGCCAGTGGG GCA    TCC
                                ||||||||||||||  |||    |||
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                                AACTTCGGTTATTT TGT     AGG
                                      A   TTCGA
GAM943  DCTN3     3'  GGAAGCTTTGTATTTATTGGCT 24322            _   CCAA_
           TCAA                  TTGAAGCCAGTGGG GCA     TCC
                                ||||||||||||| |||     |||
                                AACTTCGGTTATTT TGT     AGG
                                      A   TTCGA
GAM943  DKFZP434P0721 3'  GGATTTTTTTGTCTTTTGGCTT 64463          T     CC__
           TAA                   TTGAAGCCAG GGGGCA    AATCC
                                |||||||||| ||||||    |||||
                                AATTTCGGTT TTCTGT    TTAGG
                                      _     TTTT
GAM943  DKFZP564J047 3'  GGTGTGATTCTTTGGCTTCAA  50445          T   __
                                TTGAAGCCAG GGG  GCACC
                                |||||||||| |||  |||||
                                AACTTCGGTT CTT  TGTGG
                                      T   AG
GAM943  DKFZP586C1619 3'  GGAGTTCCCCCATTGTCTTTGG 62620    TG   C       CACCAA
                                T  AAG CAGTGGGG     TCC
                                |  ||| ||||||||     |||
                                G  TTC GTTACCCC     AGG
                                 GT   T      CTTG__
GAM943  DKFZp761O0113 5'  GTGTTTTATTGATTTCAA    37898       GC
                                TTGAA  CAGTGGGGCAC
                                |||||  ||||||||||
                                AACTT  GTTATTTTGTG
                                   TA
GAM943  DKFZp762P2111 3'  GGCAGTTCCACTGGGTTCAG   87636       G        A_
                                TTGAA CCAGTGGGGC  CC
                                |||||  ||||||||||  ||
                                GACTT GGTCACCTTG  GG
                                   G         AC
GAM943  E2IG5     3'  GTGTTTTATTGTTTTGA     27640    TG    C
                                T  AAGC AGTGGGGCAC
                                |  ||||  ||||||||||
                                A  TTTG TTATTTTGTG
                                 GT   _
GAM943  FLJ10350  3'  GGTCCTCTCTGTTGTTTT    97253       __   T    C
                                GAAGC  CAG GGGG ACC
                                |||||  |||  |||| |||
                                TTTTG  GTC CTCC TGG
                                   TT   T   _
GAM943  FLJ12687  3'  GGGTTTTCTTGGTTTTAA    46755          TG    A
                                TTGAAGCCAG  GGGC CC
                                ||||||||||  ||||  ||
                                AATTTTGGTT  TTTG GG
                                      CT   _
GAM943  FLJ12783  3'  GGTTAACCCACTGGTTTCAA   49488             GC_
                                TTGAAGCCAGTGGG   ACC
                                ||||||||||||||   |||
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                                AACTTTGGTCACCC  TGG
                                      AAT
GAM943  FLJ12998  3'  GGACATTTTCTCATTGGTTTT  43150          CACCAA
                                GAAGCCAGTGGGG    TCC
                                ||||||||||||    |||
                                TTTTGGTTACTCT    AGG
                                      TTTAC_
GAM943  FLJ13940  3'  GGACTGGTGCCCCACAGGCTTT 47309       A       A
          AA                    TTGAAGCC GTGGGGCACCA TCC
                                |||||||| |||||||||| |||
                                AATTTCGG CACCCCGTGGT AGG
                                     A         C
GAM943  FLJ14084  3'  GTGCTTTGGTGGTTTTAA   41595        G GG
                                TTGAAGCCA T  GGCAC
                                ||||||||| |  |||||
                                AATTTTGGT G  TCGTG
                                      G TT
GAM943  FLJ14721  3'  GGACCCTCCTGGTTTTAA   52643         TG  CA
                                TTGAAGCCAG  GGG  CC
                                ||||||||||  |||  ||
                                AATTTTGGTC  CCC  GG
                                      CT  A_
GAM943  FLJ14800  3'  GGTGGTCCCACTCGCTTTGG  52687  TG  C     _
                                T  AAGC AGTGGGGC ACC
                                |  |||| |||||||| |||
                                G  TTCG TCACCCTG TGG
                                 GT   C      G
GAM943  FLJ20313  5'  GGAGCCCCCACTGGCTCG   35413    A       _ A
                                TGA GCCAGTGGGG C CC
                                ||| |||||||||| | ||
                                GCT CGGTCACCCC G GG
                                  _       C A
GAM943  FLJ20847  3'  GGACTCTACTGGTTTGAG   96486   G         CA
                                TT AAGCCAGTGGGG  CC
                                || ||||||||||||  ||
                                GA TTTGGTCATCTC  GG
                                 G         A_
GAM943  FLJ21438  5'  GGAGCCCCACTGCTTTCAG   62197      C       A
                                TTGAAG CAGTGGGGC CC
                                |||||| |||||||| ||
                                GACTTT GTCACCCCG GG
                                    C       A
GAM943  FLJ21459  3'  GGCTGCCTTGCTGGTTTTGG  44806  TG     TG   _
                                T  AAGCCAG  GGGCA CC
                                |  |||||||  ||||| ||
                                G  TTTGGTC  TCCGT GG
                                 GT      GT    C
GAM943  FLJ22649  3'  GGTTTGTTTTTTGGTTTTGG  41923  TG     T   __
                                T  AAGCCAG GGGGC  ACC
                                |  ||||||| |||||  |||
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                                G  TTTGGTT TTTTG  TGG
                                 GT      _    TT
GAM943  FLJ22679  3'  GGATTTTCTTACTGGTTTC   35182          CACC
                                GAAGCCAGTGGGG   AATCC
                                ||||||||||||   |||||
                                CTTTGGTCATTCT   TTAGG
                                       T___
GAM943  FLJ22679  3'  GGATTTTCTTACTGGTTTC   35183          CACC
                                GAAGCCAGTGGGG   AATCC
                                ||||||||||||   |||||
                                CTTTGGTCATTCT   TTAGG
                                       T___
GAM943  FLJ23375  3'  GGATTGGTGGGTGAGCTTTAG  46950       _ GTGGGG
                                TTGAAGC CA     CACCAATCC
                                |||||||  ||     |||||||||
                                GATTTCG GT     GTGGTTAGG
                                     A  GG____
GAM943  FLJ23510  3'  GGACACTTTGGTGTCCCACTGG 45626     A          ____
           CCTCG                    TGA GCCAGTGGGGCACCAA    TCC
                                |||  ||||||||||||||||   |||
                                GCT CGGTCACCCTGTGGTT    AGG
                                  C             TCAC
GAM943  FLJ32356  3'  GGACCAGGTCTTGCTTGGCTTC 59025       _ TG    ACCAA
           G                     TGAAGCCA G  GGGC     TCC
                                ||||||||  |  ||||     |||
                                GCTTCGGT C  TCTG     AGG
                                     T GT    GACC_
GAM943  GLE1L    3'  CGGGTGCTATTACCTGCTGGTT 9475    TG      TG _____    AATCC
           TTGA                    T  AAGCCAG  GG    GCACC
                                |  |||||||  ||    |||||
                                A  TTTGGTC  CC    CGTGG
                                 GT      GT  ATTAT    G   CC
GAM943  GMEB2    5'  GATTGGGGCTGGCTTTGA    25663    TG      GGGGCA
                                T  AAGCCAGT     CCAATC
                                |  ||||||||     ||||||
                                A  TTCGGTCG     GGTTAG
                                 GT       G_____
GAM943  GRWD     3'  GGCGTCCCACTGGCTCTGA   49784    GA         A
                                TT  AGCCAGTGGGGC CC
                                ||  ||||||||||| ||
                                AG  TCGGTCACCCTG GG
                                  TC          C
GAM943  GTPBP5   3'  GGGTGTGAATTCGGTGGTTTTG 65980    TG     G   ___    AATCC
           A                     T  AAGCCA TGGG   GCACC
                                |  ||||||  ||||   |||||
                                A  TTTGGT GCTT   TGTGG
                                 GT     G    AAG    G   C
GAM943  HMGN4    3'  GGATTCATCCTGCTGGTTTTA  22031        TG   CACC
                                TGAAGCCAG  GGG    AATCC
                                |||||||||  |||    |||||
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                                ATTTTGGTC  CCT   TTAGG
                                     GT   AC__
GAM943  HSGT1    5'  GGATTTCCGCTGGCTTCAG   24390          CA
                                TTGAAGCCAGTGGGG  CC
                                ||||||||||||||  ||
                                GACTTCGGTCGCCTT  GG
                                       TA
GAM943  HSXIAPAF1 3'  CGGGTTTTATTCGTTGGGCTTT 34460       _____     A  AATCC
          AA                    TTGAAGCC    AGTGGGGC CC
                                ||||||||    |||||||| ||
                                AATTTCGG    TTATTTTG GG
                                     GTTGC      _    CC
GAM943  HUMZD58C02 3'  GGTTGCGTCTCATTGGCTCAG  80578     A       AC    C
                                TTGA GCCAGTGGGGC  CAATC
                                |||| ||||||||||  |||||
                                GACT CGGTTACTCTG  GTTGG
                                  _       C_    A
GAM943  IMAGE145052 5'  GGATTGTAAGCTGCTGGTTTT  27328       GG   AC_
                                GAAGCCAGT  GGC   CAATCC
                                |||||||||  |||  ||||||
                                TTTTGGTCG  TCG   GTTAGG
                                     __  AAT
GAM943  IMP-2    3'  GGGCTTCTGCAGGCTTCAG   22609       A _    A
                                TTGAAGCC GT GGGGC CC
                                |||||||| || ||||| ||
                                GACTTCGG CG CTTCG GG
                                     A  T    _
GAM943  KCNJ14   5'  CGGTGAAGGTTCCCGTTGGCTT 26242   TG        _____   AATCC
          TGG                   T  AAGCCAGTGGGG    CACC
                                |  ||||||||||||    ||||
                                G  TTCGGTTGCCCT    GTGG
                                 GT         TGGAA     CC
GAM943  KIAA0252  3'  GATTCTGTTTTGCTGCTTTGG  63456   TG   C  TG    CC   C
                                T  AAGC AG  GGGCA  AATC
                                |  |||| ||  |||||  ||||
                                G  TTCG TC  TTTGT  TTAG
                                 GT   _ GT    C_   T
GAM943  KIAA0268  3'  GGATTTCATTGGCTTCAA    70542          GG CA
                                TTGAAGCCAGTG  G  CC
                                ||||||||||||  |  ||
                                AACTTCGGTTAC  T  GG
                                       TT A_
GAM943  KIAA0280  3'  GGTGCTTGCCTCATGGCTTTGG 93309   TG     GT_ __
                                T  AAGCCA   GG  GGCACC
                                |  ||||||   ||  ||||||
                                G  TTCGGT   CC  TCGTGG
                                 GT     ACT  GT
GAM943  KIAA0317  3'  GGACTGGTTCTGCTGTTTTTGG 29745   TG   C   TG  GC   A
                                T  AAG CAG  GG  ACCA TCC
                                |  ||| |||  ||  |||| |||
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                                G  TTT GTC  CT  TGGT AGG
                                 GT   T   GT __    C
GAM943  KIAA0337 3' GGGTTTGTTTTGTTCTGTTTGG 29481   TG     _ TG    ___  C
              TTTTGG                  T  AAGCCA G  GGGC   AC AATCC
                                |  |||||| |  ||||   || |||||
                                G  TTTGGT T  CTTG   TG TTGGG
                                 GT     T GT    TTT  T
GAM943  KIAA0431 3' CGGGCATCCCCCCATTAGGTTTC 31548         _      CA___  AATCC
              AA                   TTGAAGCC AGTGGGGG    CC
                                |||||||| |||||||     ||
                                AACTTTGG TTACCCC     GG
                                     A      CTACG     CC
GAM943  KIAA0450 5' GGGTCCTGCTGGCTGCAG    28369     A     TG    A
                                TTG AGCCAG  GGGC CC
                                ||| ||||||  |||| ||
                                GAC TCGGTC  CCTG GG
                                  G     GT   _
GAM943  KIAA0459 3' GGGCCCTATTGGGTTTTAG   61654         _       A
                                TTGAAGCC AGTGGGGC CC
                                |||||||| |||||||| ||
                                GATTTTGG TTATCCCG GG
                                     G       _
GAM943  KIAA0472 3' GGGCTCTGCAGGCTTTAG    72360         A TG    A
                                TTGAAGCC G  GGGC CC
                                |||||||| |  |||| ||
                                GATTTCGG C  CTCG GG
                                     A GT    _
GAM943  KIAA0475 3' GTGTTCTATGGGTTTCAA    30126         A
                                TTGAAGCC GTGGGGCAC
                                |||||||| |||||||||
                                AACTTTGG TATCTTGTG
                                     G
GAM943  KIAA0493 5' GGCAGTCCTCTGGTTTTGG   64935   TG      T    A_
                                T  AAGCCAG GGGGC  CC
                                |  ||||||| |||||  ||
                                G  TTTGGTC TCCTG  GG
                                 GT      _    AC
GAM943  KIAA0939 3' GGGGGCTTCACTGGCTTCG   62718            A_
                                TGAAGCCAGTGGGGC  CC
                                ||||||||||||||  ||
                                GCTTCGGTCACTTCG  GG
                                       GG
GAM943  KIAA1086 3' GGGCATCTTGCTGGCTCTAA  71288     A     TG __  A
                                TTG AGCCAG  GG  GC CC
                                ||| ||||||  ||  || ||
                                AAT TCGGTC  TC  CG GG
                                  C     GT  TA  _
GAM943  KIAA1131 3' GATCCCTGTTTTGCTGGCTTT 62524         TG    CCA   C
                                GAAGCCAG  GGGCA   ATC
                                ||||||||  |||||   |||
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                                TTTCGGTC  TTTGT   TAG
                                    GT    CCC
GAM943  KIAA1255  3'  GTCCTGTTTTCCATTGGCTTCA 67745            C  CAATCC
            G                    TTGAAGCCAGTGGGG AC
                                 ||||||||||||||| ||
                                 GACTTCGGTTACCTT TG
                                       T  TCCTG
GAM943  KIAA1320  5'  GGTGGTTTTGTTGGTTTT    69845        TG   _
                                 GAAGCCAG  GGGC ACC
                                 ||||||||  |||| |||
                                 TTTTGGTT  TTTG TGG
                                    GT   G
GAM943  KIAA1391  3'  GGATTGGTCCTGTCATGTGGTT 67853         _  __  C
            TTAG                   TTGAAGCCA GTG  GGG ACCAATCC
                                 ||||||||| |||  ||| ||||||||
                                 GATTTTGGT TAC  TCC TGGTTAGG
                                    G  TG  _
GAM943  KIAA1431  3'  CGGTTTTGCCTTTGTTGGTTTT 63680          TG _  ___  AATCC
            AA                   TTGAAGCCAG  G GGC   ACC
                                 ||||||||||  | |||   |||
                                 AATTTTGGTT  T CCG   TGG
                                    GT T   TTT     CC
GAM943  KIAA1545  3'  GGCGGCTCCTGTGGGCTTCAG  61336        AGT_    A_
                                 TTGAAGCC   GGGGC  CC
                                 ||||||||   |||||  ||
                                 GACTTCGG   CCTCG  GG
                                    GTGT    GC
GAM943  KIAA1795  3'  GGGTTGGTTAGATTGATTTCAG 72618      GC   GGGGC
                                 TTGAA  CAGT    ACCAATCC
                                 |||||  ||||    ||||||||
                                 GACTT  GTTA    TGGTTGGG
                                   TA   GAT__
GAM943  KIAA1913  5'  GGTTTCCCACAGGTTTTGG   74320   TG    A    C
                                 T  AAGCC GTGGGG ACC
                                 |  ||||| |||||| |||
                                 G  TTTGG CACCCT TGG
                                  GT    A    T
GAM943  KIAA1922  3'  GGGTGCAGGGTTCTGTTGGCTC 74001    A    TG   A  A__
            CAG                    TTG AGCCAG  GGGC CC   ATCC
                                 ||| ||||||  |||| ||   ||||
                                 GAC TCGGTT  CTTG GG   TGGG
                                   C     GT   _ ACG
GAM943  KREMEN2   3'  GGTGGTCTCTGGTTTCG    44719        T   G
                                 TGAAGCCAG GGG CACC
                                 |||||||||  ||| ||||
                                 GCTTTGGTC TCT GTGG
                                       _  G
GAM943  LCP       3'  TGCACCTGTTGGTTTTAA    27479         TG  _
                                 TTGAAGCCAG  GG GCA
                                 ||||||||||  || |||
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                                AATTTTGGTT  CC CGT
                                      GT  A
GAM943  LRRFIP1   3'  GGTGCTCTACTGCTTTAA    17615        C
                                TTGAAGC AGTGGGGCACC
                                ||||||| ||||||||||
                                AATTTCG TCATCTCGTGG
                                      _
GAM943  LZ16     5'  GGACACACCTCCATTGGATTTA 26095       G        CACCAA
           A                     TTGAA CCAGTGGGG     TCC
                                ||||| |||||||||      |||
                                AATTT GGTTACCTC     AGG
                                   A        CACAC_
GAM943  MARCO    5'  GGAGCATTTCTGCTGGCTCCAG 23190     A     TG ___  A
                                TTG AGCCAG  GG   GC CC
                                ||| ||||||  ||   || ||
                                GAC TCGGTC  CT   CG GG
                                  C     GT  TTA  A
GAM943  MEF-2    3'  GGATGTGATTTTGGTTGGTTTT 65025          TG  __  CA
           AA                     TTGAAGCCAG  GGG  CAC  ATCC
                                ||||||||||  |||  |||  ||||
                                AATTTTGGTT  TTT  GTG  TAGG
                                      GG   TA  __
GAM943  MEGF10   5'  GTGTCTTGGCTGGCTTTGG   51609   TG      G _
                                T  AAGCCAGT G GGCAC
                                |  |||||||| | |||||
                                G  TTCGGTCG T CTGTG
                                 GT       G T
GAM943  MGC12837 3'  GGGTTGGTATGCTGGCTTTAG  52171          GGGC
                                TTGAAGCCAGTG   ACCAATCC
                                ||||||||||||   ||||||||
                                GATTTCGGTCGT   TGGTTGGG
                                       A___
GAM943  MGC13007 5'  GGAATTGGTTCCACTGTGTTTC 51280       _     GC    _
           GA                     TTGAAGC CAGTGGG  ACCAAT CC
                                ||||||| |||||||  |||||| ||
                                AGCTTTG GTCACCT  TGGTTA GG
                                    T      __     A
GAM943  MGC19595 5'  GGTGGCCTCGTTGGCTTTA   54183            _
                                TGAAGCCAGTGGGGC ACC
                                |||||||||||||| |||
                                ATTTCGGTTGCTCCG TGG
                                         G
GAM943  MGC2752   5'  GGTCGAGGGTGATTCGCTGGCT 79083           G   AAT__
           TTAA                    TTGAAGCCAGTGGG CACC    CC
                                |||||||||||||| ||||    ||
                                AATTTCGGTCGCTT GTGG    GG
                                       A   GAGCT
GAM943  MGC34923 5'  GGGTTCTTGATCTCACTGACTT 59198       C      _ CC
           CAA                    TTGAAG CAGTGGGG CA  AATCC
                                |||||| |||||||| ||  |||||
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                                AACTTC GTCACTCT GT  TTGGG
                                   A       A  TC
GAM943  MGC5139   3' GATTTACCACTGGTTTTA    74573          GGCACC
                                TGAAGCCAGTGG     AATC
                                ||||||||||||     ||||
                                ATTTTGGTCACC     TTAG
                                      AT____
GAM943  MGC5508   3' GTGCTTGGTTGGTTTTAA    44270         TG
                                TTGAAGCCAG  GGGCAC
                                ||||||||||  ||||||
                                AATTTTGGTT  TTCGTG
                                      GG
GAM943  NUP54     5' GATTTGGTACTGGTTTTGG   60725   TG      GGGGC    _
                                T  AAGCCAGT    ACCAA TC
                                |  ||||||||    ||||| ||
                                G  TTTGGTCA    TGGTT AG
                                 GT      _____    T
GAM943  NYD-SP15  3' GGTTGTCTCATGGCTTTGA   48848   TG     G     _
                                T  AAGCCA TGGGGCA CC
                                |  |||||| ||||||| ||
                                A  TTCGGT ACTCTGT GG
                                 GT     _      T
GAM943  OAZ1      5' GAGGTTTTCCTGGTTTCG    15976         T GG C   AA
                                TGAAGCCAG G  G ACC  TC
                                |||||||||  |  | |||  ||
                                GCTTTGGTC C  T TGG  AG
                                      _ TT _   __
GAM943  OLFM3     3' GGAGTTGTCTTTGTGGTTTCAA 83025         GT     CCAA
                                TTGAAGCCA  GGGGCA    TCC
                                |||||||||  ||||||    |||
                                AACTTTGGT  TTCTGT    AGG
                                      GT     TG__
GAM943  PB1       3' GGGTTTTTGTTTTCTTGGTTTT 36878   TG     TG    CC
            GG                    T  AAGCCAG  GGGCA  AATCC
                                |  |||||||  |||||  |||||
                                G  TTTGGTT  TTTGT  TTGGG
                                 GT      CT    TT
GAM943  PEF       3' TGCTCTGCTCGGCTTCAG    25683         _ TG
                                TTGAAGCC AG  GGGCA
                                ||||||||  ||  |||||
                                GACTTCGG TC  CTCGT
                                     C  GT
GAM943  PP1057    3' CGGGTGAGCACGCTTGTTGGTT 49252          TG  G_____    AATCC
            TCAA                   TTGAAGCCAG  GG     CACC
                                ||||||||||  ||     ||||
                                AACTTTGGTT  TC     GTGG
                                      GT  GCACGA   G   CC
GAM943  PRO2958   3' GTGCTCTGTGGCTTTGG    38250   TG     G
                                T  AAGCCA TGGGGCAC
                                |  |||||| ||||||||
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                                G  TTCGGT GTCTCGTG
                                 GT     _
GAM943  PTPRT    3'  GATTTAGCCTTGTTGGTTTTAA 56495          TG    ACC
                                TTGAAGCCAG  GGGC   AATC
                                ||||||||||  ||||   ||||
                                AATTTTGGTT  TCCG   TTAG
                                      GT    AT_
GAM943  RYK      3'  GGAGGCTTTTGCTGTTTTTAA  83509       C   TG  _  A_
                                TTGAAG CAG  GG GC  CC
                                ||||||  |||  || ||  ||
                                AATTTT GTC  TT CG  GG
                                   T   GT  T  GA
GAM943  SCAMP5   3'  GGAGGCTCTCTGGCTTTAG   58060          T    A_
                                TTGAAGCCAG GGGGC  CC
                                ||||||||||  |||||  ||
                                GATTTCGGTC TCTCG  GG
                                      _    GA
GAM943  SEC8     3'  GGATTCTTTCTCTCTGGTTTTG 41738   TG     T   CACC
              G                  T  AAGCCAG GGGG    AATCC
                                 |  |||||||  ||||    |||||
                                 G  TTTGGTC CTCT    TTAGG
                                  GT      T    TTC_
GAM943  SLC6A13  3'  GGGCGAGACTTGCTGGCTTCG  34004          TG  ____  A
                                TGAAGCCAG  GG    GC CC
                                |||||||||  ||    || ||
                                GCTTCGGTC  TC    CG GG
                                      GT  AGAG  _
GAM943  SZF1     3'  GGGTTCTTGGTCTTGCTGACTT 32731       C   TG    ACC_
              CAA                  TTGAAG CAG  GGGC    AATCC
                                   ||||||  |||  ||||    |||||
                                   AACTTC GTC  TCTG    TTGGG
                                      A  GT    GTTC
GAM943  TBLR1    3'  GGGTATTATGCTCTGTTGGTTT 45429          TG    CCA_
              T                   GAAGCCAG  GGGCA    ATCC
                                  ||||||||  |||||    ||||
                                  TTTTGGTT  CTCGT    TGGG
                                       GT    ATTA
GAM943  TOM1     3'  GGGGCCCCATGGCTTTGG    19697   TG     G     A
                                T  AAGCCA TGGGGC CC
                                |  ||||||  ||||||  ||
                                G  TTCGGT ACCCCG GG
                                 GT     _     G
GAM943  TOR2A    3'  GGTCCCCCATGGTTTTAG    56189         G    C
                                TTGAAGCCA TGGGG ACC
                                |||||||||  |||||  |||
                                GATTTTGGT ACCCC TGG
                                      _    C
GAM943  TXNL2    3'  GCCTCGTGCCACACTGGCTTTG 22581   TG        G    CAATCC
              A                   T  AAGCCAGTG GGCAC
                                  |  |||||||||  |||||
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                                A  TTCGGTCAC CCGTG
                                 GT        A     CTCCG
GAM943  UBCE7IP5  3'  GTGCTCAGCTGGCTTCAG    30850          G
                                TTGAAGCCAGT GGGCAC
                                |||||||||||| ||||||
                                GACTTCGGTCG CTCGTG
                                      A
GAM943  YME1L1    3'  GGATGCTTGCTGGTTTTA    58436        TG  G  _
                                TGAAGCCAG  GG CA CC
                                |||||||||  || || ||
                                ATTTTGGTC  TC GT GG
                                     GT  _  A
GAM943  ZID       3'  GGATATCTGTTCTACTGTTTTA 22784       C       CCA
              A                  TTGAAGC AGTGGGGCA   ATCC
                                 ||||||| |||||||||   ||||
                                 AATTTTG TCATCTTGT   TAGG
                                     _       CTA
GAM943  ZNF221    5'  GGCTGCCTCACTGCTTCAA    26268       C       _
                                TTGAAGC AGTGGGGCA CC
                                ||||||| ||||||||| ||
                                AACTTCG TCACTCCGT GG
                                     _       C
GAM943  LOC113201 3'  ACCCAGTGCTGTATTGGCTTCA 57351          G     CAATCC
              G                  TTGAAGCCAGTG GGCAC
                                 |||||||||||| |||||
                                 GACTTCGGTTAT TCGTG
                                       G     ACCCAG
GAM943  LOC127352 3'  GGATACTTCTGACTGGTTTTAA 75149          G   CACCA
                                TTGAAGCCAGT GGG     ATCC
                                |||||||||||| |||     ||||
                                AATTTTGGTCA TCT     TAGG
                                       G   TCA__
GAM943  LOC127703 3'  GTGCCTCTCTGGCTTTAG    75180          T
                                TTGAAGCCAG GGGGCAC
                                |||||||||| |||||||
                                GATTTCGGTC CTCCGTG
                                       T
GAM943  LOC134359 3'  GGGTTAGAAGTCTTTTGGTTTT 75663         T     ACC_
              AA                  TTGAAGCCAG GGGGC    AATCC
                                  |||||||||| |||||    |||||
                                  AATTTTGGTT TTCTG    TTGGG
                                       _     AAGA
GAM943  LOC136015 3'  GGATATTTTACTTGGCTTTA   76705        _      CA_
                                TGAAGCC AGTGGGG   CC
                                ||||||| |||||||   ||
                                ATTTCGG TCATTTT   GG
                                     T      ATA
GAM943  LOC144755 3'  GGCGCCTTGGTGGCTTTGG   84101    TG     G     A
                                T  AAGCCA TGGGGC CC
                                |  |||||| |||||| ||
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                                 G  TTCGGT GTTCCG GG
                                  GT     G     C
GAM943   LOC145622 3'  GGGTTCTTGGTCTCACTGACTT 77821       C       ACC_
             CAA                    TTGAAG CAGTGGGGC    AATCC
                                 |||||| |||||||||   |||||
                                 AACTTC GTCACTCTG    TTGGG
                                    A        GTTC
GAM943   LOC145781 3'  GGAACCCTGTGGCTTCAA    77957         G    CA
                                 TTGAAGCCA TGGGG  CC
                                 ||||||||| |||||  ||
                                 AACTTCGGT GTCCC  GG
                                       _    AA
GAM943   LOC146455 5'  GGAGGCACTTTGCTGTCTTCAA 78462       C   TG   CA  AA
                                 TTGAAG CAG  GGG  CC  TCC
                                 |||||| |||  |||  ||  |||
                                 AACTTC GTC  TTC  GG  AGG
                                    T   GT   AC  __
GAM943   LOC150159 3'  GATGTGCTTTGCTGGTTTTAG  58261          TG     CA
                                 TTGAAGCCAG  GGGCAC  ATC
                                 ||||||||||  ||||||  |||
                                 GATTTTGGTC  TTCGTG  TAG
                                       GT     __
GAM943   LOC150406 3'  GGGTTGTGTGGGCATTGGTTCA 80673      G     GGG  _
             G                   TTGAA CCAGTG   CAC CAATCC
                                 ||||| ||||||   ||| ||||||
                                 GACTT GGTTAC   GTG GTTGGG
                                    _     GG_   T
GAM943   LOC150848 5'  GTGTCTTGTGGTTTTAA     86319         A TG
                                 TTGAAGCC G  GGGCAC
                                 |||||||| |  ||||||
                                 AATTTTGG T  TCTGTG
                                      _ GT
GAM943   LOC151610 3'  GGATGGCCCTCCTGGCTTCAG  81097          TG    ACCA
                                 TTGAAGCCAG  GGGC    ATCC
                                 ||||||||||  ||||    ||||
                                 GACTTCGGTC  CCCG    TAGG
                                       CT    G___
GAM943   LOC153205 3'  GGACTTTATTAGGCTTTAG    87162         _      CA
                                 TTGAAGCC AGTGGGG  CC
                                 |||||||| |||||||  ||
                                 GATTTCGG TTATTTC  GG
                                      A      A_
GAM943   LOC153443 3'  GTGCTTCACTGGTTCAG     81689       G
                                 TTGAA CCAGTGGGGCAC
                                 ||||| ||||||||||||
                                 GACTT GGTCACTTCGTG
                                    _
GAM943   LOC154084 3'  GGAACTTTAGTGGCTTCAA    87381         G    CA
                                 TTGAAGCCA TGGGG  CC
                                 |||||||| |||||  ||
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                                AACTTCGGT ATTTC  GG
                                     G    AA
GAM943  LOC154788 3'  GGATATTTTACTTGGCTTTA  87460       _     CA_
                                TGAAGCC AGTGGGG  CC
                                ||||||| |||||||  ||
                                ATTTCGG TCATTTT  GG
                                    T      ATA
GAM943  LOC154877 3'  GGCTGGTCTCCTGGCTTCAA  87560        TG  G  _
                                TTGAAGCCAG  GG CA CC
                                ||||||||||  || || ||
                                AACTTCGGTC  CT GT GG
                                      CT  G  C
GAM943  LOC154881 3'  GGACAGCCTCACTGGTATCAG  82072     A        A__
                                TTGA GCCAGTGGGGC  CC
                                |||| ||||||||||  ||
                                GACT TGGTCACTCCG  GG
                                  A         ACA
GAM943  LOC155063 3'  GGGTGCAGCCTTGTTGGTTGCA 87646    A    TG   ACCA
          G                      TTG AGCCAG  GGGC   ATCC
                                ||| ||||||  ||||   ||||
                                GAC TTGGTT  TCCG   TGGG
                                  G    GT   ACG_
GAM943  LOC157556 5'  GGATTTAAATCCTGGCTTCAG  87783        T  GGCACC
                                TTGAAGCCAG GG     AATCC
                                |||||||||| ||     |||||
                                GACTTCGGTC CT     TTAGG
                                      _  AAAT__
GAM943  LOC158062 3'  GGCTGCCCTGCTGGCTGCAA  87963    A    TG    _
                                TTG AGCCAG  GGGCA CC
                                ||| ||||||  ||||| ||
                                AAC TCGGTC  CCCGT GG
                                  G    GT   C
GAM943  LOC158160 3'  GTGCCACCACTGGCTTTGG   73475   TG       _
                                T  AAGCCAGTGG GGCAC
                                |  |||||||||| |||||
                                G  TTCGGTCACC CCGTG
                                 GT        A
GAM943  LOC159199 5'  GGATCCACCCTGCTGGCTTCG  83064        TG   CACCA
                                TGAAGCCAG  GGG    ATCC
                                |||||||||  |||    ||||
                                GCTTCGGTC  CCC    TAGG
                                      GT   ACC__
GAM943  LOC163882 3'  GGAGTTACCTTATGGTTTCAG  83041        GT_ _  A
                                TTGAAGCCA   GG GGC CC
                                |||||||||   || ||| ||
                                GACTTTGGT   CC TTG GG
                                      ATT  A   A
GAM943  LOC197201 3'  GGAATTCCGCTGGCATTAG   89278     A        CA
                                TTGA GCCAGTGGGG  CC
                                |||| ||||||||||  ||
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                                GATT CGGTCGCCTT  GG
                                  A        AA
GAM943  LOC197201 3'  GGAATTCCGCTGGCATTAG   89279     A        CA
                                TTGA GCCAGTGGGG  CC
                                |||| ||||||||||  ||
                                GATT CGGTCGCCTT  GG
                                  A        AA
GAM943  LOC197201 3'  GGAATTCCGCTGGCATTAG   89280     A        CA
                                TTGA GCCAGTGGGG  CC
                                |||| ||||||||||  ||
                                GATT CGGTCGCCTT  GG
                                  A        AA
GAM943  LOC197201 3'  GGAATTCCGCTGGCATTAG   89281     A        CA
                                TTGA GCCAGTGGGG  CC
                                |||| ||||||||||  ||
                                GATT CGGTCGCCTT  GG
                                  A        AA
GAM943  LOC197201 3'  GGAATTCCGCTGGCATTAG   89282     A        CA
                                TTGA GCCAGTGGGG  CC
                                |||| ||||||||||  ||
                                GATT CGGTCGCCTT  GG
                                  A        AA
GAM943  LOC197201 3'  GGAATTCCGCTGGCATTAG   89283     A        CA
                                TTGA GCCAGTGGGG  CC
                                |||| ||||||||||  ||
                                GATT CGGTCGCCTT  GG
                                  A        AA
GAM943  LOC197201 3'  GGAATTCCGCTGGCATTAG   89284     A        CA
                                TTGA GCCAGTGGGG  CC
                                |||| ||||||||||  ||
                                GATT CGGTCGCCTT  GG
                                  A        AA
GAM943  LOC197201 3'  GGAATTCCGCTGGCATTAG   89285     A        CA
                                TTGA GCCAGTGGGG  CC
                                |||| ||||||||||  ||
                                GATT CGGTCGCCTT  GG
                                  A        AA
GAM943  LOC197201 3'  GGAATTCCGCTGGCATTAG   89286     A        CA
                                TTGA GCCAGTGGGG  CC
                                |||| ||||||||||  ||
                                GATT CGGTCGCCTT  GG
                                  A        AA
GAM943  LOC199231 3'  GGGTCATTCTTGTTTGGCTTTA 91818         _ TG   C__   AATCC
          G                      TTGAAGCCA G  GGG   ACC
                                |||||||||  |  |||   |||
                                GATTTCGGT T  TCT   TGG
                                     T GT   TAC   G   C
GAM943  LOC199974 3'  GGATACTTCTGACTGGTTTTGA 89892   TG       G   CACCA
                                T  AAGCCAGT GGG     ATCC
                                |  |||||||| |||     ||||
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                                A  TTTGGTCA TCT    TAGG
                                 GT       G   TCA__
GAM943   LOC200261 5'  GGCCAGCCTCGTTGTCTTCAG  90052       C       A__
                                TTGAAG CAGTGGGGC   CC
                                |||||| |||||||||   ||
                                GACTTC GTTGCTCCG   GG
                                   T        ACC
GAM943   LOC200781 3'  GGATTCTGGCCCCTGGCTTCAG 91723          T   G  CC
                                TTGAAGCCAG GGG CA  AATCC
                                |||||||||| ||| ||  |||||
                                GACTTCGGTC CCC GT  TTAGG
                                      _   G  C_
GAM943   LOC200830 5'  GGGTTCATGGTCTCGCTGACTT 91730       C       ACC_
            CAA                    TTGAAG CAGTGGGGC    AATCC
                                |||||| |||||||||    |||||
                                AACTTC GTCGCTCTG    TTGGG
                                   A        GTAC
GAM943   LOC203286 3'  GGTGGCTCTGCTGGCATCG    92148     A     TG    _
                                TGA GCCAG  GGGC ACC
                                ||| |||||  |||| |||
                                GCT CGGTC  CTCG TGG
                                  A    GT    G
GAM943   LOC220776 3'  GTGCTTGACTGGTTTCAA     68935           G
                                TTGAAGCCAGT GGGCAC
                                |||||||||| ||||||
                                AACTTTGGTCA TTCGTG
                                      G
GAM943   LOC220906 3'  GGAAGCATGTGTTTTGTTGTTT 93036    TG    C  TG     CAA__
            TGG                    T  AAGC AG  GGGCAC     TCC
                                |  |||| ||  ||||||     |||
                                G  TTTG TT  TTTGTG     AGG
                                 GT    _  GT     TACGA
GAM943   LOC220980 5'  GGGTCTGAACCCTCTGGCTTCA 94770          T   GC___   AATCC
            G                     TTGAAGCCAG GGG     ACC
                                |||||||||| |||     |||
                                GACTTCGGTC CCC     TGG
                                      T   AAGTC   G   C
GAM943   LOC221042 3'  GGGTTAATTTCCTATTGCTTCA 94806       C      CACC
            G                     TTGAAGC AGTGGGG    AATCC
                                ||||||| |||||||    |||||
                                GACTTCG TTATCCT    TTGGG
                                   _      TTAA
GAM943   LOC221312 3'  GGATTATACATTTTATTGCCTT 93558       C       CACC_
            CAG                    TTGAAG CAGTGGGG     AATCC
                                |||||| ||||||||     |||||
                                GACTTC GTTATTTT     TTAGG
                                   C       ACATA
GAM943   LOC221692 3'  GGTTGGTCAATGGCTTTGA   93856    TG     G  GGGC
                                T  AAGCCA TG    ACCAATC
                                |  |||||| ||    |||||||
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                                A  TTCGGT AC    TGGTTGG
                                 GT     A _____
GAM943   LOC222701 5'  GGAGATGGTTTCGCTGGTTCCA 94431     A       GG  ACCAA
                A                 TTG AGCCAGTG  GC     TCC
                                  ||| ||||||||  ||     |||
                                  AAC TTGGTCGC  TG     AGG
                                    C       TT  GTAG_
GAM943   LOC253019 5'  GATTGAGTGTTGGTTCGA    97110       G   GTGGG   _
                                  TTGAA CCA     GCAC CAATC
                                  ||||| |||     |||| |||||
                                  AGCTT GGT     TGTG GTTAG
                                     _  _____   A
GAM943   LOC253296 3'  GGGCCCTCACTGGCTGCAG   96123     A       _    A
                                  TTG AGCCAGTG GGGC CC
                                  ||| |||||||| |||| ||
                                  GAC TCGGTCAC CCCG GG
                                    G       T   _
GAM943   LOC253298 5'  GGGCCCTCACTGGCTGCAG   99012     A       _    A
                                  TTG AGCCAGTG GGGC CC
                                  ||| |||||||| |||| ||
                                  GAC TCGGTCAC CCCG GG
                                    G       T   _
GAM943   LOC253975 5'  GATTGAGTGTTGGTTCGA    97686       G   GTGGG   _
                                  TTGAA CCA     GCAC CAATC
                                  ||||| |||     |||| |||||
                                  AGCTT GGT     TGTG GTTAG
                                     _  _____   A
GAM943   LOC255645 3'  GGGCACCCCTACAGGTTTTAG  98476         A     CA__
                                  TTGAAGCC GTGGGG    CC
                                  |||||||| ||||||    ||
                                  GATTTTGG CATCCC    GG
                                       A     CACG
GAM943   LOC256222 3'  GGAACTCATTGTCTGTACTGGC 99016    TG       _    CCAA__
                TTTGA                   T  AAGCCAGTG GGGCA      TCC
                                  |  |||||||| |||||     |||
                                  A  TTCGGTCAT TCTGT      AGG
                                   GT        G     TACTCA
GAM943   LOC257570 3'  GGGCCCTCACTGGCTGCAG   99669     A       _    A
                                  TTG AGCCAGTG GGGC CC
                                  ||| |||||||| |||| ||
                                  GAC TCGGTCAC CCCG GG
                                    G       T   _
GAM943   LOC257571 5'  GGGCCCTCACTGGCTGCAG   99802     A       _    A
                                  TTG AGCCAGTG GGGC CC
                                  ||| |||||||| |||| ||
                                  GAC TCGGTCAC CCCG GG
                                    G       T   _
GAM943   LOC58489  3'  GGATTTGGGGGTTCTTTGGTTT 72936          T     A_   _
                TAA                   TTGAAGCCAG GGGGC  CCAA TCC
                                  |||||||||| |||||  |||| |||
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                                AATTTTGGTT TCTTG  GGTT AGG
                                      _    GG   T
GAM943  LOC90297  5' GGGCCCTCACTGGCTCCAG   62851    A      _   A
                                TTG AGCCAGTG GGGC CC
                                ||| |||||||| |||| ||
                                GAC TCGGTCAC CCCG GG
                                  C       T   _
GAM943  LOC90529  3' GAAATGTGCCCTAGTGGTTTTG 63861   TG     G      CAATCC
           G                     T  AAGCCA TGGGGCAC
                                |  |||||| ||||||||
                                G  TTTGGT ATCCCGTG
                                 GT     G       TAAAG
GAM943  LOC90785  3' GGGTTCGTGGTCTCACTGGCTT 64718              _  C
           CAG                     TTGAAGCCAGTGGGGC AC AATCC
                                |||||||||||||||| || |||||
                                GACTTCGGTCACTCTG TG TTGGG
                                        G  C
GAM943  LOC90785  3' GGGTTCGTGGTCTCGCTGACTT 64719       C       _  C
           CAA                     TTGAAG CAGTGGGGC AC AATCC
                                |||||| ||||||||| || |||||
                                AACTTC GTCGCTCTG TG TTGGG
                                   A        G  C
GAM943  LOC91149  3' GGAGCCTCCCCTACAGGTTTCA 65692         A     CACCAA
           G                     TTGAAGCC GTGGGG     TCC
                                ||||||| ||||||     |||
                                GACTTTGG CATCCC     AGG
                                     A     CTCCG_
GAM943  LOC91156  5' GGATATGATCTCTGCTGGCTCT 65712    GA     TG   CAC  _
           GA                     TT  AGCCAG  GGG   CA ATCC
                                ||  ||||||  |||   || ||||
                                AG  TCGGTC  CTC   GT TAGG
                                 TC     GT   TA_  A
GAM943  LOC91179  3' GGTTGCGTCTCATTGGCTCAG  65767     A         AC    C
                                TTGA GCCAGTGGGGC  CAATC
                                |||| ||||||||||  |||||
                                GACT CGGTTACTCTG  GTTGG
                                  _         C_    A
GAM943  LOC91397  3' GGACACCCTGTGCTGGCTTTAG 66500           __    CA_
                                TTGAAGCCAGT  GGGG   CC
                                ||||||||||  ||||   ||
                                GATTTCGGTCG  TCCC   GG
                                       TG    ACA
GAM943  LOC91759  3' GGAAAATGCCTTTGGTGGCTTT 67693         GT_     CCAA
           AA                     TTGAAGCCA   GGGGCA    TCC
                                |||||||||   ||||||   |||
                                AATTTCGGT   TTCCGT    AGG
                                     GGT     AAA_
GAM943  LOC91948  3' GGGTTCGTGGTCTCGCTGGCTC 68239      A         _  C
           AG                     TTGA GCCAGTGGGGC AC AATCC
                                |||| |||||||||| || |||||
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                                GACT CGGTCGCTCTG TG TTGGG
                                  _        G  C
GAM943  LOC91948  3'  GGGTTCGTGGTCTCGCTGGCTT 68240            _  C
            CAG                   TTGAAGCCAGTGGGGC AC AATCC
                                  ||||||||||||||| || |||||
                                  GACTTCGGTCGCTCTG TG TTGGG
                                        G  C
GAM943  LOC91948  3'  GGGTTCTTGGTCTCACTGACTT 68241       C       ACC_
            CAA                   TTGAAG CAGTGGGGC    AATCC
                                  |||||| |||||||||    |||||
                                  AACTTC GTCACTCTG    TTGGG
                                     A        GTTC
GAM943  LOC92840  3'  GGCAGCTCCCACTGGTCTCG   57248     AG      _  A_
                                  TGA  CCAGTGGG GC  CC
                                  |||  |||||||| ||  ||
                                  GCT  GGTCACCC CG  GG
                                    CT       T  AC
GAM943  LOC92876  5'  GGGTTTTTATGGTTTTAG    71351         GT    A
                                  TTGAAGCCA  GGGGC CC
                                  |||||||||  ||||| ||
                                  GATTTTGGT  TTTTG GG
                                       AT    _
GAM944  TRPC5     3'  AAATTCTACTGTCTTCCAAG   25922         ATTAT
                                  CTTGGAAGA    GAATTT
                                  |||||||||    ||||||
                                  GAACCTTCT    CTTAAA
                                       GTCAT
GAM944  TRPV3     3'  AAATCCAAGATTCTTCCAGG   96812           A  A
                                  CTTGGAAGAATT TG ATTT
                                  |||||||||||| || ||||
                                  GGACCTTCTTAG AC TAAA
                                        A  C
GAM944  CDC14B    3'  AAATTTTTTTTTCTTCCAA    53984         TTAT
                                  TTGGAAGAA    GAATTT
                                  |||||||||    ||||||
                                  AACCTTCTT    TTTAAA
                                       TTTT
GAM944  FLJ20171  3'  AAATTCTTAACTTCTTCCAAGG 35171           _   T
                                  CCTTGGAAGAA TTA GAATTT
                                  |||||||||||| ||| ||||||
                                  GGAACCTTCTT AAT CTTAAA
                                        C   T
GAM944  KIAA0513  3'  AAATTCACCATATCCAAGGG   29000         AGAATTA
                                  CCCTTGGA      TGAATTT
                                  ||||||||      |||||||
                                  GGGAACCT      ACTTAAA
                                     ATACC__
GAM944  LOC257358 3'  AAATGCAGCATTTCTCCAAGGG 98896          AG   TA  A
            TA                    TACCCTTGGA  AAT  TG ATTT
                                  ||||||||||  |||  || ||||
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                                ATGGGAACCT  TTA  AC TAAA
                                     CT   CG  G
GAM945  ADAR     3'  CAGTGACCCTCCCTACTCTTCT 8480        TCC   A  A
             T                    AGGAAGA   AGG AG GTCACTG
                                  |||||||   ||| || |||||||
                                  TTCTTCT   TCC TC CAGTGAC
                                     CA_   C  C
GAM945  ADAR     3'  CAGTGACCCTCCCTACTCTTCT 32348       TCC   A  A
             T                    AGGAAGA   AGG AG GTCACTG
                                  |||||||   ||| || |||||||
                                  TTCTTCT   TCC TC CAGTGAC
                                     CA_   C  C
GAM945  ADAR     3'  CAGTGACCCTCCCTACTCTTCT 32355       TCC   A  A
             T                    AGGAAGA   AGG AG GTCACTG
                                  |||||||   ||| || |||||||
                                  TTCTTCT   TCC TC CAGTGAC
                                     CA_   C  C
GAM945  ADRA1A   5'  AGGAGTCTCCTGGATCTTC   7286          A  G  A
                                  GAAGATCCAGGA GA TC CT
                                  |||||||||||| || || ||
                                  CTTCTAGGTCCT CT AG GA
                                        _  G  _
GAM945  ADRA1A   5'  AGGAGTCTCCTGGATCTTC   53947         A  G  A
                                  GAAGATCCAGGA GA TC CT
                                  |||||||||||| || || ||
                                  CTTCTAGGTCCT CT AG GA
                                        _  G  _
GAM945  ADRA1A   5'  AGGAGTCTCCTGGATCTTC   53949         A  G  A
                                  GAAGATCCAGGA GA TC CT
                                  |||||||||||| || || ||
                                  CTTCTAGGTCCT CT AG GA
                                        _  G  _
GAM945  ALDH3B1  3'  CTCCCTCCTGGGTCTTCC    93157         A_
                                  GGAAGATCCAGGA  GAG
                                  ||||||||||||  |||
                                  CCTTCTGGGTCCT  CTC
                                         CC
GAM945  CLDN5    3'  CAGTGACTTGGCCTGGACCTCC 13815   A  A    AA
             C                    GG AG TCCAGG  GAGTCACTG
                                  || || ||||||  |||||||||
                                  CC TC AGGTCC  TTCAGTGAC
                                   C  C     GG
GAM945  DR1      5'  AGTGCCCCTGGATCTTGCC   60084   _       AAGA T
                                  GG AAGATCCAGG    G CACT
                                  || ||||||||||    | ||||
                                  CC TTCTAGGTCC    C GTGA
                                   G        C____ _
GAM945  FADD     3'  CAGCACTCTCTAAATCTTCCT  15124        CCA   A   CA
                                  AGGAAGAT   GGA GAGT  CTG
                                  ||||||||   ||| ||||  |||
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                                TCCTTCTA  TCT CTCA  GAC
                                   AA_  _   C_
GAM945  HAO2    3'  CTCTTGCCTAAATCTTCCT   33702       CC  _
                                AGGAAGAT  AGG AAGAG
                                ||||||||  ||| |||||
                                TCCTTCTA  TCC TTCTC
                                   AA  G
GAM945  HOXB9   3'  CAGTCCTCCCTAGCTCTTCC  43997      TCC  AA  TC
                                GGAAGA  AGG  GAG  ACTG
                                ||||||  |||  |||  ||||
                                CCTTCT  TCC  CTC  TGAC
                                   CGA  __  C_
GAM945  MADH7   3'  TCTGCTCCTGGATCTCCCT   20929    A       __
                                AGG AGATCCAGGA  AGA
                                ||| ||||||||||  |||
                                TCC TCTAGGTCCT  TCT
                                  C        CG
GAM945  MAP4    3'  TTCTCCCTGGATCTACCT    11457    A       A
                                AGG AGATCCAGG AGAG
                                ||| |||||||| ||||
                                TCC TCTAGGTCC TCTT
                                  A       C
GAM945  MAP4    3'  TTCTCCCTGGATCTACCT    48802    A       A
                                AGG AGATCCAGG AGAG
                                ||| |||||||| ||||
                                TCC TCTAGGTCC TCTT
                                  A       C
GAM945  MC1R    5'  GACTCCTTCCTGCTTCCT    11478      ATC     _
                                AGGAAG  CAGGAAG AGTC
                                ||||||  ||||||| ||||
                                TCCTTC  GTCCTTC TCAG
                                   ___     C
GAM945  MMP25   3'  CAGTGACCCCCTAGTGCTTCCT 42695      ATCC  AAGA
                                AGGAAG   AGG   GTCACTG
                                ||||||   |||   |||||||
                                TCCTTC   TCC   CAGTGAC
                                   GTGA  CC__
GAM945  MOG     5'  CAGCACTGCCCTCCAAGATCTT 11668       CA  AG__  CA
           CC                   GGAAGATC  GGA   AGT  CTG
                                ||||||||  |||   |||  |||
                                CCTTCTAG  CCT   TCA  GAC
                                   AA  CCCG  C_
GAM945  OPHN1   3'  ACTCTTCCCTGAACTTCCT   11904      A  CA
                                AGGAAG TC  GGAAGAGT
                                |||||| ||  ||||||||
                                TCCTTC AG  CCTTCTCA
                                   A  TC
GAM945  PUM2    3'  CAGTTGAATTCCTAGTCTTCCT 31665       CC    GAGTC
                                AGGAAGAT  AGGAA    ACTG
                                ||||||||  |||||    ||||
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                                TCCTTCTG  TCCTT    TGAC
                                    A_    AAGT_
GAM945  PXN      3'  AGTGACCCACCCTAGATCTTCC 12666        C   AAGA
                                GGAAGATC AGG   GTCACT
                                |||||||| |||   ||||||
                                CCTTCTAG TCC   CAGTGA
                                    A   CACC
GAM945  SKI      3'  CAGCGACAAGGACCCAGGTCTT 13168        CA  AAGA_  A
            CCT                   AGGAAGATC  GG    GTC CTG
                                |||||||||  ||    ||| |||
                                TCCTTCTGG  CC    CAG GAC
                                    AC  AGGAA   C
GAM945  SYNGR3   3'  GGGTCTCCGGGACCTCCCT   16122    A  A   A   A  G
                                AGG AG TCC GGA GA TC
                                ||| || ||| ||| || ||
                                TCC TC AGG CCT CT GG
                                  C  C   G   _  G
GAM945  VNN3     3'  CAGTGACTCTCAGTGTCCCCCT 55315    AA   CCAG  A
                                AGG  GAT   GA GAGTCACTG
                                |||  |||   || |||||||||
                                TCC  CTG   CT CTCAGTGAC
                                  CC   TGA_  _
GAM945  C20orf20  3'  AGGAGCCCCTGGTCTTCC    37391       T    AAGA  CA
                                GGAAGA CCAGG   GT  CT
                                |||||| |||||   ||  ||
                                CCTTCT GGTCC   CG  GA
                                    _    C___  AG
GAM945  CAT56    3'  CAGTTGCCTCCTGGATCTTCTT 48277           A A  C
                                AGGAAGATCCAGGA G GT ACTG
                                |||||||||||||| | || ||||
                                TTCTTCTAGGTCCT C CG TGAC
                                        _ _  T
GAM945  CLIPR-59  3'  CAGGACCCCCCAAGTCTTCCT  32013        CCA  AAGA   A
                                AGGAAGAT   GG   GTC CTG
                                ||||||||   ||   ||| |||
                                TCCTTCTG   CC   CAG GAC
                                    AA_  CCC_  _
GAM945  DKFZp762A227 3'  CAGCTATGCTTCCTGGCTCTCC 34698     A   T      A  CA
            CT                    AGG AGA CCAGGAAG GT  CTG
                                ||| ||| ||||||| ||  |||
                                TCC TCT GGTCCTTC TA  GAC
                                  C   C       G  TC
GAM945  DKFZp762A227 3'  CAGCTATGCTTCCTGGCTCTCC 26881     A   T      A  CA
            CT                    AGG AGA CCAGGAAG GT  CTG
                                ||| ||| |||||||| ||  |||
                                TCC TCT GGTCCTTC TA  GAC
                                  C   C       G  TC
GAM945  DNAL4    5'  CAGGGCCTGCTTCCTGAATCTC 20420      A   C      A__   A
            CT                    AGGA GAT CAGGAAG   GTC CTG
                                |||| ||| |||||||   ||| |||
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                                TCCT CTA GTCCTTC   CGG GAC
                                  _  A      GTC  _
GAM945  FLJ13204  3'  CAGTGACTCCTGAGAGACATTC 45756      GA__ _    AGA
            C                    GGAA   TC CAGGA  GTCACTG
                                ||||   || |||||  |||||||
                                CCTT   AG GTCCT  CAGTGAC
                                  ACAG  A   ___
GAM945  FLJ13441  3'  CAGTGCCTCCTCTTCCTGGATC 43910      A          T___
            CTCCT                  AGGA GATCCAGGAAGAG   CACTG
                                |||| ||||||||||||   |||||
                                TCCT CTAGGTCCTTCTC   GTGAC
                                  C          CTCC
GAM945  FLJ22393  3'  AGAGGTCCCTGGTCTTCC    47775       T    AA  G  A
                                GGAAGA CCAGG  GA TC CT
                                |||||| |||||  || || ||
                                CCTTCT GGTCC  CT GG GA
                                  _    __ _ A
GAM945  FLJ25467  3'  CAGTAGATCCTGGGTCTCCC   59205    A       AGAG  _
                                GG AGATCCAGGA   TC ACTG
                                || ||||||||||   || ||||
                                CC TCTGGGTCCT   AG TGAC
                                 C        ____ A
GAM945  GMFB      3'  CAGCAACTTTTTTCCTGGGATC 15938      A   _   __   CA
            CTCCT                  AGGA GATCC AGGAA  GAGT  CTG
                                |||| ||||| |||||  ||||  |||
                                TCCT CTAGG TCCTT  TTCA  GAC
                                  C    G    TT   AC
GAM945  HES6      3'  CTCCCTGGATCTCCT      38459     A      AA
                                AGGA GATCCAGG  GAG
                                |||| ||||||||  |||
                                TCCT CTAGGTCC  CTC
                                  _      __
GAM945  HSPC065   3'  TGGGCTTCCTGGGTCCCCCT   27166     AA        AG
                                AGG  GATCCAGGAAG  TCA
                                |||  ||||||||||  |||
                                TCC  CTGGGTCCTTC  GGT
                                  CC         G_
GAM945  KIAA0173  3'  AGCAGCCCTAGGTCTTCCT   28380         C   AAGA  CA
                                AGGAAGATC AGG   GT  CT
                                |||||||| |||   ||  ||
                                TCCTTCTGG TCC   CG  GA
                                     A  ____  AC
GAM945  KIAA0193  3'  CAGCTGACTTCCCTGGATCTTC 29313          AA    _
            C                   GGAAGATCCAGG  GAGTCA CTG
                                ||||||||||||  |||||| |||
                                CCTTCTAGGTCC  TTCAGT GAC
                                       C_     C
GAM945  KIAA0295  3'  GCTCTCCTGATCTTCCT    68666         C   A
                                AGGAAGATC AGGA GAGT
                                |||||||| |||| ||||
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                                TCCTTCTAG TCCT CTCG
                                      _   _
GAM945  KIAA0451 3' CAGTTCTAATCTCCCAAATCTT 29766       CCA  A   GTC__
            TCT                  AGGAAGAT   GG AGA    ACTG
                                 ||||||||   || |||    ||||
                                 TCTTTCTA   CC TCT    TGAC
                                    AA_  C   AATCT
GAM945  KIAA0459 3' CAGTGACCCTAGGATCTTTC   61647        _   AAGA
                                 GGAAGATCC AGG    GTCACTG
                                 |||||||||  |||    |||||||
                                 CTTTCTAGG TCC    CAGTGAC
                                    A   ____
GAM945  KIAA1737 3' AGGAAACCTTCATGGATCTTCC 67930         G    AG_  A
                                 GGAAGATCCA GAAG   TC CT
                                 ||||||||||  ||||   || ||
                                 CCTTCTAGGT CTTC   AG GA
                                    A    CAA  _
GAM945  KIAA1877 3' TGAATCTTCACTAAATCTTCCT 66765       CC  _    G
                                 AGGAAGAT  AG GAAGA TCA
                                 ||||||||  || ||||| |||
                                 TCCTTCTA  TC CTTCT AGT
                                    AA  A    A
GAM945  MGC16121 3' AGTGTGCCTAGATTTTCCT   52256        C   AAGAGT
                                 AGGAAGATC AGG     CACT
                                 |||||||||  |||     ||||
                                 TCCTTTTAG TCC     GTGA
                                    A   GT____
GAM945  MGC3169  3' AGTGAGCTGAGATCTTCC    44182        _   GAAGAG
                                 GGAAGATC CAG     TCACT
                                 ||||||||  |||     |||||
                                 CCTTCTAG GTC     AGTGA
                                    A   G_____
GAM945  MGC4643  3' GCCTCCCTGGTCTTCCT     52141        T    A  A
                                 AGGAAGA CCAGG AG GT
                                 |||||||  ||||| || ||
                                 TCCTTCT GGTCC TC CG
                                    _    C  _
GAM945  MY014    3' ACTCTTTTTTTTTTCCT     48879        TCC
                                 AGGAAGA   AGGAAGAGT
                                 |||||||   |||||||||
                                 TCCTTTT   TTTTTCTCA
                                    T__
GAM945  NPTXR    3' CAGCTGTTATCTGCCAGATCTT 55207       CA  A   GT_  _
            CC                   GGAAGATC  GG AGA   CA CTG
                                 ||||||||  || |||   || |||
                                 CCTTCTAG  CC TCT   GT GAC
                                    A_  G   ATT  C
GAM945  NPTXR    3' CAGCTGTTATCTGCCAGATCTT 27428       CA  A   GT_  _
            CC                   GGAAGATC  GG AGA   CA CTG
                                 ||||||||  || |||   || |||
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                                CCTTCTAG  CC TCT   GT GAC
                                    A_  G   ATT  C
GAM945  phospho1  3'  AGTATTTCCTGGTCCTCC    83242     A  T       AGTC
                                GGA GA CCAGGAAG    ACT
                                ||| || ||||||||    |||
                                CCT CT GGTCCTTT    TGA
                                  C  _       A___
GAM945  SEC14L2   3'  AGTGACTCAGAGCTTCCT    25794       A  CAGGAA
                                AGGAAG TC     GAGTCACT
                                |||||| ||     ||||||||
                                TCCTTC AG     CTCAGTGA
                                   G  A_____
GAM945  SNPH      3'  CAGTGACCCTTTTCCTTCCT   28901       ATCCA    A
                                AGGAAG     GGAAG GTCACTG
                                ||||||     ||||| |||||||
                                TCCTTC     TTTTC CAGTGAC
                                   C____     C
GAM945  TEB4      3'  TGTTCTCCCTGGATCTTCT    61287          A    T
                                GGAAGATCCAGG AGAG CA
                                |||||||||||| |||| ||
                                TCTTCTAGGTCC TCTT GT
                                      C    _
GAM945  TRIM35    3'  GTCATCTTCCTGGAGCTTCCT  61517       A        GTC
                                AGGAAG TCCAGGAAGA   AC
                                |||||| ||||||||||   ||
                                TCCTTC AGGTCCTTCT   TG
                                   G         AC_
GAM945  TUBB4     5'  GACTCCTTCCTGCTTCCT     71149       ATC      _
                                AGGAAG   CAGGAAG AGTC
                                ||||||   ||||||| ||||
                                TCCTTC   GTCCTTC TCAG
                                   ___       C
GAM945  LOC149657 3'  GCTCCCCTTCCTGGCCCTCCC  85716    A  AT      ___
                                GG AG  CCAGGAA   GAGT
                                || ||  |||||||   ||||
                                CC TC  GGTCCTT   CTCG
                                 C  CC      CCC
GAM945  LOC150967 5'  GGCCTCCCAGATCTTTCT     80884         CA   A A
                                AGGAAGATC  GGA G GTC
                                |||||||||  ||| | |||
                                TCTTTCTAG  CCT C CGG
                                     AC  _ _
GAM945  LOC151979 3'  TTCTTCCTGGTCCCCCT      81256     AA  T
                                AGG  GA CCAGGAAGAG
                                |||  || ||||||||||
                                TCC  CT GGTCCTTCTT
                                  CC  _
GAM945  LOC152275 3'  CTCCTCCTGGTCTTCCT      86795        T     A
                                AGGAAGA CCAGGA GAG
                                ||||||| |||||| |||
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                                TCCTTCT GGTCCT CTC
                                   _     C
GAM945  LOC158527 5'  ACTTTCCCACATCTTCCT    82838       CCA  A
                                AGGAAGAT   GG AGAGT
                                ||||||||   || |||||
                                TCCTTCTA   CC TTTCA
                                    CA_  C
GAM945  LOC158549 5'  CAGTCACTCCCAGTTCTTCC   88217      TCCA  AA    C
                                GGAAGA    GG  GAGT ACTG
                                ||||||    ||  |||| ||||
                                CCTTCT    CC  CTCA TGAC
                                   TGA_  __    C
GAM945  LOC158809 5'  GCCTTCCTAGTCTTCCT     88258       CC      A
                                AGGAAGAT  AGGAAG GT
                                ||||||||  ||||||  ||
                                TCCTTCTG  TCCTTC CG
                                    A_     _
GAM945  LOC220895 3'  AGGATCCCTGGGTCTTCC    92489          AAGA   A
                                GGAAGATCCAGG    GTC CT
                                ||||||||||||    |||  ||
                                CCTTCTGGGTCC    TAG GA
                                      C___   _
GAM945  LOC253992 3'  TGGCCCTCCTGGCTCTTCCT   98427       T     A A
                                AGGAAGA CCAGGA G GTCA
                                ||||||| |||||| | ||||
                                TCCTTCT GGTCCT C CGGT
                                    C     _ C
GAM945  LOC51236  3'  GCTCCCTAAGTCTTCCT     33623       CC   AA
                                AGGAAGAT  AGG  GAGT
                                ||||||||  |||  ||||
                                TCCTTCTG  TCC  CTCG
                                    AA   __
GAM946  ADAT1     3'  AGCCTGGCCAACCTGGTGAAA  24909       T
                                TTTCACCA GTTGGCCAGGCT
                                |||||||| ||||||||||||
                                AAAGTGGT CAACCGGTCCGA
                                    C
GAM946  AICDA     3'  ACCAGCCTGGCCAACATGG    40686           C
                                CCATGTTGGCCAGGCT GT
                                |||||||||||||||  ||
                                GGTACAACCGGTCCGA CA
                                      C
GAM946  ALDH3B1   3'  AGCCTGGCTAACATGGCGAAA  93149     A
                                TTTC CCATGTTGGCCAGGCT
                                ||||  ||||||||||||||||
                                AAAG GGTACAATCGGTCCGA
                                  C
GAM946  ALDH8A1   3'  AGCCTAGGCAACATGGTGAAA  42910          G  _
                                TTTCACCATGTTG CC AGGCT
                                |||||||||||| || |||||
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                                AAAGTGGTACAAC GG TCCGA
                                      _ A
GAM946  ALPP    3' CCTGGCTAACACGGTGAAA  69414       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                   C
GAM946  ANKH    3' ACCAGCCTGGCCAACATGGCGA 55062     A           C
           AA                    TTTC CCATGTTGGCCAGGCT GT
                                 |||| |||||||||||||| ||
                                 AAAG GGTACAACCGGTCCGA CA
                                   C           C
GAM946  APOL1   3' CCTGGCTAACACAGTGAAA  14735      CA
                                TTTCAC  TGTTGGCCAGG
                                ||||||  ||||||||||
                                AAAGTG  ACAATCGGTCC
                                   AC
GAM946  ATP1A2  3' CGAGCCTGGCCAACATGGTGAA 7363
           A                     TTTCACCATGTTGGCCAGGCTCG
                                 |||||||||||||||||||||||
                                 AAAGTGGTACAACCGGTCCGAGC

GAM946  BCAS1   3' AGCCTGGCCAACATCATGAAA  14706     CC
                                TTTCA  ATGTTGGCCAGGCT
                                |||||  ||||||||||||||
                                AAAGT  TACAACCGGTCCGA
                                   AC
GAM946  BHMT2   3' ACCAGCCTGACCAACATGGTGA 34724           C    C
           AA                    TTTCACCATGTTGG CAGGCT GT
                                 |||||||||||||| |||||| ||
                                 AAAGTGGTACAACC GTCCGA CA
                                       A    C
GAM946  BRCA1   3' ACCAGCCTGGCCAACATGGTGA 24534             C
           AA                    TTTCACCATGTTGGCCAGGCT GT
                                 |||||||||||||||||||| ||
                                 AAAGTGGTACAACCGGTCCGA CA
                                       C
GAM946  BRCA1   3' ACCAGCCTGGCCAACATGGTGA 24535             C
           AA                    TTTCACCATGTTGGCCAGGCT GT
                                 |||||||||||||||||||| ||
                                 AAAGTGGTACAACCGGTCCGA CA
                                       C
GAM946  BRCA1   3' ACCAGCCTGGCCAACATGGTGA 24536             C
           AA                    TTTCACCATGTTGGCCAGGCT GT
                                 |||||||||||||||||||| ||
                                 AAAGTGGTACAACCGGTCCGA CA
                                       C
GAM946  BRCA1   3' ACCAGCCTGGCCAACATGGTGA 24537             C
           AA                    TTTCACCATGTTGGCCAGGCT GT
                                 |||||||||||||||||||| ||
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                                  AAAGTGGTACAACCGGTCCGA CA
                                        C
GAM946  BRCA1    5'  AGCCTGACCAACGTGGTGAAA  24539          C
                                  TTTCACCATGTTGG CAGGCT
                                  |||||||||||||| ||||||
                                  AAAGTGGTGCAACC GTCCGA
                                        A
GAM946  C21orf5  3'  ACCAGCCTGACCAACATGGTGA 18879          C     C
           GA                       TTTCACCATGTTGG CAGGCT GT
                                  |||||||||||||| |||||| ||
                                  AGAGTGGTACAACC GTCCGA CA
                                        A     C
GAM946  C5R1     3'  AGGCTGGCCAGCATGGTGAAA  9971             G
                                  TTTCACCATGTTGGCCAG CT
                                  |||||||||||||||||| ||
                                  AAAGTGGTACGACCGGTC GA
                                        G
GAM946  CASP10   3'  ACCAGCCTGGCCAATACGG   53193    A        C
                                  CC TGTTGGCCAGGCT GT
                                  || |||||||||||| ||
                                  GG ATAACCGGTCCGA CA
                                   C          C
GAM946  CASP10   3'  ACCAGCCTGGCCAATACGG   53194    A        C
                                  CC TGTTGGCCAGGCT GT
                                  || |||||||||||| ||
                                  GG ATAACCGGTCCGA CA
                                   C          C
GAM946  CD68     3'  ACCAGCCTGGCCAACATGGTGA 60497              C
           AA                       TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                        C
GAM946  CEACAM5  3'  CCTGCCAACATCGTGAAA    16423      C      C
                                  TTTCAC ATGTTGGC AGG
                                  |||||| |||||||| |||
                                  AAAGTG TACAACCG TCC
                                     C       A
GAM946  CHST5    3'  ACCAGCCTGGCCAACATAGTGA 25083      C          C
           AA                       TTTCAC ATGTTGGCCAGGCT GT
                                  |||||| |||||||||||||| ||
                                  AAAGTG TACAACCGGTCCGA CA
                                     A          C
GAM946  COG7     3'  ACCAGCCTGACCAACATGGTGA 68249          C     C
           AA                       TTTCACCATGTTGG CAGGCT GT
                                  |||||||||||||| |||||| ||
                                  AAAGTGGTACAACC GTCCGA CA
                                        A     C
GAM946  COPA     3'  ACTGCCTGGCCAACATGG    16474            TC
                                  CCATGTTGGCCAGGC  GT
                                  ||||||||||||||  ||
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                                GGTACAACCGGTCCG  CA
                                      TC
GAM946  CORO2A   3'  ACCAGCCTGACCAACATGGTGA 14097          C     C
           AA                   TTTCACCATGTTGG CAGGCT GT
                                |||||||||||||| ||||||  ||
                                AAAGTGGTACAACC GTCCGA CA
                                      A     C
GAM946  CPM      3'  ACCAGCCTGACCAACATGGTGA 60400          C     C
           AA                   TTTCACCATGTTGG CAGGCT GT
                                |||||||||||||| ||||||  ||
                                AAAGTGGTACAACC GTCCGA CA
                                      A     C
GAM946  CPT2     3'  CCTGGCCAACATGGTGAAA   5423
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||||
                                AAAGTGGTACAACCGGTCC

GAM946  CRACC    3'  ACCAGCCTGGCCAACATGGTGA 41302              C
           AA                   TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                      C
GAM946  CTSS     3'  AGCCTGGCTAACATGGTGAAA  15817
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||
                                AAAGTGGTACAATCGGTCCGA

GAM946  CUBN     3'  AGCCTGGCCAGCATGGTGAAA  8416
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||
                                AAAGTGGTACGACCGGTCCGA

GAM946  CYP4F3   3'  ACCAGCCTGGCCAATATGGTGA 7988               C
           AA                   TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTATAACCGGTCCGA CA
                                      C
GAM946  DAPP1    3'  AGCCTGGCCAACATGATGAAA  27676      C
                                TTTCA CATGTTGGCCAGGCT
                                |||||  ||||||||||||||
                                AAAGT GTACAACCGGTCCGA
                                   A
GAM946  DBT      3'  ACAGCCTGGCCAACATGGTGAA 10356              C
           A                    TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                      C
GAM946  DBT      3'  CCTGGCCAACATGGTGAAA   10371
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||||
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                                AAAGTGGTACAACCGGTCC

GAM946  DCLRE1C  3'  ACAGCCTGGCCAACACAGTGAA 42816       CA          C
                A                TTTCAC  TGTTGGCCAGGCT GT
                                 ||||||  |||||||||||||| ||
                                 AAAGTG  ACAACCGGTCCGA CA
                                    AC
GAM946  DFFA    3'  CCTGGCTAACATGGTGAAA   16591
                                 TTTCACCATGTTGGCCAGG
                                 |||||||||||||||||||
                                 AAAGTGGTACAATCGGTCC

GAM946  DMC1    3'  AGCCTGGCCAACATGGAGAAA  23937     A
                                 TTTC CCATGTTGGCCAGGCT
                                 |||| ||||||||||||||||
                                 AAAG GGTACAACCGGTCCGA
                                    A
GAM946  DNASE2  3'  ACCAGCCTGGCCAACATGGTGA 9094                  C
                AA               TTTCACCATGTTGGCCAGGCT GT
                                 |||||||||||||||||||| ||
                                 AAAGTGGTACAACCGGTCCGA CA
                                              C
GAM946  EGFL4   3'  ACCAGCCTGGCCAATATGGTGA 62449                 C
                AA               TTTCACCATGTTGGCCAGGCT GT
                                 |||||||||||||||||||| ||
                                 AAAGTGGTATAACCGGTCCGA CA
                                              C
GAM946  EGFL5   3'  ACCAGCCTGGTCAACATGGCGA 87901     A           C
                AA               TTTC CCATGTTGGCCAGGCT GT
                                 |||| ||||||||||||||| ||
                                 AAAG GGTACAACTGGTCCGA CA
                                    C            C
GAM946  F2R     3'  CCTGGCTAACACGGTGAAA   10564       A
                                 TTTCACC TGTTGGCCAGG
                                 ||||||| ||||||||||
                                 AAAGTGG ACAATCGGTCC
                                     C
GAM946  F2RL3   3'  ACCAGCCTGAGCAACATGGT  15483         GC    C
                                 ACCATGTTG  CAGGCT GT
                                 |||||||||  |||||| ||
                                 TGGTACAAC  GTCCGA CA
                                       GA    C
GAM946  F2RL3   3'  AGCCTGGCTAACATGGTGAAA  15493
                                 TTTCACCATGTTGGCCAGGCT
                                 |||||||||||||||||||||
                                 AAAGTGGTACAATCGGTCCGA

GAM946  FANCD2  3'  ACAGCCTGGCCAACATAGTGAA 53527       C          C
                A                TTTCAC ATGTTGGCCAGGCT GT
                                 ||||||| |||||||||||||| ||
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                                AAAGTG TACAACCGGTCCGA CA
                                   A
GAM946  FCMD     3'  ACCAGCCTGGCCAACATAGTGA 23022       C          C
                 AA                TTTCAC ATGTTGGCCAGGCT GT
                                   |||||| |||||||||||||| ||
                                   AAAGTG TACAACCGGTCCGA CA
                                      A           C
GAM946  FGFR1    3'  ACCAGCCCGGCCAACATGGTGA 7012              A   C
                 AA                TTTCACCATGTTGGCC GGCT GT
                                   |||||||||||||||| |||| ||
                                   AAAGTGGTACAACCGG CCGA CA
                                            C   C
GAM946  FGFR2    3'  ACCAGCCTGGCCAACATGGTGA 43769               C
                 AA                TTTCACCATGTTGGCCAGGCT GT
                                   |||||||||||||||||||| ||
                                   AAAGTGGTACAACCGGTCCGA CA
                                               C
GAM946  FLI1     3'  AGCCTAGCCAACGTGGTGAAA  77105           C
                                   TTTCACCATGTTGGC AGGCT
                                   |||||||||||||| |||||
                                   AAAGTGGTGCAACCG TCCGA
                                            A
GAM946  FUT6     3'  CCTGGCCAATATGGTGAAA   5636
                                   TTTCACCATGTTGGCCAGG
                                   |||||||||||||||||
                                   AAAGTGGTATAACCGGTCC

GAM946  GAS7     3'  CCTGGCTAACATGGTGAAA   20846
                                   TTTCACCATGTTGGCCAGG
                                   |||||||||||||||||
                                   AAAGTGGTACAATCGGTCC

GAM946  GGCX     3'  ACCAGCCTGGCCAACATGG   7700            C
                                   CCATGTTGGCCAGGCT GT
                                   |||||||||||||| ||
                                   GGTACAACCGGTCCGA CA
                                            C
GAM946  GNE      3'  CGCCCTGGCTAACATGGTGAAA 19667              CT
                                   TTTCACCATGTTGGCCAGG  CG
                                   |||||||||||||||||  ||
                                   AAAGTGGTACAATCGGTCC  GC
                                            C_
GAM946  HCS      3'  ACCAGCCTGGTCAACATGGCGA 38960      A          C
                 AA                TTTC CCATGTTGGCCAGGCT GT
                                   |||| |||||||||||||| ||
                                   AAAG GGTACAACTGGTCCGA CA
                                     C           C
GAM946  HIP1     3'  ACTAGCCTGGCCAACATGGTGA 19244              C
                 AA                TTTCACCATGTTGGCCAGGCT GT
                                   |||||||||||||||||||| ||
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                                AAAGTGGTACAACCGGTCCGA CA
                                             T
GAM946  HIP1    3'  AGCCTGTCCAACATGGTGAAA  19247          C
                                TTTCACCATGTTGG CAGGCT
                                |||||||||||||| ||||||
                                AAAGTGGTACAACC GTCCGA
                                       T
GAM946  HLA-E   3'  CCTGGCTAACACGGTGAAA   92673       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                   C
GAM946  HSPA5   3'  CTTTGCCAACATGGTGAAA   19285          C
                                TTTCACCATGTTGGC AGG
                                |||||||||||||| |||
                                AAAGTGGTACAACCG TTC
                                       T
GAM946  HUNK    3'  AGCCTGGGCAACATGGTGAAA  28175          G
                                TTTCACCATGTTG CCAGGCT
                                |||||||||||| |||||||
                                AAAGTGGTACAAC GGTCCGA
                                      G
GAM946  IAPP    3'  AGCCTGACCAACGTGGTGAAA  6435          C
                                TTTCACCATGTTGG CAGGCT
                                |||||||||||| ||||||
                                AAAGTGGTGCAACC GTCCGA
                                       A
GAM946  IFIT4   3'  CCTGGCTAACACAGTGAAA   71492       CA
                                TTTCAC  TGTTGGCCAGG
                                ||||||  ||||||||||
                                AAAGTG  ACAATCGGTCC
                                   AC
GAM946  IFNAR1  3'  AGCCTGGCCAACGTGGTGAAA  7134
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||
                                AAAGTGGTGCAACCGGTCCGA

GAM946  IL10    3'  ACCAGCCTGGTCAACATGGTGA 6919              C
            AA                  TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTACAACTGGTCCGA CA
                                             C
GAM946  IL13RA1 3'  ACCAGCCTGACCAAAATGGTGA 9565        G   C    C
            AA                  TTTCACCAT TTGG CAGGCT GT
                                ||||||||| |||| |||||| ||
                                AAAGTGGTA AACC GTCCGA CA
                                      A   A    C
GAM946  IL17R   3'  AGCCTGGCCAACATGGTGAAA  27548
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||
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                                AAAGTGGTACAACCGGTCCGA

GAM946  IL18     3'  ACCAGCCTGACCAACATGGTGA 9586              C     C
                AA                    TTTCACCATGTTGG CAGGCT GT
                                      |||||||||||||| ||||||| ||
                                      AAAGTGGTACAACC GTCCGA CA
                                            A     C
GAM946  IL1R1    3'  ACCAGCCCAGCCAACATGG   7918           CA   C
                                      CCATGTTGGC  GGCT GT
                                      ||||||||||  |||| ||
                                      GGTACAACCG  CCGA CA
                                            AC    C
GAM946  IRAK4    3'  ACGGCCTGGCCAACATGGTGAA 61836                  C
                A                     TTTCACCATGTTGGCCAGGCT GT
                                      |||||||||||||||||||| ||
                                      AAAGTGGTACAACCGGTCCGG CA
                                                  C
GAM946  KAI1     3'  CCTGGCTAACATGGTGAAA   11122
                                      TTTCACCATGTTGGCCAGG
                                      |||||||||||||||||
                                      AAAGTGGTACAATCGGTCC

GAM946  KCNA7    3'  CCTGGCTAACACGGTGAAA   49896        A
                                      TTTCACC TGTTGGCCAGG
                                      ||||||| ||||||||||
                                      AAAGTGG ACAATCGGTCC
                                           C
GAM946  KCNJ5    3'  CCTGGCTAACACGGTGAAA   7972         A
                                      TTTCACC TGTTGGCCAGG
                                      ||||||| ||||||||||
                                      AAAGTGG ACAATCGGTCC
                                           C
GAM946  KIF3B    3'  AGCCTGGCCAACATGGTGGAA  17800
                                      TTTCACCATGTTGGCCAGGCT
                                      |||||||||||||||||||
                                      AAGGTGGTACAACCGGTCCGA

GAM946  LAMC2    3'  ACCAGCCTGGCCAACATGGTGA 19905                  C
                AA                    TTTCACCATGTTGGCCAGGCT GT
                                      |||||||||||||||||||| ||
                                      AAAGTGGTACAACCGGTCCGA CA
                                                  C
GAM946  LAMP2    3'  ACCAGCCTGGCCAACATGGTGA 26565                 C
                AA                    TTTCACCATGTTGGCCAGGCT GT
                                      |||||||||||||||||||| ||
                                      AAAGTGGTACAACCGGTCCGA CA
                                                  C
GAM946  LEP      3'  CCTGGCCAACATGGTGAAA   5858
                                      TTTCACCATGTTGGCCAGG
                                      |||||||||||||||||
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                                AAAGTGGTACAACCGGTCC

GAM946  LILRB1   3'  CTTGGCCAACATGGTGAAA   22872
                                TTTCACCATGTTGGCCAGG
                                ||||||||||||||||||
                                AAAGTGGTACAACCGGTTC

GAM946  MAFF     3'  ACCAGCCTGGACAACATGGTGA 25570            G      C
              AA                  TTTCACCATGTTG CCAGGCT GT
                                  |||||||||||| ||||||| ||
                                  AAAGTGGTACAAC GGTCCGA CA
                                        A      C
GAM946  MCM4     3'  ACAGCCTAGCCAAGATGGTGAA 62572          G    C    C
              A                   TTTCACCAT TTGGC AGGCT GT
                                  ||||||||| ||||| ||||| ||
                                  AAAGTGGTA AACCG TCCGA CA
                                       G    A    C
GAM946  MLLT4    3'  CCTGGCTAACACGGTGAAA   21037       A
                                TTTCACC TGTTGGCCAGG
                                |||||||  ||||||||||
                                AAAGTGG ACAATCGGTCC
                                    C
GAM946  MOG      3'  ACCAGCCTGGCCAACATGGTGA 11664               C
              AA                  TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                              C
GAM946  MS4A1    3'  ACCAGCCTGGCCAACATAGTGA 5543       C          C
              AA                  TTTCAC ATGTTGGCCAGGCT GT
                                  ||||||  ||||||||||||| ||
                                  AAAGTG TACAACCGGTCCGA CA
                                     A          C
GAM946  MSH3     3'  ACAGCCTGGCCAACATGG    11684             C
                                CCATGTTGGCCAGGCT GT
                                ||||||||||||||| ||
                                GGTACAACCGGTCCGA CA
                                        C
GAM946  MTMR8    3'  CCTGGCTAACACGGTGAAA   31909       A
                                TTTCACC TGTTGGCCAGG
                                |||||||  ||||||||||
                                AAAGTGG ACAATCGGTCC
                                    C
GAM946  MYO1B    3'  ACTAGCCTGGCCAACATGG   25238             C
                                CCATGTTGGCCAGGCT GT
                                |||||||||||||| ||
                                GGTACAACCGGTCCGA CA
                                        T
GAM946  NFKBIL2  3'  CCTGGCTAACATGGTGAAA   26450
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||||
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                                AAAGTGGTACAATCGGTCC

GAM946  NPHS1    3'  ACCAGCCTGGCCAACATGGT   17363              C
                                ACCATGTTGGCCAGGCT GT
                                |||||||||||||||| ||
                                TGGTACAACCGGTCCGA CA
                                      C
GAM946  NUP62    3'  ACCAGCCTGGCCAACATGGTGA 25640                C
              AA                  TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                        C
GAM946  OPA3     3'  ACAGCCTGGCCAACATGGTGAA 47835                C
              A                   TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                        C
GAM946  OPTN     3'  AGCCTGGCCAACATGGCGGAA  42047      A
                                TTTC CCATGTTGGCCAGGCT
                                |||| ||||||||||||||||
                                AAGG GGTACAACCGGTCCGA
                                  C
GAM946  PA2G4    3'  ACCAGCCTAACCAACATGGCGA 71820      A        CC     C
              AA                  TTTC CCATGTTGG  AGGCT GT
                                  |||| |||||||||  ||||| ||
                                  AAAG GGTACAACC  TCCGA CA
                                    C        AA     C
GAM946  PAICS    3'  ACCAGCCTGGCCAACATGGTGA 22253                C
              AA                  TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                        C
GAM946  PCDH11X  3'  CCTGGCTAACACGGTGAAA    28010        A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                    C
GAM946  PCDH11Y  3'  CCTGGCTAACATGGTGAAA    53159
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||
                                AAAGTGGTACAATCGGTCC

GAM946  PDE4C    3'  ACAGCCTGGCCAACATGGTGAA 8090                 C
              A                   TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                        C
GAM946  PHKB     3'  ACCAGCCCAGCCAACATGGTGA 6093             CA   C
              AA                  TTTCACCATGTTGGC  GGCT GT
                                  |||||||||||||||  |||| ||
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                                  AAAGTGGTACAACCG  CCGA CA
                                        AC    C
GAM946  POLH     3'  ACCAGCCTGGCCAACATGG   22467              C
                                  CCATGTTGGCCAGGCT GT
                                  |||||||||||||||| ||
                                  GGTACAACCGGTCCGA CA
                                        C
GAM946  PPP1R12B 3'  CCTGGCTAACACGGTGAAA   50352        A
                                  TTTCACC TGTTGGCCAGG
                                  ||||||| ||||||||||
                                  AAAGTGG ACAATCGGTCC
                                     C
GAM946  PRKY     3'  ACCAGCCTGGCCAACATGATGA 12356       C            C
              AA                    TTTCA CATGTTGGCCAGGCT GT
                                  ||||| |||||||||||||| ||
                                  AAAGT GTACAACCGGTCCGA CA
                                     A             C
GAM946  PSD      5'  CCTGGCCAACGTAGTGAAA   12435       C
                                  TTTCAC ATGTTGGCCAGG
                                  |||||| ||||||||||||
                                  AAAGTG TGCAACCGGTCC
                                     A
GAM946  PSMB2    3'  ACCAGCCTGGCCAACATGGTGA 12455                  C
              AA                    TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                           C
GAM946  PSMB2    3'  CCTGACCAACATGGTGAAA   12466             C
                                  TTTCACCATGTTGG CAGG
                                  |||||||||||||| ||||
                                  AAAGTGGTACAACC GTCC
                                        A
GAM946  PSMB9    3'  AGCCTGACCAATATGGTGAAA  12484             C
                                  TTTCACCATGTTGG CAGGCT
                                  |||||||||||||| ||||||
                                  AAAGTGGTATAACC GTCCGA
                                        A
GAM946  PSMB9    3'  AGTCTGGCCAACATGGAGAAA  12488      A
                                  TTTC CCATGTTGGCCAGGCT
                                  |||| ||||||||||||||||
                                  AAAG GGTACAACCGGTCTGA
                                     A
GAM946  PSMD5    3'  ACAGCCTGGCCAATATGG     18551              C
                                  CCATGTTGGCCAGGCT GT
                                  |||||||||||||||| ||
                                  GGTATAACCGGTCCGA CA
                                        C
GAM946  PTGIS    3'  ACCAGCCTGGCCAACATGGCGA 8185       A            C
              AA                    TTTC CCATGTTGGCCAGGCT GT
                                  |||| |||||||||||||||| ||
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                                AAAG GGTACAACCGGTCCGA CA
                                  C            C
GAM946  RAB7L1   3' CCTGGCCAACATACTGAAA   15403      CC
                                TTTCA  ATGTTGGCCAGG
                                |||||  ||||||||||||
                                AAAGT  TACAACCGGTCC
                                   CA
GAM946  RBBP5    3' AGCCTGGCCAACGTGGTGAAA  18574
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||||
                                AAAGTGGTGCAACCGGTCCGA

GAM946  RBL1     3' AGCCTGACCAACATGGAGAAA  12782     A       C
                                TTTC CCATGTTGG CAGGCT
                                ||||  |||||||| ||||||
                                AAAG GGTACAACC GTCCGA
                                  A       A
GAM946  RBM3     3' AGCCTGACCAACATGGTGAAA  71002           C
                                TTTCACCATGTTGG CAGGCT
                                |||||||||||||  ||||||
                                AAAGTGGTACAACC GTCCGA
                                        A
GAM946  RFC2     3' AGCCTGGCCAACATGGGGAAA  12835     A
                                TTTC CCATGTTGGCCAGGCT
                                ||||  ||||||||||||||||
                                AAAG GGTACAACCGGTCCGA
                                  G
GAM946  SCAP2    3' AGCCAGGCCAACATGGTGAAA  15420             A
                                TTTCACCATGTTGGCC GGCT
                                ||||||||||||||||  ||||
                                AAAGTGGTACAACCGG CCGA
                                        A
GAM946  SLC17A5  3' AGCCTGGCCAGCATGGTGAAA  25825
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||||
                                AAAGTGGTACGACCGGTCCGA

GAM946  SLC28A2  3' CCTGGCTAACACGGTGAAA   16148       A
                                TTTCACC TGTTGGCCAGG
                                |||||||  ||||||||||
                                AAAGTGG ACAATCGGTCC
                                    C
GAM946  SLC2A3   3' AGTCTGGCCAACATCGTGAAA  23638       C
                                TTTCAC ATGTTGGCCAGGCT
                                ||||||  ||||||||||||||
                                AAAGTG TACAACCGGTCTGA
                                    C
GAM946  SLC2A6   3' ACCAGCCTGGCCAACATGGTGA 34565                C
              AA                  TTTCACCATGTTGGCCAGGCT GT
                                ||||||||||||||||||||  ||
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                                AAAGTGGTACAACCGGTCCGA CA
                                             C
GAM946  SLC31A1  3'  AGTCTGGCCAACATGGGGAAA  10272      A
                                TTTC CCATGTTGGCCAGGCT
                                |||| ||||||||||||||||
                                AAAG GGTACAACCGGTCTGA
                                  G
GAM946  SMG1     3'  CCTGGCTAACACGGTGAAA   31347       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                    C
GAM946  STAT3    3'  CCTGGCTAACACGGTGAAA   13434       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                    C
GAM946  SUDD     3'  ACCAGCCTGGGCAACATGGCGA 15149     A      G      C
              AA                  TTTC CCATGTTG CCAGGCT GT
                                |||| |||||||| ||||||| ||
                                AAAG GGTACAAC GGTCCGA CA
                                  C       G      C
GAM946  SULT2A1  3'  CCTGGCCAACATGATGAAA   72226      C
                                TTTCA CATGTTGGCCAGG
                                ||||| ||||||||||||
                                AAAGT GTACAACCGGTCC
                                   A
GAM946  SULT2A1  3'  CCTGGCTAACACGGTGAAA   72227       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                    C
GAM946  SUV39H2  3'  AGCCTGGCCATCATGGTGAAA  45451          T
                                TTTCACCATG TGGCCAGGCT
                                |||||||||| ||||||||||
                                AAAGTGGTAC ACCGGTCCGA
                                      T
GAM946  SWAP70   3'  AGCCTGGCCAACCTGGTGAAA  71858        T
                                TTTCACCA GTTGGCCAGGCT
                                |||||||| ||||||||||||
                                AAAGTGGT CAACCGGTCCGA
                                    C
GAM946  TACC1    3'  CCTAGGCAACATGGTGAAA   21869           G  _
                                TTTCACCATGTTG CC AGG
                                |||||||||||| || |||
                                AAAGTGGTACAAC GG TCC
                                      _  A
GAM946  TBX6     3'  AGCCTGCCAACATGGTGAAA  55807            C
                                TTTCACCATGTTGGC AGGCT
                                |||||||||||||| |||||
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                                AAAGTGGTACAACCG TCCGA
                                      _
GAM946  TCF7    3'  ACCAGCCTGGCCAACATGGTGA 13611                C
                AA                TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                        C
GAM946  TCTA    3'  ACCAGCCTGACCAACATGGTGA 42486          C     C
                AA                TTTCACCATGTTGG CAGGCT GT
                                  |||||||||||||| |||||| ||
                                  AAAGTGGTACAACC GTCCGA CA
                                        A     C
GAM946  TEP1    3'  CCTGGCTAACATAGTGAAA   24045       C
                                  TTTCAC ATGTTGGCCAGG
                                  |||||| ||||||||||||
                                  AAAGTG TACAATCGGTCC
                                     A
GAM946  TNFRSF1B 3'  ACCAGCCTGGCCAACATGGT   8379              C
                                  ACCATGTTGGCCAGGCT GT
                                  |||||||||||||||| ||
                                  TGGTACAACCGGTCCGA CA
                                        C
GAM946  TPM4    3'  ACCAGCCCAGCCAACATGGCGA 13829      A        CA    C
                AA                TTTC CCATGTTGGC  GGCT GT
                                  |||| ||||||||||  |||| ||
                                  AAAG GGTACAACCG  CCGA CA
                                    C         AC    C
GAM946  TRIM14   3'  ACTAGCCTGGCCAAGATGGTGA 29500          G          C
                AA                TTTCACCAT TTGGCCAGGCT GT
                                  ||||||||| |||||||||||| ||
                                  AAAGTGGTA AACCGGTCCGA CA
                                       G          T
GAM946  TRPM8    3'  ACCAGCCTGGCCAACATGG    44203              C
                                  CCATGTTGGCCAGGCT GT
                                  |||||||||||||||| ||
                                  GGTACAACCGGTCCGA CA
                                        C
GAM946  TSNAX    3'  AGCCTGACCAACGTGGCGAAA  21150      A        C
                                  TTTC CCATGTTGG CAGGCT
                                  |||| ||||||||| ||||||
                                  AAAG GGTGCAACC GTCCGA
                                    C         A
GAM946  UPK1B    3'  ACCAGCCTGGCCAACATGGTGA 23696                C
                AA                TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                        C
GAM946  USP14    3'  AGCCTGGCCACATGGTGAAA   18927           T
                                  TTTCACCATGT GGCCAGGCT
                                  |||||||||| |||||||||
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                                AAAGTGGTACA CCGGTCCGA
                                    _
GAM946  VDR     3'  CCTGACCAACATGGAGAAA   6342      A       C
                                TTTC CCATGTTGG CAGG
                                |||| ||||||||| ||||
                                AAAG GGTACAACC GTCC
                                  A       A
GAM946  VHL     3'  ACAGCCTGGCCAACATGGTGAA 6813                 C
            A                    TTTCACCATGTTGGCCAGGCT GT
                                 |||||||||||||||||||| ||
                                 AAAGTGGTACAACCGGTCCGA CA
                                               C
GAM946  VHL     3'  ACCAGCCTGGCCAACATGGT  6816              C
                                 ACCATGTTGGCCAGGCT GT
                                 |||||||||||||||| ||
                                 TGGTACAACCGGTCCGA CA
                                           C
GAM946  VHL     3'  AGCCTGGCTAACATGGTGAAA  6830
                                 TTTCACCATGTTGGCCAGGCT
                                 ||||||||||||||||||||
                                 AAAGTGGTACAATCGGTCCGA

GAM946  VPS41   3'  AGCCTGACCAACATGGAGAAA  27686     A       C
                                 TTTC CCATGTTGG CAGGCT
                                 |||| ||||||||| ||||||
                                 AAAG GGTACAACC GTCCGA
                                   A       A
GAM946  WIG1    3'  CCTGGCTAACACAGTGAAA   96099       CA
                                 TTTCAC  TGTTGGCCAGG
                                 ||||||  ||||||||||
                                 AAAGTG  ACAATCGGTCC
                                    AC
GAM946  XT3     3'  AGCCTGGCCAACATGGCGAAA  39902     A
                                 TTTC CCATGTTGGCCAGGCT
                                 |||| ||||||||||||||||
                                 AAAG GGTACAACCGGTCCGA
                                   C
GAM946  ZNF264  3'  ACCAGCCTGGCCAACATGG   14182             C
                                 CCATGTTGGCCAGGCT GT
                                 |||||||||||||||| ||
                                 GGTACAACCGGTCCGA CA
                                           C
GAM946  ZNF36   3'  ACCAGCCTGGCCAACATGGT  95573             C
                                 ACCATGTTGGCCAGGCT GT
                                 |||||||||||||||| ||
                                 TGGTACAACCGGTCCGA CA
                                           C
GAM946  AGMAT   3'  AGCCTGCCCAACATGGTGAAA  45733            C
                                 TTTCACCATGTTGG CAGGCT
                                 |||||||||||||| ||||||
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                                AAAGTGGTACAACC GTCCGA
                                       C
GAM946  AKAP11   3'  ACCAGCCTGGGCAACATGGTGA 58455          G     C
           AA                   TTTCACCATGTTG CCAGGCT GT
                                |||||||||||| ||||||| ||
                                AAAGTGGTACAAC GGTCCGA CA
                                       G     C
GAM946  ALTE     3'  ACAGCCTGGCCAACATGGCGAA 60992     A          C
           A                    TTTC CCATGTTGGCCAGGCT GT
                                |||| |||||||||||||| ||
                                AAAG GGTACAACCGGTCCGA CA
                                  C
GAM946  ALTE     3'  ACCAGCCTGGCCAACATGGCGA 60994     A          C
           AA                   TTTC CCATGTTGGCCAGGCT GT
                                |||| |||||||||||||| ||
                                AAAG GGTACAACCGGTCCGA CA
                                  C            C
GAM946  ALTE     3'  GCCAACCAACATGGTGAAA   61004          CCA
                                TTTCACCATGTTGG  GGC
                                |||||||||||||  |||
                                AAAGTGGTACAACC  CCG
                                       AA_
GAM946  AP1GBP1  3'  ACCAGCCTGGCCAACACAATGA 24340     CCA        C
           AA                   TTTCA  TGTTGGCCAGGCT GT
                                |||||  |||||||||||| ||
                                AAAGT  ACAACCGGTCCGA CA
                                  AAC          C
GAM946  APXL2    3'  CCTGGCTAACACGGTGAAA   75675       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                    C
GAM946  ARNTL2   3'  ACCAGCCTGGCCAATATGGTGA 39832              C
           AA                   TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTATAACCGGTCCGA CA
                                          C
GAM946  ARNTL2   3'  CCTGGCCAACATGGTGAAA   39845
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||
                                AAAGTGGTACAACCGGTCC

GAM946  ARSDR1   3'  ACCAGCCTGGCCAACATGGTGA 32621              C
           AA                   TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                          C
GAM946  ASAHL    3'  ACAGCCTGGCCAACATGGTGAA 64310              C
           A                    TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
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                                AAAGTGGTACAACCGGTCCGA CA
                                              C
GAM946  ASB13   3'  AGCCTGGCCAACTTGATGAAA  45541      C  T
                                TTTCA CA GTTGGCCAGGCT
                                ||||| || ||||||||||||
                                AAAGT GT CAACCGGTCCGA
                                   A  T
GAM946  BANP    3'  ACCAGCCTGACCAATATGG   66798        C     C
                                CCATGTTGG CAGGCT GT
                                ||||||||| |||||| ||
                                GGTATAACC GTCCGA CA
                                      A     C
GAM946  BFAR    3'  AGCTTGGCCAACATGGTGAAA  61421
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||||
                                AAAGTGGTACAACCGGTTCGA

GAM946  BIA2    3'  ACAGCCTGGCCAACATGGTGAA 71786                  C
              A                  TTTCACCATGTTGGCCAGGCT GT
                                ||||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                              C
GAM946  BIRC1   3'  AGCCTGGCCAGCATGGTGAAA  16986
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||||
                                AAAGTGGTACGACCGGTCCGA

GAM946  BIVM    3'  CCTGGCTAACATGGTGAAA   35156
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||||
                                AAAGTGGTACAATCGGTCC

GAM946  BLOV1   3'  AGCCTGACCAACATGGAGAAA  76788      A       C
                                TTTC CCATGTTGG CAGGCT
                                |||| ||||||||| ||||||
                                AAAG GGTACAACC GTCCGA
                                   A       A
GAM946  BTN3A2  3'  CCTGGCTAACACGGTGAAA   23875        A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                     C
GAM946  C1orf33 3'  CCTGGCTAACACGGTGAAA   32983        A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                     C
GAM946  C1orf34 3'  ACCAGCCTGGCCAACATGGTGA 61292                  C
              AA                   TTTCACCATGTTGGCCAGGCT GT
                                ||||||||||||||||||||| ||
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                                  AAAGTGGTACAACCGGTCCGA CA
                                        C
GAM946  C1QTNF2  3'  ACCAGCCTGACCAACATGG   49965        C    C
                                  CCATGTTGG CAGGCT GT
                                  ||||||||| |||||| ||
                                  GGTACAACC GTCCGA CA
                                     A     C
GAM946  C20orf106 3'  ACCAGCCTGGCCAACATGGTGA 55887              C
          GA                    TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AGAGTGGTACAACCGGTCCGA CA
                                        C
GAM946  C20orf106 3'  AGCCTGGCCAACACGGTGAAA  55893       A
                                  TTTCACC TGTTGGCCAGGCT
                                  ||||||| ||||||||||||
                                  AAAGTGG ACAACCGGTCCGA
                                     C
GAM946  C20orf106 3'  CTGGGCAACATGGTGAAA    55903          G
                                  TTTCACCATGTTG CCAG
                                  |||||||||||| ||||
                                  AAAGTGGTACAAC GGTC
                                        G
GAM946  C20orf108 3'  ACAGCCTGGCCAACATGATGAA 55872      C          C
          A                     TTTCA CATGTTGGCCAGGCT GT
                                  ||||| |||||||||||||| ||
                                  AAAGT GTACAACCGGTCCGA CA
                                     A
GAM946  C20orf12  3'  AGCCTGACCAACATGGAGAAA  36843     A      C
                                  TTTC CCATGTTGG CAGGCT
                                  |||| ||||||||| ||||||
                                  AAAG GGTACAACC GTCCGA
                                     A       A
GAM946  C20orf175 3'  ACAGCCTGGCCAACATGATGAA 55918      C          C
          A                     TTTCA CATGTTGGCCAGGCT GT
                                  ||||| |||||||||||||| ||
                                  AAAGT GTACAACCGGTCCGA CA
                                     A
GAM946  C20orf177 3'  AGCCTGACCAACATGGAGAAA  62825     A      C
                                  TTTC CCATGTTGG CAGGCT
                                  |||| ||||||||| ||||||
                                  AAAG GGTACAACC GTCCGA
                                     A       A
GAM946  C20orf183 3'  CGTCCTGGCTAACATGGTGAAA 48532              CT
                                  TTTCACCATGTTGGCCAGG  CG
                                  ||||||||||||||||||  ||
                                  AAAGTGGTACAATCGGTCC  GC
                                        T_
GAM946  C20orf29  3'  ACAGCCTGGCCAACATAGTGAA 37702      C          C
          A                     TTTCAC ATGTTGGCCAGGCT GT
                                  |||||| |||||||||||||| ||
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                                AAAGTG TACAACCGGTCCGA CA
                                   A
GAM946  C22orf19  3'  ACAGCCTGGCCGACATGGTGAA 14807                C
             A                   TTTCACCATGTTGGCCAGGCT GT
                                 |||||||||||||||||||| ||
                                 AAAGTGGTACAGCCGGTCCGA CA
                                               C
GAM946  C22orf19  3'  ACCGGCCTGGCCAACATGGTGA 14809                C
             AA                   TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGG CA
                                               C
GAM946  C2F       3'  AGCCTGGCCAACGTGGTGAAA  22001
                                 TTTCACCATGTTGGCCAGGCT
                                 ||||||||||||||||||||
                                 AAAGTGGTGCAACCGGTCCGA

GAM946  C4S-2     3'  CCTGGCCAACATGGTGAAA   38448
                                 TTTCACCATGTTGGCCAGG
                                 |||||||||||||||||
                                 AAAGTGGTACAACCGGTCC

GAM946  C6orf29   3'  ACAGCCTGGCCAACATGGTGAA 52450                C
             A                   TTTCACCATGTTGGCCAGGCT GT
                                 |||||||||||||||||||| ||
                                 AAAGTGGTACAACCGGTCCGA CA
                                               C
GAM946  C6orf5    3'  ACCAGCCTGGCCAACATGGTGA 31959                C
             AA                   TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                               C
GAM946  C6orf5    3'  CCTGGCTAACACGGTGAAA   31986        A
                                 TTTCACC TGTTGGCCAGG
                                 |||||||  ||||||||||
                                 AAAGTGG ACAATCGGTCC
                                     C
GAM946  C8orf2    3'  CCTGGCCAACATGCGAAA    24151      AC
                                 TTTC  CATGTTGGCCAGG
                                 ||||  ||||||||||||
                                 AAAG  GTACAACCGGTCC
                                   C_
GAM946  CALN1     3'  AGCCTGGCCAACGTGGTGAAA  49657
                                 TTTCACCATGTTGGCCAGGCT
                                 ||||||||||||||||||||
                                 AAAGTGGTGCAACCGGTCCGA

GAM946  CAMKK2    5'  AGCCTGGACAACATGGTGAAA  22614            G
                                 TTTCACCATGTTG CCAGGCT
                                 ||||||||||||| |||||||
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                                AAAGTGGTACAAC GGTCCGA
                                      A
GAM946  CBCIP2   3'  ACCAGCCTGGCCAACATGGTGA 52646                  C
                AA                    TTTCACCATGTTGGCCAGGCT GT
                                      |||||||||||||||||||| ||
                                      AAAGTGGTACAACCGGTCCGA CA
                                            C
GAM946  CCR6     3'  ACAGCCTGGCCAACATGGCGAA 49392      A        C
                A                      TTTC CCATGTTGGCCAGGCT GT
                                       |||| |||||||||||||||| ||
                                       AAAG GGTACAACCGGTCCGA CA
                                         C
GAM946  CCR6     3'  ACCAGCCTGGCCAACATGGCGA 49394      A        C
                AA                     TTTC CCATGTTGGCCAGGCT GT
                                       |||| |||||||||||||||| ||
                                       AAAG GGTACAACCGGTCCGA CA
                                         C           C
GAM946  CDT1     3'  CCTGGCGAACATGGTGAAA   78160          G
                                       TTTCACCATGTT GCCAGG
                                       |||||||||||| ||||||
                                       AAAGTGGTACAA CGGTCC
                                             G
GAM946  cerk     3'  AGCCTGCCCAACATGGTGAAA  43157            C
                                       TTTCACCATGTTGG CAGGCT
                                       |||||||||||||| ||||||
                                       AAAGTGGTACAACC GTCCGA
                                              C
GAM946  CG012    5'  AGCTTGGCCAACATAGTGAAA  84142       C
                                       TTTCAC ATGTTGGCCAGGCT
                                       |||||| ||||||||||||||
                                       AAAGTG TACAACCGGTTCGA
                                          A
GAM946  CLDN15   3'  ACCAGCCTGGCCAACATGGTGA 57366                  C
                AA                     TTTCACCATGTTGGCCAGGCT GT
                                       |||||||||||||||||||| ||
                                       AAAGTGGTACAACCGGTCCGA CA
                                             C
GAM946  CNNM1    3'  ACCAGCCTGGCCAACATGGTGA 40113                  C
                AA                     TTTCACCATGTTGGCCAGGCT GT
                                       |||||||||||||||||||| ||
                                       AAAGTGGTACAACCGGTCCGA CA
                                             C
GAM946  CPR2     3'  CCTGGCCAACATTGTGAAA   48831        C
                                       TTTCAC ATGTTGGCCAGG
                                       |||||| ||||||||||||
                                       AAAGTG TACAACCGGTCC
                                          T
GAM946  CRTAM    3'  ACCAGCCTGGCCAACATAGTGA 39468        C          C
                AA                     TTTCAC ATGTTGGCCAGGCT GT
                                       |||||| |||||||||||||| ||
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                                  AAAGTG TACAACCGGTCCGA CA
                                     A           C
GAM946  D21S2056E 3'  CTGACCAACATGGAGAAA    14865      A       C
                                  TTTC CCATGTTGG CAG
                                  |||| ||||||||| |||
                                  AAAG GGTACAACC GTC
                                    A       A
GAM946  DAPK2     3'  ACCAGCCTGGGCAACATGG   27509        G      C
                                  CCATGTTG CCAGGCT GT
                                  |||||||| ||||||| ||
                                  GGTACAAC GGTCCGA CA
                                       G      C
GAM946  DDX34     3'  AGCCTGACCAACATGGAGAAA  28657      A       C
                                  TTTC CCATGTTGG CAGGCT
                                  |||| ||||||||| ||||||
                                  AAAG GGTACAACC GTCCGA
                                    A       A
GAM946  DDX34     3'  CCTGGCTAACACGGTGAAA    28668        A
                                  TTTCACC TGTTGGCCAGG
                                  ||||||| ||||||||||
                                  AAAGTGG ACAATCGGTCC
                                       C
GAM946  DEGS      3'  ACCAGCCTGGCCAACACGGTGA 14797        A          C
          AA                        TTTCACC TGTTGGCCAGGCT GT
                                  ||||||| |||||||||||| ||
                                  AAAGTGG ACAACCGGTCCGA CA
                                       C          C
GAM946  DIS3      3'  ACCAGCCTGGCCAACATGGT   30909              C
                                  ACCATGTTGGCCAGGCT GT
                                  |||||||||||||||| ||
                                  TGGTACAACCGGTCCGA CA
                                            C
GAM946  DJ122O8.2 3'  ACCAGCCTGGCCAACATGGTGA 40390                 C
          AA                        TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                               C
GAM946  dJ383J4.3 3'  ACCAGCCTGGCCAACATGGTGA 67487                 C
          AA                        TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                               C
GAM946  DKFZP434B168 3'  CCTGGCTAACACAGTGAAA   31865       CA
                                  TTTCAC  TGTTGGCCAGG
                                  ||||||  ||||||||||
                                  AAAGTG  ACAATCGGTCC
                                     AC
GAM946  DKFZP434C171 3'  CCTGGCTAACACAGTGAAA   32190       CA
                                  TTTCAC  TGTTGGCCAGG
                                  ||||||  ||||||||||
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                                AAAGTG  ACAATCGGTCC
                                   AC
GAM946  DKFZp434E0519 3'  ACAGCCTGGGCAACATGGTGAA 50979          G      C
           A                    TTTCACCATGTTG CCAGGCT GT
                                |||||||||||| ||||||| ||
                                AAAGTGGTACAAC GGTCCGA CA
                                      G      C
GAM946  DKFZp434E2220 5'  AGCCTGGCCAATATGGTGAAA  34705
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||
                                AAAGTGGTATAACCGGTCCGA

GAM946  DKFZP434F091 3'  ACCAGCCTGGCCAACATGGTGA 31891              C
           AA                   TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                           C
GAM946  DKFZp434G171 3'  ACCAGCCTGGCCAACACGG    80226    A         C
                                CC TGTTGGCCAGGCT GT
                                || |||||||||||| ||
                                GG ACAACCGGTCCGA CA
                                 C          C
GAM946  DKFZp434G171 3'  ACCAGCCTGGCCAACATGGTGA 80227              C
           AA                   TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                           C
GAM946  DKFZP434I1735 3'  ACCAGCCTGACCAACATGGTGA 89161          C    C
           AA                   TTTCACCATGTTGG CAGGCT GT
                                |||||||||||||| |||||| ||
                                AAAGTGGTACAACC GTCCGA CA
                                      A    C
GAM946  DKFZP434P0721 3'  ACAAGCCTGGCCAACATGATGA 64451      C          C
           AG                   TTTCA CATGTTGGCCAGGCT GT
                                ||||| |||||||||||||| ||
                                GAAGT GTACAACCGGTCCGA CA
                                   A          A
GAM946  DKFZp547C176 3'  CCTGGCCAACATGGTGAAA    67800
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||
                                AAAGTGGTACAACCGGTCC

GAM946  DKFZp547G183 3'  ACCAGCCTGGCCAACATGGCGA 38636     A          C
           AA                   TTTC CCATGTTGGCCAGGCT GT
                                |||| |||||||||||||| ||
                                AAAG GGTACAACCGGTCCGA CA
                                   C          C
GAM946  DKFZp547I094 3'  ACCAGCCTGGGCAACATGGTGA 50549          G      C
           AA                   TTTCACCATGTTG CCAGGCT GT
                                |||||||||||| ||||||| ||
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                                AAAGTGGTACAAC GGTCCGA CA
                                      G      C
GAM946  DKFZP564A022 3'  CCTGGCTAACATGGTGAAA   48972
                                TTTCACCATGTTGGCCAGG
                                ||||||||||||||||||
                                AAAGTGGTACAATCGGTCC

GAM946  DKFZP564B1023 3'  ACCAGCCTGGGCAACATGGTGA 49355           G      C
          AA                    TTTCACCATGTTG CCAGGCT GT
                                |||||||||||| ||||||| ||
                                AAAGTGGTACAAC GGTCCGA CA
                                      G      C
GAM946  DKFZP564B1023 3'  AGCCTAACCAACATGGAGAAA  49358      A       CC
                                TTTC CCATGTTGG  AGGCT
                                |||| |||||||||  |||||
                                AAAG GGTACAACC  TCCGA
                                  A        AA
GAM946  DKFZP564I052 3'  CCTGGCCAACATGGTGAAA   67283
                                TTTCACCATGTTGGCCAGG
                                ||||||||||||||||||
                                AAAGTGGTACAACCGGTCC

GAM946  DKFZp564K142 3'  CCTGGCCAACATGGTGAAA   50431
                                TTTCACCATGTTGGCCAGG
                                ||||||||||||||||||
                                AAAGTGGTACAACCGGTCC

GAM946  DKFZP564M182 3'  CCTGGCCAACATGGTGAAA   78625
                                TTTCACCATGTTGGCCAGG
                                ||||||||||||||||||
                                AAAGTGGTACAACCGGTCC

GAM946  DKFZP586C1324 3'  ACCAGCCTGGCCAACATGGTGA 70351                C
          AA                    TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                            C
GAM946  DKFZP586D2223 3'  ACCAGCCTGGCCAACATGGTTA 38283     C            C
          AA                    TTT ACCATGTTGGCCAGGCT GT
                                ||| |||||||||||||||| ||
                                AAA TGGTACAACCGGTCCGA CA
                                  T             C
GAM946  DKFZp727G131 3'  ACCAGCCTGGCCAACATGGTGA 59690               C
          AA                    TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                            C
GAM946  DKFZp761J139 5'  CCTGGGCAACATGGTGAAA   51104           G
                                TTTCACCATGTTG CCAGG
                                |||||||||||| |||||
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                                AAAGTGGTACAAC GGTCC
                                      G
GAM946  DRF1     3'  AGCTTGGCCAACATGGCGAAA  47735      A
                                TTTC CCATGTTGGCCAGGCT
                                |||| ||||||||||||||||
                                AAAG GGTACAACCGGTTCGA
                                  C
GAM946  DRF1     3'  AGCCTGACCAACGTGGTGAAA  47734             C
                                TTTCACCATGTTGG CAGGCT
                                |||||||||||||| ||||||
                                AAAGTGGTGCAACC GTCCGA
                                      A
GAM946  ERAP140  3'  AGTCTGGCCAACATGGTGAAA  75701
                                TTTCACCATGTTGGCCAGGCT
                                ||||||||||||||||||||
                                AAAGTGGTACAACCGGTCTGA

GAM946  ERGL     3'  CCTGGCCAACATGGTGAAA    96731
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||||
                                AAAGTGGTACAACCGGTCC

GAM946  FBXO27   3'  ACCAGCCTGGCCAACATGGTGA 74995                  C
                AA                TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                                C
GAM946  FBXO6    3'  CCTGGCCAACACGGTGAAA    37991        A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAACCGGTCC
                                    C
GAM946  FBXO9    3'  ACCAGCCTGGGCAACATGG    54236        G      C
                                CCATGTTG CCAGGCT GT
                                |||||||| ||||||| ||
                                GGTACAAC GGTCCGA CA
                                     G      C
GAM946  FKBP14   3'  ACAGCCTGGCCAACATGGTGAA 36054                  C
                A                 TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                                C
GAM946  FKSG17   3'  ACAGCCTGGCCAACATGATGAA 50147       C            C
                A                 TTTCA CATGTTGGCCAGGCT GT
                                  ||||| |||||||||||||| ||
                                  AAAGT GTACAACCGGTCCGA CA
                                    A
GAM946  FLJ10008 3'  CCTGGCTAACATGGTGAAA    36183
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||||
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                                AAAGTGGTACAATCGGTCC

GAM946  FLJ10043  3'  ACCAGCCTGGCCAACAAGGCGA 36224      A  A          C
                AA                  TTTC CC TGTTGGCCAGGCT GT
                                    |||| || |||||||||||||| ||
                                    AAAG GG ACAACCGGTCCGA CA
                                      C  A           C
GAM946  FLJ10058  3'  AGCCTGGCCAACATGGTG    36257
                                    CACCATGTTGGCCAGGCT
                                    ||||||||||||||||||
                                    GTGGTACAACCGGTCCGA

GAM946  FLJ10460  3'  ACCAGCCTGGCCAACATGGCGA 36604      A            C
                AA                  TTTC CCATGTTGGCCAGGCT GT
                                    |||| |||||||||||||||| ||
                                    AAAG GGTACAACCGGTCCGA CA
                                      C             C
GAM946  FLJ10460  3'  AGCCTTGACAACATGGTGAAA  36610            GCC
                                    TTTCACCATGTTG   AGGCT
                                    ||||||||||||   |||||
                                    AAAGTGGTACAAC   TCCGA
                                          AGT
GAM946  FLJ10520  3'  AGCCTGACCAACATGGTGAAA  36696             C
                                    TTTCACCATGTTGG CAGGCT
                                    |||||||||||||| ||||||
                                    AAAGTGGTACAACC GTCCGA
                                          A
GAM946  FLJ10547  3'  ACCAGCCTGACCAACATGGTGA 36770             C     C
                AA                  TTTCACCATGTTGG CAGGCT GT
                                    |||||||||||||| |||||| ||
                                    AAAGTGGTACAACC GTCCGA CA
                                          A     C
GAM946  FLJ10607  3'  ACCAGCCTGACCAAAATGGTGA 77620         G    C     C
                AA                  TTTCACCAT TTGG CAGGCT GT
                                    ||||||||| |||| |||||| ||
                                    AAAGTGGTA AACC GTCCGA CA
                                        A    A     C
GAM946  FLJ10650  3'  ACCAGCCTGGCCAACATGGTGA 36895                 C
                GA                  TTTCACCATGTTGGCCAGGCT GT
                                    |||||||||||||||||||| ||
                                    AGAGTGGTACAACCGGTCCGA CA
                                             C
GAM946  FLJ10704  3'  ACCAGCCTGGCCAACATGGTGA 36972                 C
                AA                  TTTCACCATGTTGGCCAGGCT GT
                                    |||||||||||||||||||| ||
                                    AAAGTGGTACAACCGGTCCGA CA
                                             C
GAM946  FLJ10781  3'  AGCTTGACCAACATGGTGAAA  37166             C
                                    TTTCACCATGTTGG CAGGCT
                                    |||||||||||||| ||||||
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                                AAAGTGGTACAACC GTTCGA
                                      A
GAM946  FLJ10803  3'  ACCAGCCTGACCAACATGG   37191        C     C
                                CCATGTTGG CAGGCT GT
                                ||||||||| |||||| ||
                                GGTACAACC GTCCGA CA
                                     A     C
GAM946  FLJ10803  3'  ACCAGCCTGGGCAACATGGTGA 37192          G      C
          AA                     TTTCACCATGTTG CCAGGCT GT
                                 |||||||||||| ||||||| ||
                                 AAAGTGGTACAAC GGTCCGA CA
                                       G      C
GAM946  FLJ10936  3'  ACCGGCCTGGCCAACGTGGTGA 37437                C
          AA                     TTTCACCATGTTGGCCAGGCT GT
                                 |||||||||||||||||||| ||
                                 AAAGTGGTGCAACCGGTCCGG CA
                                          C
GAM946  FLJ10989  3'  AGCCTGGTCAACATGGTGAAA  37494
                                TTTCACCATGTTGGCCAGGCT
                                ||||||||||||||||||||
                                AAAGTGGTACAACTGGTCCGA

GAM946  FLJ11029  3'  ACCAGCCTGGCCAACATGGTGA 61628                C
          AA                     TTTCACCATGTTGGCCAGGCT GT
                                 |||||||||||||||||||| ||
                                 AAAGTGGTACAACCGGTCCGA CA
                                          C
GAM946  FLJ11042  3'  CTTGGGCAACATGGTGAAA   37564          G
                                TTTCACCATGTTG CCAGG
                                |||||||||||| |||||
                                AAAGTGGTACAAC GGTTC
                                      G
GAM946  FLJ11126  3'  ACAGCCTGGCCAACATGATGAA 37644      C          C
          A                      TTTCA CATGTTGGCCAGGCT GT
                                 ||||| |||||||||||||| ||
                                 AAAGT GTACAACCGGTCCGA CA
                                    A
GAM946  FLJ11136  3'  AGCTTGGCCAAGATGGTGAAA  37664         G
                                TTTCACCAT TTGGCCAGGCT
                                ||||||||| ||||||||||
                                AAAGTGGTA AACCGGTTCGA
                                     G
GAM946  FLJ11151  3'  AGCCTGGCCAACATGGTGAAA  68467
                                TTTCACCATGTTGGCCAGGCT
                                ||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGA

GAM946  FLJ11370  3'  ACCAGCCTGGCCAACATGGTGA 46959                C
          AA                     TTTCACCATGTTGGCCAGGCT GT
                                 |||||||||||||||||||| ||
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                                AAAGTGGTACAACCGGTCCGA CA
                                          C
GAM946  FLJ11577 3' ACCGGCCTGGCCAATATGGTGA 47953              C
              AA                  TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTATAACCGGTCCGG CA
                                          C
GAM946  FLJ11700 3' ACCAGCCTGGCCAACATGGTGA 46553              C
              AA                  TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                          C
GAM946  FLJ11722 3' CCTGGCCAACACAGTGAAA   46996      CA
                                  TTTCAC  TGTTGGCCAGG
                                  ||||||  ||||||||||
                                  AAAGTG  ACAACCGGTCC
                                     AC
GAM946  FLJ11722 3' CCTGGCCAACATGGTGAAA   46998
                                  TTTCACCATGTTGGCCAGG
                                  ||||||||||||||||||
                                  AAAGTGGTACAACCGGTCC

GAM946  FLJ11726 3' ACAGCCTGGCCAACATGGTGAA 47011              C
              A                   TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                          C
GAM946  FLJ11996 3' ACAGCCTGGCCAACATGGTGAA 47045              C
              A                   TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                          C
GAM946  FLJ11996 3' ACCAGCCTGACCAACATGGTGA 47046          C   C
              AA                  TTTCACCATGTTGG CAGGCT GT
                                  |||||||||||||| |||||| ||
                                  AAAGTGGTACAACC GTCCGA CA
                                        A   C
GAM946  FLJ12190 3' AGGCTGGTCAACATGGCGAAA  47561     A       G
                                  TTTC CCATGTTGGCCAG CT
                                  |||| ||||||||||||| ||
                                  AAAG GGTACAACTGGTC GA
                                    C         G
GAM946  FLJ12294 3' ACCAGCCTGGCCAACATGGTGA 47704              C
              AA                  TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                          C
GAM946  FLJ12298 3' ACCAGCCTGGCCAACATGGTGA 50591              C
              AA                  TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
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                                AAAGTGGTACAACCGGTCCGA CA
                                      C
GAM946  FLJ12331  3'  ACCAGCCTGGCCAACATGG   47106            C
                                CCATGTTGGCCAGGCT GT
                                |||||||||||||||| ||
                                GGTACAACCGGTCCGA CA
                                     C
GAM946  FLJ12363  3'  ACCAGCCTGACCAACATGGTGA 50625          C    C
          AA                     TTTCACCATGTTGG CAGGCT GT
                                |||||||||||||| |||||| ||
                                AAAGTGGTACAACC GTCCGA CA
                                      A    C
GAM946  FLJ12448  3'  ACCAGCCTGGCCAACATGGCGA 43473     A          C
          GA                     TTTC CCATGTTGGCCAGGCT GT
                                |||| |||||||||||||| ||
                                AGAG GGTACAACCGGTCCGA CA
                                  C            C
GAM946  FLJ12547  3'  CGTCCTGGCCGACATGGTGAAA 47131              CT
                                TTTCACCATGTTGGCCAGG  CG
                                |||||||||||||||||  ||
                                AAAGTGGTACAGCCGGTCC  GC
                                      T_
GAM946  FLJ12586  3'  AGCCTGGCCAGCATGGTGAAA  45204
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||
                                AAAGTGGTACGACCGGTCCGA

GAM946  FLJ12606  3'  CCTGGCCAACACGGTGAAA   46065       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAACCGGTCC
                                    C
GAM946  FLJ12606  3'  CCTGGGCAACATGGTGAAA   46066          G
                                TTTCACCATGTTG CCAGG
                                |||||||||||| |||||
                                AAAGTGGTACAAC GGTCC
                                      G
GAM946  FLJ12660  3'  ACCAGCCTGACCAACATGGTGA 47890          C    C
          AA                     TTTCACCATGTTGG CAGGCT GT
                                |||||||||||||| |||||| ||
                                AAAGTGGTACAACC GTCCGA CA
                                      A    C
GAM946  FLJ12666  3'  CCTGGCCAATATGGTGAAA   45068
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||||
                                AAAGTGGTATAACCGGTCC

GAM946  FLJ12671  3'  AGCCTGGCCAACATGGCGAA  49100     A
                                TTC CCATGTTGGCCAGGCT
                                ||| ||||||||||||||
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                                AAG GGTACAACCGGTCCGA
                                  C
GAM946  FLJ12800  3'  ACCAGCCTGGCCAACATGGTGA 43523                C
                AA                TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                              C
GAM946  FLJ12921  3'  CCTGGCTAACACGGTGAAA   46397        A
                                  TTTCACC TGTTGGCCAGG
                                  ||||||| ||||||||||
                                  AAAGTGG ACAATCGGTCC
                                     C
GAM946  FLJ13117  3'  ACCAGCCTGGCCAACATGGTGA 43800                C
                AA                TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                              C
GAM946  FLJ13162  3'  AGCCTGACCAACATGGAGAAA  47179      A       C
                                  TTTC CCATGTTGG CAGGCT
                                  |||| ||||||||| ||||||
                                  AAAG GGTACAACC GTCCGA
                                    A       A
GAM946  FLJ13193  3'  AGCCAGGCCAACATGGTGAAA  50706              A
                                  TTTCACCATGTTGGCC GGCT
                                  |||||||||||||| ||||
                                  AAAGTGGTACAACCGG CCGA
                                               A
GAM946  FLJ13193  3'  CCTGGCCAACATGGTGAAA   50721
                                  TTTCACCATGTTGGCCAGG
                                  |||||||||||||||||
                                  AAAGTGGTACAACCGGTCC

GAM946  FLJ13305  3'  CCTGGCTAACACGATGAAA   91709       CCA
                                  TTTCA   TGTTGGCCAGG
                                  |||||   ||||||||||
                                  AAAGT   ACAATCGGTCC
                                     AGC
GAM946  FLJ13352  3'  ACAGCCTGGGCAACATGGTGAA 45045           G      C
                A                 TTTCACCATGTTG CCAGGCT GT
                                  |||||||||||| ||||||| ||
                                  AAAGTGGTACAAC GGTCCGA CA
                                           G      C
GAM946  FLJ13448  3'  ACAGCCTGGTCAACATGGCGAA 47875      A           C
                A                 TTTC CCATGTTGGCCAGGCT GT
                                  |||| |||||||||||||| ||
                                  AAAG GGTACAACTGGTCCGA CA
                                    C
GAM946  FLJ13456  3'  CCTGGCCAACGTGGTGAAA   66541
                                  TTTCACCATGTTGGCCAGG
                                  |||||||||||||||||
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                                AAAGTGGTGCAACCGGTCC

GAM946  FLJ13621  3'  CCTGGCCAACATGGTGAAA   47222
                                TTTCACCATGTTGGCCAGG
                                ||||||||||||||||||
                                AAAGTGGTACAACCGGTCC

GAM946  FLJ13659  3'  ACCAGCCTGACCAACATGGTGA 48025            C     C
          AA                      TTTCACCATGTTGG CAGGCT GT
                                  |||||||||||||| |||||| ||
                                  AAAGTGGTACAACC GTCCGA CA
                                           A     C
GAM946  FLJ13769  3'  AGCCTGGCCAGCATGGTGAAA  47243
                                TTTCACCATGTTGGCCAGGCT
                                ||||||||||||||||||||
                                AAAGTGGTACGACCGGTCCGA

GAM946  FLJ13769  3'  GAGCCTGGCCAACATAGCGAAA 47251      ACC
                                TTTC   ATGTTGGCCAGGCTC
                                ||||   ||||||||||||||
                                AAAG   TACAACCGGTCCGAG
                                  CGA
GAM946  FLJ13848  3'  ACCAGCCTGGTCAACATGG    45813            C
                                CCATGTTGGCCAGGCT GT
                                |||||||||||||| ||
                                GGTACAACTGGTCCGA CA
                                         C
GAM946  FLJ13984  3'  ACCAGCCTGGACAACATGG    45798        G      C
                                CCATGTTG CCAGGCT GT
                                |||||||| ||||||| ||
                                GGTACAAC GGTCCGA CA
                                     A      C
GAM946  FLJ14100  3'  CCTGGCTAACACGGTGAAA    47331        A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                    C
GAM946  FLJ14117  3'  ACCAGCCTGGCCAACATGG    43210            C
                                CCATGTTGGCCAGGCT GT
                                |||||||||||||| ||
                                GGTACAACCGGTCCGA CA
                                         C
GAM946  FLJ14117  3'  CCTGGCCAACATGGTGAAA    43223
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||||
                                AAAGTGGTACAACCGGTCC

GAM946  FLJ14117  3'  CCTGGCCAACGTGGTGAAA    43224
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||||
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                                AAAGTGGTGCAACCGGTCC

GAM946  FLJ14225  3'  CCTGGCTAACACGGTGAAA   46384        A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                    C
GAM946  FLJ14251  3'  ACAGCCTGGCCAACATAGTGAA 46467       C           C
              A                  TTTCAC ATGTTGGCCAGGCT GT
                                 |||||| |||||||||||||| ||
                                 AAAGTG TACAACCGGTCCGA CA
                                    A
GAM946  FLJ14251  3'  CCTGGCCAACATGGTGAAA   46478
                                TTTCACCATGTTGGCCAGG
                                ||||||||||||||||||
                                AAAGTGGTACAACCGGTCC

GAM946  FLJ14280  3'  ACCAGCCTAGGCAACATGGCGA 46517     A      G _    C
              AA                  TTTC CCATGTTG CC AGGCT GT
                                  |||| |||||||| || ||||| ||
                                  AAAG GGTACAAC GG TCCGA CA
                                    C       _ A    C
GAM946  FLJ14326  3'  ACCAGCCTGGCCAACAGGTGAA 50757        A          C
              A                  TTTCACC TGTTGGCCAGGCT GT
                                 ||||||| |||||||||||| ||
                                 AAAGTGG ACAACCGGTCCGA CA
                                    _          C
GAM946  FLJ14327  3'  AGCTGGCCAACACGGTGAAA   46673        A        G
                                TTTCACC TGTTGGCCAG CT
                                ||||||| |||||||||| ||
                                AAAGTGG ACAACCGGTC GA
                                    C
GAM946  FLJ14345  3'  AGGCTGGCCAACACGGTGAAA  45654        A        G
                                TTTCACC TGTTGGCCAG CT
                                ||||||| |||||||||| ||
                                AAAGTGG ACAACCGGTC GA
                                    C        G
GAM946  FLJ14346  3'  CCCGGCTAACACGGTGAAA   47360        A       A
                                TTTCACC TGTTGGCC GG
                                ||||||| |||||||| ||
                                AAAGTGG ACAATCGG CC
                                    C       C
GAM946  FLJ14397  3'  AGCCTGACCAACATGGAGAAA  52312      A       C
                                TTTC CCATGTTGG CAGGCT
                                |||| ||||||||| ||||||
                                AAAG GGTACAACC GTCCGA
                                  A       A
GAM946  FLJ14397  3'  CCTGGCTAACACGGTGAAA   52323        A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
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                                AAAGTGG ACAATCGGTCC
                                    C
GAM946  FLJ14399  3'  AGCCTGGGCAACATGGTGAAA  52338          G
                                TTTCACCATGTTG CCAGGCT
                                ||||||||||||| |||||||
                                AAAGTGGTACAAC GGTCCGA
                                      G
GAM946  FLJ14457  3'  CCTGGCTAACACAGTGAAA   52403      CA
                                TTTCAC  TGTTGGCCAGG
                                ||||||  ||||||||||
                                AAAGTG  ACAATCGGTCC
                                   AC
GAM946  FLJ14466  3'  AGCCTGACCAACATGGAGAAA  52416     A       C
                                TTTC CCATGTTGG CAGGCT
                                |||| ||||||||| ||||||
                                AAAG GGTACAACC GTCCGA
                                  A       A
GAM946  FLJ14490  3'  CTGGCTAACATGGTGAAA    52442
                                TTTCACCATGTTGGCCAG
                                ||||||||||||||||||
                                AAAGTGGTACAATCGGTC

GAM946  FLJ14641  3'  CCTGGCCAACATGGTGAAA   52555
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||||
                                AAAGTGGTACAACCGGTCC

GAM946  FLJ20004  3'  ACCAGCCTGGCCAACATGGTGA 34742                C
            AA                    TTTCACCATGTTGGCCAGGCT GT
                                ||||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                      C
GAM946  FLJ20004  3'  AGCCTGGCCAACATGGTGAAG  34745
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||||
                                GAAGTGGTACAACCGGTCCGA

GAM946  FLJ20004  3'  CTGACCAACATGGAGAAA    34758     A       C
                                TTTC CCATGTTGG CAG
                                |||| ||||||||| |||
                                AAAG GGTACAACC GTC
                                  A       A
GAM946  FLJ20006  3'  ACCAGCCTGACCAACATGG   34774        C     C
                                CCATGTTGG CAGGCT GT
                                ||||||||| |||||| ||
                                GGTACAACC GTCCGA CA
                                     A     C
GAM946  FLJ20006  3'  AGCCTTGGCCAACATGGCGAAA 34776     A        _
                                TTTC CCATGTTGGCCA GGCT
                                |||| |||||||||||| ||||
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                                AAAG GGTACAACCGGT CCGA
                                  C          T
GAM946  FLJ20013  3'  ACCAGCCTGGCCAACACGGTGA 34790        A          C
                      AA                    TTTCACC TGTTGGCCAGGCT GT
                                            ||||||| ||||||||||||| ||
                                            AAAGTGG ACAACCGGTCCGA CA
                                               C           C
GAM946  FLJ20034  3'  CCTAGCCAACATGGTGAAA    34843             C
                                            TTTCACCATGTTGGC AGG
                                            ||||||||||||||| |||
                                            AAAGTGGTACAACCG TCC
                                                     A
GAM946  FLJ20045  3'  ACCAGCCTGGCCAAATGGTGAA 34869         G          C
                      A                     TTTCACCAT TTGGCCAGGCT GT
                                            ||||||||| |||||||||| ||
                                            AAAGTGGTA AACCGGTCCGA CA
                                                _          C
GAM946  FLJ20055  3'  CCTGGCTAACACGGTGAAA    34907        A
                                            TTTCACC TGTTGGCCAGG
                                            ||||||| ||||||||||
                                            AAAGTGG ACAATCGGTCC
                                               C
GAM946  FLJ20059  3'  AGCCTGACCAACATGGAGAAA  34920      A        C
                                            TTTC CCATGTTGG CAGGCT
                                            |||| ||||||||| ||||||
                                            AAAG GGTACAACC GTCCGA
                                              A        A
GAM946  FLJ20069  3'  ACCAGCCTGACCAACATGGTGA 34943             C     C
                      AA                    TTTCACCATGTTGG CAGGCT GT
                                            |||||||||||||| |||||| ||
                                            AAAGTGGTACAACC GTCCGA CA
                                                     A     C
GAM946  FLJ20139  3'  AGCCTGGGCAACATGGTGAAA  35110            G
                                            TTTCACCATGTTG CCAGGCT
                                            |||||||||||| |||||||
                                            AAAGTGGTACAAC GGTCCGA
                                                     G
GAM946  FLJ20139  3'  CTGGGCAACATGGTGAAA     35118             G
                                            TTTCACCATGTTG CCAG
                                            |||||||||||| ||||
                                            AAAGTGGTACAAC GGTC
                                                     G
GAM946  FLJ20211  3'  ACAGCCTGGCCAACATAGTGAA 35249        C          C
                      A                     TTTCAC ATGTTGGCCAGGCT GT
                                            |||||| |||||||||||||| ||
                                            AAAGTG TACAACCGGTCCGA CA
                                               A
GAM946  FLJ20306  3'  CTGGCCAACGTGGTGAAA     35392
                                            TTTCACCATGTTGGCCAG
                                            ||||||||||||||||||
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                                AAAGTGGTGCAACCGGTC

GAM946  FLJ20340 3' TGTCCTGGACAACATGGTGAAA 35463          G    CT
                                TTTCACCATGTTG CCAGG  CG
                                |||||||||||| |||||  ||
                                AAAGTGGTACAAC GGTCC  GT
                                      A    T_
GAM946  FLJ20359 3' AGCCTGCCCAACATGGTGAAA  35512          C
                                TTTCACCATGTTGG CAGGCT
                                |||||||||||||| ||||||
                                AAAGTGGTACAACC GTCCGA
                                      C
GAM946  FLJ20413 3' CCTGGCTAACACGGTGAAA   35593       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                    C
GAM946  FLJ20464 3' AGCCTGACCAACATGGAGAAA  35682     A      C
                                TTTC CCATGTTGG CAGGCT
                                |||| ||||||||| ||||||
                                AAAG GGTACAACC GTCCGA
                                  A       A
GAM946  FLJ20627 3' ACAAGCCTGGCCAACATGGTGA 35905              C
           AA                     TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                        A
GAM946  FLJ20671 3' ACAAGCCTGGGCAACATGGTGA 35931          G     C
           AA                     TTTCACCATGTTG CCAGGCT GT
                                  |||||||||||| ||||||| ||
                                  AAAGTGGTACAAC GGTCCGA CA
                                        G     A
GAM946  FLJ20686 3' ACCAGCCTGGCCAACACGGTGA 35950       A         C
           GA                     TTTCACC TGTTGGCCAGGCT GT
                                  ||||||| |||||||||||| ||
                                  AGAGTGG ACAACCGGTCCGA CA
                                      C         C
GAM946  FLJ20700 3' CTGGCCAACAGAATGAAA    36008      CCA
                                TTTCA  TGTTGGCCAG
                                |||||  ||||||||||
                                AAAGT  ACAACCGGTC
                                   AAG
GAM946  FLJ20783 3' CCTGGCTAACACGGTGAAA   36098       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                    C
GAM946  FLJ20808 3' CCTGGCTAACACGGTGAAA   36118       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
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                                AAAGTGG ACAATCGGTCC
                                    C
GAM946  FLJ20825  3'  AGCCTGACCAACATGGAGAAA  36140      A       C
                                TTTC CCATGTTGG CAGGCT
                                |||| ||||||||| ||||||
                                AAAG GGTACAACC GTCCGA
                                  A       A
GAM946  FLJ20972  3'  AGCCTGACCAACATGGAGAAA  47378      A       C
                                TTTC CCATGTTGG CAGGCT
                                |||| ||||||||| ||||||
                                AAAG GGTACAACC GTCCGA
                                  A       A
GAM946  FLJ21106  3'  CCTGGCTAACACGGTGAAA    47693      A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                    C
GAM946  FLJ21162  3'  AGCCTGGCCAGCATGGTGAAA  46365
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||||
                                AAAGTGGTACGACCGGTCCGA

GAM946  FLJ21369  3'  ACCAGCCTGGCCAACATGGTGA 46045                C
          GA                    TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AGAGTGGTACAACCGGTCCGA CA
                                      C
GAM946  FLJ21551  3'  CCTGGCCAACCTGGTGAAA    46035      T
                                TTTCACCA GTTGGCCAGG
                                |||||||| |||||||||
                                AAAGTGGT CAACCGGTCC
                                    C
GAM946  FLJ21657  3'  ACCAGCCTGGCCAACATGGTGA 42792                C
          AA                    TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                      C
GAM946  FLJ21687  3'  AGCCTGGCCAAGATGGTGAAA  46289        G
                                TTTCACCAT TTGGCCAGGCT
                                ||||||||| ||||||||||
                                AAAGTGGTA AACCGGTCCGA
                                     G
GAM946  FLJ21777  3'  ACCAGCCTGGCCAACATGGTGA 50829                C
          AA                    TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                      C
GAM946  FLJ21870  3'  ACCAGCCTGGCCAACATGGTGA 43739                C
          AA                    TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
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                                AAAGTGGTACAACCGGTCCGA CA
                                             C
GAM946  FLJ22054  3'  AGCCTGGCCAACATGGTGAAA  96043
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGA

GAM946  FLJ22167  3'  ACCAGCCTGGCCAACATAGTGA 44854       C           C
          AA                    TTTCAC ATGTTGGCCAGGCT GT
                                ||||||| ||||||||||||||| ||
                                AAAGTG TACAACCGGTCCGA CA
                                   A           C
GAM946  FLJ22313  3'  AGCCTGGCAAACATGGCGAAA  42575     A     G
                                TTTC CCATGTT GCCAGGCT
                                |||| ||||||| ||||||||
                                AAAG GGTACAA CGGTCCGA
                                  C      A
GAM946  FLJ22474  3'  ACCAGCCTGGCCAACACGGTGA 45608       A           C
          AA                    TTTCACC TGTTGGCCAGGCT GT
                                ||||||| |||||||||||||| ||
                                AAAGTGG ACAACCGGTCCGA CA
                                   C           C
GAM946  FLJ22814  3'  AGCCTGGCCAGCATGGCGAAA  46710     A
                                TTTC CCATGTTGGCCAGGCT
                                |||| ||||||||||||||||
                                AAAG GGTACGACCGGTCCGA
                                  C
GAM946  FLJ22814  3'  CCTGGCTAACATGGTGAAA   46723
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||||
                                AAAGTGGTACAATCGGTCC

GAM946  FLJ22965  3'  GCCTGGGCAACATGGTGAAA  42300           G
                                TTTCACCATGTTG CCAGGC
                                |||||||||||| ||||||
                                AAAGTGGTACAAC GGTCCG
                                        G
GAM946  FLJ23022  3'  ACCAGCCTGGCCAACATGGTGA 47488                 C
          AA                    TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                             C
GAM946  FLJ23040  3'  ACCAGCCTGGCCAACATGATGA 47979      C           C
          AA                    TTTCA CATGTTGGCCAGGCT GT
                                ||||| |||||||||||||| ||
                                AAAGT GTACAACCGGTCCGA CA
                                   A           C
GAM946  FLJ23042  3'  AGCCTGACCAACATGGAGAAA  47934     A       C
                                TTTC CCATGTTGG CAGGCT
                                |||| ||||||||| ||||||
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                                AAAG GGTACAACC GTCCGA
                                  A       A
GAM946  FLJ23112  3'  CCTGGCCAACATGTTGAAA   46810      C
                                TTTCA CATGTTGGCCAGG
                                ||||| ||||||||||||
                                AAAGT GTACAACCGGTCC
                                   T
GAM946  FLJ23235  3'  CCTGGCCAACATGGTGAAA   46878
                                TTTCACCATGTTGGCCAGG
                                ||||||||||||||||||
                                AAAGTGGTACAACCGGTCC

GAM946  FLJ23499  3'  ACAGCCTGACCAACATGGTGAA 43119          C     C
          A                   TTTCACCATGTTGG CAGGCT GT
                              |||||||||||||| |||||| ||
                              AAAGTGGTACAACC GTCCGA CA
                                       A     C
GAM946  FLJ23537  3'  CCTGACCAACATGGAGAAA   88918     A       C
                                TTTC CCATGTTGG CAGG
                                |||| ||||||||| ||||
                                AAAG GGTACAACC GTCC
                                  A       A
GAM946  FLJ25012  3'  ACAGCCTGGGCAACATGGTGAA 58703          G     C
          A                   TTTCACCATGTTG CCAGGCT GT
                              |||||||||||| ||||||| ||
                              AAAGTGGTACAAC GGTCCGA CA
                                       G     T
GAM946  FLJ25012  3'  CTGGCTAACATGGTGAAA    58710
                                TTTCACCATGTTGGCCAG
                                ||||||||||||||||||
                                AAAGTGGTACAATCGGTC

GAM946  FLJ30681  3'  ACCAGCCTGACCAACATGGTGA 93428          C     C
          AA                    TTTCACCATGTTGG CAGGCT GT
                              |||||||||||| |||||| ||
                              AAAGTGGTACAACC GTCCGA CA
                                       A     C
GAM946  FLJ31168  3'  ACCAGCCTGGCCAACATGGTGA 59173                C
          AA                    TTTCACCATGTTGGCCAGGCT GT
                              |||||||||||||||||||| ||
                              AAAGTGGTACAACCGGTCCGA CA
                                          C
GAM946  FLJ31455  3'  ACCAGCCTGGCCAACATGGTGA 59276                C
          AA                    TTTCACCATGTTGGCCAGGCT GT
                              |||||||||||||||||||| ||
                              AAAGTGGTACAACCGGTCCGA CA
                                          C
GAM946  FLJ31737  3'  ACCAGCCTGGCCAACATGGTGA 59343                C
          AA                    TTTCACCATGTTGGCCAGGCT GT
                              |||||||||||||||||||| ||
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                                AAAGTGGTACAACCGGTCCGA CA
                                                    C
GAM946  FLJ31952  3'  AGCTTGGCCAACATGGAGAAA  59040      A
                                TTTC CCATGTTGGCCAGGCT
                                |||| ||||||||||||||||
                                AAAG GGTACAACCGGTTCGA
                                  A
GAM946  FLJ32915  5'  AGCCTGGCCAACATGGTGAAA  59423
                                TTTCACCATGTTGGCCAGGCT
                                ||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGA

GAM946  FRSB      3'  AGCCTGACCAACATGATGAAA  20287      C       C
                                TTTCA CATGTTGG CAGGCT
                                ||||| |||||||| ||||||
                                AAAGT GTACAACC GTCCGA
                                   A       A
GAM946  GLTP      3'  ACCAGCCTGGCCAACATGGTGA 33577                C
              AA                  TTTCACCATGTTGGCCAGGCT GT
                                ||||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                                    C
GAM946  GMPPB     3'  ACAGCCCGCCCTCTGGTGAAA  26214        TGTT  CA   C
                                TTTCACCA   GGC  GGCT GT
                                ||||||||   |||  |||| ||
                                AAAGTGGT   CCG  CCGA CA
                                     CTC_  C_   A
GAM946  GNB4      3'  AGCCTACCCAACATGGTGAAA  41562           CC
                                TTTCACCATGTTGG  AGGCT
                                ||||||||||||||  |||||
                                AAAGTGGTACAACC  TCCGA
                                          CA
GAM946  GP5       3'  AGCTGGCCAAGATGGTGAAA   16861        G       G
                                TTTCACCAT TTGGCCAG CT
                                |||||||| |||||||| ||
                                AAAGTGGTA AACCGGTC GA
                                     G      _
GAM946  GTPBP5    3'  CCTGGCTAACACAGTGAAA   65972       CA
                                TTTCAC  TGTTGGCCAGG
                                ||||||  ||||||||||
                                AAAGTG  ACAATCGGTCC
                                   AC
GAM946  HES2      3'  CTTGGCTAACACGGTGAAA   39374        A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTTC
                                   C
GAM946  HIG2      3'  AGCCTCGCCAACATGGCGAAA  26195      A        C
                                TTTC CCATGTTGGC AGGCT
                                |||| |||||||||| |||||
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                                AAAG GGTACAACCG TCCGA
                                  C        C
GAM946  HRH4     3'  CCTGGCCAACATGGTGAAA   41536
                                TTTCACCATGTTGGCCAGG
                                ||||||||||||||||||
                                AAAGTGGTACAACCGGTCC

GAM946  HSH2     3'  ACAGCCTGGCCAACATGGTGAA 52732                  C
                A                TTTCACCATGTTGGCCAGGCT GT
                                 |||||||||||||||||||| ||
                                 AAAGTGGTACAACCGGTCCGA CA
                                                C
GAM946  HSPC031  3'  ACCAGCCTGGCCAACATGGTGA 32744                   C
                AA                TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                                C
GAM946  HSPC043  3'  ACAGCCTGGCCAACATGGTGAA 68343                   C
                A                 TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                                C
GAM946  HYPK     3'  ACCAGCCTGGCCAACATGTGAA 33510        C          C
                A                 TTTCAC ATGTTGGCCAGGCT GT
                                  |||||| |||||||||||||| ||
                                  AAAGTG TACAACCGGTCCGA CA
                                     _            C
GAM946  IL10RB   3'  ACCAGCCTGGCCAATATGGTGA 7121                   C
                AA                TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTATAACCGGTCCGA CA
                                                C
GAM946  IMAGE:4907098 3'  ACCAGCCTGGCCAATATGGTGA 57751                    C
                AA                TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTATAACCGGTCCGA CA
                                                C
GAM946  JAM1     3'  AGCCTGACCAACATGGAGAAA  34217      A        C
                                TTTC CCATGTTGG CAGGCT
                                |||| ||||||||| ||||||
                                AAAG GGTACAACC GTCCGA
                                  A        A
GAM946  KALI     3'  AGCCTGGCCAACTTGGTGAAA  54688          T
                                TTTCACCA GTTGGCCAGGCT
                                |||||||| ||||||||||||
                                AAAGTGGT CAACCGGTCCGA
                                      T
GAM946  KBRAS2   3'  AGCCTGGCCAACATTGTGAAA  34617        C
                                TTTCAC ATGTTGGCCAGGCT
                                |||||| ||||||||||||||
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                                AAAGTG TACAACCGGTCCGA
                                   T
GAM946  KCNH6    3' CCTGGCTAACACGGTGAAA   48572       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                   C
GAM946  KIAA0042 3' ACCGGCCTGGCCAACATGGTGA 30230              C
             AA                   TTTCACCATGTTGGCCAGGCT GT
                                ||||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGG CA
                                      C
GAM946  KIAA0057 3' ACCAGCCTGGCCAACATGGTGA 25396              C
             AA                   TTTCACCATGTTGGCCAGGCT GT
                                ||||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                      C
GAM946  KIAA0090 3' ACAGCCTGGCCAACATGGTGAA 89806              C
             A                    TTTCACCATGTTGGCCAGGCT GT
                                ||||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                      C
GAM946  KIAA0159 3' AGCCTGACCAACATGGAGAAA  30137     A      C
                                TTTC CCATGTTGG CAGGCT
                                |||| ||||||||| ||||||
                                AAAG GGTACAACC GTCCGA
                                  A       A
GAM946  KIAA0184 3' CCTGGCTAACATGGTGAAA   65808
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||
                                AAAGTGGTACAATCGGTCC

GAM946  KIAA0266 3' ACCAGCCTGAACAACATGGTGA 41631          GC    C
             AA                   TTTCACCATGTTG  CAGGCT GT
                                ||||||||||||  |||||| ||
                                AAAGTGGTACAAC  GTCCGA CA
                                      AA    C
GAM946  KIAA0355 3' ACCAGCCTGGCCAATATGGTGA 28695              C
             AA                   TTTCACCATGTTGGCCAGGCT GT
                                ||||||||||||||||||||| ||
                                AAAGTGGTATAACCGGTCCGA CA
                                      C
GAM946  KIAA0446 5' CCTGGCTAACATGGTGAAA   69448
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||
                                AAAGTGGTACAATCGGTCC

GAM946  KIAA0447 3' ACCAGCCTGGCCAACATGATGA 72102      C       C
             AA                   TTTCA CATGTTGGCCAGGCT GT
                                ||||| ||||||||||||| ||
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                                AAAGT GTACAACCGGTCCGA CA
                                   A           C
GAM946  KIAA0472 3' AGCCTGGCCAACATGGTGAAA  72332
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGA

GAM946  KIAA0547 3' ACCAGCCTGGCCAATATGGTGA 29584                C
             AA                   TTTCACCATGTTGGCCAGGCT GT
                                ||||||||||||||||||||| ||
                                AAAGTGGTATAACCGGTCCGA CA
                                             C
GAM946  KIAA0547 3' CCTGGTCAACATGGTGAAA   29592
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||||
                                AAAGTGGTACAACTGGTCC

GAM946  KIAA0557 3' CCTGGCCAACATGGTGAAA   78552
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||||
                                AAAGTGGTACAACCGGTCC

GAM946  KIAA0563 3' CCTGGCTAACATGGTGAAA   29877
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||||
                                AAAGTGGTACAATCGGTCC

GAM946  KIAA0596 3' AGCCTGGCCAACATGGTGAAA  63480
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGA

GAM946  KIAA0618 3' AGCCTGGCCAACATGGAGAAA  29842      A
                                TTTC CCATGTTGGCCAGGCT
                                |||| ||||||||||||||||
                                AAAG GGTACAACCGGTCCGA
                                   A
GAM946  KIAA0694 3' AGCTTGGCCAACATGGTGAAG  72962
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||||
                                GAAGTGGTACAACCGGTTCGA

GAM946  KIAA0794 3' AGCCTGAGCAACATGGTGAAA  81222            GC
                                TTTCACCATGTTG  CAGGCT
                                ||||||||||||  ||||||
                                AAAGTGGTACAAC  GTCCGA
                                         GA
GAM946  KIAA0795 3' ACCAGCCTGGCCAACATGGTGA 47227                C
             AA                   TTTCACCATGTTGGCCAGGCT GT
                                ||||||||||||||||||||| ||
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                                AAAGTGGTACAACCGGTCCGA CA
                                              C
GAM946  KIAA0825 3' AGCTTGACCAACATGGAGAAA 61680      A       C
                                TTTC CCATGTTGG CAGGCT
                                |||| ||||||||| ||||||
                                AAAG GGTACAACC GTTCGA
                                  A       A
GAM946  KIAA0831 3' AGCCTGGCTAACATGGTGAAA 30627
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||||
                                AAAGTGGTACAATCGGTCCGA

GAM946  KIAA0872 3' AGCCTGACCAACATGGTGAAA 30737            C
                                TTTCACCATGTTGG CAGGCT
                                |||||||||||||| ||||||
                                AAAGTGGTACAACC GTCCGA
                                        A
GAM946  KIAA0872 3' AGCCTGGCCAGCATGGCGAAA 30738      A
                                TTTC CCATGTTGGCCAGGCT
                                |||| ||||||||||||||||
                                AAAG GGTACGACCGGTCCGA
                                  C
GAM946  KIAA0884 3' AGTCTGGTCAACATGGTGAAA 70748
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||||
                                AAAGTGGTACAACTGGTCTGA

GAM946  KIAA0889 3' ACCGGTCTGGCCAACATGGTGA 31746                  C
                AA                TTTCACCATGTTGGCCAGGCT GT
                                ||||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCTGG CA
                                              C
GAM946  KIAA0889 3' AGCCTGGCCAATATGGTGAAA 31752
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||||
                                AAAGTGGTATAACCGGTCCGA

GAM946  KIAA0894 3' AGCGTGGCCAACATGATGAAA 30323      C       G
                                TTTCA CATGTTGGCCA GCT
                                ||||| |||||||||| |||
                                AAAGT GTACAACCGGT CGA
                                  A         G
GAM946  KIAA0907 3' AGCGTGGCTAACACGGTGAAA 30863       A       G
                                TTTCACC TGTTGGCCA GCT
                                ||||||| ||||||||| |||
                                AAAGTGG ACAATCGGT CGA
                                    C       G
GAM946  KIAA0907 3' AGCTTGGCCAACATAGTGAAA 30864       C
                                TTTCAC ATGTTGGCCAGGCT
                                |||||| ||||||||||||||
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                                AAAGTG TACAACCGGTTCGA
                                   A
GAM946  KIAA0953 3' ACCAGCCTGATCAACATGGTGA 67318          GC     C
                AA                  TTTCACCATGTTG  CAGGCT GT
                                    |||||||||||||  |||||| ||
                                    AAAGTGGTACAAC  GTCCGA CA
                                       TA     C
GAM946  KIAA0961 3' AGCCTGACCATCATGGTGAAA  30389         T   C
                                    TTTCACCATG TGG CAGGCT
                                    |||||||||| ||| ||||||
                                    AAAGTGGTAC ACC GTCCGA
                                       T   A
GAM946  KIAA0981 3' ACCAGCCTGGCCAACATGACGA 62080      AC           C
                AA                  TTTC  CATGTTGGCCAGGCT GT
                                    ||||  |||||||||||||| ||
                                    AAAG  GTACAACCGGTCCGA CA
                                      CA            C
GAM946  KIAA1001 3' ACAGCCTGGCCAACATGGTGAA 30994                C
                A                   TTTCACCATGTTGGCCAGGCT GT
                                    |||||||||||||||||||| ||
                                    AAAGTGGTACAACCGGTCCGA CA
                                                  C
GAM946  KIAA1001 3' ACAGCCTGGCCAACATGGTGAA 30995                C
                A                   TTTCACCATGTTGGCCAGGCT GT
                                    |||||||||||||||||||| ||
                                    AAAGTGGTACAACCGGTCCGA CA
                                                  C
GAM946  KIAA1032 3' ACCAGCCTGGCCAACATGGCGA 66718      A           C
                AA                  TTTC CCATGTTGGCCAGGCT GT
                                    |||| |||||||||||||| ||
                                    AAAG GGTACAACCGGTCCGA CA
                                      C             C
GAM946  KIAA1086 3' ACCGGCCTGGTCAACATGGTGA 71277                C
                AA                  TTTCACCATGTTGGCCAGGCT GT
                                    |||||||||||||||||||| ||
                                    AAAGTGGTACAACTGGTCCGG CA
                                                  C
GAM946  KIAA1130 3' ACCAGCCTGACCAAAATGGTGA 63073         G   C    C
                AA                  TTTCACCAT TTGG CAGGCT GT
                                    ||||||||| |||| |||||| ||
                                    AAAGTGGTA AACC GTCCGA CA
                                          A   A    C
GAM946  KIAA1160 3' CCTGGCCAACATGGTGAAA   40755
                                    TTTCACCATGTTGGCCAGG
                                    |||||||||||||||||
                                    AAAGTGGTACAACCGGTCC

GAM946  KIAA1164 3' ACAGCCTGGCCAACATGG    70027             C
                                    CCATGTTGGCCAGGCT GT
                                    |||||||||||||| ||
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                                GGTACAACCGGTCCGA CA
                                       C
GAM946  KIAA1164  3'  AGCCTGGCCAGCATGGTGAAA  70031
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||||
                                AAAGTGGTACGACCGGTCCGA

GAM946  KIAA1191  3'  ACCAGCCTGGCCAACATGGTGA 40327                  C
              AA                  TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                         C
GAM946  KIAA1202  3'  CCTGGCTAACACGGTGAAA   72487        A
                                TTTCACC TGTTGGCCAGG
                                |||||||  ||||||||||
                                AAAGTGG ACAATCGGTCC
                                    C
GAM946  KIAA1228  3'  AGCCTGGCCAACATGGAGAAA  65665      A
                                TTTC CCATGTTGGCCAGGCT
                                ||||  ||||||||||||||||
                                AAAG GGTACAACCGGTCCGA
                                  A
GAM946  KIAA1244  3'  AGGCTGGACAACATGGTGAAA  72439            G   G
                                TTTCACCATGTTG CCAG CT
                                ||||||||||||  ||||  ||
                                AAAGTGGTACAAC GGTC GA
                                       A   G
GAM946  KIAA1253  3'  ACCAGCCTGGGCAACATGGTGA 93545            G      C
              AA                  TTTCACCATGTTG CCAGGCT GT
                                  |||||||||||||  |||||||  ||
                                  AAAGTGGTACAAC GGTCCGA CA
                                       G      C
GAM946  KIAA1257  3'  AGCCTGGCTAACACGGTGAAA  63389        A
                                TTTCACC TGTTGGCCAGGCT
                                |||||||  ||||||||||||||
                                AAAGTGG ACAATCGGTCCGA
                                    C
GAM946  KIAA1271  3'  ACCAGCCTGGCCAACAGGGTGA 70123        A          C
              AA                  TTTCACC TGTTGGCCAGGCT GT
                                  |||||||  |||||||||||||  ||
                                  AAAGTGG ACAACCGGTCCGA CA
                                     G           C
GAM946  KIAA1276  3'  ACCAGCCTGGCCAATATGGTGA 67026                  C
              AA                  TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTATAACCGGTCCGA CA
                                         C
GAM946  KIAA1328  3'  CCTGGCTAACACGGTGAAA   62321        A
                                TTTCACC TGTTGGCCAGG
                                |||||||  ||||||||||
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                                AAAGTGG ACAATCGGTCC
                                    C
GAM946  KIAA1348 3' AGCCTGACCAACATGGAGAAA  69117      A       C
                                TTTC CCATGTTGG CAGGCT
                                |||| ||||||||| ||||||
                                AAAG GGTACAACC GTCCGA
                                  A       A
GAM946  KIAA1364 3' ACCAGCCTGGCCAACATAATGA 64340      CC          C
            AA                    TTTCA  ATGTTGGCCAGGCT GT
                                |||||  |||||||||||||| ||
                                AAAGT  TACAACCGGTCCGA CA
                                  AA          C
GAM946  KIAA1404 3' ACCAGCCTGACCAACATGGCGA 62678      A       C     C
            AA                    TTTC CCATGTTGG CAGGCT GT
                                |||| ||||||||| |||||| ||
                                AAAG GGTACAACC GTCCGA CA
                                  C       A     C
GAM946  KIAA1456 3' ACCAGCCTGACCAACATGGTGA 67522            C     C
            AA                    TTTCACCATGTTGG CAGGCT GT
                                |||||||||||||| |||||| ||
                                AAAGTGGTACAACC GTCCGA CA
                                        A     C
GAM946  KIAA1456 5' CCTGACCAACATGGAGAAA   67545      A       C
                                TTTC CCATGTTGG CAGG
                                |||| ||||||||| ||||
                                AAAG GGTACAACC GTCC
                                  A       A
GAM946  KIAA1473 3' AGCCTGACCAACATGGAGAAA  71203      A       C
                                TTTC CCATGTTGG CAGGCT
                                |||| ||||||||| ||||||
                                AAAG GGTACAACC GTCCGA
                                  A       A
GAM946  KIAA1614 3' AGTCTGGCCCACATGGTGAAA  70661          T
                                TTTCACCATGT GGCCAGGCT
                                |||||||||| |||||||||
                                AAAGTGGTACA CCGGTCTGA
                                      C
GAM946  KIAA1630 3' ACCAGCCTGGCCAACACGGTGA 38652       A          C
            AA                    TTTCACC TGTTGGCCAGGCT GT
                                ||||||| |||||||||||| ||
                                AAAGTGG ACAACCGGTCCGA CA
                                    C          C
GAM946  KIAA1641 3' ACAGCCTGGCCAATATGGTGAA 81014                C
            A                     TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTATAACCGGTCCGA CA
                                          C
GAM946  KIAA1656 5' CCTGGCCAACATGGTGAAA   66365
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||
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                                AAAGTGGTACAACCGGTCC

GAM946  KIAA1674  3'  CCTGGCTAACACGGTGAAA   69336       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                    C
GAM946  KIAA1724  3'  CCTGAGCAACATGGCGAAA   67613     A     GC
                                TTTC CCATGTTG  CAGG
                                |||| ||||||||  ||||
                                AAAG GGTACAAC  GTCC
                                  C       GA
GAM946  KIAA1751  3'  ACCAGCCTGGCCAACATGGTGA 72147               C
            AA                    TTTCACCATGTTGGCCAGGCT GT
                                ||||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                        C
GAM946  KIAA1811  5'  ACCAGCCTGACCAACATGGTGA 65414          C    C
            AA                    TTTCACCATGTTGG CAGGCT GT
                                |||||||||||||| |||||| ||
                                AAAGTGGTACAACC GTCCGA CA
                                      A    C
GAM946  KIAA1829  3'  AGCCTGACCAACATGGAGAAA  62630     A      C
                                TTTC CCATGTTGG CAGGCT
                                |||| ||||||||| ||||||
                                AAAG GGTACAACC GTCCGA
                                  A       A
GAM946  KIAA1841  3'  AGCCTGGCCAACGTGGTGAAA  80845
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||
                                AAAGTGGTGCAACCGGTCCGA

GAM946  KIAA1872  3'  AGCCTGGCCAACATGGTGAAA  63591
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGA

GAM946  KIAA1872  3'  AGGCTGGCCAACATGGTGAAA  63594              G
                                TTTCACCATGTTGGCCAG CT
                                |||||||||||||||| ||
                                AAAGTGGTACAACCGGTC GA
                                      G
GAM946  KIAA1941  3'  ACCAGCCTGGCCAACATGGTGA 75331               C
            AA                    TTTCACCATGTTGGCCAGGCT GT
                                ||||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                        C
GAM946  KIAA1948  3'  CCTGGCTAACACGGTGAAA   83302       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
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                                AAAGTGG ACAATCGGTCC
                                    C
GAM946  KIAA1951  3'  CCTGGCTAACACGGTGAAA   74151       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                    C
GAM946  KIAA1954  3'  ACCAGCCTGGACAACATGGTGA 78221          G     C
            AA                    TTTCACCATGTTG CCAGGCT GT
                                ||||||||||||| ||||||| ||
                                AAAGTGGTACAAC GGTCCGA CA
                                      A     C
GAM946  KIAA1969  3'  CCTGGCCAACATGGTGAAA   79476
                                TTTCACCATGTTGGCCAGG
                                ||||||||||||||||||
                                AAAGTGGTACAACCGGTCC

GAM946  KLHL8     3'  ACCAGCCTGACCAACATGGTGA 63502          C     C
            AA                    TTTCACCATGTTGG CAGGCT GT
                                ||||||||||||| |||||| ||
                                AAAGTGGTACAACC GTCCGA CA
                                      A     C
GAM946  KR18      3'  AGCCTGACCAACATGGAGAAA  53878     A       C
                                TTTC CCATGTTGG CAGGCT
                                |||| ||||||||| ||||||
                                AAAG GGTACAACC GTCCGA
                                  A       A
GAM946  KR18      3'  AGCCTGGCCAGCATAGTGAAA  53879      C
                                TTTCAC ATGTTGGCCAGGCT
                                |||||| ||||||||||||||
                                AAAGTG TACGACCGGTCCGA
                                   A
GAM946  KREMEN    3'  ACCAGCCTGGCCAACATGGCGA 50221     A           C
            AA                    TTTC CCATGTTGGCCAGGCT GT
                                |||| |||||||||||||| ||
                                AAAG GGTACAACCGGTCCGA CA
                                  C             C
GAM946  LAP1B     3'  ACCAGCCTGGCCAACATGGTGA 65186               C
            AA                    TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                      C
GAM946  LIAS      3'  ACAGCCTGGCCAACATGGTGAA 71160              C
            A                     TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                      C
GAM946  LIM       3'  AGCCTGGCCAACATGGTGAAA  22313
                                TTTCACCATGTTGGCCAGGCT
                                ||||||||||||||||||||
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                                AAAGTGGTACAACCGGTCCGA

GAM946  LIM      3'  CCTGGCCAACATGGTGAAA   22323
                                TTTCACCATGTTGGCCAGG
                                ||||||||||||||||||
                                AAAGTGGTACAACCGGTCC

GAM946  LRG      3'  CTTGGCTAACATGGTGAAA   54819
                                TTTCACCATGTTGGCCAGG
                                ||||||||||||||||||
                                AAAGTGGTACAATCGGTTC

GAM946  LRRFIP1  3'  AGCCTGGCCAACATGGTGAAA  17606
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGA

GAM946  LSR68    3'  ACCAGCCTGGCCGACATGGCGA 38546      A             C
              AA                  TTTC CCATGTTGGCCAGGCT GT
                                  |||| |||||||||||||| ||
                                  AAAG GGTACAGCCGGTCCGA CA
                                    C            C
GAM946  LYSAL1   3'  CCTGGCTAACACGGTGAAA   18121        A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                    C
GAM946  MACF1    3'  ACCAGCCTGGCCAACATGGTGA 53425                 C
              AA                  TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                              C
GAM946  MACF1    3'  CCTGGCTAACACGGTGAAA   53427        A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                    C
GAM946  MAWBP    3'  ACCAGCCTGGCCAACATGGTGA 42372                 C
              AA                  TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                              C
GAM946  MCAM     3'  CCTGGCTAACACGGTGAAA   22460        A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                    C
GAM946  MESDC2   3'  AGCCTGGCCAACATGGTGAAG  72906
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||||
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                                GAAGTGGTACAACCGGTCCGA

GAM946  MGC10765 3' ACAGCCTGACCAACATGGTGAA 44550          C     C
             A                   TTTCACCATGTTGG CAGGCT GT
                                 ||||||||||||| |||||| ||
                                 AAAGTGGTACAACC GTCCGA CA
                                       A     C
GAM946  MGC10771 3' ACCAGCCTGGCCAACATGGTGA 44709              C
             AA                   TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                        C
GAM946  MGC10814 5' AGCCTGGCCAACATGGTGAAA  52011
                                  TTTCACCATGTTGGCCAGGCT
                                  ||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGA

GAM946  MGC10999 3' CCTGGCCAACATGGTGAAA    51193
                                  TTTCACCATGTTGGCCAGG
                                  |||||||||||||||||
                                  AAAGTGGTACAACCGGTCC

GAM946  MGC11386 3' CCTGGCCAACATGGTGAAA    53062
                                  TTTCACCATGTTGGCCAGG
                                  |||||||||||||||||
                                  AAAGTGGTACAACCGGTCC

GAM946  MGC13017 3' ACAGCCTGGCCAACACGATGAA 55566      CCA          C
             A                   TTTCA   TGTTGGCCAGGCT GT
                                 |||||   |||||||||||| ||
                                 AAAGT   ACAACCGGTCCGA CA
                                    AGC
GAM946  MGC13053 3' AGCCTAGCCAACATGGTGAAA  52094            C
                                  TTTCACCATGTTGGC AGGCT
                                  |||||||||||||| |||||
                                  AAAGTGGTACAACCG TCCGA
                                        A
GAM946  MGC14126 3' ACAGCCTAGCCAACATGGTGAA 52933           C    C
             A                   TTTCACCATGTTGGC AGGCT GT
                                 |||||||||||||| ||||| ||
                                 AAAGTGGTACAACCG TCCGA CA
                                       A    C
GAM946  MGC14407 3' ACCAGCCTAGCCTACATGGTGA 52965         T  C    C
             AA                   TTTCACCATGT GGC AGGCT GT
                                  |||||||||| ||| ||||| ||
                                  AAAGTGGTACA CCG TCCGA CA
                                        T  A    C
GAM946  MGC14799 3' CCGACCAACATGGTGAAA    51326           CCA
                                  TTTCACCATGTTGG   GG
                                  ||||||||||||||   ||
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                                AAAGTGGTACAACC   CC
                                      AG_
GAM946  MGC15397  3'  ACCAGCCTGGCCAAGATGGTGA 55547         G         C
              AA                  TTTCACCAT TTGGCCAGGCT GT
                                  ||||||||| |||||||||| ||
                                  AAAGTGGTA AACCGGTCCGA CA
                                       G          C
GAM946  MGC16142  3'  AGCCTGGCCAACGTGATGAAA  52259       C
                                  TTTCA CATGTTGGCCAGGCT
                                  ||||| ||||||||||||||
                                  AAAGT GTGCAACCGGTCCGA
                                     A
GAM946  MGC16703  3'  CCTGGCTAACACGGTGAAA    73493        A
                                  TTTCACC TGTTGGCCAGG
                                  ||||||| ||||||||||
                                  AAAGTGG ACAATCGGTCC
                                      C
GAM946  MGC20235  3'  ACCAGCCTGGTCAACATGGTGA 59544                 C
              AA                  TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACTGGTCCGA CA
                                                C
GAM946  MGC20496  3'  ACCAGCCTGGTCAACATGGT   54525              C
                                  ACCATGTTGGCCAGGCT GT
                                  |||||||||||||||| ||
                                  TGGTACAACTGGTCCGA CA
                                        C
GAM946  MGC2562   3'  ACCAGCCTGGCCAAACATGGTG 51412           _       C
              AAA                   TTTCACCATGTT GGCCAGGCT GT
                                  |||||||||||| ||||||||| ||
                                  AAAGTGGTACAA CCGGTCCGA CA
                                         A        C
GAM946  MGC2562   3'  AGTTTGGGCAACATGGCGAAA  51423      A       G
                                  TTTC CCATGTTG CCAGGCT
                                  |||| |||||||| |||||||
                                  AAAG GGTACAAC GGTTTGA
                                     C       G
GAM946  MGC2562   3'  CCTGCCCAACATGGTGAAA    51439             C
                                  TTTCACCATGTTGG CAGG
                                  |||||||||||||| ||||
                                  AAAGTGGTACAACC GTCC
                                        C
GAM946  MGC2663   3'  CCTGGCCAACATGGTGAAA    44334
                                  TTTCACCATGTTGGCCAGG
                                  ||||||||||||||||||
                                  AAAGTGGTACAACCGGTCC

GAM946  MGC26641  3'  ACCAGCCTGGTCAACATGGTGA 59319                 C
              AA                  TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
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                                AAAGTGGTACAACTGGTCCGA CA
                                      C
GAM946  MGC2731  3' AGCCTGACCAACATGGAGAAA  44158     A       C
                                TTTC CCATGTTGG CAGGCT
                                |||| ||||||||| ||||||
                                AAAG GGTACAACC GTCCGA
                                  A       A
GAM946  MGC29891 3' CCTGGCTAACACGGTGAAA   58861       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                    C
GAM946  MGC29937 3' ACCAGCCTGACCAACATGGTGA 58724           C     C
          AA                      TTTCACCATGTTGG CAGGCT GT
                                ||||||||||||| |||||| ||
                                AAAGTGGTACAACC GTCCGA CA
                                        A     C
GAM946  MGC3169  3' AGCTTGGCCAACATGGTGAAA  44179
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||
                                AAAGTGGTACAACCGGTTCGA

GAM946  MGC3207  3' CCTGGCTAACATGGTGAAA   63235
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||
                                AAAGTGGTACAATCGGTCC

GAM946  MGC39350 3' ACAGCCTGGCCAACATGGCGAA 59311     A           C
          A                      TTTC CCATGTTGGCCAGGCT GT
                                |||| |||||||||||||| ||
                                AAAG GGTACAACCGGTCCGA CA
                                  C
GAM946  MGC4248  3' ACCAGCCTGAGCAACATGGCGA 51307     A       GC     C
          AA                      TTTC CCATGTTG  CAGGCT GT
                                |||| ||||||||  |||||| ||
                                AAAG GGTACAAC  GTCCGA CA
                                  C       GA     C
GAM946  MGC4562  3' CCTGGCTAACACGGTGAAA   56738       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                    C
GAM946  MGC4663  3' GTCGTGGCTAACACGGTGAAA  44790       A       _
                                TTTCACC TGTTGGCCA GGC
                                ||||||| ||||||||| |||
                                AAAGTGG ACAATCGGT CTG
                                    C       G
GAM946  MGC5457  3' AGCCTGGCCAGCATGGTGAAA  51934
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||
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                                AAAGTGGTACGACCGGTCCGA

GAM946  MOST2    5'  ACAGCCTGGCCAACATGGT   40046              C
                                ACCATGTTGGCCAGGCT GT
                                |||||||||||||||| ||
                                TGGTACAACCGGTCCGA CA
                                      C
GAM946  MRPS10   3'  CCTGGCTAACACGGTGAAA   36816       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                    C
GAM946  MYO3B    3'  ACCAGCCTGACCAACATGGTGA 58104           C     C
                AA                TTTCACCATGTTGG CAGGCT GT
                                ||||||||||||| |||||| ||
                                AAAGTGGTACAACC GTCCGA CA
                                      A     C
GAM946  N4BP2    3'  AGCCTGGCCAACATGGTGAA   36933
                                TTCACCATGTTGGCCAGGCT
                                ||||||||||||||||||||
                                AAGTGGTACAACCGGTCCGA

GAM946  NBR2     3'  ACCAGCCTGGCCAACATAGCGA 20613      ACC          C
                GA                TTTC   ATGTTGGCCAGGCT GT
                                ||||   |||||||||||||| ||
                                AGAG   TACAACCGGTCCGA CA
                                  CGA           C
GAM946  NDUFC2   3'  CTTGGGCAACATGGTGAAA   17029           G
                                TTTCACCATGTTG CCAGG
                                |||||||||||| |||||
                                AAAGTGGTACAAC GGTTC
                                      G
GAM946  NMNAT    3'  ACCAGCCTGGCCAATATGGTGA 43274               C
                AA                TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTATAACCGGTCCGA CA
                                      C
GAM946  NMT2     3'  TCTGGCCAACATAGTGAAA   17860       C
                                TTTCAC ATGTTGGCCAGG
                                |||||| ||||||||||||
                                AAAGTG TACAACCGGTCT
                                   A
GAM946  NPTXR    3'  AGCCTGGCCAACGTGGTGAAA  27425
                                TTTCACCATGTTGGCCAGGCT
                                ||||||||||||||||||||
                                AAAGTGGTGCAACCGGTCCGA

GAM946  ORC6L    3'  ACCAGCCTGGCCAACATGGTGA 27485               C
                AA                TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
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                                AAAGTGGTACAACCGGTCCGA CA
                                             C
GAM946  PAFAH2   3'  CCTGGCCAACATGGTGAAA   6499
                                TTTCACCATGTTGGCCAGG
                                ||||||||||||||||||
                                AAAGTGGTACAACCGGTCC

GAM946  PB1      3'  ACCAGCCTGACCAACATGGTGA 36868            C     C
          AA                      TTTCACCATGTTGG CAGGCT GT
                                  |||||||||||||| |||||| ||
                                  AAAGTGGTACAACC GTCCGA CA
                                         A     C
GAM946  PB1      3'  AGCCTGGCCAACGTGGTGAAA  36870
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||||
                                AAAGTGGTGCAACCGGTCCGA

GAM946  PDCD7    3'  CCTGGCTAACACGGTGAAA   72602       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                     C
GAM946  phorbolin-1 3'  CCTGGCTAACACGGTGAAA   90208       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                     C
GAM946  PIWIL2   3'  CCTGGCCAACATGGTGAAA   36543
                                TTTCACCATGTTGGCCAGG
                                ||||||||||||||||||
                                AAAGTGGTACAACCGGTCC

GAM946  PNPASE   3'  CCTGGCTAACACGGTGAAA   71438       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                     C
GAM946  POFUT1   3'  AGCCTGGCCAACATGGTGAA   70969
                                TTCACCATGTTGGCCAGGCT
                                ||||||||||||||||||
                                AAGTGGTACAACCGGTCCGA

GAM946  PPP1R3B  3'  ACCAGCCTGGCCAACATGGTGA 45126                C
          AA                      TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                             C
GAM946  PPP1R3B  3'  CCTGGCTAACACGGTGAAA   45139       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
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                                AAAGTGG ACAATCGGTCC
                                    C
GAM946  PRDM14   3'  ACCAGCCTGGGCAACATGGTGA 44703          G      C
                AA                  TTTCACCATGTTG CCAGGCT GT
                                    ||||||||||||| ||||||| ||
                                    AAAGTGGTACAAC GGTCCGA CA
                                          G      C
GAM946  PRIC285  3'  CCTGGCCAACATGGTGAAA   62113
                                    TTTCACCATGTTGGCCAGG
                                    ||||||||||||||||||
                                    AAAGTGGTACAACCGGTCC

GAM946  PRO0618  3'  CCTGGCTAACATGGTGAAA   27052
                                    TTTCACCATGTTGGCCAGG
                                    ||||||||||||||||||
                                    AAAGTGGTACAATCGGTCC

GAM946  PRO0628  3'  CCTGGCCAACACGGTGAAA   27061        A
                                    TTTCACC TGTTGGCCAGG
                                    ||||||| ||||||||||
                                    AAAGTGG ACAACCGGTCC
                                        C
GAM946  PRO1048  3'  CCTGGCTAACATGGTGAAA   38110
                                    TTTCACCATGTTGGCCAGG
                                    ||||||||||||||||||
                                    AAAGTGGTACAATCGGTCC

GAM946  PRO2015  3'  ACCAGCCTGGCCAACATGGCGA 38152      A           C
                AA                  TTTC CCATGTTGGCCAGGCT GT
                                    |||| |||||||||||||| ||
                                    AAAG GGTACAACCGGTCCGA CA
                                      C             C
GAM946  PRO2198  5'  ACCAGCCTGGCCAAGATGGCGA 38402      A   G         C
                AA                  TTTC CCAT TTGGCCAGGCT GT
                                    |||| |||| |||||||||| ||
                                    AAAG GGTA AACCGGTCCGA CA
                                      C   G         C
GAM946  PRO2730  3'  AGCCTGACCAACATGGAGAAA  48176      A       C
                                    TTTC CCATGTTGG CAGGCT
                                    |||| |||||||| ||||||
                                    AAAG GGTACAACC GTCCGA
                                      A       A
GAM946  PRO2859  3'  CCTGGCCAACATGGTGAAG   38209
                                    TTTCACCATGTTGGCCAGG
                                    ||||||||||||||||||
                                    GAAGTGGTACAACCGGTCC

GAM946  PRO2893  3'  AGCCTGACCAACATGGAGAAA  38427      A       C
                                    TTTC CCATGTTGG CAGGCT
                                    |||| |||||||| ||||||
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                                AAAG GGTACAACC GTCCGA
                                  A       A
GAM946  PRO2949  3'  CCTGGCTAACACGGTGAAA   38221       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                    C
GAM946  PRO2964  3'  CCTGGCTAACACGGTGAAA   38258       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                    C
GAM946  PRPF4    3'  ACGAGCCTGGGCAACATGG   17463       G
                                CCATGTTG CCAGGCTCGT
                                |||||||| ||||||||||
                                GGTACAAC GGTCCGAGCA
                                     G
GAM946  PSR      3'  ACCAGCCTGGCCAACACGGTGA 65770       A          C
            AA                    TTTCACC TGTTGGCCAGGCT GT
                                  ||||||| |||||||||||| ||
                                  AAAGTGG ACAACCGGTCCGA CA
                                      C           C
GAM946  PTK6     3'  CCTGGCTAACACGGTGAAA   21072       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                    C
GAM946  PXMP4    3'  ACCAGCCTGGGCAACATGGTGA 24328           G      C
            AA                    TTTCACCATGTTG CCAGGCT GT
                                  |||||||||||| ||||||| ||
                                  AAAGTGGTACAAC GGTCCGA CA
                                        G      C
GAM946  RAB4B    5'  AGCCTGACCAACATGGAGAAA  32897      A       C
                                TTTC CCATGTTGG CAGGCT
                                |||| ||||||||| ||||||
                                AAAG GGTACAACC GTCCGA
                                  A       A
GAM946  RAD51    3'  AGCTTGGCCAAGATGGTGAAA  56827         G
                                TTTCACCAT TTGGCCAGGCT
                                ||||||||| ||||||||||
                                AAAGTGGTA AACCGGTTCGA
                                     G
GAM946  RHOBTB3  3'  ACAGCCTGGCCAAAACAGTGAA 30417       CATG         C
            A                     TTTCAC    TTGGCCAGGCT GT
                                  ||||||    |||||||||| ||
                                  AAAGTG    AACCGGTCCGA CA
                                     ACAA
GAM946  RNO2     5'  ACAGCCTGGCCAACATGGTGAA 53909                C
            A                     TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
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                                AAAGTGGTACAACCGGTCCGA CA
                                              C
GAM946  RNO2    3'  AGCCTGGCCAAGATGGTGAAA  53918          G
                                TTTCACCAT TTGGCCAGGCT
                                |||||||| ||||||||||
                                AAAGTGGTA AACCGGTCCGA
                                   G
GAM946  RNO2    5'  AGCCTGGCCAGCACGGTGAAA  53919         A
                                TTTCACC TGTTGGCCAGGCT
                                ||||||| ||||||||||||
                                AAAGTGG ACGACCGGTCCGA
                                   C
GAM946  RoXaN   3'  ACCAGCCTGGCCAACATAATGA 47267       CC            C
          AA                      TTTCA  ATGTTGGCCAGGCT GT
                                  |||||  |||||||||||||| ||
                                  AAAGT  TACAACCGGTCCGA CA
                                     AA            C
GAM946  RoXaN   3'  CCTGGCTAACACGGTGAAA   47284         A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                   C
GAM946  RoXaN   3'  CCTGGCTAACATGGTGAAA   47285
                                TTTCACCATGTTGGCCAGG
                                ||||||||||||||||||
                                AAAGTGGTACAATCGGTCC

GAM946  RPP14   3'  ACCAGCCTGGCCAACATGGTGA 60218                  C
          AA                      TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                                C
GAM946  RRP4    3'  ACAGCCTGGCCAACAAGGTGAA 27349         A          C
          A                       TTTCACC TGTTGGCCAGGCT GT
                                  ||||||| |||||||||||| ||
                                  AAAGTGG ACAACCGGTCCGA CA
                                     A
GAM946  SC65    3'  ACCAGCCTGGCCAACATGATGA 22281       C            C
          GA                      TTTCA CATGTTGGCCAGGCT GT
                                  ||||| |||||||||||||| ||
                                  AGAGT GTACAACCGGTCCGA CA
                                     A            C
GAM946  SC65    3'  ACCTGCCTGGCCAACATGGTGA 22283                  TC
          AA                      TTTCACCATGTTGGCCAGGC  GT
                                  |||||||||||||||||||  ||
                                  AAAGTGGTACAACCGGTCCG  CA
                                                TC
GAM946  SCIN    3'  ACCAGCCTGGCCAACATGGCGA 53596      A            C
          AA                      TTTC CCATGTTGGCCAGGCT GT
                                  |||| |||||||||||||| ||
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                                AAAG GGTACAACCGGTCCGA CA
                                  C             C
GAM946  SCYA5    3'  AGCCTGGCCAACATGATGAAA  12956       C
                                TTTCA CATGTTGGCCAGGCT
                                ||||| ||||||||||||||||
                                AAAGT GTACAACCGGTCCGA
                                   A
GAM946  SERF1B   3'  ACCAGCCTGGGCAACATGGCGA 43684      A       G       C
              AA                  TTTC CCATGTTG CCAGGCT GT
                                ||||| |||||||| ||||||| ||
                                AAAG GGTACAAC GGTCCGA CA
                                  C       G       C
GAM946  SGKL     3'  CCTGGGCAACATGGCGAAA   26059      A       G
                                TTTC CCATGTTG CCAGG
                                ||||| |||||||| |||||
                                AAAG GGTACAAC GGTCC
                                  C       G
GAM946  SLC7A11  3'  AGCCTGACCAACATGGAGAAA  27528      A       C
                                TTTC CCATGTTGG CAGGCT
                                ||||| ||||||||| ||||||
                                AAAG GGTACAACC GTCCGA
                                  A       A
GAM946  Spir-2   3'  ACAGCCTGGCCAACATGATGAA 71153       C             C
              A                  TTTCA CATGTTGGCCAGGCT GT
                                ||||| |||||||||||||| ||
                                AAAGT GTACAACCGGTCCGA CA
                                   A
GAM946  SPRY4    3'  ACCAGCCTGGCCAACATAGTGA 48988       C             C
              AA                  TTTCAC ATGTTGGCCAGGCT GT
                                ||||||| |||||||||||||| ||
                                AAAGTG TACAACCGGTCCGA CA
                                   A            C
GAM946  SPTLC2   3'  ACCAGCCTGGCCAACATGGTGA 17974                  C
              AA                  TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                                C
GAM946  SPTLC2   3'  AGTCTGGCCAACATGGCGAAA  17979      A
                                TTTC CCATGTTGGCCAGGCT
                                |||| ||||||||||||||||
                                AAAG GGTACAACCGGTCTGA
                                  C
GAM946  SS18L1   3'  AGCCTGACCAACATGGAGAAA  65946      A       C
                                TTTC CCATGTTGG CAGGCT
                                |||| ||||||||| ||||||
                                AAAG GGTACAACC GTCCGA
                                  A       A
GAM946  SSR3     3'  CCTGGCCAACATGGTGAAA   24034
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||||
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                                AAAGTGGTACAACCGGTCC

GAM946  SYAP1    3'  AGCCTTGCCAACATAGTGAAA  52466       C       C
                                TTTCAC ATGTTGGC AGGCT
                                |||||| |||||||| |||||
                                AAAGTG TACAACCG TCCGA
                                   A       T
GAM946  TA-LRRP  3'  AGTCTGGCCAACCTGGTGAAA  31708         T
                                TTTCACCA GTTGGCCAGGCT
                                |||||||| ||||||||||||
                                AAAGTGGT CAACCGGTCTGA
                                     C
GAM946  TACTILE  3'  CCTGGCTAACACAGTGAAA   20585       CA
                                TTTCAC  TGTTGGCCAGG
                                ||||||  ||||||||||
                                AAAGTG  ACAATCGGTCC
                                   AC
GAM946  TDP1     5'  AGCCCGGGCAACATGGTGAAA  37599           G  A
                                TTTCACCATGTTG CC GGCT
                                |||||||||||| || ||||
                                AAAGTGGTACAAC GG CCGA
                                      G  C
GAM946  THEA     3'  ACCAGCCTGGGCAACATGGTGA 66863           G      C
           AA                     TTTCACCATGTTG CCAGGCT GT
                                |||||||||||| ||||||| ||
                                AAAGTGGTACAAC GGTCCGA CA
                                      G      C
GAM946  THEA     3'  AGCCTGGCCAACATGGTGAAA  66870
                                TTTCACCATGTTGGCCAGGCT
                                ||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGA

GAM946  THEA     3'  AGTCTGGCCAACATGGCGAAA  66873      A
                                TTTC CCATGTTGGCCAGGCT
                                |||| ||||||||||||||||
                                AAAG GGTACAACCGGTCTGA
                                  C
GAM946  TIP47    3'  AGCCAGGCCAACATGGTGAAA  20599            A
                                TTTCACCATGTTGGCC GGCT
                                |||||||||||||| ||||
                                AAAGTGGTACAACCGG CCGA
                                      A
GAM946  TMG4     3'  ACCAGCCTGGCCAACATGGTGA 44210                C
           AA                     TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                        C
GAM946  TRIM38   3'  ACCAGCCTGGCCAACATGGTGA 22049                C
           AA                     TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
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                                AAAGTGGTACAACCGGTCCGA CA
                                              C
GAM946  TXNL2    3'  ACCAGCCTGAGCAACATGGCGA 22575      A       GC     C
                AA                TTTC CCATGTTG  CAGGCT GT
                                  |||| ||||||||  |||||| ||
                                  AAAG GGTACAAC  GTCCGA CA
                                    C       GA     C
GAM946  UBCE7IP5 3'  ACCAGCCTGGCCAACATGGCAA 30839     CA             C
                GA                TTT  CCATGTTGGCCAGGCT GT
                                  |||  |||||||||||||||| ||
                                  AGA  GGTACAACCGGTCCGA CA
                                    AC             C
GAM946  ust3     3'  CCTGGCCAACATGGTGAAA   94852
                                  TTTCACCATGTTGGCCAGG
                                  ||||||||||||||||||
                                  AAAGTGGTACAACCGGTCC

GAM946  VIT1     5'  ACCAGCCTGGCCAACATGGTGA 38596                  C
                AA                TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                              C
GAM946  VPS4B    3'  AGTCTGGCCAACATGGTGAAA  18018
                                  TTTCACCATGTTGGCCAGGCT
                                  ||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCTGA

GAM946  WBSCR21   3'  ACCAGCCTGGCCAACATGGTGA 49291                   C
                AA                TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                              C
GAM946  WBSCR23   3'  ACCAGCCTGGCCAACATGGTGA 47406                   C
                AA                TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                              C
GAM946  WSB1     3'  AGCCTGGCAAACATGATGAAA  56961       C     G
                                  TTTCA CATGTT GCCAGGCT
                                  ||||| |||||| ||||||||
                                  AAAGT GTACAA CGGTCCGA
                                    A     A
GAM946  WSB1     3'  AGCCTGGCAAACATGATGAAA  56962       C     G
                                  TTTCA CATGTT GCCAGGCT
                                  ||||| |||||| ||||||||
                                  AAAGT GTACAA CGGTCCGA
                                    A     A
GAM946  YME1L1   3'  ACCAGCCTGGCCAACATGGTGA 58416                  C
                AA                TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
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                                AAAGTGGTACAACCGGTCCGA CA
                                      C
GAM946  YME1L1   3'  AGCCTGGCCAACGTGGTGAAA  58421
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||||
                                AAAGTGGTGCAACCGGTCCGA

GAM946  ZAK      3'  ACCAGCCTGGCCAACATGGTGA 34097                C
            AA                   TTTCACCATGTTGGCCAGGCT GT
                                ||||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                      C
GAM946  ZFP106   3'  ACCAGCCTGGCCAACATAGTGA 42710       C          C
            AA                   TTTCAC ATGTTGGCCAGGCT GT
                                |||||| |||||||||||||| ||
                                AAAGTG TACAACCGGTCCGA CA
                                   A          C
GAM946  ZFP106   3'  ACCAGCCTGGCCAACATGG   42711             C
                                CCATGTTGGCCAGGCT GT
                                |||||||||||||||| ||
                                GGTACAACCGGTCCGA CA
                                     C
GAM946  ZNF197   3'  ACCAGCCTGACCAACATGGTGA 23750            C     C
            AA                   TTTCACCATGTTGG CAGGCT GT
                                |||||||||||||| |||||| ||
                                AAAGTGGTACAACC GTCCGA CA
                                     A     C
GAM946  ZNF271   3'  AGCCTGACCAACATGGTGAAA  96955            C
                                TTTCACCATGTTGG CAGGCT
                                |||||||||||||| ||||||
                                AAAGTGGTACAACC GTCCGA
                                     A
GAM946  ZNF297B  5'  ACCAGCCTGGCCAACATAGTGA 26636       C          C
            AA                   TTTCAC ATGTTGGCCAGGCT GT
                                |||||| |||||||||||||| ||
                                AAAGTG TACAACCGGTCCGA CA
                                   A          C
GAM946  ZNF333   3'  AGCCTGGCCAACATGGTGAAA  51584
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGA

GAM946  ZNF33A   3'  ACCAGCCTGGTCAACATGGTGA 92989                C
            AA                   TTTCACCATGTTGGCCAGGCT GT
                                ||||||||||||||||||||| ||
                                AAAGTGGTACAACTGGTCCGA CA
                                      C
GAM946  ZNF347   3'  ACCAGCCTGACCAACATGGCGA 51816      A       C     C
            AA                   TTTC CCATGTTGG CAGGCT GT
                                |||| ||||||||| |||||| ||
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                                AAAG GGTACAACC GTCCGA CA
                                  C       A    C
GAM946  LOC112687 3'  ACAGCCTGGCCAACATGGTGAA 73215              C
                A                  TTTCACCATGTTGGCCAGGCT GT
                                   |||||||||||||||||||| ||
                                   AAAGTGGTACAACCGGTCCGA CA
                                         C
GAM946  LOC113523 3'  ACCAGCCCGGGCAACATGG   73407       G A   C
                                   CCATGTTG CC GGCT GT
                                   |||||||| || |||| ||
                                   GGTACAAC GG CCGA CA
                                      G C   C
GAM946  LOC115129 5'  ACCAGCCTGGCCAACATGGTGA 73597              C
                                   TCACCATGTTGGCCAGGCT GT
                                   |||||||||||||||||| ||
                                   AGTGGTACAACCGGTCCGA CA
                                         C
GAM946  LOC115129 5'  AGCCTGGCCAACATGGTGAAG  73602
                                   TTTCACCATGTTGGCCAGGCT
                                   ||||||||||||||||||||
                                   GAAGTGGTACAACCGGTCCGA

GAM946  LOC115196 3'  CCTGGCTAACACAGTGAAA   73656       CA
                                   TTTCAC  TGTTGGCCAGG
                                   ||||||  ||||||||||
                                   AAAGTG  ACAATCGGTCC
                                     AC
GAM946  LOC115273 3'  ACCAGCCTGGCCAACATGGTGA 73743              C
                AA                   TTTCACCATGTTGGCCAGGCT GT
                                   |||||||||||||||||||| ||
                                   AAAGTGGTACAACCGGTCCGA CA
                                         C
GAM946  LOC116143 3'  ACCAGCCTGGCCAACATGGTCA 74171    C         C
                AA                   TTT ACCATGTTGGCCAGGCT GT
                                   ||| |||||||||||||||| ||
                                   AAA TGGTACAACCGGTCCGA CA
                                     C           C
GAM946  LOC116143 3'  CCTGGCTAACATGGTGAAA   74183
                                   TTTCACCATGTTGGCCAGG
                                   |||||||||||||||||||
                                   AAAGTGGTACAATCGGTCC

GAM946  LOC116228 3'  ACAGCCTGGCCAACAGGGTGAA 74222       A       C
                A                  TTTCACC TGTTGGCCAGGCT GT
                                   ||||||| |||||||||||| ||
                                   AAAGTGG ACAACCGGTCCGA CA
                                      G
GAM946  LOC116236 3'  CCTGGCTAACACAGTGAAA   74242       CA
                                   TTTCAC  TGTTGGCCAGG
                                   ||||||  ||||||||||
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                                AAAGTG  ACAATCGGTCC
                                   AC
GAM946   LOC116349 3'  CCTGGCTAACATGGTGAAA    74274
                                TTTCACCATGTTGGCCAGG
                                ||||||||||||||||||
                                AAAGTGGTACAATCGGTCC

GAM946   LOC118471 3'  ACCAGCCTGGGCAACATGGTGA 74348           G      C
           AA                     TTTCACCATGTTG CCAGGCT GT
                                  |||||||||||| ||||||| ||
                                  AAAGTGGTACAAC GGTCCGA CA
                                        G      C
GAM946   LOC119504 5'  AGCCTGACCAACATGGAGAAA  74440      A        C
                                TTTC CCATGTTGG CAGGCT
                                |||| ||||||||| ||||||
                                AAAG GGTACAACC GTCCGA
                                  A        A
GAM946   LOC122704 3'  AGCCTGGTCAACATGGTGAAA  74599
                                TTTCACCATGTTGGCCAGGCT
                                ||||||||||||||||||||
                                AAAGTGGTACAACTGGTCCGA

GAM946   LOC124602 3'  ACCAGCCTGGCCAACATGGCGA 74782      A             C
           AA                     TTTC CCATGTTGGCCAGGCT GT
                                  |||| |||||||||||||| ||
                                  AAAG GGTACAACCGGTCCGA CA
                                    C              C
GAM946   LOC126282 3'  CCTGGCCAACATGGTGAAA    74953
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||||
                                AAAGTGGTACAACCGGTCC

GAM946   LOC126282 3'  CCTGGCTAACACGGTGAAA    74954        A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                     C
GAM946   LOC126669 3'  ACCAGCCTGGCCAACATGGTGA 75917                  C
           AA                     TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                           C
GAM946   LOC127262 3'  AGCCTGGGCAACATGGTGAAA  76591           G
                                TTTCACCATGTTG CCAGGCT
                                |||||||||||| |||||||
                                AAAGTGGTACAAC GGTCCGA
                                        G
GAM946   LOC127294 3'  ACCAGCCTGGCCAACATGACGA 75142      AC            C
           AA                     TTTC  CATGTTGGCCAGGCT GT
                                  ||||  |||||||||||||| ||
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                                AAAG  GTACAACCGGTCCGA CA
                                  CA            C
GAM946   LOC127428 3'  ACCAGCCTGGCCAACATGGCGA 75151      A            C
                 AA                 TTTC CCATGTTGGCCAGGCT GT
                                    |||| |||||||||||||||| ||
                                    AAAG GGTACAACCGGTCCGA CA
                                      C             C
GAM946   LOC130026 3'  CCTGGCTAACATGGTGAAA   57436
                                    TTTCACCATGTTGGCCAGG
                                    ||||||||||||||||||
                                    AAAGTGGTACAATCGGTCC

GAM946   LOC130535 3'  CCTGGCCAGCATGGTGAAA   76651
                                    TTTCACCATGTTGGCCAGG
                                    ||||||||||||||||||
                                    AAAGTGGTACGACCGGTCC

GAM946   LOC130589 3'  CCTGGCTAACACGGTGAAA   57930        A
                                    TTTCACC TGTTGGCCAGG
                                    ||||||| ||||||||||
                                    AAAGTGG ACAATCGGTCC
                                       C
GAM946   LOC131744 3'  ACCAGCCTGACCAACATGGTGA 76386            C     C
                 AA                 TTTCACCATGTTGG CAGGCT GT
                                    |||||||||||||| |||||| ||
                                    AAAGTGGTACAACC GTCCGA CA
                                          A     C
GAM946   LOC131965 3'  ACCAGCCTGGCCAACATGGTGA 75514                 C
                 GA                 TTTCACCATGTTGGCCAGGCT GT
                                    |||||||||||||||||||| ||
                                    AGAGTGGTACAACCGGTCCGA CA
                                             C
GAM946   LOC131965 3'  AGTGTGGGCAACATGGTGAAA  75517           G   G
                                    TTTCACCATGTTG CCA GCT
                                    |||||||||||| ||| |||
                                    AAAGTGGTACAAC GGT TGA
                                          G   G
GAM946   LOC133926 3'  CCTGGCTAACACGGTGAAA   75631        A
                                    TTTCACC TGTTGGCCAGG
                                    ||||||| ||||||||||
                                    AAAGTGG ACAATCGGTCC
                                       C
GAM946   LOC134147 3'  ACCAGCCTGGCCAACATGGTGA 57950                 C
                 AA                 TTTCACCATGTTGGCCAGGCT GT
                                    |||||||||||||||||||| ||
                                    AAAGTGGTACAACCGGTCCGA CA
                                             C
GAM946   LOC134147 3'  ACCAGCCTGGCCAACATGGTGA 57951                 C
                 GA                 TTTCACCATGTTGGCCAGGCT GT
                                    |||||||||||||||||||| ||
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                                AGAGTGGTACAACCGGTCCGA CA
                                      C
GAM946  LOC137362 3'  ACAGCCTGGCCAACATGGTGAA 75774                C
            A                  TTTCACCATGTTGGCCAGGCT GT
                               |||||||||||||||||||| ||
                               AAAGTGGTACAACCGGTCCGA CA
                                      C
GAM946  LOC138241 3'  AGCCTGGCCAACATGGCGGAA  75831      A
                               TTTC CCATGTTGGCCAGGCT
                               |||| ||||||||||||||||
                               AAGG GGTACAACCGGTCCGA
                                 C
GAM946  LOC138389 3'  ACCAGCCTGGCCAAAATGATGA 76724      C  G         C
            AA                   TTTCA CAT TTGGCCAGGCT GT
                               ||||| ||| |||||||||| ||
                               AAAGT GTA AACCGGTCCGA CA
                                  A  A         C
GAM946  LOC138428 3'  ACCAGCCTGGCCAACATGGTGA 75851                C
            AA                   TTTCACCATGTTGGCCAGGCT GT
                               |||||||||||||||||||| ||
                               AAAGTGGTACAACCGGTCCGA CA
                                      C
GAM946  LOC139422 3'  CTTGGCTAACACAGTGAAA   76349       CA
                               TTTCAC  TGTTGGCCAGG
                               ||||||  ||||||||||
                               AAAGTG  ACAATCGGTTC
                                  AC
GAM946  LOC142779 3'  CCTGGCCAACATGGTGAAA   76905
                               TTTCACCATGTTGGCCAGG
                               |||||||||||||||||
                               AAAGTGGTACAACCGGTCC

GAM946  LOC142927 3'  ACAGCCTGGGCAACATGGCGAA 76938      A      G      C
            A                  TTTC CCATGTTG CCAGGCT GT
                               |||| |||||||| ||||||| ||
                               AAAG GGTACAAC GGTCCGA CA
                                 C       G
GAM946  LOC142948 3'  CCTGGCCAACATGGTGAAA   83776
                               TTTCACCATGTTGGCCAGG
                               |||||||||||||||||
                               AAAGTGGTACAACCGGTCC

GAM946  LOC143196 3'  CCTGGCCAACATGGTGAAA   83802
                               TTTCACCATGTTGGCCAGG
                               |||||||||||||||||
                               AAAGTGGTACAACCGGTCC

GAM946  LOC143310 3'  CCTGGCTAACATGGTGAAA   77043
                               TTTCACCATGTTGGCCAGG
                               |||||||||||||||||
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                                AAAGTGGTACAATCGGTCC

GAM946  LOC143465 3'  ACAGCCTGGCCAACATGGTGAA 83863                C
                A                TTTCACCATGTTGGCCAGGCT GT
                                 |||||||||||||||||||| ||
                                 AAAGTGGTACAACCGGTCCGA CA
                                           C
GAM946  LOC143888 3'  ACCAGCCTGGCCAACATGGTGA 77163                C
                AA                TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                           C
GAM946  LOC144289 3'  AGCCTGGCCACCATGGTGAAA  83948          T
                                  TTTCACCATG TGGCCAGGCT
                                  |||||||||| ||||||||||
                                  AAAGTGGTAC ACCGGTCCGA
                                        C
GAM946  LOC144465 3'  AGCCTGACCAACATGGAGAAA  77337      A       C
                                  TTTC CCATGTTGG CAGGCT
                                  |||| ||||||||| ||||||
                                  AAAG GGTACAACC GTCCGA
                                    A       A
GAM946  LOC144465 3'  AGCCTGGCCAACATGGAGAAA  77338      A
                                  TTTC CCATGTTGGCCAGGCT
                                  |||| ||||||||||||||||
                                  AAAG GGTACAACCGGTCCGA
                                    A
GAM946  LOC144481 3'  ACCAGCCTGGCCAACATGG    84008              C
                                  CCATGTTGGCCAGGCT GT
                                  |||||||||||||||| ||
                                  GGTACAACCGGTCCGA CA
                                           C
GAM946  LOC144486 3'  ACGACCCTGGCCAACATGGTGA 83999                C
                AA                TTTCACCATGTTGGCCAGG TCGT
                                  |||||||||||||||||| ||||
                                  AAAGTGGTACAACCGGTCC AGCA
                                           C
GAM946  LOC144524 3'  ACTAGCCTGGCCAACACGGTGA 84047        A       C
                AA                TTTCACC TGTTGGCCAGGCT GT
                                  ||||||| |||||||||||| ||
                                  AAAGTGG ACAACCGGTCCGA CA
                                     C          T
GAM946  LOC144563 3'  ACCAGCCTGGCCAACATGGTGA 77388                C
                AA                TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                           C
GAM946  LOC144583 3'  AGCCTGGCCAACATGGTGAAA  77409
                                  TTTCACCATGTTGGCCAGGCT
                                  ||||||||||||||||||||
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                                AAAGTGGTACAACCGGTCCGA

GAM946  LOC144817 3'  CCGGCCAACATAGTGAAA    77514       C       A
                                TTTCAC ATGTTGGCC GG
                                |||||| ||||||||| ||
                                AAAGTG TACAACCGG CC
                                   A
GAM946  LOC144817 3'  CCTGGCTAACACGGTGAAA    77515       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                    C
GAM946  LOC144845 3'  ACCAGCCTGGCCAACATGGT   57448             C
                                ACCATGTTGGCCAGGCT GT
                                |||||||||||||||| ||
                                TGGTACAACCGGTCCGA CA
                                       C
GAM946  LOC145216 3'  ACCAGCCTGACCAACATG    84212       C     C
                                CATGTTGG CAGGCT GT
                                |||||||| |||||| ||
                                GTACAACC GTCCGA CA
                                    A     C
GAM946  LOC145231 3'  ACTAGCCTGACCAACATGGTGA 84236           C     C
          AA                      TTTCACCATGTTGG CAGGCT GT
                                  |||||||||||||| |||||| ||
                                  AAAGTGGTACAACC GTCCGA CA
                                        A     T
GAM946  LOC145387 3'  ACCAGCCTGGCCAATATGGTGA 84324                 C
          AA                      TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTATAACCGGTCCGA CA
                                         C
GAM946  LOC145387 3'  ACCAGCCTGGGCAACATGG    84325       G     C
                                CCATGTTG CCAGGCT GT
                                |||||||| ||||||| ||
                                GGTACAAC GGTCCGA CA
                                    G     C
GAM946  LOC145482 3'  ACCAGCCTGGCCAACACGGTGA 77736       A         C
          AA                      TTTCACC TGTTGGCCAGGCT GT
                                  ||||||| |||||||||||| ||
                                  AAAGTGG ACAACCGGTCCGA CA
                                     C          C
GAM946  LOC145662 3'  ACCAGCCTGGCCAAGATGGTGA 77830         G         C
          AA                      TTTCACCAT TTGGCCAGGCT GT
                                  ||||||||| |||||||||| ||
                                  AAAGTGGTA AACCGGTCCGA CA
                                      G         C
GAM946  LOC145663 3'  CCTGGCTAACATGGTGAAA    84420
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||||
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                                AAAGTGGTACAATCGGTCC

GAM946  LOC145663 3'  CCTGGTCAACATGATGAAA   84421      C
                                TTTCA CATGTTGGCCAGG
                                ||||| ||||||||||||
                                AAAGT GTACAACTGGTCC
                                   A
GAM946  LOC145757 3'  ACCAGCCTGGCCAACATGGTGA 77910                C
                  AA                TTTCACCATGTTGGCCAGGCT GT
                                    |||||||||||||||||||| ||
                                    AAAGTGGTACAACCGGTCCGA CA
                                                 C
GAM946  LOC145820 3'  CCTGGCTAACATGGTGAAA   77976
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||||
                                AAAGTGGTACAATCGGTCC

GAM946  LOC146059 3'  ACAGCCTGGCCAACATGG    78079             C
                                CCATGTTGGCCAGGCT GT
                                |||||||||||||||| ||
                                GGTACAACCGGTCCGA CA
                                          C
GAM946  LOC146332 3'  CCTGGCCAACATGGTGAAA   78355
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||||
                                AAAGTGGTACAACCGGTCC

GAM946  LOC146667 3'  CCTGGCTAACATGGTGAAA   84708
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||||
                                AAAGTGGTACAATCGGTCC

GAM946  LOC146669 3'  ACAGCCTGGCCAACATGGCGAA 78655      A          C
                  A                 TTTC CCATGTTGGCCAGGCT GT
                                    |||| ||||||||||||||| ||
                                    AAAG GGTACAACCGGTCCGA CA
                                      C
GAM946  LOC146713 3'  ACCAGCCTGGCCAACATGGCGA 84719      A          C
                  AA                TTTC CCATGTTGGCCAGGCT GT
                                    |||| ||||||||||||||| ||
                                    AAAG GGTACAACCGGTCCGA CA
                                      C           C
GAM946  LOC146723 3'  AGCCTGGCCAACATGGAGAAA  78673      A
                                TTTC CCATGTTGGCCAGGCT
                                |||| ||||||||||||||||
                                AAAG GGTACAACCGGTCCGA
                                   A
GAM946  LOC146728 5'  ACAGCCTGGCCAACATGGTGAA 84755                C
                  A                 TTTCACCATGTTGGCCAGGCT GT
                                    |||||||||||||||||||| ||
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                                  AAAGTGGTACAACCGGTCCGA CA
                                                      C
GAM946  LOC146756 3'  ACCAGCCTGACCAACATGGTGA 84790            C     C
                AA                  TTTCACCATGTTGG CAGGCT GT
                                    ||||||||||||| |||||| ||
                                    AAAGTGGTACAACC GTCCGA CA
                                              A     C
GAM946  LOC146780 3'  CCTGGCTAACATGGTGAAA   84818
                                    TTTCACCATGTTGGCCAGG
                                    ||||||||||||||||||
                                    AAAGTGGTACAATCGGTCC

GAM946  LOC146895 3'  AGCCTGGCCAACGTGATGAAA  84859      C
                                    TTTCA CATGTTGGCCAGGCT
                                    ||||| |||||||||||||
                                    AAAGT GTGCAACCGGTCCGA
                                       A
GAM946  LOC146901 3'  ACCAGCCTGGCCAACATGGTGA 84879                C
                AA                  TTTCACCATGTTGGCCAGGCT GT
                                    |||||||||||||||||||| ||
                                    AAAGTGGTACAACCGGTCCGA CA
                                                      C
GAM946  LOC147057 3'  CCTGGCCAACACGGTGAAA   84980       A
                                    TTTCACC TGTTGGCCAGG
                                    ||||||| ||||||||||
                                    AAAGTGG ACAACCGGTCC
                                       C
GAM946  LOC147071 3'  CCTGGCTAACATGGTGAAA   73360
                                    TTTCACCATGTTGGCCAGG
                                    ||||||||||||||||||
                                    AAAGTGGTACAATCGGTCC

GAM946  LOC147180 5'  AGCCTGTCCAACATGGTGAAA  85092            C
                                    TTTCACCATGTTGG CAGGCT
                                    ||||||||||||| ||||||
                                    AAAGTGGTACAACC GTCCGA
                                              T
GAM946  LOC147649 3'  CCTGGCCAACACGGTGAAA   79059       A
                                    TTTCACC TGTTGGCCAGG
                                    ||||||| ||||||||||
                                    AAAGTGG ACAACCGGTCC
                                       C
GAM946  LOC147660 3'  CGTCCTGGCTAACACGGTGAAA 79026       A        CT
                                    TTTCACC TGTTGGCCAGG  CG
                                    ||||||| ||||||||||  ||
                                    AAAGTGG ACAATCGGTCC  GC
                                       C         T_
GAM946  LOC147664 3'  AGCCTGACCAACATGGAGAAA  79039      A       C
                                    TTTC CCATGTTGG CAGGCT
                                    |||| ||||||||| ||||||
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                                AAAG GGTACAACC GTCCGA
                                  A       A
GAM946  LOC147727 5'  ACCAGCCTGGCCAACATGGTGA 79118                C
                AA                  TTTCACCATGTTGGCCAGGCT GT
                                    ||||||||||||||||||||| ||
                                    AAAGTGGTACAACCGGTCCGA CA
                                                 C
GAM946  LOC147727 5'  AGCCTGGCCAGCATGGTGAAA  79124
                                    TTTCACCATGTTGGCCAGGCT
                                    ||||||||||||||||||||
                                    AAAGTGGTACGACCGGTCCGA

GAM946  LOC147990 3'  AGCCTGGCCAACATGGTGGAA  85211
                                    TTTCACCATGTTGGCCAGGCT
                                    ||||||||||||||||||||
                                    AAGGTGGTACAACCGGTCCGA

GAM946  LOC148397 3'  AGCCTGACCAACATGGAGAAA  79557      A       C
                                    TTTC CCATGTTGG CAGGCT
                                    |||| ||||||||| ||||||
                                    AAAG GGTACAACC GTCCGA
                                      A       A
GAM946  LOC148534 3'  AGCTTGGCCAACATGGTGAAA  79627
                                    TTTCACCATGTTGGCCAGGCT
                                    ||||||||||||||||||||
                                    AAAGTGGTACAACCGGTTCGA

GAM946  LOC148758 5'  AGTCTGGCCCACATGGTGAAA  79718           T
                                    TTTCACCATGT GGCCAGGCT
                                    |||||||||| |||||||||
                                    AAAGTGGTACA CCGGTCTGA
                                           C
GAM946  LOC148809 5'  ACCAGCCTGGCCAACACAGTGA 79743        CA          C
                AA                  TTTCAC  TGTTGGCCAGGCT GT
                                    ||||||  |||||||||||| ||
                                    AAAGTG  ACAACCGGTCCGA CA
                                       AC          C
GAM946  LOC148809 3'  CTGGCCAACATGGTGGAA    79753
                                    TTTCACCATGTTGGCCAG
                                    ||||||||||||||||
                                    AAGGTGGTACAACCGGTC

GAM946  LOC148918 5'  ACCAGCCTGGCCAACATGGTGA 79812                C
                AA                  TTTCACCATGTTGGCCAGGCT GT
                                    ||||||||||||||||||||| ||
                                    AAAGTGGTACAACCGGTCCGA CA
                                                 C
GAM946  LOC148936 3'  CCTGGCCAACATGGTGAAA   85450
                                    TTTCACCATGTTGGCCAGG
                                    |||||||||||||||||
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                                AAAGTGGTACAACCGGTCC

GAM946  LOC148938 3'  CCTGGCCAACATGGTGAAA   85433
                                TTTCACCATGTTGGCCAGG
                                ||||||||||||||||||
                                AAAGTGGTACAACCGGTCC

GAM946  LOC148946 3'  CCGGCCAACATGGTGAAA    85466              A
                                TTTCACCATGTTGGCC GG
                                |||||||||||||||| ||
                                AAAGTGGTACAACCGG CC
                                      A
GAM946  LOC149073 3'  ACCAGCCTGACCAACATGGCGA 85477     A       C     C
          AA                     TTTC CCATGTTGG CAGGCT GT
                                ||||| ||||||||| |||||| ||
                                AAAG GGTACAACC GTCCGA CA
                                  C       A     C
GAM946  LOC149113 3'  ACAGCCTAGCCAAGATGGTGAA 79894         G    C     C
          A                      TTTCACCAT TTGGC AGGCT GT
                                ||||||||| ||||| ||||| ||
                                AAAGTGGTA AACCG TCCGA CA
                                     G    A    C
GAM946  LOC149113 5'  ACCAGCCTGACCAACATGGTGA 79896            C     C
          AA                     TTTCACCATGTTGG CAGGCT GT
                                |||||||||||||| |||||| ||
                                AAAGTGGTACAACC GTCCGA CA
                                      A     C
GAM946  LOC149194 5'  AGCCTGGCTAACATGGTGAAA  79976
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||||
                                AAAGTGGTACAATCGGTCCGA

GAM946  LOC149271 3'  ACTAGCCTGGTCAACATGGTGA 79992                C
          AA                     TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTACAACTGGTCCGA CA
                                       T
GAM946  LOC149319 3'  ACCAGCCTGGCCAACATGGTGA 80063                C
          AA                     TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                       C
GAM946  LOC149460 3'  ACTAGCCTGGCCAATATGGT   85603            C
                                ACCATGTTGGCCAGGCT GT
                                |||||||||||||||| ||
                                TGGTATAACCGGTCCGA CA
                                       T
GAM946  LOC149464 5'  ACCAGCCTGGGCAACATGGT   85581         G     C
                                ACCATGTTG CCAGGCT GT
                                ||||||||| ||||||| ||
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                                TGGTACAAC GGTCCGA CA
                                     G      C
GAM946   LOC149628 3'  AGTCTGGCCAACATGGTGAAA  80275
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||||
                                AAAGTGGTACAACCGGTCTGA

GAM946   LOC149668 3'  AGCTTGGCCAATATAGTGAAA  85691       C
                                TTTCAC ATGTTGGCCAGGCT
                                ||||||| ||||||||||||||
                                AAAGTG TATAACCGGTTCGA
                                   A
GAM946   LOC149705 3'  ACCAGCCTGGCCAACATGGTGA 85770                C
           AA                     TTTCACCATGTTGGCCAGGCT GT
                                ||||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                        C
GAM946   LOC149705 3'  ACCAGCCTGGCCAACATGGTGA 85771                C
           AA                     TTTCACCATGTTGGCCAGGCT GT
                                ||||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                        C
GAM946   LOC149710 3'  AGCCTGACCAACATGGAGAAA  80328      A       C
                                TTTC CCATGTTGG CAGGCT
                                |||| ||||||||| ||||||
                                AAAG GGTACAACC GTCCGA
                                  A       A
GAM946   LOC150185 3'  AGCCTGACCAACATGGTAGAA  86059      _       C
                                TTC ACCATGTTGG CAGGCT
                                ||| |||||||||| ||||||
                                AAG TGGTACAACC GTCCGA
                                  A       A
GAM946   LOC150299 3'  CCTGGCCAACATGGTGAAA   86166
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||||
                                AAAGTGGTACAACCGGTCC

GAM946   LOC150319 3'  AGCTTGACCAACATGGAGAAA  80461      A       C
                                TTTC CCATGTTGG CAGGCT
                                |||| ||||||||| ||||||
                                AAAG GGTACAACC GTTCGA
                                  A       A
GAM946   LOC150343 3'  AGCCTGGCCAACATGGTGGAA  80488
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||||
                                AAGGTGGTACAACCGGTCCGA

GAM946   LOC150358 3'  ACCAGCCTGGCCAACATGGTGA 86082                C
                                TCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||| ||
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                                AGTGGTACAACCGGTCCGA CA
                                      C
GAM946  LOC150358 3'  CCTGGCTAACACAGTGAAA   86094       CA
                                TTTCAC  TGTTGGCCAGG
                                ||||||  ||||||||||
                                AAAGTG  ACAATCGGTCC
                                   AC
GAM946  LOC150372 3'  AGCCTGGCCAACGTGGTGAAA  80603
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||||
                                AAAGTGGTGCAACCGGTCCGA

GAM946  LOC150481 3'  CCTGGCCAACATGGTGAAA   80697
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||||
                                AAAGTGGTACAACCGGTCC

GAM946  LOC150630 3'  AGCCTGACCAACATGGAGAAA  86286     A       C
                                TTTC CCATGTTGG CAGGCT
                                |||| ||||||||| ||||||
                                AAAG GGTACAACC GTCCGA
                                  A       A
GAM946  LOC150935 3'  ACCAGCCTGGCCAACATGGTGA 80822               C
          AA                      TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                      C
GAM946  LOC150960 3'  ACCAGCCTGGGCAACATGGTGA 80862          G    C
          AA                      TTTCACCATGTTG CCAGGCT GT
                                |||||||||||| ||||||| ||
                                AAAGTGGTACAAC GGTCCGA CA
                                     G    C
GAM946  LOC151196 3'  ACCAGCCTGGCCAACATGGTGA 86445               C
          AA                      TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                      C
GAM946  LOC151429 3'  AGCCTTGCCAACATGGTGAAA  86518          C
                                TTTCACCATGTTGGC AGGCT
                                |||||||||||||| |||||
                                AAAGTGGTACAACCG TCCGA
                                       T
GAM946  LOC151429 3'  CCTGGCTAACACGGTGAAA   86532       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                   C
GAM946  LOC151446 3'  ACAGCCTAGGCAACATGGTGAA 86563          G _   C
          A                       TTTCACCATGTTG CC AGGCT GT
                                |||||||||||| || ||||| ||
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                                AAAGTGGTACAAC GG TCCGA CA
                                      _ A    C
GAM946  LOC151556 3'  ACCAGCCTGGCCAACATGGCGA 81073     A           C
          AA                    TTTC CCATGTTGGCCAGGCT GT
                                |||| |||||||||||||||| ||
                                AAAG GGTACAACCGGTCCGA CA
                                  C            C
GAM946  LOC151602 3'  AGCCTGGCCAACATGGTGAAA  81102
                                TTTCACCATGTTGGCCAGGCT
                                ||||||||||||||||||||
                                AAAGTGGTACAACCGGTCCGA

GAM946  LOC151614 3'  CCTGGCTAACACAGTGAAA   81120       CA
                                TTTCAC  TGTTGGCCAGG
                                ||||||  ||||||||||
                                AAAGTG  ACAATCGGTCC
                                   AC
GAM946  LOC151632 3'  ACCAGCCTGGCCAAAATGGTGA 86636         G         C
          AA                    TTTCACCAT TTGGCCAGGCT GT
                                ||||||||| |||||||||| ||
                                AAAGTGGTA AACCGGTCCGA CA
                                     A          C
GAM946  LOC151720 3'  CCTGGCTAACATGGTGAAA   81150
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||
                                AAAGTGGTACAATCGGTCC

GAM946  LOC151904 3'  ACCAGCCTGGCCAACATGGTGA 81196                 C
          AA                    TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                              C
GAM946  LOC152106 3'  ACCAGCCCAGCCAACATGGCGA 70589      A        CA   C
          AA                    TTTC CCATGTTGGC  GGCT GT
                                |||| ||||||||||  |||| ||
                                AAAG GGTACAACCG  CCGA CA
                                  C         AC   C
GAM946  LOC152283 3'  AGCCTGGTCAACATAGTGAAA  86861       C
                                TTTCAC ATGTTGGCCAGGCT
                                ||||||  ||||||||||||||
                                AAAGTG TACAACTGGTCCGA
                                   A
GAM946  LOC152313 3'  CCTGGCTAACACGGTGAAA   86848        A
                                TTTCACC TGTTGGCCAGG
                                |||||||  ||||||||||
                                AAAGTGG ACAATCGGTCC
                                    C
GAM946  LOC152317 3'  ACCAGCCTGGGCAACATGGTGA 86820           G      C
          AA                    TTTCACCATGTTG CCAGGCT GT
                                |||||||||||||  |||||||  ||
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                                AAAGTGGTACAAC GGTCCGA CA
                                      G      C
GAM946   LOC152426 3'  CCTGGCTAACATGGTGAAA    86894
                                TTTCACCATGTTGGCCAGG
                                ||||||||||||||||||
                                AAAGTGGTACAATCGGTCC

GAM946   LOC152445 3'  ACCAGCCTGGCCAACATGATGA 86924       C            C
           AA                     TTTCA CATGTTGGCCAGGCT GT
                                  ||||| |||||||||||||| ||
                                  AAAGT GTACAACCGGTCCGA CA
                                    A             C
GAM946   LOC152445 3'  AGCCTGACCAACATGGAGAAA  86929      A        C
                                  TTTC CCATGTTGG CAGGCT
                                  |||| ||||||||| ||||||
                                  AAAG GGTACAACC GTCCGA
                                    A        A
GAM946   LOC152627 5'  ACTAGCCTGGCCAACATGGTGA 81498                  C
           AA                     TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                              T
GAM946   LOC152804 3'  ACCAGCCTGGCCAACATGGTGA 87063                  C
           AA                     TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                              C
GAM946   LOC152804 3'  CCTAGTCAACATGGTGAAA    87076             C
                                  TTTCACCATGTTGGC AGG
                                  |||||||||||||| |||
                                  AAAGTGGTACAACTG TCC
                                           A
GAM946   LOC152926 3'  ACAGCCTGGCCAACATGGTGAA 81625                  C
           A                       TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                              C
GAM946   LOC153077 3'  CCTGGCTAACACAGTGAAA    87121        CA
                                  TTTCAC  TGTTGGCCAGG
                                  ||||||  ||||||||||
                                  AAAGTG  ACAATCGGTCC
                                     AC
GAM946   LOC153146 3'  AGCCTGGGCAACATGGTGAAA  87139             G
                                  TTTCACCATGTTG CCAGGCT
                                  |||||||||||| |||||||
                                  AAAGTGGTACAAC GGTCCGA
                                           G
GAM946   LOC153260 3'  ACCAGCCTGACCAACATGGTGA 81665             C     C
           AA                     TTTCACCATGTTGG CAGGCT GT
                                  |||||||||||||| |||||| ||
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                                AAAGTGGTACAACC GTCCGA CA
                                      A     C
GAM946  LOC153338 3'  ACGCCAGCCTGGCCAACATGGT 87191                  __
          GAAA                  TTTCACCATGTTGGCCAGGCT  CGT
                                |||||||||||||||||||||  |||
                                AAAGTGGTACAACCGGTCCGA  GCA
                                      CC
GAM946  LOC153579 3'  AGCCTGGCTAACACAGTGAAA  81762       CA
                                TTTCAC  TGTTGGCCAGGCT
                                ||||||  ||||||||||||
                                AAAGTG  ACAATCGGTCCGA
                                   AC
GAM946  LOC153642 3'  CCTGGCCAACATGGTGAAA   81785
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||||
                                AAAGTGGTACAACCGGTCC

GAM946  LOC153682 3'  CCTGGCTAACACAGTGAAA   87271       CA
                                TTTCAC  TGTTGGCCAGG
                                ||||||  ||||||||||
                                AAAGTG  ACAATCGGTCC
                                   AC
GAM946  LOC153727 3'  CCTGGCCAACATGGTGAAA   87361
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||||
                                AAAGTGGTACAACCGGTCC

GAM946  LOC154089 3'  ACAGCCTAGGCAACATGGTGAA 81937           G _    C
          A                     TTTCACCATGTTG CC AGGCT GT
                                ||||||||||||| || ||||| ||
                                AAAGTGGTACAAC GG TCCGA CA
                                      _ A    C
GAM946  LOC154403 3'  ACCAGCCTAGCCAAGATGGTGA 81961         G    C    C
          AA                      TTTCACCAT TTGGC AGGCT GT
                                |||||||| ||||| ||||| ||
                                AAAGTGGTA AACCG TCCGA CA
                                     G    A    C
GAM946  LOC154403 5'  ACCAGCCTGACCAACATGGTGA 81962           C     C
          AA                      TTTCACCATGTTGG CAGGCT GT
                                |||||||||||||| |||||| ||
                                AAAGTGGTACAACC GTCCGA CA
                                      A     C
GAM946  LOC154739 5'  ACCAGCCTGACCAACATGGTGA 87425           C     C
          AA                      TTTCACCATGTTGG CAGGCT GT
                                |||||||||||||| |||||| ||
                                AAAGTGGTACAACC GTCCGA CA
                                      A     C
GAM946  LOC154992 3'  ACCAGCCTAGCCAAGATGGTGA 82123         G    C    C
          AA                      TTTCACCAT TTGGC AGGCT GT
                                |||||||| ||||| ||||| ||
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                                AAAGTGGTA AACCG TCCGA CA
                                     G    A    C
GAM946  LOC154992 5'  ACCAGCCTGACCAACATGGTGA 82124          C    C
                AA                TTTCACCATGTTGG CAGGCT GT
                                  ||||||||||||| |||||| ||
                                  AAAGTGGTACAACC GTCCGA CA
                                        A    C
GAM946  LOC155006 3'  AGCCTGGCCAACATGGTGAAA  82158
                                  TTTCACCATGTTGGCCAGGCT
                                  |||||||||||||||||||||
                                  AAAGTGGTACAACCGGTCCGA

GAM946  LOC155072 3'  CCTGGCTAACATGGTGAAA   87660
                                  TTTCACCATGTTGGCCAGG
                                  ||||||||||||||||||
                                  AAAGTGGTACAATCGGTCC

GAM946  LOC155072 3'  CCTGGCTAACATGGTGAAA   87661
                                  TTTCACCATGTTGGCCAGG
                                  ||||||||||||||||||
                                  AAAGTGGTACAATCGGTCC

GAM946  LOC155376 3'  ACCAGCCTGGCCAACATGGTGA 82235                C
                AA                TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                        C
GAM946  LOC157292 5'  AGCCTGGCCAACTTGGTGAAA  87695        T
                                  TTTCACCA GTTGGCCAGGCT
                                  |||||||| ||||||||||||
                                  AAAGTGGT CAACCGGTCCGA
                                       T
GAM946  LOC157464 5'  ACCAGCCTGGCCAACATGG   87741             C
                                  CCATGTTGGCCAGGCT GT
                                  |||||||||||||| ||
                                  GGTACAACCGGTCCGA CA
                                        C
GAM946  LOC157657 3'  ACCAGCCTGGCCAACATG    82426             C
                                  CATGTTGGCCAGGCT GT
                                  |||||||||||||| ||
                                  GTACAACCGGTCCGA CA
                                        C
GAM946  LOC157660 3'  ACCAGCCTGACCAACATGGTGA 87797          C    C
                AA                TTTCACCATGTTGG CAGGCT GT
                                  ||||||||||||| |||||| ||
                                  AAAGTGGTACAACC GTCCGA CA
                                        A    C
GAM946  LOC157983 3'  CCTGGCCAACGTGGTGAAA   82540
                                  TTTCACCATGTTGGCCAGG
                                  ||||||||||||||||||
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                                AAAGTGGTGCAACCGGTCC

GAM946  LOC158191 3'  CCTGGCCAACATGGTGAAA   82669
                                TTTCACCATGTTGGCCAGG
                                ||||||||||||||||||
                                AAAGTGGTACAACCGGTCC

GAM946  LOC158288 3'  CCTGGCTAACACAGTGAAA   88019       CA
                                TTTCAC  TGTTGGCCAGG
                                ||||||  ||||||||||
                                AAAGTG  ACAATCGGTCC
                                   AC
GAM946  LOC158292 5'  ACCAGCCTAGCCAACATGCTGA 88032      C       C    C
           AA                     TTTCA CATGTTGGC AGGCT GT
                                ||||| ||||||||| ||||| ||
                                AAAGT GTACAACCG TCCGA CA
                                   C       A    C
GAM946  LOC158292 5'  CCTGGCTAACACGGTGAAA   88047       A
                                TTTCACC TGTTGGCCAGG
                                |||||||  ||||||||||
                                AAAGTGG ACAATCGGTCC
                                    C
GAM946  LOC158677 5'  ACCAGCCTGGCCAACATGGCGA 88241     A            C
           AA                     TTTC CCATGTTGGCCAGGCT GT
                                ||||  ||||||||||||||| ||
                                AAAG GGTACAACCGGTCCGA CA
                                  C             C
GAM946  LOC158819 5'  ACCAGCCTGGCCAACATGGTGA 88261                 C
           AA                     TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                             C
GAM946  LOC158819 3'  ACCAGCCTGGCCAAGATGGTGA 88262         G         C
           AA                     TTTCACCAT TTGGCCAGGCT GT
                                |||||||| |||||||||| ||
                                AAAGTGGTA AACCGGTCCGA CA
                                     G         C
GAM946  LOC158863 3'  AGCCTGGCCAGCATAGTGAAA  88294       C
                                TTTCAC ATGTTGGCCAGGCT
                                ||||||  ||||||||||||||
                                AAAGTG TACGACCGGTCCGA
                                   A
GAM946  LOC158987 3'  ACCAGCCTGGCCAACATGGTGA 88317                 C
           AA                     TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                             C
GAM946  LOC159036 3'  ACCAGCCTGACCAATATGGTGA 88338           C     C
           AA                     TTTCACCATGTTGG CAGGCT GT
                                ||||||||||||||  |||||| ||
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                                AAAGTGGTATAACC GTCCGA CA
                                      A     C
GAM946  LOC159053 3'  ACAGCCTGGCCAACATGGTGAA 88354                C
              A                  TTTCACCATGTTGGCCAGGCT GT
                                 |||||||||||||||||||| ||
                                 AAAGTGGTACAACCGGTCCGA CA
                                       C
GAM946  LOC159053 3'  CCTGGCTAACACGGTGAAA   88369       A
                                 TTTCACC TGTTGGCCAGG
                                 ||||||| ||||||||||
                                 AAAGTGG ACAATCGGTCC
                                    C
GAM946  LOC159110 3'  ACCAGCCTGGCCAACATGGTGA 82982                C
              AA                   TTTCACCATGTTGGCCAGGCT GT
                                   |||||||||||||||||||| ||
                                   AAAGTGGTACAACCGGTCCGA CA
                                         C
GAM946  LOC159116 3'  ACCAGCCTGGCCAACATGGTGA 82965                C
              AA                   TTTCACCATGTTGGCCAGGCT GT
                                   |||||||||||||||||||| ||
                                   AAAGTGGTACAACCGGTCCGA CA
                                         C
GAM946  LOC170395 3'  AGCCTGGCCAACATGGAGAAA  76861      A
                                 TTTC CCATGTTGGCCAGGCT
                                 |||| ||||||||||||||
                                 AAAG GGTACAACCGGTCCGA
                                   A
GAM946  LOC196047 5'  ACCAGCCTGGCCAACATGGTGA 91136                C
              AA                   TTTCACCATGTTGGCCAGGCT GT
                                   |||||||||||||||||||| ||
                                   AAAGTGGTACAACCGGTCCGA CA
                                         C
GAM946  LOC196540 3'  ACCAGCCTGGACAACATGGTGA 91194          G     C
              AA                   TTTCACCATGTTG CCAGGCT GT
                                   |||||||||||| ||||||| ||
                                   AAAGTGGTACAAC GGTCCGA CA
                                         A     C
GAM946  LOC197196 3'  ACCAGCCTGGCCAACATGATGA 91289      C          C
              AA                   TTTCA CATGTTGGCCAGGCT GT
                                   ||||| |||||||||||||| ||
                                   AAAGT GTACAACCGGTCCGA CA
                                     A           C
GAM946  LOC197196 3'  ACCAGCCTGGCCAACATGATGA 91290      C          C
              AA                   TTTCA CATGTTGGCCAGGCT GT
                                   ||||| |||||||||||||| ||
                                   AAAGT GTACAACCGGTCCGA CA
                                     A           C
GAM946  LOC197201 3'  ACAGCCTGGGCAACATGGCGAA 89259      A     G     C
              A                    TTTC CCATGTTG CCAGGCT GT
                                   |||| |||||||| ||||||| ||
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                                AAAG GGTACAAC GGTCCGA CA
                                  C       G
GAM946   LOC197201 3'  AGCCTGACCAACATGGAGAAA  89263      A       C
                                TTTC CCATGTTGG CAGGCT
                                |||| ||||||||| ||||||
                                AAAG GGTACAACC GTCCGA
                                  A       A
GAM946   LOC197319 3'  CCTGGCCAACACAGTGAAA   89318       CA
                                TTTCAC  TGTTGGCCAGG
                                ||||||  ||||||||||
                                AAAGTG  ACAACCGGTCC
                                   AC
GAM946   LOC197319 3'  CCTGGCCAACATGGTGAAA   89320
                                TTTCACCATGTTGGCCAGG
                                ||||||||||||||||||
                                AAAGTGGTACAACCGGTCC

GAM946   LOC199733 3'  ACCAGCCCAGGCAACATGGTGA 91429           G  A_   C
           AA                     TTTCACCATGTTG CC  GGCT GT
                                |||||||||||| ||  |||| ||
                                AAAGTGGTACAAC GG  CCGA CA
                                       _ AC   C
GAM946   LOC199733 3'  CCTGGCTAACATGGTGAAA   91438
                                TTTCACCATGTTGGCCAGG
                                ||||||||||||||||||
                                AAAGTGGTACAATCGGTCC

GAM946   LOC199858 3'  CCTGGCTAACACGGCGAAA   89796     A  A
                                TTTC CC TGTTGGCCAGG
                                |||| || ||||||||||
                                AAAG GG ACAATCGGTCC
                                  C  C
GAM946   LOC200014 3'  ACCAGCCTGGCCAACATGGTGA 89911                C
           AA                     TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                          C
GAM946   LOC200251 3'  AGCTTGACCAACATGGTGAAA  90057           C
                                TTTCACCATGTTGG CAGGCT
                                |||||||||||| ||||||
                                AAAGTGGTACAACC GTTCGA
                                       A
GAM946   LOC200728 3'  CCTGGCTAACACGGTGAAA   91683       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                   C
GAM946   LOC200731 3'  AGCCTTACCAACATGATGAAA  91689      C       CC
                                TTTCA CATGTTGG  AGGCT
                                ||||| ||||||||  |||||
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                                AAAGT GTACAACC  TCCGA
                                  A       AT
GAM946   LOC200803 3'  ACCAGCCTGGCCAACATGGTGA 90294                C
                 AA                TTTCACCATGTTGGCCAGGCT GT
                                   |||||||||||||||||||| ||
                                   AAAGTGGTACAACCGGTCCGA CA
                                                C
GAM946   LOC200904 3'  AGCCTGACCAACGTGGTGAAA  91772           C
                                   TTTCACCATGTTGG CAGGCT
                                   |||||||||||||| ||||||
                                   AAAGTGGTGCAACC GTCCGA
                                            A
GAM946   LOC200918 3'  ACCAGCCTGGCCAACATGGTGA 90362                C
                 AA                TTTCACCATGTTGGCCAGGCT GT
                                   |||||||||||||||||||| ||
                                   AAAGTGGTACAACCGGTCCGA CA
                                                C
GAM946   LOC200940 3'  ACCAGCCTGGCCAACATAGCGA 90382      ACC          C
                 AA                TTTC   ATGTTGGCCAGGCT GT
                                   ||||   |||||||||||||| ||
                                   AAAG   TACAACCGGTCCGA CA
                                     CGA           C
GAM946   LOC201173 3'  CCTGGCTAACATGGTGAAA    88680
                                   TTTCACCATGTTGGCCAGG
                                   |||||||||||||||||
                                   AAAGTGGTACAATCGGTCC

GAM946   LOC201182 5'  AGCCTGGCCAACATTGTGAAA  91331       C
                                   TTTCAC ATGTTGGCCAGGCT
                                   |||||| ||||||||||||||
                                   AAAGTG TACAACCGGTCCGA
                                      T
GAM946   LOC201220 3'  CCTGGCTAACATGGTGAAA    88715
                                   TTTCACCATGTTGGCCAGG
                                   |||||||||||||||||
                                   AAAGTGGTACAATCGGTCC

GAM946   LOC201627 3'  ACCAGCCTGGCCAACATGGTGA 90444                C
                 AA                TTTCACCATGTTGGCCAGGCT GT
                                   |||||||||||||||||||| ||
                                   AAAGTGGTACAACCGGTCCGA CA
                                                C
GAM946   LOC201810 3'  ACAGCCTGACCAACATGGTGAA 90497           C    C
                 A                  TTTCACCATGTTGG CAGGCT GT
                                   |||||||||||||| |||||| ||
                                   AAAGTGGTACAACC GTCCGA CA
                                            A    C
GAM946   LOC201868 3'  ACCAGCCTAGCCAAGATGGTGA 90510        G   C   C
                 AA                TTTCACCAT TTGGC AGGCT GT
                                   |||||||| ||||| ||||| ||
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                                AAAGTGGTA AACCG TCCGA CA
                                    G    A    C
GAM946  LOC201868 5'  ACCAGCCTGACCAACATGGTGA 90511          C     C
                AA                TTTCACCATGTTGG CAGGCT GT
                                  ||||||||||||| |||||| ||
                                  AAAGTGGTACAACC GTCCGA CA
                                       A     C
GAM946  LOC201895 3'  ACCAGCCTGGCCAACATGGTGA 90537              C
                AA                TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                        C
GAM946  LOC201911 3'  AGCCTGACCAACATGGAGAAA  91859     A      C
                                  TTTC CCATGTTGG CAGGCT
                                  |||| ||||||||| ||||||
                                  AAAG GGTACAACC GTCCGA
                                    A       A
GAM946  LOC201931 3'  CCTGGCTAACACGGTGAAA   90564       A
                                  TTTCACC TGTTGGCCAGG
                                  ||||||| ||||||||||
                                  AAAGTGG ACAATCGGTCC
                                     C
GAM946  LOC202020 3'  ACCAGCCTGGCCAACATAGTGA 90594      C          C
                AA                TTTCAC ATGTTGGCCAGGCT GT
                                  |||||| |||||||||||| ||
                                  AAAGTG TACAACCGGTCCGA CA
                                     A          C
GAM946  LOC202038 3'  CCTGGCTAACACGGTGAAA   90621       A
                                  TTTCACC TGTTGGCCAGG
                                  ||||||| ||||||||||
                                  AAAGTGG ACAATCGGTCC
                                     C
GAM946  LOC202052 3'  ACCAGCCTGGCCAACACAGTGA 91894      CA         C
                AA                TTTCAC  TGTTGGCCAGGCT GT
                                  ||||||  |||||||||||| ||
                                  AAAGTG  ACAACCGGTCCGA CA
                                     AC          C
GAM946  LOC202134 5'  ACCGGCCTGGCCAACATGGTGA 91913              C
                AA                TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGG CA
                                        C
GAM946  LOC202868 3'  CCTGGCTAACATGGTGAAA   91997
                                  TTTCACCATGTTGGCCAGG
                                  |||||||||||||||||
                                  AAAGTGGTACAATCGGTCC

GAM946  LOC202868 3'  CCTGGCTAACATGGTGAAA   91998
                                  TTTCACCATGTTGGCCAGG
                                  |||||||||||||||||
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                                AAAGTGGTACAATCGGTCC

GAM946  LOC203025 3'  ACCAGCCTGGCCAACATGGTGA 90736                C
                AA                TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                                C
GAM946  LOC203083 3'  ACCAGCCTGGCCAACATGGTGA 92078                C
                AA                TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                                C
GAM946  LOC203276 3'  CCTGGCCAACATGGTGAAA   92120
                                  TTTCACCATGTTGGCCAGG
                                  |||||||||||||||||||
                                  AAAGTGGTACAACCGGTCC

GAM946  LOC203289 3'  CCTGGCCAACGTGGTGAAA   90867
                                  TTTCACCATGTTGGCCAGG
                                  |||||||||||||||||||
                                  AAAGTGGTGCAACCGGTCC

GAM946  LOC203305 3'  CCTGGCCAACATGGTGAAA   92173
                                  TTTCACCATGTTGGCCAGG
                                  |||||||||||||||||||
                                  AAAGTGGTACAACCGGTCC

GAM946  LOC203378 3'  ACCAGCCTGGCCAACATGG   92269              C
                                  CCATGTTGGCCAGGCT GT
                                  |||||||||||||||| ||
                                  GGTACAACCGGTCCGA CA
                                              C
GAM946  LOC203378 3'  AGCCTGGCAAACATGGCGAAA  92272      A      G
                                  TTTC CCATGTT GCCAGGCT
                                  |||| ||||||| ||||||||
                                  AAAG GGTACAA CGGTCCGA
                                    C      A
GAM946  LOC203397 3'  ACCAGCCTGGCCAACATGGCGA 90895      A            C
                AA                TTTC CCATGTTGGCCAGGCT GT
                                  |||| |||||||||||||| ||
                                  AAAG GGTACAACCGGTCCGA CA
                                    C             C
GAM946  LOC219376 3'  ACAGCCTGGCCAACATGGTGAA 95510                C
                A                 TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                                C
GAM946  LOC219540 3'  AGCTTGGCCAACATGGCGAAA  95238      A
                                  TTTC CCATGTTGGCCAGGCT
                                  |||| ||||||||||||||||
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                                AAAG GGTACAACCGGTTCGA
                                  C
GAM946  LOC219627 3'  AGCCTGACCAACATGGAGAAA  93794      A       C
                                TTTC CCATGTTGG CAGGCT
                                |||| ||||||||| ||||||
                                AAAG GGTACAACC GTCCGA
                                  A       A
GAM946  LOC219627 3'  CCTGGCCAACATGGTGAAA   93805
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||||
                                AAAGTGGTACAACCGGTCC

GAM946  LOC219649 3'  ACCAGCCTGGCCAACATGGTGA 94537                C
          AA                    TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                        C
GAM946  LOC219649 3'  CCTGGCTAACACGGTGAAA   94550       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                   C
GAM946  LOC219722 5'  ACAGCCTGACCAACATGGTGAA 94671          C     C
          A                     TTTCACCATGTTGG CAGGCT GT
                                |||||||||||| |||||| ||
                                AAAGTGGTACAACC GTCCGA CA
                                      A     T
GAM946  LOC220370 3'  ACCAGCCTGGCCAACATGGTGA 94390                C
          AA                    TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                        C
GAM946  LOC220575 3'  ACAGCCTGGGCAACATGGTGAA 76809          G     C
          A                     TTTCACCATGTTG CCAGGCT GT
                                |||||||||||| ||||||| ||
                                AAAGTGGTACAAC GGTCCGA CA
                                      G     C
GAM946  LOC220662 3'  AGCCTGGCCAACGTGGTGAAA  92802
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||||
                                AAAGTGGTGCAACCGGTCCGA

GAM946  LOC221042 3'  TCTGGCCAACATGGTGAAA   94808
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||||
                                AAAGTGGTACAACCGGTCT

GAM946  LOC221271 3'  CCTGGCTAACACAGTGAAA   93509       CA
                                TTTCAC  TGTTGGCCAGG
                                ||||||  ||||||||||
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                                AAAGTG  ACAATCGGTCC
                                   AC
GAM946  LOC221271 3'  CCTGGCTAACACGGTGAAA   93510       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                   C
GAM946  LOC221410 3'  CCTGGCTAACATGGTGAAA   93693
                                TTTCACCATGTTGGCCAGG
                                ||||||||||||||||||
                                AAAGTGGTACAATCGGTCC

GAM946  LOC221474 3'  AGCCTGGCCAACATAGGGAAA  93987     A _
                                TTTC CC ATGTTGGCCAGGCT
                                |||| || ||||||||||||||
                                AAAG GG TACAACCGGTCCGA
                                  _ A
GAM946  LOC221477 3'  ACCAGCCTGGCCAACAGGGTGA 93761       A         C
           AA                     TTTCACC TGTTGGCCAGGCT GT
                                ||||||| |||||||||||||| ||
                                AAAGTGG ACAACCGGTCCGA CA
                                   G          C
GAM946  LOC221490 3'  ACCAGCCTGACCAATATGGTGA 95295           C     C
           AA                     TTTCACCATGTTGG CAGGCT GT
                                |||||||||||||| |||||| ||
                                AAAGTGGTATAACC GTCCGA CA
                                      A     C
GAM946  LOC221543 3'  ACCAGCCTGGCCAACATGGTGA 95353                 C
           AA                     TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                      C
GAM946  LOC221543 3'  ACCAGCCTGGCCAACATGGTGA 95354                 C
           AA                     TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                      C
GAM946  LOC221543 5'  CCTGGCTAACACGGTGAAA   95371       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                   C
GAM946  LOC221550 3'  ACCAGCCTGGCCAACATGG   93741             C
                                CCATGTTGGCCAGGCT GT
                                |||||||||||||||| ||
                                GGTACAACCGGTCCGA CA
                                      C
GAM946  LOC221641 5'  ACCAGCCTGACCAACATGGTGA 95337           C     C
           AA                     TTTCACCATGTTGG CAGGCT GT
                                |||||||||||||| |||||| ||
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                                AAAGTGGTACAACC GTCCGA CA
                                      A     C
GAM946  LOC221795 3'  ACCAGCCTGGACAACATGGTGA 94064          G     C
                AA              TTTCACCATGTTG CCAGGCT GT
                                |||||||||||| ||||||| ||
                                AAAGTGGTACAAC GGTCCGA CA
                                      A     C
GAM946  LOC221943 5'  ACCAGCCTGGCCAACATGGCGA 95614     A          C
                AA              TTTC CCATGTTGGCCAGGCT GT
                                |||| ||||||||||||||| ||
                                AAAG GGTACAACCGGTCCGA CA
                                  C           C
GAM946  LOC221954 5'  ACCAGCCTGGCCAACATGGTGA 95636               C
                AA              TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                      C
GAM946  LOC222060 5'  ACCAGCCTGGTCAACATGGTGA 95747               C
                AA              TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTACAACTGGTCCGA CA
                                      C
GAM946  LOC222160 5'  CCTGGCTAACACGGTGAAA  95782       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                    C
GAM946  LOC222182 3'  ACCAGCCTGGCCAACATGGTGA 95850               C
                AA              TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                      C
GAM946  LOC222865 3'  CCTGGCTAACACGGTGAAA  94444       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                    C
GAM946  LOC253532 3'  ACAGCCTGGCCAACATGGTGAA 97724               C
                A               TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                      C
GAM946  LOC253612 5'  ACCAGCCTGACCAACATGGTGA 98541          C    C
                AA              TTTCACCATGTTGG CAGGCT GT
                                |||||||||||||| |||||| ||
                                AAAGTGGTACAACC GTCCGA CA
                                      A     C
GAM946  LOC253778 5'  ACCAGCCTGGCCAACATGGTGA 96521               C
                AA              TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
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                                AAAGTGGTACAACCGGTCCGA CA
                                           C
GAM946  LOC253840 3'  CTGGCCAACATGGAGAAA    97912      A
                                TTTC CCATGTTGGCCAG
                                |||| ||||||||||||
                                AAAG GGTACAACCGGTC
                                   A
GAM946  LOC253927 3'  CCTGGCAAACATGGTGAAA   96728           G
                                TTTCACCATGTT GCCAGG
                                |||||||||||| ||||||
                                AAAGTGGTACAA CGGTCC
                                      A
GAM946  LOC254041 5'  CCTGGCCAACATGGGGAAA   96555      A
                                TTTC CCATGTTGGCCAGG
                                |||| ||||||||||||||
                                AAAG GGTACAACCGGTCC
                                   G
GAM946  LOC254045 3'  ACAGCCTGGCCAACATGG    98257             C
                                CCATGTTGGCCAGGCT GT
                                |||||||||||||||| ||
                                GGTACAACCGGTCCGA CA
                                      C
GAM946  LOC254100 3'  ACCAGCCTGGCCAACATAGTGA 98145       C          C
          AA                      TTTCAC ATGTTGGCCAGGCT GT
                                |||||| |||||||||||||| ||
                                AAAGTG TACAACCGGTCCGA CA
                                   A          C
GAM946  LOC254176 3'  ACCAGCCTGGCCAACATGGTGA 99159                C
          AA                      TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                           C
GAM946  LOC254243 3'  CCTGGCCAACATGGTGAAA   99259
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||
                                AAAGTGGTACAACCGGTCC

GAM946  LOC254249 5'  ACCAGCCTGGGCAACATGGTGA 97179           G     C
          AA                      TTTCACCATGTTG CCAGGCT GT
                                |||||||||||| ||||||| ||
                                AAAGTGGTACAAC GGTCCGA CA
                                      G     C
GAM946  LOC254266 3'  CCTGGCTAACACAGTGAAA   99199       CA
                                TTTCAC  TGTTGGCCAGG
                                ||||||  ||||||||||
                                AAAGTG  ACAATCGGTCC
                                   AC
GAM946  LOC254351 3'  GCCTGGGCAACATGGTGAAA  96691           G
                                TTTCACCATGTTG CCAGGC
                                |||||||||||| ||||||
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                                AAAGTGGTACAAC GGTCCG
                                      G
GAM946  LOC254531 5'  ACCAGCCTGACCAACATGG   96657        C     C
                                CCATGTTGG CAGGCT GT
                                ||||||||| |||||| ||
                                GGTACAACC GTCCGA CA
                                    A     C
GAM946  LOC254808 3'  CCTGGCTAACACGGTGAAA   98805       A
                                TTTCACC TGTTGGCCAGG
                                ||||||| ||||||||||
                                AAAGTGG ACAATCGGTCC
                                   C
GAM946  LOC254875 3'  ACCAGCCTGGCCAACATGGTGA 97768                C
          AA                     TTTCACCATGTTGGCCAGGCT GT
                                ||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                          C
GAM946  LOC255042 3'  ACAGCCTGGCCAATACGATGAA 97024      CCA          C
          A                      TTTCA   TGTTGGCCAGGCT GT
                                |||||   |||||||||||| ||
                                AAAGT   ATAACCGGTCCGA CA
                                   AGC
GAM946  LOC255042 3'  ACCAGCCTGGACAACATGGTGA 97026           G      C
          AA                     TTTCACCATGTTG CCAGGCT GT
                                |||||||||||| ||||||| ||
                                AAAGTGGTACAAC GGTCCGA CA
                                      A      C
GAM946  LOC255177 3'  AGCCAGACCAACATGATGAAA  98386      C       CCA
                                TTTCA CATGTTGG   GGCT
                                ||||| ||||||||   ||||
                                AAAGT GTACAACC   CCGA
                                   A       AGA
GAM946  LOC255196 3'  AGCCGGGCCAACATGGTGAAA  98947              A
                                TTTCACCATGTTGGCC GGCT
                                |||||||||||||| ||||
                                AAAGTGGTACAACCGG CCGA
                                         G
GAM946  LOC255231 3'  ACCAGCCTGGGCAACATGG    97113        G      C
                                CCATGTTG CCAGGCT GT
                                |||||||| ||||||| ||
                                GGTACAAC GGTCCGA CA
                                     G      C
GAM946  LOC255252 3'  AGCGTGGCCAACATGAGGAAA  96704      AC         G
                                TTTC  CATGTTGGCCA GCT
                                ||||  |||||||||| |||
                                AAAG  GTACAACCGGT CGA
                                   GA          G
GAM946  LOC255328 3'  ACCAGCCTGGCCAACATGGCGA 98330      A            C
          AA                     TTTC CCATGTTGGCCAGGCT GT
                                |||| |||||||||||||| ||
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                                AAAG GGTACAACCGGTCCGA CA
                                  C            C
GAM946  LOC255671 3'  ACAGCCTGGCCCACATGGTGAA 99059          T       C
                A                  TTTCACCATGT GGCCAGGCT GT
                                   |||||||||| ||||||||| ||
                                   AAAGTGGTACA CCGGTCCGA CA
                                         C       C
GAM946  LOC255937 3'  ACCAGCCTGACCAACATGGTGA 97675            C     C
                AA                  TTTCACCATGTTGG CAGGCT GT
                                    |||||||||||||| |||||| ||
                                    AAAGTGGTACAACC GTCCGA CA
                                          A     C
GAM946  LOC255971 3'  AGTCTGGCCAATATGGTGAAA  98307
                                    TTTCACCATGTTGGCCAGGCT
                                    ||||||||||||||||||||
                                    AAAGTGGTATAACCGGTCTGA

GAM946  LOC256267 3'  ACAGCCTGGCCAACATGGTGAA 98602                 C
                A                  TTTCACCATGTTGGCCAGGCT GT
                                   |||||||||||||||||||| ||
                                   AAAGTGGTACAACCGGTCCGA CA
                                               C
GAM946  LOC256277 3'  ACCAGCCTGGCCAACATGGTGA 96347                  C
                AA                  TTTCACCATGTTGGCCAGGCT GT
                                    |||||||||||||||||||| ||
                                    AAAGTGGTACAACCGGTCCGA CA
                                               C
GAM946  LOC256515 3'  ACCAGCCTGGCCAACATGGTGA 98201                  C
                AA                  TTTCACCATGTTGGCCAGGCT GT
                                    |||||||||||||||||||| ||
                                    AAAGTGGTACAACCGGTCCGA CA
                                               C
GAM946  LOC256520 3'  ACAGCCTGGCCAACATGGTGAA 97659                  C
                A                  TTTCACCATGTTGGCCAGGCT GT
                                   |||||||||||||||||||| ||
                                   AAAGTGGTACAACCGGTCCGA CA
                                               C
GAM946  LOC256544 3'  CCTGGCCAACGTGGTGAAA    97931
                                   TTTCACCATGTTGGCCAGG
                                   |||||||||||||||||
                                   AAAGTGGTGCAACCGGTCC

GAM946  LOC257180 3'  ACTAGCCTGGCCAACATAGTGA 97311        C           C
                AA                  TTTCAC ATGTTGGCCAGGCT GT
                                    |||||| |||||||||||||| ||
                                    AAAGTG TACAACCGGTCCGA CA
                                       A           T
GAM946  LOC257495 3'  ACCAGCCTGGCCAACATGG    99568              C
                                   CCATGTTGGCCAGGCT GT
                                   |||||||||||||||| ||
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                                  GGTACAACCGGTCCGA CA
                                        C
GAM946  LOC257539 3'  CCTGGCTAACACGGTGAAA   99547       A
                                  TTTCACC TGTTGGCCAGG
                                  ||||||| ||||||||||
                                  AAAGTGG ACAATCGGTCC
                                     C
GAM946  LOC257576 3'  ACCAGCCTGGCCAACATGG   99705            C
                                  CCATGTTGGCCAGGCT GT
                                  |||||||||||||||| ||
                                  GGTACAACCGGTCCGA CA
                                        C
GAM946  LOC257578 3'  CCTGGCTAACACGGTGAAA   99659       A
                                  TTTCACC TGTTGGCCAGG
                                  ||||||| ||||||||||
                                  AAAGTGG ACAATCGGTCC
                                     C
GAM946  LOC257596 3'  ACAGCCTGGCCAACATGGTGAA 99755               C
          A                        TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                           C
GAM946  LOC257596 3'  ACCAGCCTGGCCAACATGGTGA 99757               C
          AA                       TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                           C
GAM946  LOC257596 5'  CCTGGCTAACACGGTGAAA   99774       A
                                  TTTCACC TGTTGGCCAGG
                                  ||||||| ||||||||||
                                  AAAGTGG ACAATCGGTCC
                                     C
GAM946  LOC51122  3'  CCTGGCTAACATGGTGAAA   66194
                                  TTTCACCATGTTGGCCAGG
                                  ||||||||||||||||||
                                  AAAGTGGTACAATCGGTCC

GAM946  LOC51145  3'  ACAGCCTGGCCAACATGGTGAA 32915               C
          A                        TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                           C
GAM946  LOC51279  3'  CCTGGCCAACATGGTGAAA   33753
                                  TTTCACCATGTTGGCCAGG
                                  ||||||||||||||||||
                                  AAAGTGGTACAACCGGTCC

GAM946  LOC51333  3'  ACCAGCCTGGCCAACATGGTGA 34048               C
          AA                       TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
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                                AAAGTGGTACAACCGGTCCGA CA
                                           C
GAM946  LOC51759  3' AGCCTGACCAACATGGAGAAA  73167      A        C
                                TTTC CCATGTTGG CAGGCT
                                |||| ||||||||| ||||||
                                AAAG GGTACAACC GTCCGA
                                  A        A
GAM946  LOC55974  3' CCTGACTAACATGGTGAAA    38744              C
                                TTTCACCATGTTGG CAGG
                                |||||||||||||| ||||
                                AAAGTGGTACAATC GTCC
                                       A
GAM946  LOC57118  3' ACCAGCCTGACCAACATGGTGA 40212              C     C
          AA                      TTTCACCATGTTGG CAGGCT GT
                                |||||||||||||| |||||| ||
                                AAAGTGGTACAACC GTCCGA CA
                                       A     C
GAM946  LOC63929  3' AGCCTGGCCAACGTGGTGAAA  42277
                                TTTCACCATGTTGGCCAGGCT
                                |||||||||||||||||||||
                                AAAGTGGTGCAACCGGTCCGA

GAM946  LOC85479  5' CCTGGCTAACACAGTGAAA    53563        CA
                                TTTCAC  TGTTGGCCAGG
                                ||||||  ||||||||||
                                AAAGTG  ACAATCGGTCC
                                   AC
GAM946  LOC89890  3' ACCAGCCTGGCCAACATGGTGA 61199                  C
          AA                      TTTCACCATGTTGGCCAGGCT GT
                                |||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                           C
GAM946  LOC90038  3' CCTGGCCAACATGGTGAAA    61802
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||
                                AAAGTGGTACAACCGGTCC

GAM946  LOC90092  3' ACAGCCTGGCCAACATAATGAA 62048       CC           C
          A                      TTTCA  ATGTTGGCCAGGCT GT
                                |||||  |||||||||||||| ||
                                AAAGT  TACAACCGGTCCGA CA
                                   AA
GAM946  LOC90092  3' ACCAGCCTGGCCAACATGG    62050              C
                                CCATGTTGGCCAGGCT GT
                                |||||||||||||||| ||
                                GGTACAACCGGTCCGA CA
                                       C
GAM946  LOC90155  5' AGCCTGGCCAACATGGTGAA   62360
                                TTCACCATGTTGGCCAGGCT
                                ||||||||||||||||||||
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                                AAGTGGTACAACCGGTCCGA

GAM946  LOC90233  3'  ACCAGCCTGGGCAACATGGTGA 57187          G      C
                AA                TTTCACCATGTTG CCAGGCT GT
                                  |||||||||||| ||||||| ||
                                  AAAGTGGTACAAC GGTCCGA CA
                                        G      C
GAM946  LOC90321  3'  ACCAGCCTGGCCAATATGGTGA 62926                C
                AA                TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTATAACCGGTCCGA CA
                                           C
GAM946  LOC90509  3'  CCTGGCTAACACGGTGAAA   63791       A
                                  TTTCACC TGTTGGCCAGG
                                  ||||||| ||||||||||
                                  AAAGTGG ACAATCGGTCC
                                      C
GAM946  LOC90573  3'  ACCAGCCTGGCCAACATG    63952           C
                                  CATGTTGGCCAGGCT GT
                                  |||||||||||||| ||
                                  GTACAACCGGTCCGA CA
                                           C
GAM946  LOC90785  3'  AGCCTGGCCAACGTGGTGAAA  64707
                                  TTTCACCATGTTGGCCAGGCT
                                  ||||||||||||||||||||
                                  AAAGTGGTGCAACCGGTCCGA

GAM946  LOC90841  5'  ACCAGCCTGGCCAACATGGTGA 64861                C
                AA                TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                           C
GAM946  LOC90918  5'  ACCAGCCTGACCAACATGGTGA 64992          C     C
                AA                TTTCACCATGTTGG CAGGCT GT
                                  |||||||||||||| |||||| ||
                                  AAAGTGGTACAACC GTCCGA CA
                                        A     C
GAM946  LOC90979  3'  CCTGGCCAACATGGTGAAA   65137
                                  TTTCACCATGTTGGCCAGG
                                  |||||||||||||||||||
                                  AAAGTGGTACAACCGGTCC

GAM946  LOC91056  3'  AGCCTGGCCAGCATGGCGAAA  96399      A
                                  TTTC CCATGTTGGCCAGGCT
                                  |||| ||||||||||||||||
                                  AAAG GGTACGACCGGTCCGA
                                    C
GAM946  LOC91064  3'  ACCAGCCTGGCCAACATGGTGA 65384                C
                AA                TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
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                                AAAGTGGTACAACCGGTCCGA CA
                                      C
GAM946  LOC91115  3' CCTGGCCAACATAGTGAAA   65560       C
                                TTTCAC ATGTTGGCCAGG
                                |||||| ||||||||||||
                                AAAGTG TACAACCGGTCC
                                   A
GAM946  LOC91250  5' AGCCTGGCCAACTTAGTGAAA  65905       CAT
                                TTTCAC   GTTGGCCAGGCT
                                ||||||   ||||||||||||
                                AAAGTG   CAACCGGTCCGA
                                   ATT
GAM946  LOC91286  3' ACCAGCCCGGCCAACATGGTGA 66055             A   C
           AA                     TTTCACCATGTTGGCC GGCT GT
                                  |||||||||||||||| |||| ||
                                  AAAGTGGTACAACCGG CCGA CA
                                        C   C
GAM946  LOC91380  3' AGCCTGGCCAACATGGCGAAA  66433      A
                                TTTC CCATGTTGGCCAGGCT
                                |||| ||||||||||||||||
                                AAAG GGTACAACCGGTCCGA
                                  C
GAM946  LOC91397  3' ACCTGCCTGGGCAACATGG    66495        G     TC
                                CCATGTTG CCAGGC  GT
                                |||||||| ||||||  ||
                                GGTACAAC GGTCCG  CA
                                     G     TC
GAM946  LOC91442  3' AGCCTGGCCAACATGGAGAAA  66639      A
                                TTTC CCATGTTGGCCAGGCT
                                |||| ||||||||||||||||
                                AAAG GGTACAACCGGTCCGA
                                  A
GAM946  LOC91574  3' ACCAGCCTGGCCAACATGGTGA 67106                C
           AA                     TTTCACCATGTTGGCCAGGCT GT
                                  |||||||||||||||||||| ||
                                  AAAGTGGTACAACCGGTCCGA CA
                                        C
GAM946  LOC91660  3' ACCAGCCTAGCCAACATGG    67400         C    C
                                CCATGTTGGC AGGCT GT
                                ||||||||| ||||| ||
                                GGTACAACCG TCCGA CA
                                      A    C
GAM946  LOC91750  3' CCTGGCCAATATGGTGAAA    67651
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||||
                                AAAGTGGTATAACCGGTCC

GAM946  LOC91948  3' ACCAGCCTGGCCAACATGGCGA 68231      A           C
           AA                     TTTC CCATGTTGGCCAGGCT GT
                                  |||| |||||||||||||||| ||
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                                AAAG GGTACAACCGGTCCGA CA
                                  C             C
GAM946  LOC92078  3'  ACAGCCTGGCCAACATGGCGAA 68584      A            C
                    A                TTTC CCATGTTGGCCAGGCT GT
                                     |||| |||||||||||||||| ||
                                AAAG GGTACAACCGGTCCGA CA
                                  C
GAM946  LOC92223  3'  ACCAGCCTGACCAATATGATGA 69043      C       C     C
                    AA               TTTCA CATGTTGG CAGGCT GT
                                     ||||| |||||||| |||||| ||
                                AAAGT GTATAACC GTCCGA CA
                                   A       A     C
GAM946  LOC92228  3'  AGGTTGGCCAACATGGTGAGA  69068              G
                                TTTCACCATGTTGGCCAG CT
                                |||||||||||||||||| ||
                                AGAGTGGTACAACCGGTT GA
                                         G
GAM946  LOC92267  3'  ACCAGCCTGACCAATATGGTGA 69160            C     C
                    AA               TTTCACCATGTTGG CAGGCT GT
                                     |||||||||||||| |||||| ||
                                AAAGTGGTATAACC GTCCGA CA
                                       A     C
GAM946  LOC92270  5'  ACAAGCCTGGCCAACATGGTGA 69182                C
                    AA               TTTCACCATGTTGGCCAGGCT GT
                                     |||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                         A
GAM946  LOC92283  3'  CCTGGCTAACATGGTGAAA   69303
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||
                                AAAGTGGTACAATCGGTCC

GAM946  LOC92299  3'  CCTGGCCAACATGGTGAAA   69365
                                TTTCACCATGTTGGCCAGG
                                |||||||||||||||||
                                AAAGTGGTACAACCGGTCC

GAM946  LOC92360  3'  ACCAGCCTGGCCAACATGGCGA 69621      A            C
                    AA               TTTC CCATGTTGGCCAGGCT GT
                                     |||| |||||||||||||||| ||
                                AAAG GGTACAACCGGTCCGA CA
                                  C             C
GAM946  LOC92405  3'  ACAGCCTGGCCAACATGGTGAA 69706                C
                    A                TTTCACCATGTTGGCCAGGCT GT
                                     |||||||||||||||||||| ||
                                AAAGTGGTACAACCGGTCCGA CA
                                         C
GAM946  LOC92421  3'  AGCCTGACCAACATGAAGAAA  69722      AC       C
                                TTTC  CATGTTGG CAGGCT
                                ||||  |||||||| ||||||
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                                AAAG  GTACAACC GTCCGA
                                  AA       A
GAM946  LOC92465  5'  ACAGCCTGGCCAACATGGTGAA 69930                C
            A                    TTTCACCATGTTGGCCAGGCT GT
                                 |||||||||||||||||||| ||
                                 AAAGTGGTACAACCGGTCCGA CA
                                           C
GAM946  LOC92465  3'  ACCAGCCTGGGCAACATGG   69933        G      C
                                 CCATGTTG CCAGGCT GT
                                 |||||||| ||||||| ||
                                 GGTACAAC GGTCCGA CA
                                     G      C
GAM946  LOC92466  3'  ACCAGCCTGGCCAACATGGTGA 69959              C
            AA                     TTTCACCATGTTGGCCAGGCT GT
                                   |||||||||||||||||||| ||
                                   AAAGTGGTACAACCGGTCCGA CA
                                           C
GAM946  LOC92482  3'  ACCAGCCTGGCCAACATGGTGA 70013              C
            AA                     TTTCACCATGTTGGCCAGGCT GT
                                   |||||||||||||||||||| ||
                                   AAAGTGGTACAACCGGTCCGA CA
                                           C
GAM946  LOC92499  5'  CCTGGCCAACATGGGGAAA   70106      A
                                 TTTC CCATGTTGGCCAGG
                                 |||| ||||||||||||
                                 AAAG GGTACAACCGGTCC
                                   G
GAM946  LOC92573  3'  AGCCTGGCCAGCATGGTGAAA  70368
                                 TTTCACCATGTTGGCCAGGCT
                                 ||||||||||||||||||||
                                 AAAGTGGTACGACCGGTCCGA

GAM946  LOC92661  5'  AGCTTGGCCAACATGGGAAA   70617      A
                                 TTTC CCATGTTGGCCAGGCT
                                 |||| ||||||||||||||
                                 AAAG GGTACAACCGGTTCGA
                                   _
GAM946  LOC92771  3'  ACCAGCCTGGCCAACATGGTGA 54205              C
            AA                     TTTCACCATGTTGGCCAGGCT GT
                                   |||||||||||||||||||| ||
                                   AAAGTGGTACAACCGGTCCGA CA
                                           C
GAM946  LOC93070  3'  ACCAGCCTGGCCAACATGGTGA 71801              C
            AA                     TTTCACCATGTTGGCCAGGCT GT
                                   |||||||||||||||||||| ||
                                   AAAGTGGTACAACCGGTCCGA CA
                                           C
GAM946  LOC93132  5'  ACCAGCCTGACCAACATGGTGA 71970          C   C
            AA                     TTTCACCATGTTGG CAGGCT GT
                                   |||||||||||||| |||||| ||
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                                AAAGTGGTACAACC GTCCGA CA
                                       A     C
GAM946  LOC93613  3'  AGCCTTGGCAACATGGTGAAA  73069          G  _
                                TTTCACCATGTTG CCA GGCT
                                ||||||||||||| ||| ||||
                                AAAGTGGTACAAC GGT CCGA
                                      _  T
GAM946  LOC96597  5'  CCTGGCCAACATGGCGAAA   67455     A
                                TTTC CCATGTTGGCCAGG
                                |||| ||||||||||||||
                                AAAG GGTACAACCGGTCC
                                  C
GAM947  HRH1      3'  CTCAAACATGTTTAGAGTGGA  7819      A    TGG
                                TCCA TCTGA   GCATGTTTGAG
                                |||| |||||   ||||||||||
                                AGGT AGATT   TGTACAAACTC
                                  G    ___
GAM947  TRIM37    3'  CTCAAATTTGTCATCAG     31625       G  T
                                CTGATGG CA GTTTGAG
                                ||||||| || |||||||
                                GACTACT GT TAAACTC
                                   _  T
GAM947  HTMP10    3'  CTCAAAAAAGCCATCAGATCTG 53758    CA       G ATG
          A                      TC  ATCTGATGG C   TTTGAG
                                ||  |||||||| |   ||||||
                                AG  TAGACTACC G   AAACTC
                                 TC       _ AAA
GAM947  PAK2      5'  CTCAAATATCACCAAACTAGA  67140     A__  GC
                                TCTG   TGG  ATGTTTGAG
                                ||||   |||  |||||||||
                                AGAT   ACC  TATAAACTC
                                  CAA   AC
GAM947  SEMA6A    3'  CTCGAGTACCCACCAGA     40818     A   CA
                                TCTG TGGG  TGTTTGAG
                                |||| ||||  ||||||||
                                AGAC ACCC  ATGAGCTC
                                  C   __
GAM947  TTY7      3'  TCAAACATGCAGGCTGGA    50019     AT  GATGG
                                TCCA  CT    GCATGTTTGA
                                ||||  ||    ||||||||||
                                AGGT  GA    CGTACAAACT
                                  CG  _____
GAM947  LOC144766 3'  CTCAAACATGAGAAGACTGGG  77481     A   GATGGG
                                TCCA TCT     CATGTTTGAG
                                |||| |||     ||||||||||
                                GGGT AGA     GTACAAACTC
                                  C  AGA___
GAM947  LOC201685 5'  TAAACACCCATCAGATGGA   91845     A       CA
                                TCCA TCTGATGGG  TGTTTG
                                |||| |||||||||  ||||||
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                                AGGT AGACTACCC  ACAAAT
                                  _      __
GAM947  LOC221596 5'  CTCAAACAAAACTCAGATT   93623       TG GCA
                                AATCTGA  G   TGTTTGAG
                                |||||||  |   ||||||||
                                TTAGACT  C   ACAAACTC
                                   __ AAA
GAM947  LOC93622  3'  CTCTGCAGACCATCAGAT    57729        GCA   TT
                                ATCTGATGG   TGT  GAG
                                |||||||||   |||  |||
                                TAGACTACC   ACG  CTC
                                     AG_   T_
GAM948  A1BG      3'  TGACCTCCCAGGCTCAA     56300      A   AGAGGC
                                TTGA CCTG     GGAGGTTA
                                |||| ||||     ||||||||
                                AACT GGAC     CCTCCAGT
                                  C   _______
GAM948  ADAMTS4   3'  CCTCCGCCTCCCGGGTTCAA   18756        A
                                TTGAACCTG GAGGCGGAGG
                                ||||||||| ||||||||||
                                AACTTGGGC CTCCGCCTCC
                                     C
GAM948  ALDH1B1   3'  AACCTCCGCCTCCCAGATTCAA 7310       C   A
                                TTGAA CTG GAGGCGGAGGTT
                                ||||| ||| ||||||||||||
                                AACTT GAC CTCCGCCTCCAA
                                   A   C
GAM948  APM1      3'  AACCTTTGCCTCCCAGGTTTAA 17748        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AATTTGGAC CTCCGTTTCCAA
                                     C
GAM948  APPBP2    3'  AACCTCCGCCTCCCGGGTTC   22112       A
                                GAACCTG GAGGCGGAGGTT
                                ||||||| ||||||||||||
                                CTTGGGC CTCCGCCTCCAA
                                    C
GAM948  APPL      3'  CTCCGCCTCCCAGGTTCA    24947        A
                                TGAACCTG GAGGCGGAG
                                |||||||| |||||||||
                                ACTTGGAC CTCCGCCTC
                                     C
GAM948  ARCN1     3'  AACCTCCGCCTCCTGGGTTCAA 9739         GA
                                TTGAACCT  GAGGCGGAGGTT
                                ||||||||  ||||||||||||
                                AACTTGGG  CTCCGCCTCCAA
                                     TC
GAM948  ATP1B2    3'  AACTTCCGCATCCCAGGTTCAA 9822         A  G
                                TTGAACCTG GA GCGGAGGTT
                                ||||||||| || |||||||||
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                                AACTTGGAC CT CGCCTTCAA
                                     C  A
GAM948  ATP6V1A1  3'  GCCTTCGCCTCCCGGGTTCAA  9869          A
                                TTGAACCTG GAGGCGGAGGT
                                ||||||||| ||||||||||
                                AACTTGGGC CTCCGCTTCCG
                                     C
GAM948  ATP8B2    3'  AACCTCCACCTCCTGGGTTCAA 65825        GA    C
                                TTGAACCT  GAGG GGAGGTT
                                ||||||||  |||| |||||||
                                AACTTGGG  CTCC CCTCCAA
                                    TC    A
GAM948  ATP8B2    3'  GCCCCGCCCCTCAGGCCCAG  65838     AA     A     A
                                TTG  CCTGAG GGCGG GGT
                                |||  |||||| ||||| |||
                                GAC  GGACTC CCGCC CCG
                                  CC     C    _
GAM948  BRIP1     3'  AACCTTCACCTCCAGGTTCAA  50200         A    C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGAC CTCC CTTCCAA
                                     _    A
GAM948  C18orf1   3'  GCTCCCACCCCCCAGGTTCAA  60866         AGA  C  AG
                                TTGAACCTG   GG GG  GT
                                |||||||||   || ||  ||
                                AACTTGGAC   CC CC  CG
                                     CCC  A  CT
GAM948  C7        3'  AACCTCCGCCTCCTGGGTTGAA 6971     G    GA
                                TT AACCT  GAGGCGGAGGTT
                                || |||||  ||||||||||||
                                AA TTGGG  CTCCGCCTCCAA
                                 G    TC
GAM948  CASP10    3'  TCTCGACCTCCCAGGCTCAA   53227     A    A    _  _
                                TTGA CCTG GAGG CG GA
                                |||| |||| |||| || ||
                                AACT GGAC CTCC GC CT
                                  C    C    A  T
GAM948  CASP10    3'  TCTCGACCTCCCAGGCTCAA   53266     A    A    _  _
                                TTGA CCTG GAGG CG GA
                                |||| |||| |||| || ||
                                AACT GGAC CTCC GC CT
                                  C    C    A  T
GAM948  CCNF      3'  GTAACCTCCGCCTCCCGG    10084     A
                                CTG GAGGCGGAGGTTAC
                                ||| ||||||||||||||
                                GGC CTCCGCCTCCAATG
                                  C
GAM948  CDH17     3'  AACCTCCGCCTCCTGGGTTCA  15780        GA
                                TGAACCT  GAGGCGGAGGTT
                                |||||||  ||||||||||||
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                                ACTTGGG  CTCCGCCTCCAA
                                    TC
GAM948  CIAS1    5' GCCTCCACCTCCCGGGTTCAA  18100        A    C
                                TTGAACCTG GAGG GGAGGT
                                ||||||||| |||| ||||||
                                AACTTGGGC CTCC CCTCCG
                                    C    A
GAM948  CLECSF12 3' AACCTCCGCCCCCTGGGTTCAA 77199        G  A_
                                TTGAACCT AG  GGCGGAGGTT
                                |||||||| ||  ||||||||||
                                AACTTGGG TC  CCGCCTCCAA
                                    _ CC
GAM948  COX15    3' AACCTCCACTTCCCAGGTTCAA 55273         A    C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGAC CTTC CCTCCAA
                                    C    A
GAM948  CRTAP    3' AACCTCCGCCTCTTGGGTTCAA 22070        TG
                                TTGAACC  AGAGGCGGAGGTT
                                |||||||  |||||||||||||
                                AACTTGG  TCTCCGCCTCCAA
                                    GT
GAM948  CXCL16   3' AACCCCCATCTCCCAGGTTCAA 42154         A  GC  A
                                TTGAACCTG GAG  GG GGTT
                                ||||||||| |||  || ||||
                                AACTTGGAC CTC  CC CCAA
                                    C   TA  C
GAM948  CYP1A2   3' AACCTCCACCTCGCAGGTTCAA 7488         A    C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGAC CTCC CCTCCAA
                                    G    A
GAM948  CYP1A2   3' AACCTCCGCCTCCCATGTTCAA 7489        C  A
                                TTGAAC TG GAGGCGGAGGTT
                                |||||| || ||||||||||||
                                AACTTG AC CTCCGCCTCCAA
                                   T  C
GAM948  CYP1A2   3' AACCTCTGCCTCCCAGGTTCAA 7490         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGTCTCCAA
                                    C
GAM948  CYP8B1   3' AACCTCTGCCTCCCGGGTTCAA 16527         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGTCTCCAA
                                    C
GAM948  DFFB     3' AACCTCCGCCTCTCAGGTTCAA 88745
                                TTGAACCTGAGAGGCGGAGGTT
                                ||||||||||||||||||||||
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                                AACTTGGACTCTCCGCCTCCAA

GAM948  DHFR    3'  AACCTCCGCCTTCCCAGATTCA 7634      C   A_
                                TGAA CTG  GAGGCGGAGGTT
                                |||| |||  ||||||||||||
                                ACTT GAC  TTCCGCCTCCAA
                                  A   CC
GAM948  DIAPH2   3'  GTAACCTCAAACTCCCAGGCTC 23010     A   A   GCG
          AA                      TTGA CCTG GAG   GAGGTTAC
                                |||| |||| |||   ||||||||
                                AACT GGAC CTC   CTCCAATG
                                  C   C   AAA
GAM948  DISC1    3'  AACCTCTACCTCCCAGGTTCAA 38493         A   CG
                                TTGAACCTG GAGG  GAGGTT
                                ||||||||| ||||  ||||||
                                AACTTGGAC CTCC  CTCCAA
                                     C   AT
GAM948  DSCR3    3'  AACCTCCACCTCCCAGGTTCAA 21298         A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGAC CTCC CCTCCAA
                                     C   A
GAM948  EIF2S3   3'  AACCTCTGCCCCCCGGGTTCAA 9201          AGA
                                TTGAACCTG   GGCGGAGGTT
                                |||||||||   ||||||||||
                                AACTTGGGC   CCGTCTCCAA
                                     CCC
GAM948  EPB72    3'  AACCTCCGCCTCCTGGGTTCAA 15862         GA
                                TTGAACCT  GAGGCGGAGGTT
                                ||||||||  ||||||||||||
                                AACTTGGG  CTCCGCCTCCAA
                                    TC
GAM948  FANCE    3'  GTAACCTCTGCCTCCCAGGCTC 41900     A   A
          GA                      TTGA CCTG GAGGCGGAGGTTAC
                                |||| |||| ||||||||||||||
                                AGCT GGAC CTCCGTCTCCAATG
                                  C   C
GAM948  FANCF    3'  AACCTCTGCCTCCCAGGATCAA 42965     A   A
                                TTGA CCTG GAGGCGGAGGTT
                                |||| |||| ||||||||||||
                                AACT GGAC CTCCGTCTCCAA
                                  A   C
GAM948  FCAR     3'  AACCTTCGCCTCCCAGGTTCAA 56624         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGCTTCCAA
                                     C
GAM948  FCRH1    3'  AACGCCTGCCTCTCAGGCTCAA 54723     A         AG
                                TTGA CCTGAGAGGCGG  GTT
                                |||| ||||||||||||  |||
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                                AACT GGACTCTCCGTC  CAA
                                  C          CG
GAM948  FEZ1    3'  AACCTCCACCTCCCAGGTTCAA 42861         A    C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGAC CTCC CCTCCAA
                                     C    A
GAM948  GM2A    3'  AACCTCCGCCTCCTGGGTTCAA 68368         GA
                                TTGAACCT  GAGGCGGAGGTT
                                ||||||||  ||||||||||||
                                AACTTGGG  CTCCGCCTCCAA
                                     TC
GAM948  GPR56   5'  GTAACCTCCACCTCCCGGGTTC 20276         A   C
              AA                  TTGAACCTG GAGG GGAGGTTAC
                                ||||||||| |||| |||||||||
                                AACTTGGGC CTCC CCTCCAATG
                                     C    A
GAM948  GPR81   3'  AACCTCTGCCTCCCGGGTTCAA 51728         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGTCTCCAA
                                     C
GAM948  GRAF    3'  AACCTCCGCCTCCCGGGTTCAA 31218         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGCCTCCAA
                                     C
GAM948  HCS     3'  AACCTCCGCCTTCCAGGTTCAA 38954         AG
                                TTGAACCTG  AGGCGGAGGTT
                                |||||||||  ||||||||||
                                AACTTGGAC  TCCGCCTCCAA
                                     CT
GAM948  HCS     3'  AACCTCCGCCTTCCAGTTGCAA 38955     AAC   AG
                                TTG   CTG  AGGCGGAGGTT
                                |||   |||  ||||||||||
                                AAC   GAC  TCCGCCTCCAA
                                  GTT   CT
GAM948  HTR1D   3'  AACCTCCGCATCCCGGGTTCAA 7831          A  G
                                TTGAACCTG GA GCGGAGGTT
                                ||||||||| || |||||||||
                                AACTTGGGC CT CGCCTCCAA
                                     C  A
GAM948  IGF1    3'  AACCTCCACCTCCTGGGTTTAA 7056          GA   C
                                TTGAACCT  GAGG GGAGGTT
                                ||||||||  |||| |||||||
                                AATTTGGG  CTCC CCTCCAA
                                     TC   A
GAM948  IL11    3'  CTCCACCTCCCGGGTTCAA   7181          A   C
                                TTGAACCTG GAGG GGAG
                                ||||||||| |||| ||||
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                                AACTTGGGC CTCC CCTC
                                     C    A
GAM948  ITGAM    3'  AACCTCCGCCTCCCGGGTTCAA 72303          A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGCCTCCAA
                                     C
GAM948  JAK3     3'  AACCTCTGCTTCCCAGGTTCAA 5817           A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTTCGTCTCCAA
                                     C
GAM948  LILRA3   3'  AACCTCCGCCTCTCGGGTTCAA 97018
                                TTGAACCTGAGAGGCGGAGGTT
                                ||||||||||||||||||||||
                                AACTTGGGCTCTCCGCCTCCAA

GAM948  LOXL2    3'  AACCCCCACCCCTTGTTTTTCA 11349      CC_   A C A
           A                     TTGAA   TGAG GG GG GGTT
                                |||||   |||| || || ||||
                                AACTT   GTTC CC CC CCAA
                                   TTT   C A C
GAM948  LYZ      3'  AACCTCCACCTCCCGGGTTCA  5886         A   C
                                TGAACCTG GAGG GGAGGTT
                                |||||||| |||| |||||||
                                ACTTGGGC CTCC CCTCCAA
                                     C    A
GAM948  MAK      3'  AACCTCCACCTCCTGGGTTCAA 20932        GA   C
                                TTGAACCT  GAGG GGAGGTT
                                ||||||||  |||| |||||||
                                AACTTGGG  CTCC CCTCCAA
                                     TC    A
GAM948  MEF2A    5'  AACCTCCGCCTCCAGGTTCAA  19985         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGCCTCCAA
                                                _
GAM948  MEFV     3'  AACCTCCACCTCCCAGGTTCAA 5914          A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGAC CTCC CCTCCAA
                                     C    A
GAM948  MEFV     3'  AACCTCCGCCTCCCAGGTTCAA 5915          A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGCCTCCAA
                                     C
GAM948  MHC2TA   3'  AACCTCCGCCTCTTGGGTTCAA 5962         TG
                                TTGAACC  AGAGGCGGAGGTT
                                |||||||  ||||||||||||
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                                AACTTGG  TCTCCGCCTCCAA
                                    GT
GAM948  MICB     3'  AACCTCTGCCTCCCAGGTTCAA 21015          A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGTCTCCAA
                                    C
GAM948  MLANA    3'  TAACCTCCGCCTCCCAGGTTCA 19770          A
          A                      TTGAACCTG GAGGCGGAGGTTA
                                ||||||||| |||||||||||||
                                AACTTGGAC CTCCGCCTCCAAT
                                    C
GAM948  MPL      3'  AACCTCCACCTCCGGGTTCAA  19332         A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGGC CTCC CCTCCAA
                                    _   A
GAM948  MPL      3'  AACCTCTGCCTCCCGGGTTCAA 19333          A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGTCTCCAA
                                    C
GAM948  MYCL2    3'  AACCTCTGCCTCCCGGGTTCAA 19367          A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGTCTCCAA
                                    C
GAM948  NCOA6    5'  GTAACCTCCGTCTCCCAGGTTC 26843          A
          AA                     TTGAACCTG GAGGCGGAGGTTAC
                                ||||||||| ||||||||||||||
                                AACTTGGAC CTCTGCCTCCAATG
                                    C
GAM948  NQO1     3'  AACCTCTGCCTCCCAGGTTC   8036          A
                                GAACCTG GAGGCGGAGGTT
                                ||||||| ||||||||||||
                                CTTGGAC CTCCGTCTCCAA
                                    C
GAM948  PCDHB11  3'  CCTCCGCCTCTCGGGTTCAA  38920
                                TTGAACCTGAGAGGCGGAGG
                                ||||||||||||||||||||
                                AACTTGGGCTCTCCGCCTCC

GAM948  PCDHB9   3'  AACCTCCGCCTCCCAGGTTCAA 39433          A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGCCTCCAA
                                    C
GAM948  PDCL     3'  AACCTCCACCTCCTGGGTTCAA 19392          GA   C
                                TTGAACCT  GAGG GGAGGTT
                                ||||||||  |||| |||||||
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                                AACTTGGG  CTCC CCTCCAA
                                    TC    A
GAM948  PDE6B    3'  AACCTCCACCTCCCAGGTTCAA 6066          A    C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGAC CTCC CCTCCAA
                                    C    A
GAM948  PER2     3'  AACCTCTGCCTCCCAGGTTCAA 43335         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGTCTCCAA
                                    C
GAM948  PIGR     3'  AACCTCCGCCTCCCAGGTT   72980       A
                                AACCTG GAGGCGGAGGTT
                                |||||| ||||||||||||
                                TTGGAC CTCCGCCTCCAA
                                  C
GAM948  PIK3C2B  3'  AAAATCTGCCTCCCGGGTTCAA 12083         A       GG
                                TTGAACCTG GAGGCGGA  TT
                                ||||||||| ||||||||  ||
                                AACTTGGGC CTCCGTCT  AA
                                    C       AA
GAM948  PIK3CD   3'  GTAACCTCCGCCTCCCAGGTTC 18496         A
          AA                      TTGAACCTG GAGGCGGAGGTTAC
                                ||||||||| ||||||||||||||
                                AACTTGGAC CTCCGCCTCCAATG
                                    C
GAM948  PON1     3'  AACTTCTACCTCCGAGGTTCAA 6533          GA   CG
                                TTGAACCT  GAGG  GAGGTT
                                ||||||||  ||||  ||||||
                                AACTTGGA  CTCC  CTTCAA
                                    GC    AT
GAM948  PSMB2    3'  AACCTCCGCCTCCCGGGCCCAA 12454     AA   A
                                TTG  CCTG GAGGCGGAGGTT
                                |||  |||| ||||||||||||
                                AAC  GGGC CTCCGCCTCCAA
                                  CC    C
GAM948  PTGES    3'  GCCTCCGCCTCCCGGGTTCAA  18062         A
                                TTGAACCTG GAGGCGGAGGT
                                ||||||||| ||||||||||
                                AACTTGGGC CTCCGCCTCCG
                                    C
GAM948  PTGIS    3'  AACCTCCACCTCCTGGGTTTAA 8181          GA   C
                                TTGAACCT  GAGG GGAGGTT
                                ||||||||  |||| |||||||
                                AATTTGGG  CTCC CCTCCAA
                                    TC    A
GAM948  RAB36    3'  AACCTCTGCCTCCCAGGTTGAA 18147    G     A
                                TT AACCTG GAGGCGGAGGTT
                                || |||||| ||||||||||||
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                                AA TTGGAC CTCCGTCTCCAA
                                 G     C
GAM948  RABL2A   3'  AACCTCTGACTCCCTGGTTCAA 26400       TGA   G
                                TTGAACC   GAG CGGAGGTT
                                |||||||   ||| ||||||||
                                AACTTGG   CTC GTCTCCAA
                                    TCC   A
GAM948  RABL2B   3'  AACCTCTGACTCCCTGGTTCAA 23967       TGA   G
                                TTGAACC   GAG CGGAGGTT
                                |||||||   ||| ||||||||
                                AACTTGG   CTC GTCTCCAA
                                    TCC   A
GAM948  RBBP9    3'  ACCTGCACCTCCCGGGTTCAA  70676        A    CGG
                                TTGAACCTG GAGG   AGGT
                                ||||||||| ||||   ||||
                                AACTTGGGC CTCC   TCCA
                                      C    ACG
GAM948  RHD      3'  AACCTCCGCCTCCCAGGTTCAA 32796        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGCCTCCAA
                                      C
GAM948  RHD      3'  AACCTCCGCCTCCCAGGTTCAA 33126        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGCCTCCAA
                                      C
GAM948  SAS      3'  AACCTCTGCCTCCCGGGTTCAA 21088        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGTCTCCAA
                                      C
GAM948  SEDL     3'  AACCTCCACCTCCCGGGTTCAA 28061        A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGGC CTCC CCTCCAA
                                      C    A
GAM948  SEDL     3'  AACCTCCACCTCCTGGGTTCAA 28062       GA   C
                                TTGAACCT  GAGG GGAGGTT
                                ||||||||  |||| |||||||
                                AACTTGGG  CTCC CCTCCAA
                                      TC    A
GAM948  SEDL     3'  AACCTCCGCCTCCCAGGTTCAG 28063        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                GACTTGGAC CTCCGCCTCCAA
                                      C
GAM948  SEPN1    3'  AACCTCCACCTCCCAGGTTCAA 66955        A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
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                                AACTTGGAC CTCC CCTCCAA
                                     C    A
GAM948  SH3BP2   3'  ACCTCCGCCTCTCTAGTTCAA  13045       CT
                                TTGAAC  GAGAGGCGGAGGT
                                ||||||  ||||||||||||
                                AACTTG  CTCTCCGCCTCCA
                                   AT
GAM948  SHOX     3'  ACCTCCGCCCCCCGGGTTCAA  6558         AGA
                                TTGAACCTG   GGCGGAGGT
                                |||||||||   |||||||||
                                AACTTGGGC   CCGCCTCCA
                                     CCC
GAM948  SHOX     3'  AACCTCCGCCTCCCGAGTTCAA 23508       C  A
                                TTGAAC TG GAGGCGGAGGTT
                                ||||||  || ||||||||||||
                                AACTTG GC CTCCGCCTCCAA
                                   A  C
GAM948  SLC14A2  5'  AACCTCCACCTCCCAGGTTCAA 24102         A    C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGAC CTCC CCTCCAA
                                     C    A
GAM948  SLC15A1  3'  AACCTCCGCCTCCCAGGTTCAA 18632         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGCCTCCAA
                                     C
GAM948  SLC7A6   5'  AACCTCCGACTCCCTGGTTCAA 15634        TGA   G
                                TTGAACC   GAG CGGAGGTT
                                |||||||   ||| ||||||||
                                AACTTGG   CTC GCCTCCAA
                                    TCC   A
GAM948  SMAC     5'  AACCTCTGCCTCCCAGGTTCAA 58009         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGTCTCCAA
                                     C
GAM948  SNAP23   3'  AACCTCCGCCTCCCTGGTTCAA 56328        TGA
                                TTGAACC   GAGGCGGAGGTT
                                |||||||   ||||||||||||
                                AACTTGG   CTCCGCCTCCAA
                                    TCC
GAM948  SNAP23   3'  AACCTCCGCCTCCCTGGTTCAA 15128        TGA
                                TTGAACC   GAGGCGGAGGTT
                                |||||||   ||||||||||||
                                AACTTGG   CTCCGCCTCCAA
                                    TCC
GAM948  SNX15    3'  AACCTCCACCTCCCAGGTTCAA 74110         A    C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
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                                AACTTGGAC CTCC CCTCCAA
                                     C    A
GAM948  SS18     3'  AACCTCCGCCTCCCAGGTTCAA 20100          A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGCCTCCAA
                                     C
GAM948  SULT2B1  5'  AACCTCCGCCTCCTGGGTTCAA 17217         GA
                                TTGAACCT  GAGGCGGAGGTT
                                ||||||||  ||||||||||||
                                AACTTGGG  CTCCGCCTCCAA
                                     TC
GAM948  TAPBP    3'  AACCTCCGCCTCCTGGGTTCAA 13535         GA
                                TTGAACCT  GAGGCGGAGGTT
                                ||||||||  ||||||||||||
                                AACTTGGG  CTCCGCCTCCAA
                                     TC
GAM948  TAT      3'  AACCTCCACCTCCTGGGTTCAA 6242          GA   C
                                TTGAACCT  GAGG GGAGGTT
                                ||||||||  ||||  |||||||
                                AACTTGGG  CTCC CCTCCAA
                                     TC   A
GAM948  TBXA2R   3'  AACCTCCACCTCCCGGGTTCAA 8332          A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| ||||  |||||||
                                AACTTGGGC CTCC CCTCCAA
                                     C    A
GAM948  TBXA2R   3'  AACCTCCGCCTCCCGGGTTCAA 8333          A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGCCTCCAA
                                     C
GAM948  TMC1     5'  AACCTCCGCCTCCCAGGTTCAA 57705         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGCCTCCAA
                                     C
GAM948  TNFRSF10B 3'  AACCTCCGCCTCCTGGGTTCAA 15206        GA
                                TTGAACCT  GAGGCGGAGGTT
                                ||||||||  ||||||||||||
                                AACTTGGG  CTCCGCCTCCAA
                                     TC
GAM948  TRIM9    5'  AACCTCCGCCTCCCAGGTTCAA 31433         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGCCTCCAA
                                     C
GAM948  TRPV1    3'  AACCTCCGCCTCCTGGATTC  38678    C  GA
                                GAA CT  GAGGCGGAGGTT
                                ||| ||  ||||||||||||
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                                CTT GG  CTCCGCCTCCAA
                                  A  TC
GAM948  TRPV1   3' AACCTCTGCCTCCCGGGTTCAA 38679         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGTCTCCAA
                                     C
GAM948  TRPV1   3' AACCTCCGCCTCCTGGATTC  55643    C  GA
                                GAA CT  GAGGCGGAGGTT
                                ||| ||  ||||||||||||
                                CTT GG  CTCCGCCTCCAA
                                  A  TC
GAM948  TRPV1   3' AACCTCTGCCTCCCGGGTTCAA 55644         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGTCTCCAA
                                     C
GAM948  TRPV1   3' AACCTCCGCCTCCTGGATTC  55694    C  GA
                                GAA CT  GAGGCGGAGGTT
                                ||| ||  ||||||||||||
                                CTT GG  CTCCGCCTCCAA
                                  A  TC
GAM948  TRPV1   3' AACCTCTGCCTCCCGGGTTCAA 55695         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGTCTCCAA
                                     C
GAM948  TRPV1   3' AACCTCCGCCTCCTGGATTC  55725    C  GA
                                GAA CT  GAGGCGGAGGTT
                                ||| ||  ||||||||||||
                                CTT GG  CTCCGCCTCCAA
                                  A  TC
GAM948  TRPV1   3' AACCTCTGCCTCCCGGGTTCAA 55726         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGTCTCCAA
                                     C
GAM948  VENTX2  3' AACCTCCGCCTCCTGGGTTCAA 27848        GA
                                TTGAACCT  GAGGCGGAGGTT
                                ||||||||  ||||||||||||
                                AACTTGGG  CTCCGCCTCCAA
                                     TC
GAM948  WHSC1   3' AACCTCCGCCTCCTTGGTTC  56685      TGA
                                GAACC  GAGGCGGAGGTT
                                |||||  ||||||||||||
                                CTTGG  CTCCGCCTCCAA
                                   TTC
GAM948  WISP2   5' TCCGCCTCCCAGGCTCAA   15278     A   A
                                TTGA CCTG GAGGCGGA
                                |||| |||| ||||||||
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                                AACT GGAC CTCCGCCT
                                  C   C
GAM948  ZNF157   3' ACCTTCGCCTCCCGGGTTCAA 14321        A
                                TTGAACCTG GAGGCGGAGGT
                                ||||||||| ||||||||||
                                AACTTGGGC CTCCGCTTCCA
                                    C
GAM948  ZNF264   3' AACCTCCGCCTCCTGGGTTCAA 14175       GA
                                TTGAACCT  GAGGCGGAGGTT
                                ||||||||  ||||||||||||
                                AACTTGGG  CTCCGCCTCCAA
                                   TC
GAM948  ZNF264   3' AACCTCTGCCTCCCGGGTTCAA 14176        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGTCTCCAA
                                    C
GAM948  ZNF74    5' AACCTCTGCTTCCCGGGTTCAA 14251        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTTCGTCTCCAA
                                    C
GAM948  AP3S2    3' AACCTCTGCTTCCCGGGTTCAA 20636        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTTCGTCTCCAA
                                    C
GAM948  APXL2    5' AACTTCCGCCTCCCGGGTTCAA 75665        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGCCTTCAA
                                    C
GAM948  ARHGAP5  5' AACCCCCACCTCCCAGGTTCAA 77590        A   C A
                                TTGAACCTG GAGG GG GGTT
                                ||||||||| |||| || ||||
                                AACTTGGAC CTCC CC CCAA
                                    C   A C
GAM948  ASB16    5' AACCTCCGCCTCCCGGGTTCAA 70482        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGCCTCCAA
                                    C
GAM948  ASE-1    3' AACCTCCGCCTCCTGGGTTC  24963       GA
                                GAACCT  GAGGCGGAGGTT
                                ||||||  ||||||||||||
                                CTTGGG  CTCCGCCTCCAA
                                   TC
GAM948  BAG5     3' AACCTCCACCTCCCAGGTTCAA 18031        A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
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                                AACTTGGAC CTCC CCTCCAA
                                     C    A
GAM948  BNIP-S   3'  AACCTCCGCCTCCCGGTTCAA  57081        T A
                                TTGAACC G GAGGCGGAGGTT
                                ||||||| | ||||||||||||
                                AACTTGG C CTCCGCCTCCAA
                                    _ C
GAM948  BTN3A1   3'  AACCTCCACCTCCTGGGTTCAA 23882         GA   C
                                TTGAACCT  GAGG GGAGGTT
                                ||||||||  |||| |||||||
                                AACTTGGG  CTCC CCTCCAA
                                     TC   A
GAM948  C13orf1  3'  AACCTCTGCTTCCCAGGTTTAA 40342         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AATTTGGAC CTTCGTCTCCAA
                                     C
GAM948  C1orf24  3'  AACCTCCGCCTCCTGGGTTCAG 54777         GA
                                TTGAACCT  GAGGCGGAGGTT
                                ||||||||  ||||||||||||
                                GACTTGGG  CTCCGCCTCCAA
                                     TC
GAM948  C1QTNF6  3'  AACCTCTGCCTCCCGGGTTCAA 49979         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGTCTCCAA
                                     C
GAM948  C3F      3'  AACCTCCACCTCCTGGGTTCAA 20469         GA   C
                                TTGAACCT  GAGG GGAGGTT
                                ||||||||  |||| |||||||
                                AACTTGGG  CTCC CCTCCAA
                                     TC   A
GAM948  C9orf9   3'  AACCTCCACCTCCAGGTTCAA  39002         A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGAC CTCC CCTCCAA
                                     _    A
GAM948  C9orf9   3'  AACCTCCGCCTCCCAGGTTCA  39003         A
                                TGAACCTG GAGGCGGAGGTT
                                |||||||| ||||||||||||
                                ACTTGGAC CTCCGCCTCCAA
                                     C
GAM948  CDC14B   3'  AACCTCCTTCTCCCAGGTTCAA 53993         A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGAC CTCT CCTCCAA
                                     C    T
GAM948  CENPH    3'  AACCTCTGCCTCCCGGGTTCAA 43560         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
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                                AACTTGGGC CTCCGTCTCCAA
                                     C
GAM948  CHRAC1   3'  AACCTCCGCCTCCCAGGTTCAA 34325        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGCCTCCAA
                                     C
GAM948  CIP29    3'  AACCTCTGTCTCCCGGGTTCAA 51363        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCTGTCTCCAA
                                     C
GAM948  COLEC12  3'  AACCCCCACATCCCGGGTTCAA 48602        A  GGC  A
                                TTGAACCTG GA   GG GGTT
                                ||||||||| ||   || ||||
                                AACTTGGGC CT   CC CCAA
                                     C  ACA  C
GAM948  CYLC2    3'  AGCCTCCACCTTCAGGTTCAA  9031         G   C
                                TTGAACCTGA AGG GGAGGTT
                                |||||||||| ||| |||||||
                                AACTTGGACT TCC CCTCCGA
                                      _   A
GAM948  DBR1     3'  AACCTCCGCCTCCCAGGTTCAA 33052        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGCCTCCAA
                                     C
GAM948  DKFZP434B044 3'  AACTGCCGCCTCCCGGGTTCAA 49706        A      A
                                TTGAACCTG GAGGCGG GGTT
                                ||||||||| ||||||| ||||
                                AACTTGGGC CTCCGCC TCAA
                                     C      G
GAM948  DKFZP434D146 3'  AACCTCTGCTTCCTAGGTTCAA 32127        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAT CTTCGTCTCCAA
                                     C
GAM948  DKFZp434E2220 5'  AACCTCCGCCTCCCGGGTTCAA 34701        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGCCTCCAA
                                     C
GAM948  DKFZp434F142 3'  AACCTCTGCAGGCCCAA     51028     AA   GAGAG
                                TTG  CCT     GCGGAGGTT
                                |||  |||     |||||||||
                                AAC  GGA     CGTCTCCAA
                                  CC  _____
GAM948  DKFZP434J037 3'  ACCTCCGCCTCCCGGGTTCAA  48937        A
                                TTGAACCTG GAGGCGGAGGT
                                ||||||||| ||||||||||
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                                AACTTGGGC CTCCGCCTCCA
                                     C
GAM948  DKFZp547H025 3'  AACCTCCACCTCCTGGGTTCAA 39761        GA   C
                                TTGAACCT  GAGG GGAGGTT
                                ||||||||  |||| |||||||
                                AACTTGGG  CTCC CCTCCAA
                                    TC    A
GAM948  DKFZP564O0523 3'  AACCTCCACCTCCCGGGTTCAA 50413         A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGGC CTCC CCTCCAA
                                     C    A
GAM948  DKFZp761N1114 3'  AACCTCCGCCTCCCAGTTTCAA 79769      C   A
                                TTGAA CTG GAGGCGGAGGTT
                                ||||| ||| ||||||||||||
                                AACTT GAC CTCCGCCTCCAA
                                   T   C
GAM948  DKFZp762L0311 3'  AACCTTTGCCTCCTAGGTTCAA 38670         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAT CTCCGTTTCCAA
                                     C
GAM948  DKFZp762P2111 3'  AACCTCCGCCTCTCGGGTTCAG 87619
                                TTGAACCTGAGAGGCGGAGGTT
                                ||||||||||||||||||||||
                                GACTTGGGCTCTCCGCCTCCAA

GAM948  EREG     3'  AACCTCACCTCCCGGGTTCAA  9297         A   CG
                                TTGAACCTG GAGG  GAGGTT
                                ||||||||| ||||  ||||||
                                AACTTGGGC CTCC  CTCCAA
                                     C    A_
GAM948  EVI5     3'  AACTTCCGCTTCCCAGGTTCAA 20186         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTTCGCCTTCAA
                                     C
GAM948  FER1L4   3'  AACCTCCACCTCCTGGGTTCAA 48103        GA   C
                                TTGAACCT  GAGG GGAGGTT
                                ||||||||  |||| |||||||
                                AACTTGGG  CTCC CCTCCAA
                                    TC    A
GAM948  FER1L4   3'  AACCTCCACCTCCTGGGTTCAA 48104        GA   C
                                TTGAACCT  GAGG GGAGGTT
                                ||||||||  |||| |||||||
                                AACTTGGG  CTCC CCTCCAA
                                    TC    A
GAM948  FLJ00024  5'  AACCTCTGCCTCCCAGGTTCAA 64487         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
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                                AACTTGGAC CTCCGTCTCCAA
                                    C
GAM948  FLJ10232  3'  AACCTCCGCCTCCCGGGTTCAA 36368        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGCCTCCAA
                                    C
GAM948  FLJ10346  5'  AAGCTCCACCTCCCAGGTTCA  36516       A   C   G
                                TGAACCTG GAGG GGAG TT
                                |||||||| |||| |||| ||
                                ACTTGGAC CTCC CCTC AA
                                    C   A   G
GAM948  FLJ10535  3'  AACCTCTGCCTCCCAGGTTCAA 36731        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGTCTCCAA
                                    C
GAM948  FLJ10901  3'  AACCCCCGTCTCCCGGGTTCAA 37347        A     A
                                TTGAACCTG GAGGCGG GGTT
                                ||||||||| ||||||| ||||
                                AACTTGGGC CTCTGCC CCAA
                                    C     C
GAM948  FLJ12363  3'  AACCTCCACCTCCCGGGTTCAG 50622        A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                GACTTGGGC CTCC CCTCCAA
                                    C   A
GAM948  FLJ12409  3'  AACCTCCGCCTCACAGCTTCAA 47764      C   A
                                TTGAA CTG GAGGCGGAGGTT
                                ||||| ||| ||||||||||||
                                AACTT GAC CTCCGCCTCCAA
                                  C   A
GAM948  FLJ12572  5'  AACCTCTGCCTCCCAGGTTCAA 43538        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGTCTCCAA
                                    C
GAM948  FLJ12586  3'  AACCTCTGCCTCCCAGGTTCAA 45202        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGTCTCCAA
                                    C
GAM948  FLJ12649  3'  AACCTCCGCCTCCTCATCTCAA 45082      ACC   _
                                TTGA   TGAG AGGCGGAGGTT
                                ||||   |||| ||||||||||||
                                AACT   ACTC TCCGCCTCCAA
                                  CT_   C
GAM948  FLJ12687  3'  AACCTCCGCCTCCCGGGTTCAA 46736        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
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                                AACTTGGGC CTCCGCCTCCAA
                                     C
GAM948  FLJ12747  3' AACCTCTGCCTCCCGGGTCCAA 50659    A    A
                                TTG ACCTG GAGGCGGAGGTT
                                ||| ||||| ||||||||||||
                                AAC TGGGC CTCCGTCTCCAA
                                  C    C
GAM948  FLJ12903  3' AACCTCCGCCTCCTGGGTTCAA 43059       GA
                                TTGAACCT  GAGGCGGAGGTT
                                ||||||||  ||||||||||||
                                AACTTGGG  CTCCGCCTCCAA
                                     TC
GAM948  FLJ12960  3' AACCTCCACCTCCTGGGTTCA  45286       GA   C
                                TGAACCT  GAGG GGAGGTT
                                |||||||  |||| |||||||
                                ACTTGGG  CTCC CCTCCAA
                                    TC   A
GAM948  FLJ12973  3' AACCTCCGCCTCCCAGGTTCAA 46633       A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGCCTCCAA
                                     C
GAM948  FLJ13072  5' AACCTCTGCCTCACAGGCTCAA 91376    A   A
                                TTGA CCTG GAGGCGGAGGTT
                                |||| |||| ||||||||||||
                                AACT GGAC CTCCGTCTCCAA
                                  C   A
GAM948  FLJ13193  3' GCTTCCATCTCCCAGGTTCAA  50727       A  GC
                                TTGAACCTG GAG  GGAGGT
                                ||||||||| |||  ||||||
                                AACTTGGAC CTC  CCTTCG
                                     C  TA
GAM948  FLJ13952  3' AACCCCCGCTTCCCGGGTTCAA 45998       A     A
                                TTGAACCTG GAGGCGG GGTT
                                ||||||||| ||||||| ||||
                                AACTTGGGC CTTCGCC CCAA
                                     C      C
GAM948  FLJ14803  3' AACTTCTGCCTCCCAGGCTCAA 52690    A   A
                                TTGA CCTG GAGGCGGAGGTT
                                |||| |||| ||||||||||||
                                AACT GGAC CTCCGTCTTCAA
                                  C   C
GAM948  FLJ14950  3' AACCTCCACCTCCCAGGTTCAA 52774       A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGAC CTCC CCTCCAA
                                     C   A
GAM948  FLJ14957  3' AACCTCTGCCTCCCTGGTTCAA 52800       TGA
                                TTGAACC   GAGGCGGAGGTT
                                |||||||   ||||||||||||
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                                AACTTGG   CTCCGTCTCCAA
                                    TCC
GAM948  FLJ20004  3' AACCTCCGCCTCCCGGCTTCAA 96991      C   A
                                TTGAA CTG GAGGCGGAGGTT
                                ||||| ||| ||||||||||||
                                AACTT GGC CTCCGCCTCCAA
                                   C   C
GAM948  FLJ20034  3' AACCTCTGCCTCCCGGGTTCAA 34826         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGTCTCCAA
                                      C
GAM948  FLJ20344  3' AACCTCCGCCTCTTGGGTTCAA 35470        TG
                                TTGAACC  AGAGGCGGAGGTT
                                |||||||  ||||||||||||
                                AACTTGG  TCTCCGCCTCCAA
                                    GT
GAM948  FLJ20671  3' GTAATCTCCGCCTCCCAGGCTC 35942      A   A
          AA                      TTGA CCTG GAGGCGGAGGTTAC
                                ||||| |||| ||||||||||||||
                                AACT GGAC CTCCGCCTCTAATG
                                  C   C
GAM948  FLJ21302  3' AACCTCCGCCTCCTGGGTTCAA 43496        GA
                                TTGAACCT  GAGGCGGAGGTT
                                ||||||||  ||||||||||||
                                AACTTGGG  CTCCGCCTCCAA
                                     TC
GAM948  FLJ21459  3' CTCCGCCTCCCGGGTTCAA   44802         A
                                TTGAACCTG GAGGCGGAG
                                ||||||||| |||||||||
                                AACTTGGGC CTCCGCCTC
                                      C
GAM948  FLJ22002  3' AACCTCCGCCTCCCAGGTTCAA 46187         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGCCTCCAA
                                      C
GAM948  FLJ22529  3' ACCACCACCCAGGTTCAA    45934         AGA  C  A
                                TTGAACCTG   GG GG GGT
                                |||||||||   || || |||
                                AACTTGGAC   CC CC CCA
                                     ___  A  A
GAM948  FLJ22531  5' AACCTCCACCTCCCAGGTTCAA 45369         A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGAC CTCC CCTCCAA
                                      C   A
GAM948  FLJ22794  3' AACTTCCACCTCCCAGGTTCAA 93232         A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
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                                AACTTGGAC CTCC CCTTCAA
                                      C    A
GAM948   FLJ23024  3'  AACCTCTGCCTCCCGGGTTCAA 46832          A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGTCTCCAA
                                      C
GAM948   FLJ23053  3'  AAGCTCCGCCTCCCAGGTTCA  43552          A        G
                                TGAACCTG GAGGCGGAG TT
                                |||||||| ||||||||| ||
                                ACTTGGAC CTCCGCCTC AA
                                      C        G
GAM948   FLJ23356  3'  GCCTCTGCCTCCCAGGTTCAA  50923          A
                                TTGAACCTG GAGGCGGAGGT
                                ||||||||| ||||||||||
                                AACTTGGAC CTCCGTCTCCG
                                      C
GAM948   FLJ23392  3'  AACCTCTGCCTCCCAGGTTCAA 45866          A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGTCTCCAA
                                      C
GAM948   FLJ23519  3'  AAGCTCCGCCTCCCAAGTTCA  50939       C  A        G
                                TGAAC TG GAGGCGGAG TT
                                ||||| || ||||||||| ||
                                ACTTG AC CTCCGCCTC AA
                                   A  C        G
GAM948   FLJ23556  3'  AACTTGCGCCTCCCGGGTTCAA 46417          A     G
                                TTGAACCTG GAGGCG AGGTT
                                ||||||||| |||||| |||||
                                AACTTGGGC CTCCGC TTCAA
                                      C     G
GAM948   FLJ23563  3'  AACCTCTGCCTCCCAGGTTCAA 68206          A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGTCTCCAA
                                      C
GAM948   FLJ25416  5'  AACCTCCGCATCCTAGGTTCAA 59443          A  G
                                TTGAACCTG GA GCGGAGGTT
                                ||||||||| || |||||||||
                                AACTTGGAT CT CGCCTCCAA
                                      C  A
GAM948   FLJ32865  3'  AACCTCTGCCTCCCGGGTTCAA 58793          A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGTCTCCAA
                                      C
GAM948   GAL3ST-4  3'  AACCTCTGCCTCCCAGGTTCAA 45271          A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
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                                AACTTGGAC CTCCGTCTCCAA
                                     C
GAM948  GMPPB    5'  AACCTCCACCTCCCGGGTTCAA 97426          A    C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGGC CTCC CCTCCAA
                                     C    A
GAM948  GOLGA3   3'  AAGCTCCGCCTCCCAGGTTCA  20876         A        G
                                TGAACCTG GAGGCGGAG TT
                                |||||||| ||||||||| ||
                                ACTTGGAC CTCCGCCTC AA
                                     C        G
GAM948  GP5      3'  AGCCTCCGCCCTCCAGGTTCAA 16860          _  A
                                TTGAACCTG AG GGCGGAGGTT
                                ||||||||| || ||||||||||
                                AACTTGGAC TC CCGCCTCCGA
                                     C  _
GAM948  GRWD     3'  AACCTCCGCCTCCTGGGTT   49768       GA
                                AACCT  GAGGCGGAGGTT
                                |||||  ||||||||||||
                                TTGGG  CTCCGCCTCCAA
                                   TC
GAM948  GTPBG3   3'  AACCTCCACCTCCCGGGTTCAA 51884          A    C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGGC CTCC CCTCCAA
                                     C    A
GAM948  H-plk    5'  AACCTCCACCTCCCAGGTTCAG 32375          A    C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                GACTTGGAC CTCC CCTCCAA
                                     C    A
GAM948  ICK      3'  AACCTCTGCCTCCCAGGTTCAA 30587          A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGTCTCCAA
                                     C
GAM948  JAM1     3'  GTAACCTCCGCCTCCCGGGTTC 58523          A
           AA                     TTGAACCTG GAGGCGGAGGTTAC
                                ||||||||| ||||||||||||||
                                AACTTGGGC CTCCGCCTCCAATG
                                     C
GAM948  JAM1     3'  GTAACCTCCGCCTCCCGGGTTC 58550          A
           AA                     TTGAACCTG GAGGCGGAGGTTAC
                                ||||||||| ||||||||||||||
                                AACTTGGGC CTCCGCCTCCAATG
                                     C
GAM948  JAM1     3'  GTAACCTCCGCCTCCCGGGTTC 58579          A
           AA                     TTGAACCTG GAGGCGGAGGTTAC
                                ||||||||| ||||||||||||||
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                                AACTTGGGC CTCCGCCTCCAATG
                                     C
GAM948  JAM1     3'  GTAACCTCCGCCTCCCGGGTTC 34239          A
              AA                   TTGAACCTG GAGGCGGAGGTTAC
                                   ||||||||| ||||||||||||||
                                   AACTTGGGC CTCCGCCTCCAATG
                                        C
GAM948  KIAA0063 3'  AACCTCCACCTCCTGGTTCAA  30244        TGA    C
                                   TTGAACC   GAGG GGAGGTT
                                   |||||||   |||| |||||||
                                   AACTTGG   CTCC CCTCCAA
                                      TC_    A
GAM948  KIAA0210 5'  AATCTCCGCCTCCCAGATTCAA 29142       C   A
                                   TTGAA CTG GAGGCGGAGGTT
                                   ||||| ||| ||||||||||||
                                   AACTT GAC CTCCGCCTCTAA
                                     A   C
GAM948  KIAA0426 3'  AACCTCCGCCTCCCAGGTTCAA 28912          A
                                   TTGAACCTG GAGGCGGAGGTT
                                   ||||||||| ||||||||||||
                                   AACTTGGAC CTCCGCCTCCAA
                                        C
GAM948  KIAA0459 3'  AACCTCCACCTCCCGGGTTCAA 61638          A    C
                                   TTGAACCTG GAGG GGAGGTT
                                   ||||||||| |||| |||||||
                                   AACTTGGGC CTCC CCTCCAA
                                        C    A
GAM948  KIAA0475 3'  AACCTCCGTCTCCCAGGTTCAA 30103          A
                                   TTGAACCTG GAGGCGGAGGTT
                                   ||||||||| ||||||||||||
                                   AACTTGGAC CTCTGCCTCCAA
                                        C
GAM948  KIAA0495 3'  AACCTCCGTCTCCCAGGTTCAA 63253          A
                                   TTGAACCTG GAGGCGGAGGTT
                                   ||||||||| ||||||||||||
                                   AACTTGGAC CTCTGCCTCCAA
                                        C
GAM948  KIAA0513 3'  AACCTCCACCTCCCGGGTTCAA 29001          A    C
                                   TTGAACCTG GAGG GGAGGTT
                                   ||||||||| |||| |||||||
                                   AACTTGGGC CTCC CCTCCAA
                                        C    A
GAM948  KIAA0527 3'  AACCTCTGCCTCCCAAGTTCAA 97483       C  A
                                   TTGAAC TG GAGGCGGAGGTT
                                   |||||| || ||||||||||||
                                   AACTTG AC CTCCGTCTCCAA
                                      A  C
GAM948  KIAA0544 3'  AACCTCCGCCTCCCGGGTTCAA 71452          A
                                   TTGAACCTG GAGGCGGAGGTT
                                   ||||||||| ||||||||||||
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                                AACTTGGGC CTCCGCCTCCAA
                                     C
GAM948  KIAA0557 3' AACCTCCACCTCCCAGGTTCAA 78536        A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGAC CTCC CCTCCAA
                                     C   A
GAM948  KIAA0561 3' AACCTCCGCCTCCCAAGTTCAA 66458      C A
                                TTGAAC TG GAGGCGGAGGTT
                                |||||| || ||||||||||||
                                AACTTG AC CTCCGCCTCCAA
                                   A C
GAM948  KIAA0562 3' AACCTCCGCCTCCCGGGTTCGA 28809       A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AGCTTGGGC CTCCGCCTCCAA
                                     C
GAM948  KIAA0563 5' AACCTCTGCCTCCCGGGTTCAA 29863       A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGTCTCCAA
                                     C
GAM948  KIAA0594 3' AACCTCCGCCTCCCGGGTTCAA 65501       A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGCCTCCAA
                                     C
GAM948  KIAA0599 3' AACCTCCGCCTCCCAGGTTCAA 77681       A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGCCTCCAA
                                     C
GAM948  KIAA0643 5' GCCTCTGCCTCCCAGGTTCAA  45978       A
                                TTGAACCTG GAGGCGGAGGT
                                ||||||||| ||||||||||
                                AACTTGGAC CTCCGTCTCCG
                                     C
GAM948  KIAA0663 5' AACCTCCGCCTCCCGGGTTCAA 29787       A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGCCTCCAA
                                     C
GAM948  KIAA0720 3' AACCTCTGCCTCCCGGGTTCAA 62972       A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGTCTCCAA
                                     C
GAM948  KIAA0798 3' AACCCCGCCTCCCAGGTTCAA  28436       A     A
                                TTGAACCTG GAGGCGG GGTT
                                ||||||||| ||||||| ||||
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                                AACTTGGAC CTCCGCC CCAA
                                     C      _
GAM948  KIAA0841  3'  AACCTCCGCCTCCCAGGTTCAA 71884         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGCCTCCAA
                                     C
GAM948  KIAA0889  3'  GTAACCTCCGCCTCCTGGGTTC 31782        GA
          AA                     TTGAACCT  GAGGCGGAGGTTAC
                                ||||||||  ||||||||||||||
                                AACTTGGG  CTCCGCCTCCAATG
                                     TC
GAM948  KIAA0924  3'  AACCCCCCGCCCCCCGGGTTCAA 30344         AGA    A
                                TTGAACCTG   GGCGG GGTT
                                |||||||||   ||||| ||||
                                AACTTGGGC   CCGCC CCAA
                                     CCC    C
GAM948  KIAA1028  3'  AACCTCCACCTTCCAGGTTCAA 93584         AG   C
                                TTGAACCTG  AGG GGAGGTT
                                |||||||||  ||| |||||||
                                AACTTGGAC  TCC CCTCCAA
                                     CT   A
GAM948  KIAA1040  3'  AACCTCTGCTTCCCGGGTTCAA 72673         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTTCGTCTCCAA
                                     C
GAM948  KIAA1041  3'  AACCTCCGCCTCCCGGGTTCAA 30814         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGCCTCCAA
                                     C
GAM948  KIAA1054  3'  AACCTCCGCCTCCCAGGTTCAA 68956         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGCCTCCAA
                                     C
GAM948  KIAA1128  3'  AACTTCTGCCTCCCGGGTTCAA 68993         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGTCTTCAA
                                     C
GAM948  KIAA1161  5'  AACCCCTCCTCCTAGGTTCAA  82633        A   C  A
                                TTGAACCTG GAGG GG GGTT
                                ||||||||| |||| || ||||
                                AACTTGGAT CTCC CC CCAA
                                     C   T  _
GAM948  KIAA1170  3'  AACCTCCGCCTCCCGGGTTCAA 70401         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
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                                AACTTGGGC CTCCGCCTCCAA
                                     C
GAM948  KIAA1193 3' AACCTCCGCCTCCTGAGTTCA  68259      C GA
                                TGAAC T  GAGGCGGAGGTT
                                ||||| |  ||||||||||||
                                ACTTG G  CTCCGCCTCCAA
                                   A TC
GAM948  KIAA1198 3' AACCTCCACTTCTCAGGTTCAA 63966            C
                                TTGAACCTGAGAGG GGAGGTT
                                |||||||||||||| |||||||
                                AACTTGGACTCTTC CCTCCAA
                                       A
GAM948  KIAA1198 3' AACCTCCGCCTCCCGGATTCAA 63967      C   A
                                TTGAA CTG GAGGCGGAGGTT
                                ||||| ||| ||||||||||||
                                AACTT GGC CTCCGCCTCCAA
                                   A   C
GAM948  KIAA1198 3' AACCTCTGCCTCCCAGGTCAA  63968     A    A
                                TTGA CCTG GAGGCGGAGGTT
                                |||| |||| ||||||||||||
                                AACT GGAC CTCCGTCTCCAA
                                  _    C
GAM948  KIAA1198 3' AATCTCTGCCTCCCAGGTTCAA 63973          A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGTCTCTAA
                                     C
GAM948  KIAA1257 3' AACCTCCGCCTCCCGGGTTCAA 63381          A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGCCTCCAA
                                     C
GAM948  KIAA1373 3' AACCTCCACCTCCCAGGTTCAA 71498          A    C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGAC CTCC CCTCCAA
                                     C    A
GAM948  KIAA1443 3' AAGCTCCGCCTCCCAGGTTCA  64562          A        G
                                TGAACCTG GAGGCGGAG TT
                                |||||||| ||||||||| ||
                                ACTTGGAC CTCCGCCTC AA
                                     C        G
GAM948  KIAA1465 3' CTTCCGCCTCCCGGGTTCAA   61495          A
                                TTGAACCTG GAGGCGGAGG
                                ||||||||| ||||||||||
                                AACTTGGGC CTCCGCCTTC
                                     C
GAM948  KIAA1473 3' AACCTCCGTCTCCAGGGTTCAA 71200          GA
                                TTGAACCT  GAGGCGGAGGTT
                                ||||||||  ||||||||||||
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                                AACTTGGG  CTCTGCCTCCAA
                                    AC
GAM948  KIAA1497 5' AACCTCTGCCTCCCAGGTTCAA 68103         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGTCTCCAA
                                    C
GAM948  KIAA1508 3' AACCTCCGCCTCCTGGGATCAA 62530      A  GA
                                TTGA CCT  GAGGCGGAGGTT
                                |||| |||  ||||||||||||
                                AACT GGG  CTCCGCCTCCAA
                                  A  TC
GAM948  KIAA1571 3' AACCTCCACCTCCCGGGTTCAA 61608         A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGGC CTCC CCTCCAA
                                    C   A
GAM948  KIAA1615 3' AACCTCCACCTCCCAGGTTCAA 69260         A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGAC CTCC CCTCCAA
                                    C   A
GAM948  KIAA1617 3' AACCTCTCTCTCCCGGGTTCAA 93064         A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGGC CTCT TCTCCAA
                                    C   C
GAM948  KIAA1649 3' AACCTCCGCAGCCAGACTCAA  51207     AC  AGAG
                                TTGA  CTG   GCGGAGGTT
                                ||||  |||   |||||||||
                                AACT  GAC   CGCCTCCAA
                                  CA  CGA_
GAM948  KIAA1655 3' AACCTCCGCCTCCCAGGTTCAA 67166         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGCCTCCAA
                                    C
GAM948  KIAA1655 3' GTAACCTCCACCTCCCGTGTTC 67197       C A   C
           AA                    TTGAAC TG GAGG GGAGGTTAC
                                ||||||| || |||| |||||||||
                                AACTTG GC CTCC CCTCCAATG
                                   T  C   A
GAM948  KIAA1715 3' GTAATTCAGCTTCTCAGATTCA 68689      C       G  G
           A                     TTGAA CTGAGAGGC GAG TTAC
                                ||||| ||||||||| ||| ||||
                                AACTT GACTCTTCG CTT AATG
                                  A       A  _
GAM948  KIAA1737 3' AACCTCCGCCTCCTGGGTTCAA 67925         GA
                                TTGAACCT  GAGGCGGAGGTT
                                ||||||||  ||||||||||||
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                                AACTTGGG  CTCCGCCTCCAA
                                     TC
GAM948  KIAA1784  3'  AACCTCCGCCTCCCGGGTTCAA 65735         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGCCTCCAA
                                     C
GAM948  KIAA1854  3'  GCAAAGCCTCTCAGATTCAA  72209      C       GGAG
                                TTGAA CTGAGAGGC   GT
                                ||||| |||||||||   ||
                                AACTT GACTCTCCG   CG
                                   A       AAA_
GAM948  KIAA1922  5'  AACCTCCGCCTCCCAGGTTCAA 73977         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGCCTCCAA
                                     C
GAM948  KIAA1924  3'  AAGCTCCGCCTCCCAGGTTCA  74035        A       G
                                TGAACCTG GAGGCGGAG TT
                                |||||||| ||||||||| ||
                                ACTTGGAC CTCCGCCTC AA
                                     C       G
GAM948  KIAA1971  3'  AACCTCCACCTCCCAGGTTCAA 74662         A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGAC CTCC CCTCCAA
                                     C   A
GAM948  KIAA1987  5'  AATCTCCGCCTCCCAGGTTCAA 89376         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGCCTCTAA
                                     C
GAM948  KLK7      3'  AACCTCCGCCTCCTGGGTTCAA 18532        GA
                                TTGAACCT  GAGGCGGAGGTT
                                ||||||||  ||||||||||||
                                AACTTGGG  CTCCGCCTCCAA
                                     TC
GAM948  KLK7      3'  AACCTCCGCCTCCTGGGTTCAA 58381        GA
                                TTGAACCT  GAGGCGGAGGTT
                                ||||||||  ||||||||||||
                                AACTTGGG  CTCCGCCTCCAA
                                     TC
GAM948  LAMP3     3'  AACCTCCGCCTCCCGGGTTCAA 60188         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGCCTCCAA
                                     C
GAM948  LY75      3'  AATCTCCGCCTCCCAGGTTCAA 11383         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
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                                AACTTGGAC CTCCGCCTCTAA
                                     C
GAM948  MCLC     3'  AACCTCCACCTCCCAGGTTCAA 31371          A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGAC CTCC CCTCCAA
                                     C   A
GAM948  MEF-2    3'  AACCTCCGCCTCCTGGATTCAA 65011       C  GA
                                TTGAA CT  GAGGCGGAGGTT
                                ||||| ||  ||||||||||||
                                AACTT GG  CTCCGCCTCCAA
                                   A  TC
GAM948  MGC1842  3'  AACCTCCGCCTCCTGGGTTCAA 66243         GA
                                TTGAACCT  GAGGCGGAGGTT
                                ||||||||  ||||||||||||
                                AACTTGGG  CTCCGCCTCCAA
                                     TC
GAM948  MGC3329  3'  AACCCCCGCCTCCCGGGTTCAG 44236          A      A
                                TTGAACCTG GAGGCGG GGTT
                                ||||||||| ||||||| ||||
                                GACTTGGGC CTCCGCC CCAA
                                     C      C
GAM948  MGC5149  3'  AACCTCTGCCTCCCAGGTTCAA 72747          A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGTCTCCAA
                                     C
GAM948  MKRN4    3'  AACCTCCGTCTTCCGGGTTCAA 48443          AG
                                TTGAACCTG  AGGCGGAGGTT
                                |||||||||  ||||||||||||
                                AACTTGGGC  TCTGCCTCCAA
                                     CT
GAM948  MLZE     5'  AACCTCTGCCTCCCGGGTTCAA 49442          A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGTCTCCAA
                                     C
GAM948  moblak   3'  AAGCTCCGCCTCCCAGATTCA  56378      C  A       G
                                TGAA CTG GAGGCGGAG TT
                                |||| ||| ||||||||| ||
                                ACTT GAC CTCCGCCTC AA
                                   A  C        G
GAM948  MOCS3    3'  AACCTCCGCCTCCCAGGTTCAA 27922          A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGCCTCCAA
                                     C
GAM948  MRPL20   3'  AACCTCGTCTCCCGGGTTCAA  36196          A     G
                                TTGAACCTG GAGGCG AGGTT
                                ||||||||| |||||| |||||
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                                AACTTGGGC CTCTGC TCCAA
                                    C     _
GAM948  MRPL44   3'  AACCTCCACCTCACAGGTTCAA 43588        A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGAC CTCC CCTCCAA
                                    A   A
GAM948  MRPS27   3'  AACCTCCGACTCCCAGGTTCAA 31313        A  G
                                TTGAACCTG GAG CGGAGGTT
                                ||||||||| ||| ||||||||
                                AACTTGGAC CTC GCCTCCAA
                                    C  A
GAM948  MtFMT    3'  AACCTCCGCCTCCCAGGTTCAA 58324        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGCCTCCAA
                                    C
GAM948  NDP52    3'  GCCTCTGCCTCCCAGGTTCAA  20672        A
                                TTGAACCTG GAGGCGGAGGT
                                ||||||||| ||||||||||
                                AACTTGGAC CTCCGTCTCCG
                                    C
GAM948  NDUFB1   5'  AACCTCTGCCTCCCGAGTTCAA 17012       C  A
                                TTGAAC TG GAGGCGGAGGTT
                                |||||| || ||||||||||||
                                AACTTG GC CTCCGTCTCCAA
                                   A  C
GAM948  NDUFC2   3'  AACCTCCACCTCCTGGGTTCAA 17017        GA   C
                                TTGAACCT  GAGG GGAGGTT
                                ||||||||  |||| |||||||
                                AACTTGGG  CTCC CCTCCAA
                                    TC   A
GAM948  NFAT5    3'  AGCCTCCACCTCCCAGGTTCAA 57783        A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGAC CTCC CCTCCGA
                                    C   A
GAM948  NINJ2    3'  ACCTCCGCCTCCCAGGTTCAA  33714        A
                                TTGAACCTG GAGGCGGAGGT
                                ||||||||| ||||||||||
                                AACTTGGAC CTCCGCCTCCA
                                    C
GAM948  NOSIP    5'  ACCTTCGCCTCCCAGGTTCAA  32540        A
                                TTGAACCTG GAGGCGGAGGT
                                ||||||||| ||||||||||
                                AACTTGGAC CTCCGCTTCCA
                                    C
GAM948  Nup43    3'  AACCTCCACCTCCCGGGTTCAA 45336        A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
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                                AACTTGGGC CTCC CCTCCAA
                                    C    A
GAM948  NXN      3'  AACCTCCGCCCCCAAGGTTCAA 42657        GAGA
                                TTGAACCT   GGCGGAGGTT
                                ||||||||   ||||||||||
                                AACTTGGA   CCGCCTCCAA
                                    ACCC
GAM948  OSBPL2   3'  AACCTCCGCCTCCCGGGTTCAA 29893         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGCCTCCAA
                                    C
GAM948  OSBPL2   3'  AACCTCCGCCTCCCGGGTTCAA 58475         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGCCTCCAA
                                    C
GAM948  PELI1    5'  AACCTCCTCCTCCCGGGTTCAA 40612         A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGGC CTCC CCTCCAA
                                    C   T
GAM948  PELI1    5'  AACCTCTGCCTCCAGGTTCAA  40613         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGTCTCCAA
                                    _
GAM948  PRO0365  5'  AACCTCTGTCTCCCAGGTTCAG 26973         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                GACTTGGAC CTCTGTCTCCAA
                                    C
GAM948  PRO2955  3'  AACCTCTGCCTCCCGGGTTCAA 38227         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGTCTCCAA
                                    C
GAM948  PSTPIP2  3'  AACCTCTGCCTCCCGGGTTCAA 44643         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGTCTCCAA
                                    C
GAM948  RAB21    3'  AAGCTCCACCTCCCAGGTTCA  31076         A   C   G
                                TGAACCTG GAGG GGAG TT
                                |||||||| |||| |||| ||
                                ACTTGGAC CTCC CCTC AA
                                    C   A   G
GAM948  RAB33B   3'  AACCTCCGCCTCCCAGGTTCAA 49309         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
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                                  AACTTGGAC CTCCGCCTCCAA
                                       C
GAM948  RAI      5' AACCTCCGCCTCCTGGGTTCAA 22847        GA
                                  TTGAACCT  GAGGCGGAGGTT
                                  ||||||||  ||||||||||||
                                  AACTTGGG  CTCCGCCTCCAA
                                       TC
GAM948  RES4-25  3' AACCTCCACCTCCTGGGTTCAA 65255        GA   C
                                  TTGAACCT  GAGG GGAGGTT
                                  ||||||||  ||||  |||||||
                                  AACTTGGG  CTCC CCTCCAA
                                       TC   A
GAM948  SC4MOL   3' AACCTCTGCCTCCCAGTTCAA  23099       C  A
                                  TTGAAC TG GAGGCGGAGGTT
                                  ||||||  ||  ||||||||||||
                                  AACTTG AC CTCCGTCTCCAA
                                     _  C
GAM948  SCAND2   3' AACATCTGCCTCCCGGGTTCAA 42140         A      G
                                  TTGAACCTG GAGGCGGA GTT
                                  |||||||||  ||||||||  |||
                                  AACTTGGGC CTCCGTCT CAA
                                       C       A
GAM948  SCYA16   3' GTAACCTCCACCTCCCAGGCTC 17175     A   A   C
          AA                        TTGA CCTG GAGG GGAGGTTAC
                                  ||||  ||||  ||||  |||||||||
                                  AACT GGAC CTCC CCTCCAATG
                                    C   C   A
GAM948  SERF1B   3' AACCTCCGCCTCCCGGGTTCAA 43682         A
                                  TTGAACCTG GAGGCGGAGGTT
                                  |||||||||  ||||||||||||
                                  AACTTGGGC CTCCGCCTCCAA
                                       C
GAM948  SIRPB1   3' AACCCCCGCCTCCAGGGTTCAA 21349        GA      A
                                  TTGAACCT  GAGGCGG GGTT
                                  ||||||||  |||||||  ||||
                                  AACTTGGG  CTCCGCC CCAA
                                       AC      C
GAM948  SLC11A1  3' AACCTCCACCTTCTGGGTTCAA 60152        GA   C
                                  TTGAACCT  GAGG GGAGGTT
                                  ||||||||  ||||  |||||||
                                  AACTTGGG  TTCC CCTCCAA
                                       TC   A
GAM948  SLC12A8  3' AACCTCTGCTTCCCGAGTTCAA 45227       C  A
                                  TTGAAC TG GAGGCGGAGGTT
                                  ||||||  ||  ||||||||||||
                                  AACTTG GC CTTCGTCTCCAA
                                     A  C
GAM948  STAF65(gamma) 3'  AACCTCTGCCTCCCAGGTTCAA 30055         A
                                  TTGAACCTG GAGGCGGAGGTT
                                  |||||||||  ||||||||||||
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                                  AACTTGGAC CTCCGTCTCCAA
                                       C
GAM948  SYT13    3'  AACCTCCGCCTCCCAAGTTCAA 95090       C  A
                                  TTGAAC TG GAGGCGGAGGTT
                                  ||||||  || ||||||||||||
                                  AACTTG AC CTCCGCCTCCAA
                                     A  C
GAM948  TADA3L   3'  AAGCTCCGCCTCCCAGGTTCA  56800         A        G
                                  TGAACCTG GAGGCGGAG TT
                                  ||||||||  |||||||||  ||
                                  ACTTGGAC CTCCGCCTC AA
                                       C        G
GAM948  TCL6     5'  GCCTTCACCTCCCGGGTTCAA  40482         A    C
                                  TTGAACCTG GAGG GGAGGT
                                  |||||||||  ||||  ||||||
                                  AACTTGGGC CTCC CTTCCG
                                       C    A
GAM948  TCL6     5'  GCCTTCACCTCCCGGGTTCAA  27762         A    C
                                  TTGAACCTG GAGG GGAGGT
                                  |||||||||  ||||  ||||||
                                  AACTTGGGC CTCC CTTCCG
                                       C    A
GAM948  TCL6     5'  GCCTTCACCTCCCGGGTTCAA  25910         A    C
                                  TTGAACCTG GAGG GGAGGT
                                  |||||||||  ||||  ||||||
                                  AACTTGGGC CTCC CTTCCG
                                       C    A
GAM948  TCL6     5'  GCCTTCACCTCCCGGGTTCAA  40513         A    C
                                  TTGAACCTG GAGG GGAGGT
                                  |||||||||  ||||  ||||||
                                  AACTTGGGC CTCC CTTCCG
                                       C    A
GAM948  TRIM16   3'  CTCCGCCTCCCGAGTTCAA   22370       C  A
                                  TTGAAC TG GAGGCGGAG
                                  ||||||  || |||||||||
                                  AACTTG GC CTCCGCCTC
                                     A  C
GAM948  TRIM5    3'  AACCTCCACCTCTCAGATTCAA 53455      C       C
                                  TTGAA CTGAGAGG GGAGGTT
                                  |||||  ||||||||  |||||||
                                  AACTT GACTCTCC CCTCCAA
                                     A       A
GAM948  TU12B1-TY 3'  AACCTCTGCCTCCCGGGTTCAA 33813          A
                                  TTGAACCTG GAGGCGGAGGTT
                                  |||||||||  ||||||||||||
                                  AACTTGGGC CTCCGTCTCCAA
                                       C
GAM948  TU12B1-TY 3'  AACCTCTTGCCTCCCAGGTTCA 33814          A    _
              A                    TTGAACCTG GAGGCG GAGGTT
                                  |||||||||  ||||||  ||||||
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                                AACTTGGAC CTCCGT CTCCAA
                                     C     T
GAM948  UBF-fl   3'  AACCTCTGCCTCCCAAGTTCAA 52612       C  A
                                TTGAAC TG GAGGCGGAGGTT
                                |||||| || ||||||||||||
                                AACTTG AC CTCCGTCTCCAA
                                   A  C
GAM948  VPS33A   3'  AACCTCCACCTCCTAGGTTCAA 43603         A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGAT CTCC CCTCCAA
                                     C   A
GAM948  WBSCR23  3'  AACCTCCGCCTCTCAGGTTCAA 47404
                                TTGAACCTGAGAGGCGGAGGTT
                                ||||||||||||||||||||||
                                AACTTGGACTCTCCGCCTCCAA

GAM948  ZNF221   3'  AAGCTCCGCCTCCCAAGTTCA  26259      C  A       G
                                TGAAC TG GAGGCGGAG TT
                                ||||| || ||||||||| ||
                                ACTTG AC CTCCGCCTC AA
                                   A  C        G
GAM948  ZNF338   3'  AACGTCCGCCTCCCAGGTTCAA 42247         A       G
                                TTGAACCTG GAGGCGGA GTT
                                ||||||||| |||||||| |||
                                AACTTGGAC CTCCGCCT CAA
                                     C       G
GAM948  ZNF339   3'  AACCTTGACCTCCCAGGCTCAG 41386      A   A   CG
                                TTGA CCTG GAGG  GAGGTT
                                |||| |||| ||||  ||||||
                                GACT GGAC CTCC  TTCCAA
                                  C   C   AG
GAM948  ZTL1     3'  AACCTCTGCCTCCCGGGTTCAA 44136         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGTCTCCAA
                                     C
GAM948  LOC113675 5'  AACCTCCGCCTCCCGGGTTCAA 57376         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGCCTCCAA
                                     C
GAM948  LOC115219 5'  AACCTCCGCCTCCTGGGTTCAA 73679        GA
                                TTGAACCT  GAGGCGGAGGTT
                                ||||||||  ||||||||||||
                                AACTTGGG  CTCCGCCTCCAA
                                     TC
GAM948  LOC120224 5'  AACCTCCCTCTCCCGGGTTCAA 57875         A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
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                                AACTTGGGC CTCT CCTCCAA
                                     C    C
GAM948   LOC120939 3'  GTAACCTCCACCTCCCGGATTC 76768      C   A    C
              AA                    TTGAA CTG GAGG GGAGGTTAC
                                    ||||| ||| |||| |||||||||
                                    AACTT GGC CTCC CCTCCAATG
                                      A   C    A
GAM948   LOC121504 3'  GCCTCCGCCTCCCGGGTTCAA  74548          A
                                    TTGAACCTG GAGGCGGAGGT
                                    ||||||||| ||||||||||
                                    AACTTGGGC CTCCGCCTCCG
                                         C
GAM948   LOC126364 3'  AACCTCCGCCTCCTGGGTTCAA 76177         GA
                                    TTGAACCT  GAGGCGGAGGTT
                                    ||||||||  ||||||||||||
                                    AACTTGGG  CTCCGCCTCCAA
                                         TC
GAM948   LOC126661 3'  AACCTCCGCCTCCCAGGTTCAA 75042          A
                                    TTGAACCTG GAGGCGGAGGTT
                                    ||||||||| ||||||||||||
                                    AACTTGGAC CTCCGCCTCCAA
                                         C
GAM948   LOC128077 3'  AACCTCCGCCTCCCAGATTCA  75193      C   A
                                    TGAA CTG GAGGCGGAGGTT
                                    |||| ||| ||||||||||||
                                    ACTT GAC CTCCGCCTCCAA
                                      A   C
GAM948   LOC128989 3'  AACCTCCGCCTCCCAAGTTCAA 75302       C  A
                                    TTGAAC TG GAGGCGGAGGTT
                                    |||||| || ||||||||||||
                                    AACTTG AC CTCCGCCTCCAA
                                       A  C
GAM948   LOC130813 3'  AACCTCCGCCTCCTAGGTCCAG 76256      A    A
                                    TTG ACCTG GAGGCGGAGGTT
                                    ||| ||||| ||||||||||||
                                    GAC TGGAT CTCCGCCTCCAA
                                      C    C
GAM948   LOC132625 3'  AACCTCCACCTCCCGGGTTCAA 76424          A   C
                                    TTGAACCTG GAGG GGAGGTT
                                    ||||||||| |||| |||||||
                                    AACTTGGGC CTCC CCTCCAA
                                         C   A
GAM948   LOC133686 3'  AACCTCCATCTCCCAGGTTCAA 75609          A  GC
                                    TTGAACCTG GAG  GGAGGTT
                                    ||||||||| |||  |||||||
                                    AACTTGGAC CTC  CCTCCAA
                                         C  TA
GAM948   LOC135154 3'  AACTTCCGCCCCGCCAGGTTCA 75713          AGA_
              A                      TTGAACCTG   GGCGGAGGTT
                                    |||||||||   ||||||||||
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                                AACTTGGAC    CCGCCTTCAA
                                     CGCC
GAM948   LOC135293 3'  AACCTCTGCCTCCCAGGTTCAA 76671          A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGTCTCCAA
                                     C
GAM948   LOC135763 3'  AACCTCCGCCTCCTGGGTTCAA 57552         GA
                                TTGAACCT  GAGGCGGAGGTT
                                ||||||||  ||||||||||||
                                AACTTGGG  CTCCGCCTCCAA
                                     TC
GAM948   LOC135818 3'  AACCTCCGCCTCCCAGGTTCAA 75740          A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGCCTCCAA
                                     C
GAM948   LOC142937 5'  GCCCGCGCTTCTCAAGCTCAA  57445     ACC       GA
                                TTGA   TGAGAGGCG  GGT
                                ||||   |||||||||  |||
                                AACT   ACTCTTCGC  CCG
                                  CGA        GC
GAM948   LOC143241 5'  AACCTCTGCCTCCCGGGTTCAA 57971          A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGTCTCCAA
                                     C
GAM948   LOC144317 5'  AACCTCTTCCTCCCAGGTTCAA 77283          A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGAC CTCC TCTCCAA
                                     C   T
GAM948   LOC144742 5'  AACCTTCGCCTCCCGGGTTCAA 77452          A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGCTTCCAA
                                     C
GAM948   LOC144871 3'  ACCTCCCGGGTTCAA       84115          AGAGGC
                                TTGAACCTG     GGAGGT
                                |||||||||     ||||||
                                AACTTGGGC     CCTCCA
                                              _____
GAM948   LOC145082 5'  GCCTCATCTCCCAGGCTCAA  84191      A   A   CG
                                TTGA CCTG GAGG  GAGGT
                                |||| |||| ||||  |||||
                                AACT GGAC CTCT  CTCCG
                                  C   C   A_
GAM948   LOC145268 5'  AACCTCCACCCGCCGGGTTCAA 77564          AGA  C
                                TTGAACCTG   GG GGAGGTT
                                |||||||||   || |||||||
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                                AACTTGGGC   CC CCTCCAA
                                     CGC  A
GAM948   LOC145622 3'  AACTTCTGCCTCCCGGGTTCAA 77798        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGTCTTCAA
                                     C
GAM948   LOC145757 5'  AACCTCTGCCTCCCAGGTTCAA 77909        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGTCTCCAA
                                     C
GAM948   LOC145813 5'  AACCTTGACGTCCCAGGTTCAA 84502        AGA   __
                                TTGAACCTG   GGCG  GAGGTT
                                |||||||||   ||||  ||||||
                                AACTTGGAC   CTGC  TTCCAA
                                     C__    AG
GAM948   LOC146050 3'  AACCTCTGCTTCCCGGGTTCAA 78093        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTTCGTCTCCAA
                                     C
GAM948   LOC146229 3'  AACCTCCACCTCCCGGGTTCAA 78236        A    C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGGC CTCC CCTCCAA
                                     C    A
GAM948   LOC146346 5'  AACTTCTGCCTCCTAGGTTCAA 78378        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAT CTCCGTCTTCAA
                                     C
GAM948   LOC146784 5'  AACCTCCACCTCCCAGGTTCAA 78699        A    C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGAC CTCC CCTCCAA
                                     C    A
GAM948   LOC146820 5'  AACCTCCGCATCCCGGGTTCAA 78736        A  G
                                TTGAACCTG GA GCGGAGGTT
                                ||||||||| || |||||||||
                                AACTTGGGC CT CGCCTCCAA
                                     C  A
GAM948   LOC146839 3'  AACCTCCGCCTCCTGGGTTCA  84830       GA
                                TGAACCT  GAGGCGGAGGTT
                                |||||||  ||||||||||||
                                ACTTGGG  CTCCGCCTCCAA
                                    TC
GAM948   LOC146909 3'  AACCTCCGCCTCCTGGGTTCAA 78751        GA
                                TTGAACCT  GAGGCGGAGGTT
                                ||||||||  ||||||||||||
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                                AACTTGGG  CTCCGCCTCCAA
                                    TC
GAM948   LOC146909 3'  AAGCTCCGCCTCCCAGGTTCA  78753        A       G
                                TGAACCTG GAGGCGGAG TT
                                |||||||| ||||||||| ||
                                ACTTGGAC CTCCGCCTC AA
                                    C       G
GAM948   LOC146952 5'  AACCTCCACCTCTCAGGTTCAA 84917            C
                                TTGAACCTGAGAGG GGAGGTT
                                |||||||||||||| |||||||
                                AACTTGGACTCTCC CCTCCAA
                                      A
GAM948   LOC147071 5'  AACCTCTGCCTCCCAGGTTCAA 73342        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGTCTCCAA
                                    C
GAM948   LOC147166 3'  CTCCGCCTCCCGAGTTCAA   78887      C  A
                                TTGAAC TG GAGGCGGAG
                                |||||| || |||||||||
                                AACTTG GC CTCCGCCTC
                                   A  C
GAM948   LOC147276 3'  AACGTCTGCCTCCCGGGTTCAA 78944        A       G
                                TTGAACCTG GAGGCGGA GTT
                                ||||||||| |||||||| |||
                                AACTTGGGC CTCCGTCT CAA
                                    C       G
GAM948   LOC147660 3'  AACCTCCGCCTCCTGGGTTCAA 79021        GA
                                TTGAACCT  GAGGCGGAGGTT
                                ||||||||  ||||||||||||
                                AACTTGGG  CTCCGCCTCCAA
                                    TC
GAM948   LOC147694 3'  AAGCTCCGCCTCCCAGGTTCA  79086        A       G
                                TGAACCTG GAGGCGGAG TT
                                |||||||| ||||||||| ||
                                ACTTGGAC CTCCGCCTC AA
                                    C       G
GAM948   LOC147817 3'  AACCTCCACCTCCCAGGTTCAA 79160        A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGAC CTCC CCTCCAA
                                    C   A
GAM948   LOC148137 3'  AACCTCCACCTCCCGGGTTCAA 59084        A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGGC CTCC CCTCCAA
                                    C   A
GAM948   LOC148189 5'  AACCTCCACCTCCTGGGTTCAA 79439        GA   C
                                TTGAACCT  GAGG GGAGGTT
                                ||||||||  |||| |||||||
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                                AACTTGGG  CTCC CCTCCAA
                                    TC    A
GAM948   LOC148709 3'  AACCTCCGCCTCCTGGGTCCAA 79684     A    GA
                                TTG ACCT  GAGGCGGAGGTT
                                ||| ||||  ||||||||||||
                                AAC TGGG  CTCCGCCTCCAA
                                  C    TC
GAM948   LOC148760 3'  TAAAATCCTGCTCAGGTTCAA  85366          AGGC   GG
                                TTGAACCTGAG    GGA  TTA
                                ||||||||||    |||  |||
                                AACTTGGACTC    CCT  AAT
                                      GT__   AA
GAM948   LOC148887 5'  AACATCTGCCTCCCGGGTTCAA 85385         A       G
                                TTGAACCTG GAGGCGGA GTT
                                |||||||| |||||||| |||
                                AACTTGGGC CTCCGTCT CAA
                                      C       A
GAM948   LOC149478 3'  CTCCGCCTCCCGGGTTCAA    80167         A
                                TTGAACCTG GAGGCGGAG
                                ||||||||| |||||||||
                                AACTTGGGC CTCCGCCTC
                                      C
GAM948   LOC149506 3'  AACTTCCACCTCCCGGGTTCAA 85619         A    C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGGC CTCC CCTTCAA
                                      C    A
GAM948   LOC149577 3'  AACCTCCACCTCCCAGGTTCAA 85657         A    C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGAC CTCC CCTCCAA
                                      C    A
GAM948   LOC149577 3'  AACCTTGGCCTCCTAGGTTCAA 85658         A     G
                                TTGAACCTG GAGGC GAGGTT
                                ||||||||| ||||| ||||||
                                AACTTGGAT CTCCG TTCCAA
                                      C     G
GAM948   LOC149703 5'  AACCTCTACCTCCCAGGTTCAA 85811         A    CG
                                TTGAACCTG GAGG  GAGGTT
                                ||||||||| ||||  ||||||
                                AACTTGGAC CTCC  CTCCAA
                                      C    AT
GAM948   LOC149711 3'  AACCTCTGCTTCCCGGGTTCAA 85828         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTTCGTCTCCAA
                                      C
GAM948   LOC149821 5'  AAGCTCCGCCTCCCAGGTTCA  85923         A       G
                                TGAACCTG GAGGCGGAG TT
                                |||||||| ||||||||| ||
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                                ACTTGGAC CTCCGCCTC AA
                                    C        G
GAM948   LOC150397 3'  AACCTCCGCCTCCCGGGTTCAA 80647          A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGCCTCCAA
                                    C
GAM948   LOC150587 3'  TTTGCCTCCAAAGTTCAA    86247       C_  A
                                TTGAAC  TG GAGGCGGA
                                ||||||  || ||||||||
                                AACTTG  AC CTCCGTTT
                                   AA  _
GAM948   LOC150960 3'  AACCTCCGCCTCCCAGGTTCAA 80858          A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGCCTCCAA
                                    C
GAM948   LOC151475 5'  AACCTCCACCTCCCAGGTTCAA 86578          A    C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGAC CTCC CCTCCAA
                                    C    A
GAM948   LOC151701 3'  AACCTCCACTTTCCGGGTTCAA 86658          AG   C
                                TTGAACCTG  AGG GGAGGTT
                                |||||||||  ||| |||||||
                                AACTTGGGC  TTC CCTCCAA
                                    CT   A
GAM948   LOC151826 3'  AACCTCCGCCTCCTGAGGTTCA 81171         G  _
          A                      TTGAACCT AG AGGCGGAGGTT
                                ||||||||| || ||||||||||
                                AACTTGGA TC TCCGCCTCCAA
                                    G  C
GAM948   LOC152300 3'  AAGCTCTGCCTCTCAGGTTCAA 81375                G
                                TTGAACCTGAGAGGCGGAG TT
                                |||||||||||||||||| ||
                                AACTTGGACTCTCCGTCTC AA
                                       G
GAM948   LOC152343 3'  AACCTCCGCCTCCCAGGTTCAA 81411          A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGCCTCCAA
                                    C
GAM948   LOC152582 5'  AACCTCTGCCTCCCAGGTGCAA 86988      A    A
                                TTG ACCTG GAGGCGGAGGTT
                                ||| ||||| ||||||||||||
                                AAC TGGAC CTCCGTCTCCAA
                                  G    C
GAM948   LOC152719 5'  AACCTCTGCCTCCCGGGTTCAA 87007          A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
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                                AACTTGGGC CTCCGTCTCCAA
                                     C
GAM948  LOC152794 5'  AACCTCTACCTCCCAGGTTCAA 81550        A   CG
                                TTGAACCTG GAGG  GAGGTT
                                ||||||||| ||||  ||||||
                                AACTTGGAC CTCC  CTCCAA
                                     C   AT
GAM948  LOC152851 3'  AACCTCCACCCATGGGTTCAA  81585        AGA  C
                                TTGAACCTG   GG GGAGGTT
                                |||||||||   || |||||||
                                AACTTGGGT   CC CCTCCAA
                                     AC_  A
GAM948  LOC152925 3'  ACCTCTGCCTCCCAGGTTCAA  81613        A
                                TTGAACCTG GAGGCGGAGGT
                                ||||||||| ||||||||||
                                AACTTGGAC CTCCGTCTCCA
                                     C
GAM948  LOC153077 3'  AACCTCCGCCTCCTGGGTTCAA 87098        GA
                                TTGAACCT  GAGGCGGAGGTT
                                ||||||||  ||||||||||||
                                AACTTGGG  CTCCGCCTCCAA
                                     TC
GAM948  LOC153606 5'  CCTCTGCCTCCCAGGTTCAA   87255        A
                                TTGAACCTG GAGGCGGAGG
                                ||||||||| |||||||||
                                AACTTGGAC CTCCGTCTCC
                                     C
GAM948  LOC153688 3'  AACCTCCACCTCCCCGGGTTCA 87278        A_   C
          A                      TTGAACCTG  GAGG GGAGGTT
                                ||||||||||  |||| |||||||
                                AACTTGGGC  CTCC CCTCCAA
                                     CC   A
GAM948  LOC153811 3'  AAGCTCCGCCTCCCAGGATCAA 81817      A   A       G
                                TTGA CCTG GAGGCGGAG TT
                                |||| |||| ||||||||| ||
                                AACT GGAC CTCCGCCTC AA
                                   A   C       G
GAM948  LOC153883 5'  AACCTCCACCCTGCAGGTTCAA 81881        _ A  C
                                TTGAACCTG AG GG GGAGGTT
                                ||||||||| || || |||||||
                                AACTTGGAC TC CC CCTCCAA
                                     G  _  A
GAM948  LOC154075 3'  AACCTCCGCCTCCTGGGTTCAA 81950        GA
                                TTGAACCT  GAGGCGGAGGTT
                                ||||||||  ||||||||||||
                                AACTTGGG  CTCCGCCTCCAA
                                     TC
GAM948  LOC154282 5'  AACCTCCACCTCCCAGGTTCAA 87395        A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
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                                AACTTGGAC CTCC CCTCCAA
                                     C    A
GAM948   LOC154726 5'  AACCTCCGCCTCCCAGGTTCAA 82002         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGCCTCCAA
                                     C
GAM948   LOC154877 3'  AACCTCCGCCTTCCGGGTTCA  87510        AG
                                TGAACCTG  AGGCGGAGGTT
                                ||||||||  ||||||||||||
                                ACTTGGGC  TCCGCCTCCAA
                                    CT
GAM948   LOC154930 3'  GTAACCTCTGCCTTCCAGGTTC 82095         AG
           AA                     TTGAACCTG  AGGCGGAGGTTAC
                                ||||||||||  ||||||||||||||
                                AACTTGGAC  TCCGTCTCCAATG
                                     CT
GAM948   LOC157247 5'  AACCTCCACCCCCCCAGGTTCAA 82277         AGA  C
                                TTGAACCTG   GG GGAGGTT
                                |||||||||   || |||||||
                                AACTTGGAC   CC CCTCCAA
                                     CCC  A
GAM948   LOC157798 5'  AACCTCCGCCTCCCAGGTTCAA 87847         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGCCTCCAA
                                     C
GAM948   LOC158014 5'  AATCTCCGCCTCCCCAGTTCAA 82547       C  A_
                                TTGAAC TG  GAGGCGGAGGTT
                                |||||| ||  ||||||||||||
                                AACTTG AC  CTCCGCCTCTAA
                                   _  CC
GAM948   LOC158476 3'  AACCTCCGCCCCCTGGGTTCAA 88170        G  A_
                                TTGAACCT AG  GGCGGAGGTT
                                |||||||| ||  ||||||||||
                                AACTTGGG TC  CCGCCTCCAA
                                     _  CC
GAM948   LOC158668 3'  AACCTCTGCCTCCCGGGTTCAA 69890         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGTCTCCAA
                                     C
GAM948   LOC160646 3'  TCCGCCTCCCAGGTTCAA    83122         A
                                TTGAACCTG GAGGCGGA
                                ||||||||| ||||||||
                                AACTTGGAC CTCCGCCT
                                     C
GAM948   LOC161829 3'  AACCTCCGCCTCCCGGGTTCAA 83177         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
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                                AACTTGGGC CTCCGCCTCCAA
                                      C
GAM948  LOC169611 3'  AATCTCCGCCTCCCGGGTTCAA 83628        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGCCTCTAA
                                      C
GAM948  LOC196047 5'  AACCTCCGCCTCCCAGGTTCAA 91132        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGCCTCCAA
                                      C
GAM948  LOC196411 3'  AACCTCCGCCTCCCGGGTTCAA 89035        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGCCTCCAA
                                      C
GAM948  LOC196529 3'  AACCTCCACCTCCCGGGTTCAA 89113        A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGGC CTCC CCTCCAA
                                      C   A
GAM948  LOC196529 3'  AACCTCCACCTCGCGGGTTTAA 89114        A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AATTTGGGC CTCC CCTCCAA
                                      G   A
GAM948  LOC197358 3'  AACCTCCGCCTCCCGGGTTCA  89401        A
                                TGAACCTG GAGGCGGAGGTT
                                |||||||| ||||||||||||
                                ACTTGGGC CTCCGCCTCCAA
                                      C
GAM948  LOC199725 5'  AACCTTCGCCTCCCGAGTTCAA 91404       C  A
                                TTGAAC TG GAGGCGGAGGTT
                                |||||| || ||||||||||||
                                AACTTG GC CTCCGCTTCCAA
                                     A  C
GAM948  LOC199786 3'  AACCTCCGCCTCCCGGGTTCAA 89728        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGCCTCCAA
                                      C
GAM948  LOC199906 3'  AACCTCCGCCTACTGGGTTCAA 89837        AG
                                TTGAACCTG  AGGCGGAGGTT
                                |||||||||  ||||||||||||
                                AACTTGGGT  TCCGCCTCCAA
                                      CA
GAM948  LOC200014 3'  AACCCCCACCTCCCAGGTTCAA 89908        A   C  A
                                TTGAACCTG GAGG GG GGTT
                                ||||||||| |||| || ||||
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                                AACTTGGAC CTCC CC CCAA
                                      C    A  C
GAM948   LOC200310 3'  AACCTCTGCCTCCCAGGTTTAA 66313          A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AATTTGGAC CTCCGTCTCCAA
                                      C
GAM948   LOC200314 3'  AACCTCCACCTCCCGGGTTCAA 91582          A    C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGGC CTCC CCTCCAA
                                      C    A
GAM948   LOC200339 3'  AACCTCTGCCTCCCAGGTTCA  91610          A
                                TGAACCTG GAGGCGGAGGTT
                                |||||||| ||||||||||||
                                ACTTGGAC CTCCGTCTCCAA
                                      C
GAM948   LOC200845 5'  AACCTCCGCCTCTCGGGTTCAA 90308
                                TTGAACCTGAGAGGCGGAGGTT
                                ||||||||||||||||||||||
                                AACTTGGGCTCTCCGCCTCCAA

GAM948   LOC200860 3'  AACCTCCACCTCCCAGGTTCAA 91735          A    C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGAC CTCC CCTCCAA
                                      C    A
GAM948   LOC201173 5'  AACCTCTGCCTCCCAGGTTCAA 88661          A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGTCTCCAA
                                      C
GAM948   LOC201220 5'  AACCTCTGCCTCCCAGGTTCAA 88697          A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGTCTCCAA
                                      C
GAM948   LOC201294 3'  AACCTCCGCCTCCGGGTTCAA  89565          A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGCCTCCAA
                                      _
GAM948   LOC201294 3'  AACCTCCGCCTCCTGGGTTCAA 89566          GA
                                TTGAACCT  GAGGCGGAGGTT
                                ||||||||  ||||||||||||
                                AACTTGGG  CTCCGCCTCCAA
                                      TC
GAM948   LOC201411 3'  AACCTCTGCCTCCCAGGTTCAA 63627          A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
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                                AACTTGGAC CTCCGTCTCCAA
                                      C
GAM948   LOC201626 3'  AACCTCCGCCCCCTGGGTTTAA 90420        G  A_
                                TTGAACCT AG  GGCGGAGGTT
                                |||||||| ||  ||||||||||
                                AATTTGGG TC  CCGCCTCCAA
                                     _  CC
GAM948   LOC201696 3'  GCCACTGCCTCCCAGGTTCAA  63821        A      A
                                TTGAACCTG GAGGCGG GGT
                                ||||||||| ||||||| |||
                                AACTTGGAC CTCCGTC CCG
                                      C      A
GAM948   LOC202025 3'  AACCTCCGCCTCCCAGGTTCAA 91880        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGCCTCCAA
                                      C
GAM948   LOC202934 3'  AACCTCTGCCTCCCAGGTTCAA 92021        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGTCTCCAA
                                      C
GAM948   LOC203197 3'  AACCCCCGCCACCTAGGTTCAA 90796        AGA    A
                                TTGAACCTG   GGCGG GGTT
                                |||||||||   ||||| ||||
                                AACTTGGAT   CCGCC CCAA
                                      CCA    C
GAM948   LOC203297 5'  AACCTCTGCCTCCCAGGTTCAA 75867        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGTCTCCAA
                                      C
GAM948   LOC203339 3'  AACCACTGCCTCCCAGGTTCAA 92202        A      A
                                TTGAACCTG GAGGCGG GGTT
                                ||||||||| ||||||| ||||
                                AACTTGGAC CTCCGTC CCAA
                                      C      A
GAM948   LOC203350 3'  AACCTCCGCCTCCCAGGTTCAA 92221        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGCCTCCAA
                                      C
GAM948   LOC203378 3'  AACCTCTGCCTCCCGGGTTCAA 92266        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGTCTCCAA
                                      C
GAM948   LOC219445 5'  GCCTCCGCCTCCCTGGTTCAA  93206       TGA
                                TTGAACC   GAGGCGGAGGT
                                |||||||   ||||||||||
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                                AACTTGG   CTCCGCCTCCG
                                    TCC
GAM948   LOC219673 5'  GCCTCTGCCTCCCAGGTTCAA  94625         A
                                TTGAACCTG GAGGCGGAGGT
                                ||||||||| ||||||||||
                                AACTTGGAC CTCCGTCTCCG
                                     C
GAM948   LOC219735 3'  AACCTCTGCCTCCCAGGTTCA  94718         A
                                TGAACCTG GAGGCGGAGGTT
                                |||||||| ||||||||||
                                ACTTGGAC CTCCGTCTCCAA
                                     C
GAM948   LOC220064 3'  GTAACCTCCGCCTCCTGAATTC 95069       CC GA
           AA                     TTGAA  T  GAGGCGGAGGTTAC
                                ||||| | ||||||||||||||
                                AACTT  G  CTCCGCCTCCAATG
                                   AA TC
GAM948   LOC220074 3'  AACCTCAGCCTCCCAGGTTCAA 59946         A     G
                                TTGAACCTG GAGGC GAGGTT
                                ||||||||| ||||| ||||||
                                AACTTGGAC CTCCG CTCCAA
                                     C     A
GAM948   LOC220074 3'  AACCTCCGCCTGCTGGGTTCAA 59947         G  _
                                TTGAACCT AG AGGCGGAGGTT
                                |||||||| || ||||||||||
                                AACTTGGG TC TCCGCCTCCAA
                                     _  G
GAM948   LOC220662 3'  AACCTCCACCTCCAGGGTTCAG 92796         GA    C
                                TTGAACCT  GAGG GGAGGTT
                                ||||||||  |||| |||||||
                                GACTTGGG  CTCC CCTCCAA
                                     AC    A
GAM948   LOC220662 3'  AACCTCCACTTCCTAGGTTCAA 92797         A    C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGAT CTTC CCTCCAA
                                     C    A
GAM948   LOC221122 3'  AAGCTCCGCCTCCCAGGTTCAA 95085         A        G
                                TTGAACCTG GAGGCGGAG TT
                                ||||||||| ||||||||| ||
                                AACTTGGAC CTCCGCCTC AA
                                     C        G
GAM948   LOC221271 3'  AACCTCTGCCTCCCTGGTTCAA 93482        TGA
                                TTGAACC   GAGGCGGAGGTT
                                |||||||   ||||||||||||
                                AACTTGG   CTCCGTCTCCAA
                                    TCC
GAM948   LOC221296 3'  AACCTCCACCTCCCGGGTTCAA 93597         A    C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
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                                AACTTGGGC CTCC CCTCCAA
                                    C    A
GAM948   LOC222068 3'  AACATCTGCCTCCCGGGTTCAA 94263         A       G
                                TTGAACCTG GAGGCGGA GTT
                                ||||||||| |||||||| |||
                                AACTTGGGC CTCCGTCT CAA
                                    C       A
GAM948   LOC222070 5'  AACCTCTGCCTCCCAGGTTCAA 95802         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGTCTCCAA
                                    C
GAM948   LOC245771 5'  AACCCCCGTCTCCCGGGTTCAA 94461         A       A
                                TTGAACCTG GAGGCGG GGTT
                                ||||||||| ||||||| ||||
                                AACTTGGGC CTCTGCC CCAA
                                    C       C
GAM948   LOC253612 5'  AACCTCCGCCTCCCGGGTT    98540       A
                                AACCTG GAGGCGGAGGTT
                                |||||| ||||||||||||
                                TTGGGC CTCCGCCTCCAA
                                   C
GAM948   LOC253664 3'  AACCTCTGCCTCCCGGGTTCAA 96451         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGTCTCCAA
                                    C
GAM948   LOC253666 5'  AACCTCCGCCTCCCAGGTTCAA 96754         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGCCTCCAA
                                    C
GAM948   LOC253666 5'  ACCTCCGCCTCCCAGGTTCAA  96755         A
                                TTGAACCTG GAGGCGGAGGT
                                ||||||||| ||||||||||
                                AACTTGGAC CTCCGCCTCCA
                                    C
GAM948   LOC254058 5'  CTCTGCCTCCCAGGTTCAA    99146         A
                                TTGAACCTG GAGGCGGAG
                                ||||||||| |||||||||
                                AACTTGGAC CTCCGTCTC
                                    C
GAM948   LOC254268 3'  AACCTTTGTCTCCCGGGCTCAA 97132      A    A
                                TTGA CCTG GAGGCGGAGGTT
                                |||| |||| ||||||||||||
                                AACT GGGC CTCTGTTTCCAA
                                  C   C
GAM948   LOC255177 3'  CCTCCACCTCCCAGGTTCAA   98391         A    C
                                TTGAACCTG GAGG GGAGG
                                ||||||||| |||| |||||
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                                  AACTTGGAC CTCC CCTCC
                                        C    A
GAM948   LOC255308 3'  AATCTCTGCCTCCCAGGTTCAA 96172          A
                                  TTGAACCTG GAGGCGGAGGTT
                                  ||||||||| ||||||||||||
                                  AACTTGGAC CTCCGTCTCTAA
                                        C
GAM948   LOC255497 3'  AACCTCCGCCTCCTGAGTTCAA 98977        C GA
                                  TTGAAC T  GAGGCGGAGGTT
                                  |||||| |  ||||||||||||
                                  AACTTG G  CTCCGCCTCCAA
                                     A TC
GAM948   LOC255919 3'  AACCTCTGCCTCCCAGGTTCAA 96738          A
                                  TTGAACCTG GAGGCGGAGGTT
                                  ||||||||| ||||||||||||
                                  AACTTGGAC CTCCGTCTCCAA
                                        C
GAM948   LOC256360 5'  AAGCTCCGCCTCCCAGGTTCAA 98325          A        G
                                  TTGAACCTG GAGGCGGAG TT
                                  ||||||||| ||||||||| ||
                                  AACTTGGAC CTCCGCCTC AA
                                        C         G
GAM948   LOC257465 3'  GCCTCCGCCTCCCGAGTTCAA  82497        C  A
                                  TTGAAC TG GAGGCGGAGGT
                                  |||||| || ||||||||||||
                                  AACTTG GC CTCCGCCTCCG
                                     A  C
GAM948   LOC51193  5'  AACCTCCGCCTCCCGGATTCAG 33351        C   A
                                  TTGAA CTG GAGGCGGAGGTT
                                  ||||| ||| ||||||||||||
                                  GACTT GGC CTCCGCCTCCAA
                                     A   C
GAM948   LOC51219  5'  AACCTCCGCCTCCCGGATTCAA 33536        C   A
                                  TTGAA CTG GAGGCGGAGGTT
                                  ||||| ||| ||||||||||||
                                  AACTT GGC CTCCGCCTCCAA
                                     A   C
GAM948   LOC51601  5'  ACCTCCACCTCCCGGGTTCAA  32498          A    C
                                  TTGAACCTG GAGG GGAGGT
                                  ||||||||| |||| ||||||
                                  AACTTGGGC CTCC CCTCCA
                                        C    A
GAM948   LOC57107  3'  AACCTCCGCCTCCTGGGTTCAA 40175          GA
                                  TTGAACCT  GAGGCGGAGGTT
                                  ||||||||  ||||||||||||
                                  AACTTGGG  CTCCGCCTCCAA
                                        TC
GAM948   LOC57146  3'  AACCTCCAACTCCCAGGTTCAA 40284          A   GC
                                  TTGAACCTG GAG  GGAGGTT
                                  ||||||||| |||  |||||||
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                                AACTTGGAC CTC  CCTCCAA
                                    C   AA
GAM948  LOC81034  3' AACCTCCACCTCCCGGGTTCA  48577       A   C
                                TGAACCTG GAGG GGAGGTT
                                |||||||| |||| |||||||
                                ACTTGGGC CTCC CCTCCAA
                                    C   A
GAM948  LOC89231  3' AACCTTCCTCTCCCAGGTTCAA 94290       A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGAC CTCT CTTCCAA
                                    C   C
GAM948  LOC89932  3' AACCTCCACCTCCTGGGTTCAA 61434       GA   C
                                TTGAACCT  GAGG GGAGGTT
                                ||||||||  |||| |||||||
                                AACTTGGG  CTCC CCTCCAA
                                    TC   A
GAM948  LOC90288  3' AACCTCCACCTCCCGGGTTCAA 62762       A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGGC CTCC CCTCCAA
                                    C   A
GAM948  LOC90333  5' AACCTCCACTTCCCAGGTTCAA 62952       A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGAC CTTC CCTCCAA
                                    C   A
GAM948  LOC90333  3' AACCTCCTCCTCCCAGGTTCAA 62953       A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGAC CTCC CCTCCAA
                                    C   T
GAM948  LOC90371  5' AACCTCCACCTCCCAGGTTCAA 63155       A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGAC CTCC CCTCCAA
                                    C   A
GAM948  LOC90459  3' AACCTCCGCCTCCTGGGCTCAG 63544     A  GA
                                TTGA CCT  GAGGCGGAGGTT
                                |||| |||  ||||||||||||
                                GACT GGG  CTCCGCCTCCAA
                                  C  TC
GAM948  LOC90485  3' AACCTCCGCCTCCCGGGTTCAA 63682       A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGCCTCCAA
                                    C
GAM948  LOC90768  5' TCTGCCCCCCAGGTTCAA    64655       AGA
                                TTGAACCTG   GGCGGA
                                |||||||||   ||||||
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                                AACTTGGAC   CCGTCT
                                      CCC
GAM948  LOC91115 3' AACCTCCACCTCCCAGGTTCA  65529        A   C
                                TGAACCTG GAGG GGAGGTT
                                |||||||| |||| |||||||
                                ACTTGGAC CTCC CCTCCAA
                                     C   A
GAM948  LOC91115 3' AACCTCCGCCTCCCAGGTTCAA 65530         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGAC CTCCGCCTCCAA
                                      C
GAM948  LOC91308 3' AACCTCCACCTCCCGGGTTCAA 66158         A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGGC CTCC CCTCCAA
                                      C   A
GAM948  LOC91893 3' TAAGCTCCACCTCCCAGGTTCA 68079         A   C   G
                                TGAACCTG GAGG GGAG TTA
                                |||||||| |||| |||| |||
                                ACTTGGAC CTCC CCTC AAT
                                     C   A   G
GAM948  LOC92267 3' AACCTCCACCTCCCGGGTTCAA 69158         A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
                                AACTTGGGC CTCC CCTCCAA
                                      C   A
GAM948  LOC92283 3' AACCTCCGCCACCCAGGTT   69295       AGA
                                AACCTG   GGCGGAGGTT
                                ||||||   ||||||||||
                                TTGGAC   CCGCCTCCAA
                                   CCA
GAM948  LOC92303 3' AACCTCTGCCCTCCAGGTTCAA 69378         _ A
                                TTGAACCTG AG GGCGGAGGTT
                                ||||||||| || ||||||||||
                                AACTTGGAC TC CCGTCTCCAA
                                      C _
GAM948  LOC92689 3' AACCTCCGCCTCCTGGGTTCAA 70764         GA
                                TTGAACCT  GAGGCGGAGGTT
                                ||||||||  ||||||||||||
                                AACTTGGG  CTCCGCCTCCAA
                                     TC
GAM948  LOC92697 5' AACCTCCGCCTCCCGGGTTCAA 70798         A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGCCTCCAA
                                      C
GAM948  LOC92841 3' AACCTCCTCCTCCCGGGTTCAA 71234         A   C
                                TTGAACCTG GAGG GGAGGTT
                                ||||||||| |||| |||||||
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                                AACTTGGGC CTCC CCTCCAA
                                    C   T
GAM948  LOC93132  5' AACCTCCGCCTCCCGGGTTCAA 71969        A
                                TTGAACCTG GAGGCGGAGGTT
                                ||||||||| ||||||||||||
                                AACTTGGGC CTCCGCCTCCAA
                                    C
GAM948  LOC93349  3' AACCTCTGCCTCCCGGATTCAA 57258      C   A
                                TTGAA CTG GAGGCGGAGGTT
                                ||||| ||| ||||||||||||
                                AACTT GGC CTCCGTCTCCAA
                                  A   C
GAM949  ABCA3    5' TCCTATTTCCTGCGGGTTGC   8447       A   T
                                GCAACCC CAG AGGTAGGA
                                ||||||| ||| ||||||||
                                CGTTGGG GTC TTTATCCT
                                    C   C
GAM949  ABCC5    3' CCTACCTCAGGTTGCTG     20295       CACAGT
                                CAGCAACC     AGGTAGG
                                ||||||||     |||||||
                                GTCGTTGG     TCCATCC
                                    AC____
GAM949  ADAMTS13 5' CCCCGTCTGTGGGTTTCTG   58141    C       TA  TA
                                CAG AACCCACAG  GG  GG
                                ||| |||||||||  ||  ||
                                GTC TTGGGTGTC  CC  CC
                                  T       TG  __
GAM949  ADAMTS13 5' CCCCGTCTGTGGGTTTCTG   58144    C       TA  TA
                                CAG AACCCACAG  GG  GG
                                ||| |||||||||  ||  ||
                                GTC TTGGGTGTC  CC  CC
                                  T       TG  __
GAM949  ADAMTS13 5' CCCCGTCTGTGGGTTTCTG   58152    C       TA  TA
                                CAG AACCCACAG  GG  GG
                                ||| |||||||||  ||  ||
                                GTC TTGGGTGTC  CC  CC
                                  T       TG  __
GAM949  ARHGEF12 3' TCTGAACTCTGTGGGTTGCT  31649          T  GTA
                                AGCAACCCACAG AG   GGA
                                |||||||||||| ||   |||
                                TCGTTGGGTGTC TC   TCT
                                      _  AAG
GAM949  ATP2B4   5' TCTACTACTACAGTTGCTG   70849       CCAC    G
                                CAGCAAC   AGTAG TAGG
                                |||||||   ||||| ||||
                                GTCGTTG   TCATC ATCT
                                    ACA_    _
GAM949  ATP6V0D1 3' CTCCCTTCTGTGGGTCGCT   17437    A      T   T
                                AGC ACCCACAG AGG AG
                                ||| |||||||| ||| ||
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                                TCG TGGGTGTC TCC TC
                                  C       T   C
GAM949  CASP10   3'  TTCCTACTTGGTCTGGCCACTG 53230     CAAC   CAG
                                CAG    CCA   TAGGTAGGAA
                                |||    |||   ||||||||||
                                GTC    GGT   GTTCATCCTT
                                  ACC_   CTG
GAM949  CDK10    3'  CTTCCTGGTGATGGGTTACTG  54837     C     _  G    T
                                CAG AACCCA CA TAGG AGG
                                ||| |||||| || |||| |||
                                GTC TTGGGT GT GTCC TTC
                                  A     A  G   _
GAM949  CLC      3'  TTTCCCAGGGTATCTGTGGGTT 26028          TAGGTA__
              GC                  GCAACCCACAG       GGAAA
                                ||||||||||        |||||
                                CGTTGGGTGTC       CCTTT
                                      TATGGGAC
GAM949  CYP4F3   3'  CTTCCTTATGGGTATGCTG    8006       _    CAGT   T
                                CAGCA ACCCA    AGG AGG
                                ||||| |||||    ||| |||
                                GTCGT TGGGT    TCC TTC
                                  A     AT__   _
GAM949  DDEF2    3'  TTTCCTACTGAGTGTACCACTG 15292     CAACC   AGTA
                                CAG    CAC    GGTAGGAAA
                                |||    |||    |||||||||
                                GTC    GTG    TCATCCTTT
                                  ACCAT   AG__
GAM949  EXTL1    5'  CCTAGCCCTGACTGTGGGTGGC 16734    A       _   __
                                GC ACCCACAGT AGG  TAGG
                                || |||||||| |||  ||||
                                CG TGGGTGTCA TCC  ATCC
                                 G       G   CG
GAM949  FBXL7    3'  CTCCTACTGTAGGCTCCTG    25493     CAA  C       T
                                CAG   CC ACAGTAGG AG
                                |||   || |||||||| ||
                                GTC   GG TGTCATCC TC
                                  CTC  A       _
GAM949  GCK      5'  TCCCCACGCTGGCTGCTG     5685       AC   CA  A  TA
                                CAGCA  CCA  GT GG  GGA
                                |||||  |||  || ||  |||
                                GTCGT  GGT  CA CC  CCT
                                  C_   CG  _  __
GAM949  HLA-DMA  3'  TTCCCACCTGGGGACTCTG    21503     CAA   ACAG    A
                                CAG   CCC    TAGGT GGAA
                                |||   |||    ||||| ||||
                                GTC   GGG    GTCCA CCTT
                                  TCA  _____     C
GAM949  IGF1     3'  TTTTACCCTGGGTTGCTG     7089          CAGTA
                                CAGCAACCCA    GGTAGGA
                                ||||||||||    |||||||
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                                GTCGTTGGGT    CCATTTT
                                      C____
GAM949  IL1F5   3'  TCCCCCACTGGATGGTGCT   25378     A  CA_   A  TA
                                AGCA CC   CAGT GG  GGA
                                |||| ||   |||| ||  |||
                                TCGT GG   GTCA CC  CCT
                                  _  TAG    C  __
GAM949  KIF5B   3'  TTTCCTACCTACTCTTCTTGT  16932     CCCAC
                                GCAA    AGTAGGTAGGAAA
                                ||||    ||||||||||||
                                TGTT    TCATCCATCCTTT
                                  CTTC_
GAM949  LMO4    3'  CCTACTTCTAATTTGCTG    23181       CCCAC  T
                                CAGCAA    AG AGGTAGG
                                ||||||    || |||||||
                                GTCGTT    TC TTCATCC
                                   TAA__  _
GAM949  LPIN2   3'  CCTCCTTTGTGGGTCGC     28429    A      T   T
                                GC ACCCACAG AGG AGG
                                || ||||||||| ||| |||
                                CG TGGGTGTT TCC TCC
                                 C       _  _
GAM949  MFAP4   3'  CTTCCTCACTGTGGACCCCTG  69789     CAAC      _   T
                                CAG   CCACAGT AGG AGG
                                |||   ||||||| ||| |||
                                GTC   GGTGTCA TCC TTC
                                  CCCA      C  _
GAM949  MLLT7   3'  CCACCCCTGCTGTGGGTT    21040           TA_
                                AACCCACAGTAGG   GG
                                ||||||||||||   ||
                                TTGGGTGTCGTCC   CC
                                       CCA
GAM949  NFE2L1  3'  TTCCTCTTCTGGGACTGCTG   13636      AC  A   T   T
                                CAGCA  CC CAG AGG AGGAA
                                |||||  || ||| ||| |||||
                                GTCGT  GG GTC TTC TCCTT
                                   CA  _  _  _
GAM949  NPM1    5'  TCCTACCTAAGTGCGTGC    11823     ACC   AG
                                GCA   CAC  TAGGTAGGA
                                |||   |||  |||||||||
                                CGT   GTG  ATCCATCCT
                                  GC_   A_
GAM949  NTE     5'  CCTGCCTGCAGGCTGCTG    22949      A  CACA
                                CAGCA CC    GTAGGTAGG
                                ||||| ||    |||||||||
                                GTCGT GG    CGTCCGTCC
                                   C  A___
GAM949  PCSK1   3'  TCTCCCACTGAGTTTGCTG   6516       CCCA   A  T
                                CAGCAA    CAGT GG AGG
                                ||||||    |||| || |||
```

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                                GTCGTT   GTCA CC TCT
                                   TGA_   C  _
GAM949  PFKP    3'  CCTGCAGCCACCGTGGACTGTC 12062    _ AC   A  AG__
           TG                    CAG CA  CCAC GT   GTAGG
                                 ||| ||  |||| ||   |||||
                                 GTC GT  GGTG CA   CGTCC
                                   T  CA   C  CCGA
GAM949  PRPS1   3'  TTCCTGCTATGTAATTGCT   12403     CCC   GTA
                                 AGCAA   ACA   GGTAGGAA
                                 |||||   |||   ||||||||
                                 TCGTT   TGT   TCGTCCTT
                                   AA_   A__
GAM949  RNMT    3'  TCCTACCTAAGTCAGTCACT   15058   CA  CC  AG
                                 AG  AC  AC  TAGGTAGGA
                                 ||  ||  ||  |||||||||
                                 TC  TG  TG  ATCCATCCT
                                  AC  AC  A_
GAM949  RNPEPL1  3'  TCCAGCCTGGGACTGCTG   37218     A_   CAGTA  A
                                 CAGCA  CCCA    GGT GGA
                                 |||||  ||||    ||| |||
                                 GTCGT  GGGT    CCG CCT
                                   CA   _____   A
GAM949  SLIT2   5'  CCTGGCACTCTGGGTTGCT   17723        C   AGG
                                 AGCAACCCA AGT   TAGG
                                 |||||||||| |||   ||||
                                 TCGTTGGGT TCA   GTCC
                                      C   CG_
GAM949  SRC     3'  TCCTGGAGCTCTGTGGGTCTCT 19452    CA      T  G__
           G                     CAG  ACCCACAG AG   TAGGA
                                 |||  |||||||| ||   |||||
                                 GTC  TGGGTGTC TC   GTCCT
                                   TC       _ GAG
GAM949  TARDBP   3'  CCTACCCCTTTGTCAACTGCTG 24786     ACCC   TA_
                                 CAGCA   ACAG   GGTAGG
                                 |||||   ||||   ||||||
                                 GTCGT   TGTT   CCATCC
                                   CAAC   TCC
GAM949  TGM2    3'  CCTCCTGAGCCTGTGGGT    17242        ___   T
                                 ACCCACAG   TAGG AGG
                                 ||||||||   |||| |||
                                 TGGGTGTC   GTCC TCC
                                      CGA   _
GAM949  TK1     3'  TCCTACCCACTGGTCTGCT   13770     AC   CA  A
                                 AGCA  CCA  GT GGTAGGA
                                 ||||  |||  || |||||||
                                 TCGT  GGT  CA CCATCCT
                                   CT   __  C
GAM949  TM4SF2  3'  TTTCCTACCTTCTTCAGGCTGC 17254     A  CAC  T
                                 GCA CC   AG AGGTAGGAAA
                                 ||| ||   || ||||||||||
```

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                                CGT GG   TC TCCATCCTTT
                                  C  ACT  T
GAM949  TMPRSS2  3'  TTCCAATGCTGTGGGTT     20174          GGTA
                                AACCCACAGTA    GGAA
                                ||||||||||    ||||
                                TTGGGTGTCGT    CCTT
                                      AA__
GAM949  TPS1     3'  TTCCTACCCAGGTGGCGACTGC 61107     AC__    AGTA
                                GCA    CCAC    GGTAGGAA
                                |||    ||||    ||||||||
                                CGT    GGTG    CCATCCTT
                                  CAGC    GAC_
GAM949  TPSB1    3'  TTCCTACCCAGGTGGCGACTGC 13839     AC__    AGTA
                                GCA    CCAC    GGTAGGAA
                                |||    ||||    ||||||||
                                CGT    GGTG    CCATCCTT
                                  CAGC    GAC_
GAM949  USP14    3'  TCTGATGTACTGTGGATTGT   18941     C       G  A
                                GCAA CCACAGTA GT GGA
                                |||| |||||||| || |||
                                TGTT GGTGTCAT TA TCT
                                  A       G  G
GAM949  VANGL2   3'  CCTTGACACCATAGGGCTGCTG 72092      A   ACA  A   ____
                                CAGCA CCC   GT GGT    AGG
                                ||||| |||   || |||    |||
                                GTCGT GGG   TA CCA    TCC
                                   C   A__  _   CAGT
GAM949  VANGL2   3'  TCTCCATGCTGTGAACTGCTG  72094      ACC      _  T
                                CAGCA   CACAGTA GG AGG
                                |||||   ||||||| || |||
                                GTCGT   GTGTCGT CC TCT
                                   CAA      A  _
GAM949  BATF     3'  CCCACCACTGTGGGTTGC    22145          A   A
                                GCAACCCACAGT GGT GG
                                |||||||||||| ||| ||
                                CGTTGGGTGTCA CCA CC
                                      _  C
GAM949  C20orf126 3'  CTTCCCAACAATGGCCTGCTG  48732      AC   CA  A  T
                                CAGCA  CCA  GT GG AGG
                                |||||  |||  || || |||
                                GTCGT  GGT  CA CC TTC
                                   CC   AA  A  C
GAM949  C20orf29  3'  TTCCTGAGCCTAGAGCTGCTG  37714      ACCCACAG    __
                                CAGCA       TAGGT  AGGAA
                                |||||       |||||  |||||
                                GTCGT       ATCCG  TCCTT
                                   CGAG____     AG
GAM949  CHERP    3'  TTTCCTGTAGCTGTGAATTGTT 22136      CC     AGG
                                AGCAA  CACAGT   TAGGAAA
                                |||||  ||||||   |||||||
```

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                                TTGTT  GTGTCG   GTCCTTT
                                  AA     AT_
GAM949  CLONE24945 3'  TCTGACTTACCTGGACCGCTG  32254      AAC   CA     A
                                CAGC   CCA  GTAGGT GGA
                                ||||   |||  |||||| |||
                                GTCG   GGT  CATTCA TCT
                                  CCA   C_     G
GAM949  DDX34    3'  CTTCCTGCTGCAGGGTGCTG   28671      A   A_     T
                                CAGCA CCC  CAGTAGG AGG
                                ||||| |||  ||||||| |||
                                GTCGT GGG  GTCGTCC TTC
                                  _  AC      _
GAM949  DKFZp434N035 3'  TTTCCTTTTTTTGTGGCTACTG 51067     CAAC     TAGGT
                                CAG    CCACAG     AGGAAA
                                |||    ||||||     ||||||
                                GTC    GGTGTT     TCCTTT
                                  ATC_     TTTT_
GAM949  DKFZP564C186 3'  CCCACAACTGTGGGCTGCTG   72842      A      AG  A
                                CAGCA CCCACAGT  GT GG
                                ||||| ||||||||  || ||
                                GTCGT GGGTGTCA  CA CC
                                  C       A_  C
GAM949  DKFZP564I1171 3'  CCTCCAGCTGTGGGTTGGC    72044    _       A  T
                                GC AACCCACAGT GG AGG
                                || |||||||||| || |||
                                CG TTGGGTGTCG CC TCC
                                 G        A  _
GAM949  DKFZP564K0822 3'  TTGTGCTACTGTGAACGCTG   95699     AACC      G  G
                                CAGC    CACAGTAG TA GA
                                ||||    |||||||| || ||
                                GTCG    GTGTCATC GT TT
                                  CAA_       _  G
GAM949  DKFZp762L0311 3'  TCCTACCTCCTGAGTAACTG   38674     CA  CCA   T
                                CAG  AC   CAG AGGTAGGA
                                |||  ||   ||| ||||||||
                                GTC  TG   GTC TCCATCCT
                                  AA  A__   C
GAM949  DKFZp762P2111 3'  TCACACCACTGCGGACGCTG   87642     AAC  A    A   AG
                                CAGC   CC CAGT GGT  GA
                                ||||   || |||| |||  ||
                                GTCG   GG GTCA CCA  CT
                                  CA_  C    _   CA
GAM949  DQX1     5'  CCTGGCTCTGCGGGTTGCTG   56910         A   T  G
                                CAGCAACCC CAG AG TAGG
                                ||||||||| ||| || ||||
                                GTCGTTGGG GTC TC GTCC
                                     C   _  G
GAM949  ERF      3'  CCTGTCTCTGTGGGTTTCT    22437     C       T  GT
                                AG AACCCACAG AG  AGG
                                || |||||||| ||  |||
```

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                                TC TTGGGTGTC TC  TCC
                                 T       _ TG
GAM949  FADS2    3'  TCCCCATCTCGGGGCTGCTG  16218      A  ACAGT   A_
                                CAGCA CCC    AGGT  GGA
                                ||||| |||    ||||  |||
                                GTCGT GGG    TCTA  CCT
                                   C  GC___   CC
GAM949  FAF1     5'  TTCCTGTCCGGGCTGCTG   23900      A  ACAGTA  _
                                CAGCA CCC     GG TAGGAA
                                ||||| |||     || ||||||
                                GTCGT GGG     CC GTCCTT
                                   C  ______ T
GAM949  FBXO27   3'  TCTACCTACTGCAGCTGCTG  75016      ACCCA
                                CAGCA    CAGTAGGTAGG
                                |||||    ||||||||||
                                GTCGT    GTCATCCATCT
                                   CGAC_
GAM949  FLJ10420 3'  CCTCACTGTGGGCAGCTG    36590      AA      _
                                CAGC  CCCACAGT AGG
                                ||||  |||||||| |||
                                GTCG  GGGTGTCA TCC
                                  AC       C
GAM949  FLJ10650 3'  TCTCACTTTCCTGTGGGTTGCT 36904           T_   AG
          G                      CAGCAACCCACAG  AGGT  GA
                                ||||||||||||  ||||  ||
                                GTCGTTGGGTGTC  TTCA  CT
                                       CT   CT
GAM949  FLJ14810 3'  TCCTACCTGGGGCAGCTG    52704     AA  ACAG
                                CAGC  CCC   TAGGTAGGA
                                ||||  |||   |||||||||
                                GTCG  GGG   GTCCATCCT
                                  AC  _____
GAM949  FLJ20712 3'  TTCCCTTCTCTGGAGTTGCT  36036      CCA  T  TA
                                AGCAAC   CAG AGG  GGAA
                                ||||||   ||| |||  ||||
                                TCGTTG   GTC TCT  CCTT
                                   AG_  _  TC
GAM949  FLJ31168 3'  CCTACCTTTTGGCTTCTG    59180    C  C   CAGT
                                CAG AA CCA    AGGTAGG
                                ||| || |||    |||||||
                                GTC TT GGT    TCCATCC
                                  _ C  TT__
GAM949  FLJ32915 3'  CCTATCAATATGAGTTGCTG  59431       C  CA  A
                                CAGCAAC CA  GT GGTAGG
                                ||||||| ||  || ||||||
                                GTCGTTG GT  TA CTATCC
                                    A  A_  A
GAM949  GPR64    3'  TTCCTACCTACATCTGCT    20445     ACCCACA
                                AGCA     GTAGGTAGGAA
                                ||||     ||||||||||
```

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                                TCGT      CATCCATCCTT
                                  CTA_____
GAM949  GRASP1   3' TTCCTACCCCCTAGGATGCT  39710      A  CAC  TA
                                AGCA CC   AG  GGTAGGAA
                                |||| ||   ||  ||||||||
                                TCGT GG   TC  CCATCCTT
                                  A  A__  CC
GAM949  GTPBP1   3' TCCTGCTTGCGGACTGCTG   16269      AC  ACA
                                CAGCA  CC   GTAGGTAGGA
                                |||||  ||   ||||||||||
                                GTCGT  GG   CGTTCGTCCT
                                  CA  ___
GAM949  HIC2     3' CCTCCCGGGCTGTGGGCAGC  65865    AA       A_  T
                                GC  CCCACAGT  GG AGG
                                ||  ||||||||  || |||
                                CG  GGGTGTCG  CC TCC
                                 AC       GG  C
GAM949  ICAM4    3' CCTCCTCACTGTGGGCGCTG  42593     AA       _   T
                                CAGC  CCCACAGT AGG AGG
                                ||||  |||||||| ||| |||
                                GTCG  GGGTGTCA TCC TCC
                                  C_       C   _
GAM949  IMAGE3451454 3' TTCCTCTGGATGGGGCTGCT  54941      A   A  GTA  T
                                AGCA CCC CA   GG AGGAA
                                |||| ||| ||   || |||||
                                TCGT GGG GT   TC TCCTT
                                  C   _  AGG  _
GAM949  KIAA0161 3' TTCCTGCCTGAAATTGCTG   29212       CCCACAG
                                CAGCAA      TAGGTAGGAA
                                ||||||      ||||||||||
                                GTCGTT      GTCCGTCCTT
                                   AAA_____
GAM949  KIAA0427 3' TTTCTAAATGCAGGTTGCTG  29395        CACA   GG
                                CAGCAACC    GTA  TAGGAA
                                ||||||||    |||  ||||||
                                GTCGTTGG    CGT  ATCTTT
                                     A___   AA
GAM949  KIAA0444 3' CTTCCCACATGTGGGTTGTTG  63000           _  A  T
                                CAGCAACCCACA GT GG AGG
                                |||||||||||| || || |||
                                GTTGTTGGGTGT CA CC TTC
                                       A  C  _
GAM949  KIAA0447 3' TCCTACCTGTGGGGGTT     72131      A  G
                                AACCC CA TAGGTAGGA
                                ||||| || |||||||||
                                TTGGG GT GTCCATCCT
                                  G  _
GAM949  KIAA0451 3' CCTCCTGTTGTAGTTGC     29770      CC       T
                                GCAAC  ACAGTAGG AGG
                                |||||  |||||||| |||
```

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                                CGTTG  TGTTGTCC TCC
                                  A_       _
GAM949  KIAA0469 3' TTCCCTCTGCTGTGGGTTCTG  30002     C          TA
                                CAG AACCCACAGTAGG  GGAA
                                ||| ||||||||||||  ||||
                                GTC TTGGGTGTCGTCT  CCTT
                                  _          C_
GAM949  KIAA0493 3' TTTCTTATGACTGTGAGTCACT 64942    CA  C     AG
                                AG  AC CACAGT  GTAGGAAA
                                ||  || ||||||  ||||||||
                                TC  TG GTGTCA  TATTCTTT
                                 AC  A     G_
GAM949  KIAA0757 3' CCTGAGGCCACTGTGAATTTGC 21256       CC_     A  ___
           TG                    CAGCAA   CACAGT GGT   AGG
                                ||||||   |||||| |||   |||
                                GTCGTT   GTGTCA CCG   TCC
                                   TAA     _  GAG
GAM949  KIAA0781 3' CTTACACTATATGTTGCT    68056       CCACA   _
                                AGCAAC    GTAG GTAGG
                                ||||||    |||| |||||
                                TCGTTG    TATC CATTC
                                   TA___    A
GAM949  KIAA1456 5' CTGTGACTACTGTGGGCCACTG 67554     CAA        GTA_
                                CAG   CCCACAGTAG   GG
                                |||   ||||||||||   ||
                                GTC   GGGTGTCATC   TC
                                  ACC        AGTG
GAM949  KIAA1724 3' TTTCCTTTAACCATGGGTTGT  67627        CA  AGGT
                                GCAACCCA  GT   AGGAAA
                                ||||||||  ||   ||||||
                                TGTTGGGT  CA   TCCTTT
                                    AC  ATT_
GAM949  KIAA1784 5' TCCCTCGGGCTGCTGGTTGCTG 65756         CA   AGGTA
                                CAGCAACC  CAGT    GGA
                                ||||||||  ||||    |||
                                GTCGTTGG  GTCG    CCT
                                    TC    GGCTC
GAM949  KIAA1908 3' CCCCCACTGTGGGCAGCTG   73784     AA       A  TA
                                CAGC  CCCACAGT GG  GG
                                ||||  |||||||| ||  ||
                                GTCG  GGGTGTCA CC  CC
                                  AC       C  __
GAM949  KIAA1908 5' TCAGGACCACTGTGGGTGC   73800     A       A   AG_
                                GCA CCCACAGT GGT   GA
                                ||| |||||||| |||   ||
                                CGT GGGTGTCA CCA   CT
                                  _       _  GGA
GAM949  KLHL4    3' TTCAGGCCACTATGGCTGCTG  39422      AC   C   A   AG
                                CAGCA  CCA AGT GGT  GAA
                                |||||  ||| ||| |||  |||
```

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                                GTCGT  GGT TCA CCG  CTT
                                  C_   A   _   GA
GAM949  LBP-9    3'  TTTCCTGTGCTTACGGG    28052    ACA     __
                                CCC   GTAGGT  AGGAAA
                                |||   ||||||  ||||||
                                GGG   CATTCG  TCCTTT
                                  ___     TG
GAM949  LCHN     3'  TCCTCTGCAATGTGGGTTGCTG 87479          __   GT
                                CAGCAACCCACA  GTAG  AGGA
                                ||||||||||||  ||||  ||||
                                GTCGTTGGGTGT  CGTC  TCCT
                                      AA   __
GAM949  MGC13071 5'  TTTCCCACCTTGTGGGT    52067       GT    A
                                ACCCACA  AGGT GGAAA
                                |||||||  |||| |||||
                                TGGGTGT  TCCA CCTTT
                                   __   C
GAM949  MGC14799 5'  CTTACCGCCGGCTGCTG    51327      A  CACA  A
                                CAGCA CC    GT GGTAGG
                                ||||| ||    || ||||||
                                GTCGT GG    CG CCATTC
                                  C  C___  _
GAM949  MGC21738 3'  TTCCTGTTGGTGTGAGATGC   59581     ACC   G   G
                                GCA   CACA TAG TAGGAA
                                |||   |||| ||| ||||||
                                CGT   GTGT GTT GTCCTT
                                  AGA   G   _
GAM949  MGC2477  3'  TCCTACCTAATGGCCTACTG   44312    CAAC   CAG
                                CAG    CCA   TAGGTAGGA
                                |||    |||   |||||||||
                                GTC    GGT   ATCCATCCT
                                  ATCC   A__
GAM949  MGC34923 3'  CCTCTAGACTGGGGGCTGC   59196     A   A    A_  T
                                GCA CCC CAGT  GG AGG
                                ||| ||| ||||  || |||
                                CGT GGG GTCA  TC TCC
                                  C   G    GA  _
GAM949  MGC5139  5'  TTTCCTGCCCCGTAGGTTGC   74577       C  AGTA
                                GCAACC AC    GGTAGGAAA
                                ||||||  ||   |||||||||
                                CGTTGG TG    CCGTCCTTT
                                   A  CC__
GAM949  MGC5528  5'  TTTCCTACCTTCCGGCTGCT   44275     A  CACAGT
                                AGCA CC     AGGTAGGAAA
                                ||||  ||     ||||||||||
                                TCGT GG     TCCATCCTTT
                                  C  CCT____
GAM949  MRPS10   3'  TTGCCTACCAGGGTTACTG   36824     C    ACA
                                CAG AACCC   GTAGGTAG
                                |||  |||||   ||||||||
```

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                              GTC TTGGG   CATCCGTT
                                A    AC_
GAM949  OATPRP4  3' ACCTACTGTGAGTTCTG    48982    C  C
                              CAG AAC CACAGTAGGT
                              ||| ||| ||||||||||
                              GTC TTG GTGTCATCCA
                                _  A
GAM949  P66    3' CCAGTGCCACTGTGGGTGACT  40736   CA      A   __
                              AG  ACCCACAGT GGTA  GG
                              ||  ||||||||| ||||  ||
                              TC  TGGGTGTCA CCGT  CC
                               AG        _   GA
GAM949  PDZD2   3' TTCTTTAAACCACAGGTTGTTG 81738        CACA  A  ___
                              CAGCAACC   GT GGT   AGGAA
                              ||||||||   || |||   |||||
                              GTTGTTGG   CA CCA   TTCTT
                                   A___  _   AAT
GAM949  PPFIA4   3' CCTGCCATCAGGTTGCTG    70839       CACA  A
                              CAGCAACC   GT GGTAGG
                              ||||||||   || ||||||
                              GTCGTTGG   TA CCGTCC
                                   AC__  _
GAM949  PPM1G    5' TTTCCTGCACCTGAGGCCGC   12224    AAC  A   TAG
                              GC   CC CAG   GTAGGAAA
                              ||   || |||   ||||||||
                              CG   GG GTC   CGTCCTTT
                               CC_  A   CA_
GAM949  PRO0611  5' CCTATTTGCAGGCTGCT    26859     A  CACA
                              AGCA CC    GTAGGTAGG
                              |||| ||    |||||||||
                              TCGT GG    CGTTTATCC
                                C  A___
GAM949  RAD51    3' CTTCCTGTTGTGACTGC     12746     ACC       T
                              GCA   CACAGTAGG AGG
                              |||   ||||||||| |||
                              CGT   GTGTTGTCC TTC
                                CA_       _
GAM949  RAD51    3' CTTCCTGTTGTGACTGC     56831     ACC       T
                              GCA   CACAGTAGG AGG
                              |||   ||||||||| |||
                              CGT   GTGTTGTCC TTC
                                CA_       _
GAM949  RBM5     3' TCCCCTTATGTGGGTTGC    20508         GT   TA
                              GCAACCCACA  AGG  GGA
                              ||||||||||  |||  |||
                              CGTTGGGTGT  TCC  CCT
                                    AT  __
GAM949  SDCCAG43 3' CCCCCCATGCCAGTGGGCTGCT 70893      A    A_  _  TA
           G                   CAGCA CCCAC  GTA GG  GG
                              ||||| |||||  ||| ||  ||
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                                GTCGT GGGTG  CGT CC  CC
                                   C    AC   A  CC
GAM949  SLC4A11   5'  CCTAGGGTGGCGTGGGTTGC  50164        A  AGG__
                                GCAACCCAC GT    TAGG
                                ||||||||| ||    ||||
                                CGTTGGGTG CG    ATCC
                                     _ GTGGG
GAM949  STK38L    3'  TTTCCTTTCCTGTGGGCATGCT 69690      A_     TA  T
          G                      CAGCA  CCCACAG  GG AGGAAA
                                |||||  |||||||  || ||||||
                                GTCGT  GGGTGTC  CT TCCTTT
                                   AC      __  T
GAM949  STX12     3'  CCTACCTTATAAGGGTTGCTG  66950        ACAGT
                                CAGCAACCC    AGGTAGG
                                |||||||||    |||||||
                                GTCGTTGGG    TCCATCC
                                     AATAT
GAM949  WHIP      5'  TCCGCGTGCGCACGGGTTGCTG 39709        ACA_  G  A
                                CAGCAACCC   GTA GT GGA
                                |||||||||   ||| || |||
                                GTCGTTGGG   CGT CG CCT
                                     CACG   G  _
GAM949  WSB1      3'  CCCACCTACTCCAATATTTGCT 56970      CCCAC__     A
          G                      CAGCAA      AGTAGGT GG
                                ||||||      ||||||| ||
                                GTCGTT      TCATCCA CC
                                   TATAACC      C
GAM949  WWP1      5'  TCTCCGTCTCAGGTTGCTG   81261       CAC  TA  T
                                CAGCAACC   AG  GG AGG
                                ||||||||   ||  || |||
                                GTCGTTGG   TC  CC TCT
                                     AC_  TG  _
GAM949  ZNF225    5'  TCCGTTACTGTGAGGTTGCTG  26274        _     GGTA
                                CAGCAACC CACAGTA   GGA
                                |||||||| |||||||   |||
                                GTCGTTGG GTGTCAT   CCT
                                     A      TG__
GAM949  ZNF323    3'  TCTCCTGTGTGGATGACTG   48821    _ AC    G   T
                                CAG CA  CCACA TAGG AGG
                                ||| ||  ||||| |||| |||
                                GTC GT  GGTGT GTCC TCT
                                  A  A_    _   _
GAM949  LOC127281 3'  CCTGGGGACCACTGTGGGTTCC 75134     C        A  ____
          TG                     CAG AACCCACAGT GGT   AGG
                                ||| ||||||||||| |||   |||
                                GTC TTGGGTGTCA CCA   TCC
                                  C        _  GGGG
GAM949  LOC138639 3'  TTCCCACTCCCTTGGGTTGCTG 75885         C  TA  A
                                CAGCAACCCA AG  GGT GGAA
                                |||||||||| ||  ||| ||||
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```
                                GTCGTTGGGT TC  TCA CCTT
                                      _ CC   C
GAM949   LOC143392 3'  TCCTAGCTGCCTGCAAATTGTC 83854    A    CCCA  _   G
             A                   C GCAA    CAG TAG TAGGA
                                 | ||||    ||| ||| |||||
                                 A TGTT    GTC GTC ATCCT
                                  C    AAAC   C   G
GAM949   LOC147151 5'  TTCCCCACTTCGAGAGGTTGCT 78899         CACAGT    A_
             G                   CAGCAACC     AGGT  GGAA
                                 ||||||||     ||||  ||||
                                 GTCGTTGG     TTCA  CCTT
                                      AGAGC_   CC
GAM949   LOC147858 5'  TCCTACCTGTGCTGGGACGC   79269    AA   _ G
                                 GC  CCCA CA TAGGTAGGA
                                 ||  |||| || |||||||||
                                 CG  GGGT GT GTCCATCCT
                                  CA    C _
GAM949   LOC148525 3'  TTTCCCACTGCTTACTGTGAGT 79625    C   C         ___
             TCT                   AG AAC CACAGTAGGTA   GGAAA
                                 || ||| ||||||||||   |||||
                                 TC TTG GTGTCATTCGT   CCTTT
                                  _  A          CAC
GAM949   LOC149086 5'  TTACCACTGTGGGCCGCTG    85497      AA       A
                                 CAGC  CCCACAGT GGTAG
                                 ||||  |||||||| |||||
                                 GTCG  GGGTGTCA CCATT
                                   CC       _
GAM949   LOC149685 5'  CCTCCCTGTGGGTTTGCTG    80296       _      TA  T
                                 CAGCAA CCCACAG  GG AGG
                                 |||||| |||||||  || |||
                                 GTCGTT GGGTGTC  CC TCC
                                    T      __ _
GAM949   LOC150848 3'  TCTCCTATTAGTGCAAATGGCT 86320     AACC__  _     T
                                 AGC      CAC AGTAGG AGG
                                 |||      ||| |||||| |||
                                 TCG      GTG TTATCC TCT
                                   GTAAAC   A     _
GAM949   LOC151438 5'  CTTGTTCACTGCAGGTTGCTG  86556         CA    AG
                                 CAGCAACC  CAGT  GTAGG
                                 ||||||||  ||||  |||||
                                 GTCGTTGG  GTCA  TGTTC
                                      AC    CT
GAM949   LOC151584 5'  TTCCTGCCACTAAAATTGCTG  86629       CCCAC   A
                                 CAGCAA     AGT GGTAGGAA
                                 ||||||     ||| ||||||||
                                 GTCGTT     TCA CCGTCCTT
                                    AAAA_   _
GAM949   LOC152633 5'  TCCGCGCCACGGCTGCTG     86999      A  CACA  A   A_
                                 CAGCA CC    GT GGT  GGA
                                 ||||| ||    || |||  |||
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                                GTCGT GG    CA CCG  CCT
                                  C _____ _   CG
GAM949   LOC153364 5'  TTCCCACCCTCACTGCGGGCCT 81680     CAA   A    A__   A
            CTG                    CAG   CCC CAGT   GGT GGAA
                                |||   ||| ||||   ||| ||||
                                GTC   GGG GTCA   CCA CCTT
                                  TCC   C    CTC   C
GAM949   LOC154743 3'  TTTGTGCTTATTGTGAATTGC  82019      CC         G
                                GCAA  CACAGTAGGTA GAA
                                ||||  |||||||||| |||
                                CGTT  GTGTTATTCGT TTT
                                  AA         G
GAM949   LOC162048 5'  TCCCCACCTTGGCCTGCTG    83203       AC   CAGT    A_
                                CAGCA  CCA    AGGT  GGA
                                |||||  |||    ||||  |||
                                GTCGT  GGT    TCCA  CCT
                                  CC   _____    CC
GAM949   LOC162137 3'  TTCCCCGCCTGCTGGTCGC    88484    A   CAC      A_
                                GC ACC   AGTAGGT  GGAA
                                || |||   |||||||  ||||
                                CG TGG   TCGTCCG  CCTT
                                 C   ___       CC
GAM949   LOC165229 5'  TTCCTGCTTCCACAGTTCGCT  83362     _   CCACAGT
                                AGC AAC       AGGTAGGAA
                                ||| |||       |||||||||
                                TCG TTG       TTCGTCCTT
                                  C   ACACC__
GAM949   LOC196023 3'  TTTCTACTACTGTAAGCT     88950     AACCC      G
                                AGC     ACAGTAG TAGGAA
                                |||     ||||||| ||||||
                                TCG     TGTCATC ATCTTT
                                  AA___       _
GAM949   LOC196418 5'  TTCAGCCACTGTGGGCCCTG   89053     CAA       A   A
                                CAG   CCCACAGT GGT GGA
                                |||   |||||||| ||| |||
                                GTC   GGGTGTCA CCG CTT
                                  CC_       _   A
GAM949   LOC199692 3'  TTTCCTGCTTCTTTGGGTTGC  59928         C  T
                                GCAACCCA AG AGGTAGGAAA
                                |||||||| || ||||||||||
                                CGTTGGGT TC TTCGTCCTTT
                                     T  _
GAM949   LOC199990 3'  CCCCTACGTGTGGGTTGC     89905          _    TA
                                GCAACCCACA GTAGG  GG
                                |||||||||| |||||  ||
                                CGTTGGGTGT CATCC  CC
                                      G    __
GAM949   LOC201164 3'  CCTCCCTGCGGGCTGCTG     89491       A   ACA    T
                                CAGCA CCC   GTAGG AGG
                                ||||| |||   ||||| |||
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                                GTCGT GGG   CGTCC TCC
                                  C  ___    C
GAM949  LOC201505 5'  TCCTACCTGTGCTGGGACGC  91355    AA   _  G
                                GC  CCCA CA TAGGTAGGA
                                ||  |||| || |||||||||
                                CG  GGGT GT GTCCATCCT
                                 CA   C  _
GAM949  LOC204970 3'  TTTCCTGCCTGCAGAGCGCTG  90971     AACCCACA
                                CAGC       GTAGGTAGGAAA
                                ||||       ||||||||||||
                                GTCG       CGTCCGTCCTTT
                                  CGAGA___
GAM949  LOC221398 3'  TTTCCTATAGACTGTAAGCT   92666    AACCC    AG
                                AGC    ACAGT  GTAGGAAA
                                |||    |||||  ||||||||
                                TCG    TGTCA  TATCCTTT
                                  AA___    GA
GAM949  LOC253216 5'  TCCTGGCACTGTGGGCCCTG   96633    CAA      AGG
                                CAG   CCCACAGT   TAGGA
                                |||   ||||||||   |||||
                                GTC   GGGTGTCA   GTCCT
                                  CC_      CG_
GAM949  LOC254413 5'  CCTCCAAGGCACTGTGGGCTGC 98911     A      A____  T
                                GCA CCCACAGT    GG AGG
                                ||| ||||||||    || |||
                                CGT GGGTGTCA    CC TCC
                                  C       CGGAA  _
GAM949  LOC255452 5'  TCCCCCAGGTGGGCTGTCTG   99401    _  A    AGTA  TA
                                CAG CA CCCAC    GG  GGA
                                ||| || |||||    ||  |||
                                GTC GT GGGTG    CC  CCT
                                  T  C    GA__  C_
GAM949  LOC255783 3'  CCTCCTGCTGTGGGATGCTG   96973      A        T
                                CAGCA CCCACAGTAGG AGG
                                ||||| |||||||||| |||
                                GTCGT GGGTGTCGTCC TCC
                                   A         _
GAM949  LOC255855 5'  TCTCCCATTTTGTAGGTTGC   97961      C   TA_  T
                                GCAACC ACAG   GG AGG
                                |||||| ||||   || |||
                                CGTTGG TGTT   CC TCT
                                   A   TTA  C
GAM949  LOC256223 5'  TTCCCCACTTCGAGAGGTTGCT 96883        CACAGT   A_
          G                      CAGCAACC     AGGT  GGAA
                                 ||||||||     ||||  ||||
                                 GTCGTTGG     TTCA  CCTT
                                    AGAGC_    CC
GAM949  LOC56920  3'  TTCCCCAGGCCAGGGTTGCTG  39801        ACA  A_  TA
                                CAGCAACCC   GT  GG  GGAA
                                |||||||||   ||  ||  ||||
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                                GTCGTTGGG  CG  CC  CCTT
                                     AC_  GA  __
GAM949  LOC90313  3'  CCTCCTTGTTGGTTGCTG   62896       C  GT  T
                                CAGCAACC ACA  AGG AGG
                                |||||||| |||  ||| |||
                                GTCGTTGG TGT  TCC TCC
                                    T  __  _
GAM949  LOC90538  3'  TCCTGTTCTGTGGGTTGT   63901         TAGG
                                GCAACCCACAG   TAGGA
                                ||||||||||   |||||
                                TGTTGGGTGTC   GTCCT
                                      TT__
GAM949  LOC91585  5'  TTTCCTACTCTGAGTTACTG  67162    C  CCA  TA
                                CAG AAC  CAG  GGTAGGAAA
                                ||| |||  |||  |||||||||
                                GTC TTG  GTC  TCATCCTTT
                                  A  A__  __
GAM949  LOC92876  5'  TCTCCCATTTTGTAGGTTGC  71352      C   TA_  T
                                GCAACC ACAG  GG AGG
                                |||||| ||||  || |||
                                CGTTGG TGTT  CC TCT
                                   A   TTA  C
GAM950  IRS1    3'  CCATAGATGGTTCTCAATTGTA 19874     C        TGAAC
                                TACA ATTGAGAACC    ATGG
                                |||| ||||||||||    ||||
                                ATGT TAACTCTTGG    TACC
                                  _        TAGA_
GAM950  SERPINF1  3'  CCTGTAAGGTTTCAATG    12038       A  GA  T
                                CATTGAGA CCT  ACA GG
                                |||||||| |||  ||| ||
                                GTAACTTT GGA  TGT CC
                                    _  A_  _
GAM950  HSA243396 3'  CCATGTTCAGCAATGTCAATG  37844      GAAC_
                                CATTGA   CTGAACATGG
                                ||||||   ||||||||||
                                GTAACT   GACTTGTACC
                                   GTAAC
GAM950  KIAA1387  3'  CAGGAATTTTCAATATGTA   71444     C      __
                                TACA ATTGAGAA  CCTG
                                |||| ||||||||  ||||
                                ATGT TAACTTTT  GGAC
                                  A       AA
GAM950  MGC16063  3'  TTCAAATTCCAATGTGTA    54930        A  CC
                                TACACATTG GAA  TGAA
                                ||||||||| |||  ||||
                                ATGTGTAAC CTT  ACTT
                                      _  AA
GAM950  SMCR8   3'  CCATGCTCAGGTTTGACTATGT 59253     TGA_      A
                                ACAT   GAACCTGA CATGG
                                ||||   |||||||| |||||
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                                TGTA   TTTGGACT GTACC
                                  TCAG      C
GAM950  UPLC1    3'  CCATGCTAGGCCCCAATGT   35227      AGAA   AA
                                ACATTG   CCTG  CATGG
                                ||||||   ||||  |||||
                                TGTAAC   GGAT  GTACC
                                   CCC_   C_
GAM950  ZNF334   3'  CCATAAGTCAACCCTCAATGT  36637       AACC   AC_
                                ACATTGAG   TGA   ATGG
                                ||||||||   |||   ||||
                                TGTAACTC   ACT   TACC
                                    CCA_   GAA
GAM950  LOC145082 3'  TATGGAATGCCCTTAATGTGTA 84196          AACCTGAA
                                TACACATTGAG      CATG
                                ||||||||||       ||||
                                ATGTGTAATTC      GTAT
                                      CCGTAAG_
GAM950  LOC157723 3'  CCAAGTAAGGTTCTCAAATGT  82465      _      GA  A
                                ACATT GAGAACCT  AC TGG
                                ||||| ||||||||  || |||
                                TGTAA CTCTTGGA  TG ACC
                                   A       A_  A
GAM950  LOC219988 5'  CCATGTTCGGCCCCCAATG   93262      AGAAC
                                CATTG    CTGAACATGG
                                |||||    ||||||||||
                                GTAAC    GGCTTGTACC
                                   CCCC_
GAM951  CHAD     3'  GGAAGGCTGAGCCTCTC     8855       TA   CTGC
                                GAGAG  CTC   GTCTTCC
                                |||||  |||   |||||||
                                CTCTC  GAG   CGGAAGG
                                   C_   T___
GAM951  DSG1     5'  AGGAAGGCAGAAACACCTC   10449     A  ACTC   GT
                                GAG GT   CTGC  CTTCCT
                                ||| ||   ||||  ||||||
                                CTC CA   GACG  GAAGGA
                                  _  CAAA   __
GAM951  MID1     3'  AAGATGTAGAAGTCCCTC    6351      T_   C
                                GAG  ACT CTGCGTCTT
                                |||  ||| |||||||||
                                CTC  TGA GATGTAGAA
                                  CC   A
GAM951  OTOF     3'  AGGAAGACTCCTGAAACCCTC  17828     A  AC  CTGC
                                GAG GT  TC    GTCTTCCT
                                ||| ||  ||    ||||||||
                                CTC CA  AG    CAGAAGGA
                                  C  A_  TCCT
GAM951  RNMT     3'  AGGACATCCAAGGGTACTCTC  15047        T   GCGTCT
                                GAGAGTAC CCT      TCCT
                                |||||||| |||      ||||
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                                CTCTCATG GGA     AGGA
                                     _  ACCTAC
GAM951  SCN3A    5'  AGGAAGACACGTTATACCCT  23612    A  CTCC  C
                                AG GTA   TG GTCTTCCT
                                || |||   || ||||||||
                                TC CAT   GC CAGAAGGA
                                 C  ATT_  A
GAM951  SFRS7    3'  GGAAGGCGATACTCTC     60148       CTCCTG
                                GAGAGTA    CGTCTTCC
                                |||||||    ||||||||
                                CTCTCAT    GCGGAAGG
                                    A_____
GAM951  SLC13A4  5'  AAGACGAAGGAGGACTCTC   25857      A   G
                                GAGAGT CTCCT CGTCTT
                                |||||| ||||| ||||||
                                CTCTCA GAGGA GCAGAA
                                   G    A
GAM951  SSX2     3'  AGGAAGATGACGAGTAACTC  97962     _   CTG
                                GAGT ACTC  CGTCTTCCT
                                |||| ||||  |||||||||
                                CTCA TGAG  GTAGAAGGA
                                  A   CA_
GAM951  TGFBR2   3'  AAGATTCAAGAGTATTCTC   13725        C  C
                                GAGAGTACTC TG GTCTT
                                |||||||||| || |||||
                                CTCTTATGAG AC TAGAA
                                      A  T
GAM951  TNFRSF11A 3'  AGGAAGACCACCCGGCATTCTC 15187      A  CC_  C
                                GAGAGT CT  TG GTCTTCCT
                                |||||| ||  || ||||||||
                                CTCTTA GG  AC CAGAAGGA
                                   C  CCC  _
GAM951  AP3M2    3'  AGGAAGACCCGTACTCTC    23299       TCCT C
                                GAGAGTAC   G GTCTTCCT
                                ||||||||   | ||||||||
                                CTCTCATG   C CAGAAGGA
                                     ____ C
GAM951  CALN1    3'  AGGAAGACACAGAATTCTTTC 49658     TACTC  C
                                GAGAG    CTG GTCTTCCT
                                |||||    ||| ||||||||
                                CTTTC    GAC CAGAAGGA
                                   TTAA_   A
GAM951  DAMS     5'  AGGAAATTCAAGTACTCT    42084       CC  C  C
                                AGAGTACT  TG GT TTCCT
                                ||||||||  || || |||||
                                TCTCATGA  AC TA AAGGA
                                     __  T  _
GAM951  DKFZP727M111 5'  AGGCCAGGAGGACCCTC    32055    A  A    C
                                GAG GT CTCCTG GTCT
                                ||| || |||||| ||||
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                                CTC CA GAGGAC CGGA
                                  C  G     _
GAM951  FLJ14486 5'  AGGAAGGTTCAAGTCTCTC   52434      T   CC  CG
                                GAGAG ACT  TG  TCTTCCT
                                ||||| |||  ||  |||||||
                                CTCTC TGA  AC  GGAAGGA
                                  _  __  TT
GAM951  FUSIP1   3'  AGGAAGACAGCCATAGTCTC  22780     T   CCT  _
                                GAG ACT   GC GTCTTCCT
                                ||| |||   || ||||||||
                                CTC TGA   CG CAGAAGGA
                                  _  TAC  A
GAM951  HIC      3'  GAAGATTGAGTACTCT      68048          CTGC
                                AGAGTACTC    GTCTTC
                                |||||||||    ||||||
                                TCTCATGAG    TAGAAG
                                     T___
GAM951  IL22R    3'  AGGAAATGCAGGGAAACTC   41467      AC       C
                                GAGT  TCCTGCGT TTCCT
                                ||||  |||||||| |||||
                                CTCA  GGGACGTA AAGGA
                                  AA       _
GAM951  KIAA0472 3'  AGGAGGGGTAAGTACTCTC   72334         CC   G
                                GAGAGTACT  TGC TCTTCCT
                                |||||||||  ||| |||||||
                                CTCTCATGA  ATG GGGAGGA
                                           __  _
GAM951  KIAA1229 3'  AGGATGTAAAAGTTCTCTC   62750      T   CC
                                GAGAG ACT  TGCGTCTT
                                ||||| |||  ||||||||
                                CTCTC TGA  ATGTAGGA
                                   T   AA
GAM951  LAK-4P   3'  AGGAAGACAGTTTCGCCTCTC  24394      TACTCCT  _
                                GAGAG      GC GTCTTCCT
                                |||||      || ||||||||
                                CTCTC      TG CAGAAGGA
                                   CGCTT__  A
GAM951  MRPS35   3'  AGGTCCTCAGGAGTATTCTC   41819           CGTCTT
                                GAGAGTACTCCTG     CCT
                                ||||||||||||      |||
                                CTCTTATGAGGAC     GGA
                                      TCCT__
GAM951  OBTP     5'  AGGATCTGCAAGGAGGACCCTC 34663     A  A    _  TCT
                                GAG GT CTCCT GCG   TCCT
                                ||| || ||||| |||   ||||
                                CTC CA GAGGA CGT   AGGA
                                  C  G    A   CT_
GAM951  RI58     3'  AGATCAGGAATACTCTT     25774        C    C
                                GAGAGTA TCCTG GTCT
                                ||||||| ||||| ||||
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                                TTCTCAT AGGAC TAGA
                                   A    _
GAM951  SMBP     3'  AAGACAGAAGTGTACTCTC   72620        TC  GC_
                                GAGAGTAC  CT   GTCTT
                                ||||||||  ||   |||||
                                CTCTCATG  GA   CAGAA
                                    T_  AGA
GAM951  SNTG1    5'  AGGACTCTGAGGAGTACTCTT  39099          G  TCT
                                GAGAGTACTCCT CG   TCCT
                                ||||||||||||| ||   ||||
                                TTCTCATGAGGA GT   AGGA
                                      _ CTC
GAM951  SNX11    3'  AGGACCAGGAGTATCTC     26169      G       C
                                GAGA TACTCCTG GTCTT
                                |||| |||||||| |||||
                                CTCT ATGAGGAC CAGGA

                                  _      _
GAM951  TTY7     3'  AGGAAGACACAGGTAGCT    50015     ACT    C
                                AGT   CCTG GTCTTCCT
                                |||   |||| ||||||||
                                TCG   GGAC CAGAAGGA
                                  AT_    A
GAM951  LOC123872 5' GGAAAGAGGGTACTCTC     74710          _ GCGTC
                                GAGAGTACTC CT    TTCC
                                |||||||||| ||    ||||
                                CTCTCATGGG GA    AAGG
                                     A ______
GAM951  LOC138389 3' AGGAAGACTTGCAAGTCTCTC  76725      T   CC   __
                                GAGAG ACT  TGC  GTCTTCCT
                                ||||| |||  |||  ||||||||
                                CTCTC TGA  ACG  CAGAAGGA
                                   _  __   TT
GAM951  LOC143943 3' AGGAAGATCAGCAGCCTCTC   83911      TA  C   C
                                GAGAG  CT CTG GTCTTCCT
                                |||||  || ||| ||||||||
                                CTCTC  GA GAC TAGAAGGA
                                   C_  C   _
GAM951  LOC145009 5' AAGAAACAAAGGAGTACTTTC  60965          GCG__
                                GAGAGTACTCCT    TCTT
                                ||||||||||||    ||||
                                CTTTCATGAGGA    AGAA
                                      AACAA
GAM951  LOC147976 5' AGGAAGACTGGGGTACCCTC   79285     A      TGC
                                GAG GTACTCC   GTCTTCCT
                                ||| |||||||   ||||||||
                                CTC CATGGGG   CAGAAGGA
                                  C      T__
GAM951  LOC151512 3' AGGAAGACAATGCTTGTACCTC 86611     A   TCCT ___
                                GAG GTAC   GC   GTCTTCCT
                                ||| ||||   ||   ||||||||
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                                CTC CATG   CG   CAGAAGGA
                                  _   TT__  TAA
GAM951  LOC158801 3'  GAAAACACAAGAAGTATTCT  88255       _ C  C  C
                                AGAGTACT C TG GT TTC
                                |||||||| | || || |||
                                TCTTATGA G AC CA AAG
                                    A A  A  A
GAM951  LOC206426 3'  GAAGCGAGGTGCACTCTC   91099      ACT  G  T
                                GAGAGT   CCT CG CTTC
                                ||||||   ||| || ||||
                                CTCTCA   GGA GC GAAG
                                   CGT   _ _
GAM951  LOC254337 5'  GGAAAGGGGAGTATCTC    98012     G     GCGTC
                                GAGA TACTCCT    TTCC
                                |||| |||||||    ||||
                                CTCT ATGAGGG    AAGG
                                  _     GA___
GAM951  LOC256790 5'  AGTGCAGGAGTGCCCTC    96489    A        T
                                GAG GTACTCCTGCG CT
                                ||| ||||||||||| ||
                                CTC CGTGAGGACGT GA
                                  C        _
GAM951  LOC256946 3'  AGGAAGACAGCCATAGTCTC  96182    T  CCT  _
                                GAG ACT   GC GTCTTCCT
                                ||| |||   || ||||||||
                                CTC TGA   CG CAGAAGGA
                                  _  TAC  A
GAM951  LOC257396 5'  GAAATGTAGGAGCATCTC   98922    GTA      C
                                GAGA   CTCCTGCGT TTC
                                ||||   ||||||||| |||
                                CTCT   GAGGATGTA AAG
                                  AC_       _
GAM951  LOC257408 3'  AGGGCACCAGGAGTACCTC  97797    A      C  CT
                                GAG GTACTCCTG GT  TCCT
                                ||| ||||||||| ||  ||||
                                CTC CATGAGGAC CA  GGGA
                                  _       _ C_
GAM951  LOC257453 3'  AGGAAGATGACGAGTAACTC  82927    _   CTG
                                GAGT ACTC   CGTCTTCCT
                                |||| ||||   |||||||||
                                CTCA TGAG   GTAGAAGGA
                                  A   CA_
GAM951  LOC51066  3'  AGGAAGATGGCCGACACTCTC 32500      AC  CTG
                                GAGAGT  TC   CGTCTTCCT
                                ||||||  ||   |||||||||
                                CTCTCA  AG   GTAGAAGGA
                                   C_  CCG
GAM952  DLEC1    3'  CATCTGGCCCTCCCTTG    24716      A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
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                                GTTCC TCCCG TC TAC
                                  C    G  _
GAM952  DLEC1    3'  CATCTGGCCCTCCCTTG    24728      A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                  C    G  _
GAM952  PIP5K1A  3'  TATCCCACCCTGCCTTGATA  14520       A   CA  C
                                TATCAAGG AGGG  GG GTG
                                |||||||| ||||  || |||
                                ATAGTTCC TCCC  CC TAT
                                    G   A_  C
GAM952  SOX11    3'  ACCCACCCCCCCCTTGGTA    13308       AA   CA  C
                                TATCAAGG  GGG  GG GT
                                ||||||||  |||  || ||
                                ATGGTTCC  CCC  CC CA
                                    CC   A_  _
GAM952  CHL1     3'  TGTTACCTTTCCTCAATA    22768     CA      CA
                                TAT  AGGAAGGG  GGCG
                                |||  ||||||||  ||||
                                ATA  TCCTTTCC  TTGT
                                  AC       A_
GAM952  EPB41L1  3'  CATTCTGCCCTTCCCTGA    71104     A        C
                                TCA GGAAGGGCAGG GTG
                                ||| ||||||||||| |||
                                AGT CCTTCCCGTCT TAC
                                  C          _
GAM952  FLJ00060 3'  CATACCCCCTGCCCTCCTCTGA 61741     _   A      CGTG
                                TCA AGGA GGGCAGG    ATG
                                ||| |||| |||||||    |||
                                AGT TCCT CCCGTCC    TAC
                                  C    _      CCCA
GAM952  FLJ10898 5'  CACCACAGCCCTTTCTCAATA  60126     CA       AGGC
                                TAT  AGGAAGGGC    GTG
                                |||  |||||||||    |||
                                ATA  TCTTTCCCG    CAC
                                  AC        ACAC
GAM952  FLJ22557 3'  ATCATCCCATCCTTAATA    45581     C    A   CAGGC
                                TAT AAGGA GGG     GTGAT
                                ||| ||||| |||     |||||
                                ATA TTCCT CCC     TACTA
                                  A    A  _____
GAM952  KIAA0574 3'  CATCCCCTGCCCTCCCCTGA   69808     A  A      CGT
                                TCA GG AGGGCAGG   GATG
                                ||| || ||||||||   ||||
                                AGT CC TCCCGTCC   CTAC
                                  C  C       C__
GAM952  KIAA0632 3'  CACCTCAGAAACCCTTCCTTGA 32071          CA___  C
                                TCAAGGAAGGG    GG GTG
                                ||||||||||     || |||
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                                AGTTCCTTCCC    CT CAC
                                     AAAGA  C
GAM952  KIAA1045  3'  CATCACATGTCCTTCC     71599        GGC
                                GGAAGGGCA   GTGATG
                                |||||||||   ||||||
                                CCTTCCTGT   CACTAC
                                     A__
GAM952  KIAA1354  5'  CAGTGACTGCCTTCCCTTGATA 61572       A     G _
                                TATCAAGG AGGGCAG CG TG
                                |||||||| ||||||| || ||
                                ATAGTTCC TTCCGTC GT AC
                                     C      A  G
GAM952  MGC20460  5'  CACCGCCTCCTACCCTTCTT   54901       C___    _
                                AGGAAGGG    AGGCG TG
                                ||||||||    ||||| ||
                                TTCTTCCC    TCCGC AC
                                     ATCC    C
GAM952  LOC158476 3'  CACGCCCGCCCCCCCCATTGA  88186     _ AA_   A
                                TCAA GG   GGGC GGCGTG
                                |||| ||   |||| ||||||
                                AGTT CC   CCCG CCGCAC
                                  A  CCC    C
GAM952  LOC90459  3'  CACACCCGCCTAATTTTTG   63550      A_   A  C
                                CAAGGA  GGGC GG GTG
                                ||||||  |||| || |||
                                GTTTTT  TCCG CC CAC
                                    AA    C  A
GAM953  ANPEP     3'  GCTCCAGGGCCAGATGAGC   8565        _ AGGGG
                                GCTCATTTG C    GGAGC
                                ||||||||| |    |||||
                                CGAGTAGAC G    CCTCG
                                     C GGA__
GAM953  CLU       3'  GCTCCCCCCAAGATGAGC    10213       GCA
                                GCTCATTT   GGGGGGAGC
                                ||||||||   |||||||||
                                CGAGTAGA   CCCCCCTCG
                                     A__
GAM953  F13A1     3'  CTCAGCCTTGCAAATAGC    92710    C       GG
                                GCT ATTTGCAGGG  GAG
                                ||| ||||||||||  |||
                                CGA TAAACGTTCC  CTC
                                  _        GA
GAM953  HRH2      3'  GCTCCCTTTTAAAAGGAGC   42510    A  GC
                                GCTC TTT  AGGGGGGAGC
                                |||| |||  ||||||||||
                                CGAG AAA  TTTTCCCTCG
                                  G  A_
GAM953  IFNGR2    3'  CTTGACTTTGGCAAATGAGC  19848         _   GG
                                GCTCATTTGC AGGG  GAG
                                |||||||||| ||||  |||
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                                CGAGTAAACG TTTC  TTC
                                      G    AG
GAM953  PAK4     3'  TCCAGCCCCTGCAGCAAATGA  20829       ___       __
                                TCATT   TGCAGGGG  GGA
                                |||||   ||||||||  |||
                                AGTAA   ACGTCCCC  CCT
                                   ACG        GA
GAM953  PIM2     3'  CCCAATCCTACAAAGGAGC    60651      A    C    __
                                GCTC TTTG AGGG  GGG
                                |||| |||| ||||  |||
                                CGAG AAAC TCCT  CCC
                                  G    A    AA
GAM953  PKHD1    5'  TTTGGCTGGGACACAAACGAGT 57721      A    CAGGGGGG
                                GCTC TTTG       AGCCAAA
                                |||| ||||       |||||||
                                TGAG AAAC       TCGGTTT
                                  C    ACAGGG__
GAM953  PLAT     3'  CTCCTCAAAAGCAAATGAG    53395         AGG_
                                CTCATTTGC    GGGGAG
                                |||||||||    ||||||
                                GAGTAAACG    CTCCTC
                                      AAAA
GAM953  RAI2     3'  TTTGACTTTTCACAAATGAGT  41717         CAGG GG   C
                                GCTCATTTG    G  GAG CAAA
                                |||||||||    |  ||| ||||
                                TGAGTAAAC    C  TTC GTTT
                                      A___ TT   A
GAM953  TGFB3    3'  GGCTCCGGGCAAATGGC     13719    T      AGGGG
                                GC CATTTGC     GGAGCC
                                || |||||||     ||||||
                                CG GTAAACG     CCTCGG
                                 _      GG___
GAM953  BTN2A2   3'  TCCAGCCTACAGATGAGC    23771         C   GG
                                GCTCATTTG AGG  GGA
                                ||||||||| |||  |||
                                CGAGTAGAC TCC  CCT
                                      A   GA
GAM953  C20orf72 5'  TTCGACCGTTGCAAATAG    54609    C       G  G_
                                CT ATTTGCAG GG  GAG
                                || |||||||| ||  |||
                                GA TAAACGTT CC  CTT
                                 _      G  AG
GAM953  C6orf37  3'  CTAACTCTTGACAAATGAGT   68092         _     GG
                                GCTCATTTG CAGGGG  AG
                                ||||||||| ||||||  ||
                                TGAGTAAAC GTTCTC  TC
                                      A     AA
GAM953  DOC2A    3'  GCTAGTCCCTGCAAATATGC   14563    TC         GG
                                GC  ATTTGCAGGGG  AGC
                                ||  ||||||||||  |||
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                                CG  TAAACGTCCCT  TCG
                                 TA         GA
GAM953  FADS1     3'  GCTCCATAAGCAAGTGAGC   26382          AGGGG
                                GCTCATTTGC    GGAGC
                                ||||||||||    |||||
                                CGAGTGAACG    CCTCG
                                     AATA_
GAM953  FLJ20413  3'  CTCAATCCCTGCAAATGA    35595           G_
                                TCATTTGCAGGGG  GAG
                                ||||||||||||  |||
                                AGTAAACGTCCCT  CTC
                                      AA
GAM953  HTATIP2   3'  CTTATGACCGTGCAAATGAGC  22167          G  GG__
                                GCTCATTTGCA GG   GAG
                                ||||||||||| ||   |||
                                CGAGTAAACGT CC   TTC
                                     G  AGTA
GAM953  KIAA1423  3'  CCCAACCCACTAAATGAGC   62392          CA  __
                                GCTCATTTG  GGG  GGG
                                |||||||||  |||  |||
                                CGAGTAAAT  CCC  CCC
                                     CA   AA
GAM953  MFN1      3'  TTCAACTTGAAAATGAGC    54322         G   GG
                                GCTCATTT CAGG  GGA
                                ||||||||  ||||  |||
                                CGAGTAAA GTTC  CTT
                                     A    AA
GAM953  MGC15619  3'  GCCTTAATTGAAAATGAGC   51402         G   GG   A
                                GCTCATTT CAG  GGG GC
                                ||||||||  |||  ||| ||
                                CGAGTAAA GTT  TTC CG
                                     A   AA  _
GAM953  MGEA6     5'  GCTCCCCCCGCAGCCGGC    21013     CAT    A
                                GCT   TTGC GGGGGGAGC
                                |||   ||||  |||||||||
                                CGG   GACG CCCCCCTCG
                                  CC_   _
GAM953  NMT1      3'  GCTCCCCTTCTGAATCAGC   41147     C   TG   _
                                GCT ATT  CAGG GGGGAGC
                                ||| |||  |||| |||||||
                                CGA TAA  GTCT CCCCTCG
                                  C   __   T
GAM953  P114-RHO-GEF 3'  CTCAGCCCCCGGGAAATGAGC  31669        GCA    __
                                GCTCATTT   GGGGG  GAG
                                ||||||||   |||||  |||
                                CGAGTAAA   CCCCC  CTC
                                     GGG    GA
GAM953  TRPV5     5'  CTCAGCTCTGCAAAGAGC    39522      A       GG
                                GCTC TTTGCAGGG  GAG
                                ||||  |||||||||  |||
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                                CGAG AAACGTCTC  CTC
                                  _       GA
GAM953  LOC126961 3'  GGCTCCCCCCCGCGCGTGA    75121     T   A
                                TCAT TGC GGGGGGAGCC
                                |||| ||| ||||||||||
                                AGTG GCG CCCCCCTCGG
                                  C   _
GAM953  LOC143915 3'  CTCCCCTCGGGCAACAAGC    83906     CAT   A_
                                GCT   TTGC  GGGGGGAG
                                |||   ||||  ||||||||
                                CGA   AACG  CTCCCCTC
                                  AC_   GG
GAM953  LOC145623 5'  TTGGCAGCTCCAGCAAATGAGC 84398          AG   GA
                                GCTCATTTGC  GGGG  GCCAA
                                ||||||||||  ||||  |||||
                                CGAGTAAACG  CCTC  CGGTT
                                      A_   GA
GAM953  LOC146268 3'  CCCGGGAATCTGCAAATGAGC  78335          _____
                                GCTCATTTGCAGG    GGG
                                ||||||||||||    |||
                                CGAGTAAACGTCT    CCC
                                       AAGGG
GAM953  LOC148887 3'  GGCTCCCCCGCATGCGC     85405    T  TT   AG
                                GC CA  TGC  GGGGGAGCC
                                || ||  |||  |||||||||
                                CG GT  ACG  CCCCCTCGG
                                 C  __   __
GAM953  LOC207043 3'  GCTCCCCCCGGGTATCAGC    91078     CATT   A_
                                GCT   TGC  GGGGGGAGC
                                |||   |||  |||||||||
                                CGA   ATG  CCCCCCTCG
                                  CT__   GG
GAM953  LOC253786 5'  TTAACTTTTGCAAATGAGC    98836           GG
                                GCTCATTTGCAGGGG  AG
                                ||||||||||||||  ||
                                CGAGTAAACGTTTTC  TT
                                       AA
GAM953  LOC253974 3'  TTTGGCTCCCCCCTGCAAATGA 99286
                  GC                GCTCATTTGCAGGGGGGAGCCAAA
                                ||||||||||||||||||||||||||
                                CGAGTAAACGTCCCCCCTCGGTTT

GAM953  LOC256905 3'  TCCATGTCCCTGCAAATGA    98663          ___
                                TCATTTGCAGGGG   GGA
                                ||||||||||||   |||
                                AGTAAACGTCCCT   CCT
                                       GTA
GAM953  LOC257395 3'  GGCTCCCCCCCGCGCGTGA    97149     T   A
                                TCAT TGC GGGGGGAGCC
                                |||| ||| ||||||||||
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                                AGTG GCG CCCCCCTCGG
                                  C  _
GAM953  LOC90233  3'  CCCAGGTCCTGCAAAGGAGC  57193     A      ___
                                GCTC TTTGCAGGG  GGG
                                |||| |||||||||  |||
                                CGAG AAACGTCCT  CCC
                                  G       GGA
GAM954  ACT     5'  CCACAATCCAGGGGGCCAT  40420       CCG  AAC
                                ATGGCCCCT  GGA  TGTGG
                                |||||||||  |||  |||||
                                TACCGGGGG  CCT  ACACC
                                    A__  A__
GAM954  ADAM11  3'  GCCACAGCTCAACTCGGGGGC  41490     TC  AAA__
                                GCCCC  CGGG   CTGTGGC
                                |||||  ||||   |||||||
                                CGGGG  GCTC   GACACCG
                                  __   AACTC
GAM954  ADAM11  3'  GCCACAGCTCAACTCGGGGGC  11487     TC  AAA__
                                GCCCC  CGGG   CTGTGGC
                                |||||  ||||   |||||||
                                CGGGG  GCTC   GACACCG
                                  __   AACTC
GAM954  CDC34   3'  GCCGCACCCCGGAGGAGCCA  16390     C      AAAC
                                TGGC CCTCCGGG   TGTGGC
                                |||| ||||||||   ||||||
                                ACCG GGAGGCCC   ACGCCG
                                  A      C___
GAM954  CRI1    3'  GCCACAGTTATCAAAGGCTA  27537     CCTCCG  A
                                TGGCC    GG AACTGTGGC
                                |||||    || |||||||||
                                ATCGG    CT TTGACACCG
                                  AAA___  A
GAM954  FLII    3'  GCCACAGTCCCCAGTAGCC  10656    CC  CC  AA
                                GGC  CT  GGG  ACTGTGGC
                                |||  ||  |||  ||||||||
                                CCG  GA  CCC  TGACACCG
                                  AT  __  C_
GAM954  FZD10   3'  GCCCACCCCCAGGAAGGCCA  24214     CC  _  AAAC  T
                                TGGCC  TCC GGG   TG GGC
                                |||||  ||| |||   || |||
                                ACCGG  AGG CCC   AC CCG
                                  A_  A  CC__  _
GAM954  GNA11   5'  CCACAGCCCCGGGGGCCG   76585      TC   AAA
                                TGGCCCC  CGGG  CTGTGG
                                |||||||  ||||  ||||||
                                GCCGGGG  GCCC  GACACC
                                   __   C__
GAM954  IGHMBP2  3'  GCCACAGAGGAGCGGAGGGGCC 10984        GGAAA
                                GGCCCCTCCG   CTGTGGC
                                ||||||||||   |||||||
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                                CCGGGGAGGC    GACACCG
                                      GAGGA
GAM954  MAGEA3   5' CCAGAGGCCCCCGGAGGAGC  19315   C      AAA  G
                                GC CCTCCGGG  CT TGG
                                || ||||||||  || |||
                                CG GGAGGCCC  GA ACC
                                 A       CCG  G
GAM954  PYGB     3' CCAGGGGTCCCGGAGGAACC  12687   CC       AA  G
                                GG  CCTCCGGGA  CT TGG
                                ||  |||||||||  || |||
                                CC  GGAGGCCCT  GG ACC
                                 AA       G_  G
GAM954  PYGB     3' CCATGTTTCCAGGAGGGGCCAT 12689          G     T
                                ATGGCCCCTCC GGAAAC GTGG
                                |||||||||||| |||||| ||||
                                TACCGGGGAGG CCTTTG TACC
                                      A     _
GAM954  SLC6A6   3' GCCACAGTCCTTCCTGGGGC  13183      TCC    __
                                GCCCC  GGGAA  ACTGTGGC
                                |||||  |||||  ||||||||
                                CGGGG  TCCTT  TGACACCG
                                   ___    CC
GAM954  UBTF     3' CCATTCCTTCCCAGAGGGGCC 27252        C    ACT
                                GGCCCCTC GGGAA  GTGG
                                |||||||| |||||  ||||
                                CCGGGGAG CCCTT  TACC
                                     A    CCT
GAM954  CBCIP2   3' GCCACACGGACTCAGAGGGGCC 52658         C   AAAC
           A                     TGGCCCCTC GGG   TGTGGC
                                |||||||||| |||   ||||||
                                ACCGGGGAG CTC   ACACCG
                                      A  AGGC
GAM954  FEM-2    3' GCCACAGTCCCATGAGGGCC  28316     C  C_   AA
                                GGCCC TC  GGGA  CTGTGGC
                                ||||| ||  ||||  |||||||
                                CCGGG AG  CCCT  GACACCG
                                   _ TA   __
GAM954  FLJ10199 3' GCCACAGTTGAGAAGCGGAGGG 71755          GGA___
           GCCA                  TGGCCCCTCCG     AACTGTGGC
                                ||||||||||      |||||||||
                                ACCGGGGAGGC     TTGACACCG
                                      GAAGAG
GAM954  FLJ11715 3' ACAGTGTCCCCAGGAGGCCAT  44972       _  CC   A
                                ATGGCC CCT  GGGA ACTGT
                                |||||| |||  |||| |||||
                                TACCGG GGA  CCCT TGACA
                                   A  C_   G
GAM954  FLJ12505 5' CCCGGTCCCGGAGCAGCCA   45713     CC      AA  T
                                TGGC  CTCCGGGA  CTG GG
                                ||||  ||||||||  ||| ||
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                                ACCG  GAGGCCCT  GGC CC
                                  AC       __  _
GAM954  KIAA0828  3'  GTTTCCCAGGAAGGCCAT    82119       CC  _
                                ATGGCC  TCC GGGAAAC
                                ||||||  ||| |||||||
                                TACCGG  AGG CCCTTTG
                                   A_   A
GAM954  KIAA1190  3'  CCACAGTTCTGGGAGCC     71643     CCC   G    A
                                GGC   TCC GGAA CTGTGG
                                |||   ||| |||| ||||||
                                CCG   AGG TCTT GACACC
                                  ___   G   _
GAM954  KIAA1297  5'  CCATGCCCAGAAGGCCA     72634      CC  C   AAAC
                                TGGCC  TC GGG    TGTGG
                                |||||  || |||    |||||
                                ACCGG  AG CCC    GTACC
                                   A_  A  ____
GAM954  PASK      5'  GCCACAGAGTTGGGGGGCCAT  31415        T    GAAA
                                ATGGCCCC CCGG    CTGTGGC
                                |||||||| ||||    |||||||
                                TACCGGGG GGTT    GACACCG
                                     _    GA__
GAM954  PCDH17    3'  GCCACAGTTCCCTGCAGCCA   27836     CCCTC    A
                                TGGC    CGGG AACTGTGGC
                                ||||    |||| |||||||||
                                ACCG    GTCC TTGACACCG
                                  AC___    C
GAM954  RIL       3'  CCATGCTGCCCTGAAGGGGCCA 14885        C    AAACT
                                TGGCCCCT CGGG    GTGG
                                |||||||| ||||    ||||
                                ACCGGGGA GTCC    TACC
                                     A   CGTCG
GAM954  SREC      3'  GCAGTGCTCCCGGAGGGGCC   14905          A_
                                GGCCCCTCCGGGA  ACTGT
                                ||||||||||||  |||||
                                CCGGGGAGGCCCT  TGACG
                                       CG
GAM954  TRAF2     3'  GCCGGCTCACGGAGGGGCCA   41236         G  AACTG
                                TGGCCCCTCCG GA    TGGC
                                ||||||||||| ||    ||||
                                ACCGGGGAGGC CT    GCCG
                                      A  CG___
GAM954  LOC123242 5'  CCACAGCCCACCTGGAGGCCA  76111      CC     AAA_
                                TGGCC  TCCGGG    CTGTGG
                                |||||  ||||||    ||||||
                                ACCGG  AGGTCC    GACACC
                                  __      ACCC
GAM954  LOC124460 5'  CCAAGAGCTCGAAGGGGCCAT  76559        C    AAA  G
                                ATGGCCCCT CGGG   CT TGG
                                |||||||| ||||   || |||
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                                TACCGGGGA GCTC   GA ACC
                                     A    GA_  _
GAM954   LOC132166 3'  GCCAGCGCCCGAGGGGGCCA  75537       TC    AAACTG
                                TGGCCCC  CGGG     TGGC
                                |||||||  ||||     ||||
                                ACCGGGG  GCCC     ACCG
                                    GA    GCG___
GAM954   LOC146958 5'  GCCACAGTCTCAAGTGGACAT  84944     G  C  CC    AA
                                ATG CC CT  GGGA  CTGTGGC
                                ||| || ||  ||||  |||||||
                                TAC GG GA  CTCT  GACACCG
                                  A  T  A_   __
GAM954   LOC149420 3'  GCCACAGTTTCCTAAGCGC   80155    CC  CC
                                GC  CT  GGGAAACTGTGGC
                                ||  ||  ||||||||||||||
                                CG  GA  TCCTTTGACACCG
                                 C_  A_
GAM954   LOC152317 3'  GCCACAGTCTGGGAGAGCCA   86831     CC    G   AA
                                TGGC  CTCC GGA  CTGTGGC
                                ||||  |||| |||  |||||||
                                ACCG  GAGG TCT  GACACCG
                                  A_   G   __
GAM954   LOC157450 3'  CCACAGCTTCCCGGGTCAT   71531       CTCC    A
                                ATGGCCC    GGGAA CTGTGG
                                |||||||    ||||| ||||||
                                TACTGGG    CCCTT GACACC
                                     _____    C
GAM954   LOC157807 5'  GCCACAGTTTCAGCAGACCAT  82513     CCC  CCGG
                                ATGG   CT    GAAACTGTGGC
                                ||||   ||    ||||||||||||
                                TACC   GA    CTTTGACACCG
                                  A__  CGA_
GAM954   LOC157923 5'  GCCACAGTCCAGAGAAGGCCA  82526      C_   C  GAA
                                TGGCC  CTC GG   ACTGTGGC
                                |||||  ||| ||   ||||||||
                                ACCGG  GAG CC   TGACACCG
                                   AA   A  ___
GAM954   LOC158510 5'  CCAGAGGCCCCCGGAGGAGC   82833    C       AAA  G
                                GC CCTCCGGG   CT TGG
                                || ||||||||   || |||
                                CG GGAGGCCC   GA ACC
                                 A       CCG  G
GAM954   LOC196860 3'  CCACAGTTCCCCGGAAAGTGCT 91214     CCC_     A
                                GGC    TCCGGG AACTGTGG
                                |||    |||||| ||||||||
                                TCG    AGGCCC TTGACACC
                                  TGAA     C
GAM954   LOC203235 5'  GCCAGGGCCCCCCAGAGGGGCC  92099         C   AAA  G
                                GGCCCCTC GGG   CT TGGC
                                |||||||| |||   || ||||
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                                CCGGGGAG CCC   GG ACCG
                                    A   CC_  G
GAM954   LOC220739 3'  GCCACAGTAGGAGGGGCCA   94521         GGGAA
                                TGGCCCCTCC    ACTGTGGC
                                ||||||||||    ||||||||
                                ACCGGGGAGG    TGACACCG
                                    A____
GAM954   LOC222166 5'  CCCGGCCCCGGAGGAGCC    95733    C       AAA   T
                                GGC CCTCCGGG   CTG GG
                                ||| ||||||||   ||| ||
                                CCG GGAGGCCC   GGC CC
                                  A       C__   _
GAM954   LOC253001 5'  CCACAGCCCACCTGGAGGCCA  97990      CC     AAA_
                                TGGCC  TCCGGG   CTGTGG
                                |||||  ||||||   ||||||
                                ACCGG  AGGTCC   GACACC
                                   __     ACCC
GAM954   LOC254057 3'  GCCCCTATCCCAGAGGGGCC   98782        C    AACTGT
                                GGCCCCTC GGGA     GGC
                                |||||||| ||||     |||
                                CCGGGGAG CCCT     CCG
                                    A   ATCC__
GAM954   LOC92558  3'  GCCACCTCCCAGAGGGGCC    70312        C    AACT
                                GGCCCCTC GGGA   GTGGC
                                |||||||| ||||   |||||
                                CCGGGGAG CCCT   CACCG
                                    A   C___
GAM954   LOC93626  5'  CCACAGCCCCGGGGGCCG    73128       TC    AAA
                                TGGCCCC  CGGG   CTGTGG
                                |||||||  ||||   ||||||
                                GCCGGGG  GCCC   GACACC
                                   __   C__
GAM955   CNN2      3'  CCAGCTTATACTGCTCCAT    16458         GTC    T
                                ATGGAGCAGTA   AAGTT GG
                                ||||||||||   ||||| ||
                                TACCTCGTCAT   TTCGA CC
                                    A__    _
GAM955   COL4A3    3'  CCAAACAATATTGCTCCAT    49380         GTCAA
                                ATGGAGCAGTA    GTTTGG
                                ||||||||||    ||||||
                                TACCTCGTTAT    CAAACC
                                    AA___
GAM955   COL4A3    3'  CCAAACAATATTGCTCCAT    49381         GTCAA
                                ATGGAGCAGTA    GTTTGG
                                ||||||||||    ||||||
                                TACCTCGTTAT    CAAACC
                                    AA___
GAM955   COL4A3    3'  CCAAACAATATTGCTCCAT    5400          GTCAA
                                ATGGAGCAGTA    GTTTGG
                                ||||||||||    ||||||
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                                TACCTCGTTAT    CAAACC
                                      AA___
GAM955  GRIK3    3' GGCCAAACTCACCTGCCCC   7720    A   TA  CA
                                GG GCAG  GT  AGTTTGGCC
                                || ||||  ||  |||||||||
                                CC CGTC  CA  TCAAACCGG
                                 C   __  C_
GAM955  IGF1     3' CCAAATGTTACTGCTC     7064         T  AG
                                GAGCAGTAG CA  TTTGG
                                |||||||||  ||  |||||
                                CTCGTCATT GT  AAACC
                                      _ __
GAM955  NHLH1    5' GGCCAAGCCCACCACTTCCA  20021     GC   A  CAA
                                TGGA  AGT GT   GTTTGGCC
                                ||||  ||| ||   ||||||||
                                ACCT  TCA CA   CGAACCGG
                                  __   C  CC_
GAM955  TNFSF5   3' CCAAAACGGGCCCTGCTCCAT  5367         TA   AAG
                                ATGGAGCAG  GTC   TTTGG
                                |||||||||  |||   |||||
                                TACCTCGTC  CGG   AAACC
                                     C_   GCA
GAM955  BTBD3    3' GCCAAACTCTTCTCTCCA    31028      C  T  TCA
                                TGGAG AG AG   AGTTTGGC
                                ||||| || ||   ||||||||
                                ACCTC TC TC   TCAAACCG
                                  _  T  ___
GAM955  C3IP1    3' GCTACCTGATTACTGCCCCAT  41578     A        A  TT
                                ATGG GCAGTAGTCA GT  GGC
                                |||| ||||||||||  ||  |||
                                TACC CGTCATTAGT CA  TCG
                                  C         C  __
GAM955  FAM3A    3' GCCAAACCCGGTGGCTGCTTCA 41731          AG  AA
          T                      ATGGAGCAGT  TC  GTTTGGC
                                |||||||||  ||  |||||||
                                TACTTCGTCG  GG  CAAACCG
                                      GT  CC
GAM955  FLJ14824 3' GCCAAACTTGCCTTTGCTTCA  52716        T  T
                                TGGAGCAG AG CAAGTTTGGC
                                ||||||||  || ||||||||||
                                ACTTCGTT TC GTTCAAACCG
                                     _  C
GAM955  FLJ20689 3' GACGCAACTACTGCTACAT   35962     G       CAA
                                ATG AGCAGTAGT   GTT
                                ||| |||||||||   |||
                                TAC TCGTCATCA   CAG
                                  A        ACG
GAM955  FLJ32894 3' GGCCAAACTTCCCCGCCTCCA  59000      CA  AGTC
                                TGGAG  GT    AAGTTTGGCC
                                |||||  ||   ||||||||||
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                                ACCTC  CG    TTCAAACCGG
                                   __  CCCC
GAM955  KIAA0339  3'  GGCCAGATTCATCAACCACTGC 71966    G     A  CA___
              TGCA                   TG AGCAGT GT     AGTTTGGCC
                                || |||||| ||    |||||||||
                                AC TCGTCA CA     TTAGACCGG
                                 G     C  ACTAC
GAM955  KIAA1280  5'  CCAAACTTGACTACCGTCAT   70275     AGCA
                                ATGG    GTAGTCAAGTTTGG
                                ||||    ||||||||||||||
                                TACT    CATCAGTTCAAACC
                                  GC__
GAM955  KIAA1870  5'  AACTTGACCACTGCCACA    50575    GA    A
                                TG  GCAGT GTCAAGTT
                                ||  ||||| ||||||||
                                AC  CGTCA CAGTTCAA
                                 AC     C
GAM955  PI4KII    3'  CCAAACCTGACCTGAACTTA   37948    T  AG   TA    A
                                A GG  CAG  GTCA GTTTGG
                                | ||  |||  |||| ||||||
                                A TC  GTC  CAGT CAAACC
                                 T  AA   __    C
GAM955  SSBP3     3'  GCCAAACTTTTTATTCCAT    36550      GCA    TC
                                ATGGA   GTAG  AAGTTTGGC
                                |||||   ||||  |||||||||
                                TACCT   TATT  TTCAAACCG
                                   ____    T_
GAM955  LOC127540 5'  GGCCAAACTCGACAAAGCCCG  75172     A  AGTA   A
                                TGG GC    GTC AGTTTGGCC
                                ||| ||    ||| |||||||||
                                GCC CG    CAG TCAAACCGG
                                  _  AAA_   C
GAM955  LOC158798 5'  GCCACCTACCACTGCTCC    82874        A  CA  TT
                                GGAGCAGT GT  AG  TGGC
                                |||||||| ||  ||  ||||
                                CCTCGTCA CA  TC  ACCG
                                     C  __  C_
GAM955  LOC196812 3'  GGCCACAACTAACCATGCCCCA 91127      A   GTA  CA   _
              T                   ATGG GCA   GT  AGTT TGGCC
                                |||| |||   ||  |||| |||||
                                TACC CGT   CA  TCAA ACCGG
                                  C   AC_  A_   C
GAM955  LOC199953 3'  GCCACTCACCACTGCTGCCA   89885     _     A  CA   TT
                                TGG AGCAGT GT  AGT  GGC
                                ||| |||||| ||  |||  |||
                                ACC TCGTCA CA  TCA  CCG
                                  G     C  C_   __
GAM955  LOC220020 3'  AACTTGTTCAACCCTGCTCCAT 95040         TAGT___
                                ATGGAGCAG      CAAGTT
                                |||||||||      ||||||
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                                TACCTCGTC      GTTCAA
                                     CCAACTT
GAM956  AKAP1    3'  ACTATGGGTTCTCTTCGCAAA  14472      A  CTT      C
                                TTTGT GA   GGAACCCA AGT
                                |||||| ||   |||||||| |||
                                AAACG CT   TCTTGGGT TCA
                                   _ TC_       A
GAM956  AKAP1    3'  ACTATGGGTTCTCTTCGCAAA  58373      A  CTT      C
                                TTTGT GA   GGAACCCA AGT
                                |||||| ||   |||||||| |||
                                AAACG CT   TCTTGGGT TCA
                                   _ TC_       A
GAM956  EGF      3'  ACTATAGGTTTTGGTTCCACAA 10488      A  C TG    CAC
                                TTGT GA T  GAACC   AGT
                                |||| || |  |||||   |||
                                AACA CT G  TTTGG   TCA
                                  C  T GT    ATA
GAM956  EZH1     3'  GACTGTGGGTTCCAAATTAC   10551      AC
                                GTAG  TTGGAACCCACAGTC
                                ||||  ||||||||||||||||
                                CATT  AACCTTGGGTGTCAG
                                  A_
GAM956  STAC     3'  GACTGTGGAGTAATAGCCACAA 13427      AGA  TGGA  _
           A                     TTTGT   CT    AC CCACAGTC
                                |||||   ||    || ||||||||
                                AAACA   GA    TG GGTGTCAG
                                   CC_  TAA_  A
GAM956  CCR1     3'  GACTGTGGGCTCCATTC     8927     CT    A
                                GA  TGGA CCCACAGTC
                                ||  |||| |||||||||
                                CT  ACCT GGGTGTCAG
                                 T_    C
GAM956  FLJ10483 3'  GACTGTGGAAGAGATTACAAA  36652       A   GGAAC
                                TTTGTAG CTT     CCACAGTC
                                ||||||| |||     ||||||||
                                AAACATT GAG     GGTGTCAG
                                    A   AA___
GAM956  KIAA1871 3'  ACTGTAAGAGTCTACAAA    61890          GGAACCC
                                TTTGTAGACTT      ACAGT
                                ||||||||||       |||||
                                AAACATCTGAG      TGTCA
                                      AA_____
GAM956  LOC150821 3'  GGGTTCCACATCCACAAA    60944      A  CT
                                TTTGT GA  TGGAACCC
                                ||||| ||  ||||||||
                                AAACA CT  ACCTTGGG
                                   C  AC
GAM956  LOC151057 3'  ACTGTGGGTACACCTATAAA  86379       ACT  GA
                                TTTGTAG   TG  ACCCACAGT
                                |||||||   ||  |||||||||
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                                AAATATC   AC  TGGGTGTCA
                                    C__  A_
GAM956  LOC157507 5'  ACTGTAAAAGTCTGCAAA    82377          GGAACCC
                                TTTGTAGACTT      ACAGT
                                ||||||||||      |||||
                                AAACGTCTGAA      TGTCA
                                      AA_____
GAM956  LOC203339 5'  GGATTCCCAGTCTACAAA    92214          T   C
                                TTTGTAGACT GGAA CC
                                |||||||||| |||| ||
                                AAACATCTGA CCTT GG
                                      C   A
GAM956  LOC51030  3'  ACTGTAAATTAAACCAATCTAC 32695        C   AACCC___
           AAA                    TTTGTAGA TTGG       ACAGT
                                |||||||| ||||       |||||
                                AAACATCT AACC       TGTCA
                                    _   AAATTAAA
GAM956  LOC90906  3'  GACTGTGGATCCCAAACTTTGC 64951       C_   AAC
           A                     TGTAGA  TTGG   CCACAGTC
                                |||||||  ||||   ||||||||
                                ACGTTT  AACC   GGTGTCAG
                                   CA    CTA
GAM957  FLJ22332  5'  GGAAAGAAAACTACATCACA   45637      G  A      _______
                                TGTG AT TAGTTTTC     CC
                                |||| || ||||||||     ||
                                ACAC TA ATCAAAAG     GG
                                  _ C       AAA___
GAM958  AMACR     3'  TTGTATGCATGGAAACATGGA  69103      ATC        G
                                TCCAT   TCCATGCATG CGG
                                |||||   |||||||||| |||
                                AGGTA   AGGTACGTAT GTT
                                   CAA        _
GAM958  BCL2L11   3'  TCGCCCAGAGATATGGA     57615          CA  CAT    G
                                TCCATATCTC  TG   GGCG A
                                |||||||||  ||   |||| |
                                AGGTATAGAG  AC   CCGC T
                                      __ ___    G
GAM958  BCL2L11   3'  TCGCCCAGAGATATGGA     57616          CA  CAT    G
                                TCCATATCTC  TG   GGCG A
                                |||||||||  ||   |||| |
                                AGGTATAGAG  AC   CCGC T
                                      __ ___    G
GAM958  FGFR2     5'  CGTCCACATGGAGATATGGA   5559             CA   _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __   T
GAM958  FGFR2     5'  CGTCCACATGGAGATATGGA   43633            CA   _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
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                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM958  FGFR2   5' CGTCCACATGGAGATATGGA  43638          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM958  FGFR2   5' CGTCCACATGGAGATATGGA  43642          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM958  FGFR2   5' CGTCCACATGGAGATATGGA  43652          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM958  FGFR2   5' CGTCCACATGGAGATATGGA  43665          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM958  FGFR2   5' CGTCCACATGGAGATATGGA  43674          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM958  FGFR2   5' CGTCCACATGGAGATATGGA  43678          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM958  FGFR2   5' CGTCCACATGGAGATATGGA  43763          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM958  FGFR2   5' CGTCCACATGGAGATATGGA  43767          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM958  FGFR2   5' CGTCCACATGGAGATATGGA  43771          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM958  MAP3K14 3' ATCCGCCACGTGAAGAGA   15541     CA  A
                                TCTC  TGC TGGCGGAT
                                ||||  ||| ||||||||
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                                AGAG  GTG ACCGCCTA
                                  AA  C
GAM958  KIAA0819  3'  CCCCAGCATCACAGGAGACATG 64330      A    ____   A  C
            GA                    TCCAT TCTCC   ATGC TGG GG
                                  ||||| |||||   |||| ||| ||
                                  AGGTA AGAGG   TACG ACC CC
                                    C    ACAC  _  _
GAM958  PORIMIN   3'  CATACATGGAGTATGGA    54702       T     C
                                  TCCATA CTCCATG ATG
                                  |||||| ||||||| |||
                                  AGGTAT GAGGTAC TAC
                                     _     A
GAM958  RDC1      3'  CCGGCACGGGATATGGA    72832        T  A  A
                                  TCCATATC CC TGC TGG
                                  |||||||| || ||| |||
                                  AGGTATAG GG ACG GCC
                                      _ C  _
GAM958  VEZATIN   3'  ATCCGCCACAACAGACAATG  34656    A_  CCA  CA
                                  CAT  TCT  TG  TGGCGGAT
                                  |||  |||  ||  ||||||||
                                  GTA  AGA  AC  ACCGCCTA
                                    AC  CA_ __
GAM958  LOC147645 5'  ATCCGCTGGTGGCAGAGACACG 79065    ATA   CA  AT__
            G                     CC  TCTC  TGC   GGCGGAT
                                  ||  ||||  |||   |||||||
                                  GG  AGAG  ACG   TCGCCTA
                                   CAC   __  GTGG
GAM958  LOC199775 3'  TTGCTGCATCAGAGATATG   89726       C_   TG
                                  CATATCTC  ATGCA  GCGG
                                  ||||||||  |||||  ||||
                                  GTATAGAG  TACGT  CGTT
                                       AC    __
GAM958  LOC51279  3'  CCGCTATTAGAGTATGGA    33752       T  CATGC
                                  TCCATA CTC    ATGGCGG
                                  |||||| |||    |||||||
                                  AGGTAT GAG    TATCGCC
                                     _  AT___
GAM959  SCAMP1    3'  GCTAAATAAATATTCTCC    54500    T    C
                                  GGA AATATT ATTTAGC
                                  ||| |||||| |||||||
                                  CCT TTATAA TAAATCG
                                    C    A
GAM959  SCAMP1    3'  GCTAAATAAATATTCTCC    54501    T    C
                                  GGA AATATT ATTTAGC
                                  ||| |||||| |||||||
                                  CCT TTATAA TAAATCG
                                    C    A
GAM959  NX-17     3'  TGAATATCAGCCCCTAATA   40706       ATA_
                                  TATTAGGG   ATATTCA
                                  ||||||||   |||||||
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                                ATAATCCC   TATAAGT
                                    CGAC
GAM959  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
           TA                    TATTAGGGATAATATTCATTTAGC
                                 ||||||||||||||||||||||
                                 ATAATCCCTATTATAAGTAAATCG

GAM960  DLEC1    3'  CATCTGGCCCTCCCTTG    24716      A    A  C
                                 CAAGG AGGGC GG GTG
                                 ||||| ||||| || |||
                                 GTTCC TCCCG TC TAC
                                   C    G  _
GAM960  DLEC1    3'  CATCTGGCCCTCCCTTG    24717      A    A  C
                                 CAAGG AGGGC GG GTG
                                 ||||| ||||| || |||
                                 GTTCC TCCCG TC TAC
                                   C    G  _
GAM960  PIP5K1A  3'  TATCCCACCCTGCCTTGATA  14520        A   CA  C
                                 TATCAAGG AGGG  GG GTG
                                 |||||||| ||||  || |||
                                 ATAGTTCC TCCC  CC TAT
                                    G   A_  C
GAM960  SOX11    3'  ACCCACCCCCCCTTGGTA    13308        AA   CA  C
                                 TATCAAGG  GGG  GG GT
                                 ||||||||  |||  || ||
                                 ATGGTTCC  CCC  CC CA
                                    CC   A_  _
GAM960  CHL1     3'  TGTTACCTTTCCTCAATA    22768     CA      CA
                                 TAT  AGGAAGGG  GGCG
                                 |||  ||||||||  ||||
                                 ATA  TCCTTTCC  TTGT
                                   AC       A_
GAM960  EPB41L1  3'  CATTCTGCCCTTCCCTGA    71104     A        C
                                 TCA GGAAGGGCAGG GTG
                                 ||| |||||||||| |||
                                 AGT CCTTCCCGTCT TAC
                                   C         _
GAM960  FLJ00060 3'  CATACCCCCTGCCCTCCTCTGA 61741     _   A     CGTG
                                 TCA AGGA GGGCAGG   ATG
                                 ||| |||| |||||||   |||
                                 AGT TCCT CCCGTCC   TAC
                                   C   _     CCCA
GAM960  FLJ10898 5'  CACCACAGCCCTTTCTCAATA  60126     CA       AGGC
                                 TAT  AGGAAGGGC   GTG
                                 |||  |||||||||   |||
                                 ATA  TCTTTCCCG   CAC
                                   AC       ACAC
GAM960  FLJ22557 3'  ATCATCCCATCCTTAATA    45581     C    A  CAGGC
                                 TAT AAGGA GGG    GTGAT
                                 ||| ||||| |||    |||||
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                                ATA TTCCT CCC     TACTA
                                  A     A  _____
GAM960  KIAA0574  3'  CATCCCCTGCCCTCCCCTGA   69808     A  A       CGT
                                TCA GG AGGGCAGG   GATG
                                ||| || ||||||||   ||||
                                AGT CC TCCCGTCC   CTAC
                                  C  C       C__
GAM960  KIAA0632  3'  CACCTCAGAAACCCTTCCTTGA 32071           CA___  C
                                TCAAGGAAGGG     GG GTG
                                ||||||||||     || |||
                                AGTTCCTTCCC     CT CAC
                                      AAAGA  C
GAM960  KIAA1045  3'  CATCACATGTCCTTCC      71599          GGC
                                GGAAGGGCA   GTGATG
                                |||||||||   ||||||
                                CCTTCCTGT   CACTAC
                                     A__
GAM960  KIAA1354  5'  CAGTGACTGCCTTCCCTTGATA 61572         A      G  _
                                TATCAAGG AGGGCAG CG TG
                                |||||||| ||||||| || ||
                                ATAGTTCC TTCCGTC GT AC
                                     C      A  G
GAM960  MGC20460  5'  CACCGCCTCCTACCCTTCTT   54901         C___    _
                                AGGAAGGG    AGGCG TG
                                ||||||||    ||||| ||
                                TTCTTCCC    TCCGC AC
                                     ATCC     C
GAM960  LOC158476 3'  CACGCCCGCCCCCCCCCATTGA  88186      _  AA_    A
                                TCAA GG   GGGC GGCGTG
                                ||||  ||   ||||  ||||||
                                AGTT CC   CCCG CCGCAC
                                  A  CCC    C
GAM960  LOC90459  3'  CACACCCGCCTAATTTTTG    63550       A_    A  C
                                CAAGGA  GGGC GG GTG
                                ||||||  ||||  || |||
                                GTTTTT  TCCG CC CAC
                                   AA    C  A
GAM961  EIF1A     3'  TAATGGTTCTTACTGCTAAGA  90009     CC   T  GG
                                TC  AGC GG  AGAACCATTA
                                ||  |||  ||  ||||||||||
                                AG  TCG TC  TCTTGGTAAT
                                 AA   _  AT
GAM961  HOXB6     5'  GGCTCTCACGTTGGGAC     60541         T GG    A
                                GTCCCAGC G  GAGA CC
                                ||||||||  |  ||||  ||
                                CAGGGTTG C  CTCT GG
                                     _ A_    C
GAM961  HOXC9     3'  TAATGATTCCCAGCCCAGGA   61928     CA_      GAAC
                                TCC   GCTGGGGA    CATTA
                                |||   ||||||||    |||||
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                                AGG  CGACCCTT   GTAAT
                                  ACC      A___
GAM961  ZNF2     5'  GGCTCGCTCTCCCAGCTAAGGC 41158    CC     _  AA__
                                GTC  AGCTGGG GAG   CC
                                |||  ||||||| |||   ||
                                CGG  TCGACCC CTC   GG
                                  AA      T  GCTC
GAM961  C3orf4   3'  TAATGACCCTCCAGAGCTGGGA 39596       GG   AAC
                                TCCCAGCT  GGAG  CATTA
                                ||||||||  ||||  |||||
                                AGGGTCGA  CCTC  GTAAT
                                    GA   CCA
GAM961  F-LAN-1  3'  TAATGAGACCCAGCTGGGA   61918         GAGAAC
                                TCCCAGCTGGG    CATTA
                                ||||||||||     |||||
                                AGGGTCGACCC    GTAAT
                                      AGA___
GAM961  FLJ23420 3'  AATGGTTCTCATTTGGCT    47533    TG  _
                                AGC  GG GAGAACCATT
                                |||  || ||||||||||
                                TCG  TT CTCTTGGTAA
                                  GT  A
GAM961  NOL4     3'  AATAGTTCAAGATCCAGCTG   15035       GA__   C
                                CAGCTGGG   GAAC ATT
                                ||||||||   |||| |||
                                GTCGACCT   CTTG TAA
                                    AGAA   A
GAM961  TREX1    5'  AATGGCTCCAGCTGG      54378         AGAA
                                CCAGCTGGGG   CCATT
                                ||||||||||   |||||
                                GGTCGACCTC   GGTAA
                                      ____
GAM961  TREX1    5'  AATGGCTCCAGCTGG      54385         AGAA
                                CCAGCTGGGG   CCATT
                                ||||||||||   |||||
                                GGTCGACCTC   GGTAA
                                      ____
GAM961  LOC144519 3'  AATGGTCATCCAGGAC     77361     CAGC   GA  A
                                GTCC   TGGG  GA CCATT
                                ||||   ||||  || |||||
                                CAGG   ACCT  CT GGTAA
                                  ____   A_  _
GAM961  LOC149460 5'  GTAATGTCCAGTCCCCAGCCAG 85613    CA      GAAC_
          G                      CC  GCTGGGGA    CATTAC
                                 ||  ||||||||    ||||||
                                 GG  CGACCCCT    GTAATG
                                  AC      GACCT
GAM961  LOC149461 3'  GTAATGTCCAGTCCCCAGCCAG 80203    CA      GAAC_
          G                      CC  GCTGGGGA    CATTAC
                                 ||  ||||||||    ||||||
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                              GG  CGACCCCT    GTAATG
                               AC       GACCT
GAM961  LOC93097  5'  AATGGTTCTAATCCTGG    71879     CT  GG
                              CCAG  GG  AGAACCATT
                              ||||  ||  |||||||||
                              GGTC  CT  TCTTGGTAA
                                __  AA
GAM962  ABCA2     3'  TGGAGAAGCTGACCCTGCTGGC 97878        A  T   GAAA__
           CAGG                   CCTGGCCA CA GGT     CTCCA
                              |||||||| || |||     |||||
                              GGACCGGT GT CCA     GAGGT
                                   C  C   GTCGAA
GAM962  ABCA2     3'  TGGAGAAGCTGACCCTGCTGGC 9634         A  T   GAAA__
           CAGG                   CCTGGCCA CA GGT     CTCCA
                              |||||||| || |||     |||||
                              GGACCGGT GT CCA     GAGGT
                                   C  C   GTCGAA
GAM962  ADAMTS4   3'  GGGGTTTCACCATGTTGGCCAG 18767
           G                    CCTGGCCAACATGGTGAAACTCC
                              ||||||||||||||||||||||
                              GGACCGGTTGTACCACTTTGGGG

GAM962  ADAMTS4   3'  GGGTTTCACCATGTTGGCCAGG 18769
                              CCTGGCCAACATGGTGAAACTC
                              |||||||||||||||||||||
                              GGACCGGTTGTACCACTTTGGG

GAM962  ADCY6     5'  TTCACCATCTTGGCCAGG    31595         C
                              CCTGGCCAA ATGGTGAA
                              |||||||| ||||||||
                              GGACCGGTT TACCACTT
                                   C
GAM962  AGR2      3'  GAGTCAACTCTGGCCAGG    22162         ACAT   GAA
                              CCTGGCCA    GGT   ACTC
                              ||||||||    |||   ||||
                              GGACCGGT    TCA   TGAG
                                   C___    AC_
GAM962  AKAP13    3'  TGGAATCTACTGCCTGCTGGCC 91258         A  T   GAAAC__
           AGG                    CCTGGCCA CA GGT      TCCA
                              |||||||| || |||      ||||
                              GGACCGGT GT CCG      AGGT
                                   C  _   TCATCTA
GAM962  ALDH1B1   3'  TTCACCATTTTGGCCAGG    7332          C
                              CCTGGCCAA ATGGTGAA
                              |||||||| ||||||||
                              GGACCGGTT TACCACTT
                                    T
GAM962  APAF1     3'  GGGGTTTCACCATGTTGGCCGG 25977
           G                    CCTGGCCAACATGGTGAAACTCC
                              ||||||||||||||||||||||
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                                GGGCCGGTTGTACCACTTTGGGG

GAM962  APAF1    3'  GGGGTTTCACCATGTTGGCCGG 8590
                G                CCTGGCCAACATGGTGAAACTCC
                                 ||||||||||||||||||||||
                                 GGGCCGGTTGTACCACTTTGGGG

GAM962  APM1     3'  GGGTTTCACCATATTGGCCAGG 17787          C
                                 CCTGGCCAA ATGGTGAAACTC
                                 |||||||| ||||||||||
                                 GGACCGGTT TACCACTTTGGG
                                       A
GAM962  APM1     3'  TGGAGTTTCCCTCTGTTGCCAG 17796       C   T_  T
                G                CCTGGC AACA  GG GAAACTCCA
                                 |||||| ||||  || |||||||||
                                 GGACCG TTGT  CC CTTTGAGGT
                                    _   CT  _
GAM962  APOL1    3'  TGGGGTTTCACCATGTTGGCCA 14747
                GG                 CCTGGCCAACATGGTGAAACTCCA
                                   ||||||||||||||||||||||||
                                   GGACCGGTTGTACCACTTTGGGGT

GAM962  APPL     3'  TTCACCGTGTTAGCCAGG    24961       C
                                 CCTGGC AACATGGTGAA
                                 |||||| ||||||||||
                                 GGACCG TTGTGCCACTT
                                    A
GAM962  ARSF     5'  GGCTCTCACCATGTTGACCAGG 65210      C        AACT
                                 CCTGG CAACATGGTGA   CC
                                 ||||| ||||||||||   ||
                                 GGACC GTTGTACCACT   GG
                                    A         CTC_
GAM962  ATM      3'  TTCACCATATTGCCCAGG    57151      C  C
                                 CCTGG CAA ATGGTGAA
                                 ||||| ||| ||||||||
                                 GGACC GTT TACCACTT
                                    C  A
GAM962  ATP5G3   5'  GGAATTCCCCGGCCTGGCCAGG 9860         ACA  T  AC
                                 CCTGGCCA   TGG GAA  TCC
                                 ||||||||   ||| |||  |||
                                 GGACCGGT   GCC CTT  AGG
                                      CCG   C   A_
GAM962  ATP6V1A1 3'  GGGGTTTCACCATATTGGTCAG 9871          C
                G                 CCTGGCCAA ATGGTGAAACTCC
                                  |||||||||  ||||||||||||
                                  GGACTGGTT TACCACTTTGGGG
                                       A
GAM962  ATP8B2   3'  GTTTCACCATGTTGGCCAGG   65848
                                 CCTGGCCAACATGGTGAAAC
                                 ||||||||||||||||||
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                                GGACCGGTTGTACCACTTTG

GAM962  AXL     3'  GAGTCTCACTGTGTCACCCAGG 9906       CCA       A
                                CCTGG  ACATGGTGA ACTC
                                |||||  ||||||||| ||||
                                GGACC  TGTGTCACT TGAG
                                   CAC       C
GAM962  AXL     3'  GGGTTTCACCATGTTGGCCAGG 9908
                                CCTGGCCAACATGGTGAAACTC
                                |||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGG

GAM962  AXL     3'  GAGTCTCACTGTGTCACCCAGG 41887      CCA       A
                                CCTGG  ACATGGTGA ACTC
                                |||||  ||||||||| ||||
                                GGACC  TGTGTCACT TGAG
                                   CAC       C
GAM962  AXL     3'  GGGTTTCACCATGTTGGCCAGG 41890
                                CCTGGCCAACATGGTGAAACTC
                                |||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGG

GAM962  BRIP1   3'  TGGGGTTTCACCATGTTGGCCA 50215
            GG                    CCTGGCCAACATGGTGAAACTCCA
                                |||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGGT

GAM962  BSN     3'  GGAGCAGACCTCCATGTGGCCA 14386        A    TGAAA__
            GG                    CCTGGCCA CATGG      CTCC
                                |||||||| |||||      ||||
                                GGACCGGT GTACC      GAGG
                                   _    TCCAGAC
GAM962  C7      3'  TGGGTTTCACCATGTTGGCCA  6990              T
                                TGGCCAACATGGTGAAAC CCA
                                |||||||||||||||| |||
                                ACCGGTTGTACCACTTTG GGT
                                                _
GAM962  CASP2   3'  GGGTTTCACCATGTTAGCCGGG 8716       C
                                CCTGGC AACATGGTGAAACTC
                                |||||| ||||||||||||||
                                GGGCCG TTGTACCACTTTGGG
                                   A
GAM962  CASP2   3'  GGGTTTCACCATGTTAGCCGGG 53292      C
                                CCTGGC AACATGGTGAAACTC
                                |||||| ||||||||||||||
                                GGGCCG TTGTACCACTTTGGG
                                   A
GAM962  CASP2   3'  GGGTTTCACCATGTTAGCCGGG 53308      C
                                CCTGGC AACATGGTGAAACTC
                                |||||| ||||||||||||||
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                                GGGCCG TTGTACCACTTTGGG
                                   A
GAM962  CASP2    3'  GGGTTTCACCATGTTAGCCGGG 53340       C
                                CCTGGC AACATGGTGAAACTC
                                |||||| ||||||||||||||
                                GGGCCG TTGTACCACTTTGGG
                                   A
GAM962  CCNF     3'  GGGATTTCACCATGTTGGCCAG 10081              CT
              G                  CCTGGCCAACATGGTGAAA  CC
                                 |||||||||||||||||  ||
                                 GGACCGGTTGTACCACTTT  GG
                                          AG
GAM962  CHST6    3'  GAGTTTATCATGCTGGACA   41501    G  A       A
                                TG CCA CATGGTGAA CTC
                                || ||| ||||||||| |||
                                AC GGT GTACTATTT GAG
                                 A  C       _
GAM962  CLECSF11 5'  TGGGGTTTCACTATGTTGGCCA 56150
              GG                  CCTGGCCAACATGGTGAAACTCCA
                                  ||||||||||||||||||||||||
                                  GGACCGGTTGTATCACTTTGGGGT

GAM962  CMAR    5'  GAGTCTCGCTGTGTTGCCA   19031     C       A
                                TGGC AACATGGTGA ACTC
                                |||| |||||||||| ||||
                                ACCG TTGTGTCGCT TGAG
                                  _        C
GAM962  CNGA1    5'  TGGGATTTCACCATGTTGGCCA 60246              CT
                                TGGCCAACATGGTGAAA  CCA
                                |||||||||||||||  |||
                                ACCGGTTGTACCACTTT  GGT
                                          AG
GAM962  COX15    3'  TTCACCACATTGGCCGGG    55292         CA
                                CCTGGCCAA  TGGTGAA
                                |||||||||  |||||||
                                GGGCCGGTT  ACCACTT
                                      AC
GAM962  CR1      3'  GGGGTTTCACCATGTTAGCCAG 6946       C
              G                  CCTGGC AACATGGTGAAACTCC
                                 ||||||  ||||||||||||||||
                                 GGACCG TTGTACCACTTTGGGG
                                    A
GAM962  CXCL16   3'  GGGGTTTCACCATGTTGACCAG 42174      C
              G                  CCTGG CAACATGGTGAAACTCC
                                 |||||  ||||||||||||||||
                                 GGACC GTTGTACCACTTTGGGG
                                    A
GAM962  CYP1A2   3'  GGGTTTCACCATGTTGGTCAG  7520
                                CTGGCCAACATGGTGAAACTC
                                |||||||||||||||||||||
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                                GACTGGTTGTACCACTTTGGG

GAM962  CYP1A2   3'  TGGGGTTTCACCATGTTGGCCA 7531
            GG                   CCTGGCCAACATGGTGAAACTCCA
                                 ||||||||||||||||||||||||
                                 GGACCGGTTGTACCACTTTGGGGT

GAM962  DFFB     3'  GGGGTTTCACCATGTTGGCCAG 88777
            G                    CCTGGCCAACATGGTGAAACTCC
                                 |||||||||||||||||||||||
                                 GGACCGGTTGTACCACTTTGGGG

GAM962  DFFB     3'  GGGGTTTCACCATGTTGGTCAG 88779
            G                    CCTGGCCAACATGGTGAAACTCC
                                 ||||||||||||||||||||||||
                                 GGACTGGTTGTACCACTTTGGGG

GAM962  DFFB     3'  TGGAGTTTCACTTTTGTTGCCC 88789      C     T_
            AGG                    CCTGG CAACA  GGTGAAACTCCA
                                   ||||| |||||  ||||||||||||
                                   GGACC GTTGT  TCACTTTGAGGT
                                      C     TT
GAM962  DHFR     3'  TGGGGTTTCACCATGTTGGTCA 7660
            GG                   CCTGGCCAACATGGTGAAACTCCA
                                 ||||||||||||||||||||||||||
                                 GGACTGGTTGTACCACTTTGGGGT

GAM962  DISC1    3'  TTCACCATGTTGGCTAGG     38521
                                 CCTGGCCAACATGGTGAA
                                 ||||||||||||||||||
                                 GGATCGGTTGTACCACTT

GAM962  DSCR3     3'  TTCACCATCTTGGCCAGG     21327          C
                                 CCTGGCCAA ATGGTGAA
                                 |||||||| ||||||||
                                 GGACCGGTT TACCACTT
                                       C
GAM962  EHD2     3'  GGGGTTTCACCATGTTGGCCAG 28226
            G                    CCTGGCCAACATGGTGAAACTCC
                                 |||||||||||||||||||||||
                                 GGACCGGTTGTACCACTTTGGGG

GAM962  EPB72    3'  GGGGTTTCACCATGTTGGCCAG 15879
            G                    CCTGGCCAACATGGTGAAACTCC
                                 |||||||||||||||||||||||
                                 GGACCGGTTGTACCACTTTGGGG

GAM962  F2RL2    3'  GGGGTTTCACCATGTTGACCAG 15899       C
            G                    CCTGG CAACATGGTGAAACTCC
                                 ||||| ||||||||||||||||
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                                GGACC GTTGTACCACTTTGGGG
                                  A
GAM962  F2RL3    3'  GGAGTTTCACCATGTTGGCCAG 15523
            G                    CCTGGCCAACATGGTGAAACTCC
                                 ||||||||||||||||||||||
                                 GGACCGGTTGTACCACTTTGAGG

GAM962  F3      3'  TTCACCATCTTGGCCAGG    67685          C
                                 CCTGGCCAA ATGGTGAA
                                 |||||||| ||||||||
                                 GGACCGGTT TACCACTT
                                       C
GAM962  FANCF    3'  GGGGTTTCACCATGCTGGCCAG 42983         A
            G                    CCTGGCCA CATGGTGAAACTCC
                                 |||||||| ||||||||||||||
                                 GGACCGGT GTACCACTTTGGGG
                                      C
GAM962  FCAR     3'  GGGTTTCACCATGTTGGCCAGG 56639
                                 CCTGGCCAACATGGTGAAACTC
                                 |||||||||||||||||||||
                                 GGACCGGTTGTACCACTTTGGG

GAM962  FEZ1     3'  GGAGTTTCACCATGTTGGCCAG 42871
            G                    CCTGGCCAACATGGTGAAACTCC
                                 ||||||||||||||||||||||
                                 GGACCGGTTGTACCACTTTGAGG

GAM962  FEZ1     3'  TGAAGTTTCATTCTATCGCCCA 42875      CCAACAT       C
            GG                     CCTGG      GGTGAAACT CA
                                 |||||      ||||||||| ||
                                 GGACC      TTACTTTGA GT
                                    CGCTATC        A
GAM962  FGF5     3'  GGGGTTTCACCATGTTGGTCAG 53664
            G                    CCTGGCCAACATGGTGAAACTCC
                                 ||||||||||||||||||||||
                                 GGACTGGTTGTACCACTTTGGGG

GAM962  FGF5     3'  GGGGTTTCACCATGTTGGTCAG 16762
            G                    CCTGGCCAACATGGTGAAACTCC
                                 ||||||||||||||||||||||
                                 GGACTGGTTGTACCACTTTGGGG

GAM962  FUT1     3'  GGGTTTCACCATGTTGGCCGGG 5605
                                 CCTGGCCAACATGGTGAAACTC
                                 |||||||||||||||||||||
                                 GGGCCGGTTGTACCACTTTGGG

GAM962  FUT5     3'  GGAGTCTTTGGTGGCCAGG   10729         A  T  TGAA
                                 CCTGGCCA CA GG    ACTCC
                                 |||||||| || ||    |||||
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                                GGACCGGT GT TC    TGAGG
                                     G  T  ____
GAM962   FUT6     3'  GGAGTCTTCGGTGGCCAGG    5641          A ATGG   _
                                CCTGGCCA C    TGAA ACTCC
                                |||||||| |    |||| ||||||
                                GGACCGGT G    GCTT TGAGG
                                     _ ____    C
GAM962   G6PC     3'  TTCATCATGTTGGCCAGG     5668
                                CCTGGCCAACATGGTGAA
                                ||||||||||||||||||
                                GGACCGGTTGTACTACTT

GAM962   GHR      3'  GGGGTTTCACCATGTTGGCCAG 5705
                G                CCTGGCCAACATGGTGAAACTCC
                                 ||||||||||||||||||||||
                                 GGACCGGTTGTACCACTTTGGGG

GAM962   GM2A     3'  TGGGGTTTCACCATGTTGGCCA 68391
                GG                 CCTGGCCAACATGGTGAAACTCCA
                                   ||||||||||||||||||||||||
                                   GGACCGGTTGTACCACTTTGGGGT

GAM962   GNE      3'  GGGTTTCACCATGTTGGCCAGG 19676
                                   CCTGGCCAACATGGTGAAACTC
                                   |||||||||||||||||||||
                                   GGACCGGTTGTACCACTTTGGG

GAM962   GRM7     5'  TGGGTTTCACCATGTTGGCCAG 7792                  T
                G                  CCTGGCCAACATGGTGAAAC CCA
                                   |||||||||||||||||| |||
                                   GGACCGGTTGTACCACTTTG GGT
                                                      _
GAM962   HCS      3'  TGGTGTTTCACCATGTTGGCCA 38996                T
                G                  CTGGCCAACATGGTGAAAC CCA
                                   |||||||||||||||||| |||
                                   GACCGGTTGTACCACTTTG GGT
                                                T
GAM962   HTR1D    3'  TTCATCATGTTGGCCAGG     7851
                                   CCTGGCCAACATGGTGAA
                                   ||||||||||||||||
                                   GGACCGGTTGTACTACTT

GAM962   IL11     3'  GGGTTTCACCATGTTGGCCAGG 7193
                                   CCTGGCCAACATGGTGAAACTC
                                   |||||||||||||||||||||
                                   GGACCGGTTGTACCACTTTGGG

GAM962   INMT     3'  GGAGTTTCGCTCTGTCGCCCAG 23220       CCA   T
                G                  CCTGG   ACA GGTGAAACTCC
                                   |||||   ||| ||||||||||
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                                GGACC   TGT TCGCTTTGAGG
                                   CGC   C
GAM962  INMT     3'  TTCACCGTGTTAGCCAGG    23232        C
                                CCTGGC AACATGGTGAA
                                |||||| ||||||||||
                                GGACCG TTGTGCCACTT
                                   A
GAM962  JAK3     3'  TGAGGTTTCACCATGATGGCCA 5834          A          TC
             GG                   CCTGGCCA CATGGTGAAAC  CA
                                |||||||| ||||||||||  ||
                                GGACCGGT GTACCACTTTG  GT
                                    A          GA
GAM962  JRK      3'  GAGTCCAATGTACCATGTTGCC 87828      C         AA____
             CAG                   CTGG CAACATGGTG      ACTC
                                |||| ||||||||||      ||||
                                GACC GTTGTACCAT      TGAG
                                   C         GTAACC
GAM962  LLGL1    3'  TGGGGTTTCACCATGTTAGCCA 67425        C
             GG                   CCTGGC AACATGGTGAAACTCCA
                                |||||| ||||||||||||||||
                                GGACCG TTGTACCACTTTGGGGT
                                   A
GAM962  LNK      3'  GGGTTTCACCATGTTGGCCAGG 19649
                                CCTGGCCAACATGGTGAAACTC
                                |||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGG

GAM962  LNK      3'  TGGAGTTTCTCTTGTCAACCGG 19654       CCA   T  T
             G                    CCTGG   ACA GG GAAACTCCA
                                |||||   ||| || |||||||||
                                GGGCC   TGT TC CTTTGAGGT
                                   AAC   _  T
GAM962  LTB4R    5'  GGGGTTTCACCATGTTGGCCAG 7470
             G                    CCTGGCCAACATGGTGAAACTCC
                                |||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGG

GAM962  LYZ      3'  TTCACCGTGTTAGCCAGG     5905         C
                                CCTGGC AACATGGTGAA
                                |||||| ||||||||||
                                GGACCG TTGTGCCACTT
                                   A
GAM962  MAK      3'  GGGTTTCACCATGTTGGTCAGG 20950
                                CCTGGCCAACATGGTGAAACTC
                                |||||||||||||||||||||
                                GGACTGGTTGTACCACTTTGGG

GAM962  MDM2     3'  TTCACCGTGTTAGCCAGG     23464        C
                                CCTGGC AACATGGTGAA
                                |||||| ||||||||||
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                                GGACCG TTGTGCCACTT
                                   A
GAM962  MDM2    3'  TTCACCGTGTTAGCCAGG    23477       C
                                CCTGGC AACATGGTGAA
                                |||||| ||||||||||
                                GGACCG TTGTGCCACTT
                                   A
GAM962  MDM2    3'  TTCACCGTGTTAGCCAGG    23490       C
                                CCTGGC AACATGGTGAA
                                |||||| ||||||||||
                                GGACCG TTGTGCCACTT
                                   A
GAM962  MDM2    3'  TTCACCGTGTTAGCCAGG    23504       C
                                CCTGGC AACATGGTGAA
                                |||||| ||||||||||
                                GGACCG TTGTGCCACTT
                                   A
GAM962  MDM2    3'  TTCACCGTGTTAGCCAGG    11502       C
                                CCTGGC AACATGGTGAA
                                |||||| ||||||||||
                                GGACCG TTGTGCCACTT
                                   A
GAM962  MEF2A   5'  TGGAGTTTCACCATGTTGGCCA 20003
            GG                    CCTGGCCAACATGGTGAAACTCCA
                                |||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGAGGT

GAM962  MEFV    3'  GGGGTTTCACCATGTTAGCCAG 5942        C
            G                     CCTGGC AACATGGTGAAACTCC
                                |||||| ||||||||||||||||
                                GGACCG TTGTACCACTTTGGGG
                                   A
GAM962  MEFV    3'  TTCATCATGTTGGCCAGG    5956
                                CCTGGCCAACATGGTGAA
                                ||||||||||||||||||
                                GGACCGGTTGTACTACTT

GAM962  MLANA   3'  TGGAGTTTCGCTTTTGTTGCCC 19773      C    T_
            AGG                   CCTGG CAACA  GGTGAAACTCCA
                                ||||| |||||  ||||||||||||
                                GGACC GTTGT  TCGCTTTGAGGT
                                   C    TT
GAM962  MPL     3'  GGTTTTCACCACGTTGGCCAGG 19358          A       CT
                                CCTGGCCAAC TGGTGAAA  CC
                                |||||||||| ||||||||  ||
                                GGACCGGTTG ACCACTTT  GG
                                      C       T_
GAM962  MRPL49  3'  TGGGGTTTCACCATGTTGGCCA 70176
            GG                    CCTGGCCAACATGGTGAAACTCCA
                                ||||||||||||||||||||||||
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                                GGACCGGTTGTACCACTTTGGGGT

GAM962  MUS81    3'  GAATTCCCTGGTCAGG      47819         ACAT  T   AC
                                CCTGGCCA    GG GAA  TC
                                ||||||||    || |||  ||
                                GGACTGGT    CC CTT  AG
                                    _____ _   A_
GAM962  MYCL2    3'  TGGGGTTTCACCACATTGGCCA 19383          CA
           GG                     CCTGGCCAA  TGGTGAAACTCCA
                                ||||||||||  ||||||||||||
                                GGACCGGTT  ACCACTTTGGGGT
                                     AC
GAM962  NCOA6    5'  TTCATCATGTTGGCCAGG    26852
                                CCTGGCCAACATGGTGAA
                                ||||||||||||||||||
                                GGACCGGTTGTACTACTT

GAM962  NDRG3    3'  TGGAGTTTCACCATGTTGGCCA 50129
           GG                     CCTGGCCAACATGGTGAAACTCCA
                                ||||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGAGGT

GAM962  NPTX1    3'  GGAGCCAGGCCTGGCCAGG    11838         ACAT   GAAA
                                CCTGGCCA    GGT    CTCC
                                ||||||||    |||    ||||
                                GGACCGGT    CCG    GAGG
                                    _____  GACC
GAM962  NQO1     3'  GGCGTTTCACCATGTTGGCCAG 8051                  T
           G                     CCTGGCCAACATGGTGAAAC CC
                                ||||||||||||||||||| ||
                                GGACCGGTTGTACCACTTTG GG
                                          C
GAM962  PCDHA9   3'  TTCATCATGTTGGCCAGG    26631
                                CCTGGCCAACATGGTGAA
                                ||||||||||||||||||
                                GGACCGGTTGTACTACTT

GAM962  PCDHB11  3'  GGGGTTTCACCACGTTGGCCGG 38928           A
           G                     CCTGGCCAAC TGGTGAAACTCC
                                ||||||||||  ||||||||||||
                                GGGCCGGTTG ACCACTTTGGGG
                                     C
GAM962  PCSK1    3'  TGGTCATGTTGGTCA       6517            TGAAACT
                                TGGCCAACATGG      CCA
                                ||||||||||||      |||
                                ACTGGTTGTACT      GGT
                                          _______
GAM962  PDE6B    3'  TGGGGTTTCACCATATTGGGCA 6081       G   C
           GG                     CCTG CCAA ATGGTGAAACTCCA
                                ||||  |||| ||||||||||||||
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                                GGAC GGTT TACCACTTTGGGGT
                                  G    A
GAM962   PER2     3'  GGGTTTCACCATGTTGGCCAGG 43357
                                CCTGGCCAACATGGTGAAACTC
                                |||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGG

GAM962   PER2     3'  TGGAGTTTCTTTTTGCCCAGG  43363       C   CATGGT
                                CCTGG CAA     GAAACTCCA
                                ||||| |||     |||||||||
                                GGACC GTT     CTTTGAGGT
                                  C   TTT___
GAM962   PIGR     3'  AGTCTCACTGTGTCACCCAG   72989      CCA        A
                                CTGG   ACATGGTGA ACT
                                ||||   ||||||||| |||
                                GACC   TGTGTCACT TGA
                                  CAC        C
GAM962   PIGR     3'  TTCACCGTGTTAGCCAGG     73016       C
                                CCTGGC AACATGGTGAA
                                ||||||| ||||||||||
                                GGACCG TTGTGCCACTT
                                   A
GAM962   PIK3C2B  3'  GGGGTTTCACCATGTTGGCCAG 12106
           G                     CCTGGCCAACATGGTGAAACTCC
                                 ||||||||||||||||||||||
                                 GGACCGGTTGTACCACTTTGGGG

GAM962   POU2AF1  3'  GGGGTTTCACCATGTTGGCCAG 21747
           G                     CCTGGCCAACATGGTGAAACTCC
                                 ||||||||||||||||||||||
                                 GGACCGGTTGTACCACTTTGGGG

GAM962   PRKR     3'  GGGTTTCACCATGTTGGCCAGG 12351
                                CCTGGCCAACATGGTGAAACTC
                                |||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGG

GAM962   PRKWNK3  3'  TGGGGTTTCACTATGTTGGCCA 62243
           G                     CTGGCCAACATGGTGAAACTCCA
                                 ||||||||||||||||||||||
                                 GACCGGTTGTATCACTTTGGGGT

GAM962   PRM1     5'  GAGTTCCACCTGCTGACAGG   12393      GC  A  T    A
                                CCTG  CA CA GGTG AACTC
                                ||||  || || |||| |||||
                                GGAC  GT GT CCAC TTGAG
                                  A_  C  _    C
GAM962   PTGES    3'  GGGTTCACCATGTTGCCCAGG  18067       C          A
                                CCTGG CAACATGGTGAA CTC
                                ||||| |||||||||||| |||
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                                GGACC GTTGTACCACTT GGG
                                  C         _
GAM962  PTGIS    3'  TTCACCGTATTAGCCAGG    8235        C  C
                                CCTGGC AA ATGGTGAA
                                |||||| || ||||||||
                                GGACCG TT TGCCACTT
                                   A  A
GAM962  RAB36    3'  TTCACCATGTTAGCCAGG    18187       C
                                CCTGGC AACATGGTGAA
                                |||||| ||||||||||
                                GGACCG TTGTACCACTT
                                   A
GAM962  RABL2A   3'  TTCACCATGTTGCCCAGG    26416       C
                                CCTGG CAACATGGTGAA
                                ||||| ||||||||||
                                GGACC GTTGTACCACTT
                                  C
GAM962  RABL2B   3'  TTCACCATGTTGCCCAGG    23990       C
                                CCTGG CAACATGGTGAA
                                ||||| ||||||||||
                                GGACC GTTGTACCACTT
                                  C
GAM962  RBBP9    3'  GGGTTTCACCATGTTGGCCAGG 70695
                                CCTGGCCAACATGGTGAAACTC
                                ||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGG

GAM962  RBM8A    3'  GAGTCTTGCTGTGTTACCCAGG 18808       CC      TG A
                                CCTGG  AACATGG  A ACTC
                                |||||  |||||||  | ||||
                                GGACC  TTGTGTC  T TGAG
                                   CA      GT C
GAM962  RHD      3'  TGGGGTTTCACCATGTTGGCCA 32842
                GG                  CCTGGCCAACATGGTGAAACTCCA
                                ||||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGGT

GAM962  RHD      3'  TTCACCATGTTGGCTAGG    32843
                                CCTGGCCAACATGGTGAA
                                ||||||||||||||||
                                GGATCGGTTGTACCACTT

GAM962  RHD      3'  TGGGGTTTCACCATGTTGGCCA 33152
                GG                  CCTGGCCAACATGGTGAAACTCCA
                                ||||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGGT

GAM962  RHD      3'  TTCACCATGTTGGCTAGG    33153
                                CCTGGCCAACATGGTGAA
                                ||||||||||||||||
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                                GGATCGGTTGTACCACTT

GAM962  RNMT     3'  GAGTTGGGAGTATATTGGTCAG 15052          C   GTGA_
              G                   CCTGGCCAA ATG     AACTC
                                  ||||||||| |||     |||||
                                  GGACTGGTT TAT     TTGAG
                                       A   GAGGG
GAM962  RPH3AL   3'  TGGGGTTTCTCCATGTTGGCCA 23745             T
              GG                    CCTGGCCAACATGG GAAACTCCA
                                  |||||||||||||| |||||||||
                                  GGACCGGTTGTACC CTTTGGGGT
                                         T
GAM962  RPP30    3'  TTCACCGTGTTAGCCAGG    22211        C
                                  CCTGGC AACATGGTGAA
                                  |||||| ||||||||||
                                  GGACCG TTGTGCCACTT
                                     A
GAM962  SAS      3'  GGGTTTCACCATGTTAGTCAGG 21105        C
                                  CCTGGC AACATGGTGAAACTC
                                  |||||| ||||||||||||||
                                  GGACTG TTGTACCACTTTGGG
                                     A
GAM962  SCML2    3'  TGGAGTTTCACTCTTGTGCCCA 21433       CCA   T_
              GG                    CCTGG   ACA  GGTGAAACTCCA
                                  |||||   |||  ||||||||||||
                                  GGACC   TGT  TCACTTTGAGGT
                                     CG_   TC
GAM962  SEDL     3'  GGGTTTCACCATATTGGTCAGG 28103          C
                                  CCTGGCCAA ATGGTGAAACTC
                                  ||||||||| ||||||||||||
                                  GGACTGGTT TACCACTTTGGG
                                       A
GAM962  SEDL     3'  GGGTTTCACCATATTGGTCAGG 28104          C
                                  CCTGGCCAA ATGGTGAAACTC
                                  ||||||||| ||||||||||||
                                  GGACTGGTT TACCACTTTGGG
                                       A
GAM962  SEDL     3'  TGGAGTTTCGCTCTGTTGTCCA 28115       C    T
              GG                    CCTGG CAACA GGTGAAACTCCA
                                  ||||| ||||| ||||||||||||
                                  GGACC GTTGT TCGCTTTGAGGT
                                     T    C
GAM962  SEPN1    3'  TGGGGTTTCACCATATTGGTCA 66984          C
              GG                    CCTGGCCAA ATGGTGAAACTCCA
                                  ||||||||| ||||||||||||||
                                  GGACTGGTT TACCACTTTGGGGT
                                       A
GAM962  SERPINB9 3'  TTCACCGTGTTAGCCAGG    16036        C
                                  CCTGGC AACATGGTGAA
                                  |||||| ||||||||||
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                                GGACCG TTGTGCCACTT
                                   A
GAM962  SH3BP2   3'  GGGGTTTCACCATGTTGGCCAG 13081
           G                    CCTGGCCAACATGGTGAAACTCC
                                ||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGG

GAM962  SH3GL3   5'  TGGGTTTCACCATGTTGGCCA  13116              T
                                TGGCCAACATGGTGAAAC CCA
                                |||||||||||||||||  |||
                                ACCGGTTGTACCACTTTG GGT
                                                  _
GAM962  SHOX     3'  GTTTCACCGTGTTGGCCAGG   6583
                                CCTGGCCAACATGGTGAAAC
                                ||||||||||||||||||||
                                GGACCGGTTGTGCCACTTTG

GAM962  SHOX     3'  TGGGGTTTGACCATGTTGGCCA 23524              G
           GG                     CCTGGCCAACATGGT AAACTCCA
                                  |||||||||||||| ||||||||
                                  GGACCGGTTGTACCA TTTGGGGT
                                           G
GAM962  SLA2     3'  TGGGGTTTCACCACATTGGCCA 50897          CA
           GG                     CCTGGCCAA  TGGTGAAACTCCA
                                  |||||||||  ||||||||||||
                                  GGACCGGTT  ACCACTTTGGGGT
                                       AC
GAM962  SLC12A4  3'  TGGAGTCGAGGTCTTGGCCAGG 18630         C  GG   AA
                                CCTGGCCAA AT  TGA  CTCCA
                                |||||||||  ||  |||  |||||
                                GGACCGGTT TG  GCT  GAGGT
                                     C  GA  __
GAM962  SLC14A2  5'  GGGGTTTCACCACATTGGCCAG 24122          CA
           G                     CCTGGCCAA  TGGTGAAACTCC
                                 |||||||||  ||||||||||||
                                 GGACCGGTT  ACCACTTTGGGG
                                      AC
GAM962  SLC15A1  3'  TGGGGTTTCACCATGTTAACCA 18650       CC
           GG                     CCTGG  AACATGGTGAAACTCCA
                                  |||||  ||||||||||||||||
                                  GGACC  TTGTACCACTTTGGGGT
                                    AA
GAM962  SMAC     5'  TGGGGTTTCACCATGTTGGTCA 58031
           GG                     CCTGGCCAACATGGTGAAACTCCA
                                  ||||||||||||||||||||||||
                                  GGACTGGTTGTACCACTTTGGGGT

GAM962  SNX15    3'  TGGAGTCTCGCTGTGTCGCCCA 74133      CCA       A
           G                      CTGG   ACATGGTGA ACTCCA
                                  ||||   ||||||||| ||||||
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                                GACC   TGTGTCGCT TGAGGT
                                  CGC        C
GAM962  SPN      3'  GAGTTTCGCTTTGTCGCCCAGG 13377      CCA   T
                                CCTGG   ACA GGTGAAACTC
                                ||||||   ||| ||||||||||
                                GGACC   TGT TCGCTTTGAG
                                   CGC   T
GAM962  SPN      3'  TTCACCATGTTGGCTAGG    13384
                                CCTGGCCAACATGGTGAA
                                ||||||||||||||||||
                                GGATCGGTTGTACCACTT

GAM962  SPON1    3'  TGGAGCTTCCACCTGGCCAGG  63126        ACAT   _  A
                                CCTGGCCA   GGTG AA CTCCA
                                ||||||||   |||| || |||||
                                GGACCGGT   CCAC TT GAGGT
                                     ____   C  C
GAM962  SULT2A1  3'  TTACCACGGTTGGCCAGG    72233         A_
                                CCTGGCCAAC  TGGTGA
                                ||||||||||  ||||||
                                GGACCGGTTG  ACCATT
                                      GC
GAM962  SULT2B1  5'  GGGGTTTCACCATGTTGGCCAG 17223
           G                    CCTGGCCAACATGGTGAAACTCC
                                ||||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGG

GAM962  TAPBP    3'  GGGGTTTCACCATGTTGGCCAG 13572
           G                    CCTGGCCAACATGGTGAAACTCC
                                ||||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGG

GAM962  TAPBP    3'  TTCACCGTGTTAGCCAGG    13592       C
                                CCTGGC AACATGGTGAA
                                ||||||  ||||||||||
                                GGACCG TTGTGCCACTT
                                   A
GAM962  TAPBP    3'  TTCACCGTGTTAGCCAGG    13593       C
                                CCTGGC AACATGGTGAA
                                ||||||  ||||||||||
                                GGACCG TTGTGCCACTT
                                   A
GAM962  TAT      3'  GGGTTTCACCATGTTAGCCAGG 6258        C
                                CCTGGC AACATGGTGAAACTC
                                ||||||  |||||||||||||||
                                GGACCG TTGTACCACTTTGGG
                                   A
GAM962  TBXA2R   3'  TTCACCGTGTTGGCCAGG    8372
                                CCTGGCCAACATGGTGAA
                                ||||||||||||||||||
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                                GGACCGGTTGTGCCACTT

GAM962  TDGF1    3'  GGGGTTTCACCATATTGGCCAG 13659         C
                                CTGGCCAA ATGGTGAAACTCC
                                |||||||| ||||||||||||
                                GACCGGTT TACCACTTTGGGG
                                     A
GAM962  TERF1    3'  GGGGTTTCACCATGCTGGTCAG 34395         A
           G                     CCTGGCCA CATGGTGAAACTCC
                                |||||||| ||||||||||||||
                                GGACTGGT GTACCACTTTGGGG
                                     C
GAM962  TERF2    3'  TTCACCGTGTTAGCCAGG    20164        C
                                CCTGGC AACATGGTGAA
                                |||||| ||||||||||
                                GGACCG TTGTGCCACTT
                                   A
GAM962  TES      3'  GGTTTTCACCATGTTAGCCAGG 72465        C          CT
                                CCTGGC AACATGGTGAAA  CC
                                |||||| ||||||||||||  ||
                                GGACCG TTGTACCACTTT  GG
                                   A          T_
GAM962  TIM3     3'  GGGTTTCACCATGTTGGCCAG  52358
                                CTGGCCAACATGGTGAAACTC
                                |||||||||||||||||||||
                                GACCGGTTGTACCACTTTGGG

GAM962  TMPRSS3  3'  GGGTTTCACCATGTTGGCCAGG 51520
                                CCTGGCCAACATGGTGAAACTC
                                |||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGG

GAM962  TMPRSS3  3'  GGGTTTCACCATGTTGGCCAGG 51547
                                CCTGGCCAACATGGTGAAACTC
                                |||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGG

GAM962  TMPRSS3  3'  GGGTTTCACCATGTTGGCCAGG 44030
                                CCTGGCCAACATGGTGAAACTC
                                |||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGG

GAM962  TNFRSF10B 3'  GGGGTTTCACCATGTTGGTCAG 15229
           G                     CCTGGCCAACATGGTGAAACTCC
                                |||||||||||||||||||||||
                                GGACTGGTTGTACCACTTTGGGG

GAM962  TP53BP2  5'  GAGTTTCATCATGTTGGCCAGG 19462
                                CCTGGCCAACATGGTGAAACTC
                                |||||||||||||||||||||
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                                GGACCGGTTGTACTACTTTGAG

GAM962  TPMT     3'  GGGGTTTCACCATGTTGGTCAG 6316
                G                CCTGGCCAACATGGTGAAACTCC
                                 ||||||||||||||||||||||
                                 GGACTGGTTGTACCACTTTGGGG

GAM962  TRAF5    3'  GAGTTTCATTGTCACCCAGG  17276      CCAAC TG
                                 CCTGG    A  GTGAAACTC
                                 |||||    |  |||||||||
                                 GGACC    T  TACTTTGAG
                                    CAC__ GT
GAM962  TRAF5    3'  GGAGTTTTGCCATGTTGGCCA  17278          TG
                                 TGGCCAACATGG  AAACTCC
                                 ||||||||||||  |||||||
                                 ACCGGTTGTACC  TTTGAGG
                                        GT
GAM962  TRPM6    3'  TGGGGTTTCACCATGTTGGCCA 35038
                GG                 CCTGGCCAACATGGTGAAACTCCA
                                   ||||||||||||||||||||||||
                                   GGACCGGTTGTACCACTTTGGGGT

GAM962  TRPV1    3'  GGGGTTTCACCATGTTGGCCAG 38701
                G                CCTGGCCAACATGGTGAAACTCC
                                 ||||||||||||||||||||||
                                 GGACCGGTTGTACCACTTTGGGG

GAM962  TRPV1    3'  TGGGGTTTCGCCATGTTGGCCA 38708
                GG                 CCTGGCCAACATGGTGAAACTCCA
                                   ||||||||||||||||||||||||
                                   GGACCGGTTGTACCGCTTTGGGGT

GAM962  TRPV1    3'  TGGGGTTTCGCCATGTTGGCCA 55693
                GG                 CCTGGCCAACATGGTGAAACTCCA
                                   ||||||||||||||||||||||||
                                   GGACCGGTTGTACCGCTTTGGGGT

GAM962  TRPV1    3'  GGGGTTTCACCATGTTGGCCAG 55717
                G                CCTGGCCAACATGGTGAAACTCC
                                 ||||||||||||||||||||||
                                 GGACCGGTTGTACCACTTTGGGG

GAM962  TRPV1    3'  TGGGGTTTCGCCATGTTGGCCA 55724
                GG                 CCTGGCCAACATGGTGAAACTCCA
                                   ||||||||||||||||||||||||
                                   GGACCGGTTGTACCGCTTTGGGGT

GAM962  TRPV1    3'  GGGGTTTCACCATGTTGGCCAG 55748
                G                CCTGGCCAACATGGTGAAACTCC
                                 ||||||||||||||||||||||
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                                GGACCGGTTGTACCACTTTGGGG

GAM962  TRPV1    3'  TGGGGTTTCGCCATGTTGGCCA 55755
                GG                  CCTGGCCAACATGGTGAAACTCCA
                                    ||||||||||||||||||||||||
                                    GGACCGGTTGTACCGCTTTGGGGT

GAM962  TRPV1    3'  GGGGTTTCACCATGTTGGCCAG 55682
                G                   CCTGGCCAACATGGTGAAACTCC
                                    |||||||||||||||||||||||
                                    GGACCGGTTGTACCACTTTGGGG

GAM962  TUFT1    3'  TTCACCATACTGGCTAGG    39680        AC
                                    CCTGGCCA  ATGGTGAA
                                    ||||||||  ||||||||
                                    GGATCGGT  TACCACTT
                                         CA
GAM962  UGDH     3'  TTCACCATGTGAGCCAGG    14006       CA
                                    CCTGGC  ACATGGTGAA
                                    ||||||  ||||||||||
                                    GGACCG  TGTACCACTT
                                       AG
GAM962  VENTX2   3'  TGGGGTTTCACCATGTTAGCCA 27870       C
                GG                  CCTGGC AACATGGTGAAACTCCA
                                    ||||||| ||||||||||||||||
                                    GGACCG TTGTACCACTTTGGGGT
                                       A
GAM962  VHL      3'  GTTTCGCCATGTTGGCCAGG   6873
                                    CCTGGCCAACATGGTGAAAC
                                    ||||||||||||||||||||
                                    GGACCGGTTGTACCGCTTTG

GAM962  VHL      3'  TTCACCATGTTGTCCAGG     6882       C
                                    CCTGG CAACATGGTGAA
                                    ||||| ||||||||||||
                                    GGACC GTTGTACCACTT
                                       T
GAM962  VIPR2    3'  GGGTTTCACCATGTTAGCCAGG 14071       C
                                    CCTGGC AACATGGTGAAACTC
                                    |||||| |||||||||||||||
                                    GGACCG TTGTACCACTTTGGG
                                       A
GAM962  WHSC1    3'  AGCTTCCTCTGGCCAGG     56689        ACAT  T   A
                                    CCTGGCCA    GG GAA CT
                                    ||||||||    || ||| ||
                                    GGACCGGT    TC CTT GA
                                         C___  _   C
GAM962  WHSC1    3'  GAGTCTCACCCTGTTGGCCAGG 56696          T    A
                                    CCTGGCCAACA GGTGA ACTC
                                    |||||||||| ||||| ||||
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                                GGACCGGTTGT CCACT TGAG
                                      C    C
GAM962  WHSC1    3'  GGGTTTCGCCATATTGGCCAGG 56699         C
                                CCTGGCCAA ATGGTGAAACTC
                                ||||||||| ||||||||||||
                                GGACCGGTT TACCGCTTTGGG
                                     A
GAM962  XRCC2    3'  GGGGTTTCACCATGTTGGCCAG 19507
           G                     CCTGGCCAACATGGTGAAACTCC
                                ||||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGG

GAM962  YES1     3'  AGTTTCACCGTGTTAGCCAGG  19529       C
                                CCTGGC AACATGGTGAAACT
                                |||||| ||||||||||||||
                                GGACCG TTGTGCCACTTTGA
                                   A
GAM962  ZNF157   3'  GGGTTTCACCATGTTGGCCAGG 14335
                                CCTGGCCAACATGGTGAAACTC
                                |||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGG

GAM962  ZNF264   3'  TTCACCATCTTGGCCAGG    14237         C
                                CCTGGCCAA ATGGTGAA
                                ||||||||| ||||||||
                                GGACCGGTT TACCACTT
                                     C
GAM962  AD024    5'  GAGTCCGGCTGTTGGCTAG   40711          __  TGAA
                                CTGGCCAACA  TGG   ACTC
                                ||||||||||  |||   ||||
                                GATCGGTTGT  GCC   TGAG
                                     CG  ____
GAM962  AGMAT    3'  GAGTTTTGCTTGTCACCCAGG  45741      CCA  T  TG
                                CCTGG   ACA GG  AAACTC
                                |||||   ||| ||  ||||||
                                GGACC   TGT TC  TTTGAG
                                   CAC  _  GT
GAM962  AGTRL2   5'  TCAAATGGCATTTGGCCAGG   18958         ____  GG
                                CCTGGCCAA   CAT  TGA
                                |||||||||   |||  |||
                                GGACCGGTT   GTA  ACT
                                     TACG   A_
GAM962  ANAPC11  5'  GGAGTTTCGTCATGTTGGCCAG 33634           GT
           G                     CCTGGCCAACATG  GAAACTCC
                                ||||||||||||||  ||||||||
                                GGACCGGTTGTAC  CTTTGAGG
                                      TG
GAM962  ANGPTL4  3'  TGGAGCTTCACTCCTTGCTGGC 32761        A  T__     A
           CAGG                    CCTGGCCA CA   GGTGAA CTCCA
                                ||||||||  ||   |||||| |||||
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                                GGACCGGT GT   TCACTT GAGGT
                                    C  TCC     C
GAM962   AP3S2     3'  GGGTTTCACCATGTTGGCCAGG 20655
                                CCTGGCCAACATGGTGAAACTC
                                ||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGG

GAM962   ARHF      3'  GGGTTTCACCATGTTGGCCAGG 39274
                                CCTGGCCAACATGGTGAAACTC
                                ||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGG

GAM962   ARHGAP11A 3'  GGTTTCACCGTGTTAGCCAGG  29455       C
                                CCTGGC AACATGGTGAAACT
                                |||||| ||||||||||||||
                                GGACCG TTGTGCCACTTTGG
                                   A
GAM962   ASB16     3'  GGGGTCTCGCCATGTTGGCCAG 55985              A
            G                    CCTGGCCAACATGGTGA ACTCC
                                ||||||||||||||||| |||||
                                GGACCGGTTGTACCGCT TGGGG
                                          C
GAM962   ASE-1     3'  GGGGTTTCACCATATTGGCCAG 24985         C
            G                    CCTGGCCAA ATGGTGAAACTCC
                                |||||||||  ||||||||||||
                                GGACCGGTT TACCACTTTGGGG
                                    A
GAM962   ASE-1     3'  TGGGGTTTCACCACGTTAGCCA 24998       C   A
            GG                     CCTGGC AAC TGGTGAAACTCCA
                                |||||| ||| ||||||||||||
                                GGACCG TTG ACCACTTTGGGGT
                                   A   C
GAM962   ATP1B4    3'  GGGTTTCACCATGTTGGCCAGG 24849
                                CCTGGCCAACATGGTGAAACTC
                                ||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGG

GAM962   BA108L7.2 3'  TGGAGTTTCACTATTTTGCCCA 49083       C   C
            GG                     CCTGG CAA ATGGTGAAACTCCA
                                ||||| ||| ||||||||||||||
                                GGACC GTT TATCACTTTGAGGT
                                   C   T
GAM962   BA108L7.2 3'  GGGGTTTCACCATGTTGGCCAG 49079
            G                    CCTGGCCAACATGGTGAAACTCC
                                |||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGG

GAM962   BAGE      3'  TGGAGTTTCACTGTGTCAGCCA 8642        CA
            GG                     CCTGGC  ACATGGTGAAACTCCA
                                ||||||  ||||||||||||||||
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                                GGACCG  TGTGTCACTTTGAGGT
                                   AC
GAM962  BNIP-S   3'  GGGGTTTCACCATGTTGGCCAG 57093
             G                   CCTGGCCAACATGGTGAAACTCC
                                 ||||||||||||||||||||||
                                 GGACCGGTTGTACCACTTTGGGG

GAM962  BTN3A1   3'  GAGGGTTCACTATGTTGGCCAG 23893              A_
             G                   CCTGGCCAACATGGTGAA  CTC
                                 ||||||||||||||||||  |||
                                 GGACCGGTTGTATCACTT  GAG
                                       GG
GAM962  C11orf17 3'  GGGGTTTAACCATGTTGGCCAG 40584            G
             G                   CCTGGCCAACATGGT AAACTCC
                                 ||||||||||||||| |||||||
                                 GGACCGGTTGTACCA TTTGGGG
                                       A
GAM962  C13orf1  3'  TTCACCATGTTGTCCAGG    40374      C
                                 CCTGG CAACATGGTGAA
                                 ||||| ||||||||||||
                                 GGACC GTTGTACCACTT
                                    T
GAM962  C1orf24  3'  TGGGTTTTCACCATGTTGGCCA 54799              CT
             GG                    CCTGGCCAACATGGTGAAA  CCA
                                   ||||||||||||||||||  |||
                                   GGACCGGTTGTACCACTTT  GGT
                                         TG
GAM962  C1QTNF6  3'  TGGGGTTTCACCATATTGGCCA 49998         C
             GG                    CCTGGCCAA ATGGTGAAACTCCA
                                   |||||||| ||||||||||||||
                                   GGACCGGTT TACCACTTTGGGGT
                                      A
GAM962  C20orf102 3'  GAGTTTTGCACCAGCAGG    55509      G CAACA    __
                                 CCTG C    TGGTG  AAACTC
                                 |||| |    |||||  ||||||
                                 GGAC G    ACCAC  TTTGAG
                                   _ _____    GT
GAM962  C21orf25  3'  TGGAGTCTCACCATGTTGGTCA 64305              A
             GG                    CCTGGCCAACATGGTGA ACTCCA
                                   |||||||||||||||| ||||||
                                   GGACTGGTTGTACCACT TGAGGT
                                         C
GAM962  C21orf25  3'  TGGAGTTTCACTCTGTTGCCCA 64306      C    T
             GG                    CCTGG CAACA GGTGAAACTCCA
                                   ||||| ||||| ||||||||||||
                                   GGACC GTTGT TCACTTTGAGGT
                                     C    C
GAM962  C3F      3'  GGGATTTCACCACGTTGGCCAG 20480          A      CT
             G                     CCTGGCCAAC TGGTGAAA  CC
                                   |||||||||| ||||||||  ||
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                                  GGACCGGTTG ACCACTTT  GG
                                        C       AG
GAM962  C9orf14  5'  TTCACCCTGTTGGCCAGG    87961          T
                                  CCTGGCCAACA GGTGAA
                                  |||||||||| ||||||
                                  GGACCGGTTGT CCACTT
                                        C
GAM962  C9orf9   3'  GGGGCTTCACCACGTTGGCCAG 39029         A      A
          G                        CCTGGCCAAC TGGTGAA CTCC
                                  |||||||||| ||||||| ||||
                                  GGACCGGTTG ACCACTT GGGG
                                        C      C
GAM962  C9orf9   3'  GTTTCACCATGTTAGCCAGG   39035       C
                                  CCTGGC AACATGGTGAAAC
                                  |||||| ||||||||||||
                                  GGACCG TTGTACCACTTTG
                                     A
GAM962  CCRN4L   3'  TTCACCGTGTTAGCCAGG    25075       C
                                  CCTGGC AACATGGTGAA
                                  |||||| ||||||||||
                                  GGACCG TTGTGCCACTT
                                     A
GAM962  CDC14B   3'  GGGTTTCACCATGTTGGCCAGG 54010
                                  CCTGGCCAACATGGTGAAACTC
                                  |||||||||||||||||||||
                                  GGACCGGTTGTACCACTTTGGG

GAM962  CHRAC1   3'  GGGGTTCACCATGTTGGCCAGG 34337               A
                                  CCTGGCCAACATGGTGAA CTCC
                                  |||||||||||||||| ||||
                                  GGACCGGTTGTACCACTT GGGG
                                                _
GAM962  CIP29    3'  TTCACCATGTTGCCCAGG    51384       C
                                  CCTGG CAACATGGTGAA
                                  ||||| ||||||||||
                                  GGACC GTTGTACCACTT
                                     C
GAM962  COQ7     3'  AGTCTCACTATGTCGCCAGG   32852       CA       A
                                  CCTGGC  ACATGGTGA ACT
                                  ||||||  ||||||||| |||
                                  GGACCG  TGTATCACT TGA
                                     C_       C
GAM962  CPSF2    3'  GGGTTTCACCATGTTGGCCAGG 62277
                                  CCTGGCCAACATGGTGAAACTC
                                  |||||||||||||||||||||
                                  GGACCGGTTGTACCACTTTGGG

GAM962  CYB5-M   3'  TGGAGCCAAGACGATTGGCCAG 48336        CA  GTGAAA
                                  CTGGCCAA  TG     CTCCA
                                  ||||||||  ||     |||||
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                                GACCGGTT  GC     GAGGT
                                     A_  AGAACC
GAM962  CYB5-M    3'  TGGAGCCAAGACGATTGGCCAG 96204         CA  GTGAAA
                                CTGGCCAA  TG     CTCCA
                                ||||||||  ||     |||||
                                GACCGGTT  GC     GAGGT
                                     A_  AGAACC
GAM962  DBR1      3'  TTCACCGTGTTGGCCAGG    33072
                                CCTGGCCAACATGGTGAA
                                ||||||||||||||||||
                                GGACCGGTTGTGCCACTT

GAM962  DKFZP434C212 3'  GGGGTTTCACCATGTTGGCCAG 69494
           G                     CCTGGCCAACATGGTGAAACTCC
                                ||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGG

GAM962  DKFZP434D146 3'  TTCATCATGTTGGCCAGG    32143
                                CCTGGCCAACATGGTGAA
                                ||||||||||||||||||
                                GGACCGGTTGTACTACTT

GAM962  DKFZp434E0519 3'  TGGAGTTTGAGATCAGCCTGG  51003    T   CAACA   G__
                                CC GGC    TGGT   AAACTCCA
                                || |||    ||||   ||||||||
                                GG CCG    ACTA   TTTGAGGT
                                 T  _____   GAG
GAM962  DKFZP434F0318 3'  GGGTTTCGCCATGTTGGCCAGG 48763
                                CCTGGCCAACATGGTGAAACTC
                                |||||||||||||||||||||
                                GGACCGGTTGTACCGCTTTGGG

GAM962  DKFZp434F1719 3'  TGGGATTTCGCCATGTTGGCCA 51018              CT
           GG                    CCTGGCCAACATGGTGAAA  CCA
                                ||||||||||||||||||  |||
                                GGACCGGTTGTACCGCTTT  GGT
                                      AG
GAM962  DKFZP434P0111 3'  TGGAATTTCACCAACCAACAAG 67964     GGCCAACA      C
           G                     CCT       TGGTGAAA TCCA
                                |||       |||||||| ||||
                                GGA       ACCACTTT AGGT
                                  ACAACCA_       A
GAM962  DKFZp547H025 3'  TGAGGTTTCACCATGTTGGCCA 39780              TC
           GG                    CCTGGCCAACATGGTGAAAC  CA
                                ||||||||||||||||||  ||
                                GGACCGGTTGTACCACTTTG  GT
                                      GA
GAM962  DKFZP564G092 5'  GGATTTCACCATGTTGGCCAGG 32165              C
                                CCTGGCCAACATGGTGAAA TCC
                                ||||||||||||||||||| |||
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                                GGACCGGTTGTACCACTTT AGG

                                                _
GAM962  DKFZP564O0523 3'  TGGGTTTTCACCATATTGGTCA 50425          C        CT
          GG                    CCTGGCCAA ATGGTGAAA  CCA
                                |||||||| |||||||||  |||
                                GGACTGGTT TACCACTTT  GGT
                                    A        TG
GAM962  DKFZp761J139 5'  TGGGGTTTGACCATGTTGGCCA 51116              G
          GG                    CCTGGCCAACATGGT AAACTCCA
                                |||||||||||||| ||||||||
                                GGACCGGTTGTACCA TTTGGGGT
                                      G
GAM962  DKFZp761N1114 3'  TTCACCGTGTTAGCCAGG    79792       C
                                CCTGGC AACATGGTGAA
                                |||||| ||||||||||
                                GGACCG TTGTGCCACTT
                                   A
GAM962  DRIL2    3'  GAGCACCATTTGGCCAG     22351         C     AAA
                                CTGGCCAA ATGGTG   CTC
                                |||||||| ||||||   |||
                                GACCGGTT TACCAC   GAG

                                  _     ____
GAM962  DRIM     3'  GGATTTCGCCATGTTGGCCAGG 27954                C
                                CCTGGCCAACATGGTGAAA TCC
                                |||||||||||||||||| |||
                                GGACCGGTTGTACCGCTTT AGG

                                                _
GAM962  DSCR6    3'  GGTTTCACCATGTTGGTCAGG  39072
                                CCTGGCCAACATGGTGAAACT
                                |||||||||||||||||||||
                                GGACTGGTTGTACCACTTTGG

GAM962  EREG     3'  GGGGTTTCACCATGTTGGCCAG 9311
          G                      CCTGGCCAACATGGTGAAACTCC
                                 |||||||||||||||||||||||
                                 GGACCGGTTGTACCACTTTGGGG

GAM962  FEM-2    3'  TGAAGTTTCACCATGTGGAGG  28322     GG   A          C
                                CCT  CCA CATGGTGAAACT CA
                                |||  ||| ||||||||||| ||
                                GGA  GGT GTACCACTTTGA GT
                                  __  _          A
GAM962  FER1L4   3'  TTCACCATGTTGTCCAGG    48141       C
                                CCTGG CAACATGGTGAA
                                ||||| ||||||||||
                                GGACC GTTGTACCACTT
                                   T
GAM962  FKBP9    3'  TTCACCGTGTTGGCCAGG    95725
                                CCTGGCCAACATGGTGAA
                                ||||||||||||||||
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                                GGACCGGTTGTGCCACTT

GAM962  FLJ00060  5'  TGGAATTTCACCATGTTAGCCA 61758       C         C
                GG                  CCTGGC AACATGGTGAAA TCCA
                                    |||||| |||||||||||| ||||
                                    GGACCG TTGTACCACTTT AGGT
                                       A          A
GAM962  FLJ10094  3'  ACCATGTGAACCTGGCCAGG  36294          _____
                                    CCTGGCCA    ACATGGT
                                    ||||||||    |||||||
                                    GGACCGGT    TGTACCA
                                        CCAAG
GAM962  FLJ10298  3'  GGGGTTTCACCATGTTGGTCAG 36460
                G                   CCTGGCCAACATGGTGAAACTCC
                                    ||||||||||||||||||||||
                                    GGACTGGTTGTACCACTTTGGGG

GAM962  FLJ10346  5'  GGGTTTCACCATGTTGACCAGG 36527       C
                                    CCTGG CAACATGGTGAAACTC
                                    ||||| ||||||||||||||||
                                    GGACC GTTGTACCACTTTGGG
                                       A
GAM962  FLJ10535  3'  TGGGGTTTCACCATGTTGGCCA 36759
                GG                  CCTGGCCAACATGGTGAAACTCCA
                                    ||||||||||||||||||||||||
                                    GGACCGGTTGTACCACTTTGGGGT

GAM962  FLJ10713  3'  TGGGGTTTCACCATGTTGGCCA 37011
                GG                  CCTGGCCAACATGGTGAAACTCCA
                                    ||||||||||||||||||||||||
                                    GGACCGGTTGTACCACTTTGGGGT

GAM962  FLJ10846  3'  GGGTCTCACCATGTTAGCCAGG 37289       C         A
                                    CCTGGC AACATGGTGA ACTC
                                    |||||| |||||||||| ||||
                                    GGACCG TTGTACCACT TGGG
                                       A          C
GAM962  FLJ10901  3'  TTCATCATGTTGGCCAGG    37377
                                    CCTGGCCAACATGGTGAA
                                    ||||||||||||||||||
                                    GGACCGGTTGTACTACTT

GAM962  FLJ10956  3'  GGGGTTTCACCATGTTGGCCAG 37471
                G                   CCTGGCCAACATGGTGAAACTCC
                                    ||||||||||||||||||||||||
                                    GGACCGGTTGTACCACTTTGGGG

GAM962  FLJ12190  3'  TGGAACTTTTCATCTGCTTGGC 47575          _  T      C__
                CAGG                    CCTGGCCAA CA GGTGAAA   TCCA
                                    |||||||| || |||||||   ||||
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                                GGACCGGTT GT CTACTTT   AGGT
                                     C _      TCA
GAM962  FLJ12363  3'  TGGGGTTTCACCATGTTGGCCA 50646
              GG                   CCTGGCCAACATGGTGAAACTCCA
                                   ||||||||||||||||||||||||
                                   GGACCGGTTGTACCACTTTGGGGT

GAM962  FLJ12687  3'  GGGTTTCACCATGTTGGCCAGG 46754
                                   CCTGGCCAACATGGTGAAACTC
                                   |||||||||||||||||||||||
                                   GGACCGGTTGTACCACTTTGGG

GAM962  FLJ12888  3'  GAGTTTTGCTATGTTGCCCAG  46889      C       TG
                                   CTGG CAACATGG  AAACTC
                                   |||| ||||||||  ||||||
                                   GACC GTTGTATC  TTTGAG
                                     C       GT
GAM962  FLJ12973  3'  TTCATCATGTTGGCCAGG    46647
                                   CCTGGCCAACATGGTGAA
                                   ||||||||||||||||||
                                   GGACCGGTTGTACTACTT

GAM962  FLJ13072  5'  GGGTTTCACCATGTTGGACAGG 91394      G
                                   CCTG CCAACATGGTGAAACTC
                                   |||| ||||||||||||||||
                                   GGAC GGTTGTACCACTTTGGG
                                     A
GAM962  FLJ13114  3'  TGGAGTTTCACCATGTTACCCA 44914       CC
              GG                   CCTGG  AACATGGTGAAACTCCA
                                   |||||  ||||||||||||||||
                                   GGACC  TTGTACCACTTTGAGGT
                                     CA
GAM962  FLJ13188  3'  GAGTTTTGCTGTGTTGGTCAGG 42191             TG
                                   CCTGGCCAACATGG  AAACTC
                                   ||||||||||||||  ||||||
                                   GGACTGGTTGTGTC  TTTGAG
                                           GT
GAM962  FLJ13197  3'  GAGTTTCACCATGTTGGCCAGG 45181
                                   CCTGGCCAACATGGTGAAACTC
                                   |||||||||||||||||||||||
                                   GGACCGGTTGTACCACTTTGAG

GAM962  FLJ13305  5'  TGGGGTTTCACCATGTTGGCCA 91718
              G                    CTGGCCAACATGGTGAAACTCCA
                                   ||||||||||||||||||||||||
                                   GACCGGTTGTACCACTTTGGGGT

GAM962  FLJ13456  3'  GAGTTTCACTCTGTCGCC    66549     CA   T
                                   GGC  ACA GGTGAAACTC
                                   |||  ||| ||||||||||
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                                CCG  TGT TCACTTTGAG
                                  C_  C
GAM962  FLJ13910  3'  GAGTACCATGTGGCCAGG    43251        A     GAA
                                CCTGGCCA CATGGT   ACTC
                                |||||||| ||||||   ||||
                                GGACCGGT GTACCA   TGAG
                                      _     ____
GAM962  FLJ13952  3'  GGGTTTCACCACGTTGGCCAGG 46017          A
                                CCTGGCCAAC TGGTGAAACTC
                                |||||||||| ||||||||||
                                GGACCGGTTG ACCACTTTGGG
                                      C
GAM962  FLJ14950  3'  GGGTTTCACCATGTTGGCCAGG 52795
                                CCTGGCCAACATGGTGAAACTC
                                |||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGG

GAM962  FLJ14957  3'  GGGGTTTCACCATGTTGGTCAG 52825
                  G              CCTGGCCAACATGGTGAAACTCC
                                 |||||||||||||||||||||||
                                 GGACTGGTTGTACCACTTTGGGG

GAM962  FLJ20045  3'  TGGGGATTCACCATGTTGGTCA 34897               A
                  GG               CCTGGCCAACATGGTGAA CTCCA
                                   |||||||||||||||| |||||
                                   GGACTGGTTGTACCACTT GGGGT
                                            A
GAM962  FLJ20344  3'  GGGTTTCACCATGTTGGCCAG  35484
                                CTGGCCAACATGGTGAAACTC
                                |||||||||||||||||||
                                GACCGGTTGTACCACTTTGGG

GAM962  FLJ20507  3'  GGGTTTCACCATGTTGGCCAGG 35748
                                CCTGGCCAACATGGTGAAACTC
                                |||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGG

GAM962  FLJ20507  3'  GGGTTTCACCATGTTGGCCAGG 60852
                                CCTGGCCAACATGGTGAAACTC
                                |||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGG

GAM962  FLJ20511  3'  AGTTTCACCGTGTTAGCCA   35766      C
                                TGGC AACATGGTGAAACT
                                |||| ||||||||||||
                                ACCG TTGTGCCACTTTGA
                                  A
GAM962  FLJ20700  3'  GGGTTTCACCATATTGACCAGG 36017       C  C
                                CCTGG CAA ATGGTGAAACTC
                                ||||| ||| ||||||||||||
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                                GGACC GTT TACCACTTTGGG
                                  A   A
GAM962  FLJ20712  5'  GGAATTTCACCATCAGG     36035      GCCAAC        C
                                CCTG      ATGGTGAAA TCC
                                ||||      ||||||||| |||
                                GGAC      TACCACTTT AGG
                                  _______         A
GAM962  FLJ20813  3'  TGGGCTTTCACTACGTTAGCCA 36137       C   A       CT
          GG                      CCTGGC AAC TGGTGAAA  CCA
                                ||||||| ||| ||||||||  |||
                                GGACCG TTG ATCACTTT  GGT
                                   A   C       CG
GAM962  FLJ21302  3'  GGGTTTCACCATGTTGGCCAGG 43511
                                CCTGGCCAACATGGTGAAACTC
                                |||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGG

GAM962  FLJ21324  5'  TGGGGTTTCACCATGTTGGCCA 92862
                                TGGCCAACATGGTGAAACTCCA
                                |||||||||||||||||||||
                                ACCGGTTGTACCACTTTGGGGT

GAM962  FLJ21603  3'  TTCACCCTGTTAGCCAGG    45784       C    T
                                CCTGGC AACA GGTGAA
                                |||||| |||| ||||||
                                GGACCG TTGT CCACTT
                                   A    C
GAM962  FLJ21977  3'  GGAGCTGTACTTGGCCAGG    50873         ACAT    AAA
                                CCTGGCCA    GGTG   CTCC
                                ||||||||    ||||   ||||
                                GGACCGGT    TCAT   GAGG
                                     ____    GTC
GAM962  FLJ22329  3'  GGGGTTTCACCATGTTGGCCAG 45405
                                CTGGCCAACATGGTGAAACTCC
                                |||||||||||||||||||||
                                GACCGGTTGTACCACTTTGGGG

GAM962  FLJ22474  3'  GAGAAGACCATGTTGGCCGGG  45613             GAAA
                                CCTGGCCAACATGGT    CTC
                                ||||||||||||||    |||
                                GGGCCGGTTGTACCA    GAG
                                        GAA_
GAM962  FLJ22529  3'  GGGTTTCACCACATTGGCCAGG 45947         CA
                                CCTGGCCAA  TGGTGAAACTC
                                |||||||||  ||||||||||
                                GGACCGGTT  ACCACTTTGGG
                                     AC
GAM962  FLJ22529  3'  TTCATCATGTTGGCCAGG    45957
                                CCTGGCCAACATGGTGAA
                                ||||||||||||||||||
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                                GGACCGGTTGTACTACTT

GAM962  FLJ22794  3'  GGGTTTCACCATGTTGGTCAGG 93251
                                CCTGGCCAACATGGTGAAACTC
                                ||||||||||||||||||||||
                                GGACTGGTTGTACCACTTTGGG

GAM962  FLJ22969  3'  TTCACCATGTTGCCCAGG    69220      C
                                CCTGG CAACATGGTGAA
                                ||||| ||||||||||||
                                GGACC GTTGTACCACTT
                                   C
GAM962  FLJ23024  3'  GGGGTTTCACCATGTTGGCCAG 46844
                G                CCTGGCCAACATGGTGAAACTCC
                                ||||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGG

GAM962  FLJ23392  3'  GGGTTTCACCATGTTGGCCAGG 45899
                                CCTGGCCAACATGGTGAAACTC
                                |||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGG

GAM962  FLJ23392  3'  TTCACCGTGTTAGCCAGG    45913      C
                                CCTGGC AACATGGTGAA
                                |||||| ||||||||||
                                GGACCG TTGTGCCACTT
                                   A
GAM962  FLJ23556  3'  GGGCTTCACCATGTTGGCCAGG 46447              A
                                CCTGGCCAACATGGTGAA CTC
                                |||||||||||||||||| |||
                                GGACCGGTTGTACCACTT GGG
                                         C
GAM962  FLJ23556  3'  TGGAGTTTTGCTCTGTCACCCA 46462      CCA  T  TG
                GG                CCTGG  ACA GG  AAACTCCA
                                |||||  ||| ||  ||||||||
                                GGACC  TGT TC  TTTGAGGT
                                   CAC  C  GT
GAM962  FLJ23556  3'  TTCACCGTGTTAGCCAGG    46463      C
                                CCTGGC AACATGGTGAA
                                |||||| ||||||||||
                                GGACCG TTGTGCCACTT
                                   A
GAM962  FLJ25416  5'  TGGGGTTTCACCATGTTGGCCA 59458
                GG                CCTGGCCAACATGGTGAAACTCCA
                                ||||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGGT

GAM962  FLJ30532  3'  GGATTTCACTATGTTGGCCAGG 59223              C
                                CCTGGCCAACATGGTGAAA TCC
                                |||||||||||||||||| |||
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                                GGACCGGTTGTATCACTTT AGG
                                                    _
GAM962  FLJ31101  3'  TTCACCATGTTGGCCAGG    36172
                                CCTGGCCAACATGGTGAA
                                ||||||||||||||||||
                                GGACCGGTTGTACCACTT

GAM962  FLJ31153  3'  TGGGGTTTCACCATGCTGGCCA 58757         A
           GG                    CCTGGCCA CATGGTGAAACTCCA
                                 |||||||| ||||||||||||||||
                                 GGACCGGT GTACCACTTTGGGGT
                                      C
GAM962  FLJ32334  3'  TGGAGTCAGGGCTATGTTGCCC 58609       C       GAA_
           AGG                    CCTGG CAACATGGT    ACTCCA
                                  ||||| |||||||||    ||||||
                                  GGACC GTTGTATCG    TGAGGT
                                     C        GGAC
GAM962  GGA2      3'  GGATTTCACCATGTTGGCCAGG 57673                 C
                                CCTGGCCAACATGGTGAAA TCC
                                |||||||||||||||||| |||
                                GGACCGGTTGTACCACTTT AGG
                                                    _
GAM962  GGA2      3'  GGATTTCACCATGTTGGCCAGG 31169                 C
                                CCTGGCCAACATGGTGAAA TCC
                                |||||||||||||||||| |||
                                GGACCGGTTGTACCACTTT AGG
                                                    _
GAM962  GMPPB     5'  GGGTTTCACCAGGTTGGCCAGG 97458           A
                                CCTGGCCAAC TGGTGAAACTC
                                |||||||||| ||||||||||
                                GGACCGGTTG ACCACTTTGGG
                                      G
GAM962  GNG4      3'  GGGGTTTCACCATGTTGGTCAG 16850
           G                     CCTGGCCAACATGGTGAAACTCC
                                 |||||||||||||||||||||||
                                 GGACTGGTTGTACCACTTTGGGG

GAM962  GOLGA3    3'  TGGGGTTTCACCATGTTGGCCA 20899
           GG                    CCTGGCCAACATGGTGAAACTCCA
                                 ||||||||||||||||||||||||
                                 GGACCGGTTGTACCACTTTGGGGT

GAM962  GREB1     3'  GGGGTTTCACCATGTTAGCCAG 28574       C
           G                     CCTGGC AACATGGTGAAACTCC
                                 |||||| ||||||||||||||||
                                 GGACCG TTGTACCACTTTGGGG
                                    A
GAM962  GRWD      3'  GGGGTTTCACCATGTTGGCCAG 49786
           G                     CCTGGCCAACATGGTGAAACTCC
                                 ||||||||||||||||||||||||
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                                GGACCGGTTGTACCACTTTGGGG

GAM962  GTF2E1   3'  GGGTTTCACCATGTTAGCCAGG 19802       C
                                CCTGGC AACATGGTGAAACTC
                                |||||| ||||||||||||||||
                                GGACCG TTGTACCACTTTGGG
                                   A
GAM962  GTPBG3   3'  GGTTTCACCATGTTGACCAGG  51903      C
                                CCTGG CAACATGGTGAAACT
                                ||||| ||||||||||||||||
                                GGACC GTTGTACCACTTTGG
                                   A
GAM962  H-plk    5'  TGGAGTCTTGCTGTGTCACCAG 32390      CCA     TG A
           G                     CCTGG   ACATGG  A ACTCCA
                                |||||   ||||||  | ||||||
                                GGACC   TGTGTC  T TGAGGT
                                   AC_     GT C
GAM962  H2AV     3'  TGGGGTTTCACCATGTTGGCCA 57638
           G                     CTGGCCAACATGGTGAAACTCCA
                                ||||||||||||||||||||||||
                                GACCGGTTGTACCACTTTGGGGT

GAM962  HRH4     3'  GGAGTTTTGCCAGCCTGG    41542    T   CAACA   TG
                                CC GGC    TGG  AAACTCC
                                || |||    |||  |||||||
                                GG CCG    ACC  TTTGAGG
                                 T  _____  GT
GAM962  HSNOV1   3'  TTCACCATGTTGCCCAGG    34445      C
                                CCTGG CAACATGGTGAA
                                ||||| ||||||||||||
                                GGACC GTTGTACCACTT
                                   C
GAM962  HSPC065  3'  TGGGGTTTCACCATGTTGGCCA 27167
           GG                    CCTGGCCAACATGGTGAAACTCCA
                                ||||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGGT

GAM962  HSPC065  3'  TGGGGTTTCACGATGTTGGCCA 27168          G
           GG                    CCTGGCCAACAT GTGAAACTCCA
                                |||||||||||| ||||||||||
                                GGACCGGTTGTA CACTTTGGGGT
                                      G
GAM962  HSPC232  3'  TGGGGTTCACCATGTTGGCCAG 33659              A
           G                     CCTGGCCAACATGGTGAA CTCCA
                                |||||||||||||||| |||||
                                GGACCGGTTGTACCACTT GGGGT
                                                 _
GAM962  HT002    3'  TTCACCGTGTTGGCCAGG    26804
                                CCTGGCCAACATGGTGAA
                                ||||||||||||||||
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                                GGACCGGTTGTGCCACTT

GAM962  JM11     3'  GGTTTCACCATATTGGCCAGG  54369          C
                                CCTGGCCAA ATGGTGAAACT
                                ||||||||| ||||||||||
                                GGACCGGTT TACCACTTTGG
                                      A
GAM962  KIAA0022 3'  GGAGTCTCACTGTGCTGCCCAG 30283       C  A       A
           G                     CCTGG CA CATGGTGA ACTCC
                                ||||| || |||||||| |||||
                                GGACC GT GTGTCACT TGAGG
                                   C  C       C
GAM962  KIAA0087 3'  TTCACCATCTTGGCCAGG    29350          C
                                CCTGGCCAA ATGGTGAA
                                ||||||||| ||||||||
                                GGACCGGTT TACCACTT
                                      C
GAM962  KIAA0161 3'  GGGGTTTCACCATGTTGGCCAG 29205
           G                     CCTGGCCAACATGGTGAAACTCC
                                ||||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGG

GAM962  KIAA0186 3'  GAGTTTTACCATGTTGGCCAGG 41110
                                CCTGGCCAACATGGTGAAACTC
                                |||||||||||||||||||||||
                                GGACCGGTTGTACCATTTTGAG

GAM962  KIAA0186 3'  TGGGGTTTCACCATGTTGGCCA 41124
           GG                      CCTGGCCAACATGGTGAAACTCCA
                                ||||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGGT

GAM962  KIAA0186 3'  TTCACCATGTTGGCCAGG    41128
                                CCTGGCCAACATGGTGAA
                                ||||||||||||||||
                                GGACCGGTTGTACCACTT

GAM962  KIAA0205 3'  TGGGGTTTCACCATGTTGGCCA 30220
           GG                      CCTGGCCAACATGGTGAAACTCCA
                                ||||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGGT

GAM962  KIAA0210 5'  GGAGTTTCACCATGTTGGCCAG 29167
           G                     CCTGGCCAACATGGTGAAACTCC
                                ||||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGAGG

GAM962  KIAA0210 5'  GGGGTTTCACTATATTGGCCAG 29169          C
           G                     CCTGGCCAA ATGGTGAAACTCC
                                ||||||||| ||||||||||||
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                                GGACCGGTT TATCACTTTGGGG
                                     A
GAM962  KIAA0426 3' GGGGTTTCACCATGTTGGCCAG 28929
                G                CCTGGCCAACATGGTGAAACTCC
                                 ||||||||||||||||||||||
                                 GGACCGGTTGTACCACTTTGGGG

GAM962  KIAA0459 3' GGGGTTTCACCATGTTAGCCAG 61656       C
                G                CCTGGC AACATGGTGAAACTCC
                                 |||||| ||||||||||||||||
                                 GGACCG TTGTACCACTTTGGGG
                                    A
GAM962  KIAA0475 3' GGGTTTCACCATGTTGGCCAGG 30124
                                 CCTGGCCAACATGGTGAAACTC
                                 |||||||||||||||||||||
                                 GGACCGGTTGTACCACTTTGGG

GAM962  KIAA0495 3' TGGGATTTCACCATGTTGGCCA 63277                CT
                GG               CCTGGCCAACATGGTGAAA  CCA
                                 |||||||||||||||||  |||
                                 GGACCGGTTGTACCACTTT  GGT
                                           AG
GAM962  KIAA0513 5' GGGTTTCGCCATGTTGGCCAGG 29045
                                 CCTGGCCAACATGGTGAAACTC
                                 |||||||||||||||||||||
                                 GGACCGGTTGTACCGCTTTGGG

GAM962  KIAA0513 3' TGGGGTTTCACCATGCTGGCCA 29054         A
                GG               CCTGGCCA CATGGTGAAACTCCA
                                 ||||||||| ||||||||||||||
                                 GGACCGGT GTACCACTTTGGGGT
                                      C
GAM962  KIAA0527 3' TGGAGTTTCACCATGTTGGCCA 97502
                GG               CCTGGCCAACATGGTGAAACTCCA
                                 ||||||||||||||||||||||||
                                 GGACCGGTTGTACCACTTTGAGGT

GAM962  KIAA0544 3' TTCACCATGTTGGCCGGG    71479
                                 CCTGGCCAACATGGTGAA
                                 ||||||||||||||||
                                 GGGCCGGTTGTACCACTT

GAM962  KIAA0561 3' GGGGTTTCACCATGTTGGTCAG 66484
                G                CCTGGCCAACATGGTGAAACTCC
                                 ||||||||||||||||||||||||
                                 GGACTGGTTGTACCACTTTGGGG

GAM962  KIAA0562 3' GGGGTTTCACCATATTGGCCAG 28828          C
                G                CCTGGCCAA ATGGTGAAACTCC
                                 |||||||| ||||||||||||
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                                GGACCGGTT TACCACTTTGGGG
                                     A
GAM962  KIAA0563  5'  GGAGTTTCGCCATGTTGGTCAG 29885
              G                   CCTGGCCAACATGGTGAAACTCC
                                  ||||||||||||||||||||||
                                  GGACTGGTTGTACCGCTTTGAGG

GAM962  KIAA0594  3'  TTCAGCATATTGGCCAGG    65522         C   G
                                  CCTGGCCAA ATG TGAA
                                  ||||||||| ||| ||||
                                  GGACCGGTT TAC ACTT
                                       A   G
GAM962  KIAA0682  3'  TGGGTTTCACCATGTAGACCAG 30033       CCA          T
              G                   CCTGG   ACATGGTGAAAC CCA
                                  |||||   |||||||||||| |||
                                  GGACC   TGTACCACTTTG GGT
                                    AGA         _
GAM962  KIAA0682  3'  TTCACCATGTGGGCCAGG    30036        A
                                  CCTGGCC ACATGGTGAA
                                  ||||||| ||||||||||
                                  GGACCGG TGTACCACTT
                                      G
GAM962  KIAA0720  3'  GGCATTTCACCATATTGGTCAG 62987          C        CT
              G                   CCTGGCCAA ATGGTGAAA  CC
                                  ||||||||| ||||||||  ||
                                  GGACTGGTT TACCACTTT  GG
                                       A        AC
GAM962  KIAA0737  3'  GGGTTTCACCATGTTGGCCAGG 29814
                                  CCTGGCCAACATGGTGAAACTC
                                  |||||||||||||||||||||
                                  GGACCGGTTGTACCACTTTGGG

GAM962  KIAA0774  5'  TTTCACCATGTGCAGG      93408      G CA
                                  CCTG C  ACATGGTGAAA
                                  |||| |  ||||||||||
                                  GGAC G  TGTACCACTTT
                                    _ ——
GAM962  KIAA0831  5'  GGGGTTTCACCATGTTGGCCAG 30645
              G                   CCTGGCCAACATGGTGAAACTCC
                                  ||||||||||||||||||||||||
                                  GGACCGGTTGTACCACTTTGGGG

GAM962  KIAA0831  3'  TTCACCATGTTGGCCAGG    30658
                                  CCTGGCCAACATGGTGAA
                                  ||||||||||||||||||
                                  GGACCGGTTGTACCACTT

GAM962  KIAA0841  3'  GGAGCTTTACCATGTTGGTCAG 71898                A
              G                   CCTGGCCAACATGGTGAA CTCC
                                  |||||||||||||||||| ||||
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                                GGACTGGTTGTACCATTT GAGG
                                          C
GAM962  KIAA0884 3' TTCACCATGTTGCCCAGG    70762      C
                                CCTGG CAACATGGTGAA
                                ||||| ||||||||||||
                                GGACC GTTGTACCACTT
                                   C
GAM962  KIAA0924 3' TGGGGTTTCACCATATTGGCCA 30378         C
           GG                    CCTGGCCAA ATGGTGAAACTCCA
                                ||||||||| ||||||||||||||
                                GGACCGGTT TACCACTTTGGGGT
                                     A
GAM962  KIAA0931 3' GGGGTTTCACCATGTTGGCCAG 68015
           G                     CCTGGCCAACATGGTGAAACTCC
                                ||||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGG

GAM962  KIAA0961 3' TGGGGTTTCACCATGTTGGCCA 30415
           GG                    CCTGGCCAACATGGTGAAACTCCA
                                ||||||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGGT

GAM962  KIAA1026 3' GAGATTTCACCATGTTGGCCAG 71739                 _
           G                     CCTGGCCAACATGGTGAAA CTC
                                |||||||||||||||||| |||
                                GGACCGGTTGTACCACTTT GAG
                                          A
GAM962  KIAA1054 3' TGGAGTTTCACTCTGTTGCCCA 68973      C    T
           GG                    CCTGG CAACA GGTGAAACTCCA
                                ||||| ||||| ||||||||||||
                                GGACC GTTGT TCACTTTGAGGT
                                   C    C
GAM962  KIAA1161 5' TGGGGTTTACCATGTTGGCCAG 82653              A
           G                     CCTGGCCAACATGGTGAA CTCCA
                                |||||||||||||||||| |||||
                                GGACCGGTTGTACCATTT GGGGT
                                          _
GAM962  KIAA1170 3' GGGTTTCACCATGTTAGCCAGG 70420       C
                                CCTGGC AACATGGTGAAACTC
                                |||||| ||||||||||||||
                                GGACCG TTGTACCACTTTGGG
                                   A
GAM962  KIAA1185 3' TTCACCATTTTGACCAGG    63297      C  C
                                CCTGG CAA ATGGTGAA
                                ||||| ||| ||||||||
                                GGACC GTT TACCACTT
                                   A  T
GAM962  KIAA1198 3' GGGGTTTCACCATGTTGGCCAG 64048
           G                     CCTGGCCAACATGGTGAAACTCC
                                ||||||||||||||||||||||||
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                                GGACCGGTTGTACCACTTTGGGG

GAM962  KIAA1198 3' GGGGTTTCACCATGTTGGCCAG 64049
              G                  CCTGGCCAACATGGTGAAACTCC
                                 ||||||||||||||||||||||
                                 GGACCGGTTGTACCACTTTGGGG

GAM962  KIAA1198 3' GTTTCACCATGTTGACCAGG  64059      C
                                 CCTGG CAACATGGTGAAAC
                                 ||||| |||||||||||||
                                 GGACC GTTGTACCACTTTG
                                    A
GAM962  KIAA1198 3' TGGGGTTTCACCATGTTGACCA 64071      C
              GG                   CCTGG CAACATGGTGAAACTCCA
                                 ||||| ||||||||||||||||||
                                 GGACC GTTGTACCACTTTGGGGT
                                    A
GAM962  KIAA1198 3' TTCACCGTGTTAGCCAGG    64074      C
                                 CCTGGC AACATGGTGAA
                                 |||||| ||||||||||
                                 GGACCG TTGTGCCACTT
                                    A
GAM962  KIAA1200 3' GGGGTTTCACCATGTTGGCCAG 63040
              G                  CCTGGCCAACATGGTGAAACTCC
                                 ||||||||||||||||||||||
                                 GGACCGGTTGTACCACTTTGGGG

GAM962  KIAA1209 3' TTCATCATGTTGGCCAGG    61411
                                 CCTGGCCAACATGGTGAA
                                 ||||||||||||||||||
                                 GGACCGGTTGTACTACTT

GAM962  KIAA1210 3' GGGGTTTCACCATGTTGGCCAG 98077
              G                  CCTGGCCAACATGGTGAAACTCC
                                 ||||||||||||||||||||||
                                 GGACCGGTTGTACCACTTTGGGG

GAM962  KIAA1254 3' TGGGGTTTCACCATGTTGGCCA 70569
              GG                   CCTGGCCAACATGGTGAAACTCCA
                                 ||||||||||||||||||||||||
                                 GGACCGGTTGTACCACTTTGGGGT

GAM962  KIAA1320 5' TTCACCATGTTGGCCAGG    69854
                                 CCTGGCCAACATGGTGAA
                                 ||||||||||||||||||
                                 GGACCGGTTGTACCACTT

GAM962  KIAA1328 5' TTCACCGTGTTAGCCAGG    62337      C
                                 CCTGGC AACATGGTGAA
                                 |||||| ||||||||||
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                                GGACCG TTGTGCCACTT
                                   A
GAM962  KIAA1443 3' GGGTTTCATCATGTTAGCCAGG 64576       C
                                CCTGGC AACATGGTGAAACTC
                                |||||| ||||||||||||||
                                GGACCG TTGTACTACTTTGGG
                                   A
GAM962  KIAA1456 3' TTCACCGTGTTAGCCAGG    67573       C
                                CCTGGC AACATGGTGAA
                                |||||| ||||||||||
                                GGACCG TTGTGCCACTT
                                   A
GAM962  KIAA1465 3' GGGGTTTCACCATGTTGGCCAG 61505
           G                     CCTGGCCAACATGGTGAAACTCC
                                 ||||||||||||||||||||||
                                 GGACCGGTTGTACCACTTTGGGG

GAM962  KIAA1467 3' GGGGTTTCACCATGTTGGCCAG 72072
           G                     CCTGGCCAACATGGTGAAACTCC
                                 ||||||||||||||||||||||
                                 GGACCGGTTGTACCACTTTGGGG

GAM962  KIAA1508 3' AGTTTCATCCGGCCGGG     62541        AACAT
                                CCTGGCC    GGTGAAACT
                                |||||||    |||||||||
                                GGGCCGG    CTACTTTGA
                                   C____
GAM962  KIAA1508 3' GGTTTCACCATGTTGGTCAGG  62559
                                CCTGGCCAACATGGTGAAACT
                                |||||||||||||||||||||
                                GGACTGGTTGTACCACTTTGG

GAM962  KIAA1571 3' GGGGTTTCACTATGTTGGCCAG 61619
           G                     CCTGGCCAACATGGTGAAACTCC
                                 ||||||||||||||||||||||
                                 GGACCGGTTGTATCACTTTGGGG

GAM962  KIAA1615 3' TGGAGTTTCACCACGTTGGCCA 69290         A
                                TGGCCAAC TGGTGAAACTCCA
                                |||||||| ||||||||||||
                                ACCGGTTG ACCACTTTGAGGT
                                   C
GAM962  KIAA1617 3' GGGTTTCACCATGTTGGTCAGG 93080
                                CCTGGCCAACATGGTGAAACTC
                                |||||||||||||||||||||
                                GGACTGGTTGTACCACTTTGGG

GAM962  KIAA1655 3' GGTTTCACCATGTTGGCCAGG  67196
                                CCTGGCCAACATGGTGAAACT
                                |||||||||||||||||||||
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                                GGACCGGTTGTACCACTTTGG

GAM962  KIAA1668 3' TTCACCGTGTTAACCAGG    67085      CC
                                CCTGG  AACATGGTGAA
                                |||||  ||||||||||
                                GGACC  TTGTGCCACTT
                                   AA
GAM962  KIAA1821 3' GAGCCACCATGCCTGGCCAGG  72266       A_     AAA
                                CCTGGCCA  CATGGTG   CTC
                                ||||||||  |||||||   |||
                                GGACCGGT  GTACCAC   GAG
                                     CC      C__
GAM962  KIAA1829 3' GGGGTTTCACCACATTGGTCAG 62652        CA
           G                     CCTGGCCAA  TGGTGAAACTCC
                                |||||||||  ||||||||||||
                                GGACTGGTT  ACCACTTTGGGG
                                     AC
GAM962  KIAA1843 3' GGAGCCTGCACAATTGGCTAG  62884       CATG   AAA_
                                CTGGCCAA    GTG    CTCC
                                ||||||||    |||    ||||
                                GATCGGTT    CAC    GAGG
                                     AA__   GTCC
GAM962  KIAA1858 3' GAGCCGCTGCCCTGGCCAGG   67721       ACA    AAA
                                CCTGGCCA   TGGTG   CTC
                                ||||||||   |||||   |||
                                GGACCGGT   GTCGC   GAG
                                     CCC    C__
GAM962  KIAA1877 3' TTCACCGTGTTAGCCAGG    66766       C
                                CCTGGC AACATGGTGAA
                                ||||||| ||||||||||
                                GGACCG TTGTGCCACTT
                                   A
GAM962  KIAA1962 3' TGGAGTCTCACTATGTTGCCCA 82802      C         A
           G                     CTGG CAACATGGTGA ACTCCA
                                |||| |||||||||| ||||||
                                GACC GTTGTATCACT TGAGGT
                                  C         C
GAM962  KIAA1971 3' TTCACCGTGTTAGCCAGG    74700       C
                                CCTGGC AACATGGTGAA
                                ||||||| ||||||||||
                                GGACCG TTGTGCCACTT
                                   A
GAM962  KIAA1975 5' TGGGGTTTCACCATGTTAACCA 74433      CC
           GG                    CCTGG  AACATGGTGAAACTCCA
                                |||||  ||||||||||||||||
                                GGACC  TTGTACCACTTTGGGGT
                                   AA
GAM962  KIAA1987 5' GGTTTCACCATATTGGCCAGG  89387        C
                                CCTGGCCAA ATGGTGAAACT
                                ||||||||| ||||||||||
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                                GGACCGGTT TACCACTTTGG
                                     A
GAM962  KLK7     3'  GGGTTTCACCATGTTGGCCAG  18547
                                CTGGCCAACATGGTGAAACTC
                                ||||||||||||||||||||
                                GACCGGTTGTACCACTTTGGG

GAM962  KLK7     3'  GGGTTTCACCATGTTGGCCAG  58393
                                CTGGCCAACATGGTGAAACTC
                                ||||||||||||||||||||
                                GACCGGTTGTACCACTTTGGG

GAM962  LAMP3    3'  GGGGTTTCACCATGTTGGCCAG 60207
                                CTGGCCAACATGGTGAAACTCC
                                |||||||||||||||||||||
                                GACCGGTTGTACCACTTTGGGG

GAM962  LIN-28   3'  TGGAGTCTCGCTGTGTCACCCA 45472      CCA       A
              GG                  CCTGG   ACATGGTGA ACTCCA
                                |||||   ||||||||| ||||||
                                GGACC   TGTGTCGCT TGAGGT
                                  CAC       C
GAM962  LY75     3'  TGGGGTTTCACCATGTTGGCCA 11401
              GG                  CCTGGCCAACATGGTGAAACTCCA
                                |||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGGT

GAM962  MAP-1    3'  GGGGTTTCACCATGTTGGCCAG 42446
              G                   CCTGGCCAACATGGTGAAACTCC
                                |||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGG

GAM962  MCLC     3'  TGGGGTTTCACCATGTTGGTCA 31388
              GG                  CCTGGCCAACATGGTGAAACTCCA
                                |||||||||||||||||||||||
                                GGACTGGTTGTACCACTTTGGGGT

GAM962  MEF-2    3'  TGGGTTTCACCATGTTGGTCAG 65033              T
              G                   CCTGGCCAACATGGTGAAAC CCA
                                |||||||||||||||||| |||
                                GGACTGGTTGTACCACTTTG GGT
                                          _
GAM962  MGC12518 3'  TGAGGGTTTCACCATGTTGGCC 64782                _
              AGG                   CCTGGCCAACATGGTGAAACTC CA
                                |||||||||||||||||||| ||
                                GGACCGGTTGTACCACTTTGGG GT
                                      A
GAM962  MGC13204 3'  GGTTTCTCCATGTTGGCCAGG  49630          T
                                CCTGGCCAACATGG GAAACT
                                ||||||||||||| ||||||
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                                GGACCGGTTGTACC CTTTGG
                                       T
GAM962  MGC1842  3' GGCTTCGCCATGTTGGCCAGG  66258              A
                                CCTGGCCAACATGGTGAA CT
                                |||||||||||||||||| ||
                                GGACCGGTTGTACCGCTT GG
                                      C
GAM962  MGC21675 3' TGGGGTTTCACCATGTTGGTCA 54600
           GG                    CCTGGCCAACATGGTGAAACTCCA
                                |||||||||||||||||||||||||
                                GGACTGGTTGTACCACTTTGGGGT

GAM962  MGC22014 3' AGTTTTATTAGCCAG       65110       CAACA
                                CTGGC    TGGTGAAACT
                                |||||    ||||||||||
                                GACCG    ATTATTTTGA
                                  _____
GAM962  MGC2474  3' TTCACCATGTTGGCTAGG    43971
                                CCTGGCCAACATGGTGAA
                                ||||||||||||||||||
                                GGATCGGTTGTACCACTT

GAM962  MGC2603  3' GGTTTCACCATATTAGCCAGG  44080       C  C
                                CCTGGC AA ATGGTGAAACT
                                |||||| || ||||||||||
                                GGACCG TT TACCACTTTGG
                                   A  A
GAM962  MGC4638  3' TTCAACATGTTGGCCAGG    49746            G
                                CCTGGCCAACATG TGAA
                                |||||||||||| ||||
                                GGACCGGTTGTAC ACTT
                                      A
GAM962  MGC4766  5' TTCACCGTGTTAGCCAGG    49565       C
                                CCTGGC AACATGGTGAA
                                |||||| ||||||||||
                                GGACCG TTGTGCCACTT
                                   A
GAM962  MGC5149  3' TGGGGTTTCACCACATTGGCCA 72763         CA
           GG                    CCTGGCCAA  TGGTGAAACTCCA
                                |||||||||  ||||||||||||
                                GGACCGGTT  ACCACTTTGGGGT
                                     AC
GAM962  MKRN4    3' GGGGTTTCACCATATTGGTCAG 48470         C
           G                     CCTGGCCAA ATGGTGAAACTCC
                                |||||||||  ||||||||||||
                                GGACTGGTT TACCACTTTGGGG
                                     A
GAM962  moblak   3' AGATTTCACCATGTTGGCCAGG 56384                _
                                CCTGGCCAACATGGTGAAA CT
                                |||||||||||||||||| ||
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                                GGACCGGTTGTACCACTTT GA
                                                    A
GAM962  moblak   3'  TTCACCGTGTTAGCCAGG    56414       C
                                CCTGGC AACATGGTGAA
                                |||||| ||||||||||
                                GGACCG TTGTGCCACTT
                                   A
GAM962  MRPS27   3'  TGGGGTTTCACCATGTTGGTCA 31336
           GG                     CCTGGCCAACATGGTGAAACTCCA
                                |||||||||||||||||||||||
                                GGACTGGTTGTACCACTTTGGGGT

GAM962  MtFMT    3'  TGGGGTTTCACCATGTTGGTCA 58340
           GG                     CCTGGCCAACATGGTGAAACTCCA
                                |||||||||||||||||||||||
                                GGACTGGTTGTACCACTTTGGGGT

GAM962  MYO5C    3'  GGTTTCACCATGTTGGCCAGG  38725
                                CCTGGCCAACATGGTGAAACT
                                |||||||||||||||||||
                                GGACCGGTTGTACCACTTTGG

GAM962  NDP52    3'  GGGTTTCACTATGTTGGCCAGG 20674
                                CCTGGCCAACATGGTGAAACTC
                                |||||||||||||||||||
                                GGACCGGTTGTATCACTTTGGG

GAM962  NDUFC2   3'  GGGGTTTCACCATGTTGGCCA  17033
                                TGGCCAACATGGTGAAACTCC
                                |||||||||||||||||||
                                ACCGGTTGTACCACTTTGGGG

GAM962  Nup43    3'  GGGTTTCACCATGTTGGCCAGG 45351
                                CCTGGCCAACATGGTGAAACTC
                                |||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGG

GAM962  NXN      3'  TTCACCATGTTGGCTAGG    42686
                                CCTGGCCAACATGGTGAA
                                ||||||||||||||||
                                GGATCGGTTGTACCACTT

GAM962  OCT11    3'  TGGGGTTTCACCATGTTGGTCA 27595
           GG                     CCTGGCCAACATGGTGAAACTCCA
                                |||||||||||||||||||||||
                                GGACTGGTTGTACCACTTTGGGGT

GAM962  OR51E2   3'  GAGTTTCACCATGTTGGCCAGG 48511
                                CCTGGCCAACATGGTGAAACTC
                                |||||||||||||||||||||
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                                GGACCGGTTGTACCACTTTGAG

GAM962  OSBPL2   3'  GGGTTTTCACCATGTTGGTCAG 29904                CT
            G                   CCTGGCCAACATGGTGAAA  CC
                                |||||||||||||||||  ||
                                GGACTGGTTGTACCACTTT  GG
                                      TG
GAM962  OSBPL2   3'  GGGTTTTCACCATGTTGGTCAG 58490                CT
            G                   CCTGGCCAACATGGTGAAA  CC
                                |||||||||||||||||  ||
                                GGACTGGTTGTACCACTTT  GG
                                      TG
GAM962  PDZ-GEF1 3'  GTTTGCACATGGCCAGG    27282        ACATG  _
                                CCTGGCCA    GTG AAAC
                                ||||||||    ||| ||||
                                GGACCGGT    CAC TTTG
                                    A____   G
GAM962  PELI1    5'  TGGGGTTTCACCATGTTGGCCA 40663
            GG                    CCTGGCCAACATGGTGAAACTCCA
                                ||||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGGT

GAM962  PELI1    5'  TTCACCATGTTGCCCAGG    40665      C
                                CCTGG CAACATGGTGAA
                                ||||| ||||||||||
                                GGACC GTTGTACCACTT
                                   C
GAM962  PP1201   3'  GAGTCATACGTGTGGCCAGG   42457        A   _   AA
                                CCTGGCCA CATG GTGA  CTC
                                |||||||| |||| ||||  |||
                                GGACCGGT GTGC TACT  GAG
                                    _   A   __
GAM962  PRO0365  5'  GGGGTTTCACTATGTTGGCCAG 26990
            G                   CCTGGCCAACATGGTGAAACTCC
                                |||||||||||||||||||||||
                                GGACCGGTTGTATCACTTTGGGG

GAM962  PRO0899  5'  TGGGGACACCATGTTGCCCAGG 38315      C        AAA
                                CCTGG CAACATGGTG   CTCCA
                                ||||| ||||||||||   |||||
                                GGACC GTTGTACCAC   GGGGT
                                   C        A__
GAM962  RAB21    3'  GGGGTTTCACCAGGTTAGCCAG 31094       C   A
            G                   CCTGGC AAC TGGTGAAACTCC
                                ||||||| ||| ||||||||||||
                                GGACCG TTG ACCACTTTGGGG
                                   A   G
GAM962  RAB33B   3'  TGGGGTTTCACCATGTTGGCCA 49338
            GG                    CCTGGCCAACATGGTGAAACTCCA
                                ||||||||||||||||||||||||
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                                GGACCGGTTGTACCACTTTGGGGT

GAM962  RASSF2   3'  TTCACCATCTTGGCCAGG    29115          C
                                CCTGGCCAA ATGGTGAA
                                ||||||||| ||||||||
                                GGACCGGTT TACCACTT
                                     C
GAM962  RNF8     3'  GGGTTTCACCATGTTGGCCAGG 15571
                                CCTGGCCAACATGGTGAAACTC
                                ||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGG

GAM962  SCAMP-4  3'  GAGTTTCACTCTGTCGCCCAGG 55349      CCA   T
                                CCTGG   ACA GGTGAAACTC
                                |||||   ||| ||||||||||
                                GGACC   TGT TCACTTTGAG
                                   CGC   C
GAM962  SCAMP-4  3'  TGGGGTTTCACCATGTTGGCCA 55357
                GG                 CCTGGCCAACATGGTGAAACTCCA
                                ||||||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGGT

GAM962  SCYA22   3'  GAGGCTTCACCATGTTGGCCAG 92597              A_
                G                  CCTGGCCAACATGGTGAA  CTC
                                |||||||||||||||||  |||
                                GGACCGGTTGTACCACTT  GAG
                                        CG
GAM962  SCYA22   3'  GGTTTCACCATATTGGCCAGG  92603          C
                                CCTGGCCAA ATGGTGAAACT
                                ||||||||| ||||||||||
                                GGACCGGTT TACCACTTTGG
                                     A
GAM962  SERF1B   3'  TGGGGTTTCACCATGTTGGCCA 43708
                GG                 CCTGGCCAACATGGTGAAACTCCA
                                ||||||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGGT

GAM962  SFXN2    3'  GGGGTTTCACCATGCTGGCCAG 74380         A
                                CTGGCCA CATGGTGAAACTCC
                                ||||||| |||||||||||||
                                GACCGGT GTACCACTTTGGGG
                                     C
GAM962  SH3KBP1  5'  GAGTTTGACTACCAGG      66946       CCAACA   G
                                CCTGG     TGGT AAACTC
                                |||||     |||| ||||||
                                GGACC     ATCA TTTGAG
                                   _______   G
GAM962  SLC12A8  3'  GGGTTTCACCATGTTGGCCAGG 45242
                                CCTGGCCAACATGGTGAAACTC
                                ||||||||||||||||||||||
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                                GGACCGGTTGTACCACTTTGGG

GAM962  SLC16A4   3'  GGGGTTTCACCATGTTAGCCAG 17455       C
              G                  CCTGGC AACATGGTGAAACTCC
                                 |||||| ||||||||||||||||
                                 GGACCG TTGTACCACTTTGGGG
                                    A
GAM962  SLC19A3   3'  TGGGGTTTCACAATGTTGGCCA 48254          G
              GG                   CCTGGCCAACAT GTGAAACTCCA
                                   |||||||||||| ||||||||||
                                   GGACCGGTTGTA CACTTTGGGGT
                                         A
GAM962  SLC6A14   3'  AGTTTCCCCATGTTGGCCAGG  24303           T
                                   CCTGGCCAACATGG GAAACT
                                   |||||||||||||| ||||||
                                   GGACCGGTTGTACC CTTTGA
                                         C
GAM962  SREC      3'  GGGTTTCACCATGTTAGCCAGG 14907       C
                                   CCTGGC AACATGGTGAAACTC
                                   |||||| |||||||||||||||
                                   GGACCG TTGTACCACTTTGGG
                                      A
GAM962  SS-56     3'  GGAGTTTCACCATGTTAGCTAG 60355       C
              G                    CCTGGC AACATGGTGAAACTCC
                                   |||||| ||||||||||||||||
                                   GGATCG TTGTACCACTTTGAGG
                                      A
GAM962  STAF65(gamma) 3'  TTCACCGTGTTGGCCAGG    30077
                                   CCTGGCCAACATGGTGAA
                                   ||||||||||||||||||
                                   GGACCGGTTGTGCCACTT

GAM962  STOML2    3'  GGAGCTGGGCTTGGCCAGG   26485        ACAT   GAAA
                                   CCTGGCCA   GGT   CTCC
                                   ||||||||   |||   ||||
                                   GGACCGGT   TCG   GAGG
                                        ____  GGTC
GAM962  SULT1C2   3'  TTCACCGTGTTAGCCAGG    22725       C
                                   CCTGGC AACATGGTGAA
                                   |||||| ||||||||||
                                   GGACCG TTGTGCCACTT
                                      A
GAM962  SYT13     3'  TGGGGTTTCACCATGTTGGCCA 95109
              GG                   CCTGGCCAACATGGTGAAACTCCA
                                   ||||||||||||||||||||||||
                                   GGACCGGTTGTACCACTTTGGGGT

GAM962  TADA3L   3'  TTCACCGTGTTAGCCAGG    56817       C
                                   CCTGGC AACATGGTGAA
                                   |||||| ||||||||||
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                                GGACCG TTGTGCCACTT
                                   A
GAM962  TBC1D2   5' GGAGATCATCTTGGCCAG   37932       CAT   AA
                                CTGGCCAA  GGTGA CTCC
                                ||||||||  ||||| ||||
                                GACCGGTT  CTACT GAGG
                                   ___    A_
GAM962  TCL6     5' GGTTTCACCATGTTGGCCAGG 40489
                                CCTGGCCAACATGGTGAAACT
                                ||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGG

GAM962  TCL6     5' GGTTTCACCATGTTGGCCAGG 40516
                                CCTGGCCAACATGGTGAAACT
                                ||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGG

GAM962  TCL6     5' GGTTTCACCATGTTGGCCAGG 27766
                                CCTGGCCAACATGGTGAAACT
                                ||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGG

GAM962  TCL6     3' TTCACCGTGTTAGCCAGG    27771       C
                                CCTGGC AACATGGTGAA
                                |||||| ||||||||||
                                GGACCG TTGTGCCACTT
                                   A
GAM962  TCL6     5' GGTTTCACCATGTTGGCCAGG 25914
                                CCTGGCCAACATGGTGAAACT
                                ||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGG

GAM962  TCL6     3' TTCACCGTGTTAGCCAGG    25919       C
                                CCTGGC AACATGGTGAA
                                |||||| ||||||||||
                                GGACCG TTGTGCCACTT
                                   A
GAM962  TERA     3' GGGGTTTCACCACGTTGGCCAG 41420          A
           G                     CCTGGCCAAC TGGTGAAACTCC
                                 |||||||||| ||||||||||||
                                 GGACCGGTTG ACCACTTTGGGG
                                      C
GAM962  TGIF2    3' TTCACCATCTTGGCCAGG    41761         C
                                CCTGGCCAA ATGGTGAA
                                |||||||| ||||||||
                                GGACCGGTT TACCACTT
                                      C
GAM962  TRIM16   3' TGGGGTTTCACCATGTTGGCCA 22382
           GG                    CCTGGCCAACATGGTGAAACTCCA
                                 ||||||||||||||||||||||||
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                                GGACCGGTTGTACCACTTTGGGGT

GAM962  TRIM6    3'  TTCACCGTGTTGGCCAGG    55190
                                CCTGGCCAACATGGTGAA
                                ||||||||||||||||||
                                GGACCGGTTGTGCCACTT

GAM962  TU12B1-TY 3'  GGGGTTTCACCATGTTGGCCAG 33856
                G                CCTGGCCAACATGGTGAAACTCC
                                 ||||||||||||||||||||||||
                                 GGACCGGTTGTACCACTTTGGGG

GAM962  TU12B1-TY 3'  TGGGGTTTCACCATGTTGGCCA 33864
                GG               CCTGGCCAACATGGTGAAACTCCA
                                 ||||||||||||||||||||||||
                                 GGACCGGTTGTACCACTTTGGGGT

GAM962  TUCAN    3'  GAGTTTTGCTATGTTGGCCAGG 30979          TG
                                 CCTGGCCAACATGG  AAACTC
                                 ||||||||||||||  ||||||
                                 GGACCGGTTGTATC  TTTGAG
                                        GT
GAM962  TUCAN    3'  TTCACCATTTTGGCCAGG    30993       C
                                 CCTGGCCAA ATGGTGAA
                                 |||||||||  ||||||||
                                 GGACCGGTT TACCACTT
                                       T
GAM962  UBF-fl   3'  TGGGGTTTCACCATGCTGGCCA 52637       A
                GG               CCTGGCCA CATGGTGAAACTCCA
                                 ||||||||  ||||||||||||||||
                                 GGACCGGT GTACCACTTTGGGGT
                                      C
GAM962  UBF-fl   3'  TTCACCATGCTGGCCAGG    52639       A
                                 CCTGGCCA CATGGTGAA
                                 ||||||||  |||||||||
                                 GGACCGGT GTACCACTT
                                      C
GAM962  VDU1     3'  TGGGGTTTCACCATGTTGGCCA 31131
                GG               CCTGGCCAACATGGTGAAACTCCA
                                 ||||||||||||||||||||||||
                                 GGACCGGTTGTACCACTTTGGGGT

GAM962  VPS33A   3'  TGGTGTTTCACCATGTTGGCCA 43618             T
                GG               CCTGGCCAACATGGTGAAAC CCA
                                 ||||||||||||||||||  |||
                                 GGACCGGTTGTACCACTTTG GGT
                                                T
GAM962  WBSCR23  3'  GGGGTTTCACCATGTTGGCCAG 47440
                G                CCTGGCCAACATGGTGAAACTCC
                                 ||||||||||||||||||||||
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                                GGACCGGTTGTACCACTTTGGGG

GAM962  ZNF221    3'  TTCACCGTGTTAGCCAGG    26272       C
                                CCTGGC AACATGGTGAA
                                |||||| ||||||||||
                                GGACCG TTGTGCCACTT
                                   A
GAM962  LOC112817 3'  GAGTTTCACTCTGTCACCCAGG 57328      CCA   T
                                CCTGG   ACA GGTGAAACTC
                                |||||   ||| ||||||||||
                                GGACC   TGT TCACTTTGAG
                                   CAC   C
GAM962  LOC112817 3'  TTCACCGTGTTGGCCAGG    57336
                                CCTGGCCAACATGGTGAA
                                ||||||||||||||||||
                                GGACCGGTTGTGCCACTT

GAM962  LOC113523 5'  GGGTTTCACCATGTTAGCCAG  73429      C
                                CTGGC AACATGGTGAAACTC
                                ||||| ||||||||||||||
                                GACCG TTGTACCACTTTGGG
                                   A
GAM962  LOC115219 5'  TTCATCATGTTGGCCAGG    73711
                                CCTGGCCAACATGGTGAA
                                ||||||||||||||||||
                                GGACCGGTTGTACTACTT

GAM962  LOC119392 3'  TGGGTTTCACCACGTTGGCCAG 59819          A       T
           G                     CCTGGCCAAC TGGTGAAAC CCA
                                ||||||||| ||||||||| |||
                                GGACCGGTTG ACCACTTTG GGT
                                      C       _
GAM962  LOC120114 3'  TGGGGTTTCACCATGTTGGCCA 76055
           GG                    CCTGGCCAACATGGTGAAACTCCA
                                ||||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGGT

GAM962  LOC120224 5'  TGGAGTTTTGCTTTTGTCACCC 57897      CCA   T_  TG
           AGG                   CCTGG   ACA  GG  AAACTCCA
                                |||||   |||  ||  ||||||||
                                GGACC   TGT  TC  TTTGAGGT
                                   CAC   TT  GT
GAM962  LOC121504 3'  GGGGTTTCACCATGTTGGCCAG 74551
           G                     CCTGGCCAACATGGTGAAACTCC
                                |||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGG

GAM962  LOC124216 3'  GGTTTCACCATGTTGGCCAGG  74738
                                CCTGGCCAACATGGTGAAACT
                                |||||||||||||||||||||
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                                GGACCGGTTGTACCACTTTGG

GAM962   LOC126364 3'  TGGGGTTTCGCCATGTTGGCCA 76202
                GG                CCTGGCCAACATGGTGAAACTCCA
                                  ||||||||||||||||||||||||
                                  GGACCGGTTGTACCGCTTTGGGGT

GAM962   LOC126661 3'  TGGGGTTTCACCATGTTGGCCA 75067
                G                 CTGGCCAACATGGTGAAACTCCA
                                  ||||||||||||||||||||||||
                                  GACCGGTTGTACCACTTTGGGGT

GAM962   LOC126661 3'  TTCACCATGTTGCCCAGG    75068      C
                                  CCTGG CAACATGGTGAA
                                  ||||| ||||||||||||
                                  GGACC GTTGTACCACTT
                                     C
GAM962   LOC126669 3'  AGTCTCGCTGTGTTGCCCAGG  75922      C         A
                                  CCTGG CAACATGGTGA ACT
                                  ||||| |||||||||||| |||
                                  GGACC GTTGTGTCGCT TGA
                                     C         C
GAM962   LOC128077 3'  GGGGTTTCACCATGTTAGCCAG 75223       C
                G                 CCTGGC AACATGGTGAAACTCC
                                  |||||| ||||||||||||||||
                                  GGACCG TTGTACCACTTTGGGG
                                     A
GAM962   LOC128077 3'  GGGTTTCACCATGTTGGCCAGG 75225
                                  CCTGGCCAACATGGTGAAACTC
                                  |||||||||||||||||||||||
                                  GGACCGGTTGTACCACTTTGGG

GAM962   LOC128989 3'  GGGGTTTCACCATGTTGGTCAG 75322
                G                 CCTGGCCAACATGGTGAAACTCC
                                  ||||||||||||||||||||||||
                                  GGACTGGTTGTACCACTTTGGGG

GAM962   LOC130813 3'  GGGTCTCACTATGTTGACCAGG 76278      C         A
                                  CCTGG CAACATGGTGA ACTC
                                  ||||| |||||||||||| ||||
                                  GGACC GTTGTATCACT TGGG
                                     A         C
GAM962   LOC131308 3'  GAGTTTTGTCACGTTGGCCAGG 75495          A   TG
                                  CCTGGCCAAC TGG  AAACTC
                                  |||||||||| |||  ||||||
                                  GGACCGGTTG ACT  TTTGAG
                                        C  GT
GAM962   LOC132241 5'  TGGGTTTCACTATGTTGGCCAG 75567                T
                G                 CCTGGCCAACATGGTGAAAC CCA
                                  |||||||||||||||||||| |||
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                                GGACCGGTTGTATCACTTTG GGT
                                                  _
GAM962   LOC132625 3'  TGGGGTTTCACCATGTTGGCCA 76446
                GG                CCTGGCCAACATGGTGAAACTCCA
                                  ||||||||||||||||||||||||
                                  GGACCGGTTGTACCACTTTGGGGT

GAM962   LOC133686 3'  TGGGGATTCACCATGTTGGTCA 75623              A
                GG                CCTGGCCAACATGGTGAA CTCCA
                                  |||||||||||||||| |||||
                                  GGACTGGTTGTACCACTT GGGGT
                                        A
GAM962   LOC135154 3'  GGTTTCACCATGTTAGCCAGG  75734       C
                                  CCTGGC AACATGGTGAAACT
                                  |||||| ||||||||||||||
                                  GGACCG TTGTACCACTTTGG
                                     A
GAM962   LOC135293 3'  GGCATTTCACCATGTTGGCCAG 76688              CT
                G                  CCTGGCCAACATGGTGAAA  CC
                                  ||||||||||||||||||  ||
                                  GGACCGGTTGTACCACTTT  GG
                                        AC
GAM962   LOC142820 5'  GGAGTTTTGCCATGTTGTCCAG 76917       C       TG
                G                  CCTGG CAACATGG  AAACTCC
                                  ||||| ||||||||  |||||||
                                  GGACC GTTGTACC  TTTGAGG
                                     T       GT
GAM962   LOC143187 3'  TGGAGTTTCACCATGTTGGCCA 59766
                GG                CCTGGCCAACATGGTGAAACTCCA
                                  ||||||||||||||||||||||||
                                  GGACCGGTTGTACCACTTTGAGGT

GAM962   LOC143465 3'  TGGGGCATAGCTGGCCAGG   83879        ACATG   AAA
                                  CCTGGCCA    GTG   CTCCA
                                  ||||||||    |||   |||||
                                  GGACCGGT    TAC   GGGGT
                                       CGA__   ___
GAM962   LOC143916 3'  TTCACCTTGTTGGCCAGG    77149          T
                                  CCTGGCCAACA GGTGAA
                                  |||||||||| ||||||
                                  GGACCGGTTGT CCACTT
                                        T
GAM962   LOC144524 5'  GGGTTTCACCGTGTTAGCCAGG 84058       C
                                  CCTGGC AACATGGTGAAACTC
                                  |||||| |||||||||||||||
                                  GGACCG TTGTGCCACTTTGGG
                                     A
GAM962   LOC144742 5'  GGTTTTCACCATGTTGGCCAGG 77464              CT
                                  CCTGGCCAACATGGTGAAA  CC
                                  ||||||||||||||||||  ||
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                                GGACCGGTTGTACCACTTT  GG
                                           T_
GAM962   LOC145268 5'  GAGTTTCACCATGTTGGCCAGG 77580
                                CCTGGCCAACATGGTGAAACTC
                                |||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGAG

GAM962   LOC145384 3'  GGTTTCACTACATTGACCAGG  77717      C   CA
                                CCTGG CAA  TGGTGAAACT
                                ||||| |||  ||||||||||
                                GGACC GTT  ATCACTTTGG
                                   A   AC
GAM962   LOC145622 3'  TTCACCACGTTGGCCAGG    77829          A
                                CCTGGCCAAC TGGTGAA
                                |||||||||| |||||||
                                GGACCGGTTG ACCACTT
                                      C
GAM962   LOC146050 3'  TGGGGTTTCACCATGTTGGCCA 78127
                   GG                CCTGGCCAACATGGTGAAACTCCA
                                |||||||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGGT

GAM962   LOC146229 3'  GGGGTTTCACCATGTTGGCCAG 78295
                   G                 CCTGGCCAACATGGTGAAACTCC
                                |||||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGG

GAM962   LOC146229 3'  GGGGTTTCACCATGTTGGCCAG 78296
                   G                 CCTGGCCAACATGGTGAAACTCC
                                |||||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGG

GAM962   LOC146229 3'  GGGTTTCACCATATTGGCCAGG 78299          C
                                CCTGGCCAA ATGGTGAAACTC
                                ||||||||| ||||||||||||
                                GGACCGGTT TACCACTTTGGG
                                      A
GAM962   LOC146429 5'  GGGTTTCACCATGATAGCCAGG 84672       CAA
                                CCTGGC   CATGGTGAAACTC
                                ||||||   ||||||||||||
                                GGACCG   GTACCACTTTGGG
                                   ATA
GAM962   LOC146603 5'  TTCACCGTGTTAGCCAGG    78609       C
                                CCTGGC AACATGGTGAA
                                |||||| ||||||||||
                                GGACCG TTGTGCCACTT
                                   A
GAM962   LOC146784 5'  TGGGGTTTCACCATGTTGGCCA 78721
                   GG                CCTGGCCAACATGGTGAAACTCCA
                                |||||||||||||||||||||||||||
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                                GGACCGGTTGTACCACTTTGGGGT

GAM962   LOC146839 3'  TTCACCGTGTTAGCCAGG    84857       C
                                CCTGGC AACATGGTGAA
                                |||||| ||||||||||
                                GGACCG TTGTGCCACTT
                                   A
GAM962   LOC146894 3'  TGGGGTTTCACCATGTTGGCCA 59869
            GG                    CCTGGCCAACATGGTGAAACTCCA
                                |||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGGT

GAM962   LOC146901 3'  GGGGTTTCACCATGTTGGCCAG 84908
            G                     CCTGGCCAACATGGTGAAACTCC
                                |||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGG

GAM962   LOC146909 3'  TTCACCGTGTTAGCCAGG    78790       C
                                CCTGGC AACATGGTGAA
                                |||||| ||||||||||
                                GGACCG TTGTGCCACTT
                                   A
GAM962   LOC146952 5'  GGGTTTCACCACATTGGCCAGG 84931          CA
                                CCTGGCCAA  TGGTGAAACTC
                                |||||||||  ||||||||||
                                GGACCGGTT  ACCACTTTGGG
                                     AC
GAM962   LOC147063 5'  TGGAGTTTGAGACCAGCCTGG  85019    T   CAACA   G__
                                CC GGC    TGGT   AAACTCCA
                                || |||    ||||  ||||||||
                                GG CCG    ACCA   TTTGAGGT
                                 T  _____   GAG
GAM962   LOC147071 5'  GGAGTTTCACCATGTTGGTTAG 73368
            G                     CCTGGCCAACATGGTGAAACTCC
                                |||||||||||||||||||||||
                                GGATTGGTTGTACCACTTTGAGG

GAM962   LOC147080 5'  GGTTTCACCATGTTAGCCAGG  85045       C
                                CCTGGC AACATGGTGAAACT
                                |||||| ||||||||||||||
                                GGACCG TTGTACCACTTTGG
                                   A
GAM962   LOC147166 3'  TGGGGTTTCACCATGTTGGCCA 78898
            GG                    CCTGGCCAACATGGTGAAACTCCA
                                |||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGGT

GAM962   LOC147429 3'  TGGGGTTTCACCATGTTAGTCA 79002       C
            GG                    CCTGGC AACATGGTGAAACTCCA
                                |||||| ||||||||||||||||
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                                GGACTG TTGTACCACTTTGGGGT
                                   A
GAM962   LOC147694 3'  TTCACCGTGTTAGCCAGG    79110       C
                                CCTGGC AACATGGTGAA
                                |||||| ||||||||||
                                GGACCG TTGTGCCACTT
                                   A
GAM962   LOC147817 3'  GGAGTTTCACCATATTGGCTGG 79184   TG    C
                                C  GCCAA ATGGTGAAACTCC
                                |  ||||| ||||||||||||
                                G  CGGTT TACCACTTTGAGG
                                 GT    A
GAM962   LOC147817 3'  TTCACCATGTTGGCAAGG    79198     G
                                CCT GCCAACATGGTGAA
                                ||| ||||||||||||||
                                GGA CGGTTGTACCACTT
                                  A
GAM962   LOC147841 3'  TGGAGTTTCACCATGGTGGTCA 79233         A
            GG                    CCTGGCCA CATGGTGAAACTCCA
                                |||||||| ||||||||||||||||
                                GGACTGGT GTACCACTTTGAGGT
                                    G
GAM962   LOC147990 3'  TTCAGCATATTGACCAGG    85242       C   C   G
                                CCTGG CAA ATG TGAA
                                ||||| ||| ||| ||||
                                GGACC GTT TAC ACTT
                                   A   A   G
GAM962   LOC148147 3'  TTCACCTTGTTGGCCAGG    79408           T
                                CCTGGCCAACA GGTGAA
                                |||||||||||| ||||||
                                GGACCGGTTGT CCACTT
                                       T
GAM962   LOC148189 5'  GGGGTTTCACCATGTTGACCAG 79452       C
            G                    CCTGG CAACATGGTGAAACTCC
                                ||||| ||||||||||||||||
                                GGACC GTTGTACCACTTTGGGG
                                   A
GAM962   LOC148195 3'  GGTTTCACCACATTGGTCAGG  85287          CA
                                CCTGGCCAA  TGGTGAAACT
                                |||||||||  ||||||||||
                                GGACTGGTT  ACCACTTTGG
                                     AC
GAM962   LOC148887 5'  GGGTTTCACCATGTTGGTCAGG 85408
                                CCTGGCCAACATGGTGAAACTC
                                |||||||||||||||||||||
                                GGACTGGTTGTACCACTTTGGG

GAM962   LOC149301 5'  GGAGTTTTTTAAGTTACCCAG  80017      CC   A   T
                                CTGG  AAC TGG GAAACTCC
                                ||||  ||| ||| ||||||||
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                                GACC  TTG ATT TTTTGAGG
                                  CA  A  _
GAM962   LOC149478 3'  GGGGTTTCACCATGTTGGCCAG 80174
                 G                 CCTGGCCAACATGGTGAAACTCC
                                   ||||||||||||||||||||||
                                   GGACCGGTTGTACCACTTTGGGG

GAM962   LOC149506 3'  GAGGGTTCACCACGTTGGCCAG 85636          A      A_
                 G                 CCTGGCCAAC TGGTGAA  CTC
                                   |||||||||| |||||||  |||
                                   GGACCGGTTG ACCACTT  GAG
                                         C      GG
GAM962   LOC149692 3'  GAGTTTTCACCATGTTGACCAG 85738       C          _
                 G                 CCTGG CAACATGGTGAAA CTC
                                   ||||| ||||||||||||| |||
                                   GGACC GTTGTACCACTTT GAG
                                     A           T
GAM962   LOC149692 3'  GGGTTTCACCATGTTGGCCAGG 85741
                                   CCTGGCCAACATGGTGAAACTC
                                   |||||||||||||||||||||||
                                   GGACCGGTTGTACCACTTTGGG

GAM962   LOC149821 5'  GGAGTTTCACCGTGTTAGCCAG 85935        C
                 G                 CCTGGC AACATGGTGAAACTCC
                                   ||||||| ||||||||||||||||
                                   GGACCG TTGTGCCACTTTGAGG
                                      A
GAM962   LOC150054 5'  TGGGGTTTCCCATGTTGGCCAG 85979             T
                 G                 CCTGGCCAACATGG GAAACTCCA
                                   |||||||||||||| |||||||||
                                   GGACCGGTTGTACC CTTTGGGGT
                                                _
GAM962   LOC150166 5'  TTCACCATGTTGTCCAGG    86047       C
                                   CCTGG CAACATGGTGAA
                                   ||||| ||||||||||||
                                   GGACC GTTGTACCACTT
                                     T
GAM962   LOC150225 3'  GGTTTCACCATGTCGGCCAGG  86200         A
                                   CCTGGCC ACATGGTGAAACT
                                   ||||||| |||||||||||||
                                   GGACCGG TGTACCACTTTGG
                                       C
GAM962   LOC150282 5'  TGGCGTTTCACCATGTTGGCCA 80547                  T
                 GG                  CCTGGCCAACATGGTGAAAC CCA
                                   |||||||||||||||||| |||
                                   GGACCGGTTGTACCACTTTG GGT
                                             C
GAM962   LOC150397 3'  AGTTTCACCGTGTTGACCAGG  80652       C
                                   CCTGG CAACATGGTGAAACT
                                   ||||| ||||||||||||||
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                                GGACC GTTGTGCCACTTTGA
                                   A
GAM962   LOC151050 5'  GAGTTTCACCATGTTGGCCA   80918
                                TGGCCAACATGGTGAAACTC
                                ||||||||||||||||||||
                                ACCGGTTGTACCACTTTGAG

GAM962   LOC151057 3'  GGGGTTTCACCATGTTGGCCAG 86391
            G                    CCTGGCCAACATGGTGAAACTCC
                                ||||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGG

GAM962   LOC151201 3'  TTCACCATGTTGGCTAGG    86492
                                CCTGGCCAACATGGTGAA
                                ||||||||||||||||||
                                GGATCGGTTGTACCACTT

GAM962   LOC151475 5'  GGTTTCACCATGTTGGCCAGG  86599
                                CCTGGCCAACATGGTGAAACT
                                |||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGG

GAM962   LOC151701 3'  GGGGTTTCACCATGTTGGCCAG 86677
            G                    CCTGGCCAACATGGTGAAACTCC
                                ||||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGG

GAM962   LOC152137 3'  GGGTTTCACCATGTTGGCCAGG 81322
                                CCTGGCCAACATGGTGAAACTC
                                |||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGG

GAM962   LOC152300 3'  GGGTTTCACCATATTGGCCAGG 81386          C
                                CCTGGCCAA ATGGTGAAACTC
                                ||||||||| ||||||||||||
                                GGACCGGTT TACCACTTTGGG
                                      A
GAM962   LOC152343 3'  TGGAGTCTTGCTGTGTCACCCA 81440       CCA     TG A
            GG                    CCTGG   ACATGG  A ACTCCA
                                |||||   ||||||  | |||||||
                                GGACC   TGTGTC  T TGAGGT
                                   CAC     GT C
GAM962   LOC152343 3'  TGGGTTTCACCATGTTGCCCAG 81441       C           T
            G                    CCTGG CAACATGGTGAAAC CCA
                                ||||| ||||||||||||| |||
                                GGACC GTTGTACCACTTTG GGT
                                   C          _
GAM962   LOC152445 3'  TGGAGTCAAGGTGATGGCCAGG 86973         A   GG   AA
                                CCTGGCCA CAT  TGA  CTCCA
                                |||||||| |||  |||  |||||
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                                GGACCGGT GTG  ACT  GAGGT
                                     A   GA   __
GAM962   LOC152719 5'  GGGGTTTCACCATGTTGGTCAG 87035
                 G                  CCTGGCCAACATGGTGAAACTCC
                                    ||||||||||||||||||||||
                                    GGACTGGTTGTACCACTTTGGGG

GAM962   LOC152719 5'  GGGTTTCACCATGTTAGCCAGG 87038       C
                                    CCTGGC AACATGGTGAAACTC
                                    |||||| ||||||||||||||
                                    GGACCG TTGTACCACTTTGGG
                                       A
GAM962   LOC152794 5'  TTCATCATGTTGGCCAGG    81568
                                    CCTGGCCAACATGGTGAA
                                    ||||||||||||||||||
                                    GGACCGGTTGTACTACTT

GAM962   LOC152851 3'  TGGAGTTTCACTCTTCTGGCC  81599       ACAT
                                    GGCCA    GGTGAAACTCCA
                                    |||||    ||||||||||||
                                    CCGGT    TCACTTTGAGGT
                                       CTTC
GAM962   LOC153077 3'  TGGGGCTTCACCATGTTGGCCA 87135                A
                 GG                   CCTGGCCAACATGGTGAA CTCCA
                                    |||||||||||||||||| |||||
                                    GGACCGGTTGTACCACTT GGGGT
                                                 C
GAM962   LOC153606 5'  GGGTTTCACCATGTTGGCCAGG 87259
                                    CCTGGCCAACATGGTGAAACTC
                                    |||||||||||||||||||||||
                                    GGACCGGTTGTACCACTTTGGG

GAM962   LOC153688 3'  GGGTTTCACCATGTTGGCCGGG 87327
                                    CCTGGCCAACATGGTGAAACTC
                                    |||||||||||||||||||||||
                                    GGGCCGGTTGTACCACTTTGGG

GAM962   LOC153733 3'  TGGAGTTTGACACTAGCCTGG  81803    T   CAACA    __
                                    CC GGC     TGGTG  AAACTCCA
                                    || |||     |||||  ||||||||
                                    GG CCG     ATCAC  TTTGAGGT
                                     T  _____     AG
GAM962   LOC153811 3'  GAGCTTCTCCATGTTGCCCAGG 81835       C       T   A
                                    CCTGG CAACATGG GAA CTC
                                    ||||| |||||||| ||| |||
                                    GGACC GTTGTACC CTT GAG
                                       C       T   C
GAM962   LOC153811 3'  GGTTTCACCACGTTGGCCAGG  81845          A
                                    CCTGGCCAAC TGGTGAAACT
                                    |||||||||| ||||||||||
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                                GGACCGGTTG ACCACTTTGG
                                      C
GAM962   LOC154282 5'  TGGTGTTTCACCATGTTGGCCA 87415                T
            GG                    CCTGGCCAACATGGTGAAAC CCA
                                  |||||||||||||||||||| |||
                                  GGACCGGTTGTACCACTTTG GGT
                                           T
GAM962   LOC154877 3'  TTCACCATGTTGCCCAGG    87585      C
                                  CCTGG CAACATGGTGAA
                                  ||||| ||||||||||||
                                  GGACC GTTGTACCACTT
                                     C
GAM962   LOC155372 3'  GGAATTTCACCATGGTGGCCA  82260       A        C
                                  TGGCCA CATGGTGAAA TCC
                                  |||||| |||||||||| |||
                                  ACCGGT GTACCACTTT AGG
                                      G         A
GAM962   LOC157247 5'  GGGGTTTCACCAGTGTTGGCCA 82304              _
            GG                    CCTGGCCAACA TGGTGAAACTCC
                                  |||||||||||| ||||||||||||
                                  GGACCGGTTGT ACCACTTTGGGG
                                        G
GAM962   LOC157506 3'  GGGGTTTCACCATGTTGGTCAG 82371
            G                      CCTGGCCAACATGGTGAAACTCC
                                   ||||||||||||||||||||||
                                   GGACTGGTTGTACCACTTTGGGG

GAM962   LOC157623 3'  TGGAGTTTCACCATATTGCCCA 82416       C   C
            GG                    CCTGG CAA ATGGTGAAACTCCA
                                  ||||| ||| ||||||||||||||
                                  GGACC GTT TACCACTTTGAGGT
                                     C   A
GAM962   LOC157798 5'  GGAGTCTTGCTGTGTCACCAGG 87861       CCA      TG A
                                  CCTGG   ACATGG  A ACTCC
                                  |||||   ||||||  | |||||
                                  GGACC   TGTGTC  T TGAGG
                                     AC_      GT C
GAM962   LOC157798 5'  TTCACCTTGTTGGCCAGG    87868           T
                                  CCTGGCCAACA GGTGAA
                                  |||||||||||| ||||||
                                  GGACCGGTTGT CCACTT
                                        T
GAM962   LOC158014 5'  GGAGTTTCACCATGTTAGCCAG 82563        C
            G                      CCTGGC AACATGGTGAAACTCC
                                   |||||| ||||||||||||||||
                                   GGACCG TTGTACCACTTTGAGG
                                      A
GAM962   LOC158310 5'  GGGTTTCACAATGTTGACCAGG 88085       C      G
                                  CCTGG CAACAT GTGAAACTC
                                  ||||| |||||| |||||||||
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                                GGACC GTTGTA CACTTTGGG
                                   A     A
GAM962   LOC158402 5'  TTCACCGTGTTGGCCAGG    88154
                                CCTGGCCAACATGGTGAA
                                ||||||||||||||||||
                                GGACCGGTTGTGCCACTT

GAM962   LOC158476 3'  GGGTTTCACCATATTGGCCAGG 88198          C
                                CCTGGCCAA ATGGTGAAACTC
                                ||||||||| ||||||||||||
                                GGACCGGTT TACCACTTTGGG
                                      A
GAM962   LOC158476 3'  GGGTTTCACCATGTTGGTCAGG 88200
                                CCTGGCCAACATGGTGAAACTC
                                |||||||||||||||||||||||
                                GGACTGGTTGTACCACTTTGGG

GAM962   LOC158549 5'  TTCACCGTGTTAGCCAGG    88232       C
                                CCTGGC AACATGGTGAA
                                ||||||| ||||||||||
                                GGACCG TTGTGCCACTT
                                   A
GAM962   LOC158668 3'  TGGGGTTTCACCATGCTGGTCA 69909         A
            GG                    CCTGGCCA CATGGTGAAACTCCA
                                ||||||||| ||||||||||||||||
                                GGACTGGT GTACCACTTTGGGGT
                                     C
GAM962   LOC158865 5'  TTCACCGTGTTGGCCAGG    88311
                                CCTGGCCAACATGGTGAA
                                ||||||||||||||||||
                                GGACCGGTTGTGCCACTT

GAM962   LOC160646 3'  TGGGGCTTCACCATGTTGGCCA 83126                A
            GG                    CCTGGCCAACATGGTGAA CTCCA
                                |||||||||||||||||| |||||
                                GGACCGGTTGTACCACTT GGGGT
                                           C
GAM962   LOC161829 3'  TGGGGTTTCACCATGTTGGCCA 83196
            GG                    CCTGGCCAACATGGTGAAACTCCA
                                |||||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGGT

GAM962   LOC162427 3'  TGGGGTTTCACCATGTTGGCCA 83234
            GG                    CCTGGCCAACATGGTGAAACTCCA
                                |||||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGGT

GAM962   LOC163688 5'  GAGCACCAGCTGGCCAGG    57750        ACA    AAA
                                CCTGGCCA   TGGTG   CTC
                                ||||||||   |||||   |||
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                                GGACCGGT   ACCAC   GAG
                                    CG_    ___
GAM962   LOC166206 3'  GAGTCTCCTCCTGGCCAGG    83513         ACAT  T_  A
                                CCTGGCCA    GG  GA ACTC
                                ||||||||    ||  || ||||
                                GGACCGGT    CC  CT TGAG
                                    ____  TC  C
GAM962   LOC169611 3'  GGATTTCACCATGTTGGCCAGG 83653                 C
                                CCTGGCCAACATGGTGAAA TCC
                                ||||||||||||||||||| |||
                                GGACCGGTTGTACCACTTT AGG
                                                   _
GAM962   LOC169611 3'  GGGGTTTCACCACGTTGGCCAG 83655           A
           G                     CCTGGCCAAC TGGTGAAACTCC
                                ||||||||||| ||||||||||||
                                GGACCGGTTG ACCACTTTGGGG
                                      C
GAM962   LOC170082 5'  TGGGGTTTCACCATGTTAGCCA 83451        C
           GG                    CCTGGC AACATGGTGAAACTCCA
                                |||||| ||||||||||||||||
                                GGACCG TTGTACCACTTTGGGGT
                                   A
GAM962   LOC196047 5'  GGGTTTCACCATGTCGGCCAGG 91161         A
                                CCTGGCC ACATGGTGAAACTC
                                ||||||| ||||||||||||||
                                GGACCGG TGTACCACTTTGGG
                                    C
GAM962   LOC196264 3'  TTCACCATTTTGGCCAGG     88995          C
                                CCTGGCCAA ATGGTGAA
                                ||||||||| ||||||||
                                GGACCGGTT TACCACTT
                                      T
GAM962   LOC196411 3'  TGGGGTTTCACTATGTTGGCCA 89051
           GG                    CCTGGCCAACATGGTGAAACTCCA
                                ||||||||||||||||||||||||
                                GGACCGGTTGTATCACTTTGGGGT

GAM962   LOC196528 3'  TTTCATTTGGCCAGG       89111          CATG
                                CCTGGCCAA    GTGAAA
                                |||||||||    ||||||
                                GGACCGGTT    TACTTT
                                     ____
GAM962   LOC196529 3'  GGGTTTCACTACGTTGGCCAGG 89137           A
                                CCTGGCCAAC TGGTGAAACTC
                                |||||||||| ||||||||||
                                GGACCGGTTG ATCACTTTGGG
                                      C
GAM962   LOC197358 3'  TGGGGTTTCACCATGTTGATCA 89449      GC
           GG                    CCTG  CAACATGGTGAAACTCCA
                                ||||  ||||||||||||||||||
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                                GGAC  GTTGTACCACTTTGGGGT
                                  TA
GAM962   LOC197358 3'  TTCATCATGTTGGCCAGG    89450
                                CCTGGCCAACATGGTGAA
                                ||||||||||||||||||
                                GGACCGGTTGTACTACTT

GAM962   LOC199699 3'  GAGTTTCACCATATTAGCCTGG 89675    T   C  C
                                CC GGC AA ATGGTGAAACTC
                                || ||| || ||||||||||||
                                GG CCG TT TACCACTTTGAG
                                 T   A  A
GAM962   LOC199699 3'  TTCACCGTGTTAGCCAGG    89687       C
                                CCTGGC AACATGGTGAA
                                |||||| ||||||||||
                                GGACCG TTGTGCCACTT
                                   A
GAM962   LOC199725 5'  GGGATTTCACCATGTTGGTCAG 91423                CT
           G                     CCTGGCCAACATGGTGAAA  CC
                                ||||||||||||||||||  ||
                                GGACTGGTTGTACCACTTT  GG
                                          AG
GAM962   LOC199786 3'  GGTTTCACCATGTTGGTCAGG  89762
                                CCTGGCCAACATGGTGAAACT
                                |||||||||||||||||||
                                GGACTGGTTGTACCACTTTGG

GAM962   LOC199786 3'  TGGGGTTTCACCATGTTGGCCA 89771
           GG                     CCTGGCCAACATGGTGAAACTCCA
                                |||||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGGGT

GAM962   LOC200000 3'  GAGTTTCAGTGGTCCA      91521     _   A ATGG
                                TGG CCA C    TGAAACTC
                                ||| ||| |    ||||||||
                                ACC GGT G    ACTTTGAG
                                  T   _ _____
GAM962   LOC200014 3'  GGTGTTTCACCATGTTGGTCAG 89942                 T
           G                     CCTGGCCAACATGGTGAAAC CC
                                |||||||||||||||||| ||
                                GGACTGGTTGTACCACTTTG GG
                                          T
GAM962   LOC200169 5'  GGAGTTTCACCATGTTGGCCA  91559
                                TGGCCAACATGGTGAAACTCC
                                |||||||||||||||||||
                                ACCGGTTGTACCACTTTGAGG

GAM962   LOC200310 3'  GGGGTTTCACCATGTTGGTCAG 66331
           G                     CCTGGCCAACATGGTGAAACTCC
                                |||||||||||||||||||||
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                                GGACTGGTTGTACCACTTTGGGG

GAM962   LOC200314 3'  TGGGGTTTCACCACGTTGGCCA 91607          A
                 G                  CTGGCCAAC TGGTGAAACTCCA
                                    ||||||||| ||||||||||||
                                    GACCGGTTG ACCACTTTGGGGT
                                       C
GAM962   LOC200316 3'  GGAGTTTCACTCTGTCGCCCAG 90185      CCA   T
                                    CTGG   ACA GGTGAAACTCC
                                    ||||   ||| ||||||||||
                                    GACC   TGT TCACTTTGAGG
                                      CGC   C
GAM962   LOC200316 3'  TGGGTTTCACCATGTTGGCCAG 90199                T
                 G                  CCTGGCCAACATGGTGAAAC CCA
                                    |||||||||||||||||| |||
                                    GGACCGGTTGTACCACTTTG GGT
                                                       _
GAM962   LOC201173 5'  GGAGTTTCACCATGTTGGTCAG 88689
                 G                  CCTGGCCAACATGGTGAAACTCC
                                    ||||||||||||||||||||||
                                    GGACTGGTTGTACCACTTTGAGG

GAM962   LOC201220 5'  TGGAGTTTCACCATGTTGGTCA 88729
                 GG                   CCTGGCCAACATGGTGAAACTCCA
                                      ||||||||||||||||||||||
                                      GGACTGGTTGTACCACTTTGAGGT

GAM962   LOC201294 3'  GGGGTTTCACCATGTTGGCCAG 89591
                 G                  CCTGGCCAACATGGTGAAACTCC
                                    ||||||||||||||||||||||
                                    GGACCGGTTGTACCACTTTGGGG

GAM962   LOC201411 3'  GGGTTTCACCATGTTGGTCAGG 63646
                                    CCTGGCCAACATGGTGAAACTC
                                    |||||||||||||||||||
                                    GGACTGGTTGTACCACTTTGGG

GAM962   LOC201626 3'  TGGGGTTTCGCCACGTTGGCCA 90440          A
                 GG                   CCTGGCCAAC TGGTGAAACTCCA
                                      |||||||||| ||||||||||||
                                      GGACCGGTTG ACCGCTTTGGGGT
                                         C
GAM962   LOC202460 5'  TTCACCATGTAGGCCAGG    90685        A
                                    CCTGGCC ACATGGTGAA
                                    ||||||| ||||||||||
                                    GGACCGG TGTACCACTT
                                       A
GAM962   LOC202934 3'  GAGCCACCACACTTGGCCAG   92040        CA_    AAA
                                    CTGGCCAA   TGGTG   CTC
                                    ||||||||   |||||   |||
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                                GACCGGTT   ACCAC   GAG
                                     CAC    C__
GAM962   LOC202934 3'  GGGTTTCACCACGTTGGCCAGG 92045          A
                                CCTGGCCAAC TGGTGAAACTC
                                |||||||||| ||||||||||
                                GGACCGGTTG ACCACTTTGGG
                                      C
GAM962   LOC203197 3'  TGGGGTTTCGCCATGTTGGCCA 90821
                                TGGCCAACATGGTGAAACTCCA
                                |||||||||||||||||||||
                                ACCGGTTGTACCGCTTTGGGGT

GAM962   LOC203339 3'  TGGGGTTTCACCATGTTTGCCA 92219       C
           GG                     CCTGGC AACATGGTGAAACTCCA
                                |||||| ||||||||||||||||
                                GGACCG TTGTACCACTTTGGGGT
                                    T
GAM962   LOC203350 3'  TTCACCGTGTTGGCCAGG    92252
                                CCTGGCCAACATGGTGAA
                                ||||||||||||||||
                                GGACCGGTTGTGCCACTT

GAM962   LOC204804 3'  TTCACCTTGTTGGCCAGG    91057          T
                                CCTGGCCAACA GGTGAA
                                |||||||||| ||||||
                                GGACCGGTTGT CCACTT
                                      T
GAM962   LOC205251 5'  GGGTTTCACCATGTTAACCAG  92359     CC
                                CTGG  AACATGGTGAAACTC
                                ||||  ||||||||||||||
                                GACC  TTGTACCACTTTGGG
                                  AA
GAM962   LOC219445 5'  GGTGTTTCACCATATTGGCCAG 93214         C        T
           G                     CCTGGCCAA ATGGTGAAAC CC
                                ||||||||| |||||||||| ||
                                GGACCGGTT TACCACTTTG GG
                                      A         T
GAM962   LOC219445 5'  TTCACCGTGTTAGCCAGG    93219       C
                                CCTGGC AACATGGTGAA
                                |||||| ||||||||||
                                GGACCG TTGTGCCACTT
                                   A
GAM962   LOC219673 5'  TTCACCATGTTGGCCAGG    94637
                                CCTGGCCAACATGGTGAA
                                ||||||||||||||||
                                GGACCGGTTGTACCACTT

GAM962   LOC219731 5'  GAGTCTTGCTATGTTGTCCAGG 94708       C       TG A
                                CCTGG CAACATGG  A ACTC
                                ||||| ||||||||  | ||||
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                                GGACC GTTGTATC  T TGAG
                                   T       GT C
GAM962   LOC219731 5'  GAGTTTCGTCATGTTGCCCAGG 94709       C       GT
                                CCTGG CAACATG  GAAACTC
                                |||||| |||||||  |||||||
                                GGACC GTTGTAC  CTTTGAG
                                   C       TG
GAM962   LOC219735 3'  TTCACCGTGTTAGCCAGG     94738        C
                                CCTGGC AACATGGTGAA
                                |||||| ||||||||||
                                GGACCG TTGTGCCACTT
                                   A
GAM962   LOC219894 3'  TTCACCGTGTTAGCCAGG     94912        C
                                CCTGGC AACATGGTGAA
                                |||||| ||||||||||
                                GGACCG TTGTGCCACTT
                                   A
GAM962   LOC220074 3'  GGGGTTTCACCATGTTAGCCAG 59987        C
            G                    CCTGGC AACATGGTGAAACTCC
                                |||||| ||||||||||||||||
                                GGACCG TTGTACCACTTTGGGG
                                   A
GAM962   LOC220074 3'  GGTTTCGCCATGTTGGCCAGG  59990
                                CCTGGCCAACATGGTGAAACT
                                |||||||||||||||||||||
                                GGACCGGTTGTACCGCTTTGG

GAM962   LOC220074 3'  TGGGGTTTCGCCATGTTGGCCA 60001
            GG                    CCTGGCCAACATGGTGAAACTCCA
                                |||||||||||||||||||||||||
                                GGACCGGTTGTACCGCTTTGGGGT

GAM962   LOC221060 3'  GGTGTTTCACCATGTTAGTCAG 94834        C           T
            G                    CCTGGC AACATGGTGAAAC CC
                                |||||| |||||||||||| ||
                                GGACTG TTGTACCACTTTG GG
                                   A           T
GAM962   LOC221271 3'  GAATTTCACCATGCTTTGGG   93516     TG CCAA         C
                                CC  G    CATGGTGAAA TC
                                ||  |    |||||||||| ||
                                GG  T    GTACCACTTT AG
                                 GT TC__         A
GAM962   LOC221296 3'  GGGGTTTCACCATGCTGGCCAG 93613          A
            G                    CCTGGCCA CATGGTGAAACTCC
                                |||||||| ||||||||||||||
                                GGACCGGT GTACCACTTTGGGG
                                     C
GAM962   LOC222031 3'  TTCAACATGTTGGCCAGG     95691             G
                                CCTGGCCAACATG TGAA
                                |||||||||||| ||||
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                                GGACCGGTTGTAC ACTT
                                      A
GAM962   LOC222070 5'  GGTGTTTCACCATGTTGGCCAG 95819                T
                G                    CCTGGCCAACATGGTGAAAC CC
                                     |||||||||||||||||| ||
                                     GGACCGGTTGTACCACTTTG GG
                                           T
GAM962   LOC222224 5'  GGGTTTCACCATGTTGGCCAGG 95875
                                     CCTGGCCAACATGGTGAAACTC
                                     |||||||||||||||||||||
                                     GGACCGGTTGTACCACTTTGGG

GAM962   LOC245771 5'  TTCATCATGTTGGCCAGG    94492
                                     CCTGGCCAACATGGTGAA
                                     ||||||||||||||||
                                     GGACCGGTTGTACTACTT

GAM962   LOC253436 3'  AGTTTTATTTGTTGCCCAGG   98110      C    T
                                     CCTGG CAACA GGTGAAACT
                                     ||||| ||||| |||||||||
                                     GGACC GTTGT TTATTTTGA
                                        C    _
GAM962   LOC253612 5'  GAGTTTTGCCATGTTGGCCAGG 98551            TG
                                     CCTGGCCAACATGG  AAACTC
                                     ||||||||||||  ||||||
                                     GGACCGGTTGTACC  TTTGAG
                                           GT
GAM962   LOC253666 3'  GGGGTTTCACCATGTTCGCCAG 96763       C
                G                    CCTGGC AACATGGTGAAACTCC
                                     ||||||| ||||||||||||||||
                                     GGACCG TTGTACCACTTTGGGG
                                        C
GAM962   LOC253842 5'  GTTTCACCACGTTAGCCAGG   99242       C   A
                                     CCTGGC AAC TGGTGAAAC
                                     |||||| ||| |||||||||
                                     GGACCG TTG ACCACTTTG
                                        A   C
GAM962   LOC254018 5'  TGGGGTTTCGCCATGTTAGCCA 98744       C
                GG                     CCTGGC AACATGGTGAAACTCCA
                                       |||||| |||||||||||||||||
                                       GGACCG TTGTACCGCTTTGGGGT
                                          A
GAM962   LOC254057 3'  GAGATCTATGCTGGCCAGG    98781        A    TGAAA
                                     CCTGGCCA CATGG    CTC
                                     |||||||| |||||    |||
                                     GGACCGGT GTATC    GAG
                                          C    TA___
GAM962   LOC254268 3'  TGGGGTTTCACCATGTTGGCCA 97147
                GG                     CCTGGCCAACATGGTGAAACTCCA
                                       ||||||||||||||||||||||||
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                                GGACCGGTTGTACCACTTTGGGGT

GAM962   LOC254295 5'  TTCACCGTGTTAGCCAGG    97899       C
                                CCTGGC AACATGGTGAA
                                |||||| ||||||||||
                                GGACCG TTGTGCCACTT
                                   A
GAM962   LOC254655 3'  GGGGTTTCACCATGTTGGCCAG 97222
           G                     CCTGGCCAACATGGTGAAACTCC
                                 ||||||||||||||||||||||
                                 GGACCGGTTGTACCACTTTGGGG

GAM962   LOC255037 3'  AGTCTCGCTGTGTCACCCAGG  98437      CCA       A
                                CCTGG   ACATGGTGA ACT
                                |||||   ||||||||| |||
                                GGACC   TGTGTCGCT TGA
                                   CAC       C
GAM962   LOC255465 3'  GAGCCACCACACTTGGCCAG   99115       CA_    AAA
                                CTGGCCAA   TGGTG   CTC
                                ||||||||   |||||   |||
                                GACCGGTT   ACCAC   GAG
                                     CAC    C__
GAM962   LOC255465 3'  GGGTTTCACCATGTTGGCCAGG 99120
                                CCTGGCCAACATGGTGAAACTC
                                |||||||||||||||||||||
                                GGACCGGTTGTACCACTTTGGG

GAM962   LOC255497 3'  GGGGTTTCACCATGTTGGCCAG 98989
           G                     CCTGGCCAACATGGTGAAACTCC
                                 ||||||||||||||||||||||
                                 GGACCGGTTGTACCACTTTGGGG

GAM962   LOC255927 5'  TTCACCATCTTGGCCAGG    97714         C
                                CCTGGCCAA ATGGTGAA
                                |||||||| ||||||||
                                GGACCGGTT TACCACTT
                                      C
GAM962   LOC256221 3'  TTCACCGTGTTAGCCAGG    96922       C
                                CCTGGC AACATGGTGAA
                                |||||| ||||||||||
                                GGACCG TTGTGCCACTT
                                   A
GAM962   LOC256306 3'  GGGGTTTCACCATGTTGGCCAG 98519
           G                     CCTGGCCAACATGGTGAAACTCC
                                 ||||||||||||||||||||||
                                 GGACCGGTTGTACCACTTTGGGG

GAM962   LOC257463 3'  TGGAGTCTTGCTATGTTGCCCA 71627      C       TG A
           GG                    CCTGG CAACATGG  A ACTCCA
                                 ||||| ||||||||  | ||||||
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                                GGACC GTTGTATC  T TGAGGT
                                  C       GT C
GAM962  LOC257465 3'  TGGTGTTTCACCATGTTGGCCA 82504                T
           GG                    CCTGGCCAACATGGTGAAAC CCA
                                 |||||||||||||||||||| |||
                                 GGACCGGTTGTACCACTTTG GGT
                                                T
GAM962  LOC257486 3'  GGGGTTTCACCATGTTGGCCAG 69777
           G                     CCTGGCCAACATGGTGAAACTCC
                                 |||||||||||||||||||||||
                                 GGACCGGTTGTACCACTTTGGGG

GAM962  LOC51159  5'  GGGATTTCACCATGTTGGCCAG 33032               CT
           G                     CCTGGCCAACATGGTGAAA  CC
                                 ||||||||||||||||||  ||
                                 GGACCGGTTGTACCACTTT  GG
                                               AG
GAM962  LOC51696  3'  GTTTCACCATGTTAGCTAGG   33090       C
                                 CCTGGC AACATGGTGAAAC
                                 |||||| ||||||||||||
                                 GGATCG TTGTACCACTTTG
                                    A
GAM962  LOC55893  3'  GGAGTTTGGGCTCTGTTGGCTA 38490         T   G_
                                 TGGCCAACA GGT  AAACTCC
                                 |||||||| |||  |||||||
                                 ATCGGTTGT TCG  TTTGAGG
                                       C   GG
GAM962  LOC57146  3'  TGGGGTTTCACCATGTTGGTCA 40300
           GG                    CCTGGCCAACATGGTGAAACTCCA
                                 ||||||||||||||||||||||||
                                 GGACTGGTTGTACCACTTTGGGGT

GAM962  LOC81034  3'  TGGGGTTTCACCATGTTAGCCA 48599       C
           GG                    CCTGGC AACATGGTGAAACTCCA
                                 |||||| ||||||||||||||||
                                 GGACCG TTGTACCACTTTGGGGT
                                    A
GAM962  LOC89932  3'  TGGGGTTTCACCATGTTGGCCA 61478
           GG                    CCTGGCCAACATGGTGAAACTCCA
                                 ||||||||||||||||||||||||
                                 GGACCGGTTGTACCACTTTGGGGT

GAM962  LOC90133  3'  TGGAGCTGCAGACGCTGGCTAG 62292         ACA  G_  AAA
           G                     CCTGGCCA   TG  TG   CTCCA
                                 ||||||||   ||  ||   |||||
                                 GGATCGGT   GC  AC   GAGGT
                                      C__  AG  GTC
GAM962  LOC90288  3'  TGGGGTTTCACCATATTGGTCA 62804         C
           GG                    CCTGGCCAA ATGGTGAAACTCCA
                                 |||||||| ||||||||||||||
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                                GGACTGGTT TACCACTTTGGGGT
                                     A
GAM962  LOC90333  3'  TGGGTTTCACCGTGTTAGCCAG 62968      C          T
                                CTGGC AACATGGTGAAAC CCA
                                ||||| |||||||||||| |||
                                GACCG TTGTGCCACTTTG GGT
                                   A          _
GAM962  LOC90459  3'  GGGGTTTCACCATGTTGGTCAG 63558
              G                  CCTGGCCAACATGGTGAAACTCC
                                 ||||||||||||||||||||||
                                 GGACTGGTTGTACCACTTTGGGG

GAM962  LOC90485  3'  GGGTTTCACCATGTTGGCCAGG 63704
                                 CCTGGCCAACATGGTGAAACTC
                                 |||||||||||||||||||||
                                 GGACCGGTTGTACCACTTTGGG

GAM962  LOC90485  3'  TTCACCATGTTGGCTAGG    63715
                                 CCTGGCCAACATGGTGAA
                                 ||||||||||||||||||
                                 GGATCGGTTGTACCACTT

GAM962  LOC90591  3'  GGAGTTTCATCGTGTTAGCCAG 64176       C
              G                  CCTGGC AACATGGTGAAACTCC
                                 |||||| ||||||||||||||||
                                 GGACCG TTGTGCTACTTTGAGG
                                    A
GAM962  LOC90591  3'  GGGGCTTCACTATGTTGGCCAG 64178              A
              G                  CCTGGCCAACATGGTGAA CTCC
                                 |||||||||||||||||| ||||
                                 GGACCGGTTGTATCACTT GGGG
                                           C
GAM962  LOC91250  5'  TTCATCATGTTGGCCAGG    65926
                                 CCTGGCCAACATGGTGAA
                                 ||||||||||||||||||
                                 GGACCGGTTGTACTACTT

GAM962  LOC91893  3'  TTCACCGTGTTAGCCAGG    68082       C
                                 CCTGGC AACATGGTGAA
                                 |||||| ||||||||||
                                 GGACCG TTGTGCCACTT
                                    A
GAM962  LOC92017  3'  GGAATTTTTATTATCCAGG   68491      CCAAC       C_
                                 CCTGG    ATGGTGAAA  TCC
                                 |||||    |||||||||  |||
                                 GGACC    TATTATTTT  AGG
                                    _____       TA
GAM962  LOC92267  3'  TGGGGTTTCACCATATTGGCCA 69181         C
              GG                   CCTGGCCAA ATGGTGAAACTCCA
                                   ||||||||| ||||||||||||||
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                                GGACCGGTT TACCACTTTGGGGT
                                     A
GAM962  LOC92303  3'  TGGGTTTCACCATGTTGGCCAG 69399                T
            G                    CCTGGCCAACATGGTGAAAC CCA
                                 |||||||||||||||||| |||
                                 GGACCGGTTGTACCACTTTG GGT
                                                  _
GAM962  LOC92689  3'  GGGTTTCACCATGTTGGCCAGG 70778
                                 CCTGGCCAACATGGTGAAACTC
                                 |||||||||||||||||||||
                                 GGACCGGTTGTACCACTTTGGG

GAM962  LOC92841  3'  GGGGTTTCACCATGTTAGCCAG 71259       C
            G                    CCTGGC AACATGGTGAAACTCC
                                 |||||| ||||||||||||||||
                                 GGACCG TTGTACCACTTTGGGG
                                    A
GAM962  LOC93206  3'  GGAGTTTCCCTCTGTTGCCCAG 72191      C    T_  T
            G                    CCTGG CAACA  GG GAAACTCC
                                 ||||| |||||  || ||||||||
                                 GGACC GTTGT  CC CTTTGAGG
                                   C    CT  _
GAM962  LOC93349  3'  GGGGTTTCACTATGTTGGCCAG 57273
            G                    CCTGGCCAACATGGTGAAACTCC
                                 |||||||||||||||||||||||
                                 GGACCGGTTGTATCACTTTGGGG

GAM962  LOC93408  5'  GAGTTTCACCATGTTGCTTAGG 57286      C
                                 CCTGG CAACATGGTGAAACTC
                                 ||||| ||||||||||||||||
                                 GGATT GTTGTACCACTTTGAG
                                   C
GAM963  SCAMP1    3'  GCTAAATAAATATTCTCC    18013    T    C
                                 GGA AATATT ATTTAGC
                                 ||| |||||| |||||||
                                 CCT TTATAA TAAATCG
                                   C     A
GAM963  SCAMP1    3'  GCTAAATAAATATTCTCC    54501    T    C
                                 GGA AATATT ATTTAGC
                                 ||| |||||| |||||||
                                 CCT TTATAA TAAATCG
                                   C     A
GAM963  NX-17     3'  TGAATATCAGCCCCTAATA   40706       ATA_
                                 TATTAGGG   ATATTCA
                                 ||||||||   |||||||
                                 ATAATCCC   TATAAGT
                                      CGAC
GAM963  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
            TA                     TATTAGGGATAATATTCATTTAGC
                                 ||||||||||||||||||||||||
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                                ATAATCCCTATTATAAGTAAATCG

GAM964  G6PD    5'  GGCTGCGAGCGCGGAGGGC   6388        ACATG  _
                                GCCCTCT    GC TTCGCAGCC
                                |||||||    || |||||||||
                                CGGGAGG    CG GAGCGTCGG
                                    ______ C
GAM964  HKE4    3'  GGCTAAATGGGGCCATGAAGAA 23711    C   A       C__
          GGC                     GCC TCT CATGGCTTCG   AGCC
                                |||  ||| ||||||||||   ||||
                                CGG AGA GTACCGGGGT   TCGG
                                  A   A        AAA
GAM964  HTRA3   3'  GCTGCGGGGTGTGAGG     90582     T  ATG
                                CCTC AC   GCTTCGCAGC
                                ||||  ||   ||||||||||
                                GGAG TG   TGGGGCGTCG
                                  _  ___
GAM964  MATK    3'  GGGCTGGCCCACGTAGGGGGC  58451        AT_  TTCG
                                GCCCTCTAC   GGC   CAGCCC
                                |||||||||   |||   ||||||
                                CGGGGGATG   CCG   GTCGGG
                                     CAC  _____
GAM964  MATK    3'  GGGCTGGCCCACGTAGGGGGC  58452        AT_  TTCG
                                GCCCTCTAC   GGC   CAGCCC
                                |||||||||   |||   ||||||
                                CGGGGGATG   CCG   GTCGGG
                                     CAC  _____
GAM964  MATK    3'  GGGCTGGCCCACGTAGGGGGC  11466        AT_  TTCG
                                GCCCTCTAC   GGC   CAGCCC
                                |||||||||   |||   ||||||
                                CGGGGGATG   CCG   GTCGGG
                                     CAC  _____
GAM964  MGEA5   5'  GGCTGCGGCTGACAAAGGGC  25222      CTACAT   TT
                                GCCCT     GGC  CGCAGCC
                                |||||     |||  |||||||
                                CGGGA     TCG  GCGTCGG
                                   AACAG_  __
GAM964  RAD50   3'  GGGCATTGCCATGTGGAAGGC  56821     C        TTCGCA
                                GCC TCTACATGGC     GCCC
                                |||  ||||||||||     ||||
                                CGG AGGTGTACCG     CGGG
                                  A         TTA___
GAM964  RAD50   3'  GGGCATTGCCATGTGGAAGGC  20412     C        TTCGCA
                                GCC TCTACATGGC     GCCC
                                |||  ||||||||||     ||||
                                CGG AGGTGTACCG     CGGG
                                  A         TTA___
GAM964  RBBP9   3'  GGATCAGAGCCATGTGGAGAGC 70693     C          CGCAG
                                GC CTCTACATGGCTT     CC
                                ||  ||||||||||||     ||
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                                CG GAGGTGTACCGAG    GG
                                 A          ACTA_
GAM964  TMEPAI   3' GGGCTGCGTAGGTGAAAAGGC 39829    CTCTA   GG  T
                                GCC    CAT  CT CGCAGCCC
                                |||    |||  || ||||||||
                                CGG    GTG  GA GCGTCGGG
                                  AAAA_  __  T
GAM964  TNFRSF1B  5' GGGCTGCGAGGGCGCGAGGGC 8399       TACA  G
                                GCCCTC   TG CTTCGCAGCCC
                                ||||||   || ||||||||||
                                CGGGAG   GC GGAGCGTCGGG
                                   C___  G
GAM964  C20orf139 5' GGCTGGGCCATGCAGAAGGG  85921     _ A     TCG
                                CCCT CT CATGGCT   CAGCC
                                |||| || |||||||   |||||
                                GGGA GA GTACCGG   GTCGG
                                  A  C     ___
GAM964  DKFZP586M1019 5' GCTGCGGTCGCAGAGG     32172      ACA   TT
                                CCTCT   TGGC  CGCAGC
                                |||||   ||||  ||||||
                                GGAGA   GCTG  GCGTCG
                                  C__   __
GAM964  FLJ10511  5' GGCTGCGAACCGAAGGGC    36689      CTACA   C
                                GCCCT    TGG TTCGCAGCC
                                |||||    ||| |||||||||
                                CGGGA    GCC AAGCGTCGG
                                  A____  _
GAM964  FLJ12592  3' TTGCTGAAGCCACGTAGAAGC  50657    CC    A     _
                                GC  TCTAC TGGCTTC GCAG
                                ||  ||||| ||||||| ||||
                                CG  AGATG ACCGAAG CGTT
                                 A_    C      T
GAM964  FLJ13782  3' GGCCTGCTGCCATGTGAGAGC  46703    C   T     TTC   _
                                GC CTC ACATGGC   GCAG CC
                                || ||| |||||||   |||| ||
                                CG GAG TGTACCG   CGTC GG
                                 A  _      T__   C
GAM964  FLJ22173  5' GGCTGCGGGGTCCAAGAGG   47399      ACA  _
                                CCTCT   TGG CTTCGCAGCC
                                |||||   ||| ||||||||||
                                GGAGA   ACC GGGGCGTCGG
                                  ___   T
GAM964  FLJ22938  3' CTGGGTTCAAGTAGAGGGC   45483        A  CT  G
                                GCCCTCTAC TGG  TC CAG
                                ||||||||| |||  || |||
                                CGGGAGATG ACT  GG GTC
                                     A  T_ _
GAM964  GABBR1   5' GCCGCGGGGGCCGTAGGAAGC  41861    CC    AT    _ A
                                GC  TCTAC  GGCTTC GC GC
                                ||  |||||  |||||| || ||
```

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                                CG  GGATG  CCGGGG CG CG
                                 AA    __     G  C
GAM964  GCHFR    3'  GCCCAAGCCAATAAAGGGC   19148      C  CA     C_
                                GCCCT TA  TGGCTT  GC
                                |||||  ||  ||||||  ||
                                CGGGA AT  ACCGAA  CG
                                   A  A_     CC
GAM964  HSJ001348 5'  GGCTGCGAAGGTTCCAGAAGGG 62858      CTACA  ___
           C                     GCCCT    TGG   CTTCGCAGCC
                                |||||    |||  ||||||||||
                                CGGGA    ACC   GAAGCGTCGG
                                   AG___  TTG
GAM964  HSPC142   5'  GCCGAAGCCACACAGGAGC   27187    _  CTACA      CA
                                GC CCT    TGGCTTCG  GC
                                || |||    ||||||||  ||
                                CG GGA    ACCGAAGC  CG
                                 A  CAC__      __
GAM964  KIAA1821  3'  GGCTGCGAGGTAGTAGA     72269      ATG
                                TCTAC   GCTTCGCAGCC
                                |||||   ||||||||||
                                AGATG   TGGAGCGTCGG
                                   A__
GAM964  MAPK8IP3  3'  GGGCTGCGCCCGTGTGAGGGC  54143       T     CTT
                                GCCCTC ACATGG   CGCAGCCC
                                |||||| ||||||   ||||||||
                                CGGGAG TGTGCC   GCGTCGGG
                                   _     C__
GAM964  MGC10871  3'  GGGCTGCGGTCATATATGAG   96428     _ C    TT
                                CTC TA ATGGC  CGCAGCCC
                                ||| || |||||  ||||||||
                                GAG AT TACTG  GCGTCGGG
                                  T  A    __
GAM964  MGC12904  3'  GGGCCCTAGGCCATGGAGA   49163     A      CGCA
                                TCT CATGGCTT    GCCC
                                ||| ||||||||    ||||
                                AGA GTACCGGA    CGGG
                                  G       TCC_
GAM964  MGC15873  3'  GCTGCGGGGCTGGAGAAGGC   53006     C   ACAT
                                GCC TCT    GGCTTCGCAGC
                                ||| |||    ||||||||||
                                CGG AGA    TCGGGGCGTCG
                                  A   GG__
GAM964  N4BP3     5'  GCTGCGACGCGCAAGGGC    66857      CTACA  _  T
                                GCCCT    TG GC TCGCAGC
                                |||||    || || |||||||
                                CGGGA    AC CG AGCGTCG
                                   _____  G  C
GAM964  SEMA4B    3'  GGCTGTGGCCACACGAGAGG   69599      ACA_   TT
                                CCTCT    TGGC  CGCAGCC
                                |||||    ||||  |||||||
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                                GGAGA   ACCG  GTGTCGG
                                  GCAC   __
GAM964  LOC143188 5'  GCTGAGAAGCCATACAGGGGC  83793     T  AC      G
                                GCCC CT  ATGGCTTC CAGC
                                |||| ||  |||||||| ||||
                                CGGG GA  TACCGAAG GTCG
                                  _ CA       A
GAM964  LOC146713 5'  GCCATTCCGTGTAGAGGGC   84733          CTTC
                                GCCCTCTACATGG   GC
                                ||||||||||||   ||
                                CGGGAGATGTGCC   CG
                                       TTAC
GAM964  LOC196051 5'  GCTGCGGGAGCCGCGGAGAGC  88958   C   ACA     _
                                GC CTCT   TGGCTTC GCAGC
                                || ||||   ||||||| |||||
                                CG GAGG   GCCGAGG CGTCG
                                 A   C__      G
GAM964  LOC200169 5'  GCGGGGCCGTACAGAGAGC   91557   C   AC
                                GC CTCT  ATGGCTTCGC
                                || ||||  ||||||||||
                                CG GAGA  TGCCGGGGCG
                                 A   CA
GAM964  LOC221228 3'  GGGCTGCGTCTGCAAAGGGGC  93420     T  ACATG  TT_
                                GCCC CT    GC   CGCAGCCC
                                |||| ||    ||   ||||||||
                                CGGG GA    CG   GCGTCGGG
                                  _ AA___  TCT
GAM964  LOC257065 5'  GGCTGCGAAGAACGCAGAAGC  99473   CC   ACATGG
                                GC  TCT     CTTCGCAGCC
                                ||  |||     ||||||||||
                                CG  AGA     GAAGCGTCGG
                                 A_   CGCAA_
GAM964  LOC51762  3'  CTGCAGCACACCTAGAGGGC   33705       CA  _   TC
                                GCCCTCTA  TG GCT  GCAG
                                ||||||||  || |||  ||||
                                CGGGAGAT  AC CGA  CGTC
                                     CC  A   __
GAM965  FLJ22332  5'  GGAAAGAAAACTACATCACA   45637     G  A      _______
                                TGTG AT TAGTTTTC     CC
                                |||| || ||||||||     ||
                                ACAC TA ATCAAAAG     GG
                                  _ C       AAA___
GAM966  AMACR     3'  TTGTATGCATGGAAACATGGA  69103      ATC       G
                                TCCAT   TCCATGCATG CGG
                                |||||   |||||||||| |||
                                AGGTA   AGGTACGTAT GTT
                                  CAA       _
GAM966  BCL2L11   3'  TCGCCCAGAGATATGGA     57615         CA  CAT   G
                                TCCATATCTC  TG   GGCG A
                                ||||||||||  ||   |||| |
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                                AGGTATAGAG  AC   CCGC T
                                   __ ____   G
GAM966  BCL2L11  3' TCGCCCAGAGATATGGA    57616        CA CAT   G
                                TCCATATCTC  TG   GGCG A
                                ||||||||||  ||   |||| |
                                AGGTATAGAG  AC   CCGC T
                                   __ ____   G
GAM966  FGFR2    5' CGTCCACATGGAGATATGGA  43633          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                   __  T
GAM966  FGFR2    5' CGTCCACATGGAGATATGGA  43638          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                   __  T
GAM966  FGFR2    5' CGTCCACATGGAGATATGGA  43642          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                   __  T
GAM966  FGFR2    5' CGTCCACATGGAGATATGGA  43652          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                   __  T
GAM966  FGFR2    5' CGTCCACATGGAGATATGGA  43665          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                   __  T
GAM966  FGFR2    5' CGTCCACATGGAGATATGGA  43674          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                   __  T
GAM966  FGFR2    5' CGTCCACATGGAGATATGGA  43678          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                   __  T
GAM966  FGFR2    5' CGTCCACATGGAGATATGGA  43763          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                   __  T
GAM966  FGFR2    5' CGTCCACATGGAGATATGGA  43767          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
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                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM966  FGFR2    5'  CGTCCACATGGAGATATGGA  43771          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM966  FGFR2    5'  CGTCCACATGGAGATATGGA  5559           CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM966  MAP3K14  3'  ATCCGCCACGTGAAGAGA   15541     CA  A
                                TCTC  TGC TGGCGGAT
                                ||||  ||| ||||||||
                                AGAG  GTG ACCGCCTA
                                  AA  C
GAM966  KIAA0819 3'  CCCCAGCATCACAGGAGACATG 64330      A   ____   A  C
           GA                     TCCAT TCTCC   ATGC TGG GG
                                ||||| |||||   |||| ||| ||
                                AGGTA AGAGG   TACG ACC CC
                                  C    ACAC   _  _
GAM966  PORIMIN  3'  CATACATGGAGTATGGA    54702       T     C
                                TCCATA CTCCATG ATG
                                |||||| ||||||| |||
                                AGGTAT GAGGTAC TAC
                                   _     A
GAM966  RDC1     3'  CCGGCACGGGATATGGA     72832        T  A  A
                                TCCATATC CC TGC TGG
                                |||||||| || ||| |||
                                AGGTATAG GG ACG GCC
                                    _ C  _
GAM966  VEZATIN  3'  ATCCGCCACAACAGACAATG  34656    A_  CCA  CA
                                CAT  TCT   TG  TGGCGGAT
                                |||  |||   ||  ||||||||
                                GTA  AGA   AC  ACCGCCTA
                                  AC   CA_ __
GAM966  LOC147645 5'  ATCCGCTGGTGGCAGAGACACG 79065    ATA   CA  AT__
           G                     CC   TCTC  TGC   GGCGGAT
                                ||   ||||  |||   |||||||
                                GG   AGAG  ACG   TCGCCTA
                                 CAC   __  GTGG
GAM966  LOC199775 3'  TTGCTGCATCAGAGATATG   89726       C_   TG
                                CATATCTC  ATGCA  GCGG
                                ||||||||  |||||  ||||
                                GTATAGAG  TACGT  CGTT
                                    AC    __
GAM966  LOC51279  3'  CCGCTATTAGAGTATGGA    33752       T  CATGC
                                TCCATA CTC    ATGGCGG
                                ||||||  |||    |||||||
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                                AGGTAT GAG    TATCGCC
                                   _  AT___
GAM967  CCND2    3'  TAGATGAACCTGCAGCAAGCAG 10054      CCCGG  T_   C
                                CTGCTT    TGC  GTTCA CTA
                                ||||||    |||  ||||| |||
                                GACGAA    ACG  CAAGT GAT
                                   CG___  TC    A
GAM967  CYP3A5   5'  AGGCAAACAGCCCAGCAAACAG 7583      TCCC___  T    CA
           CAG                    CTGCT      GG GCTGTT  CCT
                                |||||      || ||||||  |||
                                GACGA      CC CGACAA  GGA
                                   CAAACGA  _     AC
GAM967  DNASE1L1 3'  AGCAAACACCGGGAAACA    23014    C       C_
                                TG TTCCCGGTG  TGTT
                                || |||||||||  ||||
                                AC AAGGGCCAC  ACGA
                                 A        AA
GAM967  EGLN2    5'  AGGCAAGAGAACCAGGAGGCAG 55776       C   G  G  CA
                                CTGCTTCC GGT CT TT  CCT
                                |||||||| ||| || ||  |||
                                GACGGAGG CCA GA AA  GGA
                                     A   A  G  C_
GAM967  FANCC    3'  AGGTGCCACCGGGAAG      71031         CTGTT
                                CTTCCCGGTG    CACCT
                                ||||||||||    |||||
                                GAAGGGCCAC    GTGGA
                                      C_____
GAM967  NDUFS2   5'  TAGGTGAGAAGCCAAGAAGGAG 17044    G   CC   GCTG
                                CT CTTC  GGT   TTCACCTA
                                || ||||  |||   ||||||||
                                GA GAAG  CCG   GAGTGGAT
                                 G   AA   AA__
GAM967  NEK6     3'  AGGCAAAAGGCATCGGGAAGCA 27701             GTTCA
           G                     CTGCTTCCCGGTGCT    CCT
                                |||||||||||||||    |||
                                GACGAAGGGCTACGG    GGA
                                         AAAAC
GAM967  REGL     3'  TAGGTGAACATTCCAGGAA   22502     C  TGC
                                TTCC GG   TGTTCACCTA
                                |||| ||   ||||||||||
                                AAGG CC   ACAAGTGGAT
                                  A  TT_
GAM967  SEZ6L    5'  AGGTGAACTCTGCCAGGAAGCA 41202       C    CT
           G                     CTGCTTCC GGTG  GTTCACCT
                                |||||||| ||||  ||||||||
                                GACGAAGG CCGT  CAAGTGGA
                                     A    CT
GAM967  SFRP4    3'  AGCAGCACCAGAAACAG     13029     C   CC
                                CTG TTC  GGTGCTGTT
                                ||| |||  |||||||||
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                                GAC AAG  CCACGACGA
                                  A  A_
GAM967  SPG4     3'  AGATGAAAGTATTCCAGGAACA 30807     C   C __   G   C
                G                  CTG TTCC GG  TGCT TTCA CT
                                   ||| |||| ||  |||| |||| ||
                                   GAC AAGG CC  ATGA AAGT GA
                                     _   A  TT   _   A
GAM967  BANP     5'  TAGGTGAACACTGAGAAGGCAG 66804      _  C   GCT
                                   CTGC TTC CGGT   GTTCACCTA
                                   |||| ||| ||||   |||||||||
                                   GACG AAG GTCA   CAAGTGGAT
                                     G  A   ___
GAM967  C14orf4  5'  GTCTGCAGCACCAGGAAG    67921       C       TC
                                   CTTCC GGTGCTGT  AC
                                   ||||| ||||||||  ||
                                   GAAGG CCACGACG  TG
                                      A       TC
GAM967  C6orf37  3'  TAGGTGAAACCAAAAAGC    68094     CCC   GCTG
                                   GCTT   GGT   TTCACCTA
                                   ||||   |||   ||||||||
                                   CGAA   CCA   AAGTGGAT
                                     AAA   _____
GAM967  CCR7     3'  GACAACACTGGGAAACAG    10223     C       C
                                   CTG TTCCCGGTG TGTT
                                   ||| |||||||| ||||
                                   GAC AAGGGTCAC ACAG
                                     A       A
GAM967  DKFZP586F1524 3'  AGGCTTGGTCACCGGGAAG    32103          _   TTCA
                                   CTTCCCGGTG CTG   CCT
                                   |||||||||| |||   |||
                                   GAAGGGCCAC GGT   GGA
                                         T  TC__
GAM967  FLJ14153  3'  AGGTGAACTTCAGGAAAGACAG 43010     _  C  GG  CT
                                   CTG CTT CC  TG  GTTCACCT
                                   ||| ||| ||  ||  ||||||||
                                   GAC GAA GG  AC  CAAGTGGA
                                     A  A __  TT
GAM967  GPR      5'  GTGAGGGGCTGGGAAGCAG   24294          G  GT
                                   CTGCTTCCCGGT CT  TCAC
                                   |||||||||||| ||  ||||
                                   GACGAAGGGTCG GG  AGTG
                                         G  __
GAM967  H2AFJ    3'  AGGTAAACAGCATTCTAGCA   37379      TCCC       C
                                   TGCT   GGTGCTGTT ACCT
                                   ||||   |||||||| ||||
                                   ACGA   TTACGACAA TGGA
                                     TC__       A
GAM967  KIAA0125  3'  GTGACAACCGGGAACA     61128    C      GC   T
                                   TG TTCCCGGT  TGT CAC
                                   || ||||||||  ||| |||
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                                AC AAGGGCCA  ACA GTG
                                 _      __  _
GAM967  KIAA0427 3'  AGATGAAGCTTCCCAGCCGGGA 29371    C      _______  GT  C
              AACA                  TG TTCCCGGT     GCT  TCA CT
                                || ||||||||     |||  ||| ||
                                AC AAGGGCCG     CGA  AGT GA
                                 A       ACCCTT   __  A
GAM967  KIAA0993 3'  AGGTGAACAGCACAAGAAG   64817     CCG
                                CTTC   GTGCTGTTCACCT
                                ||||   ||||||||||||||
                                GAAG   CACGACAAGTGGA
                                  AA_
GAM967  KIAA1163 3'  GACATGTCTCCCAGGAAGCAG  79649        C  T__  _
                                CTGCTTCC GG   GC TGTT
                                |||||||| ||   || ||||
                                GACGAAGG CC   TG ACAG
                                     A  CTC  T
GAM967  MGC13071 3'  AGGTGGCCCCCCAGGAAGCAG  52064        C  TGCT  T
                                CTGCTTCC GG    GT CACCT
                                |||||||| ||    || |||||
                                GACGAAGG CC    CG GTGGA
                                     A  CCC_  _
GAM967  MGC16142 3'  AGATGAACTCTGGAAGCAG    52258        C  TGCT    C
                                CTGCTTCC GG    GTTCA CT
                                |||||||| ||    ||||| ||
                                GACGAAGG CT    CAAGT GA
                                     T _____    A
GAM967  MGC2562  3'  AGGTTTCCACAGGAAGCAG    51422        CG   CTGTTC
                                CTGCTTCC  GTG     ACCT
                                ||||||||  |||     ||||
                                GACGAAGG  CAC     TGGA
                                     A_   CTT___
GAM967  MGC4832  3'  AGTAGTACCAGGAAGTAG    59655        C
                                CTGCTTCC GGTGCTGTT
                                |||||||| |||||||||
                                GATGAAGG CCATGATGA
                                     A
GAM967  PLSCR2   5'  AGGCTGGACACACTGGGAAACA 40147    C       C    _
              G                   CTG TTCCCGGTG TGTTCA CCT
                                ||| ||||||||| |||||| |||
                                GAC AAGGGTCAC ACAGGT GGA
                                  A       _     C
GAM967  TSLRP    5'  AACAAACCCGGGAGCAG     25929        C   GC
                                CTGCTTCC GGT  TGTT
                                |||||||| |||  ||||
                                GACGAGGG CCA  ACAA
                                     C   A_
GAM967  LOC147172 3'  GAGCAGCAGGAAGCA      78902        CGG
                                TGCTTCC   TGCTGTTC
                                |||||||   ||||||||
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                                ACGAAGG  ACGACGAG
                                   ___
GAM967  LOC149501 3'  GTGAACAGCTGAGGCAG    75801       CCGGT
                                CTGCTTC    GCTGTTCAC
                                |||||||    |||||||||
                                GACGGAG    CGACAAGTG
                                   T____
GAM967  LOC157503 3'  AGGTGAACAGCAAATGGAAG  87762     CGG
                                CTTCC  TGCTGTTCACCT
                                |||||  ||||||||||||
                                GAAGG  ACGACAAGTGGA
                                  TAA
GAM967  LOC158434 5'  AGGCGAAGGACAGGACAGCAG 88159     _  CG  G  GT  A
                                CTGCT TCC  GT CT  TC CCT
                                ||||| |||  || ||  || |||
                                GACGA AGG  CA GA  AG GGA
                                   C  A_  G  __  C
GAM967  LOC199221 5'  GGCAGCTCCAGGAAGCAG   81168       C  T
                                CTGCTTCC GG GCTGTT
                                |||||||| || ||||||
                                GACGAAGG CC CGACGG
                                    A  T
GAM967  LOC203411 5'  TGAACAAAACAGGAAGTAG   92315       CG  GC
                                CTGCTTCC  GT  TGTTCA
                                ||||||||  ||  ||||||
                                GATGAAGG  CA  ACAAGT
                                    A_  AA
GAM967  LOC205355 5'  GAACTTAACACTGGGAAACAG  92362    C       CT__
                                CTG TTCCCGGTG   GTTC
                                ||| |||||||||   ||||
                                GAC AAGGGTCAC   CAAG
                                  A       AATT
GAM967  LOC58504  3'  GGCAGCCACCGGGAACAG    41406    C       _
                                CTG TTCCCGGTG CTGTT
                                ||| ||||||||| |||||
                                GAC AAGGGCCAC GACGG
                                  _       C
GAM968  FLRT1    3'  CCCACGCAGCTCTCCCGCCACT 60365       ACCA__    CG_
           GGCCA                  TGGCCAGT    AGAGT  GTGGG
                                |||||||     |||||  |||||
                                ACCGGTCA    TCTCG  CACCC
                                    CCGCCC    ACG
GAM968  MYF6     3'  CCCACCGACCCTTCCTGGCC  11735      TACC  A
                                GGCCAG   AAG GTCGGTGGG
                                ||||||   ||| |||||||||
                                CCGGTC   TTC CAGCCACCC
                                   C___  C
GAM968  NFIC     3'  CCTGCCGACTCCCAGCCCGGCC 20012     A_  ACCAA     TG
           A                   TGGCC  GT   GAGTCGG  GG
                                |||||  ||   |||||||  ||
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                                ACCGG CG    CTCAGCC CC
                                  CC ACC__      GT
GAM968  PPY      3' CCCTCTGCACCCTTGGCTCTGG 12254        TA    A _   T
            CCA                   TGGCCAG  CCAAG GT CGG GGG
                                  ||||||| ||||| || ||| |||
                                  ACCGGTC  GGTTC CA GTC CCC
                                     TC    C C   T
GAM968  PTPN7    3' CCAGGTCTTCAACACTGGCCA  12593        ACC_   G  GG
                                  TGGCCAGT   AAGA TC  TGG
                                  ||||||||   |||| ||  |||
                                  ACCGGTCA   TTCT GG  ACC
                                     CAAC   _ __
GAM968  PTPN7    3' CCAGGTCTTCAACACTGGCCA  55459        ACC_   G  GG
                                  TGGCCAGT   AAGA TC  TGG
                                  ||||||||   |||| ||  |||
                                  ACCGGTCA   TTCT GG  ACC
                                     CAAC   _ __
GAM968  PTPN7    3' CCAGGTCTTCAACACTGGCCA  55466        ACC_   G  GG
                                  TGGCCAGT   AAGA TC  TGG
                                  ||||||||   |||| ||  |||
                                  ACCGGTCA   TTCT GG  ACC
                                     CAAC   _ __
GAM968  ARTN     3' GACTCTGGCACTGGCCA     15613        A   A
                                  TGGCCAGT CCA GAGTC
                                  |||||||| ||| |||||
                                  ACCGGTCA GGT CTCAG
                                     C   _
GAM968  ARTN     3' GACTCTGGCACTGGCCA     55109        A   A
                                  TGGCCAGT CCA GAGTC
                                  |||||||| ||| |||||
                                  ACCGGTCA GGT CTCAG
                                     C   _
GAM968  ARTN     3' GACTCTGGCACTGGCCA     55117        A   A
                                  TGGCCAGT CCA GAGTC
                                  |||||||| ||| |||||
                                  ACCGGTCA GGT CTCAG
                                     C   _
GAM968  ARTN     3' GACTCTGGCACTGGCCA     55137        A   A
                                  TGGCCAGT CCA GAGTC
                                  |||||||| ||| |||||
                                  ACCGGTCA GGT CTCAG
                                     C   _
GAM968  C1QTNF6  3' CCTGCCCTCAGTGACTGGCCA 49991        ACCAA  TC  TG
                                  TGGCCAGT    GAG  GG  GG
                                  ||||||||    |||  ||  ||
                                  ACCGGTCA    CTC  CC  CC
                                     GTGA_   __  GT
GAM968  DKFZP434G1415 3' CTGATACCCTTGGTATAACCA 49269     CCA      A__
                                  TGG  GTACCAAG  GTCGG
                                  |||  ||||||||  |||||
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                                ACC   TATGGTTC   TAGTC
                                  AA_       CCA
GAM968  DKFZP586F1524 3'  CTGGCTCTTAGCACTGACC    32106    C    ACC
                                GG CAGT   AAGAGTCGG
                                || ||||   |||||||||
                                CC GTCA   TTCTCGGTC
                                 A    CGA
GAM968  DKFZp761B1514 3'  CCCACCGACCCGCCACCTGCCA 51139      C  TACCAAGA
                                TGGC AG       GTCGGTGGG
                                |||| ||       |||||||||
                                ACCG TC       CAGCCACCC
                                  _ CACCGCC_
GAM968  KIAA0843  5'  CCTCTGGCTCCCGACACTGGCC 30798        ACCAA      T
                                GGCCAGT    GAGTCGG GG
                                |||||||    ||||||| ||
                                CCGGTCA    CTCGGTC CC
                                    CAGCC      T
GAM968  KIAA1755  3'  CCACCCTTCATACTGGCCA    62007         CC   AGTC
                                TGGCCAGTA  AAG   GGTGG
                                |||||||||  |||   |||||
                                ACCGGTCAT  TTC   CCACC
                                     AC  _____
GAM968  KREMEN    3'  ACCCTCAGGACTGGCCA     50222         A  AA   TC
                                TGGCCAGT CC  GAG  GGT
                                |||||||| ||  |||  |||
                                ACCGGTCA GG  CTC  CCA
                                    _ A_  __
GAM968  N4BP3     3'  CCCAGTCTGTCTTGGCACTGGC 66846         A     GT  __
            CA                    TGGCCAGT CCAAGA  CGG  TGGG
                                |||||||| ||||||  |||  ||||
                                ACCGGTCA GGTTCT  GTC  ACCC
                                    C     __   TG
GAM968  PRO1843   5'  CCCACTTCTTAGCTACTGGCCA 38141         CC_   GTC
                                TGGCCAGTA   AAGA   GGTGGG
                                |||||||||   ||||   ||||||
                                ACCGGTCAT   TTCT   TCACCC
                                     CGA   ___
GAM968  STI2      3'  CCCACCGACCCCGGGCTGGCTA 90406         A  AAGA
                                TGGCCAGT CC   GTCGGTGGG
                                |||||||| ||   |||||||||
                                ATCGGTCG GG   CAGCCACCC
                                    _ CCC_
GAM968  LOC118611 5'  CCCCCGGCTCTGGCCA      75995       GTACCAA      T
                                TGGCCA      GAGTCGG GGG
                                ||||||      ||||||| |||
                                ACCGGT      CTCGGCC CCC
                                  _______     _
GAM968  LOC149076 3'  CCCAGTCTACCTCGGTGCTGGC 79874           A  A  C  _
            CA                    TGGCCAGTACC AG GT GG TGGG
                                |||||||||| || || || ||||
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                                ACCGGTCGTGG TC CA CT ACCC
                                      C  _  T  G
GAM968  LOC256306 5'  TGACTCTTGATCTGGCCA    98521       TAC
                                TGGCCAG   CAAGAGTCG
                                |||||||   |||||||||
                                ACCGGTC   GTTCTCAGT
                                    TA_
GAM968  LOC90379  3'  CCCACCGACTGATGACCGGC   63202    A  AC  AG
                                GCC GT  CA  AGTCGGTGGG
                                ||| ||  ||  ||||||||||
                                CGG CA  GT  TCAGCCACCC
                                  C  __  AG
GAM969  CR1       3'  TTAATTTACTAGAAAGGCATGA 6953        C_   TGCATC
           A                     TTCATGCC  TCT     GTTAA
                                ||||||||  |||     |||||
                                AAGTACGG  AGA     TAATT
                                    AA   TCATT_
GAM969  LOC135932 3'  TTAACAATGGGTTGGTATGAA  76700       CT  TG   C
                                TTCATGCC  CT  CAT GTTAA
                                ||||||||  ||  ||| |||||
                                AAGTATGG  GG  GTA CAATT
                                    TT  __   A
GAM969  LOC150279 3'  TGAAGCAACAGGGCATGAA    80484        C    A
                                TTCATGCCCT TTGC TCG
                                |||||||||| |||| |||
                                AAGTACGGGA AACG AGT
                                      C    A
GAM969  LOC161829 5'  TAACGATGGAGGACAGTGAA   83194      GCCC    G
                                TTCAT    TCTT CATCGTTA
                                |||||    |||| ||||||||
                                AAGTG    AGGA GTAGCAAT
                                   AC__    G
GAM969  LOC199918 3'  TAACAATGCTGGTATGAA    91475       CTCTT    C
                                TTCATGCC     GCAT GTTA
                                ||||||||     |||| ||||
                                AAGTATGG     CGTA CAAT
                                    T____    A
GAM969  LOC54516  3'  TAACTTTTAAGAGGGATGAA   39284      G       CATC
                                TTCAT CCCTCTTG    GTTA
                                ||||| ||||||||    ||||
                                AAGTA GGGAGAAT    CAAT
                                   _       TTT_
GAM969  LOC92181  5'  ACGCAGCAAGAGGGATGAA    68940      G       AT
                                TTCAT CCCTCTTGC  CGT
                                ||||| |||||||||  |||
                                AAGTA GGGAGAACG  GCA
                                   _       AC
GAM970  LILRB4    3'  ATATGCCCAGCTGCACAG    23383     _  T
                                TTG GC GCTGGGCATAT
                                ||| || ||||||||||
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                                GAC CG CGACCCGTATA
                                  A  T
GAM970  DKFZP566C243 3'  GCTCTGCAGCCAATGCAGA   31811            T
                                TCTGCATTGGCTGC GGGC
                                |||||||||||||| ||||
                                AGACGTAACCGACG CTCG
                                       T
GAM970  FLJ20034  3'  CATACCCAGCAGCCTGCAGA  34838      TT       CA
                                TCTGCA  GGCTGCTGGG  TATG
                                ||||||  ||||||||||  ||||
                                AGACGT  CCGACGACCC  ATAC
                                  __      __
GAM970  LOC149837 3'  CATATGCCCCCATCAAGCAGA  85892      A   C  CT
                                TCTGC TTGG TG  GGGCATATG
                                ||||| |||| ||  |||||||||
                                AGACG AACT AC  CCCGTATAC
                                  _   _  C_
GAM970  LOC155438 3'  CAGAACAGCCAATGCAGG    87683           __
                                TCTGCATTGGCTG  CTG
                                ||||||||||||  |||
                                GGACGTAACCGAC  GAC
                                       AA
GAM970  LOC163682 5'  ATGCAGCAGCCATGCAGA    88397       T     GG
                                TCTGCAT GGCTGCT  GCAT
                                |||||||  |||||||  ||||
                                AGACGTA CCGACGA  CGTA
                                  _     __
GAM971  ADAM11   3'  GCCGGATTTGCTCCCACCACGG 41491        AA   __
                                CCGTGGTG  GGGCA  TCCGGC
                                ||||||||  |||||  ||||||
                                GGCACCAC  CTCGT  AGGCCG
                                    C_    TT
GAM971  AP2B1    3'  CCTGTTGCCTCCACCACGG   8891         AA   TCC
                                CCGTGGTG  GGGCA   GG
                                ||||||||  |||||   ||
                                GGCACCAC  TCCGT   CC
                                    C_    TGT
GAM971  BCL7A    3'  GCTGGGCCCCACCACGG     40986        AA   AT
                                CCGTGGTG  GGGC  CCGGC
                                ||||||||  ||||  |||||
                                GGCACCAC  CCCG  GGTCG
                                  __    __
GAM971  CARD4    3'  GTTGGACACCCCCCACCATGGT 21442         AA  CA
                                ACCGTGGTG  GGG  TCCGGC
                                |||||||||  |||  ||||||
                                TGGTACCAC  CCC  AGGTTG
                                    CC   AC
GAM971  FBN1     3'  CCAGTGCATCCTTCATCAC   65038          __   CC
                                GTGGTGAAGG  GCAT  GG
                                ||||||||||  ||||  ||
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                                CACTACTTCC  CGTG  CC
                                      TA    A_
GAM971  FGF12    3'  CCATATCCTTCACCAGGT    41059     G       GC  CC
                                ACC TGGTGAAGG  AT  GG
                                ||| |||||||||  ||  ||
                                TGG ACCACTTCC  TA  CC
                                  _       TA  __
GAM971  IRS1     5'  GCCTCCGCCCCCCACCCGGT   19878     T   AA   ATCC
                                ACCG GGTG  GGGC   GGC
                                |||| ||||  ||||   |||
                                TGGC CCAC  CCCG   CCG
                                  _   CC   CCT_
GAM971  PPP1R12A 3'  GCCAAATGCCCTCTTATC    11753      _     CC
                                GGTGA AGGGCAT  GGC
                                ||||| |||||||  |||
                                CTATT TCCCGTA  CCG
                                   C      AA
GAM971  RFX2     3'  GCCGGATGCCCCGAGGCGG   7159      GG  AA
                                CCGT  TG  GGGCATCCGGC
                                ||||  ||  ||||||||||
                                GGCG  GC  CCCGTAGGCCG
                                  GA  __
GAM971  RNMT     3'  GCCTGCACCTCACCACG     15055       A  _  TCC
                                CGTGGTGA GG GCA   GGC
                                |||||||| || |||   |||
                                GCACCACT CC CGT   CCG
                                     _ A  ____
GAM971  SOX11    3'  CCGGGCCCTCACCACG      13313       A   AT
                                CGTGGTGA GGGC  CCGG
                                |||||||| ||||  ||||
                                GCACCACT CCCG  GGCC
                                     _   __
GAM971  SPTBN2   3'  GCCTCTGTCCCTCACCACGGT  23693        A    TCC
                                ACCGTGGTGA GGGCA   GGC
                                |||||||||| |||||   |||
                                TGGCACCACT CCTGT   CCG
                                      C    CT_
GAM971  TEM7     3'  GCCAGATGCCCTGCTCCTGG   40264    T  TGA      C
                                CCG GG   AGGGCATC GGC
                                ||| ||   |||||||| |||
                                GGT CC   TCCCGTAG CCG
                                  _ TCG       A
GAM971  TLR4     5'  GCCTCAGCCCTTCACCCCG    57503    T       ATCC
                                CG GGTGAAGGGC    GGC
                                || ||||||||||    |||
                                GC CCACTTCCCG    CCG
                                 C         ACT_
GAM971  AP1S2    5'  GCCGGGTGTCCTCCCCAC     15348     T  A
                                GTGG GA GGGCATCCGGC
                                |||| || ||||||||||
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                                CACC CT CCTGTGGGCCG
                                  C  _
GAM971  DKFZP564C1940 3'  CCCAGTCCCTTCACCAC     26743          C  CC
                                GTGGTGAAGGG AT  GG
                                |||||||||| ||  ||
                                CACCACTTCCC TG  CC
                                      _  AC
GAM971  FLJ20320  3'  CCGGATGCCACACCAGG     35420    G    AAG
                                CC TGGTG   GGCATCCGG
                                || |||||   |||||||||
                                GG ACCAC   CCGTAGGCC
                                 _    A__
GAM971  GGA2      3'  CCAATCATGTCCTTCACCACTG 57656    C          CC__
          T                      AC GTGGTGAAGGGCAT    GG
                                || ||||||||||||||    ||
                                TG CACCACTTCCTGTA    CC
                                 T           CTAA
GAM971  GGA2      3'  CCAATCATGTCCTTCACCACTG 57657    C          CC__
          T                      AC GTGGTGAAGGGCAT    GG
                                || ||||||||||||||    ||
                                TG CACCACTTCCTGTA    CC
                                 T           CTAA
GAM971  GGA2      3'  CCAGGGCCTGCTTCACCAC    57659         __  A  C
                                GTGGTGAAG  GGC TC GG
                                |||||||||  ||| || ||
                                CACCACTTC  CCG GG CC
                                      GT  _  A
GAM971  GGA2      3'  CCAGGGCCTGCTTCACCAC    57660         __  A  C
                                GTGGTGAAG  GGC TC GG
                                |||||||||  ||| || ||
                                CACCACTTC  CCG GG CC
                                      GT  _  A
GAM971  KIAA0280  3'  GCCGGATGCCCTGTGTCAT    93304     GT A
                                GTG  G AGGGCATCCGGC
                                |||  | ||||||||||||
                                TAC  T TCCCGTAGGCCG
                                  TG G
GAM971  KIAA0633  3'  GCCAATTGCTCTTCATCAC    95703           TCC
                                GTGGTGAAGGGCA   GGC
                                ||||||||||||   |||
                                CACTACTTCTCGT   CCG
                                       TAA
GAM971  KIAA1196  3'  GCTTGATGCCCTTCAACAC    62150     G         C
                                GTG TGAAGGGCATC GGC
                                ||| ||||||||||| |||
                                CAC ACTTCCCGTAG TCG
                                  A         T
GAM971  KIAA1915  3'  CCAGGGTCCACCACGGT     73666         GAA    A  C
                                ACCGTGGT   GGGC TC GG
                                ||||||||   |||| || ||
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                                TGGCACCA  CCTG GG CC
                                    ___   _ A
GAM971  MGC4737  5' GCCAGGTGCCCTCACCAC   49644       A     C
                                GTGGTGA GGGCATC GGC
                                ||||||| ||||||| |||
                                CACCACT CCCGTGG CCG
                                   _     A
GAM971  MGC5508  3' GCCGGATGCCCCACACACCGC 44266      AA__
                                GTGGTG   GGGCATCCGGC
                                ||||||   |||||||||||
                                CGCCAC   CCCGTAGGCCG
                                   ACAC
GAM971  N4BP3    3' GCCAGATGCCTTGATCAC   66853     GA      C
                                GTGGT  AGGGCATC GGC
                                |||||  |||||||| |||
                                CACTA  TTCCGTAG CCG
                                   G_      A
GAM971  OBSCN    3' GCCAGAGCAGCTTCACCAC   71189       G_  A  C
                                GTGGTGAAG  GC TC GGC
                                |||||||||  || || |||
                                CACCACTTC  CG AG CCG
                                     GA  _  A
GAM971  p25      3' CCGGATGCCCCCAGCAC    23828    G  AA
                                GTG TG  GGGCATCCGG
                                ||| ||  ||||||||||
                                CAC AC  CCCGTAGGCC
                                  G  C_
GAM971  LOC124045 3' GCCAGGGGTGTCCACCAGAGT  76537   CG   GAA     __
                                AC  TGGT   GGGCATCC  GGC
                                ||  ||||   ||||||||  |||
                                TG  ACCA   CCTGTGGG  CCG
                                 AG    ___       GA
GAM971  LOC148764 5' GCCGGGGATGCCTCACCAAGGT 79738    G     AG     __
                                ACC TGGTGA  GGCATCC  GGC
                                ||| ||||||  |||||||  |||
                                TGG ACCACT  CCGTAGG  CCG
                                  A     __       GG
GAM971  LOC150067 3' GCCTAGCCTTTACCACG     60962          G ATCC
                                CGTGGTGAAGG C    GGC
                                |||||||||||  |    |||
                                GCACCATTTCC G    CCG
                                      _ AT__
GAM971  LOC155438 3' GCCGAATGATGCCCTTCACCA  87684            ___
                                TGGTGAAGGGCATC   CGGC
                                ||||||||||||||   ||||
                                ACCACTTCCCGTAG   GCCG
                                         TAA
GAM971  LOC163231 5' GCCAGTCATTCACCACAGG   83333    _      G   ATCC
                                CC GTGGTGAA GGC    GGC
                                || ||||||| |||    |||
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                                GG CACCACTT CTG    CCG
                                 A       A  A___
GAM971  LOC219513 5'  GCCGCTGCCGCCACCACGGT  95985        AAG   TC
                                ACCGTGGTG  GGCA  CGGC
                                |||||||||  ||||  ||||
                                TGGCACCAC  CCGT  GCCG
                                     CG_   C_
GAM971  LOC219942 3'  CCATTTGCCCTTCGCCAC    94991          TCC
                                GTGGTGAAGGGCA  GG
                                ||||||||||||  ||
                                CACCGCTTCCCGT  CC
                                       TTA
GAM971  LOC221763 3'  GCCGCGGTCTTACCACGGT   95436        AA   ATC
                                ACCGTGGTG  GGGC  CGGC
                                |||||||||  ||||  ||||
                                TGGCACCAT  TCTG  GCCG
                                     __   GC_
GAM971  LOC254617 5'  CCTGATCCTCCACCGCGG    99278        A  GC  C
                                CCGTGGTG AGG  ATC GG
                                ||||||||| |||  ||| ||
                                GGCGCCAC TCC  TAG CC
                                     C   __   T
GAM971  LOC257042 3'  CCAATCTCCTCACCACG     98680        A  C  CC
                                CGTGGTGA GGG AT  GG
                                |||||||| ||| ||  ||
                                GCACCACT CCT TA  CC
                                     _  C  A_
GAM971  LOC51072  3'  GCCTAGCCTTTACCACG     32547          G ATCC
                                CGTGGTGAAGG C   GGC
                                |||||||||||  |   |||
                                GCACCATTTCC G   CCG
                                      _ AT__
GAM972  FLJ12488  3'  ATGTAGGCAGGCCTGCAGA   49156        A  ATGAA
                                TTTGCAG CT    GCCTACAT
                                |||||||  ||    ||||||||
                                AGACGTC GG    CGGATGTA
                                     C  A____
GAM972  FLJ20716  3'  ATGCCGCTTCAAGTCTGCAAA  36037         A    CTA
                                TTTGCAGACT TGAAGC  CAT
                                |||||||||| ||||||  |||
                                AAACGTCTGA ACTTCG  GTA
                                      _     CC_
GAM972  KIAA0247  3'  CATGCAGGCTTCACAGCTTAA  29065     C  A  A      A
                                TTG AG CT TGAAGCCT CATG
                                ||| || || |||||||| ||||
                                AAT TC GA ACTTCGGA GTAC
                                  _  _  C       C
GAM972  LOC158364 5'  GTAGACGTCAAAGTCTGCAAA  82756         A  AGC
                                TTTGCAGACT TGA  CTAC
                                |||||||||| |||  ||||
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                                AAACGTCTGA ACT   GATG
                                     A   GCA
GAM972  LOC253613 5'  GTAGACGTCAAAGTCTGCAAA  97917          A   AGC
                                TTTGCAGACT TGA   CTAC
                                |||||||||| |||   ||||
                                AAACGTCTGA ACT   GATG
                                     A   GCA
GAM973  ADRB3    5'  GATGGCCCAGGCTGGGGA    5248         GACC  A
                                TCTCCAGT    GG CCATC
                                ||||||||    || |||||
                                AGGGGTCG    CC GGTAG
                                   GAC_  _
GAM973  ARHGEF6  3'  GATGGGGAAGGTCACTGGA   68758          GGA_
                                TCCAGTGACC    CCATC
                                ||||||||||    |||||
                                AGGTCACTGG    GGTAG
                                     AAGG
GAM973  ARSA     3'  GATGGCTCCTCACTGGG     6670         CC  _
                                TCCAGTGA  GGA CCATC
                                ||||||||  ||| |||||
                                GGGTCACT  CCT GGTAG
                                   __   C
GAM973  EGLN2    5'  GATGGTCCGGGCTGGGGA    34519         GA
                                TCTCCAGT  CCGGACCATC
                                ||||||||  ||||||||||
                                AGGGGTCG  GGCCTGGTAG
                                   __
GAM973  ELF3     3'  GATGGCCCCTCCACTGGGGA  16683          ACC  A
                                TCTCCAGTG   GG CCATC
                                |||||||||   || |||||
                                AGGGGTCAC   CC GGTAG
                                     CTC  C
GAM973  FUT5     3'  GATGGTGCCTACTGGGGA    10728         ACC  _
                                TCTCCAGTG   GG ACCATC
                                |||||||||   || ||||||
                                AGGGGTCAT   CC TGGTAG
                                   ___  G
GAM973  ITPR3    3'  GATGCTCATCACTGGAGA    11086         CCG  C
                                TCTCCAGTGA   GA CATC
                                ||||||||||   || ||||
                                AGAGGTCACT   CT GTAG
                                     A__  C
GAM973  KCNK3    3'  ATGGTCGCACTGGAGG      11169         ACCG
                                TCTCCAGTG    GACCAT
                                |||||||||    ||||||
                                GGAGGTCAC    CTGGTA
                                     G___
GAM973  MAX      3'  ATGGTCCTGTGGCTGGGGA   59703         G  C
                                TCTCCAGT AC GGACCAT
                                |||||||| || |||||||
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                                AGGGGTCG TG CCTGGTA
                                    G  T
GAM973  PLA2G5   5' ATGTTCCGACTGGAGA     8113        GAC   C
                                TCTCCAGT   CGGA CAT
                                ||||||||   |||| |||
                                AGAGGTCA   GCCT GTA
                                    ____   T
GAM973  RAD52    3' GATGGTTCATATCATGAAGA  57036    CCA   CC_
                                TCT   GTGA   GGACCATC
                                |||   ||||   ||||||||
                                AGA   TACT   CTTGGTAG
                                  AG_   ATA
GAM973  WFS1     3' GATGGTCCGCCACGAGGA    21166    A_  AC
                                TCC  GTG  CGGACCATC
                                |||  |||  |||||||||
                                AGG  CAC  GCCTGGTAG
                                  AG   C_
GAM973  WNT3A    3' ATGGTCCGCTTTCCTGGAG   53608      T  C__
                                CTCCAG GA   CGGACCAT
                                |||||| ||   ||||||||
                                GAGGTC CT   GCCTGGTA
                                   _ TTC
GAM973  ABCA12   5' GATGGTTTTCACTGAGGA    32242    TC    CC
                                TC  CAGTGA  GGACCATC
                                ||  ||||||  ||||||||
                                AG  GTCACT  TTTGGTAG
                                 GA     __
GAM973  C11orf24 5' GATGGTCCAGGCTGGGA     42533    T    GACC
                                TC CCAGT    GGACCATC
                                || |||||    ||||||||
                                AG GGTCG    CCTGGTAG
                                 _    GA__
GAM973  DKFZP434O125 3' GGTGGGGGGGCTACTGGAGA   65587        A  GGA
                                TCTCCAGTG CC   CCATC
                                ||||||||| ||   |||||
                                AGAGGTCAT GG   GGTGG
                                    C  GG_
GAM973  DKFZP564O0423 3' GATGACCAACACTGGAGA    93351        ACC  AC
                                TCTCCAGTG   GG  CATC
                                |||||||||   ||  ||||
                                AGAGGTCAC   CC  GTAG
                                    AA_  A_
GAM973  FLJ13659  3' GATAATTCATACTGGAGA    48032        ACC   CC
                                TCTCCAGTG   GGA  ATC
                                |||||||||   |||  |||
                                AGAGGTCAT   CTT  TAG
                                    A__   AA
GAM973  FLJ13659  3' GATAATTCATACTGGAGA    48033        ACC   CC
                                TCTCCAGTG   GGA  ATC
                                |||||||||   |||  |||
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                                AGAGGTCAT  CTT  TAG
                                    A__  AA
GAM973  FLJ20195  5'  ATGTTCTGGCCACTGGGGA  35213       A    C
                                TCTCCAGTG CCGGA CAT
                                ||||||||| ||||| |||
                                AGGGGTCAC GGTCT GTA
                                    C    T
GAM973  FLJ22938  3'  GATGGAGGTGCAGCTGGAGA  45487      _ _  GGA
                                TCTCCAG TG ACC  CCATC
                                ||||||| || |||  |||||
                                AGAGGTC AC TGG  GGTAG
                                   G  G  A__
GAM973  FLJ30567  3'  GATGGGGCTGGTCACTGGA  59475        A_
                                TCCAGTGACCGG  CCATC
                                ||||||||||||  |||||
                                AGGTCACTGGTC  GGTAG
                                      GG
GAM973  FLJ31300  3'  ATGATCACTTACTGGGGA  58928        CCG  C
                                TCTCCAGTGA  GA CAT
                                ||||||||||  || |||
                                AGGGGTCATT  CT GTA
                                    CA_  A
GAM973  H-plk   3'  GATGATTCATACTGGAGA  32385       ACC  C
                                TCTCCAGTG  GGA CATC
                                |||||||||  ||| ||||
                                AGAGGTCAT  CTT GTAG
                                    A__  A
GAM973  HDAC11  3'  GATGGCCCAGGAGGTGCTGGAG 46138      G  _____  A
                                CTCCAGT ACC   GG CCATC
                                ||||||| |||   || |||||
                                GAGGTCG TGG   CC GGTAG
                                   _  AGGA  C
GAM973  HMP19   3'  ATGGCCGAGCTGGAGA  88858       GAC  A
                                TCTCCAGT  CGG CCAT
                                ||||||||  ||| ||||
                                AGAGGTCG  GCC GGTA
                                    A__  _
GAM973  KIAA0087  3'  GATGATTGTATACTGGAGG  29344       AC  AC
                                TCTCCAGTG  CGG  CATC
                                |||||||||  |||  ||||
                                GGAGGTCAT  GTT  GTAG
                                    AT  A_
GAM973  KIAA0852  5'  GATGTATCCCACTGGAG  30765       ACC  C_
                                CTCCAGTG  GGA  CATC
                                ||||||||  |||  ||||
                                GAGGTCAC  CCT  GTAG
                                    ___  AT
GAM973  KIAA1607  3'  GATGGGTCGCTTACTGGA  64537       C  GA
                                TCCAGTGA CG  CCATC
                                ||||||||  ||  |||||
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                                AGGTCATT GC  GGTAG
                                    C  TG
GAM973  KIAA1889 5' GATGGAGGTTTTACTGGA    73882       __   GGA
                                TCCAGT  GACC   CCATC
                                ||||||  ||||   |||||
                                AGGTCA  TTGG   GGTAG
                                   TT   A__
GAM973  KIAA1915 3' GATGGGTGGTCACTGAGA    73668     C      GA
                                TCTC AGTGACCG  CCATC
                                |||| ||||||||  |||||
                                AGAG TCACTGGT  GGTAG
                                  _      G_
GAM973  KIAA1969 3' GATAATTCATACTGGAGA    79480        ACC   CC
                                TCTCCAGTG   GGA  ATC
                                |||||||||   |||  |||
                                AGAGGTCAT   CTT  TAG
                                     A__   AA
GAM973  PXMP4    3' GATGCTGTTCTACTGGAGA   24333        _ C   AC
                                TCTCCAGT GA CGG  CATC
                                |||||||| || |||  ||||
                                AGAGGTCA CT GTC  GTAG
                                     T  T  __
GAM973  RALGPS1A 3' GATGTCTGTAACCACTGGGGA 28331         AC__    C
                                TCTCCAGTG    CGGAC ATC
                                |||||||||    ||||| |||
                                AGGGGTCAC    GTCTG TAG
                                     CAAT    _
GAM973  SBB103   5' GATGGAGCTTGTCACTGGGA   20523    T      C  A_
                                TC CCAGTGAC GG  CCATC
                                || ||||||||  ||  |||||
                                AG GGTCACTG TC  GGTAG
                                 _      T  GA
GAM973  SIAT8C   5' GATGGCAGCCTCGCTGGA    32446        CC  A__
                                TCCAGTGA  GG   CCATC
                                ||||||||  ||   |||||
                                AGGTCGCT  CC   GGTAG
                                     __  GAC
GAM973  ZNF273   3' GATAATTCATACTGGAGA    82100        ACC   CC
                                TCTCCAGTG   GGA  ATC
                                |||||||||   |||  |||
                                AGAGGTCAT   CTT  TAG
                                     A__   AA
GAM973  ZNF273   5' GATAATTCATACTGGAGA    82101        ACC   CC
                                TCTCCAGTG   GGA  ATC
                                |||||||||   |||  |||
                                AGAGGTCAT   CTT  TAG
                                     A__   AA
GAM973  ZNF273   5' GATAGTTCATACTGGAGA    82102        ACC    C
                                TCTCCAGTG   GGAC ATC
                                |||||||||   |||| |||
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                                AGAGGTCAT   CTTG TAG
                                     A__    A
GAM973   LOC129563 3'  GATGATTGATACTGGAG     75393        AC   AC
                                CTCCAGTG  CGG  CATC
                                ||||||||  |||  ||||
                                GAGGTCAT  GTT  GTAG
                                    A_   A_
GAM973   LOC132617 3'  GATGGTCTCTGCTCAAGA    76417     CC    ACC
                                TCT  AGTG   GGACCATC
                                |||  ||||   ||||||||
                                AGA  TCGT   TCTGGTAG
                                  AC    C__
GAM973   LOC143958 5'  GATGGTCCAGATTATGAG    77129     CA    CC_
                                CTC  GTGA   GGACCATC
                                |||  ||||   ||||||||
                                GAG  TATT   CCTGGTAG
                                  __    AGA
GAM973   LOC144262 5'  ATGCGTCTGGACCACTGGGGA  77258         A_     _
                                TCTCCAGTG  CCGGAC CAT
                                |||||||||  ||||||  |||
                                AGGGGTCAC  GGTCTG GTA
                                     CA     C
GAM973   LOC147165 5'  GATGGTCCTTGTAGGAGA    85084      A TG CC
                                TCTCC G  A  GGACCATC
                                |||||  |  |  ||||||||
                                AGAGG T  T  CCTGGTAG
                                   A GT __
GAM973   LOC150271 5'  GATGGTCCTAGGTCAGGA    86138     AG    __
                                TCC  TGACC  GGACCATC
                                |||  |||||  ||||||||
                                AGG  ACTGG  CCTGGTAG
                                  __     AT
GAM973   LOC158357 5'  GATGGTCCGGAGCGAGG     82760     CA  GA
                                TCTC  GT  CCGGACCATC
                                ||||  ||  ||||||||||
                                GGAG  CG  GGCCTGGTAG
                                  __ A_
GAM973   LOC203286 5'  GATGGTCCCGACATTGAGA   92145     C    ACC
                                TCTC AGTG   GGACCATC
                                |||| ||||   ||||||||
                                AGAG TTAC   CCTGGTAG
                                  _    AGC
GAM973   LOC220846 5'  GATGGCCCAGGCTGGGGA    92484        GACC  A
                                TCTCCAGT    GG CCATC
                                ||||||||    || |||||
                                AGGGGTCG    CC GGTAG
                                     GAC_  _
GAM973   LOC221833 3'  ATGGTTTGTACAACTGGAGA  94113        GAC_
                                TCTCCAGT    CGGACCAT
                                ||||||||    ||||||||
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                                AGAGGTCA   GTTTGGTA
                                    ACAT
GAM973  LOC51136  5' GATGGCCCCGACTGAAGG   32845    C   GAC  A_
                                TCT CAGT  CGG  CCATC
                                ||| ||||  |||  |||||
                                GGA GTCA  GCC  GGTAG
                                  A   ___  CC
GAM973  LOC90643  3' GATCAGCCATGTCACTGAAGA  64440    C     C_  ACC
                                TCT CAGTGAC  GG  ATC
                                ||| |||||||  ||  |||
                                AGA GTCACTG  CC  TAG
                                  A     TA  GAC
GAM973  LOC91156  5' GATGGTCCCTTTGGCAGA   65710    _   TGACC
                                TCT CCAG   GGACCATC
                                ||| ||||   ||||||||
                                AGA GGTT   CCTGGTAG
                                  C   TC___
GAM973  LOC91812  5' GATGGTCCAGGGCATTGGAGG  67817        A  _
                                TCTCCAGTG CC GGACCATC
                                ||||||||| || ||||||||
                                GGAGGTTAC GG CCTGGTAG
                                     G  A
GAM973  LOC91813  5' GATGGTCCAGGGCATTGGAGG  67841        A  _
                                TCTCCAGTG CC GGACCATC
                                ||||||||| || ||||||||
                                GGAGGTTAC GG CCTGGTAG
                                     G  A
GAM973  LOC93512  5' GATGGTCCTTGTAGGAGA   72876     A TG CC
                                TCTCC G  A  GGACCATC
                                ||||| |  |  ||||||||
                                AGAGG T  T  CCTGGTAG
                                   A GT __
GAM974  CDKN2C    3' TCCCCTTTTGCCAATCTCA   8848       _  C   CTGT
                                TGAGATTG CA AAG   GGA
                                |||||||| || |||   |||
                                ACTCTAAC GT TTC   CCT
                                     C  T   C___
GAM974  CDKN2C    3' TCCCCTTTTGCCAATCTCA   55318       _  C   CTGT
                                TGAGATTG CA AAG   GGA
                                |||||||| || |||   |||
                                ACTCTAAC GT TTC   CCT
                                     C  T   C___
GAM974  NDRG1     3' TCCTCCACAGCCCCAACCTC   60314    A   CACAA     A
                                GAG TTG    GCTGTGGA GA
                                ||| |||    |||||||| ||
                                CTC AAC    CGACACCT CT
                                  C   CC___      C
GAM974  PXF       3' CTTCCACAACTCAGTCTGCA   12653   _    CACA  C
                                TG AGATTG   AG TGTGGAAG
                                || ||||||   || ||||||||
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                                AC TCTGAC    TC ACACCTTC
                                 G     _____ A
GAM974  RB1      5'  TCCTCCACAGCTCGCTGGCTC  92556     ATT  ACA       A
                                GAG   GC   AGCTGTGGA GA
                                |||   ||   |||||||||| ||
                                CTC   CG   TCGACACCT CT
                                  GGT  C__        C
GAM974  SIP1     3'  CTTAACCTGTGCAATTCA    14620      A      AGCT  GG
                                TGAG TTGCACA    GT  AAG
                                |||| |||||||    ||  |||
                                ACTT AACGTGT    CA  TTC
                                  _      C___  A_
GAM974  SIRT1    3'  TCTGTACTTGTACAAACTCA   25290      A   C    C  TG
                                TGAG TTG ACAAG TG  GA
                                |||| ||| ||||| ||  ||
                                ACTC AAC TGTTC AT  CT
                                  A   A    _ GT
GAM974  STXBP1   3'  TCCTCCACAGCCTGTCA     13480    C   A       A
                                TG ACA GCTGTGGA GA
                                || ||| |||||||| ||
                                AC TGT CGACACCT CT
                                 _  C       C
GAM974  ARL8     5'  CCTCGCTGCGCGATCTCA    94812          A  A  T T
                                TGAGATTGC CA GC G GG
                                ||||||||| || || | ||
                                ACTCTAGCG GT CG C CC
                                      C  _  _ T
GAM974  BAG5     5'  CTTCCACCTCGCCACCTCA   18038      ATT  ACA  CT
                                TGAG   GC   AG  GTGGAAG
                                ||||   ||   ||  |||||||
                                ACTC   CG   TC  CACCTTC
                                  CAC  C__  __
GAM974  DXS1357E 3'  CTTCCACAGCTCATAGCTCGTC 20433     T_  ACA_
                                GAT  GC    AGCTGTGGAAG
                                |||  ||    ||||||||||
                                CTG  CG    TCGACACCTTC
                                  CT  ATAC
GAM974  FASTK    3'  CTTCCCCGTTGTGAATCTCA  47686       G    GC  T
                                TGAGATT CACAA  TG GGAAG
                                ||||||| |||||  || |||||
                                ACTCTAA GTGTT  GC CCTTC
                                    _    __  C
GAM974  FASTK    3'  CTTCCCCGTTGTGAATCTCA  53402       G    GC  T
                                TGAGATT CACAA  TG GGAAG
                                ||||||| |||||  || |||||
                                ACTCTAA GTGTT  GC CCTTC
                                    _    __  C
GAM974  FLJ13154 3'  CTTCCACAGCCCGGGTTCTC  45109     TT  ACAA
                                GAGA  GC    GCTGTGGAAG
                                ||||  ||    ||||||||||
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                                CTCT  TG   CGACACCTTC
                                  __ GGCC
GAM974  FLJ14824  3'  TCTTCCACAGCCCTGAGGTCTT 52719      TG  CAA
           A                    TGAGAT  CA   GCTGTGGAAGA
                                |||||| ||  ||||||||||
                                ATTCTG  GT   CGACACCTTCT
                                   GA  CC_
GAM974  FLJ22415  3'  TCTCCCACTCTATACTAATCTC 93122       CACA  CT   A
           A                    TGAGATTG   AG  GTGG AGA
                                |||||||   ||  |||| |||
                                ACTCTAAT   TC  CACC TCT
                                     CATA  T_   C
GAM974  GABARAPL1 3'  TCCCGGTTGCAATCTCA    49425        CAA   T
                                TGAGATTGCA   GCTG GGA
                                ||||||||||   |||| |||
                                ACTCTAACGT   TGGC CCT
                                      ____   _
GAM974  GABARAPL3 3'  TCCCAGTTGCAATCTCA    51789        CAA   T
                                TGAGATTGCA   GCTG GGA
                                ||||||||||   |||| |||
                                ACTCTAACGT   TGAC CCT
                                      ____   _
GAM974  HES2    3'  TCTGGGAAGCCTGTGCAATTCA 39379    A     A   GTGGA
                                TGAG TTGCACA GCT    AGA
                                |||| ||||||| |||    |||
                                ACTT AACGTGT CGA    TCT
                                  _     C   AGGG_
GAM974  HSJ1    3'  TCCTCCACAGCTTGCCGC    23087    A_       A
                                GC  CAAGCTGTGGA GA
                                ||  |||||||||| ||
                                CG  GTTCGACACCT CT
                                 CC         C
GAM974  ITPK1   3'  CCATCGCTTCTGCACACCTCA  27229    AT_   C   T
                                TGAG   TGCA AAGC GTGG
                                ||||   |||| |||| ||||
                                ACTC   ACGT TTCG TACC
                                  CAC    C   C
GAM974  KIAA1508  3'  TGCAATTGTGCAATCTCA    62566         GC
                                TGAGATTGCACAA  TGTG
                                ||||||||||||  ||||
                                ACTCTAACGTGTT  ACGT
                                       A_
GAM974  KIAA1950  3'  TCACAGCTCGCGCACCCTCA   94185    AT   ACA
                                TGAG  TGC   AGCTGTGG
                                ||||  |||   ||||||||
                                ACTC  ACG   TCGACACT
                                  CC   CGC
GAM974  KRT6IRS   3'  CTTCCTCTGTTGCAACCTCA   54229    A    CAA  TGT
                                TGAG TTGCA   GC   GGAAG
                                |||| |||||   ||   |||||
```

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                                ACTC AACGT   TG   CCTTC
                                  C     ___  TCT
GAM974  LGI3     3'  TTCATGGCCGTGAATCCCA   58399    A    G   AA
                                TG GATT CAC  GCTGTGGA
                                || |||| |||  ||||||||
                                AC CTAA GTG  CGGTACTT
                                 C    _   C_
GAM974  NUDT4    3'  TCTCCCACCATGTGCAGTCTCA 39383          AGCT    A
                                TGAGATTGCACA    GTGG AGA
                                ||||||||||||    |||| |||
                                ACTCTGACGTGT    CACC TCT
                                       AC__    C
GAM974  P311     3'  TCTTCCACAACTCAAACTC   17678     A   CACA  C
                                GAG TTG    AG TGTGGAAGA
                                ||| |||    || |||||||||
                                CTC AAC    TC ACACCTTCT
                                  A  _____  A
GAM974  RAI17    3'  TCCTCCACCATCACAATCTCA  92910        CACAAGCT    A
                                TGAGATTG       GTGGA GA
                                ||||||||       ||||| ||
                                ACTCTAAC       CACCT CT
                                     ACTAC___     C
GAM974  ST7L     3'  CTTGCGAACTTATACAGTCTCA 35338        CAC   CTG  G
                                TGAGATTG   AAG   TG AAG
                                ||||||||   |||   || |||
                                ACTCTGAC   TTC   GC TTC
                                     ATA   AA_  G
GAM974  ST7L     3'  CTTGCGAACTTATACAGTCTCA 57815        CAC   CTG  G
                                TGAGATTG   AAG   TG AAG
                                ||||||||   |||   || |||
                                ACTCTGAC   TTC   GC TTC
                                     ATA   AA_  G
GAM974  ST7L     3'  CTTGCGAACTTATACAGTCTCA 58282        CAC   CTG  G
                                TGAGATTG   AAG   TG AAG
                                ||||||||   |||   || |||
                                ACTCTGAC   TTC   GC TTC
                                     ATA   AA_  G
GAM974  LOC146336 3'  TCCTCCACAGCCCCCAGCTTCC 78375    A  TT  ACAA_      A
           CA                    TG GA  GC    GCTGTGGA GA
                                || ||  ||    |||||||| ||
                                AC CT  CG    CGACACCT CT
                                 C  T_  ACCCC       C
GAM974  LOC147343 5'  TCCTCCACAGCCCTGTCA    85133    C   A_      A
                                TG ACA  GCTGTGGA GA
                                || |||  |||||||| ||
                                AC TGT  CGACACCT CT
                                 _  CC       C
GAM974  LOC153196 3'  TCCTCCATTAATGTACAATCTC 87172        C   AGCT    A
                                GAGATTG ACA    GTGGA GA
                                ||||||| |||    ||||| ||
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                                CTCTAAC TGT    TACCT CT
                                    A   AAT_     C
GAM974   LOC154877 3'  TCTCCCACAGCTCACTTCCCTC 87579      TTGCACA_       A
             TC                    GAGA        AGCTGTGG AGA
                                   ||||        |||||||| |||
                                   CTCT        TCGACACC TCT
                                     CCCTTCAC        C
GAM974   LOC157653 5'  TCTCCCACAGCTCTGTCCA    82447    C  _       A
                                   TG ACA AGCTGTGG AGA
                                   || ||| |||||||| |||
                                   AC TGT TCGACACC TCT
                                    C  C       C
GAM974   LOC158130 3'  CTCCCACAGCTAATAATTCTCA 69705       TTGCACA       A
                                   TGAGA       AGCTGTGG AG
                                   |||||       |||||||| ||
                                   ACTCT       TCGACACC TC
                                      TAATAA_       C
GAM974   LOC165639 5'  CTTCCACAAAGGCAATTCA    88601      A    ACAAGC
                                   TGAG TTGC      TGTGGAAG
                                   |||| ||||      ||||||||
                                   ACTT AACG      ACACCTTC
                                     _    GAA____
GAM974   LOC200982 3'  TCAGGCTGCTTGTGCAAACTCA 91814      A         T  G_
                                   TGAG TTGCACAAGC GT  GA
                                   |||| |||||||||| ||  ||
                                   ACTC AACGTGTTCG CG  CT
                                     A         T  GA
GAM974   LOC205100 5'  TCCTCCACAGCCCATGAGCCCT 92391     ATT  A  A__       A
             C                      GAG   GC CA   GCTGTGGA GA
                                   |||   || ||   |||||||| ||
                                   CTC   CG GT   CGACACCT CT
                                     C__  A  ACC        C
GAM974   LOC221037 5'  TCTTCCACATCAGATTGCATCT 94777       T   CAAGC_
             CA                      TGAGAT GCA      TGTGGAAGA
                                   ||||||| |||      |||||||||
                                   ACTCTA CGT      ACACCTTCT
                                      _   TAGACT
GAM974   LOC222136 3'  CTCCCACAGCTTGTGCCCTC   94288     ATT           A
                                   GAG   GCACAAGCTGTGG AG
                                   |||   |||||||||||||| ||
                                   CTC   CGTGTTCGACACC TC
                                     C__            C
GAM974   LOC222681 5'  CTTCCACAACTCAGGCAATTCA 94427      A    ACA  C
                                   TGAG TTGC   AG TGTGGAAG
                                   |||| ||||   || ||||||||
                                   ACTT AACG   TC ACACCTTC
                                     _    GAC  A
GAM974   LOC257507 5'  CTTCCACAACTCAGGCAATTCA 99614      A    ACA  C
                                   TGAG TTGC   AG TGTGGAAG
                                   |||| ||||   || ||||||||
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                                ACTT AACG   TC ACACCTTC
                                  _   GAC  A
GAM974  LOC257625 5'  CTTCCACAACTCAGGCAATTCA 99734      A    ACA  C
                                TGAG TTGC   AG TGTGGAAG
                                |||| ||||   || ||||||||
                                ACTT AACG   TC ACACCTTC
                                  _   GAC  A
GAM975  EIF1A    3'  AAGACCATGTCTACTAATTACA 90001      C     GTCAG
             AA                   TTTG AATTGG    ATGGTCTT
                                |||| ||||||    ||||||||
                                AAAC TTAATC    TACCAGAA
                                  A     ATCTG
GAM976  ALPL     3'  CCAAGGGCCAAACCCA      6645      A       GG
                                TGG TTTGGCTTT  TGG
                                ||| |||||||||  |||
                                ACC AAACCGGGA  ACC
                                  C       __
GAM976  ATF5     3'  CCACCAAACCACCCAA      24818      ATT   C
                                TTGG   TGG TTTGGTGG
                                ||||   ||| ||||||||
                                AACC   ACC AAACCACC
                                  C__   _
GAM976  BARHL1   3'  CCGAAGGGCCAAATGCCAA   39636      _       GG
                                TTGG ATTTGGCTTT  TGG
                                |||| ||||||||||  |||
                                AACC TAAACCGGGA  GCC
                                  G        A_
GAM976  BCL11B   3'  CCACCACATAAATCTCAA    43483     _     GCTT
                                TTG GATTTG    TGGTGG
                                ||| ||||||    ||||||
                                AAC CTAAAT    ACCACC
                                  T     AC__
GAM976  BLAME    3'  TCCACCAAAAAAACACAA    39658     GA   GGC
                                TTG  TTT   TTTGGTGGA
                                |||  |||   |||||||||
                                AAC  AAA   AAACCACCT
                                  AC   A__
GAM976  CDR2     3'  TCCTAATATATCCAAATCCAA  76530         CTT  GT_
                                TTGGATTTGG   TG   GGA
                                ||||||||||   ||   |||
                                AACCTAAACC   AT   CCT
                                      TAT  AAT
GAM976  COL3A1   3'  TCCACCAAATACAATTCAA    5398        T GC
                                TTGGATT G  TTTGGTGGA
                                |||||||  |  |||||||||
                                AACTTAA C  AAACCACCT
                                    _ AT
GAM976  CTSK     3'  TCCAGCCAGCCAAATCCA     6372          TT  _
                                TGGATTTGGCT  GG TGGA
                                ||||||||||  || ||||
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                                ACCTAAACCGA  CC ACCT
                                      __ G
GAM976  FBXL7    3'  TCCACCAAAGAATGCAA     25499     G   TGG
                                TTG ATT   CTTTGGTGGA
                                ||| |||   ||||||||||
                                AAC TAA   GAAACCACCT
                                  G  ___
GAM976  FLT1     3'  TCCACCAAGATCTAAATCCAA  10663         C_
                                TTGGATTTGG  TTTGGTGGA
                                ||||||||||  |||||||||
                                AACCTAAATC  GAACCACCT
                                      TA
GAM976  GAGED2   5'  TCCACAGGCAGATCCAA     56756         G  TTG
                                TTGGATTTG CT   GTGGA
                                ||||||||| ||   |||||
                                AACCTAGAC GA   CACCT
                                     G  ___
GAM976  GNB2     3'  TCCATAAAGGAGCCAATTCCAA 19173       T      TG__
                                TTGGA TTGGCTT    GTGGA
                                ||||| |||||||    |||||
                                AACCT AACCGAG    TACCT
                                   T      GAAA
GAM976  IGFBP3   3'  CCGGAGGCCAAACCCAA     6999       A       GG
                                TTGG TTTGGCTTT  TGG
                                |||| |||||||||  |||
                                AACC AAACCGGAG  GCC
                                  C        __
GAM976  ITGA6    3'  TCCACCCCACAACCCAA     5794       A  _   CTTT
                                TTGG TT TGG    GGTGGA
                                |||| || |||    ||||||
                                AACC AA ACC    CCACCT
                                  C  C  _____
GAM976  JUP      3'  CCAAACCCCCAAAATCCAA   11107         ___  C
                                TTGGATTT   GG TTTGG
                                ||||||||   || |||||
                                AACCTAAA   CC AAACC
                                     ACC  C
GAM976  KCNE2    3'  CCACGAGGCAAATCCAA     18893         G   TG
                                TTGGATTTG CTT  GTGG
                                ||||||||| |||  ||||
                                AACCTAAAC GAG  CACC
                                     G  __
GAM976  LDLR     3'  TCCACCAATCTCTAAGCCAA  6743       A    CT_
                                TTGG TTTGG   TTGGTGGA
                                |||| |||||   ||||||||
                                AACC GAATC   AACCACCT
                                   _    TCT
GAM976  MKKS     5'  TCAGAAGAGCCAAATCCAG   38752            GG
                                TTGGATTTGGCTTT  TGG
                                ||||||||||||||  |||
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                                GACCTAAACCGAGA  ACT
                                      AG
GAM976  PLAG1    3'  TCCACCTTTCACATCCAA    12150       T  CTTT
                                TTGGAT TGG   GGTGGA
                                |||||| |||   ||||||
                                AACCTA ACT   CCACCT
                                   C  TT__
GAM976  PUM1     3'  CCACTGGCAAATCCAA     28646        G  TT
                                TTGGATTTG CT  GGTGG
                                ||||||||| ||  |||||
                                AACCTAAAC GG  TCACC
                                     _ __
GAM976  SCN7A    5'  TCCACCATGTGAATGCCAA   12948     AT  G  TT
                                TTGG  TT GC  TGGTGGA
                                ||||  || ||  |||||||
                                AACC  AA TG  ACCACCT
                                  GT  G  T_
GAM976  SCRT1    3'  TCCTCTGCCAAATCCGA     49371          TTT  T
                                TTGGATTTGGC   GG GGA
                                ||||||||||   || |||
                                AGCCTAAACCG   TC CCT
                                      ___  T
GAM976  SORCS2   3'  TCCACCTGTCCCCCAGACCCAA 40806      A    CTTT__
                                TTGG TTTGG     GGTGGA
                                |||| |||||     ||||||
                                AACC AGACC     CCACCT
                                  C    CCCTGT
GAM976  ALS2CR3  5'  TCCATGTGACCAAATCCA    31184         C  TG
                                TGGATTTGG TT  GTGGA
                                ||||||||| ||  |||||
                                ACCTAAACC AG  TACCT
                                     _  TG
GAM976  C6orf37  3'  TCCATTAAATCAAATCCAA   68095          C
                                TTGGATTTGG TTTGGTGGA
                                |||||||||| |||||||||
                                AACCTAAACT AAATTACCT
                                     _
GAM976  COPS7B   3'  TCCACCAATGCCATCCCAA   43001      ATT   T
                                TTGG   TGGC TTGGTGGA
                                ||||   |||| ||||||||
                                AACC   ACCG AACCACCT
                                  CT_   T
GAM976  DDX17    3'  CCACCAAAATGATCCAG     48780       TGGC
                                TTGGATT    TTTGGTGG
                                |||||||    ||||||||
                                GACCTAG    AAACCACC
                                    TA__
GAM976  DDX17    3'  CCACCAAAATGATCCAG     22124       TGGC
                                TTGGATT    TTTGGTGG
                                |||||||    ||||||||
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                                GACCTAG   AAACCACC
                                   TA__
GAM976  DKFZP434J193 3'  CCAGGAGGCAAACCCAA    71558     A   G   GG
                                TTGG TTTG CTTT  TGG
                                |||| |||| ||||  |||
                                AACC AAAC GAGG  ACC
                                  C   G   __
GAM976  DKFZP586N2124 5'  CCACCAAAGTCCTGCCAG    31857     ATTT
                                TTGG   GGCTTTGGTGG
                                ||||   ||||||||||
                                GACC   CTGAAACCACC
                                  GTC_
GAM976  FBX30    3'  TCCACCTCCCAAATCCAG    53749         CTTT
                                TTGGATTTGG   GGTGGA
                                ||||||||||   ||||||
                                GACCTAAACC   CCACCT
                                     CT__
GAM976  FIBL-6   3'  TCCTGAAAGCCAAACCAA    73298     A       GGT
                                TTGG TTTGGCTTT   GGA
                                |||| |||||||||   |||
                                AACC AAACCGAAA   CCT
                                  _       GT_
GAM976  FLJ00024  5'  CCACCAAGAGGGACTCCAA    64490      _  GG   T
                                TTGGA TTT  CTT GGTGG
                                ||||| |||  ||| |||||
                                AACCT AGG  GAA CCACC
                                  C   GA  _
GAM976  FLJ00024  3'  TCCAGCTTGCCAAACCCA    64506     A     TTT  _
                                TGG TTTGGC   GG TGGA
                                ||| ||||||   || ||||
                                ACC AAACCG   TC ACCT
                                  C     T__  G
GAM976  FLJ13544  3'  TCCACCAAAAAATACCAA    47209     _   GGC
                                TTGG ATTT   TTTGGTGGA
                                |||| ||||   |||||||||
                                AACC TAAA   AAACCACCT
                                  A   ____
GAM976  FLJ14642  3'  TCAGGAAACCAAGTCCAA    52582         C   GG
                                TTGGATTTGG TTT  TGG
                                |||||||||| |||  |||
                                AACCTGAACC AAA  ACT
                                     _  GG
GAM976  FLJ20054  3'  CCAAGAAAGCCAAATACAA    39308     G       GG
                                TTG ATTTGGCTTT  TGG
                                ||| ||||||||||  |||
                                AAC TAAACCGAAA  ACC
                                  A        GA
GAM976  GOLGA1    3'  CCAGCAGGCCAAACCCA     10847     A      T G
                                TGG TTTGGCTT G TGG
                                ||| |||||||| | |||
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                                ACC AAACCGGA C ACC
                                  C       _ G
GAM976  H17      3'  CCACCAGGGCAATCCA      34513       TG
                                TGGATT  GCTTTGGTGG
                                ||||||  ||||||||||
                                ACCTAA  CGGGACCACC
                                  __
GAM976  HCC8     3'  TCTTTGGACCAAATCCAA    33695         C  TG T
                                TTGGATTTGG TT  G GGA
                                |||||||||| ||  | |||
                                AACCTAAACC AG  T TCT
                                     _  GT _
GAM976  HSJ001348 3'  TCCACCAAAAACAAATACAA  62860     G    GC
                                TTG ATTTG  TTTGGTGGA
                                ||| |||||  |||||||||
                                AAC TAAAC  AAACCACCT
                                  A    AA
GAM976  IMP-2    3'  CCACCAAACCAACCAA      22607      AT   C
                                TTGG  TTGG TTTGGTGG
                                ||||  |||| ||||||||
                                AACC  AACC AAACCACC
                                  __   _
GAM976  KIAA0040 3'  TCAGAAGAGCCAAACCCAG   28494      A       GG
                                TTGG TTTGGCTTT  TGG
                                |||| |||||||||  |||
                                GACC AAACCGAGA  ACT
                                  C        AG
GAM976  KIAA0140 3'  CCGGACAGCCGAACCCAA    28510      A     __
                                TTGG TTTGGCT  TTGG
                                |||| |||||||  ||||
                                AACC AAGCCGA  GGCC
                                  C      CA
GAM976  KIAA0564 3'  CCACCAAAAAGTCCCTCCA   66790      TTT   __
                                TGGA   GGCTT  TGGTGG
                                ||||   |||||  ||||||
                                ACCT   CTGAA  ACCACC
                                  CC_    AA
GAM976  KIAA1030 3'  CCACTGTGCCAGATCCAA    94975          TT
                                TTGGATTTGGC  TGGTGG
                                ||||||||||  ||||||
                                AACCTAGACCG  GTCACC
                                     T_
GAM976  KIAA1484 3'  CCACACGAACAAAATCCAA   70521        GGC   _
                                TTGGATTT   TTTG GTGG
                                ||||||||   |||| ||||
                                AACCTAAA   AAGC CACC
                                    AC_    A
GAM976  KIAA1762 3'  CCACCAACGGCAAATCCAA   64529         G  _
                                TTGGATTTG CT TTGGTGG
                                ||||||||| || |||||||
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                                AACCTAAAC GG AACCACC
                                     _ C
GAM976  KIAA1975  5'  TCCACCTGCCAGAATCCAA   74430      _    TTT
                                TTGGAT TTGGC  GGTGGA
                                |||||| |||||  ||||||
                                AACCTA GACCG  CCACCT
                                   A    T__
GAM976  MGC5601   5'  TCACGGGCAGTCAAATCCAA  48260         _  G
                                TTGGATTTGGCT TT GTGG
                                |||||||||||| || ||||
                                AACCTAAACTGA GG CACT
                                      C  G
GAM976  RALGPS1A  3'  TCCATTTTCCAAGTCCAA   28337        CTTT
                                TTGGATTTGG   GGTGGA
                                ||||||||||   ||||||
                                AACCTGAACC   TTACCT
                                      TT__
GAM976  SCAMP5    3'  CCAGATCCCCAAATCTAA   58056        C__
                                TTGGATTTGG  TTTGG
                                ||||||||||  |||||
                                AATCTAAACC  AGACC
                                      CCT
GAM976  TBLR1     3'  TCCACTACAGCCAAATCTAA  45430         T
                                TTGGATTTGGCT TGGTGGA
                                |||||||||||| |||||||
                                AATCTAAACCGA ATCACCT
                                      C
GAM976  TTTY2     5'  TCCGTGGAGCCAATCCAA   88391       T   TGG
                                TTGGATT GGCTT  TGGA
                                ||||||| |||||  ||||
                                AACCTAA CCGAG  GCCT
                                   _   GT_
GAM976  WAP1      3'  TCCACCAAAAATGCCCAAT   80341    T  ___
                                ATT GGC  TTTGGTGGA
                                ||| |||  |||||||||
                                TAA CCG  AAACCACCT
                                  C  TAA
GAM976  LOC143274 3'  TCCACCAAGTTGGTATTCAA  77023      _ TG   T
                                TTGGAT T  GCTT GGTGGA
                                |||||| |  |||| ||||||
                                AACTTA G  TGAA CCACCT
                                   T GT   _
GAM976  LOC145719 5'  CCAAGAGCCAAATCCA     84460         GG
                                TGGATTTGGCTTT  TGG
                                ||||||||||||  |||
                                ACCTAAACCGAGA  ACC
                                      __
GAM976  LOC145720 5'  CCAAGAGCCAAATCCA     84446         GG
                                TGGATTTGGCTTT  TGG
                                ||||||||||||  |||
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                                ACCTAAACCGAGA  ACC
                                     __
GAM976  LOC146958 3'  TCCACCACCCCCTCAAATCCAG 84945          CTT__
                                TTGGATTTGG    TGGTGGA
                                ||||||||||    |||||||
                                GACCTAAACT    ACCACCT
                                     CCCCC
GAM976  LOC151201 3'  TCAGTAATCCAAATCCAA    86488          CT   G
                                TTGGATTTGG  TTG TGG
                                ||||||||||  ||| |||
                                AACCTAAACC  AAT ACT
                                     T_   G
GAM976  LOC152275 3'  TCCTTGCTGACAAATCCAA    86799         GCT TG  __
                                TTGGATTTG   T  GT  GGA
                                |||||||||   |  ||  |||
                                AACCTAAAC   A  CG  CCT
                                     ___ GT  TT
GAM976  LOC153077 3'  CCAAAGGCCAAATCCA      87116           GG
                                TGGATTTGGCTTT  TGG
                                ||||||||||||  |||
                                ACCTAAACCGGAA  ACC
                                     __
GAM976  LOC157376 3'  TCTGTAAACCAGATCCAA    82355          C   G TG
                                TTGGATTTGG TTT G  GA
                                |||||||||| ||| |  ||
                                AACCTAGACC AAA T  CT
                                     _  _ GT
GAM976  LOC159148 5'  TCCGTGGAGCCAATCCAA    88393        T    TGG
                                TTGGATT GGCTT   TGGA
                                ||||||| |||||   ||||
                                AACCTAA CCGAG   GCCT
                                    _    GT_
GAM976  LOC160391 3'  TCCACCGCTAGAAACCCA    88440     A__     TTT
                                TGG   TTTGGC   GGTGGA
                                |||   ||||||   ||||||
                                ACC   AGATCG   CCACCT
                                  CAA     ___
GAM976  LOC166929 3'  TCCACCAAAACCCTCTA     83556      TTT  C
                                TGGA   GG TTTGGTGGA
                                ||||   || |||||||||
                                ATCT   CC AAACCACCT
                                  C__  A
GAM976  LOC197114 5'  CCAAGAGCCAAATCCA      91265           GG
                                TGGATTTGGCTTT  TGG
                                ||||||||||||  |||
                                ACCTAAACCGAGA  ACC
                                     __
GAM976  LOC197117 5'  CCAAGAGCCAAATCCA      91278           GG
                                TGGATTTGGCTTT  TGG
                                ||||||||||||  |||
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                                ACCTAAACCGAGA  ACC
                                      __
GAM976  LOC200014 3'  TCCACCAAAGTCCTAATCTAA  89947       T_
                                TTGGATT  GGCTTTGGTGGA
                                |||||||  ||||||||||||
                                AATCTAA  CTGAAACCACCT
                                   TC
GAM976  LOC200197 3'  CCACCACTAGAAATCCAG    90015       GG  T_
                                TTGGATTT  CT  TGGTGG
                                |||||||||  ||  ||||||
                                GACCTAAA  GA  ACCACC
                                   __  TC
GAM976  LOC203297 5'  CCACCAAGAGGGACTCCAA   75869      _  GG   T
                                TTGGA TTT  CTT GGTGG
                                ||||| |||  ||| |||||
                                AACCT AGG  GAA CCACC
                                  C   GA  _
GAM976  LOC219855 3'  TCCACCAAAGGAGCCCAG    93143     AT  GG
                                TTGG  TT  CTTTGGTGGA
                                ||||  ||  ||||||||||
                                GACC  AG  GAAACCACCT
                                  CG  __
GAM976  LOC221738 5'  CTGCTAAGCCTAATCCAA    95413       T    T  TG
                                TTGGATT GGCTT GG  G
                                ||||||| ||||| ||  |
                                AACCTAA CCGAA TC  C
                                   T    _  GT
GAM976  LOC253626 5'  TCCATGCGCCAATCCAA     99014       T   TTTG
                                TTGGATT GGC    GTGGA
                                ||||||| |||    |||||
                                AACCTAA CCG    TACCT
                                   _   CG__
GAM976  LOC253943 5'  TCCACCAATGTCAATCCA    97849       T   T
                                TGGATT GGC TTGGTGGA
                                |||||| ||| ||||||||
                                ACCTAA CTG AACCACCT
                                   _  T
GAM976  LOC256306 3'  CCACTCCTTCCAGATCCAA   98507         CTTT
                                TTGGATTTGG   GGTGG
                                ||||||||||   |||||
                                AACCTAGACC   TCACC
                                     TTCC
GAM976  LOC51308  3'  CCAAGAGGGCCAAACCCA    33961     A       GG
                                TGG TTTGGCTTT  TGG
                                ||| |||||||||  |||
                                ACC AAACCGGGA  ACC
                                  C        GA
GAM976  LOC58525  5'  CCACCAGGGCCAAGCCCAA   79342     AT
                                TTGG  TTGGCTTTGGTGG
                                ||||  ||||||||||||
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                                AACC  AACCGGGACCACC
                                  CG
GAM976  LOC91156 3' CCGGGAAGCCAATCCCAA    65708     AT      GG
                                TTGG  TTGGCTTT  TGG
                                ||||  ||||||||  |||
                                AACC  AACCGAAG  GCC
                                  CT      G_
GAM976  LOC92691 3' TCGGGGTAACCAAATCCA    57241         ___
                                TGGATTTGG   CTTTGG
                                |||||||||   ||||||
                                ACCTAAACC   GGGGCT
                                     AAT
GAM977  ADAR     3' CTGCAGGGCGGGCAAGG     32361    A    CAG  T
                                CC TGCCC   GC CCTGCAG
                                || |||||   || |||||||
                                GG ACGGG   CG GGACGTC
                                 A    ___ _
GAM977  AIRE     3' TGGGAGCCTGAGGCATGAGAA  7247     C     C
                                TTC CATGCC CAGGCTCCTG
                                ||| |||||| ||||||||||
                                AAG GTACGG GTCCGAGGGT
                                  A     A
GAM977  ANG      5' GCAGGAGCCTGTGTTGG     8557     T  CC
                                CCA GC  CAGGCTCCTGC
                                ||| ||  ||||||||||
                                GGT TG  GTCCGAGGACG
                                  _  T_
GAM977  BCAS1    3' CTCGGGAGCCCAACGCACGAGA 14711     CCA   CCCA      C
           A                     TTC   TGC    GGCTCCTG AG
                                |||   |||    |||||||| ||
                                AAG   ACG    CCGAGGGC TC
                                  AGC   CAAC       _
GAM977  DAG1     3' CTGCAGGATGTAACATGG    16553      CCCCAG  _
                                CCATG     GC TCCTGCAG
                                |||||     || ||||||||
                                GGTAC     TG AGGACGTC
                                   AA____  T
GAM977  GPRK7    3' CGGGAGCCTGAGGCAGGAGAA  58313     _  A    C
                                TTC CC TGCC CAGGCTCCTG
                                ||| || |||| ||||||||||
                                AAG GG ACGG GTCCGAGGGC
                                  A  _    A
GAM977  KIF1B    3' TGGGAGCCTGAGGCAGGAGAA  31273     _  A    C
                                TTC CC TGCC CAGGCTCCTG
                                ||| || |||| ||||||||||
                                AAG GG ACGG GTCCGAGGGT
                                  A  _    A
GAM977  NCAM1    5' CTGCAGGGGGGGGGGCACAGAA 7040      CCA     AGG
                                TTC   TGCCCC   CTCCTGCAG
                                |||   ||||||   |||||||||
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                                AAG  ACGGGG  GGGGACGTC
                                  AC_    GG_
GAM977  NOS1    3'  CTGCAGGGTCCCCAAGGATGG  7095      G  CCA_  CT
                                CCAT CC   GG  CCTGCAG
                                |||| ||   ||  |||||||
                                GGTA GG   CC  GGACGTC
                                  _ AACC  TG
GAM977  PDGFRB  3'  TGCCCCAGGGACATGGGAA   66584       _  CA  CTCCT
                                TTCCCATG CCC  GG   GCA
                                |||||||| |||  ||   |||
                                AAGGGTAC GGG  CC   CGT
                                    A  AC  _____
GAM977  RAB31   3'  CTGCAGGGGGCGGGGCAGGAA  23440     CA    AGG
                                TTCC  TGCCCC  CTCCTGCAG
                                ||||  ||||||  |||||||||
                                AAGG  ACGGGG  GGGGACGTC
                                  __    CG_
GAM977  SCN4A   3'  CTGCGTTCCCAGACCATGGGAA 6200        CCCCA  CTCC
                                TTCCCATG   GG   TGCAG
                                ||||||||   ||   |||||
                                AAGGGTAC   CC   GCGTC
                                    CAGAC  TT__
GAM977  WHSC1   3'  CTGCAATGACTGCAGGGCTGGG 24667      T   __  GCTCC
          AA                  TTCCCA GCCC  CAG   TGCAG
                              |||||| ||||  |||   |||||
                              AAGGGT CGGG  GTC   ACGTC
                                _   AC   AGTA_
GAM977  WHSC1   3'  CTGCAATGACTGCAGGGCTGGG 24668      T   __  GCTCC
          AA                  TTCCCA GCCC  CAG   TGCAG
                              |||||| ||||  |||   |||||
                              AAGGGT CGGG  GTC   ACGTC
                                _   AC   AGTA_
GAM977  WHSC1   3'  CTGCAATGACTGCAGGGCTGGG 24669      T   __  GCTCC
          AA                  TTCCCA GCCC  CAG   TGCAG
                              |||||| ||||  |||   |||||
                              AAGGGT CGGG  GTC   ACGTC
                                _   AC   AGTA_
GAM977  ZFP36L1 3'  CTGCAGGAAGGAAGGCTG   18201   T  __  AGGC
                              CA GCC  CC   TCCTGCAG
                              || |||  ||   ||||||||
                              GT CGG  GG   AGGACGTC
                                _  AA  A___
GAM977  C20orf64 5' CAAGAGCCCTTCCTGCAGGGAA 54334      A  CCCA__   C
                              TTCCC TGC    GGCTC TG
                              ||||| |||    ||||| ||
                              AAGGG ACG    CCGAG AC
                                _  TCCTTC   A
GAM977  DRIL2   3'  CTGCAGGGTGTGGGCAGAGAA  22350    CCA   C G  T
                              TTC  TGCCC A GC CCTGCAG
                              |||  ||||| | || |||||||
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                                AAG   ACGGG T TG GGACGTC
                                  AG_     _ G  _
GAM977  FEM-2     3'  CTGCAGGGCCAAGCCACAGGAA 28312      CAT_  CCCA   T
                                TTCC    GC    GGC CCTGCAG
                                ||||    ||    ||| |||||||
                                AAGG    CG    CCG GGACGTC
                                  ACAC  AA__   _
GAM977  FLJ10737  3'  CTGCAGTCCAAGCTGAACATGG 37054        CCCCA    C___
           GAA                    TTCCCATG    GGCT    CTGCAG
                                ||||||||    ||||    ||||||
                                AAGGGTAC    TCGA    GACGTC
                                    AAG__    ACCT
GAM977  FLJ10898  5'  CTGCCAAACCTGCAACATGGGA 60133        CCC    CTCCT
           A                     TTCCCATG   CAGG    GCAG
                                ||||||||   ||||    ||||
                                AAGGGTAC   GTCC    CGTC
                                    AAC    AAAC_
GAM977  FLJ11618  3'  CTGCAGGGGGAAGAGCCGGGAA 42624      AT  CCCAGG
                                TTCCC  GC     CTCCTGCAG
                                |||||  ||     |||||||||
                                AAGGG  CG     GGGGACGTC
                                  C_  AGAAG_
GAM977  FLJ12287  5'  TGCCTCTGGGGCCTGGGAA   42564       T       CTCCT
                                TTCCCA GCCCCAGG    GCA
                                |||||| ||||||||    |||
                                AAGGGT CGGGGTCT    CGT
                                    C       C_____
GAM977  FLJ14129  3'  TGGGAGCCTGGGGCAGGAGAA  48814     _  A
                                TTC CC TGCCCCAGGCTCCTG
                                ||| || ||||||||||||||
                                AAG GG ACGGGGTCCGAGGGT
                                  A  _
GAM977  KIAA0187  3'  CTGCAGGAGGAGGAACAGAGAA 29250     CCA  CC  AGG
                                TTC   TG  CC   CTCCTGCAG
                                |||   ||  ||   |||||||||
                                AAG   AC  GG   GAGGACGTC
                                  AG_  AA  AG_
GAM977  KIAA0416  5'  GGAAAGCCTGGGACACAGAA   32093     CCA  C      __
                                TTC   TG CCCAGGC  TCC
                                |||   || |||||||  |||
                                AAG   AC GGGTCCG  AGG
                                  AC_  A      AA
GAM977  KIAA1266  3'  CTGCAAGGGCGAGCATGGGA   66695        CCCAG    C
                                TCCCATGC    GCTC TGCAG
                                ||||||||    |||| |||||
                                AGGGTACG    CGGG ACGTC
                                    AG____    A
GAM977  KIAA1483  3'  CTGCAGGGAAAAGGATATAGGA 70434      C   C  CAGG T
           A                     TTCC ATG CC    C CCTGCAG
                                |||| ||| ||    | |||||||
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                                AAGG TAT GG    G GGACGTC
                                  A  A  AAAA _
GAM977  KIAA1706  3'  TGCAGTGAGAGCATGGGA    94372        CCCAGG  _
                                TCCCATGC     CTC CTGCA
                                ||||||||     ||| |||||
                                AGGGTACG     GAG GACGT
                                    A_____   T
GAM977  KIAA1715  3'  CTCAGGAGCCTGAGGCAGGAGA 68684     _ A   C       C
           A                     TTC CC TGCC CAGGCTCCTG AG
                                 ||| || |||| |||||||||| ||
                                 AAG GG ACGG GTCCGAGGAC TC
                                   A _   A        _
GAM977  KIAA1981  3'  CAGGAGCCAAGGTCACAGAA   89710    CCA  C  CA
                                 TTC   TG CC  GGCTCCTG
                                 |||   || ||  ||||||||
                                 AAG   AC GG  CCGAGGAC
                                   AC_  T  AA
GAM977  MCAM      3'  CAGGAACCTGGGGGCCTGTGAA 22457     C  T    _  C
                                 TTC CA GCCCC AGG TCCTG
                                 ||| || ||||| ||| |||||
                                 AAG GT CGGGG TCC AGGAC
                                   T  C    G   A
GAM977  MRPS24    3'  CTGCAGAGAATGGAAACGTGGG 50130        CC_   GG   C
           AA                    TTCCCATG   CCA  CTC TGCAG
                                 ||||||||   |||  ||| |||||
                                 AAGGGTGC   GGT  GAG ACGTC
                                     AAA   AA   _
GAM977  MSE55     3'  TGCAGGACAGACATGGGAG   23916        CCCCAGGC
                                 TTCCCATG       TCCTGCA
                                 ||||||||       |||||||
                                 GAGGGTAC       AGGACGT
                                     AGAC____
GAM977  OS4       3'  CTGCTTTGTGCTAAAAGCATGG 20388         CCCA   TCCT_
           GAA                     TTCCCATGC    GGC    GCAG
                                 |||||||||    |||    ||||
                                 AAGGGTACG    TCG    CGTC
                                      AAAA   TGTTT
GAM977  PASK      5'  CAGGGTCTCGCCTGGGGCATTA 31405     CC         ____
           GAA                     TTC  ATGCCCCAGGC    TCCTG
                                 |||  ||||||||||    |||||
                                 AAG  TACGGGGTCCG    GGGAC
                                   AT         CTCT
GAM977  PRO1163   3'  CTGAATGAGCCTGGGGCA    38323          CTG
                                 TGCCCCAGGCTC   CAG
                                 ||||||||||||   |||
                                 ACGGGGTCCGAG   GTC
                                        TAA
GAM977  THEA      3'  CTCAGGAAGCTGAGGCACAAGA 66887     CCA    C   GC    C
           A                      TTC   TGCC CAG  TCCTG AG
                                  |||   |||| |||  ||||| ||
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                                AAG   ACGG GTC  AGGAC TC
                                  AAC    A   GA    _
GAM977  WFDC3    3'  GCTGACCAGAGCATGGGAA   98702        CCCA  C  CT
                                TTCCCATGC    GG TC  GC
                                |||||||||    || ||  ||
                                AAGGGTACG    CC AG  CG
                                     AGA_  _  T_
GAM977  LOC122726 5'  CTGCAGGAAACACTGAGGCTTG 76103       T   C   GC__
          GGAA                    TTCCCA GCC CAG    TCCTGCAG
                                |||||| ||| |||    ||||||||
                                AAGGGT CGG GTC    AGGACGTC
                                   T   A   ACAA
GAM977  LOC129303 3'  CTGCAGGAATTGGGGGCTGGGA 75373       T     AG C
          A                      TTCCCA GCCCC  G TCCTGCAG
                                |||||| |||||  | ||||||||
                                AAGGGT CGGGG  T AGGACGTC
                                   _    GT A
GAM977  LOC132617 5'  CTGCAGATCGAGGCATGGGA   76415        CCA  CTC
                                TCCCATGCC   GG   CTGCAG
                                |||||||||   ||   ||||||
                                AGGGTACGG   CT   GACGTC
                                     AG_  A__
GAM977  LOC145945 5'  AGGGCCTGGACCATAGAA    84563     CC   CC     T
                                TTC  ATG  CCAGGC CCT
                                |||  |||  |||||| |||
                                AAG  TAC  GGTCCG GGA
                                  A_   CA     _
GAM977  LOC146332 3'  CAGGAGCCTGGGGCCTGTGGA  78353     _  T
                                TCC CA GCCCCAGGCTCCTG
                                ||| || ||||||||||||||
                                AGG GT CGGGGTCCGAGGAC
                                  T  C
GAM977  LOC146714 5'  TGCAGGGCAGGCACAGGGA   84754      A_    CCAG  T
                                TCCC  TGCC    GC CCTGCA
                                ||||  ||||    || ||||||
                                AGGG  ACGG    CG GGACGT
                                   AC    A___  _
GAM977  LOC147958 3'  CTGCAGGGCAGGCAGCAGAA   88523     CCA    CCAG  T
                                TTC   TGCC    GC CCTGCAG
                                |||   ||||    || |||||||
                                AAG   ACGG    CG GGACGTC
                                   ACG    A___  _
GAM977  LOC149501 3'  CTGCAAGAGCCTGGCTGGGAA  75800       T   CC     C
                                TTCCCA GCC  AGGCTC TGCAG
                                |||||| |||  |||||| |||||
                                AAGGGT CGG  TCCGAG ACGTC
                                   _   __     A
GAM977  LOC150397 3'  CAGGAGCCTGAGTGAAGGA   80655     CA   CC
                                TCC  TGC  CAGGCTCCTG
                                |||  |||  ||||||||||
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                                AGG  GTG  GTCCGAGGAC
                                  AA   A_
GAM977   LOC150397 3'  GCAGGAGCCTGCAGGAGA    80664    _  A   CCC
                                TC CC TGC   AGGCTCCTGC
                                || || |||   ||||||||||
                                AG GG ACG   TCCGAGGACG
                                 A  _  ___
GAM977   LOC150517 5'  CTGCAGGTAGGAGCACAGAA   80725    CCA   C  AGGCT
                                TTC   TGC CC    CCTGCAG
                                |||   ||| ||    |||||||
                                AAG   ACG GG    GGACGTC
                                  AC_   A  AT___
GAM977   LOC153688 3'  TGGGAGGCTGGGGCATGAGAA  87341     C        G
                                TTC CATGCCCCAG CTCCTG
                                ||| |||||||||| ||||||
                                AAG GTACGGGGTC GAGGGT
                                  A         G
GAM977   LOC154849 3'  CTGCAGGAGGTGGAAGATG   60941    GCC   GG
                                CAT   CCA  CTCCTGCAG
                                |||   |||  |||||||||
                                GTA   GGT  GAGGACGTC
                                  GAA   G_
GAM977   LOC162137 3'  GCAGGAGCTTCCCATAAAGAA  88480    CC_   CCCC
                                TTC   ATG    AGGCTCCTGC
                                |||   |||    ||||||||||
                                AAG   TAC    TTCGAGGACG
                                  AAA   CC__
GAM977   LOC219654 3'  CAGGAGCCCAGGGGATGGGAA  92925        G   CA
                                TTCCCAT CCC  GGCTCCTG
                                ||||||| |||  ||||||||
                                AAGGGTA GGG  CCGAGGAC
                                    G   AC
GAM977   LOC254552 5'  CAGGAGCCCGGGGCTGG     96422     T    A
                                CCA GCCCC GGCTCCTG
                                ||| ||||| ||||||||
                                GGT CGGGG CCGAGGAC
                                  _     C
GAM977   LOC255042 3'  CTCGGGAGCCTGAGGCAGGAGA 97042     _  A   C        C
            A                    TTC CC TGCC CAGGCTCCTG AG
                                ||| || |||| |||||||||| ||
                                AAG GG ACGG GTCCGAGGGC TC
                                  A  _    A         _
GAM977   LOC257000 3'  CTGCAGGACTCAGAGCATGG   98587       CCCA  C
                                CCATGC    GG TCCTGCAG
                                ||||||    || ||||||||
                                GGTACG    TC AGGACGTC
                                   AGAC  _
GAM977   LOC91750  3'  TGGGGGCCTGAGGCACGAGAA  67659     CCA    C
                                TTC   TGCC CAGGCTCCTG
                                |||   |||| ||||||||||
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                                AAG   ACGG GTCCGGGGGT
                                  AGC    A
GAM978  HRH1     3'  AAATGTGCCCTTTTGGCCGG   7812     A       AA  TCA
                                CC GGCCAAAA  GC   ACATTT
                                || ||||||||  ||   ||||||
                                GG CCGGTTTT  CG   TGTAAA
                                  _       CC  ___
GAM978  SHANK2   3'  GTTGAACTTCTTCTTTGGCCTC 25531   C       A   C___
           A                     C AGGCCAAA AAG    TCAAC
                                | ||||||| |||    |||||
                                A TCCGGTTT TTC    AGTTG
                                 C       C   TTCA
GAM978  SPTA1    3'  AAATGTTGAGCTTCTATATTTC 13387     CCAAAA_
           TG                     CAGG      AAGCTCAACATTT
                                ||||      ||||||||||||
                                GTCT      TTCGAGTTGTAAA
                                  TTATATC
GAM978  FLJ13189 3'  TTGAACCTTTTTTGCCTGG    46498       C      C_
                                CCAGGC AAAAAAG  TCAA
                                |||||| |||||||  ||||
                                GGTCCG TTTTTTC  AGTT
                                   _      CA
GAM978  FLJ20208 3'  AAATGCAGGCTTTTTAGCC    35240     CA       CAA
                                GGC  AAAAAGCT   CATTT
                                |||  ||||||||   |||||
                                CCG  TTTTTCGG   GTAAA
                                  A_       AC_
GAM978  FLJ22944 3'  AAATGTTGGGATTTGAACCC   47866    CCAAA   G
                                GG     AAA CTCAACATTT
                                ||     ||| ||||||||||
                                CC     TTT GGGTTGTAAA
                                 CAAG_   A
GAM978  KIAA1843 3'  AAATGTTGACTGAACCTGACCT 62880      C  AAAA_  C
           G                     CAGG CA     AG TCAACATTT
                                |||| ||     || |||||||||
                                GTCC GT     TC AGTTGTAAA
                                  A  CCAAG  _
GAM978  KIAA1975 3'  AAATGTTGATTTTTCTGACC   74407    C  A    C
                                GG CA AAAAG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM978  MRIP2    3'  AAATGTTGATTTTTCTGACC   56789    C  A    C
                                GG CA AAAAG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM978  PKNOX2   3'  GTCTAGCTTTTTTGGCGTG   92532    G         CA
                                CA GCCAAAAAAGCT  AC
                                || ||||||||||||  ||
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                                GT CGGTTTTTTCGA  TG
                                 G          TC
GAM978  LOC118704 3'  AAATGTTGATTTTTCTGACC   74359    C  A    C
                                GG CA AAAAG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM978  LOC118706 3'  AAATGTTGATTTTTCTGACC   74361    C  A    C
                                GG CA AAAAG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM978  LOC123036 3'  AAATGTTTGCAGTTTTGGCT   74645        AA  TC
                                GGCCAAAA  GC  AACATTT
                                ||||||||  ||  |||||||
                                TCGGTTTT  CG  TTGTAAA
                                     GA  T_
GAM978  LOC123624 3'  AAATGTTGGGCTTCTGTGCCT  76134     _  AAA
                                AGGC CA   AAGCTCAACATTT
                                |||| ||   ||||||||||||
                                TCCG GT   TTCGGGTTGTAAA
                                  T  C__
GAM978  LOC126917 3'  TGAGCTTTCTAGGCCTGG    75100       AAA
                                CCAGGCC   AAAGCTCA
                                |||||||   ||||||||
                                GGTCCGG   TTTCGAGT
                                     ATC
GAM978  LOC143158 3'  AAATGTTGATTTTTCTGACC   76997    C  A    C
                                GG CA AAAAG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM978  LOC143425 3'  TTGGGCTTCTCTGGCCTG    89017       AAA
                                CAGGCCA   AAGCTCAA
                                |||||||   ||||||||
                                GTCCGGT   TTCGGGTT
                                     CTC
GAM978  LOC195979 3'  AAATGTTGATTTTTCTGACC   88928    C  A    C
                                GG CA AAAAG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM978  LOC219672 5'  AATGGTGCTTTTTGGCTGG    92963     G     A  TCAA
                                CCAG CCAAAAA GC    CATT
                                |||| ||||||| ||    ||||
                                GGTC GGTTTTT CG    GTAA
                                  _      _  TG__
GAM978  LOC220466 3'  AAATGTTGATTTTTCTGACC   74398    C  A    C
                                GG CA AAAAG TCAACATTT
                                || || ||||| |||||||||
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                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM978  LOC254105 3'  AGGTGTGGCCCCCTTGGCCTGG 96416         AAAA  CA
                                CCAGGCCAA   GCT  ACATTT
                                |||||||||   |||  ||||||
                                GGTCCGGTT   CGG  TGTGGA
                                     CCCC  __
GAM978  LOC255319 3'  AAATGTTGATTTTTCTGACC  96152    C  A    C
                                GG CA AAAAG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM978  LOC91300  5'  GTTGAGCTTTTCTGGCCCGG  96238    A    A
                                CC GGCCA AAAAGCTCAAC
                                || ||||| ||||||||||
                                GG CCGGT TTTTCGAGTTG
                                 C    C
GAM978  LOC91300  5'  GTTGAGCTTTTCTGGCCCGG  96239    A    A
                                CC GGCCA AAAAGCTCAAC
                                || ||||| ||||||||||
                                GG CCGGT TTTTCGAGTTG
                                 C    C
GAM978  LOC91660  5'  AAATGTTTATCTTCTTTTTGGC 67399         __  CTC
           TT                    AGGCCAAAAA  AG   AACATTT
                                ||||||||||  ||   |||||||
                                TTCGGTTTTT  TC   TTGTAAA
                                     CT  TAT
GAM979  FLJ10307  3'  TGAAACAAATCTTTGCCAAG  36479          C   GTG
                                TTTGGCAAAGA TTG   CA
                                |||||||||||| |||   ||
                                GAACCGTTTCT AAC   GT
                                      A   AAA
GAM979  FLJ21369  3'  CATCAAGTTTCACCAAA     46048      CAA
                                TTTGG   AGACTTGGTG
                                |||||   ||||||||||
                                AAACC   TTTGAACTAC
                                   AC_
GAM979  IMAP1     3'  TTTGCAACTTTGCCAAA     56237         ACTTGG
                                TTTGGCAAAG     TGCAGA
                                |||||||||      ||||||
                                AAACCGTTTC     ACGTTT
                                     A_____
GAM979  KIAA0258  3'  CATTCAGCCTTTGCCAAA    29464          A  TG
                                TTTGGCAAAG CT  GTG
                                |||||||||| ||  |||
                                AAACCGTTTC GA  TAC
                                      C  CT
GAM979  KIAA1243  3'  TGCCAAGTATTTGCCAAA    74030          G
                                TTTGGCAAA ACTTGGTG
                                |||||||| ||||||||
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                                AAACCGTTT TGAACCGT
                                     A
GAM979  NET-5    3'  CATCTGCATATGCGTATTTGCC 22892        G  TTG_
            AAA                   TTTGGCAAA AC    GTGCAGATG
                                  ||||||||| ||    |||||||||
                                  AAACCGTTT TG    TACGTCTAC
                                       A  CGTA
GAM979  PRO0902  5'  CATCAAGTGTCTGCCAAA    54963       AAG
                                  TTTGGCA   ACTTGGTG
                                  |||||||   ||||||||
                                  AAACCGT   TGAACTAC
                                      CTG
GAM979  SIMRP7   3'  CATCTGCAAACGCTTTGCCAA  93968        ACTTGG
                                  TTGGCAAAG     TGCAGATG
                                  |||||||||     ||||||||
                                  AACCGTTTC     ACGTCTAC
                                       GCAA__
GAM979  LOC145824 3'  CAGCAAACTTTGCCAAA     77983         AC   G
                                  TTTGGCAAAG  TTG TG
                                  ||||||||||  ||| ||
                                  AAACCGTTTC  AAC AC
                                       A_   G
GAM979  LOC151643 3'  ATCTGAGCCTTTGCCAA     81136        GACTT   G
                                  TTGGCAAA    GGT CAGAT
                                  ||||||||    ||| |||||
                                  AACCGTTT    CCG GTCTA
                                        _____  A
GAM979  LOC169026 3'  CATCTGTGCCATCTCTGC    83601     A   CT   TG
                                  GCA AGA  TGG  CAGATG
                                  ||| |||  |||  ||||||
                                  CGT TCT  ACC  GTCTAC
                                    C   __   GT
GAM979  LOC200197 3'  CATCTGCACCTGCACTCCCAAA 90014      CAA  ACTT
                                  TTTGG   AG   GGTGCAGATG
                                  |||||   ||   ||||||||||
                                  AAACC   TC   CCACGTCTAC
                                     C__  ACGT
GAM979  LOC222223 3'  GTCAAGTACCTTGCCAAA    95885        AGACTT    A_
                                  TTTGGCAA     GGTGC  GAT
                                  ||||||||     |||||  |||
                                  AAACCGTT     CCATG  CTG
                                        _______    AA
GAM979  LOC90906  3'  CATTTGTCAGCCCTTGCCAAA  64948        A ACTT   __
                                  TTTGGCAA G    GGT  GCAGATG
                                  |||||||| |    |||  |||||||
                                  AAACCGTT C    CCG  TGTTTAC
                                        _ _____  AC
GAM979  LOC91137  3'  CATCTGACTTCAATATTTGCCA 57859         GAC    TG_
            AA                    TTTGGCAAA   TTGG   CAGATG
                                  |||||||||   ||||   ||||||
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                                AAACCGTTT  AACT  GTCTAC
                                    AT_   TCA
GAM980  MEN1     5' CAGAATCCATGTACCTTTGCTA 56343          _____
                                TAGCAAAGGTGCA    TCTG
                                ||||||||||||    ||||
                                ATCGTTTCCATGT    AGAC
                                     ACCTA
GAM980  FLJ20294 3' CGGATGTCTGCACCTTCGCT  35352    A      TCTGT
                                AGC AAGGTGCA    CATCCG
                                ||| ||||||||    ||||||
                                TCG TTCCACGT    GTAGGC
                                  C      CT___
GAM980  KIAA1727 3' GATGGATGCACGTTCACTA   64762    CA  G
                                TAG  AA GTGCATCTGTC
                                |||  || ||||||||||
                                ATC  TT CACGTAGGTAG
                                  AC  G
GAM980  MGC10715 3' GGGGCAATGCACCTTTGC    44501         C   AT
                                GCAAAGGTGCAT TGTC  CC
                                |||||||||||| ||||  ||
                                CGTTTCCACGTA ACGG  GG
                                      _   __
GAM980  LOC201283 3' TGACAAACCACCTCTGCTA  61055     A    CATC
                                TAGCA AGGTG   TGTCA
                                ||||| |||||   |||||
                                ATCGT TCCAC   ACAGT
                                   C    CAA_
GAM980  LOC51110 3' GATTTCTATGCACCTTTACT  32626   C       CT__
                                AG AAAGGTGCAT   GTC
                                || ||||||||||   |||
                                TC TTTCCACGTA   TAG
                                 A        TCTT
GAM981  RAB33A   3' ACCTGCTTGTTTCCATACAAAT 17738     A       TGAA
                                ATTT TGTGGAAGC   CAGGT
                                |||| |||||||||   |||||
                                TAAA ATACCTTTG   GTCCA
                                  C       TTC_
GAM981  FLJ32942 3' TACTCAGAAGCTTCCAAATAAA 58722      G      GAACA
                                TTTAT TGGAAGCT    GGTA
                                ||||| ||||||||    ||||
                                AAATA ACCTTCGA    TCAT
                                   A      AGAC_
GAM981  KIAA0776 3' ACCTGATTTTCACACAAAT   65449     A      CTGAA
                                ATTT TGTGGAAG    CAGGT
                                |||| ||||||||    |||||
                                TAAA ACACTTTT    GTCCA
                                  C      A____
GAM981  PRO0456  5' TACCTGTTCTGGATATTTCACA 27009          GCT___
           TAAAT                 ATTTATGTGGAA     GAACAGGTA
                                ||||||||||||     |||||||||
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                                TAAATACACTTT    CTTGTCCAT
                                      ATAGGT
GAM981  ZNF259   3' ACCCTCCTTCCACATAA    73021         CT  ACA
                                TTATGTGGAAG  GA  GGT
                                ||||||||||  ||  |||
                                AATACACCTTC  CT  CCA
                                      __ C__
GAM981  LOC121344 3' ACCTGTTCTCTGGCCTCACA  74499     AA  ___
                                TGTGG  GCT  GAACAGGT
                                |||||  |||  ||||||||
                                ACACT  CGG  CTTGTCCA
                                   C_  TCT
GAM982  BCAT1    5' AGGTGGGCAGGAGCCAGTGA  66783        CAC  TG
                                TCGCTGGCTCC  TT  TCT
                                ||||||||||  ||  |||
                                AGTGACCGAGG  GG  GGA
                                      AC_  GT
GAM982  BCL2     3' GCATGGGAGCCACGA     7149     C      CTT
                                TCG TGGCTCCCA  TGT
                                ||| |||||||||  |||
                                AGC ACCGAGGGT  ACG
                                  _     ___
GAM982  CDX2     5' GCGAGGAGCCAGCGG      8852         CACT
                                TCGCTGGCTCC   TTGT
                                ||||||||||   ||||
                                GGCGACCGAGG   AGCG
                                      ____
GAM982  FAAH     3' AGAAGGAGAAGCCAGTGA   97235       CCCA  TG
                                TCGCTGGCT   CTT  TCT
                                |||||||||   |||  |||
                                AGTGACCGA   GAG  AGA
                                     A___   GA
GAM982  FADD     5' AGACCTGGCCAGGGCCAGCGA  15121        CCA  TT
                                TCGCTGGCTC  CT  GTCT
                                ||||||||||  ||  ||||
                                AGCGACCGGG  GG  CAGA
                                      ACC  TC
GAM982  FCMD     3' ACATAAGTGGGAACCAAAGA  23021   GC  C     _
                                TC  TGG TCCCACTT TGT
                                ||  ||| |||||||| |||
                                AG  ACC AGGGTGAA ACA
                                 AA  A      T
GAM982  FOXD2    5' AGAACCCTGGGAGCCAGGA   16783   G       CTTTG
                                TC CTGGCTCCCA    TCT
                                || ||||||||||    |||
                                AG GACCGAGGGT    AGA
                                 _       CCCA_
GAM982  GNGT2    3' AGACCCCCAGGGAGCCAGTGA 49809          ACTTT
                                TCGCTGGCTCCC    GTCT
                                ||||||||||||    ||||
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                                AGTGACCGAGGG    CAGA
                                      ACCCC
GAM982  GRIA3    5'  GGGGTGTAAGAGCCAGCGA   7714         C__
                                TCGCTGGCTC  CACTTT
                                ||||||||||  ||||||
                                AGCGACCGAG  GTGGGG
                                      AAT
GAM982  GRIA3    5'  GGGGTGTAAGAGCCAGCGA   7715         C__
                                TCGCTGGCTC  CACTTT
                                ||||||||||  ||||||
                                AGCGACCGAG  GTGGGG
                                      AAT
GAM982  IFNAR2   3'  ACAGGGAAGAGCCATCGA    7893     C    CCA
                                TCG TGGCTC  CTTTGT
                                ||| ||||||  ||||||
                                AGC ACCGAG  GGGACA
                                  T     AA_
GAM982  MDFI     5'  GCACCCGGGAGCCAGCGG    19981          ACTT
                                TCGCTGGCTCCC   TGT
                                ||||||||||||   |||
                                GGCGACCGAGGG   ACG
                                      CCC_
GAM982  OAS1     3'  AGACAAAGCTCCTCAGTGA   34146       CTCCCA
                                TCGCTGG     CTTTGTCT
                                |||||||     ||||||||
                                AGTGACT     GAAACAGA
                                    CCTC__
GAM982  PLAB     5'  AGACAAGGAGAGCCAGGA    66426    G     CCA
                                TC CTGGCTC  CTTTGTCT
                                || |||||||  ||||||||
                                AG GACCGAG  GGAACAGA
                                 _      A__
GAM982  RLN2     3'  AGACAAAGTGAAGCCGC     18583    T   CC
                                GC GGCT  CACTTTGTCT
                                || ||||  ||||||||||
                                CG CCGA  GTGAAACAGA
                                 _   A_
GAM982  SDS      3'  AAGGTCGGCAGCCAGCGA    23377        _ C
                                TCGCTGGCT CC ACTTT
                                ||||||||| || |||||
                                AGCGACCGA GG TGGAA
                                      C  C
GAM982  SEPN1    3'  GGACTGCGGGAGCCAGCG    66975          ACTTT
                                CGCTGGCTCCC    GTCT
                                ||||||||||     ||||
                                GCGACCGAGGG    CAGG
                                      CGT__
GAM982  SLC2A1   3'  GGGCCTGTGGGAGCCTGC    22517    T       TTT
                                GC GGCTCCCAC   GTCT
                                || |||||||||   ||||
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                                CG CCGAGGGTG   CGGG
                                 T        TC_
GAM982  SLC9A3R2  3'  AGACAGAGAGAGAGCGAGCGA  62098      G    CCA
                                TCGCT GCTC   CTTTGTCT
                                ||||| ||||   ||||||||
                                AGCGA CGAG   GAGACAGA
                                   G    AGA
GAM982  STK19     3'  GGCTTGGGAGCCAGGA      51614    G        CTTT
                                TC CTGGCTCCCA    GTC
                                || ||||||||||    |||
                                AG GACCGAGGGT    CGG
                                 _        T___
GAM982  STK19     3'  GGCTTGGGAGCCAGGA      16098    G        CTTT
                                TC CTGGCTCCCA    GTC
                                || ||||||||||    |||
                                AG GACCGAGGGT    CGG
                                 _        T___
GAM982  TUFT1     3'  AGGCCTGGTGAGAGCCAGTGA  39668          C    TT
                                TCGCTGGCTC CACT  GTCT
                                |||||||||| ||||  ||||
                                AGTGACCGAG GTGG  CGGA
                                      A    TC
GAM982  C20orf32  5'  AGACAAAGTGAGACGTCAG    40138      _  C
                                CTGGC TC CACTTTGTCT
                                ||||| || ||||||||||
                                GACTG AG GTGAAACAGA
                                   C  A
GAM982  DKFZP564I052 3'  AGACAAAGTTTTAACCAATGA  67277     C   CTCCC
                                TCG TGG     ACTTTGTCT
                                ||| |||     |||||||||
                                AGT ACC     TGAAACAGA
                                  A   AATTT
GAM982  DKFZP727M111 5'  AGACAAGCTGGAGCCAG     32052         CAC
                                CTGGCTCC   TTTGTCT
                                ||||||||   |||||||
                                GACCGAGG   GAACAGA
                                     TC_
GAM982  DREV1     3'  AGACAAAGCAATAGTCACGA   32617     C    CCCA
                                TCG TGGCT    CTTTGTCT
                                ||| |||||    ||||||||
                                AGC ACTGA    GAAACAGA
                                  _     TAAC
GAM982  FLJ11588  5'  GGGGCGGAAGCCGAGCGA    45123      _   C  A
                                TCGCT GGCT CC CTTT
                                ||||| |||| || ||||
                                AGCGA CCGA GG GGGG
                                   G    A  C
GAM982  FLJ12089  3'  AGATCTGGGAGCCAGC      44948          CTTT
                                GCTGGCTCCCA    GTCT
                                ||||||||||    ||||
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                                CGACCGAGGGT   TAGA
                                      C___
GAM982  FLJ12221  5'  GGGCGCGGGAGCCGGCGA   63221         ACTT
                                TCGCTGGCTCCC   TGTCT
                                ||||||||||||  |||||
                                AGCGGCCGAGGG   GCGGG
                                      C___
GAM982  FLJ21596  3'  ACAAAATGGAGTGTAAGCGG  46112     G__   CAC
                                TCGCT  GCTCC  TTTGT
                                |||||  |||||  |||||
                                GGCGA  TGAGG  AAACA
                                   ATG   TA_
GAM982  GALNT12   3'  GACTGTGGAGCCAGGA     45316   G     C  TTT
                                TC CTGGCTCC AC  GTC
                                || ||||||| ||  |||
                                AG GACCGAGG TG  CAG
                                 _      _ T__
GAM982  HIC2      3'  AGTCGTGTGCAGGAGCCAGC  65858       __  TT  T
                                GCTGGCTCC  CAC  TG CT
                                |||||||||  |||  || ||
                                CGACCGAGG  GTG  GC GA
                                     AC   T_  T
GAM982  HSPC156   5'  GGCGCGGGAGCCGCGA     27189     T     ACTT
                                TCGC GGCTCCC   TGTC
                                |||| |||||||   ||||
                                AGCG CCGAGGG   GCGG
                                  _     C___
GAM982  KCNH8     3'  AGAGTGTGAGGAGCCAGGGA  58904   G     _  TTTG
                                TC CTGGCTCC CAC   TCT
                                || |||||||| |||   |||
                                AG GACCGAGG GTG   AGA
                                 G      A  TG__
GAM982  KIAA0523  5'  AGGTGCCAGGAGCCAGGA   68355   G     ___
                                TC CTGGCTCC  CACTT
                                || ||||||||  |||||
                                AG GACCGAGG  GTGGA
                                 _      ACC
GAM982  KIAA0876  3'  GGGCGACAGGAGCCAGCGG  65318        CACT
                                TCGCTGGCTCC   TTGTCT
                                ||||||||||   ||||||
                                GGCGACCGAGG   AGCGGG
                                      AC__
GAM982  KIAA1322  3'  AGACGGAGGAGCGAGC     73107    G   CAC
                                GCT GCTCC  TTTGTCT
                                ||| |||||  |||||||
                                CGA CGAGG  AGGCAGA
                                  G   ___
GAM982  KIAA1483  3'  AGACAAAACAGGAGCCAG   70430       CAC
                                CTGGCTCC  TTTGTCT
                                ||||||||  |||||||
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                                GACCGAGG   AAACAGA
                                     ACA
GAM982  KIAA1656 3'  GGGCGGTGGGAGCCAGT     66379          TT
                                GCTGGCTCCCACT  GTCT
                                ||||||||||||  ||||
                                TGACCGAGGGTGG  CGGG
                                                __
GAM982  KIAA1822 3'  AGCCGGGGTGGGAACCAGGA  68178    G   C       T
                                TC CTGG TCCCACTTTG CT
                                || |||| |||||||||| ||
                                AG GACC AGGGTGGGGC GA
                                 _   A        C
GAM982  LENG9    3'  AGACAAAGCAGGAGCGTGC   75022    TG    CA
                                GC  GCTCC  CTTTGTCT
                                ||  |||||  ||||||||
                                CG  CGAGG  GAAACAGA
                                 TG    AC
GAM982  MGC1842  3'  AGACAAAGCCTTTGGCCAAGA  66244    GC    CCCA_
                                TC  TGGCT    CTTTGTCT
                                ||  |||||    ||||||||
                                AG  ACCGG    GAAACAGA
                                 A_    TTTCC
GAM982  MGC4737  5'  GGCGAGTGCCAGCGA      49646        TCCC    T
                                TCGCTGGC    ACTT GTC
                                ||||||||    |||| |||
                                AGCGACCG    TGAG CGG
                                             _____   _
GAM982  p25      3'  AGACATGCGGGAGCCAGGA   23822    G       ACTT
                                TC CTGGCTCCC    TGTCT
                                || |||||||||    |||||
                                AG GACCGAGGG    ACAGA
                                 _       CGT_
GAM982  PRO0132  5'  AGGCCTAGGAGCTAGCGA    26936          CACTTT
                                TCGCTGGCTCC     GTCT
                                ||||||||||      ||||
                                AGCGATCGAGG     CGGA
                                       ATC___
GAM982  RANBP1   5'  AGGCCGCGGAGCCAGCGA    12762          CACTTT
                                TCGCTGGCTCC     GTCT
                                ||||||||||      ||||
                                AGCGACCGAGG     CGGA
                                       CGC___
GAM982  SDCCAG3  3'  AGACATTGTCATAAAAGCCAGT 22800         CCC___  TT
           GA                    TCGCTGGCT     AC  TGTCT
                                ||||||||||      ||  |||||
                                AGTGACCGA     TG  ACAGA
                                      AAATAC  TT
GAM982  LOC134701 5'  AGAGGGGCGGAGAGGCAGCGA  75694       G  _  A   G
                                TCGCTG CTC CC CTTT TCT
                                |||||| ||| || |||| |||
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                                AGCGAC GAG GG GGGG AGA
                                   G   A C   _
GAM982   LOC145694 5'  AGGCGGCGGCAGCCAGCGA   84439         C  A  TT
                                TCGCTGGCT CC CT  GTCT
                                ||||||||| || ||  ||||
                                AGCGACCGA GG GG  CGGA
                                     C  C  __
GAM982   LOC145826 5'  GGGTGCAGGAGCCAGGGA    84530    G       __
                                TC CTGGCTCC  CACTT
                                || ||||||||  |||||
                                AG GACCGAGG  GTGGG
                                 G       AC
GAM982   LOC149773 3'  AGACAAAGTGGTTGGCGA    80289      TG CTC
                                TCGC  G   CCACTTTGTCT
                                ||||  |   ||||||||||
                                AGCG  T   GGTGAAACAGA
                                  GT ___
GAM982   LOC151429 5'  GGGCATGAAAGCCAGGA     86543    G     CC  CTT
                                TC CTGGCT  CA   TGTCT
                                || ||||||  ||   |||||
                                AG GACCGA  GT   ACGGG
                                 _     AA  ___
GAM982   LOC151963 5'  AAAGCCTGGGAGCCTGCGA   81214      T       __
                                TCGC GGCTCCCA  CTTT
                                |||| ||||||||  ||||
                                AGCG CCGAGGGT  GAAA
                                   T       CC
GAM982   LOC152441 5'  AGACAAAATGGGACCAG     86914      C    C
                                CTGG TCCCA TTTGTCT
                                |||| ||||| |||||||
                                GACC AGGGT AAACAGA
                                   _    A
GAM982   LOC158943 5'  AGGCCGCGGAGCCAGCGA    61149           CACTTT
                                TCGCTGGCTCC     GTCT
                                ||||||||||     ||||
                                AGCGACCGAGG     CGGA
                                      CGC___
GAM982   LOC196759 5'  GCTGGTGGGAGCCAGGA     88913    G          TT
                                TC CTGGCTCCCACT  GT
                                || ||||||||||||  ||
                                AG GACCGAGGGTGG  CG
                                 _          T_
GAM982   LOC199864 5'  GCTGGTGGGAGCCAGGA     91460    G          TT
                                TC CTGGCTCCCACT  GT
                                || ||||||||||||  ||
                                AG GACCGAGGGTGG  CG
                                 _          T_
GAM982   LOC200933 5'  GGCGATGAGAACAGCGA     91794       GC  C  CT
                                TCGCTG  TC CA  TTGTC
                                ||||||  || ||  |||||
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                                AGCGAC  AG GT  AGCGG
                                   A_  A  __
GAM982  LOC206973 5'  AGATCTGGCACGGGGGCCAGCG 91110          A__  TT
          A                     TCGCTGGCTCCC   CT  GTCT
                                ||||||||||||   ||  ||||
                                AGCGACCGGGGG   GG  TAGA
                                      CAC  TC
GAM982  LOC221399 5'  AGACAGTGTTGAGCCAGC    95482       C_   TT
                                GCTGGCTC  CACT  GTCT
                                ||||||||  ||||  ||||
                                CGACCGAG  GTGA  CAGA
                                    TT   __
GAM982  LOC254205 5'  GATCAAGAGCCAGTGA     98465        CCACT  _
                                TCGCTGGCTC    TTG TC
                                ||||||||||    ||| ||
                                AGTGACCGAG    AAC AG
                                      _____  T
GAM982  LOC58525  3'  GGGCGCCGGGAGCCAGC     79349        ACTT
                                GCTGGCTCCC    TGTCT
                                ||||||||||    |||||
                                CGACCGAGGG    GCGGG
                                     CC__
GAM983  CADPS    5'  GCCCACCCGGGAGAGCTGAT   65824       CGAC    AC
                                ATCAGCTC    TTTGG  GGGC
                                ||||||||    |||||  ||||
                                TAGTCGAG    GGGCC  CCCG
                                    A___     CA
GAM983  CRSP9    5'  CCAGTGTAAAGCCAGAGCTGA  16225       CGA    G  G
                                TCAGCTC   CTTTG AC GG
                                |||||||   ||||| || ||
                                AGTCGAG   GAAAT TG CC
                                   ACC    G  A
GAM983  DKFZP434B103 3'  TGCCCTTTGAAGTCGGA     32228        TG  C
                                TCCGACTT  GA GGGCA
                                ||||||||  || |||||
                                AGGCTGAA  TT CCCGT
                                    GT  _
GAM983  DTX2     5'  TGCCCAGGCCGAGCCGGAGCTG 72420        A   T  AC_
                                CAGCTCCG CTT GG   GGGCA
                                ||||||||  ||| ||   |||||
                                GTCGAGGC GAG CC   CCCGT
                                    C   _  GGA
GAM983  FLJ10404  5'  TGCCCCGACGAGTCGGAACT   39315    C       T GAC
                                AG TCCGACTT G   GGGCA
                                || |||||||| |   |||||
                                TC AGGCTGAG C   CCCGT
                                 A       _ AGC
GAM983  KIAA1100  3'  GCCCGCCACGGAGCTG      30442        ACTT   A
                                CAGCTCCG    TGG CGGGC
                                ||||||||    ||| |||||
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                                GTCGAGGC   ACC GCCCG
                                    _____  _
GAM983  MGC13170  5'  CCCACCTGGGCCAGAGCTGGT  52129       CGA  TT  AC
                                ATCAGCTC  CT  GG  GGG
                                ||||||||  ||  ||  |||
                                TGGTCGAG  GG  CC  CCC
                                    ACC  GT  A_
GAM983  P2RXL1   3'  TGCCCAGGTAGCTGGAGCTGAT 19564        A  TTGGAC
                                ATCAGCTCCG CT     GGGCA
                                |||||||||| ||     |||||
                                TAGTCGAGGT GA     CCCGT
                                     C  TGGA__
GAM983  LOC140095 5'  TGCCCACCCAACTCCTGGAGCT 76370       ACT_   AC
          G                      CAGCTCCG   TTGG  GGGCA
                                ||||||||   ||||  |||||
                                GTCGAGGT   AACC  CCCGT
                                    CCTC   CA
GAM984  AANAT    3'  AGTGGAGAGAGCAGGGCTAAA  8438         ACA  A
                                TTTGGTTTTG  TC TTCATT
                                ||||||||||  || ||||||
                                AAATCGGGAC  AG AGGTGA
                                     GAG  _
GAM984  ABCB10   3'  GGTGTTGAGAGCTGAGGA   24904     TG   _
                                TTTT  GTTTT GACATC
                                ||||  ||||| ||||||
                                AGGA  CGAGA TTGTGG
                                  GT    G
GAM984  ABCB4    5'  GATGGTGGTAGAGCTGGAG   38760    TG    A
                                TTT  GTTTTG CATCATT
                                |||  |||||| |||||||
                                GAG  CGAGAT GTGGTAG
                                  GT    G
GAM984  ACK1     3'  GATGGAGCAAGGCCAAGG   20513         A__
                                TTTTGGTTTTG  CATC
                                ||||||||||  ||||
                                GGAACCGGAAC  GTAG
                                     GAG
GAM984  ACP1     3'  GATAATGTCAAAATCATGAA  24014    T        CAT
                                TTT TGGTTTTGACAT  TC
                                ||| ||||||||||||  ||
                                AAG ACTAAAACTGTA  AG
                                  T         AT_
GAM984  ACTB     3'  AGTGGGTGGAGGCAGCCAGGG  8463       TT  ACA
                                TTTTGGT  TG  TCATTCATT
                                |||||||  ||  |||||||||
                                GGGACCG  AC  GGTGGGTGA
                                    __ GGA
GAM984  ADAM22   3'  AATGAGCATGCAGGGCTAAGG  41664         A  CA
                                TTTTGGTTTTG CAT  TTCATT
                                |||||||||| |||  ||||||
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                                GGAATCGGGAC GTA  GAGTAA
                                      _  C_
GAM984  ADAM22   3'  AATGAGCATGCAGGGCTAAGG  41663          A  CA
                                TTTTGGTTTTG CAT  TTCATT
                                |||||||||||  |||  ||||||
                                GGAATCGGGAC GTA  GAGTAA
                                      _  C_
GAM984  ADAMTS5  3'  AATGTGGTTAATGCCAAAAA  23857        T    AT
                                TTTTTGGT TTGAC  CATT
                                ||||||||  |||||  ||||
                                AAAAACCG AATTG  GTAA
                                     T    GT
GAM984  ADCY6    3'  ATTGATGTCAGGTCAGGAGCTG 40944     TG  _______     ATTCATT
           GAAG                   TTTT  GTTT     TGACATC
                                ||||  ||||     |||||||
                                GAAG  CGAG     ACTGTAG
                                  GT   GACTGG        TTAC
GAM984  ADD2     3'  GATGGATGGAAGAGCTATAAG  34381     T     GA   AT
                                TTT TGGTTTT  CATC  TC
                                |||  |||||||  ||||  ||
                                GAA ATCGAGA  GTAG  AG
                                  T      AG   GT
GAM984  ADD2     3'  GATGGATGGAAGAGCTATAAG  34382     T     GA   AT
                                TTT TGGTTTT  CATC  TC
                                |||  |||||||  ||||  ||
                                GAA ATCGAGA  GTAG  AG
                                  T      AG   GT
GAM984  ADD2     3'  GGTGCTGTGAGGACCAGGGA   34383          G  T
                                TTTTTGGTTTT ACA CATT
                                ||||||||||| ||| ||||
                                AGGGACCAGGA TGT GTGG
                                      G  C
GAM984  ADK      5'  GGTGGGCTGTAGAGCCAAAG   22991          ACA_
                                TTTTGGTTTTG   TCATT
                                ||||||||||   |||||
                                GAAACCGAGAT   GGTGG
                                      GTCG
GAM984  ADRA2B   3'  AGTGGGTTGTTGAGGCCAGAG  7295          TG  TC
                                TTTTGGTTT  ACA  ATTCATT
                                |||||||||  |||  |||||||
                                GAGACCGGA  TGT  TGGGTGA
                                     GT  __
GAM984  AGR2     3'  GATGAGGCAGATGGAGATCAGA 22163          GA   A__
           G                     TTTTGGTTTT  CATC   TTCATT
                                ||||||||||  ||||  ||||||
                                GAGACTAGAG  GTAG   GAGTAG
                                      __   ACG
GAM984  AGR2     5'  GGTGGGTGAGGAAATCCAGA   22164      T  GACA
                                TTTGG TTT    TCATTCATT
                                |||||  |||   |||||||||
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                                AGACC AAA   AGTGGGTGG
                                  T  GG__
GAM984  AGRN    3'  GATGGCTCCGAAGCCAGAAA  79585          A___
                                TTTTTGGTTTTG   CATC
                                ||||||||||||   ||||
                                AAAGACCGAAGC   GTAG
                                     CTCG
GAM984  AGTR1   3'  GATGAATGTGTTGATTTGAGAA 50261     TG TT TG  T
                                TTTT  G  T  ACA CATTCATT
                                ||||  |  |  ||| ||||||||
                                AAGA  T  A  TGT GTAAGTAG
                                  GT T_ GT  _
GAM984  ALDH3A2 3'  GGTGGATGGTCTGGACAAGAA  69802      G  TT  AT
                                TTTTTG TT  GAC  CATTCATT
                                ||||||  ||  |||  ||||||||
                                AAGAAC AG  CTG  GTAGGTGG
                                   _  GT  __
GAM984  ALDH8A1 3'  AATGCTGCAAAACCAAAAA   42908          A  T
                                TTTTTGGTTTTG CA CATT
                                |||||||||||| || ||||
                                AAAAACCAAAAC GT GTAA
                                     _  C
GAM984  ALEX3   3'  TGTATGTTAATGCTGGAAG   33972     TG  T     _
                                TTTT  GT TTGACAT CA
                                ||||  ||  |||||||  ||
                                GAAG  CG AATTGTA GT
                                  GT  T      T
GAM984  AMPD3   3'  GTGAGTGATGCTCAGGGGC   6657    G    _
                                G TTTTGA CATCATTCAT
                                |  ||||||  ||||||||||
                                C GGGACT GTAGTGAGTG
                                 G     C
GAM984  AP1B1   3'  AGTGAGGTGGGGACCAAAG   8515          G  A
                                TTTTGGTTTT AC TCATT
                                ||||||||||  ||  |||||
                                GAAACCAGGG TG AGTGA
                                     G  G
GAM984  APOB48R 3'  GGTGGGAGGATCGCTTGAGACC 38588         TG C__   A_
          AGGAG                   TTTTTGGTTT  A   ATC  TTCATT
                                ||||||||||  |   |||  ||||||
                                GAGGACCAGA  T   TAG  GGGTGG
                                     GT CGC   GA
GAM984  APTX    5'  GGTGAGGAAATTGAGACTAGGG 35151         TG CA  A
                                TTTTGGTTT  A  TC TTCATT
                                |||||||||  |  ||  ||||||
                                GGGATCAGA  T  AG GAGTGG
                                     GT AA  _
GAM984  ARSD    3'  GATGGCTTGAGACCAGGAG   9799          TG __
                                TTTTTGGTTT  A  CATC
                                ||||||||||  |  ||||
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                                GAGGACCAGA  T  GTAG
                                     GT CG
GAM984  ASL     3'  AGTGGGGACAGTCAGGGACTGG 72393     TG   _   ATCA
           AGA                    TTTT  GTTT TGAC   TTCATT
                                  ||||  |||| ||||   ||||||
                                  AGAG  CAGG ACTG   GGGTGA
                                    GT   G   ACAG
GAM984  ASL     3'  TGCGAGGATGCTTGAGGCCAGG 72397        TG _   A  ATT
           AG                     TTTTTGGTTT  A CATC TTC
                                  ||||||||||  | |||| |||
                                  GAGGACCGGA  T GTAG GAG
                                     GT C   _  CGTG
GAM984  ATP10C  3'  AGTGATTTCGGACCGAAG    44664        T  C
                                  TTTTGGTTT GA ATCATT
                                  |||||||| || ||||||
                                  GAAGCCAGG CT TAGTGA
                                     _ T
GAM984  ATP1A2  3'  GGTGAGTGCAAGAGCCTGAGA  7368     T    GACAT
                                  TTTT GGTTTT   CATTCATT
                                  |||| ||||||   ||||||||
                                  AGAG CCGAGA   GTGAGTGG
                                    T    AC___
GAM984  ATP8B2  3'  GAATGGTTTGGAGCTGGGAG  65835    TG   TG C
                                  TTTT  GTTT  A ATCATTC
                                  ||||  ||||  | |||||||
                                  GAGG  CGAG  T TGGTAAG
                                    GT   GT _
GAM984  ATP8B2  5'  GAGGCTGTCAAGATCGGGGA  65837          TCA
                                  TTTTTGGTTTTGACA  TTC
                                  ||||||||||||||  |||
                                  AGGGGCTAGAACTGT  GAG
                                       CG_
GAM984  ATSV    3'  GGTGGGTTGAGACCAGGAA   16310        TG  A
                                  TTTTTGGTTT  AC TCATT
                                  ||||||||||  || |||||
                                  AAGGACCAGA  TG GGTGG
                                     GT  _
GAM984  ATSV    3'  GGTGGTGGGTTGAGACCAGGAA 16311        TG  A   T
                                  TTTTTGGTTT  AC TCAT CATT
                                  ||||||||||  || |||| ||||
                                  AAGGACCAGA  TG GGTG GTGG
                                     GT  _   _
GAM984  AXIN2   3'  GGTGAACTGTTGGAGCCCGAAG 17390    T    TG   TCA
                                  TTTT GGTTT  ACA   TTCATT
                                  |||| |||||  |||   ||||||
                                  GAAG CCGAG  TGT   AAGTGG
                                    C    GT   C__
GAM984  B3GAT1  3'  AATGAGTTTGTTATAAATCAGA 55048        _    TC
           AA                     TTTTTGGTTT TGACA  ATTCATT
                                  |||||||||| |||||  |||||||
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                                AAAGACTAAA ATTGT  TGAGTAA
                                     T    T_
GAM984  B3GAT1   3'  AATGAGTTTGTTATAAATCAGA 55049         _    TC
           AA                  TTTTTGGTTT TGACA  ATTCATT
                               |||||||||| |||||  |||||||
                               AAAGACTAAA ATTGT  TGAGTAA
                                     T    T_
GAM984  B3GAT1   3'  GGTGGGTGGGACTCAGTCCAGA 55056       TT   CA_
           GA                  TTTTTGG  TTGA   TCATTCATT
                               |||||||  ||||   |||||||||
                               AGAGACC  GACT   GGTGGGTGG
                                  T_   CAG
GAM984  B3GAT1   3'  GGTGGGTGGGACTCAGTCCAGA 55057       TT   CA_
           GA                  TTTTTGG  TTGA   TCATTCATT
                               |||||||  ||||   |||||||||
                               AGAGACC  GACT   GGTGGGTGG
                                  T_   CAG
GAM984  BACH2    5'  TGAATGATAAAGCCAGAAG   41789         GAC
                               TTTTTGGTTTT   ATCATTCA
                               ||||||||||   ||||||||
                               GAAGACCGAAA   TAGTAAGT
                                     ___
GAM984  BCKDHA   3'  GGTGAGGGCACATTCAGGACTA 62943          CATCA__
           GAAG                  TTTTTGGTTTTGA      TTCATT
                               ||||||||||||      ||||||
                               GAAGATCAGGACT      GAGTGG
                                     TACACGG
GAM984  BGN      3'  GATGGGGAGGCAGAGCCAGGAA 9925          ACA  A
                               TTTTTGGTTTTG   TC TTCATT
                               ||||||||||||   || ||||||
                               AAGGACCGAGAC   AG GGGTAG
                                     GG_  _
GAM984  BHLHB3   3'  GATGGATGAGAAGGCCAGAA   48486         GACA
                               TTTTGGTTTT    TCATTCATT
                               ||||||||||    |||||||||
                               AAGACCGGAA    AGTAGGTAG
                                     G___
GAM984  BMP4     5'  GGTGAGTGTGGCATCCGAGCTG 8663      TG   T ___  T
           AGG                   TTT  GTTT GA   CA CATTCATT
                               |||  |||| ||   || ||||||||
                               GGA  CGAG CT   GT GTGAGTGG
                                 GT    C  ACG  _
GAM984  BMPR1A   3'  TGATGCCAAGGCCAAAAG    16329          A
                               TTTTTGGTTTTG CATCA
                               |||||||||||| |||||
                               GAAAACCGGAAC GTAGT
                                     C
GAM984  BRAF     3'  AATGAGTGAGAGAGTTCAGGAG 16337       GT   GACA
                               TTTTTG  TTT    TCATTCATT
                               ||||||  |||    |||||||||
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                                GAGGAC  GAG    AGTGAGTAA
                                   TT   AG__
GAM984  BRCA1    3'  AATGAGCATGATTTTGAAGTCA 24533      GT  TG C    __
             GAG                    TTTTG  TT  A ATCAT  TCATT
                                |||||  ||  | |||||  |||||
                                GAGAC  AA  T TAGTA  AGTAA
                                   TG  GT T    CG
GAM984  BRCA2    3'  GTGGGAGGAGTGCTTGAGGCCA 5345          TG _   CA   ATT
             GGAG                    TTTTTGGTTT  A CAT  TTC
                                ||||||||||  | |||  |||
                                GAGGACCGGA  T GTG  GAG
                                      GT C   AG   GGTGG
GAM984  BRDT     3'  AATGAATGGTAAAAGATCAAAA 9952          GAC
                                TTTTGGTTTT   ATCATTCATT
                                ||||||||||   ||||||||||
                                AAAACTAGAA   TGGTAAGTAA
                                      AA_
GAM984  CA11     5'  GTGGGTTAGGAACCAAGAG   8684          _   A
                                TTTTTGGTTT TGAC TCAT
                                |||||||||| |||| ||||
                                GAGAACCAAG ATTG GGTG
                                      G   _
GAM984  CA3      3'  ATGAATGATCACTAGAAC    18995       AC_
                                GTTTTG   ATCATTCAT
                                ||||||   |||||||||
                                CAAGAT   TAGTAAGTA
                                   CAC
GAM984  CA3      3'  TAGTGAATGATGACACTTGAAG 18998      GT  TG ____
             TCAAAG                 TTTTG  TT  A   CATCATTCATT   A
                                |||||  ||  |   ||||||||||  |
                                GAAAC  AA  T   GTAGTAAGTGA   T
                                   TG  GT CACA
GAM984  CACNB1   3'  GATGTATTGCTAGAGCCAGGAG 7409          _____
                                TTTTTGGTTTTG    ACATC
                                ||||||||||    |||||
                                GAGGACCGAGAT    TGTAG
                                      CGTTA
GAM984  CANX     3'  GATGTTTGTTAGACCAGAAA   88867         T___
                                TTTTTGGTTT   GACATC
                                ||||||||||   ||||||
                                AAAGACCAGA   TTGTAG
                                      TTGT
GAM984  CAPZA1   5'  GATGGAGGCCAGAAGCCAAGAA 73026         GACATCA
                                TTTTTGGTTTT     TTCATT
                                ||||||||||     ||||||
                                AAGAACCGAAG     AGGTAG
                                      ACCGG__
GAM984  CAST     5'  AGTGAATCGCCTTCCAAACCAG 10018         T  CATC_
             GAG                    TTTTTGGTTT GA    ATTCATT
                                |||||||||| ||    |||||||
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                                GAGGACCAAA CT    TAAGTGA
                                     C  TCCGC
GAM984  CAST    3'  GGTGGATGGTGACTTTTGAAGA 10019     TG TTTTGA
                                TTTT  G    CATCATTCATT
                                ||||  |    ||||||||||
                                AGAA  T    GTGGTAGGTGG
                                  GT TTCA__
GAM984  CCNK    5'  GGTGAGTGACCCACCGACTGAG 77796    TG   TTGACA
           G                     TTT  GTT    TCATTCATT
                                 |||  |||    |||||||||
                                 GGA  CAG    AGTGAGTGG
                                   GT   CCACCC
GAM984  CCR2    3'  AGGGATAGTGGGGTCAGGGCTG 7220     TG      AT    CATT
          AGAG                     TTTT  GTTTTGAC  CATT
                                   ||||  ||||||||  ||||
                                   GAGA  CGGGACTG  GTGA
                                     GT      GG    TAGGGAG
GAM984  CD38    3'  TGGTGCAGAGCTGAAGA    60264     TG    A
                                   TTTT  GTTTTG CATCA
                                   ||||  ||||||  |||||
                                   AGAA  CGAGAC GTGGT
                                     GT    _
GAM984  CD4     3'  GATGGATGCAGATCCAGAG   7046       T   A   AT
                                   TTTTGG TTTG CATC  TC
                                   ||||||  ||||  ||||  ||
                                   GAGACC AGAC GTAG  AG
                                      T   _   GT
GAM984  CD59    3'  AATGAATGATGCTTTTCTGAAA 7029     TG TTTTGA
          A                        TTTT  G    CATCATTCATT
                                   ||||  |    ||||||||||
                                   AAAA  C    GTAGTAAGTAA
                                     GT TTTTC_
GAM984  CD59    3'  GGGTGAATGTGGTTATGGCCGA 7030       TT   AT
          AAA                        TTTTTGGT  TGAC  CATTCATT
                                     ||||||||  ||||  ||||||||
                                     AAAAGCCG  ATTG  GTAAGTGG
                                        GT   GT      GT
GAM984  CD79B   3'  AATGGACTCGGAGCCGAGG   41488         CA
                                   TTTTGGTTTTGA  TCATT
                                   ||||||||||||  |||||
                                   GGAGCCGAGGCT  GGTAA
                                         CA
GAM984  CDH13   3'  GGTGGGTGGAAACTAAGA    8836         G  A
                                   TTTTGGTTTT AC TCATT
                                   ||||||||||  ||  |||||
                                   AGAATCAAAG TG GGTGG
                                         G  _
GAM984  CELL    3'  AATGGGTGGGGGCCGACCATAG 10165    T    TTGACA
          A                        TTT TGGTT    TCATTCATT
                                   |||  |||||    |||||||||
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                                AGA ACCAG     GGTGGGTAA
                                  T    CCGGG_
GAM984  CELSR3   3'  AGTGGCTGTGCAGGGCTGGGG  9183      TG     A  T  TT
                                TTT  GTTTTG CA CA  CATT
                                |||  |||||| || ||  ||||
                                GGG  CGGGAC GT GT  GTGA
                                  GT     _ _  CG
GAM984  CKAP1    5'  GATCTGGTGCCAGAGCCGGGAA 73901          A    T_
                                TTTTTGGTTTTG CATCA  TC
                                |||||||||||| |||||  ||
                                AAGGGCCGAGAC GTGGT  AG
                                       C    CT
GAM984  CLCN7    3'  GCTGTGATGTTGAGAGCTGAGA 8910      TG    _      TCATT
           A                     TTTT  GTTTT GACATCAT
                                ||||  ||||| ||||||||
                                AAGA  CGAGA TTGTAGTG
                                  GT    G       TCG
GAM984  CLDN14   5'  AATGGACCCGGAGCCGAGAG   58469          ACA
                                TTTTTGGTTTTG   TCATT
                                ||||||||||||   |||||
                                GAGAGCCGAGGC   GGTAA
                                       CCA
GAM984  CLN6     3'  GGTGGGGCAGAGGCCAGGAG   35838         GA___
                                TTTTTGGTTTT    CATC
                                ||||||||||    ||||
                                GAGGACCGGAG    GTGG
                                       ACGGG
GAM984  CNN1     3'  AGTGGGTACCCCCAGGACCAGA 8941          ACATC
           AG                     TTTTTGGTTTTG    ATTCATT
                                ||||||||||||    |||||||
                                GAAGACCAGGAC    TGGGTGA
                                       CCCCA
GAM984  CNP      3'  GATGGGGAGATCGGGGCCAGAG 53622          CA  A
                                TTTTGGTTTTGA  TC TTCATT
                                ||||||||||||  || ||||||
                                GAGACCGGGGCT  AG GGGTAG
                                       AG  _
GAM984  COG6     3'  TGGTGTTCAAACCAAAGA    73254         T
                                TTTTTGGTTT GACATCA
                                ||||||||| |||||||
                                AGAAACCAAA TTGTGGT
                                      C
GAM984  COG7     3'  GATGGATCATGAAGCCAGGAG  68253        TGA   C
                                TTTTTGGTTT   CAT ATTCATT
                                |||||||||   ||| |||||||
                                GAGGACCGAA   GTA TAGGTAG
                                      ___   C
GAM984  CORO1C   3'  AATGTTGCCAAAACCAAAAG   27504          A  T
                                TTTTTGGTTTTG CA CATT
                                |||||||||||| || ||||
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                                GAAAACCAAAAC GT GTAA
                                      C  T
GAM984  CORO2B   5' AATGAGGGAGGCAGGGCTAGAG 65171          ACA  A
                                TTTTGGTTTTG   TC TTCATT
                                ||||||||||   || ||||||
                                GAGATCGGGAC   AG GAGTAA
                                      GG_  G
GAM984  CORO2B   5' GATGCCTGGAATTTCGGAGCTA 65173          CA__  TT
           GAAG                  TTTTTGGTTTTGA   TCA  CATT
                                ||||||||||||   |||  ||||
                                GAAGATCGAGGCT   GGT  GTAG
                                      TTAA   CC
GAM984  CRAT     3' GATTGTCTGGGGCCGAGG    7478          _   _
                                TTTTGGTTTT GACA TC
                                |||||||||| |||| ||
                                GGAGCCGGGG CTGT AG
                                      T   T
GAM984  CRIM1    3' CATTTTGAGTTGAAATCAAAAA 33601         TG  A  TTCATT
                                TTTTTGGTTT  AC TCA
                                ||||||||||  || |||
                                AAAAACTAAA  TG AGT
                                      GT  _  TTTACA
GAM984  CSNK1D   3' CGAAATGTTAACACCGGGAG  10314        T     CA   ATT
                                TTTTTGGT TTGACAT  TTC
                                |||||||| |||||||  |||
                                GAGGGCCA AATTGTA  AAG
                                     C      __  CT
GAM984  CSNK1D   3' TCGAAATGTTAACACCGGGAG 10316        T     CA   ATT
                                TTTTTGGT TTGACAT  TTC
                                |||||||| |||||||  |||
                                GAGGGCCA AATTGTA  AAG
                                     C      __  CTA
GAM984  CSNK1G3  3' AGTGAATGGAATGGACCAA   16508        TGACA
                                TTGGTTT    TCATTCATT
                                |||||||    |||||||||
                                AACCAGG    GGTAAGTGA
                                     TAA__
GAM984  CSPG3    3' GATGCTCAGTGTTAAAACTGAA 16519     TG        CATT
           A                     TTT  GTTTTGACAT    CATT
                                |||  ||||||||||   ||||
                                AAA  CAAAATTGTG   GTAG
                                  GT        ACTC
GAM984  CXCR4    3' AGTGAATCACGTAAAGCTAGAA 14413          ACATC
           A                     TTTTTGGTTTTG    ATTCATT
                                ||||||||||||    |||||||
                                AAAGATCGAAAT    TAAGTGA
                                      GCAC_
GAM984  CXCR6    3' GAATGCTGAAACCAAGG     22675         TGA  T
                                TTTTGGTTT   CA CATTC
                                |||||||||   || |||||
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                                GGAACCAAA  GT GTAAG
                                    ___ C
GAM984  CYB561   3'  GATCGTGTGCGAGGCCAGGAG  10351          _   CAT
                                TTTTTGGTTTTG ACAT  TC
                                |||||||||||| ||||  ||
                                GAGGACCGGAGC TGTG  AG
                                     G   CT_
GAM984  CYP2A6   3'  GGTGGGCGGGGCCAGGGA   7535          A_
                                TTTTTGGTTTTG  CATC
                                |||||||||||  ||||
                                AGGGACCGGGGC  GTGG
                                     GG
GAM984  DAZ      3'  GATGGATGAAACTGAGATTGGA 15826     TG    ACA
           AG                    TTTT  GTTTTG  TCATTCATT
                                ||||  ||||||  |||||||||
                                GAAG  TAGAGT  AGTAGGTAG
                                  GT    CAA
GAM984  DAZ      3'  GATGGATGAAACTGAGATTGGA 15827     TG    ACA
           AG                    TTTT  GTTTTG  TCATTCATT
                                ||||  ||||||  |||||||||
                                GAAG  TAGAGT  AGTAGGTAG
                                  GT    CAA
GAM984  DCTN1    5'  GGTGAGTGGGTACAGACTAGGA 43760        TG  A
           G                     TTTTTGGTTT  AC TCATTCATT
                                ||||||||||  || |||||||||
                                GAGGATCAGA  TG GGTGAGTGG
                                     CA  _
GAM984  DDB2     3'  AGTGGGTGGTAGCAGAGGGATC 5455        ___  AC
           AAG                    TTTGGTT  TTG  ATCATTCATT
                                |||||||  |||  ||||||||||
                                GAACTAG  GAC  TGGTGGGTGA
                                   GGA  GA
GAM984  DIO3     3'  TTGGTGTCTGCTTTGGGACCAG 9075          _______    ATTCATT
           AG                    TTTTGGTTTT    GACATC
                                ||||||||||    ||||||
                                GAGACCAGGG    CTGTGG
                                     TTTCGT       TTA
GAM984  DMD      3'  AATGATTCTCAAGATCAAAG  5459          C_
                                TTTTGGTTTTGA  ATCATT
                                ||||||||||||  ||||||
                                GAAACTAGAACT  TAGTAA
                                     CT
GAM984  DNAI2    3'  AATGAATCGTAACAATGCCAAA 43784        T  AC  C
           AA                    TTTTTGGT TTG  AT ATTCATT
                                ||||||||| |||  || |||||||
                                AAAAACCG AAC  TG TAAGTAA
                                   T  AA  C
GAM984  DOK1     3'  AGTGGGGCAGATGGCAGGGCTG 9108      TG    A   A__
           AGGA                   TTTT  GTTTTG CATC   TTCATT
                                ||||  |||||| ||||  ||||||
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                                AGGA  CGGGAC GTAG   GGGTGA
                                  GT     G    ACG
GAM984   DPP6     5'  GGTGGGGAGTGGGAACCGGAGA 56323          G  A  A
                                TTTTTGGTTTT AC TC TTCATT
                                |||||||||| || || ||||||
                                AGAGGCCAAGG TG AG GGGTGG
                                      G  _  _
GAM984   DSC1     3'  AATGGGCAGTCAGAATTAGGGA 44597            ATCA
                                TTTTTGGTTTTGAC    TTCATT
                                ||||||||||||||    ||||||
                                AGGGATTAAGACTG    GGGTAA
                                      AC__
GAM984   DSC1     3'  AATGGGCAGTCAGAATTAGGGA 18238            ATCA
                                TTTTTGGTTTTGAC    TTCATT
                                ||||||||||||||    ||||||
                                AGGGATTAAGACTG    GGGTAA
                                      AC__
GAM984   DTNA     5'  ATCAAGGATGGTGGCAGAATTA 9140           A       ATT
            AAG                   TTTTGGTTTTG CATCATTC
                                |||||||||| ||||||||
                                GAAATTAAGAC GTGGTAGG
                                      G       AACTAT
GAM984   EFEMP1   5'  AATGGGTGTAAGGAACTGGAAA 38772      TG    GACAT
                                TTTT  GTTTT    CATTCATT
                                ||||  |||||    ||||||||
                                AAAG  CAAGG    GTGGGTAA
                                  GT    AAT__
GAM984   EGR4     5'  GGTGAGTGCCCGAAGCCAGGAG 10495          ACAT
                                TTTTTGGTTTTG    CATTCATT
                                ||||||||||||    ||||||||
                                GAGGACCGAAGC    GTGAGTGG
                                      CC__
GAM984   EHHADH   3'  GATTGTTTGAGGCCAGAAA    10500          TG _  _
                                TTTTTGGTTT  A CA TC
                                ||||||||||  | || ||
                                AAAGACCGGA  T GT AG
                                      GT T  T
GAM984   EMX2     3'  AATGGTGTTTAAAGACCGAAAA 88952           __
                                TTTTTGGTTTT  GACATCATT
                                ||||||||||  |||||||||
                                AAAAGCCAGAA  TTGTGGTAA
                                      AT
GAM984   EPHA8    3'  GGTGGATGATGTGTCATGAATG 40438      G   _    __
            AGGAG                   TTTTT GTTT TGACA  TCATTCATT
                                ||||| |||| |||||  |||||||||
                                GAGGA TAAG ACTGT  AGTAGGTGG
                                  G   T    GT
GAM984   EPHB2    3'  GGTGACCTGGCCAGAGCCAAGA 34348          A_  __    CATT
            A                    TTTTTGGTTTTG  CA  TCATT
                                ||||||||||||  ||  |||||
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                                AAGAACCGAGAC  GT  AGTGG
                                      CG  CC       T
GAM984  EPHB4    3'  GATGGGTGCGTTCCCGCAGACC 16709         T____  AT
           AAAGA                  TTTTTGGTTT    GAC  CATTCATT
                                  ||||||||||    |||  ||||||||
                                  AGAAACCAGA    TTG  GTGGGTAG
                                       CGCCC   C_
GAM984  EPM2A    3'  GATGGGCTGTTTTAAGACCAGA 20236          C  CA
           G                     TTTTGGTTTTGA AT  TTCATT
                                 ||||||||||||  ||  ||||||
                                 GAGACCAGAATT TG  GGGTAG
                                       T  TC
GAM984  ESRRA    3'  GGTGTCAGAAGCTGGGAA    16723      TG  _
                                 TTTT  GTT TTGACATC
                                 ||||  |||  ||||||||
                                 AAGG  CGA GACTGTGG
                                   GT   A
GAM984  ETF1     3'  GTGATATGACAAGACCAGAGA  17591           ACA   _   T
                                 TTTTTGGTTTTG   TCAT TCAT
                                 ||||||||||||   ||||  ||||
                                 AGAGACCAGAAC   AGTA AGTG
                                       ___    T   T
GAM984  ETV3     5'  GGTGGATGAGGAGGAGCCGGAG 19122          GACA
           A                      TTTTTGGTTTT    TCATTCATT
                                  ||||||||||    |||||||||
                                  AGAGGCCGAGG    AGTAGGTGG
                                       AGG_
GAM984  EYA1     3'  ATAATGTTGTCAAGACCAAAAG 6696             T    CATT
                                 TTTTTGGTTTTGACA CATT
                                 ||||||||||||||| ||||
                                 GAAAACCAGAACTGT GTAA
                                       T    TAG
GAM984  EYA2     3'  GACCCAGATGTTGGACACCAGG 19124         _ TG    ATTCATT
           AA                     TTTTTGGT TT  ACATC
                                  ||||||||  ||  |||||
                                  AAGGACCA AG  TGTAG
                                      C  GT    ACCCAG
GAM984  FBN1     3'  AATGGTGCTTATTAAGACCAAA 65036           ____      CATT
           GA                     TTTTTGGTTTTGA    CATCATT
                                  ||||||||||||    |||||||
                                  AGAAACCAGAATT    GTGGTAA
                                       ATTC         T
GAM984  FCN2     3'  AATGATCTTAACACCGGAAA   15915        T   C
                                 TTTTTGGT TTGA ATCATT
                                 ||||||||  ||||  ||||||
                                 AAAGGCCA AATT TAGTAA
                                      C    C
GAM984  FOLR1    5'  AGTGAGGGCTGGGGTCGGGAC  34115        AT  ___
                                 GTTTTGAC  CA   TTCATT
                                 ||||||||  ||   ||||||
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                                CAGGGCTG  GT   GAGTGA
                                    GG  CGG
GAM984  FOXP2    5'  CTCCTATGAAGTTGAAACCGGG 27946         TG  A    TCATT
          AA                     TTTTTGGTTT  AC TCAT
                                 ||||||||||  || ||||
                                 AAGGGCCAAA  TG AGTA
                                     GT  A    TCCTCA
GAM984  FPGS     3'  AATGGATCAGCCAAGGCCGAGA 18263          ACATC
                                 TTTTGGTTTTG    ATTCATT
                                 ||||||||||||   |||||||
                                 AGAGCCGGAAC    TAGGTAA
                                      CGAC_
GAM984  FPGS     3'  GTGGGTGGTGTCCTGAAGC   18268      __
                                 GTTTT  GACATCATTCAT
                                 |||||  ||||||||||||
                                 CGAAG  CTGTGGTGGGTG
                                    TC
GAM984  FREB     3'  ATTCTGCTGTCTAGATCAGGAA 52190         T    T  TTCATT
                                 TTTTTGGTTT GACA CA
                                 |||||||||| ||||| ||
                                 AAGGACTAGA CTGT GT
                                      T    C  CTTAA
GAM984  FUT3     3'  GATTGATTGAGGCCAAGAG   5622          TG CA   T
                                 TTTTTGGTTT  A  TCA TC
                                 |||||||||  |  ||| ||
                                 GAGAACCGGA  T  AGT AG
                                      GT __   T
GAM984  FXYD6    3'  GATGGATGGAGGGAGAGCAGAG 42092      G    GACA
                                 TTTTG TTTT    TCATTCATT
                                 ||||| ||||    |||||||||
                                 GAGAC AGAG    GGTAGGTAG
                                    G    GGA_
GAM984  FZD10    5'  GGTGGAGAGCCGGGGCCAG   24217         ACA  A
                                 TTGGTTTTG   TC TTCATT
                                 |||||||||   || ||||||
                                 GACCGGGGC   AG AGGTGG
                                      CG_  _
GAM984  GABRA1   5'  AGTGAGTGAGAGGCAGAGCGAG 7691      G     ACA_
          GA                     TTTT GTTTTG    TCATTCATT
                                 |||| ||||||    |||||||||
                                 AGGA CGAGAC    AGTGAGTGA
                                    G     GGAG
GAM984  GALGT    5'  AGTGGGACGCGGAGCCAGGGA  9417           ACA_
                                 TTTTTGGTTTTG    TCATT
                                 ||||||||||||    |||||
                                 AGGGACCGAGGC    GGTGA
                                      GCAG
GAM984  GARP     3'  AATGAAAAGCTTAGGACCGGAA 19775          CATCA
          G                      TTTTTGGTTTTGA    TTCATT
                                 ||||||||||||     ||||||
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                                  GAAGGCCAGGATT    AAGTAA
                                        CGAA_
GAM984  GAS11   3' AGTGAGGTTAGGCCCAGAGA  9427       TT    A
                                  TTTTTGG  TTGAC TCATT
                                  |||||||  ||||| |||||
                                  AGAGACC  GATTG AGTGA
                                      CG    G
GAM984  GAS11   3' GGTAGGTGATGTAGGACCAGGG 9431          A    TC
                                  TTTTGGTTTTG CATCAT  ATT
                                  |||||||||||| ||||||  |||
                                  GGGACCAGGAT GTAGTG  TGG
                                        _     GA
GAM984  GCNT2   5' AGTGGGGTGGGGCCAAAAA  9451         TT ACA
                                  TTTTTGGTT  G   TCATT
                                  |||||||||  |   |||||
                                  AAAAACCGG  T   GGTGA
                                       GG GG_
GAM984  GM2A    3' GGTGAATGAGGCAGATGGGAAA 68386     G    T ACA
                                  TTTTT GTTT G   TCATTCATT
                                  ||||| |||| |   |||||||||
                                  AAAGG TAGA C   AGTAAGTGG
                                     G    _ GG_
GAM984  GNAI3   3' GTGGAGTGTTGAGACCAGA   22444       TG   CA    T
                                  TTTGGTTT  ACAT  TTCAT
                                  ||||||||  ||||  |||||
                                  AGACCAGA  TGTG  AGGTG
                                       GT   __    T
GAM984  GPC1    3' GATGTTTTGGGATCAGGAG   10860         __
                                  TTTTTGGTTTT  GACATC
                                  ||||||||||  ||||||
                                  GAGGACTAGGG  TTGTAG
                                        TT
GAM984  GPC1    3' GGTGACACAGGTCAGGGCTCAG 10863     _      ATCAT
          A                        TTTG GTTTTGAC    TCATT
                                  |||| ||||||||    |||||
                                  AGAC CGGGACTG    AGTGG
                                    T       GACAC
GAM984  GPR87   5' AATGAAAGAAATCAAACCAGGA 43906        T  CA  A
          A                        TTTTTGGTTT GA  TC TTCATT
                                  |||||||||| ||  || ||||||
                                  AAGGACCAAA CT  AG AAGTAA
                                        _  AA  A
GAM984  HK2     3' AATGAAACCAAAGCCAGGAG  5751          ACA
                                  TTTTTGGTTTTG  TCATT
                                  ||||||||||||  |||||
                                  GAGGACCGAAAC  AGTAA
                                        CAA
GAM984  HOXC4   5' GGTGGAGTTGCCGAAGCTGGGG 28250     TG    A  TCA
          G                        TTTT  GTTTTG CA   TTCATT
                                  ||||  |||||| ||   ||||||
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                                GGGG  CGAAGC GT   AGGTGG
                                  GT     C  TG_
GAM984  HOXD4    5'  GGTGAGTGGAAGGGCCACGGA  28264    TT      GACA
                                TT  TGGTTTT    TCATTCATT
                                ||  |||||||    |||||||||
                                AG  ACCGGGA    GGTGAGTGG
                                 GC      A___
GAM984  HPS4     5'  GGCACTGATGTTTGAACTGGAA 42228      TG    T      TTCATT
            A                    TTTT  GTTT GACATCA
                                ||||  |||| |||||||
                                AAAG  CAAG TTGTAGT
                                  GT    T      CACGG
GAM984  HRC      5'  GGTGGACAGAGACCGAAAG    10971           GA__
                                TTTTTGGTTTT    CATC
                                ||||||||||    ||||
                                GAAAGCCAGAG    GTGG
                                       ACAG
GAM984  HRG      3'  ATGGTATTGAAACTAAAAA    6425           TG C
                                TTTTTGGTTT  A ATCAT
                                ||||||||||  | |||||
                                AAAAATCAAA  T TGGTA
                                      GT A
GAM984  HRH1     3'  GGTGGGCAGATCATTTGAGGCC 7824           TG C__   A_
            AGGAG                   TTTTTGGTTT  A   ATC  TTCATT
                                ||||||||||  |   |||  ||||||
                                GAGGACCGGA  T   TAG  GGGTGG
                                      GT TAC   AC
GAM984  HSPA1B   3'  GGTGGACTGTTGGGACTCAAG  19274      _   TG   TCA
                                TTTG GTTT  ACA   TTCATT
                                |||| ||||  |||   ||||||
                                GAAC CAGG  TGT   AGGTGG
                                  T    GT   C__
GAM984  HTR2A    3'  GATGTAACTGTGTCAGGATTGA 7104       TG        CA  _
            GGA                    TTTT  GTTTTGACAT  TT CATT
                                ||||  ||||||||||  || ||||
                                AGGA  TAGGACTGTG  AA GTAG
                                  GT         TC  T
GAM984  IGJ      3'  ATGAATTTGAAACCAGGG     58958          TG CATC
                                TTTTGGTTT  A    ATTCAT
                                |||||||||  |   ||||||
                                GGGACCAAA  T    TAAGTA
                                     GT _____
GAM984  IGSF3    5'  AATGAGAGATTAGGAGCTGGGA 9523       TG    GAC   A
            G                    TTTT  GTTTT   ATC TTCATT
                                ||||  |||||   ||| |||||||
                                GAGG  CGAGG   TAG GAGTAA
                                  GT    AT_   A
GAM984  IL21     5'  AGTGAAAACGAGACCAAGG    41726           ACA
                                TTTTGGTTTTG   TCATT
                                ||||||||||   |||||
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                                GGAACCAGAGC   AGTGA
                                      AAA
GAM984  IL5     3'  GAATGAGGGCCAAGAA      7947          TGACA
                                TTTTTGGTTT    TCATTC
                                ||||||||||    ||||||
                                AAGAACCGGG    AGTAAG
                                      _____
GAM984  IRTA2    3'  AGTGGGTCTGTGTAGAGCCTGA 49230      T     A   C_
            GA                    TTTT GGTTTTG CAT  ATTCATT
                                ||||| ||||||| |||  |||||||
                                AGAG CCGAGAT GTG  TGGGTGA
                                  T      _  TC
GAM984  ISGF3G   5'  GGTGGGCCTCAAAGCCGGG   21408          ____
                                TTTGGTTTTGA   CATC
                                ||||||||||    ||||
                                GGGCCGAAACT   GTGG
                                      CCGG
GAM984  ITGA1    5'  AGTGAGATTTCAGAGACCAAGA 64270         _   C   AT
            G                    TTTTTGGTTT TGA ATC  TCATT
                                ||||||||| ||| |||  |||||
                                GAGAACCAGA ACT TAG  AGTGA
                                      G   T  __
GAM984  ITGBL1   3'  GGTGGGTAGAGGCCAGGGA   17737          GA__
                                TTTTTGGTTTT   CATC
                                ||||||||||    ||||
                                AGGGACCGGAG   GTGG
                                      ATGG
GAM984  ITK      3'  GGTGAATATGTACTGAGCTAGG 19884         TG_   C
            AG                    TTTTTGGTTT   ACAT ATTCATT
                                ||||||||||   |||| |||||||
                                GAGGATCGAG   TGTA TAAGTGG
                                      TCA   _
GAM984  IVD      5'  GATTGGTGGAGCTAAGAG    11092          TGA    T
                                TTTTTGGTTT   CATCA TC
                                ||||||||||   ||||| ||
                                GAGAATCGAG   GTGGT AG
                                      ___     T
GAM984  JAM3     3'  GATTGTCTAAGGCCAAAG    52490          _   _
                                TTTTGGTTTT GACA TC
                                ||||||||| |||| ||
                                GAAACCGGAA CTGT AG
                                      T   T
GAM984  KL       3'  TGAATGACAAGATTAGGAA   17744          ACA     TT
                                TTTTTGGTTTTG   TCATTCA
                                ||||||||||||   |||||||
                                AAGGATTAGAAC   AGTAAGT
                                      ___     T
GAM984  KPNB2    3'  AGTGGATGTGAAGAAGCAAAAA 11225       G   GA  T
                                TTTTTG TTTT  CA CATTCATT
                                |||||| ||||  || ||||||||
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                                AAAAAC AAGA  GT GTAGGTGA
                                   G   A_ _
GAM984  KRT16    5'  GATGACTTCAGGACCAAG    96889          CA
                                TTTGGTTTTGA  TCATT
                                ||||||||||  |||||
                                GAACCAGGACT  AGTAG
                                      TC
GAM984  L1CAM    3'  GGTGGGGTCTCCTCAGGACCAG 43990           CATCA_
           GG                    TTTTGGTTTTGA    TTCATT
                                ||||||||||||    ||||||
                                GGGACCAGGACT    GGGTGG
                                      CCTCTG
GAM984  LAMP2    3'  AGTGGGTGGATCACTTGAGGCC 11277          TG CA___
           AGGAG                   TTTTTGGTTT  A    TCATTCATT
                                ||||||||||  |    |||||||||
                                GAGGACCGGA  T    GGTGGGTGA
                                      GT CACTA
GAM984  LAMP2    3'  GGTGGATCACTTGAGGCCAGGA 26576          TG CATC
           G                     TTTTTGGTTT  A    ATTCATT
                                ||||||||||  |    |||||||
                                GAGGACCGGA  T    TAGGTGG
                                      GT CAC_
GAM984  LGALS3BP 3'  GGTGGTGAGAACCGGAGA    69860          G  _
                                TTTTTGGTTTT AC ATC
                                ||||||||||| || |||
                                AGAGGCCAAGA TG TGG
                                      G  G
GAM984  LIG3     5'  GGTGAGCGCCGGAGCCGGAGA  11317          ACA_
                                TTTTTGGTTTTG    TCATT
                                ||||||||||||    |||||
                                AGAGGCCGAGGC    AGTGG
                                      CGCG
GAM984  LOH11CR2A 3'  AATGTAATGTCAAGATCA    28266          CATT
                                TGGTTTTGACAT    CATT
                                ||||||||||||    ||||
                                ACTAGAACTGTA    GTAA
                                      AT__
GAM984  LPIN1    5'  GATGAAGGGCAAGACCGGGG   67989          ACATCA
                                TTTTGGTTTTG     TTCATT
                                ||||||||||      ||||||
                                GGGGCCAGAAC     AAGTAG
                                      GGG___
GAM984  LRP5     3'  GATGGGGTGGGCAGGGCTGGGA 11363      TG     A_   AT_  ATT
           G                     TTTT  GTTTTG  CATC   TC
                                ||||  ||||||  ||||   ||
                                GAGG  CGGGAC  GTGG   AG
                                  GT     GG    GGT
GAM984  LUM      3'  GGTGGTAGATATTGAGGCCAAG 11379          TG C   AT
           AA                    TTTTTGGTTT  A ATC  TCATT
                                ||||||||||  | |||  |||||
```

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                                AAGAACCGGA  T TAG  GGTGG
                                     GT A   AT
GAM984  LZTR1    3'  AGTGGGTGGCACCTGCCAGGCC 23165         T A  ____
            AAGG                    TTTTGGTTT G CA    TCATTCATT
                                    ||||||||| | ||    |||||||||
                                    GGAACCGGA C GT    GGTGGGTGA
                                         _ C  CCAC
GAM984  M6A      5'  GAGAGGTGTCAGGGCTGGGAG  39556      TG         A
                                    TTTT  GTTTTGACATC TTC
                                    ||||  |||||||||| |||
                                    GAGG  CGGGACTGTGG GAG
                                      GT         A
GAM984  MADD     3'  GATGGAGTGGTCGAGGCTAG   56211          ATCA
                                    TTGGTTTTGAC    TTCATT
                                    ||||||||||    ||||||
                                    GATCGGAGCTG    AGGTAG
                                          GTG_
GAM984  MADD     3'  GATGGAGTGGTCGAGGCTAG   56212          ATCA
                                    TTGGTTTTGAC    TTCATT
                                    ||||||||||    ||||||
                                    GATCGGAGCTG    AGGTAG
                                          GTG_
GAM984  MAFF     3'  AGTGGTTGTGTTGGGACCAAAA 25572         TG   T  TT
                                    TTTTGGTTT  ACA CA  CATT
                                    |||||||||  ||| ||  ||||
                                    AAAACCAGG  TGT GT  GTGA
                                         GT   _  TG
GAM984  MAGEC1   3'  GGTGGAGGGCCTGGTTGAGGCT 19597      TG    TG  ATCA___
            GGAGA                   TTTT  GTTT  AC      TTCATT
                                    ||||  ||||  ||      ||||||
                                    AGAG  CGGA  TG      AGGTGG
                                      GT    GT  GTCCGGG
GAM984  MAN2A2   3'  GATTGTCATGGCCAGAGA    21511         TT    _
                                    TTTTTGGT  TGACA TC
                                    ||||||||  ||||| ||
                                    AGAGACCG  ACTGT AG
                                         GT    T
GAM984  MAP1B    3'  AATGGCTTCTATGATCAGAACT 20958      TG      _  CAT__
            GGGAA                   TTTT  GTTTTGA CAT     TCATT
                                    ||||  ||||||| |||     |||||
                                    AAGG  CAAGACT GTA     GGTAA
                                      GT      A   TCTTC
GAM984  MAP3K14  3'  GATGGACATGATCAGTGCTAAG 15547         T   _  CA
            GA                      TTTTTGGT TTGA CAT  TTCATT
                                    |||||||| |||| |||  ||||||
                                    AGGAATCG GACT GTA  AGGTAG
                                         T   A  C_
GAM984  MAP3K7IP1 3'  TGGTGTGGAACCAGGGA     21492          G
                                    TTTTTGGTTTT ACATCA
                                    |||||||||| ||||||
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                                AGGGACCAAGG TGTGGT
                                          _
GAM984  MAT1A    3'  AGTGAGTGGCCCTTTCGGATCC 92494        T    CA___
              AGGGA                  TTTTTGG TTTGA    TCATTCATT
                                     ||||||| |||||    |||||||||
                                     AGGGACC AGGCT    GGTGAGTGA
                                        T    TTCCC
GAM984  MBP      3'  AATGAGTGTCTATGAATCAAAG 91350         TGACAT
                                     TTTTGGTTT     CATTCATT
                                     |||||||||     ||||||||
                                     GAAACTAAG     GTGAGTAA
                                          TATCT_
GAM984  MCM6     3'  AGTGAAGTTGGAACCAAA    20974        TG  A
                                     TTTGGTTT  AC TCATT
                                     ||||||||  || |||||
                                     AAACCAAG  TG AGTGA
                                          GT  A
GAM984  MEN1     5'  AATGAGCCAAGACTAGAG    56339          ACA
                                     TTTTGGTTTTG   TCATT
                                     ||||||||||   |||||
                                     GAGATCAGAAC   AGTAA
                                           CG_
GAM984  MKKS     5'  GGTGGTACAGAATCAAAAG   38751          A__
                                     TTTTTGGTTTTG   CATC
                                     ||||||||||||   ||||
                                     GAAAACTAAGAC   GTGG
                                           ATG
GAM984  MLLT4    3'  AATGAGTTTGCAAAGCCGG   21036        A  TC
                                     TTGGTTTTG CA  ATTCATT
                                     ||||||||| ||  |||||||
                                     GGCCGAAAC GT  TGAGTAA
                                          _  T_
GAM984  MOCS2    3'  AATGTTGGCAGAACTGGAAA  16969      TG     A  T
                                     TTTT  GTTTTG CA CATT
                                     ||||  |||||| || ||||
                                     AAAG  CAAGAC GT GTAA
                                        GT     G  T
GAM984  MRE11A   3'  AATGAAAATGTTACAAGCTAAG 20004          _     CA
              AG                       TTTTTGGTTT TGACAT  TTCATT
                                       |||||||||| ||||||  ||||||
                                       GAGAATCGAA ATTGTA  AAGTAA
                                            C     A_
GAM984  MS4A3    3'  GATGGGAGGGTTAAGGCTCAGG 21545      _       A  A
                                     TTTG GTTTTGAC TC TTCATT
                                     |||| |||||||| || ||||||
                                     GGAC CGGAATTG GG GGGTAG
                                        T       _ A
GAM984  MTERF    5'  AGTGGATGGGTGCAGTTCAGGA 23716        TT   ACA
              G                        TTTTTGG  TTG   TCATTCATT
                                       |||||||  |||   |||||||||
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                                GAGGACT  GAC   GGTAGGTGA
                                   T_   GTG
GAM984  MTMR3    3'  GGTGGATCATGGTGAGGACTAG 41165          G  _  C
           GG                    TTTTGGTTTT AC AT ATTCATT
                                 |||||||||| || || |||||||
                                 GGGATCAGGA TG TA TAGGTGG
                                    G  G  C
GAM984  MTMR3    3'  GGTGGTCAGAGCCAGGAG    41166           _
                                 TTTTTGGTTTTGAC ATC
                                 |||||||||||||| |||
                                 GAGGACCGAGACTG TGG
                                       G
GAM984  MTMR3    3'  TGGGAGGATGGTGGTCAGAGCC 41172           _     ATT
           AGGAG                  TTTTTGGTTTTGAC ATCATTC
                                  |||||||||||||| |||||||
                                  GAGGACCGAGACTG TGGTAGG
                                        G      AGGGTG
GAM984  MXI1     3'  AATGAATGAGGTCTGGGCTAGG 56120        TT   A
                                 TTTGGTT  GAC TCATTCATT
                                 |||||||  ||| |||||||||
                                 GGATCGG  CTG AGTAAGTAA
                                    GT   G
GAM984  MXI1     3'  AATGAATGAGGTCTGGGCTAGG 56121        TT   A
                                 TTTGGTT  GAC TCATTCATT
                                 |||||||  ||| |||||||||
                                 GGATCGG  CTG AGTAAGTAA
                                    GT   G
GAM984  MYBL2    3'  GATGGGGGATGTGGCCAGGG   11727         TTG    A
                                 TTTTGGTT   ACATC TTCATT
                                 ||||||||   ||||| ||||||
                                 GGGACCGG   TGTAG GGGTAG
                                     ___     G
GAM984  MYO1D    3'  AATGAGTTGCCTGTCAAAGGCT 72237     TG  _     TC__
           GGAG                    TTT  GT TTTGACA    ATTCATT
                                   |||  || |||||||    |||||||
                                   GAG  CG AAACTGT    TGAGTAA
                                     GT  G      CCGT
GAM984  NAGA     3'  AATGAGTTGAGACCATGGA    6035     TT     TG  A
                                 TT  TGGTTT  AC TCATT
                                 ||  ||||||  || |||||
                                 AG  ACCAGA  TG AGTAA
                                   GT     GT  _
GAM984  NDRG1    3'  TGGGATTCATGTCGAGGCTAGA 60315            C_   ATT
           G                      TTTTGGTTTTGACAT  ATTC
                                  |||||||||||||||  ||||
                                  GAGATCGGAGCTGTA  TAGG
                                        CT    GTG
GAM984  NDRG2    3'  TGATGTTAAGGTGGAGAG    33195       G TT
                                 TTTTT G  TTGACATCA
                                 ||||| |  |||||||||
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                                GAGAG T  AATTGTAGT
                                  G GG
GAM984  NDUFS6   3'  GGTGTTGCTGTCATGGCTGAAA 17046     TG  TT    T  TT
           A                     TTTT  GT  TGACA CA  CATT
                                 ||||  ||  |||||  ||  ||||
                                 AAAA  CG  ACTGT GT  GTGG
                                   GT  GT    C  T_
GAM984  NEDD4L   5'  GGTAGGGTGCGGGACCGGGG   31607          A    AT_
                                 TTTTGGTTTTG CATC   TC
                                 ||||||||||| ||||   ||
                                 GGGGCCAGGGC GTGG   GG
                                       _   GAT
GAM984  NEFH     3'  AATGAATGAGCAGTTAGAA    41141        A__
                                 TTTTGAC   TCATTCATT
                                 |||||||   |||||||||
                                 AAGATTG   AGTAAGTAA
                                     ACG
GAM984  NGB      3'  AGTGGGAGCAGAATCAGAA    41459          ACA
                                 TTTTGGTTTTG   TCATT
                                 ||||||||||   |||||
                                 AAGACTAAGAC   GGTGA
                                       GAG
GAM984  NOLA1    5'  GGTGGGTGTGTGCGCAAGGCCA 39125          A_  _
           GGG                     TTTTGGTTTTG  CAT CATTCATT
                                 ||||||||||  ||| ||||||||
                                 GGGACCGGAAC  GTG GTGGGTGG
                                       GC   T
GAM984  NPHP1    3'  AATGATGGAACCAAAAA     63137          TGA
                                 TTTTTGGTTT   CATCATT
                                 |||||||||   |||||||
                                 AAAAACCAAG   GTAGTAA
                                       ___
GAM984  NPY2R    3'  AGTGGCTTGGGTCAGGATCAAA 8065            A   T_
           GA                      TTTTTGGTTTTGAC TCA  TCATT
                                 |||||||||||||| |||  |||||
                                 AGAAACTAGGACTG GGT  GGTGA
                                       _   TC
GAM984  NR2E3    3'  AATGGGGAGAATAAGCCAGAAA 33417          TGACA  A
                                 TTTTTGGTTT    TC TTCATT
                                 |||||||||     || ||||||
                                 AAAGACCGAA    AG GGGTAA
                                       TAAG_  _
GAM984  NR2F6    3'  AATGATCATGAAACCAAAAA   19103          GAC
                                 TTTTTGGTTTT   ATCATT
                                 ||||||||||   ||||||
                                 AAAAACCAAAG   TAGTAA
                                       TAC
GAM984  NR4A2    5'  AATGAATGAAGAGAGACGCGGA 21646        _    GACA
           GA                      TTTTTG GTTTT   TCATTCATT
                                 ||||||  |||||   |||||||||
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                                AGAGGC CAGAG    AGTAAGTAA
                                   G     AGA_
GAM984  NRG1     5'  GGTGGGTGGCTGCGGGGC    16904       A  _
                                GTTTTG CA TCATTCATT
                                |||||| || |||||||||
                                CGGGGC GT GGTGGGTGG
                                   _  C
GAM984  NSMAF    3'  TGGTGAATGTGCAATGTTAGTA 14554          _     ____
           ATTAGAAG                  TTTTTGGTT TTGACAT    CATTCATT   G
                                |||||||||| |||||||    ||||||||  |
                                GAAGATTAA GATTGTA    GTAAGTGG   T
                                      T      ACGT
GAM984  NVL      3'  AATGAATGAGGCCAAGCTGAAG 11866     TG    TGACA
                                TTT  GTTT     TCATTCATT
                                |||  ||||    |||||||||
                                GAA  CGAA     AGTAAGTAA
                                  GT    CCGG_
GAM984  OCRL     5'  GGTGGGTGGGTGTGGGGACGCG 9630        _    G    _
           GGAG                    TTTTTG GTTTT ACATC ATTCATT
                                |||||| ||||| ||||| |||||||
                                GAGGGC CAGGG TGTGG TGGGTGG
                                   G    G    G
GAM984  OTOR     3'  AATGGGTAAATTGAGACCAGAA 39754          TG CATC
           A                     TTTTTGGTTT  A    ATTCATT
                                |||||||||| |   |||||||
                                AAAGACCAGA  T    TGGGTAA
                                      GT AAA_
GAM984  P23      3'  AATGAGTGATTTTTCTTAGAAG 22750       G     C____
           CAGAG                   TTTTG TTTTGA     ATCATTCATT
                                ||||| ||||||    ||||||||||
                                GAGAC AAGATT     TAGTGAGTAA
                                   G     CTTTT
GAM984  PABPN1   5'  AGTGGATGATGGTGCCAA    17355       TTTGA
                                TTGGT     CATCATTCATT
                                |||||     ||||||||||
                                AACCG     GTAGTAGGTGA
                                   TG___
GAM984  PCLO     3'  GATGGACCAGTCAAGCCAGAAG 95887          T   ATCA
                                TTTTTGGTTT GAC    TTCATT
                                |||||||||| |||    ||||||
                                GAAGACCGAA CTG    AGGTAG
                                      _   ACC_
GAM984  PDE4A    3'  GATGAGGCAGGGCCAGG     21684          ACA
                                TTTGGTTTTG   TCATT
                                ||||||||||   |||||
                                GGACCGGGAC   AGTAG
                                      GG_
GAM984  PHKA2    3'  GATGTATGTTAAAGCCACAGA  6089      T         _
                                TTT TGGTTTTGACAT CATT
                                ||| |||||||||||| ||||
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                                AGA ACCGAAATTGTA GTAG
                                  C          T
GAM984  PHTF1    3'  AATGAATGGTGTTTCCGGAGG  22761       TTTT
                                TTTTTGG    GACATCATTCATT
                                |||||||    ||||||||||||
                                GGAGGCC    TTGTGGTAAGTAA
                                   T___
GAM984  PHYH     3'  AGTGAATGATTTGGAGCTTAGG 21702     T    TG C
                                TTT GGTTT  A ATCATTCATT
                                ||| |||||  | ||||||||||
                                GGA TCGAG  T TAGTAAGTGA
                                  T    GT _
GAM984  PKNOX1   3'  AATGATTGGTTGTAAGCCAAGG 17097        TG  _  T
                                TTTTGGTTT  ACA TCA TCATT
                                |||||||||  ||| ||| |||||
                                GGAACCGAA  TGT GGT AGTAA
                                     __  T  T
GAM984  PLCB4    3'  GATGATATCTGAAACCAGAGA  8120          _  C
                                TTTTTGGTTTT GA ATCATT
                                |||||||||| || ||||||
                                AGAGACCAAAG CT TAGTAG
                                      T  A
GAM984  PMP2     3'  AATGGATGATTCCAAAGC    12184       AC
                                GTTTTG  ATCATTCATT
                                ||||||  ||||||||||
                                CGAAAC  TAGTAGGTAA
                                   CT
GAM984  POLG     3'  AGTGGGTTCAGAACCAAGA   12201          CA
                                TTTTGGTTTTGA  TCATT
                                ||||||||||||  |||||
                                AGAACCAAGACT  GGTGA
                                      TG
GAM984  POU2AF1  3'  GGTGGGTGGGGACAGGCCAG  21749       TGACA
                                TTGGTTT    TCATTCATT
                                |||||||    |||||||||
                                GACCGGA    GGTGGGTGG
                                    CAGG_
GAM984  POU4F1   3'  AGTGAGTGGGAGCACAGCTGAA 21759     TG  T  ACA
           AA                     TTTT  GTT TG  TCATTCATT
                                ||||  ||| ||  |||||||||
                                AAAA  CGA AC  GGTGAGTGA
                                  GT  C  GAG
GAM984  PPIC     3'  AGTGGTGCTATTTTAAAACTAA 8131          _____     CATT
           AAA                    TTTTTGGTTTTGA    CATCATT
                                ||||||||||||||    |||||||
                                AAAAATCAAAATT    GTGGTGA
                                      TTATC       T
GAM984  PPP2R2B  3'  AGTGAGCTTGGCAGGGCCAGG  17117        A  TCA
                                TTTGGTTTTG CA   TTCATT
                                |||||||||| ||   ||||||
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                                GGACCGGGAC GT   GAGTGA
                                     G  TC_
GAM984  PPP2R2B  3'  ATGGGTGGAGTCCAGAAA    17118       TTTTG  AT
                                TTTTTGG    AC  CATTCAT
                                |||||||    ||  |||||||
                                AAAGACC    TG  GTGGGTA
                                   _____  AG
GAM984  PPT2     5'  AGTGGGGAGAATCAAGGCGGGG 18945      G      CA_  A
          AA                     TTTTT GTTTTGA   TC TTCATT
                                 |||||  |||||||   ||  ||||||
                                 AAGGG CGGAACT   AG GGGTGA
                                   G      AAG  _
GAM984  PROS1    3'  GATGAATGCTCTTTGAAGCCAA 88813        TG CAT_
          G                      TTTGGTTT  A    CATTCATT
                                 ||||||||  |    ||||||||
                                 GAACCGAA  T    GTAAGTAG
                                     GT TCTC
GAM984  PROS1    3'  GATGGATGTATACGAAGCTGGA 88814     TG     ACAT
          A                      TTT  GTTTTG    CATTCATT
                                 |||  ||||||    ||||||||
                                 AAG  CGAAGC    GTAGGTAG
                                   GT     ATAT
GAM984  PRX2     3'  GTTTGTGTATTAAAACCAAAAA 33309           CAT   TCATT
                                 TTTTTGGTTTTGA   CAT
                                 ||||||||||||   |||
                                 AAAAACCAAAATT   GTG
                                        AT_   TTTGA
GAM984  PSAP     3'  GATGCTGGGGTGTGGGGGTTGG 69883     TG TT  G    ATT_
          AAG                    TTTT  G  TT ACATC    CATT
                                 ||||  |  || |||||    ||||
                                 GAAG  T  GG TGTGG    GTAG
                                   GT GG  G    GGTC
GAM984  PTHR1    3'  AGTGGATGGACAGATGGACCAA 6143          TGACA_
          AAG                    TTTTTGGTTT     TCATTCATT
                                 ||||||||||     |||||||||
                                 GAAAACCAGG     GGTAGGTGA
                                      TAGACA
GAM984  PVR      3'  GATGAATGCCCAGGAGCTGAGG 22492      TG     GACAT
          A                      TTTT  GTTTT    CATTCATT
                                 ||||  |||||    ||||||||
                                 AGGA  CGAGG    GTAAGTAG
                                   GT    ACCC_
GAM984  RAD50    3'  GATGTGATTAAAGCTAAGGA   20410          ___
                                 TTTTTGGTTTTG   ACATC
                                 ||||||||||||   |||||
                                 AGGAATCGAAAT   TGTAG
                                        TAG
GAM984  RALBP1   3'  GATGTTGTTCAAACCAGAAA   23275         T    T
                                 TTTTTGGTTT GACA CATT
                                 |||||||||| |||| ||||
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                                AAAGACCAAA TTGT GTAG
                                     C    T
GAM984  RAMP1    3'  GATGAGTGGTTTGTGATTAAAA 20725         T   C
                G                    TTTTTGGTT TGA ATCATTCATT
                                     ||||||||| ||| ||||||||||
                                     GAAAATTAG GTT TGGTGAGTAG
                                          T  _
GAM984  RARB     5'  ATTCATGATTCGGGGCTGGGAA 32886      TG      C     TCATT
                                     TTTT  GTTTTGA ATCAT
                                     ||||  ||||||| |||||
                                     AAGG  CGGGGCT TAGTA
                                       GT      _    CTTAA
GAM984  RBM3     5'  AGTGGTCGTTGTCAAGGACCGG 71003          _     TCAT
                GAG                   TTTTTGGTT TTGACA    TCATT
                                     ||||||||| ||||||    |||||
                                     GAGGGCCAG AACTGT    GGTGA
                                          G     TGCT
GAM984  RGS6     3'  GGTGAATGGGCAGACCAGAAA  16281          TGACA
                                     TTTTTGGTTT    TCATTCATT
                                     ||||||||||    |||||||||
                                     AAAGACCAGA    GGTAAGTGG
                                          CG___
GAM984  ROCK2    3'  AATGGATGGTGTTGGAACTAA  66608        TG
                                     TTGGTTT  ACATCATTCATT
                                     |||||||  ||||||||||||
                                     AATCAAG  TGTGGTAGGTAA
                                        GT
GAM984  RPH3AL   3'  GGTGAGCATCAGAGCCAGAG   23737           CA_
                                     TTTTGGTTTTGA   TCATT
                                     ||||||||||||   |||||
                                     GAGACCGAGACT   AGTGG
                                           ACG
GAM984  RPP30    3'  AATGGAGTAGAGCCAGAG    22185           A AT
                                     TTTTGGTTTTG C  CATT
                                     |||||||||| |  ||||
                                     GAGACCGAGAT G  GTAA
                                          _ AG
GAM984  RUNX3    3'  GATTTGAGTCAGAACTGGAAA  16365      TG       A   T_
                                     TTTT  GTTTTGAC TCA  TC
                                     ||||  |||||||| |||  ||
                                     AAAG  CAAGACTG AGT  AG
                                       GT       _   TT
GAM984  SACM2L   5'  GGTGAAGTGGTTAGAGCTGAAA 42885      TG       ATCA
                G                    TTTT  GTTTTGAC    TTCATT
                                     ||||  ||||||||    ||||||
                                     GAAA  CGAGATTG    AAGTGG
                                       GT       GTG_
GAM984  SAFB     5'  AGTGGGCGGCGGAGCCAGGG   12934           ACA_
                                     TTTTGGTTTTG    TCATT
                                     ||||||||||    |||||
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                                GGGACCGAGGC   GGTGA
                                      GGCG
GAM984  SCAMP1   5' GGTGGGTGACGCCGAGAGCCAG 54503         GACA_
           AGA                  TTTTTGGTTTT    TCATTCATT
                                ||||||||||    ||||||||
                                AGAGACCGAGA    AGTGGGTGG
                                      GCCGC
GAM984  SERPINA5 3' AGTGGATGAGGGCCACCAGGAA 7117        TTTGACA
                                TTTTTGGT      TCATTCATT
                                ||||||||      ||||||||
                                AAGGACCA      AGTAGGTGA
                                   CCGGG__
GAM984  SIGLEC11 3' AGTGGGTGGATCACAAGTCAGG 54648      GT  _  CA
           AG                   TTTTTG  TT TGA  TCATTCATT
                                ||||||  || |||  ||||||||
                                GAGGAC  AA ACT  GGTGGGTGA
                                   TG  C   A_
GAM984  SKP2     3' AATGAGTGCTTAAACTAAAAA  21114         TGACAT
                                TTTTTGGTTT     CATTCATT
                                ||||||||||     ||||||||
                                AAAAATCAAA     GTGAGTAA
                                      TTC___
GAM984  SLC13A4  5' AATGATTTCTTCAAGGCCGAG  25858         CATCAT
                                TTTGGTTTTGA     TCATT
                                ||||||||||     |||||
                                GAGCCGGAACT     AGTAA
                                      TCTTT_
GAM984  SLC15A1  3' GATGAGGAAGACTTCAGAATTG 18643     TG     CA  A__
           GGAA                 TTTT  GTTTTGA  TC   TTCATT
                                ||||  |||||||  ||   ||||||
                                AAGG  TAAGACT  AG   GAGTAG
                                  GT      TC  AAG
GAM984  SLC22A12 5' GGTGAGTGGAGGCAGGAGCCA  58691       GACA_
                                TGGTTTT    TCATTCATT
                                |||||||    ||||||||
                                ACCGAGG    GGTGAGTGG
                                   ACGGA
GAM984  SLC22A2  3' GATGGCAGCAAGACCAAAAG   60280          A___
                                TTTTTGGTTTTG    CATC
                                ||||||||||||    ||||
                                GAAAACCAGAAC    GTAG
                                      GACG
GAM984  SLC25A19 5' GATGGACATTGTGTGGGCCAGA 41690        TG   TCA
           G                    TTTTGGTTT  ACA   TTCATT
                                |||||||||  |||   ||||||
                                GAGACCGGG  TGT   AGGTAG
                                      TG   TAC
GAM984  SLC2A6   3' GGTGGATTACCCAAGGCCAGGA 34574          ACATC
           G                    TTTTTGGTTTTG    ATTCATT
                                ||||||||||||    |||||||
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                                GAGGACCGGAAC    TAGGTGG
                                      CCAT_
GAM984  SLC6A12  3'  GATGAGGAACCTGGAGACCAAA 13193          GACATCA
           GA                   TTTTTGGTTTT      TTCATT
                                ||||||||||      ||||||
                                AGAAACCAGAG      GAGTAG
                                      GTCCAAG
GAM984  SMARCD2  3'  GGTGAATGGGGAGGCTGGGAG  13264     TG    GACA
                                TTTT  GTTTT    TCATTCATT
                                ||||  |||||   |||||||||
                                GAGG  CGGAG    GGTAAGTGG
                                  GT    G___
GAM984  SNAI2    3'  AATGAGTTCTGTATGAAACTGA 13238     TG    _   TC
           GA                   TTT  GTTTTG ACA  ATTCATT
                                |||  |||||| |||  |||||||
                                AGA  CAAAGT TGT  TGAGTAA
                                  GT     A   CT
GAM984  SNCAIP   5'  AATGAAAGTGATGACCAAAAG  97608        TTTGA    __
                                TTTTTGGT    CATCAT  TCATT
                                ||||||||    ||||||  |||||
                                GAAAACCA    GTAGTG  AGTAA
                                      _____     AA
GAM984  SNX5     3'  AATGAATGTGAAAGAAAGCCAA 27786         GACAT_
           G                    TTTGGTTTT     CATTCATT
                                |||||||||     ||||||||
                                GAACCGAAA     GTAAGTAA
                                      GAAAGT
GAM984  SNX6     3'  AGTGGATGAATGCTGGACCGAG 41442          TGA  _
           AG                   TTTTTGGTTT   CAT CATTCATT
                                ||||||||||   ||| ||||||||
                                GAGAGCCAGG   GTA GTAGGTGA
                                      TC_   A
GAM984  SNX9     3'  GATGGAAAAGTGTAGGGACTGA 33120     TG   TG   CA_
           GAA                    TTTT  GTTT  ACAT   TTCATT
                                ||||  ||||  ||||   ||||||
                                AAGA  CAGG  TGTG   AGGTAG
                                  GT   GA    AAA
GAM984  SOST     3'  AATGAATCATGACCGAAAG    48222         T   CA
                                TTTTTGGTT TGA  TCATT
                                |||||||| |||  |||||
                                GAAAGCCAG ACT  AGTAA
                                      T   A_
GAM984  SPAG11   3'  GGTGGATCGGCTTCAGAGGCCA 33676         _    CA  _
           GGAG                    TTTTTGGT TTTGA  TC ATTCATT
                                |||||||| |||||  || |||||||
                                GAGGACCG AGACT  GG TAGGTGG
                                      G    TC  C
GAM984  SPARC    3'  AAGGATGGTTTTGGGACTAGAG 13343         TG C      ATT
                                TTTTGGTTT  A ATCATTC
                                |||||||||  | |||||||
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                                GAGATCAGG  T TGGTAGG
                                    GT T      AA
GAM984  SPG4     3'  AGTGAATGGTAGAAGACACAAG 30808       _    GAC
            AA                    TTTTTG GTTTT   ATCATTCATT
                                  ||||||| |||||   ||||||||||
                                  AAGAAC CAGAA   TGGTAAGTGA
                                     A    GA_
GAM984  SRD5A2   5'  AATGAGTAGTGTAAAACAAAGA 60116       G    A  C
                                  TTTTTG TTTTG CAT ATTCATT
                                  ||||||| ||||| ||| |||||||
                                  AGAAAC AAAAT GTG TGAGTAA
                                     _    _  A
GAM984  SRRM2    3'  ATTGTGATGGTGGTTGGGACTG 33383     TG   TG _    T  T
            GAG                     TTT  GTTT  AC ATCAT CAT
                                  |||  ||||  || ||||| |||
                                  GAG  CAGG  TG TGGTA GTG
                                    GT   GT  G    _  TTAG
GAM984  SRRM2    3'  TGGAGTCAGGGCCAGGGA    33387            AT
                                  TTTTTGGTTTTGAC  CA
                                  ||||||||||||||  ||
                                  AGGGACCGGGACTG  GT
                                         AG
GAM984  STK10    3'  GGTGGGGTCAGGGTCCAAGA   21136       _      AT
                                  TTTTGG TTTTGAC  CATT
                                  |||||| |||||||  ||||
                                  AGAACC GGGACTG  GTGG
                                     T      GG
GAM984  STK24    5'  GGTGAATGGAAGAAGGAGCGAG 14549       G    GACA
            AA                    TTTTTG TTTT    TCATTCATT
                                  |||||| ||||    |||||||||
                                  AAGAGC AGGA    GGTAAGTGG
                                     G    AGAA
GAM984  SURF5    3'  TGTTGTCAGAGTTGGGAG    56920       GG       T
                                  TTTTT  TTTTGACA CA
                                  |||||  |||||||| ||
                                  GAGGG  GAGACTGT GT
                                     TT       T
GAM984  SURF5    3'  TGTTGTCAGAGTTGGGAG    56921       GG       T
                                  TTTTT  TTTTGACA CA
                                  |||||  |||||||| ||
                                  GAGGG  GAGACTGT GT
                                     TT       T
GAM984  SYN3     3'  AGTGGGGTCCTGAGGCCAAGAA 14477           __  AT   CATT
                                  TTTTTGGTTTT  GAC  CATT
                                  ||||||||||  |||  ||||
                                  AAGAACCGGAG  CTG  GTGA
                                        TC   GG
GAM984  SYN3     3'  AGTGGGGTCCTGAGGCCAAGAA 14478           __  AT   CATT
                                  TTTTTGGTTTT  GAC  CATT
                                  ||||||||||  |||  ||||
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                                AAGAACCGGAG CTG GTGA
                                      TC  GG
GAM984  SYN3    3' AGTGGGGTCCTGAGGCCAAGAA 14479        __  AT   CATT
                                TTTTTGGTTTT GAC CATT
                                |||||||||| ||| ||||
                                AAGAACCGGAG CTG GTGA
                                      TC  GG
GAM984  TARBP2  3' GATGAATGGGAATGAAATCAGG 16069        ACA
          G                    TTTTGGTTTTG  TCATTCATT
                               ||||||||||  |||||||||
                               GGGACTAAAGT  GGTAAGTAG
                                     AAG
GAM984  TARBP2  3' GATGAATGGGAATGAAATCAGG 16070        ACA
          G                    TTTTGGTTTTG  TCATTCATT
                               ||||||||||  |||||||||
                               GGGACTAAAGT  GGTAAGTAG
                                     AAG
GAM984  TARBP2  3' GATGGTCTTCGAAACCGGGG  16071        C_
                               TTTTGGTTTTGA ATCATT
                               |||||||||||  ||||||
                               GGGGCCAAAGCT TGGTAG
                                     TC
GAM984  TAX1BP1 5' GATGGCGGATCAGGATCGGAAG 21215         CA AT
                               TTTTTGGTTTTGA TC TCATT
                               |||||||||||| || |||||
                               GAAGGCTAGGACT AG GGTAG
                                     __ GC
GAM984  TCF3    3' AATGGGGCATTTTGTTGGGACC 71268      TG  TCA___
          AG                   TTGGTTT ACA    TTCATT
                               |||||||  |||    ||||||
                               GACCAGG TGT    GGGTAA
                                  GT  TTTACG
GAM984  TEM5    5' GATGGGTTGATGGGCGCCGGGG 52301      TTTGA  _
                               TTTTGGT   CATCA TTCATT
                               |||||||   ||||| ||||||
                               GGGGCCG   GTAGT GGGTAG
                                  CGG__   T
GAM984  TFR2    3' AATGATTCAGGGTCAGGGA  13697      TT  C
                               TTTTTGG TTGA ATCATT
                               |||||||  |||| ||||||
                               AGGGACT  GACT TAGTAA
                                  GG  _
GAM984  TFR2    3' TGAATGATTCAGGGTCAGGGA 13699      TT  C     TT
                               TTTTTGG TTGA ATCATTCA
                               |||||||  |||| ||||||||
                               AGGGACT  GACT TAGTAAGT
                                  GG  _      T
GAM984  TGFBR2  3' TGGTGTTAAGATTTGAAG   13736    TG
                               TTTT GTTTTGACATCA
                               ||||  ||||||||||||
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                                GAAG  TAGAATTGTGGT
                                  TT
GAM984  TGFBR3   3'  AGTGAGGAGATGCGGCCAAAGA 13738        TT  A   A_
                                TTTTTGGT  TG CATC  TTCATT
                                ||||||||  || ||||  ||||||
                                AGAAACCG  GC GTAG  GAGTGA
                                    __ _   AG
GAM984  TIMM8A   3'  AGTGTTTGATTGTCAATGCTGG 15833     TG  T    _  TT
           AGA                    TTTT  GT TTGACA TCA  CATT
                                ||||  || |||||| |||  ||||
                                AGAG  CG AACTGT AGT  GTGA
                                  GT  T     T   TT
GAM984  TIMP4    3'  GATGTACAGAATCAGAAG    13756          _
                                TTTTTGGTTTTG ACATC
                                |||||||||||| |||||
                                GAAGACTAAGAC TGTAG
                                       A
GAM984  TLE1     3'  AATGGAGCACCAAGGCCAAG   18666         ACATCA
                                TTTGGTTTTG     TTCATT
                                ||||||||||     ||||||
                                GAACCGGAAC     AGGTAA
                                     CACG__
GAM984  TLL2     3'  ATATGGATGGATGTCAGGACTA 25880             _    T
           AAAA                   TTTTTGGTTTTGACATC ATTCAT
                                |||||||||||||||| ||||||
                                AAAAATCAGGACTGTAG TAGGTA
                                        G     TAA
GAM984  TLL2     3'  GATGGATGTCAGGACTAAAAA  25883             AT
                                TTTTTGGTTTTGACATC  TC
                                ||||||||||||||||  ||
                                AAAAATCAGGACTGTAG  AG
                                        GT
GAM984  TMPRSS2  3'  AATGAATGATTCTACAGCTAGG 20171        TT_  C
           A                     TTTTGGTT   GA ATCATTCATT
                                ||||||||   || ||||||||||
                                AGGATCGA   CT TAGTAAGTAA
                                     CAT  _
GAM984  TNFAIP2  3'  AATGGAAGACAGAACTGGAAG  21914     TG     ACA  A
                                TTTT  GTTTTG   TC TTCATT
                                ||||  ||||||   || ||||||
                                GAAG  CAAGAC   AG AGGTAA
                                  GT     ___  A
GAM984  TNFRSF10B 3'  ATGAGTCGGGACCAAAGA    15217            A
                                TTTTTGGTTTTGAC TCAT
                                |||||||||||||| ||||
                                AGAAACCAGGGCTG AGTA
                                          _
GAM984  TNFSF15  3'  GGTGGGTGGATCATCTAAGGCC 18869          _  CA__
           GGGAG                  TTTTTGGTTTT GA    TCATTCATT
                                |||||||||| ||    |||||||||
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                                GAGGGCCGGAA CT    GGTGGGTGG
                                      T  ACTA
GAM984  TNFSF8   3'  GGTGTGGTATAGAACCAGAAA  8802          ____
                                TTTTTGGTTTTG    ACATC
                                ||||||||||||   |||||
                                AAAGACCAAGAT    TGTGG
                                      ATGG
GAM984  TNP1     3'  GATGTTAGATCAAAGCCAGAGA 60161          _____
                                TTTTTGGTTTTGA    CATC
                                ||||||||||||    ||||
                                AGAGACCGAAACT    GTAG
                                      AGATT
GAM984  TNP2     3'  AATGAATGGGGGTAGGATGCCA 19456       TTTG_  A_
           AGAA                    TTTTTGGT    AC  TCATTCATT
                                ||||||||    ||  |||||||||
                                AAGAACCG    TG  GGTAAGTAA
                                     TAGGA  GG
GAM984  TOP3A    3'  AATGAGTTAACCAGGACCAAG  17258         ACATC
                                TTTGGTTTTG    ATTCATT
                                ||||||||||    |||||||
                                GAACCAGGAC    TGAGTAA
                                      CAAT_
GAM984  TRAF5    3'  AGTGGGTGATGTAGTTACAAAG 17267       GTTTTG
           A                     TTTTTG     ACATCATTCATT
                                ||||||     ||||||||||||
                                AGAAAC     TGTAGTGGGTGA
                                   ATTGA_
GAM984  TRHR     3'  AATGGATGACAAAGAAATTGAG 13857     TG    GACA
           AA                     TTTT  GTTTT   TCATTCATT
                                ||||  |||||   |||||||||
                                AAGA  TAAAG   AGTAGGTAA
                                  GT    AAAC
GAM984  TRIM34   5'  GTGGAGTGTCGGAGTCAG    56111    GT      CA    T
                                TTG  TTTGACAT  TTCAT
                                |||  ||||||||  |||||
                                GAC  AGGCTGTG  AGGTG
                                  TG       __     T
GAM984  TRIM9    3'  AATGGGTGGTGGGGTGCTAGAG 31434       TTTGA
                                TTTTGGT    CATCATTCATT
                                |||||||    ||||||||||||
                                GAGATCG    GTGGTGGGTAA
                                     TGGG_
GAM984  TTC3     3'  AGTGTGTTGAATCCGAAGA   13880       T  TG   T
                                TTTTTGG TT  ACA CATT
                                ||||||| ||  ||| ||||
                                AGAAGCC AA  TGT GTGA
                                     T  GT   _
GAM984  UBE2B    3'  AATGAAGAAAGTAAAACCA   13932        ACA  A
                                TGGTTTTG   TC TTCATT
                                ||||||||   || ||||||
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                                ACCAAAAT   AG AAGTAA
                                    GAA  _
GAM984  UCP3     3'  AGTGGATGACGTGAAGCCA   13979       G  A
                                TGGTTTT AC TCATTCATT
                                ||||||| || |||||||||
                                ACCGAAG TG AGTAGGTGA
                                   _  C
GAM984  UGT1A1   3'  GGTGGGTGGTGTATTTGAGAA  6629      TG TTTTG
                                TTTT  G    ACATCATTCATT
                                ||||  |    ||||||||||||
                                AAGA  T    TGTGGTGGGTGG
                                  GT TA___
GAM984  UGT1A4   3'  GGTGGGTGGTGTATTTGAGAA  24056     TG TTTTG
                                TTTT  G    ACATCATTCATT
                                ||||  |    ||||||||||||
                                AAGA  T    TGTGGTGGGTGG
                                  GT TA___
GAM984  UGT1A9   3'  GGTGGGTGGTGTATTTGAGAA  41052     TG TTTTG
                                TTTT  G    ACATCATTCATT
                                ||||  |    ||||||||||||
                                AAGA  T    TGTGGTGGGTGG
                                  GT TA___
GAM984  UNC13    3'  GGTGGGCCTGAACAAAAGCCAA 22099         GACA  __
           AAA                    TTTTTGGTTTT   TCA  TTCATT
                                  ||||||||||    |||  ||||||
                                  AAAAACCGAAA   AGT  GGGTGG
                                        ACA_  CC
GAM984  VDAC1    3'  GGTGGATGTGATGAAGCCAA   14036       A  T
                                TTGGTTTTG CA CATTCATT
                                ||||||||| || ||||||||
                                AACCGAAGT GT GTAGGTGG
                                    A  _
GAM984  WBP2     3'  GGTGGCTGCTGGGTGGGGCCGG 73389        TT A_  T  TT
           GAA                    TTTTTGGTT  G  CA CA  CATT
                                  |||||||||  |  || ||  ||||
                                  AAGGGCCGG  T  GT GT  GTGG
                                       GG GG  C  CG
GAM984  WDR3     3'  AGTGTCATGGATCTTAGAGCTA 23266          C  ATT__
           AAAA                   TTTTTGGTTTTGA ATC    CATT
                                  |||||||||||| |||    ||||
                                  AAAAATCGAGATT TAG    GTGA
                                        C  GTACT
GAM984  WISP1    3'  GTGGGTCAAACCAAGAA     55941         T  A
                                TTTTTGGTTT GAC TCAT
                                |||||||||| ||| ||||
                                AAGAACCAAA CTG GGTG
                                   _  _
GAM984  WNT10B   5'  GGTGAGAGCAAAGCCAGAG   14128         ACA
                                TTTTGGTTTTG  TCATT
                                ||||||||||  |||||
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                                GAGACCGAAAC   AGTGG
                                      GAG
GAM984  WRB     3'  GATGGATACAGCCGCGAGGCTA 17329          ACATC__
            AAAA                   TTTTTGGTTTTG      ATTCATT
                                   ||||||||||||      |||||||
                                   AAAAATCGGAGC      TAGGTAG
                                         GCCGACA
GAM984  WWP2    3'  GGTGGCTGTTCGGGACTGAGAG 61727      TG     _ _    CATT
                                   TTTT  GTTTTGA CA TCATT
                                   ||||  ||||||| || |||||
                                   GAGA  CAGGGCT GT GGTGG
                                     GT      T  C       T
GAM984  XPNPEP1  3'  AGTGAATAAAAATGTCAGAACT 40200          C___
                                   GGTTTTGACAT    ATTCATT
                                   ||||||||||||   |||||||
                                   TCAAGACTGTA    TAAGTGA
                                         AAAA
GAM984  XRCC3   3'  GGTGATTCTCAGGGCTGGAG   19521     TG      C_
                                   TTT  GTTTTGA  ATCATT
                                   |||  |||||||  ||||||
                                   GAG  CGGGACT  TAGTGG
                                     GT      CT
GAM984  XYLB    3'  AGTGAGTGGTGTCCTTTGGAGG 18828      TG TTTT
                                   TTTT  G    GACATCATTCATT
                                   ||||  |    ||||||||||||
                                   GGAG  T    CTGTGGTGAGTGA
                                     GT TC__
GAM984  ZFX     5'  AGTGGATGTTCAAGATTAAGA  14163          CAT
                                   TTTTGGTTTTGA   CATTCATT
                                   ||||||||||||   ||||||||
                                   AGAATTAGAACT   GTAGGTGA
                                          T__
GAM984  ZNF10   3'  AGAAATGATGGTTAGAATCAGG 31815          _     CATT
            AG                       TTTTTGGTTTTGAC ATCATT
                                   |||||||||||||| ||||||
                                   GAGGACTAAGATTG TAGTAA
                                          G     AGA
GAM984  ZNF137  3'  AGTGGATAATGGAAACTGAAAG 14307      TG    GA   C
                                   TTTT  GTTTT  CAT ATTCATT
                                   ||||  |||||  ||| |||||||
                                   GAAA  CAAAG  GTA TAGGTGA
                                     GT    __   A
GAM984  ZNF151  3'  GATGGATGGCACCCTGGAACCG 14316          GACA__
            GGAA                     TTTTTGGTTTT     TCATTCATT
                                   ||||||||||||     |||||||||
                                   AAGGGCCAAGG     GGTAGGTAG
                                         TCCCAC
GAM984  ZNF161  3'  GATGAAATGCCAGAATTAAAA  24081          A   CA
                                   TTTTGGTTTTG CAT  TTCATT
                                   |||||||||||  |||  ||||||
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                                AAAATTAAGAC GTA  AAGTAG
                                      C  __
GAM984  ZNF174   3'  GATGAGTGATCTACCAGAAA  14352        TTTGAC
                                TTTTTGGT     ATCATTCATT
                                ||||||||     ||||||||||
                                AAAGACCA     TAGTGAGTAG
                                    TC____
GAM984  ZNF20    3'  AATGTTGTTATGGCTGGAAA  64127     TG  TT    T
                                TTTT  GT  TGACA CATT
                                ||||  ||  ||||| ||||
                                AAAG  CG  ATTGT GTAA
                                  GT  GT    T
GAM984  ZNF266   5'  AGTGAGTGAGTGTGGATAGAGA 89690      GGTT  G  _
           G                     TTTTT   TT ACA TCATTCATT
                                |||||   || ||| |||||||||
                                GAGAG   AG TGT AGTGAGTGA
                                   AT__  G  G
GAM984  ZNF278   3'  AATGCTGTTGGGAACCAGGAA  50262        _ TG  T
                                TTTTTGGTT T  ACA CATT
                                ||||||||| |  ||| ||||
                                AAGGACCAA G  TGT GTAA
                                     G GT  C
GAM984  ZNF278   3'  AATGCTGTTGGGAACCAGGAA  50263        _ TG  T
                                TTTTTGGTT T  ACA CATT
                                ||||||||| |  ||| ||||
                                AAGGACCAA G  TGT GTAA
                                     G GT  C
GAM984  ZNF35    5'  GATGACTGCAGAATTGAGAG  14240     TG    A  _
                                TTTT  GTTTTG CA TCATT
                                ||||  |||||| || |||||
                                GAGA  TAAGAC GT AGTAG
                                  GT     _  C
GAM984  ZNFN2A1  3'  AGTGGGTGGAGGGTCAGAG  61389       A__
                                TTTTGAC   TCATTCATT
                                |||||||   |||||||||
                                GAGACTG   GGTGGGTGA
                                    GGA
GAM984  ADAMTS10 3'  GGTGAGACGGAGCCGGAAG  48981          ACA
                                TTTTTGGTTTTG   TCATT
                                ||||||||||||   |||||
                                GAAGGCCGAGGC   AGTGG
                                       AG_
GAM984  ADAMTSL1 3'  AGTGCTGGTAGTCAAAATTAAA 54611           _   TT
           AA                    TTTTTGGTTTTGAC ATCA  CATT
                                |||||||||||||| ||||  ||||
                                AAAAATTAAAACTG TGGT  GTGA
                                       A   C_
GAM984  AF020591 3'  GGTGGGTGGATCACGAGGTCAG 27915      GT   ACA_
           GAG                   TTTTTG  TTTG   TCATTCATT
                                ||||||  ||||   |||||||||
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                                GAGGAC  GAGC   GGTGGGTGG
                                   TG   ACTA
GAM984  AF9Q34   3'  GGTGGGTGAGCTCTCAGGCCGA 51720         T_  CA
           GAG                   TTTTTGGTTT  GA  TCATTCATT
                                 ||||||||||  ||  |||||||||
                                 GAGAGCCGGA  CT  AGTGGGTGG
                                     CT  CG
GAM984  AHCYL1   3'  AATGAGCATGGCTTGTTAAGAT 22771           __   __
           CAGGAG                TTTTTGGTTTTGACA  TCAT  TCATT
                                 ||||||||||||||  ||||  |||||
                                 GAGGACTAGAATTGT  GGTA  AGTAA
                                       TC   CG
GAM984  AIF1     3'  GGATGATGGGATTGAAG     17928     TG   TGA
                                 TTT  GTTT   CATCATTC
                                 |||  ||||   ||||||||
                                 GAA  TAGG   GTAGTAGG
                                   GT   ____
GAM984  AIG-1    3'  GAAATATGTTAAAGTCAAAG   32757      GT      CA
                                 TTTTG  TTTGACAT  TTC
                                 |||||  ||||||||  |||
                                 GAAAC  AAATTGTA  AAG
                                    TG       TA
GAM984  AK5      3'  AATGCATGTTTGTTAGAATGGA 24926      G       T_  T
           AA                    TTTT GTTTTGACA  CAT CATT
                                 ||||  |||||||||  |||  ||||
                                 AAAG TAAGATTGT  GTA GTAA
                                   G       TT   C
GAM984  AKAP12   3'  AATGAATGCTGCTGCTGAGACT 58472     TG    GA  T___
           GAAGA                   TTTT  GTTTT  CA   CATTCATT
                                 ||||  |||||  ||   ||||||||
                                 AGAA  CAGAG  GT   GTAAGTAA
                                   GT    TC  CGTC
GAM984  ALK7     3'  AGTGAGTGAGTGAGTACAGAAG 76240       GTT  G  A
                                 TTTTTG   TT AC TCATTCATT
                                 ||||||   || || |||||||||
                                 GAAGAC   GA TG AGTGAGTGA
                                    AT_  G  _
GAM984  ALK7     3'  GATGATCCAAGACCAAAAG    76243          AC
                                 TTTTTGGTTTTG  ATCATT
                                 ||||||||||||  ||||||
                                 GAAAACCAGAAC  TAGTAG
                                       C_
GAM984  AMOTL1   3'  AATGGGCGAAATCCAGGCCAGG 74010         T  CA  A
           AG                    TTTTTGGTTT GA  TC TTCATT
                                 ||||||||||  ||  ||  ||||||
                                 GAGGACCGGA CT  AG GGGTAA
                                       C  AA  C
GAM984  AP1S3    3'  AATGAATGAAATCAATTACGG  75424     GTT   CA
                                 TTG   TTGA  TCATTCATT
                                 |||   ||||  |||||||||
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                                GGC   AACT  AGTAAGTAA
                                  ATT    AA
GAM984  AP1S3    3'  AATGAATGCAGTAAAATTGAAA 75425      TG     ACAT
            A                    TTTT  GTTTTG    CATTCATT
                                 ||||  ||||||    ||||||||
                                 AAAA  TAAAAT    GTAAGTAA
                                   GT     GAC_
GAM984  Apg4B    3'  AGTGGGTGTGTGGGAAACCTGA 26180      T     GA  _
            AG                   TTTT GGTTTT  CAT CATTCATT
                                 |||| ||||||  ||| ||||||||
                                 GAAG CCAAAG  GTG GTGGGTGA
                                   T     G_   T
GAM984  Apg4B    3'  TTAGGTGGTTTAGGGCCAAAAG 26187           C     CATT
                                 TTTTTGGTTTTGA ATCATT
                                 |||||||||||| ||||||
                                 GAAAACCGGGATT TGGTGG
                                        _     ATTG
GAM984  APOA1BP  3'  AATGGACTGTTAGATGCCAAAA 59240         _      TCA
            A                    TTTTTGGT TTTGACA   TTCATT
                                 |||||||| |||||||   ||||||
                                 AAAAACCG AGATTGT   AGGTAA
                                     T      C__
GAM984  APOA1BP  3'  AGTGAATGGTGGAAGTCAGAGA 59241       GT   GA
                                 TTTTTG  TTT  CATCATTCATT
                                 ||||||  |||  ||||||||||
                                 AGAGAC  AAG  GTGGTAAGTGA
                                    TG  __
GAM984  APOL6    3'  AATGGAGCTTGCAGGGCTGAGA 48371      TG     A  TCA
            G                    TTTT  GTTTTG CA   TTCATT
                                 ||||  |||||| ||   ||||||
                                 GAGA  CGGGAC GT   AGGTAA
                                   GT     _  TCG
GAM984  APOL6    3'  AGTGAGTGGTGAATGAATGTGA 48372      TG    TGA
            AG                   TTTT  GTTT   CATCATTCATT
                                 ||||  ||||   ||||||||||
                                 GAAG  TAAG   GTGGTGAGTGA
                                   TG    TAA
GAM984  APOL6    3'  GGTGAATGAATGTGAAGGCC   48374       G   _
                                 GGTTTT ACAT CATTCATT
                                 |||||| |||| ||||||||
                                 CCGGAA TGTA GTAAGTGG
                                    G   A
GAM984  APPD     3'  GATGGGTGGTTGCAAAACAAAA 44462      G     AC
            AA                   TTTTT GTTTTG  ATCATTCATT
                                 ||||| ||||||  ||||||||||
                                 AAAAA CAAAAC  TGGTGGGTAG
                                   A     GT
GAM984  AQP9     3'  GATGAATTTGAGAAGCCAAA   40940         GA  TC
                                 TTTGGTTTT  CA  ATTCATT
                                 |||||||||  ||  |||||||
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                                AAACCGAAG  GT  TAAGTAG
                                    A_  T_
GAM984  ARHGAP11A 5'  AGTGGATGTGAGTGAGGATCAA 29442          G  AT_
           GGA                   TTTTTGGTTTT AC   CATTCATT
                                 |||||||||| ||   ||||||||
                                 AGGAACTAGGA TG   GTAGGTGA
                                     G  AGT
GAM984  ARHGAP11A 3'  GATGAAATGTTGAATTTGAAGA 29451      TG T  TG    CA
                                 TTTT  G TT  ACAT  TTCATT
                                 ||||  | ||  ||||  ||||||
                                 AGAA  T AA  TGTA  AAGTAG
                                   GT T  GT   __
GAM984  BA108L7.2 3'  AATGTACAATGTTAAGACAGGG 49058      TG         CATT
           AA                    TTTT  GTTTTGACAT    CATT
                                 ||||  ||||||||||    ||||
                                 AAGG  CAGAATTGTA    GTAA
                                   GA         ACAT
GAM984  BAF53A    5'  GGTGGGTGGCGGTGGAAGTTAA 66036      GG    G  A_
           GGG                   TTTTT  TTTT AC  TCATTCATT
                                 |||||  |||| ||  |||||||||
                                 GGGAA  GAAG TG  GGTGGGTGG
                                   TT    G  GC
GAM984  BC022889  3'  GATGAAATCCAAGCCAAAG    84627         T  CA
                                 TTTTGGTTT GA  TCATT
                                 |||||||| ||  |||||
                                 GAAACCGAA CT  AGTAG
                                     C  AA
GAM984  BHLHB2    5'  TGCATCTCAAAGCCGAAGA    14767           C  _
                                 TTTTTGGTTTTGA AT CA
                                 |||||||||||| || ||
                                 AGAAGCCGAAACT TA GT
                                       C  C
GAM984  BLR1      5'  AGTGATTTGTTCAAAATTGAAA 53111      TG      _  TCAT
                                 TTT  GTTTTGA CA    TCATT
                                 |||  ||||||| ||    |||||
                                 AAA  TAAAACT GT    AGTGA
                                   GT      T  TT__
GAM984  BLR1      3'  GATGAGTGGAGGTTAAGGCTGA 53114      TG       A_
           GGA                   TTTT  GTTTTGAC  TCATTCATT
                                 ||||  ||||||||  |||||||||
                                 AGGA  CGGAATTG  GGTGAGTAG
                                   GT       GA
GAM984  BM040     5'  GGTGGCGGAGTTAAAGTCAAAG 38051      GT     A  AT
                                 TTTTG  TTTGAC TC  TCATT
                                 |||||  ||||||  ||  |||||
                                 GAAAC  AAATTG AG  GGTGG
                                   TG     _  GC
GAM984  BRAL1     5'  GATGGGGTGGGGACTGAGAA   41808      TG    G  AT
                                 TTTT  GTTTT AC  CATT
                                 ||||  |||||  ||  ||||
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                                AAGA  CAGGG TG  GTAG
                                  GT    G  GG
GAM984  BRD2    5'  GGTGTCTGAGATCGGGGA    18799          _
                                TTTTTGGTTTT GACATC
                                |||||||||| ||||||
                                AGGGGCTAGAG CTGTGG
                                      T
GAM984  BRD3    5'  GTGAGTGAGCTGCCGGAG    24775       TTTGACA
                                TTTTGGT     TCATTCAT
                                |||||||     ||||||||
                                GAGGCCG     AGTGAGTG
                                   TCG____
GAM984  BTN3A1  5'  GGTGATTTTCAATGTTGGGACT 23895     _   TG   CAT___
          CAAA                    TTTG GTTT  ACAT     TCATT
                                |||| ||||  ||||     |||||
                                AAAC CAGG  TGTA     AGTGG
                                  T   GT    ACTTTT
GAM984  BTN3A2  3'  AGTGGTCGAGTGAAGATTGAAA 23870     TG    G  A  AT
          A                     TTTT  GTTTT AC TC  TCATT
                                ||||  ||||| || ||  |||||
                                AAAA  TAGAA TG AG  GGTGA
                                  GT    G  _  CT
GAM984  C11orf9  3'  AATGGAAGGATGGAGCTAGAAA 26112         TGA   A_
                                TTTTTGGTTT   CATC  TTCATT
                                |||||||||   ||||  ||||||
                                AAAGATCGAG   GTAG  AGGTAA
                                     ___    GA
GAM984  C13orf1  3'  AACATGAGTGTTAGAATTAGAA 40341           _   TCATT
          A                     TTTTTGGTTTTGACA TCAT
                                ||||||||||||||| ||||
                                AAAGATTAAGATTGT AGTA
                                      G   CAA
GAM984  C17orf26 3'  AATGAGTCGAACTAGACCAGAA 58262         ____   A   CATT
          G                     TTTTTGGTT   TTGAC TCATT
                                |||||||||   ||||| |||||
                                GAAGACCAG   AGCTG AGTAA
                                     ATCA   _
GAM984  C17orf26 3'  AGCACTGATGATCAAAATTGAA 58263     TG     _   TTCATT
          GA                    TTTT  GTTTTGA CATCA
                                ||||  ||||||| |||||
                                AGAA  TAAAACT GTAGT
                                  GT     A    CACGA
GAM984  C17orf26 5'  GATGGAAGTGCAGTGGGGGCTG 58266     TG    G  AT  __
          GAGA                    TTTT  GTTTT AC  CAT  TCATT
                                ||||  ||||| ||  |||  |||||
                                AGAG  CGGGG TG  GTG  GGTAG
                                  GT    G  AC   AA
GAM984  C1orf28  3'  GGTGATTTTGAAACCTAGAA  44845     T    TG C
                                TTTT GGTTT  A ATCATT
                                |||| |||||  | ||||||
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                                AAGA CCAAA  T TAGTGG
                                  T    GT T
GAM984  C20orf111 5'  GATGGTACCCGTTAGCAGCCAG 33628        _    ATCAT
           AAG                    TTTTTGGTT TTGAC    TCATT
                                  ||||||||| |||||    |||||
                                  GAAGACCGA GATTG    GGTAG
                                      C    CCCAT
GAM984  C20orf12  5'  AATGGATTTGTTGGATCAAAAC 36840          __ TC__
           TAAAGA                 TTTTTGGTTTTGA  CA   ATTCATT
                                  ||||||||||||| ||   |||||||
                                  AGAAATCAAAACT  GT   TAGGTAA
                                        AG  TGTT
GAM984  C20orf12  3'  TGCACATGGTTCAAAGCTAAAA 36853          C    TCATT
           G                       TTTTTGGTTTTGA ATCAT
                                  ||||||||||||| |||||
                                  GAAAATCGAAACT TGGTA
                                        _    CACGTT
GAM984  C20orf13  3'  GTGATATGTCAGAACTGAAGA  35273     TG       CAT   T
                                  TTTT  GTTTTGACAT   TCAT
                                  ||||  ||||||||||   ||||
                                  AGAA  CAAGACTGTA   AGTG
                                    GT        T__    T
GAM984  C20orf177 5'  GGTGAATGAATCTCATCAGAAA 62838        TTT  CA
                                  TTTTTGGT   GA  TCATTCATT
                                  ||||||||   ||  |||||||||
                                  AAAGACTA   CT  AGTAAGTGG
                                       CT_  A_
GAM984  C20orf40  5'  AGTGATGTCAAGGTTGGGG   26763     TG TT
                                  TTT  G  TTGACATCATT
                                  |||  |  ||||||||||
                                  GGG  T  AACTGTAGTGA
                                    GT GG
GAM984  C20orf46  5'  AGTGAGGGATGCAGAGCCAGGG 37733          A    A
           A                       TTTTTGGTTTTG CATC TTCATT
                                  |||||||||||| |||| ||||||
                                  AGGGACCGAGAC GTAG GAGTGA
                                        _    G
GAM984  C20orf98  3'  GGTGGGTGAAGAAGGCTGGAGG 72008     TG    GACA
                                  TTTT  GTTTT    TCATTCATT
                                  ||||  |||||    |||||||||
                                  GGAG  CGGAA    AGTGGGTGG
                                    GT    GA__
GAM984  C3IP1     3'  AGTGAACAAATGTTGGGATGAG 41576      G    TG    CA_
           AGA                     TTTTT GTTT  ACAT   TTCATT
                                  ||||| ||||  ||||   ||||||
                                  AGAGA TAGG  TGTA   AAGTGA
                                    G   GT    AAC
GAM984  C4orf6    5'  AGTGAGGTCATGACCAGAAA   20438         T    A
                                  TTTTTGGTT TGAC TCATT
                                  ||||||||| |||| |||||
```

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                                AAAGACCAG ACTG AGTGA
                                     T   G
GAM984  C8orf6   5'  AATGATAATTGTTAACAGCTAG 90777        _     TCAT
           AAA                    TTTTTGGTT TTGACA   TCATT
                                  ||||||||| ||||||   |||||
                                  AAAGATCGA AATTGT   AGTAA
                                       C     TAAT
GAM984  C8orf6   3'  GATGGATGGACTGGAGCTAGAG 90781        TT ACA
                                  TTTTGGTT  G   TCATTCATT
                                  ||||||||  |   |||||||||
                                  GAGATCGA  T   GGTAGGTAG
                                       GG CA_
GAM984  C8orf6   3'  GATGGATGGATGGACTGGAG   90782    TG   TTGA   _
                                  TTT  GTT    CATC ATTCATT
                                  |||  |||    |||| |||||||
                                  GAG  CAG    GTAG TAGGTAG
                                    GT   ____   G
GAM984  C9orf14  5'  AATGAGTTAGTCAAGGCTGAGG 87950    TG      ATC
                                  TTT  GTTTTGAC   ATTCATT
                                  |||  ||||||||   |||||||
                                  GGA  CGGAACTG   TGAGTAA
                                    GT       AT_
GAM984  CABYR    3'  GATGGGCGACACCAAGAA    25172        T   A_
                                  TTTTTGGT TTG  CATC
                                  |||||||| |||  ||||
                                  AAGAACCA AGC  GTAG
                                       C   GG
GAM984  CAP350   3'  AATGAGTGTGTGCACCAAAGA  29701        TTTG   T
                                  TTTTTGGT    ACA CATTCATT
                                  ||||||||    ||| ||||||||
                                  AGAAACCA    TGT GTGAGTAA
                                       CG__   _
GAM984  CCNB3    3'  CTTGGATATGTTGAAGCTGGAG 54467    TG    TG    C    TT
                                  TTT  GTTT  ACAT ATTCA
                                  |||  ||||  |||| |||||
                                  GAG  CGAA  TGTA TAGGT
                                    GT   GT   _    TCC
GAM984  CCNI     3'  AATGAGAACATGCAAAATCAGG 23364          A   CA_
           AA                     TTTTTGGTTTTG CAT   TTCATT
                                  ||||||||||||| |||   ||||||
                                  AAGGACTAAAAC GTA   GAGTAA
                                         _  CAA
GAM984  CCR1     3'  GATGAATGAGCAAAACCAAA   8928          ACA
                                  TTTGGTTTTG   TCATTCATT
                                  ||||||||||   |||||||||
                                  AAACCAAAAC   AGTAAGTAG
                                       G__
GAM984  CDCA4    3'  AGTGAGACCTGGGTGAAAATCA 36085          G  A   ___
           GGAG                      TTTTTGGTTTT AC TCA   TTCATT
                                  |||||||||| || |||   ||||||
```

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                                GAGGACTAAAA TG GGT   GAGTGA
                                      G _  CCA
GAM984  CES2    3' GATGGCTTGAGGCCAGAGG   15263         TG __
                                TTTTTGGTTT  A  CATC
                                ||||||||||  |  ||||
                                GGAGACCGGA  T  GTAG
                                      GT CG
GAM984  CES2    3' GATGGGAGGATGGCTTGAGGCC 15264        TG __   A_
           AGAG                   TTTTGGTTT  A  CATC  TTCATT
                                ||||||||||  |  ||||  ||||||
                                GAGACCGGA  T  GTAG  GGGTAG
                                      GT CG   GA
GAM984  CG012   5' AATGAATGAAGTGAATTACAAA 84140      GTT  G  A
           A                    TTTTG   TT AC TCATTCATT
                                |||||   || || |||||||||
                                AAAAC   AA TG AGTAAGTAA
                                   ATT  G  A
GAM984  CGI-96  3' TGGCTGGAGGTGCAGGGCCAGG 32296          A   A   TT
           AG                     TTTTTGGTTTTG CATC TTCA
                                ||||||||||||| |||| ||||
                                GAGGACCGGGAC GTGG AGGT
                                      _   _   CGGTA
GAM984  CHST8   5' GATGAGTTCCCGAGGCCAGGAG 42692          ACATC
                                TTTTTGGTTTTG    ATTCATT
                                ||||||||||||    |||||||
                                GAGGACCGGAGC    TGAGTAG
                                      CCT__
GAM984  CLIC5   3' AATGAGTGGTTTTTGAGCTA  34184       T  C
                                TGGTTT GA ATCATTCATT
                                ||||||| || ||||||||||
                                ATCGAG TT TGGTGAGTAA
                                   T  T
GAM984  CLONE24945 3' GGTGGGTGAAAGGACCCAGGAA 32253        T   GACA
                                TTTTTGG TTT   TCATTCATT
                                ||||||| |||   |||||||||
                                AAGGACC AGG   AGTGGGTGG
                                     C  AA__
GAM984  CLSTN3  5' AGTGAAGGGATCAGGACTGAAA 28873     TG      CA  A
                                TTT  GTTTTGA  TC TTCATT
                                |||  |||||||  || ||||||
                                AAA  CAGGACT  GG AAGTGA
                                  GT      AG  _
GAM984  COPS7B  5' GACAGATTTCAAGGCCAGAGA  43000          C   AT
                                TTTTTGGTTTTGA ATC  TC
                                |||||||||||||| |||  ||
                                AGAGACCGGAACT TAG  AG
                                      T   AC
GAM984  COQ7    3' GGTGGAGTTCAGGATCAGAA   32859          CATCA
                                TTTTGGTTTTGA    TTCATT
                                ||||||||||||    ||||||
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                                AAGACTAGGACT    AGGTGG
                                      TG___
GAM984  CSMD1    5'  GATTGAGTTGAAGTCAAGAG  73515      GT  TG  A   T
                                TTTTTG  TT  AC TCA TC
                                ||||||  ||  || ||| ||
                                GAGAAC  AA  TG AGT AG
                                   TG  GT  _   T
GAM984  CTPS2    3'  GATGAGACTCAAGACTAAA   39566         CA_
                                TTTGGTTTTGA   TCATT
                                ||||||||||   |||||
                                AAATCAGAACT   AGTAG
                                      CAG
GAM984  CX46.6   3'  AATGGGTGGTGGTCAGGGCC  40306         _
                                GGTTTTGAC ATCATTCATT
                                ||||||||| ||||||||||
                                CCGGGACTG TGGTGGGTAA
                                      G
GAM984  CYB5-M   3'  GGTGGGAAGATCGCTTGAGGCC 96203         TG C__   A   ATT
           AAGAG                   TTTTTGGTTT  A   ATC TTC
                                ||||||||||  |   ||| |||
                                GAGAACCGGA  T   TAG AGG
                                      GT CGC   A   GTGG
GAM984  CYP2A13  3'  GGTGGGCGGGGCCAGGGA    7547          A_
                                TTTTTGGTTTTG  CATC
                                ||||||||||||  ||||
                                AGGGACCGGGGC  GTGG
                                      GG
GAM984  CYP2A7   3'  GGTGGGCGGGGCCAGGGA    7540          A_
                                TTTTTGGTTTTG  CATC
                                ||||||||||||  ||||
                                AGGGACCGGGGC  GTGG
                                      GG
GAM984  D15Wsu75e 3'  AGTGGATGAGGTCTGGGCTGGA 67221     TG   TT   A
           G                     TTT  GTT  GAC TCATTCATT
                                |||  |||  ||| |||||||||
                                GAG  CGG  CTG AGTAGGTGA
                                  GT   GT   G
GAM984  DDX33    3'  TAATGAATGAATCATAGTTATA 39788        T   A_____
           ACCAGGG                  TTTTGGTT TGAC     TCATTCATT   A
                                |||||||| ||||     |||||||||   |
                                GGGACCAA ATTG     AGTAAGTAA   T
                                     T    ATACTA
GAM984  dJ383J4.3 3'  GGTGGATCATTTGAGGCCAGGA 67496         TG C  C
           A                     TTTTTGGTTT  A AT ATTCATT
                                ||||||||||  | || |||||||
                                AAGGACCGGA  T TA TAGGTGG
                                      GT _  C
GAM984  dJ383J4.3 3'  GGTGGGTGGATCATTTGAGGCC 67497         TG CA___
           AGGAA                    TTTTTGGTTT  A    TCATTCATT
                                ||||||||||  |    |||||||||
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                                AAGGACCGGA T    GGTGGGTGG
                                     GT TACTA
GAM984  DJ434O14.3 5'  AGTGGCTTGAGTTGGAGCCTGG 48212    TT   TG A  T_
          GA                    TTT GGTTT AC TCA TCATT
                                ||| ||||| || ||| |||||
                                AGG CCGAG TG AGT GGTGA
                                  GT   GT _  TC
GAM984  DKFZp434A1520 3'  AATGAATGATTATCAAATTAAA 61767        T C_
          G                    TTTTGGTTT GA ATCATTCATT
                               ||||||||| ||  ||||||||||
                               GAAATTAAA CT  TAGTAAGTAA
                                     _ AT
GAM984  DKFZP434B195 3'  GGTGGCGTCATGAGCTGAAG  49250    TG  _   AT
                               TTT GTTT TGAC CATT
                               ||| |||| ||||  ||||
                               GAA CGAG ACTG GTGG
                                 GT   T   CG
GAM984  DKFZP434C171 3'  GGTGGGTGGATCACAAGGTTGG 32197    TG TT  ACA_
          GAG                   TTTT G TTG   TCATTCATT
                               |||| | |||   |||||||||
                               GAGG T AAC   GGTGGGTGG
                                 GT GG  ACTA
GAM984  DKFZP434F091 5'  AATGGAGTGTGGGAGCTGAAAG 31890    TG   G   CA
                               TTTT GTTTT ACAT TTCATT
                               |||| ||||| ||||  ||||||
                               GAAA CGAGG TGTG AGGTAA
                                 GT   G  __
GAM984  DKFZP434F091 3'  GATGGGGTGTGGGACCAA   31895       G   AT_
                               TTGGTTTT ACATC  TC
                               |||||||| |||||  ||
                               AACCAGGG TGTGG  AG
                                    _   GGT
GAM984  DKFZp434F1719 3'  AATGGATCATGAGGATCAGAGA 51005         GA  C
                               TTTTTGGTTTT CAT ATTCATT
                               |||||||||||  ||| |||||||
                               AGAGACTAGGA GTA TAGGTAA
                                     __  C
GAM984  DKFZp434F1719 3'  TTGATGACTTCCTCAAGGCCAA 51019          _______  ATTCATT
          GG                   TTTTGGTTTTGA    CATC
                               ||||||||||||    ||||
                               GGAACCGGAACT    GTAG
                                     CCTTCA     TTA
GAM984  DKFZP434F1735 5'  AGTGAAGAGATGAGGCTGGAGA 32113    TG   TGA  A_
                               TTTT GTTT  CATC TTCATT
                               |||| ||||  |||| ||||||
                               AGAG CGGA  GTAG AAGTGA
                                 GT   ___   AG
GAM984  DKFZp434G0522 3'  GGTGGGTGGCCCAGGCCAGGG 34530        T ACA
                               TTTTGGTTT G  TCATTCATT
                               ||||||||| |  |||||||||
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                                GGGACCGGA C   GGTGGGTGG
                                    _ CC_
GAM984   DKFZP434I0714 5'  GATGTGGCAAAACCAAGGA   86993          __
                                TTTTTGGTTTTG  ACATC
                                ||||||||||||  |||||
                                AGGAACCAAAAC  TGTAG
                                    GG
GAM984   DKFZP434J193 3'  AATGAGCCTAGAGCCAGGAG   71554          ACA
                                TTTTTGGTTTTG   TCATT
                                ||||||||||||   |||||
                                GAGGACCGAGAT   AGTAA
                                    CCG
GAM984   DKFZP434J193 5'  AGTGCAGCAGAACCAAAAG   71556          ACAT
                                TTTTTGGTTTTG    CATT
                                ||||||||||||    ||||
                                GAAAACCAAGAC    GTGA
                                    GAC_
GAM984   DKFZP434K028 3'  AGTGGGAGCAGGGCCAGGAG   94858          ACA
                                TTTTTGGTTTTG   TCATT
                                ||||||||||||   |||||
                                GAGGACCGGGAC   GGTGA
                                    GAG
GAM984   DKFZP434K0427 3'  AGTGAATAATTTTAAAACCA   50497        C  C
                                TGGTTTTGA AT ATTCATT
                                |||||||||  || |||||||
                                ACCAAAATT TA TAAGTGA
                                    T  A
GAM984   DKFZp434K114 3'  GGTGACTTGAATGTCAGATTCA 61386      GT      _  T_
           AGG                  TTTTG  TTTGACAT CA  TCATT
                                |||||  ||||||||  ||  |||||
                                GGAAC  AGACTGTA GT  AGTGG
                                   TT       A  TC
GAM984   DKFZP434K1172 5'  TCCTGTGAGTCAGGACTGAAAG 49266     TG      A    TCATT
                                TTTT  GTTTTGAC TCAT
                                ||||  ||||||||  ||||
                                GAAA  CAGGACTG AGTG
                                   GT       _    TCCTA
GAM984   DKFZP434K1772 5'  GGTGCGGCCGGGGCCAGAGA   68339          A___
                                TTTTTGGTTTTG    CATC
                                ||||||||||||    ||||
                                AGAGACCGGGGC    GTGG
                                    CGGC
GAM984   DKFZp434O0515 5'  AGTGAGAAGTGTAAGGCTAGAG 66509          A   CA
                                TTTTGGTTTTG CAT  TTCATT
                                ||||||||||| |||  ||||||
                                GAGATCGGAAT GTG  GAGTGA
                                    _   AA
GAM984   DKFZP547E1010 5'  GATGCATATATGTCGAAAACAA 32174       G       CATT_
           AAG                  TTTTTG TTTTGACAT    CATT
                                ||||||  |||||||||    ||||
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                                GAAAAC AAAGCTGTA    GTAG
                                   A        TATAC
GAM984  DKFZP564D166 3'  GATGAGAACAGGACCAGA    48396          ACA
                                TTTGGTTTTG   TCATT
                                ||||||||||   |||||
                                AGACCAGGAC   AGTAG
                                     AAG
GAM984  DKFZP564G092 5'  GGTGAGAGATGTTAAAAGTAGG 32166       G        A
          AA                     TTTTTG TTTTGACATC TTCATT
                                ||||||| |||||||||| |||||||
                                AAGGAT AAAATTGTAG GAGTGG
                                   G         A
GAM984  DKFZP564J102 3'  GTGAGATGTTAGACCGAGAG   66650          T     AT    T
                                TTTTTGGTTT GACATC  TCAT
                                |||||||||| |||||||  ||||
                                GAGAGCCAGA TTGTAG  AGTG
                                      _     __
GAM984  DKFZP564K2062 3'  GGTGTGGGCAAGGCTGAAGA   31853      TG     ____
                                TTTT  GTTTTG   ACATC
                                ||||  ||||||   |||||
                                AGAA  CGGAAC   TGTGG
                                  GT     GGG
GAM984  DKFZP564L2423 3'  GTTGGTGTAAAAATCAAGAG   63022          G     TT
                                TTTTTGGTTTT ACATCA  C
                                |||||||||| |||||||  |
                                GAGAACTAAAA TGTGGT  G
                                      A     TG
GAM984  DKFZp566H0824 5'  AATGAAGAAACAGAGGCCAAGA 34475          GACA  A
          G                      TTTTTGGTTTT    TC TTCATT
                                |||||||||||    || ||||||
                                GAGAACCGGAG    AG AAGTAA
                                      ACAA  _
GAM984  DKFZP566K0524 3'  GGTGAACAGTCCAAAACTAAAA 69878          _  ATCA
                                TTTTGGTTTTG AC    TTCATT
                                |||||||||| ||    ||||||
                                AAAATCAAAAC TG    AAGTGG
                                      C  AC__
GAM984  DKFZP566M114 5'  GGTGATCGGAGCTTGAAA    50449      T      _
                                TTTT GGTTTTGA CATC
                                |||| |||||||| ||||
                                AAAG TCGAGGCT GTGG
                                  T       A
GAM984  DKFZP586C1619 3'  GATGGAAGGTAAGGGCCAGGAG 62618          G  ATCA
                                TTTTTGGTTTT AC    TTCATT
                                |||||||||| ||    ||||||
                                GAGGACCGGGA TG    AGGTAG
                                      A  GA__
GAM984  DKFZP586M0622 5'  AGTGAATGAAAAAATTAAGAA  32101          GACA
                                TTTTTGGTTTT    TCATTCATT
                                ||||||||||    |||||||||
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                                AAGAATTAAAA    AGTAAGTGA
                                      A___
GAM984  DKFZP727M111 5'  GATGCTGTCGAGACCGAAG    32060            T
                                TTTTGGTTTTGACA CATT
                                |||||||||||||| ||||
                                GAAGCCAGAGCTGT GTAG
                                       C
GAM984  DKFZp761B0514 3'  GGTGAGTGGAGAGCAGAGCCAG 51147           ACA_
           GAG                    TTTTTGGTTTTG    TCATTCATT
                                |||||||||||    |||||||||
                                GAGGACCGAGAC    GGTGAGTGG
                                       GAGA
GAM984  DKFZP761C169 3'  AATGAATGTTGTAGGAATGAGG 68415     G    TG   T
           A                     TTTT GTTT  ACA CATTCATT
                                |||| ||||  ||| ||||||||
                                AGGA TAAG  TGT GTAAGTAA
                                  G    GA   T
GAM984  DKFZp761G2113 3'  AATGGGTCCGGTGCTTGGAGCT 70462     TG    TG _   __
           GAGG                    TTT  GTTT  A CATC  ATTCATT
                                |||  ||||  | ||||  |||||||
                                GGA  CGAG  T GTGG  TGGGTAA
                                  GT    GT C    CC
GAM984  DKFZP762D096 5'  GGTGGGCCAGGACCGGGGA    66182           A__
                                TTTTTGGTTTTG   CATC
                                ||||||||||||   ||||
                                AGGGGCCAGGAC   GTGG
                                       CGG
GAM984  DNAM-1    5'  ACCAAGAGGGTGTTGAGGCTAG 22682          TG    A   ATT
           GAG                    TTTTTGGTTT  ACATC TTC
                                ||||||||||  ||||| |||
                                GAGGATCGGA  TGTGG GAG
                                      GT    _   AACCAG
GAM984  DRF1      3'  GGTGGACCACTTGAGGCCAGGA 47754          TG CATCA
           G                     TTTTTGGTTT  A    TTCATT
                                ||||||||||  |    ||||||
                                GAGGACCGGA  T    AGGTGG
                                      GT CACC_
GAM984  DT1P1A10  3'  AGTGAGTGTGGGTGTGGCTGGA 62245     TG   TTG  AT_
           G                     TTT  GTT   AC   CATTCATT
                                |||  |||   ||  ||||||||
                                GAG  CGG   TG   GTGAGTGA
                                  GT   TG_  GGT
GAM984  DXS9928E  3'  AGTGCACGTGTCAGAGCTGGAG 17473     TG        CATT
                                TTT  GTTTTGACAT    CATT
                                |||  ||||||||||    ||||
                                GAG  CGAGACTGTG    GTGA
                                  GT        CAC_
GAM984  EHM2      3'  GATGATTCAATATCAAGAA    39417         T    C
                                TTTTTGGT TTGA ATCATT
                                |||||||| |||| ||||||
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                                AAGAACTA AACT TAGTAG
                                    T  _
GAM984  ERF     3'  GGTGGGTGGGTGCCCAGGGCTA 22441          A_  _
           GGGG                  TTTTTGGTTTTG  CATC ATTCATT
                                 ||||||||||||  |||| |||||||
                                 GGGGATCGGGAC  GTGG TGGGTGG
                                     CC   G
GAM984  F-LAN-1  3'  AGTGTAATTTCTTAGAGCCAAA 61917          CATCATT
           AA                    TTTTTGGTTTTGA      CATT
                                 ||||||||||||||      ||||
                                 AAAAACCGAGATT      GTGA
                                     CTTTAAT
GAM984  FAPP2    3'  GGTGAACCAAGGTCAAACTGGA 51957     TG   T  ATCA_
           AA                    TTTT  GTTT GAC    TTCATT
                                 ||||  |||| |||    ||||||
                                 AAAG  CAAA CTG    AAGTGG
                                   GT   _  GAACC
GAM984  FBXO25   5'  TGGGTCAGGACTGGAGA    25151     TG      A
                                 TTTT  GTTTTGAC TCA
                                 ||||  |||||||| |||
                                 AGAG  CAGGACTG GGT
                                   GT      _
GAM984  FBXO9    3'  AGTGAATCCCTTAGGACTGGAA 54239     TG      CATC
                                 TTT  GTTTTGA   ATTCATT
                                 |||  |||||||   |||||||
                                 AAG  CAGGATT   TAAGTGA
                                   GT     CCC_
GAM984  FKBP3    5'  ATTGGTGTCTAATTCAGAATCG 10640          _______    ATTCATT
           AAGA                   TTTTTGGTTTT     GACATC
                                  ||||||||||     ||||||
                                  AGAAGCTAAGA     CTGTGG
                                      CTTAAT       TTAC
GAM984  FLB6421  5'  GGTGGATGATCATGACTCAGAG 39646      _  T  CA
                                 TTTTG GTT TGA  TCATTCATT
                                 |||||  ||| |||  |||||||||
                                 GAGAC CAG ACT  AGTAGGTGG
                                   T  T  __
GAM984  FLJ00060 3'  GGTGGGTGGATCACGAGGTCAG 61751      GT   ACA_
           GAG                    TTTTTG  TTTG   TCATTCATT
                                  ||||||  ||||   |||||||||
                                  GAGGAC  GAGC   GGTGGGTGG
                                    TG   ACTA
GAM984  FLJ10035 3'  GACAGGTGTCAGAGCAGGGAG  36213     TG       AT
                                 TTTT  GTTTTGACATC  TC
                                 ||||  ||||||||||  ||
                                 GAGG  CGAGACTGTGG  AG
                                   GA         AC
GAM984  FLJ10101 3'  GGTGCTTGTGTCAAAACCAAGG 45602           T  TT
           A                     TTTTTGGTTTTGACA CA  CATT
                                 |||||||||||||| ||  ||||
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                                AGGAACCAAAACTGT GT  GTGG
                                        _ TC
GAM984  FLJ10111  5'  GGTGGGCCTCAAAGCCGGG   36303         ____
                                TTTGGTTTTGA   CATC
                                ||||||||||   ||||
                                GGGCCGAAACT   GTGG
                                    CCGG
GAM984  FLJ10157  3'  GATGGTGCTAGTCAAGATGAAA 36330     G      ATCAT
          A                      TTTT GTTTTGAC    TCATT
                                ||||| ||||||||    ||||||
                                AAAA TAGAACTG    GGTAG
                                  G       ATCGT
GAM984  FLJ10178  3'  AGTGTGTTGATGTTAAAGTCAA 36339     GT       TT_
          AG                     TTTTG  TTTGACATCA   CATT
                                ||||||  ||||||||||   ||||
                                GAAAC  AAATTGTAGT   GTGA
                                   TG        TGT
GAM984  FLJ10297  3'  AATGAATGTACAGAGCCAGA   36435        ACAT
                                TTTGGTTTTG   CATTCATT
                                ||||||||||   ||||||||
                                AGACCGAGAC   GTAAGTAA
                                     AT__
GAM984  FLJ10326  3'  GATGGGAGTCAAAATCAGAA   36502          A_
                                TTTTGGTTTTGAC  TCATT
                                ||||||||||||  |||||
                                AAGACTAAAACTG  GGTAG
                                     AG
GAM984  FLJ10378  5'  GATGTTGTAAGATCAGAGA   36567         __
                                TTTTTGGTTTT  GACATC
                                ||||||||||  ||||||
                                AGAGACTAGAA  TTGTAG
                                     TG
GAM984  FLJ10477  3'  AATGTAAGTTGGTTTCAAGATT 36640     TG     C   TT___
          GGGGA                    TTTT  GTTTTGA ATCA    CATT
                                ||||  ||||||| ||||    ||||
                                AGGG  TAGAACT TGGT    GTAA
                                  GT      T    TGAAT
GAM984  FLJ10493  3'  GATGAGCTCTACAAGGCCAAAA 36673          ACATCA
          A                      TTTTTGGTTTTG     TTCATT
                                ||||||||||||     ||||||
                                AAAAACCGGAAC     GAGTAG
                                     ATCTC_
GAM984  FLJ10520  3'  ATGAGTGATAGGTCAAAGC   36699        __
                                GTTTTGAC  ATCATTCAT
                                ||||||||  |||||||||
                                CGAAACTG  TAGTGAGTA
                                    GA
GAM984  FLJ10579  3'  GGTGGATGAACTTCAAAGCTA  36828        CA_
                                TGGTTTTGA   TCATTCATT
                                |||||||||   |||||||||
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                                ATCGAAACT   AGTAGGTGG
                                     TCA
GAM984  FLJ10604  3'  GGTGATTTCAAGCCAGGGA   36859         T  C
                                TTTTTGGTTT GA ATCATT
                                |||||||||| || ||||||
                                AGGGACCGAA CT TAGTGG
                                      _  T
GAM984  FLJ10652  3'  AATGGATGGTATTCACCGGGGA 36906        TTT  C
                                TTTTTGGT   GA ATCATTCATT
                                ||||||||   || ||||||||||
                                AGGGGCCA   TT TGGTAGGTAA
                                     C__  A
GAM984  FLJ10716  3'  GATGGGTGGTGTTTGTAAC   37017     TT_
                                GTT   GACATCATTCATT
                                |||   ||||||||||||
                                CAA   TTGTGGTGGGTAG
                                  TGT
GAM984  FLJ10738  3'  AGTGACTTGTCAAGACTTAAAA 37056      T        TCAT
                                TTTT GGTTTTGACA    TCATT
                                |||| ||||||||||    |||||
                                AAAA TCAGAACTGT    AGTGA
                                   T        TC__
GAM984  FLJ10761  3'  GATGGGTGGGGGCCAAGAA   37131          G  A    CATT
                                TTTTTGGTTTT AC TCATT
                                |||||||||| || |||||
                                AAGAACCGGGG TG GGTAG
                                      G  _       T
GAM984  FLJ10781  5'  GTGGGTGATGCTGAAAGC    37175   G    GA
                                G TTTT  CATCATTCAT
                                | ||||  ||||||||||
                                C AAAG  GTAGTGGGTG
                                 G    TC
GAM984  FLJ10815  3'  GGTGGGTGATGGAGAAGGCTGA 37235      TG    GA_
          GAA                     TTTT  GTTTT   CATCATTCATT
                                ||||  |||||   ||||||||||
                                AAGA  CGGAA   GTAGTGGGTGG
                                   GT    GAG
GAM984  FLJ10922  3'  GATCAGGGTGTCTAGGCTGAAG 37402     TG   T     AT__  ATT
                                TTT  GTTT GACATC    TC
                                |||  |||| ||||||    ||
                                GAA  CGGA CTGTGG    AG
                                  GT   T     GACT
GAM984  FLJ10986  5'  GGTGGAGAACAGAAACCAGAGA 37491          GACA  A
                                TTTTTGGTTTT    TC TTCATT
                                ||||||||||    || ||||||
                                AGAGACCAAAG    AG AGGTGG
                                      ACA_  _
GAM984  FLJ11068  5'  AGTGAATGAGCCGTGCCAAAAA 37586        TT  ACA
                                TTTTTGGT  TG   TCATTCATT
                                ||||||||  ||   |||||||||
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                                AAAAACCG  GC   AGTAAGTGA
                                    T_  CG_
GAM984  FLJ11151  3'  GATGGGTGGTCTCTTGGGATCA 68478        TG C__
          GAA                    TTTTGGTTT  A   ATCATTCATT
                                 |||||||||  |   ||||||||||
                                 AAGACTAGG  T   TGGTGGGTAG
                                     GT CTC
GAM984  FLJ11164  3'  GGTGGGTGGAGTTGACCAGAGA 37701         TT   AT
                                 TTTTTGGTT  GAC  CATTCATT
                                 |||||||||  |||  ||||||||
                                 AGAGACCAG  TTG  GTGGGTGG
                                     __  AG
GAM984  FLJ11267  3'  GATGCCAGGTCAGGGCTGAAGA 39498      TG       AT__    CATT
                                 TTTT  GTTTTGAC    CATT
                                 ||||  ||||||||    ||||
                                 AGAA  CGGGACTG    GTAG
                                   GT       GACC
GAM984  FLJ11336  5'  AGTGGAGCTCAGTGCCAGAG   37833       T    CATCA
                                 TTTTGGT TTGA     TTCATT
                                 |||||||  ||||    ||||||
                                 GAGACCG GACT     AGGTGA
                                     T   CG___
GAM984  FLJ11710  5'  GGTGGGAGGACTGATTGAGGCC 46248          TG _  _  A_
          AGGAG                  TTTTTGGTTT  A CA TC  TTCATT
                                 ||||||||||  | || ||  ||||||
                                 GAGGACCGGA  T GT AG  GGGTGG
                                     GT A  C  GA
GAM984  FLJ11722  3'  GGTGGATCACGAGGCCAGGAG  47006          ACATC
                                 TTTTTGGTTTTG     ATTCATT
                                 ||||||||||||     |||||||
                                 GAGGACCGGAGC     TAGGTGG
                                     AC___
GAM984  FLJ11838  3'  AATGGATGTATAAAAAAATCAA 45427         GACAT_
          G                      TTTGGTTTT      CATTCATT
                                 |||||||||      ||||||||
                                 GAACTAAAA      GTAGGTAA
                                     AAATAT
GAM984  FLJ12057  5'  AACCTGAAGATGCTGGGACCAG 45793          GA    A    TT
          AGA                    TTTTTGGTTTT  CATC TTCA
                                 ||||||||||||  |||| ||||
                                 AGAGACCAGGG  GTAG AAGT
                                     TC    _    CCAAG
GAM984  FLJ12389  5'  AGTGGCTGTCAGTGCTGGAAG  60896      TG  T     _
                                 TTTT  GT TTGACA TCATT
                                 ||||  || |||||| |||||
                                 GAAG  CG GACTGT GGTGA
                                   GT  T     C
GAM984  FLJ12448  3'  GGTGGATCAATTGAGGCCAGGA 43480         TG CATC
          G                      TTTTTGGTTT  A    ATTCATT
                                 ||||||||||  |    |||||||
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                                GAGGACCGGA T   TAGGTGG
                                     GT AAC_
GAM984  FLJ12505  3' GGTCTTCAGAACCAAAAA   45716          C_
                                TTTTTGGTTTTGA ATC
                                |||||||||||| |||
                                AAAAACCAAGACT TGG
                                   TC
GAM984  FLJ12568  3' AATGAAGATTTAAACCAAAGA 47138         TGAC  A
                                TTTTTGGTTT   ATC TTCATT
                                |||||||||   ||| ||||||
                                AGAAACCAAA   TAG AAGTAA
                                     TT__  _
GAM984  FLJ12688  3' GTCCTCTGGTGTCGAGATGGAA 73556     G         TTCATT
           AA                    TTTTT GTTTTGACATCA
                                |||||| ||||||||||||
                                AAAAG TAGAGCTGTGGT
                                   G         CTCCTGG
GAM984  FLJ12761  5' GGTGAGTGGGGCCAGCGGGGCT 44924   TG    ACA___
           GGA                   TT GTTTTG    TCATTCATT
                                || ||||||    |||||||||
                                AG CGGGGC    GGTGAGTGG
                                 GT    GACCGG
GAM984  FLJ12800  3' GGTGGGTCAGTTGAGGTCAGGA 43532      GT TG ATC
           G                     TTTTTG TT AC  ATTCATT
                                |||||| || ||  |||||||
                                GAGGAC GA TG  TGGGTGG
                                   TG GT AC_
GAM984  FLJ12800  3' GGTGGTTGAGTCAGGACCA   43533        A  TT
                                TGGTTTTGAC TCA CATT
                                |||||||||| |||  ||||
                                ACCAGGACTG AGT GTGG
                                     _  TG
GAM984  FLJ13081  3' AATGAATGTGGCTTTTGGGGGC 46168      G  TG ____  T
           AAAAG                  TTTTTG TTT  A   CA CATTCATT
                                |||||| |||  |   || ||||||||
                                GAAAAC GGG  T   GT GTAAGTAA
                                   G  GT TTCG  _
GAM984  FLJ13096  3' AATTTTGTTTGTTAAGGCTAGG 47172           T_  TTCATT
           AA                    TTTTTGGTTTTGACA  CA
                                |||||||||||||||  ||
                                AAGGATCGGAATTGT  GT
                                      TT  TTTAA
GAM984  FLJ13119  5' GATGGGTGGGGCTTTGGAATTG 45021   TG   TG CA__
           AG                    TT  GTTT  A   TCATTCATT
                                || ||||  |   |||||||||
                                GA  TAAG  T   GGTGGGTAG
                                 GT   GT TCGG
GAM984  FLJ13479  5' GGTGAAGCCAAAGCCAGAGA  45556          A___
                                TTTTTGGTTTTG   CATC
                                ||||||||||||   ||||
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                                AGAGACCGAAAC   GTGG
                                       CGAA
GAM984  FLJ13491  5' GGCTGTGTTAGCGCCAAGGA  45221       T    T  TT
                                TTTTTGGT TTGACA CA  C
                                |||||||| |||||| ||  |
                                AGGAACCG GATTGT GT  G
                                     C    _ CG
GAM984  FLJ13614  5' AATGGATGATGTTGAAGTTG  58197   GG  TG
                                T  TTT  ACATCATTCATT
                                |  |||  ||||||||||||
                                G  GAA  TGTAGTAGGTAA
                                 TT   GT
GAM984  FLJ13621  5' AGTGGGGGACTCGAGGCCTGAG 47216     T      CA  A
           G                     TTTT GGTTTTGA  TC TTCATT
                                |||| ||||||||  || ||||||
                                GGAG CCGGAGCT  AG GGGTGA
                                  T      C_  G
GAM984  FLJ13693  3' GATGGATGTGGGGAGAGTGGAA 46074    TT G   GA  T
           G                     TTT  G TTTT  CA CATTCATT
                                |||  | ||||  || ||||||||
                                GAA  T AGAG  GT GTAGGTAG
                                  GG G   GG  _
GAM984  FLJ13725  5' ATTAGTGTCTCCTGTGAGACCA 68828          _______    CATTCATT
           AGGA                    TTTTTGGTTTT     GACAT
                                |||||||||||     |||||
                                AGGAACCAGAG     CTGTG
                                      TGTCCT    A   TTAC
GAM984  FLJ13962  3' GATGGAGAGGTGGTGGCCGAGA 46319        TTGA   A_
           G                     TTTTTGGTT    CATC  TTCATT
                                |||||||||   ||||  ||||||
                                GAGAGCCGG   GTGG  AGGTAG
                                     TG__    AG
GAM984  FLJ14054  3' GGTGGATAATTGAAACCAAGAG 44969         TG CATC
                                TTTTTGGTTT  A    ATTCATT
                                |||||||||| |   |||||||
                                GAGAACCAAA  T    TAGGTGG
                                      GT AA__
GAM984  FLJ14129  3' GGTGGGCGCGAGGCCGAGG   48812          ACA
                                TTTTGGTTTTG   TCATT
                                ||||||||||   |||||
                                GGAGCCGGAGC   GGTGG
                                      GCG
GAM984  FLJ14260  3' AATGAATGAGATGACTAA    47349       TTGACA
                                TTGGTT     TCATTCATT
                                ||||||     |||||||||
                                AATCAG     AGTAAGTAA
                                   TAG___
GAM984  FLJ14490  3' GATGGGTCGGGAAGCTGGAGA  52443     TG    __   A
                                TTTT  GTTTT  GAC TCATT
                                ||||  |||||  ||| |||||
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                                AGAG  CGAAG  CTG GGTAG
                                  GT     GG  _
GAM984  FLJ14627  5'  GTGAATCAGGTGTTAAGG    52547          __
                                TTTTGACATC  ATTCAT
                                ||||||||||  ||||||
                                GGAATTGTGG  TAAGTG
                                      AC
GAM984  FLJ14641  3'  GATGAAGAAATATGTCATAATT 52559        T     CA___
           AGAG                    TTTTGGTT TGACAT     TTCATT
                                ||||||||| |||||||     |||||||
                                GAGATTAA ACTGTA     AAGTAG
                                     T     TAAAG
GAM984  FLJ14855  3'  GGTGACTCAGAGCTAAGAA   53765           __
                                TTTTTGGTTTTGA  CATC
                                ||||||||||||  ||||
                                AAGAATCGAGACT  GTGG
                                        CA
GAM984  FLJ14936  3'  AGTGAGTGAAAGAAGCCAAGGG 51126          GACA
                                TTTTTGGTTTT    TCATTCATT
                                ||||||||||    |||||||||
                                GGGAACCGAAG    AGTGAGTGA
                                      AA__
GAM984  FLJ20038  3'  GATACTTCAAAACCAAAAA   34864           C__
                                TTTTTGGTTTTGA   ATC
                                ||||||||||||   |||
                                AAAAACCAAAACT   TAG
                                        TCA
GAM984  FLJ20150  3'  GATGGCTTAAAGCCAGAAA   35142           __
                                TTTTTGGTTTTGA  CATC
                                ||||||||||||  ||||
                                AAAGACCGAAATT  GTAG
                                        CG
GAM984  FLJ20150  3'  GGTGATGGCTTAAAGCCAGAAA 35144           __
                                TTTTTGGTTTTGA  CATCATT
                                ||||||||||||  |||||||
                                AAAGACCGAAATT  GTAGTGG
                                        CG
GAM984  FLJ20156  3'  ATGATTTCAAAGCCAAAAA   35148           C
                                TTTTTGGTTTTGA ATCAT
                                ||||||||||||| |||||
                                AAAAACCGAAACT TAGTA
                                        T
GAM984  FLJ20209  3'  GTGGATGGAATACCAGAGA   86707        T  GACA
                                TTTTTGGT TT    TCATTCAT
                                |||||||| ||    ||||||||
                                AGAGACCA AA    GGTAGGTG
                                     T  _____
GAM984  FLJ20249  3'  GATGAGAAGGATGGCGGGGCTA 80221           A    AT__
           GGGA                    TTTTTGGTTTTG CATC    TCATT
                                ||||||||||| ||||    |||||
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                                AGGGATCGGGGC GTAG   AGTAG
                                      G   GAAG
GAM984  FLJ20255 3' TAATGGTGTTGATTGCAGACTG 35301    TG  _____ TG      CATT
           GAG                  TTT  GTT    T  ACATCATT
                                ||| |||    | ||||||||
                                GAG  CAG    A  TGTGGTAA
                                  GT   ACGTT GT         TT
GAM984  FLJ20257 5' AGTGGTTTCGGGGCCGGGA   39481          C
                                TTTTGGTTTTGA ATCATT
                                |||||||||||| ||||||
                                AGGGCCGGGGCT TGGTGA
                                       T
GAM984  FLJ20273 3' AATGAGTGACTCGACCAAA   39243       TT  CA
                                TTTGGTT  GA  TCATTCATT
                                |||||||  ||  |||||||||
                                AAACCAG  CT  AGTGAGTAA
                                   __  C_
GAM984  FLJ20378 3' GATGGGTGAGGAGTCAGGGCCG 35554          A__
           A                    TTGGTTTTGAC   TCATTCATT
                                ||||||||||   |||||||||
                                AGCCGGGACTG   AGTGGGTAG
                                      AGG
GAM984  FLJ20378 3' GATGGGTGAGGGCAGGGCTGA  35555   TG    ACA
                                T  GTTTTG   TCATTCATT
                                |  ||||||   |||||||||
                                A  CGGGAC   AGTGGGTAG
                                 GT    GGG
GAM984  FLJ20378 3' GGTGGATGAGGGGGCAGGGCTG 35559   TG    ACA__
           A                     T  GTTTTG    TCATTCATT
                                 |  ||||||    |||||||||
                                 A  CGGGAC    AGTAGGTGG
                                  GT    GGGGG
GAM984  FLJ20378 3' GGTGGGTGAGGGCAGGGCTGA  35561   TG    ACA
                                T  GTTTTG   TCATTCATT
                                |  ||||||   |||||||||
                                A  CGGGAC   AGTGGGTGG
                                 GT    GGG
GAM984  FLJ20378 3' GGTGGGTGAGGGCAGGGCTGA  35562   TG    ACA
                                T  GTTTTG   TCATTCATT
                                |  ||||||   |||||||||
                                A  CGGGAC   AGTGGGTGG
                                 GT    GGG
GAM984  FLJ20378 3' GGTGGGTGAGGGCAGGGCTGA  35563   TG    ACA
                                T  GTTTTG   TCATTCATT
                                |  ||||||   |||||||||
                                A  CGGGAC   AGTGGGTGG
                                 GT    GGG
GAM984  FLJ20378 3' GGTGGGTGAGGGCAGGGCTGA  35564   TG    ACA
                                T  GTTTTG   TCATTCATT
                                |  ||||||   |||||||||
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                                A  CGGGAC   AGTGGGTGG
                                 GT     GGG
GAM984  FLJ20378  3'  GGTGGGTGAGGGGGCAGGGCTG 35565    TG     ACA__
           A                     T  GTTTTG    TCATTCATT
                                |  ||||||    |||||||||
                                A  CGGGAC    AGTGGGTGG
                                 GT     GGGGG
GAM984  FLJ20417  3'  GACCCATGTCTAGGACCAGGAG 35602          _    CAT
                                TTTTTGGTTTT GACAT   TC
                                |||||||||||| |||||   ||
                                GAGGACCAGGA CTGTA   AG
                                       T    CCC
GAM984  FLJ20419  3'  GATGTTTAATGTGTTTAAAGCT 35605      TG      _ T   ___
           GGGAA                    TTTT  GTTTTGA CA CATT   CATT
                                ||||  ||||||| || ||||   ||||
                                AAGG  CGAAATT GT GTAA   GTAG
                                  GT      T _   TTT
GAM984  FLJ20477  3'  AATGGGAGAAGTGTCAGACACT 35706         _     __ A
           AGAGA                    TTTTTGGT TTTGACA  TC TTCATT
                                |||||||| |||||||  || ||||||
                                AGAGATCA AGACTGT  AG GGGTAA
                                     C      GA  A
GAM984  FLJ20485  5'  AATGGGCAAAGACCAAAGA   39288          GACA
                                TTTTTGGTTTT   TCATT
                                ||||||||||   |||||
                                AGAAACCAGAA   GGTAA
                                      ACG_
GAM984  FLJ20513  3'  GATGAGTGTTGTGATTGGAACT 35786   TG   TG _  __
           GA                     T  GTTT  A CAT  CATTCATT
                                |  ||||  | |||  ||||||||
                                A  CAAG  T GTG  GTGAGTAG
                                 GT   GT A   TT
GAM984  FLJ20542  3'  GGTGCATGGCGAGGCCAAGAA  50745          A  _
                                TTTTTGGTTTTG CAT CATT
                                |||||||||||| ||| ||||
                                AAGAACCGGAGC GTA GTGG
                                       G   C
GAM984  FLJ20542  3'  GGTGGGCCAGGCAGAGCCGGAG 50746          ACATCA
           A                     TTTTTGGTTTTG     TTCATT
                                ||||||||||||     ||||||
                                AGAGGCCGAGAC     GGGTGG
                                      GGACC_
GAM984  FLJ20605  3'  GATGAGTGATGGATCCACTAGG 35871       TTTGA
           G                     TTTTGGT    CATCATTCATT
                                |||||||    ||||||||||
                                GGGATCA    GTAGTGAGTAG
                                    CCTAG
GAM984  FLJ20625  3'  GATGGGGTGGGGGCCAAAAG   35898          G  AT
                                TTTTTGGTTTT AC  CATT
                                |||||||||| ||  ||||
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                                GAAAACCGGGG TG  GTAG
                                      G  GG
GAM984  FLJ20666  3'  AATGGATCAGAAGAACCAGAG  37657          GACATC
                                TTTTGGTTTT     ATTCATT
                                ||||||||||     |||||||
                                GAGACCAAGA     TAGGTAA
                                      AGAC__
GAM984  FLJ20686  3'  GGTGGATCACTTGAGGCCAGGA 35954          TG CATC
          G                      TTTTTGGTTT  A    ATTCATT
                                ||||||||||  |   |||||||
                                GAGGACCGGA  T    TAGGTGG
                                      GT CAC_
GAM984  FLJ20686  3'  GGTGGGTGGATCACTTGAGGCC 35955          TG CA___
          AGGAG                    TTTTTGGTTT  A    TCATTCATT
                                ||||||||||  |    |||||||||
                                GAGGACCGGA  T    GGTGGGTGG
                                      GT CACTA
GAM984  FLJ20694  5'  ATTTTGATGTCTAGAATCAGGG 35971          _      TTCATT
                                TTTTGGTTTT GACATCA
                                |||||||||| |||||||
                                GGGACTAAGA CTGTAGT
                                      T      TTTA
GAM984  FLJ20712  5'  AGTGAAACGGCAGAATCAGAAG 36032           ACATCA
                                TTTTTGGTTTTG     TTCATT
                                ||||||||||||     ||||||
                                GAAGACTAAGAC     AAGTGA
                                      GGCA__
GAM984  FLJ20958  3'  AATGGATGAAGTGATCAAAG   42304         TTG  A
                                TTTTGGTT   AC TCATTCATT
                                ||||||||   || |||||||||
                                GAAACTAG   TG AGTAGGTAA
                                     ___  A
GAM984  FLJ21044  3'  GATGAGTGGGGCTAGCTGAAG  42569     TG   TTGACA
                                TTT  GTT     TCATTCATT
                                |||  |||     |||||||||
                                GAA  CGA     GGTGAGTAG
                                  GT   TCGG__
GAM984  FLJ21126  3'  CTATTTGATGTTAAGCCAGGGA 91928          T      TTCATT
                                TTTTTGGTTT GACATCA
                                |||||||||| |||||||
                                AGGGACCGAA TTGTAGT
                                      _      TTATCA
GAM984  FLJ21148  3'  GGTGATGTGTTTTAGGATTGAG 46307     TG     ____       CATT
          AA                     TTTT  GTTTTG   ACATCATT
                                ||||  ||||||   ||||||||
                                AAGA  TAGGAT   TGTAGTGG
                                  GT     TTTG        T
GAM984  FLJ21162  3'  GGTGGATTGCTTTGAGGCCAGG 46374          TG CATC
          AG                     TTTTTGGTTT  A   ATTCATT
                                ||||||||||  |   |||||||
```

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                                GAGGACCGGA  T    TAGGTGG
                                     GT TCGT
GAM984  FLJ21596 3' AGTGGATGGTTGCTGAGTGAAT 46113         TGAC____
           CAGAG                  TTTTGGTTT       ATCATTCATT
                                |||||||||       ||||||||||
                                GAGACTAAG       TGGTAGGTGA
                                     TGAGTCGT
GAM984  FLJ21596 3' TGATGTCAAAGCCCAAAA    46124      T
                                TTTT GGTTTTGACATCA
                                |||| ||||||||||||
                                AAAA CCGAAACTGTAGT
                                  C
GAM984  FLJ21628 3' AATGAATGATTTTGGAGTTAGA 48367       GG   TG C
           AA                    TTTTT  TTT  A ATCATTCATT
                                |||||  |||  | ||||||||||
                                AAAGA  GAG  T TAGTAAGTAA
                                   TT   GT T
GAM984  FLJ21820 3' AATCGGATGTTAGAAGCTAGGA 41916         _       ATTCATT
           A                     TTTTTGGTT TTGACATC
                                |||||||| ||||||||
                                AAGGATCGA GATTGTAG
                                     A       GCTAA
GAM984  FLJ21870 3' GGTGGATCACTTGAGGCCAGGA 43748          TG CATC
           G                     TTTTTGGTTT  A    ATTCATT
                                |||||||||  |   |||||||
                                GAGGACCGGA  T    TAGGTGG
                                     GT CAC_
GAM984  FLJ21870 3' GGTGGGTCGGAGGCAAAGCCAA 43749           ACA __
           GGA                     TTTTTGGTTTTG   TC  ATTCATT
                                ||||||||||||   ||  |||||||
                                AGGAACCGAAAC   AG  TGGGTGG
                                      GG_  GC
GAM984  FLJ22002 3' AATTAAAGATTGTCAAGACCAA 46189            _  ATTCATT
           AAA                     TTTTTGGTTTTGACA TC
                                |||||||||||||| ||
                                AAAAACCAGAACTGT AG
                                        T  AAATTAA
GAM984  FLJ22035 3' GAAGATGAGGTTAGGACTGAGA 44828      TG       A    CATT
           A                     TTTT  GTTTTGAC TCATT
                                ||||  |||||||| |||||
                                AAGA  CAGGATTG AGTAG
                                   GT       G    AAG
GAM984  FLJ22035 3' GATGAGGTTAGGACTGAGAA   44829      TG       A
                                TTTT  GTTTTGAC TCATT
                                ||||  |||||||| |||||
                                AAGA  CAGGATTG AGTAG
                                   GT       G
GAM984  FLJ22127 3' AGTGGACTTGTTGAAACAGGAA 43197      TG   TG   TCA
           G                     TTTT  GTTT  ACA   TTCATT
                                ||||  ||||  |||   ||||||
```

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                                GAAG  CAAA  TGT   AGGTGA
                                  GA    GT   TC_
GAM984   FLJ22246  3'  GATGGTTAAGGGCCGGGAG    48213          GA__
                                TTTTTGGTTTT    CATC
                                ||||||||||    ||||
                                GAGGGCCGGGA    GTAG
                                      ATTG
GAM984   FLJ22477  3'  AGTGAGTGGTCCACACAGGTGC 45666        _    AC___
           CAGGAG                 TTTTTGGT TTTG     ATCATTCATT
                                ||||||||| ||||    ||||||||||
                                GAGGACCG GGAC     TGGTGAGTGA
                                     T    ACACC
GAM984   FLJ22551  5'  GGTGAGTGTAGAGGAGGCTGAA 45562      TG     GACAT
           AG                    TTTT  GTTTT     CATTCATT
                                ||||  |||||     ||||||||
                                GAAA  CGGAG     GTGAGTGG
                                  GT     GAGAT
GAM984   FLJ22659  5'  GGTGTGTCCGAGCCGAAGA    46831          T    T
                                TTTTTGGTTT GACA CATT
                                ||||||||||| |||| ||||
                                AGAAGCCGAG CTGT GTGG
                                      C    _
GAM984   FLJ22672  3'  GATGCATGCGTGTCCAGGCTGA 46596      TG    T    _   T
           AGA                    TTTT  GTTT GACAT CAT CATT
                                ||||  |||| ||||| ||| ||||
                                AGAA  CGGA CTGTG GTA GTAG
                                  GT    C     C   C
GAM984   FLJ22746  3'  AGTGGTTCTTGTTACAAACCAA 45916          _     TCAT
           AGA                    TTTTTGGTTT TGACA    TCATT
                                ||||||||||| |||||    |||||
                                AGAAACCAAA ATTGT    GGTGA
                                      C     TCTT
GAM984   FLJ23093  5'  GATGGGGAGGTCAGGTCTGGGA 45325      TG T      A  A
           A                     TTTT  G TTTGAC TC TTCATT
                                ||||  | |||||| || ||||||
                                AAGG  C GGACTG AG GGGTAG
                                  GT T     G  _
GAM984   FLJ23129  3'  AGTGGATAGAACAAGATCGAGG 45785           ACA  _
           A                     TTTTTGGTTTTG   TC ATTCATT
                                ||||||||||||   || |||||||
                                AGGAGCTAGAAC   AG TAGGTGA
                                      A__  A
GAM984   FLJ23191  3'  TGCCGGTTGGTGTCAAAGATAG 45012       G          TT ATT
           AG                     TTTTG TTTTGACATCA  C
                                |||||  ||||||||||  |
                                GAGAT GAAACTGTGGT  G
                                  A          TG CCGTA
GAM984   FLJ23420  5'  AGTGCTGGCGGAACCGGAGA   47535           A  T
                                TTTTTGGTTTTG CA CATT
                                ||||||||||| || ||||
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                                AGAGGCCAAGGC GT GTGA
                                      G  C
GAM984  FLJ23420  3'  AGTGGGTCCAGGCCAGGAG   47536        T  A
                                TTTTTGGTTT GAC TCATT
                                |||||||||| ||| |||||
                                GAGGACCGGA CTG GGTGA
                                     C  _
GAM984  FLJ23510  3'  AGTGTAAGTCAGGGCTAAAGG  45622          AT_
                                TTTTTGGTTTTGAC  CATT
                                |||||||||||||  ||||
                                GGAAATCGGGACTG  GTGA
                                      AAT
GAM984  FLJ25415  3'  AATGTATCAAGACCAAGAA   59171          CAT
                                TTTTTGGTTTTGA  CATT
                                ||||||||||||  ||||
                                AAGAACCAGAACT  GTAA
                                      AT_
GAM984  FLJ30213  3'  GGTGTTAAGGCTCAGGAG    59403      _
                                TTTTTG GTTTTGACATC
                                |||||| ||||||||||
                                GAGGAC CGGAATTGTGG
                                   T
GAM984  FLJ31300  3'  AGTGGCCTCTGTCAGGGCCAGG 58927          TCAT
          G                      TTTTGGTTTTGACA   TCATT
                                |||||||||||||   |||||
                                GGGACCGGGACTGT   GGTGA
                                      CTCC
GAM984  FLJ31455  3'  GGTGAGTGGATTACAAGGTCAG 59288      GT   ACA_
          GAG                     TTTTTG  TTTG   TCATTCATT
                                ||||||  ||||   |||||||||
                                GAGGAC  GAAC   GGTGAGTGG
                                   TG   ATTA
GAM984  FLJ31737  3'  GGTGGGTGGATCACGAAGTCAA 59351      GT   ACA_
          GAG                     TTTTTG  TTTG   TCATTCATT
                                ||||||  ||||   |||||||||
                                GAGAAC  AAGC   GGTGGGTGG
                                   TG   ACTA
GAM984  FLJ32332  5'  GATGTGAGTTTGGGGCTGAAGA 58944     TG   TG CA   _
                                TTTT  GTTT  A  TCAT TC
                                ||||  ||||  |  |||| ||
                                AGAA  CGGG  T  AGTG AG
                                  GT   GT TG   T
GAM984  FLJ32356  3'  GGTGTTAGTGCAGGACCGGAAG 59027          A  CATT
                                TTTTTGGTTTTG CAT   CATT
                                |||||||||||| |||   ||||
                                GAAGGCCAGGAC GTG   GTGG
                                      _  ATT_
GAM984  FLJ32468  5'  AGTGAATCCCAGAGACCAAGAG 59707          GACATC
                                TTTTTGGTTTT    ATTCATT
                                ||||||||||    |||||||
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                                GAGAACCAGAG     TAAGTGA
                                      ACCC__
GAM984  FLJ32762  3'  AGTGGATGGGAGCGAAGTAAGG 59481      GG    ACA
          AG                    TTTTT  TTTTG   TCATTCATT
                                |||||  |||||   |||||||||
                                GAGGA  GAAGC   GGTAGGTGA
                                  AT    GAG
GAM984  FLJ32861  5'  AATGGAAACCCAAAGCCAAAG  59379          ACATCA
                                TTTTGGTTTTG     TTCATT
                                ||||||||||      ||||||
                                GAAACCGAAAC     AGGTAA
                                      CCAA__
GAM984  FLJ32865  3'  AGTGGGTGGAGACCAGAGA   58800          G  A
                                TTTTTGGTTTT AC TCATT
                                |||||||||| || |||||
                                AGAGACCAGAG TG GGTGA
                                      G  _
GAM984  FLJ32865  3'  GATGGCTCCAAGGCCAAGGA   58813          A___
                                TTTTTGGTTTTG    CATC
                                ||||||||||||    ||||
                                AGGAACCGGAAC    GTAG
                                      CTCG
GAM984  G4        3'  GGTGATCATGGGAGCCAGAG   92639         ___  _
                                TTTTGGTTT   TGA CATC
                                |||||||||   ||| ||||
                                GAGACCGAG   ACT GTGG
                                     GGT   A
GAM984  GAB1      3'  AATGAGTAGAGTTGAAGTCAAA 10745      GT  TG  A  _
          G                     TTTTG  TT  AC TC ATTCATT
                                |||||  ||  || || |||||||
                                GAAAC  AA  TG AG TGAGTAA
                                   TG  GT  _  A
GAM984  GABARAPL1 3'  GGTGGACAAGTTGGGGCCAGAG 49423          TG  ATCA
          A                     TTTTTGGTTT  AC    TTCATT
                                ||||||||||  ||    ||||||
                                AGAGACCGGG  TG    AGGTGG
                                      GT  AAC_
GAM984  GALNT5    5'  GGATGATGGAGCTAGAG     72511          TGA
                                TTTTGGTTT   CATCATTC
                                |||||||||   ||||||||
                                GAGATCGAG   GTAGTAGG
                                      ___
GAM984  GBL       3'  GGTGTGTGGAGACTGGAGA   42572      TG    G   T
                                TTTT  GTTTT ACA CATT
                                ||||  ||||| ||| ||||
                                AGAG  CAGAG TGT GTGG
                                  GT    G  _
GAM984  GHITM     3'  GGTGAATGTGAAAACTAAAG   27675          G   _
                                TTTTGGTTTT ACAT CATT
                                |||||||||| |||| ||||
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                                GAAATCAAAA TGTA GTGG
                                     G   A
GAM984  GIT2    3'  GTGAATGGTGTTTAAAAT    29414       _
                                GTTTTGA CATCATTCAT
                                ||||||| ||||||||||
                                TAAAATT GTGGTAAGTG
                                    T
GAM984  GLYAT   3'  GTGGATGGTGGATGAAAAG   93273     G   TTGA
                                TTTTT GTT   CATCATTCAT
                                ||||| |||   ||||||||||
                                GAAAA TAG   GTGGTAGGTG
                                  G  ____
GAM984  GMEB2   3'  GGTCTGCAGAACCAAAGA    25666          AC_
                                TTTTTGGTTTTG  ATC
                                ||||||||||||  |||
                                AGAAACCAAGAC  TGG
                                      GTC
GAM984  GPR72   3'  CCCATGTGATGTGAAAACTAAA 70314          G     TCATT
            AG                    TTTTTGGTTTT ACATCAT
                                ||||||||||| |||||||
                                GAAAATCAAAA TGTAGTG
                                      G     TACCCC
GAM984  GPR9    3'  GATCGTCAGGACCAAAAA    9487            _
                                TTTTTGGTTTTGAC ATC
                                |||||||||||||| |||
                                AAAAACCAGGACTG TAG
                                       C
GAM984  GR6     5'  AGTGATTGGGCTGTCGGAATCA 24742           __  T
            AAGA                   TTTTTGGTTTTGACA  TCA TCATT
                                ||||||||||||||  ||| |||||
                                AGAAACTAAGGCTGT  GGT AGTGA
                                       CG   T
GAM984  GREB1   3'  AGTGGGTGAGAATGAAAACTTG 28556     T     GACA_
            AGA                    TTTT GGTTTT    TCATTCATT
                                |||| ||||||    |||||||||
                                AGAG TCAAAA    AGTGGGTGA
                                  T     GTAAG
GAM984  GREB1   3'  CCCTCATGCTGTTGAGGCTAAA 28561        TG   T   TCATT
            G                     TTTTGGTTT  ACA CAT
                                |||||||||  ||| |||
                                GAAATCGGA  TGT GTA
                                     GT   C   CTCCCG
GAM984  GRIN3A  5'  AATGAAGTCGGCGCTGGGG   56776    TG  T    A
                                TTT  GT TTGAC TCATT
                                |||  || ||||| |||||
                                GGG  CG GGCTG AGTAA
                                  GT  C    A
GAM984  GTF3C2  3'  AATGGGTGTATGGAGAACTGAA 9509      TG    GA  _
            AA                    TTTT  GTTTT  CAT CATTCATT
                                ||||  |||||  ||| ||||||||
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                                AAAA  CAAGA  GTA GTGGGTAA
                                  GT    G_   T
GAM984  H-L(3)MBT 3'  AGTGGGAGACAGAGCCGGGG   31922          ACA  A
                                TTTTGGTTTTG   TC TTCATT
                                ||||||||||   || ||||||
                                GGGGCCGAGAC   AG GGGTGA
                                      ___  A
GAM984  HBXAP    5'  AGTGAAAAATATACAAGACCAG 33879          ACATCA_
          AAG                     TTTTTGGTTTTG      TTCATT
                                ||||||||||||      ||||||
                                GAAGACCAGAAC      AAGTGA
                                      ATATAAA
GAM984  HGC6.1.1  3'  AGTGACCGTCAAGACCGGGGA  27608           A_
                                TTTTTGGTTTTGAC  TCATT
                                ||||||||||||||  |||||
                                AGGGGCCAGAACTG  AGTGA
                                      CC
GAM984  HGRG8    3'  TGATTTCAAAGCTGAGAA    33215     TG     C
                                TTTT  GTTTTGA ATCA
                                ||||  ||||||| ||||
                                AAGA  CGAAACT TAGT
                                  GT      T
GAM984  HRK      3'  GGTGGGGCCGGAGCCGAGA   15072          ACA
                                TTTTGGTTTTG   TCATT
                                ||||||||||   |||||
                                AGAGCCGAGGC   GGTGG
                                      CGG
GAM984  HSA243666 3'  AGTGAAATGACAGAGGCCAAAG 34554          GACA    _
          A                      TTTTTGGTTTT    TCATT CATT
                                ||||||||||    ||||| ||||
                                AGAAACCGGAG    AGTAA GTGA
                                      AC__     A
GAM984  HSN44A4A  3'  ACGAGTGATGCCGAAGA     31734       TTTTGA       ATT
                                TTTTTGG     CATCATTC
                                |||||||     ||||||||
                                AGAAGCC     GTAGTGAG
                                    _______      CAA
GAM984  HSPC157   5'  AATGAAATGATAGGCCGAGGA  27190          TGAC    _
                                TTTTTGGTTT    ATCATT CATT
                                ||||||||||    |||||| ||||
                                AGGAGCCGGA    TAGTAA GTAA
                                      ____     A
GAM984  HT002    3'  AGTGGGTGCCCTGGTTAGGGCT 26787      TG      AT___
          GAGGA                    TTTT  GTTTTGAC    CATTCATT
                                ||||  ||||||||    ||||||||
                                AGGA  CGGGATTG    GTGGGTGA
                                  GT       GTCCC
GAM984  HT002    3'  GATGAGGAAACAAGGCTGGAAG 26790      TG     ACA  A
                                TTTT  GTTTTG   TC TTCATT
                                ||||  ||||||   || ||||||
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                                GAAG  CGGAAC   AG GAGTAG
                                  GT     AA_  _
GAM984  HTCD37   3'  AGTGGTGTGATCATGAACCAAA 68296         _  ___      CATT
           G                     TTTTGGTTT TGA   CATCATT
                                 |||||||||  |||   |||||||
                                 GAAACCAAG ACT   GTGGTGA
                                       T   AGT         T
GAM984  IF2      5'  AGTGGGTCTGTGAGAGACCGAA 32479         G_   TC
                                 TTTGGTTTT  ACA  ATTCATT
                                 |||||||||  |||  |||||||
                                 AAGCCAGAG  TGT  TGGGTGA
                                       AG   C_
GAM984  IMP-2    3'  GGTGAACGTGTTCAAAGCCAAG 22610          _   CA
                                 TTTGGTTTTGA CAT  TTCATT
                                 ||||||||||| |||  ||||||
                                 GAACCGAAACT GTG  AAGTGG
                                        T   C_
GAM984  INSM2    3'  GATTGGTGTCAAACTTAAGGA  51855        T         T
                                 TTTTTGG TTTGACATCA TC
                                 |||||||  |||||||||| ||
                                 AGGAATT AAACTGTGGT AG
                                      C         T
GAM984  IRO039700 5'  GGTGGCACGGTCAGGGCTGGGG 38531      TG       ATCAT
           A                      TTTT  GTTTTGAC     TCATT
                                  ||||  ||||||||     |||||
                                  AGGG  CGGGACTG     GGTGG
                                    GT       GCAC_
GAM984  jdp2     3'  TGATGCGAAGCTGGAGA     56204      TG     A
                                 TTTT  GTTTTG CATCA
                                 ||||  |||||| |||||
                                 AGAG  CGAAGC GTAGT
                                   GT     _
GAM984  JM11     3'  GATGAGCCTTGAAGCCAGGG   54364         TG CA_
                                 TTTTGGTTT  A   TCATT
                                 |||||||||  |   |||||
                                 GGGACCGAA  T   AGTAG
                                       GT CCG
GAM984  KCNN1    3'  GATGAATGTGGGAATCAGAAA  11181          G   _
                                 TTTTTGGTTTT ACAT CATT
                                 |||||||||||  |||| ||||
                                 AAAGACTAAGG TGTA GTAG
                                        G    A
GAM984  KEAP1    5'  GTGGAGGCGGAGCCGGAG    25431          ACATCA
                                 TTTTGGTTTTG     TTCAT
                                 ||||||||||      |||||
                                 GAGGCCGAGGC     AGGTG
                                        GG____
GAM984  KIAA0009 3'  AATGAATGATGGCAACGAGG   28341      GTT   A
                                 TTTTG   TTG CATCATTCATT
                                 |||||   |||  ||||||||||
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                                GGAGC   AAC GTAGTAAGTAA
                                   ___  G
GAM984  KIAA0020 5' GATGAATCAGCAGCCAAGAA  30266        _   __
                                TTTTTGGTT TTGA  CATC
                                ||||||||| ||||  ||||
                                AAGAACCGA GACT  GTAG
                                    C    AA
GAM984  KIAA0084 3' AATGACCCAGTGTTAGAATGCA 68703      _       CAT_
          AGAG                    TTTTTG GTTTTGACAT    TCATT
                                ||||||| ||||||||||    |||||
                                GAGAAC TAAGATTGTG    AGTAA
                                   G         ACCC
GAM984  KIAA0125 3' AGTGCTGCGGTCAGGGCCAGGG 29556           ATCATT
                                TTTTGGTTTTGAC     CATT
                                ||||||||||||     ||||
                                GGGACCGGGACTG     GTGA
                                      GCGTC_
GAM984  KIAA0125 5' AGTGCTGCGGTCAGGGCCGGGG 29557           ATCATT
                                TTTTGGTTTTGAC     CATT
                                ||||||||||||     ||||
                                GGGGCCGGGACTG     GTGA
                                      GCGTC_
GAM984  KIAA0171 3' GATAGGTGATGTTGGGATGGAA 28548      G   TG      TC
          AA                     TTTTT GTTT  ACATCAT  ATT
                                ||||| ||||  |||||||  |||
                                AAAAG TAGG  TGTAGTG  TAG
                                   G   GT      GA
GAM984  KIAA0173 3' GATGGGTATTTGTAGGGCCGGA 28383          A  TC_
          G                      TTTTGGTTTTG CA   ATTCATT
                                |||||||||||  ||   |||||||
                                GAGGCCGGGAT GT   TGGGTAG
                                      _  TTA
GAM984  KIAA0174 3' GTGAGTGAGAATCAAGGC    79296        CA_
                                GTTTTGA   TCATTCAT
                                |||||||   ||||||||
                                CGGAACT   AGTGAGTG
                                    AAG
GAM984  KIAA0317 3' GTGGTGTCAGAACTGGAAA   29747      TG
                                TTTT  GTTTTGACATCAT
                                ||||  ||||||||||||
                                AAAG  CAAGACTGTGGTG
                                  GT
GAM984  KIAA0319 5' AGTGATGCTCAGGGCCAG    29697          _
                                TTGGTTTTGA CATCATT
                                |||||||||| |||||||
                                GACCGGGACT GTAGTGA
                                      C
GAM984  KIAA0435 3' ATCGATGGTGTCAAGGCAAAAA 29658       G          CATT
                                TTTTTG TTTTGACATCATT
                                |||||| ||||||||||||
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                                AAAAAC GGAACTGTGGTAG
                                  _          CTAA
GAM984  KIAA0438 3' ATGTGATTTGATGTTAACACTA 29732        T       T_   T
            GAGA                  TTTTTGGT TTGACATCA  TCAT
                                |||||||| |||||||||  ||||
                                AGAGATCA AATTGTAGT  AGTG
                                    C       TT    TAA
GAM984  KIAA0450 3' GGCGGGTGTCGGGGCCAGGG   28365             AT
                                TTTTGGTTTTGACATC  TC
                                |||||||||||||||  ||
                                GGGACCGGGGCTGTGG  GG
                                          GC
GAM984  KIAA0495 5' GGTGGGTGGCAGTCGGGGCTGA 63271    TG      A_
                                T  GTTTTGAC  TCATTCATT
                                |  ||||||||  |||||||||
                                A  CGGGGCTG  GGTGGGTGG
                                 GT       AC
GAM984  KIAA0542 3' ATTGATGGCACCCTTGAGACCA 66661          TG _______   ATTCATT
            AGAG                  TTTTTGGTTT  A     CATC
                                |||||||||| |     ||||
                                GAGAACCAGA  T     GTAG
                                      GT CCCACG      TTAC
GAM984  KIAA0555 5' GATGGATGAAATCAAAGCCAAG 60743           CA
            GA                  TTTTTGGTTTTGA  TCATTCATT
                                ||||||||||||  |||||||||
                                AGGAACCGAAACT  AGTAGGTAG
                                     AA
GAM984  KIAA0561 3' GATGAAGTTCAAGCCAGAAA   66480          T   A
                                TTTTTGGTTT GAC TCATT
                                |||||||||| ||| |||||
                                AAAGACCGAA TTG AGTAG
                                      C   A
GAM984  KIAA0570 3' GGTGGATTGCTTGAAACCAGGA 28851          TG _  TC
            G                   TTTTTGGTTT  A CA  ATTCATT
                                ||||||||||  | ||  |||||||
                                GAGGACCAAA  T GT  TAGGTGG
                                      GT C  __
GAM984  KIAA0570 3' GGTGGGTGGATTGCTTGAAACC 28852          TG _  __
            AGGAG                 TTTTTGGTTT  A CA  TCATTCATT
                                ||||||||||  | ||  |||||||||
                                GAGGACCAAA  T GT  GGTGGGTGG
                                      GT C  TA
GAM984  KIAA0603 3' AGTGAAACAAAGCCAGAG    29835           ACA
                                TTTTGGTTTTG   TCATT
                                ||||||||||   |||||
                                GAGACCGAAAC   AGTGA
                                     AA_
GAM984  KIAA0625 3' AGTGAATGTTGTAAAAGTTGAA 31178      GG    G   T
            A                   TTTT  TTTT ACA CATTCATT
                                ||||  |||| ||| ||||||||
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                                AAAG  GAAA TGT GTAAGTGA
                                  TT   A  T
GAM984  KIAA0638 3' ATTGGTGCCTTGCTTAGAGCCA 72828          _______   ATTCATT
            GAAG                  TTTTTGGTTTTGA    CATC
                                  ||||||||||||     ||||
                                  GAAGACCGAGATT    GTGG
                                        CGTTCC     TTAC
GAM984  KIAA0644 3' TAATGGATGGTGGGATGCTGAG 29727    TG  TTTGA
            G                   TTT  GT    CATCATTCATT  A
                                |||  ||    ||||||||||  |
                                GGA  CG    GTGGTAGGTAA  T
                                  GT  TAGG_
GAM984  KIAA0648 3' GGTGGATGATTCTGTTAGAG  83542        ___
                                TTTTGACA   TCATTCATT
                                ||||||||   |||||||||
                                GAGATTGT   AGTAGGTGG
                                     CTT
GAM984  KIAA0674 5' TGAAGTTAGGATCAGGAA    61246           A
                                TTTTTGGTTTTGAC TCA
                                |||||||||||||| |||
                                AAGGACTAGGATTG AGT
                                       A
GAM984  KIAA0677 3' GGTGGGTGATTCTGTCAACAGA 28534      GTT    ___
            AA                    TTTTTG   TTGACA   TCATTCATT
                                  ||||||   ||||||   |||||||||
                                  AAAGAC   AACTGT   AGTGGGTGG
                                     ___      CTT
GAM984  KIAA0701 3' AGTGGCAGTCAAAACTGAAA   70093    TG      A_
                                TTT  GTTTTGAC  TCATT
                                |||  ||||||||  |||||
                                AAA  CAAAACTG  GGTGA
                                  GT       AC
GAM984  KIAA0737 3' GTGGGGTGGTGGTGGGGTTGAA 29819     TG TT  GA      ATT
            GA                    TTTT  G  TT  CATCATTC
                                  ||||  |  ||  ||||||||
                                  AGAA  T  GG  GTGGTGGG
                                    GT GG  TG       GTGG
GAM984  KIAA0798 3' GATGAATGCTATCAATGTCAGA 28448       TT   CAT
            AA                    TTTTTGG  TTGA   CATTCATT
                                  |||||||  ||||   ||||||||
                                  AAAGACT  AACT   GTAAGTAG
                                     GT    ATC
GAM984  KIAA0826 3' GGTGTACAAAGCTAAAGA    83528          _
                                TTTTTGGTTTTG ACATC
                                |||||||||||| |||||
                                AGAAATCGAAAC TGTGG
                                       A
GAM984  KIAA0853 3' AATGAAGCAGAGCCAGGAA   31209           ACA
                                TTTTTGGTTTTG   TCATT
                                ||||||||||||   |||||
```

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                                AAGGACCGAGAC   AGTAA
                                      GA_
GAM984  KIAA0870  3'  GGTGTGGTTGTTGGAGCCGGAG 82384        TG  _   TCATT
                                TTTTGGTTT  ACA TCAT
                                |||||||||  ||| ||||
                                GAGGCCGAG  TGT GGTG
                                     GT   T   TGG
GAM984  KIAA0961  5'  GGTGGCGGTTAGTTGGGGCCAG 30406        TG __  AT
          GGA                    TTTTTGGTTT  AC  ATC  TCATT
                                |||||||||||  ||  |||  |||||
                                AGGGACCGGG  TG  TGG  GGTGG
                                     GT  AT   C_
GAM984  KIAA0963  3'  GGTGGGGAGCAGGGCCAAGG   31034        ACA_
                                TTTTGGTTTTG    TCATT
                                ||||||||||    |||||
                                GGAACCGGGAC    GGTGG
                                      GAGG
GAM984  KIAA1018  3'  AATGAATGTTATTAGGACAAGA 31054      G     CAT
          A                     TTTTTG TTTTGA   CATTCATT
                                ||||||| |||||||   ||||||||
                                AAGAAC AGGATT   GTAAGTAA
                                   _     ATT
GAM984  KIAA1052  3'  GCTGCGGGGTATCAGGGCCGGG 30944          C   ATT  TT
          AG                    TTTTTGGTTTTGA ATC   CA
                                ||||||||||||| |||   ||
                                GAGGGCCGGGACT TGG   GT
                                      A   GGC  CGG
GAM984  KIAA1075  3'  GATGGGTGTGTGAGGGGTGAGG 62386      G   G   T
          A                     TTTTTG TTTT ACA CATTCATT
                                ||||||| |||| ||| ||||||||
                                AGGAGT GGGA TGT GTGGGTAG
                                   G   G  _
GAM984  KIAA1076  3'  GTGAAGGTGGAATCAGAGA    66126        TGA   A
                                TTTTTGGTTT   CATC TTCAT
                                ||||||||||   |||| |||||
                                AGAGACTAAG   GTGG AAGTG
                                     ____   _
GAM984  KIAA1085  5'  AGTGGTGGTAAAAGCCAAGAG  40732         GA_
                                TTTTTGGTTTT   CATCATT
                                ||||||||||   |||||||
                                GAGAACCGAAA   GTGGTGA
                                      ATG
GAM984  KIAA1089  3'  GATGCAGGGTGGTTGGGGCCAG 69430         TG  _  ATT
          GAG                    TTTTTGGTTT  AC ATC   CATT
                                ||||||||||  || |||   ||||
                                GAGGACCGGG  TG TGG   GTAG
                                      GT  G   GAC
GAM984  KIAA1089  3'  GTGAATGGCGCACCAAGAG   69432        TTT ACA
                                TTTTTGGT   G   TCATTCAT
                                ||||||||   |   ||||||||
```

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                                GAGAACCA  C  GGTAAGTG
                                    ___ GC_
GAM984  KIAA1102 3' TTTTTTGTTGTTAAGACTGGGG 69587     TG       T  TTCATT
            A                    TTTT  GTTTTGACA CA
                                 ||||  ||||||||| ||
                                 AGGG  CAGAATTGT GT
                                   GT       T  TTTTTG
GAM984  KIAA1110 3' GGTGGGGGGCCGTGGGGGCCAGG 62504          G  ATCA
            GA                   TTTTTGGTTTT AC    TTCATT
                                 |||||||||||| ||    ||||||
                                 AGGGACCGGGG TG    GGGTGG
                                       G  CCGG
GAM984  KIAA1161 3' GGTGGAGCTGCCCAAGACCA  82647        A_  TCA
                                 TGGTTTTG  CA   TTCATT
                                 ||||||||  ||   ||||||
                                 ACCAGAAC  GT   AGGTGG
                                     CC  CG_
GAM984  KIAA1184 3' AATGAATGATTTAATCAAAAA  42921         TTGAC
                                 TTTTTGGTT    ATCATTCATT
                                 |||||||||    ||||||||||
                                 AAAAACTAA    TAGTAAGTAA
                                      TT___
GAM984  KIAA1184 3' GATGAGACTGTGAGGCCAAAAG 42929          G   TCA
                                 TTTTTGGTTTT ACA   TTCATT
                                 |||||||||||| |||   ||||||
                                 GAAAACCGGAG TGT   GAGTAG
                                       _   CA_
GAM984  KIAA1189 3' GATGGATTCCTGTAGAACTAGA 72508          ACATC
            G                    TTTTGGTTTTG    ATTCATT
                                 ||||||||||     |||||||
                                 GAGATCAAGAT    TAGGTAG
                                       GTCCT
GAM984  KIAA1233 3' AGTGATAGTGTCAGGATGGAG  63753     G        CAT
                                 TTT GTTTTGACAT   TCATT
                                 ||| ||||||||||   |||||
                                 GAG TAGGACTGTG   AGTGA
                                   G        AT_
GAM984  KIAA1283 5' GGTGAGCCGGTGGTGCAGAGCC 72524          A     _____
            AGGGA                   TTTTTGGTTTTG CATCAT    TCATT
                                    |||||||||||| ||||||    |||||
                                    AGGGACCGAGAC GTGGTG    AGTGG
                                          _     GCCG
GAM984  KIAA1319 3' AATGACTTGTAATGTCGTGATT 40786         T     __  T_
            AAAAA                   TTTTTGGTT TGACAT  CA  TCATT
                                    |||||||||| ||||||  ||  |||||
                                    AAAAATTAG GCTGTA  GT  AGTAA
                                          T     AT  TC
GAM984  KIAA1344 3' AGTGAGTAGAGGCCAGGGA   72865          G  A
                                    TTTTTGGTTTT AC TCATT
                                    |||||||||| || |||||
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                                AGGGACCGGAG TG AGTGA
                                      A  _
GAM984  KIAA1373  3'  AGTGAAAGTGAAACCAGAA   71501          ACA
                                TTTTGGTTTTG   TCATT
                                ||||||||||   |||||
                                AAGACCAAAGT   AGTGA
                                      GAA
GAM984  KIAA1437  3'  AATGGATGGTTTGGGTATTAAA 61211        _  TG C
          AA                    TTTTTGGT TT  A ATCATTCATT
                                |||||||| ||  | ||||||||||
                                AAAAATTA GG  T TGGTAGGTAA
                                     T  GT _
GAM984  KIAA1449  3'  TTTATGGTGTCAGAATAAAGG  40844     G          TCATT
                                TTTT GTTTTGACATCAT
                                |||| ||||||||||||
                                GGAA TAAGACTGTGGTA
                                  A          TTTA
GAM984  KIAA1486  3'  GGTGGGTGGATCACAAGGTCAG 67977      GT    ACA_
          GAG                     TTTTTG  TTTG    TCATTCATT
                                |||||||  ||||    |||||||||
                                GAGGAC  GAAC    GGTGGGTGG
                                   TG    ACTA
GAM984  KIAA1508  3'  GGTGGGTGGATCACAAGGTCGG 62555      GT    ACA_
          GAG                     TTTTTG  TTTG    TCATTCATT
                                |||||||  ||||    |||||||||
                                GAGGGC  GAAC    GGTGGGTGG
                                   TG    ACTA
GAM984  KIAA1511  3'  GGTGAGTGAGGGACAGAGGCCA 70728         GACA__
          GGA                     TTTTGGTTTT     TCATTCATT
                                ||||||||||     |||||||||
                                AGGACCGGAG     AGTGAGTGG
                                     ACAGGG
GAM984  KIAA1674  5'  GGTGACTCCAGACCAAGGA   69347          T  __
                                TTTTTGGTTT GA  CATC
                                |||||||||| ||  ||||
                                AGGAACCAGA CT  GTGG
                                     C  CA
GAM984  KIAA1705  3'  AATGTGTGTGTCAAGATACGGA 72854       _       T   T
          GA                    TTTTTG GTTTTGACA CAT CATT
                                |||||| ||||||||| ||| ||||
                                AGAGGC TAGAACTGT GTG GTAA
                                   A       _  T
GAM984  KIAA1751  3'  GGTGGAAGTCAGGGCTGAGG  72164     TG      ATCA
                                TTT  GTTTTGAC    TTCATT
                                |||  ||||||||   ||||||
                                GGA  CGGGACTG    AGGTGG
                                  GT       A___
GAM984  KIAA1755  3'  AGTGGGCGTCAGAACCAGGG  62005           A_
                                TTTTGGTTTTGAC  TCATT
                                ||||||||||||  |||||
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                                GGGACCAAGACTG GGTGA
                                      CG
GAM984  KIAA1826 3' AGTGAATAGTTGAAGCTAG   67791      TG ATC
                                TTGGTTT AC  ATTCATT
                                ||||||| ||  |||||||
                                GATCGAA TG  TAAGTGA
                                   GT A__
GAM984  KIAA1871 3' AATGAATGCAGTAAAACTAGGA 61889         ACAT
           A                    TTTTTGGTTTTG  CATTCATT
                                ||||||||||||  ||||||||
                                AAGGATCAAAAT  GTAAGTAA
                                      GAC_
GAM984  KIAA1913 5' AGTGAGACCAGGACTGAGAA  74314    TG    ACA
                                TTTT GTTTTG  TCATT
                                ||||  ||||||  |||||
                                AAGA CAGGAC  AGTGA
                                  GT    CAG
GAM984  KIAA1932 3' AGTGAGTGGAGGCCAGGGA   73821        G A
                                TTTTTGGTTTT AC TCATT
                                |||||||||||  || |||||
                                AGGGACCGGAG TG AGTGA
                                      G _
GAM984  KIAA1941 3' GGTGGAGCAGGTGGAGGCTGAA 75344    TG   G ATCA
           G                    TTT GTTTT AC   TTCATT
                                |||  ||||| ||   ||||||
                                GAA CGGAG TG   AGGTGG
                                  GT   G GACG
GAM984  KIAA1948 3' GATTGCTTGAGGCCAGAAG   83304       TG _ _
                                TTTTTGGTTT A CA TC
                                ||||||||||  | || ||
                                GAAGACCGGA T GT AG
                                      GT C T
GAM984  KIAA1954 3' AATGTTCTGATTCAGGATCAGA 78219        C   TT_
           G                    TTTTGGTTTTGA ATCA  CATT
                                ||||||||||||| ||||  ||||
                                GAGACTAGGACT TAGT  GTAA
                                      _   CTT
GAM984  KIAA1954 3' GATGAAGACTGAAAGCCAAAGA 78225        GA _ A
                                TTTTTGGTTTT CA TC TTCATT
                                ||||||||||  || || ||||||
                                AGAAACCGAAA GT AG AAGTAG
                                      __ C _
GAM984  KIAA1969 3' GGTGGGTGGATCACAAGGTCAA 79481     GT   ACA_
           GAG                    TTTTTG TTTG   TCATTCATT
                                ||||||  ||||  |||||||||
                                GAGAAC GAAC   GGTGGGTGG
                                   TG   ACTA
GAM984  KREMEN   3' GGTGGATCACTTGAGGCCAGGA 50236        TG CATC
           A                    TTTTTGGTTT A   ATTCATT
                                ||||||||||  |   |||||||
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                                AAGGACCGGA  T    TAGGTGG
                                      GT CAC_
GAM984  L3MBTL   3'  GATGAATGATGTGTTCACAAA  70086     GTTTTG
                                TTTG     ACATCATTCATT
                                ||||     ||||||||||||
                                AAAC     TGTAGTAAGTAG
                                  ACTTG_
GAM984  LCE      3'  AGTGAGTTTGCCAAAACCAAAG 44257          A  TC
                                TTTTGGTTTTG CA  ATTCATT
                                |||||||||||  ||  |||||||
                                GAAACCAAAAC GT  TGAGTGA
                                       C  T_
GAM984  LGI2     3'  GGTGGGTGAAACTAAGAG    36928          A_
                                TTTTTGGTTTTG  CATC
                                ||||||||||||  ||||
                                GAGAATCAAAGT  GTGG
                                       GG
GAM984  LHX6     3'  GGTGAGTGTGCCAAGCTCAGGA 27646      GT    A  T
                                TTTTG  TTTG CA CATTCATT
                                |||||  ||||  ||  ||||||||
                                AGGAC  GAAC GT GTGAGTGG
                                   TC    C  _
GAM984  LIG-1    3'  GATGAAACTGAGCTGGGACTGG 64613     TG   TT ACA  __
             AAA                   TTTT  GTT  G   TCA  TTCATT
                                ||||  |||  |   |||  ||||||
                                AAAG  CAG  T   AGT  AAGTAG
                                  GT   GG CG_   CA
GAM984  LIP8     5'  GGTGGTCGTCGGGGCAGAGGA  89525      G       _
                                TTTTT GTTTTGAC ATCATT
                                |||||  ||||||||  ||||||
                                AGGAG CGGGGCTG TGGTGG
                                   A       C
GAM984  LRP1B    5'  GATTCTGTGTAGAGCCGAGGA  38276          A   CAT_
                                TTTTTGGTTTTG CAT    TC
                                ||||||||||||  |||    ||
                                AGGAGCCGAGAT GTG    AG
                                       _  TCTT
GAM984  LSFR2    3'  GCCTCTGGTCTCGGGGCCAGGA 61187           C    TTCATT
             A                    TTTTTGGTTTTGA ATCA
                                ||||||||||||  ||||
                                AAGGACCGGGGCT TGGT
                                      C    CTCCG
GAM984  LYPLA3   3'  AGTGGGTGACTGGCCACAGGCC 25558          _  A_  _
             GAGAA                  TTTTTGGTTT TG  CA TCATTCATT
                                ||||||||||  ||  ||  |||||||||
                                AAGAGCCGGA AC  GT AGTGGGTGA
                                      C  CG  C
GAM984  MAB21L2  5'  GATTTTGTGAGGGCCAAAAG  22241          G   TCAT
                                TTTTTGGTTTT ACA    TC
                                ||||||||||  |||    ||
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                                GAAAACCGGGA TGT    AG
                                      G   TTT_
GAM984  MACMARCKS 3'  GGTGGGTGATCTCTAAGCT   43728      T  C
                                GGTTT GA ATCATTCATT
                                ||||| || ||||||||||
                                TCGAA CT TAGTGGGTGG
                                   T  C
GAM984  MAGE-E1   3'  AATGGATGTGGATATGGCCGAG 48672         TTGA_  T
           GA                    TTTTTGGTT    CA CATTCATT
                                ||||||||||    || ||||||||
                                AGGAGCCGG    GT GTAGGTAA
                                     TATAG  _
GAM984  MDS018    3'  GATGGATGTTGGCAAAATAGGA 41825     TG     A  T
           G                     TTT  GTTTTG CA CATTCATT
                                |||  |||||| || ||||||||
                                GAG  TAAAAC GT GTAGGTAG
                                  GA     G  T
GAM984  MDS018    3'  GATGGGTGAGGCAAGCCAGGAG 41826          T ACA
                                TTTTTGGTTT G   TCATTCATT
                                |||||||||| |   |||||||||
                                GAGGACCGAA C   AGTGGGTAG
                                     _ GG_
GAM984  MFN1      5'  GGTGATAGTTGGAGCGGAGA   54321      G    TG  _
                                TTTT GTTT  AC ATCATT
                                |||| ||||  || ||||||
                                AGAG CGAG  TG TAGTGG
                                  G    GT  A
GAM984  MFN2      3'  GATGGATGGTGGAAGGTGGGGA 30226     TT G    GA
                                TTT  G TTTT  CATCATTCATT
                                |||  | ||||  ||||||||||
                                AGG  T GAAG  GTGGTAGGTAG
                                  GG G   __
GAM984  MGC10646  3'  GGTGAAGTAGTCAGGACCATGA 52078     T        ATCA
           A                     TTT TGGTTTTGAC    TTCATT
                                ||| ||||||||||    ||||||
                                AAG ACCAGGACTG    AAGTGG
                                  T        ATG_
GAM984  MGC10765  3'  GGTGGGTGGATCACAAGGTCAG 44566       GT    ACA_
           GAG                    TTTTTG  TTTG    TCATTCATT
                                ||||||  ||||    |||||||||
                                GAGGAC  GAAC    GGTGGGTGG
                                   TG    ACTA
GAM984  MGC11335  3'  GATGAGTCTGGGTGAAGCCAGA 48770          A_  TC
           G                     TTTTGGTTTTG  CA  ATTCATT
                                ||||||||||  ||  |||||||
                                GAGACCGAAGT  GT  TGAGTAG
                                     GG  C_
GAM984  MGC11352  3'  GGTGGGTGGTGGAGTGCTGAA  65437    TG  TTTGA
                                TT  GT    CATCATTCATT
                                ||  ||    ||||||||||
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                                AA  CG    GTGGTGGGTGG
                                 GT  TGAG_
GAM984  MGC1223  3' AATGTTAGGTGTTGACATTGAG 49047     TG  T TG    ATT
           AA                    TTTT  GT T  ACATC   CATT
                                 ||||  || |  |||||   ||||
                                 AAGA  TA A  TGTGG   GTAA
                                   GT  C GT    ATT
GAM984  MGC12921 5' TGGTGACGGGGCCAGAGA    64517          A
                                 TTTTTGGTTTTG CATCA
                                 ||||||||||||| |||||
                                 AGAGACCGGGGC GTGGT
                                        A
GAM984  MGC13033 5' AATGTGCAAAACTGGAGA    49545     TG     A  T
                                 TTTT  GTTTTG CA CATT
                                 ||||  |||||| || ||||
                                 AGAG  CAAAAC GT GTAA
                                   GT     _ _
GAM984  MGC13269 3' GATGAATTTTTTTTACAGCCAA 52164        T   CATC_
           AAA                    TTTTTGGTT TGA    ATTCATT
                                 |||||||||| |||    |||||||
                                 AAAAACCGA ATT    TAAGTAG
                                      C   TTTTT
GAM984  MGC14407 3' GACTGATGTCAGGGATGGAGA  52973      GG         T
                                 TTTTT  TTTTGACATCA TC
                                 |||||  |||||||||| ||
                                 AGAGG  GGGACTGTAGT AG
                                    TA         C
GAM984  MGC14407 3' GGTGGATCACTTGAGGCCGGGA 52974          TG CATC
           G                      TTTTTGGTTT  A    ATTCATT
                                 ||||||||||  |   |||||||
                                 GAGGGCCGGA  T    TAGGTGG
                                       GT CAC_
GAM984  MGC14407 3' GGTGGGTGGATCACTTGAGGCC 52975          TG CA___
           GGGAG                    TTTTTGGTTT  A    TCATTCATT
                                 ||||||||||  |    |||||||||
                                 GAGGGCCGGA  T    GGTGGGTGG
                                       GT CACTA
GAM984  MGC14433 3' GGTGAATGAGGTTGTTTGGAAA 52954      TG TTTT   A
                                 TTTT  G    GAC TCATTCATT
                                 ||||  |    ||| |||||||||
                                 AAAG  T    TTG AGTAAGTGG
                                   GT TG__   G
GAM984  MGC15482 5' GGTGGAGGCCTAGCCGGAGCCG 52856          ACATCA__
           AGA                    TTTTGGTTTTG       TTCATT
                                 ||||||||||||       ||||||
                                 AGAGCCGAGGC       AGGTGG
                                       CGATCCGG
GAM984  MGC15634 3' GCATGTGGTTCAGAATTGAGAA 52241      TG      C     TCATT
                                 TTTT  GTTTTGA ATCAT
                                 ||||  ||||||| |||||
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                                AAGA  TAAGACT TGGTG
                                  GT      _     TACGA
GAM984  MGC16028  3'  AATGAGCTTAAAGCTAAAGA   54618           CA
                                TTTTTGGTTTTGA  TCATT
                                |||||||||||||  |||||
                                AGAAATCGAAATT  AGTAA
                                     CG
GAM984  MGC18257  3'  AGTGCAGCAGAACCAAAAA    57547           ACAT
                                TTTTTGGTTTTG    CATT
                                ||||||||||||    ||||
                                AAAAACCAAGAC    GTGA
                                     GAC_
GAM984  MGC20496  3'  GGTGGGTGAGGTGCAGATGACC 54531          __  _ A
          AGGAG                    TTTTTGGTT  TTG AC TCATTCATT
                                |||||||||  ||| || |||||||||
                                GAGGACCAG  GAC TG AGTGGGTGG
                                     TA   G  G
GAM984  MGC21688  3'  GGTGGGTGGCTTTAGAATTAAG 58916           CA
          G                     TTTTGGTTTTGA  TCATTCATT
                                ||||||||||||  |||||||||
                                GGAATTAAGATT  GGTGGGTGG
                                     TC
GAM984  MGC22679  5'  GGCTGATGTTTAAAACTGAAGA 59172      TG      _     TT
                                TTTT  GTTTTGA CATCA  C
                                ||||  ||||||| |||||  |
                                AGAA  CAAAATT GTAGT  G
                                  GT      T    CG
GAM984  MGC2628   3'  GGTGGATGCCTAGAGGCTGAAG 44201      TG    GACAT
          G                     TTTT  GTTTT    CATTCATT
                                ||||  |||||    ||||||||
                                GGAA  CGGAG    GTAGGTGG
                                  GT    ATCC_
GAM984  MGC26610  5'  GATGGCGATCCAGGCCAAGAA  58962          T ____
                                TTTTTGGTTT GA    CATC
                                ||||||||||  ||    ||||
                                AAGAACCGGA CT    GTAG
                                     C  AGCG
GAM984  MGC3178   3'  GATGCATTTGATCTCAAGACCA 48719           C    TT__
          AAGA                    TTTTTGGTTTTGA ATCA    CATT
                                ||||||||||||| ||||    ||||
                                AGAAACCAGAACT TAGT    GTAG
                                     C    TTAC
GAM984  MGC3329   3'  GGTGGCTGTTGGTCAGGACGGG 44249      G      AT_  TT
          AAG                     TTTTT GTTTTGAC   CA  CATT
                                ||||| ||||||||   ||  ||||
                                GAAGG CAGGACTG   GT  GTGG
                                  G       GTT  CG
GAM984  MGC3329   3'  GGTGGGTGGTGGGGAATCTGGG 44250     TG T   GA
          AG                    TTTT  G TTT  CATCATTCATT
                                ||||  | |||  ||||||||||
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                                GAGG  C AAG  GTGGTGGGTGG
                                  GT T   GG
GAM984   MGC4368   3' GGTGGGAGGATTGCTTGAGGCC 44727          TG _  _  A_
            AGGAG                   TTTTTGGTTT  A CA TC  TTCATT
                                    ||||||||||  | || ||  ||||||
                                    GAGGACCGGA  T GT AG  GGGTGG
                                          GT C  T  GA
GAM984   MGC4638   3' GATGTCAGGGACTAGGGA    49737          _
                                    TTTTTGGTTT TGACATC
                                    |||||||||| |||||||
                                    AGGGATCAGG ACTGTAG
                                          G
GAM984   MGC4771   3' GGTGAGTGGATCACGAGGTCAG 52004       GT    ACA_
            GAG                     TTTTTG  TTTG    TCATTCATT
                                    ||||||  ||||    |||||||||
                                    GAGGAC  GAGC    GGTGAGTGG
                                       TG    ACTA
GAM984   MGC5139   5' AATGGGTGATGCTGCCAAG    74565       TTTGA
                                    TTTGGT    CATCATTCATT
                                    ||||||    ||||||||||
                                    GAACCG    GTAGTGGGTAA
                                       TC___
GAM984   MGC5306   3' AACATGGTGTCTGGAGTTAAAG 44370      GG   _      TCATT
                                    TTTT  TTTT GACATCAT
                                    ||||  |||| ||||||||
                                    GAAA  GAGG CTGTGGTA
                                      TT   T      CAA
GAM984   MGC5391   3' AATGCAGTCAGAACCTGGGA   52194     TT       AT
                                    TTT  GGTTTTGAC  CATT
                                    |||  |||||||||  ||||
                                    AGG  CCAAGACTG  GTAA
                                      GT       AC
GAM984   MGC5457   3' AATGAATGGCATGGCCGGG    51930       TT  ACA
                                    TTTGGT  TG   TCATTCATT
                                    ||||||  ||   |||||||||
                                    GGGCCG  AC   GGTAAGTAA
                                       GT  ___
GAM984   MGC9753   3' GGTGAATGTGTCCACAGTTGAG 54198      GG  TT_   T
            AG                      TTTTT  TT   GACA CATTCATT
                                    |||||  ||   |||| ||||||||
                                    GAGAG  GA   CTGT GTAAGTGG
                                      TT  CAC   _
GAM984   MPPE1    3' GATCATGTTAGAATCAAG    43818           CAT
                                    TTTGGTTTTGACAT   TC
                                    ||||||||||||||   ||
                                    GAACTAAGATTGTA   AG
                                          CT_
GAM984   MRPS27    3' AATGAGAGATGGGTTGGGGCTT 31314     T    TG  __   A
            GAAG                    TTTT GGTTT  AC  ATC TTCATT
                                    |||| |||||  ||  ||| ||||||
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                                GAAG TCGGG  TG  TAG GAGTAA
                                  T    GT  GG   A
GAM984  MRPS27   3'  AGTGAACTCAAGGCCATGAA  31320    T       CA
                                TTT TGGTTTTGA  TCATT
                                ||| |||||||||  |||||
                                AAG ACCGGAACT  AGTGA
                                  T       CA
GAM984  MSTP031  3'  GGTGGATAGGTACAGGATTGGG 50168     TG    _  ATC
          AG                    TTTT  GTTTTG AC   ATTCATT
                                ||||  |||||| ||   |||||||
                                GAGG  TAGGAC TG   TAGGTGG
                                  GT     A  GA_
GAM984  MYH10    5'  GGTGAGTCAGGTGCTGGGAA  69673     TG _     A
                                TTTT  GT TTTGAC TCATT
                                ||||  || |||||| |||||
                                AAGG  CG GGACTG AGTGG
                                  GT  T     _
GAM984  MYO18B   3'  AATGAATGAATGAGCCAAAGA  51881         TGACA
                                TTTTTGGTTT    TCATTCATT
                                ||||||||||    |||||||||
                                AGAAACCGAG    AGTAAGTAA
                                      TA___
GAM984  MYT1L    5'  GATGGAGGTGGACACCGAGGA  67365        TTTGA   A
                                TTTTTGGT    CATC TTCATT
                                ||||||||    |||| ||||||
                                AGGAGCCA    GTGG AGGTAG
                                     CAG__   _
GAM984  NAP1L1   3'  TGGGTTAGAGCTAGAGA     58303           A
                                TTTTTGGTTTTGAC TCA
                                |||||||||||||| |||
                                AGAGATCGAGATTG GGT
                                                _
GAM984  NASP     3'  GATGGCTCAGGACTAGAGG    68579           __
                                TTTTTGGTTTTGA  CATC
                                ||||||||||||  ||||
                                GGAGATCAGGACT  GTAG
                                       CG
GAM984  NBR2     3'  AGTGGAAGCGAAGCCGAAAA   20616          ACA
                                TTTTTGGTTTTG   TCATT
                                ||||||||||||   |||||
                                AAAAGCCGAAGC   GGTGA
                                       GAA
GAM984  NET-5    3'  GTGGGTGGAGTGCCAGGGA   22895        TTTG  AT
                                TTTTTGGT    AC  CATTCAT
                                ||||||||    ||  |||||||
                                AGGGACCG    TG  GTGGGTG
                                     _____  AG
GAM984  NFASC    3'  AGTGTTCCGGCAGGACCAGAAG 70851          ACAT__
                                TTTTTGGTTTTG     CATT
                                ||||||||||||     ||||
```

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                                GAAGACCAGGAC     GTGA
                                      GGCCTT
GAM984  NR1I3    3'  AGTGGGAAAATGCTGGGACCAA 18876         GA   CA_
            AGA                    TTTTTGGTTTT  CAT   TTCATT
                                   ||||||||||  |||   ||||||
                                   AGAAACCAGGG  GTA   GGGTGA
                                         TC   AAA
GAM984  NSG-X    3'  CCCAGGATGGCTGTTGGGATTA 27727         TG   _     ATT
            GGAG                   TTTTTGGTTT  ACA TCATTC
                                   ||||||||||  ||| ||||||
                                   GAGGATTAGG  TGT GGTAGG
                                         GT   C     ACCCT
GAM984  NYD-SP11 5'  GATGAAGAGCAAAACTGAGGA  50056     TG     ACATCA
                                   TTTT  GTTTTG     TTCATT
                                   ||||  ||||||     ||||||
                                   AGGA  CAAAAC     AAGTAG
                                     GT     GAG___
GAM984  OR2C3    3'  GATACATGTTAAAATTAGAG   75976           CAT
                                   TTTTGGTTTTGACAT   TC
                                   ||||||||||||||   ||
                                   GAGATTAAAATTGTA   AG
                                         CAT
GAM984  OSBPL8   5'  GGTGGACCTCGGGGCCGAAAG  40848           ____
                                   TTTTTGGTTTTGA    CATC
                                   ||||||||||||    ||||
                                   GAAAGCCGGGGCT    GTGG
                                         CCAG
GAM984  OVGP1    3'  CCCCTCTGGTGTCAGAAACCAG 11919         _       TTCATT
            GGA                    TTTTTGGTT TTGACATCA
                                   |||||||| |||||||||
                                   AGGGACCAA GACTGTGGT
                                        A        CTCCCCG
GAM984  P15-2    3'  AATGAATGGTAGTAGAACTAA  38625         AC
                                   TTGGTTTTG  ATCATTCATT
                                   |||||||||  ||||||||||
                                   AATCAAGAT  TGGTAAGTAA
                                        GA
GAM984  P8       3'  AATGGAGGGGCAGAGCCAGGAA 25674          ACA  A
                                   TTTTTGGTTTTG   TC TTCATT
                                   ||||||||||||   || ||||||
                                   AAGGACCGAGAC   GG AGGTAA
                                         GG_  _
GAM984  PADI1    3'  AGTGGGTGAGCGGGAACCTGAA 62699      T     GACA
            A                       TTTT GGTTTT    TCATTCATT
                                   ||||  ||||||    |||||||||
                                   AAAG CCAAGG    AGTGGGTGA
                                     T     GCG_
GAM984  PAFAH2   3'  AGTGGAAGAGATGAAGCCAAAG 6493           ACA  A
                                   TTTTGGTTTTG   TC TTCATT
                                   ||||||||||   || ||||||
```

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                                GAAACCGAAGT   AG AGGTGA
                                      AG_  A
GAM984  PAGE-5   3'  AATGAAGACTGAAACCAAGAA  56195          ACA  A
                                TTTTTGGTTTTG   TC TTCATT
                                ||||||||||||   || ||||||
                                AAGAACCAAAGT   AG AAGTAA
                                      C__  _
GAM984  PAGE-5   5'  AGTGAATGTGTGGAGGAGCCAG 56196        GA  _
                                TTGGTTTT  CAT CATTCATT
                                ||||||||  ||| ||||||||
                                GACCGAGG  GTG GTAAGTGA
                                     AG   T
GAM984  PARG1    3'  GATTGTCAACAACTGAAAG   17868      TG  _    _
                                TTTT  GTT TTGACA TC
                                ||||  ||| |||||| ||
                                GAAA  CAA AACTGT AG
                                  GT   C     T
GAM984  PELI1    5'  TGATGAATGATTTTCTGTTAAA 40661           _____
           ACTAGA                TTTGGTTTTGACA    TCATTCATT   G
                                ||||||||||||||    |||||||||  |
                                AGATCAAAATTGT    AGTAAGTAG   T
                                      CTTTT
GAM984  PLEKHA4  5'  AATGAGTGAGAGAGAGACTGGA 40878      TG    GACA
           AG                   TTTT  GTTTT    TCATTCATT
                                ||||  |||||   |||||||||
                                GAAG  CAGAG    AGTGAGTAA
                                  GT    AGAG
GAM984  POLYDOM  3'  GGTGGATCACGAGGTCAGGAGT 44688      TG _      A ___
           TGGAGA                TTTT  G TTTTGAC TC   ATTCATT
                                ||||  | ||||||| ||   |||||||
                                AGAG  T AGGACTG AG   TAGGTGG
                                  GT G      G  CAC
GAM984  PP1044   5'  GGTGGGCGCAGGACCGAG    41676          ACA
                                TTTGGTTTTG   TCATT
                                ||||||||||   |||||
                                GAGCCAGGAC   GGTGG
                                      GCG
GAM984  PP3501   3'  CGTGGGTGCCGGGACTGGGGA  41680      TG     ACAT      T
                                TTTT  GTTTTG    CATTCAT
                                ||||  ||||||   |||||||
                                AGGG  CAGGGC    GTGGGTG
                                  GT     C___      CT
GAM984  PP591    5'  GGTGGCCCTTGAAGCCAGGAG  48149         TG ____
                                TTTTTGGTTT  A    CATC
                                ||||||||||  |   ||||
                                GAGGACCGAA  T   GTGG
                                      GT CCCG
GAM984  PPFIA4   3'  GGATGGTGAGGCTGGGAG    70843      TG   TGA
                                TTTT  GTTT   CATCATTC
                                ||||  ||||   ||||||||
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                                GAGG  CGGA   GTGGTAGG
                                  GT   ___
GAM984  PPFIA4   3' GGGATGATGGAACCGAGGG   70844         TGA      ATT
                                TTTTTGGTTT   CATCATTC
                                ||||||||||   ||||||||
                                GGGAGCCAAG   GTAGTAGG
                                      ___       GT
GAM984  PPIL4    3' GATGAAGAGGCAGAATTGAGAG 58221     TG     ACA  A
                                TTTT  GTTTTG   TC TTCATT
                                ||||  ||||||   || ||||||
                                GAGA  TAAGAC   AG AAGTAG
                                  GT     GG_  _
GAM984  PPP1R13B 3' GGTGGTTGGGGTTGGGGCTGGG 31659     TG   TG  AT  TT
           G                     TTT  GTTT  AC  CA  CATT
                                |||  ||||  ||  ||  ||||
                                GGG  CGGG  TG  GT  GTGG
                                  GT   GT  GG  TG
GAM984  PPP1R14C 3' AGTGTTAAGTGTCAAGGTGAGA 48926      G TT      CATT
           AA                    TTTTT G  TTGACAT    CATT
                                ||||| |  |||||||    ||||
                                AAAGA T  AACTGTG    GTGA
                                   G GG      AATT
GAM984  PRAX-1   3' GGTGAAGGTCAGAGCTAAA   17657          A_
                                TTTGGTTTTGAC  TCATT
                                ||||||||||||  |||||
                                AAATCGAGACTG  AGTGG
                                      GA
GAM984  PRKAG3   3' GGATGATGAAATTAAGGA    34290         TGA
                                TTTTTGGTTT   CATCATTC
                                ||||||||||   ||||||||
                                AGGAATTAAA   GTAGTAGG
                                      ___
GAM984  PRO0478  3' GTGTCTCAAAATCAAAAA    27034          CAT
                                TTTTTGGTTTTGA   CAT
                                ||||||||||||   |||
                                AAAAACTAAAACT   GTG
                                      CT_
GAM984  PRO1048  5' GATGGCTTGAGGCCAGGAA   38114         TG __
                                TTTTTGGTTT  A  CATC
                                ||||||||||  |  ||||
                                AAGGACCGGA  T  GTAG
                                     GT CG
GAM984  PRO1992  3' AATGACCATTCAAGACCAGA   26892          CA__
                                TTTGGTTTTGA    TCATT
                                ||||||||||    |||||
                                AGACCAGAACT    AGTAA
                                      TACC
GAM984  PRO2012  3' AATGAACATCTAAAACCAAGAA 38386           ACATCA
                                TTTTTGGTTTTG     TTCATT
                                ||||||||||||     ||||||
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                                AAGAACCAAAAT     AAGTAA
                                      CTAC__
GAM984  PRO2405  5'  GATGATCAGCATCGAGAA    38416        T   _
                                TTTTTGGT TTGA CATC
                                |||||||| |||| ||||
                                AAGAGCTA GACT GTAG
                                     C    A
GAM984  PRO2605  3'  GGTGGGTGAGGTGGCAGCTGGG 96509     TG   TTG  A
          GA                    TTTT  GTT   AC TCATTCATT
                                ||||  |||   || |||||||||
                                AGGG  CGA   TG AGTGGGTGG
                                  GT   CGG  G
GAM984  PRRDH    5'  GATGAATGGTCAGAGTCAGG   32326     GT     AT
                                TTTG  TTTGAC  CATTCATT
                                ||||  ||||||  ||||||||
                                GGAC  AGACTG  GTAAGTAG
                                  TG     __
GAM984  PSTPIP2  3'  GATGAGGGACAGAACCAGAA   44656         ACA  A
                                TTTTGGTTTTG   TC TTCATT
                                ||||||||||   || ||||||
                                AAGACCAAGAC   AG GAGTAG
                                      ___  G
GAM984  PTDSS2   3'  CGTGGATGATGGGGTCAGAGA  48624       TT TGA        T
                                TTTTTGG  T   CATCATTCAT
                                |||||||  |   ||||||||||
                                AGAGACT  G   GTAGTAGGTG
                                    GG ___         CA
GAM984  PTK9     3'  TGAGTTAAAGCTAGAAA     12555            A
                                TTTTTGGTTTTGAC TCA
                                |||||||||||||| |||
                                AAAGATCGAAATTG AGT
                                      _
GAM984  PTK9L    3'  AGTGGGGTCAGTCAGGGCTGGG 24420     TG       ATCA
          G                      TTT  GTTTTGAC    TTCATT
                                |||  ||||||||   ||||||
                                GGG  CGGGACTG    GGGTGA
                                  GT       ACTG
GAM984  PTPN9    3'  GACATGATCAAAACCAAAAA   12597          CA   _
                                TTTTTGGTTTTGA  TCAT TC
                                ||||||||||||  |||| ||
                                AAAAACCAAAACT  AGTA AG
                                      __   C
GAM984  RAB21    3'  AGTGGAGTTTGTGACCAGAGA  31083        TTG   TCA
                                TTTTTGGTT   ACA   TTCATT
                                |||||||||   |||   ||||||
                                AGAGACCAG   TGT   AGGTGA
                                     ___  TTG
GAM984  RAB40A   5'  GGTGAGTGGGCTCAGGCAGAAG 82944       GT    CA
                                TTTTTG  TTTGA  TCATTCATT
                                ||||||  |||||  |||||||||
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                                GAAGAC  GGACT  GGTGAGTGG
                                  __     CG
GAM984   RBM12    3'  GATGGTATCGAAAACCAGAAA  21282          _  C
                                TTTTTGGTTTT GA ATCATT
                                |||||||||||  ||  ||||||
                                AAAGACCAAAA CT TGGTAG
                                      G  A
GAM984   RERG     3'  TAGAAGATGTAGAATTAGAGA  53002           A   A   ATT
                                TTTTTGGTTTTG CATC TTC
                                ||||||||||||  ||||  |||
                                AGAGATTAAGAT GTAG AAG
                                      _   _  ATG
GAM984   RIP60    3'  AATGAATGCTCTGGGCTAGA   26358        TT  CAT
                                TTTGGTT  GA   CATTCATT
                                |||||||  ||   ||||||||
                                AGATCGG  CT   GTAAGTAA
                                    GT  C__
GAM984   RNAHP    3'  AATGATGGTCGGAATGGGGAA  24777       G      _
                                TTTTT GTTTTGAC ATCATT
                                |||||  ||||||||  ||||||
                                AAGGG TAAGGCTG TAGTAA
                                   G       G
GAM984   RNF9     3'  GGTGGAGATCAGAAGCCAGGGA 23239           GAC   A
                                TTTTTGGTTTT   ATC TTCATT
                                ||||||||||   |||  ||||||
                                AGGGACCGAAG   TAG AGGTGG
                                      AC_  _
GAM984   RNP24    3'  GATGATGGGTTTAAAATTAAAA 23325           ___      CATT
           G                     TTTTTGGTTTTGA   CATCATT
                                ||||||||||||   |||||||
                                GAAAATTAAAATT   GTAGTAG
                                      TGG
GAM984   RPP14    5'  AGTGGGTGTGATCAGCACTGGA 60221      TG  T   _  T
           AA                     TTTT  GT TTGA CA CATTCATT
                                ||||  ||  ||||  ||  ||||||||
                                AAAG  CA GACT GT GTGGGTGA
                                   GT  C    A  _
GAM984   RRP4     3'  TGTGGATGATTCAGAGTTAAAA 27366      GG     C       T
           G                     TTTTT  TTTTGA ATCATTCAT
                                |||||  ||||||  |||||||||
                                GAAAA  GAGACT TAGTAGGTG
                                   TT     _       TT
GAM984   S164     5'  AATGGGAATGCAAGGCCAGAAA 61429           A   CA
                                TTTTTGGTTTTG CAT  TTCATT
                                ||||||||||||  |||  ||||||
                                AAAGACCGGAAC GTA  GGGTAA
                                      _  A_
GAM984   SC65     3'  GGTGGATCACTTGAGGCCAGGA 22299          TG CATC
           G                     TTTTTGGTTT  A    ATTCATT
                                ||||||||||  |   |||||||
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                                GAGGACCGGA T   TAGGTGG
                                     GT CAC_
GAM984  SC65    3' GGTGGGTGGATCACTTGAGGCC 22300        TG CA___
          AGGAG                 TTTTTGGTTT A    TCATTCATT
                                |||||||||| |    |||||||||
                                GAGGACCGGA T    GGTGGGTGG
                                     GT CACTA
GAM984  SCAND1  3' AATGAGTTTTGGCAGCGCCAAA 54391       T  A  TC
          AA                   TTTTTGGT TTG CA  ATTCATT
                               |||||||| ||| ||  |||||||
                               AAAAACCG GAC GT  TGAGTAA
                                   C  G  TT
GAM984  SCYB11  3' ATGAATGACAATCAGAAT   88834       CA_
                               GTTTTGA  TCATTCAT
                               |||||||  ||||||||
                               TAAGACT  AGTAAGTA
                                   AAC
GAM984  SCYB11  3' GGTGGGTGAAAGGACCAAAAA 88837         GACA
                               TTTTTGGTTTT   TCATTCATT
                               ||||||||||   |||||||||
                               AAAAACCAGGA   AGTGGGTGG
                                     A___
GAM984  sdolf   3' GGTGAGCCCTTGACAGGGCTAG 54315         A  TCA_
          AGA                  TTTTTGGTTTTG CA   TTCATT
                               ||||||||||| ||   ||||||
                               AGAGATCGGGAC GT   GAGTGG
                                     A  TCCC
GAM984  SE70-2  3' AATGAATGTTTTCAAAACTGAA 42345   TG     CAT
                               TT  GTTTTGA  CATTCATT
                               ||  |||||||  ||||||||
                               AA  CAAAACT  GTAAGTAA
                                GT     TTT
GAM984  SEC31B-1 3' GATGGGTGCTGAGCAGAACCAA 31927         A_  T
          GAG                  TTTTTGGTTTTG  CA CATTCATT
                               ||||||||||||  || ||||||||
                               GAGAACCAAGAC  GT GTGGGTAG
                                     GA  C
GAM984  SELB    3' GATGGGTTGCTGGGGCCAGGAG 62592         GA  TC
                               TTTTTGGTTTT  CA  ATTCATT
                               ||||||||||  ||  |||||||
                               GAGGACCGGGG  GT  TGGGTAG
                                     TC  __
GAM984  SLC11A1 3' GGTGGGTGGGGTGAGGGCTTGA 60160    T    G  AT
          G                    TTT GGTTTT AC  CATTCATT
                               ||| |||||| ||  ||||||||
                               GAG TCGGGA TG  GTGGGTGG
                                 T    G  GG
GAM984  SLC19A3 3' GTGGGAGTTTTGCTTGAGGCCA 48249        TG _  TC   ATT
          GAG                  TTTTGGTTT  A CA  ATTC
                               |||||||||  | ||  ||||
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                                GAGACCGGA  T GT  TGAG
                                     GT C  TT    GGTGG
GAM984  SLC26A1  3'  AATGACCCTTAGGGCCAGGAA  57053          CA_
                                TTTTTGGTTTTGA   TCATT
                                ||||||||||||   |||||
                                AAGGACCGGGATT   AGTAA
                                     CCC
GAM984  SLC26A6  5'  GATGCGTCGGGACCGAGG    43582          __
                                TTTTGGTTTTGAC  ATC
                                ||||||||||||  |||
                                GGAGCCAGGGCTG  TAG
                                     CG
GAM984  SLC39A3  3'  AGTGGGTGGAGGCCAGAGA   58598         G  A
                                TTTTTGGTTTT AC TCATT
                                |||||||||| || |||||
                                AGAGACCGGAG TG GGTGA
                                     G  _
GAM984  SMA3     3'  AATGAGCGAGTGAACCAAGAA  23252        TG  A  A
                                TTTTTGGTTT  AC TC TTCATT
                                ||||||||||  || || ||||||
                                AAGAACCAAG  TG AG GAGTAA
                                     __  _  C
GAM984  SMOC1    3'  GGTGTTGTTGGGGCCTGAGA   42415     T    TG   T
                                TTTT GGTTT  ACA CATT
                                |||| |||||  ||| ||||
                                AGAG CCGGG  TGT GTGG
                                  T    GT   T
GAM984  SMOC2    3'  GCTGGTGTTGGCAGCCGGGG   72821       _ TG     TT
                                TTTTGGTT T  ACATCA  C
                                ||||||||  |  ||||||  |
                                GGGGCCGA G  TGTGGT  G
                                     C GT     CG
GAM984  SNAP29   3'  GATCAGTGTTAGAATGGGAAA  17713      G        CAT
                                TTTTT GTTTTGACAT   TC
                                |||||  ||||||||||   ||
                                AAAGG TAAGATTGTG   AG
                                   G         ACT
GAM984  SPEC1    5'  AGTGGGTTGTCCAAACACCAGG 40002        _   _  TC
           GA                     TTTTTGGT TTTG ACA  ATTCATT
                                |||||||| |||| |||  |||||||
                                AGGGACCA AAAC TGT  TGGGTGA
                                     C   C  __
GAM984  SPEC1    3'  GGTGGGTGAGATTATCAAAGCT 40009     TG      CA___
           GAAG                     TTT  GTTTTGA    TCATTCATT
                                |||  |||||||    |||||||||
                                GAA  CGAAACT    AGTGGGTGG
                                  GT      ATTAG
GAM984  SQV7L    5'  GAATGTGAAGCCAGAG      71095          ACAT
                                TTTTGGTTTTG   CATTC
                                ||||||||||   |||||
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                                GAGACCGAAGT   GTAAG
                                      ____
GAM984  SQV7L   5' GGTGGGCATAGCCAAAAA   71098        T  A_
                                TTTTTGGTT TG  CATC
                                ||||||||| ||  ||||
                                AAAAACCGA AC  GTGG
                                     T  GG
GAM984  STAB1   3' GGTGGATGGGGCAGGAGGGGCT 66037    TG   GACA___
           GAGG                  TTT  GTTTT     TCATTCATT
                                |||  |||||     |||||||||
                                GGA  CGGGG     GGTAGGTGG
                                  GT    AGGACGG
GAM984  STAG2   3' ATGGGTGAATACCAAAAG   71088       TTTGACA
                                TTTTTGGT     TCATTCAT
                                ||||||||     ||||||||
                                GAAAACCA     AGTGGGTA
                                     TA_____
GAM984  STATI2  5' GATGAGTTTCCACTAAGGCCAG 96191         ACATC_
           GG                    TTTTGGTTTTG     ATTCATT
                                ||||||||||     |||||||
                                GGGACCGGAAT     TGAGTAG
                                      CACCTT
GAM984  SUN1    3' GGTGGATCACTTGAGGCCGGGA 47918         TG CATC
           G                     TTTTTGGTTT  A   ATTCATT
                                |||||||||| |   |||||||
                                GAGGGCCGGA  T   TAGGTGG
                                     GT CAC_
GAM984  SV2B    5' AATGAATGATGGTTATTGAAA  29946    TG  TTTGA
                                TTT  GT    CATCATTCATT
                                |||  ||    ||||||||||
                                AAA  TA    GTAGTAAGTAA
                                  GT  TTG__
GAM984  SYNPO2  3' AGTGATATCAAACATCAGGAA  72386       _    C
                                TTTTTGGT TTTGA ATCATT
                                |||||||| ||||| |||||||
                                AAGGACTA AAACT TAGTGA
                                     C    A
GAM984  SYT12   5' AGTGAGTAGGAGGCCGAAG   96375        G_  A
                                TTTTGGTTTT  AC TCATT
                                ||||||||||  || |||||
                                GAAGCCGGAG  TG AGTGA
                                     GA  _
GAM984  TACTILE 3' GGTGGGTGGATCACGAGGTCAG 20591      GT   ACA_
           GAG                    TTTTTG  TTTG   TCATTCATT
                                ||||||  ||||   |||||||||
                                GAGGAC  GAGC   GGTGGGTGG
                                   TG   ACTA
GAM984  TAF5L   3' GATGAGTGATCAAGAATTAGAG 27722         GAC
                                TTTTGGTTTT   ATCATTCATT
                                ||||||||||   ||||||||||
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                                GAGATTAAGA   TAGTGAGTAG
                                     AC_
GAM984   TAF5L    3'  GGTGGGTGGGTTTGATTGAGAA 27724      TG   TT   A
                                TTTT  GTT  GAC TCATTCATT
                                |||| |||  ||| |||||||||
                                AAGA  TAG  TTG GGTGGGTGG
                                  GT   T_  _
GAM984   TCL6     5'  AGTGGATGGCCAAGTCCAAG   40461       T    ACA
                                TTTGG TTTG   TCATTCATT
                                ||||| ||||  |||||||||
                                GAACC GAAC   GGTAGGTGA
                                  T   C__
GAM984   TCL6     5'  AGTGTGTGTGGAGCCAAAGA   40462          G   _
                                TTTTTGGTTTT ACAT CATT
                                |||||||||| |||| ||||
                                AGAAACCGAGG TGTG GTGA
                                     _   T
GAM984   TCL6     3'  GATGGATGGCTGTTAAACGATC 40479          __    _
            GAAAA                  TTTTTGGTT  TTGACA TCATTCATT
                                |||||||||  |||||| |||||||||
                                AAAAGCTAG  AATTGT GGTAGGTAG
                                     CA     C
GAM984   TCL6     3'  GGTGGAGGAACAGGGCTGGAAA 40487      TG     ACA  A
                                TTTT  GTTTTG   TC TTCATT
                                ||||  ||||||   || ||||||
                                AAAG  CGGGAC   AG AGGTGG
                                  GT     A__  G
GAM984   TED      3'  AGTGAATGGGAGGGCGGGCCTG 32262     TT    TGACA_
            GAG                    TTT  GGTTT     TCATTCATT
                                |||  |||||     |||||||||
                                GAG  CCGGG     GGTAAGTGA
                                  GT    CGGGAG
GAM984   TIAM2    3'  GATGGAGAGCTGGTGGGGCCGA 25869         TT ACA__  A
            AGA                    TTTTTGGTT  G    TC TTCATT
                                ||||||||| |    || ||||||
                                AGAAGCCGG  T    AG AGGTAG
                                     GG GGTCG  _
GAM984   TINF2    3'  GATGGGTAGAACAAGACTGAGA 25872      TG     ACA  _
            A                     TTTT  GTTTTG   TC ATTCATT
                                ||||  ||||||   || |||||||
                                AAGA  CAGAAC   AG TGGGTAG
                                  GT     A__  A
GAM984   TINF2    3'  GGTGAGTGGGAAGGAGCAGAAA 25874       G   GACA
                                TTTTTG TTTT    TCATTCATT
                                |||||| ||||   |||||||||
                                AAAGAC AGGA    GGTGAGTGG
                                   G   AG__
GAM984   TONDU    5'  GGTGATGGTCCAGAATTAAGAG 33222          A__
                                TTTTTGGTTTTG   CATCATT
                                ||||||||||||  |||||||
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                                GAGAATTAAGAC  GTAGTGG
                                      CTG
GAM984  TPD52    3'  AGTGGATGAAGGTGGGTATTGG 18669    TG  T  G  A_
          GG                   TTT  GT TT AC  TCATTCATT
                               |||  || || ||  |||||||||
                               GGG  TA GG TG  AGTAGGTGA
                                 GT  T  G  GA
GAM984  TRIAD3   3'  GGGCGGATGAGTTGAGGTCGGG 96136      GT  TG  A    ATT
          AG                   TTTTTG  TT  AC TCATTC
                               ||||||  ||  || ||||||
                               GAGGGC  GA  TG AGTAGG
                                  TG  GT  _    CGGGC
GAM984  TRIM4    3'  AATGGCAGTGTTGGGATTAAAA 53403        TG   CAT
                               TTTTGGTTT  ACAT  TCATT
                               |||||||||  ||||  |||||
                               AAAATTAGG  TGTG  GGTAA
                                     GT   AC_
GAM984  TSC22    3'  AATGGATGACACAAAACTATGA 21211    T      ACA
          G                    TTT TGGTTTTG  TCATTCATT
                               ||| ||||||||  |||||||||
                               GAG ATCAAAAC  AGTAGGTAA
                                 T      AC_
GAM984  TSPAN-2  3'  AGTGAGTGTTTATAGGACTAAA 20374         ACAT
          AA                   TTTTTGGTTTTG   CATTCATT
                               ||||||||||||   ||||||||
                               AAAAATCAGGAT   GTGAGTGA
                                     ATTT
GAM984  TTTY12   5'  TGCTTCATGTGTACAGGACTAA 50030         _  T  TCATT
          GAA                   TTTTTGGTTTTG ACA CAT
                               |||||||||||| ||| |||
                               AAGAATCAGGAC TGT GTA
                                     A  _  CTTCGTG
GAM984  UBE3B    3'  GATGCCGGATTCGAAGCCAGGA 77445          C  ATT
          A                    TTTTTGGTTTTGA ATC  CATT
                               |||||||||||| |||  ||||
                               AAGGACCGAAGCT TAG  GTAG
                                     _  GCC
GAM984  ust3     5'  AGTGGGGTCAGGATCAAAA   94850          AT
                               TTTTGGTTTTGAC  CATT
                               ||||||||||||  ||||
                               AAAACTAGGACTG  GTGA
                                     GG
GAM984  VCX-2r   3'  AATGAATGTGTTGCAAATTGAA 96315     TG  _   T
          AA                   TTTT  GTTT TGACA CATTCATT
                               ||||  |||| ||||| ||||||||
                               AAAA  TAAA GTTGT GTAAGTAA
                                 GT   C   _
GAM984  VCX-8r   3'  AATGAATGTGTTGCAAATTGAA 33496     TG  _   T
          AA                   TTTT  GTTT TGACA CATTCATT
                               ||||  |||| ||||| ||||||||
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                                AAAA  TAAA GTTGT GTAAGTAA
                                  GT    C    _
GAM984  WBSCR17   3'  GATGGAGCTGGGTCAAGGACCA 82217         _    ATCA_
           GGGA                   TTTTTGGTT TTGAC    TTCATT
                                |||||||||  |||||    ||||||
                                AGGGACCAG AACTG    AGGTAG
                                     G    GGTCG
GAM984  WBSCR21   3'  GATGACTTGAGGCCAGGAG   49302         TG __
                                TTTTTGGTTT  A  CATC
                                ||||||||||  |  ||||
                                GAGGACCGGA  T  GTAG
                                     GT CA
GAM984  WBSCR22   3'  GGTGGGAGGATCATTTGAGGCC 34470         TG C__   A_
           AGGAG                  TTTTTGGTTT  A   ATC  TTCATT
                                ||||||||||  |   |||  ||||||
                                GAGGACCGGA  T   TAG  GGGTGG
                                     GT TAC   GA
GAM984  WDR9      3'  TAGAGTGTACAGGGCTAAAAG  39085          ACAT    ATT
                                TTTTTGGTTTTG    CATTC
                                ||||||||||||    |||||
                                GAAAATCGGGAC    GTGAG
                                      AT__     ATA
GAM984  WFDC3     3'  GATGAGAATTGTCAAGCTGGAG 98701      TG    T    TCA
           A                    TTTT  GTTT GACA   TTCATT
                                ||||  |||| ||||   ||||||
                                AGAG  CGAA CTGT   GAGTAG
                                  GT    _    TAA
GAM984  XLKD1     3'  GGTGGGTTGAAAGCCAAGGA   22925          _   A
                                TTTTTGGTTTT GAC TCATT
                                |||||||||||  ||| |||||
                                AGGAACCGAAA TTG GGTGG
                                     G   _
GAM984  YME1L1    3'  GGTGGATTGCTTGAGGCCAGGA 58437         TG _  TC
           G                    TTTTTGGTTT  A CA  ATTCATT
                                ||||||||||  | ||  |||||||
                                GAGGACCGGA  T GT  TAGGTGG
                                     GT C  __
GAM984  ZNF271    5'  GGTGAGAACAAGACCAAGA    96967          ACA
                                TTTTGGTTTTG   TCATT
                                ||||||||||   |||||
                                AGAACCAGAAC   AGTGG
                                      AAG
GAM984  ZNF297B   5'  GGTGGATCACTTGAAGCCAGGA 26668         TG CATC
           A                    TTTTTGGTTT  A    ATTCATT
                                ||||||||||  |    |||||||
                                AAGGACCGAA  T    TAGGTGG
                                     GT CAC_
GAM984  ZNF338    3'  AATGAGGGGTTGGAATTAAA   42248        TG  ATCA
                                TTTGGTTT  AC    TTCATT
                                ||||||||  ||    ||||||
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                                AAATTAAG  TG   GAGTAA
                                    GT  GG__
GAM984  ZNF361   5'  ATTGATGGCAGTTTTGGAGCCA 38271        TG _____   ATTCATT
          GAAG                   TTTTTGGTTT  A     CATC
                                 ||||||||||  |     ||||
                                 GAAGACCGAG  T     GTAG
                                     GT TTGACG      TTAC
GAM984  ZNF384   3'  TTTGGGCTGATGTAAGACTAGA 56799         A   _   TT
          G                     TTTTGGTTTTG CATCA TTCA
                                ||||||||||| ||||| ||||
                                GAGATCAGAAT GTAGT GGGT
                                      _   C   TTG
GAM984  ZWINT    3'  GATGGATGGTGGGAACAGGAAA 23905     TG    GA
                                TTTT  GTTTT  CATCATTCATT
                                ||||  |||||  ||||||||||
                                AAAG  CAAGG  GTGGTAGGTAG
                                  GA   __
GAM984  LOC113091 5'  GGTGGATGCATGGTGGGGCC   73315      GA  _
                                GGTTTT  CAT CATTCATT
                                ||||||  ||| ||||||||
                                CCGGGG  GTA GTAGGTGG
                                   TG   C
GAM984  LOC114928 3'  AATGAATATCAAAACTGAAAA  57390     TG      CATC
                                TTTT  GTTTTGA   ATTCATT
                                ||||  |||||||   |||||||
                                AAAA  CAAAACT   TAAGTAA
                                  GT      A___
GAM984  LOC114932 3'  GATTGGAGGTCAAAGTCAAAAG 73091      GT     A  AT_
                                TTTTTG  TTTGAC TC   TC
                                ||||||  |||||| ||   ||
                                GAAAAC  AAACTG AG   AG
                                   TG     G  GTT
GAM984  LOC115004 3'  GATGTCATGTTTAAACTGGAAG 73549     TG   _____
                                TTTT  GTTT    TGACATC
                                ||||  ||||    |||||||
                                GAAG  CAAA    ACTGTAG
                                  GT    TTTGT
GAM984  LOC115110 5'  GGTGAAGGATTTGAGTCCAGAA 72183       T  TG C   A
          G                     TTTTTGG TT  A ATC TTCATT
                                ||||||| ||  | ||| ||||||
                                GAAGACC GA  T TAG AAGTGG
                                    T  GT _   G
GAM984  LOC115123 3'  GATGATAATCAAAATCAAAAA  73593          C_
                                TTTTTGGTTTTGA  ATCATT
                                ||||||||||||  ||||||
                                AAAAACTAAAACT  TAGTAG
                                       AA
GAM984  LOC115209 3'  AATGATGTTTGAAGTGAAAA   59806      G   T
                                TTTTTG TTT GACATCATT
                                |||||| ||| |||||||||
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                                AAAAGT AAG TTGTAGTAA
                                   G   T
GAM984   LOC115297 3'  GATGAATAAGGACCAGAAA    73260          GA__
                                TTTTTGGTTTT    CATC
                                ||||||||||    ||||
                                AAAGACCAGGA    GTAG
                                      ATAA
GAM984   LOC115297 3'  GATGAGTAGATAAGACCATAAG 73261     T      GAC  _
                                TTT TGGTTTT   ATC ATTCATT
                                ||| |||||||   ||| |||||||
                                GAA ACCAGAA   TAG TGAGTAG
                                  T      ___   A
GAM984   LOC115708 3'  AGTGGGTGACCCTAATGCCAGG 73912        T   ACA
            AG                    TTTTTGGT TTG   TCATTCATT
                                ||||||||| |||   |||||||||
                                GAGGACCG AAT   AGTGGGTGA
                                     T   CCC
GAM984   LOC116236 3'  GGTGGGTGGATCACGAGGTCAG 74247       GT    ACA_
            GAG                    TTTTTG  TTTG    TCATTCATT
                                ||||||  ||||    |||||||||
                                GAGGAC  GAGC    GGTGGGTGG
                                   TG    ACTA
GAM984   LOC116437 3'  AATGGATGGGCAGGGATCTGAG 74323      T     GACA
            A                     TTTT GGTTTT    TCATTCATT
                                |||| ||||||    |||||||||
                                AGAG CTAGGG    GGTAGGTAA
                                  T     ACG_
GAM984   LOC118812 3'  AATGAATCAGAGCTGAGA    74363     TG      CA
                                TTT  GTTTTGA  TCATT
                                |||  |||||||  |||||
                                AGA  CGAGACT  AGTAA
                                  GT      A_
GAM984   LOC118851 5'  GATGTGTTAATACCAGAAG    76015        T     T
                                TTTTTGGT TTGACA CATT
                                |||||||| |||||| ||||
                                GAAGACCA AATTGT GTAG
                                     T     _
GAM984   LOC120400 3'  GATAAGGGATGCAAAACCAAGA 76062           A    AT___  ATT
            G                     TTTTTGGTTTTG CATC     TC
                                |||||||||||| ||||     ||
                                GAGAACCAAAAC GTAG     AG
                                      _    GGAAT
GAM984   LOC121642 5'  AATGAAAATGTGAAACTAGGAA 74561          G    CA
                                TTTTTGGTTTT ACAT  TTCATT
                                |||||||||| ||||  ||||||
                                AAGGATCAAAG TGTA  AAGTAA
                                      _    A_
GAM984   LOC122786 3'  GATGGAGTGGTCAAAATCATAA 74621     T        ATCA
            G                     TTT TGGTTTTGAC    TTCATT
                                |||  ||||||||||    ||||||
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                                GAA ACTAAAACTG    AGGTAG
                                  T        GTG_
GAM984   LOC123876 3'  GAACTGTCAGGGTCAGAG    74716       TT     TCA
                                TTTTGG  TTGACA   TTC
                                ||||||  ||||||   |||
                                GAGACT  GACTGT   AAG
                                   GG     C__
GAM984   LOC124145 3'  GATGGATGTTAAAGGATAAAAA 74724       G_       AT  ATT
                                TTTTTG  TTTTGACATC  TC
                                ||||||  ||||||||||  ||
                                AAAAAT  GAAATTGTAG  AG
                                   AG         GT
GAM984   LOC124222 3'  GGTGTCCAGGGCTAGGGA    74755          _
                                TTTTTGGTTTTG ACATC
                                |||||||||||| |||||
                                AGGGATCGGGAC TGTGG
                                       C
GAM984   LOC124460 5'  GATGGGGAAATCAAGGCCTGGA 76562     TT       CA  A
            G                    TTT  GGTTTTGA  TC TTCATT
                                |||  ||||||||  || ||||||
                                GAG  CCGGAACT  AG GGGTAG
                                  GT       AA  _
GAM984   LOC124842 3'  AATGGAAGCGGTCAGACTGGAG 76156     TG    T   ATCA
                                TTT  GTTT GAC    TTCATT
                                |||  |||| |||    ||||||
                                GAG  CAGA CTG    AGGTAA
                                  GT   _  GCGA
GAM984   LOC126031 5'  GGTGGGGAGGCAGGGCCA    74903        ACA  A
                                TGGTTTTG   TC TTCATT
                                ||||||||   || ||||||
                                ACCGGGAC   AG GGGTGG
                                     GG_  _
GAM984   LOC126167 3'  AAAAGAATGGTGTCCAGATTGG 74927      TG    T        ATT
            GAG                    TTTT  GTTT GACATCATTC
                                ||||  |||| ||||||||||
                                GAGG  TAGA CTGTGGTAAG
                                  GT    C         AAAAC
GAM984   LOC126208 3'  GACGTGCAAGACCAAGAG    74929          _ A
                                TTTTTGGTTTTG AC TC
                                |||||||||||| || ||
                                GAGAACCAGAAC TG AG
                                       G  C
GAM984   LOC126282 3'  GTCGCTTGATGTAAAAGCCAAA 74966          G     TTCATT
            AG                    TTTTTGGTTTT ACATCA
                                |||||||||||| ||||||
                                GAAAACCGAAA TGTAGT
                                       A     TCGCTGG
GAM984   LOC126302 3'  AATGATGTTAAAGTAAGAA    74982      GG
                                TTTT  TTTTGACATCATT
                                ||||  ||||||||||||
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                                AAGA  GAAATTGTAGTAA
                                  AT
GAM984   LOC127133 3'  GATGATCAAGAACCAGAAG   75130          _ _
                                TTTTTGGTTTT GA CATC
                                |||||||||| || ||||
                                GAAGACCAAGA CT GTAG
                                      A  A
GAM984   LOC127534 3'  GGTGGGAGGGTCACGGCTGAGA 75971     TG  TT   A  A
           G                     TTTT  GT  TGAC TC TTCATT
                                ||||  ||  |||| || ||||||
                                GAGA  CG  ACTG GG GGGTGG
                                  GT  GC   _ A
GAM984   LOC128239 3'  GATGTCAGTGGAACCAGAG   75237         ___
                                TTTTGGTTT   TGACATC
                                |||||||||   |||||||
                                GAGACCAAG   ACTGTAG
                                     GTG
GAM984   LOC128338 3'  GATGAATGCTGATAATCAGGAA 75251         TTGA  T
                                TTTTTGGTT    CA CATTCATT
                                |||||||||    || ||||||||
                                AAGGACTAA    GT GTAAGTAG
                                     TA__  C
GAM984   LOC128954 5'  GGTGGCTGAGACCAGGGA    76306          A_
                                TTTTTGGTTTTG  CATC
                                ||||||||||||  ||||
                                AGGGACCAGAGT  GTGG
                                      CG
GAM984   LOC130612 5'  AGTGACGTCAGGAGCAGAG   75465      G      A
                                TTTTG TTTTGAC TCATT
                                ||||| ||||||| |||||
                                GAGAC AGGACTG AGTGA
                                   G      C
GAM984   LOC130813 3'  GGTGGGTGTGGGTGGGGAC   76279      G  AT_
                                GTTTT AC   CATTCATT
                                ||||| ||   ||||||||
                                CAGGG TG   GTGGGTGG
                                   G  GGT
GAM984   LOC130951 3'  GATGATCACTTGAGGCCAGGAG 57941          TG C__     CATT
                                TTTTTGGTTT  A   ATCATT
                                ||||||||||  |   ||||||
                                GAGGACCGGA  T   TAGTAG
                                      GT CAC
GAM984   LOC133957 3'  AGTGACTCGAGGCCAGG     59847          CA
                                TTTGGTTTTGA  TCATT
                                ||||||||||  |||||
                                GGACCGGAGCT  AGTGA
                                      C_
GAM984   LOC135932 3'  AATGGGTTGGTATGAAGGCCAG 76693          GAC   _
           AAG                    TTTTTGGTTTT   ATCA TTCATT
                                ||||||||||   |||| ||||||
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                                GAAGACCGGAA   TGGT GGGTAA
                                      GTA    T
GAM984   LOC137492 3'  AATGGGACACAAAACCAAA    75791          ACA_
                                TTTGGTTTTG    TCATT
                                ||||||||||    |||||
                                AAACCAAAAC    GGTAA
                                      ACAG
GAM984   LOC138399 3'  AATGGATGACAATAAGAGCTTA 75847      T     GACA_
           AAG                    TTTT GGTTTT    TCATTCATT
                                ||||| ||||||    |||||||||
                                GAAA TCGAGA    AGTAGGTAA
                                  T     ATAAC
GAM984   LOC138639 3'  AGTGGGATCAGAGGCAGGAA   75878       G     CA
                                TTTTTG TTTTGA  TCATT
                                |||||| ||||||  |||||
                                AAGGAC GAGACT  GGTGA
                                    G     AG
GAM984   LOC139728 5'  GGATTAATGGTGGAGCCAGAG  75902         TGA      C
                                TTTTGGTTT   CATCATT ATT
                                |||||||||   ||||||| |||
                                GAGACCGAG   GTGGTAA TAG
                                      ___      T   GG
GAM984   LOC139795 3'  AATGAAGACTGAAACCAAGAA  75909          ACA  A
                                TTTTTGGTTTTG   TC TTCATT
                                ||||||||||||   || ||||||
                                AAGAACCAAAGT   AG AAGTAA
                                      C__  _
GAM984   LOC142955 5'  GGTGAATGATGTTAATCAG    76963       TT
                                TTGGT  TGACATCATTCATT
                                |||||  ||||||||||||||
                                GACTA  ATTGTAGTAAGTGG

GAM984   LOC143338 3'  ATGGTGTCAGACTAAAGA     77056          T
                                TTTTTGGTTT GACATCAT
                                |||||||||| ||||||||
                                AGAAATCAGA CTGTGGTA

GAM984   LOC143677 3'  ATGGATGGTGGCCCAGG      83892       TTTTGA
                                TTTGG      CATCATTCAT
                                |||||      ||||||||||
                                GGACC      GTGGTAGGTA
                                   CG____
GAM984   LOC143680 3'  CTGCTGATGGTGTTGTAATTAG 83902          T         CATT
           AAA                    TTTTTGGTT TGACATCATT
                                ||||||||| ||||||||||
                                AAAGATTAA GTTGTGGTAG
                                      T         TCGTCG
GAM984   LOC143902 3'  AGTGAGTACTTGTGTTAAAATA 77118       G         C___
           AAGAA                    TTTTT GTTTTGACAT    ATTCATT
                                ||||| ||||||||||    |||||||
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                                AAGAA TAAAATTGTG    TGAGTGA
                                  A         TTCA
GAM984   LOC143914 5'  AGCCTGGGTGTCTGAGACCGGG 77108          _     ATTCATT
           AG                    TTTTTGGTTTT GACATC
                                 |||||||||| ||||||
                                 GAGGGCCAGAG CTGTGG
                                       T     GTCCGA
GAM984   LOC143920 3'  GGTGAGTGCAAAGAGCTGGAAA 77116     TG    GACAT
                                 TTTT  GTTTT    CATTCATT
                                 ||||  |||||    ||||||||
                                 AAAG  CGAGA    GTGAGTGG
                                   GT    AAC__
GAM984   LOC144266 5'  GGTGTGGCTGGCAGAACTAGAA 77267          A _   TCATT
           G                     TTTTTGGTTTTG CA TCAT
                                 |||||||||||| || ||||
                                 GAAGATCAAGAC GT GGTG
                                       G  C    TGG
GAM984   LOC144347 3'  GGCGGATGTTGAGCCAGGAG   77307       T TG    AT
                                 TTTTTGGT T  ACATC  TC
                                 |||||||| |  |||||  ||
                                 GAGGACCG A  TGTAG  GG
                                     _ GT    GC
GAM984   LOC144481 3'  GATGGCTTGAGGCCAGGAG    84020        TG __
                                 TTTTTGGTTT  A  CATC
                                 |||||||||  |  ||||
                                 GAGGACCGGA  T  GTAG
                                       GT CG
GAM984   LOC144776 3'  GATGAGCAAAGCCAGAGA    77491         A_
                                 TTTTTGGTTTTG  CATC
                                 ||||||||||||  ||||
                                 AGAGACCGAAAC  GTAG
                                       GA
GAM984   LOC144811 3'  GTGTGGGCATGAGTTAGGGCTG 84108     TG      A   __   T
           GAAA                    TTTT  GTTTTGAC TCAT  TCAT
                                 ||||  |||||||| ||||  ||||
                                 AAAG  CGGGATTG AGTA  GGTG
                                   GT      _   CG   TGG
GAM984   LOC145501 3'  GATGTGCAGGGCTGGGAG    77768     TG    _
                                 TTTT  GTTTTG ACATC
                                 ||||  |||||| |||||
                                 GAGG  CGGGAC TGTAG
                                   GT    G
GAM984   LOC145508 3'  GATGACACCAAGTACAGAACCA 77776          _ ATCAT_
           AAAG                    TTTTTGGTTTTG AC     TCATT
                                 |||||||||||| ||     |||||
                                 GAAAACCAAGAC TG     AGTAG
                                       A  AACCAC
GAM984   LOC145566 5'  GATAAGTGTCAGGAGCAGAAG  77788       G       CAT
                                 TTTTTG TTTTGACAT   TC
                                 |||||| |||||||||   ||
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                                GAAGAC AGGACTGTG   AG
                                   G        AAT
GAM984   LOC145609 5'  GGTGGAGGTCTTCAGTGCCGAG 84367       T   C_  A
            G                    TTTTGGT TTGA  ATC TTCATT
                                 ||||||| ||||  ||| ||||||
                                 GGAGCCG GACT  TGG AGGTGG
                                    T   TC  _
GAM984   LOC145663 3'  GATTTGTACAGAGCTAGAGA   84425          _  TCAT
                                 TTTTTGGTTTTG ACA   TC
                                 |||||||||||| |||   ||
                                 AGAGATCGAGAC TGT   AG
                                       A  TT__
GAM984   LOC145719 5'  GTTTATGGTGTAGGGGCTGGGA 84468     TG   TG     TCATT
            G                    TTTT  GTTT  ACATCAT
                                 ||||  ||||  |||||||
                                 GAGG  CGGG  TGTGGTA
                                   GT   GA     TTTGG
GAM984   LOC145720 5'  GTTTATGGTGTAGGGGCTGGGA 84454     TG   TG     TCATT
            G                    TTTT  GTTT  ACATCAT
                                 ||||  ||||  |||||||
                                 GAGG  CGGG  TGTGGTA
                                   GT   GA     TTTGG
GAM984   LOC145725 3'  GGTGGGGGGATTTTGGGGCCG   77886      TG C   A
                                 TGGTTT  A ATC TTCATT
                                 ||||||  | ||| ||||||
                                 GCCGGG  T TAG GGGTGG
                                    GT T   G
GAM984   LOC145732 3'  GGTGGGGGGATTTTGGGGCCG   77898      TG C   A
                                 TGGTTT  A ATC TTCATT
                                 ||||||  | ||| ||||||
                                 GCCGGG  T TAG GGGTGG
                                    GT T   G
GAM984   LOC145761 5'  GTGGGAAGGTTTCAAGACTGAG 84484     TG     C   A   ATT
            GA                   TTTT  GTTTTGA ATC TTC
                                 ||||  ||||||| ||| |||
                                 AGGA  CAGAACT TGG AGG
                                   GT      T   A   GTGA
GAM984   LOC145783 3'  AGTGAGTGCAGTAAAGACCGG  77947       G  AT
                                 TTGGTTTT AC  CATTCATT
                                 |||||||| ||  ||||||||
                                 GGCCAGAA TG  GTGAGTGA
                                      A  AC
GAM984   LOC145815 5'  GATGGGTGAGAAGGCTAGGA   84519         GACA
                                 TTTTGGTTTT   TCATTCATT
                                 ||||||||||   |||||||||
                                 AGGATCGGAA   AGTGGGTAG
                                       G___
GAM984   LOC145825 5'  AGTGGGTGTCAACAAGCCAAAG 84535         __     ATTCATT
                                 TTTTGGTTT  TGACATC
                                 |||||||||  |||||||
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                                GAAACCGAA  ACTGTGG
                                    CA      GTGA
GAM984   LOC145826 5'  GGTGAGTGGGTGCAGGAGCCAG 84532          GA   _
                GGA                  TTTTTGGTTTT  CATC ATTCATT
                                     ||||||||||  |||| |||||||
                                     AGGGACCGAGG  GTGG TGAGTGG
                                       AC   G
GAM984   LOC145858 3'  AATGGGTGGCAAACAACATCAG 77999        T   ACA_
                GAA                  TTTTTGGT TTG    TCATTCATT
                                     |||||||| |||    |||||||||
                                     AAGGACTA AAC    GGTGGGTAA
                                        C   AAAC
GAM984   LOC145858 3'  ATGATGCTGAAGCCAGAAG    78000          GA
                                     TTTTTGGTTTT  CATCAT
                                     ||||||||||  ||||||
                                     GAAGACCGAAG  GTAGTA
                                       TC
GAM984   LOC145871 5'  GGTGGGGAACTGGTTAAAACCA 84552           ATCA__
                AAA                  TTTTGGTTTTGAC     TTCATT
                                     ||||||||||||      ||||||
                                     AAAACCAAAATTG     GGGTGG
                                       GTCAAG
GAM984   LOC145873 3'  GATGGAGTCAGGGCGGGG     78012     G       AT
                                     TTT GTTTTGAC  CATT
                                     ||| ||||||||  ||||
                                     GGG CGGGACTG  GTAG
                                       G       AG
GAM984   LOC146062 5'  AATGTCAGACTTTGGGGCCAGA 78142          TG CA  ATT
                AA                   TTTTTGGTTT  A  TC   CATT
                                     ||||||||||  |  ||   ||||
                                     AAAGACCGGG  T  AG   GTAA
                                        GT TC  ACT
GAM984   LOC146227 3'  TGGTGCGGAGCTGAAAG     78218      TG     A
                                     TTTT  GTTTTG CATCA
                                     ||||  |||||| |||||
                                     GAAA  CGAGGC GTGGT
                                       GT     _
GAM984   LOC146346 5'  GGTGAGGTCATTGTGGGGACCA 78403          G   TCA__
                GGGA                 TTTTTGGTTTT ACA     TTCATT
                                     ||||||||||| |||     ||||||
                                     AGGGACCAGGG TGT     GAGTGG
                                       G   TACTG
GAM984   LOC146429 3'  GATGGGACCAAAGTCAAGGCC  84668         ATCA__
                                     GGTTTTGAC     TTCATT
                                     |||||||||     ||||||
                                     CCGGAACTG     GGGTAG
                                        AAACCA
GAM984   LOC146499 3'  ATGGTGTCAGACTAAAG     71365          T
                                     TTTTGGTTT GACATCAT
                                     |||||||| ||||||||
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                                GAAATCAGA CTGTGGTA
                                        _
GAM984   LOC146603 5'  GGTGAGGCTGAAAGCCAAAGA  78602          GA  TCA
                                TTTTTGGTTTT  CA   TTCATT
                                |||||||||||  ||   ||||||
                                AGAAACCGAAA  GT   GAGTGG
                                      __ CG_
GAM984   LOC146667 5'  GCTGTTTCAGGGCCAGGG    84713          CAT  TT
                                TTTTGGTTTTGA   CA  C
                                ||||||||||||   ||  |
                                GGGACCGGGACT   GT  G
                                      TT_  CG
GAM984   LOC146822 3'  AGTGGGTGAGGGGACCAGGAG  78745          TGACA
                                TTTTTGGTTT    TCATTCATT
                                |||||||||     |||||||||
                                GAGGACCAGG    AGTGGGTGA
                                      GG___
GAM984   LOC146901 3'  ATCTTTGGTGTCAGATCCAAAA 84890        T        TTCATT
           A                     TTTTTGG TTTGACATCA
                                 |||||||  ||||||||||
                                 AAAAACC AGACTGTGGT
                                    T        TTCTA
GAM984   LOC146957 3'  AATGGTACTTTGAGGCCAGGAG 78810          TG C__
                                TTTTTGGTTT  A   ATCATT
                                |||||||||  |   ||||||
                                GAGGACCGGA  T   TGGTAA
                                      GT TCA
GAM984   LOC147004 3'  AGTGGATGAAACTGAAGCCTAG 84965      T      ACA
           AA                    TTTT GGTTTTG   TCATTCATT
                                 ||||  |||||||   |||||||||
                                 AAGA CCGAAGT   AGTAGGTGA
                                   T      CAA
GAM984   LOC147118 5'  GGTGTTCGGGATCAAGAG    85063           _
                                TTTTTGGTTTTGA CATC
                                |||||||||||| ||||
                                GAGAACTAGGGCT GTGG
                                      T
GAM984   LOC147165 3'  GGTGGGTGATGGCTCCGGGAG  85088        TTTTGA
                                TTTTTGG     CATCATTCATT
                                |||||||     ||||||||||
                                GAGGGCC     GTAGTGGGTGG
                                    TCG___
GAM984   LOC147176 3'  ATGGTGTCAGACTAAAG     61145         T
                                TTTTGGTTT GACATCAT
                                |||||||| ||||||||
                                GAAATCAGA CTGTGGTA
                                        _
GAM984   LOC147407 5'  GCTCAGATGATGTCACAGGTTA 76820        TT _        CATT
           AAAA                   TTTTTGG  T TGACATCATT
                                  |||||||  | ||||||||||
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                                AAAAATT  A ACTGTAGTAG
                                   GG C        ACTCGG
GAM984  LOC147817 5'  GATGAGAAAAGTTGGAGCTGGA 79180     TG   TG  ATCA
          GA                     TTTT  GTTT  AC   TTCATT
                                 ||||  ||||  ||   ||||||
                                 AGAG  CGAG  TG   GAGTAG
                                   GT   GT  AAAA
GAM984  LOC148014 3'  GGTGGACGATGCCAGGAA    79313        T  A_
                                 TTTTTGGT TTG  CATC
                                 ||||||||  |||  ||||
                                 AAGGACCG AGC  GTGG
                                     T  AG
GAM984  LOC148166 5'  GATGAGTGAGTGCCAGGGGCTG 79416     TG    GA_ _
          GGGA                    TTTT  GTTTT  CA TCATTCATT
                                  ||||  |||||  || |||||||||
                                  AGGG  CGGGG  GT AGTGAGTAG
                                    GT    ACC  G
GAM984  LOC148166 3'  GGTGGGAGGATTGCTTGAGACC 79419         TG _ _ A_
          AGGAG                    TTTTTGGTTT  A CA TC  TTCATT
                                   ||||||||||  | || ||  ||||||
                                   GAGGACCAGA  T GT AG  GGGTGG
                                      GT C  T  GA
GAM984  LOC148183 3'  AGTGAGAGTTTCAGGACCAGG  85260          C  CA
                                  TTTGGTTTTGA AT  TTCATT
                                  ||||||||||| ||  ||||||
                                  GGACCAGGACT TG  GAGTGA
                                     T  A_
GAM984  LOC148343 3'  GGTGGATTGCTTGAGGCCAGGA 79547         TG _  TC
          G                      TTTTTGGTTT  A CA  ATTCATT
                                 ||||||||||  | ||  |||||||
                                 GAGGACCGGA  T GT  TAGGTGG
                                    GT C  __
GAM984  LOC148397 5'  AGTGGATTTAGGATAAAACCGA 79559          ACATC_
          GAA                     TTTTTGGTTTTG     ATTCATT
                                  ||||||||||||     |||||||
                                  AAGAGCCAAAAT     TAGGTGA
                                      AGGATT
GAM984  LOC148697 3'  AATGGATGAGTGCTGGACGAAG 79670      G   TGACA
          AA                      TTTTT GTTT    TCATTCATT
                                  |||||  ||||    |||||||||
                                  AAGAA CAGG    AGTAGGTAA
                                    G   TCGTG
GAM984  LOC148709 5'  GGTGGGCATAGGCCAGAAG   79697         _  A_
                                 TTTTTGGTTT TG  CATC
                                 ||||||||||  ||  ||||
                                 GAAGACCGGA AC  GTGG
                                     T  GG
GAM984  LOC148760 3'  AATGAATGAATTGAATTGAAAG 85359     TG   TGACA
                                 TTTT  GTTT    TCATTCATT
                                 ||||  ||||    |||||||||
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                                GAAA  TAAG    AGTAAGTAA
                                  GT    TTA__
GAM984   LOC148823 3'  GATGAGATGCTTGGGACCAGAA 59893          TG _   AT
           G                     TTTTTGGTTT  A CATC  TCATT
                                 ||||||||||  | ||||  |||||
                                 GAAGACCAGG  T GTAG  AGTAG
                                       GT C   __
GAM984   LOC148887 5'  GATGGGCAGAAGCCGGAAA   85402          GA__
                                 TTTTTGGTTTT   CATC
                                 ||||||||||    ||||
                                 AAAGGCCGAAG   GTAG
                                       ACGG
GAM984   LOC148930 3'  AGTGGATGTTGGAAAAACCAAA 79840          GA  T
           G                     TTTTGGTTTT  CA CATTCATT
                                 ||||||||||  || ||||||||
                                 GAAACCAAAA  GT GTAGGTGA
                                       AG  T
GAM984   LOC148936 5'  GATGTGAGATGTGGAGTCAAGA 85455       GT   G    ATT
           G                     TTTTTG  TTT ACATC   CATT
                                 ||||||  ||| |||||   ||||
                                 GAGAAC  AGG TGTAG   GTAG
                                    TG   _    AGT
GAM984   LOC149076 3'  GGTGCTGCTAAGACCGAGAA   79882          A  T
                                 TTTTTGGTTTTG CA CATT
                                 ||||||||||||| || ||||
                                 AAGAGCCAGAAT GT GTGG
                                       C  C
GAM984   LOC149095 5'  GATGAGTGGTGCTTCCCCAAAA 79892       TTTTGA
                                 TTTTGG     CATCATTCATT
                                 ||||||     ||||||||||
                                 AAAACC     GTGGTGAGTAG
                                    CCTTC_
GAM984   LOC149113 3'  AATGAGGTAGGAGAGTCAGAAT 79893           A_  AT___
           TAGAGA                  TTTTTGGTTTTGAC  TC    TCATT
                                 ||||||||||||||  ||    |||||
                                 AGAGATTAAGACTG  AG    AGTAA
                                       AG  GATGG
GAM984   LOC149117 3'  AGTGATCTGGGACCAAAGA   85507         TT AC
                                 TTTTTGGTT  G  ATCATT
                                 |||||||||  |  ||||||
                                 AGAAACCAG  T  TAGTGA
                                       GG C_
GAM984   LOC149153 3'  AATGAGTGGGGACAAGTCACAG 85525     GT_   ACA
           A                     TTTG   TTTG   TCATTCATT
                                 ||||   ||||   |||||||||
                                 AGAC   GAAC   GGTGAGTAA
                                   ACT    AGG
GAM984   LOC149153 3'  GGTGAGTGGGACTAAAAGCCAG 85529         GACA_
           GA                    TTTTGGTTTT    TCATTCATT
                                 ||||||||||    |||||||||
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                                AGGACCGAAA    GGTGAGTGG
                                    ATCAG
GAM984  LOC149267 3'  GATGGGGGTCCAGAGCTAAG  57478        _ A_
                                TTTGGTTTTG AC  TCATT
                                |||||||||| ||  |||||
                                GAATCGAGAC TG  GGTAG
                                    C  GG
GAM984  LOC149271 5'  AGTGAGTGATGGAGGAGGAACT 79995        GA___
          AGAA                    TTTTGGTTTT    CATCATTCATT
                                |||||||||    ||||||||||
                                AAGATCAAGG    GTAGTGAGTGA
                                    AGGAG
GAM984  LOC149426 3'  GATGGGGCAGGACCAGAA    85573         ACA
                                TTTTGGTTTTG   TCATT
                                ||||||||||   |||||
                                AAGACCAGGAC   GGTAG
                                    GG_
GAM984  LOC149448 3'  GGTGGGAGGATCGGTTGAGGCC 85580        TG __  A_
          AGGAG                   TTTTTGGTTT  AC  ATC  TTCATT
                                |||||||||  ||  |||  ||||||
                                GAGGACCGGA  TG  TAG  GGGTGG
                                    GT  GC   GA
GAM984  LOC149464 5'  GATGGGTAGGGAGTGAGATCAG 85592        ACA  _
          AG                    TTTTGGTTTTG   TC ATTCATT
                                ||||||||||   || |||||||
                                GAGACTAGAGT   GG TGGGTAG
                                    GAG  A
GAM984  LOC149703 3'  GATGGGGGTCAAAGCAAAGAA  85822      G      A_
                                TTTTT GTTTTGAC  TCATT
                                ||||| ||||||||  |||||
                                AAGAA CGAAACTG  GGTAG
                                   A       GG
GAM984  LOC149706 5'  AGTGGGTGGGCAGGACTGGAA  85801     TG     ACA
                                TTT  GTTTTG   TCATTCATT
                                |||  ||||||   |||||||||
                                AAG  CAGGAC   GGTGGGTGA
                                  GT     G__
GAM984  LOC149706 5'  GGTGGGTGGAATCCCAAGGCTG 85808     TG     ACA__
          GGG                     TTT  GTTTTG    TCATTCATT
                                |||  ||||||    |||||||||
                                GGG  CGGAAC    GGTGGGTGG
                                  GT     CCTAA
GAM984  LOC149832 5'  GGTGGATGTCCTCAGGGGCCAA 85868        _  CAT
          GAA                     TTTTTGGTTT TGA   CATTCATT
                                |||||||||| |||   ||||||||
                                AAGAACCGGG ACT   GTAGGTGG
                                    G   CCT
GAM984  LOC149837 5'  AATGAGGATCACACAGACCAAG 85889        _ AC   A
          AG                      TTTTTGGTTT TG  ATC TTCATT
                                |||||||||| ||  ||| ||||||
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                                GAGAACCAGA AC  TAG GAGTAA
                                      C  AC   _
GAM984   LOC149844 3'  AATGAATGGTAAAGACTTGGAG 80343     TT     GAC
                                TTT  GGTTTT   ATCATTCATT
                                |||  ||||||   ||||||||||
                                GAG  TCAGAA   TGGTAAGTAA
                                  GT     A__
GAM984   LOC149844 3'  AATGAGTGGTAAAGTCAAGGTC 80344    TG _      ___
           TGGG                   TT  G TTTTGAC   ATCATTCATT
                                || | |||||||   ||||||||||
                                GG  C GGAACTG   TGGTGAGTAA
                                 GT T      AAA
GAM984   LOC149844 3'  GATGGTGCTGTCAAGGCTATGG 80345    TT        T   T
           A                    TT  TGGTTTTGACA CAT CATT
                                ||  |||||||||||| ||| ||||
                                AG  ATCGGAACTGT GTG GTAG
                                 GT         C  _
GAM984   LOC149911 3'  AGTGAGTGAAGAGTCAAA    85872       A__
                                TTTGAC   TCATTCATT
                                ||||||   |||||||||
                                AAACTG   AGTGAGTGA
                                   AGA
GAM984   LOC149935 3'  TGATGGTTATCATGGTGTCAGT 60937      TG TT       _____
           GTTGGAAG               TTTT  G  TTGACATCAT    TCATT   G
                                ||||  |  ||||||||||    |||||  |
                                GAAG  T  GACTGTGGTA    GGTAG   T
                                  GT GT        CTATT
GAM984   LOC149992 5'  GGCGGGTGCGGGACTGAAGA   80377     TG     A    AT
                                TTTT  GTTTTG CATC  TC
                                ||||  |||||| ||||  ||
                                AGAA  CAGGGC GTGG  GG
                                  GT     _    GC
GAM984   LOC150051 3'  GGTGATCTTGTTGAAAACAAAA 85954       G   TG   TCAT
           A                    TTTTTG TTT  ACA    TCATT
                                ||||||| |||  |||    |||||
                                AAAAAC AAA  TGT    AGTGG
                                   A   GT   TCT_
GAM984   LOC150142 5'  AGTGAAGGAATTAGGGCCGAG  80400          CA  A
                                TTTGGTTTTGA  TC TTCATT
                                ||||||||||  || ||||||
                                GAGCCGGGATT  AG AAGTGA
                                      A_  G
GAM984   LOC150197 3'  GATGGATTAAAGTGGAACCAAG 80423        TT ACATC
                                TTTGGTT  G    ATTCATT
                                |||||||  |    |||||||
                                GAACCAA  T    TAGGTAG
                                    GG GAAAT
GAM984   LOC150197 3'  GGTGGGCTCAGGGCCAGGG   80426           ___
                                TTTTGGTTTTGA   CATC
                                ||||||||||||   ||||
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                                GGGACCGGGACT  GTGG
                                      CGG
GAM984  LOC150245 5' GGTGGGGACAAGGCCGGGAG  86118          ACA
                                TTTTTGGTTTTG  TCATT
                                ||||||||||||  |||||
                                GAGGGCCGGAAC  GGTGG
                                      AGG
GAM984  LOC150271 5' AGTGAATGTCAAGGCAGGAAG  86132     TG       _
                                TTTT  GTTTTGACAT CATT
                                ||||  |||||||||| ||||
                                GAAG  CGGAACTGTA GTGA
                                  GA        A
GAM984  LOC150271 5' AGTGAGTGAAGGGAACCTGGGA 86133    TT    GACA
                                TTT  GGTTTT   TCATTCATT
                                |||  ||||||   |||||||||
                                AGG  CCAAGG   AGTGAGTGA
                                  GT    GA__
GAM984  LOC150299 3' GATGAAGCTTCATGTCGGACTA 86168        T    CA___
           AAG                    TTTTGGTTT GACAT    TTCATT
                                |||||||||  |||||    ||||||
                                GAAATCAGG CTGTA    AAGTAG
                                     _    CTTCG
GAM984  LOC150378 3' GATGGGTGGCAGAAAGCAGGAG 80557      G   GACA
                                TTTTTG TTTT   TCATTCATT
                                ||||||  ||||   |||||||||
                                GAGGAC AAAG   GGTGGGTAG
                                   G   AC__
GAM984  LOC150481 3' GGTGGGTGGATCACGAGGTCAA 80713      GT   ACA_
           GAG                    TTTTTG  TTTG   TCATTCATT
                                ||||||  ||||   |||||||||
                                GAGAAC  GAGC   GGTGGGTGG
                                   TG   ACTA
GAM984  LOC150519 3' GATGAATGAAGAAATCAGAGG  80730         GACA
                                TTTTTGGTTTT   TCATTCATT
                                ||||||||||   |||||||||
                                GGAGACTAAAG   AGTAAGTAG
                                      A___
GAM984  LOC150527 3' TAGTGAGTGGTGCTACGGAAAG 80734    TG   GA_____
           GCTGGGAG                TTTT  GTTTT     CATCATTCATT  A
                                ||||  |||||     ||||||||||  |
                                GAGG  CGGAA     GTGGTGAGTGA  T
                                  GT    AGGCATC
GAM984  LOC150622 5' GATGGATGAGTTACAGAACTGG 80764    TG    ACA_
           AG                   TTT  GTTTTG   TCATTCATT
                                |||  ||||||   |||||||||
                                GAG  CAAGAC   AGTAGGTAG
                                  GT    ATTG
GAM984  LOC150819 5' AGTGAAATTGAGTCAGAAC   86308        A  __
                                GTTTTGAC TCA  TTCATT
                                |||||||| |||  ||||||
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                                CAAGACTG AGT  AAGTGA
                                    _  TA
GAM984  LOC150889 5'  GGTGTCTGGTCTTGGAGTCAAG 80817      GT  TG C   TT
          AA                    TTTTTG  TT  A ATCA  CATT
                                ||||||  ||  | ||||  ||||
                                AAGAAC  AG  T TGGT  GTGG
                                   TG  GT C   CT
GAM984  LOC150946 3'  GATCTATGTCGAGACTGAGG  86347    TG       CAT
                                TTT  GTTTTGACAT   TC
                                |||  ||||||||||   ||
                                GGA  CAGAGCTGTA   AG
                                  GT        TCT
GAM984  LOC151007 3'  AATGAATGGTGTAAGCTGAA  80899    TG   TG
                                TT  GTTT  ACATCATTCATT
                                ||  ||||  ||||||||||||
                                AA  CGAA  TGTGGTAAGTAA
                                 GT   __
GAM984  LOC151009 3'  GGTGAATGATCCTGCCAGGA  86374       TTTGAC
                                TTTTGGT     ATCATTCATT
                                |||||||     ||||||||||
                                AGGACCG     TAGTAAGTGG
                                    TCC___
GAM984  LOC151056 3'  AATGAGGTTGTCGAGACTGGGA 80922     TG       TCA
          A                      TTTT  GTTTTGACA   TTCATT
                                 ||||  |||||||||   ||||||
                                 AAGG  CAGAGCTGT   GAGTAA
                                   GT        TG_
GAM984  LOC151121 5'  AATGAAAATAAATCCAGACCAA 80931         T  CATCA_
          GAA                     TTTTTGGTTT GA     TTCATT
                                  ||||||||||  ||     ||||||
                                  AAGAACCAGA CT     AAGTAA
                                       C  AAATAA
GAM984  LOC151124 5'  GATGGACTGGATGTTGGAACAG 86415     TG   TG    A__
          GAAG                      TTTT  GTTT  ACATC   TTCATT
                                    ||||  ||||  |||||   ||||||
                                    GAAG  CAAG  TGTAG   AGGTAG
                                      GA   GT    GTC
GAM984  LOC151361 5'  GATGGATGGTTCCGGCCAGAG  86504       TT  C
                                TTTTGGTT  GA ATCATTCATT
                                ||||||||  || ||||||||||
                                GAGACCGG  CT TGGTAGGTAG
                                    C_  _
GAM984  LOC151996 5'  GATGAGGCCCGTCAGAGTCAAG 86721      GT     ATCA
          AG                      TTTTTG  TTTGAC    TTCATT
                                  ||||||  ||||||    ||||||
                                  GAGAAC  AGACTG    GAGTAG
                                     TG     CCCG
GAM984  LOC152002 3'  GAACTGTCGGGACCAGGAA   81267            TCA
                                TTTTTGGTTTTGACA   TTC
                                |||||||||||||||   |||
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                                AAGGACCAGGGCTGT   AAG
                                      C__
GAM984   LOC152078 3'  ATGAATGAATTGTCAAAA    81285        __
                                TTTTGACA  TCATTCAT
                                ||||||||  ||||||||
                                AAAACTGT  AGTAAGTA
                                    TA
GAM984   LOC152215 3'  AATGCAGATGTTAAGGATTGGA 81330     TG  _      ATT
           AA                     TTTT  GTT TTGACATC   CATT
                                ||||  ||| ||||||||   ||||
                                AAAG  TAG AATTGTAG   GTAA
                                  GT   G       AC_
GAM984   LOC152263 3'  GTGAGTTGTCAGATCAAAG    86858        T   TC     T
                                TTTTGGTTT GACA  ATTCAT
                                ||||||||| ||||  ||||||
                                GAAACTAGA CTGT  TGAGTG
                                    _   __     T
GAM984   LOC152286 5'  GATGATTTCAGAACCTGAGA   86809     T      C
                                TTTT GGTTTTGA ATCATT
                                |||| |||||||| ||||||
                                AGAG CCAAGACT TAGTAG
                                  T       T
GAM984   LOC152399 3'  GATGAATGAGGTCATGCTGGGA 59898     TG  TT    A
           A                     TTTT  GT  TGAC TCATTCATT
                                ||||  ||  |||| |||||||||
                                AAGG  CG  ACTG AGTAAGTAG
                                  GT  T_   G
GAM984   LOC152441 3'  AGTGAAGGACGCTGAGACCAAG 86915          ACA  A
           AA                     TTTTTGGTTTTG   TC TTCATT
                                ||||||||||||   || ||||||
                                AAGAACCAGAGT   AG AAGTGA
                                      CGC  G
GAM984   LOC152441 5'  GGTGAGGATGTGGGGGTTGAAA 86919     TG TT  G    A
           G                      TTTT  G  TT ACATC TTCATT
                                ||||  |  || ||||| ||||||
                                GAAA  T  GG TGTAG GAGTGG
                                  GT GG  G    _
GAM984   LOC152790 5'  AGTGAGTTTTGGGGCCAGA    87057        TG CATC
                                TTTGGTTT  A    ATTCATT
                                ||||||||  |    |||||||
                                AGACCGGG  T    TGAGTGA
                                    GT T___
GAM984   LOC152790 5'  AGTGGGTAAGGTGTGAAGATTA 87058          G    __
           AAGA                    TTTTTGGTTTT ACATC  ATTCATT
                                ||||||||||| |||||  |||||||
                                AGAAATTAGAA TGTGG  TGGGTGA
                                      G    AA
GAM984   LOC152794 5'  GGTGAATGGAATGAGCTGGAG  81560     TG    TGACA
                                TTT  GTTT     TCATTCATT
                                |||  ||||    |||||||||
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                                GAG  CGAG    GGTAAGTGG
                                  GT   TAA__
GAM984   LOC152925 3'  AGTGAAAGAAGTGAGAACTAGG 81615          G  A  A
           AA                     TTTTTGGTTTT AC TC TTCATT
                                  |||||||||||| || || ||||||
                                  AAGGATCAAGA TG AG AAGTGA
                                        G  A  A
GAM984   LOC153232 3'  AGTGAGAGACCTTGGGACCAG  87177        TG CA  A
                                  TTGGTTT  A  TC TTCATT
                                  |||||||  |  || ||||||
                                  GACCAGG  T  AG GAGTGA
                                      GT CC  A
GAM984   LOC153453 5'  AGTGGATGGGAAAAACCAAAA  81697          GACA
                                  TTTTGGTTTT   TCATTCATT
                                  ||||||||||   |||||||||
                                  AAAACCAAAA   GGTAGGTGA
                                       AG__
GAM984   LOC153514 5'  GATGGATGGGATGACCTGGGA  81711     TT   TTGACA
                                  TTT  GGTT     TCATTCATT
                                  |||  ||||     |||||||||
                                  AGG  CCAG     GGTAGGTAG
                                    GT   TAG___
GAM984   LOC153561 3'  GGTGGGAGGATTGCTTGAGGCC 81752          TG _  _  A_
           AGGAG                    TTTTTGGTTT  A CA TC  TTCATT
                                  ||||||||||  | || ||  ||||||
                                  GAGGACCGGA  T GT AG  GGGTGG
                                       GT C  T  GA
GAM984   LOC153592 3'  GATGTGGGTCAGAGGCAGAGA  87246       G      A   _
                                  TTTTTG TTTTGAC TCAT TC
                                  |||||| ||||||| |||| ||
                                  AGAGAC GAGACTG GGTG AG
                                     G      _   T
GAM984   LOC153651 3'  ATGAATTTGGAATCAAGAA   81797          TG CATC
                                  TTTTTGGTTT  A   ATTCAT
                                  ||||||||||  |   ||||||
                                  AAGAACTAAG  T   TAAGTA
                                       GT ____
GAM984   LOC153727 3'  GATGAATGCTGCAGAGGCCAAA 87363         GA  T
                                  TTTGGTTTT  CA CATTCATT
                                  |||||||||  || ||||||||
                                  AAACCGGAG  GT GTAAGTAG
                                       AC  C
GAM984   LOC153733 5'  GTGGTTTCGGAGTCGAGGA   81802       GT    C
                                  TTTTTG  TTTGA ATCAT
                                  ||||||  ||||| |||||
                                  AGGAGC  AGGCT TGGTG
                                     TG    T
GAM984   LOC154084 5'  AGTGAGTGATTGGAACTTAGAG 87376      T    TG CA
                                  TTTT GGTTT  A  TCATTCATT
                                  |||| |||||  |  |||||||||
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                                GAGA TCAAG  T  AGTGAGTGA
                                  T    GT __
GAM984   LOC154403 3'  TAGGAGAGTCAGAATTAGAGA  81982          A  A   ATT
                                TTTTTGGTTTTGAC TC TTC
                                |||||||||||||| || |||
                                AGAGATTAAGACTG AG AGG
                                       _ _  ATG
GAM984   LOC154790 5'  GATGGGTGAAAGAAATCAAGA  82042        GACA
                                TTTTGGTTTT   TCATTCATT
                                ||||||||||   |||||||||
                                AGAACTAAAG   AGTGGGTAG
                                     AA__
GAM984   LOC154790 5'  TGCTGGCTGTGATTCAGAGCCA 82043          C   __  TT
           GAAG                   TTTTTGGTTTTGA ATCAT  TCA
                                |||||||||||||| |||||  |||
                                GAAGACCGAGACT TAGTG  GGT
                                      _    TC  CGTG
GAM984   LOC154992 3'  TAGGAGAGTCAGAATTAGAGA  82141          A  A   ATT
                                TTTTTGGTTTTGAC TC TTC
                                |||||||||||||| || |||
                                AGAGATTAAGACTG AG AGG
                                       _ _  ATG
GAM984   LOC155036 5'  GGTGACTGGTTGGAGCCTGGAA 87615    TT   TG  AT  T
                                TTT  GGTTT  AC  CA TCATT
                                |||  |||||  ||  || |||||
                                AAG  CCGAG  TG  GT AGTGG
                                  GT    GT  __  C
GAM984   LOC155054 3'  AGTGAAGAAATGTTACAGCCAG 82198        T    CA_
           GAA                    TTTTTGGTT TGACAT   TTCATT
                                |||||||||  ||||||   ||||||
                                AAGGACCGA ATTGTA   AAGTGA
                                     C     AAG
GAM984   LOC155081 5'  GATGAATCTGAGGAGGAGCCGG 82213         GACA  __
           AGA                    TTTTTGGTTTT   TCA  TTCATT
                                ||||||||||   |||  ||||||
                                AGAGGCCGAGG   AGT  AAGTAG
                                      AGG_  CT
GAM984   LOC157226 5'  AATGAGCAGCAAGGCCGAGA   64637         ACA_
                                TTTTGGTTTTG   TCATT
                                ||||||||||   |||||
                                AGAGCCGGAAC   AGTAA
                                      GACG
GAM984   LOC157273 5'  GGTGAGGCTGGATGAAGCCAGG 87725         GA_  TCA
           G                     TTTTGGTTTT   CA   TTCATT
                                ||||||||||   ||   ||||||
                                GGGACCGAAG   GT   GAGTGG
                                      TAG  CG_
GAM984   LOC157586 3'  GATGGAGTTCACCGAGGCTGAG 82400     TG    ACATCA
           AG                     TTTT  GTTTTG    TTCATT
                                ||||  ||||||    ||||||
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                                GAGA  CGGAGC     AGGTAG
                                  GT     CACTTG
GAM984   LOC157621 3'  AGTGGATGTGGAGGGAATTGAA 87788     TG    GA_  T
           G                     TTT  GTTTT   CA CATTCATT
                                 |||  |||||   || ||||||||
                                 GAA  TAAGG   GT GTAGGTGA
                                   GT    GAG  _
GAM984   LOC157622 3'  AGTGGATGTGGAGGGAATTGAA 87795     TG    GA_  T
           G                     TTT  GTTTT   CA CATTCATT
                                 |||  |||||   || ||||||||
                                 GAA  TAAGG   GT GTAGGTGA
                                   GT    GAG  _
GAM984   LOC157660 3'  GGTGAGATTGTCAAAATGGGA  87806     G       TCA
                                 TTT GTTTTGACA   TTCATT
                                 |||  |||||||||   ||||||
                                 AGG TAAAACTGT   GAGTGG
                                   G       TA_
GAM984   LOC157663 3'  GGTGTCTAGAATTAAAGA     82453          _
                                 TTTTTGGTTTT GACATC
                                 ||||||||||| ||||||
                                 AGAAATTAAGA CTGTGG
                                        T
GAM984   LOC157858 3'  GTGATGTTAAATCAGAAA     87894          T
                                 TTTTTGGTTT GACATCAT
                                 |||||||||| ||||||||
                                 AAAGACTAAA TTGTAGTG
                                           _
GAM984   LOC157958 3'  AATGGCAAAAGTCACAGCCGGA 82527         T    ATCAT
           G                     TTTTGGTT TGAC     TCATT
                                 |||||||| ||||     |||||
                                 GAGGCCGA ACTG     GGTAA
                                      C    AAAAC
GAM984   LOC158088 5'  AGTGGGATCGGAGGCCAGAAG  87969          _  CA
                                 TTTTTGGTTTT GA  TCATT
                                 |||||||||| ||  |||||
                                 GAAGACCGGAG CT  GGTGA
                                        G  AG
GAM984   LOC158088 3'  GGTGGGTGGATCACGAGGTCAG 87976       GT    ACA_
           GAG                     TTTTTG  TTTG    TCATTCATT
                                 ||||||  ||||   |||||||||
                                 GAGGAC  GAGC    GGTGGGTGG
                                    TG    ACTA
GAM984   LOC158107 3'  GAATGTTCAGGATTAAAAG    87981           CAT
                                 TTTTTGGTTTTGA   CATTC
                                 ||||||||||||   |||||
                                 GAAAATTAGGACT   GTAAG
                                         T__
GAM984   LOC158117 3'  GGTGGGGTCAGGGCTGGGG    82613     TG       AT
                                 TTT  GTTTTGAC  CATT
                                 |||  ||||||||  ||||
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                                GGG  CGGGACTG  GTGG
                                  GT       GG
GAM984   LOC158125 5'  GGTGAGTGAGCTGGGAGCCAAG 82620         GACA
                                TTTGGTTTT    TCATTCATT
                                |||||||||    |||||||||
                                GAACCGAGG    AGTGAGTGG
                                     GTCG
GAM984   LOC158187 3'  GGTGGGTGGATCACGAGGTCAG 87996       GT    ACA_
           GAG                    TTTTTG  TTTG    TCATTCATT
                                |||||||  ||||    |||||||||
                                GAGGAC  GAGC    GGTGGGTGG
                                   TG    ACTA
GAM984   LOC158236 5'  GATGGGTGCTCAGAGGAGCTAA 88009         GACAT_
           GG                     TTTTGGTTTT     CATTCATT
                                ||||||||||     ||||||||
                                GGAATCGAGG     GTGGGTAG
                                     AGACTC
GAM984   LOC158276 3'  ATGGTGTCAGACTAAAGA     82735          T
                                TTTTTGGTTT GACATCAT
                                |||||||||| ||||||||
                                AGAAATCAGA CTGTGGTA
                                          _
GAM984   LOC158281 3'  AATGAGTGATTTTTCTTAGAAG 82733       G     C____
           CAGAG                    TTTTG TTTTGA     ATCATTCATT
                                |||||  ||||||    ||||||||||
                                GAGAC AAGATT    TAGTGAGTAA
                                   G     CTTTT
GAM984   LOC158288 3'  GGTGGGCAGATCTCAAGGTCAG 88029       GT    C   A_
           GAG                    TTTTTG  TTTGA ATC  TTCATT
                                |||||||  |||||  |||  ||||||
                                GAGGAC  GAACT TAG  GGGTGG
                                   TG    C   AC
GAM984   LOC158310 5'  GGTGAGTGGTGTTCTACTGGAA 88086      TG  TTT
           G                     TTTT  GT   GACATCATTCATT
                                ||||  ||   ||||||||||||||
                                GAAG  CA   TTGTGGTGAGTGG
                                  GT  TC_
GAM984   LOC158314 3'  GATGAATACCTGGCAGGGTCAG 88096        TT   A  TC_
           GGA                    TTTTTGG  TTG CA   ATTCATT
                                |||||||  ||| ||   |||||||
                                AGGGACT  GAC GT   TAAGTAG
                                    GG   G  CCA
GAM984   LOC158476 5'  AATGAGATATAGACCAAGAA   88172          TGACA
                                TTTTTGGTTT     TCATT
                                ||||||||||     |||||
                                AAGAACCAGA     AGTAA
                                     TATAG
GAM984   LOC158661 3'  TGGTGGATGGAAAAGTTGTGGA 82855          G  _______
           ACCAAAGA                 TTTTTGGTTTT ACA     TCATTCATT   G
                                |||||||||| |||     |||||||||   |
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                                AGAAACCAAGG TGT     GGTAGGTGG   T
                                      _   TGAAAA
GAM984   LOC159089 3'  GTTCCAATGGTGTGAGAACTAG 88382          G       CATT
            GAG                    TTTTTGGTTTT ACATCATT
                                   |||||||||| ||||||||
                                   GAGGATCAAGA TGTGGTAA
                                         G       CCTTGT
GAM984   LOC159110 3'  AGTGATATGAAGTTAAAACCAG 82983           A   _
            GAG                    TTTTTGGTTTTGAC TCAT TCATT
                                   |||||||||||||| |||| |||||
                                   GAGGACCAAAATTG AGTA AGTGA
                                         A   T
GAM984   LOC159116 3'  AGTGATATGAAGTTAAAACCAG 82966           A   _
            GAG                    TTTTTGGTTTTGAC TCAT TCATT
                                   |||||||||||||| |||| |||||
                                   GAGGACCAAAATTG AGTA AGTGA
                                         A   T
GAM984   LOC159199 5'  GATGAATGGGGAGACCGGGAG  83061          GACA
                                   TTTTTGGTTTT   TCATTCATT
                                   ||||||||||    |||||||||
                                   GAGGGCCAGAG   GGTAAGTAG
                                         G___
GAM984   LOC159199 5'  TGATGGATGATGGCCTGTTGGA 83069     TG    GA_____
            AATTGAGA               TTT  GTTTT       CATCATTCATT   G
                                   |||  |||||       ||||||||||   |
                                   AGA  TAAAG       GTAGTAGGTAG   T
                                     GT    GTTGTCCG
GAM984   LOC159982 5'  AGTGAAGTTTTGGTTAAAATCG 88432           ATCA__
            GAAA                   TTTTTGGTTTTGAC     TTCATT
                                   |||||||||||||     ||||||
                                   AAAGGCTAAAATTG     AAGTGA
                                         GTTTTG
GAM984   LOC161003 3'  ATTTTGATGTTAAGAACAAAAG 59911        G         TTCATT
                                   TTTTTG TTTTGACATCA
                                   |||||| ||||||||||
                                   GAAAAC AGAATTGTAGT
                                      A         TTTAG
GAM984   LOC161356 5'  GGTGAAACAAAGATCTTAAAAC 83145           C   A____
            TAAAGA                 TTTTTGGTTTTGA ATC    TTCATT
                                   |||||||||||| |||    ||||||
                                   AGAAATCAAAATT TAG    AAGTGG
                                         C   AAACA
GAM984   LOC161514 3'  GATGGGCAGGATGAAGGCCAGG 88455          GA   AT__
            G                       TTTTGGTTTT  CATC   TCATT
                                   ||||||||||  ||||   |||||
                                   GGGACCGGAA  GTAG   GGTAG
                                         __   GACG
GAM984   LOC161635 5'  GGATGATGGGGTCAGAAG    98355        TT TGA
                                   TTTTTGG  T   CATCATTC
                                   |||||||  |   ||||||||
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                                GAAGACT  G   GTAGTAGG
                                   GG ___
GAM984   LOC162333 5'  GGTGGGCACAGCCGAGGCCGAG 88498          ACATCA
            GA                   TTTTTGGTTTTG     TTCATT
                                 ||||||||||||     ||||||
                                 AGGAGCCGGAGC     GGGTGG
                                       CGACAC
GAM984   LOC162333 5'  GGTTGGTGTCAATGCTGAAAA  88499     TG  T       TT
                                 TTTT  GT TTGACATCA  C
                                 ||||  || |||||||||  |
                                 AAAA  CG AACTGTGGT  G
                                   GT  T       TG
GAM984   LOC164295 5'  TAGTGAGGTCAAGCGGACACCG 83398        _____     A    CATT
            AAGA                 TTTTTGGT    TTTGAC TCATT
                                 ||||||||    |||||| |||||
                                 AGAAGCCA    GAACTG AGTGA
                                    CAGGC     G       TT
GAM984   LOC168346 5'  ATGAAGCAGAAACCAAGAA   83577          GACATCA
                                 TTTTTGGTTTT      TTCAT
                                 ||||||||||      |||||
                                 AAGAACCAAAG      AAGTA
                                       ACG____
GAM984   LOC169270 3'  GATGAGATGTATAGCTGGGG   83611     TG   TTG    AT
                                 TTT  GTT   ACATC  TCATT
                                 |||  |||   |||||  |||||
                                 GGG  CGA   TGTAG  AGTAG
                                   GT   TA_    __
GAM984   LOC169831 5'  GATGATATTGATGGTGAGACTA 83671          GA    T__
            GAGA                 TTTTTGGTTTT  CATCA   TCATT
                                 ||||||||||  |||||   |||||
                                 AGAGATCAGAG  GTAGT   AGTAG
                                       TG    TAT
GAM984   LOC170106 5'  GATGAGTGTGAGAGCTGGGA   83452     TG    G    CAT
                                 TTT  GTTTT ACAT   TCATT
                                 |||  ||||| ||||   |||||
                                 AGG  CGAGA TGTG   AGTAG
                                   GT    G   ___
GAM984   LOC170127 5'  GGTGGTGCTCTGGGGCCGGGAA 83461          _ _
                                 TTTTTGGTTTT GA CATCATT
                                 |||||||||| || |||||||
                                 AAGGGCCGGGG CT GTGGTGG
                                       T  C
GAM984   LOC170372 5'  AATGGATTGGTTAAAGCCAGA  76856          ATC
                                 TTTGGTTTTGAC   ATTCATT
                                 ||||||||||||   |||||||
                                 AGACCGAAATTG   TAGGTAA
                                       GT_
GAM984   LOC196320 3'  AGTGGATGGAGGAGAAGATCGA 89009          GACA_
            GGA                  TTTTTGGTTTT    TCATTCATT
                                 ||||||||||    |||||||||
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                                AGGAGCTAGAA    GGTAGGTGA
                                      GAGGA
GAM984  LOC196394 3' GATGATCAATGCTAGGAA    89030       T   _
                                TTTTTGGT TTGA CATC
                                |||||||| |||| ||||
                                AAGGATCG AACT GTAG
                                     T   A
GAM984  LOC196477 3' AATGAGCTTGGAATCAAGAG  89061         TG CA
                                TTTTTGGTTT  A  TCATT
                                ||||||||||  |  |||||
                                GAGAACTAAG  T  AGTAA
                                      GT CG
GAM984  LOC196500 3' GGTGGGTGGGAGGTGAGCTGGG 89086    TG   TGACA
           G                     TTT  GTTT    TCATTCATT
                                |||  ||||    |||||||||
                                GGG  CGAG    GGTGGGTGG
                                  GT   TGGAG
GAM984  LOC196955 5' CTTCTGGTGCCAGGACCAAGGA 77867          A    TTCATT
                                TTTTTGGTTTTG CATCA
                                |||||||||||| |||||
                                AGGAACCAGGAC GTGGT
                                       C    CTTCC
GAM984  LOC196957 3' GGTGGGGGATTTTGGGGCCG   89192      TG C   A
                                TGGTTT  A ATC TTCATT
                                ||||||  | ||| ||||||
                                GCCGGG  T TAG GGGTGG
                                   GT T   G
GAM984  LOC196961 3' GGTGGGGGATTTTGGGGCCG   89205      TG C   A
                                TGGTTT  A ATC TTCATT
                                ||||||  | ||| ||||||
                                GCCGGG  T TAG GGGTGG
                                   GT T   G
GAM984  LOC196993 3' AATGATAATACTCACAGCCAAG 91237        T   CATCAT
           AG                     TTTTTGGTT TGA     TCATT
                                |||||||| |||     |||||
                                GAGAACCGA ACT     AGTAA
                                     C   CATAAT
GAM984  LOC197003 3' AGTGAAGGTCAAGACCAGG    89212         A_
                                TTTGGTTTTGAC  TCATT
                                ||||||||||||  |||||
                                GGACCAGAACTG  AGTGA
                                       GA
GAM984  LOC197085 5' GGTGGAGAAGCTGTTAGAACAG 89221     TG       ___  A
           GAGA                    TTTT  GTTTTGACA   TC TTCATT
                                ||||  |||||||||   || ||||||
                                AGAG  CAAGATTGT   AG AGGTGG
                                  GA       CGA  _
GAM984  LOC197114 5' GTTTATGGTGTAGGGGCTGGGA 91274     TG   TG      TCATT
           G                     TTTT  GTTT  ACATCAT
                                ||||  ||||  |||||||
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                                GAGG  CGGG  TGTGGTA
                                  GT    GA      TTTGG
GAM984   LOC197115 5'  GGTGGAGAAGCTGTTAGAACAG 89226      TG       ___  A
                GAGA                TTTT  GTTTTGACA   TC TTCATT
                                |||| |||||||||  || ||||||
                                AGAG  CAAGATTGT   AG AGGTGG
                                  GA       CGA  _
GAM984   LOC197117 5'  GTTTATGGTGTAGGGGCTGGGA 91285      TG    TG      TCATT
                G                   TTTT  GTTT  ACATCAT
                                |||| |||| |||||||
                                GAGG  CGGG  TGTGGTA
                                  GT    GA      TTTGG
GAM984   LOC197138 3'  GGTGGGGGGATTTTGGGGCCG   89254       TG C   A
                                TGGTTT  A ATC TTCATT
                                ||||||  | ||| ||||||
                                GCCGGG  T TAG GGGTGG
                                   GT T   G
GAM984   LOC197209 5'  AGTGAATGAGGGGGGCTCAGA  88656      _    GACA
                                TTTG GTTTT    TCATTCATT
                                |||| |||||    |||||||||
                                AGAC CGGGG    AGTAAGTGA
                                  T    GG__
GAM984   LOC197259 3'  AATGAGGCCAATCAAGACCAGA 89296           CATCA
                AG                  TTTTTGGTTTTGA     TTCATT
                                ||||||||||||||    ||||||
                                GAAGACCAGAACT    GAGTAA
                                       AACCG
GAM984   LOC197285 3'  GGTGAGTGAGGTGGAGGAGCTG 89154    TG    GA __
                AA                  TT  GTTTT  CA  TCATTCATT
                                ||  |||||  ||  |||||||||
                                AA  CGAGG  GT  AGTGAGTGG
                                 GT    AG  GG
GAM984   LOC197319 3'  GGTGGGTGGATCACAAGGTCAG 89326       GT    ACA_
                GAG                   TTTTTG  TTTG    TCATTCATT
                                ||||||  ||||   |||||||||
                                GAGGAC  GAAC    GGTGGGTGG
                                   TG    ACTA
GAM984   LOC197322 5'  AGTGGACATCATCAAGACTGGA 91309      TG      CATCA
                GG                  TTTT  GTTTTGA     TTCATT
                                ||||  |||||||    ||||||
                                GGAG  CAGAACT    AGGTGA
                                  GT      ACTAC
GAM984   LOC197331 3'  GATGGAATTCACCGAGGCCGAG 61561           ACATCA
                AG                  TTTTTGGTTTTG     TTCATT
                                ||||||||||||     ||||||
                                GAGAGCCGGAGC     AGGTAG
                                       CACTTA
GAM984   LOC197335 5'  GGCTGTGTCGGAGCTGAGG   89333     TG       T  TT
                                TTT  GTTTTGACA CA  C
                                |||  ||||||||| ||  |
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                                GGA  CGAGGCTGT GT  G
                                  GT        _ CG
GAM984   LOC197414 3'  ATGGAGATGGTGCTAGAAG   89455        TTTGA   A
                                TTTTTGGT    CATC TTCAT
                                ||||||||    |||| |||||
                                GAAGATCG    GTAG AGGTA
                                    TG___   _
GAM984   LOC199675 3'  GATGAATGAATAGGACTGAGAG 89641      TG     ACA
                                TTTT  GTTTTG   TCATTCATT
                                ||||  ||||||   |||||||||
                                GAGA  CAGGAT   AGTAAGTAG
                                  GT     A__
GAM984   LOC199729 3'  GATGAACATGTCAAAATTGA   73393    TG        CA
                                T  GTTTTGACAT  TTCATT
                                |  ||||||||||  ||||||
                                A  TAAAACTGTA  AAGTAG
                                 GT        C_
GAM984   LOC199886 3'  AATGAATGTTAATAGGAATTGG 89823      TG    GACAT_
           AAA                    TTTT  GTTTT     CATTCATT
                                ||||  |||||     ||||||||
                                AAAG  TAAGG     GTAAGTAA
                                  GT    ATAATT
GAM984   LOC199906 5'  GGTGAACTGCTTGTTAGGACCA 89858             T_ _
           AAAG                   TTTTTGGTTTTGACA  CA TTCATT
                                ||||||||||||||  || ||||||
                                GAAAACCAGGATTGT  GT AAGTGG
                                       TC  C
GAM984   LOC199936 3'  GGTGGGGTGTGCTGAGCCGAGG 91484         TG_    AT
                                TTTTGGTTT   ACATC  TCATT
                                |||||||||   |||||  |||||
                                GGAGCCGAG   TGTGG  GGTGG
                                     TCG    __
GAM984   LOC199986 5'  AATGGATGAGTCACAGCTGAA  91502    TG   T    A
                                TT  GTT TGAC TCATTCATT
                                ||  ||| |||| |||||||||
                                AA  CGA ACTG AGTAGGTAA
                                 GT   C   _
GAM984   LOC200000 3'  GAGGGTCAAGATCGAGGA    91520            A_
                                TTTTTGGTTTTGAC  TC
                                ||||||||||||||  ||
                                AGGAGCTAGAACTG  AG
                                       GG
GAM984   LOC200010 3'  GGTGGCTGTCAGACCCGAAG   91527       T     _
                                TTTTGG TTTGACA TCATT
                                |||||| ||||||| |||||
                                GAAGCC AGACTGT GGTGG
                                   C      C
GAM984   LOC200197 3'  GATGGTTTTAGGATTAAAAG   90018            C
                                TTTTTGGTTTTGA ATCATT
                                |||||||||||| ||||||
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                                GAAAATTAGGATT TGGTAG
                                       T
GAM984  LOC200251 5' AATGATGTCTAAATTAGAG   90054        T
                                TTTTGGTTT GACATCATT
                                ||||||||| |||||||||
                                GAGATTAAA CTGTAGTAA
                                      T
GAM984  LOC200282 3' AATGAATGAAATCTAAACT   90095     T  CA
                                GGTTT GA  TCATTCATT
                                ||||| ||  |||||||||
                                TCAAA CT  AGTAAGTAA
                                   T  AA
GAM984  LOC200301 3' GGTGAGTGAGCCCACGCCAGGA 90148       TT  ACA
           G                     TTTTTGGT  TG   TCATTCATT
                                ||||||||  ||   |||||||||
                                GAGGACCG  AC   AGTGAGTGG
                                     C_  CCG
GAM984  LOC200352 3' GATGAGGCAAAGCTAGA     90234        ACA
                                TTTGGTTTTG   TCATT
                                ||||||||||   |||||
                                AGATCGAAAC   AGTAG
                                      GG_
GAM984  LOC200407 5' GATGCTGCCAGAATCAGAAG   91629          A  T
                                TTTTTGGTTTTG CA CATT
                                |||||||||||| || ||||
                                GAAGACTAAGAC GT GTAG
                                       C  C
GAM984  LOC200448 5' TTCCTTTGGTCTCAAGACTAGA 90247          C    TTCATT
           GA                     TTTTTGGTTTTGA ATCA
                                |||||||||||||| ||||
                                AGAGATCAGAACT TGGT
                                       C    TTCCTTA
GAM984  LOC200743 5' GATGAGGAAATTGAGGCACAGA 91720       _   TG CA  A
           GA                     TTTTTG GTTT  A  TC TTCATT
                                |||||| ||||  |  || ||||||
                                AGAGAC CGGA  T  AG GAGTAG
                                   A   GT AA  _
GAM984  LOC201109 3' GATGCTTGTCGAGGTCGGGA   91328     GT     T_
                                TTTTG  TTTGACA  CATT
                                |||||  |||||||  ||||
                                AGGGC  GAGCTGT  GTAG
                                   TG      TC
GAM984  LOC201139 3' GATGACTTCAGGACCAAG    89508         CA
                                TTTGGTTTTGA  TCATT
                                ||||||||||  |||||
                                GAACCAGGACT  AGTAG
                                       TC
GAM984  LOC201181 5' GACTGGGGTTGGAGCCAGGG   89513        TG  AT  T
                                TTTTGGTTT  AC  CA TC
                                |||||||||  ||  || ||
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                                GGGACCGAG  TG  GT AG
                                     GT  GG  C
GAM984   LOC201211 5'  AATGAGACCGAGACCAAGA   91026          ACA
                                TTTTGGTTTTG   TCATT
                                ||||||||||   |||||
                                AGAACCAGAGC   AGTAA
                                     CAG
GAM984   LOC201249 3'  AATGAGTAAGTTAACAGCCAGA 89542        _    ATC
           GA                    TTTTTGGTT TTGAC   ATTCATT
                                |||||||| |||||   |||||||
                                AGAGACCGA AATTG   TGAGTAA
                                     C    AA_
GAM984   LOC201456 3'  AATTTTGATGTCCGAGTTAAGA 89614      GG   T     TTCATT
           A                     TTTTT  TTT GACATCA
                                |||||  ||| |||||||
                                AAGAA  GAG CTGTAGT
                                   TT   C      TTTAA
GAM984   LOC201696 5'  GTGGAAATGATGTCAAGA    63825          __
                                TTTTGACATCA  TTCAT
                                ||||||||||  |||||
                                AGAACTGTAGT  AGGTG
                                     AA
GAM984   LOC201868 3'  AGGAGAGTCAGAATTAGAGA   90513           A  A   ATT
                                TTTTTGGTTTTGAC TC TTC
                                |||||||||||||| || |||
                                AGAGATTAAGACTG AG AGG
                                      _ _   AT
GAM984   LOC201910 3'  AGTGAGAATTCAAAACTGGAA  90550     TG      CA__
                                TTT  GTTTTGA    TCATT
                                |||  |||||||   |||||
                                AAG  CAAAACT    AGTGA
                                  GT      TAAG
GAM984   LOC201911 3'  GATGGGGGCGCTTGGCGAGGCC 91864          A  TCA___
           AAGGA                   TTTTTGGTTTTG CA     TTCATT
                                |||||||||||| ||     ||||||
                                AGGAACCGGAGC GT     GGGTAG
                                      G  TCGCGG
GAM984   LOC202347 3'  GATGAGTGTGCTGAAGGTGGGG 91946     TT G    GA  T
           A                     TTT  G TTTT  CA CATTCATT
                                |||  | ||||  || ||||||||
                                AGG  T GAAG  GT GTGAGTAG
                                  GG G    TC  _
GAM984   LOC202404 5'  GGGGGAATGGCTCAGGATCGGA 90651          CA     ATT
           AA                    TTTTTGGTTTTGA  TCATTC
                                ||||||||||||  ||||||
                                AAAGGCTAGGACT  GGTAAG
                                      C_     GGGGT
GAM984   LOC202551 3'  GAGGGTTAAGATCAAAGA    60749           A_
                                TTTTTGGTTTTGAC  TC
                                ||||||||||||||  ||
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                                AGAAACTAGAATTG  AG
                                      GG
GAM984   LOC202915 3'  GATGGGTCACAGAACCAG    92018        __    A
                                TTGGTTT  TGAC TCATT
                                |||||||  |||| |||||
                                GACCAAG  ACTG GGTAG
                                   AC   _
GAM984   LOC203232 3'  GATGGAATTCACCGAGGCCGAG 71919           ACATCA
           AG                     TTTTTGGTTTTG     TTCATT
                                |||||||||||     ||||||
                                GAGAGCCGGAGC     AGGTAG
                                      CACTTA
GAM984   LOC203245 5'  GGTGGGTGAGGGGCGAGGCTGA 90825      TG     ACA_
           GGA                    TTTT  GTTTTG    TCATTCATT
                                ||||  ||||||   |||||||||
                                AGGA  CGGAGC    AGTGGGTGG
                                  GT     GGGG
GAM984   LOC203275 3'  GGTGGGGTCAGGGCTGGGG    90856     TG      AT
                                TTT  GTTTTGAC  CATT
                                |||  ||||||||  ||||
                                GGG  CGGGACTG  GTGG
                                  GT       GG
GAM984   LOC203286 3'  GGTGGGTGAGGCCAGAAG    92149          A_
                                TTTTTGGTTTTG  CATC
                                ||||||||||||  ||||
                                GAAGACCGGAGT  GTGG
                                      GG
GAM984   LOC203369 3'  AGTGGGTCATGAGACCAGAAG  90879          __    A
                                TTTTTGGTTT  TGAC TCATT
                                ||||||||||  |||| |||||
                                GAAGACCAGA  ACTG GGTGA
                                   GT   _
GAM984   LOC203504 3'  AGTGATACAGAGCTGGAG    92318     TG     AC
                                TTT  GTTTTG  ATCATT
                                |||  ||||||  ||||||
                                GAG  CGAGAC  TAGTGA
                                  GT     A_
GAM984   LOC203569 3'  AATGAAGACTGAAACCAAGAA  90947           ACA  A
                                TTTTTGGTTTTG   TC TTCATT
                                ||||||||||||   || ||||||
                                AAGAACCAAAGT   AG AAGTAA
                                      C__  _
GAM984   LOC203668 5'  GGTGGGGAGCCGGAGCTGGAAG 90987      TG     ACA  A
                                TTTT  GTTTTG   TC TTCATT
                                ||||  ||||||   || ||||||
                                GAAG  CGAGGC   AG GGGTGG
                                  GT     CG_  _
GAM984   LOC204285 5'  AGTGACTACTGGTGTTGGGATC 91014     TT    TG     T___
           TGGAG                  TTT  GGTTT  ACATCA    TCATT
                                |||  |||||  ||||||   |||||
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                                GAG  CTAGG  TGTGGT    AGTGA
                                  GT    GT     CATC
GAM984   LOC205251 5'  AATGAAGCTTCCGTAAAAACCA 92351          G  ATCA__
             AAAG                   TTTTTGGTTTT AC     TTCATT
                                |||||||||| ||     ||||||
                                GAAAACCAAAA TG     AAGTAA
                                      A  CCTTCG
GAM984   LOC205418 5'  GATGGGCAGCAGAACCGAAG   92373          ACA_
                                TTTTGGTTTTG    TCATT
                                ||||||||||    |||||
                                GAAGCCAAGAC    GGTAG
                                      GACG
GAM984   LOC206324 5'  GTGAGTGATGAGACTGGGAA   92401      TG    TGA        T
                                TTTT  GTTT   CATCATTCAT
                                ||||  ||||   ||||||||||
                                AAGG  CAGA   GTAGTGAGTG
                                  GT    ___         T
GAM984   LOC206338 5'  AATGGGTGGATCATCCAGAAA  91089       TTT   CA
                                TTTTTGG   TGA  TCATTCATT
                                |||||||   |||  |||||||||
                                AAAGACC   ACT  GGTGGGTAA
                                    T__   A_
GAM984   LOC219287 3'  GGTGGATGGGCCCCATGCCAAG 95217        TTTGACA
             GA                   TTTTTGGT      TCATTCATT
                                ||||||||      |||||||||
                                AGGAACCG      GGTAGGTGG
                                     TACCCCG
GAM984   LOC219347 5'  GATGGACGAAGCCAAGAG    94578           A_
                                TTTTTGGTTTTG  CATC
                                ||||||||||||  ||||
                                GAGAACCGAAGC  GTAG
                                      AG
GAM984   LOC219376 3'  GATGAATGTGCTATTCATAAGC 95516          _  ____  T
             TAGAAA                 TTTTTGGTTT TGA    CA CATTCATT
                                |||||||||| |||    || ||||||||
                                AAAGATCGAA ACT    GT GTAAGTAG
                                      T   TATC  _
GAM984   LOC219397 3'  GGTGGGTGGGAATAAACTAAAA 95119          TGACA
             G                   TTTTTGGTTT    TCATTCATT
                                ||||||||||    |||||||||
                                GAAAATCAAA    GGTGGGTGG
                                      TAAG_
GAM984   LOC219627 3'  GGTGAGGCAGGGCTGAAAA   93810      TG     ACA
                                TTTT  GTTTTG   TCATT
                                ||||  ||||||   |||||
                                AAAA  CGGGAC   AGTGG
                                  GT     GG_
GAM984   LOC219690 5'  GATGAATCATTTCAGGCTGGAA 94664      TG   T  C  C
             G                   TTTT  GTTT GA AT ATTCATT
                                ||||  |||| || || |||||||
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                                GAAG  CGGA CT TA TAAGTAG
                                  GT    _ T  C
GAM984   LOC219736 5'  ATCTTTGATGGTAAAGCCAAAG 94740          A    TTCATT
           A                    TTTTTGGTTTTG CATCA
                                |||||||||||| |||||
                                AGAAACCGAAAT GTAGT
                                       G    TTCTAA
GAM984   LOC219848 3'  AATGAATCACAGAACCAAAGA  93123          ACATC
                                TTTTTGGTTTTG    ATTCATT
                                ||||||||||||    |||||||
                                AGAAACCAAGAC    TAAGTAA
                                       AC___
GAM984   LOC219920 5'  GGTGGAATCAGAGCCGAAG   94959          ___
                                TTTTGGTTTTGA   CATC
                                ||||||||||||   ||||
                                GAAGCCGAGACT   GTGG
                                       AAG
GAM984   LOC219920 5'  GGTGGGTGTTGGGGAGAC    94960      GA  T
                                GTTTT  CA CATTCATT
                                |||||  || ||||||||
                                CAGAG  GT GTGGGTGG
                                   GG  T
GAM984   LOC219940 3'  GGTGGAGTCTCAGAGTCCAGGG 95003       _    CATCA
           A                    TTTTTGG TTTTGA    TTCATT
                                ||||||| ||||||    ||||||
                                AGGGACC GAGACT    AGGTGG
                                     T    CTG__
GAM984   LOC219972 3'  AATGAAAGATGGGTAAAAACTG 93277     TG    GA__   A
           GAAA                   TTTT  GTTTT   CATC TTCATT
                                ||||  |||||   |||| ||||||
                                AAAG  CAAAA   GTAG AAGTAA
                                  GT    ATGG   A
GAM984   LOC219988 5'  AGTGAGGATGATGAGACAAAAG 93257      G    A   A
           A                    TTTTT GTTTTG CATC TTCATT
                                ||||| |||||| |||| ||||||
                                AGAAA CAGAGT GTAG GAGTGA
                                   A    A   _
GAM984   LOC220020 5'  GATGGGTGGTTGAAACCG    95047      TG  AT
                                TGGTTT  AC  CATTCATT
                                ||||||  ||  ||||||||
                                GCCAAA  TG  GTGGGTAG
                                   GT  __
GAM984   LOC220020 5'  GGTGAGGTGGGGCCAGAAA   95051        TT ACA
                                TTTTTGGTT  G   TCATT
                                |||||||||  |   |||||
                                AAAGACCGG  T   AGTGG
                                      GG GG_
GAM984   LOC220020 5'  GGTGGATGATACTGCCAAGAA  95052        TTTGAC
                                TTTTTGGT     ATCATTCATT
                                ||||||||     ||||||||||
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                                AAGAACCG     TAGTAGGTGG
                                     TCA___
GAM984   LOC220058 3'  AGTGGAACAGAACCAAAGA   93378          ACA
                                TTTTTGGTTTTG   TCATT
                                ||||||||||||  |||||
                                AGAAACCAAGAC   GGTGA
                                      AA_
GAM984   LOC220064 3'  GATGGATGAACAGAGACCGAA 95067        GACA
                                TTTGGTTTT    TCATTCATT
                                |||||||||    |||||||||
                                AAGCCAGAG    AGTAGGTAG
                                     ACA_
GAM984   LOC220164 5'  GTGAGTCAGAGCTGGAG     93446     TG       A
                                TTT  GTTTTGAC TCAT
                                |||  |||||||| ||||
                                GAG  CGAGACTG AGTG
                                  GT       _
GAM984   LOC220469 3'  AATGGATAATGATGGCCAGAAG 76891         TTGA   C
                                TTTTTGGTT    CAT ATTCATT
                                |||||||||    ||| |||||||
                                GAAGACCGG    GTA TAGGTAA
                                     TA__   A
GAM984   LOC220514 5'  GATGAGCTGAGCTTCAAGGCTG 61075      TG      CA_  _
            GGGA                    TTTT  GTTTTGA   TCA TTCATT
                                ||||  |||||||   ||| ||||||
                                AGGG  CGGAACT   AGT GAGTAG
                                  GT      TCG   C
GAM984   LOC220567 3'  GGTGGGAGGATCGCTTGAGACC 92437          TG C__   A_
            AGGAG                   TTTTTGGTTT  A   ATC  TTCATT
                                ||||||||||  |   |||  ||||||
                                GAGGACCAGA  T   TAG  GGGTGG
                                     GT CGC   GA
GAM984   LOC220883 3'  ATGAGTAGATAGCCAAAGA   92890        TTGAC  _
                                TTTTTGGTT    ATC ATTCAT
                                |||||||||    ||| ||||||
                                AGAAACCGA    TAG TGAGTA
                                     _____  A
GAM984   LOC220929 5'  CTGAAGTGTTAAAGTTAGAAG  93040      GG       CA   TT
                                TTTTT  TTTTGACAT  TTCA
                                |||||  |||||||||  ||||
                                GAAGA  GAAATTGTG  AAGT
                                   TT        __    CA
GAM984   LOC220936 3'  GATGACTAATGTCAGAGGCAGG 93042      G       CAT
            G                    TTTTG TTTTGACAT   TCATT
                                |||||  |||||||||   |||||
                                GGGAC GAGACTGTA   AGTAG
                                   G        ATC
GAM984   LOC221088 3'  AGTGTCCTGATGCAAAGTTGAA 94886      GG    A    TT_
            AG                   TTTTT  TTTTG CATCA   CATT
                                |||||  |||||  |||||   ||||
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                                GAAAG  GAAAC GTAGT   GTGA
                                   TT    _    CCT
GAM984   LOC221092 5'  AGTGAAAAGTCAAAACCAG   94865          ATCA
                                TTGGTTTTGAC   TTCATT
                                ||||||||||   ||||||
                                GACCAAAACTG   AAGTGA
                                      AA__
GAM984   LOC221271 5'  AATGAGCCGGAGCCGGAG    93483          ACA
                                TTTTGGTTTTG   TCATT
                                ||||||||||   |||||
                                GAGGCCGAGGC   AGTAA
                                      CG_
GAM984   LOC221300 3'  AATGAAATATGTCAGGACAGAA 93573      G        CA
            AG                    TTTTT GTTTTGACAT  TTCATT
                                |||||  ||||||||||  ||||||
                                GAAAG CAGGACTGTA  AAGTAA
                                   A         TA
GAM984   LOC221336 3'  AGTGATGCATCAAACCAGAGA  93889         __  A
                                TTTTTGGTTT  TG CATCATT
                                ||||||||||  || |||||||
                                AGAGACCAAA  AC GTAGTGA
                                      CT  _
GAM984   LOC221398 3'  AATGAATGAATAACTAAGA    92663        TTGACA
                                TTTTGGTT     TCATTCATT
                                ||||||||     |||||||||
                                AGAATCAA     AGTAAGTAA
                                     TA____
GAM984   LOC221421 3'  GATGGGCTTGACGGAGCCAGGA 93892          A  TCA
            G                    TTTTTGGTTTTG CA   TTCATT
                                ||||||||||||  ||   ||||||
                                GAGGACCGAGGC GT   GGGTAG
                                      A  TC_
GAM984   LOC221479 5'  GGTTGGTGTTGGGCCGGAG    93845        T TG     TT
                                TTTTGGT T  ACATCA  C
                                |||||||  |  ||||||  |
                                GAGGCCG G  TGTGGT  G
                                    _ GT     TG
GAM984   LOC221495 5'  GCGGGATGATGCGGGGCCGGGA 95496          A       ATT
            G                    TTTTTGGTTTTG CATCATTC
                                ||||||||||| ||||||||
                                GAGGGCCGGGGC GTAGTAGG
                                      _       GCGC
GAM984   LOC221547 3'  AGTGAATGTGGCAGTTCAAAAA 92652        TT   A  T
                                TTTTTGG  TTG CA CATTCATT
                                |||||||  ||| || ||||||||
                                AAAAACT  GAC GT GTAAGTGA
                                    T_   G  _
GAM984   LOC221683 5'  GATTATGTCCAAACTGAGAA   95328      TG    T    CAT
                                TTTT  GTTT GACAT   TC
                                ||||  |||| |||||   ||
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                                AAGA  CAAA CTGTA   AG
                                  GT    C    TT_
GAM984   LOC221738 3'  GATGAATGCAAATCAGAACCAA 95414          CAT_
                                TTGGTTTTGA    CATTCATT
                                ||||||||||    ||||||||
                                AACCAAGACT    GTAAGTAG
                                     AAAC
GAM984   LOC221752 3'  ATGGGATTTTTGTTGGGATTGA 95423     TG   TG   TC_   ATT
           AGA                    TTTT  GTTT  ACA   ATTC
                                ||||  ||||  |||   ||||
                                AGAA  TAGG  TGT   TAGG
                                  GT    GT   TTT    GTAA
GAM984   LOC221755 3'  ACAGGATGATGATAAAGCCAGA 94006          A       ATT
           G                     TTTTGGTTTTG CATCATTC
                                ||||||||||| ||||||||
                                GAGACCGAAAT GTAGTAGG
                                     A       ACAA
GAM984   LOC221794 5'  GACTGTGCCAAAGCTGAGAA   95531     TG     A  T  T
                                TTTT  GTTTTG CA CA TC
                                ||||  |||||| || || ||
                                AAGA  CGAAAC GT GT AG
                                  GT     C  _  C
GAM984   LOC221915 3'  GGTGAAGAGGCAGAACCGAGG  95569          ACA  A
                                TTTTGGTTTTG   TC TTCATT
                                ||||||||||   || ||||||
                                GGAGCCAAGAC   AG AAGTGG
                                     GG_  _
GAM984   LOC221915 3'  GGTGACGGTGTCAGGACAGAGG 95570     G         AT
                                TTTT GTTTTGACATC  TCATT
                                |||| ||||||||||  |||||
                                GGAG CAGGACTGTGG  AGTGG
                                  A         C_
GAM984   LOC221943 5'  GGTGGATCACCTGAGGCCAGGA 95624          GACATC
           A                     TTTTTGGTTTT     ATTCATT
                                ||||||||||     |||||||
                                AAGGACCGGAG     TAGGTGG
                                     TCCAC_
GAM984   LOC222066 3'  GATGGCCTGAGGCCAGGAG    94321          GA__
                                TTTTTGGTTTT    CATC
                                ||||||||||    ||||
                                GAGGACCGGAG    GTAG
                                     TCCG
GAM984   LOC222161 5'  AATGAATTGCAATAAAACTAAG 94375          ACATC
           AA                     TTTTTGGTTTTG    ATTCATT
                                ||||||||||||    |||||||
                                AAGAATCAAAAT    TAAGTAA
                                     AACGT
GAM984   LOC222182 3'  GGTGGATCGCTTGAGGCCAGGA 95859          TG CATC
           A                     TTTTTGGTTT  A   ATTCATT
                                ||||||||||  |   |||||||
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                                AAGGACCGGA  T    TAGGTGG
                                      GT CGC_
GAM984   LOC222228 5'  GATGAATCTGAGGAGGAGCCGG 95954          GACA   __
            AGA                    TTTTTGGTTTT    TCA  TTCATT
                                   ||||||||||    |||  ||||||
                                   AGAGGCCGAGG    AGT  AAGTAG
                                         AGG_   CT
GAM984   LOC222678 5'  AATGAAAAATGTGAGACCAAAG 94415          G    CA
            A                      TTTTTGGTTTT ACAT  TTCATT
                                   ||||||||||| ||||  ||||||
                                   AGAAACCAGAG TGTA  AAGTAA
                                         _    AA
GAM984   LOC245727 3'  GGTGGGGGGATTTTGGGGCCG   92762       TG C   A
                                   TGGTTT  A ATC TTCATT
                                   ||||||  | ||| ||||||
                                   GCCGGG  T TAG GGGTGG
                                       GT T   G
GAM984   LOC245728 3'  GTGTTTCAAGACCAAAAA    92768           CAT
                                   TTTTTGGTTTTGA   CAT
                                   ||||||||||||   |||
                                   AAAAACCAGAACT   GTG
                                          TT_
GAM984   LOC252983 5'  GATGGTCGTTTGAAGCCAGGAG 96934          TG _ _     CATT
                                   TTTTTGGTTT  A C ATCATT
                                   ||||||||||  | | ||||||
                                   GAGGACCGAA  T G TGGTAG
                                         GT T C
GAM984   LOC253187 5'  AGTGAATGGATACAGAGCTGAA 98901    TG     ACA
                                   TT  GTTTTG   TCATTCATT
                                   ||  ||||||   |||||||||
                                   AA  CGAGAC   GGTAAGTGA
                                    GT     ATA
GAM984   LOC253205 5'  GATTGTCGGAGTCCAGAA     99429       _      _
                                   TTTTGG TTTTGACA TC
                                   |||||| |||||||| ||
                                   AAGACC GAGGCTGT AG
                                       T       T
GAM984   LOC253286 5'  AATCCTGGTGTCAAAGGCTAAA 99421          _        TTCATT
            AA                       TTTTTGGT TTTGACATCA
                                   |||||||| ||||||||||
                                   AAAAATCG AAACTGTGGT
                                        G         CCTAA
GAM984   LOC253549 3'  GTGGGGCTGATGTCGAAA     98576          __
                                   TTTTGACATCA  TTCAT
                                   ||||||||||  |||||
                                   AAAGCTGTAGT  GGGTG
                                         CG
GAM984   LOC253596 5'  GATGAGTGGTGCTTCCCCAAAA 97232       TTTTGA
                                   TTTTGG     CATCATTCATT
                                   ||||||     ||||||||||
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                                AAAACC     GTGGTGAGTAG
                                   CCTTC_
GAM984   LOC253639 5'  GATGAGGCCAGAACTGAGAA   97515     TG     ACA
                                TTTT  GTTTTG   TCATT
                                ||||  ||||||   |||||
                                AAGA  CAAGAC   AGTAG
                                  GT     CGG
GAM984   LOC253641 5'  AGTGTTCACAGTCAGAGCTGAG 99410     TG      ATCATT
           GG                     TTTT  GTTTTGAC     CATT
                                ||||  ||||||||     ||||
                                GGGA  CGAGACTG     GTGA
                                  GT       ACACTT
GAM984   LOC253664 3'  AGTGAGTGTCATTTCAGACATT 96457     TG  _    CAT__
           GAGAA                    TTTT  GT TTTGA    CATTCATT
                                ||||  || |||||    ||||||||
                                AAGA  TA AGACT    GTGAGTGA
                                  GT  C    TTACT
GAM984   LOC253718 5'  GATGCTGGGTGAGGACCAAGGA 99405         G  A   TT
                                TTTTTGGTTTT AC TCA  CATT
                                |||||||||||| || |||  ||||
                                AGGAACCAGGA TG GGT  GTAG
                                      G  _   C_
GAM984   LOC253724 3'  GTGGATCCGGAGCCGGAGA    98237          ACATC
                                TTTTTGGTTTTG    ATTCAT
                                ||||||||||||    ||||||
                                AGAGGCCGAGGC    TAGGTG
                                      C_____
GAM984   LOC253737 5'  AGTGGAGAGGCGAAGCTGA    97981    TG     ACA  A
                                T  GTTTTG   TC TTCATT
                                |  ||||||   || ||||||
                                A  CGAAGC   AG AGGTGA
                                 GT     GG_  _
GAM984   LOC253832 3'  CTACAAGTGGTGTGGGAATCAG 96591          G       CATT
           GGA                     TTTTTGGTTTT ACATCATT
                                |||||||||||| ||||||||
                                AGGGACTAAGG TGTGGTGA
                                      G       ACATCC
GAM984   LOC253912 3'  AGTGGAAGTCAGGACCAGGG   99206          ATCA
                                TTTTGGTTTTGAC    TTCATT
                                ||||||||||||    ||||||
                                GGGACCAGGACTG    AGGTGA
                                      A___
GAM984   LOC253936 3'  GATGGAATTCACCGAGGCCGAG 96319          ACATCA
           AG                      TTTTTGGTTTTG     TTCATT
                                ||||||||||||     ||||||
                                GAGAGCCGGAGC     AGGTAG
                                      CACTTA
GAM984   LOC253974 5'  GGTGTCACTGTTGAAATCGGAG 99283         TG   TCATT
                                TTTTGGTTT  ACA    CATT
                                |||||||||  |||    ||||
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                                GAGGCTAAA  TGT    GTGG
                                     GT   CACT_
GAM984   LOC253978 5'  GAGTGTTGGAGACCAGGAA   99456          GA  T
                                TTTTTGGTTTT  CA CATTC
                                ||||||||||  || |||||
                                AAGGACCAGAG  GT GTGAG
                                     __  T
GAM984   LOC253992 3'  GATGAAAAGACAAGACCAGGG  98425           ACATCA
                                TTTTGGTTTTG     TTCATT
                                ||||||||||     ||||||
                                GGGACCAGAAC     AAGTAG
                                     AGAA__
GAM984   LOC254045 3'  GATGGCTTGAGGCCAGGAG   98270          TG __
                                TTTTTGGTTT  A  CATC
                                |||||||||  |  ||||
                                GAGGACCGGA  T  GTAG
                                     GT CG
GAM984   LOC254100 3'  GATGTCTTGAGATCAGGAG   98157           __
                                TTTTTGGTTTT  GACATC
                                ||||||||||  ||||||
                                GAGGACTAGAG  CTGTAG
                                     TT
GAM984   LOC254128 3'  AGTGTATGTGTTGGGATGGGAG 97357      G   TG  T  T
           A                     TTTTT GTTT  ACA CAT CATT
                                |||||  ||||  ||| ||| ||||
                                AGAGG TAGG  TGT GTA GTGA
                                   G   GT  _  T
GAM984   LOC254173 3'  AGTGGTGTGAGGTCAAGAG   98641      GT  G
                                TTTTTG  TTT ACATCATT
                                ||||||  ||| ||||||||
                                GAGAAC  GAG TGTGGTGA
                                    TG  _
GAM984   LOC254228 3'  GACTGGTGTCTGAAGTTGGGG  97651     GG  _     T
                                TTTT  TTTT GACATCA TC
                                ||||  |||| ||||||| ||
                                GGGG  GAAG CTGTGGT AG
                                   TT   T     C
GAM984   LOC254345 5'  GGTGGTTATTTTAAAGCCAAGA 99468          C  CAT
           G                     TTTTTGGTTTTGA AT   TCATT
                                ||||||||||||| ||   |||||
                                GAGAACCGAAATT TA   GGTGG
                                     T  TT_
GAM984   LOC254419 5'  GATTATTCAAAGCCAAAAG   99374          C__
                                TTTTTGGTTTTGA   ATC
                                ||||||||||||   |||
                                GAAAACCGAAACT   TAG
                                     TAT
GAM984   LOC254440 3'  AATGAATGATTCACGAATCAGG 98845        _  C
                                TTTGGTTT TGA ATCATTCATT
                                |||||||| ||| ||||||||||
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                                GGACTAAG ACT TAGTAAGTAA
                                    C  _
GAM984  LOC254471 3'  GATGAGACACGAAATCAAGAA  99000          ACA_
                                TTTTTGGTTTTG   TCATT
                                ||||||||||||   |||||
                                AAGAACTAAAGC   AGTAG
                                   ACAG
GAM984  LOC254517 5'  GGTGGAGAAGCTGTTAGAACAG 96637     TG      ___  A
          GAGA                    TTTT  GTTTTGACA   TC TTCATT
                                ||||  |||||||||   || ||||||
                                AGAG  CAAGATTGT   AG AGGTGG
                                  GA       CGA  _
GAM984  LOC254517 5'  GGTGGAGAAGCTGTTAGAACAG 96638     TG      ___  A
          GAGA                    TTTT  GTTTTGACA   TC TTCATT
                                ||||  |||||||||   || ||||||
                                AGAG  CAAGATTGT   AG AGGTGG
                                  GA       CGA  _
GAM984  LOC254848 5'  AATGAGTGAAGAGGAACCAGGG 98878          GACA
          A                      TTTTTGGTTTT   TCATTCATT
                                ||||||||||   |||||||||
                                AGGGACCAAGG   AGTGAGTAA
                                    AGA_
GAM984  LOC254866 5'  GGTAGGGTGCGGGACCGGGG  98570          A   AT_
                                TTTTGGTTTTG CATC   TC
                                |||||||||| ||||  ||
                                GGGGCCAGGGC GTGG   GG
                                   _   GAT
GAM984  LOC254964 5'  GGTGGAGAAGCTGTTAGAACAG 96700     TG      ___  A
          GAGA                    TTTT  GTTTTGACA   TC TTCATT
                                ||||  |||||||||   || ||||||
                                AGAG  CAAGATTGT   AG AGGTGG
                                  GA       CGA  _
GAM984  LOC255031 3'  GTGAATGAATGACTAGAA    99043        TTGACA
                                TTTTGGTT     TCATTCAT
                                ||||||||     ||||||||
                                AAGATCAG     AGTAAGTG
                                   TA____
GAM984  LOC255131 5'  GGTGAACTTGGATGTCATGGAT 97692         _     A___
          TAAAAA                  TTTTTGGTTT TGACATC   TTCATT
                                |||||||||| |||||||   ||||||
                                AAAAATTAGG ACTGTAG   AAGTGG
                                    T      GTTC
GAM984  LOC255177 3'  GATGAGTGGACACCAACTAGAG 98394         TTGACA
          A                      TTTTTGGTT     TCATTCATT
                                |||||||||     |||||||||
                                AGAGATCAA     GGTGAGTAG
                                   CCACA_
GAM984  LOC255327 5'  TGGTGGATGGAAAAGTTGTGGA 97950          G  _______
          ACCAAGGA                TTTTTGGTTTT ACA     TCATTCATT  G
                                |||||||||| |||     |||||||||  |
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                                AGGAACCAAGG TGT     GGTAGGTGG   T
                                      _   TGAAAA
GAM984   LOC255338 5'  AGTGAATGTAGTAAAATGGGAA 97630      G     ACAT
            A                    TTTTT GTTTTG    CATTCATT
                                 ||||| ||||||    ||||||||
                                 AAAGG TAAAAT    GTAAGTGA
                                    G     GAT_
GAM984   LOC255565 3'  AGTGACTTCGAGACCAGGAA   96801           CA
                                 TTTTTGGTTTTGA  TCATT
                                 ||||||||||||  |||||
                                 AAGGACCAGAGCT  AGTGA
                                       TC
GAM984   LOC255671 3'  GGTGAGCTGTTGTTGGAGCT   99073      TG   T  _
                                 GGTTT  ACA CA TTCATT
                                 |||||  ||| || ||||||
                                 TCGAG  TGT GT GAGTGG
                                    GT   T  C
GAM984   LOC255926 3'  AATGCTGTCGGGACTGAG    97823    TG       T
                                 TT  GTTTTGACA CATT
                                 ||  |||||||||| ||||
                                 GA  CAGGGCTGT GTAA
                                  GT       C
GAM984   LOC256355 5'  GATGGGGCCGGGGCCAAGA    97752          A___
                                 TTTTGGTTTTG    CATC
                                 ||||||||||    ||||
                                 AGAACCGGGGC    GTAG
                                       CGGG
GAM984   LOC256369 5'  TGATGCTTGGGGCTAGAAA    96612          TG _
                                 TTTTTGGTTT  A CATCA
                                 ||||||||||  | |||||
                                 AAAGATCGGG  T GTAGT
                                      GT C
GAM984   LOC256596 5'  AGTGAGGCGAGGATGAAGCCGA 98730           ACA  A_
            GAG                     TTTTTGGTTTTG   TC  TTCATT
                                 ||||||||||||   ||  ||||||
                                 GAGAGCCGAAGT   AG  GAGTGA
                                       AGG  CG
GAM984   LOC257096 5'  GATGAAGATGCTGTGGAAGCTG 97628     TG    G   T   __
            AGG                     TTT  GTTTT ACA CAT  TCATT
                                 |||  ||||| ||| |||  |||||
                                 GGA  CGAAG TGT GTA  AGTAG
                                   GT    G   C   GA
GAM984   LOC257464 5'  AATGAATGCACAATACCAAGAA 91238        T   ACAT
                                 TTTTTGGT TTG    CATTCATT
                                 ||||||||  |||    ||||||||
                                 AAGAACCA AAC    GTAAGTAA
                                      T   AC__
GAM984   LOC257464 5'  AGTGAAACTGGGGTCAAGGGCC 91240          _    AT  __
            AAAGA                   TTTTTGGTT TTGAC  CA  TTCATT
                                 |||||||||  |||||  ||  ||||||
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                                AGAAACCGG AACTG  GT  AAGTGA
                                     G    GG  CA
GAM984  LOC257554 3'  GGTGATCATGGGAGCCAGAG   99534          ___  _
                                TTTTGGTTT   TGA CATC
                                |||||||||   ||| ||||
                                GAGACCGAG   ACT GTGG
                                     GGT   A
GAM984  LOC257577 3'  AGTGAATGTGGCAGTTCAAAAA 99671        TT   A  T
                                TTTTTGG  TTG CA CATTCATT
                                |||||||  ||| || ||||||||
                                AAAAACT  GAC GT GTAAGTGA
                                   T_  G  _
GAM984  LOC51000  5'  AATGGATGAGGTCGGGGTGGAA 32538      G TT    A
           GA                     TTTTT G  TTGAC TCATTCATT
                                |||||  |  ||||| |||||||||
                                AGAAG T  GGCTG AGTAGGTAA
                                   G GG    G
GAM984  LOC51035  3'  ATGGTGCAAGGCCAGGAA    32391           A
                                TTTTTGGTTTTG CATCAT
                                ||||||||||| ||||||
                                AAGGACCGGAAC GTGGTA
                                          _
GAM984  LOC51049  3'  AGTGAATGCTTCAAAATAAAAG 32455      G      CAT
                                TTTT GTTTTGA   CATTCATT
                                |||| |||||||   ||||||||
                                GAAA TAAAACT   GTAAGTGA
                                  A      TC_
GAM984  LOC51134  5'  AGTGGGTGCCTGTGGTTGGAGC 32792    TT     TG  AT____
           TGTGGA                  TT  TGGTTT  AC     CATTCATT
                                ||  ||||||  ||     ||||||||
                                AG  GTCGAG  TG     GTGGGTGA
                                 GT     GT  GTGTCC
GAM984  LOC51218  3'  TGGTGTTCGGGCTAAGAA    33535         TT
                                TTTTTGGTT  GACATCA
                                |||||||||  |||||||
                                AAGAATCGG  TTGTGGT
                                     GC
GAM984  LOC51279  3'  GGTGGGTGGATCACGAGGTCAG 33762       GT    ACA_
           GAG                     TTTTTG  TTTG    TCATTCATT
                                ||||||  ||||    |||||||||
                                GAGGAC  GAGC    GGTGGGTGG
                                   TG    ACTA
GAM984  LOC51315  5'  GATGAGTGAGAGTGGAGAATTG 34011    TG  _   G  A_
           GA                     TT  GT TTT AC  TCATTCATT
                                ||  || ||| ||  |||||||||
                                AG  TA GAG TG  AGTGAGTAG
                                 GT  A   G  AG
GAM984  LOC54499  3'  GTTGTCTTGGTGTAGGAATTGG 71159     TG    TG     TT_  TT
           AAA                     TTTT  GTTT  ACATCA   CA
                                ||||  ||||  ||||||   ||
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                                AAAG  TAAG  TGTGGT   GT
                                  GT    GA     TCT  TGA
GAM984  LOC55974  3' GATGATTGATTGGGGCCTAGGA 38746     T    TG CA   T
                                TTTT GGTTT  A  TCA TCATT
                                |||| |||||  |  ||| |||||
                                AGGA CCGGG  T  AGT AGTAG
                                  T    GT __   T
GAM984  LOC56959  5' GATGGAAGTACAAAATCAGAG  82811          _  A  AT
                                TTTTGGTTTTG AC TC  TC
                                |||||||||||| || ||  ||
                                GAGACTAAAAC TG AG  AG
                                       A  A  GT
GAM984  LOC57115  3' AATGAATGAAGAGATCCAAAAA 40206        _   GACA
                                TTTTTGG TTTT    TCATTCATT
                                ||||||| ||||    |||||||||
                                AAAAACC AGAG    AGTAAGTAA
                                    T   A___
GAM984  LOC63929  3' GGTGGATCTCTTGAGACCAGGA 42283         TG CATC
          G                      TTTTTGGTTT  A    ATTCATT
                                |||||||||| |    |||||||
                                GAGGACCAGA  T    TAGGTGG
                                      GT CTC_
GAM984  LOC84524  3' AATGGATGGGACAGAGAGCTGG 51656     TG    GACA_
          GA                     TTT  GTTTT    TCATTCATT
                                |||  |||||    |||||||||
                                AGG  CGAGA    GGTAGGTAA
                                  GT    GACAG
GAM984  LOC84570  5' GGTGGGAAGCGAAGCCGAGA   51685          ACA_
                                TTTTGGTTTTG    TCATT
                                ||||||||||    |||||
                                AGAGCCGAAGC    GGTGG
                                       GAAG
GAM984  LOC85414  3' AATGTTTATGGTGACAAAATTA 53549          A     T__
          AAG                     TTTTGGTTTTG CATCAT   CATT
                                |||||||||| ||||||   ||||
                                GAAATTAAAAC GTGGTA   GTAA
                                       A     TTT
GAM984  LOC85479  5' AATGGAAACTATAGAACCAAAA 53556          ACATCA
          A                      TTTTTGGTTTTG     TTCATT
                                ||||||||||||     ||||||
                                AAAAACCAAGAT     AGGTAA
                                       ATCAA_
GAM984  LOC89135  3' AATGAATGGTAAAGACTTGGAG 60945     TT     GAC
                                TTT  GGTTTT   ATCATTCATT
                                |||  ||||||   ||||||||||
                                GAG  TCAGAA   TGGTAAGTAA
                                  GT     A__
GAM984  LOC89135  3' GATGGTGCTGTCAAGGCTATGG 60946    TT         T   T
          A                      TT  TGGTTTTGACA CAT CATT
                                ||  ||||||||||| ||| ||||
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                                AG  ATCGGAACTGT GTG GTAG
                                 GT         C  _
GAM984  LOC90019  3' AGTGGGTGAACAGAGGTGAGAA 57522       G    ACA
                                TTTTTG TTTTG   TCATTCATT
                                |||||| |||||   |||||||||
                                AAGAGT GAGAC   AGTGGGTGA
                                   G    A__
GAM984  LOC90092  3' AGTGGGTGGAGGCCAGGGG   62054          G  A
                                TTTTTGGTTTT AC TCATT
                                |||||||||||| || |||||
                                GGGGACCGGAG TG GGTGA
                                      G  _
GAM984  LOC90119  5' GATGGGTGCTGGTGGGGCCTGG 62209     TT     GA  T
           AG                     TTT  GGTTTT  CA CATTCATT
                                |||  ||||||  || ||||||||
                                GAG  CCGGGG  GT GTGGGTAG
                                  GT     TG  C
GAM984  LOC90139  3' AATGAGTGATGTCTGCCAGG   56262       TTT
                                TTTGGT   GACATCATTCATT
                                ||||||   ||||||||||||||
                                GGACCG   CTGTAGTGAGTAA
                                   T__
GAM984  LOC90297  3' AGTGGACTGAGTAGAACTGGAG 62849      TG     A A  _
           G                     TTTT  GTTTTG C TCA TTCATT
                                ||||  |||||| | ||| ||||||
                                GGAG  CAAGAT G AGT AGGTGA
                                  GT     _ _  C
GAM984  LOC90520  5' GATGGGGGTACTCACAGCCAGG 63838         T   C_   A
           G                     TTTTGGTT TGA  ATC TTCATT
                                |||||||| |||  ||| ||||||
                                GGGACCGA ACT  TGG GGGTAG
                                     C   CA  _
GAM984  LOC90564  3' TGAATGTAAAGACTGGAAG   63937      TG    GACAT
                                TTTT  GTTTT    CATTCA
                                ||||  |||||    ||||||
                                GAAG  CAGAA    GTAAGT
                                  GT    AT___
GAM984  LOC90573  3' GGTGGGTGAATTGCTTGAGGTC 63960       GT  TG _  __
           AGGAA                   TTTTTG  TT  A CA  TCATTCATT
                                ||||||  ||  | ||  |||||||||
                                AAGGAC  GA  T GT  AGTGGGTGG
                                   TG  GT C  TA
GAM984  LOC90620  3' AGTGAATGCACCTCAGAGTCCA 64326       _     CAT_
           AGA                     TTTTGG TTTTGA    CATTCATT
                                ||||||| ||||||   ||||||||
                                AGAACC GAGACT    GTAAGTGA
                                   T     CCAC
GAM984  LOC90841  5' CTGGGTGATAGAGCTGGAG   64868     TG    GAC      TT
                                TTT  GTTTT   ATCATTCA
                                |||  |||||   ||||||||
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                                GAG  CGAGA   TAGTGGGT
                                  GT    ___      CC
GAM984  LOC90850  3' GAATGTTCAGGATTAAAAG   64881          CAT
                                TTTTTGGTTTTGA   CATTC
                                ||||||||||||   |||||
                                GAAAATTAGGACT   GTAAG
                                       T__
GAM984  LOC90957  3' TTGGAGTGTCAAGGGTGAGAG  65093      G       CA    TT
                                TTTTTG TTTTGACAT  TTCA
                                ||||||| |||||||||  ||||
                                GAGAGT GGAACTGTG  AGGT
                                   G        __   TT
GAM984  LOC90981  3' GATGCTTCTTCAAGGCTAAGAA 65142          _____
                                TTTTTGGTTTTGA    CATC
                                ||||||||||||    ||||
                                AAGAATCGGAACT    GTAG
                                       TCTTC
GAM984  LOC91069  3' AGTGGAAGCTCATCATGACCAG 65397        T   CATCA_
           AAA                    TTTTTGGTT TGA     TTCATT
                                ||||||||| |||     ||||||
                                AAAGACCAG ACT     AGGTGA
                                     T   ACTCGA
GAM984  LOC91097  5' GGTGGTAACGGTTGGGGTCAGG 65464       TT TG  ATCAT
           AA                    TTTTTGG  T  AC    TCATT
                                |||||||  |  ||    |||||
                                AAGGACT  G  TG    GGTGG
                                    GG GT  GCAAT
GAM984  LOC91156  5' AGCCACTGGTGGTCAAGGCTGG 65704     TG      _   TTCATT
           GAA                    TTTT  GTTTTGAC ATCA
                                ||||  |||||||| ||||
                                AAGG  CGGAACTG TGGT
                                  GT       G   CACCGA
GAM984  LOC91156  5' GGTGGTCAAGGCTGGGAA    65713     TG      _
                                TTTT  GTTTTGAC ATC
                                ||||  |||||||| |||
                                AAGG  CGGAACTG TGG
                                  GT       G
GAM984  LOC91286  5' AATGGATGATGTTAAAAACTAA 66054         _
           G                     TTTGGTTTT GACATCATTCATT
                                |||||||| ||||||||||||
                                GAATCAAAA TTGTAGTAGGTAA
                                     A
GAM984  LOC91409  3' GGTGGGCAGGACCAGGGA    66573          A_
                                TTTTTGGTTTTG  CATC
                                ||||||||||||  ||||
                                AGGGACCAGGAC  GTGG
                                       GG
GAM984  LOC91450  5' GGTGGGCAGTCAGGGCCTAGGA 66657     T       ATCA
                                TTTT GGTTTTGAC    TTCATT
                                |||| |||||||||    ||||||
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                                AGGA CCGGGACTG    GGGTGG
                                  T       AC__
GAM984  LOC91547  3' GGTGGGTGCTTTGAACCAGGAA 67005        TGACAT
                                TTTTTGGTTT     CATTCATT
                                ||||||||||     ||||||||
                                AAGGACCAAG     GTGGGTGG
                                    TTTC__
GAM984  LOC91585  5' AATGGATTAGTGCTAGGAGCCA 67157         GA_  C_
           AGGA                   TTTTTGGTTTT   CAT  ATTCATT
                                ||||||||||||   |||  |||||||
                                AGGAACCGAGG   GTG  TAGGTAA
                                    ATC   AT
GAM984  LOC91695  3' TGGCTGGAGGTGCAGGGCCAGG 67512          A   A   TT
           AG                     TTTTTGGTTTTG CATC TTCA
                                ||||||||||||| |||| ||||
                                GAGGACCGGGAC GTGG AGGT
                                    _   _   CGGTA
GAM984  LOC91948  3' GATGAACTTAAAGCTGAAAA  68236     TG     ___
                                TTTT  GTTTTGA   CATC
                                ||||  |||||||   ||||
                                AAAA  CGAAATT   GTAG
                                  GT      CAA
GAM984  LOC91948  3' GGTGGATCACTTGAAGCCAGGA 68242        TG CATC
           G                     TTTTTGGTTT  A    ATTCATT
                                ||||||||||  |   |||||||
                                GAGGACCGAA  T    TAGGTGG
                                    GT CAC_
GAM984  LOC91948  3' GGTGGGTGGATCACTTGAAGCC 68243        TG CA___
           AGGAG                   TTTTTGGTTT  A    TCATTCATT
                                ||||||||||  |    |||||||||
                                GAGGACCGAA  T    GGTGGGTGG
                                    GT CACTA
GAM984  LOC91963  5' GGTGGGTTACTTGAGGCCAGGA 68323        TG CATC
           G                     TTTTTGGTTT  A    ATTCATT
                                ||||||||||  |   |||||||
                                GAGGACCGGA  T    TGGGTGG
                                    GT CAT_
GAM984  LOC92080  3' AGTGAGTGGGTGGGGTGCAGGA 68618      GT   G  A
           G                     TTTTTG  TTT AC TCATTCATT
                                ||||||  ||| || |||||||||
                                GAGGAC  GGG TG GGTGAGTGA
                                   GT   G  _
GAM984  LOC92080  3' AGTGGGTGGGGTGCAGGAGACA 68619      G_    _ AT
           GAGA                    TTTTTG  TTTTG AC  CATTCATT
                                ||||||  ||||| ||  ||||||||
                                AGAGAC  AGGAC TG  GTGGGTGA
                                   AG    G  GG
GAM984  LOC92340  3' GGTGAATGGTGTCTGCATTAAA 69566       TTT
           A                     TTTTGGT   GACATCATTCATT
                                |||||||   |||||||||||||
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                                AAAATTA  CTGTGGTAAGTGG
                                    CGT
GAM984  LOC92558  3'  GATGGGTGGACTGGAGGCAGCT 70311     TG  _  GA  __
          GGAAA                   TTTT  GTT TT  CA  TCATTCATT
                                |||| ||| ||  ||  |||||||||
                                AAAG  CGA GG  GT  GGTGGGTAG
                                  GT   C  AG  CA
GAM984  LOC93052  3'  GATGAGGTTGTGGAACTAGAAA 71770          G   TCA
                                TTTTTGGTTTT ACA  TTCATT
                                |||||||||| |||  ||||||
                                AAAGATCAAGG TGT  GAGTAG
                                      _  TG_
GAM984  LOC93132  5'  AGTGAGTGAAGAAGAACCAGA  71978         GACA
                                TTTGGTTTT   TCATTCATT
                                |||||||||   |||||||||
                                AGACCAAGA   AGTGAGTGA
                                     AGA_
GAM984  LOC93512  3'  GGTGGGTGATGGCTCCGGGAG  72879        TTTTGA
                                TTTTTGG     CATCATTCATT
                                |||||||     ||||||||||
                                GAGGGCC     GTAGTGGGTGG
                                    TCG___
GAM984  LOC93624  5'  GATGAGGAAAATCAGGCCAGAG 73102         T  CATCA
                                TTTTGGTTT GA    TTCATT
                                |||||||| ||    ||||||
                                GAGACCGGA CT    GAGTAG
                                      _ AAAAG
GAM984  LOC96573  3'  AATGGATGATGGACTTTGGCT  63869      TTGA__
                                GGTT     CATCATTCATT
                                ||||     ||||||||||
                                TCGG     GTAGTAGGTAA
                                  TTTCAG
GAM985  C18orf1   3'  TGCCACCAGAGTAGAGTCT   60875     A  _   GG
                                AGA CTC ATTT  TGGTGGCA
                                ||| ||| ||||  ||||||||
                                TCT GAG TGAG  ACCACCGT
                                  _  A   __
GAM985  CDH11     3'  TTGCCACCCTCCAGAATCCTGA 54461      AACTCA    T_
                                TCAG     TTTGG  GGTGGCAA
                                ||||     |||||  ||||||||
                                AGTC     AGACC  CCACCGTT
                                  CTA___     TC
GAM985  ELK1      3'  CCACCACCACCCCTTCTGG    19088       CTCATT
                                TCAGAA     TGGTGGTGG
                                ||||||     |||||||||
                                GGTCTT     ACCACCACC
                                   CCCC__
GAM985  EYA4      3'  TGGTACACACCAAATGAGT    15887          _  G
                                ACTCATTTGGTG GTG CA
                                |||||||||||| ||| ||
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                                TGAGTAAACCAC CAT GT
                                      A   G
GAM985  F2RL3    3'  TGCCACCACCTTGACCCTGG  15530     AAC   TTT
                                TCAG  TCA  GGTGGTGGCA
                                ||||  |||  ||||||||||
                                GGTC  AGT  CCACCACCGT
                                  CC_  T__
GAM985  FANCG    3'  TGCCACCACCAAGTCATTGA  17338     AACTC
                                TCAG   ATTTGGTGGTGGCA
                                ||||   ||||||||||||||
                                AGTT   TGAACCACCACCGT
                                  AC___
GAM985  FMNL     5'  GCCACCACCTCCGGGCACTGA 20869     AA  ATTT
                                TCAG CTC   GGTGGTGGC
                                |||| |||   |||||||||
                                AGTC GGG   CCACCACCG
                                  AC  CCT_
GAM985  FUT7     3'  TGCCACGTCCATAGTTCTGA  16808       CATT  TG
                                TCAGAACT   TGG  GTGGCA
                                ||||||||   |||  ||||||
                                AGTCTTGA   ACC  CACCGT
                                     T___  TG
GAM985  LAMC2    3'  TGCCACCTTCAAGTTCTGG   19910       CATT  T
                                TCAGAACT   TGG GGTGGCA
                                ||||||||   ||| |||||||
                                GGTCTTGA   ACT CCACCGT
                                     ____  T
GAM985  M17S2    5'  TCGCCACCTGAGGCCTGA    20912     AA   TTT
                                TCAG  CTCA  GGTGGTGG
                                ||||  ||||  ||||||||
                                AGTC  GAGT  CCACCGCT
                                  CG   ___
GAM985  M17S2    5'  TCGCCACCTGAGGCCTGA    20913     AA   TTT
                                TCAG  CTCA  GGTGGTGG
                                ||||  ||||  ||||||||
                                AGTC  GAGT  CCACCGCT
                                  CG   ___
GAM985  MYEOV    5'  TCACCACCTGCTGAGCTCTG  57849     A   TTT
                                CAGA CTCA  GGTGGTGG
                                |||| ||||  ||||||||
                                GTCT GAGT  CCACCACT
                                  C   CGT
GAM985  NR5A2    3'  TTGCCATTTTAAATATGTTCTG 15119       TC    T
           A                     TCAGAAC  ATTTGG GGTGGCAA
                                 |||||||  |||||| ||||||||
                                 AGTCTTG  TAAATT TTACCGTT
                                    TA    _
GAM985  NUP62    5'  CCGCCACCAGAGTCCGGA    25646    AGA   ATT
                                TC   ACTC   TGGTGGTGG
                                ||   ||||   |||||||||
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                              AG  TGAG  ACCACCGCC
                               GCC  ___
GAM985  NUP62    5' CCGCCACCAGAGTCCGGA   25647   AGA   ATT
                              TC  ACTC  TGGTGGTGG
                              ||  ||||  |||||||||
                              AG  TGAG  ACCACCGCC
                               GCC  ___
GAM985  PPP2R2B  3' CCACCACCCCTGAGTCCCTGA 17120    A_   TTT
                              TCAG ACTCA  GGTGGTGG
                              |||| |||||  ||||||||
                              AGTC TGAGT  CCACCACC
                                CC   CC_
GAM985  RGS14    5' CCGCCACCGTGCAAGCTCTGG 22398     A CATT
                              TCAGA CT   TGGTGGTGG
                              ||||| ||   |||||||||
                              GGTCT GA   GCCACCGCC
                                 C ACGT
GAM985  SMURF1   3' CTGCCACCAGATCGAATTTCGA 94046   AG C _      TG
                              TC AA TC ATTTGGTGG G
                              ||  || || ||||||||| |
                              AG TT AG TAGACCACC C
                               CT A C       GT
GAM985  SYNGR1   3' CCACCACCTGGTTAAGTCTCGA 17497   _ ACTC TT
                              TC AGA   AT GGTGGTGG
                              || |||   ||  ||||||||
                              AG TCT   TG CCACCACC
                               C  GAAT GT
GAM985  20D7-FC4 5' CCACCACCACCTAGGTCCTGA 61563    A  CATT
                              TCAG ACT   TGGTGGTGG
                              |||| |||   |||||||||
                              AGTC TGG   ACCACCACC
                                C  ATCC
GAM985  CXYorf1  3' CCACCACCACCCCCAGCTCCTG 82905    AA_ CATT_
           A                   TCAG  CT   TGGTGGTGG
                              ||||  ||   |||||||||
                              AGTC  GA   ACCACCACC
                                CTC CCCCC
GAM985  FLJ00026 3' TTATTCCCAAATGGACTCTGA 65623    AC     TG
                              TCAGA TCATTTGG GTGG
                              ||||| |||||||| ||||
                              AGTCT GGTAAACC TATT
                                 CA      CT
GAM985  FLJ11113 3' CCACCACCACAGGGTGCT   37631   A  ATT
                              AG ACTC  TGGTGGTGG
                              || ||||  |||||||||
                              TC TGGG  ACCACCACC
                               G  AC_
GAM985  FLJ13322 5' TCGCCACCTGGCGACCCTGA  45633    AAC A TT
                              TCAG  TC T GGTGGTGG
                              ||||  || | ||||||||
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                                AGTC  AG G  CCACCGCT
                                  CC_  C GT
GAM985  FLJ20038  3'  CTGTGTCCAAATGGGTTCTGA  34863           TG TG
                                TCAGAACTCATTTGG  G  G
                                ||||||||||||||  |  |
                                AGTCTTGGGTAAACC  T  C
                                       TG GT
GAM985  FLJ20130  5'  TTGCCACCACCACTAGTTC   35085     CATT
                                GAACT   TGGTGGTGGCAA
                                |||||   ||||||||||||
                                CTTGA   ACCACCACCGTT
                                  TC__
GAM985  FLJ20856  3'  CCACCACCTGTGTGAACTTGA  47863     AAC   TT_
                                TCAG  TCAT  GGTGGTGG
                                ||||  ||||  ||||||||
                                AGTT  AGTG  CCACCACC
                                  CA_   TGT
GAM985  FLJ22059  3'  CCACCACCTTGTAAGTTCT   43052      C  TT
                                AGAACT AT  GGTGGTGG
                                ||||||  ||  ||||||||
                                TCTTGA TG  CCACCACC
                                   A  TT
GAM985  FLJ32468  5'  TGCCACCACCCTGATCT    59714    AC   TTT
                                AGA  TCA   GGTGGTGGCA
                                |||  |||   ||||||||||
                                TCT  AGT   CCACCACCGT
                                  __   C__
GAM985  FRAG1     5'  GCCACCACCGCGTGGGTCTGA  27945      A    T
                                TCAGA CTCAT TGGTGGTGGC
                                ||||| ||||| ||||||||||
                                AGTCT GGGTG GCCACCACCG
                                  _    C
GAM985  GTPBP2    3'  TTGCCACCCTGTGCTGAGGCCT 39387     AA   TT_  T
           GA                   TCAG  CTCA   TGG GGTGGCAA
                                ||||  ||||   ||| ||||||||
                                AGTC  GAGT   GTC CCACCGTT
                                  CG   CGT  _
GAM985  H2BFQ     3'  TTGATGAATCCAAATGAGCTCT 60078     A       TGGTGG
                                AGA CTCATTTGG     CAA
                                ||| |||||||||     |||
                                TCT GAGTAAACC     GTT
                                  C        TAAGTA
GAM985  HSC3      5'  CCACCACCAGCAGAGCCTGA  59730     AA   AT
                                TCAG  CTC  TTGGTGGTGG
                                ||||  |||  ||||||||||
                                AGTC  GAG  GACCACCACC
                                  C_   AC
GAM985  KIAA0229  3'  TGCCACCACCACGTCCTG    94030     A  TCATT
                                CAG AC    TGGTGGTGGCA
                                ||| ||    ||||||||||
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                                GTC TG    ACCACCACCGT
                                  C  C____
GAM985  KIAA0423  5'  CCACCACCACCTGACAACCCTG 89180    AAC__   TT
                                CAG    TCA  TGGTGGTGG
                                |||    |||  |||||||||
                                GTC    AGT  ACCACCACC
                                  CCAAC   CC
GAM985  KIAA0970  3'  TGCCACCACCATCAGAATTC   30621    C  ATT
                                GAA TC   TGGTGGTGGCA
                                ||| ||   ||||||||||
                                CTT AG   ACCACCACCGT
                                  A  ACT
GAM985  KIAA1055  5'  CCACCACCAAAGAGCTGA    66654     AA   A
                                TCAG  CTC TTTGGTGGTGG
                                ||||  ||| ||||||||||
                                AGTC  GAG AAACCACCACC
                                   __   _
GAM985  MGC23445  5'  TGCCACCACCATGCCTGA    58775     AACT  TT
                                TCAG    CA  TGGTGGTGGCA
                                ||||    ||  ||||||||||
                                AGTC    GT  ACCACCACCGT
                                  C___  __
GAM985  MSTP032   3'  TCACCAAATAGGTTCTGA    48207       TC
                                TCAGAAC  ATTTGGTGG
                                |||||||  |||||||||
                                AGTCTTG  TAAACCACT
                                    GA
GAM985  RAB3IL1   3'  TGCCACCACCAGGAGGATTTC  26370    C  A_
                                GAA TC  TTTGGTGGTGGCA
                                ||| ||  ||||||||||||
                                CTT AG  GGACCACCACCGT
                                  T  GA
GAM985  RIN1      3'  TGCCACCACCTTTGTCTGA   16277      ACT  TTT
                                TCAGA   CA   GGTGGTGGCA
                                |||||   ||   ||||||||||
                                AGTCT   GT   CCACCACCGT
                                   ___  TT_
GAM985  SEC15L    3'  CCAAACCAAATGAACTCTGG   72729      AC       GG
                                TCAGA  TCATTTGGT  TGG
                                |||||  |||||||||  |||
                                GGTCT  AGTAAACCA  ACC
                                   CA       A_
GAM985  SEC8      3'  GCCACCCCTAATTTCTGA    41736       CTC   T  T
                                TCAGAA   ATT GG GGTGGC
                                ||||||   ||| || ||||||
                                AGTCTT   TAA CC CCACCG
                                   ___   T  _
GAM985  TRIM5     3'  TCACCAATGAATGAGTCCT   53478    A      GG
                                AG ACTCATTT  TGGTGG
                                || ||||||||  ||||||
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                                TC TGAGTAAG  ACCACT
                                 C       TA
GAM985   LOC120892 5'  TTGAAGTTTCCAAATGAGTTT  74478          TGGTGG
                                GAACTCATTTGG     CAA
                                ||||||||||||     |||
                                TTTGAGTAAACC     GTT
                                      TTTGAA
GAM985   LOC146056 3'  CCACCACCTCCTGAATTCTG   78077      C   TTT
                                CAGAA TCA   GGTGGTGG
                                ||||| |||   ||||||||
                                GTCTT AGT   CCACCACC
                                   A   CCT
GAM985   LOC146237 3'  CCACCACCACCACCTTCATGA  84606     _   CTCATT
                                TCA GAA     TGGTGGTGG
                                ||| |||     |||||||||
                                AGT CTT     ACCACCACC
                                  A   CCACC_
GAM985   LOC148231 3'  TTGCCACCAAGGAGCTGCTGA  79492      AA_   A       TG
                                TCAG   CTC TTTGGTGG  G
                                ||||   ||| ||||||||  |
                                AGTC   GAG GAACCACC  T
                                   GTC   _       GT
GAM985   LOC148508 3'  TTACCATCAAATGAATTGTGA  85312     G  C
                                TCA AA TCATTTGGTGGTGG
                                ||| || ||||||||||||||
                                AGT TT AGTAAACTACCATT
                                  G  A
GAM985   LOC149420 3'  TTGAAGAAACCAAATGAGCTC  80160     A        GGTGG
                                GA CTCATTTGGT     CAA
                                || ||||||||||     |||
                                CT GAGTAAACCA     GTT
                                 C         AAGAA
GAM985   LOC154089 3'  TGCCACCTACCAAACTCTGG   81946      ACTCA     _
                                TCAGA     TTTGGT GGTGGCA
                                |||||     |||||| |||||||
                                GGTCT     AAACCA CCACCGT
                                   C____      T
GAM985   LOC155368 3'  TGCCTATTAAATGAGCTC    82265    A        GT
                                GA CTCATTTGGTG  GGCA
                                || ||||||||||  ||||
                                CT GAGTAAATTAT  CCGT
                                 C          __
GAM985   LOC158947 3'  TGAACACCAAATGAATTC    82930     C        GTGG
                                GAA TCATTTGGTG    CA
                                ||| ||||||||||    ||
                                CTT AGTAAACCAC    GT
                                  A         AA__
GAM985   LOC199870 3'  TGCCACCCTCTGAACTTTGA   89805      AC   TTT  T
                                TCAGA  TCA   GG GGTGGCA
                                |||||  |||   || |||||||
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                                AGTTT  AGT   TC CCACCGT
                                  CA   C__  _
GAM985   LOC200093 3'  CCACCACCACCCCCAGCTCCTG 63763      AA_  CATT_
           A                     TCAG   CT    TGGTGGTGG
                                 ||||   ||    |||||||||
                                 AGTC   GA    ACCACCACC
                                   CTC  CCCCC
GAM985   LOC221794 5'  CCACCACCATGAATGGTCTGA  95530      A T   __
                                 TCAGA C CATT  TGGTGGTGG
                                 ||||| | ||||  |||||||||
                                 AGTCT G GTAA  ACCACCACC
                                   _ _   GT
GAM985   LOC253650 3'  TTGCCACCATCTTGGAGCTC   97874    A   ATTT
                                 GA CTC    GGTGGTGGCAA
                                 || |||    ||||||||||
                                 CT GAG    CTACCACCGTT
                                  C   GTT_
GAM985   LOC253943 3'  CTACCACTTAATGAATCT    97844     AC    T
                                 AGA  TCATT GGTGGTGG
                                 |||  ||||| ||||||||
                                 TCT  AGTAA TCACCATC
                                   A_    T
GAM985   LOC54550  3'  CCAGGCGCCAAATAAACCCTGG 78184      AACTC       G_
                                 TCAG    ATTTGGTG  TGG
                                 ||||    ||||||||  |||
                                 GGTC    TAAACCGC  ACC
                                   CCAAA       GG
GAM985   LOC91040  3'  CCACCACCACCCCCAGCTCCTG 65337      AA_  CATT_
           A                     TCAG   CT    TGGTGGTGG
                                 ||||   ||    |||||||||
                                 AGTC   GA    ACCACCACC
                                   CTC  CCCCC
GAM985   LOC91963  3'  TCACCCAAAATGATACCCTGA  68326     AAC_     GGT
                                 TCAG    TCATTT   GGTGG
                                 ||||    ||||||   |||||
                                 AGTC    AGTAAA   CCACT
                                   CCAT     AC_
GAM985   LOC92230  5'  CTACCACCTATGAGCTCTGG   69084      A     TT
                                 TCAGA CTCAT  GGTGGTGG
                                 ||||| |||||  ||||||||
                                 GGTCT GAGTA  CCACCATC
                                   C    T_
GAM986   GNPI      3'  CCTCAGGGACTCTCCAGCACCA 19618         CAAAAAG  GA
           A                     TTGGTGCTGG      CC  AGG
                                 ||||||||||      ||  |||
                                 AACCACGACC      GG  TCC
                                       TCTCAG_  AC
GAM986   ISGF3G    3'  CCTCAGGAACAGCTCCAGCACC 21406         CAAAAAG  GA
           AA                    TTGGTGCTGG      CC  AGG
                                 ||||||||||      ||  |||
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                                AACCACGACC      GG  TCC
                                      TCGACAA  AC
GAM986  POLR2A   5' CCTCCGGCTTTTTCCTCCCAA 8127      TGCT  C       A
                                TTGG    GG AAAAAGCCG AGG
                                ||||    || |||||||||| |||
                                AACC    CC TTTTTCGGC TCC
                                  CT__  _       C
GAM986  PPP1R12B 3' CCTTCAGCTTTTTACATTAACC 50353    GC_  GC      C
                                GGT   TG  AAAAAGC GAAGG
                                |||   ||  ||||||| |||||
                                CCA   AC  TTTTTCG CTTCC
                                  ATT  A_     A
GAM986  PPP1R12B 3' CCTTCAGCTTTTTACATTAACC 50372    GC_  GC      C
                                GGT   TG  AAAAAGC GAAGG
                                |||   ||  ||||||| |||||
                                CCA   AC  TTTTTCG CTTCC
                                  ATT  A_     A
GAM986  PPP1R12B 3' CCTTCAGCTTTTTACATTAACC 50386    GC_  GC      C
                                GGT   TG  AAAAAGC GAAGG
                                |||   ||  ||||||| |||||
                                CCA   AC  TTTTTCG CTTCC
                                  ATT  A_     A
GAM986  RAI3     3' CCTCAGCAGCTCCCCAGCACCA 15619         CAAAAA  C  A
          A                      TTGGTGCTGG     GC GA GG
                                ||||||||||     || || ||
                                AACCACGACC     CG CT CC
                                      CCTCGA  A  _
GAM986  AQP9     3' CTTGCTTCCTGCCAGCACCAA  40939          AA   CG
                                TTGGTGCTGGCA  AAGC  AAG
                                ||||||||||||  ||||  |||
                                AACCACGACCGT  TTCG  TTC
                                       CC   __
GAM986  DKFZP586G1122 3' CCATTCTTTTCACCAGCACC   61937        CA    CC  A
                                GGTGCTGG  AAAAG  GA GG
                                ||||||||  |||||  || ||
                                CCACGACC  TTTTC  TT CC
                                     AC    __  A
GAM986  FLJ10111  3' CCTCAGGAACAGCTCCAGCACC 36301         CAAAAAG  GA
          AA                     TTGGTGCTGG      CC  AGG
                                ||||||||||      ||  |||
                                AACCACGACC      GG  TCC
                                      TCGACAA  AC
GAM986  FLJ10884  5' CTTTTTCGCCAGGCACCAA   39354        _   _
                                TTGGTGC TGGC AAAAAG
                                ||||||| |||| ||||||
                                AACCACG ACCG TTTTTC
                                    G   C
GAM986  KIAA0169 5' CGCCTCTGCCAGCACCGA    73179          AAA  C
                                TTGGTGCTGGCA   AG CG
                                ||||||||||||   || ||
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                                AGCCACGACCGT   TC GC
                                      C__  C
GAM986  LENEP    3'  CCTCCTCTCCCCACCAGCACCA 38477        CAAAA  CC  A
                                TGGTGCTGG    AG  GA GG
                                |||||||||    ||  || ||
                                ACCACGACC    TC  CT CC
                                     ACCCC  TC  _
GAM986  RASGRP4  3'  CCTGAGCCCTGACAGCACCAA  54744        G  AAAA  CGA
                                TTGGTGCTG CA   GC   AGG
                                ||||||||| ||   ||   |||
                                AACCACGAC GT   CG   TCC
                                     A  CC__  AG_
GAM986  LOC152274 3'  CCTTCGACTTCCTCATGGCACC 81338        GCAAA   C
          A                      TGGTGCTG    AAG CGAAGG
                                |||||||||    ||| ||||||
                                ACCACGGT    TTC GCTTCC
                                     ACTCC   A
GAM986  LOC157226 5'  CCCTCAGCGCCGCCGACACCAA 64638       C   AAAAA  C  A
                                TTGGTG TGGC    GC GA GG
                                |||||| ||||    || || ||
                                AACCAC GCCG    CG CT CC
                                   A   CCG__  A  C
GAM986  LOC157931 3'  CCTTTCCTCTGCCAGCACCA   87939        AAA  CC
                                TGGTGCTGGCA   AG  GAAGG
                                ||||||||||   ||  |||||
                                ACCACGACCGT   TC  TTTCC
                                      C__  C_
GAM986  LOC220573 5'  CGGCTCTCTGCCAGCATCAA   70204         AAA
                                TTGGTGCTGGCA   AGCCG
                                ||||||||||||   |||||
                                AACTACGACCGT   TCGGC
                                      CTC
GAM986  LOC255809 3'  CCTTCGGCTCCTCAGGACCA   98581     G   CAAAA
                                TGGT CTGG    AGCCGAAGG
                                |||| ||||    |||||||||
                                ACCA GACT    TCGGCTTCC
                                  G   CC___
GAM986  LOC256158 5'  CCTGCTCCCCACCAGCACCAA  99489        CAAAA   CGA
                                TTGGTGCTGG    AGC   AGG
                                ||||||||||    |||   |||
                                AACCACGACC    TCG   TCC
                                     ACCCC   ___
GAM986  LOC256380 5'  CCCTCTGCATCCCACAGCACCA 97674        GCAAAAA  C  A
          A                      TTGGTGCTG      GC GA GG
                                |||||||||      || || ||
                                AACCACGAC      CG CT CC
                                     ACCCTA_  T  C
GAM986  LOC51754  5'  GCTCCTTTGCCAGCACCGA   71582          A_
                                TTGGTGCTGGCAAA  AGC
                                ||||||||||||||  |||
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                                AGCCACGACCGTTT  TCG
                                       CC
GAM986  LOC90786  5'  CCTCCAACTTTTTGTTTTCCAA 64731      TGCT       CCGA
                                TTGG   GGCAAAAAG   AGG
                                ||||   |||||||||   |||
                                AACC   TTGTTTTTC   TCC
                                  TT__       AACC
GAM987  CDH12     3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM987  GOCAP1    3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM987  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT    98090      T    AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT     TTATTC
                                  _   GTCA_
GAM987  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
          A                      TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM987  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM987  HMP19     3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
          TA                     TACA   TCC    GAAGAATAAG
                                ||||   |||   ||||||||||
                                ATGT   AGG    TTTCTTATTC
                                  AAA_   ATTG
GAM987  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68742              _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                          G
GAM987  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM987  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748      CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
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                                TGAG    TCTTCTTATTC
                                  TACCG
GAM987  KIAA1906 3'  CTTATTCTTCTTGACTTTTGG  73571    CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM987  OSBPL11  3'  CTTAATTTCCCAAGAGTGGTG  43206       CCAA   AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                     AACC   A_
GAM987  YME1L1   3'  TCATTCTTGATGTGGTGTA   58438       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                     TA_    A
GAM987  ZNF262   3'  CTTATTTTGTTTGGGAGT    18723       A
                                ACTCCCAAG AGAATAAG
                                |||||||||  ||||||||
                                TGAGGGTTT TTTTATTC
                                     G
GAM987  LOC91960 3'  TGTGGCTTGGAACGTGGTGTA  68294       TC_    AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
                                ATGTGGTG   GGTTC   TGT
                                     CAA    GG__
GAM988  CDH12    3'  CTTATCATTTAAAGTGGTGTA  15777       CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM988  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007     CA       G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC       G
GAM988  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090     T   AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                   _   GTCA_
GAM988  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877     CACTCCCA
          A                      TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM988  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126       CCCAAGAA
                                TACACCACT      GAATAAG
                                |||||||||      |||||||
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                                ATGTGGTGA      TTTATTC
                                     AGACG___
GAM988  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
            TA                    TACA   TCC   GAAGAATAAG
                                  ||||   |||   ||||||||||
                                  ATGT   AGG   TTTCTTATTC
                                    AAA_   ATTG
GAM988  KIAA1719 3'  TCTGTCTTGGGAGTGGTGTA  68742           _
                                  TACACCACTCCCAAGA AGA
                                  |||||||||||||||| |||
                                  ATGTGGTGAGGGTTCT TCT
                                           G
GAM988  KIAA1853 3'  TTTTTCTTGGAAGCAGTG    69929    CA  C
                                  CAC  CT CCAAGAAGAA
                                  |||  || ||||||||||
                                  GTG  GA GGTTCTTTTT
                                    AC  A
GAM988  KIAA1877 3'  CTTATTCTTCTGCCATGAGT  66748     CCA__
                                  ACTC    AGAAGAATAAG
                                  ||||    ||||||||||
                                  TGAG    TCTTCTTATTC
                                    TACCG
GAM988  KIAA1906 3'  CTTATTCTTCTTGACTTTTGG  73571    CTCC_
                                  CCA    CAAGAAGAATAAG
                                  |||    ||||||||||||
                                  GGT    GTTCTTCTTATTC
                                    TTTCA
GAM988  OSBPL11  3'  CTTAATTTCCCAAGAGTGGTG  43206       CCAA   AA
                                  CACCACTC   GAAG  TAAG
                                  ||||||||   ||||  ||||
                                  GTGGTGAG   CTTT  ATTC
                                       AACC   A_
GAM988  YME1L1   3'  TCATTCTTGATGTGGTGTA   58438       TCC    _
                                  TACACCAC   CAAGAA GA
                                  ||||||||   |||||| ||
                                  ATGTGGTG   GTTCTT CT
                                       TA_     A
GAM988  ZNF262   3'  CTTATTTTGTTTGGGAGT    18723        A
                                  ACTCCCAAG AGAATAAG
                                  |||||||||  ||||||||
                                  TGAGGGTTT TTTTATTC
                                       G
GAM988  LOC91960 3'  TGTGGCTTGGAACGTGGTGTA  68294       TC_   AAGA
                                  TACACCAC   CCAAG   ATA
                                  ||||||||   |||||   |||
                                  ATGTGGTG   GGTTC   TGT
                                       CAA    GG__
GAM989  ARNT2    3'  GTGGTCTGCTTGTCCTTCA   30090    C   _
                                  TGA AGGA GGGCAGACCAC
                                  ||| |||| ||||||||||
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                                ACT TCCT TTCGTCTGGTG
                                  _   G
GAM989  ATP8B2   5' GGTCTGCCCTCCCCCACTCA  65842    A  ACA
                                TGA TG   GGAGGGCAGACC
                                ||| ||   ||||||||||||
                                ACT AC   CCTCCCGTCTGG
                                  C  CC_
GAM989  CHGB     3' TGATCTGTTTTTCACCACTTCA 10195     _ ACA        C
                                TGAA TG   GGAGGGCAGA CA
                                |||| ||   |||||||||| ||
                                ACTT AC   CTTTTTGTCT GT
                                  C  CA_        A
GAM989  EN2      3' TGTGGTCTGTGTCGCTGTC   9276       _ GG
                                GACAG GA  GCAGACCACA
                                ||||| ||  ||||||||||
                                CTGTC CT  TGTCTGGTGT
                                   G  G_
GAM989  ENDOGL1  3' TGTGGTCTCGCCGTGTCATCCA 18827    A    GGAG  _
                                TG ATGACA    GGC AGACCACA
                                || |||||||   ||| ||||||||
                                AC TACTGT    CCG TCTGGTGT
                                 C     G___   C
GAM989  FGFR1    3' TGTGGCCTGCCTTCACCCCACT 32374     A  ACAG       A
          CA                      TGA TG    GAGGGCAG CCACA
                                ||| ||    |||||||| |||||
                                ACT AC    CTTCCGTC GGTGT
                                  C  CCCA       C
GAM989  FGFR1    3' TGTGGCCTGCCTTCACCCCACT 7024      A  ACAG       A
          CA                      TGA TG    GAGGGCAG CCACA
                                ||| ||    |||||||| |||||
                                ACT AC    CTTCCGTC GGTGT
                                  C  CCCA       C
GAM989  GFPT2    3' GTGGAGCCCCTCCTGCATCCA  18843    A  A      CAGA
                                TG ATG CAGGAGGG    CCAC
                                || ||| ||||||||    ||||
                                AC TAC GTCCTCCC    GGTG
                                 C  _       CGA_
GAM989  HPS1     3' GTCTGCCTTTGCATCCTGTC   5766        _____
                                GACAGGA     GGGCAGAC
                                |||||||     ||||||||
                                CTGTCCT     TCCGTCTG
                                    ACGTT
GAM989  LOXL2    3' GTGGTCAACTCCTGTCTTCA   11353      T      GGCA
                                TGAA GACAGGAG    GACCAC
                                |||| ||||||||    ||||||
                                ACTT CTGTCCTC    CTGGTG
                                  _       AA__
GAM989  MGA      3' GTAACCCCTGTTCTGTCTTCA  63468      T     __    CAG
                                TGAA GACAGG  AGGG   AC
                                |||| ||||||  ||||   ||
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                                ACTT CTGTCT  TCCC   TG
                                  _     TG    CAA
GAM989  NDRG2    3'  TGTGGAGGGTGCCCTCCCGTC  33196     A      GA__
                                GAC GGAGGGCA    CCACA
                                ||| ||||||||    |||||
                                CTG CCTCCCGT    GGTGT
                                  C       GGGA
GAM989  PHB      3'  TGTGGCCTCCGTCCTGTCA    12071        G  C  A
                                TGACAGGA GG AG CCACA
                                |||||||| || || |||||
                                ACTGTCCT CC TC GGTGT
                                     G  _  C
GAM989  PIK3R3   3'  TGCAGTCTGCCCTCCTGCTC   61712    _          CA
                                GA CAGGAGGGCAGAC  CA
                                || ||||||||||||  ||
                                CT GTCCTCCCGTCTG  GT
                                 C           AC
GAM989  PIP5K1A  3'  TGTCCTACCCCCCTGTCTTCA  14522     T     A   C  AC
                                TGAA GACAGG GGG AG  CA
                                |||| |||||| ||| ||  ||
                                ACTT CTGTCC CCC TC  GT
                                  _     C   A  CT
GAM989  SLC14A2  5'  GTTTGCTCTGTCACCCA     24126    AA     GAG
                                TG  TGACAG   GGCAGAC
                                ||  ||||||   |||||||
                                AC  ACTGTC   TCGTTTG
                                 CC     ____
GAM989  WARS     3'  TCTGCCCTCCTGTCACCCA    67868    AA
                                TG  TGACAGGAGGGCAGA
                                ||  ||||||||||||||
                                AC  ACTGTCCTCCCGTCT
                                 CC
GAM989  AOP2     3'  GTCCTCTCCTGTCACCCA    18136    AA         CA
                                TG  TGACAGGAGGG  GAC
                                ||  ||||||||||  |||
                                AC  ACTGTCCTCTC  CTG
                                 CC         __
GAM989  C12orf22 3'  GTAACCTGCCTTCCTTCA    48710     C        ACC
                                TGA AGGAGGGCAG   AC
                                ||| |||||||||   ||
                                ACT TCCTTCCGTC   TG
                                  _         CAA
GAM989  C20orf150 3'  GTCTCAGCCTGTCATTC     66014          AG GC
                                GAATGACAGG  G  AGAC
                                ||||||||||  |  ||||
                                CTTACTGTCC  C  TCTG
                                      GA __
GAM989  CHST3    3'  GTGGACTCCAGTCATTCA    16242         A   GGCAGA
                                TGAATGAC GGAG     CCAC
                                |||||||| ||||     ||||
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                                ACTTACTG CCTC     GGTG
                                     A   A_____
GAM989  FLJ10199  3'  CTCCCTCCTGTCTCTCA    71753    AT       C
                                TGA  GACAGGAGGG AG
                                |||  |||||||||| ||
                                ACT  CTGTCCTCCC TC
                                  CT       _
GAM989  FLJ10922  3'  GGCCCCCTCCTGTCATTC    37404           CAGA
                                GAATGACAGGAGGG   CC
                                ||||||||||||||   ||
                                CTTACTGTCCTCCC   GG
                                         CC__
GAM989  FOXP1     3'  TGTAGCTTTCTGTCACTCA   52049    A       __
                                TGA TGACAGGAGG  GCA
                                ||| ||||||||||  |||
                                ACT ACTGTCTTTC  TGT
                                  C        GA
GAM989  FTCD      3'  GGTACTGGCCCTGTCCTCA   22839    AT    AG G  _
                                TGA  GACAGG  G CAG ACC
                                |||  ||||||  | ||| |||
                                ACT  CTGTCC  C GTC TGG
                                  C_     __ G  A
GAM989  KIAA0557  3'  GTGACCTGCCCTTTTTCTCATT 78575      C_       AC
           C                     GAATGA  AGGAGGGCAG  CAC
                                ||||||  ||||||||||  |||
                                CTTACT  TTTTCCCGTC  GTG
                                   CT        CA
GAM989  KIAA0889  3'  CTGCTCTCCTGCCACCCA   31774    AA  A
                                TG  TG CAGGAGGGCAG
                                ||  || ||||||||||
                                AC  AC GTCCTCTCGTC
                                 CC  C
GAM989  KIAA1399  3'  TGTGGTCTGCCCTGCTCTCA  70796    C  G
                                TGA AG AGGGCAGACCACA
                                ||| || ||||||||||||
                                ACT TC TCCCGTCTGGTGT
                                  C  G
GAM989  LAMB4     5'  TGTAATCTGCAATTGTCTTCA  82083     T    GAGG    CC
                                TGAA GACAG   GCAGA  ACA
                                |||| |||||   |||||  |||
                                ACTT CTGTT   CGTCT  TGT
                                   _    AA__    AA
GAM989  PM5       3'  TGGACCCTCCTGTCACTC    27385    A       CAGA
                                GA TGACAGGAGGG   CCA
                                || ||||||||||   |||
                                CT ACTGTCCTCCC   GGT
                                 C        A___
GAM989  RHOBTB2   3'  CTGGTTTCCTGTCACTCA    61599    A       G
                                TGA TGACAGGAGG CAG
                                ||| |||||||||| |||
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                                ACT ACTGTCCTTT GTC
                                  C        G
GAM989  SLC16A4   3'  GTGATCCGCCCGCCTTGTC   17457       A_   A  C
                                GACAGG  GGGC GA CAC
                                ||||||  |||| || |||
                                CTGTTC  CCCG CT GTG
                                   CG    C  A
GAM989  SRCRB4D   3'  TGACCTCAGCCTGTCATCG   55798     A      A__  _
                                TGA TGACAGG   GGG CA
                                ||| |||||||   ||| ||
                                GCT ACTGTCC   TCC GT
                                  _      GAC   A
GAM989  TCF-3     3'  TGTGACATTTCCTGTTACCCA  49244    AA        GCAGAC
                                TG  TGACAGGAGG     CACA
                                ||  ||||||||||     ||||
                                AC  ATTGTCCTTT     GTGT
                                 CC         ACA___
GAM989  VAV3      3'  TGTAGCCTGCCCTCTCATCA   21480     CA       ACC
                                TGA  GGAGGGCAG   ACA
                                |||  |||||||||   |||
                                ACT  TCTCCCGTC   TGT
                                  AC        CGA
GAM989  LOC112885 3'  GGTCCCTCCTGTCATTC     57341            CAG
                                GAATGACAGGAGGG   ACC
                                ||||||||||||||   |||
                                CTTACTGTCCTCCC   TGG
                                                 ___
GAM989  LOC130813 3'  GTCTCCCCTCCTGCGATTCA   76281       GA       C
                                TGAAT  CAGGAGGG AGAC
                                |||||  |||||||| ||||
                                ACTTA  GTCCTCCC TCTG
                                   GC       C
GAM989  LOC133923 5'  TGCGGTTCCTGTTACTCA     76461     A       G_
                                TGA TGACAGGAG  GCA
                                ||| |||||||||  |||
                                ACT ATTGTCCTT  CGT
                                  C        GG
GAM989  LOC152215 3'  GTGACCTGCAGTCATTCA     81331         AGGAGG    AC
                                TGAATGAC     GCAG  CAC
                                ||||||||     ||||  |||
                                ACTTACTG     CGTC  GTG
                                     A_____    CA
GAM989  LOC160662 5'  TGACACTCCTGTCATTCA     83127           GG_
                                TGAATGACAGGAG   CA
                                ||||||||||||||  ||
                                ACTTACTGTCCTC   GT
                                        ACA
GAM989  LOC167147 5'  TGTGGTCTTTAATCTGTCCTTC 83561      T     AG  C
             A                   TGAA GACAGG  GG AGACCACA
                                ||||  ||||||  || ||||||||
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                                ACTT CTGTCT  TT TCTGGTGT
                                  C     AA  _
GAM989  LOC170409 3'  TGGTCTGCCCCCCTGTCCTCA  83747     AT     A
                                TGA  GACAGG GGGCAGACCA
                                |||  |||||| ||||||||||
                                ACT  CTGTCC CCCGTCTGGT
                                  C_     C
GAM989  LOC203107 3'  GTAATCCCTATATCTGTCTTCA 90795      T     ___    CAG
                                TGAA GACAGG   AGGG   AC
                                |||| ||||||   ||||   ||
                                ACTT CTGTCT   TCCC   TG
                                  _     ATA    TAA
GAM989  LOC220538 3'  CTGTCTCCTGTCATGCA     92429    A         G
                                TG ATGACAGGAGG CAG
                                || |||||||||| |||
                                AC TACTGTCCTCT GTC
                                 G         _
GAM989  LOC222183 3'  TGATCTGCTCTGTCACTTCA   95832     _     GAG     C
                                TGAA TGACAG   GGCAGA CA
                                |||| ||||||   |||||| ||
                                ACTT ACTGTC   TCGTCT GT
                                  C     ___     A
GAM989  LOC254824 3'  GTGGTCTAGGGGCTGTCATTC  98412         GAGGGC
                                GAATGACAG     AGACCAC
                                |||||||||     |||||||
                                CTTACTGTC     TCTGGTG
                                     GGGGA_
GAM989  LOC91974  5'  TGTGACCCTGCTCCTGTCA    68366        GG    AC_
                                TGACAGGA  GCAG   CACA
                                ||||||||  ||||   ||||
                                ACTGTCCT  CGTC   GTGT
                                     __    CCA
GAM990  FLJ21438  5'  CAAAACGCTTCCCCCCATCCCA 62190       GAGATTATC
                                TGGGA        AAGCGTTTTG
                                |||||        ||||||||||
                                ACCCT        TTCGCAAAAC
                                   ACCCCCC__
GAM990  FLJ32334  3'  AAAACGCTATTCCTTCCCA    58605        A  TTATCA
                                TGGGAG GA     AGCGTTTT
                                |||||| ||     ||||||||
                                ACCCTT CT     TCGCAAAA
                                   C  TA____
GAM990  HHLA2     3'  CAATGTACTTTGTAATCTCCCC 23953      A       C   CG T
          CA                      TGGG GAGATTAT AAG  T TTG
                                |||| |||||||| |||  | |||
                                ACCC CTCTAATG TTC  G AAC
                                  C       T   AT T
GAM991  ADAT1     3'  CCAGCAAAGAATGAAGGC     24914     __         C
                                GTC  CATTCTTTGC GG
                                |||  |||||||||| ||
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                                CGG  GTAAGAAACG CC
                                  AA         A
GAM991  M17S2     5'  CCGGTAGCGGACGGTCCTT   20910          ATTCT
                                AAGGACCGTCC    TTGCCGG
                                ||||||||||    |||||||
                                TTCCTGGCAGG    GATGGCC
                                      C_____
GAM991  ST14      5'  CCGGCAGGGACGACGCCT    42042     AC    CAT
                                AGG  CGTC   TCTTTGCCGG
                                |||  ||||   ||||||||||
                                TCC  GCAG   AGGGACGGCC
                                  __    C__
GAM991  HTGN29    5'  GCCAACTGTGTGGCGGTCC    39885         _   TC  T
                                GGACCGTC CAT  TT GC
                                |||||||| |||  || ||
                                CCTGGCGG GTG  AA CG
                                     T   TC  C
GAM991  PMAIP1    3'  GCAAGAATGGAAGACCCTT    41211      ACCG        T
                                AAGG    TCCATTCTT GC
                                ||||    ||||||||| ||
                                TTCC    AGGTAAGAA CG
                                  CAGA        _
GAM991  LOC144278 3'  GCCAGCAAAGACTGCTCGATGG 77274          ___  T      C
           TCCT                    AGGACCGTC   CA TCTTTGC GGC
                                |||||||||   || ||||||| |||
                                TCCTGGTAG   GT AGAAACG CCG
                                     CTC  C      A
GAM991  LOC147976 3'  CCGGTGAATGAAGACCCT    79287     ACC   CA   _  TG
                                AGG   GTC  TTC TT  CCGG
                                |||   |||  ||| ||  ||||
                                TCC   CAG  AAG AA  GGCC
                                  ___   __   T  GT
GAM991  LOC254263 5'  GCCGGCAGCGGACGCGCC    96367    AC     ATTCT
                                GG  CGTCC    TTGCCGGC
                                ||  |||||    ||||||||
                                CC  GCAGG    GACGGCCG
                                 GC    C_____
GAM992  CDH12     3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM992  GOCAP1    3'  ATTGTTCTTGGGAGCAGTGTA  43007       CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC         G
GAM992  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090       T    AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||    ||||||
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                                TGGTG GGGT    TTATTC
                                  _   GTCA_
GAM992  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
          A                      TACAC       AGAAGAATAAG
                                 |||||       ||||||||||
                                 ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM992  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                 TACACCACT       GAATAAG
                                 |||||||||       |||||||
                                 ATGTGGTGA       TTTATTC
                                      AGACG___
GAM992  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
          TA                     TACA   TCC   GAAGAATAAG
                                 ||||   |||   ||||||||||
                                 ATGT   AGG   TTTCTTATTC
                                   AAA_  ATTG
GAM992  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA  68742              _
                                 TACACCACTCCCAAGA AGA
                                 |||||||||||||||| |||
                                 ATGTGGTGAGGGTTCT TCT
                                           G
GAM992  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                 CAC  CT CCAAGAAGAA
                                 |||  || ||||||||||
                                 GTG  GA GGTTCTTTTT
                                   AC  A
GAM992  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748     CCA__
                                 ACTC    AGAAGAATAAG
                                 ||||    ||||||||||
                                 TGAG    TCTTCTTATTC
                                   TACCG
GAM992  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                                 CCA    CAAGAAGAATAAG
                                 |||    ||||||||||||
                                 GGT    GTTCTTCTTATTC
                                   TTTCA
GAM992  OSBPL11   3'  CTTAATTTCCCAAGAGTGGTG  43206        CCAA    AA
                                 CACCACTC    GAAG  TAAG
                                 ||||||||    ||||  ||||
                                 GTGGTGAG    CTTT  ATTC
                                      AACC    A_
GAM992  YME1L1    3'  TCATTCTTGATGTGGTGTA    58438        TCC     _
                                 TACACCAC   CAAGAA GA
                                 ||||||||   |||||| ||
                                 ATGTGGTG   GTTCTT CT
                                      TA_     A
GAM992  ZNF262    3'  CTTATTTTGTTTGGGAGT     18723         A
                                 ACTCCCAAG AGAATAAG
                                 |||||||||  ||||||||
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                                TGAGGGTTT TTTTATTC
                                     G
GAM992  LOC91960  3'  TGTGGCTTGGAACGTGGTGTA  68294        TC_    AAGA
                                TACACCAC   CCAAG    ATA
                                ||||||||   |||||    |||
                                ATGTGGTG   GGTTC    TGT
                                     CAA    GG__
GAM993  FGF2      5'  CCGCCGGCTCGCCGCGCAC    10617        G  CCA
                                GTGCGCGG GA   GCCGGCGG
                                |||||||| ||   ||||||||
                                CACGCGCC CT   CGGCCGCC
                                     G ___
GAM993  LBX1      5'  GGCTGGTCCCCGCGCCCGA    22669     T
                                TCG GCGCGGGGACCAGCC
                                ||| ||||||||||||||
                                AGC CGCGCCCCTGGTCGG
                                  C
GAM993  DKFZP761E1824 5'  CCGCCGGCTGGTCCCCTCCCCG 67035     C___
              C                    GCG    GGGGACCAGCCGGCGG
                                ||||    ||||||||||||||||
                                CGC    CCCCTGGTCGGCCGCC
                                  CCCT
GAM993  G4        5'  CCGGGAGCGGTCCCCGCGCAC  92636          AG__
                                GTGCGCGGGGACC    CCGG
                                ||||||||||||    ||||
                                CACGCGCCCCTGG    GGCC
                                      CGAG
GAM993  KIAA0415  3'  CGCCGGCTAGCCCCGCCA    94161    C     ACC
                                TG GCGGGG   AGCCGGCG
                                || ||||||   ||||||||
                                AC CGCCCC   TCGGCCGC
                                 _     GA_
GAM993  KIAA1600  5'  CCGCCGAGCCGCCCGCGCAC   71941        GACCA  _
                                GTGCGCGGG     GC CGGCGG
                                |||||||||     || ||||||
                                CACGCGCCC     CG GCCGCC
                                      GC___  A
GAM993  MGC10772  5'  GCCGGCGCGCGCACGA      48292         GGGACCA
                                TCGTGCGCG      GCCGGC
                                |||||||||      ||||||
                                AGCACGCGC      CGGCCG
                                      G_______
GAM993  TGIF2     5'  CCGCCGGGACGCCCCGCGCCGA 41744     T       ACCAG
                                TCG GCGCGGGG     CCGGCGG
                                ||| ||||||||     |||||||
                                AGC CGCGCCCC     GGCCGCC
                                  _       GCAG_
GAM993  LOC200186 5'  CCGGCGGCCCCCGCGCGC    91564          A  A
                                GTGCGCGGGG CC GCCGG
                                |||||||||| || |||||
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                                CGCGCGCCCC GG CGGCC
                                      C  _
GAM993  LOC254116 3'  CCACCAACTGGTCCAACTGAC  97424    G  CGG     CC  C
                                GT CG   GGACCAG  GG GG
                                || ||   |||||||  || ||
                                CA GT   CCTGGTC  CC CC
                                 _ CAA      AA  A
GAM993  LOC257554 5'  CCGGGAGCGGTCCCCGCGCAC  99532           AG__
                                GTGCGCGGGGACC   CCGG
                                ||||||||||||    ||||
                                CACGCGCCCCTGG   GGCC
                                       CGAG
GAM994  LFG     3'  CCAGCTGCCACACCCCCGACA  77230    C  A  A    TG  GAC
                                TG CG GG TGTGG  GC   TGG
                                || || || |||||  ||   |||
                                AC GC CC ACACC  CG   ACC
                                 A  C  C    GT  ___
GAM994  RB1CC1    5'  CCAGTCGCCTGGGCCCCTCGGC 29434       ATGT  ___
                                GCCGAGG   GGT   GGCGACTGG
                                |||||||   |||   |||||||||
                                CGGCTCC   CCG   CCGCTGACC
                                    _____  GGT
GAM994  SHANK2    3'  CCAGTCTCCCCACACCCCAGCA 25526    CGA  A    T  C
                                TGC   GG TGTGG GG GACTGG
                                |||   || ||||| || ||||||
                                ACG   CC ACACC CC CTGACC
                                  AC_  C    _  T
GAM994  STAU    3'  CCAGCAGATCCACACCCTGGGC 17195     G   A    TGGCGA
           A                     TGCC AGG TGTGG     CTGG
                                ||||  ||| |||||      ||||
                                ACGG TCC ACACC     GACC
                                  G   C    TAGAC_
GAM994  STAU    3'  CCAGCAGATCCACACCCTGGGC 34350     G   A    TGGCGA
           A                     TGCC AGG TGTGG     CTGG
                                ||||  ||| |||||      ||||
                                ACGG TCC ACACC     GACC
                                  G   C    TAGAC_
GAM994  STAU    3'  CCAGCAGATCCACACCCTGGGC 34353     G   A    TGGCGA
           A                     TGCC AGG TGTGG     CTGG
                                ||||  ||| |||||      ||||
                                ACGG TCC ACACC     GACC
                                  G   C    TAGAC_
GAM994  STAU    3'  CCAGCAGATCCACACCCTGGGC 34356     G   A    TGGCGA
           A                     TGCC AGG TGTGG     CTGG
                                ||||  ||| |||||      ||||
                                ACGG TCC ACACC     GACC
                                  G   C    TAGAC_
GAM994  C5orf4  3'  CCAGTCGCCACTTCACCC    33425    A  T
                                GG TG GGTGGCGACTGG
                                || || ||||||||||||
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                                CC AC TCACCGCTGACC
                                 C  T
GAM994  C5orf4   3'  CCAGTCGCCACTTCACCC    51487    A  T
                                GG TG GGTGGCGACTGG
                                || || ||||||||||||
                                CC AC TCACCGCTGACC
                                 C  T
GAM994  KIAA0618 5'  CCAGCCCTTCACATCCTCAGC  29849    C        T  CGA
                                GC GAGGATGTGG GG   CTGG
                                || ||||||||||  ||   ||||
                                CG CTCCTACACT CC   GACC
                                 A        T  C__
GAM994  PALM     3'  CCAGTCACCACCTGCAGCCTCG 11961        A  _    C
           GCA                     TGCCGAGG TGT GGTGG GACTGG
                                |||||||| ||| ||||| ||||||
                                ACGGCTCC ACG CCACC CTGACC
                                     G  T    A
GAM994  SEMA6A   5'  CCAGCATCACCACACCCGCGGC 40817      A  A      CGA
           A                     TGCCG GG TGTGGTGG   CTGG
                                ||||| || ||||||||   ||||
                                ACGGC CC ACACCACT   GACC
                                   G  C       AC_
GAM994  LOC118987 5'  CCAGCCGCCCGATGTCCTC   74394        GGT   A
                                GAGGATGT   GGCG CTGG
                                ||||||||   |||| ||||
                                CTCCTGTA   CCGC GACC
                                     GC_   C
GAM994  LOC125297 5'  CAGCCGCCGCCCCGGGCA    74866     GA  ATGT     A
                                TGCC  GG    GGTGGCG CTG
                                ||||  ||    ||||||| |||
                                ACGG  CC    CCGCCGC GAC
                                  G_  ____      C
GAM994  LOC150406 3'  CCAGTGTCTCCACATCCTCGTC 80671    C        T   G
           A                     TG CGAGGATGTGG GGC ACTGG
                                || |||||||||| ||| |||||
                                AC GCTCCTACACC CTG TGACC
                                 T         T  _
GAM994  LOC152992 3'  CCAGCTTTCTCCACATCCTC   81642         T  CGA
                                GAGGATGTGG GG   CTGG
                                |||||||||  ||   ||||
                                CTCCTACACC CT   GACC
                                      T  TTC
GAM994  LOC196540 3'  CCAATCACCACCACAGCCTGCA 91198     CG   A      C  C
                                TGC  AGG TGTGGTGG GA TGG
                                |||  ||| ||||||| || |||
                                ACG  TCC ACACCACC CT ACC
                                  __  G      A  A
GAM994  LOC254038 5'  CAGCCGCCGCCCCGGGCA    96954     GA  ATGT     A
                                TGCC  GG    GGTGGCG CTG
                                ||||  ||    ||||||| |||
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                                ACGG  CC    CCGCCGC GAC
                                  G_ _____      C
GAM994  LOC255452 5'  CCAGCTCCCCACATCCCCTGCA 99391     CGA       T  CGA
                                TGC   GGATGTGG GG   CTGG
                                |||   |||||||| ||   ||||
                                ACG   CCTACACC CC   GACC
                                  TCC       _  TC_
GAM994  LOC256987 3'  CCAGTCATTCTCATCCTCGG   97640         T  TGGC
                                CCGAGGATG GG    GACTGG
                                ||||||||| ||    ||||||
                                GGCTCCTAC CT    CTGACC
                                      T  TA__
GAM995  SCAMP1    3'  GCTAAATAAATATTCTCC    18013     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM995  SCAMP1    3'  GCTAAATAAATATTCTCC    54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM995  NX-17     3'  TGAATATCAGCCCCTAATA    40706         ATA_
                                TATTAGGG    ATATTCA
                                ||||||||    |||||||
                                ATAATCCC    TATAAGT
                                     CGAC
GAM995  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
              TA                  TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM996  ABCB6     3'  TATTTCATCCTGGTCTTGGGG  20300       C     CCTC
                                TCCCGA ACCAG    ATGGAATA
                                |||||| |||||    ||||||||
                                GGGGTT TGGTC    TACTTTAT
                                   C     C___
GAM996  ABL1      3'  TGTTCTGTGGGGGTCATCAGGG 24610      GACACCAG
              A                   TCCC       CCTCATGGAATA
                                ||||       ||||||||||||
                                AGGG       GGGGTGTCTTGT
                                  ACTACTG_
GAM996  ATF5      3'  TGTTTCGTGAAGGTGTTGGAGA 24826    _      AGCC
                                TC CCGACACC    TCATGGAATA
                                || ||||||||    ||||||||||
                                AG GGTTGTGG    AGTGCTTTGT
                                 A       A___
GAM996  CISH      3'  TTCTCCTTGGGGTTGGTGTCAG 59670     _          T   ATA
              GG                  CCC GACACCAGCCTCA GGA
                                ||| |||||||||||| |||
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                                GGG CTGTGGTTGGGGT CCT
                                  A          T  CTTA
GAM996  CRSP8    3'  GTTTTGTGGGGCTTGGG    81859     ACACC     TG
                                CCCG    AGCCTCA  GAAT
                                ||||    |||||||  ||||
                                GGGT    TCGGGGT  TTTG
                                  _____     GT
GAM996  FGFRL1   3'  TGTGGGCTGGGGTTGGGG    41911       A     T
                                TCCCGAC CCAGCC CATG
                                ||||||| |||||| ||||
                                GGGGTTG GGTCGG GTGT
                                   G    _
GAM996  HOXB9    3'  TGTTTCGTGATTTCTTTGGGG  44001      CACC  CC_
                                TCCCGA   AG   TCATGGAATA
                                ||||||   ||  ||||||||||
                                GGGGTT   TC   AGTGCTTTGT
                                   ____  TTT
GAM996  KLHL3    3'  TGGGGATGAGGCTGGGGTTGGG 88854       A       GGAATA
            A                    TCCCGAC CCAGCCTCAT
                                ||||||| ||||||||||
                                AGGGTTG GGTCGGAGTA
                                   G        GGGGT
GAM996  LBR      5'  TGTTCCACGCTCCGCGGTGTTG 60072         A  CTCA__
            GGG                   TCCCGACACC GC     TGGAATA
                                ||||||||||  ||     |||||||
                                GGGGTTGTGG CG     ACCTTGT
                                     _  CCTCGC
GAM996  MBL2     3'  TATTTCATGAAAATTGTGGGGA 5912      G   CCAGCC
                                TCCC ACA     TCATGGAATA
                                |||| |||     ||||||||||
                                AGGG TGT     AGTACTTTAT
                                  G   TAAA__
GAM996  NHP2L1   3'  TGTTCTGTGAGGTTGTTCGG   18451     CAC
                                CCGA   CAGCCTCATGGAATA
                                ||||   ||||||||||||||||
                                GGCT   GTTGGAGTGTCTTGT
                                  T__
GAM996  PXN      3'  GTTCTGTGATTATTGGGG    12674       CACCAGCC
                                TCCCGA       TCATGGAAT
                                ||||||       |||||||||
                                GGGGTT       AGTGTCTTG
                                   ATT_____
GAM996  SLC38A3  3'  TGAGGGTGGGGCTGGTGTAGGG 23376      G          GGAATA
            A                    TCCC ACACCAGCCTCAT
                                ||||| ||||||||||||
                                AGGG TGTGGTCGGGGTG
                                  A          GGAGT
GAM996  SLC6A8   3'  TATTCCGTCCTGGGTGTCTGGG 20075     _     AGCCTC
                                CCC GACACC     ATGGAATA
                                ||| ||||||     ||||||||
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                                GGG CTGTGG     TGCCTTAT
                                  T     GTCC__
GAM996  TCTE1L   3'  TATTTTGTACCTAAGGTGATGG 71527      A    AGCCTC TG
              GG                   TCCCG CACC     A  GAATA
                                |||||  ||||     |  |||||
                                GGGGT GTGG     T  TTTAT
                                  A    AATCCA GT
GAM996  CLSTN1   3'  TGTTCCTAATTTGGTGTGGGG  30793     G      CCTCAT
                                CCC ACACCAG     GGAATA
                                |||  |||||||     ||||||
                                GGG TGTGGTT     CCTTGT
                                  G      TAAT__
GAM996  DDX18    3'  TGTTTTGTGAGGATTTTTGTGG 23200    G   CCAG_    TG
                                CC ACA    CCTCA  GAATA
                                ||  |||     |||||  |||||
                                GG TGT    GGAGT  TTTGT
                                 _   TTTTA    GT
GAM996  DKFZP434H0820 3'  CAGGGGCTGGTTTTGGGG    64581       C        A
                                TCCCGA ACCAGCCTC TG
                                ||||||  |||||||||  ||
                                GGGGTT TGGTCGGGG AC
                                   T        _
GAM996  DKFZP564K2062 3'  TGTTTCATGGGATGGGTGTGGG 31854      G     AG_  T
              A                   TCCC  ACACC   CC CATGGAATA
                                ||||  |||||   ||  |||||||||
                                AGGG  TGTGG   GG GTACTTTGT
                                  _     GTA  _
GAM996  DKFZp761G2113 3'  TATTCTGTACTTGTGGTTTGGG 70470       C    GCCTC
              G                   TCCCGA ACCA     ATGGAATA
                                ||||||  ||||     ||||||||
                                GGGGTT TGGT     TGTCTTAT
                                   _    GTTCA
GAM996  DNAJC5   3'  TGTTCCATGTCTGTGTTGTGGA 62144     _      C  CCT
                                TCC CGACAC AG   CATGGAATA
                                |||  ||||||  ||   |||||||||
                                AGG GTTGTG TC   GTACCTTGT
                                  T     _  T__
GAM996  FASTK    5'  TGGGCCGGGGTGGGTGTTGGGG 47691          A     AT  AA
                                TCCCGACACC GCCTC  GG  TA
                                ||||||||||  |||||  ||  ||
                                GGGGTTGTGG TGGGG  CC  GT
                                      G     __  GG
GAM996  FBXO25   3'  TGTTCTGTGAGGTGGGTG    25152      A
                                CACC GCCTCATGGAATA
                                ||||  ||||||||||||
                                GTGG TGGAGTGTCTTGT
                                  G
GAM996  FLJ00012  3'  CAGGGGTTGGGGTTGGGA    74457        A       A
                                TCCCGAC CCAGCCTC TG
                                |||||||  ||||||||  ||
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                                AGGGTTG GGTTGGGG AC
                                   G      _
GAM996  FLJ10008  3'  TGTTCCCTCCGCTGGTGTCGTG 36195    _        CTCAT
            G                    CC CGACACCAGC     GGAATA
                                 || |||||||||     ||||||
                                 GG GCTGTGGTCG     CCTTGT
                                  T         CCTC_
GAM996  FLJ20184  3'  TGTTTTATGAGACTTGCTGGGA 35200       A  CC  C
                                 TCCCG CA  AG CTCATGGAATA
                                 ||||| ||  || ||||||||||
                                 AGGGT GT  TC GAGTATTTTGT
                                    C  __  A
GAM996  FLJ20371  3'  TAGGTTATGGGAGTTGGTGTTG 35540            _      AA
            GGA                     TCCCGACACCAGC CTCATGG  TA
                                 |||||||||||| |||||||  ||
                                 AGGGTTGTGGTTG GGGTATT  AT
                                         A      GG
GAM996  FLJ22035  3'  TGTTTTGTGAGGGTTTGGGG   44831       C   AGC    TG
                                 TCCCGA ACC   CTCA  GAATA
                                 |||||| |||   ||||  |||||
                                 GGGGTT TGG   GAGT  TTTGT
                                    _  ___    GT
GAM996  HSGP25L2G 3'  AGGGATGTGAGGCTGCTGTTGG 62866         C        GAATA
            GG                     TCCCGACA CAGCCTCATG
                                 ||||||||| ||||||||||
                                 GGGGTTGT GTCGGAGTGT
                                      C         AGGGAC
GAM996  KIAA0476  3'  TTCGTGCTGATGTTGGGG    30043         C    CTC
                                 TCCCGACA CAGC   ATGGA
                                 |||||||| ||||   |||||
                                 GGGGTTGT GTCG   TGCTT
                                      A   ____
GAM996  KIAA1553  3'  TGTTCCATGAAACCTGTTGG   93571       CCAGCC
                                 CCGACA     TCATGGAATA
                                 ||||||     ||||||||||
                                 GGTTGT     AGTACCTTGT
                                    CCAA__
GAM996  KIAA1831  3'  ATTTCATGGAATTTGGGA    64520       CACCAGCC
                                 TCCCGA       TCATGGAAT
                                 ||||||       |||||||||
                                 AGGGTT       GGTACTTTA
                                    TAA_____
GAM996  MKRN2    3'  TCGTCTGGTTGGTGTTGGGG   72850            TC
                                 TCCCGACACCAGCC  ATGG
                                 ||||||||||||||  ||||
                                 GGGGTTGTGGTTGG  TGCT
                                          TC
GAM996  R3HDM    5'  TCCGGGCTGGTGATGGGG    31718       A       CAT
                                 TCCCG CACCAGCCT   GGA
                                 ||||| |||||||||   |||
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                                GGGGT GTGGTCGGG   CCT
                                  A       ___
GAM996  SEPW1    3'  TGTTCTCGTGGCTGCTGTTGGG 13016        C     TCAT
            G                    TCCCGACA CAGCC    GGAATA
                                 |||||||| |||||    ||||||
                                 GGGGTTGT GTCGG    TCTTGT
                                    C     TGC_
GAM996  TNFAIP3  3'  TTCTGGTTGTTGTTGGGG    21911        C     TCAT
                                 TCCCGACA CAGCC    GGAA
                                 |||||||| |||||    ||||
                                 GGGGTTGT GTTGG    TCTT
                                    T    _____
GAM996  TOMM70A  3'  TGTTTCATGTCTAGGTGTTGTG 29740     _      AGCCT
            GG                   TCC CGACACC     CATGGAATA
                                 ||| |||||||     |||||||||
                                 GGG GTTGTGG     GTACTTTGT
                                   T      ATCT_
GAM996  LOC121219 5'  TGTTCTATGGGTGGGTGGGGG  74492     GA    A   T
                                 CCC  CACC GCC CATGGAATA
                                 |||  |||| ||| |||||||||
                                 GGG  GTGG TGG GTATCTTGT
                                   G_   G   _
GAM996  LOC143286 5'  TATGCACAGGCTTGTGTTGGGG 83848         C     ___
                                 TCCCGACAC AGCCT   CATG
                                 |||||||| |||||   ||||
                                 GGGGTTGTG TCGGA   GTAT
                                      T    CAC
GAM996  LOC145662 3'  TCGGTGAGGTTGGAGTTGGGG  77838        A        G
                                 TCCCGAC CCAGCCTCAT GA
                                 ||||||| |||||||||| ||
                                 GGGGTTG GGTTGGAGTG CT
                                    A        G
GAM996  LOC145846 5'  ATTTTATGGGGTGTGGAGG   84544    GA   CA
                                 CC  CAC  GCCTCATGGAAT
                                 ||  |||  ||||||||||||
                                 GG  GTG  TGGGGTATTTTA
                                  AG  __
GAM996  LOC146176 3'  GTTCTATGGACATTTGGGA   78193       CACCAGCC
                                 TCCCGA       TCATGGAAT
                                 ||||||       |||||||||
                                 AGGGTT       GGTATCTTG
                                    TACA_____
GAM996  LOC146488 3'  TATTCCATCCTGGGTGTCTGGG 71362     _     AGCCTC
                                 CCC GACACC      ATGGAATA
                                 ||| ||||||      ||||||||
                                 GGG CTGTGG      TACCTTAT
                                   T     GTCC__
GAM996  LOC148479 3'  CTTCCACTGTGTTGGGG     79612         C  CCTCA    TA
                                 TCCCGACAC AG    TGGAA
                                 |||||||| ||    |||||
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                                GGGGTTGTG TC    ACCTT
                                   _ _____    CG
GAM996  LOC219899 3'  GTTCTGTTTAGGTTTGGGA   93134      CACCA   C_
                                TCCCGA    GCCT  ATGGAAT
                                ||||||    ||||  |||||||
                                AGGGTT    TGGA  TGTCTTG
                                   _____   TT
GAM996  LOC254122 3'  TGGGGGATGGTGTTGGGA    96398         G_
                                TCCCGACACCA  CCTCA
                                ||||||||||  |||||
                                AGGGTTGTGGT  GGGGT
                                      AG
GAM996  LOC257490 5'  TCCAGGTTGGTGTCTGGG    99561    _        CAT
                                CCC GACACCAGCCT   GGA
                                ||| ||||||||||   |||
                                GGG CTGTGGTTGGA   CCT
                                  T        ___
GAM996  LOC90499  5'  TGTTTGGTGGTTGCTGTTGGGG 63746       C    TC  G
                                TCCCGACA CAGCC  AT GAATA
                                |||||||| |||||  || |||||
                                GGGGTTGT GTTGG  TG TTTGT
                                     C    __ G
GAM997  C20orf39  3'  ATGATTGCCAAATGATGCC   46570       CA     TG
                                GGCATCAT  TGGCAAT  T
                                ||||||||  |||||||  |
                                CCGTAGTA  ACCGTTA  A
                                     A_     GT
GAM997  DIS3     3'  ACAATACACGTGATGATGTC   30908          GCA
                                GGCATCATCATG   ATTGT
                                ||||||||||||  |||||
                                CTGTAGTAGTGC   TAACA
                                      ACA
GAM997  FBXO27   3'  ATAGTGAGCCATGATCATACC  75002    C  C      A_
                                GG AT ATCATGGC  ATTGT
                                || || ||||||||  |||||
                                CC TA TAGTACCG  TGATA
                                 A  C       AG
GAM997  FLJ32334  3'  GCCTGTTGCCATGATAAGGCC  58608    ATC        T_
                                GGC   ATCATGGCAAT  GT
                                |||   ||||||||||| ||
                                CCG   TAGTACCGTTG  CG
                                  GAA         TC
GAM997  KIAA1855  3'  TGACAATCAGCTCGTGCC    93959      CATCAT  A_
                                GGCAT     GGC  ATTGTCA
                                |||||     |||  |||||||
                                CCGTG     TCG  TAACAGT
                                   C_____  AC
GAM997  PP1665   5'  GCGCTCCCATGATGATACC   48638    C       CAAT
                                GG ATCATCATGG    TGT
                                || ||||||||||   |||
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                                CC TAGTAGTACC    GCG
                                 A         CTC_
GAM997  LOC152317 5'  ATGAAGTTGACCATGACAATGG 86822    ATCA_     _    G
           C                      GC     TCATGG CAATT TCAT
                                  ||     |||||| ||||| ||||
                                  CG     AGTACC GTTGA AGTA
                                   GTAAC      A    _
GAM997  LOC157562 5'  ACAGTGAGCCATGATCACACC  87769    CATC       A_
                                  GG    ATCATGGC  ATTGT
                                  ||    ||||||||  |||||
                                  CC    TAGTACCG  TGACA
                                   ACAC       AG
GAM997  LOC89932  5'  ATGGCGGCTGCCATGGCAATGC 61446      CA       A
           C                      GGCAT  TCATGGCA TTGTCAT
                                  |||||  |||||||| |||||||
                                  CCGTA  GGTACCGT GGCGGTA
                                     AC       C
GAM997  LOC90288  3'  ATGACCCACGCCCATTATGATG 62772         C    _ AATT
           CCG                      CGGCATCAT ATGG C    GTCAT
                                  |||||||||  |||| |    |||||
                                  GCCGTAGTA TACC G    CAGTA
                                       T    C CACC
GAM998  CDH12     3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                  TACACCACT    GAA  ATAAG
                                  |||||||||    |||  |||||
                                  ATGTGGTGA    TTT  TATTC
                                       AA___   AC
GAM998  GOCAP1    3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                  TACAC  CTCCCAAGAA AAT
                                  |||||  |||||||||| |||
                                  ATGTG  GAGGGTTCTT TTA
                                     AC         G
GAM998  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT    98090       T    AGAAG
                                  ACCAC CCCA     AATAAG
                                  ||||| ||||     ||||||
                                  TGGTG GGGT     TTATTC
                                     _    GTCA_
GAM998  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
           A                      TACAC       AGAAGAATAAG
                                  |||||       ||||||||||
                                  ATGTG       TCTTCTTATTC
                                     TACTCCC_
GAM998  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                  TACACCACT       GAATAAG
                                  |||||||||       |||||||
                                  ATGTGGTGA       TTTATTC
                                       AGACG___
GAM998  HMP19     3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
           TA                       TACA    TCC    GAAGAATAAG
                                  ||||    |||    ||||||||||
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                              ATGT   AGG   TTTCTTATTC
                                AAA_  ATTG
GAM998  KIAA1579 3' TACTCTTAGTGGTGTA     37154        CCCAAG   A
                              TACACCACT     AAGA TA
                              |||||||||     |||| ||
                              ATGTGGTGA     TTCT AT
                                    _______   C
GAM998  KIAA1719 3' TCTGTCTTGGGAGTGGTGTA  68742             _
                              TACACCACTCCCAAGA AGA
                              |||||||||||||||| |||
                              ATGTGGTGAGGGTTCT TCT
                                        G
GAM998  KIAA1853 3' TTTTTCTTGGAAGCAGTG    69929    CA  C
                              CAC  CT CCAAGAAGAA
                              |||  || ||||||||||
                              GTG  GA GGTTCTTTTT
                                AC  A
GAM998  KIAA1877 3' CTTATTCTTCTGCCATGAGT  66748     CCA__
                              ACTC    AGAAGAATAAG
                              ||||    ||||||||||
                              TGAG    TCTTCTTATTC
                                TACCG
GAM998  KIAA1906 3' CTTATTCTTCTTGACTTTTGG 73571    CTCC_
                              CCA    CAAGAAGAATAAG
                              |||    ||||||||||||
                              GGT    GTTCTTCTTATTC
                                TTTCA
GAM998  OSBPL11  3' CTTAATTTCCCAAGAGTGGTG 43206       CCAA   AA
                              CACCACTC   GAAG  TAAG
                              ||||||||   ||||  ||||
                              GTGGTGAG   CTTT  ATTC
                                   AACC   A_
GAM998  YME1L1   3' TCATTCTTGATGTGGTGTA   58438       TCC    _
                              TACACCAC   CAAGAA GA
                              ||||||||   |||||| ||
                              ATGTGGTG   GTTCTT CT
                                   TA_    A
GAM998  YME1L1   3' TCATTCTTGATGTGGTGTA   27323       TCC    _
                              TACACCAC   CAAGAA GA
                              ||||||||   |||||| ||
                              ATGTGGTG   GTTCTT CT
                                   TA_    A
GAM998  ZNF262   3' CTTATTTTGTTTGGGAGT    18723        A
                              ACTCCCAAG AGAATAAG
                              ||||||||| ||||||||
                              TGAGGGTTT TTTTATTC
                                   G
GAM998  LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_   AAGA
                              TACACCAC   CCAAG   ATA
                              ||||||||   |||||   |||
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                                ATGTGGTG  GGTTC   TGT
                                    CAA   GG__
GAM999  SCAMP1   3' GCTAAATAAATATTCTCC   18013    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM999  SCAMP1   3' GCTAAATAAATATTCTCC   54501    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM999  NX-17    3' TGAATATCAGCCCCTAATA   40706       ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM999  LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
            TA                   TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM1000 SCAMP1   3' GCTAAATAAATATTCTCC   54500    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1000 SCAMP1   3' GCTAAATAAATATTCTCC   54501    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1000 NX-17    3' TGAATATCAGCCCCTAATA   40706       ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM1000 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
            TA                   TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM1001 GNPI     3' AATCAGAAAAAAAATATCTG  19617      GC  C
                                TAGATG  TT TTTCTGATT
                                ||||||  || |||||||||
                                GTCTAT  AA AAAGACTAA
                                   AA  A
GAM1001 HEPH     5' AAGAAGACCATCTATAAA    29646         _
                                TTTATAGATGG CTTCTT
                                |||||||||| ||||||
```

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                                AAATATCTACC GAAGAA
                                      A
GAM1001  PAX6     5'  CAGAAAGGATGCCTCATAAA   6064       A  T  _
                                TTTAT GA GGC TTCTTTCTG
                                ||||| || ||| |||||||||
                                AAATA CT CCG AGGAAAGAC
                                   _ _  T
GAM1001  PAX6     5'  CAGAAAGGATGCCTCATAAA   9632       A  T  _
                                TTTAT GA GGC TTCTTTCTG
                                ||||| || ||| |||||||||
                                AAATA CT CCG AGGAAAGAC
                                   _ _  T
GAM1001  LOC157507 5'  AAAGAAGCCATCCATGAA    82375      A
                                TTTAT GATGGCTTCTTT
                                ||||| ||||||||||||
                                AAGTA CTACCGAAGAAA
                                   C
GAM1001  LOC91380  5'  AAAGAAGCCATTTATAAA    66429
                                TTTATAGATGGCTTCTTT
                                ||||||||||||||||||
                                AAATATTTACCGAAGAAA

GAM1002  LILRB4    3'  GACAGTATATCATGACCACACT 23387          GTGT_  CA
            GG                    TCAGTGTGGTCA    TAC  TC
                                  ||||||||||||    |||  ||
                                  GGTCACACCAGT    ATG  AG
                                        ACTAT   AC
GAM1002  MST1R    3'  GGACTCAGCAGTGACCACAC   11708        G   ACCA
                                GTGTGGTCA TGTT    TCC
                                ||||||||| ||||    |||
                                CACACCAGT ACGA    AGG
                                     G   CTC_
GAM1002  MYLK     5'  AACATCTTCTGACACACTGA   98791        G   ____
                                TCAGTGTG TCAG    TGTT
                                |||||||| ||||    ||||
                                AGTCACAC AGTC    ACAA
                                     _   TTCT
GAM1002  C20orf50  3'  GGACAACACCATTGGACCACAC 70613          A____    A_
            TGG                   TCAGTGTGGTC    GTGTT  CC
                                  ||||||||||||    |||||  ||
                                  GGTCACACCAG    CACAA  GG
                                        GTTAC    CA
GAM1002  DKFZp761H079 3'  GACTTAGCAACCACACTGA   59385         CAG    CCA
                                TCAGTGTGGT   TGTTA   TC
                                ||||||||||   |||||   ||
                                AGTCACACCA   ACGAT   AG
                                     ____    TC_
GAM1002  FLJ21945  3'  GATGGTAACACCACTTCTCACT 48094       T  TCA_
            G                     CAGTG GG    GTGTTACCATC
                                  |||||  ||    ||||||||||||
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                                GTCAC CT   CACAATGGTAG
                                   T  TCAC
GAM1002  FLJ22344  3'  GGATAATAATATAACACACTGA 45590       GTCA    CC
                                TCAGTGTG   GTGTTA  ATCC
                                ||||||||   ||||||  ||||
                                AGTCACAC   TATAAT  TAGG
                                     AA__     AA
GAM1002  KIAA0265  3'  ATGGTATGACCAGCACTGA   70438      _    GTGT
                                TCAGTG TGGTCA   TACCAT
                                |||||| ||||||   ||||||
                                AGTCAC ACCAGT   ATGGTA
                                   G    ____
GAM1002  KIAA0418  3'  GGATGGGGGGTGCCCACACTGA  28297       TCA TG TA
                                TCAGTGTGG  G  T  CCATCC
                                |||||||||  |  |  ||||||
                                AGTCACACC  C  G  GGTAGG
                                     ___ GT GG
GAM1002  KIAA1243  3'  ATGGTAAATGTTCCATACTGA  74022       TCAGTG
                                TCAGTGTGG    TTACCAT
                                |||||||||    |||||||
                                AGTCATACC    AATGGTA
                                     TTGTA_
GAM1002  MGC13057  3'  GGATGACAACACTTTGACTGT  51285   TG   __   AC
                                G  GTCA  GTGTT  CATCC
                                |  ||||  |||||  |||||
                                T  CAGT  CACAA  GTAGG
                                 GT   TT   CA
GAM1002  NIR3      3'  GGACCTACAACCACACTGA   66831       CA   TTA
                                TCAGTGTGGT  GTG   CC
                                ||||||||||  |||   ||
                                AGTCACACCA  CAT   GG
                                     A_   CCA
GAM1002  PDZ-GEF1  3'  GGACAGGGTGTGGCCACAC   27281       GTGT   A__
                                GTGTGGTCA   TACC   TCC
                                |||||||||   ||||  |||
                                CACACCGGT   GTGG   AGG
                                     ____    GAC
GAM1002  TED       3'  GGACAGACCTCCACCACACTGA 32270       C_  T   A__
                                TCAGTGTGGT  AG GTT   CC
                                |||||||||  || |||   ||
                                AGTCACACCA  TC CAG   GG
                                     CC  _   ACA
GAM1002  LOC145098 5'  GGTACAAACACGACACTGA   77538      G  CAG   T
                                TCAGTGT GT   TGT ACC
                                ||||||| ||   ||| |||
                                AGTCACA CA   ACA TGG
                                    G  CAA   _
GAM1002  LOC147042 3'  GGACGATTCCTGACCACACTG  84995         T_   A_
                                CAGTGTGGTCAG  GTT  CC
                                ||||||||||||  |||  ||
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                                GTCACACCAGTC  TAG  GG
                                      CT   CA
GAM1002  LOC149837 3'  GATGGCAACATTACATTGA   85897       GTCA    A
                                TCAGTGTG   GTGTT CCATC
                                ||||||||   ||||| |||||
                                AGTTACAT   TACAA GGTAG
                                    _____    C
GAM1002  LOC150271 5'  GGACGTTCACAACCACACTGA  86142        CA   TT  CA
                                TCAGTGTGGT  GTG  AC  TCC
                                ||||||||||  |||  ||  |||
                                AGTCACACCA  CAC  TG  AGG
                                     A_   T_  C_
GAM1002  LOC151438 3'  GGATGATGCAGTGACCACAC   86560       G   TAC
                                GTGTGGTCA TGT   CATCC
                                |||||||| |||   |||||
                                CACACCAGT ACG   GTAGG
                                     G   TA_
GAM1002  LOC169026 5'  GACCTACCAACAACACTGA    83602       ____   C  T
                                TCAGTGT    GGT AG GTT
                                |||||||    ||| || |||
                                AGTCACA    CCA TC CAG
                                    ACAA  _ _
GAM1002  LOC90309  3'  GATGGTAACAGACACTGG    62873       GGTCAG
                                TCAGTGT     TGTTACCATC
                                |||||||     ||||||||||
                                GGTCACA     ACAATGGTAG
                                    G_____
GAM1002  LOC92340  3'  GGACAGCAACACCGACACCACC 69564     __   TG   A    ACCA
           GTGA                    TCA  GTG  GTC GTGTT    TCC
                                |||  |||  ||| |||||   |||
                                AGT  CAC  CAG CACAA    AGG
                                  GC   CA   C    CGAC
GAM1003  MAP1A    3'  TATACCATTCACATCCCAG   11442     AA   CA
                                CTGG  GTG  AATGGTGTG
                                ||||  |||  |||||||||
                                GACC  TAC  TTACCATAT
                                  C_   AC
GAM1003  MAP3K9   3'  CACTGCCTATCTGCACTTCCAG 61359          A  _  _
                                CTGGAAGTGCA AT GGT GTG
                                |||||||||| || ||| |||
                                GACCTTCACGT TA CCG CAC
                                     C  T   T
GAM1003  MYO1C    3'  AAAGACTCGAACTTCCAG    61849        GCAAAT  T  G
                                CTGGAAGT     GG GT TTT
                                ||||||||     || || |||
                                GACCTTCA     CT CA AAA
                                    AG____  _  G
GAM1003  PELI1    5'  CAAATACGGGCATTTACACTTT 40629         C    G_
           CAG                    CTGGAAGTG AAATG  TGTGTTTG
                                |||||||| |||||  ||||||||
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                                GACTTTCAC TTTAC  GCATAAAC
                                     A    GG
GAM1003  PIP5K1C   3'  CAAACACTGGTTTGCATCCCAG 71296     AA       GGT
                                CTGG  GTGCAAAT   GTGTTTG
                                ||||  ||||||||   |||||||
                                GACC  TACGTTTG   CACAAAC
                                  C_      GT_
GAM1003  LOC131368 3'  CAAACTGTTTTTTGCACTTC   76373         TGGTGT
                                GAAGTGCAAA     GTTTG
                                ||||||||||     |||||
                                CTTCACGTTT     CAAAC
                                      TTTGT_
GAM1003  LOC144817 3'  CAAACACACCCTGCCTCCCCCA 77507     A__  T   AAT
             G                   CTGG   AG GCA   GGTGTGTTTG
                                ||||   || |||   ||||||||||
                                GACC   TC CGT   CCACACAAAC
                                  CCC  _   C__
GAM1003  LOC154739 3'  CATGCCACCGCACTTCCAG    87434         AAA
                                CTGGAAGTGC   TGGTGTG
                                ||||||||||   |||||||
                                GACCTTCACG   ACCGTAC
                                      CC_
GAM1003  LOC165229 5'  ATGCCCATCCACACTTCCAG   83360         CAA   T
                                CTGGAAGTG   ATGG GTGT
                                |||||||||   |||| ||||
                                GACCTTCAC   TACC CGTA
                                      ACC   _
GAM1003  LOC201696 5'  CATCCATTTGCCTCCCAG    63814     A  T      T
                                CTGG AG GCAAATGG GTG
                                |||| || |||||||| |||
                                GACC TC CGTTTACC TAC
                                  C  _       _
GAM1003  LOC203276 3'  CATGCCACTGCACTTCCAG    92115         AA
                                CTGGAAGTGCA  TGGTGTG
                                ||||||||||   |||||||
                                GACCTTCACGT  ACCGTAC
                                      C_
GAM1003  LOC203305 3'  CATGCCACTGCACTTCCAG    92168         AA
                                CTGGAAGTGCA  TGGTGTG
                                ||||||||||   |||||||
                                GACCTTCACGT  ACCGTAC
                                      C_
GAM1003  LOC254243 3'  CATGCCACTGCACTTCCAG    99254         AA
                                CTGGAAGTGCA  TGGTGTG
                                ||||||||||   |||||||
                                GACCTTCACGT  ACCGTAC
                                      C_
GAM1003  LOC90038  3'  CATGCCACTGCACTTCCAG    61797         AA
                                CTGGAAGTGCA  TGGTGTG
                                ||||||||||   |||||||
```

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                                GACCTTCACGT  ACCGTAC
                                      C_
GAM1004  APOD     5'  CAGGTCCCTTCTCCAGCCAC  9706       CTTTC
                                GTGGC    GAGGGACCTG
                                |||||    ||||||||||
                                CACCG    TTCCCTGGAC
                                   ACCTC
GAM1004  ITGAL    3'  AGATCCCAGCTCACGTCA    11039       GC  TTCGA   C
                                TGACGTG  CT    GGGA CT
                                |||||||  ||    |||| ||
                                ACTGCAC  GA    CCCT GA
                                    TC  _____   A
GAM1004  RCE1     3'  AGGTCCCAGGAGCCAC      18889      CT   GA
                                GTGGC  TTC  GGGACCT
                                |||||  |||  |||||||
                                CACCG  AGG  CCCTGGA
                                   __  A_
GAM1004  TAF1C    3'  CAGGTCCCTCAGTTCTCACG   20264      CCT  C
                                CGTGG   TT GAGGGACCTG
                                |||||   || ||||||||||
                                GCACT   GA CTCCCTGGAC
                                   CTT  _
GAM1004  TCIRG1   5'  CAGGCCCCCGGGGGGCCGC   21330       TT  A   A
                                GTGGCCT  CG GGG CCTG
                                |||||||  || ||| ||||
                                CGCCGGG  GC CCC GGAC
                                    GG  C  _
GAM1004  FLJ10521 3'  CAGGCCTGACCAAGGCCACG  36718        TCGA   A
                                CGTGGCCTT    GGG CCTG
                                |||||||||    ||| ||||
                                GCACCGGAA    TCC GGAC
                                     CCAG   _
GAM1004  KIAA1893 3'  GTCCCTTGTGACCACTCA    73591     C   CCTTT
                                TGA GTGG    CGAGGGAC
                                ||| ||||    ||||||||
                                ACT CACC    GTTCCCTG
                                  _   AGT__
GAM1004  KIAA1924 3'  AGGTCCCCAAGCCATGTCA   74039        CTTTCGA
                                TGACGTGGC     GGGACCT
                                |||||||||     |||||||
                                ACTGTACCG     CCCTGGA
                                     AAC_____
GAM1004  PRAX-1   3'  CAGGAAGGAGAAAGGCCAAGCC 17654    ACG       GAGGGA
            A                    TG   TGGCCTTTC     CCTG
                                ||   |||||||||     ||||
                                AC   ACCGGAAAG     GGAC
                                 CGA       AGGAA_
GAM1004  LOC127281 3'  AGACCCAAGCCCACGTCA    75132        C   TCGA   AC
                                TGACGTGG CTT    GGG  CT
                                |||||||| |||    |||  ||
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                                ACTGCACC GAA    CCC  GA
                                    C  _____  A_
GAM1004  LOC201252 5'  CAGGTCCCCAAAGCCAC     89547      C  CGA
                                GTGGC TTT   GGGACCTG
                                ||||| |||   ||||||||
                                CACCG AAA   CCCTGGAC
                                  _  C__
GAM1005  A1BG     3'  ATTTTTTGTAGAGATGAGTCTC 56280     A  CC       T
           A                     TGA AC  CATCTCTAC AAAAAT
                                ||| ||  ||||||||| ||||||
                                ACT TG  GTAGAGATG TTTTTA
                                  C A_       T
GAM1005  A1BG     3'  TTTTTAGTAGAGATGGGGTTTC 56303
           A                     TGAAACCCCATCTCTACTAAAAA
                                |||||||||||||||||||||||
                                ACTTTGGGGTAGAGATGATTTTT

GAM1005  ACADSB   3'  AGTAGAGATGGGGTTTTA    9643
                                TGAAACCCCATCTCTACT
                                ||||||||||||||||||
                                ATTTTGGGGTAGAGATGA

GAM1005  ADAMTS4  3'  ATTTTTAGTAGAGACAGGGTTT 18752        CA
           CA                   TGAAACCC  TCTCTACTAAAAAT
                                ||||||||  ||||||||||||||
                                ACTTTGGG  AGAGATGATTTTTA
                                    AC
GAM1005  ADAMTS4  3'  ATTTTTAGTAGAGACGGGGTTT 18753         A
           CA                   TGAAACCCC TCTCTACTAAAAAT
                                |||||||||| ||||||||||||||
                                ACTTTGGGG AGAGATGATTTTTA
                                    C
GAM1005  ADCY6    5'  ATTTTTAGTAGAGACGAGGTTT 31586       CCA
           CA                   TGAAACC   TCTCTACTAAAAAT
                                |||||||   ||||||||||||||
                                ACTTTGG   AGAGATGATTTTTA
                                    AGC
GAM1005  AIM1     3'  TTTTTGTAGAGATGGGGTTTCA 93475             T
                                TGAAACCCCATCTCTAC AAAAA
                                |||||||||||||||| |||||
                                ACTTTGGGGTAGAGATG TTTTT
                                                _
GAM1005  ALDH1B1  3'  ATTTTTAGTAGAGATGAGGTTT 7317        C
           CA                   TGAAACC CATCTCTACTAAAAAT
                                ||||||| ||||||||||||||||
                                ACTTTGG GTAGAGATGATTTTTA
                                    A
GAM1005  APAF1    3'  ATTTTTAGTAGAGACGGGGTTT 8581          A
           CA                   TGAAACCCC TCTCTACTAAAAAT
                                ||||||||| ||||||||||||||
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                                ACTTTGGGG AGAGATGATTTTTA
                                     C
GAM1005  APAF1    3'  ATTTTTAGTAGAGACGGGGTTT 25963          A
                CA                  TGAAACCCC TCTCTACTAAAAAT
                                    ||||||||| ||||||||||||||
                                ACTTTGGGG AGAGATGATTTTTA
                                     C
GAM1005  APM1     3'  ATTTTTAGTAAAGACAGGGTTT 17760         CA  C
                CA                  TGAAACCC  TCT TACTAAAAAT
                                    ||||||||  ||| ||||||||||
                                ACTTTGGG  AGA ATGATTTTTA
                                     AC  A
GAM1005  APM1     3'  ATTTTTAGTAGAAATGGGGTTT 17761          C
                C                    GAAACCCCAT TCTACTAAAAAT
                                    |||||||||| ||||||||||||
                                CTTTGGGGTA AGATGATTTTTA
                                      A
GAM1005  APM1     3'  ATTTTTCGTAGAGACGGGGTTT 17762          A      T
                CA                  TGAAACCCC TCTCTAC AAAAAT
                                    ||||||||| ||||||| ||||||
                                ACTTTGGGG AGAGATG TTTTTA
                                     C      C
GAM1005  APOL1    3'  ATTTTTAATAGAGATGGGGTTT 14729              C
                CA                  TGAAACCCCATCTCTA TAAAAAT
                                    |||||||||||||||| |||||||
                                ACTTTGGGGTAGAGAT ATTTTTA
                                         A
GAM1005  APPL     3'  ATTTTTAGTAGAGACGGGGTTT 24943          A
                CA                  TGAAACCCC TCTCTACTAAAAAT
                                    ||||||||| ||||||||||||||
                                ACTTTGGGG AGAGATGATTTTTA
                                     C
GAM1005  AQP6     3'  ATTTTTAGTAGAGATGGGGTTT 9724
                CA                  TGAAACCCCATCTCTACTAAAAAT
                                    |||||||||||||||||||||||||
                                ACTTTGGGGTAGAGATGATTTTTA

GAM1005  AQP6     3'  ATTTTTAGTAGAGATGGGGTTT 54984
                CA                  TGAAACCCCATCTCTACTAAAAAT
                                    |||||||||||||||||||||||||
                                ACTTTGGGGTAGAGATGATTTTTA

GAM1005  ARCN1    3'  TTTTAGTAGAGACGGGGTTTCA 9761           A
                                    TGAAACCCC TCTCTACTAAAA
                                    |||||||||| ||||||||||||
                                ACTTTGGGG AGAGATGATTTT
                                     C
GAM1005  ATP6V1A1 3'  ATTTTTAGTAGAAACGGGGTTT 9865          ATC
                CA                  TGAAACCCC   TCTACTAAAAAT
                                    |||||||||   ||||||||||||
```

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                                ACTTTGGGG  AGATGATTTTTA
                                     CAA
GAM1005 ATP7A    3' ATTTTTCAGTAGAGACGGGGTT 5316         A      _
            TC                   GAAACCCC TCTCTACT AAAAAT
                                 |||||||| |||||||| ||||||
                                 CTTTGGGG AGAGATGA TTTTTA
                                     C       C
GAM1005 ATP8B2   3' ATTTTTAGTAGAGATGTTTCA 65830       CCC
                                 TGAAAC   ATCTCTACTAAAAAT
                                 ||||||   ||||||||||||||||
                                 ACTTTG   TAGAGATGATTTTTA
                                      ___
GAM1005 AXL      3' ATTTTTAGTAGAGACAGGGTTT 9901         CA
            CA                   TGAAACCC  TCTCTACTAAAAAT
                                 ||||||||  ||||||||||||||
                                 ACTTTGGG  AGAGATGATTTTTA
                                     AC
GAM1005 AXL      3' ATTTTTAGTAGAGACAGGGTTT 41877        CA
            CA                   TGAAACCC  TCTCTACTAAAAAT
                                 ||||||||  ||||||||||||||
                                 ACTTTGGG  AGAGATGATTTTTA
                                     AC
GAM1005 B4GALT5  3' ATTTTTAGTAGAGACAGGGGTT 17682        A_
            TC                   GAAACCCC  TCTCTACTAAAAAT
                                 ||||||||  ||||||||||||||
                                 CTTTGGGG  AGAGATGATTTTTA
                                     AC
GAM1005 BRIP1    3' ATTTTTAGTAGAGATGGGGTTT 50207
            CA                   TGAAACCCCATCTCTACTAAAAAT
                                 |||||||||||||||||||||||||
                                 ACTTTGGGGTAGAGATGATTTTTA

GAM1005 C7       3' ATTTTTAGTAGAGATGGGTTTC 6981         C
            A                    TGAAACCC ATCTCTACTAAAAAT
                                 ||||||||  ||||||||||||||
                                 ACTTTGGG TAGAGATGATTTTTA
                                      _
GAM1005 CASP10   3' TTTTTTGTGGAGATGGGGTTTC 53231            T
            A                    TGAAACCCCATCTCTAC AAAAA
                                 |||||||||||||||| |||||
                                 ACTTTGGGGTAGAGGTG TTTTT
                                           T
GAM1005 CASP10   3' TTTTTTGTGGAGATGGGGTTTC 53269            T
            A                    TGAAACCCCATCTCTAC AAAAA
                                 |||||||||||||||| |||||
                                 ACTTTGGGGTAGAGGTG TTTTT
                                           T
GAM1005 CASP2    3' ATTTTTAGTAGAGACAGGGTTT 53286        CA
            CA                   TGAAACCC  TCTCTACTAAAAAT
                                 ||||||||  ||||||||||||||
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                                ACTTTGGG AGAGATGATTTTTA
                                   AC
GAM1005 CASP2   3' ATTTTTAGTAGAGACAGGGTTT 53302       CA
           CA                   TGAAACCC TCTCTACTAAAAAT
                                |||||||| ||||||||||||||
                                ACTTTGGG AGAGATGATTTTTA
                                   AC
GAM1005 CASP2   3' ATTTTTAGTAGAGACAGGGTTT 53323       CA
           CA                   TGAAACCC TCTCTACTAAAAAT
                                |||||||| ||||||||||||||
                                ACTTTGGG AGAGATGATTTTTA
                                   AC
GAM1005 CASP2   3' ATTTTTAGTAGAGACAGGGTTT 8705        CA
           CA                   TGAAACCC TCTCTACTAAAAAT
                                |||||||| ||||||||||||||
                                ACTTTGGG AGAGATGATTTTTA
                                   AC
GAM1005 CASP8   3' ATTTTTAGTAGAGACAGGGTTT 8746        CA
           CA                   TGAAACCC TCTCTACTAAAAAT
                                |||||||| ||||||||||||||
                                ACTTTGGG AGAGATGATTTTTA
                                   AC
GAM1005 CASP8   3' ATTTTTAGTAGAGACAGGGTTT 54070       CA
           CA                   TGAAACCC TCTCTACTAAAAAT
                                |||||||| ||||||||||||||
                                ACTTTGGG AGAGATGATTTTTA
                                   AC
GAM1005 CASP8   3' ATTTTTAGTAGAGACAGGGTTT 54095       CA
           CA                   TGAAACCC TCTCTACTAAAAAT
                                |||||||| ||||||||||||||
                                ACTTTGGG AGAGATGATTTTTA
                                   AC
GAM1005 CASP8   3' ATTTTTAGTAGAGACAGGGTTT 54111       CA
           CA                   TGAAACCC TCTCTACTAAAAAT
                                |||||||| ||||||||||||||
                                ACTTTGGG AGAGATGATTTTTA
                                   AC
GAM1005 CBFA2T2 3' ATTTTTAGTGGAGACGGGGTTT 18701        A
           C                    GAAACCCC TCTCTACTAAAAAT
                                |||||||| ||||||||||||||
                                CTTTGGGG AGAGGTGATTTTTA
                                   C
GAM1005 CCNF    3' ATTTTCGGTAGAGACGGGATTT 10067      C  A     TA
           CA                   TGAAA CCC TCTCTAC  AAAAT
                                ||||| ||| |||||||  |||||
                                ACTTT GGG AGAGATG  TTTTA
                                  A  C     GC
GAM1005 CDC6    3' ATTTTTAGTAGAGACAGGGTTT 8817        CA
           TA                   TGAAACCC TCTCTACTAAAAAT
                                |||||||| ||||||||||||||
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                                ATTTTGGG  AGAGATGATTTTTA
                                    AC
GAM1005  CDH17    3'  ATTTTTAATAGAGACGGGGTTT 15781        A     C
             C                   GAAACCCC TCTCTA TAAAAAT
                                 |||||||| |||||| |||||||
                                 CTTTGGGG AGAGAT ATTTTTA
                                     C     A
GAM1005  CLECSF11  5'  ATTTTTAGTAGAGATGGGGTTT 56147
             CA                    TGAAACCCCATCTCTACTAAAAAT
                                   ||||||||||||||||||||||||
                                   ACTTTGGGGTAGAGATGATTTTTA

GAM1005  CLECSF12  3'  TTTTTAGTAGAGACAGGGTTTC 77223       CA
                                GAAACCC  TCTCTACTAAAAA
                                |||||||  ||||||||||||
                                CTTTGGG  AGAGATGATTTTT
                                    AC
GAM1005  CNGA1     5'  ATTTTTAGTAGAGATGGGATTT 60235      C
             CA                    TGAAA CCCATCTCTACTAAAAAT
                                   ||||| |||||||||||||||||
                                   ACTTT GGGTAGAGATGATTTTTA
                                     A
GAM1005  CNN2      3'  ATTTTTAGTAGAGATGGGGTTT 16457
             C                     GAAACCCCATCTCTACTAAAAAT
                                   ||||||||||||||||||||||||
                                   CTTTGGGGTAGAGATGATTTTTA

GAM1005  COX15     3'  ATTTTTAGTAGAGAAGGGGTTT 55278         A
             CA                    TGAAACCCC TCTCTACTAAAAAT
                                   ||||||||| ||||||||||||||
                                   ACTTTGGGG AGAGATGATTTTTA
                                       A
GAM1005  CR1       3'  ATTTTTAGTAGAGACGGGGTTT 6939          A
             CA                    TGAAACCCC TCTCTACTAAAAAT
                                   ||||||||| ||||||||||||||
                                   ACTTTGGGG AGAGATGATTTTTA
                                       C
GAM1005  CXCL16    3'  ATTTTTAGTAGAGACGGGGTTT 42161         A
             CA                    TGAAACCCC TCTCTACTAAAAAT
                                   ||||||||| ||||||||||||||
                                   ACTTTGGGG AGAGATGATTTTTA
                                       C
GAM1005  CYP1A2    3'  ATTTTTAGTAGAGACGAGGTTT 7503        CCA
             CA                    TGAAACC   TCTCTACTAAAAAT
                                   |||||||   ||||||||||||||
                                   ACTTTGG   AGAGATGATTTTTA
                                       AGC
GAM1005  CYP1A2    3'  ATTTTTGGTAGAGACGGGTTTC 7504         CA
             A                     TGAAACCC  TCTCTACTAAAAAT
                                   ||||||||  ||||||||||||||
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                                ACTTTGGG  AGAGATGGTTTTTA
                                    C_
GAM1005  CYP1A2   3'  TTTTAGTGGAGATGGGGTTTCA 7533
                                TGAAACCCCATCTCTACTAAAA
                                ||||||||||||||||||||||
                                ACTTTGGGGTAGAGGTGATTTT

GAM1005  CYP2B6   3'  ATTTTTAGTAGAGATGGGGTTT 7552
           CA                     TGAAACCCCATCTCTACTAAAAAT
                                ||||||||||||||||||||||||
                                ACTTTGGGGTAGAGATGATTTTTA

GAM1005  CYP51    3'  ATTTTTAGTAGAGACGGGGGTT 7611          A_
           TCA                     TGAAACCCC  TCTCTACTAAAAAT
                                ||||||||| ||||||||||||||
                                ACTTTGGGG  AGAGATGATTTTTA
                                    GC
GAM1005  CYP8B1   3'  ATTTTTAGTAGAGACGGCGTTT 16530       C  A
           CA                     TGAAAC CC TCTCTACTAAAAAT
                                ||||||| || ||||||||||||||
                                ACTTTG GG AGAGATGATTTTTA
                                   C  C
GAM1005  DFFB     3'  ATTTTTAGTAGAGACGGGGTTT 88760          A
           CA                     TGAAACCCC TCTCTACTAAAAAT
                                ||||||||| ||||||||||||||
                                ACTTTGGGG AGAGATGATTTTTA
                                    C
GAM1005  DFFB     3'  TTTAGTAGAAACGGGGTTTCA  88792          ATC
                                TGAAACCCC   TCTACTAAA
                                |||||||||   |||||||||
                                ACTTTGGGG   AGATGATTT
                                    CAA
GAM1005  DHFR     3'  ATTTTTAGTAGAGATGGGGTTT 7643
           CA                     TGAAACCCCATCTCTACTAAAAAT
                                ||||||||||||||||||||||||
                                ACTTTGGGGTAGAGATGATTTTTA

GAM1005  DISC1    3'  ATTTTTAGTAGAGACAGGGCTT 38501      A   CA
           CA                     TGAA CCC  TCTCTACTAAAAAT
                                |||| |||  ||||||||||||||
                                ACTT GGG  AGAGATGATTTTTA
                                  C   AC
GAM1005  DSC3     3'  ATTTTTAATAGAGACGGGGTTT 44614          A     C
           CA                     TGAAACCCC TCTCTA TAAAAAT
                                |||||||||  |||||| |||||||
                                ACTTTGGGG AGAGAT ATTTTTA
                                    C     A
GAM1005  DSC3     3'  ATTTTTAATAGAGACGGGGTTT 10434          A     C
           CA                     TGAAACCCC TCTCTA TAAAAAT
                                |||||||||  |||||| |||||||
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                                ACTTTGGGG AGAGAT ATTTTTA
                                     C     A
GAM1005  DSCR3    3'  ATTTTTAGTAGAGACGGGGCTT 21307      A    A
              CA                   TGAA CCCC TCTCTACTAAAAAT
                                   |||| |||| ||||||||||||||
                                   ACTT GGGG AGAGATGATTTTTA
                                     C   C
GAM1005  EHD2     3'  AGTAGAGACGGGGTTTCA    28214          A
                                   TGAAACCCC TCTCTACT
                                   |||||||| ||||||||
                                   ACTTTGGGG AGAGATGA
                                        C
GAM1005  EIF2S3   3'  TTAGTAGAGACGGGGTTTCA  9216           A
                                   TGAAACCCC TCTCTACTAA
                                   |||||||| ||||||||||
                                   ACTTTGGGG AGAGATGATT
                                        C
GAM1005  EPB72    3'  TTTTTAGTAGAGACGGGGTTTC 15883          A
              A                    TGAAACCCC TCTCTACTAAAAA
                                   ||||||||| ||||||||||||
                                   ACTTTGGGG AGAGATGATTTTT
                                        C
GAM1005  F2RL2    3'  ATTTTTAGTAGAGACGGGGTTT 15893          A
              CA                   TGAAACCCC TCTCTACTAAAAAT
                                   ||||||||| ||||||||||||||
                                   ACTTTGGGG AGAGATGATTTTTA
                                        C
GAM1005  F3       3'  TTTTTAGTAGAGATGGGGTTTC 67687
              A                    TGAAACCCCATCTCTACTAAAAA
                                   |||||||||||||||||||||||
                                   ACTTTGGGGTAGAGATGATTTTT

GAM1005  FANCF    3'  ATTTTTAGTAGAGACGGGGTTT 42974          A
              CA                   TGAAACCCC TCTCTACTAAAAAT
                                   ||||||||| ||||||||||||||
                                   ACTTTGGGG AGAGATGATTTTTA
                                        C
GAM1005  FCAR     3'  ATTTTTAGTAGAGATGGGGTTT 10583
              CA                   TGAAACCCCATCTCTACTAAAAAT
                                   |||||||||||||||||||||||
                                   ACTTTGGGGTAGAGATGATTTTTA

GAM1005  FCAR     3'  ATTTTTAGTAGAGATGGGGTTT 56561
              CA                   TGAAACCCCATCTCTACTAAAAAT
                                   |||||||||||||||||||||||
                                   ACTTTGGGGTAGAGATGATTTTTA

GAM1005  FCAR     3'  ATTTTTAGTAGAGATGGGGTTT 56590
              CA                   TGAAACCCCATCTCTACTAAAAAT
                                   |||||||||||||||||||||||
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                                ACTTTGGGGTAGAGATGATTTTTA

GAM1005  FCAR     3'  ATTTTTAGTAGAGATGGGGTTT 56602
                CA                TGAAACCCCATCTCTACTAAAAAT
                                  |||||||||||||||||||||||
                                  ACTTTGGGGTAGAGATGATTTTTA

GAM1005  FCAR     3'  ATTTTTAGTAGAGATGGGGTTT 56614
                CA                TGAAACCCCATCTCTACTAAAAAT
                                  |||||||||||||||||||||||
                                  ACTTTGGGGTAGAGATGATTTTTA

GAM1005  FCGR2A   3'  TTTTTAGTAGAGACAGGGTTTC 80035       CA
                                  GAAACCC  TCTCTACTAAAAA
                                  |||||||  ||||||||||||
                                  CTTTGGG  AGAGATGATTTTT
                                       AC
GAM1005  FGF5     3'  ATTTTTAGTAGAGACGGGGTTT 53651         A
                CA                TGAAACCCC TCTCTACTAAAAAT
                                  |||||||||  ||||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                       C
GAM1005  FGF5     3'  ATTTTTAGTAGAGACGGGGTTT 16758         A
                CA                TGAAACCCC TCTCTACTAAAAAT
                                  |||||||||  ||||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                       C
GAM1005  FUT1     3'  ATTTTTAGTAGAGACAGGGTTT 5584         CA
                CA                TGAAACCC  TCTCTACTAAAAAT
                                  ||||||||  ||||||||||||||
                                  ACTTTGGG  AGAGATGATTTTTA
                                       AC
GAM1005  FUT1     3'  ATTTTTAGTAGAGACGGGGTTT 5585          A
                CA                TGAAACCCC TCTCTACTAAAAAT
                                  |||||||||  ||||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                       C
GAM1005  G6PC     3'  TTTTAGAAGAGATGGGATTTCA 5669       C       A
                                  TGAAA CCCATCTCT CTAAAA
                                  |||||  |||||||||  ||||||
                                  ACTTT GGGTAGAGA GATTTT
                                     A       A
GAM1005  GHR      3'  TTTTAGCAGAGACGGGGTTTCA 5708          A    A
                                  TGAAACCCC TCTCT CTAAAA
                                  |||||||||  |||||  ||||||
                                  ACTTTGGGG AGAGA GATTTT
                                       C    C
GAM1005  GM2A     3'  ATTTTTAGTAGAGATGGGGTTT 68376
                CA                TGAAACCCCATCTCTACTAAAAAT
                                  |||||||||||||||||||||||
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```
                                ACTTTGGGGTAGAGATGATTTTTA

GAM1005  GNE      3'  ATTTTTAGTGGACAGGGTTTCA 19662          CATC
                                TGAAACCC    TCTACTAAAAAT
                                ||||||||    ||||||||||||
                                ACTTTGGG    AGGTGATTTTTA
                                     AC__
GAM1005  GPR81     3'  ATTTTTAGTACAGACGGGGTTT 51737           A   C
              CA                   TGAAACCCC TCT TACTAAAAAT
                                ||||||||| ||| ||||||||||
                                ACTTTGGGG AGA ATGATTTTTA
                                     C   C
GAM1005  GPR81     3'  ATTTTTAGTAGAGACAGGGTTT 51738         CA
              T                    GAAACCC  TCTCTACTAAAAAT
                                |||||||  ||||||||||||||
                                TTTTGGG  AGAGATGATTTTTA
                                     AC
GAM1005  GRM7      5'  ATTTTTAGTAGAGATTGGGTTT 7782           C
              CA                   TGAAACCC ATCTCTACTAAAAAT
                                ||||||||| ||||||||||||||||
                                ACTTTGGG TAGAGATGATTTTTA
                                     T
GAM1005  HCS       3'  ATTTTTAGTGGAGATGGTGTTT 38969         C
              CA                   TGAAAC CCATCTCTACTAAAAAT
                                ||||||| ||||||||||||||||||
                                ACTTTG GGTAGAGGTGATTTTTA
                                    T
GAM1005  HCS       3'  TTTTTAGTAGAGACAGGGTTTC 38998         CA
                                GAAACCC  TCTCTACTAAAAA
                                |||||||  ||||||||||||
                                CTTTGGG  AGAGATGATTTTT
                                     AC
GAM1005  HLCS      5'  ATTTTTAGTAGAGGCGGGGGTT 6406           A_
              TCA                   TGAAACCCC  TCTCTACTAAAAAT
                                |||||||||  ||||||||||||||
                                ACTTTGGGG  GGAGATGATTTTTA
                                     GC
GAM1005  HTR1D     3'  ATTTTTAATAAAGACGGGGTTT 7839           A   C  C
              CA                   TGAAACCCC TCT TA TAAAAAT
                                ||||||||| ||| || |||||||
                                ACTTTGGGG AGA AT ATTTTTA
                                     C   A  A
GAM1005  HTR1E     5'  ATTTTTAGTGGAGACGGGATTT 7859         C   A
              CA                   TGAAA CCC TCTCTACTAAAAAT
                                ||||| ||| ||||||||||||||
                                ACTTT GGG AGAGGTGATTTTTA
                                    A   C
GAM1005  HUNK      3'  TTTTGTAGAAATGGGGTTTC  28198           C     T
                                GAAACCCCAT TCTAC AAAA
                                ||||||||||  ||||| ||||
```

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                                CTTTGGGGTA AGATG TTTT
                                    A    _
GAM1005  HYAL4    5'  ATTTTTAGTAGAGATGGGGTTT 25365
              CA                  TGAAACCCCATCTCTACTAAAAAT
                                  |||||||||||||||||||||||
                                  ACTTTGGGGTAGAGATGATTTTTA

GAM1005  IFNAR2   3'  ATTTTTAGTGGAGACAGGATTT 7897       C  CA
              TA                  TGAAA CC  TCTCTACTAAAAAT
                                  ||||| ||  ||||||||||||||
                                  ATTTT GG  AGAGGTGATTTTTA
                                    A  AC
GAM1005  IGF1     3'  ATTTTTAATAGAGACGGGGTTT 7061          A     C
              TA                  TGAAACCCC TCTCTA TAAAAAT
                                  |||||||||| |||||| |||||||
                                  ATTTTGGGG AGAGAT ATTTTTA
                                       C     A
GAM1005  IL11     3'  ATTTTTAGTAGAGACAGGGTTT 7179         CA
              CA                  TGAAACCC  TCTCTACTAAAAAT
                                  ||||||||  ||||||||||||||
                                  ACTTTGGG  AGAGATGATTTTTA
                                      AC
GAM1005  INMT     3'  ATTTTTAGTAGATATGGGGTTT 23209           C
              CA                  TGAAACCCCAT TCTACTAAAAAT
                                  ||||||||||| ||||||||||||
                                  ACTTTGGGGTA AGATGATTTTTA
                                        T
GAM1005  JAK3     3'  ATTTTTAATAGAGATGAGGTTT 5827         C       C
              CA                  TGAAACC CATCTCTA TAAAAAT
                                  ||||||| |||||||| |||||||
                                  ACTTTGG GTAGAGAT ATTTTTA
                                      A       A
GAM1005  LLGL1    3'  ATTTTTAGTAGAGATGGGGTTT 67415
              CA                  TGAAACCCCATCTCTACTAAAAAT
                                  |||||||||||||||||||||||
                                  ACTTTGGGGTAGAGATGATTTTTA

GAM1005  LNK      3'  ATTTTTAGTAGAGACAGGGTTT 19633         CA
              CA                  TGAAACCC  TCTCTACTAAAAAT
                                  ||||||||  ||||||||||||||
                                  ACTTTGGG  AGAGATGATTTTTA
                                      AC
GAM1005  LTB4R    5'  ATTTTTAGTAGAGACGGGGTTT 7460          A
              CA                  TGAAACCCC TCTCTACTAAAAAT
                                  |||||||||| |||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                       C
GAM1005  LYZ      3'  ATTTTTAGTAGAGACAGGGTTT 5892         CA
              CA                  TGAAACCC  TCTCTACTAAAAAT
                                  ||||||||  ||||||||||||||
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                                ACTTTGGG  AGAGATGATTTTTA
                                    AC
GAM1005  MAK     3'  TTAGTAGAGACAGGGTTTCA  20955        CA
                                TGAAACCC  TCTCTACTAA
                                ||||||||  ||||||||||
                                ACTTTGGG  AGAGATGATT
                                    AC
GAM1005  MDM2    3'  TTTTAGTAGAGACAGGGTTTCA 11504        CA
                                TGAAACCC  TCTCTACTAAAA
                                ||||||||  ||||||||||||
                                ACTTTGGG  AGAGATGATTTT
                                    AC
GAM1005  MDM2    3'  TTTTAGTAGAGACAGGGTTTCA 23466        CA
                                TGAAACCC  TCTCTACTAAAA
                                ||||||||  ||||||||||||
                                ACTTTGGG  AGAGATGATTTT
                                    AC
GAM1005  MDM2    3'  TTTTAGTAGAGACAGGGTTTCA 23479        CA
                                TGAAACCC  TCTCTACTAAAA
                                ||||||||  ||||||||||||
                                ACTTTGGG  AGAGATGATTTT
                                    AC
GAM1005  MDM2    3'  TTTTAGTAGAGACAGGGTTTCA 23492        CA
                                TGAAACCC  TCTCTACTAAAA
                                ||||||||  ||||||||||||
                                ACTTTGGG  AGAGATGATTTT
                                    AC
GAM1005  MDM2    3'  TTTTAGTAGAGACAGGGTTTCA 23506        CA
                                TGAAACCC  TCTCTACTAAAA
                                ||||||||  ||||||||||||
                                ACTTTGGG  AGAGATGATTTT
                                    AC
GAM1005  MEF2A   5'  ATTTTTAGTAGAGATGGAGTTT 19992       C
            CA                    TGAAAC CCATCTCTACTAAAAAT
                                ||||||  ||||||||||||||||
                                ACTTTG GGTAGAGATGATTTTTA
                                   A
GAM1005  MEFV    3'  ATTTTTAGTAGACATGAGGTTT 5928        C  C
            CA                    TGAAACC CAT TCTACTAAAAAT
                                |||||||  |||  ||||||||||||
                                ACTTTGG GTA AGATGATTTTTA
                                    A  C
GAM1005  MEFV    3'  ATTTTTAGTAGAGACGGGGGTT 5929         A_
            TCA                    TGAAACCCC  TCTCTACTAAAAAT
                                |||||||||  ||||||||||||||
                                ACTTTGGGG  AGAGATGATTTTTA
                                     GC
GAM1005  MHC2TA  3'  TTTTTAGCGGAGACGGAGTCCC 5999     AA  C  A    TA
            A                     TG  AC CC TCTC  CTAAAAA
                                ||  || || ||||  |||||||
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                                AC  TG GG AGAG  GATTTTT
                                 CC  A  C    GC
GAM1005  MICB     3'  ATTTTTTGTAGAGACGGGGTTT 21019         A      T
              C                   GAAACCCC TCTCTAC AAAAAT
                                  |||||||| ||||||| ||||||
                                  CTTTGGGG AGAGATG TTTTTA
                                      C      T
GAM1005  MLANA    3'  TTTTAGTAGAGACGGGGTTTC  19774         A
                                  GAAACCCC TCTCTACTAAAA
                                  |||||||| ||||||||||||
                                  CTTTGGGG AGAGATGATTTT
                                      C
GAM1005  MPL      3'  ATTTTTAGTAGAGACAGGGTTT 19341         CA
              T                   GAAACCC  TCTCTACTAAAAAT
                                  |||||||  ||||||||||||||
                                  TTTTGGG  AGAGATGATTTTTA
                                      AC
GAM1005  MRPL49   3'  ATTTTTAGTAGAGATGGGGTTT 70162
              CA                    TGAAACCCCATCTCTACTAAAAAT
                                    |||||||||||||||||||||||||
                                    ACTTTGGGGTAGAGATGATTTTTA

GAM1005  MTR      3'  AGTAGAGACAGGATTTCA    6013        C  CA
                                  TGAAA CC  TCTCTACT
                                  ||||| ||  ||||||||
                                  ACTTT GG  AGAGATGA
                                     A  AC
GAM1005  MYCL2    3'  ATTTTTAGTAGAGATGGGGTTT 19371
              CA                    TGAAACCCCATCTCTACTAAAAAT
                                    |||||||||||||||||||||||||
                                    ACTTTGGGGTAGAGATGATTTTTA

GAM1005  NDRG3    3'  ATTTTTAGTAGAGATGGAGTTT 50118        C
              CA                    TGAAAC CCATCTCTACTAAAAAT
                                    ||||||  ||||||||||||||||
                                    ACTTTG GGTAGAGATGATTTTTA
                                       A
GAM1005  NQO1     3'  ATTTTTAGTAGAGACGGCGTTT 8043         C  A
              CA                    TGAAAC CC TCTCTACTAAAAAT
                                    ||||||  || ||||||||||||||
                                    ACTTTG GG AGAGATGATTTTTA
                                       C  C
GAM1005  PCDHA9   3'  ATTTTTAGTAGAGATGGGGTTT 26612
              CA                    TGAAACCCCATCTCTACTAAAAAT
                                    |||||||||||||||||||||||||
                                    ACTTTGGGGTAGAGATGATTTTTA

GAM1005  PCDHA9   3'  ATTTTTAGTAGAGATGGGGTTT 26613
              CA                    TGAAACCCCATCTCTACTAAAAAT
                                    ||||||||||||||||||||||||
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                                ACTTTGGGGTAGAGATGATTTTTA

GAM1005  PCDHB11   3'  TTTAGTAGAGACGGGGTTTCA  38932          A
                                TGAAACCCC TCTCTACTAAA
                                ||||||||| ||||||||||
                                ACTTTGGGG AGAGATGATTT
                                     C
GAM1005  PCDHB9    3'  ATTTTCAGTAGAGACGGGTTTC 39438         CA       A
              A                  TGAAACCC  TCTCTACT AAAAT
                                 |||||||| ||||||| |||||
                                 ACTTTGGG  AGAGATGA TTTTA
                                     C_       C
GAM1005  PDE6B     3'  ATTTTCAGTACAGATGGGGTTT 6071            C    A
              CA                   TGAAACCCCATCT TACT AAAAT
                                   |||||||||||| |||| |||||
                                   ACTTTGGGGTAGA ATGA TTTTA
                                        C   C
GAM1005  PER2      3'  ATTTTTAGTAGAGACAGGGTTT 43344         CA
              CA                   TGAAACCC  TCTCTACTAAAAAT
                                   |||||||| ||||||||||||||
                                   ACTTTGGG  AGAGATGATTTTTA
                                       AC
GAM1005  PIGR      3'  ATTTTTAGTAGAGACAGGGTTT 72990         CA
              CA                   TGAAACCC  TCTCTACTAAAAAT
                                   |||||||| ||||||||||||||
                                   ACTTTGGG  AGAGATGATTTTTA
                                       AC
GAM1005  PIK3C2B   3'  ATTTTTAGTAGAGACGGGGTTT 12091         A
              CA                   TGAAACCCC TCTCTACTAAAAAT
                                   ||||||||| ||||||||||||||
                                   ACTTTGGGG AGAGATGATTTTTA
                                       C
GAM1005  PIK3CD    3'  TTTTAGTAGAGACGGGGGTTTC 18505         A_
              A                    TGAAACCCC  TCTCTACTAAAA
                                   |||||||||  ||||||||||||
                                   ACTTTGGGG  AGAGATGATTTT
                                       GC
GAM1005  PMCHL1    3'  ATTTTTAGTAGAGGCAAGGTTT 49912        CCA
              CA                   TGAAACC   TCTCTACTAAAAAT
                                   |||||||   ||||||||||||||
                                   ACTTTGG   GGAGATGATTTTTA
                                      AAC
GAM1005  POU2AF1   3'  ATTTTTAGTAGAGACGGGGTTT 21732         A
              CA                   TGAAACCCC TCTCTACTAAAAAT
                                   ||||||||| ||||||||||||||
                                   ACTTTGGGG AGAGATGATTTTTA
                                       C
GAM1005  PPEF2     3'  ATTTTTAGTAGACACAGGGTTT 21771        CATC
              C                     GAAACCC    TCTACTAAAAAT
                                    |||||||    ||||||||||||
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                                CTTTGGG    AGATGATTTTTA
                                    ACAC
GAM1005  PPID     3'  ATTTTTAGTAGAGATGGGGTTT 88821
                 CA                  TGAAACCCCATCTCTACTAAAAAT
                                     |||||||||||||||||||||||
                                     ACTTTGGGGTAGAGATGATTTTTA

GAM1005  PPT2     3'  ATTTTTAGTAGAGACGGGGTTT 18947          A
                 TA                  TGAAACCCC TCTCTACTAAAAAT
                                     |||||||||| ||||||||||||||
                                     ATTTTGGGG AGAGATGATTTTTA
                                         C
GAM1005  PPT2     3'  ATTTTTAGTAGAGACGGGGTTT 57799          A
                 TA                  TGAAACCCC TCTCTACTAAAAAT
                                     |||||||||| ||||||||||||||
                                     ATTTTGGGG AGAGATGATTTTTA
                                         C
GAM1005  PRKR     3'  TTTTTAATAAAGACAGGGTTTC 12354         CA   C  C
                 A                    TGAAACCC  TCT TA TAAAAA
                                     ||||||||  ||| || ||||||
                                     ACTTTGGG  AGA AT ATTTTT
                                         AC   A  A
GAM1005  PRKWNK3  3'  ATTTTTAGTAGAGGATGGGGTT 62226           _
                 TCA                   TGAAACCCCATC TCTACTAAAAAT
                                     ||||||||||||| ||||||||||||
                                     ACTTTGGGGTAG AGATGATTTTTA
                                           G
GAM1005  PTGES    3'  ATTTTTAGTAGAGACGGGTTCA 18057      AC   A
                                     TGAA  CCC TCTCTACTAAAAAT
                                     ||||  ||| ||||||||||||||
                                     ACTT  GGG AGAGATGATTTTTA
                                       __   C
GAM1005  PTGIS    3'  ATTTTTAGTAGAGACGGGGTTT 8195          A
                 C                    GAAACCCC TCTCTACTAAAAAT
                                     |||||||| ||||||||||||||
                                     CTTTGGGG AGAGATGATTTTTA
                                         C
GAM1005  PTGIS    3'  ATTTTTAGTAGAGATGGGATTT 8196        C
                 CA                   TGAAA CCCATCTCTACTAAAAAT
                                     ||||| |||||||||||||||||
                                     ACTTT GGGTAGAGATGATTTTTA
                                        A
GAM1005  RAB36    3'  ATTTTTAGTAGAGAGAGGTTTC 18155        CCA
                 A                    TGAAACC   TCTCTACTAAAAAT
                                     |||||||   ||||||||||||||
                                     ACTTTGG   AGAGATGATTTTTA
                                         AG_
GAM1005  RAB36    3'  ATTTTTAGTAGAGATGGGGTTT 18156
                 C                    GAAACCCCATCTCTACTAAAAAT
                                     |||||||||||||||||||||||
```

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                                CTTTGGGGTAGAGATGATTTTTA

GAM1005  RABL2A   3'  ATTTTTAGTAGAGACGGGGTTT 26406          A
                CA                  TGAAACCCC TCTCTACTAAAAAT
                                    ||||||||| ||||||||||||||
                                    ACTTTGGGG AGAGATGATTTTTA
                                         C
GAM1005  RABL2B   3'  ATTTTTAGTAGAGACGGGGTTT 23974          A
                CA                  TGAAACCCC TCTCTACTAAAAAT
                                    ||||||||| ||||||||||||||
                                    ACTTTGGGG AGAGATGATTTTTA
                                         C
GAM1005  RBBP9    3'  ATTTTTAGTAGAGACAGGGTTT 70684         CA
                CA                  TGAAACCC  TCTCTACTAAAAAT
                                    ||||||||  ||||||||||||||
                                    ACTTTGGG  AGAGATGATTTTTA
                                         AC
GAM1005  RGS9     5'  TTTTAGTAAAGACGGGGTTTT  15175        A  C
                                    GAAACCCC TCT TACTAAAA
                                    ||||||||  ||| ||||||||
                                    TTTTGGGG AGA ATGATTTT
                                         C  A
GAM1005  RHD      3'  ATTTTTACTTGACAGGGTTTCA 32816         CA  TCTAC
                                    TGAAACCC  TC    TAAAAAT
                                    ||||||||  ||    |||||||
                                    ACTTTGGG  AG    ATTTTTA
                                         AC  TTC__
GAM1005  RHD      3'  ATTTTTAGTAAAGATGGGGTTT 32817           C
                CA                  TGAAACCCCATCT TACTAAAAAT
                                    |||||||||||||  ||||||||||
                                    ACTTTGGGGTAGA ATGATTTTTA
                                              A
GAM1005  RHD      3'  ATTTTTACTTGACAGGGTTTCA 33136         CA  TCTAC
                                    TGAAACCC  TC    TAAAAAT
                                    ||||||||  ||    |||||||
                                    ACTTTGGG  AG    ATTTTTA
                                         AC  TTC__
GAM1005  RHD      3'  ATTTTTAGTAAAGATGGGGTTT 33137           C
                CA                  TGAAACCCCATCT TACTAAAAAT
                                    |||||||||||||  ||||||||||
                                    ACTTTGGGGTAGA ATGATTTTTA
                                              A
GAM1005  RPH3AL   3'  ATTTTTAGAAGAGATGGGGTTT 23730            A
                C                    GAAACCCCATCTCT CTAAAAAT
                                    ||||||||||||||  ||||||||
                                    CTTTGGGGTAGAGA GATTTTTA
                                              A
GAM1005  RPP30    3'  TTTAGCAGAGACGGGGTTTCA  22212         A    A
                                    TGAAACCCC TCTCT CTAAA
                                    |||||||||  ||||| |||||
```

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                                ACTTTGGGG AGAGA GATTT
                                    C    C
GAM1005 SAS     3' ATTTTTAGTAGAGACAGGGTTT 21096        CA
            CA                   TGAAACCC  TCTCTACTAAAAAT
                                 ||||||||  ||||||||||||||
                                 ACTTTGGG  AGAGATGATTTTTA
                                     AC
GAM1005 SCML2   3' TTTTGTAGAGATGGGGTTTC  21436            T
                                 GAAACCCCATCTCTAC AAAA
                                 |||||||||||||||| ||||
                                 CTTTGGGGTAGAGATG TTTT
                                                 _
GAM1005 SEDL    3' ATTTTTAGTAGAGACAGGGTTT 28078        CA
            CA                   TGAAACCC  TCTCTACTAAAAAT
                                 ||||||||  ||||||||||||||
                                 ACTTTGGG  AGAGATGATTTTTA
                                     AC
GAM1005 SEDL    3' ATTTTTAGTAGAGACAGGGTTT 28079        CA
            CA                   TGAAACCC  TCTCTACTAAAAAT
                                 ||||||||  ||||||||||||||
                                 ACTTTGGG  AGAGATGATTTTTA
                                     AC
GAM1005 SEDL    3' TTTTTAGTAGAGACGGGGTTTC 28118         A
                                 GAAACCCC TCTCTACTAAAAA
                                 |||||||| ||||||||||||
                                 CTTTGGGG AGAGATGATTTTT
                                     C
GAM1005 SEPN1   3' ATTTTTAGTAGAGATGGGGTTT 66961
            CA                   TGAAACCCCATCTCTACTAAAAAT
                                 |||||||||||||||||||||||||
                                 ACTTTGGGGTAGAGATGATTTTTA

GAM1005 SERPINB9 3' ATTTTTAGTAGAGACGGGGTTT 16009         A
            CA                   TGAAACCCC TCTCTACTAAAAAT
                                 |||||||||  ||||||||||||||
                                 ACTTTGGGG AGAGATGATTTTTA
                                     C
GAM1005 SERPINB9 3' ATTTTTCAGTAGAGACGGGGTT 16010         A      _
            TC                   GAAACCCC TCTCTACT AAAAAT
                                 |||||||| |||||||| ||||||
                                 CTTTGGGG AGAGATGA TTTTTA
                                     C       C
GAM1005 SH3BP2  3' ATTTTTAGTAGAGACGGGATTT 13050       C  A
            TA                   TGAAA CCC TCTCTACTAAAAAT
                                 |||||  ||| ||||||||||||||
                                 ATTTT GGG AGAGATGATTTTTA
                                   A  C
GAM1005 SH3BP2  3' ATTTTTAGTGGAACCGGGGTTT 13051         ATC
            CA                   TGAAACCCC   TCTACTAAAAAT
                                 |||||||||   ||||||||||||
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                                ACTTTGGGG  AGGTGATTTTTA
                                     CCA
GAM1005  SH3GL3   5'  AGTAGAGATGGGTTTCA    13104        C
                                TGAAACCC ATCTCTACT
                                |||||||| |||||||||
                                ACTTTGGG TAGAGATGA
                                     _
GAM1005  SHOX     3'  ATTTTCAGTAGAGATGGGGTTT 23516             A
                                AAACCCCATCTCTACT AAAAT
                                |||||||||||||||| |||||
                                TTTGGGGTAGAGATGA TTTTA
                                        C
GAM1005  SHOX     3'  ATTTATAGTAGAGACGGCGTTT 6564       C  A       A
            CA                    TGAAAC CC TCTCTACTA AAAT
                                |||||| || ||||||||| ||||
                                ACTTTG GG AGAGATGAT TTTA
                                   C  C       A
GAM1005  SIL      3'  ATTTTTAGTAGAGACTGGTTTC 13153       CCA
                                GAAACC   TCTCTACTAAAAAT
                                ||||||   |||||||||||||
                                CTTTGG   AGAGATGATTTTTA
                                   TC_
GAM1005  SLA2     3'  ATTTTTAGTAGACATGGGGTTT 50881          C
            CA                    TGAAACCCCAT TCTACTAAAAAT
                                |||||||||| ||||||||||
                                ACTTTGGGGTA AGATGATTTTTA
                                      C
GAM1005  SLC14A2  5'  ATTTTTAGTAGAGACGGGGTTT 24110         A
            CA                    TGAAACCCC TCTCTACTAAAAAT
                                ||||||||| ||||||||||||||
                                ACTTTGGGG AGAGATGATTTTTA
                                     C
GAM1005  SLC15A1  3'  ATTTTTAGTAGAGATGGGGTTT 18636
            CA                    TGAAACCCCATCTCTACTAAAAAT
                                |||||||||||||||||||||||
                                ACTTTGGGGTAGAGATGATTTTTA

GAM1005  SLC17A5  3'  TTTTGTAGAGATGGGGTCTC  25837    A          T
                                GA ACCCCATCTCTAC AAAA
                                || |||||||||||| ||||
                                CT TGGGGTAGAGATG TTTT
                                 C          _
GAM1005  SMAC     5'  AGTAGAGATGGGGTTTCA    58015
                                TGAAACCCCATCTCTACT
                                ||||||||||||||||||
                                ACTTTGGGGTAGAGATGA

GAM1005  SNAP23   3'  ATTTTTAGTAGAGACAGGGTTT 56335        CA
            CA                    TGAAACCC  TCTCTACTAAAAAT
                                ||||||||  ||||||||||||||
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                                ACTTTGGG  AGAGATGATTTTTA
                                    AC
GAM1005  SNAP23   3'  ATTTTTAGTAGAGACAGGGTTT 15136        CA
             CA                   TGAAACCC  TCTCTACTAAAAAT
                                  ||||||||  ||||||||||||||
                                  ACTTTGGG  AGAGATGATTTTTA
                                      AC
GAM1005  SNX15    3'  ATTTTCAGTAGGGACGGGGTTA 74115    A     A       A
             CA                   TG AACCCC TCTCTACT AAAAT
                                  || |||||| |||||||| |||||
                                  AC TTGGGG AGGGATGA TTTTA
                                   A     C       C
GAM1005  SPN      3'  ATTTTTGGTAGAGATGGGGTTT 13370
             CA                   TGAAACCCCATCTCTACTAAAAAT
                                  |||||||||||||||||||||||||
                                  ACTTTGGGGTAGAGATGGTTTTTA

GAM1005  TAPBP    3'  ATTTTTAGTAGAGACGGGGTTT 13552         A
             CA                   TGAAACCCC TCTCTACTAAAAAT
                                  |||||||||  ||||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                      C
GAM1005  TAPBP    3'  TTTTTAGTAGAGACGGGGTTTC 13594         A
             A                    TGAAACCCC TCTCTACTAAAAA
                                  |||||||||  |||||||||||||
                                  ACTTTGGGG AGAGATGATTTTT
                                      C
GAM1005  TAPBP    3'  TTTTTAGTAGAGACGGGGTTTC 13595         A
             A                    TGAAACCCC TCTCTACTAAAAA
                                  |||||||||  |||||||||||||
                                  ACTTTGGGG AGAGATGATTTTT
                                      C
GAM1005  TAT      3'  ATTTTTAGTAGAGACAGGGTTT 6250          CA
             CA                   TGAAACCC  TCTCTACTAAAAAT
                                  ||||||||  ||||||||||||||
                                  ACTTTGGG  AGAGATGATTTTTA
                                      AC
GAM1005  TBXA2R   3'  ATTTTTAGTAGAGACGGGGTTT 8345          A
             CA                   TGAAACCCC TCTCTACTAAAAAT
                                  |||||||||  |||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                      C
GAM1005  TDGF1    3'  TTTTAGTAGAGATGGGGGTTTC 13665         _
             A                    TGAAACCCC ATCTCTACTAAAA
                                  |||||||||  |||||||||||||
                                  ACTTTGGGG TAGAGATGATTTT
                                      G
GAM1005  TERF1    3'  ATTTTTAGTAGAGGCGGGGTTT 34389         AT
             CA                   TGAAACCCC  CTCTACTAAAAAT
                                  |||||||||  |||||||||||||
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                                ACTTTGGGG  GAGATGATTTTTA
                                     CG
GAM1005  TERF2    3'  ATTTTTAGTAGAGACGGGGTTT 20145         A
              CA                   TGAAACCCC TCTCTACTAAAAAT
                                   ||||||||| ||||||||||||||
                                   ACTTTGGGG AGAGATGATTTTTA
                                        C
GAM1005  TES      3'  ATTTTTAGTAGAGACAGGTTTT 72460       C  CA
              CA                   TGAAA CC  TCTCTACTAAAAAT
                                   ||||| ||  ||||||||||||||
                                   ACTTT GG  AGAGATGATTTTTA
                                     T  AC
GAM1005  TIM3     3'  ATTTTTAGTAGAGACAGGGTTT 52352         CA
              CA                   TGAAACCC  TCTCTACTAAAAAT
                                   ||||||||  ||||||||||||||
                                   ACTTTGGG  AGAGATGATTTTTA
                                        AC
GAM1005  TMPRSS3  3'  ATTTTTAGTAGAGACAGGGTTT 51512         CA
              CA                   TGAAACCC  TCTCTACTAAAAAT
                                   ||||||||  ||||||||||||||
                                   ACTTTGGG  AGAGATGATTTTTA
                                        AC
GAM1005  TMPRSS3  3'  ATTTTTAGTAGAGACAGGGTTT 51540         CA
              CA                   TGAAACCC  TCTCTACTAAAAAT
                                   ||||||||  ||||||||||||||
                                   ACTTTGGG  AGAGATGATTTTTA
                                        AC
GAM1005  TMPRSS3  3'  ATTTTTAGTAGAGACAGGGTTT 44015         CA
              CA                   TGAAACCC  TCTCTACTAAAAAT
                                   ||||||||  ||||||||||||||
                                   ACTTTGGG  AGAGATGATTTTTA
                                        AC
GAM1005  TNFRSF10B 3'  ATTTTTAGTAGAGACGGGGTTT 15218         A
              CA                   TGAAACCCC TCTCTACTAAAAAT
                                   ||||||||| ||||||||||||||
                                   ACTTTGGGG AGAGATGATTTTTA
                                        C
GAM1005  TP53     3'  TTTTGTAGAGATGGGGTCTCA  6809      A          T
                                   TGA ACCCCATCTCTAC AAAA
                                   ||| |||||||||||| ||||
                                   ACT TGGGGTAGAGATG TTTT
                                     C          _
GAM1005  TPMT     3'  TTTTTAGTGGAGACGGGGTTTC 6322          A
              A                     TGAAACCCC TCTCTACTAAAAA
                                   ||||||||| ||||||||||||
                                   ACTTTGGGG AGAGGTGATTTTT
                                        C
GAM1005  TRAF5    3'  ATTTTTAGTAGAGACGGAGTTT 17268       C  A
              T                     GAAAC CC TCTCTACTAAAAAT
                                   ||||| || ||||||||||||||
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                                TTTTG GG AGAGATGATTTTTA
                                  A  C
GAM1005  TRIM9    5'  AGTAGAGACGGGGTTTCA    31444          A
                                TGAAACCCC TCTCTACT
                                ||||||||| ||||||||
                                ACTTTGGGG AGAGATGA
                                    C
GAM1005  TRPM6    3'  ATTTTTAGTAGAGATGGGGTTT 35027
              CA                  TGAAACCCCATCTCTACTAAAAAT
                                  ||||||||||||||||||||||||
                                  ACTTTGGGGTAGAGATGATTTTTA

GAM1005  TRPV1    3'  ATTTTTAATAGAGACGGGGTTT 38689          A     C
              CA                  TGAAACCCC TCTCTA TAAAAAT
                                  ||||||||| |||||| |||||||
                                  ACTTTGGGG AGAGAT ATTTTTA
                                      C     A
GAM1005  TRPV1    3'  ATTTTTAATAGAGACGGGGTTT 55660          A     C
              CA                  TGAAACCCC TCTCTA TAAAAAT
                                  ||||||||| |||||| |||||||
                                  ACTTTGGGG AGAGAT ATTTTTA
                                      C     A
GAM1005  TRPV1    3'  ATTTTTAATAGAGACGGGGTTT 55705          A     C
              CA                  TGAAACCCC TCTCTA TAAAAAT
                                  ||||||||| |||||| |||||||
                                  ACTTTGGGG AGAGAT ATTTTTA
                                      C     A
GAM1005  TRPV1    3'  ATTTTTAATAGAGACGGGGTTT 55736          A     C
              CA                  TGAAACCCC TCTCTA TAAAAAT
                                  ||||||||| |||||| |||||||
                                  ACTTTGGGG AGAGAT ATTTTTA
                                      C     A
GAM1005  TUFT1    3'  ATTTTTAGTAGAGATGGGGTTT 39670
              CA                  TGAAACCCCATCTCTACTAAAAAT
                                  ||||||||||||||||||||||||
                                  ACTTTGGGGTAGAGATGATTTTTA

GAM1005  UGDH     3'  ATTTTTAGTAGAGACAGGGTTT 13992          CA
              CA                  TGAAACCC  TCTCTACTAAAAAT
                                  ||||||||  ||||||||||||||
                                  ACTTTGGG  AGAGATGATTTTTA
                                      AC
GAM1005  VENTX2   3'  ATTTTTAGTAGAAATGGGGTTT 27857            C
              CA                  TGAAACCCCAT TCTACTAAAAAT
                                  |||||||||||| ||||||||||||
                                  ACTTTGGGGTA AGATGATTTTTA
                                       A
GAM1005  VHL      3'  TTTTAGTAGAGACAGTGTTTC  6886        CCCA
                                GAAAC    TCTCTACTAAAA
                                |||||    ||||||||||||
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                                CTTTG   AGAGATGATTTT
                                  TGAC
GAM1005  VHL      3'  TTTTTAGTGGAGACGGGGTTTC 6887          A
              A                  TGAAACCCC TCTCTACTAAAAA
                                 ||||||||| ||||||||||||
                                 ACTTTGGGG AGAGGTGATTTTT
                                     C
GAM1005  VIPR2    3'  ATTTTTAGTAGAGACAGGGTTT 14059         CA
              CA                   TGAAACCC  TCTCTACTAAAAAT
                                 ||||||||  ||||||||||||||
                                 ACTTTGGG  AGAGATGATTTTTA
                                     AC
GAM1005  WHSC1    3'  ATTTTTAGTAGAGACAGGGTTT 56691         CA
              C                   GAAACCC  TCTCTACTAAAAAT
                                 |||||||  ||||||||||||||
                                 CTTTGGG  AGAGATGATTTTTA
                                     AC
GAM1005  XRCC2    3'  ATTTTTAATAGAGACGGGGTTT 19493          A     C
              CA                   TGAAACCCC TCTCTA TAAAAAT
                                 |||||||||| |||||| |||||||
                                 ACTTTGGGG AGAGAT ATTTTTA
                                     C     A
GAM1005  YES1     3'  ATTTTTAGTAGAGACGCAGTTT 19530        CCCA
              CA                   TGAAAC    TCTCTACTAAAAAT
                                 ||||||    ||||||||||||||
                                 ACTTTG    AGAGATGATTTTTA
                                    ACGC
GAM1005  ZNF133   5'  ATTTTTAGTAGAGACGGAGTTT 14292        C  A
              CA                   TGAAAC CC TCTCTACTAAAAAT
                                 |||||| || ||||||||||||||
                                 ACTTTG GG AGAGATGATTTTTA
                                    A  C
GAM1005  ZNF157   3'  ATTTTTAGTAAAGACGGGTTTC 14328         CA   C
              A                   TGAAACCC  TCT TACTAAAAAT
                                 ||||||||  ||| ||||||||||
                                 ACTTTGGG  AGA ATGATTTTTA
                                     C_   A
GAM1005  ZNF264   3'  ATTTTTAGTAGAGACGGGGTTT 14198          A
              CA                   TGAAACCCC TCTCTACTAAAAAT
                                 |||||||||| ||||||||||||||
                                 ACTTTGGGG AGAGATGATTTTTA
                                     C
GAM1005  ZNF264   3'  ATTTTTAGTAGAGACGGGGTTT 14199          A
              CA                   TGAAACCCC TCTCTACTAAAAAT
                                 |||||||||| ||||||||||||||
                                 ACTTTGGGG AGAGATGATTTTTA
                                     C
GAM1005  ZNF74    5'  ATTTTTAGTAGAGACGGGGTTT 14257          A
              T                   GAAACCCC TCTCTACTAAAAAT
                                 |||||||| ||||||||||||||
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                                TTTTGGGG AGAGATGATTTTTA
                                     C
GAM1005  AAK1     3'  ATTTTTAGTAGAGATGGGGTTT 30517
                C                    GAAACCCCATCTCTACTAAAAAT
                                     |||||||||||||||||||||||
                                     CTTTGGGGTAGAGATGATTTTTA

GAM1005  AP3S2    3'  TTTAGTAGAGACAGGGTTTCA  20661        CA
                                     TGAAACCC  TCTCTACTAAA
                                     ||||||||  ||||||||||
                                     ACTTTGGG  AGAGATGATTT
                                          AC
GAM1005  ARHF     3'  ATTTTTAGTAGAGACAGGGTTT 39262        CA
                CA                     TGAAACCC  TCTCTACTAAAAAT
                                     ||||||||  ||||||||||||||
                                     ACTTTGGG  AGAGATGATTTTTA
                                          AC
GAM1005  ARHGAP11A 3'  ATTTTTAGTAGAGACGGTTTCA 29443        CCA
                                     TGAAACC   TCTCTACTAAAAAT
                                     |||||||   |||||||||||||
                                     ACTTTGG   AGAGATGATTTTTA
                                          C__
GAM1005  ARHGAP5  5'  ATTTTTAGTAGAGATGGGGTTT 77596
                C                    GAAACCCCATCTCTACTAAAAAT
                                     |||||||||||||||||||||||
                                     CTTTGGGGTAGAGATGATTTTTA

GAM1005  ASB16    3'  ATTTTTGGTGGAGACGGGGTCT 55973    A    A
                C                    GA ACCCC TCTCTACTAAAAAT
                                     || ||||| |||||||||||||
                                     CT TGGGG AGAGGTGGTTTTTA
                                      C    C
GAM1005  ASE-1    3'  ATTTTTAGTAGAGACAGGGGTT 24971         A_
                TCA                    TGAAACCCC  TCTCTACTAAAAAT
                                     |||||||||  ||||||||||||||
                                     ACTTTGGGG  AGAGATGATTTTTA
                                          AC
GAM1005  ASE-1    3'  TTTTTAGTAGAGATGGGGTTTC 25001
                A                    TGAAACCCCATCTCTACTAAAAA
                                     |||||||||||||||||||||||
                                     ACTTTGGGGTAGAGATGATTTTT

GAM1005  ATP1B4   3'  ATTTTTGGCGGAGACAGGGTTT 24836        CA   TA
                CA                     TGAAACCC  TCTC  CTAAAAAT
                                     ||||||||  ||||  ||||||||
                                     ACTTTGGG  AGAG  GGTTTTTA
                                          AC   GC
GAM1005  BA108L7.2 3'  ATTTTTAGCAGAGATGGGGGTT 49066         _    A
                TCA                    TGAAACCCC ATCTCT CTAAAAAT
                                     |||||||||  ||||||  ||||||||
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                                ACTTTGGGG TAGAGA GATTTTTA
                                     G     C
GAM1005  BM-002   3'  ATTTTTAGCAGAGACAGGG   34006     CA    A
                                CCC  TCTCT CTAAAAAT
                                |||  ||||| ||||||||
                                GGG  AGAGA GATTTTTA
                                  AC    C
GAM1005  BNIP-S   3'  ATTTTTAGTAGAGACGGGGTTT 57087          A
            CA                    TGAAACCCC TCTCTACTAAAAAT
                                |||||||||| ||||||||||||||
                                ACTTTGGGG AGAGATGATTTTTA
                                     C
GAM1005  BTN3A1   3'  TTTTAGTACAGATGAGGGTTCA 23897      A  _    C
                                TGAA CCC CATCT TACTAAAA
                                |||| ||| ||||| ||||||||
                                ACTT GGG GTAGA ATGATTTT
                                  _  A    C
GAM1005  C11orf17 3'  ATTTTTAGTAGAGACGGGGTTT 40576        A
                                AAACCCC TCTCTACTAAAAAT
                                ||||||| ||||||||||||||
                                TTTGGGG AGAGATGATTTTTA
                                    C
GAM1005  C13orf1  3'  ATTTTTAGTAGAGATGGGGTTT 40355
            CA                    TGAAACCCCATCTCTACTAAAAAT
                                |||||||||||||||||||||||
                                ACTTTGGGGTAGAGATGATTTTTA

GAM1005  C1orf24  3'  ATTTTTGGTGGAGATGGGTTTT 54783       C
            CA                    TGAAA CCCATCTCTACTAAAAAT
                                ||||| ||||||||||||||||||
                                ACTTT GGGTAGAGGTGGTTTTTA
                                   T
GAM1005  C1QTNF6  3'  ATTTTTAGTAGAGATGGGGTTT 49989
            CA                    TGAAACCCCATCTCTACTAAAAAT
                                |||||||||||||||||||||||
                                ACTTTGGGGTAGAGATGATTTTTA

GAM1005  C20orf142 3'  ATTTTTAGTAGAGATGGGGTTT 75272
            C                     GAAACCCCATCTCTACTAAAAAT
                                |||||||||||||||||||||||
                                CTTTGGGGTAGAGATGATTTTTA

GAM1005  C21orf25 3'  TTTAGTAGAAATGGAGTCTCA  64308     A  C    C
                                TGA AC CCAT TCTACTAAA
                                ||| || |||| |||||||||
                                ACT TG GGTA AGATGATTT
                                  C  A    A
GAM1005  C6orf5   3'  ATTTTTAGTAGAGACAGGGTTT 31974          CA
            CA                    TGAAACCC  TCTCTACTAAAAAT
                                ||||||||  ||||||||||||||
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                                ACTTTGGG  AGAGATGATTTTTA
                                    AC
GAM1005  C9orf9   3'  ATTTTTAGTAGAGACAGCGTTT 39010       CCCA
              CA                  TGAAAC   TCTCTACTAAAAAT
                                  ||||||   ||||||||||||||
                                  ACTTTG   AGAGATGATTTTTA
                                     CGAC
GAM1005  C9orf9   3'  TTTTTAGTAGAGACGGGGCTTC 39041     A   A
              A                   TGAA CCCC TCTCTACTAAAAA
                                  |||| |||| ||||||||||||
                                  ACTT GGGG AGAGATGATTTTT
                                    C   C
GAM1005  CARD6    3'  ATTTTTAGTAGAGGCAGGGTTT 51838       CA
              C                   GAAACCC  TCTCTACTAAAAAT
                                  |||||||  ||||||||||||||
                                  CTTTGGG  GGAGATGATTTTTA
                                      AC
GAM1005  CCRN4L   3'  ATTTTTAGTAGAGACGGGGTTT 25067        A
              CA                  TGAAACCCC TCTCTACTAAAAAT
                                  |||||||||  |||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                       C
GAM1005  CDC14B   3'  ATTTTTAGTAGAGACAGGGTTT 54001        CA
              CA                  TGAAACCC  TCTCTACTAAAAAT
                                  ||||||||  |||||||||||||
                                  ACTTTGGG  AGAGATGATTTTTA
                                      AC
GAM1005  CEACAM8  3'  ATTTTTAGTAGAGACGGGGTTT 10177        A
              CA                  TGAAACCCC TCTCTACTAAAAAT
                                  |||||||||  |||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                       C
GAM1005  CENPH    3'  TTTTAGTAGAGACGGGGTTTCA 43574        A
                                  TGAAACCCC TCTCTACTAAAA
                                  |||||||||  ||||||||||||
                                  ACTTTGGGG AGAGATGATTTT
                                       C
GAM1005  CHRAC1   3'  TTTTTAGTAGAGACGGGGTTCA 34340     A   A
                                  TGAA CCCC TCTCTACTAAAAA
                                  |||| |||| ||||||||||||
                                  ACTT GGGG AGAGATGATTTTT
                                    _   C
GAM1005  CHSY1    3'  ATTTTTAGTAGAGACGGGGTTT 30564        A
              CA                  TGAAACCCC TCTCTACTAAAAAT
                                  |||||||||  |||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                       C
GAM1005  CIP29    3'  ATTTTTAGTAGAGACGGGGTTT 51371        A
              CA                  TGAAACCCC TCTCTACTAAAAAT
                                  |||||||||  |||||||||||||
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                                ACTTTGGGG AGAGATGATTTTTA
                                    C
GAM1005  COLEC12   3'  ATTTTTAGTAGAGAGGGGTTTC 48606          A
            A                    TGAAACCCC TCTCTACTAAAAAT
                                 ||||||||| ||||||||||||||
                                 ACTTTGGGG AGAGATGATTTTTA
                                 _
GAM1005  CPSF2     3'  ATTTTTAGTAGAGACGGGGTTT 62263         A
            C                    GAAACCCC TCTCTACTAAAAAT
                                 |||||||| ||||||||||||||
                                 CTTTGGGG AGAGATGATTTTTA
                                    C
GAM1005  CPSF2     3'  ATTTTTGGTAGAGACAGGGTTT 62264        CA
            CA                    TGAAACCC  TCTCTACTAAAAAT
                                  |||||||| ||||||||||||||
                                  ACTTTGGG  AGAGATGGTTTTTA
                                     AC
GAM1005  DBR1      3'  ATTTTTAGTAATGACAGGGTTT 33061        CA  TC
            CA                    TGAAACCC  TC  TACTAAAAAT
                                  |||||||| ||  ||||||||||
                                  ACTTTGGG  AG  ATGATTTTTA
                                     AC  TA
GAM1005  DKFZp434A2417 3'  ATTTTTAGTAGAGACGGGGTTT 66674         A
            C                    GAAACCCC TCTCTACTAAAAAT
                                 |||||||| ||||||||||||||
                                 CTTTGGGG AGAGATGATTTTTA
                                    C
GAM1005  DKFZP434B044 3'  ATTTTTAGTAGAGATGGGGTTT 49711
            CA                    TGAAACCCCATCTCTACTAAAAAT
                                  |||||||||||||||||||||||||
                                  ACTTTGGGGTAGAGATGATTTTTA

GAM1005  DKFZP434C212 3'  ATTTTTAGTAGAAACGGGGTTT 69482          ATC
            CA                    TGAAACCCC   TCTACTAAAAAT
                                  |||||||||   ||||||||||||
                                  ACTTTGGGG   AGATGATTTTTA
                                      CAA
GAM1005  DKFZP434D146 3'  ATTTTTAGTAGAGACAGGGTTT 32132         CA
            CA                    TGAAACCC  TCTCTACTAAAAAT
                                  |||||||| ||||||||||||||
                                  ACTTTGGG  AGAGATGATTTTTA
                                     AC
GAM1005  DKFZP434F0318 3'  ATTTTTAGTAGAGACAGGGTTT 48745        CA
            C                     GAAACCC  TCTCTACTAAAAAT
                                  ||||||| ||||||||||||||
                                  CTTTGGG  AGAGATGATTTTTA
                                     AC
GAM1005  DKFZp434F1719 3'  TTTTTAGTAGAGATGGGATTTC 51021      C
                                  GAAA CCCATCTCTACTAAAAA
                                  |||| |||||||||||||||
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                                CTTT GGGTAGAGATGATTTTT
                                  A
GAM1005  DKFZP434J037 3'  ATTTTTAGTAGAGACAGGGTTT 48940        CA
            C                      GAAACCC  TCTCTACTAAAAAT
                                   |||||||  |||||||||||||
                                   CTTTGGG  AGAGATGATTTTTA
                                      AC
GAM1005  DKFZp547H025 3'  ATTTTTAGTAGAGATGAGGTTT 39771        C
            CA                       TGAAACC CATCTCTACTAAAAAT
                                   ||||||| ||||||||||||||||
                                   ACTTTGG GTAGAGATGATTTTTA
                                      A
GAM1005  DKFZP564G092 5'  ATTTTTAGTAGAGACAGGATTT 32154       C  CA
            CA                       TGAAA CC  TCTCTACTAAAAAT
                                   ||||| ||  |||||||||||||
                                   ACTTT GG  AGAGATGATTTTTA
                                      A  AC
GAM1005  DKFZP564O0423 3'  TTTTCATAGAGATGGGGTCTCA 93362     A          CT
                                   TGA ACCCCATCTCTA  AAAA
                                   ||| ||||||||||||  ||||
                                   ACT TGGGGTAGAGAT  TTTT
                                     C          AC
GAM1005  DKFZP564O0523 3'  AGTAGAGATGGGTTTTCA     50417       C
                                   TGAAA CCCATCTCTACT
                                   ||||| ||||||||||||
                                   ACTTT GGGTAGAGATGA
                                      T
GAM1005  DKFZp761J139 5'  ATTTTTAGTAGAGATGGGGTTT 51102
                                   AAACCCCATCTCTACTAAAAAT
                                   |||||||||||||||||||||
                                   TTTGGGGTAGAGATGATTTTTA

GAM1005  DKFZp761N1114 3'  ATTTTTAGTAGAGACGGGATTT 79775       C   A
            CA                       TGAAA CCC TCTCTACTAAAAAT
                                   ||||| ||| ||||||||||||||
                                   ACTTT GGG AGAGATGATTTTTA
                                      A   C
GAM1005  DKFZp761O0113 5'  ATTTTTGGTGGAGACGGGGTTT 37889         A
            C                      GAAACCCC TCTCTACTAAAAAT
                                   ||||||||  ||||||||||||||
                                   CTTTGGGG AGAGGTGGTTTTTA
                                      C
GAM1005  DKFZp762P2111 3'  ATTTTTAGTAGAGACAGGGTTT 87625         CA
            CA                       TGAAACCC  TCTCTACTAAAAAT
                                   ||||||||  ||||||||||||||
                                   ACTTTGGG  AGAGATGATTTTTA
                                      AC
GAM1005  DSCR6    3'  ATTTTTAGTAGAGACTCGGTTT 39058        CCA
            CA                       TGAAACC   TCTCTACTAAAAAT
                                   |||||||   ||||||||||||||
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                                ACTTTGG  AGAGATGATTTTTA
                                   CTC
GAM1005 EREG    3' ATTTTTAGTAGAGGCGGGGTTT 9302         AT
            CA                   TGAAACCCC CTCTACTAAAAAT
                                 ||||||||| ||||||||||||
                                 ACTTTGGGG GAGATGATTTTTA
                                    CG
GAM1005 EVI5    3' ATTTTTAGTAGAGATGGGGTTT 20198
            C                     GAAACCCCATCTCTACTAAAAAT
                                  ||||||||||||||||||||||
                                  CTTTGGGGTAGAGATGATTTTTA

GAM1005 EVI5    3' ATTTTTAGTAGAGATGGGGTTT 20199
            CA                   TGAAACCCCATCTCTACTAAAAAT
                                 ||||||||||||||||||||||
                                 ACTTTGGGGTAGAGATGATTTTTA

GAM1005 FBP17   3' ATTTTTAGTAGAGACAGGGTTT 73147        CA
            CA                   TGAAACCC TCTCTACTAAAAAT
                                 |||||||| ||||||||||||
                                 ACTTTGGG AGAGATGATTTTTA
                                    AC
GAM1005 FER1L4  3' ATTTTTAGTAGAGACAGGGTTT 48113        CA
            CA                   TGAAACCC TCTCTACTAAAAAT
                                 |||||||| ||||||||||||
                                 ACTTTGGG AGAGATGATTTTTA
                                    AC
GAM1005 FKBP9   3' ATTTTTGGTAGAGACGGGGTTT 95713         A
            CA                   TGAAACCCC TCTCTACTAAAAAT
                                 ||||||||| ||||||||||||
                                 ACTTTGGGG AGAGATGGTTTTTA
                                    C
GAM1005 FLJ00060 5' ATTTTTAGTAGAGATGGAATTT 61737      CC
            CA                   TGAAA CCATCTCTACTAAAAAT
                                 ||||| ||||||||||||||||
                                 ACTTT GGTAGAGATGATTTTTA
                                   AA
GAM1005 FLJ10232 3' ATTTTTAGTAGAGGTGGGGTTT 36373
            CA                   TGAAACCCCATCTCTACTAAAAAT
                                 ||||||||||||||||||||||
                                 ACTTTGGGGTGGAGATGATTTTTA

GAM1005 FLJ10298 3' ATTTTTAGTAGAGACGGGGTTT 36454         A
            CA                   TGAAACCCC TCTCTACTAAAAAT
                                 ||||||||| ||||||||||||
                                 ACTTTGGGG AGAGATGATTTTTA
                                    C
GAM1005 FLJ10346 5' ATTTTTAGTAGAGGCAGGGTTT 36521        CA
            CA                   TGAAACCC TCTCTACTAAAAAT
                                 |||||||| ||||||||||||
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                                ACTTTGGG  GGAGATGATTTTTA
                                     AC
GAM1005  FLJ10352  3'  TTTGGTGGAGATGAAATTTCA  50475      CCC
                                TGAAA   CATCTCTACTAAA
                                |||||   ||||||||||||||
                                ACTTT   GTAGAGGTGGTTT
                                   AAA
GAM1005  FLJ10535  3'  ATTTTTAGTAGAGATGGGGTTT 36739
            CA                    TGAAACCCCATCTCTACTAAAAAT
                                  |||||||||||||||||||||||||
                                  ACTTTGGGGTAGAGATGATTTTTA

GAM1005  FLJ10560  3'  ATTTTTAGTAGAGACGGGGTTT 36792          A
            CA                    TGAAACCCC TCTCTACTAAAAAT
                                  |||||||||| ||||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                       C
GAM1005  FLJ10713  3'  ATTTTTAGTAGAGATGGGGTTT 36999
            CA                    TGAAACCCCATCTCTACTAAAAAT
                                  |||||||||||||||||||||||||
                                  ACTTTGGGGTAGAGATGATTTTTA

GAM1005  FLJ10846  3'  TTTTCAGTAGAGACAGGGTCTC 37295     A    CA       A
            A                     TGA ACCC  TCTCTACT AAAA
                                  ||| ||||  |||||||| ||||
                                  ACT TGGG  AGAGATGA TTTT
                                    C    AC       C
GAM1005  FLJ10901  3'  ATTTTTAGTAGAGATGGGGTTT 37354
            CA                    TGAAACCCCATCTCTACTAAAAAT
                                  |||||||||||||||||||||||||
                                  ACTTTGGGGTAGAGATGATTTTTA

GAM1005  FLJ10956  3'  ATTTTTAGTGGAGACGGGGTTT 37462          A
            CA                    TGAAACCCC TCTCTACTAAAAAT
                                  |||||||||| ||||||||||||||
                                  ACTTTGGGG AGAGGTGATTTTTA
                                       C
GAM1005  FLJ11800  3'  TTTTTAGTAGAAATGAGGTCTC 47044    A   C   C
                                GA ACC CAT TCTACTAAAAA
                                || ||| ||| ||||||||||
                                CT TGG GTA AGATGATTTTT
                                 C   A   A
GAM1005  FLJ12363  3'  ATTTTTAGTGGGGATGGGGTTT 50629
            CA                    TGAAACCCCATCTCTACTAAAAAT
                                  |||||||||||||||||||||||||
                                  ACTTTGGGGTAGGGGTGATTTTTA

GAM1005  FLJ12488  5'  TTAGTAGACATGAGTTCA    49160      ACCC   C
                                TGAA    CAT TCTACTAA
                                ||||    ||| ||||||||
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                                ACTT    GTA AGATGATT
                                  GA__   C
GAM1005  FLJ12581  3'  ATTTTTAGTAGAGACAGGGTTT 46330         CA
                CA                  TGAAACCC  TCTCTACTAAAAAT
                                    ||||||||  ||||||||||||||
                                    ACTTTGGG  AGAGATGATTTTTA
                                        AC
GAM1005  FLJ12649  3'  TTTTAGTAGAGATAGGGTTTTA 45099         C
                                    TGAAACCC ATCTCTACTAAAA
                                    |||||||| ||||||||||||
                                    ATTTTGGG TAGAGATGATTTT
                                        A
GAM1005  FLJ12668  3'  ATTTTTAGTAGAGATGAGGTTT 47155         C
                CA                  TGAAACC CATCTCTACTAAAAAT
                                    ||||||| |||||||||||||||
                                    ACTTTGG GTAGAGATGATTTTTA
                                        A
GAM1005  FLJ12687  3'  ATTTTTGGTAGAGACAGGGTTT 46746         CA
                CA                  TGAAACCC  TCTCTACTAAAAAT
                                    ||||||||  ||||||||||||||
                                    ACTTTGGG  AGAGATGGTTTTTA
                                        AC
GAM1005  FLJ12687  3'  TTTTTTTTTGGGATGGGGTCTC 46760     A        TACT
                A                    TGA ACCCCATCTC    AAAAA
                                    ||| ||||||||||    |||||
                                    ACT TGGGGTAGGG    TTTTT
                                      C         TTTT
GAM1005  FLJ12787  3'  TTTTAGTAGAGACGGGGTTTCA 50700          A
                                    TGAAACCCC TCTCTACTAAAA
                                    ||||||||| ||||||||||||
                                    ACTTTGGGG AGAGATGATTTT
                                        C
GAM1005  FLJ12876  3'  ATTTTTAGTAGAGACGGGGTTT 43086          A
                CA                  TGAAACCCC TCTCTACTAAAAAT
                                    ||||||||| |||||||||||||
                                    ACTTTGGGG AGAGATGATTTTTA
                                        C
GAM1005  FLJ12903  3'  TTTTTAGTAGAGACAGGATTTC 43081      C  CA
                                    GAAA CC  TCTCTACTAAAAA
                                    |||| ||  ||||||||||||
                                    CTTT GG  AGAGATGATTTTT
                                      A  AC
GAM1005  FLJ12960  3'  ATTTTTAGTAGAGATGGGGTTT 45291
                CA                  TGAAACCCCATCTCTACTAAAAAT
                                    |||||||||||||||||||||||
                                    ACTTTGGGGTAGAGATGATTTTTA

GAM1005  FLJ12973  3'  ATTTTTAGTAGAGATGGGGTTT 46640
                CA                  TGAAACCCCATCTCTACTAAAAAT
                                    |||||||||||||||||||||||
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                                ACTTTGGGGTAGAGATGATTTTTA

GAM1005  FLJ12975  3'  ATTTTTAGTAGAGACAGGGTTC 70185    A    CA
                CA                  TG AACCC  TCTCTACTAAAAAT
                                    || |||||  ||||||||||||||
                                    AC TTGGG  AGAGATGATTTTTA
                                     C    AC
GAM1005  FLJ12975  3'  ATTTTTGGTAAAGACGGGGTTT 70186        A  C
                C                    GAAACCCC TCT TACTAAAAAT
                                    |||||||| ||| ||||||||||
                                    CTTTGGGG AGA ATGGTTTTTA
                                         C  A
GAM1005  FLJ13072  5'  ATTTTTAGTAGAGACAGGGTTT 91387        CA
                CA                  TGAAACCC  TCTCTACTAAAAAT
                                    ||||||||  ||||||||||||||
                                    ACTTTGGG  AGAGATGATTTTTA
                                         AC
GAM1005  FLJ13114  3'  ATTTTTAGTAGAGATGGAGTTT 44896       C
                CA                  TGAAAC CCATCTCTACTAAAAAT
                                    ||||||| |||||||||||||||||
                                    ACTTTG GGTAGAGATGATTTTTA
                                       A
GAM1005  FLJ13188  3'  ATTTTTAGTAGAGACAGAGTTT 42188      CCCA
                T                    GAAAC    TCTCTACTAAAAAT
                                    |||||    ||||||||||||||
                                    TTTTG    AGAGATGATTTTTA
                                       AGAC
GAM1005  FLJ13197  3'  ATTTTTAGTAGAGACAAGAGTT 45175      CCCA_
                TC                   GAAAC    TCTCTACTAAAAAT
                                    |||||    ||||||||||||||
                                    CTTTG    AGAGATGATTTTTA
                                       AGAAC
GAM1005  FLJ13952  3'  ATTTTTAATAGAGACGGGTTTC 46005        CA     C
                A                    TGAAACCC  TCTCTA TAAAAAT
                                    ||||||||  |||||| |||||||
                                    ACTTTGGG  AGAGAT ATTTTTA
                                         C_     A
GAM1005  FLJ14442  3'  ATTTTTAGCAGAGATGGGGTTT 52376             A
                TA                   TGAAACCCCATCTCT CTAAAAAT
                                    |||||||||||||| ||||||||
                                    ATTTTGGGGTAGAGA GATTTTTA
                                              C
GAM1005  FLJ14950  3'  ATTTTTAGTAGAGACAGGGTTT 52782        CA
                CA                  TGAAACCC  TCTCTACTAAAAAT
                                    ||||||||  ||||||||||||||
                                    ACTTTGGG  AGAGATGATTTTTA
                                         AC
GAM1005  FLJ14957  3'  TTTAGTAGAGACGGGGTTTCA  52830         A
                                    TGAAACCCC TCTCTACTAAA
                                    ||||||||| ||||||||||
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                                ACTTTGGGG AGAGATGATTT
                                     C
GAM1005  FLJ20034  3'  TTTTTAGTAGAGATGGGGTCTC 34859    A
                                GA ACCCCATCTCTACTAAAAA
                                || ||||||||||||||||||
                                CT TGGGGTAGAGATGATTTTT
                                 C
GAM1005  FLJ20045  3'  ATTTTTAGTAGAAATGGGGATT 34874     A     C
           CA                    TGAA CCCCAT TCTACTAAAAAT
                                 |||| |||||| ||||||||||||
                                 ACTT GGGGTA AGATGATTTTTA
                                   A     A
GAM1005  FLJ20079  3'  ATTTTTAGTAGAGACAGGGTTT 34967       CA
           C                     GAAACCC  TCTCTACTAAAAAT
                                 |||||||  ||||||||||||||
                                 CTTTGGG  AGAGATGATTTTTA
                                      AC
GAM1005  FLJ20136  3'  ATTTTTAGTAGAGATGAGTTTC 35092       CC
           A                     TGAAAC  CATCTCTACTAAAAAT
                                 ||||||  ||||||||||||||||
                                 ACTTTG  GTAGAGATGATTTTTA
                                    A_
GAM1005  FLJ20344  3'  ATTTTTAGTAGAGACAGGGTTT 35477       CA
           CA                    TGAAACCC  TCTCTACTAAAAAT
                                 ||||||||  ||||||||||||||
                                 ACTTTGGG  AGAGATGATTTTTA
                                      AC
GAM1005  FLJ20507  3'  ATTTTTAGTAGAGACAGGGTTT 35732       CA
           CA                    TGAAACCC  TCTCTACTAAAAAT
                                 ||||||||  ||||||||||||||
                                 ACTTTGGG  AGAGATGATTTTTA
                                      AC
GAM1005  FLJ20507  3'  ATTTTTAGTAGAGACAGGGTTT 60840       CA
           CA                    TGAAACCC  TCTCTACTAAAAAT
                                 ||||||||  ||||||||||||||
                                 ACTTTGGG  AGAGATGATTTTTA
                                      AC
GAM1005  FLJ20700  3'  ATTTTTAGTAGAGACGGGTTTC 35997       CA
           A                     TGAAACCC  TCTCTACTAAAAAT
                                 ||||||||  ||||||||||||||
                                 ACTTTGGG  AGAGATGATTTTTA
                                      C_
GAM1005  FLJ20813  3'  ATTTTTAGTAGAGATGGGCTTT 36127      C
           CA                    TGAAA CCCATCTCTACTAAAAAT
                                 ||||| |||||||||||||||||
                                 ACTTT GGGTAGAGATGATTTTTA
                                   C
GAM1005  FLJ21302  3'  ATTTTTAGTAGAGACAGGGTTT 43505       CA
           CA                    TGAAACCC  TCTCTACTAAAAAT
                                 ||||||||  ||||||||||||||
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                                ACTTTGGG  AGAGATGATTTTTA
                                    AC
GAM1005  FLJ21324  5'  ATTTTTAGTAGAGATGGGGTTT 92845
              CA                  TGAAACCCCATCTCTACTAAAAAT
                                  |||||||||||||||||||||||
                                  ACTTTGGGGTAGAGATGATTTTTA

GAM1005  FLJ21603  3'  ATTTTTAGTAGAGATGGGGTTT 45768
              CA                  TGAAACCCCATCTCTACTAAAAAT
                                  |||||||||||||||||||||||
                                  ACTTTGGGGTAGAGATGATTTTTA

GAM1005  FLJ22002  3'  ATTTTTAATAGAGATGAGGTTT 46193       C       C
              C                   GAAACC CATCTCTA TAAAAAT
                                  ||||||| |||||||| |||||||
                                  CTTTGG GTAGAGAT ATTTTTA
                                     A       A
GAM1005  FLJ22167  5'  ATTTTTAGTAGAGATGGGGTCT 44861     A
              CA                  TGA ACCCCATCTCTACTAAAAAT
                                  ||| ||||||||||||||||||||
                                  ACT TGGGGTAGAGATGATTTTTA
                                    C
GAM1005  FLJ22329  3'  ATTTTTAGTAGAGACGGGGTTT 45394         A
              CA                  TGAAACCCC TCTCTACTAAAAAT
                                  |||||||||| ||||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                      C
GAM1005  FLJ22529  3'  ATTTTTAGTAGAGACAGGGTTT 45940        CA
              CA                  TGAAACCC  TCTCTACTAAAAAT
                                  ||||||||  ||||||||||||||
                                  ACTTTGGG  AGAGATGATTTTTA
                                      AC
GAM1005  FLJ22529  3'  TTTAGTAGAGACAGGGTTTCA  45959        CA
                                  TGAAACCC  TCTCTACTAAA
                                  ||||||||  ||||||||||
                                  ACTTTGGG  AGAGATGATTT
                                      AC
GAM1005  FLJ22684  3'  ATTTTTACTAGAGACAGGGTTT 47466        CA     C
              CA                  TGAAACCC  TCTCTA TAAAAAT
                                  ||||||||  |||||| |||||||
                                  ACTTTGGG  AGAGAT ATTTTTA
                                      AC     C
GAM1005  FLJ22794  3'  ATTTTTAGTAGAGACAGGGTTT 93239        CA
              CA                  TGAAACCC  TCTCTACTAAAAAT
                                  ||||||||  ||||||||||||||
                                  ACTTTGGG  AGAGATGATTTTTA
                                      AC
GAM1005  FLJ22800  3'  ATTTTTAGTAGAGATGGGG   45991
                                  CCCCATCTCTACTAAAAAT
                                  ||||||||||||||||||
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                                GGGGTAGAGATGATTTTTA

GAM1005  FLJ22969  3' ATTTTTTGTAGAGACAGGGTTT 69198        CA      T
                CA                  TGAAACCC  TCTCTAC AAAAAT
                                    ||||||||  |||||||  ||||||
                                    ACTTTGGG  AGAGATG TTTTTA
                                        AC      T
GAM1005  FLJ23024  3' ATTTTTAGTAGAGACGGGGTTT 46838         A
                CA                  TGAAACCCC TCTCTACTAAAAAT
                                    |||||||||  ||||||||||||||
                                    ACTTTGGGG AGAGATGATTTTTA
                                        C
GAM1005  FLJ23392  3' ATTTTTAGTAGAGACAGGGTTT 45881        CA
                CA                  TGAAACCC  TCTCTACTAAAAAT
                                    ||||||||  ||||||||||||||
                                    ACTTTGGG  AGAGATGATTTTTA
                                        AC
GAM1005  FLJ23392  3' ATTTTTAGTAGAGACAGGGTTT 45882        CA
                CA                  TGAAACCC  TCTCTACTAAAAAT
                                    ||||||||  ||||||||||||||
                                    ACTTTGGG  AGAGATGATTTTTA
                                        AC
GAM1005  FLJ23392  3' TTTTTAGTAGAGACGGGGTTTC 45915         A
                A                   TGAAACCCC TCTCTACTAAAAA
                                    |||||||||  |||||||||||||
                                    ACTTTGGGG AGAGATGATTTTT
                                        C
GAM1005  FLJ23519  3' TTTTAGTAGAGATGGGGTTTCA 50969
                                    TGAAACCCCATCTCTACTAAAA
                                    ||||||||||||||||||||||
                                    ACTTTGGGGTAGAGATGATTTT

GAM1005  FLJ23556  3' ATTTTTAGCAGAGACGGGGTTT 46429         A    A
                CA                  TGAAACCCC TCTCT CTAAAAAT
                                    |||||||||  |||||  ||||||||
                                    ACTTTGGGG AGAGA GATTTTTA
                                        C    C
GAM1005  FLJ23556  3' ATTTTTAGTAGAGACCGGGCTT 46430      A   CA
                CA                  TGAA CCC  TCTCTACTAAAAAT
                                    ||||  |||  ||||||||||||||
                                    ACTT GGG  AGAGATGATTTTTA
                                      C   CC
GAM1005  FLJ23563  3' ATTTTTAGTAGAGACAGGGTT  68210       CA
                                    AACCC  TCTCTACTAAAAAT
                                    |||||  |||||||||||||
                                    TTGGG  AGAGATGATTTTTA
                                      AC
GAM1005  FLJ25416  5' TTTAGTGGAGATGGGGTTTCA  59462
                                    TGAAACCCCATCTCTACTAAA
                                    |||||||||||||||||||||
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                                ACTTTGGGGTAGAGGTGATTT

GAM1005  FLJ30532  3'  ATTTTTAGTAGAGACAGGATTT 59216      C  CA
             CA                   TGAAA CC  TCTCTACTAAAAAT
                                  ||||| ||  ||||||||||||||
                                  ACTTT GG  AGAGATGATTTTTA
                                    A  AC
GAM1005  FLJ31101  3'  ATTTTTAGTAAAGACGGGG   36157     A   C
                                  CCCC TCT TACTAAAAAT
                                  |||| ||| ||||||||||
                                  GGGG AGA ATGATTTTTA
                                    C   A
GAM1005  FLJ31153  3'  ATTTTTAGTAGAGATGGGGTTT 58744
             CA                   TGAAACCCCATCTCTACTAAAAAT
                                  |||||||||||||||||||||||||
                                  ACTTTGGGGTAGAGATGATTTTTA

GAM1005  FLJ32865  3'  ATTTTTAGTAGAGACGGGGTTT 58801        A
             C                    GAAACCCC TCTCTACTAAAAAT
                                  |||||||| ||||||||||||||
                                  CTTTGGGG AGAGATGATTTTTA
                                       C
GAM1005  FLJ32894  3'  AGTAGAGATGGGATTTCA    58991      C
                                  TGAAA CCCATCTCTACT
                                  ||||| ||||||||||||
                                  ACTTT GGGTAGAGATGA
                                    A
GAM1005  GGA2      3'  ATTTTTAGTAGAGACAGGATTT 57652      C  CA
             CA                   TGAAA CC  TCTCTACTAAAAAT
                                  ||||| ||  ||||||||||||||
                                  ACTTT GG  AGAGATGATTTTTA
                                    A  AC
GAM1005  GGA2      3'  ATTTTTAGTAGAGACAGGATTT 31158      C  CA
             CA                   TGAAA CC  TCTCTACTAAAAAT
                                  ||||| ||  ||||||||||||||
                                  ACTTT GG  AGAGATGATTTTTA
                                    A  AC
GAM1005  GMPPB     5'  ATTTTTAGTAGAGACAGGGTTT 97437        CA
             CA                   TGAAACCC  TCTCTACTAAAAAT
                                  ||||||||  ||||||||||||||
                                  ACTTTGGG  AGAGATGATTTTTA
                                       AC
GAM1005  GNG4      3'  ATTTTTAGTAAAGACGGGGTTT 16842        A   C
             CA                   TGAAACCCC TCT TACTAAAAAT
                                  ||||||||| ||| ||||||||||
                                  ACTTTGGGG AGA ATGATTTTTA
                                       C   A
GAM1005  GOLGA3    3'  ATTTTTAGTAGCAATGGGGTTT 20883          CT
             CA                   TGAAACCCCAT  CTACTAAAAAT
                                  ||||||||||  ||||||||||
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                                ACTTTGGGGTA  GATGATTTTTA
                                      AC
GAM1005  GREB1    3'  TTTTTAGTAGAGACGGGGTTTC 28584          A
                A                  TGAAACCCC TCTCTACTAAAAA
                                   ||||||||| ||||||||||||
                                   ACTTTGGGG AGAGATGATTTTT
                                       C
GAM1005  GREB1    3'  TTTTTAGTAGAGATGGGGTTTC 28585
                                   GAAACCCCATCTCTACTAAAAA
                                   ||||||||||||||||||||||
                                   CTTTGGGGTAGAGATGATTTTT

GAM1005  GRWD     3'  ATTTTTAGTAGAGACGGGGTTT 49775          A
                CA                   TGAAACCCC TCTCTACTAAAAAT
                                   ||||||||| ||||||||||||||
                                   ACTTTGGGG AGAGATGATTTTTA
                                       C
GAM1005  GTF2E1   3'  ATTTTTAGTAGAGGCAGGGTTT 19792         CA
                CA                   TGAAACCC  TCTCTACTAAAAAT
                                   ||||||||  ||||||||||||||
                                   ACTTTGGG  GGAGATGATTTTTA
                                       AC
GAM1005  GTPBG3   3'  ATTTTTAGTAGAGACAAGGTTT 51890        CCA
                CA                   TGAAACC   TCTCTACTAAAAAT
                                   |||||||   ||||||||||||||
                                   ACTTTGG   AGAGATGATTTTTA
                                       AAC
GAM1005  H2AV     3'  ATTTTTAGTAGACGTGGGGTTT 57627           C
                CA                   TGAAACCCCAT TCTACTAAAAAT
                                   |||||||||||| ||||||||||||
                                   ACTTTGGGGTG AGATGATTTTTA
                                         C
GAM1005  HCA4     3'  TTTTAGTAGAGACGGGGTTTT  78048          A
                                   GAAACCCC TCTCTACTAAAA
                                   |||||||| ||||||||||||
                                   TTTTGGGG AGAGATGATTTT
                                       C
GAM1005  HRH4     3'  ATTTTTAGTAGAGATGAGGTTT 41528        C
                T                   GAAACC CATCTCTACTAAAAAT
                                   |||||| |||||||||||||||||
                                   TTTTGG GTAGAGATGATTTTTA
                                      A
GAM1005  HRH4     3'  TTTCTGTAGAGATGAAGTCTCA 41555     A  CC        TA
                                   TGA AC  CATCTCTAC  AAA
                                   ||| ||  |||||||||  |||
                                   ACT TG  GTAGAGATG  TTT
                                     C  AA        TC
GAM1005  HSMPP8   3'  ATTTTTAGTAGAGATGGGGTTT 95126
                                   AAACCCCATCTCTACTAAAAAT
                                   |||||||||||||||||||||||
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                                TTTGGGGTAGAGATGATTTTTA

GAM1005  HSNOV1   3'  ATTTTTAGTAGACATGGGGTTT 34429          C
             CA                  TGAAACCCCAT TCTACTAAAAAT
                                 |||||||||||| ||||||||||||
                                 ACTTTGGGGTA AGATGATTTTTA
                                       C
GAM1005  HSPC065  3'  ATTTTTAGTAGAGATGGGGTTT 27143
             CA                  TGAAACCCCATCTCTACTAAAAAT
                                 |||||||||||||||||||||||||
                                 ACTTTGGGGTAGAGATGATTTTTA

GAM1005  HSPC065  3'  ATTTTTAGTAGAGATGGGGTTT 27144
             CA                  TGAAACCCCATCTCTACTAAAAAT
                                 |||||||||||||||||||||||||
                                 ACTTTGGGGTAGAGATGATTTTTA

GAM1005  HSPC232  3'  ATTTTTTGTAGAGATGGGGTTC 33656     A         T
             A                    TGAA CCCCATCTCTAC AAAAAT
                                  |||| |||||||||||| ||||||
                                  ACTT GGGGTAGAGATG TTTTTA
                                    _         T
GAM1005  ICK      3'  ATTTTTAGTAGAGACGGGGTTT 30592         A
             CA                   TGAAACCCC TCTCTACTAAAAAT
                                  |||||||||| ||||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                       C
GAM1005  JAM1     3'  TTTTTAGTAGAGACAGGGTTTC 34251         CA
             A                    TGAAACCC  TCTCTACTAAAAA
                                  ||||||||  ||||||||||||||
                                  ACTTTGGG  AGAGATGATTTTT
                                       AC
GAM1005  JAM1     3'  TTTTTAGTAGAGACAGGGTTTC 58527         CA
             A                    TGAAACCC  TCTCTACTAAAAA
                                  ||||||||  ||||||||||||||
                                  ACTTTGGG  AGAGATGATTTTT
                                       AC
GAM1005  JAM1     3'  TTTTTAGTAGAGACAGGGTTTC 58554         CA
             A                    TGAAACCC  TCTCTACTAAAAA
                                  ||||||||  ||||||||||||||
                                  ACTTTGGG  AGAGATGATTTTT
                                       AC
GAM1005  JAM1     3'  TTTTTAGTAGAGACAGGGTTTC 58584         CA
             A                    TGAAACCC  TCTCTACTAAAAA
                                  ||||||||  ||||||||||||||
                                  ACTTTGGG  AGAGATGATTTTT
                                       AC
GAM1005  JM11     3'  TTAGTAGAGACAAGGTTTCA  54376         CCA
                                  TGAAACC   TCTCTACTAA
                                  |||||||   ||||||||||
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                                ACTTTGG   AGAGATGATT
                                    AAC
GAM1005  KIAA0022  3'  ATTTTTGGTAGAGACGGGGTTT 30276        A
             C                   GAAACCCC TCTCTACTAAAAAT
                                 |||||||| ||||||||||||||
                                 CTTTGGGG AGAGATGGTTTTTA
                                     C
GAM1005  KIAA0063  3'  ATTTTTAGTAGAGATGGGGTTT 30252
             C                   GAAACCCCATCTCTACTAAAAAT
                                 |||||||||||||||||||||||
                                 CTTTGGGGTAGAGATGATTTTTA

GAM1005  KIAA0087  3'  ATTTTTAGTAGAGATGGGGTTT 29340
             CA                    TGAAACCCCATCTCTACTAAAAAT
                                   |||||||||||||||||||||||
                                   ACTTTGGGGTAGAGATGATTTTTA

GAM1005  KIAA0161  3'  ATTTTCAGTAGAGACGGGGTTT 29192         A       A
             CA                    TGAAACCCC TCTCTACT AAAAT
                                   ||||||||| |||||||| |||||
                                   ACTTTGGGG AGAGATGA TTTTA
                                       C       C
GAM1005  KIAA0186  3'  ATTTTTAGTAGAGACAGAGTTT 41099        CCCA
             TA                    TGAAAC    TCTCTACTAAAAAT
                                   ||||||    ||||||||||||||
                                   ATTTTG    AGAGATGATTTTTA
                                      AGAC
GAM1005  KIAA0186  3'  ATTTTTTGTGGAGATGGGGTTT 41100              T
             CA                    TGAAACCCCATCTCTAC AAAAAT
                                   |||||||||||||||| ||||||
                                   ACTTTGGGGTAGAGGTG TTTTTA
                                             T
GAM1005  KIAA0205  3'  ATTTTTAGTAGAGATGGGGTTT 30203
             CA                    TGAAACCCCATCTCTACTAAAAAT
                                   |||||||||||||||||||||||
                                   ACTTTGGGGTAGAGATGATTTTTA

GAM1005  KIAA0210  5'  ATTTTTAGTAGAGACGGGGTTT 29149         A
             CA                    TGAAACCCC TCTCTACTAAAAAT
                                   ||||||||| ||||||||||||||
                                   ACTTTGGGG AGAGATGATTTTTA
                                       C
GAM1005  KIAA0391  3'  ATTTTTAGTAGAGACGGGTTTT 28601       C   A
             CA                    TGAAA CCC TCTCTACTAAAAAT
                                   ||||| ||| |||||||||||||
                                   ACTTT GGG AGAGATGATTTTTA
                                     T   C
GAM1005  KIAA0426  3'  ATTTTTAGTAGAGACGGGGTTT 28920         A
             CA                    TGAAACCCC TCTCTACTAAAAAT
                                   ||||||||| |||||||||||||
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                                ACTTTGGGG AGAGATGATTTTTA
                                    C
GAM1005  KIAA0459  3'  ATTTTTAGTAGAGACGGGGTTT 61646          A
                CA                TGAAACCCC TCTCTACTAAAAAT
                                  ||||||||| ||||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                    C
GAM1005  KIAA0469  3'  ATTTTTAGTAGAGACGGGATTT 29971       C   A
                CA                TGAAA CCC TCTCTACTAAAAAT
                                  ||||| ||| ||||||||||||||
                                  ACTTT GGG AGAGATGATTTTTA
                                    A   C
GAM1005  KIAA0472  5'  ATTTTCAGTAGAGACGGGGTCT 72336    A    A       A
                C                 GA ACCCC TCTCTACT AAAAT
                                  || ||||| |||||||| |||||
                                  CT TGGGG AGAGATGA TTTTA
                                   C    C       C
GAM1005  KIAA0475  3'  ATTTTTAGTGGAGACAGGGTTT 30111         CA
                C                 GAAACCC  TCTCTACTAAAAAT
                                  |||||||  ||||||||||||||
                                  CTTTGGG  AGAGGTGATTTTTA
                                     AC
GAM1005  KIAA0495  3'  ATTTTTAGTAGAGATGGGATTT 63260       C
                CA                TGAAA CCCATCTCTACTAAAAAT
                                  ||||| |||||||||||||||||
                                  ACTTT GGGTAGAGATGATTTTTA
                                    A
GAM1005  KIAA0513  3'  ATTTTTGGTAGAGATGGGGTTT 29019
                CA                TGAAACCCCATCTCTACTAAAAAT
                                  |||||||||||||||||||||||||
                                  ACTTTGGGGTAGAGATGGTTTTTA

GAM1005  KIAA0513  5'  TTTTTAGTAGAGACAGGGTTTC 29061         CA
                                  GAAACCC  TCTCTACTAAAAA
                                  |||||||  |||||||||||||
                                  CTTTGGG  AGAGATGATTTTT
                                     AC
GAM1005  KIAA0527  3'  ATTTTTAGTAGAGATGGAGTTT 97490         C
                CA                TGAAAC CCATCTCTACTAAAAAT
                                  ||||||| |||||||||||||||||
                                  ACTTTG GGTAGAGATGATTTTTA
                                    A
GAM1005  KIAA0532  3'  ATTTTTTCTAGAGATGAGGTCT 71317     A  C       CT
                CA                TGA ACC CATCTCTA  AAAAAT
                                  ||| ||| ||||||||  ||||||
                                  ACT TGG GTAGAGAT  TTTTTA
                                    C  A       CT
GAM1005  KIAA0544  3'  ATTTTTAGTAGAGAAGGGATTT 71458       C   A
                CA                TGAAA CCC TCTCTACTAAAAAT
                                  ||||| ||| ||||||||||||||
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```
                                ACTTT GGG AGAGATGATTTTTA
                                  A   A
GAM1005  KIAA0555  3'  ATTTTTAGTAGAGACAGGGTTT 29545        CA
                CA                TGAAACCC  TCTCTACTAAAAAT
                                  ||||||||  ||||||||||||||
                                  ACTTTGGG  AGAGATGATTTTTA
                                      AC
GAM1005  KIAA0557  3'  ATTTTTAGTAGAGATGGGGTTT 78547
                C                  GAAACCCCATCTCTACTAAAAAT
                                   ||||||||||||||||||||||
                                   CTTTGGGGTAGAGATGATTTTTA

GAM1005  KIAA0561  3'  ATTTTTAGTACAGACGGGGTTT 66466         A   C
                CA                TGAAACCCC TCT TACTAAAAAT
                                  |||||||||| ||| ||||||||||
                                  ACTTTGGGG AGA ATGATTTTTA
                                      C   C
GAM1005  KIAA0562  3'  ATTTTTAGTAGAGACGGGGTTT 28816         A
                CA                TGAAACCCC TCTCTACTAAAAAT
                                  |||||||||| ||||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                      C
GAM1005  KIAA0563  5'  ATTTTTAGTAGAGGCGGAGTTT 29869      C  AT
                C                  GAAAC CC  CTCTACTAAAAAT
                                   |||||  ||  |||||||||||||
                                   CTTTG GG  GAGATGATTTTTA
                                     A  CG
GAM1005  KIAA0594  3'  TTTTAGTAGAGATGGGGTTTCA 65523
                                  TGAAACCCCATCTCTACTAAAA
                                  ||||||||||||||||||||||
                                  ACTTTGGGGTAGAGATGATTTT

GAM1005  KIAA0599  3'  ATTTTTAGTAGAGACGGGGTTT 77686         A
                C                  GAAACCCC TCTCTACTAAAAAT
                                   ||||||||  ||||||||||||||
                                   CTTTGGGG AGAGATGATTTTTA
                                       C
GAM1005  KIAA0682  3'  ATTTTTCATAGAGACTGGGTTT 30016         CA     CT
                CA                TGAAACCC  TCTCTA  AAAAAT
                                  ||||||||  ||||||  ||||||
                                  ACTTTGGG  AGAGAT  TTTTTA
                                      TC     AC
GAM1005  KIAA0682  3'  ATTTTTGGTAGACGGGGTTTCA 30017          ATC
                                  TGAAACCCC   TCTACTAAAAAT
                                  |||||||||   ||||||||||||
                                  ACTTTGGGG   AGATGGTTTTTA
                                      C__
GAM1005  KIAA0720  3'  ATTTTAAGTAGAGACGGCATTT 62974      CC  A      A
                CA                TGAAA  CC TCTCTACT AAAAT
                                  |||||  ||  |||||||| |||||
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                                ACTTT  GG AGAGATGA TTTTA
                                  AC  C       A
GAM1005  KIAA0737  3'  AGTAGAGATGGGGTCTCA    29801     A
                                TGA ACCCCATCTCTACT
                                ||| ||||||||||||||
                                ACT TGGGGTAGAGATGA
                                  C
GAM1005  KIAA0737  3'  ATTTTTAGTAGAGACAGGGTTT 29802         CA
              CA                  TGAAACCC  TCTCTACTAAAAAT
                                ||||||||  ||||||||||||||
                                ACTTTGGG  AGAGATGATTTTTA
                                    AC
GAM1005  KIAA0798  3'  ATTTTTGGTAGAGACGGGGTTT 28442         A
              CA                  TGAAACCCC TCTCTACTAAAAAT
                                ||||||||| ||||||||||||||
                                ACTTTGGGG AGAGATGGTTTTTA
                                    C
GAM1005  KIAA0841  3'  TTTTAGTAGGGACGGGGTTTCA 71909         A
                                TGAAACCCC TCTCTACTAAAA
                                ||||||||| ||||||||||||
                                ACTTTGGGG AGGGATGATTTT
                                    C
GAM1005  KIAA0861  3'  ATTTTTAGTAGAGACGGGGTTT 90342         A
              C                   GAAACCCC TCTCTACTAAAAAT
                                ||||||||| ||||||||||||||
                                CTTTGGGG AGAGATGATTTTTA
                                    C
GAM1005  KIAA0889  3'  TTTTTGGTGGAGACGGGGTTTC 31793         A
              A                   TGAAACCCC TCTCTACTAAAAA
                                ||||||||| ||||||||||||
                                ACTTTGGGG AGAGGTGGTTTTT
                                    C
GAM1005  KIAA0924  3'  ATTTTTGGCAGAGATGGGGTTT 30355             A
              CA                  TGAAACCCCATCTCT CTAAAAAT
                                |||||||||||||| ||||||||
                                ACTTTGGGGTAGAGA GGTTTTTA
                                      C
GAM1005  KIAA0931  3'  TTTTTTTTAGAGACGGGGTTTC 68027         A     CT
              A                   TGAAACCCC TCTCTA  AAAAA
                                ||||||||| ||||||  |||||
                                ACTTTGGGG AGAGAT  TTTTT
                                    C     TT
GAM1005  KIAA0961  3'  ATTTTTAGTGGAGATGGGGTTT 30392
              CA                  TGAAACCCCATCTCTACTAAAAAT
                                ||||||||||||||||||||||||
                                ACTTTGGGGTAGAGGTGATTTTTA

GAM1005  KIAA1026  3'  ATTTTTAGTAGAGATGAGATTT 71732       CCC
              CA                  TGAAA   CATCTCTACTAAAAAT
                                |||||   ||||||||||||||||
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                                ACTTT   GTAGAGATGATTTTTA
                                  AGA
GAM1005  KIAA1028  3'  ATTTTTAGTAGAGATGGGGTTT 93586
              CA                  TGAAACCCCATCTCTACTAAAAAT
                                  |||||||||||||||||||||||
                                  ACTTTGGGGTAGAGATGATTTTTA

GAM1005  KIAA1040  3'  ATTTTTAGTAGAGATGGGGTTT 72682
              CA                  TGAAACCCCATCTCTACTAAAAAT
                                  |||||||||||||||||||||||
                                  ACTTTGGGGTAGAGATGATTTTTA

GAM1005  KIAA1041  3'  TTTTAGTAGAGATGGGGTTTCA 30838
                                  TGAAACCCCATCTCTACTAAAA
                                  ||||||||||||||||||||
                                  ACTTTGGGGTAGAGATGATTTT

GAM1005  KIAA1054  3'  TTTTAGTAGAGGTGGGGTTTCA 68976
                                  TGAAACCCCATCTCTACTAAAA
                                  ||||||||||||||||||||
                                  ACTTTGGGGTGGAGATGATTTT

GAM1005  KIAA1110  3'  AGCAGAGATGGGGCTCA    62498    AA       A
                                  TGA  CCCCATCTCT CT
                                  |||  |||||||||| ||
                                  ACT  GGGGTAGAGA GA
                                    C_        C
GAM1005  KIAA1115  5'  ATTTTTGGTAGAGACAGGGTTT 30687       CA
              C                    GAAACCC  TCTCTACTAAAAAT
                                  |||||||  |||||||||||||
                                  CTTTGGG  AGAGATGGTTTTTA
                                      AC
GAM1005  KIAA1128  3'  ATTTTTAGTAGAGATGAGATTT 68997      CCC
              CA                    TGAAA   CATCTCTACTAAAAAT
                                  |||||   ||||||||||||||||
                                  ACTTT   GTAGAGATGATTTTTA
                                    AGA
GAM1005  KIAA1143  3'  ATTTTTAATAGAGACGGGGTTT 69229        A    C
              CA                    TGAAACCCC TCTCTA TAAAAAT
                                  |||||||||  ||||||  |||||||
                                  ACTTTGGGG AGAGAT ATTTTTA
                                       C     A
GAM1005  KIAA1161  5'  TTTTTAGTAGAGATGGGGTTT  82655
                                  AAACCCCATCTCTACTAAAAA
                                  |||||||||||||||||||||
                                  TTTGGGGTAGAGATGATTTTT

GAM1005  KIAA1170  3'  ATTTTTAGTAGAAACAGGGTTT 70410       CATC
              CA                    TGAAACCC    TCTACTAAAAAT
                                  ||||||||    ||||||||||||
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                                ACTTTGGG   AGATGATTTTTA
                                    ACAA
GAM1005  KIAA1185  3'  ATTTTTAGTAGAGACGGGGTTT 63284        A
             CA                   TGAAACCCC TCTCTACTAAAAAT
                                  ||||||||| ||||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                      C
GAM1005  KIAA1193  3'  ATTTTTTGTAGAGATGGGGTTT 68263             T
             C                    GAAACCCCATCTCTAC AAAAAT
                                  |||||||||||||||| ||||||
                                  CTTTGGGGTAGAGATG TTTTTA
                                           T
GAM1005  KIAA1198  3'  ATTTTTAGTAGAGACAGTGTTT 64004       CCCA
             CA                   TGAAAC   TCTCTACTAAAAAT
                                  ||||||   ||||||||||||||
                                  ACTTTG   AGAGATGATTTTTA
                                     TGAC
GAM1005  KIAA1198  3'  ATTTTTAGTAGAGACGGGGTTT 64005        A
             CA                   TGAAACCCC TCTCTACTAAAAAT
                                  ||||||||| ||||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                      C
GAM1005  KIAA1198  3'  ATTTTTAGTAGAGACGGGGTTT 64006        A
             CA                   TGAAACCCC TCTCTACTAAAAAT
                                  ||||||||| ||||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                      C
GAM1005  KIAA1198  3'  ATTTTTAGTAGAGATGGGGTTT 64007
             CA                   TGAAACCCCATCTCTACTAAAAAT
                                  |||||||||||||||||||||||
                                  ACTTTGGGGTAGAGATGATTTTTA

GAM1005  KIAA1198  3'  ATTTTTAGTGGAGACGGGGTTT 64008        A
             CA                   TGAAACCCC TCTCTACTAAAAAT
                                  ||||||||| ||||||||||||||
                                  ACTTTGGGG AGAGGTGATTTTTA
                                      C
GAM1005  KIAA1198  3'  TTTTAGTAGAGATGGGGTTTC  64076
                                  GAAACCCCATCTCTACTAAAA
                                  |||||||||||||||||||
                                  CTTTGGGGTAGAGATGATTTT

GAM1005  KIAA1200  3'  ATTTTTAGTAGAGACGGGGTTT 63032        A
             CA                   TGAAACCCC TCTCTACTAAAAAT
                                  ||||||||| ||||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                      C
GAM1005  KIAA1209  3'  AGTAGAGGCGGGGTTTCA    61400        AT
                                  TGAAACCCC  CTCTACT
                                  |||||||||  |||||||
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                                ACTTTGGGG  GAGATGA
                                     CG
GAM1005  KIAA1210  3'  ATTTTTAGTAGAGACGGGGTTT 98065         A
              CA                  TGAAACCCC TCTCTACTAAAAAT
                                  ||||||||| ||||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                       C
GAM1005  KIAA1254  3'  ATTTTTAGTAGAGATGGGGTTT 70556
              CA                  TGAAACCCCATCTCTACTAAAAAT
                                  |||||||||||||||||||||||
                                  ACTTTGGGGTAGAGATGATTTTTA

GAM1005  KIAA1257  3'  ATTTTTGGTAGAGACGAGGTTT 63391        CCA
              C                    GAAACC   TCTCTACTAAAAAT
                                  ||||||   ||||||||||||||
                                  CTTTGG   AGAGATGGTTTTTA
                                      AGC
GAM1005  KIAA1257  3'  ATTTTTTGTAGAGATGGGGTTT 63392              T
              CA                  TGAAACCCCATCTCTAC AAAAAT
                                  |||||||||||||||| ||||||
                                  ACTTTGGGGTAGAGATG TTTTTA
                                             T
GAM1005  KIAA1287  3'  ATTTTTAGTAAAGACGGGGGTT 78933        A_   C
              T                    AAACCCC  TCT TACTAAAAAT
                                  |||||||  ||| ||||||||||
                                  TTTGGGG  AGA ATGATTTTTA
                                       GC   A
GAM1005  KIAA1320  5'  ATTTTTAGTAGAGATGGGATTT 69833       C
              CA                  TGAAA CCCATCTCTACTAAAAAT
                                  ||||| ||||||||||||||||||
                                  ACTTT GGGTAGAGATGATTTTTA
                                     A
GAM1005  KIAA1328  3'  AGCAGAGATGGGCTTTCA    62315       C        A
                                  TGAAA CCCATCTCT CT
                                  ||||| ||||||||| ||
                                  ACTTT GGGTAGAGA GA
                                     C        C
GAM1005  KIAA1373  3'  ATTTTTAGTAGAGATGGGGTTT 71502
              TA                  TGAAACCCCATCTCTACTAAAAAT
                                  |||||||||||||||||||||||
                                  ATTTTGGGGTAGAGATGATTTTTA

GAM1005  KIAA1443  3'  ATTTTTAGTAGAGACGGGTTTC 64566         CA
              A                    TGAAACCC  TCTCTACTAAAAAT
                                  ||||||||  ||||||||||||||
                                  ACTTTGGG  AGAGATGATTTTTA
                                       C_
GAM1005  KIAA1456  3'  ATTTTTAGGAGAGACGGGGTTT 67533         A    A
              CA                  TGAAACCCC TCTCT CTAAAAAT
                                  ||||||||| ||||| ||||||||
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                                ACTTTGGGG AGAGA GATTTTTA
                                    C    G
GAM1005  KIAA1465  3'  ATTTTTAGTAGAGACGGGGTTT 61486        A
              CA                  TGAAACCCC TCTCTACTAAAAAT
                                  ||||||||| ||||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                      C
GAM1005  KIAA1467  3'  ATTTTTAGTAGAGACGGGGTTT 72061        A
              CA                  TGAAACCCC TCTCTACTAAAAAT
                                  ||||||||| ||||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                      C
GAM1005  KIAA1493  3'  ATTTTTAGTAGAGATGGGGTTT 64835
              CA                  TGAAACCCCATCTCTACTAAAAAT
                                  |||||||||||||||||||||||
                                  ACTTTGGGGTAGAGATGATTTTTA

GAM1005  KIAA1497  5'  ATTTTTAGTAGAGACAGGGTTT 68114        CA
              CA                  TGAAACCC  TCTCTACTAAAAAT
                                  ||||||||  ||||||||||||||
                                  ACTTTGGG  AGAGATGATTTTTA
                                      AC
GAM1005  KIAA1530  3'  ATTTTTAGTAGAGACGGGATTT 68548      C   A
              CA                  TGAAA CCC TCTCTACTAAAAAT
                                  ||||| ||| ||||||||||||||
                                  ACTTT GGG AGAGATGATTTTTA
                                     A   C
GAM1005  KIAA1530  3'  ATTTTTTGTAGAGATGAGGTCT 68549     A   C       T
              CA                  TGA ACC CATCTCTAC AAAAAT
                                  ||| ||| ||||||||| ||||||
                                  ACT TGG GTAGAGATG TTTTTA
                                    C   A        T
GAM1005  KIAA1571  3'  ATTTTTAGTAGAGTTGGGGGTT 61612         AT_
              TCA                   TGAAACCCC   CTCTACTAAAAAT
                                  |||||||||   ||||||||||||
                                  ACTTTGGGG   GAGATGATTTTTA
                                       GTT
GAM1005  KIAA1615  3'  ATTTTTAGTAGAGACGGG    69269     A
                                  CCC TCTCTACTAAAAAT
                                  ||| ||||||||||||||
                                  GGG AGAGATGATTTTTA
                                    C
GAM1005  KIAA1615  3'  TTTTAGTAGATATGGAGTTTCA 69294       C    C
                                  TGAAAC CCAT TCTACTAAAA
                                  |||||| |||| ||||||||||
                                  ACTTTG GGTA AGATGATTTT
                                     A    T
GAM1005  KIAA1617  3'  ATTTTTGGTAGAGACAGGGTTT 93071        CA
              CA                  TGAAACCC  TCTCTACTAAAAAT
                                  ||||||||  ||||||||||||||
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                                ACTTTGGG  AGAGATGGTTTTTA
                                    AC
GAM1005  KIAA1649  3'  ATTTTTGTAGAGATGAGGTTTC 51217        C        T
              A                  TGAAACC CATCTCTAC AAAAAT
                                 ||||||| ||||||||| ||||||
                                 ACTTTGG GTAGAGATG TTTTTA
                                    A       _
GAM1005  KIAA1655  3'  ATTTTTAGTAGAGACAGGTTTC 67175        CCA
              A                  TGAAACC   TCTCTACTAAAAAT
                                 |||||||   ||||||||||||||
                                 ACTTTGG   AGAGATGATTTTTA
                                    AC_
GAM1005  KIAA1655  3'  ATTTTTAGTAGAGACGAGGTGT 67176     A   CCA
              CA                   TGA ACC   TCTCTACTAAAAAT
                                 ||| |||   ||||||||||||||
                                 ACT TGG   AGAGATGATTTTTA
                                   G   AGC
GAM1005  KIAA1668  3'  ATTTTTAGTAGAGACGGGGTTT 67060         A
              CA                   TGAAACCCC TCTCTACTAAAAAT
                                 ||||||||| ||||||||||||||
                                 ACTTTGGGG AGAGATGATTTTTA
                                     C
GAM1005  KIAA1674  3'  TTTTGGTAAATATGGTTTCA   69353        CCATCTC
                                 TGAAACC      TACTAAAA
                                 |||||||      ||||||||
                                 ACTTTGG      ATGGTTTT
                                    TATAA__
GAM1005  KIAA1712  3'  ATTTTTGTAGAGACAGGGTTTC 68150         CA      T
              A                  TGAAACCC  TCTCTAC AAAAAT
                                 ||||||||  ||||||| ||||||
                                 ACTTTGGG  AGAGATG TTTTTA
                                    AC      _
GAM1005  KIAA1727  3'  TTTTGTAGAGATGGGATCTCA  64768     AAC         T
                                 TGA   CCCATCTCTAC AAAA
                                 |||   |||||||||| ||||
                                 ACT   GGGTAGAGATG TTTT
                                   CTA         _
GAM1005  KIAA1737  3'  ATTTTTAGTAGAAATGGGGTTT 67933           C
              TA                   TGAAACCCCAT TCTACTAAAAAT
                                 |||||||||| ||||||||||||
                                 ATTTTGGGGTA AGATGATTTTTA
                                       A
GAM1005  KIAA1784  3'  TTTTAGTAGAAACGGGGTTTCA 65758         ATC
                                 TGAAACCCC   TCTACTAAAA
                                 |||||||||   ||||||||||
                                 ACTTTGGGG   AGATGATTTT
                                      CAA
GAM1005  KIAA1829  3'  ATTTTTAGTAGAGACGGGGTTT 62633         A
              CA                   TGAAACCCC TCTCTACTAAAAAT
                                 ||||||||| ||||||||||||||
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                                ACTTTGGGG AGAGATGATTTTTA
                                     C
GAM1005 KIAA1877 3' ATTTTTAGTAGAGACAGGGTTT 66741        CA
            CA                   TGAAACCC  TCTCTACTAAAAAT
                                 ||||||||  ||||||||||||||
                                 ACTTTGGG  AGAGATGATTTTTA
                                     AC
GAM1005 KIAA1922 5' ATTTTTGGTGGAGATGGGGTTT 73988
            C                    GAAACCCCATCTCTACTAAAAAT
                                 |||||||||||||||||||||||
                                 CTTTGGGGTAGAGGTGGTTTTTA

GAM1005 KIAA1924 3' ATTTTTAGTAGAGATAGGCTTT 74041      C  C
            CA                   TGAAA CC ATCTCTACTAAAAAT
                                 |||||  ||  ||||||||||||||
                                 ACTTT GG TAGAGATGATTTTTA
                                    C  A
GAM1005 KIAA1924 3' TTTTTGTAGAGATAGGGTTTCA 74066        C       T
                                 TGAAACCC ATCTCTAC AAAAA
                                 ||||||||  ||||||||  |||||
                                 ACTTTGGG TAGAGATG TTTTT
                                     A      _
GAM1005 KIAA1971 3' TTTTTAGTAGAGACGAGGTTTC 74701        CCA
            A                    TGAAACC   TCTCTACTAAAAA
                                 |||||||   ||||||||||||
                                 ACTTTGG   AGAGATGATTTTT
                                     AGC
GAM1005 KIAA1975 5' ATTTTTAGTAGAGATGGGGTTT 74415
            CA                   TGAAACCCCATCTCTACTAAAAAT
                                 |||||||||||||||||||||||||
                                 ACTTTGGGGTAGAGATGATTTTTA

GAM1005 KLK7     3' ATTTTTACTAGAGACAGGGTTT 58388         CA     C
            CA                   TGAAACCC  TCTCTA TAAAAAT
                                 ||||||||  ||||||  |||||||
                                 ACTTTGGG  AGAGAT ATTTTTA
                                     AC     C
GAM1005 KLK7     3' ATTTTTACTAGAGACAGGGTTT 18541         CA     C
            CA                   TGAAACCC  TCTCTA TAAAAAT
                                 ||||||||  ||||||  |||||||
                                 ACTTTGGG  AGAGAT ATTTTTA
                                     AC     C
GAM1005 LAMP3    3' ATTTTTATTATAGACGGGGTTT 60198         A  C  C
            CA                   TGAAACCCC TCT TA TAAAAAT
                                 |||||||||  |||  ||  |||||||
                                 ACTTTGGGG AGA AT ATTTTTA
                                     C  T  T
GAM1005 LNIR     3' TTTTTTTTAGAGATGGAGTCTC 48877     A  C       CT
            A                    TGA AC CCATCTCTA  AAAAA
                                 |||  ||  |||||||||  |||||
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                                ACT TG GGTAGAGAT  TTTTT
                                  C A       TT
GAM1005  LY75     3'  ATTTTTAGTAGAGATGGGGTTT 11389
                CA                  TGAAACCCCATCTCTACTAAAAAT
                                    ||||||||||||||||||||||||
                                    ACTTTGGGGTAGAGATGATTTTTA

GAM1005  MAP-1    3'  AGTAGAGACGGGGTTTCA    42436         A
                                    TGAAACCCC TCTCTACT
                                    |||||||||  ||||||||
                                    ACTTTGGGG AGAGATGA
                                          C
GAM1005  MCLC     3'  TTTTTAGTAGAGATGGGGTTTC 31390
                A                    TGAAACCCCATCTCTACTAAAAA
                                    |||||||||||||||||||||||
                                    ACTTTGGGGTAGAGATGATTTTT

GAM1005  MEF-2    3'  ATTTTTAGTAGAGACTGGGTTT 65018         CA
                CA                  TGAAACCC  TCTCTACTAAAAAT
                                    ||||||||  ||||||||||||||
                                    ACTTTGGG  AGAGATGATTTTTA
                                         TC
GAM1005  MGC10200 3'  TTTTTGGAGAGATGGGGTTTCA 59654              A
                                    TGAAACCCCATCTCT CTAAAAA
                                    ||||||||||||||| |||||||
                                    ACTTTGGGGTAGAGA GGTTTTT
                                                  _
GAM1005  MGC12466 3'  TTTTTATAGAGATGGGATCTC  79802    AAC        C
                                    GA   CCCATCTCTA TAAAAA
                                    ||   ||||||||||| ||||||
                                    CT   GGGTAGAGAT ATTTTT
                                     CTA        _
GAM1005  MGC12518 3'  ATTTTTAGTAGAGTGAGGGTTT 64774          _  T
                CA                  TGAAACCC CA CTCTACTAAAAAT
                                    |||||||| || ||||||||||||
                                    ACTTTGGG GT GAGATGATTTTTA
                                         A  _
GAM1005  MGC13204 3'  ATTTTTAGTAGAGATGTGGTTT 49626        C
                C                    GAAACC CATCTCTACTAAAAAT
                                    ||||||| ||||||||||||||||
                                    CTTTGG GTAGAGATGATTTTTA
                                       T
GAM1005  MGC1842   3'  ATTTTTAGTAGAGACCAGGCTT 66249     A  CCA
                C                    GAA CC   TCTCTACTAAAAAT
                                    ||| ||   ||||||||||||||
                                    CTT GG   AGAGATGATTTTTA
                                      C  ACC
GAM1005  MGC20235 3'  TTTTTGGTAGAGACAGAGTCTC 59566     A  CCCA
                A                    TGA AC    TCTCTACTAAAAA
                                    ||| ||    |||||||||||||
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                              ACT TG    AGAGATGGTTTTT
                                C  AGAC
GAM1005  MGC21675  3'  ATTTTTAGTAGAGATGGGGTTT 54587
             CA                 TGAAACCCCATCTCTACTAAAAAT
                                |||||||||||||||||||||||
                                ACTTTGGGGTAGAGATGATTTTTA

GAM1005  MGC2474   3'  ATTTTTAGTAGAGATGGGGTTT 43951
             CA                 TGAAACCCCATCTCTACTAAAAAT
                                |||||||||||||||||||||||
                                ACTTTGGGGTAGAGATGATTTTTA

GAM1005  MGC2474   3'  TTTTTGCAGAGATGGGGTT   43974          AC
                                AACCCCATCTCT  TAAAAA
                                ||||||||||||  ||||||
                                TTGGGGTAGAGA  GTTTTT
                                      C_
GAM1005  MGC2477   5'  ATTTTTAGTAGAGAAAGAGTTT 44291       CCCA
             CA                 TGAAAC   TCTCTACTAAAAAT
                                ||||||   ||||||||||||||
                                ACTTTG   AGAGATGATTTTTA
                                   AGAA
GAM1005  MGC2603   3'  ATTTTTAGTAGAGACGAGGTTT 44071       CCA
             CA                 TGAAACC  TCTCTACTAAAAAT
                                |||||||  ||||||||||||||
                                ACTTTGG  AGAGATGATTTTTA
                                   AGC
GAM1005  MGC29898  3'  ATTTGCTTGTAGAGATGGGATC 59583    AAC        TAA_
             TCA                  TGA  CCCATCTCTAC   AAAT
                                  |||  ||||||||||   ||||
                                  ACT  GGGTAGAGATG   TTTA
                                    CTA        TTCG
GAM1005  MGC3113   3'  TTTTGTAGAGACAGGGTTTC  44065       CA     T
                                GAAACCC  TCTCTAC AAAA
                                |||||||  ||||||| ||||
                                CTTTGGG  AGAGATG TTTT
                                   AC     _
GAM1005  MGC4638   3'  TTAGTAGAAACGAGGTTTCA  49745       CCATC
                                TGAAACC    TCTACTAA
                                |||||||    ||||||||
                                ACTTTGG    AGATGATT
                                   AGCAA
GAM1005  MGC4766   5'  AGTAGAGACGGGGTTTCA    49555        A
                                TGAAACCCC TCTCTACT
                                ||||||||| ||||||||
                                ACTTTGGGG AGAGATGA
                                     C
GAM1005  MGC5149   3'  ATTTTTAGCAGAGATGGGGTTT 72755           A
             CA                 TGAAACCCCATCTCT CTAAAAAT
                                |||||||||||||| ||||||||
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                                ACTTTGGGGTAGAGA GATTTTTA
                                        C
GAM1005  MKRN4    3'  ATTTTTAGTAGAAACGGGGTTT 48453          ATC
              CA                  TGAAACCCC   TCTACTAAAAAT
                                  |||||||||   ||||||||||||
                                  ACTTTGGGG   AGATGATTTTTA
                                       CAA
GAM1005  MLZE     5'  ATTTTCAGTAGAGACAGGGTTT 49448         CA       A
              CA                  TGAAACCC  TCTCTACT AAAAT
                                  ||||||||  |||||||| |||||
                                  ACTTTGGG  AGAGATGA TTTTA
                                       AC       C
GAM1005  moblak   3'  TTTTAGTAGAGACAAGATTTCA 56417       CCCCA
                                  TGAAA     TCTCTACTAAAA
                                  |||||     ||||||||||||
                                  ACTTT     AGAGATGATTTT
                                     AGAAC
GAM1005  moblak   3'  TTTTAGTAGAGACAGGGTTTCA 56418         CA
                                  TGAAACCC  TCTCTACTAAAA
                                  ||||||||  ||||||||||||
                                  ACTTTGGG  AGAGATGATTTT
                                       AC
GAM1005  MOCS3    3'  ATTTTTAGTACAGAGGGGGTTT 27927          A   C
              CA                  TGAAACCCC TCT TACTAAAAAT
                                  |||||||||| ||| ||||||||||
                                  ACTTTGGGG AGA ATGATTTTTA
                                       G   C
GAM1005  MRPL20   3'  ATTTTTAGTAGAGACCGGGTTC 36200     A     CA
              CG                  TG AACCC  TCTCTACTAAAAAT
                                  || |||||  ||||||||||||||
                                  GC TTGGG  AGAGATGATTTTTA
                                   C     CC
GAM1005  MRPL44   3'  ATTTTTGGTAGAGATGGGGTTT 43592
              CA                  TGAAACCCCATCTCTACTAAAAAT
                                  |||||||||||||||||||||||||
                                  ACTTTGGGGTAGAGATGGTTTTTA

GAM1005  MRPS27   3'  ATTTTTAGTAGAGATGGGGTTT 31323
              CA                  TGAAACCCCATCTCTACTAAAAAT
                                  |||||||||||||||||||||||||
                                  ACTTTGGGGTAGAGATGATTTTTA

GAM1005  MtFMT    3'  ATTTTTAGTAGAGATGGGGTTT 58331
              CA                  TGAAACCCCATCTCTACTAAAAAT
                                  |||||||||||||||||||||||||
                                  ACTTTGGGGTAGAGATGATTTTTA

GAM1005  MYO5C    3'  ATTTTTAGTGGAGACAGGTTTC 38713         CCA
              A                    TGAAACC   TCTCTACTAAAAAT
                                  |||||||   ||||||||||||||
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                                ACTTTGG   AGAGGTGATTTTTA
                                   AC_
GAM1005  NDP52    3'  TTTTTAGTAGAGACAGGGTTTC 20681        CA
              A                    TGAAACCC  TCTCTACTAAAAA
                                   ||||||||  ||||||||||||
                                   ACTTTGGG  AGAGATGATTTTT
                                      AC
GAM1005  NDUFC2   3'  TTTTTAGTAGAGACGGGGTTTC 17040         A
              A                    TGAAACCCC TCTCTACTAAAAA
                                   |||||||||| ||||||||||||
                                   ACTTTGGGG AGAGATGATTTTT
                                       C
GAM1005  NINJ2    3'  ATTTTTAGTAGAGACGGGGTTT 33718         A
              C                    GAAACCCC TCTCTACTAAAAAT
                                   |||||||| ||||||||||||||
                                   CTTTGGGG AGAGATGATTTTTA
                                      C
GAM1005  Nup43    3'  TTTTAGTGGAGATGGGGTTTCA 45361
                                   TGAAACCCCATCTCTACTAAAA
                                   ||||||||||||||||||||||
                                   ACTTTGGGGTAGAGGTGATTTT

GAM1005  NXN      3'  ATTTTTAGTAGAGATGGGGTTT 42668
              CA                     TGAAACCCCATCTCTACTAAAAAT
                                     ||||||||||||||||||||||||
                                     ACTTTGGGGTAGAGATGATTTTTA

GAM1005  OCT11    3'  ATTTTTAGTAGAGATGGGGTTT 27584
              CA                     TGAAACCCCATCTCTACTAAAAAT
                                     ||||||||||||||||||||||||
                                     ACTTTGGGGTAGAGATGATTTTTA

GAM1005  OR51E2   3'  TTTTTAGTAGAGACAGAGTTTC 48523        CCCA
              A                    TGAAAC    TCTCTACTAAAAA
                                   ||||||    ||||||||||||
                                   ACTTTG    AGAGATGATTTTT
                                      AGAC
GAM1005  OSBPL2   3'  ATTTTTAGTAGACACGGGTTTT 29896       C   ATC
              CA                     TGAAA CCC   TCTACTAAAAAT
                                     ||||| |||   ||||||||||||
                                     ACTTT GGG   AGATGATTTTTA
                                        T   CAC
GAM1005  OSBPL2   3'  ATTTTTAGTAGACACGGGTTTT 58479       C   ATC
              CA                     TGAAA CCC   TCTACTAAAAAT
                                     ||||| |||   ||||||||||||
                                     ACTTT GGG   AGATGATTTTTA
                                        T   CAC
GAM1005  PELI1    5'  ATTTTTAGTAGAGACCAGGTTT 40627       CCA
                                     AAACC   TCTCTACTAAAAAT
                                     |||||   ||||||||||||||
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                                TTTGG   AGAGATGATTTTTA
                                  ACC
GAM1005  PELI1    5'  ATTTTTAGTAGAGACGGGGTTT 40628          A
                CA                  TGAAACCCC TCTCTACTAAAAAT
                                    ||||||||| ||||||||||||||
                                    ACTTTGGGG AGAGATGATTTTTA
                                      C
GAM1005  PELI1    5'  TTAGTGGAGATGGGGTTTCA   40664
                                    TGAAACCCCATCTCTACTAA
                                    ||||||||||||||||||||
                                    ACTTTGGGGTAGAGGTGATT

GAM1005  PIP3-E   3'  ATTTTTAGTAGAGACCGGGGTT 67346         A_
                T                    AAACCCC  TCTCTACTAAAAAT
                                    |||||||  ||||||||||||||
                                    TTTGGGG  AGAGATGATTTTTA
                                      CC
GAM1005  PRO0365  5'  ATTTTCAGTAGAGACGGGGTTT 26978          A       A
                CA                  TGAAACCCC TCTCTACT AAAAT
                                    ||||||||| |||||||| |||||
                                    ACTTTGGGG AGAGATGA TTTTA
                                      C       C
GAM1005  PRO1843  5'  ATTTTTAGTTTCAAGGTTTCA  38139        CCATCTCT
                                    TGAAACC       ACTAAAAAT
                                    |||||||       |||||||||
                                    ACTTTGG       TGATTTTTA
                                      AACTT___
GAM1005  PRO1992  3'  ATTTTTAGTAGAGATGGGGTTT 26896
                TA                  TGAAACCCCATCTCTACTAAAAAT
                                    ||||||||||||||||||||||||
                                    ATTTTGGGGTAGAGATGATTTTTA

GAM1005  PRO2955  3'  ATTTTTAGTAGAGACAGGGTTT 38234          CA
                TA                  TGAAACCC  TCTCTACTAAAAAT
                                    ||||||||  ||||||||||||||
                                    ATTTTGGG  AGAGATGATTTTTA
                                      AC
GAM1005  PSPH     3'  ATTTTTAGTAGAGACGGGGTTT 17130          A
                                    AAACCCC TCTCTACTAAAAAT
                                    ||||||| |||||||||||||
                                    TTTGGGG AGAGATGATTTTTA
                                      C
GAM1005  PSTPIP2  3'  ATTTTTAGTAGAGACAGGGTTT 44650          CA
                TA                  TGAAACCC  TCTCTACTAAAAAT
                                    ||||||||  ||||||||||||||
                                    ATTTTGGG  AGAGATGATTTTTA
                                      AC
GAM1005  PTPRR    5'  GGAGAGGTGGAATTTCA     12628       CC       A
                                    TGAAA  CCATCTCT CT
                                    |||||  |||||||| ||
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                                ACTTT  GGTGGAGA GG
                                  AA      _
GAM1005  RAB21    3'  ATTTTTAGTAGAGACGGGGTTT 31084          A
                CA                  TGAAACCCC TCTCTACTAAAAAT
                                    ||||||||| ||||||||||||||
                                    ACTTTGGGG AGAGATGATTTTTA
                                      C
GAM1005  RAB33B   3'  ATTTTTAGTATAGATGGGGTTT 49320            C
                CA                  TGAAACCCCATCT TACTAAAAAT
                                    |||||||||||| |||||||||
                                    ACTTTGGGGTAGA ATGATTTTTA
                                          T
GAM1005  RAI      5'  ATTTTTAGTAGAGACAGGGTT  22850       CA
                                    AACCC  TCTCTACTAAAAAT
                                    |||||  ||||||||||||||
                                    TTGGG  AGAGATGATTTTTA
                                      AC
GAM1005  RAP140   3'  ATTTTTAGTAGAGACAGGGTTT 31509          CA
                CA                  TGAAACCC  TCTCTACTAAAAAT
                                    ||||||||  ||||||||||||||
                                    ACTTTGGG  AGAGATGATTTTTA
                                      AC
GAM1005  RASSF2   3'  TTTTAGTAGAGGTGGGGTTTCA 29117
                                    TGAAACCCCATCTCTACTAAAA
                                    ||||||||||||||||||||||
                                    ACTTTGGGGTGGAGATGATTTT

GAM1005  RES4-25  3'  ATTTTTAGTAGAGACGGGGTTT 65261          A
                C                    GAAACCCC TCTCTACTAAAAAT
                                    |||||||| ||||||||||||||
                                    CTTTGGGG AGAGATGATTTTTA
                                      C
GAM1005  RNF8     3'  TTTCTGTAGAGACAGGGTTTCA 15580          CA      TA
                                    TGAAACCC  TCTCTAC  AAA
                                    ||||||||  |||||||  |||
                                    ACTTTGGG  AGAGATG  TTT
                                      AC      TC
GAM1005  RNO2     5'  TTTTTAGTGGAGATGGGGTGTC 53945     A
                A                    TGA ACCCCATCTCTACTAAAAA
                                    ||| ||||||||||||||||||
                                    ACT TGGGGTAGAGGTGATTTTT
                                      G
GAM1005  SC4MOL   3'  ATTTTTGTAGAGATGGGGTTTC 23102              T
                                    GAAACCCCATCTCTAC AAAAAT
                                    |||||||||||||||| ||||||
                                    CTTTGGGGTAGAGATG TTTTTA
                                                  _
GAM1005  SCAMP-4  3'  ATTTTTAGTACAGATGGGGTTT 55339            C
                CA                  TGAAACCCCATCT TACTAAAAAT
                                    |||||||||||| |||||||||
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                                ACTTTGGGGTAGA ATGATTTTTA
                                      C
GAM1005  SCYA16   3'  ATTTTTGGTAGAGACGGGATTC 17167     A   CA
                                GAA CCC  TCTCTACTAAAAAT
                                ||| |||  ||||||||||||||
                                CTT GGG  AGAGATGGTTTTTA
                                  A   C_
GAM1005  SCYA22   3'  ATTTTTAGTAGAGACAGGTTTC 92580        CCA
            A                    TGAAACC   TCTCTACTAAAAAT
                                ||||||||   ||||||||||||||
                                ACTTTGG   AGAGATGATTTTTA
                                    AC_
GAM1005  SCYA22   3'  ATTTTTAGTAGAGACGAGGCTT 92581      A  CCA
            CA                     TGAA CC   TCTCTACTAAAAAT
                                ||||| ||   ||||||||||||||
                                ACTT GG   AGAGATGATTTTTA
                                  C  AGC
GAM1005  SCYA28   3'  TTTTTGTTACAGACGGGGTTTC 39547         A   C  C
            A                    TGAAACCCC TCT TA TAAAAA
                                |||||||||| ||| || ||||||
                                ACTTTGGGG AGA AT GTTTTT
                                     C   C  T
GAM1005  SERF1B   3'  TTAGTAGAGATGGGGTTTCA   43710
                                TGAAACCCCATCTCTACTAA
                                ||||||||||||||||||||
                                ACTTTGGGGTAGAGATGATT

GAM1005  SFXN2    3'  TTTTAGTGGAGACGGGGTTTCA 74388          A
                                TGAAACCCC TCTCTACTAAAA
                                ||||||||| ||||||||||||
                                ACTTTGGGG AGAGGTGATTTT
                                     C
GAM1005  SIRPB1   3'  ATTTTTAGTAGAGATGGGGTTT 21357
            C                    GAAACCCCATCTCTACTAAAAAT
                                |||||||||||||||||||||||
                                CTTTGGGGTAGAGATGATTTTTA

GAM1005  SLC12A8  3'  ATTTTTACTGGAGACAGGGTTT 45233         CA     C
            CA                     TGAAACCC  TCTCTA TAAAAAT
                                ||||||||  ||||||| |||||||
                                ACTTTGGG  AGAGGT ATTTTTA
                                    AC     C
GAM1005  SLC16A4  3'  ATTTTTAGTAGAGGCGGGGTTT 17447          AT
            CA                     TGAAACCCC  CTCTACTAAAAAT
                                |||||||||  ||||||||||||||
                                ACTTTGGGG  GAGATGATTTTTA
                                     CG
GAM1005  SLC19A3  3'  ATTTTTAGTGGAGATGGGGTTT 48237
            CA                     TGAAACCCCATCTCTACTAAAAAT
                                |||||||||||||||||||||||||
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                                ACTTTGGGGTAGAGGTGATTTTTA

GAM1005 SLC2A10  3' ATTTTTAGCAGAGATGGGGTTT 48544              A
             CA                   TGAAACCCCATCTCT CTAAAAAT
                                  ||||||||||||||| ||||||||
                                  ACTTTGGGGTAGAGA GATTTTTA
                                           C
GAM1005 SLC6A14  3' ATTTTTAGTAGAGGCGAAGTTT 24304       CCCA
             C                    GAAAC   TCTCTACTAAAAAT
                                  |||||   ||||||||||||||
                                  CTTTG   GGAGATGATTTTTA
                                    AAGC
GAM1005 SREC     3' TTTAATAGAGACAGGGTTTCA 14912         CA    C
                                  TGAAACCC  TCTCTA TAAA
                                  ||||||||  |||||| ||||
                                  ACTTTGGG  AGAGAT ATTT
                                       AC     A
GAM1005 SS-56    3' ATTTTTAGTAGAGACGGAGTTT 60345       C  A
             CA                   TGAAAC CC TCTCTACTAAAAAT
                                  |||||| || ||||||||||||||
                                  ACTTTG GG AGAGATGATTTTTA
                                     A  C
GAM1005 STAF65(gamma) 3'  ATTTTTAGTAGAGATGAGGTTT 30063        C
             CA                   TGAAACC CATCTCTACTAAAAAT
                                  ||||||| ||||||||||||||||
                                  ACTTTGG GTAGAGATGATTTTTA
                                      A
GAM1005 STARD7   3' AGTAGAGATGGAGTTTCA    58368       C
                                  TGAAAC CCATCTCTACT
                                  |||||| ||||||||||
                                  ACTTTG GGTAGAGATGA
                                     A
GAM1005 STARD7   3' AGTAGAGATGGAGTTTCA    39735       C
                                  TGAAAC CCATCTCTACT
                                  |||||| ||||||||||
                                  ACTTTG GGTAGAGATGA
                                     A
GAM1005 SULT1C2  3' TTAGTAGAGACGAGGTTTCA  22724        CCA
                                  TGAAACC   TCTCTACTAA
                                  |||||||   ||||||||||
                                  ACTTTGG   AGAGATGATT
                                      AGC
GAM1005 SUN1     3' ATTTTTAGTAGAGACAGGGTTT 47909         CA
             CA                   TGAAACCC  TCTCTACTAAAAAT
                                  ||||||||  ||||||||||||||
                                  ACTTTGGG  AGAGATGATTTTTA
                                       AC
GAM1005 SYT13    3' TTTTAGTAGAGATGGGGTTTCA 95113
                                  TGAAACCCCATCTCTACTAAAA
                                  ||||||||||||||||||||||
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                                ACTTTGGGGTAGAGATGATTTT

GAM1005  TADA3L   3'  ATTTTTAGTAGAGACGGGGTTT 56805          A
              CA                  TGAAACCCC TCTCTACTAAAAAT
                                  ||||||||| ||||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                       C
GAM1005  TBCC     3'  ATTTTTAGTAGAGACGGGGTTT 13601          A
              C                    GAAACCCC TCTCTACTAAAAAT
                                  |||||||| ||||||||||||||
                                  CTTTGGGG AGAGATGATTTTTA
                                       C
GAM1005  TCL6     3'  ATTTTTAGTAGAGACAGGGTTT 25902          CA
              CA                  TGAAACCC  TCTCTACTAAAAAT
                                  |||||||| ||||||||||||||
                                  ACTTTGGG  AGAGATGATTTTTA
                                       AC
GAM1005  TCL6     5'  ATTTTTAGTAGAGACGAGGTTT 25903          CCA
              CA                  TGAAACC   TCTCTACTAAAAAT
                                  ||||||| ||||||||||||||
                                  ACTTTGG   AGAGATGATTTTTA
                                       AGC
GAM1005  TCL6     3'  ATTTTTAGTAGAGACAGGGTTT 27754          CA
              CA                  TGAAACCC  TCTCTACTAAAAAT
                                  |||||||| ||||||||||||||
                                  ACTTTGGG  AGAGATGATTTTTA
                                       AC
GAM1005  TCL6     5'  ATTTTTAGTAGAGACGAGGTTT 27755          CCA
              CA                  TGAAACC   TCTCTACTAAAAAT
                                  ||||||| ||||||||||||||
                                  ACTTTGG   AGAGATGATTTTTA
                                       AGC
GAM1005  TCL6     5'  ATTTTTAGTAGAGACGAGGTTT 40463          CCA
              CA                  TGAAACC   TCTCTACTAAAAAT
                                  ||||||| ||||||||||||||
                                  ACTTTGG   AGAGATGATTTTTA
                                       AGC
GAM1005  TCL6     5'  ATTTTTAGTAGAGACGAGGTTT 40507          CCA
              CA                  TGAAACC   TCTCTACTAAAAAT
                                  ||||||| ||||||||||||||
                                  ACTTTGG   AGAGATGATTTTTA
                                       AGC
GAM1005  TERA     3'  TTTTAGTAGAGACGGGGTTTCA 41428           A
                                  TGAAACCCC TCTCTACTAAAA
                                  ||||||||| ||||||||||||
                                  ACTTTGGGG AGAGATGATTTT
                                       C
GAM1005  TGIF2    3'  TTTTAGTAGAGACGGGGTTTCA 41762           A
                                  TGAAACCCC TCTCTACTAAAA
                                  ||||||||| ||||||||||||
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                                ACTTTGGGG AGAGATGATTTT
                                     C
GAM1005  THEA     3'  ATTTTTAGTGGAGATGGGGTTT 66874
                 CA                TGAAACCCCATCTCTACTAAAAAT
                                   |||||||||||||||||||||||
                                   ACTTTGGGGTAGAGGTGATTTTTA

GAM1005  TRIM16   3'  ATTTTTAGTAGAGATGGGGTTT 22366
                 CA                TGAAACCCCATCTCTACTAAAAAT
                                   |||||||||||||||||||||||
                                   ACTTTGGGGTAGAGATGATTTTTA

GAM1005  TRIM5    3'  ATTTTCAGTAGAGACGGGGTTT 53465        A       A
                 C                 GAAACCCC TCTCTACT AAAAT
                                   |||||||| |||||||| |||||
                                   CTTTGGGG AGAGATGA TTTTA
                                       C       C
GAM1005  TRIM5    3'  ATTTTCAGTAGAGACGGGGTTT 53538        A       A
                 C                 GAAACCCC TCTCTACT AAAAT
                                   |||||||| |||||||| |||||
                                   CTTTGGGG AGAGATGA TTTTA
                                       C       C
GAM1005  TRIM6    3'  ATTTTTATAGAGATAGGGTTTC 55174        C      C
                 A                 TGAAACCC ATCTCTA TAAAAAT
                                   |||||||| ||||||| |||||||
                                   ACTTTGGG TAGAGAT ATTTTTA
                                       A     _
GAM1005  TU12B1-TY 3'  ATTTCTAGTAGAGATGGGGTTT 33830              A
                 C                 GAAACCCCATCTCTACTA AAAT
                                   |||||||||||||||||| ||||
                                   CTTTGGGGTAGAGATGAT TTTA
                                             C
GAM1005  TU12B1-TY 3'  ATTTTTAGTAGAGACGGGGTTT 33831         A
                 CA                TGAAACCCC TCTCTACTAAAAAT
                                   ||||||||| ||||||||||||||
                                   ACTTTGGGG AGAGATGATTTTTA
                                       C
GAM1005  TU12B1-TY 3'  TTTTAATAGAGATGGGGTTTCA 33870             C
                                   TGAAACCCCATCTCTA TAAAA
                                   |||||||||||||||| |||||
                                   ACTTTGGGGTAGAGAT ATTTT
                                             A
GAM1005  TUCAN    3'  ATTTTTAGTAGAGACAGAGTTT 30966      CCCA
                 T                 GAAAC   TCTCTACTAAAAAT
                                   |||||   |||||||||||||
                                   TTTTG   AGAGATGATTTTTA
                                     AGAC
GAM1005  TUCAN    3'  ATTTTTAGTAGAGACAGGGTTT 30967        CA
                 CA                TGAAACCC  TCTCTACTAAAAAT
                                   ||||||||  ||||||||||||||
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                                ACTTTGGG  AGAGATGATTTTTA
                                    AC
GAM1005  TUSP     3'  ATTTTTAATAGAGATGGGGTTT 40016            C
             T                   GAAACCCCATCTCTA TAAAAAT
                                 ||||||||||||||| |||||||
                                 TTTTGGGGTAGAGAT ATTTTTA
                                       A
GAM1005  TXI1     5'  GGTAGGACGGGGTCTCA     37972     A    A  T
                                 TGA ACCCC TC CTACT
                                 ||| ||||| || |||||
                                 ACT TGGGG AG GATGG
                                   C    C  _
GAM1005  UBF-fl   3'  ATTTCTATTAGCAATGGGGTTT 52619          CT   C  A
             CA                    TGAAACCCCAT  CTA TA AAAT
                                   ||||||||||  ||| || ||||
                                   ACTTTGGGGTA  GAT AT TTTA
                                         AC   T  C
GAM1005  VDU1     3'  TTTTAGTAGAGATGGGGTTTCA 31133
                                 TGAAACCCCATCTCTACTAAAA
                                 ||||||||||||||||||||||
                                 ACTTTGGGGTAGAGATGATTTT

GAM1005  VPS33A   3'  ATTTTTAGTAGCCATGGTGTTT 43610       C    CT
             CA                    TGAAAC CCAT  CTACTAAAAAT
                                   |||||| ||||  ||||||||||
                                   ACTTTG GGTA  GATGATTTTTA
                                      T    CC
GAM1005  WBSCR23  3'  ATTTTTAGTAGAGACGGGGTTT 47416         A
             CA                    TGAAACCCC TCTCTACTAAAAAT
                                   |||||||| ||||||||||||||
                                   ACTTTGGGG AGAGATGATTTTTA
                                         C
GAM1005  ZNF221   3'  ATTTTTAGTAAAAACGGGGTTT 26266          ATCTC
             CA                    TGAAACCCC     TACTAAAAAT
                                   |||||||||     ||||||||||
                                   ACTTTGGGG     ATGATTTTTA
                                         CAAAA
GAM1005  ZNF228   3'  TTTAATGAGAGGGGTTTCA   60601          A    TAC
                                 TGAAACCCC TCTC   TAAA
                                 ||||||||| ||||   ||||
                                 ACTTTGGGG AGAG   ATTT
                                      _    TA_
GAM1005  ZNF338   3'  TTTAATAGAGGCGGGGTTTCA  42264          AT    C
                                 TGAAACCCC  CTCTA TAAA
                                 |||||||||  ||||| ||||
                                 ACTTTGGGG  GAGAT ATTT
                                      CG    A
GAM1005  ZTL1     3'  ATTTTTAGTAGAGACGGGGCTT 44138      A   A
             CA                    TGAA CCCC TCTCTACTAAAAAT
                                   |||| |||| ||||||||||||||
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                                ACTT GGGG AGAGATGATTTTTA
                                  C    C
GAM1005  LOC112687 3'  ATTTTTAGTAGAGATGGGGTTT 73220
                                AAACCCCATCTCTACTAAAAAT
                                |||||||||||||||||||||
                                TTTGGGGTAGAGATGATTTTTA

GAM1005  LOC112817 3'  ATTTTTAGCAGAGATGGGGTTT 57317              A
              CA                  TGAAACCCCATCTCT CTAAAAAT
                                |||||||||||||||| ||||||||
                                ACTTTGGGGTAGAGA GATTTTTA
                                        C
GAM1005  LOC115219 5'  ATTTTTGGTAGAGACGGGGTTT 73689          A
              CA                  TGAAACCCC TCTCTACTAAAAAT
                                |||||||||| ||||||||||||||
                                ACTTTGGGG AGAGATGGTTTTTA
                                     C
GAM1005  LOC115648 3'  TTTTTAGTGGAGACGGGGTTTC 60035          A
              A                   TGAAACCCC TCTCTACTAAAAA
                                |||||||||| |||||||||||||
                                ACTTTGGGG AGAGGTGATTTTT
                                     C
GAM1005  LOC119392 3'  ATTTTTAGTAGAGACTGGGTTT 59811         CA
              CA                  TGAAACCC  TCTCTACTAAAAAT
                                |||||||| ||||||||||||||
                                ACTTTGGG  AGAGATGATTTTTA
                                     TC
GAM1005  LOC120114 3'  ATTTTTAGTAGAGATGGGGTTT 76041
              CA                  TGAAACCCCATCTCTACTAAAAAT
                                |||||||||||||||||||||||||
                                ACTTTGGGGTAGAGATGATTTTTA

GAM1005  LOC120224 5'  TTTAGTAGAGACAGGGTTTCA  57899         CA
                                TGAAACCC  TCTCTACTAAA
                                |||||||| ||||||||||
                                ACTTTGGG  AGAGATGATTT
                                     AC
GAM1005  LOC120939 3'  ATTTTTAGTGGAGAGGGGGTTT 76756          A
              CA                  TGAAACCCC TCTCTACTAAAAAT
                                |||||||||| |||||||||||||
                                ACTTTGGGG AGAGGTGATTTTTA
                                      G
GAM1005  LOC124216 3'  ATTTTTAGTAGAGATGGTTTCA 74734         CC
                                TGAAACC  ATCTCTACTAAAAAT
                                |||||||  |||||||||||||||
                                ACTTTGG  TAGAGATGATTTTTA
                                         —
GAM1005  LOC126661 3'  ATTTTTAGTAGAGATGGGGTTT 75051
              CA                  TGAAACCCCATCTCTACTAAAAAT
                                |||||||||||||||||||||||||
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                                ACTTTGGGGTAGAGATGATTTTTA

GAM1005  LOC126669 3'  ATTTTTAGTAGAGATGGGGTTT 75925
                C                GAAACCCCATCTCTACTAAAAAT
                                 |||||||||||||||||||||||
                                 CTTTGGGGTAGAGATGATTTTTA

GAM1005  LOC128077 3'  ATTTTTAGTAGAGACAGGGTTT 75205        CA
                CA                 TGAAACCC  TCTCTACTAAAAAT
                                   ||||||||  ||||||||||||||
                                   ACTTTGGG  AGAGATGATTTTTA
                                       AC
GAM1005  LOC128077 3'  ATTTTTAGTAGAGACGGGGTTT 75206         A
                CA                 TGAAACCCC TCTCTACTAAAAAT
                                   ||||||||| |||||||||||||
                                   ACTTTGGGG AGAGATGATTTTTA
                                        C
GAM1005  LOC128989 3'  TTTTTAGTAGAGACGGGGTTTC 75328         A
                A                  TGAAACCCC TCTCTACTAAAAA
                                   ||||||||| |||||||||||||
                                   ACTTTGGGG AGAGATGATTTTT
                                        C
GAM1005  LOC129880 3'  TTTTTGGTGGAGACGGGGTTTC 75410         A
                                   GAAACCCC TCTCTACTAAAAA
                                   ||||||||  |||||||||||||
                                   CTTTGGGG AGAGGTGGTTTTT
                                       C
GAM1005  LOC130813 3'  ATTTTTAGTAGAGATGGGGTTT 76266
                C                  GAAACCCCATCTCTACTAAAAAT
                                   |||||||||||||||||||||||
                                   CTTTGGGGTAGAGATGATTTTTA

GAM1005  LOC130813 3'  TTTTATGTAGAGATAGGGTCTC 76284     A   C      _
                A                  TGA ACCC ATCTCTAC TAAAA
                                   |||  ||||  ||||||||  |||||
                                   ACT TGGG TAGAGATG ATTTT
                                     C   A       T
GAM1005  LOC132241 5'  ATTTTTAGTAGAGAGTGGGTTT 75554         CA
                CA                 TGAAACCC  TCTCTACTAAAAAT
                                   ||||||||  ||||||||||||||
                                   ACTTTGGG  AGAGATGATTTTTA
                                       TG
GAM1005  LOC132625 3'  ATTTTTAGTAGAGATGGGGTTT 76435
                CA                 TGAAACCCCATCTCTACTAAAAAT
                                   |||||||||||||||||||||||
                                   ACTTTGGGGTAGAGATGATTTTTA

GAM1005  LOC133686 3'  ATTTTTAGTAGATATGGGGATT 75612      A     C
                CA                 TGAA CCCCAT TCTACTAAAAAT
                                   ||||  ||||||  ||||||||||||
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                                ACTT GGGGTA AGATGATTTTTA
                                  A     T
GAM1005  LOC135154 3'  ATTTTTAGTAAAGACAAGGTTT 75722        CCA   C
                 CA              TGAAACC   TCT TACTAAAAAT
                                 |||||||   ||| ||||||||||
                                 ACTTTGG   AGA ATGATTTTTA
                                    AAC   A
GAM1005  LOC135293 3'  ATTTTTAGTAGAGACGGCATTT 76678      CC  A
                 CA              TGAAA  CC TCTCTACTAAAAAT
                                 |||||  || ||||||||||||||
                                 ACTTT  GG AGAGATGATTTTTA
                                   AC  C
GAM1005  LOC135818 3'  TTTTTAGTAGAGATGGGGTTTC 75757
                                 GAAACCCCATCTCTACTAAAAA
                                 |||||||||||||||||||||||
                                 CTTTGGGGTAGAGATGATTTTT

GAM1005  LOC143187 3'  TTTTTGTAGAGATGGAGTTTCA 59769       C         T
                                 TGAAAC CCATCTCTAC AAAAA
                                 |||||| |||||||||| |||||
                                 ACTTTG GGTAGAGATG TTTTT
                                    A        _
GAM1005  LOC143916 3'  TTTTAGTAGAGATGGGGTTTCA 77153
                                 TGAAACCCCATCTCTACTAAAA
                                 |||||||||||||||||||||||
                                 ACTTTGGGGTAGAGATGATTTT

GAM1005  LOC144317 5'  ATTTTTAGTAGAGACTGGGGTT 77289          _
                 TC              GAAACCCCA TCTCTACTAAAAAT
                                 |||||||||| ||||||||||||||
                                 CTTTGGGGT AGAGATGATTTTTA
                                      C
GAM1005  LOC144524 5'  ATTTTTAGTAGAAACCGGGTTT 84049         CATC
                 CA              TGAAACCC    TCTACTAAAAAT
                                 ||||||||    ||||||||||||
                                 ACTTTGGG    AGATGATTTTTA
                                     CCAA
GAM1005  LOC144667 3'  TTTTTGTAGAGATGGGGTCTC  84094    A          T
                                 GA ACCCCATCTCTAC AAAAA
                                 || |||||||||||| |||||
                                 CT TGGGGTAGAGATG TTTTT
                                  C          _
GAM1005  LOC144742 5'  ATTTTTAGTAGAGACAGGTTTT 77454       C  CA
                 CA              TGAAA CC  TCTCTACTAAAAAT
                                 ||||| ||  ||||||||||||||
                                 ACTTT GG  AGAGATGATTTTTA
                                   T  AC
GAM1005  LOC144871 3'  ATTTTTAGTAGAAATGGGGTTT 84120           C
                 CA              TGAAACCCCAT TCTACTAAAAAT
                                 |||||||||| ||||||||||||
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                                ACTTTGGGGTA AGATGATTTTTA
                                      A
GAM1005  LOC145009 3'  ATTTTTAGTAGAGACAGGGTTT 60969        CA
                CA                TGAAACCC  TCTCTACTAAAAAT
                                  ||||||||  ||||||||||||||
                                  ACTTTGGG  AGAGATGATTTTTA
                                      AC
GAM1005  LOC145268 5'  ATTTTTAGTAGAGACAGAGTTT 77572       CCCA
                CA                TGAAAC    TCTCTACTAAAAAT
                                  ||||||    ||||||||||||||
                                  ACTTTG    AGAGATGATTTTTA
                                     AGAC
GAM1005  LOC145622 3'  ATTTTTAGTAGAGAGGGGGTTT 77804         A
                CA                TGAAACCCC TCTCTACTAAAAAT
                                  |||||||||| ||||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                       G
GAM1005  LOC146050 3'  ATTTTTAGTAGAGATGGGGTTT 78103
                C                  GAAACCCCATCTCTACTAAAAAT
                                   |||||||||||||||||||||||
                                   CTTTGGGGTAGAGATGATTTTTA

GAM1005  LOC146050 3'  ATTTTTAGTAGAGATGGGGTTT 78104
                CA                TGAAACCCCATCTCTACTAAAAAT
                                  |||||||||||||||||||||||
                                  ACTTTGGGGTAGAGATGATTTTTA

GAM1005  LOC146229 3'  ATTTTTAATAGAGACGGGGTTT 78261         A     C
                CA                TGAAACCCC TCTCTA TAAAAAT
                                  ||||||||| |||||| |||||||
                                  ACTTTGGGG AGAGAT ATTTTTA
                                       C     A
GAM1005  LOC146229 3'  ATTTTTAGTAGAGACGGGGTTT 78262         A
                TA                TGAAACCCC TCTCTACTAAAAAT
                                  ||||||||| ||||||||||||||
                                  ATTTTGGGG AGAGATGATTTTTA
                                       C
GAM1005  LOC146229 3'  ATTTTTAGTAGTGACGGGGTTT 78263         A  T
                CA                TGAAACCCC TC CTACTAAAAAT
                                  ||||||||| || ||||||||||
                                  ACTTTGGGG AG GATGATTTTTA
                                       C  T
GAM1005  LOC146346 5'  ATTTTTAGTAGAGACAGGATTT 78387       C  CA
                CA                TGAAA CC  TCTCTACTAAAAAT
                                  ||||| ||  ||||||||||||||
                                  ACTTT GG  AGAGATGATTTTTA
                                     A  AC
GAM1005  LOC146346 5'  ATTTTTAGTAGAGACGGGGTTT 78388         A
                CA                TGAAACCCC TCTCTACTAAAAAT
                                  ||||||||| |||||||||||||||
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                                ACTTTGGGG AGAGATGATTTTTA
                                     C
GAM1005  LOC146429 5'  ATTTTTAGTAAAGACAGGGTTT 84661        CA   C
                 CA                TGAAACCC  TCT TACTAAAAAT
                                   |||||||||  ||| ||||||||||
                                   ACTTTGGG  AGA ATGATTTTTA
                                        AC   A
GAM1005  LOC146603 5'  ATTTTCAGTAGAGACGGGGTTT 78590          A       A
                 CA                TGAAACCCC TCTCTACT AAAAT
                                   |||||||||| |||||||| |||||
                                   ACTTTGGGG AGAGATGA TTTTA
                                        C       C
GAM1005  LOC146784 5'  TTTTTAGTAGAGATGGGGTTTC 78722
                 A                 TGAAACCCCATCTCTACTAAAAA
                                   |||||||||||||||||||||||
                                   ACTTTGGGGTAGAGATGATTTTT

GAM1005  LOC146839 3'  TTTTTAGTAGAGACGGGGTTTC 84858          A
                 A                 TGAAACCCC TCTCTACTAAAAA
                                   ||||||||| ||||||||||||
                                   ACTTTGGGG AGAGATGATTTTT
                                        C
GAM1005  LOC146894 3'  TTTTAGTAGAGATGGGGTTTCA 59870
                                   TGAAACCCCATCTCTACTAAAA
                                   |||||||||||||||||||||
                                   ACTTTGGGGTAGAGATGATTTT

GAM1005  LOC146901 3'  ATTTTTAACAGAGACGGGGTTT 84891          A     AC
                 CA                TGAAACCCC TCTCT  TAAAAAT
                                   ||||||||| |||||  |||||||
                                   ACTTTGGGG AGAGA  ATTTTTA
                                        C    CA
GAM1005  LOC146909 3'  ATTTTTAGTAGAGATGGGGTTT 78761
                 CA                TGAAACCCCATCTCTACTAAAAAT
                                   |||||||||||||||||||||||
                                   ACTTTGGGGTAGAGATGATTTTTA

GAM1005  LOC146952 5'  ATTTTTAGTAGAGACAGGGTTT 84923          CA
                 CA                TGAAACCC  TCTCTACTAAAAAT
                                   ||||||||  ||||||||||||||
                                   ACTTTGGG  AGAGATGATTTTTA
                                        AC
GAM1005  LOC147054 3'  ATTTTTAGTAGGGATGGGGTTT 85002
                 C                 GAAACCCCATCTCTACTAAAAAT
                                   |||||||||||||||||||||||
                                   CTTTGGGGTAGGGATGATTTTTA

GAM1005  LOC147071 5'  ATTTTTAGTAGAGACGGAGTTT 73352        C  A
                 CA                TGAAAC CC TCTCTACTAAAAAT
                                   |||||| || ||||||||||||||
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                                ACTTTG GG AGAGATGATTTTTA
                                   A  C
GAM1005  LOC147080 5'  ATTTTCAGTAGAGACAAGGTTT 85027        CCA       A
              CA                  TGAAACC   TCTCTACT AAAAT
                                  ||||||| ||||||||| |||||
                                  ACTTTGG   AGAGATGA TTTTA
                                     AAC       C
GAM1005  LOC147166 3'  ATTTTTAGTAGAGATGGGGTTT 78883
              CA                  TGAAACCCCATCTCTACTAAAAAT
                                  |||||||||||||||||||||||
                                  ACTTTGGGGTAGAGATGATTTTTA

GAM1005  LOC147276 3'  ATTTTTAGTAGAGACGGGGCTT 78952     A    A
              C                    GAA CCCC TCTCTACTAAAAAT
                                  ||| |||| ||||||||||||||
                                  CTT GGGG AGAGATGATTTTTA
                                    C    C
GAM1005  LOC147429 3'  ATTTTTAGTAGAGATGGGGTTT 78993
              CA                  TGAAACCCCATCTCTACTAAAAAT
                                  |||||||||||||||||||||||
                                  ACTTTGGGGTAGAGATGATTTTTA

GAM1005  LOC147694 3'  ATTTTTAGTAGAGACGGGGTTT 79090          A
              CA                  TGAAACCCC TCTCTACTAAAAAT
                                  ||||||||| ||||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                     C
GAM1005  LOC147817 3'  ATTTTTAGTAGAGACAGGGCTT 79168      A   CA
              CA                  TGAA CCC  TCTCTACTAAAAAT
                                  |||| |||  ||||||||||||||
                                  ACTT GGG  AGAGATGATTTTTA
                                    C   AC
GAM1005  LOC147817 3'  ATTTTTAGTAGAGACGGAGTTT 79169       C  A
              CA                  TGAAAC CC TCTCTACTAAAAAT
                                  |||||| || ||||||||||||||
                                  ACTTTG GG AGAGATGATTTTTA
                                     A  C
GAM1005  LOC147841 3'  TTTGGTAGAGATGGAGTTTCA  79234       C
                                  TGAAAC CCATCTCTACTAAA
                                  |||||| ||||||||||||||
                                  ACTTTG GGTAGAGATGGTTT
                                     A
GAM1005  LOC147990 3'  ATTTTTACTAGAGACGGGGTTT 85212          A     C
              CA                  TGAAACCCC TCTCTA TAAAAAT
                                  ||||||||| |||||| |||||||
                                  ACTTTGGGG AGAGAT ATTTTTA
                                     C     C
GAM1005  LOC148137 3'  ATTTTTAGTAGAGACGGTGTTT 59089       C  A
              CA                  TGAAAC CC TCTCTACTAAAAAT
                                  |||||| || ||||||||||||||
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                                ACTTTG GG AGAGATGATTTTTA
                                   T  C
GAM1005  LOC148147 3'  ATTTTTGTAGAGATGAGGTTTC 79391        C        T
              A                  TGAAACC CATCTCTAC AAAAAT
                                 ||||||| ||||||||| ||||||
                                 ACTTTGG GTAGAGATG TTTTTA
                                    A       _
GAM1005  LOC148189 5'  ATTTTTAGTAGAGACGGGGTTT 79446          A
              CA                   TGAAACCCC TCTCTACTAAAAAT
                                   ||||||||| |||||||||||||
                                   ACTTTGGGG AGAGATGATTTTTA
                                       C
GAM1005  LOC148195 3'  ATTTTCAGTAGAGACAGGTTTC 85270        CCA       A
              A                    TGAAACC   TCTCTACT AAAAT
                                   |||||||   |||||||| |||||
                                   ACTTTGG   AGAGATGA TTTTA
                                      AC_       C
GAM1005  LOC148195 5'  TTTTTAGTGACGGGGTCTCA   85301     A     A  TCT
                                   TGA ACCCC TC   ACTAAAAA
                                   ||| ||||| ||   ||||||||
                                   ACT TGGGG AG   TGATTTTT
                                     C    C ____
GAM1005  LOC148709 3'  ATTTTTAGTAGAGACAGGGTTT 79688        CA
              C                    GAAACCC  TCTCTACTAAAAAT
                                   |||||||  |||||||||||||
                                   CTTTGGG  AGAGATGATTTTTA
                                      AC
GAM1005  LOC148887 5'  ATTTTTAGTAGAGACAGGGTTT 85392         CA
              CA                   TGAAACCC  TCTCTACTAAAAAT
                                   ||||||||  |||||||||||||
                                   ACTTTGGG  AGAGATGATTTTTA
                                      AC
GAM1005  LOC149171 5'  ATTTTTAGTAGAGATGGGGTTT 79963
              C                    GAAACCCCATCTCTACTAAAAAT
                                   |||||||||||||||||||||||
                                   CTTTGGGGTAGAGATGATTTTTA

GAM1005  LOC149421 3'  ATTTTTAGTAGAGACGGGGTTT 80140          A
              CA                   TGAAACCCC TCTCTACTAAAAAT
                                   ||||||||| |||||||||||||
                                   ACTTTGGGG AGAGATGATTTTTA
                                       C
GAM1005  LOC149478 3'  ATTTTTAGTAGAGACGGGGGTT 80164          A_
              TCA                   TGAAACCCC  TCTCTACTAAAAAT
                                    |||||||||  |||||||||||||
                                    ACTTTGGGG  AGAGATGATTTTTA
                                       GC
GAM1005  LOC149506 3'  ATTTTTAGTAGAGACGAGGGTT 85625      A   CA_
              CA                    TGAA CCC   TCTCTACTAAAAAT
                                    |||| |||   |||||||||||||
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                                ACTT GGG   AGAGATGATTTTTA
                                  _   AGC
GAM1005  LOC149577 3'  ATTTTTAGTAGAGACAGGCTTT 85665      C  CA
              C                   GAAA CC  TCTCTACTAAAAAT
                                  ||||| ||  ||||||||||||||
                                  CTTT GG  AGAGATGATTTTTA
                                    C  AC
GAM1005  LOC149577 3'  TTTAGTAGAGATGGGGTTTT   85685
                                  GAAACCCCATCTCTACTAAA
                                  ||||||||||||||||||||
                                  TTTTGGGGTAGAGATGATTT

GAM1005  LOC149692 3'  ATTTTTAGTAGAGACAGGGTTT 85727         CA
              CA                    TGAAACCC  TCTCTACTAAAAAT
                                  ||||||||  ||||||||||||||
                                  ACTTTGGG  AGAGATGATTTTTA
                                       AC
GAM1005  LOC149692 3'  TTTTAGTAGAGACGAGTTTTCA 85749       CCCCA
                                  TGAAA     TCTCTACTAAAA
                                  ||||||     ||||||||||||
                                  ACTTT     AGAGATGATTTT
                                     TGAGC
GAM1005  LOC149703 5'  ATTTTTAGTAGAGACGGGGTTT 85816         A
              T                    GAAACCCC TCTCTACTAAAAAT
                                  |||||||| ||||||||||||||
                                  TTTTGGGG AGAGATGATTTTTA
                                       C
GAM1005  LOC149711 3'  ATTTTTAGTAGAGATGGGGTTT 85840
              TA                    TGAAACCCCATCTCTACTAAAAAT
                                  |||||||||||||||||||||||||
                                  ATTTTGGGGTAGAGATGATTTTTA

GAM1005  LOC149821 5'  ATTTTTAGTACAGACGGAGTTT 85929       C  A   C
              CA                    TGAAAC CC TCT TACTAAAAAT
                                  |||||| || ||| ||||||||||
                                  ACTTTG GG AGA ATGATTTTTA
                                     A  C   C
GAM1005  LOC150166 5'  TTTTGTAGAAATGGGGTTTCA  86048          C     T
                                  TGAAACCCCAT TCTAC AAAA
                                  |||||||||||| ||||| ||||
                                  ACTTTGGGGTA AGATG TTTT
                                        A    _
GAM1005  LOC150282 5'  ATTTTTAGTAGAGATGGCGTTT 80537       C
              CA                    TGAAAC CCATCTCTACTAAAAAT
                                  |||||| ||||||||||||||||||
                                  ACTTTG GGTAGAGATGATTTTTA
                                     C
GAM1005  LOC150397 3'  ATTTTTAGTAGAGACGCAGTTT 80654       CCCA
              CA                    TGAAAC    TCTCTACTAAAAAT
                                  ||||||    ||||||||||||||
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                                ACTTTG    AGAGATGATTTTTA
                                   ACGC
GAM1005  LOC150630 5'  ATTTTTAGTAGAGAGGGGGTTT 86291          A
              CA                  TGAAACCCC TCTCTACTAAAAAT
                                  ||||||||| ||||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                     G
GAM1005  LOC150960 3'  AGTAGAGATGGGGTCTCA     80866     A
                                  TGA ACCCCATCTCTACT
                                  ||| ||||||||||||||
                                  ACT TGGGGTAGAGATGA
                                    C
GAM1005  LOC151050 5'  ATTTTTAGTAGAGACAGAGTTT 80916        CCCA
              CA                  TGAAAC    TCTCTACTAAAAAT
                                  ||||||    ||||||||||||||
                                  ACTTTG    AGAGATGATTTTTA
                                     AGAC
GAM1005  LOC151057 3'  TTAGTAGAGACGGGGTTTCA   86401          A
                                  TGAAACCCC TCTCTACTAA
                                  ||||||||| ||||||||||
                                  ACTTTGGGG AGAGATGATT
                                     C
GAM1005  LOC151201 3'  ATTTTTAGTAGAGACGGGGTTT 86467          A
              CA                  TGAAACCCC TCTCTACTAAAAAT
                                  ||||||||| ||||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                     C
GAM1005  LOC151475 5'  ATTTTTAGTAGAGACGAGGTTT 86584        CCA
              CA                  TGAAACC   TCTCTACTAAAAAT
                                  |||||||   ||||||||||||||
                                  ACTTTGG   AGAGATGATTTTTA
                                     AGC
GAM1005  LOC151701 3'  ATTTTTAGTAGAGACGGGGTTT 86667          A
              CA                  TGAAACCCC TCTCTACTAAAAAT
                                  ||||||||| ||||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                     C
GAM1005  LOC151826 3'  TTTTTAGTAGAGACAGGGTTTC 81191         CA
              A                    TGAAACCC  TCTCTACTAAAAA
                                   ||||||||  |||||||||||||
                                   ACTTTGGG  AGAGATGATTTTT
                                      AC
GAM1005  LOC151979 5'  TTTTTAGTAGAGACGGGGTTTC 81258          A
              A                    TGAAACCCC TCTCTACTAAAAA
                                   ||||||||| |||||||||||||
                                   ACTTTGGGG AGAGATGATTTTT
                                      C
GAM1005  LOC152137 3'  ATTTTTAGTAAAGAGCGGGTTT 81308         CA   C
              CA                   TGAAACCC  TCT TACTAAAAAT
                                   ||||||||  ||| ||||||||||
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                                ACTTTGGG  AGA ATGATTTTTA
                                    CG   A
GAM1005  LOC152220 3'  ATTTTTAGTAGAGACAGAGTCT 86760     A  CCCA
             CA                   TGA AC    TCTCTACTAAAAAT
                                  ||| ||    ||||||||||||||
                                  ACT TG    AGAGATGATTTTTA
                                    C  AGAC
GAM1005  LOC152300 3'  TTTTTAGTAGAGACAGGGTTTC 81392         CA
             A                    TGAAACCC  TCTCTACTAAAAA
                                  ||||||||  ||||||||||||||
                                  ACTTTGGG  AGAGATGATTTTT
                                      AC
GAM1005  LOC152343 3'  ATTTTTAGTAGAGAGGGGGTGT 81420     A     A
             CA                   TGA ACCCC TCTCTACTAAAAAT
                                  ||| ||||| ||||||||||||||
                                  ACT TGGGG AGAGATGATTTTTA
                                    G     G
GAM1005  LOC152445 3'  ATTTTTAATAGAGACAGGGTTT 86935         CA      C
             CA                   TGAAACCC  TCTCTA TAAAAAT
                                  ||||||||  ||||||| |||||||
                                  ACTTTGGG  AGAGAT ATTTTTA
                                      AC      A
GAM1005  LOC152620 3'  ATTTTTAGTAGAGGCGGGGTTA 60705    A      AT
             CA                   TG AACCCC  CTCTACTAAAAAT
                                  || ||||||  ||||||||||||||
                                  AC TTGGGG  GAGATGATTTTTA
                                   A     CG
GAM1005  LOC152719 5'  ATTTTTAGTTGAGACGGGGTTT 87016          A    T
             CA                   TGAAACCCC TCTC ACTAAAAAT
                                  ||||||||| |||| |||||||||
                                  ACTTTGGGG AGAG TGATTTTTA
                                      C    T
GAM1005  LOC152794 5'  ATTTTTTGTGGAGATGGGGTTT 81555               T
             CA                   TGAAACCCCATCTCTAC AAAAAT
                                  |||||||||||||||| ||||||
                                  ACTTTGGGGTAGAGGTG TTTTTA
                                            T
GAM1005  LOC152851 3'  TTTTTAGTAGAGACAGGATTTC 81601       C  CA
             A                    TGAAA CC  TCTCTACTAAAAA
                                  ||||| ||  ||||||||||||||
                                  ACTTT GG  AGAGATGATTTTT
                                     A  AC
GAM1005  LOC153077 3'  ATTTTTAGTAGAGATGGGGCTT 87112      A
             CA                   TGAA CCCCATCTCTACTAAAAAT
                                  |||| ||||||||||||||||||
                                  ACTT GGGGTAGAGATGATTTTTA
                                    C
GAM1005  LOC153606 5'  TTTTAGTAGAGATAGGGTTTCA 87262         C
                                  TGAAACCC ATCTCTACTAAAA
                                  |||||||| ||||||||||||
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                                ACTTTGGG TAGAGATGATTTT
                                    A
GAM1005  LOC153688 3'  ATTTTTAGTAGAGACAGGGTTT 87295        CA
             CA                  TGAAACCC  TCTCTACTAAAAAT
                                 ||||||||  ||||||||||||||
                                ACTTTGGG  AGAGATGATTTTTA
                                    AC
GAM1005  LOC153688 3'  ATTTTTGGATAGAGACAGGATT 87296     C  CA    _
             TC                  GAAA CC  TCTCTA CTAAAAAT
                                 ||||  ||  ||||||  ||||||||
                                CTTT GG  AGAGAT GGTTTTTA
                                  A  AC     A
GAM1005  LOC153811 3'  ATTTTTAGTAGAAACGAGGTTT 81824       CCATC
             CA                  TGAAACC    TCTACTAAAAAT
                                 |||||||    ||||||||||||
                                ACTTTGG    AGATGATTTTTA
                                    AGCAA
GAM1005  LOC153883 5'  AGTAGAAATGGGGTTTTA    81886         C
                                TGAAACCCCAT TCTACT
                                ||||||||||| ||||||
                                ATTTTGGGGTA AGATGA
                                      A
GAM1005  LOC154282 5'  TTTTTAGTAGAGATGGTGTTTC 87416       C
             A                   TGAAAC CCATCTCTACTAAAAA
                                 ||||||  ||||||||||||||||
                                ACTTTG GGTAGAGATGATTTTT
                                    T
GAM1005  LOC154877 5'  ATTTTTAGTAGAGATGGGGTTT 87528
             T                   GAAACCCCATCTCTACTAAAAAT
                                 |||||||||||||||||||||||
                                TTTTGGGGTAGAGATGATTTTTA

GAM1005  LOC154877 3'  ATTTTTAGTAGAGTCGGGGGTTT 87529         AT
             CA                  TGAAACCCC  CTCTACTAAAAAT
                                 |||||||||  ||||||||||||
                                ACTTTGGGG  GAGATGATTTTTA
                                     CT
GAM1005  LOC154877 3'  TTTTTGGTGGAGACAGGGTCTC 87587     A   CA
             A                   TGA ACCC  TCTCTACTAAAAA
                                 |||  ||||  ||||||||||||
                                ACT TGGG  AGAGGTGGTTTTT
                                  C   AC
GAM1005  LOC154930 3'  TTTTTAGTAGAGACAGGATTTT 82098      C  CA
             A                   TGAAA CC  TCTCTACTAAAAA
                                 |||||  ||  ||||||||||||
                                ATTTT GG  AGAGATGATTTTT
                                  A  AC
GAM1005  LOC157247 5'  ATTTTTGGTAGAGACGGGGTTT 82286         A
             CA                  TGAAACCCC TCTCTACTAAAAAT
                                 |||||||||  ||||||||||||||
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                                ACTTTGGGG AGAGATGGTTTTTA
                                     C
GAM1005  LOC157506 3'  ATTTTTAGTAGAGACGGGGTTT 82363          A
              CA                  TGAAACCCC TCTCTACTAAAAAT
                                  ||||||||| ||||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                     C
GAM1005  LOC157623 3'  ATTTTTGCAGAGATGGAGTTTC 82411        C       AC
              A                    TGAAAC CCATCTCT  TAAAAAT
                                   |||||| ||||||||  |||||||
                                   ACTTTG GGTAGAGA  GTTTTTA
                                      A       C_
GAM1005  LOC157798 5'  ATTTTTAGTAGAGACGGGGTTT 87854          A
              CA                  TGAAACCCC TCTCTACTAAAAAT
                                  ||||||||| ||||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                     C
GAM1005  LOC157858 5'  ATTTTTACTAGAGACAGGGTTT 87883         CA      C
              CA                  TGAAACCC  TCTCTA TAAAAAT
                                  ||||||||  |||||| |||||||
                                  ACTTTGGG  AGAGAT ATTTTTA
                                     AC      C
GAM1005  LOC158014 5'  ATTTTTAGTAGAGACGGAGTTT 82554        C  A
              CA                  TGAAAC CC TCTCTACTAAAAAT
                                  |||||| || ||||||||||||||
                                  ACTTTG GG AGAGATGATTTTTA
                                     A  C
GAM1005  LOC158014 5'  ATTTTTTTTTGAGATGGGGTCT 82555     A         TACT
              C                    GA ACCCCATCTC    AAAAAT
                                   || ||||||||||    ||||||
                                   CT TGGGGTAGAG    TTTTTA
                                    C         TTTT
GAM1005  LOC158310 5'  ATTTTTAATAGAGACAGGGTTT 88076         CA      C
              CA                  TGAAACCC  TCTCTA TAAAAAT
                                  ||||||||  |||||| |||||||
                                  ACTTTGGG  AGAGAT ATTTTTA
                                     AC      A
GAM1005  LOC158402 5'  ATTTTTAGTAGAGAGGGGGGTT 88142          A_
              TCA                  TGAAACCCC  TCTCTACTAAAAAT
                                   |||||||||  |||||||||||||
                                   ACTTTGGGG  AGAGATGATTTTTA
                                      GG
GAM1005  LOC158476 3'  ATTTTTGTAGAGACAGGGTTTC 88185         CA      T
              A                    TGAAACCC  TCTCTAC AAAAAT
                                   ||||||||  ||||||| ||||||
                                   ACTTTGGG  AGAGATG TTTTTA
                                      AC      _
GAM1005  LOC158476 3'  TTTGGTAGAGACAGGGTTTCA  88211         CA
                                   TGAAACCC  TCTCTACTAAA
                                   ||||||||  ||||||||||
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                                ACTTTGGG  AGAGATGGTTT
                                    AC
GAM1005  LOC158549 5'  ATTTTTAGTAGAGATAGGGGTT 88216          _
              TCA                  TGAAACCCC ATCTCTACTAAAAAT
                                   ||||||||| ||||||||||||||||
                                   ACTTTGGGG TAGAGATGATTTTTA
                                     A
GAM1005  LOC158668 3'  ATTTTTAGTAGAGGTGGGGTTT 69894
              CA                   TGAAACCCCATCTCTACTAAAAAT
                                   |||||||||||||||||||||||||
                                   ACTTTGGGGTGGAGATGATTTTTA

GAM1005  LOC158865 5'  ATTTTTAGTAGAGATGGGG    88305
                                   CCCCATCTCTACTAAAAAT
                                   ||||||||||||||||||
                                   GGGGTAGAGATGATTTTTA

GAM1005  LOC160646 3'  ATTTTTAGTAGAGATGGGGCTT 83107      A
              CA                   TGAA CCCCATCTCTACTAAAAAT
                                   |||| ||||||||||||||||||
                                   ACTT GGGGTAGAGATGATTTTTA
                                     C
GAM1005  LOC161829 3'  ATTTTTAGTAGAGATGGGGTTT 83184
              CA                   TGAAACCCCATCTCTACTAAAAAT
                                   |||||||||||||||||||||||||
                                   ACTTTGGGGTAGAGATGATTTTTA

GAM1005  LOC162427 3'  ATTTTTAGTAGAAATGGGGTTT 83224           C
              CA                   TGAAACCCCAT TCTACTAAAAAT
                                   |||||||||||| ||||||||||||
                                   ACTTTGGGGTA AGATGATTTTTA
                                      A
GAM1005  LOC169286 5'  TTTATGGAACAGATGGGGCTCG 83615     AA       CTA   A
                                   TGA  CCCCATCT   CTA AAA
                                   |||  ||||||||   ||| |||
                                   GCT  GGGGTAGA   GGT TTT
                                     C_       CAA   A
GAM1005  LOC169611 3'  ATTTTTAGTAGAGACAGGATTT 83636       C  CA
              CA                   TGAAA CC  TCTCTACTAAAAAT
                                   ||||| ||  ||||||||||||||
                                   ACTTT GG  AGAGATGATTTTTA
                                     A  AC
GAM1005  LOC169611 3'  ATTTTTAGTAGAGACAGGGGTT 83637          A_
              TCA                   TGAAACCCC  TCTCTACTAAAAAT
                                   |||||||||  ||||||||||||||
                                   ACTTTGGGG  AGAGATGATTTTTA
                                      AC
GAM1005  LOC170082 5'  ATTTTTAGTAGAGATGGGGTTT 83440
              CA                   TGAAACCCCATCTCTACTAAAAAT
                                   |||||||||||||||||||||||||
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                                ACTTTGGGGTAGAGATGATTTTTA

GAM1005  LOC196047 5'  TTAGTAGAGCCAGGGTTTCA   91169         CAT
                                TGAAACCC   CTCTACTAA
                                ||||||||   |||||||||
                                ACTTTGGG   GAGATGATT
                                     ACC
GAM1005  LOC196264 3'  TTTTTAGTAGAGACGGGGTTTC 88997          A
              A                  TGAAACCCC TCTCTACTAAAAA
                                 |||||||||| ||||||||||||
                                 ACTTTGGGG AGAGATGATTTTT
                                      C
GAM1005  LOC196411 3'  ATTTTTAGTAGAGATGGGGTTT 89041
              CA                   TGAAACCCCATCTCTACTAAAAAT
                                   |||||||||||||||||||||||
                                   ACTTTGGGGTAGAGATGATTTTTA

GAM1005  LOC196529 3'  ATTTTTAGTTGAGACAGGGTTT 89124         CA    T
              CA                   TGAAACCC  TCTC ACTAAAAAT
                                   ||||||||  |||| |||||||||
                                   ACTTTGGG  AGAG TGATTTTTA
                                        AC    T
GAM1005  LOC196529 3'  TTTTAGTAGAGATGGTGTTTC  89147       C
                                GAAAC CCATCTCTACTAAAA
                                ||||| ||||||||||||||
                                CTTTG GGTAGAGATGATTTT
                                   T
GAM1005  LOC197358 3'  ATTTTTAGTAGAGATGGGGTTT 89422
              CA                   TGAAACCCCATCTCTACTAAAAAT
                                   |||||||||||||||||||||||
                                   ACTTTGGGGTAGAGATGATTTTTA

GAM1005  LOC197358 3'  TTTTAGTAGAGACGGGGTTTCA 89453          A
                                TGAAACCCC TCTCTACTAAAA
                                |||||||||| ||||||||||||
                                ACTTTGGGG AGAGATGATTTT
                                     C
GAM1005  LOC199699 3'  ATTTTTAGTAAAGACAGGGTTT 89667         CA   C
              CA                   TGAAACCC  TCT TACTAAAAAT
                                   |||||||||  ||| ||||||||||
                                   ACTTTGGG  AGA ATGATTTTTA
                                        AC   A
GAM1005  LOC199699 3'  ATTTTTAGTAGAGACAGAGTTT 89668        CCCA
              CA                   TGAAAC    TCTCTACTAAAAAT
                                   ||||||    ||||||||||||||
                                   ACTTTG    AGAGATGATTTTTA
                                      AGAC
GAM1005  LOC199725 5'  ATTTTTAGTAGAGACGGGATTT 91410       C   A
              CA                   TGAAA CCC TCTCTACTAAAAAT
                                   ||||| ||| |||||||||||||
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                                ACTTT GGG AGAGATGATTTTTA
                                  A  C
GAM1005  LOC199786 3'  TTTTAGTAGAGACGGTGGTTTC 89773      _  A
                                GAAACC CC TCTCTACTAAAA
                                |||||| || ||||||||||||
                                CTTTGG GG AGAGATGATTTT
                                   T  C
GAM1005  LOC199786 3'  TTTTTAGTAGAGATGGGGTTTC 89775
              A                  TGAAACCCCATCTCTACTAAAAA
                                 |||||||||||||||||||||||
                                 ACTTTGGGGTAGAGATGATTTTT

GAM1005  LOC199906 3'  ATTTTTAGTAAAGACAGGGTTT 89846       CA  C
              CA                  TGAAACCC  TCT TACTAAAAAT
                                  ||||||||  ||| ||||||||||
                                  ACTTTGGG  AGA ATGATTTTTA
                                       AC  A
GAM1005  LOC200014 3'  ATTTTTAGTAGAGACGGTGTTT 89920      C  A
              CA                  TGAAAC CC TCTCTACTAAAAAT
                                  |||||| || ||||||||||||||
                                  ACTTTG GG AGAGATGATTTTTA
                                     T  C
GAM1005  LOC200169 5'  ATTTTTAGTAGAGACGGAGTTT 91552      C  A
              CA                  TGAAAC CC TCTCTACTAAAAAT
                                  |||||| || ||||||||||||||
                                  ACTTTG GG AGAGATGATTTTTA
                                     A  C
GAM1005  LOC200301 5'  ATTTTTAGTAGAGACGGGGTTT 90134        A
              CA                  TGAAACCCC TCTCTACTAAAAAT
                                  |||||||||| ||||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                       C
GAM1005  LOC200310 3'  ATTTTTAGTAGAGACGGGGTTT 66321        A
              CA                  TGAAACCCC TCTCTACTAAAAAT
                                  |||||||||| ||||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                       C
GAM1005  LOC200314 3'  TAGTAGAGATGGGGTTTCA   91602
                                TGAAACCCCATCTCTACTA
                                |||||||||||||||||||
                                ACTTTGGGGTAGAGATGAT

GAM1005  LOC200316 5'  ATTTTTAGTAGAGACGGGGTTT 90172        A
              C                   GAAACCCC TCTCTACTAAAAAT
                                  |||||||| ||||||||||||||
                                  CTTTGGGG AGAGATGATTTTTA
                                       C
GAM1005  LOC200316 3'  ATTTTTAGTAGTGACTGGGTTT 90173        CA  T
              CA                  TGAAACCC  TC CTACTAAAAAT
                                  ||||||||  || ||||||||||
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                                ACTTTGGG  AG GATGATTTTTA
                                    TC  T
GAM1005  LOC200339 3'  ATTTTTAGTAGAGATGGGATTT 91613      C
              T                  GAAA CCCATCTCTACTAAAAAT
                                 |||| ||||||||||||||||||
                                 TTTT GGGTAGAGATGATTTTTA
                                   A
GAM1005  LOC200407 3'  ATTTTTAGTAGAGACAGGGTTT 91626       CA
              T                  GAAACCC  TCTCTACTAAAAAT
                                 |||||||  |||||||||||||
                                 TTTTGGG  AGAGATGATTTTTA
                                    AC
GAM1005  LOC200845 5'  ATTTTTAGTAGAGATGGGGTTT 90312
              CA                   TGAAACCCCATCTCTACTAAAAAT
                                 |||||||||||||||||||||||||
                                 ACTTTGGGGTAGAGATGATTTTTA

GAM1005  LOC200860 3'  ATTTTTAGTAGAGACGGGGTTT 91740        A
              C                  GAAACCCC TCTCTACTAAAAAT
                                 ||||||||| |||||||||||||
                                 CTTTGGGG AGAGATGATTTTTA
                                    C
GAM1005  LOC201164 3'  ATTTTTAGTAGAGACAGGGTTT 89488        CA
              CA                   TGAAACCC  TCTCTACTAAAAAT
                                 ||||||||  |||||||||||||
                                 ACTTTGGG  AGAGATGATTTTTA
                                    AC
GAM1005  LOC201173 5'  ATTTTTAGTAGAGACGGAGTTT 88671       C  A
              CA                   TGAAAC CC TCTCTACTAAAAAT
                                 ||||||| || |||||||||||||
                                 ACTTTG GG AGAGATGATTTTTA
                                    A  C
GAM1005  LOC201220 5'  ATTTTTAGTAGAGATGGAGTTT 88706       C
              CA                   TGAAAC CCATCTCTACTAAAAAT
                                 |||||| ||||||||||||||||||
                                 ACTTTG GGTAGAGATGATTTTTA
                                    A
GAM1005  LOC201294 3'  ATTTTTAGTAGAGACGGGGTTT 89576        A
              CA                   TGAAACCCC TCTCTACTAAAAAT
                                 ||||||||| |||||||||||||
                                 ACTTTGGGG AGAGATGATTTTTA
                                     C
GAM1005  LOC201411 3'  ATTTTTAGTAGAGACAGGGTTT 63637        CA
              CA                   TGAAACCC  TCTCTACTAAAAAT
                                 ||||||||  |||||||||||||
                                 ACTTTGGG  AGAGATGATTTTTA
                                    AC
GAM1005  LOC201626 3'  ATTTTTAGTAGAAATGGGGTTT 90427        C
              C                  GAAACCCCAT TCTACTAAAAAT
                                 |||||||||| ||||||||||||
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                                CTTTGGGGTA AGATGATTTTTA
                                     A
GAM1005  LOC201627 3'  ATTTTTAGTAGAGATGGGGTTT 90449
                C                GAAACCCCATCTCTACTAAAAAT
                                 ||||||||||||||||||||||
                                 CTTTGGGGTAGAGATGATTTTTA

GAM1005  LOC201696 3'  ATTTTTAGTAGAGACGAGGTTT 63812       CCA
                C                GAAACC   TCTCTACTAAAAAT
                                 ||||||   ||||||||||||||
                                 CTTTGG   AGAGATGATTTTTA
                                    AGC
GAM1005  LOC202460 5'  ATTTTTAGTAGAGATGGGGTTT 90668
                CA                 TGAAACCCCATCTCTACTAAAAAT
                                   ||||||||||||||||||||||||
                                   ACTTTGGGGTAGAGATGATTTTTA

GAM1005  LOC202908 5'  ATTTTTTGTAGAGATGAGGTTT 90712       C       T
                CA                 TGAAACC CATCTCTAC AAAAAT
                                   |||||||  |||||||||  ||||||
                                   ACTTTGG GTAGAGATG TTTTTA
                                      A        T
GAM1005  LOC202934 3'  ATTTTTAGTAGAGACAGGGTTT 92027        CA
                CA                 TGAAACCC  TCTCTACTAAAAAT
                                   ||||||||  ||||||||||||||
                                   ACTTTGGG  AGAGATGATTTTTA
                                      AC
GAM1005  LOC203197 3'  TTTTTAGTAGAGATGGGGTTTC 90823
                                   GAAACCCCATCTCTACTAAAAA
                                   ||||||||||||||||||||||
                                   CTTTGGGGTAGAGATGATTTTT

GAM1005  LOC203339 3'  ATTTTTAGTAGAGATGGGGTTT 92207
                CA                 TGAAACCCCATCTCTACTAAAAAT
                                   ||||||||||||||||||||||||
                                   ACTTTGGGGTAGAGATGATTTTTA

GAM1005  LOC203350 3'  ATTTTTATTAGAGACGGGGTTT 92229         A     C
                CA                 TGAAACCCC TCTCTA TAAAAAT
                                   |||||||||  ||||||  |||||||
                                   ACTTTGGGG AGAGAT ATTTTTA
                                      C     T
GAM1005  LOC203378 3'  ATTTTTAGTAGAGATGGGATTT 92278       C
                TA                 TGAAA CCCATCTCTACTAAAAAT
                                   |||||  |||||||||||||||||
                                   ATTTT GGGTAGAGATGATTTTTA
                                     A
GAM1005  LOC204804 3'  ATTTTTAGTAGAGATGAGGTTT 91035        C
                CA                 TGAAACC CATCTCTACTAAAAAT
                                   |||||||  ||||||||||||||||
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                                ACTTTGG GTAGAGATGATTTTTA
                                    A
GAM1005  LOC219445 5'  AGTAGGGACGGGGTTTCA    93198         A
                                TGAAACCCC TCTCTACT
                                ||||||||| ||||||||
                                ACTTTGGGG AGGGATGA
                                    C
GAM1005  LOC219445 5'  TTTTTAGTAGAGACGGTGTTTC 93220       C  A
           A                     TGAAAC CC TCTCTACTAAAAA
                                ||||||| || ||||||||||||
                                ACTTTG GG AGAGATGATTTTT
                                   T  C
GAM1005  LOC219673 5'  ATTTTTGTAGAAAAGGGGTTTC 94611         ATC    T
           A                     TGAAACCCC   TCTAC AAAAAT
                                |||||||||   ||||| ||||||
                                ACTTTGGGG   AGATG TTTTTA
                                    AAA   _
GAM1005  LOC219673 5'  TTTTTGTAGAGATGAGGTCTCA 94638     A  C       T
                                TGA ACC CATCTCTAC AAAAA
                                ||| ||| ||||||||| |||||
                                ACT TGG GTAGAGATG TTTTT
                                  C  A       _
GAM1005  LOC219735 3'  ATTTTTAGTAGAGACGGGGTTT 94724         A
           CA                    TGAAACCCC TCTCTACTAAAAAT
                                ||||||||| ||||||||||||||
                                ACTTTGGGG AGAGATGATTTTTA
                                    C
GAM1005  LOC219894 3'  ATTTTTAGTAGAGATGGGGTTT 94899
           CA                    TGAAACCCCATCTCTACTAAAAAT
                                |||||||||||||||||||||||||
                                ACTTTGGGGTAGAGATGATTTTTA

GAM1005  LOC220064 3'  ATTTTTAGTAGAGATGGGGTTT 95061
           T                     GAAACCCCATCTCTACTAAAAAT
                                |||||||||||||||||||||||||
                                TTTTGGGGTAGAGATGATTTTTA

GAM1005  LOC220074 3'  ATTTTTAGTAGAGACGGGGTTT 59964         A
           CA                    TGAAACCCC TCTCTACTAAAAAT
                                ||||||||| ||||||||||||||
                                ACTTTGGGG AGAGATGATTTTTA
                                    C
GAM1005  LOC220074 3'  ATTTTTAGTAGAGATGGGGTTT 59965
           C                     GAAACCCCATCTCTACTAAAAAT
                                |||||||||||||||||||||||||
                                CTTTGGGGTAGAGATGATTTTTA

GAM1005  LOC220074 3'  TTTTAGTAGAGACAAGGTTTC  60002       CCA
                                GAAACC   TCTCTACTAAAA
                                ||||||   ||||||||||||
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                                CTTTGG   AGAGATGATTTT
                                   AAC
GAM1005  LOC220575 3'  TTTTTAGTAGAAATGAGGTCTC 76818    A  C  C
                                GA ACC CAT TCTACTAAAAA
                                || ||| ||| ||||||||||
                                CT TGG GTA AGATGATTTTT
                                 C  A  A
GAM1005  LOC221060 3'  ATTTTTAGTACAGACGGTGTTT 94829      C  A  C
            CA                    TGAAAC CC TCT TACTAAAAAT
                                |||||| || ||| ||||||||||
                                ACTTTG GG AGA ATGATTTTTA
                                   T  C  C
GAM1005  LOC221271 3'  AGTAGAGAGGGGGGTTTCA    93495        A
                                TGAAACCCC TCTCTACT
                                ||||||||| ||||||||
                                ACTTTGGGG AGAGATGA
                                      G
GAM1005  LOC221296 3'  ATTTTTAGTAGAGACGGGGTTT 93605         A
            CA                    TGAAACCCC TCTCTACTAAAAAT
                                ||||||||| ||||||||||||||
                                ACTTTGGGG AGAGATGATTTTTA
                                      C
GAM1005  LOC221964 3'  ATTTTTAGTAGAGACAGGGTTT 95600       CA
            T                    GAAACCC  TCTCTACTAAAAAT
                                ||||||| ||||||||||||||
                                TTTTGGG  AGAGATGATTTTTA
                                   AC
GAM1005  LOC222031 3'  ATTTTTAGTAGAGACGAGGTTT 95670       CCA
            CA                    TGAAACC   TCTCTACTAAAAAT
                                ||||||| ||||||||||||||
                                ACTTTGG   AGAGATGATTTTTA
                                   AGC
GAM1005  LOC222068 3'  ATTTTTAGTAGAGATGGGGTTT 94270
            TA                    TGAAACCCCATCTCTACTAAAAAT
                                ||||||||||||||||||||||||
                                ATTTTGGGGTAGAGATGATTTTTA

GAM1005  LOC222070 5'  ATTTTTAGTGGAGACGGTGTTT 95809       C  A
            CA                    TGAAAC CC TCTCTACTAAAAAT
                                |||||| || ||||||||||||||
                                ACTTTG GG AGAGGTGATTTTTA
                                   T  C
GAM1005  LOC222224 5'  ATTTTTTGTAGAGACAGGGTTT 95870        CA      T
            CA                    TGAAACCC  TCTCTAC AAAAAT
                                |||||||| ||||||| ||||||
                                ACTTTGGG  AGAGATG TTTTTA
                                   AC      T
GAM1005  LOC245771 5'  ATTTTTAGTAGAGATGGGGTTT 94468
            CA                    TGAAACCCCATCTCTACTAAAAAT
                                |||||||||||||||||||||||||
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                                ACTTTGGGGTAGAGATGATTTTTA

GAM1005  LOC253664 3'  ATTTTCAGTAGAGATGGGGTTT 96459                A
                C                GAAACCCCATCTCTACT AAAAT
                                 ||||||||||||||||| |||||
                                 CTTTGGGGTAGAGATGA TTTTA
                                       C
GAM1005  LOC253666 3'  AGTAGAGACGGGGTTTCA    96760          A
                                 TGAAACCCC TCTCTACT
                                 |||||||||  ||||||||
                                 ACTTTGGGG AGAGATGA
                                      C
GAM1005  LOC253805 3'  ATTTTTAGTGGAGATAGGGTTT 98168          C
                CA               TGAAACCC ATCTCTACTAAAAAT
                                 ||||||||  ||||||||||||||||
                                 ACTTTGGG TAGAGGTGATTTTTA
                                     A
GAM1005  LOC253842 5'  ATTTTTAGTAGAAACATTGTTT 99234        CCCATC
                CA               TGAAAC     TCTACTAAAAAT
                                 ||||||     ||||||||||||
                                 ACTTTG     AGATGATTTTTA
                                   TTACAA
GAM1005  LOC253981 3'  ATTTTTAGGAGAGACGGGGTTT 97530          A    A
                CA               TGAAACCCC TCTCT CTAAAAAT
                                 |||||||||  |||||  ||||||||
                                 ACTTTGGGG AGAGA GATTTTTA
                                      C    G
GAM1005  LOC253981 3'  ATTTTTAGTAGAGACGGGGTAT 97531     A    A
                CA               TGA ACCCC TCTCTACTAAAAAT
                                 |||  |||||  ||||||||||||||
                                 ACT TGGGG AGAGATGATTTTTA
                                   A    C
GAM1005  LOC254018 5'  TTTTTAGTAGAGATGGGGTTTC 98745
                                 GAAACCCCATCTCTACTAAAAA
                                 |||||||||||||||||||||
                                 CTTTGGGGTAGAGATGATTTTT

GAM1005  LOC254100 3'  ATTTTTTGTAGAGATGGGGTTT 98147                T
                C                GAAACCCCATCTCTAC AAAAAT
                                 ||||||||||||||||  ||||||
                                 CTTTGGGGTAGAGATG TTTTTA
                                       T
GAM1005  LOC254268 3'  ATTTTTGGTAGAGATGGGGTTT 97139
                CA               TGAAACCCCATCTCTACTAAAAAT
                                 |||||||||||||||||||||||
                                 ACTTTGGGGTAGAGATGGTTTTTA

GAM1005  LOC254295 5'  ATTTTTAGTAGAGACGGGGTTT 97888          A
                CA               TGAAACCCC TCTCTACTAAAAAT
                                 |||||||||  ||||||||||||||
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                                ACTTTGGGG AGAGATGATTTTTA
                                     C
GAM1005  LOC254655 3'  ATTTTTAGTAGAGACGGGGTTT 97215          A
              CA                  TGAAACCCC TCTCTACTAAAAAT
                                  ||||||||| ||||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                       C
GAM1005  LOC254672 3'  ATTTTTAGTAGAGGCAAGGTTT 96290        CCA
              CA                  TGAAACC   TCTCTACTAAAAAT
                                  |||||||   ||||||||||||||
                                  ACTTTGG   GGAGATGATTTTTA
                                     AAC
GAM1005  LOC255308 3'  TTAGTAGAGACGGGGTTTC    96181         A
                                  GAAACCCC TCTCTACTAA
                                  |||||||| ||||||||||
                                  CTTTGGGG AGAGATGATT
                                       C
GAM1005  LOC255465 3'  ATTTTTAGTAGAGACGGGTTTC 99103         CA
              A                    TGAAACCC  TCTCTACTAAAAAT
                                   |||||||| ||||||||||||||
                                   ACTTTGGG  AGAGATGATTTTTA
                                       C_
GAM1005  LOC255497 3'  ATTTTTAGTAGAGACGGGGTTT 98984          A
              CA                  TGAAACCCC TCTCTACTAAAAAT
                                  ||||||||| ||||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                       C
GAM1005  LOC255927 5'  ATTTGTAGTAGAGACGGGGTTT 97710          A        A
              CA                  TGAAACCCC TCTCTACTA AAAT
                                  ||||||||| ||||||||| ||||
                                  ACTTTGGGG AGAGATGAT TTTA
                                       C        G
GAM1005  LOC256221 3'  TTTTTAGTAGAGACGGGGTTTC 96923          A
              A                    TGAAACCCC TCTCTACTAAAAA
                                   ||||||||| |||||||||||||
                                   ACTTTGGGG AGAGATGATTTTT
                                       C
GAM1005  LOC256267 3'  ATTTTTAGTAGAGATGGG     98605
                                  CCCATCTCTACTAAAAAT
                                  ||||||||||||||||||
                                  GGGTAGAGATGATTTTTA

GAM1005  LOC256306 3'  ATTTTTAGTAGAGACGGGGTTT 98505          A
              CA                  TGAAACCCC TCTCTACTAAAAAT
                                  ||||||||| ||||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                       C
GAM1005  LOC257465 3'  TTTTAGTAGAGATGGTGTTTCA 82505        C
                                  TGAAAC CCATCTCTACTAAAA
                                  |||||| ||||||||||||||
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                                ACTTTG GGTAGAGATGATTTT
                                   T
GAM1005  LOC257486 3'  ATTTTTAGTAGAGACGGGGTTT 69766          A
              CA                  TGAAACCCC TCTCTACTAAAAAT
                                  ||||||||| ||||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                    C
GAM1005  LOC51008  5'  ATTTCTAGTAGAGATGGGGTTT 32529              A
              C                   GAAACCCCATCTCTACTA AAAT
                                  |||||||||||||||||| ||||
                                  CTTTGGGGTAGAGATGAT TTTA
                                           C
GAM1005  LOC51159  5'  TTTTAGTAGAGACGGGATTTCA 33035      C   A
                                  TGAAA CCC TCTCTACTAAAA
                                  ||||| ||| ||||||||||||
                                  ACTTT GGG AGAGATGATTTT
                                     A   C
GAM1005  LOC51193  5'  ATTTTCAGTCGAGACGGGGTTT 33360        A   T   A
              C                   GAAACCCC TCTC ACT AAAAT
                                  |||||||| |||| ||| |||||
                                  CTTTGGGG AGAG TGA TTTTA
                                       C   C   C
GAM1005  LOC51200  3'  TTTTTAGTAGAGACAGGGTTTC 33443        CA
                                  GAAACCC  TCTCTACTAAAAA
                                  |||||||  ||||||||||||
                                  CTTTGGG  AGAGATGATTTTT
                                       AC
GAM1005  LOC51219  5'  ATTTTTAGTGGAGACGGGGTTT 33539        A
              C                   GAAACCCC TCTCTACTAAAAAT
                                  |||||||| ||||||||||||||
                                  CTTTGGGG AGAGGTGATTTTTA
                                       C
GAM1005  LOC51696  3'  ATTTTTAGTAGAGACAGCGTTT 33078       CCCA
              CA                    TGAAAC    TCTCTACTAAAAAT
                                    ||||||    ||||||||||||||
                                    ACTTTG    AGAGATGATTTTTA
                                       CGAC
GAM1005  LOC56181  5'  ATTTTTAGTAGAGACAGGGCTT 97270      A   CA
              CA                    TGAA CCC  TCTCTACTAAAAAT
                                    |||| |||  ||||||||||||||
                                    ACTT GGG  AGAGATGATTTTTA
                                      C   AC
GAM1005  LOC57107  3'  ATTTTTAGTAGAGATGGGGTTT 40181
              CA                    TGAAACCCCATCTCTACTAAAAAT
                                    |||||||||||||||||||||||||
                                    ACTTTGGGGTAGAGATGATTTTTA

GAM1005  LOC57146  3'  TTTTTAGTACAGATGGGGTTTC 40301            C
              A                     TGAAACCCCATCT TACTAAAAA
                                    |||||||||||| |||||||||
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                                ACTTTGGGGTAGA ATGATTTTT
                                      C
GAM1005  LOC81034  3'  ATTTTGAGTAGAAATGGGGTTT 48585          C     A
                CA                TGAAACCCCAT TCTACT AAAAT
                                  |||||||||||| |||||| |||||
                                  ACTTTGGGGTA AGATGA TTTTA
                                        A     G
GAM1005  LOC89919  3'  ATTTTTATTAGAGACGGGGTTT 61371          A     C
                CA                TGAAACCCC TCTCTA TAAAAAT
                                  ||||||||| |||||| |||||||
                                  ACTTTGGGG AGAGAT ATTTTTA
                                       C     T
GAM1005  LOC89932  3'  ATTTTTAGTAGAGACGGGGTTT 61448          A
                C                  GAAACCCC TCTCTACTAAAAAT
                                   |||||||| ||||||||||||||
                                   CTTTGGGG AGAGATGATTTTTA
                                       C
GAM1005  LOC89932  3'  ATTTTTAGTTGAGATGGGGTTT 61449             T
                CA                TGAAACCCCATCTC ACTAAAAAT
                                  |||||||||||||| |||||||||
                                  ACTTTGGGGTAGAG TGATTTTTA
                                         T
GAM1005  LOC90288  3'  ATTTTTAGTAGAGACGGGGTTT 62774          A
                CA                TGAAACCCC TCTCTACTAAAAAT
                                  ||||||||| |||||||||||||
                                  ACTTTGGGG AGAGATGATTTTTA
                                       C
GAM1005  LOC90288  3'  ATTTTTAGTAGAGATGGGGTTT 62775
                CA                TGAAACCCCATCTCTACTAAAAAT
                                  |||||||||||||||||||||||
                                  ACTTTGGGGTAGAGATGATTTTTA

GAM1005  LOC90333  3'  TTTTTAGTAGAGACTGGGTTTC 62970         CA
                A                  TGAAACCC  TCTCTACTAAAAA
                                   |||||||  ||||||||||||
                                   ACTTTGGG  AGAGATGATTTTT
                                       TC
GAM1005  LOC90459  3'  ATTTTTGGTAGAGGCGGGGTTT 63548          AT
                CA                TGAAACCCC  CTCTACTAAAAAT
                                  |||||||||  |||||||||||||
                                  ACTTTGGGG  GAGATGGTTTTTA
                                       CG
GAM1005  LOC90485  3'  ATTTTTAGTAGAGGCAGGGTTT 63689         CA
                CA                TGAAACCC  TCTCTACTAAAAAT
                                  |||||||  ||||||||||||||
                                  ACTTTGGG  GGAGATGATTTTTA
                                       AC
GAM1005  LOC90485  3'  TTTTAGTAGAGGCGGGGTTTCA 63717          AT
                                  TGAAACCCC  CTCTACTAAAA
                                  |||||||||  ||||||||||
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                                ACTTTGGGG  GAGATGATTTT
                                     CG
GAM1005  LOC90591  3'  ATTTTTAGTAGAGACGGGGCTT 64149      A    A
             CA                   TGAA CCCC TCTCTACTAAAAAT
                                  |||| |||| ||||||||||||||
                                  ACTT GGGG AGAGATGATTTTTA
                                    C    C
GAM1005  LOC90591  3'  ATTTTTAGTAGAGATGAGGTCT 64150     A   C
             CA                   TGA ACC CATCTCTACTAAAAAT
                                  ||| ||| ||||||||||||||||
                                  ACT TGG GTAGAGATGATTTTTA
                                    C   A
GAM1005  LOC90591  3'  TTTTTAGTAGAGACGGAGTTTC 64199       C  A
             A                     TGAAAC CC TCTCTACTAAAAA
                                  |||||| || ||||||||||||
                                  ACTTTG GG AGAGATGATTTTT
                                     A  C
GAM1005  LOC90784  5'  ATTTTTAGTAGAGATGGGGTTT 64691
             CA                   TGAAACCCCATCTCTACTAAAAAT
                                  |||||||||||||||||||||||||
                                  ACTTTGGGGTAGAGATGATTTTTA

GAM1005  LOC91115  3'  ATTTTTAGTAGAGATGGGGTTT 65550
             CA                   TGAAACCCCATCTCTACTAAAAAT
                                  |||||||||||||||||||||||||
                                  ACTTTGGGGTAGAGATGATTTTTA

GAM1005  LOC91115  3'  ATTTTTAGTAGAGATGGGGTTT 65551
             CA                   TGAAACCCCATCTCTACTAAAAAT
                                  |||||||||||||||||||||||||
                                  ACTTTGGGGTAGAGATGATTTTTA

GAM1005  LOC91250  5'  ATTTTTAGTAGAGATGGGGTTT 65908
             CA                   TGAAACCCCATCTCTACTAAAAAT
                                  |||||||||||||||||||||||||
                                  ACTTTGGGGTAGAGATGATTTTTA

GAM1005  LOC91291  5'  TTTTAGTAGAGACAAGGTTTCA 66096       CCA
                                  TGAAACC   TCTCTACTAAAA
                                  |||||||   ||||||||||||
                                  ACTTTGG   AGAGATGATTTT
                                     AAC
GAM1005  LOC91308  3'  ATTTTTAGTAGAGACGGGGTTT 66162       A
                                  AAACCCC TCTCTACTAAAAAT
                                  ||||||| ||||||||||||||
                                  TTTGGGG AGAGATGATTTTTA
                                     C
GAM1005  LOC91373  3'  ATTTTTAGTAGAGATGGGGTTT 66408
                                  AAACCCCATCTCTACTAAAAAT
                                  |||||||||||||||||||||
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                                TTTGGGGTAGAGATGATTTTTA

GAM1005 LOC91893 3' ATTTTTAGTAGAGACGAGGTTT 68068       CCA
             CA                  TGAAACC  TCTCTACTAAAAAT
                                 |||||||  ||||||||||||||
                                 ACTTTGG  AGAGATGATTTTTA
                                    AGC
GAM1005 LOC91963 3' ATTTTTTGTAGAGGTGAGGTCT 68312    A  C       T
             CA                  TGA ACC CATCTCTAC AAAAAT
                                 ||| ||| ||||||||| ||||||
                                 ACT TGG GTGGAGATG TTTTTA
                                   C  A       T
GAM1005 LOC92148 5' TTTTTAGGAGAGACGGGGTTTC 68891        A    A
             A                   TGAAACCCC TCTCT CTAAAAA
                                 |||||||||| ||||| |||||||
                                 ACTTTGGGG AGAGA GATTTTT
                                      C    G
GAM1005 LOC92267 3' ATTTTTAGTAGAGATGGGGTTT 69164
             CA                  TGAAACCCCATCTCTACTAAAAAT
                                 |||||||||||||||||||||||||
                                 ACTTTGGGGTAGAGATGATTTTTA

GAM1005 LOC92303 3' ATTTTCAGTAGAGATGGGTTTC 69386       C       A
             A                   TGAAACCC ATCTCTACT AAAAT
                                 |||||||| ||||||||| |||||
                                 ACTTTGGG TAGAGATGA TTTTA
                                      _       C
GAM1005 LOC92466 3' ATTTTTAGTAGAGATGGG    69961
                                 CCCATCTCTACTAAAAAT
                                 |||||||||||||||||
                                 GGGTAGAGATGATTTTTA

GAM1005 LOC92661 5' ATTTTTAGTAGAGGCGGGGTTT 70619        AT
             CA                  TGAAACCCC  CTCTACTAAAAAT
                                 |||||||||  ||||||||||||
                                 ACTTTGGGG  GAGATGATTTTTA
                                      CG
GAM1005 LOC92689 3' ATTTTTAGTAGAGACAGGGTTT 70771        CA
             CA                  TGAAACCC  TCTCTACTAAAAAT
                                 ||||||||  ||||||||||||||
                                 ACTTTGGG  AGAGATGATTTTTA
                                    AC
GAM1005 LOC92697 5' ATTTTTAGTACAGATAGGGTTT 70804       C    C
             C                    GAAACCC ATCT TACTAAAAAT
                                 ||||||| |||| ||||||||||
                                 CTTTGGG TAGA ATGATTTTTA
                                    A   C
GAM1005 LOC92697 5' TTTTTGGTGGAGACGGGGTTTC 70820        A
                                 GAAACCCC TCTCTACTAAAAA
                                 |||||||| |||||||||||||
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                                CTTTGGGG AGAGGTGGTTTTT
                                     C
GAM1005  LOC92841  3'  AGTAGAGACGGGGTTTCA    71247          A
                                TGAAACCCC TCTCTACT
                                ||||||||| ||||||||
                                ACTTTGGGG AGAGATGA
                                     C
GAM1005  LOC92841  3'  TTTTAGTAGAGACAGGGTTTCA 71267         CA
                                TGAAACCC  TCTCTACTAAAA
                                ||||||||  ||||||||||||
                                ACTTTGGG  AGAGATGATTTT
                                     AC
GAM1005  LOC93129  3'  TTTTTTGTAGAGACGGGGTTTC 71960         A      T
                                GAAACCCC TCTCTAC AAAAA
                                |||||||| ||||||| |||||
                                CTTTGGGG AGAGATG TTTTT
                                     C      T
GAM1005  LOC93349  3'  ATTTTTAGTAGAGACGGGGTTT 57264          A
            CA                    TGAAACCCC TCTCTACTAAAAAT
                                |||||||||| ||||||||||||||
                                ACTTTGGGG AGAGATGATTTTTA
                                     C
GAM1006  CDH12     3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM1006  GOCAP1    3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC         G
GAM1006  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT    98090       T    AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT     TTATTC
                                   _    GTCA_
GAM1006  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
            A                    TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM1006  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM1006  HMP19     3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
            TA                    TACA    TCC    GAAGAATAAG
                                ||||    |||    ||||||||||
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                                ATGT   AGG   TTTCTTATTC
                                  AAA_  ATTG
GAM1006 KIAA1719 3' TCTGTCTTGGGAGTGGTGTA  68742           _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                         G
GAM1006 KIAA1853 3' TTTTTCTTGGAAGCAGTG   69929    CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM1006 KIAA1877 3' CTTATTCTTCTGCCATGAGT  66748     CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM1006 KIAA1906 3' CTTATTCTTCTTGACTTTTGG 73571    CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM1006 OSBPL11  3' CTTAATTTCCCAAGAGTGGTG 43206       CCAA   AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                     AACC   A_
GAM1006 YME1L1   3' TCATTCTTGATGTGGTGTA   58438       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                     TA_    A
GAM1006 ZNF262   3' CTTATTTTGTTTGGGAGT    18723        A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                     G
GAM1006 LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_    AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
                                ATGTGGTG   GGTTC   TGT
                                     CAA    GG__
GAM1007 CDH12    3' CTTATCATTTAAAGTGGTGTA 15777       CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM1007 GOCAP1   3' ATTGTTCTTGGGAGCAGTGTA 43007      CA       G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
```

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                                ATGTG  GAGGGTTCTT TTA
                                   AC         G
GAM1007  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT    98090       T    AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||     ||||||
                                TGGTG GGGT     TTATTC
                                   _    GTCA_
GAM1007  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
            A                    TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM1007  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM1007  HMP19     3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
            TA                    TACA    TCC    GAAGAATAAG
                                ||||    |||    ||||||||||
                                ATGT    AGG    TTTCTTATTC
                                   AAA_   ATTG
GAM1007  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68742             _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                         G
GAM1007  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM1007  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748      CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM1007  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM1007  OSBPL11   3'  CTTAATTTCCCAAGAGTGGTG  43206         CCAA    AA
                                CACCACTC    GAAG  TAAG
                                ||||||||    ||||  ||||
                                GTGGTGAG    CTTT  ATTC
                                     AACC    A_
GAM1007  YME1L1    3'  TCATTCTTGATGTGGTGTA    58438         TCC     _
                                TACACCAC   CAAGAA GA
                                ||||||||   |||||| ||
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                                ATGTGGTG  GTTCTT CT
                                    TA_     A
GAM1007 ZNF262   3' CTTATTTTGTTTGGGAGT    18723         A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                    G
GAM1007 LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294        TC_    AAGA
                                TACACCAC  CCAAG   ATA
                                ||||||||  |||||   |||
                                ATGTGGTG  GGTTC   TGT
                                    CAA    GG__
GAM1008 ADRB3    3' GTTCTCCAGGCTCTGTGGCCCA 5250      C    C  A
          G                      CTG GCTAC AGA CCTGGAGAAC
                                ||| ||||| ||| ||||||||||
                                GAC CGGTG TCT GGACCTCTTG
                                  C    _  C
GAM1008 CKTSF1B1 3' CTCCAGACTCTGGGAGAGGC  26293    G_ A    AC
                                GC  CT CCAGA  CTGGAG
                                ||  || |||||  ||||||
                                CG  GA GGTCT  GACCTC
                                 GA  G    CA
GAM1008 CPS1     3' TCTCCAGGCTGGAGTGCAG   10288       A   AA
                                CTGCGCT CCAG  CCTGGAGA
                                ||||||| ||||  ||||||||
                                GACGTGA GGTC  GGACCTCT
                                    _   __
GAM1008 FUS      3' TCCCCAGGTTCTGGAACAGC  18278    A__        A
                                GCT   CCAGAACCTGG GA
                                |||   |||||||||| ||
                                CGA   GGTCTTGGACC CT
                                  CAA         C
GAM1008 HTR3B    5' TTCCATCTGGTAGGCA     21218    G      ACC
                                TGC CTACCAGA   TGGAG
                                ||| ||||||||   |||||
                                ACG GATGGTCT   ACCTT
                                   _      ___
GAM1008 KLK8     5' TCCCCAGGCTCTAGTGCAG   24212       ACC  A    A
                                CTGCGCT   AGA CCTGG GA
                                |||||||   ||| ||||| ||
                                GACGTGA   TCT GGACC CT
                                    ___   C    C
GAM1008 KLK8     5' TCCCCAGGCTCTAGTGCAG   58585       ACC  A    A
                                CTGCGCT   AGA CCTGG GA
                                |||||||   ||| ||||| ||
                                GACGTGA   TCT GGACC CT
                                    ___   C    C
GAM1008 KLK8     5' TCCCCAGGCTCTAGTGCAG   58586       ACC  A    A
                                CTGCGCT   AGA CCTGG GA
                                |||||||   ||| ||||| ||
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                                GACGTGA   TCT GGACC CT
                                   ___  C    C
GAM1008  KLK8    5'  TCCCCAGGCTCTAGTGCAG   58587       ACC  A    A
                                CTGCGCT   AGA CCTGG GA
                                |||||||   ||| ||||| ||
                                GACGTGA   TCT GGACC CT
                                   ___  C    C
GAM1008  LHX4    3'  TCAGTGCTTTGGTAGCACA   54044    C       AC_
                                TG GCTACCAGA   CTGG
                                || |||||||||   ||||
                                AC CGATGGTTT   GACT
                                 A        CGT
GAM1008  MEF2A   5'  CCAGGCTGAAGTGCAG     19994       AC   AA
                                CTGCGCT  CAG  CCTGG
                                |||||||  |||  |||||
                                GACGTGA  GTC  GGACC
                                   A_  __
GAM1008  NR2E1   5'  TTGGGTTCCGGCAGCGCGG   13794       A  A    TG
                                CTGCGCT CC GAACC  G
                                ||||||| || |||||  |
                                GGCGCGA GG CTTGG  T
                                   C  C    GT
GAM1008  NRG2    5'  CTCCAGGTCCTGGCGCACAG   18081    C  TA   A
                                CTG GC  CCAG ACCTGGAG
                                |||  ||  |||| ||||||||
                                GAC CG  GGTC TGGACCTC
                                  A  C_   C
GAM1008  NRG2    5'  CTCCAGGTCCTGGCGCACAG   26534    C  TA   A
                                CTG GC  CCAG ACCTGGAG
                                |||  ||  |||| ||||||||
                                GAC CG  GGTC TGGACCTC
                                  A  C_   C
GAM1008  NRG2    5'  CTCCAGGTCCTGGCGCACAG   26535    C  TA   A
                                CTG GC  CCAG ACCTGGAG
                                |||  ||  |||| ||||||||
                                GAC CG  GGTC TGGACCTC
                                  A  C_   C
GAM1008  NRG2    5'  CTCCAGGTCCTGGCGCACAG   26536    C  TA   A
                                CTG GC  CCAG ACCTGGAG
                                |||  ||  |||| ||||||||
                                GAC CG  GGTC TGGACCTC
                                  A  C_   C
GAM1008  NRG2    5'  CTCCAGGTCCTGGCGCACAG   26537    C  TA   A
                                CTG GC  CCAG ACCTGGAG
                                |||  ||  |||| ||||||||
                                GAC CG  GGTC TGGACCTC
                                  A  C_   C
GAM1008  NRG2    5'  CTCCAGGTCCTGGCGCACAG   26538    C  TA   A
                                CTG GC  CCAG ACCTGGAG
                                |||  ||  |||| ||||||||
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                                GAC CG  GGTC TGGACCTC
                                  A  C_   C
GAM1008  OGT     5'  TTGGGTTCTGGTGGCGCAG   14598            TG
                                CTGCGCTACCAGAACC  G
                                |||||||||||||||  |
                                GACGCGGTGGTCTTGG  T
                                          GT
GAM1008  P2RY6   3'  CTCCAGGTCCTGGGCAG    15996     GCTA   A
                                CTGC   CCAG ACCTGGAG
                                ||||   |||| ||||||||
                                GACG   GGTC TGGACCTC
                                  ____   C
GAM1008  PTGFR   3'  TTCCAGGTCTGGCAGACAG   8179     CG  A    A
                                CTG  CT CCAGA CCTGGAG
                                |||  || ||||| |||||||
                                GAC  GA GGTCT GGACCTT
                                  A_  C    _
GAM1008  PTGIS   3'  GTTCTCCAGATGGAGAAACAG  8224     CG_  A   GAAC
                                CTG   CT CCA   CTGGAGAAC
                                |||   || |||   |||||||||
                                GAC   GA GGT   GACCTCTTG
                                  AAA  _   A___
GAM1008  STX7    3'  TTTTTCTGGTTCACAACAGCAC 14543    C   ACCA_    T
           A                     TG GCT    GAACC GGAGAA
                                || |||    ||||| ||||||
                                AC CGA    CTTGG CTTTTT
                                 A  CAACA    T
GAM1008  TCP10   3'  TCAGGGCTCCAATAGTGCAG   17239        CCA  A_
                                CTGCGCTA   GA  CCTGG
                                ||||||||   ||  |||||
                                GACGTGAT   CT  GGACT
                                     AAC  CG
GAM1008  C20orf59  5'  GTTCCCATCCTGGTAGCCCAG  42235     C       AACC   A
                                CTG GCTACCAG    TGG GAAC
                                ||| ||||||||    ||| ||||
                                GAC CGATGGTC    ACC CTTG
                                  C       CT__   _
GAM1008  DKFZP586B2420 3'  TCCCTGTGGCTACAGTAGCGCA 75490         C__  A_  CT
           G                     CTGCGCTAC   AG  AC  GGA
                                |||||||||   ||  ||  |||
                                GACGCGATG   TC  TG  CCT
                                     ACA  GG  TC
GAM1008  FLJ23392  3'  CCAGGCTGGAGTGCAG     45885        A   AA
                                CTGCGCT CCAG  CCTGG
                                ||||||| ||||  |||||
                                GACGTGA GGTC  GGACC
                                       _   __
GAM1008  FLJ30092  3'  GTTCTCCAGCCTGGGCAACAG  59341     C_  TA   AAC
                                CTG  GC  CCAG   CTGGAGAAC
                                |||  ||  ||||   |||||||||
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                                GAC  CG  GGTC   GACCTCTTG
                                  AA  __   C__
GAM1008 HN1L     3' GTTCTCCAGTGATGTAGACAG  58619    CG   CAGAAC
                                CTG  CTAC     CTGGAGAAC
                                |||  ||||     |||||||||
                                GAC  GATG     GACCTCTTG
                                  A_   TAGT__
GAM1008 IL14     5' TTCTCCAGGTCCCTTGTTCCAG 97166    CGCT  C  A_
                                CTG   AC AG  ACCTGGAGAA
                                |||   || ||  ||||||||||
                                GAC   TG TC  TGGACCTCTT
                                  CT__  T  CC
GAM1008 KIAA0557 3' CCCGGTTCTGGCGGCACAG   78550    C  TA      T
                                CTG GC  CCAGAACC GG
                                ||| ||  |||||||| ||
                                GAC CG  GGTCTTGG CC
                                  A  GC       C
GAM1008 KIAA0806 5' CTCCTTTTCTAGCAGGCAG   29720     __  ACC   CCT
                                CTGC  GCT   AGAA   GGAG
                                ||||  |||   ||||   ||||
                                GACG  CGA   TCTT   CCTC
                                   GA   ___    TT_
GAM1008 KIAA0913 3' TCAGTTCCCTGGTAGCACAG  69534    C      AAC_
                                CTG GCTACCAG    CTGG
                                ||| ||||||||    ||||
                                GAC CGATGGTC    GACT
                                  A       CCTT
GAM1008 KIAA1691 3' GTTCTCCAGGCCTAGGGCCAG  94135    C   ACC  AA
                                CTG GCT   AG  CCTGGAGAAC
                                ||| |||   ||  ||||||||||
                                GAC CGG   TC  GGACCTCTTG
                                  _   GA_  C_
GAM1008 MRPL10   3' TTCTCCAGGTCCAAGGCAG   59834     G  ACCA  A
                                CTGC CT    GA CCTGGAGAA
                                |||| ||    || |||||||||
                                GACG GA    CT GGACCTCTT
                                  _  AC__  _
GAM1008 MY050    3' TTCTCCAGCGGCAGGGCAG   51918     G  A  AGAAC
                                CTGC CT CC    CTGGAGAA
                                |||| || ||    ||||||||
                                GACG GA GG    GACCTCTT
                                  G  C  C____
GAM1008 PRKWNK2  5' CAGCGCTGGTAGCGCAG     92192          AAC
                                CTGCGCTACCAG   CTG
                                ||||||||||||   |||
                                GACGCGATGGTC   GAC
                                       GC_
GAM1008 RYBP     5' TTCTCAGCTGGTGGCACA    60176    C      AACCTG
                                TG GCTACCAG     GAGAA
                                || ||||||||     |||||
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                                AC CGGTGGTC     CTCTT
                                 A       GA____
GAM1008  SPINT1   3'  GTTCTCCAACATCACAGCCCAG 63334     C   ACCA  ACC
                                CTG GCT    GA   TGGAGAAC
                                ||| |||    ||   ||||||||
                                GAC CGA    CT   ACCTCTTG
                                  C   CA__  ACA
GAM1008  SREC     3'  CCAGGCTGGAGTGCAG      14899        A    AA
                                CTGCGCT CCAG  CCTGG
                                ||||||| ||||  |||||
                                GACGTGA GGTC  GGACC
                                      _   __
GAM1008  TAF5L    3'  TTCAGAGAATTTGGTAGCACAG 27725     C        AC__
                                CTG GCTACCAGA    CTGGA
                                ||| |||||||||    |||||
                                GAC CGATGGTTT    GACTT
                                  A        AAGA
GAM1008  USP8     5'  TTCCGTCCTGGTAGCCA     18942    C       A  CT
                                TG GCTACCAG AC  GGAG
                                || ||||||||  ||  ||||
                                AC CGATGGTC TG  CCTT
                                 _       C  __
GAM1008  LOC139770 3'  TTCTCCAGGTTGTTGC      75908    T  CAG
                                GC AC   AACCTGGAGAA
                                || ||   ||||||||||
                                CG TG   TTGGACCTCTT
                                 T  ____
GAM1008  LOC143677 3'  GTTCTCCAGATCCCGTGGC    83899      CA  AC
                                GCTAC  GA  CTGGAGAAC
                                |||||  ||  |||||||||
                                CGGTG  CT  GACCTCTTG
                                   CC  A_
GAM1008  LOC149706 5'  CTCGGTTCTCCAACAGCCCAG  85802     C   ACC__     TG
                                CTG GCT    AGAACC  GAG
                                ||| |||    ||||||  |||
                                GAC CGA    TCTTGG  CTC
                                  C   CAACC     __
GAM1008  LOC153364 5'  CCCCGTGCTGGTGGCGCAG    81679           A  CT
                                CTGCGCTACCAG AC  GG
                                |||||||||||| ||  ||
                                GACGCGGTGGTC TG  CC
                                       G  CC
GAM1008  LOC154860 5'  CTCGGTTCAGGTAGCACA    87502    C     A    TG
                                TG GCTACC GAACC  GAG
                                || |||||| |||||  |||
                                AC CGATGG CTTGG  CTC
                                 A     A    __
GAM1008  LOC157931 3'  TCTCCAGGCCCCCATGGGCCAG 87945     C  TA   GAA___
                                CTG GC  CCA     CCTGGAGA
                                ||| ||  |||     ||||||||
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                                GAC CG  GGT     GGACCTCT
                                  _ __   ACCCCC
GAM1008  LOC158056 5'  TCTCCAGGCCCCAGGTGCCAG  82597     C  T   AGAA_
                                CTG GC ACC    CCTGGAGA
                                ||| || |||    ||||||||
                                GAC CG TGG    GGACCTCT
                                  _ _  ACCCC
GAM1008  LOC164173 5'  CTCCCGGGCTGGTAGCGC    83053         AA  T
                                GCGCTACCAG  CC GGAG
                                ||||||||||  || ||||
                                CGCGATGGTC  GG CCTC
                                      G_  C
GAM1008  LOC202052 3'  TCTCCAGGCTGTTTGCTCA   91904    C  TAC   AA
                                TG GC   CAG  CCTGGAGA
                                || ||   |||  ||||||||
                                AC CG   GTC  GGACCTCT
                                 T  TTT  __
GAM1008  LOC219722 5'  TTCTCCAGAGCTAGCACAG   94693     C   ACC  AAC
                                CTG GCT   AG   CTGGAGAA
                                ||| |||   ||   ||||||||
                                GAC CGA   TC   GACCTCTT
                                  A   ____  GA_
GAM1008  LOC220846 3'  GTTCTCCAGGCTCTGTGGCCCA 92485     C    C   A
           G                     CTG GCTAC AGA CCTGGAGAAC
                                ||| ||||| ||| ||||||||||
                                GAC CGGTG TCT GGACCTCTTG
                                  C    _  C
GAM1008  LOC221540 3'  CTCCAGGTCTTGGAAGACAG   95478    CG  A   GA
                                CTG  CT CCA  ACCTGGAG
                                |||  || |||  ||||||||
                                GAC  GA GGT  TGGACCTC
                                  A_  A   TC
GAM1008  LOC255743 5'  TCCAGGTGTTCTGGTACACAG  97604     CGC     __
                                CTG   TACCAGA  ACCTGGA
                                |||   |||||||  |||||||
                                GAC   ATGGTCT  TGGACCT
                                  AC_      TG
GAM1008  LOC256542 5'  CTCATTTCTCATAGCGCAG   97289        CC   CCTG
                                CTGCGCTA  AGAA    GAG
                                ||||||||  ||||    |||
                                GACGCGAT  TCTT    CTC
                                     AC    TA__
GAM1008  LOC257545 3'  CTCCAGGTCTTGGAAGACAG   99642     CG  A   GA
                                CTG  CT CCA  ACCTGGAG
                                |||  || |||  ||||||||
                                GAC  GA GGT  TGGACCTC
                                  A_  A   TC
GAM1008  LOC257598 3'  CTCCAGGTCTTGGAAGACAG   99750     CG  A   GA
                                CTG  CT CCA  ACCTGGAG
                                |||  || |||  ||||||||
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                                GAC  GA GGT  TGGACCTC
                                  A_  A   TC
GAM1008  LOC51333  3'  GTTCTCCAGGCTCAGGTGCCA  34056    C  T   A  A
                                TG GC ACC GA CCTGGAGAAC
                                || || ||| || ||||||||||
                                AC CG TGG CT GGACCTCTTG
                                 _ _   A  C
GAM1008  LOC90110  5'  TTCTCCAGCCTGGGCAACGGAG 62183    G  CTA_   AAC
                                CT CG    CCAG   CTGGAGAA
                                || ||    ||||   ||||||||
                                GA GC    GGTC   GACCTCTT
                                 G  AACG   C__
GAM1008  LOC90170  5'  CCTGTTCTGGTGCACAG     62375     C  T       CT
                                CTG GC ACCAGAAC  GG
                                ||| || ||||||||  ||
                                GAC CG TGGTCTTG  CC
                                  A  _       T_
GAM1008  LOC91960  3'  GTTCTCCAAGCTGCTGGCACAG 68291     C    C   AACC
                                CTG GCTA CAG    TGGAGAAC
                                ||| |||| |||    ||||||||
                                GAC CGGT GTC    ACCTCTTG
                                  A   C   GA__
GAM1009  AIRE     3'  TGGGAGCCTGAGGCATGAGAA  7247      C     C
                                TTC CATGCC CAGGCTCCTG
                                ||| |||||| ||||||||||
                                AAG GTACGG GTCCGAGGGT
                                  A     A
GAM1009  BCAS1    3'  CTCGGGAGCCCAACGCACGAGA 14711     CCA   CCCA      C
             A                   TTC   TGC    GGCTCCTG AG
                                |||   |||    |||||||| ||
                                AAG   ACG    CCGAGGGC TC
                                  AGC   CAAC       _
GAM1009  DAG1     3'  CTGCAGGATGTAACATGG    16553       CCCCAG  _
                                CCATG     GC TCCTGCAG
                                |||||     || ||||||||
                                GGTAC     TG AGGACGTC
                                   AA____  T
GAM1009  GPRK7    3'  CGGGAGCCTGAGGCAGGAGAA  58313     _  A   C
                                TTC CC TGCC CAGGCTCCTG
                                ||| || |||| ||||||||||
                                AAG GG ACGG GTCCGAGGGC
                                  A  _    A
GAM1009  KIF1B    3'  TGGGAGCCTGAGGCAGGAGAA  31273     _  A   C
                                TTC CC TGCC CAGGCTCCTG
                                ||| || |||| ||||||||||
                                AAG GG ACGG GTCCGAGGGT
                                  A  _    A
GAM1009  NCAM1    5'  CTGCAGGGGGGGGGGCACAGAA 7040      CCA     AGG
                                TTC   TGCCCC   CTCCTGCAG
                                |||   ||||||   |||||||||
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                                AAG  ACGGGG  GGGGACGTC
                                  AC_    GG_
GAM1009 NOS1    3' CTGCAGGGTCCCCAAGGATGG 7095     G CCA_ CT
                                CCAT CC   GG CCTGCAG
                                |||| ||   || |||||||
                                GGTA GG   CC GGACGTC
                                  _ AACC TG
GAM1009 PDGFRB  3' TGCCCCAGGGACATGGGAA  66584      _  CA CTCCT
                                TTCCCATG CCC GG   GCA
                                |||||||| ||| ||   |||
                                AAGGGTAC GGG CC   CGT
                                    A AC _____
GAM1009 RAB31   3' CTGCAGGGGGCGGGGCAGGAA 23440    CA    AGG
                                TTCC TGCCCC  CTCCTGCAG
                                ||||  ||||||  |||||||||
                                AAGG ACGGGG  GGGGACGTC
                                  __    CG_
GAM1009 SCN4A   3' CTGCGTTCCCAGACCATGGGAA 6200       CCCCA CTCC
                                TTCCCATG   GG  TGCAG
                                ||||||||   ||  |||||
                                AAGGGTAC   CC  GCGTC
                                    CAGAC TT__
GAM1009 WHSC1   3' CTGCAATGACTGCAGGGCTGGG 24667     T  __ GCTCC
          AA                  TTCCCA GCCC CAG   TGCAG
                              |||||| |||| |||   |||||
                              AAGGGT CGGG GTC   ACGTC
                                 _  AC  AGTA_
GAM1009 WHSC1   3' CTGCAATGACTGCAGGGCTGGG 24668     T  __ GCTCC
          AA                  TTCCCA GCCC CAG   TGCAG
                              |||||| |||| |||   |||||
                              AAGGGT CGGG GTC   ACGTC
                                 _  AC  AGTA_
GAM1009 WHSC1   3' CTGCAATGACTGCAGGGCTGGG 24669     T  __ GCTCC
          AA                  TTCCCA GCCC CAG   TGCAG
                              |||||| |||| |||   |||||
                              AAGGGT CGGG GTC   ACGTC
                                 _  AC  AGTA_
GAM1009 ZFP36L1 3' CTGCAGGAAGGAAGGCTG   18201   T  __ AGGC
                              CA GCC CC   TCCTGCAG
                              || ||| ||   ||||||||
                              GT CGG GG   AGGACGTC
                               _  AA A___
GAM1009 C20orf64 5' CAAGAGCCCTTCCTGCAGGGAA 54334     A  CCCA__   C
                              TTCCC TGC    GGCTC TG
                              ||||| |||    ||||| ||
                              AAGGG ACG    CCGAG AC
                                 _  TCCTTC   A
GAM1009 DRIL2   3' CTGCAGGGTGTGGGCAGAGAA 22350    CCA   C G  T
                              TTC  TGCCC A GC CCTGCAG
                              |||  ||||| | || |||||||
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                                AAG   ACGGG T TG GGACGTC
                                  AG_     _ G  _
GAM1009  FEM-2    3'  CTGCAGGGCCAAGCCACAGGAA 28312      CAT_  CCCA   T
                                TTCC    GC    GGC CCTGCAG
                                ||||    ||    ||| |||||||
                                AAGG    CG    CCG GGACGTC
                                  ACAC  AA__   _
GAM1009  FLJ10737 3'  CTGCAGTCCAAGCTGAACATGG 37054        CCCCA    C___
           GAA                    TTCCCATG    GGCT    CTGCAG
                                ||||||||    ||||    ||||||
                                AAGGGTAC    TCGA    GACGTC
                                    AAG__    ACCT
GAM1009  FLJ10898 5'  CTGCCAAACCTGCAACATGGGA 60133        CCC    CTCCT
           A                     TTCCCATG   CAGG    GCAG
                                ||||||||   ||||    ||||
                                AAGGGTAC   GTCC    CGTC
                                    AAC    AAAC_
GAM1009  FLJ11618 3'  CTGCAGGGGGAAGAGCCGGGAA 42624      AT  CCCAGG
                                TTCCC  GC     CTCCTGCAG
                                |||||  ||     |||||||||
                                AAGGG  CG     GGGGACGTC
                                  C_  AGAAG_
GAM1009  FLJ12287 5'  TGCCTCTGGGGCCTGGGAA    42564       T       CTCCT
                                TTCCCA GCCCCAGG     GCA
                                |||||| ||||||||     |||
                                AAGGGT CGGGGTCT     CGT
                                   C       C_____
GAM1009  FLJ14129 3'  TGGGAGCCTGGGGCAGGAGAA  48814     _  A
                                TTC CC TGCCCCAGGCTCCTG
                                ||| || ||||||||||||||
                                AAG GG ACGGGGTCCGAGGGT
                                  A  _
GAM1009  KIAA0187 3'  CTGCAGGAGGAGGAACAGAGAA 29250     CCA  CC  AGG
                                TTC   TG  CC   CTCCTGCAG
                                |||   ||  ||   |||||||||
                                AAG   AC  GG   GAGGACGTC
                                  AG_  AA  AG_
GAM1009  KIAA0416 5'  GGAAAGCCTGGGACACAGAA   32093     CCA  C      __
                                TTC   TG CCCAGGC  TCC
                                |||   || |||||||  |||
                                AAG   AC GGGTCCG  AGG
                                  AC_  A      AA
GAM1009  KIAA1266 3'  CTGCAAGGGCGAGCATGGGA   66695        CCCAG    C
                                TCCCATGC    GCTC TGCAG
                                ||||||||    |||| |||||
                                AGGGTACG    CGGG ACGTC
                                    AG___    A
GAM1009  KIAA1483 3'  CTGCAGGGAAAAGGATATAGGA 70434      C   C  CAGG T
           A                     TTCC ATG CC    C CCTGCAG
                                |||| ||| ||    | |||||||
```

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                                AAGG TAT GG    G GGACGTC
                                  A  A  AAAA _
GAM1009  KIAA1706  3'  TGCAGTGAGAGCATGGGA    94372        CCCAGG  _
                                TCCCATGC     CTC CTGCA
                                ||||||||     ||| |||||
                                AGGGTACG     GAG GACGT
                                    A_____   T
GAM1009  KIAA1715  3'  CTCAGGAGCCTGAGGCAGGAGA 68684     _ A   C       C
            A                    TTC CC TGCC CAGGCTCCTG AG
                                 ||| || |||| |||||||||| ||
                                 AAG GG ACGG GTCCGAGGAC TC
                                   A _   A        _
GAM1009  KIAA1981  3'  CAGGAGCCAAGGTCACAGAA   89710     CCA  C  CA
                                 TTC   TG CC  GGCTCCTG
                                 |||   || ||  ||||||||
                                 AAG   AC GG  CCGAGGAC
                                   AC_  T  AA
GAM1009  MCAM      3'  CAGGAACCTGGGGGCCTGTGAA 22457     C  T    _   C
                                 TTC CA GCCCC AGG TCCTG
                                 ||| || ||||| ||| |||||
                                 AAG GT CGGGG TCC AGGAC
                                   T  C    G   A
GAM1009  MRPS24    3'  CTGCAGAGAATGGAAACGTGGG 50130        CC_   GG   C
            AA                   TTCCCATG   CCA  CTC TGCAG
                                 ||||||||   |||  ||| |||||
                                 AAGGGTGC   GGT  GAG ACGTC
                                     AAA   AA   _
GAM1009  MSE55    3'  TGCAGGACAGACATGGGAG    23916        CCCCAGGC
                                 TTCCCATG       TCCTGCA
                                 ||||||||       |||||||
                                 GAGGGTAC       AGGACGT
                                     AGAC____
GAM1009  OS4       3'  CTGCTTTGTGCTAAAAGCATGG 20388         CCCA   TCCT_
            GAA                    TTCCCATGC    GGC    GCAG
                                   |||||||||    |||    ||||
                                   AAGGGTACG    TCG    CGTC
                                        AAAA   TGTTT
GAM1009  PASK      5'  CAGGGTCTCGCCTGGGGCATTA 31405     CC         ____
            GAA                    TTC  ATGCCCCAGGC    TCCTG
                                   |||  ||||||||||    |||||
                                   AAG  TACGGGGTCCG    GGGAC
                                     AT         CTCT
GAM1009  PRO1163   3'  CTGAATGAGCCTGGGGCA    38323          CTG
                                   TGCCCCAGGCTC   CAG
                                   ||||||||||||   |||
                                   ACGGGGTCCGAG   GTC
                                          TAA
GAM1009  THEA      3'  CTCAGGAAGCTGAGGCACAAGA 66887     CCA   C   GC    C
            A                      TTC   TGCC CAG  TCCTG AG
                                   |||   |||| |||  ||||| ||
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                                AAG   ACGG GTC  AGGAC TC
                                  AAC    A   GA    _
GAM1009  WFDC3    3'  GCTGACCAGAGCATGGGAA   98702        CCCA  C  CT
                                TTCCCATGC    GG TC  GC
                                |||||||||    || ||  ||
                                AAGGGTACG    CC AG  CG
                                     AGA_  _  T_
GAM1009  LOC122726 5'  CTGCAGGAAACACTGAGGCTTG 76103       T   C   GC__
           GGAA                    TTCCCA GCC CAG    TCCTGCAG
                                |||||| ||| |||    ||||||||
                                AAGGGT CGG GTC    AGGACGTC
                                   T   A   ACAA
GAM1009  LOC129303 3'  CTGCAGGAATTGGGGGCTGGGA 75373       T    AG C
           A                     TTCCCA GCCCC  G TCCTGCAG
                                |||||| |||||  | ||||||||
                                AAGGGT CGGGG  T AGGACGTC
                                   _    GT A
GAM1009  LOC132617 5'  CTGCAGATCGAGGCATGGGA   76415        CCA  CTC
                                TCCCATGCC   GG   CTGCAG
                                |||||||||   ||   ||||||
                                AGGGTACGG   CT   GACGTC
                                     AG_  A__
GAM1009  LOC145945 5'  AGGGCCTGGACCATAGAA    84563     CC   CC     T
                                TTC  ATG  CCAGGC CCT
                                |||  |||  |||||| |||
                                AAG  TAC  GGTCCG GGA
                                  A_   CA     _
GAM1009  LOC146332 3'  CAGGAGCCTGGGGCCTGTGGA  78353     _  T
                                TCC CA GCCCCAGGCTCCTG
                                ||| || ||||||||||||||
                                AGG GT CGGGGTCCGAGGAC
                                  T  C
GAM1009  LOC146714 5'  TGCAGGGCAGGCACAGGGA   84754      A_   CCAG  T
                                TCCC  TGCC    GC CCTGCA
                                ||||  ||||    || ||||||
                                AGGG  ACGG    CG GGACGT
                                   AC    A___  _
GAM1009  LOC147958 3'  CTGCAGGGCAGGCAGCAGAA   88523     CCA    CCAG  T
                                TTC   TGCC    GC CCTGCAG
                                |||   ||||    || |||||||
                                AAG   ACGG    CG GGACGTC
                                  ACG    A___  _
GAM1009  LOC149501 3'  CTGCAAGAGCCTGGCTGGGAA  75800       T   CC     C
                                TTCCCA GCC  AGGCTC TGCAG
                                |||||| |||  |||||| |||||
                                AAGGGT CGG  TCCGAG ACGTC
                                   _   __     A
GAM1009  LOC150397 3'  CAGGAGCCTGAGTGAAGGA   80655     CA   CC
                                TCC  TGC  CAGGCTCCTG
                                |||  |||  ||||||||||
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                                AGG  GTG  GTCCGAGGAC
                                  AA   A_
GAM1009  LOC150397 3'  GCAGGAGCCTGCAGGAGA    80664    _ A   CCC
                                TC CC TGC   AGGCTCCTGC
                                || || |||   ||||||||||
                                AG GG ACG   TCCGAGGACG
                                 A  _  ____
GAM1009  LOC150517 5'  CTGCAGGTAGGAGCACAGAA   80725     CCA   C  AGGCT
                                TTC   TGC CC    CCTGCAG
                                |||   ||| ||    |||||||
                                AAG   ACG GG    GGACGTC
                                  AC_   A  AT____
GAM1009  LOC153688 3'  TGGGAGGCTGGGGCATGAGAA  87341     C        G
                                TTC CATGCCCCAG CTCCTG
                                ||| |||||||||| ||||||
                                AAG GTACGGGGTC GAGGGT
                                  A         G
GAM1009  LOC154849 3'  CTGCAGGAGGTGGAAGATG    60941     GCC   GG
                                CAT   CCA  CTCCTGCAG
                                |||   |||  |||||||||
                                GTA   GGT  GAGGACGTC
                                  GAA   G_
GAM1009  LOC162137 3'  GCAGGAGCTTCCCATAAAGAA  88480     CC_   CCCC
                                TTC   ATG    AGGCTCCTGC
                                |||   |||    ||||||||||
                                AAG   TAC    TTCGAGGACG
                                  AAA   CC__
GAM1009  LOC219654 3'  CAGGAGCCCAGGGGATGGGAA  92925        G   CA
                                TTCCCAT CCC  GGCTCCTG
                                ||||||| |||  ||||||||
                                AAGGGTA GGG  CCGAGGAC
                                    G   AC
GAM1009  LOC254552 5'  CAGGAGCCCGGGGCTGG     96422     T     A
                                CCA GCCCC GGCTCCTG
                                ||| ||||| ||||||||
                                GGT CGGGG CCGAGGAC
                                  _     C
GAM1009  LOC255042 3'  CTCGGGAGCCTGAGGCAGGAGA 97042     _ A    C        C
            A                    TTC CC TGCC CAGGCTCCTG AG
                                ||| || |||| |||||||||| ||
                                AAG GG ACGG GTCCGAGGGC TC
                                  A  _    A         _
GAM1009  LOC257000 3'  CTGCAGGACTCAGAGCATGG   98587       CCCA  C
                                CCATGC    GG TCCTGCAG
                                ||||||    || ||||||||
                                GGTACG    TC AGGACGTC
                                    AGAC  _
GAM1009  LOC91750  3'  TGGGGGCCTGAGGCACGAGAA  67659     CCA    C
                                TTC   TGCC CAGGCTCCTG
                                |||   |||| ||||||||||
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                                AAG   ACGG GTCCGGGGGT
                                  AGC    A
GAM1010  SCAMP1   3'  GCTAAATAAATATTCTCC    54500     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1010  SCAMP1   3'  GCTAAATAAATATTCTCC    54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1010  NX-17    3'  TGAATATCAGCCCCTAATA    40706         ATA_
                                TATTAGGG    ATATTCA
                                ||||||||    |||||||
                                ATAATCCC    TATAAGT
                                     CGAC
GAM1010  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
              TA                  TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM1011  ADAMTS3   3'  TTGCTGCTACTTTGTGCAAGA  27273     _ _    TGAAA
                                TCT G ACAG     AGCAGCAA
                                ||| | ||||     ||||||||
                                AGA C TGTT     TCGTCGTT
                                  A G    TCA__
GAM1011  ADAMTS4   3'  TGTTGCTGCCTCATGCTAAGA  18778     GACA    AAA
                                TCT    GTGA   GCAGCAACA
                                |||    ||||   |||||||||
                                AGA    TACT   CGTCGTTGT
                                  ATCG    C__
GAM1011  ADH1B     3'  CTGTCTCAGTTTTCACTGTCG  73040          _____
                                TGACAGTGAAAA     GCAG
                                ||||||||||||     ||||
                                GCTGTCACTTTT     TGTC
                                       GACTC
GAM1011  ATP1B3    3'  TTGTTACTGCTTTTATTTAGCA 9844       ACAGTG       C
              GA                  TCTG      AAAAGCAG AACAA
                                ||||      |||||||| |||||
                                AGAC      TTTTCGTC TTGTT
                                  GATTTA       A
GAM1011  B3GALT5   5'  TGTCACGTGATTCCTGTCAGA  53738         T   AA  A__
                                TCTGACAG GAA  GC   GCA
                                |||||||| |||  ||   |||
                                AGACTGTC CTT  TG   TGT
                                     _  AG  CAC
GAM1011  BPAG1     5'  TGCCACTTTTCACCGTTAGA   9950         A       CA
                                TCTGAC GTGAAAAG  GCA
                                |||||| ||||||||  |||
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                                AGATTG CACTTTTC  CGT
                                   C       AC
GAM1011  CD86     3'  TGCTTCTTTTCACTTCAGA   23539      C       C
                                TCTGA AGTGAAAAG AGCA
                                ||||| ||||||||| ||||
                                AGACT TCACTTTTC TCGT
                                   _       T
GAM1011  CHST5    5'  TGTTGCTGCCTACCAGG     25093     ACA   AAAA
                                TCTG   GTG   GCAGCAACA
                                ||||   |||   |||||||||
                                GGAC   CAT   CGTCGTTGT
                                   ___   C___
GAM1011  DDX6     5'  TGCTGCTTACCGTTCAGA    16568      _ A   AAA
                                TCTGA C GTG   AGCAGCA
                                ||||| | |||   |||||||
                                AGACT G CAT   TCGTCGT
                                   T C   ___
GAM1011  DUOX1    3'  TTGGGCTCCCCACTGTCAGA   34294         AAA   AG
                                TCTGACAGTG   AGC  CAA
                                ||||||||||   |||  |||
                                AGACTGTCAC   TCG  GTT
                                      CCC   G_
GAM1011  GEMIN5   3'  TGTTGACTCTCCTGTCAGA   90648        T  AAAG
                                TCTGACAG GA    CAGCA
                                |||||||| ||    |||||
                                AGACTGTC CT    GTTGT
                                     _ CTCA
GAM1011  HK2      3'  TTGTTACTGATTCTCCTGTCAG 5753        T  A  G   C
            A                    TCTGACAG GA AA CAG AACAA
                                ||||||||| || || ||| |||||
                                AGACTGTC CT TT GTC TTGTT
                                     _ C  A   A
GAM1011  PDE6H    3'  GTTCTCTTACTGTCAGA     21692          AA  C
                                TCTGACAGTGA  AG AGC
                                ||||||||||  || |||
                                AGACTGTCATT  TC TTG
                                      C_  _
GAM1011  PRDM2    5'  CTGTTACCACTTGTTAGA    32418        _   AAA
                                TCTGACA GTG   AGCAG
                                |||||||  |||   |||||
                                AGATTGT CAC   TTGTC
                                    T   CA_
GAM1011  PSEN1    5'  TTGCTGCTGCTTCCCTCTCAGA 24627      C  T   A_
                                TCTGA AG GAA  AGCAGCAA
                                ||||| || |||  ||||||||
                                AGACT TC CTT  TCGTCGTT
                                   C  C   CG
GAM1011  RAP1A    3'  TTGTGTTTTACTGTCAGA    12766           A
                                TCTGACAGTGAAA GCAG
                                |||||||||||| ||||
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                                AGACTGTCATTTT TGTT
                                       G
GAM1011  RCN1     3'  TGCTGTGTATTTTAACTACCAG 12797      AC   G   ___
              A                  TCTG  AGT AAAA   GCAGCA
                                 ||||  ||| ||||   ||||||
                                 AGAC  TCA TTTT   TGTCGT
                                   CA   A    ATG
GAM1011  RRM2B    3'  TTGTTAGATACACTGTCAGA   68438          AAAAGC
                                 TCTGACAGTG     AGCAA
                                 ||||||||||     |||||
                                 AGACTGTCAC     TTGTT
                                       ATAGA_
GAM1011  SNX9     3'  GTTACGCCTTTCACTGCCA    33124    A       A  AGC
                                 TG CAGTGAAA GC   AAC
                                 || |||||||| ||   |||
                                 AC GTCACTTT CG   TTG
                                  C       C  CA_
GAM1011  SOX12    3'  TGTTACTCCATTGTCAGA     23688          AAA  C
                                 TCTGACAGTG   AG AGCA
                                 ||||||||||   || ||||
                                 AGACTGTTAC   TC TTGT
                                       C__  A
GAM1011  XPR1     3'  TTGCTGCTGCTTTAGAGTCCTG 17625    T_   AG    A_
              A                  TC  GAC  TGAA  AGCAGCAA
                                 ||  |||  ||||  ||||||||
                                 AG  CTG  ATTT  TCGTCGTT
                                  TC   AG    CG
GAM1011  DKFZP566M114 3'  TTGTACATTTCACTGTCA    50451           AGCA
                                 TGACAGTGAAA    GCAA
                                 ||||||||||    ||||
                                 ACTGTCACTTT    TGTT
                                       ACA_
GAM1011  ERAP140  3'  TTGTCCAGTGGCCTCCTGTCAG 75709         T  AAA  A  A__
              A                  TCTGACAG GA   GC GC   ACAA
                                 |||||||| ||   || ||   ||||
                                 AGACTGTC CT   CG TG   TGTT
                                      _  C__  G  ACC
GAM1011  FHX      3'  TTGTTCTTTCTCTGTCAGA    37925         T    A C
                                 TCTGACAG GAAA G AGCAA
                                 |||||||| |||| | |||||
                                 AGACTGTC CTTT C TTGTT
                                      T    _ _
GAM1011  FLJ22055 3'  TTGCTGCTCTTCACCAGA    45851      ACA    A
                                 TCTG   GTGAA AGCAGCAA
                                 ||||   ||||| ||||||||
                                 AGAC   CACTT TCGTCGTT
                                   ___     C
GAM1011  FREQ     3'  TTGCTGCTGCTTTGCAGAGTCA 27379      AG  A       A
                                 TGAC  TG AAAGCAGCA CAA
                                 ||||  || |||||||| |||
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                                ACTG  AC TTTCGTCGT GTT
                                  AG  G       C
GAM1011  GMEB2    5'  TGTTGCCGCTCGTTTTTGTCAG 25671        T  AA   A
             G                   TCTGACAG GA  AGC GCAACA
                                 |||||||| ||  ||| ||||||
                                 GGACTGTT TT  TCG CGTTGT
                                     T  GC   C
GAM1011  KIAA0174 3'  TTGTCCGTTTCCTGTCAGA   79297        T   AGCA
                                 TCTGACAG GAAA   GCAA
                                 |||||||| ||||   ||||
                                 AGACTGTC CTTT   TGTT
                                     _   GCC_
GAM1011  KIAA0247 3'  GCCTTCCCATCTGTCAGA    29073        _  AA   CA
                                 TCTGACAG TG  AAG  GC
                                 |||||||| ||  |||  ||
                                 AGACTGTC AC  TTC  CG
                                     T  CC   __
GAM1011  KIAA0342 3'  TTGCTGCTGCTCTGGGCCAGG  71145     A__   TGAAA
                                 TCTG   CAG    AGCAGCAA
                                 ||||   |||    ||||||||
                                 GGAC   GTC    TCGTCGTT
                                   CGG   TCG__
GAM1011  KIAA1145 3'  TGTCTCTCCTTTCATTGTCAGA 66241           A C  CA
                                 TCTGACAGTGAAA G AG  ACA
                                 |||||||||||| | ||  |||
                                 AGACTGTTACTTT C TC  TGT
                                       _ C  TC
GAM1011  KIAA1317 3'  TTGTCACTGGAAGTACTGTCA  87220        AAAAG   CA
                                 TGACAGTG    CAG  ACAA
                                 ||||||||    |||  ||||
                                 ACTGTCAT    GTC  TGTT
                                     GAAG_   AC
GAM1011  KIAA1323 3'  TTGCTGCTAGATTATATCAGG  63727      CA   AA_
                                 TCTGA  GTGA   AGCAGCAA
                                 |||||  ||||   ||||||||
                                 GGACT  TATT   TCGTCGTT
                                   A_    AGA
GAM1011  KIAA1466 5'  TTGCTGTACTTCAATGCCA   72411    A  G   AA
                                 TG CA TGAA  GCAGCAA
                                 || || ||||  |||||||
                                 AC GT ACTT  TGTCGTT
                                  C  A   CA
GAM1011  KLHL6    3'  CTGTCCTTCACTGTAAGA    56170     G      AA
                                 TCT ACAGTGAA  GCAG
                                 ||| ||||||||  ||||
                                 AGA TGTCACTT  TGTC
                                   A       CC
GAM1011  LGI2     3'  TTGCTGCTATTGCACTGCCAG  36930     A    _  A
                                 CTG CAGTG AA AGCAGCAA
                                 ||| ||||| || ||||||||
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                                GAC GTCAC TT TCGTCGTT
                                  C    G  A
GAM1011 LMOD1    3' TGTCAGCCCTCACTGTCAG   25108         AAA  A_
                                CTGACAGTGA   GC  GCA
                                ||||||||||   ||  |||
                                GACTGTCACT   CG  TGT
                                     CC_  AC
GAM1011 MBLR     3' TTGCTACCACTTTGCTGTTCAA 50547    __    TG  AAGC_
           GA                     TCT  GACAG  AA    AGCAA
                                |||  |||||  ||    |||||
                                AGA  TTGTC  TT    TCGTT
                                  AC    GT  CACCA
GAM1011 MGC26954 3' TTGCTGCTTCCAGACCAGA   59495     ACAG  AA
                                TCTG    TG  AAGCAGCAA
                                ||||    ||  |||||||||
                                AGAC    AC  TTCGTCGTT
                                  CAG_  C_
GAM1011 MYT1L    3' TTGCTGCTGTAACTTACCAGA  67368     AC_  GAAA
                                TCTG   AGT   AGCAGCAA
                                ||||   |||   ||||||||
                                AGAC   TCA   TCGTCGTT
                                  CAT   ATG_
GAM1011 PRO2037  3' TTGCACAGGCTTTCACTGTAAG 38397     G       A  A___
           A                     TCT ACAGTGAAA GC    GCAA
                                |||  |||||||| ||    ||||
                                AGA TGTCACTTT CG    CGTT
                                  A       _  GACA
GAM1011 SNURF    3' TGTTGCTGCGACTGCCAG    20263     A    GAAAA
                                CTG CAGT    GCAGCAACA
                                |||  ||||    |||||||||
                                GAC GTCA    CGTCGTTGT
                                  C   G____
GAM1011 SPOP     3' TTGCTGCCACTGACCACCAGG  14536     A____    AAAA
                                TCTG    CAGTG   GCAGCAA
                                ||||    |||||   |||||||
                                GGAC    GTCAC   CGTCGTT
                                  CACCA   _____
GAM1011 SPRY4    3' TGCTGCTCACTGTCA       49036         AAA
                                TGACAGTGA   GCAGCA
                                |||||||||   ||||||
                                ACTGTCACT   CGTCGT
                                      ___
GAM1011 STXBP3   3' TTGCTGCTGCTTTGTAGA    24399     A   TGAAA
                                TCTG CAG    AGCAGCAA
                                |||| |||    ||||||||
                                AGAT GTT    TCGTCGTT
                                  _  TCG__
GAM1011 THTPA    5' TGGAGACCTGTCACTGTCAGA  44512         AAAA   CAA__
                                TCTGACAGTG   GCAG    CA
                                ||||||||||   ||||    ||
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                                AGACTGTCAC   TGTC    GT
                                     ____    CAGAG
GAM1011  UBE2D3   3'  TTGTTTAAGCCTTCCACTGTTA 13946         A  A  AGC
            GA                    TCTGACAGTG AA GC   AACAA
                                  |||||||||| || ||   |||||
                                  AGATTGTCAC TT CG   TTGTT
                                       C  C  AAT
GAM1011  VEZATIN  3'  TTGTTGCTGCTTCTCTAGTGGA 34657     G  AGT  A
                                  TCT AC   GA AAGCAGCAACAA
                                  ||| ||   || ||||||||||||
                                  AGG TG   CT TTCGTCGTTGTT
                                    _  AT_  C
GAM1011  LOC132671 3'  TTGACTTCTTCACTGTCA    59844          _  _
                                  TGACAGTGAA AAG CAG
                                  |||||||||| ||| |||
                                  ACTGTCACTT TTC GTT
                                       C   A
GAM1011  LOC143524 3'  TTGTTGCTACTTTGATTCATCA 77096      CAGTGA   C
            GA                    TCTGA     AAAG AGCAACAA
                                  |||||      |||| ||||||||
                                  AGACT     TTTC TCGTTGTT
                                     ACTTAG    A
GAM1011  LOC145758 5'  TTGCTGCTGTGACTTCAGA   84488      C   GAAA
                                  TCTGA AGT    AGCAGCAA
                                  ||||| |||    ||||||||
                                  AGACT TCA    TCGTCGTT
                                     _   GTG_
GAM1011  LOC152286 3'  TGTTGGCATCCACTGTCAGG   86816         AAAA  AG
                                  TCTGACAGTG    GC  CAACA
                                  ||||||||||    ||  |||||
                                  GGACTGTCAC    CG  GTTGT
                                       CTA_  __
GAM1011  LOC153020 3'  TGCTGCTGCTTCCTGCAGA   81648      A   T   A_
                                  TCTG CAG GAA  AGCAGCA
                                  |||| ||| |||  |||||||
                                  AGAC GTC CTT  TCGTCGT
                                     _   _   CG
GAM1011  LOC153579 5'  TTGCTGCTACCTGCCAGG    81775      A   TGAAA
                                  TCTG CAG     AGCAGCAA
                                  |||| |||     ||||||||
                                  GGAC GTC     TCGTCGTT
                                     C   CA___
GAM1011  LOC163231 5'  TGTGGGATCCTGTTCACTGTCA 83336           A  CAGCA_
            GA                    TCTGACAGTGAA AG      ACA
                                  |||||||||||| ||      |||
                                  AGACTGTCACTT TC      TGT
                                         G  CTAGGG
GAM1011  LOC166602 5'  TTGCTGCTACCTCGTTGTTCAG 83538      _     AA_
                                  CTGA CAGTGA   AGCAGCAA
                                  |||| ||||||   ||||||||
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                                GACT GTTGCT   TCGTCGTT
                                  T     CCA
GAM1011  LOC196878 5'  TTGCTGCTGCTTCTCCAGA   89178     ACAGT  A      A
                                TCTG    GA AAGCAGCA CAA
                                ||||    || |||||||| |||
                                AGAC    CT TTCGTCGT GTT
                                  _____ C       C
GAM1011  LOC197003 3'  TTGCTGCCTATCACTGTCA   89217        AAA
                                TGACAGTGA   GCAGCAA
                                |||||||||   |||||||
                                ACTGTCACT   CGTCGTT
                                     ATC
GAM1011  LOC253272 3'  TTGCTACCACTTTGCTGTTCAA 97108    __    TG  AAGC_
           GA                     TCT  GACAG  AA    AGCAA
                                |||  |||||  ||    |||||
                                AGA  TTGTC  TT    TCGTT
                                  AC    GT  CACCA
GAM1011  LOC255515 3'  TTGTTGCTACTTTGGTTCATCA 97814     CAGTGA   C
           GA                     TCTGA     AAAG AGCAACAA
                                |||||     |||| ||||||||
                                AGACT     TTTC TCGTTGTT
                                   ACTTGG   A
GAM1011  LOC255736 3'  TTGTTGCTGCTTGGAGAGATCA 97077    CAGTGAA
                                TGA      AAGCAGCAACAA
                                |||      ||||||||||||
                                ACT      TTCGTCGTTGTT
                                  AGAGAGG
GAM1011  LOC256895 3'  GCTCCCTTTCCCTGTCAGA   98654       T   AGC
                                TCTGACAG GAAA   AGC
                                |||||||| ||||   |||
                                AGACTGTC CTTT   TCG
                                     C    CCC
GAM1011  LOC257407 5'  TGCCTTCTCCCTGTCAGA    98761       T  A   CA
                                TCTGACAG GA AAG  GCA
                                |||||||| || |||  |||
                                AGACTGTC CT TTC  CGT
                                     C  C   __
GAM1011  LOC92997  3'  TGCCTTCTCCCTGTCAGA    71640       T  A   CA
                                TCTGACAG GA AAG  GCA
                                |||||||| || |||  |||
                                AGACTGTC CT TTC  CGT
                                     C  C   __
GAM1012  SCAMP1    3'  GCTAAATAAATATTCTCC    54500    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1012  SCAMP1    3'  GCTAAATAAATATTCTCC    54501    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
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                                CCT TTATAA TAAATCG
                                  C     A
GAM1012 NX-17    3' TGAATATCAGCCCCTAATA   40706        ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM1012 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
             TA                   TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM1013 ADCY6    3' CCAGATCAGGTCACTCTGCCCC 40945    ACA AT    _  C
                                GG  CA  GTGGC TGA CTGG
                                ||  ||  ||||| ||| ||||
                                CC  GT  CACTG ACT GACC
                                 CC_ CT    G  A
GAM1013 HMG20A   3' CAGATGCTTTGTGTCCTG    37061         TGT  TGAC
                                CAGGACACAA  GGC   CTG
                                ||||||||||  |||   |||
                                GTCCTGTGTT  TCG   GAC
                                      ___  TA__
GAM1013 HTR6     5' CCAAATAGCCACACTGTGTCCT 7890         A      ACC
                                AGGACACA TGTGGCTG  TGG
                                |||||||| ||||||||  |||
                                TCCTGTGT ACACCGAT  ACC
                                    C       AA_
GAM1013 JRK      5' CCAGGCCAGGCGTGTGTCCTG  87819        ATG  G   A
                                CAGGACACA  TG CTG CCTGG
                                |||||||||  || ||| |||||
                                GTCCTGTGT  GC GAC GGACC
                                      ___ G  C
GAM1013 KCNS2    3' TAGCCACTTGTGTCCTG     68852         T
                                CAGGACACAA GTGGCTG
                                |||||||||| |||||||
                                GTCCTGTGTT CACCGAT
                                      _
GAM1013 LY6E     3' CCAGGTCAGGCCCACCCCCTG  11381     ACACAA  T  _
                                CAGG     TG GGC TGACCTGG
                                ||||     || ||| ||||||||
                                GTCC     AC CCG ACTGGACC
                                  CCC___  _  G
GAM1013 MID1     3' TTGGCCACATTTTGCCCTG   53903     A  C      TG
                                CAGG CA AATGTGGC  A
                                |||| || ||||||||  |
                                GTCC GT TTACACCG  T
                                  C  T      GT
GAM1013 MPP2     3' CCAGATTTCTCCAATGTGTCCT 60516        A  TG CT  C
             G                   CAGGACACA TG  G  GA CTGG
                                |||||||||  ||  |  ||  ||||
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                                GTCCTGTGT AC  C  TT GACC
                                     A  CT T_  A
GAM1013  PYCR1    3'  CCAGGGAGGGGCCACATCACTT 70640     CACA      GA__
              CC                   GGA   ATGTGGCT   CCTGG
                                   |||   ||||||||   |||||
                                   CCT   TACACCGG   GGACC
                                     TCAC      GGAG
GAM1013  RALBP1   3'  CAGGTCAGCGCTGCGCCTG   23273     ACACAAT   G
                                   CAGG      GTG CTGACCTG
                                   ||||      ||| ||||||||
                                   GTCC      CGC GACTGGAC
                                     GCGT___  _
GAM1013  RBP5     3'  CCAGGTCAAGGTCTGGCGTCC  49799     A_  ATGT   __
                                   GGAC  CA   GGCT  GACCTGG
                                   ||||  ||   ||||  |||||||
                                   CCTG  GT   CTGG  CTGGACC
                                     CG  ____   AA
GAM1013  SCNN1B   3'  CCAGGCCAGAGCTTGTGTCCT  6214        T  GG   A
                                   AGGACACAA GT  CTG CCTGG
                                   |||||||||  ||  ||| |||||
                                   TCCTGTGTT CG  GAC GGACC
                                        _  A_   C
GAM1013  SEPN1    3'  CAGGCTCCCTGTGTCCTG    66964        ATGT  CT  _
                                   CAGGACACA    GG  GA CCTG
                                   |||||||||    ||  || ||||
                                   GTCCTGTGT    CC  CT GGAC
                                        ____  __  C
GAM1013  TRIM37   3'  CCAAACTTTGCCATTGTGCTCC 31624      _   AT    TGACC_
              TG                     CAGGA CACA  GTGGC     TGG
                                   |||||  ||||  |||||      |||
                                   GTCCT GTGT  TACCG     ACC
                                     C    __     TTTCAA
GAM1013  VCL      3'  CCATGAACACACTGTGTCCTG  14032        A   GCTGACC
                                   CAGGACACA TGTG      TGG
                                   |||||||||  ||||      |||
                                   GTCCTGTGT ACAC      ACC
                                        C    AAGT___
GAM1013  C20orf163 3'  CCAGAGCACAGCTGCATCCTG  55802      CACAA  TG   AC__
                                   CAGGA    TG  GCTG   CTGG
                                   |||||    ||  ||||   ||||
                                   GTCCT    AC  CGAC   GACC
                                     _____  GT   ACGA
GAM1013  C20orf80  5'  CCAGGTCACATACTCGTCCTG  65882      ACAAT   GC
                                   CAGGAC    GTG  TGACCTGG
                                   ||||||    |||  ||||||||
                                   GTCCTG    CAT  ACTGGACC
                                     CT___   AC
GAM1013  DDM36    3'  CCAGGTCAGAACGGTGCC    40916    A   AA   GG
                                   GG CAC  TGT  CTGACCTGG
                                   || |||  |||  |||||||||
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                                CC GTG  GCA  GACTGGACC
                                 _  __   A_
GAM1013  DKFZP727M111 3'  CCAGACGAAGAACATTGTGTCC 32056          GG  GAC_
           T                     AGGACACAATGT  CT    CTGG
                                 ||||||||||||  ||    ||||
                                 TCCTGTGTTACA  GA    GACC
                                       A_  AGCA
GAM1013  FBXL9    3'  CCAGGTCAGTAACCAGCCCTG  25138     ACACAAT  G
                                 CAGG      GT GCTGACCTGG
                                 ||||      || ||||||||||
                                 GTCC      CA TGACTGGACC
                                   CGAC___  A
GAM1013  FGD3     3'  CAGGGACAGCCACATCCTG   73277      CACAA      A_
                                 CAGGA    TGTGGCTG  CCTG
                                 |||||    ||||||||  ||||
                                 GTCCT    ACACCGAC  GGAC
                                   _____       AG
GAM1013  FLJ10193 3'  CAGGTACACATTGTTCCTG   57360      C      GCTG
                                 CAGGA ACAATGTG    ACCTG
                                 ||||| ||||||||    |||||
                                 GTCCT TGTTACAC    TGGAC
                                   _       A___
GAM1013  FLJ14816 3'  CAGCCACACTGTGACCTG    52707     A   A
                                 CAGG CACA TGTGGCTG
                                 |||| |||| ||||||||
                                 GTCC GTGT ACACCGAC
                                   A   C
GAM1013  IL18BP   3'  CAGGTCAGACCCAGTCCTG   20309      ACAA  T  _
                                 CAGGAC    TG GG CTGACCTG
                                 ||||||    || || ||||||||
                                 GTCCTG    AC CC GACTGGAC
                                    ____  _  A
GAM1013  KIAA1198 3'  CAGGTCAAAGCAATCCTG    64010      CACAA   GGC
                                 CAGGA    TGT   TGACCTG
                                 |||||    |||   |||||||
                                 GTCCT    ACG   ACTGGAC
                                   A____   AA_
GAM1013  NSE1     3'  CCAGGTCTCCTGACATTGTGTT 59677          _  CT
           C                     GGACACAATGT GG  GACCTGG
                                 ||||||||||| ||  |||||||
                                 CTTGTGTTACA TC  CTGGACC
                                       G  CT
GAM1013  SKIL     5'  CCAGACCATTGCATTGACCCTG 19446      ACA    TG C  AC
                                 CAGG   CAATG  G TG  CTGG
                                 ||||   |||||  | ||  ||||
                                 GTCC   GTTAC  T AC  GACC
                                   CA_    GT _  CA
GAM1013  SRF      3'  CAGGTCAGCCCTGTGTCT    13393       ATGT
                                 GGACACA    GGCTGACCTG
                                 |||||||    ||||||||||
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                                TCTGTGT   CCGACTGGAC
                                   C___
GAM1013  WDR5B    3'  CCAAATAGTATACATTGTACCT 39344     AC      _   ACC
                                AGG  ACAATGTG GCTG   TGG
                                |||  |||||||| ||||   |||
                                TCC  TGTTACAT TGAT   ACC
                                  A_      A   AA_
GAM1013  LOC115574 3'  CCAGGTCAGAGATGTCCCCTG  73849     AC   ATGTGG
                                CAGG  ACA     CTGACCTGG
                                ||||  |||     |||||||||
                                GTCC  TGT     GACTGGACC
                                  CC   AGA___
GAM1013  LOC149373 5'  CCAGGTCAGGCCCGATTTGTCC 80091       CAA  T   _
              TG                  CAGGACA   TG GGC TGACCTGG
                                |||||||   || ||| ||||||||
                                GTCCTGT   GC CCG ACTGGACC
                                   TTA  _   G
GAM1013  LOC150538 3'  CAGGCCGGATTGTGTTCTG    80736         G    TGAC
                                CAGGACACAAT TGGC    CTG
                                ||||||||||| ||||    |||
                                GTCTTGTGTTA GCCG    GAC
                                      G    _____
GAM1013  LOC152317 5'  CCAAGTCAGCCATCTGTCCT   86825       CAAT       C
                                AGGACA    GTGGCTGAC TGG
                                ||||||    ||||||||| |||
                                TCCTGT    TACCGACTG ACC
                                   C___        A
GAM1013  LOC169436 3'  CCAGGTGTTGGCCACCTACCCT 83618      ACACAAT      __
              G                  CAGG      GTGGCTG  ACCTGG
                                ||||      |||||||  ||||||
                                GTCC      CACCGGT  TGGACC
                                  CATC___      TG
GAM1013  LOC199991 3'  CCAGGCCAGCCCTCAGCCATCC 91514      CACAA  T_    A
              T                   AGGA    TG  GGCTG CCTGG
                                ||||    ||  ||||| |||||
                                TCCT    AC  CCGAC GGACC
                                  ACCG_  TC    C
GAM1013  LOC200081 3'  CCAGGTCAGGAATGTGGGCC   89973    A_   ATGTGG
                                GG  CACA     CTGACCTGG
                                ||  ||||     |||||||||
                                CC  GTGT     GACTGGACC
                                 GG    AAG___
GAM1013  LOC201514 3'  CGGGAGCCACATTGCACTCTG  89633      ACA        GA
                                CAGG   CAATGTGGCT  CCTG
                                ||||   ||||||||||  ||||
                                GTCT   GTTACACCGA  GGGC
                                  CAC         __
GAM1013  LOC254130 3'  CCAGAACACAGCTGTGTCCT   97380         A_   GCTGAC
                                AGGACACA  TGTG     CTGG
                                ||||||||  ||||     ||||
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                                TCCTGTGT  ACAC     GACC
                                    CG    AA____
GAM1014  APOB48R   3'  GCCTGCCCTGGTTCCTCCCCA  38587    AA         ACCT
                                TG  GAGGAATCAGG    GGC
                                ||  ||||||||||    |||
                                AC  CTCCTTGGTCC    CCG
                                 CC         CGT_
GAM1014  ARHGDIB   5'  GAGCCAGGGTTTCCTCTTCA  8615          TCAGGA
                                TGAAGAGGAA     CCTGGCTC
                                ||||||||||     ||||||||
                                ACTTCTCCTT     GGACCGAG
                                     TG____
GAM1014  BAP1      3'  AGCCAGGTCTTCTCTCTTCA  17393         AATC
                                TGAAGAGG    AGGACCTGGCT
                                ||||||||    ||||||||||
                                ACTTCTCT    TTCTGGACCGA
                                    C___
GAM1014  LIMK1     3'  GAGCCAGGCCCTGACTTGCCTT 11335      AG  A     A
              C                  GAAG  GA TCAGG CCTGGCTC
                                 ||||  || ||||| ||||||||
                                 CTTC  TT AGTCC GGACCGAG
                                   CG  C    C
GAM1014  LIMK1     3'  GAGCCAGGCCCTGACTTGCCTT 11336      AG  A     A
              C                  GAAG  GA TCAGG CCTGGCTC
                                 ||||  || ||||| ||||||||
                                 CTTC  TT AGTCC GGACCGAG
                                   CG  C    C
GAM1014  NRXN2     5'  GAACCAGGTCTCCGTCCCTCTT 57820        A  CA       C
              C                  GAAGAGG AT  GGACCTGG TC
                                 |||||||  ||  |||||||| ||
                                 CTTCTCC TG  TCTGGACC AG
                                     C  CC       A
GAM1014  PVRL2     3'  AGCCAGGCCCGGCCCTC     12650      AA  A  A
                                 GAGG  TC GG CCTGGCT
                                 ||||  || ||  |||||||
                                 CTCC  GG CC GGACCGA
                                   C_  C  _
GAM1014  RAD1      5'  GAGCCGCCTCGCTCCTCTTCA  12644         ATC   ACC
                                TGAAGAGGA   AGG   TGGCTC
                                |||||||||   |||   ||||||
                                ACTTCTCCT   TCC   GCCGAG
                                     CGC   ___
GAM1014  RAD1      5'  GAGCCGCCTCGCTCCTCTTCA  12645         ATC   ACC
                                TGAAGAGGA   AGG   TGGCTC
                                |||||||||   |||   ||||||
                                ACTTCTCCT   TCC   GCCGAG
                                     CGC   ___
GAM1014  RAD1      5'  GAGCCGCCTCGCTCCTCTTCA  12646         ATC   ACC
                                TGAAGAGGA   AGG   TGGCTC
                                |||||||||   |||   ||||||
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                                ACTTCTCCT  TCC  GCCGAG
                                     CGC  ___
GAM1014 RASAL1   3' AGCCAGGGGGCCCTCTTCA  17402      AA AGGA
                                TGAAGAGG TC   CCTGGCT
                                |||||||| ||   |||||||
                                ACTTCTCC GG   GGACCGA
                                     CG _____
GAM1014 SERPINB4 3' CCAAATCATACTTTCTCTTCA 65878       TCAG CC
                                TGAAGAGGAA   GA TGG
                                ||||||||||   || |||
                                ACTTCTCTTT   CT ACC
                                      CATA AA
GAM1014 SLC2A5   3' AGCCAAATTCATCCTCTT   13177      ATCA  CC
                                AAGAGGA   GGA TGGCT
                                |||||||   |||  |||||
                                TTCTCCT   CTT ACCGA
                                    A___  AA
GAM1014 SLC30A3  3' GAGCCAGGTCCATACCCCTTC 14399    A AATCA
                                GAAG GG    GGACCTGGCTC
                                |||| ||    ||||||||||
                                CTTC CC    CCTGGACCGAG
                                  _ CATA_
GAM1014 TFE3     3' GAGCCAGGCCCCACCCCTTC  22538    A AATCA A
                                GAAG GG    GG CCTGGCTC
                                |||| ||    || ||||||||
                                CTTC CC    CC GGACCGAG
                                  _ CACC_ _
GAM1014 BM039    5' AGCCAGGTCCTAACGGAGCCT 38048    AA ___
                                AGG TC  AGGACCTGGCT
                                ||| ||  ||||||||||
                                TCC GG  TCCTGGACCGA
                                 GA CAA
GAM1014 C14orf4  5' AGCCCCAATTCTTCTTCA   67896       CA ACCT
                                TGAAGAGGAAT GG   GGCT
                                |||||||||| ||   ||||
                                ACTTCTTCTTA CC   CCGA
                                      A_ _____
GAM1014 CNNM3    3' GACCAGGTGGATCCTCTTTA  34807       A AGG    C
                                TGAAGAGGA TC  ACCTGG TC
                                ||||||||| ||  |||||| ||
                                ATTTCTCCT AG  TGGACC AG
                                     _ G__    A
GAM1014 CSTF3    3' GAACCACATTTTGTTCCCTCTT 9001       AAT   CC  C
           CA                  TGAAGAGG  CAGGA TGG TC
                               ||||||||  |||||  ||| ||
                               ACTTCTCC  GTTTT ACC AG
                                    CTT   AC  A
GAM1014 DNAJC6   3' GAACCAGGTCCCACCTCCCCA 29494   AA  AATCA     C
                               TG GAGG   GGACCTGG TC
                               ||  ||||   |||||||| ||
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                                AC  CTCC    CCTGGACC AG
                                 CC   AC___      A
GAM1014  FLJ10415  3'  AGGCCTGACTCCCTTTCA   36584      A  A    A
                                TGAAG GGA TCAGG CCT
                                ||||| ||| ||||| |||
                                ACTTT CCT AGTCC GGA
                                   C  C    _
GAM1014  FLJ20069  3'  CCAAATGGAATTTCTCTTCA  34949          _ AGGACC
                                TGAAGAGGAAT C     TGG
                                |||||||||||| |     |||
                                ACTTCTCTTTA G     ACC
                                       A GTAA__
GAM1014  FLJ21276  3'  GAGCAGTTCCAATTCCTCTCA  45259     A     CA  C  G
                                TGA GAGGAAT  GGA CTG CTC
                                ||| |||||||  ||| ||| |||
                                ACT CTCCTTA  CCT GAC GAG
                                  _      A_  T  _
GAM1014  FLJ21736  5'  GAGCCAAGTCCCTTCCATTCCT 46783    A      CA___   C
            TTCCA                   TG AGAGGAAT    GGAC TGGCTC
                                || |||||||||    |||| ||||||
                                AC TTTCCTTA    CCTG ACCGAG
                                 C       CCTTC   A
GAM1014  FSD1     3'  GAGCCAGGCACCCTCCTCTGTC 44540    _     ATCA  A_
            A                    TGA AGAGGA   GG  CCTGGCTC
                                ||| ||||||   ||  ||||||||
                                ACT TCTCCT   CC  GGACCGAG
                                  G     C___  AC
GAM1014  GTF3C4   5'  GAGCCAGGTCTCCACCTCTGCA 25207    A    AATCA
                                TG AGAGG    GGACCTGGCTC
                                || |||||    ||||||||||
                                AC TCTCC    TCTGGACCGAG
                                 G    ACC__
GAM1014  KIAA0453  3'  GAGCCAGGCCAGTGCTTCC   69606     T  __  A
                                GGAA CA  GG CCTGGCTC
                                |||| ||  || ||||||||
                                CCTT GT  CC GGACCGAG
                                  C  GA  _
GAM1014  KIAA0710  3'  GAGCCAGATTCATTCCTTCTTC 30187       _   CA  C
            A                    TGAAGA GGAAT  GGA CTGGCTC
                                |||||| |||||  ||| |||||||
                                ACTTCT CCTTA  CTT GACCGAG
                                   T    __   A
GAM1014  KIAA0939  3'  AGCCAGCCACCCCTCTTCA   62708       AATCA  AC
                                TGAAGAGG    GG  CTGGCT
                                ||||||||    ||  ||||||
                                ACTTCTCC    CC  GACCGA
                                     CCA__  __
GAM1014  KIAA1025  3'  AGCCAGGTCTCTCCTCTCA   64672    A    ATCA
                                TGA GAGGA   GGACCTGGCT
                                ||| |||||   ||||||||||
```

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                                ACT CTCCT    TCTGGACCGA
                                  _    C___
GAM1014 KIAA1463 3' AGCCACTTTGTGACTCCCTTCA 72734      A   A   G  CC
                                TGAAG GGA TCA GA  TGGCT
                                ||||| ||| ||| ||  |||||
                                ACTTC CCT AGT TT  ACCGA
                                  _  C   G  TC
GAM1014 KIAA1524 5' AGGATCCTGATTCCTCTTCA   73836            _
                                TGAAGAGGAATCAGGA CCT
                                |||||||||||||||| |||
                                ACTTCTCCTTAGTCCT GGA
                                           A
GAM1014 LBP-9    3' CAGGCTCCTGATTCCTCTTC   28044            _
                                GAAGAGGAATCAGGA CCTG
                                |||||||||||||| ||||
                                CTTCTCCTTAGTCCT GGAC
                                           C
GAM1014 MAPK8IP3 3' AGCCAGGCCACTCCTTCA    54135   A    ATCA  A
                                A GAGGA    GG CCTGGCT
                                | |||||    || |||||||
                                A TTCCT    CC GGACCGA
                                 C    CA__ _
GAM1014 MGC2628  3' AGCCAGGTGTCCTCTTGCA   44194   _     ATCAGG
                                TG AAGAGGA     ACCTGGCT
                                || |||||||     ||||||||
                                AC TTCTCCT     TGGACCGA
                                 G      G_____
GAM1014 p25      3' GAGCCAGGAGAGCACCCTTC   23834     A  AA_  AGGA
                                GAAG GG   TC    CCTGGCTC
                                |||| ||   ||    ||||||||
                                CTTC CC   AG    GGACCGAG
                                  _  ACG  A___
GAM1014 SMARCF1  3' GAGCCAGGCCAGCCTCCTC   21189      ATCA  A
                                GAGGA    GG CCTGGCTC
                                |||||    || ||||||||
                                CTCCT    CC GGACCGAG
                                   CCGA  _
GAM1014 TRIP-Br2 3' AGCCAGGCCCCCAGGTCTTCTC 29259     A    ATCA_  A
           A                     TGA GAGGA     GG CCTGGCT
                                ||| |||||     || |||||||
                                ACT CTTCT     CC GGACCGA
                                  _    GGACC  C
GAM1014 USP2     3' AGCCAAGAGCCCTCTTCA    16107        AA  AGGACC
                                TGAAGAGG  TC     TGGCT
                                ||||||||  ||     |||||
                                ACTTCTCC  AG     ACCGA
                                     CG  A_____
GAM1014 LOC147343 5' AGCCATAACTCTTCTTCA    85123         ATCA GACC
                                TGAAGAGGA    G    TGGCT
                                |||||||||    |    |||||
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                                ACTTCTTCT   C   ACCGA
                                     _____ AAT_
GAM1014  LOC150333 5'  AGCCAGAGATTCCTCCTC    86211    A      AGGAC
                                GA GAGGAATC    CTGGCT
                                || ||||||||    ||||||
                                CT CTCCTTAG    GACCGA
                                 C       A_____
GAM1014  LOC196527 3'  GAGCCAGGCCCTCTCACCCCT  89099    A  AATC   A
                                AG GG    AGG CCTGGCTC
                                || ||    ||| ||||||||
                                TC CC    TCC GGACCGAG
                                 C  ACTC   C
GAM1014  LOC220567 3'  GCCTGCCCTGGTTCCTCCCCA  92436    AA        ACCT
                                TG  GAGGAATCAGG    GGC
                                ||  ||||||||||    |||
                                AC  CTCCTTGGTCC    CCG
                                 CC         CGT_
GAM1014  LOC253776 3'  AGCCAGGCCCTTTCCTCT    99292       TC   A
                                AGAGGAA  AGG CCTGGCT
                                |||||||  ||| |||||||
                                TCTCCTT  TCC GGACCGA
                                    __   C
GAM1014  LOC253816 3'  GAGCCAGACCATTTCTTCCCCA 96041    AA     TCA  AC
                                TG  GAGGAA   GG  CTGGCTC
                                ||  ||||||   ||  |||||||
                                AC  CTTCTT   CC  GACCGAG
                                 CC     TA_  A_
GAM1014  LOC254122 3'  AGCCAAGACTCCTCTTCA    96393         A  AGGACC
                                TGAAGAGGA TC      TGGCT
                                |||||||||| ||      |||||
                                ACTTCTCCT AG      ACCGA
                                     C  A_____
GAM1014  LOC255299 5'  GAACCATGTACTGACGTCCTCT 99336         A_   G  C   C
            TCA                    TGAAGAGGA  TCAG AC TGG TC
                                |||||||||  |||| || ||| ||
                                ACTTCTCCT  AGTC TG ACC AG
                                     GC    A  T   A
GAM1014  LOC256283 5'  GAGCCAGGTCCTCCTCCTCCTC 98823    A    ATC
                                GA GAGGA   AGGACCTGGCTC
                                || |||||   ||||||||||||
                                CT CTCCT   TCCTGGACCGAG
                                 C    CC_
GAM1014  LOC51125  3'  GAGTGTCCCTACCTCCTCTCCA 32742    A     ATCA_   CTG
                                TG AGAGGA    GGAC   GCTC
                                || ||||||    ||||   ||||
                                AC TCTCCT    CCTG   TGAG
                                 C     CCATC   ____
GAM1014  LOC51149  5'  AGCCAGGCCCCCGCTTCA    32971       A  AATCA  A
                                TGAAG GG    GG CCTGGCT
                                ||||| ||    || |||||||
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                                ACTTC CC    CC GGACCGA
                                  G _____ C
GAM1014 LOC51161 3' GAGCCAGGTCCTAGCTGTTCTC 33041      ATC__
                                GAGGA    AGGACCTGGCTC
                                |||||    ||||||||||||
                                CTCTT    TCCTGGACCGAG
                                  GTCGA
GAM1014 LOC91663 3' AGGCTCCCGTTCCCTCTCCA  57221    A   _  CA  _
                                TG AGAGG AAT  GGA CCT
                                || ||||| |||  ||| |||
                                AC TCTCC TTG  CCT GGA
                                 C    C  C_  C
GAM1014 LOC92249 3' AGCCTCTATCTCCTCTTCA   69104        ATCA  CCT
                                TGAAGAGGA   GGA  GGCT
                                |||||||||   |||  ||||
                                ACTTCTCCT   TCT  CCGA
                                     CTA_  ___
GAM1015 ADCY2    3' ACCCCCATCTCTGCAAAAAAAT 65641       A    G
            A                    TATTTT TTGCAG AGGTGGGGGT
                                 |||||| |||||| ||||||||||
                                 ATAAAA AACGTC TCTACCCCCA
                                    A    _
GAM1015 CST1     3' CCCCCACCTCCTGCAATTAAA  10329     T
                                 TTT ATTGCAGGAGGTGGGGG
                                 ||| ||||||||||||||||
                                 AAA TAACGTCCTCCACCCCC
                                   T
GAM1015 CST2     3' ACCCCCACCTCCTGCAATTAAA 8995      T
                                 TTT ATTGCAGGAGGTGGGGGT
                                 ||| |||||||||||||||||
                                 AAA TAACGTCCTCCACCCCCA
                                   T
GAM1015 CST3     3' ACCCCCACCTCCTGCAATAAAA 5432
            TA                     TATTTTATTGCAGGAGGTGGGGGT
                                   ||||||||||||||||||||||||
                                   ATAAAATAACGTCCTCCACCCCCA

GAM1015 CST4     3' ACCCCCACCTCCTGCAATTAAA 10332     T
                                 TTT ATTGCAGGAGGTGGGGGT
                                 ||| |||||||||||||||||
                                 AAA TAACGTCCTCCACCCCCA
                                   T
GAM1015 ICA1     3' ACCCCCATCTCTACAAAAAATA 18307       A  CA
                                 TATTTT TTG  GGAGGTGGGGGT
                                 |||||| |||  ||||||||||||
                                 ATAAAA AAC  TCTCTACCCCCA
                                    _  A_
GAM1015 IL10RA   3' ACCCCCACCCCTCTGCCAAAGT 60377       ATT   _ A
            A                    TATTTT   GCAG G GGTGGGGGT
                                 ||||||   |||| | |||||||||
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                                ATGAAA  CGTC C CCACCCCCA
                                   C__   T C
GAM1015  PRG2     3'  ACCTCCCTGCAATAAAATG   12259          _
                                TATTTTATTGCAGG AGGT
                                |||||||||||||| ||||
                                GTAAAATAACGTCC TCCA
                                      C
GAM1015  C20orf139 3'  CGCCTCCTGCAATAAAA    85918           TG
                                TTTTATTGCAGGAGG  G
                                ||||||||||||||  |
                                AAAATAACGTCCTCC  C
                                       GT
GAM1015  DC13     3'  CTTATCTCCTTCAATAAAATA  39879         C
                                TATTTTATTG AGGAGGTGGG
                                |||||||||| ||||||||||
                                ATAAAATAAC TCCTCTATTC
                                      T
GAM1015  DKFZp761N1114 3'  CCTTTCCTAAAATAAAATA   79781        GC    T
                                TATTTTATT  AGGAGG GG
                                |||||||||  ||||||  ||
                                ATAAAATAA  TCCTTT CC
                                     AA    _
GAM1015  FBXO27   3'  ACCCCCATCGCTACAAAAAATA 74997      A  C  GA
                                TATTTT TTG AG  GGTGGGGGT
                                |||||| ||| ||  |||||||||
                                ATAAAA AAC TC  CTACCCCCA
                                   _  A  G_
GAM1015  FLJ20013  3'  ACCCCCATCTCTACAAAAAATA 34791      A  CA
                                TATTTT TTG  GGAGGTGGGGGT
                                |||||| |||  ||||||||||||
                                ATAAAA AAC  TCTCTACCCCCA
                                   _  A_
GAM1015  HGC6.2   5'  ACCCCCACCTCACTTACAA   27618    C_ _
                                TTG  AG GAGGTGGGGGT
                                |||  || ||||||||||
                                AAC  TC CTCCACCCCCA
                                  AT  A
GAM1015  MGC4840  3'  CCCCATTTCTACAAAAAATA  72021      A  CA
                                TATTTT TTG  GGAGGTGGGG
                                |||||| |||  ||||||||||
                                ATAAAA AAC  TCTTTACCCC
                                   _  A_
GAM1015  TSA1902  3'  CCTAAAGTCCTGCAATAAAAT  41722          GG_
                                ATTTTATTGCAGGA  TGGG
                                ||||||||||||||  ||||
                                TAAAATAACGTCCT  ATCC
                                      GAA
GAM1015  LOC130507 3'  CCTATCGTTCTACAATAAAATA 75455        C   _
                                TATTTTATTG AGGA GGTGGG
                                |||||||||| |||| ||||||
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                                ATAAAATAAC TCTT CTATCC
                                      A   G
GAM1015  LOC143188 3'  ACCCCCACCTCCTCATTA    83789    T  C
                                TA TG AGGAGGTGGGGGT
                                || || ||||||||||||
                                AT AC TCCTCCACCCCCA
                                 T  _
GAM1015  LOC91191  3'  ACCCCCACCCCAAATTAAAATG 65800       TTGCA  A
                                TATTTTA    GG GGTGGGGGT
                                |||||||    || |||||||||
                                GTAAAAT    CC CCACCCCCA
                                    TAAA_  _
GAM1016  DIAPH2    3'  GCAGTCTCACAATCTTCTTTC  23007     _   CCAA_
                                GAAA AAG    GAGACTGC
                                |||| |||    ||||||||
                                CTTT TTC    CTCTGACG
                                  C   TAACA
GAM1016  EGLN3     3'  CAATCTCCCTGCTACTTCTTGC 42209       AA   CAA    C
             A                   TGTAAGAA  AGC   GAGA TG
                                ||||||||  |||   |||| ||
                                ACGTTCTT  TCG   CTCT AC
                                     CA   TCC    A
GAM1016  EGLN3     3'  CAATCTCCCTGCTACTTCTTGC 54047       AA   CAA    C
             A                   TGTAAGAA  AGC   GAGA TG
                                ||||||||  |||   |||| ||
                                ACGTTCTT  TCG   CTCT AC
                                     CA   TCC    A
GAM1016  GABRE     5'  CTCTGGCTTTTCCTCTCA    42073    TA  A      A
                                TG  AG AAAAGCCA GAG
                                ||  || |||||||| |||
                                AC  TC TTTTCGGT CTC
                                 TC  C      _
GAM1016  POLA      3'  GCAGTCTTTCCTCTCTTACA   34198       AAA  CCA
                                TGTAAGA   AG   AGAGACTGC
                                |||||||   ||   |||||||||
                                ACATTCT   TC   TTTCTGACG
                                    C__  C__
GAM1016  PSG5      3'  CAGTCCAAAATTGCTTTTTCTT 12444    T       CAAGA__
             CA                   TG AAGAAAAAGC      GACTG
                                || ||||||||||      |||||
                                AC TTCTTTTTCG      CTGAC
                                 _        TTAAAAC
GAM1016  SOCS5     3'  GCAGTGTTAGGCTTTTTCATAC 26681      A       AA  G
             A                   TGTA GAAAAAGCC  GA ACTGC
                                |||| |||||||||  || |||||
                                ACAT CTTTTTCGG  TT TGACG
                                  A       A_  G
GAM1016  BPES      3'  GCAGACCTCTTGGCCTTCTCTC 43797     A  A  A      A_
             ACA                   TGT AGA AA GCCAAGAG  CTGC
                                ||| ||| || ||||||||  ||||
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                                ACA TCT TT CGGTTCTC  GACG
                                  C   C  C       CA
GAM1016  C1orf16   3'  GCAGTCTCCCAGCCTCCACTTT 29913    T   AAAAA  CAA
              CA                   TG AAG    GC   GAGACTGC
                                || |||    ||   ||||||||
                                AC TTC    CG   CTCTGACG
                                 T   ACCTC  ACC
GAM1016  C20orf108 3'  CAATCTCAGCTTTTCTTA    55874        A  CAA    C
                                TAAGAAAA GC   GAGA TG
                                |||||||| ||   |||| ||
                                ATTCTTTT CG   CTCT AC
                                     _ A__    A
GAM1016  GAB3      3'  CTCTTGGCCTTTTCCCAC    55518    AA    A
                                GT  GAAAA GCCAAGAG
                                ||  ||||| ||||||||
                                CA  CTTTT CGGTTCTC
                                 CC    C
GAM1016  KIAA0451  5'  TCGTTTGGCTTCTTCTCAC   29783    A   A      A
                                GT AGAA AAGCCAAG GA
                                || |||| |||||||| ||
                                CA TCTT TTCGGTTT CT
                                 C   C       G
GAM1016  KIAA1323  3'  AGTTGCCTTTCTTACA      63721         AA  CAAGA
                                TGTAAGAAA  GC    GACT
                                |||||||||  ||    ||||
                                ACATTCTTT  CG    TTGA
                                     C_  _____
GAM1016  KIAA1966  3'  GCAGCCTCTTGTTTTTTTC   56725       C     A
                                GAAAAAG CAAGAG CTGC
                                ||||||| |||||| ||||
                                CTTTTTT GTTCTC GACG
                                    T     C
GAM1016  NAP1L2    5'  GCAGTCTCCGGCTCTCTCCTGC 42012     A  AAA    AA
              A                   TGTA GA   AGCC  GAGACTGC
                                |||| ||   ||||  ||||||||
                                ACGT CT   TCGG  CTCTGACG
                                  C  CTC    C_
GAM1016  NR6A1     3'  GCAGCCAATGCATTTTCTTACA 54017          A  CAAGAGA
                                TGTAAGAAAA GC      CTGC
                                |||||||||| ||      ||||
                                ACATTCTTTT CG      GACG
                                      A  TAACC__
GAM1016  NR6A1     3'  GCAGCCAATGCATTTTCTTACA 54023          A  CAAGAGA
                                TGTAAGAAAA GC      CTGC
                                |||||||||| ||      ||||
                                ACATTCTTTT CG      GACG
                                      A  TAACC__
GAM1016  NR6A1     3'  GCAGCCAATGCATTTTCTTACA 9446           A  CAAGAGA
                                TGTAAGAAAA GC      CTGC
                                |||||||||| ||      ||||
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                                ACATTCTTTT CG      GACG
                                      A  TAACC__
GAM1016  LOC127002 5'  GCAGTCTCTCTGTCTCTTAC   75126       AAAA  CA
                                GTAAGA    GC  AGAGACTGC
                                ||||||    ||  |||||||||
                                CATTCT    TG  TCTCTGACG
                                   C___  TC
GAM1016  LOC144681 3'  CAGTCTTACCATCTTCTTACA  84095        AAAGCCAA
                                TGTAAGAA       GAGACTG
                                ||||||||       |||||||
                                ACATTCTT       TTCTGAC
                                     CTACCA__
GAM1016  LOC144970 3'  CAGCCTCTTGGCTTCT      77530     AAA        A
                                AGA   AGCCAAGAG CTG
                                |||   ||||||||| |||
                                TCT   TCGGTTCTC GAC
                                  ___        C
GAM1016  LOC150279 3'  TAGTCAGTTTTTCTTACA     80483           G CAAGA
                                TGTAAGAAAAA C     GACTG
                                |||||||||||  |     |||||
                                ACATTCTTTTT G     CTGAT
                                      _ A____
GAM1016  LOC152453 5'  GTTTCTTGGCTCTTCCTCCCA  81478     TA  A  A
                                TG  AG AA AGCCAAGAGAC
                                ||  || ||  ||||||||||
                                AC  TC TT TCGGTTCTTTG
                                 CC  C  C
GAM1017  HYAL2     3'  AAGCCCAGGAGGGCATCCATAC 53700
            CA                    TGGTATGGATGCCCTCCTGGGTTT
                                ||||||||||||||||||||||||
                                ACCATACCTACGGGAGGACCCGAA

GAM1017  C1orf17   3'  AAACCCTCCCAGGCATCCCATA 68761         _     CTCCT
            CCA                    TGGTATGG ATGCC     GGGTTT
                                ||||||||  |||||     ||||||
                                ACCATACC TACGG     CCCAAA
                                     C     ACCCT
GAM1017  C20orf139 5'  ACCTGGGAGCATCCACACCA   85913      A      CC   TG
                                TGGT TGGATGC  TCC  GGT
                                ||||  |||||||  |||  |||
                                ACCA ACCTACG  AGG  CCA
                                  C       __   GT
GAM1017  DKFZp547I224 5'  CAGAAAGGACATCCACACCA   39951      A     C   C_
                                TGGT TGGATG CCT  CTG
                                ||||  ||||||  |||  |||
                                ACCA ACCTAC GGA  GAC
                                  C     A   AA
GAM1017  FLJ23510  5'  AAACCCAGGAGGAGAGCCTCCA 45620      T  ___
                                TGGA GC   CCTCCTGGGTTT
                                ||||  ||   ||||||||||||
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                                ACCT CG   GGAGGACCCAAA
                                  C  AGA
GAM1017 HSPC072   5' AAACCCAGAAGGACAACTCTCC 27171     TAT  A  C   C
             A                    TGG   GG TG CCT CTGGGTTT
                                  |||   || || ||| ||||||||
                                  ACC   TC AC GGA GACCCAAA
                                    TC_  A  A   A
GAM1017 KIAA0923  3' AAACCCAGGACTCCACAC    26703    A    TGCCC
                                  GT TGGA    TCCTGGGTTT
                                  || ||||    ||||||||||
                                  CA ACCT    AGGACCCAAA
                                   C   C____
GAM1017 NYD-SP12  3' AGGCAAGGGCATCCACTCCA   50070     TA        __
                                  TGG  TGGATGCCCT  CCT
                                  |||  ||||||||||  |||
                                  ACC  ACCTACGGGA  GGA
                                    TC         AC
GAM1017 PISD      5' AAACCCAGGAAGCGGCGCCACC 27541      AT  A   _ _
             A                    TGGT  GG TGCC CT CCTGGGTTT
                                  ||||  || |||| || |||||||||
                                  ACCA  CC GCGG GA GGACCCAAA
                                    __ _   C  A
GAM1017 SIRPB1    3'  AAACCCAGGAAAGCAGTCTCCA 21348       ___   CC
             T                    ATGGA   TGC  TCCTGGGTTT
                                  |||||   |||  ||||||||||
                                  TACCT   ACG  AGGACCCAAA
                                     CTG   AA
GAM1017 LOC154007 3'  AGGTTCAGAGGAATCCATACCA 81922          GC    C  GG
                                  TGGTATGGAT  CCTC TG  TTT
                                  ||||||||||  |||| ||  |||
                                  ACCATACCTA  GGAG AC  GGA
                                        A_    _ TT
GAM1017 LOC161734 3'  CAGAAAGGACATCCACACCA   88461      A     C   C_
                                  TGGT TGGATG CCT  CTG
                                  |||| ||||||  |||  |||
                                  ACCA ACCTAC GGA  GAC
                                    C     A   AA
GAM1017 LOC90593  3'  CAGAAAGGACAACCACACCA   64202      A   A  C   C_
                                  TGGT TGG TG CCT  CTG
                                  |||| ||| || |||  |||
                                  ACCA ACC AC GGA  GAC
                                    C   A  A   AA
GAM1017 LOC92080  3'  GGGAGGGCACCCACCCA     68632     TA   A
                                  TGG  TGG TGCCCTCCT
                                  |||  ||| |||||||||
                                  ACC  ACC ACGGGAGGG
                                    C_   C
GAM1018 CALM1     3'  TGCATGCAGCTTGACGATTGAG 23538         AT__   TTA
                                  TTCAATCG    GCT   CATGCA
                                  ||||||||    |||   ||||||
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                                GAGTTAGC   CGA  GTACGT
                                    AGTT  C__
GAM1018 MTMR2    3' TGCATGTAAAAGATGTATT   32913     ____
                                GATGC   TTTACATGCA
                                |||||   ||||||||||
                                TTATG   AAATGTACGT
                                   TAGA
GAM1018 TTC3     5' TGCATGTAAAACATTTGGT   13888     _ C
                                ATCGA TG TTTACATGCA
                                ||||| || ||||||||||
                                TGGTT AC AAATGTACGT
                                   T  A
GAM1018 WISP1    3' TGCATGTATTAGCTCACTGAA 55942     ATC  T  T_
                                TTCA  GA GCT  TACATGCA
                                ||||  || |||  ||||||||
                                AAGT  CT CGA  ATGTACGT
                                  CA_ _  TT
GAM1018 FLJ20758 5' CATTTAATGCATTGATTGAA  36080         T  C
                                TTCAATCGATGC TTA ATG
                                |||||||||||| ||| |||
                                AAGTTAGTTACG AAT TAC
                                       T  T
GAM1018 KIAA1372 5' CATGTAAAGTTGATGGAA   93319    A   AT
                                TTC ATCG  GCTTTACATG
                                ||| ||||  ||||||||||
                                AAG TAGT  TGAAATGTAC
                                  G   __
GAM1018 MGC12466 3' CATGTAAGGAAGATTAGAA  79794    _   GATG
                                TTC AATC   CTTTACATG
                                ||| ||||   |||||||||
                                AAG TTAG   GGAATGTAC
                                  A   AA__
GAM1018 LOC254987 3' TGCATGTAAGTGTTGACTGA  97411    A      T
                                TCA TCGATGCTT ACATGCA
                                ||| ||||||||| |||||||
                                AGT AGTTGTGAA TGTACGT
                                  C       _
GAM1018 LOC85479  5' TGCATAAGGGAGCATCAAATGA 53572     ATC      AC_
            A                    TTCA  GATGCTTT  ATGCA
                                ||||  ||||||||  |||||
                                AAGT  CTACGAGG  TACGT
                                   AAA      GAA
GAM1019 COL4A4   3' ACGAAACAAAGACAATTTAT  5402     TT      A
                                GTA  ATTGTCTTT TTTCGT
                                |||  ||||||||| ||||||
                                TAT  TAACAGAAA AAAGCA
                                  T_       C
GAM1019 EIF4G3   3' ACAAAATAAAGACAAACATTGC 15000    TTA_        C
                                GTA   TTGTCTTTATTT GT
                                |||   |||||||||||| ||
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                                CGT    AACAGAAATAAA CA
                                  TACA          A
GAM1020 ALDH3A2  3' CTCATCAGTCGTTCATGGTCA 69799     G  T    ACA
                                TGA CT TGAA   ACTGATGAG
                                ||| || ||||   |||||||||
                                ACT GG ACTT   TGACTACTC
                                  _  T   GC_
GAM1020 CALCR    3' CAGCTTCAAAGCTTAA      9983           ACAA
                                TTGAGCTTTGAA   CTG
                                ||||||||||||   |||
                                AATTCGAAACTT   GAC
                                       C___
GAM1020 DLEC1    3' CTCATCAGTTGAGGGCAGCTC  24722      TTGAAA
                                GAGCT     CAACTGATGAG
                                |||||     ||||||||||
                                CTCGA     GTTGACTACTC
                                   CGGGA_
GAM1020 DLEC1    3' CTCATCAGTTGAGGGCAGCTC  24732      TTGAAA
                                GAGCT     CAACTGATGAG
                                |||||     ||||||||||
                                CTCGA     GTTGACTACTC
                                   CGGGA_
GAM1020 FBXL7    3' CATCAGTTGCTTTTACTCAG   25488      CTT    _
                                TTGAG   TGAAA CAACTGATG
                                |||||   ||||| |||||||||
                                GACTC   ATTTT GTTGACTAC
                                   ___     C
GAM1020 MECP2    3' CTCACCAGCTGTGTCCGGCCCA 18398     A   TT  A   A   A
            G                    TTG GCT  GA ACA CTG TGAG
                                ||| |||  || ||| ||| ||||
                                GAC CGG  CT TGT GAC ACTC
                                  C   C_  G   C   C
GAM1020 RNF4     3' CACCAGTTGTTCTCAG      12880      CTTTGA       A
                                TTGAG     AACAACTG TG
                                |||||     |||||||| ||
                                GACTC     TTGTTGAC AC
                                  _______       C
GAM1020 SLC12A7  3' CATCAACAAAGTTCAA      22737          AAACAAC
                                TTGAGCTTTG      TGATG
                                ||||||||||      |||||
                                AACTTGAAAC      ACTAC
                                      A_______
GAM1020 TBX1     3' TCAGGTTTCAGAGCCCAA    21140     A        AA
                                TTG GCTTTGAAAC  CTGA
                                ||| ||||||||||  ||||
                                AAC CGAGACTTTG  GACT
                                  C         __
GAM1020 ZNF36    3' CTCATCAGTCATTCACTGATCA 95581     GCTT    ACA
            G                    TTGA    TGAA   ACTGATGAG
                                ||||    ||||   |||||||||
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                                GACT   ACTT  TGACTACTC
                                  AGTC   AC_
GAM1020 AKAP8    3' CAGGTTTCAAAGCTGAA    20733   G       AA
                                TT AGCTTTGAAAC  CTG
                                || ||||||||||  |||
                                AA TCGAAACTTTG  GAC
                                 G        __
GAM1020 ANKT     3' TTATCACCTTAAAGCTCAA   33461         AACAAC
                                TTGAGCTTTGA     TGATGA
                                ||||||||||     ||||||
                                AACTCGAAATT     ACTATT
                                      CC____
GAM1020 BZW1     3' CTCCAGATATCCTAAAGCTCAA 28586        AAACAA  AT
                                TTGAGCTTTG     CTG  GAG
                                |||||||||     |||  |||
                                AACTCGAAAT     GAC  CTC
                                      CCTATA  __
GAM1020 FBXO21   3' CTCATCAGTCAAATCCAAAGTC 54348     G    AAACA_
                AA                  TTGA CTTTG     ACTGATGAG
                                ||||| |||||     |||||||||
                                AACT GAAAC     TGACTACTC
                                  _    CTAAAC
GAM1020 FHOD2    5' CATACATACATTCAAAAGCTCA 74261        _  ACAACTG
                A                   TTGAGCTTT GAA      ATG
                                ||||||||| |||      |||
                                AACTCGAAA CTT      TAC
                                     A   ACATACA
GAM1020 KIAA0316 3' CTCACCAAAAGTTTTTCCCAAA 70244        ____   AAC  A
                GCTCAA                 TTGAGCTTTG   AAAC   TG TGAG
                                ||||||||||   ||||  || ||||
                                AACTCGAAAC   TTTG   AC ACTC
                                     CCTT   AAA  C
GAM1020 KIAA1240 3' TGTCTTATTCTCAAAGCTCAA  67296         AACAACT
                                TTGAGCTTTGA      GATG
                                ||||||||||      ||||
                                AACTCGAAACT      CTGT
                                      CTTATT_
GAM1020 MGC10966 5' CTCACCACCATCCCAGAGCTCA 49684         AAACAAC  A
                A                   TTGAGCTTTG      TG TGAG
                                ||||||||||      || ||||
                                AACTCGAGAC      AC ACTC
                                     CCTACC_  C
GAM1020 LOC118786 5' CTCATCAGTCACATGGCCCAG  76009    A   T  AAACA
                                TTG GCT TG    ACTGATGAG
                                ||| ||| ||    |||||||||
                                GAC CGG AC    TGACTACTC
                                  C   T  AC___
GAM1020 LOC145739 3' TCATTCTTCAAAGCCCAG    77906     A       ACAACT
                                TTG GCTTTGAA     GATGA
                                ||| ||||||||     |||||
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                                GAC CGAAACTT      TTACT
                                  C       C_____
GAM1020  LOC150113 3'  TCATCCTCCAAGGCTCAA    88571          AAACAACT
                                TTGAGCTTTG       GATGA
                                ||||||||||       |||||
                                AACTCGGAAC       CTACT
                                     CTC_____
GAM1020  LOC150311 5'  TCATCAGCCAAAACTCAA    80568       C    AAACAA
                                TTGAG TTTG     CTGATGA
                                ||||| ||||     |||||||
                                AACTC AAAC     GACTACT
                                   A    C_____
GAM1020  LOC151579 3'  CTCCAGATATCCTAAAGCTCAA 69987          AAACAA   AT
                                TTGAGCTTTG     CTG  GAG
                                ||||||||||     |||  |||
                                AACTCGAAAT     GAC  CTC
                                     CCTATA   __
GAM1020  LOC154739 5'  GGTCCATTTCAAAGCGCAA    87441     A        CA_
                                TTG GCTTTGAAA   ACT
                                ||| |||||||||   |||
                                AAC CGAAACTTT   TGG
                                  G        ACC
GAM1020  LOC254556 3'  CACCAGTTGTTCTCAG      96256       CTTTGA       A
                                TTGAG     AACAACTG TG
                                |||||     |||||||| ||
                                GACTC     TTGTTGAC AC
                                   _______       C
GAM1020  LOC256337 3'  CTCATCAGAAACAAAGACTCAA 96342       _    AAACAA
                                TTGAG CTTTG     CTGATGAG
                                ||||| |||||     ||||||||
                                AACTC GAAAC     GACTACTC
                                   A     AAA___
GAM1020  LOC257058 5'  AGTCCTATTTCAAGCTCAA    99346         T    CA__
                                TTGAGCTT GAAA    ACT
                                |||||||| ||||    |||
                                AACTCGAA CTTT    TGA
                                     _    ATCC
GAM1020  LOC257068 3'  CTCATCAGTCATTCAGAAATCA 97505      GC      ACA
            A                    TTGA  TTTGAA   ACTGATGAG
                                ||||  ||||||   |||||||||
                                AACT  AGACTT   TGACTACTC
                                   AA     AC_
GAM1020  LOC51030  3'  TTAGTCTGTCTCAAAGCTC    32697         A  _
                                GAGCTTTGA ACA ACTGA
                                ||||||||| ||| |||||
                                CTCGAAACT TGT TGATT
                                     C   C
GAM1020  LOC91522  3'  CTCATCAGCCTCCAAACTCAA  66916       C    AAACAA
                                TTGAG TTTG     CTGATGAG
                                ||||| ||||     ||||||||
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                                AACTC AAAC     GACTACTC
                                  _   CTCC__
GAM1021  ABL1     3'  ACAAACGGAGCCCCTG      18953         GG
                                CAGGGGCTTT  GTTTGT
                                ||||||||||  ||||||
                                GTCCCCGAGG  CAAACA
                                     __
GAM1021  ABL1     3'  ACAAACGGAGCCCCTG      24605         GG
                                CAGGGGCTTT  GTTTGT
                                ||||||||||  ||||||
                                GTCCCCGAGG  CAAACA
                                     __
GAM1021  DNMT3B   3'  ACAAACCCAAGGGCAGGG    23545    AGGG  _
                                CC   GCT TTGGGTTTGT
                                ||   ||| ||||||||||
                                GG   CGG AACCCAAACA
                                 GA__  G
GAM1021  EPHB2    3'  AACCAAGCGCCTGGAG       16696       G   TG
                                CTCCAGG GCTT  GGTT
                                ||||||| ||||  ||||
                                GAGGTCC CGAA  CCAA
                                    G   __
GAM1021  EPHB2    3'  AACCAAGCGCCTGGAG       34343       G   TG
                                CTCCAGG GCTT  GGTT
                                ||||||| ||||  ||||
                                GAGGTCC CGAA  CCAA
                                    G   __
GAM1021  FCN2     3'  ACAAATGCTGCCCTCTGGAG   32342       _   TTTGG
                                CTCCAG GGGC    GTTTGT
                                ||||||| ||||    ||||||
                                GAGGTC CCCG    TAAACA
                                   T   TCG__
GAM1021  FCN2     3'  ACAAATGCTGCCCTCTGGAG   32343       _   TTTGG
                                CTCCAG GGGC    GTTTGT
                                ||||||| ||||    ||||||
                                GAGGTC CCCG    TAAACA
                                   T   TCG__
GAM1021  IRAK1    3'  ACAGTGAGAAGCCCCTGGA    9605          GGGT
                                TCCAGGGGCTTT   TTGT
                                ||||||||||||   ||||
                                AGGTCCCCGAAG   GACA
                                     AGT_
GAM1021  KLHL3    3'  ACAATACAGACCCTGGAG     88841        GC   GGT
                                CTCCAGGG  TTTG  TTGT
                                ||||||||  ||||  ||||
                                GAGGTCCC  AGAC  AACA
                                    __   AT_
GAM1021  LRP1     5'  ACAAGGGGAGCCCCCAGAG   11356     CA      GGG
                                CTC  GGGGCTTT  TTTGT
                                |||  ||||||||  |||||
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                                GAG  CCCCGAGG   GAACA
                                  AC       G__
GAM1021  MID1     5'  ACAAACCCCCATCCTGGG    53901        GCTTT
                                TCCAGGG    GGGTTTGT
                                |||||||    ||||||||
                                GGGTCCT    CCCAAACA
                                   ACC__
GAM1021  NT5C2    3'  ACAAAGGAACAAGCCCCCAGA  25250    CA      T GG__
                                TC  GGGGCTT G    TTTGT
                                ||  ||||||| |    |||||
                                AG  CCCCGAA C    AAACA
                                 AC       _ AAGG
GAM1021  PDE7A    3'  ACAAACTGCCTCCTGGAG    66131        _   TTTG
                                CTCCAGG GGC    GGTTTGT
                                ||||||| |||    |||||||
                                GAGGTCC CCG    TCAAACA
                                   T  _____
GAM1021  SLC2A6   3'  ACAAACCTGCACCCTGGG    34564        _  TTT
                                TCCAGGG GC   GGGTTTGT
                                ||||||| ||   ||||||||
                                GGGTCCC CG   TCCAAACA
                                   A  ___
GAM1021  DKFZP434B103 3'  ACAAACCCAGGGCTGAG     32221     CAGG
                                CTC    GGCTTTGGGTTTGT
                                |||    ||||||||||||||
                                GAG    TCGGGACCCAAACA
                                  _____
GAM1021  DKFZp761B1514 3'  ACGGTGTAAAGTCCCCTGGA   51137        _    GGT
                                TCCAGGGG CTTTG   TTGT
                                |||||||| |||||   ||||
                                AGGTCCCC GAAAT   GGCA
                                    T    GT_
GAM1021  DKFZp761O17121 3'  ACAGGAGAAGCTCCCCAGAG   51130     CA  _    GGGT
                                CTC  GGG GCTTT    TTGT
                                |||  ||| |||||    ||||
                                GAG  CCC CGAAG    GACA
                                  AC   T    AG__
GAM1021  DRCTNNB1A 3'  ACAATTTGCTCAAAGCCCTGGA 51807        G       ___
                                TCCAGGG CTTTGGGT   TTGT
                                ||||||| ||||||||   ||||
                                AGGTCCC GAAACTCG   AACA
                                   _       TTT
GAM1021  FLJ10569  5'  ACAAACCCAATTTTTAAGA   36825    CAG   CT
                                TC   GGG  TTGGGTTTGT
                                ||   |||  ||||||||||
                                AG   TTT  AACCCAAACA
                                 AA_   TT
GAM1021  FLJ12572  3'  ACAAACCTGGATGCCACCTGGA 43539        _  _  TG
            G                    CTCCAGG GGC TT  GGTTTGT
                                ||||||| ||| ||  |||||||
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                                GAGGTCC CCG AG  CCAAACA
                                    A   T  GT
GAM1021  FLJ23186  5'  ACAAGGAAAGCCCCTGGAG   61037          GGG
                                CTCCAGGGGCTTT   TTTGT
                                ||||||||||||   |||||
                                GAGGTCCCCGAAA   GAACA
                                   G__
GAM1021  FLJ25410  5'  ACAAGGCAGCTCCTGGA    58770         TTGGG
                                TCCAGGGGCT    TTTGT
                                ||||||||||    |||||
                                AGGTCCTCGA    GAACA
                                    CG___
GAM1021  HPIP      3'  ACAAACCCTAGGCCCTTG    40423         T
                                CAGGGGCTT GGGTTTGT
                                ||||||||| ||||||||
                                GTTCCCGGA CCCAAACA
                                    T
GAM1021  KIAA0255  3'  ACAAGAAAATCCCCTGGA    29126        CT  GGG
                                TCCAGGGG  TT   TTTGT
                                ||||||||  ||   |||||
                                AGGTCCCC  AA   GAACA
                                    T_  AA_
GAM1021  KIAA1100  5'  ACAAAGAGAGAGGCCCCGGA   30436     A       GGG_
                                TCC GGGGCTTT    TTTGT
                                ||| ||||||||    |||||
                                AGG CCCCGGAG    AAACA
                                  _       AGAG
GAM1021  KIAA1432  5'  ACAAACCCAGAATCCCAGGAG  67299      A   GC
                                CTCC GGG  TTTGGGTTTGT
                                |||| |||  ||||||||||
                                GAGG CCC  AGACCCAAACA
                                  A   TA
GAM1021  KIAA1656  3'  ACAAACCACTTGCCCTGGA    66354        G TTTG
                                TCCAGGG C    GGTTTGT
                                ||||||| |    |||||||
                                AGGTCCC G    CCAAACA
                                    _ TTCA
GAM1021  KIAA1666  3'  ACAAGCCAACCCCTGAGAG    65853     _     CTTTG
                                CTC CAGGGG     GGTTTGT
                                ||| ||||||     |||||||
                                GAG GTCCCC     CCGAACA
                                  A     AA___
GAM1021  LRRFIP2   3'  ACAAACCCAAAGGGGGAG    35293      AGGGG
                                CTCC     CTTTGGGTTTGT
                                ||||     ||||||||||||
                                GAGG     GAAACCCAAACA
                                  GG___
GAM1021  MANBAL    3'  ACAAACTTCCTGAGCCTCTG   42213         T __
                                CAGGGGCTT GG  GTTTGT
                                ||||||||| ||  ||||||
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                                GTCTCCGAG CC  CAAACA
                                     T  TT
GAM1021  MARCO    3'  AACTGAGCAGCCTCTGGAG   23188          _ G
                                CTCCAGGGGCT TT GGTT
                                |||||||||| || ||||
                                GAGGTCTCCGA GA TCAA
                                      C  G
GAM1021  MGC11034 3'  GGGCAAAAGCCCCTGGAG    49574           GG
                                CTCCAGGGGCTTT  GTTT
                                ||||||||||||  ||||
                                GAGGTCCCCGAAA  CGGG
                                       A_
GAM1021  MGC13523 5'  ACAAACCCAGCGTCCCTG    54168        T
                                CAGGGGC TTGGGTTTGT
                                ||||||| |||||||||
                                GTCCCTG GACCCAAACA
                                    C
GAM1021  OMD      5'  ACAAATTCATCAACCCCTG   18460       CTT_
                                CAGGGG   TGGGTTTGT
                                ||||||   |||||||||
                                GTCCCC   ACTTAAACA
                                   AACT
GAM1021  PRO1048  3'  ACAAGTGCAAACCCATGGA   38100     G  C   G
                                TCCA GGG TTTG GTTTGT
                                |||| ||| |||| ||||||
                                AGGT CCC AAAC TGAACA
                                  A  _   G
GAM1021  Rabip4R  3'  ACATGAAAAGCCCCCGGAG   36272     A      GGGTT
                                CTCC GGGGCTTT    TGT
                                |||| ||||||||    |||
                                GAGG CCCCGAAA    ACA
                                  C       AGT__
GAM1021  SCAND1   5'  ACAAAGAGTGACGCCCGGAG   33795     AG   _  TGGG
                                CTCC  GGGC TT   TTTGT
                                ||||  |||| ||   |||||
                                GAGG  CCCG AG   AAACA
                                  __   C  TGAG
GAM1021  SCAND1   5'  ACAAAGAGTGACGCCCGGAG   54392     AG   _  TGGG
                                CTCC  GGGC TT   TTTGT
                                ||||  |||| ||   |||||
                                GAGG  CCCG AG   AAACA
                                  __   C  TGAG
GAM1021  SEMA4G   5'  ACAGTGGAAGACCCTGGAG   96321        G   GGGT
                                CTCCAGGG CTTT   TTGT
                                |||||||| ||||   ||||
                                GAGGTCCC GAAG   GACA
                                    A   GT__
GAM1021  SNRPD1   3'  ACAAATCAGGTAGCCCCTG   23661        TTG_
                                CAGGGGCT   GGTTTGT
                                ||||||||   |||||||
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                                GTCCCCGA   CTAAACA
                                    TGGA
GAM1021  SS18L1   3'  CATGCAGCCCCTGGAG     65952          TTGG  T
                                CTCCAGGGGCT   GT TG
                                ||||||||||   || ||
                                GAGGTCCCCGA   CG AC
                                      ____  T
GAM1021  STAF65(gamma) 5'  CCGAGGAAACCCCTGGAG    30065         ___
                                CTCCAGGGG  CTTTGG
                                |||||||||  ||||||
                                GAGGTCCCC  GGAGCC
                                     AAA
GAM1021  TRPV6    3'  ACAAAAACCAAACACCCAGAG  38461    CA  GC    G_
                                CTC  GGG  TTTGG  TTTGT
                                |||  |||  |||||  |||||
                                GAG  CCC  AAACC  AAACA
                                  A_  AC    AA
GAM1021  LOC145127 3'  ACAAGGTGAGCTCCTGGAG   77541          TGGG
                                CTCCAGGGGCTT   TTTGT
                                ||||||||||||   |||||
                                GAGGTCCTCGAG   GAACA
                                      TG__
GAM1021  LOC146272 5'  AGCCTCAGAAACCCCCAGAG  78324    CA   C_   _
                                CTC  GGGG  TTTG GGTT
                                |||  ||||  |||| ||||
                                GAG  CCCC  AGAC CCGA
                                  AC   AA   T
GAM1021  LOC146475 5'  ACAAACCAAGGAACACCTGGAG 84688       GG__    G
                                CTCCAGG   CTTTGG TTTGT
                                |||||||   |||||| |||||
                                GAGGTCC   GGAACC AAACA
                                    ACAA    _
GAM1021  LOC148987 3'  ACCCTGAAAGCCCCTGAGAG  79852    _       __
                                CTC CAGGGGCTTT  GGGT
                                ||| ||||||||||  ||||
                                GAG GTCCCCGAAA  CCCA
                                  A        GT
GAM1021  LOC150221 3'  ACAAGCCAACCCCTGAGAG   65877    _    CTTTG
                                CTC CAGGGG    GGTTTGT
                                ||| ||||||    |||||||
                                GAG GTCCCC    CCGAACA
                                  A     AA___
GAM1021  LOC157349 3'  ACAAAAGAAGCCCATGGAG   82326     G     GGG
                                CTCCA GGGCTTT   TTTGT
                                ||||| |||||||   |||||
                                GAGGT CCCGAAG   AAACA
                                   A      A__
GAM1021  LOC162333 5'  ACGAGAAAGGCCCCAGAG    88485    CA      GGGT
                                CTC  GGGGCTTT   TTGT
                                |||  ||||||||   ||||
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                                GAG  CCCCGGAA    AGCA
                                  A_       AG__
GAM1021  LOC170037 5'  GGTCCAAAGCCCCAGGAG    88596      A        GT
                                CTCC GGGGCTTTGG  T
                                |||| ||||||||||  |
                                GAGG CCCCGAAACC  G
                                  A         TG
GAM1021  LOC197285 3'  ACAAGGTGAGCTCCTGGAG    89149           TGGG
                                CTCCAGGGGCTT    TTTGT
                                ||||||||||||    |||||
                                GAGGTCCTCGAG    GAACA
                                       TG__
GAM1021  LOC197322 5'  ACAAGGTCAGCGCCCTGGAG   91308        _   TT  G
                                CTCCAGGG GCT  GG TTTGT
                                |||||||| |||  || |||||
                                GAGGTCCC CGA  CT GAACA
                                     G   __  G
GAM1021  LOC91917  3'  ACAAGGTGAGCTCCTGGAG    68139           TGGG
                                CTCCAGGGGCTT    TTTGT
                                ||||||||||||    |||||
                                GAGGTCCTCGAG    GAACA
                                       TG__
GAM1022  AKAP1     3'  ACTATGGGTTCTCTTCGCAAA  14472       A  CTT       C
                                TTTGT GA   GGAACCCA AGT
                                ||||| ||   |||||||| |||
                                AAACG CT   TCTTGGGT TCA
                                   _  TC_       A
GAM1022  AKAP1     3'  ACTATGGGTTCTCTTCGCAAA  58373       A  CTT       C
                                TTTGT GA   GGAACCCA AGT
                                ||||| ||   |||||||| |||
                                AAACG CT   TCTTGGGT TCA
                                   _  TC_       A
GAM1022  EGF       3'  ACTATAGGTTTTGGTTCCACAA 10488      A  C TG    CAC
                                TTGT GA T  GAACC   AGT
                                |||| || |  |||||   |||
                                AACA CT G  TTTGG   TCA
                                  C  T GT    ATA
GAM1022  EZH1      3'  GACTGTGGGTTCCAAATTAC   10551      AC
                                GTAG  TTGGAACCCACAGTC
                                ||||  ||||||||||||||||
                                CATT  AACCTTGGGTGTCAG
                                  A_
GAM1022  STAC      3'  GACTGTGGAGTAATAGCCACAA 13427       AGA  TGGA  _
              A                  TTTGT   CT    AC CCACAGTC
                                |||||   ||    || ||||||||
                                AAACA   GA    TG GGTGTCAG
                                  CC_  TAA_  A
GAM1022  CCR1      3'  GACTGTGGGCTCCATTC     8927     CT    A
                                GA  TGGA CCCACAGTC
                                ||  |||| |||||||||
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                                CT  ACCT GGGTGTCAG
                                 T_   C
GAM1022  FLJ10483  3'  GACTGTGGAAGAGATTACAAA  36652       A   GGAAC
                                TTTGTAG CTT    CCACAGTC
                                ||||||| |||    ||||||||
                                AAACATT GAG    GGTGTCAG
                                   A   AA___
GAM1022  KIAA1871  3'  ACTGTAAGAGTCTACAAA    61890         GGAACCC
                                TTTGTAGACTT      ACAGT
                                ||||||||||      |||||
                                AAACATCTGAG      TGTCA
                                      AA_____
GAM1022  LOC150821 3'  GGGTTCCACATCCACAAA    60944      A  CT
                                TTTGT GA  TGGAACCC
                                ||||| ||  ||||||||
                                AAACA CT  ACCTTGGG
                                   C  AC
GAM1022  LOC151057 3'  ACTGTGGGTACACCTATAAA   86379       ACT  GA
                                TTTGTAG   TG  ACCCACAGT
                                |||||||   ||  |||||||||
                                AAATATC   AC  TGGGTGTCA
                                   C__  A_
GAM1022  LOC157507 5'  ACTGTAAAAGTCTGCAAA    82377         GGAACCC
                                TTTGTAGACTT      ACAGT
                                ||||||||||      |||||
                                AAACGTCTGAA      TGTCA
                                      AA_____
GAM1022  LOC203339 5'  GGATTCCCAGTCTACAAA    92214         T    C
                                TTTGTAGACT GGAA CC
                                |||||||||| |||| ||
                                AAACATCTGA CCTT GG
                                      C    A
GAM1022  LOC51030  3'  ACTGTAAATTAAACCAATCTAC 32695        C    AACCC___
            AAA                   TTTGTAGA TTGG       ACAGT
                                |||||||| ||||       |||||
                                AAACATCT AACC       TGTCA
                                   _   AAATTAAA
GAM1022  LOC90906  3'  GACTGTGGATCCCAAACTTTGC 64951       C_   AAC
            A                    TGTAGA  TTGG   CCACAGTC
                                ||||||  ||||   ||||||||
                                ACGTTT  AACC   GGTGTCAG
                                   CA    CTA
GAM1023  CDH12    3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                      AA___   AC
GAM1023  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007       CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
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                                ATGTG  GAGGGTTCTT TTA
                                   AC         G
GAM1023  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT    98090       T    AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||     ||||||
                                TGGTG GGGT     TTATTC
                                  _    GTCA_
GAM1023  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
           A                     TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM1023  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM1023  HMP19     3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
           TA                    TACA    TCC    GAAGAATAAG
                                ||||    |||    ||||||||||
                                ATGT    AGG    TTTCTTATTC
                                  AAA_   ATTG
GAM1023  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68742             _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                         G
GAM1023  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM1023  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748      CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM1023  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM1023  OSBPL11   3'  CTTAATTTCCCAAGAGTGGTG  43206        CCAA    AA
                                CACCACTC    GAAG  TAAG
                                ||||||||    ||||  ||||
                                GTGGTGAG    CTTT  ATTC
                                     AACC    A_
GAM1023  YME1L1    3'  TCATTCTTGATGTGGTGTA    58438         TCC     _
                                TACACCAC   CAAGAA GA
                                ||||||||   |||||| ||
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                                ATGTGGTG  GTTCTT CT
                                    TA_    A
GAM1023 ZNF262   3' CTTATTTTGTTTGGGAGT   18723       A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                   G
GAM1023 LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_   AAGA
                                TACACCAC  CCAAG   ATA
                                ||||||||  |||||   |||
                                ATGTGGTG  GGTTC   TGT
                                    CAA   GG__
GAM1024 ELOVL4   3' ACAACTGGAAATAAAGT    42988      AC
                                ACTTTG  TTCCGGTTGT
                                ||||||  ||||||||||
                                TGAAAT  AAGGTCAACA
                                   A_
GAM1024 RENT1    3' GCGCTGCACACCGAAAGCCCAA 12816    A_  C   _   T
            A                    TTTG  CTT CGGT TGTA CGC
                                ||||  ||| |||| |||| |||
                                AAAC  GAA GCCA ACGT GCG
                                  CC  A   C   C
GAM1024 SLC16A2  3' ACAATCTCCTTGGAGTCAAAG 22520        C____
                                CTTTGACTTC    GGTTGT
                                ||||||||||    ||||||
                                GAAACTGAGG    CTAACA
                                      TTCCT
GAM1024 CLSTN1   3' GACGCATGGCCCGAAGTCAAAG 30789        C  __  TA
            T                    ACTTTGACTTC GGT  TG  TC
                                ||||||||||| |||  ||  ||
                                TGAAACTGAAG CCG  AC  AG
                                      C  GT  GC
GAM1024 DNAM-1   3' GACATCACCAACAGTCAAAG  22683       TCC  T  A
                                CTTTGACT  GGT GT TC
                                ||||||||  ||| || ||
                                GAAACTGA  CCA TA AG
                                    CAA   C  C
GAM1024 FBXO8    5' ACAATAGGAAACGTCAAA    25158      __   G
                                TTTGAC  TTCC GTTGT
                                ||||||  |||| |||||
                                AAACTG  AAGG TAACA
                                   CA   A
GAM1024 FLJ20315 3' ACAACAAAGGAAAAGCAAAGT 35414      AC_   G__
                                ACTTTG  TTCC  GTTGT
                                ||||||  ||||  |||||
                                TGAAAC  AAGG  CAACA
                                   GAA   AAA
GAM1024 PRO1853  3' GGTAACAAAAGTCAAAGT    38380       CCGG  _
                                ACTTTGACTT   TTGT ATC
                                ||||||||||   |||| |||
```

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                                TGAAACTGAA    AACA TGG
                                      ____    A
GAM1024  SUCLG1    3'  GTACAACTGGAAGCCAAA    15243      A
                                TTTG CTTCCGGTTGTAT
                                |||| ||||||||||||
                                AAAC GAAGGTCAACATG
                                  C
GAM1024  LOC114987 3'  GCAATGTGAAGAATCAAAGT   59797        __    CG
                                ACTTTGA  CTTC  GTTGT
                                |||||||  ||||  |||||
                                TGAAACT  GAAG  TAACG
                                    AA    TG
GAM1024  LOC154062 3'  ACAATGGAAAAATGTCAAAGT  81936        ____    G
                                ACTTTGAC    TTCCG TTGT
                                ||||||||    ||||| ||||
                                TGAAACTG    AAGGT AACA
                                     TAAA    _
GAM1024  LOC158709 5'  GCAATTCTGGAAGTCAAA    82865          __
                                TTTGACTTCCGG  TTGT
                                ||||||||||||  ||||
                                AAACTGAAGGTC  AACG
                                       TT
GAM1024  LOC170284 5'  GCAACAGGATCGGAAGCCAAAG 83477       A       GTATC
           T                     ACTTTG CTTCCGGTT    GC
                                ||||||| |||||||||    ||
                                TGAAAC GAAGGCTAG    CG
                                   C        GACAA
GAM1024  LOC253461 3'  ACATGCCGGAAGCCAAAG    98023      A      _
                                CTTTG CTTCCGGT TGT
                                ||||| |||||||| |||
                                GAAAC GAAGGCCG ACA
                                  C       T
GAM1024  LOC56959  5'  ACAATGTAGAGATGTCAAAGT  82810        T  CG___
                                ACTTTGAC TC    GTTGT
                                |||||||| ||    |||||
                                TGAAACTG AG    TAACA
                                     T  AGATG
GAM1025  HRH1      3'  CTCAAACATGTTTAGAGTGGA  7819      A    TGG
                                TCCA TCTGA   GCATGTTTGAG
                                |||| |||||   ||||||||||
                                AGGT AGATT   TGTACAAACTC
                                  G    ___
GAM1025  TRIM37    3'  CTCAAATTTGTCATCAG     31625       G  T
                                CTGATGG CA GTTTGAG
                                ||||||| || |||||||
                                GACTACT GT TAAACTC
                                     _ T
GAM1025  HTMP10    3'  CTCAAAAAAGCCATCAGATCTG 53758    CA       G ATG
           A                     TC  ATCTGATGG C   TTTGAG
                                ||  |||||||| |   ||||||
```

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                                AG  TAGACTACC G   AAACTC
                                 TC        _ AAA
GAM1025  PAK2     5'  CTCAAATATCACCAAACTAGA  67140      A__   GC
                                TCTG   TGG  ATGTTTGAG
                                ||||   |||  |||||||||
                                AGAT   ACC  TATAAACTC
                                  CAA   AC
GAM1025  SEMA6A   3'  CTCGAGTACCCACCAGA     40818      A   CA
                                TCTG TGGG  TGTTTGAG
                                |||| ||||  ||||||||
                                AGAC ACCC  ATGAGCTC
                                  C   __
GAM1025  TTY7     3'  TCAAACATGCAGGCTGGA    50019      AT  GATGG
                                TCCA  CT    GCATGTTTGA
                                ||||  ||    ||||||||||
                                AGGT  GA    CGTACAAACT
                                  CG  _____
GAM1025  LOC144766 3'  CTCAAACATGAGAAGACTGGG  77481      A   GATGGG
                                TCCA TCT     CATGTTTGAG
                                |||| |||     ||||||||||
                                GGGT AGA     GTACAAACTC
                                  C   AGA___
GAM1025  LOC201685 5'  TAAACACCCATCAGATGGA   91845      A       CA
                                TCCA TCTGATGGG  TGTTTG
                                |||| |||||||||  ||||||
                                AGGT AGACTACCC  ACAAAT
                                  _       __
GAM1025  LOC221596 5'  CTCAAACAAAACTCAGATT   93623        TG GCA
                                AATCTGA  G   TGTTTGAG
                                |||||||  |   ||||||||
                                TTAGACT  C   ACAAACTC
                                   __ AAA
GAM1025  LOC93622  3'  CTCTGCAGACCATCAGAT    57729         GCA   TT
                                ATCTGATGG   TGT  GAG
                                |||||||||   |||  |||
                                TAGACTACC   ACG  CTC
                                     AG_   T_
GAM1026  ABCC3     3'  TCTTTGACCACGTCATCGGGCC 39622           CCACAG
            A                    TGGCCTGATGAT     CGGAGA
                                 ||||||||||||     ||||||
                                 ACCGGGCTACTG     GTTTCT
                                       CACCA_
GAM1026  ADAMTS3   3'  TCTCTATAGATCGTCAGCTCA  27272    GC       CACAGC
                                 TG  CTGATGATC     GGAGA
                                 ||  |||||||||     |||||
                                 AC  GACTGCTAG     TCTCT
                                  TC        ATA___
GAM1026  AIM1      3'  TTTTTGAGACAGGATCTCAGGC 93474        T    ACAG_
            T                    GGCCTGA GATCC     CGGAGA
                                 ||||||| |||||     ||||||
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                              TCGGACT CTAGG    GTTTTT
                                 _    ACAGA
GAM1026 ALOX5AP  3' TCTCTGCTGAATATGGGGTT  9679      G  ATCCA
                              GGCCT ATG    CAGCGGAGA
                              ||||| |||    |||||||||
                              TTGGG TAT    GTCGTCTCT
                                 G  AA___
GAM1026 ANXA5    5' TTTCCGTTGCTTGGATCAGTC 8570     CTGA    __
                              GGC   TGATCCA CAGCGGAGA
                              |||   ||||||| |||||||||
                              CTG   ACTAGGT GTTGCCTTT
                                _____     TC
GAM1026 ARHGEF12 3' TCTCTGCTGTCCAGTAGGCT  31648      A ATCC
                              GGCCTG TG   ACAGCGGAGA
                              |||||| ||   ||||||||||
                              TCGGAT AC   TGTCGTCTCT
                                 G  C___
GAM1026 ASGR1    3' TTCTGCAGTTTGCAGGTTA   9806       ATGATCC A
                              TGGCCTG     AC GCGGAG
                              |||||||     || ||||||
                              ATTGGAC     TG CGTCTT
                                  GTT_____ A
GAM1026 CACNA1C  3' TCTGGGGATGGGCGTCGGGCC 7403        A   CAG_
                              GGCCTGATG TCCA   CGGA
                              ||||||||| ||||   ||||
                              CCGGGCTGC GGGT   GTCT
                                    _   AGGG
GAM1026 CD2AP    3' TTTCCAGCAGATTTCAGGCT  25082      T   CACA _
                              GGCCTGA GATC   GC GGAGA
                              ||||||| ||||   || |||||
                              TCGGACT TTAG   CG CCTTT
                                 _   A___  A
GAM1026 CELSR2   3' TCTTTGCTGTGATGTGGGT   9200      ATGATC
                              GCCTG    CACAGCGGAGA
                              |||||    ||||||||||
                              TGGGT    GTGTCGTTTCT
                                 GTA___
GAM1026 CNTFR    3' TCTCTGTTGCCACCATCAG   10240     ATCCA
                              CTGATG   CAGCGGAGA
                              ||||||   |||||||||
                              GACTAC   GTTGTCTCT
                                 CACC_
GAM1026 CRH     3' TTTTTGTTGTGGTCTGAGCCA 7484     CTGAT  T
                              TGGC    GA CCACAGCGGAGA
                              ||||    || ||||||||||||
                              ACCG    CT GGTGTTGTTTTT
                                AGT__ _
GAM1026 CYBB     3' TTCCAGATCATTAGGACA    76855   G       CACAGC
                              TG CCTGATGATC    GGAG
                              || ||||||||||    ||||
```

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                                AC GGATTACTAG     CCTT
                                 A        A_____
GAM1026 DMRT2    3' CTTTGCTTCTTGTAGGCTA   22652       AT_  TCCAC
                                TGGCCTG   GA    AGCGGAG
                                |||||||   ||    |||||||
                                ATCGGAT   CT    TCGTTTC
                                    GTT  _____
GAM1026 DNCI1    3' TCTCTGCTGCTGTTGAGGTTA 92712       GA   CCA
                                TGGCCT  TGAT   CAGCGGAGA
                                ||||||  ||||   |||||||||
                                ATTGGA  GTTG   GTCGTCTCT
                                    __    TC_
GAM1026 DNMT3B   3' TTTTTGCTAATTTTTAGGCT   23551       T   CCAC
                                GGCCTGA GAT    AGCGGAGA
                                ||||||| |||    ||||||||
                                TCGGATT TTA    TCGTTTTT
                                    T   A___
GAM1026 FBXW7    3' TCTCCAGTGGTCATTGGGC   37591     TG    T    AGC
                                GCC  ATGA CCAC   GGAGA
                                |||  |||| ||||   |||||
                                CGG  TACT GGTG   CCTCT
                                  GT    _    A__
GAM1026 GALNT1   3' TTTTTGTTTGGTTTGTGGGCT  40403      G TG T   C
                                GGCCT A  A CCA AGCGGAGA
                                ||||| |  | ||| ||||||||
                                TCGGG T  T GGT TTGTTTTT
                                   _ GT T   _
GAM1026 HDAC4    3' TCTCTGACCACATCGTCAGG   21253         CCACAG
                                CCTGATGAT     CGGAGA
                                |||||||||     ||||||
                                GGACTGCTA     GTCTCT
                                     CACCA_
GAM1026 IL1RL2   3' TTTCTGCTGCAGGATGAGGCTA 60163       GATG    A_
                                TGGCCT    ATCC  CAGCGGAGA
                                ||||||    ||||  |||||||||
                                ATCGGA    TAGG  GTCGTCTTT
                                    G___    AC
GAM1026 ITK      3' TTTTTGCTCAAACCATCAGG   19887        ATCCAC
                                CCTGATG     AGCGGAGA
                                |||||||     ||||||||
                                GGACTAC     TCGTTTTT
                                    CAAAC_
GAM1026 KDR      3' TCTCTGAATGATTATTAGCCA  11200      C       CACAG
                                TGGC TGATGATC     CGGAGA
                                |||| ||||||||     ||||||
                                ACCG ATTATTAG     GTCTCT
                                   _       TAA__
GAM1026 MAOA     3' AAGGCTGTGTCATTGGGCCA   5907       TG    TC     GGAGA
                                TGGCC  ATGA  CACAGC
                                |||||  ||||  ||||||
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                                ACCGG  TACT  GTGTCG
                                  GT   __     GAAA
GAM1026  MMP14    3'  TCTTCGTTGCTCAGTCAGTCA  18432      C    GATCCA
                                TGGC TGAT     CAGCGGAGA
                                |||| ||||     |||||||||
                                ACTG ACTG     GTTGCTTCT
                                  _    ACTC__
GAM1026  MPP2     3'  TCTTCGCTGCAGCGTCAGCCA  60523      C     ATCCA
                                TGGC TGATG    CAGCGGAGA
                                |||| |||||    |||||||||
                                ACCG ACTGC    GTCGCTTCT
                                  _    GAC__
GAM1026  MX1      3'  TCTCTGCTTATCCGTTAGCC   11723      C     ATCCAC
                                GGC TGATG     AGCGGAGA
                                ||| |||||     ||||||||
                                CCG ATTGC     TCGTCTCT
                                  _    CTAT__
GAM1026  MYB      3'  TTTTTGTTGTGGTACAACAG   60285      A  AT
                                CTG TG  CCACAGCGGAGA
                                ||| ||  ||||||||||||
                                GAC AC  GGTGTTGTTTTT
                                  A  AT
GAM1026  NT5C3    3'  TTTTTGTAATTTGGGTTATTAT 33662      C        CA__
            GCT                   GGC TGATGATCCA    GCGGAGA
                                ||| ||||||||||    |||||||
                                TCG ATTATTGGGT    TGTTTTT
                                  T        TTAA
GAM1026  OGDH     3'  TCTTTGCTGTGCCAAAGCAGGT 92753        ATGATC
            CA                    TGGCCTG     CACAGCGGAGA
                                |||||||     ||||||||||
                                ACTGGAC     GTGTCGTTTCT
                                    GAAACC
GAM1026  OSR1     3'  TCTCTGTTGCTTCTATTGGCC  18839      TGAT  TCCA
                                GGCC    GA    CAGCGGAGA
                                ||||    ||    |||||||||
                                CCGG    CT    GTTGTCTCT
                                  TTAT  TC__
GAM1026  PCDH1    5'  TTGTGCTTGTGAATTATTGGGT 51581      TG    C   _   G  A
            TA                    TGGCC  ATGAT CACA GCG AG
                                |||||  ||||| |||| ||| ||
                                ATTGG  TATTA GTGT CGT TT
                                  GT    A   T   G
GAM1026  POLR2H   3'  TCTCTGCCAAGTCACTCAGGTC 21722        _    CCACA
            A                     TGGCCTGA TGAT     GCGGAGA
                                |||||||| ||||     |||||||
                                ACTGGACT ACTG     CGTCTCT
                                    C    AAC__
GAM1026  POLS     3'  TCTAAGTTGGGTCATCGTGTC  23782     C        CA  GG
                                GGC TGATGATCCA  GC  AGA
                                ||| ||||||||||  ||  |||
```

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                                CTG GCTACTGGGT  TG  TCT
                                  T        __ AA
GAM1026  PPP2R5C   3'  TTTCCACGTGATTGTTACGCCA 12251     C   TG   C  AGC
                                TGGC TGA  ATC AC   GGAGA
                                |||| |||  ||| ||   |||||
                                ACCG ATT  TAG TG   CCTTT
                                  C   GT   _  CA_
GAM1026  PRNP      3'  TTTCTGCAATGTTATTATTGGC 6133      T     C_  CA
               T                 GGCC GATGAT  CA  GCGGAGA
                                |||| ||||||  ||  |||||||
                                TCGG TTATTA  GT  CGTCTTT
                                  _     TT  AA
GAM1026  RAD21     3'  TTTTTGTTGCTTATCGGGTT   21838         TCCA
                                GGCCTGATGA    CAGCGGAGA
                                ||||||||||    |||||||||
                                TTGGGCTATT    GTTGTTTTT
                                      C___
GAM1026  RAD51L1   3'  TCTCTGCTAAAACATTTGGTT  56880     T   ATCCAC
                                GGCC GATG     AGCGGAGA
                                |||| ||||     ||||||||
                                TTGG TTAC     TCGTCTCT
                                  T   AAAA__
GAM1026  RENT1     3'  TTTCTGCGGGGCATCAGGCT   12820         AT  ACA
                                GGCCTGATG  CC   GCGGAGA
                                |||||||||  ||   |||||||
                                TCGGACTAC  GG   CGTCTTT
                                     GG  ___
GAM1026  RLN2      3'  TCTTTGTTAGATATTAGGTC   18584         A  CAC
                                GGCCTGATG TC   AGCGGAGA
                                |||||||||  ||   ||||||||
                                CTGGATTAT AG   TTGTTTCT
                                     _  A__
GAM1026  RLN2      3'  TCTTTGTTAGATATTAGGTC   18585         A  CAC
                                GGCCTGATG TC   AGCGGAGA
                                |||||||||  ||   ||||||||
                                CTGGATTAT AG   TTGTTTCT
                                     _  A__
GAM1026  SCN1A     3'  TTTCTGTTGAGAAATAGGCTA  90269       ATGA  CA
                                TGGCCTG    TC  CAGCGGAGA
                                |||||||    ||  |||||||||
                                ATCGGAT    AG  GTTGTCTTT
                                    AA__  A_
GAM1026  SLC7A1    5'  TCTTTGCTGCAAGATCGAGGCT 13199      GA    CA_
                                GGCCT  TGATC   CAGCGGAGA
                                |||||  |||||   |||||||||
                                TCGGA  GCTAG   GTCGTTTCT
                                   __     AAC
GAM1026  SORCS2    3'  TCTCTGCTGTTTGGGTTGGGTT 40808      GAT    __
                                GGCCT   GATCC  ACAGCGGAGA
                                |||||   |||||  ||||||||||
```

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                              TTGGG  TTGGG  TGTCGTCTCT
                                 ___    TT
GAM1026 SQSTM1   3' TTTCTGCTGGAAGCTGTCAGGC 15332       GATCCA
            T                  GGCCTGAT    CAGCGGAGA
                               ||||||||    |||||||||
                               TCGGACTG    GTCGTCTTT
                                  TCGAAG
GAM1026 TCP10    3' CTTTGTTGTTTGCAGGCCA   17237      ATGATCC
                               TGGCCTG     ACAGCGGAG
                               |||||||     |||||||||
                               ACCGGAC     TGTTGTTTC
                                  GTT____
GAM1026 TFG      5' TCTCGCTAGGCTTGTTGGGTCA 21382     TG TG T  AC   G
                               TGGCC  A  A CC  AGCG AGA
                               |||||  |  | ||  |||| |||
                               ACTGG  T  T GG  TCGC TCT
                                  GT GT C  A_   _
GAM1026 TMEPAI   3' TCTCCGTGAAGTCGTCAGCC  39830    C     CCACA
                               GGC TGATGAT    GCGGAGA
                               ||| |||||||    |||||||
                               CCG ACTGCTG    TGCCTCT
                                 _     AAG__
GAM1026 TRPM8    3' TCTCCAGTTGATCATTGGG   44209    TG    C  AGC
                               CC  ATGATC AC   GGAGA
                               ||  |||||| ||   |||||
                               GG  TACTAG TG   CCTCT
                                GT     T  A__
GAM1026 UNG      3' TTTTTGCTGTTAGTCGGGTTA  56027       GATCC
                               TGGCCTGAT    ACAGCGGAGA
                               |||||||||    ||||||||||
                               ATTGGGCTG    TGTCGTTTTT
                                    AT___
GAM1026 VCP      3' TTTCTGTTGTAGTTTGGGGC   75892     GAT   CC
                               GCCT   GAT  ACAGCGGAGA
                               ||||   |||  ||||||||||
                               CGGG   TTG  TGTTGTCTTT
                                 GT_   A_
GAM1026 ZNF265   3' TCTTTGCTGCGTTTATGTAGGT 19578      _   TCCA
            T                  GGCCTG ATGA    CAGCGGAGA
                               ||||||| ||||    |||||||||
                               TTGGAT TATT    GTCGTTTCT
                                  G    TGC_
GAM1026 ZNF74    5' TCTCGAGGATATATCGGGTT   14266       _   ACAGCG
                               GGCCTGATG ATCC     GAGA
                               ||||||||| ||||     ||||
                               TTGGGCTAT TAGG     CTCT
                                    A    AG____
GAM1026 ABCC13   3' TTTTTGTTTAGATCATCAGGT  57813        CAC
                               GCCTGATGATC   AGCGGAGA
                               ||||||||||   ||||||||
```

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                                TGGACTACTAG  TTGTTTTT
                                      AT_
GAM1026 AFAP    3' TTTTGCTGCCTTCGGGTCA   41614       TGATCCA
                                TGGCCTGA     CAGCGGAG
                                ||||||||     ||||||||
                                ACTGGGCT     GTCGTTTT
                                     TCC____
GAM1026 AMOT    3' TTTTTGTTGTTACACTGTTGGG 56551    TG  GATCC_
             T                   GCC  AT    ACAGCGGAGA
                                 |||  ||    ||||||||||
                                 TGG  TG    TGTTGTTTTT
                                   GT  TCACAT
GAM1026 BRD3    3' TTTTGCTTTCATAGGTCA    24776       A   TCCAC
                                TGGCCTG TGA    AGCGGAG
                                ||||||| |||    |||||||
                                ACTGGAT ACT    TCGTTTT
                                    _  T____
GAM1026 C20orf46 5' TTCTGCTTATGTTAGGGTA   37737    G    GATCCAC
                                TG CCTGAT     AGCGGAG
                                || ||||||     |||||||
                                AT GGATTG     TCGTCTT
                                 G     TAT____
GAM1026 C5orf6   3' CTCTGCTGTAGATTGGCT    33950     TGAT    C
                                GGCC    GATC ACAGCGGAG
                                ||||    |||| |||||||||
                                TCGG    TTAG TGTCGTCTC
                                   ____    A
GAM1026 C6.1A    3' CTTCAGGATCTTGGGCTA    44531      TG T    ACAGC
                                TGGCC  A GATCC    GGAG
                                |||||  | |||||    ||||
                                ATCGG  T CTAGG    CTTC
                                   GT _    A____
GAM1026 C6orf33  3' TTTCTGTTCTGGGTTATTGGG  56724    TG      C
                                CC  ATGATCCA AGCGGAGA
                                ||  |||||||| ||||||||
                                GG  TATTGGGT TTGTCTTT
                                 GT       C
GAM1026 CKAP4    3' TCTCTGCTTCTGCATTTGGTT  23348     T   ATCCAC
                                GGCC GATG     AGCGGAGA
                                |||| ||||     ||||||||
                                TTGG TTAC     TCGTCTCT
                                  T   GTCT__
GAM1026 CNOT7    3' TCTCAGTTGGTTGTTAGGTT   55060       TG  CCA   G
                                GGCCTGA  AT   CAGC GAGA
                                |||||||  ||   |||| ||||
                                TTGGATT  TG   GTTG CTCT
                                    GT  ___    A
GAM1026 CSR1     3' TTTCTGCTGGCCAGGTGGGCCA 33187       A_  ATCCA
                                TGGCCTG  TG    CAGCGGAGA
                                |||||||  ||    |||||||||
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                                ACCGGGT  AC    GTCGTCTTT
                                   GG  CG___
GAM1026  DGKD     3'  CTCTCGAGTCATCAGGCTA   60104          CCACAG  _
                                TGGCCTGATGAT     CG GAG
                                ||||||||||||     || |||
                                ATCGGACTACTG     GC CTC
                                    A_____  T
GAM1026  DKFZP566G1424 3'  TCTTAGTGGTGGATCATCAGGT 85946            A  G
                                GCCTGATGATCCAC GC GAGA
                                |||||||||||||| || ||||
                                TGGACTACTAGGTG TG TTCT
                                     G  A
GAM1026  DKFZP586I2223 3'  TCTCTGTTTAAGTATCAGCTA  55774      C    ATCCAC
                                TGGC TGATG     AGCGGAGA
                                |||| |||||     ||||||||
                                ATCG ACTAT     TTGTCTCT
                                  _    GAAT__
GAM1026  DKFZP586I2223 3'  TCTCTGTTTAAGTATCAGCTA  55775      C    ATCCAC
                                TGGC TGATG     AGCGGAGA
                                |||| |||||     ||||||||
                                ATCG ACTAT     TTGTCTCT
                                  _    GAAT__
GAM1026  DOK4     3'  TTTTTGTTGTTTTTTGGGTT   36667      TG T  TCC
                                GGCC  A GA   ACAGCGGAGA
                                ||||  | ||   ||||||||||
                                TTGG  T TT   TGTTGTTTTT
                                  GT T  ___
GAM1026  DRCTNNB1A 5'  TCTCCCGGCTGGGTTGTCAGTC 51811      C   TG T  A   __
            A                    TGGC TGA  A CC CAGC  GGAGA
                                ||||  |||  | || ||||  |||||
                                ACTG ACT  T GG GTCG  CCTCT
                                  _  GT _  _   GC
GAM1026  FBXO30   3'  TTTTGTTATTGTTATGCCA   50492      C   TG  CCAC
                                TGGC TGA  AT    AGCGGAG
                                |||| |||  ||    |||||||
                                ACCG ATT  TA    TTGTTTT
                                  T   GT  _____
GAM1026  FKBP9    3'  TCTCCGTTTGTCGCCAGGCT   95724       A    CCAC
                                GGCCTG TGAT    AGCGGAGA
                                ||||||  ||||    ||||||||
                                TCGGAC GCTG    TTGCCTCT
                                   C    T___
GAM1026  FLJ00001  3'  TCTTTGCTCCTTGTCAGAGTT  82717     _    TG TCCAC
                                GGC CTGA  A     AGCGGAGA
                                |||  ||||  |     ||||||||
                                TTG GACT  T     TCGTTTCT
                                  A   GT CC___
GAM1026  FLJ10058  3'  TTTTTGTTGTCTGTGTTGAGTC 36269      CT    ATCC
            A                    TGGC  GATG    ACAGCGGAGA
                                ||||  ||||    ||||||||||
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                                ACTG  TTGT   TGTTGTTTTT
                                  AG   GTC_
GAM1026  FLJ10379  3'  TCTTTGTTGACACAGTAGGGCT 36569      GA_  ATCCA
                                GGCCT  TG   CAGCGGAGA
                                |||||  ||   |||||||||
                                TCGGG  AC   GTTGTTTCT
                                  ATG  ACA__
GAM1026  FLJ10546  3'  TTTTTGTTGTTGTTGTTGGGCT 60187     TG TG  CC
                                GGCC  A  AT  ACAGCGGAGA
                                ||||  |  ||  ||||||||||
                                TCGG  T  TG  TGTTGTTTTT
                                  GT GT  T_
GAM1026  FLJ10925  5'  TTCTGCTGGTGTTGCGCT    37415    C   GATCCA
                                GGC TGAT     CAGCGGAG
                                ||| ||||     ||||||||
                                TCG GTTG     GTCGTCTT
                                  C   TG____
GAM1026  FLJ11117  3'  CTCTGCTGCATGGGGCTA    37634      G  ATCCA
                                TGGCCT ATG    CAGCGGAG
                                |||||| |||    ||||||||
                                ATCGGG TAC    GTCGTCTC
                                   G  _____
GAM1026  FLJ11273  3'  TTTTTGTCACTTATTTCAGGTT 37778       TGATCCACA
           A                     TGGCCTGA       GCGGAGA
                                |||||||        |||||||
                                ATTGGACT       TGTTTTT
                                     TTATTCAC_
GAM1026  FLJ13081  3'  TTTTTATGGGATCATCAG    46173         A  GC
                                CTGATGATCC CA  GGAGA
                                |||||||||| ||  |||||
                                GACTACTAGG GT  TTTTT
                                     _  A_
GAM1026  FLJ13154  3'  TCGGCTGTTGTGGGTTGCAGGT 45112       A         A_
           T                     GGCCTG TGATCCACAGCGG  GA
                                ||||||  ||||||||||||  ||
                                TTGGAC GTTGGGTGTTGTC  CT
                                   _          GG
GAM1026  FLJ13204  3'  TCTGCCCCTGTGATTGGGCCA  45760      TG  GATC    C  _
                                TGGCC  AT   CACAG GG AGA
                                |||||  ||   ||||| || |||
                                ACCGG  TA   GTGTC CC TCT
                                   GT  ____    C  G
GAM1026  FLJ14855  3'  TTTTCGTTGGCTGGCAGGTT   53767      ATGAT  __
                                GGCCTG    CCA  CAGCGGAGA
                                ||||||    |||  |||||||||
                                TTGGAC    GGT  GTTGCTTTT
                                   _____  CG
GAM1026  FLJ20392  5'  TTTCTGCTGTGGCCTTAG    35578     TGAT
                                CTGA   CCACAGCGGAGA
                                ||||   ||||||||||||
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                                GATT   GGTGTCGTCTTT
                                  CC__
GAM1026  FLJ20699  3'  TCTCTGTTGTCTCATTGTGTT  35991    C     TCC
                                GGC TGATGA   ACAGCGGAGA
                                ||| ||||||   ||||||||||
                                TTG GTTACT   TGTTGTCTCT
                                  T     C__
GAM1026  FLJ32865  3'  CTCCGTGTTGGTCAGGCT    58807       TGAT   CA
                                GGCCTGA    CCA  GCGGAG
                                |||||||    |||  ||||||
                                TCGGACT    GGT  TGCCTC
                                    _____  TG
GAM1026  G4        5'  TCTCTGCTGCGTGTTCGCGGGC 92642        A   TCCA_
              CA                  TGGCCTG TGA    CAGCGGAGA
                                |||||||  |||    |||||||||
                                ACCGGGC GCT    GTCGTCTCT
                                    _   TGTGC
GAM1026  gm117     3'  TGATATTGTGGGTTATTATGCC 79591      C          CGGAGA
              A                   TGGC TGATGATCCACAG
                                ||||  ||||||||||||
                                ACCG ATTATTGGGTGTT
                                  T           ATAGTT
GAM1026  HBOA      3'  TTTTTGATCTGTATTGGGCTA  23934      TG  GATCC   __
                                TGGCC  AT    ACAG  CGGAGA
                                |||||  ||    ||||  ||||||
                                ATCGG  TA    TGTC  GTTTTT
                                   GT  ______   TA
GAM1026  HCA4      3'  TTTTTGCTACATATTAAGGTCA 57747       GA    CCAC
                                TGGCCT  TGAT    AGCGGAGA
                                ||||||  ||||   ||||||||
                                ACTGGA  ATTA    TCGTTTTT
                                    __    TACA
GAM1026  HSPC195   5'  TCTCTGTTGTGGGCAGCAGGGC 81869       GA_  A
              CA                  TGGCCT   TG TCCACAGCGGAGA
                                ||||||   || ||||||||||||
                                ACCGGG   AC GGGTGTTGTCTCT
                                   ACG  _
GAM1026  ICK       3'  TTTCTTAGTAGGTCATTGGTT  30602      T      C  AGC
                                GGCC GATGATC AC   GGAGA
                                |||| ||||||| ||   |||||
                                TTGG TTACTGG TG   TCTTT
                                  _      A  AT_
GAM1026  KIAA0152  3'  TTTTCGCTGTGACTTGGGTC   28985      TG TGATC
                                GGCC  A    CACAGCGGAGA
                                ||||  |    ||||||||||
                                CTGG  T    GTGTCGCTTTT
                                  GT CA___
GAM1026  KIAA0205  3'  TCTCTGGAGCAGTCATTGGTT  30219      T     CCACAG
                                GGCC GATGAT     CGGAGA
                                |||| ||||||     ||||||
```

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                              TTGG TTACTG     GTCTCT
                                _     ACGAG_
GAM1026  KIAA0349  3'  TCTCTGTGGTCTGTTGGGTCA  93919      TG   AT     C
                              TGGCC  ATG  CCACAG GGA
                              |||||  |||  ||||||| |||
                              ACTGG  TGT  GGTGTC TCT
                                 GT   CT     _
GAM1026  KIAA0446  3'  TCTTTGGAGGGGTTATTAGGTT 69462           ACAG
                              GGCCTGATGATCC    CGGAGA
                              ||||||||||||||   ||||||
                              TTGGATTATTGGG    GTTTCT
                                     GAG_
GAM1026  KIAA0449  3'  TTTCTGCTGTTTCTGATGGGTC 34642        AT_  TCC
            A                  TGGCCTG   GA   ACAGCGGAGA
                              |||||||   ||   ||||||||||
                              ACTGGGT   CT   TGTCGTCTTT
                                  AGT  T__
GAM1026  KIAA0475  3'  TTTTTGTTGTAAGTCAGG    30133       GATCC
                              CCTGAT    ACAGCGGAGA
                              ||||||    ||||||||||
                              GGACTG    TGTTGTTTTT
                                 AA___
GAM1026  KIAA0819  3'  TTTCCGTTCTGTTTTGGGCCA  64339      TG TGATC  C
                              TGGCC  A    CA AGCGGAGA
                              |||||  |    || ||||||||
                              ACCGG  T    GT TTGCCTTT
                                 GT TT___  C
GAM1026  KIAA1007  3'  TCTCTGTTGTACGTGTCAGTCT 95224     C     ATCC
            A                  TGG CTGATG    ACAGCGGAGA
                              |||  ||||||    ||||||||||
                              ATC GACTGT    TGTTGTCTCT
                                T     GCA_
GAM1026  KIAA1014  3'  TTTCTGTTGTATCACAATCAGG 65962       GATCC_
            T                  GCCTGAT     ACAGCGGAGA
                              |||||||     ||||||||||
                              TGGACTA     TGTTGTCTTT
                                  ACACTA
GAM1026  KIAA1026  3'  TTTTTGTTTGGTTCGTCGGTT  71747     T    T   C
                              GGCC GATGA CCA AGCGGAGA
                              |||| ||||| ||| ||||||||
                              TTGG CTGCT GGT TTGTTTTT
                                _     T   _
GAM1026  KIAA1054  3'  TCTTTGCTGTGGGACTGGCC   68972     TGATGA
                              GGCC     TCCACAGCGGAGA
                              ||||     ||||||||||||||
                              CCGG     GGGTGTCGTTTCT
                                TCA___
GAM1026  KIAA1084  3'  TTTTGAAATCTGGTTGTCAGGC 30506        TG   CACAG_    A
            CA                   TGGCCTGA  ATC     CGGAG
                              ||||||||  |||     |||||
```

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                              ACCGGACT  TGG     GTTTT
                                  GT   TCTAAA
GAM1026  KIAA1196  3'  TCTCTGGCTTCATCCTTGGGCC 62155      TG T   CCAC  _
            A                  TGGCC  A GAT    AGC GGAGA
                               ||||||  | |||   ||| |||||
                               ACCGG  T CTA    TCG TCTCT
                                  GT C   CT__   G
GAM1026  KIAA1209  3'  TTTTCGTTGTTTTCAGGT    61412       TGATCC
                               GCCTGA     ACAGCGGAGA
                               ||||||     ||||||||||
                               TGGACT     TGTTGCTTTT
                                  TT____
GAM1026  KIAA1363  3'  TTTTTGTTGTGTTTTTGGTTA  69793      TGAT  TC
                               TGGCC    GA  CACAGCGGAGA
                               |||||    ||  ||||||||||
                               ATTGG    TT  GTGTTGTTTTT
                                  T___  TT
GAM1026  KIAA1416  3'  TTTTTGCTGTGAAGGTCAAGCT 87759     C    GATC
                               GGC TGAT    CACAGCGGAGA
                               ||| ||||    ||||||||||
                               TCG ACTG    GTGTCGTTTTT
                                 A   GAA_
GAM1026  KIAA1430  3'  TCTTTGTTGCCACATGTCAGG  81651       GATCCA
                               CCTGAT     CAGCGGAGA
                               ||||||     |||||||||
                               GGACTG     GTTGTTTCT
                                  TACACC
GAM1026  KIAA1557  3'  TTTCTGCTGTGTCCTTAGG    61788      T  TC
                               CCTGA GA  CACAGCGGAGA
                               ||||| ||  ||||||||||
                               GGATT CT  GTGTCGTCTTT
                                  C  __
GAM1026  KIAA1673  3'  TTTTCGTATTGCCATCGGGTT  71333        ATC  CA
                               GGCCTGATG   CA  GCGGAGA
                               |||||||||   ||  |||||||
                               TTGGGCTAC   GT  TGCTTTT
                                    C__  TA
GAM1026  KIAA1712  3'  CTCCGTGTTGGTCAGGCT    68156       TGAT   CA
                               GGCCTGA    CCA  GCGGAG
                               |||||||    |||  ||||||
                               TCGGACT    GGT  TGCCTC
                                  ____   TG
GAM1026  KIAA1789  5'  CTTTGAAATGATTAGGTCA   67701         G  CCACAG
                               TGGCCTGAT AT     CGGAG
                               ||||||||| ||     |||||
                               ACTGGATTA TA     GTTTC
                                    G  AA____
GAM1026  KIAA1821  3'  TTTGGCCTGGGTGTTAGGTCA  72277         G    CA  G
                               TGGCCTGAT ATCCA  GC GAG
                               ||||||||| |||||  || |||
```

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                                ACTGGATTG TGGGT  CG TTT
                                      _    C_  G
GAM1026 KIAA1910 3' TCTCTGCTGCTTTTGTTGGTGC 73717    _ TG TG TCCA
            T                    GGC C  A  A   CAGCGGAGA
                                 ||| |  | |   |||||||||
                                 TCG G  T  T   GTCGTCTCT
                                   T GT GT TTC_
GAM1026 KIAA1949 5' TCTTTGTGCCGAGATTGTCAGT 99703    C   TG   CACA_
            CT                   GG CTGA  ATC    GCGGAGA
                                 || ||||  |||    |||||||
                                 TC GACT  TAG    TGTTTCT
                                  T   GT   AGCCG
GAM1026 KIF13B   3' TTTCTAGGAAGGTCTTTGGGTC 31575      TG T   CACAGC
            A                    TGGCC  A GATC     GGAGA
                                 |||||  | ||||     |||||
                                 ACTGG  T CTGG     TCTTT
                                    GT T   AAGGA_
GAM1026 KIF13B   3' TTTCTAGGAAGGTCTTTGGGTC 31576      TG T   CACAGC
            A                    TGGCC  A GATC     GGAGA
                                 |||||  | ||||     |||||
                                 ACTGG  T CTGG     TCTTT
                                    GT T   AAGGA_
GAM1026 LEC3     3' TTTTTAATGGGATTTTTAGGTC 31535        T    A  GC
            A                    TGGCCTGA GATCC CA  GGAGA
                                 |||||||| ||||| ||  |||||
                                 ACTGGATT TTAGG GT  TTTTT
                                      T    _  AA
GAM1026 MESDC2   3' TTCTGTTGTACTCAGGGCA   72927    G    TGATCC
                                 TG CCTGA     ACAGCGGAG
                                 || |||||     |||||||||
                                 AC GGACT     TGTTGTCTT
                                  G    CA____
GAM1026 MGC20253 3' TCTCTGTTGTGGTGGGCATAGG 58678      A  AT__
            T                    GCCTG TG   CCACAGCGGAGA
                                 ||||| ||   ||||||||||||
                                 TGGAT AC   GGTGTTGTCTCT
                                    _  GGGT
GAM1026 MGC2217  3' TCTTCATCTGGTCTTGGGTCA  44431      TG T  T   CAGC
                                 TGGCC  A GA CCA   GGAGA
                                 |||||  | || |||   |||||
                                 ACTGG  T CT GGT    CTTCT
                                    GT _  _   CTA_
GAM1026 NLI-IF   3' TCTCTGCTGCCAAATTGGGCC  41346     TG  GATCCA
                                 GGCC  AT     CAGCGGAGA
                                 ||||  ||     |||||||||
                                 CCGG  TA     GTCGTCTCT
                                   GT  AACC__
GAM1026 OLIG1    3' TTTCCGCTGTTCCTCAGCGGGC 97338       A   TCC
            C                    GGCCTG TGA   ACAGCGGAGA
                                 |||||| |||   ||||||||||
```

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                                CCGGGC ACT   TGTCGCCTTT
                                   G   CCT
GAM1026 PCDH20   3' TTTTTGTTGTTGTTTAGGTT  43427       TGATCC
                                GGCCTGA     ACAGCGGAGA
                                |||||||     ||||||||||
                                TTGGATT     TGTTGTTTTT
                                    TGT___
GAM1026 PJA1     3' TTTTTGTTGCATGTTATGGGTC 42567      G    CCA
                                GGCCT ATGAT   CAGCGGAGA
                                ||||| |||||   |||||||||
                                CTGGG TATTG   GTTGTTTTT
                                   _    TAC
GAM1026 PP1665   3' TTGATGGGTCATGGGCCA    48644       G      _
                                TGGCCT ATGATCCA CAG
                                |||||| |||||||| |||
                                ACCGGG TACTGGGT GTT
                                   _       A
GAM1026 PPP1R10  3' TTTTGTGCAGGGTCTTGGGTTA 12234      TG T    ACA
                                TGGCC  A GATCC   GCGGAG
                                |||||  | |||||   ||||||
                                ATTGG  T CTGGG   TGTTTT
                                   GT _    ACG
GAM1026 PPP1R3B  3' TTCTGCTGTGTTTAGGACA   45149    G    TGATC
                                TG CCTGA    CACAGCGGAG
                                || |||||    ||||||||||
                                AC GGATT    GTGTCGTCTT
                                 A    T____
GAM1026 PRO0902  5' TCTTTGGGTGGGGTGTTGGGCT 54972     TG   AT   AG
                                GGCC  ATG  CCAC  CGGAGA
                                ||||  |||  ||||  ||||||
                                TCGG  TGT  GGTG  GTTTCT
                                  GT   GG   G_
GAM1026 SEC24A   3' TTTTTGTTTTGTTTTAATGGGT 83570       A   TC  C
            TA                   TGGCCTG TGA  CA AGCGGAGA
                                |||||||  |||  ||  ||||||||
                                ATTGGGT ATT  GT TTGTTTTT
                                    A   TT  T
GAM1026 SH3BGRL2 3' TTTTTGCTGCAGAATCAG    49681      GA  CA
                                CTGAT  TC  CAGCGGAGA
                                |||||  ||  |||||||||
                                GACTA  AG  GTCGTTTTT
                                   __  AC
GAM1026 SLC2A12  3' TTTCTGAGCAGGATATCAGGTT 59743         A   ACAG
            A                    TGGCCTGATG TCC    CGGAGA
                                ||||||||||  |||    ||||||
                                ATTGGACTAT AGG    GTCTTT
                                      _  ACGA
GAM1026 SPRY4    3' TTTCTGCTGTGGGTAACTGC   49041    CTGATG
                                GC     ATCCACAGCGGAGA
                                ||     ||||||||||||||
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                                CG     TGGGTGTCGTCTTT
                                 TCAA__
GAM1026  STAG2    3'  TCTTTGCAAGCAGTCTTCAGGT 71089        T   CCACA
              TA                  TGGCCTGA GAT     GCGGAGA
                                  |||||||| |||     |||||||
                                  ATTGGACT CTG     CGTTTCT
                                     T   ACGAA
GAM1026  TNFAIP3  3'  TTTCTGGTTGTTGTTGGGGCA  21912    G  TG   ATCC    _
                                  TG CC  ATG    ACAGC GGAGA
                                  || ||  |||    ||||| |||||
                                  AC GG  TGT    TGTTG TCTTT
                                   G  GT  ____     G
GAM1026  TU12B1-TY 3'  CTCCATGGTGGTCAGGCT    33845        TGAT    AGC
                                  GGCCTGA    CCAC   GGAG
                                  |||||||    ||||   ||||
                                  TCGGACT    GGTG   CCTC
                                     ____    GTA
GAM1026  WIT-1    5'  TCTTTGTTGTGGGTAACGTT   32399     __
                                  GATG  ATCCACAGCGGAGA
                                  ||||  ||||||||||||||
                                  TTGC  TGGGTGTTGTTTCT
                                    AA
GAM1026  LOC115704 3'  CTCTGCTGAATCAGAGCT    73907     _    GATCCA
                                  GGC CTGAT     CAGCGGAG
                                  ||| |||||     ||||||||
                                  TCG GACTA     GTCGTCTC
                                    A    A_____
GAM1026  LOC138649 5'  TTTGGGGGTGGATCGCGGGTT  75877       A       AG_
                                  GGCCTG TGATCCAC   CGGA
                                  |||||| ||||||||   ||||
                                  TTGGGC GCTAGGTG   GTTT
                                     _       GGG
GAM1026  LOC139221 3'  TTCTGCTGTTGATGGGTTA    76331       GATG   C
                                  TGGCCT    ATC ACAGCGGAG
                                  ||||||    ||| |||||||||
                                  ATTGGG    TAG TGTCGTCTT
                                     ____   T
GAM1026  LOC143286 5'  TCTTCAGCAGTGATTGTCAGCC 83849     C   TG   C  A  _
              A                   TGGC TGA  ATC AC GC GGAGA
                                  |||| |||  ||| || || |||||
                                  ACCG ACT  TAG TG CG CTTCT
                                    _  GT   _  A  A
GAM1026  LOC144161 3'  TTTCCGAAGTTGATTGGGCT   83935      GAT    C  AG
                                  GGCCT   GATC AC  CGGAGA
                                  |||||   |||| ||  ||||||
                                  TCGGG   TTAG TG  GCCTTT
                                     ___   T  AA
GAM1026  LOC145241 5'  TTTCTGGCTACTGTCAGGCT   63530        GATCCAC  _
                                  GGCCTGAT      AGC GGAGA
                                  ||||||||      ||| |||||
```

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                                TCGGACTG      TCG TCTTT
                                    TCA____   G
GAM1026  LOC145623 3'  TTTCTGTTATCTTGTCAGTGTT 84399     _   TG TCCAC
                                GGC CTGA  A     AGCGGAGA
                                ||| ||||  |     ||||||||
                                TTG GACT  T     TTGTCTTT
                                  T   GT CTA__
GAM1026  LOC145739 3'  TCTCTGTTTGTTAATCATTAGT 77907    C       CC   _
              CT                  GG CTGATGAT  ACAG CGGAGA
                                || ||||||||  |||| ||||||
                                TC GATTACTA  TGTT GTCTCT
                                 T       AT   T
GAM1026  LOC145815 3'  TCCAGTGGATTGTTGGCCA   84523      T  TG     AGC
                                TGGCC GA  ATCCAC   GGA
                                ||||| ||  ||||||   |||
                                ACCGG TT  TAGGTG   CCT
                                   _ GT     A__
GAM1026  LOC145828 5'  TTTTTGCTTTGTCCTCATAGGT 84543       A   TC_  C
              TA                  TGGCCTG TGA   CA AGCGGAGA
                                ||||||| |||   || ||||||||
                                ATTGGAT ACT   GT TCGTTTTT
                                    _  CCT  T
GAM1026  LOC146184 5'  TTTTTGCTGTCACATTTAGGT  84598       TGATCC
                                GCCTGA     ACAGCGGAGA
                                ||||||     ||||||||||
                                TGGATT     TGTCGTTTTT
                                   TACAC_
GAM1026  LOC146481 5'  TTTCTTGTGGTCAGTTGGGTTA 78489      TG  GAT     C
                                TGGCC  AT   CCACAG GGAG
                                |||||  ||   |||||| ||||
                                ATTGG  TG   GGTGTT CTTT
                                   GT  ACT     _
GAM1026  LOC146794 3'  TCAATGTGGGGCATCAGGCCA  84825         AT    GCG
                                TGGCCTGATG  CCACA   GA
                                ||||||||||  |||||   ||
                                ACCGGACTAC  GGTGT   CT
                                      GG    AA_
GAM1026  LOC149077 3'  TCTCTGCTGTGGCAGTAGGT   79890      A  AT
                                GCCTG TG  CCACAGCGGAGA
                                ||||| ||  ||||||||||||
                                TGGAT AC  GGTGTCGTCTCT
                                  G  __
GAM1026  LOC149103 3'  CTTTGTTGGTATTGTGCCA    79938     CTG TG  CCA
                                TGGC   A  AT   CAGCGGAG
                                ||||   |  ||   ||||||||
                                ACCG   T  TA   GTTGTTTC
                                  ___ GT  TG_
GAM1026  LOC149465 3'  TCTTTGCTGTTGGATCAGACCA 80194     CCTGA      _
                                TGG     TGATCCA CAGCGGAGA
                                |||     ||||||| |||||||||
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                                ACC    ACTAGGT GTCGTTTCT
                                  AG___      T
GAM1026  LOC150622 3'  TTTCTGTTACATCCATTGAGGT 80771       _   ATCCAC
                CA                  TGGCCT GATG     AGCGGAGA
                                    |||||| ||||     ||||||||
                                    ACTGGA TTAC     TTGTCTTT
                                       G   CTACA_
GAM1026  LOC150848 5'  TCTTTGCTAATCTATTGGCC   86321     TGAT   CCAC
                                    GGCC   GAT   AGCGGAGA
                                    ||||   |||   ||||||||
                                    CCGG   CTA   TCGTTTCT
                                      TTAT   A___
GAM1026  LOC151361 3'  TCTTTGCTGCCAGCCATCAGGT 86507        ATCCA
                                    GCCTGATG    CAGCGGAGA
                                    ||||||||    |||||||||
                                    TGGACTAC    GTCGTTTCT
                                        CGACC
GAM1026  LOC151361 3'  TTCTGTATGTCTTAGGCCA   86509        T   CCACA
                                    TGGCCTGA GAT    GCGGAG
                                    |||||||| |||    ||||||
                                    ACCGGATT CTG    TGTCTT
                                        _   TA___
GAM1026  LOC151610 3'  TCTTTGCTGAATCCAGATGGGT 81099       GA_  ATCCA
                TA                  TGGCCT   TG    CAGCGGAGA
                                    ||||||   ||    |||||||||
                                    ATTGGG   AC    GTCGTTTCT
                                       TAG  CTAA_
GAM1026  LOC151827 5'  TCTTCGCTGGCCCGGCAGGCC  81193       ATGATCCA
                                    GGCCTG       CAGCGGAGA
                                    ||||||       |||||||||
                                    CCGGAC       GTCGCTTCT
                                       GGCCCG__
GAM1026  LOC154222 3'  CTCTGTTCTTATCAGGGCA   87390    G       TCCAC
                                    TG CCTGATGA    AGCGGAG
                                    || ||||||||    |||||||
                                    AC GGACTATT    TTGTCTC
                                     G       C____
GAM1026  LOC158318 5'  TCTTTGTTGAAGACATTGGGC  88103    TG   A  CA
                                    GCC  ATG TC  CAGCGGAGA
                                    |||  ||| ||  |||||||||
                                    CGG  TAC AG  GTTGTTTCT
                                      GT   _  AA
GAM1026  LOC164121 5'  TCAAGGTGGGCGTCGGGCT    83050        A    AGCG
                                    GGCCTGATG TCCAC    GA
                                    ||||||||| |||||    ||
                                    TCGGGCTGC GGGTG    CT
                                         _    GAA_
GAM1026  LOC196528 3'  TCTCAGGTGATCATCAGG     89109        C  AGCG
                                    CCTGATGATC AC    GAGA
                                    |||||||||| ||    ||||
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                                GGACTACTAG TG    CTCT
                                      _  GA__
GAM1026  LOC200081 3'  TTTCCATGAGGTTATCGGACCA 89978     C      T  A  GC
                                TGG CTGATGA CC CA  GGAGA
                                ||| ||||||| || ||  |||||
                                ACC GGCTATT GG GT  CCTTT
                                  A      _  A  A_
GAM1026  LOC200268 3'  CTCTAGACTATTAGGCTA    90084          A  CACAGC
                                TGGCCTGATG TC     GGAG
                                ||||||||||  ||      ||||
                                ATCGGATTAT AG     TCTC
                                      C  A_____
GAM1026  LOC201164 3'  TTCTGTTACTTCGGGTCA    89505         TGATCCAC
                                TGGCCTGA       AGCGGAG
                                ||||||||       |||||||
                                ACTGGGCT       TTGTCTT
                                     TCA_____
GAM1026  LOC201475 5'  TCTTTAAGTGTGGTCATCAGGT 89623           T    GC_
              CA                  TGGCCTGATGA CCACA   GGAGA
                                ||||||||||| |||||   |||||
                                ACTGGACTACT GGTGT   TTTCT
                                      _    GAA
GAM1026  LOC202460 5'  TCTTTGTGACCTGTTGTTAGGC 90678       TG  CCACA
                                GCCTGA  AT    GCGGAGA
                                ||||||  ||    |||||||
                                CGGATT  TG    TGTTTCT
                                   GT  TCCAG
GAM1026  LOC202934 5'  TTGAGGTGCATCATTAGGTT   92058          C   AG
                                GGCCTGATGAT CAC  CGG
                                |||||||||||  |||  |||
                                TTGGATTACTA GTG  GTT
                                      C   GA
GAM1026  LOC219654 3'  TTTCTGTTTCCCGTTATTGGGT 92944      TG    CCAC
              T                  GGCC  ATGAT    AGCGGAGA
                                ||||  |||||    ||||||||
                                TTGG  TATTG    TTGTCTTT
                                  GT    CCCT
GAM1026  LOC219690 3'  TCTCCTGCACCGGTTATTAAGC 94668      C       CACA  _
              CA                  TGGC TGATGATC    GC GGAGA
                                |||| ||||||||    || |||||
                                ACCG ATTATTGG    CG CCTCT
                                  A       CCA_  T
GAM1026  LOC220883 3'  TTTTTGATCTGTATTGGGCTA  92894      TG  GATCC   __
                                TGGCC  AT    ACAG  CGGAGA
                                |||||  ||    ||||  ||||||
                                ATCGG  TA    TGTC  GTTTTT
                                  GT  _____    TA
GAM1026  LOC221416 3'  CTCTGTCATCGTCAGGCT    95406          CCACA
                                GGCCTGATGAT    GCGGAG
                                ||||||||||    ||||||
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                                TCGGACTGCTA    TGTCTC
                                      C____
GAM1026  LOC221687 3'  TCTTTGTTGTGTGATGCAGGT  93873      ATG  _
                                GCCTG  ATC CACAGCGGAGA
                                |||||  ||| ||||||||||
                                TGGAC  TAG GTGTTGTTTCT
                                   G__  T
GAM1026  LOC221975 3'  CTCTGCTTGTTATTGGTTA   94190      T    CCAC
                                TGGCC GATGAT   AGCGGAG
                                ||||| ||||||   |||||||
                                ATTGG TTATTG   TCGTCTC
                                   _    T___
GAM1026  LOC253263 3'  TTTCTGCCTCCCCTCTTTGGGT 98820      TG T  TCCACA
            TA                   TGGCC  A GA    GCGGAGA
                                ||||| | ||    |||||||
                                ATTGG  T CT    CGTCTTT
                                   GT T  CCCCTC
GAM1026  LOC254249 5'  TTTCTGTTGCAGAGTTAGGC   97189       GA  CA
                                GCCTGAT  TC  CAGCGGAGA
                                |||||||  ||  |||||||||
                                CGGATTG  AG  GTTGTCTTT
                                   __ AC
GAM1026  LOC254351 5'  CTCCGTGTTGGTCGGGCT    96687       TGAT   CA
                                GGCCTGA   CCA  GCGGAG
                                |||||||   |||  ||||||
                                TCGGGCT   GGT  TGCCTC
                                   _____  TG
GAM1026  LOC255465 5'  TTGAGGTGCATCATTAGGTT   99132         C   AG
                                GGCCTGATGAT CAC  CGG
                                |||||||||||| |||  |||
                                TTGGATTACTA GTG  GTT
                                      C   GA
GAM1026  LOC257554 5'  TCTCTGCTGCGTGTTCGCGGGC 99537       A   TCCA_
            CA                   TGGCCTG TGA    CAGCGGAGA
                                ||||||| |||    |||||||||
                                ACCGGGC GCT    GTCGTCTCT
                                   _  TGTGC
GAM1026  LOC90408  5'  TTCTGCTGTGCCAGGGCT    63349      GATGATC
                                GGCCT      CACAGCGGAG
                                |||||      ||||||||||
                                TCGGG      GTGTCGTCTT
                                   ACC_____
GAM1026  LOC91496  5'  TTTTTGTTGTTGTTTTTGGGCC 66814      TG T   CC
            A                    TGGCC  A GAT  ACAGCGGAGA
                                ||||| | |||  ||||||||||
                                ACCGG  T TTG  TGTTGTTTTT
                                   GT T   T_
GAM1026  LOC92231  3'  TCCATTGTGGCGTCATTAGGTT 69095          _     C   GA
            A                    TGGCCTGATGAT CCACAG GGA
                                |||||||||||| |||||| |||
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                                ATTGGATTACTG GGTGTT CCT
                                      C     A
GAM1026 LOC92973 5' TTTCTGCTGTATGACTTTGGTC 71596      TGATGATCC
             A                   TGGCC       ACAGCGGAGA
                                 |||||       ||||||||||
                                 ACTGG       TGTCGTCTTT
                                   TTTCAGTA_
GAM1027 CHAD    3' GGAAGGCTGAGCCTCTC     8855       TA  CTGC
                                 GAGAG  CTC   GTCTTCC
                                 |||||  |||   |||||||
                                 CTCTC  GAG   CGGAAGG
                                   C_   T___
GAM1027 DSG1    5' AGGAAGGCAGAAACACCTC   10449     A  ACTC   GT
                                 GAG GT   CTGC  CTTCCT
                                 ||| ||   ||||  ||||||
                                 CTC CA   GACG  GAAGGA
                                   _  CAAA   __
GAM1027 MID1    3' AAGATGTAGAAGTCCCTC    6351      T_  C
                                 GAG  ACT CTGCGTCTT
                                 |||  ||| |||||||||
                                 CTC  TGA GATGTAGAA
                                   CC   A
GAM1027 OTOF    3' AGGAAGACTCCTGAAACCCTC 17828     A  AC  CTGC
                                 GAG GT  TC   GTCTTCCT
                                 ||| ||  ||   ||||||||
                                 CTC CA  AG   CAGAAGGA
                                   C  A_  TCCT
GAM1027 RNMT    3' AGGACATCCAAGGGTACTCTC 15047        T   GCGTCT
                                 GAGAGTAC CCT     TCCT
                                 |||||||| |||     ||||
                                 CTCTCATG GGA     AGGA
                                      _  ACCTAC
GAM1027 SCN3A   5' AGGAAGACACGTTATACCCT  23612    A  CTCC  C
                                 AG GTA   TG GTCTTCCT
                                 || |||   || ||||||||
                                 TC CAT   GC CAGAAGGA
                                  C  ATT_  A
GAM1027 SFRS7   3' GGAAGGCGATACTCTC      60148       CTCCTG
                                 GAGAGTA     CGTCTTCC
                                 |||||||     ||||||||
                                 CTCTCAT     GCGGAAGG
                                    A_____
GAM1027 SLC13A4 5' AAGACGAAGGAGGACTCTC   25857      A   G
                                 GAGAGT CTCCT CGTCTT
                                 |||||| ||||| ||||||
                                 CTCTCA GAGGA GCAGAA
                                    G    A
GAM1027 SSX2    3' AGGAAGATGACGAGTAACTC  97962     _   CTG
                                 GAGT ACTC   CGTCTTCCT
                                 |||| ||||   |||||||||
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                                CTCA TGAG   GTAGAAGGA
                                  A    CA_
GAM1027  TGFBR2   3'  AAGATTCAAGAGTATTCTC    13725          C  C
                                GAGAGTACTC TG GTCTT
                                |||||||||| || |||||
                                CTCTTATGAG AC TAGAA
                                     A  T
GAM1027  TNFRSF11A 3'  AGGAAGACCACCCGGCATTCTC 15187        A  CC_  C
                                GAGAGT CT   TG GTCTTCCT
                                |||||| ||   || ||||||||
                                CTCTTA GG   AC CAGAAGGA
                                   C  CCC  _
GAM1027  AP3M2    3'  AGGAAGACCCGTACTCTC     23299         TCCT C
                                GAGAGTAC    G GTCTTCCT
                                ||||||||    | ||||||||
                                CTCTCATG    C CAGAAGGA
                                     _____ C
GAM1027  CALN1    3'  AGGAAGACACAGAATTCTTTC  49658       TACTC   C
                                GAGAG     CTG GTCTTCCT
                                |||||     ||| ||||||||
                                CTTTC     GAC CAGAAGGA
                                   TTAA_   A
GAM1027  DAMS     5'  AGGAAATTCAAGTACTCT    42084         CC  C  C
                                AGAGTACT  TG GT TTCCT
                                ||||||||  || || |||||
                                TCTCATGA  AC TA AAGGA
                                     __  T  _
GAM1027  DKFZP727M111 5'  AGGCCAGGAGGACCCTC     32055     A  A     C
                                GAG GT CTCCTG GTCT
                                ||| || |||||| ||||
                                CTC CA GAGGAC CGGA
                                  C  G     _
GAM1027  FLJ14486 5'  AGGAAGGTTCAAGTCTCTC    52434       T   CC  CG
                                GAGAG ACT  TG  TCTTCCT
                                ||||| |||  ||  |||||||
                                CTCTC TGA  AC  GGAAGGA
                                   _  __  TT
GAM1027  FUSIP1   3'  AGGAAGACAGCCATAGTCTC   22780     T   CCT  _
                                GAG ACT   GC GTCTTCCT
                                ||| |||   || ||||||||
                                CTC TGA   CG CAGAAGGA
                                  _   TAC  A
GAM1027  HIC      3'  GAAGATTGAGTACTCT      68048          CTGC
                                AGAGTACTC    GTCTTC
                                |||||||||    ||||||
                                TCTCATGAG    TAGAAG
                                     T____
GAM1027  IL22R    3'  AGGAAATGCAGGGAAACTC   41467      AC       C
                                GAGT  TCCTGCGT TTCCT
                                ||||  |||||||| |||||
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                                CTCA  GGGACGTA AAGGA
                                  AA      _
GAM1027  KIAA0472  3'  AGGAGGGGTAAGTACTCTC   72334        CC   G
                                GAGAGTACT  TGC TCTTCCT
                                |||||||||  ||| |||||||
                                CTCTCATGA  ATG GGGAGGA
                                     __  _
GAM1027  KIAA1229  3'  AGGATGTAAAAGTTCTCTC   62750      T   CC
                                GAGAG ACT  TGCGTCTT
                                |||||| |||  ||||||||
                                CTCTC TGA  ATGTAGGA
                                   T   AA
GAM1027  LAK-4P    3'  AGGAAGACAGTTTCGCCTCTC  24394      TACTCCT  _
                                GAGAG      GC GTCTTCCT
                                |||||      || ||||||||
                                CTCTC      TG CAGAAGGA
                                   CGCTT__  A
GAM1027  MRPS35    3'  AGGTCCTCAGGAGTATTCTC   41819           CGTCTT
                                GAGAGTACTCCTG     CCT
                                ||||||||||||      |||
                                CTCTTATGAGGAC     GGA
                                       TCCT__
GAM1027  OBTP      5'  AGGATCTGCAAGGAGGACCCTC 34663     A  A    _   TCT
                                GAG GT CTCCT GCG   TCCT
                                ||| || ||||| |||   ||||
                                CTC CA GAGGA CGT   AGGA
                                  C  G    A   CT_
GAM1027  RI58      3'  AGATCAGGAATACTCTT     25774        C    C
                                GAGAGTA TCCTG GTCT
                                |||||||  ||||| ||||
                                TTCTCAT AGGAC TAGA
                                    A    _
GAM1027  SMBP      3'  AAGACAGAAGTGTACTCTC   72620        TC  GC_
                                GAGAGTAC  CT   GTCTT
                                ||||||||  ||   |||||
                                CTCTCATG  GA   CAGAA
                                     T_  AGA
GAM1027  SNTG1     5'  AGGACTCTGAGGAGTACTCTT  39099           G  TCT
                                GAGAGTACTCCT CG   TCCT
                                ||||||||||| ||   ||||
                                TTCTCATGAGGA GT   AGGA
                                       _  CTC
GAM1027  SNX11     3'  AGGACCAGGAGTATCTC     26169      G       C
                                GAGA TACTCCTG GTCTT
                                |||| |||||||| |||||
                                CTCT ATGAGGAC CAGGA
                                  _       _
GAM1027  TTY7      3'  AGGAAGACACAGGTAGCT    50015     ACT    C
                                AGT   CCTG GTCTTCCT
                                |||   |||| ||||||||
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                                TCG   GGAC CAGAAGGA
                                  AT_    A
GAM1027  LOC123872 5'  GGAAAGAGGGTACTCTC     74710          _  GCGTC
                                GAGAGTACTC CT     TTCC
                                |||||||||| ||     ||||
                                CTCTCATGGG GA     AAGG
                                     A  _____
GAM1027  LOC138389 3'  AGGAAGACTTGCAAGTCTCTC  76725       T   CC  __
                                GAGAG ACT  TGC  GTCTTCCT
                                ||||| |||  |||  ||||||||
                                CTCTC TGA  ACG  CAGAAGGA
                                   _  __  TT
GAM1027  LOC143943 3'  AGGAAGATCAGCAGCCTCTC   83911       TA  C   C
                                GAGAG  CT CTG GTCTTCCT
                                |||||  || ||| ||||||||
                                CTCTC  GA GAC TAGAAGGA
                                   C_  C   _
GAM1027  LOC145009 5'  AAGAAACAAAGGAGTACTTTC  60965           GCG__
                                GAGAGTACTCCT     TCTT
                                ||||||||||||     ||||
                                CTTTCATGAGGA     AGAA
                                      AACAA
GAM1027  LOC147976 5'  AGGAAGACTGGGGTACCCTC   79285     A      TGC
                                GAG GTACTCC   GTCTTCCT
                                ||| |||||||   ||||||||
                                CTC CATGGGG   CAGAAGGA
                                  C      T__
GAM1027  LOC151512 3'  AGGAAGACAATGCTTGTACCTC 86611     A   TCCT ___
                                GAG GTAC    GC   GTCTTCCT
                                ||| ||||    ||   ||||||||
                                CTC CATG    CG   CAGAAGGA
                                  _    TT__  TAA
GAM1027  LOC158801 3'  GAAAACACAAGAAGTATTCT   88255        _ C  C  C
                                AGAGTACT C TG GT TTC
                                |||||||| | || || |||
                                TCTTATGA G AC CA AAG
                                     A A  A  A
GAM1027  LOC206426 3'  GAAGCGAGGTGCACTCTC    91099       ACT   G  T
                                GAGAGT   CCT CG CTTC
                                ||||||   ||| || ||||
                                CTCTCA   GGA GC GAAG
                                   CGT   _  _
GAM1027  LOC254337 5'  GGAAAGGGGAGTATCTC     98012      G      GCGTC
                                GAGA TACTCCT     TTCC
                                |||| |||||||     ||||
                                CTCT ATGAGGG     AAGG
                                  _      GA___
GAM1027  LOC256790 5'  AGTGCAGGAGTGCCCTC     96489     A         T
                                GAG GTACTCCTGCG CT
                                ||| ||||||||||| ||
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                                CTC CGTGAGGACGT GA
                                  C         _
GAM1027  LOC256946 3'  AGGAAGACAGCCATAGTCTC   96182     T   CCT  _
                                GAG ACT   GC GTCTTCCT
                                ||| |||   || ||||||||
                                CTC TGA   CG CAGAAGGA
                                  _   TAC  A
GAM1027  LOC257396 5'  GAAATGTAGGAGCATCTC     98922      GTA        C
                                GAGA   CTCCTGCGT TTC
                                ||||   ||||||||| |||
                                CTCT   GAGGATGTA AAG
                                  AC_        _
GAM1027  LOC257408 3'  AGGGCACCAGGAGTACCTC    97797     A        C  CT
                                GAG GTACTCCTG GT  TCCT
                                ||| ||||||||| ||  ||||
                                CTC CATGAGGAC CA  GGGA
                                  _        _ C_
GAM1027  LOC257453 3'  AGGAAGATGACGAGTAACTC   82927      _    CTG
                                GAGT ACTC   CGTCTTCCT
                                |||| ||||   |||||||||
                                CTCA TGAG   GTAGAAGGA
                                  A   CA_
GAM1027  LOC51066  3'  AGGAAGATGGCCGACACTCTC  32500       AC  CTG
                                GAGAGT  TC   CGTCTTCCT
                                ||||||  ||   |||||||||
                                CTCTCA  AG   GTAGAAGGA
                                   C_  CCG
GAM1028  IRS1      3'  CCATAGATGGTTCTCAATTGTA 19874      C         TGAAC
                                TACA ATTGAGAACC     ATGG
                                |||| ||||||||||     ||||
                                ATGT TAACTCTTGG     TACC
                                  _         TAGA_
GAM1028  SERPINF1  3'  CCTGTAAGGTTTCAATG      12038         A   GA   T
                                CATTGAGA CCT  ACA GG
                                |||||||| |||  ||| ||
                                GTAACTTT GGA  TGT CC
                                     _   A_   _
GAM1028  HSA243396 3'  CCATGTTCAGCAATGTCAATG  37844       GAAC_
                                CATTGA    CTGAACATGG
                                ||||||    ||||||||||
                                GTAACT    GACTTGTACC
                                   GTAAC
GAM1028  KIAA1387  3'  CAGGAATTTTCAATATGTA    71444      C       __
                                TACA ATTGAGAA  CCTG
                                |||| ||||||||  ||||
                                ATGT TAACTTTT  GGAC
                                  A       AA
GAM1028  MGC16063  3'  TTCAAATTCCAATGTGTA     54930          A   CC
                                TACACATTG GAA  TGAA
                                ||||||||| |||  ||||
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                                ATGTGTAAC CTT  ACTT
                                      _  AA
GAM1028  SMCR8    3'  CCATGCTCAGGTTTGACTATGT 59253     TGA_      A
                                ACAT   GAACCTGA CATGG
                                ||||   |||||||| |||||
                                TGTA   TTTGGACT GTACC
                                  TCAG      C
GAM1028  UPLC1    3'  CCATGCTAGGCCCCAATGT   35227      AGAA   AA
                                ACATTG   CCTG  CATGG
                                ||||||   ||||  |||||
                                TGTAAC   GGAT  GTACC
                                   CCC_   C_
GAM1028  ZNF334   3'  CCATAAGTCAACCCTCAATGT  36637       AACC   AC_
                                ACATTGAG   TGA   ATGG
                                ||||||||   |||   ||||
                                TGTAACTC   ACT   TACC
                                     CCA_  GAA
GAM1028  LOC145082 3'  TATGGAATGCCCTTAATGTGTA 84196         AACCTGAA
                                TACACATTGAG      CATG
                                ||||||||||       ||||
                                ATGTGTAATTC      GTAT
                                      CCGTAAG_
GAM1028  LOC157723 3'  CCAAGTAAGGTTCTCAAATGT  82465     _      GA  A
                                ACATT GAGAACCT  AC TGG
                                ||||| ||||||||  || |||
                                TGTAA CTCTTGGA  TG ACC
                                   A      A_  A
GAM1028  LOC219988 5'  CCATGTTCGGCCCCCAATG   93262     AGAAC
                                CATTG    CTGAACATGG
                                |||||    ||||||||||
                                GTAAC    GGCTTGTACC
                                   CCCC_
GAM1029  ATP6V0C  3'  CCCCAGTAGTTGGTCTTGTA  88658       CTG  _  A
                                TACAAGATCA   ACT CTG GG
                                ||||||||||   ||| ||| ||
                                ATGTTCTGGT   TGA GAC CC
                                      ___   T   C
GAM1029  DLX4     3'  GTCCCCAGAACCCTTGGTCTTG 57114       CTGAC   A
                                CAAGATCA     TCTG GGAC
                                ||||||||     |||| ||||
                                GTTCTGGT     AGAC CCTG
                                     TCCCA    C
GAM1029  MNT      3'  TCCTCAGAGGCTGAGCCTGTA  40089     AGA   CTGA
                                TACA   TCA   CTCTGAGGA
                                ||||   |||   |||||||||
                                ATGT   AGT   GAGACTCCT
                                  CCG   CG__
GAM1029  SIAH2    3'  TCTCATCAGTGATCTT      18616          CTC
                                AAGATCACTGA   TGAGG
                                ||||||||||   |||||
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                                TTCTAGTGACT   ACTCT
                                    ___
GAM1029  TCF2     3'  GTCCCCAGAACCAGCTGCAGAT 6617     AGAT  _   AC    A
              G                   CA    CA CTG  TCTG GGAC
                                  ||    || |||  |||| ||||
                                  GT    GT GAC  AGAC CCTG
                                   AGAC  C   CA    C
GAM1029  TCL1A    3'  CCTGGACCAGTGGTCT      42017         AC   G
                                  AGATCACTG  TCT AGG
                                  |||||||||  ||| |||
                                  TCTGGTGAC  AGG TCC
                                       C_   _
GAM1029  TOB1     3'  TTTTGAGTCAGTGTCTT     20437      T        T
                                  AAGA CACTGACTC GAG
                                  |||| |||||||| |||
                                  TTCT GTGACTGAG TTT
                                    _        T
GAM1029  VNN1     3'  TCCTCAGAGCAATTCTCTGTA  17423      _   TCAC  A
                                  TACA AGA    TG CTCTGAGGA
                                  |||| |||    || |||||||||
                                  ATGT TCT    AC GAGACTCCT
                                    C   TA__  _
GAM1029  BMF      5'  CCTCAGAGTCAAACTTTGTG   54280       ATCAC
                                  TACAAG     TGACTCTGAGG
                                  ||||||     ||||||||||
                                  GTGTTT     ACTGAGACTCC
                                     CAA__
GAM1029  DDX33    3'  GTCCTCAGTGCGTGACCCTGT  39786     AGA    T ACT
                                  ACA   TCAC G   CTGAGGAC
                                  |||   |||| |   ||||||||
                                  TGT   AGTG C   GACTCCTG
                                    CCC    _ GT_
GAM1029  FLJ20364 3'  CCTCAGAGCCATGTATTTG   35528      AT  C  A
                                  CAAG  CA TG CTCTGAGG
                                  ||||  || || ||||||||
                                  GTTT  GT AC GAGACTCC
                                    AT  _  C
GAM1029  HMGN4    3'  TCCTTTCCCCAGTGATTTGTA  22034      A       ACTCT
                                  TACA GATCACTG     GAGGA
                                  |||| ||||||||     |||||
                                  ATGT TTAGTGAC     TTCCT
                                    _        CCCT_
GAM1029  KIAA0377 3'  CCTCAGAGCCAGTCTCT     28501     TC    A
                                  AGA  ACTG CTCTGAGG
                                  |||  |||| ||||||||
                                  TCT  TGAC GAGACTCC
                                    C_    C
GAM1029  KIAA0449 3'  TCCCCAGCACTCATGATCTTG  34639         C   CT_   A
                                  CAAGATCA TGA   CTG GGA
                                  |||||||| |||   ||| |||
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                                GTTCTAGT ACT   GAC CCT
                                     _  CAC   C
GAM1029 KIAA1061 3' GTCCTCAGAGTGCATTTCCTG 71723    A  TCAC  _
                                CA GA    TG ACTCTGAGGAC
                                || ||    || ||||||||||
                                GT CT    AC TGAGACTCCTG
                                 C  TT__  G
GAM1029 KIAA1535 3' GTCCTCAGCTCAAGAATCCTGT 80214     A   CAC   CT
             A                   TACA GAT   TGA  CTGAGGAC
                                 |||| |||   |||  ||||||||
                                 ATGT CTA   ACT  GACTCCTG
                                   C   AGA   C_
GAM1029 LCHN     3'  TCCTCAGAGTATGTCTTG    87478       CACTG
                                 CAAGAT    ACTCTGAGGA
                                 ||||||    ||||||||||
                                 GTTCTG    TGAGACTCCT
                                    TA___
GAM1029 MAGEH1   3'  TCATAATCTATGATCTTGTA   26772         CT  CTC
                                 TACAAGATCA  GA   TGA
                                 |||||||||  ||   |||
                                 ATGTTCTAGT  CT   ACT
                                       AT  AAT
GAM1029 LOC154789 5'  TCCTCAGAGCTCTCCTGTG   82034     A  TCACT  _
                                 TACA GA    GA CTCTGAGGA
                                 |||| ||    || |||||||||
                                 GTGT CT    CT GAGACTCCT
                                   C  _____  C
GAM1029 LOC197201 3'  TCCTCAGAAGGTATTTGTA   89289      ATC   GAC
                                 TACAAG   ACT   TCTGAGGA
                                 ||||||   |||   ||||||||
                                 ATGTTT   TGG   AGACTCCT
                                    A__   A__
GAM1029 LOC255193 3'  CCTCAGAGTCAGGCCTGTA   97103     AGATCA
                                 TACA     CTGACTCTGAGG
                                 ||||     ||||||||||||
                                 ATGT     GACTGAGACTCC
                                   CCG___
GAM1029 LOC96597  5'  TCCCCAGAATTCTCTTGT    67468      TCACT  C_   A
                                 ACAAGA    GA  TCTG GGA
                                 ||||||    ||  |||| |||
                                 TGTTCT    CT  AGAC CCT
                                    _____  TA   C
GAM1030 BBS4     3'  ATTTGCCCAAAGGGAATCCAGA 53447        G_  G_   A
             ACA                   TGTTCTGGA  CT  TTGG CAAAT
                                   |||||||||  ||  |||| |||||
                                   ACAAGACCT  GG  AACC GTTTA
                                        AA  GA   C
GAM1030 CENTD2   3'  CCAACAAACTCCAGAACA    31539         C_
                                   TGTTCTGGAG  TGTTGG
                                   ||||||||||  ||||||
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                                ACAAGACCTC  ACAACC
                                      AA
GAM1030  HAMP     3'  TCCTGCTGCCCCAGAACA    41289        A  T  T
                                TGTTCTGG GC GT GGA
                                |||||||| || || |||
                                ACAAGACC CG CG CCT
                                     C  T  T
GAM1030  ITGA11   3'  TCTGCCGGCCCCCAGGACA   25213        A_   TT
                                TGTTCTGG  GCTG  GGA
                                ||||||||  ||||  |||
                                ACAGGACC  CGGC  TCT
                                     CC    CG
GAM1030  KITLG    3'  ATTTGCATGGCTCCAGAA    8023           TGGA
                                TTCTGGAGCTGT    CAAAT
                                ||||||||||||    |||||
                                AAGACCTCGGTA    GTTTA
                                       C___
GAM1030  MAPK4    5'  CCTGGGCAGCTCCAGATCA    12300    T         __
                                TG TCTGGAGCTGTT  GG
                                || ||||||||||||  ||
                                AC AGACCTCGACGG  CC
                                 T          GT
GAM1030  MGAT2    3'  ATTTGTCCAAACAGGACA    11557        GAGCTG
                                TGTTCTG     TTGGACAAAT
                                |||||||     ||||||||||
                                ACAGGAC     AACCTGTTTA
                                    A_____
GAM1030  PSPHL    5'  TTGTCATACAGCTCCAAACA   94499     C        TG
                                TGTT TGGAGCTGT  GACAA
                                |||| |||||||||  |||||
                                ACAA ACCTCGACA  CTGTT
                                  _        TA
GAM1030  TTC3     3'  TATTTGTCCAACAACTGTCAGA 13885         _ C
              ATA                   TGTTCTGG AG TGTTGGACAAATA
                                |||||||| || ||||||||||||
                                ATAAGACT TC ACAACCTGTTTAT
                                     G  A
GAM1030  H2BFQ    3'  TTTAAGAGAACTCCAGGACA   60079          __ G
                                TGTTCTGGAG  CT TTGGA
                                ||||||||||  || |||||
                                ACAGGACCTC  GA AATTT
                                      AA  G
GAM1030  LRG      3'  TCCATCCATGCTTCCTAGAACA 54825       _  _ _ T_
                                TGTTCT GGA GC TG  TGGA
                                |||||| ||| || ||  ||||
                                ACAAGA CCT CG AC  ACCT
                                   T  T  T  CT
GAM1030  NMT2     3'  ATTTGTCCATGTAACAGAACA  17852        GA  TGT
                                TGTTCTG  GC   TGGACAAAT
                                |||||||  ||   |||||||||
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                                ACAAGAC  TG   ACCTGTTTA
                                    AA  T__
GAM1030  NYD-SP21  3'  TATTTGTCCAATCTAGATTCAG 51863        G  __
             AACA                   TGTTCTGGA CT  GTTGGACAAATA
                                ||||||||| ||  ||||||||||||
                                ACAAGACTT GA  TAACCTGTTTAT
                                    A  TC
GAM1030  PSPH     3'  TTGTCGTACAGCTCCAAACA  17143     C       TG
                                TGTT TGGAGCTGT  GACAA
                                |||| |||||||||  |||||
                                ACAA ACCTCGACA  CTGTT
                                  _       TG
GAM1030  LOC122258 3'  CCACCAGCCTCCGGAACA    59820         _  T
                                TGTTCTGGAG CTG TGG
                                |||||||||| ||| |||
                                ACAAGGCCTC GAC ACC
                                    C   C
GAM1030  LOC151826 3'  ATTTGTCCAACCTAGCACA   81176    T   AGCT
                                TGT CTGG   GTTGGACAAAT
                                ||| ||||   ||||||||||||
                                ACA GATC   CAACCTGTTTA
                                  C   ____
GAM1030  LOC169611 3'  TCCAGTGGCAGCTCCAGAA   83663          ___
                                TTCTGGAGCTGT   TGGA
                                ||||||||||||  ||||
                                AAGACCTCGACG   ACCT
                                    GTG
GAM1030  LOC196746 3'  TCAGAGCAGCTCCAAGACA   88903    TC       G_
                                TGT  TGGAGCTGTT  GA
                                |||  ||||||||||  ||
                                ACA  ACCTCGACGA  CT
                                  GA        GA
GAM1030  LOC253142 5'  TTGCTAGGATGCCCCAGAATA  99230       A  TG_   A
                                TGTTCTGG GC   TTGG CAA
                                |||||||| ||   |||| |||
                                ATAAGACC CG   GATC GTT
                                    C  TAG   _
GAM1031  C1orf6   3'  CTCTCTGGACAGGAATTAACA  39694    G  GC
                                TGT GA  CCTGTCCAGAGAG
                                ||| ||  ||||||||||||
                                ACA TT  GGACAGGTCTCTC
                                  A  AA
GAM1031  MYLK2    3'  CTCCCCAGACAGGGCTCCA   53584          CA__
                                TGGAGCCCTGTC   GAG
                                ||||||||||||   |||
                                ACCTCGGGACAG   CTC
                                    ACCC
GAM1031  PKIG     3'  CTCATGGAGCTCCACAGA    23926    A      CCTG   _
                                TC TGTGGAGC   TCCA GAG
                                || ||||||||   |||| |||
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                                AG ACACCTCG    AGGT CTC
                                 _      _____    A
GAM1031  STK6     3'  CTCCCTATTCAGAAAGCTCCAC 14587         C__   TCC  A
              AT                   ATGTGGAGC   CTG   AG GAG
                                |||||||||   |||   || |||
                                TACACCTCG   GAC   TC CTC
                                     AAA   TTA  C
GAM1031  THBD     3'  CTCAGACAGAACCCCTACATGA 6276         AGCC_    CA
                                TCATGTGG    CTGTC  GAG
                                ||||||||    |||||  |||
                                AGTACATC    GACAG  CTC
                                     CCCAA    A_
GAM1031  CNNM4    3'  CTCCCCAGTGGGCCCACATGA  39863         A    TGTCCA
                                TCATGTGG GCCC     GAG
                                |||||||| ||||     |||
                                AGTACACC CGGG     CTC
                                     _   TGACCC
GAM1031  FLJ10352 3'  CTCTCTGGACAAAGCATC    50471    _ CC
                                GA GC  TGTCCAGAGAG
                                || ||  ||||||||||||
                                CT CG  ACAGGTCTCTC
                                 A  AA
GAM1031  FLJ10352 3'  CTCTTAAGGAGCCTCACATGA  50472       GA  _  GTCC
                                TCATGTG  GC CCT    AGAG
                                |||||||  || |||    ||||
                                AGTACAC  CG GGA    TCTC
                                     TC  A   AT__
GAM1031  FLJ21977 5'  GGACAAAGCTCACATGA     50872        G   CC
                                TCATGTG AGC  TGTCC
                                ||||||| |||  |||||
                                AGTACAC TCG  ACAGG
                                     _   AA
GAM1031  KIAA0461 3'  CTCTGGACAAAGGATCATACA  71395      _  G  C_
                                TGTG GA CC  TGTCCAGAG
                                |||| || ||  |||||||||
                                ACAT CT GG  ACAGGTCTC
                                  A  A  AA
GAM1031  KIAA1130 3'  CTCTGGGCTTCCTCCACATGG  63090          CCCT
                                TCATGTGGAG    GTCCAGAG
                                ||||||||||    ||||||||
                                GGTACACCTC    CGGGTCTC
                                     CTT_
GAM1031  MGC10471 5'  CTCTGCCAGGCTCCACAAGA   48765    A       C  TC
                                TC TGTGGAGCC TG  CAGAG
                                || |||||||| ||  |||||
                                AG ACACCTCGG AC  GTCTC
                                 A        _  C_
GAM1031  LOC146562 3'  TCTCTGGACCCCACGTGA    58255        AGCCCT
                                TCATGTGG     GTCCAGAGA
                                ||||||||     |||||||||
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                                AGTGCACC     CAGGTCTCT
                                    C_____
GAM1031  LOC148753 3'  CTCCAACAGCCCCACATGG   85371        A  CC   CCA
                                TCATGTGG GC  TGT   GAG
                                |||||||| ||  |||   |||
                                GGTACACC CG  ACA   CTC
                                    C  __   AC_
GAM1031  LOC148946 3'  CTCTAAGGAGGACCCTACATGA 85467        AG_  CTG   AG
                                TCATGTGG   CC   TCC  AGAG
                                ||||||||   ||   |||  ||||
                                AGTACATC   GG   AGG  TCTC
                                    CCA  ___   AA
GAM1031  LOC154739 5'  TCTCTGGCCCTCCACTGA    87446    T     CCCT T
                                TCA GTGGAG    G CCAGAGA
                                ||| ||||||    | |||||||
                                AGT CACCTC    C GGTCTCT
                                  _     C___ _
GAM1031  LOC166341 3'  CTCCCAGTGGGCCCCACATGA  83514        A    TGTCCA
                                TCATGTGG GCCC     GAG
                                |||||||| ||||     |||
                                AGTACACC CGGG     CTC
                                    C    TGACC_
GAM1031  LOC203276 3'  TCTCTGGCCCTCCACTGA    92133    T     CCCT T
                                TCA GTGGAG    G CCAGAGA
                                ||| ||||||    | |||||||
                                AGT CACCTC    C GGTCTCT
                                  _     C___ _
GAM1031  LOC203305 3'  TCTCTGGCCCTCCACTGA    92186    T     CCCT T
                                TCA GTGGAG    G CCAGAGA
                                ||| ||||||    | |||||||
                                AGT CACCTC    C GGTCTCT
                                  _     C___ _
GAM1031  LOC204084 5'  CTCTCTGGACAGACTGACA   90996     GG  CC
                                TGT  AG  CTGTCCAGAGAG
                                |||  ||  ||||||||||||
                                ACA  TC  GACAGGTCTCTC
                                  G_  A_
GAM1031  LOC254243 3'  TCTCTGGCCCTCCACTGA    99272    T     CCCT T
                                TCA GTGGAG    G CCAGAGA
                                ||| ||||||    | |||||||
                                AGT CACCTC    C GGTCTCT
                                  _     C___ _
GAM1031  LOC90038  3'  TCTCTGGCCCTCCACTGA    61816    T     CCCT T
                                TCA GTGGAG    G CCAGAGA
                                ||| ||||||    | |||||||
                                AGT CACCTC    C GGTCTCT
                                  _     C___ _
GAM1031  LOC91661  3'  CTCCCCACCCCGGGCTCCAACA 57212     _     T__  CCA
                                TGT GGAGCCC   GT   GAG
                                ||| |||||||   ||   |||
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                                ACA CCTCGGG  CA  CTC
                                  A      CCC  CCC
GAM1031  LOC93444  5'  CTCTCCAGACAGGGTACAACTT 72825     T  GGA       CA
              GA                   TCA GT   GCCCTGTC  GAGAG
                                ||| ||   ||||||||  |||||
                                AGT CA   TGGGACAG  CTCTC
                                  T  ACA       AC
GAM1032  IL17R    3'  GGGGAATCCACACAGCCCGCT  27559     AGA       ATGG
                                AGC   TTGTGTGGA    TCCT
                                |||   |||||||||    ||||
                                TCG   GACACACCT    GGGG
                                  CCC        AA__
GAM1032  MAN1A1   3'  AGGACCATCTTTATGACCTGCT 93555       A TG  T   A
              T                    AAGCAG T  TG GGA TGGTCCT
                                |||||| |  || ||| |||||||
                                TTCGTC A  AT TCT ACCAGGA
                                   C GT  T   _
GAM1032  DNAJC6   3'  AGAACCACCGCATTCCACCCTG 29489     ATT___     AA    C
              C                    GCAG     GTGTGG  TGGT CT
                                ||||     ||||||  |||| ||
                                CGTC     TACGCC  ACCA GA
                                  CCACCT     __    A
GAM1032  FLJ20489  3'  GAATGGTCCTAGGACACAAATC 35712         _  T_______  ATGG
              TGCTT                AAGCAGATT GTG       GGA    TC
                                ||||||||| |||       |||    ||
                                TTCGTCTAA CAC       CCT    AG
                                     A   AGGA___T   GGTA
GAM1032  FLJ21551  3'  ATTCCACATAATCCACTT    46029     CA
                                AAG  GATTGTGTGGAAT
                                |||  ||||||||||||
                                TTC  CTAATACACCTTA
                                  AC
GAM1032  KIAA1045  3'  ACCACTCCAAGTCTGCT     71598        GTG    A
                                AGCAGATT   TGGA TGGT
                                ||||||||   |||| ||||
                                TCGTCTGA   ACCT ACCA
                                     ___    C
GAM1032  KIAA1613  3'  GGACTCAACAAATCTGC     65441       G   GGAAT
                                GCAGATT TGT    GGTCC
                                ||||||| |||    |||||
                                CGTCTAA ACA    TCAGG
                                   _  AC___
GAM1032  KIAA1889  5'  GATATTTCCACACAATATACTT 73881     CAG        TG
                                AAG   ATTGTGTGGAA  GTC
                                |||   ||||||||||  |||
                                TTC   TAACACACCTT  TAG
                                  ATA         TA
GAM1032  LASP1    3'  AGGAAGCCCACCAATCTGC    21573        T    AATGG
                                GCAGATTG GTGG    TCCT
                                |||||||| ||||    ||||
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                                CGTCTAAC CACC    AGGA
                                    _   CGA__
GAM1032  RCD-8    3'  GGCTGAGCCACACAACTC    27522   _      AA
                                GA TTGTGTGG  TGGTC
                                || |||||||  |||||
                                CT AACACACC  GTCGG
                                 C       GA
GAM1032  STK39    3'  ACCAATTTACAATCTGACT    26009   _      TGGAA
                                AG CAGATTGTG    TGGT
                                || |||||||||    ||||
                                TC GTCTAACAT    ACCA
                                 A       TTA__
GAM1032  LOC143279 5'  AGAACCACCACCAATTTGC    77019       T   AA   C
                                GCAGATTG GTGG  TGGT CT
                                |||||||| ||||  |||| ||
                                CGTTTAAC CACC  ACCA GA
                                    _   __   A
GAM1032  LOC219673 5'  ATTCCACACAACCAGCTT    94610     AGA
                                AAGC   TTGTGTGGAAT
                                ||||   ||||||||||||
                                TTCG   AACACACCTTA
                                  ACC
GAM1032  LOC220827 3'  ACCATTCCACCAGCTGCT    92879     A   T
                                AGCAG TTG GTGGAATGGT
                                ||||| ||| ||||||||||
                                TCGTC GAC CACCTTACCA
                                   _  _
GAM1032  LOC222160 3'  GACCACCCCCATTGTTCTGC   95786     TT_   T  AA
                                GCAGA   GTG GG  TGGTC
                                |||||   ||| ||  |||||
                                CGTCT   TAC CC  ACCAG
                                   TGT   _  CC
GAM1032  LOC51644  3'  ACCACCTTCATAAACTGCT    32663     A    T_  AA
                                AGCAG TTGTG  GG  TGGT
                                ||||| |||||  ||  ||||
                                TCGTC AATAC  CC  ACCA
                                   A    TT  __
GAM1033  ARF1     3'  GTGGAACCTCTTACTGCTTTCA 71198       C   A  A_
                                TGAAAGCAG AAGA GT  TGC
                                ||||||||| |||| ||  |||
                                ACTTTCGTC TTCT CA  GTG
                                     A   C  AG
GAM1033  BCL11B   3'  TCAGCATGTGTCTGCCATTTCA 57580     GCA   A  AG
                                TGAAA   GCA GA  TATGCTGA
                                |||||   ||| ||  ||||||||
                                ACTTT   CGT CT  GTACGACT
                                   AC_   _  GT
GAM1033  BRF2     5'  TACTTCTTGCTGCCTCA     37567     AA
                                TGA  GCAGCAAGAAGTA
                                |||  ||||||||||||
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                                ACT  CGTCGTTCTTCAT
                                  C_
GAM1033  CRHR1    3'  CAGCAATGCCCTGCCTTGCTGC 16502      A       AA___   _
              CTTCA                    TGAA GCAGCAAG     GTAT GCTG
                                ||||  ||||||||     ||||  ||||
                                ACTT CGTCGTTC     CGTA CGAC
                                  C       CGTCC    A
GAM1033  LAMP2    3'  TCAAATATTTCTTGCTGCTT   26578              GC
                                AAGCAGCAAGAAGTAT  TGA
                                ||||||||||||||||  |||
                                TTCGTCGTTCTTTATA  ACT
                                          A_
GAM1033  SORT1    3'  CAGCTCTGTTTCTGCTGCTTCC 12926    A       A    TAT_
              A                     TG AAGCAGCA GAAG    GCTG
                                ||  ||||||||  ||||    ||||
                                AC TTCGTCGT CTTT    CGAC
                                 C       _    GTCT
GAM1033  TLR2     5'  TGCTCTTTCACTGCTTTCA    13777          C__    A
                                TGAAAGCAG   AAGA GTA
                                |||||||||   ||||  |||
                                ACTTTCGTC   TTCT CGT
                                      ACT    _
GAM1033  UGT2B4   3'  TCAGCATACTTTGGATCCATTT 72415       GCAGCAA
              CA                    TGAAA      GAAGTATGCTGA
                                |||||      ||||||||||||
                                ACTTT      TTTCATACGACT
                                   ACCTAGG
GAM1033  7h3      3'  TCGGCCCTCTTGCTGCTGCCA  53436    AA        A TAT
                                TG  AGCAGCAAGA G   GCTGA
                                ||  ||||||||||  |   |||||
                                AC  TCGTCGTTCT C   CGGCT
                                 CG         _ C__
GAM1033  DCOHM    3'  AGTTATCTTGCTGCCTCA    50510     AA        AGTAT
                                TGA  GCAGCAAGA     GCT
                                |||  |||||||||     |||
                                ACT  CGTCGTTCT     TGA
                                  C_        AT___
GAM1033  FLJ10874 3'  GGTATGTTCTAACTGCTTCCA  37327    A     CA    G
                                TG AAGCAG  AGAA TATGCT
                                ||  ||||||  ||||  ||||||
                                AC TTCGTC  TCTT GTATGG
                                 C     AA   _
GAM1033  FLJ20489 3'  TCAGAGTGCCCTTGCTGC    35713         AA    G
                                GCAGCAAG  GTAT CTGA
                                ||||||||  ||||  ||||
                                CGTCGTTC  CGTG GACT
                                      C_    A
GAM1033  FLJ21709 3'  CAGTGTTCTTGTTACTTCCA   78479    A   C       AGT
                                TG AAG AGCAAGA   ATGCTG
                                ||  |||  |||||||   ||||||
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                                AC TTC TTGTTCT   TGTGAC
                                 C   A     ___
GAM1033  FLJ21977  3'  CAGGCCACACCCCTTGCTGTCT 50868     AA       AA  A  __
              CA                   TGA  GCAGCAAG  GT TG  CTG
                                |||  ||||||||  || ||  |||
                                ACT  TGTCGTTC  CA AC  GAC
                                  C_       CC  C  CG
GAM1033  FLJ23112  3'  CAGTATCCTGCTGCTTCA    46809      A     A  AGTA
                                TGAA GCAGCA GA    TGCTG
                                |||| |||||| ||    |||||
                                ACTT CGTCGT CT    ATGAC
                                  _     C  ____
GAM1033  GFRA4     3'  AGCCGGCCCTGGTGCTTTCA   42417         G  AGAA  AT
                                TGAAAGCA CA    GT  GCT
                                |||||||| ||    ||  |||
                                ACTTTCGT GT    CG  CGA
                                     G  CC__  GC
GAM1033  GIT1      3'  CAGCCCCTTGCTGCTCTC    26717    A       AAGTAT
                                GA AGCAGCAAG     GCTG
                                || |||||||||     ||||
                                CT TCGTCGTTC     CGAC
                                 C        CC____
GAM1033  HPCAL4    3'  TCAGCAGTTTTTGCTGCTTCA  33212      A        GTA
                                TGAA GCAGCAAGAA   TGCTGA
                                |||| ||||||||||   ||||||
                                ACTT CGTCGTTTTT   ACGACT
                                  _         G__
GAM1033  HSU79275  3'  CAGCACCCTCTGCTGCTTCA   66920      A     A  A TA
                                TGAA GCAGCA GA G  TGCTG
                                |||| |||||| || |  |||||
                                ACTT CGTCGT CT C  ACGAC
                                  _     _ _ CC
GAM1033  KIAA0552  3'  CAGCCTCTTTCTGCTTTCA    28988         C    AGTAT
                                TGAAAGCAG AAGA     GCTG
                                |||||||| ||||     ||||
                                ACTTTCGTC TTCT     CGAC
                                     T    C____
GAM1033  KIAA0912  3'  TCAGTTTCCTATTGCTGCTTCC 65044    A       GA  TAT
              A                   TG AAGCAGCAA  AG   GCTGA
                                || |||||||||  ||   |||||
                                AC TTCGTCGTT  TC   TGACT
                                 C        A_  CTT
GAM1033  KIAA0937  3'  TCAGCCGGCTTCTTGCTACTTC 93227    A  C        AT
              CA                   TG AAG AGCAAGAAGT  GCTGA
                                || ||| ||||||||||  |||||
                                AC TTC TCGTTCTTCG  CGACT
                                 C  A         GC
GAM1033  KIAA1157  3'  CAGCAGCTCCGCTGTTTTCA   72697          AA  A  A
                                TGAAAGCAGC  GA GT TGCTG
                                ||||||||||  || || |||||
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                                ACTTTTGTCG  CT CG ACGAC
                                      C_  _  _
GAM1033  KIAA1259  3'  CAGCCTGAGCTTGCTGCCCTC  50797    AA       AAG  T
                                GA  GCAGCAAG   TA GCTG
                                ||  ||||||||   || ||||
                                CT  CGTCGTTC   GT CGAC
                                 CC       GA_  C
GAM1033  MAPKAPK3  3'  CAGCATACTTTCCCTGC     17343      CAA
                                GCAG   GAAGTATGCTG
                                ||||   ||||||||||
                                CGTC   TTTCATACGAC
                                  CC_
GAM1033  SLC11A2   3'  TCAGCACAAAGCTGCTGCTTTT 7052           A AAGTA
              A                  TGAAAGCAGCA G     TGCTGA
                                ||||||||||| |     ||||||
                                ATTTTCGTCGT C     ACGACT
                                      _ GAAAC
GAM1033  LOC130536 5'  TCATGTAGCCCCTTGCTGCCAT 76246     AA       AA  A  _
              CA                   TGA  GCAGCAAG  GT TGC TGA
                                |||  ||||||||  || ||| |||
                                ACT  CGTCGTTC  CG ATG ACT
                                  AC       CC  _   T
GAM1033  LOC145826 5'  TCAGCATAGAAAAGGCTGCTTT 84533         AAGAAG
                                AAAGCAGC      TATGCTGA
                                ||||||||      ||||||||
                                TTTCGTCG      ATACGACT
                                     GAAAAG
GAM1033  LOC148056 3'  TCAGCTCCTCCTGCTGCTTCCG 85249    A       A  A TAT
                                TG AAGCAGCA GA G   GCTGA
                                || |||||||| || |   |||||
                                GC TTCGTCGT CT C   CGACT
                                 C       C  _ CT_
GAM1033  LOC159121 3'  CACATTTTCTCACTGCTTTC   88385         CA    T   C
                                GAAAGCAG  AGAAG ATG TG
                                ||||||||  ||||| ||| ||
                                CTTTCGTC  TCTTT TAC AC
                                     AC    _  _
GAM1033  LOC204804 3'  TCAGCCCAGTCCTGGTGCTTTC 91053         G  A  AGTAT
              A                  TGAAAGCA CA GA     GCTGA
                                ||||||||  || ||     |||||
                                ACTTTCGT GT CT     CGACT
                                     G  C  GACC_
GAM1033  LOC221760 3'  CAGCTACCTCTTGCTGTTCTCA 95427     A        A   T
                                TGA AGCAGCAAGA GTA GCTG
                                ||| |||||||||| ||| ||||
                                ACT TTGTCGTTCT CAT CGAC
                                  C         C   _
GAM1033  LOC253143 3'  CAGCAAGCTCCTGCTTTCA    98728          CAA  A  A
                                TGAAAGCAG   GA GT TGCTG
                                |||||||||   || || |||||
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                                ACTTTCGTC   CT CG ACGAC
                                    ___  _  A
GAM1034  CDH12    3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                    AA___   AC
GAM1034  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC         G
GAM1034  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090       T    AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||     ||||||
                                TGGTG GGGT     TTATTC
                                   _    GTCA_
GAM1034  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
             A                   TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM1034  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                    AGACG___
GAM1034  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
             TA                   TACA    TCC    GAAGAATAAG
                                ||||    |||    ||||||||||
                                ATGT    AGG    TTTCTTATTC
                                  AAA_   ATTG
GAM1034  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68742             _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                          G
GAM1034  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM1034  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748      CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM1034  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
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                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM1034  OSBPL11   3'  CTTAATTTCCCAAGAGTGGTG  43206       CCAA   AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                    AACC   A_
GAM1034  YME1L1    3'  TCATTCTTGATGTGGTGTA   58438       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                    TA_    A
GAM1034  ZNF262    3'  CTTATTTTGTTTGGGAGT    18723       A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                    G
GAM1034  LOC91960  3'  TGTGGCTTGGAACGTGGTGTA  68294       TC_    AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
                                ATGTGGTG   GGTTC   TGT
                                    CAA    GG__
GAM1035  ADCY8     5'  GGGGCTGCGTGGCTCACAGCG  8503      C_  G   GAC
                                CGCTG  AGC CACG   CCCC
                                |||||  ||| ||||   ||||
                                GCGAC  TCG GTGC   GGGG
                                  AC   _    GTC
GAM1035  ANKH      3'  GGCGGGTGGCACGCTGCAGC   55070       CACGG   _
                                GCTGCAGCG    ACCC CC
                                |||||||||    ||||  ||
                                CGACGTCGC    TGGG GG
                                    ACGG_    C
GAM1035  ATBF1     5'  GGGCGGTGCGCGCTGCA     23529       AC G   _
                                TGCAGCGC  G ACC CCC
                                ||||||||  |  ||| |||
                                ACGTCGCG  C TGG GGG
                                    __ G   C
GAM1035  ATM       5'  GGGATCTGCGCTGCAGC     5299        C  A
                                GCTGCAGCGCA GG CCC
                                ||||||||||| ||  |||
                                CGACGTCGCGT CT GGG
                                    _  A
GAM1035  ATP5J     5'  GGGCTCCACGTGCAGCGT    9856        G  CAC   C
                                ACGCTGCA CG   GGA CCC
                                ||||||||  ||   |||  |||
                                TGCGACGT GC   CCT GGG
                                    _  A__   C
GAM1035  BAALC     5'  GGAGCTCCGCGCGGCTGCAGCG 46093       _  A   CCC
                                CGCTGCAGC GC CGGA   CC
                                |||||||||  ||  ||||   ||
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                                GCGACGTCG CG GCCT   GG
                                     G  C    CGA
GAM1035  C21orf33  3'  GGGGATGTGCTGCAGTG     17382          CGGA  C
                                CGCTGCAGCGCA    CC CC
                                ||||||||||||    || ||
                                GTGACGTCGTGT    GG GG
                                       A___  A
GAM1035  CACNG7   3'  GGGGGGTCTCCCTGCAATG   49943    C    CGCAC
                                CG TGCAG    GGACCCCCC
                                || |||||    |||||||||
                                GT ACGTC    TCTGGGGGG
                                 A    CC___
GAM1035  CD1D     5'  GGGAGGTGTCAGGCTGCAGC   80270       GCACG  _ _
                                GCTGCAGC    GAC CC CCC
                                ||||||||    ||| || |||
                                CGACGTCG    CTG GG GGG
                                     GA___   T  A
GAM1035  CELSR3   5'  GGGAGGCGGCAGCAGCGT    9188        AGC  A  GA  _
                                ACGCTGC   GC CG  CC CCC
                                |||||||   || ||  || |||
                                TGCGACG   CG GC  GG GGG
                                    A__  _  __  A
GAM1035  CPT2     5'  GGACCCCCCAAGGAGCGGCTGC 5426         _ AC________  ACCC
            GGCG                  CGCTGCAGC GC       GG    CC
                                |||||||||  ||       ||    ||
                                GCGGCGTCG CG       CC    GG
                                     G  AGGAA___C  CCCA
GAM1035  DGCR2    3'  GGGAGGCCTGTCTGAAGC    18905     G   C   C  A  _
                                GCT CAG GCA GG CC CCC
                                ||| ||| ||| || || |||
                                CGA GTC TGT CC GG GGG
                                  A  _  _  _  A
GAM1035  DRIL1    3'  GGGGGTCCAGGTGGGCCACA   19079    CA  G   __
                                TG  GC CAC  GGACCCCC
                                ||  || |||  ||||||||
                                AC  CG GTG  CCTGGGGG
                                 AC  G   GA
GAM1035  DXYS155E 3'  GGAGGCCGAGCTGCGGCG    18690        GCA   A  C
                                CGCTGCAGC   CGG CC CC
                                |||||||||   ||| || ||
                                GCGGCGTCG   GCC GG GG
                                     A__   _  A
GAM1035  G22P1    5'  GGGGGTCCGTTAGTCAGC    9408      CA  GC
                                GCTG  GC  ACGGACCCCC
                                ||||  ||  ||||||||||
                                CGAC  TG  TGCCTGGGGG
                                  __  AT
GAM1035  HEPH     5'  GGGGTCTGCAGTGCAGC     29651       G GCA
                                GCTGCA C   CGGACCCC
                                ||||||  |   ||||||||
```

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                                CGACGT G   GTCTGGGG
                                   _ AC_
GAM1035  HERC2    3'  GGTCCGCCTGTGCGCGT     17427      TGCA    __
                                ACGC    GCGCA  CGGACC
                                ||||    |||||  ||||||
                                TGCG    CGTGT  GCCTGG
                                  ____     CC
GAM1035  HUS1     3'  GGGGTGTCACAGCTGCAGC    92740        GCACG  _
                                GCTGCAGC     GAC CCCC
                                ||||||||     ||| ||||
                                CGACGTCG     CTG GGGG
                                     ACA__   T
GAM1035  JAG2     5'  GGCCCGCGCGCCGCGGCG     11096       A    A   A
                                CGCTGC GCGC CGG CC
                                |||||| |||| ||| ||
                                GCGGCG CGCG GCC GG
                                   C    C   C
GAM1035  KCNA6    5'  GGAGAGCCGAGCCGCTGCAGC  11138         _ A   ACCC
                                GCTGCAGCG C CGG    CC
                                ||||||||| | |||    ||
                                CGACGTCGC G GCC    GG
                                     C A   GAGA
GAM1035  KLKB1    3'  GGGGGGTCCTCATCTGCAAAGC 7982      __    CGCAC
                                GCT  GCAG    GGACCCCCC
                                |||  ||||    |||||||||
                                CGA  CGTC    CCTGGGGGG
                                  AA    TACT_
GAM1035  LRRC2    3'  GGAGGTCGAGGCTGCAGTGT   44752         GCACG   C
                                ACGCTGCAGC     GACC CC
                                ||||||||||     |||| ||
                                TGTGACGTCG     CTGG GG
                                     GAG__    A
GAM1035  LYN      5'  GGGCCAGACGCGCTGCAGC    11405         AC__  A
                                GCTGCAGCGC    GG CCC
                                ||||||||||    || |||
                                CGACGTCGCG    CC GGG
                                     CAGA  _
GAM1035  LZTR1    3'  GGAGTGCAGGCTGCAGCG     23173         __    GGA
                                CGCTGCAGC  GCAC   CC
                                |||||||||  ||||   ||
                                GCGACGTCG  CGTG   GG
                                     GA    A__
GAM1035  MUC4     3'  GGAGGCGTGTGCTGCAGC     37881           GA  C
                                GCTGCAGCGCACG  CC CC
                                ||||||||||||  || ||
                                CGACGTCGTGTGC  GG GG
                                      __  A
GAM1035  MUC4     3'  GGCTGGCACGTGCAGCGT     37882         GC_  A   A
                                ACGCTGCA   GC CGG CC
                                ||||||||   || ||| ||
```

```
                                TGCGACGT   CG GTC GG
                                    GCA  _  _
GAM1035  NPAS2    5'  GGGACCCGCGCGGCTGCGGC   11822        _  A   AC
                                GCTGCAGC GC CGG  CCC
                                |||||||| || |||  |||
                                CGGCGTCG CG GCC  GGG
                                    G  C   CA
GAM1035  PET112L  3'  GGAGGGTCCGGTGAGGCTGCAG 17081        G_  _    _
            C                    GCTGCAGC  CAC GGACCC CC
                                |||||||||  ||| |||||| ||
                                CGACGTCG  GTG CCTGGG GG
                                    GA  G     A
GAM1035  SLC30A3  5'  GGACTCCGCGCGCCACAGTCG  14401    _  CA   A   CC
                                CG CTG  GCGC CGGA  CC
                                || |||  |||| ||||  ||
                                GC GAC  CGCG GCCT  GG
                                 T  AC   C   CA
GAM1035  SLC30A3  3'  GGAGGACTCCGCTGCAGC    14402        CAC  A  C
                                GCTGCAGCG   GG CC CC
                                |||||||||   || || ||
                                CGACGTCGC   TC GG GG
                                    C__  A  A
GAM1035  TAF6     5'  GGAGATCCTGTGACTGTAGCGT 20114        _   C   CCC
                                ACGCTGCAG CGCA GGA   CC
                                |||||||||| |||| |||   ||
                                TGCGATGTC GTGT CCT   GG
                                    A   _  AGA
GAM1035  UBE2G2   3'  GGGGCCCTGTAGCTGCAGC   65492        _  C  A
                                GCTGCAGC GCA GG CCCC
                                |||||||| ||| || ||||
                                CGACGTCG TGT CC GGGG
                                    A  C  _
GAM1035  VIPR2    3'  GGGAGGCAGGTGGACGCTGCAG 14068        __   GGA  _
                                CTGCAGCG  CAC   CC CCC
                                ||||||||  |||   || |||
                                GACGTCGC  GTG   GG GGG
                                    AG   GAC  A
GAM1035  WHSC1    3'  GGGAGCCCCGTAGGGCGCTGCA 24676        ___   ACC_
            G                    CTGCAGCGC   ACGG   CCC
                                |||||||||  ||||   |||
                                GACGTCGCG   TGCC   GGG
                                    GGA   CCGA
GAM1035  WHSC1    3'  GGGAGCCCCGTAGGGCGCTGCA 24677        ___   ACC_
            G                    CTGCAGCGC   ACGG   CCC
                                |||||||||  ||||   |||
                                GACGTCGCG   TGCC   GGG
                                    GGA   CCGA
GAM1035  WHSC1    3'  GGGAGCCCCGTAGGGCGCTGCA 24678        ___   ACC_
            G                    CTGCAGCGC   ACGG   CCC
                                |||||||||  ||||   |||
```

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                                GACGTCGCG  TGCC   GGG
                                     GGA   CCGA
GAM1035 ZNF161   5' GGGGGGTCGGCCGCCGCAGC  24082     A  CA  G
                                GCTGC GCG  CG ACCCCCC
                                ||||| |||  || |||||||
                                CGACG CGC  GC TGGGGGG
                                   C  CG  _
GAM1035 ADAR3    3' GGGGTTTTAGCTGCAGC    38635       GCAC
                                GCTGCAGC   GGACCCC
                                ||||||||   |||||||
                                CGACGTCG   TTTGGGG
                                     AT__
GAM1035 ALOX15B  5' GGGGAGCCCCGCTCTGCAGC  8554       C  AC  AC
                                GCTGCAG GC  GG  CCCC
                                ||||||| ||  ||  ||||
                                CGACGTC CG  CC  GGGG
                                    T  CC  GA
GAM1035 APOF     3' GGGAGGTCGAGGCTGCAGCG  9694        GCACG  _
                                CGCTGCAGC    GACC CCC
                                |||||||||    |||| |||
                                GCGACGTCG    CTGG GGG
                                     GAG__   A
GAM1035 BCCIP    3' GGAGGGTCCCAGCTGCAGTGT 33806        GCAC    _
                                ACGCTGCAGC   GGACCC CC
                                ||||||||||   |||||| ||
                                TGTGACGTCG   CCTGGG GG
                                      AC__     A
GAM1035 BICD2    3' GGGGCGCCGCACGCTGCAGC  70915       CA  AC
                                GCTGCAGCG  CGG  CCCC
                                |||||||||  |||  ||||
                                CGACGTCGC  GCC  GGGG
                                     AC   GC
GAM1035 C1orf34  3' GGGGCTGTGTGCCACAGGGT  61316   G  CA     A
                                AC CTG  GCGCACGG CCCC
                                || |||  |||||||| ||||
                                TG GAC  CGTGTGTC GGGG
                                 G  AC      _
GAM1035 CBX3     5' GGAGGGCCGGAGACGCTGCAG 33898       CA__  A  _
                                CTGCAGCG   CGG CCC CC
                                ||||||||   ||| ||| ||
                                GACGTCGC   GCC GGG GG
                                     AGAG  _  A
GAM1035 CTNNBIP1 5' GGCCGCCGCGCGCTGCGCG   40044    T     A  ACC
                                CGC GCAGCGC CGG   CC
                                ||| ||||||| |||   ||
                                GCG CGTCGCG GCC   GG
                                  _     C  GCC
GAM1035 DKFZp762M136 3' GGGAAATCCGGCTGCGGC   65324       GCA   CC_
                                GCTGCAGC   CGGA  CCC
                                ||||||||   ||||  |||
```

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                                CGGCGTCG  GCCT  GGG
                                   ___   AAA
GAM1035 EFS2    5' GGGAGCACCGCTCTGCAGCG  20776       C  AC  ACC_
                                CGCTGCAG GC  GG   CCC
                                |||||||| ||  ||   |||
                                GCGACGTC CG  CC   GGG
                                   T  __  ACGA
GAM1035 EPSIN   5' GGAGGTGTGCGCTGCAGGT   26211   G       GG  C
                                AC CTGCAGCGCAC  ACC CC
                                || ||||||||||  ||| ||
                                TG GACGTCGCGTG  TGG GG
                                 _        __  A
GAM1035 FADS1   3' GGAGGTCAAGCCTGCAGCG   26383       C  ACG   C
                                CGCTGCAG GC   GACC CC
                                |||||||| ||   |||| ||
                                GCGACGTC CG   CTGG GG
                                   _ AA_   A
GAM1035 FGF19   3' GGGGCTGTGGTACCTGCAGCGT 18857        CG__    A
                                ACGCTGCAG   CACGG CCCC
                                |||||||||   ||||| ||||
                                TGCGACGTC   GTGTC GGGG
                                   CATG   _
GAM1035 FLJ00060 5' GGGAGGCTGGATCACGCTGCAG 61749        CA___  A  _
            C                    GCTGCAGCG    CGG CC CCC
                                |||||||||    ||| || |||
                                CGACGTCGC    GTC GG GGG
                                   ACTAG  _ A
GAM1035 FLJ11078 3' GGGGGTCCCTGTGCAGC    37596     AGC  C
                                GCTGC  GCA GGACCCCC
                                |||||  ||| ||||||||
                                CGACG  TGT CCTGGGGG
                                  ___  C
GAM1035 FLJ20195 3' GGGACCCAGCGGCTGCAGCG  35221        _  AC  A
                                CGCTGCAGC GC  GG CCC
                                ||||||||| ||  || |||
                                GCGACGTCG CG  CC GGG
                                   G  AC  A
GAM1035 FLJ22037 5' GGGAGGCAAGTCAGAGCTGCAG 95536        GCACG  ___  _
            CG                   CGCTGCAGC    GAC   CC CCC
                                |||||||||    |||   || |||
                                GCGACGTCG    CTG   GG GGG
                                   AGA__   AAC  A
GAM1035 FLJ22596 5' GGGGGGTCCATGGACAGTG   47644     CAGCG  C
                                CGCTG    CA GGACCCCCC
                                |||||    || |||||||||
                                GTGAC    GT CCTGGGGGG
                                  AG___  A
GAM1035 GPR108  3' GGGGGTCCATGTGGACCAG   69631    CAG   C
                                CTG  CGCA GGACCCCC
                                |||  |||| ||||||||
```

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                                GAC   GTGT CCTGGGGG
                                  CAG    A
GAM1035  GS3955    5'  GGGAGCCCTGCGCTGCAGC    41624          C  AC
                                GCTGCAGCGCA GG  CCC
                                |||||||||| ||  |||
                                CGACGTCGCGT CC  GGG
                                      C  GA
GAM1035  HSPC067   5'  GGAAACCCGTGCGCGGCTGCG  27170     T  A       ACCC
                                CGC GC GCGCACGG    CC
                                ||| || ||||||||    ||
                                GCG CG CGCGTGCC    GG
                                  T  G       CAAA
GAM1035  KIAA0450  3'  GGAGGGCCCCGTGTGCGGCA   28364     A       A_  _
                                TGC GCGCACGG  CCC CC
                                ||| ||||||||  ||| ||
                                ACG CGTGTGCC  GGG GG
                                  G       CC   A
GAM1035  KIAA0450  5'  GGGGAACCCTCCTTGCTAGCGT 28368       _    CGCAC  AC
                                ACGCT GCAG     GG  CCCC
                                ||||| ||||     ||  ||||
                                TGCGA CGTT     CC  GGGG
                                   T    CCTC_  AA
GAM1035  KIAA0469  3'  GGGAGGCCTGGCGCTGCAGCG  29987          A   A  _
                                CGCTGCAGCGC CGG CC CCC
                                |||||||||| ||| || |||
                                GCGACGTCGCG GTC GG GGG
                                      _   C  A
GAM1035  KIAA0683  5'  GGGGAATCGGCTGCAGCG    32765         GCA   AC
                                CGCTGCAGC   CGG  CCCC
                                |||||||||   |||  ||||
                                GCGACGTCG   GCT  GGGG
                                     ____   AA
GAM1035  KIAA0987  5'  GTTCGCCGCCGCTGCAGCG   25510          _ A_
                                CGCTGCAGCG C  CGGAC
                                |||||||||| |  |||||
                                GCGACGTCGC G  GCTTG
                                      C CC
GAM1035  KIAA1643  3'  GGTGGGGCCACGCTGCAG    65157         CAC  A   _
                                CTGCAGCG   GG CCCC CC
                                ||||||||   || |||| ||
                                GACGTCGC   CC GGGG GG
                                    A__  _    T
GAM1035  KIAA1922  5'  GGAGGACCTGCTGCAGC     73999         CAC  A  C
                                GCTGCAGCG   GG CC CC
                                |||||||||   || || ||
                                CGACGTCGT   CC GG GG
                                     ____  A  A
GAM1035  KLF5      3'  GGGGAGTGTGTGCAGCGT    9961          G    GGA
                                ACGCTGCA CGCAC   CCCC
                                |||||||| |||||   ||||
```

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                                TGCGACGT GTGTG   GGGG
                                    _    A__
GAM1035 LANCL2   3' GGAGAGTCTGTTTGCTGCAG  38620       C     CC_
                                CTGCAGCG ACGGAC   CC
                                |||||||| ||||||   ||
                                GACGTCGT TGTCTG   GG
                                     T     AGA
GAM1035 MESDC1   5' GGAGGCCGAAAGCTGCAGC   42901       GCA   A  C
                                GCTGCAGC   CGG CC CC
                                ||||||||   ||| || ||
                                CGACGTCG   GCC GG GG
                                     AAA   _  A
GAM1035 MGC2749  3' GGGGGTCTCAGGGCAGCAGC  44171      A  GCAC
                                GCTGC GC    GGACCCCC
                                ||||| ||    ||||||||
                                CGACG CG    TCTGGGGG
                                   A  GGAC
GAM1035 MGC3062  5' GGGGCGGGGGCGCTGCGGC   44154         ACGGA  _
                                GCTGCAGCGC    CC CCCC
                                ||||||||||    || ||||
                                CGGCGTCGCG    GG GGGG
                                      GG___  C
GAM1035 MGC35558 3' GGAGCTGTCCGTGCACACAGCG 59416       CAGC       CC__
           T                     ACGCTG    GCACGGAC    CC
                                 ||||||    ||||||||    ||
                                 TGCGAC    CGTGCCTG    GG
                                    ACA_       TCGA
GAM1035 MGC4737  5' GGGGGACCTGTGCCTGCAG   49647      C     AC
                                CTGCAG GCACGG  CCCCC
                                |||||| ||||||  |||||
                                GACGTC CGTGTC  GGGGG
                                    _     CA
GAM1035 PPP4R1L  5' GGAAGGTTTGTGCTGCA     80324         CG    CC
                                TGCAGCGCA  GACC  CC
                                |||||||||  ||||  ||
                                ACGTCGTGT  TTGG  GG
                                     __    AA
GAM1035 PRKWNK2  3' GGATCTGGCCCGCGCTGCAGC  92199          A___    C
                                GCTGCAGCGC    CGGA CC
                                ||||||||||    |||| ||
                                CGACGTCGCG    GTCT GG
                                      CCCG    A
GAM1035 PTK9L    3' GGAGGGCTGGCAGCTGAACGC  24421    TG_   _ A  A  _
                                GC   CAGC GC CGG CCC CC
                                ||   |||| || ||| ||| ||
                                CG   GTCG CG GTC GGG GG
                                 CAA   A  _  _  A
GAM1035 SEMA3C   5' GGAGCCGCGCGCCGCGGCG   22108       A   A  AC
                                CGCTGC GCGC CGG  CC
                                |||||| |||| |||  ||
```

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                                GCGGCG CGCG GCC  GG
                                   C   C   GA
GAM1035  SEMA3C   5'  GGGTGCCGCGGCACTGCAGCG  22110        C  A_  _
                                CGCTGCAG GC  CGG ACCC
                                |||||||| ||  ||| ||||
                                GCGACGTC CG  GCC TGGG
                                     A  GC   G
GAM1035  SFXN5    3'  GGACCCCCCAAGAGGCCGCTGC 58654    G      _ AC________  ACCC
            AGGGT                   AC CTGCAGCG C        GG    CC
                                || |||||||| |        ||    ||
                                TG GACGTCGC G        CC    GG
                                 G       C GAGAA___C  CCCA
GAM1035  SH120    5'  GGGGGCCTGTGGCCCCAGCGT  33391       CA  G    A
                                ACGCTG  GC CACGG CCCCC
                                ||||||  || ||||| |||||
                                TGCGAC  CG GTGTC GGGGG
                                   CC  _    C
GAM1035  SLIT1    3'  GGGGCCCCAGCCGCTGCAGC   13232         _ AC  A
                                GCTGCAGCG C  GG CCCC
                                ||||||||| |  || ||||
                                CGACGTCGC G  CC GGGG
                                     C AC  C
GAM1035  TLE4     3'  GGGGCGGCAGCTGCAGC     68515         _  A  GA
                                GCTGCAGC GC CG  CCCC
                                |||||||| || ||  ||||
                                CGACGTCG CG GC  GGGG
                                     A  _  __
GAM1035  TLK2     3'  GGGGGGTCCCTGATGCAGTG   78808        GCG  C
                                CGCTGCA   CA GGACCCCCC
                                |||||||   || |||||||||
                                GTGACGT   GT CCTGGGGGG
                                   A__  C
GAM1035  WBSCR16  3'  GGAGGACCCTGCGTGCAGTGT  96151         G   C  A  C
                                ACGCTGCA CGCA GG CC CC
                                |||||||| |||| || || ||
                                TGTGACGT GCGT CC GG GG
                                     _   C  A  A
GAM1035  LOC124512 5'  GGGGGTCCGGGCCCAGCG    74781       CAGC  A
                                CGCTG   GC CGGACCCCC
                                |||||   || |||||||||
                                GCGAC   CG GCCTGGGGG
                                  C___  G
GAM1035  LOC132617 5'  GGCTTCGTGCGCTACAGCGT   76419        C         C
                                ACGCTG AGCGCACGGA CC
                                |||||| |||||||||| ||
                                TGCGAC TCGCGTGCTT GG
                                   A         C
GAM1035  LOC138050 5'  GGGAAGCCTAGTGCTGCAGC   75816          AC  ACC
                                GCTGCAGCGC  GG   CCC
                                |||||||||  ||   |||
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                                CGACGTCGTG  CC   GGG
                                      AT  GAA
GAM1035  LOC143666 5'  GGCCTGCGTGGCTGCAGCG   83885        G   GACC
                                CGCTGCAGC CACG   CC
                                ||||||||| ||||   ||
                                GCGACGTCG GTGC   GG
                                     _   GTCC
GAM1035  LOC144017 5'  GGAGTCGCTGCTGCAGC     83930        _ ACG   C
                                GCTGCAGC GC   GAC CC
                                |||||||| ||   ||| ||
                                CGACGTCG CG   CTG GG
                                     T ____  A
GAM1035  LOC145842 5'  GGCCGTTGGCTGCAGCGT    77994         G _  A
                                ACGCTGCAGC CA CGG CC
                                |||||||||| || ||| ||
                                TGCGACGTCG GT GCC GG
                                     _ T  _
GAM1035  LOC147599 3'  GGAGAGTCCGTGCGTAAAGCAG 85164      A__        CC_
           C                     GCTGC   GCGCACGGAC   CC
                                |||||   ||||||||||   ||
                                CGACG   TGCGTGCCTG   GG
                                   AAA         AGA
GAM1035  LOC158376 5'  GGGGGGTCCTGGCCGCAGC   88136      A  G  C
                                GCTGC GC CA GGACCCCCC
                                ||||| || || |||||||||
                                CGACG CG GT CCTGGGGGG
                                   C  _  _
GAM1035  LOC196394 5'  GGCTTCAGACGCTGCAGCG   89031         CAC   C
                                CGCTGCAGCG   GGA CC
                                ||||||||||   ||| ||
                                GCGACGTCGC   CTT GG
                                      AGA   C
GAM1035  LOC200269 3'  GGGAAGCCCATGGTTGCAGTGT 90074         G  C  ACC_
                                ACGCTGCAGC CA GG    CCC
                                |||||||||| || ||    |||
                                TGTGACGTTG GT CC    GGG
                                     _  A  CGAA
GAM1035  LOC201191 3'  GGCCAGTGGGCGCTGCAGC   91345         __  _  A
                                GCTGCAGCGC  AC GG CC
                                |||||||||  || || ||
                                CGACGTCGCG  TG CC GG
                                      GG  A  _
GAM1035  LOC201705 5'  GGGGATGGGTGGCTGCAGC   91855        G   GGAC
                                GCTGCAGC CAC    CCCC
                                |||||||| |||    ||||
                                CGACGTCG GTG    GGGG
                                     _  GGTA
GAM1035  LOC203428 5'  GGAAACCCGTGCGCGGCTGCG  90927     T  A       ACCC
                                CGC GC GCGCACGG    CC
                                ||| || ||||||||    ||
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                                GCG CG CGCGTGCC   GG
                                  T G      CAAA
GAM1035  LOC204970 3'  GGGTCTTCACGCTACAGGT   90967    G  C   CAC
                                AC CTG AGCG  GGACCC
                                || ||| ||||  ||||||
                                TG GAC TCGC  TCTGGG
                                 _  A   ACT
GAM1035  LOC221218 5'  GGGCCGTGCGCTGCAGC    93418           A
                                GCTGCAGCGCACGG CCC
                                |||||||||||||| |||
                                CGACGTCGCGTGCC GGG
                                              _
GAM1035  LOC254808 5'  GGGAGTATCGCTGCAGCGT   98809         CACGG  C
                                ACGCTGCAGCG    AC CCC
                                ||||||||||    || |||
                                TGCGACGTCGC    TG GGG
                                      TA___  A
GAM1035  LOC81569  3'  GGGAGGCATTGCTGCAGGT   62675    G      CACGGA  _
                                AC CTGCAGCG    CC CCC
                                || ||||||||    || |||
                                TG GACGTCGT    GG GGG
                                 _      TAC___  A
GAM1035  LOC90297  3'  GGGGGGCCCCGCTGCAGC    62852        CAC  A
                                GCTGCAGCG  GG CCCCCC
                                |||||||||  || ||||||
                                CGACGTCGC  CC GGGGGG
                                     C__  _
GAM1035  LOC91035  5'  GGTGGTGCCTGCAGCGT     65303        C   GG
                                ACGCTGCAG GCAC  ACC
                                ||||||||| ||||  |||
                                TGCGACGTC CGTG  TGG
                                     _   G_
GAM1036  ABR       5'  CGCGATGAGGGTCGGGTTTCGG 42000        A   AAAGAG
                                CTGAAGCC GAC    ATCGTG
                                |||||||| |||    ||||||
                                GGCTTTGG CTG    TAGCGC
                                     G  GGAG__
GAM1036  ACTB      3'  TTTTTTTGTTTTGTTTTGG   8467    TG   C
                                C  AAGC AGACAAAGAGA
                                |  |||| ||||||||||
                                G  TTTG TTTGTTTTTTT
                                 GT   T
GAM1036  ADAR      3'  TGCGGTCTTGATTAGGTTTCAG 32366        A  CAAA
                                CTGAAGCC GA   GAGATCGTG
                                |||||||| ||   |||||||||
                                GACTTTGG TT   TTCTGGCGT
                                     A  AG__
GAM1036  ALOX15    3'  TATGATTTTTTTGTTGTTGTT  8550     CA_
                                AGC  GACAAAGAGATCGTG
                                |||  ||||||||||||||
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                                TTG  TTGTTTTTTTAGTAT
                                  TTG
GAM1036 ANKH    3' TTCCCTTTTTTTTGTTTTGTTT 55078   TG   C        TCGTG
            TGG                    C  AAGC AGACAAAGAGA
                                | ||||| ||||||||||
                                G  TTTG TTTGTTTTTTT
                                 GT   T         TCCCTTG
GAM1036 APAF1   3' ATGATTTTTTTGCCTTGG   25962     A_
                                CCAG  CAAAGAGATCGT
                                ||||  ||||||||||||
                                GGTT  GTTTTTTTAGTA
                                  CC
GAM1036 ATF5    3' ATGAAATGTTTGGCCTTAG   24816     A      AAGAGA
                                CTGA GCCAGACA     TCGT
                                |||| ||||||||      ||||
                                GATT CGGTTTGT     AGTA
                                  C       AA_____
GAM1036 CACNG2  5' ATTTATTTTTTTTGGCTTTAG  21399          C   _
                                CTGAAGCCAGA AAAG AGAT
                                |||||||||||| ||||| ||||
                                GATTTCGGTTT TTTT TTTA
                                       T   A
GAM1036 CALU    3' GTGATCTCTTTGCAGAGCTATA 8696      A   CAGA        GTG
            G                   CTG AGC    CAAAGAGATC
                                ||| |||    ||||||||||
                                GAT TCG    GTTTCTCTAG
                                  A   AGAC         TGT
GAM1036 CBFB    3' TATGAATGAATTTGGTTGGTTT 10039    TG      A    GAGA_
            TGG                    C  AAGCCAG CAAA     TCGTG
                                |  ||||||| ||||     |||||
                                G  TTTGGTT GTTT     AGTAT
                                 GT      G    AAGTA
GAM1036 CBFB    3' TATGAATGAATTTGGTTGGTTT 43443    TG      A    GAGA_
            TGG                    C  AAGCCAG CAAA     TCGTG
                                |  ||||||| ||||     |||||
                                G  TTTGGTT GTTT     AGTAT
                                 GT      G    AAGTA
GAM1036 CHRNA7  3' TACGGTTTCTTTGTTACTTTAG 7442        CCA
                                CTGAAG   GACAAAGAGATCGTG
                                ||||||   ||||||||||||||||
                                GATTTC   TTGTTTCTTTGGCAT
                                   A__
GAM1036 COL11A2 3' GGTCTCCCTGGCCTCAG     55633      A    ACAAA
                                CTGA GCCAG     GAGATC
                                |||| |||||     ||||||
                                GACT CGGTC     CTCTGG
                                  C    C_____
GAM1036 DRIL1   3' TGTTTTCATTTTTGTCTGCTTT 19082        C        _  TCGTG
            AG                    CTGAAGC AGACAAAGA GA
                                ||||||| ||||||||| ||
```

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                                GATTTCG TCTGTTTTT CT
                                   _       A  TTTGTG
GAM1036  ETS2     3'  GTTTGTTTGTTTGTTTTTGG  19118   TG  C      G
                                C  AAG CAGACAAA AGAT
                                |  ||| |||||||| ||||
                                G  TTT GTTTGTTT TTTG
                                 GT   T       G
GAM1036  FMR1     3'  TATGTTGACATTTGTTTGGTTA 10681     A        GAGAT_
              TAG                  CTG AGCCAGACAAA     CGTG
                                ||| ||||||||||      ||||
                                GAT TTGGTTTGTTT     GTAT
                                  A         ACAGTT
GAM1036  FOXO1A   3'  GTTTCTTTTCTGGTTTTAG   10653          C
                                CTGAAGCCAGA AAAGAGAT
                                |||||||||| ||||||||
                                GATTTTGGTCT TTTCTTTG

                                   _
GAM1036  GLS      3'  AAAGATCTTTTTGTTTTGGCTT 30460          _        GTG
              TAG                  CTGAAGCCAGA CAAAGAGATC
                                |||||||||| ||||||||||
                                GATTTCGGTTT GTTTTTCTAG
                                      T         AAAC
GAM1036  HCS      3'  TGCGATCTCGGCTGGCTGCAG  38995     A     ACAAA
                                CTG AGCCAG     GAGATCGTG
                                ||| ||||||     |||||||||
                                GAC TCGGTC     CTCTAGCGT
                                  G     GG___
GAM1036  KPNA3    3'  CATGATTTCCTAAACTGTTTTA 11222        C  ACAAA
              G                   CTGAAGC AG     GAGATCGTG
                                ||||||| ||     |||||||||
                                GATTTTG TC     CTTTAGTAC
                                   _  AAATC
GAM1036  LDLR     3'  CGTGATAAGCCTTTCTGGTTTC 6734           CAAAGAG
              GG                    CTGAAGCCAGA      ATCGTG
                                ||||||||||       ||||||
                                GGCTTTGGTCT      TAGTGC
                                      TTCCGAA
GAM1036  LZTS1    3'  GGTTTCTTGTTTGGTTT     41037          A
                                AAGCCAGACAA GAGATC
                                |||||||||| ||||||
                                TTTGGTTTGTT CTTTGG

                                   _
GAM1036  MTMR8    3'  CGTGTAGTTGTCTGGTTTCAG  31910           AGAGAT
                                CTGAAGCCAGACAA      CG
                                ||||||||||||||      ||
                                GACTTTGGTCTGTT      GC
                                      GATGT_
GAM1036  NDRG1    3'  CATGGTTTTTGAAGGCTTTAG  60308         AGACAA
                                CTGAAGCC     AGAGATCGTG
                                ||||||||     ||||||||||
```

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                                GATTTCGG     TTTTTGGTAC
                                     AAG___
GAM1036  PTGIR    3'  GTGATCTCTGCCCTGTCTTCGG 8180       C   ACAA      GTG
                                CTGAAG CAG    AGAGATC
                                ||||||| |||    |||||||
                                GGCTTC GTC    TCTCTAG
                                   T   CCG_      TGT
GAM1036  RNF4     3'  CGTGGTTCCAGTCTGGTTGCAG 12882     A       AAA   AT_
                                CTG AGCCAGAC   GAG   CG
                                ||| ||||||||   |||   ||
                                GAC TTGGTCTG   CTT   GC
                                  G       AC_   GGT
GAM1036  SGCD     3'  GGCCTTTTTTGGCTTTAG    6215          CAA    AT
                                CTGAAGCCAGA   AGAG  C
                                ||||||||||   ||||  |
                                GATTTCGGTTT   TTTC  G
                                      ___    CG
GAM1036  SMURF1   3'  GTGGTTTCTTTGTTGTTGTTTT 94051      CA_         GTG
                                GAAGC   GACAAAGAGATC
                                |||||   ||||||||||||
                                TTTTG   TTGTTTCTTTGG
                                   TTG          TGT
GAM1036  SNX3     3'  TATGCTCAGTTTTGTTTTGTTT 15044    TG    C       A_  T
            TGG                   C  AAGC AGACAAAG  GA CGTG
                                |  |||| ||||||||  || ||||
                                G  TTTG TTTGTTTT  CT GTAT
                                 GT    T       GA  C
GAM1036  TMPRSS3  3'  CATGATTTCTTTGTAGCATTTG 44018    TG  _  CAG
            G                    C  AA GC   ACAAAGAGATCGTG
                                |  || ||   ||||||||||||||
                                G  TT CG   TGTTTCTTTAGTAC
                                 GT  A  A__
GAM1036  TRIM8    3'  GATTTTGTTTTGGTTTTGG    48854    TG       CAAA
                                C  AAGCCAGA    GAGATC
                                |  ||||||||    ||||||
                                G  TTTGGTTT    TTTTAG
                                 GT       TG__
GAM1036  ZNF198   3'  TGGGGTTTTTGTTTTGTTTTGG 14364    TG    C       GA
                                C  AAGC AGACAAAGA  TCG
                                |  |||| |||||||||  |||
                                G  TTTG TTTGTTTTT  GGT
                                 GT    T       GG
GAM1036  A4GALT   3'  CTTTGTTCTTTTCTGGTTTTGG 34299    TG       C     ATCGTG
                                C  AAGCCAGA AAAGAG
                                |  |||||||| ||||||
                                G  TTTGGTCT TTTCTT
                                 GT       _     GTTTCG
GAM1036  AB026190 3'  CATGGTTTTTTGTTGTTTTC   27830      CCA    A
                                GAAG   GACAA GAGATCGTG
                                ||||   ||||| |||||||||
```

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                                CTTT   TTGTT TTTTGGTAC
                                  TG_    _
GAM1036  AKAP11    3'  GTTTGTTTGTTTGTTTTAG   58465        C      G
                                CTGAAGC AGACAAA AGAT
                                ||||||| ||||||| ||||
                                GATTTTG TTTGTTT TTTG
                                    _      G
GAM1036  BTBD3     5'  ATCAGCTTTGTTGGTTTCAG   31027          A    A_
                                CTGAAGCCAG CAAAG  GAT
                                |||||||||| |||||  |||
                                GACTTTGGTT GTTTC  CTA
                                      _    GA
GAM1036  C20orf108 3'  CATGATTTGGATTGGTTTTAG  55877          A_  AAGA
                                CTGAAGCCAG  CA    GATCGTG
                                ||||||||||  ||    |||||||
                                GATTTTGGTT  GT    TTAGTAC
                                      AG  ____
GAM1036  CTCF      3'  TTTCTTTTTTTGGCTTTGG    22681    TG      C
                                C  AAGCCAGA AAAGAGA
                                |  |||||||| |||||||
                                G  TTCGGTTT TTTCTTT
                                 GT       T
GAM1036  DDX34     3'  CACGCATATATGTTTGGTTTTA 28661             AAGAG  _
              G                   CTGAAGCCAGACA     AT CGTG
                                ||||||||||||     || ||||
                                GATTTTGGTTTGT     TA GCAC
                                      ATA__  C
GAM1036  DKFZP434E2135 5'  GAATTTTTTTTTTGTTTTGTTT 48687         C          TCGTG
              TAG                   CTGAAGC AGACAAAGAGA
                                ||||||| ||||||||||
                                GATTTTG TTTGTTTTTTT
                                    T          TTTAAGA
GAM1036  DKFZp547I224 5'  TATGATCTGTAGTTTGTTTGCT 39961        C       G___
              TTTAG                   CTGAAG CAGACAAA    AGATCGTG
                                |||||| ||||||||    ||||||||
                                GATTTT GTTTGTTT    TCTAGTAT
                                    C       GATG
GAM1036  ESM1      3'  GCTTTTTTTTTTTTTTTGGCTT 23850    TG       C      TCGTG
              TGG                   C  AAGCCAGA AAAGAGA
                                |  |||||||| |||||||
                                G  TTCGGTTT TTTTTTT
                                 GT       T      TTTTCGT
GAM1036  FLJ10687  3'  TCAGCTTTTTTTTGTTTGTTTT 36950         C          TCGTG
              AG                    CTGAAGC AGACAAAGAGA
                                ||||||| ||||||||||
                                GATTTTG TTTGTTTTTTT
                                    _          TCGACTC
GAM1036  FLJ10803  3'  GTGGTTTCTCTGATGGTTCTGG 37207    GA    GA  A      GTG
                                CT  AGCCA  CA AGAGATC
                                ||  |||||  || |||||||
```

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                                GG  TTGGT  GT TCTTTGG
                                 TC    A_ C      TGT
GAM1036  FLJ10811  3'  TATGATTTAGTTTTTGGTTTT  37227         C  AG
                                GAAGCCAGA AA  AGATCGTG
                                |||||||||  ||  ||||||||
                                TTTTGGTTT TT  TTTAGTAT
                                      _  GA
GAM1036  FLJ13576  5'  CTTTTTGGTTTGGTTTTGG   42808   TG       _
                                C  AAGCCAGAC AAAGAG
                                |  |||||||||  ||||||
                                G  TTTGGTTTG TTTTTC
                                 GT        G
GAM1036  FLJ13855  3'  GTCTATTTGTCTGTCTTCAG   43854       C       G
                                CTGAAG CAGACAAA AGAT
                                ||||||  ||||||||  ||||
                                GACTTC GTCTGTTT TCTG
                                    T       A
GAM1036  FLJ20130  3'  CTGGCATTTTATTTGGTTTTAG 35083          CA   GA   TG
                                CTGAAGCCAGA  AAGA  TCG
                                ||||||||||  ||||  |||
                                GATTTTGGTTT  TTTT  GGT
                                      A_   AC   CA
GAM1036  FLJ20950  3'  CATGGTTTCTGTTACTCATGGT 46940         _ CAA__
            TTCAG                  CTGAAGCCA GA    AGAGATCGTG
                                |||||||||  ||    ||||||||||
                                GACTTTGGT CT    TCTTTGGTAC
                                      A  CATTG
GAM1036  FLJ21945  3'  TATGGTTTCTCTGAGGCTTT   48095       AGA  A
                                GAAGCC   CA AGAGATCGTG
                                ||||||   ||  ||||||||||
                                TTTCGG   GT TCTTTGGTAT
                                   A__  C
GAM1036  FLJ31890  5'  TATGATTTCTGCTCTGGCTTT  92986         CAA
                                GAAGCCAGA   AGAGATCGTG
                                |||||||||   ||||||||||
                                TTTCGGTCT   TCTTTAGTAT
                                      CG_
GAM1036  H2AV     3'  GGTAATTTGTTGGCTTTAG   25761          A   GAG
                                CTGAAGCCAG CAAA   ATC
                                ||||||||||  ||||   |||
                                GATTTCGGTT GTTT   TGG
                                      _   AA_
GAM1036  HARC     3'  CACTTTATTTTTGTTTGGTTTT 35916             GATC
                                GAAGCCAGACAAAGA   GTG
                                ||||||||||||||||   |||
                                TTTTGGTTTGTTTTT   CAC
                                         ATTT
GAM1036  KIAA0121  3'  ACGGCGTGTTTGGTTCGG    73043       G      AAGAGA
                                CTGAA CCAGACA     TCGT
                                |||||  |||||||      ||||
```

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                                GGCTT GGTTTGT     GGCA
                                  _      GC____
GAM1036  KIAA0186  3' CTCTTTTTTGGTTTTGG    41107   TG      C
                                C  AAGCCAGA AAAGAG
                                |  |||||||| ||||||
                                G  TTTGGTTT TTTCTC
                                 GT      _
GAM1036  KIAA0247  3' TATGAGTTTGTTTGGTTTTA  29076           GAGA
                                TGAAGCCAGACAAA   TCGTG
                                ||||||||||||||   |||||
                                ATTTTGGTTTGTTT   AGTAT
                                        G___
GAM1036  KIAA0337  3' TGTTTTGTTCTGTTTGGTTTTG 29485   TG       AA__    CGTG
            G                    C  AAGCCAGACA   GAGAT
                                |  ||||||||||   |||||
                                G  TTTGGTTTGT   TTTTG
                                 GT        CTTG    T
GAM1036  KIAA0416  3' CATGATTTTTGTGGCATTTAG  32088      _   GACAA
                                CTGAA GCCA    AGAGATCGTG
                                ||||| ||||    ||||||||||
                                GATTT CGGT    TTTTTAGTAC
                                   A   G____
GAM1036  KIAA0451  3' TATTTTATTTTGTTTGGTTTTA 29780            A  TCGTG
                                TGAAGCCAGACAAAG GA
                                |||||||||||||| ||
                                ATTTTGGTTTGTTTT TT
                                         A  TTAT
GAM1036  KIAA0545  3' ACGATCTTTTTCTATCAG    63840     AGCC   CA
                                CTGA   AGA  AAGAGATCGT
                                ||||   |||  ||||||||||
                                GACT   TCT  TTTTCTAGCA
                                  A___   __
GAM1036  KIAA0645  3' GTTTGTTTGTTTGTTTTTGG   28525   TG   C      G
                                C  AAG CAGACAAA AGAT
                                |  ||| |||||||| ||||
                                G  TTT GTTTGTTT TTTG
                                 GT   T      G
GAM1036  KIAA0660  3' TTAATTTTTTTTTTGGCTTTGG 25472   TG      C      CGTG
                                C  AAGCCAGA AAAGAGAT
                                |  |||||||| ||||||||
                                G  TTCGGTTT TTTTTTTA
                                 GT       _       ATTG
GAM1036  KIAA1068  3' GTGGTTTGTTTCTGGTTTACAG 31688    _      CA  G    GTG
                                CTG AAGCCAGA  AA AGATC
                                |||  ||||||||  ||  |||||
                                GAC TTTGGTCT  TT TTTGG
                                  A       __  G    TGT
GAM1036  KIAA1210  3' CACGGTCTTTTTCTTTTGT   98066    C   C
                                GC AGA AAAGAGATCGTG
                                ||  |||  ||||||||||||
```

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                                TG TTT TTTTTCTGGCAC
                                 T  C
GAM1036 KIAA1317 3' CGGCCTTTTGTTTGTTTTAG  87210       C     A  AT
                                CTGAAGC AGACAA GAG  CG
                                ||||||| |||||| |||  ||
                                GATTTTG TTTGTT TTC  GC
                                    _    _  CG
GAM1036 KIAA1671 3' TATGTCATTTTTGTTTGCTTTA 66288       C       _ T
            G                    CTGAAGC AGACAAAGA GA CGTG
                                ||||||| ||||||||| || ||||
                                GATTTCG TTTGTTTTT CT GTAT
                                    _       A  _
GAM1036 KIAA1710 5' CGCGGTCTCTCAGGTTTTGG  63177   TG    A  CAAA
                                C  AAGCC GA   GAGATCGTG
                                |  ||||| ||   |||||||||
                                G  TTTGG CT   CTCTGGCGC
                                 GT    A  ____
GAM1036 KIAA1728 3' TATGAAATTGTTTGGCTTT   68954          AGAGA
                                GAAGCCAGACAA    TCGTG
                                ||||||||||||    |||||
                                TTTCGGTTTGTT    AGTAT
                                      AA___
GAM1036 MEF-2    3' GATTTTGGTTGGTTTTA     65023         ACAAA
                                TGAAGCCAG    GAGATC
                                |||||||||    ||||||
                                ATTTTGGTT    TTTTAG
                                     GG___
GAM1036 MGC23937 3' CATTTTGTTTAGTTTGGTTTTA 59600          _  G  TCGTG
            G                    CTGAAGCCAGAC AAA AGA
                                ||||||||||||| ||| |||
                                GATTTTGGTTTG TTT TTT
                                      A  G  TAC
GAM1036 MGC4643  3' GATGATGGCTGCCTGGTTTCAG 52140         ACAA  AG    G
                                CTGAAGCCAG   AG  ATCGT
                                ||||||||||   ||  |||||
                                GACTTTGGTC   TC  TAGTA
                                      CG__  GG    GT
GAM1036 N4BP3    3' CATGGTTTCATTTTGCTTTGG  66845   TG   C   CAAA
                                C  AAGC AGA   GAGATCGTG
                                |  |||| |||   |||||||||
                                G  TTCG TTT   CTTTGGTAC
                                 GT   T  A___
GAM1036 NCKX3    3' TGGGATTTTGTTTGGTTT    40730          AGA  TG
                                AAGCCAGACAAAG  TCG
                                ||||||||||||   |||
                                TTTGGTTTGTTTT  GGT
                                      AG_  T
GAM1036 OSR2     3' GTTGTTTTGTTTGCTTTGG   54858   TG   C      A
                                C  AAGC AGACAAAG GAT
                                |  |||| |||||||| |||
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                                G  TTCG TTTGTTTT TTG
                                 GT   _      G
GAM1036  PANK     3'  CATGATTTGCTGTTGGTTTCA  57159         A  AAG
                                TGAAGCCAG CA   AGATCGTG
                                ||||||||| ||   ||||||||
                                ACTTTGGTT GT   TTTAGTAC
                                     _ CG_
GAM1036  PCDH20   3'  GTCATTTGTTTGTTTTTAG   43425       C       GA
                                CTGAAG CAGACAAA  GAT
                                |||||| ||||||||  |||
                                GATTTT GTTTGTTT  CTG
                                   T       A_
GAM1036  RASSF2   3'  GCTAATTTTTTTGTGTGGTTTT 29102         G        CGTG
              AG                  CTGAAGCCA ACAAAGAGAT
                                |||||||| ||||||||||
                                GATTTTGGT TGTTTTTTTA
                                     G         ATCGG
GAM1036  RNF8     3'  GTGGTCTTTTTCCTTGCTTT   15572      C  AC       GTG
                                GAAGC AG  AAAGAGATC
                                ||||| ||  |||||||||
                                TTTCG TC  TTTTTCTGG
                                   T  C_       TGT
GAM1036  SPRY4    3'  ATTTGTTTGTTTGTTTTAG   48996        C      G
                                CTGAAGC AGACAAA AGAT
                                ||||||| ||||||| ||||
                                GATTTTG TTTGTTT TTTA
                                    _      G
GAM1036  TREX1    5'  GTGATTTCTTGCCCAGGTTCCA 50616     A    AGACA       GTG
              G                   CTG AGCC     AAGAGATC
                                ||| ||||     ||||||||
                                GAC TTGG     TTCTTTAG
                                  C    ACCCG       TGT
GAM1036  ZNF297B  3'  CAGAGCTCTGTTGTCTGGTTTT 26649            _    A  GTG
              AG                  CTGAAGCCAGACAA AGAG TC
                                |||||||||||||| |||| ||
                                GATTTTGGTCTGTT TCTC AG
                                        G   G  AC
GAM1036  LOC113523 5'  CACGATCTCTTTCGCCGGCTCG 73414      A   AGAC
              G                   CTGA GCC    AAAGAGATCGTG
                                |||| |||    ||||||||||||
                                GGCT CGG    TTTCTCTAGCAC
                                  _  CCGC
GAM1036  LOC113523 3'  TATGATTTTTTTGTTTGTTCA  73433      GC
                                TGAA  CAGACAAAGAGATCGTG
                                ||||  ||||||||||||||||
                                ACTT  GTTTGTTTTTTTAGTAT
                                   __
GAM1036  LOC121599 3'  ATGGTTTACTGGCATCGG    74558      A    ACAAAG
                                CTGA GCCAG     AGATCGT
                                |||| |||||     |||||||
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                                GGCT CGGTC     TTTGGTA
                                  A    A_____
GAM1036  LOC125704 3'  TGCGGTCTCTTTCCAGCTTCAG 74883       CA  CA
                                CTGAAGC  GA  AAGAGATCGTG
                                |||||||  ||  ||||||||||
                                GACTTCG  CT  TTCTCTGGCGT
                                   AC  __
GAM1036  LOC128077 3'  GGTTTTTTTTTGGTTTT     75227         CA
                                GAAGCCAGA  AAGAGATC
                                |||||||||  ||||||||
                                TTTTGGTTT  TTTTTTGG
                                     __
GAM1036  LOC145439 5'  CATGATTTCTTAATGGGATTCA 77726      G_  GACA
            G                    CTGAA  CCA    AAGAGATCGTG
                                |||||  |||    ||||||||||
                                GACTT  GGT    TTCTTTAGTAC
                                   AG   AA__
GAM1036  LOC145900 5'  CATGATTTCTTTGTTTGCTC   78022    A  C
                                GA GC AGACAAAGAGATCGTG
                                || || ||||||||||||||||
                                CT CG TTTGTTTCTTTAGTAC
                                 _ _
GAM1036  LOC145926 3'  TACGGTTTCTTTGTTACTTTAG 78033       CCA
                                CTGAAG   GACAAAGAGATCGTG
                                ||||||   ||||||||||||||
                                GATTTC   TTGTTTCTTTGGCAT
                                   A__
GAM1036  LOC150174 3'  CAGATTTTTTTTGTTTTGTTTT 80432   TG   C        _  GTG
            GG                   C  AAGC AGACAAAGAGA TC
                                |  |||| |||||||||| ||
                                G  TTTG TTTGTTTTTTT AG
                                 GT   T         T  AC
GAM1036  LOC150213 3'  CAGATTTTTTTTGTTTTGTTTT 75351   TG   C        _  GTG
            GG                   C  AAGC AGACAAAGAGA TC
                                |  |||| |||||||||| ||
                                G  TTTG TTTGTTTTTTT AG
                                 GT   T         T  AC
GAM1036  LOC150696 3'  GGTCTGCTGGGTTTCAG     59164         _  A  AAGA
                                CTGAAGCC AG CA    GATC
                                |||||||| || ||    ||||
                                GACTTTGG TC GT    CTGG
                                   G  _  _____
GAM1036  LOC151414 5'  CATGGAGATATCTGGTTTCAG  81034          CAAAGAGA
                                CTGAAGCCAGA       TCGTG
                                ||||||||||        |||||
                                GACTTTGGTCT       GGTAC
                                     ATAGA___
GAM1036  LOC153339 5'  TGTTTGTTTTGGTTTGGTTTTG 87202   TG       __  G   CGTG
            G                    C  AAGCCAGAC  AAA AGAT
                                |  |||||||||  ||| ||||
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                                G  TTTGGTTTG  TTT TTTG
                                 GT       GT   G    T
GAM1036  LOC158156 3'  TATGGGACACATGTTTAGGTTT 82629    TG    _    AAGAGA
                TGG                  C  AAGCC AGACA     TCGTG
                                |  ||||| |||||     |||||
                                G  TTTGG TTTGT     GGTAT
                                 GT     A     ACACAG
GAM1036  LOC159250 5'  TGTTCTGTTTTGTTTTGGTTTT 88428    TG      _    _  TCGTG
                GG                   C  AAGCCAGA CAAAG AGA
                                |  |||||||| ||||| |||
                                G  TTTGGTTT GTTTT TCT
                                 GT       T    G   TGT
GAM1036  LOC196326 5'  CGCGGTTTTTTTGCGGCCGTTC 92340     __   AGA
                                GAA  GCC   CAAAGAGATCGTG
                                |||  |||   ||||||||||||
                                CTT  CGG   GTTTTTTTGGCGC
                                  GC   C__
GAM1036  LOC199231 3'  TTCTTGTTTGGCTTTAG     91819            A
                                CTGAAGCCAGACAA GAG
                                |||||||||||||| |||
                                GATTTCGGTTTGTT CTT
                                          _
GAM1036  LOC202986 5'  CATGGTCTTCTTGAGCTTTGG  92063    TG    CAGA   AG
                                C  AAGC    CAA  AGATCGTG
                                |  ||||    |||  ||||||||
                                G  TTCG    GTT  TCTGGTAC
                                 GT    A___   CT
GAM1036  LOC220763 5'  CATGATTGGGCAGTTTGGTGTT 73734    TG A      AAAGA
                GG                   C  A GCCAGAC     GATCGTG
                                |  | |||||||     |||||||
                                G  T TGGTTTG     TTAGTAC
                                 GT G      ACGGG
GAM1036  LOC222256 3'  CATGGTTATGTCTGGTTTCA   95909           AAGA
                                TGAAGCCAGACA    GATCGTG
                                ||||||||||||    |||||||
                                ACTTTGGTCTGT    TTGGTAC
                                       A___
GAM1036  LOC253443 5'  ATCCAATTGTTTGGTTTCAG   97557             AGA
                                CTGAAGCCAGACAA   GAT
                                ||||||||||||||   |||
                                GACTTTGGTTTGTT   CTA
                                         AAC
GAM1036  LOC254556 3'  CGTGGTTCCAGTCTGGTTGCAG 96258     A       AAA   AT_
                                CTG AGCCAGAC   GAG   CG
                                ||| ||||||||   |||   ||
                                GAC TTGGTCTG   CTT   GC
                                  G       AC_   GGT
GAM1036  LOC254936 5'  CATGATTTCTTTGTTTGCTC   96651    A  C
                                GA GC AGACAAAGAGATCGTG
                                || || ||||||||||||||||
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                                CT CG TTTGTTTCTTTAGTAC
                                 _ _
GAM1036 LOC256364 5' CACGGGGAGGTGGTTGGTTTTG 96441   TG     A  AAGAGA
             G                    C  AAGCCAG CA     TCGTG
                                  |  ||||||| ||     |||||
                                  G  TTTGGTT GT     GGCAC
                                   GT      G  GGAGG_
GAM1036 LOC257486 3' CACGGTCTTTTTCTTTTGT   69767    C   C
                                  GC AGA AAAGAGATCGTG
                                  || ||| ||||||||||||
                                  TG TTT TTTTTCTGGCAC
                                   T   C
GAM1036 LOC51267  3' GGAATTCTTTTTGTTTGTTTCA 33675       C         TCGTG
             G                    CTGAAGC AGACAAAGAGA
                                  |||||||| ||||||||||
                                  GACTTTG TTTGTTTTTCT
                                      _         TAAGGA
GAM1036 LOC90785  3' CGTGGTCTCACTGGCTTCAG  64714         ACAAA
                                  CTGAAGCCAG    GAGATCGTG
                                  ||||||||||    |||||||||
                                  GACTTCGGTC    CTCTGGTGC
                                        A____
GAM1036 LOC91373  3' TTTTTTTGTTTGTTTTAG    66422       C
                                  CTGAAGC AGACAAAGAGA
                                  |||||||| ||||||||||
                                  GATTTTG TTTGTTTTTTT
                                      _
GAM1036 LOC91948  3' CGTGGTCTCGCTGGCTTCAG  68235         ACAAA
                                  CTGAAGCCAG    GAGATCGTG
                                  ||||||||||    |||||||||
                                  GACTTCGGTC    CTCTGGTGC
                                        G____
GAM1036 LOC91948  3' GTGGTCTCGCTGGCTCAG    68245     A    ACAAA
                                  CTGA GCCAG    GAGATCGT
                                  |||| |||||    ||||||||
                                  GACT CGGTC    CTCTGGTG
                                    _    G____
GAM1037 AIPL1    3'  TGGGGGTCATCTCGGTGATTTT 60537      C  ATCATG
             TG                     TAGGAA TAC     GACTTCCA
                                    ||||||| |||     ||||||||
                                    GTTTTT GTG     CTGGGGGT
                                       A   GCTCTA
GAM1037 AKAP13   3'  TGGGGGAAAGATGGAGTTCCTA 91259       A   ATGGA
                                  TAGGAACT CATC     CTTCCA
                                  |||||||| ||||     ||||||
                                  ATCCTTGA GTAG     GGGGGT
                                       G    AAA__
GAM1037 APLP2    3'  TGGTAACCTGTGGTGTATTTTT 92545      C        ACTT
             A                      TAGGAA TACATCATGG    CCA
                                    |||||| ||||||||||    |||
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                                ATTTTT ATGTGGTGTC    GGT
                                   _        CAAT
GAM1037  ARNT2    3'  GGAAGTTTGGGGGGTCTTA   30087      A  ACA   TG
                                TAGGA CT   TCA  GACTTCC
                                |||||| ||   |||  |||||||
                                ATTCT GG   GGT  TTGAAGG
                                   _ GG_   __
GAM1037  ASH2L    3'  TGGGGGTTTTGTTTTTGTTTTT 72013        TACAT  T
            G                    TAGGAAC    CA GGACTTCCA
                                |||||||    || |||||||||
                                GTTTTTG    GT TTTGGGGGT
                                    TTTTT  _
GAM1037  BACE     3'  TGGAAAATGATCTAGTTCCTG  58093         C    GGAC
                                TAGGAACTA ATCAT    TTCCA
                                ||||||||| |||||    |||||
                                GTCCTTGAT TAGTA    AAGGT
                                     C    A___
GAM1037  BDP1     5'  GGGAGGGCGTAGTTCCTA    37969          ATCAT GA
                                TAGGAACTAC    G  CTTCC
                                ||||||||||    |  |||||
                                ATCCTTGATG    C  GAGGG
                                      _____ GG
GAM1037  BMP1     3'  TGGAGGTCCGAGATGGCTTCT  21537      CTA    A
                                GGAA   CATC TGGACTTCCA
                                ||||   |||| ||||||||||
                                TCTT   GTAG GCCTGGAGGT
                                  CG_    A
GAM1037  CDC25B   3'  TGGGAAAGATGGTGTGGTGTCC 41856       _        GGAC
            TG                   TAGGA ACTACATCAT    TTCCA
                                ||||| ||||||||||    |||||
                                GTCCT TGGTGTGGTA    AGGGT
                                   G         GAA_
GAM1037  CKTSF1B1 3'  TGGAAGTCTGTAAGTTGTTTTT 26297       T  ATC
                                AGGAAC AC   ATGGACTTCCA
                                |||||| ||   ||||||||||
                                TTTTTG TG   TGTCTGAAGGT
                                   T  AA_
GAM1037  CNP      3'  GCTTCCATGTGTGCTGTGGTTC 53624          T A________   ACTT
            CTG                    TAGGAACTACA C       TGG    C
                                ||||||||||| |       |||    |
                                GTCCTTGGTGT G       ACC    G
                                      C TGTGT      TTCA
GAM1037  CYP26A1  3'  TGGAAGTGTACATATGAGTTTT 55125        A   CA_  G
            TA                   TAGGAACT CAT   TG ACTTCCA
                                |||||||| |||   || |||||||
                                ATTTTTGA GTA   AT TGAAGGT
                                   _   TAC  G
GAM1037  DDX11    3'  GCTTCCATGTGCGGTGTGGTTC 16578           AT________  ACTT
            CTG                    TAGGAACTACATC        GG    C
                                ||||||||||||        ||    |
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                                GTCCTTGGTGTGG       CC    G
                                      CGTGT   A  TTCA
GAM1037  EVI2A    5'  TGTCATCTGTGGTTTGGTTTTT 27224         C       CTTCCA
             A                    TAGGAACTA ATCATGGA
                                  ||||||||| ||||||||
                                  ATTTTTGGT TGGTGTCT
                                        T       ACTGT
GAM1037  FOXO1A   3'  TGGAGGTTGGTTTTGTAGTTCT 10655         TC  G
                                  GGAACTACA  AT GACTTCCA
                                  |||||||||  || ||||||||
                                  TCTTGATGT  TG TTGGAGGT
                                        TT  G
GAM1037  FZD1     3'  GGAAAGATGTGGTTACTG    14499     G       ATGGAC
                                  TAG AACTACATC     TTCC
                                  ||| |||||||||     ||||
                                  GTC TTGGTGTAG     AAGG
                                    A       A_____
GAM1037  GAS7     3'  GGCGCGTGGTGGGTTTTTG   20855        A      GA
                                  TAGGAACT CATCATG  CT
                                  |||||||| |||||||  ||
                                  GTTTTTGG GTGGTGC  GG
                                       _      GC
GAM1037  GPR48    3'  GGGGGTTTAATAGTATCTG   38096     A    CATCA
                                  TAGG ACTA    TGGACTTCC
                                  |||| ||||    |||||||||
                                  GTCT TGAT    ATTTGGGGG
                                    A   A____
GAM1037  GPR85    3'  GCTTCCATGTATTATGTGGTTT 39105          CA_______   ACTT
             TTG                    TAGGAACTACAT       TGG    C
                                    ||||||||||||       |||   |
                                    GTTTTTGGTGTA       ACC    G
                                          TTATGT     TTCA
GAM1037  HDAC7A   3'  GGGAGTCCTGTGCTTCCTG   31834       C    TCAT
                                  TAGGAA TACA    GGACTTCC
                                  |||||| ||||    ||||||||
                                  GTCCTT GTGT    CCTGAGGG
                                     C    ____
GAM1037  HTR2C    3'  TGGAAGAATTCATGATGCTAGT 7874          _       __
             TCTTA                   TAGGAACTA CATCATGGA  CTTCCA
                                     |||||||| |||||||||  ||||||
                                     ATTCTTGAT GTAGTACTT  GAAGGT
                                          C        AA
GAM1037  IL10RA   3'  TGGGAGTCCATGGTGTCATGCC 60384    AACT
                                  GG    ACATCATGGACTTCCA
                                  ||    ||||||||||||||||
                                  CC    TGTGGTACCTGAGGGT
                                    GTAC
GAM1037  INPP5A   3'  TGGAAGTGACCGGTCTGGTTCC 19868         C   AT  __
             TA                     TAGGAACTA ATC  GG  ACTTCCA
                                    ||||||||| |||  ||  |||||||
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                                ATCCTTGGT TGG  CC  TGAAGGT
                                    C   __  AG
GAM1037  LHX4     3'  TGGAAGTCCTCCGCTGATTCCT 54045       CTACATCAT
              A                  TAGGAA       GGACTTCCA
                                 ||||||       |||||||||
                                 ATCCTT       CCTGAAGGT
                                    AGTCGCCT_
GAM1037  LNK      3'  GTTTACAGATGTAGTTCTTG   19650           A_
                                 TAGGAACTACATC  TGGAC
                                 ||||||||||||  |||||
                                 GTTCTTGATGTAG  ATTTG
                                       AC
GAM1037  MC1R     3'  GCTTCCATGTGTGGTCTGGTTC 11479         C  A_______  ACTT
              CTG                   TAGGAACTA ATC       TGG   C
                                 |||||||| |||       |||   |
                                 GTCCTTGGT TGG       ACC   G
                                     C   TGTGT     TTCA
GAM1037  MMP19    5'  TGGAGGGGAGGGTGAGGTTCCT 11644        A   ATGGA
              A                  TAGGAACT CATC    CTTCCA
                                 ||||||||| ||||    ||||||
                                 ATCCTTGG GTGG    GGAGGT
                                     A   GAGG_
GAM1037  NCOA3    3'  AGAATCCTTGGTGTGGTTTCTG 22560           T  C  CA
                                 TAGGAACTACATCA GGA TTC
                                 |||||||||||||| ||| |||
                                 GTCTTTGGTGTGGT CCT AAG
                                       T   _  AT
GAM1037  NCOA6    5'  TCAAGTGTGGTGTAGTTTTTG  26848           GG   CCA
                                 TAGGAACTACATCAT  ACTT
                                 ||||||||||||||  ||||
                                 GTTTTTGATGTGGTG  TGAA
                                       __   CTG
GAM1037  NEU3     3'  TGGAAGACAAGGATGTGGTCCT 22836      A     A_  GA
              G                  TAGGA CTACATC  TG  CTTCCA
                                 |||||  |||||||  ||  ||||||
                                 GTCCT GGTGTAG  AC  GAAGGT
                                    _      GA  A_
GAM1037  OLIG2    3'  TGGGGGTTCTGTTGGCTTTTTA 20551       CTA  T  T
                                 TAGGAA   CA CA GGACTTCCA
                                 ||||||   || || |||||||||
                                 ATTTTT   GT GT CTTGGGGGT
                                    CG_  T  _
GAM1037  PRDM4    3'  TGGAAGTTTAGGGTAGATCTTG 25744      A   ATCA
                                 TAGGA CTAC    TGGACTTCCA
                                 |||||  ||||   ||||||||||
                                 GTTCT GATG    ATTTGAAGGT
                                    A   GG__
GAM1037  PYGB     3'  TGGGGGTCAGGGTGGTTTT   12692        ATCATG
                                 GGAACTAC     GACTTCCA
                                 ||||||||     ||||||||
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                                TTTTGGTG     CTGGGGGT
                                     GGA___
GAM1037  RFC1     3'  TGGAAGTTTGGGTTATTCCTA  12831       CT  A   TG
                                TAGGAA  AC TCA  GACTTCCA
                                ||||||  || |||  ||||||||
                                ATCCTT  TG GGT  TTGAAGGT
                                   AT  _  __
GAM1037  RLN1     3'  GGACTTCCATGTATGATTGTAG 23581          _ A_______   ACTT
              TTTCTG                  TAGGAACTACA TC       TGG    CC
                                ||||||||||| ||       |||    ||
                                GTCTTTGATGT AG       ACC    GG
                                      T  TATGT     TTCA
GAM1037  SIP      3'  TGGGGTAAAGATGGGTTTTTA  27735        A    ATGG   T
                                TAGGAACT CATC    ACT CCA
                                |||||||| ||||    ||| |||
                                ATTTTTGG GTAG    TGG GGT
                                     _    AAA_  _
GAM1037  SLC2A2   3'  TTTATGGTGTGTTCCTA     6219         T
                                TAGGAAC ACATCATGGA
                                ||||||| ||||||||||
                                ATCCTTG TGTGGTATTT
                                     _
GAM1037  SLC2A3   3'  TGGAGGGTAAATGATGTGGTGC 23650      A        GGA_
              CTG                   TAGG ACTACATCAT    CTTCCA
                                |||| ||||||||||    ||||||
                                GTCC TGGTGTAGTA    GGAGGT
                                   G         AATG
GAM1037  SLC6A2   3'  TGATTTCGTGACTGTAGTTTTT 8310           _      CTTCCA
              G                    TAGGAACTACA TCATGGA
                                ||||||||||| |||||||
                                GTTTTTGATGT AGTGCTT
                                      C      TAGT
GAM1037  SLC9A1   3'  GGAGCAGGGGTGGTTTCTA    70929          AT A  GAC
                                TAGGAACTAC  C TG   TTCC
                                ||||||||||  | ||   ||||
                                ATCTTTGGTG  G AC   GAGG
                                      GG _  ___
GAM1037  SOST     3'  TGGGGGCAACTGTAGATGTGGT 48225           _   A__
              TTCTA                  TAGGAACTACATC ATGG   CTTCCA
                                ||||||||||||| ||||   ||||||
                                ATCTTTGGTGTAG TGTC   GGGGGT
                                        A    AAC
GAM1037  TCF3     3'  GGGGGTTCTCTTGGTTTT    71274        CATCAT
                                GGAACTA     GGACTTCC
                                |||||||     ||||||||
                                TTTTGGT     CTTGGGGG
                                     TCT___
GAM1037  TNFRSF8  3'  TGGAGGAAGTGATAGTTTCTG  8799         CA    GGA
                                TAGGAACTA  TCAT   CTTCCA
                                |||||||||  ||||   ||||||
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                                GTCTTTGAT  AGTG   GGAGGT
                                     __    AA_
GAM1037  VSNL1    3'  GGAAGTGTATTGGTTTCTG   14082        CATC   G
                                TAGGAACTA    ATG ACTTCC
                                |||||||||    ||| ||||||
                                GTCTTTGGT    TAT TGAAGG
                                     ____   G
GAM1037  WISP1    3'  TGGAGGTTTACCGGTTGTTT   55943      T  ATCA
                                GAAC AC    TGGACTTCCA
                                |||| ||    ||||||||||
                                TTTG TG    ATTTGGAGGT
                                  T  GCC_
GAM1037  WNT3     3'  GGATGGTGTGTGGTTTTTA    48436          CATGG  _
                                TAGGAACTACAT     ACT TCC
                                ||||||||||||     ||| |||
                                ATTTTTGGTGTG     TGG AGG
                                     ______  T
GAM1037  ABLIM    3'  ATGTCCAATCATGTGTGTGGTT 22977          _ ____    TTCCA
              CCTG                  TAGGAACTACAT CA    TGGAC
                                |||||||||||| ||    |||||
                                GTCCTTGGTGTG GT    ACCTG
                                      T  ACTA     T   AC
GAM1037  ABLIM    3'  GGAAGGCGTGTGGTTCTT     22981          CATGGA
                                AGGAACTACAT     CTTCC
                                ||||||||||      |||||
                                TTCTTGGTGTG     GAAGG
                                     CG____
GAM1037  ATP10D   3'  TGGAGGTTTCTATGAGGTTCTT 73530        ACA     __
              A                   TAGGAACT   TCATGGA  CTTCCA
                                ||||||||   |||||||  ||||||
                                ATTCTTGG   AGTATCT  GGAGGT
                                     ___      TT
GAM1037  BRAL1    5'  TGGAAGTCCTGGATAGTTCC   41810       CA   T
                                GGAACTA  TCA GGACTTCCA
                                |||||||  ||| |||||||||
                                CCTTGAT  GGT CCTGAAGGT
                                    A_  _
GAM1037  C20orf121 3'  TGGGGGGTGGTGATCTGGTTCT 44525         C    GGA
              TA                   TAGGAACTA ATCAT   CTTCCA
                                |||||||||  |||||   ||||||
                                ATTCTTGGT TAGTG   GGGGGT
                                     C    GTG
GAM1037  ChGn     3'  TGGAGGTTTTGATGGTGTTT   37777      TA    T
                                GAAC  CATCA GGACTTCCA
                                ||||  |||||  |||||||||
                                TTTG  GTAGT TTTGGAGGT
                                  TG    _
GAM1037  DIS3     3'  TGGAGGTTTATGGTCTGTTCT  30926       TAC
                                GGAAC   ATCATGGACTTCCA
                                |||||   ||||||||||||||
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                                TCTTG  TGGTATTTGGAGGT
                                  TC_
GAM1037  DKFZP434C212 3'  GCTTCCATGTGGGATGTGGTTT 69491          AT_______  ACTT
           CTG                    TAGGAACTACATC       GG   C
                                  ||||||||||||        ||   |
                                  GTCTTTGGTGTAG       CC   G
                                        GGTGT  A  TTCA
GAM1037  DSCR1L1  3'  GGAGGTTTTTGGTTTTTC   20626     CTAC   TG
                                  GGAA   ATCA  GACTTCC
                                  ||||   ||||  |||||||
                                  CTTT   TGGT  TTGGAGG
                                    T___   TT
GAM1037  EPSTI1   3'  TGGGGGTCTTTTTAGATTTTA  53828      A  CATCAT
                                  TAGGA CTA     GGACTTCCA
                                  ||||| |||     |||||||||
                                  ATTTT GAT     TCTGGGGGT
                                     A  TTT___
GAM1037  FLJ10057  3'  GCTTCCATGTGTGGTGCAGTTT 36252        A   A_______  ACTT
           CTG                    TAGGAACT CATC       TGG   C
                                  |||||||| ||||       |||   |
                                  GTCTTTGA GTGG       ACC   G
                                      C   TGTGT     TTCA
GAM1037  FLJ12827  5'  TGGAAGTCCGTGACTGTTTCCT 45694       CT  _
           G                     TAGGAA  ACA TCATGGACTTCCA
                                 ||||||  ||| ||||||||||||
                                 GTCCTT  TGT AGTGCCTGAAGGT
                                    __  C
GAM1037  FLJ12847  3'  CCATGTGTTGTGGTTCTTA   45077          T__
                                  TAGGAACTACA   CATGG
                                  ||||||||||   |||||
                                  ATTCTTGGTGT   GTACC
                                        TGT
GAM1037  FLJ13096  3'  GGGTCATTGATGAGTTCTTA   47175        A    TG
                                  TAGGAACT CATCA  GACTT
                                  |||||||| |||||  |||||
                                  ATTCTTGA GTAGT  CTGGG
                                     _    TA
GAM1037  FLJ13441  3'  TGGGGTGTGGGTGGTGGGTTTT 43922        A    GG  _
           TA                     TAGGAACT CATCAT  AC TTCCA
                                  |||||||| ||||||  || |||||
                                  ATTTTTGG GTGGTG  TG GGGGT
                                     _    GG  T
GAM1037  FLJ22474  3'  GGGAGTCAGTAGTTTCCTA   45617      _   ATCATG
                                  TAGGAA CTAC     GACTTCC
                                  |||||| ||||     |||||||
                                  ATCCTT GATG     CTGAGGG
                                     T   A_____
GAM1037  FLJ23309  3'  GCTTCCATGTATGATGTGCTTT 46591      C    A_______  ACTT
           TTA                    TAGGAA TACATC       TGG   C
                                  |||||| ||||||       |||   |
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                                ATTTTT GTGTAG       ACC    G
                                   C     TATGT     TTCA
GAM1037  FLJ23462  3'  TGGAGTGGGGTGTAGTT     46223         ATGG   T
                                AACTACATC    ACT CCA
                                |||||||||    ||| |||
                                TTGATGTGG    TGA GGT
                                     GG__   _
GAM1037  GCN2      5'  TCCAGATGTAGTTCCTG     63439           A
                                TAGGAACTACATC TGGA
                                |||||||||||| ||||
                                GTCCTTGATGTAG ACCT
                                          _
GAM1037  GPT2      3'  TGGAAGTTACATCTGTGAAGTT 56774         A   C_   _
             TCTG                   TAGGAACT CAT  ATG GACTTCCA
                                |||||||| |||  ||| ||||||||
                                GTCTTTGA GTG  TAC TTGAAGGT
                                     A   TC   A
GAM1037  GTF3C1    3'  GGGAGTTGGTGCTTCTTG    9508        CTACAT   G
                                TAGGAA     CAT GACTTCC
                                ||||||     ||| |||||||
                                GTTCTT     GTG TTGAGGG
                                   C_____   G
GAM1037  HEAB      3'  TCCATATGTGGTTCTTA     23362           C
                                TAGGAACTACAT ATGGA
                                |||||||||||| |||||
                                ATTCTTGGTGTA TACCT
                                          _
GAM1037  HSPC055   5'  TGGAGGTTTTCTTGGTTCCTG  27120         CATCAT
                                TAGGAACTA     GGACTTCCA
                                |||||||||     |||||||||
                                GTCCTTGGT     TTTGGAGGT
                                     TCT___
GAM1037  KIAA0144  3'  GGAAGGCATGTAGTTTC     29944          CATGGA
                                GGAACTACAT     CTTCC
                                ||||||||||     |||||
                                CTTTGATGTA     GAAGG
                                     CG____
GAM1037  KIAA0173  3'  TGGAAGGAGATGTGGTTTCT   28384           ATGGA
                                AGGAACTACATC    CTTCCA
                                ||||||||||||    ||||||
                                TCTTTGGTGTAG    GAAGGT
                                      AG___
GAM1037  KIAA0173  3'  TGGGGGCCCTGGTGTGGTTGCT 28386     G        T  A
             G                   TAG AACTACATCA GG CTTCCA
                                ||| |||||||||| || ||||||
                                GTC TTGGTGTGGT CC GGGGGT
                                  G        C  _
GAM1037  KIAA0247  3'  TGGTCTGAATGGTGTAGTTGCT 29079     G         __    TCCA
             G                   TAG AACTACATCAT  GGACT
                                ||| ||||||||||  |||||
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                                GTC TTGATGTGGTA  TCTGG
                                  G         AG    T
GAM1037  KIAA0365  3'  TGGAAGTTTTCTTTTGTTTCTG 79372       TACATCAT
                                TAGGAAC       GGACTTCCA
                                |||||||       |||||||||
                                GTCTTTG       TTTGAAGGT
                                    TTTTCT__
GAM1037  KIAA0515  3'  TGGGGGTTTTGTTTGGTTCCTG 64558         CAT  T
                                TAGGAACTA   CA GGACTTCCA
                                |||||||||   || |||||||||
                                GTCCTTGGT   GT TTTGGGGGT
                                    TT_ _
GAM1037  KIAA0532  3'  GCTTCCATGTGTGATTTAGTTT 71323         C   A________   ACTT
            TTG                   TAGGAACTA ATC       TGG    C
                                |||||||||| |||       |||    |
                                GTTTTTGAT TAG       ACC    G
                                    T   TGTGT     TTCA
GAM1037  KIAA0630  3'  TGGAACACAGGTCTAGTTTCTA 90954         C   A  GAC
                                TAGGAACTA ATC TG   TTCCA
                                |||||||||| ||| ||   |||||
                                ATCTTTGAT TGG AC   AAGGT
                                    C   _  AC_
GAM1037  KIAA0767  3'  TGGAGAGAAGCTGTAGTTTTTA 61259          TCATGGAC
                                TAGGAACTACA       TTCCA
                                ||||||||||       |||||
                                ATTTTTGATGT       GAGGT
                                     CGAAGA__
GAM1037  KIAA0931  3'  TGGCAGCCATGGTGTATTTTTG 68022       C        A  T
                                TAGGAA TACATCATGG CT CCA
                                |||||| |||||||||| || |||
                                GTTTTT ATGTGGTACC GA GGT
                                   _        _ C
GAM1037  KIAA1045  3'  TGGAAGTCCATCTTGTTCCCTG 71613     AACT   TC
                                TAGG    ACA  ATGGACTTCCA
                                ||||    |||  ||||||||||||
                                GTCC    TGT  TACCTGAAGGT
                                  CT__   TC
GAM1037  KIAA1069  3'  GGGGCAGGAGTGGTTCTTA    68531         A  A  GAC
                                TAGGAACTAC TC TG   TTCC
                                |||||||||| || ||   ||||
                                ATTCTTGGTG AG AC   GGGG
                                     _  G  ___
GAM1037  KIAA1078  3'  GGAAAGATTTAGTTCTTG     65717         C   ATGGAC
                                TAGGAACTA ATC     TTCC
                                |||||||||| |||     ||||
                                GTTCTTGAT TAG     AAGG
                                    T   A_____
GAM1037  KIAA1128  3'  GTCTATGGTGTATTTTTG     69009        C
                                TAGGAA TACATCATGGAC
                                |||||| ||||||||||||
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                                GTTTTT ATGTGGTATCTG
                                      _
GAM1037 KIAA1240 3' TGGGAGTCCAATTTGGTTTC  67295       C  CA
                                GGAACTA AT  TGGACTTCCA
                                ||||||| ||  ||||||||||
                                CTTTGGT TA  ACCTGAGGGT
                                   T __
GAM1037 KIAA1320 3' GGATGTTGGTGGGTTTTTG   69844       ACAT   G   T
                                TAGGAACT    CAT GAC TCC
                                ||||||||    ||| ||| |||
                                GTTTTTGG    GTG TTG AGG
                                     ____   G   T
GAM1037 KIAA1323 5' TGGAAGTTTGTGGAACATCTTG 63726      ACTACA   TG
                                TAGGA     TCA  GACTTCCA
                                |||||     |||  ||||||||
                                GTTCT     GGT  TTGAAGGT
                                   ACAA__   GT
GAM1037 KIAA1726 3' AGCTATGATGTGCTTCTTG   67825       C        A
                                TAGGAA TACATCATGG CT
                                |||||| |||||||||| ||
                                GTTCTT GTGTAGTATC GA
                                   C        _
GAM1037 MDS026   3' TGGAGGCCCGGTGTGGTTCC  38061          AT  A
                                GGAACTACATC  GG CTTCCA
                                |||||||||||  || ||||||
                                CCTTGGTGTGG  CC GGAGGT
                                      C_ _
GAM1037 METAP1   3' TGGGAGTATGTGTGTGAAGTTT 73037        A  _   G
           TTA                    TAGGAACT CAT CATG ACTTCCA
                                ||||||||| ||| |||| |||||||
                                ATTTTTGA GTG GTGT TGAGGGT
                                     A  T   A
GAM1037 MGC22014 3' GGGGGTCTTTCGGTTTTTG   65117        ACATCAT
                                TAGGAACT      GGACTTCC
                                ||||||||      ||||||||
                                GTTTTTGG      TCTGGGGG
                                     CTT____
GAM1037 MGC3103  3' TGGGAGTCCCTCCCTGGTTTTT 44067        CATCAT
           A                    TAGGAACTA     GGACTTCCA
                                |||||||||     |||||||||
                                ATTTTTGGT     CCTGAGGGT
                                     CCCTC_
GAM1037 MGC32043 3' TGGGAAAAGGAGTGGTTTCTG  58670         A  ATGGAC
                                TAGGAACTAC TC     TTCCA
                                |||||||||| ||     |||||
                                GTCTTTGGTG AG     AGGGT
                                     _  GAAA__
GAM1037 MO25     3' GGCCGTGATGTGGTGTCCTG   33292       _         A
                                TAGGA ACTACATCATGG CT
                                ||||| |||||||||||| ||
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                                GTCCT TGGTGTAGTGCC GG
                                  G         _
GAM1037  NAV3     3'  GCTTCCATGGATGATGTATTTT 30453       C     A_______   ACTT
             CTA                    TAGGAA TACATC       TGG    C
                                    |||||| ||||||       |||    |
                                    ATCTTT ATGTAG       ACC    G
                                      T     TAGGT     TTCA
GAM1037  OIP5     3'  TGGAGGGGAAATGCAGTTTCTA 63445        A   CATGGA
                                    TAGGAACT CAT     CTTCCA
                                    |||||||| |||     ||||||
                                    ATCTTTGA GTA     GGAGGT
                                         C   AAGG__
GAM1037  OLFM3    3'  TGGGAGTTGTCTTTGTGGTTTC 83029         TCATG
                                    GGAACTACA    GACTTCCA
                                    |||||||||    ||||||||
                                    CTTTGGTGT    TTGAGGGT
                                          TTCTG
GAM1037  OSBPL6   3'  AGCTATGTGTGGTTTCTG    51686          T    A
                                    TAGGAACTACA CATGG CT
                                    |||||||||||| ||||| ||
                                    GTCTTTGGTGT GTATC GA
                                                _    _
GAM1037  PPAP2C   3'  GCTTCCATGTATATGTGGTTTT 14931          CA______   ACTT
             TA                     TAGGAACTACAT       TGG    C
                                    ||||||||||||       |||    |
                                    ATTTTTGGTGTA       ACC    G
                                          TATGT     TTCA
GAM1037  PRC1     3'  GGGAGTCTGTTTGTTCC     15629       TACATC
                                    GGAAC     ATGGACTTCC
                                    |||||     ||||||||||
                                    CCTTG     TGTCTGAGGG
                                      TT____
GAM1037  PRO0641  3'  TGGAAGTACATAGGGTTTGGTT 27069         C   __   G
             TTTG                     TAGGAACTA ATC  ATG ACTTCCA
                                    ||||||||| |||  ||| |||||||
                                    GTTTTTGGT TGG  TAC TGAAGGT
                                          T   GA   A
GAM1037  RPIA     3'  TGGGGGTTTCTTCATATTCCTG 58595       CTACATCAT
                                    TAGGAA        GGACTTCCA
                                    ||||||        |||||||||
                                    GTCCTT        TTTGGGGGT
                                       ATACTTC__
GAM1037  RYK      3'  GCTTCCATGGATGGTGTGGTGC 83508      A       A_______   ACTT
             CTG                      TAGG ACTACATC       TGG    C
                                    |||| ||||||||       |||    |
                                    GTCC TGGTGTGG       ACC    G
                                      G       TAGGT     TTCA
GAM1037  SCYA22   3'  TGGAGTGCAATGGTGTGGTCTT 92615       A       _ G   T
             G                        TAGGA CTACATCAT G ACT CCA
                                    ||||| ||||||||| | ||| |||
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                                GTTCT GGTGTGGTA C TGA GGT
                                  _       A G  _
GAM1037  SMOC2    3'  TGGAAGTTTGTGATGTACGGCC 72822    AAC      TG
                                GG  TACATCA  GACTTCCA
                                ||  |||||||  ||||||||
                                CC  ATGTAGT  TTGAAGGT
                                 GGC      GT
GAM1037  ST13     3'  GCTTCCATGGATATGTGGTTCC 15432          CA_______  ACTT
           TG                    TAGGAACTACAT      TGG   C
                                ||||||||||||      |||   |
                                GTCCTTGGTGTA      ACC   G
                                      TAGGT     TTCA
GAM1037  TMSNB    3'  TGACCTTTGTGTATGTAGTTCT 42078          _ TG  CT  CA
           TG                    TAGGAACTACAT CA  GA  TC
                                ||||||||||||| ||  ||  ||
                                GTTCTTGATGTA GT  TT  AG
                                      T  GT  CC  T
GAM1037  TREX1    5'  TGGAACAAGAGGTGGTGTGGCT 50617      A       GGAC__
           CCTG                   TAGGA CTACATCAT     TTCCA
                                ||||| |||||||||     |||||
                                GTCCT GGTGTGGTG     AAGGT
                                  C       GAGAAC
GAM1037  TREX1    5'  TGGAACAAGAGGTGGTGTGGCT 50618      A       GGAC__
           CCTG                   TAGGA CTACATCAT     TTCCA
                                ||||| |||||||||     |||||
                                GTCCT GGTGTGGTG     AAGGT
                                  C       GAGAAC
GAM1037  TUSP     5'  TGGACTAGTGGTGTGGTGTTTG 40033     A       GGACT
                                TAGG ACTACATCAT     TCCA
                                |||| ||||||||||     ||||
                                GTTT TGGTGTGGTG     AGGT
                                  G       ATC__
GAM1037  U5-116KD 3'  GGGAGTTGTTGGGTTCCTG   16185       ACAT  TG
                                TAGGAACT   CA  GACTTCC
                                ||||||||   ||  |||||||
                                GTCCTTGG   GT  TTGAGGG
                                     _____  TG
GAM1037  VDAC3    5'  GGAGGTCTTTGGTTTC      20182       CATCAT
                                GGAACTA     GGACTTCC
                                |||||||     ||||||||
                                CTTTGGT     TCTGGAGG
                                    T_____
GAM1037  WDR13    5'  TGGGAGTTCGTGACATCTCC   35845     ACTACA
                                GGA     TCATGGACTTCCA
                                |||     |||||||||||||
                                CCT     AGTGCTTGAGGGT
                                  CTAC__
GAM1037  LOC116071 3'  TGGAAGTTCAGTTTTGGTGTCT 57422     GA   CATCA
           G                     TAG  ACTA    TGGACTTCCA
                                |||  ||||    ||||||||||
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                                GTC  TGGT    ACTTGAAGGT
                                  TG   TTTG_
GAM1037  LOC123036 5'  TGGAAGTTTGTGTCTTTTGCTG 74649    G  CTACAT  TG
                                TAG AA     CA  GACTTCCA
                                ||| ||     ||  ||||||||
                                GTC TT     GT  TTGAAGGT
                                  G  TTCT__  GT
GAM1037  LOC124912 3'  TGGGAAATGTGGTTTGGTTCCT 74821        C     GAC
            G                    TAGGAACTA ATCATG   TTCCA
                                |||||||||| ||||||   |||||
                                GTCCTTGGT TGGTGT   AGGGT
                                      T     AA_
GAM1037  LOC126917 3'  GGTGTAATGTGGTTTCTG    75098          CA  G
                                TAGGAACTACAT  TG ACT
                                ||||||||||||  || |||
                                GTCTTTGGTGTA  AT TGG
                                       __  G
GAM1037  LOC144195 3'  TGGAGGGTAAATGATGTGGTGC 60990     A        GGA_
            CTG                    TAGG ACTACATCAT    CTTCCA
                                |||| ||||||||||    ||||||
                                GTCC TGGTGTAGTA    GGAGGT
                                  G         AATG
GAM1037  LOC145813 3'  TGGGGGCCAGTGTGTGGTTTTT 84513          CA   A
            A                    TAGGAACTACAT  TGG CTTCCA
                                ||||||||||||  ||| ||||||
                                ATTTTTGGTGTG  ACC GGGGGT
                                       TG  _
GAM1037  LOC145945 5'  GGGAGTCAGTGTTTCCTA    84568       CT    CATG
                                TAGGAA  ACAT    GACTTCC
                                ||||||  ||||    |||||||
                                ATCCTT  TGTG    CTGAGGG
                                   __    A___
GAM1037  LOC147991 3'  TGGGGGTTTTTTGTTTGTTTCT 79303       T_   TCAT
            G                    TAGGAAC  ACA    GGACTTCCA
                                |||||||  |||    |||||||||
                                GTCTTTG  TGT    TTTGGGGGT
                                    TT   TT__
GAM1037  LOC148823 3'  GCTTCCATGGATGTGTAGTTTC 59894          T A________   ACTT
            TG                     TAGGAACTACA C       TGG    C
                                |||||||||||  |       |||    |
                                GTCTTTGATGT G       ACC    G
                                      _ TAGGT     TTCA
GAM1037  LOC149052 3'  GCTTCCATGGATATGTGGTTCC 79873          CA_______   ACTT
            TG                     TAGGAACTACAT       TGG    C
                                ||||||||||||       |||    |
                                GTCCTTGGTGTA       ACC    G
                                       TAGGT     TTCA
GAM1037  LOC151040 5'  TGGAGAGAGTTGTAGTTCCTG  80910          TCATGGAC
                                TAGGAACTACA       TTCCA
                                ||||||||||       |||||
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                                GTCCTTGATGT       GAGGT
                                      TGAGA___
GAM1037  LOC151556 5'  GCTTCCATGTATGGTGTATTTC 81080       C     A________   ACTT
                CTG                    TAGGAA TACATC       TGG    C
                                       |||||| ||||||       |||    |
                                       GTCCTT ATGTGG       ACC    G
                                          T     TATGT     TTCA
GAM1037  LOC153651 3'  TGGGAGAACAATGGGGTTTCTA 81798        TA   CA  GA
                                       TAGGAAC  CAT  TG  CTTCCA
                                       |||||||  |||  ||  ||||||
                                       ATCTTTG  GTA  AC  GAGGGT
                                           GG   __  AA
GAM1037  LOC161378 5'  GGGAGTCTGCAGCTTCCTG    83149       _  A  TCATG
                                       TAGGAA CT CA     GACTTCC
                                       |||||| || ||     |||||||
                                       GTCCTT GA GT     CTGAGGG
                                           C  C  _____
GAM1037  LOC166713 5'  GGCCGTGGTGTGGTCCTG     88613      A         A
                                       TAGGA CTACATCATGG CT
                                       ||||| ||||||||||| ||
                                       GTCCT GGTGTGGTGCC GG
                                         _          _
GAM1037  LOC170082 3'  GGACTTCCATGTATGTGTGTAG 83445           _ A________   ACTT
                TTTTTA                  TAGGAACTACAT C       TGG    CC
                                        |||||||||||| |       |||    ||
                                        ATTTTTGATGTG G       ACC    GG
                                              T TATGT     TTCA
GAM1037  LOC196746 3'  GGAGGTTTGCGTGTTTCTG    88900       T  ATCA GG
                                       TAGGAAC AC    T  ACTTCC
                                       |||||||  ||    |  ||||||
                                       GTCTTTG TG    G  TGGAGG
                                           _  C___ TT
GAM1037  LOC199678 3'  GGGGGTCAGGGGTTCCTG    91369        ACATCATG
                                       TAGGAACT       GACTTCC
                                       ||||||||       |||||||
                                       GTCCTTGG       CTGGGGG
                                            GGA_____
GAM1037  LOC202347 3'  TGGAAGTTCAGCAAAGTTTC   91951       ACATCA
                                       GGAACT     TGGACTTCCA
                                       ||||||     ||||||||||
                                       CTTTGA     ACTTGAAGGT
                                           AACG__
GAM1037  LOC204084 5'  GGAAGGCGATGAGTTTCTG    90998        A   ATGGA
                                       TAGGAACT CATC     CTTCC
                                       |||||||| ||||     |||||
                                       GTCTTTGA GTAG     GAAGG
                                           _    CG___
GAM1037  LOC221087 3'  GCTTCCATGGGTGGTGTGTTCC 94863       T    A________   ACTT
                TA                     TAGGAAC ACATC       TGG    C
                                       ||||||| |||||       |||    |
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                                ATCCTTG TGTGG       ACC    G
                                   _    TGGGT      TTCA
GAM1037  LOC221692 3'  TGGGAGTTCCCTCCTTCTGGTT 93861         CATCAT__
            CTTG                  TAGGAACTA       GGACTTCCA
                                  |||||||||       |||||||||
                                  GTTCTTGGT       CTTGAGGGT
                                     CTTCCTCC
GAM1037  LOC255811 3'  TGGGGGTTTTGTTTTTGTTTTT 96310         TACAT  T
            G                     TAGGAAC    CA GGACTTCCA
                                  |||||||     || |||||||||
                                  GTTTTTG     GT TTTGGGGGT
                                     TTTTT  _
GAM1037  LOC51141  3'  CCCTAATTTGTGGTTAGTTTCT 69146         C    TG  CTTCCA
            A                     TAGGAACTA ATCA  GA
                                  |||||||||| ||||  ||
                                  ATCTTTGAT TGGT  TT
                                     _    GT  AATCCCG
GAM1037  LOC58489  3'  GGGGGTTCTTTGGTTTT     72937        CATCAT
                                  GGAACTA     GGACTTCC
                                  |||||||     ||||||||
                                  TTTTGGT     CTTGGGGG
                                     TT____
GAM1037  LOC90670  3'  TGGAAGTCCTAAATTATTCTTG 64485        CTACATCAT
                                  TAGGAA        GGACTTCCA
                                  ||||||        |||||||||
                                  GTTCTT        CCTGAAGGT
                                     ATTAAAT__
GAM1037  LOC91069  3'  TGGAACAGGGGGTGTGGTTTCT 65407            ATGGAC
            G                     TAGGAACTACATC     TTCCA
                                  ||||||||||||      |||||
                                  GTCTTTGGTGTGG     AAGGT
                                        GGGAC_
GAM1037  LOC91442  5'  GGACTTCCATGGGACGGTGGGG 66645        TA    AT_________  ACTT
            TTCCTG                  TAGGAAC  CATC        GG    CC
                                  |||||||  ||||        ||    ||
                                  GTCCTTG  GTGG        CC    GG
                                     GG    CAGGGT    A  TTCA
GAM1038  CASP2    3'  GGTTGGACCTATTGCCA     53293       CA
                                  TGGCAA  GGGTCCAATT
                                  ||||||  ||||||||||
                                  ACCGTT  TCCAGGTTGG
                                     A_
GAM1038  CASP2    3'  GGTTGGACCTATTGCCA     53309       CA
                                  TGGCAA  GGGTCCAATT
                                  ||||||  ||||||||||
                                  ACCGTT  TCCAGGTTGG
                                     A_
GAM1038  CASP2    3'  GGTTGGACCTATTGCCA     53344       CA
                                  TGGCAA  GGGTCCAATT
                                  ||||||  ||||||||||
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                                ACCGTT  TCCAGGTTGG
                                   A_
GAM1038  CASP2    3'  GGTTGGACCTATTGCCA    8717       CA
                                TGGCAA  GGGTCCAATT
                                ||||||  ||||||||||
                                ACCGTT  TCCAGGTTGG
                                   A_
GAM1038  CHST6    3'  GAACTTCTGACCCTGTTACC   41500    C       CAATT
                                GG AACAGGGTC    GGTTC
                                || |||||||||    |||||
                                CC TTGTCCCAG    TCAAG
                                 A       TCT__
GAM1038  FVT1     3'  GATGAGTTGGACCCATTGCCA  10735      CA        G
                                TGGCAA  GGGTCCAATT GTT
                                ||||||  |||||||||| |||
                                ACCGTT  CCCAGGTTGA TAG
                                   A_        G
GAM1038  HK1      3'  GGAACCAACCAACAAACAATGC 54260      ACAGG_  CCAA
            CA                    TGGCA     GT    TTGGTTCC
                                |||||     ||    ||||||||
                                ACCGT     CA    AACCAAGG
                                   AACAAA  ACC_
GAM1038  HK1      3'  GGAACCAACCAACAAACAATGC 54263      ACAGG_  CCAA
            CA                    TGGCA     GT    TTGGTTCC
                                |||||     ||    ||||||||
                                ACCGT     CA    AACCAAGG
                                   AACAAA  ACC_
GAM1038  HK1      3'  GGAACCAACCAACAAACAATGC 54266      ACAGG_  CCAA
            CA                    TGGCA     GT    TTGGTTCC
                                |||||     ||    ||||||||
                                ACCGT     CA    AACCAAGG
                                   AACAAA  ACC_
GAM1038  HK1      3'  GGAACCAACCAACAAACAATGC 54269      ACAGG_  CCAA
            CA                    TGGCA     GT    TTGGTTCC
                                |||||     ||    ||||||||
                                ACCGT     CA    AACCAAGG
                                   AACAAA  ACC_
GAM1038  HK1      3'  GGAACCAACCAACAAACAATGC 5747       ACAGG_  CCAA
            CA                    TGGCA     GT    TTGGTTCC
                                |||||     ||    ||||||||
                                ACCGT     CA    AACCAAGG
                                   AACAAA  ACC_
GAM1038  HPGD     3'  AACCAATTTTGCCACAGCCA  7808      AACAG   CC
                                TGGC    GGT  AATTGGTT
                                ||||    |||  ||||||||
                                ACCG    CCG  TTAACCAA
                                  ACA__   TT
GAM1038  MGA      5'  AACCACGTACCCTGTTGCC   63463          CCAAT
                                GGCAACAGGGT    TGGTT
                                ||||||||||     |||||
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                                CCGTTGTCCCA    ACCAA
                                      TGC__
GAM1038 PACSIN1  3' GGAACCAGGGCTGCCCCACCGC 93884    AACA   CCAA
            C                  GGC   GGGT   TTGGTTCC
                               |||   ||||   ||||||||
                               CCG   CCCG   GACCAAGG
                                 CCAC   TCGG
GAM1038 RRM1     3' GGCTTTGCTGGACCCTGTTGC  8282          ATT_
                               GCAACAGGGTCCA   GGTT
                               ||||||||||||   ||||
                               CGTTGTCCCAGGT   TCGG
                                      CGTT
GAM1038 STARD5   3' AACCAGGCCCTGTTGCC    48314         CAAT
                               GGCAACAGGGTC   TGGTT
                               ||||||||||||   |||||
                               CCGTTGTCCCGG   ACCAA
                                     _____
GAM1038 ARHGEF9  5' GGAACCAAGCACCCCGTCCCCA 31488    CA  A   CCAA
                               TGG  AC GGGT   TTGGTTCC
                               |||  || ||||   ||||||||
                               ACC  TG CCCA   AACCAAGG
                                 CC  C   CG__
GAM1038 KIAA0444 3' GGCCCTGGACTCTGTTACCA  63002    C        ATT
                               TGG AACAGGGTCCA   GGTT
                               ||| ||||||||||   ||||
                               ACC TTGTCTCAGGT   CCGG
                                 A        C__
GAM1038 KIAA1115 3' GCCCAGCCCTGTTGCCA    30693         CCAAT   TT
                               TGGCAACAGGGT    TGG  C
                               ||||||||||||    |||  |
                               ACCGTTGTCCCG    ACC  G
                                      _____  CT
GAM1038 MGC10471  5' GGAAGCCTGTGGACCCTCTGCC 48766      AC      ATT   _
            A                   TGGCA  AGGGTCCA   GGTT CC
                               |||||  ||||||||   |||| ||
                               ACCGT  TCCCAGGT   CCGA GG
                                  C_      GT_    A
GAM1038 P114-RHO-GEF 3' GGAACCAGAGCCCCACAGCCA  31672     AACA   CCAA
                               TGGC   GGGT   TTGGTTCC
                               ||||   ||||   ||||||||
                               ACCG   CCCG   GACCAAGG
                                 ACAC   A___
GAM1038 SDC3     3' GAGCCCAGACCCTGTCTCCA  28475    CA      CAATT
                               TGG  ACAGGGTC    GGTTC
                               |||  ||||||||    |||||
                               ACC  TGTCCCAG    CCGAG
                                 TC       AC___
GAM1038 SEMA4F   3' GAACTTTAGACCCTGTAGCCA  16209     A       CAATT
                               TGGC ACAGGGTC    GGTTC
                               |||| ||||||||    |||||
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                                ACCG TGTCCCAG    TCAAG
                                  A      ATT__
GAM1038  LOC144874 5'  GAATCCAAACTCTGTTACCA  84113    C      CCAA   _
                                TGG AACAGGGT   TTGG TTC
                                ||| ||||||||   |||| |||
                                ACC TTGTCTCA   AACC AAG
                                  A      ____   T
GAM1038  LOC145815 5'  GACTGAACCTCTGTTGCCA   84518        _  CCAA TG
                                TGGCAACAG GGT   T  GTT
                                ||||||||| |||   |  |||
                                ACCGTTGTC CCA   A  CAG
                                      T  ____ GT
GAM1038  LOC147080 5'  GGACCCCCAAACCTGTTGCCA  85041         GTCCAATT
                                TGGCAACAGG      GGTTC
                                ||||||||||      |||||
                                ACCGTTGTCC      CCAGG
                                      AAACCC__
GAM1038  LOC149576 3'  GTCCGGACCCTGTTGCC     80225          AATT  TT
                                GGCAACAGGGTCC   GG  C
                                ||||||||||||   ||  |
                                CCGTTGTCCCAGG   CC  G
                                      ____  TC
GAM1038  LOC154084 5'  GGAACTTAGAGACTCCTGTTGC 87380         _  CAATT
           CA                   TGGCAACAGG GTC    GGTTCC
                                |||||||||| |||    ||||||
                                ACCGTTGTCC CAG    TCAAGG
                                      T  AGAT_
GAM1038  LOC154092 3'  AACCAAATCCTGTTGTCA    87365          CCAA
                                TGGCAACAGGGT   TTGGTT
                                ||||||||||||   ||||||
                                ACTGTTGTCCTA   AACCAA
                                      ____
GAM1038  LOC158402 5'  GGACCTCTGGACCCTCTACCA  88149    CAAC      ATT
                                TGG   AGGGTCCA  GGTTC
                                |||   ||||||||  |||||
                                ACC   TCCCAGGT  CCAGG
                                  ATC_      CT_
GAM1038  LOC221468 3'  AGTCACTTGGACCCTGTTCCA  60004    C         T  GT
                                TGG AACAGGGTCCAA TG  T
                                ||| ||||||||||| ||  |
                                ACC TTGTCCCAGGTT AC  A
                                  _         C  TG
GAM1039  ABCB9    5'  AGCACCCGCCCACCTCCA    39515        A  ___
                                TGGAGGTGG GC   TGCT
                                |||||||| ||   ||||
                                ACCTCCACC CG   ACGA
                                      _ CCC
GAM1039  COPA     3'  AGCAGCTTTCTTTCCTGTCA  16476      T    TG
                                TGACA GGAGG  GAGCTGCT
                                ||||| |||||  ||||||||
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                                ACTGT CCTTT  TTCGACGA
                                   _    CT
GAM1039  ETV6    3'  AGCCTGGGACTCCATGTCA   10542         GT__  A
                                TGACATGGAG   GG GCT
                                ||||||||||   || |||
                                ACTGTACCTC   TC CGA
                                     AGGG  _
GAM1039  FGF23   3'  CAGCTTCTTCCCAGTCA    40555     A   A  T
                                TGAC TGG GG GGAGCTG
                                |||| ||| || |||||||
                                ACTG ACC CT CTTCGAC
                                  _  _  T
GAM1039  FUT3    5'  AGCAGGCAACCACCATGTCA  5619        A   GGAG
                                TGACATGG GGT   CTGCT
                                |||||||| |||   |||||
                                ACTGTACC CCA   GACGA
                                     A   ACG_
GAM1039  GYS1    3'  AGCAGATGGTCCTCCATTTCA  89779    C      TGGAG
                                TGA ATGGAGG    CTGCT
                                ||| |||||||    |||||
                                ACT TACCTCC    GACGA
                                  T      TGGTA
GAM1039  HLA-DMA  3'  AGCAGCTTCGGCCATCCA    21500     _  _
                                TGGA GGT GGAGCTGCT
                                |||| ||| |||||||||
                                ACCT CCG CTTCGACGA
                                  A  G
GAM1039  LMO4    3'  AGTGCCAGCTCCATGCCA    23178    A     G  A
                                TG CATGGAG TGG GCT
                                || ||||||| ||| |||
                                AC GTACCTC ACC TGA
                                 C      G  G
GAM1039  LOH11CR2A 5'  AGCAGCTCCAGGGATGTC    28267      GGAGG
                                GACAT    TGGAGCTGCT
                                |||||    ||||||||||
                                CTGTA    ACCTCGACGA
                                   GGG__
GAM1039  PAX5    3'  AGCAGCTCTTTTCCAGATCA   34121     CA    T
                                TGA  TGGAGG GGAGCTGCT
                                |||  |||||| |||||||||
                                ACT  ACCTTT TCTCGACGA
                                  AG    _
GAM1039  PDE4D    3'  AGTTTTTTCACCTCCATGTCA  73963            CT
                                TGACATGGAGGTGGAG  GCT
                                ||||||||||||||||  |||
                                ACTGTACCTCCACTTT  TGA
                                          TT
GAM1039  PGK1    3'  AGCTAAAACCTTCCATGTCA   6086         _  GG_
                                TGACATGGA GGT   AGCT
                                ||||||||| |||   ||||
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                                ACTGTACCT CCA   TCGA
                                     T   AAA
GAM1039  SHC1     5'  AGCAGCCCCTCTTTCACCTCA  13120     CA     T  A
                                TGA  TGGAGG GG GCTGCT
                                |||  |||||| || ||||||
                                ACT  ACTTTC CC CGACGA
                                  CC      T  C
GAM1039  SHOX     3'  GGTGCCCACCACCATGTCA   6580         A    A  T
                                TGACATGG GGTGG GC GCT
                                |||||||| ||||| || |||
                                ACTGTACC CCACC CG TGG
                                     A    _ _
GAM1039  SSPN     3'  AGTCCTTCCCACCTCCAGTCA  18683      A       _  CT
                                TGAC TGGAGGTGG AG  GCT
                                |||| ||||||||| ||  |||
                                ACTG ACCTCCACC TT  TGA
                                  _       C  CC
GAM1039  TK2      3'  GCTGCCAACTCCATGTCA    17251          G  _
                                TGACATGGAG TGG AGC
                                |||||||||| ||| |||
                                ACTGTACCTC ACC TCG
                                     A  G
GAM1039  TLR9     3'  CGGTGCCACCTCCACACTCA   34307     CA_       A
                                TGA   TGGAGGTGG GCTG
                                |||   ||||||||| ||||
                                ACT   ACCTCCACC TGGC
                                  CAC        G
GAM1039  WDR1     3'  AGCGCCACCTCCAGATCA    18845     CA       A
                                TGA  TGGAGGTGG GCT
                                |||  ||||||||| |||
                                ACT  ACCTCCACC CGA
                                  AG        G
GAM1039  WDR1     3'  AGCGCCACCTCCAGATCA    18846     CA       A
                                TGA  TGGAGGTGG GCT
                                |||  ||||||||| |||
                                ACT  ACCTCCACC CGA
                                  AG        G
GAM1039  CITED1   5'  CAGCTCCAGCTGGCAGCATCA  15969     CA_  G_  G
                                TGA   TG  AG TGGAGCTG
                                |||   ||  || ||||||||
                                ACT   AC  TC ACCTCGAC
                                  ACG  GG  G
GAM1039  CXorf2   5'  AGCACTAGCCCCCATGTC    9625         A   GG  C
                                GACATGG GGT  AG TGCT
                                |||||||  |||  ||  ||||
                                CTGTACC CCG  TC ACGA
                                     C   A_  _
GAM1039  DKFZp434N074 5'  AGCAGCTCGATGTCATGTTA   63328         AG  G
                                TGACATGG  GT GAGCTGCT
                                ||||||||  ||  ||||||||
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                                ATTGTACT  TA CTCGACGA
                                    G_  G
GAM1039  FER1L3   3'  AGCAGGTTACGCCATGTCA   26523       AG   AG
                                TGACATGG  GTGG  CTGCT
                                ||||||||  ||||  |||||
                                ACTGTACC  CATT  GACGA
                                    G_   G_
GAM1039  FLJ12668 3'  AGCAATTCTCCTATGTCA    47154       A  T   GC
                                TGACATGG GG GGA  TGCT
                                |||||||| || |||  ||||
                                ACTGTATC CT CTT  ACGA
                                    _ _  A_
GAM1039  FLJ20174 5'  AGCAGCCCCACATCTCCA    35189      __   A
                                TGGAG  GTGG GCTGCT
                                |||||  |||| ||||||
                                ACCTC  CACC CGACGA
                                   TA   C
GAM1039  FLJ20209 3'  AGCAGCTCTGGGCTGCCA    86705    A  __
                                TGG GGT  GGAGCTGCT
                                ||| |||  |||||||||
                                ACC TCG  TCTCGACGA
                                  G  GG
GAM1039  FLJ21019 3'  AGCAGCTCTTCTCCTCCATGCC 46803    A      T__
           A                     TG CATGGAGG   GGAGCTGCT
                                || ||||||||   |||||||||
                                AC GTACCTCC   TCTCGACGA
                                 C       TCT
GAM1039  FLJ23556 3'  AGCAGCACGAGTCTCCAT    46428       __ GA
                                ATGGAGG  TG  GCTGCT
                                |||||||  ||  ||||||
                                TACCTCT  GC  CGACGA
                                    GA  A_
GAM1039  GGA2     3'  CAGCTCTGGTTCTTGCCA    57655    A  T   G
                                TG CA GGAG TGGAGCTG
                                || || |||| ||||||||
                                AC GT TCTT GTCTCGAC
                                 C  _   G
GAM1039  GGA2     3'  CAGCTCTGGTTCTTGCCA    31161    A  T   G
                                TG CA GGAG TGGAGCTG
                                || || |||| ||||||||
                                AC GT TCTT GTCTCGAC
                                 C  _   G
GAM1039  IMP13    5'  GGCCCACCTCCCTGCCA     28458    A  T      A
                                TG CA GGAGGTGG GCT
                                || || |||||||| |||
                                AC GT CCTCCACC CGG
                                 C  C       _
GAM1039  KCND1    3'  AGCAGCTGCTGCCGTGTCA   18336        A   GG
                                TGACATGG GGT  AGCTGCT
                                |||||||| |||  |||||||
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                                ACTGTGCC TCG  TCGACGA
                                    G  __
GAM1039  KIAA0172  5'  AGCATAACCTTCATGTCA    65593          GGA
                                TGACATGGAGGT  GCT
                                ||||||||||||  |||
                                ACTGTACTTCCA  CGA
                                      ATA
GAM1039  KIAA0226  3'  GGTTTCACCTGCATGTCA    64262       G
                                TGACATG AGGTGGAGCT
                                ||||||| |||||||||
                                ACTGTAC TCCACTTTGG
                                    G
GAM1039  KIAA0265  3'  AGCAGCTCCATTAGTCCA    70437     __
                                TGGA  GGTGGAGCTGCT
                                ||||  ||||||||||||
                                ACCT  TTACCTCGACGA
                                  GA
GAM1039  KIAA0747  3'  AGCAGCTCAGGCCCCCATGTC  31618       A  G_
                                GACATGG GGT  GAGCTGCT
                                ||||||| |||  ||||||||
                                CTGTACC CCG  CTCGACGA
                                    C  GA
GAM1039  KIAA0748  3'  CAGCCCCACCCCTATCTC    29612    C   A    A
                                GA ATGG GGTGG GCTG
                                || |||| ||||| ||||
                                CT TATC CCACC CGAC
                                 C   C    C
GAM1039  KIAA0888  5'  AGCAGCCGCCGGCTCCATTCA  63924    C    G  A_
                                TGA ATGGAG TGG  GCTGCT
                                ||| |||||| |||  ||||||
                                ACT TACCTC GCC  CGACGA
                                  _    G  GC
GAM1039  KIAA1190  3'  AGCAGCCTATCCCCATGTC   71641       A    A
                                GACATGG GGTGG GCTGCT
                                ||||||| ||||| ||||||
                                CTGTACC CTATC CGACGA
                                    C   _
GAM1039  KIAA1317  5'  AGCAGCTCACTACCATCCA   87208     _  __
                                TGGA GGTG  GAGCTGCT
                                |||| ||||  ||||||||
                                ACCT CCAT  CTCGACGA
                                  A   CA
GAM1039  KIAA1979  3'  AGCAGGCAGACCTTCCACATCA 89646    CA  _  GGAG
                                TGA  TGGA GGT   CTGCT
                                |||  |||| |||   |||||
                                ACT  ACCT CCA   GACGA
                                  AC   T  GACG
GAM1039  LATS1     3'  AGCCACCACCTCCATATC    60908    C       A_
                                GA ATGGAGGTGG  GCT
                                || ||||||||||  |||
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                                CT TACCTCCACC  CGA
                                 A        AC
GAM1039  MGC16279  5'  AGCAGCTCCGAGGGAATGTC   52980      GGAGG
                                GACAT    TGGAGCTGCT
                                |||||    ||||||||||
                                CTGTA    GCCTCGACGA
                                   AGGGA
GAM1039  MGC2628   3'  AGCAGGCACCCACCTCCCTGCC 44193    A  T      A_  _
           A                     TG CA GGAGGTGG  GC TGCT
                                 || || ||||||||  || ||||
                                 AC GT CCTCCACC  CG ACGA
                                  C  C       CA  G
GAM1039  P450RAI-2 3'  AGTCCCTTCCACCTCTATGCCA 39569    A          CT_
                                TG CATGGAGGTGGAG   GCT
                                || ||||||||||||   |||
                                AC GTATCTCCACCTT   TGA
                                 C           CCC
GAM1039  PIPPIN    3'  AGCAGCTCTCCTCCCCACTCA  80506    CAT_    T
                                TGA    GGAGG GGAGCTGCT
                                |||    ||||| |||||||||
                                ACT    CCTCC TCTCGACGA
                                  CACC    _
GAM1039  RNF24     3'  AGCCTCATCTCCATGTCA    24276           GA
                                TGACATGGAGGTG  GCT
                                ||||||||||||  |||
                                ACTGTACCTCTAC  CGA
                                       TC
GAM1039  SCYA22    3'  AGCAGCTGGTAATTCCATTTCA 92577     C     GTGG_
                                TGA ATGGAG     AGCTGCT
                                ||| ||||||     |||||||
                                ACT TACCTT     TCGACGA
                                  T     AATGG
GAM1039  SCYA22    3'  AGCCCTACCTCCCTGCCA    92578    A  T      A
                                TG CA GGAGGTGG GCT
                                || || |||||||| |||
                                AC GT CCTCCATC CGA
                                 C  C       C
GAM1039  SEC14L1   3'  AGCAGCTCTCGCATCCACTTCA 13002     CA   G   _
                                TGA  TGGA GTG GAGCTGCT
                                |||  |||| ||| ||||||||
                                ACT  ACCT CGC CTCGACGA
                                  TC   A   T
GAM1039  SLC38A1   5'  GGCGGACACCTCCACATC    48424    CA      GAG
                                GA  TGGAGGTG   CTGCT
                                ||  ||||||||   |||||
                                CT  ACCTCCAC   GGCGG
                                 AC       A__
GAM1039  SNURF     3'  AGCAACCCCACCTCCAGGCA  20260    ACA       AGC
                                TG   TGGAGGTGG   TGCT
                                ||   |||||||||   ||||
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                                AC   ACCTCCACC   ACGA
                                 GG_       CCA
GAM1039  SYNPO2   3'  AGCAGCTCTGGTCTGTCA    72383      T  AGGT
                                TGACA GG    GGAGCTGCT
                                ||||| ||    |||||||||
                                ACTGT CT    TCTCGACGA
                                   _ GG__
GAM1039  TCL6     5'  GGTGCCCACCACCATGCCA   40486    A    A    A  T
                                TG CATGG GGTGG GC GCT
                                || ||||| ||||| || |||
                                AC GTACC CCACC CG TGG
                                 C    A    _ _
GAM1039  TRIM2    5'  AGCCGGCCCCCCCATGTCA    31596        A  T  AGCT
                                TGACATGG GG GG    GCT
                                |||||||| || ||    |||
                                ACTGTACC CC CC    CGA
                                     _ _  GGC_
GAM1039  LOC146958 5'  AGCACACCTCACCTCCATG   84938          AGC_
                                CATGGAGGTGG    TGCT
                                ||||||||||    ||||
                                GTACCTCCACT    ACGA
                                      CCAC
GAM1039  LOC149132 5'  AGCAATCCTACCATGTCA    79923        AGGT   GC
                                TGACATGG    GGA  TGCT
                                ||||||||    |||  ||||
                                ACTGTACC    CCT  ACGA
                                     AT__   A_
GAM1039  LOC149721 5'  AGCAGCTCCACTCACCTCCTGC 80314    A  T    _____
            CA                    TG CA GGAGGT    GGAGCTGCT
                                || || ||||||    |||||||||
                                AC GT CCTCCA    CCTCGACGA
                                 C  _     CTCA
GAM1039  LOC154215 3'  AGCAGCTCCAGTGTGTC     81953       GAGG
                                GACATG    TGGAGCTGCT
                                ||||||    ||||||||||
                                CTGTGT    ACCTCGACGA
                                   G___
GAM1039  LOC154761 3'  CAGCTCCACTATAAGTC     82020     A  GA
                                GAC TG  GGTGGAGCTG
                                ||| ||  ||||||||||
                                CTG AT  TCACCTCGAC
                                  A  A_
GAM1039  LOC155072 3'  AGCAGCTCCGACCACACCAT   87652      A__  _
                                ATGG   GGT GGAGCTGCT
                                ||||   ||| |||||||||
                                TACC   CCA CCTCGACGA
                                  ACA   G
GAM1039  LOC163682 5'  AGCAGCTCAGTCACAGTCA    88395     A  GA  TG
                                TGAC TG  GG  GAGCTGCT
                                |||| ||  ||  ||||||||
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                                ACTG AC  CT  CTCGACGA
                                  _ A_  GA
GAM1039  LOC168576 5'  GGCCCACCTCCATCCCA     83593    AC        A
                                TG  ATGGAGGTGG GCT
                                ||  |||||||||| |||
                                AC  TACCTCCACC CGG
                                 CC         _
GAM1039  LOC202868 3'  AGCAGCTCCGACCACACCAT   91986      A__  _
                                ATGG   GGT GGAGCTGCT
                                ||||   ||| |||||||||
                                TACC   CCA CCTCGACGA
                                  ACA   G
GAM1039  LOC202908 5'  AGCAGTCCTACCATGTCA    90707         _  TGGA
                                TGACATGG AGG    GCTGCT
                                |||||||| |||    ||||||
                                ACTGTACC TCC    TGACGA
                                    A  _____
GAM1039  LOC221398 3'  AGCAGCACCTCCTCCATGCA   92664    A      T  A
                                TG CATGGAGG GG GCTGCT
                                || |||||||| || ||||||
                                AC GTACCTCC CC CGACGA
                                 _       T  A
GAM1039  LOC222057 5'  AGCAATCCTACCATGTCA    94344        AGGT   GC
                                TGACATGG    GGA  TGCT
                                ||||||||    |||  ||||
                                ACTGTACC    CCT  ACGA
                                    AT__   A_
GAM1039  LOC253981 3'  AGACCCGCCTCCATGTCA    97527            AG
                                TGACATGGAGGTGG  CT
                                ||||||||||||||  ||
                                ACTGTACCTCCGCC  GA
                                       CA
GAM1039  LOC254314 3'  CAGCTCCATTTCTGTGCA    98234    A
                                TG CATGGAGGTGGAGCTG
                                || ||||||||||||||||
                                AC GTGTCTTTACCTCGAC
                                 _
GAM1039  LOC255975 5'  AGCAATCCTACCATGTCA    97569        AGGT   GC
                                TGACATGG    GGA  TGCT
                                ||||||||    |||  ||||
                                ACTGTACC    CCT  ACGA
                                    AT__   A_
GAM1039  LOC256878 5'  AGCAATCCTACCATGTCA    98682        AGGT   GC
                                TGACATGG    GGA  TGCT
                                ||||||||    |||  ||||
                                ACTGTACC    CCT  ACGA
                                    AT__   A_
GAM1039  LOC257426 3'  AGCAGCCGGCTCCATG      67215        G  GA
                                CATGGAG TG  GCTGCT
                                ||||||| ||  ||||||
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                                GTACCTC GC  CGACGA
                                   G  __
GAM1040  ATRN     3'  GGAAGAGGCATTTTACCTTCC  24858      TG    GC
                                GGAAG  AGGA  GCCTCTTCC
                                |||||  ||||  |||||||||
                                CCTTC  TTTT  CGGAGAAGG
                                   CA    A_
GAM1040  C21orf33  3'  GGAAATTGCAGCTCCTCAGCCC 17381      AAG       _  CTC
            CCA                    TGGG   TGAGGAGC GC   TTCC
                                ||||   |||||||| ||   ||||
                                ACCC   ACTCCTCG CG   AAGG
                                  CCG       A  TTA
GAM1040  CPSF6    3'  GAAGAGGATCACCTTCCA    23791       A    GGAGCG
                                TGGGA GTGA     CCTCTTC
                                |||||  ||||     |||||||
                                ACCTT CACT     GGAGAAG
                                   C    A_____
GAM1040  CYLN2    3'  GGAAACCCCTCTCCTCACCTCC 14092       A       CGCCTC
            CA                     TGGGA GTGAGGAG     TTCC
                                |||||  ||||||||      ||||
                                ACCCT CACTCCTC     AAGG
                                   C       TCCCCA
GAM1040  DCTN1    5'  GGACTTGCTCCTCAGCCCCCA  43758      AAG       CC
                                TGGG   TGAGGAGCG  TCT
                                ||||   |||||||||  |||
                                ACCC   ACTCCTCGT  AGG
                                  CCG        TC
GAM1040  DTR      3'  GGCCCTCCACTCCTCATCCCCA 10456      AA       C_____
                                TGGG  GTGAGGAG     GCC
                                ||||  ||||||||     |||
                                ACCC  TACTCCTC     CGG
                                  C_       ACCTCC
GAM1040  EPHB2    3'  GGAAGTCCTTGCCCACTTCCCA 34347          A  AGCGCCT
                                TGGGAAGTG GG      CTTCC
                                |||||||||  ||      |||||
                                ACCCTTCAC CC      GAAGG
                                     _  GTTCCT_
GAM1040  HFE      3'  GAAGAGGCACCTGTCCCA    6398       AGTG   AGC
                                TGGGA    AGG   GCCTCTTC
                                |||||    |||   ||||||||
                                ACCCT    TCC   CGGAGAAG
                                   G___    A__
GAM1040  HHIP     3'  GAAGAGATTATTTGACTTCCCA 42754         G   AGCGC
                                TGGGAAGT AGG    CTCTTC
                                ||||||||  |||    ||||||
                                ACCCTTCA TTT    GAGAAG
                                     G   ATTA_
GAM1040  PMP22    3'  GAAGATACCTCCCTCCCA    6120       A T    AGCGCC
                                TGGGA G GAGG     TCTTC
                                |||||  |  ||||     |||||
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                                ACCCT C CTCC     AGAAG
                                   _ C   AT____
GAM1040  RB1      3'  AAGAGGCGCTTCTCCCC    92551     AAGT
                                GGG   GAGGAGCGCCTCTT
                                |||   ||||||||||||||
                                CCC   CTCTTCGCGGAGAA
                                 _____
GAM1040  THBD     3'  GAAGACCCTCCCCGCACCCC  6277      AA  A   CGCC
                                GGG  GTG GGAG   TCTTC
                                |||  ||| ||||   |||||
                                CCC  CGC CCTC   AGAAG
                                  CA  C   CC__
GAM1040  C11orf9  3'  AGAGCGCCCCCTACTTCCCA  26115        A A   C
                                TGGGAAGTG GG GCGC TCT
                                ||||||||| || |||| |||
                                ACCCTTCAT CC CGCG AGA
                                     C  C   _
GAM1040  C1QTNF7  3'  AGAGGCACTCTTCACTTCCCA  50000           C
                                TGGGAAGTGAGGAG GCCTCT
                                |||||||||||||| ||||||
                                ACCCTTCACTTCTC CGGAGA
                                        A
GAM1040  C1QTNF7  3'  AGAGGTGCTCCTCACTTCCCA  50001
                                TGGGAAGTGAGGAGCGCCTCT
                                ||||||||||||||||||||
                                ACCCTTCACTCCTCGTGGAGA

GAM1040  C1QTNF7  3'  AGGTGCTCCCCACTTCCCA   50002        A
                                TGGGAAGTG GGAGCGCCT
                                ||||||||| |||||||||
                                ACCCTTCAC CCTCGTGGA
                                     C
GAM1040  FLJ11856 5'  GAAGAAGTCTTCACTTCCCA  44851          AGC  C
                                TGGGAAGTGAGG   GC TCTTC
                                ||||||||||||   || |||||
                                ACCCTTCACTTC   TG AGAAG
                                       ___  A
GAM1040  FLJ20374 5'  AAGCCTCACTCCTCACGTCCCA 35545      A       CGCCT
                                TGGGA GTGAGGAG     CTT
                                ||||| ||||||||     |||
                                ACCCT CACTCCTC     GAA
                                   G       ACTCC
GAM1040  KIAA0552 3'  GGTGCACTGCCCACTTCCCA  28994        A  A___
                                TGGGAAGTG GG    GCGCC
                                ||||||||| ||    |||||
                                ACCCTTCAC CC    CGTGG
                                     _  GTCA
GAM1040  MGC20576 5'  GCCCCCTCCCCACTTCCCA   59083        A   C__
                                TGGGAAGTG GGAG   GC
                                ||||||||| ||||   ||
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                                ACCCTTCAC CCTC   CG
                                      C    CCC
GAM1040  OASIS    3'  GAAAAGGCTCCACTTCCCA    54564          A  AGC    C
                                TGGGAAGTG GG   GCCT TTC
                                ||||||||| ||   |||| |||
                                ACCCTTCAC CT   CGGA AAG
                                     _ ___    A
GAM1040  ZNF31    5'  AAGAGAGTGCTGTCCTCACTCC 65612     A       __   _
              CC                  GGG AGTGAGGA  GCGC CTCTT
                                ||| ||||||||  |||| |||||
                                CCC TCACTCCT  CGTG GAGAA
                                  C       GT    A
GAM1040  LOC146287 5'  AAGAGGCCTCAGCTTCCCA    84629         GAG   C
                                TGGGAAGT   GAG GCCTCTT
                                ||||||||   ||| |||||||
                                ACCCTTCG   CTC CGGAGAA
                                     A__   _
GAM1040  LOC146346 5'  AAGAGGCCTTCCCTTCCCA    78379         TGA    C
                                TGGGAAG   GGAG GCCTCTT
                                |||||||   |||| |||||||
                                ACCCTTC   CCTT CGGAGAA
                                     ___    C
GAM1040  LOC149194 3'  GGAGGCTGGCTTCTCACTCCCC 79985      A         __
              A                   TGGG AGTGAGGAGC  GCCTCT
                                |||| ||||||||||  ||||||
                                ACCC TCACTCTTCG  CGGAGG
                                  C         GT
GAM1040  LOC164832 3'  AAGAAGGATTCACTTCCCA    83346          GGAGCG  _
                                TGGGAAGTGA      CCT CTT
                                ||||||||||      ||| |||
                                ACCCTTCACT      GGA GAA
                                     TA_____   A
GAM1040  LOC256614 3'  GCACCTCCTCACCTCCCA     98199       A       C_
                                TGGGA GTGAGGAG  GC
                                ||||| ||||||||  ||
                                ACCCT CACTCCTC  CG
                                   C       CA
GAM1040  LOC257206 3'  AAGAGACCAGCCCGCTTCCCA  98891          A  AGCGC
                                TGGGAAGTG GG     CTCTT
                                ||||||||| ||     |||||
                                ACCCTTCGC CC     GAGAA
                                     _  GACCA
GAM1041  LILRB4    3'  ATATGCCCAGCTGCACAG     23383     _  T
                                TTG GC GCTGGGCATAT
                                ||| || ||||||||||
                                GAC CG CGACCCGTATA
                                  A  T
GAM1041  DKFZP566C243 3'  GCTCTGCAGCCAATGCAGA    31811             T
                                TCTGCATTGGCTGC GGGC
                                |||||||||||||| ||||
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                                AGACGTAACCGACG CTCG
                                       T
GAM1041  FLJ20034  3'  CATACCCAGCAGCCTGCAGA  34838      TT       CA
                                TCTGCA  GGCTGCTGGG  TATG
                                ||||||  ||||||||||  ||||
                                AGACGT  CCGACGACCC  ATAC
                                  __       __
GAM1041  KIAA0240  3'  ATGCCCCAGCCAATACA    94035    C      CT
                                TG ATTGGCTG  GGGCAT
                                || ||||||||  ||||||
                                AC TAACCGAC  CCCGTA
                                 A      __
GAM1041  LOC149837 3'  CATATGCCCCCATCAAGCAGA  85892      A   C  CT
                                TCTGC TTGG TG  GGGCATATG
                                ||||| |||| ||  |||||||||
                                AGACG AACT AC  CCCGTATAC
                                  _   _ C_
GAM1041  LOC155438 3'  CAGAACAGCCAATGCAGG    87683          __
                                TCTGCATTGGCTG  CTG
                                ||||||||||||  |||
                                GGACGTAACCGAC  GAC
                                       AA
GAM1041  LOC163682 5'  ATGCAGCAGCCATGCAGA    88397       T     GG
                                TCTGCAT GGCTGCT  GCAT
                                |||||||  |||||||  ||||
                                AGACGTA CCGACGA  CGTA
                                  _     __
GAM1042  CR1      3'  TTAATTTACTAGAAAGGCATGA 6953         C   CATC
            A                    TTCATGCCT TTTG   GTTAA
                                |||||||||  ||||   |||||
                                AAGTACGGA AGAT   TAATT
                                      A   CATT
GAM1042  TIA1     3'  TTAACTATTAAGAGGCAGAA   42104     A      TGCATC
                                TTC TGCCTCTT     GTTAA
                                |||  ||||||||     |||||
                                AAG ACGGAGAA     CAATT
                                  _       TTAT__
GAM1042  NYD-SP25  3'  AGCTTGAAAGAGGTATGAA   54301          G  TC
                                TTCATGCCTCTTT CA  GTT
                                ||||||||||||  ||  |||
                                AAGTATGGAGAAA GT  CGA
                                       _ T_
GAM1042  VAV3     3'  TGGTACAAAGAAGCAGAA    21479     A  C     C
                                TTC TGC TCTTTG ATCG
                                |||  |||  ||||||  ||||
                                AAG ACG AGAAAC TGGT
                                  _  A     A
GAM1042  LOC135932 3'  TTAACAATGGGTTGGTATGAA  76700        T_  TTG   C
                                TTCATGCC  CT   CAT GTTAA
                                ||||||||  ||   |||  |||||
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                                AAGTATGG  GG   GTA CAATT
                                    TT  ___   A
GAM1042  LOC143310 5'  TTAACTTAAAAGAGGCAT    77053         GCATC
                                ATGCCTCTTT    GTTAA
                                ||||||||||    |||||
                                TACGGAGAAA    CAATT
                                     ATT__
GAM1042  LOC199918 3'  TAACAATGCTGGTATGAA    91475        TCTTT   C
                                TTCATGCC    GCAT GTTA
                                ||||||||    |||| ||||
                                AAGTATGG    CGTA CAAT
                                    T____   A
GAM1043  BCAT1    3'  AGAAAACAAAGAGGCATACT   66782    C       AAT
                                AG ATGCCTCTT   TTTTCT
                                || |||||||||   ||||||
                                TC TACGGAGAA   AAAAGA
                                 A        AC_
GAM1043  ETF1     3'  AGAAAAATTAAATTGCTGC    17587     T  CTC
                                GCA GC   TTAATTTTTCT
                                ||| ||   ||||||||||
                                CGT CG   AATTAAAAAGA
                                  _  TTA
GAM1043  EXTL2    5'  AGAAGGATAGATGCACGCTA   9325      A   C   TA
                                TAGC TGC TCT  ATTTTTCT
                                |||| ||| |||  ||||||||
                                ATCG ACG AGA  TAGGAAGA
                                  C   T   __
GAM1043  FOXE1    3'  AGAAAAATTAAGTTAGGGCA   16777      ___
                                TGCCT   CTTAATTTTTCT
                                |||||   ||||||||||||
                                ACGGG   GAATTAAAAAGA
                                   ATT
GAM1043  FZD3     3'  AGAAAAATGCTGGAACATGCT  34257      CC   TA_
                                AGCATG  TCT   ATTTTTCT
                                ||||||  |||   ||||||||
                                TCGTAC  AGG   TAAAAAGA
                                    A_   TCG
GAM1043  RRM2B    3'  AAAAATTAAGAGTGTGTT    68429       C
                                AGCATGC TCTTAATTTTT
                                ||||||| ||||||||||
                                TTGTGTG AGAATTAAAAA
                                        _
GAM1043  ZNF132   3'  AGAAAAATTACCTCCATGCT   14286      CCTCT
                                AGCATG    TAATTTTTCT
                                ||||||    ||||||||||
                                TCGTAC    ATTAAAAAGA
                                   CTCC_
GAM1043  BAP29    3'  AGAAAAATATAAGCATGTTA   61331       CTCTTA
                                TAGCATGC     ATTTTTCT
                                ||||||||     ||||||||
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                                ATTGTACG     TAAAAAGA
                                    AATA__
GAM1043  FAM8A1    3'  AGAAAAATCTGGCATACTG   33197    C    TCTTA
                                TAG ATGCC    ATTTTTCT
                                ||| |||||    ||||||||
                                GTC TACGG    TAAAAAGA
                                  A    TC___
GAM1043  FLJ10648  3'  AGAAAAATTAGGTTCCATGC  36888     CCT
                                GCATG  CTTAATTTTTCT
                                |||||  ||||||||||||
                                CGTAC  GGATTAAAAAGA
                                   CTT
GAM1043  FLJ10970  3'  AGAAAAATCAAGATAGGCCTG 37476   T  __   A
                                CA GCC  TCTT ATTTTTCT
                                || |||  |||| ||||||||
                                GT CGG  AGAA TAAAAAGA
                                 C  AT   C
GAM1043  FLJ14735  3'  AAAAACTGATGAGGCATGC   52663       _  A
                                GCATGCCTC TTA TTTTT
                                ||||||||| ||| |||||
                                CGTACGGAG AGT AAAAA
                                     T  C
GAM1043  KIAA0830  3'  AGAAAAATAGCGGAGGCA   70266      TA_
                                TGCCTCT  ATTTTTCT
                                |||||||  ||||||||
                                ACGGAGG  TAAAAAGA
                                    CGA
GAM1043  KIAA0907  3'  AGAAAAATTAAGCTGGGCA  30862     __
                                TGCCT  CTTAATTTTTCT
                                |||||  ||||||||||||
                                ACGGG  GAATTAAAAAGA
                                   TC
GAM1043  KIAA1348  3'  AGAAACTTTGAGCCATGCTA  69116      CCT   TT
                                TAGCATG  CTTAA  TTTCT
                                |||||||  |||||  |||||
                                ATCGTAC  GAGTT  AAAGA
                                    C__    TC
GAM1043  PLAGL2    3'  AGAAATGAAAGGCATGC    70952      C  ATT
                                GCATGCCT TTA  TTTCT
                                |||||||| |||  |||||
                                CGTACGGA AGT  AAAGA
                                    A  ___
GAM1043  RNF2      3'  AGAAAAATTAAATTGGTAGT  24256   A  TC_
                                GC TGCC  TTAATTTTTCT
                                || ||||  ||||||||||
                                TG ATGG  AATTAAAAAGA
                                 _  TTA
GAM1043  LOC143146 3'  AGAAAATGGCCGAGGCATGCTA 60763         TTAAT
                                TAGCATGCCTC    TTTTCT
                                ||||||||||    ||||||
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                                ATCGTACGGAG    AAAAGA
                                     CCGGT
GAM1043  LOC146059 3'  AGAAAAGTCCAGAGATGC    78082     GC   TA
                                GCAT  CTCT  ATTTTTCT
                                ||||  ||||  ||||||||
                                CGTA  GAGA  TGAAAAGA
                                  __   CC
GAM1043  LOC151391 3'  AGAAAGATCAAAGCATGC    86511      CTC  A
                                GCATGC   TT ATTTTTCT
                                ||||||   || ||||||||
                                CGTACG   AA TAGAAAGA
                                   A__  C
GAM1043  LOC157507 5'  AAAGAAGAGGAGGCAACTA   82374    CA      AA
                                TAG  TGCCTCTT  TTTTT
                                |||  ||||||||  |||||
                                ATC  ACGGAGGA  AGAAA
                                  A_       GA
GAM1043  LOC158434 3'  AAAAATTACAAGGCATGC    88156       CT
                                GCATGCCT  TAATTTTT
                                ||||||||  ||||||||
                                CGTACGGA  ATTAAAAA
                                     AC
GAM1043  LOC220020 5'  AGAAAACAGGTGAAGGCATGC  95043       _ TTAAT
                                GCATGCCT C    TTTTCT
                                |||||||| |    ||||||
                                CGTACGGA G    AAAAGA
                                     A TGGAC
GAM1043  LOC221979 3'  AGAGTGCAGAAGGCATGC    94216       _  TA
                                GCATGCCT CT  ATTTT
                                |||||||| ||  |||||
                                CGTACGGA GA  TGAGA
                                     A  CG
GAM1043  LOC92078  3'  AGAAATCCGAAGAGGCAGCTA  68588     A      AATT
                                TAGC TGCCTCTT    TTTCT
                                |||| ||||||||    |||||
                                ATCG ACGGAGAA    AAAGA
                                  _       GCCT
GAM1043  LOC92080  5'  AGAAAAATCAAGACCATGTTA  68617       CC   A
                                TAGCATG  TCTT ATTTTTCT
                                |||||||  |||| ||||||||
                                ATTGTAC  AGAA TAAAAAGA
                                    C_   C
GAM1044  SCAMP1    3'  GCTAAATAAATATTCTCC    54500    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1044  SCAMP1    3'  GCTAAATAAATATTCTCC    54501    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
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                                CCT TTATAA TAAATCG
                                  C     A
GAM1044  NX-17    3'  TGAATATCAGCCCCTAATA   40706        ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM1044  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
             TA                   TATTAGGGATAATATTCATTTAGC
                                  ||||||||||||||||||||||||
                                  ATAATCCCTATTATAAGTAAATCG

GAM1045  BCAT1    3'  AGAAAACAAAGAGGCATACT   66782    C       AAT
                                AG ATGCCTCTT   TTTTCT
                                || |||||||||   ||||||
                                TC TACGGAGAA   AAAAGA
                                 A        AC_
GAM1045  ETF1     3'  AGAAAAATTAAATTGCTGC    17587     T  CTC
                                GCA GC   TTAATTTTTCT
                                ||| ||   ||||||||||
                                CGT CG   AATTAAAAAGA
                                  _  TTA
GAM1045  EXTL2    5'  AGAAGGATAGATGCACGCTA   9325      A   C   TA
                                TAGC TGC TCT  ATTTTTCT
                                |||| ||| |||  ||||||||
                                ATCG ACG AGA  TAGGAAGA
                                  C   T   __
GAM1045  FOXE1    3'  AGAAAAATTAAGTTAGGGCA   16777      ___
                                TGCCT   CTTAATTTTTCT
                                |||||   ||||||||||||
                                ACGGG   GAATTAAAAAGA
                                   ATT
GAM1045  FZD3     3'  AGAAAAATGCTGGAACATGCT  34257       CC   TA_
                                AGCATG  TCT   ATTTTTCT
                                ||||||  |||   ||||||||
                                TCGTAC  AGG   TAAAAAGA
                                    A_   TCG
GAM1045  RRM2B    3'  AAAAATTAAGAGTGTGTT    68429       C
                                AGCATGC TCTTAATTTTT
                                ||||||| ||||||||||
                                TTGTGTG AGAATTAAAAA
                                        _
GAM1045  ZNF132   3'  AGAAAAATTACCTCCATGCT   14286       CCTCT
                                AGCATG    TAATTTTTCT
                                ||||||    ||||||||||
                                TCGTAC    ATTAAAAAGA
                                   CTCC_
GAM1045  BAP29    3'  AGAAAAATATAAGCATGTTA   61331        CTCTTA
                                TAGCATGC     ATTTTTCT
                                ||||||||     ||||||||
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                                ATTGTACG     TAAAAAGA
                                    AATA__
GAM1045  FAM8A1    3'  AGAAAAATCTGGCATACTG   33197    C    TCTTA
                                TAG ATGCC    ATTTTTCT
                                ||| |||||    ||||||||
                                GTC TACGG    TAAAAAGA
                                  A    TC___
GAM1045  FLJ10648  3'  AGAAAAATTAGGTTCCATGC  36888     CCT
                                GCATG  CTTAATTTTTCT
                                |||||  ||||||||||||
                                CGTAC  GGATTAAAAAGA
                                   CTT
GAM1045  FLJ10970  3'  AGAAAAATCAAGATAGGCCTG 37476   T  __   A
                                CA GCC  TCTT ATTTTTCT
                                || |||  |||| ||||||||
                                GT CGG  AGAA TAAAAAGA
                                 C  AT   C
GAM1045  FLJ14735  3'  AAAAACTGATGAGGCATGC   52663       _  A
                                GCATGCCTC TTA TTTTT
                                ||||||||| ||| |||||
                                CGTACGGAG AGT AAAAA
                                     T  C
GAM1045  KIAA0830  3'  AGAAAAATAGCGGAGGCA   70266      TA_
                                TGCCTCT  ATTTTTCT
                                |||||||  ||||||||
                                ACGGAGG  TAAAAAGA
                                    CGA
GAM1045  KIAA0907  3'  AGAAAAATTAAGCTGGGCA  30862     __
                                TGCCT  CTTAATTTTTCT
                                |||||  ||||||||||||
                                ACGGG  GAATTAAAAAGA
                                   TC
GAM1045  KIAA1348  3'  AGAAACTTTGAGCCATGCTA  69116      CCT   TT
                                TAGCATG  CTTAA  TTTCT
                                |||||||  |||||  |||||
                                ATCGTAC  GAGTT  AAAGA
                                    C__    TC
GAM1045  PLAGL2    3'  AGAAATGAAAGGCATGC    70952       C  ATT
                                GCATGCCT TTA  TTTCT
                                |||||||| |||  |||||
                                CGTACGGA AGT  AAAGA
                                    A  ___
GAM1045  RNF2      3'  AGAAAAATTAAATTGGTAGT  24256   A  TC_
                                GC TGCC  TTAATTTTTCT
                                || ||||  ||||||||||
                                TG ATGG  AATTAAAAAGA
                                 _  TTA
GAM1045  LOC143146 3'  AGAAAATGGCCGAGGCATGCTA 60763         TTAAT
                                TAGCATGCCTC    TTTTCT
                                ||||||||||    ||||||
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                                ATCGTACGGAG    AAAAGA
                                     CCGGT
GAM1045  LOC146059 3'  AGAAAAGTCCAGAGATGC    78082     GC   TA
                                GCAT  CTCT  ATTTTTCT
                                |||| |||| ||||||||
                                CGTA  GAGA  TGAAAAGA
                                  __   CC
GAM1045  LOC151391 3'  AGAAAGATCAAAGCATGC    86511      CTC  A
                                GCATGC   TT ATTTTTCT
                                ||||||  || ||||||||
                                CGTACG   AA TAGAAAGA
                                   A__  C
GAM1045  LOC157507 5'  AAAGAAGAGGAGGCAACTA   82374    CA      AA
                                TAG  TGCCTCTT  TTTTT
                                |||  ||||||||  |||||
                                ATC  ACGGAGGA  AGAAA
                                  A_      GA
GAM1045  LOC158434 3'  AAAAATTACAAGGCATGC    88156       CT
                                GCATGCCT  TAATTTTT
                                ||||||||  ||||||||
                                CGTACGGA  ATTAAAAA
                                     AC
GAM1045  LOC220020 5'  AGAAAACAGGTGAAGGCATGC  95043       _ TTAAT
                                GCATGCCT C    TTTTCT
                                |||||||| |    ||||||
                                CGTACGGA G    AAAAGA
                                     A TGGAC
GAM1045  LOC221979 3'  AGAGTGCAGAAGGCATGC    94216       _  TA
                                GCATGCCT CT  ATTTT
                                |||||||| ||  |||||
                                CGTACGGA GA  TGAGA
                                     A  CG
GAM1045  LOC92078  3'  AGAAATCCGAAGAGGCAGCTA  68588     A      AATT
                                TAGC TGCCTCTT   TTTCT
                                |||| ||||||||   |||||
                                ATCG ACGGAGAA   AAAGA
                                  _      GCCT
GAM1045  LOC92080  5'  AGAAAAATCAAGACCATGTTA  68617       CC   A
                                TAGCATG  TCTT ATTTTTCT
                                |||||||  |||| ||||||||
                                ATTGTAC  AGAA TAAAAAGA
                                    C_   C
GAM1046  DLEC1     3'  CATCTGGCCCTCCCTTG     24716      A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                  C    G  _
GAM1046  DLEC1     3'  CATCTGGCCCTCCCTTG     24728      A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
```

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                                GTTCC TCCCG TC TAC
                                  C    G  _
GAM1046 PIP5K1A  3' TATCCCACCCTGCCTTGATA  14520       A   CA  C
                                TATCAAGG AGGG  GG GTG
                                |||||||| ||||  || |||
                                ATAGTTCC TCCC  CC TAT
                                    G   A_  C
GAM1046 SOX11    3' ACCCACCCCCCCTTGGTA    13308       AA   CA  C
                                TATCAAGG  GGG  GG GT
                                ||||||||  |||  || ||
                                ATGGTTCC  CCC  CC CA
                                    CC   A_  _
GAM1046 CHL1     3' TGTTACCTTTCCTCAATA    22768     CA      CA
                                TAT  AGGAAGGG  GGCG
                                |||  ||||||||  ||||
                                ATA  TCCTTTCC  TTGT
                                  AC       A_
GAM1046 EPB41L1  3' CATTCTGCCCTTCCCTGA    71104     A        C
                                TCA GGAAGGGCAGG GTG
                                ||| ||||||||||| |||
                                AGT CCTTCCCGTCT TAC
                                  C         _
GAM1046 FLJ00060 3' CATACCCCCTGCCCTCCTCTGA 61741     _   A      CGTG
                                TCA AGGA GGGCAGG   ATG
                                ||| |||| |||||||   |||
                                AGT TCCT CCCGTCC   TAC
                                  C   _      CCCA
GAM1046 FLJ10898 5' CACCACAGCCCTTTCTCAATA  60126     CA       AGGC
                                TAT  AGGAAGGGC   GTG
                                |||  |||||||||   |||
                                ATA  TCTTTCCCG   CAC
                                  AC       ACAC
GAM1046 FLJ22557 3' ATCATCCCATCCTTAATA    45581     C    A   CAGGC
                                TAT AAGGA GGG    GTGAT
                                ||| ||||| |||    |||||
                                ATA TTCCT CCC    TACTA
                                  A    A  _____
GAM1046 KIAA0574 3' CATCCCCTGCCCTCCCCTGA   69808     A  A      CGT
                                TCA GG AGGGCAGG   GATG
                                ||| || ||||||||   ||||
                                AGT CC TCCCGTCC   CTAC
                                  C  C       C__
GAM1046 KIAA0632 3' CACCTCAGAAACCCTTCCTTGA 32071          CA___  C
                                TCAAGGAAGGG    GG GTG
                                ||||||||||    || |||
                                AGTTCCTTCCC    CT CAC
                                      AAAGA  C
GAM1046 KIAA1045 3' CATCACATGTCCTTCC      71599         GGC
                                GGAAGGGCA   GTGATG
                                |||||||||   ||||||
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                                CCTTCCTGT   CACTAC
                                    A__
GAM1046  KIAA1354  5'  CAGTGACTGCCTTCCCTTGATA 61572        A      G  _
                                TATCAAGG AGGGCAG CG TG
                                |||||||| ||||||| || ||
                                ATAGTTCC TTCCGTC GT AC
                                    C      A  G
GAM1046  MGC20460  5'  CACCGCCTCCTACCCTTCTT   54901        C___    _
                                AGGAAGGG    AGGCG TG
                                ||||||||    ||||| ||
                                TTCTTCCC    TCCGC AC
                                    ATCC     C
GAM1046  LOC158476 3'  CACGCCCGCCCCCCCCCATTGA  88186     _ AA_   A
                                TCAA GG   GGGC GGCGTG
                                |||| ||   |||| ||||||
                                AGTT CC   CCCG CCGCAC
                                  A  CCC    C
GAM1046  LOC90459  3'  CACACCCGCCTAATTTTTG    63550       A_   A  C
                                CAAGGA  GGGC GG GTG
                                ||||||  |||| || |||
                                GTTTTT  TCCG CC CAC
                                   AA    C  A
GAM1047  ADAMTS3   3'  ACAATGCATCTGACTGCAA    27270        _  A T   C
                                TTGCAGTC GA G CGT GT
                                |||||||| || | ||| ||
                                AACGTCAG CT C GTA CA
                                    T  A _   A
GAM1047  NICN1     3'  TGGCGACTTCATCTGCAA    51261       TC
                                TTGCAG  GAAGTCGTCG
                                ||||||  ||||||||||
                                AACGTC  CTTCAGCGGT
                                   TA
GAM1047  PNMA5     3'  ACTGTGACCTCGACTGCAG    73967         A    TC
                                TTGCAGTCGA GTCG  GT
                                |||||||||| ||||  ||
                                GACGTCAGCT CAGT  CA
                                     C    GT
GAM1047  LOC152845 5'  GCGGTGACCTCAGCTGCAA    60958       C  A   GT
                                TTGCAGT GA GTC  CGT
                                ||||||| || |||  |||
                                AACGTCG CT CAG  GCG
                                    A  C   TG
GAM1048  AMD1      3'  CGCAAAAAGAGAACAC      9682        CC     C
                                GTGTTC  CTTTT TGCG
                                ||||||  ||||| ||||
                                CACAAG  GAAAA ACGC
                                   A_    _
GAM1048  APRT      3'  GCTGCCCACAGGGAACAC     6666         CTTTTC  C
                                GTGTTCCC     TG GCAGC
                                ||||||||     || |||||
```

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                                CACAAGGG     AC CGTCG
                                     AC____  C
GAM1048 AR      5'  GGCTGCACGCGGAGAGAAC   5276      CCCT      __
                                GTTC   TTTCTGC  GCAGCC
                                ||||   |||||||  ||||||
                                CAAG   AGAGGCG  CGTCGG
                                  ____      CA
GAM1048 CD63    5'  GCCGCGGCGGGAGAGGAACGC  10117       CC      _ A
                                GTGTTCC  TTTTCTGC GC GC
                                |||||||  |||||||| || ||
                                CGCAAGG  AGAGGGCG CG CG
                                   __       G  C
GAM1048 DGKG    5'  GGCTGCGCAGGCGGGAAGAC   9042    G    CTTT
                                GT TTCCC    TCTGCGCAGCC
                                || |||||    ||||||||||
                                CA AAGGG    GGACGCGTCGG
                                 G    C___
GAM1048 DTNA    3'  GGCCACACAGAGGAGGAAGAC  53208    CC       CGCA
                                GTT  CCTTTTCTG    GCC
                                |||  |||||||||    |||
                                CAG  GGAGGAGAC    CGG
                                  AA        ACAC
GAM1048 DTNA    3'  GGCCACACAGAGGAGGAAGAC  53276    CC       CGCA
                                GTT  CCTTTTCTG    GCC
                                |||  |||||||||    |||
                                CAG  GGAGGAGAC    CGG
                                  AA        ACAC
GAM1048 DUOX1   5'  GGCCGCAGCTGGAAGAGGAAAA 34292    CC      _ _ A
            C                    GTT  CCTTTTCT GC GC GCC
                                |||  |||||||| || || |||
                                CAA  GGAGAAGG CG CG CGG
                                  AA       T  A  C
GAM1048 FCN2    3'  GGCTGCACACCTGGTGGGAGAA 32346       _   TTTTC_  C
            CAC                    GTGTTC CCC     TG GCAGCC
                                |||||| |||     || ||||||
                                CACAAG GGG     AC CGTCGG
                                   A   TGGTCC  A
GAM1048 MGAM    3'  GCAAAGAAAAGGCAAACAC   72811      CC       GC
                                GTGTT  CCTTTTCT  GC
                                |||||  ||||||||  ||
                                CACAA  GGAAAAGA  CG
                                   AC       AA
GAM1048 PITX2   3'  GCTATATAGAGAAAAGGAAACC 6156     __   CC      CGC
            AC                    GTG  TTCC  TTTTCTG   AGC
                                |||  ||||  |||||||  |||
                                CAC  AAGG  AAGAGAT   TCG
                                  CA   AA      ATA
GAM1048 PPP1R3C 3'  GGCTATGGAAAAGAAAGACAC  19424      CCC       CGC
                                GTGTT   CTTTTCTG   AGCC
                                |||||   ||||||||   ||||
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                                CACAG  GAAAAGGT  TCGG
                                  AAA      A__
GAM1048 RXRG    5' GCTGCACAGGAGAGGAACAT  23611       CC     C
                                GTGTTCC  TTTTCTG GCAGC
                                |||||||  ||||||| |||||
                                TACAAGG  AGAGGAC CGTCG
                                   __      A
GAM1048 SDC4    3' GCTGCGGTGAGGGGAAC    12998        TTCTG
                                GTTCCCCTT   CGCAGC
                                |||||||||   ||||||
                                CAAGGGGAG   GCGTCG
                                    TG___
GAM1048 SORCS2  3' GGCCACAGGACAAGGGGAGCAC 40804          _    CGCA
                                GTGTTCCCCTT TTCTG   GCC
                                |||||||||| |||||   |||
                                CACGAGGGGAA AGGAC   CGG
                                    C    AC__
GAM1048 TLX1    3' CTGCACCCAGGAGGGGAACAC  19821         TT  C__
                                GTGTTCCCCTT  CTG  GCAG
                                ||||||||||  |||  ||||
                                CACAAGGGGAG  GAC  CGTC
                                   __  CCA
GAM1048 DKFZp586I021 3' GCCACGCCAGGAGGAGGACAC  51083      C    CT  CA
                                GTGTTC CCTTTT  GCG  GC
                                |||||| ||||||  |||  ||
                                CACAGG GGAGGA  CGC  CG
                                  A     C_  AC
GAM1048 DKFZP586I2223 3' GGCTGCACAGAGGGGAACAT  55768       TTT   C
                                GTGTTCCCC   TCTG GCAGCC
                                |||||||||   |||| ||||||
                                TACAAGGGG   AGAC CGTCGG
                                   ___   A
GAM1048 DKFZP586I2223 3' GGCTGCACAGAGGGGAACAT  55770       TTT   C
                                GTGTTCCCC   TCTG GCAGCC
                                |||||||||   |||| ||||||
                                TACAAGGGG   AGAC CGTCGG
                                   ___   A
GAM1048 DKFZP586I2223 3' GGCTGCACAGAGGGGAACAT  31880       TTT   C
                                GTGTTCCCC   TCTG GCAGCC
                                |||||||||   |||| ||||||
                                TACAAGGGG   AGAC CGTCGG
                                   ___   A
GAM1048 FLJ10904  3' GCCAAAAAAGGGAACAT    37382       C   C  C
                                GTGTTCCC TTTT TG GC
                                |||||||| |||| || ||
                                TACAAGGG AAAA AC CG
                                   _   A  _
GAM1048 FLJ23554  3' GTGGAGAAAAGAAACAC    46071      CCC     G
                                GTGTT   CTTTTCT CGC
                                |||||   ||||||| |||
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                                CACAA   GAAAAGA GTG
                                  A__      G
GAM1048  HSPC155   3'  GGCTGCACAGGGAAGGGAAAGA 33522    G  C    TT   C
             C                     GT TT CCCTT  CTG GCAGCC
                                   || || |||||  ||| ||||||
                                   CA AA GGGAA  GAC CGTCGG
                                    G  A    GG   A
GAM1048  KIAA0649  3'  GGCTGCAAGGAAGGGAAACA   29714     C     T  GC
                                   TGTT CCCTTT CT  GCAGCC
                                   |||| |||||| ||  ||||||
                                   ACAA GGGAAG GA  CGTCGG
                                     A     _ A_
GAM1048  KIAA0711  5'  GCTGCAGAGAGAGACAC     30150      CCCCT    GC
                                   GTGTT    TTTCT  GCAGC
                                   |||||    |||||  |||||
                                   CACAG    AGAGA  CGTCG
                                     _____    GA
GAM1048  KIAA1303  3'  CGCTGAAAGGGGAAACAC    66604      C       T
                                   GTGTT CCCTTTTC GCG
                                   |||||| |||||||| |||
                                   CACAA GGGGAAAG CGC
                                     A       T
GAM1048  KIAA1317  3'  GCAGGAAAAGGGGAAGAC    87213    G         GC
                                   GT TTCCCCTTTTCT  GC
                                   || ||||||||||||  ||
                                   CA AAGGGGAAAAGG  CG
                                    G          A_
GAM1048  KIAA1706  5'  GCCGCAGGTGGAAGAGGAAC   94367      C   __     CA
                                   GTTCC CTTT  TCTGCG  GC
                                   ||||| ||||  ||||||  ||
                                   CAAGG GAAG  GGACGC  CG
                                     A   GT     __
GAM1048  KIAA1908  5'  GGCTGCGCCCCTGGGGACAC   73792     T    TTTTCT
                                   GTGT CCCC     GCGCAGCC
                                   |||| ||||     ||||||||
                                   CACA GGGG     CGCGTCGG
                                     _   TCCC__
GAM1048  NTPBP     3'  GCCAAGGAAAAGGGAAACAT   24393      C       GC_
                                   GTGTT CCCTTTTCT   GC
                                   ||||| |||||||||   ||
                                   TACAA GGGAAAAGG   CG
                                     A        AAC
GAM1048  NUDT11    3'  GGCTGCTATTAGAGGGGAACAC 60659          TC  C
                                   GTGTTCCCCTTT  TG GCAGCC
                                   ||||||||||||  || ||||||
                                   CACAAGGGGAGA  AT CGTCGG
                                          TT  _
GAM1048  PDZD2     5'  CTGCGAAAAAGGGGAA      81722          CTG
                                   TTCCCCTTTT   CGCAG
                                   ||||||||||   |||||
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                                AAGGGGAAAA  GCGTC
                                     A__
GAM1048 PRO0899  5' GCCGCACAGCAGGGGAGAAAC 38311   G_     TTT  C  A
                                GT  TTCCCCT  CTG GC GC
                                ||  |||||||  ||| || ||
                                CA  GAGGGGA  GAC CG CG
                                 AA      C__  A  C
GAM1048 SARM     3' GGCCACAGCAGAAAAGAGAGCA 31298      CC       GCA_
             C                   GTGTTC  CTTTTCTGC   GCC
                                ||||||  |||||||||   |||
                                CACGAG  GAAAAGACG   CGG
                                   A_       ACAC
GAM1048 LOC139904 5' GGCCGCGCTGGAGGGGTACAC  76368     T     TCT   A
                                GTGT CCCCTTT  GCGC GCC
                                |||| |||||||  |||| |||
                                CACA GGGGAGG  CGCG CGG
                                  T      T__   C
GAM1048 LOC253430 5' GGCTGCGGCGGCAGAGGAACA  97974      C  TTT   _
                                TGTTCC CT   CTGC GCAGCC
                                |||||| ||   |||| ||||||
                                ACAAGG GA   GGCG CGTCGG
                                   A  C__   G
GAM1048 LOC256015 5' GTAAGAAAAGGAAAACAC    99454      CC       GC
                                GTGTT  CCTTTTCT  GC
                                |||||  ||||||||  ||
                                CACAA  GGAAAAGA  TG
                                   AA       A_
GAM1048 LOC257235 3' GCAAGAAAAGAAAAGGAACAC  98842      C___     GC
                                GTGTTCC   CTTTTCT  GC
                                |||||||   |||||||  ||
                                CACAAGG   GAAAAGA  CG
                                    AAAA      A_
GAM1048 LOC54466  3' CTGAGTAGAGAGGAACAC    39173       CCT     G
                                GTGTTCC   TTTCTGC CAG
                                |||||||   ||||||| |||
                                CACAAGG   AGAGATG GTC
                                   ___       A
GAM1048 LOC86651  5' GGCTACAAGGAGAAAAGGAACA 69311      CC     GCGC
                                TGTTCC  TTTTCT   AGCC
                                ||||||  ||||||   ||||
                                ACAAGG  AAGAGG   TCGG
                                   AA     AACA
GAM1048 LOC91813  5' GCTACGCTGGGGAACAT     67844        TTTTCT   C
                                GTGTTCCCC     GCG AGC
                                |||||||||     ||| |||
                                TACAAGGGG     CGC TCG
                                     T_____   A
GAM1049 ADAM19   3' GCACTTTCCTGGTGCCC     53841          CTTG
                                GGGCATCAGGAAA   GC
                                ||||||||||||   ||
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                                CCCGTGGTCCTTT  CG
                                      CA__
GAM1049 CADPS   3' CTGATTTCCTGATGTCC   65823          C TG
                                GGGCATCAGGAAA T  G
                                |||||||||||| |  |
                                CCTGTAGTCCTTT A  C
                                      _ GT
GAM1049 CSNK1A1  5' GTGTTCCGTTTCCTGCCGCCC 10313    AT      TT GC
                                GGGC  CAGGAAAC  G  CAC
                                ||||  ||||||||  |  |||
                                CCCG  GTCCTTTG  C  GTG
                                  CC      C_ TT
GAM1049 EHD3    3' TGTGGCCCTCACTGATGCCC  28206       _ AACTT
                                GGGCATCAG GA    GGCCACA
                                ||||||||| ||    |||||||
                                CCCGTAGTC CT    CCGGTGT
                                     A  C____
GAM1049 FKBP2   5' CTGTGGCCTCCCCTGACCCCC 55120    CA    AAACTT
                                GGG  TCAGG     GGCCACAG
                                |||  |||||     ||||||||
                                CCC  AGTCC     CCGGTGTC
                                  CC    CCT___
GAM1049 MBD3    3' CTGCGGCCAGTCCCTGGTGCCC 15391        AA   T    A
                                GGGCATCAGG  ACT GGCC CAG
                                ||||||||||  ||| |||| |||
                                CCCGTGGTCC  TGA CCGG GTC
                                     C_  _   C
GAM1049 MGAT4B  3' CTGTGGCCAGCCCTGAAGCCC  27340     A    AAAC
                                GGGC TCAGG   TTGGCCACAG
                                |||| |||||   ||||||||||
                                CCCG AGTCC   GACCGGTGTC
                                  A    C___
GAM1049 MGAT4B  3' CTGTGGCCAGCCCTGAAGCCC  55027     A    AAAC
                                GGGC TCAGG   TTGGCCACAG
                                |||| |||||   ||||||||||
                                CCCG AGTCC   GACCGGTGTC
                                  A    C___
GAM1049 NPR1    3' TGTGGATTCCTGATCCC    88743    C      ACTTGG
                                GGG ATCAGGAA     CCACA
                                ||| ||||||||     |||||
                                CCC TAGTCCTT     GGTGT
                                  _      A_____
GAM1049 TNXB    5' CCAGAGCTCGCTGATGCCC   51633        _ AAC
                                GGGCATCAG GA   TTGG
                                ||||||||| ||   ||||
                                CCCGTAGTC CT   GACC
                                     G  CGA
GAM1049 WASF3   3' CTGCTCCTTTAGTTTCCTGACA 22811    CA       T__ CCA
            CCT                 GGG  TCAGGAAACT   GG   CAG
                                |||  ||||||||||   ||   |||
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                                TCC  AGTCCTTTGA   CC   GTC
                                  AC         TTT  TC_
GAM1049  BM039     5'  GTGCAGTCCCCTGTGCCC    38049      T   AA   TG  C
                                GGGCA CAGG  ACT  GC AC
                                ||||| ||||  |||  || ||
                                CCCGT GTCC  TGA  CG TG
                                  _    CC   __ _
GAM1049  C21orf18  3'  CCATAGTTTCCTGACCC     34303     CA        _
                                GGG  TCAGGAAACT TGG
                                |||  |||||||||| |||
                                CCC  AGTCCTTTGA ACC
                                  __         T
GAM1049  CPA5      3'  CTGTGGCTCCTCCCGAAACCC  55367     CA  A   AACTT
                                GGG  TC GGA    GGCCACAG
                                |||  || |||    ||||||||
                                CCC  AG CCT    TCGGTGTC
                                  AA  C   CC___
GAM1049  DJ37E16.5 3'  TGTGGCCAAGCCCCACCC    40100     CATCA  AAA
                                GGG    GG   CTTGGCCACA
                                |||    ||   ||||||||||
                                CCC    CC   GAACCGGTGT
                                  A_____  CC_
GAM1049  FLJ13725  3'  CCATGGGTTCCTGGTGCCC    68830           A  _
                                GGGCATCAGGAA CT TGG
                                |||||||||||| || |||
                                CCCGTGGTCCTT GG ACC
                                       G  T
GAM1049  FLJ21347  3'  CTGTGGCCATCCCTGAGCACC  43384    _ A    AAACT
                                GG GC TCAGG    TGGCCACAG
                                || || |||||    |||||||||
                                CC CG AGTCC    ACCGGTGTC
                                  A  _    CT___
GAM1049  HIP-55    3'  CTGTGGCCAAGCCCTGAGTGGC 26774    G  _    AAA
              C                  GG CA TCAGG   CTTGGCCACAG
                                || || |||||   ||||||||||
                                CC GT AGTCC   GAACCGGTGTC
                                  G  G    C__
GAM1049  jdp2      3'  GCGGGGCCCTGATGCCC     56202          AAA   G
                                GGGCATCAGG   CTT GC
                                |||||||||   ||| ||
                                CCCGTAGTCC   GGG CG
                                      C__   G
GAM1049  KIAA0295  3'  TGGCAGATCCTGATGCCT    68677          AACTTG
                                GGGCATCAGGA     GCCA
                                ||||||||||     ||||
                                TCCGTAGTCCT     CGGT
                                       AGA___
GAM1049  KIAA0435  3'  TGTGAGCCCCCTGATGCC    29668         AAACTT  _
                                GGCATCAGG     GGC CACA
                                |||||||||     ||| ||||
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                              CCGTAGTCC     CCG GTGT
                                   C_____   A
GAM1049 KIAA0978 3' GCCAGGTTGCCCGATGCCC   70995       A  A
                              GGGCATC GG AACTTGGC
                              ||||||| || ||||||||
                              CCCGTAG CC TTGGACCG
                                  C  G
GAM1049 KIAA1171 3' TGGCCAAGCCTGGCGTTGCCT 89348      ___    AAA
                              GGGCA  TCAGG  CTTGGCCA
                              |||||  |||||  ||||||||
                              TCCGT  GGTCC  GAACCGGT
                                TGC   ___
GAM1049 MGC15416 3' TGGCCAAGGGCCGAACCC    57348    CA  A  AAA
                              GGG  TC GG  CTTGGCCA
                              |||  || ||  ||||||||
                              CCC  AG CC  GAACCGGT
                                A_ _  GG_
GAM1049 MGC15416 3' TGGCCAAGGGCCGAACCC    51407    CA  A  AAA
                              GGG  TC GG  CTTGGCCA
                              |||  || ||  ||||||||
                              CCC  AG CC  GAACCGGT
                                A_ _  GG_
GAM1049 MGC16703 3' GTGGCCAAGATCGCCAGTGCCC 73497      CA  AAA_
                              GGGCAT  GG   CTTGGCCAC
                              ||||||  ||   |||||||||
                              CCCGTG  CC   GAACCGGTG
                                 A_  GCTA
GAM1049 MGC20255 3' GTGGCCAAGCCTGAAGGACCC 54543    CA__    AAA
                              GGG   TCAGG  CTTGGCCAC
                              |||   |||||  |||||||||
                              CCC   AGTCC  GAACCGGTG
                                AGGA   ___
GAM1049 MGC3035  5' GCCAAAACCCCCTGATGCTC  44403       AAAC_
                              GGGCATCAGG    TTGGC
                              ||||||||||    |||||
                              CTCGTAGTCC    AACCG
                                   CCCAA
GAM1049 NR5A1    3' TGGTTCATTTTCTGATGCCC  18276         CTT
                              GGGCATCAGGAAA  GGCCA
                              ||||||||||||  |||||
                              CCCGTAGTCTTTT  TTGGT
                                     AC_
GAM1049 PCDH16   5' CTGTGGCCTGAGCCCTGCACCC 73183    CAT   AAA  _
                              GGG  CAGG  CTT GGCCACAG
                              |||  ||||  ||| ||||||||
                              CCC  GTCC  GAG CCGGTGTC
                                AC_   C__  T
GAM1049 PLPL     3' TTAAATTTCCTGGTACCC    39821    C      C
                              GGG ATCAGGAAA TTGG
                              ||| ||||||||| ||||
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                                CCC TGGTCCTTT AATT
                                  A       A
GAM1049  PME-1    3'  CTGTGGCCTGTCCCTATTGCCC 32868      TC   AA  TT
                                GGGCA  AGG  AC  GGCCACAG
                                |||||  |||  ||  ||||||||
                                CCCGT  TCC  TG  CCGGTGTC
                                   TA  C_  T_
GAM1049  SEMA4G   5'  CTGTGGCTGGGACCCTGGCACC 96329     CA    AAA  TG
            C                    GGG  TCAGG   CT  GCCACAG
                                |||  |||||   ||  |||||||
                                CCC  GGTCC   GG  CGGTGTC
                                  AC    CA_  GT
GAM1049  SLC2A10  3'  GCGCATCTCTTCCTGATTCCC  48554     C       ACT_  _
                                GGG ATCAGGAA    TG GC
                                ||| ||||||||    || ||
                                CCC TAGTCCTT    AC CG
                                  T       CTCT  G
GAM1049  TXNL2    3'  GCAGTAGCTTCCTGATGCCT   22580          A  TG_
                                GGGCATCAGGAA CT   GC
                                ||||||||||| ||   ||
                                TCCGTAGTCCTT GA   CG
                                      C  TGA
GAM1049  LOC127435 3'  CTGTGGCCAGGTGCCTGCCACC 76608     CAT    AA
            C                    GGG   CAGG  ACTTGGCCACAG
                                |||   ||||  ||||||||||||
                                CCC   GTCC  TGGACCGGTGTC
                                  ACC    G_
GAM1049  LOC131827 3'  TGTGTCTCTCCTGACACTC    75504     CA     AACTT   C
                                GGG  TCAGGA     GGC ACA
                                |||  ||||||     ||| |||
                                CTC  AGTCCT     CTG TGT
                                  AC     CT___   _
GAM1049  LOC145623 5'  CTGCAGCCAAACTTTTCTGGAC 84391     CA       C_    CA
            C                    GG  TCAGGAAA  TTGGC  CAG
                                ||  ||||||||  |||||  |||
                                CC  GGTCTTTT  AACCG  GTC
                                 A_       CA    AC
GAM1049  LOC146336 5'  TGTGGCCGCCCCTGCACCC    78376     CAT    AAACT
                                GGG   CAGG    TGGCCACA
                                |||   ||||    ||||||||
                                CCC   GTCC    GCCGGTGT
                                  AC_   CC___
GAM1049  LOC150319 3'  CTGTGGCTGTGTCCCCACGCCC 80470      ATCA   A  TT
                                GGGC    GGA AC  GGCCACAG
                                ||||    ||| ||  ||||||||
                                CCCG    CCT TG  TCGGTGTC
                                  CACC   G  __
GAM1049  LOC152110 5'  TGGAAGCTTCCTGATGCCT    81293          A   GG
                                GGGCATCAGGAA CTT  CCA
                                |||||||||||| |||  |||
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                                TCCGTAGTCCTT GAA  GGT
                                      C  __
GAM1049  LOC221178 3'  TGTGACCGCCTGATGTCC    95179         AAACT   C
                                GGGCATCAGG    TGG CACA
                                ||||||||||    ||| ||||
                                CCTGTAGTCC    GCC GTGT
                                      _____  A
GAM1049  LOC92223  3'  GTGGCCAAGGGCTGCCC    69054      TCAG AAA
                                GGGCA   G   CTTGGCCAC
                                |||||   |   |||||||||
                                CCCGT   C   GAACCGGTG
                                   _____ GG_
GAM1050  ATP8B2    5'  ACTTACTTCCTGTTCCTCCTC  65829      TTCCT       C
                                GAGGA    ACAGGAAG AAGT
                                |||||    |||||||| ||||
                                CTCCT    TGTCCTTC TTCA
                                   CCT__       A
GAM1050  HMGA2     3'  CTCCCTGTAGTGAATCCTC   14453        _      A
                                GAGGATTC CTACAGG AG
                                |||||||| ||||||| ||
                                CTCCTAAG GATGTCC TC
                                     T      C
GAM1050  RUNX1     3'  TACTGTATTCCCACAAGGAATC 10030        ACA_   GCA
            C                    GGATTCCT   GGAA   AGTA
                                |||||||    ||||   ||||
                                CCTAAGGA   CCTT   TCAT
                                     ACAC   ATG
GAM1050  SLC25A13  3'  ACTTGCTTTTAAAATCC    27286      CCTACA
                                GGATT     GGAAGCAAGT
                                |||||     ||||||||||
                                CCTAA     TTTTCGTTCA
                                   AA_____
GAM1050  TRIM14    3'  ACTATGCTGCAGGAATCCT   29501        ACAGGA   _
                                AGGATTCCT     AGCA AGT
                                |||||||||     |||| |||
                                TCCTAAGGA     TCGT TCA
                                     CG_____   A
GAM1050  C20orf21  3'  TACTTGCTCCAAAAGACCCTC  35572     AT  CTACA   A
                                GAGG  TC    GGA GCAAGTA
                                ||||  ||    ||| |||||||
                                CTCC  AG    CCT CGTTCAT
                                  C_  AAAA_  _
GAM1050  DKFZP434F091 5'  TACCCGCTCCCTAGGATTCC   31897     T   AC   A   AA
                                GGA TCCT  AGG AGC  GTA
                                ||| ||||  ||| |||  |||
                                CCT AGGA  TCC TCG  CAT
                                  T   __   C   CC
GAM1050  DKFZp564A176 3'  ACTTGCTTCCTGCAGCACCTC  50970      ATTC  A
                                GAGG   CT CAGGAAGCAAGT
                                ||||   || ||||||||||||
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                                CTCC    GA GTCCTTCGTTCA
                                  AC__  C
GAM1050  FLJ22056  3'  ACCTGCTTCCTAAAGGCAACCC 42828     A  _   AC       A
              T                    AGG TT CCT  AGGAAGCA GT
                                   ||| || |||  |||||||| ||
                                   TCC AA GGA  TCCTTCGT CA
                                     C  C   AA       C
GAM1050  HSA249128 3'  TACTTGTTTACTGTAGGAATCC 34562            G
              T                    AGGATTCCTACAG AAGCAAGTA
                                   |||||||||||| |||||||||
                                   TCCTAAGGATGTC TTTGTTCAT
                                            A
GAM1050  KIAA0397  3'  ACTTGCTCTGAGGAATCCC    62341    A      A   GA
                                   G GGATTCCT CAG  AGCAAGT
                                   | |||||||| |||  |||||||
                                   C CCTAAGGA GTC  TCGTTCA
                                   _       _  ___
GAM1050  KIAA1493  3'  TACTTGGGAGCTGTCAGAATCC 64843        CT    GAAG
              TC                     GAGGATTC  ACAG    CAAGTA
                                   ||||||||  ||||    ||||||
                                   CTCCTAAG  TGTC    GTTCAT
                                       AC    GAGG
GAM1050  TA-KRP    3'  CTTTTACGTTGGAATCCTC    51673         T  A_
                                   GAGGATTCC AC  GGAAG
                                   |||||||||  ||  |||||
                                   CTCCTAAGG TG  TTTTC
                                         T  CA
GAM1050  LOC129526 3'  TTTCCTGCAGGAACCCTC     75390      A    A
                                   GAGG TTCCT CAGGAAG
                                   |||| ||||| |||||||
                                   CTCC AAGGA GTCCTTT
                                     C     C
GAM1050  LOC153232 5'  CTTCCTGCAGGCATCCTC     87183       T   A
                                   GAGGAT CCT CAGGAAG
                                   |||||| ||| |||||||
                                   CTCCTA GGA GTCCTTC
                                      C   C
GAM1051  ACCN1     3'  CCACCTCCACGTCTGTCTTGTA 8457            AA_  ACAA
                                   TACAAGACAGGC   GA    GTGG
                                   ||||||||||||   ||    ||||
                                   ATGTTCTGTCTG   CT    CACC
                                          CAC  C___
GAM1051  FGFR1     3'  CACTTGTTCTGTACTTGT     7016       CA_
                                   ACAGG   AGAACAAGTG
                                   |||||   ||||||||||
                                   TGTTC   TCTTGTTCAC
                                      ATG
GAM1051  OPHN1     3'  CTTGACTCTTGCCTGCCT     11909     A       A_
                                   AG CAGGCAAGA  CAAG
                                   || |||||||||  ||||
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```
                                TC GTCCGTTCT  GTTC
                                 C        CA
GAM1051  BCL2L1   3'  CCACCCTTGGCCTGTCT     57586         _  AACAA
                                AGACAGGC AAG    GTGG
                                |||||||| |||    ||||
                                TCTGTCCG TTC    CACC
                                    G  C____
GAM1051  CABP2    3'  CAGTGCCCTTGCCTGCCTT   49128    A      AA  AG
                                AAG CAGGCAAG  CA  TG
                                ||| ||||||||  ||  ||
                                TTC GTCCGTTC  GT  AC
                                  C       CC  G_
GAM1051  CST9L    5'  TGTCCTTCCTGTCCTGTA    55515     A    C   A
                                TACA GACAGG AAG ACA
                                |||| |||||| ||| |||
                                ATGT CTGTCC TTC TGT
                                  C     _  C
GAM1051  FLJ14154 3'  CCACTCCGCTGCCTGTTCTTG  46225      _     A AACA
                                CAAGA CAGGCA G    AGTGG
                                ||||| |||||| |    |||||
                                GTTCT GTCCGT C    TCACC
                                   T     _ GCC_
GAM1051  FLJ30213 3'  CCACTTGTTAGTTTATCTTG   59401      C    AAG
                                CAAGA AGGC   AACAAGTGG
                                ||||| ||||   |||||||||
                                GTTCT TTTG   TTGTTCACC
                                   A   A__
GAM1051  KIAA1041 3'  CCACTCATCTAGGTTGTCTTG  30819        GCA   ACA
                                CAAGACAG   AGA   AGTGG
                                ||||||||   |||   |||||
                                GTTCTGTT   TCT   TCACC
                                    GGA   AC_
GAM1051  KIAA1111 3'  CCACTCCCGTCACCTGCCTTGT 97944      A    CAA  ACA_
                                ACAAG CAGG   GA    AGTGG
                                ||||| ||||   ||    |||||
                                TGTTC GTCC   CT    TCACC
                                   C    A__  GCCC
GAM1051  KIAA1764 5'  CCACTGTCACTTGCCTGCCTTG 69827      A       AACA
                                CAAG CAGGCAAG    AGTGG
                                |||| ||||||||    |||||
                                GTTC GTCCGTTC    TCACC
                                  C       ACTG
GAM1051  LSM5     3'  CCACTTACTTTTCTGTC     25568       C   AAC
                                GACAGG AAG   AAGTGG
                                |||||| |||   ||||||
                                CTGTCT TTC   TTCACC
                                   T   A__
GAM1051  MAD4     3'  CCACCCAGTAGTCCTGCCTGTC 22271         A  ACAA___
              T                  AGACAGGCA GA      GTGG
                                |||||||| ||      ||||
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                                TCTGTCCGT CT      CACC
                                     C  GATGACC
GAM1051  p25      3'  CCGCCCTTGCCTGTCT      23827          AACAA
                                AGACAGGCAAG     GTGG
                                ||||||||||     ||||
                                TCTGTCCGTTC     CGCC
                                      C_____
GAM1051  RABAC1    3'  CCACCCCTGCCCATGCCTGTCC 22220    A       AGAA  A__
              TG                    CA GACAGGCA    CA   GTGG
                                || ||||||||    ||   ||||
                                GT CTGTCCGT    GT   CACC
                                 C       ACCC  CCC
GAM1051  SEMA5A    3'  CAAGAGTCCTTCCTGTCTT    15590         C   A  AAG
                                AAGACAGG AAG AC   TG
                                |||||||| ||| ||   ||
                                TTCTGTCC TTC TG   AC
                                     _   C  AGA
GAM1051  TRIM16    3'  CCACTGCGCCCTGCCTGTTTGT 22367      A       AGAACA
              A                     TACA GACAGGCA      AGTGG
                                |||| ||||||||      |||||
                                ATGT TTGTCCGT      TCACC
                                   _       CCCGCG
GAM1051  TSGA14    3'  CCACTGAAAATTGCCTGTCCTG 38665    A       GAACA
                                CA GACAGGCAA     AGTGG
                                || |||||||||     |||||
                                GT CTGTCCGTT     TCACC
                                 C        AAAAG
GAM1051  LOC142948 5'  GCTGCCTTGCCTGCCTTCA    83778    C   A       AACA
                                A AAG CAGGCAAG    AGT
                                | ||| ||||||||    |||
                                A TTC GTCCGTTC    TCG
                                 C   C       CG__
GAM1051  LOC147166 3'  CCACTGCGCCCTGCCTGTTTGT 78884      A       AGAACA
              A                     TACA GACAGGCA      AGTGG
                                |||| ||||||||      |||||
                                ATGT TTGTCCGT      TCACC
                                   _       CCCGCG
GAM1051  LOC149134 3'  CAGTGTCCCTGCTTGTCCTG   85518    A       AGA   AG
                                CA GACAGGCA   ACA  TG
                                || ||||||||   |||  ||
                                GT CTGTTCGT   TGT  AC
                                 C       CCC   G_
GAM1051  LOC197003 3'  CCACTCCCTACCTGTCTT    89213         CA  AACA
                                AAGACAGG  AG    AGTGG
                                ||||||||  ||    |||||
                                TTCTGTCC  TC    TCACC
                                     A_  CC__
GAM1051  LOC221362 5'  CCAAACTCTTGCCTTTCTTGTA 95399         C       ACAAG
                                TACAAGA AGGCAAGA     TGG
                                ||||||| ||||||||     |||
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                                ATGTTCT TCCGTTCT    ACC
                                    T       CAA__
GAM1051  LOC222066 5'  CCACCTGCCCTGCCTGTT    94316        A AA  A
                                GACAGGCA G  CA GTGG
                                |||||||| |  || ||||
                                TTGTCCGT C  GT CACC
                                    _ CC  C
GAM1051  LOC223009 5'  CCAGATTCCTGCCTGTCT    96032        A   CAAG
                                AGACAGGCA GAA    TGG
                                ||||||||| |||    |||
                                TCTGTCCGT CTT    ACC
                                     C   AG__
GAM1051  LOC81501  3'  CCACATGATCTTGCCTGT    48631         A  A
                                ACAGGCAAGA CA GTGG
                                |||||||||| || ||||
                                TGTCCGTTCT GT CACC
                                     A  A
GAM1051  LOC90141  3'  CCATGCCTTGCCTGTCCTG   62301    A        AACAA
                                CA GACAGGCAAG    GTGG
                                || ||||||||||    ||||
                                GT CTGTCCGTTC    TACC
                                 C        CG___
GAM1052  GNA11     3'  CGTCGTGGCCTGGATCCTCTG  76588          A  T  T
                                TAGAGGATCCA GCT ACG ACG
                                |||||||||||| ||| ||| |||
                                GTCTCCTAGGT CGG TGC TGC
                                     C  _  _
GAM1052  KIAA0150  3'  GCGCACAGGCCGGCTGGATCCT 71882        A  TAC__  A
                                AGGATCCA GCT    GT CGC
                                |||||||| |||    || |||
                                TCCTAGGT CGG    CA GCG
                                    _  CCGGA  C
GAM1052  KIAA1695  3'  ACGCATTGACTTGGATCT    47830         C  ___
                                GGATCCAAG TTA   CGT
                                ||||||||| |||   |||
                                TCTAGGTTC AGT   GCA
                                    _  TAC
GAM1052  LOC152274 3'  CGAAGCCTGGTCCTCTA     81339        T  A  A
                                TAGAGGA CCA GCTT CG
                                ||||||| ||| |||| ||
                                ATCTCCT GGT CGAA GC
                                    _  C   _
GAM1052  LOC93626  3'  CGTCGTGGCCTGGATCCTCTG  73129          A  T  T
                                TAGAGGATCCA GCT ACG ACG
                                |||||||||||| ||| ||| |||
                                GTCTCCTAGGT CGG TGC TGC
                                     C  _  _
GAM1053  PML       3'  CTGAAGACCCACTGAGGA    53802    G  ATAA  AT
                                TC TCA   GG  GTCTTCAG
                                || |||   ||  ||||||||
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                                AG AGT   CC  CAGAAGTC
                                 G  CA__ __
GAM1053  TLL1     3'  CTGAAGTGTTCTTTTTGAC   25875      T     T
                                GTCAA AAGGATG CTTCAG
                                ||||| ||||||| ||||||
                                CAGTT TTCTTGT GAAGTC
                                   T     _
GAM1053  KIAA1715  3'  CTCTGCTCACCATCCTTATCAC 68685    CA       TCTT_
                                GT  ATAAGGATG    CAGAG
                                ||  |||||||||    |||||
                                CA  TATTCCTAC    GTCTC
                                 C_       CACTC
GAM1053  MGC4737   5'  CTGAAGACATAATTGAC     49642       AAGG
                                GTCAAT    ATGTCTTCAG
                                ||||||    ||||||||||
                                CAGTTA    TACAGAAGTC
                                   A___
GAM1053  LOC196214 5'  CTGAAGACAAGCTGATGA    91177       ATAA GA
                                TCGTCA    G  TGTCTTCAG
                                ||||||    |  |||||||||
                                AGTAGT    C  ACAGAAGTC
                                   _____ GA
GAM1054  HADHB     5'  CTCGCGGACGTCAGCCAAGATT 5738          _ _  A   A
              CCA                  TGGAATCTTG C GGC TCC CGAG
                                ||||||||||  | ||| ||| ||||
                                ACCTTAGAAC G CTG AGG GCTC
                                     C A   C   C
GAM1054  BHLHB2    5'  CTCAAAGCCGAAGATTCCA    14763        G    ATCCAC
                                TGGAATCTT CGGC     GAG
                                ||||||||| ||||     |||
                                ACCTTAGAA GCCG     CTC
                                     _    AAA___
GAM1054  CPSF1     3'  CGTGGATGCCGTCACCACCA   65160     AATCTT
                                TGG     GCGGCATCCACG
                                |||     ||||||||||||
                                ACC     TGCCGTAGGTGC
                                  ACCAC_
GAM1054  DKFZP434K0427 3'  TCTCACAGATGTGCTGTATCC  50500     ATCT       CCAC__
                                GGA    TGCGGCAT     GAGA
                                |||    ||||||||     ||||
                                CCT    ATGTCGTG     CTCT
                                  _____       TAGACA
GAM1054  FLJ14166  3'  TCTCGGTTCCGGAAGATTCCA  44992         G   CATCCA
                                TGGAATCTT CGG     CGAGA
                                ||||||||| |||     |||||
                                ACCTTAGAA GCC     GCTCT
                                     G   TTG___
GAM1054  FLJ20618  3'  TCTCACAAGGCTGCACCAGATT 35888         __     ATCCAC
              CCA                  TGGAATCT  TGCGGC     GAGA
                                ||||||||  ||||||     ||||
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                                ACCTTAGA  ACGTCG     CTCT
                                    CC     GAACA_
GAM1054  LOC125988 5'  TCTCAGAGCCGCAAGACACCA  74900     AA       A  CAC
                                TGG  TCTTGCGGC TC   GAGA
                                |||  |||||||||  ||   ||||
                                ACC  AGAACGCCG AG   CTCT
                                  AC        _  A__
GAM1054  LOC148697 3'  TCTCGTGGACACCCACATCTCA 79681    GA  CT  C  CA
                                TG  AT  TG GG  TCCACGAGA
                                ||  ||  || ||  |||||||||
                                AC  TA  AC CC  AGGTGCTCT
                                 TC  C_  _  AC
GAM1054  LOC195977 3'  GGATGCCGCCCAAGATTCC   88933         __
                                GGAATCTT  GCGGCATCC
                                ||||||||  |||||||||
                                CCTTAGAA  CGCCGTAGG
                                    CC
GAM1055  ABR      3'  TGTACACTTGTCAGGCAGA   42011       CC     A  C
                                TTTGCC  TGGCAA TG ACA
                                ||||||  |||||| || |||
                                AGACGG  ACTGTT AC TGT
                                   __     C  A
GAM1055  ABR      3'  TGTACACTTGTCAGGCAGA   8456        CC     A  C
                                TTTGCC  TGGCAA TG ACA
                                ||||||  |||||| || |||
                                AGACGG  ACTGTT AC TGT
                                   __     C  A
GAM1055  GM2A     3'  TGTGTTTGCCAAGGCCAAA   68392      C  C
                                TTTG CC TGGCAAATGCA
                                ||||  || ||||||||||
                                AAAC GG ACCGTTTGTGT
                                  C  A
GAM1055  SAG      5'  TGTAGAAGTTGCCAGGGACAGA 6774       C        ATGC_
                                TTTG CCCTGGCAA     ACA
                                ||||  |||||||||     |||
                                AGAC GGGACCGTT     TGT
                                  A        GAAGA
GAM1055  TRPC6    3'  TGTGCATTTACCAAGAGGT   17291     C  _  C
                                GCC CT GG AAATGCACA
                                |||  ||  ||  |||||||||
                                TGG GA CC TTTACGTGT
                                  A  A  A
GAM1055  DKFZp434K1210 3'  TGACTTTTACCAGGGGCAAA   34692          C   TG_
                                TTTGCCCCTGG AAA   CA
                                ||||||||||| |||   ||
                                AAACGGGGACC TTT   GT
                                       A   TCA
GAM1055  DKFZP434P0111 3'  GTGTGCATTTTTCAGAAGG   67961    C_   C
                                CC  CTGG AAATGCACAC
                                ||  |||| ||||||||||
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                                GG  GACT TTTACGTGTG
                                 AA    T
GAM1055  DKFZp547F072 5'  TGTCCAGCCAGGGGCAGA    51089          AAA  C
                                TTTGCCCCTGGC   TG ACA
                                ||||||||||||   || |||
                                AGACGGGGACCG   AC TGT
                                       ____  C
GAM1055  DKFZP564O0463 3'  TGTGTGCATTTGCCCATTGGGG 27128        T___
           TAAA                    TTTGCCCC    GGCAAATGCACACA
                                ||||||||    ||||||||||||||
                                AAATGGGG    CCGTTTACGTGTGT
                                     TTAC
GAM1055  EFA6R    3'  TGTGTGCAATACCAAGGGCA   31643      C   CAAA
                                TGCCC TGG    TGCACACA
                                ||||| |||    ||||||||
                                ACGGG ACC    ACGTGTGT
                                   A   ATA_
GAM1055  FLJ12122  5'  GTGTGTTGCCAGGGGCAGA   47095          AAT
                                TTTGCCCCTGGCA   GCACAC
                                ||||||||||||   ||||||
                                AGACGGGGACCGT   TGTGTG
                                          ___
GAM1055  HRIHFB2436 3'  GTTCATTGCCAGGAGCAGA   27572      C       A  C
                                TTTGC CCTGGCAA TG AC
                                ||||| |||||||| || ||
                                AGACG GGACCGTT AC TG
                                   A       _ T
GAM1055  KIAA0377  3'  TGTAGTTGTGCCAGGGACAGA  28504      C       AA__
                                TTTG CCCTGGCA    TGCA
                                |||| ||||||||    ||||
                                AGAC GGGACCGT    ATGT
                                  A       GTTG
GAM1055  KIAA1036  3'  TGCTCAGTGCCAGGGGCAGA   30498          AAT_
                                TTTGCCCCTGGCA    GCA
                                ||||||||||||    |||
                                AGACGGGGACCGT    CGT
                                       GACT
GAM1055  KIAA1280  5'  TGTGCATTTACCATGTA     70293     CCC   C
                                TGC   TGG AAATGCACA
                                |||   ||| |||||||||
                                ATG   ACC TTTACGTGT
                                  T__   A
GAM1055  MGC2217   3'  GTACATTCACTAGGGGCAAA   44430         CA    C
                                TTTGCCCCTGG  AATG AC
                                ||||||||||  |||| ||
                                AAACGGGGATC  TTAC TG
                                       AC    A
GAM1055  POT1     3'  TGTTATTTGCCAAAGACAGA   31889      CCCC       C
                                TTTG    TGGCAAATG ACA
                                ||||    ||||||||| |||
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                                AGAC    ACCGTTTAT TGT
                                  AGAA       _
GAM1055  LOC124145 3'  TGTATTTGCCAACAACAAA    74725      CCCC
                                TTTG    TGGCAAATGCA
                                ||||    ||||||||||
                                AAAC    ACCGTTTATGT
                                  AACA
GAM1055  LOC131870 3'  TGGCATCAGGGGCAAA      75512          GCAA    A
                                TTTGCCCCTG    ATGC CA
                                ||||||||||    |||| ||
                                AAACGGGGAC    TACG GT
                                      _____   _
GAM1055  LOC145483 3'  TGCATATCCCCAGGGGGCAAA  77762        _   CAA_
                                TTTGCCCC TGG    ATGCA
                                |||||||| |||    |||||
                                AAACGGGG ACC    TACGT
                                     G   CCTA
GAM1055  LOC145945 5'  GTGTCCCTGCACCAGGGGCAAA 84569           CAAA   _____
                                TTTGCCCCTGG    TGC    ACAC
                                ||||||||||    |||    ||||
                                AAACGGGGACC    ACG    TGTG
                                      _____  TCCC
GAM1055  LOC146227 3'  GTGGGTGTTTGCAGAGACAAA  78217      CCC   G      A
                                TTTG   CTG CAAATGC CAC
                                ||||   ||| ||||||| |||
                                AAAC   GAC GTTTGTG GTG
                                  AGA   _      G
GAM1055  LOC148918 5'  TGCATGGTGACCACCAGGGGCA 79834           _____  A_
            AG                    TTTGCCCCTGG    CA  ATGCA
                                ||||||||||    ||  |||||
                                GAACGGGGACC    GT  TACGT
                                      ACCA  GG
GAM1055  LOC151610 3'  TGTGTGCATCAACCGAGCAGA  81100      CCC   CAA
                                TTTGC   TGG   ATGCACACA
                                |||||   |||   |||||||||
                                AGACG   GCC   TACGTGTGT
                                  A__   AAC
GAM1055  LOC152098 5'  TGGAATTTTGCTAGGAACAAA  81294      CC        TGCA
                                TTTG  CCTGGCAAA    CA
                                ||||  |||||||||    ||
                                AAAC  GGATCGTTT    GT
                                  AA        TAAG
GAM1055  LOC155061 3'  TGTGTGCACTCTCAGAGGGCA  82195       _   CAAA
                                TGCCC CTGG    TGCACACA
                                ||||| ||||    ||||||||
                                ACGGG GACT    ACGTGTGT
                                  A    CTC_
GAM1055  LOC90538  3'  TGTGTTAAGTGCCAGGGGCA   63903           AAT_
                                TGCCCCTGGCA    GCACA
                                ||||||||||    |||||
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                                ACGGGGACCGT   TGTGT
                                      GAAT
GAM1056  CCNDBP1   5'  TGCTCTCCCCCGCTGCATCCT  54472        AA__    T
                                AGGATGCAG   GGAGA CA
                                |||||||||   ||||| ||
                                TCCTACGTC   CCTCT GT
                                     GCCC    C
GAM1056  CHAT      5'  GCAGGTCCACACCTCTGCATCC 40970        A  AGATC  _
                                GGATGCAGA GG    ACC GC
                                |||||||||  ||    ||| ||
                                CCTACGTCT CC    TGG CG
                                     _  ACACC   A
GAM1056  COG7      5'  GGCTCGCTCGCTTCTGCATCC  68256        _  ATCACC
                                GGATGCAGAAG GAG     GCC
                                ||||||||||| |||     |||
                                CCTACGTCTTC CTC     CGG
                                      G   GCT___
GAM1056  DAP       3'  GGCAGTAGGGTACCCTGCGTCC 72948        AA  AGA  _  C
           T                     AGGATGCAG  GG   TC AC GCC
                                 |||||||||  ||   || || |||
                                 TCCTGCGTC  CC   GG TG CGG
                                      __  ATG  A  A
GAM1056  DMD       3'  GGCAGCGCATTGTTTTGCATCC 15679        G  GATCACC
           T                     AGGATGCAGAA GA      GCC
                                 ||||||||||| ||      |||
                                 TCCTACGTTTT TT      CGG
                                      G  ACGCGA_
GAM1056  DMD       3'  GGCAGCGCATTGTTTTGCATCC 15682        G  GATCACC
           T                     AGGATGCAGAA GA      GCC
                                 ||||||||||| ||      |||
                                 TCCTACGTTTT TT      CGG
                                      G  ACGCGA_
GAM1056  DMD       3'  GGCAGCGCATTGTTTTGCATCC 15686        G  GATCACC
           T                     AGGATGCAGAA GA      GCC
                                 ||||||||||| ||      |||
                                 TCCTACGTTTT TT      CGG
                                      G  ACGCGA_
GAM1056  DMD       3'  GGCAGCGCATTGTTTTGCATCC 15690        G  GATCACC
           T                     AGGATGCAGAA GA      GCC
                                 ||||||||||| ||      |||
                                 TCCTACGTTTT TT      CGG
                                      G  ACGCGA_
GAM1056  DMD       3'  GGCAGCGCATTGTTTTGCATCC 15694        G  GATCACC
           T                     AGGATGCAGAA GA      GCC
                                 ||||||||||| ||      |||
                                 TCCTACGTTTT TT      CGG
                                      G  ACGCGA_
GAM1056  DMD       3'  GGCAGCGCATTGTTTTGCATCC 15698        G  GATCACC
           T                     AGGATGCAGAA GA      GCC
                                 ||||||||||| ||      |||
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                                TCCTACGTTTT TT      CGG
                                      G  ACGCGA_
GAM1056  DMD     3'  GGCAGCGCATTGTTTTGCATCC 15702          G  GATCACC
                T                AGGATGCAGAA GA      GCC
                                 |||||||||| ||      |||
                                TCCTACGTTTT TT      CGG
                                      G  ACGCGA_
GAM1056  DMD     3'  GGCAGCGCATTGTTTTGCATCC 15706          G  GATCACC
                T                AGGATGCAGAA GA      GCC
                                 |||||||||| ||      |||
                                TCCTACGTTTT TT      CGG
                                      G  ACGCGA_
GAM1056  DMD     3'  GGCAGCGCATTGTTTTGCATCC 15709          G  GATCACC
                T                AGGATGCAGAA GA      GCC
                                 |||||||||| ||      |||
                                TCCTACGTTTT TT      CGG
                                      G  ACGCGA_
GAM1056  DMD     3'  GGCAGCGCATTGTTTTGCATCC 15712          G  GATCACC
                T                AGGATGCAGAA GA      GCC
                                 |||||||||| ||      |||
                                TCCTACGTTTT TT      CGG
                                      G  ACGCGA_
GAM1056  DMD     3'  GGCAGCGCATTGTTTTGCATCC 15716          G  GATCACC
                T                AGGATGCAGAA GA      GCC
                                 |||||||||| ||      |||
                                TCCTACGTTTT TT      CGG
                                      G  ACGCGA_
GAM1056  DMD     3'  GGCAGCGCATTGTTTTGCATCC 15724          G  GATCACC
                T                AGGATGCAGAA GA      GCC
                                 |||||||||| ||      |||
                                TCCTACGTTTT TT      CGG
                                      G  ACGCGA_
GAM1056  DMD     3'  GGCAGCGCATTGTTTTGCATCC 5466           G  GATCACC
                T                AGGATGCAGAA GA      GCC
                                 |||||||||| ||      |||
                                TCCTACGTTTT TT      CGG
                                      G  ACGCGA_
GAM1056  FAT     3'  CGGGGACCTTCTGCATACC    19130    _       AGA  A
                                GG ATGCAGAAGG   TC CCG
                                || ||||||||||   || |||
                                CC TACGTCTTCC   AG GGC
                                 A        ___  G
GAM1056  GNB1    3'  GTAGTGGCTTCTCCATCCT    10839       C    GAGA   CG
                                AGGATG AGAAG    TCAC  C
                                ||||||  |||||   ||||  |
                                TCCTAC TCTTC    GGTG  G
                                   C     _____    AT
GAM1056  HAP1    3'  GACCCTCCTTCCCATCCT    15475       CA      A_
                                AGGATG  GAAGGAG  TC
                                ||||||  |||||||  ||
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                                TCCTAC  CTTCCTC  AG
                                   C_      CC
GAM1056  INSRR    3'  GGCCCTCCTTCCGCCTCCT   68991      T  A      ATCA
                                AGGA GC GAAGGAG    CC
                                |||| || |||||||    ||
                                TCCT CG CTTCCTC    GG
                                  C  C      CC__
GAM1056  MVK      3'  GGCATGGTCTGCCCTCTGCATC 61280          A  _     CC
              CT                   AGGATGCAGA GG AGATCA  GCC
                                |||||||||| || ||||||  |||
                                TCCTACGTCT CC TCTGGT  CGG
                                      C  G     A_
GAM1056  SIAT7D   5'  GGCGGTGAAAAACCTACGTCCT 27705       CAGA   AGA_
                                AGGATG    AGG    TCACCGCC
                                ||||||    |||    ||||||||
                                TCCTGC    TCC    AGTGGCGG
                                   A___   AAAA
GAM1056  UBQLN1   5'  GCGGCGTGCTCTGCATTCT   26476          AGGA ATCA
                                AGGATGCAGA    G    CCGC
                                ||||||||||    |    ||||
                                TCTTACGTCT    C    GGCG
                                      _____ GTGC
GAM1056  CALP     5'  GTCTCGCTTCTGCACCCT    48173     A       _
                                AGG TGCAGAAG GAGAT
                                ||| |||||||| |||||
                                TCC ACGTCTTC CTCTG
                                  C       G
GAM1056  CECR6    3'  GGTGTCCTTCTGCACCCT    49933     A        GAT
                                AGG TGCAGAAGGA   CACC
                                ||| ||||||||||   ||||
                                TCC ACGTCTTCCT   GTGG
                                  C        ____
GAM1056  CENTB1   5'  GTGCCTCCACCTGCATCC    28869        AA    AT
                                GGATGCAG  GGAG  CAC
                                ||||||||  ||||  |||
                                CCTACGTC  CCTC  GTG
                                     CA    C_
GAM1056  FLJ14327 3'  GCGGTACTTCTCTGCATCT   46685         A    ATC
                                GGATGCAGA GGAG   ACCGC
                                ||||||||| ||||   |||||
                                TCTACGTCT CTTC   TGGCG
                                      _    A__
GAM1056  FLJ14800 3'  GCCCTCTATCTCCTTCTAATCC 52686       GC         CACC_
              T                   AGGAT  AGAAGGAGAT    GC
                                |||||  ||||||||||    ||
                                TCCTA  TCTTCCTCTA    CG
                                   A_         TCTCC
GAM1056  GMPPB    5'  GATCACCCCCCCTGCATCCT   97451         AA__  A
                                AGGATGCAG    GG GATC
                                |||||||||    || ||||
```

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                                TCCTACGTC    CC CTAG
                                     CCCC  A
GAM1056  GRIN3A   3'  GACTCTCCTTCAACATCCT    56782       CA       _
                                AGGATG  GAAGGAGA TC
                                ||||||  |||||||| ||
                                TCCTAC  CTTCCTCT AG
                                   AA       C
GAM1056  HELO1    5'  GGTGTCTCCTTCTACATCC    41797      C        T
                                GGATG AGAAGGAGA CACC
                                ||||| ||||||||| ||||
                                CCTAC TCTTCCTCT GTGG
                                  A       _
GAM1056  KCNT1    3'  GGCGGTGACCCCGCAGAGCACC 62492    A   AGAA_ AGA
             C                   GG TGC    GG   TCACCGCC
                                || |||    ||   ||||||||
                                CC ACG    CC   AGTGGCGG
                                 C   AGACG  CC_
GAM1056  KCNT1    3'  GGTCCTCATCCTCTTCTGCACC 62494     A      GA   C___
             CT                   AGG TGCAGAAG  GAT    ACC
                                ||| ||||||||  |||    |||
                                TCC ACGTCTTC  CTA    TGG
                                  C       TC   CTCC
GAM1056  KIAA1272 3'  GGCAGCTTGCTTCTGCACCC   70732    A      _   ATCACC
                                GG TGCAGAAG GAG     GCC
                                || |||||||| |||     |||
                                CC ACGTCTTC TTC     CGG
                                 C       G   GA____
GAM1056  KIAA1671 3'  GCCTGCGTCTCCTTTTGCACCC 66284    A          CACC
                                GG TGCAGAAGGAGAT    GC
                                || ||||||||||||    ||
                                CC ACGTTTTCCTCTG    CG
                                 C           CGTC
GAM1056  MGC33345 3'  CGGTGGCCCCTGCATCT     58921        AA  AGA
                                GGATGCAG  GG   TCACCG
                                ||||||||  ||   ||||||
                                TCTACGTC  CC   GGTGGC
                                     C_  ___
GAM1056  NUDEL    3'  GGCGGCTGTCCCTGTGCATCCT 48700        GA   A   CA
                                AGGATGCA  AGG GAT  CCGCC
                                ||||||||  ||| |||  |||||
                                TCCTACGT  TCC CTG  GGCGG
                                     G_  _   TC
GAM1056  P450RAI-2 3'  GCGTCTCCTCCTCCTGCGCCC  39575    A    A    ATCAC
                                GG TGCAG AGGAG     CGC
                                || ||||| |||||     |||
                                CC GCGTC TCCTC     GCG
                                 C    C     CTCT_
GAM1056  phospho1 3'  CGGTGTCTCCTTGCATCC    83245        GA     T
                                GGATGCA  AGGAGA CACCG
                                |||||||  |||||| |||||
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                                CCTACGT  TCCTCT GTGGC
                                   __    _
GAM1056  RPIA     3'  GCAGTGATCTCCTGATGC    58592     GA        C
                                GCA  AGGAGATCAC GC
                                |||  |||||||||| ||
                                CGT  TCCTCTAGTG CG
                                  AG         A
GAM1056  SCRG1    5'  GCCTTGTCTCCTTCCACTCC   24416     _ CA       T  CC
                                GGA TG  GAAGGAGA CA  GC
                                ||| ||  |||||||| ||  ||
                                CCT AC  CTTCCTCT GT  CG
                                  C __       _ TC
GAM1056  LOC123242 5'  GGCGGTGACCCAGACATGCCT  76119     _  CAGAA  AGA
                                AGG ATG    GG   TCACCGCC
                                ||| |||    ||   ||||||||
                                TCC TAC    CC   AGTGGCGG
                                  G   AGAC_ ___
GAM1056  LOC147093 5'  GCGCCTCCTTCTGCACCC    85057    A         ATCAC
                                GG TGCAGAAGGAG    CGC
                                || ||||||||||     |||
                                CC ACGTCTTCCTC    GCG
                                 C         C____
GAM1056  LOC154282 3'  GGCAGCAACCTTTGCTTTCTGC 87409     A        AGATCACC___
            AGCCT                  AGG TGCAGAAGG         GCC
                                ||| |||||||||         |||
                                TCC ACGTCTTTC         CGG
                                  G        GTTTCCAACGA
GAM1056  LOC154881 3'  GGCAGTGATCTCCTGTTCCCT  82074     AT   GAA       C
                                AGG  GCA   GGAGATCAC GCC
                                |||  |||   ||||||||| |||
                                TCC  TGT   CCTCTAGTG CGG
                                  CT   ___        A
GAM1056  LOC154881 3'  GGCCTTGACCCCTTCTGCTTCC 82075     T       AGA   CC
                                GGA GCAGAAGG   TCA  GCC
                                ||| ||||||||   |||  |||
                                CCT CGTCTTCC   AGT  CGG
                                  T       CC_   TC
GAM1056  LOC165070 5'  GGCAGTGTGAGCTCTGCGTCC  83350         AGGAGAT   C
                                GGATGCAGA      CAC GCC
                                |||||||||      ||| |||
                                CCTGCGTCT      GTG CGG
                                     CGAGT__   A
GAM1056  LOC220370 3'  GGCGGCCTTCCCCTGCAGTCCT 94401     _    AA    ATCA
                                AGGA TGCAG  GGAG    CCGCC
                                |||| |||||  ||||    |||||
                                TCCT ACGTC  CTTC    GGCGG
                                  G    CC    C___
GAM1056  LOC253001 5'  GGCGGTGACCCAGACATGCCT  97997     _  CAGAA  AGA
                                AGG ATG    GG   TCACCGCC
                                ||| |||    ||   ||||||||
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                                TCC TAC    CC   AGTGGCGG
                                  G   AGAC_ ___
GAM1056 LOC91353 3' GCGTCTCTCTCTGCATCC    61160        AG    TCAC
                                GGATGCAGA  GAGA    CGC
                                |||||||||  ||||    |||
                                CCTACGTCT  CTCT    GCG
                                     CT    _____
GAM1056 LOC91397 5' GCATATCCCTTCTGCATCCT   66497           A   CACC
                                AGGATGCAGAAGG GAT    GC
                                |||||||||||||| |||    ||
                                TCCTACGTCTTCC CTA    CG
                                       _  TA__
GAM1057 HLF      3' ATCGAGGCTTGTGATGACG    10931         CA    AAA
                                CGTCATCAT  AAGTC   GAT
                                |||||||||  |||||   |||
                                GCAGTAGTG  TTCGG   CTA
                                     __    AG_
GAM1057 MGA      3' TATCCTTGACTTCAATGATGCA 63469      T__     CA      A  ___
             GTGGA                 TCCG   CATCAT  AAGTCAA GAT   A
                                ||||   ||||||  ||||||| |||   |
                                AGGT   GTAGTA  TTCAGTT CTA   T
                                  GAC     AC      C  ___
GAM1057 C9orf5   3' ATCTTTGACTCCGTTGTGTGC  50101    T  _  TCAA
                                G CAT CA    AGTCAAAGAT
                                | ||| ||    ||||||||||
                                C GTG GT    TCAGTTTCTA
                                _  T  TGCC
GAM1057 DKFZP434B172 3' ATCTTTGACTCTAATAAGTGTG 70575      T   CAA____
             AT                   GTCA CAT      AGTCAAAGAT
                                ||||| |||      ||||||||||
                                TAGT GTG      TCAGTTTCTA
                                  _   AATAATC
GAM1057 KIAA1764  3' ATCTTATTGTGATGATGA    69825         A   CA
                                TCATCATCA AGT  AAGAT
                                |||||||||  |||  |||||
                                AGTAGTAGT TTA  TTCTA
                                     G   __
GAM1057 MGC12335 3' ATCTTTGACCTTCGTGGAGGA  52202     GT   CATCAAA
                                TCC  CAT      GTCAAAGAT
                                |||  |||      |||||||||
                                AGG  GTG      CAGTTTCTA
                                  AG   CTTC___
GAM1057 SS18L1   3' ATCTTTGGATAAATGCTGAC   65948      T   CAAAG
                                GTCA CAT    TCAAAGAT
                                |||| |||    ||||||||
                                CAGT GTA    GGTTTCTA
                                  C   AATA_
GAM1057 LOC200854 3' ATCCATGGATAATGATGACG   88810         CAAAG   AA
                                CGTCATCAT    TCA  GAT
                                |||||||||    |||  |||
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                                GCAGTAGTA    GGT  CTA
                                     ATA__   AC
GAM1058  CERD4    3'  GGGCGTCCCTGGCTCACCA   24881        CA_  _
                                TGGTGAGCC   GA GCCC
                                |||||||||   || ||||
                                ACCACTCGG   CT CGGG
                                     TCC  G
GAM1058  CPNE7    3'  GGGCCCGGCTCTGGGGCCCCCA 27793    TGAG       C A
                                TGG    CCCAGAGCC G GCCC
                                |||    ||||||||| | ||||
                                ACC    GGGTCTCGG C CGGG
                                  CCCG        _ C
GAM1058  DHCR24   3'  GGGCTCATTCTTCTTGGCTCAC 29302        C    CCC_
            CA                    TGGTGAGCC AGAG    GAGCCC
                                |||||||||| ||||    ||||||
                                ACCACTCGG TCTT    CTCGGG
                                     T    CTTA
GAM1058  DTNA     3'  GCCTTGTTCCCCATGGCTCACC 53271        CA___    CCGA
            A                     TGGTGAGCC    GAGC    GC
                                |||||||||    ||||    ||
                                ACCACTCGG    CTTG    CG
                                     TACCC    TTC_
GAM1058  DTNA     3'  GCCTTGTTCCCCATGGCTCACC 53273        CA___    CCGA
            A                     TGGTGAGCC    GAGC    GC
                                |||||||||    ||||    ||
                                ACCACTCGG    CTTG    CG
                                     TACCC    TTC_
GAM1058  DTNA     3'  GCCTTGTTCCCCATGGCTCACC 53278        CA___    CCGA
            A                     TGGTGAGCC    GAGC    GC
                                |||||||||    ||||    ||
                                ACCACTCGG    CTTG    CG
                                     TACCC    TTC_
GAM1058  DTNA     3'  GCCTTGTTCCCCATGGCTCACC 9147         CA___    CCGA
            A                     TGGTGAGCC    GAGC    GC
                                |||||||||    ||||    ||
                                ACCACTCGG    CTTG    CG
                                     TACCC    TTC_
GAM1058  EGFL3    3'  GGCTCCTGCGGGCTCACCA   63301        AGA  CC
                                TGGTGAGCCC   GC  GAGCC
                                ||||||||||   ||  |||||
                                ACCACTCGGG   CG  CTCGG
                                      ___  TC
GAM1058  EGFL4    3'  GCCGGCTGGGCTCCCA      62468     T      AGC   A
                                TGG GAGCCCAG   CCG GC
                                ||| ||||||||   ||| ||
                                ACC CTCGGGTC   GGC CG
                                  _      ___   _
GAM1058  EN2      3'  TCGGCTCCATGCTCACCA    9273         CCA    C
                                TGGTGAGC   GAGCC GA
                                ||||||||   ||||| ||
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                                ACCACTCG  CTCGG CT
                                    TAC   _
GAM1058 GRM3    5' GCCCGGGTGCAGGCTCACC  7745       CAGA   A
                                GGTGAGCC  GCCCG GC
                                ||||||||  ||||| ||
                                CCACTCGG  TGGGC CG
                                    ACG_  C
GAM1058 HDGF    5' GCTCGGGCCGGGGGCCACCA  16899     A  AGA
                                TGGTG GCCC  GCCCGAGC
                                ||||| ||||  ||||||||
                                ACCAC CGGG  CGGGCTCG
                                  _  GGC
GAM1058 HIP12   3' GGGCTTGGCCCTAGGCCCTCCA 66818   TGA  C A  C
                                TGG  GCC AG GCC GAGCCC
                                |||  ||| || ||| ||||||
                                ACC  CGG TC CGG TTCGGG
                                  TCC  A C  _
GAM1058 HOXC6   3' GGGCTCGGACCCTGAACTCA  16910    CC  AGC
                                TGAG  CAG  CCGAGCCC
                                ||||  |||  ||||||||
                                ACTC  GTC  GGCTCGGG
                                  AA  CCA
GAM1058 IRS1    5' GGGCTCTCTCCTGGGCTCAGCA 19879   G      _ CCC
                                TG TGAGCCCAG AG  GAGCCC
                                || |||||||| ||  ||||||
                                AC ACTCGGGTC TC  CTCGGG
                                 G       C  T__
GAM1058 ITGA5   3' GCTCGGGCCCCTGCACCA   61934     AGCC  A_
                                TGGTG   CAG  GCCCGAGC
                                |||||   |||  ||||||||
                                ACCAC   GTC  CGGGCTCG
                                  _____  CC
GAM1058 MECP2   3' GGGCAGCCTCTGGGCCCAC  18409    A     CCCGA
                                GTG GCCCAGAG   GCCC
                                ||| ||||||||   ||||
                                CAC CGGGTCTC   CGGG
                                  C      CGA__
GAM1058 MHC2TA  3' GTTCAGCTCCAGCTCACCA  5992       CCA  CC
                                TGGTGAGC  GAGC  GAGC
                                ||||||||  ||||  ||||
                                ACCACTCG  CTCG  CTTG
                                    AC_   A_
GAM1058 PEA15   5' GGGCTCGGGCTCCGGCTC   15013     CA
                                GAGCC  GAGCCCGAGCCC
                                |||||  ||||||||||||
                                CTCGG  CTCGGGCTCGGG
                                  C_
GAM1058 PIG3    5' GGGCTCGGGCTTTGTCACC  18080     GCC
                                GGTGA  CAGAGCCCGAGCCC
                                |||||  ||||||||||||||
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                              CCACT  GTTTCGGGCTCGGG
                                ___
GAM1058 PTPRF   5' GGGCTCGGGCTCCGGCTC   12609     CA
                              GAGCC GAGCCCGAGCCC
                              ||||| ||||||||||||
                              CTCGG CTCGGGCTCGGG
                                 C_
GAM1058 PTPRF   5' GGGCTCGGGCTCCGGCTC   56139     CA
                              GAGCC GAGCCCGAGCCC
                              ||||| ||||||||||||
                              CTCGG CTCGGGCTCGGG
                                 C_
GAM1058 PUNC    5' GGCTCGGGCTCTGGGGCCTAC 91230    A  _
                              GTG GCCC AGAGCCCGAGCC
                              ||| |||| ||||||||||||
                              CAT CGGG TCTCGGGCTCGG
                                C   G
GAM1058 RRAD    3' GGCTCAGACTCTGGGTCCC   16048   T G     CCC
                              GG GA CCCAGAG  GAGCC
                              || || |||||||  |||||
                              CC CT GGGTCTC  CTCGG
                               _ _     AGA
GAM1058 SOX13   3' GGTCTGCCCTGGGCTCATCA  20283         A CCGA
                              TGGTGAGCCCAG GC   GCC
                              |||||||||||| ||   |||
                              ACTACTCGGGTC CG   TGG
                                     C  TC__
GAM1058 TMEM1   5' GGCTCGGGCTCCGGCTGGGCC 13804    G_   CA
                              GGT  AGCC  GAGCCCGAGCC
                              |||  ||||  ||||||||||||
                              CCG  TCGG  CTCGGGCTCGG
                                GG   C_
GAM1058 USP1    5' GGGCTCGGGGCAGGGACTCACC 14020      _  AGAG
                              GGTGAG CCC   CCCGAGCCC
                              |||||| |||   |||||||||
                              CCACTC GGG   GGGCTCGGG
                                 A  ACG_
GAM1058 ARHGEF9 3' GGGCTCGGGACTGGCCACCA  31489     A  C  AG
                              TGGTG GCC AG  CCCGAGCCC
                              ||||| ||| ||  |||||||||
                              ACCAC CGG TC  GGGCTCGGG
                                _  _ A_
GAM1058 ATP6V1B1 5' GGCTCAGACACTGGGCTCCCA 9880     T      AGCCC
                              TGG GAGCCCAG    GAGCC
                              ||| ||||||||    |||||
                              ACC CTCGGGTC    CTCGG
                                _      ACAGA
GAM1058 CNNM4   5' GCTTGCCTCGAGCTCACCA   39867       CCA  CC
                              TGGTGAGC   GAG  CGAGC
                              ||||||||   |||  |||||
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                                ACCACTCG  CTC  GTTCG
                                    AG_  C_
GAM1058 FLJ12704 3' GGTGGCCCTGGGCTCAC    47171        A  CGA
                                GTGAGCCCAG GCC  GCC
                                |||||||||| |||  |||
                                CACTCGGGTC CGG  TGG
                                    C  ___
GAM1058 FLJ13441 3' GCTACTCCCAGGCTTCACCA  43914     _  CA_  CCCG
                                TGGTGA GCC  GAG  AGC
                                |||||| |||  |||  |||
                                ACCACT CGG  CTC  TCG
                                   T  ACC  A___
GAM1058 FLJ14549 5' GGCCCGAGGTGGCTCACCA  52498       CAGA  _ A
                                TGGTGAGCC  GCC CG GCC
                                |||||||||  ||| || |||
                                ACCACTCGG  TGG GC CGG
                                    ____  A  C
GAM1058 FLJ22341 3' GGGCCCGGGCTCTGGACC  45115   GAGC       A
                                GGT  CCAGAGCCCG GCCC
                                |||  |||||||||| ||||
                                CCA  GGTCTCGGGC CGGG
                                 ____       C
GAM1058 FLJ22969 3' GGCTCAGCATGGGCTCAGCA  69212   G      GA  CC
                                TG TGAGCCCA  GC  GAGCC
                                || ||||||||  ||  |||||
                                AC ACTCGGGT  CG  CTCGG
                                 G      A_  A_
GAM1058 GMPPB   5' GGGCCATGGCTGGGCTCCCA  97456    T     GA  CGA
                                TGG GAGCCCA  GCC  GCCC
                                ||| |||||||  |||  ||||
                                ACC CTCGGGT  CGG  CGGG
                                  _     __  TAC
GAM1058 HSU47926 3' GGCTAGCCTGGAGCTCACCA  27309       _  A  CCG
                                TGGTGAGC CCAG GC  AGCC
                                |||||||| |||| ||  ||||
                                ACCACTCG GGTC CG  TCGG
                                    A  _ A__
GAM1058 IGFALS  3' GGACTCAGGCCCCCACCTGGCT 18315       C  A_____  C  _
            CACC                GGTGAGCC AG     GCC GAG CC
                                |||||||| ||     ||| ||| ||
                                CCACTCGG TC     CGG CTC GG
                                    _ CACCCC  A  A
GAM1058 ITPK1   3' GGGCGTCCTCTGGGCCCCCCA 27234    TGA      CCCGA
                                TGG  GCCCAGAG   GCCC
                                |||  ||||||||   ||||
                                ACC  CGGGTCTC   CGGG
                                  CCC      CTG__
GAM1058 KATII   5' GGACTTTGCCGGGCTCGCCA  33166        ___  C
                                TGGTGAGCCC  AGAG CC
                                ||||||||||  |||| ||
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                                ACCGCTCGGG   TTTC GG
                                     CCG    A
GAM1058  KIAA1052  3'  GGACCCGATTTCTCTGGGCCCA 30945     A       CC__  AG_
             C                    GTG GCCCAGAG    CG   CC
                                  ||| ||||||||    ||   ||
                                  CAC CGGGTCTC    GC   GG
                                    C       TTTA  CCA
GAM1058  KIAA1904  3'  GGGCTCAGGCCCTGGGCTCTGA 73874     ___       A   C
             ACC                    GGT   GAGCCCAG GCC GAGCCC
                                  |||   |||||||| ||| ||||||
                                  CCA   CTCGGGTC CGG CTCGGG
                                    AGT       C   A
GAM1058  MAPKAPK2  3'  GCTCGGGCCCTGGAGGCTGC   17662    G   __   A
                                  GT AGCC  CAG GCCCGAGC
                                  || ||||  ||| ||||||||
                                  CG TCGG  GTC CGGGCTCG
                                   _    AG   C
GAM1058  MRVI1    5'  GGGTCTTCTCCAGGCTCAC    56097        CA   CCC   _
                                  GTGAGCC  GAG   GAG CCC
                                  |||||||  |||   ||| |||
                                  CACTCGG  CTC   TTC GGG
                                      AC   ___   T
GAM1058  PCBP4    5'  CTCCTTCTGGGCTGACCA     40280      G        CCC
                                  TGGT AGCCCAGAG   GAG
                                  |||| |||||||||   |||
                                  ACCA TCGGGTCTT   CTC
                                    G        C__
GAM1058  PLSCR2   5'  GGCTGACCACCTGGGCTCCCA  40149     T       AGCCCG
                                  TGG GAGCCCAG      AGCC
                                  ||| ||||||||      ||||
                                  ACC CTCGGGTC      TCGG
                                    _       CACCAG
GAM1058  PNMA5    3'  GGCCCGGGCTCTGCTCA     73974       CC       A
                                  TGAGC  AGAGCCCG GCC
                                  |||||  |||||||| |||
                                  ACTCG  TCTCGGGC CGG
                                     __        C
GAM1058  PTPRU    5'  GGGCTCGGGCTCCGGGGGCGGC 56524    G  AG   A
             G                     TG TG  CCC GAGCCCGAGCCC
                                   || ||  ||| ||||||||||||
                                   GC GC  GGG CTCGGGCTCGGG
                                    G  GG   C
GAM1058  PTPRU    5'  GGGCTCGGGCTCCGGGGGCGGC 56528    G  AG   A
             G                     TG TG  CCC GAGCCCGAGCCC
                                   || ||  ||| ||||||||||||
                                   GC GC  GGG CTCGGGCTCGGG
                                    G  GG   C
GAM1058  PTPRU    5'  GGGCTCGGGCTCCGGGGGCGGC 20324    G  AG   A
             G                     TG TG  CCC GAGCCCGAGCCC
                                   || ||  ||| ||||||||||||
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                                GC GC  GGG CTCGGGCTCGGG
                                 G  GG   C
GAM1058  RASSF2   3'  GGGTTCTCCAGGTTCACCA   29105        C__
                                TGGTGAGCC   AGAGCCC
                                |||||||||   |||||||
                                ACCACTTGG   TCTTGGG
                                     ACC
GAM1058  STK38L   3'  CTCAGGTAGCTGCATCACCA  69688      GCC   A_   C
                                TGGTGA   CAG  GCC GAG
                                ||||||   |||  ||| |||
                                ACCACT   GTC  TGG CTC
                                   AC_   GA   A
GAM1058  TESK2    3'  GGCTCAACTTCTGGGCTCCCA 63885     T        CCC
                                TGG GAGCCCAGAG   GAGCC
                                ||| ||||||||||   |||||
                                ACC CTCGGGTCTT   CTCGG
                                  _        CAA
GAM1058  TNK1     5'  GGGCCTGCCCTGAGCTCACCA  15650        C   A  CCGA
                                TGGTGAGC CAG GC    GCCC
                                |||||||| ||| ||    ||||
                                ACCACTCG GTC CG    CGGG
                                     A   C  TC__
GAM1058  LOC120072 5'  GGACTTGCTGGGCTCAC     74458          AGCC   _
                                GTGAGCCCAG    CGAG CC
                                ||||||||||    |||| ||
                                CACTCGGGTC    GTTC GG
                                      _____    A
GAM1058  LOC124739 3'  GGGCAGGCTCCAGGCTCACC   74810        CA    CGA
                                GGTGAGCC  GAGCC   GCCC
                                ||||||||  |||||   ||||
                                CCACTCGG  CTCGG   CGGG
                                     AC    A__
GAM1058  LOC145468 3'  TGTGGCTCTGGACTCACCA    74258        C      _
                                TGGTGAG CCAGAGCC CG
                                ||||||| |||||||| ||
                                ACCACTC GGTCTCGG GT
                                     A       T
GAM1058  LOC145858 5'  GGGCATCTCCTGAAGCTCACCA 78003        C_   A____
                                TGGTGAGC  CAG    GCCC
                                ||||||||  |||    ||||
                                ACCACTCG  GTC    CGGG
                                     AA   CTCTA
GAM1058  LOC149372 5'  GGCTCTGTGGAGCTCACCA    80104         _   __
                                TGGTGAGC CCA  GAGCC
                                |||||||| |||  |||||
                                ACCACTCG GGT  CTCGG
                                     A   GT
GAM1058  LOC150155 3'  TGTGGCTTTGGACTCACCA    71419        C      _
                                TGGTGAG CCAGAGCC CG
                                ||||||| |||||||| ||
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                                ACCACTC GGTTTCGG GT
                                    A       T
GAM1058  LOC162048 5'  GGGCCTGCTGGGCTCTCCA    83200     T       A__
                                TGG GAGCCCAG   GCCC
                                ||| ||||||||   ||||
                                ACC CTCGGGTC   CGGG
                                  T       GTC
GAM1058  LOC199780 5'  GCTTCTCTGGGCTCCCA     79483     T        CCC
                                TGG GAGCCCAGAG   GAGC
                                ||| ||||||||||   ||||
                                ACC CTCGGGTCTC   TTCG
                                  _       ____
GAM1058  LOC200933 5'  GGGCTCGGGCTCTGGGGCCGC  91796     AG
                                GTG  CCCAGAGCCCGAGCCC
                                |||  ||||||||||||||||
                                CGC  GGGTCTCGGGCTCGGG
                                  CG
GAM1058  LOC201245 5'  GGGCCTACCCTGAGCTCACCA  88735        C   A_____
                                TGGTGAGC CAG     GCCC
                                |||||||| |||     ||||
                                ACCACTCG GTC     CGGG
                                     A   CCATC
GAM1058  LOC201689 5'  GGGCTGACTTGGCTCTGGGATC 67735       G        CG____
            ACCA                    TGGTGA CCCAGAGCC     AGCCC
                                ||||||| |||||||||     |||||
                                ACCACT GGGTCTCGG     TCGGG
                                    A        TTCAG
GAM1058  LOC202451 3'  GGCTCGGGCCCTGACACTGCCA 91956      G  CC_   A
                                TGGT AG   CAG GCCCGAGCC
                                |||| ||   ||| |||||||||
                                ACCG TC   GTC CGGGCTCGG
                                  _  ACA   C
GAM1058  LOC205327 3'  GCCCAGGCTGTGTGGTTCACCA 91070          _  G    CGA
                                TGGTGAGCC CA AGCC   GC
                                ||||||||| || ||||   ||
                                ACCACTTGG GT TCGG   CG
                                      T  G    ACC
GAM1058  LOC253502 3'  GGGCCCGGCTCTGGGGCCCCCA 96222     TGAG        C A
                                TGG    CCCAGAGCC G GCCC
                                |||    ||||||||| | ||||
                                ACC    GGGTCTCGG C CGGG
                                  CCCG        _ C
GAM1058  LOC256230 5'  GGGCTCTTGCGTCTCCAGCTCA 99317         CC_   _  CC
            CCA                   TGGTGAGC   AGA GC  GAGCCC
                                ||||||||   ||| ||  ||||||
                                ACCACTCG   TCT CG  CTCGGG
                                     ACC   G  TT
GAM1058  LOC256231 5'  GGGCTCTTGCGTCTCCAGCTCA 99320         CC_   _  CC
            CCA                   TGGTGAGC   AGA GC  GAGCCC
                                ||||||||   ||| ||  ||||||
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                                ACCACTCG  TCT CG  CTCGGG
                                    ACC  G  TT
GAM1058  LOC51200  3'  GGGCTCGATCTTGGCTCACCA  33438       C  GCC
                                TGGTGAGCC AGA  CGAGCCC
                                ||||||||| |||  |||||||
                                ACCACTCGG TCT  GCTCGGG
                                     T  A__
GAM1058  LOC92078  3'  GGGCACATCTGGGCTCACTA  68608         ___
                                TGGTGAGCCCAGA  GCCC
                                ||||||||||||  ||||
                                ATCACTCGGGTCT  CGGG
                                       ACA
GAM1059  HRH1     3'  CTCAAACATGTTTAGAGTGGA  7819      A    TGG
                                TCCA TCTGA  GCATGTTTGAG
                                |||| |||||  ||||||||||
                                AGGT AGATT  TGTACAAACTC
                                  G   ___
GAM1059  TRIM37   3'  CTCAAATTTGTCATCAG    31625       G  T
                                CTGATGG CA GTTTGAG
                                ||||||| || |||||||
                                GACTACT GT TAAACTC
                                    _  T
GAM1059  HTMP10   3'  CTCAAAAAAGCCATCAGATCTG 53758    CA       G ATG
           A                     TC  ATCTGATGG C  TTTGAG
                                ||  ||||||||| |  ||||||
                                AG  TAGACTACC G  AAACTC
                                 TC       _ AAA
GAM1059  PAK2     5'  CTCAAATATCACCAAACTAGA  67140     A__  GC
                                TCTG  TGG  ATGTTTGAG
                                ||||  |||  |||||||||
                                AGAT  ACC  TATAAACTC
                                  CAA  AC
GAM1059  SEMA6A   3'  CTCGAGTACCCACCAGA    40818     A   CA
                                TCTG TGGG  TGTTTGAG
                                |||| ||||  ||||||||
                                AGAC ACCC  ATGAGCTC
                                  C  __
GAM1059  TTY7     3'  TCAAACATGCAGGCTGGA    50019     AT  GATGG
                                TCCA  CT    GCATGTTTGA
                                ||||  ||    ||||||||||
                                AGGT  GA    CGTACAAACT
                                  CG  _____
GAM1059  LOC144766 3'  CTCAAACATGAGAAGACTGGG  77481     A  GATGGG
                                TCCA TCT     CATGTTTGAG
                                |||| |||     ||||||||||
                                GGGT AGA     GTACAAACTC
                                  C  AGA___
GAM1059  LOC201685 5'  TAAACACCCATCAGATGGA   91845     A       CA
                                TCCA TCTGATGGG  TGTTTG
                                |||| |||||||||  ||||||
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                                AGGT AGACTACCC  ACAAAT
                                  _      __
GAM1059  LOC221596 5'  CTCAAACAAAACTCAGATT   93623       TG GCA
                                AATCTGA  G   TGTTTGAG
                                |||||||  |   ||||||||
                                TTAGACT  C   ACAAACTC
                                   __ AAA
GAM1059  LOC93622  3'  CTCTGCAGACCATCAGAT    57729        GCA   TT
                                ATCTGATGG   TGT  GAG
                                |||||||||   |||  |||
                                TAGACTACC   ACG  CTC
                                     AG_   T_
GAM1060  ANKTM1    3'  AGATGTTATTATGCTATAGC   24695    C    C_
                                GC ATAGC  AGTAACATCT
                                || |||||  ||||||||||
                                CG TATCG  TTATTGTAGA
                                 A    TA
GAM1060  CLN5      3'  AGATGTTACTGGTCTGTG    22428      _
                                CATAG CCAGTAACATCT
                                ||||| ||||||||||||
                                GTGTC GGTCATTGTAGA
                                   T
GAM1060  PIP5K1B   3'  AGACGTGAGCACAGTTATGGCA 14524        CA_  A_  A
                                TGCCATAGC   GT  AC TCT
                                |||||||||   ||  || |||
                                ACGGTATTG   CG  TG AGA
                                     ACA  AG  C
GAM1060  PYGO2     3'  AGAGTTCCTGGTTATGGCA   64682          T   A
                                TGCCATAGCCAG AAC TCT
                                |||||||||||| ||| |||
                                ACGGTATTGGTC TTG AGA
                                       C  _
GAM1060  RBM8A     3'  AGATGTTAAGATCTTATGGCA  18803        CCAG_
                                TGCCATAG    TAACATCT
                                ||||||||    ||||||||
                                ACGGTATT    ATTGTAGA
                                    CTAGA
GAM1060  SFRS2IP   5'  AGATGTTAGTAGCTATGCA   17535    C    CAG
                                TGC ATAGC   TAACATCT
                                ||| |||||   ||||||||
                                ACG TATCG   ATTGTAGA
                                  _    ATG
GAM1060  TMOD      3'  AGATCAACATGGCTATGGTA   13809         GTAAC
                                TGCCATAGCCA    ATCT
                                ||||||||||    ||||
                                ATGGTATCGGT    TAGA
                                       ACAAC
GAM1060  TRPM7     3'  AGATGCTTGTTGGCCACGGG   62816    ATA_      _
                                CC    GCCAGTAA CATCT
                                ||    |||||||| |||||
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                                GG   CGGTTGTT GTAGA
                                 GCAC      C
GAM1060 FLJ11827 3' AGATGTTACCATTGGGGGTA  47677    ATAG  ___
                                TGCC   CCA  GTAACATCT
                                ||||   |||  |||||||||
                                ATGG   GGT  CATTGTAGA
                                  G___  TAC
GAM1060 KCNMB2   3' AGATGCTACTTGTTGGTA   20683     TA C   A
                                TGCCA  GC AGTA CATCT
                                |||||  || |||| |||||
                                ATGGT  TG TCAT GTAGA
                                   __ T   C
GAM1060 KIAA0016 3' AGACTTACTGGCTGTAGCA   29307    C       CA
                                TGC ATAGCCAGTAA  TCT
                                ||| ||||||||||  |||
                                ACG TGTCGGTCATT  AGA
                                  A        C_
GAM1060 MGC10955 3' AGATGTTGTAGCCATGGC    52031     A  CAG
                                GCCAT GC   TAACATCT
                                ||||| ||   ||||||||
                                CGGTA CG   GTTGTAGA
                                   C  AT_
GAM1060 RAB40A   5' AGGTGGACTGGCTACAGG    82942    A_     AA
                                CC  TAGCCAGT  CATCT
                                ||  ||||||||  |||||
                                GG  ATCGGTCA  GTGGA
                                 AC       G_
GAM1060 LOC144289 5' AGATGTTACCAGCCAGTGGC  83947     A_  CA
                                GCCAT  GC  GTAACATCT
                                |||||  ||  |||||||||
                                CGGTG  CG  CATTGTAGA
                                   AC  AC
GAM1060 LOC148293 5' AGATGTTGGGTTAATAGCA   79526    CA_   AG
                                TGC   TAGCC  TAACATCT
                                |||   |||||  ||||||||
                                ACG   ATTGG  GTTGTAGA
                                  ATA    __
GAM1060 LOC170037 5' AGATGTTAATAACTATAGCA  88593    C   CCAG
                                TGC ATAG    TAACATCT
                                ||| ||||    ||||||||
                                ACG TATC    ATTGTAGA
                                  A   AATA
GAM1060 LOC257451 3' AGAGTTCCTGGTTATGGCA   97294         T  A
                                TGCCATAGCCAG AAC TCT
                                |||||||||||| ||| |||
                                ACGGTATTGGTC TTG AGA
                                        C  _
GAM1060 LOC55829  3' AGATGTTGCCTCTAGGCA    38033     A  CCA
                                TGCC TAG   GTAACATCT
                                |||| |||   |||||||||
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                                ACGG ATC   CGTTGTAGA
                                  _   TC_
GAM1060  LOC90049  3'  AGATGTTGGGTTAATAGCA   61874     CA_    AG
                                TGC   TAGCC  TAACATCT
                                |||   |||||  ||||||||
                                ACG   ATTGG  GTTGTAGA
                                  ATA    __
GAM1061  BACE      5'  CTGGCCCAGGGCCCTGCA    25032     AAA    A
                                TGCA   GCCC GGGTTAG
                                ||||   |||| |||||||
                                ACGT   CGGG CCCGGTC
                                  CC_    A
GAM1061  BACE      5'  CTGGCCCAGGGCCCTGCA    58084     AAA    A
                                TGCA   GCCC GGGTTAG
                                ||||   |||| |||||||
                                ACGT   CGGG CCCGGTC
                                  CC_    A
GAM1061  CERD4     3'  TTCCTCTGGGTGGGCTTTGGCA 24885     A       GGGTT
                                TGC AAAGCCCA     AGGAA
                                ||| ||||||||     |||||
                                ACG TTTCGGGT     TCCTT
                                  G       GGGTC
GAM1061  DMRT2     3'  CCTAATCTGGACTTTTGCA    22650        C     G
                                TGCAAAAG CCAGG TTAGG
                                |||||||| ||||| |||||
                                ACGTTTTC GGTCT AATCC
                                    A    _
GAM1061  EBAF      3'  CCATTCTGGACTTTTGTA     66025        C      TA
                                TGCAAAAG CCAGGGT  GG
                                |||||||| |||||||  ||
                                ATGTTTTC GGTCTTA  CC
                                    A      __
GAM1061  ESR1      3'  CCTTCCCTGGGCCTTTGC     5512        A       TT
                                GCAAA GCCCAGGG  AGG
                                ||||| ||||||||  |||
                                CGTTT CGGGTCCC  TCC
                                  C       T_
GAM1061  GJA4      3'  CCCTCTGGCCTTTTGCA      60083        C     TTA
                                TGCAAAAG CCAGGG   GG
                                |||||||| ||||||   ||
                                ACGTTTTC GGTCTC   CC
                                    C     ___
GAM1061  GPR56     3'  TCCCGGGCTGGGCTTTTG     20278         G G TA
                                CAAAAGCCCA G T  GGA
                                |||||||||| | |  |||
                                GTTTTCGGGT C G  CCT
                                    _ G GC
GAM1061  LENG4     3'  CCTGGCCCGGGCCTTGCA     44418       AA    A
                                TGCAA  GCCC GGGTTAGG
                                |||||  |||| ||||||||
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                                ACGTT  CGGG CCCGGTCC
                                  C_   _
GAM1061  MAT1A    3'  GGCTCCTTGTGGGCCTGGGCTC 92503    AA      G ___   A
                CTG                CA  AGCCCAGG TT   AGGA CC
                                   ||  |||||||| ||   |||| ||
                                   GT  TCGGGTCC GG   TCCT GG
                                    CC       G  TGT    C
GAM1061  MYOG     3'  CCCTGGGGGGGCCAAACTTTTGC 60067       ________
                  A                 TGCAAAAG       CCCAGGG
                                    ||||||||       |||||||
                                    ACGTTTTC       GGGTCCC
                                         AAACCGGG
GAM1061  OGG1     3'  TCTACCCCTGGGCTTTTG    34167           T
                                    CAAAAGCCCAGGG TAGG
                                    |||||||||||| ||||
                                    GTTTTCGGGTCCC ATCT
                                          C
GAM1061  OGG1     3'  TCTACCCCTGGGCTTTTG    34170           T
                                    CAAAAGCCCAGGG TAGG
                                    |||||||||||| ||||
                                    GTTTTCGGGTCCC ATCT
                                          C
GAM1061  OGG1     3'  TCTACCCCTGGGCTTTTG    34171           T
                                    CAAAAGCCCAGGG TAGG
                                    |||||||||||| ||||
                                    GTTTTCGGGTCCC ATCT
                                          C
GAM1061  OGG1     3'  TCTACCCCTGGGCTTTTG    34172           T
                                    CAAAAGCCCAGGG TAGG
                                    |||||||||||| ||||
                                    GTTTTCGGGTCCC ATCT
                                          C
GAM1061  PSEN1    3'  TTCCCGGCTGGACTTTTGCA   5244        C   GG  TA
                                    TGCAAAAG CCA  GT  GGAA
                                    |||||||| |||  ||  ||||
                                    ACGTTTTC GGT  CG  CCTT
                                         A   __  GC
GAM1061  PSEN1    3'  TTCCCGGCTGGACTTTTGCA   24625       C   GG  TA
                                    TGCAAAAG CCA  GT  GGAA
                                    |||||||| |||  ||  ||||
                                    ACGTTTTC GGT  CG  CCTT
                                         A   __  GC
GAM1061  PTMS     3'  GGCTCCCTGCTCTGGGCCCTGC 12565     AAA       TA  A
                  A                 TGCA   GCCCAGGGT  GGA CC
                                    ||||   |||||||||  ||| ||
                                    ACGT   CGGGTCTCG  CCT GG
                                      CC_        TC   C
GAM1061  TGFBR2   3'  GGTTCCATCTTTCTGGGCTCCT 13733    AA       TTA_
                  G                 CA  AGCCCAGGG   GGAACC
                                    ||  |||||||||   ||||||
```

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                                GT  TCGGGTCTT   CCTTGG
                                 CC       TCTA
GAM1061  TGFBR3   3'  TGACCCTGGGCTTCTGTA    13741     A
                                TGCA AAGCCCAGGGTTA
                                |||| ||||||||||||
                                ATGT TTCGGGTCCCAGT
                                  C
GAM1061  UBE1     3'  GGTTCCCATTTGGCTTCTGGCA 13925    AA_    C   GTTA
                                TGC   AAGCC AGG   GGAACC
                                |||   ||||| |||   ||||||
                                ACG   TTCGG TTT   CCTTGG
                                  GTC    _  AC__
GAM1061  BCL2L1   3'  CCAGATCTGGTCCCTTGCA   57587     AA_  CA    A
                                TGCAA   GCC  GGGTT GG
                                |||||   |||  ||||| ||
                                ACGTT   TGG  TCTAG CC
                                   CCC   __    A
GAM1061  C1orf34  3'  TCCTTTCCCGAAGCTTTTGCA  61323        CCA   TT
                                TGCAAAAGC   GGG  AGGA
                                |||||||||   |||  ||||
                                ACGTTTTCG   CCC  TCCT
                                     AAG   TT
GAM1061  DKFZP434C1715 3'  GGTTCAGATCTGGGCTTTGCA  87357       A     GTTAG
                                TGCAAA GCCCAGG    GAACC
                                |||||| |||||||    |||||
                                ACGTTT CGGGTCT    CTTGG
                                   _     AGA__
GAM1061  DKFZP547L112 5'  GGCCCCGCAGAGCCCTGGACTC 67133    AAA  C     TA___  AA
           TGGCA                  TGC   AG CCAGGGT    GG  CC
                                |||   || |||||||    ||  ||
                                ACG   TC GGTCCCG    CC  GG
                                  GTC  A      AGACG  CC
GAM1061  DKFZP761D0211 3'  CCTTCCCTGGGTCTCTGCA   50178     AAA      TT
                                TGCA   GCCCAGGG  AGG
                                ||||   ||||||||  |||
                                ACGT   TGGGTCCC  TCC
                                  CTC       T_
GAM1061  E2F6     3'  TCCTTTCAGGTTTTTGCA    10475         CA   TT
                                TGCAAAAGCC  GGG  AGGA
                                |||||||||  |||  ||||
                                ACGTTTTTGG  CTT  TCCT
                                     A_   __
GAM1061  FLJ20211  3'  CCTTCCTGGGCCTCTGTA    35259     AAA      TT
                                TGCA   GCCCAGGG  AGG
                                ||||   ||||||||  |||
                                ATGT   CGGGTCCT  TCC
                                  CTC       __
GAM1061  GREB1    3'  TTCTGGCTTCTGGACTCTGCA  28583     AA  C    _
                                TGCA  AG CCAGG GTTAGGA
                                ||||  ||  ||||| |||||||
```

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                                ACGT  TC GGTCT CGGTCTT
                                  C_ A    T
GAM1061  GS3955   3'  TCCTGGAGTCTGATGCTTTTGC 41627        C_   G_
             A                   TGCAAAAGC  CAGG  TTAGGA
                                 |||||||||  ||||  ||||||
                                 ACGTTTTCG  GTCT  GGTCCT
                                      TA   GA
GAM1061  GS3955   5'  TCTGTGCCCAGCTTTTGCA   41628        CCA   TA
                                 TGCAAAAGC   GGGT  GGA
                                 |||||||||   ||||  |||
                                 ACGTTTTCG   CCCG  TCT
                                      A__   TG
GAM1061  KCNK17   3'  CCTGATTTTAAGCTTTGCA   49592       A  CC
                                 TGCAAA GC  AGGGTTAGG
                                 ||||||  ||  |||||||||
                                 ACGTTT CG  TTTTAGTCC
                                    _  AA
GAM1061  KIAA0125 3'  CCTCCTGGGCTTCTGC      61126     A       GTT
                                 GCA AAGCCCAGG   AGG
                                 ||| |||||||||   |||
                                 CGT TTCGGGTCC   TCC
                                   C       ___
GAM1061  KIAA0193 3'  GGTTTGGCCTGGGCTTT     29316          GTTAG
                                 AAAGCCCAGG    GAACC
                                 ||||||||||    |||||
                                 TTTCGGGTCC    TTTGG
                                      GG___
GAM1061  KIAA0494 5'  TTCCCAACCCTGGAAGGCA   29406     AAAAGC       A
                                 TGC     CCAGGGTT GGAA
                                 |||     |||||||| ||||
                                 ACG     GGTCCCAA CCTT
                                   GAA___       C
GAM1061  KIAA0514 3'  AGCCCCAGGGTAGGTTTCTGCA 28737      _  ___    A_
                                 TGCA AAA   GCCC  GGGTT
                                 |||| |||   ||||  |||||
                                 ACGT TTT   TGGG  CCCGA
                                   C   GGA   AC
GAM1061  KIAA0668 3'  GGCTGCCCCCTTGGGCTCTTGC 67123       A       TTA  AA_
             A                   TGCAA AGCCCAGGG   GG   CC
                                 |||||  |||||||||   ||   ||
                                 ACGTT TCGGGTTCC   CC   GG
                                    C        C__  GTC
GAM1061  KIAA0700 3'  CCTGGCCCTGGCCCCTGCA   72517     AAA   C
                                 TGCA   GCC AGGGTTAGG
                                 ||||   ||| |||||||||
                                 ACGT   CGG TCCCGGTCC
                                   CCC   _
GAM1061  KIAA0705 3'  GGTTCCCTTGTGGGGGCTTTGG 25483     A      AGGGTTA
             CA                    TGC AAAGCCC      GGAACC
                                   ||| |||||||      ||||||
```

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                                ACG TTTCGGG      CCTTGG
                                  G      GGTGTTC
GAM1061  KIAA0937  3'  CCTTTTCCCCTGGGCTTTTG  93225           TT__
                                CAAAAGCCCAGGG    AGG
                                ||||||||||||    |||
                                GTTTTCGGGTCCC    TCC
                                      CTTT
GAM1061  KIAA1190  3'  GGTTCCTGTTTTACTAGCTTTT 71654    C     CC  GGT__
           ACA                    TG AAAAGC  AG    TAGGAACC
                                || ||||||  ||    ||||||||
                                AC TTTTCG  TC    GTCCTTGG
                                 A     A_  ATTTT
GAM1061  KIAA1337  3'  CCCGGCTTGGGCTTCTGCA   73058      A       G TA
                                TGCA AAGCCCAGG T  GG
                                |||| |||||||| |  ||
                                ACGT TTCGGGTTC G  CC
                                  C       _ GC
GAM1061  KIAA1432  5'  GGTTCATTCCTGGGCTT     67308          TTAG
                                AAGCCCAGGG    GAACC
                                ||||||||||    |||||
                                TTCGGGTCCT    CTTGG
                                      TA__
GAM1061  KIAA1530  5'  GTCCTCTTGGCCTCTGCA    68567      AA  C    GTT    A
                                TGCA  AG CCAGG   AGGA C
                                ||||  || |||||   |||| |
                                ACGT  TC GGTTC   TCCT G
                                  C_  C     ___    C
GAM1061  KIAA1877  3'  TCTACCCTGCAGCTTTTGCA   66764         C_     TA
                                TGCAAAAGC  CAGGGT  GGA
                                |||||||||  ||||||  |||
                                ACGTTTTCG  GTCCCA  TCT
                                     AC     __
GAM1061  KIAA1985  3'  TTCCTGGTTCCAGGCTTTGCA  45019       A   CA GG
                                TGCAAA GCC  G  TTAGGAA
                                |||||| |||  |  |||||||
                                ACGTTT CGG  C  GGTCCTT
                                   _   AC TT
GAM1061  MGC13170  5'  GTCTCCTGGGTCCTGCA     52132      AAA      GTTA   A
                                TGCA   GCCCAGG    GGA C
                                ||||   |||||||    ||| |
                                ACGT   TGGGTCC    TCT G
                                  CC_       _____   C
GAM1061  MGC15429  3'  GACCCCATGGGCCAGCCCTTGC 52212       AA_____    __
           A                    TGCAA     GCCCA  GGGTT
                                |||||     |||||  |||||
                                ACGTT     CGGGT  CCCAG
                                   CCCGAC    AC
GAM1061  MR       3'  GGTTCCTAATAAAAAGCCTTT  49148     A  CCAGG
                                AAA GC     GTTAGGAACC
                                ||| ||     ||||||||||
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                                TTT CG    TAATCCTTGG
                                  C  AAAAA
GAM1061  my048    5'  CCTGTCCTGGGTCCCCGCA   55368    AAAA      T
                                TGC   GCCCAGGGT AGG
                                |||   |||||||||| |||
                                ACG   TGGGTCCTG TCC
                                  CCCC       _
GAM1061  NPTXR    3'  TGACCCTGGGCTTCGCA    55219    AA
                                TGC  AAGCCCAGGGTTA
                                |||  ||||||||||||
                                ACG  TTCGGGTCCCAGT
                                  C_
GAM1061  NPTXR    3'  TGACCCTGGGCTTCGCA    27446    AA
                                TGC  AAGCCCAGGGTTA
                                |||  ||||||||||||
                                ACG  TTCGGGTCCCAGT
                                  C_
GAM1061  OAZ2     3'  GGCTCCTGAGTATAGGCTTTTC 11880   C     CAGGG    A
                A                TG AAAAGCC    TTAGGA CC
                                || |||||||    |||||| ||
                                AC TTTTCGG    AGTCCT GG
                                 _     ATATG    C
GAM1061  SLC31A2  3'  TCCTAGTTGGCAATTTTGCA  60762      GC_   GG
                                TGCAAAA   CCAG  TTAGGA
                                |||||||   ||||  ||||||
                                ACGTTTT   GGTT  GATCCT
                                    AAC   __
GAM1061  SV2B     3'  AGCTCTGCAGACTTTTGCA   29947      CC__
                                TGCAAAAG   CAGGGTT
                                ||||||||   |||||||
                                ACGTTTTC   GTCTCGA
                                     AGAC
GAM1061  Ubc6p    3'  GGCTCCTAGGTTTAGCTTTT   55193     CC   G    A
                                AAAAGC  AGG TTAGGA CC
                                ||||||  ||| |||||| ||
                                TTTTCG  TTT GATCCT GG
                                   A_   G    C
GAM1061  UBP1     3'  GTTCCTAGAAGCAGCCTTTGC  27995     A  CCAGGG
                                GCAAA GC     TTAGGAAC
                                ||||| ||     ||||||||
                                CGTTT CG     GATCCTTG
                                  C  ACGAA_
GAM1061  ZNF286   5'  TCTAACCCAGGCCTTTCA    40670    C   A   CA
                                TG AAA GCC  GGGTTAGG
                                || ||| |||  ||||||||
                                AC TTT CGG  CCCAATCT
                                 _  C   A_
GAM1061  LOC112476 3'  CCGCCCACCTGGGCTTTTCA  59784    C        GTTA_
                                TG AAAAGCCCAGG    GG
                                || ||||||||||     ||
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                                AC TTTTCGGGTCC    CC
                                 _         ACCCG
GAM1061  LOC113201 5' CCGAGGCCTGGGCTTCTGC   57355    A       G  A
                                GCA AAGCCCAGG TT GG
                                ||| ||||||||| || ||
                                CGT TTCGGGTCC GA CC
                                  C        G  G
GAM1061  LOC118738 3' TTCGAATCTGGGCTCTTTCA  76008   C  A      GTTA
                                TG AA AGCCCAGG   GGA
                                || || ||||||||   |||
                                AC TT TCGGGTCT   CTT
                                 T  C       AAG_
GAM1061  LOC118976 5' TTTGGACCTTGACTTCTGCA  74390    A   CC      AG
                                TGCA AAG  CAGGGTT  GA
                                |||| |||  |||||||  ||
                                ACGT TTC  GTTCCAG  TT
                                  C   A_      GT
GAM1061  LOC120856 3' TTCCTGAGCTAGGCCTTTG   74476    A   CA  G
                                CAAA GCC  GG TTAGGAA
                                |||| |||  || |||||||
                                GTTT CGG  TC AGTCCTT
                                  C   A_  G
GAM1061  LOC134553 3' TTTTATGGCCTGGGCTTT    75690         GT_
                                AAAGCCCAGG   TAGGA
                                ||||||||||   |||||
                                TTTCGGGTCC   ATTTT
                                     GGT
GAM1061  LOC149421 3' AGCCCTGCCGGACTTTGGCA  80139    A   _ __
                                TGC AAAG CC  CAGGGTT
                                ||| |||| ||  |||||||
                                ACG TTTC GG  GTCCCGA
                                  G    A  CC
GAM1061  LOC151568 3' GTGTTAGCCCTAGGCTCCTGTA 57496     AA   C      GA
                                TGCA  AGCC AGGGTTAG  AC
                                ||||  |||| ||||||||  ||
                                ATGT  TCGG TCCCGATT  TG
                                  CC   A      G_
GAM1061  LOC153688 3' CCTGCTCTGGCTTCTGCA    87308    A    C    T
                                TGCA AAGCC AGGGT AGG
                                |||| ||||| ||||| |||
                                ACGT TTCGG TCTCG TCC
                                  C    _    _
GAM1061  LOC154007 3' GGCCCCTAGCTCTAAGTCCTTG 81928      AA  CC       AA
           CA                    TGCAA  GC  AGGGTTAGG  CC
                                |||||  ||  |||||||||  ||
                                ACGTT  TG  TCTCGATCC  GG
                                   CC  AA       CC
GAM1061  LOC162417 3' TTCCTTTGGGTCTTGCA     83215      AA     GGTT
                                TGCAA  GCCCAG   AGGAA
                                |||||  ||||||   |||||
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                                ACGTT  TGGGTT    TCCTT
                                  C_     ____
GAM1061  LOC199678 3'  GGTTCCTGTCCCCAAACTTCGC 91370     AA   CCCA   T
             A                    TGC  AAG    GGG TAGGAACC
                                  |||  |||    ||| ||||||||
                                  ACG  TTC    CCC GTCCTTGG
                                    C_   AAAC   T
GAM1061  LOC201294 5'  AGCCCCAGGCTCTTTGCA    89575       _    CA
                                  TGCAAA AGCC  GGGTT
                                  ||||||| ||||  |||||
                                  ACGTTT TCGG  CCCGA
                                     C    AC
GAM1061  LOC201799 3'  AACACCTGGGCCTTTACA    90486    C   A      _
                                  TG AAA GCCCAGG GTT
                                  || ||| ||||||| |||
                                  AC TTT CGGGTCC CAA
                                   A  C      A
GAM1061  LOC202266 3'  CCTCTCCTGGGCTTCTG     91936    A        TT
                                  CA AAGCCCAGGG  AGG
                                  || ||||||||||  |||
                                  GT TTCGGGTCCT  TCC
                                   C         C_
GAM1061  LOC203197 3'  CCCCCTGGCCTTTGCA      90808       A   C    TTA
                                  TGCAAA GCC AGGG   GG
                                  |||||| ||| ||||   ||
                                  ACGTTT CGG TCCC   CC
                                     C   _   ____
GAM1061  LOC203427 3'  AACTCCTGGGCTCATGCA    90916      AA       _
                                  TGCA  AGCCCAGG GTT
                                  ||||  |||||||| |||
                                  ACGT  TCGGGTCC CAA
                                    AC       T
GAM1061  LOC220549 3'  TTCTTCCGGGCTTTT       94513         A   TT
                                  AAAAGCCC GGG  AGGA
                                  |||||||| |||  ||||
                                  TTTTCGGG CCT  TCTT
                                        _  __
GAM1061  LOC220776 3'  GTCCCTCCAGGGCTTTTCA   68934    C       A  GTT   A
                                  TG AAAAGCCC GG   AGG AC
                                  || |||||||| ||   ||| ||
                                  AC TTTTCGGG CC   TCC TG
                                   _       A ____   C
GAM1061  LOC221415 5'  CCACGCGCCTGGGCTCTGCA   95499      AA       _ TA
                                  TGCA  AGCCCAGG GT  GG
                                  ||||  |||||||| ||  ||
                                  ACGT  TCGGGTCC CG  CC
                                    C_       G  CA
GAM1061  LOC222008 5'  TTCCAGCCTGGGCTCCGCA   95661     AAA       G  A
                                  TGC   AGCCCAGG TT GGAA
                                  |||   |||||||| || ||||
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                                ACG   TCGGGTCC GA CCTT
                                  CC_       _ _
GAM1061  LOC256230 5'  CCCCCTGGGCTCTTGC      99315      A        TTA
                                GCAA AGCCCAGGG   GG
                                |||| |||||||||   ||
                                CGTT TCGGGTCCC   CC
                                  C       ____
GAM1061  LOC256231 5'  CCCCCTGGGCTCTTGC      99318      A        TTA
                                GCAA AGCCCAGGG   GG
                                |||| |||||||||   ||
                                CGTT TCGGGTCCC   CC
                                  C       ____
GAM1061  LOC257206 5'  TTCAACCTCAAACTTTTGCA   98894         CCCA     A
                                TGCAAAAG    GGGTT GGA
                                ||||||||    ||||| |||
                                ACGTTTTC    TCCAA CTT
                                     AAAC     _
GAM1061  LOC51162  5'  CCACGCCTGGGCTCCAGCA    66396     AAA       _  TA
                                TGC   AGCCCAGG GT  GG
                                |||   |||||||| ||  ||
                                ACG   TCGGGTCC CA  CC
                                  ACC       G  __
GAM1061  LOC51162  5'  CCACGCCTGGGCTCCAGCA    33048     AAA       _  TA
                                TGC   AGCCCAGG GT  GG
                                |||   |||||||| ||  ||
                                ACG   TCGGGTCC CA  CC
                                  ACC       G  __
GAM1061  LOC90630  5'  CCTAATCTGGACTCATTGCA   64390      A_  C     G
                                TGCAA  AG CCAGG TTAGG
                                |||||  || ||||| |||||
                                ACGTT  TC GGTCT AATCC
                                   AC  A     _
GAM1061  LOC90784  5'  GTCACTGGCCCTAGGTTTCTGC 64699      A     C       GA
            A                    TGCA AAGCC AGGGTTAG  AC
                                |||| ||||| ||||||||  ||
                                ACGT TTTGG TCCCGGTC  TG
                                  C     A       AC
GAM1061  LOC91208  5'  CCTAATCTGGACTCATTGCA   65852      A_  C     G
                                TGCAA  AG CCAGG TTAGG
                                |||||  || ||||| |||||
                                ACGTT  TC GGTCT AATCC
                                   AC  A     _
GAM1061  LOC92558  3'  CTTGGTGTTGGGCTTTGCA    70310       A     G TT
                                TGCAAA GCCCAG G  AGG
                                |||||| |||||| |  |||
                                ACGTTT CGGGTT T  TTC
                                   _     G GG
GAM1061  LOC96597  5'  TCAAGCCCTGACCTTTGCA    67465       A CC      A
                                TGCAAA G  CAGGGTT GG
                                |||||| |  ||||||| ||
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                                ACGTTT C  GTCCCGA CT
                                   _ CA      A
GAM1062  CNTN2    5'  AGCCTCCAGCTGGGCT      18656      TTTA        A
                                AGCT    CAGCTGGAG CT
                                ||||    ||||||||| ||
                                TCGG    GTCGACCTC GA
                                  ____         C
GAM1062  GALNT7   3'  CAGCTGAAAAGCTTCAA      55087           A
                                TTGAAGCTTTT CAGCTG
                                |||||||||| ||||||
                                AACTTCGAAAA GTCGAC
                                           _
GAM1062  JAM3     3'  CTCATTTATAAAAGCTTCAA   52488           CAGCTG
                                TTGAAGCTTTTA     GAG
                                ||||||||||||     |||
                                AACTTCGAAAAT     CTC
                                       ATTTA_
GAM1062  KLRD1    5'  TCTCCAGCTCAGCTTCAA    24710        TTTAC
                                TTGAAGCT    AGCTGGAGA
                                ||||||||    |||||||||
                                AACTTCGA    TCGACCTCT
                                     C____
GAM1062  KLRD1    5'  TCTCCAGCTCAGCTTCAA    11215        TTTAC
                                TTGAAGCT    AGCTGGAGA
                                ||||||||    |||||||||
                                AACTTCGA    TCGACCTCT
                                     C____
GAM1062  TEM7     3'  AGCCTCCAGCTATCTGCTCA   40243     A  TTTTAC       A
                                TGA GC      AGCTGGAG CT
                                ||| ||      |||||||| ||
                                ACT CG      TCGACCTC GA
                                  _ TCTA__       C
GAM1062  TEX13B   3'  TCTGGCTGCAAAAGCCTCAG   66171     A     A    TG
                                TTGA GCTTTT CAGC  GA
                                |||| |||||| ||||  ||
                                GACT CGAAAA GTCG  CT
                                  C     C    GT
GAM1062  ZNF236   3'  TCTCTGTTTTAAAGCTTCAA   24738          TAC   T
                                TTGAAGCTTT   AGC GGAGA
                                ||||||||||   ||| |||||
                                AACTTCGAAA   TTG TCTCT
                                     TT_  _
GAM1062  FLJ10512 3'  AGTCTATATTGTAAAAGC    36691          CTGG
                                GCTTTTACAG    AGACT
                                ||||||||||    |||||
                                CGAAAATGTT    TCTGA
                                     ATA_
GAM1062  H2AV     3'  GTTTCACAAAAGCTTCAA     57633          ACAGCTG
                                TTGAAGCTTTT      GAGAC
                                ||||||||||       |||||
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                                AACTTCGAAAA      CTTTG
                                      CA_____
GAM1062  KIAA1884  3'  CCATAAAGGCTTCAA      73721          CAGC
                                TTGAAGCTTTTA    TGG
                                ||||||||||||    |||
                                AACTTCGGAAAT    ACC
                                      _____
GAM1062  KIAA1893  3'  AGTCTGAGTGGCAGAAGCTTCA 73586          ACA   GG
              A                  TTGAAGCTTTT   GCT  AGACT
                                 ||||||||||||  |||  |||||
                                 AACTTCGAAGA   TGA  TCTGA
                                       CGG   G_
GAM1062  LOC154792 3'  AGCCTCCAGAGAAAAGATTCAA 87462      G    ACAG     A
                                 TTGAA CTTTT    CTGGAG CT
                                 |||||  |||||    ||||||  ||
                                 AACTT GAAAA    GACCTC GA
                                    A    GA__     C
GAM1062  LOC199232 3'  AGTTTTTGTACAAAAGCTTCAA 90411          ACA  T
                                 TTGAAGCTTTT   GC GGAGACT
                                 ||||||||||||  ||  |||||||
                                 AACTTCGAAAA   TG TTTTTGA
                                       CA_  _
GAM1062  LOC221543 5'  AGTCTCCAAGGAAAACTTGCAA 95362     _  C    ACAGC
                                 TTG AAG TTTT     TGGAGACT
                                 |||  |||  ||||    ||||||||
                                 AAC TTC AAAG     ACCTCTGA
                                   G   A    GA___
GAM1062  LOC255533 5'  AGTCTATAATGTAAAAGCTTGA 98752    G         GCTGG
              A                   TT AAGCTTTTACA     AGACT
                                  ||  ||||||||||     |||||
                                  AA TTCGAAAATGT     TCTGA
                                   G          AATA_
GAM1062  LOC257596 5'  AGTCTCCAAGGAAAACTTGCAA 99765     _  C    ACAGC
                                 TTG AAG TTTT     TGGAGACT
                                 |||  |||  ||||    ||||||||
                                 AAC TTC AAAG     ACCTCTGA
                                   G   A    GA___
GAM1063  AASS     3'  GAGTCTCGCTCTGTCACCCAGG 20460       CC
                                 CCTGGG  ACAGAGCGAGACTC
                                 ||||||  ||||||||||||||
                                 GGACCC  TGTCTCGCTCTGAG
                                    AC
GAM1063  ACP1     3'  CTCACTTGAAGGCCCAGGT   24012         ACA   C
                                 ACCTGGGCC   GAG GAG
                                 |||||||||   |||  |||
                                 TGGACCCGG   TTC CTC
                                       AAG   A
GAM1063  ACP1     3'  CTCACTTGAAGGCCCAGGT   16286         ACA   C
                                 ACCTGGGCC   GAG GAG
                                 |||||||||   |||  |||
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                                TGGACCCGG   TTC CTC
                                     AAG   A
GAM1063  ADAMTS4   3'  GAATCTCGCTCTGTCGCCCAGG 18760        C          C
                                CCTGGGC ACAGAGCGAGA TC
                                ||||||| |||||||||| ||
                                GGACCCG TGTCTCGCTCT AG
                                    C         A
GAM1063  ATP7A     3'  GAGTCTTGTTTTGCAGCCCAGG 5324         CA
                                CCTGGGC  CAGAGCGAGACTC
                                |||||||  ||||||||||||
                                GGACCCG  GTTTTGTTCTGAG
                                    AC
GAM1063  CASP2     3'  GAGTCTCGCTCTGTCGCCCAGG 8710         C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| ||||||||||||
                                GGACCCG TGTCTCGCTCTGAG
                                    C
GAM1063  CASP2     3'  GAGTCTCGCTCTGTCGCCCAGG 53289        C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| ||||||||||||
                                GGACCCG TGTCTCGCTCTGAG
                                    C
GAM1063  CASP2     3'  GAGTCTCGCTCTGTCGCCCAGG 53305        C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| ||||||||||||
                                GGACCCG TGTCTCGCTCTGAG
                                    C
GAM1063  CASP2     3'  GAGTCTCGCTCTGTCGCCCAGG 53334        C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| ||||||||||||
                                GGACCCG TGTCTCGCTCTGAG
                                    C
GAM1063  CASP8     3'  GAATCTCGCTCTGTCGCCCAGG 54075        C          C
                                CCTGGGC ACAGAGCGAGA TC
                                ||||||| |||||||||| ||
                                GGACCCG TGTCTCGCTCT AG
                                    C         A
GAM1063  CASP8     3'  GAATCTCGCTCTGTCGCCCAGG 54098        C          C
                                CCTGGGC ACAGAGCGAGA TC
                                ||||||| |||||||||| ||
                                GGACCCG TGTCTCGCTCT AG
                                    C         A
GAM1063  CASP8     3'  GAATCTCGCTCTGTCGCCCAGG 54114        C          C
                                CCTGGGC ACAGAGCGAGA TC
                                ||||||| |||||||||| ||
                                GGACCCG TGTCTCGCTCT AG
                                    C         A
GAM1063  CASP8     3'  GAATCTCGCTCTGTCGCCCAGG 8752         C          C
                                CCTGGGC ACAGAGCGAGA TC
                                ||||||| |||||||||| ||
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                                GGACCCG TGTCTCGCTCT AG
                                    C         A
GAM1063  CNGA1    5'  GAGTCTCGCTCTTCGCCCAGG  60241       CAC
                                CCTGGGC   AGAGCGAGACTC
                                |||||||   ||||||||||||
                                GGACCCG   TCTCGCTCTGAG
                                    CT_
GAM1063  COX10    3'  AGTTATCCTGTGGCCAGGTG   8946        G     AGC  _
                                CACCTGG CCACAG   GA GACT
                                ||||||| ||||||   || ||||
                                GTGGACC GGTGTC   CT TTGA
                                    _     ____ A
GAM1063  CRTAP    3'  GAGTCTCGCTCTCTTGCCCAGG 22081       CAC
                                CCTGGGC   AGAGCGAGACTC
                                |||||||   ||||||||||||
                                GGACCCG   TCTCGCTCTGAG
                                    TTC
GAM1063  CXCL16   3'  GAGTCTCGCTCTGTCATCCAGG 42170       CC
                                CCTGGG  ACAGAGCGAGACTC
                                ||||||  ||||||||||||||
                                GGACCT  TGTCTCGCTCTGAG
                                   AC
GAM1063  CYP4F3   3'  GAGTCTCGCTCTGTTGCCCAGG 8009        C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| ||||||||||||||
                                GGACCCG TGTCTCGCTCTGAG
                                    T
GAM1063  CYP51    3'  GAGTCTCGCTCTGTTGCCCAGG 7617        C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| ||||||||||||||
                                GGACCCG TGTCTCGCTCTGAG
                                    T
GAM1063  DSC3     3'  GAGTCTCGCTCTGACGCACAGG 10442     G  CA
                                CCTG GC  CAGAGCGAGACTC
                                ||||  ||  ||||||||||||
                                GGAC CG  GTCTCGCTCTGAG
                                  A  CA
GAM1063  DSC3     3'  GAGTCTCGCTCTGACGCACAGG 44624     G  CA
                                CCTG GC  CAGAGCGAGACTC
                                ||||  ||  ||||||||||||
                                GGAC CG  GTCTCGCTCTGAG
                                  A  CA
GAM1063  ECEL1    5'  GCATCCCGTAGCCCAGGTG   17890        C  A_  _
                                CACCTGGGC AC  GA GC
                                |||||||||  ||  ||  ||
                                GTGGACCCG TG  CT CG
                                     A  CC  A
GAM1063  FANCA    3'  GAGGGGCTCGGTGGCCCAGGTG 5541           A    GAGA
                                CACCTGGGCCAC GAGC    CTC
                                |||||||||||| ||||    |||
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                                GTGGACCCGGTG CTCG    GAG
                                      G    GG__
GAM1063  FCN2     3'  GAGTCCCGCTCTGTTCATACAG 32344     GGCC_       A
                                CTG     ACAGAGCG GACTC
                                |||     |||||||| |||||
                                GAC     TGTCTCGC CTGAG
                                  ATACT       C
GAM1063  FHL2     5'  GAGTCTCGCTTTGTCGCCCAGG 9367          C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| ||||||||||||||
                                GGACCCG TGTTTCGCTCTGAG
                                    C
GAM1063  FUT1     3'  GAGTCTTGCTCTGTAGCCCAGG 5596          C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| ||||||||||||||
                                GGACCCG TGTCTCGTTCTGAG
                                    A
GAM1063  GHR      3'  GAGTCTCGCTCTGTCGCCAGG  5701        G C
                                CCTGG C ACAGAGCGAGACTC
                                ||||| | ||||||||||||||
                                GGACC G TGTCTCGCTCTGAG
                                   _ C
GAM1063  GRAF     3'  GAGTCTCACTCTGTGGCCCAGG 31238             C
                                CCTGGGCCACAGAG GAGACTC
                                |||||||||||||| |||||||
                                GGACCCGGTGTCTC CTCTGAG
                                      A
GAM1063  ITGAM    3'  GAGTCTCGCTCTGTCACCCAGG 72312        CC
                                CCTGGG  ACAGAGCGAGACTC
                                ||||||  ||||||||||||||
                                GGACCC  TGTCTCGCTCTGAG
                                   AC
GAM1063  LIF      3'  AGCTCCTCCTGTGGCCCGG   11301          _  C   A
                                CTGGGCCACAG AG GAG CT
                                |||||||||| || ||| ||
                                GGCCCGGTGTC TC CTC GA
                                      C  _   _
GAM1063  LTB4R    5'  GAGTCTCGCTCTGTCATTCAGG 7465        CC
                                CCTGGG  ACAGAGCGAGACTC
                                ||||||  ||||||||||||||
                                GGACTT  TGTCTCGCTCTGAG
                                   AC
GAM1063  MEFV     3'  TCTTGCTCTGTGGCCCAGG   5952
                                CCTGGGCCACAGAGCGAGA
                                |||||||||||||||||
                                GGACCCGGTGTCTCGTTCT

GAM1063  NDRG3    3'  GAGTCTCGCTGTTACCCAGG  50123       CC   GA
                                CCTGGG  ACA  GCGAGACTC
                                ||||||  |||  |||||||||
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                                GGACCC  TGT  CGCTCTGAG
                                   AT  __
GAM1063  PCDHA9   3'  GAGTCTCGCTCTGTTGCCCAGG 26622       C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| |||||||||||||
                                GGACCCG TGTCTCGCTCTGAG
                                    T
GAM1063  PCDHB9   3'  GAGTCTCGCTCTGTCGCCCAGG 39446       C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| |||||||||||||
                                GGACCCG TGTCTCGCTCTGAG
                                    C
GAM1063  PDCL     3'  GAGTCTCGCTCTGTCACCCAGG 19397      CC
                                CCTGGG  ACAGAGCGAGACTC
                                ||||||  ||||||||||||||
                                GGACCC  TGTCTCGCTCTGAG
                                   AC
GAM1063  PIK3C2B  3'  GAGTCTCGCCCTGTCGCCAGG  12102     G C   A
                                CCTGG C ACAG GCGAGACTC
                                ||||| | |||| |||||||||
                                GGACC G TGTC CGCTCTGAG
                                  _ C   C
GAM1063  PKD1     3'  GAGTGTGCTGTATGGCCCAGG  6103       CAG   AG
                                CCTGGGCCA  AGCG  ACTC
                                |||||||||  ||||  ||||
                                GGACCCGGT  TCGT  TGAG
                                     ATG   G_
GAM1063  PLA2G4B  3'  GCTCGGGCTCAGGTG      18693        ACAGAG   A
                                CACCTGGGCC     CGAG C
                                ||||||||||     |||| |
                                GTGGACTCGG     GCTC G
                                      _______   C
GAM1063  PPP3CC   3'  GAGTCCTGCCGTGGCTCAGGTG 20028          AGA  A
                                CACCTGGGCCAC  GCG GACTC
                                ||||||||||||  ||| |||||
                                GTGGACTCGGTG  CGT CTGAG
                                      C__  C
GAM1063  PRKR     3'  GAGTCTCGCTCTGTTGCCCAGG 12347       C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| |||||||||||||
                                GGACCCG TGTCTCGCTCTGAG
                                    T
GAM1063  PTGIS    3'  GAGTCTCGCTCTGCTGCCCAGG 8211        CA
                                CCTGGGC  CAGAGCGAGACTC
                                |||||||  ||||||||||||
                                GGACCCG  GTCTCGCTCTGAG
                                   TC
GAM1063  RABL2A   3'  GAGTCTCGCTCTGTCGCCAGG  26408     G C
                                CCTGG C ACAGAGCGAGACTC
                                ||||| | ||||||||||||||
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                                GGACC G TGTCTCGCTCTGAG
                                   _ C
GAM1063  RABL2B   3'  GAGTCTCGCTCTGTCGCCAGG  23979      G C
                                CCTGG C ACAGAGCGAGACTC
                                ||||| | ||||||||||||||
                                GGACC G TGTCTCGCTCTGAG
                                   _ C
GAM1063  SNAP23   3'  GAGTCTCGCTCTCTTGTCCAGG 56337       CAC
                                CCTGGGC   AGAGCGAGACTC
                                |||||||   ||||||||||||
                                GGACCTG   TCTCGCTCTGAG
                                    TTC
GAM1063  SNAP23   3'  GAGTCTCGCTCTCTTGTCCAGG 15140       CAC
                                CCTGGGC   AGAGCGAGACTC
                                |||||||   ||||||||||||
                                GGACCTG   TCTCGCTCTGAG
                                    TTC
GAM1063  SNX15    3'  GAGTCTCGCTGTGTCGCCCAG  74121      C   G
                                CTGGGC ACA AGCGAGACTC
                                |||||| ||| ||||||||||
                                GACCCG TGT TCGCTCTGAG
                                   C   G
GAM1063  TAPBP    3'  GAGTCTCGCTCTGTCGCCCAGG 13565       C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| ||||||||||||||
                                GGACCCG TGTCTCGCTCTGAG
                                    C
GAM1063  TAPBP    3'  GAGTCTCGCTCTGTTGCCCAGG 13566       C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| ||||||||||||||
                                GGACCCG TGTCTCGCTCTGAG
                                    T
GAM1063  TBXA2R   3'  GAGTCTCACTCTGTGGCCCAG  8359          C
                                CTGGGCCACAGAG GAGACTC
                                |||||||||||| |||||||
                                GACCCGGTGTCTC CTCTGAG
                                       A
GAM1063  TERF2    3'  GAGTCTCGCTCTGTCACCCAGG 20153       CC
                                CCTGGG  ACAGAGCGAGACTC
                                ||||||  ||||||||||||||
                                GGACCC  TGTCTCGCTCTGAG
                                   AC
GAM1063  TJP1     5'  GTCTTGCCCTGTGGTCCAGG   13766         A
                                CCTGGGCCACAG GCGAGAC
                                |||||||||||| |||||||
                                GGACCTGGTGTC CGTTCTG
                                       C
GAM1063  TMPRSS3  3'  GAGTCTCGCTCTGTTGCCCAGG 51517       C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| ||||||||||||||
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                                GGACCCG TGTCTCGCTCTGAG
                                    T
GAM1063  TMPRSS3   3'  GAGTCTCGCTCTGTTGCCCAGG 51544        C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| ||||||||||||||
                                GGACCCG TGTCTCGCTCTGAG
                                    T
GAM1063  TMPRSS3   3'  GAGTCTCGCTCTGTTGCCCAGG 44026        C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| ||||||||||||||
                                GGACCCG TGTCTCGCTCTGAG
                                    T
GAM1063  TRIM9     5'  GAGTCTCGCTCTGTCGCCCAGG 31454        C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| ||||||||||||||
                                GGACCCG TGTCTCGCTCTGAG
                                    C
GAM1063  YES1      3'  GAGTCTCGCTCTGCCGCCCAGG 19538        CA
                                CCTGGGC  CAGAGCGAGACTC
                                |||||||  ||||||||||||
                                GGACCCG  GTCTCGCTCTGAG
                                    CC
GAM1063  APOL2     3'  GAGTCTCGCTCTATCGCCCAGG 48790        CAC
                                CCTGGGC   AGAGCGAGACTC
                                |||||||   ||||||||||||
                                GGACCCG   TCTCGCTCTGAG
                                    CTA
GAM1063  ASE-1     3'  GAGTCTCGCTCTGTCGCCCAGG 24981        C
            T                    ACCTGGGC ACAGAGCGAGACTC
                                ||||||||| ||||||||||||||
                                TGGACCCG TGTCTCGCTCTGAG
                                     C
GAM1063  BNIP-S    3'  GAGTCTCGCTCTGTCGCCAGG  57090      G C
                                CCTGG C ACAGAGCGAGACTC
                                ||||| | ||||||||||||||
                                GGACC G TGTCTCGCTCTGAG
                                   _ C
GAM1063  C1orf24   3'  GAGTCTCGCTCTGTCGCCAAGG 54791     G   C
                                CCT GGC ACAGAGCGAGACTC
                                ||| ||| ||||||||||||||
                                GGA CCG TGTCTCGCTCTGAG
                                  A   C
GAM1063  C6orf5    3'  GAGTCTCGCTCTGTCGTCCAGG 31993        C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| ||||||||||||||
                                GGACCTG TGTCTCGCTCTGAG
                                    C
GAM1063  C9orf9    3'  GAGTCTCGCTCTGTCGCCCAGG 39023        C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| ||||||||||||||
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                                GGACCCG TGTCTCGCTCTGAG
                                    C
GAM1063  CCRN4L    3'  GAGTCTCGCTCTGTTGCCTAGG 25069        C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| ||||||||||||||
                                GGATCCG TGTCTCGCTCTGAG
                                    T
GAM1063  CEACAM8   3'  GAATCTCGCTCTGTCGCCCAGG 10180        C          C
                                CCTGGGC ACAGAGCGAGA TC
                                ||||||| |||||||||| ||
                                GGACCCG TGTCTCGCTCT AG
                                    C          A
GAM1063  CENPH     3'  GAGTCTCGCTTTGTTGCCCAG  43567       C
                                CTGGGC ACAGAGCGAGACTC
                                |||||| ||||||||||||||
                                GACCCG TGTTTCGCTCTGAG
                                    T
GAM1063  DKFZp547H025 3'  GAGTCTCGCTCCATTGCCCAGG 39774         CACA
                                CCTGGGC    GAGCGAGACTC
                                |||||||    ||||||||||
                                GGACCCG    CTCGCTCTGAG
                                    TTAC
GAM1063  EREG      3'  GAGTCTCGCTCTGTTGCCCAGG 9308          C
              T                  ACCTGGGC ACAGAGCGAGACTC
                                 ||||||||| |||||||||||||
                                 TGGACCCG TGTCTCGCTCTGAG
                                     T
GAM1063  FBP17     3'  GAGTCTCGCTCTATTGTTCAG  73151        CAC
                                CTGGGC   AGAGCGAGACTC
                                ||||||   ||||||||||||
                                GACTTG   TCTCGCTCTGAG
                                   TTA
GAM1063  FLJ10597  3'  GAGTAGAGGCTGTGGCCCAGG  36836            AGCGAG
                                CCTGGGCCACAG      ACTC
                                ||||||||||||      ||||
                                GGACCCGGTGTC      TGAG
                                      GGAGA_
GAM1063  FLJ10687  3'  GAGTCTCGCTTTGTTGCCCAGG 36947        C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| |||||||||||||
                                GGACCCG TGTTTCGCTCTGAG
                                    T
GAM1063  FLJ10901  3'  GAGTCTCGCTCTGTCGCCCAGG 37364        C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| |||||||||||||
                                GGACCCG TGTCTCGCTCTGAG
                                    C
GAM1063  FLJ10936  3'  GAGTCTCACACTGTGGCCCAGG 37444             AGC
                                CCTGGGCCACAG   GAGACTC
                                ||||||||||||   |||||||
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                                GGACCCGGTGTC  CTCTGAG
                                      ACA
GAM1063  FLJ10998  3' AGTCTCGCTCTGTCACCCA   37517     CC
                                TGGG  ACAGAGCGAGACT
                                ||||  ||||||||||||
                                ACCC  TGTCTCGCTCTGA
                                  AC
GAM1063  FLJ12572  5' GAGTCTCGCTCTGTCACCCAGG 43542      CC
                                CCTGGG  ACAGAGCGAGACTC
                                ||||||  |||||||||||||
                                GGACCC  TGTCTCGCTCTGAG
                                   AC
GAM1063  FLJ12876  3' GAGTCTCGCTCTGTCACCCAGG 43093      CC
                                CCTGGG  ACAGAGCGAGACTC
                                ||||||  |||||||||||||
                                GGACCC  TGTCTCGCTCTGAG
                                   AC
GAM1063  FLJ13330  3' GAGCCTGGGCACGTGGCCCAGG 47666        AGA  G_  A
                                CCTGGGCCAC  GC  AG CTC
                                ||||||||||  ||  || |||
                                GGACCCGGTG  CG  TC GAG
                                      CA_  GG  C
GAM1063  FLJ14327  3' GAGCCCTCCTGTGTCCCAGGTG 46681       C    AGC   A_
                                CACCTGGG CACAG  GAG  CTC
                                |||||||| |||||  |||  |||
                                GTGGACCC GTGTC  CTC  GAG
                                     T    ___  CC
GAM1063  FLJ20139  3' AGTCTCACAGTGGGCCAGG   35111     G   AGAGC
                                CCTGG CCAC    GAGACT
                                ||||| ||||    ||||||
                                GGACC GGTG    CTCTGA
                                  G   ACA__
GAM1063  FLJ20154  3' AGACTCGGTGGCCCAGG    73302        AGAG   A
                                CCTGGGCCAC   CGAG CT
                                ||||||||||   |||| ||
                                GGACCCGGTG   GCTC GA
                                     ____   A
GAM1063  FLJ21324  5' AGTCTCGCTCTGACACCCAGG  92842      CCA
                                CCTGGG  CAGAGCGAGACT
                                ||||||  ||||||||||||
                                GGACCC  GTCTCGCTCTGA
                                   ACA
GAM1063  FLJ22169  3' GAGCAGGGTTCCTGTGGCCCAG 44233         _  GAGA
           G                    CCTGGGCCACAG AGC   CTC
                                ||||||||||| |||   |||
                                GGACCCGGTGTC TTG   GAG
                                      C  GGAC
GAM1063  FLJ31153  3' GAGTCTCGCTCTGTCACCCAG  58749     CC
                                CTGGG  ACAGAGCGAGACTC
                                |||||  |||||||||||||
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                                GACCC  TGTCTCGCTCTGAG
                                  AC
GAM1063  GMPPB    5'  GAGTCTCGCTCTGTTGCCCAGG 97450       C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| ||||||||||||||
                                GGACCCG TGTCTCGCTCTGAG
                                   T
GAM1063  GNG4     3'  GAGTCTCGCTCTGTCACCCAGG 16846      CC
                                CCTGGG  ACAGAGCGAGACTC
                                ||||||  ||||||||||||||
                                GGACCC  TGTCTCGCTCTGAG
                                  AC
GAM1063  GOLGA3   3'  GAGTCTCGCTTTGTTGCCCAGG 20889       C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| ||||||||||||||
                                GGACCCG TGTTTCGCTCTGAG
                                   T
GAM1063  GTPBG3   3'  GAGTCTCGCTCTGTCACCCAGG 51898      CC
                                CCTGGG  ACAGAGCGAGACTC
                                ||||||  ||||||||||||||
                                GGACCC  TGTCTCGCTCTGAG
                                  AC
GAM1063  JAM1     3'  GAGTCTCGCTCTGTCACCCAGG 58516      CC
                                CCTGGG  ACAGAGCGAGACTC
                                ||||||  ||||||||||||||
                                GGACCC  TGTCTCGCTCTGAG
                                  AC
GAM1063  JAM1     3'  GAGTCTCGCTCTGTCACCCAGG 58544      CC
                                CCTGGG  ACAGAGCGAGACTC
                                ||||||  ||||||||||||||
                                GGACCC  TGTCTCGCTCTGAG
                                  AC
GAM1063  JAM1     3'  GAGTCTCGCTCTGTCACCCAGG 58573      CC
                                CCTGGG  ACAGAGCGAGACTC
                                ||||||  ||||||||||||||
                                GGACCC  TGTCTCGCTCTGAG
                                  AC
GAM1063  JAM1     3'  GAGTCTCGCTCTGTCACCCAGG 34230      CC
                                CCTGGG  ACAGAGCGAGACTC
                                ||||||  ||||||||||||||
                                GGACCC  TGTCTCGCTCTGAG
                                  AC
GAM1063  KIAA0057 3'  AGTCTGTGAGGTGGCCCA    25402       AGA  G
                                TGGGCCAC   GC AGACT
                                ||||||||   || |||||
                                ACCCGGTG   TG TCTGA
                                    GAG  _
GAM1063  KIAA0189 3'  GAGCAGAGCCAGGCCCAGGTG  28943         ACAGA  GAGA
                                CACCTGGGCC    GC   CTC
                                ||||||||||    ||   |||
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                                GTGGACCCGG    CG   GAG
                                      AC___  AGAC
GAM1063  KIAA0296  5'  CTCTCAGTGACCTCAGGTG   28773      _ C  __
                                CACCTG GG CAC  AGAG
                                |||||| || |||  ||||
                                GTGGAC CC GTG  TCTC
                                   T  A   AC
GAM1063  KIAA0469  3'  GAGTCTCGCTCTGTCACCCAGG 29983      CC
                                CCTGGG  ACAGAGCGAGACTC
                                ||||||  ||||||||||||||
                                GGACCC  TGTCTCGCTCTGAG
                                   AC
GAM1063  KIAA0737  3'  GAGTCTCGCTCTGTCACCCAGG 29811      CC
                                CCTGGG  ACAGAGCGAGACTC
                                ||||||  ||||||||||||||
                                GGACCC  TGTCTCGCTCTGAG
                                   AC
GAM1063  KIAA0831  3'  GAGTCTCGCTCAGCTGCCCAGG 30640       CACA
                                CCTGGGC   GAGCGAGACTC
                                |||||||   ||||||||||
                                GGACCCG   CTCGCTCTGAG
                                   TCGA
GAM1063  KIAA0861  3'  GAGTCTCGCTCTGTCGCCCAGG 90350       C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| ||||||||||||||
                                GGACCCG TGTCTCGCTCTGAG
                                   C
GAM1063  KIAA0961  3'  GAGTCTCGCTCTTTCGCCCAGG 30401       CAC
                                CCTGGGC   AGAGCGAGACTC
                                |||||||   ||||||||||||
                                GGACCCG   TCTCGCTCTGAG
                                   CTT
GAM1063  KIAA1040  3'  GAGTCTCGCTCTGTCACCCAGG 72688      CC
                                CCTGGG  ACAGAGCGAGACTC
                                ||||||  ||||||||||||||
                                GGACCC  TGTCTCGCTCTGAG
                                   AC
GAM1063  KIAA1143  3'  GAGTCTCGCTCTGTCACCCAGG 69243      CC
                                CCTGGG  ACAGAGCGAGACTC
                                ||||||  ||||||||||||||
                                GGACCC  TGTCTCGCTCTGAG
                                   AC
GAM1063  KIAA1185  3'  GAGTCTCGCTCTGTCGCCAGG  63286     G C
                                CCTGG C ACAGAGCGAGACTC
                                ||||| | ||||||||||||||
                                GGACC G TGTCTCGCTCTGAG
                                   _ C
GAM1063  KIAA1210  3'  GAGTCTCGCTCTGTTACCCAG  98072     CC
                                CTGGG  ACAGAGCGAGACTC
                                |||||  ||||||||||||||
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                                GACCC  TGTCTCGCTCTGAG
                                   AT
GAM1063  KIAA1271  3'  GCCCTGTTGGCCCAGGTG    70140          _  A
                                CACCTGGGCCA CAG GC
                                |||||||||||  ||| ||
                                GTGGACCCGGT GTC CG
                                      T  C
GAM1063  KIAA1320  5'  GAGTCTCGCCCTGTCACCCAGG 69841       CC   A
                                CCTGGG  ACAG GCGAGACTC
                                ||||||  |||| |||||||||
                                GGACCC  TGTC CGCTCTGAG
                                   AC   C
GAM1063  KIAA1456  3'  GAGTCTCGCTCTGTCGCCCAGG 67558       C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| ||||||||||||||
                                GGACCCG TGTCTCGCTCTGAG
                                    C
GAM1063  KIAA1649  5'  GAGTCTCACTGTGTTGCCCAGG 51239       C  G  C
            T                    ACCTGGGC ACA AG GAGACTC
                                ||||||||  ||| || |||||||
                                TGGACCCG TGT TC CTCTGAG
                                     T  G  A
GAM1063  KIAA1668  3'  GAGTCTCGCTCTGTCGCCCAGG 67071       C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| ||||||||||||||
                                GGACCCG TGTCTCGCTCTGAG
                                    C
GAM1063  KIAA1719  3'  AGTCTCTTTAGCCCAGGT    68723        CACA  C
                                ACCTGGGC   GAG GAGACT
                                ||||||||   ||| ||||||
                                TGGACCCG   TTT CTCTGA
                                     A___  _
GAM1063  KIAA1829  3'  GAGTCTCGCTCTGTTGCCCAGG 62645       C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| ||||||||||||||
                                GGACCCG TGTCTCGCTCTGAG
                                    T
GAM1063  KIAA1978  3'  GAGCTTGACTATGGACCA    74893    G  C  AG   A
                                TGG CCA AG  CGAG CTC
                                ||| ||| ||  |||| |||
                                ACC GGT TC  GTTC GAG
                                  A  A A_   _
GAM1063  LIN-28    3'  GAGTCTCGCTGTGTCACCCAGG 45469       CC  G
                                CCTGGG  ACA AGCGAGACTC
                                ||||||  ||| ||||||||||
                                GGACCC  TGT TCGCTCTGAG
                                   AC   G
GAM1063  MAP-1     3'  GAGTCTCGCTCTGTCACCCAGG 42442       CC
                                CCTGGG  ACAGAGCGAGACTC
                                ||||||  ||||||||||||||
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                                GGACCC  TGTCTCGCTCTGAG
                                   AC
GAM1063  MGC13017  3'  GAGTCTTGCTCTGTTGCCCAGG 55574        C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| |||||||||||||||
                                GGACCCG TGTCTCGTTCTGAG
                                    T
GAM1063  MGC23445  5'  AGCCTCGCCACCCCGGGTG   58772        CCACAGA    A
                                CACCTGGG      GCGAG CT
                                ||||||||      ||||| ||
                                GTGGGCCC      CGCTC GA
                                     CAC____     C
GAM1063  MGC2603   3'  GAGTCTCGCTCTGTCGCCAGG  44074      G C
                                CCTGG C ACAGAGCGAGACTC
                                ||||| | |||||||||||||||
                                GGACC G TGTCTCGCTCTGAG
                                  _ C
GAM1063  MGC3262   5'  GAGCCCCAGCCACGCCGGCCCA 44051         ACAGA_  GAGA_
            GGTG                   CACCTGGGCC     GC    CTC
                                |||||||||      ||    |||
                                GTGGACCCGG     CG    GAG
                                     CCGCAC  ACCCC
GAM1063  MGC4638   3'  GAGTCTCGCTCTGTCACCAGG  49736      GCC
                                CCTGG   ACAGAGCGAGACTC
                                |||||   ||||||||||||||
                                GGACC   TGTCTCGCTCTGAG
                                  AC_
GAM1063  MYO5C     3'  GAGTCTCGCTCTATCGCCAGG  38720      G CAC
                                CCTGG C   AGAGCGAGACTC
                                ||||| |   ||||||||||||
                                GGACC G   TCTCGCTCTGAG
                                  _ CTA
GAM1063  NY-BR-1   3'  CGAATCTCGCTCTGCACTCCAG 54851         CA_____        C ___
            CCTAGGTG                CACCTGGGC      CAGAGCGAGA TC   G
                                |||||||||      |||||||||| ||   |
                                GTGGATCCG      GTCTCGCTCT AG   C
                                     ACCTCAC        A ___
GAM1063  OSBPL5    3'  GAGCCCCGAGTGGCCCAGG   73063         AGAG  AGA
                                CCTGGGCCAC    CG   CTC
                                ||||||||||    ||   |||
                                GGACCCGGTG    GC   GAG
                                     A___  CCC
GAM1063  P114-RHO-GEF 3'  AGCCTTGTTCTGCACCCCA   31667      CCA        A
                                TGGG   CAGAGCGAG CT
                                ||||   ||||||||| ||
                                ACCC   GTCTTGTTC GA
                                  CAC        C
GAM1063  PLAA      3'  GAGCCCTCTATGTGGTCCAGG  16187          GAGC   A_
                                CCTGGGCCACA    GAG  CTC
                                ||||||||||    |||  |||
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                                GGACCTGGTGT   CTC  GAG
                                      AT__   CC
GAM1063  POLE3    3'  GAGTCTCTCACTCTGTGGCCCA 34316          C__
              GG                  CCTGGGCCACAGAG   GAGACTC
                                  ||||||||||||||   |||||||
                                  GGACCCGGTGTCTC   CTCTGAG
                                        ACT
GAM1063  PP5395   5'  CGCGGCTGTGACCCAAGTG   72585    C   C    A_
                                  CAC TGGG CACAG  GCG
                                  ||| |||| |||||  |||
                                  GTG ACCC GTGTC  CGC
                                    A   A    GG
GAM1063  PRO0365  5'  GAGTCTCGCTCTGTCGCCAGG  26983      G C
                                  CCTGG C ACAGAGCGAGACTC
                                  ||||| | ||||||||||||||
                                  GGACC G TGTCTCGCTCTGAG
                                    _ C
GAM1063  RAB21    3'  GAGTCTCGCTCTGTCACCCAGG 31090      CC
                                  CCTGGG  ACAGAGCGAGACTC
                                  ||||||  ||||||||||||||
                                  GGACCC  TGTCTCGCTCTGAG
                                     AC
GAM1063  RAB33B   3'  GAGTCTCGCTCTGTCTCCAGG  49327      CC
                                  CCTGGG  ACAGAGCGAGACTC
                                  ||||||  ||||||||||||||
                                  GGACCT  TGTCTCGCTCTGAG
                                     C_
GAM1063  RAP140   3'  GAGTCTCGCTCTGTCGCCCA   31516     C
                                  TGGGC ACAGAGCGAGACTC
                                  ||||| |||||||||||||
                                  ACCCG TGTCTCGCTCTGAG
                                    C
GAM1063  SARM     3'  AGCTAGCCTGTGGCCCAG    31277         A  G  A
                                  CTGGGCCACAG GC AG CT
                                  |||||||||| || || ||
                                  GACCCGGTGTC CG TC GA
                                        _  A  _
GAM1063  SH120    5'  GAGGGGGCCTGTGGCCCCAG   33390      _    A  GAGA
                                  CTGGG CCACAG GC   CTC
                                  ||||| |||||| ||   |||
                                  GACCC GGTGTC CG   GAG
                                    C     _  GGG_
GAM1063  SLC12A8  3'  GAGTCTCGCCTTGTCACCCAGG 45238      CC   A
                                  CCTGGG  ACAG GCGAGACTC
                                  ||||||  |||| |||||||||
                                  GGACCC  TGTT CGCTCTGAG
                                     AC   C
GAM1063  SLC16A4  3'  GAGTCTCGCTCTTTCGCCCAGG 17452       CAC
                                  CCTGGGC   AGAGCGAGACTC
                                  |||||||   ||||||||||||
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                                GGACCCG   TCTCGCTCTGAG
                                    CTT
GAM1063  SULT1C2   3'  GAGTCTCGCTCTGTCGCCCAGG 22715       C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| |||||||||||||
                                GGACCCG TGTCTCGCTCTGAG
                                    C
GAM1063  TOM1      3'  AGCTGCGGCGGCCCAGGT    19695        ACAGA  G  A
                                ACCTGGGCC    GC AG CT
                                |||||||||    || || ||
                                TGGACCCGG    CG TC GA
                                     CGG__  _ _
GAM1063  TPC2      3'  AGTCCTTTGCGTGTGGCCCA  58192        GA   __
                                TGGGCCACA  GCGA  GACT
                                |||||||||  ||||  ||||
                                ACCCGGTGT  CGTT  CTGA
                                     G_    TC
GAM1063  TRIM6     3'  GAATCTCGCTCTGTCGCCCAGG 55180       C        C
                                CCTGGGC ACAGAGCGAGA TC
                                ||||||| |||||||||| ||
                                GGACCCG TGTCTCGCTCT AG
                                    C         A
GAM1063  TUCAN     3'  GAGTCTCGCTCTGTCATCTAGG 30978       CC
                                CCTGGG  ACAGAGCGAGACTC
                                ||||||  ||||||||||||||
                                GGATCT  TGTCTCGCTCTGAG
                                   AC
GAM1063  UBF-fl    3'  GAGTCTCGCTCTGTCTCCCAGG 52624       CC
                                CCTGGG  ACAGAGCGAGACTC
                                ||||||  ||||||||||||||
                                GGACCC  TGTCTCGCTCTGAG
                                   TC
GAM1063  ZNF338    3'  GAGTCTCGCTCTGTTTCCCAGG 42257       CC
                                CCTGGG  ACAGAGCGAGACTC
                                ||||||  ||||||||||||||
                                GGACCC  TGTCTCGCTCTGAG
                                   TT
GAM1063  LOC112687 3'  GAGTCTCGCCCTGTCACCCAGG 73236       CC   A
                                CCTGGG  ACAG GCGAGACTC
                                ||||||  ||||  |||||||||
                                GGACCC  TGTC CGCTCTGAG
                                   AC   C
GAM1063  LOC126669 3'  AGTCTCGCTGTGTTGCCCAGG  75923       C  G
                                CCTGGGC ACA AGCGAGACT
                                ||||||| ||| |||||||||
                                GGACCCG TGT TCGCTCTGA
                                    T  G
GAM1063  LOC127435 3'  TGCTCTGTGGCCAGGTG     76611        G
                                CACCTGG CCACAGAGCG
                                ||||||| ||||||||||
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                                GTGGACC GGTGTCTCGT
                                    _
GAM1063  LOC129676 5'  GAGTCTCGGACTCCGGCCCAGG 76234        ACA  __
                                CCTGGGCC   GAG  CGAGACTC
                                ||||||||   |||  ||||||||
                                GGACCCGG   CTC  GCTCTGAG
                                    C__   AG
GAM1063  LOC132228 3'  AGCCTCGCTTTGGGTGGCCCAA 75543    _     __       A
           GG                     CCT GGGCCAC  AGAGCGAG CT
                                ||| |||||||  |||||||| ||
                                GGA CCCGGTG  TTTCGCTC GA
                                  A      GG       C
GAM1063  LOC135293 3'  GAGCCTCGCTCTGTTGCCCAGG 76685       C        A
                                CCTGGGC ACAGAGCGAG CTC
                                |||||||  |||||||||| |||
                                GGACCCG TGTCTCGCTC GAG
                                    T         C
GAM1063  LOC135763 3'  GAGTCTCGCTCCGTCACCCAGG 57559       CC  A
                                CCTGGG  AC GAGCGAGACTC
                                ||||||  ||  ||||||||||||
                                GGACCC  TG CTCGCTCTGAG
                                   AC  C
GAM1063  LOC144114 5'  AGTGCCGTGGCCCAGGTG    83083          AGA  GAG
                                CACCTGGGCCAC   GC   ACT
                                ||||||||||||   ||   |||
                                GTGGACCCGGTG   CG   TGA
                                      C__  ___
GAM1063  LOC144248 5'  GAGTCTCGCTCTTTCGCCCAGG 77253       CAC
                                CCTGGGC   AGAGCGAGACTC
                                |||||||   ||||||||||||
                                GGACCCG   TCTCGCTCTGAG
                                    CTT
GAM1063  LOC145009 3'  GAGTCTCGCTCTGTCGCCCAGG 60975       C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| ||||||||||||||
                                GGACCCG TGTCTCGCTCTGAG
                                    C
GAM1063  LOC145757 5'  GAGTCTCGCTCTGTCGCCCAGG 77932       C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| ||||||||||||||
                                GGACCCG TGTCTCGCTCTGAG
                                    C
GAM1063  LOC146229 3'  GAGTCTCGCTCTGTCGCCCAGG 78286       C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| ||||||||||||||
                                GGACCCG TGTCTCGCTCTGAG
                                    C
GAM1063  LOC146429 5'  GAGTCTCGCTCTGTCACCAGG  84666      GCC
                                CCTGG   ACAGAGCGAGACTC
                                |||||   ||||||||||||||
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                                GGACC   TGTCTCGCTCTGAG
                                  AC_
GAM1063  LOC146603 5'  GAGTCTCGCTCTGTCGCCCAGG 78596       C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| ||||||||||||||
                                GGACCCG TGTCTCGCTCTGAG
                                    C
GAM1063  LOC146909 3'  GAGTCTCGCTCTGTCGCCCAGG 78773       C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| ||||||||||||||
                                GGACCCG TGTCTCGCTCTGAG
                                    C
GAM1063  LOC147817 3'  GAGTCTCGCTCTGTCACCCAGG 79179       CC
                                CCTGGG  ACAGAGCGAGACTC
                                ||||||  ||||||||||||||
                                GGACCC  TGTCTCGCTCTGAG
                                   AC
GAM1063  LOC148188 3'  GAGCTGAGGCTGCGGCCCAGG  79456        A  AG_ G  A
                                CCTGGGCC CAG   C AG CTC
                                |||||||| |||   | || |||
                                GGACCCGG GTC   G TC GAG
                                    C   GGA _  _
GAM1063  LOC148189 5'  GAGTCTCGCTCTGTCACCAGG  79449      GCC
                                CCTGG   ACAGAGCGAGACTC
                                |||||   ||||||||||||||
                                GGACC   TGTCTCGCTCTGAG
                                  AC_
GAM1063  LOC149506 3'  GAGTCTCGCTGTTGCCCAGG   85637       C  GA
                                CCTGGGC ACA  GCGAGACTC
                                ||||||| |||  |||||||||
                                GGACCCG TGT  CGCTCTGAG
                                    T  __
GAM1063  LOC149577 3'  GAGTCTCGCTTTGTTGCCCAGG 85678       C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| ||||||||||||||
                                GGACCCG TGTTTCGCTCTGAG
                                    T
GAM1063  LOC149692 3'  GAGTCTCGCTCTGTCACCCAGG 85737       CC
                                CCTGGG  ACAGAGCGAGACTC
                                ||||||  ||||||||||||||
                                GGACCC  TGTCTCGCTCTGAG
                                   AC
GAM1063  LOC150054 5'  GAGCCCTCCCGTGGCCCAGG   85973        A_  CGAGA
                                CCTGGGCCAC  GAG    CTC
                                ||||||||||  |||    |||
                                GGACCCGGTG  CTC    GAG
                                     CC  CC___
GAM1063  LOC150157 5'  GAGCCAGCAGTGTGGCTCAGGT 86024          GA  GAGA
            G                   CACCTGGGCCACA  GC   CTC
                                ||||||||||||  ||   |||
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                                GTGGACTCGGTGT  CG    GAG
                                       GA  ACC_
GAM1063  LOC151475 5'  GAGTCTTGCTCTGTGGCCCAGG 86594
                                CCTGGGCCACAGAGCGAGACTC
                                |||||||||||||||||||||
                                GGACCCGGTGTCTCGTTCTGAG

GAM1063  LOC151701 3'  GAGTCTCGCTCTGTCGCCCAGG 86673        C
                                CCTGGGC ACAGAGCGAGACTC
                                |||||||  ||||||||||||||
                                GGACCCG TGTCTCGCTCTGAG
                                     C
GAM1063  LOC152137 3'  GAGTCTCGCCCTGTCACACAGG 81318      GGCC    A
                                CCTG    ACAG GCGAGACTC
                                ||||    |||| |||||||||
                                GGAC    TGTC CGCTCTGAG
                                   ACAC    C
GAM1063  LOC152245 3'  GAGTCTCGCTCTGTCGCCCAGG 86778        C
                                CCTGGGC ACAGAGCGAGACTC
                                |||||||  ||||||||||||||
                                GGACCCG TGTCTCGCTCTGAG
                                     C
GAM1063  LOC153811 5'  TCTCGCTCTGTCACCCAGG    81854       CC
                                CCTGGG  ACAGAGCGAGA
                                ||||||  ||||||||||
                                GGACCC  TGTCTCGCTCT
                                    AC
GAM1063  LOC154282 5'  GAGTCTCGCTCTGTCGCCAGGT 87405       G C
                                ACCTGG C ACAGAGCGAGACTC
                                |||||| | ||||||||||||||
                                TGGACC G TGTCTCGCTCTGAG
                                   _ C
GAM1063  LOC154877 3'  GAGTCTCGCTCTGTCGCCCAGG 87554        C
                                CCTGGGC ACAGAGCGAGACTC
                                |||||||  ||||||||||||||
                                GGACCCG TGTCTCGCTCTGAG
                                     C
GAM1063  LOC157349 5'  GTCTTGCCCTGGGGCCCAGGTG 82348          A   A
                                CACCTGGGCC CAG GCGAGAC
                                |||||||||| ||| |||||||
                                GTGGACCCGG GTC CGTTCTG
                                      G   C
GAM1063  LOC157506 3'  GAGTCTCGCTCTGTCACCAGG  82368      GCC
                                CCTGG   ACAGAGCGAGACTC
                                |||||   ||||||||||||||
                                GGACC   TGTCTCGCTCTGAG
                                   AC_
GAM1063  LOC197358 3'  GAGTCTCGCTCTTGTCGCCCAG 89434        C   _
             G                   CCTGGGC ACA GAGCGAGACTC
                                 |||||||  ||| ||||||||||
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                                GGACCCG TGT CTCGCTCTGAG
                                    C   T
GAM1063  LOC199699 3'  GAGTCTCGCTCTGTCGCCCAGG 89674        C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| |||||||||||||
                                GGACCCG TGTCTCGCTCTGAG
                                    C
GAM1063  LOC199936 5'  GAGTCTCGCTCTGTCACCCAGG 91482       CC
                                CCTGGG  ACAGAGCGAGACTC
                                ||||||  ||||||||||||||
                                GGACCC  TGTCTCGCTCTGAG
                                   AC
GAM1063  LOC201164 3'  GAGTCTCACTCTGTGGCCCAGG 89496             C
                                CCTGGGCCACAGAG GAGACTC
                                |||||||||||||| |||||||
                                GGACCCGGTGTCTC CTCTGAG
                                       A
GAM1063  LOC201294 3'  GAGTCTCGCTCTGTCGCCCAGG 89585        C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| |||||||||||||
                                GGACCCG TGTCTCGCTCTGAG
                                    C
GAM1063  LOC203378 3'  GAGTCTCGCTCTGTCGCCCAGG 92290        C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| |||||||||||||
                                GGACCCG TGTCTCGCTCTGAG
                                    C
GAM1063  LOC203429 3'  AGTCCCGGAGTTTGTGGCCAAA 90928     CTG       G__  A
            GTG                    CAC   GGCCACAGA   CG GACT
                                |||   |||||||||   || ||||
                                GTG   CCGGTGTTT   GC CTGA
                                  AAA        GAG  C
GAM1063  LOC219445 5'  GAGTCTCGCTTTGTTGCCCAGG 93205        C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| |||||||||||||
                                GGACCCG TGTTTCGCTCTGAG
                                    T
GAM1063  LOC219529 5'  CTCCTGAGCCCAGGTG      94566         CA   AGC
                                CACCTGGGC  CAG   GAG
                                |||||||||  |||   |||
                                GTGGACCCG  GTC   CTC
                                     A_  ___
GAM1063  LOC220074 3'  GAGTCTCGCTCTGTCACCCAGG 59983       CC
                                CCTGGG  ACAGAGCGAGACTC
                                ||||||  ||||||||||||||
                                GGACCC  TGTCTCGCTCTGAG
                                   AC
GAM1063  LOC220662 3'  AGTCTCGCCGTTGCCCAGG    92805        C  AGA
                                CCTGGGC AC   GCGAGACT
                                ||||||| ||   ||||||||
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                                GGACCCG TG   CGCTCTGA
                                   T  C__
GAM1063  LOC245771 5'  GAGTCTCGCTCTGTCGCCCAGG 94478        C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| ||||||||||||||
                                GGACCCG TGTCTCGCTCTGAG
                                   C
GAM1063  LOC253296 5'  AGTCCCCGGCCGTGACCCAGG  96122       C   AGAG  A_
                                CCTGGG CAC    CG  GACT
                                |||||| |||    ||  ||||
                                GGACCC GTG    GC  CTGA
                                   A   CCG_  CC
GAM1063  LOC253612 5'  GAGTCTCGCTCTGTCTCCCAGG 98550       CC
                                CCTGGG  ACAGAGCGAGACTC
                                ||||||  ||||||||||||||
                                GGACCC  TGTCTCGCTCTGAG
                                   TC
GAM1063  LOC253664 3'  GAGTCTCGCTCTGTTGCCCAGG 96467        C
                                CCTGGGC ACAGAGCGAGACTC
                                ||||||| ||||||||||||||
                                GGACCCG TGTCTCGCTCTGAG
                                   T
GAM1063  LOC255037 3'  AGTCTCGCTGTGTCACCCAGG  98438       CC   G
                                CCTGGG  ACA AGCGAGACT
                                ||||||  ||| |||||||||
                                GGACCC  TGT TCGCTCTGA
                                   AC   G
GAM1063  LOC255919 3'  GAGTCTCGCTCTGTTGCCAGG  96746      G C
                                CCTGG C ACAGAGCGAGACTC
                                ||||| | ||||||||||||||
                                GGACC G TGTCTCGCTCTGAG
                                  _ T
GAM1063  LOC256221 3'  GAGTCTCGCTCTGTAACTCAGG 96911       CC
                                CCTGGG  ACAGAGCGAGACTC
                                ||||||  ||||||||||||||
                                GGACTC  TGTCTCGCTCTGAG
                                   AA
GAM1063  LOC257486 3'  GAGTCTCGCTCTGTTACCCAG  69773      CC
                                CTGGG  ACAGAGCGAGACTC
                                |||||  ||||||||||||||
                                GACCC  TGTCTCGCTCTGAG
                                  AT
GAM1063  LOC257570 5'  AGTCCCCGGCCGTGACCCAGG  99668       C   AGAG  A_
                                CCTGGG CAC    CG  GACT
                                |||||| |||    ||  ||||
                                GGACCC GTG    GC  CTGA
                                   A   CCG_  CC
GAM1063  LOC56181  5'  GAGTCTCGCTCTGTCACCCAGG 97276        CC
            T                    ACCTGGG  ACAGAGCGAGACTC
                                ||||||| ||||||||||||||
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                                TGGACCC  TGTCTCGCTCTGAG
                                   AC
GAM1063  LOC90591  3'  GAGTCTCGCTCTGTCACCCAGG 64173       CC
                                CCTGGG  ACAGAGCGAGACTC
                                ||||||  ||||||||||||||
                                GGACCC  TGTCTCGCTCTGAG
                                   AC
GAM1063  LOC91291  5'  GAGTCTCGCTCTGTCGCCCAG  66090       C
                                CTGGGC ACAGAGCGAGACTC
                                |||||| ||||||||||||||
                                GACCCG TGTCTCGCTCTGAG
                                   C
GAM1063  LOC91893  3'  GAGTCTTGCTCTGCCGCCCAGG 68074       CA
                                CCTGGGC  CAGAGCGAGACTC
                                |||||||  ||||||||||||
                                GGACCCG  GTCTCGTTCTGAG
                                   CC
GAM1063  LOC92017  5'  GAGGCAGGGCTCTGTGGCCCAG 68490            GAGA_
            G                    CCTGGGCCACAGAGC    CTC
                                ||||||||||||||    |||
                                GGACCCGGTGTCTCG    GAG
                                      GGACG
GAM1063  LOC92148  5'  GAGTCTCGCCCTGCCGCCCAGG 68880       CA   A
                                CCTGGGC  CAG GCGAGACTC
                                |||||||  ||| |||||||||
                                GGACCCG  GTC CGCTCTGAG
                                   CC   C
GAM1063  LOC93070  3'  GAGTCTCACACTGTGGCCCAGG 71809          AGC
                                CCTGGGCCACAG   GAGACTC
                                ||||||||||||  |||||||
                                GGACCCGGTGTC   CTCTGAG
                                      ACA
GAM1063  LOC93132  5'  GAGTCTCGCTCTGTCACCAGG  71991      GCC
                                CCTGG   ACAGAGCGAGACTC
                                |||||   ||||||||||||||
                                GGACC   TGTCTCGCTCTGAG
                                   AC_
GAM1064  LTB       3'  CGGGCCTCTCTGGTACACG   11370     AA  G  A
                                CGT  TA CG AGAGGCCCG
                                |||  || || |||||||||
                                GCA  AT GT TCTCCGGGC
                                  C_  G  C
GAM1064  P114-RHO-GEF 3'  GCGGGCCTCTAGCTTCAGCCA  31671      GTAAT   GA
                                TGGC    AGC  AGAGGCCCGC
                                ||||    |||  ||||||||||
                                ACCG    TCG  TCTCCGGGCG
                                   ACT__   A_
GAM1064  LOC137593 3'  GCAGACCTCATAGCTGTTACAC 75795     C       GAA    CCC
            CA                    TGG GTAATAGC   GAGG   GC
                                ||| ||||||||   ||||   ||
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                                ACC CATTGTCG   CTCC   CG
                                  A       ATA    AGA
GAM1064  LOC255480 5'  GCGGGCCTCTTTCCAACCAGCC 98286      GTAATAGC
             A                   TGGC       GAAGAGGCCCGC
                                 ||||       ||||||||||||
                                 ACCG       TTTCTCCGGGCG
                                   ACCAACC_
GAM1065  AXIN1    3'  CCCGCCCCCGCTTGGCA     61535    A       A  A
                                 TG CCAAGCGGG GG TGGG
                                 || |||||||| || ||||
                                 AC GGTTCGCCC CC GCCC
                                  _       _ _
GAM1065  CFL1     3'  CCCCATTCCCCACCTGGTCCTC 19745    T    AGC   A
                                 GA GACCA   GGG GGATGGGG
                                 || |||||   ||| ||||||||
                                 CT CTGGT   CCC CTTACCCC
                                  C    CCA  _
GAM1065  GJA5     3'  CCCTGTCCCCACCCGGTCA    75166      AAGCG  A
                                 TGACC     GG GGATGGGG
                                 |||||     || ||||||||
                                 ACTGG     CC CCTGTCCC
                                    CCCA_ _
GAM1065  HTRA3    5'  CCCGCCGGCCCCCGCCCGGTCT 90578    T    AA    A  A  _
             C                   GA GACC  GCGGG GG TGG GGG
                                 || ||||  ||||| || ||| |||
                                 CT CTGG  CGCCC CC GCC CCC
                                  _   CC    _ G   G
GAM1065  IHPK2    5'  CCCCATCTCCCCGCCATC    62515     ACCAA    AG
                                 GATG    GCGGG  GATGGGG
                                 ||||    |||||  |||||||
                                 CTAC    CGCCC  CTACCCC
                                   ______    CT
GAM1065  MAP3K9   3'  CCCCCACCCTCCACAGTCTTC  61361    T   CAAGCG    A
                                 GA GAC     GGAGG TGGGGG
                                 || |||     ||||| ||||||
                                 CT CTG     CCTCC ACCCCC
                                  T   ACA___    C
GAM1065  MEF2D    3'  CCCCGGGCTCCTCCCGCT    20981          ___
                                 AGCGGGAGGA   TGGGG
                                 ||||||||||   |||||
                                 TCGCCCTCCT   GCCCC
                                       CGG
GAM1065  MVP      5'  CCCCACCTACCAGTCATC    34360       CAAGC  G   A
                                 GATGAC    GG AGG TGGGG
                                 ||||||    || ||| |||||
                                 CTACTG    CC TCC ACCCC
                                    A_____  A   _
GAM1065  NTSR1    3'  CCCCACAAGCCTGGTCATC   11853         A  GGGAGGA
                                 GATGACCA GC      TGGGG
                                 |||||||| ||      |||||
```

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                                CTACTGGT CG      ACCCC
                                    C  AAC____
GAM1065  PCSK5    5'  CCGCTCCCGCTGGTCATC    21673        A      GA
                                GATGACCA GCGGGAG  TGG
                                |||||||| |||||||  |||
                                CTACTGGT CGCCCTC  GCC
                                    _      __
GAM1065  PTPRA    3'  CCCCCATCCCCACCACTGATAT 55949     ACCA  C  GA_
              C                  GATG   AG GG   GGATGGGGG
                                 ||||   || ||   |||||||||
                                 CTAT   TC CC   CCTACCCCC
                                   AG__  A  ACC
GAM1065  PTPRA    3'  CCCCCATCCCCACCACTGATAT 55951     ACCA  C  GA_
              C                  GATG   AG GG   GGATGGGGG
                                 ||||   || ||   |||||||||
                                 CTAT   TC CC   CCTACCCCC
                                   AG__  A  ACC
GAM1065  PTPRA    3'  CCCCCATCCCCACCACTGATAT 12602     ACCA  C  GA_
              C                  GATG   AG GG   GGATGGGGG
                                 ||||   || ||   |||||||||
                                 CTAT   TC CC   CCTACCCCC
                                   AG__  A  ACC
GAM1065  SLC15A1  3'  CCCACCCCACATTGGTCATC   18640        GCG  A  A
                                GATGACCAA   GG GG TGGG
                                |||||||||   || || ||||
                                CTACTGGTT   CC CC ACCC
                                     ACA  _  _
GAM1065  SLC9A3R2 3'  CCCCCATCCTGCCCCTGC    62100      ___
                                GCGGG   AGGATGGGGG
                                |||||   ||||||||||
                                CGTCC   TCCTACCCCC
                                   CCG
GAM1065  SNTB1    5'  CCCCGCGTCCTCCCCCCGGCCA 41046    A  AAGC       _
                                TG CC    GGGAGGATG GGGG
                                || ||    ||||||||| ||||
                                AC GG    CCCTCCTGC CCCC
                                 C  CCC_       G
GAM1065  SPOCK    3'  CCCCCATCCCAAATTGACCATT 63472     AC   GCGGGA
                                GATG  CAA     GGATGGGGG
                                ||||  |||     |||||||||
                                TTAC  GTT     CCTACCCCC
                                  CA   AAAC__
GAM1065  TCF7     3'  CCCCCATCCCCCACTGCCACA  13619    ACCA  C   A
                                TG    AG GGG GGATGGGGG
                                ||    || ||| |||||||||
                                AC    TC CCC CCTACCCCC
                                 ACCG  A  _
GAM1065  FLJ14810 3'  CCCCCACCCAGCTCCCGGCCGT 52698     A  AAGC   ___  A
              C                  GATG CC    GGGA   GG TGGGGG
                                 |||| ||    ||||   || ||||||
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                                CTGC GG   CCCT  CC ACCCCC
                                  C ____   CGA  C
GAM1065  GRIN3A   3'  CCCCCATCCTCACACCCACTCA 56779      CCAAGCGG
                TC                  GATGA      GAGGATGGGGG
                                    |||||      ||||||||||
                                    CTACT      CTCCTACCCCC
                                       CACCCACA
GAM1065  KIAA1096 3'  CCTTGCCCCCACTCAGTCATC  69059      CA  C   A  A
                                    GATGAC  AG GGG GG TGGGG
                                    ||||||  || ||| || |||||
                                    CTACTG  TC CCC CC GTTCC
                                       AC  A  _ _
GAM1065  MGC16703 3'  CCACCTCCCCCTGGCCA    73490    A   A C     A
                                    TG CCA G GGGAGG TGG
                                    || ||| | |||||| |||
                                    AC GGT C CCCTCC ACC
                                     C  _ C     _
GAM1065  NMT1     3'  CCCCCACCCTCTGCCACCCAGT 41145    GACCAA   GA  A
                C                    GAT     GCGG  GG TGGGGG
                                    |||     ||||  || ||||||
                                    CTG     CGTC  CC ACCCCC
                                      ACCCAC   TC  _
GAM1065  SPR1     3'  CCTACCTCCCACCCGGTCTTC  26812    T   AAGC     A
                                    GA GACC    GGGAGG TGGG
                                    || ||||    |||||| ||||
                                    CT CTGG    CCCTCC ATCC
                                     T   CCCA     _
GAM1065  T2BP     5'  CCCCCATCCTGCGCCCAGTCTC 70536    T   CAA   GG
                                    GA GAC   GCG  AGGATGGGGG
                                    || |||   |||  ||||||||||
                                    CT CTG   CGC  TCCTACCCCC
                                     _   ACC   G_
GAM1065  TOR1B    3'  CCCCTCCCGCCTGTCCATC    27968      AC  A       AT
                                    GATG  CA GCGGGAGG  GG
                                    ||||  || ||||||||  ||
                                    CTAC  GT CGCCCTCC  CC
                                      CT  C       __
GAM1065  LOC146745 5'  CCCCCATAGCCACTCAGTCTTC 78691    T   CA  C  GAGG
                                    GA GAC  AG GG    ATGGGGG
                                    || |||  || ||    |||||||
                                    CT CTG  TC CC    TACCCCC
                                     T   AC  A  GA__
GAM1065  LOC149711 3'  CCCTCTCCCTGCTCAACCATC  85846      ACCA     AG  T
                                    GATG    AGCGGG  GA GGG
                                    ||||    ||||||  || |||
                                    CTAC    TCGTCC  CT CCC
                                      CAAC     CT  _
GAM1065  LOC153480 5'  CCCCCACCCCCCGACGTCCTC  73274    T   CAAG    A  A
                                    GA GAC    CGGG GG TGGGGG
                                    || |||    |||| || ||||||
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                                CT CTG    GCCC CC ACCCCC
                                 C   CA__    _ C
GAM1065  LOC157292 3'  CCCAGGAGTCACGCTTAGTCAT 87697       C    _ AGGA
              C                   GATGAC AAGCG GG    TGGG
                                  |||||| ||||| ||    ||||
                                  CTACTG TTCGC CT    ACCC
                                     A     A  GAGG
GAM1065  LOC162333 5'  CCCCCATCCCCAATAGCACATC 88490      ACCAAGCG  A
                                  GATG       GG GGATGGGGG
                                  ||||       || |||||||||
                                  CTAC       CC CCTACCCCC
                                    ACGATAA_  _
GAM1065  LOC197350 3'  CCCCCATCCCCCCGGTTTCCTC 89400    T  CC  G    A
                                  GA GA  AA CGGG GGATGGGGG
                                  || ||  || |||| |||||||||
                                  CT CT  TT GCCC CCTACCCCC
                                   C  __  G    C
GAM1065  LOC201243 5'  CCCCCATAGCCACTCAGTCTTC 89540    T   CA  C  GAGG
                                  GA GAC  AG GG    ATGGGGG
                                  || |||  || ||    |||||||
                                  CT CTG  TC CC    TACCCCC
                                   T   AC  A  GA__
GAM1065  LOC253991 5'  CCCGCCGCCGCCCGGTCA    99409       AA    GA  A
                                  TGACC  GCGG  GG TGGG
                                  |||||  ||||  || ||||
                                  ACTGG  CGCC  CC GCCC
                                     CC    G_  _
GAM1065  LOC51092  3'  CCCCTTCGTCCCACCTGGTC   32591       AGC    G  T
                                  GACCA   GGGA GA GGGG
                                  |||||   |||| || ||||
                                  CTGGT   CCCT CT CCCC
                                     CCA    G  T
GAM1066  CDH12     3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                  TACACCACT    GAA  ATAAG
                                  |||||||||    |||  |||||
                                  ATGTGGTGA    TTT  TATTC
                                        AA____   AC
GAM1066  GOCAP1    3'  ATTGTTCTTGGGAGCAGTGTA  43007       CA         G
                                  TACAC  CTCCCAAGAA AAT
                                  |||||  |||||||||| |||
                                  ATGTG  GAGGGTTCTT TTA
                                     AC         G
GAM1066  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT    98090       T    AGAAG
                                  ACCAC CCCA     AATAAG
                                  ||||| ||||     ||||||
                                  TGGTG GGGT     TTATTC
                                     _    GTCA_
GAM1066  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
              A                    TACAC       AGAAGAATAAG
                                  |||||       ||||||||||
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                              ATGTG      TCTTCTTATTC
                                 TACTCCC_
GAM1066 FLJ21791 3' CTTATTTGCAGAAGTGGTGTA 62126        CCCAAGAA
                              TACACCACT      GAATAAG
                              |||||||||      |||||||
                              ATGTGGTGA      TTTATTC
                                   AGACG___
GAM1066 HMP19    3' CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
           TA                   TACA   TCC   GAAGAATAAG
                              ||||   |||   ||||||||||
                              ATGT   AGG   TTTCTTATTC
                                AAA_  ATTG
GAM1066 KIAA1719 3' TCTGTCTTGGGAGTGGTGTA  68742             _
                              TACACCACTCCCAAGA AGA
                              |||||||||||||||| |||
                              ATGTGGTGAGGGTTCT TCT
                                        G
GAM1066 KIAA1853 3' TTTTTCTTGGAAGCAGTG    69929    CA  C
                              CAC  CT CCAAGAAGAA
                              |||  || ||||||||||
                              GTG  GA GGTTCTTTTT
                                AC  A
GAM1066 KIAA1877 3' CTTATTCTTCTGCCATGAGT  66748     CCA__
                              ACTC    AGAAGAATAAG
                              ||||    ||||||||||
                              TGAG    TCTTCTTATTC
                                TACCG
GAM1066 KIAA1906 3' CTTATTCTTCTTGACTTTTGG 73571    CTCC_
                              CCA    CAAGAAGAATAAG
                              |||    ||||||||||||
                              GGT    GTTCTTCTTATTC
                                TTTCA
GAM1066 OSBPL11  3' CTTAATTTCCCAAGAGTGGTG 43206        CCAA   AA
                              CACCACTC   GAAG  TAAG
                              ||||||||   ||||  ||||
                              GTGGTGAG   CTTT  ATTC
                                   AACC   A_
GAM1066 YME1L1   3' TCATTCTTGATGTGGTGTA   58438       TCC    _
                              TACACCAC   CAAGAA GA
                              ||||||||   |||||| ||
                              ATGTGGTG   GTTCTT CT
                                   TA_     A
GAM1066 ZNF262   3' CTTATTTTGTTTGGGAGT    18723        A
                              ACTCCCAAG AGAATAAG
                              ||||||||| ||||||||
                              TGAGGGTTT TTTTATTC
                                   G
GAM1066 LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294        TC_    AAGA
                              TACACCAC   CCAAG   ATA
                              ||||||||   |||||   |||
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                                ATGTGGTG  GGTTC   TGT
                                    CAA    GG__
GAM1067 CSNK1G2  3' CAACCAAAATGCTGCACCAAAG 8987         TCACTACC
                                CTTTGGTGC      TGGTTG
                                |||||||||      ||||||
                                GAAACCACG      ACCAAC
                                    TCGTAAA_
GAM1067 LMO2     5' AACCAGGCCACCAAGAGG    19933      _   CTCACTA
                                CCTTT GGTG     CCTGGTT
                                ||||| ||||     |||||||
                                GGAGA CCAC     GGACCAA
                                  A   C_______
GAM1067 MIPOL1   3' CAACACTGTGTAAACACCAAAG 77588       CT__  TACCTG
                                CTTTGGTG   CAC    GTTG
                                ||||||||   |||    ||||
                                GAAACCAC   GTG    CAAC
                                    AAAT   TCA___
GAM1067 TNFAIP2  3' AACCAGGCAACACCAAGG   21913       CTCACTA
                                CTTTGGTG     CCTGGTT
                                ||||||||     |||||||
                                GGAACCAC     GGACCAA
                                    AAC____
GAM1067 C21orf100 3' AGCCAAGGAACACCAAAG   59504       C  A  ACC
                                CTTTGGTG TC CT   TGGTT
                                |||||||| || ||   |||||
                                GAAACCAC AG GA   ACCGA
                                    A  _  ___
GAM1067 GPR9     5' AACCACAAGCACCAAAG     9484          CACTACC
                                CTTTGGTGCT     TGGTT
                                ||||||||||     |||||
                                GAAACCACGA     ACCAA
                                    AC_____
GAM1067 KIAA1466  3' CAACATTTATATAGAGCACCAA 72407          ACTACCTG_
            AGG                   CCTTTGGTGCTC       GTTG
                                ||||||||||||       ||||
                                GGAAACCACGAG       CAAC
                                      ATATATTTA
GAM1067 MGC2491   3' CAACCAGGTAGTGAGCACCAAA 44094
            GG                    CCTTTGGTGCTCACTACCTGGTTG
                                ||||||||||||||||||||||||
                                GGAAACCACGAGTGATGGACCAAC

GAM1067 PRO2015   3' GCCAATGAGACCAAAGG     38162       G   CTACC
                                CCTTTGGT CTCA    TGGT
                                |||||||| ||||    ||||
                                GGAAACCA GAGT    ACCG
                                    _   A____
GAM1067 LOC158293 3' ACCAGCAGAACACCAAAGG   82744        C  ACTAC
                                CCTTTGGTG TC    CTGGT
                                ||||||||| ||    |||||
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                                GGAAACCAC AG    GACCA
                                     A  AC___
GAM1067  LOC219347 3'  AACTAACAAGCACCAAGG    94569          CACTACC
                                CTTTGGTGCT      TGGTT
                                ||||||||||      |||||
                                GGAACCACGA      ATCAA
                                     ACA____
GAM1067  LOC256130 3'  ATGAGGCAATGAGACACCAAAG 97755         _   CTA   G
           G                     CCTTTGGTG CTCA   CCT GT
                                ||||||||| ||||   ||| ||
                                GGAAACCAC GAGT   GGA TA
                                     A   AAC   G
GAM1067  LOC92231  3'  CAACCAGGTAACAAAACTAAAG 69089        GCTCAC
                                CTTTGGT     TACCTGGTTG
                                |||||||     ||||||||||
                                GAAATCA     ATGGACCAAC
                                    AAACA_
GAM1068  ANK3     5'  AGTCTGACAAAACACCATTCCA 8562       AAC   AGAG
                                TGGAA   GTG   GTCAGACT
                                |||||   |||   ||||||||
                                ACCTT   CAC   CAGTCTGA
                                  AC_   AAAA
GAM1068  FGFR2    5'  GAGTCCTTTCTTCCTCTCGTTC 43775     AA   T   _   TCA_
           CCCA                  TGG  AACG GAG AGG   GACTC
                                ||| |||| ||| |||   |||||
                                ACC  TTGC CTC TTC   CTGAG
                                  CC   T   C   TTTC
GAM1068  FGFR2    5'  GAGTCCTTTCTTCCTCTCGTTC 5562      AA   T   _   TCA_
           CCCA                  TGG  AACG GAG AGG   GACTC
                                ||| |||| ||| |||   |||||
                                ACC  TTGC CTC TTC   CTGAG
                                  CC   T   C   TTTC
GAM1068  IL10     3'  AGCCTGACCACGCTTTCTA   6921        A   GAGA     A
                                TGGAAA CGT   GGTCAG CT
                                |||||| |||   |||||| ||
                                ATCTTT GCA   CCAGTC GA
                                   C   ____     C
GAM1068  SORCS1   3'  TCCGATACTGCAACGTTTTCCA 54684          GAGAG_   A
                                TGGAAAACGT     GTC GA
                                ||||||||||     ||| ||
                                ACCTTTTGCA     TAG CT
                                     ACGTCA   C
GAM1068  ARHGEF2  3'  GAGCCCTGACCTCATCTTCCA  17551      AACGT   _      A_
                                TGGAA    GA GAGGTCAG  CTC
                                |||||    || ||||||||  |||
                                ACCTT    CT CTCCAGTC  GAG
                                   _____  A       CC
GAM1068  ARPP-21  3'  GTCTTACCTCTCAGCTCCCCA  33295     AAAACG       C
                                TGG     TGAGAGGT AGAC
                                |||     |||||||| ||||
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                                ACC      ACTCTCCA TCTG
                                  CCTCG_       T
GAM1068  DKFZP434P1750 3'  GAGTCTGGAGCCTCTCATCTCC 32025     AAAC        __
                                GGA    GTGAGAGGT  CAGACTC
                                |||    |||||||||  |||||||
                                CCT    TACTCTCCG  GTCTGAG
                                  C___         AG
GAM1068  GS3955    3'  GAGCCCTGTCCTCACGTTCCCA 41620     AA       A  T   A_
                                TGG  AACGTGAG GG CAG  CTC
                                |||  |||||||| || |||  |||
                                ACC  TTGCACTC CT GTC  GAG
                                  C_       _ _   CC
GAM1068  KIAA1705  3'  GAGTCTGACAAAACCTTCTCCA 72855      A  C  GAGAG
                                TGGA AA GT     GTCAGACTC
                                |||| || ||     |||||||||
                                ACCT TT CA     CAGTCTGAG
                                  C  C  AAA__
GAM1068  LOC145333 5'  AGTCTGATATCTTCACATTCTC 84288     A  C    _  G
              C                  GGA AA GTGA GA GTCAGACT
                                |||| || |||| || ||||||||
                                CCT TT CACT CT TAGTCTGA
                                  C  A    T  A
GAM1068  LOC153684 5'  TTGTCTCTCACACTTTTCA    87264       AC       T
                                TGGAAA  GTGAGAGG CAG
                                ||||||  |||||||| |||
                                ACTTTT  CACTCTCT GTT
                                   CA       _
GAM1068  LOC196319 5'  AGCCTGACCTCTCTCTACTGCC 91188     AAAACGT        A
              A                   TGG       GAGAGGTCAG CT
                                |||       |||||||||| ||
                                ACC       CTCTCCAGTC GA
                                  GTCATCT         C
GAM1068  LOC197358 5'  AGTCTGACCTCTCTGGACCTCC 89419     AAA_  T
                                GGA    CG GAGAGGTCAGACT
                                |||    || ||||||||||||
                                CCT    GT CTCTCCAGTCTGA
                                  CCAG  _
GAM1068  LOC199678 3'  GCCCTTATCAGTTTTCCA     91366         __     A
                                TGGAAAAC  GTGAG GGT
                                ||||||||  ||||| |||
                                ACCTTTTG  TATTC CCG
                                     AC    _
GAM1068  LOC51066  3'  GAGCCTGCCATTCACGTTTGCC 32502     A       A  T   A
              A                   TGG AAACGTGAG GG CAG CTC
                                ||| ||||||||| || ||| |||
                                ACC TTTGCACTT CC GTC GAG
                                  G        A _   C
GAM1069  FADD      3'  ACAGACCACCTGCTTCTGA    15120       C    A   AC
                                TCAGA GCAG TGG  TCTGT
                                ||||| |||| |||  |||||
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                                AGTCT CGTC ACC  AGACA
                                  T   C  __
GAM1069  SLC22A11  3'  TACAGAGCCCTCATCTGT    38078        A__
                                GCAGATGG  CTCTGTA
                                ||||||||  |||||||
                                TGTCTACT  GAGACAT
                                    CCC
GAM1069  C9orf7    3'  GGGCCCATCTGCGTCTGA    34584           A
                                TCAGACGCAGATGG CTC
                                |||||||||||||| |||
                                AGTCTGCGTCTACC GGG
                                         C
GAM1069  LOC133688 5'  CGCACAGAGTCCTTAGC     75607    A  T       A
                                GC GA GGACTCTGT CG
                                || || |||||||| ||
                                CG TT CCTGAGACA GC
                                 A  _       C
GAM1069  LOC253256 5'  ACAGGGTCACCTGCATCTGA   97985      C    ATG
                                TCAGA GCAG   GACTCTGT
                                ||||| ||||   ||||||||
                                AGTCT CGTC   CTGGGACA
                                   A    CA_
GAM1070  ABCE1     3'  GTCTTTGCACTATATTACCA   60262     _      A   TG
                                TGG AATATAGT GTA  GAGAC
                                ||| |||||||| |||  |||||
                                ACC TTATATCA CGT  TTCTG
                                  A       _  __
GAM1070  ACADL     3'  TGGTTTTTACCACTGTACTCCA 9640      A     A   TG
                                TGGA TATAGT GTA  GAGACCA
                                |||| ||||||| |||  |||||||
                                ACCT ATGTCA CAT  TTTTGGT
                                  C     C  __
GAM1070  GPR85     3'  TCTTGTAGCTACTATATTCCA  39108           ATG
                                TGGAATATAGTAGT   GAGA
                                ||||||||||||||   ||||
                                ACCTTATATCATCG   TTCT
                                         ATG
GAM1070  HLA-DQA1  3'  CTCCATCTATAATCTCCA    98032      AT  A    T
                                TGGA  AT GTAG ATGGAG
                                ||||  || |||| ||||||
                                ACCT  TA TATC TACCTC
                                  C_  A   _
GAM1070  LPO       3'  TGGTCCCTTAGAGCTCCATATC 68463     A   __  AG  T  A
             CCA                   TGG ATAT  AGT  TA GG GACCA
                                ||| ||||  |||  || || |||||
                                ACC TATA  TCG  AT CC CTGGT
                                  C   CC   AG  T  _
GAM1070  OPA3      3'  TTGTACCACTGTATTCCA    47852          A   TG
                                TGGAATATAGT GTA  G
                                |||||||||| |||  |
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                                ACCTTATGTCA CAT  T
                                      C   GT
GAM1070 RPP30    3' TCTCCTGACCTCATATTCCA  22210       _ TA  AT
                                TGGAATAT AG  GT  GGAGA
                                |||||||| ||  ||  |||||
                                ACCTTATA TC  CA  CCTCT
                                     C __  GT
GAM1070 CAMKK2   5' TCGTGCTACTGCACTCCA   22632     ATA
                                TGGA   TAGTAGTATGG
                                ||||   ||||||||||
                                ACCT   GTCATCGTGCT
                                  CAC
GAM1070 DKFZP434K1772 3' GGTCTCCCCACCAACTCCA   68337     ATATA  A_  AT
                                TGGA    GT  GT  GGAGACC
                                ||||    ||  ||  |||||||
                                ACCT    CA  CA  CCTCTGG
                                  _____  AC  CC
GAM1070 DKFZp761O132 5' GTCCCTGCTACTATCTCCA   51173     AT       T  A
                                TGGA  ATAGTAGTA GG GAC
                                ||||  |||||||||| || |||
                                ACCT  TATCATCGT CC CTG
                                  C_       _ _
GAM1070 FLJ12650  3' GGTCTCCACCATATTC     44823       A  AGTAT
                                GAATAT GT    GGAGACC
                                |||||| ||    |||||||
                                CTTATA CA    CCTCTGG
                                   C _____
GAM1070 FLJ20170  3' TGGTCACACCACTGTATTCCA  35170          A  AT GA
                                TGGAATATAGT GT  G  GACCA
                                |||||||||||| ||  |  |||||
                                ACCTTATGTCA CA  C  CTGGT
                                      C  __ A_
GAM1070 FLJ20306  3' TTGTACCACTGTATTCCA    35404          A   TG
                                TGGAATATAGT GTA  G
                                |||||||||||| |||  |
                                ACCTTATGTCA CAT  T
                                      C   GT
GAM1070 GLCCI1   3' TGGCCTCCACCCTATGTTCCA  94172         TAGTA    A
                                TGGAATATAG    TGGAG CCA
                                ||||||||||    ||||| |||
                                ACCTTGTATC    ACCTC GGT
                                     CC___    C
GAM1070 KIAA0391  3' TCATGCTACTGCACTCCA    28620     ATA
                                TGGA   TAGTAGTATGG
                                ||||   ||||||||||
                                ACCT   GTCATCGTACT
                                  CAC
GAM1070 KIAA1727  3' TGGTCTCCACAGGTCTTTCCA  64767      TAT  TAGTA
                                TGGAA   AG    TGGAGACCA
                                |||||   ||    |||||||||
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                                ACCTT  TC    ACCTCTGGT
                                   ___ TGGAC
GAM1070 KIAA1853 3' TGGTCTCCAGCCCCACTTCC  69927    ATAT  AGTA_
                                GGA   AGT    TGGAGACCA
                                |||   |||    |||||||||
                                CCT   TCA    ACCTCTGGT
                                  _____  CCCCG
GAM1070 MGC4248  3' TCACACCACTGTATTCCA   51318          A  A
                                TGGAATATAGT GT TGG
                                |||||||||||  || |||
                                ACCTTATGTCA CA ACT
                                      C  C
GAM1070 ZFP106   3' TCATACTACTGCACTCCA   42740      ATA
                                TGGA  TAGTAGTATGG
                                ||||  ||||||||||
                                ACCT  GTCATCATACT
                                  CAC
GAM1070 LOC147040 5' TGGGGGGCACACTATATTCCA 78838          A  ATGGAGA
                                TGGAATATAGT GT      CCA
                                ||||||||||  ||      |||
                                ACCTTATATCA CA      GGT
                                      _ CGGGG__
GAM1070 LOC150245 3' TGGTCTCCACATCTCCCCTCCA 86121      ATAT  TAGTA
                                TGGA   AG    TGGAGACCA
                                ||||   ||    |||||||||
                                ACCT   TC    ACCTCTGGT
                                  CCCC  TAC__
GAM1070 LOC157663 3' GTCTCCATAATTATATTC    82454         AG
                                GAATATAGT  TATGGAGAC
                                |||||||||  |||||||||
                                CTTATATTA  ATACCTCTG
                                      __
GAM1070 LOC253681 5' TGGGGGGCACACTATATTCCA  96843          A  ATGGAGA
                                TGGAATATAGT GT      CCA
                                ||||||||||  ||      |||
                                ACCTTATATCA CA      GGT
                                      _ CGGGG__
GAM1070 LOC254428 3' TGGTCTCCAGCCACCCCTACCC 97200     AATA  TA  A__
           CA                     TGG   TAG  GT   TGGAGACCA
                                |||   |||  ||   |||||||||
                                ACC   ATC  CA   ACCTCTGGT
                                  CC__   CC  CCG
GAM1070 LOC257429 3' CTCCATCTATAATCTCCA    97696      AT  A   T
                                TGGA  AT GTAG ATGGAG
                                ||||  || |||| ||||||
                                ACCT  TA TATC TACCTC
                                  C_  A   _
GAM1071 CALCRL   3' ACCTCTTCCTGTCTTAC     20526      A  ATTTC  _
                                GTGA GA    CAG AAGAGGT
                                ||||  ||    ||| |||||||
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                                CATT CT    GTC TTCTCCA
                                  _ _____  C
GAM1071  EBAF     3'  TCTGGCAAATTCTTCACT    66031          _
                                AGTGAAGAATTT CCAGA
                                |||||||||||| |||||
                                TCACTTCTTAAA GGTCT
                                      C
GAM1071  MAP1B    3'  AACTTTGTTTCCAGAAATTCTT 20957         CA  __
              CA                  TGAAGAATTTC  GAA  GAGGTT
                                |||||||||||  |||  ||||||
                                ACTTCTTAAAG  CTT  TTTCAA
                                      AC   TG
GAM1071  MAP1B    3'  AACTTTGTTTCCAGAAATTCTT 50088         CA  __
              CA                  TGAAGAATTTC  GAA  GAGGTT
                                |||||||||||  |||  ||||||
                                ACTTCTTAAAG  CTT  TTTCAA
                                      AC   TG
GAM1071  MAP3K14  3'  ACCTCTTCCAGATTTCTC    15540    AG    CCA
                                GA  AATTT   GAAGAGGT
                                ||  |||||   ||||||||
                                CT  TTAGA   CTTCTCCA
                                 CT    C__
GAM1071  MMP10    3'  TTTCTGGAATTCTTCACT    11606          T
                                AGTGAAGAATT CCAGAAG
                                |||||||||||  |||||||
                                TCACTTCTTAA GGTCTTT
                                           _
GAM1071  CSEN     3'  TTTCTGGAAATTCTTCCCT   26464    T
                                AG GAAGAATTTCCAGAAG
                                ||  ||||||||||||||||
                                TC CTTCTTAAAGGTCTTT
                                 C
GAM1071  NMT1     3'  AACCCCTTCTGGGACTTCA   41142      AAT       A
                                TGAAG   TTCCAGAAG GGTT
                                |||||   |||||||||  ||||
                                ACTTC   AGGGTCTTC CCAA
                                   ___        C
GAM1071  LOC149086 3'  AACCTCTTCCTGCTGTCCCTCC 85488     A  AATTTC  _
              AC                  GTG AG     CAG AAGAGGTT
                                |||  ||     |||  ||||||||
                                CAC TC     GTC TTCTCCAA
                                  C  CCTGTC   C
GAM1071  LOC158230 3'  ACCTCTCCCTCTTCTTCCT    82698    T     TTTCCA  A
                                AG GAAGAA     GA GAGGT
                                ||  ||||||     ||  |||||
                                TC CTTCTT     CT CTCCA
                                 _     CTCC__  _
GAM1071  LOC163231 5'  AACCTCTTCACTCTCTCCCACT 83327      A_   ATTTCCA
                                AGTG  AGA      GAAGAGGTT
                                ||||  |||      |||||||||
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                                TCAC  TCT      CTTCTCCAA
                                  CC   CTCA___
GAM1071  LOC163231 5'  AACCTCTTCACTGTCACCCACT 83328      AA_  ATTTCCA
                                AGTG   GA      GAAGAGGTT
                                ||||   ||      |||||||||
                                TCAC   CT      CTTCTCCAA
                                  CCA  GTCA___
GAM1071  LOC199883 3'  AACCTCCTCTGGAGGTCCTC   91461    A  A       A
                                GA GA TTTCCAGA GAGGTT
                                || || |||||||| ||||||
                                CT CT GGAGGTCT CTCCAA
                                 C  _       C
GAM1071  LOC200020 3'  AACCTCCTCTGGAGGTCCTC   91532    A  A       A
                                GA GA TTTCCAGA GAGGTT
                                || || |||||||| ||||||
                                CT CT GGAGGTCT CTCCAA
                                 C  _       C
GAM1071  LOC257364 3'  CCCTGGGAAATTCCCCACT    96643      AA       AGA  A
                                AGTG  GAATTTCC   AG GG
                                ||||  ||||||||   || ||
                                TCAC  CTTAAAGG   TC CC
                                  CC       G__  _
GAM1071  LOC92697  3'  AACCTCTTCCAGAAAGTCCCAG 70799     GAA  A    CA
            CT                    AGT   GA TTTC  GAAGAGGTT
                                |||   || ||||  |||||||||
                                TCG   CT AAAG  CTTCTCCAA
                                  ACC  G    AC
GAM1072  DLEC1    3'  CATCTGGCCCTCCCTTG     96278      A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                   C    G  _
GAM1072  DLEC1    3'  CATCTGGCCCTCCCTTG     96279      A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                   C    G  _
GAM1072  PIP5K1A  3'  TATCCCACCCTGCCTTGATA   14520        A   CA  C
                                TATCAAGG AGGG  GG GTG
                                |||||||| ||||  || |||
                                ATAGTTCC TCCC  CC TAT
                                     G    A_  C
GAM1072  SOX11    3'  ACCCACCCCCCCTTGGTA    13308        AA   CA  C
                                TATCAAGG  GGG  GG GT
                                ||||||||  |||  || ||
                                ATGGTTCC  CCC  CC CA
                                     CC   A_  _
GAM1072  CHL1     3'  TGTTACCTTTCCTCAATA    22768     CA      CA
                                TAT  AGGAAGGG  GGCG
                                |||  ||||||||  ||||
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                                ATA  TCCTTTCC  TTGT
                                  AC       A_
GAM1072  EPB41L1   3'  CATTCTGCCCTTCCCTGA    71104     A         C
                                TCA GGAAGGGCAGG GTG
                                ||| |||||||||| |||
                                AGT CCTTCCCGTCT TAC
                                  C         _
GAM1072  FLJ00060  3'  CATACCCCCTGCCCTCCTCTGA 61741     _   A      CGTG
                                TCA AGGA GGGCAGG    ATG
                                ||| |||| |||||||    |||
                                AGT TCCT CCCGTCC    TAC
                                  C   _      CCCA
GAM1072  FLJ10898  5'  CACCACAGCCCTTTCTCAATA  60126     CA       AGGC
                                TAT  AGGAAGGGC    GTG
                                |||  |||||||||    |||
                                ATA  TCTTTCCCG    CAC
                                  AC        ACAC
GAM1072  FLJ22557  3'  ATCATCCCATCCTTAATA    45581     C    A   CAGGC
                                TAT AAGGA GGG    GTGAT
                                ||| ||||| |||    |||||
                                ATA TTCCT CCC    TACTA
                                  A    A  _____
GAM1072  KIAA0574  3'  CATCCCCTGCCCTCCCCTGA   69808     A  A      CGT
                                TCA GG AGGGCAGG   GATG
                                ||| || ||||||||   ||||
                                AGT CC TCCCGTCC   CTAC
                                  C  C       C__
GAM1072  KIAA0632  3'  CACCTCAGAAACCCTTCCTTGA 32071          CA___  C
                                TCAAGGAAGGG     GG GTG
                                ||||||||||     || |||
                                AGTTCCTTCCC     CT CAC
                                      AAAGA  C
GAM1072  KIAA1045  3'  CATCACATGTCCTTCC      71599          GGC
                                GGAAGGGCA   GTGATG
                                |||||||||   ||||||
                                CCTTCCTGT   CACTAC
                                     A__
GAM1072  KIAA1354  5'  CAGTGACTGCCTTCCCTTGATA 61572        A      G  _
                                TATCAAGG AGGGCAG CG TG
                                |||||||| ||||||| || ||
                                ATAGTTCC TTCCGTC GT AC
                                     C      A  G
GAM1072  MGC20460  5'  CACCGCCTCCTACCCTTCTT   54901        C___    _
                                AGGAAGGG    AGGCG TG
                                ||||||||    ||||| ||
                                TTCTTCCC    TCCGC AC
                                     ATCC     C
GAM1072  LOC158476 3'  CACGCCCGCCCCCCCCCATTGA  88186      _ AA_   A
                                TCAA GG   GGGC GGCGTG
                                |||| ||   |||| ||||||
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                                AGTT CC   CCCG CCGCAC
                                  A  CCC    C
GAM1072  LOC90459  3'  CACACCCGCCTAATTTTTG   63550       A_   A  C
                                CAAGGA  GGGC GG GTG
                                ||||||  |||| || |||
                                GTTTTT  TCCG CC CAC
                                   AA    C  A
GAM1073  BACE      3'  CTGGAGCTCACCCAAGGTCACC 25031          CC__
           AA                    TTGGTGACCTTG   AGCTCCAG
                                ||||||||||||   ||||||||
                                AACCACTGGAAC   TCGAGGTC
                                      CCAC
GAM1073  BACE      3'  CTGGAGCTCACCCAAGGTCACC 58083          CC__
           AA                    TTGGTGACCTTG   AGCTCCAG
                                ||||||||||||   ||||||||
                                AACCACTGGAAC   TCGAGGTC
                                      CCAC
GAM1073  CXorf6    3'  CTGTAGCAAACACCACCAAGT  19705        ACC_   __
                                ACTTGGTG   TTGC  CAG
                                ||||||||   ||||  |||
                                TGAACCAC   AACG  GTC
                                    CACA   AT
GAM1073  CYFIP2    5'  CTGGAGCCGGAGGTCACCAAG  73965          TG  A
                                CTTGGTGACCT  CC GCTCCAG
                                ||||||||||  || |||||||
                                GAACCACTGGA  GG CGAGGTC
                                      __ C
GAM1073  FUT1      3'  GAGCAAGCATTCACCAAGT   5595          CCT   CA
                                ACTTGGTGA   TGC  GCTC
                                |||||||||   |||  ||||
                                TGAACCACT   ACG  CGAG
                                     T__   AA
GAM1073  HNF3G     3'  CTGGAGCTCACACCACGAAG  72799     G   ACCT  CC
                                CTT GTG    TG  AGCTCCAG
                                ||| |||    ||  ||||||||
                                GAA CAC    AC  TCGAGGTC
                                  G   C___  AC
GAM1073  KLHL1     3'  CTGAAACTGGCAAACACAAAG  40872     G   ACC      CTC
                                CTT GTG   TTGCCAG   CAG
                                ||| |||   |||||||   |||
                                GAA CAC   AACGGTC   GTC
                                  A   A__      AAA
GAM1073  PIGN      3'  CTGGAAGGAAATCACCAGGT   25602         ___    G
                                ACTTGGTGA   CCTT CCAG
                                |||||||||   |||| ||||
                                TGGACCACT   GGAA GGTC
                                     AAA    _
GAM1073  SMARCD2   5'  GGAATTAAGATCGCCAAGT   13262         C    CCAGC
                                ACTTGGTGA CTTG    TCC
                                ||||||||| ||||    |||
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                                TGAACCGCT GAAT    AGG
                                     A   TA___
GAM1073  AF020591  3'  CTGAAACTGTGTATTACCAAG  27910       CCT  _  CTC
                                CTTGGTGA  TGC CAG  CAG
                                ||||||||  ||| |||  |||
                                GAACCATT  ATG GTC  GTC
                                    ___  T  AAA
GAM1073  CGGBP1   3'  AGTTGGCAAGATCTCCAAG   14749     T  C
                                CTTGG GA CTTGCCAGCT
                                ||||| || ||||||||||
                                GAACC CT GAACGGTTGA
                                   T  A
GAM1073  DCOHM    3'  GGACTTCAGGGTCACCAAG   50532         CC  C
                                CTTGGTGACCTTG  AG TCC
                                ||||||||||||  || |||
                                GAACCACTGGGAC  TC AGG
                                       T_  _
GAM1073  DEFCAP   3'  CTGGAGCTGGCAAGACC    53387    GAC
                                GGT  CTTGCCAGCTCCAG
                                |||  ||||||||||||||
                                CCA  GAACGGTCGAGGTC
                                 ___
GAM1073  DEFCAP   3'  CTGGAGCTGGCAAGACC    53390    GAC
                                GGT  CTTGCCAGCTCCAG
                                |||  ||||||||||||||
                                CCA  GAACGGTCGAGGTC
                                 ___
GAM1073  DEFCAP   3'  CTGGAGCTGGCAAGACC    30614    GAC
                                GGT  CTTGCCAGCTCCAG
                                |||  ||||||||||||||
                                CCA  GAACGGTCGAGGTC
                                 ___
GAM1073  DKFZP434C128 3'  GAGCTGGTATAGCCACCAG   65470      ACCT
                                TTGGTG   TGCCAGCTC
                                ||||||   |||||||||
                                GACCAC   ATGGTCGAG
                                   CGAT
GAM1073  DKFZp434N035 3'  CTGGAGCTGGCGGAGACCAA  51062     GA  TT
                                TTGGT  CC  GCCAGCTCCAG
                                |||||  ||  ||||||||||||
                                AACCA  GG  CGGTCGAGGTC
                                  GA  __
GAM1073  FLJ11800  3'  CTGTGAGCAATGCCACCAAGT  47039       ACCTT  CA_  _
                                ACTTGGTG   GC  GCTC CAG
                                ||||||||   ||  |||| |||
                                TGAACCAC   CG  CGAG GTC
                                    _____ TAA  T
GAM1073  FLJ12595  3'  CTGGAGCTGACAAACCCAA   47149    TGACC  C
                                TTGG   TTG CAGCTCCAG
                                ||||   ||| |||||||||
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                                AACC    AAC GTCGAGGTC
                                  CA___   A
GAM1073 FLJ14768 3' GGAGCTGGGGGACCA      52676     GA  TG
                                TGGT  CCT  CCAGCTCC
                                ||||  |||  ||||||||
                                ACCA  GGG  GGTCGAGG
                                  __  __
GAM1073 HNT      3' CTGGAGCTGGCCATCCCAA   33699     T  CCTT
                                TTGG GA   GCCAGCTCCAG
                                |||| ||   ||||||||||
                                AACC CT   CGGTCGAGGTC
                                  _ AC__
GAM1073 KIAA0431 3' TGGAGCTGTTTCCCCAAGT   31556      T  CCTTGC
                                ACTTGG GA    CAGCTCCA
                                |||||| ||    ||||||||
                                TGAACC CT    GTCGAGGT
                                   C  TT____
GAM1073 KIAA1061 3' GGAGGCAAAGTCACCAA     71722       C    AGC
                                TTGGTGAC TTGCC   TCC
                                |||||||| |||||   |||
                                AACCACTG AACGG   AGG
                                    A    ___
GAM1073 KIAA1668 3' CTGGAGCTGGCGCCACCAA   67068      ACCT
                                TTGGTG   TGCCAGCTCCAG
                                ||||||   ||||||||||||
                                AACCAC   GCGGTCGAGGTC
                                   C___
GAM1073 KLF12    3' CTGGAGCTCCAAAATCATCCAA 24361     _  CC   CC
                                TTGG TGA  TTG  AGCTCCAG
                                |||| |||  |||  ||||||||
                                AACC ACT  AAC  TCGAGGTC
                                  T  AA  C_
GAM1073 MGC2574  3' CTGGAGCTGGCACTCCAA    44283     TGACCT
                                TTGG     TGCCAGCTCCAG
                                ||||     ||||||||||||
                                AACC     ACGGTCGAGGTC
                                  TC____
GAM1073 MGC4796  3' GGAGCTGGGTACCCAAG     62168     TG   TTGC
                                CTTGG  ACC    CAGCTCC
                                |||||  |||    |||||||
                                GAACC  TGG    GTCGAGG
                                   CA  ____
GAM1073 NISCH    3' CTGGAGCTGCCAGCACCAAG   24190       ACC   C
                                CTTGGTG   TTG CAGCTCCAG
                                |||||||   ||| |||||||||
                                GAACCAC   GAC GTCGAGGTC
                                    ___  C
GAM1073 RASGRF2  3' CTGTGGAACAGAAGGCCACCAA 61699         A    GCCAG TC
             GT                   ACTTGGTG CCTT    C  CAG
                                |||||||| ||||    |  |||
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                                TGAACCAC GGAA    G  GTC
                                    C    GACAA GT
GAM1073  SIAT4B   5'  GAGCTGGCAGCCAGG      23635       GACCT
                                CTTGGT    TGCCAGCTC
                                ||||||    |||||||||
                                GGACCG    ACGGTCGAG
                                  _____
GAM1073  SLC21A12  5'  CTGAAGCCTCGAGGTCACCAGG 33447           CCA   C
                                CTTGGTGACCTTG   GCT CAG
                                ||||||||||||   ||| |||
                                GGACCACTGGAGC   CGA GTC
                                      TC_   A
GAM1073  SLC26A10  5'  CTGTGGACACAAGATACCAAGT 56845        AC    CCAG TC
                                ACTTGGTG  CTTG    C  CAG
                                ||||||||  ||||    |  |||
                                TGAACCAT  GAAC    G  GTC
                                    A_    ACA_ GT
GAM1073  LOC146237 3'  AGCCCAAGGTCAACAAG     84604      G       CCA
                                CTTG TGACCTTG   GCT
                                |||| ||||||||   |||
                                GAAC ACTGGAAC   CGA
                                  A       C__
GAM1073  LOC147219 3'  CTGACAAAGCAGAAATCACCAA 85112         CC_    CAGCTC
           GT                    ACTTGGTGA   TTGC     CAG
                                |||||||||   ||||     |||
                                TGAACCACT   GACG     GTC
                                    AAA    AAACA_
GAM1073  LOC147859 5'  TGGAGCTATCATACCAAG    88518        ACCT  CC
                                CTTGGTG    TG  AGCTCCA
                                |||||||    ||  |||||||
                                GAACCAT    AC  TCGAGGT
                                   _____  TA
GAM1073  LOC157254 5'  CTGGAGCTACTTCTCACCAA   82310        CCTTGCC
                                TTGGTGA      AGCTCCAG
                                |||||||      ||||||||
                                AACCACT      TCGAGGTC
                                    CTTCA__
GAM1073  LOC157931 5'  CTGGAGCTTTCAAACCCCAA   87941      TGACC   CC
                                TTGG    TTG  AGCTCCAG
                                ||||    |||  ||||||||
                                AACC    AAC  TCGAGGTC
                                  CCA__   TT
GAM1073  LOC161589 3'  CTGGAGCTGGCAAGGTAGCCAA 83156        G
           GT                    ACTTGGT ACCTTGCCAGCTCCAG
                                |||||||  ||||||||||||||||
                                TGAACCG TGGAACGGTCGAGGTC
                                    A
GAM1073  LOC196549 3'  CTGGAGGAGGAGATCACCAAGT 59920         C  TG  AG
                                ACTTGGTGA CT  CC  CTCCAG
                                |||||||| ||  ||  ||||||
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                                TGAACCACT GA  GG  GAGGTC
                                     A  __  AG
GAM1073  LOC220575 3'  CTGTGAGCAATGCCACCAAGT  76814        ACCTT  CA_   _
                                ACTTGGTG    GC   GCTC CAG
                                ||||||||    ||   |||| |||
                                TGAACCAC    CG   CGAG GTC
                                     _____  TAA    T
GAM1073  LOC51762  3'  CTGAAAGCACAGGTCACCCAG  33704    T      _  ___
                                CT GGTGACCT TGC   CAG
                                || |||||||| |||   |||
                                GA CCACTGGA ACG   GTC
                                 C       C   AAA
GAM1073  LOC92340  3'  GGCCGTCCAGGGTCACCAAG   69565          CCA_
                                CTTGGTGACCTTG    GCT
                                ||||||||||||    |||
                                GAACCACTGGGAC    CGG
                                       CTGC
GAM1073  LOC93624  5'  CTGAAGCGCAAGATCACCAAG  73101        C    CA   C
                                CTTGGTGA CTTGC  GCT CAG
                                |||||||| |||||  ||| |||
                                GAACCACT GAACG  CGA GTC
                                     A     __   A
GAM1074  DPYSL2    3'  CCAGTTCAGAAGTGCTAA    9115      A   CTTTA
                                TTAG ACT    CTGAACTGG
                                |||| |||    |||||||||
                                AATC TGA    GACTTGACC
                                  G   A____
GAM1074  ARHGEF9   3'  CAGCAACAAGAGAGTTCTAA   31481          ACTGAA
                                TTAGAACTCTTT     CTG
                                ||||||||||||     |||
                                AATCTTGAGAGA     GAC
                                       ACAAC_
GAM1074  LOC123342 5'  CAGCAGAAAAGAGTTCTAA    76124          A   AA
                                TTAGAACTCTTT CTG  CTG
                                |||||||||||| |||  |||
                                AATCTTGAGAAA GAC  GAC
                                       A  __
GAM1075  ENC1      3'  AAGCCCAACTGTGGGTCCG    14644        GCT   GA_
                                CGGACCCA   CAGT   GCTT
                                ||||||||   ||||   ||||
                                GCCTGGGT   GTCA   CGAA
                                     ___    ACC
GAM1075  KNS2      3'  TGGGGCATGAGCTGGGCCC    19896    A       GTGA
                                GG CCCAGCTCA    GCTTCG
                                || |||||||||    ||||||
                                CC GGGTCGAGT    CGGGGT
                                 C        A___
GAM1075  SLC21A9   3'  AGAGCACTGAGCTGGACCC    24378    AC        AG
                                GG  CCAGCTCAGTG  CT
                                ||  ||||||||||  ||
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                                CC  GGTCGAGTCAC  GA
                                 CA         GA
GAM1075  FLJ10769  3'  CGACTGCACTGACTGGGTCC   37143        C     AGCT
                                GGACCCAG TCAGTG    TCG
                                |||||||| ||||||    |||
                                CCTGGGTC AGTCAC    AGC
                                     _     GTC_
GAM1075  KIAA0339  3'  CGATTTGGCCGGAGCCGGATCC 71963     C  A    A_  G  CT
                                GGA CC GCTC  GT AG  TCG
                                ||| || ||||  || ||  |||
                                CCT GG CGAG  CG TT  AGC
                                  A  C    GC  G  T_
GAM1075  KIAA0459  3'  CGAAGCCCACACATGAGCT    61650       ____   A
                                AGCTCA   GTG GCTTCG
                                ||||||   ||| ||||||
                                TCGAGT   CAC CGAAGC
                                    ACA   C
GAM1075  PP3501    3'  CGAAGCTCTGACCCAGGCC    41679    A  CAGC   GT
                                GG CC    TCA  GAGCTTCG
                                || ||    |||  ||||||||
                                CC GG    AGT  CTCGAAGC
                                 _  ACCC   __
GAM1075  ZDHHC3    5'  CGAAGCCCGAGGCCGGGTCC   33929       A   CAG  A
                                GGACCC GCT   TG GCTTCG
                                |||||| |||   || ||||||
                                CCTGGG CGG   GC CGAAGC
                                    C   A__  C
GAM1075  LOC162083 5'  AAGATTCACCAATGCTGAGTCC 83204      C    TCA_    _
                                GGAC CAGC    GTGAG CTT
                                |||| ||||    ||||| |||
                                CCTG GTCG    CACTT GAA
                                  A    TAAC    A
GAM1075  LOC91661  3'  CGAAGCTGACACTGAGTT    57210         __
                                AGCTCAGTG  AGCTTCG
                                |||||||||  |||||||
                                TTGAGTCAC  TCGAAGC
                                     AG
GAM1076  CHC1      3'  GTGTCCATGGGACAAAAAAGAA 8863         G  G_
                                TTCTTTTT TG  CTGTGGACAC
                                |||||||| ||  ||||||||||
                                AAGAAAAA AC  GGTACCTGTG
                                     _  AG
GAM1076  CTBP2     3'  TCAAATCACAAAAAGAA     9004           CTG
                                TTCTTTTTGTGG   TGG
                                ||||||||||||   |||
                                AAGAAAAACACT   ACT
                                      AA_
GAM1076  CTBP2     3'  TCAAATCACAAAAAGAA     43315          CTG
                                TTCTTTTTGTGG   TGG
                                ||||||||||||   |||
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                                AAGAAAAACACT   ACT
                                      AA_
GAM1076  GARS     3'  TGTCCACTTTACAAAAGAA   10758       T   CT
                                TTCTTTTT GTGG  GTGGACA
                                |||||||  ||||  |||||||
                                AAGAAAA CATT  CACCTGT
                                    _   T_
GAM1076  GRIN2A   3'  GTGCCTGCCACAAAAA      7723         TGT  A
                                TTTTTGTGGC   GG CAC
                                |||||||||   || |||
                                AAAAACACCG   CC GTG
                                      T__  _
GAM1076  HHLA1    5'  TCCACCACAAAAGAA       20338       T   CTG
                                TTCTTTT GTGG   TGGA
                                |||||||  ||||   ||||
                                AAGAAAA CACC   ACCT
                                    _   ___
GAM1076  LOH11CR2A 3'  CCATCCAGAAAAAGAA      28269        G   CT
                                TTCTTTTT TGG  GTGG
                                ||||||||  |||  ||||
                                AAGAAAAA ACC  TACC
                                     G  __
GAM1076  MTM1     3'  GTGTCACTCCATAAAAAGAA   6006          CT   G
                                TTCTTTTTGTGG  GTG ACAC
                                ||||||||||||  ||| ||||
                                AAGAAAAATACC  CAC TGTG
                                      T_  _
GAM1076  NDRG3    3'  TCCACATATCCACAAGAA    50127        C__
                                TTTTTGTGG   TGTGGA
                                |||||||||   ||||||
                                AAGAACACC   ACACCT
                                     TAT
GAM1076  NPHP1    3'  GTCAAAAGCACAAAAAGAA   63148         G  GTG
                                TTCTTTTTGTG CT   GAC
                                ||||||||||| ||   |||
                                AAGAAAAAACAC GA   CTG
                                     _  AAA
GAM1076  PAIP2    3'  TGTCCCCATCAAAAAGAA    33645        _  CTGT
                                TTCTTTTTG TGG    GGACA
                                |||||||||  |||   |||||
                                AAGAAAAAC ACC    CCTGT
                                     T  _____
GAM1076  PCDH11X  3'  TGTCACACACACAAAAA     53138        GC   _
                                TTTTTGTG  TGTG GACA
                                ||||||||  |||| ||||
                                AAAAACAC  ACAC CTGT
                                     __   A
GAM1076  PCDH11X  3'  TGTCACACACACAAAAA     53145        GC   _
                                TTTTTGTG  TGTG GACA
                                ||||||||  |||| ||||
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                                AAAAACAC  ACAC CTGT
                                    __    A
GAM1076  PCDH11Y   3'  TGTCACACACACAAAAA     53190        GC   _
                                TTTTTGTG  TGTG GACA
                                ||||||||  |||| ||||
                                AAAAACAC  ACAC CTGT
                                    __    A
GAM1076  PTGES     3'  GTGTCTGCCAAAAAAA      18070      G    TGT
                                TTTTT TGGC   GGACAC
                                ||||| ||||   ||||||
                                AAAAA ACCG   TCTGTG
                                   A   ___
GAM1076  RP42      3'  GTGCCCACATATAAAAA      40568        GC    A
                                TTTTTGTG  TGTGG CAC
                                ||||||||  ||||| |||
                                AAAAATAT  ACACC GTG
                                    __    C
GAM1076  RPL8      3'  GTGTTTATGCCAAAAAAA    53946      G    T
                                TTTTT TGGC GTGGACAC
                                ||||| |||| ||||||||
                                AAAAA ACCG TATTTGTG
                                   A   _
GAM1076  RPL8      3'  GTGTTTATGCCAAAAAAA    8267       G    T
                                TTTTT TGGC GTGGACAC
                                ||||| |||| ||||||||
                                AAAAA ACCG TATTTGTG
                                   A   _
GAM1076  SRD5A2    5'  TGTCCACAACAATATGAA    60120     TTT    GGC
                                TTC   TTGT   TGTGGACA
                                |||   ||||   ||||||||
                                AAG   AACA   ACACCTGT
                                  TAT   ____
GAM1076  TGFBR2    3'  GTGTCCACAAGGACAAGAA   13734        GGC
                                TTTTTGT   TGTGGACAC
                                |||||||   |||||||||
                                AAGAACA   ACACCTGTG
                                    GGA
GAM1076  UCP3      3'  TGTAAATGCCACAAAGAAGAA  43316        _    T  GG
                                TTCTTTTT GTGGC GT  ACA
                                |||||||| ||||| ||  |||
                                AAGAAGAA CACCG TA  TGT
                                    A    _  AA
GAM1076  UMOD      3'  GTGCTCCAGCCACAGAAAAGAA 14010       _        TG A
                                TTCTTT TTGTGGCTG  G CAC
                                |||||| |||||||||  | |||
                                AAGAAA GACACCGAC  C GTG
                                   A        CT _
GAM1076  WARS      3'  TGCCCCCTCCCAAAAAGAA   67869         T  CTGT  A
                                TTCTTTTTG GG    GG CA
                                ||||||||| ||    || ||
```

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                                AAGAAAAAC CC    CC GT
                                     _ TCCC  _
GAM1076  C1orf16   3'  GCAGTGCAACAAAAAGAA    29914          _ _
                                TTCTTTTTGT G GCTGT
                                |||||||||| | |||||
                                AAGAAAAACA C TGACG
                                     A G
GAM1076  C1orf2    3'  CACTGGCTGGCACAAAAAGAA  22727          ___  _
                                TTCTTTTTGTG   GCT GTG
                                ||||||||||   ||| |||
                                AAGAAAAACAC   CGG CAC
                                     GGT   T
GAM1076  C1orf2    3'  CACTGGCTGGCACAAAAAGAA  96264          ___  _
                                TTCTTTTTGTG   GCT GTG
                                ||||||||||   ||| |||
                                AAGAAAAACAC   CGG CAC
                                     GGT   T
GAM1076  C20orf42  3'  TGTTCTGCCACACAAAGAA    35064       T     TGT
                                TTCTTT TGTGGC   GGACA
                                |||||| ||||||   |||||
                                AAGAAA ACACCG   CTTGT
                                   C     T__
GAM1076  DIO2      3'  CACAAGGCCAGAAAAAGAA    7664        G    __
                                TTCTTTTT TGGCT  GTG
                                |||||||| |||||  |||
                                AAGAAAAA ACCGG  CAC
                                     G     AA
GAM1076  DIO2      3'  CACAAGGCCAGAAAAAGAA    26547       G    __
                                TTCTTTTT TGGCT  GTG
                                |||||||| |||||  |||
                                AAGAAAAA ACCGG  CAC
                                     G     AA
GAM1076  FLJ11004  5'  TGTCTATGCCAAAAAAAGAA   37534       G    T
                                TTCTTTTT TGGC GTGGACA
                                |||||||| |||| |||||||
                                AAGAAAAA ACCG TATCTGT
                                     A   _
GAM1076  FLJ11026  3'  TCTGCCACATAAAAGAA      37549       _     TGT
                                TTCTTTT TGTGGC   GGA
                                ||||||| ||||||   |||
                                AAGAAAA ACACCG   TCT
                                     T     ___
GAM1076  FLJ13031  5'  TCCACAGCTCAGAGAAGAA    45514       GT
                                TTCTTTTT  GGCTGTGGA
                                ||||||||  |||||||||
                                AAGAAGAG  TCGACACCT
                                     AC
GAM1076  FLJ20281  3'  TGTCCAAAACAAGAAAGAA    92623       G  GCTG
                                TTCTTTTT TG    TGGACA
                                |||||||| ||    ||||||
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                                AAGAAAGA AC    ACCTGT
                                    _ AAA_
GAM1076  FLJ20464  3'  ACATCCACAAAGAAAGAG    35676        __    C
                                TTCTTTTT  TGTGG TGT
                                |||||||  ||||| |||
                                GAGAAAG  ACACC ACA
                                   AA     T
GAM1076  FLJ20506  3'  GTTTTAAGCCACTAAAAA    35724      _     GT
                                TTTTT GTGGCT  GGAC
                                ||||| ||||||  ||||
                                AAAAA CACCGA  TTTG
                                  T     AT
GAM1076  FLJ21777  3'  GTGTTATGCCACAAACAGAA   50849     T       TGTG
                                TTCT TTTGTGGC    GACAC
                                |||| ||||||||    |||||
                                AAGA AAACACCG    TTGTG
                                  C       TA__
GAM1076  FLJ22233  3'  CCATCTGCCACAAACAGAA    46956     T       T_
                                TTCT TTTGTGGC  GTGG
                                |||| ||||||||  ||||
                                AAGA AAACACCG  TACC
                                  C       TC
GAM1076  HSPC133   3'  TACAAGTTTCACAAAAAGAA   27185          __  _
                                TTCTTTTTGTG  GCT GTG
                                ||||||||||  ||| |||
                                AAGAAAAACAC  TGA CAT
                                      TT   A
GAM1076  HSPC195   3'  GTCCCTAGCATAAAAAGAA    81867          G   T
                                TTCTTTTTGTG CTG GGAC
                                |||||||||| ||| ||||
                                AAGAAAAATAC GAT CCTG
                                      _   C
GAM1076  KIAA0552  3'  GTCCAACCACAAAAGAA     28996        T   CTG
                                TTCTTTT GTGG   TGGAC
                                ||||||| ||||   |||||
                                AAGAAAA CACC   ACCTG
                                   _   A__
GAM1076  KIAA1229  3'  CAATTGCCACAAAGAGAA    62752           TG_
                                TTCTTTTTGTGGC   TG
                                ||||||||||||   ||
                                AAGAGAAACACCG   AC
                                    TTA
GAM1076  KIAA1437  5'  GTCCATGGAGCAAAAGGAA   61216         GG
                                TTCTTTTTGT  CTGTGGAC
                                ||||||||||  ||||||||
                                AAGGAAAACG  GGTACCTG
                                   A_
GAM1076  KIAA1726  3'  GTGTTTAACCACAAAAA     67833         CTG
                                TTTTTGTGG   TGGACAC
                                |||||||||   |||||||
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                                AAAAACACC  ATTTGTG
                                     A__
GAM1076 LHFPL2   3' TCTACAACAAAAAGAA     70500        GGC
                                TTCTTTTTGT  TGTGGA
                                ||||||||||  ||||||
                                AAGAAAAACA  ACATCT
                                      ___
GAM1076 MGC10848 3' TCCACAGAGGGGAGAGAA   48307       GTGG
                                TTCTTTTT   CTGTGGA
                                ||||||||   |||||||
                                AAGAGAGG   GACACCT
                                     GGA_
GAM1076 NESHBP   3' TCCACAAATTCTTAAAAAGA  31860       T  C__
                                TCTTTTTG GG  TGTGGA
                                |||||||| ||  ||||||
                                AGAAAAAT CT  ACACCT
                                     T  TAA
GAM1076 PASK     3' TCCACAACAATCATAAAAA   31420       C___
                                TTTTTGTGG   TGTGGA
                                |||||||||   ||||||
                                AAAAATACT   ACACCT
                                     AACA
GAM1076 PDZD2    5' GTCCACAACCAAGAGGAA    81731       TG  C
                                TTCTTTT  TGG TGTGGAC
                                |||||||  ||| |||||||
                                AAGGAGA  ACC ACACCTG
                                   __  A
GAM1076 PP1628   5' TGTCCACATTAGAAAAA    48084      G  C
                                TTTTT TGG TGTGGACA
                                ||||| ||| ||||||||
                                AAAAA ATT ACACCTGT
                                  G  _
GAM1076 PPP1R1A  3' GTACCCAGTGAACACACAAAAA 23095       _____   T _
                                TTTTTGTG    GCTG GG AC
                                ||||||||    |||| || ||
                                AAAAACAC    TGAC CC TG
                                     ACAAG   _ A
GAM1076 PRO0245  5' CCCAGTCCAAAGAAGAA    26955       G  _  T
                                TTCTTTTT TGG CTG GG
                                |||||||| ||| ||| ||
                                AAGAAGAA ACC GAC CC
                                     _  T  _
GAM1076 SKD3     3' TGTTAGTCACAAAAA      48728         GTG
                                TTTTTGTGGCT  GACA
                                ||||||||||  ||||
                                AAAAACACTGA  TTGT
                                      ___
GAM1076 TUCAN    3' ACAGAACCACCAAAAAGAA   30958       _  __
                                TTCTTTTTG TGG  CTGT
                                ||||||||| |||  ||||
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                                AAGAAAAAC ACC  GACA
                                     C   AA
GAM1076  LOC115648 3'  TGTCTATCACAAAAA      60034        GCT
                                TTTTTGTG  GTGGACA
                                ||||||||  |||||||
                                AAAAACAC  TATCTGT
                                    ___
GAM1076  LOC137492 3'  GTGCCATCTCACAAAAGAA   75794       T   CT   A
                                TTCTTTT GTGG  GTGG CAC
                                ||||||| ||||  |||| |||
                                AAGAAAA CACT  TACC GTG
                                   _   C_   _
GAM1076  LOC145676 5'  CATAAGGAACCACAAGAAGAA 77844          C____
                                TTCTTTTTGTGG    TGTG
                                ||||||||||||    ||||
                                AAGAAGAACACC    ATAC
                                      AAGGA
GAM1076  LOC146723 3'  CTATTCAGCCACAAAAAGGA  78679           __
                                TTCTTTTTGTGGCTG  TGG
                                ||||||||||||||  |||
                                AGGAAAAACACCGAC  ATC
                                       TT
GAM1076  LOC149649 5'  TGTTCTCACCACAAAAA     85707        C  T
                                TTTTTGTGG TG GGACA
                                |||||||| || |||||
                                AAAAACACC AC CTTGT
                                   _ T
GAM1076  LOC158431 3'  GTACCCACCCAAAAGGAA    88167        T  C  T  _
                                TTCTTTTTG GG TG GG AC
                                |||||||| || || || ||
                                AAGGAAAAC CC AC CC TG
                                   _ _ _ A
GAM1076  LOC159982 5'  TCCATTTGCACAGAAAGAA   88435         GCT
                                TTCTTTTTGTG  GTGGA
                                ||||||||||  |||||
                                AAGAAAGACAC  TACCT
                                      GTT
GAM1076  LOC220705 3'  GTGTCCTGCTACAAAAAGA   92868         TGT
                                TCTTTTTGTGGC  GGACAC
                                ||||||||||||  ||||||
                                AGAAAAACATCG  CCTGTG
                                      T__
GAM1076  LOC256435 3'  TGTCCTGCCCCACCACAAAAGG 97167          CT__ _
           AA                    TTCTTTTTGTGG   GT GGACA
                                ||||||||||||   || |||||
                                AAGGAAAACACC   CG CCTGT
                                      ACCC  T
GAM1076  LOC57107  3'  TCCAATTACAGAAAGAA    40194         GCTG
                                TTCTTTTTGTG   TGGA
                                ||||||||||   ||||
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                                AAGAAAGACAT   ACCT
                                      TA__
GAM1076 LOC90843 3' GTGTCTCACACACAAAAAGAA 64878         GC   _
                                TTCTTTTTGTG  TGTG GACAC
                                ||||||||||  |||| |||||
                                AAGAAAAACAC  ACAC CTGTG
                                      __   T
GAM1077 ADAT1    3' AGGCAGGCAGATCACTTGAGGT 24910        __    CA  CA
           CAGG                  CCTGACCTC  GTGATC  CC  CCT
                                ||||||||  ||||||  ||  |||
                                GGACTGGAG  CACTAG  GG  GGA
                                     TT     AC  AC
GAM1077 ALDH8A1  3' AGGTGGGTGGATCACTTGAG  42911    __
                                CTC  GTGATCCACCCACCT
                                |||  ||||||||||||||
                                GAG  CACTAGGTGGGTGGA
                                  TT
GAM1077 ALPP     3' AGGTGGGCGGATCACGAGGTCA 69405           A
           GG                    CCTGACCTCGTGATCC CCCACCT
                                |||||||||||||| |||||||
                                GGACTGGAGCACTAGG GGGTGGA
                                       C
GAM1077 AP3S1    5' GGCGAGATTACGAGGCGAGG  8897     GA       CAC
                                CCT  CCTCGTGATC   CC
                                |||  ||||||||||   ||
                                GGA  GGAGCATTAG   GG
                                  GC        AGC
GAM1077 APOL1    3' AGGCGGGCGGATCACGAGGTCA 14727           A   A
           GG                    CCTGACCTCGTGATCC CCC CCT
                                |||||||||||||| ||| |||
                                GGACTGGAGCACTAGG GGG GGA
                                       C   C
GAM1077 ATM      3' AGGTGAGCGGATCACAAGGTCA 5286        C      ACC
           GG                    CCTGACCT GTGATCC   CACCT
                                |||||||| |||||||   |||||
                                GGACTGGA CACTAGG   GTGGA
                                    A      CGA
GAM1077 ATM      3' AGGTGAGCGGATCACAAGGTCA 57129       C      ACC
           GG                    CCTGACCT GTGATCC   CACCT
                                |||||||| |||||||   |||||
                                GGACTGGA CACTAGG   GTGGA
                                    A      CGA
GAM1077 ATP1A2   3' AGGCAGGTGGATCATGAGGTCA 7356             CA
           GG                    CCTGACCTCGTGATCCACC  CCT
                                |||||||||||||||||  |||
                                GGACTGGAGTACTAGGTGG  GGA
                                       AC
GAM1077 BCAS1    3' AGGCAGGTGGATCACCTGAGGT 14707        __       CA
           CAGG                  CCTGACCTC  GTGATCCACC  CCT
                                |||||||||  ||||||||||  |||
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                                GGACTGGAG CACTAGGTGG GGA
                                   TC       AC
GAM1077 BHMT2   3' AGGCGGGCGGATCACCTGAGGT 34728      __    A  A
          CAG                CTGACCTC GTGATCC CCC CCT
                             |||||||| ||||||| ||| |||
                             GACTGGAG CACTAGG GGG GGA
                                TC     C  C
GAM1077 BRCA1   3' AGGTGGGCAGATCACTGGAGGT 24444      __    CA
          CAGG               CCTGACCTC GTGATC CCCACCT
                             ||||||||| |||||| |||||||
                             GGACTGGAG CACTAG GGGTGGA
                                GT     AC
GAM1077 BRCA1   3' AGGTGGGCAGATCACTGGAGGT 24454      __    CA
          CAGG               CCTGACCTC GTGATC CCCACCT
                             ||||||||| |||||| |||||||
                             GGACTGGAG CACTAG GGGTGGA
                                GT     AC
GAM1077 BRCA1   3' AGGTGGGCAGATCACTGGAGGT 24467      __    CA
          CAGG               CCTGACCTC GTGATC CCCACCT
                             ||||||||| |||||| |||||||
                             GGACTGGAG CACTAG GGGTGGA
                                GT     AC
GAM1077 BRCA1   3' AGGTGGGCAGATCACTGGAGGT 24476      __    CA
          CAGG               CCTGACCTC GTGATC CCCACCT
                             ||||||||| |||||| |||||||
                             GGACTGGAG CACTAG GGGTGGA
                                GT     AC
GAM1077 BRCA1   3' AGGTGGGCAGATCACTGGAGGT 24484      __    CA
          CAGG               CCTGACCTC GTGATC CCCACCT
                             ||||||||| |||||| |||||||
                             GGACTGGAG CACTAG GGGTGGA
                                GT     AC
GAM1077 BRCA1   3' AGGTGGGCAGATCACTGGAGGT 24492      __    CA
          CAGG               CCTGACCTC GTGATC CCCACCT
                             ||||||||| |||||| |||||||
                             GGACTGGAG CACTAG GGGTGGA
                                GT     AC
GAM1077 BRCA1   3' AGGTGGGCAGATCACTGGAGGT 24501      __    CA
          CAGG               CCTGACCTC GTGATC CCCACCT
                             ||||||||| |||||| |||||||
                             GGACTGGAG CACTAG GGGTGGA
                                GT     AC
GAM1077 BRCA1   3' AGGTGGGCAGATCACTGGAGGT 24511      __    CA
          CAGG               CCTGACCTC GTGATC CCCACCT
                             ||||||||| |||||| |||||||
                             GGACTGGAG CACTAG GGGTGGA
                                GT     AC
GAM1077 BRCA1   3' AGGTGGGCAGATCACTGGAGGT 24519      __    CA
          CAGG               CCTGACCTC GTGATC CCCACCT
                             ||||||||| |||||| |||||||
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                                GGACTGGAG  CACTAG  GGGTGGA
                                    GT     AC
GAM1077 BRCA1    3' AGGTGGGCAGATCACTGGAGGT 24527        __     CA
           CAGG                  CCTGACCTC  GTGATC  CCCACCT
                                 |||||||||  ||||||  |||||||
                                 GGACTGGAG  CACTAG  GGGTGGA
                                    GT     AC
GAM1077 BRCA1    3' AGGTGGGCAGATCACTGGAGGT 24540        __     CA
           CAGG                  CCTGACCTC  GTGATC  CCCACCT
                                 |||||||||  ||||||  |||||||
                                 GGACTGGAG  CACTAG  GGGTGGA
                                    GT     AC
GAM1077 C21orf5  3' AGGCAGGCAGATCACTTGAGGT 18882        __     CA  CA
           CAGG                  CCTGACCTC  GTGATC  CC  CCT
                                 |||||||||  ||||||  ||  |||
                                 GGACTGGAG  CACTAG  GG  GGA
                                    TT     AC  AC
GAM1077 C5R1     3' AGGTGGGTGGATCACCTGAGGT 9972         __
           CA                     TGACCTC  GTGATCCACCCACCT
                                  |||||||  ||||||||||||||||
                                  ACTGGAG  CACTAGGTGGGTGGA
                                     TC
GAM1077 CARKL    3' GTGGGTGAATCACCTGAGGTCA 26107        __     C
           GG                     CCTGACCTC  GTGAT CACCCAC
                                  |||||||||  |||||  |||||||
                                  GGACTGGAG  CACTA GTGGGTG
                                     TC     A
GAM1077 CASP10   3' AGGCAGGCAGATCACTTGAGGT 53216        __     CA  CA
           CAGG                  CCTGACCTC  GTGATC  CC  CCT
                                 |||||||||  ||||||  ||  |||
                                 GGACTGGAG  CACTAG  GG  GGA
                                    TT     AC  AC
GAM1077 CASP10   3' AGGCAGGCAGATCACTTGAGGT 53243        __     CA  CA
           CAGG                  CCTGACCTC  GTGATC  CC  CCT
                                 |||||||||  ||||||  ||  |||
                                 GGACTGGAG  CACTAG  GG  GGA
                                    TT     AC  AC
GAM1077 CASP6    3' AGGTGGGCGGATCACCTGAGGT 53361        __      A
           CGGG                  CCTGACCTC  GTGATCC CCCACCT
                                 |||||||||  |||||||  |||||||
                                 GGGCTGGAG  CACTAGG GGGTGGA
                                    TC      C
GAM1077 CASP6    3' AGGTGGGCGGATCACCTGAGGT 8729         __      A
           CGGG                  CCTGACCTC  GTGATCC CCCACCT
                                 |||||||||  |||||||  |||||||
                                 GGGCTGGAG  CACTAGG GGGTGGA
                                    TC      C
GAM1077 CD68     3' AGGCAGGTGGATCACTGGAGGT 60500        __       CA
           CAGG                  CCTGACCTC  GTGATCCACC  CCT
                                 |||||||||  ||||||||||  |||
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                                GGACTGGAG  CACTAGGTGG  GGA
                                    GT         AC
GAM1077  CHST5    3'  AGGCGGGTGGATCACCTGAGGT 25085          __         A
            CAGG                    CCTGACCTC  GTGATCCACCC CCT
                                    |||||||||  |||||||||||  |||
                                    GGACTGGAG  CACTAGGTGGG GGA
                                       TC          C
GAM1077  CORO2A   3'  AGGCTGGTGGATCACGAGGTCA 14099               CA
            G                     CTGACCTCGTGATCCACC  CCT
                                  ||||||||||||||||||  |||
                                  GACTGGAGCACTAGGTGG  GGA
                                        TC
GAM1077  CORO2A   3'  AGGTGGGCGGATTGCTTGAGGT 14100          __ TG    A
            CGGG                    CCTGACCTC  G  ATCC CCCACCT
                                    |||||||||  |  |||| |||||||
                                    GGGCTGGAG  C  TAGG GGGTGGA
                                       TT GT    C
GAM1077  CORO2A   3'  AGGCTGGTGGATCACGAGGTCA 54491               CA
            G                     CTGACCTCGTGATCCACC  CCT
                                  ||||||||||||||||||  |||
                                  GACTGGAGCACTAGGTGG  GGA
                                        TC
GAM1077  CORO2A   3'  AGGTGGGCGGATTGCTTGAGGT 54492          __ TG    A
            CGGG                    CCTGACCTC  G  ATCC CCCACCT
                                    |||||||||  |  |||| |||||||
                                    GGGCTGGAG  C  TAGG GGGTGGA
                                       TT GT    C
GAM1077  COX11    5'  AGGCGGGTGGGTGTTAGTTCAG 16485      C  CG G       A
                                    CTGA CT  T ATCCACCC CCT
                                    ||||  ||  |  |||||||| |||
                                    GACT GA  G TGGGTGGG GGA
                                      T  TT _       C
GAM1077  CPM      3'  AGGTGGGCGGATCACCCTGAGG 60402          ___       A
            TTAGG                   CCTGACCTC   GTGATCC CCCACCT
                                    |||||||||   |||||||  |||||||
                                    GGATTGGAG   CACTAGG GGGTGGA
                                       TCC       C
GAM1077  CPT2     3'  AGGCGGGTGGATCACTTGAGGT 5420           __         A
            CAGG                    CCTGACCTC  GTGATCCACCC CCT
                                    |||||||||  |||||||||||  |||
                                    GGACTGGAG  CACTAGGTGGG GGA
                                       TT          C
GAM1077  CRACC    3'  AGGTGGGTGGGTCATCTGAGGT 41306          __
            CAGG                    CCTGACCTC  GTGATCCACCCACCT
                                    |||||||||  ||||||||||||||||
                                    GGACTGGAG  TACTGGGTGGGTGGA
                                       TC
GAM1077  CYP4F3   3'  AGGTGGGCAGATCATGAGGTCA 7992              CA
            GG                      CCTGACCTCGTGATC  CCCACCT
                                    ||||||||||||||  |||||||
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                                GGACTGGAGTACTAG  GGGTGGA
                                      AC
GAM1077  DDOST    3'  AGGCAGGCGGCTCACGAGGTCA 19059          T  A  CA
                GG                  CCTGACCTCGTGA CC CC  CCT
                                    ||||||||||||| || ||  |||
                                    GGACTGGAGCACT GG GG  GGA
                                          C  C  AC
GAM1077  DMC1     3'  AGGCAGGTGGATCACTTGAGGT 23938        __       CA
                CAGG                  CCTGACCTC  GTGATCCACC  CCT
                                    |||||||||  ||||||||||  |||
                                    GGACTGGAG  CACTAGGTGG  GGA
                                       TT         AC
GAM1077  DNASE2   3'  AGATGGGCAGATCACTTGAGGT 9097         __     CA    C
                CAGG                  CCTGACCTC  GTGATC  CCCA CT
                                    |||||||||  ||||||  |||| ||
                                    GGACTGGAG  CACTAG  GGGT GA
                                       TT     AC    A
GAM1077  DVL3     3'  GGTGGATCACTTGAGGTCGGG  16650        __
                                    CCTGACCTC  GTGATCCACC
                                    |||||||||  ||||||||||
                                    GGGCTGGAG  CACTAGGTGG
                                       TT
GAM1077  EGFL5    3'  AGGCGGGTGGATCACAAGGTCA 87905        C         A
                GG                  CCTGACCT GTGATCCACCC CCT
                                    |||||||| ||||||||||| |||
                                    GGACTGGA CACTAGGTGGG GGA
                                       A          C
GAM1077  F2R      3'  AGGCGGGTGGATCACGAGGTCA 10562              A
                GG                  CCTGACCTCGTGATCCACCC CCT
                                    |||||||||||||||||||| |||
                                    GGACTGGAGCACTAGGTGGG GGA
                                                C
GAM1077  F2RL3    3'  AGGCGGATGGATCACTTGAG   15495    __      C  A
                                    CTC  GTGATCCA CC CCT
                                    |||  |||||||| || |||
                                    GAG  CACTAGGT GG GGA
                                      TT       A  C
GAM1077  FANCD2   3'  GTGGGCAGATCACAAGGTCAGG 53532        C     CA
                                    CCTGACCT GTGATC  CCCAC
                                    |||||||| ||||||  |||||
                                    GGACTGGA CACTAG  GGGTG
                                       A     AC
GAM1077  FCMD     3'  AGGCAGGTGGATCACTTGAGG  23025     __       CA
                                    CCTC  GTGATCCACC  CCT
                                    ||||  ||||||||||  |||
                                    GGAG  CACTAGGTGG  GGA
                                      TT         AC
GAM1077  FGFR2    3'  AGGCAGGCGGATCATGAGGTCA 43649             A  CA
                GG                  CCTGACCTCGTGATCC CC  CCT
                                    |||||||||||||||| ||  |||
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                                GGACTGGAGTACTAGG GG  GGA
                                      C  AC
GAM1077  FGFR2    3'  AGGCAGGCGGATCATGAGGTCA 43662            A  CA
              GG                  CCTGACCTCGTGATCC CC  CCT
                                  |||||||||||||||| ||  |||
                                  GGACTGGAGTACTAGG GG  GGA
                                      C  AC
GAM1077  FUT1     3'  GGCAGGAGCACGAGGTCTGG   5601     T       A   AC
                                  CC GACCTCGTG TCC  CC
                                  || |||||||| |||  ||
                                  GG CTGGAGCAC AGG  GG
                                   T        G   AC
GAM1077  FUT6     3'  AGGCAGGCGGATCACAAGGTCA 5628         C      A  CA
              GG                  CCTGACCT GTGATCC CC  CCT
                                  |||||||| ||||||| ||  |||
                                  GGACTGGA CACTAGG GG  GGA
                                      A      C  AC
GAM1077  GAS7     3'  AGGTGGGCAGATCACGAGGTCA 20839            CA
              GG                  CCTGACCTCGTGATC  CCCACCT
                                  ||||||||||||||  |||||||
                                  GGACTGGAGCACTAG  GGGTGGA
                                        AC
GAM1077  GNE      3'  AGGCGGGCGGATCACGAGGTCA 19661             A   A
              GG                  CCTGACCTCGTGATCC CCC CCT
                                  |||||||||||||||| ||| |||
                                  GGACTGGAGCACTAGG GGG GGA
                                        C   C
GAM1077  GP2      3'  AGGCAGGTGGATCACCTGAGGT 9479          __       CA
              CAG                  CTGACCTC  GTGATCCACC  CCT
                                  ||||||||  ||||||||||  |||
                                  GACTGGAG  CACTAGGTGG  GGA
                                      TC         AC
GAM1077  GPR81    3'  GGCGGATCACCTGAGGTCAGG  51752         __      A
                                  CCTGACCTC  GTGATCC CC
                                  |||||||||  |||||||  ||
                                  GGACTGGAG  CACTAGG GG
                                      TC       C
GAM1077  GPRK7    3'  AGGCAGATGGATCATGAGGTCA 58309             CCCA
              GG                  CCTGACCTCGTGATCCA    CCT
                                  ||||||||||||||||    |||
                                  GGACTGGAGTACTAGGT    GGA
                                        AGAC
GAM1077  GRAF     3'  AGGCGGGCGGATCACGAGGTCA 31221             A   A
              GG                  CCTGACCTCGTGATCC CCC CCT
                                  |||||||||||||||| ||| |||
                                  GGACTGGAGCACTAGG GGG GGA
                                        C   C
GAM1077  GRM6     3'  AGGCAGGTGGATCACCTGAGGT 7758         __       CA
                                  ACCTC  GTGATCCACC  CCT
                                  |||||  ||||||||||  |||
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                                TGGAG  CACTAGGTGG  GGA
                                   TC         AC
GAM1077  HCR     3'  GTGGGTGGGGACAGACCAG   92645     AC  C  GA
                                CTG  CT GT  TCCACCCAC
                                |||  || ||  |||||||||
                                GAC  GA CA  GGGTGGGTG
                                  CA  _  G_
GAM1077  HCS     3'  AGGCAGGCAGATCACTTGAGGT 38966          __     CA  CA
            CGGG                  CCTGACCTC  GTGATC  CC  CCT
                                |||||||||  ||||||  ||  |||
                                GGGCTGGAG  CACTAG  GG  GGA
                                     TT      AC  AC
GAM1077  HLA-E   3'  AGGAGGGCAGATCACGAGGTCA 92669             CA   A
            GG                    CCTGACCTCGTGATC  CCC CCT
                                ||||||||||||||  ||| |||
                                GGACTGGAGCACTAG  GGG GGA
                                        AC   A
GAM1077  HSPA5   3'  AGGCGGGTGGATCACAAGGTCA 19277       C         A
                                TGACCT GTGATCCACCC CCT
                                ||||||  |||||||||| |||
                                ACTGGA CACTAGGTGGG GGA
                                   A          C
GAM1077  IAPP    3'  AGGCAGGCAGATCACAAGGTCA 6437         C     CA  CA
            GG                    CCTGACCT GTGATC  CC  CCT
                                |||||||| ||||||  ||  |||
                                GGACTGGA CACTAG  GG  GGA
                                     A     AC  AC
GAM1077  IFIT4   3'  AGGTGGGCGGATCACGAGGTCT 71489    T          A
            GG                    CC GACCTCGTGATCC CCCACCT
                                ||  ||||||||||||| |||||||
                                GG CTGGAGCACTAGG GGGTGGA
                                 T           C
GAM1077  IFNAR1  3'  AGGCAGGCAGATCATGAGGTCA 7135             CA  CA
                                TGACCTCGTGATC  CC  CCT
                                ||||||||||||  ||  |||
                                ACTGGAGTACTAG  GG  GGA
                                        AC  AC
GAM1077  IL10    3'  AGGCGGGTGGATCACTTGAGGT 6922          __        A
            CAGG                  CCTGACCTC  GTGATCCACCC CCT
                                |||||||||  |||||||||| |||
                                GGACTGGAG  CACTAGGTGGG GGA
                                     TT          C
GAM1077  IL13RA1 3'  AGGCGGGCGGATCACTCGAGGT 9566          __      A  A
            CAGG                  CCTGACCTC  GTGATCC CCC CCT
                                |||||||||  |||||| ||| |||
                                GGACTGGAG  CACTAGG GGG GGA
                                     CT      C   C
GAM1077  IL17R   3'  AGGCAGGTGGATCACTCTGAGG 27549          ___       CA
            TCAGG                 CCTGACCTC   GTGATCCACC  CCT
                                |||||||||   ||||||||||  |||
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                                GGACTGGAG  CACTAGGTGG  GGA
                                    TCT        AC
GAM1077  IL18    3'  AGGCGGGCAGATCACCAGAGGT 9587          __    CA  A
            CAGG                  CCTGACCTC  GTGATC  CCC CCT
                                  |||||||||  ||||||  ||| |||
                                  GGACTGGAG  CACTAG  GGG GGA
                                    AC     AC   C
GAM1077  IL1R1   3'  GTGGGTGGATCACCAGAGGTCA 7924          __
            GG                    CCTGACCTC  GTGATCCACCCAC
                                  |||||||||  ||||||||||||
                                  GGACTGGAG  CACTAGGTGGGTG
                                    AC
GAM1077  IRAK4   3'  AGGCAGGCAGATCACCTGAGGT 61839        __    CA  CA
            CA                    TGACCTC  GTGATC  CC  CCT
                                  |||||||  ||||||  ||  |||
                                  ACTGGAG  CACTAG  GG  GGA
                                    TC     AC  AC
GAM1077  KAI1    3'  AGGCGGGTGGATCACGAGGTCA 11118              A
            GG                    CCTGACCTCGTGATCCACCC CCT
                                  |||||||||||||||||| |||
                                  GGACTGGAGCACTAGGTGGG GGA
                                            C
GAM1077  KCNA7   3'  AGGTGGGCAAATTACGAGGTCA 49888           CCA
            GG                    CCTGACCTCGTGAT   CCCACCT
                                  ||||||||||||   |||||||
                                  GGACTGGAGCATTA   GGGTGGA
                                      AAC
GAM1077  KCNJ15  5'  AGGTGGGTGAAGGGGAGCGAGG 11159       GA  ___
                                  CCTCGT  TCC   ACCCACCT
                                  ||||||  |||   ||||||||
                                  GGAGCG  GGG   TGGGTGGA
                                     AG   AAG
GAM1077  KCNJ5   3'  AGGCGGGTGGATCATGAGGTCA 7966              A
            GG                    CCTGACCTCGTGATCCACCC CCT
                                  |||||||||||||||||| |||
                                  GGACTGGAGTACTAGGTGGG GGA
                                            C
GAM1077  KIF1B   3'  AGGCGGGCAGATCACGAGATCA 31262      C     CA  A
            GG                    CCTGA CTCGTGATC  CCC CCT
                                  |||||  |||||||||  ||| |||
                                  GGACT GAGCACTAG  GGG GGA
                                     A       AC   C
GAM1077  KIF3B   3'  AGGTGGGTGGACCACCTGAGGT 17801        __  A
            TAGG                   CCTGACCTC  GTG TCCACCCACCT
                                  |||||||||  ||| ||||||||||
                                  GGATTGGAG  CAC AGGTGGGTGGA
                                     TC   C
GAM1077  LAMC2   3'  GGGTGGATCACCCGAGGTCAGG 38768         __
                                  CCTGACCTC  GTGATCCACCC
                                  |||||||||  ||||||||||
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                                GGACTGGAG  CACTAGGTGGG
                                     CC
GAM1077  LAMP2    3'  GTGGGTGGATCACTTGAGG   26577     __
                                CCTC  GTGATCCACCCAC
                                ||||  ||||||||||||
                                GGAG  CACTAGGTGGGTG
                                  TT
GAM1077  LDLR     3'  AGGCGGGTGGATCATGAGGTCA 6724              A
              GG                  CCTGACCTCGTGATCCACCC CCT
                                ||||||||||||||||||| |||
                                GGACTGGAGTACTAGGTGGG GGA
                                           C
GAM1077  LILRB1   3'  AGGCGGGCAGATCACGAGTTCA 22869     C      CA  A
              GG                  CCTGA CTCGTGATC  CCC CCT
                                ||||| |||||||||  ||| |||
                                GGACT GAGCACTAG  GGG GGA
                                   T       AC  C
GAM1077  LRRC2    3'  AGATGGGTGAATCATGAGGTCA 44735          C    C
              GG                  CCTGACCTCGTGAT CACCCA CT
                                ||||||||||||| |||||| ||
                                GGACTGGAGTACTA GTGGGT GA
                                        A     A
GAM1077  LRRC2    3'  GTGGGTGGATCACCTGAGGT   44758     __
                                ACCTC  GTGATCCACCCAC
                                |||||  ||||||||||||
                                TGGAG  CACTAGGTGGGTG
                                  TC
GAM1077  LUZP1    3'  AGGCAGGCGGATCACAAGGTCA 54396       C     A  CA
              GG                  CCTGACCT GTGATCC CC  CCT
                                ||||||||  |||||||  ||  |||
                                GGACTGGA CACTAGG GG  GGA
                                     A      C  AC
GAM1077  MCM4     3'  GGTGGATCATGAGGTCAGG   62582
                                CCTGACCTCGTGATCCACC
                                |||||||||||||||||||
                                GGACTGGAGTACTAGGTGG


GAM1077  MLLT4    3'  AGGCGGGCAGATCACGAGGTCA 72897           CA  A
              GG                  CCTGACCTCGTGATC  CCC CCT
                                ||||||||||||||  ||| |||
                                GGACTGGAGCACTAG  GGG GGA
                                        AC  C
GAM1077  MOG      3'  AGGCGGGCGAATCACGAGGTCA 11666          CCA  A
              GG                  CCTGACCTCGTGAT   CCC CCT
                                ||||||||||||||   ||| |||
                                GGACTGGAGCACTA   GGG GGA
                                        AGC  C
GAM1077  MS4A1    3'  AGGTGGGCAGATCACGAAGTCA 5544       C      CA
              G                   CTGAC TCGTGATC  CCCACCT
                                ||||| ||||||||  |||||||
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                                GACTG AGCACTAG  GGGTGGA
                                  A       AC
GAM1077  MSH3     3'  AGGTAGGCAGATCACCTGAGGT 11687          __     CA  C
              CAGG                  CCTGACCTC  GTGATC  CC ACCT
                                    |||||||||  ||||||  || ||||
                                    GGACTGGAG  CACTAG  GG TGGA
                                      TC      AC  A
GAM1077  MTMR8    3'  AGGCGGGCGGATCATGAGGTCA 31902              A   A
              GG                    CCTGACCTCGTGATCC CCC CCT
                                    |||||||||||||||| ||| |||
                                    GGACTGGAGTACTAGG GGG GGA
                                          C   C
GAM1077  MYO1B    3'  AGGCAGGTGGATCACCTCAGGT 25239         C__         CA
              CAGG                  CCTGACCT   GTGATCCACC  CCT
                                    ||||||||   ||||||||||  |||
                                    GGACTGGA   CACTAGGTGG  GGA
                                       CTC         AC
GAM1077  MYO1C    3'  GGGCAGATAACCTGAGGTCAGG 61869          TG__   CA
                                    CCTGACCTCG    ATC  CCC
                                    ||||||||||    |||  |||
                                    GGACTGGAGT    TAG  GGG
                                       CCAA   AC
GAM1077  NFKBIL2  3'  AGGCGGGCGGATCACGAGGTCA 26442              A   A
              GG                    CCTGACCTCGTGATCC CCC CCT
                                    |||||||||||||||| ||| |||
                                    GGACTGGAGCACTAGG GGG GGA
                                          C   C
GAM1077  NPHP1    3'  AGGTGGGTGGATCACCTGAGGT 63139          __
              CAGG                  CCTGACCTC  GTGATCCACCCACCT
                                    |||||||||  ||||||||||||||
                                    GGACTGGAG  CACTAGGTGGGTGGA
                                       TC
GAM1077  NPHS1    3'  AGGCGGGTGGATCACCTGAGGT 17365          __         A
              CAGG                  CCTGACCTC  GTGATCCACCC CCT
                                    |||||||||  |||||||||| |||
                                    GGACTGGAG  CACTAGGTGGG GGA
                                       TC          C
GAM1077  NT5C2    3'  GGCGGATCACCTGAGGTCGGG  25265          __     A
                                    CCTGACCTC  GTGATCC CC
                                    |||||||||  |||||| ||
                                    GGGCTGGAG  CACTAGG GG
                                       TC      C
GAM1077  NUP62    3'  AGGCGGGCAGATGACTTGAGGT 33780          __ G   CA   A
              CAGG                  CCTGACCTC  GT ATC  CCC CCT
                                    |||||||||  || |||  ||| |||
                                    GGACTGGAG  CA TAG  GGG GGA
                                       TT  G   AC   C
GAM1077  OPA3     3'  AGGCGGGCGGATCACTTGAGGT 47839          __     A   A
              CAGG                  CCTGACCTC  GTGATCC CCC CCT
                                    |||||||||  ||||||| ||| |||
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                                GGACTGGAG  CACTAGG GGG GGA
                                    TT      C   C
GAM1077  OPTN     3'  AGGTGGGTGGATCACTTGGGGT 42048          __
              CAGG                  CCTGACCTC  GTGATCCACCCACCT
                                    |||||||||  ||||||||||||||||
                                    GGACTGGGG  CACTAGGTGGGTGGA
                                        TT
GAM1077  P2RX7    3'  AGGCAGGCAGATCACCTGAGGT 11925          __     CA  CA
              CGGG                  CCTGACCTC  GTGATC  CC  CCT
                                    |||||||||  ||||||  ||  |||
                                    GGGCTGGAG  CACTAG  GG  GGA
                                        TC      AC  AC
GAM1077  PA2G4    3'  AGGCGGGTGGATCACCTGAGGT 71822          __         A
              CA                      TGACCTC  GTGATCCACCC CCT
                                    |||||||  |||||||||||| |||
                                    ACTGGAG  CACTAGGTGGG GGA
                                        TC          C
GAM1077  PCDH11X  3'  AGGCGGGTGGATCACGAGGTCA 53124                 A
              GG                    CCTGACCTCGTGATCCACCC CCT
                                    |||||||||||||||||||| |||
                                    GGACTGGAGCACTAGGTGGG GGA
                                                C
GAM1077  PCDH11X  3'  AGGTGGGTGGATCACCTGAGGT 53125          __
              CAGG                  CCTGACCTC  GTGATCCACCCACCT
                                    |||||||||  ||||||||||||||||
                                    GGACTGGAG  CACTAGGTGGGTGGA
                                        TC
GAM1077  PCDH11Y  3'  AGGCGGGTGGATCACCTGAGGT 53152          __         A
              CAGG                  CCTGACCTC  GTGATCCACCC CCT
                                    |||||||||  ||||||||||| |||
                                    GGACTGGAG  CACTAGGTGGG GGA
                                        TC          C
GAM1077  PCDH11Y  3'  AGGCGGGTGGATCACGAGGTCA 53153                 A
              GG                    CCTGACCTCGTGATCCACCC CCT
                                    |||||||||||||||||||| |||
                                    GGACTGGAGCACTAGGTGGG GGA
                                                C
GAM1077  PCDH11Y  3'  AGGCGGGTGGATCACCTGAGGT 53175          __         A
              CAGG                  CCTGACCTC  GTGATCCACCC CCT
                                    |||||||||  ||||||||||| |||
                                    GGACTGGAG  CACTAGGTGGG GGA
                                        TC          C
GAM1077  PCDH11Y  3'  AGGCGGGTGGATCACGAGGTCA 53176                 A
              GG                    CCTGACCTCGTGATCCACCC CCT
                                    |||||||||||||||||||| |||
                                    GGACTGGAGCACTAGGTGGG GGA
                                                C
GAM1077  PCDHB9   3'  AGGCGGGCAGATCACCTTAGGT 39437        C__     CA  A
              CA                    TGACCT   GTGATC  CCC CCT
                                    ||||||   ||||||  ||| |||
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                                ACTGGA  CACTAG  GGG GGA
                                   TTC     AC  C
GAM1077  PDE4C    3'  AGGCAGGTGGATCACCTGAGGT 8095          __       CA
            TAGG                   CCTGACCTC  GTGATCCACC  CCT
                                   |||||||||  ||||||||||  |||
                                   GGATTGGAG  CACTAGGTGG  GGA
                                      TC         AC
GAM1077  PHKB     3'  AGGCAGGTGGATCACTTGAGGT 6095          __       CA
            TAGG                   CCTGACCTC  GTGATCCACC  CCT
                                   |||||||||  ||||||||||  |||
                                   GGATTGGAG  CACTAGGTGG  GGA
                                      TT         AC
GAM1077  PIK3R2   3'  GGGCGGATCTTTTGAGGTCGGG 18517         T__    A
                                   CCTGACCTCG   GATCC CCC
                                   ||||||||||   ||||| |||
                                   GGGCTGGAGT   CTAGG GGG
                                      TTT    C
GAM1077  PLA2G2D  3'  AGGCAGGCAGATCACCTGGGGT 25706         __     CA  CA
            CAGG                   CCTGACCTC  GTGATC  CC  CCT
                                   |||||||||  ||||||  ||  |||
                                   GGACTGGGG  CACTAG  GG  GGA
                                      TC     AC  AC
GAM1077  POLH     3'  AGGCAGACAGATCACCTGAGGT 22469         __     CACCCA
            CAGG                   CCTGACCTC  GTGATC     CCT
                                   |||||||||  ||||||     |||
                                   GGACTGGAG  CACTAG     GGA
                                      TC     ACAGAC
GAM1077  POLH     3'  AGGCGGGCAGATCACGAGGTCA 22471           CA  A
            GG                     CCTGACCTCGTGATC  CCC CCT
                                   ||||||||||||||  ||| |||
                                   GGACTGGAGCACTAG  GGG GGA
                                         AC  C
GAM1077  PPP1R12B 3'  AGGTGGACAGATCACGAGGTCA 50377           CAC
            GG                     CCTGACCTCGTGATC  CCACCT
                                   ||||||||||||||  ||||||
                                   GGACTGGAGCACTAG  GGTGGA
                                         ACA
GAM1077  PRKY     3'  AGGCAGGCAGATCACCTGAGGT 12361         __     CA  CA
            CAGG                   CCTGACCTC  GTGATC  CC  CCT
                                   |||||||||  ||||||  ||  |||
                                   GGACTGGAG  CACTAG  GG  GGA
                                      TC     AC  AC
GAM1077  PSMB2    3'  AGGCGGGCGGATCACGAGGTCA 12460           A  A
                                   TGACCTCGTGATCC CCC CCT
                                   |||||||||||||| ||| |||
                                   ACTGGAGCACTAGG GGG GGA
                                         C  C
GAM1077  PSMB9    3'  AGGCAGGCGGATCACCTGAGGT 12485         __     A  CA
            CAGG                   CCTGACCTC  GTGATCC CC  CCT
                                   |||||||||  |||||||  ||  |||
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                                GGACTGGAG  CACTAGG GG  GGA
                                     TC      C  AC
GAM1077  PSMB9    3'  AGGTGGGCAGATCTTTTAAGGT 12487        CGT__    CA
             CAGG                   CCTGACCT    GATC  CCCACCT
                                ||||||||    ||||  |||||||
                                GGACTGGA    CTAG  GGGTGGA
                                     ATTTT    AC
GAM1077  PTAFR    3'  AGGTGGGCAGATCATGGGTCA  8162       T      CA
                                TGACC CGTGATC  CCCACCT
                                |||||  |||||||  |||||||
                                ACTGG GTACTAG  GGGTGGA
                                   _      AC
GAM1077  PTGIS    3'  AGGTGGGCGGATCACTTGAGGT 8192          __      A
             CGGG                   CCTGACCTC  GTGATCC CCCACCT
                                |||||||||  |||||||  |||||||
                                GGGCTGGAG  CACTAGG GGGTGGA
                                     TT      C
GAM1077  PTPRF    3'  AGGTGAATAGCACAGGTTAGG  12605        C   ATCCACC
                                CCTGACCT GTG      CACCT
                                ||||||||  |||      |||||
                                GGATTGGA CAC      GTGGA
                                     _   GATAA__
GAM1077  PTPRF    3'  AGGTGAATAGCACAGGTTAGG  56134        C   ATCCACC
                                CCTGACCT GTG      CACCT
                                ||||||||  |||      |||||
                                GGATTGGA CAC      GTGGA
                                     _   GATAA__
GAM1077  RAB3B    3'  AGGCGGGTGGATCATGAGGTCA 12700                A
             GG                     CCTGACCTCGTGATCCACCC CCT
                                ||||||||||||||||||  |||
                                GGACTGGAGTACTAGGTGGG GGA
                                           C
GAM1077  RAB7L1   3'  AGGCAGGTGGATCGCCTGAGGT 15399          __        CA
             CAGG                   CCTGACCTC  GTGATCCACC  CCT
                                |||||||||  ||||||||||  |||
                                GGACTGGAG  CGCTAGGTGG  GGA
                                     TC         AC
GAM1077  RAD1     3'  AGGTGGGCGGATCACCTGAGGT 12638          __      A
             CAGG                   CCTGACCTC  GTGATCC CCCACCT
                                |||||||||  |||||||  |||||||
                                GGACTGGAG  CACTAGG GGGTGGA
                                     TC      C
GAM1077  RAD1     3'  AGGTGGGCGGATCACCTGAGGT 56652          __      A
             CAGG                   CCTGACCTC  GTGATCC CCCACCT
                                |||||||||  |||||||  |||||||
                                GGACTGGAG  CACTAGG GGGTGGA
                                     TC      C
GAM1077  RAD1     3'  AGGTGGGCGGATCACCTGAGGT 56748          __      A
             CAGG                   CCTGACCTC  GTGATCC CCCACCT
                                |||||||||  |||||||  |||||||
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                                GGACTGGAG  CACTAGG GGGTGGA
                                     TC      C
GAM1077  RAD51L1   5'  GGGCGGATCACGAGGTCAGG   56879             A
                                CCTGACCTCGTGATCC CCC
                                |||||||||||||||| |||
                                GGACTGGAGCACTAGG GGG
                                        C
GAM1077  RBBP5     3'  AGGCGGGTGGATCACCCGAGGT 18575          __         A
           CAGG                   CCTGACCTC  GTGATCCACCC CCT
                                |||||||||  |||||||||||| |||
                                GGACTGGAG  CACTAGGTGGG GGA
                                     CC         C
GAM1077  RFC2      3'  AGGCAGGTGGATCACCTGAGGT 12836          __        CA
           CAG                    CTGACCTC  GTGATCCACC  CCT
                                |||||||||  ||||||||||  |||
                                GACTGGAG  CACTAGGTGG  GGA
                                     TC         AC
GAM1077  SIGLEC11  3'  GTGGGTGGATCACAAGTCAGG  54655       CTC
                                CCTGAC   GTGATCCACCCAC
                                ||||||   ||||||||||||||
                                GGACTG   CACTAGGTGGGTG
                                   AA_
GAM1077  SIM2      3'  AGGTGGGCGGATCACCTGAGGT 24797          __      A
           CAGG                   CCTGACCTC  GTGATCC CCCACCT
                                |||||||||  |||||||  |||||||
                                GGACTGGAG  CACTAGG GGGTGGA
                                     TC      C
GAM1077  SLC14A2   3'  AGGCGGGTGGATCACGAGGTCA 24109               A
           GG                     CCTGACCTCGTGATCCACCC CCT
                                |||||||||||||||||||| |||
                                GGACTGGAGCACTAGGTGGG GGA
                                        C
GAM1077  SLC17A5   3'  AGGTGGGCGAATCATGAGATCA 25827       C       CCA
           GG                     CCTGA CTCGTGAT   CCCACCT
                                |||||  ||||||||   |||||||
                                GGACT GAGTACTA   GGGTGGA
                                   A       AGC
GAM1077  SLC26A2   3'  AGGCTTCTGGATCACAAAGTCA 5473       CTC       CCCA
                                TGAC   GTGATCCA    CCT
                                ||||   ||||||||    |||
                                ACTG   CACTAGGT    GGA
                                   AAA       CTTC
GAM1077  SLC26A4   3'  AGGCGGGTGGATCACGAGGTCA 6520               A
           GG                     CCTGACCTCGTGATCCACCC CCT
                                |||||||||||||||||||| |||
                                GGACTGGAGCACTAGGTGGG GGA
                                        C
GAM1077  SLC28A2   3'  AGGCGGGCGGATCGCAGGGTCA 16144        TC      A  A
           GG                     CCTGACC  GTGATCC CCC CCT
                                |||||||  ||||||| ||| |||
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                                GGACTGG  CGCTAGG GGG GGA
                                   GA      C   C
GAM1077  SMG1     3'  AGGCGGGCGGATCATGAGGTTA 31340              A   A
                GG                  CCTGACCTCGTGATCC CCC CCT
                                    ||||||||||||||| ||| |||
                                    GGATTGGAGTACTAGG GGG GGA
                                          C   C
GAM1077  SRGAP1   5'  GGCGGGTGGATTACCTGG    72718    TC         A
                                    CC  GTGATCCACCC CC
                                    ||  ||||||||||| ||
                                    GG  CATTAGGTGGG GG
                                     TC          C
GAM1077  STAT3    3'  AGGCCGAGGCGGATCATAAGGT 58377         CG     A  CA__
                CAGG                CCTGACCT  TGATCC CC    CCT
                                    ||||||||  ||||||  ||    |||
                                    GGACTGGA  ACTAGG GG    GGA
                                       AT      C  AGCC
GAM1077  STAT3    3'  AGGCCGAGGCGGATCATAAGGT 13431         CG     A  CA__
                CAGG                CCTGACCT  TGATCC CC    CCT
                                    ||||||||  ||||||  ||    |||
                                    GGACTGGA  ACTAGG GG    GGA
                                       AT      C  AGCC
GAM1077  SUDD     3'  AGGCGGGTGGATCACTTGAGGT 15152          __         A
                CAGG                CCTGACCTC  GTGATCCACCC CCT
                                    |||||||||  ||||||||||| |||
                                    GGACTGGAG  CACTAGGTGGG GGA
                                         TT          C
GAM1077  SULT2A1  3'  GGGCGGATCACGAGGTCAGG   72231              A
                                    CCTGACCTCGTGATCC CCC
                                    ||||||||||||||| |||
                                    GGACTGGAGCACTAGG GGG
                                          C
GAM1077  SWAP70   3'  AGGCGGGTGGATCACCTGAGGT 71860          __         A
                CAGG                CCTGACCTC  GTGATCCACCC CCT
                                    |||||||||  ||||||||||| |||
                                    GGACTGGAG  CACTAGGTGGG GGA
                                       TC          C
GAM1077  TCTA     3'  AGGCAGGCAGATCACGAGGTCA 42488             CA  CA
                GG                  CCTGACCTCGTGATC  CC  CCT
                                    ||||||||||||||  ||  |||
                                    GGACTGGAGCACTAG  GG  GGA
                                          AC  AC
GAM1077  TEP1     3'  AGGTGGGCAGATCACGAGGTCA 24044             CA
                GG                  CCTGACCTCGTGATC  CCCACCT
                                    ||||||||||||||  |||||||
                                    GGACTGGAGCACTAG  GGGTGGA
                                          AC
GAM1077  TNFRSF10A 3'  AGGCGGGTGGATCACTTGAGGT 15237          __         A
                CAG                  CTGACCTC  GTGATCCACCC CCT
                                    ||||||||  |||||||||| |||
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                                GACTGGAG  CACTAGGTGGG GGA
                                    TT         C
GAM1077  TNFRSF1B  3'  AGGCGGGTGGATCACCTGAGGT 8383          __         A
           TAGG                   CCTGACCTC  GTGATCCACCC CCT
                                  |||||||||  |||||||||||| |||
                                  GGATTGGAG  CACTAGGTGGG GGA
                                     TC         C
GAM1077  TNFSF10   3'  AGGTGGGTAGATCACGAGATCA 15086     C       C
                                  TGA CTCGTGATC ACCCACCT
                                  ||| |||||||||  ||||||||
                                  ACT GAGCACTAG TGGGTGGA
                                    A       A
GAM1077  TNFSF14   3'  AGGCAGGCGGATCACCTGAGGT 15075          __      A  CA
           CAGG                   CCTGACCTC  GTGATCC CC  CCT
                                  |||||||||  |||||||  ||  |||
                                  GGACTGGAG  CACTAGG GG  GGA
                                     TC      C  AC
GAM1077  TRIM14    3'  GTGGGTGGATCACAAGGTCAGG 53777         C
                                  CCTGACCT GTGATCCACCCAC
                                  ||||||||  ||||||||||||
                                  GGACTGGA CACTAGGTGGGTG
                                     A
GAM1077  TRIM9     5'  AGGCAGGCGGACCACCTGAGGT 31442       __  A   A  CA
                                  ACCTC  GTG TCC CC  CCT
                                  |||||  ||| ||| ||  |||
                                  TGGAG  CAC AGG GG  GGA
                                    TC   C   C  AC
GAM1077  TSNAX     3'  AGGTAGGCAGATCACGAGGTCA 21151            CA  C
                                  TGACCTCGTGATC  CC ACCT
                                  ||||||||||||  ||  ||||
                                  ACTGGAGCACTAG  GG TGGA
                                        AC  A
GAM1077  UBE2G2    3'  AGGCAGGTAGATCACAAGGTCA 65476         C     C   CA
           GG                     CCTGACCT GTGATC ACC  CCT
                                  ||||||||  ||||||  |||  |||
                                  GGACTGGA CACTAG TGG  GGA
                                     A     A   AC
GAM1077  UBE2G2    3'  AGGCGGGCGGATCATGAGGTCA 65477              A   A
           GG                     CCTGACCTCGTGATCC CCC CCT
                                  ||||||||||||||| ||| |||
                                  GGACTGGAGTACTAGG GGG GGA
                                        C   C
GAM1077  UC28      3'  AGGTGGGTGGATCACCTGAGGT 41583          __
           CGGG                   CCTGACCTC  GTGATCCACCCACCT
                                  |||||||||  ||||||||||||||||
                                  GGGCTGGAG  CACTAGGTGGGTGGA
                                     TC
GAM1077  UPK1B     3'  AGGTGGGCAGATCACCTGAGGT 23698          __     CA
           CAGG                   CCTGACCTC  GTGATC  CCCACCT
                                  |||||||||  ||||||  |||||||
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                                GGACTGGAG  CACTAG  GGGTGGA
                                     TC     AC
GAM1077  VDR     3'  AGGTAGGTGGATCACCTGAGGT 6337          __        C
              CGGG                   CCTGACCTC  GTGATCCACC ACCT
                                |||||||||  |||||||||| ||||
                                GGGCTGGAG  CACTAGGTGG TGGA
                                     TC         A
GAM1077  VHL     3'  AGGCGGATGGATCACCTGAGGT 6832          __      C  A
              CAGG                   CCTGACCTC  GTGATCCA CC CCT
                                |||||||||  ||||||| || |||
                                GGACTGGAG  CACTAGGT GG GGA
                                     TC       A  C
GAM1077  VHL     3'  AGGCGGGTGGATCACGACGTCA 6833        C          A
              GG                     CCTGAC TCGTGATCCACCC CCT
                                ||||||| |||||||||||| |||
                                GGACTG AGCACTAGGTGGG GGA
                                   C           C
GAM1077  VHL     3'  AGGTGGGCAGATCACCTGAGGT 6834          __     CA
              CAGG                   CCTGACCTC  GTGATC  CCCACCT
                                |||||||||  ||||||  |||||||
                                GGACTGGAG  CACTAG  GGGTGGA
                                     TC     AC
GAM1077  VHL     3'  GGCAGATCATCTGAGGTCAGG  6866          __     CA
                                CCTGACCTC  GTGATC  CC
                                |||||||||  ||||||  ||
                                GGACTGGAG  TACTAG  GG
                                     TC     AC
GAM1077  WIG1    3'  GGCGGATCACGAGGTCAGG   96103              A
                                CCTGACCTCGTGATCC CC
                                |||||||||||||||| ||
                                GGACTGGAGCACTAGG GG
                                          C
GAM1077  XT3     3'  AGGTGGGTGGATCACTTGAGGT 39903          __
              CAGG                   CCTGACCTC  GTGATCCACCCACCT
                                |||||||||  ||||||||||||||||
                                GGACTGGAG  CACTAGGTGGGTGGA
                                     TT
GAM1077  ZNF14   3'  AGGCGGGCAGATCATTTGAGGT 41055         __     CA  A
              CAG                    CTGACCTC  GTGATC  CCC CCT
                                |||||||||  ||||||  ||| |||
                                GACTGGAG  TACTAG  GGG GGA
                                     TT     AC  C
GAM1077  ZNF264  3'  AGGCGGGTGGATCACCTGAGG  14196      __        A
                                CCTC  GTGATCCACCC CCT
                                ||||  |||||||||| |||
                                GGAG  CACTAGGTGGG GGA
                                  TC         C
GAM1077  ZNF266  3'  AGGTGAGTAACTTCAAATGAGG 89689       __  TCC_  C
                                CCTCG  TGA   AC CACCT
                                |||||  |||   || |||||
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                                GGAGT  ACT    TG GTGGA
                                  AA   TCAA  A
GAM1077  ZNF36    3'  AGGTGAGCGGATCACCTGAGGT 95575          __      ACC
            CAGG                  CCTGACCTC  GTGATCC   CACCT
                                  |||||||||  |||||||   |||||
                                  GGACTGGAG  CACTAGG   GTGGA
                                     TC      CGA
GAM1077  AF020591 3'  AGGCAGGTGGATCACTTGAG   27902     __       CA
                                  CTC  GTGATCCACC  CCT
                                  |||  ||||||||||  |||
                                  GAG  CACTAGGTGG  GGA
                                    TT        AC
GAM1077  AF020591  3'  AGGTGGGTGGATCACGAGGTCA 27903
            GG                    CCTGACCTCGTGATCCACCCACCT
                                  |||||||||||||||||||||||||
                                  GGACTGGAGCACTAGGTGGGTGGA

GAM1077  AKR1D1   3'  AGGTGGGCAGATCAGGAGGTCA 21129          G     CA
            GG                    CCTGACCTC TGATC  CCCACCT
                                  |||||||||  |||||  |||||||
                                  GGACTGGAG ACTAG  GGGTGGA
                                     G     AC
GAM1077  ALTE     3'  AGGTGGGCAGATCAGCTGAGGT 17576          __    CA
            CAGG                  CCTGACCTCG  TGATC  CCCACCT
                                  ||||||||||  |||||  |||||||
                                  GGACTGGAGT  ACTAG  GGGTGGA
                                     CG     AC
GAM1077  ALTE     3'  AGGTGGGCAGATCAGCTGAGGT 60997          __    CA
            CAGG                  CCTGACCTCG  TGATC  CCCACCT
                                  ||||||||||  |||||  |||||||
                                  GGACTGGAGT  ACTAG  GGGTGGA
                                     CG     AC
GAM1077  APXL2    3'  AGGCGGGCGGATCACAAGGTCA 75669        C      A   A
            GG                    CCTGACCT GTGATCC CCC CCT
                                  ||||||||  |||||||  |||  |||
                                  GGACTGGA CACTAGG GGG GGA
                                     A      C   C
GAM1077  ARNTL2   3'  GGGCAGATCACTTGAGGTCAGG 39855          __     CA
                                  CCTGACCTC  GTGATC  CCC
                                  |||||||||  ||||||  |||
                                  GGACTGGAG  CACTAG  GGG
                                     TT     AC
GAM1077  ARNTL2   3'  GTGGGCGGATCACGAGGTCAGG 39856              A
                                  CCTGACCTCGTGATCC CCCAC
                                  ||||||||||||||| |||||
                                  GGACTGGAGCACTAGG GGGTG
                                            C
GAM1077  ASAHL    3'  AGGCGGGTGGATCACTTGAGGT 64313          __         A
            CAGG                  CCTGACCTC  GTGATCCACCC CCT
                                  |||||||||  ||||||||||| |||
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                                GGACTGGAG  CACTAGGTGGG GGA
                                     TT         C
GAM1077 BAF53A   5' AGGTGGGTGGCGGTGGAAGTTA 66035     C  GTGAT
                                TGAC TC    CCACCCACCT
                                |||| ||    ||||||||||
                                ATTG AG    GGTGGGTGGA
                                  A  GTGGC
GAM1077 BIA2     3' AGGCGGGTGGATCACAAGCTCA 71790      C  C        A
           GG                   CCTGA CT GTGATCCACCC CCT
                                |||||| || |||||||||||| |||
                                GGACT GA CACTAGGTGGG GGA
                                  C  A         C
GAM1077 BTN3A2   3' AGGAGGGCGGATCACAAGGTCA 23869       C     A  A
           GG                   CCTGACCT GTGATCC CCC CCT
                                |||||||| ||||||| ||| |||
                                GGACTGGA CACTAGG GGG GGA
                                     A      C  A
GAM1077 C12orf2  3' AGGTGGGAGAATCACAAGGTCA 83678       C    CCA
           GG                   CCTGACCT GTGAT   CCCACCT
                                |||||||| |||||   |||||||
                                GGACTGGA CACTA   GGGTGGA
                                     A    AGA
GAM1077 C13orf1  3' AGGCGGGAGGATCACAAGGTCA 40352       C     A  A
           GG                   CCTGACCT GTGATCC CCC CCT
                                |||||||| ||||||| ||| |||
                                GGACTGGA CACTAGG GGG GGA
                                     A      A  C
GAM1077 C1orf33  3' AGGTGGGCAGATCATAAGGTCA 32978       CG    CA
           GG                   CCTGACCT  TGATC  CCCACCT
                                ||||||||  |||||  |||||||
                                GGACTGGA  ACTAG  GGGTGGA
                                     AT    AC
GAM1077 C1orf34  3' AGGCGGGCGGATAGCTTGAGGT 61297         TG__   A  A
           CAGG                   CCTGACCTCG   ATCC CCC CCT
                                |||||||||    |||| ||| |||
                                GGACTGGAGT   TAGG GGG GGA
                                      TCGA   C  C
GAM1077 C1QTNF2  3' AGGTGGACGGATCATTTGAGGT 49968         __     AC
           CAGG                   CCTGACCTC  GTGATCC  CCACCT
                                |||||||||  |||||||  ||||||
                                GGACTGGAG  TACTAGG  GGTGGA
                                     TT      CA
GAM1077 C20orf106 3' AGGCGGGTGAATCACGAGGTCA 55894           C    A
           GG                   CCTGACCTCGTGAT CACCC CCT
                                |||||||||||||| ||||| |||
                                GGACTGGAGCACTA GTGGG GGA
                                       A    C
GAM1077 C20orf106 3' GGGCAGATCACTTGAGGTCAGG 55911         __     CA
                                CCTGACCTC  GTGATC  CCC
                                |||||||||  ||||||  |||
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                                GGACTGGAG  CACTAG  GGG
                                     TT      AC
GAM1077  C20orf175 3'  AGGCAGGCGGATTACCTGAGGT 55921          __      A  CA
              CAGG                   CCTGACCTC  GTGATCC CC  CCT
                                |||||||||  |||||||  ||  |||
                                GGACTGGAG  CATTAGG GG  GGA
                                     TC      C  AC
GAM1077  C20orf177 3'  AGGCAGGCGGATCACCTGAGGT 62826          __      A  CA
              CGGG                   CCTGACCTC  GTGATCC CC  CCT
                                |||||||||  |||||||  ||  |||
                                GGGCTGGAG  CACTAGG GG  GGA
                                     TC      C  AC
GAM1077  C20orf183 3'  AGGCGGGCGGATCAATAGGTCA 48527         CG     A   A
              GG                     CCTGACCT  TGATCC CCC CCT
                                |||||||||  |||||| |||  |||
                                GGACTGGA  ACTAGG GGG GGA
                                     TA     C   C
GAM1077  C21orf108 3'  AGGCGGGTGAATCACCTGAGGT 90109          __     C     A
              CAGG                   CCTGACCTC  GTGAT CACCC CCT
                                |||||||||  |||||  |||||  |||
                                GGACTGGAG  CACTA GTGGG GGA
                                     TC     A     C
GAM1077  C22orf19  3'  AGGCGGGTGGATCACTTGAGGT 14815          __         A
              CAGG                   CCTGACCTC  GTGATCCACCC CCT
                                |||||||||  ||||||||||  |||
                                GGACTGGAG  CACTAGGTGGG GGA
                                     TT          C
GAM1077  C2F      3'  AGGCGGGTGGATCACTTGCGG  22002     ACCTC         A
                                CTG    GTGATCCACCC CCT
                                |||    ||||||||||  |||
                                GGC    CACTAGGTGGG GGA
                                  GTT__          C
GAM1077  C6orf5   3'  AGGCAGGCAGATCATTTGAGGT 31970          __     CA  CA
              CAGG                   CCTGACCTC  GTGATC  CC  CCT
                                |||||||||  ||||||  ||  |||
                                GGACTGGAG  TACTAG  GG  GGA
                                     TT      AC  AC
GAM1077  C6orf5   3'  AGGCAGGCGGATCATGAGGTCA 31971               A  CA
              GG                     CCTGACCTCGTGATCC CC  CCT
                                |||||||||||||||  ||  |||
                                GGACTGGAGTACTAGG GG  GGA
                                          C  AC
GAM1077  C8orf2   3'  AGGCAGGCGGATCACCTGAGGT 24143          __     A  CA
              TAGG                   CCTGACCTC  GTGATCC CC  CCT
                                |||||||||  |||||||  ||  |||
                                GGATTGGAG  CACTAGG GG  GGA
                                     TC      C  AC
GAM1077  CAMKK2   5'  AGGCGGGTGGATCACGAGGTCA 22616                 A
              GG                     CCTGACCTCGTGATCCACCC CCT
                                |||||||||||||||||||  |||
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                                GGACTGGAGCACTAGGTGGG GGA
                                      C
GAM1077 CBCIP2    3'  AGGTGGGCGGATCACTTGAGGT 52650          __      A
            CAGG                  CCTGACCTC  GTGATCC CCCACCT
                                  |||||||||  |||||||| |||||||
                                  GGACTGGAG  CACTAGG GGGTGGA
                                     TT       C
GAM1077 CCR6      3'  AGATGGGTGGATCACTTGAGGT 49396          __          C
            CAGG                  CCTGACCTC  GTGATCCACCCA CT
                                  |||||||||  |||||||||||| ||
                                  GGACTGGAG  CACTAGGTGGGT GA
                                     TT           A
GAM1077 CCR6      3'  AGATGGGTGGATCACTTGAGGT 16437          __          C
            CAGG                  CCTGACCTC  GTGATCCACCCA CT
                                  |||||||||  |||||||||||| ||
                                  GGACTGGAG  CACTAGGTGGGT GA
                                     TT           A
GAM1077 CDT1      3'  AGGTGGGCAGATCACGAGGTCA 78156            CA
                                  TGACCTCGTGATC  CCCACCT
                                  ||||||||||||  |||||||
                                  ACTGGAGCACTAG  GGGTGGA
                                        AC
GAM1077 cerk      3'  AGGCGGGTGGATCACCTAAGGT 43158          C__         A
            CAGG                  CCTGACCT   GTGATCCACCC CCT
                                  ||||||||   |||||||||| |||
                                  GGACTGGA   CACTAGGTGGG GGA
                                     ATC          C
GAM1077 CGRP-RCP  3'  AGGCAGGCGGATCACCTGAGGT 27884          __      A  CA
            CAGG                  CCTGACCTC  GTGATCC CC  CCT
                                  |||||||||  ||||||| ||  |||
                                  GGACTGGAG  CACTAGG GG  GGA
                                     TC       C  AC
GAM1077 CLDN15    3'  AGGTGGGTGGATTACTTGAGGT 57368          __
            CAGG                  CCTGACCTC  GTGATCCACCCACCT
                                  |||||||||  ||||||||||||||
                                  GGACTGGAG  CATTAGGTGGGTGGA
                                     TT
GAM1077 COE2      3'  AGGTGGGCAGATCACTTGAGGT 64903          __      CA
            CGGG                  CCTGACCTC  GTGATC  CCCACCT
                                  |||||||||  ||||||  |||||||
                                  GGGCTGGAG  CACTAG  GGGTGGA
                                     TT      AC
GAM1077 CRTAM     3'  AGGTAGGCAGATCACTTGAGGT 39470          __      CA  C
            CAGG                  CCTGACCTC  GTGATC  CC ACCT
                                  |||||||||  ||||||  || ||||
                                  GGACTGGAG  CACTAG  GG TGGA
                                     TT      AC  A
GAM1077 CSAD      3'  AGGCGGGTGGATCACTTGAGGT 32577          __          A
            CAGG                  CCTGACCTC  GTGATCCACCC CCT
                                  |||||||||  |||||||||| |||
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                                GGACTGGAG  CACTAGGTGGG GGA
                                     TT         C
GAM1077  DDX34    3'  AGGCGGGCAGATCACCTGAGGT 28659         __     CA   A
            CAGG                   CCTGACCTC  GTGATC  CCC CCT
                                |||||||||  ||||||  ||| |||
                                GGACTGGAG  CACTAG  GGG GGA
                                     TC     AC   C
GAM1077  DEGS     3'  AGGTGGGTGGATCACCTGAGGT 14800         __
            CAGG                   CCTGACCTC  GTGATCCACCCACCT
                                |||||||||  ||||||||||||||||
                                GGACTGGAG  CACTAGGTGGGTGGA
                                     TC
GAM1077  DKFZp434C0923 3'  AGGTGGGTGGGACTATGCCAGG 34644      ACCT    A_
                                CCTG    CGTG  TCCACCCACCT
                                ||||    ||||  ||||||||||
                                GGAC    GTAT  GGGTGGGTGGA
                                  C___    CA
GAM1077  DKFZP434C171 3'  AGGTGGGTGGATCACAAGGTTG 32182    TG    C
            GG                   CC  ACCT GTGATCCACCCACCT
                                ||  |||| ||||||||||||||
                                GG  TGGA CACTAGGTGGGTGGA
                                 GT    A
GAM1077  DKFZp434E2220 5'  AGGCGGGTGGATCATGAGGTCA 34706                A
            GG                   CCTGACCTCGTGATCCACCC CCT
                                |||||||||||||||||| |||
                                GGACTGGAGTACTAGGTGGG GGA
                                          C
GAM1077  DKFZp434G0522 3'  AGGTGGGTGGCCCAGGCCAGG  34529      A   CGTGAT
                                CCTG CCT      CCACCCACCT
                                |||| |||     ||||||||||
                                GGAC GGA     GGTGGGTGGA
                                  C   CCC___
GAM1077  DKFZp434G171 3'  AGGCAGGCAGATCACTTGAGGT 80232          __     CA  CA
            CAGG                   CCTGACCTC  GTGATC  CC  CCT
                                |||||||||  ||||||  ||  |||
                                GGACTGGAG  CACTAG  GG  GGA
                                     TT     AC  AC
GAM1077  DKFZp434G171 3'  AGGTGGGTGGATCACCTGAGGT 80233          __
            CAGG                   CCTGACCTC  GTGATCCACCCACCT
                                |||||||||  ||||||||||||||||
                                GGACTGGAG  CACTAGGTGGGTGGA
                                     TC
GAM1077  DKFZP434I1735 3'  AGGCGGGCGGATCACGAAGTCG 89164       C        A   A
            GG                   CCTGAC TCGTGATCC CCC CCT
                                ||||||  |||||||||  ||| |||
                                GGGCTG AGCACTAGG GGG GGA
                                   A        C   C
GAM1077  DKFZP434N1511 3'  AGGCGGGAGGATCATGAGGTCA 93050              A   A
            GG                   CCTGACCTCGTGATCC CCC CCT
                                ||||||||||||||| ||| |||
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                                GGACTGGAGTACTAGG GGG GGA
                                     A   C
GAM1077  DKFZp547C176 3'  AGGCGGGCGGATCACGAGGTCA 67796            A   A
                                TGACCTCGTGATCC CCC CCT
                                |||||||||||||| ||| |||
                                ACTGGAGCACTAGG GGG GGA
                                     C   C
GAM1077  DKFZP564A022 3'  AGGCGGGTAGATCACAAGGTCA 48969        C     C    A
           GG                    CCTGACCT GTGATC ACCC CCT
                                |||||||| |||||| |||| |||
                                GGACTGGA CACTAG TGGG GGA
                                    A     A    C
GAM1077  DKFZp564K142 3'  AGGCAGGCAGATCACGAGGTCA 50429            CA  CA
           GG                    CCTGACCTCGTGATC  CC  CCT
                                |||||||||||||||  ||  |||
                                GGACTGGAGCACTAG  GG  GGA
                                     AC  AC
GAM1077  DKFZp566H0824 3'  AGGCAGGTGGATCATGAGATCA 34476      C          CA
           GG                    CCTGA CTCGTGATCCACC  CCT
                                ||||| ||||||||||||  |||
                                GGACT GAGTACTAGGTGG  GGA
                                   A           AC
GAM1077  DKFZP586C1324 3'  AGGCAGGTGGATCACAAGGTTG 70353    TG   C        CA
           GG                    CC  ACCT GTGATCCACC  CCT
                                ||  |||| ||||||||||  |||
                                GG  TGGA CACTAGGTGG  GGA
                                 GT   A         AC
GAM1077  DKFZP761G1913 3'  AGGTGGGTGGATCACTTGAGGT 49692          __
           CAGG                    CCTGACCTC  GTGATCCACCCACCT
                                |||||||||  ||||||||||||||||
                                GGACTGGAG  CACTAGGTGGGTGGA
                                     TT
GAM1077  DRF1     3'  AGGCGGGTGGATCACAAGGTCA 47736       C         A
                                TGACCT GTGATCCACCC CCT
                                |||||| |||||||||| |||
                                ACTGGA CACTAGGTGGG GGA
                                   A         C
GAM1077  DRF1     3'  AGGTGGGTGGACCACTTGAGG  47737      __  A
                                CCTC  GTG TCCACCCACCT
                                ||||  ||| ||||||||||
                                GGAG  CAC AGGTGGGTGGA
                                  TT   C
GAM1077  ERAP140   3'  AGGCAGGTGGATCACTCAAGGT 75699     C__       CA
                                ACCT   GTGATCCACC  CCT
                                ||||   ||||||||||  |||
                                TGGA   CACTAGGTGG  GGA
                                  ACT         AC
GAM1077  ET       3'  AGGTGGGTGGATCGCCTGAGGT 44464         __
           CGGG                    CCTGACCTC  GTGATCCACCCACCT
                                |||||||||  ||||||||||||||||
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                                GGGCTGGAG CGCTAGGTGGGTGGA
                                   TC
GAM1077 FBXO27   3' AGGCAGGCGGATCACCTGAGGT 75000        __     A CA
           CAGG                 CCTGACCTC GTGATCC CC CCT
                                ||||||||| ||||||| || |||
                                GGACTGGAG CACTAGG GG GGA
                                   TC      C AC
GAM1077 FBXO6    3' AGGCAGGTGGATCACGAGGTCA 37987             CA
           GG                   CCTGACCTCGTGATCCACC CCT
                                |||||||||||||||||| |||
                                GGACTGGAGCACTAGGTGG GGA
                                         AC
GAM1077 FKBP14   3' AGGCGGGCGGATCACCTGAGGT 36060      __    A A
                                ACCTC GTGATCC CCC CCT
                                ||||| ||||||| ||| |||
                                TGGAG CACTAGG GGG GGA
                                   TC      C C
GAM1077 FKSG17   3' AGGCAGGCAGATCATCTGAGGT 50150       __    CA CA
           CA                   TGACCTC GTGATC CC CCT
                                ||||||| |||||| || |||
                                ACTGGAG TACTAG GG GGA
                                   TC     AC AC
GAM1077 FLJ00060 3' AGGTGGGTGGATCACGAGGTCA 61735
           GG                   CCTGACCTCGTGATCCACCCACCT
                                |||||||||||||||||||||||
                                GGACTGGAGCACTAGGTGGGTGGA

GAM1077 FLJ10008 3' AGGCGGACGGATCACGAGGTCA 36178            AC A
           GG                   CCTGACCTCGTGATCC CC CCT
                                |||||||||||||||  || |||
                                GGACTGGAGCACTAGG GG GGA
                                      CA C
GAM1077 FLJ10043 3' AGGCAGGTGGATCACTTGAGGT 36227        __      CA
           CAGG                 CCTGACCTC GTGATCCACC CCT
                                ||||||||| |||||||||| |||
                                GGACTGGAG CACTAGGTGG GGA
                                   TT       AC
GAM1077 FLJ10058 3' AGGCAAGTGGATCACTTGAGGT 36258        __      CCA
           CAGG                 CCTGACCTC GTGATCCAC  CCT
                                ||||||||| ||||||||  |||
                                GGACTGGAG CACTAGGTG  GGA
                                   TT       AAC
GAM1077 FLJ10244 3' AGGCGGGTGGATCACTTGAGGT 36397        __      A
           CAGG                 CCTGACCTC GTGATCCACCC CCT
                                ||||||||| |||||||||| |||
                                GGACTGGAG CACTAGGTGGG GGA
                                   TT       C
GAM1077 FLJ10460 3' AGATGGGTGGATCACCTGAGGT 36609        __      C
           CAGG                 CCTGACCTC GTGATCCACCCA CT
                                ||||||||| |||||||||||| ||
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                                GGACTGGAG  CACTAGGTGGGT GA
                                    TC          A
GAM1077  FLJ10460  3'  AGGTGGGCAGATCATGAGGTCA 36611            CA
            GG                   CCTGACCTCGTGATC  CCCACCT
                                 ||||||||||||||  |||||||
                                 GGACTGGAGTACTAG  GGGTGGA
                                        AC
GAM1077  FLJ10547  3'  AGGTGAGTGGATCACCTGAGGT 36772        __       C
            CAG                   CTGACCTC  GTGATCCAC CACCT
                                  ||||||||  |||||||||  |||||
                                  GACTGGAG  CACTAGGTG GTGGA
                                     TC        A
GAM1077  FLJ10607  3'  AGGTGGGCAGATCACAAGGTCA 77623        C     CA
            GG                   CCTGACCT GTGATC  CCCACCT
                                 ||||||||  ||||||  |||||||
                                 GGACTGGA CACTAG  GGGTGGA
                                     A     AC
GAM1077  FLJ10613  3'  AGGTGGGCGGATCACCTGAGGT 39334        __      A
            CGGG                  CCTGACCTC  GTGATCC CCCACCT
                                  |||||||||  |||||||  |||||||
                                  GGGCTGGAG  CACTAGG GGGTGGA
                                     TC       C
GAM1077  FLJ10650  3'  AGGTGGGCAGATCACTTGAGGT 36898        __     CA
            CAGG                  CCTGACCTC  GTGATC  CCCACCT
                                  |||||||||  ||||||  |||||||
                                  GGACTGGAG  CACTAG  GGGTGGA
                                     TT      AC
GAM1077  FLJ10704  3'  AGGCAGGTGGATCACCTGAGGT 36973        __       CA
            CAGG                  CCTGACCTC  GTGATCCACC  CCT
                                  |||||||||  ||||||||||  |||
                                  GGACTGGAG  CACTAGGTGG  GGA
                                     TC         AC
GAM1077  FLJ10724  3'  AGATGGGTGTTATCAAGGCCAG 37036     A  CG   C_     C
                                  CTG CCT  TGAT  CACCCA CT
                                  ||| |||  ||||  |||||| ||
                                  GAC GGA  ACTA  GTGGGT GA
                                    C  __   TT     A
GAM1077  FLJ10781  3'  AGGCAGGTCGATCACGAGGTCA 37167            C  CA
            GG                   CCTGACCTCGTGATC ACC  CCT
                                 ||||||||||||||| |||  |||
                                 GGACTGGAGCACTAG TGG  GGA
                                        C  AC
GAM1077  FLJ10826  3'  AGGCAGGCGGATCACCTGAGGT 37241        __     A  CA
            CAGG                  CCTGACCTC  GTGATCC CC  CCT
                                  |||||||||  |||||||  ||  |||
                                  GGACTGGAG  CACTAGG GG  GGA
                                     TC       C  AC
GAM1077  FLJ10891  3'  AGGTGGATAGATCACTTGAGGT 37339        __     CAC
            CA                    TGACCTC  GTGATC   CCACCT
                                  |||||||  ||||||   ||||||
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                                ACTGGAG  CACTAG   GGTGGA
                                   TT     ATA
GAM1077  FLJ10932  3'  AGGTGGGCAGATCACGAGGTGA 37423     G        CA
                GG                 CCT ACCTCGTGATC  CCCACCT
                                   ||| ||||||||||  |||||||
                                   GGA TGGAGCACTAG  GGGTGGA
                                     G         AC
GAM1077  FLJ10989  3'  AGGCGAGCGGATCATGAGGTCA 37495            ACCCA
                G                   CTGACCTCGTGATCC    CCT
                                   ||||||||||||||    |||
                                   GACTGGAGTACTAGG    GGA
                                            CGAGC
GAM1077  FLJ11029  3'  AGGCAGGTGGATCACCTGAGGT 61631         __        CA
                CAGG                  CCTGACCTC  GTGATCCACC  CCT
                                   |||||||||  ||||||||||  |||
                                   GGACTGGAG  CACTAGGTGG  GGA
                                        TC         AC
GAM1077  FLJ11106  3'  AGGCGGGCGGATCACGAGGTCA 37617             A   A
                GG                   CCTGACCTCGTGATCC CCC CCT
                                   |||||||||||||||| ||| |||
                                   GGACTGGAGCACTAGG GGG GGA
                                            C   C
GAM1077  FLJ11164  3'  AGGTGGGTGGAGTTGACCAG   37697    ACC   TGA
                                   CTG   TCG   TCCACCCACCT
                                   |||   |||   ||||||||||
                                   GAC   AGT   AGGTGGGTGGA
                                     C__   TG_
GAM1077  FLJ11370  3'  AGGCAGGCAGATCACCTGAGGT 46960         __     CA  CA
                CAG                   CTGACCTC  GTGATC  CC  CCT
                                   ||||||||  ||||||  ||  |||
                                   GACTGGAG  CACTAG  GG  GGA
                                        TC     AC  AC
GAM1077  FLJ11637  3'  AGGCAGGCGGATCACGAGGTCA 46980             A  CA
                GG                   CCTGACCTCGTGATCC CC  CCT
                                   |||||||||||||||| ||  |||
                                   GGACTGGAGCACTAGG GG  GGA
                                            C  AC
GAM1077  FLJ11722  3'  AGGCAGGTGGATCACGAGGCCA 46991      A          CA
                GG                   CCTG CCTCGTGATCCACC  CCT
                                   ||||  ||||||||||||||  |||
                                   GGAC GGAGCACTAGGTGG  GGA
                                     C           AC
GAM1077  FLJ11722  3'  AGGTGGGTGGATCATGAAGTCA 46992       C
                GG                   CCTGAC TCGTGATCCACCCACCT
                                   ||||||  ||||||||||||||||
                                   GGACTG AGTACTAGGTGGGTGGA
                                      A
GAM1077  FLJ11726  3'  AGGCAGGTGGATCACGATGTCA 47014       C         CA
                GG                   CCTGAC TCGTGATCCACC  CCT
                                   ||||||  ||||||||||||  |||
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                                GGACTG AGCACTAGGTGG  GGA
                                   T          AC
GAM1077  FLJ11996  3'  AGGCAGGCGGATCACAAGGTCA 47052        C      A  CA
                GG                  CCTGACCT GTGATCC CC  CCT
                                    |||||||| ||||||| ||  |||
                                    GGACTGGA CACTAGG GG  GGA
                                       A      C  AC
GAM1077  FLJ11996  3'  AGGCGAGTGGATCACTTGAGGT 47053         __       CCA
                CAGG                CCTGACCTC  GTGATCCAC   CCT
                                    |||||||||  |||||||||   |||
                                    GGACTGGAG  CACTAGGTG   GGA
                                       TT        AGC
GAM1077  FLJ12056  3'  AGGCAGGCGGATCACCTGAGGT 46816         __      A  CA
                CAGG                CCTGACCTC  GTGATCC CC  CCT
                                    |||||||||  |||||||| ||  |||
                                    GGACTGGAG  CACTAGG GG  GGA
                                       TC      C  AC
GAM1077  FLJ12078  3'  AGGCAGGCGGATCATGAGGTCG 47076             A  CA
                G                    CTGACCTCGTGATCC CC  CCT
                                    |||||||||||||| ||  |||
                                    GGCTGGAGTACTAGG GG  GGA
                                          C  AC
GAM1077  FLJ12178  3'  AGGCAGGCGGATCATGAGGTCA 47827             A  CA
                GG                  CCTGACCTCGTGATCC CC  CCT
                                    |||||||||||||| ||  |||
                                    GGACTGGAGTACTAGG GG  GGA
                                          C  AC
GAM1077  FLJ12190  3'  AGGCGGGTGAATCCCTTAAGGT 47560        CGT__  C    A
                CAGG                CCTGACCT    GAT CACCC CCT
                                    ||||||||    ||| ||||| |||
                                    GGACTGGA    CTA GTGGG GGA
                                       ATTCC   A    C
GAM1077  FLJ12294  3'  AGGTGGGCAGATCACGAGGTCA 47706             CA
                GG                  CCTGACCTCGTGATC  CCCACCT
                                    |||||||||||||||  |||||||
                                    GGACTGGAGCACTAG  GGGTGGA
                                          AC
GAM1077  FLJ12331  3'  AGGTGGGCAATCATTTGAGGTC 47108         __    CCA
                AGG                  CCTGACCTC  GTGAT   CCCACCT
                                    |||||||||  |||||   |||||||
                                    GGACTGGAG  TACTA   GGGTGGA
                                       TT     AC_
GAM1077  FLJ12517  3'  AGGTGAGGCCCAATGAGGTCAG 43715          GATCCA _
                G                    CCTGACCTCGT     CC CACCT
                                    ||||||||||      || |||||
                                    GGACTGGAGTA     GG GTGGA
                                          ACCC__  A
GAM1077  FLJ12547  3'  AGGCGGGAGGATCATGAGGTCA 47128             A  A
                GG                  CCTGACCTCGTGATCC CCC CCT
                                    |||||||||||||||| ||| |||
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                                GGACTGGAGTACTAGG GGG GGA
                                      A   C
GAM1077  FLJ12606  3'  AGGCGGGTGGATCACGAGGTCA 46061                A
              GG                  CCTGACCTCGTGATCCACCC CCT
                                  |||||||||||||||||||| |||
                                  GGACTGGAGCACTAGGTGGG GGA
                                        C
GAM1077  FLJ12660  3'  AGGTGGGTGGATCATGAGGTCA 47892
              GG                  CCTGACCTCGTGATCCACCCACCT
                                  |||||||||||||||||||||||||
                                  GGACTGGAGTACTAGGTGGGTGGA

GAM1077  FLJ12921  3'  AGGCGGGCGGATCACGAGGTCA 46392             A   A
              GG                  CCTGACCTCGTGATCC CCC CCT
                                  |||||||||||||||| ||| |||
                                  GGACTGGAGCACTAGG GGG GGA
                                        C   C
GAM1077  FLJ13117  3'  AGGCGGGTGGATCACTAGGTCA 43802         C         A
              GG                  CCTGACCT GTGATCCACCC CCT
                                  |||||||| |||||||||| |||
                                  GGACTGGA CACTAGGTGGG GGA
                                       T          C
GAM1077  FLJ13193  3'  AGGCGGGCAGATCACTTGAGGT 50708          __     CA   A
              CGGG                  CCTGACCTC  GTGATC  CCC CCT
                                    |||||||||  ||||||  ||| |||
                                    GGGCTGGAG  CACTAG  GGG GGA
                                         TT      AC   C
GAM1077  FLJ13193  3'  AGGCGGGTGGATCACAAGGTCA 50709        C         A
                                  TGACCT GTGATCCACCC CCT
                                  ||||||| |||||||||| |||
                                  ACTGGA CACTAGGTGGG GGA
                                     A          C
GAM1077  FLJ13193  3'  GGTAGATCATTTGAGGTCAGG  50732          __     C
                                  CCTGACCTC  GTGATC ACC
                                  |||||||||  |||||| |||
                                  GGACTGGAG  TACTAG TGG
                                       TT      A
GAM1077  FLJ13305  3'  GGGTGGATCACGAGGTCAGG   91716
                                  CCTGACCTCGTGATCCACCC
                                  ||||||||||||||||||||
                                  GGACTGGAGCACTAGGTGGG

GAM1077  FLJ13448  3'  AGGTGGGCAGATCAGTTGAGGT 47879          __     CA
              CAGG                  CCTGACCTCG  TGATC  CCCACCT
                                    ||||||||||  |||||  |||||||
                                    GGACTGGAGT  ACTAG  GGGTGGA
                                         TG     AC
GAM1077  FLJ13456  3'  AGGTGGGTGGATCACAAGGTCA 66528         C
              GG                  CCTGACCT GTGATCCACCCACCT
                                  |||||||| ||||||||||||||
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                                GGACTGGA CACTAGGTGGGTGGA
                                    A
GAM1077  FLJ13621  3'  AGGCGGGTGGATCACTTGAG   47215     __        A
                                CTC  GTGATCCACCC CCT
                                |||  |||||||||||| |||
                                GAG  CACTAGGTGGG GGA
                                  TT         C
GAM1077  FLJ13769  3'  AGGTGGGTAGATCATTTGAGGT 47244         __     C
           CAGG                   CCTGACCTC  GTGATC ACCCACCT
                                |||||||||  |||||| ||||||||
                                GGACTGGAG  TACTAG TGGGTGGA
                                     TT     A
GAM1077  FLJ13848  3'  AGGCAGGCGGGTCACCTGAGGT 45815         __      A  CA
           CAGG                   CCTGACCTC  GTGATCC CC  CCT
                                |||||||||  |||||| ||  |||
                                GGACTGGAG  CACTGGG GG  GGA
                                     TC      C  AC
GAM1077  FLJ13952  3'  AGATGGGTGGATCACCTGAGGT 46003         __         C
           CAGG                   CCTGACCTC  GTGATCCACCCA CT
                                |||||||||  |||||||||||| ||
                                GGACTGGAG  CACTAGGTGGGT GA
                                     TC         A
GAM1077  FLJ14100  3'  AGGCGGGCGGATCACGAGGTCA 47328             A   A
           GG                     CCTGACCTCGTGATCC CCC CCT
                                |||||||||||||||| ||| |||
                                GGACTGGAGCACTAGG GGG GGA
                                       C   C
GAM1077  FLJ14107  5'  AGGTGGGTGCTCTGCAAAGTTA 47345       CTC  _  TC
           GG                     CCTGAC   GT GA  CACCCACCT
                                ||||||   || ||  |||||||||
                                GGATTG   CG CT  GTGGGTGGA
                                   AAA  T  C_
GAM1077  FLJ14117  3'  AGGTGGGCGGATCATGAGGTCA 43217             A
           GG                     CCTGACCTCGTGATCC CCCACCT
                                |||||||||||||||| |||||||
                                GGACTGGAGTACTAGG GGGTGGA
                                       C
GAM1077  FLJ14225  3'  AGGCGGGCGGATCATGAGGTCA 46382             A   A
           GG                     CCTGACCTCGTGATCC CCC CCT
                                |||||||||||||||| ||| |||
                                GGACTGGAGTACTAGG GGG GGA
                                       C   C
GAM1077  FLJ14251  3'  AGATGGGCGGATCACGAGGTCA 46472             A    C
           GG                     CCTGACCTCGTGATCC CCCA CT
                                |||||||||||||||| |||| ||
                                GGACTGGAGCACTAGG GGGT GA
                                       C    A
GAM1077  FLJ14251  3'  AGGTGGGTGGATCACTGG    46473    TC
                                CC  GTGATCCACCCACCT
                                ||  ||||||||||||||
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                              GG  CACTAGGTGGGTGGA
                               T_
GAM1077  FLJ14326  3'  AGGCGGGTGGATCACTTGAGGT 50759          __         A
              CAGG                  CCTGACCTC  GTGATCCACCC CCT
                                    |||||||||  |||||||||||| |||
                                    GGACTGGAG  CACTAGGTGGG GGA
                                         TT          C
GAM1077  FLJ14346  3'  AGGCGGGCGGATCTCGAGGTCA 47356          T    A   A
              GG                    CCTGACCTCG GATCC CCC CCT
                                    |||||||||| ||||| ||| |||
                                    GGACTGGAGC CTAGG GGG GGA
                                         T    C   C
GAM1077  FLJ14397  3'  AGGCAGGCGGATCACCTGAGGT 52313          __      A  CA
              CGGG                  CCTGACCTC  GTGATCC CC  CCT
                                    |||||||||  ||||||| ||  |||
                                    GGGCTGGAG  CACTAGG GG  GGA
                                         TC       C  AC
GAM1077  FLJ14397  3'  AGGCAGGCGGATCATGAGGTCA 52314              A  CA
              GG                    CCTGACCTCGTGATCC CC  CCT
                                    |||||||||||||||| ||  |||
                                    GGACTGGAGTACTAGG GG  GGA
                                              C  AC
GAM1077  FLJ14457  3'  AGGCGGACAGATCACGAGGTCA 52400             CAC  A
              GG                    CCTGACCTCGTGATC   CC CCT
                                    |||||||||||||||   || |||
                                    GGACTGGAGCACTAG   GG GGA
                                              ACA  C
GAM1077  FLJ14466  3'  AGGCGGGCAGATCACTTGAGGT 52419          __     CA   A
              CGGG                  CCTGACCTC  GTGATC  CCC CCT
                                    |||||||||  ||||||  ||| |||
                                    GGGCTGGAG  CACTAG  GGG GGA
                                         TT      AC   C
GAM1077  FLJ14621  3'  AGGCGGGTGGATCAAGAGGTCA 52532          G         A
              GG                    CCTGACCTC TGATCCACCC CCT
                                    |||||||||  |||||||||| |||
                                    GGACTGGAG ACTAGGTGGG GGA
                                         A          C
GAM1077  FLJ14641  3'  GGGTGGATCATGAGGTCAGG   52564
                                    CCTGACCTCGTGATCCACCC
                                    ||||||||||||||||||||
                                    GGACTGGAGTACTAGGTGGG

GAM1077  FLJ20004  3'  AGATGGGCGGATCACCTGAGGT 96995          __     A   C
              CAGG                  CCTGACCTC  GTGATCC CCCA CT
                                    |||||||||  ||||||| |||| ||
                                    GGACTGGAG  CACTAGG GGGT GA
                                         TC       C    A
GAM1077  FLJ20004  3'  AGGCGGGCAGATCACTTGAGGT 34746          __     CA   A
              CAGG                  CCTGACCTC  GTGATC  CCC CCT
                                    |||||||||  ||||||  ||| |||
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                                GGACTGGAG  CACTAG  GGG GGA
                                    TT     AC   C
GAM1077  FLJ20034  3' AGGCAGGTGGATCATTTGAGGT 34834        __       CA
                   CAGG                 CCTGACCTC  GTGATCCACC  CCT
                                |||||||||  ||||||||||  |||
                                GGACTGGAG  TACTAGGTGG  GGA
                                    TT         AC
GAM1077  FLJ20045  3' AGGTAGGTGGATCACCCAAGGT 34871        C__       C
                   CAGG                 CCTGACCT   GTGATCCACC ACCT
                                ||||||||   ||||||||||  ||||
                                GGACTGGA   CACTAGGTGG TGGA
                                    ACC        A
GAM1077  FLJ20055  3' AGGCTGGCAGATCACAAGGTCA 34904        C     CAC  _
                   GG                   CCTGACCT GTGATC   CCA CCT
                                ||||||||  ||||||   ||| |||
                                GGACTGGA CACTAG   GGT GGA
                                    A     AC_  C
GAM1077  FLJ20059  3' AGGTGGATAGATCACTTGAGGT 34921        __     CAC
                   CAGG                 CCTGACCTC  GTGATC   CCACCT
                                |||||||||  ||||||   ||||||
                                GGACTGGAG  CACTAG   GGTGGA
                                    TT     ATA
GAM1077  FLJ20069  3' AGGCAGGTGGATCACCTAAGGT 34945        C__       CA
                   CAGG                 CCTGACCT   GTGATCCACC  CCT
                                ||||||||   ||||||||||  |||
                                GGACTGGA   CACTAGGTGG  GGA
                                    ATC        AC
GAM1077  FLJ20211  3' AGGTGGGCGGATCACCTGAGGT 35254        __     A
                   CAG                  CTGACCTC  GTGATCC CCCACCT
                                ||||||||  |||||||  |||||||
                                GACTGGAG  CACTAGG GGGTGGA
                                    TC      C
GAM1077  FLJ20306  3' GGGAGGATCACGAGGTCA    35398          A
                                TGACCTCGTGATCC CCC
                                ||||||||||||||  |||
                                ACTGGAGCACTAGG GGG
                                       A
GAM1077  FLJ20340  3' AGGCAGGGGAACACAAGGTCAG 35449        C  A  A  CA
                   G                   CCTGACCT GTG TCC CC  CCT
                                ||||||||  |||  |||  ||  |||
                                GGACTGGA CAC AGG GG  GGA
                                    A  A  _  AC
GAM1077  FLJ20359  3' AGGCAGGCGAATCACGAGGTCA 35513           CCA  CA
                   GG                   CCTGACCTCGTGAT   CC  CCT
                                ||||||||||||||   ||  |||
                                GGACTGGAGCACTA   GG  GGA
                                       AGC  AC
GAM1077  FLJ20413  3' AGGCGGGCGGATCACAAGGTCA 35589        C      A  A
                   GG                   CCTGACCT GTGATCC CCC CCT
                                ||||||||  |||||||  |||  |||
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                                GGACTGGA CACTAGG GGG GGA
                                   A      C   C
GAM1077  FLJ20456  3' AGGCAGGCGGATCACAGGGTCG 35661        TC      A  CA
             GG                  CCTGACC  GTGATCC CC  CCT
                                 |||||||  |||||||  ||  |||
                                 GGGCTGG  CACTAGG GG  GGA
                                    GA      C  AC
GAM1077  FLJ20464  3' AGGCAGGCGGATCACCTGAGGT 35684          __      A  CA
             CGGG                CCTGACCTC  GTGATCC CC  CCT
                                 |||||||||  |||||||  ||  |||
                                 GGGCTGGAG  CACTAGG GG  GGA
                                    TC      C  AC
GAM1077  FLJ20464  3' AGGCGGGCGGATCACCTGAGGT 35685          __      A   A
             CGGG                CCTGACCTC  GTGATCC CCC CCT
                                 |||||||||  |||||||  |||  |||
                                 GGGCTGGAG  CACTAGG GGG GGA
                                    TC      C   C
GAM1077  FLJ20546  3' AGGCAGGCAGATCACCTGAGGT 35805          __     CA  CA
             CGGG                CCTGACCTC  GTGATC  CC  CCT
                                 |||||||||  ||||||  ||  |||
                                 GGGCTGGAG  CACTAG  GG  GGA
                                    TC      AC  AC
GAM1077  FLJ20686  3' AGGTGGGTGGATCACTTGAGG  35951      __
                                 CCTC  GTGATCCACCCACCT
                                 ||||  ||||||||||||||
                                 GGAG  CACTAGGTGGGTGGA
                                   TT
GAM1077  FLJ20694  3' AGGTGGGCGGATCACCTGAGGT 35970          __      A
             CAGG                CCTGACCTC  GTGATCC CCCACCT
                                 |||||||||  |||||||  |||||||
                                 GGACTGGAG  CACTAGG GGGTGGA
                                    TC      C
GAM1077  FLJ20700  3' AGGCGGGCAGATCACAAGGTCA 35996        C     CA   A
             GG                  CCTGACCT GTGATC  CCC CCT
                                 ||||||||  ||||||  |||  |||
                                 GGACTGGA CACTAG  GGG GGA
                                    A     AC   C
GAM1077  FLJ20783  3' AGGCGGGCGGATCACGAGGTCA 36095             A   A
             GG                  CCTGACCTCGTGATCC CCC CCT
                                 ||||||||||||||||  |||  |||
                                 GGACTGGAGCACTAGG GGG GGA
                                       C   C
GAM1077  FLJ20808  3' AGGTGGGCAGATCACGAGCTCA 36117      C       CA
             GG                  CCTGA CTCGTGATC  CCCACCT
                                 |||||  |||||||||  |||||||
                                 GGACT GAGCACTAG  GGGTGGA
                                   C        AC
GAM1077  FLJ20825  3' AGGCGGGCAGATCATCTGAGGT 36141          __     CA   A
             CAGG                CCTGACCTC  GTGATC  CCC CCT
                                 |||||||||  ||||||  |||  |||
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                                GGACTGGAG  TACTAG  GGG GGA
                                     TC     AC   C
GAM1077  FLJ20972  3'  AGGTGGGCGGATCACCTGAGGT 47379         __      A
              CAGG                  CCTGACCTC  GTGATCC CCCACCT
                                |||||||||  |||||||  |||||||
                                GGACTGGAG  CACTAGG GGGTGGA
                                     TC      C
GAM1077  FLJ21106  3'  AGGCGGGTGTATCACGAGGTCA 47692            C     A
              GG                   CCTGACCTCGTGAT CACCC CCT
                                |||||||||||||| ||||| |||
                                GGACTGGAGCACTA GTGGG GGA
                                        T    C
GAM1077  FLJ21144  3'  AGATGGGTGGATCACCTGAG   43187     __          C
                                CTC  GTGATCCACCCA CT
                                |||  |||||||||||| ||
                                GAG  CACTAGGTGGGT GA
                                  TC          A
GAM1077  FLJ21369  3'  GGGTGGATCACCTGAGGTCAG  46054         __
                                CTGACCTC  GTGATCCACCC
                                ||||||||  ||||||||||
                                GACTGGAG  CACTAGGTGGG
                                     TC
GAM1077  FLJ21551  3'  AGGCAGGTGGATTGCCTGAGGT 46027         __ TG       CA
              CAG                   CTGACCTC  G  ATCCACC  CCT
                                |||||||| |  |||||||  |||
                                GACTGGAG  C  TAGGTGG  GGA
                                     TC GT      AC
GAM1077  FLJ21687  3'  AGGCTGGTGGATCACGAGGTCA 46290              CA
                                TGACCTCGTGATCCACC  CCT
                                ||||||||||||||||  |||
                                ACTGGAGCACTAGGTGG  GGA
                                        TC
GAM1077  FLJ21870  3'  AGGCAGGTGGATCACTTGAGG  43741     __         CA
                                CCTC  GTGATCCACC  CCT
                                ||||  ||||||||||  |||
                                GGAG  CACTAGGTGG  GGA
                                  TT         AC
GAM1077  FLJ22167  3'  AGGCGGGTGGATCACCTGAGGT 44860          __         A
              CAGG                  CCTGACCTC  GTGATCCACCC CCT
                                |||||||||  |||||||||| |||
                                GGACTGGAG  CACTAGGTGGG GGA
                                     TC          C
GAM1077  FLJ22596  3'  AGGCAGGTGGATCATTTGAGGT 47640          __         CA
              CAGG                  CCTGACCTC  GTGATCCACC  CCT
                                |||||||||  ||||||||||  |||
                                GGACTGGAG  TACTAGGTGG  GGA
                                     TT         AC
GAM1077  FLJ22692  3'  AGGCAGGCGGATCACAAGGTCA 47477         C       A  CA
              GG                    CCTGACCT GTGATCC CC  CCT
                                |||||||| |||||||  ||  |||
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                                GGACTGGA CACTAGG GG  GGA
                                   A      C  AC
GAM1077  FLJ22814  3'  AGGCGGGGGGGATCACAAGGTCA 46712        C      A  A
                GG                  CCTGACCT GTGATCC CCC CCT
                                    |||||||| ||||||| ||| |||
                                    GGACTGGA CACTAGG GGG GGA
                                       A      G   C
GAM1077  FLJ23040  3'  GGTGGATCATCTGAGGTCAGG  47989         __
                                    CCTGACCTC  GTGATCCACC
                                    |||||||||  ||||||||||
                                    GGACTGGAG  TACTAGGTGG
                                          TC
GAM1077  FLJ23042  3'  AGGCGGGCGGATCACCTGAGGT 47936       __      A  A
                                    ACCTC  GTGATCC CCC CCT
                                    |||||  ||||||| ||| |||
                                    TGGAG  CACTAGG GGG GGA
                                       TC      C   C
GAM1077  FLJ23112  3'  AGGCGGGTGGATCACCTGAGGT 46808          __         A
                CAGG                   CCTGACCTC  GTGATCCACCC CCT
                                    |||||||||  |||||||||||| |||
                                    GGACTGGAG  CACTAGGTGGG GGA
                                          TC          C
GAM1077  FLJ23120  3'  AGGCGGGTGGATCACGAGGTCA 86324                 A
                GG                  CCTGACCTCGTGATCCACCC CCT
                                    |||||||||||||||||| |||
                                    GGACTGGAGCACTAGGTGGG GGA
                                                C
GAM1077  FLJ23185  3'  AGGCAGGTGGAGAGGATGAGG  47508       GA__     CA
                                    CCTCGT    TCCACC  CCT
                                    ||||||    ||||||  |||
                                    GGAGTA    AGGTGG  GGA
                                       GGAG      AC
GAM1077  FLJ23235  3'  AGGTGGGAGGATCATGAGGTCA 46875              A
                                    TGACCTCGTGATCC CCCACCT
                                    |||||||||||||| |||||||
                                    ACTGGAGTACTAGG GGGTGGA
                                             A
GAM1077  FLJ23360  3'  AGGCGGGTGGATCACCTAAGGT 43822         C__         A
                CAGG                   CCTGACCT   GTGATCCACCC CCT
                                    ||||||||   |||||||||||| |||
                                    GGACTGGA   CACTAGGTGGG GGA
                                          ATC          C
GAM1077  FLJ23499  3'  AGGCAGGTGGATCACGTGAGGT 43126          __         CA
                CAGG                   CCTGACCTC  GTGATCCACC  CCT
                                    |||||||||  ||||||||||  |||
                                    GGACTGGAG  CACTAGGTGG  GGA
                                          TG         AC
GAM1077  FLJ23499  3'  AGGTGGGTGGATCACCTGAGGT 43127          __
                CAGG                   CCTGACCTC  GTGATCCACCCACCT
                                    |||||||||  ||||||||||||||
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                                GGACTGGAG  CACTAGGTGGGTGGA
                                    TC
GAM1077  FLJ23878  3'  AGGCGGGCAGATCACGAGGTCA 59366            CA   A
            GG                   CCTGACCTCGTGATC  CCC CCT
                                 ||||||||||||||  ||| |||
                                 GGACTGGAGCACTAG  GGG GGA
                                       AC   C
GAM1077  FLJ25012  3'  AGGCAGGTGGATCATGAGGTCA 58707              CA
            GG                   CCTGACCTCGTGATCCACC  CCT
                                 ||||||||||||||||||  |||
                                 GGACTGGAGTACTAGGTGG  GGA
                                       AC
GAM1077  FLJ30681  3'  AGGCGGGGAGATCACAAGGTCA 93430        C     CA   A
            GG                   CCTGACCT GTGATC  CCC CCT
                                 ||||||||  ||||||  ||| |||
                                 GGACTGGA CACTAG  GGG GGA
                                    A     AG   C
GAM1077  FLJ31455  3'  AGGTGAGTGGATTACAAGGTCA 59279        C       C
            GG                   CCTGACCT GTGATCCAC CACCT
                                 ||||||||  |||||||||  |||||
                                 GGACTGGA CATTAGGTG GTGGA
                                    A        A
GAM1077  FLJ31455  3'  GTGGGCAGATCACCTGAGGTCA 59290          __     CA
            GG                   CCTGACCTC  GTGATC  CCCAC
                                 |||||||||  ||||||  |||||
                                 GGACTGGAG  CACTAG  GGGTG
                                       TC     AC
GAM1077  FLJ31737  3'  AGGTGGGTGGATCACGAAGTCA 59346      C
                                 TGAC TCGTGATCCACCCACCT
                                 ||||  ||||||||||||||||
                                 ACTG AGCACTAGGTGGGTGGA
                                   A
GAM1077  FLJ31952  3'  AGGCAGGTGGATCACCTGAGGT 59041          __        CA
            CAGG                    CCTGACCTC  GTGATCCACC  CCT
                                 |||||||||  ||||||||||  |||
                                 GGACTGGAG  CACTAGGTGG  GGA
                                       TC         AC
GAM1077  FLJ32915  5'  AGGCGGGCAGATCACCTGAGGT 59425          __     CA   A
            TAGG                    CCTGACCTC  GTGATC  CCC CCT
                                 |||||||||  ||||||  ||| |||
                                 GGATTGGAG  CACTAG  GGG GGA
                                       TC     AC   C
GAM1077  FUSIP1    3'  AGGCGGGCGGATCACGAGGTCA 55033            A   A
            GG                   CCTGACCTCGTGATCC CCC CCT
                                 ||||||||||||||| ||| |||
                                 GGACTGGAGCACTAGG GGG GGA
                                       C   C
GAM1077  G4        3'  AGGCAAGTGGATTAGGGGGTCT 92634    T     G       CCA
            GG                   CC GACCTC TGATCCAC   CCT
                                 || |||||| ||||||||   |||
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                                GG CTGGGG ATTAGGTG   GGA
                                 T     G       AAC
GAM1077  GABARAPL3 3'  GGTGGACAAGTTGGGGTCAG   51787          ___  A
                                CTGACCTCG   TG TCCACC
                                |||||||||   || ||||||
                                GACTGGGGT   AC AGGTGG
                                     TGA  _
GAM1077  GALNT6   3'  AGGCAGGTGGATCACCTGAGGT 24238          __        CA
            CAG                    CTGACCTC  GTGATCCACC  CCT
                                |||||||||  ||||||||||  |||
                                GACTGGAG  CACTAGGTGG  GGA
                                     TC         AC
GAM1077  GLTP     3'  AGGCGGGTGGATCACCTGAGGT 33580          __        A
            CGGG                   CCTGACCTC  GTGATCCACCC CCT
                                |||||||||  |||||||||||  |||
                                GGGCTGGAG  CACTAGGTGGG GGA
                                     TC          C
GAM1077  GNB4     3'  AGGTGGGCAGATCACTTGAGGT 41563          __     CA
            CAGG                   CCTGACCTC  GTGATC  CCCACCT
                                |||||||||  ||||||  |||||||
                                GGACTGGAG  CACTAG  GGGTGGA
                                     TT      AC
GAM1077  GP5      3'  AGGTGGGTGGATCACAGGTCAG 16862         C
            G                     CCTGACCT GTGATCCACCCACCT
                                |||||||| ||||||||||||||
                                GGACTGGA CACTAGGTGGGTGGA
                                     _
GAM1077  GRID1    3'  AGGTGGGTGGACCAGTACTCCA 69021      ACCTCG  A
            GG                     CCTG      TG TCCACCCACCT
                                ||||      || ||||||||||
                                GGAC      AC AGGTGGGTGGA
                                  CTCATG  C
GAM1077  GTPBP5   3'  AGGCTGGTGGATCACAAGGTCA 65966         C         CA
            GG                     CCTGACCT GTGATCCACC  CCT
                                |||||||| ||||||||||  |||
                                GGACTGGA CACTAGGTGG  GGA
                                     A          TC
GAM1077  HES2     3'  AGGCGGGCAGATCACGAGGTCA 39368              CA   A
            GG                     CCTGACCTCGTGATC  CCC CCT
                                ||||||||||||||  ||| |||
                                GGACTGGAGCACTAG  GGG GGA
                                        AC   C
GAM1077  HIG2     3'  AGGTGGGTGGATCACCTGAGGT 26197          __
            CAGG                   CCTGACCTC  GTGATCCACCCACCT
                                |||||||||  ||||||||||||||
                                GGACTGGAG  CACTAGGTGGGTGGA
                                     TC
GAM1077  HRH4     3'  AGGTGGGCGGATCATGAGGTCA 41527              A
            GG                     CCTGACCTCGTGATCC CCCACCT
                                |||||||||||||| |||||||
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                                GGACTGGAGTACTAGG GGGTGGA
                                       C
GAM1077 HSH2     3' AGGCAGGCAGATCGCTTGAGGT 52735        __     CA CA
           CAGG                  CCTGACCTC GTGATC CC CCT
                                 ||||||||| ||||||  ||  |||
                                 GGACTGGAG CGCTAG GG GGA
                                    TT     AC AC
GAM1077 HSPC031  3' AGGCGGACGGATCACTTGAGGT 32747        __     AC A
           TAGG                  CCTGACCTC GTGATCC CC CCT
                                 ||||||||| |||||||  || |||
                                 GGATTGGAG CACTAGG GG GGA
                                    TT      CA C
GAM1077 HYPK     3' AGGCAGGTAGATCACGAGGTCA 33512           C   CA
           GG                    CCTGACCTCGTGATC ACC CCT
                                 |||||||||||||| |||  |||
                                 GGACTGGAGCACTAG TGG GGA
                                       A   AC
GAM1077 IL-23R   3' AGGTGGGTGGATCACCTGAGGT 59127        __
           CAGG                  CCTGACCTC GTGATCCACCCACCT
                                 |||||||||  ||||||||||||||
                                 GGACTGGAG CACTAGGTGGGTGGA
                                    TC
GAM1077 IL10RB   3' AGGCAGGCGGATCACTTGAGGT 7122         __     A CA
           CAGG                  CCTGACCTC GTGATCC CC CCT
                                 |||||||||  |||||||  ||  |||
                                 GGACTGGAG CACTAGG GG GGA
                                    TT      C AC
GAM1077 IMAGE:4907098 3' GGTCGGATCATGAGGTCA    93327          _
                                 TGACCTCGTGATCC ACC
                                 |||||||||||||| |||
                                 ACTGGAGTACTAGG TGG
                                       C
GAM1077 JAM1     3' AGGCAGGCGGATCACCTGAGGT 58509        __     A CA
           CAGG                  CCTGACCTC GTGATCC CC CCT
                                 |||||||||  |||||||  ||  |||
                                 GGACTGGAG CACTAGG GG GGA
                                    TC      C AC
GAM1077 JAM1     3' AGGCAGGCGGATCACCTGAGGT 58537        __     A CA
           CAGG                  CCTGACCTC GTGATCC CC CCT
                                 |||||||||  |||||||  ||  |||
                                 GGACTGGAG CACTAGG GG GGA
                                    TC      C AC
GAM1077 JAM1     3' AGGCAGGCGGATCACCTGAGGT 58565        __     A CA
           CAGG                  CCTGACCTC GTGATCC CC CCT
                                 |||||||||  |||||||  ||  |||
                                 GGACTGGAG CACTAGG GG GGA
                                    TC      C AC
GAM1077 JAM1     3' AGGCAGGCGGATCACCTGAGGT 34218        __     A CA
           CAGG                  CCTGACCTC GTGATCC CC CCT
                                 |||||||||  |||||||  ||  |||
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                                GGACTGGAG  CACTAGG GG  GGA
                                     TC      C  AC
GAM1077  KIAA0042  3'  AGGCGGGCAGATCACAAGGTCA 30231        C     CA   A
              GG                  CCTGACCT GTGATC  CCC CCT
                                  |||||||| ||||||  ||| |||
                                  GGACTGGA CACTAG  GGG GGA
                                      A     AC   C
GAM1077  KIAA0057  3'  AGGTGGGCAGATCACCTGAGGT 25401         __     CA
              TAGG                  CCTGACCTC  GTGATC  CCCACCT
                                  |||||||||  ||||||  |||||||
                                  GGATTGGAG  CACTAG  GGGTGGA
                                       TC     AC
GAM1077  KIAA0082  3'  GGCAGGTATGAGGTCAG     93783          GATCC   CA
                                  CTGACCTCGT    ACC  CC
                                  ||||||||||    |||  ||
                                  GACTGGAGTA    TGG  GG
                                        _____   AC
GAM1077  KIAA0090  3'  AGGCAGGCAGATCATTTGAGGT 89810         __     CA  CA
              CAGG                  CCTGACCTC  GTGATC  CC  CCT
                                  |||||||||  ||||||  ||  |||
                                  GGACTGGAG  TACTAG  GG  GGA
                                       TT     AC  AC
GAM1077  KIAA0184  3'  AGGCGAGCAGATCACGAGGTCA 65803             CACCCA
              GG                  CCTGACCTCGTGATC     CCT
                                  ||||||||||||||     |||
                                  GGACTGGAGCACTAG     GGA
                                        ACGAGC
GAM1077  KIAA0186  3'  AGATGGGTGGATCACTTGAG   41097     __         C
                                  CTC  GTGATCCACCCA CT
                                  |||  |||||||||||| ||
                                  GAG  CACTAGGTGGGT GA
                                    TT          A
GAM1077  KIAA0226  3'  GGCGGATCATGAGGTCAGG    64260              A
                                  CCTGACCTCGTGATCC CC
                                  |||||||||||||||| ||
                                  GGACTGGAGTACTAGG GG
                                        C
GAM1077  KIAA0252  3'  AGGCGGGTGGATCACCTGAGGT 63450         __         A
              CAGG                  CCTGACCTC  GTGATCCACCC CCT
                                  |||||||||  |||||||||| |||
                                  GGACTGGAG  CACTAGGTGGG GGA
                                       TC          C
GAM1077  KIAA0266  3'  AGATGGGTGGATCATGAGGTCA 41634                C
              G                    CTGACCTCGTGATCCACCCA CT
                                  |||||||||||||||||| ||
                                  GACTGGAGTACTAGGTGGGT GA
                                         A
GAM1077  KIAA0266  3'  AGATGGGTGGATCATGAGGTCA 41635                C
              G                    CTGACCTCGTGATCCACCCA CT
                                  |||||||||||||||||| ||
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                                GACTGGAGTACTAGGTGGGT GA
                                       A
GAM1077  KIAA0355  3'  AGGCAGGTGGATCACCTAAGGT 28698        C__        CA
              CAGG                  CCTGACCT   GTGATCCACC  CCT
                                    ||||||||   ||||||||||  |||
                                    GGACTGGA   CACTAGGTGG  GGA
                                       ATC         AC
GAM1077  KIAA0408  3'  AGGTGGGGGGGATCACGAGGTCA 28792              A
              GG                    CCTGACCTCGTGATCC CCCACCT
                                    ||||||||||||||| |||||||
                                    GGACTGGAGCACTAGG GGGTGGA
                                          G
GAM1077  KIAA0419  3'  AGGTGGGTGGATCACCTGAGGT 28857         __
              CAGG                  CCTGACCTC  GTGATCCACCCACCT
                                    |||||||||  ||||||||||||||||
                                    GGACTGGAG  CACTAGGTGGGTGGA
                                       TC
GAM1077  KIAA0441  3'  AGGTGGGCGGATCACGAGGTCA 29623              A
              GG                    CCTGACCTCGTGATCC CCCACCT
                                    ||||||||||||||| |||||||
                                    GGACTGGAGCACTAGG GGGTGGA
                                          C
GAM1077  KIAA0445  5'  AGGCAGGCAGATCGCCTGAGGT 28635         __     CA  CA
              CAGG                  CCTGACCTC  GTGATC  CC  CCT
                                    |||||||||  ||||||  ||  |||
                                    GGACTGGAG  CGCTAG  GG  GGA
                                       TC      AC  AC
GAM1077  KIAA0446  5'  AGGCGGGTGGATCACGAGGTCA 69441                A
              GG                    CCTGACCTCGTGATCCACCC CCT
                                    |||||||||||||||||| |||
                                    GGACTGGAGCACTAGGTGGG GGA
                                          C
GAM1077  KIAA0514  3'  AGGTGGGTGGAGAGAGGGCAGG 28739      A    GTGA
                                    CCTG CCTC    TCCACCCACCT
                                    |||| ||||    ||||||||||
                                    GGAC GGAG    AGGTGGGTGGA
                                      G    AG__
GAM1077  KIAA0547  3'  AGGTGGGCAGATCACAAGGTTA 29587         C     CA
              GG                    CCTGACCT GTGATC  CCCACCT
                                    ||||||| ||||||  |||||||
                                    GGATTGGA CACTAG  GGGTGGA
                                       A      AC
GAM1077  KIAA0557  3'  AGGCAGGTGGATCACAAGGTCA 78546         C         CA
              GG                    CCTGACCT GTGATCCACC  CCT
                                    |||||||| ||||||||||  |||
                                    GGACTGGA CACTAGGTGG  GGA
                                       A         AC
GAM1077  KIAA0563  3'  AGGCGGGCGGATCATGAGGTCA 29868              A   A
              GG                    CCTGACCTCGTGATCC CCC CCT
                                    |||||||||||||||| ||| |||
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                              GGACTGGAGTACTAGG GGG GGA
                                    C   C
GAM1077  KIAA0565  3'  AGGTGGGTGGATCACCTGAGGT 67431        __
            CAGG                 CCTGACCTC  GTGATCCACCCACCT
                                 |||||||||  ||||||||||||||
                                 GGACTGGAG  CACTAGGTGGGTGGA
                                    TC
GAM1077  KIAA0596  3'  AGGCGGGTGGATCACCTGAGGT 63481        __        A
            TAGG                 CCTGACCTC  GTGATCCACCC CCT
                                 |||||||||  |||||||||| |||
                                 GGATTGGAG  CACTAGGTGGG GGA
                                    TC         C
GAM1077  KIAA0618  3'  AGGTGGGCAGATCACCTGAGGT 29843        __     CA
            CAGG                 CCTGACCTC  GTGATC  CCCACCT
                                 |||||||||  ||||||  |||||||
                                 GGACTGGAG  CACTAG  GGGTGGA
                                    TC     AC
GAM1077  KIAA0628  3'  AGGCGGGCGGATCGCTTGAGGT 29526        __     A   A
            CAGG                 CCTGACCTC  GTGATCC CCC CCT
                                 |||||||||  ||||||| ||| |||
                                 GGACTGGAG  CGCTAGG GGG GGA
                                    TT      C   C
GAM1077  KIAA0635  3'  AGGCGAGTGGATTTCCTAAGGT 28410        CGT__     CCA
            CAGG                 CCTGACCT    GATCCAC   CCT
                                 ||||||||    |||||||   |||
                                 GGACTGGA    TTAGGTG   GGA
                                    ATCCT      AGC
GAM1077  KIAA0694  3'  GGCGGATCCCGAGGTCAGG   72971         T    A
                              CCTGACCTCG GATCC CC
                              ||||||||||| ||||| ||
                              GGACTGGAGC CTAGG GG
                                    C    C
GAM1077  KIAA0752  3'  GGGCGGATCAGCAGAGGTCAGG 67633        _ _    A
                              CCTGACCTC G TGATCC CCC
                              |||||||||  | ||||||  |||
                              GGACTGGAG C ACTAGG GGG
                                    A G     C
GAM1077  KIAA0794  3'  AGGTGGGCAGATCACCTAAGGT 81223        C__     CA
            CAGG                 CCTGACCT   GTGATC  CCCACCT
                                 ||||||||   ||||||  |||||||
                                 GGACTGGA   CACTAG  GGGTGGA
                                    ATC      AC
GAM1077  KIAA0798  3'  AGGTGGGTGGATCACTTGAGGT 28441        __
            CGGG                 CCTGACCTC  GTGATCCACCCACCT
                                 |||||||||  ||||||||||||||
                                 GGGCTGGAG  CACTAGGTGGGTGGA
                                    TT
GAM1077  KIAA0831  3'  AGGCAGGCGGATCACTTGAGGT 30628        __      A  CA
            CAGG                 CCTGACCTC  GTGATCC CC  CCT
                                 |||||||||  ||||||| ||  |||
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                                GGACTGGAG  CACTAGG GG  GGA
                                     TT      C  AC
GAM1077  KIAA0831  5'  GGTGGATCACCTGAGGTTAGG  30652          __
                                CCTGACCTC  GTGATCCACC
                                |||||||||  ||||||||||
                                GGATTGGAG  CACTAGGTGG
                                     TC
GAM1077  KIAA0872  3'  AGGCGGGCAGATCACGAGGTTA 30740             CA   A
              GG                  CCTGACCTCGTGATC  CCC CCT
                                  ||||||||||||||  ||| |||
                                  GGATTGGAGCACTAG  GGG GGA
                                        AC   C
GAM1077  KIAA0872  3'  AGGCGGGTGGGTCACCTGAGGT 30741          __         A
              CAGG                  CCTGACCTC  GTGATCCACCC CCT
                                    |||||||||  |||||||||||  |||
                                    GGACTGGAG  CACTGGGTGGG GGA
                                         TC          C
GAM1077  KIAA0884  3'  AGGCAGGTGGATCACCTGAGGT 70746          __         CA
              CAGG                  CCTGACCTC  GTGATCCACC  CCT
                                    |||||||||  ||||||||||  |||
                                    GGACTGGAG  CACTAGGTGG  GGA
                                         TC         AC
GAM1077  KIAA0889  3'  AGGCGGGTGGATCACAAGGTCA 31754          C          A
              GG                    CCTGACCT GTGATCCACCC CCT
                                    ||||||||  ||||||||||  |||
                                    GGACTGGA CACTAGGTGGG GGA
                                         A          C
GAM1077  KIAA0889  3'  AGGTGGGTGGATCGCCTGAG   31756     __
                                CTC  GTGATCCACCCACCT
                                |||  ||||||||||||||
                                GAG  CGCTAGGTGGGTGGA
                                  TC
GAM1077  KIAA0894  3'  AGGCAAGTGGATCACTTGAGGT 30325          __         CCA
              CAGG                  CCTGACCTC  GTGATCCAC   CCT
                                    |||||||||  |||||||||   |||
                                    GGACTGGAG  CACTAGGTG   GGA
                                         TT         AAC
GAM1077  KIAA0907  3'  AGGTGGGCAGATCACCTAAGGT 30865          C__      CA
              CAGG                  CCTGACCT   GTGATC  CCCACCT
                                    |||||||   ||||||  |||||||
                                    GGACTGGA   CACTAG  GGGTGGA
                                         ATC      AC
GAM1077  KIAA0907  3'  AGGTGGGCGGATAACCTGAGGT 30866           TG__    A
              CAGG                  CCTGACCTCG    ATCC CCCACCT
                                    ||||||||||    |||| |||||||
                                    GGACTGGAGT    TAGG GGGTGGA
                                          CCAA    C
GAM1077  KIAA0930  3'  AGATGGGTGGATCACCTGAG   71061     __          C
                                CTC  GTGATCCACCCA CT
                                |||  ||||||||||| ||
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                                GAG  CACTAGGTGGGT GA
                                  TC          A
GAM1077  KIAA0953  3'  AGGCAGGTGGATCACCTGAGGT 67321          __        CA
                TAGG                  CCTGACCTC  GTGATCCACC  CCT
                                |||||||||  ||||||||||  |||
                                GGATTGGAG  CACTAGGTGG  GGA
                                    TC         AC
GAM1077  KIAA0961  3'  GGCAGATCATGAGGTCAGG   30404             CA
                                CCTGACCTCGTGATC  CC
                                ||||||||||||||  ||
                                GGACTGGAGTACTAG  GG
                                        AC
GAM1077  KIAA0981  3'  AGGCAGGCAGATCACCTGAGGT 62083          __     CA  CA
                CAGG                  CCTGACCTC  GTGATC  CC  CCT
                                |||||||||  ||||||  ||  |||
                                GGACTGGAG  CACTAG  GG  GGA
                                    TC     AC  AC
GAM1077  KIAA1001  3'  AGGTGGGTGGATCACTGGGTCA 31000         C
                GG                  CCTGACCT GTGATCCACCCACCT
                                |||||||| ||||||||||||||
                                GGACTGGG CACTAGGTGGGTGGA
                                    T
GAM1077  KIAA1086  3'  AGGTGGGCAGATCGCCTGAGGT 71280          __     CA
                CAGG                  CCTGACCTC  GTGATC  CCCACCT
                                |||||||||  ||||||  |||||||
                                GGACTGGAG  CGCTAG  GGGTGGA
                                    TC     AC
GAM1077  KIAA1130  3'  AGATGGGTGGATCATGAGGTCA 63075                C
                GG                  CCTGACCTCGTGATCCACCCA CT
                                |||||||||||||||||||| ||
                                GGACTGGAGTACTAGGTGGGT GA
                                        A
GAM1077  KIAA1155  3'  GTGGGTGGGGAGAACAGG    62918     AC   GTGA
                                CCTG  CTC    TCCACCCAC
                                ||||  |||   |||||||||
                                GGAC  GAG    GGGTGGGTG
                                  AA  _____
GAM1077  KIAA1160  3'  AGGCGGGCGGGTCACGAGGTCA 40751            A   A
                                TGACCTCGTGATCC CCC CCT
                                |||||||||||||| ||| |||
                                ACTGGAGCACTGGG GGG GGA
                                        C   C
GAM1077  KIAA1164  3'  AGGCAGGTGGATCACCTGAG   70032     __        CA
                                CTC  GTGATCCACC  CCT
                                |||  ||||||||||  |||
                                GAG  CACTAGGTGG  GGA
                                  TC         AC
GAM1077  KIAA1191  3'  AGGTAGGTGGATACCTGAGGTC 40330          TG_     C
                AGG                  CCTGACCTCG   ATCCACC ACCT
                                |||||||||   |||||||  ||||
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                                GGACTGGAGT   TAGGTGG TGGA
                                     CCA      A
GAM1077  KIAA1202  3'  AGGCAGGTGGATCACGAGGTCA 72484                CA
                GG                  CCTGACCTCGTGATCCACC  CCT
                                    ||||||||||||||||||  |||
                                    GGACTGGAGCACTAGGTGG  GGA
                                          AC
GAM1077  KIAA1228  3'  AGGCGGGCGGATGACCTGAGGT 65667          __ G   A  A
                CAGG                CCTGACCTC  GT ATCC CCC CCT
                                    |||||||||  || |||| ||| |||
                                    GGACTGGAG  CA TAGG GGG GGA
                                       TC  G   C  C
GAM1077  KIAA1257  3'  AGGCGGGTGGATCACGAGGTCA 63390                A
                GG                  CCTGACCTCGTGATCCACCC CCT
                                    |||||||||||||||||| |||
                                    GGACTGGAGCACTAGGTGGG GGA
                                          C
GAM1077  KIAA1277  3'  AGGCAGGTGGATCACCTGAGGT 65068          __       CA
                CAGG                CCTGACCTC  GTGATCCACC  CCT
                                    |||||||||  ||||||||||  |||
                                    GGACTGGAG  CACTAGGTGG  GGA
                                       TC         AC
GAM1077  KIAA1328  3'  AGGCAGCCGGATCATGAGGTCA 62316              ACCCA
                GG                  CCTGACCTCGTGATCC    CCT
                                    ||||||||||||||||    |||
                                    GGACTGGAGTACTAGG    GGA
                                          CCGAC
GAM1077  KIAA1348  3'  AGGCGGATGGATCACCTGAGGT 69118          __      C  A
                CGGG                CCTGACCTC  GTGATCCA CC CCT
                                    |||||||||  |||||||| || |||
                                    GGGCTGGAG  CACTAGGT GG GGA
                                       TC       A  C
GAM1077  KIAA1404  3'  AGGCAGGCGGATCACGAGGTCA 62681              A  CA
                GG                  CCTGACCTCGTGATCC CC  CCT
                                    |||||||||||||||| ||  |||
                                    GGACTGGAGCACTAGG GG  GGA
                                          C  AC
GAM1077  KIAA1456  5'  AGGCAGGCGGATCACCTGAGGT 67530       __     A  CA
                                    ACCTC  GTGATCC CC  CCT
                                    |||||  ||||||| ||  |||
                                    TGGAG  CACTAGG GG  GGA
                                      TC      C  AC
GAM1077  KIAA1456  3'  AGGTGGGTGGATCAGCTGAGGT 67532          __
                CAGG                CCTGACCTCG  TGATCCACCCACCT
                                    ||||||||||  ||||||||||||||
                                    GGACTGGAGT  ACTAGGTGGGTGGA
                                       CG
GAM1077  KIAA1473  3'  AGGTGGGTAGATCACCTGAGGT 71204          __     C
                CGGG                CCTGACCTC  GTGATC ACCCACCT
                                    |||||||||  ||||||  ||||||||
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                                GGGCTGGAG  CACTAG TGGGTGGA
                                    TC     A
GAM1077  KIAA1486  3'  AGGTGGGTGGATCACAAGGTCA 67968        C
             GG                   CCTGACCT GTGATCCACCCACCT
                                  |||||||| ||||||||||||||
                                  GGACTGGA CACTAGGTGGGTGGA
                                      A
GAM1077  KIAA1508  3'  AGGTGGGTGGATCACAAGGTCG 62540        C
             GG                   CCTGACCT GTGATCCACCCACCT
                                  |||||||| ||||||||||||||
                                  GGGCTGGA CACTAGGTGGGTGGA
                                      A
GAM1077  KIAA1559  3'  AGGTGGGTGGATCACTTGAGG  73445     __
                                  CCTC  GTGATCCACCCACCT
                                  ||||  ||||||||||||||
                                  GGAG  CACTAGGTGGGTGGA
                                    TT
GAM1077  KIAA1674  3'  AGGCGAGTGGATCACGAGGTCA 69329             CCA
             GG                   CCTGACCTCGTGATCCAC   CCT
                                  |||||||||||||||||   |||
                                  GGACTGGAGCACTAGGTG   GGA
                                           AGC
GAM1077  KIAA1715  3'  AGGCGGGCAGATCATCTGGGGT 68681        __    CA   A
             CAGG                 CCTGACCTC  GTGATC  CCC CCT
                                  |||||||||  ||||||  ||| |||
                                  GGACTGGGG  TACTAG  GGG GGA
                                      TC     AC   C
GAM1077  KIAA1811  5'  AGGTGGGCAAATCACAAGGTCA 65416        C    CCA
             GG                   CCTGACCT GTGAT   CCCACCT
                                  |||||||| |||||   |||||||
                                  GGACTGGA CACTA   GGGTGGA
                                      A     AAC
GAM1077  KIAA1829  3'  AGGTGGGCAGATCACCTGAGGT 62631        __    CA
             CAGG                 CCTGACCTC  GTGATC  CCCACCT
                                  |||||||||  ||||||  |||||||
                                  GGACTGGAG  CACTAG  GGGTGGA
                                      TC     AC
GAM1077  KIAA1841  3'  AGGCGGGCAGATCACCTGAGGT 80847        __    CA   A
             CAGG                 CCTGACCTC  GTGATC  CCC CCT
                                  |||||||||  ||||||  ||| |||
                                  GGACTGGAG  CACTAG  GGG GGA
                                      TC     AC   C
GAM1077  KIAA1871  3'  CTAGGTGGGCAGATCACGAGGT 61900          CA    ___
             CA                    TGACCTCGTGATC  CCCACCT   AG
                                   ||||||||||||  |||||||  ||
                                   ACTGGAGCACTAG  GGGTGGA   TC
                                         AC     ___
GAM1077  KIAA1872  3'  AGGTGGGTGGATCACCTGAGGT 63595        __
             CAGG                 CCTGACCTC  GTGATCCACCCACCT
                                  |||||||||  ||||||||||||||
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                                GGACTGGAG  CACTAGGTGGGTGGA
                                     TC
GAM1077  KIAA1872  3'  GGTGGATCACCTGAGGTCAGG  63615        __
                                CCTGACCTC  GTGATCCACC
                                |||||||||  ||||||||||
                                GGACTGGAG  CACTAGGTGG
                                     TC
GAM1077  KIAA1941  3'  AGGTGGGCGGATCACAAGGTCA 75333        C      A
              GG                  CCTGACCT GTGATCC CCCACCT
                                  |||||||| ||||||| |||||||
                                  GGACTGGA CACTAGG GGGTGGA
                                       A      C
GAM1077  KIAA1948  3'  AGGCAGGTGGATCGTGAGGTCA 83292              CA
              GG                  CCTGACCTCGTGATCCACC  CCT
                                  ||||||||||||||||||  |||
                                  GGACTGGAGTGCTAGGTGG  GGA
                                            AC
GAM1077  KIAA1951  3'  AGGCGGGCAGATCACGAGGTCA 74145            CA   A
              GG                  CCTGACCTCGTGATC  CCC CCT
                                  ||||||||||||||  ||| |||
                                  GGACTGGAGCACTAG  GGG GGA
                                         AC   C
GAM1077  KIAA1958  3'  AGGTGGGCAGATCACTTGAGGT 82775        __     CA
              CAGG                  CCTGACCTC  GTGATC  CCCACCT
                                    |||||||||  ||||||  |||||||
                                    GGACTGGAG  CACTAG  GGGTGGA
                                         TT      AC
GAM1077  KIAA1969  3'  AGGTGGGTGGATCACAAGGTCA 79472       C
                                TGACCT GTGATCCACCCACCT
                                ||||||  ||||||||||||||
                                ACTGGA CACTAGGTGGGTGGA
                                   A
GAM1077  KIAA1979  3'  AGGTGGGTAAATCACTTGAGGT 89648        __    CC
              CAGG                  CCTGACCTC  GTGAT  ACCCACCT
                                    |||||||||  |||||  ||||||||
                                    GGACTGGAG  CACTA  TGGGTGGA
                                         TT     AA
GAM1077  KLHL8    3'  AGGTGGGTGGACCACCTGAG   63505    __  A
                                CTC  GTG TCCACCCACCT
                                |||  ||| ||||||||||
                                GAG  CAC AGGTGGGTGGA
                                  TC   C
GAM1077  KR18     3'  AGGCAGGTGGATCACCTGAGGT 53880        __       CA
              CGGG                  CCTGACCTC  GTGATCCACC  CCT
                                    |||||||||  ||||||||||  |||
                                    GGGCTGGAG  CACTAGGTGG  GGA
                                         TC         AC
GAM1077  LAP1B    3'  AGGCAGGTGGATCACCTGAGGT 65187        __       CA
              CAG                   CTGACCTC  GTGATCCACC  CCT
                                    ||||||||  ||||||||||  |||
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                                GACTGGAG  CACTAGGTGG  GGA
                                    TC         AC
GAM1077  LHPP     5'  AGGCAGGTGGATCACGAGGTCA 42357                CA
                GG                    CCTGACCTCGTGATCCACC  CCT
                                      ||||||||||||||||||  |||
                                      GGACTGGAGCACTAGGTGG  GGA
                                            AC
GAM1077  LIAS     3'  AGGCGGGTGGATCACCTGAGGT 71163          __         A
                CAGG                    CCTGACCTC  GTGATCCACCC CCT
                                        |||||||||  |||||||||| |||
                                        GGACTGGAG  CACTAGGTGGG GGA
                                            TC          C
GAM1077  LIM      3'  AGGTGGGTGGACCACATGAGGT 22314           A__
                CAGG                    CCTGACCTCGTG   TCCACCCACCT
                                        ||||||||||||   ||||||||||
                                        GGACTGGAGTAC   AGGTGGGTGGA
                                              ACC
GAM1077  LIM      3'  GGGCGGATCATGAGGTCA    22332             A
                                        TGACCTCGTGATCC CCC
                                        |||||||||||||| |||
                                        ACTGGAGTACTAGG GGG
                                              C
GAM1077  LRG      3'  AGGTGGGCGGATCACGAAGTCA 54813       C       A
                GG                    CCTGAC TCGTGATCC CCCACCT
                                      ||||||  |||||||||  |||||||
                                      GGACTG AGCACTAGG GGGTGGA
                                         A        C
GAM1077  LRRFIP1   3'  AGGCAGGTGGATCACCTGAGGT 17607        __        CA
                CA                    TGACCTC  GTGATCCACC  CCT
                                      |||||||  ||||||||||  |||
                                      ACTGGAG  CACTAGGTGG  GGA
                                         TC         AC
GAM1077  LSR68    3'  AGGCGGGTGGACCACCTGAGGT 38548          __  A      A
                CAGG                    CCTGACCTC  GTG TCCACCC CCT
                                        |||||||||  |||  |||||||  |||
                                        GGACTGGAG  CAC AGGTGGG GGA
                                             TC   C      C
GAM1077  LYSAL1   3'  AGGCGGGCGGATCATGAGGTCA 18120              A  A
                GG                    CCTGACCTCGTGATCC CCC CCT
                                      ||||||||||||||||  |||  |||
                                      GGACTGGAGTACTAGG GGG GGA
                                              C   C
GAM1077  MACF1    3'  AGGCAGGCGGATCACGAAGTCA 53492       C       A  CA
                GG                    CCTGAC TCGTGATCC CC  CCT
                                      ||||||  |||||||||  ||  |||
                                      GGACTG AGCACTAGG GG  GGA
                                         A        C  AC
GAM1077  MAWBP    3'  AGGTGGGTGGATCACCTGAGGT 42376          __
                CAGG                    CCTGACCTC  GTGATCCACCCACCT
                                        |||||||||  ||||||||||||||||
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                                GGACTGGAG  CACTAGGTGGGTGGA
                                     TC
GAM1077  MED6     3'  AGGCAGGTGGATCACCTGAG   19610     __        CA
                                CTC  GTGATCCACC  CCT
                                |||  ||||||||||  |||
                                GAG  CACTAGGTGG  GGA
                                  TC         AC
GAM1077  MESDC2   3'  AGGTGGGTGGATCAGTTGAGGT 72907          __
            CAGG                    CCTGACCTCG  TGATCCACCCACCT
                                |||||||||  ||||||||||||||
                                GGACTGGAGT  ACTAGGTGGGTGGA
                                     TG
GAM1077  MGC10765 3'  AGGTGGGTGGATCACAAGGTCA 44553         C
            GG                    CCTGACCT GTGATCCACCCACCT
                                |||||||| ||||||||||||||
                                GGACTGGA CACTAGGTGGGTGGA
                                     A
GAM1077  MGC10771 3'  GGGTGGATTACCTGAGGTCAGG 44715          __
                                CCTGACCTC  GTGATCCACCC
                                |||||||||  ||||||||||
                                GGACTGGAG  CATTAGGTGGG
                                     TC
GAM1077  MGC10814 5'  AGGTGGGTGGATCACCTGAGGT 52012          __
            CAGG                    CCTGACCTC  GTGATCCACCCACCT
                                |||||||||  ||||||||||||||
                                GGACTGGAG  CACTAGGTGGGTGGA
                                     TC
GAM1077  MGC10999 3'  AGGCGGGTGGATCATCTGAGGT 51189          __         A
            CAGG                    CCTGACCTC  GTGATCCACCC CCT
                                |||||||||  |||||||||| |||
                                GGACTGGAG  TACTAGGTGGG GGA
                                     TC         C
GAM1077  MGC11287 5'  AGGCAGACGGATCACTTGAGGT 49610          __      ACCCA
            CAGG                    CCTGACCTC  GTGATCC    CCT
                                |||||||||  |||||||    |||
                                GGACTGGAG  CACTAGG    GGA
                                     TT      CAGAC
GAM1077  MGC13017 3'  AGGTGAGCAGATCACCTGAGGT 55569          __     CACC
            TAGG                    CCTGACCTC  GTGATC    CACCT
                                |||||||||  ||||||   |||||
                                GGATTGGAG  CACTAG    GTGGA
                                     TC     ACGA
GAM1077  MGC13053 3'  AGGCAGGCGGATCATGAGGTCA 52095              A  CA
            GG                    CCTGACCTCGTGATCC CC  CCT
                                |||||||||||||||| ||  |||
                                GGACTGGAGTACTAGG GG  GGA
                                       C  AC
GAM1077  MGC14126 3'  AGGCGGGTGGATCACCTAAGGT 52936         C__         A
            CAGG                    CCTGACCT   GTGATCCACCC CCT
                                ||||||||   |||||||||| |||
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                                GGACTGGA  CACTAGGTGGG GGA
                                    ATC        C
GAM1077 MGC14407 3' AGGTGGGTGGATCACTTGAGG 52968    __
                                CCTC GTGATCCACCCACCT
                                |||| ||||||||||||||
                                GGAG CACTAGGTGGGTGGA
                                  TT
GAM1077 MGC14799 3' AGGCGGGCGGATCATGAGGTCA 51323           A  A
           GG                    CCTGACCTCGTGATCC CCC CCT
                                ||||||||||||||| ||| |||
                                GGACTGGAGTACTAGG GGG GGA
                                        C  C
GAM1077 MGC14817 3' AGGCAGGTGGATCACGAGGTCA 51335            CA
           G                     CTGACCTCGTGATCCACC  CCT
                                |||||||||||||||||  |||
                                GACTGGAGCACTAGGTGG  GGA
                                      AC
GAM1077 MGC15397 3' AGGCCGGTGATTCACAAGGTCA 55549       C   TC   CA
           GG                    CCTGACCT GTGA  CACC  CCT
                                |||||||| ||||  ||||  |||
                                GGACTGGA CACT  GTGG  GGA
                                    A   TA   CC
GAM1077 MGC16385 3' GGGCGGATCACCTGAGGTCAGG 59541        __     A
                                CCTGACCTC  GTGATCC CCC
                                |||||||||  ||||||| |||
                                GGACTGGAG  CACTAGG GGG
                                     TC      C
GAM1077 MGC16703 3' AGGCAGGCAGATCACGAGGTCA 73486           CA  CA
           GG                    CCTGACCTCGTGATC  CC  CCT
                                ||||||||||||||  ||  |||
                                GGACTGGAGCACTAG  GG  GGA
                                       AC  AC
GAM1077 MGC20235 3' GTGGGTGGATCGCTTGAGG   59560    __
                                CCTC  GTGATCCACCCAC
                                ||||  ||||||||||||
                                GGAG  CGCTAGGTGGGTG
                                  TT
GAM1077 MGC20496 3' AGGCAGGCAGATCACCTGAGGT 54528        __    CA  CA
           CAGG                   CCTGACCTC  GTGATC  CC  CCT
                                |||||||||  ||||||  ||  |||
                                GGACTGGAG  CACTAG  GG  GGA
                                     TC     AC  AC
GAM1077 MGC23244 3' AGGCGGGTGGAACACTTGAGGT 58826        __  A     A
           CAGG                   CCTGACCTC  GTG TCCACCC CCT
                                |||||||||  ||| ||||||| |||
                                GGACTGGAG  CAC AGGTGGG GGA
                                     TT  A     C
GAM1077 MGC2562  3' AGGCGGGTGGATCACTTGAG  51419    __        A
                                CTC  GTGATCCACCC CCT
                                |||  |||||||||| |||
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                                GAG  CACTAGGTGGG GGA
                                  TT         C
GAM1077  MGC2562   3'  AGGTGGGCAGATCATGAGGTCA 51420              CA
                GG                  CCTGACCTCGTGATC  CCCACCT
                                    ||||||||||||||  |||||||
                                    GGACTGGAGTACTAG  GGGTGGA
                                           AC
GAM1077  MGC2562   3'  AGGTGGGCGGATCACCTGAGGT 51421         __      A
                CAG                   CTGACCTC  GTGATCC CCCACCT
                                      ||||||||  |||||||  |||||||
                                      GACTGGAG  CACTAGG GGGTGGA
                                          TC       C
GAM1077  MGC2663   3'  AGGTGGGTGGATCACTTGAGGT 44328         __
                CAGG                  CCTGACCTC  GTGATCCACCCACCT
                                      |||||||||  ||||||||||||||
                                      GGACTGGAG  CACTAGGTGGGTGGA
                                          TT
GAM1077  MGC26641  3'  GGTGGACCATGAGGTCAGG    59325           A
                                      CCTGACCTCGTG TCCACC
                                      ||||||||||| ||||||
                                      GGACTGGAGTAC AGGTGG
                                             C
GAM1077  MGC2731   3'  AGGTGGGCGGATCACCTGAGGT 44159         __      A
                CGGG                  CCTGACCTC  GTGATCC CCCACCT
                                      |||||||||  |||||||  |||||||
                                      GGGCTGGAG  CACTAGG GGGTGGA
                                          TC       C
GAM1077  MGC29891  3'  AGGCGGGCGGATCACGAGGTCA 58848              A   A
                G                     CTGACCTCGTGATCC CCC CCT
                                      ||||||||||||||| ||| |||
                                      GACTGGAGCACTAGG GGG GGA
                                             C   C
GAM1077  MGC3169   3'  AGGCGGGCAGATCACCTGAGGT 44181         __     CA   A
                CAGG                  CCTGACCTC  GTGATC  CCC CCT
                                      |||||||||  ||||||  ||| |||
                                      GGACTGGAG  CACTAG  GGG GGA
                                          TC      AC   C
GAM1077  MGC3207   3'  AGGCAGGTGGATCACAAGATCA 63231       C  C         CA
                GG                    CCTGA CT GTGATCCACC  CCT
                                      ||||| || ||||||||||  |||
                                      GGACT GA CACTAGGTGG  GGA
                                        A  A         AC
GAM1077  MGC39350  3'  AGGCGGGCGGATCACCTGAGGT 59315         __      A   A
                CAGG                  CCTGACCTC  GTGATCC CCC CCT
                                      |||||||||  |||||||  ||| |||
                                      GGACTGGAG  CACTAGG GGG GGA
                                          TC       C   C
GAM1077  MGC4562   3'  AGGCGGGCGGATCACGAGGTCA 56732              A   A
                GG                    CCTGACCTCGTGATCC CCC CCT
                                      |||||||||||||||  ||| |||
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                                GGACTGGAGCACTAGG GGG GGA
                                      C   C
GAM1077  MGC4663   3'  AGGCGGGCGGATCACGAAATCA 44781      CC       A   A
              GG                 CCTGA  TCGTGATCC CCC CCT
                                 |||||  ||||||||| ||| |||
                                 GGACT  AGCACTAGG GGG GGA
                                   AA       C   C
GAM1077  MGC4771   3'  AGGTGAGTGGATCACGAGGTCA 51999              C
              GG                 CCTGACCTCGTGATCCAC CACCT
                                 ||||||||||||||||| |||||
                                 GGACTGGAGCACTAGGTG GTGGA
                                       A
GAM1077  MGC4771   3'  GGTGGGTGGATGCCGAGG    52005      TG
                                 CCTCG  ATCCACCCACC
                                 |||||  ||||||||||
                                 GGAGC  TAGGTGGGTGG
                                   CG
GAM1077  MGC5254   3'  AGGTGGGTGGATCATGAGGTCA 51387
              GG                 CCTGACCTCGTGATCCACCCACCT
                                 ||||||||||||||||||||||||
                                 GGACTGGAGTACTAGGTGGGTGGA

GAM1077  MGC5384   3'  AGGCAGGCAGATCACGGGGTCA 49087            CA  CA
              GG                 CCTGACCTCGTGATC  CC  CCT
                                 |||||||||||||||  ||  |||
                                 GGACTGGGGCACTAG  GG  GGA
                                       AC  AC
GAM1077  MGC5457   3'  AGGAAGGCAAATCACAAGGTCA 51935        C    CCA  CA
              GG                 CCTGACCT GTGAT   CC  CCT
                                 ||||||||| |||||   ||  |||
                                 GGACTGGA CACTA   GG  GGA
                                    A     AAC  AA
GAM1077  MOST2     5'  AGGCAGGCAGATCACTTGAGGT 40051          __     CA  CA
              CAGG                  CCTGACCTC  GTGATC  CC  CCT
                                    |||||||||  ||||||  ||  |||
                                    GGACTGGAG  CACTAG  GG  GGA
                                       TT      AC  AC
GAM1077  MRP63     3'  AGGCGGGCGGATCACTTGAGGT 44042          __      A   A
              CAGG                  CCTGACCTC  GTGATCC CCC CCT
                                    |||||||||  |||||||  ||| |||
                                    GGACTGGAG  CACTAGG GGG GGA
                                       TT      C   C
GAM1077  MRPL48    5'  AGGCGGGCGGATCACCTGAGGT 32654          __      A   A
              CGGG                  CCTGACCTC  GTGATCC CCC CCT
                                    |||||||||  |||||||  ||| |||
                                    GGGCTGGAG  CACTAGG GGG GGA
                                       TC      C   C
GAM1077  MRPL56    3'  AGGTGGGTGGATCACCTGAGGT 52751          __
              CAGG                  CCTGACCTC  GTGATCCACCCACCT
                                    |||||||||  ||||||||||||||
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                                GGACTGGAG  CACTAGGTGGGTGGA
                                     TC
GAM1077  MRPS10   3'  AGGCAGGCGGATCACGAGGTCA 36812            A  CA
                                TGACCTCGTGATCC CC  CCT
                                |||||||||||||| ||  |||
                                ACTGGAGCACTAGG GG  GGA
                                     C  AC
GAM1077  My015    3'  GGCGGATCACCTGAGGTCAGG  67233          __     A
                                CCTGACCTC  GTGATCC CC
                                |||||||||  ||||||| ||
                                GGACTGGAG  CACTAGG GG
                                     TC      C
GAM1077  MYO3B    3'  AGATGGGCGGATCATGAAGTCA 58106       C       A   C
           GG                     CCTGAC TCGTGATCC CCCA CT
                                |||||| ||||||||| |||| ||
                                GGACTG AGTACTAGG GGGT GA
                                   A        C   A
GAM1077  N4BP2    3'  AGGTAGGTGGATCGCCTGAGGT 36934          __       C
           CAG                    CTGACCTC  GTGATCCACC ACCT
                                ||||||||  |||||||||| ||||
                                GACTGGAG  CGCTAGGTGG TGGA
                                     TC         A
GAM1077  NMNAT    3'  GTGGGTGGATCACGTGAGGTCA 43291        __
                                TGACCTC  GTGATCCACCCAC
                                |||||||  ||||||||||||
                                ACTGGAG  CACTAGGTGGGTG
                                   TG
GAM1077  NMT2     3'  AGGTGGGCAGATCATGAGGTCA 17851            CA
           GG                     CCTGACCTCGTGATC  CCCACCT
                                ||||||||||||||  |||||||
                                GGACTGGAGTACTAG  GGGTGGA
                                      AC
GAM1077  NPTXR    3'  GGCAGATCACTTGAGGTCAGG  55213          __     CA
                                CCTGACCTC  GTGATC  CC
                                |||||||||  ||||||  ||
                                GGACTGGAG  CACTAG  GG
                                     TT      AC
GAM1077  NPTXR    3'  GGTAGACATCCGCGAGGTCAG  55216           A___  C
                                CTGACCTCGTG    TC ACC
                                ||||||||||    || |||
                                GACTGGAGCGC    AG TGG
                                      CTAC  A
GAM1077  NPTXR    3'  GGCAGATCACTTGAGGTCAGG  27439          __     CA
                                CCTGACCTC  GTGATC  CC
                                |||||||||  ||||||  ||
                                GGACTGGAG  CACTAG  GG
                                     TT      AC
GAM1077  NPTXR    3'  GGTAGACATCCGCGAGGTCAG  27442           A___  C
                                CTGACCTCGTG    TC ACC
                                ||||||||||    || |||
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                                GACTGGAGCGC   AG TGG
                                     CTAC  A
GAM1077  OCLM     5'  AGGTGGGTGGATCATCTGAGGT 42584          __
              CAGG                  CCTGACCTC  GTGATCCACCCACCT
                                    |||||||||  ||||||||||||||
                                    GGACTGGAG  TACTAGGTGGGTGGA
                                       TC
GAM1077  ORC6L    3'  AGGTGGGTGGATCACCTGAGGT 27487          __
              CAGG                  CCTGACCTC  GTGATCCACCCACCT
                                    |||||||||  ||||||||||||||
                                    GGACTGGAG  CACTAGGTGGGTGGA
                                       TC
GAM1077  OS-9     3'  AGGTGGGTAGAGAGAGCAAGG  23318     GAC   GTGA  C
                                    CCT   CTC    TC ACCCACCT
                                    |||   |||    || ||||||||
                                    GGA   GAG    AG TGGGTGGA
                                      AC_   AG__  A
GAM1077  PB1      3'  AGATGGGTGGATTACCTGAGGT 37572          __          C
              CAGG                  CCTGACCTC  GTGATCCACCCA CT
                                    |||||||||  |||||||||||| ||
                                    GGACTGGAG  CATTAGGTGGGT GA
                                       TC          A
GAM1077  PB1      3'  AGGCGGGCAGATCACGAGATCA 37573       C        CA   A
              GG                    CCTGA CTCGTGATC  CCC CCT
                                    ||||| |||||||||  ||| |||
                                    GGACT GAGCACTAG  GGG GGA
                                       A        AC   C
GAM1077  PDCD7    3'  AGGCGGGCCGATCACGAGGTCA 72597             CA   A
              GG                    CCTGACCTCGTGATC  CCC CCT
                                    ||||||||||||||  ||| |||
                                    GGACTGGAGCACTAG  GGG GGA
                                             CC   C
GAM1077  phorbolin-1 3'  AGGCGGGTGGATCACGAGGTCA 90204                A
              GG                    CCTGACCTCGTGATCCACCC CCT
                                    |||||||||||||||||| |||
                                    GGACTGGAGCACTAGGTGGG GGA
                                               C
GAM1077  PHYHIP   3'  AGGTGGGTAGCCCAGGTTCAGG 29287       _  CGTGATCC
                                    CCTGA CCT       ACCCACCT
                                    ||||| |||       ||||||||
                                    GGACT GGA       TGGGTGGA
                                       T   CCCGA___
GAM1077  PIP5K1C  3'  GGCAGGGGCAGAGGTCAG    71306        G  AT  A  CA
                                    CTGACCTC TG  CC CC  CC
                                    |||||||| ||  || ||  ||
                                    GACTGGAG AC  GG GG  GG
                                         _  __  _  AC
GAM1077  PIWIL2   3'  AGGCGGGTGGATCATGAGGTCA 36539                A
              GG                    CCTGACCTCGTGATCCACCC CCT
                                    |||||||||||||||||| |||
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                                GGACTGGAGTACTAGGTGGG GGA
                                      C
GAM1077 PNPASE   3' AGGCAGGCGGATCATGAGATCA 71436      C       A  CA
           GG                   CCTGA CTCGTGATCC CC  CCT
                                ||||| |||||||||| ||  |||
                                GGACT GAGTACTAGG GG  GGA
                                  A        C  AC
GAM1077 POLYDOM  3' AGGAGGGTGGATCACGAGGTCA 44683              A
           GG                   CCTGACCTCGTGATCCACCC CCT
                                |||||||||||||||||||| |||
                                GGACTGGAGCACTAGGTGGG GGA
                                      A
GAM1077 PPP1R3B  3' AGGCAGGTGGATCACGAGGTCA 45130              CA
           GG                   CCTGACCTCGTGATCCACC  CCT
                                |||||||||||||||||||  |||
                                GGACTGGAGCACTAGGTGG  GGA
                                      AC
GAM1077 PPP1R3B  3' AGGCGGGCAGCTCACCTGAGGT 45131        __   TCCA  A
           CAGG                   CCTGACCTC  GTGA   CCC CCT
                                |||||||||  ||||   ||| |||
                                GGACTGGAG  CACT   GGG GGA
                                     TC   CGAC  C
GAM1077 PRIC285  3' AGGCGGGCAGATCACCTGAGGT 62107        __    CA  A
           CAGG                   CCTGACCTC  GTGATC  CCC CCT
                                |||||||||  ||||||  ||| |||
                                GGACTGGAG  CACTAG  GGG GGA
                                     TC     AC  C
GAM1077 PRO0255  3' AGGCGGGCAGATCACCTGAGGT 26964       __    CA  A
           CA                     TGACCTC  GTGATC  CCC CCT
                                |||||||  ||||||  ||| |||
                                ACTGGAG  CACTAG  GGG GGA
                                     TC     AC  C
GAM1077 PRO0456  3' AGGTGGATGGATCACCTGAG  27003    __     C
                                CTC  GTGATCCA CCACCT
                                |||  |||||||| ||||||
                                GAG  CACTAGGT GGTGGA
                                  TC       A
GAM1077 PRO0478  3' AGGCGGGCAGATCATGAGGTCA 27017            CA  A
           GG                   CCTGACCTCGTGATC  CCC CCT
                                ||||||||||||||  ||| |||
                                GGACTGGAGTACTAG  GGG GGA
                                       AC  C
GAM1077 PRO0478  5' AGGTGAGCAGATCACCTGAGGT 27018        __    CACC
           CAGG                   CCTGACCTC  GTGATC   CACCT
                                |||||||||  ||||||   |||||
                                GGACTGGAG  CACTAG   GTGGA
                                     TC     ACGA
GAM1077 PRO0618  3' AGGCGGGAAGATCACAAGGTCA 27045       C    CA  A
           GG                   CCTGACCT GTGATC  CCC CCT
                                |||||||| ||||||  ||| |||
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                                GGACTGGA CACTAG  GGG GGA
                                   A     AA  C
GAM1077  PRO0628  3'  AGGCTGGTGGATCACGAGGTCA 27060                CA
                GG                  CCTGACCTCGTGATCCACC  CCT
                                    ||||||||||||||||||  |||
                                    GGACTGGAGCACTAGGTGG  GGA
                                       TC
GAM1077  PRO1048  3'  AGGCGGGCGGATCATGAGGTCA 38103              A  A
                GG                  CCTGACCTCGTGATCC CCC CCT
                                    |||||||||||||||| ||| |||
                                    GGACTGGAGTACTAGG GGG GGA
                                       C  C
GAM1077  PRO2198  5'  AGGTGGGTGGATCACTTGAGGT 38404          __
                CAGG                  CCTGACCTC  GTGATCCACCCACCT
                                    |||||||||  ||||||||||||||||
                                    GGACTGGAG  CACTAGGTGGGTGGA
                                       TT
GAM1077  PRO2266  3'  GGCAGGTAGGCAAGGTAGG   38185     A  CG  A  C  CA
                                    CCTG CCT  TG TC ACC  CC
                                    ||||  |||  || || |||  ||
                                    GGAT GGA  AC GG TGG  GG
                                      _  __  _  A  AC
GAM1077  PRO2730  3'  AGGCGGGCGGATCACCGGAGGT 48178          __      A  A
                CGGG                  CCTGACCTC  GTGATCC CCC CCT
                                    |||||||||  |||||||  ||| |||
                                    GGGCTGGAG  CACTAGG GGG GGA
                                       GC      C  C
GAM1077  PRO2859  3'  AGGTGGGCAGATCACCTGAGGT 38207          __     CA
                CAG                   CTGACCTC  GTGATC  CCCACCT
                                    ||||||||  ||||||  |||||||
                                    GACTGGAG  CACTAG  GGGTGGA
                                       TC     AC
GAM1077  PRO2893  3'  AGGCGGGCGGATCATCTGAGGT 38428          __     A  A
                CAGG                  CCTGACCTC  GTGATCC CCC CCT
                                    |||||||||  |||||||  ||| |||
                                    GGACTGGAG  TACTAGG GGG GGA
                                       TC      C  C
GAM1077  PRO2949  3'  GGGCGGATCACGAGGTCAGG   38225              A
                                    CCTGACCTCGTGATCC CCC
                                    ||||||||||||||| |||
                                    GGACTGGAGCACTAGG GGG
                                       C
GAM1077  PRO2964  3'  AGGCTGGCGGATCATGAGGTCA 38252              A  CA
                GG                  CCTGACCTCGTGATCC CC  CCT
                                    |||||||||||||||  ||  |||
                                    GGACTGGAGTACTAGG GG  GGA
                                       C  TC
GAM1077  PSK      5'  GGACTGGACCGCGAGGTCAG  32879          A   C_
                                    CTGACCTCGTG TCCA  CC
                                    ||||||||||| ||||  ||
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                                GACTGGAGCGC AGGT  GG
                                      C    CA
GAM1077  PTK6     3'  AGGCAGGTGGATCACGAGGTCA 21067                CA
                 GG                  CCTGACCTCGTGATCCACC  CCT
                                     ||||||||||||||||||  |||
                                     GGACTGGAGCACTAGGTGG  GGA
                                           AC
GAM1077  PTRF     3'  AGGTGGGCGGATCACCTGAGGT 64232          __     A
                 CAGG                 CCTGACCTC  GTGATCC CCCACCT
                                     |||||||||  |||||||  |||||||
                                     GGACTGGAG  CACTAGG GGGTGGA
                                          TC      C
GAM1077  PXMP4    3'  AGGCAGGTGGATCACTTGAG   24330     __        CA
                                     CTC  GTGATCCACC  CCT
                                     |||  ||||||||||  |||
                                     GAG  CACTAGGTGG  GGA
                                       TT         AC
GAM1077  RAB4B    5'  AGGCAGGCGGATCACCTGAGGT 32898          __      A  CA
                 CGGG                 CCTGACCTC  GTGATCC CC  CCT
                                     |||||||||  |||||||  ||  |||
                                     GGGCTGGAG  CACTAGG GG  GGA
                                          TC      C  AC
GAM1077  RAD51    3'  AGGCAGGTGGATCGCTTGAGCC 12744     AC  __        CA
                 AG                   CTG  CTC  GTGATCCACC  CCT
                                     |||  |||  ||||||||||  |||
                                     GAC  GAG  CGCTAGGTGG  GGA
                                       C_   TT         AC
GAM1077  RAD51    3'  AGGCAGGTGGATCGCTTGAGCC 56828     AC  __        CA
                 AG                   CTG  CTC  GTGATCCACC  CCT
                                     |||  |||  ||||||||||  |||
                                     GAC  GAG  CGCTAGGTGG  GGA
                                       C_   TT         AC
GAM1077  RBM14    3'  AGGTGGGTAGGGTTACAGATCC 21990     AC_  C      _
                 AG                   CTG   CT GTGATCC ACCCACCT
                                     |||   ||  |||||||  ||||||||
                                     GAC   GA CATTGGG TGGGTGGA
                                       CTA  _       A
GAM1077  RNO2     3'  AGGCAGGTGGATCACGAGGTCA 53920                CA
                 GG                   CCTGACCTCGTGATCCACC  CCT
                                     ||||||||||||||||||  |||
                                     GGACTGGAGCACTAGGTGG  GGA
                                           AC
GAM1077  RNO2     5'  AGGCGGGCAGATCACTGAGGTC 53921          _     CA  A
                 AGG                   CCTGACCTC GTGATC  CCC CCT
                                     |||||||||  ||||||  |||  |||
                                     GGACTGGAG  CACTAG  GGG GGA
                                          T      AC   C
GAM1077  RoXaN    3'  AGGCGGGTGGATCACGAGGTCA 47272                 A
                 GG                   CCTGACCTCGTGATCCACCC CCT
                                     ||||||||||||||||||  |||
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                                GGACTGGAGCACTAGGTGGG GGA
                                      C
GAM1077 RRP4    3' AGGCGGGCAGATCACCTGAGGT 27353       __    CA  A
          CA                  TGACCTC  GTGATC  CCC CCT
                              |||||||  ||||||  ||| |||
                              ACTGGAG  CACTAG  GGG GGA
                                 TC     AC  C
GAM1077 SC65    3' AGGTGGGTGGATCACTTGAGG  22285     __
                              CCTC  GTGATCCACCCACCT
                              ||||  ||||||||||||||
                              GGAG  CACTAGGTGGGTGGA
                                TT
GAM1077 SCIN    3' AGGTAGGCGGATCACTGGGGTC 53597        _     A  C
          AGG                   CCTGACCTC GTGATCC CC ACCT
                              |||||||| ||||||| || ||||
                              GGACTGGGG CACTAGG GG TGGA
                                   T      C  A
GAM1077 SCN12A  3' AGGCAGGTGGATCACGAGGTCA 27077             CA
                              TGACCTCGTGATCCACC  CCT
                              ||||||||||||||||  |||
                              ACTGGAGCACTAGGTGG  GGA
                                        AC
GAM1077 SCYA5   3' AGGTGGGTGGATCACTTGAGGT 12958        __
          CAGG                  CCTGACCTC  GTGATCCACCCACCT
                              |||||||||  ||||||||||||||
                              GGACTGGAG  CACTAGGTGGGTGGA
                                   TT
GAM1077 SEF     3' AGGTGAAGCTCACGGGGCCAGG 69993     A      TCCACC
                              CCTG CCTCGTGA     CACCT
                              |||| ||||||||     |||||
                              GGAC GGGGCACT     GTGGA
                                C       CGAA__
GAM1077 SEMA3E  3' AGGCGGGTGGATCATGAGGTCA 25803               A
          GG                    CCTGACCTCGTGATCCACCC CCT
                              |||||||||||||||||| |||
                              GGACTGGAGTACTAGGTGGG GGA
                                        C
GAM1077 SGKL    3' AGGCGGGCAGATCACCTGAGGT 26053        __    CA  A
          CAGG                  CCTGACCTC  GTGATC  CCC CCT
                              |||||||||  ||||||  ||| |||
                              GGACTGGAG  CACTAG  GGG GGA
                                   TC     AC  C
GAM1077 SMA3    3' AGGCAGGCGGATCACTTGAGGT 23255        __     A  CA
          CAGG                  CCTGACCTC  GTGATCC CC  CCT
                              |||||||||  |||||||  ||  |||
                              GGACTGGAG  CACTAGG GG  GGA
                                   TT      C  AC
GAM1077 SMARCF1 3' AGGTGGGTGACCCAGGACAG  38038    A  CGTGATC
                              CTG CCT      CACCCACCT
                              ||| |||      |||||||||
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                                GAC GGA      GTGGGTGGA
                                  A  CCCA___
GAM1077  SNAPC1   3'  AGGTGGGCGGATCACGAGGTCA 13272              A
              GG                   CCTGACCTCGTGATCC CCCACCT
                                   |||||||||||||||| |||||||
                                   GGACTGGAGCACTAGG GGGTGGA
                                            C
GAM1077  SPRY4    3'  AGGCAGGTGGATCACGAGGTCA 48993               CA
              GG                   CCTGACCTCGTGATCCACC  CCT
                                   |||||||||||||||||||  |||
                                   GGACTGGAGCACTAGGTGG  GGA
                                            AC
GAM1077  SPRY4    3'  AGGTGGGTGGATCACGAGGTCA 48995
              GG                   CCTGACCTCGTGATCCACCCACCT
                                   ||||||||||||||||||||||||
                                   GGACTGGAGCACTAGGTGGGTGGA

GAM1077  SS18L1   3'  GGGCGGATCACCTGAGGTCGGG 65958          __      A
                                   CCTGACCTC  GTGATCC CCC
                                   |||||||||  ||||||| |||
                                   GGGCTGGAG  CACTAGG GGG
                                         TC       C
GAM1077  SUN1     3'  AGGCGGGTGGATCACTTGAGG  47908      __         A
                                   CCTC  GTGATCCACCC CCT
                                   ||||  |||||||||||| |||
                                   GGAG  CACTAGGTGGG GGA
                                     TT          C
GAM1077  SYAP1    3'  AGGTGGGCAGATCACCGGAGGT 52467          __     CA
              CAGG                   CCTGACCTC  GTGATC  CCCACCT
                                   |||||||||  ||||||  |||||||
                                   GGACTGGAG  CACTAG  GGGTGGA
                                         GC      AC
GAM1077  TA-LRRP  3'  AGATGGGCGGATTGCTTGAGGT 31707          __ TG    A    C
              CAGG                   CCTGACCTC  G  ATCC CCCA CT
                                   |||||||||  |  |||| |||| ||
                                   GGACTGGAG  C  TAGG GGGT GA
                                         TT GT    C    A
GAM1077  TACTILE  3'  AGGTGGGTGGATCACGAGGTCA 20581
              GG                   CCTGACCTCGTGATCCACCCACCT
                                   ||||||||||||||||||||||||
                                   GGACTGGAGCACTAGGTGGGTGGA

GAM1077  TAO1     5'  GGACTGGACCGCGAGGTCAG   17718          A    C_
                                   CTGACCTCGTG TCCA  CC
                                   |||||||||||  ||||  ||
                                   GACTGGAGCGC AGGT  GG
                                         C    CA
GAM1077  THEA     3'  AGGTGGGCAGATCACCTGAGGT 66872          __     CA
              CAGG                   CCTGACCTC  GTGATC  CCCACCT
                                   |||||||||  ||||||  |||||||
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                                GGACTGGAG  CACTAG  GGGTGGA
                                     TC     AC
GAM1077  TIP47    3'  AGGCGGGCGGAACACCTGAGGT 20600        __  A  A  A
              CAGG                   CCTGACCTC  GTG TCC CCC CCT
                                |||||||||  ||| ||| ||| |||
                                GGACTGGAG  CAC AGG GGG GGA
                                     TC  A  C  C
GAM1077  TRIAD3   3'  AGGCGGGCGGATGAGTTGAGGT 96129         TG__  A  A
              CGGG                   CCTGACCTCG   ATCC CCC CCT
                                |||||||||||   |||| ||| |||
                                GGGCTGGAGT   TAGG GGG GGA
                                      TGAG   C  C
GAM1077  TRIM38   3'  AGGCAGGTGGATCACTTGAGGT 22051         __       CA
              CAGG                   CCTGACCTC  GTGATCCACC  CCT
                                |||||||||  ||||||||||  |||
                                GGACTGGAG  CACTAGGTGG  GGA
                                     TT        AC
GAM1077  UBCE7IP5 3'  AGGTGGGTGGATCACTTGAGGT 30841        __
              CAGG                   CCTGACCTC  GTGATCCACCCACCT
                                |||||||||  ||||||||||||||||
                                GGACTGGAG  CACTAGGTGGGTGGA
                                     TT
GAM1077  ust3     3'  AGGCGGGCAGATCATGAGGTCA 94849            CA  A
              G                    CTGACCTCGTGATC  CCC CCT
                                ||||||||||||||  ||| |||
                                GACTGGAGTACTAG  GGG GGA
                                       AC  C
GAM1077  VIT1     5'  AGGTGGGTGGATCATTTGAGGT 38599        __
              CAGG                   CCTGACCTC  GTGATCCACCCACCT
                                |||||||||  ||||||||||||||||
                                GGACTGGAG  TACTAGGTGGGTGGA
                                     TT
GAM1077  WDR13    5'  AGATGGGTGGAGAATGTCA   35840     CTC  GA      C
                                TGAC   GT  TCCACCCA CT
                                ||||   ||  |||||||| ||
                                ACTG   TA  AGGTGGGT GA
                                  ___  AG       A
GAM1077  WSB1     3'  AGGCGGGCAAATCACCTGAGGT 56963        __    CCA  A
              CAG                    CTGACCTC  GTGAT   CCC CCT
                                |||||||  |||||   ||| |||
                                GACTGGAG  CACTA   GGG GGA
                                     TC    AAC  C
GAM1077  WSB1     3'  AGGCGGGCAAATCACCTGAGGT 56988        __    CCA  A
              CAG                    CTGACCTC  GTGAT   CCC CCT
                                |||||||  |||||   ||| |||
                                GACTGGAG  CACTA   GGG GGA
                                     TC    AAC  C
GAM1077  YME1L1   3'  AGGCGGGCAAATCACCTGAGGT 58423        __    CCA  A
              CA                     TGACCTC  GTGAT   CCC CCT
                                |||||||  |||||   ||| |||
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                                ACTGGAG  CACTA   GGG GGA
                                   TC    AAC   C
GAM1077  YME1L1    3'  AGGCGGGCAAATCACCTGAGGT 27317       __    CCA   A
            CA                   TGACCTC  GTGAT   CCC CCT
                                |||||||  |||||   ||| |||
                                ACTGGAG  CACTA   GGG GGA
                                   TC    AAC   C
GAM1077  ZFD25     3'  AGGTGGGTGGATCACCTGAGG  33105     __
                                CCTC  GTGATCCACCCACCT
                                ||||  ||||||||||||||
                                GGAG  CACTAGGTGGGTGGA
                                  TC
GAM1077  ZFP106    3'  AGGCGGGTGGATCACTCAAGGT 42713        C__        A
            CAGG                   CCTGACCT   GTGATCCACCC CCT
                                |||||||   |||||||||| |||
                                GGACTGGA   CACTAGGTGGG GGA
                                    ACT         C
GAM1077  ZNF197    3'  GTGGATCACCTGAGGTCAGG   23758         __
                                CCTGACCTC  GTGATCCAC
                                |||||||||  |||||||||
                                GGACTGGAG  CACTAGGTG
                                    TC
GAM1077  ZNF297B   3'  AGATGGGTGGATCACCTGAGGT 26640          __         C
            CAGG                   CCTGACCTC  GTGATCCACCCA CT
                                |||||||||  |||||||||||| ||
                                GGACTGGAG  CACTAGGTGGGT GA
                                    TC          A
GAM1077  ZNF297B   5'  AGGTGGGTGGATCATGCGGTCA 26642        T
            GG                   CCTGACC CGTGATCCACCCACCT
                                |||||||  ||||||||||||||||
                                GGACTGG GTACTAGGTGGGTGGA
                                   C
GAM1077  ZNF33A    3'  AGGCGGGTGGATCACAAGGTCA 92991         C         A
            GG                   CCTGACCT GTGATCCACCC CCT
                                |||||||| |||||||||| |||
                                GGACTGGA CACTAGGTGGG GGA
                                    A          C
GAM1077  ZNF347    3'  AGGCAGGTGGATCACCTGAGGT 51818          __        CA
            CAGG                   CCTGACCTC  GTGATCCACC  CCT
                                |||||||||  ||||||||||  |||
                                GGACTGGAG  CACTAGGTGG  GGA
                                    TC         AC
GAM1077  LOC115129 5'  AGGCAGGTGGATCACCTGAGGT 73604          __        CA
            CAGG                   CCTGACCTC  GTGATCCACC  CCT
                                |||||||||  ||||||||||  |||
                                GGACTGGAG  CACTAGGTGG  GGA
                                    TC         AC
GAM1077  LOC115196 3'  AGGCGGGTGGATCATGAGGTCA 73648                A
            GG                   CCTGACCTCGTGATCCACCC CCT
                                |||||||||||||||||||| |||
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                                GGACTGGAGTACTAGGTGGG GGA
                                      C
GAM1077  LOC115442 3'  AGATGGTGTGGTCTACGAGGTC 73055          AT   _  C
            AGG                  CCTGACCTCGTG  CCAC CCA CT
                                 ||||||||||||  |||| ||| ||
                                 GGACTGGAGCAT  GGTG GGT GA
                                       CT   T   A
GAM1077  LOC116143 3'  AGGCGGGTGAATCACGAGGTCA 74175            C    A
            GG                   CCTGACCTCGTGAT CACCC CCT
                                 |||||||||||||| ||||| |||
                                 GGACTGGAGCACTA GTGGG GGA
                                       A    C
GAM1077  LOC116143 3'  AGGCGGGTGGATCAGAAGGTCA 74176        CG        A
            GG                   CCTGACCT  TGATCCACCC CCT
                                 ||||||||  |||||||||| |||
                                 GGACTGGA  ACTAGGTGGG GGA
                                     AG        C
GAM1077  LOC116236 3'  AGGTGGGTGGATCACGAGGTCA 74237
            GG                   CCTGACCTCGTGATCCACCCACCT
                                 ||||||||||||||||||||||||
                                 GGACTGGAGCACTAGGTGGGTGGA

GAM1077  LOC116349 3'  AGGCAGGTAGATCATGAGGTCA 74270            C   CA
            GG                   CCTGACCTCGTGATC ACC  CCT
                                 ||||||||||||||| |||  |||
                                 GGACTGGAGTACTAG TGG  GGA
                                       A   AC
GAM1077  LOC119504 5'  AGGCAGGTGGATCACCTGAGGT 74441         __        CA
            CGGG                 CCTGACCTC  GTGATCCACC  CCT
                                 |||||||||  ||||||||||  |||
                                 GGGCTGGAG  CACTAGGTGG  GGA
                                     TC        AC
GAM1077  LOC121457 3'  AGGTGGGCAGATCACGAAGTCA 74508       C       CA
            GG                   CCTGAC TCGTGATC  CCCACCT
                                 ||||||  ||||||||  |||||||
                                 GGACTG AGCACTAG  GGGTGGA
                                    A       AC
GAM1077  LOC124944 5'  GTGAACATGAGGTCAGG     74836           ATC
                                 CCTGACCTCGTG   CAC
                                 ||||||||||||   |||
                                 GGACTGGAGTAC   GTG
                                       AA_
GAM1077  LOC126282 3'  AGGCGGGCGGATCACGAGGTCA 74943             A   A
            GG                   CCTGACCTCGTGATCC CCC CCT
                                 ||||||||||||||| ||| |||
                                 GGACTGGAGCACTAGG GGG GGA
                                       C   C
GAM1077  LOC126669 3'  AGGCAGGCAGATCACGTGAGGT 75921         __     CA  CA
            CAGG                 CCTGACCTC  GTGATC  CC  CCT
                                 |||||||||  ||||||  ||  |||
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                                GGACTGGAG  CACTAG  GG  GGA
                                     TG     AC  AC
GAM1077  LOC127294 3'  AGGCGGGCAGATCACCTGAGGT 75144          __     CA   A
              CAGG                   CCTGACCTC  GTGATC  CCC CCT
                                |||||||||  ||||||  ||| |||
                                GGACTGGAG  CACTAG  GGG GGA
                                     TC     AC   C
GAM1077  LOC127348 3'  AGGTGGTATTGACAGAGGTCAG 75148         G  A  CAC_
              G                   CCTGACCTC TG TC    CCACCT
                                |||||||||  ||  ||    ||||||
                                GGACTGGAG AC AG    GGTGGA
                                     _  _  TTAT
GAM1077  LOC127428 3'  AGGCAGGCAGATCACCTGAGGT 75154          __     CA  CA
              CAGG                   CCTGACCTC  GTGATC  CC  CCT
                                |||||||||  ||||||  ||  |||
                                GGACTGGAG  CACTAG  GG  GGA
                                     TC     AC  AC
GAM1077  LOC129452 3'  AGGCAAGTGCTGTTGCGAGGTC 75382         TG  C_   CCA
              G                   TGACCTCG  AT  CAC   CCT
                                |||||||||  ||  |||   |||
                                GCTGGAGC  TG  GTG   GGA
                                     GT  TC   AAC
GAM1077  LOC130026 3'  AGGCAGGCGGATCACGAGGTCA 57431              A  CA
              GG                   CCTGACCTCGTGATCC CC  CCT
                                |||||||||||||||  ||  |||
                                GGACTGGAGCACTAGG GG  GGA
                                        C  AC
GAM1077  LOC130535 3'  AGGCAGGTGGATCACCTGAGGT 76640          __        CA
              CAGG                   CCTGACCTC  GTGATCCACC  CCT
                                |||||||||  ||||||||||  |||
                                GGACTGGAG  CACTAGGTGG  GGA
                                     TC         AC
GAM1077  LOC130535 3'  AGGCAGGTGGATCATGAGGTCA 76641              CA
                                TGACCTCGTGATCCACC  CCT
                                ||||||||||||||||  |||
                                ACTGGAGTACTAGGTGG  GGA
                                        AC
GAM1077  LOC130589 3'  AGGCAGGCGGATCACGAGGTCA 57927              A  CA
              GG                   CCTGACCTCGTGATCC CC  CCT
                                |||||||||||||||  ||  |||
                                GGACTGGAGCACTAGG GG  GGA
                                        C  AC
GAM1077  LOC130951 3'  GGTGGATGAGGTCAG      57943        GTG
                                CTGACCTC   ATCCACC
                                ||||||||   |||||||
                                GACTGGAG   TAGGTGG
                                        ___
GAM1077  LOC131744 3'  AGGTGGGTGAATCACATGAGGT 76387          __    C
              CAGG                   CCTGACCTC  GTGAT CACCCACCT
                                |||||||||  |||||  |||||||||
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                                GGACTGGAG  CACTA GTGGGTGGA
                                    TA     A
GAM1077  LOC133926 3'  AGGTGGACGGATCACGAGGTCA 75627              AC
              GG                  CCTGACCTCGTGATCC  CCACCT
                                  ||||||||||||||||  ||||||
                                  GGACTGGAGCACTAGG  GGTGGA
                                        CA
GAM1077  LOC134147 3'  AGGTGGGTGGATCACTTGAGGT 57954          __
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GAM1077  LOC134147 3'  GTGGGTGGATCACCTGAGGTCA 57965          __
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                                  GGACTGGAG  CACTAGGTGGGTG
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GAM1077  LOC137362 3'  AGGCGGGTGGGTCACCTGAGGT 75781          __         A
              CAGG                  CCTGACCTC  GTGATCCACCC CCT
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                                  GGACTGGAG  CACTGGGTGGG GGA
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GAM1077  LOC139422 3'  AGGCAGGCGGATCATGAGGTCA 76341              A  CA
              GG                  CCTGACCTCGTGATCC CC  CCT
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                                        C  AC
GAM1077  LOC142779 3'  AGGTGGGCAGATCACAAGGTCA 76900        C     CA
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GAM1077  LOC142927 3'  AGGTGGGCGAATCACCTGAGGT 76942          __    CCA
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GAM1077  LOC143196 3'  AGGCGGGTGGATCACGAGGTC  83799              A
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GAM1077  LOC143310 3'  AGGTGGGCCGATCACGAGGTCA 77033             CA
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GAM1077  LOC143465 3'  GGCAGATCACCTGAGGTTA   83875         __     CA
                                  TGACCTC  GTGATC  CC
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                                   TC     AC
GAM1077  LOC143888 3'  AGATGGGCGGATCTTTTGAGGT 77165         T__    A   C
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GAM1077  LOC143943 3'  AGGCGGGCGGATCACGAGGTCA 83912             A  A
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                                         C  C
GAM1077  LOC144289 3'  AGGTGGGTGGATCACTTGAGGT 83949         __
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GAM1077  LOC144465 3'  AGGCGGGCGGATCACCTGAGGT 77339         __     A  A
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                                     TC      C  C
GAM1077  LOC144481 3'  AGGCAAGTGAAGCACTTGAGGT 84010         __  ATC  CCA
            CAGG                   CCTGACCTC  GTG   CAC   CCT
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                                     TT   GAA   AAC
GAM1077  LOC144486 3'  AGGCAGGTGGATCACCTGAGGT 84000         __       CA
            CAGG                   CCTGACCTC  GTGATCCACC  CCT
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                                     TC        AC
GAM1077  LOC144524 3'  GTGGATCACCTGAGGTCAGG   84059         __
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GAM1077  LOC144563 3'  AGGCAGGCGGATCACCTTAGGT 77389        C__     A  CA
            CAGG                   CCTGACCT   GTGATCC CC  CCT
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                                     TTC      C  AC
GAM1077  LOC144583 3'  AGGTGGGCAGATCACTTGAGGT 77410         __     CA
            TAG                    CTGACCTC  GTGATC  CCCACCT
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                                     TT     AC
GAM1077  LOC144817 3'  AGGCGGGCGGATCACTAGGTCA 77503         C      A  A
            GG                     CCTGACCT GTGATCC CCC CCT
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GAM1077  LOC144817 3'  AGGTGGGCGGATCACCTGAGGT 77505         __      A
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GAM1077  LOC144845 3'  AGGCGGGCAGATCACTTGAGGT 57451         __     CA   A
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                                       TT       AC   C
GAM1077  LOC145035 3'  AGGTGGGCGGATCACTTGAGGT 84174         __      A
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                                       TT       C
GAM1077  LOC145082 5'  AGGTGGGTGGATCACCTGAG   84181     __
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GAM1077  LOC145216 3'  AGGCGGGCGGATCACCTGAGGT 84215        __      A   A
                 CA                  TGACCTC  GTGATCC CCC CCT
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                                       TC       C   C
GAM1077  LOC145231 3'  AGGCGGGTGAATCATGAGGTCA 84240             C     A
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GAM1077  LOC145299 3'  AGGCGGGTGGATCATGAGGTCA 84272               A
                 GG                    CCTGACCTCGTGATCCACCC CCT
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GAM1077  LOC145333 3'  AGGCGGGCGGATCACGAGGTCA 84287             A   A
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GAM1077  LOC145438 3'  AGGCGGGCGGATCACGAGGTCA 84307             A   A
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GAM1077  LOC145453 3'  AGGCAGGTGGATCACCTGAGGT 77652         __        CA
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GAM1077  LOC145482 3'  AGGCGGGCAGATCACTTGAGGT 77739          __     CA   A
            CAGG                   CCTGACCTC  GTGATC  CCC CCT
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GAM1077  LOC145483 3'  AGGCAGGCAGATCATCTGAGGT 77751          __     CA  CA
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GAM1077  LOC145662 3'  AGGTGGGTGGATCACCTGAGGT 77833          __
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GAM1077  LOC145663 3'  AGGCAGGCGGATTGCCTGAGGT 84411          __ TG    A  CA
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                                    TC GT    C  AC
GAM1077  LOC145663 3'  AGGCGGGCGGATCACGAGGTTA 84412              A   A
            GG                     CCTGACCTCGTGATCC CCC CCT
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GAM1077  LOC145757 3'  AGGCAGGTGGATCACTTGAGGT 77916          __         CA
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GAM1077  LOC145820 3'  AGGCGGGCGGATCACGAGGTCA 77970              A   A
            GG                     CCTGACCTCGTGATCC CCC CCT
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GAM1077  LOC145988 5'  AGGCAGGTGGATCACAAGGTCA 78059          C         CA
            GG                     CCTGACCT GTGATCCACC  CCT
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                                     A         AC
GAM1077  LOC146229 3'  AGGCGGGTGGATCACGAGGTCA 78259                A
            GG                     CCTGACCTCGTGATCCACCC CCT
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                                       C
GAM1077  LOC146332 3'  AGGCAAGCAGATCATGAGGTCA 78352              CACCCA
            GG                     CCTGACCTCGTGATC     CCT
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GAM1077  LOC146336 5'  AGGCGGGTGGATCACCTGAGG  78364      __        A
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                                  TC         C
GAM1077  LOC146667 3'  AGGCGGTTGGATCACGAGGTCA 84706              C  A
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                                      T  C
GAM1077  LOC146667 5'  AGGTGGGTAGATGCCACGAGG  84707       __  C
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GAM1077  LOC146669 3'  AGGCAGGTGGATCACCTGAGGT 78658         __       CA
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GAM1077  LOC146713 3'  AGGTGGGCAGATCACCTGAGGT 84722         __     CA
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GAM1077  LOC146723 3'  AGGCGGACAGACCACCTGAGGT 78674         __  A  CAC  A
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                                     TC   C  ACA  C
GAM1077  LOC146756 3'  AGGCGGGCGGATCACGAGGTCA 84793              A   A
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GAM1077  LOC146780 3'  AGGCGGGTGGATCACGAGGTCA 84817                A
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GAM1077  LOC146901 3'  AGGCAGGTGGATCACTTGAG  84888     __       CA
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GAM1077  LOC146923 3'  AGGCGGGCGGATCACAAGGTCA 78794         C      A   A
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GAM1077  LOC146975 5'  AGGCAGGTGGATCACGAGGTCA 78827              CA
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GAM1077  LOC147071 3'  AGGCGGGCGGATCATGAGGTCA 73351            A   A
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GAM1077  LOC147080 3'  AGGTGGGCAGATGACTTGAGGT 85026        __ G   CA
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GAM1077  LOC147180 5'  AGGCGGGCGGATCACCTGAGGT 85094        __     A   A
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GAM1077  LOC147599 3'  AGGCAGGTGGATCACTTGAGGT 85158        __       CA
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GAM1077  LOC147649 3'  AGGGGGGGGGGATCACGAGGTCA 79054            A   A
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                                        G   G
GAM1077  LOC147664 3'  AGGCAGGCAGATCACCTGAGGT 79040        __    CA  CA
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GAM1077  LOC147727 5'  AGGCGGGCGGATCACGAGGTCA 79126            A   A
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GAM1077  LOC147727 5'  AGGTGGGCGGATCACTTGAGGT 79127        __     A
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GAM1077  LOC148198 3'  AGGCGGGCGGATCACCTGAGGT 71218         __      A   A
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                                       TC      C   C
GAM1077  LOC148267 3'  AGGTGAGGAGAGGTCAGG    79512         GTGA   ACC
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GAM1077  LOC148534 3'  AGGTGGGTCGATCACTGAGGTC 79629         _     C
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GAM1077  LOC148734 3'  AGGTGGGCGGATCACAAGGTCA 79707        C      A
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GAM1077  LOC148918 5'  AGGTGGGCAGATCACCTGAGGT 79817         __     CA
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GAM1077  LOC149073 3'  AGGCAGATGGAACACTTGAGGT 85481         __  A    CCCA
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GAM1077  LOC149113 3'  AGGAGGGTGGATCACGAGGTCA 79900               A
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GAM1077  LOC149127 3'  GGTGGGGAGGAGGTCAG     85502         GTGAT CA
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GAM1077  LOC149175 3'  AGATGGGCGGATCACGAGGTCA 79946             A   C
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GAM1077  LOC149271 3'  AGGTGGGTGGATCACCTGAGGT 79994         __
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GAM1077  LOC149319 3'  AGGTGGGTGGATCACCTGAGGT 80065        __
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GAM1077  LOC149460 3'  AGGTGGGTAGATACCTGAAGTC 85605      C   TG_  C
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GAM1077  LOC149464 3'  AGGTGGGTGGATCACCTGAGGT 85584        __
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GAM1077  LOC149579 5'  AGGCAGGCAGATCGCCTGAGGT 71688        __     CA  CA
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GAM1077  LOC149628 3'  AGGCAGGTGGATTGCCTGAGGT 80274        __ TG      CA
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GAM1077  LOC149668 3'  AGGTGGGCGGATCACCTGAGGT 85693        __      A
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GAM1077  LOC149710 3'  AGGTGGGTGGATCACCTGAGGT 80329        __
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GAM1077  LOC150035 5'  AGGTGGGTGGACATCATCCAG  85956     ACCTC   A
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GAM1077  LOC150185 3'  AGGCGGGCAGATTACGAGGTCA 86061             CA   A
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GAM1077  LOC150299 3'  AGGTGGGCAGATCACGAGGTCA 86160           CA
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GAM1077  LOC150319 3'  AGGCGGACGGAACACCTGAGGT 80462       __  A  AC  A
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GAM1077  LOC150343 3'  AGGCAGGTGGATCACTTGAGGT 80489        __       CA
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GAM1077  LOC150358 3'  AGGTGTGCAGATCACAAGGTCA 86087        C     CACC
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GAM1077  LOC150358 3'  AGTTGGGCGGATCACAAGGTCA 86088        C      A    C
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GAM1077  LOC150372 3'  AGGCGGGTGGATCACTTGAGG  80605     __        A
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GAM1077  LOC150481 3'  AGGTGGGTGGATCACGAGGTCA 80692
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GAM1077  LOC150622 3'  AGGCAGGCGGATCACCTGAGGT 80753        __      A  CA
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GAM1077  LOC150630 3'  AGGCAGGCAGATCACCTGAGGT 86290      __     CA  CA
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                                          TC      AC  AC
GAM1077  LOC150935 3'  AGGTGGGCGGATCACCTGAGGT 80823        __      A
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GAM1077  LOC151196 3'  AGGCAGGTGGATCACTGAGGTC 86447        _       CA
                AGG                     CCTGACCTC GTGATCCACC  CCT
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GAM1077  LOC151248 3'  AGGCAGGCAGACCACGAGGTCA 80983          A  CA  CA
              GG                   CCTGACCTCGTG TC  CC  CCT
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GAM1077  LOC151248 3'  AGGCGGGTGGATCACAAGGTCA 80984        C         A
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GAM1077  LOC151429 3'  AGGCCGGCGGATCACGAGGTCA 86519             A  CA
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GAM1077  LOC151429 3'  AGGCGGGCAGATAACCTGAGGT 86520         TG__  CA  A
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GAM1077  LOC151556 3'  GGTGGATCACCTGAGGTCAGG  81083         __
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GAM1077  LOC151602 3'  AGGCGGACGGATCACCTGAGGT 81103         __      AC  A
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                                        TC       CA  C
GAM1077  LOC151614 3'  AGGCTGGTGGATCACGAGGTCA 81118              CA
                                   TGACCTCGTGATCCACC  CCT
                                   ||||||||||||||||  |||
                                   ACTGGAGCACTAGGTGG  GGA
                                             TC
GAM1077  LOC151720 3'  GGCGGATCACGAGGTCAGG    81157              A
                                   CCTGACCTCGTGATCC CC
                                   |||||||||||||||| ||
                                   GGACTGGAGCACTAGG GG
                                             C
GAM1077  LOC151904 3'  AGGCGGGTGGATCACATGAGG  81200      __         A
                                   CCTC  GTGATCCACCC CCT
                                   ||||  |||||||||| |||
                                   GGAG  CACTAGGTGGG GGA
                                     TA         C
GAM1077  LOC152271 3'  AGGCAGGCAGATCACCTTAGGT 81351         C__     CA  CA
              CAGG                   CCTGACCT   GTGATC  CC  CCT
                                   ||||||||   ||||||  ||  |||
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                                GGACTGGA  CACTAG  GG  GGA
                                   TTC     AC  AC
GAM1077  LOC152274 3'  AGGTGGGTAAACTGAGGCTCAG 81335      _   _  GATCC
            G                   CCTGA CCTC GT    ACCCACCT
                                ||||| |||| ||    ||||||||
                                GGACT GGAG CA    TGGGTGGA
                                  C   T  AA___
GAM1077  LOC152283 3'  AGGCGAGCAGATCACCGAAGGT 86862        _ _    CACCCA
            CAGG                  CCTGACCT CG TGATC     CCT
                                ||||||||  || |||||     |||
                                GGACTGGA GC ACTAG     GGA
                                   A  C    ACGAGC
GAM1077  LOC152313 3'  AGGCGGGCAGATCACGGGGTCA 86843             CA   A
            GG                    CCTGACCTCGTGATC  CCC CCT
                                ||||||||||||||  ||| |||
                                GGACTGGGGCACTAG  GGG GGA
                                        AC   C
GAM1077  LOC152316 3'  AGGTGGGTAGATCACTTGAG   86789    __     C
                                CTC  GTGATC ACCCACCT
                                |||  |||||| ||||||||
                                GAG  CACTAG TGGGTGGA
                                  TT     A
GAM1077  LOC152426 3'  AGGCAGGCGGATCACGAGGTCA 86888              A  CA
            GG                    CCTGACCTCGTGATCC CC  CCT
                                ||||||||||||||| ||  |||
                                GGACTGGAGCACTAGG GG  GGA
                                        C  AC
GAM1077  LOC152445 3'  AGGCAGGCGGATCACCTGAGGT 86931         __      A  CA
            CGGG                  CCTGACCTC  GTGATCC CC  CCT
                                |||||||||  ||||||| ||  |||
                                GGGCTGGAG  CACTAGG GG  GGA
                                   TC      C  AC
GAM1077  LOC152804 3'  AGGTGGGCGGATCACGTGAGGT 87069         __      A
            CAGG                  CCTGACCTC  GTGATCC CCCACCT
                                |||||||||  ||||||| |||||||
                                GGACTGGAG  CACTAGG GGGTGGA
                                   TG      C
GAM1077  LOC152926 3'  AGGTGGGTAGATCATCTGAGGT 81628         __     C
            CAGG                  CCTGACCTC  GTGATC ACCCACCT
                                |||||||||  |||||| ||||||||
                                GGACTGGAG  TACTAG TGGGTGGA
                                   TC     A
GAM1077  LOC153077 3'  AGGTGGGCGGATCATGAGGTTA 87110              A
            GG                    CCTGACCTCGTGATCC CCCACCT
                                ||||||||||||||| |||||||
                                GGATTGGAGTACTAGG GGGTGGA
                                        C
GAM1077  LOC153260 3'  AGGCGGGCAGATCACAAGGTCA 81667         C     CA   A
            GG                    CCTGACCT GTGATC  CCC CCT
                                |||||||| ||||||  ||| |||
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                                GGACTGGA CACTAG  GGG GGA
                                   A     AC   C
GAM1077  LOC153579 3'  AGGCGGGTGGATCACGAGGTCA 81763                A
              GG                  CCTGACCTCGTGATCCACCC CCT
                                  |||||||||||||||||||| |||
                                  GGACTGGAGCACTAGGTGGG GGA
                                           C
GAM1077  LOC153682 3'  AGGTGGTCGGATCACGAGGTTA 87267              AC
              GG                  CCTGACCTCGTGATCC  CCACCT
                                  ||||||||||||||||  ||||||
                                  GGATTGGAGCACTAGG  GGTGGA
                                           CT
GAM1077  LOC153688 3'  AGGCGGGTGGATCACCTGAGGT 87294         __        A
              CAGG                CCTGACCTC  GTGATCCACCC CCT
                                  |||||||||  |||||||||||| |||
                                  GGACTGGAG  CACTAGGTGGG GGA
                                     TC         C
GAM1077  LOC154403 3'  AGGAGGGTGGATCACGAGGTCA 81966                A
              G                   CTGACCTCGTGATCCACCC CCT
                                  |||||||||||||||||||| |||
                                  GACTGGAGCACTAGGTGGG GGA
                                           A
GAM1077  LOC154789 5'  GTGGGTGGAGGGACAGCAGG   82033      ACC  GTGA
                                  CCTG   TC    TCCACCCAC
                                  ||||   ||    |||||||||
                                  GGAC   AG    AGGTGGGTG
                                    GAC  GG__
GAM1077  LOC154791 3'  AGGCAGGCGGATCACCTGAGGT 82047       __      A  CA
                                  ACCTC  GTGATCC CC  CCT
                                  |||||  ||||||| ||  |||
                                  TGGAG  CACTAGG GG  GGA
                                     TC      C  AC
GAM1077  LOC154988 3'  GGTGGATCAGGGTCAG      82103         CG
                                  CTGACCT  TGATCCACC
                                  |||||||  |||||||||
                                  GACTGGG  ACTAGGTGG
                                           __
GAM1077  LOC154992 3'  AGGAGGGTGGATCACGAGGTCA 82128                A
              G                   CTGACCTCGTGATCCACCC CCT
                                  |||||||||||||||||||| |||
                                  GACTGGAGCACTAGGTGGG GGA
                                           A
GAM1077  LOC155006 3'  AGGTGGGCAGATCACTCAAGGT 82160         C__     CA
              CAGG                  CCTGACCT   GTGATC  CCCACCT
                                  ||||||||   ||||||  |||||||
                                  GGACTGGA   CACTAG  GGGTGGA
                                     ACT      AC
GAM1077  LOC155072 3'  AGGCGGGTGGATCACGAGGTCA 87653                A
              GG                  CCTGACCTCGTGATCCACCC CCT
                                  |||||||||||||||||||| |||
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                                GGACTGGAGCACTAGGTGGG GGA
                                      C
GAM1077  LOC155072 3'  AGGTAGGTGGATCATGAGGTCA 87654              C
              GG                 CCTGACCTCGTGATCCACC ACCT
                                 |||||||||||||||||| ||||
                                 GGACTGGAGTACTAGGTGG TGGA
                                       A
GAM1077  LOC157464 5'  TAGGCGGGTGAATCACTTGATT 87751       _______   C   A  ___
              GAGGTCAGG              CCTGACCTC    GTGAT CACCC CCT  A
                                 |||||||||    ||||| ||||| |||  |
                                 GGACTGGAG    CACTA GTGGG GGA  T
                                      TTAGTT   A   C  ___
GAM1077  LOC157657 3'  AGGCAGGCAGATCAGCTGAGGT 82428        __   CA  CA
              CAGG               CCTGACCTCG  TGATC  CC  CCT
                                 |||||||||  |||||  ||  |||
                                 GGACTGGAGT  ACTAG  GG  GGA
                                      CG    AC  AC
GAM1077  LOC157660 3'  AGGCCGAGGCGGATCACGAGGT 87799            A  CA__
              CAGG               CCTGACCTCGTGATCC CC   CCT
                                 |||||||||||||||| ||   |||
                                 GGACTGGAGCACTAGG GG   GGA
                                       C  AGCC
GAM1077  LOC157983 3'  AGGCGGGCGCATCACGAGGTCA 82535           CCA  A
              GG                 CCTGACCTCGTGAT   CCC CCT
                                 |||||||||||||   ||| |||
                                 GGACTGGAGCACTA   GGG GGA
                                       CGC   C
GAM1077  LOC158088 3'  AGGTGGGTGGATCACGAGGTCA 87968
              GG                 CCTGACCTCGTGATCCACCCACCT
                                 |||||||||||||||||||||||||
                                 GGACTGGAGCACTAGGTGGGTGGA

GAM1077  LOC158117 3'  AGGTAGTAGGAGAGGTCGG   82609       GTGA  _  CC
                                 CTGACCTC   TCC AC  ACCT
                                 ||||||||   ||| ||  ||||
                                 GGCTGGAG   AGG TG  TGGA
                                      _____  A  A_
GAM1077  LOC158187 3'  AGGTGGGTGGATCACGAGGTCA 87985
              GG                 CCTGACCTCGTGATCCACCCACCT
                                 |||||||||||||||||||||||||
                                 GGACTGGAGCACTAGGTGGGTGGA

GAM1077  LOC158191 3'  AGGCGGGTGGATCACGAGGTCA 82663              A
                                 TGACCTCGTGATCCACCC CCT
                                 |||||||||||||||| |||
                                 ACTGGAGCACTAGGTGGG GGA
                                       C
GAM1077  LOC158288 3'  AGGTGGGCAGATCTCAAGGTCA 88017       CGT   CA
              GG                 CCTGACCT   GATC  CCCACCT
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                                GGACTGGA  CTAG  GGGTGGA
                                    ACT   AC
GAM1077  LOC158292 5'  AGGCGGGCGGATCACAAGGTCA 88037       C     A  A
             GG                   CCTGACCT GTGATCC CCC CCT
                                  |||||||| ||||||| ||| |||
                                  GGACTGGA CACTAGG GGG GGA
                                     A      C  C
GAM1077  LOC158292 5'  GGTGGATCACGAGGTCAGG   88055
                                  CCTGACCTCGTGATCCACC
                                  ||||||||||||||||||
                                  GGACTGGAGCACTAGGTGG

GAM1077  LOC158337 3'  AGGCGGGCAGATCACGAGGTCA 88106          CA  A
                                  TGACCTCGTGATC  CCC CCT
                                  ||||||||||||  ||| |||
                                  ACTGGAGCACTAG  GGG GGA
                                        AC  C
GAM1077  LOC158677 5'  AGGTGGGTAGATCACTTGAGGT 88244        __    C
             CAGG                 CCTGACCTC  GTGATC ACCCACCT
                                  |||||||||  |||||| ||||||||
                                  GGACTGGAG  CACTAG TGGGTGGA
                                       TT     A
GAM1077  LOC158819 5'  AGGCAGGCGGATCACTTGAGGT 88268        __    A  CA
             TAGG                 CCTGACCTC  GTGATCC CC  CCT
                                  |||||||||  ||||||| ||  |||
                                  GGATTGGAG  CACTAGG GG  GGA
                                       TT     C  AC
GAM1077  LOC158819 3'  AGGCGGGTGGATCACGAGGTCA 88269             A
             GG                   CCTGACCTCGTGATCCACCC CCT
                                  |||||||||||||||||||| |||
                                  GGACTGGAGCACTAGGTGGG GGA
                                             C
GAM1077  LOC158987 3'  GGCGGATCACCTGAGGTCAGG  88327        __    A
                                  CCTGACCTC  GTGATCC CC
                                  |||||||||  ||||||| ||
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                                       TC     C
GAM1077  LOC159036 3'  AGGCGGGTGGATTACGAGGTCA 88342             A
             GG                   CCTGACCTCGTGATCCACCC CCT
                                  |||||||||||||||||||| |||
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                                             C
GAM1077  LOC159053 3'  AGGCAGGCGGGTCATGAGGTCA 88360          A  CA
             GG                   CCTGACCTCGTGATCC CC  CCT
                                  |||||||||||||||| ||  |||
                                  GGACTGGAGTACTGGG GG  GGA
                                           C  AC
GAM1077  LOC162461 3'  AGGTGGGTGGAGAGGTGAG   83235   G   GTGA
                                  CT ACCTC   TCCACCCACCT
                                  || |||||   ||||||||||
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                                GA TGGAG    AGGTGGGTGGA
                                 G    _____
GAM1077  LOC170395 3'  AGGTGGGCAGATCACCTAAGGT 76862        C__     CA
              CAGG                  CCTGACCT   GTGATC  CCCACCT
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                                    GGACTGGA   CACTAG  GGGTGGA
                                         ATC      AC
GAM1077  LOC196540 3'  AGGCAGGTGGATCACCTGAGGT 91196         __        CA
              CAGG                  CCTGACCTC  GTGATCCACC  CCT
                                    |||||||||  ||||||||||  |||
                                    GGACTGGAG  CACTAGGTGG  GGA
                                         TC         AC
GAM1077  LOC197196 3'  AGGTAGGCGGATCACCTGAGGT 91293         __      A  C
              TAGG                  CCTGACCTC  GTGATCC CC ACCT
                                    |||||||||  |||||||  ||  ||||
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                                         TC       C  A
GAM1077  LOC197196 3'  AGGTGGGTGGATCATCTGAGGT 91294         __
              CAGG                  CCTGACCTC  GTGATCCACCCACCT
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                                         TC
GAM1077  LOC197201 3'  AGGTAGGCGGATCACCTGAGGT 89265         __      A  C
              CGG                   CTGACCTC  GTGATCC CC ACCT
                                    ||||||||  |||||||  ||  ||||
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                                         TC       C  A
GAM1077  LOC197319 3'  AGGTGGGTGGATCACAAGGTCA 89313         C
              GG                     CCTGACCT GTGATCCACCCACCT
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                                          A
GAM1077  LOC197319 3'  TAGGTGGGCGGATCACAAGGTC 89328         C      A      ___
              AGG                    CCTGACCT GTGATCC CCCACCT   A
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                                     GGACTGGA CACTAGG GGGTGGA   T
                                          A      C      ___
GAM1077  LOC199676 3'  AGGTGGGCGGATCACCTGAGGT 91356         __      A
              CAGG                  CCTGACCTC  GTGATCC CCCACCT
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                                         TC       C
GAM1077  LOC199733 3'  AGGTGGGCGGATCACCTGAGGT 91433         __      A
              CAGG                  CCTGACCTC  GTGATCC CCCACCT
                                    |||||||||  |||||||  |||||||
                                    GGACTGGAG  CACTAGG GGGTGGA
                                         TC       C
GAM1077  LOC199858 3'  AGGCGGGCGGATCACCAGGTCA 89790         C      A   A
              GG                     CCTGACCT GTGATCC CCC CCT
                                     ||||||||  |||||||  |||  |||
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                                GGACTGGA CACTAGG GGG GGA
                                    C      C   C
GAM1077  LOC200014 3'  AGGCAGGTGGATCACCTGAGGT 89918         __        CA
                CAGG                CCTGACCTC  GTGATCCACC  CCT
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                                    GGACTGGAG  CACTAGGTGG  GGA
                                       TC         AC
GAM1077  LOC200317 3'  GGCAGATCACCTGAGGTCAGG  90226         __     CA
                                    CCTGACCTC  GTGATC  CC
                                    |||||||||  ||||||  ||
                                    GGACTGGAG  CACTAG  GG
                                       TC      AC
GAM1077  LOC200728 3'  AGGTGGGCAGATCATGAGGTCA 91680            CA
                G                    CTGACCTCGTGATC  CCCACCT
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                                          AC
GAM1077  LOC200731 3'  AGGCAGGTGGATCAACTGAGGT 91690         __       CA
                CAGG                CCTGACCTCG  TGATCCACC  CCT
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GAM1077  LOC200904 3'  AGGCAGGCAGATCACCTTAGGT 91773        C__     CA  CA
                CAGG                CCTGACCT   GTGATC  CC  CCT
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                                       TTC      AC  AC
GAM1077  LOC200940 3'  AGGCAGGCGGATCTCCTGAGGT 90384         T__    A  CA
                CAGG                CCTGACCTCG   GATCC CC  CCT
                                    ||||||||||   ||||| ||  |||
                                    GGACTGGAGT   CTAGG GG  GGA
                                       CCT     C  AC
GAM1077  LOC201173 3'  AGGCGGGCGGATCATGAGGTCA 88670             A   A
                GG                  CCTGACCTCGTGATCC CCC CCT
                                    |||||||||||||||| ||| |||
                                    GGACTGGAGTACTAGG GGG GGA
                                          C   C
GAM1077  LOC201220 3'  AGGTGGGCGGATCACGAGGTCA 88704             A
                GG                  CCTGACCTCGTGATCC CCCACCT
                                    |||||||||||||||| |||||||
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                                          C
GAM1077  LOC201685 3'  AGGCAGGCGGATCACCTGAGGT 91835         __      A  CA
                CAGG                CCTGACCTC  GTGATCC CC  CCT
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                                    GGACTGGAG  CACTAGG GG  GGA
                                       TC      C  AC
GAM1077  LOC201810 3'  AGGCAGATGGATCACGAGGTCA 90500             CCCA
                GG                  CCTGACCTCGTGATCCA    CCT
                                    ||||||||||||||||    |||
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                                GGACTGGAGCACTAGGT    GGA
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GAM1077  LOC201868 3'  GGGTGGATCATGAGGTCAG    90530
                                CTGACCTCGTGATCCACCC
                                ||||||||||||||||||
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GAM1077  LOC201895 3'  AGGTGGGTGGATCACTTGAGGT 90539         __
              CAGG                 CCTGACCTC  GTGATCCACCCACCT
                                ||||||||  ||||||||||||||
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GAM1077  LOC201911 3'  AGGCGGGCGGATCAACTGAGGT 91860          __     A   A
              CGGG                 CCTGACCTCG  TGATCC CCC CCT
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                                     CA     C   C
GAM1077  LOC201931 3'  GGCGGATCATGAGGTCAGG    90567              A
                                CCTGACCTCGTGATCC CC
                                |||||||||||||||| ||
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GAM1077  LOC202020 3'  AGGGGGCGAATCACGAGGTCAG 90595             CCA   A
              G                   CCTGACCTCGTGAT   CCC CCT
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                                      AGC   _
GAM1077  LOC202038 3'  AGGCGGGCGGATCACGAGGTCA 90618              A   A
              GG                    CCTGACCTCGTGATCC CCC CCT
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                                       C   C
GAM1077  LOC202052 3'  GGTGGATCACCTGAGGTCAGG  91903         __
                                CCTGACCTC  GTGATCCACC
                                |||||||||  ||||||||||
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                                     TC
GAM1077  LOC202134 5'  AGGTGGGTGGATCACCTGAGGT 91915         __
              CAGG                 CCTGACCTC  GTGATCCACCCACCT
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                                     TC
GAM1077  LOC202868 3'  AGGCGGGTGGATCACGAGGTCA 91987                A
              GG                    CCTGACCTCGTGATCCACCC CCT
                                |||||||||||||||||| |||
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                                       C
GAM1077  LOC202868 3'  AGGTAGGTGGATCATGAGGTCA 91988               C
              GG                    CCTGACCTCGTGATCCACC ACCT
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                                GGACTGGAGTACTAGGTGG TGGA
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GAM1077  LOC203025 3'  AGGCGGGTGGGTCACCTGAGGT 90742        __        A
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                                      TC         C
GAM1077  LOC203083 3'  AGGCAGGTGGATCACCTTAGGT 92080        C__       CA
              CAGG                  CCTGACCT   GTGATCCACC  CCT
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                                      TTC        AC
GAM1077  LOC203246 3'  AGGCGGGCGGATCACGAGGTCA 90827             A   A
              GG                    CCTGACCTCGTGATCC CCC CCT
                                    ||||||||||||||| ||| |||
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                                        C   C
GAM1077  LOC203275 3'  GGTAGTCGGAGAGGTCGG    90855       G_   CC
                                    CTGACCTC  TGAT  ACC
                                    ||||||||  ||||  |||
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GAM1077  LOC203289 3'  AGGCGGGCGCATCACGAGGTCA 90862           CCA   A
              GG                    CCTGACCTCGTGAT   CCC CCT
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                                        CGC   C
GAM1077  LOC203378 3'  AGGTGGGCAGATCACCTGAGGT 92275        __     CA
              CAGG                  CCTGACCTC  GTGATC  CCCACCT
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                                      TC     AC
GAM1077  LOC206338 5'  TGGGTGGATCATCCAG      91091     ACCTC
                                    CTG    GTGATCCACCCA
                                    |||    ||||||||||||
                                    GAC    TACTAGGTGGGT
                                     C____
GAM1077  LOC219347 3'  AGGTGGGTGGATCACCAGGTCA 94571        C
              GG                    CCTGACCT GTGATCCACCCACCT
                                    ||||||||  ||||||||||||||
                                    GGACTGGA CACTAGGTGGGTGGA
                                      C
GAM1077  LOC219627 3'  AGGCGGGCAGACCATGAGGTCA 93798          A  CA   A
              GG                    CCTGACCTCGTG TC  CCC CCT
                                    ||||||||||||  ||  ||| |||
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                                        C  AC   C
GAM1077  LOC219627 3'  AGGTGGGCAGATCACCTGAGGT 93799      __     CA
                                    ACCTC  GTGATC  CCCACCT
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                                TGGAG  CACTAG  GGGTGGA
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GAM1077  LOC219649 3'  AGGCGGGTGGATCACAAGGTCA 94542        C         A
             GG                   CCTGACCT GTGATCCACCC CCT
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                                     A         C
GAM1077  LOC219649 3'  GGGTGGATCACCTGAGGTCAGG 94556         __
                                  CCTGACCTC  GTGATCCACCC
                                  |||||||||  ||||||||||
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                                       TC
GAM1077  LOC219673 3'  AGGCGGGCGGATCACGAGGTCA 94609              A   A
             GG                   CCTGACCTCGTGATCC CCC CCT
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                                           C   C
GAM1077  LOC219919 3'  AGGCAGGCGGATCACCTTAGGT 94916        C__      A  CA
             CAGG                   CCTGACCT   GTGATCC CC  CCT
                                  ||||||||   ||||||| ||  |||
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                                     TTC      C  AC
GAM1077  LOC219920 5'  AGGTGGGTGTTGGGGAGACAAG 94937     GA___    TGATC
             G                    CCT    CCTCG    CACCCACCT
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                                  GGA    GGGGT    GTGGGTGGA
                                    ACAGA    T_____
GAM1077  LOC220662 3'  AGGTGGGCAGATCACGAGGTCA 92803             CA
             GG                   CCTGACCTCGTGATC  CCCACCT
                                  ||||||||||||||  |||||||
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                                           AC
GAM1077  LOC220906 3'  AGGTGGGCAGATCACCTGAGGT 93029       __     CA
                                  ACCTC  GTGATC  CCCACCT
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GAM1077  LOC221178 3'  AGGCAGGTGGATCACCTGAGGT 95164         __        CA
             CAGG                   CCTGACCTC  GTGATCCACC  CCT
                                  |||||||||  ||||||||||  |||
                                  GGACTGGAG  CACTAGGTGG  GGA
                                       TC         AC
GAM1077  LOC221271 3'  AGGTGGGCGGATCACAAGGTCA 93494        C      A
             GG                   CCTGACCT GTGATCC CCCACCT
                                  |||||||| ||||||| |||||||
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                                     A      C
GAM1077  LOC221271 3'  GGGCAGATCACGAGGTCAGG  93525             CA
                                  CCTGACCTCGTGATC  CCC
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                                      AC
GAM1077  LOC221288 3'  AGGTGGGCAGATCACGAGGTCA 95254             CA
              GG                  CCTGACCTCGTGATC  CCCACCT
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GAM1077  LOC221410 3'  AGGCAGGTAGATCATGAGGTCA 93688            C   CA
              GG                  CCTGACCTCGTGATC ACC  CCT
                                  ||||||||||||||| |||  |||
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                                      A   AC
GAM1077  LOC221474 3'  AGGTGGGCAGATCACCTGAGGT 93989         __     CA
              CAGG                  CCTGACCTC  GTGATC  CCCACCT
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                                  GGACTGGAG  CACTAG  GGGTGGA
                                      TC      AC
GAM1077  LOC221477 3'  AGGCAGGCAGATCACTTGAGGT 93767         __     CA  CA
              CAGG                  CCTGACCTC  GTGATC  CC  CCT
                                  |||||||||  ||||||  ||  |||
                                  GGACTGGAG  CACTAG  GG  GGA
                                      TT      AC  AC
GAM1077  LOC221490 3'  AGGCGGGTGGATCACAAGGTCA 95297        C         A
              GG                  CCTGACCT GTGATCCACCC CCT
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                                  GGACTGGA CACTAGGTGGG GGA
                                      A          C
GAM1077  LOC221543 3'  AGGCAGGTGGATCACCTGAGGT 95359         __        CA
              CAGG                  CCTGACCTC  GTGATCCACC  CCT
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                                  GGACTGGAG  CACTAGGTGG  GGA
                                      TC         AC
GAM1077  LOC221543 5'  AGGTGGGCGGATCACGGGGTCA 95361              A
              GG                  CCTGACCTCGTGATCC CCCACCT
                                  ||||||||||||||| |||||||
                                  GGACTGGGGCACTAGG GGGTGGA
                                        C
GAM1077  LOC221585 3'  GGGCGGATCACGAGGTGG    95279    TG         A
                                  CC  ACCTCGTGATCC CCC
                                  ||  |||||||||||| |||
                                  GG  TGGAGCACTAGG GGG
                                   __          C
GAM1077  LOC221641 5'  AGGTGGGTGGATCACTTGAGGT 95342         __
              CAGG                  CCTGACCTC  GTGATCCACCCACCT
                                  |||||||||  ||||||||||||||||
                                  GGACTGGAG  CACTAGGTGGGTGGA
                                      TT
GAM1077  LOC221766 3'  AGGTGGGCAGATCACCTGAGGT 95418         __     CA
              CAGG                  CCTGACCTC  GTGATC  CCCACCT
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                                GGACTGGAG  CACTAG  GGGTGGA
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GAM1077  LOC221795 3'  AGGCAGGCGGATCACCTTAGGT 94066        C__      A  CA
              CAGG                   CCTGACCT   GTGATCC CC  CCT
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                                GGACTGGA   CACTAGG GG  GGA
                                     TTC      C  AC
GAM1077  LOC221943 5'  AGGCGGGTGGATCACCTGAGG  95616      __         A
                                CCTC  GTGATCCACCC CCT
                                ||||  |||||||||||| |||
                                GGAG  CACTAGGTGGG GGA
                                  TC          C
GAM1077  LOC221954 5'  GTGGGCGGATCACCTGAGGTCA 95650          __      A
              GG                   CCTGACCTC  GTGATCC CCCAC
                                |||||||||  ||||||| |||||
                                GGACTGGAG  CACTAGG GGGTG
                                     TC      C
GAM1077  LOC222060 5'  AGGCGGGTGGATCCATTGAGGT 95749          T__       A
              CAGG                   CCTGACCTCG   GATCCACCC CCT
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                                GGACTGGAGT   CTAGGTGGG GGA
                                      TAC        C
GAM1077  LOC222066 3'  AGGCAGGCAGATCACCTGAGGT 94311         __     CA  CA
              CAG                    CTGACCTC  GTGATC  CC  CCT
                                |||||||  ||||||  ||  |||
                                GACTGGAG  CACTAG  GG  GGA
                                     TC      AC  AC
GAM1077  LOC222160 5'  AGATGGGCGGATCACGAGGTCA 95770              A    C
              GG                   CCTGACCTCGTGATCC CCCA CT
                                |||||||||||||||| |||| ||
                                GGACTGGAGCACTAGG GGGT GA
                                        C    A
GAM1077  LOC222182 3'  AGGCAGGTGGATCGCTTGAGG  95851      __         CA
                                CCTC  GTGATCCACC  CCT
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                                GGAG  CGCTAGGTGG  GGA
                                  TT          AC
GAM1077  LOC222256 3'  AGGTGGGCAGATCACCTAAGGT 95907         C__     CA
              CAGG                   CCTGACCT   GTGATC  CCCACCT
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                                GGACTGGA   CACTAG  GGGTGGA
                                     ATC      AC
GAM1077  LOC222865 3'  AGGCGGGTGGATCACGAGATCA 94437       C           A
              GG                   CCTGA CTCGTGATCCACCC CCT
                                |||||  |||||||||||||| |||
                                GGACT GAGCACTAGGTGGG GGA
                                  A           C
GAM1077  LOC253639 3'  AGGCGGGTGGATCATGAGGTCA 97509                 A
              GG                   CCTGACCTCGTGATCCACCC CCT
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                                GGACTGGAGTACTAGGTGGG GGA
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GAM1077  LOC253840 3'  AGGTGGGTGGATCACCTGAGGT 97909        __
            CAGG                  CCTGACCTC  GTGATCCACCCACCT
                                  |||||||||  ||||||||||||||
                                  GGACTGGAG  CACTAGGTGGGTGGA
                                    TC
GAM1077  LOC253927 3'  AGGTGGGCGGATCATGAGGTCA 96726            A
            GG                    CCTGACCTCGTGATCC CCCACCT
                                  |||||||||||||||| |||||||
                                  GGACTGGAGTACTAGG GGGTGGA
                                       C
GAM1077  LOC254045 3'  AGGCAAGTGAAGCACTTGAGGT 98260        __  ATC  CCA
            CAGG                  CCTGACCTC  GTG  CAC  CCT
                                  |||||||||  |||  |||  |||
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                                    TT  GAA  AAC
GAM1077  LOC254176 3'  AGGCAGGTGGATCACCTTAGGT 99161       C__       CA
            CAGG                  CCTGACCT  GTGATCCACC  CCT
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                                  GGACTGGA  CACTAGGTGG  GGA
                                    TTC       AC
GAM1077  LOC254266 3'  AGGCGGGCAGATCACGAGGTCA 99192           CA  A
            G                     CTGACCTCGTGATC  CCC CCT
                                  ||||||||||||||  ||| |||
                                  GACTGGAGCACTAG  GGG GGA
                                       AC  C
GAM1077  LOC254351 3'  AGGCAGTGCGACGAGGTCAGG  96682         GATC  CCA
                                  CCTGACCTCGT   CAC  CCT
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                                      GC__  AC_
GAM1077  LOC254531 5'  AGGCGGGTGGATCACCTGAGGT 96660        __       A
            CAGG                  CCTGACCTC  GTGATCCACCC CCT
                                  |||||||||  |||||||||| |||
                                  GGACTGGAG  CACTAGGTGGG GGA
                                    TC        C
GAM1077  LOC254808 3'  AGGCGGGCGGATCACGAGGTCA 98800            A  A
            GG                    CCTGACCTCGTGATCC CCC CCT
                                  |||||||||||||||| ||| |||
                                  GGACTGGAGCACTAGG GGG GGA
                                       C  C
GAM1077  LOC255042 3'  AGGCAGGCAGATCATGAGGTCA 97031           CA  CA
            GG                    CCTGACCTCGTGATC  CC  CCT
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                                  GGACTGGAGTACTAG  GG  GGA
                                       AC  AC
GAM1077  LOC255042 3'  AGGCGGGTGGATCACCTGAGGT 97032        __       A
            CAGG                  CCTGACCTC  GTGATCCACCC CCT
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GAM1077  LOC255177 3'  GGCAGATCACAAGGTCAGG   98396        C     CA
                                CCTGACCT GTGATC  CC
                                |||||||| ||||||  ||
                                GGACTGGA CACTAG  GG
                                    A     AC
GAM1077  LOC255185 3'  AGGCGGGCGGATCATGAGGTCA 96829             A   A
           GG                     CCTGACCTCGTGATCC CCC CCT
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                                          C   C
GAM1077  LOC255196 3'  AGGCGAGTGAATCACTTGAGGT 98948         __    C   CCA
           CAGG                    CCTGACCTC  GTGAT CAC   CCT
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                                GGACTGGAG  CACTA GTG   GGA
                                     TT    A   AGC
GAM1077  LOC255326 3'  AGGCGGGCAGATCACGAAGTCA 98114     C       CA   A
                                TGAC TCGTGATC  CCC CCT
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                                ACTG AGCACTAG  GGG GGA
                                  A       AC   C
GAM1077  LOC255328 3'  AGGTGGGCAGATCACGAGGTCA 98332             CA
           GG                     CCTGACCTCGTGATC  CCCACCT
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                                          AC
GAM1077  LOC255937 3'  AGGCAGGCGGATCACTTGAGGT 97676         __      A  CA
           CAGG                    CCTGACCTC  GTGATCC CC  CCT
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                                     TT       C  AC
GAM1077  LOC255971 3'  AGGCGGGCGGATCACTTGAGGT 98306         __      A   A
           CAGG                    CCTGACCTC  GTGATCC CCC CCT
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                                     TT       C   C
GAM1077  LOC256207 3'  AGGTGGGTGGATCACCTGAGGT 96870         __
           CAGG                    CCTGACCTC  GTGATCCACCCACCT
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                                     TC
GAM1077  LOC256277 3'  GGGTAGATCACTTGAGGTCAGG 96353         __     C
                                CCTGACCTC  GTGATC ACCC
                                |||||||||  ||||||  ||||
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                                     TT      A
GAM1077  LOC256515 3'  AGGCAGGCGGATTACCTTAGGT 98203         C__      A  CA
           CAGG                    CCTGACCT   GTGATCC CC  CCT
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GAM1077  LOC256544 3'  AGGCGGGCGCATCACGAGGTCA 97926           CCA  A
            GG                   CCTGACCTCGTGAT  CCC CCT
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                                       CGC  C
GAM1077  LOC256594 3'  AGGCAGGCGGATCACCTTAGGT 98853       C__     A  CA
            CAGG                  CCTGACCT  GTGATCC CC  CCT
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                                    TTC      C  AC
GAM1077  LOC257180 3'  AGGCAGGTGGATCATGAGATCA 97313     C         CA
            G                     CTGA CTCGTGATCCACC  CCT
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                                   A          AC
GAM1077  LOC257480 3'  AGGTGGGTGGATCACTTGAG  78431    __
                                 CTC  GTGATCCACCCACCT
                                 |||  ||||||||||||||
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                                   TT
GAM1077  LOC257539 3'  AGGAGGGCAGATCACGAGGTCA 99543           CA  A
            GG                   CCTGACCTCGTGATC  CCC CCT
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                                       AC  A
GAM1077  LOC257547 3'  GTGGGTGGGGACAGACCAG   99540    AC  C  GA
                                 CTG  CT GT  TCCACCCAC
                                 |||  || ||  |||||||||
                                 GAC  GA CA  GGGTGGGTG
                                   CA  _  G_
GAM1077  LOC257554 3'  AGGCAAGTGGATTAGGGGGTCT 99530    T     G      CCA
            GG                   CC GACCTC TGATCCAC   CCT
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                                  T     G       AAC
GAM1077  LOC257578 3'  AGGAGGGCAGATCACGAGGTCA 99655           CA  A
            GG                   CCTGACCTCGTGATC  CCC CCT
                                 ||||||||||||||  ||| |||
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                                       AC  A
GAM1077  LOC257596 3'  AGGCAGGTGGATCACCTGAGGT 99762        __       CA
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GAM1077  LOC257596 5'  AGGTGGGCGGATCACGGGGTCA 99764            A
            GG                   CCTGACCTCGTGATCC CCCACCT
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GAM1077  LOC257607 3'  GTGGGTGGGGACAGACCAG   99652    AC  C  GA
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                                GAC  GA CA  GGGTGGGTG
                                  CA  _  G_
GAM1077  LOC51122  3'  AGGTGGGCAAATCATGAGGTCA 66193           CCA
           GG                     CCTGACCTCGTGAT   CCCACCT
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                                         AAC
GAM1077  LOC51145  3'  AGGCAGGTGGATCACAAGGTCA 32919       C       CA
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GAM1077  LOC51279  3'  AGGTGGGTGGATCACGAGGTCA 33749
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GAM1077  LOC51336  3'  AGGCAGGCGGATCACTTGAGGT 34066         __      A  CA
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GAM1077  LOC51759  3'  AGGTGGGCGGATCACCTGAGGT 73168         __      A
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GAM1077  LOC55974  3'  AGGTGGGCGGATCGCCTGAGGT 38741         __      A
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                                         TC       C
GAM1077  LOC63929  3'  AGGCAGGTGGATCTCTTGAG   42278      T__      CA
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                                  TCT       AC
GAM1077  LOC64167  3'  GGGCGGATCACGAGGTCAGG   42541           A
                                CCTGACCTCGTGATCC CCC
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GAM1077  LOC85479  5'  AGGCTGGCGGATCACGAGGTCA 53559            A  CA
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                                GGACTGGAGCACTAGG GG  GGA
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GAM1077  LOC89890  3'  AGGCAGGTGGATCACCTGAGGT 61201        __        CA
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GAM1077  LOC90072  3'  AGGCGGGCAGATCACTAGAGGT 61946         __     CA   A
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                                        AT     AC   C
GAM1077  LOC90072  3'  AGGTGGGTGGATCGCCTGAG   61947     __
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                                       TC
GAM1077  LOC90092  3'  AGGTAGGTGGATCACCTAAGGT 62052         C__        C
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GAM1077  LOC90092  3'  AGGTGGGCGAATCACAAGGTCA 62053         C     CCA
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GAM1077  LOC90155  5'  AGGTGGGCGGATCACTTGAGGT 62361         __      A
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GAM1077  LOC90321  3'  AGGCAGGTGGATCACAAGGTCA 62928         C         CA
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                                        A         AC
GAM1077  LOC90509  3'  GGCGGATCACGAGGCCAGG    63795      A         A
                                     CCTG CCTCGTGATCC CC
                                     ||||  ||||||||||| ||
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                                       C          C
GAM1077  LOC90573  3'  AGGTGGGTGAATTGCTTGAGGT 63954         __ TG  C
                CAGG                 CCTGACCTC  G  AT CACCCACCT
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                                        TT GT  A
GAM1077  LOC90589  3'  AGGCAGGCGGACCACGAGGTCA 59772           A   A  CA
                G                     CTGACCTCGTG TCC CC  CCT
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                                GACTGGAGCAC AGG GG  GGA
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GAM1077  LOC90591  3'  AGGCAGGCAGATCACCTGAGGT 64144        __     CA  CA
                CAGG                  CCTGACCTC  GTGATC  CC  CCT
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                                        TC      AC  AC
GAM1077  LOC90591  3'  AGGCAGGTGGATCACTTGAGGT 64146        __        CA
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                                        TT         AC
GAM1077  LOC90591  3'  AGGTGGGCGGATCACGAGGTCA 64148             A
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GAM1077  LOC90624  3'  AGGCGGGCAGATCACAAGGTCA 64364        C     CA   A
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GAM1077  LOC90918  5'  GTGGGTGGATCACCTGAGGTCA 65003        __
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                                        TC
GAM1077  LOC90979  3'  GTGGGCAGATCACGAGGTCA   65138           CA
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GAM1077  LOC91115  3'  AGGCAGGCGGATCATCTGAGGT 65547        __      A  CA
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GAM1077  LOC91115  3'  AGGCAGGTGGATTGTCTGAGGT 65548        __ TG      CA
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GAM1077  LOC91286  3'  AGGTGGGTAGATCACCTGAGGT 66056        __     C
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GAM1077  LOC91380  3'  AGGCGGGTGGATCACCTGAGGT 66435        __         A
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GAM1077  LOC91547  3'  AGGTGGGCGGATCACGAGGTCA 66996             A
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GAM1077  LOC91574  3'  AGGCGGGCGGATCACTTGAGGT 67108         __     A  A
              CAGG                CCTGACCTC  GTGATCC CCC CCT
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                                      TT      C  C
GAM1077  LOC91750  3'  AGGCAGGTGGATCATAGGTCA  67646       C       CA
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GAM1077  LOC91796  5'  AGGTGGGCAGATCACCTGAGGT 67784         __     CA
              CAGG                CCTGACCTC  GTGATC  CCCACCT
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GAM1077  LOC91862  3'  AGGTGGGTGGATCACTTGAGGT 54568         __
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GAM1077  LOC91960  3'  AGGTGACATGACACAGGGTCAG 68279        TC   A  CACC
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GAM1077  LOC92078  3'  AGGTGAGTGGATCACCTGAGGT 68590         __       C
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                                      TC         A
GAM1077  LOC92283  3'  AGGCGGGCGGATCACGAGGTCA 69299             A  A
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                                        C  C
GAM1077  LOC92465  5'  AGGTGGGCAGATCTCTTGAGGT 69940          T__   CA
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GAM1077  LOC92465  3'  AGGTGGGTAGATCATTTCAG  69941     CCTC     C
                                  CTGA    GTGATC ACCCACCT
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GAM1077 LOC93132  5'  AGGCAGGTGGATCACAAGGTCA 71975         C         CA
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                                       A         AC
GAM1077 LOC93613  3'  AGGCGGGCAGATCACTTGAGGT 73070          __      CA   A
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                                       TT      AC   C
GAM1077 LOC96597  5'  AGGTGGGCGGATCACCTGAGGT 67447          __      A
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                                       TC      C
GAM1078 LDB3      3'  AAACCTTCTTGGGAGCCCGGAC 76922     CA   ACCGA
              GT                    ACG  CGG    CGGGAAGGTTT
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GAM1078 NFATC1    3'  TCCCGTCGGTCTGCACGT    21598     CA
                                    ACG  CGGACCGACGGGA
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                                    TGC  GTCTGGCTGCCCT
                                      AC
GAM1078 IL18BP    3'  AAACCTTCCCATCACTCC    20306     CC  C
                                    GGA  GA GGGAAGGTTT
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                                    CCT  CT CCCTTCCAAA
                                      CA  A
GAM1078 MGC17919  5'  AATCTTCCCTCGGCCCGCGCG  58879     A   A    C
                                    CGC CGG CCGA GGGAAGGTT
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                                    GCG GCC GGCT CCCTTCTAA
                                      C   C   _
GAM1078 LOC146756 3'  AAACCTTCCTTGCCTGCCGTGC 84789        ACCGAC
                                    GCACGG     GGGAAGGTTT
                                    ||||||     ||||||||||
                                    CGTGCC     TCCTTCCAAA
                                       GTCCGT
GAM1079 PIK3CG    3'  CTTGGATTTCAAATGCAATAGA 12122       CA   G  TC
                                    TCTAT  TAT TG  AAATCCAAG
                                    |||||  ||| ||  |||||||||
                                    AGATA  GTA AC  TTTAGGTTC
                                      AC   A __
GAM1079 B1        3'  CTTGGATTTTATTTATAATTAG 27824      TCA    T  C
              A                     TCTA   TATG GT AAATCCAAG
                                    ||||   |||| || |||||||||
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                                AGAT   ATAT TA TTTAGGTTC
                                  TA_   T  T
GAM1079  FLJ10246  3'  CTTGGATTCACACCATAT    36409      _  CA
                                ATATG TGT  AATCCAAG
                                ||||| |||  ||||||||
                                TATAC ACA  TTAGGTTC
                                  C   C_
GAM1079  KATII     3'  TTGGATTTATTATGAAGA    33170     A    TGTGTC
                                TCT TCATA     AAATCCAA
                                ||| |||||     ||||||||
                                AGA AGTAT     TTTAGGTT
                                  _    TA____
GAM1079  KIAA0553  3'  TTTATCACATATGATAGA    70455           TC
                                TCTATCATATGTG  AAA
                                ||||||||||||  |||
                                AGATAGTATACAC  TTT
                                        TA
GAM1079  LOC94431  5'  TTTGACACATATCACAGA    69153     ATC
                                TCT   ATATGTGTCAAA
                                |||   ||||||||||||
                                AGA   TATACACAGTTT
                                  CAC
GAM1080  BHMT2     3'  TGACCTGGAACCGTTCCTCAC  34740     C  AG  TC
                                GTG AG  AC  TTCCAGGTCA
                                ||| ||  ||  ||||||||||
                                CAC TC  TG  AAGGTCCAGT
                                  _ CT  CC
GAM1080  CCBL1     3'  TGACCTGGGCCTCTCCCTGC   15771     A  CTCT
                                GCAG GA    TCCAGGTCA
                                |||| ||    |||||||||
                                CGTC CT    GGGTCCAGT
                                  C  CTCC
GAM1080  CHAT      5'  GACCTCTGGAAATGTCCAC   40971     CAGA   TC    __
                                GTG    GAC  TTCCA  GGTC
                                |||    |||  |||||  ||||
                                CAC    CTG  AAGGT  CCAG
                                  _____  TA    CT
GAM1080  COX10     3'  TCTGGAAAAAGCCTCTACA   8948     C    A  C_
                                TG AGAG CT  TTCCAGG
                                || |||| ||  |||||||
                                AC TCTC GA  AAGGTCT
                                 A    C  AA
GAM1080  CYP2B6    3'  TTTGAGACAGAGTCTCACAC  7576      CA      _ _
                                GTG  GAGACTCT TC CAGG
                                |||  |||||||| || ||||
                                CAC  CTCTGAGA AG GTTT
                                  A_       C  A
GAM1080  DAPK1     3'  TTGACCTGTTTCTCTGC     18229       CTCTTC
                                GCAGAGA     CAGGTCAA
                                |||||||     ||||||||
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                                CGTCTCT     GTCCAGTT
                                   TT____
GAM1080  DNM2     3'  TTTGACCACTGTAAGTGCCTGC 18237       AG   CTTCCA
              AC                    GTGCAG  ACT     GGTCAAA
                                ||||||  |||     |||||||
                                CACGTC  TGA     CCAGTTT
                                   CG   ATGTCA
GAM1080  GCN5L2   3'  TGACCTGGAATGTCTCCAC   60531     CA    TC
                                GTG  GAGAC  TTCCAGGTCA
                                |||  |||||  ||||||||||
                                CAC  CTCTG  AAGGTCCAGT
                                  __    T_
GAM1080  MTMR2    3'  GACCTAGTCTCTGCAT      32911          CTTCC
                                GTGCAGAGACT    AGGTC
                                ||||||||||    |||||
                                TACGTCTCTGA    TCCAG

                                      _____
GAM1080  NKX3A    3'  CCTAAGGAGGGTCTCCACAC   21613     CA        C_
                                GTG  GAGACTCTTC  AGG
                                |||  ||||||||||  |||
                                CAC  CTCTGGGAGG  TCC
                                  AC         AA
GAM1080  RBM10    5'  CCGAGAAGAGTCCCTGCA    20245      A       CA
                                TGCAG GACTCTTC  GG
                                |||||| ||||||||  ||
                                ACGTC CTGAGAAG  CC
                                   C       AG
GAM1080  C5orf7   3'  TCTGATAGCGTCTCTGCAC   64601          T  TC
                                GTGCAGAGAC CT  CAGG
                                |||||||||| ||  ||||
                                CACGTCTCTG GA  GTCT
                                      C  TA
GAM1080  CHERP    3'  CTTGGAAGAACCCTGCAC    22130       AGAC
                                GTGCAG    TCTTCCAGG
                                ||||||    |||||||||
                                CACGTC    AGAAGGTTC
                                   CCA_
GAM1080  DKFZP434J154 3'  TTGACCTGTGACCTCTG     32177       ACTCT  _
                                CAGAG     TC CAGGTCAA
                                |||||     || ||||||||
                                GTCTC     AG GTCCAGTT
                                   C_____  T
GAM1080  DKFZP434J154 3'  TTGACCTGTGACCTCTG     32598       ACTCT  _
                                CAGAG     TC CAGGTCAA
                                |||||     || ||||||||
                                GTCTC     AG GTCCAGTT
                                   C_____  T
GAM1080  FLJ10936 3'  TTTGAGACAGAGTCTCACAC   37453     CA       _  _
                                GTG  GAGACTCT TC CAGG
                                |||  |||||||| || ||||
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                                CAC  CTCTGAGA AG GTTT
                                  A_       C  A
GAM1080  FLJ12875  3'  TTGACCTGGAAGCACCCCTGC  44920      AGACT
                                GCAG    CTTCCAGGTCAA
                                ||||    ||||||||||||
                                CGTC    GAAGGTCCAGTT
                                  CCCAC
GAM1080  FLJ14708  3'  TGACCTGGTGCTCTCTCTCCAC 52610     C    CTCTT
                                GTG AGAGA    CCAGGTCA
                                ||| |||||    ||||||||
                                CAC TCTCT    GGTCCAGT
                                  C    CTCGT
GAM1080  FLJ20436  3'  TCTGAGAAAGCCTCTGCAC   35628        A  C  _
                                GTGCAGAG CT TTC CAGG
                                |||||||| || ||| ||||
                                CACGTCTC GA AAG GTCT
                                     C  _  A
GAM1080  FLJ21415  3'  CTGCAAGAGAAGAGTCTTACAC 45685     CA        _____
                                GTG  GAGACTCTTC    CAG
                                |||  ||||||||||    |||
                                CAC  TTCTGAGAAG    GTC
                                  A_        AGAAC
GAM1080  FLJ32389  3'  ACCTCCCCAGACTCTGCAC   58840        AC   TCC_
                                GTGCAGAG  TCT    AGGT
                                ||||||||  |||    ||||
                                CACGTCTC  AGA    TCCA
                                     __  CCCC
GAM1080  KLF12     3'  TGACCTGGAGGTCTGC      24364       GACT
                                GCAGA    CTTCCAGGTCA
                                |||||    ||||||||||||
                                CGTCT    GGAGGTCCAGT
                                   _____
GAM1080  MPN       3'  CTTGAGCAGAGCTCTGCAC    50050        A    TC_
                                GTGCAGAG CTCT   CAGG
                                |||||||| ||||   ||||
                                CACGTCTC GAGA   GTTC
                                     _   CGA
GAM1080  SERF1B    3'  TTTGAGACAGAGTCTCGCAC   43711      A       _ _
                                GTGC GAGACTCT TC CAGG
                                |||| |||||||| || ||||
                                CACG CTCTGAGA AG GTTT
                                  _       C  A
GAM1080  LOC126528 5'  TTTGACCTCTTGACCTCTG    75035       AC  TTCC
                                CAGAG  TC    AGGTCAAA
                                |||||  ||    ||||||||
                                GTCTC  AG    TCCAGTTT
                                  C_  TTC_
GAM1080  LOC143916 3'  TGACTTAAGTCTCTGC       77147         CTTCC
                                GCAGAGACT     AGGTCA
                                |||||||||     ||||||
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                                CGTCTCTGA    TTCAGT
                                     A____
GAM1080  LOC146957 3'  GCCCAGATCTCTGCAC      78816        C   TCCA
                                GTGCAGAGA TCT    GGT
                                ||||||||| |||    |||
                                CACGTCTCT AGA    CCG
                                     _  C___
GAM1080  LOC149506 5'  ACCTGGAATCCCTGCAC     85622       A  CTC
                                GTGCAG GA   TTCCAGGT
                                |||||| ||   ||||||||
                                CACGTC CT   AAGGTCCA
                                   C  ___
GAM1080  LOC219920 5'  TTTGTAAGAATCTCTGCA    94966        C    C
                                TGCAGAGA TCTT CAGG
                                |||||||| |||| ||||
                                ACGTCTCT AGAA GTTT
                                     A    T
GAM1080  LOC51287  5'  GCTTAGAGTCTCCCAC     33804     CA       TCC
                                GTG  GAGACTCT   AGGT
                                |||  ||||||||   ||||
                                CAC  CTCTGAGA   TTCG
                                  C_       ___
GAM1080  LOC93070  3'  TTTGAGACAGAGTCTCACAC   71818     CA       _ _
                                GTG  GAGACTCT TC CAGG
                                |||  |||||||| || ||||
                                CAC  CTCTGAGA AG GTTT
                                  A_       C  A
GAM1080  LOC93259  5'  TTTGACCTGCCCACTCTCCAC  72299     C    ACTCTTC
                                GTG AGAG       CAGGTCAAA
                                ||| ||||       |||||||||
                                CAC TCTC       GTCCAGTTT
                                  C    ACCC___
GAM1081  ADAM19    3'  GCCCCTCCTCGTACTTC     43790        AAGAA     T
                                GAAGTAC     AGGAGG GT
                                |||||||     |||||| ||
                                CTTCATG     TCCTCC CG
                                     C____      C
GAM1081  CD74      3'  CCATGTCCCACCCTGTACCTCA 16380     A    AGAAA  A  TG
                                TGA GTACA     GG GG  TGG
                                ||| |||||     || ||  |||
                                ACT CATGT     CC CT  ACC
                                  C    CCCA_  _  GT
GAM1081  CST1      5'  CCTCCTCTCCTGCAGCTCCA   10330    A   A_  A  A
                                TG AGT  CA GA AGGAGG
                                || |||  || || ||||||
                                AC TCG  GT CT TCCTCC
                                 C   AC  C  C
GAM1081  CST4      5'  CCTCCTCTCCTGCAGCTCCA   10335    A   A_  A  A
                                TG AGT  CA GA AGGAGG
                                || |||  || || ||||||
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                                AC TCG  GT CT TCCTCC
                                 C   AC  C  C
GAM1081  D10S170   3'  CCCCTTTCGTACTTCA      19549        AA     A
                                TGAAGTAC  GAAAGG GG
                                ||||||||  |||||| ||
                                ACTTCATG  CTTTCC CC
                                    __     _
GAM1081  LTBP2     3'  CCACACCTCCATCCTGTA    6466       A  AA
                                TACA GA  GGAGGTGTGG
                                |||| ||  ||||||||||
                                ATGT CT  CCTCCACACC
                                  C  A_
GAM1081  PTPRF     3'  CACACCCCATGCACCTCA    12606     A  A  AGAAA  A
                                TGA GT CA     GG GGTGTG
                                ||| || ||     || ||||||
                                ACT CA GT     CC CCACAC
                                  C  C  A____  _
GAM1081  PTPRF     3'  CACACCCCATGCACCTCA    56135     A  A  AGAAA  A
                                TGA GT CA     GG GGTGTG
                                ||| || ||     || ||||||
                                ACT CA GT     CC CCACAC
                                  C  C  A____  _
GAM1081  PXN       3'  CATCTCTTCCTCATATTTCA  12668        CA  AA
                                TGAAGTA  AG  AGGAGGTG
                                |||||||  ||  ||||||||
                                ACTTTAT  TC  TTCTCTAC
                                     AC  C_
GAM1081  RBP5      3'  CCAAAGTCCTTTCTCACACTCC 49798    A   ACA      GGTG
           A                     TG AGT   AGAAAGGA   TGG
                                || |||   ||||||||   |||
                                AC TCA   TCTTTCCT   ACC
                                 C   CAC       GAA_
GAM1081  STX1A     3'  CACGCTTCCTTGCCTTCA    17207      TACAAGA
                                TGAAG      AAGGAGGTGTG
                                |||||      ||||||||||
                                ACTTC      TTCCTTCGCAC
                                   CG_____
GAM1081  TMP21     3'  CCTCCCACCTTGTACCTCA   23355     A      AAA
                                TGA GTACAAG   GGAGG
                                ||| |||||||   |||||
                                ACT CATGTTC   CCTCC
                                  C      CAC
GAM1081  ARFGAP1   3'  CACACCTGAGCTGTCCTCA   37136     A T   A AAAGG
                                TGA G ACA G     AGGTGTG
                                ||| | ||| |     |||||||
                                ACT C TGT C     TCCACAC
                                  _ C   _ GAG__
GAM1081  C12orf3   3'  GCACCCTCTTGTACTTCA    40165           AAG A
                                TGAAGTACAAGA   G GGTGT
                                ||||||||||||   | |||||
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                                ACTTCATGTTCT  C CCACG
                                      ___ _
GAM1081  FLJ10315  5'  CCACACCTCCCTGAACTTC   36492     A  AGAAA
                                GAAGT CA    GGAGGTGTGG
                                ||||| ||    ||||||||||
                                CTTCA GT    CCTCCACACC
                                  A  C____
GAM1081  FLJ13310  3'  CACTTCCCTCATACTTCA    47807      CA  AAA
                                TGAAGTA  AG   GGAGGTG
                                |||||||  ||   |||||||
                                ACTTCAT  TC   CCTTCAC
                                   AC  ___
GAM1081  FLJ20502  3'  CCATGTCTTTCTCATATTTCA  35717      CA   AAG    TG
                                TGAAGTA  AGA   GAGG  TGG
                                |||||||  |||   ||||  |||
                                ACTTTAT  TCT   TTCT  ACC
                                   AC   ___   GT
GAM1081  GGA2     3'  CCACATCATGTCCTCCCTGCAC 31162    _   ACA  AA   ___
           TTACA                TG AAGT   AG  AGGA   GGTGTGG
                                || ||||   ||  ||||   |||||||
                                AC TTCA   TC  TCCT   CTACACC
                                 A   CG_  CC   GTA
GAM1081  GGA2     3'  CCACATCATGTCCTCCCTGCAC 57658    _   ACA  AA   ___
           TTACA                TG AAGT   AG  AGGA   GGTGTGG
                                || ||||   ||  ||||   |||||||
                                AC TTCA   TC  TCCT   CTACACC
                                 A   CG_  CC   GTA
GAM1081  HNOEL-iso 3'  CCACTAAATTTCTTGTTCCTCA 39880     AGT      GGAGGT
                                TGA   ACAAGAAA     GTGG
                                |||   ||||||||     ||||
                                ACT   TGTTCTTT     CACC
                                  CCT       AAAT__
GAM1081  KIAA0907  3'  CCACACCTCCCCTTATAACTC  30871    AG  C   AAA
                                GA  TA AAG   GGAGGTGTGG
                                ||  || |||   ||||||||||
                                CT  AT TTC   CCTCCACACC
                                 CA  A   C__
GAM1081  KIAA1052  3'  CCACATCTATCTCCAATACCTC 30939     A   CAA  AAGG
           A                    TGA GTA   GA    AGGTGTGG
                                ||| |||   ||    ||||||||
                                ACT CAT   CT    TCTACACC
                                  C   AAC  CTA_
GAM1081  KIAA1505  3'  CCAGGCTTCCTTGTAC     95847      AGAA      G
                                GTACA    AGGAGGT TGG
                                |||||    ||||||| |||
                                CATGT    TCCTTCG ACC
                                   _____      G
GAM1081  KIAA1602  3'  CCACTGCCCTCCTTGCACTTC  65236      A  AGAA     T__
                                GAAGT CA    AGGAGG   GTGG
                                ||||| ||    ||||||   ||||
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                                CTTCA GT   TCCTCC  CACC
                                  C ____     CGT
GAM1081 MGC4796  3' CAAACCTCCTTGTGCCTCA  62158    A   AGAA     G
                                TGA GTACA   AGGAGGT TG
                                ||| |||||   ||||||| ||
                                ACT CGTGT   TCCTCCA AC
                                  C   ____     A
GAM1081 MYLE     3' TGCCTCCCTGCACTTCA    26692      A  AGAAA
                                TGAAGT CA   GGAGGTG
                                |||||| ||   |||||||
                                ACTTCA GT   CCTCCGT
                                   C  C____
GAM1081 PLEK2    3' CATTTCCTTCCCCATCTTCA  33609      TACAA  A
                                TGAAG   GAA GGAGGTG
                                |||||   ||| |||||||
                                ACTTC   CTT CCTTTAC
                                   TACCC  _
GAM1081 PPFIA4   3' CCACACCAGCCTCCTGTATCTC 70838    AG   A  AA  A_
              A                  TGA  TACA GA  GG  GGTGTGG
                                 |||  |||| ||  ||  |||||||
                                 ACT  ATGT CT  CC  CCACACC
                                   CT   C __ GA
GAM1081 PRO2958  3' CCAGTTCTCCTCTGCACTTCA 38247      ACA  AA   TG
                                TGAAGT  AGA  GGAGG  TGG
                                ||||||  |||  |||||  |||
                                ACTTCA  TCT  CCTCT  ACC
                                   CG_  __   TG
GAM1081 PTPRU    3' CCACACCCCCATTCCGTGCCTC 56522    A   AA  A  A
              A                  TGA GTAC  GAA GG GGTGTGG
                                 ||| ||||  ||| || |||||||
                                 ACT CGTG  CTT CC CCACACC
                                   C   C_  A  C
GAM1081 PTPRU    3' CCACACCCCCATTCCGTGCCTC 56526    A   AA  A  A
              A                  TGA GTAC  GAA GG GGTGTGG
                                 ||| ||||  ||| || |||||||
                                 ACT CGTG  CTT CC CCACACC
                                   C   C_  A  C
GAM1081 PTPRU    3' CCACACCCCCATTCCGTGCCTC 20320    A   AA  A  A
              A                  TGA GTAC  GAA GG GGTGTGG
                                 ||| ||||  ||| || |||||||
                                 ACT CGTG  CTT CC CCACACC
                                   C   C_  A  C
GAM1081 SDC3     3' CCACAGTGCCTCCCTGCAGCCT 28463    A  ACA  AAA    ___
              CA                   TGA GT   AG   GGAGGT   GTGG
                                 ||| ||   ||   ||||||   ||||
                                 ACT CG   TC   CCTCCG   CACC
                                   C  ACG  ___     TGA
GAM1081 SDCCAG43 3' CCACACCCACTTCCTATACTT  70892      CA  A   GA
                                AAGTA  AG AAG  GGTGTGG
                                |||||  || |||  |||||||
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                                TTCAT  TC TTC  CCACACC
                                  A_  C   AC
GAM1081  SE57-1   3'  CCAGATTCCTTTTATACCTCA  48166     A   CAA       G G
                                TGA GTA   GAAAGGAG T TGG
                                ||| |||   |||||||| | |||
                                ACT CAT   TTTTCCTT A ACC
                                  C   A__       _ G
GAM1081  SP2      3'  CCATGCCCCCTCTCCTGCACCT 13329    A  A  A  A   A
             C                   GA GT CA GA AGG GGTGTGG
                                || || || || ||| |||||||
                                CT CA GT CT TCC CCGTACC
                                 C  C  C  C   C
GAM1081  TLE4     3'  CCCCTTTCTTAACCTCA     68511     A  AC       A
                                TGA GT  AAGAAAGG GG
                                ||| ||  |||||||| ||
                                ACT CA  TTCTTTCC CC
                                  C  A_       _
GAM1081  LOC115442 3'  CCTCCCGCCTTGTACTCCA    73056    A       AAA
                                TG AGTACAAG   GGAGG
                                || ||||||||   |||||
                                AC TCATGTTC   CCTCC
                                 C       CGC
GAM1081  LOC134145 3'  TTTCCTTTTTGTACTTCA     75637             A
                                TGAAGTACAAGAA GGAGG
                                |||||||||||| |||||
                                ACTTCATGTTTTT CCTTT
                                                _
GAM1081  LOC142901 5'  CCGCGGTCCCTTCCTGTACCTC 61119    A    A  A   GG
                                GA GTACA GAA GGA  TGTGG
                                || ||||| ||| |||  |||||
                                CT CATGT CTT CCT  GCGCC
                                 C    C  C   G_
GAM1081  LOC145125 3'  TTCCTTCCTTGTACCTCA     77549     A      A
                                TGA GTACAAG AAGGAG
                                ||| ||||||| ||||||
                                ACT CATGTTC TTCCTT
                                  C      C
GAM1081  LOC145921 3'  CACTTCCTTCACTTCA       76525       ACAA   A
                                TGAAGT    GAA GGAGGTG
                                ||||||    ||| |||||||
                                ACTTCA    CTT CCTTCAC
                                     _____   _
GAM1081  LOC148394 3'  TACACCTCCCTTACACATCA   85303     A  AC   AAA
                                TGA GT  AAG   GGAGGTGTG
                                ||| ||  |||   |||||||||
                                ACT CA  TTC   CCTCCACAT
                                  A  CA  ___
GAM1081  LOC148397 5'  CTTCCTTTTCTGCACTCCA    79569    A   A  AG
                                TG AGT CA  AAAGGAGG
                                || ||| ||  ||||||||
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                                AC TCA GT  TTTCCTTC
                                 C   C  CT
GAM1081  LOC148824 3'  CCACAGCCTTTCCCTATACCTC 85380     A   CAA_     AGG
                A                 TGA GTA    GAAAGG   TGTGG
                                  ||| |||    ||||||   |||||
                                  ACT CAT    CTTTCC   ACACC
                                    C   ATCC     G__
GAM1081  LOC155061 3'  CGCCTCCCCTGTGCCCCA    82189    AA    A AAA
                                  TG  GTACA G   GGAGGTG
                                  ||  ||||| |   |||||||
                                  AC  CGTGT C   CCTCCGC
                                   CC     _ C__
GAM1081  LOC157918 3'  CCACACCCAAATTTGCACTTTA 87929       A    AAAGGA
                                  TGAAGT CAAG     GGTGTGG
                                  |||||| ||||     |||||||
                                  ATTTCA GTTT     CCACACC
                                      C    AAAC__
GAM1081  LOC222128 5'  TCCTTTCCTTGTACTTCA    94286          _
                                  TGAAGTACAAG AAAGGA
                                  |||||||||||| ||||||
                                  ACTTCATGTTC TTTCCT
                                         C
GAM1081  LOC254196 3'  TACACCTCCCTTACACATCA   99186     A  AC   AAA
                                  TGA GT  AAG   GGAGGTGTG
                                  ||| ||  |||   |||||||||
                                  ACT CA  TTC   CCTCCACAT
                                    A  CA  ____
GAM1081  LOC254440 3'  TTCCTTCCTTGTACCTCA    98851     A      A
                                  TGA GTACAAG AAGGAG
                                  ||| ||||||| ||||||
                                  ACT CATGTTC TTCCTT
                                    C      C
GAM1081  LOC254549 5'  TATCCCTTTCATACTTCA    97977       CAA     A
                                  TGAAGTA   GAAAGG GGTG
                                  |||||||   |||||| ||||
                                  ACTTCAT   CTTTCC CTAT
                                      A__     _
GAM1081  LOC255102 3'  CACACCCCCATGTACTTC    97800        AGAAA  A
                                  GAAGTACA     GG GGTGTG
                                  ||||||||     || ||||||
                                  CTTCATGT     CC CCACAC
                                       AC____  _
GAM1081  LOC255925 3'  CACACCCCCATGTACTTC    98235        AGAAA  A
                                  GAAGTACA     GG GGTGTG
                                  ||||||||     || ||||||
                                  CTTCATGT     CC CCACAC
                                       AC____  _
GAM1081  LOC256957 5'  ACACCTCCCCTGTACCTC    96826    A     A AAA
                                  GA GTACA G   GGAGGTGT
                                  || ||||| |   ||||||||
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                                CT CATGT C   CCTCCACA
                                 C    _ C__
GAM1081  LOC257397 5'  CCAACTGGACCTTCTTGTACTC 97952    A        A  A__   G
            CA                    TG AGTACAAGAA GG   GGT TGG
                                || |||||||||| ||   ||| |||
                                AC TCATGTTCTT CC   TCA ACC
                                 C         _  AGG   _
GAM1081  LOC89231  5'  TCCATTCCTTGTACTTCA    94302          _  A
                                TGAAGTACAAG AA GGA
                                |||||||||| || |||
                                ACTTCATGTTC TT CCT
                                      C  A
GAM1082  ABCC11   3'  CTGGATGGAAACCCTGG     53683       ATAATA
                                TTAGGG     TTCATTTAG
                                ||||||     |||||||||
                                GGTCCC     AGGTAGGTC
                                   AA____
GAM1082  ADH5     3'  GCTTCTGTGATATTATCTTTAA 7267           T   TT_
                                TTAGGGATAATAT CAT   AGC
                                |||||||||||| |||   |||
                                AATTTCTATTATA GTG   TCG
                                       _   TCT
GAM1082  AES      3'  GTTAGGTGGATACCTGCCCTGA 8525        ATAA
                                TTAGGG    TATTCATTTAGC
                                ||||||    ||||||||||||
                                AGTCCC    ATAGGTGGATTG
                                   GTCC
GAM1082  AGL      3'  GCCATTTGGGGTTATCTCTAGT 7215           A    TTTA
            A                    TATTAGGGATAAT TTCA    GC
                                |||||||||||| ||||    ||
                                ATGATCTCTATTG GGGT    CG
                                       _    TTAC
GAM1082  APAF1    3'  GTTGGATGAATAATATTAATG  25979    GG    A
                                TA  GATA TATTCATTTAGC
                                ||  |||| ||||||||||||
                                GT  TTAT ATAAGTAGGTTG
                                 AA    A
GAM1082  APM1     3'  GCTAAATGGACATCATGTTTTC 17784       GG TA___  A
            TGGTG                   TATTAG  A     AT TTCATTTAGC
                                ||||||  |     || ||||||||||
                                GTGGTC  T     TA AGGTAAATCG
                                   TT TGTAC  C
GAM1082  APXL     3'  CTAATGGTTGGCCCTGGTG    9713          A    ATTCAT
                                TATTAGGG TAAT      TTAG
                                |||||||| ||||      ||||
                                GTGGTCCC GTTG      AATC
                                     G    GT_____
GAM1082  ARF3     3'  GTTGGATGGGTCATCTGTCCTT 9781           _  _
            GGT                     ATTAGGGATA AT ATTCATTTAGC
                                |||||||||| || ||||||||||
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                                TGGTTCCTGT TA TGGGTAGGTTG
                                      C  C
GAM1082 BACE     3'  GAAGATGGGTGTTGTTTTCAAT 58086      AG            AGC
              G                  TATT  GGATAATATTCATTT
                                 ||||  ||||||||||||||
                                 GTAA  TTTGTTGTGGGTAGA
                                   CT            AG
GAM1082 BACE     3'  GCTAAGTGTGGAATTACCTGAT 58088        GATAATATT
              A                  TATTAGG        CATTTAGC
                                 |||||||        ||||||||
                                 ATAGTCC        GTGAATCG
                                     ATTAAGGT_
GAM1082 BACH2    3'  GCTGGATGTTCAGATTCCTAA  41786         AATATT
                                 TTAGGGAT     CATTTAGC
                                 ||||||||     ||||||||
                                 AATCCTTA     GTAGGTCG
                                      GACTT_
GAM1082 BAZ2A    3'  GCTAGGTGGATTTTCTCT    26512       TAAT
                                 AGGGA    ATTCATTTAGC
                                 |||||    ||||||||||
                                 TCTCT    TAGGTGGATCG
                                    TT__
GAM1082 BCL11A   3'  GCTAAATGTCTGTCTCTAA    43467         ATATT
                                 TTAGGGATA    CATTTAGC
                                 |||||||||    ||||||||
                                 AATCTCTGT    GTAAATCG
                                      CT____
GAM1082 C11orf8  3'  GCTAGCACAAAATATTGTCGCT 9624         G        CAT__
              AATA                  TATTAG GATAATATT     TTAGC
                                 ||||||| |||||||||     |||||
                                 ATAATC CTGTTATAA     GATCG
                                    G        AACAC
GAM1082 C4BPB    5'  GCTGGGTGAATTCCAGCCTGG  7389       GATAAT
                                 TTAGG     ATTCATTTAGC
                                 |||||     ||||||||||
                                 GGTCC     TAAGTGGGTCG
                                    GACCT_
GAM1082 CAMLG    3'  GCTGAGTTTGTATTATTACTGA 10002       GG      TC
              TA                   TATTAG  ATAATAT  ATTTAGC
                                 ||||||  |||||||  |||||||
                                 ATAGTC  TATTATG  TGAGTCG
                                    AT      TT
GAM1082 CAT      3'  GCTTAATGTTTATTCCTGATA  10021           TATT    T
                                 TATTAGGGATAA    CATT AGC
                                 ||||||||||||    |||| |||
                                 ATAGTCCTTATT    GTAA TCG
                                         T____    T
GAM1082 CDKN1A   3'  GTTGAATGAGAGGTTCCTAA   55271         AATA
                                 TTAGGGAT    TTCATTTAGC
                                 ||||||||    ||||||||||
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                                AATCCTTG   GAGTAAGTTG
                                    GA__
GAM1082  CHC1L    3'  GTATGAAGTATTATCTTTGA  8857           _  TTAGC
                                TTAGGGATAATATT CAT
                                |||||||||||||| |||
                                AGTTTCTATTATGA GTA
                                      A  TG
GAM1082  CLN5     3'  GCTAAGTGATCTTTCTCTGG  22431      TAATAT
                                TTAGGGA    TCATTTAGC
                                |||||||    |||||||||
                                GGTCTCT    AGTGAATCG
                                    TTCT__
GAM1082  CTRL     3'  CTGAGTGACTCCTTGA     10340      TAATAT
                                TTAGGGA    TCATTTAG
                                |||||||    ||||||||
                                AGTTCCT    AGTGAGTC
                                    C_____
GAM1082  CUL4B    3'  GTTGAGTGGACTTTTTCTC   14566     T  TA
                                GGGA AA  TTCATTTAGC
                                |||| ||  ||||||||||
                                CTCT TT  AGGTGAGTTG
                                  T  TC
GAM1082  CXorf6   3'  GTTGATTTGGGGTTTGTCTTTG 19709          TA   T_
            ATG                   TATTAGGGATAA  TTCA  TTAGC
                                |||||||||||  ||||  |||||
                                GTAGTTTCTGTT  GGGT  AGTTG
                                      TG   TT
GAM1082  DAAM2    3'  CTGAGCTGGTCCTTAATA    93902        AATATT  _
                                TATTAGGGAT    CA TTTAG
                                ||||||||||    || |||||
                                ATAATTCCTG    GT GAGTC
                                     _______  C
GAM1082  DAG1     3'  CCTGGTGAGATTATTTCTGATG 16550      GG    A    TAGC
                                TATTAG  ATAAT TTCATT
                                ||||||  ||||| ||||||
                                GTAGTC  TATTA GAGTGG
                                    TT    _    TCCA
GAM1082  DNTT     3'  GCTGAAATACTGTCTATCTCTA 73663          _  TTCA
            ATA                   TATTAGGGATA ATA   TTTAGC
                                ||||||||||| |||   ||||||
                                ATAATCTCTAT TGT   AAGTCG
                                      C  CATA
GAM1082  EIF4G2   3'  GCTAGATTTTAATATCCTTGA  9219         A  TTC
                                TTAGGGATA TA  ATTTAGC
                                |||||||||  ||  |||||||
                                AGTTCCTAT AT  TAGATCG
                                     A  TT_
GAM1082  EYA4     3'  GCTGAATGGAGTTAAACTTTAG 15885        ATAATA
            TG                    TATTAGGG    TTCATTTAGC
                                ||||||||    ||||||||||
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                                GTGATTTC     AGGTAAGTCG
                                     AAATTG
GAM1082  EZH1     3'  GCTAAGTGAAGTGTGGTCCCTG 10552        A    _
              G                   TTAGGGAT ATATT CATTTAGC
                                  |||||||| ||||| ||||||||
                                  GGTCCCTG TGTGA GTGAATCG
                                       G    A
GAM1082  FACL4    3'  TGAATTTATCTTTGATA     16747           T
                                  TATTAGGGATAA ATTCA
                                  |||||||||||| |||||
                                  ATAGTTTCTATT TAAGT
                                        _
GAM1082  FBXL7    3'  GCTGGATGCTGTCGTCTCTG   25496       TA   TT
                                  TAGGGA  ATA  CATTTAGC
                                  ||||||  |||  ||||||||
                                  GTCTCT  TGT  GTAGGTCG
                                      GC   C_
GAM1082  FLRT2    3'  TTGAATGGAATTATTTTTGATA 26007           A       C
                                  TATTAGGGATAAT TTCATTTAG
                                  |||||||||||| |||||||||
                                  ATAGTTTTTATTA AGGTAAGTT
                                        _
GAM1082  FMR2     3'  GCTGTAGTGTTGTCTTTGATA  10696             CATT
                                  TATTAGGGATAATATT    TAGC
                                  ||||||||||||||||    ||||
                                  ATAGTTTCTGTTGTGA    GTCG
                                        T____    T
GAM1082  FZD3     3'  GCTAAATGAAGCATGATTAGTC 34258        GA    A____
              TTAGTA                  TATTAGG  TAAT    TTCATTTAGC
                                  |||||||  ||||    ||||||||||
                                  ATGATTC  ATTA    AAGTAAATCG
                                      TG    GTACG
GAM1082  FZD7     3'  GCTGGGTGGGGGCCTGTTTCTG 14504     GG   ATA_
                                  TAG  ATA    TTCATTTAGC
                                  |||  |||    ||||||||||
                                  GTC  TGT    GGGTGGGTCG
                                    TT   CCGG
GAM1082  GALNT3   3'  GCTAAATGTAACTTATTCCAAG 16826      A      TATT
              TG                    TATT GGGATAA    CATTTAGC
                                  ||||  |||||||    ||||||||
                                  GTGA CCTTATT    GTAAATCG
                                    A      CAAT
GAM1082  GAN      3'  GTTAGTCTCCATTTATTCCTAG 42122           TATTCAT
              TA                    TATTAGGGATAA      TTAGC
                                  ||||||||||||      |||||
                                  ATGATCCTTATT      GATTG
                                         TACCTCT
GAM1082  GPLD1    3'  GCTGGAGGCCATTATCCTTCAT 93660     T       AT  A
              A                     TAT AGGGATAAT  TC TTTAGC
                                  ||| |||||||||  || ||||||
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                                ATA TTCCTATTA  GG AGGTCG
                                  C        CC  _
GAM1082  GRINL1A   3'  GTTAGGTGAAAGTGTTTTTGA  70069          ATA
                                TTAGGGATA   TTCATTTAGC
                                |||||||||   ||||||||||
                                AGTTTTTGT   AAGTGGATTG
                                     GA_
GAM1082  HSPG2     3'  TGGGAATTGTCTTTAGTG     19841            A
                                TATTAGGGATAAT TTCA
                                |||||||||||| ||||
                                GTGATTTCTGTTA GGGT
                                       A
GAM1082  KCND2     3'  GCTGAGTGTTCATGTTCCATGG 25383       _     ATATT
           TG                     TATTA GGGATA     CATTTAGC
                                |||||| ||||||     ||||||||
                                GTGGT CCTTGT     GTGAGTCG
                                   A     ACTT_
GAM1082  KCNK2     3'  ATGAATGAGAATTGTTTCTGGT 27237       GG     A       GC
           A                     TATTAG  ATAAT TTCATTTA
                                |||||||  |||||| ||||||||
                                ATGGTC  TGTTA GAGTAAGT
                                   TT     A       AA
GAM1082  LMCD1     3'  GTTGGGTGGTGGTAGATCCTTG 28150         AATAT_
           A                     TTAGGGAT     TCATTTAGC
                                |||||||      |||||||||
                                AGTTCCTA     GGTGGGTTG
                                     GATGGT
GAM1082  NBS1      3'  GCTGGGTGGGTGTCTGTTTTGA 70026       ATA
                                TTAGGG   ATATTCATTTAGC
                                ||||||   ||||||||||||
                                AGTTTT   TGTGGGTGGGTCG
                                   GTC
GAM1082  NDST2     3'  CTAGAAATGTCCTTAATA     14664          ATATTCA
                                TATTAGGGATA      TTTAG
                                ||||||||||       |||||
                                ATAATTCCTGT      AGATC
                                      AA_____
GAM1082  NEB       3'  GCTAATGCTTATTATTTCTAAT 17008       GG     TT    T
                                ATTAG  ATAATA  CATT AGC
                                |||||  ||||||  |||| |||
                                TAATC  TATTAT  GTAA TCG
                                   TT     TC   _
GAM1082  NEB       3'  GCTTCTGCAATATTATTTCTG  17009     GG       _  TTT
                                TAG  ATAATATT CA   AGC
                                |||  |||||||| ||   |||
                                GTC  TATTATAA GT   TCG
                                  TT       C  CT_
GAM1082  NRXN1     5'  GCTAAATGGATTTACCTAGTG  17825        GATAAT
                                TATTAGG     ATTCATTTAGC
                                |||||||     ||||||||||
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                                GTGATCC     TAGGTAAATCG
                                    ATT___
GAM1082  NSF      3'  GTTAAATGAGCTTAATGTCTTT 63750        A  __
              G                   TAGGGATA TA  TTCATTTAGC
                                  |||||||| ||  ||||||||||
                                  GTTTCTGT AT  GAGTAAATTG
                                      A  TC
GAM1082  NTSR1    3'  GCTGGATGAGACTGTCCT    11858       ATA
                                  GGGATA   TTCATTTAGC
                                  ||||||   ||||||||||
                                  TCCTGT   GAGTAGGTCG
                                     CA_
GAM1082  OGG1     3'  CTAGATGGGGCACCCTGG    34156       ATAATA
                                  TTAGGG     TTCATTTAG
                                  ||||||     |||||||||
                                  GGTCCC     GGGTAGATC
                                     ACG___
GAM1082  PCDH12   5'  GTTAAGTGACTTGTCCCAGATG 33888     A      TAT
                                  TATT GGGATAA   TCATTTAGC
                                  |||| |||||||   |||||||||
                                  GTAG CCCTGTT   AGTGAATTG
                                    A      C__
GAM1082  PIN4     3'  GCTAAGTGAATGTCAACTGTAG 21711      G  ATA
              TA                    TATTA GG   ATATTCATTTAGC
                                    ||||| ||   ||||||||||||
                                    ATGAT TC   TGTAAGTGAATCG
                                       G  AAC
GAM1082  PMX1     3'  GTTAAAGATATTTGTTGTCTTT 23572          TTCA__
              GA                    TTAGGGATAATA     TTTAGC
                                    ||||||||||||     ||||||
                                    AGTTTCTGTTGT     AAATTG
                                          TTATAG
GAM1082  PMX1     3'  GTTAAAGATATTTGTTGTCTTT 23573          TTCA__
              GA                    TTAGGGATAATA     TTTAGC
                                    ||||||||||||     ||||||
                                    AGTTTCTGTTGT     AAATTG
                                          TTATAG
GAM1082  PPARGC1  3'  GACCATGGTGTTGTTCTTGATG 26079             T   TTAGC
                                  TATTAGGGATAATAT CAT
                                  |||||||||||||| |||
                                  GTAGTTCTTGTTGTG GTA
                                        _   CCAGT
GAM1082  PPID     3'  GTCTATGAATATGATCCCTAAT 88828          A       TTAGC
              G                    TATTAGGGAT ATATTCAT
                                   |||||||||| ||||||||
                                   GTAATCCCTA TATAAGTA
                                         G       TCTG
GAM1082  PTPN7    5'  GCTGAGTGAGCCTCCCCTGG   55463       ATAATA
                                  TTAGGG     TTCATTTAGC
                                  ||||||     ||||||||||
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                                GGTCCC     GAGTGAGTCG
                                   CTCC__
GAM1082  QDPR     3'  GTTATTCAGAATGTTGTTCCTA 6147                ATT_
              ATA                   TATTAGGGATAATATTC    TAGC
                                    ||||||||||||||||    ||||
                                    ATAATCCTTGTTGTAAG    ATTG
                                          ACTT
GAM1082  RBL2     3'  GCTAAACATCCAATATTTTCTT 20041          T     CA___
              TAATG                  TATTAGGGA AATATT     TTTAGC
                                    |||||||| ||||||     ||||||
                                    GTAATTTCT TTATAA     AAATCG
                                          T     CCTAC
GAM1082  RBM8A    3'  GCTGAAATGATTTTCCTGGTA  18810          TAATAT    _
                                    TATTAGGGA     TCATT TAGC
                                    |||||||||     ||||| ||||
                                    ATGGTCCTT     AGTAA GTCG
                                          TT_____     A
GAM1082  RECK     3'  GTTAAAATGTGTTGTTCCAAAT 41199      A         TCA
              A                      TATT GGGATAATAT   TTTAGC
                                    |||| ||||||||||   ||||||
                                    ATAA CCTTGTTGTG   AAATTG
                                       A         TA_
GAM1082  RGL      3'  GTTAAGTGACACTTTTGTCTCT 31429     T       TAT__
              CATA                    TAT AGGGATAA     TCATTTAGC
                                    ||| ||||||||     |||||||||
                                    ATA TCTCTGTT     AGTGAATTG
                                      C       TTCAC
GAM1082  RHAG     3'  ATGAATATTATTCTTAAT     6153
                                    ATTAGGGATAATATTCAT
                                    ||||||||||||||||||
                                    TAATTCTTATTATAAGTA

GAM1082  ROCK2    3'  GTTGGAACTAATATATCCTTGA 66624           A    CA_
              TG                      TATTAGGGATA TATT   TTTAGC
                                    |||||||||| ||||   ||||||
                                    GTAGTTCCTAT ATAA   AGGTTG
                                          _    TCA
GAM1082  RP42     3'  AGATGAAGATTATCTTTAGTG  40564            A
                                    TATTAGGGATAAT TTCATTT
                                    |||||||||||| |||||||
                                    GTGATTTCTATTA AAGTAGA
                                          G
GAM1082  SART2    3'  ATGAATGAATATTTCCTTGATG 26250          T          GC
                                    TATTAGGGA AATATTCATTTA
                                    |||||||| ||||||||||||
                                    GTAGTTCCT TTATAAGTAAGT
                                          _          AT
GAM1082  SDPR     3'  GTTAAAGCTGTATTTTTCTTAA 17401          T     TCA
              TA                      TATTAGGGA AATAT   TTTAGC
                                    |||||||| |||||   ||||||
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                                ATAATTCTT TTATG   AAATTG
                                     T    TCG
GAM1082 SEL1L    3' GCTGAATGAATCCAATTTTTTA 18603        TAAT_
            ATG                   TATTAGGGA    ATTCATTTAGC
                                  |||||||||    ||||||||||
                                  GTAATTTTT    TAAGTAAGTCG
                                     TAACC
GAM1082 SEL1L    3' GCTGGATATTTTGTTTCTGA  18604     GG   TATTC
                                  TTAG  ATAA    ATTTAGC
                                  ||||  ||||    |||||||
                                  AGTC  TGTT    TAGGTCG
                                    TT   TTA__
GAM1082 SERPINA3 3' GCTGGATGCCTGGGTCTCTGG 61821        AATATT
                                  TTAGGGAT     CATTTAGC
                                  ||||||||     ||||||||
                                  GGTCTCTG     GTAGGTCG
                                     GGTCC_
GAM1082 SERPINB5 3' GTTGGGTGGATAAGCTATCCCT 12072        A__
            G                      TAGGGATA   TATTCATTTAGC
                                  ||||||||   ||||||||||||
                                  GTCCCTAT   ATAGGTGGGTTG
                                     CGA
GAM1082 SLC12A7  3' TGAAGCTGTCCCTGATG     22744          ATA
                                  TATTAGGGATA   TTCA
                                  ||||||||||   ||||
                                  GTAGTCCCTGT   AAGT
                                        CG_
GAM1082 SLC20A2  3' GCTGGATGGAGTATTTCTCTGA 23118        T     _
                                  TTAGGGA AATATTC ATTTAGC
                                  ||||||| ||||||| |||||||
                                  AGTCTCT TTATGAG TAGGTCG
                                     _      G
GAM1082 SLC6A6   3' GCTGAATGAGGAGGCCCTA   13184      ATAATA
                                  TAGGG     TTCATTTAGC
                                  |||||     ||||||||||
                                  ATCCC     GAGTAAGTCG
                                     GGAG__
GAM1082 SNX6     3' GTTAGTGACAGTTATTCCTGA  41443          AT    T
                                  TTAGGGATAAT  TCATT AGC
                                  ||||||||||  ||||| |||
                                  AGTCCTTATTG  AGTGA TTG
                                        AC    _
GAM1082 SOCS5    3' GTTAAATGGAAATTGTTTTAAA 26684      AG      A
            TG                    TATT  GGATAAT TTCATTTAGC
                                  ||||  ||||||| ||||||||||
                                  GTAA  TTTGTTA AGGTAAATTG
                                    AT      A
GAM1082 SOX12    3' CTGGATGGATGTTTCTGA    23685      GG  AAT
                                  TTAG  AT   ATTCATTTAG
                                  ||||  ||   ||||||||||
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                                AGTC  TG   TAGGTAGGTC
                                  TT  ___
GAM1082  SPAP1    5'  GTTGAGAAAATTATCTCTAA  57835          A   AT
                                TTAGGGATAAT TTC  TTAGC
                                |||||||||||  |||  |||||
                                AATCTCTATTA AAG  AGTTG
                                      A  __
GAM1082  SPAP1    5'  GTTGAGAAAATTATCTCTAA  57836          A   AT
                                TTAGGGATAAT TTC  TTAGC
                                |||||||||||  |||  |||||
                                AATCTCTATTA AAG  AGTTG
                                      A  __
GAM1082  SSPN     3'  GCTGAATCTCTTTATTTTCCCT 18684         T    TTC__
              GGTA                   TATTAGGGA AATA     ATTTAGC
                                |||||||||  ||||     |||||||
                                ATGGTCCCT TTAT     TAAGTCG
                                      T    TTCTC
GAM1082  STK31    3'  TGAGTTGTATCTTTAGTA    53079           AT
                                TATTAGGGATA  ATTCA
                                ||||||||||  |||||
                                ATGATTTCTAT  TGAGT
                                      GT
GAM1082  SURF5    3'  GCTAGGTGGGACTCATTCCTAA 56915         AATA
              T                  ATTAGGGAT    TTCATTTAGC
                                |||||||||    ||||||||||
                                TAATCCTTA    GGGTGGATCG
                                     CTCA
GAM1082  SURF5    3'  GCTAGGTGGGACTCATTCCTAA 56916         AATA
              T                  ATTAGGGAT    TTCATTTAGC
                                |||||||||    ||||||||||
                                TAATCCTTA    GGGTGGATCG
                                     CTCA
GAM1082  SYT1     3'  GCTAAAGATTTATTTCTAGT   20113      GG    TAT  A
                                ATTAG  ATAA   TC TTTAGC
                                |||||  ||||   ||  ||||||
                                TGATC  TATT   AG AAATCG
                                   TT   T__  _
GAM1082  TSN      3'  GCTTTCTGATGTTGCCTTAATA 17302         A     T  TTT
                                TATTAGGG TAATAT CA   AGC
                                |||||||| ||||||  ||   |||
                                ATAATTCC GTTGTA GT   TCG
                                     _     _ CTT
GAM1082  UBL3     3'  GTTAAATGAAGTTTCCTCATA  24025     T    TAATA
                                TAT AGGGA    TTCATTTAGC
                                |||  |||||    ||||||||||
                                ATA TCCTT    AAGTAAATTG
                                  C    TG___
GAM1082  VBP1     3'  GCTGGGTGATACAGATTCTGAT 14030         ATAATAT
              A                   TATTAGGG      TCATTTAGC
                                |||||||||      |||||||||
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                                ATAGTCTT      AGTGGGTCG
                                    AGACAT_
GAM1082  WHSC1L1   3'  GCTGGATGGGTACAGCTTAA   35500       GATAA
                                TTAGG     TATTCATTTAGC
                                |||||     ||||||||||||
                                AATTC     ATGGGTAGGTCG
                                   GAC__
GAM1082  XPR1      3'  GCTGGGTGGGTGGGAAATATGA 17622       GGGATAA
           TG                     TATTA      TATTCATTTAGC
                                |||||      ||||||||||||
                                GTAGT      GTGGGTGGGTCG
                                   ATAAAGG
GAM1082  ZNF255    5'  TGAATAGTATTCCATGGTG    20499       _     A
                                TATTA GGGATA TATTCA
                                ||||| |||||| ||||||
                                GTGGT CCTTAT ATAAGT
                                   A     G
GAM1082  A4GALT    3'  GCTGGGTGGGGAGGCTCTTTAG 34301        TAATA
                                TTAGGGA     TTCATTTAGC
                                |||||||     ||||||||||
                                GATTTCT     GGGTGGGTCG
                                    CGGAG
GAM1082  AKAP8     3'  CTGAATCAGTTCTCTAATA    20734         TAAT   C
                                TATTAGGGA    ATT ATTTAG
                                |||||||||    ||| ||||||
                                ATAATCTCT    TGA TAAGTC
                                      ____   C
GAM1082  AKAP8     3'  GCTGAAGTACATTGTCCTTAG  20736          ATTCA
                                TTAGGGATAAT     TTTAGC
                                ||||||||||     ||||||
                                GATTCCTGTTA     AAGTCG
                                      CATG_
GAM1082  ALLC      5'  ATTTTGTGAATATTATCTTTTG 37978      T            TTAGC
           TA                     TAT AGGGATAATATTCAT
                                ||| ||||||||||||||
                                ATG TTTCTATTATAAGTG
                                  T            TTTTAG
GAM1082  ARF4      3'  TGGAATTATTCCTAATA      83708            A
                                TATTAGGGATAAT TTCA
                                |||||||||||| ||||
                                ATAATCCTTATTA AGGT
                                      _
GAM1082  ARG99     3'  GCTAAGTGAGCTTTATCT     50012        TA
                                GGATAA  TTCATTTAGC
                                ||||||  ||||||||||
                                TCTATT  GAGTGAATCG
                                   TC
GAM1082  C12orf5   3'  CTAGATGTCATCTCTGG      40169         AATATT
                                TTAGGGAT     CATTTAG
                                ||||||||     |||||||
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                                GGTCTCTA     GTAGATC
                                     CT____
GAM1082  C1orf9    3'  TGGGTATTGTTTGTAATG    33162       G
                                TATTA GGATAATATTCA
                                ||||| ||||||||||||
                                GTAAT TTTGTTATGGGT
                                   G
GAM1082  C20orf126 3'  GCTGAATGAAGAACAGAATCTT 48734         ATAATA__
              GGTG                   TATTAGGG       TTCATTTAGC
                                ||||||||       ||||||||||
                                GTGGTTCT       AAGTAAGTCG
                                     AAGACAAG
GAM1082  C20orf142 3'  GTTAGGCACTTTTTGTCCCTGG 75287           TATTCA
              TA                   TATTAGGGATAA     TTTAGC
                                ||||||||||||     ||||||
                                ATGGTCCCTGTT     GGATTG
                                       TTTCAC
GAM1082  C20orf162 5'  CTGAATGGGCTCCTGAT     55499        ATAATA
                                ATTAGGG     TTCATTTAG
                                |||||||     |||||||||
                                TAGTCCT     GGGTAAGTC
                                     C_____
GAM1082  C6.1A     3'  GCTAGGTGACAAGTTCTTGG   44533        AATAT
                                TTAGGGAT     TCATTTAGC
                                ||||||||     |||||||||
                                GGTTCTTG     AGTGGATCG
                                     AAC__
GAM1082  C8orf4    3'  TGAGTATTGTCTATTGGTA    39692        _
                                TATTAG GGATAATATTCA
                                |||||| ||||||||||||
                                ATGGTT TCTGTTATGAGT
                                   A
GAM1082  CAMKK2    3'  CTAGATGTGGCTCCTAGTG    22619        ATAATATT
                                TATTAGGG       CATTTAG
                                ||||||||       |||||||
                                GTGATCCT       GTAGATC
                                     CGGT____
GAM1082  CBX8      3'  GTTGGAAAGATTATCTCTAG   40610          ATTCA
                                TTAGGGATAAT     TTTAGC
                                ||||||||||     ||||||
                                GATCTCTATTA     AGGTTG
                                       GAA__
GAM1082  CDC14A    3'  ATGGTTTTGTCTCTAATG     53965          TAT
                                TATTAGGGATAA   TCAT
                                ||||||||||||   ||||
                                GTAATCTCTGTT   GGTA
                                       TT_
GAM1082  CLIC2     3'  ATGAGTTTATTTCTGATA     8914        GG    T
                                TATTAG  ATAA ATTCAT
                                ||||||  |||| ||||||
```

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                                ATAGTC  TATT TGAGTA
                                   TT   _
GAM1082  CPR2     3'  GCTGAGTGAAAGGCACCCTGA  48834       ATAATA
                                TTAGGG     TTCATTTAGC
                                ||||||     ||||||||||
                                AGTCCC     AAGTGAGTCG
                                   ACGGA_
GAM1082  DCTD     3'  GCTGAATAATGAGTTGTTCCTA 10392          __  C
            G                    TTAGGGATAAT  ATT ATTTAGC
                                ||||||||||  ||| |||||||
                                GATCCTTGTTG  TAA TAAGTCG
                                      AG  _
GAM1082  DDM36    3'  GTTAGGGTCTTTACTCCCTAAT 40928         _  TATTCA
            G                    TATTAGGGA TAA     TTTAGC
                                |||||||| |||     ||||||
                                GTAATCCCT ATT     GGATTG
                                      C  TCTG__
GAM1082  DJ667H12.2 3'  GCTAGATGAAATGGCTTAATG  39478       GATA  A
                                TATTAGG   AT TTCATTTAGC
                                |||||||   || ||||||||||
                                GTAATTC   TA AAGTAGATCG
                                   GG__  _
GAM1082  DKFZP434A0225 3'  GCTAGGTGGAGTATGCTTGATA 95524       G  ATA
                                TATTAGG ATA   TTCATTTAGC
                                ||||||| |||   ||||||||||
                                ATAGTTC TAT   AGGTGGATCG
                                   G  G__
GAM1082  DKFZP434H0820 3'  GTTGGGTGGGCCCTCCCTGA   64585       TAATA
                                TTAGGGA    TTCATTTAGC
                                |||||||    ||||||||||
                                AGTCCCT    GGGTGGGTTG
                                   CCC__
GAM1082  DKFZP564O0523 3'  GCTAAGTTTTGTGTTTTTTTTA 50421         T    TC_
            GTA                    TATTAGGGA AATAT   ATTTAGC
                                ||||||||| |||||   |||||||
                                ATGATTTTT TTGTG   TGAATCG
                                      T    TTT
GAM1082  DKFZP761E2110 3'  GAGTATTTATTCCTAATA    48963          _
                                TATTAGGGATAA TATTC
                                |||||||||||| |||||
                                ATAATCCTTATT ATGAG
                                      T
GAM1082  DKFZP761F241 3'  GCTGAGTAATTGTTTCTAATG  49582       GG    ATTC
                                TATTAG  ATAAT    ATTTAGC
                                ||||||  |||||    |||||||
                                GTAATC  TGTTA    TGAGTCG
                                   TT    A___
GAM1082  DKFZP761F241 3'  GCTGAGTAATTGTTTCTAATG  49583       GG    ATTC
                                TATTAG  ATAAT    ATTTAGC
                                ||||||  |||||    |||||||
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                                GTAATC  TGTTA    TGAGTCG
                                   TT    A___
GAM1082  DKFZp761G0313 3'  AAATGAAATTATCTTTGATA   66390           A
                                TATTAGGGATAAT TTCATTT
                                ||||||||||||| |||||||
                                ATAGTTTCTATTA AAGTAAA
                                                 _
GAM1082  DKFZp761O132 5'  GCTGGATGGATGTTTGTTGA   51170     G  TA
                                TTAG GA  ATATTCATTTAGC
                                |||| ||  |||||||||||||
                                AGTT TT  TGTAGGTAGGTCG
                                  G  __
GAM1082  EIF2S1    3'  GCTGAATATTTTTTATTTCTAA 15847     GG    TATTC
                                TTAG  ATAA    ATTTAGC
                                ||||  ||||    |||||||
                                AATC  TATT    TAAGTCG
                                  TT    TTTTA
GAM1082  ENPP4     3'  GTTAAGTGGCAGAATAGCCTTA 30718        ATAATAT_
            GTG                   TATTAGGG       TCATTTAGC
                                |||||||||       |||||||||
                                GTGATTCC       GGTGAATTG
                                     GATAAGAC
GAM1082  ERAP140   3'  GTTGAATGCAATTTTTATTTTT 75707          T_  _
            GGTA                   TATTAGGGATAA  ATT CATTTAGC
                                |||||||||||  ||| ||||||||
                                ATGGTTTTTATT  TAA GTAAGTTG
                                      TT   C
GAM1082  FBX30     3'  CTAGATGGGTACCAGGTG    53745     TA  GATAA
                                TAT  GG    TATTCATTTAG
                                |||  ||    ||||||||||
                                GTG  CC    ATGGGTAGATC
                                  GA  _____
GAM1082  FLJ10300  3'  ATGAATATTTCTTTGGTA    36468         T
                                TATTAGGGA AATATTCAT
                                |||||||| |||||||||
                                ATGGTTTCT TTATAAGTA
                                                _
GAM1082  FLJ10375  5'  GTTGAATGAATGTCTGGCTC   36560     ATA_
                                GGG    ATATTCATTTAGC
                                |||    |||||||||||||
                                CTC    TGTAAGTAAGTTG
                                  GGTC
GAM1082  FLJ10656  3'  GTTAGGTGGATAGTCCTGTAGT 36909      _    AA
            G                    TATTA GGGAT  TATTCATTTAGC
                                ||||| |||||  ||||||||||||
                                GTGAT TCCTG  ATAGGTGGATTG
                                   G    __
GAM1082  FLJ10936  3'  CTGAATGGAAGTCTTGA     37442       ATAATA
                                TTAGGG     TTCATTTAG
                                ||||||     |||||||||
```

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                                AGTTCT     AGGTAAGTC
                                   GA____
GAM1082  FLJ10980  3'  GTGATGTTTGTCTCTAGTG   65254          TAT
                                TATTAGGGATAA   TCAT
                                ||||||||||||  ||||
                                GTGATCTCTGTT   AGTG
                                      TGT
GAM1082  FLJ11149  3'  GCTAAATGCTATCTTTAG    37687         ATATT
                                TTAGGGATA    CATTTAGC
                                |||||||||    ||||||||
                                GATTTCTAT    GTAAATCG
                                   C____
GAM1082  FLJ12649  3'  GCTGTCAGATTGTTTCTAATA  45094       GG    ATTCATT
                                TATTAG  ATAAT      TAGC
                                ||||||  |||||      ||||
                                ATAATC  TGTTA      GTCG
                                   TT    GACT___
GAM1082  FLJ12787  3'  ATCTGGGATGGATATTAATTTT 50689         A          AGC
            AATA                   TATTAGGG TAATATTCATTT
                                ||||||||  ||||||||||||
                                ATAATTTT ATTATAGGTAGG
                                     A          GTCTAT
GAM1082  FLJ12892  3'  GCTGAATGTTGTGTTATCACTA 68453       G       T_
            ATA                    TATTAG GATAATAT  CATTTAGC
                                ||||||  ||||||||  ||||||||
                                ATAATC CTATTGTG  GTAAGTCG
                                   A       TT
GAM1082  FLJ13194  3'  GTTGGAACATTGTTATCCTTG  47873          TTCA
                                TAGGGATAATA    TTTAGC
                                ||||||||||    ||||||
                                GTTCCTATTGT    AGGTTG
                                      TACA
GAM1082  FLJ13657  3'  GTTAGATGAGTATTTAGCTGTG 46140    G  AT_
                                TA GG   AATATTCATTTAGC
                                || ||   ||||||||||||||
                                GT TC   TTATGAGTAGATTG
                                 G  GAT
GAM1082  FLJ13769  3'  GCTGGGTGGCCTGGCCCTGGTA 47257         ATAATAT
                                TATTAGGG      TCATTTAGC
                                ||||||||      |||||||||
                                ATGGTCCC      GGTGGGTCG
                                     GGTCC__
GAM1082  FLJ14437  3'  GTGATATCCCTAGTA      51799          ATAT
                                TATTAGGGATA    TCAT
                                ||||||||||    ||||
                                ATGATCCCTAT    AGTG
                                      ____
GAM1082  FLJ14600  3'  TTAGGTGCTGGTTCCTAG    52530         AATATT
                                TTAGGGAT     CATTTAG
                                ||||||||     |||||||
```

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                              GATCCTTG     GTGGATT
                                  GTC___
GAM1082  FLJ14668  3'  GCTGTGATATATTTTCCTAGTG 52588         T    _   TT
                              TATTAGGGA AATAT TCAT  AGC
                              ||||||||| ||||| ||||  |||
                              GTGATCCTT TTATA AGTG  TCG
                                   _    T   __
GAM1082  FLJ14735  3'  TTGAGTGGATTCCTGGGTA   52670    TA   TAAT
                              TAT  GGGA   ATTCATTTAG
                              |||  ||||   ||||||||||
                              ATG  TCCT   TAGGTGAGTT
                                GG   ____
GAM1082  FLJ20127  3'  GCTAAATGAGATGTTTCTAAT  35080      GG   ATA
                              ATTAG  ATA   TTCATTTAGC
                              |||||  |||   ||||||||||
                              TAATC  TGT   GAGTAAATCG
                                 TT   A__
GAM1082  FLJ20436  3'  GCTAGGTGGGAGCTGTCTTTG  35626        ATA
                              TAGGGATA   TTCATTTAGC
                              ||||||||   ||||||||||
                              GTTTCTGT   GGGTGGATCG
                                   CGA
GAM1082  FLJ20986  5'  GCTAGGTGGATGGATGTT    44837     A_
                              GATA  TATTCATTTAGC
                              ||||  ||||||||||||
                              TTGT  GTAGGTGGATCG
                                AG
GAM1082  FLJ21596  3'  GCTGAGTGGATGGTTGCTGA   46117     G   AA
                              TTAG GAT  TATTCATTTAGC
                              |||| |||  ||||||||||||
                              AGTC TTG  GTAGGTGAGTCG
                                G   __
GAM1082  FLJ21615  3'  AACTTGAATTTATCTTTGATA  50806          T    TTTAGC
                              TATTAGGGATAA ATTCA
                              |||||||||||| |||||
                              ATAGTTTCTATT TAAGT
                                     _    TCAAA
GAM1082  FLJ22969  3'  GCTGAGTGTTTGTTTCTA    69210    GG   TATT
                              TAG  ATAA   CATTTAGC
                              |||  ||||   ||||||||
                              ATC  TGTT   GTGAGTCG
                                TT   T___
GAM1082  FLJ23024  3'  GTTGAATGAGTGAGATGTTTAG 46847      G  AA
                              TTAGG AT  TATTCATTTAGC
                              ||||| ||  ||||||||||||
                              GATTT TA  GTGAGTAAGTTG
                                 G  GA
GAM1082  FLJ23058  3'  GCTGGGTTCCGCTTTGTCCCTG 45526          TATTC_
            GT                 ATTAGGGATAA     ATTTAGC
                              ||||||||||     |||||||
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                                TGGTCCCTGTT     TGGGTCG
                                      TCGCCT
GAM1082  FLJ23416  3'  GTTAAATGCTCTGGGTTTTCTC 50934        T   ATT___
            TGATA                  TATTAGGGA AAT     CATTTAGC
                                   ||||||||| |||     ||||||||
                                   ATAGTCTCT TTG     GTAAATTG
                                         T   GGTCTC
GAM1082  FLJ23560  3'  GTTGAATAAAACAGTGTTATCT 45509            C____
            TTAAT                  ATTAGGGATAATATT     ATTTAGC
                                   ||||||||||||||     |||||||
                                   TAATTTCTATTGTGA     TAAGTTG
                                         CAAAA
GAM1082  GENX-3414 3'  GCTGAGTGAGGTGGCCTGAATG 15457     A   ATAATA
                                   TATT GGG     TTCATTTAGC
                                   |||| |||     ||||||||||
                                   GTAA TCC     GAGTGAGTCG
                                     G   GGTG__
GAM1082  GMPPB     5'  GCTGCTCTGTACTGTCCCTGGT 26223          A   TCATT
            G                       TATTAGGGATA TAT     TAGC
                                   |||||||||| |||     ||||
                                   GTGGTCCCTGT ATG     GTCG
                                         C   TCTC_
GAM1082  HSJ1      3'  GCTGGGCTTTTGTGCCCTGGTA 23082         _    TATTCA
                                   TATTAGGG ATAA     TTTAGC
                                   |||||||| ||||     ||||||
                                   ATGGTCCC TGTT     GGGTCG
                                        G    TTC___
GAM1082  HSPC228   3'  GTTAATAATTTATTTCCCTAAT 33649         T    TTCAT
            A                       TATTAGGGA AATA     TTAGC
                                   ||||||||| ||||     |||||
                                   ATAATCCCT TTAT     AATTG
                                         _    TTAAT
GAM1082  IPLA2(GAMMA) 5'  GCTGAGTGGGTGGCGACCTAG  61341       GATAA
                                   TTAGG     TATTCATTTAGC
                                   |||||     ||||||||||||
                                   GATCC     GTGGGTGAGTCG
                                      AGCG_
GAM1082  ITGB8     3'  GCTAGATGAATAAATGATTCGT 11056     G    AA__
            G                       TA GGAT    TATTCATTTAGC
                                   || ||||    ||||||||||||
                                   GT CTTA    ATAAGTAGATCG
                                    G    GTAA
GAM1082  KALI      3'  GTTGGATGGGCCCATCCTGATA 54696         ATAATA
                                   TATTAGGG     TTCATTTAGC
                                   ||||||||     ||||||||||
                                   ATAGTCCT     GGGTAGGTTG
                                        ACCC__
GAM1082  KIAA0161  3'  GTTGAGTGGACGGACTTATTCC 29208         TA___
            TG                       TAGGGATAA     TTCATTTAGC
                                   |||||||||     ||||||||||
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                                GTCCTTATT    AGGTGAGTTG
                                     CAGGC
GAM1082  KIAA0226  3'  CTGGGTCCTTCCCTGGTG    64258        TAATATTC
                                TATTAGGGA      ATTTAG
                                |||||||||      ||||||
                                GTGGTCCCT      TGGGTC
                                     TCC_____
GAM1082  KIAA0321  3'  GCTGAAGTCAGTGTCTCTGGTG 63055         ATATTCA
                                TATTAGGGATA     TTTAGC
                                ||||||||||     ||||||
                                GTGGTCTCTGT     AAGTCG
                                      GACTG__
GAM1082  KIAA0416  3'  CTGAGTGACTCTTTAATA    32091        TAATAT
                                TATTAGGGA    TCATTTAG
                                |||||||||    ||||||||
                                ATAATTTCT    AGTGAGTC
                                     C_____
GAM1082  KIAA0459  3'  GTTAGGTGGATGTGAACTTAA  61658     GATA
                                TTAGG   ATATTCATTTAGC
                                |||||   ||||||||||||
                                AATTC   TGTAGGTGGATTG
                                   AAG_
GAM1082  KIAA0711  3'  GTTAGATGAGGCTATTGCCTTG 30153       A   __
           ATG                    TATTAGGG TAATA  TTCATTTAGC
                                |||||||| |||||  ||||||||||
                                GTAGTTCC GTTAT  GAGTAGATTG
                                   _    CG
GAM1082  KIAA0769  3'  GCTAGCCAAATTGTCCTTGA   29757         ATTCAT
                                TTAGGGATAAT     TTAGC
                                ||||||||||     |||||
                                AGTTCCTGTTA     GATCG
                                      AACC__
GAM1082  KIAA0794  3'  GTTATAGGATATGGTTTCTAAT 81237      GG  A     ATT
           G                     TATTAG  AT ATATTC   TAGC
                                ||||||  || ||||||   ||||
                                GTAATC  TG TATAGG   ATTG
                                   TT  G     AT_
GAM1082  KIAA0820  3'  GTTGAATGAAGTCTGAAACTCT 69591       ATAATA__
           AGTA                   TATTAGGG       TTCATTTAGC
                                ||||||||       ||||||||||
                                ATGATCTC       AAGTAAGTTG
                                     AAAGTCTG
GAM1082  KIAA0841  3'  GCTTTCCCATGTAGTCCTTAGT 71897         A   TCATTT
           G                     TATTAGGGAT ATAT      AGC
                                ||||||||||| ||||     |||
                                GTGATTCCTG TGTA      TCG
                                      A   CCCTT_
GAM1082  KIAA1116  3'  GTTGGGTGAATTTTGTTTTTAG 30304         T
                                TTAGGGATAA ATTCATTTAGC
                                |||||||||| ||||||||||
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                                GATTTTTGTT TAAGTGGGTTG
                                      T
GAM1082  KIAA1165  3'  GCTAAAACAATATTATTTCCAG 67994      A GG       CA
              TA                  TATT G  ATAATATT  TTTAGC
                                  |||| |  ||||||||  ||||||
                                  ATGA C  TATTATAA  AAATCG
                                    C TT       CA
GAM1082  KIAA1229  3'  GCTAAATGAATGTATATT    62755      _
                                  GATA ATATTCATTTAGC
                                  |||| ||||||||||||
                                  TTAT TGTAAGTAAATCG
                                    A
GAM1082  KIAA1350  3'  GCTAAATGGATAAACCTCATA  73087     T   GATAA
                                  TAT AGG    TATTCATTTAGC
                                  ||| |||    ||||||||||||
                                  ATA TCC    ATAGGTAAATCG
                                    C   AA___
GAM1082  KIAA1372  3'  GTTGGGTGAAGTGCCCTGA   93321       ATAATA
                                  TTAGGG     TTCATTTAGC
                                  ||||||     ||||||||||
                                  AGTCCC     AAGTGGGTTG
                                     GTG___
GAM1082  KIAA1486  3'  TGAATATTGATGTCCTTA    67981        ___
                                  TAGGGATA   ATATTCA
                                  ||||||||   |||||||
                                  ATTCCTGT   TATAAGT
                                       AGT
GAM1082  KIAA1546  3'  GCTAAGAAAATGGTGTCTTTAA 68499          A    CA
              TA                  TATTAGGGATA TATT  TTTAGC
                                  |||||||||||| ||||  ||||||
                                  ATAATTTCTGT GTAA  GAATCG
                                        G    AA
GAM1082  KIAA1554  3'  GTTAGAGGCAGTATCCTTAATA 96860          ATATTCA
                                  TATTAGGGATA      TTTAGC
                                  ||||||||||      ||||||
                                  ATAATTCCTAT      AGATTG
                                        GACGG__
GAM1082  KIAA1557  3'  GCTTTAATGTTATCTTTGA   61786           CATTT
                                  TTAGGGATAATATT    AGC
                                  ||||||||||||||    |||
                                  AGTTTCTATTGTAA    TCG
                                        TT___
GAM1082  KIAA1822  3'  GTTGAGTGGGCATCTTCCT   68196     TA  A
                                  GGGA  AT TTCATTTAGC
                                  ||||  || ||||||||||
                                  TCCT  TA GGGTGAGTTG
                                    TC  C
GAM1082  KIAA1854  3'  TGATTTGTTCCTAGTA      72216          TAT
                                  TATTAGGGATAA   TCA
                                  ||||||||||||   |||
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                                ATGATCCTTGTT  AGT
                                      T__
GAM1082 KIAA1867 3' GCTGAGTGCGCTGTGCTTAGTG 96483      G  ATATT
                                TATTAGG ATA    CATTTAGC
                                ||||||| |||    ||||||||
                                GTGATTC TGT    GTGAGTCG
                                    G  CGC__
GAM1082 KIAA1878 3' GCTGAGTGAGAAGTCTTTTGTA 93369    T    AATA
                                TAT AGGGAT   TTCATTTAGC
                                ||| ||||||   ||||||||||
                                ATG TTTCTG   GAGTGAGTCG
                                  T    AA__
GAM1082 KIAA1957 3' GCTGACTGGAGTATTATTTTTC 76215    T         AT_
            ATG                   TAT AGGGATAATATTC  TTAGC
                                ||| ||||||||||||  |||||
                                GTA TTTTTATTATGAG  AGTCG
                                  C          GTC
GAM1082 KREMEN   3' GCTAGATGGATGTGTACCTGGT 50235      GATA
            G                   TATTAGG   ATATTCATTTAGC
                                |||||||   ||||||||||||
                                GTGGTCC   TGTAGGTAGATCG
                                    ATG_
GAM1082 LANO    3' TAAATGATGTCTCTGATG   47975         ATAT
                                TATTAGGGATA   TCATTTA
                                ||||||||||   |||||||
                                GTAGTCTCTGT   AGTAAAT
                                      ____
GAM1082 LCHN    3' GCTGGGCTGCCCTGTTGTTCCT 87473         TT_ _
            GA                    TTAGGGATAATA  CA TTTAGC
                                ||||||||||||  || ||||||
                                AGTCCTTGTTGT  GT GGGTCG
                                      CCC  C
GAM1082 LGP2    5' GTTAAGTGGGACTGCCCTGG  44380      ATAATA
                                TTAGGG    TTCATTTAGC
                                ||||||    ||||||||||
                                GGTCCC    GGGTGAATTG
                                   GTCA__
GAM1082 LRMP    5' GCTGGATGCCTTATCTCTGG  21586        TATT
                                TTAGGGATAA   CATTTAGC
                                |||||||||   ||||||||
                                GGTCTCTATT   GTAGGTCG
                                      CC__
GAM1082 LY6G6C  3' GCTTCTGTGTTGTCCCCAGTG 48273    A       TCATTT
                                TATT GGGATAATAT    AGC
                                |||| ||||||||||    |||
                                GTGA CCCTGTTGTG    TCG
                                  C        TCT___
GAM1082 MARK2   5' GCTGAATGGAAGTCGCTGGTA 66222      G  AATA
                                TATTAG GAT   TTCATTTAGC
                                |||||| |||   ||||||||||
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                                ATGGTC CTG    AGGTAAGTCG
                                   G   A___
GAM1082  MGC10981  3'  GCTGAGTGTCTCATGTCTTAAT 51986        ATAATATT
             G                    TATTAGGG       CATTTAGC
                                  ||||||||       ||||||||
                                  GTAATTCT       GTGAGTCG
                                      GTACTCT_
GAM1082  MGC12217  5'  GTTGAATGAATGTCTGGCTC   52288     ATA_
                                  GGG    ATATTCATTTAGC
                                  |||    ||||||||||||
                                  CTC    TGTAAGTAAGTTG
                                    GGTC
GAM1082  MGC12921  5'  CTGAGTTCCTGTCCCTGA     64514         ATATTC
                                  TTAGGGATA      ATTTAG
                                  |||||||||      ||||||
                                  AGTCCCTGT      TGAGTC
                                       CCT___
GAM1082  MGC12945  5'  GCTAAGTGGTCGGTTCCTGG   51267        AATAT
                                  TTAGGGAT     TCATTTAGC
                                  ||||||||     |||||||||
                                  GGTCCTTG     GGTGAATCG
                                       GCT__
GAM1082  MGC16142  5'  GCTAAATGGGTCGTGTGTTTCT 52265      GG   AT__
             GA                     TTAG  ATA    ATTCATTTAGC
                                    ||||  |||    ||||||||||
                                    AGTC  TGT    TGGGTAAATCG
                                      TT   GTGC
GAM1082  MGC4268   3'  GCTGAGTGTTTCCTTTGTCCTT 49544         TATT__
             GG                     TTAGGGATAA      CATTTAGC
                                    ||||||||||      ||||||||
                                    GGTTCCTGTT      GTGAGTCG
                                         TCCTTT
GAM1082  MGC4643   3'  GTTGAAGGAATATTGTTTCTAA 52146      GG        A
                                    TTAG  ATAATATTC TTTAGC
                                    ||||  ||||||||| ||||||
                                    AATC  TGTTATAAG AAGTTG
                                      TT        G
GAM1082  NCKX3     3'  GTTGAATGTTTCTGTCTGTGGT 40727       G     ATATT
             G                      TATTA GGATA     CATTTAGC
                                    |||||  |||||     ||||||||
                                    GTGGT  TCTGT     GTAAGTTG
                                       G    CTTT_
GAM1082  NEK1      3'  ATGTATATTATTTCTAATA    97560        GG      T
                                    TATTAG  ATAATAT CAT
                                    ||||||  ||||||| |||
                                    ATAATC  TATTATA GTA
                                       TT      T
GAM1082  POLYDOM   3'  GCTAGCATTGTTGTTCTTGGT  44687           TTCAT
                                    ATTAGGGATAATA     TTAGC
                                    ||||||||||||      |||||
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                                TGGTTCTTGTTGT    GATCG
                                       TAC__
GAM1082  PPM1A    3'  GCTGGGCCTGCTGCTGTTCCTA 41009          ATATTCA_
              GTA                  TATTAGGGATA       TTTAGC
                                   ||||||||||        ||||||
                                   ATGATCCTTGT       GGGTCG
                                         CGTCGTCC
GAM1082  PPP1R10  3'  GCTAAGTTCATTATTCCTCATG 12231     T       ATTC
                                   TAT AGGGATAAT    ATTTAGC
                                   ||| |||||||||    |||||||
                                   GTA TCCTTATTA    TGAATCG
                                     C        CT__
GAM1082  PRAX-1   3'  CTAAATGGCTCCTTAA      17655        TAATAT
                                   TTAGGGA     TCATTTAG
                                   |||||||     ||||||||
                                   AATTCCT     GGTAAATC
                                       C_____
GAM1082  PRO0159  5'  GCTGGGTGGGTATAGGCT    26947    ATA
                                   GG   ATATTCATTTAGC
                                   ||   ||||||||||||
                                   TC   TATGGGTGGGTCG
                                    GGA
GAM1082  PRO1430  3'  TGAGTATTGTCTATTGGTA    38357       _
                                   TATTAG GGATAATATTCA
                                   |||||| ||||||||||||
                                   ATGGTT TCTGTTATGAGT
                                       A
GAM1082  PSKH1    3'  CTGGGTGGAGTGTCCT      68797       ATA
                                   GGGATA   TTCATTTAG
                                   ||||||   |||||||||
                                   TCCTGT   AGGTGGGTC
                                       G__
GAM1082  PSMD10   3'  GTGTTGTTGTCCCCAGTG    12533      A        TT
                                   TATT GGGATAATA  CAT
                                   |||| |||||||||  |||
                                   GTGA CCCTGTTGT  GTG
                                     C        T_
GAM1082  RAB40A   5'  GTTGGGTGAATATTATTTATGA 82945     GG
                                   TTA  GATAATATTCATTTAGC
                                   |||  ||||||||||||||||
                                   AGT  TTATTATAAGTGGGTTG
                                     AT
GAM1082  RBM11    3'  TGCATATTGTTCCTAATG    59239             T
                                   TATTAGGGATAATAT CA
                                   |||||||||||||| ||
                                   GTAATCCTTGTTATA GT
                                             C
GAM1082  SCDGF-B  3'  GTTAGATGAGTGACCTAA    53634       GATAA
                                   TTAGG    TATTCATTTAGC
                                   |||||    ||||||||||||
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                                AATCC    GTGAGTAGATTG
                                  A____
GAM1082 SEMA7A   3' GCTGGGTGGCTGGTGTTCCTGA 14610        A  TT
                                TTAGGGATA TA  CATTTAGC
                                ||||||||| ||  ||||||||
                                AGTCCTTGT GT  GTGGGTCG
                                    G  CG
GAM1082 SGK2    3' GCTGGGTACGTGACTATCCCTA 33252         A_  TC
           ATA                   TATTAGGGATA  TAT  ATTTAGC
                                ||||||||||  |||  |||||||
                                ATAATCCCTAT  GTG  TGGGTCG
                                      CA   CA
GAM1082 ShrmL   3' GTTATTGGTGTTTGTTCCTGAT 40851          TAT   TT
           G                    TATTAGGGATAA   TCA  TAGC
                                ||||||||||||   |||  ||||
                                GTAGTCCTTGTT   GGT  ATTG
                                      TGT   T_
GAM1082 SLC38A4  3' GCTTTTTCATGTTATTCCTAA  36343          TCATTT
                                TTAGGGATAATAT     AGC
                                ||||||||||||      |||
                                AATCCTTATTGTA     TCG
                                      CTTTT_
GAM1082 SPTLC2   3' GCTAGTTCTCTTTTATTCTTGA 17997          TATTCAT
           TG                   TATTAGGGATAA      TTAGC
                                ||||||||||||      |||||
                                GTAGTTCTTATT      GATCG
                                      TTCTCTT
GAM1082 ST13    3' TGGATATGTGGTTCCTGATG   15434         A__
                                TATTAGGGAT   ATATTCA
                                ||||||||||   |||||||
                                GTAGTCCTTG   TATAGGT
                                     GTG
GAM1082 STRIN    3' GTTAAAATTGGGTATGTTCTTA 33232          A    __
           ATA                    TATTAGGGATA TATTCA  TTTAGC
                                ||||||||||| ||||||  ||||||
                                ATAATTCTTGT ATGGGT  AAATTG
                                      _     TA
GAM1082 SWAP2    3' GCTGCTGGTTTTATCTCTAGTG 23901          TAT   TT
                                TATTAGGGATAA   TCA  TAGC
                                ||||||||||||   |||  ||||
                                GTGATCTCTATT   GGT  GTCG
                                      TT_   C_
GAM1082 TEB4    3' GCTAGGTGAGGAAATTATTTTT 61284          A__
           AAT                    ATTAGGGATAAT   TTCATTTAGC
                                ||||||||||||   ||||||||||
                                TAATTTTTATTA   GAGTGGATCG
                                      AAG
GAM1082 TTC2    3' GTTGGATGCCCTGTGTCTCTG  13877        ATATT
                                TAGGGATA    CATTTAGC
                                ||||||||    ||||||||
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                                GTCTCTGT    GTAGGTTG
                                     GTCCC
GAM1082 UBE3B    5' GCTGGGTGATTTGTTCCTG   77446        TAT
                                TAGGGATAA   TCATTTAGC
                                |||||||||   |||||||||
                                GTCCTTGTT   AGTGGGTCG
                                     T__
GAM1082 VEST1    3' GTTAAGTGAATGGATCTAA   54764      GATAA
                                TTAGG    TATTCATTTAGC
                                |||||    ||||||||||||
                                AATCT    GTAAGTGAATTG
                                   AG___
GAM1082 WBSCR20A 5' GCTGGATGGAGTGCCCTGG   50572      ATAATA
                                TTAGGG     TTCATTTAGC
                                ||||||     ||||||||||
                                GGTCCC     AGGTAGGTCG
                                    GTG___
GAM1082 XYLT1    3' TGAACTATTCTCCTTAGTA   78416        T   _
                                TATTAGGGA AATA TTCA
                                ||||||||| |||| ||||
                                ATGATTCCT TTAT AAGT
                                     C   C
GAM1082 ZFP95    3' GCTGGATGGTATGTGTTTCTG 28120    GG   ATAT
                                TAG  ATA    TCATTTAGC
                                |||  |||    |||||||||
                                GTC  TGT    GGTAGGTCG
                                  TT   GTAT
GAM1082 ZNF197   3' GTTAAGTGAAAGGATCTTTG  23759       AATA
                                TAGGGAT    TTCATTTAGC
                                |||||||    ||||||||||
                                GTTTCTA    AAGTGAATTG
                                    GGA_
GAM1082 ZNF225   5' GCTGCAGTTTTGTCCCTGGTA 26273          T   CATT
                                TATTAGGGATAA ATT    TAGC
                                |||||||||||| |||    ||||
                                ATGGTCCCTGTT TGA    GTCG
                                       T   C___
GAM1082 ZNF33A   3' CTAACATTATCCTTGATG    92994          ATTCAT
                                TATTAGGGATAAT     TTAG
                                ||||||||||||      ||||
                                GTAGTTCCTATTA     AATC
                                       C_____
GAM1082 LOC115219 5' GCTGGGTGAGTGTGCACTTGGT 73697       GATA
                                ATTAGG    ATATTCATTTAGC
                                ||||||    ||||||||||||
                                TGGTTC    TGTGAGTGGGTCG
                                   ACG_
GAM1082 LOC122830 5' CTGAGTGAGAACCTTGG     74630       ATAATA
                                TTAGGG     TTCATTTAG
                                ||||||     |||||||||
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                                GGTTCC     GAGTGAGTC
                                   AA____
GAM1082  LOC123643 5'  TTAGATGAAGCCCCTGA     76529       ATAATA
                                TTAGGG     TTCATTTAG
                                ||||||     |||||||||
                                AGTCCC     AAGTAGATT
                                   CG____
GAM1082  LOC127703 3'  GCTGAGGCTATTGTCCCTGATG 75178            TTCA
                                TATTAGGGATAATA    TTTAGC
                                ||||||||||||||    ||||||
                                GTAGTCCCTGTTAT    GAGTCG
                                      CG__
GAM1082  LOC130502 3'  GTTGAATGGGTTTTTTTTAATG 75444         TAAT
                                TATTAGGGA    ATTCATTTAGC
                                |||||||||    ||||||||||
                                GTAATTTTT    TGGGTAAGTTG
                                   TT__
GAM1082  LOC137221 5'  GCTGGCTGAGTTTTATTTCTGA 76475       GG    T     T
            TG                    TATTAG  ATAA ATTCA TTAGC
                                ||||||  |||| ||||| |||||
                                GTAGTC  TATT TGAGT GGTCG
                                   TT    T     C
GAM1082  LOC137221 5'  TGAGTTTTATTTCTGATG    76476       GG    T
                                TATTAG  ATAA ATTCA
                                ||||||  |||| |||||
                                GTAGTC  TATT TGAGT
                                   TT    T
GAM1082  LOC143381 3'  GTTGAATGAAAAGCCTTGA    77062       ATAATA
                                TTAGGG     TTCATTTAGC
                                ||||||     ||||||||||
                                AGTTCC     AAGTAAGTTG
                                   GAA___
GAM1082  LOC144809 3'  TGACAGTGAATAATTTCTAATA 84105       GG  AA       TAGC
                                TATTAG  AT  TATTCATT
                                ||||||  ||  ||||||||
                                ATAATC  TA  ATAAGTGA
                                   TT  __       CAGTA
GAM1082  LOC145231 3'  AATGGGTATTGTCCCTAG    84234
                                TTAGGGATAATATTCATT
                                ||||||||||||||||||
                                GATCCCTGTTATGGGTAA

GAM1082  LOC146455 3'  TATTTGATTTGTCTCTGATA   78466          TAT   TT
                                TATTAGGGATAA   TCA  TA
                                ||||||||||||   |||  ||
                                ATAGTCTCTGTT   AGT  AT
                                      T__   TT
GAM1082  LOC146723 3'  GCTAAAGACCTTATCCTTG    78681         TAT  A
                                TAGGGATAA   TC TTTAGC
                                |||||||||   || ||||||
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                                GTTCCTATT   AG AAATCG
                                     CC_  _
GAM1082  LOC146990 5'  GTTGTTTTTGTGTTGTTCCTG  84956          TCATT
                                TAGGGATAATAT    TAGC
                                ||||||||||||    ||||
                                GTCCTTGTTGTG    GTTG
                                      TTTTT
GAM1082  LOC148918 5'  TGGGTATGTCTCTGGTA    79835          A
                                TATTAGGGATA TATTCA
                                |||||||||||| ||||||
                                ATGGTCTCTGT ATGGGT
                                      _
GAM1082  LOC149832 5'  GTGATTTTGTCTCTAGTG    85869          TAT
                                TATTAGGGATAA   TCAT
                                ||||||||||||   ||||
                                GTGATCTCTGTT   AGTG
                                      TT_
GAM1082  LOC149844 3'  GTTGAATGGGCTGATCCT    80347      AATA
                                GGGAT    TTCATTTAGC
                                |||||    ||||||||||
                                TCCTA    GGGTAAGTTG
                                   GTC_
GAM1082  LOC149911 3'  GCTAAGTGAGTGAAGAGTC    85874     AA__
                                GAT    TATTCATTTAGC
                                |||    ||||||||||||
                                CTG    GTGAGTGAATCG
                                  AGAA
GAM1082  LOC150372 3'  GCTGAATGAATGGGCCTGG    80617      GATAA
                                TTAGG     TATTCATTTAGC
                                |||||     ||||||||||||
                                GGTCC     GTAAGTAAGTCG
                                   GG___
GAM1082  LOC150933 3'  GTTGATTTTTGTTGTTCCTGA  86339          TTCAT
                                TTAGGGATAATA    TTAGC
                                ||||||||||||    |||||
                                AGTCCTTGTTGT    AGTTG
                                      TTTT_
GAM1082  LOC151516 3'  GCTAGAAATGCTTGTCTTTGA  81067          _   CA
                                TTAGGGATAA TATT  TTTAGC
                                |||||||||| ||||  ||||||
                                AGTTTCTGTT GTAA  AGATCG
                                     C   __
GAM1082  LOC152185 3'  CTCACTGAGTTTGTTCTTAATA 59200          T    TTTAGC
                                TATTAGGGATAA ATTCA
                                |||||||||||| |||||
                                ATAATTCTTGTT TGAGT
                                      _    CACTCT
GAM1082  LOC152245 5'  GTTGGGTGGGCACCCCCTGAT  86784        ATAATA
                                ATTAGGG     TTCATTTAGC
                                |||||||     ||||||||||
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                                TAGTCCC     GGGTGGGTTG
                                    CCAC__
GAM1082  LOC152674 5'  GTTGAGTGGAAGATGTCTTAGT 87005        ATAATA
               A                    TATTAGGG     TTCATTTAGC
                                    ||||||||     ||||||||||
                                    ATGATTCT     AGGTGAGTTG
                                        GTAGA_
GAM1082  LOC153205 3'  GCTAACAATGGTTATCTCTGA  87160          ATTCAT
                                    TTAGGGATAAT     TTAGC
                                    ||||||||||      |||||
                                    AGTCTCTATTG     AATCG
                                          GTAAC_
GAM1082  LOC157657 3'  TGGAATTATTCCTGATA     82439            A
                                    TATTAGGGATAAT TTCA
                                    |||||||||||| ||||
                                    ATAGTCCTTATTA AGGT
                                                 _
GAM1082  LOC157798 5'  CTGGATGAAACCTTAGTA     87857        ATAATA
                                    TATTAGGG     TTCATTTAG
                                    ||||||||     |||||||||
                                    ATGATTCC     AAGTAGGTC
                                        A_____
GAM1082  LOC157858 5'  GTTAAATGAGGGGCTCTCTGA  87895       TAATA
                                    TTAGGGA     TTCATTTAGC
                                    |||||||     ||||||||||
                                    AGTCTCT     GAGTAAATTG
                                        CGGG_
GAM1082  LOC161589 3'  GGCTAAATGAATATTATCCCTA 83160
               ATA                     TATTAGGGATAATATTCATTTAGC
                                       ||||||||||||||||||||||||
                                       ATAATCCCTATTATAAGTAAATCG
                                                   GA
GAM1082  LOC164971 5'  GCTAATATATTATCCTTTGGTG 83349        _        TCAT
                                    TATTAG GGATAATAT    TTAGC
                                    |||||| |||||||||    |||||
                                    GTGGTT CCTATTATA    AATCG
                                        T        T___
GAM1082  LOC170127 3'  GCTGAGTGCCTGCCCTTGATG  83460        ATAATATT
                                    TATTAGGG       CATTTAGC
                                    ||||||||       ||||||||
                                    GTAGTTCC       GTGAGTCG
                                        CGTCC___
GAM1082  LOC196394 3'  GTTGGATGAGTCATTATTTTTG 89032          _
               A                     TTAGGGATAAT ATTCATTTAGC
                                     |||||||||| ||||||||||
                                     AGTTTTTATTA TGAGTAGGTTG
                                           C
GAM1082  LOC199704 5'  GCTCCTATGAGTGTTAACCTTG 89697        A        TT_
               ATG                     TATTAGGG TAATATTCAT   AGC
                                       |||||||| ||||||||||   |||
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                                GTAGTTCC ATTGTGAGTA   TCG
                                     A         TCC
GAM1082  LOC199953 3'  TTGGGTGAGGGTCCTGGT    89887        ATAATA
                                ATTAGGG     TTCATTTAG
                                |||||||     |||||||||
                                TGGTCCT     GAGTGGGTT
                                   GG____
GAM1082  LOC200352 3'  CTAGATGCATTCCTGA      90233         AATATT
                                TTAGGGAT     CATTTAG
                                ||||||||     |||||||
                                AGTCCTTA     GTAGATC
                                     C_____
GAM1082  LOC200399 3'  GTTGGGCTGATGTTGTTGTTGG 90241       G        CA
                TG                    TATTAG GATAATATT  TTTAGC
                                |||||| |||||||||  ||||||
                                GTGGTT TTGTTGTAG  GGGTTG
                                   G        TC
GAM1082  LOC200734 3'  GCTGGAAAAGAGTATTTTTCTA 90280       GG T      A__
                ATA                   TATTAG  A AATATTC   TTTAGC
                                |||||| | |||||||   ||||||
                                ATAATC  T TTATGAG   AGGTCG
                                   TT _      AAA
GAM1082  LOC200830 3'  TGAATTGTAATTCCTGATG    91731          A   _
                                TATTAGGGAT ATA TTCA
                                |||||||||| ||| ||||
                                GTAGTCCTTA TGT AAGT
                                     A   T
GAM1082  LOC200942 3'  GTTAGGGGAGCCTTTGTCTTTA 90379           TA_   A
                GTG                   TATTAGGGATAA   TTC TTTAGC
                                ||||||||||||   ||| ||||||
                                GTGATTTCTGTT   GAG GGATTG
                                      TCC   G
GAM1082  LOC201736 5'  TGGGTATGTGCCTAGTG     90482        G   A
                                TATTAGG ATA TATTCA
                                ||||||| ||| ||||||
                                GTGATCC TGT ATGGGT
                                   G   _
GAM1082  LOC202460 5'  GCTGAGAGATATTATTCTTAG  90673            CA
                                TTAGGGATAATATT  TTTAGC
                                ||||||||||||||  ||||||
                                GATTCTTATTATAG  GAGTCG
                                      A_
GAM1082  LOC202934 5'  GCTGGATGAAATATTCT     92042        ATA
                                GGGATA   TTCATTTAGC
                                ||||||   ||||||||||
                                TCTTAT   AAGTAGGTCG
                                   A__
GAM1082  LOC203286 3'  GCTGGATGTCCAAGTCCCTG   92146        AATATT
                                TAGGGAT     CATTTAGC
                                |||||||     ||||||||
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                                GTCCCTG     GTAGGTCG
                                    AACCT_
GAM1082  LOC219902 5'  GCTAACATGTTATCTCTGA   93129          TCAT
                                TTAGGGATAATAT   TTAGC
                                ||||||||||||   |||||
                                AGTCTCTATTGTA   AATCG
                                      C___
GAM1082  LOC221496 3'  GCTGGATGAATAAACTATTT  93642      A__
                                GGATA  TATTCATTTAGC
                                |||||  ||||||||||||
                                TTTAT  ATAAGTAGGTCG
                                   CAA
GAM1082  LOC221687 3'  GTTGAATGTATATATTTCTAA 93871     GG  A  T
                                TTAG  ATA TAT CATTTAGC
                                ||||  ||| ||| ||||||||
                                AATC  TAT ATA GTAAGTTG
                                  TT  _  T
GAM1082  LOC221895 3'  GTTAGATGAGTAAACCTCTA  94106      ATAA
                                TAGGG   TATTCATTTAGC
                                |||||   ||||||||||||
                                ATCTC   ATGAGTAGATTG
                                   CAA_
GAM1082  LOC221931 3'  GCTGGGTGATGTTAGGTTTCTG 95631     GG  AATAT_
           G                     TTAG  AT     TCATTTAGC
                                ||||  ||     |||||||||
                                GGTC  TG     AGTGGGTCG
                                  TT  GATTGT
GAM1082  LOC222662 3'  GCTAAATGGGTCCATCTCTAG  94414       AAT
                                TTAGGGAT   ATTCATTTAGC
                                ||||||||   ||||||||||||
                                GATCTCTA   TGGGTAAATCG
                                     CC_
GAM1082  LOC253698 3'  GCTGAAAATGTCATTTCTAGTA 96546      GG  A    CA
                                TATTAG  AT ATATT  TTTAGC
                                ||||||  || |||||  ||||||
                                ATGATC  TA TGTAA  AAGTCG
                                    TT  C    __
GAM1082  LOC255391 5'  GTTGGGTGGGTTTCTCTGG   99458       TAAT
                                TTAGGGA   ATTCATTTAGC
                                |||||||   ||||||||||||
                                GGTCTCT   TGGGTGGGTTG
                                     T___
GAM1082  LOC255465 5'  GCTGGATGAAATATTCT     99118       ATA
                                GGGATA   TTCATTTAGC
                                ||||||   ||||||||||
                                TCTTAT   AAGTAGGTCG
                                   A__
GAM1082  LOC257481 3'  GCTGTTCCGATGGTGTCTTTGA 61763          A   CATT
           TG                    TATTAGGGATA TATT   TAGC
                                ||||||||||| ||||   ||||
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                                GTAGTTTCTGT GTAG   GTCG
                                      G   CCTT
GAM1082 LOC51316 3' ATAAATGAATGTTGTCCCTGA 60247              GC
                                TTAGGGATAATATTCATTTA
                                ||||||||||||||||||||
                                AGTCCCTGTTGTAAGTAAAT
                                      AT
GAM1082 LOC83468 3' TCTTTATGAATATTACCTTTGA 49344       A       TT  C
           TA                    TATTAGGG TAATATTCAT  AG
                                ||||||||| ||||||||||  ||
                                ATAGTTTC ATTATAAGTA  TC
                                     C        TT  TT
GAM1082 LOC90190 3' GCTAACTTTTGTGTTGACTCTG 62427       A     TCAT_
           GTG                    TATTAGGG TAATAT    TTAGC
                                ||||||||| ||||||    |||||
                                GTGGTCTC GTTGTG    AATCG
                                     A     TTTTC
GAM1082 LOC90246 3' GCTAAATGGATGTTGCTTGA  62587     GA
                                TTAGG  TAATATTCATTTAGC
                                |||||  ||||||||||||||
                                AGTTC  GTTGTAGGTAAATCG
                                  __
GAM1082 LOC91137 3' TGGTATAGTATCCTTAATA   57860         A  _
                                TATTAGGGATA TAT TCA
                                |||||||||||  ||| |||
                                ATAATTCCTAT ATA GGT
                                      G   T
GAM1082 LOC91548 5' CTGGGTGAGACCCCTGG    67008      ATAATA
                                TTAGGG     TTCATTTAG
                                ||||||     |||||||||
                                GGTCCC     GAGTGGGTC
                                   CA____
GAM1082 LOC92140 3' GCTTATGAAGTTATTTTTGATA 68826          A    TT
                                TATTAGGGATAAT TTCAT  AGC
                                |||||||||||| |||||  |||
                                ATAGTTTTTATTG AAGTA  TCG
                                       _    T_
GAM1082 LOC92283 3' TGAAGTTGTTTCTAATG     69306      GG    A
                                TATTAG  ATAAT TTCA
                                ||||||  ||||| ||||
                                GTAATC  TGTTG AAGT
                                   TT    _
GAM1082 LOC92344 3' GTTTGAGGGTATTATCTTCTGG 69578       _       ATTTAGC
           TA                    TATTAGG GATAATATTC
                                ||||||| ||||||||||
                                ATGGTCT CTATTATGGG
                                     T        AGTTTG
GAM1082 LOC92379 3' GTTAAATGTTTGATTGTTTTTG 69677          ATT_
           G                     TTAGGGATAAT    CATTTAGC
                                ||||||||||    ||||||||
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                                GGTTTTTGTTA   GTAAATTG
                                      GTTT
GAM1082 LOC92421 3' GCTGAATGAGAATCTCCTGG  69726     _  AATA
                                TTAGG GAT   TTCATTTAGC
                                ||||| |||   ||||||||||
                                GGTCC CTA   GAGTAAGTCG
                                   T  A___
GAM1082 LOC93070 3' CTGAATGGAAGTCTTGA    71806      ATAATA
                                TTAGGG    TTCATTTAG
                                ||||||    |||||||||
                                AGTTCT    AGGTAAGTC
                                   GA____
GAM1083 SCAMP1   3' GCTAAATAAATATTCTCC    18014    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1083 SCAMP1   3' GCTAAATAAATATTCTCC    54500    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1083 NX-17    3' TGAATATCAGCCCCTAATA   40706       ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                     CGAC
GAM1083 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
             TA                   TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM1084 SCAMP1   3' GCTAAATAAATATTCTCC    18013    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1084 SCAMP1   3' GCTAAATAAATATTCTCC    54501    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1084 NX-17    3' TGAATATCAGCCCCTAATA   40706       ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                     CGAC
GAM1084 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
             TA                   TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
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                                ATAATCCCTATTATAAGTAAATCG

GAM1085 SCAMP1   3' GCTAAATAAATATTCTCC    54500    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1085 SCAMP1   3' GCTAAATAAATATTCTCC    54501    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1085 NX-17    3' TGAATATCAGCCCCTAATA   40706       ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                     CGAC
GAM1085 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
             TA                   TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM1086 CELSR3   3' CAAGTTGATCTGAGTATCGTCA 9184      A    TG __  C
                                TGAC ATACT  GG  AAC TG
                                |||| |||||  ||  ||| ||
                                ACTG TATGA  CT  TTG AC
                                  C    GT  AG   A
GAM1086 FY       5' TCTTCAGGCTCCCTGCTTTGTC 10740      TACTT   A
                                GACAA    GGGA CCTGAAGA
                                |||||    |||| ||||||||
                                CTGTT    CCCT GGACTTCT
                                   TCGT_   C
GAM1086 KMO      3' CTTCAAATATAAGTATTATCA  14845    C      GGAACC
                                TGA AATACTTG     TGAAG
                                ||| ||||||||     |||||
                                ACT TTATGAAT     ACTTC
                                  A       ATAA__
GAM1086 RTN3     3' CTTCAGGTTCTCACTCATAGTC 74330     A  ACT
             A                   TGAC AT   TGGGAACCTGAAG
                                |||| ||   ||||||||||||||
                                ACTG TA   ACTCTTGGACTTC
                                  A  CTC
GAM1086 ZNF266   5' TCAGACTCTGTAGGTATTGCA  89692    A      _  AC
                                TG CAATACTTG GGA  CTGA
                                || ||||||||| |||  ||||
                                AC GTTATGGAT TCT  GACT
                                 _       G   CA
GAM1086 C1orf24  3' TCTCCAGTCCCAAGTATT    54796          AC   A
                                AATACTTGGGA  CTG AGA
                                ||||||||||  ||| |||
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                                TTATGAACCCT  GAC TCT
                                      __  C
GAM1086 IGF2AS   3'  CTTCAGGTCACCTTGTCA   33527      TACTT  GA
                                TGACAA    GG  ACCTGAAG
                                ||||||    ||  ||||||||
                                ACTGTT    CC  TGGACTTC
                                   _____  AC
GAM1086 LOC138046 3'  TCTCCATTCCCAAGCATTGCCA 75811    A   A      CC  A
                                TG CAAT CTTGGGAA  TG AGA
                                || |||| ||||||||  || |||
                                AC GTTA GAACCCTT  AC TCT
                                 C   C       __ C
GAM1086 LOC149132 5'  TCTCCAGGCCCTGAACATTCTC 79929     C   AC TG  AA   A
             A                   TGA AAT  T  GG  CCTG AGA
                                ||| |||  |  ||  |||| |||
                                ACT TTA  A  CC  GGAC TCT
                                  C   CA GT  C_   C
GAM1086 LOC152905 3'  CTTCAGGTTCTCACTCATAGTC 61094      A  ACT
             A                   TGAC AT   TGGGAACCTGAAG
                                |||| ||   ||||||||||||||
                                ACTG TA   ACTCTTGGACTTC
                                  A  CTC
GAM1086 LOC91069  3'  CTTCCAGCCAGATATTGTCA   65401       C    GAAC  _
                                TGACAATA TTGG    CTG AAG
                                |||||||| ||||    ||| |||
                                ACTGTTAT GACC    GAC TTC
                                    A   _____   C
GAM1086 LOC96597  5'  CTTTGTCCCAAGTATTCCCA   67459    AC         ACC
                                TG  AATACTTGGGA   TGAAG
                                ||  ||||||||||   |||||
                                AC  TTATGAACCCT   GTTTC
                                 CC         ___
GAM1087 CHRNA2    5'  GCTCTATTCTGTACCTGCCA   7429       TGAAGAA
                                TGGCA      GGAATAGAGC
                                |||||      ||||||||||
                                ACCGT      TCTTATCTCG
                                   CCATG__
GAM1087 CRY2      3'  GCTCCATGGTGGCTTCATGCC  72665         AAGGA  A
                                GGCATGAAG     AT GAGC
                                |||||||||     || ||||
                                CCGTACTTC     TA CTCG
                                     GGTGG  C
GAM1087 DMD       3'  GCTTTACTCTTTCATGCCA    5464          GAA   A
                                TGGCATGAA   GGA TAGAGC
                                |||||||||   ||| ||||||
                                ACCGTACTT   TCT ATTTCG
                                     ___  C
GAM1087 DMD       3'  GCTTTACTCTTTCATGCCA    5465          GAA   A
                                TGGCATGAA   GGA TAGAGC
                                |||||||||   ||| ||||||
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                                ACCGTACTT   TCT ATTTCG
                                     ___   C
GAM1087  EXTL2    3'  CTGTATTTCTTACACGCCA   9326      A  _     GA
                                TGGC TG AAGAAG  ATAG
                                |||| || ||||||  ||||
                                ACCG AC TTCTTT  TGTC
                                  C  A     A_
GAM1087  FAT2     3'  CTCTGGGTTCTTCATCCCA   9349      C       GGAA
                                TGG ATGAAGAA    TAGAG
                                ||| ||||||||    |||||
                                ACC TACTTCTT    GTCTC
                                  C       GG__
GAM1087  KRT15    3'  GCTCTATTCCCCCTCTGCC   11233      T  A AA
                                GGCA GA G  GGAATAGAGC
                                |||| || |  ||||||||||
                                CCGT CT C  CCTTATCTCG
                                  _  _ CC
GAM1087  MAK      5'  GCCGATTCCTTCATGCTA    20948        AGA     AGA
                                TGGCATGA   AGGAAT   GC
                                ||||||||   ||||||   ||
                                ATCGTACT   TCCTTA   CG
                                     ___      GCC
GAM1087  OGG1     5'  GCTCCCTGCTTTTTCATGCCA  34157           GAATA
                                TGGCATGAAGAAG    GAGC
                                ||||||||||||     ||||
                                ACCGTACTTTTTC    CTCG
                                       GTCC_
GAM1087  OPCML    3'  GCTCTACTCATTCCTTCCACCA 11899     CA  AA      _____
                                TGG  TG  GAAGGAA    TAGAGC
                                |||  ||  |||||||    ||||||
                                ACC  AC  CTTCCTT    ATCTCG
                                  __  __      ACTC
GAM1087  PDCL     5'  GCTCCATTCCTTCCGGCGCC   19398     A_  AA       A
                                GGC  TG  GAAGGAAT GAGC
                                |||  ||  |||||||| ||||
                                CCG  GC  CTTCCTTA CTCG
                                  CG  __       C
GAM1087  RRM2B    3'  GCTCCATTCTTTCCATAACA   68433    GC   AA       A
                                TG  ATG  GAAGGAAT GAGC
                                ||  |||  |||||||| ||||
                                AC  TAC  CTTTCTTA CTCG
                                  AA  __       C
GAM1087  TLL2     3'  CTATGCTTCTTCATACCA    25881     C       GA
                                TGG ATGAAGAAG  ATAG
                                ||| |||||||||  ||||
                                ACC TACTTCTTC  TATC
                                  A       G_
GAM1087  TNFSF4   3'  GCTTACATCTTCCTCAGCCA   13913      A  A    AATA
                                TGGC TGA GAAGG    GAGC
                                |||| ||| |||||    ||||
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                                ACCG ACT CTTCT    TTCG
                                  _  C    ACA_
GAM1087 ZNF289   3' CTTTATTCCCTCTCACACCA  65930    CA  A  A
                                TGG  TGA GA GGAATAGAG
                                |||  ||| || |||||||||
                                ACC  ACT CT CCTTATTTC
                                  AC   _  C
GAM1087 ZXDA     3' CTCTATTCATTCCTTGCCA   67163     TGAA  G
                                TGGCA   GAA GAATAGAG
                                |||||   ||| ||||||||
                                ACCGT   CTT CTTATCTC
                                   TC__  A
GAM1087 ARHGEF4  3' CTATTCCTTCTCCAAGCCA   53369     A  A
                                TGGC TG AGAAGGAATAG
                                |||| || ||||||||||
                                ACCG AC TCTTCCTTATC
                                  A  C
GAM1087 ASTN2    3' CTCTGCTTTCTTCCTGCCA   73557     T      AA
                                TGGCA GAAGAAGG  TAGAG
                                ||||| ||||||||  |||||
                                ACCGT CTTCTTTC  GTCTC
                                   C      __
GAM1087 ASTN2    3' GCTCTTCTTCCTTCTTCCTGCC 73560      T       T_
            A                    TGGCA GAAGAAGGAA  AGAGC
                                ||||| ||||||||||  |||||
                                ACCGT CTTCTTCCTT  TCTCG
                                   C         CT
GAM1087 BLP1     3' CTCTACTCCTTCTTCCTG    55298    T      A
                                CA GAAGAAGGA TAGAG
                                || |||||||| |||||
                                GT CTTCTTCCT ATCTC
                                 C        C
GAM1087 C8orf13  5' GCTCTGGGCCTTCTTCCTGCCA 82480      T      AA
                                TGGCA GAAGAAGG  TAGAGC
                                ||||| ||||||||  ||||||
                                ACCGT CTTCTTCC  GTCTCG
                                   C       GG
GAM1087 CAPNS2   5' CTCCATTTCATCTTTTTTCATA 51305    C        ____ A
            CCA                    TGG ATGAAGAAGGA    AT GAG
                                ||| ||||||||||    || |||
                                ACC TACTTTTTTCT    TA CTC
                                  A          ACTT  C
GAM1087 DDX17    5' GCCTATACCTTCTTCACCCCA  22125    CA       A   A
                                TGG  TGAAGAAGG ATAG GC
                                |||  ||||||||| |||| ||
                                ACC  ACTTCTTCC TATC CG
                                  CC        A   _
GAM1087 FBXO24   3' CTAATCCCCCTCATGCTA    25149        A AA   A
                                TGGCATGA G  GGA TAG
                                |||||||| |  ||| |||
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                                ATCGTACT C  CCT ATC
                                    _ CC   A
GAM1087  FLJ11259  3'  GCTCCTTCTCTTCATGCC    37769         A   ATA
                                GGCATGAAGA GGA   GAGC
                                |||||||||| |||   ||||
                                CCGTACTTCT CTT   CTCG
                                     _   C__
GAM1087  FLJ12788  3'  CTCTGTTTCTCCACCCCA    42848     CA  AAGA
                                TGG  TG   AGGAATAGAG
                                |||  ||   ||||||||||
                                ACC  AC   TCTTTGTCTC
                                  CC  C___
GAM1087  FLJ13204  3'  GCTCCCCACTCCTCTGCCA    45759      T  A  A_  AATA
                                TGGCA GA GA  GG   GAGC
                                ||||| || ||  ||   ||||
                                ACCGT CT CT  CC   CTCG
                                   _ C  CA  C___
GAM1087  FLJ23516  5'  CTCCATTCCTTCCCCACC    44886    CA  AA      A
                                GG  TG  GAAGGAAT GAG
                                ||  ||  |||||||| |||
                                CC  AC  CTTCCTTA CTC
                                 __ CC       C
GAM1087  HARSL     3'  GCTCTATTCCATACCGTGCCA  25210       AAGAA
                                TGGCATG    GGAATAGAGC
                                |||||||    ||||||||||
                                ACCGTGC    CCTTATCTCG
                                    CATA_
GAM1087  KCNH8     3'  GCTCCATCTAGGCTCTGCCA   58907      T  A AA_   ATA
                                TGGCA GA G   GGA   GAGC
                                ||||| || |   |||   ||||
                                ACCGT CT C   TCT   CTCG
                                   _ _ GGA   AC_
GAM1087  KIAA0280  3'  CTCTCTCCTCCTCATGCCA   93297       A  A   AT
                                TGGCATGA GA GGA  AGAG
                                |||||||| || |||  ||||
                                ACCGTACT CT CCT  TCTC
                                    C  _   C_
GAM1087  KIAA0286  3'  GCTCCAGGTTATCTTCATGCC  68858         AG AATA
                                GGCATGAAGA  G    GAGC
                                ||||||||||  |    ||||
                                CCGTACTTCT  T    CTCG
                                     AT GGAC
GAM1087  KIAA0290  3'  GCTCCTCCCCCTCATGCCA   66717       A AA   ATA
                                TGGCATGA G  GGA   GAGC
                                |||||||| |  |||   ||||
                                ACCGTACT C  CCT   CTCG
                                    _ CC   C__
GAM1087  KIAA0542  3'  CTCTTTCCTCCTTCATGCC   66662         A    T
                                GGCATGAAG AGGAA AGAG
                                ||||||||| ||||| ||||
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                                CCGTACTTC TCCTT TCTC
                                     C    _
GAM1087 LASP1    3' CTGAAGCCTTCTTCTGCCA   21577      T      AA_
                                TGGCA GAAGAAGG   TAG
                                ||||| ||||||||   |||
                                ACCGT CTTCTTCC   GTC
                                   _       GAA
GAM1087 MAP3K3   3' GCTCTGTTCTTCCTCAGCCA  11541     A  A   G
                                TGGC TGA GAAG AATAGAGC
                                |||| ||| |||| ||||||||
                                ACCG ACT CTTC TTGTCTCG
                                   _  C   _
GAM1087 MGC16943 3' CTTGAACCTCTTCATGTCA   55603         A  AATA
                                TGGCATGAAGA GG   GAG
                                |||||||||| ||   |||
                                ACTGTACTTCT CC   TTC
                                      _ AAG_
GAM1087 MRPL48   3' CTGTAGACCCTTTCATGCCA  32658        AA  AA  G
                                TGGCATGAAG  GG  TA AG
                                |||||||||  ||  || ||
                                ACCGTACTTT  CC  AT TC
                                      C_  AG  G
GAM1087 NRM      3' GCCTGGCTGCTTCATGCCA   99717        AAGGAA   A
                                TGGCATGAAG     TAG GC
                                |||||||||     ||| ||
                                ACCGTACTTC     GTC CG
                                      GTCG__   C
GAM1087 PHF3     3' GCTCATCATCCCTTCTTCATAC 31432     C       A  A__
            CA                    TGG ATGAAGAAGG AT   GAGC
                                ||| ||||||||| ||   ||||
                                ACC TACTTCTTCC TA   CTCG
                                  A        C  CTA
GAM1087 PPP1R16B 3' CTATTCCTCTCCACCCA     62037     CA  A   A
                                TGG  TG AGA GGAATAG
                                |||  || ||| |||||||
                                ACC  AC TCT CCTTATC
                                  C_  C  _
GAM1087 PRO1880  5' CTCTATATACTTCATGTCA   26888         AAGGA
                                TGGCATGAAG    ATAGAG
                                |||||||||    ||||||
                                ACTGTACTTC    TATCTC
                                      ATA__
GAM1087 RP4-622L5 3' GCCTGGACCTTCATGCTA   39426        AGA   AA   A
                                TGGCATGA   AGG  TAG GC
                                ||||||||   |||  ||| ||
                                ATCGTACT   TCC  GTC CG
                                     ___   AG   C
GAM1087 UPLC1    3' GCTGGCCTTCTTCCTGCCA   35228      T      AATAG
                                TGGCA GAAGAAGG    AGC
                                ||||| ||||||||    |||
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                                ACCGT CTTCTTCC    TCG
                                  C       GG___
GAM1087  LOC143158 5'  CTATTCCTCCTCCATTCCA   76999    C   A  A
                                TGG ATG AG AGGAATAG
                                ||| ||| || ||||||||
                                ACC TAC TC TCCTTATC
                                  T   C  C
GAM1087  LOC149386 5'  CTCTGAGATCTTCATGGCA   85556    G      AGGAA
                                TG CATGAAGA    TAGAG
                                || ||||||||    |||||
                                AC GTACTTCT    GTCTC
                                 G       AGA__
GAM1087  LOC151405 5'  CTCATCACTTCTTCATGACA  86514    G       GA  A
                                TG CATGAAGAAG  AT GAG
                                || ||||||||||  || |||
                                AC GTACTTCTTC  TA CTC
                                 A         AC  _
GAM1087  LOC151835 3'  CTCTCTGCCTTCATGCCA    81194         AA   ATA
                                TGGCATGAAG  GGA   GAG
                                ||||||||||  |||   |||
                                ACCGTACTTC  TCT   CTC
                                      CG   ___
GAM1087  LOC196264 3'  GCTCCATTCCTTTGACTCCA  88987    CATGAA      A
                                TGG     GAAGGAAT GAGC
                                |||     |||||||| ||||
                                ACC     TTTCCTTA CTCG
                                  TCAG__       C
GAM1087  LOC256222 5'  GCCCTTTTACTCTTTCATGCCA 99015        GA  GAAT  A
                                TGGCATGAA  AG    AG GC
                                |||||||||  ||    || ||
                                ACCGTACTT  TC    TC CG
                                      TC  ATTT  C
GAM1087  LOC256310 5'  CTGCACCTTCTTCACCCA    98097    CA       AA
                                TGG  TGAAGAAGG  TAG
                                |||  |||||||||  |||
                                ACC  ACTTCTTCC  GTC
                                  C_        AC
GAM1088  BAT3     5'  GAAGTGGCCGTCGGTGGCAGGT 17348        G   A__
                                ACCTGCTG TGA   CCACTTC
                                |||||||| |||   |||||||
                                TGGACGGT GCT   GGTGAAG
                                     G   GCC
GAM1088  CD28     3'  GAAGTGGTCAGGCAGAAGGT   21552     G   G_   A
                                ACCT CTG  TGA CCACTTC
                                |||| |||  ||| |||||||
                                TGGA GAC  ACT GGTGAAG
                                  A   GG   _
GAM1088  CLC      3'  GAAGTGGTTCAGGTTGGT    26026     T   GG
                                ACC GCT  TGAACCACTTC
                                ||| |||  ||||||||||
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                                TGG TGG  ACTTGGTGAAG
                                  T  __
GAM1088 DYRK1A   3' GAAGCTATGGAACCAGCAG   56080       GAA  ___
                                CTGCTGGT  CCA  CTTC
                                ||||||||  |||  ||||
                                GACGACCA  GGT  GAAG
                                    A__  ATC
GAM1088 DYRK1A   3' GAAGCTATGGAACCAGCAG   9163        GAA  ___
                                CTGCTGGT  CCA  CTTC
                                ||||||||  |||  ||||
                                GACGACCA  GGT  GAAG
                                    A__  ATC
GAM1088 EIF2C1   3' GAAGTGGTGTTGGCAGCA    25194      G  _
                                TGCTG TGA ACCACTTC
                                ||||| ||| ||||||||
                                ACGAC GTT TGGTGAAG
                                  G  G
GAM1088 EIF4EBP1 3' AAGTGATCATACTGGGCAGG  15849      G___   AC
                                CCTGCT   GTGA  CACTT
                                ||||||   ||||  |||||
                                GGACGG   TACT  GTGAA
                                   GTCA   A_
GAM1088 EPB72    3' GAAGTGGTTCACCCTTGAGG  15874    GCT_
                                CCT   GGTGAACCACTTC
                                |||   ||||||||||||
                                GGA   CCACTTGGTGAAG
                                  GTTC
GAM1088 EXTL1    5' GAAGCGTCTGCCAGCGGG    16736       GA  CA
                                CCTGCTGGT  AC  CTTC
                                |||||||||  ||  ||||
                                GGGCGACCG  TG  GAAG
                                     TC  C_
GAM1088 GLUL     3' GAAGTGGTTCTTAGATGGT   10809    TG   T
                                ACC  CTGG GAACCACTTC
                                |||  |||| ||||||||||
                                TGG  GATT CTTGGTGAAG
                                  TA   _
GAM1088 HAL      5' AAGGGGGCCAGCAGCAGGT   10902       G  AA  A
                                ACCTGCTG TG  CC CTT
                                |||||||| ||  || |||
                                TGGACGAC AC  GG GAA
                                    G  CG  G
GAM1088 HAP1     3' AAGGCCTTCACCAGCAAGG   15473    _      CCA
                                CCT GCTGGTGAA   CTT
                                ||| |||||||||   |||
                                GGA CGACCACTT   GAA
                                  A       CCG
GAM1088 IHPK3    5' GAAGCGGTTCACCCCACAG   55095    CT_     A
                                CTG   GGTGAACC CTTC
                                |||   |||||||| ||||
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                                GAC   CCACTTGG GAAG
                                  ACC       C
GAM1088 MEL     3' GAAGCGAGGTCCCAGAAGG   19329    G   T A A__
                                CCT CTGG GA CC   CTTC
                                ||| |||| || ||   ||||
                                GGA GACC CT GG   GAAG
                                  A   _ _ AGC
GAM1088 NRAP    3' GAAGTTTGTTCACCAGAG    56308    G       C_
                                CT CTGGTGAAC  ACTTC
                                || |||||||||  |||||
                                GA GACCACTTG  TGAAG
                                 _       TT
GAM1088 RAD23A  5' GAAGTGGTCGGCGCGCGG    18566     _ G   A
                                CTGC TG TGA CCACTTC
                                |||| || ||| |||||||
                                GGCG GC GCT GGTGAAG
                                  C G  _
GAM1088 SACM1L  3' GAAGCGGTCACTATTAGCAGG 26694       ___    A A
                                CCTGCT   GGTGA CC CTTC
                                ||||||   ||||| || ||||
                                GGACGA   TCACT GG GAAG
                                   TTA    _ C
GAM1088 SLC26A4 3' GAAATGGTTTACCTAAAAGC  6528     ____       C
                                GCT    GGTGAACCA TTC
                                |||    ||||||||| |||
                                CGA    CCATTTGGT AAG
                                  AAAT       A
GAM1088 TEAD3   3' GAAGGGAGCACAGCAGGT    13670        G  AA  A
                                ACCTGCTG TG  CC CTTC
                                |||||||| ||  || ||||
                                TGGACGAC AC  GG GAAG
                                    _ GA  _
GAM1088 TIMP3   3' GAAGCTGATGCCAGCATGT   6287     C       AAC  _
                                AC TGCTGGTG   CA CTTC
                                || ||||||||   || ||||
                                TG ACGACCGT   GT GAAG
                                 T       A__  C
GAM1088 VAPB    3' GAAGCGAGGGCACCAGCAG   17628         AA  A__
                                CTGCTGGTG  CC   CTTC
                                |||||||||  ||   ||||
                                GACGACCAC  GG   GAAG
                                     G_  AGC
GAM1088 A2BP1   5' GAAGTGGTTCTCCAAGCAG   38677      _ T
                                CTGCT GG GAACCACTTC
                                ||||| || ||||||||||
                                GACGA CC CTTGGTGAAG
                                  A  T
GAM1088 ADMP    3' GAAGTAATATTCTACCAGCAGG 59512         _   CC__
                                CCTGCTGGT GAA    ACTTC
                                ||||||||| |||    |||||
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                                GGACGACCA CTT    TGAAG
                                     T   ATAA
GAM1088  D2S448    3'  GAAGGAGGCACAGCAGGT    73891        G  AA  A_
                                ACCTGCTG TG  CC  CTTC
                                |||||||| ||  ||  ||||
                                TGGACGAC AC  GG  GAAG
                                     _  __  AG
GAM1088  DKFZP434B195 3'  AAGTGGTTTGGAAGACAG    49245     _  GG
                                CTG CT  TGAACCACTT
                                ||| ||  ||||||||||
                                GAC GA  GTTTGGTGAA
                                  A  AG
GAM1088  DKFZp566H0824 5'  GAAATGGTTCACTGAAAG    34484     GC        C
                                CT  TGGTGAACCA TTC
                                ||  |||||||||| |||
                                GA  GTCACTTGGT AAG
                                  AA         A
GAM1088  DKFZp761D0614 3'  GAAGCAGTTTTATTAGCATGT  88945    C        _ CA
                                AC TGCTGGTGAA C  CTTC
                                || |||||||||| |  ||||
                                TG ACGATTATTT G  GAAG
                                 T         T AC
GAM1088  FLJ20195  3'  GAAGCGGTGCCAGCCAGCAGGT 35219          GA__   A
                                ACCTGCTGGT    ACC CTTC
                                ||||||||||    ||| ||||
                                TGGACGACCG    TGG GAAG
                                      ACCG   C
GAM1088  FLJ21459  3'  GAAGTGGGGTGCACAGCAGGT  44805        _   AA
                                ACCTGCTG GTG  CCACTTC
                                |||||||| |||  |||||||
                                TGGACGAC CGT  GGTGAAG
                                     A   GG
GAM1088  FLJ22659  5'  GAAGTGGAGGCTCAGCAGG   46828       _  GAA
                                CCTGCTG GT   CCACTTC
                                ||||||| ||   |||||||
                                GGACGAC CG   GGTGAAG
                                     T  GA_
GAM1088  IL18BP    5'  GAAGTGGTCCAACTTGGGGT   20310     GCT   GA_
                                ACCT   GGT   ACCACTTC
                                ||||   |||   ||||||||
                                TGGG   TCA   TGGTGAAG
                                  GT_   ACC
GAM1088  IMAP1     5'  GAAGGGAAAGCAGCAGGT    56236        G GAA  A
                                ACCTGCTG T   CC CTTC
                                |||||||| |   || ||||
                                TGGACGAC G   GG GAAG
                                     _ AAA  _
GAM1088  IR1899308 3'  GAAGTGGTTCCTTGGCAG    38527      TG T
                                CTGC  G GAACCACTTC
                                ||||  | ||||||||||
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                                GACG  T CTTGGTGAAG
                                  GT C
GAM1088 KIAA0205 3' AAGTGACCAAGCCAGCAGGT  30196        GAAC_
                                ACCTGCTGGT    CACTT
                                ||||||||||    |||||
                                TGGACGACCG    GTGAA
                                     AACCA
GAM1088 KIAA0266 3' AAGTGGTTTGTCCGCTAGC   41630       ____
                                GCTGGTG   AACCACTT
                                |||||||   ||||||||
                                CGATCGC   TTGGTGAA
                                    CTGT
GAM1088 KIAA0450 5' GAAGTGGTCTTGGTGCCAGC  28356       A____
                                GCTGGTG    ACCACTTC
                                |||||||    ||||||||
                                CGACCGT    TGGTGAAG
                                    GGTTC
GAM1088 KIAA1944 3' AAGTGGTGGATCCAGCAGG   76072       TGA_
                                CCTGCTGG   ACCACTT
                                ||||||||   |||||||
                                GGACGACC   TGGTGAA
                                     TAGG
GAM1088 KIAA1950 3' GAAGTGGTTCATGCCTGT    94181    T  __
                                GC GGT  GAACCACTTC
                                || |||  ||||||||||
                                TG CCG  CTTGGTGAAG
                                 T  TA
GAM1088 LMOD1    5' GAAGTGTTCGACCAGCAGG   25100        _   C
                                CCTGCTGGT GAAC ACTTC
                                ||||||||| |||| |||||
                                GGACGACCA CTTG TGAAG
                                     G   _
GAM1088 MGC13159 3' AAGTGGTTTCATTGTAGGT   53032       T    _
                                ACCTGC GGTGAA CCACTT
                                |||||| |||||| ||||||
                                TGGATG TTACTT GGTGAA
                                   _     T
GAM1088 SHANK3   3' GAGTCAGTTCACCACAGG    66107     C      C_
                                CCTG TGGTGAAC  ACTT
                                |||| ||||||||  ||||
                                GGAC ACCACTTG  TGAG
                                   _       AC
GAM1088 SPEC1    3' GAAGTGGTTCCTGCAGTGT   40005   _   T  T
                                AC CTGC GG GAACCACTTC
                                || |||| || ||||||||||
                                TG GACG TC CTTGGTGAAG
                                 T   _ _
GAM1088 TCL6     3' GAAGTGGTTGGCAACAGG    40475     CTG  G
                                CCTG   GT AACCACTTC
                                ||||   || |||||||||
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                                GGAC   CG TTGGTGAAG
                                  AA_  G
GAM1088  TCL6     3'  GAAGTGGTTGGCAACAGG    40476      CTG  G
                                CCTG   GT AACCACTTC
                                ||||   || |||||||||
                                GGAC   CG TTGGTGAAG
                                  AA_  G
GAM1088  TRIM36   3'  GAAGTGGTTAACTTTGCA    38627     T_   G
                                TGC  GGT AACCACTTC
                                |||  ||| |||||||||
                                ACG  TCA TTGGTGAAG
                                  TT   A
GAM1088  ZFP106   3'  AAGTGGTTACTAGCCAGG    42709      _      A
                                CCTG CTGGTGA CCACTT
                                |||| ||||||| ||||||
                                GGAC GATCATT GGTGAA
                                  C      _
GAM1088  LOC116441 5'  GAAGTGGTTCTAAGCAGG    57874       GGT
                                CCTGCT   GAACCACTTC
                                ||||||   ||||||||||
                                GGACGA   CTTGGTGAAG
                                   AT_
GAM1088  LOC142955 5'  GAAGTGGTTCAACAAGGT    76960      GCTGG
                                ACCT     TGAACCACTTC
                                ||||     ||||||||||
                                TGGA     ACTTGGTGAAG
                                  ACA__
GAM1088  LOC145871 5'  GAAGTGGTTCCTTGGCAG    84550      TG T
                                CTGC  G GAACCACTTC
                                ||||  | ||||||||||
                                GACG  T CTTGGTGAAG
                                  GT C
GAM1088  LOC147495 5'  GAAGCTCGGCCAGCAGGT    85143          _  ACCA
                                ACCTGCTGGT GA    CTTC
                                |||||||||| ||    ||||
                                TGGACGACCG CT    GAAG
                                      G  C___
GAM1088  LOC157621 3'  GAAGTGGTCTCCGTGCAG    87790      _   T  A
                                CTGC TGG GA CCACTTC
                                |||| ||| || |||||||
                                GACG GCC CT GGTGAAG
                                  T   T  _
GAM1088  LOC158288 3'  AAGTGGTTCATAGGCCGGT    88014     T   G
                                ACC GCT GTGAACCACTT
                                ||| ||| ||||||||||
                                TGG CGG TACTTGGTGAA
                                  C   A
GAM1088  LOC203286 3'  GAAGCTGATCCAGCGGGT    92144         TGAAC  _
                                ACCTGCTGG     CA CTTC
                                |||||||||     || ||||
```

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                                TGGGCGACC    GT GAAG
                                     TA___  C
GAM1088  LOC204084 5'  GAAGTGGTACCTGAGCAAGG  90997    _  __  GA
                                CCT GCT  GGT  ACCACTTC
                                ||| |||  |||  ||||||||
                                GGA CGA  CCA  TGGTGAAG
                                  A  GT  __
GAM1088  LOC219653 3'  GAAGTGAGGTTTTAGCAGG  92917      GT   __
                                CCTGCTG  GAACC  ACTTC
                                |||||||  |||||  |||||
                                GGACGAT  TTTGG  TGAAG
                                    __    AG
GAM1088  LOC221337 3'  GAAGTGGTCAGACCAGGGT  93735    TG   GA_
                                ACC  CTGGT   ACCACTTC
                                |||  |||||   ||||||||
                                TGG  GACCA   TGGTGAAG
                                  __    GAC
GAM1088  LOC91156  5'  GAAGTGGCAAAGACGGCAGGT  65709       GTGAA_
                                ACCTGCTG     CCACTTC
                                ||||||||     |||||||
                                TGGACGGC     GGTGAAG
                                     AGAAAC
GAM1089  HAS2     3'  TTATGGACTGTTTGATAGATG  19229    ACC       _
                                CAT   ATCAAATGGTC ATAA
                                |||   |||||||||||| ||||
                                GTA   TAGTTTGTCAG TATT
                                  GA_         G
GAM1089  ITK      3'  TGTGGTTGATGGCATGG     19886     A     ATGG
                                CCAT CCATCAA    TCATA
                                |||| |||||||    |||||
                                GGTA GGTAGTT    GGTGT
                                  C     _____
GAM1089  LAMP2    3'  ACTAGTTGATGTATGGTA    26566       C    A
                                TACCATAC ATCAA TGGT
                                |||||||| ||||| ||||
                                ATGGTATG TAGTT ATCA
                                     _    G
GAM1089  MATN3    3'  TTATGACTGTGAAATGATTGGT 11471     TAC   CAA
             A                   TACCA   CAT   ATGGTCATAA
                                 |||||   |||   ||||||||||
                                 ATGGT   GTA   TGTCAGTATT
                                    TA_   AAG
GAM1089  SLC21A9  3'  TATGACCATCTGTGCGGTCA  24381   T   AT_  A
                                A ACC   CA ATGGTCATA
                                | |||   || |||||||||
                                A TGG   GT TACCAGTAT
                                 C   CGT  C
GAM1089  TXNRD1   3'  TGGCATTTGGTAGTATAGTA  13923    C   C      G
                                TAC ATAC ATCAAATG TCA
                                ||| |||| |||||||| |||
```

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                                ATG TATG TGGTTTAC GGT
                                  A   A      _
GAM1089 ZNF124   3' GTGGTATTTGATGGTAT    14284          G
                                ATACCATCAAATG TCAT
                                |||||||||||| ||||
                                TATGGTAGTTTAT GGTG
                                          _
GAM1089 DKFZp761H2121 3' TTATGATAGAATTGATGGT   57182       ATG_
                                ACCATCAA   GTCATAA
                                ||||||||   |||||||
                                TGGTAGTT   TAGTATT
                                    AAGA
GAM1089 FLJ12716 3' TCATTTGATGAATGGTA    41944      AC
                                TACCAT  CATCAAATGG
                                ||||||  ||||||||||
                                ATGGTA  GTAGTTTACT
                                   A_
GAM1089 KIAA0227  3' TTATAACCATTTGAGAACAGG  61355   ATACCA      C
                                CC     TCAAATGGT ATAA
                                ||     ||||||||| ||||
                                GG     AGTTTACCA TATT
                                 ACAAG_       A
GAM1089 RAB22A   3' ATGATCAAGATGGTGATGGTA  60608      _    AAA
                                TACCAT ACCATC   TGGTCAT
                                |||||| ||||||   |||||||
                                ATGGTA TGGTAG   ACTAGTA
                                   G     A__
GAM1089 SEC24A   3' TATGATCACCAATGGAATAGTA 83566    C  A   CAAA
                                TAC AT CCAT    TGGTCATA
                                ||| || ||||    ||||||||
                                ATG TA GGTA    ACTAGTAT
                                  A  A   ACC_
GAM1089 LOC146957 3' GACCTGATCTAATATGGTG   78815      CC__   AAT
                                TACCATA   ATCA   GGTC
                                |||||||   ||||   ||||
                                GTGGTAT   TAGT   CCAG
                                    AATC   ___
GAM1090 ANKH    5' CCCGCAGAGTCCCCTCGCGGC  39548    A  A_   CGG
                                GCC CGA  GGAT   CTGCGGG
                                ||| |||  ||||   |||||||
                                CGG GCT  CCTG   GACGCCC
                                  C   CC   A__
GAM1090 ANKH    5' CCCGCAGAGTCCCCTCGCGGC  55067    A  A_   CGG
                                GCC CGA  GGAT   CTGCGGG
                                ||| |||  ||||   |||||||
                                CGG GCT  CCTG   GACGCCC
                                  C   CC   A__
GAM1090 BYSL    5' CCCACGTGCGATCCTTCCCGGC 15762    AC       G _  C
                                GCC  GAAGGATCG C TG GGG
                                |||  ||||||||| | || |||
```

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                                CGG  CTTCCTAGC G GC CCC
                                  CC        _ T  A
GAM1090  EP300    5'  CGCCTCCTTGTGGCGA      9283         G    TCGGCT
                                TCGCCAC AAGGA     GCG
                                ||||||| |||||     |||
                                AGCGGTG TTCCT     CGC
                                    _    C_____
GAM1090  INSM1    5'  CCCGCAGCCGCCGCGCCCGGGC 11014     A  AA  AT___
                                GCC CG  GG    CGGCTGCGGG
                                ||| ||  ||    ||||||||||
                                CGG GC  CC    GCCGACGCCC
                                  _ __  GCGCC
GAM1090  NMI      5'  CCCGCAGCTCTCCCGCGGCG   17433      A  AA   TC
                                CGCC CG  GGA  GGCTGCGGG
                                |||| ||  |||  |||||||||
                                GCGG GC  CCT  TCGACGCCC
                                  C __   C_
GAM1090  TBX5     5'  CCCACCTCCCTTCGTGAAGA   55756    GC       ATC  C  C
                                TC  CACGAAGG   GG TG GG
                                ||  ||||||||   || || ||
                                AG  GTGCTTCC   CC AC CC
                                 AA       CT_  _  _
GAM1090  TBX5     5'  CCCACCTCCCTTCGTGAAGA   5755     GC       ATC  C  C
                                TC  CACGAAGG   GG TG GG
                                ||  ||||||||   || || ||
                                AG  GTGCTTCC   CC AC CC
                                 AA       CT_  _  _
GAM1090  BCoR     5'  CCCGCAGCCCGCTCGCGGCG   35344      A   AG ATC
                                CGCC CGA  G   GGCTGCGGG
                                |||| |||  |   |||||||||
                                GCGG GCT  C   CCGACGCCC
                                  C   __ GC_
GAM1090  BCoR     5'  CCCGCAGCCCGCTCGCGGCG   40888      A   AG ATC
                                CGCC CGA  G   GGCTGCGGG
                                |||| |||  |   |||||||||
                                GCGG GCT  C   CCGACGCCC
                                  C   __ GC_
GAM1090  CGI-142  5'  CCCGGCATCTTCGCGGCGA   32691      A     ATCG   C
                                TCGCC CGAAGG    GCTG GG
                                ||||| ||||||    |||| ||
                                AGCGG GCTTCT    CGGC CC
                                  C     A___    _
GAM1090  CRMP5    5'  CCCGCAGCTCCGGCGCCGCGGC 39702       A  AA___   TCG
           GA                     TCGCC CG    GGA   GCTGCGGG
                                ||||| ||    |||   ||||||||
                                AGCGG GC    CCT   CGACGCCC
                                  C  CGCGG   ___
GAM1090  DOC-1R   5'  CCCGCAGCCAACCCCCGAGG   20720    A  AA  ATC
                                CC CG  GG   GGCTGCGGG
                                || ||  ||   |||||||||
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                                GG GC  CC   CCGACGCCC
                                 A  CC  AA_
GAM1090  UBE2D1    5'  CCCGCAGCCGACCCCTGCCGGC 13943     ACGA   A_
                                GCC    AGG  TCGGCTGCGGG
                                |||    |||  ||||||||||
                                CGG    TCC  AGCCGACGCCC
                                  CCG_   CC
GAM1090  LOC144165 5'  CCCGCAGCCCAGCAGCCCCGCA 77193      CA  AA  ATC___
           GCGG                    TCGC  CG  GG     GGCTGCGGG
                                |||| ||  ||     |||||||||
                                GGCG  GC  CC     CCGACGCCC
                                  AC  C_  GACGAC
GAM1090  LOC157567 5'  CCACACCTTCCGCGGCGA    82391       A  _   ATCGGC  C
                                TCGCC CG AAGG     TG GG
                                ||||| || ||||     || ||
                                AGCGG GC TTCC     AC CC
                                   C  C   _______ A
GAM1090  LOC199923 3'  CCCGCAGCCGCTGGACGCGGGA 89868    G  A  AA_  AT
                                TC CC CG   GG  CGGCTGCGGG
                                || || ||   ||  ||||||||||
                                AG GG GC   TC  GCCGACGCCC
                                 _  C  AGG  __
GAM1091  ABH       3'  GCACCCAGACAAGCCAAAAACA 60463       C    CCATG_
                                TGTTT TGGT     GGGTGC
                                ||||| ||||     ||||||
                                ACAAA ACCG     CCCACG
                                   A    AACAGA
GAM1091  FGF1      3'  GCATTCCATGACCAGAAACA   53641          C
                                TGTTTCTGGTC ATGGGGTGC
                                |||||||||||| |||||||||
                                ACAAAGACCAG TACCTTACG
                                           _
GAM1091  FGF1      3'  GCATTCCATGACCAGAAACA   53644          C
                                TGTTTCTGGTC ATGGGGTGC
                                |||||||||||| |||||||||
                                ACAAAGACCAG TACCTTACG
                                           _
GAM1091  FGF1      3'  GCATTCCATGACCAGAAACA   7685           C
                                TGTTTCTGGTC ATGGGGTGC
                                |||||||||||| |||||||||
                                ACAAAGACCAG TACCTTACG
                                           _
GAM1091  NBEA      3'  GCACTTTGCACCAGAAACA    96583          C  TG
                                TGTTTCTGGT CA  GGGTGC
                                |||||||||| ||  ||||||
                                ACAAAGACCA GT  TTCACG
                                      C  __
GAM1091  PRY       5'  GCACACCACACCAGAAACA    60892          CCA   G
                                TGTTTCTGGT   TGG GTGC
                                |||||||||   ||| ||||
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                                ACAAAGACCA   ACC CACG
                                     C__   A
GAM1091  RABIF    3'  CCAACCACTAACCAGAAACA   12723        CCA  _____
                                TGTTTCTGGT   TGG    GG
                                ||||||||||   |||    ||
                                ACAAAGACCA   ACC    CC
                                     ATC   AAIII
GAM1091  UBE4A    3'  ACAGGAAATGAACCTAGAAACA 17726       _  C   GGG__
                                TGTTTCT GGT CAT    GT
                                |||||||  ||| |||    ||
                                ACAAAGA CCA GTA    CA
                                   T   A   AAGGA
GAM1091  FLJ11413 3'  CATCCCCACAGACCAGAAACA  44954         CA    _
                                TGTTTCTGGTC  TGGGG TG
                                ||||||||||  ||||| ||
                                ACAAAGACCAG  ACCCC AC
                                      AC    T
GAM1091  GLIO703  3'  GCATTCCATGACCAGAAACA   26344         C
                                TGTTTCTGGTC ATGGGGTGC
                                ||||||||||| |||||||||
                                ACAAAGACCAG TACCTTACG
                                          _
GAM1091  LOC153711 3'  GCAACATGAATCAGAAACA   87343        C   GG
                                TGTTTCTGGT CATG  GT
                                |||||||||| ||||  ||
                                ACAAAGACTA GTAC  CG
                                     A    AA
GAM1091  LOC159160 5'  GCACACCACACCAGAAACA   61153        CCA  G
                                TGTTTCTGGT   TGG GTGC
                                ||||||||||   ||| ||||
                                ACAAAGACCA   ACC CACG
                                     C__   A
GAM1091  LOC170425 3'  GCATCATCCACGAACCAGAAA  76887       CCA  __
                                TTTCTGGT   TGG  GGTGC
                                ||||||||   |||  |||||
                                AAAGACCA   ACC  CTACG
                                     AGC   TA
GAM1091  LOC197259 3'  ACCACATGAAGCAGAAACA   89297       GTC   G
                                TGTTTCTG   CATG GGT
                                ||||||||   |||| |||
                                ACAAAGAC   GTAC CCA
                                     GAA    A
GAM1091  LOC197259 5'  GCACTGGACAGAAACA      89300       G   TGGG
                                TGTTTCTG TCCA    GTGC
                                ||||||||  ||||   ||||
                                ACAAAGAC AGGT    CACG
                                          _   _____
GAM1091  LOC253664 3'  GGCGCCGGTCCACTGACCAGAA 96469         CA  _______  TGCG
            ACA                   TGTTTCTGGTC  TGG     GG   C
                                ||||||||||  |||     ||   |
```

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                                ACAAAGACCAG ACC    CC   G
                                     TC  TGGIII GCGT
GAM1092 EEF1A1   3' TGTCACAGAATTTTGAGACCCA 9181          _
           TTA                  TAATGGGTCTCAAA TTCTGTGACA
                                |||||||||||||| ||||||||||
                                ATTACCCAGAGTTT AAGACACTGT
                                       T
GAM1092 TBL2     3' TCACAGAACTGTGTTCCAT   25867     TCT  AA
                                ATGGG  CA  TTCTGTGA
                                |||||  ||  ||||||||
                                TACCT  GT  AAGACACT
                                   TGT  C_
GAM1092 TBL2     3' TCACAGAACTGTGTTCCAT   25868     TCT  AA
                                ATGGG  CA  TTCTGTGA
                                |||||  ||  ||||||||
                                TACCT  GT  AAGACACT
                                   TGT  C_
GAM1092 DKFZp434G179 3' TGTTGGCTAATTAAGACCCATT 80894        CA   CT  _
           A                    TAATGGGTCT  AATT  GT GACA
                                ||||||||||  ||||  ||  ||||
                                ATTACCCAGA  TTAA  CG TTGT
                                      A_   T_  G
GAM1092 DSCR6    3' TACTTAACCTGAGACTCATTA  39074         AA  CT
                                TAATGGGTCTCA  TT  GTG
                                ||||||||||||  ||  |||
                                ATTACTCAGAGT  AA  CAT
                                      CC  TT
GAM1092 FLJ10661 3' CACTTGGACTTGAGACCC    36916       A  T_
                                GGGTCTCAA TTC  GTG
                                |||||||||  |||  |||
                                CCCAGAGTT AGG  CAC
                                     C   TT
GAM1092 FLJ12806 3' CACAGAATTCAGAGTCCA    43389     T  A_
                                TGGG CTC  AATTCTGTG
                                ||||  |||  |||||||||
                                ACCT GAG  TTAAGACAC
                                  _  AC
GAM1092 MGC16279 3' CACTTGGACTTGAGACCC    52981       A  T_
                                GGGTCTCAA TTC  GTG
                                |||||||||  |||  |||
                                CCCAGAGTT AGG  CAC
                                     C   TT
GAM1092 MGC16279 3' CACTTGGACTTGAGACCC    63541       A  T_
                                GGGTCTCAA TTC  GTG
                                |||||||||  |||  |||
                                CCCAGAGTT AGG  CAC
                                     C   TT
GAM1092 MGC35558 3' TCACAGACCAAGCCCATTA   59419       CTCAAAT
                                TAATGGGT     TCTGTGA
                                ||||||||     |||||||
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                                ATTACCCG      AGACACT
                                    AACC___
GAM1092  LOC124961 3'  TGTCTTAATTTTAGACCCATTA 76164          C    CTGT
                                TAATGGGTCT AAATT    GACA
                                |||||||||| |||||    ||||
                                ATTACCCAGA TTTAA    CTGT
                                     T    TT__
GAM1092  LOC148371 3'  TGTCACAGAATTTTGAGACCCA 79553            _
           TTA                    TAATGGGTCTCAAA TTCTGTGACA
                                |||||||||||||| ||||||||||
                                ATTACCCAGAGTTT AAGACACTGT
                                      T
GAM1092  LOC157450 3'  CACTTGGACTTGAGACCC    71530         A  T_
                                GGGTCTCAA TTC  GTG
                                ||||||||| |||  |||
                                CCCAGAGTT AGG  CAC
                                     C   TT
GAM1092  LOC161589 3'  TGTCACAGAATTTTGAGACCCA 83162            _
           TT                     AATGGGTCTCAAA TTCTGTGACA
                                |||||||||||| ||||||||||
                                TTACCCAGAGTTT AAGACACTGT
                                      T
GAM1092  LOC163231 5'  TCACAGTGGAAACCCGTTA   83334         C  AAATT
                                TAATGGGT TC    CTGTGA
                                |||||||| ||    ||||||
                                ATTGCCCA AG    GACACT
                                    A  GT___
GAM1092  LOC196484 5'  CACTTGGACTTGAGACCC    63536         A  T_
                                GGGTCTCAA TTC  GTG
                                ||||||||| |||  |||
                                CCCAGAGTT AGG  CAC
                                     C   TT
GAM1092  LOC220073 5'  CACTTGGACTTGAGACCC    95072         A  T_
                                GGGTCTCAA TTC  GTG
                                ||||||||| |||  |||
                                CCCAGAGTT AGG  CAC
                                     C   TT
GAM1092  LOC221838 3'  TGTCACAGAATTTTGAGACCCA 94120            _
           TTA                    TAATGGGTCTCAAA TTCTGTGACA
                                |||||||||||||| ||||||||||
                                ATTACCCAGAGTTT AAGACACTGT
                                      T
GAM1092  LOC91069  3'  TACCTGGACTTGAGACCC    65404         A  T_
                                GGGTCTCAA TTC  GTG
                                ||||||||| |||  |||
                                CCCAGAGTT AGG  CAT
                                     C   TC
GAM1092  LOC91250  5'  TGTTTCAGAATTTAAAACCC  65925      CTC      T
                                GGGT   AAATTCTG GACA
                                ||||   |||||||| ||||
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                                CCCA   TTTAAGAC TTGT
                                  AAA       T
GAM1093  AKAP13    3'  TCTTTAATCAAAGGATGTCTTC 91256          CCAGCGA
                T                  GGAAGACATCC      AAAGA
                                   ||||||||||       |||||
                                   TCTTCTGTAGG      TTTCT
                                         AAACTAA
GAM1093  ATP10C    3'  TTTCCAGAGGATGTCTTTCT   44671          CCAGC
                                   AGGAAGACATCC    GAAA
                                   ||||||||||||    ||||
                                   TCTTTCTGTAGG    CTTT
                                         AGAC_
GAM1093  CARD15    3'  CTTCAAAGCAAATGTCTTCCT  42468          CCCCA  GAA_
                                   AGGAAGACAT    GC    AAG
                                   ||||||||||    ||    |||
                                   TCCTTCTGTA    CG    TTC
                                         AA___  AAAC
GAM1093  CHAC      3'  CTTTTAAAATGTTTTCCT    53954          CCCCAGCG
                                   AGGAAGACAT      AAAAG
                                   ||||||||||      |||||
                                   TCCTTTTGTA      TTTTC
                                         AAA_____
GAM1093  CHST6     3'  TCTGGGCTGGAACTGTCTTCC  41504         TCC    GAAA
                                   GGAAGACA   CCAGC    AGA
                                   ||||||||   |||||    |||
                                   CCTTCTGT   GGTCG    TCT
                                        CAA    GG__
GAM1093  CRYAA     3'  TTCTCTCAGACCGTCTTCCT   6368          A_  CCC  C
                                   AGGAAGAC  TC   AG GAA
                                   ||||||||  ||   || |||
                                   TCCTTCTG  AG   TC CTT
                                        CC  AC_  T
GAM1093  DDB1      5'  TCTTTTCGCTTGTGTCCCT   10400     AA    CCCC
                                   AGG  GACAT    AGCGAAAAGA
                                   |||  |||||    ||||||||||
                                   TCC  CTGTG    TCGCTTTTCT
                                     __     T___
GAM1093  DYRK1A    3'  TCTTCTGCACAAAGATGTCTTC 9166          CCCA_   AA
                T                  GGAAGACATC    GCG  AAGA
                                   ||||||||||    |||  ||||
                                   TCTTCTGTAG    CGT  TTCT
                                         AAACA   C_
GAM1093  DYRK1A    3'  TCTTCTGCACAAAGATGTCTTC 56082         CCCA_   AA
                T                  GGAAGACATC    GCG  AAGA
                                   ||||||||||    |||  ||||
                                   TCTTCTGTAG    CGT  TTCT
                                         AAACA   C_
GAM1093  EHF       3'  TCTGATGCCAGGGCTGTCTTCC 25128         T   CA   AAA
                T                  AGGAAGACA CCC  GCG   AGA
                                   |||||||||  |||  |||   |||
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                                TCCTTCTGT GGG  CGT   TCT
                                     C   AC   AG_
GAM1093  EIF4EBP2  3'  CTGGGAGGAATGTCTTCT    15857         __ _
                                GGAAGACAT  C CCCAG
                                |||||||||  | |||||
                                TCTTCTGTA  G GGGTC
                                     AG A
GAM1093  GALNT2    3'  TTCGCAAGTGTCTTCCT     16823          CCCCA
                                AGGAAGACAT    GCGAA
                                ||||||||||    |||||
                                TCCTTCTGTG    CGCTT
                                     AA___
GAM1093  GTF2E2    3'  TCGGGGTCTGAAGACTGTCTTC 10887         _ CC  ____
              CT                  AGGAAGACA TC  CAG   CGA
                                |||||||| ||  |||   |||
                                TCCTTCTGT AG  GTC   GCT
                                     C  AA   TGGG
GAM1093  IL2RG     3'  CTTTTCGCAGGATTCTTCCT   5779        C   CCA
                                AGGAAGA ATCC   GCGAAAAG
                                ||||||| ||||  ||||||||
                                TCCTTCT TAGG   CGCTTTTC
                                   _   A__
GAM1093  KCNK4     3'  TCGAGGCCGAAAAGTCTTCCT  53963        A__  C_  AG
                                AGGAAGAC   TC  CC  CGA
                                ||||||||   ||  ||  |||
                                TCCTTCTG   AG  GG  GCT
                                     AAA  CC  A_
GAM1093  NEBL      3'  TCTTGGGGATATCTGCCT    22142     A  C      C
                                AGG AGA ATCCCCAG GA
                                ||| ||| |||||||| ||
                                TCC TCT TAGGGGTT CT
                                  G   A      _
GAM1093  NORE1     3'  CTTTTTAAATGTCTTTCT     49525          CCCCAGC
                                AGGAAGACAT      GAAAAG
                                ||||||||||      ||||||
                                TCTTTCTGTA      TTTTTC
                                     AA_____
GAM1093  PDE4D     3'  CTTTTTTAGATGTTTTCCT    73964          CCCAGC
                                AGGAAGACATC     GAAAAG
                                ||||||||||     ||||||
                                TCCTTTTGTAG     TTTTTC
                                     AT____
GAM1093  RELA      3'  TTTGTGGATGTCTTCCT     42027           CCA
                                AGGAAGACATCC   GCGAA
                                ||||||||||||   |||||
                                TCCTTCTGTAGG   TGTTT
                                          ___
GAM1093  RPL24     5'  TCTTTTCGCCATCTTTTGTCTT 8269          TCCCCA_
              TC                  GGAAGACA      GCGAAAAGA
                                ||||||||      |||||||||
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                                CTTTCTGT      CGCTTTTCT
                                     TTTCTAC
GAM1093  SRGAP2    3'  CTGGGGGCAGAGCTGTCTTCC  75110        _______
                                GGAAGACA      TCCCCAG
                                ||||||||      |||||||
                                CCTTCTGT      GGGGGTC
                                     CGAGAC
GAM1093  STAU2     3'  CTTTCGCTCTGTCTTCC     27673         TCCCC     A
                                GGAAGACA     AGCGAA AG
                                ||||||||     |||||| ||
                                CCTTCTGT     TCGCTT TC
                                     C____      C
GAM1093  ARPP-21   3'  TTGTTGGAGATGTCTTACC   33297    _       C
                                GG AAGACATC CCAGCGA
                                || |||||||| |||||||
                                CC TTCTGTAG GGTTGTT
                                  A       A
GAM1093  CECR7     5'  TTTCTCCAGAGATGTCTTCCT  80452           CCCAGC
                                AGGAAGACATC      GAAA
                                ||||||||||      ||||
                                TCCTTCTGTAG      CTTT
                                      AGACCT
GAM1093  DKFZP434K1772 3'  TCAGCAGGGATGTCCTCC    68340     A       CA  _
                                GGA GACATCCC  GC GA
                                ||| ||||||||  || ||
                                CCT CTGTAGGG  CG CT
                                  C       A_  A
GAM1093  DKFZP434L0718 3'  CTTTTTGTTGAGAACCTCCCT  50457     A  ACA  CC
                                AGG AG   TC  CAGCGAAAAG
                                ||| ||   ||  ||||||||||
                                TCC TC   AG  GTTGTTTTTC
                                  C  CA_  A_
GAM1093  DNAJA4    3'  TTTCGGAGTGTCTTCCT     38364         TC  CAGC
                                AGGAAGACA  CC    GAAA
                                |||||||||  ||    ||||
                                TCCTTCTGT  GG    CTTT
                                     GA  _____
GAM1093  FLJ10761  3'  TTCCAGGGATGTCTCTCC    37134     _       CAGC
                                GGA AGACATCCC    GAA
                                ||| |||||||||    |||
                                CCT TCTGTAGGG    CTT
                                  C        AC__
GAM1093  FLJ12221  3'  TTTCGCCTCCTGTCTTTCT   63227          TCCCCA
                                AGGAAGACA      GCGAAA
                                |||||||||      ||||||
                                TCTTTCTGT      CGCTTT
                                     CCTC__
GAM1093  FLJ22415  5'  CTTTCCGCCTCGCGTTTTCCT  93119         ATCCCCA   A
                                AGGAAGAC       GCG AAAG
                                ||||||||       ||| ||||
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                                TCCTTTTG      CGC TTTC
                                    CGCTC__   C
GAM1093  FLJ22477  3'  TCCTGGGAAATGTTTTCCT   45678         C_    C
                                AGGAAGACAT  CCCAG GA
                                ||||||||||  ||||| ||
                                TCCTTTTGTA  GGGTC CT
                                     AA    _
GAM1093  GAL3ST-4  3'  CTCTTCGCTGGGCTCCC     45278    A  ACATC       A
                                GG AG    CCCAGCGAA AG
                                || ||    ||||||||| ||
                                CC TC    GGGTCGCTT TC
                                 C _____       C
GAM1093  HERC3     3'  CTTTTCGTACCCTGTGTCCTCC 28235     A    CCCCA
                                GGA GACAT    GCGAAAAG
                                ||| |||||    ||||||||
                                CCT CTGTG    TGCTTTTC
                                  C    TCCCA
GAM1093  HTEX4     5'  TCTTTTCGCTGGGAGAGGCTCC 93726    A  ACA  _
              C                  GG AG   TC CCCAGCGAAAAGA
                                || ||   || ||||||||||||
                                CC TC   AG GGGTCGCTTTTCT
                                 C  GG_  A
GAM1093  KIAA0193  3'  TCCTGAAGAAGCTGTCTTCC   29318        ___  CC   C
                                GGAAGACA   TC  CAG GA
                                ||||||||   ||  ||| ||
                                CCTTCTGT   AG  GTC CT
                                     CGA  AA  _
GAM1093  KIAA0418  3'  TTCGCTGGGAGTGGATTTC   28302     GA  TC
                                GGAA  CA  CCCAGCGAA
                                ||||  ||  |||||||||
                                CTTT  GT  GGGTCGCTT
                                  AG  GA
GAM1093  KIAA0459  3'  TCTGAATGAAGATGTTTTCCT  61663          CC  GCGAAA
                                AGGAAGACATC  CA     AGA
                                ||||||||||  ||     |||
                                TCCTTTTGTAG  GT     TCT
                                      AA  AAG___
GAM1093  KIAA0546  3'  TCTTTTCACTATAGGTTTTCCT 71839        ATCCCC  C
                                AGGAAGAC     AG GAAAAGA
                                ||||||||     || |||||||
                                TCCTTTTG     TC CTTTTCT
                                     GATA__  A
GAM1093  KIAA1028  3'  TCTATGATGATGTCTTCCT   93593          CC  GC
                                AGGAAGACATC  CA  GA
                                ||||||||||  ||  ||
                                TCCTTCTGTAG  GT  CT
                                      TA  AT
GAM1093  KIAA1045  3'  TCCCTATGGGATGTCACCCT   71611     AA       C_  C
                                AGG  GACATCCC  AG GA
                                |||  ||||||||  || ||
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                                TCC  CTGTAGGG  TC CT
                                  CA       TA  C
GAM1093  MAPK8IP3  3'  CTTCTCATGATGTCTTTC    54139         CCCAGC  A
                                GGAAGACATC     GA AAG
                                ||||||||||     || |||
                                CTTTCTGTAG     CT TTC
                                     TA____  C
GAM1093  MGC2647   3'  TCTGGGGTCAGGGATGTCCCC  74080    AA       CA  GAAA
                                GG  GACATCCC  GC    AGA
                                ||  ||||||||  ||    |||
                                CC  CTGTAGGG  TG    TCT
                                 C_       AC  GGG_
GAM1093  MGC3035   5'  TCTTCTGGTTGCTGTCTTCCT  44406         TCC_   C_
                                AGGAAGACA    CCAG  GA
                                |||||||||    ||||  ||
                                TCCTTCTGT    GGTC  CT
                                     CGTT    TT
GAM1093  NYD-SP11  5'  CTGACGGTGATGTCTTCC     50055          _ __
                                GGAAGACATC CC  CAG
                                |||||||||| ||  |||
                                CCTTCTGTAG GG  GTC
                                     T  CA
GAM1093  OS4       3'  TCTTTTCCTGTTGTGTCTTCC  20397         CCC   C
                                GGAAGACAT   CAG GAAAAGA
                                |||||||||   ||| |||||||
                                CCTTCTGTG   GTC CTTTTCT
                                     TT_   _
GAM1093  PDZD2     3'  TTTTGCCAAAAATGTTTTCCT  81740         CCCCA
                                AGGAAGACAT     GCGAAA
                                ||||||||||     ||||||
                                TCCTTTTGTA     CGTTTT
                                     AAAAC
GAM1093  REM       3'  TCTTTTTGTAAAAAAATCTTCC 26689        CATCCCCA
              T                  AGGAAGA       GCGAAAAGA
                                 |||||||       |||||||||
                                 TCCTTCT       TGTTTTTCT
                                     AAAAAAA_
GAM1093  RNF9      3'  CTAGGGAAATTGTCTTCCT    23237         ___    C
                                AGGAAGACA   TCCC AG
                                |||||||||   |||| ||
                                TCCTTCTGT   AGGG TC
                                     TAA    A
GAM1093  RoXaN     3'  CTGAGTTGGGGACTCCTCC    47289     A  CA      GAAA
                                GGA GA  TCCCCAGC    AG
                                ||| ||  ||||||||    ||
                                CCT CT  AGGGGTTG    TC
                                  C  C_       AG__
GAM1093  SFXN5     3'  GCTTGGGGATGCCCTTCT     58653      A_       _
                                GGAAG  CATCCCCA GC
                                |||||  |||||||| ||
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                                TCTTC  GTAGGGGT CG
                                  CC       T
GAM1093  VTI2     5'  TTTCGCTGCGGCCTTTCC    22069      ACAT  C
                                GGAAG   CC CAGCGAAA
                                |||||   || ||||||||
                                CCTTT   GG GTCGCTTT
                                  CC__  C
GAM1093  ZAK      3'  TCTTTTTTTTGGATGTCCCCT  34111     AA     CCAGC
                                AGG  GACATCC    GAAAAGA
                                |||  |||||||    |||||||
                                TCC  CTGTAGG    TTTTTCT
                                 C_     TTT__
GAM1093  LOC124470 3'  CTTTCCGTCATGTTTTCCT   76147        CCCCA   A
                                AGGAAGACAT    GCG AAAG
                                ||||||||||    ||| ||||
                                TCCTTTTGTA    TGC TTTC
                                      C____   C
GAM1093  LOC145919 3'  TTCCTCCATGTCTTCCT     78030        CCCC  C
                                AGGAAGACAT    AG GAA
                                ||||||||||    || |||
                                TCCTTCTGTA    TC CTT
                                      CC__  _
GAM1093  LOC146455 5'  TCTTTTTGTGGGAAATCTTCCT 78469       CA    CA
                                AGGAAGA  TCCC  GCGAAAAGA
                                |||||||  ||||  |||||||||
                                TCCTTCT  AGGG  TGTTTTTCT
                                   AA   __
GAM1093  LOC147124 3'  TGACTGGGATTGTCTTCCT   76808        TC    _
                                AGGAAGACA  CCCAG CG
                                |||||||||  ||||| ||
                                TCCTTCTGT  GGGTC GT
                                      TA    A
GAM1093  LOC149109 3'  CTTCCAGTGAATGGTATGTCTT 85510        _  CCA_  GAA
            CCT                   AGGAAGACAT CC   GC   AAG
                                ||||||||||| ||   ||   |||
                                TCCTTCTGTA GG    TG   TTC
                                      T  TAAG  ACC
GAM1093  LOC158857 5'  TCTTCTGTGCTGTCTTCCT   88287        TCCCCA   AA_
                                AGGAAGACA     GCG   AAGA
                                |||||||||     |||   ||||
                                TCCTTCTGT     CGT   TTCT
                                      _______  GTC
GAM1093  LOC159049 5'  TCTTCTGTGCTGTCTTCCT   88353        TCCCCA   AA_
                                AGGAAGACA     GCG   AAGA
                                |||||||||     |||   ||||
                                TCCTTCTGT     CGT   TTCT
                                      _______  GTC
GAM1093  LOC162333 5'  TCTTTTCGTTCCCATTCTTCCT 88502       CATCCCC
                                AGGAAGA      AGCGAAAAGA
                                |||||||      ||||||||||
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                                TCCTTCT      TTGCTTTTCT
                                    TACCC__
GAM1093  LOC202134 5'  TTCGCTGGTAGGCCCTTCTT   91925       ACAT  __
                                AGGAAG   CC  CCAGCGAA
                                ||||||   ||  ||||||||
                                TTCTTC   GG  GGTCGCTT
                                   CC__  AT
GAM1093  LOC256158 5'  TCCCTGGGTGAAGAGGTCTTCC 99515        A___ _    C
            T                   AGGAAGAC   TC CCCAG GA
                                ||||||||   || ||||| ||
                                TCCTTCTG   AG GGGTC CT
                                     GAGA  T    C
GAM1094  LDB1     3'  GGCCCTGCTGTGGCCACCCAGT 15312     AT      G  TA   AA
                                ACT  GGTGGTT AC  CAG  CC
                                |||  ||||||| ||  |||  ||
                                TGA  CCACCGG TG  GTC  GG
                                  C_      _ TC   CC
GAM1094  PBX3     3'  GTCCTGTAGCTATTTTATCATA 21669         T_  A     A
                                TATGGTGG  TG CTACAG AC
                                ||||||||  || ||||||  ||
                                ATACTATT  AT GATGTC TG
                                     TT  C     C
GAM1094  PLG      3'  TTCTGTAGTAAGGTGACATAG  6112        GT G  G
                                CTATG  G TT ACTACAGAA
                                |||||  | || |||||||||
                                GATAC  T GA TGATGTCTT
                                   AG G  A
GAM1094  SSRP1    5'  GGCTCTGCCCAGGCCACCACAG 13419    A       GACTA    A
                                CT TGGTGGTT     CAGA CC
                                || ||||||||     |||| ||
                                GA ACCACCGG     GTCT GG
                                 C       ACCC_   C
GAM1094  TMEM1    3'  CTGTGGTCCCCCATA       13799       T  TT
                                TATGG GG  GACTACAG
                                ||||| ||  ||||||||
                                ATACC CC  CTGGTGTC
                                   _  __
GAM1094  UVRAG    3'  GTTCTGTAACCCAGTAG     14026      GGT   TGAC
                                CTAT   GGT    TACAGAAC
                                ||||   |||    ||||||||
                                GATG   CCA    ATGTCTTG
                                  AC_   _____
GAM1094  WNT4     3'  CTGCGCCGGCAACCACCTAGT  48483      T       A  A___
                                ACTA GGTGGTTG CT    CAG
                                |||| |||||||| ||    |||
                                TGAT CCACCAAC GG    GTC
                                  _       _ CCGC
GAM1094  CDC42BPB 3'  AGTCCTGCTGACCACCTAGT   21237      T      ______
                                ACTA GGTGGTT     GACT
                                |||| |||||||     ||||
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                                TGAT CCACCAG    CTGA
                                  _     TCGTC
GAM1094 DCAMKL1  3' GGTTCTGTGCATCACCACAGT 17602    A     TGAC
                                ACT TGGTGGT   TACAGAACC
                                ||| |||||||   |||||||||
                                TGA ACCACTA   GTGTCTTGG
                                  C     C___
GAM1094 FLJ10314 3' TGTCACAACCACCATAG    36491          ACT
                                CTATGGTGGTTG  ACA
                                ||||||||||||  |||
                                GATACCACCAAC  TGT
                                      AC_
GAM1094 FLJ21919 3' GGCTCTGTAAAATCAGACCATA 43737       GG   C__    A
           GT                   ACTATGGT  TTGA  TACAGA CC
                                |||||||| ||||  |||||| ||
                                TGATACCA  GACT  ATGTCT GG
                                    __   AAA    C
GAM1094 KIAA0766 3' GTTCTGTTAGCTCACCATAG  29675       _   ACT
                                CTATGGTG GTTG  ACAGAAC
                                |||||||| ||||  |||||||
                                GATACCAC CGAT  TGTCTTG
                                     T   ___
GAM1094 KIAA0918 3' CTGTAAAGGATCACCATAG   73520         GAC
                                CTATGGTGGTT   TACAG
                                ||||||||||   |||||
                                GATACCACTAG   ATGTC
                                      GAA
GAM1094 KIAA1130 3' CTGACAACCACCACAGT    63092    A      ACTA
                                ACT TGGTGGTTG   CAG
                                ||| |||||||||   |||
                                TGA ACCACCAAC   GTC
                                  C       A___
GAM1094 KIAA1198 3' CTGCACCAACCACCACAGT   64033    A      ACTA
                                ACT TGGTGGTTG   CAG
                                ||| |||||||||   |||
                                TGA ACCACCAAC   GTC
                                  C       CAC_
GAM1094 KIAA1535 3' CTGTAGCTTGTCCCATCATA  80213       T_  _
                                TATGGTGG  TGA CTACAG
                                ||||||||  ||| ||||||
                                ATACTACC  GTT GATGTC
                                     CT   C
GAM1094 MGC10924 3' TTCTGTAATCATTGAATCAT  48312     GGT_  C
                                ATGGT   TGA TACAGAA
                                |||||   ||| |||||||
                                TACTA   ACT ATGTCTT
                                   AGTT   A
GAM1094 MGC20235 3' GTTCTGTTCCACCACCA    59561       T  CT
                                TGGTGGT GA  ACAGAAC
                                ||||||| ||  |||||||
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                                ACCACCA CT  TGTCTTG
                                   C __
GAM1094  PPIB     3'  GGCCCTGTAGTCCGCCAC    8130       T       AA
                                GTGGT GACTACAG  CC
                                ||||| ||||||||  ||
                                CACCG CTGATGTC  GG
                                   C       CC
GAM1094  Rabip4R  3'  GTTCTGCAGTCATTGACTGT   36278      GGT    A
                                ATGGT   TGACT CAGAAC
                                |||||   ||||| ||||||
                                TGTCA   ACTGA GTCTTG
                                   GTT    C
GAM1094  SHAPY    3'  GTCCTGTAGTTACCCAGC    57912   G   T       A
                                G TGG TGACTACAG AC
                                | ||| |||||||| ||
                                C ACC ATTGATGTC TG
                                 G   C       C
GAM1094  LOC148195 3'  GGTTCTGTCTTTACCACCA    85285       TGACT
                                TGGTGGT    ACAGAACC
                                |||||||    ||||||||
                                ACCACCA    TGTCTTGG
                                    TTTC_
GAM1094  LOC150837 3'  GGTCCTGAGCAAGAACCACC   80805       ___  A  A   A
                                GGTGGT   TG CT CAG ACC
                                ||||||   || || ||| |||
                                CCACCA   AC GA GTC TGG
                                   AGA  _ _   C
GAM1094  LOC150935 3'  GGTTCTGCAACCAGTTCATATG 80836    _    __     ACTA
            T                    AC TATGG  TGGTTG    CAGAACC
                                || |||||  ||||||    |||||||
                                TG ATACT  ACCAAC    GTCTTGG
                                 T    TG     _____
GAM1094  LOC151248 5'  TTCTGCAGATTTTAACCACTGT 81002          ___  A
                                ATGGTGGTTGA   CT CAGAA
                                ||||||||||   || |||||
                                TGTCACCAATT   GA GTCTT
                                      TTA  C
GAM1094  LOC163682 5'  GGTTCCACAGTCCCACCAGAGT 88414     A     TT    ACA
                                ACT TGGTGG  GACT   GAACC
                                ||| ||||||  ||||   |||||
                                TGA ACCACC  CTGA   CTTGG
                                  G     __    CAC
GAM1094  LOC169505 3'  TTCTGTAATCAATGCTG     83624      G    C
                                TGGTG TTGA TACAGAA
                                ||||| |||| |||||||
                                GTCGT AACT ATGTCTT
                                   _   A
GAM1094  LOC255042 5'  CTGCAGGTCAGACCACCGT    97044        _    A_
                                ATGGTGGT TGACT  CAG
                                |||||||| |||||  |||
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                                TGCCACCA ACTGG  GTC
                                    G    AC
GAM1095  ATP6V0C  3'  CCCCAGTAGTTGGTCTTGTA  88658        CTG  _  A
                                TACAAGATCA  ACT CTG GG
                                ||||||||||  ||| ||| ||
                                ATGTTCTGGT  TGA GAC CC
                                    ___  T  C
GAM1095  DLX4     3'  GTCCCCAGAACCCTTGGTCTTG 57114       CTGAC   A
                                CAAGATCA    TCTG GGAC
                                ||||||||    |||| ||||
                                GTTCTGGT    AGAC CCTG
                                    TCCCA   C
GAM1095  DLX4     3'  GTCCCCAGAACCCTTGGTCTTG 10421       CTGAC   A
                                CAAGATCA    TCTG GGAC
                                ||||||||    |||| ||||
                                GTTCTGGT    AGAC CCTG
                                    TCCCA   C
GAM1095  MNT      3'  TCCTCAGAGGCTGAGCCTGTA  40089     AGA  CTGA
                                TACA  TCA   CTCTGAGGA
                                ||||  |||   |||||||||
                                ATGT  AGT   GAGACTCCT
                                  CCG  CG__
GAM1095  SIAH2    3'  TCTCATCAGTGATCTT     18616         CTC
                                AAGATCACTGA  TGAGG
                                ||||||||||  |||||
                                TTCTAGTGACT  ACTCT
                                     ___
GAM1095  TCF2     3'  GTCCCCAGAACCAGCTGCAGAT 22411   AGAT  _  AC   A
           G                     CA   CA CTG  TCTG GGAC
                                ||   || |||  |||| ||||
                                GT   GT GAC  AGAC CCTG
                                 AGAC  C  CA   C
GAM1095  TCL1A    3'  CCTGGACCAGTGGTCT     42017        AC  G
                                AGATCACTG  TCT AGG
                                |||||||||  ||| |||
                                TCTGGTGAC  AGG TCC
                                    C_  _
GAM1095  TOB1     3'  TTTTGAGTCAGTGTCTT    20437     T      T
                                AAGA CACTGACTC GAG
                                |||| |||||||| |||
                                TTCT GTGACTGAG TTT
                                  _       T
GAM1095  VNN1     3'  TCCTCAGAGCAATTCTCTGTA  17423    _  TCAC  A
                                TACA AGA   TG CTCTGAGGA
                                |||| |||   || |||||||||
                                ATGT TCT   AC GAGACTCCT
                                  C  TA__  _
GAM1095  BMF      5'  CCTCAGAGTCAAACTTTGTG  54280      ATCAC
                                TACAAG    TGACTCTGAGG
                                ||||||    ||||||||||
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                                GTGTTT    ACTGAGACTCC
                                   CAA__
GAM1095  DDX33    3'  GTCCTCAGTGCGTGACCCTGT  39786    AGA   T ACT
                                ACA   TCAC G   CTGAGGAC
                                |||   |||| |   ||||||||
                                TGT   AGTG C   GACTCCTG
                                  CCC   _ GT_
GAM1095  FLJ20364 3'  CCTCAGAGCCATGTATTTG   35528     AT  C  A
                                CAAG  CA TG CTCTGAGG
                                ||||  || || ||||||||
                                GTTT  GT AC GAGACTCC
                                  AT  _  C
GAM1095  HMGN4    3'  TCCTTTCCCCAGTGATTTGTA  22034     A      ACTCT
                                TACA GATCACTG    GAGGA
                                |||| ||||||||    |||||
                                ATGT TTAGTGAC    TTCCT
                                  _      CCCT_
GAM1095  KIAA0377 3'  CCTCAGAGCCAGTCTCT    28501    TC   A
                                AGA  ACTG CTCTGAGG
                                |||  |||| ||||||||
                                TCT  TGAC GAGACTCC
                                  C_   C
GAM1095  KIAA0449 3'  TCCCCAGCACTCATGATCTTG  34639       C   CT_  A
                                CAAGATCA TGA   CTG GGA
                                |||||||| |||   ||| |||
                                GTTCTAGT ACT   GAC CCT
                                     _  CAC   C
GAM1095  KIAA1061 3'  GTCCTCAGAGTGCATTTCCTG  71723    A  TCAC  _
                                CA GA    TG ACTCTGAGGAC
                                || ||    || ||||||||||
                                GT CT    AC TGAGACTCCTG
                                 C  TT__  G
GAM1095  KIAA1535 3'  GTCCTCAGCTCAAGAATCCTGT 80214     A   CAC   CT
            A                    TACA GAT   TGA  CTGAGGAC
                                |||| |||   |||  ||||||||
                                ATGT CTA   ACT  GACTCCTG
                                  C   AGA   C_
GAM1095  LCHN     3'  TCCTCAGAGTATGTCTTG    87478       CACTG
                                CAAGAT    ACTCTGAGGA
                                ||||||    ||||||||||
                                GTTCTG    TGAGACTCCT
                                   TA___
GAM1095  MAGEH1   3'  TCATAATCTATGATCTTGTA   26772        CT  CTC
                                TACAAGATCA  GA   TGA
                                ||||||||||  ||   |||
                                ATGTTCTAGT  CT   ACT
                                      AT  AAT
GAM1095  LOC154789 5'  TCCTCAGAGCTCTCCTGTG   82034     A  TCACT  _
                                TACA GA    GA CTCTGAGGA
                                |||| ||    || |||||||||
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                                GTGT CT    CT GAGACTCCT
                                  C _____  C
GAM1095  LOC197201 3'  TCCTCAGAAGGTATTTGTA   89289      ATC  GAC
                                TACAAG  ACT  TCTGAGGA
                                ||||||  |||  ||||||||
                                ATGTTT  TGG  AGACTCCT
                                   A__  A__
GAM1095  LOC200178 3'  CCTCAGATGCCTTGTA     89998      AT  CTGAC
                                TACAAG  CA    TCTGAGG
                                ||||||  ||    |||||||
                                ATGTTC  GT    AGACTCC
                                   C_  _____
GAM1095  LOC255193 3'  CCTCAGAGTCAGGCCTGTA   97103     AGATCA
                                TACA     CTGACTCTGAGG
                                ||||     ||||||||||||
                                ATGT     GACTGAGACTCC
                                  CCG___
GAM1095  LOC96597  5'  TCCCCAGAATTCTCTTGT    67468      TCACT  C_   A
                                ACAAGA    GA  TCTG GGA
                                ||||||    ||  |||| |||
                                TGTTCT    CT  AGAC CCT
                                   _____  TA   C
GAM1096  IRS1      3'  CCATAGATGGTTCTCAATTGTA 19874     C        TGAAC
                                TACA ATTGAGAACC    ATGG
                                |||| ||||||||||    ||||
                                ATGT TAACTCTTGG    TACC
                                  _        TAGA_
GAM1096  SERPINF1  3'  CCTGTAAGGTTTCAATG     12038       A  GA  T
                                CATTGAGA CCT  ACA GG
                                |||||||| |||  ||| ||
                                GTAACTTT GGA  TGT CC
                                    _  A_  _
GAM1096  HSA243396 3'  CCATGTTCAGCAATGTCAATG  37844      GAAC_
                                CATTGA    CTGAACATGG
                                ||||||    ||||||||||
                                GTAACT    GACTTGTACC
                                   GTAAC
GAM1096  KIAA1387  3'  CAGGAATTTTCAATATGTA   71444     C      __
                                TACA ATTGAGAA  CCTG
                                |||| ||||||||  ||||
                                ATGT TAACTTTT  GGAC
                                  A       AA
GAM1096  MGC16063  3'  TTCAAATTCCAATGTGTA    54930       A  CC
                                TACACATTG GAA  TGAA
                                |||||||||| |||  ||||
                                ATGTGTAAC CTT  ACTT
                                      _  AA
GAM1096  SMCR8     3'  CCATGCTCAGGTTTGACTATGT 59253     TGA_      A
                                ACAT    GAACCTGA CATGG
                                ||||    |||||||| |||||
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                                TGTA   TTTGGACT GTACC
                                  TCAG      C
GAM1096 UPLC1    3' CCATGCTAGGCCCCAATGT   35227      AGAA   AA
                                ACATTG   CCTG  CATGG
                                ||||||   ||||  |||||
                                TGTAAC   GGAT  GTACC
                                   CCC_   C_
GAM1096 ZNF334   3' CCATAAGTCAACCCTCAATGT  36637       AACC   AC_
                                ACATTGAG   TGA   ATGG
                                ||||||||   |||   ||||
                                TGTAACTC   ACT   TACC
                                    CCA_   GAA
GAM1096 LOC145082 3' TATGGAATGCCCTTAATGTGTA 84196          AACCTGAA
                                TACACATTGAG      CATG
                                ||||||||||       ||||
                                ATGTGTAATTC      GTAT
                                      CCGTAAG_
GAM1096 LOC157723 3' CCAAGTAAGGTTCTCAAATGT  82465     _      GA  A
                                ACATT GAGAACCT  AC TGG
                                ||||| ||||||||  || |||
                                TGTAA CTCTTGGA  TG ACC
                                   A       A_  A
GAM1096 LOC219988 5' CCATGTTCGGCCCCCAATG   93262      AGAAC
                                CATTG    CTGAACATGG
                                |||||    ||||||||||
                                GTAAC    GGCTTGTACC
                                   CCCC_
GAM1097 CCND2    3' TCCCAGCAAATCATCGGGCCA  10055          CCACA  _  A
                                TGGCCTGATGAT    GC GG GA
                                ||||||||||||    || || ||
                                ACCGGGCTACTA    CG CC CT
                                      AA___  A  C
GAM1097 GCN5L2   5' CTCCGCTGCGGGGGAGGCC   60529      GATGA   A
                                GGCCT    TCC CAGCGGAG
                                |||||    ||| ||||||||
                                CCGGA    GGG GTCGCCTC
                                   GG___   C
GAM1097 GJA5     3' CTGACCAGATCATCAGCCA   19164      C      CACAG
                                TGGC TGATGATC    CGG
                                |||| ||||||||    |||
                                ACCG ACTACTAG    GTC
                                  _       ACCA_
GAM1097 HIVEP3   3' TCCCCGCTGTGGTTGGCAGCCA 44702     C  ATGAT       A
                                TGGC TG    CCACAGCGG GA
                                |||| ||    ||||||||| ||
                                ACCG AC    GGTGTCGCC CT
                                  _ GGTT_       C
GAM1097 HOXD1    5' CCGCCGGTATATTAGGCCA   44696         AT  ACA
                                TGGCCTGATG  CC   GCGG
                                |||||||||  ||   ||||
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                                ACCGGATTAT  GG   CGCC
                                      AT  C__
GAM1097  SUFU     3'  CCTTGTGACCCATCAGGCCA   32934          ATC    C
                                TGGCCTGATG   CACAG GG
                                ||||||||||   ||||| ||
                                ACCGGACTAC   GTGTT CC
                                      CCA    _
GAM1097  DKFZP586J1624 3'  CTCCGCCCAGTCACCATCAGGC 32043          ATCCACA_
           CA                    TGGCCTGATG       GCGGAG
                                ||||||||||       ||||||
                                ACCGGACTAC       CGCCTC
                                      CACTGACC
GAM1097  KIAA1671  3'  CTTTGCTTATGAATCATCAGAC 66282    C       C  C_
           C                     GG CTGATGAT CA  AGCGGAG
                                || |||||||| ||  |||||||
                                CC GACTACTA GT  TCGTTTC
                                 A       A  AT
GAM1097  LOC159110 5'  TCTCCGCTGCCCCGGTCAACCA 82995     CCTGA    CA__
                                TGG    TGATC    CAGCGGAGA
                                |||    |||||    |||||||||
                                ACC    ACTGG    GTCGCCTCT
                                  A____     CCCC
GAM1097  LOC159116 5'  TCTCCGCTGCCCCGGTCAACCA 82978     CCTGA    CA__
                                TGG    TGATC    CAGCGGAGA
                                |||    |||||    |||||||||
                                ACC    ACTGG    GTCGCCTCT
                                  A____     CCCC
GAM1097  LOC165476 5'  CTCCGCTGCCTGCTCAGCCA   88550     C   TGATCCA
                                TGGC TGA      CAGCGGAG
                                |||| |||      ||||||||
                                ACCG ACT      GTCGCCTC
                                  _   CGTCC__
GAM1097  LOC200032 5'  CTGACCAGATCATCAGCCA    85475      C       CACAG
                                TGGC TGATGATC     CGG
                                |||| ||||||||     |||
                                ACCG ACTACTAG     GTC
                                  _       ACCA_
GAM1097  LOC219654 5'  CTCCGCTGCGGAGGGGGGCC   92932      GATGA   A
                                GGCCT     TCC CAGCGGAG
                                |||||     ||| ||||||||
                                CCGGG     AGG GTCGCCTC
                                   GGG__   C
GAM1097  LOC255862 3'  TCAAATGTAGACTATCAGGCCA 96115          A  C   GCG
                                TGGCCTGATG TC ACA   GA
                                |||||||||| || |||   ||
                                ACCGGACTAT AG TGT   CT
                                      C  A   AAA
GAM1098  HAL      5'  GCCACTCCTGCATAAAGCTC   10903          TGAAAA
                                GAGCTTTATGC     GGTGGC
                                ||||||||||     ||||||
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                                CTCGAAATACG     TCACCG
                                      TCC___
GAM1098 HMGN2    3' GGCCACCTTGGCACAAAAGC  19809      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _ GG
GAM1098 NMI      5' GGCCACCTCCTCAGGAAG    17436     ATG   AA
                                CTTT   CTGA  AGGTGGCC
                                ||||   ||||  ||||||||
                                GAAG   GACT  TCCACCGG
                                  ___   CC
GAM1098 PACE     3' GGCCACCTCTCCAAGGGCTT   11944       A  CT  AAA
                                GAGCTTT TG  GA   GGTGGCC
                                ||||||| ||  ||   |||||||
                                TTCGGGA AC  CT   CCACCGG
                                   _ CT  ___
GAM1098 PYCR1    3' CCACCTTCCTCTAGAGCTC   70639       TGCT  A_
                                GAGCTTTA   GA  AAGGTGG
                                ||||||||   ||  |||||||
                                CTCGAGAT   CT  TTCCACC
                                     _____ CC
GAM1098 SDC1     3' GGCCACCTCCCCAGCATTCCAG 12991     TT_     AAA
           C                     GCT   ATGCTG   AGGTGGCC
                                |||   ||||||   ||||||||
                                CGA   TACGAC   TCCACCGG
                                  CCT     CCC
GAM1098 FLJ11560 5' GCCCAGGCCCAGCATAAAG   48008         AAAA   ___
                                CTTTATGCTG   GGT   GGC
                                ||||||||||   |||   |||
                                GAAATACGAC   CCG   CCG
                                     _____  GAC
GAM1098 KIAA0446 5' CCACCTTTTGAAGAGCTC    69446       ATGCTG
                                GAGCTTT     AAAAGGTGG
                                |||||||     |||||||||
                                CTCGAGA     TTTTCCACC
                                   AG_____
GAM1098 KIAA0971 3' GTTGTTCTCAGCATAAAGT   30677          AAA  TG
                                GCTTTATGCTGA   GG  GC
                                ||||||||||||   ||  ||
                                TGAAATACGACT   TT  TG
                                      C__  GT
GAM1098 KIAA1393 3' GGCCACCTTGGCACAAAAGC  72574      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _ GG
GAM1098 KIAA1656 3' GGCCACCTCCTCCTAGAAGCC 66377   A    ATGCT  AA
                                G GCTTT    GA  AGGTGGCC
                                | |||||    ||  ||||||||
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                                C CGAAG    CT  TCCACCGG
                                _    ATC__  CC
GAM1098  KIAA1884  3'  GCCACCTTCATCTACCAAGGCT 73728       ATGCT  A_
             C                   GAGCTTT    GA  AAGGTGGC
                                 |||||||    ||  ||||||||
                                 CTCGGAA    CT  TTCCACCG
                                     CCAT_  AC
GAM1098  PP3501    3'  GGCCACCGTTGACAGCATAAAG 41683         AAAA_
                                 CTTTATGCTG    GGTGGCC
                                 ||||||||||    |||||||
                                 GAAATACGAC    CCACCGG
                                       AGTTG
GAM1098  SDCCAG3   3'  GGTGTTCTCAGCATGAAGCTC  22803           AAA  TG
                                 GAGCTTTATGCTGA   GG  GCC
                                 ||||||||||||||   ||  |||
                                 CTCGAAGTACGACT   CT  TGG
                                        ___  TG
GAM1098  SP140     3'  GGCCACCTCCATGCAGAAGC   24327      A   TGAAA
                                 GCTTT TGC    AGGTGGCC
                                 ||||| |||    ||||||||
                                 CGAAG ACG    TCCACCGG
                                    _  TACC_
GAM1098  LOC148760 3'  GGCCACCTTCTCCAACAAGCTC 85364       TA  CT  A
                                 GAGCTT  TG  GA AAGGTGGCC
                                 ||||||  ||  || |||||||||
                                 CTCGAA  AC  CT TTCCACCGG
                                     CA  __  C
GAM1098  LOC150170 5'  ACCTGTTTCACATAAAGC    80414         C    _
                                 GCTTTATG TGAAA AGGT
                                 |||||||| ||||| ||||
                                 CGAAATAC ACTTT TCCA
                                      _    G
GAM1098  LOC150175 5'  ACCTGTTTCACATAAAGC    80453         C    _
                                 GCTTTATG TGAAA AGGT
                                 |||||||| ||||| ||||
                                 CGAAATAC ACTTT TCCA
                                      _    G
GAM1098  LOC150215 5'  ACCTGTTTCACATAAAGC    80456         C    _
                                 GCTTTATG TGAAA AGGT
                                 |||||||| ||||| ||||
                                 CGAAATAC ACTTT TCCA
                                      _    G
GAM1098  LOC150218 5'  ACCTGTTTCACATAAAGC    80525         C    _
                                 GCTTTATG TGAAA AGGT
                                 |||||||| ||||| ||||
                                 CGAAATAC ACTTT TCCA
                                      _    G
GAM1098  LOC152065 3'  GGCCACCTTCTCCTTGGCAGGC 86737       TTA   ___  A
             TC                    GAGCT   TGCT   GA AAGGTGGCC
                                   |||||   ||||   || |||||||||
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                                CTCGG  ACGG  CT TTCCACCGG
                                   ___   TTC  C
GAM1098  LOC152267 3'  GGCCACCTTGGCACAAAAGC  61036      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _  GG
GAM1098  LOC158292 5'  CCTCTGGACCCAGCATAAGGCT 88046           AAAA_  T
           C                     GAGCTTTATGCTG    GG GG
                                ||||||||||||    || ||
                                CTCGGAATACGAC    TC CC
                                       CCAGG  T
GAM1098  LOC219997 3'  GCCACCTCTTCAGCCTC    93256    CTTTAT    A
                                GAG     GCTGAA AGGTGGC
                                |||     |||||| |||||||
                                CTC     CGACTT TCCACCG
                                  _______     C
GAM1098  LOC256269 3'  GGCCACCTTGGCACAAAAGC  96608      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _  GG
GAM1098  LOC91963  5'  GGCCACCTCCTCTGAGAAGC  68321      ATGCT  AA
                                GCTTT    GA  AGGTGGCC
                                |||||    ||  ||||||||
                                CGAAG    CT  TCCACCGG
                                   AGT__  CC
GAM1099  DDX19    5'  CATCCCTCGAATCCACCAG   24337        A   CCA
                                CTGGTGGAT TGG   GGATG
                                ||||||||| |||   |||||
                                GACCACCTA GCT   CCTAC
                                     A   C__
GAM1099  RUVBL2   3'  CCTGTTTTCCACCAGAGT    22863         TATGGC
                                ACTCTGGTGGA     CAGG
                                ||||||||||     ||||
                                TGAGACCACCT     GTCC
                                      TTT___
GAM1099  C20orf162 5'  CATCCTAGCCATGCTCAGT   55498   G  GA     C
                                G TG  TATGGC AGGATG
                                | ||  |||||| ||||||
                                T AC  GTACCG TCCTAC
                                 G  TC     A
GAM1099  DKFZP727G051 3'  ATCCCCAGACCCACCAGA    70001        ATA   CCA
                                TCTGGTGG   TGG   GGAT
                                ||||||||   |||   ||||
                                AGACCACC   ACC   CCTA
                                    CAG   ___
GAM1099  FLJ10404  5'  ATCCTCCACCCACCAGAG    39314        ATA   CC
                                CTCTGGTGG   TGG  AGGAT
                                |||||||||   |||  |||||
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                                GAGACCACC  ACC  TCCTA
                                    C__  __
GAM1099  FLJ21324  5'  CATCCCATCACCCACCAGGGT  92847       ATA  CCA
                                ACTCTGGTGG  TGG  GGATG
                                ||||||||||  |||  |||||
                                TGGGACCACC  ACT  CCTAC
                                    C__  AC_
GAM1099  MGC11287  3'  ATCCCAGTCACCACCAGG   49611      ATA  CA
                                TCTGGTGG  TGGC  GGAT
                                ||||||||  ||||  ||||
                                GGACCACC  ACTG  CCTA
                                    ___  AC
GAM1099  TEX27   3'  CCTCCACCCACCAGAGT   41946       ATA  CC
                                ACTCTGGTGG  TGG  AGG
                                ||||||||||  |||  |||
                                TGAGACCACC  ACC  TCC
                                    C__  __
GAM1099  LOC145858 3'  CATCCTGCAGGGGCTCCCACCA 78001       ATAT  _____
           GAG                CTCTGGTGG   GGCC   AGGATG
                              |||||||||   ||||   ||||||
                              GAGACCACC   TCGG   TCCTAC
                                  C___   GGACG
GAM1099  LOC163231 5'  CCACTTATTCACCAGAGT   83331         __
                                ACTCTGGTGGATA  TGG
                                ||||||||||||  |||
                                TGAGACCACTTAT  ACC
                                      TC
GAM1099  LOC165246 5'  ATCCACCATCCACCAGA    83364       TA  CCA
                                TCTGGTGGA  TGG  GGAT
                                |||||||||  |||  ||||
                                AGACCACCT  ACC  CCTA
                                    __  A__
GAM1099  LOC256032 5'  GGTACCCATACCCACCAGG   99362       A   ___
                                TCTGGTGG TATGG  CC
                                |||||||| |||||  ||
                                GGACCACC ATACC  GG
                                    C   CAT
GAM1100  ABL2    5'  TGTGAGTCGCCTGGAGGCAG  24611          A_
                                CTGCCTCCAGGTGAC  GCA
                                ||||||||||||||  |||
                                GACGGAGGTCCGCTG  TGT
                                      AG
GAM1100  DYRK1B   3'  TGATTGGGGCCTGGGGCAG   17517     T    GACAG
                                CTGCC CCAGGT   CAATCA
                                ||||| ||||||   ||||||
                                GACGG GGTCCG   GTTAGT
                                  _    GG___
GAM1100  GNAZ    3'  CTGCACCCCTGTCACCTGGAGG 10827          CAAT_
                                CCTCCAGGTGACAG   CAG
                                ||||||||||||||   |||
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                                GGAGGTCCACTGTC    GTC
                                      CCCAC
GAM1100 GYPC    3' GATAGCCACCTGGAAACA   10900   CC     ACA A
                                TG TCCAGGTG  GC ATC
                                || ||||||||  || |||
                                AC AGGTCCAC  CG TAG
                                 AA      ___ A
GAM1100 GYPC    3' GATAGCCACCTGGAAACA   34143   CC     ACA A
                                TG TCCAGGTG  GC ATC
                                || ||||||||  || |||
                                AC AGGTCCAC  CG TAG
                                 AA      ___ A
GAM1100 IL1R1   3' TGAGGTCACCTGGAATCAG  7928    CC      AG
                                CTG TCCAGGTGAC CA
                                ||| ||||||||||  ||
                                GAC AGGTCCACTG GT
                                  TA       GA
GAM1100 SLC21A9 3' TGTGTCACCTGGGGCAG    24384     T      G
                                CTGCC CCAGGTGACA CA
                                ||||| ||||||||||  ||
                                GACGG GGTCCACTGT GT
                                  _       _
GAM1100 ZNF138  5' CTGATTACCTGTCTGGA    82099    GGT   C_
                                TCCA  GACAG  AATCAG
                                ||||  |||||  ||||||
                                AGGT  CTGTC  TTAGTC
                                  ___    CA
GAM1100 C8orf13 3' GTGGGTCTCCCGGAGGCAG  82482       A T  A_
                                CTGCCTCC GG GAC  GC
                                |||||||| || |||  ||
                                GACGGAGG CC CTG  TG
                                    C  T   GG
GAM1100 CHST3   3' TGTGGTCCCTGGAGGCA    16246       T  A
                                TGCCTCCAGG GAC GCA
                                |||||||||| ||| |||
                                ACGGAGGTCC CTG TGT
                                      _  G
GAM1100 CMG1    5' TGCAATGCCACCTGGGACAG  47728    C T    A __
                                CTG C CCAGGTG CA  GCA
                                ||| | ||||||| ||  |||
                                GAC G GGTCCAC GT  CGT
                                  A _     C  AA
GAM1100 DKFZP434H132 3' GATGGGCCCTGGAGGCAG   31932        TGACA A_
                                CTGCCTCCAGG    GC  ATC
                                ||||||||||    ||  |||
                                GACGGAGGTCC    CG  TAG
                                      _____ GG
GAM1100 FLJ10036 3' CTGATTGCCCTTATGGAG   96627     GG  CA
                                CTCCA  TGA  GCAATCAG
                                |||||  |||  ||||||||
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                                GAGGT  ATT  CGTTAGTC
                                  __   CC
GAM1100  FLJ11053  3'  CTGACTATCTACCTGGAGATAG 90123     C       _  C  CAA
                                CTG CTCCAGGT GA AG   TCAG
                                ||| |||||||| || ||   ||||
                                GAT GAGGTCCA CT TC   AGTC
                                  A       T  A  ___
GAM1100  FLJ11767  3'  CTGATTGTAAGCACCTGAAGGC 45059       C      ACA
             A                   TGCCT CAGGTG   GCAATCAG
                                ||||| ||||||   ||||||||
                                ACGGA GTCCAC   TGTTAGTC
                                  A     GAA
GAM1100  FLJ12691  3'  CTGATTGGTATCTGGAGACAG  45001     C        ACAG
                                CTG CTCCAGGTG    CAATCAG
                                ||| |||||||||    |||||||
                                GAC GAGGTCTAT    GTTAGTC
                                  A       G___
GAM1100  GALNT6   3'  CTGATCACCAGCTTCTCTGGAG 24247         T  C   A____
             GC                   GCCTCCAGG GA AGC     ATCAG
                                |||||||| || |||     |||||
                                CGGAGGTCT CT TCG     TAGTC
                                    _ _   ACCAC
GAM1100  H-plk    5'  CTGATTACCTGTCTGGAGCA   32381     C    GGT    C_
                                TGC TCCA   GACAG  AATCAG
                                ||| ||||   |||||  ||||||
                                ACG AGGT   CTGTC  TTAGTC
                                  _   ___    CA
GAM1100  KIAA0781  3'  GCCACCGTGGAGGCAG      68058          _   ACA
                                CTGCCTCCA GGTG   GC
                                |||||||| ||||   ||
                                GACGGAGGT CCAC   CG
                                    G   ___
GAM1100  KIAA0971  3'  CTGATTACTGTCATTACTAGAG 30670     C  __      C
                                CTC AG  GTGACAG AATCAG
                                ||| ||  ||||||| ||||||
                                GAG TC  TACTGTC TTAGTC
                                  A  AT      A
GAM1100  KIAA1344  3'  CTGATTATTACCTGGATACA   72866    CC       CAGC
                                TG  TCCAGGTGA    AATCAG
                                ||  |||||||||    ||||||
                                AC  AGGTCCATT    TTAGTC
                                  AT       A___
GAM1100  MADCAM1   3'  CTGATTGCCTCTTTGGAG    56238        T  CA
                                CTCCAGG GA  GCAATCAG
                                |||||||  ||  ||||||||
                                GAGGTTT CT  CGTTAGTC
                                    _  C_
GAM1100  MADCAM1   3'  CTGATTGCCTCTTTGGAG    56241        T  CA
                                CTCCAGG GA  GCAATCAG
                                |||||||  ||  ||||||||
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                                GAGGTTT CT  CGTTAGTC
                                    _ C_
GAM1100 MADCAM1  3' CTGATTGCCTCTTTGGAG    56244       T  CA
                                CTCCAGG GA  GCAATCAG
                                ||||||| ||  ||||||||
                                GAGGTTT CT  CGTTAGTC
                                    _ C_
GAM1100 MGC10870 5' CTGACCATGTCACCTGGAGGC 51178           GCAA
                                GCCTCCAGGTGACA   TCAG
                                ||||||||||||||   ||||
                                CGGAGGTCCACTGT   AGTC
                                       ACC_
GAM1100 MGC10924 3' CTGTATGAACACCTGGAAGCA 48311    C      _____
                                TGC TCCAGGTG    ACAG
                                ||| ||||||||    ||||
                                ACG AGGTCCAC    TGTC
                                  A       AAGTA
GAM1100 MGC14436 5' CTGACCACCTGGAGACAG    52926    C       A_
                                CTG CTCCAGGTG  CAG
                                ||| |||||||||  |||
                                GAC GAGGTCCAC  GTC
                                  A        CA
GAM1100 SYT12    3' TGATCGCTGTGGGGGCAG    96390        AGGTG    A
                                CTGCCTCC    ACAGC ATCA
                                ||||||||    ||||| ||||
                                GACGGGGG    TGTCG TAGT
                                     _____    C
GAM1100 TReP-132 3' TGTGTGTCACTTAGAGACAG  54274    C  C      _
                                CTG CTC AGGTGACA GCA
                                ||| ||| |||||||| |||
                                GAC GAG TTCACTGT TGT
                                  A  A       G
GAM1100 TReP-132 3' TGTGTGTCACTTAGAGACAG  54276    C  C      _
                                CTG CTC AGGTGACA GCA
                                ||| ||| |||||||| |||
                                GAC GAG TTCACTGT TGT
                                  A  A       G
GAM1100 TReP-132 3' TGTGTGTCACTTAGAGACAG  37915    C  C      _
                                CTG CTC AGGTGACA GCA
                                ||| ||| |||||||| |||
                                GAC GAG TTCACTGT TGT
                                  A  A       G
GAM1100 ZFD25    5' CTGATCACCTGTCTGGAGCA  33109    C   GGT    CA_
                                TGC TCCA   GACAG   ATCAG
                                ||| ||||   |||||   |||||
                                ACG AGGT   CTGTC   TAGTC
                                  _   ___    CAC
GAM1100 ZNF177   3' CTGTTATGGTCACCTGGAAACA 14356    CC       AGCAAT
            G                    CTG  TCCAGGTGAC     CAG
                                ||| ||||||||||     |||
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                                GAC  AGGTCCACTG     GTC
                                  AA         GTATT_
GAM1100  ZNF90     5'  CTGATCACCTGTCTGGAGCA   79467     C    GGT    CA_
                                TGC TCCA   GACAG   ATCAG
                                ||| ||||   |||||   |||||
                                ACG AGGT   CTGTC   TAGTC
                                  _   ___     CAC
GAM1100  LOC149606 3'  CTGAAGCACCACTGGAGGCA   80261         G  ACA  AA
                                TGCCTCCAG TG   GC  TCAG
                                ||||||||| ||   ||  ||||
                                ACGGAGGTC AC   CG  AGTC
                                      _ CA_  A_
GAM1100  LOC157663 3'  CTGAAAGTACTGTCATCTAAAA 82450     CTCC        CAA__
             GCA                   TGC    AGGTGACAG     TCAG
                                |||    |||||||||     ||||
                                ACG    TCTACTGTC     AGTC
                                  AAAA        ATGAA
GAM1100  LOC196527 3'  TGATTGTACTAGAGACAG    89102     C   CA   GACA
                                CTG CTC  GGT    GCAATCA
                                ||| |||  |||    |||||||
                                GAC GAG  TCA    TGTTAGT
                                  A  A_  _____
GAM1100  LOC221025 5'  CTGGCCACCTGGAGACAG    94785     C        A_
                                CTG CTCCAGGTG  CAG
                                ||| |||||||||  |||
                                GAC GAGGTCCAC  GTC
                                  A        CG
GAM1100  LOC253943 3'  CTGATTGCTATCATGAAGTA   97845     C  CAG    C
                                TGC TC   GTGA AGCAATCAG
                                ||| ||   |||| |||||||||
                                ATG AG   TACT TCGTTAGTC
                                  A  ___    A
GAM1100  LOC255180 3'  GATCACTGTCATCTAAAAGCAG 96732      CTCC        CA
                                CTGC    AGGTGACAG  ATC
                                ||||    |||||||||  |||
                                GACG    TCTACTGTC  TAG
                                   AAAA        AC
GAM1100  LOC256416 3'  CTGTCCACCTGGGGACAG    96059     C        _
                                CTG CTCCAGGTG ACAG
                                ||| ||||||||| ||||
                                GAC GGGGTCCAC TGTC
                                  A        C
GAM1100  LOC51673  3'  CTGTCCACCTGGGGACAG    96207     C        _
                                CTG CTCCAGGTG ACAG
                                ||| ||||||||| ||||
                                GAC GGGGTCCAC TGTC
                                  A        C
GAM1101  KLK13     3'  CAGAAGCATTCAGGCACTGCCA 32144           CGGC  G
                                TGGCAGTGCCTGA    GC TCTG
                                ||||||||||||    || ||||
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                                ACCGTCACGGACT   CG AGAC
                                      TA__  A
GAM1101  SCN4A    3'  CAGACACCTAACCCCAGGGCAC 6195          GAC  CGC___
            TGCCA                 TGGCAGTGCCT  GG    GTCTG
                                  ||||||||||  ||    |||||
                                  ACCGTCACGGG  CC    CAGAC
                                       ACC  AATCCA
GAM1101  C8orf13  3'  CAGAGCTCTGCACAAACACTGC 82471       CC  A_  C  G
            CA                    TGGCAGTG  TG  CGG GC TCTG
                                  ||||||||  ||  ||| || ||||
                                  ACCGTCAC  AC  GTC CG AGAC
                                      AA  AC   T  _
GAM1101  DKFZP434G156 5'  CAGAGTGAGTCAGGCACCTCCA 70335    CA       GG   G
                                  TGG  GTGCCTGAC  CGC TCTG
                                  |||  |||||||||  ||| ||||
                                  ACC  CACGGACTG  GTG AGAC
                                    TC       A_  _
GAM1101  FLJ12150  5'  AGACGCGCCAGACGCGCCA   45681     A   C  GAC
                                  TGGC GTG CT   GGCGCGTCT
                                  |||| ||| ||   |||||||||
                                  ACCG CGC GA   CCGCGCAGA
                                    _   A  ___
GAM1101  FLJ13725  3'  CAGGGCTCACCAGGCACTGGCA 68829    G       AC  C  G
                                  TG CAGTGCCTG  GG GC TCTG
                                  || |||||||||  || || ||||
                                  AC GTCACGGAC  CT CG GGAC
                                   G       CA  _  _
GAM1101  IR1899308 5'  AGACGCGCCGCCGCTGCC    38526       CCTGA
                                  GGCAGTG    CGGCGCGTCT
                                  |||||||    ||||||||||
                                  CCGTCGC    GCCGCGCAGA
                                     C_____
GAM1101  KIAA1193  3'  GCGCCCGGCACTGCCA      68274         TGAC
                                  TGGCAGTGCC   GGCGC
                                  ||||||||||   |||||
                                  ACCGTCACGG   CCGCG
                                       C___
GAM1101  LOC148394 5'  TGTGCACCAGACACTGCCA   85304       C   ACG
                                  TGGCAGTG CTG   GCGCG
                                  |||||||| |||   |||||
                                  ACCGTCAC GAC   CGTGT
                                      A   CA_
GAM1101  LOC153565 5'  AGGTGCGCCAGGACTACCA   81755    C   G   GAC    GT
                                  TGG AGT CCT   GGCGC  CT
                                  ||| ||| |||   |||||  ||
                                  ACC TCA GGA   CCGCG  GA
                                    A   _   ___     TG
GAM1101  LOC254196 5'  TGTGCACCAGACACTGCCA   99187       C   ACG
                                  TGGCAGTG CTG   GCGCG
                                  |||||||| |||   |||||
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                                ACCGTCAC GAC   CGTGT
                                    A   CA_
GAM1101  LOC255374 3'  CAGAGTGCACCTGACACTGCCA 97789        CCTGACG    G
                                TGGCAGTG      GCGC TCTG
                                ||||||||      |||| ||||
                                ACCGTCAC      CGTG AGAC
                                    AGTCCA_   _
GAM1102  DLEC1     3'  CATCTGGCCCTCCCTTG     24716      A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                  C    G  _
GAM1102  DLEC1     3'  CATCTGGCCCTCCCTTG     24717      A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                  C    G  _
GAM1102  PIP5K1A   3'  TATCCCACCCTGCCTTGATA   14520        A   CA  C
                                TATCAAGG AGGG  GG GTG
                                |||||||| ||||  || |||
                                ATAGTTCC TCCC  CC TAT
                                    G   A_  C
GAM1102  SOX11     3'  ACCCACCCCCCCTTGGTA    13308        AA  CA  C
                                TATCAAGG  GGG  GG GT
                                ||||||||  |||  || ||
                                ATGGTTCC  CCC  CC CA
                                    CC  A_  _
GAM1102  CHL1      3'  TGTTACCTTTCCTCAATA    22768     CA      CA
                                TAT  AGGAAGGG  GGCG
                                |||  ||||||||  ||||
                                ATA  TCCTTTCC  TTGT
                                  AC       A_
GAM1102  EPB41L1   3'  CATTCTGCCCTTCCCTGA    71104     A        C
                                TCA GGAAGGGCAGG GTG
                                ||| |||||||||| |||
                                AGT CCTTCCCGTCT TAC
                                  C         _
GAM1102  FLJ00060  3'  CATACCCCCTGCCCTCCTCTGA 61741     _   A      CGTG
                                TCA AGGA GGGCAGG    ATG
                                ||| |||| |||||||    |||
                                AGT TCCT CCCGTCC    TAC
                                  C   _      CCCA
GAM1102  FLJ10898  5'  CACCACAGCCCTTTCTCAATA  60126     CA       AGGC
                                TAT  AGGAAGGGC    GTG
                                |||  |||||||||    |||
                                ATA  TCTTTCCCG    CAC
                                  AC        ACAC
GAM1102  FLJ22557  3'  ATCATCCCATCCTTAATA    45581     C    A  CAGGC
                                TAT AAGGA GGG     GTGAT
                                ||| ||||| |||     |||||
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                                ATA TTCCT CCC     TACTA
                                  A     A  _____
GAM1102  KIAA0574  3'  CATCCCCTGCCCTCCCCTGA   69808     A  A       CGT
                                TCA GG AGGGCAGG   GATG
                                ||| || ||||||||   ||||
                                AGT CC TCCCGTCC   CTAC
                                  C  C       C__
GAM1102  KIAA0632  3'  CACCTCAGAAACCCTTCCTTGA 32071          CA___  C
                                TCAAGGAAGGG     GG GTG
                                ||||||||||     || |||
                                AGTTCCTTCCC     CT CAC
                                      AAAGA  C
GAM1102  KIAA1045  3'  CATCACATGTCCTTCC      71599          GGC
                                GGAAGGGCA   GTGATG
                                |||||||||   ||||||
                                CCTTCCTGT   CACTAC
                                     A__
GAM1102  KIAA1354  5'  CAGTGACTGCCTTCCCTTGATA 61572        A      G  _
                                TATCAAGG AGGGCAG CG TG
                                |||||||| ||||||| || ||
                                ATAGTTCC TTCCGTC GT AC
                                     C      A  G
GAM1102  MGC20460  5'  CACCGCCTCCTACCCTTCTT   54901        C___    _
                                AGGAAGGG    AGGCG TG
                                ||||||||    ||||| ||
                                TTCTTCCC    TCCGC AC
                                     ATCC     C
GAM1102  LOC158476 3'  CACGCCCGCCCCCCCCATTGA  88186      _ AA_    A
                                TCAA GG   GGGC GGCGTG
                                ||||  ||   ||||  ||||||
                                AGTT CC   CCCG CCGCAC
                                  A  CCC    C
GAM1102  LOC90459  3'  CACACCCGCCTAATTTTTG    63550       A_    A  C
                                CAAGGA  GGGC GG GTG
                                ||||||  ||||  ||  |||
                                GTTTTT  TCCG CC CAC
                                   AA    C  A
GAM1103  CSNK1G2   3'  CAACCAAAATGCTGCACCAAAG 8987          TCACTACC
                                CTTTGGTGC       TGGTTG
                                |||||||||       ||||||
                                GAAACCACG       ACCAAC
                                     TCGTAAA_
GAM1103  LMO2      5'  AACCAGGCCACCAAGAGG     19933       _    CTCACTA
                                CCTTT GGTG      CCTGGTT
                                |||||  ||||      |||||||
                                GGAGA CCAC      GGACCAA
                                  A    C_______
GAM1103  MIPOL1    3'  CAACACTGTGTAAACACCAAAG 77588         CT__   TACCTG
                                CTTTGGTG    CAC     GTTG
                                ||||||||    |||     ||||
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                                GAAACCAC   GTG     CAAC
                                     AAAT   TCA___
GAM1103  TNFAIP2   3'  AACCAGGCAACACCAAGG    21913        CTCACTA
                                CTTTGGTG      CCTGGTT
                                ||||||||      |||||||
                                GGAACCAC      GGACCAA
                                     AAC____
GAM1103  C21orf100 3'  AGCCAAGGAACACCAAAG    59504        C  A  ACC
                                CTTTGGTG TC CT   TGGTT
                                |||||||| || ||   |||||
                                GAAACCAC AG GA   ACCGA
                                     A  _  ___
GAM1103  GPR9      5'  AACCACAAGCACCAAAG     9484          CACTACC
                                CTTTGGTGCT      TGGTT
                                ||||||||||      |||||
                                GAAACCACGA      ACCAA
                                      AC_____
GAM1103  KIAA1466  3'  CAACATTTATATAGAGCACCAA 72407          ACTACCTG_
              AGG                    CCTTTGGTGCTC        GTTG
                                |||||||||||        ||||
                                GGAAACCACGAG        CAAC
                                      ATATATTTA
GAM1103  MGC2491   3'  CAACCAGGTAGTGAGCACCAAA 44094
              GG                    CCTTTGGTGCTCACTACCTGGTTG
                                |||||||||||||||||||||||
                                GGAAACCACGAGTGATGGACCAAC

GAM1103  PRO2015   3'  GCCAATGAGACCAAAGG     38162        G    CTACC
                                CCTTTGGT CTCA     TGGT
                                |||||||| ||||     ||||
                                GGAAACCA GAGT     ACCG
                                     _    A____
GAM1103  LOC158293 3'  ACCAGCAGAACACCAAAGG    82744         C  ACTAC
                                CCTTTGGTG TC     CTGGT
                                ||||||||| ||     |||||
                                GGAAACCAC AG     GACCA
                                     A  AC___
GAM1103  LOC219347 3'  AACTAACAAGCACCAAGG     94569          CACTACC
                                CTTTGGTGCT      TGGTT
                                ||||||||||      |||||
                                GGAACCACGA      ATCAA
                                      ACA____
GAM1103  LOC256130 3'  ATGAGGCAATGAGACACCAAAG 97755          _   CTA   G
              G                     CCTTTGGTG CTCA   CCT GT
                                |||||||| ||||   ||| ||
                                GGAAACCAC GAGT   GGA TA
                                     A    AAC   G
GAM1103  LOC92231  3'  CAACCAGGTAACAAAACTAAAG 69089        GCTCAC
                                CTTTGGT     TACCTGGTTG
                                |||||||     ||||||||||
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                                GAAATCA     ATGGACCAAC
                                    AAACA_
GAM1104  ACCN2    3'  TCTCCCACATCCTCTTCCCCAA 39631     AA       CC   T
                                TTG  GAAGAGGAT  GGG GG
                                |||  |||||||||  ||| ||
                                AAC  CTTCTCCTA  CCC CT
                                  CC        CA   T
GAM1104  DRD1     5'  GGCCTGGGATCCTTTCCCCAA  7671      AA  A       G GT
                                TTG  GA GAGGATCC G  GGCC
                                |||  || ||||||||  |  ||||
                                AAC  CT TTCCTAGG T  CCGG
                                  CC  _       G __
GAM1104  GA       5'  GCCACCCGGGTTCTCCTTCA   26087       AA
                                TGAAG  GAGGATCCGGGTGGC
                                |||||  ||||||||||||||
                                ACTTC  CTCTTGGGCCCACCG
                                    __
GAM1104  GABRE    3'  GGCCACCTCCCTCTTCTTCAA  18286           ATCC
                                TTGAAGAAGAGG    GGGTGGCC
                                ||||||||||||    ||||||||
                                AACTTCTTCTCC    TCCACCGG
                                      C___
GAM1104  HNRPDL   3'  GCCAGCGTCACCCTCTTCTCCA 19602     A       ATC_  GG
             A                   TTG AGAAGAGG    CG  TGGC
                                ||| ||||||||    ||  ||||
                                AAC TCTTCTCC    GC  ACCG
                                  C       CACT  G_
GAM1104  ILVBL    3'  GCTCTTGGACCCTCCTCTTCA  23379       A    A     T
                                TGAAGA GAGG TCCGGG GGC
                                ||||||| |||| |||||| |||
                                ACTTCT CTCC AGGTTC TCG
                                   C   C     _
GAM1104  MAT1A    3'  GGCCATGCTCCTCTTCCCCAG  92501     AA       TCCGG
                                TTG  GAAGAGGA    GTGGCC
                                |||  ||||||||    ||||||
                                GAC  CTTCTCCT    TACCGG
                                  CC       CG___
GAM1104  NGFR     3'  GGCCACCTGCCCCCTTCT    11801       A  ATC
                                AGAAG GG   CGGGTGGCC
                                |||||  ||   |||||||||
                                TCTTC CC   GTCCACCGG
                                   _  CC_
GAM1104  NP       3'  GGTGCCAGATCCTCTTCTCAA  6051       A        CG    G
                                TTGA GAAGAGGATC  GGTG CC
                                ||||  ||||||||||  ||||  ||
                                AACT CTTCTCCTAG  CCGT GG
                                   _        A_   _
GAM1104  PPIL1    5'  GGCCACCCAAATCCTGGTATCG 32668      AGAAG    CC
             A                   TTGA    AGGAT  GGGTGGCC
                                ||||    |||||  ||||||||
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                                AGCT    TCCTA  CCCACCGG
                                  ATGG_    AA
GAM1104  TEGT     3'  GCCACCCGGCCCTTCCTTCCTC 65227     A   _  AT
             A                    TGA GAAG AGG  CCGGGTGGC
                                  ||| |||| |||  |||||||||
                                  ACT CTTC TTC  GGCCCACCG
                                    C   C  CC
GAM1104  DKFZP434L0718 3'  CCACCACCATCTCTCTCCTCTT 50456       __   _  CCG
             CAA                    TTGAAGA  AGAG GAT   GGTGG
                                  |||||||  |||| |||   |||||
                                  AACTTCT  TCTC CTA   CCACC
                                      CC    T   CCA
GAM1104  DKFZP434P0721 3'  CACCAATCTCTTCTTCAA    64459          ATCCG
                                  TTGAAGAAGAGG    GGTG
                                  ||||||||||||    ||||
                                  AACTTCTTCTCT    CCAC
                                        AA___
GAM1104  FLJ12661  5'  GGCCATCCAAACCACCTCCTTC 47855       AA   ATCC__
             AA                     TTGAAG  GAGG     GGGTGGCC
                                  ||||||  ||||     ||||||||
                                  AACTTC  CTCC     CCTACCGG
                                     __   ACCAAA
GAM1104  FLJ13189  3'  CCACCCAGATTCTACTCATTCT 46496       ___ _    C
             TCAA                   TTGAAGA   AG AGGATC GGGTGG
                                  |||||||   || |||||| ||||||
                                  AACTTCT   TC TCTTAG CCCACC
                                      TAC  A     A
GAM1104  FLJ21458  3'  ACCATCTCCTTCTTCAA     46277         AG   CCG
                                  TTGAAGAAG  GAT   GGT
                                  |||||||||  |||   |||
                                  AACTTCTTC  CTA   CCA
                                       CT   ___
GAM1104  FLJ23420  5'  GCCCACCTCTTCTCCAA     47540     A       ATCC
                                  TTG AGAAGAGG    GGGT
                                  ||| ||||||||    ||||
                                  AAC TCTTCTCC    CCCG
                                    C       A___
GAM1104  KIAA0790  3'  ACTGAGGATCCTCTCCTCCAG  69256     A  A       G_
                                  TTG AG AGAGGATCC  GGT
                                  ||| || |||||||||  |||
                                  GAC TC TCTCCTAGG  TCA
                                    C  C        AG
GAM1104  KIAA1036  3'  GCCACCCCTATCCCTCTTCT   30492         _  CC
                                  AGAAGAGG AT  GGGTGGC
                                  |||||||| ||  |||||||
                                  TCTTCTCC TA  CCCACCG
                                      C  TC
GAM1104  PIP5K1C   3'  GGCCAGGCCTCCTCTTCCCCAG 71307     AA       T_  GGG
                                  TTG  GAAGAGGA  CC   TGGCC
                                  |||  ||||||||  ||   |||||
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                                GAC  CTTCTCCT  GG   ACCGG
                                  CC       CC  ___
GAM1104  SLC38A4   3'  GGCAATGCTCTTCTTCAA    36344          G  __
                                TTGAAGAAGAG AT  CC
                                ||||||||||| ||  ||
                                AACTTCTTCTC TA  GG
                                      G  AC
GAM1104  LOC153914 3'  TAGATCCTCTTCCTCAA     81899      A        CG
                                TTGA GAAGAGGATC  G
                                |||| ||||||||||  |
                                AACT CTTCTCCTAG  T
                                  C         AT
GAM1104  LOC256369 3'  GCATGGATCTCTTCTCCAA   96611     A      G    G
                                TTG AGAAGAG ATCCG GT
                                ||| ||||||| ||||| ||
                                AAC TCTTCTC TAGGT CG
                                  C      _    A
GAM1105  ATP10C    3'  GCATGAGTGGACGTCAGAAG   44668    C        _   GA
                                CT CTGACGTCC CTCA  TGC
                                || ||||||||| ||||  |||
                                GA GACTGCAGG GAGT  ACG
                                 A        T   __
GAM1105  BLVRB     3'  GCATTCTGGACATGAGGAGCAA 7387         GAC    CTCA
                                TTGCTCCT   GTCC   GATGC
                                ||||||||   ||||   |||||
                                AACGAGGA   CAGG   TTACG
                                     GTA   TC__
GAM1105  EGFL5     5'  GCATCTGAAATTTTCAGGTACA 87913     CT    CGTCCC
            A                    TTG  CCTGA     TCAGATGC
                                |||  |||||     ||||||||
                                AAC  GGACT     AGTCTACG
                                  AT    TTTAA_
GAM1105  GATM      3'  CACCTAAGAAGCTTAGGGGCAA 9434         C  CC  C  A
                                TTGCTCCTGA GT  CT AG TG
                                |||||||||| ||  || || ||
                                AACGGGGATT CG  GA TC AC
                                      _  AA  A  C
GAM1105  KCNK7     3'  CACCTGAGGAGGAAGCAG    20344      _  GACGTC     A
                                TTGCT CCT     CCTCAG TG
                                ||||| |||     |||||| ||
                                GACGA GGA     GGAGTC AC
                                  A  _______     C
GAM1105  KCNK7     3'  CACCTGAGGAGGAAGCAG    54054      _  GACGTC     A
                                TTGCT CCT     CCTCAG TG
                                ||||| |||     |||||| ||
                                GACGA GGA     GGAGTC AC
                                  A  _______     C
GAM1105  KCNK7     3'  CACCTGAGGAGGAAGCAG    54061      _  GACGTC     A
                                TTGCT CCT     CCTCAG TG
                                ||||| |||     |||||| ||
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                                GACGA GGA     GGAGTC AC
                                  A  _______     C
GAM1105  KCNK7    3'  CACCTGAGGAGGAAGCAG    54231      _  GACGTC     A
                                TTGCT CCT     CCTCAG TG
                                ||||| |||     |||||| ||
                                GACGA GGA     GGAGTC AC
                                  A  _______     C
GAM1105  LYL1     3'  TGAAGACGTCAGGGGCAA    19951            CC
                                TTGCTCCTGACGTC  TCA
                                ||||||||||||||  |||
                                AACGGGGACTGCAG  AGT
                                       A_
GAM1105  TMOD2    3'  CATTTGCAAACGTCAGGAG   28022          CCCT
                                CTCCTGACGT    CAGATG
                                ||||||||||    ||||||
                                GAGGACTGCA    GTTTAC
                                     AAC_
GAM1105  UBE2A    3'  GCATCTGAGAACCTTAAAGC   13927     CC   C  CC
                                GCT  TGA GT  CTCAGATGC
                                |||  ||| ||  |||||||||
                                CGA  ATT CA  GAGTCTACG
                                  A_   C  A_
GAM1105  CGB1     5'  ATCTGAGAGAGAGCAG      54128       CTGACG  C
                                TTGCTC     TC CTCAGAT
                                ||||||     || |||||||
                                GACGAG     AG GAGTCTA
                                   _______ A
GAM1105  DKFZp547N157 3'  CACCTGAGACCAGCAGGACAA  69524     C    AC_  CC   A
                                TTG TCCTG   GTC  TCAG TG
                                ||| |||||   |||  |||| ||
                                AAC AGGAC   CAG  AGTC AC
                                  _    GAC   __    C
GAM1105  DNAJB11  3'  GCAAGAGGACTCCAGGAGCAA  33306         AC    C  AGA
                                TTGCTCCTG  GTCC TC   TGC
                                |||||||||  |||| ||   |||
                                AACGAGGAC  CAGG AG   ACG
                                     CT    _  A__
GAM1105  KIAA1951 3'  CTGGAGACCCAGGAGCAA    74154         AC   C T
                                TTGCTCCTG  GTC C CAG
                                |||||||||  ||| | |||
                                AACGAGGAC  CAG G GTC
                                     C_   A _
GAM1105  OBTP     3'  GCACCCAAAGGGCAGGAGCAA  34665         ACGT    CAGA_
                                TTGCTCCTG    CCCT    TGC
                                |||||||||    ||||    |||
                                AACGAGGAC    GGGA    ACG
                                     _____    AACCC
GAM1105  TROAP    5'  GCACCCGAGAGGGTCAGGAG   19692         GT  _   AGA
                                CTCCTGAC  CC CTC   TGC
                                ||||||||  || |||   |||
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                                GAGGACTG  GG GAG   ACG
                                     __  A   CCC
GAM1105  LOC146515 3'  GCATCTGAGAATTGGAGAGCAG 78518       _ TG CGTCC
                                TTGCTC C  A    CTCAGATGC
                                |||||| |  |    |||||||||
                                GACGAG G  T    GAGTCTACG
                                   A GT AA___
GAM1105  LOC149426 3'  GCATCTGAGAAACACATGGGC  85574     C  AC  CC
                                GCTC TG  GT  CTCAGATGC
                                |||| ||  ||  |||||||||
                                CGGG AC  CA  GAGTCTACG
                                  T  A_  AA
GAM1105  LOC153577 3'  GCATCCAAGGGTGGGGAGCAG  87240        GA  T    CA
                                TTGCTCCT  CG CCCT  GATGC
                                ||||||||  || ||||  |||||
                                GACGAGGG  GT GGGA  CTACG
                                     __  _    AC
GAM1105  LOC220021 3'  GCAAGGGAGGAGCCAGGAGCAA 95023         AC TC    AGA
                                TTGCTCCTG  G  CCTC   TGC
                                |||||||||  |  ||||   |||
                                AACGAGGAC  C  GGAG   ACG
                                     __ GA    GGA
GAM1106  GAS7     3'  GCAAACACATTCTCCACCA   20850    A   T      __
                                TG TGG GAATGTGT  GC
                                || ||| ||||||||  ||
                                AC ACC CTTACACA  CG
                                 C   T       AA
GAM1106  IL1RAP   3'  TCCACACACATACATTACA   57073    A    A     C
                                TG TGGTG ATGTGTG GGA
                                || ||||| ||||||| |||
                                AC ATTAC TACACAC CCT
                                 _    A      A
GAM1106  TRIM14   3'  CGCACCCTCACCCCACCATCA  29511        AA_  T__
                                TGATGGTG   TG   GTGCG
                                ||||||||   ||   |||||
                                ACTACCAC   AC   CACGC
                                     CCC  TCC
GAM1106  DKFZP434P211 3'  TGTCCGTCTCGCTCATCATCA  28033        AT   T_
                                TGATGGTGA  GTG  GCGGACA
                                |||||||||  |||  |||||||
                                ACTACTACT  CGC  TGCCTGT
                                     __   TC
GAM1106  DKFZp761O17121 5'  TGCCACCCACTCACCATCA   51136        A  T   _
                                TGATGGTGA TG GTG CG
                                ||||||||| || ||| ||
                                ACTACCACT AC CAC GT
                                     C  C   C
GAM1106  HGC6.1.1  3'  TGTGTCCGGCCCCAGCCACCA  27617      AA  T_  G
                                TGGTG  TG  GT CGGACACA
                                |||||  ||  || ||||||||
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                                ACCAC  AC  CG GCCTGTGT
                                  CG  CC  _
GAM1106 HSPC031  3' TGTGTGGACTCCACCATCA   32750       AATGT  G  G
                                TGATGGTG    GT CG ACA
                                ||||||||    || || |||
                                ACTACCAC    CA GT TGT
                                    CT___  G  G
GAM1106 KIAA1077 5' TGTGCTGACGGCCACCCACCAT 73295       AA  TG  _  A
           CA                    TGATGGTG  TG  TG CGG CACA
                                ||||||||  ||  || ||| ||||
                                ACTACCAC  AC  GC GTC GTGT
                                    CC  CG  A  _
GAM1106 KIAA1237 3' GTCTCCACCACTCACCATCA  81301       A  T   C
                                TGATGGTGA TG GTG GGAC
                                |||||||||  || ||| ||||
                                ACTACCACT AC CAC TCTG
                                    C  _  C
GAM1106 PELI1    5' GTTTTCACTTTCACCATCA   40653        TGT   CG
                                TGATGGTGAA   GTG  GAC
                                ||||||||||   |||  |||
                                ACTACCACTT   CAC  TTG
                                    T__   TT
GAM1106 TCL6     3' TGTCTATCCATTCAGCATCA  40496      G     TG GC
                                TGATG TGAATG  T  GGACA
                                |||||  ||||||  |  |||||
                                ACTAC ACTTAC  A  TCTGT
                                  G     CT __
GAM1106 ZNF333   3' CCCACCACGGTCTCCATCA   51590      T  A   _  C
                                TGATGG GA TGTG TG GG
                                ||||||  ||  ||||  ||  ||
                                ACTACC CT GCAC AC CC
                                  T  G   C  _
GAM1106 LOC150174 3' GTCCATCTCGCTCATCATCA  80439       AT   TGC_
                                TGATGGTGA  GTG   GGAC
                                |||||||||  |||   ||||
                                ACTACTACT  CGC   CCTG
                                    __  TCTA
GAM1106 LOC150213 3' GTCCATCTCGCTCATCATCA  75358       AT   TGC_
                                TGATGGTGA  GTG   GGAC
                                |||||||||  |||   ||||
                                ACTACTACT  CGC   CCTG
                                    __  TCTA
GAM1106 LOC150236 5' GTCCATCTCGCTCATCATCA  80502       AT   TGC_
                                TGATGGTGA  GTG   GGAC
                                |||||||||  |||   ||||
                                ACTACTACT  CGC   CCTG
                                    __  TCTA
GAM1106 LOC150886 3' TGTGTCCGCCAGATCCCAACAT 86334     G  A_  G  T
           CA                    TGATG TG  AT TG GCGGACACA
                                |||||  ||  ||  ||  |||||||||
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                                ACTAC AC  TA AC CGCCTGTGT
                                   A  CC  G  _
GAM1106  LOC163944 5'  TGCTCTGACACCCACCTCA   88425    T   AAT   G   _
                                TGA GGTG  GTGT CGGA CA
                                ||| ||||  |||| |||| ||
                                ACT CCAC  CACA GTCT GT
                                  _   C__   _   C
GAM1106  LOC166793 5'  TCCGCATGCTTCACCATCA   59919        T
                                TGATGGTGAA GTGTGCGGA
                                |||||||||| |||||||||
                                ACTACCACTT CGTACGCCT
                                        _
GAM1106  LOC199858 5'  GTGGCACCACTCACCATCA   89801        A  T   GGA
                                TGATGGTGA TG GTGC  CAC
                                ||||||||| || ||||  |||
                                ACTACCACT AC CACG  GTG
                                     C  _  ____
GAM1106  LOC220522 3'  GTGTCCGCCACCAGCACCA   61144      AAT  T
                                TGGTG  GTG GCGGACAC
                                |||||  ||| ||||||||
                                ACCAC  CAC CGCCTGTG
                                   GAC  _
GAM1106  LOC222031 3'  TGTCGCCCCCACTCACCACCA  95690    A    A  TGT  G
                                TG TGGTGA TG  GCG ACA
                                || |||||| ||  ||| |||
                                AC ACCACT AC  CGC TGT
                                 C    C  CCC  _
GAM1106  LOC51161  3'  GTGCCCAGCCTCTCCACCGTCA 33044       AATGT  GC  A
                                TGATGGTG    GT  GG CAC
                                ||||||||    ||  || |||
                                ACTGCCAC    CG  CC GTG
                                     CTCTC  A_  C
GAM1107  AKAP13   5'  GACCTGCCCGGGCGGCCGCCTA 23089    AA_  TTTGA  A
                                TAG  GCC    CC GGCAGGTC
                                |||  |||    || ||||||||
                                ATC  CGG    GG CCGTCCAG
                                  CGC  CG___  C
GAM1107  AKAP13   5'  GACCTGCCCGGGCGGCCGCCTA 24219    AA_  TTTGA  A
                                TAG  GCC    CC GGCAGGTC
                                |||  |||    || ||||||||
                                ATC  CGG    GG CCGTCCAG
                                  CGC  CG___  C
GAM1107  B4GALT4  3'  GACCTGCCCAGGTATGCCTTC  15027    CCTTTG  A_
                                GAAG    ACC  GGCAGGTC
                                ||||    |||  ||||||||
                                CTTC    TGG  CCGTCCAG
                                  CGTA__  AC
GAM1107  GPM6A    3'  GTGTGGTCAGAGGCCCCTA   19175    AA       G
                                TAG  GCCTTTGACCA GC
                                |||  |||||||||| ||
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                                ATC  CGGAGACTGGT TG
                                  CC         G
GAM1107  NR5A2    3'  CTGTGAATCAAAGGCTTC    15117          CCAG
                                GAAGCCTTTGA    GCAG
                                ||||||||||    ||||
                                CTTCGGAAACT    TGTC
                                      AAG_
GAM1107  C20orf188 3'  ACCCAGGCAAAGGCTTCTG   32218           A  AGGCA
                                TAGAAGCCTTTG CC    GGT
                                ||||||||||| ||    |||
                                GTCTTCGGAAAC GG    CCA
                                      _  AC___
GAM1107  CDH24    3'  ACCTGCCTGCATGGTT     96600      TT  AC
                                AGCC  TG  CAGGCAGGT
                                ||||  ||  |||||||||
                                TTGG  AC  GTCCGTCCA
                                  T_  __
GAM1107  DCOHM    3'  GACCTGCCTGCCTTGGCCTC   50522    A   TTTGAC
                                GA GCC     CAGGCAGGTC
                                || |||     ||||||||||
                                CT CGG     GTCCGTCCAG
                                 C   TTCC__
GAM1107  FLJ10704  3'  GACCTGCCTGAGAAGCTTC   36980      C   GAC
                                GAAGC TTT   CAGGCAGGTC
                                ||||| |||   ||||||||||
                                CTTCG AAG   GTCCGTCCAG
                                   _   A__
GAM1107  FLJ12287  3'  ACCTGCCTGTCCCAGGACCCTA 42563     AAG   TT   C
                                TAG   CCT  GAC AGGCAGGT
                                |||   |||  ||| ||||||||
                                ATC   GGA  CTG TCCGTCCA
                                  CCA   CC   _
GAM1107  FLJ12443  5'  ACCTGCCTAATTACCTTC    46143     CCTT   CC
                                GAAG    TGA  AGGCAGGT
                                ||||    |||  ||||||||
                                CTTC    ATT  TCCGTCCA
                                  C___   AA
GAM1107  FLJ20203  3'  GGTCTCTGGCCAAGGCTTC    35237        T A    GC  GT
                                GAAGCCTT G CCAG  AG  C
                                |||||||| | ||||  ||  |
                                CTTCGGAA C GGTC  TC  G
                                     _ C    __  TG
GAM1107  FLJ20511  3'  GACCTGCCTGCCTCAGACTTCT 35773       CC    C_
            G                    TAGAAG  TTTGA  CAGGCAGGTC
                                ||||||  |||||  ||||||||||
                                GTCTTC  AGACT  GTCCGTCCAG
                                   __    CC
GAM1107  KIAA0408  3'  ACCTGCCTGACTTCCTGCTCCT 28790     A   CTTTGAC
            G                    TAG AGC      CAGGCAGGT
                                ||| |||      |||||||||
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                                GTC TCG      GTCCGTCCA
                                  C   TCCTTCA
GAM1107  MGC32104  3'  ACCTGTTGTCTCTGCCCAAAGG 59062     A      AC  _____
             CTCCTA                  TAG AGCCTTTG  CAG    GCAGGT
                                ||| ||||||||  |||    ||||||
                                ATC TCGGAAAC  GTC    TGTCCA
                                  C       CC   TCTGT
GAM1107  SYNCOILIN 3'  GACCTGCTTAAAAAGATTCTA  48629      GC    GACC
                                TAGAA  CTTT    AGGCAGGTC
                                |||||  ||||   |||||||||
                                ATCTT  GAAA    TTCGTCCAG
                                   A_    AA__
GAM1107  LOC140095 5'  GACCTGCCCACCCAACTCCTG  76369     A  CCT   ACCA
                                TAG AG   TTG    GGCAGGTC
                                ||| ||   |||    ||||||||
                                GTC TC   AAC    CCGTCCAG
                                  C  ___   CCAC
GAM1107  LOC144699 3'  GACCTGCCTAGCAGTTTC    77436      CTT  ACC
                                GAAGC   TG   AGGCAGGTC
                                |||||   ||   |||||||||
                                CTTTG   AC   TCCGTCCAG
                                   ___  GA_
GAM1107  LOC157653 5'  ATCTGCAGTTAAAGGCT     82440         CAG
                                AGCCTTTGAC   GCAGGT
                                ||||||||||   ||||||
                                TCGGAAATTG   CGTCTA
                                     A__
GAM1107  LOC163911 5'  ACCTGTCACTCAAAGGCCCCT  88419    AA      CCA
                                AG  GCCTTTGA   GGCAGGT
                                ||  ||||||||   |||||||
                                TC  CGGAAACT   CTGTCCA
                                 CC       CA_
GAM1107  LOC93273  3'  ACCTGCCTAACCAGGCACCTG  72379     AA   TTGACC
                                TAG  GCCT     AGGCAGGT
                                |||  ||||     ||||||||
                                GTC  CGGA     TCCGTCCA
                                  CA   CCAA__
GAM1108  CETP      5'  GAGCCTCATGTTCCGT      5373           AAGAC
                                ACGGAGCATGAG    GTTC
                                ||||||||||||    ||||
                                TGCCTTGTACTC    CGAG
                                      _____
GAM1108  GAK       3'  GGAACAGCTGATTCATGCTCC  19141         A_  AC
                                GGAGCATGAG  AG  GTTCC
                                ||||||||||  ||  |||||
                                CCTCGTACTT  TC  CAAGG
                                     AG  GA
GAM1108  PRLR      3'  AGCTCCTTTCATGCTCC     8143           A  C
                                GGAGCATGAGA GA GTT
                                |||||||||||  || |||
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                                CCTCGTACTTT CT CGA
                                      C  _
GAM1108  TIMM23   3'  GGGAGCGCCTCTGCCCCG    60773     A   T   AAGA
                                CGG GCA GAG    CGTTCCC
                                ||| ||| |||    |||||||
                                GCC CGT CTC    GCGAGGG
                                  C   _   C___
GAM1108  TRPV1    3'  GGGAACACCAGTGCTCTGT   38699        GAGAAGAC
                                ACGGAGCAT      GTTCCC
                                |||||||||      ||||||
                                TGTCTCGTG      CAAGGG
                                     ACCA____
GAM1108  TRPV1    3'  GGGAACACCAGTGCTCTGT   55678        GAGAAGAC
                                ACGGAGCAT      GTTCCC
                                |||||||||      ||||||
                                TGTCTCGTG      CAAGGG
                                     ACCA____
GAM1108  TRPV1    3'  GGGAACACCAGTGCTCTGT   55715        GAGAAGAC
                                ACGGAGCAT      GTTCCC
                                |||||||||      ||||||
                                TGTCTCGTG      CAAGGG
                                     ACCA____
GAM1108  TRPV1    3'  GGGAACACCAGTGCTCTGT   55746        GAGAAGAC
                                ACGGAGCAT      GTTCCC
                                |||||||||      ||||||
                                TGTCTCGTG      CAAGGG
                                     ACCA____
GAM1108  UBE2B    3'  GAGTTTCTTCTCATATCC    13936     GC       CG
                                GGA  ATGAGAAGA  TTC
                                |||  |||||||||  |||
                                CCT  TACTCTTCT  GAG
                                  A_        TT
GAM1108  C11orf25 3'  GAGAGGTTCTCATGCTCC    49465          GACG
                                GGAGCATGAGAA    TTC
                                ||||||||||||   |||
                                CCTCGTACTCTT    GAG
                                       GGA_
GAM1108  FLJ14735 3'  GGAGAACGTTTAATACTTC   52668     C  GAGAA      _
                                GGAG AT    GACGTTC CC
                                |||| ||    ||||||| ||
                                CTTC TA    TTGCAAG GG
                                  A  AT___      A
GAM1108  JM11     3'  GGGACATCTCATGCCCC     54365    A      AGAC
                                GG GCATGAGA    GTTCC
                                || ||||||||    |||||
                                CC CGTACTCT    CAGGG
                                 C       A___
GAM1108  KIAA1036 3'  AGCCTGGCTCCTCATGCTCAGT 30483    G       A  AC__
                                AC GAGCATGAG AG    GTT
                                || |||||||| ||    |||
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                                TG CTCGTACTC TC    CGA
                                 A        C  GGTC
GAM1108  KIAA1045  3'  GGGGAACGTCCCCAAGCCCTGT 71606      A  A  AGAA
                                ACGG GC TG    GACGTTCCCC
                                |||| || ||    ||||||||||
                                TGTC CG AC    CTGCAAGGGG
                                  C  A  CC__
GAM1108  KIAA1492  3'  GGAATCGTGTCTTCCATGCTCC 65126         A     ___
                                GGAGCATG GAAGAC   GTTCC
                                |||||||| ||||||   |||||
                                CCTCGTAC CTTCTG   TAAGG
                                     _     TGC
GAM1108  KIAA1674  3'  GAGTTTCCTCTCACCTCCGT   69340       CA    A  CG
                                ACGGAG  TGAGA GA  TTC
                                ||||||  ||||| ||  |||
                                TGCCTC  ACTCT CT  GAG
                                   C_    C  TT
GAM1108  KIAA1674  3'  GAGTTTCCTCTCACCTCCGT   69341       CA    A  CG
                                ACGGAG  TGAGA GA  TTC
                                ||||||  ||||| ||  |||
                                TGCCTC  ACTCT CT  GAG
                                   C_    C  TT
GAM1108  KIAA1674  3'  GAGTTTCCTCTCACCTCCGT   69342       CA    A  CG
                                ACGGAG  TGAGA GA  TTC
                                ||||||  ||||| ||  |||
                                TGCCTC  ACTCT CT  GAG
                                   C_    C  TT
GAM1108  KIAA1751  3'  GGGCCACATTTCACATGCTCC  72163        A   ACGTT
                                GGAGCATG GAAG    CCC
                                |||||||| ||||    |||
                                CCTCGTAC CTTT    GGG
                                     A   ACACC
GAM1108  KIAA1822  3'  GGACTCCTCATACTCTGT    68188       C    AA  C
                                ACGGAG ATGAG  GA GTTC
                                |||||| |||||  || ||||
                                TGTCTC TACTC  CT CAGG
                                   A    __ _
GAM1108  SYT12     5'  GGAACTCTCATGCCC      96384    A      AGAC
                                GG GCATGAGA   GTTCC
                                || ||||||||   |||||
                                CC CGTACTCT   CAAGG
                                 _      _____
GAM1108  LOC115207 3'  GGGAAATAAACCTCGTCATGCT 57398         GA  ACG___
            CC                   GGAGCATGA  AG     TTCCC
                                |||||||||  ||     |||||
                                CCTCGTACT  TC     AAGGG
                                     GC  CAAATA
GAM1108  LOC154789 5'  GAACTCTCACTTCTCATCTCC  82028     C       AC___
                                GGAG ATGAGAAG    GTTC
                                |||| ||||||||    ||||
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                                CCTC TACTCTTC    CAAG
                                  _      ACTCT
GAM1108  LOC170395 5'  GAGTTTCCTCTCACCTCCGT   76870      CA    A  CG
                                ACGGAG  TGAGA GA  TTC
                                ||||||  ||||| ||  |||
                                TGCCTC  ACTCT CT  GAG
                                   C_    C  TT
GAM1108  LOC170395 5'  GAGTTTCCTCTCACCTCCGT   76869      CA    A  CG
                                ACGGAG  TGAGA GA  TTC
                                ||||||  ||||| ||  |||
                                TGCCTC  ACTCT CT  GAG
                                   C_    C  TT
GAM1108  LOC92973  5'  GAAGTTTTATTTCTCATGCT   71592        ____  G
                                AGCATGAGAA    GAC TTC
                                ||||||||||    ||| |||
                                TCGTACTCTT    TTG AAG
                                      TATT  _
GAM1109  SCAMP1    3'  GCTAAATAAATATTCTCC    54500    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1109  SCAMP1    3'  GCTAAATAAATATTCTCC    54501    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1109  NX-17     3'  TGAATATCAGCCCCTAATA   40706       ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                     CGAC
GAM1109  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
            TA                   TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM1110  CENPB     3'  AGAGTGCAGAGCCCCAGATC   70110    C   T  TTG
                                GA CTGG GT   TCTGCACTCT
                                || |||| ||   ||||||||||
                                CT GACC CG   AGACGTGAGA
                                 A   C  ___
GAM1110  ITPR1     5'  GAGTGCCTGACCCAGGTCA   11073       T   TGTCT
                                TGACCTGG GTT    GCACTC
                                |||||||| |||    ||||||
                                ACTGGACC CAG    CGTGAG
                                     _  TC___
GAM1110  PRM2      3'  AGTCGCCCGAAACACCAAGT   12395    C      GTCT  _
                                AC TGGTGTTT    GC ACT
                                || ||||||||    || |||
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                                TG ACCACAAA    CG TGA
                                 A       GCC_  C
GAM1110  RAB5B    3'  GCAACAAACACCAGGCA     12709    A          C
                                TG CCTGGTGTTTGT TGC
                                || |||||||||||| |||
                                AC GGACCACAAACA ACG
                                 _          _
GAM1110  RFC1     5'  AGAGTGCAAACATTAAGCAAG  12826    G  GTT_   C
                                CT GT    TGT TGCACTCT
                                || ||    ||| ||||||||
                                GA CG    ACA ACGTGAGA
                                 A  AATT   A
GAM1110  SLC7A6   3'  AGAATAAACACCAAGGCA     15636    A  _        _
                                TG CCT GGTGTTTGT CT
                                || ||| ||||||||| ||
                                AC GGA CCACAAATA GA
                                 _  A        A
GAM1110  FLJ11850 3'  TAGACAAACACAAGGTCA     43023       G
                                TGACCT GTGTTTGTCTG
                                |||||| ||||||||||
                                ACTGGA CACAAACAGAT
                                   A
GAM1110  KIAA0712 3'  AGAGTCATCATAAAACACCAG  28865         GTC__  C
                                CTGGTGTTT     TG ACTCT
                                |||||||||     || |||||
                                GACCACAAA     AC TGAGA
                                      ATACT  _
GAM1110  MKP-7    3'  GAGTGCAAAGCCATGGCCA    67012    A  _   GTTTGTC
                                TG CC TGGT      TGCACTC
                                || || ||||      |||||||
                                AC GG ACCG      ACGTGAG
                                 C  T    AA_____
GAM1110  PP1628   5'  AGAGTGCAGAACCGTCCCAGGC 48070    A     TG TTG
            A                    TG CCTGG  T   TCTGCACTCT
                                || |||||  |   ||||||||||
                                AC GGACC  G   AGACGTGAGA
                                 _    CT CCA
GAM1110  RAB3IL1  3'  AGAACACAGACAGGGCTTCAG  26363      T  _     CAC
                                CTGG GTT TGTCTG   TCT
                                |||| ||| ||||||   |||
                                GACT CGG ACAGAC   AGA
                                  T  G     ACA
GAM1110  LOC150418 3' GCCAACAAGCACCAGATCA    66114     C         CT
                                TGA CTGGTGTTTGT  GC
                                ||| ||||||||||  ||
                                ACT GACCACGAACA  CG
                                  A          AC
GAM1110  LOC199957 3' GCCAACAAGCACCAGATCA    89888     C         CT
                                TGA CTGGTGTTTGT  GC
                                ||| ||||||||||  ||
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                                ACT GACCACGAACA  CG
                                  A         AC
GAM1110  LOC206463 3'  GCCAACAAGCACCAGATCA   91102     C        CT
                                TGA CTGGTGTTTGT  GC
                                ||| ||||||||||  ||
                                ACT GACCACGAACA  CG
                                  A         AC
GAM1110  LOC255368 5'  AGAATGACCAGAACGCCAGGCC 99352    A        GTCTG  C
              A                  TG CCTGGTGTTT    CA TCT
                                || ||||||||||    || |||
                                AC GGACCGCAAG    GT AGA
                                 C        ACCA_  A
GAM1110  LOC56270  3'  AGAATGAGGCAGACACCAGGCC 39501    A          G  C
              A                  TG CCTGGTGTTTGTCT CA TCT
                                || ||||||||||||| || |||
                                AC GGACCACAGACGGA GT AGA
                                 C           _  A
GAM1110  LOC92181  3'  AGTACAGACAAGAAGGCA    68941    A  GGTGT     C
                                TG CCT    TTGTCTG ACT
                                || |||    ||||||| |||
                                AC GGA    AACAGAC TGA
                                 _  AG___      A
GAM1111  COL13A1   5'  GCACCAACTGCTCTGCAGACA  19042    G      G TGAA
                                TGT CTGCAGAG C   GGTGC
                                ||| |||||||| |   |||||
                                ACA GACGTCTC G   CCACG
                                  _      _ TCAA
GAM1111  COL13A1   5'  GCACCAACTGCTCTGCAGACA  55851    G      G TGAA
                                TGT CTGCAGAG C   GGTGC
                                ||| |||||||| |   |||||
                                ACA GACGTCTC G   CCACG
                                  _      _ TCAA
GAM1111  COL13A1   5'  GCACCAACTGCTCTGCAGACA  55853    G      G TGAA
                                TGT CTGCAGAG C   GGTGC
                                ||| |||||||| |   |||||
                                ACA GACGTCTC G   CCACG
                                  _      _ TCAA
GAM1111  COL13A1   5'  GCACCAACTGCTCTGCAGACA  55854    G      G TGAA
                                TGT CTGCAGAG C   GGTGC
                                ||| |||||||| |   |||||
                                ACA GACGTCTC G   CCACG
                                  _      _ TCAA
GAM1111  COL13A1   5'  GCACCAACTGCTCTGCAGACA  55855    G      G TGAA
                                TGT CTGCAGAG C   GGTGC
                                ||| |||||||| |   |||||
                                ACA GACGTCTC G   CCACG
                                  _      _ TCAA
GAM1111  COL13A1   5'  GCACCAACTGCTCTGCAGACA  55856    G      G TGAA
                                TGT CTGCAGAG C   GGTGC
                                ||| |||||||| |   |||||
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                                ACA GACGTCTC G    CCACG
                                  _       _ TCAA
GAM1111  COL13A1   5'  GCACCAACTGCTCTGCAGACA  55857     G       G TGAA
                                TGT CTGCAGAG C    GGTGC
                                ||| |||||||| |    |||||
                                ACA GACGTCTC G    CCACG
                                  _       _ TCAA
GAM1111  HSD11B2   3'  GCCCAGCCACTGCAGCACA   5770          A     AA
                                TGTGCTGCAG GGCTG  GGT
                                |||||||||| |||||  |||
                                ACACGACGTC CCGAC  CCG
                                      A    __
GAM1111  KCNK4     3'  GCGTCTCCAGCCTCTGCACACA 33987     C         A  GT
                                TGTG TGCAGAGGCTG AG  GC
                                |||| |||||||||| ||  ||
                                ACAC ACGTCTCCGAC TC  CG
                                  _         C  TG
GAM1111  OVOL1     3'  GCAAAGGGTACCCCTGCAAACA 17069     GC    A  C  AAGG_
                                TGT  TGCAG GG TG    TGC
                                |||  ||||| || ||    |||
                                ACA  ACGTC CC AT    ACG
                                  A_    _ C  GGGAA
GAM1111  PRY       3'  CACCCTGTCTGCAGCAC     60891          _ CTGAA
                                GTGCTGCAGA GG    GGTG
                                |||||||||| ||    ||||
                                CACGACGTCT TC    CCAC
                                      G _____
GAM1111  TEAD3     3'  CACCTTCAGCCTCCAGCAT   13666       CA
                                GTGCTG  GAGGCTGAAGGTG
                                ||||||  ||||||||||||
                                TACGAC  CTCCGACTTCCAC
                                   __
GAM1111  DKFZP564D0462 3'  CACCTTCAGCCACAGCACA   71018        CAGA
                                TGTGCTG   GGCTGAAGGTG
                                |||||||   ||||||||||
                                ACACGAC   CCGACTTCCAC
                                    A___
GAM1111  FLJ11850  3'  GCACCTCATTGATCTGCAGCA  43022         GGC_  A
                                TGCTGCAGA   TGA GGTGC
                                |||||||||   ||| |||||
                                ACGACGTCT   ACT CCACG
                                     AGTT  _
GAM1111  FLJ13710  3'  CACCTTCAAGTCAGCAG     46097      AGA   _
                                CTGC   GGCT GAAGGTG
                                ||||   |||| |||||||
                                GACG   CTGA CTTCCAC
                                  A__    A
GAM1111  HS6ST     3'  GCAAGCGCCTTCTGCAGCACA  62730          _  T AAGG
                                TGTGCTGCAGA GGC G    TGC
                                |||||||||| ||| |    |||
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                                ACACGACGTCT CCG C   ACG
                                      T  _ GA__
GAM1111 KIAA0255 3' CACCCTCAGTGCCAGCCA   29129   T  CAGAG   A
                                TG GCTG    GCTGA GGTG
                                || ||||    ||||| ||||
                                AC CGAC    TGACT CCAC
                                 _   CG___    C
GAM1111 MGC10540 3' CACATGCGCCTGCAGCACA  51358        AG  TGAAG
                                TGTGCTGCAG  GC    GTG
                                ||||||||||  ||    |||
                                ACACGACGTC  CG    CAC
                                      CG  TA___
GAM1111 MGC16202 3' ACCAAAGCCACTGCAGCACA  51411        A   GAA
                                TGTGCTGCAG GGCT   GGT
                                |||||||||| ||||   |||
                                ACACGACGTC CCGA   CCA
                                      A   AA_
GAM1111 MGC26768 3' CATGGCCCCTGCAGCAC    58910        A   GAAG
                                GTGCTGCAG GGCT   GTG
                                ||||||||| ||||   |||
                                CACGACGTC CCGG   TAC
                                     C   _____
GAM1111 PRO2325  3' GCCATGAGCCTCTGAGCACA  98039      G      GAA
                                TGTGCT CAGAGGCT   GGT
                                |||||| ||||||||   |||
                                ACACGA GTCTCCGA   CCG
                                   _      GTA
GAM1111 RAB40A   5' CACCACCTCTGCGCACA    56015      T     CTGAA
                                TGTGC GCAGAGG    GGTG
                                ||||| |||||||    ||||
                                ACACG CGTCTCC    CCAC
                                   _     A_____
GAM1111 RNF29    5' GCACCCTTCCCTGGCAGCACA 53515       AG   CT   _
                                TGTGCTGC  AGG  GAAGG TGC
                                ||||||||  |||  ||||| |||
                                ACACGACG  TCC  CTTCC ACG
                                     G_  __    C
GAM1111 TBPL1    3' GCACCTTTTAAACCTGCTGCAC 18011     T   AGGCT
           A                     TGTGC GCAG    GAAGGTGC
                                 ||||| ||||    ||||||||
                                 ACACG CGTC    TTTCCACG
                                    T   CAAAT
GAM1111 TIGD5    5' CACCTTCAAGGCCAGCCA    52766   T  GCAGA   __
                                TG GCT    GGCT  GAAGGTG
                                || |||    ||||  |||||||
                                AC CGA    CCGG  CTTCCAC
                                 _  ______   AA
GAM1111 ZNF282   3' CACCTTCATGATGACAACAC  90693    C  _  GAGGC
                                GTG TG CA    TGAAGGTG
                                ||| || ||    ||||||||
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                                CAC AC GT     ACTTCCAC
                                  A  A  AGT__
GAM1111  LOC115051 3'  GCAAGCGCCTTCTGCAGCACA  60678          _   T AAGG
                                TGTGCTGCAGA GGC G    TGC
                                |||||||||||| ||| |    |||
                                ACACGACGTCT CCG C    ACG
                                       T   _ GA__
GAM1111  LOC132235 5'  CACCCTCAGCCTTCAC      76662     CTGCA       A
                                GTG     GAGGCTGA GGTG
                                |||     |||||||| ||||
                                CAC     TTCCGACT CCAC
                                  ______       C
GAM1111  LOC135763 3'  CACCTCTGTCCTGCAGCA     57556         A   T  A
                                TGCTGCAG GGC GA GGTG
                                |||||||| ||| || ||||
                                ACGACGTC CTG CT CCAC
                                     _   T  _
GAM1111  LOC146108 5'  CACCCCCTCTGCAGCCA      78147    T        CTGAA
                                TG GCTGCAGAGG     GGTG
                                || ||||||||||     ||||
                                AC CGACGTCTCC     CCAC
                                  _         C____
GAM1111  LOC149372 5'  CACCTCTCCTGTCTTCAGCACA 80101        CA     T_  _
                                TGTGCTG  GAGGC  GA AGGTG
                                |||||||  |||||  || |||||
                                ACACGAC  TTCTG  CT TCCAC
                                    __     TC  C
GAM1111  LOC149684 5'  GCACCTTCAGCCATCAGCA    85765      CAGA
                                TGCTG    GGCTGAAGGTGC
                                |||||    ||||||||||||
                                ACGAC    CCGACTTCCACG
                                   TA__
GAM1111  LOC157285 5'  GCACCCCAAACCTGCAGCA    87728         AGGC  AA
                                TGCTGCAG    TG  GGTGC
                                ||||||||    ||  |||||
                                ACGACGTC    AC  CCACG
                                     CAA_  C_
GAM1111  LOC159160 3'  CACCCTGTCTGCAGCAC      61152          _  CTGAA
                                GTGCTGCAGA GG     GGTG
                                |||||||||| ||     ||||
                                CACGACGTCT TC     CCAC
                                     G  ______
GAM1111  LOC196047 3'  ACCTGAATAGCCTCTGCAGAAC 91139      G          A__
            A                    TGT CTGCAGAGGCTG   AGGT
                                ||| ||||||||||||   ||||
                                ACA GACGTCTCCGAT   TCCA
                                  A          AAG
GAM1112  CDH12    3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT     GAA  ATAAG
                                |||||||||     |||  |||||
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                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM1112  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA       G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM1112  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090      T   AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                   _   GTCA_
GAM1112  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
           A                     TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM1112  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126        CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM1112  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
           TA                   TACA   TCC   GAAGAATAAG
                                ||||   |||   ||||||||||
                                ATGT   AGG   TTTCTTATTC
                                  AAA_   ATTG
GAM1112  KIAA1579  3'  TACTCTTAGTGGTGTA     37154        CCCAAG   A
                                TACACCACT     AAGA TA
                                |||||||||     |||| ||
                                ATGTGGTGA     TTCT AT
                                     _______   C
GAM1112  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA  68742            _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                          G
GAM1112  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929    CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM1112  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748     CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM1112  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571    CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
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                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM1112 OSBPL11  3' CTTAATTTCCCAAGAGTGGTG 43206       CCAA   AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                    AACC   A_
GAM1112 YME1L1   3' TCATTCTTGATGTGGTGTA   27323       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                    TA_    A
GAM1112 YME1L1   3' TCATTCTTGATGTGGTGTA   58438       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                    TA_    A
GAM1112 ZNF262   3' CTTATTTTGTTTGGGAGT    18723        A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                     G
GAM1112 LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_    AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
                                ATGTGGTG   GGTTC   TGT
                                    CAA    GG__
GAM1113 SCAMP1   3' GCTAAATAAATATTCTCC    18013    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C    A
GAM1113 SCAMP1   3' GCTAAATAAATATTCTCC    54501    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C    A
GAM1113 NX-17    3' TGAATATCAGCCCCTAATA   40706       ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM1113 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
            TA                   TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM1114 MYO1D    3' CAGCCCATCCAGCAGAGTGAGT 72241    G_ _      CGA
            CC                   GGA  CG TCTGCTGGA   GCTG
                                |||  || |||||||||   ||||
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                                CCT  GT AGACGACCT   CGAC
                                  GA  G       ACC
GAM1114  PKIG     3'  CAGCCCACACAGGAACGCTCCT 23925       CTG   GACGA
                                AGGAGCGT   CTG    GCTG
                                ||||||||   |||    ||||
                                TCCTCGCA   GAC    CGAC
                                    AG_   ACACC
GAM1114  C9orf12   5'  AGCTGACAGGCGCTCCT     43103          CTGGACG
                                AGGAGCGTCTG      AGCT
                                ||||||||||      ||||
                                TCCTCGCGGAC      TCGA
                                     AG_____
GAM1114  DKFZp434N035 3'  AGCCCGCTAGGCGCTCC     51058          C   ACGA
                                GGAGCGTCTG TGG    GCT
                                |||||||||| |||    |||
                                CCTCGCGGAT GCC    CGA
                                     C  _____
GAM1114  KIAA1169  5'  CAGCACAGAGAGACGCTCC    35876        G_   GACGA
                                GGAGCGTCT  CTG    GCTG
                                |||||||||  |||    ||||
                                CCTCGCAGA  GAC    CGAC
                                     GA   A_____
GAM1114  KIAA1600  5'  CAGCTCGTCCTCCCCGCCCC   71940    A   TCTGCT
                                GG GCG     GGACGAGCTG
                                || |||     ||||||||||
                                CC CGC     CCTGCTCGAC
                                 C   CCCT__
GAM1114  LOC157740 3'  CAGCTCATCCAACACTTGTCC  82466     G  TC  C    C
                                GGA CG  TG TGGA GAGCTG
                                ||| ||  || |||| ||||||
                                CCT GT  AC ACCT CTCGAC
                                  _  TC  A    A
GAM1114  LOC200734 3'  CAGCTCGTCCACAAGCTC    90272      GTC  C
                                GAGC   TG TGGACGAGCTG
                                ||||   || ||||||||||
                                CTCG   AC ACCTGCTCGAC
                                  A__  _
GAM1114  LOC205418 5'  CAGCCCCCTGCAGCGCTCCT   92367        T    T  ACGA
                                AGGAGCG CTGC GG    GCTG
                                ||||||| |||| ||    ||||
                                TCCTCGC GACG CC    CGAC
                                   _    T  CC__
GAM1114  LOC221061 3'  CAGTGACAACAGACAGTCCCT  94840     AG _    C  GACGA
                                AGG  C GTCTG TG    GCTG
                                |||  | ||||| ||    ||||
                                TCC  G CAGAC AC    TGAC
                                  CT A     A  AG___
GAM1114  LOC222330 5'  TCTGAGCAGACGCTGCCT    95972     _        _
                                AGG AGCGTCTGCT GGA
                                ||| |||||||||| |||
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                                TCC TCGCAGACGA TCT
                                  G        G
GAM1115 KIAA0945 5' CCCACCCCACTGACCCCGCGA 30900     AGA   TCT  TT
                                TCGC   GTCA   GT  GGTGGG
                                ||||   ||||   ||  ||||||
                                AGCG   CAGT   CA  CCACCC
                                  CCC    ___  CC
GAM1115 KIAA1691 3' CCGCCAAACGCCCTGCGA    94128       A  CATCT
                                TCGCAG GT    GTTTGGTGG
                                |||||| ||    |||||||||
                                AGCGTC CG    CAAACCGCC
                                   C  _____
GAM1115 MBLL39   3' CCCACCAAACAAAGTCTTGA  59258     C   GTCATC
                                TCG AGA     TGTTTGGTGGG
                                ||| |||     ||||||||||
                                AGT TCT     ACAAACCACCC
                                  _  GAA___
GAM1115 LOC147077 3' CCACCAAGGGCCCTGCGA    78844       A   ATCTG
                                TCGCAG GTC    TTTGGTGG
                                |||||| |||    ||||||||
                                AGCGTC CGG    GAACCACC
                                   C  _____
GAM1116 CD4     3' ACTGACCCTGTGCAGAACCTC  7042           TG    C
                                GAGGTTTTGTAT  AGGG CAGT
                                ||||||||||||  |||| ||||
                                CTCCAAGACGTG  TCCC GTCA
                                      __    A
GAM1116 GLRX    3' ACTGACCCTCAATTGTCCTCT  10802      TTTTGT      C
                                AGAGG     ATTGAGGG CAGT
                                |||||     |||||||| ||||
                                TCTCC     TAACTCCC GTCA
                                   TGT___       A
GAM1116 GPR4    5' ACTGACTCCATACATAACCTC  60572       T    T A   C
                                GAGGTT TGTAT G GGG CAGT
                                |||||| ||||| | ||| ||||
                                CTCCAA ACATA C CTC GTCA
                                   T    _ _   A
GAM1116 RAB3A   3' ACCAGCCACGGGCACAAGACCC 12696    A      A_   AG   CA
            CT                   AG GGTTTTGT  TTG  GGC  GT
                                || ||||||||  |||  |||  ||
                                TC CCAGAACA  GGC  CCG  CA
                                 C       CG   A_   AC
GAM1116 TCF8    3' ACTGATTCCAACACAAAACCCC 48425    A      A   A  GC
            T                    AG GGTTTTGT TTG GG  CAGT
                                || ||||||||  ||| ||  ||||
                                TC CCAAAACA AAC CT  GTCA
                                 C       C   _  TA
GAM1116 APCL    3' ACTGGCCCCCAACATGACC   20810     T   AT  A
                                GGTT TGT  TG GGGCCAGT
                                ||||  |||  ||  ||||||||
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                                CCAG ACA  AC CCCGGTCA
                                  T   __  C
GAM1116  DKFZP434N1511 3'  ACTGGCCCCCAAGGTCAGCTCC 93048    TT   TA_  A
                                GG  TTG   TTG GGGCCAGT
                                ||  |||   ||| ||||||||
                                CC  GAC   AAC CCCGGTCA
                                 TC   TGG   C
GAM1116  DKFZP586H2123 3'  CCATATACAAAACCTCT     62611           TGA
                                AGAGGTTTTGTAT   GG
                                ||||||||||||   ||
                                TCTCCAAAACATA   CC
                                       TA_
GAM1116  FLJ12876  3'  ACTGGGAAAATACAAAAGCTCT 43083      G       GAGGG
                                AGAG TTTTGTATT    CCAGT
                                |||| |||||||||    |||||
                                TCTC AAAACATAA    GGTCA
                                  G       AAG__
GAM1116  FPGT     3'  CTAGATACAAAGACCTCT    15180         _    G
                                AGAGGTTTT GTATT AG
                                ||||||||| ||||| ||
                                TCTCCAGAA CATAG TC
                                     A    A
GAM1116  KIAA0280  3'  ACTGGCCCCAGGATGCAAACCC 93286    A  T      GA_
            CT                   AG GG TTTGTATT   GGGCCAGT
                                || || ||||||||   ||||||||
                                TC CC AAACGTAG   CCCGGTCA
                                 _ C       GAC
GAM1116  THEA     3'  ACTGGCCATAAGCAAAACCTCT 66865          ATTGAG
                                AGAGGTTTTGT     GGCCAGT
                                ||||||||||     |||||||
                                TCTCCAAAACG     CCGGTCA
                                      AATA__
GAM1116  LOC122830 3'  ACTAACATTTCACACAAAACCT 74627         AT    GCC_
                                AGGTTTTGT  TGAGG    AGT
                                |||||||||  |||||    |||
                                TCCAAAACA  ACTTT    TCA
                                     C_    ACAA
GAM1116  LOC253815 3'  CAGCCCTCAGAACCCTC     97342      TTTT  A      CA
                                GAGG    GT TTGAGGGC  G
                                ||||    || ||||||||  |
                                CTCC    CA GACTCCCG  C
                                  _____  A       AC
GAM1116  LOC257457 3'  TCCTCCAACACAAAACCCT    63316    A      A  _
                                AG GGTTTTGT TTG AGGG
                                || |||||||| ||| ||||
                                TC CCAAAACA AAC TCCT
                                 _       C   C
GAM1116  LOC91266  5'  ACTGGCCCCCAATTCCACTCT  66018     GTTTTGT    A
                                AGAG      ATTG GGGCCAGT
                                ||||      |||| ||||||||
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                                TCTC      TAAC CCCGGTCA
                                  ACCT___   C
GAM1116 LOC92344 3' CCTCCAATAAAAACCTCT    69575        G    AG
                                AGAGGTTTT TATTG  GG
                                ||||||||| |||||  ||
                                TCTCCAAAA ATAAC  CC
                                     _    CT
GAM1117 APLP1    3' CAGCAGGGAGTCTTGAA     18967       G  AAGAA
                                TTCAAGA CT    CCTGCTG
                                ||||||| ||    |||||||
                                AAGTTCT GA    GGACGAC
                                    _ G____
GAM1117 B4GALT5  3' AGCAGGTTCCTGCCCTTGAA  17681       A  TAA
                                TTCAAG GC   GAACCTGCT
                                |||||| ||   |||||||||
                                AAGTTC CG   CTTGGACGA
                                   C  TC_
GAM1117 DDX3     3' GCAGCAGGCTTTATTTT     9057      GCT   AA
                                AAGA   AAG  CCTGCTGC
                                ||||   |||  ||||||||
                                TTTT   TTC  GGACGACG
                                  AT_  __
GAM1117 FANCA    3' GCAAAGGCTTGGCTCCCGAA  5542      AA      AA   GC
                                TTC  GAGCTAAG  CCT  TGC
                                |||  ||||||||  |||  |||
                                AAG  CTCGGTTC  GGA  ACG
                                 CC       __   A_
GAM1117 LDHB     3' GCAATCTGAGCTCTTGAA    11289         A   ACC
                                TTCAAGAGCT AGA   TGC
                                |||||||||| |||   |||
                                AAGTTCTCGA TCT   ACG
                                     G   A__
GAM1117 PPP1R12B 5' CAGCAGGTCCTATCTGA     50345     A  GCTA  A
                                TCA GA    AG ACCTGCTG
                                ||| ||    || ||||||||
                                AGT CT    TC TGGACGAC
                                  _ A___  C
GAM1117 PPP1R12B 5' CAGCAGGTCCTATCTGA     50369     A  GCTA  A
                                TCA GA    AG ACCTGCTG
                                ||| ||    || ||||||||
                                AGT CT    TC TGGACGAC
                                  _ A___  C
GAM1117 TGFBR2   3' GCAGCAGGAAGCTGCCCCTGAA 13732     AGA  TA  AA_
                                TTCA   GC  AG   CCTGCTGC
                                ||||   ||  ||   ||||||||
                                AAGT   CG  TC   GGACGACG
                                  CCC  __  GAA
GAM1117 AHCYL1   3' GCCCATTTCTTAGCTGCTGAA 22775     AG       CCT_
                                TTCA  AGCTAAGAA   GC
                                ||||  |||||||||   ||
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                                AAGT  TCGATTCTT   CG
                                  CG       TACC
GAM1117 C7orf11  3' GCAACATTTAGCTCTGGAA   57735    A      AACC
                                TTC AGAGCTAAG   TGC
                                ||| |||||||||   |||
                                AAG TCTCGATTT   ACG
                                  G       ACA_
GAM1117 CIDEB    5' CAGCAGGCAGCTCTGGAA    27795    A    AAGAA
                                TTC AGAGCT    CCTGCTG
                                ||| ||||||    |||||||
                                AAG TCTCGA    GGACGAC
                                  G     C____
GAM1117 FLJ22625 5' GCAACGTCTGGCGCTTAGCTC 45585       AA  T_ __
                                GAGCTAAG  CC  GC  TGC
                                ||||||||  ||  ||  |||
                                CTCGATTC  GG  TG  ACG
                                     GC  TC  CA
GAM1117 KIAA0247 3' GCAGCAGGTGGCAGGCTGTT  29071    G   AAGA
                                AA AGCT    ACCTGCTGC
                                || ||||    |||||||||
                                TT TCGG    TGGACGACG
                                 G   ACGG
GAM1117 KIAA0779 5' GCAGCAGGCGCTGTAGTCTC  86909    _  _ AA
                                GAG CTA AG  CCTGCTGC
                                ||| ||| ||  ||||||||
                                CTC GAT TC  GGACGACG
                                  T   G  GC
GAM1117 KIAA1155 3' GCAGGGCTGCTCAGCTCTTGAG 62913        A  AA__
                                TTCAAGAGCT AG    CCTGC
                                |||||||||| ||    |||||
                                GAGTTCTCGA TC    GGACG
                                      C  GTCG
GAM1117 KIAA1768 5' CAGCAGGACGACTCTTGAA   88895       CTAAGAA
                                TTCAAGAG      CCTGCTG
                                ||||||||      |||||||
                                AAGTTCTC      GGACGAC
                                     AGCA___
GAM1117 MGC12760 3' GCAGCAGGCCTTGTCTCTGAA 52160     A   C   AA
                                TTCA GAG TAAG  CCTGCTGC
                                |||| ||| ||||  ||||||||
                                AAGT CTC GTTC  GGACGACG
                                  _   T   C_
GAM1117 MGC4643  3' GCGCTCTTAGCTCCTGA    52142    A      ACC
                                TCA GAGCTAAGA   TGC
                                ||| |||||||||   |||
                                AGT CTCGATTCT   GCG
                                  C       C__
GAM1117 YAP      5' GCAGCATGTTCAGCTCTTGA   58205       AA   C
                                TCAAGAGCT  GAAC TGCTGC
                                |||||||||  |||| ||||||
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                                AGTTCTCGA  CTTG ACGACG
                                     __    T
GAM1117  ZMPSTE24  3'  GCAGCATGTTCCAGCTCTTGA  20730        AA    C
                                TCAAGAGCT  GAAC TGCTGC
                                |||||||||  |||| ||||||
                                AGTTCTCGA  CTTG ACGACG
                                     C_    T
GAM1117  LOC128077 3'  GCAGCTTTGTTAGCTCTT    75218        G  CCT
                                AAGAGCTAA AA   GCTGC
                                |||||||||  ||   |||||
                                TTCTCGATT TT   CGACG
                                     G  T__
GAM1117  LOC130497 3'  GCAGCCCCCTCCCAGCTCTTG  75450        AA  ACCT
                                CAAGAGCT  GA    GCTGC
                                ||||||||  ||    |||||
                                GTTCTCGA  CT    CGACG
                                     CC  CCCC
GAM1117  LOC145333 5'  GCAACAGGTTCTCCAACTTT   84297      CTA_       C
                                AGAG    AGAACCTG TGC
                                ||||    |||||||| |||
                                TTTC    TCTTGGAC ACG
                                  AACC       A
GAM1117  LOC145623 3'  CAGCAACAGCTCTTGAA     84389          AAGAACC
                                TTCAAGAGCT      TGCTG
                                ||||||||||      |||||
                                AAGTTCTCGA      ACGAC
                                     CA_____
GAM1117  LOC149579 3'  GCAGCAGGCCTTGTCTCTGAA  71692      A  C   AA
                                TTCA GAG TAAG  CCTGCTGC
                                |||| ||| ||||  ||||||||
                                AAGT CTC GTTC  GGACGACG
                                  _  T   C_
GAM1117  LOC57795  5'  CAGCAAGGAGGGCTCTTG    69864        AAGAA  _
                                CAAGAGCT    CCT GCTG
                                ||||||||    ||| ||||
                                GTTCTCGG    GGA CGAC
                                     GA___   A
GAM1117  LOC90190  3'  GCAACAAGTTGGCTCTTGAG   62426          GAACC
                                TTCAAGAGCTAA    TGC
                                ||||||||||||    |||
                                GAGTTCTCGGTT    ACG
                                      GAACA
GAM1117  LOC90639  3'  GCTTCCCAGCTCTTGAG     64411         AA   CCT
                                TTCAAGAGCT  GAA   GC
                                ||||||||||  |||   ||
                                GAGTTCTCGA  CTT   CG
                                     CC   ___
GAM1117  LOC92181  5'  CAGCACCAGCTTTTGAA     68943         AAGAACC
                                TTCAAGAGCT      TGCTG
                                ||||||||||      |||||
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                                AAGTTTTCGA      ACGAC
                                     CC_____
GAM1118 A1BG    3' TCCCACAGCAGAGCTGGACGC 56298    A  CCT      CA
                                GC TCC   TTCTGCTG  GGA
                                || |||   ||||||||  |||
                                CG AGG   GAGACGAC  CCT
                                 C  TC_       AC
GAM1118 ARHGEF6 3' AGAGAAAGGGAATGCAG    68751      C      G
                                CTGCAT CCCTTTCT CT
                                |||||| |||||||| ||
                                GACGTA GGGAAAGA GA
                                   A       _
GAM1118 B4GALT7 3' CCCCACAGAGGGGGAACAG   24377    CA     T   C  CA
                                CTG  TCCCCTT CTG TG  GG
                                |||  ||||||| ||| ||  ||
                                GAC  AGGGGGA GAC AC  CC
                                  A_      _  _ C_
GAM1118 BPAG1   3' TCCCACAGCCTTCAAGCTGCAG 9949      TCCC   TCT_   CA
                                CTGCA    CTT    GCTG  GGA
                                ||||||   |||   ||||  |||
                                GACGT    GAA    CGAC  CCT
                                   C___   CTTC    AC
GAM1118 CASP10  3' TCCTGCAGAAGCAGAAGTGCA  53226     CCCCT     ___
                                TGCAT    TTCTGCT   GCAGGA
                                |||||    |||||||  ||||||
                                ACGTG    AAGACGA   CGTCCT
                                   _____      AGA
GAM1118 CHD4    3' TCCTGCAGAAGAGACATGCAG  8877       CCCC    G
                                CTGCAT    TTTCT CTGCAGGA
                                ||||||   ||||| ||||||||
                                GACGTA    AGAGA GACGTCCT
                                   C___     A
GAM1118 CNTN2   3' TCCTGCCTGGGAGGGGAATGCA 18664      _    TT TGCT
            G                    CTGCAT CCCCT  C    GCAGGA
                                ||||||| |||||  |   ||||||
                                GACGTA GGGGA  G    CGTCCT
                                   A    GG TC__
GAM1118 DHFR    3' TCTAGGGCAGAAAGAAGTACAG 7659     C  CCC       GC
                                CTG AT   CTTTCTGCT  AGG
                                ||| ||   |||||||||  |||
                                GAC TG   GAAAGACGG  TCT
                                  A  AA_       GA
GAM1118 E48     3' CCCACAGAGGATGCAG     14913        CCTT    C  CA
                                CTGCATCC    TCTG TG  G
                                ||||||||    |||| ||  |
                                GACGTAGG    AGAC AC  C
                                     _____   _ C_
GAM1118 HTR4    3' CCTGCAGCTCCCCCAAGGTGCA 7880        CCCTTTCT
            G                    CTGCATC       GCTGCAGG
                                |||||||       ||||||||
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                                GACGTGG       CGACGTCC
                                    AACCCCCT
GAM1118 IL1B     3'  TGGCAGAAAGGGAACAG     6956      CATC
                                CTG    CCCTTTCTGCTG
                                |||    ||||||||||||
                                GAC    GGGAAAGACGGT
                                  AA__
GAM1118 LEF1     5'  TCCCACAGCGGAGCGGAGATTA 33226     C_   C  T       CA
             CAG                    CTG  ATC CC TTCTGCTG  GGA
                                |||  ||| || ||||||||  |||
                                GAC  TAG GG GAGGCGAC  CCT
                                  AT   A  C       AC
GAM1118 NPTX1    3'  CCCGCAGAGGGGGTGCAG    11832          TTCTG    A
                                CTGCATCCCCT    CTGC GG
                                ||||||||||     |||| ||
                                GACGTGGGGGA    GACG CC
                                      _____    C
GAM1118 PLA2G4C  5'  TCCCACAGGGGGAAAAGGAAAG 73809      A_   CC     G   CA
             CAG                    CTGC  TCC  TTTCT CTG  GGA
                                ||||  |||  ||||| |||  |||
                                GACG  AGG  AAGGG GAC  CCT
                                  AA   AA    G   AC
GAM1118 PRLR     5'  TCCTGCAGCAAGAGAAGGCAG  8145       ATCCC    C
                                CTGC    CTTT TGCTGCAGGA
                                ||||    |||| ||||||||||
                                GACG    GAGA ACGACGTCCT
                                  GAA__   _
GAM1118 SMT3H1   3'  CCCGCAGTGGGGATGCAG    60629          TTTCT    A
                                CTGCATCCCC    GCTGC GG
                                ||||||||||    ||||| ||
                                GACGTAGGGG    TGACG CC
                                      _____    C
GAM1118 SURF5    3'  CCTGCAGCAGAGCAGGGCGCA  23125     ATC   _
                                TGC   CCCT TTCTGCTGCAGG
                                |||   |||| ||||||||||||
                                ACG   GGGA GAGACGACGTCC
                                  C__    C
GAM1118 TRIM9    3'  CTGCAGGAGGATGTAG      54829         CCTTTC G
                                CTGCATCC     T CTGCAG
                                ||||||||     | ||||||
                                GATGTAGG     A GACGTC
                                     _______ G
GAM1118 TRPS1    3'  TCCTACACCGGAGAAAAGCAG  26926      ATCCCC     C  C
                                CTGC     TTTCTG TG AGGA
                                ||||     |||||| || ||||
                                GACG     AGAGGC AC TCCT
                                  AAA___     C  A
GAM1118 C17orf26 3'  CCTGTGGAAAGAAGAGACAG   58264     CA  CC     GCT
                                CTG  TC  CTTTCT   GCAGG
                                |||  ||  ||||||   |||||
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                                GAC  AG  GAAAGG   TGTCC
                                  AG  AA     ___
GAM1118  C20orf139 3'  CCTGGGGAAAGGGAACAG    85917     CATC      GCTG
                                CTG   CCCTTTCT   CAGG
                                |||   ||||||||   ||||
                                GAC   GGGAAAGG   GTCC
                                  AA__      G___
GAM1118  CBX6     3'  CCTGGCCTGAAAGGGGATGCAG 27411           T_  TG
                                CTGCATCCCCTTTC  GC  CAGG
                                ||||||||||||||  ||  ||||
                                GACGTAGGGGAAAG  CG  GTCC
                                        TC  __
GAM1118  CCR1     3'  CCTGGTAGAAAGAAGATG    8925      CC      TG
                                CATC  CTTTCTGC  CAGG
                                ||||  ||||||||  ||||
                                GTAG  GAAAGATG  GTCC
                                  AA       __
GAM1118  DKFZP434K1772 3'  TCCTAGGTGGAAAGGAAAGCA  68341     ATCC     TG  GC
                                TGC   CCTTTC  CT  AGGA
                                |||   ||||||  ||  ||||
                                ACG   GGAAAG  GG  TCCT
                                  AAA_     GT  A_
GAM1118  DKFZP434P0111 3'  CCTGCAGTCTGAGGAGGCA   67955     ATCC    TCT
                                TGC   CCTT   GCTGCAGG
                                |||   ||||   ||||||||
                                ACG   GGAG   TGACGTCC
                                  GA__   TC_
GAM1118  DNAJC5   3'  CTGCATAGGGGAGCAG     62137     A     TTCTGC
                                CTGC TCCCCT     TGCAG
                                |||| ||||||     |||||
                                GACG AGGGGA     ACGTC
                                  _     T_____
GAM1118  FLJ11722  5'  CCTGCAGCTGGGGACATAG   46995     CA    TTTCT
                                CTG  TCCCC    GCTGCAGG
                                |||  |||||    ||||||||
                                GAT  AGGGG    CGACGTCC
                                  AC    T____
GAM1118  FLJ12443  3'  TCCTGCAGAGAGAGGAGCCGCA 46146      ATCC      G
            G                    CTGC   CCTTTCT CTGCAGGA
                                ||||   ||||||| ||||||||
                                GACG   GGAGAGA GACGTCCT
                                  CCGA      _
GAM1118  FLJ20623  5'  TCCCGCCTGGGAAGGGATGCA  35895        C    GCT  A
                                TGCATCCC TTTCT   GC GGA
                                |||||||| |||||   || |||
                                ACGTAGGG AAGGG   CG CCT
                                     _    TC_  C
GAM1118  FLJ32865  3'  CCTGCAGCTGAGGGACGC    58806    A   CTT  T
                                GC TCCC   TC GCTGCAGG
                                || ||||   || ||||||||
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                                CG AGGG   AG CGACGTCC
                                 C   ___  T
GAM1118 IL22R    3' CCTGCAAGGCAGAAATGACAG 41469    _  CCCCT     __
                                CTG CAT    TTCTGCT  GCAGG
                                ||| |||    |||||||  |||||
                                GAC GTA    AAGACGG  CGTCC
                                  A  _____      AA
GAM1118 KIAA0409 3' CCTTGAAAGGGGAGGCAG    31681     A       TGCTGC
                                CTGC TCCCCTTTC     AGG
                                |||| |||||||||     |||
                                GACG AGGGGAAAG     TCC
                                  G       T_____
GAM1118 KIAA0455 3' CCTACAGCAGAGGCCATGCAG  72884       CC  TT     C
                                CTGCAT  CC  TCTGCTG AGG
                                ||||||  ||  ||||||| |||
                                GACGTA  GG  AGACGAC TCC
                                    CC  __      A
GAM1118 KIAA0596 3' AGCAGAAAAGGGGTGCAG    63479         C
                                CTGCATCCC TTTCTGCT
                                |||||||||| ||||||||
                                GACGTGGGG AAAGACGA
                                     A
GAM1118 KIAA1604 5' CCCGCAGGCAGAGACGCGG   64893     A  CCCTT    _  A
                                CTGC TC    TCTGC TGC GG
                                |||| ||    ||||| ||| ||
                                GGCG AG    AGACG ACG CC
                                  C  _____    G  C
GAM1118 KIAA1862 3' TCCTGCAGCCAGTGCAGATGCA 69514       CCCTTT  _
            G                    CTGCATC     CTG CTGCAGGA
                                |||||||     ||| ||||||||
                                GACGTAG     GAC GACGTCCT
                                    ACGT__   C
GAM1118 KIAA1940 3' CCCACAGCACCGGCAGGAAATG 80780    CC   T  __    CA
                                CAT  CCT TC  TGCTG  GG
                                |||  ||| ||  |||||  ||
                                GTA  GGA GG  ACGAC  CC
                                  AA   C  CC    AC
GAM1118 MGC14859 3' CCCGCTTTGAAGAGGGTGCAG  62598        C   CTGCT  A
                                CTGCATCC CTTT    GC GG
                                |||||||| ||||    || ||
                                GACGTGGG GAAG    CG CC
                                     A   TTT__  C
GAM1118 MGC15668 3' TCCTGCAGCTCTGGGGAGACCA 52244    CA_    TTTCT
            G                    CTG   TCCCC    GCTGCAGGA
                                |||   |||||    |||||||||
                                GAC   AGGGG    CGACGTCCT
                                  CAG    TCT__
GAM1118 NXPH3    3' TCCCACAGTGCTGTGGAGACTG 66348      _  C  TTTCT   CA
            CAG                   CTGCA TC CC    GCTG  GGA
                                |||||  ||  ||    ||||  |||
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                                GACGT AG GG    TGAC  CCT
                                  C  A  TGTCG    AC
GAM1118  SHAPY    5'  CCCGCAGCGGAGGGACCACAG  57907     CA_   CTT      A
                                CTG   TCCC   TCTGCTGC GG
                                |||   ||||   |||||||| ||
                                GAC   AGGG   AGGCGACG CC
                                  ACC    ___       C
GAM1118  STMN4    3'  CCTGCAGCAGGTGGGATG    48650       CTT
                                CATCCC   TCTGCTGCAGG
                                ||||||   ||||||||||
                                GTAGGG   GGACGACGTCC
                                   T__
GAM1118  TAO1     3'  CCTGCAAGGGTAGGGGA     17717       T   GC
                                TCCCCT TCT  TGCAGG
                                |||||| |||  ||||||
                                AGGGGA GGG  ACGTCC
                                   T   A_
GAM1118  TOB2     5'  CCTGCAGGGCGGAGGGACGCA  97354     A   CTT     __
                                TGC TCCC   TCTGCT  GCAGG
                                ||| ||||   ||||||  |||||
                                ACG AGGG   AGGCGG  CGTCC
                                  C    ___     GA
GAM1118  UGT2B10   3'  CAGAAAAAAAAGGGATGCAG   8411          C____
                                CTGCATCCC    TTTCTG
                                |||||||||    ||||||
                                GACGTAGGG    AAAGAC
                                     AAAAA
GAM1118  LOC116071 5'  CCTGCGGAAGGAGATCCAG   57419     C   C    TCTG
                                CTG ATC CCTT   CTGCAGG
                                ||| ||| ||||   |||||||
                                GAC TAG GGAA   GGCGTCC
                                  C   A   ____
GAM1118  LOC124302 3'  CCTGCAGAGGGAGATGGCAG   74760      _  _   TTCTG
                                CTGC ATC CCCT    CTGCAGG
                                |||| ||| ||||    |||||||
                                GACG TAG GGGA    GACGTCC
                                  G   A   _____
GAM1118  LOC139483 5'  CCTGCAGCTCCTGGAAGGGATC 76359     C    C   T___
            CAG                   CTG ATCCC TTTC   GCTGCAGG
                                ||| ||||| ||||   ||||||||
                                GAC TAGGG AAGG   CGACGTCC
                                  C    _   TCCT
GAM1118  LOC144184 5'  CCTGCAGCTCCAGGTAGACGCA 77195      A  CC   TCT
            G                    CTGC TC  CTT   GCTGCAGG
                                |||| ||  |||   ||||||||
                                GACG AG  GGA   CGACGTCC
                                  C  AT   CCT
GAM1118  LOC145078 3'  CAGCAGAAAAGGGCTACAG   60929     CAT   C
                                CTG   CCC TTTCTGCTG
                                |||   ||| |||||||||
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                                GAC   GGG AAAGACGAC
                                  ATC   A
GAM1118  LOC145694 5'  CCAACAGGCAGAGAGGAGATGC 84441        C        GCA_
              AG                   CTGCATC CCTTTCTGCT    GG
                                |||||||| ||||||||||    ||
                                GACGTAG GGAGAGACGG    CC
                                    A         ACAA
GAM1118  LOC147229 5'  CCTGCAGCCTGGGATGCG    78919         CTTTCT
                                TGCATCCC     GCTGCAGG
                                ||||||||     ||||||||
                                GCGTAGGG     CGACGTCC
                                     TC____
GAM1118  LOC148981 3'  CAGCAGAAAAGGGCTACAG   85472     CAT   C
                                CTG   CCC TTTCTGCTG
                                |||   ||| |||||||||
                                GAC   GGG AAAGACGAC
                                  ATC   A
GAM1118  LOC149657 3'  CTGCAGCCGGGAGCAG      85715     A    CTTTCT
                                CTGC TCCC     GCTGCAG
                                |||| ||||     |||||||
                                GACG AGGG     CGACGTC
                                  _    C_____
GAM1118  LOC152106 5'  CCTGCAGCAGCAGGCGGA    70594     _   TT
                                TCC CCT  CTGCTGCAGG
                                ||| |||  ||||||||||
                                AGG GGA  GACGACGTCC
                                  C   C_
GAM1118  LOC169831 3'  CCTGCAGTGCCAGAGACGCAG  83670      A  CC  TTC
                                CTGC TC  CT   TGCTGCAGG
                                |||| ||  ||   |||||||||
                                GACG AG  GA   GTGACGTCC
                                  C  A_  CC_
GAM1118  LOC196510 3'  CCCCACATGAGGGGATG     89092         TC  C  CA
                                CATCCCCTT  TG TG  GG
                                |||||||||  || ||  ||
                                GTAGGGGAG  AC AC  CC
                                     T_  _  C_
GAM1118  LOC199986 5'  CCTGCAGGTTGTTGGAGAGGCA 91509      A  C  TTTCTG
              G                   CTGC TC CC     CTGCAGG
                                |||| || ||     |||||||
                                GACG AG GG     GACGTCC
                                  G  A  TTGTTG
GAM1118  LOC200220 3'  CCCCACATGAGGGGATG     90035         TC  C  CA
                                CATCCCCTT  TG TG  GG
                                |||||||||  || ||  ||
                                GTAGGGGAG  AC AC  CC
                                     T_  _  C_
GAM1118  LOC200312 5'  CCTGCAGCAGCTGTGGAACGC  91580    A_   CCTTT
                                GC  TCC    CTGCTGCAGG
                                ||  |||    ||||||||||
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                                CG  AGG    GACGACGTCC
                                 CA   TGTC_
GAM1118  LOC219654 3'  CCCCACAGGCCAGGGAAAGCAG 92927     A_   CTT   C  CA
                                CTGC  TCCC   TCTG TG  GG
                                ||||  ||||   |||| ||  ||
                                GACG  AGGG   GGAC AC  CC
                                  AA   ACC   _  C_
GAM1118  LOC220988 3'  CAGCAGAAAAGGGCTACAG   92512    CAT   C
                                CTG   CCC TTTCTGCTG
                                |||   ||| |||||||||
                                GAC   GGG AAAGACGAC
                                 ATC   A
GAM1118  LOC222166 3'  TGGCAGAGAAGAAATGCAG   95746      CCCC
                                CTGCAT    TTTCTGCTG
                                ||||||    |||||||||
                                GACGTA    AGAGACGGT
                                   AAGA
GAM1118  LOC253954 3'  CCTGCAGCCAGAAAGTTGCAG  99022      TCCC     _
                                CTGCA    CTTTCTG CTGCAGG
                                |||||    ||||||| |||||||
                                GACGT    GAAAGAC GACGTCC
                                  T___      C
GAM1118  LOC255157 5'  TCCTGGAGAAAGGGGACTCAG  99404     CA       GCTG
                                CTG  TCCCCTTTCT    CAGGA
                                |||  ||||||||||    |||||
                                GAC  AGGGGAAAGA    GTCCT
                                 TC        G___
GAM1118  LOC256021 3'  AGCAGAAAAGGGATGTAG    98275        C
                                CTGCATCCC TTTCTGCT
                                ||||||||| ||||||||
                                GATGTAGGG AAAGACGA
                                     A
GAM1118  LOC51195  3'  TCTGAGAAAGGGGAT      33410          GCTG
                                ATCCCCTTTCT    CAGG
                                ||||||||||    ||||
                                TAGGGGAAAGA    GTCT
                                     ____
GAM1118  LOC57333  3'  CCCGCAGGAGGCAGATGCAG   74090       CC      TGCA
                                CTGCATC  CTTTCTGC    GG
                                |||||||  ||||||||    ||
                                GACGTAG  GGAGGACG    CC
                                   AC       C___
GAM1118  LOC89932  5'  CCTGCAGGCAGAGGACGCGG   61456     A   CCTT    _
                                CTGC TCC    TCTGC TGCAGG
                                |||| |||    ||||| ||||||
                                GGCG AGG    AGACG ACGTCC
                                 C   ____     G
GAM1118  LOC91409  3'  TCCTGCAGACCCAAGAGCTGCA 66575      TCCC   TCTG
           G                     CTGCA    CTT    CTGCAGGA
                                |||||    |||    ||||||||
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                                GACGT   GAA   GACGTCCT
                                  CGA_  CCCA
GAM1118 LOC91522 5' CCAAAGGACAGAAAGGAGACCC 66915    CA  C      _ GCA
           AG                    CTG  TC CCTTTCTG CT   GG
                                |||  || ||||||||| ||   ||
                                GAC  AG GGAAAGAC GG   CC
                                  CC  A       A  AAA
GAM1119 CR1L    5' CTATCATCTGCCTAAAAAACTC 90957       CCTGCTC  C
           A                     TGAGTT      GC GATGATAG
                                ||||||      || ||||||||
                                ACTCAA      CG CTACTATC
                                   AAAATC_  T
GAM1119 ITGAL   3' TATCTCGAACATGGAACTCA  11049        _ C   CC
                                TGAGTTCC TG TCG  GATG
                                |||||||| || |||  ||||
                                ACTCAAGG AC AGC  CTAT
                                     T  A   T_
GAM1119 OFD1    3' CTATCATCAGACAAAACTCA  14608      CC  C  GCC
                                TGAGTT  TG TC   GATGATAG
                                ||||||  || ||   ||||||||
                                ACTCAA  AC AG   CTACTATC
                                   A_  _  A__
GAM1119 SCN2A2  3' TGGTCAGCAAACTGGAACTCA 41013        ____   C
                                TGAGTTCC    TGCT GCCG
                                ||||||||    |||| ||||
                                ACTCAAGG    ACGA TGGT
                                     TCAA    C
GAM1119 IL18BP  3' CACCAGGACAGCAGGAACCA  20307    A       CG  GA_
                                TG GTTCCTGCT  CC   TG
                                || |||||||||  ||   ||
                                AC CAAGGACGA  GG   AC
                                  _       CA  ACC
GAM1119 KIAA0447 3' CTATCATCAGCAAATAGAGCTC 72117       CTGCTC  C
           A                     TGAGTTC     GC GATGATAG
                                |||||||     || ||||||||
                                ACTCGAG     CG CTACTATC
                                    ATAAA_  A
GAM1119 LIN-7-C  3' CATCAAAATAAGTAGGAACTCA 37753          CGCC__
                                TGAGTTCCTGCT     GATG
                                ||||||||||||     ||||
                                ACTCAAGGATGA     CTAC
                                       ATAAAA
GAM1120 SCAMP1  3' GCTAAATAAATATTCTCC    18013     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1120 SCAMP1  3' GCTAAATAAATATTCTCC    54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
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                                CCT TTATAA TAAATCG
                                  C     A
GAM1120 NX-17    3' TGAATATCAGCCCCTAATA   40706        ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM1120 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
             TA                   TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM1121 ABCB8    3' CCGGCTGCCTCCCTCCCA    24203        _
                                TGGGAGGG GGCAGCTGG
                                |||||||| |||||||||
                                ACCCTCCC CCGTCGGCC
                                    T
GAM1121 ABP1     3' CAGCCCCCAGTTCCTCCCCCA  63797     A    C   __
                                TGGG GGGGG AGCT  GGGCTG
                                |||| ||||| ||||  ||||||
                                ACCC CCTCC TTGA  CCCGAC
                                  _    _   CC
GAM1121 ACTN1    5' CAGCCCAGCCCTACTCCCTCCC 8469         CA__
                                GGGAGGGGG   GCTGGGCTG
                                |||||||||   |||||||||
                                CCCTCCCTC   CGACCCGAC
                                    ATCC
GAM1121 ADRBK1   3' TCAGGGGCTGCCCGCTCCCA  9669       G      GGG
                                TGGGAG GGGCAGCT  CTGA
                                ||||||| ||||||||  ||||
                                ACCCTC CCCGTCGG  GACT
                                   G      G__
GAM1121 ALDOA    3' CAGGCCCTGCCCCCTCCCA   5263          CT  G
                                TGGGAGGGGGGCAG  GG CTG
                                ||||||||||||  || |||
                                ACCCTCCCCCGTC  CC GAC
                                      __ G
GAM1121 AMH      3' CAGCTCGCGCCCCTTCCCA   6651          A  T
                                TGGGAGGGGGC GC GGGCTG
                                |||||||||| || ||||||
                                ACCCTTCCCCG CG CTCGAC
                                      _ _
GAM1121 AR       5' TCAGCCAACCCCCCTCACCA  5277     _     CAGCTG
                                TGG GAGGGGG     GGCTGA
                                ||| |||||||     ||||||
                                ACC CTCCCCC     CCGACT
                                  A      CAA___
GAM1121 ARF1     3' CAGCCCAGCTGTTCCCCT    71195    A
                                GG GGGGGCAGCTGGGCTG
                                || ||||||||||||||||
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                                TC CCCTTGTCGACCCGAC
                                  _
GAM1121 ARHG    3' CAACCCAGTGCCCCCTCCCA  77086          G    C
                                TGGGAGGGGGCA CTGGG TG
                                |||||||||||| ||||| ||
                                ACCCTCCCCCGT GACCC AC
                                      _    A
GAM1121 ASGR2   5' CAGCCCAGCCCAGCTCC    56041     GG  CA
                                GGAG  GG  GCTGGGCTG
                                ||||  ||  |||||||||
                                CCTC  CC  CGACCCGAC
                                  GA  __
GAM1121 ASGR2   5' CAGCCCAGCCCAGCTCC    56042     GG  CA
                                GGAG  GG  GCTGGGCTG
                                ||||  ||  |||||||||
                                CCTC  CC  CGACCCGAC
                                  GA  __
GAM1121 ASGR2   5' CAGCCCAGCTCCAGCTCC    56043     GG  C
                                GGAG  GG AGCTGGGCTG
                                ||||  || ||||||||||
                                CCTC  CC TCGACCCGAC
                                  GA  _
GAM1121 ASGR2   5' CAGCCCAGCTCCAGCTCC    56044     GG  C
                                GGAG  GG AGCTGGGCTG
                                ||||  || ||||||||||
                                CCTC  CC TCGACCCGAC
                                  GA  _
GAM1121 ASGR2   5' CAGCCCAGCTCCAGCTCC    56045     GG  C
                                GGAG  GG AGCTGGGCTG
                                ||||  || ||||||||||
                                CCTC  CC TCGACCCGAC
                                  GA  _
GAM1121 C18orf2 3' CATCCCGCCCACCCCCCA    49460     A _   AGCT   C
                                TGGG GG GGGC   GGG TG
                                |||| || ||||   ||| ||
                                ACCC CC CCCG   CCC AC
                                  C  A   ____   T
GAM1121 CACNB1  3' CAGCAACCCTGCCCCTCCCCA 7405      AG     CTGG
                                TGGG  GGGGCAG   GCTG
                                ||||  |||||||   ||||
                                ACCC  CCCCGTC   CGAC
                                  CT      CCAA
GAM1121 CACNG3  5' CCAGCCGGCCCCCGCCCCA   22564     A_    A_
                                TGGG  GGGGGC  GCTGG
                                ||||  ||||||  |||||
                                ACCC  CCCCCG  CGACC
                                  CG     GC
GAM1121 CAMLG   5' CCACTGCCACCCCTCCCA    9996          __   C
                                TGGGAGGGG  GCAG TGG
                                |||||||||  |||| |||
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                                ACCCTCCCC  CGTC ACC
                                     AC   _
GAM1121  CAV1    5'  CAGCCACCGCCCCCCTCC    10022       CA  TG_
                                GGAGGGGG  GC   GGCTG
                                ||||||||  ||   |||||
                                CCTCCCCC  CG   CCGAC
                                    __  CCA
GAM1121  CBFA2T3  3'  TCAGACGTGCTCCCTCCCA   19019         GC  GG
                                TGGGAGGGGGCA  TG  CTGA
                                ||||||||||||  ||  ||||
                                ACCCTCCCTCGT  GC  GACT
                                      __  A_
GAM1121  CD74    3'  TCAGCCCCCAGCCCCTCCCC   16381    AG    AGCT
                                GGG  GGGGC   GGGCTGA
                                |||  |||||   |||||||
                                CCC  CCCCG   CCCGACT
                                  CT    ACC_
GAM1121  CKM     5'  CAGCCCAGCCAGGTCTCCT   10198      A__
                                AGGGGGC   GCTGGGCTG
                                |||||||   |||||||||
                                TCCTCTG   CGACCCGAC
                                    GAC
GAM1121  CNP     3'  CAGCCCAGCTGCTCTGCCCA  53616     AG
                                TGGG  GGGGCAGCTGGGCTG
                                ||||  ||||||||||||||
                                ACCC  TCTCGTCGACCCGAC
                                  G_
GAM1121  COL1A1   3'  CAACCTGGCTCCCTCCCA    5391       GGC   TG  C
                                TGGGAGGG   AGC  GG TG
                                ||||||||   |||  || ||
                                ACCCTCCC   TCG  CC AC
                                     ___   GT  A
GAM1121  EGFL4    5'  TCAGACCTGCCCCCTCCCA   62474         CTGGG
                                TGGGAGGGGGGCAG    CTGA
                                ||||||||||||     ||||
                                ACCCTCCCCCCGTC    GACT
                                      CA___
GAM1121  EPHA8    3'  CAGCCCTGCCCCCCCCTCCC   40429       CA  T
                                GGGAGGGGG  GC GGGCTG
                                |||||||||  || ||||||
                                CCCTCCCCC  CG CCCGAC
                                     C_  T
GAM1121  EVX1     5'  CAGCAGCTCCGCGCCCTCCCA  10545       G  __   GG
                                TGGGAGGG GC  AGCT  GCTG
                                |||||||| ||  ||||  ||||
                                ACCCTCCC CG  TCGA  CGAC
                                     G  CC   __
GAM1121  FGFR1    3'  CAGCCACTTCATCCCCTCCCA  7018         CAGCTG
                                TGGGAGGGGG    GGCTG
                                ||||||||||    |||||
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                                ACCCTCCCCT     CCGAC
                                     ACTTCA
GAM1121  FGFR1    3'  CAGCCACTTCATCCCCTCCCA  32371          CAGCTG
                                TGGGAGGGGG     GGCTG
                                ||||||||||     |||||
                                ACCCTCCCCT     CCGAC
                                     ACTTCA
GAM1121  FOSB     3'  AGACCCTGCCCCCTGCCA    23054     G      GCT  _
                                TGG AGGGGGCA   GGG CT
                                ||| ||||||||   ||| ||
                                ACC TCCCCCGT   CCC GA
                                  G       ___   A
GAM1121  FOSB     3'  TCTAGCCACTCCCTCCCA    23058          CA
                                TGGGAGGGGG  GCTGGG
                                ||||||||||  ||||||
                                ACCCTCCCTC  CGATCT
                                     AC
GAM1121  FOXD2    5'  TCAGTCCCCCGCCCCCTCCC   16793          AGCT
                                GGGAGGGGGC   GGGCTGA
                                ||||||||||   |||||||
                                CCCTCCCCCG   CCTGACT
                                     CCC_
GAM1121  GPRK6    3'  CAGCCCTGGCCCTTCCCA    10865         G  GCT
                                TGGGAGGGG CA   GGGCTG
                                |||||||| ||   ||||||
                                ACCCTTCCC GT   CCCGAC
                                     G ___
GAM1121  GRLF1    3'  TCAGCTGCGCCCCCCTCCCA  79262          CA  TG
                                TGGGAGGGGG  GC  GGCTGA
                                ||||||||||  ||  ||||||
                                ACCCTCCCCC  CG  TCGACT
                                     CG __
GAM1121  HEPH     5'  CAGCCCTTCCCCCTCCC     57831         CAGCT
                                GGGAGGGGG    GGGCTG
                                |||||||||    ||||||
                                CCCTCCCCC    CCCGAC
                                     TT___
GAM1121  HOXC6    3'  TCAGCTCTGGACCCCCTCCC   16911         CAGCT
                                GGGAGGGGG    GGGCTGA
                                |||||||||    |||||||
                                CCCTCCCCC    CTCGACT
                                     AGGT_
GAM1121  HR       5'  CAGCTCTGGCACTGCCCCCTCC 37907           __  TG _
           CA                     TGGGAGGGGGCA  GC  G GCTG
                                ||||||||||||  ||  | ||||
                                ACCCTCCCCCGT  CG  C CGAC
                                      CA  GT T
GAM1121  IMMP2L   5'  CCAACAACGCGCCCTCTCCCA  51705          A _____
                                TGGGAGGGGGC GC    TGG
                                |||||||||| ||    |||
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                                ACCCTCTCCCG CG    ACC
                                      _ CAACA
GAM1121 IMPDH1   3' CAGCCTGGCCCCCACCCCA  7950     AG   CA TG
                                TGGG GGGG GC GGCTG
                                |||| |||| || |||||
                                ACCC CCCC CG CCGAC
                                  CA  __ GT
GAM1121 INHBC    3' CCTGGCTACCCCCTTCCA   19859       C  TG
                                TGGGAGGGGG AGC GG
                                |||||||||| ||| ||
                                ACCTTCCCCC TCG CC
                                     A  GT
GAM1121 ITGA3    3' CAGCCCCAGCCCCTTCC    11029       AGCT
                                GGAGGGGGC   GGGCTG
                                |||||||||   ||||||
                                CCTTCCCCG   CCCGAC
                                     AC__
GAM1121 ITGA3    3' CAGCCCCAGCCCCTTCC    11030       AGCT
                                GGAGGGGGC   GGGCTG
                                |||||||||   ||||||
                                CCTTCCCCG   CCCGAC
                                     AC__
GAM1121 MAFF     3' CCACACTGCCCCTCCCCA   25577     AG     C _
                                TGGG GGGGCAG TG GG
                                |||| ||||||| || ||
                                ACCC CCCCGTC AC CC
                                  CT     _ A
GAM1121 MSI1     3' CCTAGGACCGCCCCCTCCC   11698       AG__
                                GGGAGGGGGC   CTGGG
                                ||||||||||   |||||
                                CCCTCCCCCG   GATCC
                                     CCAG
GAM1121 MYL1     5' TCAACCCAACCACCATCCTCTT 55323       CAGC___   C
           CCA                   TGGGAGGGGG     TGGG TGA
                                ||||||||||      |||| |||
                                ACCTTCTCCT      ACCC ACT
                                     ACCACCA   A
GAM1121 NFIA     5' CCGCAGCCGCCCCCTCCC   70884       A  _
                                GGGAGGGGGC GCTG GG
                                |||||||||| |||| ||
                                CCCTCCCCCG CGAC CC
                                     C   G
GAM1121 NTF5     5' CAGGTGGTTGCCCCCTCCC  21630         GGG
                                GGGAGGGGGCAGCT  CTG
                                |||||||||||||  |||
                                CCCTCCCCCGTTGG  GAC
                                       TG_
GAM1121 PACSIN1  3' CAGCCCAGCCCTGTTTCCCCTC 93877      __  __
                                GAGGGG GCA GCTGGGCTG
                                |||||| ||| |||||||||
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                                CTCCCC  TGT  CGACCCGAC
                                   TT   CC
GAM1121  PCDH11X  5'  TCAACCCCTCTCCTCTCCCA  28016        C  CT   C
                                TGGGAGGGGG AG  GGG TGA
                                |||||||||| ||  ||| |||
                                ACCCTCTCCT TC  CCC ACT
                                     C  __   A
GAM1121  PCDH11Y  5'  TCAACCCCTCTCCTCTCCCA  53168        C  CT   C
                                TGGGAGGGGG AG  GGG TGA
                                |||||||||| ||  ||| |||
                                ACCCTCTCCT TC  CCC ACT
                                     C  __   A
GAM1121  PIK3R2   5'  CAACCCAGCGGACCCTCCCA  18509       GGCA     C
                                TGGGAGGG   GCTGGG TG
                                ||||||||   |||||| ||
                                ACCCTCCC   CGACCC AC
                                    AGG_    A
GAM1121  PIK4CB   3'  CCAGCTCTACCCCTCCCA   12129        GC_
                                TGGGAGGGG  AGCTGG
                                |||||||||  ||||||
                                ACCCTCCCC  TCGACC
                                     ATC
GAM1121  PIK4CB   3'  CCAGGGACCTACCCCTCCCA  12130        GC  ____
                                TGGGAGGGG  AG   CTGG
                                |||||||||  ||   ||||
                                ACCCTCCCC  TC   GACC
                                     A_  CAGG
GAM1121  PK428    5'  TCAGGGACCTCGCCCCCTCCC  14603        AGCT  G__
                                GGGAGGGGGC   GG  CTGA
                                ||||||||||   ||  ||||
                                CCCTCCCCCG   CC  GACT
                                     CT__  AGG
GAM1121  PKP2     3'  CAGCCCAGCCTTGCCCACC   17106   _   __
                                GG GGGCA  GCTGGGCTG
                                || |||||  |||||||||
                                CC CCCGT  CGACCCGAC
                                 A    TC
GAM1121  PLA2G4C  5'  CAGCCCGCGACCTCCTCCCA  73806        CA  T
                                TGGGAGGGGG  GC GGGCTG
                                ||||||||||  || ||||||
                                ACCCTCCTCC  CG CCCGAC
                                     AG  _
GAM1121  PNUTL1   3'  TCAGCACCACCCCCTCCCA   12193        CAGC  _
                                TGGGAGGGGG   TGG GCTGA
                                ||||||||||   ||| |||||
                                ACCCTCCCCC   ACC CGACT
                                     ____   A
GAM1121  PNUTL2   3'  CCATGCCGGCCCCTCCCA    55371        G A_  _
                                TGGGAGGGG C  GC TGG
                                ||||||||| |  || |||
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                                ACCCTCCCC G  CG ACC
                                     _ GC  T
GAM1121  PNUTL2   3'  CCATGCCGGCCCCTCCCA    55372        G A_  _
                                TGGGAGGGG C  GC TGG
                                |||||||||  |  || |||
                                ACCCTCCCC G  CG ACC
                                     _ GC  T
GAM1121  PNUTL2   3'  CCATGCCGGCCCCTCCCA    55373        G A_  _
                                TGGGAGGGG C  GC TGG
                                |||||||||  |  || |||
                                ACCCTCCCC G  CG ACC
                                     _ GC  T
GAM1121  POU2F2   3'  CAGCCATGCCTCCCCTCCCA  12212          CA  TG
                                TGGGAGGGGG  GC  GGCTG
                                ||||||||||  ||  |||||
                                ACCCTCCCCT  CG  CCGAC
                                     C_  TA
GAM1121  PPGB     3'  CCAGGACTGCCCCCTTCCCA  6125       _       __
                                TGGGA GGGGGGCAG  CTGG
                                |||||  ||||||||  ||||
                                ACCCT CCCCCGTC  GACC
                                   T       AG
GAM1121  PPP2R4   3'  CCAGCAGTGGCCCCTCCC    61179        G  __
                                GGGAGGGG CA  GCTGG
                                ||||||||  ||  |||||
                                CCCTCCCC GT  CGACC
                                     G  GA
GAM1121  PRCC     3'  CAGCCCAGCTGGCCTGGCCC  21063     AG   G
                                GGG  GGG CAGCTGGGCTG
                                |||  ||| ||||||||||
                                CCC  TCC GTCGACCCGAC
                                  GG   G
GAM1121  PTPRN    3'  CAGCCTCCTCCCACCACCCTCC 12624        _  CAGCT__
              CA                  TGGGAGGG GG      GGGCTG
                                |||||||  ||      ||||||
                                ACCCTCCC CC      TCCGAC
                                     A  ACCCTCC
GAM1121  RANBP3   3'  CAGCCCTCTGCCCCTGCCCA  24630      A       CT
                                TGGG GGGGGCAG  GGGCTG
                                ||||  ||||||||  ||||||
                                ACCC TCCCCGTC  CCCGAC
                                  G       T_
GAM1121  RFX1     3'  CTTGGCCGCCCCCCTCCCA   12849         _ A  TG
                                TGGGAGGGGG C GC  GG
                                ||||||||||  |  ||  ||
                                ACCCTCCCCC G CG  TC
                                     C C  GT
GAM1121  RGR      3'  TCATCCCTCACCCCCTCCCA  12861          CAGCT   C
                                TGGGAGGGGG    GGG TGA
                                ||||||||||    ||| |||
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                                ACCCTCCCCC    CCC ACT
                                     ACT__   T
GAM1121 RXRA    3' CCAGCTGGGCCCCTCCCA   12916       G_
                                TGGGAGGGG  CAGCTGG
                                |||||||||  |||||||
                                ACCCTCCCC  GTCGACC
                                     GG
GAM1121 RXRB    3' CAGCTTCCCGCCGCCCCCCCCA 42029     A     A  T  __
                                TGGG GGGGGC GC GG  GCTG
                                |||| |||||| || ||  ||||
                                ACCC CCCCCG CG CC  CGAC
                                  _     C  C  TT
GAM1121 RYR1    5' CAGCCCGCAGCCCCCTCCC   6771         A  T
                                GGGAGGGGGC GC GGGCTG
                                |||||||||| || ||||||
                                CCCTCCCCCG CG CCCGAC
                                     A  _
GAM1121 SLC22A12 3' AGCCTGCCTCCTCCCA     58681          GCTG
                                TGGGAGGGGGCA   GGCT
                                ||||||||||||   ||||
                                ACCCTCCTCCGT   CCGA
                                          ____
GAM1121 SLC7A6  3' CAGGAATTTGCTGCCCCCCACC 15638    GA       TGGG__
           A                     TGG  GGGGGCAGC     CTG
                                |||  |||||||||     |||
                                ACC  CCCCCGTCG     GAC
                                  AC       TTTAAG
GAM1121 SNCB    3' CAGTGTTGCCTCCTCCCA    13285          TGG
                                TGGGAGGGGGGCAGC  GCTG
                                ||||||||||||||  ||||
                                ACCCTCCTCCGTTG  TGAC
                                          ___
GAM1121 SNL     3' TCTCCCAGCCACCTCCTCCCA 13292        CA     CT
                                TGGGAGGGGG  GCTGGG  GA
                                ||||||||||  ||||||  ||
                                ACCCTCCTCC  CGACCC  CT
                                     AC     T_
GAM1121 SOX12   3' CAGCAGCCAGCCCCCTCC    23681        A_  GG
                                GGAGGGGGC  GCT  GCTG
                                |||||||||  |||  ||||
                                CCTCCCCCG  CGA  CGAC
                                     AC  __
GAM1121 SYNGR1  3' TCAGCCCAGAAGCCCTTCC   17512       G AG
                                GGAGGGG C  CTGGGCTGA
                                |||||||  |  |||||||||
                                CCTTCCC G  GACCCGACT
                                    _ AA
GAM1121 TAGLN   3' CAGCCCAGCCTGCCCCCT    60376        _
                                AGGGGGCAG CTGGGCTG
                                |||||||| ||||||||
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                                TCCCCCGTC GACCCGAC
                                     C
GAM1121  TCF7     3'  CCAGTGTGCACCCCTCCC    13616        _  _
                                GGGAGGGG GCA GCTGG
                                |||||||| ||| |||||
                                CCCTCCCC CGT TGACC
                                     A  G
GAM1121  TFEB     3'  CCAGGGGCACCTCCCTCCCA  93750         ___ AG
                                TGGGAGGGG  GC  CTGG
                                |||||||||  ||  ||||
                                ACCCTCCCT  CG  GACC
                                     CCA  GG
GAM1121  THRA     5'  CACTCCCTGGCCCCTCCCA   13753        G  CT  GC
                                TGGGAGGGG CAG  GG  TG
                                |||||||| |||  ||  ||
                                ACCCTCCCC GTC  CC  AC
                                     G  __ TC
GAM1121  TMEPAI   3'  CCAGCTGCTACCCCCTCCC   39826        ___
                                GGGAGGGG  GCAGCTGG
                                ||||||||  ||||||||
                                CCCTCCCC  CGTCGACC
                                     CAT
GAM1121  WARS     3'  TCAGCCCATGCCCCCTCCCA  67867          GC
                                TGGGAGGGGGCA  TGGGCTGA
                                ||||||||||||  ||||||||
                                ACCCTCCCCCGT  ACCCGACT
                                      __
GAM1121  WWP2     3'  CCGAGGCCGCCCCTCCCA    61726        G A  G_
                                TGGGAGGGG C GCT  GG
                                |||||||| | |||  ||
                                ACCCTCCCC G CGG  CC
                                     _ C  AG
GAM1121  20D7-FC4 3'  TCAGCCCCAACCCCCTCCC   61570        CAGCT
                                GGGAGGGGG    GGGCTGA
                                |||||||||    |||||||
                                CCCTCCCCC    CCCGACT
                                     AAC__
GAM1121  ANKRD2   3'  CAGCCCAGCCAGCTACCC    72587    _  A_
                                GGG GGC  GCTGGGCTG
                                ||| |||  |||||||||
                                CCC TCG  CGACCCGAC
                                  A  AC
GAM1121  Apg4B    3'  CCGTGCTGCCTCCCCCCA    26181    A      _
                                TGGG GGGGGCAGC TGG
                                |||| ||||||||| |||
                                ACCC CCTCCGTCG GCC
                                  C       T
GAM1121  ARTN     5'  CCAGCATCTACCCCCCTCCCA  15611        CA____
                                TGGGAGGGGG    GCTGG
                                ||||||||||    |||||
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                                ACCCTCCCCC     CGACC
                                     CATCTA
GAM1121 BA108L7.2 3' CCACTGCACCCCCTCCCA    49068         __   C
                                TGGGAGGGG  GCAG TGG
                                |||||||||  |||| |||
                                ACCCTCCCC  CGTC ACC
                                     CA   _
GAM1121 BICD2    3' CCGTGTTGCCCCCTCCCA    70908          _
                                TGGGAGGGGGCAGC TGG
                                |||||||||||||| |||
                                ACCCTCCCCCGTTG GCC
                                       T
GAM1121 C14orf4  3' CAACCCAACTCGACCCTCCC  67897       GGC  C   C
                                GGGAGGG   AG TGGG TG
                                |||||||   || |||| ||
                                CCCTCCC   TC ACCC AC
                                    AGC  A    A
GAM1121 C5orf6   3' TCAGCCCCACCCCCTCCC    33957        CAGCT
                                GGGAGGGGGG    GGGCTGA
                                |||||||||     |||||||
                                CCCTCCCCC     CCCGACT
                                     AC___
GAM1121 CBX6     3' CCAAAGATGCCCCCTCCCA   27408          GC__
                                TGGGAGGGGGCA   TGG
                                ||||||||||||   |||
                                ACCCTCCCCCGT   ACC
                                       AGAA
GAM1121 CNNM2    3' CAGCCCCTGCTCCTCCTCCCA 34939         C   T_
                                TGGGAGGGGG AGC  GGGCTG
                                |||||||||| |||  ||||||
                                ACCCTCCTCC TCG  CCCGAC
                                     _   TC
GAM1121 CSR1     3' TCAGGCACCACCCCCTCC    33186        CAGC  _ _
                                GGAGGGGG   TGG GC TGA
                                ||||||||   ||| || |||
                                CCTCCCCC   ACC CG ACT
                                     _____  A  G
GAM1121 DGKZ     3' CAGCCCCCGCTCCTGCCCCACC 14676     AG      CT_____
            CCA                    TGGG  GGGGCAG     GGGCTG
                                ||||  |||||||     ||||||
                                ACCC  CCCCGTC     CCCGAC
                                  CA      CTCGCC
GAM1121 DJ37E16.5 3' CCTTGCAACCCCCTCCCA   40094         CA  T
                                TGGGAGGGGG  GC GGG
                                ||||||||||  || |||
                                ACCCTCCCCC  CG TCC
                                       AA  T
GAM1121 DKFZP434J193 3' TCAACCCCAGGCCACCCCCA  71563     A  G   AG    C_
                                TGGG GG GGC  CTGGG  TGA
                                |||| || |||  |||||  |||
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                                ACCC CC CCG  GACCC  ACT
                                  _ A  __    CA
GAM1121  DKFZP434J193 3'  TCAGCTGAATCCCCTCCCA   71564         __
                                TGGGAGGGGG  CAGCTGG
                                ||||||||||  |||||||
                                ACCCTCCCCT  GTCGACT
                                     AA
GAM1121  DKFZP434N1817 3'  CAGCCCAGCCCTGCCTCCC   68719      G  CA
                                GGGAGG GG  GCTGGGCTG
                                ||||||  ||  |||||||||
                                CCCTCC TC  CGACCCGAC
                                   G  C_
GAM1121  DKFZp434P2235 3'  CATGCCCAGCCCCTCCCA    51045       GGCA     _
                                TGGGAGGG    GCTGGGC TG
                                ||||||||    ||||||| ||
                                ACCCTCCC    CGACCCG AC
                                     ____      T
GAM1121  DKFZp547J036 3'  TCAGCCCAGCCAGGCCCCCTCC 51123          A__
           C                     GGGAGGGGGC   GCTGGGCTGA
                                ||||||||||   ||||||||||
                                CCCTCCCCCG   CGACCCGACT
                                     GAC
GAM1121  DKFZp547O146 3'  CAGCCCAGCCCCGCCCTCCC   39965       _ CA
                                GGGAGGG GG  GCTGGGCTG
                                |||||||  ||  |||||||||
                                CCCTCCC CC  CGACCCGAC
                                   G  C_
GAM1121  DKFZP586G1122 3'  TCAACCCTGAACCCCTCCCA   61940        GCAGCT   C
                                TGGGAGGGG     GGG TGA
                                |||||||||     ||| |||
                                ACCCTCCCC     CCC ACT
                                     AAGT__   A
GAM1121  DKFZP586M1019 3'  CAGCCCTTCGAGCCCCCTCCC  32171         AGCT_
                                GGGAGGGGGC    GGGCTG
                                ||||||||||    ||||||
                                CCCTCCCCCG    CCCGAC
                                     AGCTT
GAM1121  DNAJC5   3'  CCAGTCTCCCCCCTCCCA    62133          C  _
                                TGGGAGGGGG AG CTGG
                                |||||||||| || ||||
                                ACCCTCCCCC TC GACC
                                     C  T
GAM1121  FBXO2    5'  CCGTAGCCGCCTCCTCCCA   25141          A   _
                                TGGGAGGGGGC GCTG GG
                                |||||||||||| |||| ||
                                ACCCTCCTCCG CGAT CC
                                     C   G
GAM1121  FLJ00007  3'  CCTTGGGCTGCCCTCCCCCA  71776      A       __
                                TGGG GGGGGCAGCT  GGG
                                |||| ||||||||||  |||
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                                ACCC CTCCCGTCGG  TCC
                                  C        GT
GAM1121  FLJ00024  3'  TCAGGGGCGCCCCTCCCA    64505        _  AG
                                TGGGAGGGG GC  CTGG
                                |||||||||  ||  ||||
                                ACCCTCCCC CG  GACT
                                     G  GG
GAM1121  FLJ10535  3'  TCAACCCATTTCCCTCCC    36757        CAGC   C
                                GGGAGGGGG   TGGG TGA
                                |||||||||   |||| |||
                                CCCTCCCTT   ACCC ACT
                                     T___   A
GAM1121  FLJ10759  3'  CAGCCCAGCCCTGACCTC    37120     __  CA
                                GAGG  GGG  GCTGGGCTG
                                ||||  |||  |||||||||
                                CTCC  TCC  CGACCCGAC
                                  AG  __
GAM1121  FLJ12387  3'  CCTTATGCACTGCCCCTCCCA  43375        ____  GCT
                                TGGGAGGGG   GCA  GGG
                                |||||||||   |||  |||
                                ACCCTCCCC   CGT  TCC
                                     GTCA  AT_
GAM1121  FLJ12681  3'  CATCCCACCCTCCTCCCA    43183        CAGC   C
                                TGGGAGGGGG   TGGG TG
                                |||||||||   |||| ||
                                ACCCTCCTCC   ACCC AC
                                     C___   T
GAM1121  FLJ12783  3'  CCAGGATTCGCCCTCTCCCA  49484        AG___
                                TGGGAGGGGGC   CTGG
                                ||||||||||    ||||
                                ACCCTCTCCCG   GACC
                                      CTTAG
GAM1121  FLJ12788  3'  CAACCAGCCCCTCTCCCA    42844        CA   GC
                                TGGGAGGGGG  GCTGG  TG
                                |||||||||  |||||  ||
                                ACCCTCTCCC  CGACC  AC
                                     __    A_
GAM1121  FLJ12875  3'  CCTTGTGTTACCCCCTCCCA  44916        CA__  T
                                TGGGAGGGGG   GC GGG
                                |||||||||   || |||
                                ACCCTCCCCC   TG TCC
                                      ATTG  T
GAM1121  FLJ13153  5'  CAGCCCAGCCCCTGCTCCC   45922     G  CA
                                GGGAG GGG  GCTGGGCTG
                                |||||  |||  |||||||||
                                CCCTC TCC  CGACCCGAC
                                  G  C_
GAM1121  FLJ14126  3'  CAGCCCCCTCTCCTCCCA    46274        CAGCT
                                TGGGAGGGGG   GGGCTG
                                ||||||||||   ||||||
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                                ACCCTCCTCT    CCCGAC
                                     CC___
GAM1121  FLJ14327  3'  CAGCCCTTTCCTCTGCCCCCAC 46676     A      CT____
            CCA                   TGGG GGGGGCAG     GGGCTG
                                  |||| ||||||||     ||||||
                                  ACCC CCCCCGTC     CCCGAC
                                    A       TCCTTT
GAM1121  FLJ14800  3'  TCAACCCCTGGCCCCCTCCC   52689         AGCT   C
                                  GGGAGGGGGC    GGG TGA
                                  ||||||||||    ||| |||
                                  CCCTCCCCCG    CCC ACT
                                       GTC_   A
GAM1121  FLJ14810  3'  CAACCCATCCCCCACCCA    52696     A    CAGC    C
                                  TGGG GGGGG    TGGG TG
                                  |||| |||||    |||| ||
                                  ACCC CCCCC    ACCC AC
                                    A    T___    A
GAM1121  FLJ20320  5'  CCTACACTGCCTCCTCCCA    35421           C_
                                  TGGGAGGGGGGCAG  TGGG
                                  ||||||||||||  ||||
                                  ACCCTCCTCCGTC  ATCC
                                         AC
GAM1121  FLJ20542  3'  CACCTCTGCCCTCTCCCA    50743           CT   C
                                  TGGGAGGGGGGCAG  GGG TG
                                  ||||||||||||  ||| ||
                                  ACCCTCTCCCGTC  TCC AC
                                              __  _
GAM1121  FLJ20850  3'  CAGCCCAGCCCTAACTGCCA  36174     G  GG  CA
                                  TGG AG  GG  GCTGGGCTG
                                  ||| ||  ||  |||||||||
                                  ACC TC  TC  CGACCCGAC
                                    G  AA  C_
GAM1121  FLJ23058  5'  TCAGCCCAGCTGGGTTCC    45528     GGGG
                                  GGAG    CAGCTGGGCTGA
                                  ||||    ||||||||||||
                                  CCTT    GTCGACCCGACT
                                    GG__
GAM1121  FLJ23604  3'  CAGCCCATGCACCCCTCCC    47546        _   GC
                                  GGGAGGGG GCA  TGGGCTG
                                  |||||||| |||  |||||||
                                  CCCTCCCC CGT  ACCCGAC
                                       A   __
GAM1121  FLJ32332  3'  CAGCCCGTGGCCCTCCCA    58942        GGCA  T
                                  TGGGAGGG    GC GGGCTG
                                  ||||||||    || ||||||
                                  ACCCTCCC    TG CCCGAC
                                       GG__  _
GAM1121  GMEB2     3'  CTGAGCCGGCCCCTCCCA    25661         G A_   G
                                  TGGGAGGGG C  GCT GG
                                  |||||||| |  ||| ||
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                                ACCCTCCCC G  CGA TC
                                     _ GC   G
GAM1121 HA-1     3' CAGCGGGCGCCTCCTCCCA   66154          A   GG
                                TGGGAGGGGGC GCT  GCTG
                                |||||||||| |||  ||||
                                ACCCTCCTCCG CGG  CGAC
                                     _  G_
GAM1121 HTCD37   3' CAGCAGAGCACTCCCTCCCA  68297         CA   GG
                                TGGGAGGGGG  GCT  GCTG
                                |||||||||  |||  ||||
                                ACCCTCCCTC  CGA  CGAC
                                     A_  GA
GAM1121 KDELR1   5' CAGCCCAGCTACCCGTTC    23296     G   C
                                GAG GGG AGCTGGGCTG
                                ||| ||| ||||||||||
                                CTT CCC TCGACCCGAC
                                  G   A
GAM1121 KIAA0275 3' CAGCCCAGCCCTGACCCCT   29323      G __
                                AGGGG CA  GCTGGGCTG
                                ||||| ||  |||||||||
                                TCCCC GT  CGACCCGAC
                                   A  CC
GAM1121 KIAA0285 3' TCAACCCTCACCCTCCTCCCA 29689         CAGCT   C
                                TGGGAGGGGG    GGG TGA
                                ||||||||||    ||| |||
                                ACCCTCCTCC    CCC ACT
                                     CACT_  A
GAM1121 KIAA0321 5' CAGCCACACCACCCTCTCCCA 63046         CAGCTG
                                TGGGAGGGGG     GGCTG
                                ||||||||||     |||||
                                ACCCTCTCCC     CCGAC
                                     ACCACA
GAM1121 KIAA0397 3' CAGCCCAGCCCTGCCCCC    62342        __
                                GGGGGCA  GCTGGGCTG
                                |||||||  |||||||||
                                CCCCCGT  CGACCCGAC
                                    CC
GAM1121 KIAA0542 3' TCAGCCAGCAGCCCCCTCCC  66668         A    G
                                GGGAGGGGGC GCTGG CTGA
                                |||||||||| ||||| ||||
                                CCCTCCCCCG CGACC GACT
                                     A    _
GAM1121 KIAA0792 3' CAGCCCAGCAGTCCCTCC    28763       G A
                                GGAGGGG C GCTGGGCTG
                                ||||||| | |||||||||
                                CCTCCCT G CGACCCGAC
                                    _ A
GAM1121 KIAA1023 3' CAGCCCAGCCTGTTCTCTCCCA 34675           _
                                TGGGAGGGGGCAG CTGGGCTG
                                |||||||||||| ||||||||
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                                ACCCTCTCTTGTC GACCCGAC
                                      C
GAM1121  KIAA1029  5'  CCAGCTGACCACCCCTCCCA  24424        __ _
                                TGGGAGGGG  G CAGCTGG
                                |||||||||  | |||||||
                                ACCCTCCCC  C GTCGACC
                                     AC A
GAM1121  KIAA1100  3'  TCAGCCTGGTCCCACCCCCA  30443     A _  CA  TG
                                TGGG GG GGG  GC  GGCTGA
                                |||| || |||  ||  ||||||
                                ACCC CC CCC  TG  CCGACT
                                  _ A  __ GT
GAM1121  KIAA1130  3'  CACGCCCACCCCCTCCCA    63078        CAGC    _
                                TGGGAGGGGG   TGGGC TG
                                ||||||||||   ||||| ||
                                ACCCTCCCCC   ACCCG AC
                                     _____   C
GAM1121  KIAA1317  5'  TCAACCCAACCTCCTCTCA   87214        CAGC   C
                                TGGGAGGGGG   TGGG TGA
                                ||||||||||   |||| |||
                                ACTCTCCTCC   ACCC ACT
                                     A___    A
GAM1121  KIAA1514  3'  CAGCCAGCTGCCCCCTTCCA  39325            G
                                TGGGAGGGGGCAGCTGG CTG
                                |||||||||||||||| |||
                                ACCTTCCCCCGTCGACC GAC
                                                _
GAM1121  KIAA1554  3'  CAACCCTGACCTTCCCCCTCCC 96852        C  CT__  C
            A                    TGGGAGGGGG AG   GGG TG
                                ||||||||||  ||   ||| ||
                                ACCCTCCCCC TC   CCC AC
                                     T  CAGT   A
GAM1121  KIAA1582  5'  CAACCCAGCTGCCTGGCCT   65984    AGG        C
                                GGG   GGGCAGCTGGG TG
                                |||   |||||||||||  ||
                                TCC   TCCGTCGACCC AC
                                  GG_         A
GAM1121  KIAA1762  3'  CAGCAGAGTCCTGCCTCCTCCC 64528          __ GG
            A                    TGGGAGGGGGCAG  CT  GCTG
                                |||||||||||||  ||  ||||
                                ACCCTCCTCCGTC  GA  CGAC
                                      CT  GA
GAM1121  KIAA1831  3'  CCATTGCTCCACGCCCTCCCA  64522        _____   C
                                TGGGAGGG    GGCAG TGG
                                ||||||||    ||||| |||
                                ACCCTCCC    TCGTT ACC
                                    GCACC   _
GAM1121  KIAA1879  5'  CCATGCTGGCCACCCCCTCC   73934        ____   _
                                GGAGGGGG   CAGC TGG
                                ||||||||   |||| |||
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                                CCTCCCCC   GTCG ACC
                                    ACCG   T
GAM1121 KIAA1893 3' CAGCCCCATCCCCTCTCCCA  73587        CAGCT
                                TGGGAGGGGG    GGGCTG
                                ||||||||||    ||||||
                                ACCCTCTCCC    CCCGAC
                                    CTAC_
GAM1121 KIAA1957 3' CCGGGACGCCCCCTCCCA    76214        AG  G
                                TGGGAGGGGGC  CT GG
                                ||||||||||  || ||
                                ACCCTCCCCCG  GG CC
                                     CA  G
GAM1121 MGC1127  3' CACCCCACACCCCTCCCA    54331        GCAGC   C
                                TGGGAGGGG    TGGG TG
                                |||||||||    |||| ||
                                ACCCTCCCC    ACCC AC
                                    AC___   C
GAM1121 MGC13057 5' CAGCAAGCCCCCCTCCCA    51283        CA   GG
                                TGGGAGGGGG  GCT  GCTG
                                ||||||||||  |||  ||||
                                ACCCTCCCCC  CGA  CGAC
                                    __  A_
GAM1121 MGC14436 5' TCAGCCGAAAGCCCCCCGCCCA 52930     A    CA   G__
                                TGGG GGGGG  GCT   GGCTGA
                                |||| |||||  |||   ||||||
                                ACCC CCCCC  CGA   CCGACT
                                  G    __  AAG
GAM1121 MGC14832 3' CAGCCACCTCATACCCCCTTCC 51339        CAGCTG___
            CA                  TGGGAGGGGG       GGCTG
                                ||||||||||       |||||
                                ACCCTTCCCC       CCGAC
                                    CATACTCCA
GAM1121 MGC15416 3' TCAGCCCGACTGCCCTCCTCCC 51406       _    C
            A                   TGGGAGG GGGCAG TGGGCTGA
                                ||||||| |||||| ||||||||
                                ACCCTCC CCCGTC GCCCGACT
                                    T     A
GAM1121 MGC15476 3' CCAGCTATGGCCCCCTCTCA  59607         ___
                                TGGGAGGGGGC   AGCTGG
                                ||||||||||   ||||||
                                ACTCTCCCCCG   TCGACC
                                     GTA
GAM1121 MGC4707  3' TCAGCCCAGCCAGTGGCCCC  44364     G ___
                                GGGG CA   GCTGGGCTGA
                                |||| ||   ||||||||||
                                CCCC GT   CGACCCGACT
                                  G  GAC
GAM1121 MIL1     3' CCAGTGGCACCCCCTCCCA   31725        CA__
                                TGGGAGGGGG   GCTGG
                                |||||||||   |||||
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                                ACCCTCCCCC   TGACC
                                     ACGG
GAM1121 NFAT5   5' CAGCCTCCCCCCCTCCCA   57761        CAGCT
                                TGGGAGGGGG   GGGCTG
                                ||||||||||   ||||||
                                ACCCTCCCCC   TCCGAC
                                     CC___
GAM1121 NKD1    3' TCAACTCTGCCCCACCCCA  53588    AG     CT  GC
                                TGGG  GGGGCAG  GG  TGA
                                ||||  |||||||  ||  |||
                                ACCC  CCCCGTC  TC  ACT
                                  CA      __  A_
GAM1121 NKD1    3' TCAGCCCACACCCTTCCCA  53589       GCAGC
                                TGGGAGGGG   TGGGCTGA
                                |||||||||   ||||||||
                                ACCCTTCCC   ACCCGACT
                                     AC___
GAM1121 OAZ2    5' CCTGCGCCGCCTCCTCCCA  11875        A  _
                                TGGGAGGGGGC GC TGGG
                                |||||||||||  || ||||
                                ACCCTCCTCCG CG GTCC
                                      C  C
GAM1121 PF1     5' TCAGGAGCGCCCCCTCCC   96834        A  GGG
                                GGGAGGGGGC GCT  CTGA
                                ||||||||||  |||  ||||
                                CCCTCCCCCG CGA  GACT
                                     _  G__
GAM1121 PIP5K1C  3' TCAGGCTCCCCGCCCCCTCC  71308       AGCT  G
                                GGAGGGGGC   GG CTGA
                                |||||||||   || ||||
                                CCTCCCCCG   TC GACT
                                     CCCC  G
GAM1121 PLAGL2   3' CAGCAATGAGCTGTCCCCCTCC 70954        _   GG__
            CA                    TGGGAGGGGG CAGCT   GCTG
                                |||||||||| |||||   ||||
                                ACCCTCCCCC GTCGA   CGAC
                                      T    GTAA
GAM1121 PPY2    3' CAGCCCAGCTCTCCCCTCC   41173       C
                                GGAGGGGG AGCTGGGCTG
                                |||||||| ||||||||||
                                CCTCCCCT TCGACCCGAC
                                     C
GAM1121 QKI     5' CAGCCCAGAGAGACCCCCCG  66042     A  GGCAG
                                TGGG GGG    CTGGGCTG
                                |||| |||    ||||||||
                                GCCC CCC    GACCCGAC
                                  _  AGAGA
GAM1121 RPH3A   3' TCAGCCCACCTCCCTCACCA  30937    _     CAGC
                                TGG GAGGGGG   TGGGCTGA
                                ||| |||||||   ||||||||
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                                ACC CTCCCTC   ACCCGACT
                                  A     C___
GAM1121 SCAMP-4  3' CAGCCTCGCCCCCTCCC    55341        AGCT
                                GGGAGGGGGC   GGGCTG
                                ||||||||||   ||||||
                                CCCTCCCCCG   TCCGAC
                                     C___
GAM1121 SCGF    5' CCAGAGGCCACCCCTCCCA   12944        __ AG
                                TGGGAGGGG  GC  CTGG
                                |||||||||  ||  ||||
                                ACCCTCCCC  CG  GACC
                                     AC  GA
GAM1121 SEC14L1  3' CATCCCCTGCCCCCTCCCA   13005          CT   C
                                TGGGAGGGGGGCAG  GGG TG
                                ||||||||||||  ||| ||
                                ACCCTCCCCCGTC  CCC AC
                                      __   T
GAM1121 SFXN5   3' AGGCTGCCTGCCCCATCCCA  58645     G     CT  G
                                TGGGA GGGGCAG  GG CT
                                |||||| |||||||  || ||
                                ACCCT CCCCGTC  TC GA
                                   A      CG  G
GAM1121 SLC26A10 5' CCAGATTGCCCCCTCTCA    56840          _
                                TGGGAGGGGGGCAG CTGG
                                |||||||||||| ||||
                                ACTCTCCCCCGTT GACC
                                      A
GAM1121 SOX17   5' TCATTCCCCACCCCCTCCC   42631       CAGC   C__
                                GGGAGGGGG   TGGG  TGA
                                |||||||||   ||||  |||
                                CCCTCCCCC   ACCC  ACT
                                     _____   CTT
GAM1121 SSH-3   3' CACCCCCGCCCCCTCCC     35788        AGCT  C
                                GGGAGGGGGC   GGG TG
                                ||||||||||   ||| ||
                                CCCTCCCCCG   CCC AC
                                     C___   C
GAM1121 STMN3   3' CAGCCCCAACACCCTTCCCA  32463       GCAGCT
                                TGGGAGGGG    GGGCTG
                                |||||||||    ||||||
                                ACCCTTCCC    CCCGAC
                                     ACAAC_
GAM1121 TACTILE  3' TCAGCCCAGACTCCTGCCA   20593    G   GCAG
                                TGG AGGGG   CTGGGCTGA
                                ||| |||||   |||||||||
                                ACC TCCTC   GACCCGACT
                                  G   A___
GAM1121 TLN1    3' CCAAGTGCCTGCCCCTCCCCA 21901     AG     _ ___
                                TGGG  GGGGCAG C   TGG
                                ||||  ||||||| |   |||
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                                ACCC  CCCCGTC G   ACC
                                  CT      C TGA
GAM1121  TOMM34    3'  CAGCCCAGCTAGCTGATC    23314    GGG  _
                                GA   GGC AGCTGGGCTG
                                ||   ||| ||||||||||
                                CT   TCG TCGACCCGAC
                                 AG_   A
GAM1121  WFDC2     3'  CAGCCCACCTGCCCTCCCC    55778     A       C
                                GGG GGGGGCAG TGGGCTG
                                ||| |||||||| |||||||
                                CCC CTCCCGTC ACCCGAC
                                  _       C
GAM1121  WFDC2     3'  CAGCCCACCTGCCCTCCCC    55779     A       C
                                GGG GGGGGCAG TGGGCTG
                                ||| |||||||| |||||||
                                CCC CTCCCGTC ACCCGAC
                                  _       C
GAM1121  YARS      3'  CAGCCCAGCATCTTCCCCCC   14853     A     CA
                                GGG GGGGG  GCTGGGCTG
                                ||| |||||  |||||||||
                                CCC CCTTC  CGACCCGAC
                                  C     TA
GAM1121  LOC112476 3'  CCTGGCCGCCTCCTCCCA    59785          A  TG
                                TGGGAGGGGGC GC  GG
                                |||||||||| ||  ||
                                ACCCTCCTCCG CG  CC
                                       C  GT
GAM1121  LOC113730 5'  CAGCCCAGACCCTCCCCCA   73499      A    CAG
                                TGGG GGGGG   CTGGGCTG
                                |||| |||||   ||||||||
                                ACCC CCTCC   GACCCGAC
                                  _    CA_
GAM1121  LOC115110 5'  CAGCCCAGCCCCGGTTCCTCCC 72173       ____   CA
                                GGGAGG   GGG  GCTGGGCTG
                                ||||||   |||  |||||||||
                                CCCTCC   CCC  CGACCCGAC
                                   TTGG  __
GAM1121  LOC116150 3'  TCAGCCCAGCTACTTCCC    57425       GGGC
                                GGGAGG   AGCTGGGCTGA
                                ||||||   ||||||||||
                                CCCTTC   TCGACCCGACT
                                   A___
GAM1121  LOC123775 3'  TCATTTCCCACCCACCCCCCA  76143     A  _  CAGC   C__
                                TGGG GG GGG   TGGG   TGA
                                |||| || |||   ||||   |||
                                ACCC CC CCC   ACCC   ACT
                                  C  A  ____   TTT
GAM1121  LOC124222 3'  CAGCCCAGAGCCTCCTC     74745        AG
                                GAGGGGGC  CTGGGCTG
                                ||||||||  ||||||||
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                                CTCCTCCG  GACCCGAC
                                   A_
GAM1121  LOC124930 3'  CACCCCCACCCCTTCCCA    74822        CAGCT   C
                                TGGGAGGGGG    GGG TG
                                ||||||||||    ||| ||
                                ACCCTTCCCC    CCC AC
                                   AC____   C
GAM1121  LOC130497 3'  GCGGGGCAGCCCCCTCCCA   75452         A   GG
                                TGGGAGGGGGC GCT  GC
                                |||||||||||| |||  ||
                                ACCCTCCCCCG CGG  CG
                                   A   GG
GAM1121  LOC134187 5'  CCACTTCTGCCCCCTTCCA   76464          C__
                                TGGGAGGGGGCAG   TGG
                                ||||||||||||   |||
                                ACCTTCCCCCGTC   ACC
                                   TTC
GAM1121  LOC138389 5'  CAGCCCAGGCACCCTCC     76728       G  AG
                                GGAGGG GC  CTGGGCTG
                                |||||| ||  ||||||||
                                CCTCCC CG  GACCCGAC
                                  A  __
GAM1121  LOC143677 3'  CACTTGGCGCCCCCTCCCA   83893         A  TG  C
                                TGGGAGGGGGC GC  GG TG
                                |||||||||||| ||  || ||
                                ACCCTCCCCCG CG  TC AC
                                   _  GT  _
GAM1121  LOC143915 5'  CCATTATCTGCCCCCTCCCA  83904          C___
                                TGGGAGGGGGCAG    TGG
                                ||||||||||||    |||
                                ACCCTCCCCCGTC    ACC
                                   TATT
GAM1121  LOC144262 5'  CCAAGTGTAGCCCCTCCCA   77259         __  GC
                                TGGGAGGGG  GCA  TGG
                                |||||||||  |||  |||
                                ACCCTCCCC  TGT  ACC
                                   GA   GA
GAM1121  LOC144402 5'  CCAAGGCGCCTCCTCCCA    77323         A  __
                                TGGGAGGGGGC GCT  GG
                                |||||||||||| |||  ||
                                ACCCTCCTCCG CGG  CC
                                   _   AA
GAM1121  LOC145678 3'  CCAGGGTGACCCCTCCCA    84432        G  G _
                                TGGGAGGGG CA C TGG
                                ||||||||| || | |||
                                ACCCTCCCC GT G ACC
                                   A  G G
GAM1121  LOC145757 3'  CAGCCCAGGCACCTCCTCCCA  77919         CAG
                                TGGGAGGGGG   CTGGGCTG
                                |||||||||   ||||||||
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                                ACCCTCCTCC   GACCCGAC
                                     ACG
GAM1121  LOC145989 3'  CCCAGCCACCTCCTCCCA    60289         CA
                                TGGGAGGGGG  GCTGGG
                                ||||||||||  ||||||
                                ACCCTCCTCC  CGACCC
                                     AC
GAM1121  LOC146562 3'  CAGCCCCCAGGCCCTCTCCCA  58251          AGCT
                                TGGGAGGGGGC   GGGCTG
                                ||||||||||    ||||||
                                ACCCTCTCCCG   CCCGAC
                                      GACC
GAM1121  LOC146782 3'  CATGCCCAGCCCCTCCCA    76804        GGCA     _
                                TGGGAGGG   GCTGGGC TG
                                ||||||||   ||||||| ||
                                ACCCTCCC   CGACCCG AC
                                    ____      T
GAM1121  LOC147136 5'  CAGCAAGCTGCCCCCTCC    78858          GG
                                GGAGGGGGCAGCT  GCTG
                                ||||||||||||  ||||
                                CCTCCCCCGTCGA  CGAC
                                       A_
GAM1121  LOC148181 5'  CAGCCCAGCTCATGCCTCCC   79430       GGGC
                                GGGAGG   AGCTGGGCTG
                                ||||||   ||||||||||
                                CCCTCC   TCGACCCGAC
                                   GTAC
GAM1121  LOC148250 5'  TCAGAGCATGCCCCCTCCCA   79495          _  GGG
                                TGGGAGGGGGCA GCT   CTGA
                                |||||||||||| |||   ||||
                                ACCCTCCCCCGT CGA   GACT
                                       A  ___
GAM1121  LOC148697 3'  CAACCCAGCTGCCTTACCT    79675     AG         C
                                GGG  GGGGCAGCTGGG TG
                                |||  |||||||||||| ||
                                TCC  TTCCGTCGACCC AC
                                  A_         A
GAM1121  LOC149134 5'  TCACATGACTGTCCCCTCCCA  85521          CT GGC
                                TGGGAGGGGGCAG  G   TGA
                                ||||||||||||  |   |||
                                ACCCTCCCCTGTC  T   ACT
                                       AG AC_
GAM1121  LOC150368 3'  CCTGACTGCCCCCTCCCA    80514          CT
                                TGGGAGGGGGCAG  GGG
                                ||||||||||||  |||
                                ACCCTCCCCCGTC  TCC
                                       AG
GAM1121  LOC150886 3'  TCAGCCCAACACGCTCCCCTCC 86333         _  AGC_
            CA                   TGGGAGGGG GC    TGGGCTGA
                                |||||||| ||    ||||||||
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                                ACCCTCCCC CG    ACCCGACT
                                     T  CACA
GAM1121  LOC151470 3'  CCATCTCTACCCCCTCCCA   81055         C  C__
                                TGGGAGGGGG AG   TGG
                                |||||||||| ||   |||
                                ACCCTCCCCC TC   ACC
                                     A  TCT
GAM1121  LOC154222 5'  TCAGCGTCACCTCCTCCCA   87393         CA  TGG
                                TGGGAGGGGG  GC   GCTGA
                                |||||||||  ||   |||||
                                ACCCTCCTCC  TG   CGACT
                                     AC  ___
GAM1121  LOC154990 5'  CAGCCCAGCTCATGCCTCCC   82147       GGGC
                                GGGAGG    AGCTGGGCTG
                                ||||||    ||||||||||
                                CCCTCC    TCGACCCGAC
                                   GTAC
GAM1121  LOC155179 3'  CAGCCCAGCCTGTTCTCTCCCA 82223           _
                                TGGGAGGGGGCAG CTGGGCTG
                                |||||||||||| ||||||||
                                ACCCTCTCTTGTC GACCCGAC
                                       C
GAM1121  LOC157349 5'  CCAGCGGGCACCACCCTCCCA  82330         _  CA___
                                TGGGAGGG GG     GCTGG
                                |||||||| ||     |||||
                                ACCCTCCC CC     CGACC
                                     A  ACGGG
GAM1121  LOC163682 3'  CAGCCCTTCCCACCCCCA     88398      A  _   CAGCT
                                TGGG GG GGG     GGGCTG
                                |||| || |||     ||||||
                                ACCC CC CCC     CCCGAC
                                  _  A   TT___
GAM1121  LOC163682 3'  CAGCCTCACCCACCCCCTCC   88399         CAGC  _
                                GGAGGGGG    TG GGCTG
                                ||||||||    || |||||
                                CCTCCCCC    AC CCGAC
                                     ACCC  T
GAM1121  LOC170393 3'  CAGCCCCTGCTTGGCCCCTCCC 83733         G  _  T_
           A                     TGGGAGGGG CA GC  GGGCTG
                                |||||||| || ||  ||||||
                                ACCCTCCCC GT CG  CCCGAC
                                     G  T  TC
GAM1121  LOC196337 5'  TCAGCCCAGCTATGGCCC     89026      ___
                                GGGC   AGCTGGGCTGA
                                ||||   ||||||||||
                                CCCG   TCGACCCGACT
                                  GTA
GAM1121  LOC200301 5'  TCAGAAATGCCCCCTCCCA    90153          GCTGGG
                                TGGGAGGGGGCA     CTGA
                                ||||||||||     ||||
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                                ACCCTCCCCCGT     GACT
                                      AAA___
GAM1121  LOC203954 5'  GGCCCCGCCCCTTCCCA     92339          AGCT
                                TGGGAGGGGGC    GGGCT
                                ||||||||||    |||||
                                ACCCTTCCCCG    CCCGG
                                      C___
GAM1121  LOC205095 3'  CCAGTGCACCCCGTCCCA     92381      _   _  G
                                TGGGA GGGG GCA CTGG
                                ||||| |||| ||| ||||
                                ACCCT CCCC CGT GACC
                                   G    A  _
GAM1121  LOC219562 3'  CATGCCCAGCCCCTCCCA     92448        GGCA      _
                                TGGGAGGG    GCTGGGC TG
                                ||||||||    ||||||| ||
                                ACCCTCCC    CGACCCG AC
                                     _____      T
GAM1121  LOC220018 5'  TCAACCCAAGGGACCCCTCCC  95030         GCAGC    C
                                GGGAGGGG     TGGG TGA
                                ||||||||     |||| |||
                                CCCTCCCC     ACCC ACT
                                     AGGGA    A
GAM1121  LOC220739 3'  TCAGCCCAGCTCTGCCTCGCA  94528    G    G  C
                                TG GAGG GG AGCTGGGCTGA
                                || |||| || ||||||||||
                                AC CTCC TC TCGACCCGACT
                                 G    G  _
GAM1121  LOC221486 3'  TCAGCCCAGCACCTGCTCCCA  92659       G   CA
                                TGGGAG GGG  GCTGGGCTGA
                                |||||| |||  ||||||||||
                                ACCCTC TCC  CGACCCGACT
                                   G   A_
GAM1121  LOC254295 5'  TCAGCCCAGCTGCTTGGCCT   97897     AGG
                                GGG   GGGCAGCTGGGCTGA
                                |||   ||||||||||||||||
                                TCC   TTCGTCGACCCGACT
                                  GG_
GAM1121  LOC255612 5'  CAGCCCCTGTCCCCCCCCA    99365      A       CT
                                TGGG GGGGGCAG  GGGCTG
                                |||| ||||||||  ||||||
                                ACCC CCCCTGTC  CCCGAC
                                   C       __
GAM1121  LOC255975 3'  CAGCCCAGCTCATGCCTCCC   97572       GGGC
                                GGGAGG    AGCTGGGCTG
                                ||||||    ||||||||||
                                CCCTCC    TCGACCCGAC
                                   GTAC
GAM1121  LOC256867 5'  CACGTCCTGCCCCCCGCCA    96511     GA      GCT   _
                                TGG  GGGGGCA   GGGC TG
                                |||  |||||||   |||| ||
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                                ACC  CCCCCGT   CCTG AC
                                  GC      ___    C
GAM1121  LOC257016 3'  TCAGCCCAGCCCACCCTC    96753      _ CA
                                GAGGG GG  GCTGGGCTGA
                                |||||  ||  ||||||||||
                                CTCCC CC  CGACCCGACT
                                   A  __
GAM1121  LOC257181 3'  CATGCCCAGCCCCTCCCA    96229        GGCA     _
                                TGGGAGGG    GCTGGGC TG
                                ||||||||    |||||||  ||
                                ACCCTCCC    CGACCCG AC
                                     _____      T
GAM1121  LOC257457 5'  CCAAGCCTGCCCCCTTCCA   63315           _ _
                                TGGGAGGGGGCAG CT GG
                                ||||||||||||| ||  ||
                                ACCTTCCCCCGTC GA CC
                                        C  A
GAM1121  LOC51107  5'  CAGCTGGCGCGCCCCTCCCA  32607         _  A  TG G
                                TGGGAGGGG GC GC  G CTG
                                |||||||||  ||  ||  |  |||
                                ACCCTCCCC CG CG  C GAC
                                     G  _  GT _
GAM1121  LOC51308  3'  CAGCAGTCGCCTCCTCCCA   33960          A   GG
                                TGGGAGGGGGC GCT  GCTG
                                ||||||||||| |||  ||||
                                ACCCTCCTCCG TGA  CGAC
                                      C  __
GAM1121  LOC51713  3'  CCGGGCGCGGCCCCCTCCCA  33228          A__   G
                                TGGGAGGGGGC   GCT GG
                                ||||||||||   ||| ||
                                ACCCTCCCCCG   CGG CC
                                      GCG   G
GAM1121  LOC91252  3'  CCAGAGCTGCCCACCTCCCA  65937        _      G_
                                TGGGAGG GGGCAGCT  GG
                                |||||||  ||||||||  ||
                                ACCCTCC CCCGTCGA  CC
                                    A       GA
GAM1121  LOC91300  5'  CAGCCCCTGCTCAGCCCCTCCC 96233         _____   CT
            A                    TGGGAGGGG   GCAG  GGGCTG
                                 |||||||||   ||||  ||||||
                                 ACCCTCCCC   CGTC  CCCGAC
                                      GACT   __
GAM1121  LOC91300  5'  CAGCCCCTGCTCAGCCCCTCCC 96234         _____   CT
            A                    TGGGAGGGG   GCAG  GGGCTG
                                 |||||||||   ||||  ||||||
                                 ACCCTCCCC   CGTC  CCCGAC
                                      GACT   __
GAM1121  LOC91409  3'  TCAGCCCAGCCCTAACCCTC  66574      GGCA_
                                GAGGG    GCTGGGCTGA
                                |||||    ||||||||||
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                                CTCCC    CGACCCGACT
                                   AATCC
GAM1121  LOC92223  5'  CAACCCGCCGCTGCCCCCTCCC 69044          __   C
                                GGGAGGGGGCAGC  TGGG TG
                                |||||||||||||  |||| ||
                                CCCTCCCCCGTCG  GCCC AC
                                     CC    A
GAM1122  CYP8B1    3'  TATCCAAAATATTGGCATTTCA 16541        TCACC__
                                TGGAATGCCA      GGATA
                                ||||||||||      |||||
                                ACTTTACGGT      CCTAT
                                     TATAAAA
GAM1122  DAZ       3'  TATCCCGATTCAGCATTTCA   83006       C__   ACC
                                TGGAATGC   ATC   GGATA
                                ||||||||   |||   |||||
                                ACTTTACG   TAG   CCTAT
                                     ACT   C__
GAM1122  FGF5      3'  TGGCTGCATAGTATTCCA    53673       C  _  _
                                TGGAATGC AT CA CCG
                                |||||||| || || |||
                                ACCTTATG TA GT GGT
                                     A  C  C
GAM1122  FGF5      3'  TGGCTGCATAGTATTCCA    53674       C  _  _
                                TGGAATGC AT CA CCG
                                |||||||| || || |||
                                ACCTTATG TA GT GGT
                                     A  C  C
GAM1122  ITGAM     3'  CCGCTGCATAGTATTCCA    72308       C  _  C
                                TGGAATGC AT CA CGG
                                |||||||| || || |||
                                ACCTTATG TA GT GCC
                                     A  C  C
GAM1122  OPHN1     3'  TGGCTGCATAGTATTCCA    11913       C  _  _
                                TGGAATGC AT CA CCG
                                |||||||| || || |||
                                ACCTTATG TA GT GGT
                                     A  C  C
GAM1122  PTGS1     3'  ATCCGGTGGCCTATTCCA    55471       CCA
                                TGGAATG   TCACCGGAT
                                |||||||   |||||||||
                                ACCTTAT   GGTGGCCTA
                                    CC_
GAM1122  AD024     3'  TGGCTGCATAGTATTCCA    40712       C  _  _
                                TGGAATGC AT CA CCG
                                |||||||| || || |||
                                ACCTTATG TA GT GGT
                                     A  C  C
GAM1122  CCR6      3'  TATCCGCCTGGCATTTCA    16447        TCAC
                                TGGAATGCCA   CGGATA
                                ||||||||||   ||||||
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                                ACTTTACGGT   GCCTAT
                                     CC__
GAM1122 HXCP2    3' TGGCTGCATAGTATTCCA    51805       C _ _
                                TGGAATGC AT CA CCG
                                |||||||| || || |||
                                ACCTTATG TA GT GGT
                                     A  C  C
GAM1122 PP3501   5' TGGCTGCATAGTATTCCA    41687       C _ _
                                TGGAATGC AT CA CCG
                                |||||||| || || |||
                                ACCTTATG TA GT GGT
                                     A  C  C
GAM1122 PSK      5' TATCCGGGGTTCATTCC     32881       CC   A
                                GGAATG  ATC CCGGATA
                                ||||||  ||| |||||||
                                CCTTAC  TGG GGCCTAT
                                   T_   _
GAM1122 SPINLW1  3' TGGCTGCATAGTATTCCA    40232       C _ _
                                TGGAATGC AT CA CCG
                                |||||||| || || |||
                                ACCTTATG TA GT GGT
                                     A  C  C
GAM1122 TRIM4    3' TGGCTGCATAGTATTCCA    53409       C _ _
                                TGGAATGC AT CA CCG
                                |||||||| || || |||
                                ACCTTATG TA GT GGT
                                     A  C  C
GAM1122 LOC124976 3' CTGGCTGCTGGCATTCCA    74841         T _
                                TGGAATGCCA CA CCGG
                                |||||||||| || ||||
                                ACCTTACGGT GT GGTC
                                      C  C
GAM1122 LOC147525 3' TATCCAAACGAGGCATTCCA  79007         A  ACC_
                                TGGAATGCC TC    GGATA
                                ||||||||| ||    |||||
                                ACCTTACGG AG    CCTAT
                                     _  CAAA
GAM1122 LOC150568 5' TATCCAATAGGAAGCATTCCA 86227         CA  ACC__
                                TGGAATGC  TC    GGATA
                                ||||||||  ||    |||||
                                ACCTTACG  AG    CCTAT
                                     A_  GATAA
GAM1122 LOC203427 3' TATCATGATGGCATTCCA    90922           CCG
                                TGGAATGCCATCA   GATA
                                ||||||||||||   ||||
                                ACCTTACGGTAGT   CTAT
                                       A__
GAM1122 LOC256905 3' TGGCTGCATAGTATTCCA    98664       C _ _
                                TGGAATGC AT CA CCG
                                |||||||| || || |||
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                                ACCTTATG TA GT GGT
                                     A  C  C
GAM1122  LOC57086  3'  TGGCTGCATAGTATTCCA    40130        C  _  _
                                TGGAATGC AT CA CCG
                                |||||||| || || |||
                                ACCTTATG TA GT GGT
                                     A  C  C
GAM1123  NDUFV3   5'  AGAAGCCAAGAGAAAGAT    41138    AG       C
                                ATT  TCTCTTGGCT CT
                                |||  |||||||||| ||
                                TAG  AGAGAACCGA GA
                                  AA        A
GAM1123  DRIL2    3'  TGCCAGGAGCCAAGAGC     22355   T         A
                                G CTCTTGGCTCCT GCA
                                | ||||||||||| |||
                                C GAGAACCGAGGA CGT
                                _          C
GAM1123  TRPC3    3'  GCCTCCAAGAGACTATCA    13859     T       CTCCTA
                                TGAT AGTCTCTTGG     GC
                                |||| ||||||||||     ||
                                ACTA TCAGAGAACC     CG
                                   _        TC_____
GAM1123  USP3     3'  AGGAGCCAAGGGGATAACA   91250    A   GT
                                TG TTA  CTCTTGGCTCCT
                                || |||  ||||||||||||
                                AC AAT  GGGAACCGAGGA
                                 _  AG
GAM1123  LOC154104 5'  GCCAGGAGCTGAGACTAGCCA  88624    AT      TT      A
                                TG  TAGTCTC  GGCTCCT GC
                                ||  |||||||  ||||||| ||
                                AC  ATCAGAG  TCGAGGA CG
                                 CG      __      C
GAM1124  GABRR2   3'  AACAATGCAGCAGCTACTGGAC 10753          CGAACAGT
                                GTCCAGTAGC       TTGTT
                                ||||||||||       |||||
                                CAGGTCATCG       AACAA
                                      ACGACGT_
GAM1124  KLHL1    3'  AACAAACTGTCCTACT      40867      CCGA
                                AGTAG   ACAGTTTGTT
                                |||||   ||||||||||
                                TCATC   TGTCAAACAA
                                  C___
GAM1124  MS4A2    5'  AACAAACTGCACCCACTGAAC  41974    C   AGCCGAA
                                GT CAGT      CAGTTTGTT
                                || ||||      |||||||||
                                CA GTCA      GTCAAACAA
                                 A   CCCAC__
GAM1124  SPK      5'  AACAAAGACCCACACTACTGGA 17872          CCGAACAG
            CA                    TGTCCAGTAG       TTTGTT
                                |||||||||       ||||||
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                                ACAGGTCATC       AAACAA
                                     ACACCCAG
GAM1124  VAPA     3'  AACAAACTGTTCGGCTACTGGA 14544
              CA                   TGTCCAGTAGCCGAACAGTTTGTT
                                   ||||||||||||||||||||||||
                                   ACAGGTCATCGGCTTGTCAAACAA

GAM1124  VAPA     3'  AACTGTTCGGCTACTGGACA  14545
                                   TGTCCAGTAGCCGAACAGTT
                                   ||||||||||||||||||||
                                   ACAGGTCATCGGCTTGTCAA

GAM1124  FLJ13315  3'  AACAAATAAAGGGCTACTG   47196        GAACA
                                   CAGTAGCC    GTTTGTT
                                   ||||||||    |||||||
                                   GTCATCGG    TAAACAA
                                       GAAA_
GAM1124  SYT13    3'  AACAAACTCTGAGGCCACCAGC 95089     CCA  A   GAAC
              A                     TGT   GT GCC    AGTTTGTT
                                   |||   || |||    ||||||||
                                   ACG   CA CGG    TCAAACAA
                                     AC_  C   AGTC
GAM1124  LOC150372 5'  AACAAACTGCCACCCTGGAC   80600       TAGCCGAA
                                   GTCCAG       CAGTTTGTT
                                   ||||||       |||||||||
                                   CAGGTC       GTCAAACAA
                                      CCACC___
GAM1124  LOC253367 3'  GGACTCGGCCAGCTGGACA   99437        A_    ACA
                                   TGTCCAGT  GCCGA   GTTT
                                   ||||||||  |||||   ||||
                                   ACAGGTCG  CGGCT   CAGG
                                       AC    ___
GAM1124  LOC51622  5'  AACAAACTGAGTTCCACTG   32203     AGCC   __
                                   CAGT   GAAC  AGTTTGTT
                                   ||||   ||||  ||||||||
                                   GTCA   CTTG  TCAAACAA
                                     C___    AG
GAM1125  SCAMP1   3'  GCTAAATAAATATTCTCC    54500     T     C
                                   GGA AATATT ATTTAGC
                                   ||| |||||| |||||||
                                   CCT TTATAA TAAATCG
                                     C     A
GAM1125  SCAMP1   3'  GCTAAATAAATATTCTCC    54501     T     C
                                   GGA AATATT ATTTAGC
                                   ||| |||||| |||||||
                                   CCT TTATAA TAAATCG
                                     C     A
GAM1125  NX-17    3'  TGAATATCAGCCCCTAATA   40706        ATA_
                                   TATTAGGG   ATATTCA
                                   ||||||||   |||||||
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                              ATAATCCC   TATAAGT
                                  CGAC
GAM1125  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
             TA                  TATTAGGGATAATATTCATTTAGC
                                 ||||||||||||||||||||||||
                                 ATAATCCCTATTATAAGTAAATCG

GAM1126  SCAMP1   3'  GCTAAATAAATATTCTCC    18013    T    C
                                 GGA AATATT ATTTAGC
                                 ||| |||||| |||||||
                                 CCT TTATAA TAAATCG
                                   C     A
GAM1126  SCAMP1   3'  GCTAAATAAATATTCTCC    54501    T    C
                                 GGA AATATT ATTTAGC
                                 ||| |||||| |||||||
                                 CCT TTATAA TAAATCG
                                   C     A
GAM1126  NX-17    3'  TGAATATCAGCCCCTAATA   40706       ATA_
                                 TATTAGGG   ATATTCA
                                 ||||||||   |||||||
                                 ATAATCCC   TATAAGT
                                     CGAC
GAM1126  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
             TA                  TATTAGGGATAATATTCATTTAGC
                                 ||||||||||||||||||||||||
                                 ATAATCCCTATTATAAGTAAATCG

GAM1127  SCAMP1   3'  GCTAAATAAATATTCTCC    54500    T    C
                                 GGA AATATT ATTTAGC
                                 ||| |||||| |||||||
                                 CCT TTATAA TAAATCG
                                   C     A
GAM1127  SCAMP1   3'  GCTAAATAAATATTCTCC    54501    T    C
                                 GGA AATATT ATTTAGC
                                 ||| |||||| |||||||
                                 CCT TTATAA TAAATCG
                                   C     A
GAM1127  NX-17    3'  TGAATATCAGCCCCTAATA   40706       ATA_
                                 TATTAGGG   ATATTCA
                                 ||||||||   |||||||
                                 ATAATCCC   TATAAGT
                                     CGAC
GAM1127  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
             TA                  TATTAGGGATAATATTCATTTAGC
                                 ||||||||||||||||||||||||
                                 ATAATCCCTATTATAAGTAAATCG

GAM1128  APOBEC1  3'  AATACCCACCTCTGTGG    20834     TGGT      C
                                 CCAC   GGAGGTGGG ATT
                                 ||||   ||||||||| |||
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                                GGTG   TCTCCACCC TAA
                                  ____       A
GAM1128  DKFZP434K0427 3'  CAATGCCCACCTCTATGCTAG  50498      __
                                CTGGT  GGAGGTGGGCATTG
                                |||||  ||||||||||||||
                                GATCG  TCTCCACCCGTAAC
                                   TA
GAM1128  LOC120973 5'  CATTAGCCACCAGTGGCA    76069          A_
                                TGCCACTGGTGG  GGTG
                                ||||||||||||  ||||
                                ACGGTGACCACC  TTAC
                                      GA
GAM1128  LOC219988 5'  CCACCTCCACAGCAGCA     93261     CA   G
                                TGC  CTG TGGAGGTGG
                                |||  ||| |||||||||
                                ACG  GAC ACCTCCACC
                                  AC  _
GAM1128  LOC255232 3'  CAATGCCCACATCACACAG   98432     _   AG
                                CTG GTGG  GTGGGCATTG
                                ||| ||||  ||||||||||
                                GAC CACT  CACCCGTAAC
                                  A   A_
GAM1129  GSTM4    3'  GTTGCATGACAGCATTGA    7796         C   T  C
                                TCAATGCTG CAT GC AC
                                ||||||||| ||| || ||
                                AGTTACGAC GTA CG TG
                                      A  _  T
GAM1129  USP6     5'  TGGAATCAACAGCAGCATTGA  92784         CA   CCA
                                TCAATGCTGC  TTG   CCA
                                ||||||||||  |||   |||
                                AGTTACGACG  AAC   GGT
                                      AC   TAA
GAM1129  FLJ20154  3'  TGATGATATTCAGACGAAGCAT 73307        GCCA   CCAC_
            TGA                   TCAATGCT    TTG    CATCA
                                |||||||    |||    |||||
                                AGTTACGA    GAC    GTAGT
                                     AGCA   TTATA
GAM1129  FLJ23468  5'  TGATGACTCTGAAAGCATTGA  45247        GC  TTGCCAC
                                TCAATGCT  CA      CATCA
                                ||||||||  ||      |||||
                                AGTTACGA  GT      GTAGT
                                     AA  CTCA___
GAM1129  LZK1     5'  TGACGGTGGCAACGGCAGCGTC 46175    A      A      A
            GG                    TC ATGCTGCC TTGCCACC TCA
                                || |||||||| |||||||| |||
                                GG TGCGACGG AACGGTGG AGT
                                  C       C       C
GAM1129  MGC10715  5'  TGATGGTGGCTTGCTATACATT 44503      CT__  CATT
                                AATG   GC   GCCACCATCA
                                ||||   ||   ||||||||||
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                                TTAC   CG   CGGTGGTAGT
                                  ATAT  TT__
GAM1129  MYT1    3'  GAGGTGGCAATGACATCAT   16980    C  C       A
                                ATG TG CATTGCCACC TC
                                ||| || |||||||||| ||
                                TAC AC GTAACGGTGG AG
                                  T  A       _
GAM1129  RNAH    3'  TGACAGTGGCTGCAGTATTGA  62661         CATT    CA
                                TCAATGCTGC   GCCAC  TCA
                                ||||||||||   |||||  |||
                                AGTTATGACG   CGGTG  AGT
                                      T___    AC
GAM1129  SEMA3E  3'  TGATGATAACAATGGTGTA   25814    T     CCAC
                                TGC GCCATTG   CATCA
                                ||| |||||||   |||||
                                ATG TGGTAAC   GTAGT
                                  _     AATA
GAM1129  LOC112724 5'  TGATGGTGACAGCAGCAGTGA  57308    A     CAT  C
                                TCA TGCTGC   TG CACCATCA
                                ||| ||||||   || ||||||||
                                AGT ACGACG   AC GTGGTAGT
                                  G     ___  A
GAM1129  LOC115749 5'  TGATGAGCTGGTGGCATGCATT 73951       _     _ CAC
           GA                     TCAATGC TGCCATT GC   CATCA
                                ||||||| ||||||| ||   |||||
                                AGTTACG ACGGTGG CG   GTAGT
                                    T      T  A__
GAM1129  LOC147515 3'  ATGGTGGCAGCAGCAGCA    85147       CA
                                TGCTGC  TTGCCACCAT
                                ||||||  ||||||||||
                                ACGACG  GACGGTGGTA
                                   AC
GAM1129  LOC149995 3'  ATGGTGGCAGCAGCAGCA    85981       CA
                                TGCTGC  TTGCCACCAT
                                ||||||  ||||||||||
                                ACGACG  GACGGTGGTA
                                   AC
GAM1129  LOC158835 3'  GGCACTTTGGTGCCAGCATTGA 82879         C  _____
                                TCAATGCTG CAT    TGCC
                                ||||||||| |||    ||||
                                AGTTACGAC GTG    ACGG
                                     C   GTTTC
GAM1129  LOC196337 5'  TGATGGCAGCAGCATTGG    89028         CAT    C
                                TCAATGCTGC   TGCCA CA
                                ||||||||||   ||||| ||
                                GGTTACGACG   ACGGT GT
                                      ___    A
GAM1129  LOC202025 3'  TGATACAAGTTAGGAGCATTGA 91892        G  ATT  CACC
                                TCAATGCT CC   GC    ATCA
                                |||||||| ||   ||    ||||
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                                AGTTACGA GG   TG    TAGT
                                    _ AT_  AACA
GAM1129  LOC51131  3'  GGTGGCAGCAGTTGA      32784     AT    CAT
                                TCA  GCTGC   TGCCACC
                                |||  |||||   |||||||
                                AGT  TGACG   ACGGTGG
                                  __    ____
GAM1129  LOC91431  5'  TGATGGCATCACATGAAAGCAT 57727        GC   _  CCA
             TGA                   TCAATGCT  CAT TG   CCATCA
                                |||||||||  ||| ||   ||||||
                                AGTTACGA  GTA AC   GGTAGT
                                    AA   C  TAC
GAM1130  AQP6     3'  GGCCCCAGGCCCCAGC      55008      A       CTC
                                GCTG GGCCTGGG   GCC
                                |||| ||||||||   |||
                                CGAC CCGGACCC   CGG
                                  C       ____
GAM1130  GCK      5'  CCCAAGCGCCCAGCAATG    5682         A  _  _
                                CATTGCTG GGC CT GGG
                                |||||||| ||| || |||
                                GTAACGAC CCG GA CCC
                                    _   C  A
GAM1130  GGT1     5'  TGTCCCCAGGCCTCAGCAA   26439            CT
                                TTGCTGAGGCCTGGG  CG
                                ||||||||||||||  ||
                                AACGACTCCGGACCC  GT
                                       CT
GAM1130  GNAT1    3'  GACGCACAGACTCAGCAAT   5721         GC   G  _
                                ATTGCTGAG  CTG GC TC
                                |||||||||  ||| || ||
                                TAACGACTC  GAC CG AG
                                    A_   A  C
GAM1130  HAS3     3'  AGGCAAGCGTGTTCTCAGCA  19231        CCT G   C
                                TGCTGAGG   G GCT GCCT
                                ||||||||   | ||| ||||
                                ACGACTCT   T CGA CGGA
                                    TG_ G   A
GAM1130  P23      3'  AGGCGAGCCCTCCCCAGCA   22751      A  CCT
                                TGCTG GG   GGGCTCGCCT
                                |||||  ||   ||||||||||
                                ACGAC CC   CCCGAGCGGA
                                  _  CT_
GAM1130  SF1      3'  AGGCAGACAGCCTCAGCAA   17339         C  GG  C
                                TTGCTGAGGC TG  CT GCCT
                                |||||||||| ||  || ||||
                                AACGACTCCG AC  GA CGGA
                                    _  A_  _
GAM1130  SYN3     3'  GTCGCCTAGTCAGACCTCAGCA 14482         C  ________  CTCG
             AT                   ATTGCTGAGG CTG      GG    C
                                |||||||||| |||      ||    |
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                                TAACGACTCC GAC      CC    G
                                     A   TGAIIIT  GCTC
GAM1130  SYN3     3'  GTCGCCTAGTCAGACCTCAGCA 56904          C  ________  CTCG
              AT                   ATTGCTGAGG CTG      GG    C
                                |||||||||| |||      ||    |
                                TAACGACTCC GAC      CC    G
                                     A   TGAIIIT  GCTC
GAM1130  SYN3     3'  GTCGCCTAGTCAGACCTCAGCA 56906          C  ________  CTCG
              AT                   ATTGCTGAGG CTG      GG    C
                                |||||||||| |||      ||    |
                                TAACGACTCC GAC      CC    G
                                     A   TGAIIIT  GCTC
GAM1130  WNT5A    3'  CTCAGAAGCATCAGCAATG   14120         G  __
                                CATTGCTGA GC  CTGGG
                                ||||||||| ||  |||||
                                GTAACGACT CG  GACTC
                                     A  AA
GAM1130  ARGBP2   5'  AGGCAAGCTTTCCCTGCAAT   14589      TG   CCT    C
                                ATTGC  AGG   GGGCT GCCT
                                |||||  |||   ||||| ||||
                                TAACG  TCC   TTCGA CGGA
                                   __   CT_    A
GAM1130  ATP9B    3'  AGGCAAGCCCAGGGCACAG   78971     AG  _    C
                                CTG  GCC TGGGCT GCCT
                                |||  ||| |||||| ||||
                                GAC  CGG ACCCGA CGGA
                                  A_   G     A
GAM1130  ATP9B    3'  AGGCAAGCCCAGGGCACAG   78972     AG  _    C
                                CTG  GCC TGGGCT GCCT
                                |||  ||| |||||| ||||
                                GAC  CGG ACCCGA CGGA
                                  A_   G     A
GAM1130  ATP9B    3'  AGGCAAGCCCAGGGCACAG   78973     AG  _    C
                                CTG  GCC TGGGCT GCCT
                                |||  ||| |||||| ||||
                                GAC  CGG ACCCGA CGGA
                                  A_   G     A
GAM1130  ATP9B    3'  AGGCGAGCCCAGGGCACAG   78974     AG  _
                                CTG  GCC TGGGCTCGCCT
                                |||  ||| ||||||||||||
                                GAC  CGG ACCCGAGCGGA
                                  A_   G
GAM1130  CALN1    3'  AGGCAAACCCAGTGGTTTCAGA 49659      G      __   CTC
              AATG                   CATT CTGAGGCC  TGGG   GCCT
                                |||| ||||||||  ||||   ||||
                                GTAA GACTTTGG  ACCC   CGGA
                                  A       TG    AAA
GAM1130  CNR2     3'  GCGAGCCTCCAGGCCCAGCAAT 10234         A     __
              G                    CATTGCTG GGCCTGG  GCTCGC
                                |||||||| |||||||  ||||||
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                                GTAACGAC CCGGACC  CGAGCG
                                   _      TC
GAM1130  DKFZp434A171 3'  GGCTCGCCTAAACATAACCTCA 71342          CCT_________  CTCG
           GCAAT                   ATTGCTGAGG         GGG    CC
                                |||||||||          |||    ||
                                TAACGACTCC         TCC    GG
                                     AATACAAAIII   GCTC
GAM1130  DKFZp762L0311 3'  GTCGCCTAGACGGGCTTCAACA 38672       C        ________  CTCG
           ATG                   CATTG TGAGGCCTG      GG    C
                                ||||| |||||||||      ||    |
                                GTAAC ACTTCGGGC      CC    G
                                   A        AGAIIIT  GCTC
GAM1130  FLJ12076  3'  AGCACCTGTGCCCTCAGCAATG 48020           _ CT_  _
                                CATTGCTGAGG C   GG GCT
                                |||||||||||  |   || |||
                                GTAACGACTCC G   CC CGA
                                      C TGT  A
GAM1130  FLJ20297  3'  AGGCAGGTGGGCCCCAGCAA   35369       A    GG  TC
                                TTGCTG GGCCT  GC  GCCT
                                ||||||  |||||  ||  ||||
                                AACGAC CCGGG  TG  CGGA
                                   C     __  GA
GAM1130  FLJ20297  3'  AGGCAGGTGGGCCCCAGCAA   36076       A    GG  TC
                                TTGCTG GGCCT  GC  GCCT
                                ||||||  |||||  ||  ||||
                                AACGAC CCGGG  TG  CGGA
                                   C     __  GA
GAM1130  KIAA1069  3'  AGTTCCAAACCCCAGCAATG   68525        A  CC   _
                                CATTGCTG GG  TGGG CT
                                ||||||||  ||  ||||  ||
                                GTAACGAC CC  ACCT GA
                                     C  AA   T
GAM1130  KIAA1272  3'  AGGCCTCACACAGGCCTCAGAA 70731      G        GGCTC_
           ATG                   CATT CTGAGGCCTG     GCCT
                                ||||  ||||||||||     ||||
                                GTAA GACTCCGGAC     CGGA
                                   A        ACACTC
GAM1130  MGC:5244  3'  GGCCGGACCTCAGCAAT     49151          _  TG
                                ATTGCTGAGG CC  GGCT
                                ||||||||||  ||  ||||
                                TAACGACTCC GG  CCGG
                                     A  __
GAM1130  LOC149194 3'  GCAAGCCCAGGTTGCCAGT   79984      A_       C
                                GCTG  GGCCTGGGCT GC
                                ||||  ||||||||||  ||
                                TGAC  TTGGACCCGA CG
                                   CG        A
GAM1130  LOC150207 3'  GGCCGGACCTCAGCAAT     80596          _  TG
                                ATTGCTGAGG CC  GGCT
                                ||||||||||  ||  ||||
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                                TAACGACTCC GG  CCGG
                                     A  __
GAM1130  LOC158281 3'  AGGCGAGCCCTCCCCAGCA   82734      A  CCT
                                TGCTG GG   GGGCTCGCCT
                                ||||| ||   ||||||||||
                                ACGAC CC   CCCGAGCGGA
                                  _ CT_
GAM1130  LOC163479 5'  AGGCATATTCAAAACTCAGCAA 83021        GCC    CTC
                                TTGCTGAG   TGGG   GCCT
                                ||||||||   ||||   ||||
                                AACGACTC   ACTT   CGGA
                                     AAA    ATA
GAM1130  LOC220020 5'  GATCCAGACCTCACCAATG   95045      C    C    C
                                CATTG TGAGG CTGGG TC
                                ||||| ||||| ||||| ||
                                GTAAC ACTCC GACCT AG
                                   C    A    _
GAM1130  LOC256286 3'  GGCCGGACCTCAGCAAT     96895         _  TG
                                ATTGCTGAGG CC  GGCT
                                |||||||||| ||  ||||
                                TAACGACTCC GG  CCGG
                                     A  __
GAM1130  LOC91632  3'  AGCCGGACCTCAGCAAT     67314         _  TG
                                ATTGCTGAGG CC  GGCT
                                |||||||||| ||  ||||
                                TAACGACTCC GG  CCGA
                                     A  __
GAM1130  LOC93538  5'  AGACGAGAACCTGCCTCAGCAA 72952         CT  G_   C
                                TTGCTGAGGC  GG  CTCG CT
                                ||||||||||  ||  |||| ||
                                AACGACTCCG  CC  GAGC GA
                                     T_  AA   A
GAM1131  ADH7     3'  AAGATTAAGGGACGGGC     7268       ACA   G
                                GCCC   TCT TTTAATCTT
                                ||||   ||| |||||||||
                                CGGG   AGG GAATTAGAA
                                  C__   _
GAM1131  ARAF1    5'  GGAAGGACTTCAGATGTGAGC  64644    C       TTTAA
                                GC CACATCTG     TCTTCC
                                || ||||||||     ||||||
                                CG GTGTAGAC     GGAAGG
                                 A       TTCA_
GAM1131  CEACAM6  3'  GGAAGACTGGCAGATTGGACCA 11756     C   C      TAA
                                TGG CCA ATCTGTT   TCTTCC
                                ||| ||| |||||||   ||||||
                                ACC GGT TAGACGG   AGAAGG
                                  A   _      TC_
GAM1131  CLECSF12 3'  GGATTACAGATGTGAGCCA    77214      C        TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
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                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1131  CYP1A2   3'  GGATTAACAGGTATGAACCA   7518     CC  C      T
                                TGG  CA ATCTGTT AATCT
                                |||  || ||||||| |||||
                                ACC  GT TGGACAA TTAGG
                                  AA  A     _
GAM1131  ENG      3'  GAACTTGAAACAGATTCAGGCC 5496       CAC       AATC
                A                TGGCC   ATCTGTTT   TTC
                                |||||   ||||||||   |||
                                ACCGG   TAGACAAA   AAG
                                  ACT       GTTC
GAM1131  ERCC3    3'  GAATAAACAGAATGGACCA   5506     C   CA      A
                                TGG CCA  TCTGTTTA TC
                                ||| |||  |||||||| ||
                                ACC GGT  AGACAAAT AG
                                  A  A_       A
GAM1131  HTLF     5'  AAGATTGCAGGATTAAGCCA   10973     CCACA    TT
                                TGGC    TCTGT  AATCTT
                                ||||    |||||  ||||||
                                ACCG    GGACG  TTAGAA
                                  AATTA    __
GAM1131  MS4A8B   3'  GATTTTAAACAGATGTTAACCA 49588     CCC          TCT
                                TGG   ACATCTGTTTAA   TC
                                |||   ||||||||||||   ||
                                ACC   TGTAGACAAATT   AG
                                  AAT          TT_
GAM1131  PRKAA2   3'  GAAGATTAAAAAGTAAAGAACC 21811     CCCACAT  G
                A                TGG      CT TTTAATCTTC
                                |||      || ||||||||||
                                ACC      GA AAATTAGAAG
                                  AAGAAAT  A
GAM1131  ASE-1    3'  GGATAACAGGTGTGAGCCA   24983     C        TA
                                TGGC CACATCTGTT  ATCT
                                |||| ||||||||||  ||||
                                ACCG GTGTGGACAA  TAGG
                                  A        __
GAM1131  CITED2   3'  GGAAGATTAAACAGATGTGGGC 21403
                CA                TGGCCCACATCTGTTTAATCTTCC
                                |||||||||||||||||||||||||
                                ACCGGGTGTAGACAAATTAGAAGG

GAM1131  DKFZP564K0322 3'  GGATTACAGATGTGAGCCA   50188     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1131  DZIP1    3'  GAAGATTATTCCAGAAGCCA   30703     CCACA    TT_
                                TGGC    TCTG   TAATCTTC
                                ||||    ||||   ||||||||
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                                ACCG    AGAC   ATTAGAAG
                                  A____    CTT
GAM1131  FLJ22969  3'  GGATTACAGATGTGAGCCA   69211     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1131  HSNOV1    3'  GGATTACAGATGTGAACCA   34437     CC      TT
                                TGG  CACATCTGT  AATCT
                                |||  |||||||||  |||||
                                ACC  GTGTAGACA  TTAGG
                                  AA       __
GAM1131  IMPACT    3'  GAATTACAGGTGTGAGCCA   38006     C       TTAATC
                                TGGC CACATCTGT     TTC
                                |||| |||||||||     |||
                                ACCG GTGTGGACA     AAG
                                  A       TT____
GAM1131  JAM1      3'  GGATTACAGATGTGAGCCA   34234     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1131  JAM1      3'  GGATTACAGATGTGAGCCA   58499     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1131  JAM1      3'  GGATTACAGATGTGAGCCA   58520     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1131  JAM1      3'  GGATTACAGATGTGAGCCA   58548     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1131  JAM1      3'  GGATTACAGATGTGAGCCA   58577     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1131  KIAA0210  5'  GAATTACAGGTGTGAGCCA   29159     C       TTAATC
                                TGGC CACATCTGT     TTC
                                |||| |||||||||     |||
                                ACCG GTGTGGACA     AAG
                                  A       TT____
GAM1131  KIAA0280  3'  GAGCATAAACAGATGTGGTCCA 93301     C          AT
                                TGG CCACATCTGTTTA  CTT
                                ||| ||||||||||||  |||
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                                ACC GGTGTAGACAAAT  GAG
                                  T          AC
GAM1131  KIAA0285  5'  GAAGATTGAGCTTGACCGGACC 29684     C  ACA  T_
             A                   TGG CC   TC  GTTTAATCTTC
                                 ||| ||   ||  ||||||||||
                                 ACC GG   AG  CGAGTTAGAAG
                                  A  CC_  TT
GAM1131  KIAA0356  3'  GGAAGACCCTCAGATGTGGCCA 66778      C      TTTAA
                                 TGGCC ACATCTG    TCTTCC
                                 ||||| |||||||    ||||||
                                 ACCGG TGTAGAC    AGAAGG
                                    _     TCCC_
GAM1131  KIAA1354  3'  GGAAGATTGTCAGCATGT    61576     _  TT
                                 ACAT CTG  TAATCTTCC
                                 |||| |||  |||||||||
                                 TGTA GAC  GTTAGAAGG
                                   C  T_
GAM1131  KIAA1466  3'  ATTAAATAGTATGGGCCA    72406       CAT
                                 TGGCCCA   CTGTTTAAT
                                 |||||||   |||||||||
                                 ACCGGGT   GATAAATTA
                                     AT_
GAM1131  KIAA1468  5'  AAGATCTTGTAGATGTGGCCA  93423      C      TTTA
                                 TGGCC ACATCTG    ATCTT
                                 ||||| |||||||    |||||
                                 ACCGG TGTAGAT    TAGAA
                                    _     GTTC
GAM1131  MRPS26    3'  GGAAGATTACAGTCTGAGGGCC 48723       A  T_   TT
             A                   TGGCCC CA  CTGT  AATCTTCC
                                 ||||||  ||  ||||  ||||||||
                                 ACCGGG GT  GACA  TTAGAAGG
                                    A  CT   __
GAM1131  PANX3     3'  AAGATTAATAAAGATGTAAACC 54765    CCC     GT_
                                 GG   ACATCT   TTAATCTT
                                 ||   ||||||   ||||||||
                                 CC   TGTAGA   AATTAGAA
                                  AAA     AAT
GAM1131  PLCL1     3'  AAGATTAAACAGATGATG    21714    _
                                 CA CATCTGTTTAATCTT
                                 || ||||||||||||||
                                 GT GTAGACAAATTAGAA
                                  A
GAM1131  SPRY4     3'  GAAGACAGAACACAGATGTGGA 49013    GC        _  AA_
             CA                    TG  CCACATCTGT TT   TCTTC
                                   ||  |||||||||| ||   |||||
                                   AC  GGTGTAGACA AA   AGAAG
                                    A_         C  GAC
GAM1131  WNT10A    3'  GAAGAGGAGATTGGACCA    48170     C   C    G TTAA
                                 TGG CCA ATCT T    TCTTC
                                 ||| ||| |||| |    |||||
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                                ACC GGT TAGA G    AGAAG
                                  A   _    G _____
GAM1131  LOC113523 5'  GGATTACAGATGTGAGCCA    73427      C        TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A        __
GAM1131  LOC124216 3'  GGATTACAGATGTGAGCCA    74736      C        TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A        __
GAM1131  LOC130639 5'  GGATTAAAGACGTGAGCCA    75480      C   A   GT
                                TGGC CAC TCT  TTAATCT
                                |||| ||| |||  |||||||
                                ACCG GTG AGA  AATTAGG
                                  A   C   __
GAM1131  LOC144202 5'  GGAAGATTCGATGGACATGGAC 77226     GC   CA     T
              A                  TG  CCA  TCTGTT AATCTTCC
                                ||  |||  ||||||| ||||||||
                                AC  GGT  AGGTAG TTAGAAGG
                                 A_   AC      C
GAM1131  LOC149171 5'  GAATTACAGGTGTGAGCCA    79967      C        TTAATC
                                TGGC CACATCTGT      TTC
                                |||| |||||||||      |||
                                ACCG GTGTGGACA      AAG
                                  A        TT_____
GAM1131  LOC150245 3'  GAAGCAAGACAGATGTGGGCC  86112              AAT
                                GGCCCACATCTGTTT   CTTC
                                ||||||||||||||   ||||
                                CCGGGTGTAGACAGA   GAAG
                                         AC_
GAM1131  LOC152620 3'  AGATTACAGATGTGAGCCA    60703      C        TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGA
                                  A        __
GAM1131  LOC153577 3'  GAAGATTTTATGTGACCA     87239     CC     CTGTTT
                                TGG  CACAT      AATCTTC
                                |||  |||||      |||||||
                                ACC  GTGTA      TTAGAAG
                                  A_     TT_____
GAM1131  LOC154930 3'  GAATAACAGGTGTGAGCCA    82091      C        TAATC
                                TGGC CACATCTGTT    TTC
                                |||| ||||||||||     |||
                                ACCG GTGTGGACAA     AAG
                                  A         T_____
GAM1131  LOC157507 5'  AAGATTAAACCATGGATG     82376       ___
                                CATCT   GTTTAATCTT
                                |||||   ||||||||||
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                                GTAGG   CAAATTAGAA
                                  TAC
GAM1131  LOC158014 5'  AGAATTACAGGTGTGAGCCA   82549     C       TTAA
                                TGGC CACATCTGT    TCT
                                |||| |||||||||    |||
                                ACCG GTGTGGACA    AGA
                                  A       TTA_
GAM1131  LOC158668 3'  AGATTACAGATGTGAGCCA    69892     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGA
                                  A       __
GAM1131  LOC170409 5'  GGATTACAGATGTGAGCCA    83745     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1131  LOC200282 5'  GAAATTACAGGTGTGAGCCA   90099     C       TTAA
                                TGGC CACATCTGT    TC
                                |||| |||||||||    ||
                                ACCG GTGTGGACA    AG
                                  A       TTAA
GAM1131  LOC220595 3'  GGAAGACCTCAGATGTGACCA  92778     CC      TTTAA
                                TGG  CACATCTG    TCTTCC
                                |||  ||||||||    ||||||
                                ACC  GTGTAGAC    AGAAGG
                                  A_      TCC__
GAM1131  LOC253805 3'  GGATTACAGATGTGAGCCA    98179     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1131  LOC56181  5'  GGATTACAGATGTGAGCCA    97278     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1131  LOC91547  3'  GGATTACAGATGTGAGCCA    67004     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1132  CCNG1     3'  TCAAAACATCACGAGATA     15774       ATT   __
                                TATCTC   GTG  GTTTTGA
                                ||||||   |||  |||||||
                                ATAGAG   CAC  CAAAACT
                                   ___   TA
GAM1132  CNR1      3'  TCAAAGTCTCAATGAAATA    32723     C     T GT
                                TAT TCATTG G  TTTGA
                                |||  ||||||  |  |||||
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                                ATA AGTAAC C  AAACT
                                  A     T TG
GAM1132 COL19A1  3' TCAAAACAAAGGATGGGATA  10265        GTG_
                                TATCTCATT   GTTTTGA
                                |||||||||   |||||||
                                ATAGGGTAG   CAAAACT
                                    GAAA
GAM1132 LMO4     3' TCAAAACTGACCATGAGATA  23187        T _
                                TATCTCAT GT GGTTTTGA
                                |||||||| || ||||||||
                                ATAGAGTA CA TCAAAACT
                                    C  G
GAM1132 MAT2A    3' TCAAAACCAGGTCCAATGA   20971       ____
                                TCATTG   TGGTTTTGA
                                ||||||   |||||||||
                                AGTAAC   ACCAAAACT
                                   CTGG
GAM1132 OXTR     3' TCAAAATCACAATGAGAT    8082
                                ATCTCATTGTGGTTTTGA
                                ||||||||||||||||||
                                TAGAGTAACACTAAAACT

GAM1132 PKIB     3' TCAAAACTCACATGGATA    51639     T  T  _
                                TATC CAT GTG GTTTTGA
                                |||| ||| ||| |||||||
                                ATAG GTA CAC CAAAACT
                                  _  _  T
GAM1132 PLAT     3' TCAAAAGCAAATGAGAT     53396       G  G
                                ATCTCATT TG TTTTGA
                                |||||||| || ||||||
                                TAGAGTAA AC AAAACT
                                    _  G
GAM1132 PLAT     3' TCAAAAGCAAATGAGAT     8118        G  G
                                ATCTCATT TG TTTTGA
                                |||||||| || ||||||
                                TAGAGTAA AC AAAACT
                                    _  G
GAM1132 SGPL1    3' TCAAGATAGACCATGAGA    92981       T  G_
                                TCTCAT GT  GTTTTGA
                                ||||||  ||  |||||||
                                AGAGTA CA  TAGAACT
                                   C  GA
GAM1132 WHSC1    3' TCATTGCCAGTGAGATA     56700       TG   TT
                                TATCTCAT  TGGT  TGA
                                ||||||||  ||||  |||
                                ATAGAGTG  ACCG  ACT
                                    __   TT
GAM1132 ZNF6     5' TCAAAACTGAGACAAGAGA   42082     A   ___
                                TCTC TTGT   GGTTTTGA
                                |||| ||||   ||||||||
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                                AGAG AACA   TCAAAACT
                                  _   GAG
GAM1132  ABLIM    3'  CAAAACCTCAAAGAGATA    11321      A   T
                                TATCTC TTG GGTTTTG
                                ||||||| ||| |||||||
                                ATAGAG AAC CCAAAAC
                                   A   T
GAM1132  ABLIM    3'  CAAAACCTCAAAGAGATA    22978      A   T
                                TATCTC TTG GGTTTTG
                                ||||||| ||| |||||||
                                ATAGAG AAC CCAAAAC
                                   A   T
GAM1132  AKAP11   3'  TCAAAACCTTCAAGTGATA   33192     TCA   T_
                                TATC   TTG  GGTTTTGA
                                ||||   |||  ||||||||
                                ATAG   AAC  CCAAAACT
                                  TG_   TT
GAM1132  C12orf2  3'  TCAAAGCCACAATGAGATA   83686
                                TATCTCATTGTGGTTTTGA
                                ||||||||||||||||||
                                ATAGAGTAACACCGAAACT

GAM1132  C20orf7  3'  TCAAAATCATTTGGAGATA   44382      ATT
                                TATCTC   GTGGTTTTGA
                                ||||||   ||||||||||
                                ATAGAG   TACTAAAACT
                                   GTT
GAM1132  CAPS2    3'  CAAAGCCAGTGAGATA     71125       TG
                                TATCTCAT  TGGTTTTG
                                ||||||||  ||||||||
                                ATAGAGTG  ACCGAAAC
                                    __
GAM1132  CED-6    3'  TCATTCCAAATGAGATA     33319       G   TTT
                                TATCTCATT TGG   TGA
                                ||||||||| |||   |||
                                ATAGAGTAA ACC   ACT
                                     _  TT_
GAM1132  DKFZP564O1863 3'  TCAAAACTACACTTGAGA    69143      T_
                                TCTCA  TGTGGTTTTGA
                                |||||  ||||||||||
                                AGAGT  ACATCAAAACT
                                   TC
GAM1132  ERp44    3'  TCAAAGCTAAAGAGATA     82604      ATTG
                                TATCTC   TGGTTTTGA
                                ||||||   |||||||||
                                ATAGAG   ATCGAAACT
                                   AA__
GAM1132  FLJ10508 3'  TCAAAACCACATTAGGGA    36685     AT_
                                TCTC   TGTGGTTTTGA
                                ||||   ||||||||||
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                                AGGG   ACACCAAAACT
                                  ATT
GAM1132  FLJ10997  3'  TCAATGGACACAGTGAAATA   37514     C       GTT_
                                TAT TCATTGTG    TTGA
                                ||| ||||||||    ||||
                                ATA AGTGACAC    AACT
                                  A       AGGT
GAM1132  FLJ12910  3'  TCAAAATTGAACACAGTGA    45005         ____
                                TCATTGTG    GTTTTGA
                                ||||||||    |||||||
                                AGTGACAC    TAAAACT
                                     AAGT
GAM1132  FLJ14129  3'  TCAAAACCCTGCATGAGATG   48813         T __
                                TATCTCAT GT  GGTTTTGA
                                |||||||| ||  ||||||||
                                GTAGAGTA CG  CCAAAACT
                                     _  TC
GAM1132  FLJ20209  3'  TCAAAACCAGATGAGAT     86708         G
                                ATCTCATT TGGTTTTGA
                                |||||||| |||||||||
                                TAGAGTAG ACCAAAACT
                                     _
GAM1132  KIAA0179  3'  TCAAAACCATGCCTGAGA    65459       TT_
                                TCTCA   GTGGTTTTGA
                                |||||   ||||||||||
                                AGAGT   TACCAAAACT
                                   CCG
GAM1132  KIAA0286  3'  TCAAGTCTGACATATGAGATA  68860         _  _  T
                                TATCTCAT TGT GG TTTGA
                                |||||||| ||| || |||||
                                ATAGAGTA ACA TC GAACT
                                     T   G  T
GAM1132  KIAA0555  3'  CAAAGTTACAATGAAATA     29546     C       GG
                                TAT TCATTGT  TTTTG
                                ||| |||||||  |||||
                                ATA AGTAACA  GAAAC
                                  A      TT
GAM1132  KIAA1198  3'  CAAAACCACGGTGAAGAT     64009      _
                                ATCT CATTGTGGTTTTG
                                |||| ||||||||||||
                                TAGA GTGGCACCAAAAC
                                  A
GAM1132  KIAA1211  3'  TCAAAAAGCAACAGTGAGA    69470         GG__
                                TCTCATTGT    TTTTGA
                                |||||||||    ||||||
                                AGAGTGACA    AAAACT
                                     ACGA
GAM1132  KIAA1229  3'  TCAAAACTACAGTGAGATA    62760
                                TATCTCATTGTGGTTTTGA
                                ||||||||||||||||||
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                                ATAGAGTGACATCAAAACT

GAM1132  MGC32104  3'  TCAAAGCCACAATGAGATA   59071
                                TATCTCATTGTGGTTTTGA
                                ||||||||||||||||||
                                ATAGAGTAACACCGAAACT

GAM1132  PRO2949   3'  CAAAACTTTATGAGGTA    38219       TGT
                                TATCTCAT  GGTTTTG
                                ||||||||  |||||||
                                ATGGAGTA  TCAAAAC
                                     TT_
GAM1132  SLC2A12   3'  TCAAAAGGTAGATGAGGTA   59742       GTGG
                                TATCTCATT   TTTTGA
                                |||||||||   ||||||
                                ATGGAGTAG   AAAACT
                                      ATGG
GAM1132  SNRPD1    3'  TCAAAGTCATATGAGAT    23663       T  GT
                                ATCTCAT GTG  TTTGA
                                ||||||| |||  |||||
                                TAGAGTA TAC  AAACT
                                    _  TG
GAM1132  TRPM3     3'  CAGCGTACACAATGAGATA   65525         GTT_
                                TATCTCATTGTG   TTG
                                ||||||||||||   |||
                                ATAGAGTAACAC   GAC
                                       ATGC
GAM1132  LOC129530 5'  CAAAATAGGATGAGATG    75383        G  G
                                TATCTCATT TG TTTTG
                                ||||||||| || |||||
                                GTAGAGTAG AT AAAAC
                                      G  _
GAM1132  LOC131368 3'  TCAGAGTTATAATGAGATA   76376         GG
                                TATCTCATTGT  TTTTGA
                                ||||||||||  ||||||
                                ATAGAGTAATA  GAGACT
                                       TT
GAM1132  LOC143915 3'  TCAAAGGCACAGCAAGATA   83908      CA    G
                                TATCT  TTGTG TTTTGA
                                |||||  ||||| ||||||
                                ATAGA  GACAC GAAACT
                                   AC    G
GAM1132  LOC145384 3'  TCAAAATCACAATGAGATA   77719
                                TATCTCATTGTGGTTTTGA
                                ||||||||||||||||||
                                ATAGAGTAACACTAAAACT

GAM1132  LOC145553 5'  TCAAGGACAAGTGAGATA    57466        G  GT
                                TATCTCATT TG  TTTGA
                                ||||||||| ||  |||||
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                                ATAGAGTGA AC  GAACT
                                     _ AG
GAM1132  LOC145945 5'  TCAAAATCCAACAGGATA    84570      CA   T
                                TATCT  TTG GGTTTTGA
                                |||||  ||| ||||||||
                                ATAGG  AAC CTAAAACT
                                   AC  _
GAM1132  LOC148166 3'  TCAAGGCTTCACCGAGATA   79422       AT  T
                                TATCTC  TG GGTTTTGA
                                ||||||  || ||||||||
                                ATAGAG  AC TCGGAACT
                                    CC  T
GAM1132  LOC149157 3'  TAAAACCACAATGAGATA    79942
                                TATCTCATTGTGGTTTTG
                                ||||||||||||||||||
                                ATAGAGTAACACCAAAAT

GAM1132  LOC157867 5'  TAAAACAACAATGAGATA    87873          G
                                TATCTCATTGT GTTTTG
                                |||||||||| ||||||
                                ATAGAGTAACA CAAAAT
                                      A
GAM1132  LOC201696 3'  CAGTGATAACAATGGGATA   63813          G  _
                                TATCTCATTGT GTT TTG
                                |||||||||| ||| |||
                                ATAGGGTAACA TAG GAC
                                      A  T
GAM1132  LOC221300 3'  TCAAAACTATAATGAGATA   93579
                                TATCTCATTGTGGTTTTGA
                                |||||||||||||||||||
                                ATAGAGTAATATCAAAACT

GAM1132  LOC221692 3'  TGAAACCACACTAAGATA    93858      CAT
                                TATCT   TGTGGTTTTG
                                |||||   ||||||||||
                                ATAGA   ACACCAAAGT
                                   ATC
GAM1132  LOC221893 3'  TCAGAGCCAATGATGATA    94097      _   TG
                                TATC TCAT  TGGTTTTGA
                                |||| ||||  |||||||||
                                ATAG AGTA  ACCGAGACT
                                  T   __
GAM1132  LOC253017 3'  TCAAAACCACAATGAGATA   97545
                                TATCTCATTGTGGTTTTGA
                                |||||||||||||||||||
                                ATAGAGTAACACCAAAACT

GAM1132  LOC256789 5'  TCAAAACCCACTGAGAT     99311       T  T
                                ATCTCA TG GGTTTTGA
                                |||||| || ||||||||
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                                TAGAGT AC CCAAAACT
                                   C  _
GAM1132 LOC91431 5'  TCATCTATCAATGAGATA    57726          _  TTT
                                TATCTCATTG TGG   TGA
                                |||||||||| |||   |||
                                ATAGAGTAAC ATC   ACT
                                      T   T__
GAM1132 LOC91650 5'  TCAAAACCATAATGGAATA   67394     CT
                                TAT  CATTGTGGTTTTGA
                                |||  ||||||||||||||
                                ATA  GTAATACCAAAACT
                                  AG
GAM1133 PIP5K1A  3'  TATCCCACCCTGCCTTGATA  14520        A   CA  C
                                TATCAAGG AGGG  GG GTG
                                |||||||| ||||  || |||
                                ATAGTTCC TCCC  CC TAT
                                     G   A_  C
GAM1133 SOX11    3'  ACCCACCCCCCCTTGGTA    13308        AA   CA  C
                                TATCAAGG  GGG  GG GT
                                ||||||||  |||  || ||
                                ATGGTTCC  CCC  CC CA
                                     CC   A_  _
GAM1133 CHL1     3'  TGTTACCTTTCCTCAATA    22768     CA      CA
                                TAT  AGGAAGGG  GGCG
                                |||  ||||||||  ||||
                                ATA  TCCTTTCC  TTGT
                                  AC       A_
GAM1133 EPB41L1  3'  CATTCTGCCCTTCCCTGA    71104     A        C
                                TCA GGAAGGGCAGG GTG
                                ||| ||||||||||| |||
                                AGT CCTTCCCGTCT TAC
                                  C         _
GAM1133 FLJ00060 3'  CATACCCCCTGCCCTCCTCTGA 61741     _   A      CGTG
                                TCA AGGA GGGCAGG    ATG
                                ||| |||| |||||||    |||
                                AGT TCCT CCCGTCC    TAC
                                  C   _      CCCA
GAM1133 FLJ10898 5'  CACCACAGCCCTTTCTCAATA  60126     CA       AGGC
                                TAT  AGGAAGGGC    GTG
                                |||  |||||||||    |||
                                ATA  TCTTTCCCG    CAC
                                  AC        ACAC
GAM1133 FLJ22557 3'  ATCATCCCATCCTTAATA    45581     C    A   CAGGC
                                TAT AAGGA GGG     GTGAT
                                ||| ||||| |||     |||||
                                ATA TTCCT CCC     TACTA
                                  A    A  _____
GAM1133 KIAA0574 3'  CATCCCCTGCCCTCCCCTGA  69808     A  A      CGT
                                TCA GG AGGGCAGG   GATG
                                ||| || ||||||||   ||||
```

```
                                AGT CC TCCCGTCC   CTAC
                                  C  C       C__
GAM1133  KIAA0632  3'  CACCTCAGAAACCCTTCCTTGA 32071          CA___  C
                                TCAAGGAAGGG     GG GTG
                                ||||||||||     || |||
                                AGTTCCTTCCC     CT CAC
                                      AAAGA  C
GAM1133  KIAA1354  5'  CAGTGACTGCCTTCCCTTGATA 61572         A      G  _
                                TATCAAGG AGGGCAG CG TG
                                |||||||| ||||||| || ||
                                ATAGTTCC TTCCGTC GT AC
                                     C      A  G
GAM1133  MGC20460  5'  CACCGCCTCCTACCCTTCTT   54901         C___    _
                                AGGAAGGG    AGGCG TG
                                ||||||||    ||||| ||
                                TTCTTCCC    TCCGC AC
                                     ATCC     C
GAM1133  LOC158476 3'  CACGCCCGCCCCCCCCATTGA  88186      _ AA_   A
                                TCAA GG   GGGC GGCGTG
                                |||| ||   |||| ||||||
                                AGTT CC   CCCG CCGCAC
                                  A  CCC    C
GAM1133  LOC90459  3'  CACACCCGCCTAATTTTTG    63550       A_   A  C
                                CAAGGA  GGGC GG GTG
                                ||||||  |||| || |||
                                GTTTTT  TCCG CC CAC
                                    AA    C  A
GAM1134  ARAF1     3'  GACTGAGCCCCCTGTCTCC    64643    A    CA    AAT  A_
                                A AGAC  AGGG   GC  AGTC
                                | ||||  ||||   ||  ||||
                                C TCTG  TCCC   CG  TCAG
                                 C    __    C__  AG
GAM1134  CHST6     3'  GGAACTGTCTTCCCTTGGTC   41502          T   AG
                                GACCAAGGGAA GCA  TCC
                                |||||||||| |||  |||
                                CTGGTTCCCTT TGT  AGG
                                      C   CA
GAM1134  CSPG4     3'  ACTTCCTCCCCTGGTTTTT    10323        A    ATGC
                                AAAGACCA GGGA    AAGT
                                |||||||| ||||    ||||
                                TTTTTGGT CCCT    TTCA
                                     C    CC__
GAM1134  DAZ       3'  ACTTGCATTTTAAAGTGTTT   83001     G  CAAG
                                AAA AC    GGAATGCAAGT
                                ||| ||    ||||||||||
                                TTT TG    TTTTACGTTCA
                                  G  AAA_
GAM1134  EMP1      3'  GACCTCATGCCATGGTCTTT   9238         A  GA   CAA
                                AAAGACCA GG  ATG   GTC
                                |||||||| ||  |||   |||
```

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                                TTTCTGGT CC  TAC   CAG
                                    A  G_   TC_
GAM1134  EPHB6    3'  GGCTGCATTCCCTGGTC     16714      A       A
                                GACCA GGGAATGCA GTC
                                ||||| ||||||||| |||
                                CTGGT CCCTTACGT CGG
                                  _       _
GAM1134  ETF1     3'  GGAACCATTTCTCTCTTGGTCT 17588          ___   CAAG
                                AGACCAAGGGA   ATG    TCC
                                ||||||||||   |||    |||
                                TCTGGTTCTCT   TAC    AGG
                                      CTT   CA__
GAM1134  GJA5     3'  GGAACTTGCATTATATGTGCTC 19166     C  AGGG_       _
              T                  AGA CA     AATGCAAGT CC
                                ||| ||     ||||||||| ||
                                TCT GT     TTACGTTCA GG
                                  C  GTATA        A
GAM1134  KCNA3    3'  GGAACGTGCCCCCTTGGTCT   11134         AAT   AG_
                                AGACCAAGGG   GCA   TCC
                                ||||||||||   |||   |||
                                TCTGGTTCCC   CGT   AGG
                                      C__   GCA
GAM1134  LFG      3'  GGACCCTCCCTTGGCTT     77238     A       ATGCAA
                                AAG CCAAGGGA      GTCC
                                ||| ||||||||      ||||
                                TTC GGTTCCCT      CAGG
                                  _       CC_____
GAM1134  MAPRE1   3'  GGAACCCATTTTCCACCTGGTC 25592         AG_   TGCAAG_
              TTT                  AAAGACCA   GGAA      TCC
                                ||||||||   ||||      |||
                                TTTCTGGT   CCTT      AGG
                                    CCA    TTACCCA
GAM1134  MSL3L1   3'  GGACTGGGCTGTTTCCTCAGCC 23290      ACCA      _  A_
              TTT                  AAAG    AGGGAAT GC  AGTCC
                                ||||    |||||||  ||  |||||
                                TTTC    TCCTTTG CG  TCAGG
                                  CGAC      T  GG
GAM1134  NXF2     5'  GGCTGACATTTCCTCAATCTTT 35600      CCA       CA
                                AAAGA   AGGGAATG  AGTC
                                |||||   ||||||||  ||||
                                TTTCT   TCCTTTAC  TCGG
                                  AAC       AG
GAM1134  NXF2     5'  GGCTGACATTTCCTCAATCTTT 35601      CCA       CA
                                AAAGA   AGGGAATG  AGTC
                                |||||   ||||||||  ||||
                                TTTCT   TCCTTTAC  TCGG
                                  AAC       AG
GAM1134  OAS2     3'  GACTTTTTCCTTGGCTTT    11868      A       TGC
                                AAAG CCAAGGGAA   AAGTC
                                |||| |||||||||   |||||
```

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                                TTTC GGTTCCTTT  TTCAG
                                  _     ___
GAM1134 PCSK1    3' GACTCATTCCCTAGATCTTT  6514      CCA      CA
                                AAAGA  AGGGAATG AGTC
                                |||||  |||||||| ||||
                                TTTCT  TCCCTTAC TCAG
                                   AGA      __
GAM1134 RPL10    3' ACCTGCATTCCCAGGGCCTT  21175    A AA      A
                                AAG CC  GGGAATGCA GT
                                ||| ||  ||||||||| ||
                                TTC GG  CCCTTACGT CA
                                  C GA       C
GAM1134 SRPX     5' GCACGCAGTCCCTTGGTCT   21948         A  AA
                                AGACCAAGGGA TGC  GT
                                |||||||||| |||  ||
                                TCTGGTTCCCT ACG  CG
                                      G  CA
GAM1134 SYNGR1   3' GAGAGGTGTTTCCTTGGCCTT 17504    A        AAG
                                AAG CCAAGGGAATGC  TC
                                ||| ||||||||||||  ||
                                TTC GGTTCCTTTGTG  AG
                                  C         GAG
GAM1134 TBX3     3' GGGACTTGCATTATCGGTT   21147    AA GG
                                GACC  G  AATGCAAGTCCC
                                ||||  |  ||||||||||||
                                TTGG  C  TTACGTTCAGGG
                                  __ TA
GAM1134 WHSC1L1  3' GGGTTAAATTCCCTTGGTCTTT 35504           GCAAGT
                                AAAGACCAAGGGAAT    CCC
                                ||||||||||||||    |||
                                TTTCTGGTTCCCTTA    GGG
                                       AATT__
GAM1134 WNT10B   3' GACTTGTTCTTGGTT      14127       GAAT
                                GACCAAGG   GCAAGTC
                                ||||||||   |||||||
                                TTGGTTCT   TGTTCAG
                                   _____
GAM1134 ARHGEF11 3' GACCCGCATGTTGCTTGGTCT 29462       G  _   AA
                                AGACCAAG GA ATGC  GTC
                                |||||||| || ||||  |||
                                TCTGGTTC TT TACG  CAG
                                    G  G   CC
GAM1134 BMF      3' GGGACCCCAGACCCCTTGGTTT 54284   A       AA_  CAA
           CC                    A AGACCAAGGG  TG  GTCCC
                                | ||||||||||  ||  |||||
                                C TTTGGTTCCC  AC  CAGGG
                                 C        CAG  CC_
GAM1134 CASPR4   3' ACTGTAGCCTTGGTCT     58103        GAA   A
                                AGACCAAGG  TGCA GT
                                |||||||||  |||| ||
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                                TCTGGTTCC  ATGT CA
                                     G__   _
GAM1134  DAZ2     3'  ACTTGCATTTTAAGTGTTT   40154      CAAG
                                AGAC   GGAATGCAAGT
                                ||||   ||||||||||
                                TTTG   TTTTACGTTCA
                                  TGAA
GAM1134  DKFZP566B183 3'  GACCTATTTCCTGGGTCT    31943       A       CAA
                                AGACC AGGGAATG  GTC
                                ||||| ||||||||  |||
                                TCTGG TCCTTTAT  CAG
                                   G       C__
GAM1134  EIF3S9   3'  GGACTTGCATCCCCATTG    14987     _  A
                                CAA GGG ATGCAAGTCC
                                ||| ||| ||||||||||
                                GTT CCC TACGTTCAGG
                                  A   C
GAM1134  FLJ10565  3'  GGACCTGTAGCTTGGTTTT   36807         GGAA    A
                                AAGACCAAG    TGCA GTCC
                                |||||||||    |||| ||||
                                TTTTGGTTC    ATGT CAGG
                                     G___    C
GAM1134  FLJ10743  3'  GAGTTGTCATTCCCTCGGCTT  37083     A  A      _  G
                                AAG CC AGGGAATG CAA TC
                                ||| || |||||||| ||| ||
                                TTC GG TCCCTTAC GTT AG
                                  _ C       T   G
GAM1134  FLJ12221  3'  GACCTGTATCTTGGTGTTT   63220     G     GGA    A
                                AAA ACCAAG   ATGCA GTC
                                ||| ||||||   ||||| |||
                                TTT TGGTTC   TATGT CAG
                                  G     ___     C
GAM1134  FLJ13441  3'  GGACTTGTCTCCTAATCTT   43916      CCAA    AT
                                AAGA    GGGA  GCAAGTCC
                                ||||    ||||  ||||||||
                                TTCT    TCCT  TGTTCAGG
                                   AA__    C_
GAM1134  FLJ23185  5'  GCTACATTCCTTGGCCTTT   47518      A     G    CA
                                AAAG CCAAGG AATG  AGT
                                |||| |||||| ||||  |||
                                TTTC GGTTCC TTAC  TCG
                                   C     _    A_
GAM1134  FLJ25471  5'  GACAGGCTTTCCTTGGCCTCC  58971    A  A       T  AA
                                A AG CCAAGGGAA GC  GTC
                                | || |||||||| ||  |||
                                C TC GGTTCCTTT CG  CAG
                                 C  C        _ GA
GAM1134  HEYL     3'  GGACTTGCATCTTGTGTTT   28132      _    GGA
                                AGAC CAAG   ATGCAAGTCC
                                |||| ||||   ||||||||||
```

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                                TTTG GTTC   TACGTTCAGG
                                  T  ____
GAM1134  HRD1     3'  GGGACCTGCCTGCCCCTGTCTT 70152       CAA   AAT   A
                T                  AAAGAC   GGG   GCA GTCCC
                                   ||||||   |||   ||| |||||
                                   TTTCTG   CCC   CGT CAGGG
                                      TC_   GTC   C
GAM1134  KIAA0893 3'  TGCATTCCTTGGTCTTT     31064          G
                                   AAAGACCAAGG AATGCA
                                   |||||||||||| ||||||
                                   TTTCTGGTTCC TTACGT
                                              _
GAM1134  KIAA1363 3'  GGGACCAAGTACCCTCTGGTCT 69792         _    A  GCAA
                TT                  AAAGACCA AGGG AT    GTCCC
                                   |||||||| |||| ||    |||||
                                   TTTCTGGT TCCC TG    CAGGG
                                        C    A  AAC_
GAM1134  KIAA1826 5'  GGAACTTGCCGTCTGGTTTTT  67792         AGG  AT     _
                                   AAAGACCA   GA  GCAAGT CC
                                   ||||||||   ||  |||||| ||
                                   TTTTTGGT   CT  CGTTCA GG
                                        ___  GC     A
GAM1134  moblak   3'  GGACTTGTCCTTGATC      56405    C    GAAT
                                   GA CAAGG    GCAAGTCC
                                   || |||||    ||||||||
                                   CT GTTCC    TGTTCAGG
                                    A    _____
GAM1134  NFKBIE   5'  GGGACTCGCATTCCCCGGTT   17054     AA       A
                                   GACC  GGGAATGC AGTCCC
                                   ||||  |||||||| ||||||
                                   TTGG  CCCTTACG TCAGGG
                                     C_       C
GAM1134  NUDT11   3'  GGACTTGCATCAGCTGCCTC   60658    CCA  G_  A
                                   GA   AG  GA TGCAAGTCC
                                   ||   ||  || |||||||||
                                   CT   TC  CT ACGTTCAGG
                                    CCG  GA  _
GAM1134  PIP3-E   3'  GGAAGCAATTCCCTTGCCTCT  67353     C_       _  AAG
                                   AGA  CAAGGGAAT GC   TCC
                                   |||  ||||||||| ||   |||
                                   TCT  GTTCCCTTA CG   AGG
                                     CC        A  A__
GAM1134  RAB25    3'  GGACCTTTCCTTGCCCTTT    73258      AC       TGCAA
                                   AAAG  CAAGGGAA    GTCC
                                   ||||  ||||||||    ||||
                                   TTTC  GTTCCTTT    CAGG
                                     CC       C____
GAM1134  SPRY2    5'  GGGACTTGCCGTTGGCGCTT   20702     A_    G GAAT
                                   AAG  CCAA G    GCAAGTCCC
                                   |||  |||| |    |||||||||
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                                TTC  GGTT C    CGTTCAGGG
                                  GC    G ____
GAM1134  ZNF317    3'  ACTTGGCCGACCCTTGGTCT   72470          AAT  _
                                AGACCAAGGG   GC AAGT
                                ||||||||||   || ||||
                                TCTGGTTCCC   CG TTCA
                                     AGC  G
GAM1134  LOC139770 3'  GGAACTTGTTTCCTTAGTCTTT 75906       C     AT     _
                                AAAGAC AAGGGA  GCAAGT CC
                                |||||| ||||||  |||||| ||
                                TTTCTG TTCCTT  TGTTCA GG
                                   A      __      A
GAM1134  LOC145761 5'  GCAGTCCTCTTTGGTCTT    84480         __    A
                                AAGACCAA  GGGA TGC
                                ||||||||  |||| |||
                                TTCTGGTT  TCCT ACG
                                     TC    G
GAM1134  LOC147669 5'  GGACTTGACTCCTGGCCTT    85185     A   A   AATG
                                AAG CCA GGG    CAAGTCC
                                ||| ||| |||    |||||||
                                TTC GGT CCT    GTTCAGG
                                  C   _   CA__
GAM1134  LOC148529 5'  GGGACTTGAGATCTGGGTCTT  85322       A   GAATG
                                AAGACC AGG     CAAGTCCC
                                |||||| |||     ||||||||
                                TTCTGG TCT     GTTCAGGG
                                   G   AGA__
GAM1134  LOC149506 3'  GCGCCTCCCTTGGTCTTT     85639           A_
                                AAAGACCAAGGGA  TGC
                                ||||||||||||  |||
                                TTTCTGGTTCCCT  GCG
                                       CC
GAM1134  LOC150245 3'  GGAAGGGCAATTCCCCTACTCT 86114      CCAA     _  AAG
           T                     AAGA    GGGAAT GC   TCC
                                ||||    |||||| ||   |||
                                TTCT    CCCTTA CG   AGG
                                  CATC      A  GGA
GAM1134  LOC151610 5'  GGAACTTGCATTGTGATAAGTT 81096      CAAGGG_       _
           TT                     AAGAC       AATGCAAGT CC
                                |||||       ||||||||| ||
                                TTTTG       TTACGTTCA GG
                                   AATAGTG        A
GAM1134  LOC152018 3'  GGGACCTGCATTTTAAATAATC 86730      CCAAG_      A
           TT                     AAGA      GGAATGCA GTCCC
                                ||||      |||||||| |||||
                                TTCT      TTTTACGT CAGGG
                                  AATAAA       C
GAM1134  LOC162333 5'  GGCCACACTCCCTTGGTC     88497          A  CAA
                                GACCAAGGGA TG   GTC
                                |||||||||| ||   |||
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                                CTGGTTCCCT AC   CGG
                                      C  AC_
GAM1134  LOC170284 5'  GGGCCATCCCCTTGGTT     83478         A   CAA
                                GACCAAGGG ATG   GTCC
                                ||||||||| |||   ||||
                                TTGGTTCCC TAC   CGGG
                                     C  ___
GAM1134  LOC170425 5'  ACTTGCATTCTGTGTTC     76882    C  AG
                                GA CA  GGAATGCAAGT
                                || ||  ||||||||||
                                CT GT  TCTTACGTTCA
                                 T  G_
GAM1134  LOC200132 3'  GGAACTTGATCTTGGTTTT    89993          GAATG    _
                                AAGACCAAGG     CAAGT CC
                                ||||||||||     ||||| ||
                                TTTTGGTTCT     GTTCA GG
                                      A____     A
GAM1134  LOC219540 5'  GGAGGGTTTCCCTTGGTCTCC  95245    A         T  AAG
                                A AGACCAAGGGAA GC   TCC
                                | ||||||||||| ||   |||
                                C TCTGGTTCCCTT TG   AGG
                                 C          _  GG_
GAM1134  LOC219920 5'  GGATTCCATTTCCTCGGCCTCC 94956    A  A  A       CA
                                A AG CC AGGGAATG  AGTCC
                                | || || ||||||||  |||||
                                C TC GG TCCTTTAC  TTAGG
                                 C  C  C       C_
GAM1134  LOC253769 5'  GACTTGCACCCTGTGATCT    99019     C  _    AA
                                AGA CA AGGG  TGCAAGTC
                                ||| || ||||  ||||||||
                                TCT GT TCCC  ACGTTCAG
                                  A  G   __
GAM1134  LOC91547  3'  GGACTCTCCCCTGTTCTTT    67003      C  A    ATGCA
                                AAAGA CA GGGA     AGTCC
                                ||||| || ||||     |||||
                                TTTCT GT CCCT     TCAGG
                                   T  C    C____
GAM1134  LOC92249  3'  GGAACTTGCACCCTGGTCTTT  69108        A   AA     _
                                AAAGACCA GGG  TGCAAGT CC
                                |||||||| |||  ||||||| ||
                                TTTCTGGT CCC  ACGTTCA GG
                                     _  __      A
GAM1135  CDH12     3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT     GAA  ATAAG
                                |||||||||     |||  |||||
                                ATGTGGTGA     TTT  TATTC
                                      AA___   AC
GAM1135  GOCAP1    3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
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                                ATGTG  GAGGGTTCTT TTA
                                   AC         G
GAM1135  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT    98090       T    AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||     ||||||
                                TGGTG GGGT     TTATTC
                                   _    GTCA_
GAM1135  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
           A                     TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM1135  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM1135  HMP19     3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
           TA                    TACA    TCC    GAAGAATAAG
                                ||||    |||    ||||||||||
                                ATGT    AGG    TTTCTTATTC
                                  AAA_   ATTG
GAM1135  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68742             _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                        G
GAM1135  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM1135  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748      CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM1135  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM1135  OSBPL11   3'  CTTAATTTCCCAAGAGTGGTG  43206        CCAA    AA
                                CACCACTC    GAAG  TAAG
                                ||||||||    ||||  ||||
                                GTGGTGAG    CTTT  ATTC
                                     AACC    A_
GAM1135  YME1L1    3'  TCATTCTTGATGTGGTGTA    58438         TCC     _
                                TACACCAC   CAAGAA GA
                                ||||||||   |||||| ||
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                                ATGTGGTG  GTTCTT CT
                                    TA_    A
GAM1135 ZNF262   3' CTTATTTTGTTTGGGAGT   18723       A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                   G
GAM1135 LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_   AAGA
                                TACACCAC  CCAAG   ATA
                                ||||||||  |||||   |||
                                ATGTGGTG  GGTTC   TGT
                                    CAA   GG__
GAM1136 ALDH1A1  3' GTGACTCTTGAAGTACTTA   7306       C   GA  G
                                TAAGTGCT CAAG  GGT GC
                                |||||||| ||||  ||| ||
                                ATTCATGA GTTC  TCA TG
                                    A   __  G
GAM1136 ARHGAP6  3' TGGCCACTGGCACACTTA    8612      CT  AGGAG
                                TAAGTG  CCA    GTGGCCA
                                ||||||  |||    |||||||
                                ATTCAC  GGT    CACCGGT
                                   AC  _____
GAM1136 ARHGAP6  3' TGGCCACTGGCACACTTA    26433     CT  AGGAG
                                TAAGTG  CCA    GTGGCCA
                                ||||||  |||    |||||||
                                ATTCAC  GGT    CACCGGT
                                   AC  _____
GAM1136 ASH1     5' GGCCACCCCCTCTTCCCCACTT 38089     CTCCA_  A
                                AAGTG     AGG GGTGGCC
                                |||||     ||| |||||||
                                TTCAC     TCC CCACCGG
                                  CCCTTC  C
GAM1136 ENG      3' GCCACTGGCTTGGAACAC    5498     C    GA
                                GTG TCCAAG  GGTGGC
                                ||| ||||||  ||||||
                                CAC AGGTTC  TCACCG
                                  A     GG
GAM1136 GALNT3   3' CACTCCACTTGAAGCACTTA   16825       C   GA _
                                TAAGTGCT CAAG  G GTG
                                |||||||| ||||  | |||
                                ATTCACGA GTTC  C CAC
                                    A   AC T
GAM1136 HDAC4    3' GTGGGGCTCTCTTGGAGCAC   21249       GA  GG
                                GTGCTCCAAG  GGT  CCAC
                                ||||||||||  |||  ||||
                                CACGAGGTTC  TCG  GGTG
                                    TC  G_
GAM1136 MASP1    3' GTGATCCCTTGGAGCAC     58217       A  G
                                GTGCTCCAAGG GGT GC
                                |||||||||| ||| ||
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                                CACGAGGTTCC CTA TG
                                      _  G
GAM1136 ROCK2    3' GTGGCCTCAAAGGCACTTA   66623       CCAAG    G
                                TAAGTGCT    GAGGT GC
                                ||||||||    ||||| ||
                                ATTCACGG    CTCCG TG
                                    AAA__    G
GAM1136 SNCAIP   3' GCCACCTATAAGCTTGGGGCAC 97609        G____
                                GTGCTCCAAG    AGGTGGC
                                ||||||||||    |||||||
                                CACGGGGTTC    TCCACCG
                                      GAATA
GAM1136 C14orf4  3' GCCACCTCCTTTGCCCT    67918    T  TCC
                                AG GC   AAGGAGGTGGC
                                || ||   ||||||||||
                                TC CG   TTCCTCCACCG
                                 C  T__
GAM1136 CLIPR-59 3' TGGTCACCCTGAAGCCCTTA  32022     T   CCAA  A
                                TAAG GCT    GG GGTGGCCA
                                |||| |||    || ||||||||
                                ATTC CGA    TC CCACTGGT
                                  C   AG__  _
GAM1136 FLJ10620 3' GTGGCCCGTGCCAAAGCACTTA 36865        CCAA  AGGT
                                TAAGTGCT    GG    GGCCAC
                                ||||||||    ||    ||||||
                                ATTCACGA    CC    CCGGTG
                                    AA__  GTGC
GAM1136 FLJ12838 3' GTTACCTAAAGCACTTA     45315        CCAAGG
                                TAAGTGCT     AGGTGGC
                                ||||||||     |||||||
                                ATTCACGA     TCCATTG
                                    AA____
GAM1136 FLJ14681 3' GTGGCTCCCCCAGAGCACTT  52597        CAA  A  TG
                                AAGTGCTC   GG GG  GCCAC
                                ||||||||   || ||  |||||
                                TTCACGAG   CC CC  CGGTG
                                    A__  _  CT
GAM1136 FLJ23360 3' GCCACCTCCTGCTGGGCAC   43831       CA_
                                GTGCTC   AGGAGGTGGC
                                ||||||   ||||||||||
                                CACGGG   TCCTCCACCG
                                   TCG
GAM1136 FLJ23375 5' GTGGCCATGCTCTTGGAGCACT 46953          AG
                                AGTGCTCCAAGG  GTGGCCAC
                                ||||||||||||  ||||||||
                                TCACGAGGTTCT  TACCGGTG
                                      CG
GAM1136 KIAA0232 3' GTAGCATGCCTGGAGCATCA  73123   A      A  AG_  G
                                A GTGCTCCA GG   GT GC
                                | ||||||| ||   || ||
```

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                                A TACGAGGT CC   CG TG
                                 C       _ GTA  A
GAM1136 KIAA0295 3' GCAGCCCCTGGGAGCAC     68665        A   A   G
                                GTGCTCC AGG GGT GC
                                ||||||| ||| ||| ||
                                CACGAGG TCC CCG CG
                                    G   _   A
GAM1136 KIAA1389 3' GTTACCTTAGAGACTTA     70319      G   CAAG
                                TAAGT CTC    GAGGTGGC
                                ||||| |||    ||||||||
                                ATTCA GAG    TTCCATTG
                                  _   A___
GAM1136 KIAA1878 3' GCAGCCCCTGGAGCAC      93367        A  A   G
                                GTGCTCCA GG GGT GC
                                |||||||| || ||| ||
                                CACGAGGT CC CCG CG
                                    _ _   A
GAM1136 KLHL8    3' GTTAACCCTGTAGCACTTA   63517        CCA   AGG
                                TAAGTGCT   AGG   TGGC
                                ||||||||   |||   ||||
                                ATTCACGA   TCC   ATTG
                                     TG_   CA_
GAM1136 KLHL8    3' TGACCACCTTTCAACACTT   63519      CTCCAA       C
                                AAGTG     GGAGGTGG CA
                                |||||     |||||||| ||
                                TTCAC     TTTCCACC GT
                                   AAC___       A
GAM1136 MGC13090 3' GTGGCCACTTGGCCAAAGCGC 52122      CCAA __
                                GTGCT    GG  AGGTGGCCAC
                                |||||    ||  ||||||||||
                                CGCGA    CC  TTCACCGGTG
                                   AA__  GG
GAM1136 MGC33177 3' ATTTACCTTAGAGCATTTA   58626        C   _
                                TAAGTGCTC AAGG AGGT
                                ||||||||| |||| ||||
                                ATTTACGAG TTCC TTTA
                                     A   A
GAM1136 PPP1R13B 3' CCATCACCTTGGAGCACT    31656          A
                                AGTGCTCCAAGG GGTGG
                                |||||||||||| |||||
                                TCACGAGGTTCC CTACC
                                       A
GAM1136 SHANK3   3' GTGACCACCTCCTTCGCAGC  66110     CC_        C
                                GCT   AAGGAGGTGG CAC
                                |||   |||||||||| |||
                                CGA   TTCCTCCACC GTG
                                  CGC         A
GAM1136 SIAT8C   5' GCCACCTCCTCGCCGGCAC   32447      CCA_
                                GTGCT    AGGAGGTGGC
                                |||||    ||||||||||
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                                CACGG   TCCTCCACCG
                                  CCGC
GAM1136 SNX11    3' GTAGCCCTAGAGCACTT    26173       CAA A  G
                                AAGTGCTC  GG GGT GC
                                ||||||||  || ||| ||
                                TTCACGAG  TC CCG TG
                                   A__ _  A
GAM1136 WAC      5' GCAGCCTTACCAGGCACTTA  56070       CCAAG   G
                                TAAGTGCT   GAGGT GC
                                ||||||||   ||||| ||
                                ATTCACGG   TTCCG CG
                                   ACCA_   A
GAM1136 YAP      5' GGCCACCCCCTCTTCCTCACTT 58206     CTCCA_  A
                                AAGTG     AGG GGTGGCC
                                |||||     ||| |||||||
                                TTCAC     TCC CCACCGG
                                  TCCTTC  C
GAM1136 YAP      5' GGCCACCCCCTCTTCCTCACTT 37332     CTCCA_  A
                                AAGTG     AGG GGTGGCC
                                |||||     ||| |||||||
                                TTCAC     TCC CCACCGG
                                  TCCTTC  C
GAM1136 LOC140275 3' ATCTCCCTTAAAGTACTTA  75295       CC  _
                                TAAGTGCT  AAGG AGGT
                                ||||||||  |||| ||||
                                ATTCATGA  TTCC TCTA
                                   AA   C
GAM1136 LOC146488 5' GTGGCCACACCTGGAACACT  71361    C   A AG
                                AGTG TCCA GG  GTGGCCAC
                                |||| |||| ||  ||||||||
                                TCAC AGGT CC  CACCGGTG
                                  A  _ A_
GAM1136 LOC146713 3' GGTCACCTCGGAGCCACT   84738    _   AAG
                                AGTG CTCC  GAGGTGGCC
                                |||| ||||  |||||||||
                                TCAC GAGG  CTCCACTGG
                                  C  ___
GAM1136 LOC147958 5' GGCCACAGGGCACTTA     88526       CAAGGAG
                                TAAGTGCTC     GTGGCC
                                |||||||||     ||||||
                                ATTCACGGG     CACCGG
                                   A_______
GAM1136 LOC148137 3' CCTCCCTCCTTGAAGCACTT  59094      C      T_
                                AAGTGCT CAAGGAGG  GG
                                ||||||| ||||||||  ||
                                TTCACGA GTTCCTCC  CC
                                   A      CT
GAM1136 LOC150203 3' GTGACCATTGTTGGAGCAC   61136       G _  G
                                GTGCTCCAA GA GGT GC
                                ||||||||| || ||| ||
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                                CACGAGGTT TT CCA TG
                                     G  A   G
GAM1136  LOC151521 3'  GTGGCCACACTTGAAACAC   86624    CTC   GAG
                                GTG   CAAG   GTGGCCAC
                                |||   ||||   ||||||||
                                CAC   GTTC   CACCGGTG
                                  AAA    A__
GAM1136  LOC151996 5'  GTAGCCATGACATTGGAGCAC  86722        GGAG    C
                                GTGCTCCAA    GTGGC AC
                                |||||||||    ||||| ||
                                CACGAGGTT    TACCG TG
                                     ACAG     A
GAM1136  LOC152790 5'  GCACGCTTCTTAAAGCACT    87060       CCA      _
                                AGTGCT   AGGAGGTG GC
                                ||||||   |||||||| ||
                                TCACGA   TTCTTCGC CG
                                   AA_       A
GAM1136  LOC153688 3'  GTGGCCACTTGATTAGAGACCT 87330    TG   C  GG
                                AG  CTC AA  AGGTGGCCAC
                                ||  ||| ||  ||||||||||
                                TC  GAG TT  TTCACCGGTG
                                 CA   A  AG
GAM1136  LOC154860 3'  GCGGCCTCTGGAGCCTTA    87505     T     AG    G
                                TAAG GCTCCA  GAGGT GC
                                |||| ||||||  ||||| ||
                                ATTC CGAGGT  CTCCG CG
                                  _     __     G
GAM1136  LOC164714 5'  GGCTGGCGTCCTTGGAGC    88587         G  _
                                GCTCCAAGGA GT GGCC
                                |||||||||| || ||||
                                CGAGGTTCCT CG TCGG
                                     G  G
GAM1136  LOC196374 3'  GCCACCTCCTTCCTGAACAC   89029     C  C__
                                GTG TC   AAGGAGGTGGC
                                ||| ||   ||||||||||
                                CAC AG   TTCCTCCACCG
                                  A  TCC
GAM1136  LOC196955 3'  GCAGGCCTTGGAGCCTTA    77868     T       AGGTG
                                TAAG GCTCCAAGG    GC
                                |||| |||||||||    ||
                                ATTC CGAGGTTCC    CG
                                  _       GGA__
GAM1136  LOC199720 3'  TGGCCAAGCTGGAGCACT    89706        AG AGG
                                AGTGCTCCA  G   TGGCCA
                                |||||||||  |   ||||||
                                TCACGAGGT  C   ACCGGT
                                     __ GA_
GAM1136  LOC200138 5'  GTGGCCACCTCCTTGGAGCACT 91543
            TA                   TAAGTGCTCCAAGGAGGTGGCCAC
                                ||||||||||||||||||||||||
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                                ATTCACGAGGTTCCTCCACCGGTG

GAM1136  LOC203378 5'  TGGTCAACCTTGGAACATT   92309     C     AGG
                                AGTG TCCAAGG   TGGCCA
                                |||| |||||||   ||||||
                                TTAC AGGTTCC   ACTGGT
                                  A      A__
GAM1136  LOC205258 5'  CACTGCTCCTCAGAGCACTTG  92361        CA    __
                                TAAGTGCTC  AGGAG  GTG
                                |||||||||  |||||  |||
                                GTTCACGAG  TCCTC  CAC
                                      AC     GT
GAM1136  LOC219654 3'  TACCCTCTGAGCACTTA     92940        CA  GA
                                TAAGTGCTC  AG  GGTG
                                |||||||||  ||  ||||
                                ATTCACGAG  TC  CCAT
                                      __  TC
GAM1136  LOC220827 3'  TGGCTACCTTAGAGCAC     92885      CAAG
                                GTGCTC    GAGGTGGCCA
                                ||||||    ||||||||||
                                CACGAG    TTCCATCGGT
                                   A___
GAM1136  LOC222160 3'  TGGCTCTCACTTTGGAGCACTT 95795           A GT
            A                    TAAGTGCTCCAAGG G  GGCCA
                                ||||||||||||||  |  |||||
                                ATTCACGAGGTTTC C  TCGGT
                                        A TC
GAM1137  CELSR3    3'  CCTCCTGCTCCCCAGTGGTGG  9186           C   TCAA
                                TCACCACTGGGGA CAG    AGG
                                |||||||||||||  |||    |||
                                GGTGGTGACCCCT GTC    TCC
                                        C   C___
GAM1137  CXCL16    3'  CCCTTGCCTACCCCAGTG    42164        ACC  T   A
                                CACTGGGG   AG CAA GG
                                ||||||||   || ||| ||
                                GTGACCCC   TC GTT CC
                                     A__  C   C
GAM1137  EPB49     3'  CCTCTGCAGTCCCCGGCAGTGA 10526     CA       CA T  A
                                TCAC  CTGGGGAC  G CA AGG
                                ||||  ||||||||  | || |||
                                AGTG  GGCCCCTG  C GT TCC
                                   AC       A_ _  C
GAM1137  FBXL11    3'  CCCATCCATGGTCCCCAGCAGT 25513     CA        GTCAAA
            G                    CAC  CTGGGGACCA     GG
                                |||  ||||||||||     ||
                                GTG  GACCCCTGGT     CC
                                  AC         ACCTAC
GAM1137  GRM7      3'  CCTTTGACTGATCAGTGTGA   7785      C    GGAC
                                TCAC ACTGG    CAGTCAAAGG
                                |||| |||||    ||||||||||
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                                AGTG TGACT    GTCAGTTTCC
                                  _    A___
GAM1137  STAU     3'  CCTTTGACCGGCCCCAG     17197       A  A
                                CTGGGG CC GTCAAAGG
                                |||||| || ||||||||
                                GACCCC GG CAGTTTCC
                                   _ C
GAM1137  ACF      3'  CCTCTAACTCGGTCCCCAATG  58035    C      _  CAA
                                CA TGGGGACC AGT   AGG
                                || |||||||| |||   |||
                                GT ACCCCTGG TCA   TCC
                                 A       C   ATC
GAM1137  C20orf130 3'  CCTTTGATCCTCCCCCAAGGTG 62413      ACT    CCA
              A                  TCACC   GGGGA   GTCAAAGG
                                |||||   |||||   ||||||||
                                AGTGG   CCCCT   TAGTTTCC
                                   AAC    CC_
GAM1137  DKFZP434B044 3'  CCTTTGACTGATGTTCAGTG   49715       GAC
                                CACTGGG   CAGTCAAAGG
                                |||||||   ||||||||||
                                GTGACTT   GTCAGTTTCC
                                    GTA
GAM1137  DKFZP762D096 3'  CCTCTGACTGGCCCCCCAGTG  66180        A_     A
                                CACTGGGG  CCAGTCA AGG
                                ||||||||  ||||||| |||
                                GTGACCCC  GGTCAGT TCC
                                     CC      C
GAM1137  DOCK3    3'  ACAGGAGCCCCAGTGGTGA    67088          A_  A
                                TCACCACTGGGG  CC GT
                                ||||||||||||  || ||
                                AGTGGTGACCCC  GG CA
                                       GA  A
GAM1137  EDR2     3'  CTGGGAGTCCCAGTGGTGA    61110          A__
                                TCACCACTGGGG   CCAG
                                ||||||||||||   ||||
                                AGTGGTGACCCT   GGTC
                                       GAG
GAM1137  FLJ10922  3'  CCCCTGACTGGTCCCCAG     37399            AA
                                CTGGGGACCAGTCA  GG
                                ||||||||||||||  ||
                                GACCCCTGGTCAGT  CC
                                       CC
GAM1137  FLJ20257  3'  CCTTTGCCCTCCCCCAGTGGGA 39485     A       ACCA T
                                TC CCACTGGGG    G CAAAGG
                                || |||||||||    | ||||||
                                AG GGTGACCCC    C GTTTCC
                                  _       CTCC _
GAM1137  GPR64    3'  CCCCTGACCGCATCCCCAGTAG 20444     C       CCA_   AA
              T                   AC ACTGGGGA    GTCA  GG
                                || ||||||||    ||||  ||
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                                TG TGACCCCT   CAGT  CC
                                 A      ACGC   CC
GAM1137 KIAA0450 3' CTCTGACCGTCAGTGGTGG   28350       GGG  CA   A
                                TCACCACT   GAC  GTCA AG
                                ||||||||   |||  |||| ||
                                GGTGGTGA   CTG  CAGT TC
                                     ___   C_   C
GAM1137 KIAA1171 3' CCTCTGACTGGGCGCACAGTGG 89342       GGGA_     A
             TG                   CACCACTG    CCAGTCA AGG
                                ||||||||    ||||||| |||
                                GTGGTGAC    GGTCAGT TCC
                                     ACGCG      C
GAM1137 KREMEN   3' CCTTTGACTTCGCCACATGG   50233    C_  G  CC
                                CCA  TGG GA  AGTCAAAGG
                                |||  ||| ||  |||||||||
                                GGT  ACC CT  TCAGTTTCC
                                  AC   G  __
GAM1137 MGC29762 3' CCTTTGACTAAGGGGGGTGTTG 59144     C   GGGGA  __
             A                   TCA CACT    CC  AGTCAAAGG
                                ||| ||||    ||  |||||||||
                                AGT GTGG    GG  TCAGTTTCC
                                  T   GG___  AA
GAM1137 OBTP     3' CCTGGATCCAGTCCCCAGCAGG 34664    A_      CA_  AA
                                CC  CTGGGGAC   GTC  AGG
                                ||  ||||||||   |||  |||
                                GG  GACCCCTG   TAG  TCC
                                 AC       ACC   G_
GAM1137 P66      3' CTGACTGTAAGTGGTGG     40740        GGGGAC     AA
                                TCACCACT     CAGTCA  G
                                ||||||||     ||||||  |
                                GGTGGTGA     GTCAGT  C
                                     AT_____     C
GAM1137 PISD     3' CTGGGGAGCCCCCAGTGGCGG  27543    A       A_____
                                TC CCACTGGGG    CCAG
                                || |||||||||    ||||
                                GG GGTGACCCC    GGTC
                                 C        CGAGG
GAM1137 RBM7     3' CCTTTGACTAAGTTGATATGG  32734     C  GG   C_
                                CCA TG  GAC  AGTCAAAGG
                                ||| ||  |||  |||||||||
                                GGT AT  TTG  TCAGTTTCC
                                  _  AG   AA
GAM1137 YEA      5' CCGCGGCGGCCCCCAGTG    52600        A  A   AAA
                                CACTGGGG CC GTC   GG
                                |||||||| || |||   ||
                                GTGACCCC GG CGG   CC
                                     C  _   CG_
GAM1137 LOC125704 3' CCTGGGGTCCCCAGTGGGA   74876    A          AGTCAA
                                TC CCACTGGGGACC     AGG
                                || ||||||||||||     |||
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                                AG GGTGACCCCTGG     TCC
                                 _         GG____
GAM1137  LOC138389 3'  CCTTCAGCTCCCCCAGTGG   76735        ACC   CA
                                CCACTGGGG   AGT  AAGG
                                |||||||||   |||  ||||
                                GGTGACCCC   TCG  TTCC
                                     C__   AC
GAM1137  LOC146714 5'  CCTTGTTCCTGCCCAGTGG   84744        GAC   TCA_
                                CCACTGGG   CAG    AAGG
                                ||||||||   |||    ||||
                                GGTGACCC   GTC    TTCC
                                    ___   CTTG
GAM1137  LOC200282 3'  ACTGCATCCCCAGTAATGA   90097     CC      C_
                                TCA  ACTGGGGA  CAGT
                                |||  ||||||||  ||||
                                AGT  TGACCCCT  GTCA
                                  AA       AC
GAM1137  LOC255739 3'  CCTTGCTGGGAGTCCCCAG   97905       ___    CA
                                CTGGGGA   CCAGT  AAGG
                                |||||||   |||||  ||||
                                GACCCCT   GGTCG  TTCC
                                   GAG    __
GAM1138  SCAMP1    3'  GCTAAATAAATATTCTCC    54500     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1138  SCAMP1    3'  GCTAAATAAATATTCTCC    54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1138  NX-17     3'  TGAATATCAGCCCCTAATA   40706        ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                     CGAC
GAM1138  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
              TA                  TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM1139  SCAMP1    3'  GCTAAATAAATATTCTCC    54500     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1139  SCAMP1    3'  GCTAAATAAATATTCTCC    54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
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                                CCT TTATAA TAAATCG
                                  C     A
GAM1139 NX-17    3' TGAATATCAGCCCCTAATA   40706        ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM1139 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
              TA                  TATTAGGGATAATATTCATTTAGC
                                  ||||||||||||||||||||||||
                                  ATAATCCCTATTATAAGTAAATCG

GAM1140 ATOX1    5' GTGGAGAGGCGCTGCTG     15750     C   A
                                CAGC AGC CCTCTTTAT
                                |||| ||| |||||||||
                                GTCG TCG GGAGAGGTG
                                  _   C
GAM1140 AXUD1    3' GGCTCTGCGGGCAGGTGCTGGC 53445         C  TA   A
                                GCCAGCACCT TT  TAGA CC
                                |||||||||| ||  |||| ||
                                CGGTCGTGGA GG  GTCT GG
                                     C  GC   C
GAM1140 BTEB1    3' GTTCTATAAAGAGAACTGCT   8671      C__
                                AGCA   CTCTTTATAGAAC
                                ||||   ||||||||||||
                                TCGT   GAGAAATATCTTG
                                  CAA
GAM1140 CYP1A1   3' GGCTCTGTGAGGGTGCTGACTG 6692     C      CT     A
                                CAG CAGCACCT  TTATAGA CC
                                ||| ||||||||  ||||||| ||
                                GTC GTCGTGGG  AGTGTCT GG
                                  A       __      C
GAM1140 EFNB2    3' CTGGGGAAAGGGCTGGCTG   15843        A  C  TA
                                CAGCCAGC CCT TT  TAG
                                |||||||| ||| ||  |||
                                GTCGGTCG GGA AG  GTC
                                    _  A  GG
GAM1140 HSPD1    3' ATGAAGAAAAAGGCTGGCTG   60809        ACC__
                                CAGCCAGC    TCTTTAT
                                ||||||||    |||||||
                                GTCGGTCG    AGAAGTA
                                    GAAAA
GAM1140 IGF1     3' TTTTATAGAGGGCTG      7090      A    TT
                                CAGC CCTCT  ATAGAA
                                |||| |||||  ||||||
                                GTCG GGAGA  TATTTT
                                  _    __
GAM1140 IL17E    3' CTGTGAAGTGCTGTCTG     43299     C     CTC
                                CAG CAGCAC   TTTATAG
                                ||| ||||||   |||||||
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                                GTC GTCGTG   AAGTGTC
                                  T    ___
GAM1140 NCOA6    5' GGTCCTTATGAAGCACTGCTG 26841      CCT      A_
                                CAGCA  CTTTATAG  ACC
                                |||||  ||||||||  |||
                                GTCGT  GAAGTATT  TGG
                                   CAC       CC
GAM1140 PHB      3' GGTTCCTGTGCAGATGCTGCTG 12070     C   CC  T   _
                                CAGC AGCA  TCT TATAG AACC
                                |||| ||||  ||| ||||| ||||
                                GTCG TCGT  AGA GTGTC TTGG
                                  _   __  C    C
GAM1140 PKHD1    3' GTTCTATGAGAAGTACTGGC   57716      C C   T
                                GCCAG AC TCTT ATAGAAC
                                ||||| || |||| |||||||
                                CGGTC TG AGAG TATCTTG
                                   A A   _
GAM1140 PTPRF    3' GGTTCCCGAGGGAGCTGCTGGC 56140        C     ATA
            TG                    CAGCCAGCA CTCTTT   GAACC
                                |||||||||| ||||||   |||||
                                GTCGGTCGT GAGGGA   CTTGG
                                     C     GCC
GAM1140 RGL      5' GGTCCTGCGTAAGGTCCGGCTG 31428      AGC   CTTTA  A
                                CAGCC   ACCT    TAG ACC
                                |||||   ||||    ||| |||
                                GTCGG   TGGA    GTC TGG
                                   CC_   ATGC_  C
GAM1140 SDC1     5' TCGGCGGGAGAGGTGCGGGC   12992     A       ATA_
                                GCC GCACCTCTTT   GA
                                ||| ||||||||||   ||
                                CGG CGTGGAGAGG   CT
                                  G        GCGG
GAM1140 SH3BP4   3' TGTGCAGAGGTGCCAGCTG   28003     CA      T
                                CAGC  GCACCTCT TATA
                                ||||  |||||||| ||||
                                GTCG  CGTGGAGA GTGT
                                   AC       C
GAM1140 SLC31A1  5' TTCGGAGAGAGAGGTGCTAGT  10281    C       ATA_
                                GC AGCACCTCTTT   GAA
                                || ||||||||||   |||
                                TG TCGTGGAGAGA   CTT
                                 A         GAGG
GAM1140 TNFRSF10C 3' GGTTCAGGTAGGCGCTGGCTG  15204       A  _  TATA
                                CAGCCAGC CCT CTT   GAACC
                                |||||||| ||| |||   |||||
                                GTCGGTCG GGA GGA   CTTGG
                                     C  T  ____
GAM1140 USP11    5' GGTTCCTTGTGGAGAAGCACTG 17385      CACC      __
            GT                    GCCAG   TCTTTATA  GAACC
                                |||||   ||||||||  |||||
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                                TGGTC   AGAGGTGT  CTTGG
                                  ACGA      TC
GAM1140  ZNF32    5'  TCATATGAAGAGGTGGTGACTG 93105    C  G        _
                                CAG CA CACCTCTTTATA GA
                                ||| || ||||||||||||| ||
                                GTC GT GTGGAGAAGTAT CT
                                  A  G          A
GAM1140  APELIN   3'  TCTAGTTAAGAGGTGCTGGCTG 34272            TA_
                                CAGCCAGCACCTCTT   TAGA
                                ||||||||||||||   ||||
                                GTCGGTCGTGGAGAA   ATCT
                                        TTG
GAM1140  C20orf46 3'  GGCCTTGTGGAAGAAGTACTGG 37735    G   C  C    _   AA
            GTG                   CA CCAG AC TCTTT ATAG  CC
                                || |||| || ||||| ||||  ||
                                GT GGTC TG AGAAG TGTT  GG
                                 G   A A    G   CC
GAM1140  CALN1    3'  GTTCTGGAGAGGCGCCGC    49670    CA  A     TA
                                GC  GC CCTCTT  TAGAAC
                                ||  || ||||||  ||||||
                                CG  CG GGAGAG  GTCTTG
                                 C_  C     __
GAM1140  caspr5   3'  TTTTGTAAGAATGCTAGCT   56255    C   CC   T
                                AGC AGCA  TCTT ATAGAA
                                ||| ||||  |||| ||||||
                                TCG TCGT  AGAA TGTTTT
                                  A   A_   _
GAM1140  CECR6    3'  GGTTTTGTGAAAGAGAGCTAGC 49934     C   AC    _
            TG                    CAGC AGC  CTCTT TATAGAACC
                                |||| |||  ||||| |||||||||
                                GTCG TCG  GAGAA GTGTTTTGG
                                  A  A_    A
GAM1140  CGI-51   5'  TCTGCGAGGCAGCGGCTG    69028      A  A_   TTTA
                                CAGCC GC  CCTC    TAGA
                                ||||| ||  ||||   ||||
                                GTCGG CG  GGAG    GTCT
                                   _ AC   C___
GAM1140  DKFZP434B195 3'  GGCTCCATAGGTTATAGGCTGG 49248        ACCTC_    A  A
            CTG                   CAGCCAGC     TTTAT GA CC
                                ||||||||     ||||| || ||
                                GTCGGTCG     GGATA CT GG
                                     GATATT    C  C
GAM1140  DKFZP564D116 3'  CTGTAGAGGAGCTAACTG    72671     CC   A    TT
                                CAG  AGC CCTCT  ATAG
                                |||  ||| |||||  ||||
                                GTC  TCG GGAGA  TGTC
                                  AA   A    __
GAM1140  DNAJC5   3'  GTTCAGCCTGAGATGCTGGCTG 62142         C   TTTATA
                                CAGCCAGCA CTC     GAAC
                                ||||||||| |||     ||||
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                                GTCGGTCGT GAG     CTTG
                                     A   TCCGA_
GAM1140  EIF5     3'  TTCTGTAGGAGATACTGGT   10510      CAC    T
                                GCCAG   CTCTT ATAGAA
                                |||||   ||||| ||||||
                                TGGTC   GAGGA TGTCTT
                                   ATA    _
GAM1140  FLJ11342 3'  TTGTGAAGAAGGACCAGCTG   37838      CAGCA  _
                                CAGC    CCT CTTTATAG
                                ||||    ||| ||||||||
                                GTCG    GGA GAAGTGTT
                                  ACCA_  A
GAM1140  FLJ20666 5'  GGTTCAATAAAGGTGCTGAATG 35928    GC      CT    A
                                CA  CAGCACCT  TTAT GAACC
                                ||  ||||||||  |||| |||||
                                GT  GTCGTGGA  AATA CTTGG
                                 AA       __    A
GAM1140  FLJ21916 3'  CTGGGCAGAGGTGCTGCT    43895     C       TTA
                                AGC AGCACCTCT   TAG
                                ||| |||||||||   |||
                                TCG TCGTGGAGA   GTC
                                  _       CGG
GAM1140  FLJ21952 5'  GTCCTGGCGAGGGCGCTGGC   42856       A_   TTTA   A
                                GCCAGC  CCTC    TAG AC
                                ||||||  ||||    ||| ||
                                CGGTCG  GGAG    GTC TG
                                   CG    CG__   C
GAM1140  FLJ32861 3'  GTTCTATTGGACAGTACTGGT  59383      C  C_   TT
                                GCCAG AC  TCT  ATAGAAC
                                ||||| ||  |||  |||||||
                                TGGTC TG  AGG  TATCTTG
                                   A  AC   T_
GAM1140  HNRPA3   3'  CTGTAAAGAAACACCTGCTG   20452     C  CACC_
                                CAGC AG    TCTTTATAG
                                |||| ||    |||||||||
                                GTCG TC    AGAAATGTC
                                  _  CACAA
GAM1140  HT002    3'  GTCCTGTGGGGAGATTCTG   26801     CAC        A
                                CAG   CTCTTTATAG AC
                                |||   ||||||||||  ||
                                GTC   GAGGGGTGTC TG
                                  TTA        C
GAM1140  KIAA1265 3'  TTTGTGAGAAGTGCAAGC    71340    CA    C    T
                                GC  GCAC TCTT ATAGA
                                ||  |||| |||| |||||
                                CG  CGTG AGAG TGTTT
                                 AA   A   _
GAM1140  KIAA1579 3'  GGTTCTTTATAGAAAAATGCTG 37152     C    CC__   T  T
            CT                   AGC AGCA    TCT TA AGAACC
                                ||| ||||    ||| || ||||||
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                                TCG TCGT    AGA AT TCTTGG
                                  _    AAAA   T  T
GAM1140 KIAA1872 3' GGTTCCTGTGGAGCCACCGGCT 63616      AGCACCT      _
             G                   CAGCC      CTTTATAG AACC
                                 |||||      |||||||| ||||
                                 GTCGG      GAGGTGTC TTGG
                                   CCACC__       C
GAM1140 LEAP-2   5' GGCCCTTGGGAAGAGGTATTAG 54809    C  C       AT_  AA
             C                   GC AG ACCTCTTT   AG  CC
                                 || || ||||||||   ||  ||
                                 CG TT TGGAGAAG   TC  GG
                                  A  A       GGT  CC
GAM1140 LRRFIP2  3' TTCTATGAGTGCTCACTG    21954     CC    CTCT
                                 CAG  AGCAC    TTATAGAA
                                 |||  |||||    ||||||||
                                 GTC  TCGTG    AGTATCTT
                                   AC    _____
GAM1140 MGC16279 5' GTCTGCAGAGGCTGGCTG    52990        AC    TTA   A
                                 CAGCCAGC  CTCT   TAG AC
                                 ||||||||  ||||   ||| ||
                                 GTCGGTCG  GAGA   GTC TG
                                      __   C__   C
GAM1140 MGC16386 3' GTTGATAGGGCGCTGGCTG   55616        A   CTT   AG
                                 CAGCCAGC CCT   TAT  AAC
                                 |||||||| |||   |||  |||
                                 GTCGGTCG GGG   ATA  TTG
                                      C   ___   G_
GAM1140 MGC2477  5' GGTGTCCAAGAAGTGCTGGC  44310        C    TATAGA
                                 GCCAGCAC TCTT      ACC
                                 ||||||||  ||||     |||
                                 CGGTCGTG AGAA      TGG
                                      A   CCTG__
GAM1140 MGC29956 3' GGCTCTGTAAGGAGAGGTGCAG 58923      CA        __      A
             CTG                   CAGC  GCACCTCTT  TATAGA CC
                                   ||||  |||||||||  |||||| ||
                                   GTCG  CGTGGAGAG  ATGTCT GG
                                     A_        GA      C
GAM1140 MGC3038  3' GGCTCATTGTAAAGTGCCTGCT 49097      CA    CTC     __ A
             G                     CAGC  GCAC   TTTATA  GA CC
                                   ||||  ||||   ||||||  || ||
                                   GTCG  CGTG   AAATGT  CT GG
                                     TC    ___      TA  C
GAM1140 PPP1R14D 3' GGCTCTCTGGGAGAAAGCTGGC 35295        AC_    TAT   A
             TG                    CAGCCAGC   CTCTT   AGA CC
                                   ||||||||   |||||   ||| ||
                                   GTCGGTCG   GAGGG   TCT GG
                                      AAA     TC_   C
GAM1140 SDC3     5' GGTTCCGAGCCCAGGAGCTGGC 28480        A   CTTTATA
             TG                    CAGCCAGC CCT      GAACC
                                   |||||||| |||      |||||
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                                GTCGGTCG GGA      CTTGG
                                     A   CCCGAGC
GAM1140  SEC23B    5'  CTCTGAGGAGCGCTGGCTG   53350        AC      T
                                CAGCCAGC  CTCTTTA AG
                                ||||||||  ||||||| ||
                                GTCGGTCG  GAGGAGT TC
                                     C_      C
GAM1140  SIMRP7    3'  CTATACAGAGGTGCTGGCTG  93970            T
                                CAGCCAGCACCTCT TATAG
                                |||||||||||||| |||||
                                GTCGGTCGTGGAGA ATATC
                                          C
GAM1140  TCL6      3'  CTGGAAAGAGGCTGCTGGCTG 40472         _      A
                                CAGCCAGCA CCTCTTT TAG
                                ||||||||| ||||||| |||
                                GTCGGTCGT GGAGAAA GTC
                                     C      G
GAM1140  LOC133993 5'  GTCTGGAGGTGCTGG       76463          TTAT   A
                                CCAGCACCTCT    AGA C
                                ||||||||||    ||| |
                                GGTCGTGGAGG    TCT G
                                      ____   C
GAM1140  LOC142901 5'  GGTTCTATAAAGAGACATTGG  61120      CAC
                                CCAG   CTCTTTATAGAACC
                                ||||   ||||||||||||||
                                GGTT   GAGAAATATCTTGG
                                  ACA
GAM1140  LOC144501 3'  TTCCTGGGAAGGCTGGCTG    84035        ACC    TATA
                                CAGCCAGC   TCTT    GAA
                                ||||||||   ||||    |||
                                GTCGGTCG   AGGG    CTT
                                     GA_    TC__
GAM1140  LOC146280 3'  CTGTGGCAGAGGTGCAGGCTG  78349       A      _
                                CAGCC GCACCTCT TTATAG
                                ||||| |||||||| ||||||
                                GTCGG CGTGGAGA GGTGTC
                                   A       C
GAM1140  LOC146895 5'  GGTTCTACAAAGAGGTCAAAGC 84870     CAGC       A
           T                     AGC    ACCTCTTT TAGAACC
                                |||    |||||||| |||||||
                                TCG    TGGAGAAA ATCTTGG
                                  AAAC       C
GAM1140  LOC150311 5'  GTTTGTTAGAGGATGCTGGCTG 80567         _    TTATA
                                CAGCCAGCA CCTCT     GAAC
                                ||||||||| |||||     ||||
                                GTCGGTCGT GGAGA     TTTG
                                     A     TTG__
GAM1140  LOC150622 5'  TCTGCCAGTTGCTGGCTG     80770         C  CTTTA
                                CAGCCAGCA CT     TAGA
                                ||||||||| ||     ||||
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                                GTCGGTCGT GA    GTCT
                                     T  CC___
GAM1140  LOC152317 5'  GGCTCTATAAAAAAAAAACTGG 86835       CACCTC_      A
              CT                   AGCCAG      TTTATAGA CC
                                   ||||||      |||||||| ||
                                   TCGGTC      AAATATCT GG
                                      AAAAAAA       C
GAM1140  LOC157918 5'  GTCCTGTGTGAAGTGCTGGT   87931        C  TT    A
                                   GCCAGCAC TC  TATAG AC
                                   |||||||| ||  ||||| ||
                                   TGGTCGTG AG  GTGTC TG
                                        A  T_    C
GAM1140  LOC163682 3'  GGCTCTGAGGGGGAGGTACTTG 88410    C  C      A_   A
              C                    GC AG ACCTCTTT  TAGA CC
                                   || || ||||||||  ||||| ||
                                   CG TC TGGAGGGG  GTCT GG
                                    T  A       GA    C
GAM1140  LOC203248 3'  TCTATGAGGAAGATGCCAGT   90846    CA   C  _
                                   GC  GCA CT CTTTATAGA
                                   ||  ||| || |||||||||
                                   TG  CGT GA GGAGTATCT
                                    AC   A  A
GAM1140  LOC220988 3'  CTGTAAAGAAACACCTGCTG   92513     C  CACC_
                                   CAGC AG     TCTTTATAG
                                   |||| ||     |||||||||
                                   GTCG TC     AGAAATGTC
                                     _  CACAA
GAM1140  LOC90170  5'  TTCTGTAAAAGCGTTGGC    62382       AC  C
                                   GCCAGC  CT TTTATAGAA
                                   ||||||  || |||||||||
                                   CGGTTG  GA AAATGTCTT
                                      C_  _
GAM1141  SCAMP1    3'  GCTAAATAAATATTCTCC     18013     T     C
                                   GGA AATATT ATTTAGC
                                   ||| |||||| |||||||
                                   CCT TTATAA TAAATCG
                                     C     A
GAM1141  SCAMP1    3'  GCTAAATAAATATTCTCC     54501     T     C
                                   GGA AATATT ATTTAGC
                                   ||| |||||| |||||||
                                   CCT TTATAA TAAATCG
                                     C     A
GAM1141  NX-17     3'  TGAATATCAGCCCCTAATA    40706        ATA_
                                   TATTAGGG    ATATTCA
                                   ||||||||    |||||||
                                   ATAATCCC    TATAAGT
                                        CGAC
GAM1141  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
              TA                   TATTAGGGATAATATTCATTTAGC
                                   |||||||||||||||||||||||
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                                ATAATCCCTATTATAAGTAAATCG

GAM1142 SCAMP1   3' GCTAAATAAATATTCTCC    18013    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1142 SCAMP1   3' GCTAAATAAATATTCTCC    54501    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1142 NX-17    3' TGAATATCAGCCCCTAATA   40706       ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                     CGAC
GAM1142 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
             TA                   TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM1143 RNASE3L  5' CATCAAGGAGCTGATAATCTA 26013        ACA  GAA
                                TAGATTGTCA  TC  TTGATG
                                ||||||||||  ||  ||||||
                                ATCTAATAGT  AG  AACTAC
                                     CG_  G__
GAM1144 PIP5K1A  3' TATCCCACCCTGCCTTGATA  14520       A   CA  C
                                TATCAAGG AGGG  GG GTG
                                |||||||| ||||  || |||
                                ATAGTTCC TCCC  CC TAT
                                     G   A_  C
GAM1144 SOX11    3' ACCCACCCCCCCTTGGTA    13308       AA  CA  C
                                TATCAAGG  GGG  GG GT
                                ||||||||  |||  || ||
                                ATGGTTCC  CCC  CC CA
                                     CC   A_  _
GAM1144 CHL1     3' TGTTACCTTTCCTCAATA    22768    CA     CA
                                TAT  AGGAAGGG  GGCG
                                |||  ||||||||  ||||
                                ATA  TCCTTTCC  TTGT
                                  AC       A_
GAM1144 EPB41L1  3' CATTCTGCCCTTCCCTGA    71104    A       C
                                TCA GGAAGGGCAGG GTG
                                ||| |||||||||| |||
                                AGT CCTTCCCGTCT TAC
                                  C        _
GAM1144 FLJ00060 3' CATACCCCCTGCCCTCCTCTGA 61741    _   A     CGTG
                                TCA AGGA GGGCAGG   ATG
                                ||| |||| |||||||   |||
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                                AGT TCCT CCCGTCC   TAC
                                  C   _     CCCA
GAM1144  FLJ10898  5'  CACCACAGCCCTTTCTCAATA  60126    CA      AGGC
                                TAT  AGGAAGGGC   GTG
                                |||  |||||||||   |||
                                ATA  TCTTTCCCG   CAC
                                  AC       ACAC
GAM1144  FLJ22557  3'  ATCATCCCATCCTTAATA   45581    C   A  CAGGC
                                TAT AAGGA GGG    GTGAT
                                ||| ||||| |||    |||||
                                ATA TTCCT CCC    TACTA
                                  A    A  _____
GAM1144  KIAA0574  3'  CATCCCCTGCCCTCCCCTGA  69808    A  A      CGT
                                TCA GG AGGGCAGG  GATG
                                ||| || ||||||||  ||||
                                AGT CC TCCCGTCC  CTAC
                                  C  C      C__
GAM1144  KIAA0632  3'  CACCTCAGAAACCCTTCCTTGA 32071         CA___  C
                                TCAAGGAAGGG    GG GTG
                                ||||||||||    || |||
                                AGTTCCTTCCC    CT CAC
                                      AAAGA  C
GAM1144  KIAA1354  5'  CAGTGACTGCCTTCCCTTGATA 61572       A     G  _
                                TATCAAGG AGGGCAG CG TG
                                |||||||| ||||||| || ||
                                ATAGTTCC TTCCGTC GT AC
                                     C      A  G
GAM1144  MGC20460  5'  CACCGCCTCCTACCCTTCTT  54901       C___    _
                                AGGAAGGG   AGGCG TG
                                ||||||||   ||||| ||
                                TTCTTCCC   TCCGC AC
                                     ATCC    C
GAM1144  LOC158476 3'  CACGCCCGCCCCCCCCATTGA  88186    _ AA_   A
                                TCAA GG   GGGC GGCGTG
                                |||| ||   |||| ||||||
                                AGTT CC   CCCG CCGCAC
                                  A  CCC   C
GAM1144  LOC90459  3'  CACACCCGCCTAATTTTTG   63550      A_   A  C
                                CAAGGA  GGGC GG GTG
                                ||||||  |||| || |||
                                GTTTTT  TCCG CC CAC
                                   AA   C  A
GAM1145  FLJ22332  5'  GGAAAGAAAACTACATCACA  45637     G  A     _______
                                TGTG AT TAGTTTTC     CC
                                |||| || ||||||||     ||
                                ACAC TA ATCAAAAG     GG
                                  _  C       AAA___
GAM1146  AMACR    3'  TTGTATGCATGGAAACATGGA  69103      ATC       G
                                TCCAT   TCCATGCATG CGG
                                |||||   |||||||||| |||
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                                AGGTA  AGGTACGTAT GTT
                                  CAA       _
GAM1146 BCL2L11  3' TCGCCCAGAGATATGGA    57615       CA CAT   G
                                TCCATATCTC TG  GGCG A
                                |||||||||| ||  |||| |
                                AGGTATAGAG AC  CCGC T
                                     __ ___   G
GAM1146 BCL2L11  3' TCGCCCAGAGATATGGA    57616       CA CAT   G
                                TCCATATCTC TG  GGCG A
                                |||||||||| ||  |||| |
                                AGGTATAGAG AC  CCGC T
                                     __ ___   G
GAM1146 FGFR2    5' CGTCCACATGGAGATATGGA  5559          CA  _
                                TCCATATCTCCATG TGG CG
                                |||||||||||||| ||| ||
                                AGGTATAGAGGTAC ACC GC
                                     __  T
GAM1146 FGFR2    5' CGTCCACATGGAGATATGGA  43633         CA  _
                                TCCATATCTCCATG TGG CG
                                |||||||||||||| ||| ||
                                AGGTATAGAGGTAC ACC GC
                                     __  T
GAM1146 FGFR2    5' CGTCCACATGGAGATATGGA  43638         CA  _
                                TCCATATCTCCATG TGG CG
                                |||||||||||||| ||| ||
                                AGGTATAGAGGTAC ACC GC
                                     __  T
GAM1146 FGFR2    5' CGTCCACATGGAGATATGGA  43642         CA  _
                                TCCATATCTCCATG TGG CG
                                |||||||||||||| ||| ||
                                AGGTATAGAGGTAC ACC GC
                                     __  T
GAM1146 FGFR2    5' CGTCCACATGGAGATATGGA  43652         CA  _
                                TCCATATCTCCATG TGG CG
                                |||||||||||||| ||| ||
                                AGGTATAGAGGTAC ACC GC
                                     __  T
GAM1146 FGFR2    5' CGTCCACATGGAGATATGGA  43665         CA  _
                                TCCATATCTCCATG TGG CG
                                |||||||||||||| ||| ||
                                AGGTATAGAGGTAC ACC GC
                                     __  T
GAM1146 FGFR2    5' CGTCCACATGGAGATATGGA  43674         CA  _
                                TCCATATCTCCATG TGG CG
                                |||||||||||||| ||| ||
                                AGGTATAGAGGTAC ACC GC
                                     __  T
GAM1146 FGFR2    5' CGTCCACATGGAGATATGGA  43678         CA  _
                                TCCATATCTCCATG TGG CG
                                |||||||||||||| ||| ||
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                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM1146  FGFR2    5'  CGTCCACATGGAGATATGGA  43763          CA  _
                                TCCATATCTCCATG  TGG CG
                                |||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM1146  FGFR2    5'  CGTCCACATGGAGATATGGA  43767          CA  _
                                TCCATATCTCCATG  TGG CG
                                |||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM1146  FGFR2    5'  CGTCCACATGGAGATATGGA  43771          CA  _
                                TCCATATCTCCATG  TGG CG
                                |||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM1146  MAP3K14  3'  ATCCGCCACGTGAAGAGA   15541     CA  A
                                TCTC  TGC TGGCGGAT
                                ||||  ||| ||||||||
                                AGAG  GTG ACCGCCTA
                                  AA  C
GAM1146  KIAA0819  3'  CCCCAGCATCACAGGAGACATG 64330      A   ____   A  C
            GA                    TCCAT TCTCC   ATGC TGG GG
                                |||||  |||||   ||||  ||| ||
                                AGGTA  AGAGG   TACG ACC CC
                                  C    ACAC   _  _
GAM1146  PORIMIN  3'  CATACATGGAGTATGGA    54702       T     C
                                TCCATA CTCCATG ATG
                                ||||||  ||||||| |||
                                AGGTAT GAGGTAC TAC
                                   _     A
GAM1146  RDC1     3'  CCGGCACGGGATATGGA    72832        T  A  A
                                TCCATATC CC TGC TGG
                                ||||||||  ||  ||| |||
                                AGGTATAG GG ACG GCC
                                     _ C  _
GAM1146  VEZATIN  3'  ATCCGCCACAACAGACAATG  34656    A_  CCA  CA
                                CAT  TCT   TG  TGGCGGAT
                                |||  |||   ||  ||||||||
                                GTA  AGA   AC  ACCGCCTA
                                  AC   CA_ __
GAM1146  LOC147645 5'  ATCCGCTGGTGGCAGAGACACG 79065    ATA   CA   AT__
            G                    CC   TCTC  TGC   GGCGGAT
                                ||   ||||  |||   |||||||
                                GG   AGAG  ACG   TCGCCTA
                                 CAC    __  GTGG
GAM1146  LOC199775 3'  TTGCTGCATCAGAGATATG   89726       C_   TG
                                CATATCTC  ATGCA  GCGG
                                ||||||||  |||||  ||||
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                                GTATAGAG  TACGT  CGTT
                                    AC    __
GAM1146 LOC51279 3' CCGCTATTAGAGTATGGA    33752      T  CATGC
                                TCCATA CTC    ATGGCGG
                                ||||||| |||    |||||||
                                AGGTAT GAG    TATCGCC
                                   _  AT___
GAM1147 MRPL11   3' ATCAGGCCTGAATAAACATCC  32649    CGG__
                                GGA    GTTCAGGCCTGAT
                                |||    ||||||||||||
                                CCT    TAAGTCCGGACTA
                                  ACAAA
GAM1147 MYOZ2    5' ATCAGGCCCAAGTGCCATCCAT 33938     CG  TCA__
                                ATGGA  GGT    GGCCTGAT
                                |||||  |||    ||||||||
                                TACCT  CCG    CCGGACTA
                                   A_  TGAAC
GAM1147 LOC145226 3' TCAGGCCCAATCCATGCCA   77561    AC_    CA
                                TGG   GGGTT  GGCCTGA
                                |||   |||||  |||||||
                                ACC   CCTAA  CCGGACT
                                  GTA    C_
GAM1147 LOC146108 5' ATCAGACCCAAGGGCCCGTTCA 78146         A__  C
                                TGGACGGGTTC   GG CTGAT
                                ||||||||||   || |||||
                                ACTTGCCCGGG   CC GACTA
                                      AAC  A
GAM1148 SCAMP1   3' GCTAAATAAATATTCTCC    54500    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1148 SCAMP1   3' GCTAAATAAATATTCTCC    54501    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1148 NX-17    3' TGAATATCAGCCCCTAATA   40706       ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM1148 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
            TA                   TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM1149 ACAT1    5' GGTGCGGGGTTGGGGAG     5238         TACAT  G
                                TTTCCTAGC    CT GTACC
                                |||||||||    || |||||
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                                GAGGGGTTG    GG CGTGG
                                     _____ G
GAM1149 ACP2    3' AGGTTGTCTGTACTTGGGAGG 9651        C   TCTGGT
                                TTTCCTAG TACA     ACCT
                                |||||||| ||||     ||||
                                GGAGGGTT ATGT     TGGA
                                    C   CTGT__
GAM1149 ADAMTS13 3' AGGTGCCAGGTGTGTGGTGGGG 58148     A     __
            A                    TCCT GCTACAT  CTGGTACCT
                                |||| |||||||  |||||||||
                                AGGG TGGTGTG  GACCGTGGA
                                  G      TG
GAM1149 AK3     5' GGTGCCAGAGGTAGGGGG    26399     AG   A
                                CCT  CTAC TCTGGTACC
                                |||  |||| |||||||||
                                GGG  GATG AGACCGTGG
                                  G_   G
GAM1149 AXIN1   3' AGGTGCCAGGTGCCTCGGAGGA 61533       T  CTA
                                TTTTCC AG   CATCTGGTACCT
                                |||||| ||   ||||||||||||
                                AGGAGG TC   GTGGACCGTGGA
                                    C  C__
GAM1149 BACH1   3' GGGTGTCAGCTACTGGGAA   8634        C  CAT   GT
                                TTCCTAG TA   CTG  ACCT
                                ||||||| ||   |||  ||||
                                AAGGGTC AT   GAC  TGGG
                                    _ C__   TG
GAM1149 BAPX1   3' GGGTGCTGAATGTAAGGAGG  8647       AGC    CT
                                TTTCCT   TACAT  GGTACCT
                                ||||||   |||||  |||||||
                                GGAGGA   ATGTA  TCGTGGG
                                    ___    AG
GAM1149 BAZ2A   3' GGGTGCCAGGTGAGGTGGAG  26513     TA   A
                                TTCC  GCT CATCTGGTACCT
                                ||||  ||| ||||||||||||
                                GAGG  TGG GTGGACCGTGGG
                                  __  A
GAM1149 BAZ2A   3' GGTACTTGCACTGGGGAG    26514       CTA  TCT
                                TTTCCTAG   CA   GGTACC
                                ||||||||   ||   ||||||
                                GAGGGGTC   GT   TCATGG
                                    AC_  ___
GAM1149 BSN     3' AGGTATCATTGCTGTGGAAAA  14376      _   TACATC
                                TTTTCC TAGC     TGGTACCT
                                |||||| ||||     ||||||||
                                AAAAGG GTCG     ACTATGGA
                                   T   TT_____
GAM1149 C4BPB   5' GGTGTCTGAGCTGGGTGAA   7390     T      A  TCT GT
                                TTT CCTAGCT CA   G  ACC
                                ||| ||||||| ||   |  |||
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                                AAG GGGTCGA GT   C  TGG
                                 T      _ ___ TG
GAM1149  CACNG6   3'  AGCTCCGGGTGCGGTTGGGGGA 49945    TT     TA      TACCT
              G                   TT  CCTAGC  CATCTGG
                                  ||  ||||||  |||||||
                                  GA  GGGTTG  GTGGGCC
                                   GG     GC      TCGA
GAM1149  CASP4    5'  AGGTGTTGGAATCCCTGGGCAA 8722      T    CTACA   GG
              A                   TTT CCTAG    TCT  TACCT
                                  ||| |||||    |||  |||||
                                  AAA GGGTC    AGG  GTGGA
                                   C    CCTA_   TT
GAM1149  CASP4    5'  AGGTGTTGGAATCCCTGGGCAA 8723      T    CTACA   GG
              A                   TTT CCTAG    TCT  TACCT
                                  ||| |||||    |||  |||||
                                  AAA GGGTC    AGG  GTGGA
                                   C    CCTA_   TT
GAM1149  CCND2    3'  AGGTACCAGGTGTCAGGAAA   10045       AGCT
                                  TTTCCT    ACATCTGGTACCT
                                  ||||||    ||||||||||||
                                  AAAGGA    TGTGGACCATGGA
                                     C___
GAM1149  CD14     5'  GGGTGCCGCTGTGTAGGAAAG  67142        GC    TC
                                  TTTTCCTA  TACA  TGGTACCT
                                  ||||||||  ||||  ||||||||
                                  GAAAGGAT  GTGT  GCCGTGGG
                                       __    C_
GAM1149  CD68     3'  GGGTTGGGGTGTGGTGGGGGGG 60507   TT   A       GGT
                                  T  CCT GCTACATCT   ACCT
                                  |  ||| |||||||||   ||||
                                  G  GGG TGGTGTGGG   TGGG
                                   GG   G       GT_
GAM1149  CDC7L1   3'  GTCTTAGGTGGGTTGGGAAGA  14494          A      T
                                  TTTTCCTAGCT CATCTGG AC
                                  |||||||||| ||||||| ||
                                  AGAAGGGTTGG GTGGATT TG
                                         _      C
GAM1149  CDKN2D   5'  GGGAGGGTGAGTTAGGGGGA   55324    TT     A    GGTA
                                  TT  CCTAGCT CATCT    CC
                                  ||  ||||||| |||||    ||
                                  AG  GGATTGA GTGGG    GG
                                   GG      _     AG__
GAM1149  CNR1     3'  GGGTGCTAGAGGATTAGTAAG  10230    A   CA__
                                  CT GCTA    TCTGGTACCT
                                  || ||||    ||||||||||
                                  GA TGAT    AGATCGTGGG
                                   A   TAGG
GAM1149  COL18A1  3'  AGGTCCCTGGGGCTAGGGGGA  48341    TT     TA  TCT  T
                                  TT  CCTAGC  CA   GG ACCT
                                  ||  ||||||  ||   || ||||
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                                AG  GGATCG  GT   CC TGGA
                                 GG     GG ___  C
GAM1149  COL4A5   5'  GGGTGCTGAAGGAGCTGCGGGA 54133      _    ACA  T
                                TTCC TAGCT   TC GGTACCT
                                |||| |||||   || |||||||
                                AGGG GTCGA   AG TCGTGGG
                                  C    GGA  _
GAM1149  COX7A2L  3'  GGATTTGGATGTGGCTATGGAA 17531      _       TG TA  T
             A                   TTTCC TAGCTACATC  G  CC
                                 ||||| ||||||||||  |  ||
                                 AAAGG ATCGGTGTAG  T  GG
                                    T         GT TA
GAM1149  CR1      5'  GGTTTGTAGATGTGCTTGGGGA 6948         _ T      GT_   T
             GA                    TTTTCCTA GC ACATCTG   ACC
                                 |||||||| || |||||||   |||
                                 AGAGGGGT CG TGTAGAT   TGG
                                      T _      GTT
GAM1149  CREBL1   3'  GGGTACCAGGTGGCCAGGTGGG 16498      G  A__
             A                   TCCTA CT   CATCTGGTACCT
                                 |||||| ||   ||||||||||||
                                 AGGGT GA   GTGGACCATGGG
                                    G  CCG
GAM1149  CYP2A6   3'  AGGTGCTTCCGAGCTGGGA   7534         ACATCT
                                 TCCTAGCT     GGTACCT
                                 ||||||||     |||||||
                                 AGGGTCGA     TCGTGGA
                                      GCCT__
GAM1149  D12S2489E 3'  TGGATGGGCTGGGGGAG     24764    TT      A
                                 TT  CCTAGCT CATCTG
                                 ||  ||||||| ||||||
                                 GA  GGGTCGG GTAGGT
                                  GG      _
GAM1149  DDX3     3'  GGAATGATAGTTGGGAAGA   9059           _  _
                                 TTTTCCTAGCTA CAT CT
                                 |||||||||||| ||| ||
                                 AGAAGGGTTGAT GTA GG
                                         A   A
GAM1149  DES      3'  AGGTGCTGGAGGTGGGAG    72590       G TACA  TG
                                 TTCCTA C    TC  GTACCT
                                 |||||| |    ||  ||||||
                                 GAGGGT G    AG  CGTGGA
                                    G _____  GT
GAM1149  DGCR2    3'  GGGTGCCAGGTGGCCAGTGAGG 18907     A   A__
                                 CCT GCT   CATCTGGTACCT
                                 ||| |||   ||||||||||||
                                 GGA TGA   GTGGACCGTGGG
                                   G   CCG
GAM1149  DYRK2    3'  GGGTGTTGGGGGTAGTGGGAGG 14557        G    AT  GG
             A                   TTTTCCTA CTAC  CT  TACCT
                                 |||||||| ||||  ||  |||||
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                                AGGAGGGT GATG  GG  GTGGG
                                     _   GG  TT
GAM1149  E2F3     3'  GGGTGTATGTTTGGGAAGA   10469         _ _
                                TTTTCCTAG C TACATCT
                                ||||||||| | |||||||
                                AGAAGGGTT G ATGTGGG
                                     T T
GAM1149  EFNB2    3'  GGAGTGGGGCTGGGGAAA    15844          TA  _
                                TTTTCCTAGC  CA TCT
                                ||||||||||  || |||
                                AAAGGGGTCG  GT AGG
                                     GG  G
GAM1149  EGLN2    3'  AGGTATGGAGAGCTGGGAGGA  54909          ACA    G
                                TTTTCCTAGCT   TCTG TACCT
                                ||||||||||   |||| |||||
                                AGGAGGGTCGA   AGGT ATGGA
                                     G__   _
GAM1149  EGLN2    3'  AGGTATGGAGAGCTGGGAGGA  54910          ACA    G
                                TTTTCCTAGCT   TCTG TACCT
                                ||||||||||   |||| |||||
                                AGGAGGGTCGA   AGGT ATGGA
                                     G__   _
GAM1149  EIF4EBP1 3'  AGGTTGATGTGCTTGGGAAAG  15850        _ T    TGGT
                                TTTTCCTA GC ACATC    ACCT
                                |||||||| || |||||    ||||
                                GAAAGGGT CG TGTAG    TGGA
                                     T _    T___
GAM1149  EIF4EBP2 3'  GGGTGCCAAATGATGGGAAGA  15859        GCTA   C
                                TTTTCCTA    CAT TGGTACCT
                                ||||||||    ||| ||||||||
                                AGAAGGGT    GTA ACCGTGGG
                                     A___   A
GAM1149  ENO2     3'  GCTGTGTGCCTGGGGGAG    10520    TT    C     CT
                                TT  CCTAG TACAT  GGT
                                ||  ||||| |||||  |||
                                GA  GGGTC GTGTG  TCG
                                 GG    C    __
GAM1149  ESRRA    3'  GGGTGTCAGAAGCTGGGAA    16722         ACA    GT
                                TTCCTAGCT   TCTG  ACCT
                                |||||||||   ||||  ||||
                                AAGGGTCGA   AGAC  TGGG
                                     ___    TG
GAM1149  EXTL1    3'  AGGTGAGAATGGAGTTGGGGGG 16733   TT      A   CTGG
                                T  CCTAGCT CAT    TACCT
                                |  ||||||| |||    |||||
                                G  GGGTTGA GTA    GTGGA
                                 GG      G   AGA_
GAM1149  EZH1     3'  GGTATCTGAAGTGGGAGAA    10553         G  ACA  T
                                TTTTCCTA CT   TC GGTACC
                                |||||||| ||   || ||||||
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                                AAGAGGGT GA   AG CTATGG
                                   _ ___  T
GAM1149  FAT2     3'  GGGTGAGTTGAGTGTGGCTGGG 9351            _ TGG_
              AGAG                  TTTTCCTAGCTACA TC    TACCT
                                    |||||||||||||| ||    |||||
                                    GAGAGGGTCGGTGT AG    GTGGG
                                          G  TTGA
GAM1149  FRK      3'  AGGTATCAAAATAGTTTAGGAA 10716         _  CATC
              AA                    TTTTCCTAG CTA    TGGTACCT
                                    |||||||| |||    ||||||||
                                    AAAAGGATT GAT    ACTATGGA
                                         T  AAA_
GAM1149  FSTL1    3'  AGGTGGCTGGCTAGGAAG    24004          __
                                    TTTCCTAGCTA  CATCT
                                    ||||||||||  |||||
                                    GAAGGATCGGT  GTGGA
                                          CG
GAM1149  FUT6     5'  AGGTGTGGTGGTTGGAAAG   5629       TA__
                                    TTTTCC    GCTACATCT
                                    ||||||    |||||||||
                                    GAAAGG    TGGTGTGGA
                                       TTGG
GAM1149  GALNS    3'  AGGTGCCCGAGGTGGCTGGGGA 6703           A  T
                                    TTCCTAGCTAC TC GGTACCT
                                    |||||||||| || |||||||
                                    AGGGGTCGGTG AG CCGTGGA
                                          G  C
GAM1149  GALNT3   3'  AGGTCCGCGTGGCTGGGGAAG  16824           ATC   T
                                    TTTTCCTAGCTAC   TGG ACCT
                                    ||||||||||||   ||| ||||
                                    GAAGGGGTCGGTG   GCC TGGA
                                           C__  _
GAM1149  GJA5     3'  AGGTGTCAGCCCTGCTAGGGAG 19161         TACAT   GT
                                    TTTCCTAGC    CTG  ACCT
                                    |||||||||    |||  ||||
                                    GAGGGATCG    GAC  TGGA
                                          TCCC_  TG
GAM1149  GJB1     3'  GGTGAGGGAGTTAGGGAGA   60638          ACA   GG
                                    TTTTCCTAGCT   TCT  TACC
                                    ||||||||||   |||  ||||
                                    AGAGGGATTGA   GGG  GTGG
                                          ___  A_
GAM1149  GLTSCR1  3'  GGGTGCTGGGAGCTGGCAGG   32302     A   CA_  TG
                                    CCT GCTA   TC  GTACCT
                                    ||| ||||   ||  ||||||
                                    GGA CGGT   GG  CGTGGG
                                      _    CGA  GT
GAM1149  GNAS     3'  AGGTGCTGGAGAATCTGGTAAA 6709       C   CTACA  TG
              A                     TTTT CTAG    TC  GTACCT
                                    |||| ||||    ||  ||||||
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                                AAAA GGTC    AG  CGTGGA
                                  T   TAAG_  GT
GAM1149  GYPC     3'  GGGTACCCGGGGGCTGGGGAAG 34144          ACA    _
                                TTTTCCTAGCT   TCTGG TACCT
                                ||||||||||   ||||| |||||
                                GAAGGGGTCGG   GGGCC ATGGG
                                      ___    C
GAM1149  HADH2    3'  GGGTACTACTCTCCAGCTTGGG 16897        _  ACATC_
            AGGA                   TTTTCCTA GCT     TGGTACCT
                                ||||||||| |||     ||||||||
                                AGGAGGGT CGA     ATCATGGG
                                     T   CCTCTC
GAM1149  HADHB    3'  GGTTTGCAGTTGGGAAAG    5741           A  TCTGGT
                                TTTTCCTAGCT CA     ACC
                                |||||||||| ||     |||
                                GAAAGGGTTGA GT     TGG
                                      C  T_____
GAM1149  HDAC4    3'  GGAATGTGAGCTGGGGGAG    21247    TT     _   _
                                TT  CCTAGCT ACAT CT
                                ||  ||||||| |||| ||
                                GA  GGGTCGA TGTA GG
                                 GG      G   A
GAM1149  HKE4     3'  AGGTGCTGGGGCTGCTGGGGGG 23709    TT     TACA  TG
            A                    TT  CCTAGC    TC  GTACCT
                                ||  ||||||   ||  ||||||
                                AG  GGGTCG    GG  CGTGGA
                                 GG     TCG_  GT
GAM1149  HOXB5    3'  GGGTGGGAAGGGGCTAGGGAG  10958         ACA   GG
                                TTTCCTAGCT   TCT  TACCT
                                ||||||||||   |||  |||||
                                GAGGGATCGG   AGG  GTGGG
                                      GGA   __
GAM1149  HYAL2    3'  GGGTACAGCTGGGCTGGGGAG  53701          A  T   G
                                TTTCCTAGCT CA CTG TACCT
                                |||||||||| || ||| |||||
                                GAGGGGTCGG GT GAC ATGGG
                                      _  C   _
GAM1149  HYOU1    3'  GGGTATCAGGTTGCTGGGGAG  60387         TAC
                                TTTCCTAGC   ATCTGGTACCT
                                |||||||||   ||||||||||
                                GAGGGGTCG   TGGACTATGGG
                                     T__
GAM1149  ID4      5'  GGGTGATCCCGGGCTAGGGGAG 9548     TT     TACAT   ___
                                TT  CCTAGC    CTGG   TACCT
                                ||  ||||||    ||||   |||||
                                GA  GGATCG    GGCC   GTGGG
                                 GG      _____    CTA
GAM1149  ILK      3'  AGGTGTCGGGACATGGTTGGGG 16925    TT      CA_   GT
            GAA                    TT  CCTAGCTA   TCTG  ACCT
                                ||  ||||||||   ||||  ||||
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                                AA  GGGTTGGT   GGGC  TGGA
                                 GG       ACA    TG
GAM1149  INPP5A   3'  AGGTGTGTCCAGGGGCTGGGGA 19863          ACA    ___
             AG                   TTTTCCTAGCT   TCTGG   TACCT
                                  ||||||||||   |||||  |||||
                                  GAAGGGGTCGG   GGACC   GTGGA
                                        ___    TGT
GAM1149  ITGA5    3'  AGGTGCTGACGGCCAGGGAGA  61931        A   ACA  T
                                  TTTTCCT GCT   TC GGTACCT
                                  |||||||  |||   || |||||||
                                  AGAGGGA CGG   AG TCGTGGA
                                      C   C__  _
GAM1149  ITPKA    3'  AGGTGCCAGCCACTAAGGGGG  11059    TT  _  CTACAT
                                  T  CCT AG     CTGGTACCT
                                  |  |||  ||     |||||||||
                                  G  GGA TC     GACCGTGGA
                                   GG   A  ACC___
GAM1149  JAM3     3'  GGGTGTCAGGATTTAAGGAAAA 52491        AGCTACA    GT
                                  TTTTCCT      TCTG  ACCT
                                  |||||||      ||||  ||||
                                  AAAAGGA      GGAC  TGGG
                                      ATTTA__    TG
GAM1149  KCNK7    3'  AAGCAGCCAGGAGTGGCTGGGG 54050           AT    ACCT
             AAG                    TTTTCCTAGCTAC  CTGGT
                                    ||||||||||||  |||||
                                    GAAGGGGTCGGTG  GACCG
                                          AG    ACGAAG
GAM1149  KCNK7    3'  AGCAGCCAGGAGTGGCTGGGGA 54052           AT    ACCT
             AG                     TTTTCCTAGCTAC  CTGGT
                                    ||||||||||||  |||||
                                    GAAGGGGTCGGTG  GACCG
                                          AG    ACGAA
GAM1149  KCNK7    3'  AGCAGCCAGGAGTGGCTGGGGA 54053           AT    ACCT
             AG                     TTTTCCTAGCTAC  CTGGT
                                    ||||||||||||  |||||
                                    GAAGGGGTCGGTG  GACCG
                                          AG    ACGAA
GAM1149  KCNK7    3'  AAGCAGCCAGGAGTGGCTGGGG 20343           AT    ACCT
             AAG                    TTTTCCTAGCTAC  CTGGT
                                    ||||||||||||  |||||
                                    GAAGGGGTCGGTG  GACCG
                                          AG    ACGAAG
GAM1149  KCNS2    3'  CAGATGTGTTAGGGAGA     68844          T
                                  TTTTCCTAGC ACATCTG
                                  ||||||||||  |||||||
                                  AGAGGGATTG TGTAGAC
                                             _
GAM1149  KRTHA2   5'  AGGTAGCTGTGGCTGAGGAGA  11240       _      T  GGT
                                  TTTCCT AGCTACA CT   ACCT
                                  ||||||  |||||||  ||   ||||
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                                AGAGGA TCGGTGT GA   TGGA
                                   G      C  ___
GAM1149  KRTHA7   5'  GGGTATAAAAGGGTTGGGAGGA 15018          ACATCTG
                                TTTTCCTAGCT      GTACCT
                                ||||||||||       ||||||
                                AGGAGGGTTGG      TATGGG
                                      GAAAA__
GAM1149  KRTHA8   5'  GGGTATAAAAGGGCTGGGAGGA 23193          ACATCTG
                                TTTTCCTAGCT      GTACCT
                                ||||||||||       ||||||
                                AGGAGGGTCGG      TATGGG
                                      GAAAA__
GAM1149  LRP5     3'  GGGTGGGCAGGGCTGGGAGAA  11364          ACAT   G_
                                TTTTCCTAGCT    CTG  TACCT
                                ||||||||||    |||  |||||
                                AAGAGGGTCGG    GAC  GTGGG
                                      ____   GG
GAM1149  LRPAP1   3'  GGTGTCGAGGCAGGAAG     11368       A   ACA  T GT
                                TTTCCT GCT   TC G  ACC
                                |||||| |||   || |  |||
                                GAAGGA CGG   AG C  TGG
                                   _   ___  _ TG
GAM1149  M6A      5'  GGTGTCAGGGCTGGGAGA    39557         ACAT   GT
                                TTTCCTAGCT    CTG  ACC
                                |||||||||    |||  |||
                                AGAGGGTCGG    GAC  TGG
                                      ____   TG
GAM1149  MAT1A    3'  GGGTACATGGTGCTGGGAGAG  92504         T  ATCTG
                                TTTTCCTAGC AC     GTACCT
                                |||||||||| ||     ||||||
                                GAGAGGGTCG TG     CATGGG
                                      _  GTA__
GAM1149  MBD3     3'  GGGTGCCAGGAGCCACTGGGA  15393       CTACA
                                TCCTAG     TCTGGTACCT
                                ||||||     ||||||||||
                                AGGGTC     GGACCGTGGG
                                   ACCGA
GAM1149  MDM4     3'  GGTACATAGTTAGGTGAA     11511      T       CATCTG
                                TTT CCTAGCTA      GTACC
                                ||| ||||||||      |||||
                                AAG GGATTGAT      CATGG
                                  T       A_____
GAM1149  MECP2    3'  AGGTACCAGTTCTTTAAGAAGA 18383       C   CTACAT
                                TTTTC TAG      CTGGTACCT
                                ||||| |||      |||||||||
                                AGAAG ATT      GACCATGGA
                                   A   TCTT__
GAM1149  MEFV     3'  AGGTGCTAGCTGCTATGGGAAA 5926        _   TACAT
                                TTTTCC TAGC     CTGGTACCT
                                |||||| ||||    |||||||||
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                                AAAGGG ATCG    GATCGTGGA
                                   T   TC___
GAM1149 MMP19   5' GGGTGCACCTGGTTGGAAGG  11638      T   CATCTG
                                TTTTCC AGCTA    GTACCT
                                |||||| |||||    ||||||
                                GGAAGG TTGGT    CGTGGG
                                   _    CCA___
GAM1149 MN1     3' GGGTGCTGGAGTTGGAGGAG  11658     AGCT  A  TG
                                TTCCT   AC TC  GTACCT
                                |||||   || ||  ||||||
                                GAGGA   TG AG  CGTGGG
                                   GGT_ _  GT
GAM1149 MTMR2   3' AGGCCTTATAGATGTGCTTGGG 32908   TT  T   T     GTA__
           GGA                     TT  CC AGC ACATCTG    CCT
                                ||  || ||| |||||||    |||
                                AG  GG TCG TGTAGAT    GGA
                                 GG  T  _     ATTCC
GAM1149 NDST1   3' AGGTCTGGTGGGGCTGGGGGAG 9526    TT    TA   T  T
                                TT  CCTAGC  CATC GG ACCT
                                ||  ||||||  |||| || ||||
                                GA  GGGTCG  GTGG TC TGGA
                                 GG     GG   _ _
GAM1149 NDUFA10 3' GGTAATGGAGTTGGGGGAA   17011    TT     A  CTGG
                                TT  CCTAGCT CAT    TACC
                                ||  ||||||| |||    ||||
                                AA  GGGTTGA GTA    ATGG
                                 GG      G  ____
GAM1149 NEU3    3' GGTGTCATGGCAGGAAG     22831      A   CATC  GT
                                TTTCCT GCTA    TG  ACC
                                |||||| ||||    ||  |||
                                GAAGGA CGGT    AC  TGG
                                   _   ____  TG
GAM1149 NEURL   3' GGTATCAGGCAGGGAGG     16133      A  TACAT
                                TTTCCT GC    CTGGTACC
                                |||||| ||    ||||||||
                                GGAGGG CG    GACTATGG
                                   A  _____
GAM1149 NFIA    3' GGTGACGTGGCTAGCGGA    70887    _     A  TGGT
                                TTC CTAGCTAC TC    ACC
                                ||| |||||||| ||    |||
                                AGG GATCGGTG AG    TGG
                                  C       C  ____
GAM1149 NPTX1   3' GGTGTCCGGGGTGGGAGAG   11839       G TACAT   _
                                TTTTCCTA C    CTGG TACC
                                |||||||| |    |||| ||||
                                GAGAGGGT G    GGCC GTGG
                                     G _____    T
GAM1149 NR2E1   3' AGGTACTAGCACTGAGGAAAA 13791       AGCTACAT
                                TTTTCCT       CTGGTACCT
                                |||||||       |||||||||
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                                AAAAGGA       GATCATGGA
                                    GTCAC___
GAM1149  Nrap     3'  GGATGTGTGCCTGGGAGAG    56310          _ _
                                TTTTCCTAG C TACATCT
                                ||||||||| | |||||||
                                GAGAGGGTC G GTGTAGG
                                     C T
GAM1149  NRL      3'  GGGTTGTTGGTGTGGGTTGGGA 21627           _     TGGT
              GAG                   TTTTCCTAGCT ACATC    ACCT
                                ||||||||||| |||||    ||||
                                GAGAGGGTTGG TGTGG    TGGG
                                      G     TTGT
GAM1149  OCRL     3'  GGGTGATCAAGGGTGTGGTTAG 9629      _          GG___
              TGGA                  TTC CTAGCTACATCT     TACCT
                                ||| ||||||||||||     |||||
                                AGG GATTGGTGTGGG     GTGGG
                                  T          AACTA
GAM1149  ORC2L    3'  AGGTGTAGATTGGGAAGA    21662          _
                                TTTTCCTAG CTACATCT
                                ||||||||| ||||||||
                                AGAAGGGTT GATGTGGA
                                     A
GAM1149  PACSIN1  3'  GGGTGCTGGGGCTTGGGG    93885      T    ACAT TG
                                TTCC AGCT    C  GTACCT
                                |||| ||||    |  ||||||
                                GGGG TCGG    G  CGTGGG
                                  T    _____ GT
GAM1149  PAX5     3'  AGGTGCTGGGGCTGGGG     34122         ACAT TG
                                TCCTAGCT    C  GTACCT
                                ||||||||    |  ||||||
                                GGGGTCGG    G  CGTGGA
                                     _____ GT
GAM1149  PIAS3    3'  GGTATGTGAGCTAGGAGAA   21448           A   CTG    T
                                TTTTCCTAGCT CAT   GTACC
                                |||||||||| |||   |||||
                                AAGAGGATCGA GTG   TATGG
                                     _  ___
GAM1149  PIK3CD   3'  GGTACCAGAAGTGTGAGAA   18495       CTA   ACA
                                TTTTC   GCT   TCTGGTACC
                                |||||   |||   |||||||||
                                AAGAG   TGA   AGACCATGG
                                   TG_  ___
GAM1149  PIR51    3'  GGAATGTTTGGTTGGGAGAA  22396           __   _
                                TTTTCCTAGCT  ACAT CT
                                ||||||||||  |||| ||
                                AAGAGGGTTGG  TGTA GG
                                      TT    A
GAM1149  PLXNB2   3'  GGGTGCCGGCACTCTGGGTGGA 25727    TT    CTACAT
                                TT  CCTAG     CTGGTACCT
                                ||  |||||     |||||||||
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                                AG  GGGTC     GGCCGTGGG
                                 GT    TCAC__
GAM1149  POU4F1   3'  GGGTGCTGGGTGTGGGGATTGG 21765      TAG__      TG
             AG                   TTCC    CTACATC  GTACCT
                                  ||||    |||||||  ||||||
                                  GAGG    GGTGTGG  CGTGGG
                                    TTAGG      GT
GAM1149  PPP2R4   3'  AGGTGCTGGGCTCCTGGGAGGG 61178         CTACA  TG
                                  TTTTCCTAG    TC  GTACCT
                                  |||||||||    ||  ||||||
                                  GGGAGGGTC    GG  CGTGGA
                                       CTC__  GT
GAM1149  PPT2     3'  AGGTGCTGCTGCTGGAGGAGA  18944       _    TA  TCTG
                                  TTTTC CTAGC  CA    GTACCT
                                  ||||| |||||  ||    ||||||
                                  AGAGG GGTCG  GT    CGTGGA
                                     A    TC  ____
GAM1149  PRKCA    5'  GCAAGAGGTGGTTGGGGGG    12286    TT       A   G
                                  T  CCTAGCTAC TCT GT
                                  |  |||||||| ||| ||
                                  G  GGGTTGGTG AGA CG
                                   GG        G   A
GAM1149  PRPS1    3'  GGGTGTTTGACTGTGACTGGGG 12402          C   _  TG
             AAG                    TTTTCCTAG TACA TC  GTACCT
                                    |||||||| |||| ||  ||||||
                                    GAAGGGGTC GTGT AG  TGTGGG
                                         A    C  TT
GAM1149  PRPSAP2  3'  GGGTGTTTGTGAGTTTGGGGAG 12406    TT  T    A   CT
                                  TT  CC AGCT CAT  GGTACCT
                                  ||  || |||| |||  |||||||
                                  GA  GG TTGA GTG  TTGTGGG
                                   GG  T    _   T_
GAM1149  PSD      5'  AGGTGCTGGCTGAGCGGGAGGA 12431         A   A  T TG
                                  TTTTCCT GCT CA C  GTACCT
                                  ||||||| ||| || |  ||||||
                                  AGGAGGG CGA GT G  CGTGGA
                                      _   _  C GT
GAM1149  PTGES    3'  GCTCAGGTGTGGGTGGGAGG   18063        G       _
                                  TTTCCTA CTACATCTG GT
                                  ||||||| |||||||| ||
                                  GGAGGGT GGTGTGGAC CG
                                       G        T
GAM1149  PTGS1    3'  AGTAATCTAGGTGTGGCTGTGA 8240       C          __  CT
             AG                     TTTC TAGCTACATCTGG  TAC
                                    |||| ||||||||||||  |||
                                    GAAG GTCGGTGTGGATC  ATG
                                      T          TA   A
GAM1149  PTGS1    3'  AGTAATCTAGGTGTGGCTGTGA 55470      C          __  CT
             AG                     TTTC TAGCTACATCTGG  TAC
                                    |||| ||||||||||||  |||
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                                GAAG GTCGGTGTGGATC  ATG
                                  T          TA  A
GAM1149  PTPN18   3'  GGTATAGTGGCTGGTGAG    27651    _      ATCTG
                                TTC CTAGCTAC    GTACC
                                ||| ||||||||    |||||
                                GAG GGTCGGTG    TATGG
                                  T      A____
GAM1149  PTPRF    3'  GAACCACAGATGTGTCTGGGAG 56136        C      GTACCT
           AG                     TTTTCCTAG TACATCTG
                                ||||||||| ||||||||
                                GAGAGGGTC GTGTAGAC
                                     T      ACCAAGA
GAM1149  PTPRN    3'  GGTGCTGCAGCCAGGAGGA   12626       A  A  TCTG
                                TTTTCCT GCT CA   GTACC
                                ||||||| ||| ||   |||||
                                AGGAGGA CGA GT   CGTGG
                                   C  C  ____
GAM1149  RAD23B   3'  GGGTTGGGAGATGTGGCTGGAA 12736      T       GGT_
           AG                     TTTTCC AGCTACATCT   ACCT
                                ||||||| ||||||||||   ||||
                                GAAAGG TCGGTGTAGA   TGGG
                                  _        GGGT
GAM1149  RASGRP2  3'  GGGTGTCGGGGCAGGAGGCTGG 20632        ACA___   GT
           GGA                    TTCCTAGCT     TCTG  ACCT
                                |||||||||     ||||  ||||
                                AGGGGTCGG     GGGC  TGGG
                                     AGGACG    TG
GAM1149  RLF      3'  GGTGGGAGGGCTAGGGAAA   25778         ACA   GG
                                TTTTCCTAGCT   TCT  TACC
                                ||||||||||   |||  ||||
                                AAAGGGATCGG   AGG  GTGG
                                     G__   __
GAM1149  RNASE1   5'  TGGTGCCCTGTAGTTGTGGGAA 64604      _      TCT     T
           G                     TTTTCC TAGCTACA   GGTACC
                                ||||||| ||||||||   ||||||
                                GAAGGG GTTGATGT   CCGTGG
                                   T      C__      TG
GAM1149  SALL2    3'  GGACTGTGGCTGGGAAG     64592          TCTG  A
                                TTTCCTAGCTACA    GT CC
                                ||||||||||||    || ||
                                GAAGGGTCGGTGT    CA GG
                                       ____  A
GAM1149  SERPINA4 3'  AGGAGGATGTGGCAGGGGAG   21703       A       GGTA
                                TTTCCT GCTACATCT    CCT
                                ||||||| |||||||||    |||
                                GAGGGG CGGTGTAGG    GGA
                                   A       A___
GAM1149  SERPINH2 3'  GGGTGCTATTGGGGTTGGGGGG 8786     TT     TA  TC
           G                     TT  CCTAGC  CA  TGGTACCT
                                ||  ||||||  ||  ||||||||
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                                GG  GGGTTG  GT  ATCGTGGG
                                 GG     GG  T_
GAM1149  SIAT8E   5'  AGGTACCCGGGGGTGGGGAAG  60550        G  ACA  T
                                TTTTCCTA CT   TC GGTACCT
                                |||||||| ||   || |||||||
                                GAAGGGGT GG   GG CCATGGA
                                     G ___  C
GAM1149  SLC22A7  3'  AGGTGCCCCTTGGGTTGGGG  22885        A  TCT
                                TCCTAGCT CA   GGTACCT
                                |||||||| ||   |||||||
                                GGGGTTGG GT   CCGTGGA
                                     _ TCC
GAM1149  SLC4A4   3'  GGAGTGGGGCTGGGGAGA    14995         TA  _
                                TTTTCCTAGC  CA TCT
                                ||||||||||  || |||
                                AGAGGGGTCG  GT AGG
                                      GG  G
GAM1149  SLC9A1   3'  GGGTACCAGGCACATGGCTGGG 70931    TT      CA__
            GGAG                   TT  CCTAGCTA    TCTGGTACCT
                                ||  ||||||||   ||||||||||
                                GA  GGGTCGGT    GGACCATGGG
                                 GG       ACAC
GAM1149  SMARCC1  3'  GGTGCTCAGGCTGGGAGG    13254         TACAT  _
                                TTTCCTAGC     CTG GTACC
                                |||||||||     ||| |||||
                                GGAGGGTCG     GAC CGTGG
                                      _____   T
GAM1149  SPTBN4   3'  GGGTGCTAGGGGGCAGGGAGG  48158       A   ACA
                                TTTCCT GCT   TCTGGTACCT
                                |||||| |||   ||||||||||
                                GGAGGG CGG   GGATCGTGGG
                                   A  G__
GAM1149  STCH     3'  AGGTATTTACAGTGGTTGGAAG 23694       T     ATCT
            A                    TTTTCC AGCTAC    GGTACCT
                                |||||| ||||||    |||||||
                                AGAAGG TTGGTG    TTATGGA
                                   _     ACAT
GAM1149  SUPT5H   5'  AGGTCTAGCATGTGGCGTAGGA 13490        _     _   T
            GG                   TTTCCTA GCTACAT CTGG ACCT
                                ||||||| ||||||| |||| ||||
                                GGAGGAT CGGTGTA GATC TGGA
                                     G      C   _
GAM1149  SUV39H1  3'  AGGTGCCAGGCACTAGGTAGA  13492     T    CTACA
                                TTT CCTAG     TCTGGTACCT
                                ||| |||||     ||||||||||
                                AGA GGATC     GGACCGTGGA
                                  T    AC___
GAM1149  TACR1    3'  GGGTCAGTATGGGTTAGGGAAA 8329           A  _  GT
                                TTTTCCTAGCT CAT CTG  ACCT
                                |||||||||| ||| |||  ||||
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                                AAAGGGATTGG GTA GAC  TGGG
                                      _  T  __
GAM1149  TCF20    3'  GGGTCACTGTGGCTGGTGAG  67504    _      TCTG  _
                                TTC CTAGCTACA   GT ACCT
                                ||| |||||||||   || ||||
                                GAG GGTCGGTGT   CA TGGG
                                  T       ____  C
GAM1149  TFAP4    3'  GGGTGTCGCAGAGCTGTGGGA  13691     _    ACATC  GT
                                TTCC TAGCT    TG  ACCT
                                |||| |||||    ||  ||||
                                AGGG GTCGA    GC  TGGG
                                  T    GAC__  TG
GAM1149  THBS1    3'  TTGTGCAGATGTAGCAGGAAAA 13750       A       G   CT
                                TTTTCCT GCTACATCTG TAC
                                ||||||| |||||||||| |||
                                AAAAGGA CGATGTAGAC GTG
                                   _       _  TTC
GAM1149  THRA     3'  AGGTGCCTGAAAGCTGGGAG  13752       ACA  T
                                TTCCTAGCT  TC GGTACCT
                                |||||||||  || |||||||
                                GAGGGTCGA  AG CCGTGGA
                                     A__  T
GAM1149  THY1     3'  GGGTACCAGCCACTGGAGGGG  21898    AG   CAT_
                                CCT  CTA   CTGGTACCT
                                |||  |||   |||||||||
                                GGG  GGT   GACCATGGG
                                  GA   CACC
GAM1149  TMEM4    5'  AGGTACCAGTTAGCGTCAGGGG 27299    TT   A__   CAT
            AG                    TT  CCT   GCTA   CTGGTACCT
                                || |||   ||||   |||||||||
                                GA  GGA   CGAT   GACCATGGA
                                 GG   CTG   T__
GAM1149  TNFRSF6B 5'  GGGTGCTGGGGACTCAGGGAG  53084      _  CTACA  TG
                                TTTCCT AG    TC  GTACCT
                                |||||| ||    ||  ||||||
                                GAGGGA TC    GG  CGTGGG
                                   C  AG___  GT
GAM1149  TOP1     3'  AGGAACAGTGTGGTTTGGGAAA 13825        _    T   GTA
            G                     TTTTCCTAG CTACA CTG   CCT
                                |||||||| ||||| |||   |||
                                GAAAGGGTT GGTGT GAC   GGA
                                     T    _  AA_
GAM1149  TOX      3'  AGGTACCAGAGATTTGCTAGGG 28960        TACA_
            AA                    TTTCCTAGC    TCTGGTACCT
                                |||||||||    ||||||||||
                                AAGGGATCG    AGACCATGGA
                                     TTTAG
GAM1149  TRIM9    3'  GGGTGCTAGAGCTGTTTAGAGA 31460      CT   TACA
            G                     TTTTC  AGC   TCTGGTACCT
                                |||||  |||   ||||||||||
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                                GAGAG TTG   AGATCGTGGG
                                  AT  TCG_
GAM1149 TRPV3   3' AGGTCGGCTTGGCTGGGAGAG 96813         CAT  GT
                                TTTTCCTAGCTA  CTG ACCT
                                ||||||||||||  ||| ||||
                                GAGAGGGTCGGT  GGC TGGA
                                     TC_  __
GAM1149 VEGFB   3' AGGTGCCGGAAGCTGCGAAG  14046    C   ACA
                                TTTC TAGCT  TCTGGTACCT
                                |||| |||||  ||||||||||
                                GAAG GTCGA  AGGCCGTGGA
                                  C   ___
GAM1149 WARS    3' GGGTGGACTTAGCTAGGGAGA 67866         CA  GGT
                                TTTTCCTAGCTA TCT  ACCT
                                ||||||||||||  |||  ||||
                                AGAGGGATCGAT  AGG  TGGG
                                     TC  ___
GAM1149 WNT3    3' GGGTGAAGTGTGTGGCTGGGCG 48437   TT       _ GG
           GA                    TT  CCTAGCTACAT CT  TACCT
                                ||  ||||||||||| ||  |||||
                                AG  GGGTCGGTGTG GA  GTGGG
                                 GC        T  A_
GAM1149 ZNF180  3' AGGTAGTACATGTAGTTGGAAG 26043     T     C  G
           A                     TTTTCC AGCTACAT TG TACCT
                                |||||| |||||||| || |||||
                                AGAAGG TTGATGTA AT ATGGA
                                   _      C  G
GAM1149 ABT1    3' AGGTGCACTTTACTGGGGAGA  26299       C  CATCTG
                                TTTTCCTAG TA    GTACCT
                                |||||||||  ||    ||||||
                                AGAGGGGTC AT    CGTGGA
                                     _ TTCA__
GAM1149 ABT1    3' GGGTGGACTGGGTTGGGAAGA  26304        ACA  GGT
                                TTTTCCTAGCT  TCT  ACCT
                                ||||||||||  |||  ||||
                                AGAAGGGTTGG  AGG  TGGG
                                     GTC  ___
GAM1149 AIBZIP  5' AGGTGTAGTGTTTGGGGAG   56470      ___
                                TTTCCTA  GCTACATCT
                                |||||||  |||||||||
                                GAGGGGT  TGATGTGGA
                                   TTG
GAM1149 AMOT    3' GGGTGTTAGGTAAGGGTTGGGG 56548       AC_  GG
           G                     TTCCTAGCT  ATCT  TACCT
                                |||||||||  ||||  |||||
                                GGGGGTTGG  TGGA  GTGGG
                                     GAA   TT
GAM1149 AP1G2   5' GGGTACCAGGTTAGGGGGAGGA 15355      AG  C
                                TTTTCCT  CTA ATCTGGTACCT
                                |||||||  ||| ||||||||||
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                                AGGAGGG  GAT TGGACCATGGG
                                   G_  _
GAM1149  APELIN   3'  CTGGGGCTGGGGGTGGCTGGGA 34265          AT TG TA  T
             GG                   TTTCCTAGCTAC  C  G  CC
                                  ||||||||||||  |  |  ||
                                  GGAGGGTCGGTG  G  C  GG
                                        GG GT GG  TCG
GAM1149  APELIN   3'  GGGTAGTGGGTGGGCTAGGGGG 34271   TT     A     G
                                  T  CCTAGCT CATCTG TACCT
                                  |  ||||||| |||||| |||||
                                  G  GGATCGG GTGGGT ATGGG
                                   GG      _     G
GAM1149  APOL6    3'  GCCTATGTGCTGGGAAAA    48373         T   CT
                                  TTTTCCTAGC ACAT  GGT
                                  ||||||||||  ||||  |||
                                  AAAAGGGTCG TGTA  CCG
                                        _   T_
GAM1149  APXL2    5'  GGGTGGAACAGGGTTGGGGAG  75682         ACAT   G__
                                  TTTCCTAGCT    CTG   TACCT
                                  ||||||||||    |||   |||||
                                  GAGGGGTTGG    GAC   GTGGG
                                        _____   AAG
GAM1149  ARHGAP9  3'  GGTGTTGGGATGGGTGAGG    51662     A   A    _ GG
                                  CCT GCT CATC T  TACC
                                  ||| ||| |||| |  ||||
                                  GGA TGG GTAG G  GTGG
                                    G   _    G TT
GAM1149  B7       3'  GGGTGCTGGTAGGAGTGGTTGG 23764       T     AT___ TG
             AGAG                     TTTTCC AGCTAC     C  GTACCT
                                  ||||||  ||||||     |  ||||||
                                  GAGAGG TTGGTG     G  CGTGGG
                                     _     AGGAT GT
GAM1149  BM-002   3'  AGGTGTATGTTGGGGAGA    34005          _
                                  TTTTCCTAGC TACATCT
                                  ||||||||||  |||||||
                                  AGAGGGGTTG ATGTGGA
                                        T
GAM1149  BMF      3'  GGGTGGGGGTTGGGAGAG    54285          A_
                                  TTTTCCTAGCT  CATCT
                                  ||||||||||||  |||||
                                  GAGAGGGTTGG  GTGGG
                                        GG
GAM1149  C12orf2  3'  AGGTGGACTGTAGATTGGGAGA 83677          _    _  GGT
             A                     TTTTCCTAG CTACA TCT   ACCT
                                  |||||||||  ||||| |||   ||||
                                  AAGAGGGTT GATGT AGG   TGGA
                                        A    C  ___
GAM1149  C1orf34  3'  TGGGGCAGGTGGGGCTGGGGAA 61326          TA     GTA  T
             G                     TTTTCCTAGC  CATCTG   CC
                                  ||||||||||  ||||||   ||
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                                GAAGGGGTCG  GTGGAC   GG
                                      GG     GG_  TC
GAM1149  C20orf142 3'  GGGTACCAGATTGTATTTAGAG 75286     _    C    _
              AA                    TTC CTAG TACA TCTGGTACCT
                                    ||| |||| |||| ||||||||||
                                    AAG GATT ATGT AGACCATGGG
                                      A   T   T
GAM1149  C20orf172 3'  AGGTGTCAGTACAGCTCGGAAA 46761       T    ACAT   GT
              G                     TTTTCC AGCT    CTG  ACCT
                                    |||||| ||||    |||  ||||
                                    GAAAGG TCGA    GAC  TGGA
                                       C    CAT_   TG
GAM1149  C20orf44  3'  GGTACAGGGCTGGGAGAA    37311          ACATCTG
                                    TTTTCCTAGCT      GTACC
                                    ||||||||||       |||||
                                    AAGAGGGTCGG      CATGG
                                          GA_____
GAM1149  C3IP1    3'  GGGTATTAGGAGTGTGGGAA   41579       GC   AT
                                    TTCCTA  TAC  CTGGTACCT
                                    ||||||  |||  |||||||||
                                    AAGGGT  GTG  GATTATGGG
                                       __   AG
GAM1149  C5orf4   3'  GGTGCTGGGTGTGCTGG     51494       T    TG
                                    CTAGC ACATC  GTACC
                                    ||||| |||||  |||||
                                    GGTCG TGTGG  CGTGG
                                       _    GT
GAM1149  CBX6     3'  AGGTGGACAGAGTTGGGGGGA  27406    TT     TACA   G_
                                    TT  CCTAGC    TCTG  TACCT
                                    ||  ||||||    ||||  |||||
                                    AG  GGGTTG    AGAC  GTGGA
                                     GG      ____    AG
GAM1149  CBX6     3'  GGGCCCCTGGGGGTGGCTGGGG 27422            AT  _  TA
              AGA                     TTTTCCTAGCTAC  CT GG  CCT
                                    ||||||||||||  ||  ||  |||
                                    AGAGGGGTCGGTG  GG CC  GGG
                                          GG  T  CC
GAM1149  CENTG1   3'  AGGATTCGAGGTGGCTGGGAGG 29352           A  TG  A
                                    TTTCCTAGCTAC TC  GT CCT
                                    |||||||||||| ||  || |||
                                    GGAGGGTCGGTG AG  TA GGA
                                          G  CT  _
GAM1149  CEP3     5'  GGTACCGCGGCCGGGAGG    22249       TA   ACATC
                                    TTTCC  GCT    TGGTACC
                                    |||||  |||    |||||||
                                    GGAGG  CGG    GCCATGG
                                       GC   C____
GAM1149  CGI-85   5'  GGGTATGAAGTGGTTGGGAGAA 32629            A  TG
                                    TTTTCCTAGCTAC TC  GTACCT
                                    |||||||||||| ||  ||||||
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                                AAGAGGGTTGGTG AG  TATGGG
                                      A  __
GAM1149  CLDN7    3'  GGTGCCGTTGGTGGGAGAG   96227        G   CATC
                                TTTTCCTA CTA    TGGTACC
                                |||||||| |||    |||||||
                                GAGAGGGT GGT    GCCGTGG
                                    _   T___
GAM1149  CLSTN3   3'  GGGGGGTTGGGTGTGGTGAGGG 28881       A       TG TA
              AG                  TTTCCT GCTACATC  G  CCT
                                |||||| ||||||||  |  |||
                                GAGGGA TGGTGTGG  T  GGG
                                   G       GT GG   GC
GAM1149  CNR2     3'  GGTATCAGATGGGATGGA    10236     TAG  A
                                TCC   CT CATCTGGTACC
                                |||   || ||||||||||
                                AGG   GG GTAGACTATGG
                                  TA_  _
GAM1149  CYP2A7   3'  AGGTGCTTCCGAGCTGGGA   7537         ACATCT
                                TCCTAGCT     GGTACCT
                                ||||||||     |||||||
                                AGGGTCGA     TCGTGGA
                                     GCCT__
GAM1149  CYP2D6   5'  GGGTGCCAGGTGTGTCCAGAGG 5452       AGC__
              A                  TCCT     TACATCTGGTACCT
                                ||||     ||||||||||||||
                                AGGA    GTGTGGACCGTGGG
                                  GACCT
GAM1149  DDX34    3'  AGGTATCAGGTGGGTGGAGGGG 28660    TT   A_   A
              AG                  TT  CCT  GCT CATCTGGTACCT
                                ||  |||  ||| ||||||||||||
                                GA  GGA  TGG GTGGACTATGGA
                                 GG   GG   _
GAM1149  DGCR6L   5'  CTGGGATGTCGTGAAGCTGGGG 53831    TT     _____     GGTACCT
              GAG                   TT  CCTAGCT     ACATCT
                                ||  |||||||    ||||||
                                GA  GGGTCGA     TGTAGG
                                 GG      AGTGC     G   TCC
GAM1149  DKFZP434A1319 5'  GGTGCCGGGCGAGGGAG     50461       A  TACAT
                                TTTCCT GC     CTGGTACC
                                |||||| ||     ||||||||
                                GAGGGA CG     GGCCGTGG
                                   G  _____
GAM1149  DKFZP434C171 3'  GGGAAGAGGTGAGGCTAGGGGA 32193    TT      A    GGTA  T
              G                   TT  CCTAGCT CATCT    CC
                                ||  ||||||| |||||    ||
                                GA  GGATCGG GTGGA    GG
                                 GG      A    GAAG
GAM1149  DKFZP564C103 3'  AGGTGCTGCCCTGGCTGGGAG  32239          CATCT
                                TTCCTAGCTA    GGTACCT
                                ||||||||||    |||||||
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                                GAGGGTCGGT    TCGTGGA
                                      CCCG_
GAM1149  DKFZP564I1171 5'  GGGTGCCCTGGCTGGGTGAG  72048    T      CATCT
                                TTT CCTAGCTA    GGTACCT
                                ||| ||||||||    |||||||
                                GAG GGGTCGGT    CCGTGGG
                                  T      C____
GAM1149  DKFZP564J157 3'  GCCCTGAGTGGCTAGGGGAA  38054    TT      A  T_
                                TT  CCTAGCTAC TC  GGT
                                ||  ||||||||| ||  |||
                                AA  GGATCGGTG AG  CCG
                                 GG        _ TC
GAM1149  DKFZP564K2062 3'  AGGCAAAGAGGTGTGGCGGGGG 31852      A       GGTA_
            A                    TTCCT GCTACATCT    CCT
                                ||||| |||||||||    |||
                                AGGGG CGGTGTGGA    GGA
                                   G        GAAAC
GAM1149  DKFZP762D096 3'  AGGTGGCTTGGGAGTTGGGAGA 66177          ACATCT  _
            A                    TTTTCCTAGCT     GGT ACCT
                                ||||||||||     ||| ||||
                                AAGAGGGTTGA     TCG TGGA
                                      GGGT__   G
GAM1149  DNAM-1   5'  GGGTGTTGAGGCTAGGAGG   22684          ___
                                TTTCCTAGCT   ACATCT
                                |||||||||   ||||||
                                GGAGGATCGG   TGTGGG
                                      AGT
GAM1149  EFS2     3'  AGGTACTAGGCTCTGGGG    20768       CTACA
                                TCCTAG    TCTGGTACCT
                                ||||||    ||||||||||
                                GGGGTC    GGATCATGGA
                                   TC___
GAM1149  ERAL1    3'  AGCTACAAAGGTGTAGCTAAGA 63310      C        G_  C
            AGA                    TTTTC TAGCTACATCT  GTA CT
                                ||||| ||||||||||  ||| ||
                                AGAAG ATCGATGTGGA  CAT GA
                                   A         AA  C
GAM1149  FADS2    3'  AGGTGCTGGTAGCTGAGGGGA  16214   TT  _    CAT TG
                                T  CCT AGCTA   C  GTACCT
                                |  ||| |||||  |  ||||||
                                A  GGA TCGAT   G  CGTGGA
                                 GG   G    ___ GT
GAM1149  FAP48    5'  AGGTGGCGGCGGCTGGGAGAG  54973          ACAT   G
                                TTTTCCTAGCT    CTG TACCT
                                ||||||||||    ||| |||||
                                GAGAGGGTCGG    GGC GTGGA
                                      C___   G
GAM1149  FEM-2    3'  GGGTGTCGGGTAGAGGGAAGA  28319        AG    AT   GT
                                TTTTCCT  CTAC  CTG  ACCT
                                |||||||  ||||  |||  ||||
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                                AGAAGGG  GATG  GGC  TGGG
                                   A_    __   TG
GAM1149  FKBP4    3'  GGGTGCTAGGGACATGGGAAAA 10642        GCTACA
                                TTTTCCTA     TCTGGTACCT
                                ||||||||     ||||||||||
                                AAAAGGGT     GGATCGTGGG
                                   ACAG__
GAM1149  FLJ10035 3'  GGTGTCAGAGCAGGGAGAA   36214        A  TACA   GT
                                TTTTCCT GC   TCTG  ACC
                                ||||||| ||   ||||  |||
                                AAGAGGG CG   AGAC  TGG
                                   A _____   TG
GAM1149  FLJ10060 5'  GGGTCCTCTGTGGGTAGGAAAA 36271        G    TCT  T
                                TTTTCCTA CTACA   GG ACCT
                                |||||||| |||||   || ||||
                                AAAAGGAT GGTGT   CC TGGG
                                   G    CT_  _
GAM1149  FLJ10300 3'  CGGGTGTGGCTGAGAGGA    36470      C
                                TTTTC TAGCTACATCTG
                                ||||| ||||||||||||
                                AGGAG GTCGGTGTGGGC
                                  A
GAM1149  FLJ10546 3'  AGGTAGGTTGAAGCTAGGAGGA 60178          A  T  GG
                                TTTTCCTAGCT CA CT  TACCT
                                |||||||||| || ||  |||||
                                AGGAGGATCGA GT GG  ATGGA
                                   A  T  __
GAM1149  FLJ10781 3'  GGGTGGGAGGGAGTTGGGGAAG 37174          ACA   GG
                                TTTTCCTAGCT   TCT  TACCT
                                ||||||||||   |||  |||||
                                GAAGGGGTTGA   AGG  GTGGG
                                   GGG   __
GAM1149  FLJ10811 3'  AGGTACAAAAGGGGCTGGGAAG 37220          ACATCTG
            A                   TTTTCCTAGCT      GTACCT
                                ||||||||||      ||||||
                                AGAAGGGTCGG      CATGGA
                                   GGAAAA_
GAM1149  FLJ10811 3'  AGGTGCCAGGTCAGCAGGAG   37221      A   AC
                                TTCCT GCT  ATCTGGTACCT
                                ||||| |||  ||||||||||
                                GAGGA CGA  TGGACCGTGGA
                                  _  C_
GAM1149  FLJ10895 3'  GGTACCAGCACCAGGAAGA   39359       AGCTACAT
                                TTTTCCT       CTGGTACC
                                |||||||       ||||||||
                                AGAAGGA       GACCATGG
                                   CCAC____
GAM1149  FLJ10901 3'  GGGTACCCCAGCCTGGGCTGGG 37370    TT      ACAT  __
            GGAG                TT  CCTAGCT    CT  GGTACCT
                                ||  |||||||    ||  |||||||
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                                GA  GGGTCGG   GA  CCATGGG
                                 GG      GTCC  CC
GAM1149  FLJ11017  5'  GGAATGTTGCTGGGGAAG    37544         T   _
                                TTTTCCTAGC ACAT CT
                                |||||||||| |||| ||
                                GAAGGGGTCG TGTA GG
                                      T   A
GAM1149  FLJ11710  3'  AGGTGTTCTAGGTGGGAAAA   46240        G  ___
                                TTTTCCTA CT   ACATCT
                                |||||||| ||   ||||||
                                AAAAGGGT GA   TGTGGA
                                     G  TCT
GAM1149  FLJ11773  5'  GGTCGTGGACTGTGGTTGGGGG 41933    TT       _   GT   T
            AG                    TT  CCTAGCTACA TCTG  ACC
                                ||  |||||||||| ||||  |||
                                GA  GGGTTGGTGT AGGT  TGG
                                 GG        C   GC
GAM1149  FLJ11996  3'  AGGTGCCTACAGGTAGGAAAA  47055        G  ACATCT
                                TTTTCCTA CT     GGTACCT
                                |||||||| ||     |||||||
                                AAAAGGAT GA     CCGTGGA
                                     G  CAT___
GAM1149  FLJ12221  3'  GGGTGGGCTCAGGGTTGGGGAA 63224          ACAT   ___
            G                    TTTTCCTAGCT   CTGG   TACCT
                                ||||||||||    ||||   |||||
                                GAAGGGGTTGG   GACT   GTGGG
                                      ____   CGG
GAM1149  FLJ12294  3'  GGTGAGCTGGCTGGGGAG    47718         CATCTGG
                                TTTCCTAGCTA      TACC
                                ||||||||||      ||||
                                GAGGGGTCGGT     GTGG
                                      CGA____
GAM1149  FLJ12428  3'  GGTTGGGGGTAGTTAGGGAGA  43266          A   GGT
                                TTTTCCTAGCTAC TCT   ACC
                                |||||||||||| |||   |||
                                AGAGGGATTGATG GGG   TGG
                                      _  GT_
GAM1149  FLJ12770  3'  GGGTGTTCCAGGTGAGCTGGGG 50681          A     __
            AAG                    TTTTCCTAGCT CATCTGG  TACCT
                                ||||||||||| |||||||  |||||
                                GAAGGGGTCGA GTGGACC  GTGGG
                                      _      TT
GAM1149  FLJ13964  3'  GGTACTACTGCTGTGAAGA   50754      C    TACATC
                                TTTTC TAGC     TGGTACC
                                ||||| ||||     |||||||
                                AGAAG GTCG     ATCATGG
                                   T   TC____
GAM1149  FLJ14084  3'  GGGTAGGGTTTAGCTGGGGGAA 41594    TT      C   GG
                                TT  CCTAGCTA ATCT  TACCT
                                ||  |||||||| ||||  |||||
```

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                                AA  GGGTCGAT TGGG  ATGGG
                                 GG       T   __
GAM1149  FLJ14249  3' AGGTGTCACATGGGGCAGGGAA 42639      A  TA   C  GT
                                TTCCT GC  CAT TG  ACCT
                                ||||| ||  ||| ||  ||||
                                AAGGG CG  GTA AC  TGGA
                                   A  GG   C  TG
GAM1149  FLJ14249  3' AGGTGTCACATGGGGCAGGGAA 42640      A  TA   C  GT
                                TTCCT GC  CAT TG  ACCT
                                ||||| ||  ||| ||  ||||
                                AAGGG CG  GTA AC  TGGA
                                   A  GG   C  TG
GAM1149  FLJ14346  3' GGGCAGAGGGTGTGGCAGGGAA 47370      A       GGTA
                                TTCCT GCTACATCT    CCT
                                ||||| |||||||||    |||
                                AAGGG CGGTGTGGG    GGG
                                   A        AGAC
GAM1149  FLJ14871  3' GGGTACCCCCAGGCTGGGGAAA 52730          ACATCT
                                TTTTCCTAGCT     GGTACCT
                                ||||||||||     |||||||
                                AAAGGGGTCGG     CCATGGG
                                      ACCC__
GAM1149  FLJ20094  3' AGGTACCATTCAAAGCAGGGGG 35044    TT   A   ACATC
           A                     TT  CCT GCT     TGGTACCT
                                ||  ||| |||    ||||||||
                                AG  GGA CGA    ACCATGGA
                                 GG  _  AACTT
GAM1149  FLJ20184  3' GGGTTAATGGAGTTAGGGGAA  35198    TT      A   CTGGT
                                TT  CCTAGCT CAT     ACCT
                                ||  ||||||| |||     ||||
                                AA  GGATTGA GTA     TGGG
                                 GG      G   AT___
GAM1149  FLJ20595  3' AGGTTGTTATTTGGTTGGGGAG 35862          C  CTGGT
                                TTTCCTAGCTA AT     ACCT
                                |||||||||| ||     ||||
                                GAGGGGTTGGT TA     TGGA
                                      T  TTGT_
GAM1149  FLJ20701  3' GGGTGGGAGTGTGGATGGGGAG 36025       G    T  GG
                                TTTCCTA CTACA CT  TACCT
                                ||||||| ||||| ||  |||||
                                GAGGGGT GGTGT GA  GTGGG
                                    A    _  GG
GAM1149  FLJ20986  3' AGGTGTTTAGGTGGCTGGAAAA 44834       T     ATCT
                                TTTTCC AGCTAC    GGTACCT
                                ||||||| ||||||    |||||||
                                AAAAGG TCGGTG    TTGTGGA
                                   _     GAT_
GAM1149  FLJ21432  3' AGGTGCTAGGTGGACCGAGC   44939     A____
                                GCT    CATCTGGTACCT
                                |||    ||||||||||||
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                                CGA    GTGGATCGTGGA
                                  GCCAG
GAM1149  FLJ21432  3'  GGGTGCTGGAGGCCATGGAGGA 44946      TA_  ACA  TG
                                TTTTCC  GCT  TC  GTACCT
                                ||||||  |||  ||  ||||||
                                AGGAGG  CGG  AG  CGTGGG
                                   TAC  ___  GT
GAM1149  FLJ21988  3'  GGGTGCCAGGCCCCTGGAAAG  42853      T  CTACA
                                TTTTCC AG    TCTGGTACCT
                                |||||| ||    ||||||||||
                                GAAAGG TC    GGACCGTGGG
                                   _ CCC__
GAM1149  FLJ22174  3'  AGGTATCGCATGTGCGGGGGAG 41957      A  T   C
                                TTTCCT GC ACAT TGGTACCT
                                |||||| || |||| ||||||||
                                GAGGGG CG TGTA GCTATGGA
                                   G  _   C
GAM1149  FLJ22215  3'  AGGTGTTCAGAAGGCTGGGGG  98635       ACA   _
                                TTCCTAGCT  TCTGG TACCT
                                |||||||||  ||||| |||||
                                GGGGGTCGG  AGACT GTGGA
                                     A__    T
GAM1149  FLJ22301  3'  GGGTATGGAGGTGGGTGGGAAA 46180       G   A   G
          G                      TTTTCCTA CTAC TCTG TACCT
                                 |||||||| |||| |||| |||||
                                 GAAAGGGT GGTG AGGT ATGGG
                                     G   G   _
GAM1149  FLJ22814  3'  AGGTAGTGATATGTGTGTTAGG 46713        _   CT_ G
          AAAA                    TTTTCCTAGC TACAT  G TACCT
                                  |||||||||| |||||  | |||||
                                  AAAAGGATTG GTGTA  T ATGGA
                                     T    TAG G
GAM1149  FLJ22938  5'  AGGACGGCTGGTGGCTGGGGAA 45480          AT_  GTA
          G                       TTTTCCTAGCTAC  CTG  CCT
                                  ||||||||||||  |||  |||
                                  GAAGGGGTCGGTG  GGC  GGA
                                        GTC  A__
GAM1149  FLJ23506  5'  GGTGGAGGTGTTGGGAAAG   46166       T  A  GGT
                                TTTTCCTAGC AC TCT  ACC
                                |||||||||| || |||  |||
                                GAAAGGGTTG TG AGG  TGG
                                     _  G  ___
GAM1149  FLJ25082  3'  GGGTGTCAGATCCTGTGAAGA  58984     C  CTAC   GT
                                TTTTC TAG   ATCTG  ACCT
                                ||||| |||   |||||  ||||
                                AGAAG GTC   TAGAC  TGGG
                                   T  C___    TG
GAM1149  FLJ30058  3'  GGTGCCAGACAGGGGAAA   59304      AGCTACA
                                TTTCCT     TCTGGTACC
                                ||||||     |||||||||
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                                AAAGGG      AGACCGTGG
                                   GAC_____
GAM1149  FLJ32452  3'  GGAAATGAGATGTGCTTAGGAA 58632         _ T     G  A_  T
              AG                    TTTTCCTA GC ACATCT GT  CC
                                ||||||||  || ||||||  ||  ||
                                GAAAGGAT CG TGTAGA TA  GG
                                     T  _     G  AA
GAM1149  FLVCR    3'  GGGTTTGTATGTGGTGGGGGAA 26762        A      CTGGT
                                TTTCCT GCTACAT     ACCT
                                ||||||  |||||||     ||||
                                AAGGGG TGGTGTA     TGGG
                                   G      TGTT_
GAM1149  G4       5'  GGGTGCTGCCTGCTGGGAAGG  92638          TACATCT
                                TTTTCCTAGC      GGTACCT
                                ||||||||||      |||||||
                                GGAAGGGTCG      TCGTGGG
                                     TCCG___
GAM1149  GFR      3'  GGGTGTAAACTGGCTGGGGAGA 25448           CATCTG
                                TTTTCCTAGCTA     GTACCT
                                ||||||||||||     ||||||
                                AGAGGGGTCGGT     TGTGGG
                                      CAAA__
GAM1149  GMEB2    3'  AGGTGGGCGGGGGCTAGGGGGA 25659    TT      ACA    G_
                                TT  CCTAGCT   TCTG  TACCT
                                ||  |||||||   ||||  |||||
                                AG  GGATCGG   GGGC  GTGGA
                                 GG       ___    GG
GAM1149  GP5      3'  CCTGACCAGATGTGGCTCGGAG 16871       T          ACCT
              G                    TTTCC AGCTACATCTGGT
                                |||||  ||||||||||||
                                GGAGG TCGGTGTAGACCA
                                   C           GTCCA
GAM1149  GTPBP2   3'  TAGGTGCCAAACTTGGTGTGGC 39386        A       _____
              CAGGAAAG                TTTTCCT GCTACATC     TGGTACCT   A
                                |||||||  ||||||||    ||||||||  |
                                GAAAGGA CGGTGTGG     ACCGTGGA   T
                                     C       TTCAA
GAM1149  HIC2     3'  GGGTAGCCCTGGGGCTGGGGGA 65872    TT     TA  TCT   _
              G                    TT  CCTAGC  CA   GGT ACCT
                                ||  ||||||  ||   ||| ||||
                                GA  GGGTCG  GT   CCG TGGG
                                 GG     GG  C__   A
GAM1149  HSA404617 3'  AGGTGTGACGGGAGGCTGGGGA 73088           ACA   G  ___
              GA                    TTTTCCTAGCT   TCT GT   ACCT
                                ||||||||||   ||| ||   ||||
                                AGAGGGGTCGG   AGG CA   TGGA
                                      ___   G  GTG
GAM1149  HSCBCIP1  5'  GGGTGCCGGCCCAGCTAGGCGG 90232    TT      ACAT
              A                    TT  CCTAGCT    CTGGTACCT
                                ||  |||||||    |||||||||
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                                AG  GGATCGA    GGCCGTGGG
                                 GC      CCC_
GAM1149  HSJ1     3'  GGGTGTCAGGGCAGTGGAGGGG 23085     AG    A__    GT
                                CCT  CTAC   TCTG  ACCT
                                |||  ||||   ||||  ||||
                                GGG  GGTG   GGAC  TGGG
                                  GA    ACG    TG
GAM1149  HSPF2    5'  AGGTGCTCAATGGTAGGGGAA  19832      AG    ATC  _
                                TTCCT  CTAC   TG GTACCT
                                |||||  ||||   || ||||||
                                AAGGG  GATG   AC CGTGGA
                                   __    GTA  T
GAM1149  IL18BP   5'  GGGCTGGTGGCTGGGGGAG   20314    TT       CAT TG  A
                                TT  CCTAGCTA   C  GT CC
                                ||  ||||||||   |  || ||
                                GA  GGGTCGGT   G  CG GG
                                 GG       ___ GT  _
GAM1149  JDD1     3'  AGGTGTTCTAGCTGGGTAGA   63910     T      ___
                                TTT CCTAGCT   ACATCT
                                |||  |||||||   ||||||
                                AGA GGGTCGA   TGTGGA
                                  T      TCT
GAM1149  KCNJ9    3'  AGGTATCAGGCACAGGCAGGAA 18364        A   ACA_
            GA                    TTTTCCT GCT    TCTGGTACCT
                                |||||||  |||    ||||||||||
                                AGAAGGA CGG    GGACTATGGA
                                   _   ACAC
GAM1149  KHDRBS3  5'  GGGTGCTGGCAGGTGCTGGCGG 22657      A    _     ___
            GA                    TCCT GCTA CATCTG   GTACCT
                                ||||  |||| ||||||   ||||||
                                AGGG CGGT GTGGAC   CGTGGG
                                   _    C     GGT
GAM1149  KIAA0042 5'  AGGTGCCGGACCCTGCGGAGG  30233     A_  TACA
                                CCT  GC    TCTGGTACCT
                                |||  ||    ||||||||||
                                GGA  CG    AGGCCGTGGA
                                  GG  TCCC
GAM1149  KIAA0161 3'  AGGCCCCAGGTGTGGTGGGGAG 29191       A         TA
            G                     TTTCCT GCTACATCTGG  CCT
                                ||||||  ||||||||||  |||
                                GGAGGG TGGTGTGGACC  GGA
                                   G          CC
GAM1149  KIAA0205 3'  GGGTGCTGAACTGTTGGGGAAG 30215          TACA  T
                                TTTTCCTAGC    TC GGTACCT
                                ||||||||||    || |||||||
                                GAAGGGGTTG    AG TCGTGGG
                                      TCA_  _
GAM1149  KIAA0237 3'  GCCTGGTCTGGCTGGGAAAG   29227           C   T
                                TTTTCCTAGCTA ATC GGT
                                ||||||||||| ||| |||
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                                GAAAGGGTCGGT TGG CCG
                                      C   T
GAM1149  KIAA0247  3' GGTGCTAGAACTAGAAGG    29075     AG   CA
                                CCT  CTA  TCTGGTACC
                                |||  |||  |||||||||
                                GGA  GAT  AGATCGTGG
                                  A_   CA
GAM1149  KIAA0285  3' GGACTGGTGGCTGGGAGG    29686          CAT TG  A
                                TTTCCTAGCTA   C  GT CC
                                ||||||||||   |  || ||
                                GGAGGGTCGGT   G  CA GG
                                      ___ GT  _
GAM1149  KIAA0326  3' GGGCATATGTGGCTGGGGAGA  64967             CTG  A
                                TTTTCCTAGCTACAT   GT CC
                                ||||||||||||||   || ||
                                AGAGGGGTCGGTGTA   CG GG
                                       TA_  _
GAM1149  KIAA0444  3' GGGAGGGTGGGCTGGGGGG    63004   TT     A    GGTA
                                T  CCTAGCT CATCT    CC
                                |  ||||||| |||||    ||
                                G  GGGTCGG GTGGG    GG
                                 GG      _    AG__
GAM1149  KIAA0472  3' AGGTGAGATTGTGGCTGGAGGA 72335       T     _  GG
                                TTTTCC AGCTACA TCT  TACCT
                                |||||| ||||||| |||  |||||
                                AGGAGG TCGGTGT AGA  GTGGA
                                   _      T  __
GAM1149  KIAA0542  3' AGGTGCTGGGCTGTCGGGGAG  66660      TA  TACA  TG
                                TTTCC  GC   TC  GTACCT
                                |||||  ||   ||  ||||||
                                GAGGG  TG   GG  CGTGGA
                                   GC  TC__  GT
GAM1149  KIAA0544  3' GGTGCTGAGGTGGGAGGA    71473     AG   A  T
                                TCCT  CTAC TC GGTACC
                                ||||  |||| || ||||||
                                AGGA  GGTG AG TCGTGG
                                  G_   G  _
GAM1149  KIAA0557  3' GGGTCTCTGTAGGTGGGAGAG  78573       G    TCT  T
                                TTTTCCTA CTACA   GG ACCT
                                |||||||| |||||   || ||||
                                GAGAGGGT GATGT   TC TGGG
                                     G    C__  _
GAM1149  KIAA0574  3' AGGTGCTGGTAGACTAGGGAA  69806       _  CAT TG
                                TTTCCTAG CTA   C  GTACCT
                                |||||||| |||   |  ||||||
                                AAGGGATC GAT   G  CGTGGA
                                     A   ___ GT
GAM1149  KIAA0638  3' AGGAGCGATGCAGTTGGGAGAG 72827          A   TG  A
                                TTTTCCTAGCT CATC  GT CCT
                                |||||||||| ||||  || |||
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                                GAGAGGGTTGA GTAG  CG GGA
                                      C   __  A
GAM1149  KIAA0668  3'  AGGTGCCAGGGCTGTGGGAGGG 67118     AG   __
                                TCCT  CTACA  TCTGGTACCT
                                ||||  |||||  ||||||||||
                                GGGA  GGTGT  GGACCGTGGA
                                  G_    CG
GAM1149  KIAA0767  3'  GGTTGCCTGGGTTGGTTGGGGG 61256   TT      C  _  _ T
            AG                    TT  CCTAGCTA ATCT GGTA CC
                                ||  |||||||| |||| |||| ||
                                GA  GGGTTGGT TGGG CCGT GG
                                 GG       _   T   T
GAM1149  KIAA0773  3'  GCTTGGTGTGGCTGTGGAGA  28725      _       T
                                TTTCC TAGCTACATC GGT
                                ||||| |||||||||| |||
                                AGAGG GTCGGTGTGG TCG
                                   T        T
GAM1149  KIAA0795  3'  TGGATGTGAGCTGGGAGG    47234         _
                                TTTCCTAGCT ACATCTG
                                |||||||||| |||||||
                                GGAGGGTCGA TGTAGGT
                                      G
GAM1149  KIAA0945  3'  GGGTGCTGGGAGAGGGTTGGGG 30904        ACA_  TG
            G                    TTCCTAGCT   TC  GTACCT
                                |||||||||   ||  ||||||
                                GGGGGGTTGG   GG  CGTGGG
                                     GAGA  GT
GAM1149  KIAA0945  3'  GGTGTCTGTCTGGGAGGA    30905        CT   TCT GT
                                TTTTCCTAG  ACA   G  ACC
                                |||||||||  |||   |  |||
                                AGGAGGGTC  TGT   C  TGG
                                     __   ___ TG
GAM1149  KIAA1143  3'  TGGATGAGCTAGGAAGA     69253          A
                                TTTTCCTAGCT CATCTG
                                |||||||||| ||||||
                                AGAAGGATCGA GTAGGT
                                      _
GAM1149  KIAA1200  3'  AGGTGCTGACAGAGTTGGAGAA 63031      _     ACA  T
            AA                    TTTTC CTAGCT   TC GGTACCT
                                ||||| ||||||   || |||||||
                                AAAAG GGTTGA   AG TCGTGGA
                                   A     GAC  _
GAM1149  KIAA1229  3'  AGGTATCAGGTGTCATTG    62751     CT
                                TAG  ACATCTGGTACCT
                                |||  ||||||||||||
                                GTT  TGTGGACTATGGA
                                  AC
GAM1149  KIAA1237  3'  GCTGGATGTGGTTAGAGGGA  81300     TC        TG
                                TTT  CTAGCTACATC  GT
                                |||  ||||||||||  ||
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                                AGG  GATTGGTGTAG  CG
                                  GA         GT
GAM1149  KIAA1244  3'  GGTTATGGGTCTGGCTGGGAAG 72450          C    GGT   T
              A                    TTTTCCTAGCTA ATCT   ACC
                                   |||||||||||| ||||   |||
                                   AGAAGGGTCGGT TGGG   TGG
                                         C    TAT
GAM1149  KIAA1274  3'  AGGTGCTCTTGGCTGGGAG   93008         CATCT
                                   TTCCTAGCTA    GGTACCT
                                   ||||||||||    |||||||
                                   GAGGGTCGGT    TCGTGGA
                                         TC___
GAM1149  KIAA1297  5'  AGGTGGGGGCTGGGGAAA    72627          A_
                                   TTTTCCTAGCT  CATCT
                                   ||||||||||  |||||
                                   AAAGGGGTCGG  GTGGA
                                         GG
GAM1149  KIAA1535  3'  AGGTATCCAAGCCTGGGGAAG  80208         _ ACATC  _
                                   TTTTCCTAG CT    TGG TACCT
                                   ||||||||| ||    ||| |||||
                                   GAAGGGGTC GA    ACC ATGGA
                                         C _____  T
GAM1149  KIAA1560  3'  GGGTGTTCCTTATCTGGGGAAG 64851         CTAC  CT  __
                                   TTTTCCTAG   AT  GG  TACCT
                                   |||||||||   ||  ||  |||||
                                   GAAGGGGTC   TA  CC  GTGGG
                                         ____ TT  TT
GAM1149  KIAA1655  3'  GGGTACCAGGTGAGGCTGGAGA 67194       T   A
              G                    TTTTCC AGCT CATCTGGTACCT
                                   |||||| |||| ||||||||||||
                                   GAGAGG TCGG GTGGACCATGGG
                                      _   A
GAM1149  KIAA1679  3'  GGGTGGAGTCTGTGGTTGTGAG 70711      C       TCTGG
              AA                    TTTTC TAGCTACA    TACCT
                                   ||||| ||||||||    |||||
                                   AAGAG GTTGGTGT    GTGGG
                                      T       CTGAG
GAM1149  KIAA1695  3'  CCCCTCCAGGTGGGGTTGGGGA 47831         TA      TACCT
              GA                    TTTTCCTAGC  CATCTGG
                                   ||||||||||  |||||||
                                   AGAGGGGTTG  GTGGACC
                                         GG      TCCCCA
GAM1149  KIAA1710  3'  GGTATCAGCTTGGGAG      63179        CTACAT
                                   TTCCTAG     CTGGTACC
                                   |||||||     ||||||||
                                   GAGGGTT     GACTATGG
                                      C_____
GAM1149  KIAA1718  3'  AGGTACTAGATAAAGGTGAAGG 64971     A_   AC_
                                   CCT  GCT   ATCTGGTACCT
                                   |||  |||   ||||||||||
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                                GGA  TGG   TAGATCATGGA
                                  AG   AAA
GAM1149  KIAA1718  3'  GGCGTGGGGTGTGGCTGGGAGG 64978              G TA  T
                                TTTCCTAGCTACATCT G  CC
                                |||||||||||||||| |  ||
                                GGAGGGTCGGTGTGGG T  GG
                                      G GC
GAM1149  KIAA1726  3'  AGGTATTAAAAACAGGGGTTGG 67826    TT      ACATC___
            GGGGA                   TT  CCTAGCT       TGGTACCT
                                ||  |||||||       ||||||||
                                AG  GGGTTGG       ATTATGGA
                                 GG      GGACAAAA
GAM1149  KIAA1765  3'  AGGCGTGTGTTAGTTAGGAAAA 71131            _   C  GTA
                                TTTTCCTAGCTA CAT TG   CCT
                                ||||||||||| ||| ||   |||
                                AAAAGGATTGAT GTG GC   GGA
                                       T   T ____
GAM1149  KIAA1821  3'  GGGTACTGGAAGTGGGAGGA   72270     AG    A  TG
                                TCCT  CTAC TC  GTACCT
                                ||||  |||| ||  ||||||
                                AGGA  GGTG AG  CATGGG
                                  G_    A  GT
GAM1149  KIAA1821  3'  GGGTGTTAGGTCAGAAGGAG   72271      AG  AC    GG
                                TTCCT  CT  ATCT  TACCT
                                |||||  ||  ||||  |||||
                                GAGGA  GA  TGGA  GTGGG
                                   A_  C_    TT
GAM1149  KIAA1854  3'  AGGTGCCAGGCCATTAGCAGG  72197     A    CA__
                                CCT GCTA    TCTGGTACCT
                                ||| ||||    ||||||||||
                                GGA CGAT    GGACCGTGGA
                                  _    TACC
GAM1149  KIAA1867  3'  GCCTGGTGTACTGGGGGGA    96482    TT    C     T
                                TT  CCTAG TACATC GGT
                                ||  ||||| |||||| |||
                                AG  GGGTC ATGTGG CCG
                                 GG    _     T
GAM1149  KIAA1906  3'  GGGTAGGGGGTGTAACTGGGGA 73572         C      GG
             G                   TTTCCTAG TACATCT  TACCT
                                |||||||| |||||||  |||||
                                GAGGGGTC ATGTGGG  ATGGG
                                     A      GG
GAM1149  KIAA1944  3'  GGGCGTGTGGAGTTGGGGGGG   76080   TT     A   C  GTA
                                T  CCTAGCT CAT TG   CCT
                                |  ||||||| ||| ||   |||
                                G  GGGTTGA GTG GC   GGG
                                 GG      G   T ____
GAM1149  KIAA1949  5'  GGGTGGGGGCTGGGGAGA    99700          A_
                                TTTTCCTAGCT  CATCT
                                ||||||||||  |||||
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                                AGAGGGGTCGG  GTGGG
                                      GG
GAM1149  LANP-L    5'  GGGTATTGGGGAAGGCAGGAAA 48882       A   ACA  TG
              G                    TTTTCCT GCT   TC  GTACCT
                                   ||||||| |||   ||  ||||||
                                   GAAAGGA CGG   GG  TATGGG
                                      _  AAG  GT
GAM1149  LCHN      3'  GGGTGTTTTAAGCTGGGGG   87475        ____
                                   TTCCTAGCT    ACATCT
                                   |||||||||    ||||||
                                   GGGGGTCGA    TGTGGG
                                         ATTT
GAM1149  LGI3      3'  GGGTGCTGGGAGCGAGGGGG  58397   TT  A   ACA  TG
                                   T  CCT GCT   TC  GTACCT
                                   |  ||| |||   ||  ||||||
                                   G  GGA CGA   GG  CGTGGG
                                    GG   G  ___  GT
GAM1149  LGP2      3'  ACTGGATGGAGTTAGGGAAA   44376         A    TG
                                   TTTTCCTAGCT CATC  GT
                                   |||||||||| ||||  ||
                                   AAAGGGATTGA GTAG  CA
                                         G   GT
GAM1149  LMOD1     3'  GGTGCCCCAGCTAGGAAG    25103         ACATCT
                                   TTTCCTAGCT     GGTACC
                                   |||||||||      ||||||
                                   GAAGGATCGA     CCGTGG
                                         CC____
GAM1149  LW-1      5'  TGGGTGTGTTAGGAGGA     32893          T
                                   TTTTCCTAGC ACATCTG
                                   |||||||||| |||||||
                                   AGGAGGATTG TGTGGGT
                                         _
GAM1149  MADHIP    3'  GGGTGGGAAAGGGTGGTTGGGG 17815    TT       A   GG__
              GGA                     TT  CCTAGCTAC TCT    TACCT
                                   ||  ||||||||| |||    |||||
                                   AG  GGGTTGGTG GGA    GTGGG
                                    GG        _  AAGG
GAM1149  MADHIP    3'  GGGTGGGAAAGGGTGGTTGGGG 17816    TT       A   GG__
              GGA                     TT  CCTAGCTAC TCT    TACCT
                                   ||  ||||||||| |||    |||||
                                   AG  GGGTTGGTG GGA    GTGGG
                                    GG        _  AAGG
GAM1149  MAP-1     3'  AGGTGTAATTGACTAGGAAG   42435        C____
                                   TTTCCTAG     TACATCT
                                   ||||||||     |||||||
                                   GAAGGATC     ATGTGGA
                                         AGTTA
GAM1149  MAP1LC3A  3'  GGGTGCTGGCTGGTGGGATGGG 51683    TT   G_   AT_ TG
              GGAG                    TT  CCTA  CTAC   C  GTACCT
                                   ||  ||||  ||||   |  ||||||
```

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                                GA  GGGT  GGTG   G  CGTGGG
                                 GG    AG    GTC GT
GAM1149  MAPK13    3'  AGATGTCGGTTGGGAGAA    12317          _
                                TTTTCCTAGCT ACATCT
                                |||||||||| ||||||
                                AAGAGGGTTGG TGTAGA
                                       C
GAM1149  MAPKAP1   3'  AGGTGTCGGGGGCCCCCTAGGA 44373        CTACA_   GT
           GGG                    TTTTCCTAG     TCTG  ACCT
                                |||||||||     ||||  ||||
                                GGGAGGATC     GGGC  TGGA
                                      CCCCGG    TG
GAM1149  MASA      3'  GGGCAAAGTGTAGTTGGTAGAA 65465      C        CTG  A
                                TTTT CTAGCTACAT   GT CC
                                |||| ||||||||||   || ||
                                AAGA GGTTGATGTG   CG GG
                                  T         AAA  _
GAM1149  MDS018    3'  GGGTGTTGCCAGGTGTGGCTGG 41828                ___
           GGAAG                   TTTTCCTAGCTACATCTGGT   ACCT
                                |||||||||||||||||||   ||||
                                GAAGGGGTCGGTGTGGACCG   TGGG
                                          TTG
GAM1149  MGC15563  5'  GGTGCCAGGCGGGGAGG     52862       A  TACAT
                                TTTCCT GC     CTGGTACC
                                |||||| ||     ||||||||
                                GGAGGG CG     GACCGTGG
                                   G  ______
GAM1149  MGC23401  5'  GGGTGCTGGGGTGCGGGGAA   59336      A  T  A  TG
                                TTCCT GC AC TC  GTACCT
                                ||||| || || ||  ||||||
                                AAGGG CG TG GG  CGTGGG
                                   G  _  _  GT
GAM1149  MGC2508   3'  GGGTGGCTCTGTGGCTGGTAGG 44507      C        TCT  _
           A                     TTTT CTAGCTACA   GGT ACCT
                                |||| |||||||||   ||| ||||
                                AGGA GGTCGGTGT   TCG TGGG
                                  T        C__   G
GAM1149  MGC2601   3'  GGGTGCTGGGGAGGGGCTGGTA 44098      C     ACA_  TG
           GGA                     TTTT CTAGCT    TC  GTACCT
                                |||| ||||||    ||  ||||||
                                AGGA GGTCGG    GG  CGTGGG
                                  T     GGAG  GT
GAM1149  MGC32104  3'  GGGTGGAGGTTGGGAAGA    59068          A_
                                TTTTCCTAGCT  CATCT
                                ||||||||||  |||||
                                AGAAGGGTTGG  GTGGG
                                       AG
GAM1149  MGC34869  3'  GGGTGTTGGCTGGGTAAGGGGA 58717    TT   A   A  T  GG
           G                     TT  CCT GCT CA CT  TACCT
                                ||  ||| ||| || ||  |||||
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                                GA  GGA TGG GT GG  GTGGG
                                 GG   A  _ C  TT
GAM1149  MGC5442   5'  GGGCCGCGATGGAGCTGGGGGA 49506    TT      A   _   A  T
             G                    TT  CCTAGCT CATC TGGT CC
                                  ||  ||||||| |||| |||| ||
                                GA  GGGTCGA GTAG GCCG GG
                                 GG      G   C   _
GAM1149  MIDORI    5'  GGGTGTTGGGGGAGACAGGAGA 74219        AG  ACA   GG
             G                    TTTTCCT  CT   TCT  TACCT
                                  |||||||  ||   |||  |||||
                                GAGAGGA  GA   GGG  GTGGG
                                    CA  GG_   TT
GAM1149  MMPL1     3'  TAGACTGTAGCTGGGAGGA    15967             _
                                TTTTCCTAGCTACA TCTG
                                |||||||||||||| ||||
                                AGGAGGGTCGATGT AGAT
                                       C
GAM1149  MR       5'  GGGTGCTGGCGGTGTGGCGGGG 49147    TT   A      __ TG
             GGG                    T  CCT GCTACAT  C  GTACCT
                                  |  ||| |||||||  |  ||||||
                                G  GGG CGGTGTG  G  CGTGGG
                                 GG   G      GC GT
GAM1149  MRPL35    3'  ACTTTGCCAGATTTGGTTAGGG 34016           C       CCT
             AAA                    TTTTCCTAGCTA ATCTGGTA
                                  |||||||||||| ||||||||
                                AAAGGGATTGGT TAGACCGT
                                       T       TTCAG
GAM1149  N4BP3     3'  GGGTGTGAGGCATGAGCTGGGG 66859    TT      A   _  GG_
             GG                     T  CCTAGCT CAT CT   TACCT
                                  |  ||||||| ||| ||   |||||
                                G  GGGTCGA GTA GG   GTGGG
                                 GG      _   C  AGT
GAM1149  NEU4      3'  GGGTGCCCCACGATAGCTGTGG 55792    TT  _     CATCT_
             GGG                    T  CC TAGCTA     GGTACCT
                                  |  || ||||||     |||||||
                                G  GG GTCGAT     CCGTGGG
                                 GG  T     AGCACC
GAM1149  NEUROG3   3'  GGGTGCTAAGGGTAAGGGAGA  41003        A   ACATC
                                TTTTCCT GCT    TGGTACCT
                                |||||||  |||    ||||||||
                                AGAGGGA TGG    ATCGTGGG
                                    A   GA___
GAM1149  NFASC     3'  GGGTGCCACCAGTGTGGGAGAG 70860        GC   ATC
                                TTTTCCTA  TAC   TGGTACCT
                                ||||||||  |||   ||||||||
                                GAGAGGGT  GTG   ACCGTGGG
                                    __   ACC
GAM1149  P66       3'  GGGTGTCCCACAAGTTGGGTGG 40743     TT      ACATCT  _
             A                      TT  CCTAGCT     GG TACCT
                                  ||  |||||||     || |||||
```

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                                AG  GGGTTGA     CC GTGGG
                                 GT      ACAC__  T
GAM1149  PADI1    3'  GGTGTGTGTGTTGGGAGGA   62704         T   CTGG
                                TTTTCCTAGC ACAT    TACC
                                |||||||||| ||||    ||||
                                AGGAGGGTTG TGTG    GTGG
                                      _    T___
GAM1149  PDE2A    5'  AGGTGCCACCTTAGTCTGGCTG 12002          C  C____
           GGGAG                   TTTCCTAGCTA AT     TGGTACCT
                                |||||||||| ||    ||||||||
                                GAGGGGTCGGT TG     ACCGTGGA
                                      C  ATTCC
GAM1149  PILR(ALPHA) 5'  AGGTGCACTGGTTTGGGGAA   26480    TT  T    CATCTG
                                TT  CC AGCTA     GTACCT
                                ||  || |||||     ||||||
                                AA  GG TTGGT     CGTGGA
                                 GG  T    CA____
GAM1149  PINK1    3'  GGTATCAACATTGGGGAAG   51565         CTACATC
                                TTTTCCTAG      TGGTACC
                                |||||||||      |||||||
                                GAAGGGGTT      ACTATGG
                                      ACA____
GAM1149  PIP3-E   3'  GGGTACTTCTCCACCTAGGGAA 67355         CTACATCT
             G                   TTTTCCTAG       GGTACCT
                                |||||||||       |||||||
                                GAAGGGATC       TCATGGG
                                      CACCTCT_
GAM1149  PM5      5'  GGTGGGTCTAGCTGGGGGAG   27383    TT      C    GGT
                                TT  CCTAGCTA ATCT   ACC
                                ||  |||||||| ||||   |||
                                GA  GGGTCGAT TGGG   TGG
                                 GG       C   ___
GAM1149  PNMA5    3'  AGGAGGGATGTGGTGGGGGGG  73968   TT   A       GGTA
                                T  CCT GCTACATCT    CCT
                                |  ||| |||||||||    |||
                                G  GGG TGGTGTAGG    GGA
                                 GG   G       GA__
GAM1149  POFUT1   3'  AGGTACTGGGGATACAGGAGAG 70970        AGCTACA  TG
                                TTTTCCT      TC  GTACCT
                                |||||||      ||  ||||||
                                GAGAGGA      GG  CATGGA
                                     CATAG__  GT
GAM1149  POMT2    3'  GGGTGCCAGAGGGTGGGAG   26320       G  ACA
                                TTCCTA CT   TCTGGTACCT
                                |||||| ||   ||||||||||
                                GAGGGT GG   AGACCGTGGG
                                   G  ___
GAM1149  PP3501   3'  GGGTGCCGGGACTGGGGAGG   41685         CTACA
                                TTTTCCTAG    TCTGGTACCT
                                |||||||||    ||||||||||
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                                GGAGGGGTC    GGGCCGTGGG
                                     A____
GAM1149 PPFIA4   3' AGGATGGTGAGGCTGGGAGGA 70836         A   TGGTA
                                TTTTCCTAGCT CATC    CCT
                                |||||||||| ||||    |||
                                AGGAGGGTCGG GTGG    GGA
                                      A   TA___
GAM1149 PPP1R16B 3' AGGTGTCAGGGCAGCTGGGGAG 62031         ACA   GT
            A                    TTTTCCTAGCT  TCTG  ACCT
                                |||||||||||  ||||  ||||
                                AGAGGGGTCGA  GGAC  TGGA
                                      CG_   TG
GAM1149 PRIC285  3' AGGTGCCAGGACTGGGAGGG  62108       CTACA
                                TTTTCCTAG    TCTGGTACCT
                                |||||||||    ||||||||||
                                GGGAGGGTC    GGACCGTGGA
                                     A____
GAM1149 PRO0255  3' GGGTGCCCAGGGCTGGCAAAA 26971     C     ACATCT
                                TTTT CTAGCT     GGTACCT
                                |||| ||||||     |||||||
                                AAAA GGTCGG     CCGTGGG
                                  C     GAC___
GAM1149 PRO2198  3' AGGTGTCATTTGCTAGTAGAA 38405     C    TACATC  GT
                                TTTT CTAGC     TG  ACCT
                                |||| |||||     ||  ||||
                                AAGA GATCG     AC  TGGA
                                  T    TTT___  TG
GAM1149 PRO2577  5' GGGTTGCTTTGTGTTAGGAGGA 38425         T  TCT   _
                                TTTTCCTAGC ACA   GGTA CCT
                                |||||||||| |||   |||| |||
                                AGGAGGATTG TGT   TCGT GGG
                                      _  T__   T
GAM1149 PRO2730  5' AGGTGTTGGGTGGGAAAA    48179       G  _
                                TTTTCCTA CTA CATCT
                                |||||||| ||| |||||
                                AAAAGGGT GGT GTGGA
                                     G  T
GAM1149 PRTD-NY3 5' GGGTGACGGGGGCTGGGAAG  48884        ACA   G
                                TTTCCTAGCT  TCTG TACCT
                                ||||||||||  |||| |||||
                                GAAGGGTCGG  GGGC GTGGG
                                     ___   A
GAM1149 PSKH1    3' GGGTGTTGGCAGCCTGGGAG  68801      _ ACAT  GG
                                TTCCTAG CT   CT  TACCT
                                ||||||| ||   ||  |||||
                                GAGGGTC GA   GG  GTGGG
                                    C  C___  TT
GAM1149 PTK6     5' GGGTGCTGGGTGTGGCTG    21081        TG
                                TAGCTACATC  GTACCT
                                ||||||||||  ||||||
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                                GTCGGTGTGG  CGTGGG
                                      GT
GAM1149  PTPRT    3'  AGGTGCTGGGGAGTGGGAGG   56485     AG   A_  TG
                                CCT  CTAC  TC  GTACCT
                                |||  ||||  ||  ||||||
                                GGA  GGTG  GG  CGTGGA
                                  G_   AG  GT
GAM1149  PYGO1    5'  GGACTGGATGGGTTAGGAGGA  83155          A   TG  A  T
                                TTTTCCTAGCT CATC  GT CC
                                |||||||||||  ||||  || ||
                                AGGAGGATTGG GTAG  CA GG
                                      _   GT  _  T
GAM1149  QSCN6    3'  GGGTGCCAGGTAGAAGCTAGGG 12569          AC_
            AG                    TTTCCTAGCT   ATCTGGTACCT
                                |||||||||   ||||||||||
                                GAGGGATCGA   TGGACCGTGGG
                                      AGA
GAM1149  RASD2    3'  GGGTGGCAGCTGGGAGAA    27465          A_
                                TTTTCCTAGCT  CATCT
                                ||||||||||  |||||
                                AAGAGGGTCGA  GTGGG
                                      CG
GAM1149  RODH-4   5'  GGGTGTGTTTGCCTAGGAGAG  14924         _ ___
                                TTTTCCTAG C   TACATCT
                                |||||||| |   |||||||
                                GAGAGGATC G   GTGTGGG
                                     C TTT
GAM1149  SENP8    5'  AGGTGCCTGAGGGTGGTTGGGG 59750          A_  T
            AG                    TTTCCTAGCTAC  TC GGTACCT
                                ||||||||||||  || |||||||
                                GAGGGGTTGGTG  AG CCGTGGA
                                      GG  T
GAM1149  SERPINH1 3'  GGGTGCTATTGGGGTTGGGGGG 16374    TT     TA  TC
            G                     TT  CCTAGC  CA  TGGTACCT
                                ||  ||||||  ||  ||||||||
                                GG  GGGTTG  GT  ATCGTGGG
                                  GG     GG  T_
GAM1149  SFXN5    3'  GGGTGCCATGGTGTTGGAGGG  58656      AGCT    _
                                TCCT    ACATC TGGTACCT
                                ||||    ||||| ||||||||
                                GGGA    TGTGG ACCGTGGG
                                   GGT_     T
GAM1149  SHANK3   3'  AGGTGCTGCTCGTGGTGGGAGG 66099        G    ATC
                                TTTCCTA CTAC   TGGTACCT
                                |||||||  ||||   ||||||||
                                GGAGGGT GGTG   GTCGTGGA
                                     _   CTC
GAM1149  SMCR5    3'  AGGTGCCCAATCTAGTTGGGGA 59244          C  CT
                                TTCCTAGCTA AT  GGTACCT
                                |||||||||| ||  |||||||
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                                AGGGGTTGAT TA  CCGTGGA
                                      C  AC
GAM1149  SNPH     3'  GGGTACACATGGGGCTGGGAGG 28906         TA   CTG
                                TTTCCTAGC  CAT   GTACCT
                                |||||||||  |||   ||||||
                                GGAGGGTCG  GTA   CATGGG
                                     GG   CA_
GAM1149  SNX7     5'  AGGTGCTGGATCTGGACGAGGA 32562      AG_   C   TG
                                TCCT   CTA ATC  GTACCT
                                ||||   ||| |||  ||||||
                                AGGA   GGT TAG  CGTGGA
                                  GCA   C   GT
GAM1149  SPEC1    5'  GGGTGGTGGTGTATCTGGGGAG 40008         C     T G
           A                     TTTTCCTAG TACATC G TACCT
                                |||||||||  ||||||  |  |||||
                                AGAGGGGTC ATGTGG T GTGGG
                                     T     _ G
GAM1149  SPRY1    3'  GGGTACCGTGGGAGCAGGGAAA 65633        A   A_   CT
                                TTTTCCT GCT  CAT  GGTACCT
                                |||||||  |||  |||  |||||||
                                AAAGGGA CGA  GTG  CCATGGG
                                    _  GG  __
GAM1149  SPRY4    3'  GGGCAGGGTGTGGTTTGGGGGG 49026    TT    _      G  A  T
           A                     TT  CCTAG CTACATCT GT CC
                                ||  |||||  ||||||||  ||  ||
                                AG  GGGTT GGTGTGGG CG GG
                                 GG    T       A  _
GAM1149  STK16    3'  GGGTGGGGGTTGGGAAAA    72588          A_
                                TTTTCCTAGCT  CATCT
                                ||||||||||  |||||
                                AAAAGGGTTGG  GTGGG
                                      GG
GAM1149  STX4A    5'  GGGTGTTGGGGTCCGCAGGGGG 17215    TT   A  TACA   GG
           A                     TT  CCT GC    TCT  TACCT
                                ||  |||  ||    |||  |||||
                                AG  GGA CG    GGG  GTGGG
                                 GG   _  CCTG   TT
GAM1149  SV2B     3'  GGGTGTGGGTTGGGGGAG    29953    TT     _
                                TT  CCTAGCT ACATCT
                                ||  |||||||  ||||||
                                GA  GGGTTGG TGTGGG
                                 GG      G
GAM1149  TA-KRP   3'  AGGTACCAGATGAATCAGGA   51670      AGCTA
                                TCCT    CATCTGGTACCT
                                ||||    ||||||||||||
                                AGGA    GTAGACCATGGA
                                  CTAA_
GAM1149  TDPGD    3'  GGTAGTGGTGCTAGGGAGA   60446         TA   CTGG
                                TTTTCCTAGC  CAT    TACC
                                ||||||||||  |||    ||||
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                                AGAGGGATCG  GTG   ATGG
                                      TG  ____
GAM1149  TOLLIP   3'  GGTGTTGGAGGTGGTGGA   39198    TA   A  GG
                                TCC  GCTAC TCT  TACC
                                |||  ||||| |||  ||||
                                AGG  TGGTG AGG  GTGG
                                  __    G   TT
GAM1149  TPD52    3'  GGGTATTGGGGGTGGCTGTGAA 18671      C      AT TG
           AG                     TTTTC TAGCTAC  C  GTACCT
                                |||||| |||||||  |  ||||||
                                GAAAG GTCGGTG  G  TATGGG
                                   T      GG GT
GAM1149  UPLC1    3'  GGGTGCTGGGCCCTGGCAGGA  35229     A   CA_  TG
                                TCCT GCTA   TC  GTACCT
                                |||| ||||   ||  ||||||
                                AGGA CGGT   GG  CGTGGG
                                  _   CCC  GT
GAM1149  VPS39    3'  GCAATGGTGTGGTTGGAGAG   63499      T       TG_
                                TTTTCC AGCTACATC   GT
                                ||||||| |||||||||   ||
                                GAGAGG TTGGTGTGG   CG
                                   _       TAA
GAM1149  XT2      3'  AGGAAAATGGGTGGTTGGGAGA 42474           A  TGGTA
           G                     TTTTCCTAGCTAC TC    CCT
                                |||||||||||| ||    |||
                                GAGAGGGTTGGTG GG    GGA
                                      _ TAAAA
GAM1149  ZFP106   3'  AGGTGTTGGGCAGTTGTGGGAA 42715      _    ACA   GG
                                TTTCC TAGCT   TCT  TACCT
                                ||||| |||||   |||  |||||
                                AAGGG GTTGA   GGG  GTGGA
                                   T    C__   TT
GAM1149  ZNF363   3'  AGGTATTCCATAAAAGTAGTTG 73834           ATC__  __
           GGAAAA                TTTTCCTAGCTAC    TGG  TACCT
                                ||||||||||||    |||  |||||
                                AAAAGGGTTGATG    ACC  ATGGA
                                      AAAAT   TT
GAM1149  LOC112885 3'  GGGTGGAGGGTTGGGGAG    57340         A__
                                TTTCCTAGCT   CATCT
                                ||||||||||   |||||
                                GAGGGGTTGG   GTGGG
                                      GAG
GAM1149  LOC113146 5'  AGGTGCTGGGGTCCCTGGGGAG 73333        CT  A  TG
                                TTTCCTAG  AC TC  GTACCT
                                ||||||||  || ||  ||||||
                                GAGGGGTC  TG GG  CGTGGA
                                     CC  _  GT
GAM1149  LOC113201 5'  AGGTGTTGGGTTTGGGGGA   57352   TT    CTAC    GG
                                T  CCTAG    ATCT  TACCT
                                |  |||||    ||||  |||||
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                                A  GGGTT    TGGG  GTGGA
                                 GG     ____    TT
GAM1149  LOC115129 3'  GGGTGCTACTGAGGCTGTGAGA 73626      C     A  TC
              A                   TTTTC TAGCT CA  TGGTACCT
                                  ||||| ||||| ||  ||||||||
                                  AAGAG GTCGG GT  ATCGTGGG
                                     T     A  C_
GAM1149  LOC118851 3'  GCTGGTGTGGCTGGCAAAA    76016      C         T
                                  TTTT CTAGCTACATC GGT
                                  |||| |||||||||| |||
                                  AAAA GGTCGGTGTGG TCG
                                    C         _
GAM1149  LOC119188 5'  GCTAAGGGTGTGGTGGGAGAA  74402         G       __
                                  TTTTCCTA CTACATCT  GGT
                                  |||||||| ||||||||  |||
                                  AAGAGGGT GGTGTGGG  TCG
                                       _       AA
GAM1149  LOC123346 3'  AGGTCCCTGTGTCGTTGGGGGA 76126    TT     T    CT  T
              G                   TT  CCTAGC ACAT  GG ACCT
                                  ||  |||||| ||||  || ||||
                                  GA  GGGTTG TGTG  CC TGGA
                                   GG     C    T_  C
GAM1149  LOC124222 3'  GGGTGTCCAGGGCTAGGGAG   74754          ACAT    _
                                  TTTCCTAGCT    CTGG TACCT
                                  ||||||||||    |||| |||||
                                  GAGGGATCGG    GACC GTGGG
                                        _____    T
GAM1149  LOC124602 3'  AGGTGTCCAGGGTTTGGGGGGA 74784    TT     CT  A     _
                                  TT  CCTAG  AC TCTGG TACCT
                                  ||  |||||  || ||||| |||||
                                  AG  GGGTT  TG GGACC GTGGA
                                   GG     __ _     T
GAM1149  LOC126297 5'  AGGAAGTTGTGGGGTTGGGGAG 74976          TA   CTGGTA
                                  TTTCCTAGC  CAT      CCT
                                  |||||||||  |||      |||
                                  GAGGGGTTG  GTG      GGA
                                        GG   TTGAA_
GAM1149  LOC126661 5'  GGGTATCCCCCGCTAGGAGAG  75060          TACATCT
                                  TTTTCCTAGC       GGTACCT
                                  ||||||||||       |||||||
                                  GAGAGGATCG       CTATGGG
                                        CCCC___
GAM1149  LOC126755 3'  AGATCGAGGTGTGTGTTGGGGG 75073    TT     _      _   ACCT
              AG                    TT  CCTAGC TACATCT GGT
                                  ||  |||||| ||||||| |||
                                  GA  GGGTTG GTGTGGA CTA
                                   GG     T      G   GA
GAM1149  LOC127002 5'  GGTGAAGGGGCTGGGGAGA   75127          ACA   GG
                                  TTTTCCTAGCT   TCT  TACC
                                  ||||||||||   |||  ||||
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                                AGAGGGGTCGG  GGA  GTGG
                                      ___  A_
GAM1149  LOC132228 3'  GGGTGTGTGTTGGTGGGGG   75547    TT _    _
                                TT  C CTAGC TACATCT
                                ||  | ||||| |||||||
                                GG  G GGTTG GTGTGGG
                                 GG T    T
GAM1149  LOC139082 5'  GGGTGGCAGGGGTTAGGGAAA  75894          ACA   G
                                TTTTCCTAGCT   TCTG TACCT
                                ||||||||||   |||| |||||
                                AAAGGGATTGG   GGAC GTGGG
                                      ___   G
GAM1149  LOC143286 5'  AGGATGTGTGTGGCGGGGAGAG 83842        A     CTG  A
                                TTTTCCT GCTACAT   GT CCT
                                ||||||| |||||||   || |||
                                GAGAGGG CGGTGTG   TA GGA
                                    G      TG_  _
GAM1149  LOC143286 5'  GGAAGGTAGCTGGGGAGA    83845          A_
                                TTTTCCTAGCTAC  TCT
                                ||||||||||||  |||
                                AGAGGGGTCGATG  AGG
                                       GA
GAM1149  LOC143287 3'  AGGATGTGTGTGGCGGGGAGAG 83826        A     CTG  A
                                TTTTCCT GCTACAT   GT CCT
                                ||||||| |||||||   || |||
                                GAGAGGG CGGTGTG   TA GGA
                                    G      TG_  _
GAM1149  LOC143287 3'  GGAAGGTAGCTGGGGAGA    83828          A_
                                TTTTCCTAGCTAC  TCT
                                ||||||||||||  |||
                                AGAGGGGTCGATG  AGG
                                       GA
GAM1149  LOC144266 5'  AGCATGGGGTGTGGCTGGCAGA 77265     C         G  ACCT
           A                     TTTT CTAGCTACATCT GT
                                ||||  |||||||||||| ||
                                AAGA GGTCGGTGTGGG TA
                                  C          G  CGA
GAM1149  LOC144587 5'  GGGTGCCGGAATTAGGAAGG   67590        CTACA
                                TTTTCCTAG    TCTGGTACCT
                                |||||||||    ||||||||||
                                GGAAGGATT    AGGCCGTGGG
                                     A____
GAM1149  LOC144755 5'  GGAATAAGGTTGTGGCTAGGAA 84100          _  G  A  T
           GA                    TTTTCCTAGCTACA TCT GT CC
                                ||||||||||||| ||| || ||
                                AGAAGGATCGGTGT GGA TA GG
                                       T   A  A
GAM1149  LOC145463 5'  GGTGTTGTGGCTGGGGAGA   71482          TCTGG
                                TTTTCCTAGCTACA    TACC
                                ||||||||||||     ||||
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                                AGAGGGGTCGGTGT    GTGG
                                       T_____
GAM1149  LOC145468 3'  GGTGCCACGCTGGAGAAGA   74256      _    TACATC
                                TTTTC CTAGC     TGGTACC
                                ||||| |||||     |||||||
                                AGAAG GGTCG     ACCGTGG
                                   A    C_____
GAM1149  LOC145717 5'  GGGTGAGTCTGTGTTTGGGGAG 67377        C   TCTGG
            A                    TTTTCCTAG TACA    TACCT
                                 ||||||||| ||||    |||||
                                 AGAGGGGTT GTGT    GTGGG
                                       T   CTGA_
GAM1149  LOC145757 3'  AGAACCAAGGTGAGCTGGGGGA 77913    TT     A    _   ACCT
            A                    TT  CCTAGCT CATCT GGT
                                 ||  ||||||| ||||| |||
                                 AA  GGGTCGA GTGGA CCA
                                  GG      _    A   AGA
GAM1149  LOC146856 3'  GGGTGTATGTTTGGGAAGA   83703        _ _
                                TTTTCCTAG C TACATCT
                                ||||||||| | |||||||
                                AGAAGGGTT G ATGTGGG
                                       T T
GAM1149  LOC147165 3'  GGGTGTTGGGTTTGTTAGGGA  85087       TAC   GG
                                TTCCTAGC   ATCT  TACCT
                                ||||||||   ||||  |||||
                                AGGGATTG   TGGG  GTGGG
                                      TT_   TT
GAM1149  LOC147178 3'  GGGAGTTATGTGGCTAGGAGG  61997           CTGGTA
                                TTTCCTAGCTACAT     CC
                                ||||||||||||||     ||
                                GGAGGATCGGTGTA     GG
                                         TTGAG_
GAM1149  LOC148304 3'  GGGTGCTGCATGCTAGGAAAG  79532         TACATCT
                                TTTTCCTAGC      GGTACCT
                                ||||||||||      |||||||
                                GAAAGGATCG      TCGTGGG
                                       TACG___
GAM1149  LOC148697 3'  GGGTACCAGTTTTGTAGGAAAA 79678       G TACAT
                                TTTTCCTA C    CTGGTACCT
                                |||||||| |    |||||||||
                                AAAAGGAT G    GACCATGGG
                                     _ TTTT_
GAM1149  LOC149010 5'  TTAGATGTATTGGGAAAG    79856       C
                                TTTTCCTAG TACATCTGG
                                ||||||||| |||||||||
                                GAAAGGGTT ATGTAGATT
                                          _
GAM1149  LOC149297 3'  GGTGCCAGGGGTGGCAGGA   85542     A    AT
                                TCCT GCTAC  CTGGTACC
                                |||| |||||  ||||||||
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                                AGGA CGGTG  GACCGTGG
                                  _    GG
GAM1149  LOC150155 3'  GGTGCCACGCTGGAGAAGA   71417      _    TACATC
                                TTTTC CTAGC     TGGTACC
                                ||||| |||||     |||||||
                                AGAAG GGTCG     ACCGTGG
                                  A    C_____
GAM1149  LOC150291 3'  AGGTGCTGGATTTTACTAAGAA 86129      C   CTAC   TG
            AA                    TTTTC TAG    ATC  GTACCT
                                ||||| |||    |||  ||||||
                                AAAAG ATC    TAG  CGTGGA
                                  A   ATTT   GT
GAM1149  LOC150967 3'  AGGTGTCGCTCATTAGGGAAA  80882       ____   T
                                TTTTCCT    AGC ACATCT
                                |||||||    ||| ||||||
                                AAAGGGA    TCG TGTGGA
                                    TTAC   C
GAM1149  LOC151124 5'  GGGTGTCTGCAGCAAGGGAG   86419      A   A  TCT GT
                                TTTCCT GCT CA   G  ACCT
                                |||||| ||| ||   |  ||||
                                GAGGGA CGA GT   C  TGGG
                                  A   C  ___ TG
GAM1149  LOC151405 5'  AGGTGTCTTTAACTGGGGAAG  86513        C  CATCT GT
                                TTTTCCTAG TA     G  ACCT
                                |||||||| ||     |  ||||
                                GAAGGGGTC AT     C  TGGA
                                    A  TT___ TG
GAM1149  LOC151414 5'  GGGCTAAAATGTAGTTGGGAAA 81038           C_   A  T
            G                   TTTTCCTAGCTACAT  TGGT CC
                                ||||||||||||||  |||| ||
                                GAAAGGGTTGATGTA  ATCG GG
                                      AA   _
GAM1149  LOC151429 5'  GGTCCCTGAGCTGGGGAAG   86545        A  TCT  T
                                TTTTCCTAGCT CA   GG ACC
                                |||||||||| ||   || |||
                                GAAGGGGTCGA GT   CC TGG
                                    _ ____  C
GAM1149  LOC151445 3'  GGTCTGCTGGCTGGGAAG    69986        CATC   T
                                TTTCCTAGCTA    TGG ACC
                                ||||||||||    ||| |||
                                GAAGGGTCGGT    GTC TGG
                                    C____   _
GAM1149  LOC151446 5'  AGGAGGGGTGGGTTGGGGAAG  86567         A    GGTA
                                TTTTCCTAGCT CATCT    CCT
                                |||||||||| |||||    |||
                                GAAGGGGTTGG GTGGG    GGA
                                    _    GA__
GAM1149  LOC151457 5'  AGGTGCCAGGGATGGGAAAG   81045       GCTACA
                                TTTTCCTA     TCTGGTACCT
                                ||||||||     ||||||||||
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                                GAAAGGGT     GGACCGTGGA
                                     AG____
GAM1149  LOC152359 3'  CAGATGGTGGTTAGGAGAA    86881           _
                                TTTTCCTAGCTAC ATCTG
                                |||||||||||| |||||
                                AAGAGGATTGGTG TAGAC
                                      G
GAM1149  LOC153196 5'  AGGTCTGGTGGGGCTGGGGGAG 87164    TT     TA    T  T
                                TT  CCTAGC  CATC GG ACCT
                                ||  ||||||  |||| || ||||
                                GA  GGGTCG  GTGG TC TGGA
                                 GG     GG   _ _
GAM1149  LOC153232 5'  AGAGCCGAGTGTGGCTGGGAAG 87176            TC    ACCT
            A                    TTTTCCTAGCTACA  TGGT
                                ||||||||||||||  ||||
                                AGAAGGGTCGGTGT  GCCG
                                      GA    AGA
GAM1149  LOC153454 3'  GGGCTTGGTGAGCTGGGGGAA  81693    TT      A    T   A
                                TT  CCTAGCT CATC GGT CC
                                ||  ||||||| |||| ||| ||
                                AA  GGGTCGA GTGG TCG GG
                                 GG      _    T   _
GAM1149  LOC154789 5'  AGGTGTTCACGGGCTGGGGGAG 82024    TT      _____
                                TT  CCTAGCT     ACATCT
                                ||  |||||||     ||||||
                                GA  GGGTCGG     TGTGGA
                                 GG      GCACT
GAM1149  LOC157254 3'  GGGTGCCAGCCACGCTGGGAGG 82314          TACAT
            G                    TTTTCCTAGC     CTGGTACCT
                                ||||||||||     |||||||||
                                GGGAGGGTCG     GACCGTGGG
                                      CACC_
GAM1149  LOC157381 3'  AGGTGTCAGCTACAAGGAGAA  87731        ___   _
                                TTTTCCT   AGCT ACATCT
                                |||||||   |||| ||||||
                                AAGAGGA   TCGA TGTGGA
                                     ACA    C
GAM1149  LOC157848 3'  AGGTAGGGGGTGGGCTGGGGGA 82516    TT      A    GG
            G                    TT  CCTAGCT CATCT  TACCT
                                ||  ||||||| |||||  |||||
                                GA  GGGTCGG GTGGG  ATGGA
                                 GG      _    GG
GAM1149  LOC158046 3'  AGGAAAGTGGGGTTGGGAGGA  59900          TA  T  GGTA
                                TTTTCCTAGC  CA CT    CCT
                                ||||||||||  || ||    |||
                                AGGAGGGTTG  GT GA    GGA
                                      GG  _  AA__
GAM1149  LOC158061 5'  GCCGTGTGGTTGGGAAGA    82584             CT
                                TTTTCCTAGCTACAT  GGT
                                ||||||||||||||  |||
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                                AGAAGGGTTGGTGTG  CCG
                                     __
GAM1149  LOC158156 3'  GGGTATTATTTATGTGGCATGG 82627        _      C__
                GAAAA                  TTTTCCTA GCTACAT   TGGTACCT
                                       |||||||| |||||||   ||||||||
                                       AAAAGGGT CGGTGTA   ATTATGGG
                                            A      TTT
GAM1149  LOC158308 3'  AGGTGTCGGGGTGTGGGGGGG  88065      AG       _ GT
                                       TCCT  CTACATCT G  ACCT
                                       ||||  |||||||| |  ||||
                                       GGGG  GGTGTGGG C  TGGA
                                         G_       G TG
GAM1149  LOC158434 3'  CGGATGTGGTTAGGGAAG    88160              TG
                                       TTTTCCTAGCTACATC  G
                                       ||||||||||||||||  |
                                       GAAGGGATTGGTGTAG  C
                                                 GT
GAM1149  LOC158434 3'  TTAACAGCTGGATGTGGTTAGG 88164              TG  ACCT
                GAAG                   TTTTCCTAGCTACATC  GT
                                       ||||||||||||||||  ||
                                       GAAGGGATTGGTGTAG  CG
                                                 GT  ACAATTC
GAM1149  LOC159036 3'  GGGTGTCAGATGAGTGTAGAGG 88350      A___   A     GT
                AA                      TTCCT    GCT CATCTG  ACCT
                                        |||||    ||| ||||||  ||||
                                        AAGGA    TGA GTAGAC  TGGG
                                           GATG  _     TG
GAM1149  LOC161528 5'  GGGTGAGTCTGTGTTTGGGGAG 83154         C    TCTGG
                A                       TTTTCCTAG TACA     TACCT
                                        |||||||||| ||||     |||||
                                        AGAGGGGTT GTGT     GTGGG
                                              T    CTGA_
GAM1149  LOC164382 3'  GGGTGCTGGACACAGTGTTGGG 88560          T  A___  TG
                GAAG                   TTTTCCTAGC AC    TC  GTACCT
                                       ||||||||||| ||    ||  ||||||
                                       GAAGGGGTTG TG    AG  CGTGGG
                                             _  ACAC  GT
GAM1149  LOC199927 3'  ACCGGAGTGGCTGGGAGG     91477            A
                                       TTTCCTAGCTAC TCTGGT
                                       |||||||||||| ||||||
                                       GGAGGGTCGGTG AGGCCA
                                                  _
GAM1149  LOC200197 3'  AGGCTGGATGTGGCTTGGGAGA 90013         _       TG  ACCT
                G                       TTTTCCTA GCTACATC  GT
                                        |||||||| ||||||||  ||
                                        GAGAGGGT CGGTGTAG  CG
                                             T       GT  GA
GAM1149  LOC200933 5'  GGGAAGTGTGGTGGGAGG     91795        G     T  GGTA
                                       TTTCCTA CTACA CT    CC
                                       ||||||| ||||| ||    ||
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                                GGAGGGT GGTGT GA    GG
                                   _    _ AG__
GAM1149  LOC201115 5'  AGGTGTTGGCTCAGGGAAG    89476        _    _
                                TTTTCCT AGCTA CATCT
                                ||||||| ||||| |||||
                                GAAGGGA TCGGT GTGGA
                                    C    T
GAM1149  LOC201689 5'  AGGTGCCAGGTCTGTAGGTAG  67730     G    __
                                CTA CTACA  TCTGGTACCT
                                ||| |||||  ||||||||||
                                GAT GATGT  GGACCGTGGA
                                  G    CT
GAM1149  LOC203069 5'  GGGTGCTGCGCAGGCAGGAAGA 90761        A   ACATCT
                                TTTTCCT GCT     GGTACCT
                                ||||||| |||     |||||||
                                AGAAGGA CGG     TCGTGGG
                                   _  ACGCG_
GAM1149  LOC203232 3'  AGGTGTCAGACACCGTGGTGGA 71914     TA    A___   GT
                                TCC  GCTAC   TCTG  ACCT
                                |||  |||||   ||||  ||||
                                AGG  TGGTG   AGAC  TGGA
                                  __    CCAC   TG
GAM1149  LOC203246 3'  GGGTGCCTTTCTTAGCTAGGAG 90837         CATCT
                                TTCCTAGCTA    GGTACCT
                                ||||||||||    |||||||
                                GAGGATCGAT    CCGTGGG
                                     TCTTT
GAM1149  LOC203273 3'  AGGTATCAGGCAGTGGCGGAGG 88882     A_    A_
                                CCT  GCTAC  TCTGGTACCT
                                |||  |||||  ||||||||||
                                GGA  CGGTG  GGACTATGGA
                                  GG    AC
GAM1149  LOC203397 3'  AGGTGTCCAGGGTTTGGGGGGA 90897    TT    CT  A    _
                                TT  CCTAG  AC TCTGG TACCT
                                ||  |||||  || ||||| |||||
                                AG  GGGTT  TG GGACC GTGGA
                                 GG    __ _    T
GAM1149  LOC203429 3'  GGGTAGAGTGGGGTTAGGGAGA 90932         TA   CTGG
                                TTTTCCTAGC  CAT    TACCT
                                ||||||||||  |||    |||||
                                AGAGGGATTG  GTG    ATGGG
                                     GG   AG__
GAM1149  LOC204720 5'  GCTATGATGTGTTGGGAAAA   92347         T    _
                                TTTTCCTAGC ACATC TGGT
                                |||||||||| ||||| ||||
                                AAAAGGGTTG TGTAG ATCG
                                     _    T
GAM1149  LOC219653 3'  AGGTGTTGGGGAAGATTTGGGG 92913         CTACA_   GG
            AAG                   TTTTCCTAG     TCT  TACCT
                                |||||||||     |||  |||||
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                              GAAGGGGTT    GGG  GTGGA
                                   TAGAAG   TT
GAM1149  LOC219920 5'  AGGTGGGTGTTGGGGAGA    94936        TA_
                              TTTTCCTAGC   CATCT
                              ||||||||||   |||||
                              AGAGGGGTTG   GTGGA
                                   TGG
GAM1149  LOC219940 3'  GGAATTGTTGGCTAGGGGAG   95002    TT      _ __
                              TT  CCTAGCTA CA  TCT
                              ||  |||||||| ||  |||
                              GA  GGATCGGT GT  AGG
                               GG       T  TA
GAM1149  LOC219942 3'  GGTGTGATGTAGTAGGAAGA   94996       G      TGG
                              TTTTCCTA CTACATC   TACC
                              |||||||| |||||||   ||||
                              AGAAGGAT GATGTAG   GTGG
                                   _      T__
GAM1149  LOC220045 5'  GGGTGCCCGTGAGCATGGGAGG 95036       _  A   CT
                              TTTCCTA GCT CAT  GGTACCT
                              ||||||| ||| |||  |||||||
                              GGAGGGT CGA GTG  CCGTGGG
                                   A  _  C_
GAM1149  LOC221410 3'  AGGAGACATGGGCTAGGGAAG  93687         ACA_  GGTA
                              TTTTCCTAGCT    TCT    CCT
                              ||||||||||    |||    |||
                              GAAGGGATCGG    AGA    GGA
                                    GTAC  ____
GAM1149  LOC221463 3'  GGGCTGGCACGTGGCTGGGAGG 93708          AT_ TG  A  T
                              TTTCCTAGCTAC   C  GT CC
                              ||||||||||||   |  || ||
                              GGAGGGTCGGTG   G  CG GG
                                    CAC GT  _
GAM1149  LOC221474 5'  GGGTGCCAGGGAGGGGTGGGAG 93998       G  ACA
           AG                   TTTTCCTA CT   TCTGGTACCT
                              ||||||||  ||   ||||||||||
                              GAGAGGGT GG   GGACCGTGGG
                                   G  GAG
GAM1149  LOC221692 3'  GGGTGCTGGGTTCCGCTTTGGT 93854      _____  TAC   TG
           GGGGA                TTCCT    AGC   ATC  GTACCT
                              |||||    |||   |||  ||||||
                              AGGGG    TCG   TGG  CGTGGG
                                 TGGTT   CCT   GT
GAM1149  LOC221751 3'  AGGTATCGCATGTGCGGGGGAG 93675      A  T   C
                              TTTCCT GC ACAT TGGTACCT
                              |||||| || |||| ||||||||
                              GAGGGG CG TGTA GCTATGGA
                                 G  _   C
GAM1149  LOC221922 5'  AGGTGCTGGAACAGTCGGGAGG 94247      TA  ACA  TG
                              TTTCC  GCT   TC  GTACCT
                              |||||  |||   ||  ||||||
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                                GGAGG  TGA   AG  CGTGGA
                                  GC   CA_  GT
GAM1149  LOC222070 5'  ATTAGGTTAGTTAGGAAGA   95808          C
                                TTTTCCTAGCTA ATCTGGT
                                |||||||||||| |||||||
                                AGAAGGATTGAT TGGATTA
                                           _
GAM1149  LOC222486 5'  GGGTACCCGCGGCTGTGGGGGA 96006    TT  _    ACATCT
                                TT  CC TAGCT     GGTACCT
                                ||  || |||||     |||||||
                                AG  GG GTCGG     CCATGGG
                                 GG  T    CGC___
GAM1149  LOC222709 5'  GGTGCCGGGCCTGGAGAG    94432       TA  TACAT
                                TTTTCC  GC    CTGGTACC
                                ||||||  ||    ||||||||
                                GAGAGG  CG    GGCCGTGG
                                   TC  _____
GAM1149  LOC245727 5'  GGGTGAGTCTGTGTTTGGGGAG 92761         C    TCTGG
           A                     TTTTCCTAG TACA     TACCT
                                |||||||||| ||||     |||||
                                AGAGGGGTT GTGT     GTGGG
                                      T    CTGA_
GAM1149  LOC245771 5'  GGGTACCCCAGCCTGGGCTGGG 94485    TT      ACAT  __
           GGAG                   TT  CCTAGCT    CT  GGTACCT
                                ||  |||||||    ||  |||||||
                                GA  GGGTCGG    GA  CCATGGG
                                 GG      GTCC  CC
GAM1149  LOC253936 3'  AGGTGTCGGACACCGTGGTGGA 96316     TA    A___    GT
                                TCC  GCTAC    TCTG  ACCT
                                |||  |||||    ||||  ||||
                                AGG  TGGTG    AGGC  TGGA
                                  __    CCAC    TG
GAM1149  LOC254027 5'  AGGTACTGGAAGGTCCATTGGG 97722         CT_  A_  TG
           AAGA                    TTTTCCTAG   AC  TC  GTACCT
                                |||||||||   ||  ||  ||||||
                                AGAAGGGTT   TG  AG  CATGGA
                                      ACC  GA  GT
GAM1149  LOC254532 3'  AGGTACCAGTGCCATGGGAAG  98446       GCTA  T
                                TTTCCTA    CA CTGGTACCT
                                |||||||    || |||||||||
                                GAAGGGT    GT GACCATGGA
                                    ACC_  _
GAM1149  LOC254806 5'  GGGTGTTAGAGGAAGCGGGGAG 97482       A   ACA   GG
           A                     TTTCCT GCT   TCT  TACCT
                                ||||||  |||   |||  |||||
                                AGAGGG CGA   AGA  GTGGG
                                   G   AGG   TT
GAM1149  LOC255736 3'  GCCCTGAGTGGCTAGGGGAA   97075    TT       A  T_
                                TT  CCTAGCTAC TC  GGT
                                ||  |||||||||  ||  |||
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                                AA  GGATCGGTG AG  CCG
                                 GG        _ TC
GAM1149  LOC256273 3'  GCCTGCTGTAGTTGGGAAG   98142          TCT
                                TTTCCTAGCTACA   GGT
                                ||||||||||||   |||
                                GAAGGGTTGATGT   CCG
                                     CGT
GAM1149  LOC256741 3'  CTAGAGTGGTTGGGAAG     98577          A
                                TTTCCTAGCTAC TCTGG
                                |||||||||||| |||||
                                GAAGGGTTGGTG AGATC
                                          _
GAM1149  LOC257554 5'  GGGTGCTGCCTGCTGGGAAGG  99533         TACATCT
                                TTTTCCTAGC      GGTACCT
                                |||||||||      |||||||
                                GGAAGGGTCG      TCGTGGG
                                     TCCG___
GAM1149  LOC51195  3'  GGGTGGATGTTGTGTGTGCTGG 33408         _    CTGG__
           GGAG                   TTTCCTAGC TACAT     TACCT
                                |||||||| |||||     |||||
                                GAGGGGTCG GTGTG     GTGGG
                                     T    TTGTAG
GAM1149  LOC51337  3'  GGGTAGCCTTGTGGCTGAGAGG 34086      C       TCT  _
                                TTTC TAGCTACA   GGT ACCT
                                |||| ||||||||   ||| ||||
                                GGAG GTCGGTGT   CCG TGGG
                                  A       T__   A
GAM1149  LOC55924  3'  GGAAGGTGGTTGGGAGAG    39394          A_
                                TTTTCCTAGCTAC  TCT
                                ||||||||||||  |||
                                GAGAGGGTTGGTG  AGG
                                     GA
GAM1149  LOC56920  3'  GGTGGGGGAGCTGGGGAAG   39798          ACA   GGT
                                TTTTCCTAGCT   TCT   ACC
                                ||||||||||   |||   |||
                                GAAGGGGTCGA   GGG   TGG
                                     GG_   ___
GAM1149  LOC57105  3'  GGGTATTAGGAAGGACAGGAAA 40171        AG  ACA
           A                    TTTTCCT  CT   TCTGGTACCT
                                |||||||  ||   ||||||||||
                                AAAAGGA  GG   GGATTATGGG
                                   CA  AA_
GAM1149  LOC58525  3'  GGGTGTCAGGGACCCGTTGGGA 79352        TACA_   GT
           G                    TTCCTAGC    TCTG  ACCT
                                ||||||||    ||||  ||||
                                GAGGGTTG    GGAC  TGGG
                                   CCCAG    TG
GAM1149  LOC90170  5'  GGTGCATGGCTGGGAGGA    62380          CATCTG
                                TTTTCCTAGCTA     GTACC
                                ||||||||||||     |||||
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                                AGGAGGGTCGGT     CGTGG
                                      A_____
GAM1149  LOC90462  5'  GGTGTCAGGACTAAGAGAA   63573      C  CTACA   GT
                                TTTTC TAG    TCTG  ACC
                                ||||| |||    ||||  |||
                                AAGAG ATC    GGAC  TGG
                                   A  A____   TG
GAM1149  LOC90525  3'  GGGTTGTCTGGAGCTGGGGAAA 63857         TACA  TG T__
                                TTTTCCTAGC   TC  G   ACCT
                                ||||||||||   ||  |   ||||
                                AAAGGGGTCG   AG  C   TGGG
                                      ____  GT TGT
GAM1149  LOC90750  5'  AGGTATTTGGAGCATGAGTTAG 64626         ACA__  TG _
            GAAG                    TTTCCTAGCT    TC  G TACCT
                                ||||||||||    ||  | |||||
                                GAAGGATTGA    AG  T ATGGA
                                      GTACG  GT T
GAM1149  LOC91461  3'  GGGTGATTCTGTACCTGGGGAG 66706        C    TCTGG
                                TTTCCTAG TACA    TACCT
                                |||||||| ||||    |||||
                                GAGGGGTC ATGT    GTGGG
                                     C   CTTA_
GAM1149  LOC91526  3'  GGGTGTTGGCTGTGGAAA    66939      _    _
                                TTTCC TAGCTA CATCT
                                ||||| |||||| |||||
                                AAAGG GTCGGT GTGGG
                                   T     T
GAM1149  LOC92080  5'  GGGTGGTGGGTGGGGCTGGGAA 68633         TA     G
            GA                    TTTTCCTAGC  CATCTG TACCT
                                ||||||||||  |||||| |||||
                                AGAAGGGTCG  GTGGGT GTGGG
                                      GG     G
GAM1149  LOC92293  3'  ACGGGATGTGGCCAGGAGAA  69316       A       G
                                TTTTCCT GCTACATCT GT
                                ||||||| ||||||||| ||
                                AAGAGGA CGGTGTAGG CA
                                     C       G
GAM1149  LOC93268  3'  GGGTACCCTGGGTTGGGA    72378        ACATCT
                                TCCTAGCT     GGTACCT
                                ||||||||     |||||||
                                AGGGTTGG     CCATGGG
                                     GTC___
GAM1149  LOC93512  3'  GGGTGTTGGGTTTGTTGGGGA  72878        TAC    GG
                                TTCCTAGC   ATCT  TACCT
                                ||||||||   ||||  |||||
                                AGGGGTTG   TGGG  GTGGG
                                     TT_    TT
GAM1150  ADH7      3'  AAGATTAAGGGACGGGC     7268       ACA   G
                                GCCC   TCT TTTAATCTT
                                ||||   ||| |||||||||
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                                CGGG   AGG GAATTAGAA
                                  C__   _
GAM1150 ARAF1    5' GGAAGGACTTCAGATGTGAGC  64644    C       TTTAA
                                GC CACATCTG    TCTTCC
                                || ||||||||    ||||||
                                CG GTGTAGAC    GGAAGG
                                 A       TTCA_
GAM1150 CEACAM6  3' GGAAGACTGGCAGATTGGACCA 11756    C   C      TAA
                                TGG CCA ATCTGTT   TCTTCC
                                ||| ||| |||||||   ||||||
                                ACC GGT TAGACGG   AGAAGG
                                  A   _      TC_
GAM1150 CLECSF12 3' GGATTACAGATGTGAGCCA   77214     C        TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1150 CYP1A2   3' GGATTAACAGGTATGAACCA   7518     CC  C      T
                                TGG  CA ATCTGTT AATCT
                                |||  || ||||||| |||||
                                ACC  GT TGGACAA TTAGG
                                  AA  A      _
GAM1150 ENG      3' GAACTTGAAACAGATTCAGGCC 5496       CAC       AATC
                   A                 TGGCC   ATCTGTTT   TTC
                                |||||   ||||||||   |||
                                ACCGG   TAGACAAA   AAG
                                   ACT       GTTC
GAM1150 ERCC3    3' GAATAAACAGAATGGACCA   5506     C   CA      A
                                TGG CCA  TCTGTTTA TC
                                ||| |||  |||||||| ||
                                ACC GGT  AGACAAAT AG
                                  A  A_       A
GAM1150 HTLF     5' AAGATTGCAGGATTAAGCCA   10973     CCACA    TT
                                TGGC    TCTGT  AATCTT
                                ||||    |||||  ||||||
                                ACCG    GGACG  TTAGAA
                                  AATTA    __
GAM1150 MS4A8B   3' GATTTTAAACAGATGTTAACCA 49588     CCC          TCT
                                TGG   ACATCTGTTTAA   TC
                                |||   ||||||||||||   ||
                                ACC   TGTAGACAAATT   AG
                                  AAT          TT_
GAM1150 PRKAA2   3' GAAGATTAAAAAGTAAAGAACC 21811     CCCACAT  G
                   A                 TGG      CT TTTAATCTTC
                                |||      || ||||||||||
                                ACC      GA AAATTAGAAG
                                  AAGAAAT  A
GAM1150 ASE-1    3' GGATAACAGGTGTGAGCCA   24983     C        TA
                                TGGC CACATCTGTT  ATCT
                                |||| ||||||||||  ||||
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                                ACCG GTGTGGACAA  TAGG
                                  A       __
GAM1150  CITED2   3'  GGAAGATTAAACAGATGTGGGC 21403
                CA                TGGCCCACATCTGTTTAATCTTCC
                                  ||||||||||||||||||||||||
                                  ACCGGGTGTAGACAAATTAGAAGG

GAM1150  DKFZP564K0322 3'  GGATTACAGATGTGAGCCA   50188     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1150  DZIP1    3'  GAAGATTATTCCAGAAGCCA  30703     CCACA   TT_
                                TGGC    TCTG   TAATCTTC
                                ||||    ||||  ||||||||
                                ACCG    AGAC   ATTAGAAG
                                  A____   CTT
GAM1150  FLJ22969 3'  GGATTACAGATGTGAGCCA   69211     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1150  HSNOV1   3'  GGATTACAGATGTGAACCA   34437     CC       TT
                                TGG  CACATCTGT  AATCT
                                |||  |||||||||  |||||
                                ACC  GTGTAGACA  TTAGG
                                  AA       __
GAM1150  IMPACT   3'  GAATTACAGGTGTGAGCCA   38006     C       TTAATC
                                TGGC CACATCTGT     TTC
                                |||| |||||||||     |||
                                ACCG GTGTGGACA     AAG
                                  A       TT____
GAM1150  JAM1     3'  GGATTACAGATGTGAGCCA   34234     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1150  JAM1     3'  GGATTACAGATGTGAGCCA   58499     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1150  JAM1     3'  GGATTACAGATGTGAGCCA   58520     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1150  JAM1     3'  GGATTACAGATGTGAGCCA   58548     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
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                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1150  JAM1     3'  GGATTACAGATGTGAGCCA    58577      C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1150  KIAA0210 5'  GAATTACAGGTGTGAGCCA    29159      C       TTAATC
                                TGGC CACATCTGT     TTC
                                |||| |||||||||      |||
                                ACCG GTGTGGACA     AAG
                                  A       TT_____
GAM1150  KIAA0280 3'  GAGCATAAACAGATGTGGTCCA 93301     C          AT
                                TGG CCACATCTGTTTA  CTT
                                ||| ||||||||||||  |||
                                ACC GGTGTAGACAAAT  GAG
                                  T          AC
GAM1150  KIAA0285 5'  GAAGATTGAGCTTGACCGGACC 29684     C  ACA  T_
              A                  TGG CC   TC  GTTTAATCTTC
                                ||| ||   ||  ||||||||||
                                ACC GG   AG  CGAGTTAGAAG
                                  A  CC_  TT
GAM1150  KIAA0356 3'  GGAAGACCCTCAGATGTGGCCA 66778      C      TTTAA
                                TGGCC ACATCTG    TCTTCC
                                ||||| |||||||    ||||||
                                ACCGG TGTAGAC    AGAAGG
                                   _      TCCC_
GAM1150  KIAA1354 3'  GGAAGATTGTCAGCATGT    61576     _  TT
                                ACAT CTG  TAATCTTCC
                                |||| |||  |||||||||
                                TGTA GAC  GTTAGAAGG
                                  C   T_
GAM1150  KIAA1466 3'  ATTAAATAGTATGGGCCA    72406       CAT
                                TGGCCCA   CTGTTTAAT
                                |||||||   |||||||||
                                ACCGGGT   GATAAATTA
                                    AT_
GAM1150  KIAA1468 5'  AAGATCTTGTAGATGTGGCCA  93423      C      TTTA
                                TGGCC ACATCTG    ATCTT
                                ||||| |||||||    |||||
                                ACCGG TGTAGAT    TAGAA
                                   _      GTTC
GAM1150  MRPS26   3'  GGAAGATTACAGTCTGAGGGCC 48723       A  T_   TT
              A                  TGGCCC CA  CTGT  AATCTTCC
                                ||||||  ||  ||||  ||||||||
                                ACCGGG GT  GACA  TTAGAAGG
                                   A  CT   __
GAM1150  PANX3    3'  AAGATTAATAAAGATGTAAACC 54765    CCC     GT_
                                GG   ACATCT   TTAATCTT
                                ||   ||||||   ||||||||
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                                CC   TGTAGA   AATTAGAA
                                 AAA     AAT
GAM1150  PLCL1    3'  AAGATTAAACAGATGATG    21714    _
                                CA CATCTGTTTAATCTT
                                || ||||||||||||||
                                GT GTAGACAAATTAGAA
                                 A
GAM1150  SPRY4    3'  GAAGACAGAACACAGATGTGGA 49013    GC        _  AA_
              CA                   TG  CCACATCTGT TT   TCTTC
                                ||  |||||||||| ||   |||||
                                AC  GGTGTAGACA AA   AGAAG
                                 A_         C  GAC
GAM1150  WNT10A   3'  GAAGAGGAGATTGGACCA    48170     C   C    G TTAA
                                TGG CCA ATCT T    TCTTC
                                ||| ||| |||| |    |||||
                                ACC GGT TAGA G    AGAAG
                                  A   _    G _____
GAM1150  LOC113523 5'  GGATTACAGATGTGAGCCA    73427      C        TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A        __
GAM1150  LOC124216 3'  GGATTACAGATGTGAGCCA    74736      C        TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A        __
GAM1150  LOC130639 5'  GGATTAAAGACGTGAGCCA    75480      C   A   GT
                                TGGC CAC TCT  TTAATCT
                                |||| ||| |||  |||||||
                                ACCG GTG AGA  AATTAGG
                                  A   C   __
GAM1150  LOC144202 5'  GGAAGATTCGATGGACATGGAC 77226     GC   CA     T
              A                   TG  CCA  TCTGTT AATCTTCC
                                ||  |||  ||||||| ||||||||
                                AC  GGT  AGGTAG TTAGAAGG
                                 A_   AC      C
GAM1150  LOC149171 5'  GAATTACAGGTGTGAGCCA    79967      C        TTAATC
                                TGGC CACATCTGT      TTC
                                |||| |||||||||      |||
                                ACCG GTGTGGACA      AAG
                                  A        TT_____
GAM1150  LOC150245 3'  GAAGCAAGACAGATGTGGGCC  86112              AAT
                                GGCCCACATCTGTTT   CTTC
                                ||||||||||||||   ||||
                                CCGGGTGTAGACAGA   GAAG
                                          AC_
GAM1150  LOC152620 3'  AGATTACAGATGTGAGCCA    60703      C        TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
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                                ACCG GTGTAGACA  TTAGA
                                  A       __
GAM1150  LOC153577 3'  GAAGATTTTATGTGACCA    87239     CC    CTGTTT
                                TGG  CACAT     AATCTTC
                                |||  |||||     |||||||
                                ACC  GTGTA     TTAGAAG
                                  A_    TT____
GAM1150  LOC154930 3'  GAATAACAGGTGTGAGCCA    82091     C       TAATC
                                TGGC CACATCTGTT    TTC
                                |||| ||||||||||    |||
                                ACCG GTGTGGACAA    AAG
                                  A        T____
GAM1150  LOC157507 5'  AAGATTAAACCATGGATG    82376      ___
                                CATCT   GTTTAATCTT
                                |||||   ||||||||||
                                GTAGG   CAAATTAGAA
                                   TAC
GAM1150  LOC158014 5'  AGAATTACAGGTGTGAGCCA   82549     C       TTAA
                                TGGC CACATCTGT    TCT
                                |||| |||||||||    |||
                                ACCG GTGTGGACA    AGA
                                  A       TTA_
GAM1150  LOC158668 3'  AGATTACAGATGTGAGCCA    69892     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGA
                                  A       __
GAM1150  LOC170409 5'  GGATTACAGATGTGAGCCA    83745     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1150  LOC200282 5'  GAAATTACAGGTGTGAGCCA   90099     C       TTAA
                                TGGC CACATCTGT    TC
                                |||| |||||||||    ||
                                ACCG GTGTGGACA    AG
                                  A       TTAA
GAM1150  LOC220595 3'  GGAAGACCTCAGATGTGACCA  92778     CC      TTTAA
                                TGG  CACATCTG    TCTTCC
                                |||  ||||||||    ||||||
                                ACC  GTGTAGAC    AGAAGG
                                  A_       TCC__
GAM1150  LOC253805 3'  GGATTACAGATGTGAGCCA    98179     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1150  LOC56181  5'  GGATTACAGATGTGAGCCA    97278     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
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                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1150  LOC91547  3'  GGATTACAGATGTGAGCCA   67004     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1151  FLJ22332  5'  GGAAAGAAAACTACATCACA   45637     G  A      _______
                                TGTG AT TAGTTTTC     CC
                                |||| || ||||||||     ||
                                ACAC TA ATCAAAAG     GG
                                  _ C       AAA___
GAM1152  AMACR     3'  TTGTATGCATGGAAACATGGA  69103      ATC        G
                                TCCAT   TCCATGCATG CGG
                                |||||   |||||||||| |||
                                AGGTA   AGGTACGTAT GTT
                                   CAA        _
GAM1152  BCL2L11   3'  TCGCCCAGAGATATGGA     57615        CA  CAT    G
                                TCCATATCTC  TG   GGCG A
                                ||||||||||  ||   |||| |
                                AGGTATAGAG  AC   CCGC T
                                     __ ___    G
GAM1152  BCL2L11   3'  TCGCCCAGAGATATGGA     57616        CA  CAT    G
                                TCCATATCTC  TG   GGCG A
                                ||||||||||  ||   |||| |
                                AGGTATAGAG  AC   CCGC T
                                     __ ___    G
GAM1152  FGFR2     5'  CGTCCACATGGAGATATGGA   5559           CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __   T
GAM1152  FGFR2     5'  CGTCCACATGGAGATATGGA   43633          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __   T
GAM1152  FGFR2     5'  CGTCCACATGGAGATATGGA   43638          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __   T
GAM1152  FGFR2     5'  CGTCCACATGGAGATATGGA   43642          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __   T
GAM1152  FGFR2     5'  CGTCCACATGGAGATATGGA   43652          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
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                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM1152  FGFR2    5'  CGTCCACATGGAGATATGGA   43665          CA  _
                                TCCATATCTCCATG  TGG CG
                                |||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM1152  FGFR2    5'  CGTCCACATGGAGATATGGA   43674          CA  _
                                TCCATATCTCCATG  TGG CG
                                |||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM1152  FGFR2    5'  CGTCCACATGGAGATATGGA   43678          CA  _
                                TCCATATCTCCATG  TGG CG
                                |||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM1152  FGFR2    5'  CGTCCACATGGAGATATGGA   43763          CA  _
                                TCCATATCTCCATG  TGG CG
                                |||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM1152  FGFR2    5'  CGTCCACATGGAGATATGGA   43767          CA  _
                                TCCATATCTCCATG  TGG CG
                                |||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM1152  FGFR2    5'  CGTCCACATGGAGATATGGA   43771          CA  _
                                TCCATATCTCCATG  TGG CG
                                |||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM1152  MAP3K14  3'  ATCCGCCACGTGAAGAGA    15541     CA  A
                                TCTC  TGC TGGCGGAT
                                ||||  ||| ||||||||
                                AGAG  GTG ACCGCCTA
                                  AA  C
GAM1152  KIAA0819  3'  CCCCAGCATCACAGGAGACATG 64330      A   ____   A  C
            GA                    TCCAT TCTCC   ATGC TGG GG
                                |||||  |||||   |||| ||| ||
                                AGGTA AGAGG   TACG ACC CC
                                  C    ACAC   _  _
GAM1152  PORIMIN  3'  CATACATGGAGTATGGA     54702       T     C
                                TCCATA CTCCATG ATG
                                ||||||  ||||||| |||
                                AGGTAT GAGGTAC TAC
                                  _     A
GAM1152  RDC1     3'  CCGGCACGGGATATGGA     72832        T  A  A
                                TCCATATC CC TGC TGG
                                ||||||||  ||  ||| |||
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                                AGGTATAG GG ACG GCC
                                    _ C  _
GAM1152 VEZATIN  3' ATCCGCCACAACAGACAATG  34656    A_  CCA  CA
                                CAT  TCT  TG  TGGCGGAT
                                |||  |||  ||  ||||||||
                                GTA  AGA  AC  ACCGCCTA
                                  AC  CA_  __
GAM1152 LOC147645 5' ATCCGCTGGTGGCAGAGACACG 79065    ATA   CA   AT__
          G                      CC  TCTC  TGC   GGCGGAT
                                ||  ||||  |||   |||||||
                                GG  AGAG  ACG   TCGCCTA
                                 CAC   __  GTGG
GAM1152 LOC199775 3' TTGCTGCATCAGAGATATG   89726       C_   TG
                                CATATCTC  ATGCA  GCGG
                                ||||||||  |||||  ||||
                                GTATAGAG  TACGT  CGTT
                                    AC   __
GAM1152 LOC51279  3' CCGCTATTAGAGTATGGA    33752      T  CATGC
                                TCCATA CTC    ATGGCGG
                                ||||||| |||    |||||||
                                AGGTAT GAG    TATCGCC
                                   _  AT___
GAM1153 FLJ22332  5' GGAAAGAAAACTACATCACA  45637     G  A     _______
                                TGTG AT TAGTTTTC     CC
                                |||| || ||||||||     ||
                                ACAC TA ATCAAAAG     GG
                                  _ C       AAA___
GAM1154 AMACR    3' TTGTATGCATGGAAACATGGA  69103      ATC       G
                                TCCAT   TCCATGCATG CGG
                                |||||   |||||||||| |||
                                AGGTA   AGGTACGTAT GTT
                                   CAA       _
GAM1154 BCL2L11  3' TCGCCCAGAGATATGGA     57615        CA  CAT   G
                                TCCATATCTC  TG   GGCG A
                                ||||||||||  ||   |||| |
                                AGGTATAGAG  AC   CCGC T
                                     __  ___    G
GAM1154 BCL2L11  3' TCGCCCAGAGATATGGA     57616        CA  CAT   G
                                TCCATATCTC  TG   GGCG A
                                ||||||||||  ||   |||| |
                                AGGTATAGAG  AC   CCGC T
                                     __  ___    G
GAM1154 FGFR2    5' CGTCCACATGGAGATATGGA   43652          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                     __  T
GAM1154 FGFR2    5' CGTCCACATGGAGATATGGA   43665          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
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                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM1154  FGFR2    5'  CGTCCACATGGAGATATGGA   43674          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM1154  FGFR2    5'  CGTCCACATGGAGATATGGA   43678          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM1154  FGFR2    5'  CGTCCACATGGAGATATGGA   43763          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM1154  FGFR2    5'  CGTCCACATGGAGATATGGA   43767          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM1154  FGFR2    5'  CGTCCACATGGAGATATGGA   43771          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM1154  FGFR2    5'  CGTCCACATGGAGATATGGA   5559           CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM1154  FGFR2    5'  CGTCCACATGGAGATATGGA   43633          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM1154  FGFR2    5'  CGTCCACATGGAGATATGGA   43638          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM1154  FGFR2    5'  CGTCCACATGGAGATATGGA   43642          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM1154  MAP3K14  3'  ATCCGCCACGTGAAGAGA    15541     CA  A
                                TCTC  TGC TGGCGGAT
                                ||||  ||| ||||||||
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                                AGAG  GTG ACCGCCTA
                                  AA  C
GAM1154  KIAA0819  3'  CCCCAGCATCACAGGAGACATG 64330      A   ____   A  C
             GA                   TCCAT TCTCC   ATGC TGG GG
                                  ||||| |||||   |||| ||| ||
                                  AGGTA AGAGG   TACG ACC CC
                                    C   ACAC  _  _
GAM1154  PORIMIN  3'  CATACATGGAGTATGGA    54702       T     C
                                  TCCATA CTCCATG ATG
                                  |||||| ||||||| |||
                                  AGGTAT GAGGTAC TAC
                                     _     A
GAM1154  RDC1     3'  CCGGCACGGGATATGGA    72832        T  A  A
                                  TCCATATC CC TGC TGG
                                  |||||||| || ||| |||
                                  AGGTATAG GG ACG GCC
                                      _ C  _
GAM1154  VEZATIN  3'  ATCCGCCACAACAGACAATG  34656    A_  CCA  CA
                                  CAT  TCT  TG  TGGCGGAT
                                  |||  |||  ||  ||||||||
                                  GTA  AGA  AC  ACCGCCTA
                                    AC  CA_ __
GAM1154  LOC147645 5'  ATCCGCTGGTGGCAGAGACACG 79065    ATA   CA  AT__
             G                    CC  TCTC  TGC   GGCGGAT
                                  ||  ||||  |||   |||||||
                                  GG  AGAG  ACG   TCGCCTA
                                   CAC   __  GTGG
GAM1154  LOC199775 3'  TTGCTGCATCAGAGATATG   89726       C_   TG
                                  CATATCTC  ATGCA  GCGG
                                  ||||||||  |||||  ||||
                                  GTATAGAG  TACGT  CGTT
                                      AC    __
GAM1154  LOC51279  3'  CCGCTATTAGAGTATGGA   33752       T  CATGC
                                  TCCATA CTC    ATGGCGG
                                  |||||| |||    |||||||
                                  AGGTAT GAG    TATCGCC
                                     _  AT___
GAM1155  FLJ20457  3'  GCCTGCCCATGTACTC     35673          TGAAG
                                  GAGTACATGGGCA    GGC
                                  ||||||||||||    |||
                                  CTCATGTACCCGT    CCG
                                                 _____
GAM1155  KIAA1550  3'  ACACTTGCACATGCCTACACAC 67147     ACA      AA_  C
             TC                    GAGT  TGGGCATG  GGG GT
                                   ||||  ||||||||  ||| ||
                                   CTCA  ATCCGTAC  TTC CA
                                     CAC      ACG  A
GAM1155  LY6G5C   3'  CGCCCTTCAGCACACTT    48275     ACATGG  A
                                  GAGT     GC TGAAGGGCG
                                  ||||     || |||||||||
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                                TTCA     CG ACTTCCCGC
                                  CA____ _
GAM1155 LOC255971 5' CGCCCTTCGAACGTACCG    98311    A   ATGGGCA
                                CG GTAC      TGAAGGGCG
                                || ||||      |||||||||
                                GC CATG      GCTTCCCGC
                                 _   CAA____
GAM1156 ACATN    5' GACTGGCTCCCGGCTTCAG   17596       AGTG  CA  A
                                TTGAAGCC   GGG  CCA TC
                                ||||||||   |||  ||| ||
                                GACTTCGG   CCC  GGT AG
                                    ____  TC  C
GAM1156 B3GALT2  3' GTGTCTCAGGCTCAA      15032     A  AG
                                TTGA GCC  TGGGGCAC
                                |||| |||  ||||||||
                                AACT CGG  ACTCTGTG
                                  _  __
GAM1156 CD164    3' GGACTAGTGCAGAGGCTTTAA 21197       AGTGGG   CAA
                                TTGAAGCC     GCAC  TCC
                                ||||||||     ||||  |||
                                AATTTCGG     CGTG  AGG
                                    AGA___   ATC
GAM1156 DRG2     3' TGGTTAGTGGCTTCAA      9131         G  GGGC
                                TTGAAGCCA TG   ACCA
                                ||||||||| ||   ||||
                                AACTTCGGT AT   TGGT
                                     G ____
GAM1156 HPS4     3' ATTGGTGCCACAAGCTTC    42226      CAG  G
                                GAAGC  TG GGCACCAAT
                                |||||  || |||||||||
                                CTTCG  AC CCGTGGTTA
                                  A__  A
GAM1156 SDPR     5' GACTGGTGCCCTGAGCTCCAA 17400     A  CAG       A
                                TTG AGC  TGGGGCACCA TC
                                ||| |||  |||||||||| ||
                                AAC TCG  GTCCCGTGGT AG
                                 C  A__        C
GAM1156 C5orf6   3' GATTGGCTGTGCCAGCTTC   33954      CAG  G  _
                                GAAGC  TGG GCA CCAATC
                                |||||  ||| ||| ||||||
                                CTTCG  ACC TGT GGTTAG
                                  ___  G  C
GAM1156 C8orf17  3' GGACCACACTGGCTGCAA    39998     A      G  CA
                                TTG AGCCAGTG GG  CC
                                ||| |||||||| ||  ||
                                AAC TCGGTCAC CC  GG
                                 G       A  A_
GAM1156 CABP5    5' GACTGGTGCCCTGCGAGCTCCA 39562    A  CA TG      A
                                TG AGC  G  GGGCACCA TC
                                || |||  |  |||||||| ||
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                                AC TCG  C  CCCGTGGT AG
                                 C   AG GT       C
GAM1156  FLJ13940  3'  GGACTGGTGCCCCACAGGCTTT 47309         A         A
              AA                   TTGAAGCC GTGGGGCACCA TCC
                                   |||||||| |||||||||| |||
                                   AATTTCGG CACCCCGTGGT AGG
                                       A         C
GAM1156  KCNMB2   3'  ATTGGTGGACTGGTTTCAA   20684          GGGG
                                   TTGAAGCCAGT   CACCAAT
                                   ||||||||||    |||||||
                                   AACTTTGGTCA   GTGGTTA
                                         G___
GAM1156  KIAA0530  3'  GATTGGTGTATAGCTTTAA   71431        CAGTGGG
                                   TTGAAGC      GCACCAATC
                                   |||||||      |||||||||
                                   AATTTCG      TGTGGTTAG
                                       ATA____
GAM1156  KIAA1522  3'  GGATTGGCCTTCCTGTGCCTCA 65607     A _  TG   AC
              A                    TTGA GC CAG  GGGC  CAATCC
                                   |||| || |||  ||||  ||||||
                                   AACT CG GTC  TCCG  GTTAGG
                                     C  T   CT   __
GAM1156  KIAA1853  3'  GGATGCCCCACTAGTCCAA   69924     AA  C       _
                                   TTG  GC AGTGGGGCA CC
                                   |||  || |||||||| ||
                                   AAC  TG TCACCCCGT GG
                                     C_ A       A
GAM1156  LOXL4    3'  GATTGGTCTAAACTTCAA    50859       CCAG   GGC
                                   TTGAAG   TGG   ACCAATC
                                   ||||||   |||   |||||||
                                   AACTTC   ATC   TGGTTAG
                                      AA__  ____
GAM1156  LSR7     5'  GGACCGGCCCTGCCCCCGGCTT 38280         AGT     ___  AA
              CAA                    TTGAAGCC   GGGGCA   CC  TCC
                                   ||||||||   ||||||   ||  |||
                                   AACTTCGG   CCCCGT   GG  AGG
                                       C__      CCC  CC
GAM1156  PLK      3'  GGACTGGTGCCCTCCTCACT   18525    CC  TG      A
                                   AG  AG  GGGCACCA TCC
                                   ||  ||  |||||||| |||
                                   TC  TC  CCCGTGGT AGG
                                    AC  CT       C
GAM1156  STK22D   3'  GGTCCCCACTGGCCGCAA    50145     AA        C
                                   TTG  GCCAGTGGGG ACC
                                   |||  |||||||||| |||
                                   AAC  CGGTCACCCC TGG
                                     GC        _
GAM1156  LOC124871 3'  TGCTGCCCCACCAGCTTCAG   74818        CA       C
                                   TTGAAGC  GTGGGGCA CA
                                   |||||||  |||||||| ||
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                                GACTTCG  CACCCCGT GT
                                    AC       C
GAM1156  LOC157349 3'  GACTGGCTGCTGGCTCCGA   82341     A     TG GGCA   A
                                TTG AGCCAG  G    CCA TC
                                ||| ||||||  |    ||| ||
                                AGC TCGGTC  C    GGT AG
                                  C     GT _____   C
GAM1156  LOC222550 5'  GGATCAATATCGTGCTGGCTT  96018         G  CACCA
                                AAGCCAGTG GG     ATCC
                                |||||||||  ||     ||||
                                TTCGGTCGT CT     TAGG
                                     G  ATAAC
GAM1157  ABCC3    3'  GCCCCTGTCATCCTCATGC   39616     _  _
                                GCA GAG ATGACAGGGGC
                                ||| ||| ||||||||||
                                CGT CTC TACTGTCCCCG
                                  A   C
GAM1157  ADORA1   5'  GCCCCTTGGTGCCCGTCTGCTG 7271         GATGA__  _
              A                  TCAGCAGA      CA GGGGC
                                 ||||||||      || |||||
                                 AGTCGTCT      GT CCCCG
                                     GCCCGTG  T
GAM1157  ALDH3A1  3'  GCCCCACTCCTCTGCTGA    7308          AT  CA
                                TCAGCAGAG  GA  GGGGC
                                |||||||||  ||  |||||
                                AGTCGTCTC  CT  CCCCG
                                     __  CA
GAM1157  BMPR2    3'  CCTGGGTCATCTCCACTGA   8666      CA       AG
                                TCAG  GAGATGAC  GGG
                                ||||  ||||||||  |||
                                AGTC  CTCTACTG  TCC
                                  AC       GG
GAM1157  CAPN11   3'  GCTCTCCAGTCTCTGCTGA   23913          GACA
                                TCAGCAGAGAT    GGGGC
                                ||||||||||    |||||
                                AGTCGTCTCTG    TCTCG
                                      ACC_
GAM1157  CBFA2T2  3'  GTTCCCAGCCTCTGCTGA    18717         A_  ACA
                                TCAGCAGAG  TG   GGGGC
                                |||||||||  ||   |||||
                                AGTCGTCTC  AC   CCTTG
                                     CG  ___
GAM1157  CCNF     3'  GCCCCTGCCCACATCTGCTGG  10079        GA  A_
                                TCAGCAGA  TG  CAGGGGC
                                ||||||||  ||  |||||||
                                GGTCGTCT  AC  GTCCCCG
                                     AC  CC
GAM1157  CSNK1G2  3'  GCCCCTCCGTTTCTTTGCTGA  8989          T   __
                                TCAGCAGAGA GAC  AGGGGC
                                |||||||||| |||  ||||||
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                                AGTCGTTTCT TTG  TCCCCG
                                      _  CC
GAM1157  FDXR    3'  CTTTGCACCTCTGCTGA    44592        A  A
                                TCAGCAGAG TG CAGGG
                                ||||||||| || |||||
                                AGTCGTCTC AC GTTTC
                                    C  _
GAM1157  GGA3    3'  CCCTGGGCATTTCTGCTGA   26585          A_
                                TCAGCAGAGATG  CAGGG
                                ||||||||||||  |||||
                                AGTCGTCTTTAC  GTCCC
                                      GG
GAM1157  GGT1    5'  GCCCCTGTCTGCTGCTGG    26427       AGAT
                                TCAGCAG   GACAGGGGC
                                |||||||   |||||||||
                                GGTCGTC   CTGTCCCCG
                                    GT__
GAM1157  LILRB1  5'  GCGAGATGCGTCTCTGCTGA  22874          A  GGG_
                                TCAGCAGAGATG CA   GC
                                |||||||||||| ||   ||
                                AGTCGTCTCTGC GT   CG
                                      _ AGAG
GAM1157  LILRB2  5'  GCGAGATGCGTCTCTGCTGA  20805          A  GGG_
                                TCAGCAGAGATG CA   GC
                                |||||||||||| ||   ||
                                AGTCGTCTCTGC GT   CG
                                      _ AGAG
GAM1157  MAFF    3'  CCCCTGTCAGTGTCCACTG   25580     CA  G _
                                CAG  GA A TGACAGGGG
                                |||  || | |||||||||
                                GTC  CT T ACTGTCCCC
                                  AC  G G
GAM1157  MAP1B   3'  CCCCAGTTCATCTCTGCTGA  20961           _ A
                                TCAGCAGAGATGA C GGGG
                                |||||||||||| | ||||
                                AGTCGTCTCTACT G CCCC
                                      T A
GAM1157  MYLK    5'  GCCCGGCTGCCTCTGCTG    54894        ATGA  __
                                CAGCAGAG   CAG  GGGC
                                ||||||||   |||  ||||
                                GTCGTCTC   GTC  CCCG
                                    C___   GG
GAM1157  PIK3R2  5'  GCCCCTGTGGTCGCCTGT    18514      A_  G
                                GCAG  GAT ACAGGGGC
                                ||||  ||| ||||||||
                                TGTC  CTG TGTCCCCG
                                  CG   G
GAM1157  PIM1    3'  GTCCCTGTCACCTCTTCCGA  92689    AGC   A
                                TC   AGAG TGACAGGGGC
                                ||   |||| ||||||||||
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                                AG  TCTC ACTGTCCCTG
                                 CCT   C
GAM1157 PSAP    3' GCCCCTTTTCTCTCTGCT   69884       T C
                                AGCAGAGA GA AGGGGC
                                |||||||| || ||||||
                                TCGTCTCT TT TCCCCG
                                    C  T
GAM1157 RRM2    3' GCCCCTGTTAAGTGGTGA   8287     G  GAGA
                                TCA CA   TGACAGGGGC
                                ||| ||   ||||||||||
                                AGT GT   ATTGTCCCCG
                                  G  GA__
GAM1157 SRRM1   3' GCCTGTGGAGTCTCTGCTGA  20696        GA  G
                                TCAGCAGAGAT  CA GGGC
                                ||||||||||  || ||||
                                AGTCGTCTCTG  GT TCCG
                                      AG  G
GAM1157 TRH     3' GCCCCTATCCCTTGTCGA   24052   A   G  AT  C
                                TC GCA AG  GA AGGGGC
                                || ||| ||  || ||||||
                                AG TGT TC  CT TCCCCG
                                 C   _  C_  A
GAM1157 UBE2I   5' CCCCGATTTCTGCTCTGCTGA  13960       AT__  CA
                                TCAGCAGAG   GA  GGGG
                                |||||||||   ||  ||||
                                AGTCGTCTC   TT  CCCC
                                     GTCT  AG
GAM1157 VNN1    3' CTTATTCAGCTCTGCTGA   17422       A   CA
                                TCAGCAGAG TGA  GGG
                                ||||||||| |||  |||
                                AGTCGTCTC ACT  TTC
                                     G   TA
GAM1157 BICD2   3' GCCCCTGTATTCTGCTGG   70913       GATG
                                TCAGCAGA   ACAGGGGC
                                ||||||||   ||||||||
                                GGTCGTCT   TGTCCCCG
                                    TA__
GAM1157 C9orf7  3' GCCCTACTCCTCTGCTGG   34583       AT  CA
                                TCAGCAGAG  GA  GGGGC
                                |||||||||  ||  |||||
                                GGTCGTCTC  CT  TCCCG
                                     __  CA
GAM1157 CBX1    3' GCCCCTGTCACATCTGACTG  23311    _   GA
                                CAG CAGA  TGACAGGGGC
                                ||| ||||  ||||||||||
                                GTC GTCT  ACTGTCCCCG
                                  A   AC
GAM1157 CGRP-RCP 3' GCCCCTTTTCTCTGCTGG   27891       TGAC
                                TCAGCAGAGA   AGGGGC
                                ||||||||||   ||||||
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                                GGTCGTCTCT   TCCCCG
                                     TT__
GAM1157 CX46.6   3' CCCCTGTCCTGAGCTGG    40310     AG  AT
                                TCAGC  AG  GACAGGGG
                                |||||  ||  ||||||||
                                GGTCG  TC  CTGTCCCC
                                   AG  __
GAM1157 DKFZP566K0524 3' CTTTCTCACCTCTGTTGA    69876        A   C
                                TCAGCAGAG TGA AGGG
                                ||||||||| ||| ||||
                                AGTTGTCTC ACT TTTC
                                     C   C
GAM1157 DNAJC6   3' GCTTTTCCATCTCTGCTG    29495          AC
                                CAGCAGAGATG  AGGGGC
                                ||||||||||  ||||||
                                GTCGTCTCTAC  TTTTCG
                                      C_
GAM1157 EAT2     3' GCCCCAGTCTCTCTGTTGA    80052         T   A
                                TCAGCAGAGA GAC GGGGC
                                |||||||||| ||| |||||
                                AGTTGTCTCT CTG CCCCG
                                     _  A
GAM1157 ET       5' GCCCCCTCAGACTCCGCTG   44472     A  A_   CA
                                CAGC GAG  TGA  GGGGC
                                |||| |||  |||  |||||
                                GTCG CTC  ACT  CCCCG
                                  C  AG  C_
GAM1157 FLJ10898 5' GCCAGTCACCTCTGCTGA    60136        A   AGG
                                TCAGCAGAG TGAC   GGC
                                ||||||||| ||||   |||
                                AGTCGTCTC ACTG   CCG
                                     C   A__
GAM1157 FLJ12891 5' GCCCCTGTGTTAGGCCGTGA  46926    __ AGA   G
                                TCA  GC   GAT ACAGGGGC
                                |||  ||   ||| ||||||||
                                AGT  CG   TTG TGTCCCCG
                                  GC  GA_  _
GAM1157 FLJ14451 3' GCCTTCCCCATCCCTGTCTGA  52396     _  A   ACA
                                TCAG CAG GATG   GGGGC
                                |||| ||| ||||   |||||
                                AGTC GTC CTAC   TTCCG
                                  T   C    CCC
GAM1157 FLJ14564 3' GCCCCTGTCTTTTCCTCTGA   77013     CA   T
                                TCAG  GAGA GACAGGGGC
                                ||||  |||| |||||||||
                                AGTC  CTTT CTGTCCCCG
                                  TC    T
GAM1157 FLJ20371 3' GCTTATCTCACCTCTGCTGG   35537        A   CAG
                                TCAGCAGAG TGA   GGGC
                                |||||||| |||   ||||
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                                GGTCGTCTC ACT   TTCG
                                     C   CTA
GAM1157  FLJ20374  5' GCCCCTCCCGCACTCTGCTGA 35551        A  AC__
                                TCAGCAGAG TG    AGGGGC
                                ||||||||| ||    ||||||
                                AGTCGTCTC AC    TCCCCG
                                     _  GCCC
GAM1157  FLJ21240  3' CCTAGTGATTCTGCTGA     46264        A G  A
                                TCAGCAGAG T AC GGG
                                ||||||||| | || |||
                                AGTCGTCTT A TG TCC
                                     _ G  A
GAM1157  FLJ31762  3' GCCCTTTAACGTCTCTGC    58766        AC_
                                GCAGAGATG   AGGGGC
                                |||||||||   ||||||
                                CGTCTCTGC   TTCCCG
                                     AAT
GAM1157  FLJ32926  3' GCCCCTTCCCTGTCTGCTGA  58636       GAT_  C
                                TCAGCAGA    GA AGGGGC
                                ||||||||    || ||||||
                                AGTCGTCT    CT TCCCCG
                                     GTCC  _
GAM1157  GREB1     5' CCCTTTCTTCGTCTCTGCTGA 28562         C__
                                TCAGCAGAGATGA   AGGGG
                                ||||||||||||   |||||
                                AGTCGTCTCTGCT   TTCCC
                                      TCT
GAM1157  KIAA0296  3' GCCCCTTTTCCCTCTGCTG   28775        AT  C
                                CAGCAGAG  GA AGGGGC
                                ||||||||  || ||||||
                                GTCGTCTC  TT TCCCCG
                                     CC  T
GAM1157  KIAA0354  3' GCCCGCTTACCTCTGCTGA   30192        A   CAG
                                TCAGCAGAG TGA   GGGC
                                ||||||||| |||   ||||
                                AGTCGTCTC ATT   CCCG
                                     C   CG_
GAM1157  KIAA0513  3' GCCATTCACTTCTGCTGA    29036        A   CAGG
                                TCAGCAGAG TGA    GGC
                                ||||||||| |||    |||
                                AGTCGTCTT ACT    CCG
                                     C   TA__
GAM1157  KIAA0618  3' GCCCCACTGGCATCTCTGT   29854        A  __
                                GCAGAGATG CA  GGGGC
                                ||||||||| ||  |||||
                                TGTCTCTAC GT  CCCCG
                                     G  CA
GAM1157  KIAA0662  3' GCCTCTGCAGCTCTGCTGA   82739        A  A
                                TCAGCAGAG TG CAGGGGC
                                ||||||||| || |||||||
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                                AGTCGTCTC AC GTCTCCG
                                     G  _
GAM1157 KIAA0748 3' CCCCTATCTCCCTTTGCTGA  29613       AT_  C
                                TCAGCAGAG  GA AGGGG
                                |||||||||  || |||||
                                AGTCGTTTC  CT TCCCC
                                     CCT  A
GAM1157 KIAA1718 3' GCATTTTCATTTCTGCTGA   64976        C  GG
                                TCAGCAGAGATGA AG  GC
                                |||||||||||||| ||  ||
                                AGTCGTCTTTACT TT  CG
                                       T  A_
GAM1157 LIMK2    5' GCCCCTGTGGGAATCTGCTGG 19923       GATG_
                                TCAGCAGA    ACAGGGGC
                                ||||||||    ||||||||
                                GGTCGTCT    TGTCCCCG
                                     AAGGG
GAM1157 MGC16385 5' GCCCCTGGACGTTTCTGC    59537       A_
                                GCAGAGATG  CAGGGGC
                                |||||||||  |||||||
                                CGTCTTTGC  GTCCCCG
                                     AG
GAM1157 MGC3123  5' CCCCTCAGGCTCTGCTGA    44343       A_  CA
                                TCAGCAGAG  TGA  GGGG
                                |||||||||  |||  ||||
                                AGTCGTCTC  ACT  CCCC
                                     GG  __
GAM1157 NPD009   5' CTGTAGCATCTCTGCTGG    40722        __
                                TCAGCAGAGATG  ACAG
                                ||||||||||||  ||||
                                GGTCGTCTCTAC  TGTC
                                       GA
GAM1157 NXPH3    3' GCCCCTTGTCGTGTGCTGA   66342      GAG    _
                                TCAGCA   ATGACA GGGGC
                                ||||||   |||||| |||||
                                AGTCGT   TGCTGT CCCCG
                                    G__     T
GAM1157 PCDH17   5' GCCCCTGCAGCTCTGCTG    27837       A  A
                                CAGCAGAG TG CAGGGGC
                                |||||||| || |||||||
                                GTCGTCTC AC GTCCCCG
                                     G  _
GAM1157 PIP5K2B  3' CCCTCCCCATCTTTGCTGA   57692        AC_
                                TCAGCAGAGATG  AGGG
                                ||||||||||||  ||||
                                AGTCGTTTCTAC  TCCC
                                       CCC
GAM1157 PM5      3' CTCCTGTCACTCTGCTGA    27381       A
                                TCAGCAGAG TGACAGGGG
                                ||||||||| |||||||||
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                                AGTCGTCTC ACTGTCCTC
                                          _
GAM1157 RIP60    3' GCCCCTGTCTTTTACTGT    26362     _  T
                                GCAG AGA GACAGGGGC
                                |||| ||| |||||||||
                                TGTC TTT CTGTCCCCG
                                  A  T
GAM1157 SLC17A6  5' GCCACTACCATTCTGCTGA   40110        A  AC  G
                                TCAGCAGAG TG  AG GGC
                                ||||||||| ||  || |||
                                AGTCGTCTT AC  TC CCG
                                     _ CA  A
GAM1157 SMCR7    3' GCTTCACATTTCTGCTGA    58240          ACA
                                TCAGCAGAGATG   GGGGC
                                ||||||||||||   |||||
                                AGTCGTCTTTAC   CTTCG
                                       A__
GAM1157 SNTA1    3' GCCCCTGTGCGGATCCTGA   13297     CA  GA  _
                                TCAG  GA  TG ACAGGGGC
                                ||||  ||  || ||||||||
                                AGTC  CT  GC TGTCCCCG
                                  __ AG  G
GAM1157 TGIF2    3' GCCCCTGTGCTGTTTCTGT   41752        __
                                GCAGAGATG  ACAGGGGC
                                |||||||||  ||||||||
                                TGTCTTTGT  TGTCCCCG
                                     CG
GAM1157 TGOLN2   3' CCTTGTCCTCCCTGCTGA    64742       A  T
                                TCAGCAG GA GACAGGG
                                ||||||| || |||||||
                                AGTCGTC CT CTGTTCC
                                    C  C
GAM1157 TRAF4    3' CCCCCGTCAGCTGCTTCTGCTG 63318       GA____   A
                                CAGCAGA     TGAC GGGG
                                |||||||     |||| ||||
                                GTCGTCT     ACTG CCCC
                                    TCGTCG    C
GAM1157 TRIM22   3' CCTGAGTTCATCTCTACTGA   21386     C      ___
                                TCAG AGAGATGA   CAGG
                                |||| ||||||||   ||||
                                AGTC TCTCTACT   GTCC
                                  A       TGA
GAM1157 LOC128402 3' GCCCCTCCAGGCTTTGCTGA  76288        A_  AC
                                TCAGCAGAG  TG  AGGGGC
                                |||||||||  ||  ||||||
                                AGTCGTTTC  AC  TCCCCG
                                     GG  C_
GAM1157 LOC143677 3' GCCCCTGTCCCTCTGCCGG   83898    A     AT
                                TC GCAGAG  GACAGGGGC
                                || ||||||  |||||||||
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                                GG CGTCTC  CTGTCCCCG
                                 C     C_
GAM1157  LOC144587 5'  CCCCTCAGGCTCTGCTGA    67589        A_   CA
                                TCAGCAGAG  TGA  GGGG
                                |||||||||  |||  ||||
                                AGTCGTCTC  ACT  CCCC
                                     GG   __
GAM1157  LOC145501 3'  GCCCCCTCTGTTCTGCTGA   77769        AT  CA
                                TCAGCAGAG  GA  GGGGC
                                |||||||||  ||  |||||
                                AGTCGTCTT  CT  CCCCG
                                     GT  C_
GAM1157  LOC145717 3'  CCCCCCTCCCTCTCTCTGA   67372     C    T_  CA
                                TCAG AGAGA  GA  GGGG
                                |||| |||||  ||  ||||
                                AGTC TCTCT  CT  CCCC
                                  _    CC  CC
GAM1157  LOC146802 3'  GCTTCCATTCTCTGCTGA    78727         TGACA
                                TCAGCAGAGA    GGGGC
                                ||||||||||    |||||
                                AGTCGTCTCT    CTTCG
                                     TAC__
GAM1157  LOC147004 3'  GCCCCTGTCACTCTCATGA   84967     GC   A
                                TCA  AGAG TGACAGGGGC
                                |||  |||| ||||||||||
                                AGT  TCTC ACTGTCCCCG
                                  AC   _
GAM1157  LOC149483 3'  CCCCGCAGTTGGCTTTGCTGA  80184        AT   A__
                                TCAGCAGAG  GAC   GGGG
                                |||||||||  |||   ||||
                                AGTCGTTTC  TTG   CCCC
                                     GG   ACG
GAM1157  LOC150054 5'  GCCCTCATCTTAATCTCTGCTG 85975         ___  CA
            A                    TCAGCAGAGAT   GA  GGGGC
                                ||||||||||   ||  |||||
                                AGTCGTCTCTA   CT  TCCCG
                                     ATT  AC
GAM1157  LOC151610 3'  GCATTGCATCTTTGCTGA    81094          A   GG
                                TCAGCAGAGATG CAG  GC
                                ||||||||||| |||  ||
                                AGTCGTTTCTAC GTT  CG
                                     _   A_
GAM1157  LOC152195 5'  GCCCCTGTACCCTGCATGA   86748     _   AGATG
                                TCA GCAG    ACAGGGGC
                                ||| ||||    ||||||||
                                AGT CGTC    TGTCCCCG
                                  A   CCA__
GAM1157  LOC163682 5'  GCCCCTGTCCATGGTGCTGA  88409       GAGAT
                                TCAGCA    GACAGGGGC
                                ||||||    |||||||||
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                                AGTCGT    CTGTCCCCG
                                   GGTAC
GAM1157  LOC199991 5'  GCCCCTTTGTCCTGCTGA    91516       A  TG C
                                TCAGCAG GA  A AGGGGC
                                ||||||| ||  | ||||||
                                AGTCGTC CT  T TCCCCG
                                   _  GT _
GAM1157  LOC201799 3'  GCCCCTGAGGGAGTCTGCTGA  90491        GATGA_
                                TCAGCAGA     CAGGGGC
                                ||||||||     |||||||
                                AGTCGTCT     GTCCCCG
                                     GAGGGA
GAM1157  LOC221025 3'  GCCCCTGTATTTTGCTGA    94787        GATG
                                TCAGCAGA    ACAGGGGC
                                ||||||||    ||||||||
                                AGTCGTTT    TGTCCCCG
                                     TA__
GAM1157  LOC221692 3'  GCCCCCCAGTTTATCTCTACT  93853    C       _ A__
                                AG AGAGATGA C   GGGGC
                                || |||||||| |   |||||
                                TC TCTCTATT G   CCCCG
                                 A       T ACC
GAM1157  LOC253971 3'  CCCAACGTCTCTCTGATGA    97852     G     T   AG_
                                TCA CAGAGA GAC   GGG
                                ||| |||||| |||   |||
                                AGT GTCTCT CTG   CCC
                                  A     _   CAA
GAM1157  LOC254531 5'  GCCCCTGTCCTTGTTGCTG    96670       A  T
                                CAGCAG GA GACAGGGGC
                                |||||| || |||||||||
                                GTCGTT TT CTGTCCCCG
                                   G  C
GAM1157  LOC51326  3'  GCCCAGTGCCCTCTGTTGA    34038        ATG  AG
                                TCAGCAGAG   AC  GGGC
                                |||||||||   ||  ||||
                                AGTTGTCTC   TG  CCCG
                                     CCG  A_
GAM1157  LOC90019  3'  GCCTCTGTCTCCCCGCTGA    57531      AGA  T
                                TCAGC   GA GACAGGGGC
                                |||||   || |||||||||
                                AGTCG   CT CTGTCTCCG
                                   CCC  _
GAM1157  LOC90462  3'  CCCCCATCATTTTTTTGA     63570      C       CA
                                TCAG AGAGATGA  GGGG
                                |||| ||||||||  ||||
                                AGTT TTTTTACT  CCCC
                                   _       AC
GAM1157  LOC92080  3'  CCCCTGAGCCTCTGCTGG     68625         ATGA
                                TCAGCAGAG    CAGGGG
                                |||||||||    ||||||
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                                GGTCGTCTC   GTCCCC
                                     CGA_
GAM1157 LOC92293 3' CCCCTGTCATCGTGGGGA   69320   AG  GA
                                TC  CA  GATGACAGGGG
                                ||  ||  ||||||||||
                                AG  GT  CTACTGTCCCC
                                 GG  G_
GAM1158 SCAMP1   3' GCTAAATAAATATTCTCC   54500    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1158 SCAMP1   3' GCTAAATAAATATTCTCC   54501    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1158 NX-17    3' TGAATATCAGCCCCTAATA   40706       ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                     CGAC
GAM1158 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
              TA                  TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM1159 APM1     3' CAAAGCTCAAAACAATCAAGA  17764     C   GAGGG
                                TCTT ATTG    TTGAGCTTTG
                                |||| ||||    ||||||||||
                                AGAA TAAC    AACTCGAAAC
                                  C   AA___
GAM1159 ATP6V1G2 3' CAAAGAAATCCTCCAAT    56193         GAG
                                ATTGGAGGGTT   CTTTG
                                ||||||||||   |||||
                                TAACCTCCTAA   GAAAC
                                     A__
GAM1159 ATP6V1G2 3' CAAAGAAATCCTCCAAT    57116         GAG
                                ATTGGAGGGTT   CTTTG
                                ||||||||||   |||||
                                TAACCTCCTAA   GAAAC
                                     A__
GAM1159 C1orf1   5' CAAAGCCCAACCCCTTAATGAA 8677       GA    A
                                TTCATTG  GGGTTG GCTTTG
                                |||||||  |||||| ||||||
                                AAGTAAT  CCCAAC CGAAAC
                                   TC     C
GAM1159 LOC254065 5' CAAAGCTTATACCTCTAAT   99289       GT
                                ATTGGAGG  TGAGCTTTG
                                ||||||||  |||||||||
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                                TAATCTCC  ATTCGAAAC
                                    AT
GAM1160  CDO1     3'  ACATGATCCCCAGACCACAACA 10162              GA
                                TGTTGTGGTCTGGGGA  ATGT
                                |||||||||||||||  ||||
                                ACAACACCAGACCCCT  TACA
                                      AG
GAM1160  SMTN     3'  ACACCCTCCCCCCCCACATACAC 23651      _    TCT     AA
              A                  TGTGT TGTGG   GGGGAG  TGT
                                |||||  |||||   ||||||  |||
                                ACACA ACACC   CCCCTC  ACA
                                   T    C__     CC
GAM1160  SMTN     3'  ACACCCTCCCCCCCCACATACAC 23652      _    TCT     AA
              A                  TGTGT TGTGG   GGGGAG  TGT
                                |||||  |||||   ||||||  |||
                                ACACA ACACC   CCCCTC  ACA
                                   T    C__     CC
GAM1160  HB-1     5'  TCCTCTGCCACACCACA     41317      T     CT
                                TGTG TGTGGT  GGGGA
                                ||||  ||||||  |||||
                                ACAC ACACCG  CTCCT
                                  C     T_
GAM1161  BACH2    3'  ATCTACCTGTATAACCCTCTG  41775       A      AT_
                                TAGAGG TTATACAG   GAT
                                ||||||  ||||||||   |||
                                GTCTCC AATATGTC   CTA
                                    C       CAT
GAM1161  CASP10   3'  ATCATTGGGTATAACCTC    53217      A     A_
                                GAGG TTATAC  GATGAT
                                ||||  ||||||  ||||||
                                CTCC AATATG  TTACTA
                                  _     GG
GAM1161  CASP10   3'  ATCATTGGGTATAACCTC    53244      A     A_
                                GAGG TTATAC  GATGAT
                                ||||  ||||||  ||||||
                                CTCC AATATG  TTACTA
                                  _     GG
GAM1161  FLJ14564 3'  CATCATCTGTAAAACCATCTA  77012      _  A  A
                                TAGA GG TT TACAGATGATG
                                ||||  ||  ||  ||||||||||
                                ATCT CC AA ATGTCTACTAC
                                  A  _  A
GAM1161  MAL2     3'  TTATCTAATAATCCTCTA     54662          AC
                                TAGAGGATTAT  AGATGA
                                ||||||||||  ||||||
                                ATCTCCTAATA  TCTATT
                                       A_
GAM1161  LOC129852 3'  AATCATCATCTTGGCCCTC    75401      AT  TAC
                                GAGG  TA   AGATGATGATT
                                ||||  ||   ||||||||||
```

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                                CTCC  GT   TCTACTACTAA
                                  CG  ___
GAM1161  LOC146050 3'  CATCATCTATAGTAAATC    78106    GG_    AC
                                GA  ATTAT  AGATGATG
                                ||  |||||  ||||||||
                                CT  TGATA  TCTACTAC
                                 AAA   __
GAM1162  AMACR     3'  TTGTATGCATGGAAACATGGA  69103      ATC        G
                                TCCAT  TCCATGCATG CGG
                                |||||  |||||||||| |||
                                AGGTA  AGGTACGTAT GTT
                                  CAA       _
GAM1162  BCL2L11   3'  TCGCCCAGAGATATGGA     57615        CA  CAT    G
                                TCCATATCTC  TG  GGCG A
                                ||||||||||  ||  |||| |
                                AGGTATAGAG  AC  CCGC T
                                     __ ___   G
GAM1162  BCL2L11   3'  TCGCCCAGAGATATGGA     57616        CA  CAT    G
                                TCCATATCTC  TG  GGCG A
                                ||||||||||  ||  |||| |
                                AGGTATAGAG  AC  CCGC T
                                     __ ___   G
GAM1162  FGFR2     5'  CGTCCACATGGAGATATGGA  5559           CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                     __  T
GAM1162  FGFR2     5'  CGTCCACATGGAGATATGGA  43633          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                     __  T
GAM1162  FGFR2     5'  CGTCCACATGGAGATATGGA  43638          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                     __  T
GAM1162  FGFR2     5'  CGTCCACATGGAGATATGGA  43642          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                     __  T
GAM1162  FGFR2     5'  CGTCCACATGGAGATATGGA  43652          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                     __  T
GAM1162  FGFR2     5'  CGTCCACATGGAGATATGGA  43665          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
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                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM1162  FGFR2    5'  CGTCCACATGGAGATATGGA  43674          CA  _
                                TCCATATCTCCATG  TGG CG
                                |||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM1162  FGFR2    5'  CGTCCACATGGAGATATGGA  43678          CA  _
                                TCCATATCTCCATG  TGG CG
                                |||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM1162  FGFR2    5'  CGTCCACATGGAGATATGGA  43763          CA  _
                                TCCATATCTCCATG  TGG CG
                                |||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM1162  FGFR2    5'  CGTCCACATGGAGATATGGA  43767          CA  _
                                TCCATATCTCCATG  TGG CG
                                |||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM1162  FGFR2    5'  CGTCCACATGGAGATATGGA  43771          CA  _
                                TCCATATCTCCATG  TGG CG
                                |||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                      __  T
GAM1162  MAP3K14  3'  ATCCGCCACGTGAAGAGA   15541     CA  A
                                TCTC  TGC TGGCGGAT
                                ||||  ||| ||||||||
                                AGAG  GTG ACCGCCTA
                                  AA  C
GAM1162  KIAA0819 3'  CCCCAGCATCACAGGAGACATG 64330      A   ____   A  C
            GA                    TCCAT TCTCC   ATGC TGG GG
                                |||||  |||||   ||||  ||| ||
                                AGGTA AGAGG   TACG ACC CC
                                  C    ACAC   _  _
GAM1162  PORIMIN  3'  CATACATGGAGTATGGA    54702       T     C
                                TCCATA CTCCATG ATG
                                ||||||  ||||||| |||
                                AGGTAT GAGGTAC TAC
                                   _      A
GAM1162  RDC1     3'  CCGGCACGGGATATGGA    72832        T  A  A
                                TCCATATC CC TGC TGG
                                ||||||||  ||  ||| |||
                                AGGTATAG GG ACG GCC
                                     _  C  _
GAM1162  VEZATIN  3'  ATCCGCCACAACAGACAATG  34656    A_  CCA  CA
                                CAT  TCT   TG  TGGCGGAT
                                |||  |||   ||  ||||||||
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                                GTA  AGA   AC  ACCGCCTA
                                  AC   CA_ __
GAM1162  LOC147645 5'  ATCCGCTGGTGGCAGAGACACG 79065    ATA   CA   AT__
             G                     CC   TCTC  TGC    GGCGGAT
                                   ||   ||||  |||    |||||||
                                   GG   AGAG  ACG    TCGCCTA
                                    CAC    __  GTGG
GAM1162  LOC199775 3'  TTGCTGCATCAGAGATATG   89726        C_    TG
                                   CATATCTC  ATGCA  GCGG
                                   ||||||||  |||||  ||||
                                   GTATAGAG  TACGT  CGTT
                                        AC    __
GAM1162  LOC51279  3'  CCGCTATTAGAGTATGGA    33752       T   CATGC
                                   TCCATA CTC    ATGGCGG
                                   ||||||| |||    |||||||
                                   AGGTAT GAG    TATCGCC
                                      _   AT___
GAM1163  FLJ22332  5'  GGAAAGAAAACTACATCACA   45637     G  A      _______
                                   TGTG AT TAGTTTTC     CC
                                   |||| || ||||||||     ||
                                   ACAC TA ATCAAAAG     GG
                                     _ C       AAA___
GAM1164  BCAT1     3'  AGAAAACAAAGAGGCATACT   66782    C       AAT
                                   AG ATGCCTCTT   TTTTCT
                                   || |||||||||   ||||||
                                   TC TACGGAGAA   AAAAGA
                                    A        AC_
GAM1164  ETF1      3'  AGAAAAATTAAATTGCTGC    17587     T  CTC
                                   GCA GC   TTAATTTTTCT
                                   ||| ||   ||||||||||
                                   CGT CG   AATTAAAAAGA
                                     _  TTA
GAM1164  EXTL2     5'  AGAAGGATAGATGCACGCTA   9325      A   C   TA
                                   TAGC TGC TCT  ATTTTTCT
                                   |||| ||| |||  ||||||||
                                   ATCG ACG AGA  TAGGAAGA
                                     C   T   __
GAM1164  FOXE1     3'  AGAAAAATTAAGTTAGGGCA   16777      ___
                                   TGCCT   CTTAATTTTTCT
                                   |||||   ||||||||||||
                                   ACGGG   GAATTAAAAAGA
                                      ATT
GAM1164  FZD3      3'  AGAAAAATGCTGGAACATGCT  34257       CC   TA_
                                   AGCATG  TCT   ATTTTTCT
                                   ||||||  |||   ||||||||
                                   TCGTAC  AGG   TAAAAAGA
                                      A_   TCG
GAM1164  RRM2B     3'  AAAAATTAAGAGTGTGTT     68429       C
                                   AGCATGC TCTTAATTTTT
                                   ||||||| ||||||||||
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                                TTGTGTG AGAATTAAAAA
                                      _
GAM1164 ZNF132   3' AGAAAAATTACCTCCATGCT  14286      CCTCT
                                AGCATG    TAATTTTTCT
                                ||||||    ||||||||||
                                TCGTAC    ATTAAAAAGA
                                   CTCC_
GAM1164 BAP29    3' AGAAAAATATAAGCATGTTA  61331       CTCTTA
                                TAGCATGC    ATTTTTCT
                                ||||||||    ||||||||
                                ATTGTACG    TAAAAAGA
                                    AATA__
GAM1164 FAM8A1   3' AGAAAAATCTGGCATACTG   33197    C    TCTTA
                                TAG ATGCC    ATTTTTCT
                                ||| |||||    ||||||||
                                GTC TACGG    TAAAAAGA
                                  A    TC___
GAM1164 FLJ10648 3' AGAAAAATTAGGTTCCATGC  36888     CCT
                                GCATG  CTTAATTTTTCT
                                |||||  ||||||||||||
                                CGTAC  GGATTAAAAAGA
                                   CTT
GAM1164 FLJ10970 3' AGAAAAATCAAGATAGGCCTG 37476   T  __   A
                                CA GCC  TCTT ATTTTTCT
                                || |||  |||| ||||||||
                                GT CGG  AGAA TAAAAAGA
                                 C  AT   C
GAM1164 FLJ14735 3' AAAAACTGATGAGGCATGC   52663       _  A
                                GCATGCCTC TTA TTTTT
                                ||||||||| ||| |||||
                                CGTACGGAG AGT AAAAA
                                      T  C
GAM1164 KIAA0830 3' AGAAAAATAGCGGAGGCA   70266      TA_
                                TGCCTCT  ATTTTTCT
                                |||||||  ||||||||
                                ACGGAGG  TAAAAAGA
                                    CGA
GAM1164 KIAA0907 3' AGAAAAATTAAGCTGGGCA  30862     __
                                TGCCT  CTTAATTTTTCT
                                |||||  ||||||||||||
                                ACGGG  GAATTAAAAAGA
                                   TC
GAM1164 KIAA1348 3' AGAAACTTTGAGCCATGCTA  69116      CCT   TT
                                TAGCATG  CTTAA  TTTCT
                                |||||||  |||||  |||||
                                ATCGTAC  GAGTT  AAAGA
                                    C__    TC
GAM1164 PLAGL2   3' AGAAATGAAAGGCATGC    70952       C  ATT
                                GCATGCCT TTA  TTTCT
                                |||||||| |||  |||||
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                                CGTACGGA AGT   AAAGA
                                     A  ___
GAM1164  RNF2     3'  AGAAAAATTAAATTGGTAGT   24256    A   TC_
                                GC TGCC   TTAATTTTTCT
                                || ||||   ||||||||||
                                TG ATGG   AATTAAAAAGA
                                 _   TTA
GAM1164  LOC143146 3'  AGAAAATGGCCGAGGCATGCTA 60763          TTAAT
                                TAGCATGCCTC    TTTTCT
                                ||||||||||    ||||||
                                ATCGTACGGAG    AAAAGA
                                      CCGGT
GAM1164  LOC146059 3'  AGAAAAGTCCAGAGATGC    78082     GC    TA
                                GCAT  CTCT  ATTTTTCT
                                ||||  ||||  ||||||||
                                CGTA  GAGA  TGAAAAGA
                                  __   CC
GAM1164  LOC151391 3'  AGAAAGATCAAAGCATGC    86511      CTC  A
                                GCATGC   TT ATTTTTCT
                                ||||||   || ||||||||
                                CGTACG   AA TAGAAAGA
                                   A__  C
GAM1164  LOC157507 5'  AAAGAAGAGGAGGCAACTA   82374    CA      AA
                                TAG  TGCCTCTT  TTTTT
                                |||  ||||||||  |||||
                                ATC  ACGGAGGA  AGAAA
                                 A_       GA
GAM1164  LOC158434 3'  AAAAATTACAAGGCATGC    88156       CT
                                GCATGCCT  TAATTTTT
                                ||||||||  ||||||||
                                CGTACGGA  ATTAAAAA
                                     AC
GAM1164  LOC220020 5'  AGAAAACAGGTGAAGGCATGC  95043       _ TTAAT
                                GCATGCCT C    TTTTCT
                                |||||||| |    ||||||
                                CGTACGGA G    AAAAGA
                                     A TGGAC
GAM1164  LOC221979 3'  AGAGTGCAGAAGGCATGC    94216       _  TA
                                GCATGCCT CT  ATTTT
                                |||||||| ||  |||||
                                CGTACGGA GA  TGAGA
                                     A  CG
GAM1164  LOC92078  3'  AGAAATCCGAAGAGGCAGCTA  68588     A      AATT
                                TAGC TGCCTCTT   TTTCT
                                |||| ||||||||   |||||
                                ATCG ACGGAGAA   AAAGA
                                  _      GCCT
GAM1164  LOC92080  5'  AGAAAAATCAAGACCATGTTA  68617       CC   A
                                TAGCATG  TCTT ATTTTTCT
                                |||||||  |||| ||||||||
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                                ATTGTAC  AGAA TAAAAAGA
                                   C_   C
GAM1165 COL19A1  3' CAGACCAAAGAGTTCACA    10261    T   C     C
                                TGT GAGC TTTTTGG CTG
                                ||| |||| ||||||| |||
                                ACA CTTG AGAAACC GAC
                                  _   _      A
GAM1165 RRM2B    3' CAAAAACTTAACATTTA     68431          CC
                                TAAATGTTGAG  TTTTTG
                                ||||||||||  ||||||
                                ATTTACAATTC  AAAAAC
                                             __
GAM1165 TCF2     3' CAGGCTGGAGCCCAGCATT   22402       A  CTT  TG
                                AATGTTG GC   TT  GCCTG
                                ||||||| ||   ||  |||||
                                TTACGAC CG   AG  CGGAC
                                   C  ___  GT
GAM1165 BY55     3' AGACAGACCTCAACATT     60061        CCTT   GC
                                AATGTTGAG    TTTG  CT
                                |||||||||    ||||  ||
                                TTACAACTC    AGAC  GA
                                   C___    A_
GAM1165 C8orf2   3' CAAGTCAGGCTGAACATT    24145       G    T_
                                AATGTT AGCCT  TTTG
                                |||||| |||||  ||||
                                TTACAA TCGGA  GAAC
                                  G    CT
GAM1165 FLJ13409 3' CAGGCTTCAACTTAACATTTA  45194          CCTTTTT
                                TAAATGTTGAG      GGCCTG
                                ||||||||||       ||||||
                                ATTTACAATTC      TCGGAC
                                    AACT___
GAM1165 FLJ22774 3' CTAAAAAGGCTGAACATTTA   64471        G
                                TAAATGTT AGCCTTTTTGG
                                |||||||| ||||||||||
                                ATTTACAA TCGGAAAAATC
                                   G
GAM1165 HSOBRGRP 3' CAGACCAAGAGCCTCAACATTT 34462          C    T  C
                                AAATGTTGAG CTTTT GG CTG
                                |||||||||| ||||| || |||
                                TTTACAACTC GAGAA CC GAC
                                   C    _ A
GAM1165 KIAA0435 3' GCTAGAACTCAGCATT      29661         CCT
                                AATGTTGAG   TTTTGGC
                                |||||||||   |||||||
                                TTACGACTC   AAGATCG
                                            ___
GAM1165 MGC10940 3' CAAAAAGTAAAAAAAGCTCAAC 51183        _________
             A                   TGTTGAGC       CTTTTTG
                                 ||||||||       |||||||
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                                ACAACTCG       GAAAAAC
                                    AAAAAAAT
GAM1165 ZIN      3' CAGGCCAGGGATTGCCCAACA 26391      A  C_
                                TGTTG GC  TTTTTGGCCTG
                                ||||| ||  ||||||||||
                                ACAAC CG  AGGGACCGGAC
                                   C  TT
GAM1165 LOC256158 5' CAGGCCACTGGAGAGCCCACA 99482     T A  _   T_
                                TGT G GC CTTT  TGGCCTG
                                ||| | || ||||  |||||||
                                ACA C CG GAGG  ACCGGAC
                                  _ C  A   TC
GAM1166 SCAMP1   3' GCTAAATAAATATTCTCC    18013    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1166 SCAMP1   3' GCTAAATAAATATTCTCC    54501    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1166 NX-17    3' TGAATATCAGCCCCTAATA   40706       ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM1166 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
             TA                   TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM1167 SCAMP1   3' GCTAAATAAATATTCTCC    54500    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1167 SCAMP1   3' GCTAAATAAATATTCTCC    54501    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1167 NX-17    3' TGAATATCAGCCCCTAATA   40706       ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM1167 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
             TA                   TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
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                                ATAATCCCTATTATAAGTAAATCG

GAM1168 ABCA1    3' CTCTTCTGAAGCTAGAAACA  19734    GC    GTGG
                                TGT  CTAGCT   AGAAGAG
                                |||  ||||||   |||||||
                                ACA  GATCGA   TCTTCTC
                                  AA     AG__
GAM1168 ATP7A    3' CTCTTCTCTAGTTTAAAACA  5321     GCCT   GT
                                TGT   AGCT  GGAGAAGAG
                                |||   ||||  |||||||||
                                ACA   TTGA  TCTCTTCTC
                                  AAAT   __
GAM1168 CEACAM1  5' CTCTCCTCCACAGGTGAAGACA 9928     GCC  G      A
                                TGT   TA CTGTGGAG AGAG
                                |||   || ||||||||| ||||
                                ACA   GT GACACCTC TCTC
                                  GAA  G       C
GAM1168 CEACAM5  5' CTCTTCTCCACAGAGGAGGACA 16424    G   AG_
                                TGT CCT   CTGTGGAGAAGAG
                                ||| |||   ||||||||||||||
                                ACA GGA   GACACCTCTTCTC
                                  _   GGA
GAM1168 COL1A1   3' CTCCTCCACAGCTGCA     5396     CT       A
                                TGC  AGCTGTGGAG AG
                                |||  |||||||||| ||
                                ACG  TCGACACCTC TC
                                  __        C
GAM1168 CSRP2    3' TCTTCATAATCTAGGCACA   8994         C_
                                TGTGCCTAG  TGTGGAGA
                                |||||||||  ||||||||
                                ACACGGATC  ATACTTCT
                                     TA
GAM1168 CYP11B1  3' CTCTTCTCTCCCACATGCACA 62864      CTAGC    ___
                                TGTGC    TGTGG   AGAAGAG
                                |||||    |||||   |||||||
                                ACACG    ACACC   TCTTCTC
                                   T_____    CTC
GAM1168 FKBP10   3' CTCCCCTCCACATCACTGACAC 41935     CC   C__     AA
            A                    TGTG  TAG   TGTGGAG  GAG
                                ||||  |||   |||||||  |||
                                ACAC  GTC   ACACCTC  CTC
                                  A_   ACT      CC
GAM1168 FRK      5' CTCTTCTCCCCACCAAGGCACA 10717       AGC  T
                                TGTGCCT   TG GGAGAAGAG
                                |||||||   || |||||||||
                                ACACGGA   AC CCTCTTCTC
                                    ACC  C
GAM1168 HDAC4    3' CTCTTCTCCACAGCAAGC    21244    CTA
                                GC   GCTGTGGAGAAGAG
                                ||   ||||||||||||||
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                                CG  CGACACCTCTTCTC
                                 AA_
GAM1168 ITGB7    3' CTCTTCTCCTTGGAGGACA   7962     G  AGCTGT
                                TGT CCT    GGAGAAGAG
                                ||| |||    |||||||||
                                ACA GGA    CCTCTTCTC
                                  _  GGTT__
GAM1168 MAGEA10  5' CTCTTTTCTACAGACACA   41085    CCTAG
                                TGTG   CTGTGGAGAAGAG
                                ||||   ||||||||||||
                                ACAC   GACATCTTTTCTC
                                  A____
GAM1168 MYEOV    3' CTCTTCCCTAACTAGACA   57846   C   C  T  A
                                TG CTAG TG GG GAAGAG
                                || |||| || || ||||||
                                AC GATC AT CC CTTCTC
                                 A   A  _  _
GAM1168 RET      3' CTCTTCTCCGTTGTAGGCTCA 40546   T   G TG
                                TG GCCTA C  TGGAGAAGAG
                                || ||||| |  ||||||||||
                                AC CGGAT G  GCCTCTTCTC
                                 T    _ TT
GAM1168 RHO      3' CTTCTCCATATAAGCA     6769     C  GC
                                TGC TA  TGTGGAGAAG
                                ||| ||  ||||||||||
                                ACG AT  ATACCTCTTC
                                  A  __
GAM1168 SERPINB4 5' CTTCATTCCACAGACACA   65879    CCTAG     __
                                TGTG   CTGTGGA  GAAG
                                ||||   |||||||  ||||
                                ACAC   GACACCT  CTTC
                                  A____     TA
GAM1168 BRD4     3' CTCTTCTCCTCCAGACACA  55250    CCTAG  T_
                                TGTG   CTG  GGAGAAGAG
                                ||||   |||  |||||||||
                                ACAC   GAC  CCTCTTCTC
                                  A____  CT
GAM1168 BY55     3' TCATTACAATAGGCACA    60064      GC   A
                                TGTGCCTA  TGTGG GA
                                ||||||||  ||||| ||
                                ACACGGAT  ACATT CT
                                    A_    A
GAM1168 C5orf6   3' CTCTTCTCCCTCTTCAGGCCA 33951   T  AGCTGT
                                TG GCCT    GGAGAAGAG
                                || ||||    |||||||||
                                AC CGGA    CCTCTTCTC
                                 _   CTTCTC
GAM1168 C6orf26  3' CTCTTCTCAAGTAGGAACA  48269    G   G  GTG
                                TGT CCTA CT   GAGAAGAG
                                ||| |||| ||   ||||||||
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                                ACA GGAT GA   CTCTTCTC
                                  A   _ A__
GAM1168 CEACAM4   5' CTCCTCTCCACAGACCACA   10193     CCTAG       A
                                TGTG    CTGTGGAGA GAG
                                ||||    ||||||||| |||
                                ACAC    GACACCTCT CTC
                                  CA___       C
GAM1168 DKFZP434P0111 3' CTCTTCTTTGCTGGACACA   67958     C    TGT
                                TGTG CTAGC   GGAGAAGAG
                                |||| |||||   |||||||||
                                ACAC GGTCG   TTTCTTCTC
                                  A    ___
GAM1168 DKFZP586N0721 3' TCTCCTCCCAAGGACA     31827     G   AGC  T   A
                                TGT CCT   TG GGAG AGA
                                ||| |||   || |||| |||
                                ACA GGA   AC CCTC TCT
                                  _  ___ _   C
GAM1168 DOCK2    3'  TCTCCCCAACATCCTAGGCACA 71402        C_  ___
                                TGTGCCTAG  TGT   GGAGA
                                |||||||||  |||   |||||
                                ACACGGATC  ACA   CCTCT
                                     CT   ACC
GAM1168 ELOVL1   3'  TCCCCACAGCTGCTCTACA   43373     CC_       A
                                TGTG   TAGCTGTGG GA
                                ||||   ||||||||| ||
                                ACAT   GTCGACACC CT
                                  CTC        C
GAM1168 ET       3'  CTCAGAAACACAGCTGGACACA 44468     C       GAGAA
                                TGTG CTAGCTGTG    GAG
                                |||| |||||||||    |||
                                ACAC GGTCGACAC    CTC
                                  A        AAAGA
GAM1168 FBX30    3'  CTCTGACAGCTGGACACA    53746     C      _
                                TGTG CTAGCTGT GGAG
                                |||| |||||||| ||||
                                ACAC GGTCGACA TCTC
                                  A       G
GAM1168 FLJ10713  3'  TCTTGAGTAGCTAGGTACA   37010          G_
                                TGTGCCTAGCTGT  GAGA
                                ||||||||||||  ||||
                                ACATGGATCGATG  TTCT
                                       AG
GAM1168 FLJ11113  5'  TCTCAGCAGCAGCCAAAGCACA 37633      _____ A    G
                                TGTGC    CT GCTGT GAGA
                                |||||    || ||||| ||||
                                ACACG    GA CGACG CTCT
                                   AAACC  _    A
GAM1168 FLJ12998  3'  CTCCTCCCTCTGTGGACACA   43148     _ _  CTGT   A
                                TGTG CC TAG    GGAG AG
                                |||| || |||    |||| ||
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                                ACAC GG GTC    CCTC TC
                                  A  T   TC__    C
GAM1168  FLJ13544  3'  CTCCTCTACTTTCTAGGCAC   47206        CT_     A
                                GTGCCTAG   GTGGAG AG
                                ||||||||   |||||| ||
                                CACGGATC   CATCTC TC
                                    TTT     C
GAM1168  FLJ23022  5'  CTTCTCCACAGGTGCCA     47495    T  CT G
                                TG GC  A CTGTGGAGAAG
                                || ||  | ||||||||||
                                AC CG  T GACACCTCTTC
                                 _  __ G
GAM1168  INPP5E    3'  CTCCTCGGGCTGTGGGCACA   73505        __    _ T
                                TGTGCCT  AGCT G GGAG
                                |||||||  |||| | ||||
                                ACACGGG  TCGG C CCTC
                                    TG    G T
GAM1168  KIAA0240  3'  CTCTTCTCCCACACATACACA  94039      CC  GC    _
                                TGTG  TA  TGTGG AGAAGAG
                                ||||  ||  ||||| |||||||
                                ACAC  AT  ACACC TCTTCTC
                                  __ AC    C
GAM1168  KIAA0321  3'  TCTTCTCCCAAGCACA      63064      CTAGC  T
                                TGTGC    TG GGAGAAGA
                                |||||    || ||||||||
                                ACACG    AC CCTCTTCT
                                  A_____ _
GAM1168  KIAA0450  3'  TCTCCACGCAGCGGCCA     28372    T   TA    __
                                TG GCC  GCTGT  GGAGA
                                || |||  |||||  |||||
                                AC CGG  CGACG  CCTCT
                                 _  __    CA
GAM1168  KIAA0563  5'  CTCTTCTCCATGTGTGCACA   29880      CTA  T
                                TGTGC   GC GTGGAGAAGAG
                                |||||   || ||||||||||
                                ACACG   TG TACCTCTTCTC
                                  TG_  _
GAM1168  KIAA0773  3'  TCTCCTGGCCCTGGGCACA    28729        __    T
                                TGTGCCTA  GCTG GGAGA
                                ||||||||  |||| |||||
                                ACACGGGT  CGGT CCTCT
                                    CC    _
GAM1168  KIAA1001  3'  TTCTGATTTCCACGGCACA    31017       TAGCT     __
                                TGTGCC    GTGGAGA  AGAG
                                ||||||    |||||||  ||||
                                ACACGG    CACCTTT  TCTT
                                  ______      AG
GAM1168  KIAA1010  3'  CTCTTCCCTTGTTAGGTACA   72540         TGT  A
                                TGTGCCTAGC   GG GAAGAG
                                ||||||||||   || ||||||
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                                ACATGGATTG   CC CTTCTC
                                     TT_ _
GAM1168 KIAA1130 3' CTCTTCTCCCAGGAGGACA   63091    G   AG   T
                                TGT CCT  CTG GGAGAAGAG
                                ||| |||  ||| |||||||||
                                ACA GGA  GAC CCTCTTCTC
                                  _  G_  _
GAM1168 KIAA1170 3' TCTCCCCCAACTTAGGCAC   70425       _ C  T_
                                GTGCCTA G TG  GGAGA
                                ||||||| | ||  |||||
                                CACGGAT C AC  CCTCT
                                    T A  CC
GAM1168 KIAA1437 3' CTCCCGGACAGCCAGGACA   61214    G  A   ___
                                TGT CCT GCTGT   GGAG
                                ||| ||| |||||   ||||
                                ACA GGA CGACA   CCTC
                                  _  C    GGC
GAM1168 KIAA1554 3' CTCTTCCTAGACAGCTCAGCAC 96857      CT    __ A
             A                   TGTGC  AGCTGT  GG GAAGAG
                                ||||| ||||||  || ||||||
                                ACACG  TCGACA  TC CTTCTC
                                   AC     GA  _
GAM1168 MIDORI   3' CTTCCCCATGGGGAGTACA   74213      _ AG     A
                                TGTGC CT  CTGTGG GAAG
                                ||||| ||  |||||| ||||
                                ACATG GG  GGTACC CTTC
                                   A __     C
GAM1168 MIG     3' CTCTTCTCCATCCTACCACA   11585     CC   CT
                                TGTG  TAG  GTGGAGAAGAG
                                ||||  |||  ||||||||||
                                ACAC  ATC  TACCTCTTCTC
                                  C_  C_
GAM1168 NTF2    3' CTCCTCTCAGCTAGGCAC    20530          T   A
                                GTGCCTAGCTG GGAG AG
                                |||||||||| |||| ||
                                CACGGATCGAC TCTC TC
                                      _   C
GAM1168 SUPT4H1  3' CTCTTCCATTCTCTTAGGCACA 13486        CT__    GA
                                TGTGCCTAG   GTGGA  AGAG
                                |||||||||   |||||  ||||
                                ACACGGATT   TACCT  TCTC
                                     CTCT    __
GAM1168 SYT12    3' CTCCTCCCGGTAGGCCA    96379    T    G  T   A
                                TG GCCTA CTG GGAG AG
                                || ||||| ||| |||| ||
                                AC CGGAT GGC CCTC TC
                                  _    _  _   C
GAM1168 VPS29    3' CTCTTCTCCAGTAATAAACA  55162    GCCTA  GT
                                TGT    GCT  GGAGAAGAG
                                |||    |||  |||||||||
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                                ACA    TGA  CCTCTTCTC
                                  AATAA  __
GAM1168  VPS29    3'  CTCTTCTCCAGTAATAAACA  33154    GCCTA  GT
                                TGT    GCT  GGAGAAGAG
                                |||    |||  |||||||||
                                ACA    TGA  CCTCTTCTC
                                  AATAA  __
GAM1168  LOC115219 3'  TCTTCTCCATTGTCACA    73709     CCTA  T
                                TGTG   GC GTGGAGAAGA
                                ||||   || ||||||||||
                                ACAC   TG TACCTCTTCT
                                  ____ T
GAM1168  LOC130074 3'  CTTCCCCAGCTGGGCATA   76626          T  A
                                TGTGCCTAGCTG GG GAAG
                                |||||||||||| || ||||
                                ATACGGGTCGAC CC CTTC
                                        _  _
GAM1168  LOC130497 3'  CTCTCCTCCATAGGGACCA   75448   TG  TAG      A
                                TG  CC   CTGTGGAG AGAG
                                ||  ||   |||||||| ||||
                                AC  GG   GATACCTC TCTC
                                 CA ___       C
GAM1168  LOC145501 3'  TCTTCTCATGGGCACA     77774       GCTGTG
                                TGTGCCTA     GAGAAGA
                                ||||||||     |||||||
                                ACACGGGT     CTCTTCT
                                    A_____
GAM1168  LOC147071 5'  CTCTTCTCCATGTGTGCACA  73363      CTA  T
                                TGTGC   GC GTGGAGAAGAG
                                |||||   || ||||||||||
                                ACACG   TG TACCTCTTCTC
                                   TG_  _
GAM1168  LOC150290 3'  CTTCTCCAGGGCACA      80588       AGCTG
                                TGTGCCT    TGGAGAAG
                                |||||||    ||||||||
                                ACACGGG    ACCTCTTC
                                     _____
GAM1168  LOC150622 5'  CTTCTTTACCTGGCACA    80763      T  CT
                                TGTGCC AG  GTGGAGAAG
                                |||||| ||  |||||||||
                                ACACGG TC  CATTTCTTC
                                     _  __
GAM1168  LOC152286 3'  CTCCTCCCCACAGCTGTTGGCA 86807     __       A  A
                                TGCC  TAGCTGTGG GA GAG
                                ||||  ||||||||| || |||
                                ACGG  GTCGACACC CT CTC
                                  TT       C  C
GAM1168  LOC170370 3'  CTTCCTGCCCTAGGCACA    83726        CT TG A
                                TGTGCCTAG  G  G GAAG
                                |||||||||  |  | ||||
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                                ACACGGATC  C  C CTTC
                                     C_ GT _
GAM1168  LOC199926 5'  CTCTGGTCCACAGCTAAGCA   91480     C        GA
                                TGC TAGCTGTGGA  AGAG
                                ||| ||||||||||  ||||
                                ACG ATCGACACCT  TCTC
                                  A         GG
GAM1168  LOC200734 3'  CTCTTCTCTACAAAGCACA    90278      CTAGC
                                TGTGC    TGTGGAGAAGAG
                                |||||    ||||||||||||
                                ACACG    ACATCTCTTCTC
                                   AA___
GAM1168  LOC201173 5'  CTCTTCTCCATGTGTGCACA   88683      CTA  T
                                TGTGC   GC GTGGAGAAGAG
                                |||||   || ||||||||||
                                ACACG   TG TACCTCTTCTC
                                   TG_  _
GAM1168  LOC201220 5'  CTCTTCTCCATGTGTGCACA   88718      CTA  T
                                TGTGC   GC GTGGAGAAGAG
                                |||||   || ||||||||||
                                ACACG   TG TACCTCTTCTC
                                   TG_  _
GAM1168  LOC202316 5'  CTCTGGTCCACAGCTAAGCA   91942     C        GA
                                TGC TAGCTGTGGA  AGAG
                                ||| ||||||||||  ||||
                                ACG ATCGACACCT  TCTC
                                  A         GG
GAM1168  LOC203508 3'  TTCTCCTCCATCAAGCTCA    90938    T   __     A
                                C AGCT  GTGGAG AGAG
                                | ||||  |||||| ||||
                                A TCGA  TACCTC TCTT
                                 C    AC     C
GAM1168  LOC220097 5'  CTCTTCTCCCACTAAGAACA   95117     GCC   C  T
                                TGT   TAG TG GGAGAAGAG
                                |||   ||| || |||||||||
                                ACA   ATC AC CCTCTTCTC
                                  AGA   _  _
GAM1168  LOC221322 5'  CTCTTCTCCTGTTAGAGGCTCA 93582    T    AGCTGT
                                TG GCCT     GGAGAAGAG
                                || ||||     |||||||||
                                AC CGGA     CCTCTTCTC
                                 T    GATTGT
GAM1168  LOC222815 5'  CTTCTCCACAGCTGGAGCCA   96023    T  _
                                TG GC CTAGCTGTGGAGAAG
                                || || ||||||||||||||
                                AC CG GGTCGACACCTCTTC
                                 _  A
GAM1168  LOC253962 5'  CTCCCCCACAGCTGCGC     98479      CT       AGAA
                                GTGC  AGCTGTGG    GAG
                                ||||  ||||||||    |||
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                                CGCG  TCGACACC   CTC
                                  __      CC__
GAM1168 LOC90564 3' CTCTTCGGCATATAGGCACA  63936       GC   GA
                                TGTGCCTA  TGTG  GAAGAG
                                ||||||||  ||||  ||||||
                                ACACGGAT  ATAC  CTTCTC
                                    __    GG
GAM1169 ABCA3    5' AGCCCTGGGCACCTCCTG    8440     AG      A
                                CAG  GGTGCCCAG GCT
                                |||  ||||||||| |||
                                GTC  CCACGGGTC CGA
                                  CT       C
GAM1169 AGRP     5' GGACCCTGGGCACCCTCT    24617          AGC
                                AGAGGGTGCCCAG   TCC
                                ||||||||||||   |||
                                TCTCCCACGGGTC   AGG
                                       CC_
GAM1169 BIN3     3' GGAGCCCTCTGGCCCCTC    38578     T   C  __
                                GAGGG GCC AGA  GCTCC
                                ||||| ||| |||  |||||
                                CTCCC CGG TCT  CGAGG
                                  _  _  CC
GAM1169 CD81     3' AGTCTGTGGGCACTCTCTG   16383          G  _
                                CAGAGGGTGCCCA AG CT
                                |||||||||||| || ||
                                GTCTCTCACGGGT TC GA
                                       G  T
GAM1169 CDKN1C   5' GAATTCCGGGCACCCCTC    5370       _    A  C
                                GAGGG TGCCC GAG TC
                                ||||| ||||| ||| ||
                                CTCCC ACGGG CTT AG
                                   C    C  A
GAM1169 CENPB    3' GGACTCTCTGGGCACCCGCTG  70117     A         C_
                                CAG GGGTGCCCAGAG  TCC
                                ||| ||||||||||||  |||
                                GTC CCCACGGGTCTC  AGG
                                  G          TC
GAM1169 COL6A2   3' GGAGCTCTAGGCCGACGCCC   10251     ____  C
                                GGGT   GCC AGAGCTCC
                                ||||   ||| ||||||||
                                CCCG   CGG TCTCGAGG
                                  CAGC   A
GAM1169 CYP1A1   3' AGCTCTGAAGAACTCTCTG   6687        GCC_
                                CAGAGGGT   CAGAGCT
                                ||||||||   |||||||
                                GTCTCTCA   GTCTCGA
                                     AGAA
GAM1169 DNLC2A   3' GAGCTCCGGAGCGCCCTCT   27197         _ A
                                AGAGGGTGC CC GAGCTC
                                ||||||||| || ||||||
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                                TCTCCCGCG GG CTCGAG
                                     A  C
GAM1169  EDN1    3'  GAGCAGGAGCATCCTCTG    10479         _  AGA
                                CAGAGGGTGC CC   GCTC
                                |||||||||| ||   ||||
                                GTCTCCTACG GG   CGAG
                                     A  A__
GAM1169  EGR1    3'  GAGCCCTGCCCTGCACCCTT   10491        C___   A
                                GAGGGTGC   CAG GCTC
                                ||||||||   ||| ||||
                                TTCCCACG   GTC CGAG
                                    TCCC   C
GAM1169  EXT2    3'  GGAATGTCTGATACCCTCTG   6381         CC   GC_
                                CAGAGGGTG  CAGA  TCC
                                |||||||| ||||  |||
                                GTCTCCCAT  GTCT  AGG
                                     A_   GTA
GAM1169  FCMD    3'  GGAACCCTCCCCCACCCTTTG 23040         CCCA  C__
                                CAGAGGGTG   GAG  TCC
                                |||||||||   |||  |||
                                GTTTCCCAC   CTC  AGG
                                     CCC_  CCA
GAM1169  FMOD    3'  AGTCCACGGGCACCCTCTG   10671          AGA_
                                CAGAGGGTGCCC   GCT
                                ||||||||||||   |||
                                GTCTCCCACGGG   TGA
                                      CACC
GAM1169  GABRE   3'  GAGCCCACTGTCACCTTCT   18283        CC  A__
                                AGAGGGTG  CAG  GCTC
                                ||||||||  |||  ||||
                                TCTTCCAC  GTC  CGAG
                                     T_  ACC
GAM1169  GABRE   3'  GAGCCCACTGTCACCTTCT   18284        CC  A__
                                AGAGGGTG  CAG  GCTC
                                ||||||||  |||  ||||
                                TCTTCCAC  GTC  CGAG
                                     T_  ACC
GAM1169  GPT     3'  GGAGCCCTGGGAGGCTCTG   19187      GGTG   A
                                CAGAG   CCCAG GCTCC
                                |||||   ||||| |||||
                                GTCTC   GGGTC CGAGG
                                   GGA_   C
GAM1169  GSPT1   3'  GAGCTCTGCTATGCCACTG   10884     AG   CC_
                                CAG  GGTG  CAGAGCTC
                                |||  ||||  ||||||||
                                GTC  CCGT  GTCTCGAG
                                  A_   ATC
GAM1169  HEM1    5'  GGAGTATGACCACCCTCTG   19241        CC  GA
                                CAGAGGGTG  CA  GCTCC
                                |||||||||  ||  |||||
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                                GTCTCCCAC  GT  TGAGG
                                     CA  A_
GAM1169  HOXA3    3'  GGACGCAGCAGCCCTCTG    48401        _  CCAGA  _
                                CAGAGGG TGC    GC TCC
                                ||||||| |||    || |||
                                GTCTCCC ACG    CG AGG
                                    G   A____  C
GAM1169  HSPA4    3'  GGAGCTCTAATTATGCTTT    90653     G   CCC
                                AGAG GTG   AGAGCTCC
                                |||| |||   ||||||||
                                TTTC TAT   TCTCGAGG
                                  G   TAA
GAM1169  IGFBP3   3'  GGAGCTCACAGCCTTCTG    7002         GCCCA
                                CAGAGGGT    GAGCTCC
                                ||||||||    |||||||
                                GTCTTCCG    CTCGAGG
                                     ACA__
GAM1169  KCNH3    3'  GAGCTTTGCCATCCCCTG    65213     A    CC
                                CAG GGGTG  CAGAGCTC
                                ||| |||||  ||||||||
                                GTC CCTAC  GTTTCGAG
                                  C    C_
GAM1169  LZTS1    3'  GGCTTTCCAGGCACCCTC    41036         C__
                                GAGGGTGCC   AGAGCT
                                |||||||||   ||||||
                                CTCCCACGG   TTTCGG
                                     ACC
GAM1169  MADD     3'  GGAACCCTGGGGCTCACCCTCT 56213         ___    AGC
                                AGAGGGTG   CCCAG   TCC
                                ||||||||   |||||   |||
                                TCTCCCAC   GGGTC   AGG
                                     TCG    CCA
GAM1169  MADD     3'  GGAACCCTGGGGCTCACCCTCT 56214         ___    AGC
                                AGAGGGTG   CCCAG   TCC
                                ||||||||   |||||   |||
                                TCTCCCAC   GGGTC   AGG
                                     TCG    CCA
GAM1169  MECP2    3'  GAACTCTGCCTGCCCTTTG   18403         CC    C
                                CAGAGGGTG  CAGAG TC
                                |||||||||  ||||| ||
                                GTTTCCCGT  GTCTC AG
                                     CC    A
GAM1169  MUCDHL   5'  GGATCCCGGACACCCTCT    88643         _ CA  GC
                                AGAGGGTG CC  GA  TCC
                                |||||||| ||  ||  |||
                                TCTCCCAC GG  CT  AGG
                                     A  CC  __
GAM1169  NCYM     5'  GGAATGGGGCACCCTTTG    21971           AGAGC
                                CAGAGGGTGCCC    TCC
                                ||||||||||||    |||
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                                GTTTCCCACGGG    AGG
                                      GTA__
GAM1169 NFKBIL2  5' GGAGCGCGCTGACGACCCTCTG 26453       GCC  A__
                                CAGAGGGT  CAG  GCTCC
                                ||||||||  |||  |||||
                                GTCTCCCA  GTC  CGAGG
                                    GCA  GCG
GAM1169 OSR1    5' GGAGCTCTGAACCCCCGCTG  18836    A  TGCC
                                CAG GGG   CAGAGCTCC
                                ||| |||   |||||||||
                                GTC CCC   GTCTCGAGG
                                  G  CCAA
GAM1169 OXTR    5' GGAGCCCCGGGCGCCCCT   8078    A     AGA
                                AG GGGTGCCC  GCTCC
                                || ||||||||  |||||
                                TC CCCGCGGG  CGAGG
                                 _      CCC
GAM1169 PACE    3' AGCTCTGGCTGAACCCTGTG  11940   G   GC__
                                CA AGGGT   CCAGAGCT
                                || |||||   ||||||||
                                GT TCCCA   GGTCTCGA
                                 G    AGTC
GAM1169 PCDHA1  3' GAGGTGGCAGCCACCCTCT   49414       _ __  GAG
                                AGAGGGTG C  CCA  CTC
                                |||||||| |  |||  |||
                                TCTCCCAC G  GGT  GAG
                                    C AC  G__
GAM1169 PCDHA10 3' GAGGTGGCAGCCACCCTCT   38791       _ __  GAG
                                AGAGGGTG C  CCA  CTC
                                |||||||| |  |||  |||
                                TCTCCCAC G  GGT  GAG
                                    C AC  G__
GAM1169 PCDHA11 3' GAGGTGGCAGCCACCCTCT   49862       _ __  GAG
                                AGAGGGTG C  CCA  CTC
                                |||||||| |  |||  |||
                                TCTCCCAC G  GGT  GAG
                                    C AC  G__
GAM1169 PCDHA12 3' GAGGTGGCAGCCACCCTCT   38799       _ __  GAG
                                AGAGGGTG C  CCA  CTC
                                |||||||| |  |||  |||
                                TCTCCCAC G  GGT  GAG
                                    C AC  G__
GAM1169 PCDHA13 3' GAGGTGGCAGCCACCCTCT   49870       _ __  GAG
                                AGAGGGTG C  CCA  CTC
                                |||||||| |  |||  |||
                                TCTCCCAC G  GGT  GAG
                                    C AC  G__
GAM1169 PCDHA2  3' GAGGTGGCAGCCACCCTCT   38806       _ __  GAG
                                AGAGGGTG C  CCA  CTC
                                |||||||| |  |||  |||
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                                TCTCCCAC G  GGT   GAG
                                    C AC   G__
GAM1169  PCDHA3   3'  GAGGTGGCAGCCACCCTCT   49807       _ __  GAG
                                AGAGGGTG C  CCA   CTC
                                |||||||| |  |||   |||
                                TCTCCCAC G  GGT   GAG
                                    C AC   G__
GAM1169  PCDHA4   3'  GAGGTGGCAGCCACCCTCT   38814       _ __  GAG
                                AGAGGGTG C  CCA   CTC
                                |||||||| |  |||   |||
                                TCTCCCAC G  GGT   GAG
                                    C AC   G__
GAM1169  PCDHA5   3'  GAGGTGGCAGCCACCCTCT   49814       _ __  GAG
                                AGAGGGTG C  CCA   CTC
                                |||||||| |  |||   |||
                                TCTCCCAC G  GGT   GAG
                                    C AC   G__
GAM1169  PCDHA6   3'  GAGGTGGCAGCCACCCTCT   38822       _ __  GAG
                                AGAGGGTG C  CCA   CTC
                                |||||||| |  |||   |||
                                TCTCCCAC G  GGT   GAG
                                    C AC   G__
GAM1169  PCDHA7   3'  GAGGTGGCAGCCACCCTCT   49827       _ __  GAG
                                AGAGGGTG C  CCA   CTC
                                |||||||| |  |||   |||
                                TCTCCCAC G  GGT   GAG
                                    C AC   G__
GAM1169  PCDHA8   3'  GAGGTGGCAGCCACCCTCT   38830       _ __  GAG
                                AGAGGGTG C  CCA   CTC
                                |||||||| |  |||   |||
                                TCTCCCAC G  GGT   GAG
                                    C AC   G__
GAM1169  PCDHA9   3'  GAGGTGGCAGCCACCCTCT   49847       _ __  GAG
                                AGAGGGTG C  CCA   CTC
                                |||||||| |  |||   |||
                                TCTCCCAC G  GGT   GAG
                                    C AC   G__
GAM1169  PCDHAC1  3'  GAGGTGGCAGCCACCCTCT   38781       _ __  GAG
                                AGAGGGTG C  CCA   CTC
                                |||||||| |  |||   |||
                                TCTCCCAC G  GGT   GAG
                                    C AC   G__
GAM1169  PCDHAC2  3'  GAGGTGGCAGCCACCCTCT   49878       _ __  GAG
                                AGAGGGTG C  CCA   CTC
                                |||||||| |  |||   |||
                                TCTCCCAC G  GGT   GAG
                                    C AC   G__
GAM1169  PDE6D    5'  GGCTCCTGGGCACCGTCTG   12017     G     _
                                CAGA GGTGCCCAG AGCT
                                |||| ||||||||| ||||
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                                GTCT CCACGGGTC TCGG
                                  G       C
GAM1169  PRG2    5'  GGAACTCCGCTCCTTCTG    12262       T  CCA   C
                                CAGAGGG GC   GAG TCC
                                ||||||| ||   ||| |||
                                GTCTTCC CG   CTC AGG
                                   T  C__   A
GAM1169  REN     3'  GAGCTGGAACACTCTCTG    6763        C_  GA
                                CAGAGGGTG  CCA  GCTC
                                |||||||||  |||  ||||
                                GTCTCTCAC  GGT  CGAG
                                     AA  __
GAM1169  REST    5'  GGAGGCCTGAGCACCCTCTG   20043         C   AG
                                CAGAGGGTGC CAG  CTCC
                                |||||||||| |||  ||||
                                GTCTCCCACG GTC  GAGG
                                      A   CG
GAM1169  ROR2    3'  GGAGCCCTGCTCCTCTCTG    17060      _  T  CC  A
                                CAGAG GG GC  AG GCTCC
                                ||||| || ||  || |||||
                                GTCTC CC CG  TC CGAGG
                                   T  T  __  C
GAM1169  SLC22A7  3'  GGAGTATCGAACCCTCTG    22886        GCCCA  _
                                CAGAGGGT    GA GCTCC
                                ||||||||    || |||||
                                GTCTCCCA    CT TGAGG
                                     AG___  A
GAM1169  SLC7A5   3'  GGAACTAGGGCACCCCTTG   14468    A      AG  C
                                CAG GGGTGCCC  AG TCC
                                ||| ||||||||  || |||
                                GTT CCCACGGG  TC AGG
                                  C       A_  A
GAM1169  SMURF1   3'  GAGCTCCGGTTCACTCTT    94047       C_  A
                                GAGGGTG  CC GAGCTC
                                |||||||  || ||||||
                                TTCTCAC  GG CTCGAG
                                     TT  C
GAM1169  SORT1    3'  GGAACCCTGAGCACTTTTT    12927        C   AGC
                                AGAGGGTGC CAG   TCC
                                |||||||||  |||   |||
                                TTTTTCACG GTC   AGG
                                      A   CCA
GAM1169  SPON2    5'  GGAGCTCCGGGCTCTGGCTG   25852    AG  T   A
                                CAG  GG GCCC GAGCTCC
                                |||  || |||| |||||||
                                GTC  TC CGGG CTCGAGG
                                  GG  T   C
GAM1169  SRC     3'  GGAGCTCTGTGGGTCTCTG    19451       GTG  _
                                CAGAGG   CC CAGAGCTCC
                                ||||||   || |||||||||
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                                GTCTCT   GG GTCTCGAGG
                                   G__  T
GAM1169  TEM7     3'  GAGCTCTGTTACAGCCCACTG  40262     A   GCC__
                                CAG GGGT    CAGAGCTC
                                ||| ||||    ||||||||
                                GTC CCCG    GTCTCGAG
                                  A   ACATT
GAM1169  ZNF289   3'  GGAATGCAGGACCCTCTG    65932       G  CAGA __
                                CAGAGGGT CC   GC  TCC
                                |||||||| ||   ||  |||
                                GTCTCCCA GG   CG  AGG
                                     _ A___  TA
GAM1169  APOA5    3'  GGAGCTCCTTAAACCCTCTG  54801       GCCCA
                                CAGAGGGT    GAGCTCC
                                ||||||||    |||||||
                                GTCTCCCA    CTCGAGG
                                     AATTC
GAM1169  ARS2     3'  AGCTCTGAGAATTTTTTG    32481       GCC
                                CAGAGGGT   CAGAGCT
                                ||||||||   |||||||
                                GTTTTTTA   GTCTCGA
                                     AGA
GAM1169  ATP9A    3'  GGAGCTCCGAAGCATCTTCT  62738       CCA_
                                AGAGGGTGC   GAGCTCC
                                |||||||||   |||||||
                                TCTTCTACG   CTCGAGG
                                     AAGC
GAM1169  BNIP-S   3'  GAGCTCTGGGTTTTAATCC   57103     _____
                                GGGT   GCCCAGAGCTC
                                ||||   ||||||||||
                                CCTA   TGGGTCTCGAG
                                  ATTT
GAM1169  BNIP-S   3'  GAGCTCTGGGTTTTTTTG    57104       T
                                CAGAGGG GCCCAGAGCTC
                                ||||||| ||||||||||
                                GTTTTTT TGGGTCTCGAG
                                     _
GAM1169  C20orf124 3'  GGAGCTCTTCCCGCCGCTG   45841     AG   CCC
                                CAG  GGTG   AGAGCTCC
                                |||  ||||   ||||||||
                                GTC  CCGC   TCTCGAGG
                                  G_   CCT
GAM1169  C22orf3  3'  GGAGCAGGGGCACCTCTG    25350       G    AGA
                                CAGAGG TGCCC   GCTCC
                                |||||| |||||   |||||
                                GTCTCC ACGGG   CGAGG
                                   _    GA_
GAM1169  C8orf13  5'  GAGCTCTGGGCCTTCTTC    82478      T_
                                GAGGG  GCCCAGAGCTC
                                |||||  ||||||||||
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                                CTTCT  CGGGTCTCGAG
                                   TC
GAM1169  CHSY1    3'  GAGCTCTGCCATTTCTTG    30570     AG    CC
                                CAG  GGTG  CAGAGCTC
                                |||  ||||  ||||||||
                                GTT  TTAC  GTCTCGAG
                                  CT    C_
GAM1169  CLSTN1   3'  GGAGCTCTGAGCACGGGCTC  30791     G__    C
                                GAG   GTGC CAGAGCTCC
                                |||   |||| |||||||||
                                CTC   CACG GTCTCGAGG
                                  GGG    A
GAM1169  CLSTN2   3'  AGCCTTGGGCACTCCCTG    42397     A        A
                                CAG GGGTGCCCAG GCT
                                ||| |||||||||| |||
                                GTC CTCACGGGTT CGA
                                  C         C
GAM1169  CNNM4    3'  GGAACTGGCCCACCCACTG   39869     A    C_   AGC
                                CAG GGGTG  CCAG   TCC
                                ||| |||||  ||||   |||
                                GTC CCCAC  GGTC   AGG
                                  A    CC    A__
GAM1169  DKFZp547E052 3'  GGAGCTCTTTGGCCTCCTG   51092     A   T   C_
                                CAG GGG GCC  AGAGCTCC
                                ||| ||| |||  ||||||||
                                GTC CTC CGG  TCTCGAGG
                                  _   _   TT
GAM1169  DKFZP586I2223 3'  GGAGCTCTTGCTCTCCTG    31878     A   T  CC
                                CAG GGG GC  AGAGCTCC
                                ||| ||| ||  ||||||||
                                GTC CTC CG  TCTCGAGG
                                  _   T  T_
GAM1169  DKFZP586I2223 3'  GGAGCTCTTGCTCTCCTG    31879     A   T  CC
                                CAG GGG GC  AGAGCTCC
                                ||| ||| ||  ||||||||
                                GTC CTC CG  TCTCGAGG
                                  _   T  T_
GAM1169  ELKS     3'  GGAGCCTCTCACCTCCTG    31192     AG    CCC   _
                                CAG  GGTG   AGAG CTCC
                                |||  ||||   |||| ||||
                                GTC  CCAC   TCTC GAGG
                                  CT    ____    C
GAM1169  FLJ00001 3'  GAGCTCTGGCCACTTCTG    82715       G  C
                                CAGAGG TG CCAGAGCTC
                                |||||| || |||||||||
                                GTCTTC AC GGTCTCGAG
                                    _ C
GAM1169  FLJ10769 3'  GGAGCTCTGAGACGCCTCCT   37146    AG    CC_
                                AG  GGTG   CAGAGCTCC
                                ||  ||||   |||||||||
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                                TC  CCGC   GTCTCGAGG
                                 CT    AGA
GAM1169  FLJ10925  5'  GGAGGTGTCGGGACCCTCTG  37413       G   A  G__
                                CAGAGGGT CCC GA   CTCC
                                |||||||| ||| ||   ||||
                                GTCTCCCA GGG CT   GAGG
                                    _  _ GTG
GAM1169  FLJ14154  3'  GAGCTCTGAGGCTCAGCCC   46231     ___  _
                                GGGT   GCC CAGAGCTC
                                ||||   ||| ||||||||
                                CCCG   CGG GTCTCGAG
                                  ACT   A
GAM1169  FLJ14280  3'  GGAATCGAGGGCACCTCTG   46521      G    A_  GC
                                CAGAGG TGCCC  GA  TCC
                                ||||||  |||||  ||  |||
                                GTCTCC ACGGG  CT  AGG
                                   _    AG  A_
GAM1169  FLJ14641  5'  GGAGCTCTCCAGCCTTTG    52562      G  CCC
                                CAGAGG TG   AGAGCTCC
                                ||||||  ||   ||||||||
                                GTTTCC AC   TCTCGAGG
                                   G  C__
GAM1169  FLJ14957  3'  GGAGGTTGAGCACCTCTG    52823      G   C   AG
                                CAGAGG TGC CAG  CTCC
                                ||||||  |||  |||  ||||
                                GTCTCC ACG GTT  GAGG
                                   _  A   G_
GAM1169  FLJ20694  3'  AGCTCTTCACCTCCTCTG    35969      __  CCC
                                CAGAGG  GTG   AGAGCT
                                ||||||  |||   ||||||
                                GTCTCC  CAC   TCTCGA
                                   TC   T__
GAM1169  FLJ21432  3'  GGAGCTCTGGAACACTCTCT  44944       C_
                                AGAGGGTG  CCAGAGCTCC
                                ||||||||  ||||||||||
                                TCTCTCAC  GGTCTCGAGG
                                    AA
GAM1169  GNG3     3'  AGATATGAGGCACCCTTTG   25205         _  GAG
                                CAGAGGGTGCC CA   CT
                                ||||||||||| ||   ||
                                GTTTCCCACGG GT   GA
                                      A  ATA
GAM1169  KCNS1    3'  GGAGCTCTGGATCTCAGCTG  11195    A_   TGC
                                CAG  GGG   CCAGAGCTCC
                                |||  |||   ||||||||||
                                GTC  CTC   GGTCTCGAGG
                                  GA   TA_
GAM1169  KIAA0189  3'  GAGCAGGGCAGCCCCCTG    28944    A   _    AGA
                                CAG GGG TGCCC   GCTC
                                ||| ||| |||||   ||||
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                              GTC CCC ACGGG   CGAG
                                C   G    A__
GAM1169  KIAA0365  3'  GGCCCTCTGGGCACCCCCT   79371    A         CT
                              AG GGGTGCCCAGAG  CC
                              || ||||||||||||  ||
                              TC CCCACGGGTCTC  GG
                               C          CC
GAM1169  KIAA0513  3'  GAGCTCTGGTGGCCCCTC    29033      T  __
                              GAGGG GCC  CAGAGCTC
                              ||||| |||  ||||||||
                              CTCCC CGG  GTCTCGAG
                                 _  TG
GAM1169  KIAA0544  3'  GGAGCCCTCCCCTGCTCTCTG  71469        GCCC_  A
                              CAGAGGGT    AG GCTCC
                              ||||||||    || |||||
                              GTCTCTCG    TC CGAGG
                                   TCCCC  C
GAM1169  KIAA0773  3'  GGAGCTCTGAGAGGTGGTCT   28726    G   ___
                              AGG TGCC   CAGAGCTCC
                              ||| ||||   |||||||||
                              TCT GTGG   GTCTCGAGG
                                G    AGA
GAM1169  KIAA0793  3'  AGCCTGGGCACACCCTG     29693    A  _      A
                              CAG GG GTGCCCAG GCT
                              ||| || |||||||| |||
                              GTC CC CACGGGTC CGA
                                _  A       _
GAM1169  KIAA0821  3'  GGAACCCTGGGCAGGGCTCTG  30609      GG_     AGC
                              CAGAG   TGCCCAG   TCC
                              |||||   |||||||   |||
                              GTCTC   ACGGGTC   AGG
                                 GGG      CCA
GAM1169  KIAA1396  3'  GAGCTCTGGCTGGCATCT    63670        ___
                              GGGTGCC   CAGAGCTC
                              |||||||   ||||||||
                              TCTACGG   GTCTCGAG
                                  TCG
GAM1169  KIAA1706  3'  GGAGCTCTAAGGGTACTT    94368        __
                              GGGTGCCC  AGAGCTCC
                              ||||||||  ||||||||
                              TTCATGGG  TCTCGAGG
                                   AA
GAM1169  KIAA1755  3'  GGAGCTCTGGTCAGTCCC    62017    __  C
                              GGG  TG CCAGAGCTCC
                              |||  || ||||||||||
                              CCC  AC GGTCTCGAGG
                                TG  T
GAM1169  KIAA1822  3'  GGAGCTCTGGGTGCGGCCTC   68190     __ TG
                              GAGG  G  CCCAGAGCTCC
                              ||||  |  ||||||||||
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                                CTCC  C  GGGTCTCGAGG
                                  GG GT
GAM1169 KIAA1838 3' GAGCCCTGCCAGCGCCCTC   65369       C__   A
                                GAGGGTGC   CAG GCTC
                                ||||||||   ||| ||||
                                CTCCCGCG   GTC CGAG
                                    ACC   C
GAM1169 KIAA1858 3' GGAGCTCTGGGCTCCGCCT   67723    AG  T
                                AG  GG GCCCAGAGCTCC
                                ||  || ||||||||||||
                                TC  CC CGGGTCTCGAGG
                                 CG  T
GAM1169 MGC14289 3' GGAGCTCTGCTGACTTCTG   55592      GTGCC
                                CAGAGG    CAGAGCTCC
                                ||||||    |||||||||
                                GTCTTC    GTCTCGAGG
                                   AGTC_
GAM1169 MGC2396  5' GGAGCTCTAGGTCGCCTCT   54559     GT   C
                                AGAGG  GCC AGAGCTCC
                                |||||  ||| ||||||||
                                TCTCC  TGG TCTCGAGG
                                  GC   A
GAM1169 MGC2654  3' GGAGCTCTGGAAGATCATC   44349    G   GC_
                                GA GGT   CCAGAGCTCC
                                || |||   ||||||||||
                                CT CTA   GGTCTCGAGG
                                 A   GAA
GAM1169 NAG73    5' GGCTCCTAGCACCCTCTG    51792        CCA
                                CAGAGGGTGC   GAGCT
                                ||||||||||   |||||
                                GTCTCCCACG   CTCGG
                                      ATC
GAM1169 NDRG4    3' GAGCTCTGGCCAGGCTGTG   40382    G  GG  C
                                CA AG  TG CCAGAGCTC
                                || ||  || |||||||||
                                GT TC  AC GGTCTCGAG
                                 G  GG  C
GAM1169 NIP30    3' CTTTGTAGGCACCTTCTG    46897         __
                                CAGAGGGTGCC  CAGAG
                                ||||||||||  |||||
                                GTCTTCCACGG  GTTTC
                                      AT
GAM1169 OATL1    3' GGAGCTCTGCTTTGGCACT   71016      _____
                                GGTGCC    CAGAGCTCC
                                ||||||    |||||||||
                                TCACGG    GTCTCGAGG
                                   TTTC
GAM1169 OLIG1    3' GGACTGTCGGGCACCCCCT   97335    A      AG_  C
                                AG GGGTGCCC   AG TCC
                                || ||||||||   || |||
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                                TC CCCACGGG  TC AGG
                                 C       CTG  _
GAM1169  PCSK7    3'  GGAATCTGAGGCATCCTCTG  17521          _   GC
                                CAGAGGGTGCC CAGA  TCC
                                |||||||||||  ||||  |||
                                GTCTCCTACGG GTCT  AGG
                                      A   A_
GAM1169  PI4KII   3'  GAGATGTGCAGCCCTCTG   37953       _  C  GAG
                                CAGAGGG TGC CA   CTC
                                |||||||  ||| ||   |||
                                GTCTCCC ACG GT   GAG
                                    G   T  A__
GAM1169  PINK1    3'  AGAACTTGGCATCCTCTG   51562          C  AG
                                CAGAGGGTGCC AG  CT
                                ||||||||||  ||  ||
                                GTCTCCTACGG TC  GA
                                      T  AA
GAM1169  PTPRT    3'  GGAGCTCTGAGGTGGCACCCT  56503        ____
                                AGGGTGCC   CAGAGCTCC
                                ||||||||   |||||||||
                                TCCCACGG   GTCTCGAGG
                                    TGGA
GAM1169  PTPRU    3'  GGCCTGGGGCACCCACTG   20323    A      _ A
                                CAG GGGTGCCC AG GCT
                                ||| |||||||| || |||
                                GTC CCCACGGG TC CGG
                                 A       G  _
GAM1169  RHOBTB3  5'  GTTCCCGGGCACTCCCTG   30430    A      A_
                                CAG GGGTGCCC  GAGC
                                ||| ||||||||  ||||
                                GTC CTCACGGG  CTTG
                                 C       CC
GAM1169  RPL34    3'  GGAGCTCTGATATATATCTG  8273     GG_  CC
                                CAGA  GTG  CAGAGCTCC
                                ||||  |||  |||||||||
                                GTCT  TAT  GTCTCGAGG
                                  ATA  A_
GAM1169  SH2D3A   5'  GAGCTCAGCCCTGGCACCCTCT 19702         CA____
            G                    CAGAGGGTGCC    GAGCTC
                                ||||||||||     ||||||
                                GTCTCCCACGG    CTCGAG
                                      TCCCGA
GAM1169  SLC26A6  3'  GGAGGTGCAGGGCACCCTT   43585        AGA  _
                                GAGGGTGCCC   GC TCC
                                ||||||||||   || |||
                                TTCCCACGGG   TG AGG
                                      ACG  G
GAM1169  STIM2    3'  GGAGCTCTGGAGCAGGACC   40859    G__  _
                                GG   TGC CCAGAGCTCC
                                ||   ||| ||||||||||
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                                CC   ACG GGTCTCGAGG
                                 AGG   A
GAM1169  VCY2IP1   3'  GGAGGCCGGGCACCCCTG    36923     A       AGAG
                                CAG GGGTGCCC    CTCC
                                ||| ||||||||    ||||
                                GTC CCCACGGG    GAGG
                                  _       CCG_
GAM1169  ZDHHC7    3'  AGCCATTGGGCACCTCTG    35316       G      A_
                                CAGAGG TGCCCAG  GCT
                                |||||| |||||||  |||
                                GTCTCC ACGGGTT  CGA
                                   _      AC
GAM1169  ZFP106    3'  GAGCTGCTCCAGCACCCTT   42727        CC_ _
                                GAGGGTGC   AG AGCTC
                                ||||||||   || |||||
                                TTCCCACG   TC TCGAG
                                     ACC  G
GAM1169  LOC118471 5'  AGCTCCCTGAGCACTCTCT   74351         C __
                                AGAGGGTGC CA  GAGCT
                                ||||||||| ||  |||||
                                TCTCTCACG GT  CTCGA
                                      A  CC
GAM1169  LOC121506 5'  GAACTCTGCTCCGGCATCCTC  74532         ____    C
                                GAGGGTGCC    CAGAG TC
                                |||||||||    ||||| ||
                                CTCCTACGG    GTCTC AG
                                      CCTC     A
GAM1169  LOC126327 3'  GGAGTTCAGGGCACCCTCT    74985          A
                                AGAGGGTGCCC GAGCTCC
                                |||||||||||| |||||||
                                TCTCCCACGGG CTTGAGG
                                       A
GAM1169  LOC126603 5'  GGAGCAGCTCAACACCCTCTG  75912         CCC  A_
                                CAGAGGGTG   AG  GCTCC
                                |||||||||   ||  |||||
                                GTCTCCCAC   TC  CGAGG
                                      AAC  GA
GAM1169  LOC138429 3'  GGAGCTCTGGGAGGCATTCTG  75864      G  G_
                                CAGAG GT  CCCAGAGCTCC
                                ||||| ||  ||||||||||||
                                GTCTT CG  GGGTCTCGAGG
                                   A  GA
GAM1169  LOC143162 3'  GAACTTGGGGCAGCCCCTG    77007     A  _    A  C
                                CAG GGG TGCCC GAG TC
                                ||| ||| ||||| ||| ||
                                GTC CCC ACGGG TTC AG
                                  _  G    G  A
GAM1169  LOC145387 5'  GGAGCTCTGGGAGCCACTC    84339     _  G
                                GAG GGT CCCAGAGCTCC
                                ||| ||| ||||||||||
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                                CTC CCG GGGTCTCGAGG
                                  A   A
GAM1169  LOC145781 3'  AGCTCTGGAACCCTGTG     77955    G    GC
                                CA AGGGT  CCAGAGCT
                                || |||||  ||||||||
                                GT TCCCA  GGTCTCGA
                                 G    A_
GAM1169  LOC146108 5'  GGAGCTCTGCACACCCCCT    78150    A    CC
                                AG GGGTG  CAGAGCTCC
                                || |||||  |||||||||
                                TC CCCAC  GTCTCGAGG
                                 C    AC
GAM1169  LOC146445 3'  GGAGCCCTCGATGGCACCCTC  84682        CA_ __
                                GAGGGTGCC   GA  GCTCC
                                |||||||||   ||  |||||
                                CTCCCACGG   CT  CGAGG
                                      TAG  CC
GAM1169  LOC147515 3'  GCTCTGGGCACCCTTTG     85150             _
                                CAGAGGGTGCCCAGAG C
                                |||||||||||||||| |
                                GTTTCCCACGGGTCTC G
                                          C
GAM1169  LOC148029 3'  GGAACTCTTTGCTCCCCTG    79319     A  T  CC   C
                                CAG GGG GC  AGAG TCC
                                ||| ||| ||  |||| |||
                                GTC CCC CG  TCTC AGG
                                  _  T  TT   A
GAM1169  LOC148837 3'  GAGCTCTGGAGTGCCCCT    85383    A   TG _
                                AG GGG  C CCAGAGCTC
                                || |||  | |||||||||
                                TC CCC  G GGTCTCGAG
                                 _  GT A
GAM1169  LOC148870 5'  GGAGCTCTGGAAGCTGATCT   79804     G_  GC
                                AGA  GGT  CCAGAGCTCC
                                |||  |||  ||||||||||
                                TCT  TCG  GGTCTCGAGG
                                  AG   AA
GAM1169  LOC149995 3'  GCTCTGGGCACCCTTTG     85985             _
                                CAGAGGGTGCCCAGAG C
                                |||||||||||||||| |
                                GTTTCCCACGGGTCTC G
                                          C
GAM1169  LOC150481 5'  GGAGCTCCCCCACCCTCT    80707        CCCA
                                AGAGGGTG   GAGCTCC
                                ||||||||   |||||||
                                TCTCCCAC   CTCGAGG
                                     CCC_
GAM1169  LOC150481 3'  GGAGCTCTAGGGCTATGTCT   80709     GGGT   _
                                AGA   GCCC AGAGCTCC
                                |||   |||| ||||||||
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                                TCT    CGGG TCTCGAGG
                                  GTAT    A
GAM1169  LOC153565 5'  GGAGCTCTACGCCTCCTG    81757     AG    CCC
                                CAG  GGTG   AGAGCTCC
                                |||  ||||   ||||||||
                                GTC  CCGC   TCTCGAGG
                                  CT    A__
GAM1169  LOC154386 3'  GGAACTCTCTATACCTTCTG   81989         CCC    C
                                CAGAGGGTG   AGAG TCC
                                |||||||||   |||| |||
                                GTCTTCCAT   TCTC AGG
                                     ATC    A
GAM1169  LOC157653 5'  GGAGCCTGCCACACCCTTT    82446        CC_   A
                                AGAGGGTG   CAG GCTCC
                                ||||||||   ||| |||||
                                TTTCCCAC   GTC CGAGG
                                     ACC   _
GAM1169  LOC157860 3'  AGTCCCTGGGCACCCCCT    87876    A        A_
                                AG GGGTGCCCAG  GCT
                                || ||||||||||  |||
                                TC CCCACGGGTC  TGA
                                 C         CC
GAM1169  LOC158191 3'  GGAGCTCACATCCAGCCTCTG  82679       G  CCCA_
                                CAGAGG TG     GAGCTCC
                                |||||| ||     |||||||
                                GTCTCC AC     CTCGAGG
                                   G  CTACA
GAM1169  LOC163183 5'  GGAGCTCTGGGACACCCTT    83324        _
                                GAGGGTG CCCAGAGCTCC
                                ||||||| ||||||||||
                                TTCCCAC GGGTCTCGAGG
                                     A
GAM1169  LOC196266 3'  GGAATCTGAGGCATCCTCTG   88653          _   GC
                                CAGAGGGTGCC CAGA  TCC
                                |||||||||| ||||  |||
                                GTCTCCTACGG GTCT  AGG
                                      A   A_
GAM1169  LOC196738 3'  GAACTTGGGGCAGCCCCTG    88892     A  _    A  C
                                CAG GGG TGCCC GAG TC
                                ||| ||| ||||| ||| ||
                                GTC CCC ACGGG TTC AG
                                  _  G    G  A
GAM1169  LOC200301 5'  GGAACATTGCACACCCTTTG   90144         CC   AGC
                                CAGAGGGTG  CAG   TCC
                                |||||||||  |||   |||
                                GTTTCCCAC  GTT   AGG
                                     AC   ACA
GAM1169  LOC200488 5'  GGAGCTTTATGCACACTC    91651     G    CC
                                GAG GTGC  AGAGCTCC
                                ||| ||||  ||||||||
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                                CTC CACG  TTTCGAGG
                                  A   TA
GAM1169  LOC201685 3'  GGAGCTCTGAGAGCAAGCTG  91843    AGGG  C__
                                CAG   TGC  CAGAGCTCC
                                |||   |||  |||||||||
                                GTC   ACG  GTCTCGAGG
                                  GA__  AGA
GAM1169  LOC203232 3'  GGAGCCCTACAACGCCACCCTC 71920       _ CC___  A
           T                     AGAGGGTG C    AG GCTCC
                                ||||||||  |    || |||||
                                TCTCCCAC G    TC CGAGG
                                     C CAACA  C
GAM1169  LOC204285 5'  GAGCTCTGGCGGAAATTTG  91018     GGG_  C
                                CAGA   TGCC AGAGCTC
                                ||||   |||| |||||||
                                GTTT   GCGG TCTCGAG
                                  AAAG   _
GAM1169  LOC221943 5'  GGAGCTCTGGTGAGCCCCTT  95622     T ___
                                GAGGG GC   CCAGAGCTCC
                                ||||| ||   ||||||||||
                                TTCCC CG   GGTCTCGAGG
                                  _ AGT
GAM1169  LOC253936 3'  GGAGCCCTACAACGCCACCCTC 96320       _ CC___  A
           T                     AGAGGGTG C    AG GCTCC
                                ||||||||  |    || |||||
                                TCTCCCAC G    TC CGAGG
                                     C CAACA  C
GAM1169  LOC254552 5'  GGAACTCCTCGCCCTTTG   96426       CCCA  C
                                CAGAGGGTG   GAG TCC
                                |||||||||   ||| |||
                                GTTTCCCGC   CTC AGG
                                     TC__  A
GAM1169  LOC254749 5'  GGTCTCAGGTACCCTCTG   97017        CA  CT
                                CAGAGGGTGCC  GAG  CC
                                ||||||||||  |||  ||
                                GTCTCCCATGG  CTC  GG
                                     A_  T_
GAM1169  LOC256158 5'  AGCCCTGAATGGCCACTCTCTG 99476       _ ___  A
                                CAGAGGGTG CC   CAG GCT
                                |||||||| ||   ||| |||
                                GTCTCTCAC GG   GTC CGA
                                     C  TAA  C
GAM1169  LOC256866 5'  GGAGCTCTGGGGTCCCTC   98014     TG
                                GAGGG  CCCAGAGCTCC
                                |||||  ||||||||||
                                CTCCC  GGGTCTCGAGG
                                  TG
GAM1169  LOC256949 3'  GAGCCCTGATCCACCCACTCTC 96983       CC_____  A
           TG                    CAGAGGGTG     CAG GCTC
                                |||||||||     ||| ||||
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                                GTCTCTCAC      GTC CGAG
                                     CCACCTA   C
GAM1169 LOC56181 5' GAGCTCTGACCTCATCTG    97275     __   GCC
                                CAGA  GGGT   CAGAGCTC
                                ||||  ||||   ||||||||
                                GTCT  TCCA   GTCTCGAG
                                  AC   ___
GAM1169 LOC90342 5' GGACTGCAAGCGCCCTCTG   63013        C__  AGC
                                CAGAGGGTGC   CAG   TCC
                                ||||||||||   |||   |||
                                GTCTCCCGCG   GTC   AGG
                                     AAC   ___
GAM1169 LOC91050 3' GGCCTGTTGAGCACCTTCTG  65377        C___  A
                                CAGAGGGTGC    CAG GCT
                                ||||||||||    ||| |||
                                GTCTTCCACG    GTC CGG
                                     AGTT  _
GAM1169 LOC92170 3' GGCCTCTGAGCACCTTCT    68909        C    _
                                AGAGGGTGC CAGAG CT
                                ||||||||| ||||| ||
                                TCTTCCACG GTCTC GG
                                     A    C
GAM1169 LOC93132 5' GAGCTCTAACGAAGCCCTCTG 71989        GCCC__
                                CAGAGGGT     AGAGCTC
                                ||||||||     |||||||
                                GTCTCCCG     TCTCGAG
                                     AAGCAA
GAM1169 LOC96597 5' GGAGCTCTAGAGGGCTGCCT  67462     _   ___
                                GGGT GCCC   AGAGCTCC
                                |||| ||||   ||||||||
                                TCCG CGGG   TCTCGAGG
                                  T    AGA
GAM1170 ASL      3' GTTTGACACAGCCTGGGCAACA 72396     GA   A      C
                                TGT  CCCA GCTGTGTC AAT
                                |||  |||| |||||||| |||
                                ACA  GGGT CGACACAG TTG
                                  AC   C       T
GAM1170 DHFR     3' GACCAGCTTGGGCAACA     7647      GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM1170 MMP19    3' GACCAGCTTGGGCAACA     11630     GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM1170 MMP19    3' GACCAGCTTGGGCAACA     43304     GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
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                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM1170  NR1I2    5'  AGATCAAAGTGGTGGGGTCACA 15294        AA  TG GTCCA
                                TGTGACCC  GC  T    ATCT
                                |||||||  ||  |    ||||
                                ACACTGGG  TG  G    TAGA
                                    G_  GT AAAC_
GAM1170  PRKY     3'  GACCAGCTTGGGCAACA     12375     GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM1170  RAD54B   3'  AGATTGTCAGCTTGGTCCACA  57062      AC      TGTC
                                TGTG  CCAAGCTG   CAATCT
                                ||||  ||||||||   ||||||
                                ACAC  GGTTCGAC   GTTAGA
                                  CT       T___
GAM1170  RCE1     3'  GATTTAACTTGGGTAACA    18890     G      C  T
                                TGT ACCCAAG TG GTC
                                ||| ||||||| || |||
                                ACA TGGGTTC AT TAG
                                  A      A  T
GAM1170  SFRS2IP  5'  GACCAGCTTGGGCAACA     17540     GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM1170  TEM7     3'  GACCAGCTTGGGCAACA     40259     GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM1170  FLJ13263 3'  AGATTGCTCCTTCAGCTCAGGG 47809      A   A_    TGTC__
            CCACA                  TGTG CCC  AGCTG     CAATCT
                                |||| |||  |||||     ||||||
                                ACAC GGG  TCGAC     GTTAGA
                                  C   AC    TTCCTC
GAM1170  FLJ14327 3'  GACCAGCTTGGGCAACA     46679     GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM1170  KIAA0172 3'  GACTGCTAGCCTGGGCACA   65596      A   A  _ _
                                TGTG CCCA GCT GT GTC
                                |||| |||| ||| || |||
                                ACAC GGGT CGA CG CAG
                                  _   C   T  T
GAM1170  KIAA1833 3'  GGACCACAGCCTGGGCACA   90753      A   A    _
                                TGTG CCCA GCTGTG TCC
                                |||| |||| |||||| |||
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                                ACAC GGGT CGACAC AGG
                                  _   C     C
GAM1170 KIAA1870 3' GACCAGCTTGGGCAACA     52901     GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM1170 MEGF11   3' ATTGGACAAATGTGGATACA   51599      AC   AGCTG
                                TGTG  CCA    TGTCCAAT
                                ||||  |||    ||||||||
                                ACAT  GGT    ACAGGTTA
                                  A_  GTAA_
GAM1170 MGC15631 3' GACCAGCCTGGGTGACA     52230     G    A   T
                                TGT ACCCA GCTG GTC
                                ||| ||||| |||| |||
                                ACA TGGGT CGAC CAG
                                  G    C   _
GAM1170 MGC32043 3' GACCAGGTCTTGGGCACA    58665      A     __  T
                                TGTG CCCAAG  CTG GTC
                                |||| ||||||  ||| |||
                                ACAC GGGTTC  GAC CAG
                                  _     TG  _
GAM1170 PLP1     3' ATTGGACATTAAGCATCACA   6755       CCCAA  __
                                TGTGA    GCT  GTGTCCAAT
                                |||||    |||  |||||||||
                                ACACT    CGA  TACAGGTTA
                                   A_____  AT
GAM1170 PTD012   3' GACCAGCTTGGGCAACA     26738     GA       T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
                                ACA  GGGTTCGAC CAG
                                  AC       _
GAM1170 STAF42   3' ATTGAATGTTTTTTGGGTCCA  54942    T       CT TG C
                                TG GACCCAAG  G  T CAAT
                                || ||||||||  |  | ||||
                                AC CTGGGTTT  T  A GTTA
                                  _       TT GT A
GAM1170 TRIM31   3' ACGCCAGCCTGGGTCACA    92649         A   _
                                TGTGACCCA GCTG TGT
                                ||||||||| |||| |||
                                ACACTGGGT CGAC GCA
                                     C   C
GAM1170 LOC142893 5' ATTGGAACATTTTTGGGTCCA  83757    T       CT   _
                                TG GACCCAAG  GTGT CCAAT
                                || ||||||||  |||| |||||
                                AC CTGGGTTT  TACA GGTTA
                                  _       T_   A
GAM1170 LOC143503 5' AGACTGGACAAAGGGGGTCACA 83882         AAGCTG     A
                                TGTGACCC     TGTCCA TCT
                                ||||||||     |||||| |||
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                                ACACTGGG     ACAGGT AGA
                                     GGAA__     C
GAM1170  LOC145824 5'  GACTTGCAGCTTGGATACACA  77986      AC_       __
                                TGTG   CCAAGCTGT  GTC
                                ||||   |||||||||  |||
                                ACAC   GGTTCGACG  CAG
                                  ATA        TT
GAM1170  LOC157603 3'  GACCAGCTTGGGCAACA     87786     GA        T
                                TGT  CCCAAGCTG GTC
                                |||  ||||||||| |||
                                ACA  GGGTTCGAC CAG
                                  AC        _
GAM1170  LOC221300 3'  GACCAGCTTGGGTAACA     93576     G         T
                                TGT ACCCAAGCTG GTC
                                ||| |||||||||| |||
                                ACA TGGGTTCGAC CAG
                                  A         _
GAM1170  LOC257608 3'  ACGCCAGCCTGGGTCACA    99664          A    _
                                TGTGACCCA GCTG TGT
                                ||||||||| ||||| |||
                                ACACTGGGT CGAC GCA
                                     C    C
GAM1170  LOC51337  3'  GACCAGAGCATCCTGGGTACA  34081      A    A___   G  _
                                TGTG CCCA    GCT TG TC
                                |||| ||||    ||| || ||
                                ACAT GGGT    CGA AC AG
                                  _    CCTA   G  C
GAM1171  ADCY1     5'  ACGACAATGTGAGCATC     94336          AG
                                GATGCTCACAT  GTTGT
                                ||||||||||  |||||
                                CTACGAGTGTA  CAGCA
                                       A_
GAM1171  C8orf1    3'  ATAGCATGATGTGAGCATC    16343          AG_
                                GATGCTCACAT   GTTGT
                                ||||||||||   |||||
                                CTACGAGTGTA   CGATA
                                       GTA
GAM1171  CDH12     3'  ATAGCTATGTGGCATCA     15776       T      G
                                TGATGC CACATAG TTGT
                                |||||| ||||||| ||||
                                ACTACG GTGTATC GATA
                                     _      _
GAM1171  HIP1      3'  ACAAACTTGTGAGCATCA     19242          T  G
                                TGATGCTCACA AG TTGT
                                |||||||||| || ||||
                                ACTACGAGTGT TC AACA
                                       _ A
GAM1171  DKFZp547I224 5'  ATGGCCTATGTGAGATCA    39948      G         TG
                                TGAT CTCACATAGGT  T
                                |||| ||||||||||  |
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                                ACTA GAGTGTATCCG  A
                                  _        GT
GAM1171  DKFZp761P1010 3'  GGCACAAATAAGCTCA     37943     T   CACA  GG
                                TGA GCT    TA  TTGTGCC
                                ||| |||    ||  |||||||
                                ACT CGA    AT  AACACGG
                                  _  _____  A_
GAM1171  FLJ13114  3'  ACAGGCCAGGTGAGCATCA    44889          ATA  _
                                TGATGCTCAC   GGT TGT
                                ||||||||||   ||| |||
                                ACTACGAGTG   CCG ACA
                                      GA_   G
GAM1171  FLJ23024  3'  TGGCACAACCTCAGCTCA    46851     T   CACAT
                                TGA GCT    AGGTTGTGCCA
                                ||| |||    ||||||||||
                                ACT CGA    TCCAACACGGT
                                  _  C_____
GAM1171  HNK-1ST   5'  ACAGCAAGGAAATGTGAGCCCC 17946    AT       AG_____
            A                    TG  GCTCACAT     GTTGT
                                ||  ||||||||     |||||
                                AC  CGAGTGTA     CGACA
                                 CC       AAGGAA
GAM1171  KIAA0459  3'  ACAATCATGTGAGCTCA     61639     T       A
                                TGA GCTCACAT GGTTGT
                                ||| |||||||| ||||||
                                ACT CGAGTGTA CTAACA
                                  _      _
GAM1171  KIAA1466  3'  ATAACCTATGAAACATCA    72405      CTCA
                                TGATG    CATAGGTTGT
                                |||||    ||||||||||
                                ACTAC    GTATCCAATA
                                   AAA_
GAM1171  KIAA1954  5'  ACAGCTTACTGAGCATCA    78220         CA
                                TGATGCTCA  TAGGTTGT
                                |||||||||  ||||||||
                                ACTACGAGT  ATTCGACA
                                      C_
GAM1171  PACSIN2   3'  ATGGCACAGATTGATGCGCACC 24296    A   T  _  TAGG
            A                    TG TGC CA CA    TTGTGCCAT
                                || ||| || ||    |||||||||
                                AC ACG GT GT    GACACGGTA
                                 C   C  A  TA__
GAM1171  PARVA     3'  GGCCCATGTGAGCATCA     37183           A  TTGT
                                TGATGCTCACAT GG    GCC
                                ||||||||||| ||    |||
                                ACTACGAGTGTA CC    CGG
                                          _ _____
GAM1171  RoXaN     3'  GCACACATGTGAGCACA     47292    A       AGGT
                                TG TGCTCACAT    TGTGC
                                || |||||||||    |||||
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                                AC ACGAGTGTA    ACACG
                                 _       C___
GAM1171  LOC148638 3'  ATGGCCATGTGAGCACA     79665    A       A   TG
                                TG TGCTCACAT GGT  T
                                || ||||||||| |||  |
                                AC ACGAGTGTA CCG  A
                                 _       _  GT
GAM1171  LOC148696 5'  GGCCAGCATTGAGCATCA    85348        CATAG    T
                                TGATGCTCA    GTTG GCC
                                |||||||||    |||| |||
                                ACTACGAGT    CGAC CGG
                                     TA___   _
GAM1171  LOC200609 5'  ATAACACTGTGCAATCATCA  91658      CTCA    _
                                TGATG   CATAG GTTGT
                                |||||   ||||| |||||
                                ACTAC   GTGTC CAATA
                                   TAAC    A
GAM1171  LOC203235 3'  ATGACACAACCTGAGAGGCACC 92097    A   CACA       C
            A                    TG TGCT    TAGGTTGTG CAT
                                || ||||    ||||||||| |||
                                AC ACGG    GTCCAACAC GTA
                                 C   AGA_       A
GAM1171  LOC219667 3'  GCCAGCCTATGCAACATCA   92948      CTCA       T
                                TGATG   CATAGGTTG GC
                                |||||   ||||||||| ||
                                ACTAC   GTATCCGAC CG
                                   AAC_       _
GAM1171  LOC220514 3'  ATGGCACAGATTGATGCGCACC 61072    A  T  _  TAGG
            A                    TG TGC CA CA    TTGTGCCAT
                                || ||| || ||   |||||||||
                                AC ACG GT GT    GACACGGTA
                                 C   C  A  TA__
GAM1171  LOC221463 3'  GGCATGGCACGTGAGCAGCA  93706    A     ATAG  TG
                                TG TGCTCAC    GT  TGCC
                                || |||||||   ||  ||||
                                AC ACGAGTG    CG  ACGG
                                 G      CA__  GT
GAM1172  ADH7    3'  AAGATTAAGGGACGGGC     7268       ACA   G
                                GCCC   TCT TTTAATCTT
                                ||||   ||| |||||||||
                                CGGG   AGG GAATTAGAA
                                  C__   _
GAM1172  ARAF1    5'  GGAAGGACTTCAGATGTGAGC  64644    C       TTTAA
                                GC CACATCTG    TCTTCC
                                || ||||||||    ||||||
                                CG GTGTAGAC    GGAAGG
                                 A       TTCA_
GAM1172  CEACAM6  3'  GGAAGACTGGCAGATTGGACCA 11756    C   C      TAA
                                TGG CCA ATCTGTT   TCTTCC
                                ||| ||| |||||||   ||||||
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                                ACC GGT TAGACGG   AGAAGG
                                  A  _      TC_
GAM1172 CLECSF12 3' GGATTACAGATGTGAGCCA   77214     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1172 CYP1A2   3' GGATTAACAGGTATGAACCA  7518     CC  C     T
                                TGG  CA ATCTGTT AATCT
                                |||  || ||||||| |||||
                                ACC  GT TGGACAA TTAGG
                                  AA  A     _
GAM1172 ENG      3' GAACTTGAAACAGATTCAGGCC 5496      CAC       AATC
            A                    TGGCC   ATCTGTTT   TTC
                                |||||   ||||||||   |||
                                ACCGG   TAGACAAA   AAG
                                   ACT       GTTC
GAM1172 ERCC3    3' GAATAAACAGAATGGACCA   5506     C   CA      A
                                TGG CCA  TCTGTTTA TC
                                ||| |||  |||||||| ||
                                ACC GGT  AGACAAAT AG
                                  A  A_       A
GAM1172 HTLF     5' AAGATTGCAGGATTAAGCCA  10973     CCACA    TT
                                TGGC    TCTGT  AATCTT
                                ||||    |||||  ||||||
                                ACCG    GGACG  TTAGAA
                                  AATTA    __
GAM1172 MS4A8B   3' GATTTTAAACAGATGTTAACCA 49588    CCC         TCT
                                TGG   ACATCTGTTTAA   TC
                                |||   ||||||||||||   ||
                                ACC   TGTAGACAAATT   AG
                                  AAT         TT_
GAM1172 PRKAA2   3' GAAGATTAAAAAGTAAAGAACC 21811    CCCACAT  G
            A                    TGG      CT TTTAATCTTC
                                |||      || ||||||||||
                                ACC      GA AAATTAGAAG
                                  AAGAAAT  A
GAM1172 ASE-1    3' GGATAACAGGTGTGAGCCA   24983     C       TA
                                TGGC CACATCTGTT  ATCT
                                |||| ||||||||||  ||||
                                ACCG GTGTGGACAA  TAGG
                                  A       __
GAM1172 CITED2   3' GGAAGATTAAACAGATGTGGGC 21403
            CA                    TGGCCCACATCTGTTTAATCTTCC
                                |||||||||||||||||||||||||
                                ACCGGGTGTAGACAAATTAGAAGG

GAM1172 DKFZP564K0322 3' GGATTACAGATGTGAGCCA   50188     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
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                                ACCG GTGTAGACA  TTAGG
                                  A      __
GAM1172 DZIP1    3' GAAGATTATTCCAGAAGCCA  30703    CCACA   TT_
                                TGGC   TCTG  TAATCTTC
                                ||||   ||||  ||||||||
                                ACCG   AGAC  ATTAGAAG
                                  A____   CTT
GAM1172 FLJ22969 3' GGATTACAGATGTGAGCCA   69211    C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A      __
GAM1172 HSNOV1   3' GGATTACAGATGTGAACCA   34437    CC      TT
                                TGG  CACATCTGT  AATCT
                                |||  |||||||||  |||||
                                ACC  GTGTAGACA  TTAGG
                                  AA      __
GAM1172 IMPACT   3' GAATTACAGGTGTGAGCCA   38006    C       TTAATC
                                TGGC CACATCTGT    TTC
                                |||| |||||||||     |||
                                ACCG GTGTGGACA    AAG
                                  A      TT____
GAM1172 JAM1     3' GGATTACAGATGTGAGCCA   34234    C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A      __
GAM1172 JAM1     3' GGATTACAGATGTGAGCCA   58499    C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A      __
GAM1172 JAM1     3' GGATTACAGATGTGAGCCA   58520    C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A      __
GAM1172 JAM1     3' GGATTACAGATGTGAGCCA   58548    C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A      __
GAM1172 JAM1     3' GGATTACAGATGTGAGCCA   58577    C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A      __
GAM1172 KIAA0210 5' GAATTACAGGTGTGAGCCA   29159    C       TTAATC
                                TGGC CACATCTGT    TTC
                                |||| |||||||||     |||
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                                ACCG GTGTGGACA     AAG
                                  A       TT____
GAM1172  KIAA0280  3'  GAGCATAAACAGATGTGGTCCA 93301     C          AT
                                TGG CCACATCTGTTTA  CTT
                                ||| ||||||||||||  |||
                                ACC GGTGTAGACAAAT  GAG
                                  T          AC
GAM1172  KIAA0285  5'  GAAGATTGAGCTTGACCGGACC 29684     C  ACA  T_
            A                    TGG CC   TC  GTTTAATCTTC
                                ||| ||   ||  ||||||||||
                                ACC GG   AG  CGAGTTAGAAG
                                  A  CC_  TT
GAM1172  KIAA0356  3'  GGAAGACCCTCAGATGTGGCCA 66778      C      TTTAA
                                TGGCC ACATCTG     TCTTCC
                                ||||| |||||||     ||||||
                                ACCGG TGTAGAC     AGAAGG
                                   _      TCCC_
GAM1172  KIAA1354  3'  GGAAGATTGTCAGCATGT    61576     _  TT
                                ACAT CTG  TAATCTTCC
                                |||| |||  |||||||||
                                TGTA GAC  GTTAGAAGG
                                  C   T_
GAM1172  KIAA1466  3'  ATTAAATAGTATGGGCCA    72406       CAT
                                TGGCCCA   CTGTTTAAT
                                |||||||   |||||||||
                                ACCGGGT   GATAAATTA
                                    AT_
GAM1172  KIAA1468  5'  AAGATCTTGTAGATGTGGCCA  93423      C      TTTA
                                TGGCC ACATCTG    ATCTT
                                ||||| |||||||    |||||
                                ACCGG TGTAGAT    TAGAA
                                   _      GTTC
GAM1172  MRPS26    3'  GGAAGATTACAGTCTGAGGGCC 48723       A  T_   TT
            A                    TGGCCC CA  CTGT  AATCTTCC
                                |||||| ||  ||||  ||||||||
                                ACCGGG GT  GACA  TTAGAAGG
                                   A  CT   __
GAM1172  PANX3     3'  AAGATTAATAAAGATGTAAACC 54765    CCC     GT_
                                GG   ACATCT   TTAATCTT
                                ||   ||||||   ||||||||
                                CC   TGTAGA   AATTAGAA
                                  AAA     AAT
GAM1172  PLCL1     3'  AAGATTAAACAGATGATG    21714    _
                                CA CATCTGTTTAATCTT
                                || ||||||||||||||
                                GT GTAGACAAATTAGAA
                                  A
GAM1172  SPRY4     3'  GAAGACAGAACACAGATGTGGA 49013    GC        _  AA_
            CA                     TG  CCACATCTGT TT   TCTTC
                                ||  |||||||||| ||   |||||
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                                AC  GGTGTAGACA AA   AGAAG
                                 A_         C  GAC
GAM1172  WNT10A    3'  GAAGAGGAGATTGGACCA    48170     C   C    G TTAA
                                TGG CCA ATCT T    TCTTC
                                ||| ||| |||| |    |||||
                                ACC GGT TAGA G    AGAAG
                                  A   _    G _____
GAM1172  LOC113523 5'  GGATTACAGATGTGAGCCA    73427      C        TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A        __
GAM1172  LOC124216 3'  GGATTACAGATGTGAGCCA    74736      C        TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A        __
GAM1172  LOC130639 5'  GGATTAAAGACGTGAGCCA    75480      C   A   GT
                                TGGC CAC TCT  TTAATCT
                                |||| ||| |||  |||||||
                                ACCG GTG AGA  AATTAGG
                                  A  C   __
GAM1172  LOC144202 5'  GGAAGATTCGATGGACATGGAC 77226     GC   CA     T
            A                    TG  CCA  TCTGTT AATCTTCC
                                ||  |||  |||||| ||||||||
                                AC  GGT  AGGTAG TTAGAAGG
                                 A_  AC     C
GAM1172  LOC149171 5'  GAATTACAGGTGTGAGCCA    79967      C        TTAATC
                                TGGC CACATCTGT      TTC
                                |||| |||||||||      |||
                                ACCG GTGTGGACA      AAG
                                  A        TT_____
GAM1172  LOC150245 3'  GAAGCAAGACAGATGTGGGCC  86112              AAT
                                GGCCCACATCTGTTT   CTTC
                                ||||||||||||||   ||||
                                CCGGGTGTAGACAGA   GAAG
                                         AC_
GAM1172  LOC152620 3'  AGATTACAGATGTGAGCCA    60703      C        TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGA
                                  A        __
GAM1172  LOC153577 3'  GAAGATTTTATGTGACCA     87239     CC     CTGTTT
                                TGG  CACAT      AATCTTC
                                |||  |||||      |||||||
                                ACC  GTGTA      TTAGAAG
                                  A_     TT_____
GAM1172  LOC154930 3'  GAATAACAGGTGTGAGCCA    82091      C        TAATC
                                TGGC CACATCTGTT    TTC
                                |||| ||||||||||    |||
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                                ACCG GTGTGGACAA    AAG
                                  A        T____
GAM1172  LOC157507 5'  AAGATTAAACCATGGATG    82376      ___
                                CATCT   GTTTAATCTT
                                |||||   ||||||||||
                                GTAGG   CAAATTAGAA
                                  TAC
GAM1172  LOC158014 5'  AGAATTACAGGTGTGAGCCA   82549      C       TTAA
                                TGGC CACATCTGT    TCT
                                |||| |||||||||    |||
                                ACCG GTGTGGACA    AGA
                                  A        TTA_
GAM1172  LOC158668 3'  AGATTACAGATGTGAGCCA    69892      C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGA
                                  A        __
GAM1172  LOC170409 5'  GGATTACAGATGTGAGCCA    83745      C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A        __
GAM1172  LOC200282 5'  GAAATTACAGGTGTGAGCCA   90099      C       TTAA
                                TGGC CACATCTGT    TC
                                |||| |||||||||    ||
                                ACCG GTGTGGACA    AG
                                  A        TTAA
GAM1172  LOC220595 3'  GGAAGACCTCAGATGTGACCA  92778     CC      TTTAA
                                TGG  CACATCTG    TCTTCC
                                |||  ||||||||    ||||||
                                ACC  GTGTAGAC    AGAAGG
                                  A_       TCC__
GAM1172  LOC253805 3'  GGATTACAGATGTGAGCCA    98179      C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A        __
GAM1172  LOC56181  5'  GGATTACAGATGTGAGCCA    97278      C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A        __
GAM1172  LOC91547  3'  GGATTACAGATGTGAGCCA    67004      C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A        __
GAM1173  CDA       3'  CCACCTGGAGAACTTCATAAAG 10127     CTG    TGCAA
                A                TCT   ATGA    TCCAGGTGG
                                |||   ||||    |||||||||
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                                AGA  TACT    AGGTCCACC
                                  AA_   TCAAG
GAM1173 DCN     3' CCACCTGGACACAACACCA  56874    A  A  CAA
                                TG TG TG   TCCAGGTGG
                                || || ||   |||||||||
                                AC AC AC   AGGTCCACC
                                 C  A  AC_
GAM1173 DOM3Z   5' CTGAATGATTGCATCATCG   19750          ___
                                TGATGATGCAATC   CAG
                                ||||||||||||   |||
                                GCTACTACGTTAG   GTC
                                       TAA
GAM1173 DOM3Z   5' CTGAATGATTGCATCATCG   51574          ___
                                TGATGATGCAATC   CAG
                                ||||||||||||   |||
                                GCTACTACGTTAG   GTC
                                       TAA
GAM1173 MTF1    3' ACCCTTGCTCCATCAGAGA   21049        AT   TCCA
                                TCTCTGATG  GCAA   GGT
                                |||||||||  ||||   |||
                                AGAGACTAC  CGTT   CCA
                                     CT   C___
GAM1173 TGFB1   3' CCACCTGGGGCCCCATTAAAGA 7251     C    AT  AA
                                TCT TGATG  GC  TCCAGGTGG
                                ||| |||||  ||  |||||||||
                                AGA ATTAC  CG  GGGTCCACC
                                  A    CC  __
GAM1173 cerk    3' TGGACCACATTATCAGAGA   43171          CAA
                                TCTCTGATGATG   TCCA
                                ||||||||||||   ||||
                                AGAGACTATTAC   AGGT
                                       ACC
GAM1173 ENPP4   3' CCAGTATTTGCATCACAGA   30714     A      TCCAGG
                                TCTG TGATGCAA     TGG
                                |||| ||||||||     |||
                                AGAC ACTACGTT     ACC
                                  _       TATG__
GAM1173 FLJ12057 3' CCACCGTCACATCATCAGA   45794         CAATCCA
                                TCTGATGATG      GGTGG
                                ||||||||||      |||||
                                AGACTACTAC      CCACC
                                     ACTG___
GAM1173 FLJ12985 3' CCTCATTACACATCAGAGA   46795        A  C   CC
                                TCTCTGATG TG AAT  AGG
                                ||||||||| || |||  |||
                                AGAGACTAC AC TTA  TCC
                                     _ A   C_
GAM1173 FLJ14011 5' CATCCTACTTCATCAGAGA   42315         TGCAATCC  _
                                TCTCTGATGA      AGG TG
                                ||||||||||      ||| ||
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                                AGAGACTACT       TCC AC
                                     TCA_____   T
GAM1173  FLJ22031  3'  CCACAATATTTCACACCATTAG 47587         A  CAATCCAG_
             AGA                   TCTCTGATG TG       GTGG
                                   ||||||||| ||       ||||
                                   AGAGATTAC AC       CACC
                                      C  ACTTTATAA
GAM1173  KIAA0121  3'  CACCTGGCCCACCAGAGG    73046       A  ATGCAAT
                                   TCTCTG TG      CCAGGTG
                                   |||||| ||      |||||||
                                   GGAGAC AC      GGTCCAC
                                      C  CC_____
GAM1173  KIAA0720  3'  CCACCTTCAGCCACCATCAGAG 62977         A  CAATCC
                                   CTCTGATG TG     AGGTGG
                                   |||||||| ||     ||||||
                                   GAGACTAC AC     TCCACC
                                        C  CGACT_
GAM1173  KIAA1437  3'  CACCTGGACTTCAGCAGA    61213      A   TGCAA
                                   TCTG TGA     TCCAGGTG
                                   |||| |||     ||||||||
                                   AGAC ACT     AGGTCCAC
                                     G   TC___
GAM1173  KIAA1710  3'  CCACGATTTAAACCATCAGAGA 63176         ATGC_   CAG
                                   TCTCTGATG    AATC   GTGG
                                   |||||||||    ||||   ||||
                                   AGAGACTAC    TTAG   CACC
                                        CAAAT   ___
GAM1173  PP1628    5'  CCACCCAAGATCTTATCAGAGA 48074         TGCA   CA_
                                   TCTCTGATGA    ATC   GGTGG
                                   ||||||||||    |||   |||||
                                   AGAGACTATT    TAG   CCACC
                                         C___    AAC
GAM1173  SARM      3'  CTTGGCCACATCATCAGA    31289          CAAT
                                   TCTGATGATG    CCAGG
                                   ||||||||||    |||||
                                   AGACTACTAC    GGTTC
                                         ACC_
GAM1173  SE57-1    3'  CACCACACATCAGAGA      48164          A  CAATCCA
                                   TCTCTGATG TG      GGTG
                                   ||||||||| ||      ||||
                                   AGAGACTAC AC      CCAC
                                        _  A_______
GAM1173  LOC129138 3'  CCACCTGGACTGGCTCAGTGA  57921    T    TGAT  AA_
                                   TC CTGA    GC   TCCAGGTGG
                                   || ||||    ||   |||||||||
                                   AG GACT    CG   AGGTCCACC
                                    T    _____  GTC
GAM1173  LOC163081 5'  CCTCACTGATCATCAGAGA    83310          G  ATCC
                                   TCTCTGATGAT CA    AGG
                                   |||||||||| ||    |||
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                                AGAGACTACTA GT    TCC
                                      _ CAC_
GAM1173  LOC199786 3'  CCATTATTTCTGCATATCAGAG 89744         A    ATCCA
             A                  TCTCTGATG TGCA     GGTGG
                                |||||||||  ||||     |||||
                                AGAGACTAT ACGT     TTACC
                                      _   CTTTA
GAM1173  LOC254122 3'  CCTTGATGACACCATCAGAGA  96394         A  CA   C
                                TCTCTGATG TG  ATC AGG
                                |||||||||  ||  |||  |||
                                AGAGACTAC AC  TAG TCC
                                      C  AG   T
GAM1173  LOC255624 3'  CCTCATTACACATCAGAGA    96162         A  C   CC
                                TCTCTGATG TG AAT  AGG
                                |||||||||  ||  |||  |||
                                AGAGACTAC AC TTA  TCC
                                      _ A   C_
GAM1173  LOC51277  3'  GGAATTCATCATCAGAGA     80841           CAA
                                TCTCTGATGATG   TCC
                                ||||||||||||   |||
                                AGAGACTACTAC   AGG
                                       TTA
GAM1174  CYP7B1    5'  ACGGTGACATTCCTGTCT     17874      _   C
                                GGAT GGAA GTCACCGT
                                ||||  ||||  ||||||||
                                TCTG CCTT CAGTGGCA
                                  T    A
GAM1174  FLOT1     3'  ACAGTGAGGTCCCACCCCT    20541      A   A  G    C
                                AGGG TGG AC TCAC GT
                                ||||  |||  ||  ||||  ||
                                TCCC ACC TG AGTG CA
                                  C   C  G    A
GAM1174  LDB1      5'  ACGGCAACGCCTTTCCCCCCT  15308      AT    ___   CA
                                AGGG  GGAA   CGT  CCGT
                                ||||  ||||   |||  ||||
                                TCCC  CCTT   GCA  GGCA
                                  C_    TCC   AC
GAM1174  MAGEA8    3'  ACAGTGTGGACCATCTCT     19318        AA  T   C
                                AGGGATGG  CG CAC GT
                                ||||||||  ||  |||  ||
                                TCTCTACC  GT GTG CA
                                     AG  _   A
GAM1174  NAV2      3'  ACGGTATGTTTCCATCCT     60788         _   C
                                GGGATGGAA CGT ACCGT
                                |||||||||  |||  |||||
                                TCCTACCTT GTA TGGCA
                                      T   _
GAM1174  PIK3CG    3'  ACAGTGAGACTCCATCTCT    12116         ACG    C
                                AGGGATGGA   TCAC GT
                                |||||||||   ||||  ||
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                                TCTCTACCT  AGTG CA
                                     CAG   A
GAM1174 SULT2A1  3' ACGGTGAAACCCCATCTCT  72221       AACG
                                AGGGATGG   TCACCGT
                                ||||||||   |||||||
                                TCTCTACC   AGTGGCA
                                     CCAA
GAM1174 TP53     5' ACGGTGACACGCTTCCCT   6790      T  AAC
                                AGGGA GG  GTCACCGT
                                |||||  ||  ||||||||
                                TCCCT TC  CAGTGGCA
                                   _  GCA
GAM1174 XRCC2    3' ACGGTGAAACCCCATCTCT  19485       AACG
                                AGGGATGG   TCACCGT
                                ||||||||   |||||||
                                TCTCTACC   AGTGGCA
                                     CCAA
GAM1174 APG3     5' ACGGCTGCACTTTCCATCCC  42826       C  _  _
                                GGGATGGAA GT CA CCGT
                                |||||||||  ||  ||  ||||
                                CCCTACCTT CA GT GGCA
                                     T  C  C
GAM1174 C20orf106 3' ACGGTGAAACCCCATCTCT  55889       AACG
                                AGGGATGG   TCACCGT
                                ||||||||   |||||||
                                TCTCTACC   AGTGGCA
                                     CCAA
GAM1174 C6orf5   3' ACGGTGAAACTCCATCTCT  31961       ACG
                                AGGGATGGA  TCACCGT
                                |||||||||  |||||||
                                TCTCTACCT  AGTGGCA
                                     CAA
GAM1174 CBX6     3' ACGGTAAGTTGGGACCCATCCC 27403       _____  GTC
           T                     AGGGATGG   AAC  ACCGT
                                 ||||||||   |||  |||||
                                 TCCCTACC   TTG  TGGCA
                                     CAGGG  AA_
GAM1174 DEGS     3' ACGGTGAAACCCCATCTCT  59265       AACG
                                AGGGATGG   TCACCGT
                                ||||||||   |||||||
                                TCTCTACC   AGTGGCA
                                     CCAA
GAM1174 DGKD     3' ACGGTGAAGATCTCCATCCTT 60101       ACG__
                                AGGGATGGA   TCACCGT
                                |||||||||   |||||||
                                TTCCTACCT   AGTGGCA
                                     CTAGA
GAM1174 DKFZP434D193 3' ACAGTGACTTATTATCCTT  90292       AAC   C
                                AGGGATGG  GTCAC GT
                                ||||||||  |||||  ||
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                                TTCCTATT   CAGTG CA
                                    ATT    A
GAM1174  DKFZP434L1123 5'  ACGAGTGCGTCCATTCCT    50493        A  T  _
                                AGGGATGGA CG CAC CGT
                                ||||||||| || ||| |||
                                TCCTTACCT GC GTG GCA
                                    _ _  A
GAM1174  FHX      3'  ACGAATGATCTTCCCATCCCT  37917        _ C   C_
                                AGGGATGG AA GTCA  CGT
                                |||||||| || ||||  |||
                                TCCCTACC TT TAGT  GCA
                                    C  C   AA
GAM1174  FLJ10520  5'  ACAGTGACATTGTCGTCCTT   36695        AAC_   C
                                AGGGATGG   GTCAC GT
                                ||||||||   ||||| ||
                                TTCCTGCT   CAGTG CA
                                    GTTA   A
GAM1174  FLJ13441  3'  ACGTGTGGCTCCAGCCCT    43907     A   AC   _
                                AGGG TGGA  GTCAC CGT
                                |||| ||||  ||||| |||
                                TCCC ACCT  CGGTG GCA
                                  G   __   T
GAM1174  FLJ14225  3'  ACGGTGAAACCCCATCTCT   46380        AACG
                                AGGGATGG   TCACCGT
                                ||||||||   |||||||
                                TCTCTACC   AGTGGCA
                                    CCAA
GAM1174  FLJ20783  3'  ACGGTGAAACCCCATCTCT   36092        AACG
                                AGGGATGG   TCACCGT
                                ||||||||   |||||||
                                TCTCTACC   AGTGGCA
                                    CCAA
GAM1174  HES2     3'  ACGGTGAAACCCCATCTCT   39366        AACG
                                AGGGATGG   TCACCGT
                                ||||||||   |||||||
                                TCTCTACC   AGTGGCA
                                    CCAA
GAM1174  KIAA0252  3'  ACGGTGAAACCCCATCTCT   63447        AACG
                                AGGGATGG   TCACCGT
                                ||||||||   |||||||
                                TCTCTACC   AGTGGCA
                                    CCAA
GAM1174  KIAA0746  3'  ACAGTGCGTGCTTCATCCCT   69984         __  T  C
                                AGGGATGGA  ACG CAC GT
                                |||||||||  ||| ||| ||
                                TCCCTACTT  TGC GTG CA
                                    CG  _  A
GAM1174  KIAA1243  3'  ACAGTGACGTTAGGATTCT   74019      GG_      C
                                GGGAT   AACGTCAC GT
                                |||||   |||||||| ||
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                                TCTTA  TTGCAGTG CA
                                  GGA      A
GAM1174 KIAA1328 3' ACGGTGAAACCCCATCTCT  62314       AACG
                                AGGGATGG  TCACCGT
                                ||||||||  |||||||
                                TCTCTACC  AGTGGCA
                                    CCAA
GAM1174 KIAA1486 3' ACGGTGAGACCCCATCTCT  67965       AACG
                                AGGGATGG  TCACCGT
                                ||||||||  |||||||
                                TCTCTACC  AGTGGCA
                                    CCAG
GAM1174 KIAA1948 3' ACGGTGAAACCCCATCTCT  83288       AACG
                                AGGGATGG  TCACCGT
                                ||||||||  |||||||
                                TCTCTACC  AGTGGCA
                                    CCAA
GAM1174 MGC13007 3' ACAGTGACGTTGTACTCT   51275    A G     C
                                AGGG TG AACGTCAC GT
                                |||| || |||||||| ||
                                TCTC AT TTGCAGTG CA
                                  _ G      A
GAM1174 MGC16142 3' ACGGTTGGCTGTTCCATCCT  52257        _  _
                                GGGATGGAAC GTCA CCGT
                                |||||||||| |||| ||||
                                TCCTACCTTG CGGT GGCA
                                     T   T
GAM1174 MGC2721  3' ACGATGCGAAACCATCCCT   52188       AA_ T C
                                AGGGATGG  CG CA CGT
                                ||||||||  || || |||
                                TCCCTACC  GC GT GCA
                                    AAA _ A
GAM1174 MGC2865  3' ACGGCATTGGCTCCATCCC   51455       AC  ___
                                GGGATGGA GTCA  CCGT
                                ||||||||  ||||  ||||
                                CCCTACCT CGGT  GGCA
                                    __   TAC
GAM1174 MGC29891 3' ACGGTGAAACTCCATCTCT   58844       ACG
                                AGGGATGGA  TCACCGT
                                |||||||||  |||||||
                                TCTCTACCT  AGTGGCA
                                    CAA
GAM1174 MGC4663  3' ACGGTGAAACCCCATCTCT   44779       AACG
                                AGGGATGG  TCACCGT
                                ||||||||  |||||||
                                TCTCTACC  AGTGGCA
                                    CCAA
GAM1174 PRDM8    5' ACGGCCTCGGCAACTCCATCCC 39970       AC_  A___
                                GGGATGGA  GTC   CCGT
                                ||||||||  |||  ||||
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                                CCCTACCT  CGG   GGCA
                                    CAA  CTCC
GAM1174 PRO2949  3' ACGGTGAAACCCCATCTCT  38217       AACG
                                AGGGATGG   TCACCGT
                                ||||||||   |||||||
                                TCTCTACC   AGTGGCA
                                    CCAA
GAM1174 RoXaN    3' ACGGTGAAACCCCATCTCT  47270       AACG
                                AGGGATGG   TCACCGT
                                ||||||||   |||||||
                                TCTCTACC   AGTGGCA
                                    CCAA
GAM1174 Rpo1-2   3' ACGGTGACAAGTCTCCTT   39208     T  AAC
                                AGGGA GG   GTCACCGT
                                |||||  ||  ||||||||
                                TTCCT CT   CAGTGGCA
                                   _  GAA
GAM1174 Rpo1-2   3' ACGGTGACAAGTCTCCTT   39209     T  AAC
                                AGGGA GG   GTCACCGT
                                |||||  ||  ||||||||
                                TTCCT CT   CAGTGGCA
                                   _  GAA
GAM1174 SE57-1   3' ACAGTGACATAAGTTCATCTC 48162       AC___    C
                                GGGATGGA    GTCAC GT
                                ||||||||    |||||  ||
                                CTCTACTT    CAGTG CA
                                    GAATA    A
GAM1174 LOC121133 5' ACAGTGACGTTTCTCTCC   76508    AT       C
                                GGG  GGAACGTCAC GT
                                |||  ||||||||||  ||
                                CCT  CTTTGCAGTG CA
                                  CT        A
GAM1174 LOC126282 3' ACGGTGAAACCCCATCTCT  74937       AACG
                                AGGGATGG   TCACCGT
                                ||||||||   |||||||
                                TCTCTACC   AGTGGCA
                                    CCAA
GAM1174 LOC126917 3' GGTGCCCCGTCTCCATCCC  75097       _  T__
                                GGGATGGA ACG  CACC
                                |||||||| |||  ||||
                                CCCTACCT TGC  GTGG
                                    C  CCC
GAM1174 LOC145482 3' ACGGTGAAACCCCATCTCT  77737       AACG
                                AGGGATGG   TCACCGT
                                ||||||||   |||||||
                                TCTCTACC   AGTGGCA
                                    CCAA
GAM1174 LOC146923 3' ACGGTGAAACCCCATCTCT  78792       AACG
                                AGGGATGG   TCACCGT
                                ||||||||   |||||||
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                                TCTCTACC   AGTGGCA
                                    CCAA
GAM1174  LOC147057 3'  ACGAGTGCCCTCCATCCC   84972       AC T  _
                                GGGATGGA  G CAC CGT
                                ||||||||  | ||| |||
                                CCCTACCT  C GTG GCA
                                    CC _   A
GAM1174  LOC149267 5'  ACAGTGGCTTCCTTCCATCCT  57474       C___   C
                                GGGATGGAA   GTCAC GT
                                |||||||||   ||||| ||
                                TCCTACCTT   CGGTG CA
                                    CCTT    A
GAM1174  LOC149912 3'  ACAGTGACACTCTATCTC   85878       AC    C
                                GGGATGGA  GTCAC GT
                                ||||||||  ||||| ||
                                CTCTATCT  CAGTG CA
                                    CA    A
GAM1174  LOC154877 3'  ACGGCACGTTCCATCTCT   87518         CA
                                AGGGATGGAACGT  CCGT
                                ||||||||||||  ||||
                                TCTCTACCTTGCA  GGCA
                                      C_
GAM1174  LOC202038 3'  ACGGTGAAACCCCATCTCT   90616       AACG
                                AGGGATGG   TCACCGT
                                ||||||||   |||||||
                                TCTCTACC   AGTGGCA
                                    CCAA
GAM1174  LOC202781 3'  ACGGTGAAACCCCGTCCCT   91966       AACG
                                AGGGATGG   TCACCGT
                                ||||||||   |||||||
                                TCCCTGCC   AGTGGCA
                                    CCAA
GAM1174  LOC203427 5'  ACGGGGCTTCCCGTCCCT   90918       AAC  A
                                AGGGATGG   GTC CCGT
                                ||||||||   ||| ||||
                                TCCCTGCC   CGG GGCA
                                    CTT  _
GAM1174  LOC221271 3'  ACGGTGAAACCCCATCTCT   93488       AACG
                                AGGGATGG   TCACCGT
                                ||||||||   |||||||
                                TCTCTACC   AGTGGCA
                                    CCAA
GAM1174  LOC257211 3'  ACGGTGAAAACCCATCTCT   97611       AACG
                                AGGGATGG   TCACCGT
                                ||||||||   |||||||
                                TCTCTACC   AGTGGCA
                                    CAAA
GAM1174  LOC92299  3'  ACGGTGAAACCCCATCTCT   69357       AACG
                                AGGGATGG   TCACCGT
                                ||||||||   |||||||
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                                TCTCTACC    AGTGGCA
                                    CCAA
GAM1174  LOC92465  5'  ATGGTGAAACTCCATCCCT    69942          ACG
                                AGGGATGGA   TCACCGT
                                |||||||||   |||||||
                                TCCCTACCT   AGTGGTA
                                    CAA
GAM1175  ACTG2     5'  GTCACTGGGAGAAGAACCTCTC 9660      C   _  GA  _
             A                   TGA AGGT CT  TC CCCAGTGAC
                                 ||| |||| ||  || |||||||||
                                 ACT TCCA GA  AG GGGTCACTG
                                   C   A __  A
GAM1175  BCL10     3'  GGTCACTGATGGGAAAACTGCC 15372     CTGA_   __
                                 GGT    TCCC  CAGTGACC
                                 |||    ||||  ||||||||
                                 CCG    AGGG  GTCACTGG
                                   TCAAA    TA
GAM1175  BIN3      3'  GGTCACTGAGGACTGGTACCT  38580      _  GA   C
                                 AGGT CT  TCC CAGTGACC
                                 |||| ||  ||| ||||||||
                                 TCCA GG  AGG GTCACTGG
                                   T  TC   A
GAM1175  CIT       3'  GGTCACTGAAAATGGGTCTTTC 70305     C  GT  GATCCC
             A                   TGA AG  CT     CAGTGACC
                                 ||| ||  ||     ||||||||
                                 ACT TC  GG     GTCACTGG
                                   T  TG  TAAAA_
GAM1175  CTSB      3'  GGCCAAACATCAGACCTGTC  65367          CCCCAG  A
                                 GACAGGTCTGAT     TG CC
                                 ||||||||||||     || ||
                                 CTGTCCAGACTA     AC GG
                                        CAA___  C
GAM1175  GRIK3     3'  GCTTGGGGACCAGAGCTGCCA  7719     A   G    A    _
                                 TG CAG TCTG TCCCCA GT
                                 || ||| |||| |||||| ||
                                 AC GTC AGAC AGGGGT CG
                                  C   G    C     T
GAM1175  KCNA7     3'  TCCTGAACCAGGCCTGTCA   49908          ATCCC   T
                                 TGACAGGTCTG    CAG GA
                                 ||||||||||     ||| ||
                                 ACTGTCCGGAC    GTC CT
                                        CAA__   _
GAM1175  LIPE      3'  GGTCACCGAGACGGCTGGACCT 19303    A       AT CCCA__
             GCA                   TG CAGGTCTG  C     GTGACC
                                   || ||||||||  |     ||||||
                                   AC GTCCAGGT  G     CACTGG
                                    _       CG CAGAGC
GAM1175  PLAC1     5'  GGCACGAGGATCAGACC     41720          CCA   A
                                 GGTCTGATCC   GTG CC
                                 ||||||||||   ||| ||
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                                CCAGACTAGG   CAC GG
                                     AG_  _
GAM1175 PRX     3' GGTCACTGGGGAAGGGTCC   40900    T  GA
                                GG CT  TCCCCAGTGACC
                                || ||  ||||||||||||
                                CC GG  AGGGGTCACTGG
                                 T  GA
GAM1175 RALBP1   3' GTCACCAGGACGGCCTGTC   23279       T   A   CCA
                                GACAGG CTG TCC   GTGAC
                                |||||| ||| |||   |||||
                                CTGTCC GGC AGG   CACTG
                                   _  _  AC_
GAM1175 SCG2     3' GGTCACTGGGGAGTCTGCTTCA 14415     CA   CT  _
                                TGA  GGT  GA TCCCCAGTGACC
                                |||  |||  || ||||||||||||
                                ACT  TCG  CT AGGGGTCACTGG
                                  __  T_  G
GAM1175 SPON1    3' GGTGGAAAGTCAAACCTGTCA  63123        C  ___  _
                                TGACAGGT TGA   TCC CC
                                |||||||| |||   ||| ||
                                ACTGTCCA ACT   AGG GG
                                     A   GAA   T
GAM1175 UBE2V1   3' GTCACCAGGGTTACTCAGACCT 42067    A       T___   CA
            GCCA                TG CAGGTCTGA   CCC  GTGAC
                                || |||||||||   |||  |||||
                                AC GTCCAGACT   GGG  CACTG
                                 C       CATT   AC
GAM1175 UBE2V1   3' GTCACCAGGGTTACTCAGACCT 42605    A       T___   CA
            GCCA                TG CAGGTCTGA   CCC  GTGAC
                                || |||||||||   |||  |||||
                                AC GTCCAGACT   GGG  CACTG
                                 C       CATT   AC
GAM1175 UBE2V1   3' GTCACCAGGGTTACTCAGACCT 13970    A       T___   CA
            GCCA                TG CAGGTCTGA   CCC  GTGAC
                                || |||||||||   |||  |||||
                                AC GTCCAGACT   GGG  CACTG
                                 C       CATT   AC
GAM1175 AF9Q34   3' GCACTGGGGTGCCTTCA    51716    C   CTGAT      A
                                TGA AGGT    CCCCAGTG C
                                ||| ||||    |||||||| |
                                ACT TCCG    GGGGTCAC G
                                  _   T_____       C
GAM1175 ASAH     3' GTCACTGGAAAGAGTGCCAGTC 16303     A   CTGA  C__
            A                    TGAC GGT   TC   CCAGTGAC
                                |||| |||   ||   ||||||||
                                ACTG CCG   AG   GGTCACTG
                                  A  TG__  AAA
GAM1175 BRPF3    3' GTCACTGGGGAGATCACTGCC  93933    C_  __
                                GGT  TGA  TCCCCAGTGAC
                                |||  |||  ||||||||||
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                                CCG  ACT  AGGGGTCACTG
                                  TC   AG
GAM1175  C21orf69  3'  GGTCACTGGGGACTCCGGC   55234     T  _
                                GTC GA TCCCCAGTGACC
                                ||| || ||||||||||||
                                CGG CT AGGGGTCACTGG
                                  C  C
GAM1175  CPXCR1    3'  ATTGAAATATCAGACCTGTCA  53506           CCC_
                                TGACAGGTCTGAT    CAGT
                                ||||||||||||    ||||
                                ACTGTCCAGACTA    GTTA
                                        TAAA
GAM1175  FLJ10081  3'  GGTCACTGAGGTAGGAAGACCT 36292         GAT__  C
             GTC                   GACAGGTCT     CC CAGTGACC
                                |||||||||     || ||||||||
                                CTGTCCAGA     GG GTCACTGG
                                     AGGAT  A
GAM1175  FLJ12587  3'  GTCACTGGGGTCCCTCACC   42783     CT__  T
                                GGT    GA CCCCAGTGAC
                                |||    || ||||||||||
                                CCA    CT GGGGTCACTG
                                  CTCC  _
GAM1175  FLJ13072  5'  TCACTGGGAAGACTGT      91399      G   GATC
                                ACAG TCT    CCCAGTGA
                                |||| |||    ||||||||
                                TGTC AGA    GGGTCACT
                                  _   A___
GAM1175  FLJ20190  3'  GTCACTGGGAGGACCTGT    35208        GATC
                                ACAGGTCT    CCCAGTGAC
                                ||||||||    |||||||||
                                TGTCCAGG    GGGTCACTG
                                    A___
GAM1175  HEL308    5'  GTCACTGAGAACGACGTC    56907     AG   T A  CC
                                GAC  GTC G TC  CAGTGAC
                                |||  ||| | ||  |||||||
                                CTG  CAG C AG  GTCACTG
                                  __   _ A  A_
GAM1175  HS6ST     3'  GTCACCAGGACCCCCAGACCTG 62731     A       A___   CCA
             CA                   TG CAGGTCTG    TCC   GTGAC
                                || ||||||||    |||   |||||
                                AC GTCCAGAC    AGG   CACTG
                                  _       CCCC   AC_
GAM1175  KIAA0350  3'  GGTCACTGGTGAGACCTTC    61832     C      G TCC
                                GA AGGTCT A   CCAGTGACC
                                || |||||| |   |||||||||
                                CT TCCAGA T   GGTCACTGG
                                  _     G ____
GAM1175  KIAA0376  3'  GTCACTGGAGATGCTCTCA    66216     CA   CTG   C
                                TGA  GGT   ATC CCAGTGAC
                                |||  |||   ||| ||||||||
```

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                                ACT  TCG   TAG GGTCACTG
                                  C_  ___   A
GAM1175 KIAA1237 3' CACTGGGGACAGTTCTG    81298    GT   A
                                CAG  CTG TCCCCAGTG
                                |||  ||| |||||||||
                                GTC  GAC AGGGGTCAC
                                  TT  _
GAM1175 KIAA1266 3' GGCCACTGGGGGGACCTGCCA  66699    A    TGAT      A
                                TG CAGGTC   CCCCAGTG CC
                                || ||||||   |||||||| ||
                                AC GTCCAG   GGGGTCAC GG
                                 C     _____      C
GAM1175 KIAA1405 5' GGCCACCAAGATCAACCTGTC 61698       C    CCCA   A
                                GACAGGT TGATC   GTG CC
                                ||||||| |||||   ||| ||
                                CTGTCCA ACTAG   CAC GG
                                    _   AAC_  C
GAM1175 KIAA1573 3' CTGATGAACAGACCTGCCA   63362    A      A  CC
                                TG CAGGTCTG TC  CAG
                                || ||||||||  ||  |||
                                AC GTCCAGAC AG  GTC
                                 C       A  TA
GAM1175 KIAA1617 3' GTCATGCATCAGACCCTGCCA 93082    A   _     CCCCA
                                TG CAGG TCTGAT    GTGAC
                                || |||| ||||||    |||||
                                AC GTCC AGACTA    TACTG
                                 C   C     CG___
GAM1175 MGC14258 3' GGTCACTGGGAACGTGCC    52947    C  ATC
                                GGT TG   CCCAGTGACC
                                ||| ||   ||||||||||
                                CCG GC   GGGTCACTGG
                                  T  AA_
GAM1175 PRO2389  3' GGCCACATCTGAACAGACCTGT 64479          A  CCCA   A
            CA                    TGACAGGTCTG TC   GTG CC
                                ||||||||||| ||   ||| ||
                                ACTGTCCAGAC AG   CAC GG
                                      A  TCTA   C
GAM1175 RNF9    3' GGTTCTTGAACCAGCCTGTCA  54507       T   ATCCC   T
                                TGACAGG CTG    CAG GACC
                                ||||||| |||    ||| ||||
                                ACTGTCC GAC    GTT TTGG
                                    _   CAA__   C
GAM1175 RNF9    3' GGTTCTTGAACCAGCCTGTCA  23240       T   ATCCC   T
                                TGACAGG CTG    CAG GACC
                                ||||||| |||    ||| ||||
                                ACTGTCC GAC    GTT TTGG
                                    _   CAA__   C
GAM1175 TU3A    3' TCACTGGGGATCTTGTTA    24185       GTCT
                                TGACAG   GATCCCCAGTGA
                                ||||||   ||||||||||||
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                                ATTGTT   CTAGGGGTCACT
                                   ____
GAM1175 XPO5     3' GGTCACTGAAAGGCCCTGT   92877     _  GATCCC
                                ACAGG TCT    CAGTGACC
                                ||||| |||    ||||||||
                                TGTCC GGA    GTCACTGG
                                  C  AA____
GAM1175 LOC115051 3' GTCACCAGGACCCCCAGACCTG 60679   A     A___  CCA
             CA                   TG CAGGTCTG   TCC  GTGAC
                                || ||||||||   |||  |||||
                                AC GTCCAGAC   AGG  CACTG
                                 _     CCCC  AC_
GAM1175 LOC121838 5' GTCACCAAACAACCTGTTA   76515       C  ATCCCCA
                                TGACAGGT TG     GTGAC
                                |||||||| ||     |||||
                                ATTGTCCA AC     CACTG
                                     _ AAAC___
GAM1175 LOC126364 3' GGTCACTGTGCCAATCCTGTCA 76196       TC  ATCCC
                                TGACAGG  TG   CAGTGACC
                                |||||||  ||   ||||||||
                                ACTGTCC  AC   GTCACTGG
                                    TA  CGT__
GAM1175 LOC147353 3' ACTCTGAATCAGACTGTCA   85134      G    CCCC
                                TGACAG TCTGAT   AGT
                                |||||| ||||||   |||
                                ACTGTC AGACTA   TCA
                                   _    AGTC
GAM1175 LOC149420 3' GTCACTGGAGTTCCTTTCA   80157    C  TCT  CC
                                TGA AGG  GAT  CCAGTGAC
                                ||| |||  |||  ||||||||
                                ACT TCC  TTG  GGTCACTG
                                  T  ___  A_
GAM1175 LOC153603 5' TCATCTGATCAGGCCCATCA  81777    CA      CCCA
                                TGA  GGTCTGATC   GTGA
                                |||  |||||||||   ||||
                                ACT  CCGGACTAG   TACT
                                  AC       TC__
GAM1175 LOC162137 5' GGCCACTGGGGGAAGCC    88481    T  GA      A
                                GG CT  TCCCCAGTG CC
                                || ||  |||||||||  ||
                                CC GA  GGGGGTCAC GG
                                 _ A_       C
GAM1175 LOC163479 5' TCACCATCAGATCCATCA    83022    CA     CCCCA
                                TGA  GGTCTGAT    GTGA
                                |||  ||||||||    ||||
                                ACT  CTAGACTA    CACT
                                  AC      C____
GAM1175 LOC203636 3' TTGGGAACCACACCTGTCA   90982       C  ATC
                                TGACAGGT TG   CCCAG
                                |||||||| ||   |||||
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                                ACTGTCCA AC   GGGTT
                                    C  CAA
GAM1175  LOC205095 5'  CACAGTCAGACCTGTC      92379          CCCCA
                                GACAGGTCTGAT    GTG
                                ||||||||||||    |||
                                CTGTCCAGACTG    CAC
                                      A____
GAM1175  LOC205095 3'  TCACTGGGAATGCCTG      92388      CTG  C
                                CAGGT   AT CCCAGTGA
                                |||||   || ||||||||
                                GTCCG   TA GGGTCACT
                                   ___  A
GAM1175  LOC253015 5'  CACTGGGGACGGTTCTGCCG   98407    A   GT   A
                                TG CAG  CTG TCCCCAGTG
                                || |||  ||| |||||||||
                                GC GTC  GGC AGGGGTCAC
                                 C   TT  _
GAM1175  LOC51146  5'  TTGAAAGATAGACCTGCCA    32931    A      A  CC_
                                TG CAGGTCTG TC   CAG
                                || ||||||||  ||   |||
                                AC GTCCAGAT AG   GTT
                                 C       _  AAA
GAM1176  CSDA      3'  CATCCAAGCAATAAAGT     14687     CCA
                                ACT   ATTGCTTGGATG
                                |||   ||||||||||||
                                TGA   TAACGAACCTAC
                                  AA_
GAM1176  DBP       5'  GACACTCGTCCAAACCACTGGA 9052       ATTGC      CA
             GT                   ACTCCA    TTGGATGA  GTC
                                ||||||    ||||||||  |||
                                TGAGGT    AACCTGCT  CAG
                                   CACCA      CA
GAM1176  EIF2B5    3'  GACCACCATCCAGGCTGAG   62204     CAATT       ACA
                                CTC    GCTTGGATG   GTC
                                |||    |||||||||   |||
                                GAG    CGGACCTAC   CAG
                                  T_____       CAC
GAM1176  GRB10     3'  GACTCAGTCAAGCAACCACAGT 19195     CCAA      GA   CA
                                ACT    TTGCTTG  TGA  GTC
                                |||    |||||||  |||  |||
                                TGA    AACGAAC  ACT  CAG
                                  CACC      TG   __
GAM1176  OLIG2     3'  GACTGCCAGCCCCATCGGAGT  20548      AAT  CTT  A  A
                                ACTCC   TG   GG TG CAGTC
                                |||||   ||   || || |||||
                                TGAGG   AC   CC AC GTCAG
                                   CT_  C__  G  C
GAM1176  PPP1R2    3'  GACTGTCACCACATTAGGAG   21784     AAT  CT   A
                                CTCC   TG  TGG TGACAGTC
                                ||||   ||  ||| ||||||||
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                                GAGG  AC  ACC ACTGTCAG
                                  ATT  __  _
GAM1176 SOX5     3'  CATCCAAGCACTGAAGT    23666    C  AT
                                ACT CA  TGCTTGGATG
                                ||| ||  ||||||||||
                                TGA GT  ACGAACCTAC
                                  A  C_
GAM1176 C1orf17  3'  CATCATGGCAGTTGGAGT   68763          TG
                                ACTCCAATTGCT  GATG
                                ||||||||||||  ||||
                                TGAGGTTGACGG  CTAC
                                       TA
GAM1176 C6orf37  3'  ACTGCCATTTTGACAGTTGGA  68090        CTT    A
                                TCCAATTG   GGATG CAGT
                                ||||||||   ||||| ||||
                                AGGTTGAC   TTTAC GTCA
                                     AGT    C
GAM1176 KIAA0227 3'  GACTGTCAATGTGTACACTGGA 61349       AT_   TTGGA
             GT                   ACTCCA   TGC    TGACAGTC
                                ||||||  |||    ||||||||
                                TGAGGT   ATG    ACTGTCAG
                                   CAC   TGTA_
GAM1176 MGC32104 3'  ACTGACAAGCAATGAAGT    59063     CCA      GATGA
                                ACT   ATTGCTTG    CAGT
                                |||   ||||||||    ||||
                                TGA   TAACGAAC    GTCA
                                  AG_      A____
GAM1176 OR7C1    3'  ACTGTCATTCTTCAATCAGA   34416    CA    CTT
                                TC  ATTG   GGATGACAGT
                                ||  ||||   ||||||||||
                                AG  TAAC   CTTACTGTCA
                                 AC    TT_
GAM1176 PDP      3'  GACCAAGATCCAAGCAATCTGA 38030    CA         GACA
                                TC  ATTGCTTGGAT    GTC
                                ||  ||||||||||    |||
                                AG  TAACGAACCTA    CAG
                                 TC         GAAC
GAM1176 RIN1     3'  ACTGCCACATCTGAGGAACTGG 16276     A  G  TG    A__
             A                    TCCA TT CT  GATG   CAGT
                                |||| || ||  ||||   ||||
                                AGGT AA GA  CTAC   GTCA
                                  C  G  GT    ACC
GAM1176 LOC123876 3'  ACTGCAAGGGAAAGCAATTG   74713         GGA__  A
                                CAATTGCTT    TG CAGT
                                |||||||||    || ||||
                                GTTAACGAA    AC GTCA
                                     AGGGA  _
GAM1176 LOC152317 5'  GACTGTGTAGACAAGCAATCTG 86829    CA       GA  _
             A                    TC  ATTGCTTG  TG ACAGTC
                                ||  ||||||||  || ||||||
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                                AG  TAACGAAC  AT TGTCAG
                                 TC       AG  G
GAM1176  LOC157663 3'  GACCAAGATCCAAGCAATCTGA 82452    CA         GACA
                                TC  ATTGCTTGGAT    GTC
                                ||  ||||||||||    |||
                                AG  TAACGAACCTA    CAG
                                 TC         GAAC
GAM1176  LOC220558 3'  CATCCAAGCAATAAAGT     92771     CCA
                                ACT   ATTGCTTGGATG
                                |||   ||||||||||||
                                TGA   TAACGAACCTAC
                                 AA_
GAM1176  LOC253039 3'  GTATTCCAAGCAACTGGAG   97865       A        TG
                                CTCCA TTGCTTGGA  AC
                                |||||  |||||||||  ||
                                GAGGT AACGAACCT  TG
                                   C        TA
GAM1177  CDH12    3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM1177  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007       CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM1177  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090       T    AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT     TTATTC
                                  _   GTCA_
GAM1177  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
            A                    TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM1177  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM1177  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
            TA                    TACA   TCC   GAAGAATAAG
                                ||||   |||   ||||||||||
                                ATGT   AGG   TTTCTTATTC
                                  AAA_   ATTG
GAM1177  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA  68742             _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
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                                ATGTGGTGAGGGTTCT TCT
                                         G
GAM1177 KIAA1853 3' TTTTTCTTGGAAGCAGTG    69929    CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM1177 KIAA1877 3' CTTATTCTTCTGCCATGAGT   66748     CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM1177 KIAA1906 3' CTTATTCTTCTTGACTTTTGG  73571    CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM1177 OSBPL11  3' CTTAATTTCCCAAGAGTGGTG 43206       CCAA   AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                     AACC   A_
GAM1177 YME1L1   3' TCATTCTTGATGTGGTGTA   58438       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||| ||
                                ATGTGGTG   GTTCTT CT
                                     TA_    A
GAM1177 ZNF262   3' CTTATTTTGTTTGGGAGT    18723        A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                     G
GAM1177 LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_   AAGA
                                TACACCAC  CCAAG   ATA
                                ||||||||  |||||   |||
                                ATGTGGTG  GGTTC   TGT
                                     CAA   GG__
GAM1178 ADCY7    3' TGAGTTGCCCCGGGCTG     8494       AACACT   __
                                CAGCCCGG    GGCA  TCA
                                ||||||||    ||||  |||
                                GTCGGGCC    CCGT  AGT
                                     _______   TG
GAM1178 ADRBK1   3' ATGATGCCACACCAAGCTGTG 9663      CC  AACAC
                                CACAGC  GG    TGGCATCAT
                                ||||||  ||    |||||||||
                                GTGTCG  CC    ACCGTAGTA
                                   AA  AC___
GAM1178 BTEB1    5' ATGTCAGTGTTCGAGGCTGT  8668      CG
                                ACAGCC  GAACACTGGCAT
                                ||||||  ||||||||||||
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                                TGTCGG  CTTGTGACTGTA
                                   AG
GAM1178 LAIR1    3'  GAGGACAGCCCGGGCTGTG   41662        AACA   GCA
                                CACAGCCCGG   CTG   TC
                                ||||||||||   |||   ||
                                GTGTCGGGCC   GAC   AG
                                     C___   AGG
GAM1178 LILRB4   3'  TGATGTCTTCCTGGCTGT    23388      C   CACT
                                ACAGCC GGAA   GGCATCA
                                ||||||  ||||   |||||||
                                TGTCGG CCTT   CTGTAGT
                                   T   _____
GAM1178 P23      3'  ATGACTTGTCAGTGTTCCAGGT 22752     G  C         __
              GT                   ACA CC GGAACACTGGCA  TCAT
                                ||| ||  ||||||||||||  ||||
                                TGT GG CCTTGTGACTGT  AGTA
                                 _  A          TC
GAM1178 PRV1     3'  TGAGCATTCAGGGCTGTG    73896        G   CACTG  A
                                CACAGCCC GAA    GC TCA
                                ||||||||  |||    ||  |||
                                GTGTCGGG CTT    CG AGT
                                    A   A_____  _
GAM1178 SOLH     5'  GGCGCCGCCGGGCTGTG     20094         AACAC   AT
                                CACAGCCCGG    TGGC  C
                                ||||||||||    ||||  |
                                GTGTCGGGCC    GCCG  G
                                      ______   CG
GAM1178 SOX5     3'  ATGCCAGTAATTCAGCTG    23665     CC   AC
                                CAGC  GGA  ACTGGCAT
                                ||||  |||  ||||||||
                                GTCG  CTT  TGACCGTA
                                  A_   AA
GAM1178 ATP10B   3'  ATGATGCCAGCACTAGCCAGCT 64103     CC  AACA__
              G                   CAGC  GG     CTGGCATCAT
                                ||||  ||     ||||||||||
                                GTCG  CC     GACCGTAGTA
                                  A_  GATCAC
GAM1178 C19orf7  3'  ATGCAGGTGTTCCAAGGTGTG  61776     G  C_      G
                                CACA CC  GGAACACT GCAT
                                ||||  ||  ||||||||  ||||
                                GTGT GG  CCTTGTGG CGTA
                                  _  AA       A
GAM1178 C1QR1    3'  ATGCCAGTGCTCCGAGCTCA  24867   C   C    A
                                A AGC CGGA CACTGGCAT
                                |  |||  ||||  |||||||||
                                A TCG GCCT GTGACCGTA
                                 C   A    C
GAM1178 CYP2A13  3'  ATGATGTCCTTCAGAGCTGTG  7546       CCG   CACT
                                CACAGC   GAA   GGCATCAT
                                ||||||   |||   ||||||||
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                                GTGTCG  CTT   CTGTAGTA
                                   AGA  C___
GAM1178 KIAA0316 3' ATGATGCCAATGAGCTGCTCTG 70243    CC  AA  C
                                CAG  CGG  CA TGGCATCAT
                                |||  |||  || |||||||||
                                GTC  GTC  GT ACCGTAGTA
                                  TC  GA  A
GAM1178 MGC4368  5' ATGATGCCAGTGGCGCTGG   44723     AA_
                                CCGG  CACTGGCATCAT
                                ||||  ||||||||||||
                                GGTC  GTGACCGTAGTA
                                  GCG
GAM1178 NBL1     3' ATGTTAGTGCCCCGCACTGTG  60045     CC  AA
                                CACAG  CGG  CACTGGCAT
                                |||||  |||  |||||||||
                                GTGTC  GCC  GTGATTGTA
                                   AC  CC
GAM1178 RNF13    5' GCTAGTACTCCGGGCTGTG   24417         AC
                                CACAGCCCGGA  ACTGGC
                                ||||||||||  ||||||
                                GTGTCGGGCCT  TGATCG
                                      CA
GAM1178 RNPC1    3' TGGGGCATCCAGGGCTGTG   34414       _  ACACTG  AT
                                CACAGCCC GGA     GC  CA
                                |||||||| |||     ||  ||
                                GTGTCGGG CCT     CG  GT
                                    A  A_____  GG
GAM1178 TIMM22   3' ATGATGCCAGCCCCGGATCCGG 78911        ACA____
            GCTG                   CAGCCCGGA      CTGGCATCAT
                                |||||||||      ||||||||||
                                GTCGGGCCT      GACCGTAGTA
                                     AGGCCCC
GAM1178 LOC143879 5' ATGATGCCACTGATCAAACCTG 77157     CCCG  A  C
                                CAG    GA CA TGGCATCAT
                                |||    || || |||||||||
                                GTC    CT GT ACCGTAGTA
                                  CAAA  A  C
GAM1178 LOC147858 5' ATGCTGCACTCCGGAGCCGTG  79267     A  _    ACACT
                                CAC GC CCGGA     GGCAT
                                ||| || |||||     |||||
                                GTG CG GGCCT     TCGTA
                                  C  A    CACG_
GAM1178 LOC149086 3' ATGGGTTGGTGTCCGGGC    85491       A  TG  A
                                GCCCGGA CAC  GC TCAT
                                ||||||| |||  || ||||
                                CGGGCCT GTG  TG GGTA
                                    _  GT  _
GAM1178 LOC200058 3' TGTCGCAGCAGCCCGGGCTG  89965         AACA  __  AT
                                CAGCCCGG   CTG  GC  CA
                                ||||||||   |||  ||  ||
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                                GTCGGGCC   GAC  CG  GT
                                    C___   GA  CT
GAM1178  LOC257364 3'  ATGCTGGGCACCCAGGGCTGTG 96641        _  AACA TG
                                CACAGCCC GG   C  GCAT
                                |||||||| ||   |  ||||
                                GTGTCGGG CC   G  CGTA
                                    A  CACG GT
GAM1178  LOC55893  5'  ATGATGCCAGGCTACCAGGC   38489     C  AACA
                                GCC GG   CTGGCATCAT
                                ||| ||   ||||||||||
                                CGG CC   GACCGTAGTA
                                  A  ATCG
GAM1179  SCAMP1    3'  GCTAAATAAATATTCTCC    54500     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1179  SCAMP1    3'  GCTAAATAAATATTCTCC    54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1179  NX-17     3'  TGAATATCAGCCCCTAATA   40706        ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM1179  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
             TA                   TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM1180  SCAMP1    3'  GCTAAATAAATATTCTCC    54500     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1180  SCAMP1    3'  GCTAAATAAATATTCTCC    54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1180  NX-17     3'  TGAATATCAGCCCCTAATA   40706        ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM1180  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
             TA                   TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
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                                ATAATCCCTATTATAAGTAAATCG

GAM1181  SCAMP1   3'  GCTAAATAAATATTCTCC    18014    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1181  SCAMP1   3'  GCTAAATAAATATTCTCC    54500    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1181  NX-17    3'  TGAATATCAGCCCCTAATA   40706       ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                     CGAC
GAM1181  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
            TA                   TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM1182  KIAA1069  3'  TGACCTACATTCAACTGCAA   68535         _  C_
                                TTGCAGTTGAA GT  GTCG
                                |||||||||||  ||  ||||
                                AACGTCAACTT CA  CAGT
                                       A  TC
GAM1182  NICN1    3'  TGGCGACTTCATCTGCAA    51261       T
                                TTGCAG TGAAGTCGTCG
                                |||||| ||||||||||
                                AACGTC ACTTCAGCGGT
                                   T
GAM1182  TEX27    3'  GCTGAACACCTGCAACTGCAA  41952        A  TC  CG
                                TTGCAGTTG AG  GT  TAGC
                                ||||||||| ||  ||  ||||
                                AACGTCAAC TC  CA  GTCG
                                     G  CA  A_
GAM1182  LOC142948 3'  TGGCCACCGGCCCAACTGCAG  83782        AA   TC  A
                                TTGCAGTTG  GTCG  GT GCCA
                                |||||||||  ||||  || ||||
                                GACGTCAAC  CGGC  CA CGGT
                                     C_   __  C
GAM1182  LOC146488 5'  GCTACAACCGCTTCAACAACAA 71359     CA      C  C
                                TTG  GTTGAAGT GT GTAGC
                                |||  |||||||| || |||||
                                AAC  CAACTTCG CA CATCG
                                  AA       C  A
GAM1182  LOC147080 3'  TGCACAACTTCAGCCACAA   85053     CA      C  C
                                TTG  GTTGAAGT GT GTA
                                |||  |||||||| || |||
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                                AAC  CGACTTCA CA CGT
                                  AC       A  _
GAM1182  LOC152845 5'  GCGGTGACCTCAGCTGCAA   60958          A   GT
                                TTGCAGTTGA GTC  CGT
                                |||||||||| |||  |||
                                AACGTCGACT CAG  GCG
                                     C   TG
GAM1182  LOC203052 3'  ACCACCATTTCAACTGCA    92073           C  C
                                TGCAGTTGAAGT GT GT
                                |||||||||||| || ||
                                ACGTCAACTTTA CA CA
                                      C  C
GAM1182  LOC204084 5'  GGCCAGACCTCCAACTGCAG  91000          A  TC   GTA
                                TTGCAGTTG AG  GTC   GCC
                                ||||||||| ||  |||   |||
                                GACGTCAAC TC  CAG   CGG
                                     C  __   AC_
GAM1183  APG5L    3'  AAGTATGTGCCACTCGAT    17936     A      TC  CG
                                ATC AGTGGCA  CA  CTT
                                ||| |||||||  ||  |||
                                TAG TCACCGT  GT  GAA
                                  C      __ AT
GAM1183  EYA1     3'  AAGCATGGATGTCAAGTG    6694     AG       C
                                CA  TGGCATCCA GCTT
                                ||  ||||||||| ||||
                                GT  ACTGTAGGT CGAA
                                 GA        A
GAM1183  GNAI3    3'  AAGCATGGATGTTAGTGA    22442     AG       C
                                TCA  TGGCATCCA GCTT
                                |||  ||||||||| ||||
                                AGT  ATTGTAGGT CGAA
                                  G_        A
GAM1183  NCOA6    3'  AAGCAGGACTGCGACTTGATA  26817         G  _  AC
                                TATCAAGT GCA TCC  GCTT
                                |||||||| ||| |||  ||||
                                ATAGTTCA CGT AGG  CGAA
                                     G  C  A_
GAM1183  ABCA10   5'  AAGCGTGGATCAGTTTAATGA  55359     AGT  __
                                TCA   GGC  ATCCACGCTT
                                |||   |||  ||||||||||
                                AGT   TTG  TAGGTGCGAA
                                  AAT   AC
GAM1183  DKFZp762K222 5'  AAGCGCTGCAGGCCACTTG   71666         ATC  _
                                CAAGTGGC   CA CGCTT
                                ||||||||   || |||||
                                GTTCACCG   GT GCGAA
                                     GAC  C
GAM1183  ENPP4    3'  AAGCAAAGACCATTTGATA   30712          CA  CAC
                                TATCAAGTGG  TC   GCTT
                                ||||||||||  ||   ||||
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                                ATAGTTTACC  AG   CGAA
                                    __  AAA
GAM1183  FLJ31952  3'  AAGCATGAGAATCACTTGA   59038        CA  _  C
                                TCAAGTGG  TC CA GCTT
                                ||||||||  || || ||||
                                AGTTCACT  AG GT CGAA
                                    A_  A  A
GAM1183  KIAA1266  3'  AAGCACGAGGTAACTTGGTA   66689        G  A  CAC
                                TATCAAGT GC TC   GCTT
                                ||||||||  || ||   ||||
                                ATGGTTCA TG AG   CGAA
                                    A  G  CA_
GAM1183  KIAA1266  3'  AAGCGTGTGTATCACTGTGA   66690     _    GC TC
                                TCA AGTG  A  CACGCTT
                                |||  ||||  |  |||||||
                                AGT TCAC  T  GTGCGAA
                                  G    TA GT
GAM1183  MGC11034  3'  AAGCAATTCTGCCACTTGAT   49569          TCCAC
                                ATCAAGTGGCA     GCTT
                                ||||||||||     ||||
                                TAGTTCACCGT     CGAA
                                     CTTAA
GAM1184  ADM      5'  GTGGGACGTCTGAGAC      8512          CTT C
                                GTCTCAGAC   G CCCAC
                                |||||||||   | |||||
                                CAGAGTCTG   C GGGTG
                                    ___ A
GAM1184  C18orf1   3'  GTGGAGGTTCTGAGAC      60869        CCTT  _
                                GTCTCAGA    GCC CCAC
                                ||||||||    ||| ||||
                                CAGAGTCT    TGG GGTG
                                    _____   A
GAM1184  CML66    3'  TGGTACCTGGAGGTCTGGACA  68785      T       GCCCC
                                TGTC CAGACCTT     ACCA
                                |||| ||||||||     ||||
                                ACAG GTCTGGAG     TGGT
                                  _       GTCCA
GAM1184  CYP4A11   3'  GGTGTTGGGTCTGAACA     7590      C       TGCCC
                                TGT TCAGACCT     CACC
                                |||  ||||||||     ||||
                                ACA AGTCTGGG     GTGG
                                  _       TT___
GAM1184  DBH      3'  GGTGGGGCCAGCGCTGAACA   7628      C    AC  T
                                TGT TCAG  CT GCCCCACC
                                |||  ||||  ||  ||||||||
                                ACA AGTC  GA CGGGGTGG
                                  _    GC  C
GAM1184  FBXL5    5'  TGGTGGGGCTCTACTGCGACA  54319      T   ACCTT
                                TGTC CAG     GCCCCACCA
                                ||||  |||     |||||||||
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                                ACAG GTC    CGGGGTGGT
                                  C  ATCT_
GAM1184  FCMD    3'  TGGGGCAAGAACTCAGAC    23050     C  AC
                                GTCT AG  CTTGCCCCA
                                |||| ||  |||||||||
                                CAGA TC  GAACGGGGT
                                  C  AA
GAM1184  FLG     3'  GGTAGATAGGTCTGGACA    71450     T     ___
                                TGTC CAGACCT   TGCC
                                |||| |||||||   ||||
                                ACAG GTCTGGA   ATGG
                                  _      TAG
GAM1184  FLG     5'  GGTAGATAGGTCTGGACA    71451     T     ___
                                TGTC CAGACCT   TGCC
                                |||| |||||||   ||||
                                ACAG GTCTGGA   ATGG
                                  _      TAG
GAM1184  GCH1    3'  TGATGGGGCAAGATGGCA    5680      TCAGAC       C
                                TGTC     CTTGCCCCA CA
                                ||||     ||||||||| ||
                                ACGG     GAACGGGGT GT
                                  TA____       A
GAM1184  ITGA5   3'  GGTGTCTCCAAGCCTGAGGCA  61935       AC   CCC_
                                TGTCTCAG  CTTG   CACC
                                ||||||||  ||||   ||||
                                ACGGAGTC  GAAC   GTGG
                                     C_   CTCT
GAM1184  KIAA0857 3'  TGATGCAGTAATCTGGGACA  67258       CC_   CC
                                TGTCTCAGA   TTGC  CA
                                |||||||||   ||||  ||
                                ACAGGGTCT   GACG  GT
                                     AAT    TA
GAM1184  LOX     5'  GGTGGAGACTGAGATA      11347       AC  TGCC
                                TGTCTCAG  CT   CCACC
                                ||||||||  ||   |||||
                                ATAGAGTC  GA   GGTGG
                                     A_  _____
GAM1184  RU2     5'  GGTGAGGCCGCTGGGACA    33448       ACCTT   C
                                TGTCTCAG    GCC CACC
                                ||||||||    ||| ||||
                                ACAGGGTC    CGG GTGG
                                     GC___   A
GAM1184  TFAP2C  3'  TGATGGGGTAATCTATAACA  13686    CTC   CC      C
                                TGT   AGA  TTGCCCCA CA
                                |||   |||  |||||||| ||
                                ACA   TCT  AATGGGGT GT
                                  ATA   __       A
GAM1184  WDR10   5'  GTGAGGCGGTTGCTGAGACA  37341       ACC    C
                                TGTCTCAG   TTGCC CAC
                                ||||||||   ||||| |||
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                                ACAGAGTC   GGCGG GTG
                                    GTT    A
GAM1184  WDR10    5'  GTGAGGCGGTTGCTGAGACA  54832       ACC    C
                                TGTCTCAG   TTGCC CAC
                                ||||||||   ||||| |||
                                ACAGAGTC   GGCGG GTG
                                    GTT    A
GAM1184  WDR10    5'  GTGAGGCGGTTGCTGAGACA  54838       ACC    C
                                TGTCTCAG   TTGCC CAC
                                ||||||||   ||||| |||
                                ACAGAGTC   GGCGG GTG
                                    GTT    A
GAM1184  WDR10    5'  GTGAGGCGGTTGCTGAGACA  54839       ACC    C
                                TGTCTCAG   TTGCC CAC
                                ||||||||   ||||| |||
                                ACAGAGTC   GGCGG GTG
                                    GTT    A
GAM1184  XPR1     3'  TGATGGGACGGTACTGAGATA  17624       _  TTGC   C
                                TGTCTCAG ACC   CCCA CA
                                ||||||||  |||   |||| ||
                                ATAGAGTC TGG   GGGT GT
                                    A  CA__   A
GAM1184  ART5     3'  TGATGGGGACTTCCTGGGACA  54871       ACCTTG    C
                                TGTCTCAG     CCCCA CA
                                ||||||||     ||||| ||
                                ACAGGGTC     GGGGT GT
                                    CTTCA_    A
GAM1184  C11orf11 3'  TGATGGGGCCTTTGAGGCA   94884       CCTT    C
                                TGTCTCAGA   GCCCCA CA
                                |||||||||   |||||| ||
                                ACGGAGTTT   CGGGGT GT
                                    C___     A
GAM1184  C21orf25 3'  TGGTAAAAAGAGGCTGAGACA  64307       A   GCCCC
                                TGTCTCAG CCTT    ACCA
                                ||||||||  ||||    ||||
                                ACAGAGTC GGAG    TGGT
                                    _   AAAAA
GAM1184  CARD11   3'  GTAGGGCGGGGACCCGGACA  51573     CAGA     C
                                TGTCT   CCTTGCCC AC
                                |||||   |||||||| ||
                                ACAGG   GGGGCGGG TG
                                   CCCA      A
GAM1184  DKFZp434A171 5'  GGTGGTTGGGGGTCTGAGA   51025         GCC
                                TCTCAGACCTT   CCACC
                                ||||||||||   |||||
                                AGAGTCTGGGG   GGTGG
                                      GTT
GAM1184  DKFZP434N178 3'  TGGTGCTACAGACTTGAGACA  72402       ACC   CCC
                                TGTCTCAG   TTG   CACCA
                                ||||||||   |||   |||||
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                                ACAGAGTT  GAC  GTGGT
                                    CA_  ATC
GAM1184 EPB41L1  3' GGTGCTGGCCTGAGGCA    71113       ACCTT  C_
                                TGTCTCAG    GCC  CACC
                                ||||||||    |||  ||||
                                ACGGAGTC    CGG  GTGG
                                    _____  TC
GAM1184 FLJ11618 3' TGGTGGGGCTTCTTCTGTAACA 42627    CT   CCTT
                                TGT  CAGA   GCCCCACCA
                                |||  ||||   |||||||||
                                ACA  GTCT   CGGGGTGGT
                                  AT   TCTT
GAM1184 FLJ12770 3' GTGAAGCCAGGTCTGAACA   50682    C      T  CC
                                TGT TCAGACCT GC  CAC
                                ||| ||||||||  ||  |||
                                ACA AGTCTGGA CG  GTG
                                  _      C  AA
GAM1184 FLJ21817 3' GGTGGGGTTTCAAGACA    42613     CA  CCTT
                                TGTCT  GA   GCCCCACC
                                |||||  ||   ||||||||
                                ACAGA  CT   TGGGGTGG
                                   A_  T___
GAM1184 FYCO1    3' TGGGTTTGGGGCCTGGGACA  44777       ACCTT    ___
                                TGTCTCAG    GCCCCA  CCA
                                ||||||||    ||||||  |||
                                ACAGGGTC    CGGGGT  GGT
                                    _____    TTG
GAM1184 KIAA1396 3' TGGTGGGTGCCCCTCTGGGACA 63677        CCTT  _
                                TGTCTCAGA   GC CCCACCA
                                |||||||||   || |||||||
                                ACAGGGTCT   CG GGGTGGT
                                     CCC_  T
GAM1184 KIAA1464 3' GGTGTGGCCTGAGATA     68822       ACCTT  C
                                TGTCTCAG    GCC CACC
                                ||||||||    ||| ||||
                                ATAGAGTC    CGG GTGG
                                    _____  T
GAM1184 KIAA1765 3' TGGTGCAGTCTGAGACA    71136        CT  C
                                TGTCTCAGAC  TGC CCA
                                ||||||||||  ||| |||
                                ACAGAGTCTG  ACG GGT
                                     __  T
GAM1184 LIP8     5' GTAGGGCAGGGGGACA     89526     CAGA     C
                                TGTCT   CCTTGCCC AC
                                |||||   |||||||| ||
                                ACAGG   GGGACGGG TG
                                   _____      A
GAM1184 MBIP     5' TGGTGGGGCGGCCTGAGA    33895      A  TT
                                TCTCAG CC  GCCCCACCA
                                ||||||  ||  |||||||||
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                                AGAGTC GG  CGGGGTGGT
                                   C  __
GAM1184  MGC15937  5'  GGTCTCAAGGTCTGAAGCA   55600    TC       CCCC
                                TG  TCAGACCTTG   ACC
                                ||  ||||||||||   |||
                                AC  AGTCTGGAAC   TGG
                                 GA        TC__
GAM1184  MGC16153  5'  GGTGAGGCAATCTGTGA    52270    T   CC    C
                                TC CAGA  TTGCC CACC
                                || ||||  ||||| ||||
                                AG GTCT  AACGG GTGG
                                 T   __    A
GAM1184  NPD009    5'  TGGTGGGGAGTCTGAGA    96751       CTTG
                                TCTCAGAC   CCCCACCA
                                ||||||||   ||||||||
                                AGAGTCTG   GGGGTGGT
                                    A___
GAM1184  NXPH3     3'  GTGGAGCCTCTGGGACA    66345       CCTT  C
                                TGTCTCAGA   GC CCAC
                                |||||||||   || ||||
                                ACAGGGTCT   CG GGTG
                                     C___  A
GAM1184  PAPOLB    5'  TGGCGGGGCGGGCGCTGA    39720     AC      A
                                TCAG  CTTGCCCC CCA
                                ||||  |||||||| |||
                                AGTC  GGGCGGGG GGT
                                  GC       C
GAM1184  PIP5K1C   3'  TGGTGTGGGGTCTGAGAC    71312         TG C
                                GTCTCAGACCT  C CCA
                                ||||||||||  | |||
                                CAGAGTCTGGG  G GGT
                                      GT T
GAM1184  PLCL1     3'  GTGTTTTAAATTCTGAGACA   21716       CC   CCC
                                TGTCTCAGA  TTG   CAC
                                |||||||||  |||   |||
                                ACAGAGTCT  AAT   GTG
                                     TA   TTT
GAM1184  PRO2533   3'  TGGGAAAGCTGTCTGAGACA   38422        __   GC
                                TGTCTCAGAC  CTT  CCCA
                                ||||||||||  |||  ||||
                                ACAGAGTCTG  GAA  GGGT
                                      TC   A_
GAM1184  RAB-R     3'  TGATGGGGCAGTGACCAGACA  21391      CAGACC      C
                                TGTCT     TTGCCCCA CA
                                |||||     |||||||| ||
                                ACAGA     GACGGGGT GT
                                   CCAGT_       A
GAM1184  RNPC2     3'  TGGTAGGCAAAGCAGTCTGAGA 18132       C___    CC
                                TCTCAGAC   TTGCC  ACCA
                                ||||||||   |||||  ||||
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                                AGAGTCTG   AACGG  TGGT
                                    ACGA    A_
GAM1184  SDC3     3'  TGGTGGGGGCCCCTGGACA   28485     T   ACCTTG
                                TGTC CAG     CCCCACCA
                                |||| |||     ||||||||
                                ACAG GTC     GGGGTGGT
                                  _   CCCG__
GAM1184  SLC26A6  3'  GCGCTCCAGGTCTGGGACA   43583          ____
                                TGTCTCAGACCT   TGC
                                ||||||||||||   |||
                                ACAGGGTCTGGA   GCG
                                       CCTC
GAM1184  SLC26A6  3'  GCGCTCCAGGTCTGGGACA   56958          ____
                                TGTCTCAGACCT   TGC
                                ||||||||||||   |||
                                ACAGGGTCTGGA   GCG
                                       CCTC
GAM1184  SLC26A6  3'  GCGCTCCAGGTCTGGGACA   57055          ____
                                TGTCTCAGACCT   TGC
                                ||||||||||||   |||
                                ACAGGGTCTGGA   GCG
                                       CCTC
GAM1184  SMAP-5   5'  TGGTTCAGGGTCTGAAACA   48663     C        CC
                                TGT TCAGACCTTG  CCA
                                ||| ||||||||||  |||
                                ACA AGTCTGGGAC  GGT
                                  A         TT
GAM1184  TLN2     5'  GTGGGGATCTTCTGAGACA   62357         CCTTG
                                TGTCTCAGA    CCCCAC
                                |||||||||    ||||||
                                ACAGAGTCT    GGGGTG
                                     TCTA_
GAM1184  VPS33B   5'  GGTGGCTGCAGGTCTGAGACA  38524           T  C_
                                TGTCTCAGACCT GC  CCACC
                                |||||||||||| ||  |||||
                                ACAGAGTCTGGA CG  GGTGG
                                       _  TC
GAM1184  LOC115704 3'  GGCAGGCTTCCTTCTGGGACA  73910         C_____
                                TGTCTCAGA     CTTGCC
                                |||||||||     ||||||
                                ACAGGGTCT     GGACGG
                                     TCCTTC
GAM1184  LOC128916 5'  TGGTGGGGAGGCCTTCTGGACA 76298      T   ___   TG
                                TGTC CAGA   CCT  CCCCACCA
                                |||| ||||   |||  ||||||||
                                ACAG GTCT   GGA  GGGGTGGT
                                  _    TCC   __
GAM1184  LOC144755 3'  TGATGGGGCAAGAGTGGGA   84102      GAC       C
                                TCTCA   CTTGCCCCA CA
                                |||||   |||||||||  ||
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                                AGGGT   GAACGGGGT GT
                                   GA_        A
GAM1184  LOC148490 3'  GGCAGCCATGAGGTCTGGGACA 79622           _______
                                TGTCTCAGACCT      TGCC
                                ||||||||||||     ||||
                                ACAGGGTCTGGA      ACGG
                                      GTACCG
GAM1184  LOC150482 5'  GGTGGTTGGGGGTCTGAGA    63751           GCC
                                TCTCAGACCTT   CCACC
                                ||||||||||   |||||
                                AGAGTCTGGGG   GGTGG
                                      GTT
GAM1184  LOC151193 5'  TGGAGCATGCTCTATCTGGGAC 80976          CCT_____   C
            A                    TGTCTCAGA      TGC CCA
                                |||||||||       ||| |||
                                ACAGGGTCT       ACG GGT
                                      ATCTCGT   A
GAM1184  LOC158972 3'  TGGAGGACACAATCTGAGACA  88316          CCT  _  _
                                TGTCTCAGA   TG CC CCA
                                |||||||||   || || |||
                                ACAGAGTCT   AC GG GGT
                                      AAC  A  A
GAM1184  LOC162427 3'  TGATGGGGCAAGGGAAGA    83233     CAGA        C
                                TCT    CCTTGCCCCA CA
                                |||    |||||||||| ||
                                AGA    GGAACGGGGT GT
                                  AG__         A
GAM1184  LOC163183 5'  GGAGGAGCTCTGGGACA     83325         CCTT  C  A
                                TGTCTCAGA    GC CC CC
                                |||||||||    || || ||
                                ACAGGGTCT    CG GG GG
                                      _____  A  A
GAM1184  LOC196214 3'  GGTGGCTGCCTGGGACA     91182         ACCTT  C_
                                TGTCTCAG     GC  CCACC
                                ||||||||     ||  |||||
                                ACAGGGTC     CG  GGTGG
                                      ______  TC
GAM1184  LOC196214 5'  TGGCGGAGACAAGCACTGAGAC 91186          AC    CC_  A
            A                    TGTCTCAG  CTTG   CC CCA
                                |||||||  ||||   || |||
                                ACAGAGTC  GAAC   GG GGT
                                      AC    AGA  C
GAM1184  LOC205418 5'  TGGTGATTCGGACCTGAGGCA  92376         A_  TTGCCC
                                TGTCTCAG  CC      CACCA
                                ||||||||  ||      |||||
                                ACGGAGTC  GG      GTGGT
                                      CA  CTTA__
GAM1184  LOC219700 3'  TGGTGGGGCAAAGGGCTGGAC  94662     T   A   _
                                GTC CAG CCTT GCCCCACCA
                                ||| ||| |||| |||||||||
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                                CAG GTC GGAA CGGGGTGGT
                                  _  G   A
GAM1184  LOC219701 3'  TGGTGGGGCAAAGGGCTGGAC  94646     T  A   _
                                GTC CAG CCTT GCCCCACCA
                                ||| ||| |||| |||||||||
                                CAG GTC GGAA CGGGGTGGT
                                  _  G   A
GAM1184  LOC257095 5'  TGGTGGGGCAGTGGGAGATA  98724       AGA  _
                                TGTCTC  CC TTGCCCCACCA
                                ||||||  || ||||||||||
                                ATAGAG  GG GACGGGGTGGT
                                   ___  T
GAM1185  ATP4A    3'  CCAAGAGTCCCAGCCCCA    7372         CAGCCT   _
                                TGGGGCTG    GGGC CTTGG
                                ||||||||    |||| |||||
                                ACCCCGAC    CCTG GAACC
                                   _______   A
GAM1185  FCER2    3'  ACCCTCTCCAGATGCAGCCCCA 10599         GC    CCTT
                                TGGGGCTGCA  CTGGG   GGT
                                ||||||||||  |||||   |||
                                ACCCCGACGT  GACCT   CCA
                                     A_    CTC_
GAM1185  FOXO1A   3'  CCAATAACCCCAGCCCCA    10649        CAGCCT  CC_
                                TGGGGCTG    GGG  TTGG
                                ||||||||    |||  ||||
                                ACCCCGAC    CCC  AACC
                                   _______  AAT
GAM1185  INPPL1   3'  ACCAAGGCCCAGCTATGGCCCC 9602        GC  C
            A                    TGGGGCT  AGC TGGGCCTTGGT
                                ||||||| ||| ||||||||||
                                ACCCCGG  TCG ACCCGGAACCA
                                   TA  _
GAM1185  LRP1     3'  CCAAACCCCAGCCCCA     11358        CAGCCT  CC
                                TGGGGCTG    GGG  TTGG
                                ||||||||    |||  ||||
                                ACCCCGAC    CCC  AACC
                                   _______  A_
GAM1185  PIM1     5'  GCCACAGCCACAGCCCCA    92686        CA  C  _
                                TGGGGCTG  GC TG GGC
                                ||||||||  || || |||
                                ACCCCGAC  CG AC CCG
                                     AC  _  A
GAM1185  PRX2     3'  GTACCAGAGACTGCAGCCC   33308         C__   ____
                                GGGCTGCAG   CTGG   GC
                                |||||||||   ||||   ||
                                CCCGACGTC   GACC   TG
                                     AGA   AIII
GAM1185  RET      3'  GGCCAAGCCTCAGCCCCA    40549        C  C  G
                                TGGGGCTG AG CT GGCC
                                |||||||| || || ||||
```

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                                ACCCCGAC TC GA CCGG
                                    _ C  A
GAM1185 SLC5A2   3' CTTGGTACCATAAGCCACAGCC 13180       CA  C__  ____ CTTG
           TCA                   TGGGGCTG  GC   TGG   GC   G
                                 ||||||||  ||   |||   ||   |
                                 ACTCCGAC  CG   ACC   TG   C
                                     AC  AAT   AIII  GTTC
GAM1185 ADAMTS10 5' ACCAAGGCCCAGAGAGGGAGGC 48979     GCAGC__
           CC                    GGGCT     CTGGGCCTTGGT
                                 |||||     ||||||||||||
                                 CCCGG     GACCCGGAACCA
                                   AGGGAGA
GAM1185 DC-TM4F2 3' CCGTGCCTAGCCACAACCCCA  48898     C  CA  C    CT
                                 TGGGG TG  GC TGGGC  TGG
                                 |||||  ||  ||  |||||  |||
                                 ACCCC AC  CG ATCCG  GCC
                                    A  AC  _    T_
GAM1185 FBXO27   3' ACCAAAACCCTCCGATCCAGCC 74994       CAGCCT_  CC
           CCA                   TGGGGCTG     GGG  TTGGT
                                 ||||||||     |||  |||||
                                 ACCCCGAC     CCC  AACCA
                                     CTAGCCT   AA
GAM1185 FLJ14249 3' GTACCAGAAGCCCAGCCCCA  42644       CA  __   ____
                                 TGGGGCTG  GC  CTGG   GC
                                 ||||||||  ||  ||||   ||
                                 ACCCCGAC  CG  GACC   TG
                                     C_  AA   AIII
GAM1185 GDF10    5' CCCTGTCAGCTGCAGCCCCA  18298         CT___
                                 TGGGGCTGCAGC    GGG
                                 ||||||||||||    |||
                                 ACCCCGACGTCG    CCC
                                       ACTGT
GAM1185 KIAA0140 3' CTTGGTACCAGCAAGCCCAGCC 28514       CA  ___   ____ CTTG
           CCA                   TGGGGCTG  GC   CTGG   GC   G
                                 ||||||||  ||   ||||   ||   |
                                 ACCCCGAC  CG   GACC   TG   C
                                     C_  AAC   AIII  GTTC
GAM1185 KIAA0444 3' CCTTTCCCCAGGCACAGCCCCA 62998       CA     CCTT
                                 TGGGGCTG  GCCTGGG   GG
                                 ||||||||  |||||||   ||
                                 ACCCCGAC  CGGACCC   CC
                                     A_     CTTT
GAM1185 KIAA0450 5' GCCCAGGCCGCACCCCA    28357     C   A
                                 TGGGG TGC GCCTGGGC
                                 |||||  ||| ||||||||
                                 ACCCC ACG CGGACCCG
                                    _  C
GAM1185 KIAA1077 3' AGCCCCAGGCTGCAGCCC    73285          C
                                 GGGCTGCAGCCTGGG CT
                                 |||||||||||||| ||
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                                CCCGACGTCGGACCC GA
                                       C
GAM1185  MGC10986  3'  GCCTTGGTACTCGCCAGGCTGC 48325          _________ CTTG
             AGCCTCA                TGGGGCTGCAGCCTGG      GC   GT
                                ||||||||||||||||      ||   ||
                                ACTCCGACGTCGGACC      TG   CG
                                       GCTCAIII  GTTC
GAM1185  MGC11352  5'  CCGTGCCTAGCCACAACCCCA  65430     C  CA  C    CT
                                TGGGG TG  GC TGGGC  TGG
                                ||||| ||  || |||||  |||
                                ACCCC AC  CG ATCCG  GCC
                                   A  AC  _    T_
GAM1185  PPP1R16B  5'  CCATGAGGCCCCAGCCCCA   62035       CAGCCT    __
                                TGGGGCTG     GGGCCT  TGG
                                ||||||||     ||||||  |||
                                ACCCCGAC     CCCGGA  ACC
                                   _______      GT
GAM1185  TM4SF11   3'  CTTGGTACTCCAGACCTGCAGC 32587         C_   _______ CTTG
             CCCA                   TGGGGCTGCAG  CTGG     GC   G
                                ||||||||||  ||||     ||   |
                                ACCCCGACGTC  GACC     TG   C
                                      CA    TCAIII  GTTC
GAM1185  LOC154834 5'  GTACACCAGGCTCAGCCCCA   87496       C     _______
                                TGGGGCTG AGCCTGG     GC
                                |||||||| |||||||     ||
                                ACCCCGAC TCGGACC     TG
                                   _      ACAIII
GAM1185  LOC200030 3'  ACCAAGACCCATCATGCCCCA  80124      TGCAGCC   C
                                TGGGGC      TGGG CTTGGT
                                ||||||      |||| ||||||
                                ACCCCG      ACCC GAACCA
                                   TACT___    A
GAM1185  LOC200030 3'  ACCAAGACCCATCATGCCCCA  80125      TGCAGCC   C
                                TGGGGC      TGGG CTTGGT
                                ||||||      |||| ||||||
                                ACCCCG      ACCC GAACCA
                                   TACT___    A
GAM1185  LOC200030 3'  ACCAAGACCCATCATGCCCCA  80126      TGCAGCC   C
                                TGGGGC      TGGG CTTGGT
                                ||||||      |||| ||||||
                                ACCCCG      ACCC GAACCA
                                   TACT___    A
GAM1185  LOC200030 3'  ACCAAGGCCCACCATGCCCCA  80127      TGCAGCC
                                TGGGGC      TGGGCCTTGGT
                                ||||||      ||||||||||
                                ACCCCG      ACCCGGAACCA
                                   TACC___
GAM1185  LOC200030 3'  ACCAAGGCCCACCATGCCCCA  80128      TGCAGCC
                                TGGGGC      TGGGCCTTGGT
                                ||||||      ||||||||||
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                                ACCCCG     ACCCGGAACCA
                                   TACC___
GAM1185 LOC221431 3' CCAAGACTCTGCAGCCC    93728       CCT  GC
                                GGGCTGCAG  GG  CTTGG
                                |||||||||  ||  |||||
                                CCCGACGTC  TC  GAACC
                                     ___  A_
GAM1186 DLEC1    3' CATCTGGCCCTCCCTTG    24716     A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                   C    G  _
GAM1186 DLEC1    3' CATCTGGCCCTCCCTTG    24728     A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                   C    G  _
GAM1186 PIP5K1A  3' TATCCCACCCTGCCTTGATA  14520       A   CA  C
                                TATCAAGG AGGG  GG GTG
                                |||||||| ||||  || |||
                                ATAGTTCC TCCC  CC TAT
                                     G   A_  C
GAM1186 SOX11    3' ACCCACCCCCCCTTGGTA    13308       AA  CA  C
                                TATCAAGG  GGG  GG GT
                                ||||||||  |||  || ||
                                ATGGTTCC  CCC  CC CA
                                     CC   A_  _
GAM1186 CHL1     3' TGTTACCTTTCCTCAATA    22768    CA     CA
                                TAT  AGGAAGGG  GGCG
                                |||  ||||||||  ||||
                                ATA  TCCTTTCC  TTGT
                                  AC       A_
GAM1186 EPB41L1  3' CATTCTGCCCTTCCCTGA    71104    A       C
                                TCA GGAAGGGCAGG GTG
                                ||| |||||||||| |||
                                AGT CCTTCCCGTCT TAC
                                  C        _
GAM1186 FLJ00060 3' CATACCCCCTGCCCTCCTCTGA 61741    _   A     CGTG
                                TCA AGGA GGGCAGG   ATG
                                ||| |||| |||||||   |||
                                AGT TCCT CCCGTCC   TAC
                                  C   _     CCCA
GAM1186 FLJ10898 5' CACCACAGCCCTTTCTCAATA 60126    CA      AGGC
                                TAT  AGGAAGGGC   GTG
                                |||  |||||||||   |||
                                ATA  TCTTTCCCG   CAC
                                  AC       ACAC
GAM1186 FLJ22557 3' ATCATCCCATCCTTAATA    45581    C    A  CAGGC
                                TAT AAGGA GGG    GTGAT
                                ||| ||||| |||    |||||
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                                ATA TTCCT CCC     TACTA
                                  A     A  _____
GAM1186  KIAA0574  3'  CATCCCCTGCCCTCCCCTGA   69808     A  A       CGT
                                TCA GG AGGGCAGG   GATG
                                ||| || ||||||||   ||||
                                AGT CC TCCCGTCC   CTAC
                                  C  C       C__
GAM1186  KIAA0632  3'  CACCTCAGAAACCCTTCCTTGA 32071           CA___  C
                                TCAAGGAAGGG     GG GTG
                                ||||||||||     || |||
                                AGTTCCTTCCC     CT CAC
                                      AAAGA  C
GAM1186  KIAA1045  3'  CATCACATGTCCTTCC      71599          GGC
                                GGAAGGGCA   GTGATG
                                |||||||||   ||||||
                                CCTTCCTGT   CACTAC
                                     A__
GAM1186  KIAA1354  5'  CAGTGACTGCCTTCCCTTGATA 61572         A      G  _
                                TATCAAGG AGGGCAG CG TG
                                |||||||| ||||||| || ||
                                ATAGTTCC TTCCGTC GT AC
                                     C      A  G
GAM1186  MGC20460  5'  CACCGCCTCCTACCCTTCTT   54901         C___    _
                                AGGAAGGG    AGGCG TG
                                ||||||||    ||||| ||
                                TTCTTCCC    TCCGC AC
                                     ATCC     C
GAM1186  LOC158476 3'  CACGCCCGCCCCCCCCATTGA  88186      _ AA_    A
                                TCAA GG   GGGC GGCGTG
                                ||||  ||   ||||  ||||||
                                AGTT CC   CCCG CCGCAC
                                  A  CCC    C
GAM1186  LOC90459  3'  CACACCCGCCTAATTTTTG    63550       A_    A  C
                                CAAGGA  GGGC GG GTG
                                ||||||  ||||  || |||
                                GTTTTT  TCCG CC CAC
                                    AA    C  A
GAM1187  ADCY2     3'  GGTCCCAGTGCCATTGGCTTCA 65651           G  _____   AATCC
            A                    TTGAAGCCAGTGG GC    ACC
                                ||||||||||||| ||    |||
                                AACTTCGGTTACC TG    TGG
                                       G  ACCC     C
GAM1187  ADD3      3'  GGAGTCCCATTGTTTCAG    34168        C       A
                                TTGAAGC AGTGGGGC CC
                                ||||||| |||||||| ||
                                GACTTTG TTACCCTG GG
                                    _       A
GAM1187  ARF1      3'  GGAACCTCTTACTGCTTTCAA  71196       C    __    CA
                                TTGAAG CAGT  GGGG  CC
                                |||||| ||||  ||||  ||
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                                AACTTT GTCA  CTCC  GG
                                   C    TT    AA
GAM1187  ARNTL    5'  GGGCCTTCATTGGTTCCGA   8627      A       _  A
                                TTG AGCCAGTGG GGC CC
                                ||| ||||||||| ||| ||
                                AGC TTGGTTACT CCG GG
                                  C        T  _
GAM1187  ATP8B2   3'  GGATTCCTTAGTCCTGCTGGCC 65841    TG A    TG    ACC__
            TTGG                   T  A GCCAG  GGGC    AATCC
                                | | |||||  ||||    |||||
                                G  T CGGTC  CCTG    TTAGG
                                 GT C    GT    ATTCC
GAM1187  BCL2     3'  GGGTTTTGTTACCTGGTTTTAA 7239          TGG    CC
                                TTGAAGCCAG   GGCA  AATCC
                                ||||||||||   ||||  |||||
                                AATTTTGGTC   TTGT  TTGGG
                                      CA_    T_
GAM1187  BCL7A    3'  GGGTCATGGGTTTTGTTGTTTT 40989    TG   C   TG    A   __
            TGG                    T  AAG CAG  GGGC CCA  ATCC
                                |  ||| |||  |||| |||  ||||
                                G  TTT GTT  TTTG GGT  TGGG
                                 GT   T   GT    _  AC
GAM1187  BRCA1    3'  GGAAAGTTCTGCTGTTTTTAG  24568       C   TG    A__
                                TTGAAG CAG  GGGC   CC
                                |||||| |||  ||||   ||
                                GATTTT GTC  CTTG   GG
                                   T   GT    AAA
GAM1187  CDYL     3'  AATTGTGTTTTATTGGTTTTGG 17886    TG           C   CC
                                T  AAGCCAGTGGGGCAC AAT
                                |  |||||||||||||| |||
                                G  TTTGGTTATTTTGTG TTA
                                 GT           _  AG
GAM1187  COLQ     3'  GGCGGCTCTTGTGGTTTCAA   55426         GT    A_
                                TTGAAGCCA  GGGGC  CC
                                |||||||||  |||||  ||
                                AACTTTGGT  TCTCG  GG
                                      GT    GC
GAM1187  COLQ     3'  GGCGGCTCTTGTGGTTTCAA   55427         GT    A_
                                TTGAAGCCA  GGGGC  CC
                                |||||||||  |||||  ||
                                AACTTTGGT  TCTCG  GG
                                      GT    GC
GAM1187  CSH2     3'  GGCTGCTCTACTGCTTCAG    40976        C       _
                                TTGAAGC AGTGGGGCA CC
                                ||||||| ||||||||| ||
                                GACTTCG TCATCTCGT GG
                                   _       C
GAM1187  CSH2     3'  GGCTGCTCTACTGCTTCAG    42945        C       _
                                TTGAAGC AGTGGGGCA CC
                                ||||||| ||||||||| ||
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                                GACTTCG TCATCTCGT GG
                                   _       C
GAM1187  CSHL1    3'  GGCTGCTCCACTGCTTCAG   42938       C       _
                                TTGAAGC AGTGGGGCA CC
                                ||||||| ||||||||| ||
                                GACTTCG TCACCTCGT GG
                                   _       C
GAM1187  CSHL1    3'  GGCTGCTCCACTGCTTCAG   8985        C       _
                                TTGAAGC AGTGGGGCA CC
                                ||||||| ||||||||| ||
                                GACTTCG TCACCTCGT GG
                                   _       C
GAM1187  CYBB     3'  GGAGCTCTATGGTTTTGA    76849   TG    G     A
                                T  AAGCCA TGGGGC CC
                                |  |||||| |||||| ||
                                A  TTTGGT ATCTCG GG
                                 GT     _     A
GAM1187  CYP1A1   3'  GGTGCTGACTGGCTTCAG    6693          G  G
                                TTGAAGCCAGT GG CACC
                                |||||||||||  || ||||
                                GACTTCGGTCA TC GTGG
                                      G  _
GAM1187  DAF      3'  GGATGCTTTCATTGTCTTTAA  6955        C     _  _
                                TTGAAG CAGTGGG GCA CC
                                |||||| ||||||| ||| ||
                                AATTTC GTTACTT CGT GG
                                   T      T   A
GAM1187  DKK1     3'  GGATATACAAGTTCTGTGGTTT 25296         G     ACCA__
            CAG                    TTGAAGCCA TGGGGC      ATCC
                                |||||||||  ||||||      ||||
                                GACTTTGGT GTCTTG      TAGG
                                      _     AACATA
GAM1187  DPYD     3'  GGGCTCTGACTGGTTTTAA   61071          _    A
                                TTGAAGCCAGT GGGGC CC
                                |||||||||||  ||||| ||
                                AATTTTGGTCA TCTCG GG
                                      G    _
GAM1187  ELMO3    5'  CGGCGCCTTGTTCCGCTGGCCT 45578     A       _____   A  AATCC
            CG                     TGA GCCAGTGG     GGC CC
                                |||  ||||||||     ||| ||
                                GCT CGGTCGCC     CCG GG
                                  C       TTGTT   C     CC
GAM1187  EPB41L2  3'  CTGTGGTGGTGTTCTGTTGGTT 9292      A     TG       ATCC
            ACAA                    TTG AGCCAG  GGGCACCA
                                |||  ||||||  ||||||||
                                AAC TTGGTT  CTTGTGGT
                                  A     GT       GGTGTCG
GAM1187  FOXF2    3'  GGATCTTCGTTGCCTTCAG   9374        C       CA
                                TTGAAG CAGTGGGG  CC
                                ||||||  ||||||||  ||
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                                GACTTC GTTGCTTC  GG
                                   C       TA
GAM1187  FZD7    3'  GGATTTTTGTTTTGTTGGCTTT 14505         TG    CC
             AA                   TTGAAGCCAG  GGGCA  AATCC
                                  ||||||||||  |||||  |||||
                                  AATTTCGGTT  TTTGT  TTAGG
                                     GT    TT
GAM1187  GARP    3'  GGCAGGCCCCGCTGGTTT    19784           A__
                                  AAGCCAGTGGGGC   CC
                                  ||||||||||||   ||
                                  TTTGGTCGCCCCG   GG
                                        GAC
GAM1187  GH1     3'  GGCTGCTCTACTGCTTCAG   42890        C       _
                                  TTGAAGC AGTGGGGCA CC
                                  |||||||  |||||||| ||
                                  GACTTCG TCATCTCGT GG
                                     _       C
GAM1187  GH2     3'  GGCTGCTCTACTGCTTCAG   10790        C       _
                                  TTGAAGC AGTGGGGCA CC
                                  |||||||  |||||||| ||
                                  GACTTCG TCATCTCGT GG
                                     _       C
GAM1187  GRM1    3'  GGATTTTTTCTTGCTGTTTTGA 7741    TG   C  TG   CACC
                                  T  AAGC AG  GGG    AATCC
                                  |  ||||  ||  |||    |||||
                                  A  TTTG TC  TCT    TTAGG
                                   GT    _  GT   TTT_
GAM1187  IL10RA  3'  GGGTCCCTGCCTTGTTGGTGTT 60382      _    TG    CCA
             CAG                    TTGAA GCCAG  GGGCA   ATCC
                                  |||||  |||||  |||||   ||||
                                  GACTT TGGTT  TCCGT   TGGG
                                     G    GT    CCC
GAM1187  INPP5A  3'  GGAGTCCGCCCCGCGGGTTTCA 19867        A      ACCAA
             G                     TTGAAGCC GTGGGGC     TCC
                                  ||||||||  |||||||    |||
                                  GACTTTGG CGCCCCG     AGG
                                       G      CCTG_
GAM1187  KCNK5   3'  GGAATCTGTTGTTGGCTTCAG  14969          TG _  CA_
                                  TTGAAGCCAG  G GG   CC
                                  ||||||||||  | ||   ||
                                  GACTTCGGTT  T TC   GG
                                        GT G  TAA
GAM1187  LAMP2   3'  CGGTAACGCTCTATCTGGTTTT 26571    TG      _     ___   AATCC
             GG                     T  AAGCCAG TGGGGC   ACC
                                  |  |||||||  ||||||   |||
                                  G  TTTGGTC ATCTCG   TGG
                                   GT      T     CAA     CC
GAM1187  LILRB1  5'  GGGCACTCCATTGGTTTTA   22876           CA_
                                  TGAAGCCAGTGGGG   CC
                                  ||||||||||||||   ||
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                                ATTTTGGTTACCTC  GG
                                       ACG
GAM1187 MAN2A1   3' GGATTGAGAATCATTGGCTTT 11436          GGCAC
                                GAAGCCAGTGG    CAATCC
                                ||||||||||    ||||||
                                TTTCGGTTACT    GTTAGG
                                      AAGA_
GAM1187 MBNL     5' GGGTTGGGTTTGTTGGTTTCA 41069        TG  G A
                                TGAAGCCAG  GG C CCAATCC
                                |||||||||  || | |||||||
                                ACTTTGGTT  TT G GGTTGGG
                                     GT  _ _
GAM1187 MYO1E    3' GGGCTGGTCCTGCTGGCTTTGA 18440   TG     TG  GC   AT
                                T  AAGCCAG  GG  ACCA  CC
                                |  |||||||  ||  ||||  ||
                                A  TTCGGTC  CC  TGGT  GG
                                 GT      GT  __   CG
GAM1187 NCKAP1   3' TGGTGCCCTGTTGGCATTAG  26470     A    TG
                                TTGA GCCAG  GGGCACCA
                                |||| |||||  ||||||||
                                GATT CGGTT  CCCGTGGT
                                   A    GT
GAM1187 NEB      5' GGGCATCTCCTGCTGCCTTCAG 17010      C   TG  ____  A
                                TTGAAG CAG  GG   GC CC
                                |||||| |||  ||   || ||
                                GACTTC GTC  CC   CG GG
                                    C   GT  TCTA  _
GAM1187 NOX5     5' GGGTTCTTGGTCTCACTGACTT 44708      C       ACC_
           CAA                    TTGAAG CAGTGGGGC   AATCC
                                  |||||| |||||||||   |||||
                                  AACTTC GTCACTCTG   TTGGG
                                     A       GTTC
GAM1187 OFD1     5' GGTCCTGCCTCGCTGCCTTCAG 14609      C       ___
                                TTGAAG CAGTGGGGC   ACC
                                |||||| |||||||||   |||
                                GACTTC GTCGCTCCG   TGG
                                    C       TCC
GAM1187 OGG1     3' GGATTCTCATTGCCTTCG    34158      C      CA
                                TGAAG CAGTGGGG  CC
                                |||||  ||||||||  ||
                                GCTTC GTTACTCT  GG
                                   C       TA
GAM1187 PFKL     3' AGGCTGCTGCCCCCTGGCTTTG 12052   TG     T     C  AT C
           G                     T  AAGCCAG GGGGCA CA  C
                                 |  ||||||| |||||| ||  |
                                 G  TTCGGTC CCCCGT GT  G
                                  GT      _     C  CG AG
GAM1187 PKNOX1   3' GGGTTCTGTTTTCTTTGGTTTC 17100         T_     CC
           GA                     TTGAAGCCAG  GGGGCA  AATCC
                                  |||||||||  ||||||  |||||
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                                AGCTTTGGTT  TTTTGT  TTGGG
                                      TC     C_
GAM1187  PSPHL    5'  GGATGCTTTCATTGGATTTGG  94498   TG  G      _  _
                                T  AA CCAGTGGG GCA CC
                                |  || |||||||| ||| ||
                                G  TT GGTTACTT CGT GG
                                 GT  A       T   A
GAM1187  RENT1    3'  GGAGTTTTGTTGTTGGTTTTAG 12818          TG ___   A
                                TTGAAGCCAG  G   GGC CC
                                ||||||||||  |   ||| ||
                                GATTTTGGTT  T   TTG GG
                                      GT GTT   A
GAM1187  RNF14    3'  CCGGTGTATATGGTCCACTGGT 16273            _______    AATCC
              TTCAG                   TTGAAGCCAGTGGG     GCACC
                                ||||||||||||||     |||||
                                GACTTTGGTCACCT     TGTGG
                                        GGTATA       CCT
GAM1187  RPL10    3'  TTCCCGGTGTTTGCTGGTTTCA 21179          TG  G    AATCC
              G                    TTGAAGCCAG  GG CACC
                                ||||||||||  || ||||
                                GACTTTGGTC  TT GTGG
                                      GT  _    CCCTTT
GAM1187  RRM1     3'  GGAGATTTAGTTTTACTGCTTT 8281     TG    C       ACCAA_
              GA                    T  AAGC AGTGGGGC     TCC
                                |  |||| ||||||||     |||
                                A  TTCG TCATTTTG     AGG
                                 GT    _       ATTTAG
GAM1187  SCAMP1   3'  GGATTTCATCCCTTACTGGTCT 54502      AG       CACC_
              CAA                    TTGA  CCAGTGGGG    AATCC
                                ||||  |||||||||    |||||
                                AACT  GGTCATTCC    TTAGG
                                  CT        CTACT
GAM1187  SEPP1    3'  GTGTTCTATTTGCTTTAA    60732        C
                                TTGAAGC AGTGGGGCAC
                                ||||||| ||||||||||
                                AATTTCG TTATCTTGTG
                                     T
GAM1187  SH3BP2   3'  GGAAAAGGGCCCCAGTGGCTTT 13077   TG     G     A  AA_
              GG                    T  AAGCCA TGGGGC CC   TCC
                                |  |||||| |||||| ||   |||
                                G  TTCGGT ACCCCG GG   AGG
                                 GT     G     _  AAA
GAM1187  SIAH2    3'  GTGTCCCATCTGGCTTCGA    18614          _
                                TTGAAGCCAG TGGGGCAC
                                |||||||||| ||||||||
                                AGCTTCGGTC ACCCTGTG
                                      T
GAM1187  SLC21A2  3'  GGTTGGCTTTCCTGGTTTCAG  20087          TG   __
                                TTGAAGCCAG  GGGC  ACC
                                |||||||||  ||||  |||
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                                GACTTTGGTC  TTCG  TGG
                                      CT    GT
GAM1187  STK18    5'  GGAGAACTTTCCGTGGTTTCAG 27326         G    CACCAA
                                TTGAAGCCA TGGGG     TCC
                                ||||||||| |||||     |||
                                GACTTTGGT GCCTT     AGG
                                      _    TCAAG_
GAM1187  SURF4    3'  GGATTGGTGCCAAGTGTTTTA  53710       CAGTGG
                                TGAAGC     GGCACCAATCC
                                ||||||     ||||||||||||
                                ATTTTG     CCGTGGTTAGG
                                   TGAA__
GAM1187  TCF21    5'  GGAGGCCTCTTGGTTTCAG   13644         T    A_
                                TTGAAGCCAG GGGGC  CC
                                |||||||||| |||||  ||
                                GACTTTGGTT CTCCG  GG
                                      _    GA
GAM1187  TFAP2C   3'  GGGGCCTTCTGGTTTTAG    13685         T    A
                                TTGAAGCCAG GGGGC CC
                                |||||||||| ||||| ||
                                GATTTTGGTC TTCCG GG
                                      _    G
GAM1187  TLL2     3'  GGAATTCCATGGGCTTCAA   25884         A     CA
                                TTGAAGCC GTGGGG  CC
                                |||||||| ||||||  ||
                                AACTTCGG TACCTT  GG
                                     G     AA
GAM1187  TRIM37   3'  GGCATTGGTGCTCTACTGTCTT 31626   TG   C          _
            TGG                    T  AAG CAGTGGGGCACCAAT CC
                                |  ||| ||||||||||||||| ||
                                G  TTC GTCATCTCGTGGTTA GG
                                 GT   T           C
GAM1187  TRIM8    3'  GATTTTGTTTTGGTTTTGG   48855   TG     TGG   CC
                                T  AAGCCAG   GGCA  AATC
                                |  |||||||   ||||  ||||
                                G  TTTGGTT   TTGT  TTAG
                                 GT      ___    T_
GAM1187  UC28     3'  GGGTCTCAATGGCTTCAG    41589         G     A
                                TTGAAGCCA TGGGGC CC
                                ||||||||| |||||| ||
                                GACTTCGGT ACTCTG GG
                                      A     _
GAM1187  USP7     3'  GATTCGCTGCTGGTGTTAA   14417     A     GG   ACC
                                TTGA GCCAGT  GGC   AATC
                                |||| ||||||  |||   ||||
                                AATT TGGTCG  TCG   TTAG
                                  G     __   C__
GAM1187  VCAM1    5'  ATCGGGCCTCACTGGCTTCAG  55635              A  AATCC
                                TTGAAGCCAGTGGGGC CC
                                |||||||||||||||| ||
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```
                                GACTTCGGTCACTCCG GG
                                       _ CTAC
GAM1187 VCAM1    5' CATCGGGCCTCACTGGCTTCAG 55636            A AATCC
                                TTGAAGCCAGTGGGGC CC
                                |||||||||||||||| ||
                                GACTTCGGTCACTCCG GG
                                       _ CTACG
GAM1187 VPS41    3' GTGCTCTGCTGGCTACGA   27696    A    TG
                                TTG AGCCAG  GGGCAC
                                ||| ||||||  ||||||
                                AGC TCGGTC  CTCGTG
                                  A     GT
GAM1187 XRCC3    5' GGGCCTCCCACAGGCTTTGA  19520   TG   A   __ A
                                T  AAGCC GTGGG  GC CC
                                |  ||||| |||||  || ||
                                A  TTCGG CACCC  CG GG
                                 GT    A    TC _
GAM1187 ZNF261   3' GCTCTGGTGATCCTGTTGGCTT 18733   TG     TG  _    ATCC
           TGG                    T  AAGCCAG  GGG CACCA
                                |  |||||||  ||| |||||
                                G  TTCGGTT  CCT GTGGT
                                 GT      GT   A    CTCG
GAM1187 AD034    3' GGAAGATGGCTTATTGGTTTTA 49748           G  CCAA
           A                     TTGAAGCCAGTGGG CA   TCC
                                |||||||||||||| ||   |||
                                AATTTTGGTTATTC GT   AGG
                                        G  AGA_
GAM1187 BTN2A2   3' GGGTTCTCAGGCCTTTGGCTTT 23770   TG     TG   ACC__
           GG                     T  AAGCCAG  GGGC    AATCC
                                |  |||||||  ||||    |||||
                                G  TTCGGTT  TCCG    TTGGG
                                 GT      __    GACTC
GAM1187 C20orf55 3' GGGTTTTGTTCTTGGCTTTGG  49478   TG    GT    CC
                                T  AAGCCA  GGGGCA  AATCC
                                |  ||||||  ||||||  |||||
                                G  TTCGGT  TCTTGT  TTGGG
                                 GT     __     T_
GAM1187 C21orf25 3' GGAACTGGGTGCTCATGTTGGT 64298         TG_     AA__
           TTTAA                  TTGAAGCCAG   GGGCACC   TCC
                                |||||||||   |||||||   |||
                                AATTTTGGTT   CTCGTGG   AGG
                                      GTA      GTCA
GAM1187 CBX6     3' GGAGACTTCTTTTTGTTGGTTT 27419         TG   CACCAA_
           TAA                    TTGAAGCCAG  GGG      TCC
                                |||||||||  |||      |||
                                AATTTTGGTT  TTT      AGG
                                      GT   TCTTCAG
GAM1187 CXorf12  5' GGGCTTCTTTCTGCTGGCTCAG 14488     A     _____    A
                                TTGA GCCAGT    GGGGC CC
                                |||| ||||||    ||||| ||
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                                GACT CGGTCG    CTTCG GG
                                  _    TCTTT    _
GAM1187 CYorf14   5' GGAGGTTTTTTGGTTTCAG   38204         T    A_
                                TTGAAGCCAG GGGGC  CC
                                |||||||||| |||||  ||
                                GACTTTGGTT TTTTG  GG
                                      _    GA
GAM1187 DCTN3    3' GGAAGCTTTGTATTTATTGGCT 44571          _  CCAA_
           TCAA                   TTGAAGCCAGTGGG GCA    TCC
                                |||||||||||||| |||    |||
                                AACTTCGGTTATTT TGT    AGG
                                      A   TTCGA
GAM1187 DCTN3    3' GGAAGCTTTGTATTTATTGGCT 24322          _  CCAA_
           TCAA                   TTGAAGCCAGTGGG GCA    TCC
                                |||||||||||||| |||    |||
                                AACTTCGGTTATTT TGT    AGG
                                      A   TTCGA
GAM1187 DKFZP434P0721 3' GGATTTTTTTGTCTTTTGGCTT 64463         T    CC__
           TAA                   TTGAAGCCAG GGGGCA    AATCC
                                |||||||||| ||||||   |||||
                                AATTTCGGTT TTCTGT    TTAGG
                                      _    TTTT
GAM1187 DKFZP564J047 3' GGTGTGATTCTTTGGCTTCAA  50445         T  __
                                TTGAAGCCAG GGG  GCACC
                                |||||||||| |||  |||||
                                AACTTCGGTT CTT  TGTGG
                                      T   AG
GAM1187 DKFZP586C1619 3' GGAGTTCCCCCATTGTCTTTGG 62620   TG   C      CACCAA
                                T  AAG CAGTGGGG     TCC
                                |  ||| ||||||||     |||
                                G  TTC GTTACCCC     AGG
                                 GT   T      CTTG__
GAM1187 DKFZp761O0113 5' GTGTTTTATTGATTTCAA    37898      GC
                                TTGAA  CAGTGGGGCAC
                                |||||  ||||||||||
                                AACTT  GTTATTTTGTG
                                   TA
GAM1187 DKFZp762P2111 3' GGCAGTTCCACTGGGTTCAG   87636      G       A_
                                TTGAA CCAGTGGGGC  CC
                                |||||  |||||||||  ||
                                GACTT GGTCACCTTG  GG
                                   G         AC
GAM1187 E2IG5    3' GTGTTTTATTGTTTTGA    27640   TG   C
                                T  AAGC AGTGGGGCAC
                                |  ||||  ||||||||||
                                A  TTTG TTATTTTGTG
                                 GT   _
GAM1187 FLJ10350  3' GGTCCTCTCTGTTGTTTT    97253      __  T   C
                                GAAGC  CAG GGGG ACC
                                |||||  |||  ||||  |||
```

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                                TTTTG  GTC CTCC TGG
                                   TT   T   _
GAM1187  FLJ12687  3'  GGGTTTTCTTGGTTTTAA    46755          TG    A
                                TTGAAGCCAG  GGGC CC
                                ||||||||||  |||| ||
                                AATTTTGGTT  TTTG GG
                                     CT   _
GAM1187  FLJ12783  3'  GGTTAACCCACTGGTTTCAA   49488            GC_
                                TTGAAGCCAGTGGG   ACC
                                ||||||||||||||   |||
                                AACTTTGGTCACCC   TGG
                                       AAT
GAM1187  FLJ12998  3'  GGACATTTTCTCATTGGTTTT  43150            CACCAA
                                GAAGCCAGTGGGG     TCC
                                ||||||||||||      |||
                                TTTTGGTTACTCT     AGG
                                       TTTAC_
GAM1187  FLJ13940  3'  GGACTGGTGCCCCACAGGCTTT 47309          A         A
            AA                    TTGAAGCC GTGGGGCACCA TCC
                                ||||||||| |||||||||| |||
                                AATTTCGG CACCCCGTGGT AGG
                                     A          C
GAM1187  FLJ14084  3'  GTGCTTTGGTGGTTTTAA    41595          G GG
                                TTGAAGCCA T  GGCAC
                                |||||||||  |  |||||
                                AATTTTGGT G  TCGTG
                                     G TT
GAM1187  FLJ14721  3'  GGACCCTCCTGGTTTTAA    52643           TG   CA
                                TTGAAGCCAG  GGG  CC
                                ||||||||||  |||  ||
                                AATTTTGGTC  CCC  GG
                                     CT   A_
GAM1187  FLJ14800  3'  GGTGGTCCCACTCGCTTTGG   52687    TG    C      _
                                T  AAGC AGTGGGGC ACC
                                |  |||| |||||||| |||
                                G  TTCG TCACCCTG TGG
                                 GT    C       G
GAM1187  FLJ20313  5'  GGAGCCCCCACTGGCTCG     35413     A        _ A
                                TGA GCCAGTGGGG C CC
                                ||| |||||||||| | ||
                                GCT CGGTCACCCC G GG
                                  _         C A
GAM1187  FLJ20847  3'  GGACTCTACTGGTTTGAG     96486     G          CA
                                TT AAGCCAGTGGGG  CC
                                || ||||||||||||  ||
                                GA TTTGGTCATCTC  GG
                                 G          A_
GAM1187  FLJ21438  5'  GGAGCCCCACTGCTTTCAG    62197       C        A
                                TTGAAG CAGTGGGGC CC
                                ||||||  ||||||||| ||
```

```
                                GACTTT GTCACCCCG GG
                                   C        A
GAM1187  FLJ21459  3'  GGCTGCCTTGCTGGTTTTGG   44806   TG      TG    _
                                T  AAGCCAG  GGGCA CC
                                |  |||||||  ||||| ||
                                G  TTTGGTC  TCCGT GG
                                 GT      GT    C
GAM1187  FLJ22649  3'  GGTTTGTTTTTTGGTTTTGG   41923   TG      T    __
                                T  AAGCCAG GGGGC  ACC
                                |  ||||||| |||||  |||
                                G  TTTGGTT TTTTG  TGG
                                 GT      _    TT
GAM1187  FLJ22679  3'  GGATTTTCTTACTGGTTTC    35183           CACC
                                GAAGCCAGTGGGG    AATCC
                                ||||||||||||    |||||
                                CTTTGGTCATTCT    TTAGG
                                        T___
GAM1187  FLJ22679  3'  GGATTTTCTTACTGGTTTC    50909           CACC
                                GAAGCCAGTGGGG    AATCC
                                ||||||||||||    |||||
                                CTTTGGTCATTCT    TTAGG
                                        T___
GAM1187  FLJ23375  3'  GGATTGGTGGGTGAGCTTTAG  46950        _  GTGGGG
                                TTGAAGC CA     CACCAATCC
                                |||||||  ||     |||||||||
                                GATTTCG GT     GTGGTTAGG
                                    A  GG____
GAM1187  FLJ23510  3'  GGACACTTTGGTGTCCCACTGG 45626     A            ____
            CCTCG                   TGA GCCAGTGGGGCACCAA    TCC
                                ||| ||||||||||||||||    |||
                                GCT CGGTCACCCTGTGGTT    AGG
                                  C             TCAC
GAM1187  FLJ32356  3'  GGACCAGGTCTTGCTTGGCTTC 59025        _ TG    ACCAA
            G                    TGAAGCCA G  GGGC     TCC
                                ||||||||  |  ||||     |||
                                GCTTCGGT C  TCTG     AGG
                                     T GT    GACC_
GAM1187  GLE1L    3'  CGGGTGCTATTACCTGCTGGTT 9475    TG      TG _____    AATCC
            TTGA                   T  AAGCCAG  GG    GCACC
                                |  |||||||  ||    |||||
                                A  TTTGGTC  CC    CGTGG
                                 GT      GT  ATTAT    G   CC
GAM1187  GMEB2    5'  GATTGGGGCTGGCTTTGA    25663    TG      GGGGCA
                                T  AAGCCAGT     CCAATC
                                |  ||||||||     ||||||
                                A  TTCGGTCG     GGTTAG
                                 GT       G_____
GAM1187  GRWD     3'  GGCGTCCCACTGGCTCTGA    49784    GA          A
                                TT  AGCCAGTGGGGC CC
                                ||  |||||||||||| ||
```

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                                AG  TCGGTCACCCTG GG
                                 TC          C
GAM1187  GTPBP5    3'  GGGTGTGAATTCGGTGGTTTTG 65980    TG     G   ___    AATCC
              A                   T  AAGCCA TGGG   GCACC
                                  |  |||||| ||||   |||||
                                  A  TTTGGT GCTT   TGTGG
                                   GT     G    AAG    G  C
GAM1187  HMGN4     3'  GGATTCATCCTGCTGGTTTTA  22031         TG   CACC
                                  TGAAGCCAG  GGG   AATCC
                                  |||||||||  |||   |||||
                                  ATTTTGGTC  CCT   TTAGG
                                        GT   AC__
GAM1187  HSGT1     5'  GGATTTCCGCTGGCTTCAG   24390             CA
                                  TTGAAGCCAGTGGGG  CC
                                  ||||||||||||||  ||
                                  GACTTCGGTCGCCTT  GG
                                           TA
GAM1187  HSXIAPAF1 3'  GGGTTTTATTCGTTGGGCTTTA 34461         _____      A  AATCC
              A                   TTGAAGCC    AGTGGGGC CC
                                  ||||||||    |||||||| ||
                                  AATTTCGG    TTATTTTG GG
                                       GTTGC      _    C
GAM1187  HUMZD58C02 3'  GGTTGCGTCTCATTGGCTCAG  80578     A        AC    C
                                  TTGA GCCAGTGGGGC  CAATC
                                  |||| ||||||||||  |||||
                                  GACT CGGTTACTCTG  GTTGG
                                    _         C_    A
GAM1187  IMAGE145052 5'  GGATTGTAAGCTGCTGGTTTT  27328         GG   AC_
                                  GAAGCCAGT  GGC   CAATCC
                                  |||||||||  |||   ||||||
                                  TTTTGGTCG  TCG   GTTAGG
                                       __   AAT
GAM1187  IMP-2     3'  GGGCTTCTGCAGGCTTCAG    22609         A  _    A
                                  TTGAAGCC GT GGGGC CC
                                  |||||||| || ||||| ||
                                  GACTTCGG CG CTTCG GG
                                       A  T    _
GAM1187  KCNJ14    5'  CGGTGAAGGTTCCCGTTGGCTT 26242    TG         _____   AATCC
              TGG                    T  AAGCCAGTGGGG    CACC
                                  |  ||||||||||||    ||||
                                  G  TTCGGTTGCCCT    GTGG
                                   GT          TGGAA      CC
GAM1187  KIAA0252  3'  GATTCTGTTTTGCTGCTTTGG  63456   TG   C  TG    CC   C
                                  T  AAGC AG  GGGCA  AATC
                                  |  |||| ||  |||||  ||||
                                  G  TTCG TC  TTTGT  TTAG
                                   GT    _ GT    C_    T
GAM1187  KIAA0268  3'  GGATTTCATTGGCTTCAA     70542           GG CA
                                  TTGAAGCCAGTG  G  CC
                                  ||||||||||||  |  ||
```

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                                AACTTCGGTTAC  T  GG
                                      TT A_
GAM1187  KIAA0280  3'  GGTGCTTGCCTCATGGCTTTGG 93309    TG     GT_ __
                                T  AAGCCA   GG  GGCACC
                                |  ||||||   ||  ||||||
                                G  TTCGGT   CC  TCGTGG
                                 GT     ACT  GT
GAM1187  KIAA0317  3'  GGACTGGTTCTGCTGTTTTTGG 29745    TG   C   TG  GC    A
                                T  AAG CAG  GG  ACCA TCC
                                |  ||| |||  ||  |||| |||
                                G  TTT GTC  CT  TGGT AGG
                                 GT   T   GT __    C
GAM1187  KIAA0337  3'  GGGTTTGTTTTGTTCTGTTTGG 29481    TG     _ TG    ___  C
            TTTTGG                  T  AAGCCA G  GGGC   AC AATCC
                                |  |||||| |  ||||   || |||||
                                G  TTTGGT T  CTTG   TG TTGGG
                                 GT     T GT    TTT  T
GAM1187  KIAA0431  3'  GGGCATCCCCCATTAGGTTTCA 31552         _      CA___  AATCC
              A                  TTGAAGCC AGTGGGG    CC
                                |||||||| |||||||     ||
                                AACTTTGG TTACCCC     GG
                                     A      CTACG    C
GAM1187  KIAA0450  5'  GGGTCCTGCTGGCTGCAG    28369     A     TG    A
                                TTG AGCCAG  GGGC CC
                                ||| ||||||  |||| ||
                                GAC TCGGTC  CCTG GG
                                  G     GT   _
GAM1187  KIAA0459  3'  GGGCCCTATTGGGTTTTAG    61654         _      A
                                TTGAAGCC AGTGGGGC CC
                                |||||||| |||||||| ||
                                GATTTTGG TTATCCCG GG
                                     G       _
GAM1187  KIAA0472  3'  GGGCTCTGCAGGCTTTAG    72360         A TG    A
                                TTGAAGCC G  GGGC CC
                                |||||||| |  |||| ||
                                GATTTCGG C  CTCG GG
                                     A GT    _
GAM1187  KIAA0475  3'  GTGTTCTATGGGTTTCAA    30126         A
                                TTGAAGCC GTGGGGCAC
                                |||||||| |||||||||
                                AACTTTGG TATCTTGTG
                                     G
GAM1187  KIAA0493  5'  GGCAGTCCTCTGGTTTTGG    64935    TG      T    A_
                                T  AAGCCAG GGGGC  CC
                                |  ||||||| |||||  ||
                                G  TTTGGTC TCCTG  GG
                                 GT      _     AC
GAM1187  KIAA0939  3'  GGGGGCTTCACTGGCTTCG    62718             A_
                                TGAAGCCAGTGGGGC  CC
                                ||||||||||||||  ||
```

```
                                GCTTCGGTCACTTCG  GG
                                       GG
GAM1187  KIAA1086  3'  GGGCATCTTGCTGGCTCTAA  71288    A    TG __ A
                                TTG AGCCAG  GG  GC CC
                                ||| ||||||  ||  || ||
                                AAT TCGGTC  TC  CG GG
                                  C     GT  TA  _
GAM1187  KIAA1131  3'  GATCCCTGTTTTGCTGGCTTT  62524       TG    CCA  C
                                GAAGCCAG  GGGCA   ATC
                                ||||||||  |||||   |||
                                TTTCGGTC  TTTGT   TAG
                                     GT    CCC
GAM1187  KIAA1255  3'  TCCTGTTTTCCATTGGCTTCAG 67746            C  CAATCC
                                TTGAAGCCAGTGGGG AC
                                |||||||||||||| ||
                                GACTTCGGTTACCTT TG
                                         T  TCCTG
GAM1187  KIAA1320  5'  GGTGGTTTTGTTGGTTTT    69845       TG   _
                                GAAGCCAG  GGGC ACC
                                ||||||||  |||| |||
                                TTTTGGTT  TTTG TGG
                                     GT   G
GAM1187  KIAA1391  3'  GGATTGGTCCTGTCATGTGGTT 67853        _  __  C
          TTAG                    TTGAAGCCA GTG  GGG ACCAATCC
                                ||||||||| |||  ||| ||||||||
                                GATTTTGGT TAC  TCC TGGTTAGG
                                     G   TG  _
GAM1187  KIAA1431  3'  CGGTTTTGCCTTTGTTGGTTTT 63680         TG _  ___  AATCC
          AA                     TTGAAGCCAG  G GGC   ACC
                                ||||||||||  | |||   |||
                                AATTTTGGTT  T CCG   TGG
                                      GT T   TTT     CC
GAM1187  KIAA1545  3'  GGCGGCTCCTGTGGGCTTCAG  61336       AGT_    A_
                                TTGAAGCC   GGGGC  CC
                                ||||||||   |||||  ||
                                GACTTCGG   CCTCG  GG
                                     GTGT    GC
GAM1187  KIAA1795  3'  GGGTTGGTTAGATTGATTTCAG 72618      GC   GGGGC
                                TTGAA  CAGT    ACCAATCC
                                |||||  ||||    ||||||||
                                GACTT  GTTA    TGGTTGGG
                                   TA   GAT__
GAM1187  KIAA1913  5'  GGTTTCCCACAGGTTTTGG   74320   TG    A    C
                                T  AAGCC GTGGGG ACC
                                |  ||||| |||||| |||
                                G  TTTGG CACCCT TGG
                                 GT    A    T
GAM1187  KIAA1922  3'  GGGTGCAGGGTTCTGTTGGCTC 74001    A    TG   A  A__
          CAG                    TTG AGCCAG  GGGC CC   ATCC
                                ||| ||||||  |||| ||   ||||
```

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                                GAC TCGGTT  CTTG GG   TGGG
                                  C     GT   _ ACG
GAM1187 LCP      3'  TGCACCTGTTGGTTTTAA    27479          TG _
                                TTGAAGCCAG  GG GCA
                                ||||||||||  || |||
                                AATTTTGGTT  CC CGT
                                      GT  A
GAM1187 LRRFIP1  3'  GGTGCTCTACTGCTTTAA    17615        C
                                TTGAAGC AGTGGGGCACC
                                ||||||| ||||||||||
                                AATTTCG TCATCTCGTGG
                                    _
GAM1187 LZ16     5'  GGACACACCTCCATTGGATTTA 26095       G        CACCAA
             A                   TTGAA CCAGTGGGG     TCC
                                ||||| |||||||||      |||
                                AATTT GGTTACCTC     AGG
                                   A        CACAC_
GAM1187 MARCO    5'  GGAGCATTTCTGCTGGCTCCAG 23190     A     TG ___ A
                                TTG AGCCAG  GG   GC CC
                                ||| ||||||  ||   || ||
                                GAC TCGGTC  CT   CG GG
                                  C     GT  TTA  A
GAM1187 MEF-2    3'  GGATGTGATTTTGGTTGGTTTT 65025          TG __  CA
             AA                   TTGAAGCCAG  GGG  CAC  ATCC
                                ||||||||||  |||  |||  ||||
                                AATTTTGGTT  TTT  GTG  TAGG
                                      GG   TA  __
GAM1187 MEGF10   5'  GTGTCTTGGCTGGCTTTGG   51609   TG      G _
                                T  AAGCCAGT G GGCAC
                                |  |||||||| | |||||
                                G  TTCGGTCG T CTGTG
                                 GT       G T
GAM1187 MGC12837 3'  GGGTTGGTATGCTGGCTTTAG  52171           GGGC
                                TTGAAGCCAGTG   ACCAATCC
                                ||||||||||||   ||||||||
                                GATTTCGGTCGT   TGGTTGGG
                                       A___
GAM1187 MGC13007 5'  GGAATTGGTTCCACTGTGTTTC 51280       _     GC     _
             GA                   TTGAAGC CAGTGGG  ACCAAT CC
                                ||||||| |||||||  |||||| ||
                                AGCTTTG GTCACCT  TGGTTA GG
                                    T      __      A
GAM1187 MGC19595 5'  GGTGGCCTCGTTGGCTTTA   54183            _
                                TGAAGCCAGTGGGGC ACC
                                |||||||||||||| |||
                                ATTTCGGTTGCTCCG TGG
                                       G
GAM1187 MGC2752  5'  GGTCGAGGGTGATTCGCTGGCT 79083           G   AAT__
             TTAA                   TTGAAGCCAGTGGG CACC    CC
                                |||||||||||||| ||||    ||
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                                AATTTCGGTCGCTT GTGG    GG
                                      A   GAGCT
GAM1187 MGC34923 5' GGGTTCTTGATCTCACTGACTT 59198      C      _ CC
            CAA                   TTGAAG CAGTGGGG CA  AATCC
                                  |||||| |||||||| ||  |||||
                                  AACTTC GTCACTCT GT  TTGGG
                                     A       A  TC
GAM1187 MGC5139  3' GATTTACCACTGGTTTTA    74573          GGCACC
                                  TGAAGCCAGTGG     AATC
                                  ||||||||||||     ||||
                                  ATTTTGGTCACC     TTAG
                                        AT____
GAM1187 MGC5508  3' GTGCTTGGTTGGTTTTAA    44270         TG
                                  TTGAAGCCAG  GGGCAC
                                  ||||||||||  ||||||
                                  AATTTTGGTT  TTCGTG
                                        GG
GAM1187 NUP54    5' GATTTGGTACTGGTTTTGG   60725   TG      GGGGC   _
                                  T  AAGCCAGT    ACCAA TC
                                  |  ||||||||    ||||| ||
                                  G  TTTGGTCA    TGGTT AG
                                   GT       _____    T
GAM1187 NYD-SP15 3' GGTTGTCTCATGGCTTTGA   48848   TG     G     _
                                  T  AAGCCA TGGGGCA CC
                                  |  |||||| ||||||| ||
                                  A  TTCGGT ACTCTGT GG
                                   GT     _      T
GAM1187 OAZ1     5' GAGGTTTTCCTGGTTTCG    15976         T GG C   AA
                                  TGAAGCCAG G  G ACC  TC
                                  ||||||||| |  | |||  ||
                                  GCTTTGGTC C  T TGG  AG
                                        _ TT _  __
GAM1187 OLFM3    3' GGAGTTGTCTTTGTGGTTTCAA 83025         GT     CCAA
                                  TTGAAGCCA  GGGGCA    TCC
                                  |||||||||  ||||||   |||
                                  AACTTTGGT  TTCTGT    AGG
                                        GT     TG__
GAM1187 PB1      3' GGGTTTTTGTTTTCTTGGTTTT 36878   TG     TG    CC
            GG                    T  AAGCCAG  GGGCA  AATCC
                                  |  |||||||  |||||  |||||
                                  G  TTTGGTT  TTTGT  TTGGG
                                   GT      CT    TT
GAM1187 PEF      3' TGCTCTGCTCGGCTTCAG    25683        _ TG
                                  TTGAAGCC AG  GGGCA
                                  ||||||||| ||  |||||
                                  GACTTCGG TC  CTCGT
                                       C  GT
GAM1187 PP1057   3' GGGTGAGCACGCTTGTTGGTTT 49256          TG  G_____   AATCC
            CAA                   TTGAAGCCAG  GG     CACC
                                  ||||||||||  ||     ||||
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                                AACTTTGGTT TC    GTGG
                                     GT GCACGA  G  C
GAM1187 PRO2958 3' GTGCTCTGTGGCTTTGG   38250  TG    G
                                T AAGCCA TGGGGCAC
                                | |||||| ||||||||
                                G TTCGGT GTCTCGTG
                                 GT    _
GAM1187 PTPRT   3' GATTTAGCCTTGTTGGTTTTAA 56495       TG   ACC
                                TTGAAGCCAG GGGC  AATC
                                |||||||||| ||||  ||||
                                AATTTTGGTT TCCG  TTAG
                                     GT   AT_
GAM1187 RYK     3' GGAGGCTTTTGCTGTTTTTAA 83509     C  TG _ A_
                                TTGAAG CAG GG GC CC
                                |||||| |||  || ||  ||
                                AATTTT GTC TT CG GG
                                   T  GT T GA
GAM1187 SCAMP5  3' GGAGGCTCTCTGGCTTTAG   58060       T   A_
                                TTGAAGCCAG GGGGC CC
                                |||||||||| |||||  ||
                                GATTTCGGTC TCTCG GG
                                     _   GA
GAM1187 SEC8    3' GGATTCTTTCTCTCTGGTTTTG 41738   TG    T  CACC
           G                     T AAGCCAG GGGG   AATCC
                                | |||||||| ||||   |||||
                                G TTTGGTC CTCT   TTAGG
                                 GT     T   TTC_
GAM1187 SLC6A13 3' GGGCGAGACTTGCTGGCTTCG 34004       TG ____ A
                                TGAAGCCAG GG   GC CC
                                ||||||||| ||   || ||
                                GCTTCGGTC TC   CG GG
                                     GT AGAG _
GAM1187 SZF1    3' GGGTTCTTGGTCTTGCTGACTT 32731     C  TG   ACC_
           CAA                    TTGAAG CAG GGGC   AATCC
                                |||||| |||  ||||   |||||
                                AACTTC GTC TCTG   TTGGG
                                   A  GT   GTTC
GAM1187 TBLR1   3' GGGTATTATGCTCTGTTGGTTT 45429       TG   CCA_
           T                    GAAGCCAG GGGCA   ATCC
                                |||||||| |||||   ||||
                                TTTTGGTT CTCGT   TGGG
                                    GT   ATTA
GAM1187 TOM1    3' GGGGCCCCATGGCTTTGG   19697  TG    G    A
                                T AAGCCA TGGGGC CC
                                | |||||| |||||| ||
                                G TTCGGT ACCCCG GG
                                 GT    _    G
GAM1187 TOR2A   3' GGTCCCCCATGGTTTTAG   56189       G   C
                                TTGAAGCCA TGGGG ACC
                                ||||||||| ||||| |||
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                                GATTTTGGT ACCCC TGG
                                      _    C
GAM1187 TXNL2    3' GCCTCGTGCCACACTGGCTTTG 22581   TG       G    CAATCC
             A                    T  AAGCCAGTG GGCAC
                                  |  ||||||||| |||||
                                  A  TTCGGTCAC CCGTG
                                   GT        A    CTCCG
GAM1187 UBCE7IP5 3' GTGCTCAGCTGGCTTCAG    30850          G
                                  TTGAAGCCAGT GGGCAC
                                  |||||||||||| ||||||
                                  GACTTCGGTCG CTCGTG
                                        A
GAM1187 YME1L1   3' GGATGCTTGCTGGTTTTA    58436         TG  G  _
                                  TGAAGCCAG  GG CA CC
                                  |||||||||  || || ||
                                  ATTTTGGTC  TC GT GG
                                       GT  _  A
GAM1187 ZID      3' GGATATCTGTTCTACTGTTTTA 22784        C       CCA
             A                    TTGAAGC AGTGGGGCA   ATCC
                                  ||||||| |||||||||   ||||
                                  AATTTTG TCATCTTGT   TAGG
                                      _       CTA
GAM1187 ZNF221   5' GGCTGCCTCACTGCTTCAA   26268       C       _
                                  TTGAAGC AGTGGGGCA CC
                                  ||||||| ||||||||| ||
                                  AACTTCG TCACTCCGT GG
                                      _       C
GAM1187 LOC113201 3' CCCAGTGCTGTATTGGCTTCAG 57354          G    CAATCC
                                  TTGAAGCCAGTG GGCAC
                                  |||||||||||| |||||
                                  GACTTCGGTTAT TCGTG
                                        G    ACCCA
GAM1187 LOC127352 3' GGATACTTCTGACTGGTTTTAA 75149          G   CACCA
                                  TTGAAGCCAGT GGG    ATCC
                                  |||||||||| |||    ||||
                                  AATTTTGGTCA TCT    TAGG
                                        G   TCA__
GAM1187 LOC127703 3' GTGCCTCTCTGGCTTTAG    75180          T
                                  TTGAAGCCAG GGGGCAC
                                  |||||||||| |||||||
                                  GATTTCGGTC CTCCGTG
                                       T
GAM1187 LOC134359 3' GGGTTAGAAGTCTTTTGGTTTT 75663         T    ACC_
             AA                    TTGAAGCCAG GGGGC   AATCC
                                  |||||||||| |||||   |||||
                                  AATTTTGGTT TTCTG   TTGGG
                                      _    AAGA
GAM1187 LOC136015 3' GGATATTTTACTTGGCTTTA  76705       _     CA_
                                  TGAAGCC AGTGGGG   CC
                                  ||||||| |||||||   ||
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                                ATTTCGG TCATTTT   GG
                                    T      ATA
GAM1187  LOC144755 3'  GGCGCCTTGGTGGCTTTGG   84101   TG     G     A
                                T  AAGCCA TGGGGC CC
                                |  |||||| |||||| ||
                                G  TTCGGT GTTCCG GG
                                 GT     G     C
GAM1187  LOC145622 3'  GGGTTCTTGGTCTCACTGACTT 77821       C       ACC_
            CAA                    TTGAAG CAGTGGGGC    AATCC
                                |||||| |||||||||    |||||
                                AACTTC GTCACTCTG    TTGGG
                                   A        GTTC
GAM1187  LOC145781 3'  GGAACCCTGTGGCTTCAA    77957         G    CA
                                TTGAAGCCA TGGGG  CC
                                ||||||||| |||||  ||
                                AACTTCGGT GTCCC  GG
                                     _    AA
GAM1187  LOC146455 5'  GGAGGCACTTTGCTGTCTTCAA 78462       C   TG   CA  AA
                                TTGAAG CAG  GGG  CC  TCC
                                |||||| |||  |||  ||  |||
                                AACTTC GTC  TTC  GG  AGG
                                   T   GT   AC  __
GAM1187  LOC150159 3'  GATGTGCTTTGCTGGTTTTAG  58261         TG     CA
                                TTGAAGCCAG  GGGCAC  ATC
                                ||||||||||  ||||||  |||
                                GATTTTGGTC  TTCGTG  TAG
                                     GT     __
GAM1187  LOC150406 3'  GGGTTGTGTGGGCATTGGTTCA 80673      G     GGG  _
            G                   TTGAA CCAGTG   CAC CAATCC
                                |||||| ||||||   ||| ||||||
                                GACTT GGTTAC   GTG GTTGGG
                                  _     GG_   T
GAM1187  LOC151610 3'  GGATGGCCCTCCTGGCTTCAG  81097         TG    ACCA
                                TTGAAGCCAG  GGGC    ATCC
                                ||||||||||  ||||    ||||
                                GACTTCGGTC  CCCG    TAGG
                                     CT    G___
GAM1187  LOC153205 3'  GGACTTTATTAGGCTTTAG    87162         _      CA
                                TTGAAGCC AGTGGGG  CC
                                |||||||| |||||||  ||
                                GATTTCGG TTATTTC  GG
                                   A      A_
GAM1187  LOC154084 3'  GGAACTTTAGTGGCTTCAA    87381         G    CA
                                TTGAAGCCA TGGGG  CC
                                ||||||||| |||||  ||
                                AACTTCGGT ATTTC  GG
                                     G    AA
GAM1187  LOC154788 3'  GGATATTTTACTTGGCTTTA   87460        _      CA_
                                TGAAGCC AGTGGGG   CC
                                ||||||| |||||||   ||
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                                ATTTCGG TCATTTT   GG
                                    T      ATA
GAM1187  LOC154877 3'  GGCTGGTCTCCTGGCTTCAA   87560         TG  G  _
                                TTGAAGCCAG  GG CA CC
                                ||||||||||  || || ||
                                AACTTCGGTC  CT GT GG
                                     CT  G  C
GAM1187  LOC154881 3'  GGACAGCCTCACTGGTATCAG  82072      A         A__
                                TTGA GCCAGTGGGGC   CC
                                |||| ||||||||||   ||
                                GACT TGGTCACTCCG   GG
                                  A          ACA
GAM1187  LOC155063 3'  GGGTGCAGCCTTGTTGGTTGCA 87646     A     TG    ACCA
           G                     TTG AGCCAG  GGGC    ATCC
                                ||| ||||||  ||||    ||||
                                GAC TTGGTT  TCCG    TGGG
                                  G     GT    ACG_
GAM1187  LOC157556 5'  GGATTTAAATCCTGGCTTCAG  87783         T  GGCACC
                                TTGAAGCCAG GG      AATCC
                                |||||||||| ||      |||||
                                GACTTCGGTC CT      TTAGG
                                      _  AAAT__
GAM1187  LOC158062 3'  GGCTGCCCTGCTGGCTGCAA   87963     A     TG    _
                                TTG AGCCAG  GGGCA CC
                                ||| ||||||  ||||| ||
                                AAC TCGGTC  CCCGT GG
                                  G     GT    C
GAM1187  LOC158160 3'  GTGCCACCACTGGCTTTGG    73475    TG        _
                                T  AAGCCAGTGG GGCAC
                                |  |||||||||| |||||
                                G  TTCGGTCACC CCGTG
                                 GT         A
GAM1187  LOC159199 5'  GGATCCACCCTGCTGGCTTCG  83064         TG   CACCA
                                TGAAGCCAG  GGG     ATCC
                                |||||||||  |||     ||||
                                GCTTCGGTC  CCC     TAGG
                                      GT   ACC__
GAM1187  LOC163882 3'  GGAGTTACCTTATGGTTTCAG  83041         GT_  _   A
                                TTGAAGCCA   GG GGC CC
                                |||||||||   || ||| ||
                                GACTTTGGT   CC TTG GG
                                      ATT  A   A
GAM1187  LOC197201 3'  GGAATTCCGCTGGCATTAG    89278      A         CA
                                TTGA GCCAGTGGGG  CC
                                |||| ||||||||||  ||
                                GATT CGGTCGCCTT  GG
                                  A         AA
GAM1187  LOC197201 3'  GGAATTCCGCTGGCATTAG    89279      A         CA
                                TTGA GCCAGTGGGG  CC
                                |||| ||||||||||  ||
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                                GATT CGGTCGCCTT  GG
                                  A        AA
GAM1187  LOC197201 3'  GGAATTCCGCTGGCATTAG   89280     A        CA
                                TTGA GCCAGTGGGG  CC
                                |||| ||||||||||  ||
                                GATT CGGTCGCCTT  GG
                                  A        AA
GAM1187  LOC197201 3'  GGAATTCCGCTGGCATTAG   89281     A        CA
                                TTGA GCCAGTGGGG  CC
                                |||| ||||||||||  ||
                                GATT CGGTCGCCTT  GG
                                  A        AA
GAM1187  LOC197201 3'  GGAATTCCGCTGGCATTAG   89282     A        CA
                                TTGA GCCAGTGGGG  CC
                                |||| ||||||||||  ||
                                GATT CGGTCGCCTT  GG
                                  A        AA
GAM1187  LOC197201 3'  GGAATTCCGCTGGCATTAG   89283     A        CA
                                TTGA GCCAGTGGGG  CC
                                |||| ||||||||||  ||
                                GATT CGGTCGCCTT  GG
                                  A        AA
GAM1187  LOC197201 3'  GGAATTCCGCTGGCATTAG   89284     A        CA
                                TTGA GCCAGTGGGG  CC
                                |||| ||||||||||  ||
                                GATT CGGTCGCCTT  GG
                                  A        AA
GAM1187  LOC197201 3'  GGAATTCCGCTGGCATTAG   89285     A        CA
                                TTGA GCCAGTGGGG  CC
                                |||| ||||||||||  ||
                                GATT CGGTCGCCTT  GG
                                  A        AA
GAM1187  LOC197201 3'  GGAATTCCGCTGGCATTAG   89286     A        CA
                                TTGA GCCAGTGGGG  CC
                                |||| ||||||||||  ||
                                GATT CGGTCGCCTT  GG
                                  A        AA
GAM1187  LOC199231 3'  GGGTCATTCTTGTTTGGCTTTA 91818         _ TG   C__   AATCC
            G                    TTGAAGCCA G  GGG   ACC
                                |||||||| |  |||   |||
                                GATTTCGGT T  TCT   TGG
                                     T GT   TAC   G
GAM1187  LOC199974 3'  GGATACTTCTGACTGGTTTTGA 89892   TG       G   CACCA
                                T  AAGCCAGT GGG     ATCC
                                |  |||||||| |||     ||||
                                A  TTTGGTCA TCT     TAGG
                                 GT       G   TCA__
GAM1187  LOC200261 5'  GGCCAGCCTCGTTGTCTTCAG  90052       C        A__
                                TTGAAG CAGTGGGGC   CC
                                ||||||  |||||||||   ||
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                                GACTTC GTTGCTCCG   GG
                                   T       ACC
GAM1187  LOC200781 3'  GGATTCTGGCCCCTGGCTTCAG 91723         T   G  CC
                                TTGAAGCCAG GGG CA  AATCC
                                |||||||||| ||| ||  |||||
                                GACTTCGGTC CCC GT  TTAGG
                                      _  G  C_
GAM1187  LOC200830 5'  GGGTTCATGGTCTCGCTGACTT 91730       C       ACC_
            CAA                   TTGAAG CAGTGGGGC    AATCC
                                |||||| |||||||||    |||||
                                AACTTC GTCGCTCTG    TTGGG
                                   A       GTAC
GAM1187  LOC203286 3'  GGTGGCTCTGCTGGCATCG   92148     A    TG   _
                                TGA GCCAG  GGGC ACC
                                ||| |||||  |||| |||
                                GCT CGGTC  CTCG TGG
                                  A    GT   G
GAM1187  LOC220776 3'  GTGCTTGACTGGTTTCAA    68935          G
                                TTGAAGCCAGT GGGCAC
                                |||||||||| ||||||
                                AACTTTGGTCA TTCGTG
                                      G
GAM1187  LOC220906 3'  GGAAGCATGTGTTTTGTTGTTT 93036   TG   C  TG     CAA__
            TGG                   T  AAGC AG  GGGCAC    TCC
                                |  |||| ||  ||||||    |||
                                G  TTTG TT  TTTGTG    AGG
                                 GT   _  GT     TACGA
GAM1187  LOC220980 5'  GGGTCTGAACCCTCTGGCTTCA 94770         T   GC___   AATCC
            G                    TTGAAGCCAG GGG     ACC
                                |||||||||| |||     |||
                                GACTTCGGTC CCC     TGG
                                      T   AAGTC   G
GAM1187  LOC221042 3'  GGGTTAATTTCCTATTGCTTCA 94806       C      CACC
            G                    TTGAAGC AGTGGGG    AATCC
                                ||||||| |||||||    |||||
                                GACTTCG TTATCCT    TTGGG
                                   _      TTAA
GAM1187  LOC221312 3'  GGATTATACATTTTATTGCCTT 93558       C       CACC_
            CAG                   TTGAAG CAGTGGGG     AATCC
                                |||||| ||||||||     |||||
                                GACTTC GTTATTTT     TTAGG
                                   C       ACATA
GAM1187  LOC221692 3'  GGTTGGTCAATGGCTTTGA   93856   TG     G  GGGC
                                T  AAGCCA TG    ACCAATC
                                |  |||||| ||    |||||||
                                A  TTCGGT AC    TGGTTGG
                                 GT     A  ____
GAM1187  LOC222701 5'  GGAGATGGTTTCGCTGGTTCCA 94431     A       GG  ACCAA
            A                    TTG AGCCAGTG  GC     TCC
                                ||| ||||||||  ||     |||
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                                AAC TTGGTCGC  TG    AGG
                                  C       TT  GTAG_
GAM1187  LOC253019 5'  GATTGAGTGTTGGTTCGA    97110      G   GTGGG   _
                                TTGAA CCA    GCAC CAATC
                                ||||| |||    |||| |||||
                                AGCTT GGT    TGTG GTTAG
                                  _  _____   A
GAM1187  LOC253296 3'  GGGCCCTCACTGGCTGCAG   96123    A      _   A
                                TTG AGCCAGTG GGGC CC
                                ||| |||||||| |||| ||
                                GAC TCGGTCAC CCCG GG
                                  G       T   _
GAM1187  LOC253298 5'  GGGCCCTCACTGGCTGCAG   99012    A      _   A
                                TTG AGCCAGTG GGGC CC
                                ||| |||||||| |||| ||
                                GAC TCGGTCAC CCCG GG
                                  G       T   _
GAM1187  LOC253975 5'  GATTGAGTGTTGGTTCGA    97686      G   GTGGG   _
                                TTGAA CCA    GCAC CAATC
                                ||||| |||    |||| |||||
                                AGCTT GGT    TGTG GTTAG
                                  _  _____   A
GAM1187  LOC255645 3'  GGGCACCCCTACAGGTTTTAG  98476        A    CA__
                                TTGAAGCC GTGGGG   CC
                                |||||||| ||||||   ||
                                GATTTTGG CATCCC   GG
                                     A    CACG
GAM1187  LOC256222 3'  GGAACTCATTGTCTGTACTGGC 99016   TG      _    CCAA__
            TTTGA                 T  AAGCCAGTG GGGCA     TCC
                                |  |||||||| |||||     |||
                                A  TTCGGTCAT TCTGT     AGG
                                 GT       G    TACTCA
GAM1187  LOC257570 3'  GGGCCCTCACTGGCTGCAG   99669    A      _   A
                                TTG AGCCAGTG GGGC CC
                                ||| |||||||| |||| ||
                                GAC TCGGTCAC CCCG GG
                                  G       T   _
GAM1187  LOC257571 5'  GGGCCCTCACTGGCTGCAG   99802    A      _   A
                                TTG AGCCAGTG GGGC CC
                                ||| |||||||| |||| ||
                                GAC TCGGTCAC CCCG GG
                                  G       T   _
GAM1187  LOC58489  3'  GGATTTGGGGGTTCTTTGGTTT 72936        T    A_   _
            TAA                   TTGAAGCCAG GGGGC  CCAA TCC
                                |||||||||| |||||  |||| |||
                                AATTTTGGTT TCTTG  GGTT AGG
                                     _    GG   T
GAM1187  LOC90297  5'  GGGCCCTCACTGGCTCCAG   62851    A      _   A
                                TTG AGCCAGTG GGGC CC
                                ||| |||||||| |||| ||
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                                GAC TCGGTCAC CCCG GG
                                  C       T   _
GAM1187 LOC90529 3' GAAATGTGCCCTAGTGGTTTTG 63861    TG     G       CAATCC
             G                   T  AAGCCA TGGGGCAC
                                 |  |||||| ||||||||
                                 G  TTTGGT ATCCCGTG
                                  GT     G       TAAAG
GAM1187 LOC90785 3' GGGTTCGTGGTCTCACTGGCTT 64718              _  C
             CAG                   TTGAAGCCAGTGGGGC AC AATCC
                                 ||||||||||||||| || |||||
                                 GACTTCGGTCACTCTG TG TTGGG
                                           G  C
GAM1187 LOC90785 3' GGGTTCGTGGTCTCGCTGACTT 64719       C       _  C
             CAA                   TTGAAG CAGTGGGGC AC AATCC
                                 |||||| ||||||||| || |||||
                                 AACTTC GTCGCTCTG TG TTGGG
                                    A        G  C
GAM1187 LOC91149 3' GGAGCCTCCCCTACAGGTTTCA 65692         A     CACCAA
             G                    TTGAAGCC GTGGGG     TCC
                                 |||||||| ||||||      |||
                                 GACTTTGG CATCCC     AGG
                                     A     CTCCG_
GAM1187 LOC91156 5' GGATATGATCTCTGCTGGCTCT 65712    GA     TG   CAC  _
             GA                    TT  AGCCAG  GGG   CA ATCC
                                 ||  ||||||  |||   || ||||
                                 AG  TCGGTC  CTC   GT TAGG
                                  TC     GT   TA_  A
GAM1187 LOC91179 3' GGTTGCGTCTCATTGGCTCAG  65767     A         AC     C
                                 TTGA GCCAGTGGGGC  CAATC
                                 ||||  ||||||||||  |||||
                                 GACT CGGTTACTCTG  GTTGG
                                   _         C_     A
GAM1187 LOC91397 3' GGACACCCTGTGCTGGCTTTAG 66500           __   CA_
                                 TTGAAGCCAGT  GGGG   CC
                                 ||||||||||  ||||   ||
                                 GATTTCGGTCG  TCCC   GG
                                        TG    ACA
GAM1187 LOC91759 3' GGAAAATGCCTTTGGTGGCTTT 67693         GT_     CCAA
             AA                    TTGAAGCCA   GGGGCA    TCC
                                 |||||||||   ||||||    |||
                                 AATTTCGGT   TTCCGT    AGG
                                      GGT     AAA_
GAM1187 LOC91948 3' GGGTTCGTGGTCTCGCTGGCTC 68239      A         _  C
             AG                    TTGA GCCAGTGGGGC AC AATCC
                                 |||| |||||||||| || |||||
                                 GACT CGGTCGCTCTG TG TTGGG
                                   _         G  C
GAM1187 LOC91948 3' GGGTTCGTGGTCTCGCTGGCTT 68240              _  C
             CAG                   TTGAAGCCAGTGGGGC AC AATCC
                                 |||||||||||||||| || |||||
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                                GACTTCGGTCGCTCTG TG TTGGG
                                       G  C
GAM1187  LOC91948  3'  GGGTTCTTGGTCTCACTGACTT 68241       C       ACC_
             CAA                    TTGAAG CAGTGGGGC    AATCC
                                |||||| |||||||||   |||||
                                AACTTC GTCACTCTG    TTGGG
                                   A        GTTC
GAM1187  LOC92840  3'  GGCAGCTCCCACTGGTCTCG   57248     AG      _  A_
                                TGA  CCAGTGGG GC  CC
                                |||  |||||||| ||  ||
                                GCT  GGTCACCC CG  GG
                                  CT       T  AC
GAM1187  LOC92876  5'  GGGTTTTTATGGTTTTAG    71351         GT    A
                                TTGAAGCCA  GGGGC CC
                                |||||||||  ||||| ||
                                GATTTTGGT  TTTTG GG
                                      AT    _
GAM1188  AKAP1     3'  ACTATGGGTTCTCTTCGCAAA  14472      A  CTT       C
                                TTTGT GA   GGAACCCA AGT
                                ||||| ||   |||||||| |||
                                AAACG CT   TCTTGGGT TCA
                                   _  TC_       A
GAM1188  AKAP1     3'  ACTATGGGTTCTCTTCGCAAA  58373      A  CTT       C
                                TTTGT GA   GGAACCCA AGT
                                ||||| ||   |||||||| |||
                                AAACG CT   TCTTGGGT TCA
                                   _  TC_       A
GAM1188  EGF       3'  ACTATAGGTTTTGGTTCCACAA 10488      A  C TG    CAC
                                TTGT GA T  GAACC   AGT
                                |||| || |  |||||   |||
                                AACA CT G  TTTGG   TCA
                                  C  T GT    ATA
GAM1188  EZH1      3'  GACTGTGGGTTCCAAATTAC   10551      AC
                                GTAG  TTGGAACCCACAGTC
                                ||||  ||||||||||||||||
                                CATT  AACCTTGGGTGTCAG
                                  A_
GAM1188  STAC      3'  GACTGTGGAGTAATAGCCACAA 13427      AGA  TGGA  _
             A                   TTTGT   CT    AC CCACAGTC
                                |||||   ||    || ||||||||
                                AAACA   GA    TG GGTGTCAG
                                   CC_  TAA_  A
GAM1188  CCR1      3'  GACTGTGGGCTCCATTC     8927     CT    A
                                GA  TGGA CCCACAGTC
                                ||  |||| |||||||||
                                CT  ACCT GGGTGTCAG
                                 T_    C
GAM1188  FLJ10483  3'  GACTGTGGAAGAGATTACAAA  36652        A   GGAAC
                                TTTGTAG CTT     CCACAGTC
                                |||||||  |||    ||||||||
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                                AAACATT GAG    GGTGTCAG
                                   A  AA___
GAM1188 KIAA1871  3' ACTGTAAGAGTCTACAAA    61890         GGAACCC
                                TTTGTAGACTT     ACAGT
                                ||||||||||      |||||
                                AAACATCTGAG     TGTCA
                                      AA_____
GAM1188 LOC150821 3' GGGTTCCACATCCACAAA    60944      A  CT
                                TTTGT GA  TGGAACCC
                                ||||| ||  ||||||||
                                AAACA CT  ACCTTGGG
                                   C  AC
GAM1188 LOC151057 3' ACTGTGGGTACACCTATAAA  86379       ACT  GA
                                TTTGTAG   TG  ACCCACAGT
                                |||||||   ||  |||||||||
                                AAATATC   AC  TGGGTGTCA
                                   C__  A_
GAM1188 LOC157507 5' ACTGTAAAAGTCTGCAAA    82377         GGAACCC
                                TTTGTAGACTT     ACAGT
                                ||||||||||      |||||
                                AAACGTCTGAA     TGTCA
                                      AA_____
GAM1188 LOC203339 5' GGATTCCCAGTCTACAAA    92214         T   C
                                TTTGTAGACT GGAA CC
                                |||||||||| |||| ||
                                AAACATCTGA CCTT GG
                                      C   A
GAM1188 LOC51030  3' ACTGTAAATTAAACCAATCTAC 32695        C   AACCC___
           AAA                    TTTGTAGA TTGG       ACAGT
                                |||||||| ||||       |||||
                                AAACATCT AACC       TGTCA
                                   _   AAATTAAA
GAM1188 LOC90906  3' GACTGTGGATCCCAAACTTTGC 64951       C_   AAC
           A                     TGTAGA  TTGG   CCACAGTC
                                ||||||  ||||   ||||||||
                                ACGTTT  AACC   GGTGTCAG
                                   CA   CTA
GAM1189 ALDH1B1   3' TGGAATATTCCTTGGATTACTC 7330    A  C      C   GTC
           A                     C AG AGTCCAAG GGA   TCCA
                                | || |||||||| |||   ||||
                                A TC TTAGGTTC CTT   AGGT
                                 C  A       _   ATA
GAM1189 CNTN2     3' AGACGGCCTTGGACTGCTTG   18654          CGGA
                                CAAGCAGTCCAAG   GTCT
                                ||||||||||||    ||||
                                GTTCGTCAGGTTC   CAGA
                                      CGG_
GAM1189 DLEU2     3' TGAAGAAATGCCAACTGCTTG  21210        CCAA   GAG   C
                                CAAGCAGT    GCG   TCT CA
                                ||||||||    |||   ||| ||
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                                GTTCGTCA   CGT   AGA GT
                                    AC__   AA_   A
GAM1189  DNMT3B   3'  AGACCTGGCTGCTTG      23546        CAAGC  A
                                CAAGCAGTC    GG GTCT
                                |||||||||    || ||||
                                GTTCGTCGG    TC CAGA
                                     ______ _
GAM1189  HUNK     3'  AGAAATTGACTGGACTGTCA  28174   A      AG   AG
                                A GCAGTCCA  CGG  TCT
                                | ||||||||  |||  |||
                                A TGTCAGGT  GTT  AGA
                                 C       CA   AA
GAM1189  ITPKB    3'  GGAAGGTTTCTTCAACTGCTTG 11068        CC   CG  GT  _
                                CAAGCAGT  AAG  GA  CT CC
                                ||||||||  |||  ||  || ||
                                GTTCGTCA  TTC  TT  GA GG
                                    AC   __  TG  A
GAM1189  NORE1    3'  GGAGGGCCTGGGCTACTTG   49527     C     A  GGAG
                                CAAG AGTCCA GC    TCTCC
                                |||| |||||| ||    |||||
                                GTTC TCGGGT CG    GGAGG
                                  A     C  _____
GAM1189  PYGO2    3'  AGAAGAGCCTGGATTGCTCA   64681   A       A  GGAG
                                C AGCAGTCCA GC    TCT
                                | |||||||||  ||    |||
                                A TCGTTAGGT CG    AGA
                                 C        C  AGA_
GAM1189  RAMP1    3'  TGGAAAGGGTCCCAGCCTAGAC 20726        CAA  __   G  __
            TGCTT                  AAGCAGTC   GC  GGA TC  TCCA
                                ||||||||   ||  ||| ||  ||||
                                TTCGTCAG   CG  CCT GG  AGGT
                                    ATC  AC   G  AA
GAM1189  TBX2     3'  AGGCCACCCGGGCTGCCTG   21143    A     AAGC  A_
                                CA GCAGTCC    GG  GTCT
                                || |||||||    ||  ||||
                                GT CGTCGGG    CC  CGGA
                                 C      C___  AC
GAM1189  TMEPAI   3'  ACTCTTGGACTGCTCC     39822   A       AGC
                                C AGCAGTCCA   GGAGT
                                | |||||||||   |||||
                                C TCGTCAGGT   TCTCA
                                 C        ___
GAM1189  ARF4     3'  AGATTTTCTAATACTGCTTG   83707        CCA  C
                                CAAGCAGT   AG GGAGTCT
                                ||||||||   || |||||||
                                GTTCGTCA   TC TTTTAGA
                                    TAA  _
GAM1189  BM036    5'  GAGACGCTGCAAATTGCTTG   70315        CCAA   A
                                CAAGCAGT    GCGG GTCTC
                                ||||||||    |||| |||||
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                                GTTCGTTA    CGTC CAGAG
                                    AA__    G
GAM1189  C20orf45  3'  GAAACCCTTGGACTATTT    32643     C       C  AG
                                AAG AGTCCAAG GG  TC
                                ||| |||||||| ||  ||
                                TTT TCAGGTTC CC  AG
                                  A       _  AA
GAM1189  E2F5      3'  GGAAACTTGGGACTGTT     10474         AAGCG    C
                                AGCAGTCC     GAGT TCC
                                ||||||||     |||| |||
                                TTGTCAGG     TTCA AGG
                                    G____    A
GAM1189  EDR1      3'  GAGAACTAGGACTGCTCA    16659    A       A  CGGAG
                                C AGCAGTCC AG     TCTC
                                | ||||||||  ||     ||||
                                A TCGTCAGG TC     AGAG
                                 C       A  A____
GAM1189  FGD3      3'  GAGCGCCCTGGACTGCT     73280          A C  A T
                                AGCAGTCCA G GG G CTC
                                ||||||||| | || | |||
                                TCGTCAGGT C CC C GAG
                                    _ _  G _
GAM1189  FLJ10751  3'  GAGAACCTTGACTGCTTG    37113         C   CGGAG   C
                                CAAGCAGTC AAG     TCT C
                                ||||||||| |||     ||| |
                                GTTCGTCAG TTC     AGA G
                                    _   CA___   A
GAM1189  FLJ10751  3'  GAGAACCTTGACTGCTTG    37276         C   CGGAG   C
                                CAAGCAGTC AAG     TCT C
                                ||||||||| |||     ||| |
                                GTTCGTCAG TTC     AGA G
                                    _   CA___   A
GAM1189  FLJ11099  3'  GGGGCGCTTGGGCCACTCA    37608    A  CA       GAGT
                                C AG  GTCCAAGCG    CTCC
                                | ||  |||||||||    ||||
                                A TC  CGGGTTCGC    GGGG
                                 C  AC        _____
GAM1189  FLJ12294  3'  TGGAAACGTCTTCAGCTGCCTG 47724    A    CC   _  GAGTC
                                CA GCAGT  AAG CG     TCCA
                                || |||||  ||| ||     ||||
                                GT CGTCG  TTC GC     AGGT
                                 C     AC   T  AA___
GAM1189  FLJ14566  3'  TGGAGACTTCTGGGAACTATTT 52502     C   _  AAGC
                                AAG AGT CC    GGAGTCTCCA
                                ||| ||| ||    ||||||||||
                                TTT TCA GG    CTTCAGAGGT
                                  A   A  GT__
GAM1189  FLJ14824  3'  AGACATTCTGCTTGAACACTTG 52714      CA  C       __
                                CAAG  GT CAAGCGGA  GTCT
                                ||||  || ||||||||  ||||
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                                GTTC  CA GTTCGTCT  CAGA
                                  A_  A       TA
GAM1189  FLJ21135  3'  TGGAGACTCCACCTGGAT    46353      AGC
                                GTCCA   GGAGTCTCCA
                                |||||   ||||||||||
                                TAGGT   CCTCAGAGGT
                                   CCA
GAM1189  FLJ21709  3'  TGGAGACTCTACTGGACTGCTT 78483          A CG
                                AAGCAGTCCA G  GAGTCTCCA
                                |||||||||| |  |||||||||
                                TTCGTCAGGT C  CTCAGAGGT
                                      _ AT
GAM1189  FLJ22944  3'  GGCCCTGCCACTGTGGACTGC  47871        A____   A
                                GCAGTCCA    GCGG GTC
                                ||||||||    |||| |||
                                CGTCAGGT    CGTC CGG
                                     GTCAC   C
GAM1189  IMPACT    3'  GAGAGTATCCTTGACTGCTT   38007        C   C  AG_
                                AAGCAGTC AAG GG   TCTC
                                |||||||| ||| ||   ||||
                                TTCGTCAG TTC CT   AGAG
                                     _  _ ATG
GAM1189  KIAA0446  3'  GAGACTTTGAACTGCT     69452       CCAAG
                                AGCAGT    CGGAGTCTC
                                ||||||    |||||||||
                                TCGTCA    GTTTCAGAG
                                   A____
GAM1189  KIAA0493  5'  GGAGACTCCCCCGACTTGCCTG 64934    A  _  CAAGC
                                CA GCA GTC    GGAGTCTCC
                                || ||| |||    |||||||||
                                GT CGT CAG    CCTCAGAGG
                                 C  T  CCC__
GAM1189  KIAA0826  3'  TGAAGACCTGCAAAGCTGCTTG 83530        CCAA   A   C
                                CAAGCAGT   GCGG GTCT CA
                                ||||||||   |||| |||| ||
                                GTTCGTCG   CGTC CAGA GT
                                     AAA_   _   A
GAM1189  KIAA1679  3'  AGACTTTCAAATTGGATTGC   70707        GC__
                                GCAGTCCAA   GGAGTCT
                                |||||||||   |||||||
                                CGTTAGGTT   TTTCAGA
                                     AAAC
GAM1189  KIAA1729  3'  AGAATGTTTTCAACTGCTTG   90587       CC_   GGAG
                                CAAGCAGT   AAGC   TCT
                                ||||||||   ||||   |||
                                GTTCGTCA   TTTG   AGA
                                     ACT   TA__
GAM1189  MBLL39    5'  TGGAGAAGCCTCGGCCACTTG 59263     CA   CAAGC  AG
                                CAAG  GTC    GG  TCTCCA
                                ||||  |||    ||  ||||||
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                                GTTC  CGG    CC  AGAGGT
                                  AC   CT___  GA
GAM1189  MBLL39    5'  TGGAGAAGCCTCGGCCACTTG  20450      CA   CAAGC  AG
                                CAAG  GTC    GG  TCTCCA
                                ||||  |||    ||  ||||||
                                GTTC  CGG    CC  AGAGGT
                                  AC   CT___  GA
GAM1189  MGC10812  5'  TGGGGTTCCACTTAGACCCTTG 49481      CA   C   C    T
                                CAAG  GTC AAG GGAG CTCCA
                                ||||  ||| ||| |||| |||||
                                GTTC  CAG TTC CCTT GGGGT
                                  C_   A   A    _
GAM1189  NRF       3'  TGAAGAAAGGAAGCTTGAACTG 34509         C    GGAG__   C
             TTTG                   CAAGCAGT CAAGC      TCT CA
                                ||||||||| |||||      ||| ||
                                GTTTGTCA GTTCG      AGA GT
                                     A     AAGGAA   A
GAM1189  PPP1R10   3'  TGGAAACGTTCCTGGACTGCT  12233         A C   _  C
                                AGCAGTCCA G GGA GT TCCA
                                ||||||||| | ||| || ||||
                                TCGTCAGGT C CTT CA AGGT
                                     _ _   G  A
GAM1189  SPRY4     3'  GGAAACTGCAGCTGCTTG    49020         CCAA    AG
                                CAAGCAGT    GCGG  TCT
                                ||||||||    ||||  |||
                                GTTCGTCG    CGTC  AGG
                                     A___    AA
GAM1189  LOC113115 3'  AGAAACTGATTTGGACTGTT   57350           _   AG
                                AGCAGTCCAAG CGG  TCT
                                ||||||||||| |||  |||
                                TTGTCAGGTTT GTC  AGA
                                     A   AA
GAM1189  LOC128933 5'  GGAGCGCCTGGCTGCTTG     76774         T   A   GAGT
                                CAAGCAG CCA GCG    CTCC
                                ||||||| ||| |||    ||||
                                GTTCGTC GGT CGC    GAGG
                                     _   C   _____
GAM1189  LOC142827 3'  AGACTCTGGACTGCTT       76921           AGCG
                                AAGCAGTCCA    GAGTCT
                                ||||||||||    ||||||
                                TTCGTCAGGT    CTCAGA
                                              _____
GAM1189  LOC149483 3'  TGGGTCTCACTTGGACTATTTG 80190      C       CG   T T
                                CAAG AGTCCAAG  GAG C CCA
                                |||| ||||||||  ||| | |||
                                GTTT TCAGGTTC  CTC G GGT
                                  A       A_   T _
GAM1189  LOC163682 3'  GAGCTCCTGGACTGC       88405         AGC    T
                                GCAGTCCA   GGAG CTC
                                ||||||||   |||| |||
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                                CGTCAGGT   CCTC GAG
                                   ___   _
GAM1189  LOC197202 5'  GGAAAGCCCGGCTGCTTG    89295        CCAAG   A  C_
                                CAAGCAGT    CGG GT  TCC
                                ||||||||    ||| ||  |||
                                GTTCGTCG    GCC CG  AGG
                                   _____  _  AA
GAM1189  LOC201931 3'  TGGAAATTATTTAACTGCTTG  90571        CCAAGCGG   C
                                CAAGCAGT       AGT TCCA
                                ||||||||       ||| ||||
                                GTTCGTCA       TTA AGGT
                                     ATTTA___   A
GAM1189  LOC202134 3'  ACCCCGCTCTGTCTTTGTTT   91912       TC_ _    A
                                AAGCAG   CA AGCGG GT
                                ||||||   || ||||| ||
                                TTTGTT   GT TCGCC CA
                                    TCT  C    C
GAM1189  LOC245806 3'  GAGACTTCAGACTTCTCA    93543    A  C    CAAGC
                                C AG AGTC    GGAGTCTC
                                | || ||||    ||||||||
                                A TC TCAG    CTTCAGAG
                                 C  T    A____
GAM1189  LOC255452 3'  TGGAGACTTGATGGGCTGCTTG 99403          AGCG
                                CAAGCAGTCCA    GAGTCTCCA
                                ||||||||||    |||||||||
                                GTTCGTCGGGT    TTCAGAGGT
                                      AG__
GAM1189  LOC256369 3'  TGGAGACTGTAAGACTG     96613      CAA  GG
                                CAGTC   GC  AGTCTCCA
                                |||||   ||  ||||||||
                                GTCAG   TG  TCAGAGGT
                                   AA_  __
GAM1189  LOC257451 3'  AGAAGAGCCTGGATTGCTCA   97293    A       A  GGAG
                                C AGCAGTCCA GC    TCT
                                | |||||||||  ||    |||
                                A TCGTTAGGT CG    AGA
                                 C        C  AGA_
GAM1189  LOC56920  3'  GAAACTCAAACCCAGACTGCCT 39796      _    CAAGCG_   C
           TG                    CAAG CAGTC      GAGT TC
                                ||||  |||||      ||||  ||
                                GTTC GTCAG      CTCA AG
                                   C    ACCCAAA    A
GAM1189  LOC90408  5'  GAAACTCAAGTCTGGGCTGCTT 63343         AG G_   C
                                AAGCAGTCCA  C  GAGT TC
                                ||||||||||  |  |||| ||
                                TTCGTCGGGT  G  CTCA AG
                                      CT AA    A
GAM1189  LOC90906  3'  AGACTGGCCTTGGACTACTTG  64947      C       CGG
                                CAAG AGTCCAAG   AGTCT
                                |||| ||||||||   |||||
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                                GTTC TCAGGTTC   TCAGA
                                  A       CGG
GAM1189  LOC91156  5'  ACTCTGCTCAGACTGCTT    65703        CA
                                AAGCAGTC  AGCGGAGT
                                ||||||||  ||||||||
                                TTCGTCAG  TCGTCTCA
                                    AC
GAM1190  DCTN4     3'  GTAATATATGTGATGCAGTG   68395      _  T
                                CACTG ATT TATATATTAC
                                ||||| ||| ||||||||||
                                GTGAC TAG GTATATAATG
                                   G   T
GAM1190  FER1L4    3'  GGTAATAAGATCAGT       48129          ATAT
                                ACTGATTTTAT    TACC
                                ||||||||||    ||||
                                TGACTAGAATA    ATGG
                                      ____
GAM1190  LOC145660 3'  ACAGGGTGACTAAAGTCA    77840        TATA     C
                                TGATTTTA    TTACCC GT
                                ||||||||    ||||||  ||
                                ACTGAAAT    AGTGGG CA
                                    C___     A
GAM1190  LOC202460 5'  GATATACAAAAATCAGTG    90672         A_
                                CACTGATTTT  TATATT
                                ||||||||||  ||||||
                                GTGACTAAAA  ATATAG
                                    AC
GAM1191  DLEC1     3'  CATCTGGCCCTCCCTTG     24716      A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| ||  |||
                                GTTCC TCCCG TC TAC
                                   C    G  _
GAM1191  DLEC1     3'  CATCTGGCCCTCCCTTG     24717      A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| ||  |||
                                GTTCC TCCCG TC TAC
                                   C    G  _
GAM1191  PIP5K1A   3'  TATCCCACCCTGCCTTGATA   14520        A   CA  C
                                TATCAAGG AGGG  GG GTG
                                |||||||| ||||  ||  |||
                                ATAGTTCC TCCC  CC TAT
                                    G   A_  C
GAM1191  SOX11     3'  ACCCACCCCCCCTTGGTA    13308        AA   CA  C
                                TATCAAGG  GGG  GG GT
                                ||||||||  |||  ||  ||
                                ATGGTTCC  CCC  CC CA
                                    CC   A_  _
GAM1191  CHL1      3'  TGTTACCTTTCCTCAATA    22768     CA      CA
                                TAT  AGGAAGGG  GGCG
                                |||  ||||||||  ||||
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                                ATA  TCCTTTCC  TTGT
                                  AC       A_
GAM1191  EPB41L1   3' CATTCTGCCCTTCCCTGA    71104     A         C
                                TCA GGAAGGGCAGG GTG
                                ||| |||||||||| |||
                                AGT CCTTCCCGTCT TAC
                                  C         _
GAM1191  FLJ00060  3' CATACCCCCTGCCCTCCTCTGA 61741     _   A      CGTG
                                TCA AGGA GGGCAGG    ATG
                                ||| |||| |||||||    |||
                                AGT TCCT CCCGTCC    TAC
                                  C   _      CCCA
GAM1191  FLJ10898  5' CACCACAGCCCTTTCTCAATA  60126     CA       AGGC
                                TAT  AGGAAGGGC    GTG
                                |||  |||||||||    |||
                                ATA  TCTTTCCCG    CAC
                                  AC        ACAC
GAM1191  FLJ22557  3' ATCATCCCATCCTTAATA    45581     C    A   CAGGC
                                TAT AAGGA GGG    GTGAT
                                ||| ||||| |||    |||||
                                ATA TTCCT CCC    TACTA
                                  A    A  _____
GAM1191  KIAA0574  3' CATCCCCTGCCCTCCCCTGA   69808     A  A      CGT
                                TCA GG AGGGCAGG   GATG
                                ||| || ||||||||   ||||
                                AGT CC TCCCGTCC   CTAC
                                  C  C       C__
GAM1191  KIAA0632  3' CACCTCAGAAACCCTTCCTTGA 32071          CA___  C
                                TCAAGGAAGGG    GG GTG
                                ||||||||||    || |||
                                AGTTCCTTCCC    CT CAC
                                      AAAGA  C
GAM1191  KIAA1045  3' CATCACATGTCCTTCC      71599         GGC
                                GGAAGGGCA   GTGATG
                                |||||||||   ||||||
                                CCTTCCTGT   CACTAC
                                     A__
GAM1191  KIAA1354  5' CAGTGACTGCCTTCCCTTGATA 61572        A      G  _
                                TATCAAGG AGGGCAG CG TG
                                |||||||| ||||||| || ||
                                ATAGTTCC TTCCGTC GT AC
                                     C      A  G
GAM1191  MGC20460  5' CACCGCCTCCTACCCTTCTT   54901        C___    _
                                AGGAAGGG    AGGCG TG
                                ||||||||    ||||| ||
                                TTCTTCCC    TCCGC AC
                                     ATCC    C
GAM1191  LOC158476 3' CACGCCCGCCCCCCCCCATTGA  88186      _ AA_   A
                                TCAA GG   GGGC GGCGTG
                                |||| ||   |||| ||||||
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                                AGTT CC   CCCG CCGCAC
                                  A  CCC    C
GAM1191 LOC90459 3' CACACCCGCCTAATTTTTG   63550       A_   A  C
                                CAAGGA  GGGC GG GTG
                                ||||||  |||| || |||
                                GTTTTT  TCCG CC CAC
                                   AA    C  A
GAM1192 COLQ     3' TCATATGGAGACCTGCAATGCA 55428        _  _  G  GGAC
             C                   GTGCATTG AGG CT CA    ATGA
                                ||||||||| ||| || ||    ||||
                                CACGTAAC TCC GA GT    TACT
                                     G   A  G  A___
GAM1192 TCP1     3' TCCCACCCCCAATGCAC     48435        A  C  CA
                                GTGCATTG GG TG  GGA
                                |||||||| || ||  |||
                                CACGTAAC CC AC  CCT
                                     C  C  __
GAM1192 FLJ13195 3' CATGTCATCCTCAATGCAT   43549          CTGCAG
                                GTGCATTGAGG     GACATG
                                ||||||||||      ||||||
                                TACGTAACTCC     CTGTAC
                                      TA_____
GAM1192 FLJ25193 5' CATGGGGTAGCCTCAACGCAT  59354      A        AGGA
                                GTGC TTGAGGCTGC    CATG
                                |||| ||||||||||    ||||
                                TACG AACTCCGATG    GTAC
                                  C         GG__
GAM1192 KIAA1010 3' CATACCGCAACCTCAATG    72539        C   A  AC
                                CATTGAGG TGC GG  ATG
                                |||||||| ||| ||  |||
                                GTAACTCC ACG CC  TAC
                                     A   _  A_
GAM1192 KIAA1814 5' CATATCCTGCAGCAGGTCTAC  70874     C  TGAG       C
                                GTG AT    GCTGCAGGA ATG
                                ||| ||    ||||||||| |||
                                CAT TG    CGACGTCCT TAC
                                  C  GA__        A
GAM1192 MRPS26   3' GTGTGTACAGCCTCAGCGCAC  48725      A       CAGG
                                GTGC TTGAGGCTG    ACAT
                                |||| |||||||||    ||||
                                CACG GACTCCGAC    TGTG
                                  C        ATG_
GAM1192 RCD-8    3' CATATCCTGCAGCTGCTGCA   27519      TTGA        C
                                TGCA    GGCTGCAGGA ATG
                                ||||    |||||||||| |||
                                ACGT    TCGACGTCCT TAC
                                  CG__         A
GAM1192 SDC3     3' CCTGCAGCCTCAACAC      28471     CA
                                GTG  TTGAGGCTGCAGG
                                |||  ||||||||||||
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                                CAC  AACTCCGACGTCC
                                  __
GAM1192  TAF5L    3'  CACGTCCTGCACTGCAAT    27719      A  C       A
                                ATTG GG TGCAGGAC TG
                                |||| || |||||||| ||
                                TAAC TC ACGTCCTG AC
                                  G  _       C
GAM1192  LOC143162 5'  CCTGCAGCCTCAAGCAC     77004      A
                                GTGC TTGAGGCTGCAGG
                                |||| ||||||||||||
                                CACG AACTCCGACGTCC
                                  _
GAM1192  LOC144563 5'  TCATTTCCACAGCCTCAACCAC 77404     CA       CA  C
                                GTG  TTGAGGCTG  GGA ATGA
                                |||  |||||||||  ||| ||||
                                CAC  AACTCCGAC  CCT TACT
                                  C_       A_  T
GAM1192  LOC145053 5'  CCTGCAGTCTCAATGCAC    84176
                                GTGCATTGAGGCTGCAGG
                                ||||||||||||||||||
                                CACGTAACTCTGACGTCC

GAM1192  LOC149703 5'  CATGTCCCTGACCCACCAATGC 85817        A_  CTG   _
           AC                     GTGCATTG  GG   CAGG ACATG
                                |||||||  ||   |||| |||||
                                CACGTAAC  CC   GTCC TGTAC
                                     CA  CA_   C
GAM1192  LOC151632 5'  TCATTTCCACAGCCTCAACCAC 86650     CA       CA  C
                                GTG  TTGAGGCTG  GGA ATGA
                                |||  |||||||||  ||| ||||
                                CAC  AACTCCGAC  CCT TACT
                                  C_       A_  T
GAM1192  LOC196738 5'  CCTGCAGCCTCAAGCAC     88889      A
                                GTGC TTGAGGCTGCAGG
                                |||| ||||||||||||
                                CACG AACTCCGACGTCC
                                  _
GAM1192  LOC200904 5'  TCATTTCCACAGCCTCAACCAC 91784     CA       CA  C
                                GTG  TTGAGGCTG  GGA ATGA
                                |||  |||||||||  ||| ||||
                                CAC  AACTCCGAC  CCT TACT
                                  C_       A_  T
GAM1192  LOC219919 5'  TCATTTCCACAGCCTCAACCAC 94932     CA       CA  C
                                GTG  TTGAGGCTG  GGA ATGA
                                |||  |||||||||  ||| ||||
                                CAC  AACTCCGAC  CCT TACT
                                  C_       A_  T
GAM1192  LOC220980 3'  CATGTCCTGCAACACTGTCC   94766    TG  T  AGGC
                                G  CA TG    TGCAGGACATG
                                |  || ||    ||||||||||
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                                C  GT AC    ACGTCCTGTAC
                                 CT  C  A___
GAM1192  LOC221795 5'  TCATTTCCACAGCCTCAACCAC 94080     CA       CA   C
                                GTG  TTGAGGCTG  GGA ATGA
                                |||  |||||||||  ||| ||||
                                CAC  AACTCCGAC  CCT TACT
                                  C_       A_   T
GAM1192  LOC256515 5'  TCATTTCCACAGCCTCAACCAC 98217     CA       CA   C
                                GTG  TTGAGGCTG  GGA ATGA
                                |||  |||||||||  ||| ||||
                                CAC  AACTCCGAC  CCT TACT
                                  C_       A_   T
GAM1192  LOC92822  3'  CCCACAACCTCAATGTAC    71181          C  CA
                                GTGCATTGAGG TG  GG
                                ||||||||||| ||  ||
                                CATGTAACTCC AC  CC
                                       A  AC
GAM1193  MEN1      3'  ACTCCGCCCCCAGCCTATGAGC 56340     _      C    T  CA
              A                  TGC CATAGGC GGGG GC  AGT
                                 ||| ||||||| |||| ||  |||
                                 ACG GTATCCG CCCC CG  TCA
                                   A      A    _ CC
GAM1193  SIX3      3'  GACCCGGCACCCCACCTGCA   19443     CAT   CC       AA
                                 TGC   AGG  GGGGTGCC  GTC
                                 |||   |||  ||||||||  |||
                                 ACG   TCC  CCCCACGG  CAG
                                   ____  A_       CC
GAM1193  KIAA0574  3'  ACATGGACCCCAACTCTATGGC 69805         CC_    G   A
              A                  TGCCATAGG   GGGGT CCA GT
                                 |||||||||   ||||| ||| ||
                                 ACGGTATCT   CCCCA GGT CA
                                       CAA    _   A
GAM1193  NKX2C     3'  GACGATGGCCCCGACCCTGGCA 59908       TA  C    GT    A_
                                 TGCCA  GG CGGG  GCCA  GTC
                                 |||||  || ||||  ||||  |||
                                 ACGGT  CC GCCC  CGGT  CAG
                                    C_  A    __    AG
GAM1193  LOC170221 3'  GACCCTGTCCCGGCCCATGCA  83469     C  A      GT CCAA
                                 TGC AT GGCCGGG  G    GTC
                                 ||| || |||||||  |    |||
                                 ACG TA CCGGCCC  T    CAG
                                   _  C       TG CC__
GAM1193  LOC257481 3'  GACCTGGCGTCTTGGCCTTCGG 61762      AT       GT    A
              CA                   TGCC  AGGCCGGG  GCCA GTC
                                   ||||  ||||||||  |||| |||
                                   ACGG  TCCGGTTC  CGGT CAG
                                     CT       TG    C
GAM1193  LOC51134  3'  ACTTGACATTTTAACCTGTGGC 32790         CC     C
              A                    TGCCATAGG  GGGGTG CAAGT
                                   |||||||||  |||||| |||||
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                                ACGGTGTCC  TTTTAC GTTCA
                                     AA     A
GAM1194  AQP6     5'  ATCCTTTCAGTGGCCTC     54983    A        CA
                                GA GCCATTGAAA  GAT
                                || ||||||||||  |||
                                CT CGGTGACTTT  CTA
                                 C        C_
GAM1194  ATP11B   3'  GATCACCCTGTTAATGGC     81126        AA   A_
                                GCCATTG  ACAG  TGATC
                                |||||||  ||||  |||||
                                CGGTAAT  TGTC  ACTAG
                                    __   CC
GAM1194  TRPC5    3'  ATCATCTGTTCTGGAACTC    25924    AG_  TT   A
                                GA   CCA  GAA CAGATGAT
                                ||   |||  ||| ||||||||
                                CT   GGT  CTT GTCTACTA
                                 CAA  __  _
GAM1194  C1orf34  3'  CATGTGTCTTCATGGCTTC    61301        T  _  G
                                GAAGCCAT GAA ACA ATG
                                |||||||| ||| ||| |||
                                CTTCGGTA CTT TGT TAC
                                     _  C  G
GAM1194  DKFZp761B1514 3'  ATCATCTGTTTGACTTC     51138      C  TTGA
                                GAAG CA    AACAGATGAT
                                |||| ||    ||||||||||
                                CTTC GT    TTGTCTACTA
                                  A _____
GAM1194  FLJ10346 5'  GATCATCTGCCCTCCTCGGCCT 36525    A   ATT  AA_
           C                     GA GCC   GA   CAGATGATC
                                || |||   ||   |||||||||
                                CT CGG   CT   GTCTACTAG
                                 C  CTC  CCC
GAM1194  FLJ12960 3'  GATCATCTGTCCCAGGT     45300     AT  AA
                                GCC  TG  ACAGATGATC
                                |||  ||  ||||||||||
                                TGG  AC  TGTCTACTAG
                                  __  CC
GAM1194  FLJ23563 3'  CACCTGTAGGCCCTGGCTTTGT 68211         TTGAA_   A
                                ACGAAGCCA      ACAG TG
                                |||||||||      |||| ||
                                TGTTTCGGT      TGTC AC
                                     CCCGGA    C
GAM1194  MGC10911 5'  TCCGTTTCAATGCCCCGT    51182     AA  C       A
                                ACG  GC ATTGAAAC GA
                                |||  || |||||||| ||
                                TGC  CG TAACTTTG CT
                                  CC  _       C
GAM1194  LOC123095 5'  TCTGTCTTTAATGGCTTC    76522           _
                                GAAGCCATTGAA ACAGA
                                |||||||||||| |||||
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                                CTTCGGTAATTT TGTCT
                                       C
GAM1194  LOC132617 5'  CTGGGGCCCAATGGCTTCGT   76416          AAA__
                                ACGAAGCCATTG    CAG
                                ||||||||||||    |||
                                TGCTTCGGTAAC    GTC
                                       CCGGG
GAM1194  LOC135138 3'  ATCATCTGTCTCTGTTGC    75710    C  T  A
                                GC AT GA ACAGATGAT
                                || || || |||||||||
                                CG TG CT TGTCTACTA
                                 T  T  C
GAM1194  LOC196860 5'  TCTGTCTTTAATGGCTTC    91217          _
                                GAAGCCATTGAA ACAGA
                                |||||||||||| |||||
                                CTTCGGTAATTT TGTCT
                                       C
GAM1194  LOC221477 3'  GATCATCTGGAGGCCGGCTTTG 93772        ATTGAAA
              T                  ACGAAGCC      CAGATGATC
                                 ||||||||      |||||||||
                                 TGTTTCGG      GTCTACTAG
                                      CCGGAG_
GAM1194  LOC56270  3'  CGTTAGCTTCAGTGGCTCCG   39505    A       ACA
                                CG AGCCATTGAA   GATG
                                || ||||||||||   ||||
                                GC TCGGTGACTT   TTGC
                                 C         CGA
GAM1195  MEP1B     5'  GCTACTTTCAACTGGAA     20998    G       TCGTC
                                TT CAGTTGAAG    GTAGC
                                || |||||||||    |||||
                                AA GTCAACTTT    CATCG
                                 G       _____
GAM1195  KIAA1069  3'  TGACCTACATTCAACTGCAA   68535          _  C_
                                TTGCAGTTGAA GT  GTCG
                                |||||||||||  ||  ||||
                                AACGTCAACTT CA  CAGT
                                       A  TC
GAM1195  NICN1     3'  TGGCGACTTCATCTGCAA    51261       T
                                TTGCAG TGAAGTCGTCG
                                ||||||  ||||||||||
                                AACGTC ACTTCAGCGGT
                                    T
GAM1195  TEX27     3'  GCTGAACACCTGCAACTGCAA  41952        A  TC  CG
                                TTGCAGTTG AG  GT  TAGC
                                |||||||||  ||  ||  ||||
                                AACGTCAAC TC  CA  GTCG
                                      G  CA  A_
GAM1195  LOC142948 3'  TGGCCACCGGCCCAACTGCAG  83782        AA    TC  A
                                TTGCAGTTG  GTCG  GT GCCA
                                |||||||||  ||||  ||  ||||
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                                GACGTCAAC  CGGC  CA CGGT
                                     C_   __  C
GAM1195  LOC146488 5'  GCTACAACCGCTTCAACAACAA 71359     CA       C  C
                                TTG  GTTGAAGT GT GTAGC
                                |||  |||||||| || |||||
                                AAC  CAACTTCG CA CATCG
                                  AA       C  A
GAM1195  LOC147080 3'  TGCACAACTTCAGCCACAA    85053     CA       C  C
                                TTG  GTTGAAGT GT GTA
                                |||  |||||||| || |||
                                AAC  CGACTTCA CA CGT
                                  AC       A  _
GAM1195  LOC152845 5'  GCGGTGACCTCAGCTGCAA    60958          A   GT
                                TTGCAGTTGA GTC  CGT
                                |||||||||| |||  |||
                                AACGTCGACT CAG  GCG
                                      C   TG
GAM1195  LOC203052 3'  ACCACCATTTCAACTGCA     92073           C  C
                                TGCAGTTGAAGT GT GT
                                |||||||||||| || ||
                                ACGTCAACTTTA CA CA
                                       C  C
GAM1195  LOC204084 5'  GGCCAGACCTCCAACTGCAG   91000         A  TC   GTA
                                TTGCAGTTG AG  GTC   GCC
                                |||||||| ||  |||   |||
                                GACGTCAAC TC  CAG   CGG
                                     C  __   AC_
GAM1196  ATRN     3'  TGATGCACAGAACACCTCT    58448      ATA       _
                                AGAG   TTCTGTGTA CA
                                ||||   ||||||||| ||
                                TCTC   AAGACACGT GT
                                  CAC        A
GAM1196  CYP51    3'  ATGAAGTGTACAAAACAACTCT 7610       ATATTCTG
                                AGAG       TGTACATTTCAT
                                ||||       ||||||||||||
                                TCTC       ACATGTGAAGTA
                                  AACAAA__
GAM1196  MAPK9    3'  AAATGAGGCAGAATATGTCT   12315     G       GTA
                                AGA ATATTCTGT   CATTT
                                ||| |||||||||   |||||
                                TCT TATAAGACG   GTAAA
                                  G        GA_
GAM1196  MAPK9    3'  AAATGAGGCAGAATATGTCT   58173     G       GTA
                                AGA ATATTCTGT   CATTT
                                ||| |||||||||   |||||
                                TCT TATAAGACG   GTAAA
                                  G        GA_
GAM1196  MAPK9    3'  AAATGAGGCAGAATATGTCT   58178     G       GTA
                                AGA ATATTCTGT   CATTT
                                ||| |||||||||   |||||
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                                TCT TATAAGACG   GTAAA
                                  G       GA_
GAM1196  MAPK9    3'  AAATGAGGCAGAATATGTCT   58181     G       GTA
                                AGA ATATTCTGT   CATTT
                                ||| |||||||||   |||||
                                TCT TATAAGACG   GTAAA
                                  G       GA_
GAM1196  CDA02    3'  GGTATACACAGAATATTCCT   68452    AG         C
                                AG  ATATTCTGTGTA ATT
                                ||  |||||||||||| |||
                                TC  TATAAGACACAT TGG
                                 CT          A
GAM1196  PLK      3'  ATGAATTGTACAGAATATTTCT 18523           GT   T
                                AGAGATATTCTGT  ACA TTCAT
                                ||||||||||||  ||| |||||
                                TCTTTATAAGACA  TGT AAGTA
                                       __   T
GAM1196  TAGAP    3'  AAATGCTTCAGAATGTCTC    57970          TGTA
                                GAGATATTCTG    CATTT
                                ||||||||||    |||||
                                CTCTGTAAGAC    GTAAA
                                      TTC_
GAM1196  LOC145009 3'  ATGAAGTGTACAAAACAACTCT 60968      ATATTCTG
                                AGAG       TGTACATTTCAT
                                ||||       ||||||||||||
                                TCTC       ACATGTGAAGTA
                                  AACAAA__
GAM1196  LOC203080 5'  ATGAAATGGACGGAAACTCTCT 90772      TA     GTA
                                AGAGA  TTCTGT   CATTTCAT
                                |||||  ||||||   ||||||||
                                TCTCT  AAGGCA   GTAAAGTA
                                   CA     G__
GAM1196  LOC221337 5'  TGAAATTCAAAATATCTC    93739        C  TGTAC
                                GAGATATT TG    ATTTCA
                                |||||||| ||    ||||||
                                CTCTATAA AC    TAAAGT
                                     A  T____
GAM1197  ADAR     3'  CCTTTGCAGAACACCAAAG   8482          CG   T_
                                CTTTGGTGTTT  GCA  GG
                                ||||||||||  |||  ||
                                GAAACCACAAG  CGT  CC
                                      A_   TT
GAM1197  ADAR     3'  CCTTTGCAGAACACCAAAG   32350         CG   T_
                                CTTTGGTGTTT  GCA  GG
                                ||||||||||  |||  ||
                                GAAACCACAAG  CGT  CC
                                      A_   TT
GAM1197  ADAR     3'  CCTTTGCAGAACACCAAAG   32358         CG   T_
                                CTTTGGTGTTT  GCA  GG
                                ||||||||||  |||  ||
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                                GAAACCACAAG  CGT  CC
                                     A_   TT
GAM1197  ATP7A    3'  CTCCATGCCCAGCCTAAA    5320       T   TC
                                TTTGG GTT  GGCATGGAG
                                ||||| |||  |||||||||
                                AAATC CGA  CCGTACCTC
                                   _   C_
GAM1197  PMP22    3'  CTCATTTAGAAAACCAAAGT   6119         G    GGCATG
                                ACTTTGGT TTTC     GAG
                                |||||||| ||||     |||
                                TGAAACCA AAAG     CTC
                                     _   ATTTA_
GAM1197  PRM2     3'  TCGCCCGAAACACCAAG     12397           CATGGA
                                TTTGGTGTTTCGG     GA
                                ||||||||||||      ||
                                GAACCACAAAGCC     CT
                                      CG____
GAM1197  TRIP15   3'  TCTCCAGAAGAAAACCAAA    16177       G    GGCA
                                TTTGGT TTTC    TGGAGA
                                |||||| ||||    ||||||
                                AAACCA AAAG    ACCTCT
                                   _    AAG_
GAM1197  ARHGEF11 5'  TCCTGATCAAGACACCAAAG   29463          C  _  T
                                CTTTGGTGTTT GG CA GGA
                                |||||||||| || || |||
                                GAAACCACAGA CT GT CCT
                                      A  A  _
GAM1197  C21orf6  3'  TGCCATAAACACCAAAGT    34202           C_
                                ACTTTGGTGTTT  GGCA
                                ||||||||||||  ||||
                                TGAAACCACAAA  CCGT
                                      TA
GAM1197  DKFZp762K2015 3'  TCTCCATGCATCAGCAAA    72894      G  TTTCG
                                TTTG TG    GCATGGAGA
                                |||| ||    |||||||||
                                AAAC AC    CGTACCTCT
                                  G  TA___
GAM1197  FLJ13544 3'  TCTCCACCAAAAAATACCAAA  47211          C__  CA
                                TTTGGTGTTT   GG  TGGAGA
                                ||||||||||   ||  ||||||
                                AAACCATAAA   CC  ACCTCT
                                     AAA  __
GAM1197  FLJ20312 3'  GTCTGTCAACAAATACACCAAA 35410         TTCGGCA  _
                                TTTGGTGT      TGG AGAC
                                ||||||||      ||| ||||
                                AAACCACA      ACT TCTG
                                    TAAACA_   G
GAM1197  FLJ20627 3'  TCTCTACTAAAAATACCAAA   35911          CGGCA
                                TTTGGTGTTT    TGGAGA
                                ||||||||||    ||||||
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                                AAACCATAAA    ATCTCT
                                     AATC_
GAM1197  FLJ32915  5'  GTCTCTATTAAAAATACCAAA  59435        CGGC
                                TTTGGTGTTT   ATGGAGAC
                                ||||||||||   ||||||||
                                AAACCATAAA   TATCTCTG
                                     AAT_
GAM1197  KIAA1695  3'  TCTCCACAACACCAAA     47833        TCGGCA
                                TTTGGTGTT    TGGAGA
                                |||||||||    ||||||
                                AAACCACAA    ACCTCT
                                     C_____
GAM1197  KIAA1884  3'  GTCTGCACAATAACACCAAA  73730        TCGGCA  G
                                TTTGGTGTT    TG AGAC
                                |||||||||    || ||||
                                AAACCACAA    AC TCTG
                                     TAAC__  G
GAM1197  NYD-SP18  3'  CTCCATGCCACTGCCAGAG   51864       _  TTC
                                CTTTGGT GT   GGCATGGAG
                                |||||||  ||  |||||||||
                                GAGACCG CA   CCGTACCTC
                                     T  ___
GAM1197  PRRDH     3'  CTCCATGCATACACCAGAG   32322        TTCG
                                CTTTGGTGT    GCATGGAG
                                |||||||||    ||||||||
                                GAGACCACA    CGTACCTC
                                     TA__
GAM1197  SSR3      3'  GTCTCTACTAAAAATACCAAA  24039        CGGCA
                                TTTGGTGTTT    TGGAGAC
                                ||||||||||    |||||||
                                AAACCATAAA    ATCTCTG
                                     AATC_
GAM1197  UNC5D     3'  TCTCCATGCCAAGTGAAAAAG  56010     GG GT  C
                                CTTT  T  TT GGCATGGAGA
                                ||||  |  || ||||||||||
                                GAAA  G  AA CCGTACCTCT
                                  AA TG  _
GAM1197  LOC133258 5'  TCTCCACCACAACACCAA    76453        TC  CA
                                TTGGTGTT  GG  TGGAGA
                                ||||||||  ||  ||||||
                                AACCACAA  CC  ACCTCT
                                     CA  __
GAM1197  LOC144577 3'  GTCTCCATGGTACAGCAAAGT  77425       G   TTCGG
                                ACTTTG TGT    CATGGAGAC
                                ||||||  |||   |||||||||
                                TGAAAC ACA    GTACCTCTG
                                   G   TG___
GAM1197  LOC145387 3'  GTCTCTATAAAAAATACCAAA  84342         CGGC
                                TTTGGTGTTT    ATGGAGAC
                                |||||||||    ||||||||
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                                AAACCATAAA   TATCTCTG
                                     AAA_
GAM1197  LOC147136 3'  GTCCCAAGGAAAACCCAAAGT  78864       TG   GGCA  A
                                ACTTTGG  TTTC   TGG GAC
                                |||||||  ||||   ||| |||
                                TGAAACC  AAAG   ACC CTG
                                   CA   GA__  _
GAM1197  LOC256867 3'  CCACGCCAAACACTGAATGT  96512   _ TG    C  A
                                AC TT  GTGTTT GGC TGG
                                || ||  |||||| ||| |||
                                TG AA  CACAAA CCG ACC
                                 T  GT     _  C
GAM1198  ADCY1   3'  CCACCGAGCAGGCACAGCACA  94339    AA      GCCT
                                TGT  TGTGCCTGT   GTGG
                                |||  |||||||||   ||||
                                ACA  ACACGGACG   CACC
                                  CG       AGC_
GAM1198  CDH1    3'  CCACAGGCATGCACCACTAC   16400    AT_   CT
                                GTA   GTGC  GTGCCTGTGG
                                |||   ||||  ||||||||||
                                CAT   CACG  TACGGACACC
                                  CAC   __
GAM1198  COL4A4   3'  GTTAGCATAAACACATCACA   5406     A    CC    CTG
                                TGT ATGTG  TGTGC   TGGC
                                ||| |||||  |||||   ||||
                                ACA TACAC  ATACG   ATTG
                                  C    AA   ___
GAM1198  IGF1R    3'  GGCCACAGGCACACAGGT    7909     __
                                GCC  TGTGCCTGTGGCC
                                |||  |||||||||||||
                                TGG  ACACGGACACCGG
                                  AC
GAM1198  NFE2L1   3'  GCCACAGGCAGCTTCTCCACA  13630     CCT__ _
                                TGTG    G TGCCTGTGGC
                                ||||    | ||||||||||
                                ACAC    C ACGGACACCG
                                   CTCTT G
GAM1198  PER2    3'  CCACAGGCGACTGCCACCACA  43345    AA  T  CTG
                                TGT  TG GC   TGCCTGTGG
                                |||  || ||   |||||||||
                                ACA  AC CG   GCGGACACC
                                  CC  _  TCA
GAM1198  TAL1    3'  CCACAGGTGTGAGCCACCACA  13524    AA  T  CT TG
                                TGT  TG GC  G  CCTGTGG
                                |||  || ||  |  |||||||
                                ACA  AC CG  T  GGACACC
                                  CC  _  AG GT
GAM1198  TMPRSS3  3'  CCACAGGTGCCCGCCACCACA  44019    AA  T  CT TG
                                TGT  TG GC  G  CCTGTGG
                                |||  || ||  |  |||||||
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                                ACA  AC CG  C  GGACACC
                                  CC  _  CC GT
GAM1198 ASB16    3' CCACAGGTGGGCAGCACCACA  55976     AA  _    GT
                                TGT  TG TGCCT  GCCTGTGG
                                |||  || |||||  ||||||||
                                ACA  AC ACGGG  TGGACACC
                                  CC  G    __
GAM1198 C(27)-3BETA-HSD 3' CCACAGGTGCACGCCACCACA  48050     AA  T  C  TG
                                TGT  TG GC TG  CCTGTGG
                                |||  || || ||  |||||||
                                ACA  AC CG AC  GGACACC
                                  CC  _  C  GT
GAM1198 FLJ10718 3' CCACAGGCACGTGCCACCACA  37026     AA  T  C
                                TGT  TG GC TGTGCCTGTGG
                                |||  || || ||||||||||
                                ACA  AC CG GCACGGACACC
                                  CC  _  T
GAM1198 FLJ20147 3' CCACAGGTGTGTGCCACCACA  35132     AA  T  C  TG
                                TGT  TG GC TG  CCTGTGG
                                |||  || || ||  |||||||
                                ACA  AC CG GT  GGACACC
                                  CC  _  T  GT
GAM1198 HIF3A    3' GCCACACAGGCACATGCACA   42655      C       __
                                TGTGC TGTGCCTGT  GGC
                                |||||| |||||||||  |||
                                ACACG ACACGGACA  CCG
                                   T       CA
GAM1198 HRH4     3' CCGTGGCCAGGCACAAGACA   41534     AA     GT__  TGT
                                TGT  TGTGCCT   GCC   GG
                                |||  |||||||   |||   ||
                                ACA  ACACGGA   CGG   CC
                                  GA      ___C   TGT
GAM1198 HSPC065  3' GGCCACGGCTTACAGACCACTA 27155      AT   C_   __   T
             CA                   TGTA  GTG  CTGT  GCC GTGGCC
                                ||||  |||  ||||  ||| ||||||
                                ACAT  CAC  GACA  CGG CACCGG
                                  __   CA   TT   _
GAM1198 IGF2AS   3' GGCCACAGGCACAGCAGCTCA  33530    T  __
                                TG GC  CTGTGCCTGTGGCC
                                ||  ||  ||||||||||||||
                                AC CG  GACACGGACACCGG
                                 T  AC
GAM1198 KIAA0089 3' GCAAGTCCCAAACACATTACA  70508         CC  T_  C
                                TGTAATGTG  TG  GC TGT
                                |||||||||  ||  || |||
                                ACATTACAC  AC  TG ACG
                                     AA  CC  A
GAM1198 KIAA1924 3' GGCCACAGGCGTGTGCCACCAC 74052     AA  T  C GT
             A                   TGT  TG GC T  GCCTGTGGCC
                                |||  || || |  ||||||||||
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                                ACA  AC CG G  CGGACACCGG
                                  CC  _  T TG
GAM1198  KIAA1981  3'  GGCCACAGACACAGAGACCAC  89716     C___     C
                                GTG    CTGTG CTGTGGCC
                                |||    ||||| ||||||||
                                CAC    GACAC GACACCGG
                                  CAGA     A
GAM1198  SBBI31    3'  GGCCACAGACACACACTGC    26730     AT   CC    C
                                GTA  GTG  TGTG CTGTGGCC
                                |||  |||  |||| ||||||||
                                CGT  CAC  ACAC GACACCGG
                                  __   __    A
GAM1198  SIMRP7    3'  GCCACAGGGGCCACCTACA    93975      AT   CCT  G
                                TGTA  GTG   GT CCTGTGGC
                                ||||  |||   || ||||||||
                                ACAT  CAC   CG GGACACCG
                                  C_   ___  G
GAM1198  LOC124222 3'  GGCCACAGGCACAAGGGCTGCA 74753     _    __
                                TGT GCCT  GTGCCTGTGGCC
                                ||| ||||  ||||||||||||
                                ACG CGGG  CACGGACACCGG
                                  T    AA
GAM1198  LOC126133 3'  GGCCACAGACATGCACCACCAC 74912      CCT    ____
           A                     TGTG   GTGC    CTGTGGCC
                                ||||   ||||    ||||||||
                                ACAC   CACG    GACACCGG
                                  CAC    TACA
GAM1198  LOC127841 5'  GGCCTCTTTCCCAGGCACATCA 75189     A        TGCCTGT
           CA                     TGT ATGTGCCTG       GGCC
                                ||| |||||||||       ||||
                                ACA TACACGGAC       CCGG
                                  C        CCTTTCT
GAM1198  LOC151521 3'  GGCCACACTTGAAACACATTAT 86623          CCTGTGCC
           A                     TGTAATGTG        TGTGGCC
                                |||||||||        |||||||
                                ATATTACAC        ACACCGG
                                      AAAGTTC_
GAM1198  LOC152220 3'  CCACAGGCACCCGCCACCACA  86761     AA  T  CT
                                TGT  TG GC  GTGCCTGTGG
                                |||  || ||  ||||||||||
                                ACA  AC CG  CACGGACACC
                                  CC  _  CC
GAM1198  LOC154449 5'  CCCACACAGGCACATTCCA    81992     T          CC  T
                                TG AATGTGCCTGTG  TG GG
                                || ||||||||||||  || ||
                                AC TTACACGGACAC  AC CC
                                  C          __  _
GAM1198  LOC91308  3'  CCACAGGTGCGTGCCACCACA  66163     AA  T  C  TG
                                TGT  TG GC TG  CCTGTGG
                                |||  || || ||  |||||||
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                                ACA  AC CG GC  GGACACC
                                  CC  _  T  GT
GAM1199  AEGL1    3'  CACCCCCGCCTTCCCCATATTT 8529          ____     TGAA
                TC                  GAAGATATG    AGGCGG    GTG
                                    |||||||||    ||||||    |||
                                    CTTTTATAC    TCCGCC    CAC
                                         CCCT     CC__
GAM1199  CEP2     3'  ACTTCACCACCTCCTTC     24195      ATAT    C
                                    GAAG    GAGG GGTGAAGT
                                    ||||    |||| ||||||||
                                    CTTC    CTCC CCACTTCA
                                      ____    A
GAM1199  DLST     3'  CACCTGTCTCATAGCCTCGA   10415      AGA       _
                                    TCGA   TATGAGGC GGTG
                                    ||||   |||||||| ||||
                                    AGCT   ATACTCTG CCAC
                                      CCG       T
GAM1199  HEXA     3'  CACTTCTGCATTATATCT     6716         G   GT
                                    AGATATGA GCG  GAAGTG
                                    |||||||| |||  ||||||
                                    TCTATATT CGT  CTTCAC
                                        A   __
GAM1199  MOCS2    3'  CACCTCACCGCCCCCCATCCCG 16970     AA   ATGA       A
                G                    TCG  GAT    GGCGGTGA GTG
                                    |||  |||    |||||||| |||
                                    GGC  CTA    CCGCCACT CAC
                                      C_   CCCC       C
GAM1199  APACD    3'  CACCTAAATACTCATATTCTCG 20520      AG      GC____
                A                    TCGA  ATATGAG     GGTG
                                    ||||  |||||||     ||||
                                    AGCT  TATACTC     CCAC
                                      CT      ATAAAT
GAM1199  APCL     3'  ACCTCACCGCCCAGTC      20809     A  A       A
                                    GAT TG GGCGGTGA GT
                                    ||| || |||||||| ||
                                    CTG AC CCGCCACT CA
                                      _  _       C
GAM1199  C20orf21 3'  CACAACCTCCATCTTCGA    35569         AT    CG
                                    TCGAAGAT  GAGG  GTG
                                    ||||||||  ||||  |||
                                    AGCTTCTA  CTCC  CAC
                                         C_    AA
GAM1199  KIAA1602 3'  CACCCCACCACCCACTGCTTCG 65235       ATA  A  C    AA
                G                    TCGAAG   TG GG GGTG  GTG
                                    ||||||   || || ||||  |||
                                    GGCTTC   AC CC CCAC  CAC
                                       GTC  _  A    CC
GAM1199  LOC222133 3'  CACTTCACCCCAACCCCTTCGA 95759       ATATGA  C
                                    TCGAAG     GG GGTGAAGTG
                                    ||||||     || |||||||||
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                                AGCTTC     CC CCACTTCAC
                                   CCCAA_ _
GAM1200 EDAR     3' GAAAAACTCAGACTTGG     42526        CGG   ATC
                                TCAAGTCT   GAG   TTTC
                                ||||||||   |||   ||||
                                GGTTCAGA   CTC   AAAG
                                     ___   AA_
GAM1200 EDG2     3' ACTTTCTACCCCACAAGACTTG 9170          C___  G____   TCTT
             ATA                  TATCAAGTCT    GG    AGA    T
                                ||||||||||    ||    |||    |
                                ATAGTTCAGA    CC    TCT    A
                                     ACAC  CAIII   TTCT
GAM1200 EDG2     3' ACTTTCTACCCCACAAGACTTG 55130         C___  G____   TCTT
             ATA                  TATCAAGTCT    GG    AGA    T
                                ||||||||||    ||    |||    |
                                ATAGTTCAGA    CC    TCT    A
                                     ACAC  CAIII   TTCT
GAM1200 KIAA1238 3' AGAAAAACCCAACAAGAGACTT 71630         _____   AGATC
             GG                   TCAAGTCTC    GGG    TTTCT
                                |||||||||    |||    |||||
                                GGTTCAGAG    CCC    AAAGA
                                     AACAA   AA___
GAM1200 MGC15606 3' AAAGATCTGGACTTAATA    59514     C     CGGG
                                TAT AAGTCT    AGATCTTT
                                ||| ||||||    ||||||||
                                ATA TTCAGG    TCTAGAAA
                                  A     _____
GAM1200 LOC157567 3' AAAGAATATGAAGGCTTGATA  82388          _  GGAGA
                                TATCAAGTCT CG     TCTTT
                                |||||||||| ||     |||||
                                ATAGTTCGGA GT     AGAAA
                                     A  ATA__
GAM1200 LOC90643  3' AAAGATCCTAATGCACTTGATG 64435         CTCG_  A
                                TATCAAGT     GG GATCTTT
                                ||||||||     || |||||||
                                GTAGTTCA     TC CTAGAAA
                                     CGTAA  _
GAM1200 LOC91373  3' AGACTCCCCCGAGACCTG    66404    A       A  _
                                CA GTCTCGGG GA TCT
                                || |||||||| || |||
                                GT CAGAGCCC CT AGA
                                 C       C  C
GAM1201 ARL4     3' TTCTCTGGTCTGATTTTG    20415         AATAT
                                TAAAATCA    CCAGAGAA
                                ||||||||    ||||||||
                                GTTTTAGT    GGTCTCTT
                                     CT___
GAM1201 CYP3A4   3' TTCTCTGGAGTATTCTATAA  34368       A   CAAATA
                                TTATA AAT     TCCAGAGAA
                                ||||| |||     |||||||||
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                                AATAT TTA     AGGTCTCTT
                                  C   TG____
GAM1201  PRKWNK3   3'  TCTTTGATACTTGATTTTTTAA 62240     T       A    C
                                TTA AAAATCAA TATC AGAGA
                                ||| |||||||| |||| |||||
                                AAT TTTTAGTT ATAG TTTCT
                                  T       C    _
GAM1201  TEM7      3'  CTCTGAACTGGATTTTATAG   40257          AAATATC
                                TTATAAAATC      CAGAG
                                ||||||||||      |||||
                                GATATTTTAG      GTCTC
                                      GTCAA__
GAM1201  ENDO180   3'  TTCTCTGTAGTTGATTTTTTAA 21270     T       ATATC
                                TTA AAAATCAA     CAGAGAA
                                ||| ||||||||     |||||||
                                AAT TTTTAGTT     GTCTCTT
                                  T       GAT__
GAM1201  FLJ12331  3'  TCTCTGGATGGCTTTTA     47115       TCAAA
                                TAAAA     TATCCAGAGA
                                |||||     ||||||||||
                                ATTTT     GTAGGTCTCT
                                   CG___
GAM1201  FLJ13110  3'  CTCTGAAGGTGATTTTGTAA   43586          AATATC
                                TTATAAAATCA      CAGAG
                                ||||||||||      |||||
                                AATGTTTTAGT      GTCTC
                                      GGAA__
GAM1201  FLJ32332  3'  TTCTCTGGCAGAGTGACTTTA  58947      A   AATAT
                                TAAA TCA     CCAGAGAA
                                |||| |||     ||||||||
                                ATTT AGT     GGTCTCTT
                                  C   GAGAC
GAM1201  KIAA0861  3'  TTCTGGTTATTTAATTTTATAG 90361         C     T
                                TTATAAAAT AAATA CCAGAG
                                ||||||||| ||||| ||||||
                                GATATTTTA TTTAT GGTCTT
                                      A     T
GAM1201  KIAA1615  3'  TCCGGTTATTTGATTTTTATAA 69288         _      T  A
                                TTATAAAA TCAAATA CC GA
                                |||||||| ||||||| || ||
                                AATATTTT AGTTTAT GG CT
                                      T      T  C
GAM1201  KIAA1829  3'  GGATATTTATTTTTATAA    62649         TC
                                TTATAAAA  AAATATCC
                                ||||||||  ||||||||
                                AATATTTT  TTTATAGG
                                      TA
GAM1201  MGC19556  3'  TCCTGGTGATTGATTTTA    54344         A  T    A
                                TAAAATCAA TA CCAG GA
                                ||||||||| || |||| ||
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                                ATTTTAGTT GT GGTC CT
                                     A  _   _
GAM1201  TPD52    3'  CTCTGTATATTTGATTCTTA  18670     _       C
                                TAA AATCAAATAT CAGAG
                                ||| |||||||||| |||||
                                ATT TTAGTTTATA GTCTC
                                  C         T
GAM1201  LOC149332 3'  TTGGGTGATCCTGATTTTATAA 85551          AA__
                                TTATAAAATCA    TATCCAG
                                ||||||||||    |||||||
                                AATATTTTAGT    GTGGGTT
                                      CCTA
GAM1201  LOC149837 5'  TCTCTGGAAGGATTTTATGA  85907          AAATA
                                TTATAAAATC     TCCAGAGA
                                |||||||||     ||||||||
                                AGTATTTTAG     AGGTCTCT
                                      GA___
GAM1201  LOC158337 3'  TCTCTGGATCTTTTATGA    88113        TCAAAT
                                TTATAAAA     ATCCAGAGA
                                ||||||||     |||||||||
                                AGTATTTT     TAGGTCTCT
                                     C_____
GAM1202  CDH12    3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM1202  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC         G
GAM1202  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090       T    AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT     TTATTC
                                   _    GTCA_
GAM1202  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
            A                    TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM1202  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM1202  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
            TA                    TACA    TCC    GAAGAATAAG
                                ||||    |||    ||||||||||
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                              ATGT   AGG   TTTCTTATTC
                                AAA_  ATTG
GAM1202 KIAA1579 3' TACTCTTAGTGGTGTA     37154        CCCAAG   A
                              TACACCACT     AAGA TA
                              |||||||||     |||| ||
                              ATGTGGTGA     TTCT AT
                                   _______   C
GAM1202 KIAA1719 3' TCTGTCTTGGGAGTGGTGTA  68742             _
                              TACACCACTCCCAAGA AGA
                              |||||||||||||||| |||
                              ATGTGGTGAGGGTTCT TCT
                                        G
GAM1202 KIAA1853 3' TTTTTCTTGGAAGCAGTG    69929    CA  C
                              CAC  CT CCAAGAAGAA
                              |||  || ||||||||||
                              GTG  GA GGTTCTTTTT
                                AC  A
GAM1202 KIAA1877 3' CTTATTCTTCTGCCATGAGT  66748     CCA__
                              ACTC    AGAAGAATAAG
                              ||||    ||||||||||
                              TGAG    TCTTCTTATTC
                                TACCG
GAM1202 KIAA1906 3' CTTATTCTTCTTGACTTTTGG 73571    CTCC_
                              CCA    CAAGAAGAATAAG
                              |||    ||||||||||||
                              GGT    GTTCTTCTTATTC
                                TTTCA
GAM1202 OSBPL11  3' CTTAATTTCCCAAGAGTGGTG 43206       CCAA   AA
                              CACCACTC   GAAG  TAAG
                              ||||||||   ||||  ||||
                              GTGGTGAG   CTTT  ATTC
                                   AACC   A_
GAM1202 YME1L1   3' TCATTCTTGATGTGGTGTA   58438       TCC    _
                              TACACCAC   CAAGAA GA
                              ||||||||   |||||| ||
                              ATGTGGTG   GTTCTT CT
                                   TA_    A
GAM1202 YME1L1   3' TCATTCTTGATGTGGTGTA   27323       TCC    _
                              TACACCAC   CAAGAA GA
                              ||||||||   |||||| ||
                              ATGTGGTG   GTTCTT CT
                                   TA_    A
GAM1202 ZNF262   3' CTTATTTTGTTTGGGAGT    18723        A
                              ACTCCCAAG AGAATAAG
                              ||||||||| ||||||||
                              TGAGGGTTT TTTTATTC
                                   G
GAM1202 LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_    AAGA
                              TACACCAC   CCAAG   ATA
                              ||||||||   |||||   |||
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                                ATGTGGTG  GGTTC   TGT
                                    CAA    GG__
GAM1203  RB1CC1   3'  GATCAGCCATAAGTAATCAGCA 29435       _    GGACA_
            ATCT                  AGATTGCT ATTACT     TGATC
                                |||||||| ||||||     |||||
                                TCTAACGA TAATGA     ACTAG
                                   C     ATACCG
GAM1203  DJ328E19.C1.1 3'  CATGCCAGTGGCAACCT    31796    A    ATT    A
                                AG TTGCT   ACTGG CATG
                                || |||||   ||||| ||||
                                TC AACGG   TGACC GTAC
                                 C    ___    _
GAM1203  KIAA1253  3'  TGGCCAATAATAGCATTCT   93551     T      C   A
                                AGA TGCTATTA TGG CA
                                ||| |||||||| ||| ||
                                TCT ACGATAAT ACC GT
                                  T       A   G
GAM1203  LOC149317 3'  CATGCCAGTGGCAACCT    80059    A    ATT    A
                                AG TTGCT   ACTGG CATG
                                || |||||   ||||| ||||
                                TC AACGG   TGACC GTAC
                                 C    ___    _
GAM1203  LOC170037 5'  GATCATGTCCAGCAGCGA    88595      ATTA
                                TTGCT    CTGGACATGATC
                                |||||    ||||||||||||
                                AGCGA    GACCTGTACTAG
                                   C___
GAM1203  LOC220638 3'  CATGCCAGTGGCAACCT    74339    A    ATT    A
                                AG TTGCT   ACTGG CATG
                                || |||||   ||||| ||||
                                TC AACGG   TGACC GTAC
                                 C    ___    _
GAM1204  CD28     3'  TGCTGAAGAACTGTTGGA    21561           T_
                                TCCAACAGTTCTTC  CA
                                ||||||||||||||  ||
                                AGGTTGTCAAGAAG  GT
                                        TC
GAM1204  CD58     3'  TTTTTGAACAACTGTTGGAA   10114          C   TC
                                TTCCAACAGTT TTC  AGA
                                |||||||||| |||  |||
                                AAGGTTGTCAA AAG  TTT
                                      C   TT
GAM1204  CELSR1   3'  GTGGCCCGAGGGGCTGTGGAA  27277       A       TCAGA
                                TTCCA CAGTTCTTC    CCAC
                                ||||| |||||||||    ||||
                                AAGGT GTCGGGGAG    GGTG
                                   _       CCC__
GAM1204  CRIM1    3'  TGGTTTGAAACAACTACTGGAA 33605      AC    C  C
                                TTCCA  AGTT TT TCAGACCA
                                |||||  |||| || ||||||||
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                                AAGGT  TCAA AA AGTTTGGT
                                   CA    C _
GAM1204  EXTL2    3'  TGAGTAAGAACTGGCAGAA   9327      CAA      _
                                TTC   CAGTTCTT CTCA
                                |||   |||||||| ||||
                                AAG   GTCAAGAA GAGT
                                  ACG       T
GAM1204  FOXE1    3'  TCTGAGAACGAACAGGAA    16782     AACA   _
                                TTCC    GTTC TTCTCAGA
                                ||||    |||| ||||||||
                                AAGG    CAAG AAGAGTCT
                                  A___    C
GAM1204  PSCDBP   3'  GTGGTCTGAGATGGGTGCTG   16270     T __
                                CAGT CT  TCTCAGACCAC
                                |||| ||  ||||||||||
                                GTCG GG  AGAGTCTGGTG
                                   T  GT
GAM1204  TRIM37   3'  TTTGGAAACTGTTGGAA     31628          CT  T
                                TTCCAACAGTT  TC CAGA
                                ||||||||||  || ||||
                                AAGGTTGTCAA  AG GTTT
                                         __ _
GAM1204  DDX36    3'  GTGGTCTGAAAAGCCAGTTTGA 40865    C   AGTT   C
                                TC AAC    CTT TCAGACCAC
                                || |||    ||| |||||||||
                                AG TTG    GAA AGTCTGGTG
                                 T   ACC_   A
GAM1204  DKFZP434E2135 3'  GTGGTTCTGAAAGAACTG    48688        C    _
                                CAGTTCTT TCAGA CCAC
                                |||||||| ||||| ||||
                                GTCAAGAA AGTCT GGTG
                                     _    T
GAM1204  FLJ10759  3'  GTGGCTTGCAAAATTGTTGGAA 37125          CTTCT  GA
                                TTCCAACAGTT    CA  CCAC
                                ||||||||||    ||  ||||
                                AAGGTTGTTAA    GT  GGTG
                                       AAC__  TC
GAM1204  FLJ10898  5'  TGAAAGAGCTGTCAGAA     60140     CA       C
                                TTC  ACAGTTCTT TCA
                                |||  ||||||||| |||
                                AAG  TGTCGAGAA AGT
                                  AC       _
GAM1204  FLJ12587  3'  TGGCCCCGAGAGAACTGCTG   42787    A      T   AGA_
                                CA CAGTTCT CTC    CCA
                                || ||||||| |||    |||
                                GT GTCAAGA GAG    GGT
                                 C      _  CCCC
GAM1204  FLJ22625  3'  TGGTCTGAAAGAAGTTGGAA   45588        AG    C
                                TTCCAAC  TTCTT TCAGACCA
                                |||||||  ||||| ||||||||
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                                AAGGTTG  AAGAA AGTCTGGT
                                   __    _
GAM1204  FLJ25082  3'  TGACTGAGAAGCATTGGAA   58985       CAGTT       AC
                                TTCCAA    CTTCTCAG  CA
                                ||||||    ||||||||  ||
                                AAGGTT    GAAGAGTC  GT
                                   AC___      A_
GAM1204  KIAA1145  3'  GTCTGAGAGAATGGAA     66240      ACAG    T
                                TTCCA    TTCT CTCAGAC
                                |||||    |||| |||||||
                                AAGGT    AAGA GAGTCTG
                                   _____   _
GAM1204  Kv6.3     3'  TGGTCTGAGAAGTGAAATAAGA 56857     CAACAGTT
              A                  TTC       CTTCTCAGACCA
                                 |||       ||||||||||||
                                 AAG       GAAGAGTCTGGT
                                   AATAAAGT
GAM1204  RNPC2     3'  GTCTGAGAAAGAAATAGGAA   18131      AACAG    _
                                TTCC     TTCTT CTCAGAC
                                ||||     ||||| |||||||
                                AAGG     AAGAA GAGTCTG
                                   ATA__     A
GAM1204  SPINLW1   3'  CTGGAAGAACTGCCAGAA    40230     CAA       T
                                TTC   CAGTTCTTC CAG
                                |||   ||||||||| |||
                                AAG   GTCAAGAAG GTC
                                   ACC       _
GAM1204  SYTL2     5'  GTGGTCTGAAGCTCTGTTGTGA 51479     _     TT  TC
              A                   TTC CAACAG  CT  TCAGACCAC
                                  ||| ||||||  ||  |||||||||
                                  AAG GTTGTC  GA  AGTCTGGTG
                                    T     TC  __
GAM1204  T2BP      3'  GTGGCCTGAATGACTGTTGGAG 70540          CTTC    A
                                TTCCAACAGTT    TCAG CCAC
                                ||||||||||    |||| ||||
                                GAGGTTGTCAG    AGTC GGTG
                                      TA__    C
GAM1204  VIT1      3'  GTTTAGACAAAACTGTTGGAA  38605          CT_   C
                                TTCCAACAGTT   TCT AGAC
                                ||||||||||   ||| ||||
                                AAGGTTGTCAA   AGA TTTG
                                      AAC   _
GAM1204  LOC130471 3'  TGGCCCAAGAAGAAGGGTGTGA 75440     CA  AG      CAGA
              A                   TTC  AC  TTCTTCT    CCA
                                  |||  ||  |||||||    |||
                                  AAG  TG  AAGAAGA    GGT
                                    TG  GG      ACCC
GAM1204  LOC144266 5'  GTGGATTCAGAAACTGCTGGAA 77268       A    CT   C  A
                                TTCCA CAGTT  TCT AG CCAC
                                ||||| |||||  ||| || ||||
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                                AAGGT GTCAA  AGA TT GGTG
                                  C    __  C  A
GAM1204  LOC149535 3'  CTAGAAGAACCCTTGGAA    80217       CA       C
                                TTCCAA  GTTCTTCT AG
                                ||||||  |||||||| ||
                                AAGGTT  CAAGAAGA TC
                                   CC       _
GAM1204  LOC158798 5'  TCTGAGAGAAGCTACTGAGA   82876    _ AC    CT
                                TC CA  AGTT  TCTCAGA
                                || ||  ||||  |||||||
                                AG GT  TCGA  AGAGTCT
                                 A  CA    AG
GAM1204  LOC158972 3'  GTGGTCTGAGAAAGCAGGTGG  88315     ACA   C
                                CCA   GTT TTCTCAGACCAC
                                |||   ||| ||||||||||||
                                GGT   CGA AAGAGTCTGGTG
                                  GGA  _
GAM1204  LOC165771 5'  TGGCCCTGGTTTAAACTGTTGA 83500    _      CTTC    A_
            GA                    TC CAACAGTT    TCAG  CCA
                                || ||||||||    ||||  |||
                                AG GTTGTCAA    GGTC  GGT
                                 A       ATTT    CC
GAM1204  LOC200933 3'  GTAGTCACTTTGGAATGTTGGA 91797        G    TCTCA   C
            A                     TTCCAACA TTCT     GAC AC
                                |||||||| ||||     ||| ||
                                AAGGTTGT AAGG     CTG TG
                                     _   TTTCA   A
GAM1204  LOC202934 5'  GTGGTCTGAGAAGATACTTG   92051    _ _
                                CA GT TCTTCTCAGACCAC
                                || || ||||||||||||||
                                GT CA AGAAGAGTCTGGTG
                                 T  T
GAM1204  LOC221968 3'  TCTTAGAAGAACTGTGAA    94155     CA         C
                                TTC  ACAGTTCTTCT AGA
                                |||  |||||||||| |||
                                AAG  TGTCAAGAAGA TCT
                                  __          T
GAM1204  LOC255465 5'  GTGGTCTGAGAAGATACTTG   99126    _ _
                                CA GT TCTTCTCAGACCAC
                                || || ||||||||||||||
                                GT CA AGAAGAGTCTGGTG
                                 T  T
GAM1204  LOC80298  5'  GGTGCTGAGAACTGTCGGGA   48065     A    TCT     _
                                TTCC ACAGT   TCTCAG ACC
                                |||| |||||   |||||| |||
                                AGGG TGTCA   AGAGTC TGG
                                  C     ___      G
GAM1204  LOC90190  3'  GTTGGAGAAGAACCATTAGAA  62431     C  CA       A
                                TTC AA  GTTCTTCTC GAC
                                ||| ||  |||||||| |||
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                                AAG TT  CAAGAAGAG TTG
                                  A  AC        G
GAM1204  LOC92283  5'  TGAGTGTAAAGAATGTTGGAA  69307         G    ____
                                TTCCAACA TTCTT    CTCA
                                |||||||| |||||    ||||
                                AAGGTTGT AAGAA    GAGT
                                     _    ATGT
GAM1205  DES      3'  CTGACCCCTCCTCACTGGCC   72591         _  A  A
                                GGCCAGTG GGA GG TCAG
                                |||||||| ||| || ||||
                                CCGGTCAC CCT CC AGTC
                                     T   C  C
GAM1205  LARGE    3'  AAAATCTGATCCTTTGAGGCT  17626      AGTGG
                                GGCC    GAAGGATCAGATTTT
                                ||||    ||||||||||||||
                                TCGG    TTTCCTAGTCTAAAA
                                  AG___
GAM1205  LARGE    3'  AAAATCTGATCCTTTGAGGCT  56924      AGTGG
                                GGCC    GAAGGATCAGATTTT
                                ||||    ||||||||||||||
                                TCGG    TTTCCTAGTCTAAAA
                                  AG___
GAM1205  FLJ32934 3'  CTGATCCTTCCCACCC      58882    CCA
                                GG   GTGGGAAGGATCAG
                                ||   ||||||||||||||
                                CC   CACCCTTCCTAGTC
                                     ___
GAM1205  HUMAGCGB 3'  AAAATCTGATCCCCTCTCTAC  26129      _  A_
                                GTGG GA  GGATCAGATTTT
                                |||| ||  ||||||||||||
                                CATC CT  CCTAGTCTAAAA
                                  T  CC
GAM1205  KCNS1    3'  AAAATCTGAAGGGCCCCTGGCC 11190       T   AAGGA
                                GGCCAG GGG    TCAGATTTT
                                |||||| |||    |||||||||
                                CCGGTC CCC    AGTCTAAAA
                                   _   GGGA_
GAM1205  TOR2A    3'  AAAGTCCCCTCCCCACCTACC  56180    CCA    A   ATCA
                                GG   GTGGG AGG    GATTTT
                                ||   ||||| |||    ||||||
                                CC   CACCC TCC    CTGAAA
                                 ATC    C   C___
GAM1205  LOC219653 3'  AAAATCCCAGTGTCCCACTGGC 92912          AGGATCA
              T                  GGCCAGTGGGA      GATTTT
                                ||||||||||||      ||||||
                                TCGGTCACCCT      CTAAAA
                                      GTGACC_
GAM1206  FBXL3A   3'  AGTCTAGCATAAACAGCA    25131       CTG
                                TGTTGT   ATGCTAGACT
                                ||||||   ||||||||||
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                                ACGACA   TACGATCTGA
                                   AA_
GAM1206 HYAL1    3' CAGTCCAGCAAATAAAGCAGTC 53702        GTCTGA   A
             A                   TGACTGTT     TGCT GACTG
                                 ||||||||     |||| |||||
                                 ACTGACGA     ACGA CTGAC
                                     AATAA_   C
GAM1206 HYAL1    3' CAGTCCAGCAAATAAAGCAGTC 24602        GTCTGA   A
             A                   TGACTGTT     TGCT GACTG
                                 ||||||||     |||| |||||
                                 ACTGACGA     ACGA CTGAC
                                     AATAA_   C
GAM1206 MAN2A2   3' AGCCCAGCATCAGGGTCA    21505      GTTGT      AGA
                                 TGACT    CTGATGCT   CT
                                 |||||    ||||||||   ||
                                 ACTGG    GACTACGA   GA
                                   _____      CCC
GAM1206 PRO0529  3' CAGTGAGTTTCAGTCAACAGTC 26855         T   T   AG
             A                   TGACTGTTG CTGA GCT  ACTG
                                 ||||||||| |||| |||  ||||
                                 ACTGACAAC GACT TGA  TGAC
                                      T   T   G_
GAM1206 LOC223073 5' CAGTGTGAAGTCAGACAACAAT 96036     C        GC  G
             CA                    TGA TGTTGTCTGAT  TA ACTG
                                 ||| ||||||||||  || ||||
                                 ACT ACAACAGACTG  GT TGAC
                                   A         AA  G
GAM1207 ABCA3    3' GCCATCAGGCAGGGA       8445        GGTGAC
                                 TCCCTG     TCTGATGGC
                                 ||||||     |||||||||
                                 AGGGAC     GGACTACCG
                                   _______
GAM1207 CEP2     3' CTATGGAATCACCCAGAGG   24197   _      C   G
                                 CC CTGGGTGA TCT ATGG
                                 || |||||||| ||| ||||
                                 GG GACCCACT AGG TATC
                                  A       A   _
GAM1207 DYT1     3' CCTGCAGGCCACCCAGGGA   5478          A T   AT
                                 TCCCTGGGTG C CTG  GG
                                 |||||||||| | |||  ||
                                 AGGGACCCAC G GAC  CC
                                      C _   GT
GAM1207 GNRH1    5' CTTGCCATCACCAGCCACAGAG 7707     C   _   GACTC
             A                   TC CTG GGT     TGATGGCAAG
                                 || ||| |||     ||||||||||
                                 AG GAC CCG     ACTACCGTTC
                                  A   A   ACC__
GAM1207 SPRR2C   3' TCATCAAAGCCATCCAGGGA  22531          A  C
                                 TCCCTGGGTG CT TGATGG
                                 |||||||||| || ||||||
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                                AGGGACCTAC GA ACTACT
                                      C  A
GAM1207  WNT5A    5'  CTTGCCATCAAAAAACTCACGG 14121     C    GACTC
              A                    TCC TGGGT    TGATGGCAAG
                                   ||| |||||    ||||||||||
                                   AGG ACTCA    ACTACCGTTC
                                     C    AAAA_
GAM1207  ARFRP1   3'  TGCCCAGTGTCACCCAGGG   13696          T  AT
                                   CCCTGGGTGAC CTG  GGCA
                                   |||||||||| |||  ||||
                                   GGGACCCACTG GAC  CCGT
                                          T  __
GAM1207  B3GNT7   3'  TCAGCGGGAGTCACCTAGG   71683           GA_
                                   CCTGGGTGACTCT  TGG
                                   ||||||||||||  |||
                                   GGATCCACTGAGG  ACT
                                           GCG
GAM1207  CEACAM4  3'  CCACCCGGGGTCACCAGG    10191      G      A_
                                   CCTGG TGACTCTG  TGG
                                   ||||| ||||||||  |||
                                   GGACC ACTGGGGC  ACC
                                      _       CC
GAM1207  DKFZP434P211 3'  TGCCACCACCCCCTCCCCAGGG 28032        T  CTC__  A
              A                    TCCCTGGG GA    TG TGGCA
                                   |||||||| ||    || |||||
                                   AGGGACCC CT    AC ACCGT
                                      _ CCCCC  C
GAM1207  FLJ10101 3'  TTCCAAAGCCTCCCAGGGA   45606        TGACT  GA   C
                                   TCCCTGGG    CT  TGG AA
                                   ||||||||    ||  ||| ||
                                   AGGGACCC    GA  ACC TT
                                        TCC__  A_  _
GAM1207  FLJ11017 3'  TCAGGGACAATCACCCAGGGA  37547          _____
                                   TCCCTGGGTGA    CTCTGA
                                   ||||||||||    ||||||
                                   AGGGACCCACT    GGGACT
                                          AACA
GAM1207  FLJ20499 3'  TGCCTGAGCCACCTCAGGGA   35714       _   A   TGAT
                                   TCCCTG GGTG CTC    GGCA
                                   |||||| |||| |||    ||||
                                   AGGGAC CCAC GAG    CCGT
                                      T   C   T___
GAM1207  FLJ23420 3'  CATCAAAATCACCTAGGGA   47538          CTC
                                   TCCCTGGGTGA   TGATG
                                   ||||||||||   |||||
                                   AGGGATCCACT   ACTAC
                                          AAA
GAM1207  KIAA0161 3'  CTTGCCATCATTCCCCAG    29200      T  CTC
                                   CTGGG GA   TGATGGCAAG
                                   ||||| ||   ||||||||||
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                                GACCC CT   ACTACCGTTC
                                   _ T__
GAM1207  KIAA0543  5'  TCTGGAGCATCACCCAGG    69522          __   _
                                CCTGGGTGA  CTCT GA
                                |||||||||  |||| ||
                                GGACCCACT  GAGG CT
                                     AC    T
GAM1207  MGC20496  3'  CCTGAAGAGCTCACCCAGAGA  54529    C      _   GAT
                                TC CTGGGTGA CTCT   GG
                                || ||||||||  ||||   ||
                                AG GACCCACT GAGA   CC
                                 A       C    AGT
GAM1207  MMEL2     3'  TGCCTGACACCCAGGGA     54233          AC  TGAT
                                TCCCTGGGTG  TC    GGCA
                                ||||||||||  ||    ||||
                                AGGGACCCAC  AG    CCGT
                                     __  T____
GAM1207  U5-116KD  3'  TGCCTGGGTCCCCAGGGA    16186        T    TGAT
                                TCCCTGGG GACTC    GGCA
                                ||||||||  |||||    ||||
                                AGGGACCC CTGGG    CCGT
                                     _     T____
GAM1207  LOC127534 3'  CCACATGAGGCCACCCAGG    75966         A_   _  A
                                CCTGGGTG  CTC TG TGG
                                ||||||||  ||| || |||
                                GGACCCAC  GAG AC ACC
                                     CG   T  _
GAM1207  LOC143188 5'  CCAGCAAAGTCCACCCAGG    83790         _   C  A
                                CCTGGGTG ACT TG TGG
                                ||||||||  ||| || |||
                                GGACCCAC TGA AC ACC
                                     C   A  G
GAM1207  LOC149464 5'  CTTGCCCAAGATCACCCAG    85591         C   GAT
                                CTGGGTGA TCT   GGCAAG
                                ||||||||  |||   ||||||
                                GACCCACT AGA   CCGTTC
                                     _   AC_
GAM1207  LOC149836 5'  ATCAGGCCACCCAGGGA      80349          A T
                                TCCCTGGGTG C CTGAT
                                ||||||||||  | |||||
                                AGGGACCCAC G GACTA
                                      C _
GAM1207  LOC149838 5'  GTCAGGCCACCCAGGGA      80358          A T
                                TCCCTGGGTG C CTGAT
                                ||||||||||  | |||||
                                AGGGACCCAC G GACTG
                                      C _
GAM1207  LOC150174 3'  TGCCACCACCCCCTCCCCAGGG 80443         T  CTC__  A
              A                  TCCCTGGG GA     TG TGGCA
                                ||||||||  ||     ||  |||||
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                                AGGGACCC CT     AC ACCGT
                                     _ CCCCC  C
GAM1207  LOC150213 3'  TGCCACCACCCCCTCCCCAGGG 75362        T  CTC__  A
              A                   TCCCTGGG GA     TG TGGCA
                                  |||||||| ||     || |||||
                                  AGGGACCC CT     AC ACCGT
                                     _ CCCCC  C
GAM1207  LOC150236 5'  TGCCACCACCCCCTCCCCAGGG 80504        T  CTC__  A
              A                   TCCCTGGG GA     TG TGGCA
                                  |||||||| ||     || |||||
                                  AGGGACCC CT     AC ACCGT
                                     _ CCCCC  C
GAM1207  LOC151429 3'  TGCCTCTGCCACCCAGGGG    86552          ACTCT  T
                                  TCCCTGGGTG     GA GGCA
                                  ||||||||||     || ||||
                                  GGGGACCCAC     CT CCGT
                                        CGT__  _
GAM1207  LOC157254 5'  TGCCATCAAAGCAGCAGGG    82316       GG  A  C
                                  CCCTG  TG CT TGATGGCA
                                  |||||  || || ||||||||
                                  GGGAC  AC GA ACTACCGT
                                     G_  _  A
GAM1207  LOC162137 5'  CTACCAGCTCGCCCAGAGA    88479     C       CT   A
                                  TC CTGGGTGA  CTG TGG
                                  || ||||||||  ||| |||
                                  AG GACCCGCT  GAC ATC
                                   A       C_   C
GAM1207  LOC165904 3'  CCAAAGGTCACCCAAAGA     83502     CC       T  GA
                                  TC  TGGGTGAC CT  TGG
                                  ||  |||||||| ||  |||
                                  AG  ACCCACTG GA  ACC
                                   AA       _  A_
GAM1207  LOC201696 3'  CTTGCCTGAGATCACCTAG    63819         _   TGAT
                                  CTGGGTGA CTC    GGCAAG
                                  |||||||| |||    ||||||
                                  GATCCACT GAG    CCGTTC
                                       A   T___
GAM1207  LOC254124 3'  GCCGAGCCACCCAGGGA      98467          A   TGAT
                                  TCCCTGGGTG CTC    GGC
                                  |||||||||| |||    |||
                                  AGGGACCCAC GAG    CCG
                                        C   _____
GAM1207  LOC51281  3'  TGCCTGAGCCACCTCAGGGA   33774       _    A   TGAT
                                  TCCCTG GGTG CTC    GGCA
                                  |||||| |||| |||    ||||
                                  AGGGAC CCAC GAG    CCGT
                                     T    C   T___
GAM1207  LOC58525  3'  TGCCATGTCAAGGCCCCCCAAA 79355    CC    TGA TC   __
              GA                    TC  TGGG   C  TGA  TGGCA
                                  ||  ||||   |  |||  |||||
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                                AG  ACCC   G  ACT  ACCGT
                                 AA    CCC GA   GT
GAM1207 LOC90050 3' CTTGCCTTGCAGTCACCCCAG 57185      _    C   T
                                CTGGG TGACT TGA GGCAAG
                                ||||| ||||| ||| ||||||
                                GACCC ACTGA GTT CCGTTC
                                   C    C  _
GAM1207 LOC93349 3' TCACACAGTCACCCGGG     57276          C  A
                                CCTGGGTGACT TG TGG
                                |||||||||||| || |||
                                GGGCCCACTGA AC ACT
                                      C  _
GAM1208 AQP3     3' CAAGGGCCACTCCCAAGAAGC  60332     CC  AAA  A
                                GTT  CT   GA TGGCCCTTG
                                |||  ||   || |||||||||
                                CGA  GA   CT ACCGGGAAC
                                  A_  ACC  C
GAM1208 CBFA2T1  3' AAGATATCTTTTCTTTAGAGAA 16357      C       T  CC__
             CT                   AGTTC CTAAAGAA GG    CTT
                                ||||| |||||||| ||    |||
                                TCAAG GATTTCTT TC    GAA
                                   A       T  TATA
GAM1208 CRHR1    3' CAAGGGCCCTCACTCAGGAAC  16501      CTAAA  AT
                                GTTCC    GA  GGCCCTTG
                                |||||    ||  ||||||||
                                CAAGG    CT  CCGGGAAC
                                   ACTCA  C_
GAM1208 KCNJ10   5' CAAGGGCCACTCCACCTCGGAC 11154     CCTAAA  A
                                GTTC     GA TGGCCCTTG
                                ||||     || |||||||||
                                CAGG     CT ACCGGGAAC
                                  CTCCAC  C
GAM1208 KIAA0857 3' CAAGGCATCTGCAGGGAACTT  67248        AA   A  GC
                                AAGTTCCCT  AGA TG  CCTTG
                                |||||||||  ||| ||  |||||
                                TTCAAGGGA  TCT AC  GGAAC
                                     CG  _ __
GAM1208 LEP      3' CAAGGGCCATGCTGAAGGGACC 5856      T    AA  A
             TT                   AAG TCCCT  AG ATGGCCCTTG
                                ||| |||||  || ||||||||||
                                TTC AGGGA  TC TACCGGGAAC
                                  C    AG  G
GAM1208 PAX5     3' AAGGGCCACGGGAACTT     34120         TAAAGAA
                                AAGTTCCC      TGGCCCTT
                                ||||||||      ||||||||
                                TTCAAGGG      ACCGGGAA
                                     C_______
GAM1208 PDE4D    3' AAGAATATTTGGGAACTT    73962         TAAA    GCC
                                AAGTTCCC   GAATG   CTT
                                ||||||||   |||||  |||
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                                TTCAAGGG   TTTAT  GAA
                                    ____    AA_
GAM1208 PITPN    3' CCATTCTTCAGGCAACTT   21712      C  A
                                AAGTT CCT AAGAATGG
                                ||||| ||| ||||||||
                                TTCAA GGA TTCTTACC
                                   C  C
GAM1208 SON      3' AAGAGGTCTGGGAACTT    55224       TAAAGAAT  _
                                AAGTTCCC      GGCC CTT
                                ||||||||      |||| |||
                                TTCAAGGG      CTGG GAA
                                    T_______  A
GAM1208 SON      3' AAGAGGTCTGGGAACTT    57985       TAAAGAAT  _
                                AAGTTCCC      GGCC CTT
                                ||||||||      |||| |||
                                TTCAAGGG      CTGG GAA
                                    T_______  A
GAM1208 AGTRL2   5' CAAGGAGTTTTCAGGGAACT  18957       AAA  T  _
                                AGTTCCCT  GAA GGC CCTTG
                                ||||||||  ||| ||| |||||
                                TCAAGGGA  CTT TTG GGAAC
                                    ___  _  A
GAM1208 C9orf16  3' CAAGGGCTGGCCTTCAGGGA  44358     A  AA
                                TCCCT AAG  TGGCCCTTG
                                ||||| |||  |||||||||
                                AGGGA TTC  GTCGGGAAC
                                   C  CG
GAM1208 DKFZP434L0117 3' CAAGGGCTGATTAGGGAACT  43239        AGAA
                                AGTTCCCTAA   TGGCCCTTG
                                ||||||||||   |||||||||
                                TCAAGGGATT   GTCGGGAAC
                                    A___
GAM1208 HPIP     3' GTTAATCTCTGGGAACTT   40427       TAA  A
                                AAGTTCCC  AGA TGGC
                                ||||||||  ||| ||||
                                TTCAAGGG  TCT ATTG
                                    TC_  A
GAM1208 KIAA0752 3' CAAGGGCCACTCTGGTTTGAGC 67630      CCTAA  A
           TT                    AAGTTC    AGA TGGCCCTTG
                                ||||||    ||| |||||||||
                                TTCGAG    TCT ACCGGGAAC
                                   TTTGG  C
GAM1208 KIAA1340 3' CTACTTTTTAGGAAACTT   69695     C      A
                                AAGTT CCTAAAGA TGG
                                ||||| |||||||| |||
                                TTCAA GGATTTTT ATC
                                   A      C
GAM1208 MGC12679 3' AGTACCCTTCAGGGGACT   52182       AAA  T  CC
                                AGTTCCCT  GAA GG  CT
                                ||||||||  ||| ||  ||
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                                TCAGGGGA  CTT CC  GA
                                    ___   C  AT
GAM1208  SDS3     3'  GTGAATTCTTTAGGGCACTT  69751      T         G_
                                AAGT CCCTAAAGAAT  GC
                                |||| ||||||||||  ||
                                TTCA GGGATTTCTTA  TG
                                  C         AG
GAM1208  STMN3    3'  CAAGTCCTCCTCAGGGAGC   32462        AAA  AT  CC
                                GTTCCCT   GA  GG  CTTG
                                |||||||   ||  ||  ||||
                                CGAGGGA   CT  TC  GAAC
                                    ___ CC  CT
GAM1208  TA-KRP   3'  TCATTCTTAGGAAACTT    51675      C    A
                                AAGTT CCTAA GAATGG
                                ||||| ||||| ||||||
                                TTCAA GGATT CTTACT
                                   A    _
GAM1208  LOC145501 3'  CAAGAGCCACCAAAAGTTAGGG 77763           AGAA___    C
           GACTT                  AAGTTCCCTAA      TGGC CTTG
                                ||||||||||      |||| ||||
                                TTCAGGGGATT      ACCG GAAC
                                     GAAAACC    A
GAM1208  LOC149373 3'  CAAGAGCCATTCTCCCTTCTGA 80090      CCCTAA_      C
           CT                   AGTT      AGAATGGC CTTG
                                ||||      |||||||| ||||
                                TCAG      TCTTACCG GAAC
                                  TCTTCCC       A
GAM1208  LOC151162 5'  CAAGGGTTTTCCTCAAGGAAC  86426      CTAAA   T
                                GTTCC     GAA GGCCCTTG
                                |||||     ||| ||||||||
                                CAAGG     CTT TTGGGAAC
                                   AACTC  _
GAM1208  LOC152286 3'  CAAGTGGCCCCCTAAGGCACTT 86802      TC   AA  AAT   _
                                AAGT  CCT  AG   GGCC CTTG
                                ||||  |||  ||   |||| ||||
                                TTCA  GGA  TC   CCGG GAAC
                                  C_   A_  CC_    T
GAM1208  LOC165693 5'  AAGGAGTCCAGGGAATTT    83484         AAAGAAT   _
                                AAGTTCCCT      GGC CCTT
                                |||||||||      ||| ||||
                                TTTAAGGGA      CTG GGAA
                                     C_______   A
GAM1208  LOC202347 5'  CAAGGGCCATTGAATGGGAACT 91944        TAAAG
                                AGTTCCC     AATGGCCCTTG
                                |||||||     ||||||||||
                                TCAAGGG     TTACCGGGAAC
                                    TAAG_
GAM1208  LOC203377 5'  CAAGGGTTTTCCTCAAGGAAC  92255      CTAAA   T
                                GTTCC     GAA GGCCCTTG
                                |||||     ||| ||||||||
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                                CAAGG    CTT TTGGGAAC
                                  AACTC  _
GAM1208 LOC254122 3' AAGGATTCTAGGGAACT    96392       AA    GGC
                                AGTTCCCT  AGAAT   CCTT
                                ||||||||  |||||   ||||
                                TCAAGGGA  TCTTA   GGAA
                                   __    ___
GAM1209 APPL    3' GTAGAGACGGGGTTTCACCGTG 24952    __
                                CAC  TGAAACCCCGTCTCTAC
                                |||  ||||||||||||||||
                                GTG  ACTTTGGGGCAGAGATG
                                  CC
GAM1209 ARCN1   3' GTAGAGACGGGGTTTCACCGTG 9757     __
                                CAC  TGAAACCCCGTCTCTAC
                                |||  ||||||||||||||||
                                GTG  ACTTTGGGGCAGAGATG
                                  CC
GAM1209 ARHGEF6  3' GGTAGAGATGGCCTCAGAGT  68760   A   AACC
                                AC CTGA   CCGTCTCTACC
                                || ||||   ||||||||||
                                TG GACT   GGTAGAGATGG
                                 A   CC__
GAM1209 CAPN1   3' GTGGGGAGGTCCCGTGTT    19013      T AA  CCG
                                AACAC G  ACC   TCTCTAC
                                ||||| |  |||   |||||||
                                TTGTG C  TGG   AGGGGTG
                                  _ CC  ___
GAM1209 CASP8   3' GTAGAGACAGGGTTTCACTGT  8760     C      C
                                ACA TGAAACCC GTCTCTAC
                                ||| |||||||| ||||||||
                                TGT ACTTTGGG CAGAGATG
                                  C       A
GAM1209 CASP8   3' GTAGAGACAGGGTTTCACTGT  54081    C      C
                                ACA TGAAACCC GTCTCTAC
                                ||| |||||||| ||||||||
                                TGT ACTTTGGG CAGAGATG
                                  C       A
GAM1209 CASP8   3' GTAGAGACAGGGTTTCACTGT  54101    C      C
                                ACA TGAAACCC GTCTCTAC
                                ||| |||||||| ||||||||
                                TGT ACTTTGGG CAGAGATG
                                  C       A
GAM1209 CASP8   3' GTAGAGACAGGGTTTCACTGT  54117    C      C
                                ACA TGAAACCC GTCTCTAC
                                ||| |||||||| ||||||||
                                TGT ACTTTGGG CAGAGATG
                                  C       A
GAM1209 CCNF    3' GGTAGAGACGGGATTTCA    10083      C
                                TGAAA CCCGTCTCTACC
                                ||||| ||||||||||||
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                                ACTTT GGGCAGAGATGG
                                  A
GAM1209  CLCN7    3'  GGCAGAGGCAACTTCAGTGT   8912         ACCCC     A
                                ACACTGAA    GTCTCT CC
                                ||||||||    |||||| ||
                                TGTGACTT    CGGAGA GG
                                    CAA__     C
GAM1209  CYP1A2   3'  GTAGAGACGAGGTTTCACTGT  7522      C      C
                                ACA TGAAACC CGTCTCTAC
                                ||| ||||||| |||||||||
                                TGT ACTTTGG GCAGAGATG
                                  C      A
GAM1209  CYP1B1   3'  AGAGACAAGTAATTTCAGTGT  5443          CCCC__
                                ACACTGAAA     GTCTCT
                                |||||||||     ||||||
                                TGTGACTTT     CAGAGA
                                    AATGAA
GAM1209  CYP51    3'  GTAGAGACGGGGGTTTCA    7619          _
                                TGAAACCCC GTCTCTAC
                                ||||||||| ||||||||
                                ACTTTGGGG CAGAGATG
                                    G
GAM1209  DSC3     3'  TAGAGACGGGGTTTCACTGT   10446     C
                                ACA TGAAACCCCGTCTCTA
                                ||| ||||||||||||||||
                                TGT ACTTTGGGGCAGAGAT
                                  C
GAM1209  DSC3     3'  TAGAGACGGGGTTTCACTGT   44634     C
                                ACA TGAAACCCCGTCTCTA
                                ||| ||||||||||||||||
                                TGT ACTTTGGGGCAGAGAT
                                  C
GAM1209  EIF2S3   3'  GTAGAGACGGGGTTTCAG    9211
                                CTGAAACCCCGTCTCTAC
                                ||||||||||||||||||
                                GACTTTGGGGCAGAGATG

GAM1209  FREB     5'  GAGAGGTTTCATGTT       52191      C      CCG
                                AACA TGAAACC   TCTC
                                |||| |||||||   ||||
                                TTGT ACTTTGG   AGAG
                                  _      ___
GAM1209  FUT1     3'  GTAGAGACGGGGTTTCATCGTG 5608      __
                                CAC  TGAAACCCCGTCTCTAC
                                |||  ||||||||||||||||
                                GTG  ACTTTGGGGCAGAGATG
                                  CT
GAM1209  HOXC9    3'  GGGAGGGTTCAGTGTT      61927          A   CG
                                AACACTGAA CCC  TCTC
                                ||||||||| |||  ||||
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                                TTGTGACTT GGG  AGGG
                                      _  __
GAM1209  JPH3     3'  GACGCGTGGGGTTCCGTGT   40676     T  A  _  C
                                ACAC GAA CCC CGT TC
                                |||| ||| ||| ||| ||
                                TGTG CTT GGG GCG AG
                                  C  G  T  C
GAM1209  KCNA3    3'  AGATGTTTTCAGTGTT      11132         CCC
                                AACACTGAAA  CGTCT
                                ||||||||||  |||||
                                TTGTGACTTT  GTAGA
                                      T__
GAM1209  LYZ      3'  GTAGAGACAGGGTTTCACCGTG 5900     __      C
                                CAC  TGAAACCC GTCTCTAC
                                |||  |||||||| ||||||||
                                GTG  ACTTTGGG CAGAGATG
                                  CC       A
GAM1209  MAP1B    5'  GTAGAGAATTTCAGTG      50091        CCCCG
                                CACTGAAA    TCTCTAC
                                ||||||||    |||||||
                                GTGACTTT    AGAGATG
                                    A____
GAM1209  MDM2     3'  GTAGAGACAGGGTTTCACCGTG 11498    __      C
                                CAC  TGAAACCC GTCTCTAC
                                |||  |||||||| ||||||||
                                GTG  ACTTTGGG CAGAGATG
                                  CC       A
GAM1209  MDM2     3'  GTAGAGACAGGGTTTCACCGTG 23460    __      C
                                CAC  TGAAACCC GTCTCTAC
                                |||  |||||||| ||||||||
                                GTG  ACTTTGGG CAGAGATG
                                  CC       A
GAM1209  MDM2     3'  GTAGAGACAGGGTTTCACCGTG 23473    __      C
                                CAC  TGAAACCC GTCTCTAC
                                |||  |||||||| ||||||||
                                GTG  ACTTTGGG CAGAGATG
                                  CC       A
GAM1209  MDM2     3'  GTAGAGACAGGGTTTCACCGTG 23486    __      C
                                CAC  TGAAACCC GTCTCTAC
                                |||  |||||||| ||||||||
                                GTG  ACTTTGGG CAGAGATG
                                  CC       A
GAM1209  MDM2     3'  GTAGAGACAGGGTTTCACCGTG 23499    __      C
                                CAC  TGAAACCC GTCTCTAC
                                |||  |||||||| ||||||||
                                GTG  ACTTTGGG CAGAGATG
                                  CC       A
GAM1209  MEFV     3'  GTAGAGACGGGGGTTTCA    5944         _
                                TGAAACCCC GTCTCTAC
                                |||||||| ||||||||
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                                ACTTTGGGG CAGAGATG
                                     G
GAM1209  MHC2TA   3'  GGTAGAGACAGGGTTTTGCCGT 5990     T__     C
             G                   CAC   GAAACCC GTCTCTACC
                                 |||   ||||||| |||||||||
                                 GTG   TTTTGGG CAGAGATGG
                                   CCG      A
GAM1209  MTR      3'  GTAGAGACAGGATTTCACTGT  6024     C    C  C
                                 ACA TGAAA CC GTCTCTAC
                                 ||| ||||| || ||||||||
                                 TGT ACTTT GG CAGAGATG
                                   C    A  A
GAM1209  PIGR     3'  GTAGAGACAGGGTTTCACCGTG 73006    __      C
                                 CAC  TGAAACCC GTCTCTAC
                                 |||  |||||||| ||||||||
                                 GTG  ACTTTGGG CAGAGATG
                                   CC       A
GAM1209  PIK3CD   3'  GTAGAGACGGGGGTTTCA    18497        _
                                 TGAAACCCC GTCTCTAC
                                 ||||||||| ||||||||
                                 ACTTTGGGG CAGAGATG
                                      G
GAM1209  PPP1R3C  3'  GTAGGGACTTCATGT      19425    C   ACCCC
                                 ACA TGAA    GTCTCTAC
                                 ||| ||||    ||||||||
                                 TGT ACTT    CAGGGATG
                                  _   _____
GAM1209  PPT2     3'  GTAGAGACGGGGTTTTAGT   18951
                                 ACTGAAACCCCGTCTCTAC
                                 ||||||||||||||||||
                                 TGATTTTGGGGCAGAGATG

GAM1209  PPT2     3'  GTAGAGACGGGGTTTTAGT   57801
                                 ACTGAAACCCCGTCTCTAC
                                 ||||||||||||||||||
                                 TGATTTTGGGGCAGAGATG

GAM1209  PTGES    3'  GTAGAGACGGGTTCACCATGTT 18068     C__   AC
                                 AACA   TGAA  CCCGTCTCTAC
                                 ||||   ||||  ||||||||||
                                 TTGT   ACTT  GGGCAGAGATG
                                   ACC   __
GAM1209  PTPRF    5'  GGCAGAGGCGGCGGCTCCAG   12608    AAA  _      A
                                 CTG   CC CCGTCTCT CC
                                 |||   || |||||||| ||
                                 GAC   GG GGCGGAGA GG
                                   CTC  C       C
GAM1209  PTPRF    5'  GGCAGAGGCGGCGGCTCCAG   56138    AAA  _      A
                                 CTG   CC CCGTCTCT CC
                                 |||   || |||||||| ||
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                                GAC   GG GGCGGAGA GG
                                  CTC  C       C
GAM1209  RARB     3'  GGCAGAAACACTTTTCAGTGTT 32889          CCCC  C   A
                                AACACTGAAA    GT TCT CC
                                ||||||||||    || ||| ||
                                TTGTGACTTT    CA AGA GG
                                      TCA_  A   C
GAM1209  RARB     3'  GGCAGAAACACTTTTCAGTGTT 8260           CCCC  C   A
                                AACACTGAAA    GT TCT CC
                                ||||||||||    || ||| ||
                                TTGTGACTTT    CA AGA GG
                                      TCA_  A   C
GAM1209  RBM8A    3'  GTAGAGACACTGGTCAGT    18811       AA  CC_
                                ACTGA  CC   GTCTCTAC
                                |||||  ||   ||||||||
                                TGACT  GG   CAGAGATG
                                  __  TCA
GAM1209  RPP30    3'  AGAGACGGGGTTTCACCGTG   22190     __
                                CAC  TGAAACCCCGTCTCT
                                |||  ||||||||||||||||
                                GTG  ACTTTGGGGCAGAGA
                                  CC
GAM1209  RPP30    5'  GGTAGAGACGGACTGCGCAGGT 22204     A   AAACC_
           T                     AAC CTG     CCGTCTCTACC
                                 ||| |||     ||||||||||
                                 TTG GAC     GGCAGAGATGG
                                  _   GCGTCA
GAM1209  SERPINB9 3'  GTAGAGACGGGGTTTCACCGTG 16027     __
                                CAC  TGAAACCCCGTCTCTAC
                                |||  |||||||||||||||||
                                GTG  ACTTTGGGGCAGAGATG
                                  CC
GAM1209  SLC3A2   5'  TAGAGACGGGGTCTGACTGTG  11524     TGAA__
                                CAC     ACCCCGTCTCTA
                                |||     ||||||||||||
                                GTG     TGGGGCAGAGAT
                                  TCAGTC
GAM1209  TAPBP    3'  GTAGAGACGGGGTTTCACCGTG 13579     __
                                CAC  TGAAACCCCGTCTCTAC
                                |||  |||||||||||||||||
                                GTG  ACTTTGGGGCAGAGATG
                                  CC
GAM1209  TAPBP    3'  GTAGAGACGGGGTTTCACCGTG 13580     __
                                CAC  TGAAACCCCGTCTCTAC
                                |||  |||||||||||||||||
                                GTG  ACTTTGGGGCAGAGATG
                                  CC
GAM1209  TBXA2R   3'  GTAGAGACGGGGTTTCACCGTG 8362      __
                                CAC  TGAAACCCCGTCTCTAC
                                |||  |||||||||||||||||
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                                GTG  ACTTTGGGGCAGAGATG
                                  CC
GAM1209  TEAD3    3'  GGTAGAGGAAGGAGTCCCAG   13674     AA  _  CG
                                CTG  AC CC  TCTCTACC
                                |||  || ||  ||||||||
                                GAC  TG GG  GGAGATGG
                                  CC  A  AA
GAM1209  TERF2    3'  GTAGAGACGGGGTTTCACCGTG 20160     __
                                CAC  TGAAACCCCGTCTCTAC
                                |||  ||||||||||||||||
                                GTG  ACTTTGGGGCAGAGATG
                                  CC
GAM1209  TEX15    3'  GTAGAGATGTTTTAAATGTT   49223     C_    CCC
                                AACA  TGAAAC   GTCTCTAC
                                ||||  ||||||   ||||||||
                                TTGT  ATTTTG   TAGAGATG
                                  AA     ___
GAM1209  UBE2V1   3'  GTAGATGTGAAGGTTTCAG    42066       C_  TC
                                CTGAAACC  CG  TCTAC
                                ||||||||  ||  |||||
                                GACTTTGG  GT  AGATG
                                    AA  GT
GAM1209  UBE2V1   3'  GTAGATGTGAAGGTTTCAG    13969       C_  TC
                                CTGAAACC  CG  TCTAC
                                ||||||||  ||  |||||
                                GACTTTGG  GT  AGATG
                                    AA  GT
GAM1209  UPF3A    3'  TAGAAACGGTTTCAGT      43734       CC  C
                                ACTGAAACC  GT TCTA
                                |||||||||  || ||||
                                TGACTTTGG  CA AGAT
                                    __  A
GAM1209  UPF3A    3'  TAGAAACGGTTTCAGT      55640       CC  C
                                ACTGAAACC  GT TCTA
                                |||||||||  || ||||
                                TGACTTTGG  CA AGAT
                                    __  A
GAM1209  WBSCR5   3'  GTAGAGATTTCTGTGTT     51630     T  ACCCC
                                AACAC GAA    GTCTCTAC
                                |||||  |||    ||||||||
                                TTGTG CTT    TAGAGATG
                                  T  _____
GAM1209  WBSCR5   3'  GTAGAGATTTCTGTGTT     42112     T  ACCCC
                                AACAC GAA    GTCTCTAC
                                |||||  |||    ||||||||
                                TTGTG CTT    TAGAGATG
                                  T  _____
GAM1209  WBSCR5   3'  GTAGAGATTTCTGTGTT     27114     T  ACCCC
                                AACAC GAA    GTCTCTAC
                                |||||  |||    ||||||||
```

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                                TTGTG CTT    TAGAGATG
                                  T  _____
GAM1209  WTAP     3'  GTAGTAGTTTCAGTGTT     18140          CCCGTCT
                                AACACTGAAAC      CTAC
                                ||||||||||       ||||
                                TTGTGACTTTG      GATG
                                      AT_____
GAM1209  ZNF133   5'  GTAGAGACGGAGTTTCAG     14297        C
                                CTGAAAC CCGTCTCTAC
                                ||||||| ||||||||||
                                GACTTTG GGCAGAGATG
                                    A
GAM1209  ALDH9    3'  GTAGAGATGATTTCAG      7347         CCC
                                CTGAAA   CGTCTCTAC
                                ||||||   |||||||||
                                GACTTT   GTAGAGATG
                                    A__
GAM1209  APOL4    3'  GGTAAAGTTTATGGAACTCAGT 48380         AACC   ___  C
             GTT                   AACACTGA    CCGT   CT TACC
                                |||||||||    ||||   || ||||
                                TTGTGACT    GGTA   GA ATGG
                                     CAA_    TTT  A
GAM1209  ARHGAP11A 3'  GTAGAGACGGTTTCACCGTGTT 29456       __       CC
                                AACAC  TGAAACC  GTCTCTAC
                                |||||  |||||||  ||||||||
                                TTGTG  ACTTTGG  CAGAGATG
                                   CC      __
GAM1209  ARHGEF9  3'  GGTAGAGTTGGGAGGTTTCAGG 31490     A       _  GT_
             GTT                   AAC CTGAAACC CC   CTCTACC
                                ||| ||||||||  ||   |||||||
                                TTG GACTTTGG GG   GAGATGG
                                  G       A  GTT
GAM1209  ASE-1    3'  GTAGAGACAGGGGTTTCA     24989          _
                                TGAAACCCC GTCTCTAC
                                ||||||||| ||||||||
                                ACTTTGGGG CAGAGATG
                                      A
GAM1209  BRAL1    5'  GGCAGAGGGGCTCAAGTTCCAG 41809     A   A  _____   G   _
             GGTT                   AAC CTG AAC     CCC TCT CT
                                ||| ||| |||     ||| ||| ||
                                TTG GAC TTG     GGG AGA GG
                                  G   C   AACTC   G   C
GAM1209  C1orf16  3'  GTAGAAGCTTTCAGTGT     29916         CCCC TC
                                ACACTGAAA    G  TCTAC
                                |||||||||    |  |||||
                                TGTGACTTT    C  AGATG
                                      ____ GA
GAM1209  C20orf36 3'  AGTTGCTGGGCTTCAGTGT   37333         A   C  CT
                                ACACTGAA CCC GT  CT
                                |||||||| ||| ||  ||
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                                TGTGACTT GGG CG  GA
                                     C   T  TT
GAM1209  CCRN4L    3'  GTAGAGACGGGGTTTCACCGTG 25073     __
                                CAC  TGAAACCCCGTCTCTAC
                                |||  ||||||||||||||||
                                GTG  ACTTTGGGGCAGAGATG
                                  CC
GAM1209  CDCA7     3'  GGTAGAGGTGGAATCTAAGTGT 50044       GAAACC  GT
              T                  AACACT     CC  CTCTACC
                                 ||||||     ||  |||||||
                                 TTGTGA     GG  GAGATGG
                                    ATCTAA  TG
GAM1209  CEACAM8   3'  GTAGAGACGGGGTTTCACTGT  10185     C
                                ACA TGAAACCCCGTCTCTAC
                                ||| ||||||||||||||||
                                TGT ACTTTGGGGCAGAGATG
                                  C
GAM1209  CENPH     3'  GTAGAGACGGGGTTTCACCGTG 43570     __
                                CAC  TGAAACCCCGTCTCTAC
                                |||  ||||||||||||||||
                                GTG  ACTTTGGGGCAGAGATG
                                  CC
GAM1209  CEPT1     3'  GTGGAGAGTTCTAATGTT    21438      C  A   CCCG
                                AACA TG AAC    TCTCTAC
                                ||||  ||  |||   |||||||
                                TTGT AT TTG    AGAGGTG
                                  A  C  _____
GAM1209  CPSF2     3'  GGTAGAGACAGGGTTTCA    62278        C
                                TGAAACCC GTCTCTACC
                                ||||||||  |||||||||
                                ACTTTGGG CAGAGATGG
                                     A
GAM1209  DKFZp761N1114 3'  GTAGAGACGGGATTTCACCGTG 79790     __    C
                                CAC  TGAAA CCCGTCTCTAC
                                |||  |||||  ||||||||||
                                GTG  ACTTT GGGCAGAGATG
                                  CC    A
GAM1209  EPN2      3'  GACGTGGAGTCATCAGTGTT   31040        A_  _  _
                                AACACTGA  AC CC CGTC
                                ||||||||  ||  ||  ||||
                                TTGTGACT  TG GG GCAG
                                     AC  A  T
GAM1209  EVI5      3'  GATACTAGGTATTCAGTGTT   20213         _  CC  C
                                AACACTGAA ACC  GT TC
                                |||||||||  |||  ||  ||
                                TTGTGACTT TGG  CA AG
                                     A   AT  T
GAM1209  FBP17     3'  GTAGAGACAGGGTTTCACCGTG 73155     __       C
                                CAC  TGAAACCC GTCTCTAC
                                |||  ||||||||  ||||||||
```

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                                GTG  ACTTTGGG CAGAGATG
                                  CC       A
GAM1209  FKBP9    3'  GGTAGAGACGGGGTTTCACCGT 95719     __
             G                   CAC  TGAAACCCCGTCTCTACC
                                 |||  ||||||||||||||||||
                                 GTG  ACTTTGGGGCAGAGATGG
                                   CC
GAM1209  FLJ10232 3'  GTAGAGGTGGGGTTTCATGTT  36383      C       GT
                                 AACA TGAAACCCC  CTCTAC
                                 ||||  |||||||||  ||||||
                                 TTGT ACTTTGGGG  GAGATG
                                   _       TG
GAM1209  FLJ10560 3'  GTAGAGACGGGGTTTCACCGTG 36799     __
                                 CAC  TGAAACCCCGTCTCTAC
                                 |||  ||||||||||||||||
                                 GTG  ACTTTGGGGCAGAGATG
                                   CC
GAM1209  FLJ12581 3'  GTAGAGACAGGGTTTCACTGT  46340     C       C
                                 ACA TGAAACCC GTCTCTAC
                                 |||  ||||||||  ||||||||
                                 TGT ACTTTGGG CAGAGATG
                                   C       A
GAM1209  FLJ12687 3'  GGTAGAGACAGGGTTTCA     46756         C
                                 TGAAACCC GTCTCTACC
                                 ||||||||  ||||||||
                                 ACTTTGGG CAGAGATGG
                                      A
GAM1209  FLJ12876 3'  GTAGAGACGGGGTTTCACTGT  43097     C
                                 ACA TGAAACCCCGTCTCTAC
                                 |||  ||||||||||||||||
                                 TGT ACTTTGGGGCAGAGATG
                                   C
GAM1209  FLJ12975 3'  GTAGAGACAGGGTTCCACCGT  70196    AC  A    C
                                 AC  TG AACCC GTCTCTAC
                                 ||  ||  |||||  ||||||||
                                 TG  AC TTGGG CAGAGATG
                                  CC  C    A
GAM1209  FLJ13072 5'  TAGAGTCGTTTTCAGTG     91398         CCC  T
                                 CACTGAAA   CG CTCTA
                                 ||||||||   ||  |||||
                                 GTGACTTT   GC GAGAT
                                      T__  T
GAM1209  FLJ13188 3'  GTAGAGACAGAGTTTTGCTGT  42193     CT    CCC
                                 ACA  GAAAC   GTCTCTAC
                                 |||  |||||   ||||||||
                                 TGT  TTTTG   CAGAGATG
                                   CG    AGA
GAM1209  FLJ20294 3'  GGTAGAGACAAACGTTGCACTG 35358    C  A   CCC_
                                 CA TG AAC    GTCTCTACC
                                 ||  ||  |||    |||||||||
```

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                                GT AC TTG    CAGAGATGG
                                 C  G   CAAA
GAM1209  FLJ20546  3'  GTAGTGGCTTCAGTGT      35813         ACCCC   T
                                ACACTGAA     GTC CTAC
                                ||||||||     ||| ||||
                                TGTGACTT     CGG GATG
                                     _____   T
GAM1209  FLJ21742  3'  GTAGAGCTTGGTTCAGTGTT   50816         A  CC T
                                AACACTGAA CC  G CTCTAC
                                ||||||||| ||  | ||||||
                                TTGTGACTT GG  C GAGATG
                                     _  TT _
GAM1209  FLJ23392  3'  GTAGAGACAGGGTTTCACCGTG 45902     __       C
                                CAC  TGAAACCC GTCTCTAC
                                |||  |||||||| ||||||||
                                GTG  ACTTTGGG CAGAGATG
                                  CC       A
GAM1209  FLJ23392  3'  GTAGAGACGGGGTTTCACCGTG 45903     __
                                CAC  TGAAACCCCGTCTCTAC
                                |||  ||||||||||||||||
                                GTG  ACTTTGGGGCAGAGATG
                                  CC
GAM1209  FLJ23556  3'  AGAGACGGGGTTTCACCGTG   46424     __
                                CAC  TGAAACCCCGTCTCT
                                |||  ||||||||||||||
                                GTG  ACTTTGGGGCAGAGA
                                  CC
GAM1209  FLJ23563  3'  GTAGAGACAGGGTTGGCCAG   68216     A__     C
                                CTG   AACCC GTCTCTAC
                                |||   ||||| ||||||||
                                GAC   TTGGG CAGAGATG
                                  CGG    A
GAM1209  FLJ31101  3'  GTAAAGACGGGGGATTTCA    36168      __       C
                                TGAAA  CCCCGTCT TAC
                                |||||  |||||||| |||
                                ACTTT  GGGGCAGA ATG
                                   AG       A
GAM1209  FLJ32865  3'  GTAGAGACGGGGTTTCTCCGTG 58818     T__
                                CAC   GAAACCCCGTCTCTAC
                                |||   ||||||||||||||||
                                GTG   CTTTGGGGCAGAGATG
                                  CCT
GAM1209  GMPPB     3'  GGTAGAGACAGGGGTTGTG    97459     TGA     _
                                CAC   AACCCC GTCTCTACC
                                |||   |||||| |||||||||
                                GTG   TTGGGG CAGAGATGG
                                  ___      A
GAM1209  ICK       3'  GTAGAGACGGGGTTTCACTGT  30598     C
                                ACA TGAAACCCCGTCTCTAC
                                ||| ||||||||||||||||
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                                TGT ACTTTGGGGCAGAGATG
                                  C
GAM1209  KIAA0140  3'  GGTGGGGGGGGGCTTAGTG    28518       AA    GTC
                                CACTGA  CCCC   TCTACC
                                ||||||  ||||   ||||||
                                GTGATT  GGGG   GGGTGG
                                   CG   ___
GAM1209  KIAA0210  5'  GTAGAGACGGAGGAGTTTCA   29170       __ _
                                TGAAA  CC CCGTCTCTAC
                                |||||  || ||||||||||
                                ACTTT  GG GGCAGAGATG
                                   GA  A
GAM1209  KIAA0256  3'  TAGAAGCAGTTATCAGTGTT   65051         _   CCC TC
                                AACACTGA AAC   G  TCTA
                                |||||||| |||   |  ||||
                                TTGTGACT TTG   C  AGAT
                                     A   A__ GA
GAM1209  KIAA0469  3'  GTAGAGACGGGATTTCACTGT  29990     C     C
                                ACA TGAAA CCCGTCTCTAC
                                ||| ||||| ||||||||||
                                TGT ACTTT GGGCAGAGATG
                                  C     A
GAM1209  KIAA0594  3'  GTAGAGATGGGGTTTCAG    65515
                                CTGAAACCCCGTCTCTAC
                                ||||||||||||||||||
                                GACTTTGGGGTAGAGATG

GAM1209  KIAA0599  3'  GTAGAGACGGGGTTTCGCCGTG 77696     __
                                CAC  TGAAACCCCGTCTCTAC
                                |||  ||||||||||||||||
                                GTG  GCTTTGGGGCAGAGATG
                                  CC
GAM1209  KIAA0798  3'  GGTAGAGACGGGGTTTCACTGT 28453     C
                                ACA TGAAACCCCGTCTCTACC
                                ||| ||||||||||||||||
                                TGT ACTTTGGGGCAGAGATGG
                                  C
GAM1209  KIAA0831  3'  GGTAGAGACGGGGGTTTTCA   30650      __
                                TGAAA  CCCCGTCTCTACC
                                |||||  ||||||||||||
                                ACTTT  GGGGCAGAGATGG
                                   TG
GAM1209  KIAA0861  3'  GTAGAGACGGGGTTTCCCCGTG 90356     T__
                                CAC   GAAACCCCGTCTCTAC
                                |||   ||||||||||||||||
                                GTG   CTTTGGGGCAGAGATG
                                  CCC
GAM1209  KIAA1204  5'  GGCAGAGACGGAGGGGCAG   69741     AAA  _      A
                                CTG   CC CCGTCTCT CC
                                |||   || ||||||| ||
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                                GAC   GG GGCAGAGA GG
                                  GG_ A       C
GAM1209  KIAA1233  3'  GGTAAGGGTTAGTTTCAGT    63757        CCCGT   _
                                ACTGAAAC     CTCT ACC
                                ||||||||     |||| |||
                                TGACTTTG     GGGA TGG
                                    ATT__    A
GAM1209  KIAA1259  3'  GTAGAGACAGAGGGGCAGTGTT 50801        AAA   ___
                                AACACTG   CCCC   GTCTCTAC
                                |||||||   ||||   ||||||||
                                TTGTGAC   GGGG   CAGAGATG
                                    ___    AGA
GAM1209  KIAA1465  3'  GGTGGGGGGGAGTTTCAGT    61506        _  GTC
                                ACTGAAAC CCC   TCTACC
                                |||||||| |||   ||||||
                                TGACTTTG GGG   GGGTGG
                                    A  ___
GAM1209  KIAA1530  3'  GTAGAGACGGGATTTCACTGT  68566     C    C
                                ACA TGAAA CCCGTCTCTAC
                                ||| ||||| ||||||||||
                                TGT ACTTT GGGCAGAGATG
                                  C    A
GAM1209  KIAA1615  3'  GTAGAGACGGGATATCTCCGTG 69280     T  AAC__
                                CAC GA     CCCGTCTCTAC
                                ||| ||     ||||||||||
                                GTG CT     GGGCAGAGATG
                                  C  CTATA
GAM1209  KIAA1617  3'  GGTAGAGACAGGGTTTCA     93081        C
                                TGAAACCC GTCTCTACC
                                |||||||| |||||||||
                                ACTTTGGG CAGAGATGG
                                    A
GAM1209  KIAA1668  3'  GTAGAGACGGGGTTTCACCGTG 67077     __
                                CAC  TGAAACCCCGTCTCTAC
                                |||  ||||||||||||||||
                                GTG  ACTTTGGGGCAGAGATG
                                  CC
GAM1209  KIAA1877  3'  GTAGAGACAGGGTTTCACCGTG 66757     __       C
                                CAC  TGAAACCC GTCTCTAC
                                |||  |||||||| ||||||||
                                GTG  ACTTTGGG CAGAGATG
                                  CC       A
GAM1209  KIAA1971  3'  GTAGAGACGAGGTTTCACCGTG 74689     __      C
                                CAC  TGAAACC CGTCTCTAC
                                |||  ||||||| |||||||||
                                GTG  ACTTTGG GCAGAGATG
                                  CC      A
GAM1209  LCHN      3'  GGTAGAGACCATTCCAGTGT   87476       AAACCCC
                                ACACTG      GTCTCTACC
                                ||||||      |||||||||
```

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                                TGTGAC      CAGAGATGG
                                   CTTAC__
GAM1209 LENG1    5' AGAGGCGGGAGCCCCAGGTT  85193     A   AAAC_
                                AAC CTG     CCCGTCTCT
                                ||| |||     |||||||||
                                TTG GAC     GGGCGGAGA
                                  _   CCCGA
GAM1209 MEGF11   3' AGAGATTTCAGTGTT       51597         ACCCC
                                AACACTGAA     GTCTCT
                                |||||||||     ||||||
                                TTGTGACTT     TAGAGA
                                              _____
GAM1209 MGC20235 3' GGTAGAGACAGAGTCTCACTGT 59557      C   A  CCC
             T                   AACA TGA AC   GTCTCTACC
                                ||||| ||| ||   |||||||||
                                TTGT ACT TG   CAGAGATGG
                                  C   C  AGA
GAM1209 MGC29667 3' GACAGGGCAACTTCAGTGTT   58987         A___   C
                                AACACTGAA    CCC GTC
                                |||||||||    ||| |||
                                TTGTGACTT    GGG CAG
                                     CAAC   A
GAM1209 MGC4766  5' GTAGAGACGGGGTTTCACCGTG 49563     __
                                CAC  TGAAACCCCGTCTCTAC
                                |||  ||||||||||||||||
                                GTG  ACTTTGGGGCAGAGATG
                                  CC
GAM1209 MGC4832  3' GGTAGAGACAGGTCTCA     59659     A   CC
                                TGA ACC  GTCTCTACC
                                ||| |||  |||||||||
                                ACT TGG  CAGAGATGG
                                  C   A_
GAM1209 moblak   3' GTAGAGACAGGGTTTCACCGTG 56408     __       C
                                CAC  TGAAACCC GTCTCTAC
                                |||  |||||||| ||||||||
                                GTG  ACTTTGGG CAGAGATG
                                  CC       A
GAM1209 NUP107   3' GTAGGGATATCAGCGTT     40237     A    AACCCC
                                AAC CTGA     GTCTCTAC
                                |||  ||||     ||||||||
                                TTG GACT     TAGGGATG
                                  C    A_____
GAM1209 OLFM3    5' GGTTGGAGGCGCTTCAG     83026       ACCC      _
                                CTGAA    CGTCTCTA CC
                                |||||    |||||||| ||
                                GACTT    GCGGAGGT GG
                                   C___       T
GAM1209 POPX1    3' GTAGAGACTTTCAGT       30476         CCCC
                                ACTGAAA    GTCTCTAC
                                |||||||    ||||||||
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                                TGACTTT   CAGAGATG
                                   ____
GAM1209 PSPH    3' GTAGAGACGGGGTTTGACCGTG 17137    TG__
                                CAC   AAACCCCGTCTCTAC
                                |||   ||||||||||||||||
                                GTG   TTTGGGGCAGAGATG
                                  CCAG
GAM1209 RAP140  3' GTAGAGACAGGGTTTCACTGT  31521    C      C
                                ACA TGAAACCC GTCTCTAC
                                ||| |||||||| ||||||||
                                TGT ACTTTGGG CAGAGATG
                                  C       A
GAM1209 RILP    3' GGCAGGACGGGGTCTCAG    49498     A      T  A
                                CTGA ACCCCGTC CT CC
                                |||| |||||||| || ||
                                GACT TGGGGCAG GA GG
                                  C       _  C
GAM1209 SEC15B  3' AGTGTTGGGGATTGTCAGTGTT 67260       AA__    TCT
                                AACACTGA   CCCCG   CT
                                ||||||||   |||||  ||
                                TTGTGACT   GGGGT   GA
                                    GTTA    TGT
GAM1209 SULT1C2 3' GTAGAGACGAGGTTTCACCGTG 22718    __     C
                                CAC  TGAAACC CGTCTCTAC
                                |||  ||||||| |||||||||
                                GTG  ACTTTGG GCAGAGATG
                                  CC      A
GAM1209 SUN1    3' GTAGAGACAGGGTTTCACTGT  47919    C      C
                                ACA TGAAACCC GTCTCTAC
                                ||| |||||||| ||||||||
                                TGT ACTTTGGG CAGAGATG
                                  C       A
GAM1209 TADA3L  3' GTAGAGACGGGGTTTCACCGTG 56812    __
                                CAC  TGAAACCCCGTCTCTAC
                                |||  ||||||||||||||||
                                GTG  ACTTTGGGGCAGAGATG
                                  CC
GAM1209 TCL6    3' GTAGAGACAGGGTTTCACCGTG 27767    __     C
                                CAC  TGAAACCC GTCTCTAC
                                |||  |||||||| ||||||||
                                GTG  ACTTTGGG CAGAGATG
                                  CC      A
GAM1209 TCL6    3' GTAGAGACAGGGTTTCACCGTG 25915    __     C
                                CAC  TGAAACCC GTCTCTAC
                                |||  |||||||| ||||||||
                                GTG  ACTTTGGG CAGAGATG
                                  CC      A
GAM1209 TLR8    5' GGTTCTCTTGACACTTCAGTGT 33977       ACCCC   TCT___
            T                    AACACTGAA   GTC    ACC
                                |||||||||   |||    |||
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                                TTGTGACTT    CAG     TGG
                                     CA___   TTCTCT
GAM1209  TRIM36   3'  TGGAGAACTTCAGTGTT     38629         ACCCCG
                                AACACTGAA     TCTCTA
                                |||||||||     ||||||
                                TTGTGACTT     AGAGGT
                                     CA____
GAM1209  ZNF221   3'  GTAAAAACGGGGTTTCACCGTG 26271     __         CTC
                                CAC  TGAAACCCCGT   TAC
                                |||  ||||||||||   |||
                                GTG  ACTTTGGGGCA   ATG
                                  CC         AAA
GAM1209  LOC115219 5'  GGTAGAGACGGGGTTTCA    73702
                                TGAAACCCCGTCTCTACC
                                ||||||||||||||||||
                                ACTTTGGGGCAGAGATGG

GAM1209  LOC115509 3'  GGCACTGGGTTTTCAGTGT    73844         _  C  C
                                ACACTGAAA CCC GT TC
                                ||||||||| ||| || ||
                                TGTGACTTT GGG CA GG
                                     T   T  C
GAM1209  LOC126669 3'  TAGAATGTTTTCAGTGT     75949         CCC   C
                                ACACTGAAA   CGT TCTA
                                |||||||||   ||| ||||
                                TGTGACTTT   GTA AGAT
                                     T__   _
GAM1209  LOC134266 3'  GGTAGGGATTGGTTCA      75646      AC  C
                                TGAA  CC GTCTCTACC
                                ||||  || |||||||||
                                ACTT  GG TAGGGATGG
                                  __  T
GAM1209  LOC145623 3'  TAGAGATTTCAGTGT       84394         ACCCC
                                ACACTGAA     GTCTCTA
                                ||||||||     |||||||
                                TGTGACTT     TAGAGAT
                                     _____
GAM1209  LOC146229 3'  GTAGAGACGGGGTTTTACCGTG 78302     __
                                CAC  TGAAACCCCGTCTCTAC
                                |||  ||||||||||||||||
                                GTG  ATTTTGGGGCAGAGATG
                                  CC
GAM1209  LOC146237 3'  GGCTGGGGGCAATTTCAGTG   84612         ____   _
                                CACTGAAA    CCCC GTC
                                ||||||||    |||| |||
                                GTGACTTT    GGGG CGG
                                     AACG    T
GAM1209  LOC146346 5'  GTAGAGACGGGGTTTCACCGTG 78404     __
                                CAC  TGAAACCCCGTCTCTAC
                                |||  ||||||||||||||||
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                                GTG  ACTTTGGGGCAGAGATG
                                  CC
GAM1209  LOC146603 5'  GTAGAGACGGGGTTTCACCGTG 78603     __
                                CAC  TGAAACCCCGTCTCTAC
                                |||  ||||||||||||||||
                                GTG  ACTTTGGGGCAGAGATG
                                  CC
GAM1209  LOC146756 3'  GGTAGCATCGTTTTCAGTG   84812        CCC  TCT
                                CACTGAAA   CG   CTACC
                                ||||||||   ||   |||||
                                GTGACTTT   GC   GATGG
                                     T__  TAC
GAM1209  LOC146839 3'  GTAGAGACGGGGTTTCACCGTG 84846     __
                                CAC  TGAAACCCCGTCTCTAC
                                |||  ||||||||||||||||
                                GTG  ACTTTGGGGCAGAGATG
                                  CC
GAM1209  LOC147080 3'  GTAGTGACGGGGTCTCAGT   85047      A      T
                                ACTGA ACCCCGTC CTAC
                                ||||| |||||||| ||||
                                TGACT TGGGGCAG GATG
                                   C       T
GAM1209  LOC147694 3'  GTAGAGACGGGGTTTCACCGTG 79104     __
                                CAC  TGAAACCCCGTCTCTAC
                                |||  ||||||||||||||||
                                GTG  ACTTTGGGGCAGAGATG
                                  CC
GAM1209  LOC148145 3'  AGAAGGGTGTCAGTGTT     85258        A   CG
                                AACACTGA ACCC  TCT
                                |||||||| ||||  |||
                                TTGTGACT TGGG  AGA
                                     G   A_
GAM1209  LOC148709 3'  GGTGTCAGAGAGCTCAGTGTT  79698        AACCCCG    ___
                                AACACTGA      TCTCT   ACC
                                ||||||||      |||||   |||
                                TTGTGACT      AGAGA   TGG
                                     CG_____     CTG
GAM1209  LOC149478 3'  GTAGAGACGGGGGTTTCA    80176         _
                                TGAAACCCC GTCTCTAC
                                ||||||||| ||||||||
                                ACTTTGGGG CAGAGATG
                                     G
GAM1209  LOC150225 3'  GTAGAGACGGTTTCACCATGT  86201     C__      CC
                                ACA   TGAAACC  GTCTCTAC
                                |||   |||||||  ||||||||
                                TGT   ACTTTGG  CAGAGATG
                                  ACC      __
GAM1209  LOC150696 3'  GGTAGGGAGTGGGTCCCAG   59163     AA   CG
                                CTG  ACCC  TCTCTACC
                                |||  ||||  ||||||||
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                                GAC  TGGG  AGGGATGG
                                  CC    TG
GAM1209  LOC150819 5'  GGTAGAGATGATTTCA      86311       CCC
                                TGAAA   CGTCTCTACC
                                |||||   ||||||||||
                                ACTTT   GTAGAGATGG
                                   A__
GAM1209  LOC151124 5'  AGAGACGGATGGTGTT      86413        AAACC
                                AACACTG     CCGTCTCT
                                |||||||     ||||||||
                                TTGTGGT     GGCAGAGA
                                   A____
GAM1209  LOC151162 5'  GGTTTTGTGAGGATTCAGTGTT 86430          A  C  TCTCT
                                AACACTGAA CC CG     ACC
                                ||||||||| || ||     |||
                                TTGTGACTT GG GT     TGG
                                      A  A  GTTT_
GAM1209  LOC151248 5'  AGCAGAGGTTTATCAGTGTT   80982         __    CCG   _
                                AACACTGA  AACC   TCT CT
                                ||||||||  ||||   ||| ||
                                TTGTGACT  TTGG   AGA GA
                                     AT    ___   C
GAM1209  LOC151826 3'  GTAGAGACAGGGTTTCACCGTG 81184      __       C
                                CAC  TGAAACCC GTCTCTAC
                                |||  |||||||| ||||||||
                                GTG  ACTTTGGG CAGAGATG
                                  CC       A
GAM1209  LOC154930 3'  GTAGAGACAGGATTTTACTGT  82096     C     C  C
                                ACA TGAAA CC GTCTCTAC
                                ||| ||||| || ||||||||
                                TGT ATTTT GG CAGAGATG
                                  C    A  A
GAM1209  LOC157247 5'  GGTAGAGACGGGGTTTCA     82305
                                TGAAACCCCGTCTCTACC
                                ||||||||||||||||||
                                ACTTTGGGGCAGAGATGG

GAM1209  LOC157464 5'  GTAGAGATCTGCAGTGTT     87750        AAACCCC
                                AACACTG      GTCTCTAC
                                |||||||      ||||||||
                                TTGTGAC      TAGAGATG
                                   GTC_____
GAM1209  LOC158476 3'  GGTAGAGACAGGGTTTCA     88201         C
                                TGAAACCC GTCTCTACC
                                |||||||| |||||||||
                                ACTTTGGG CAGAGATGG
                                     A
GAM1209  LOC169611 3'  GTAGAGACAGGGGTTTCA     83658         _
                                TGAAACCCC GTCTCTAC
                                ||||||||| ||||||||
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                                ACTTTGGGG CAGAGATG
                                     A
GAM1209  LOC199699 3'  GTAAAGACAGGGTTTCACCGTG 89679     __      C   C
                                CAC  TGAAACCC GTCT TAC
                                |||  |||||||| |||| |||
                                GTG  ACTTTGGG CAGA ATG
                                  CC       A    A
GAM1209  LOC200301 5'  GTAGAGACGGGGTTTCACCGTG 90150     __
                                CAC  TGAAACCCCGTCTCTAC
                                |||  ||||||||||||||||
                                GTG  ACTTTGGGGCAGAGATG
                                  CC
GAM1209  LOC203377 5'  GGTTTTGTGAGGATTCAGTGTT 92259         A  C  TCTCT
                                AACACTGAA CC CG     ACC
                                |||||||| || ||     |||
                                TTGTGACTT GG GT     TGG
                                     A  A  GTTT_
GAM1209  LOC219347 3'  GTAGAGACGGTGAAACACTGT  94580     C  AAACC
                                ACA TG     CCGTCTCTAC
                                ||| ||     ||||||||||
                                TGT AC     GGCAGAGATG
                                  C  AAAGT
GAM1209  LOC219735 3'  GTAGAGACGGGGTTTCACCGTG 94732     __
                                CAC  TGAAACCCCGTCTCTAC
                                |||  ||||||||||||||||
                                GTG  ACTTTGGGGCAGAGATG
                                  CC
GAM1209  LOC221964 3'  GTAGAGACAGGGTTTTGCCGTG 95609     T__      C
                                CAC   GAAACCC GTCTCTAC
                                |||   ||||||| ||||||||
                                GTG   TTTTGGG CAGAGATG
                                  CCG      A
GAM1209  LOC254228 3'  GGCAAGGAGTGTTCAGTGTT   97652         _  _  C_
                                AACACTGAA AC CC  GTC
                                |||||||| || ||  |||
                                TTGTGACTT TG GG  CGG
                                     G  A  AA
GAM1209  LOC254295 5'  GTAGAGACGGGGTTTCACCGTG 97895     __
                                CAC  TGAAACCCCGTCTCTAC
                                |||  ||||||||||||||||
                                GTG  ACTTTGGGGCAGAGATG
                                  CC
GAM1209  LOC255308 3'  GTAGAGACGGGGTTTCGG    96178
                                CTGAAACCCCGTCTCTAC
                                ||||||||||||||||
                                GGCTTTGGGGCAGAGATG

GAM1209  LOC256158 5'  GGCACGGAGGAACTTCAGTGT  99505         A__  _   C
                                ACACTGAA   CC CCGT TC
                                ||||||||   || |||| ||
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                                TGTGACTT   GG GGCA GG
                                     CAA  A    C
GAM1209  LOC256221 3'  GTAGAGACGGGGTTTCACCGTG 96917     __
                                CAC  TGAAACCCCGTCTCTAC
                                |||  ||||||||||||||||
                                GTG  ACTTTGGGGCAGAGATG
                                  CC
GAM1209  LOC54103  5'  AGTGAGTTTTAGTGTT      95883          CCCG  T
                                AACACTGAAAC    TC CT
                                ||||||||||    || ||
                                TTGTGATTTTG    AG GA
                                       ____ T
GAM1209  LOC56181  5'  GTAGAGACAGGGCTTCACTGT  97281     C    A   C
                                ACA TGAA CCC GTCTCTAC
                                ||| |||| ||| ||||||||
                                TGT ACTT GGG CAGAGATG
                                  C    C   A
GAM1209  LOC85414  3'  GGTAGAGGGTGGGGCTTCAG   53553      A    GT _
                                CTGAA CCCC  C TCTACC
                                ||||| ||||  | ||||||
                                GACTT GGGG  G AGATGG
                                   C    TG G
GAM1209  LOC90288  3'  GTAGAGACGGGGTTTCACAGTG 62795     __
                                CACT  GAAACCCCGTCTCTAC
                                ||||  ||||||||||||||||
                                GTGA  CTTTGGGGCAGAGATG
                                   CA
GAM1209  LOC90591  3'  GTAGAGACGGAGTTTCATCGTG 64182     __     C
                                CAC  TGAAAC CCGTCTCTAC
                                |||  |||||| ||||||||||
                                GTG  ACTTTG GGCAGAGATG
                                  CT     A
GAM1209  LOC91308  3'  GTAGAGACGGGGTTTAGT    66169       A
                                ACTGAA CCCCGTCTCTAC
                                ||||||| ||||||||||||
                                TGATTT GGGGCAGAGATG
                                       _
GAM1209  LOC91893  3'  GTAGAGACGAGGTTTCACCGTG 68078     __     C
                                CAC  TGAAACC CGTCTCTAC
                                |||  ||||||| |||||||||
                                GTG  ACTTTGG GCAGAGATG
                                  CC      A
GAM1210  ADRA1D    3'  TCCCTGAGGAACTGGGCAG   7284        __   GA
                                CTGCCCAG  CTTT  GGA
                                ||||||||  ||||  |||
                                GACGGGTC  GGAG  CCT
                                     AA    TC
GAM1210  ATP1B1    3'  CCTTGTAGTAAGCAGTGTT   9818        CCA   T
                                AACACTGC   GCT TGAGG
                                ||||||||   ||| |||||
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                                TTGTGACG  TGA GTTCC
                                    AA_   T
GAM1210 CBFA2T2  3' TCTGCAAACCTGGGCAGT   18719       C   A
                                ACTGCCCAG TTTG GGA
                                ||||||||| |||| |||
                                TGACGGGTC AAAC TCT
                                    C   G
GAM1210 CD72     3' ATCTCCTTCATTCTGGGCAGTG 10119        CTT  _
                                CACTGCCCAG  TGA GGAGAT
                                ||||||||||  ||| ||||||
                                GTGACGGGTC  ACT CCTCTA
                                    TT_   T
GAM1210 CNR1     3' ATCTCCTAAATGCTGGGCAATG 10229    C      TTTG
                                CA TGCCCAGC   AGGAGAT
                                || ||||||||   |||||||
                                GT ACGGGTCG   TCCTCTA
                                 A      TAAA
GAM1210 IL8RA    3' ATCTCCTCAACTCTGAGTGTT  7151       GCC  CT
                                AACACT  CAG  TTGAGGAGAT
                                ||||||  |||  ||||||||||
                                TTGTGA  GTC  AACTCCTCTA
                                   ___  TC
GAM1210 MAD2L2   3' TCCCCGCCTAGGGCAGTG    22019       _ CTT  A
                                CACTGCCC AG  TG GGA
                                |||||||| ||  || |||
                                GTGACGGG TC  GC CCT
                                    A  C__  C
GAM1210 MGAM     3' TCTGGGGAGTGGGCAGTGT   72813        G   GA
                                ACACTGCCCA CTTT  GGA
                                |||||||||| ||||  |||
                                TGTGACGGGT GAGG  TCT
                                    _   GG
GAM1210 MMP19    5' TCCCAGAGCTGGGCAGTGT   11640           A
                                ACACTGCCCAGCTTTG GGA
                                |||||||||||||||| |||
                                TGTGACGGGTCGAGAC CCT
                                                _
GAM1210 MMP19    5' TCCCAGAGCTGGGCAGTGT   11641           A
                                ACACTGCCCAGCTTTG GGA
                                |||||||||||||||| |||
                                TGTGACGGGTCGAGAC CCT
                                                _
GAM1210 PROK1    5' TCTAAGCAGGCAGTGTT     51570       CA   T
                                AACACTGCC  GCTT GA
                                |||||||||  |||| ||
                                TTGTGACGG  CGAA CT
                                    A_    T
GAM1210 SOX11    3' CCTTGGTATGCAGTGTT     13314       CCA  TT
                                AACACTGC   GCT  GAGG
                                ||||||||   |||  ||||
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                                TTGTGACG  TGG  TTCC
                                    TA_  __
GAM1210  STIM1    3'  CTCCTCAGATGAGCCGTG    60777     T  C  GC
                                CAC GC CA  TTTGAGGAG
                                ||| || ||  |||||||||
                                GTG CG GT  AGACTCCTC
                                  C  A  __
GAM1210  BIRC8    5'  CCGAGAGAGCTGGCCAGTG   54038      C       GA_
                                CACTG CCAGCTTT  GG
                                ||||| ||||||||  ||
                                GTGAC GGTCGAGA  CC
                                   C       GAG
GAM1210  CAT56    3'  ATCTTTGGGTAGAAGCTGGACA 48276     C       GA___
              GT                  ACTG CCAGCTTT    GGAGAT
                                ||||| ||||||||    ||||||
                                TGAC GGTCGAAG    TTTCTA
                                  A       ATGGG
GAM1210  CDH22    5'  CCCCGCGGCTGGGCGGCGTT  41439    A        T  A
                                AAC CTGCCCAGCT TG GG
                                ||| ||||||||| || ||
                                TTG GGCGGGTCGG GC CC
                                  C        C  C
GAM1210  CENTA2   3'  ATCTCCTCTGGCTCTGGAAGCA 37863    __  __  TT
                                TGC  CCA  GCT  GAGGAGAT
                                |||  |||  |||  ||||||||
                                ACG  GGT  CGG  CTCCTCTA
                                  AA  CT  T_
GAM1210  EIF3S9   3'  TCCCCATTGCGGGCAGTG    14988       A  TT  A
                                CACTGCCC GC  TG GGA
                                |||||||| ||  || |||
                                GTGACGGG CG  AC CCT
                                    _ TT  C
GAM1210  GPS2     5'  CTCCTCGGGAGGAGCAG     88508     _ AGC
                                CTGC CC   TTTGAGGAG
                                |||| ||   |||||||||
                                GACG GG   GGGCTCCTC
                                  A  A__
GAM1210  KIAA0574 3'  CCTTGAACTGAGCAGTGTT   69812       C   C  TG
                                AACACTGC CAG TT  AGG
                                |||||||| ||| ||  |||
                                TTGTGACG GTC AA  TCC
                                    A  _ GT
GAM1210  KIAA1096 3'  TCAAAGTGAGCAGTGTT     69060       CCA
                                AACACTGC   GCTTTGA
                                ||||||||   |||||||
                                TTGTGACG   TGAAACT
                                    AG_
GAM1210  KIAA1163 3'  ATCTCCTCTGTGTGGACAAGGT 79645     AC  C   G TTT
              T                  AAC  TG CCA C   GAGGAGAT
                                |||  || ||| |   ||||||||
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                                TTG  AC GGT G   CTCCTCTA
                                  GA  A  _ TGT
GAM1210  KIAA1464  3'  ATCCCTGTGGGTTGGGCA    68816         TG   A
                                TGCCCAGCTT  AGG GAT
                                ||||||||||  ||| |||
                                ACGGGTTGGG  TCC CTA
                                     TG  _
GAM1210  KIAA1522  3'  TCTCGGGGCACTTGGCAGTGT  65610        CA__
                                ACACTGCC    GCTTTGAGG
                                ||||||||    |||||||||
                                TGTGACGG    CGGGGCTCT
                                     TTCA
GAM1210  MGC13138  3'  TCTGAGTCCAGGCAGTGTT   54163         CA_   T
                                AACACTGCC   GCTT GA
                                |||||||||   |||| ||
                                TTGTGACGG   TGAG CT
                                     ACC    T
GAM1210  NXPH3     3'  ATCTCCCCATCAGGCTGGG   66338         __  A
                                CCCAGCTT  TG GGAGAT
                                ||||||||  || ||||||
                                GGGTCGGA  AC CCTCTA
                                     CT  C
GAM1210  RAB14     3'  CCTTGGTGCTGGCAGTGTT   33334         C   T TG
                                AACACTGCC AGC T  AGG
                                ||||||||| ||| |  |||
                                TTGTGACGG TCG G  TCC
                                     _   T GT
GAM1210  SEC24A    3'  TCTCCCTTAAGCAGTGTT    83568        CCAGCT    _
                                AACACTGC     TTGAGG AGA
                                ||||||||     |||||| |||
                                TTGTGACG     AATTCC TCT
                                     _______     C
GAM1210  ZFP36L2   3'  ATCTCTTCACTTGAACAG    23530     CC   CTT
                                CTG  CAG   TGAGGAGAT
                                |||  |||   |||||||||
                                GAC  GTT   ACTTCTCTA
                                  AA   C__
GAM1210  LOC145676 5'  ATCTCCTCAAAGCCATTGT    77843     C  CCCA
                                ACA TG    GCTTTGAGGAGAT
                                |||  ||    ||||||||||||
                                TGT AC    CGAAACTCCTCTA
                                  T  _____
GAM1210  LOC151103 5'  ATCTCTTCACTTGAACAG    86410     CC   CTT
                                CTG  CAG   TGAGGAGAT
                                |||  |||   |||||||||
                                GAC  GTT   ACTTCTCTA
                                  AA   C__
GAM1210  LOC153396 3'  TCTTCAAACTGAGCCATG    81684     CT  C   C
                                CA  GC CAG TTTGAGGA
                                ||  || ||| ||||||||
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                                GT  CG GTC AAACTTCT
                                 AC  A  _
GAM1210  LOC153894 5'  CTCCTCAAAGCTGACCAG    81878     CC
                                CTG  CAGCTTTGAGGAG
                                |||  ||||||||||||
                                GAC  GTCGAAACTCCTC
                                  CA
GAM1210  LOC202018 3'  CCAAGGAAGCAGAGCAGTGTT  90607        CCA    GA_
                                AACACTGC   GCTTT   GG
                                ||||||||   |||||   ||
                                TTGTGACG   CGAAG   CC
                                     AGA    GAA
GAM1210  LOC219700 5'  TCCATAAAGCCAAGGAGTG   94660      G  CA_    A
                                CACT CC   GCTTTG GGA
                                ||||  ||   |||||| |||
                                GTGA GG   CGAAAT CCT
                                  _  AAC     A
GAM1210  LOC220018 5'  CTCCTGGGGCAGGCAGTGT   95028        CA    G
                                ACACTGCC  GCTTT AGGAG
                                ||||||||  ||||| |||||
                                TGTGACGG  CGGGG TCCTC
                                     A_    _
GAM1210  LOC220883 3'  CCTGTGGGCAGTGGGCAGTGT  92891          __   TG
                                ACACTGCCCA  GCTT  AGG
                                ||||||||||  ||||  |||
                                TGTGACGGGT  CGGG  TCC
                                      GA   TG
GAM1210  LOC90643  3'  CTCCTCCAGGAACCATGTT   64438     C  CCCAG   T
                                AACA TG    CTT GAGGAG
                                ||||  ||    |||  ||||||
                                TTGT AC    GGA CTCCTC
                                  _  CAA__   C
GAM1210  LOC91818  3'  CTCCTCCAGGAACGATGTT   67857     C  CCCAG   T
                                AACA TG    CTT GAGGAG
                                ||||  ||    |||  ||||||
                                TTGT GC    GGA CTCCTC
                                  A  AA___   C
GAM1211  CSNK1G2   3'  GCTCGGCCCTCAGCCCTG    8990     AA
                                CAG  TTGAGGGCCGAGT
                                |||  ||||||||||||
                                GTC  GACTCCCGGCTCG
                                  CC
GAM1211  GORASP1   3'  GCATCTACCCAGCCCCAAT   49956     A   CGA
                                ATTG GGGC   GTAGATGC
                                ||||  ||||   ||||||||
                                TAAC CCCG   CATCTACG
                                  _   ACC
GAM1211  KRT13     5'  CACCTGCTCTCAATCCTG    11231     A       CGAGT  A
                                CAG ATTGAGGGC    AG TG
                                |||  |||||||||    ||  ||
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                                GTC TAACTCTCG    TC AC
                                  C       _____ C
GAM1211  SIRT3    3'  CATCCACATCCCAATTCTG   25292        A  CCGA  A
                                CAGAATTG GGG   GT GATG
                                |||||||| |||   || ||||
                                GTCTTAAC CCT   CA CTAC
                                     _  A___  C
GAM1211  WHN      3'  GCACCCACTCAGCCATTCTCT  14579    ATT  _  C   AGA
                                AGA  GAG GGC GAGT  TGC
                                |||  ||| ||| ||||  |||
                                TCT  CTT CCG CTCA  ACG
                                  ___  A  A   CCC
GAM1211  ABLIM    3'  GCATCTACTCCGCTACCCAATT 11323        AG_  C
            CTG                   CAGAATTG  GGC GAGTAGATGC
                                |||||||  ||| ||||||||||
                                GTCTTAAC  TCG CTCATCTACG
                                     CCA  C
GAM1211  ABLIM    3'  GCATCTACTCCGCTACCCAATT 22980        AG_  C
            CTG                   CAGAATTG  GGC GAGTAGATGC
                                |||||||  ||| ||||||||||
                                GTCTTAAC  TCG CTCATCTACG
                                     CCA  C
GAM1211  CALN1    3'  GCTGAGGTCAACCCTCAGTTC  49665         ____  G_
                                GAATTGAGGG   CC  AGT
                                ||||||||||   ||  |||
                                CTTGACTCCC   GG  TCG
                                      AACT  AG
GAM1211  FLJ11151 3'  CTATCGACCTCAATTC     68474        GC  G
                                GAATTGAGG  CGA TAG
                                |||||||||  ||| |||
                                CTTAACTCC  GCT ATC
                                     A_  _
GAM1211  FLJ32356 3'  CACCTCCTGGCCCTCACCCTG  59017    AAT      G  T  A
                                CAG  TGAGGGCC AG AG TG
                                |||  |||||||| || || ||
                                GTC  ACTCCCGG TC TC AC
                                  CC_      _  C  C
GAM1211  KIAA0478 3'  GCATCTGAGCCCTCAA     30179        CGAG
                                TTGAGGGC   TAGATGC
                                ||||||||   |||||||
                                AACTCCCG   GTCTACG
                                     A___
GAM1211  p25      3'  ACTCGGCTCCCATCTCTG    23821     AT  A
                                CAGA  TG GGGCCGAGT
                                ||||  || |||||||||
                                GTCT  AC CTCGGCTCA
                                  CT  C
GAM1211  LOC126423 5'  GCATTTTGCCAGCCCTCAACCC 76207    AA       CGAGT
            T                   AG  TTGAGGGC    AGATGC
                                ||  ||||||||    ||||||
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                                TC  AACTCCCG    TTTACG
                                 CC       ACCGT
GAM1211  LOC148547 5'  ATTCAACTCCCAATTCTG    79661        A   CC
                                CAGAATTG GGG  GAGT
                                |||||||| |||  ||||
                                GTCTTAAC CTC  CTTA
                                     C   AA
GAM1211  LOC163033 5'  ACCCGGCCCCAATTCTG     83283        A     A
                                CAGAATTG GGGCCG GT
                                |||||||| |||||| ||
                                GTCTTAAC CCCGGC CA
                                     _     C
GAM1211  LOC219673 3'  CACCTGAGGCCCTCAATGCTG  94614     A        GAG   A
                                CAG ATTGAGGGCC   TAG TG
                                ||| ||||||||||   ||| ||
                                GTC TAACTCCCGG   GTC AC
                                  G        A__   C
GAM1211  LOC253866 5'  GCATCGAGCTTCGGCCCCCACC 97334     AAT  A      _  A_
            CCTG                    CAG   TG GGGCCGA GT  GATGC
                                |||   || |||||||  ||  |||||
                                GTC   AC CCCGGCT CG  CTACG
                                  CCC  C      T  AG
GAM1211  LOC255975 5'  GCATCTACAGGCCCAACCTCTG 97583      ATTGA    GA
                                CAGA    GGGCC  GTAGATGC
                                ||||    |||||  ||||||||
                                GTCT    CCCGG  CATCTACG
                                  CCAA_    A_
GAM1211  LOC256158 5'  TGCGAAGCCCTCAATGCTG   99518     A       CGA
                                CAG ATTGAGGGC   GTA
                                ||| |||||||||   |||
                                GTC TAACTCCCG   CGT
                                  G        AAG
GAM1211  LOC256905 5'  GTCCTCGGCCCCCACTTCTG   98662      T  A      TA
                                CAGAA TG GGGCCGAG  GAT
                                ||||| || ||||||||  |||
                                GTCTT AC CCCGGCTC  CTG
                                   C  C       __
GAM1211  LOC51720  3'  CACCTACCCAGCATTCTG    33293       T AG  CCGA   A
                                CAGAAT G  GG    GTAG TG
                                |||||| |  ||    |||| ||
                                GTCTTA C  CC    CATC AC
                                   _ GA  _____    C
GAM1211  LOC56965  3'  GCATCTACCTGAGCCCCATCTC 39925    AT  A   _  A
                                GA  TG GGGC CG GTAGATGC
                                ||  || |||| || ||||||||
                                CT  AC CCCG GT CATCTACG
                                 CT  _    A  C
GAM1212  HRH1     3'  AAATGTGCCCTTTTGGCCGG   7812     A       A   TCA
                                CC GGCCAAAA GGC   ACATTT
                                || |||||||| |||   ||||||
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                                GG CCGGTTTT CCG   TGTAAA
                                 _       C  ___
GAM1212  POLD2    5'  TTGAACCTCCTTGGCCTGG   21721         AA   C
                                CCAGGCCAA  AGG TCAA
                                |||||||||  ||| ||||
                                GGTCCGGTT  TCC AGTT
                                     CC   A
GAM1212  SCN7A    3'  AAATGTTGAAAGCCTAAGCC   12947     CAAAA   __
                                GGC    AGGC  TCAACATTT
                                |||    ||||  |||||||||
                                CCG    TCCG  AGTTGTAAA
                                  AA___    AA
GAM1212  SHANK2   3'  GTTGAACTTCTTCTTTGGCCTC 25531   C       _   C__
              A                  C AGGCCAAA AAGG   TCAAC
                                | ||||||||| ||||   |||||
                                A TCCGGTTT TTCT   AGTTG
                                 C       C    TCA
GAM1212  SIAT8E   3'  TGAGCCTCCTGGCCTGG     60552        AAA
                                CCAGGCCA   AGGCTCA
                                ||||||||   |||||||
                                GGTCCGGT   TCCGAGT
                                     CC_
GAM1212  SLC7A8   3'  GAGCCCTTCCTGGCCTGG    25304        AA   _
                                CCAGGCCA  AAGG CTC
                                ||||||||  |||| |||
                                GGTCCGGT  TTCC GAG
                                     CC    C
GAM1212  TFAP2C   3'  TGGGAACCCCTCCTGGCCTGG  13687        AAA  _____
                                CCAGGCCA   AGG    CTCA
                                ||||||||   |||    ||||
                                GGTCCGGT   TCC    GGGT
                                     CC_   CCAA
GAM1212  TRPM2    3'  GAGCCTTGCCTGGCCTGG    13864        AA_
                                CCAGGCCA   AAGGCTC
                                ||||||||   |||||||
                                GGTCCGGT   TTCCGAG
                                     CCG
GAM1212  FLJ13189 3'  TTGAACCTTTTTTGCCTGG   46498       C      C
                                CCAGGC AAAAAGG TCAA
                                ||||||| ||||||| ||||
                                GGTCCG TTTTTCC AGTT
                                    T      A
GAM1212  FLJ20208 3'  AAATGCAGGCTTTTTAGCC   35240     C     G  CAA
                                GGC AAAAAG CT   CATTT
                                ||| |||||| ||   |||||
                                CCG TTTTTC GA   GTAAA
                                  A     G  C__
GAM1212  FLJ22944 3'  AAATGTTGGGATTTGAACCC   47866    CCAA   GG
                                GG    AAA  CTCAACATTT
                                ||    |||  ||||||||||
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                                CC   TTT  GGGTTGTAAA
                                 CAAG  A_
GAM1212 HPRP8BP  3' AAATGTTGGATGTCCAGGCT  60060     AAAAA  __
                                GGCC   GGC  TCAACATTT
                                ||||    |||  |||||||||
                                TCGG   CTG  GGTTGTAAA
                                  AC___  TA
GAM1212 KIAA0872 3' AAATGTTAAGCCTTTTGTTATT 30731    GCCA      C
           G                     CAG   AAAAGGCT AACATTT
                                |||   ||||||||  |||||||
                                GTT   TTTTCCGA TTGTAAA
                                  ATTG      A
GAM1212 KIAA1843 3' AAATGTTGACTGAACCTGACCT 62880     C  AAAA_  C
           G                     CAGG CA    GG TCAACATTT
                                ||||  ||    ||  |||||||||
                                GTCC GT    TC AGTTGTAAA
                                  A  CCAAG  _
GAM1212 KIAA1975 3' AAATGTTGATTTTTCTGACC  74407    C  A    C
                                GG CA AAAGG TCAACATTT
                                ||  ||  |||||  |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM1212 MRIP2    3' AAATGTTGATTTTTCTGACC  56789    C  A    C
                                GG CA AAAGG TCAACATTT
                                ||  ||  |||||  |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM1212 SLC26A10 5' TTGAACCCCTTTGGCCTG    56851         AA  C
                                CAGGCCAAA  GG TCAA
                                |||||||||  ||  ||||
                                GTCCGGTTT  CC AGTT
                                     CC  A
GAM1212 THEG     3'  TGAGCTTTTTGGCCTGG     33892           G
                                CCAGGCCAAAAAAG CTCA
                                ||||||||||||| ||||
                                GGTCCGGTTTTTC GAGT
                                              _
GAM1212 LOC118704 3' AAATGTTGATTTTTCTGACC  74359    C  A    C
                                GG CA AAAGG TCAACATTT
                                ||  ||  |||||  |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM1212 LOC118706 3' AAATGTTGATTTTTCTGACC  74361    C  A    C
                                GG CA AAAGG TCAACATTT
                                ||  ||  |||||  |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM1212 LOC123036 3' AAATGTTTGCAGTTTTGGCT  74645        AG  TC
                                GGCCAAAA  GC  AACATTT
                                ||||||||  ||  |||||||
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                                TCGGTTTT  CG  TTGTAAA
                                    GA  T_
GAM1212  LOC123624 3'  AAATGTTGGGCTTCTGTGCCT  76134     _  AAA
                                AGGC CA   AGGCTCAACATTT
                                |||| ||   ||||||||||||
                                TCCG GT   TTCGGGTTGTAAA
                                  T  C__
GAM1212  LOC128338 3'  AAATATTGAGCCTTTTTAATAG 75250    AGGCC          C
             G                   CC     AAAAAGGCTCAA ATTT
                                 ||     |||||||||||| ||||
                                 GG     TTTTTCCGAGTT TAAA
                                  ATAA_          A
GAM1212  LOC143158 3'  AAATGTTGATTTTTCTGACC   76997    C  A    C
                                GG CA AAAGG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM1212  LOC195979 3'  AAATGTTGATTTTTCTGACC   88928    C  A    C
                                GG CA AAAGG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM1212  LOC219672 5'  AATGGTGCTTTTTGGCTGG    92963      G       G TCAA
                                CCAG CCAAAAAG C    CATT
                                |||| |||||||| |    ||||
                                GGTC GGTTTTTC G    GTAA
                                  _       _ TG__
GAM1212  LOC220466 3'  AAATGTTGATTTTTCTGACC   74398    C  A    C
                                GG CA AAAGG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM1212  LOC254105 3'  AGGTGTGGCCCCCTTGGCCTGG 96416          AAA    CA
                                CCAGGCCAA   GGCT  ACATTT
                                |||||||||   ||||  ||||||
                                GGTCCGGTT   CCGG  TGTGGA
                                     CCC    __
GAM1212  LOC255319 3'  AAATGTTGATTTTTCTGACC   96152    C  A    C
                                GG CA AAAGG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM1212  LOC91300  5'  GTTGAGCTTTTCTGGCCCGG   96238    A    A
                                CC GGCCA AAAGGCTCAAC
                                || ||||| ||||||||||
                                GG CCGGT TTTTCGAGTTG
                                 C    C
GAM1212  LOC91300  5'  GTTGAGCTTTTCTGGCCCGG   57864    A    A
                                CC GGCCA AAAGGCTCAAC
                                || ||||| ||||||||||
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                                GG CCGGT TTTTCGAGTTG
                                 C    C
GAM1212  LOC91660  5'  AAATGTTTATCTTCTTTTTGGC 67399          CTC__
             TT                  AGGCCAAAAAGG    AACATTT
                                 ||||||||||||    |||||||
                                 TTCGGTTTTTCT    TTGTAAA
                                      TCTAT
GAM1213  ALPP     3'  GAAGCACCCAGACCCCG     69418        AAGAC  T
                                 CGGGGTCTG    TG CTTC
                                 |||||||||    || ||||
                                 GCCCCAGAC    AC GAAG
                                      CC___  _
GAM1213  ATF4     5'  ACAGCCCTCGGACCCCGAG   9809          AGA
                                 CTCGGGGTCTGA   CTGT
                                 ||||||||||||   ||||
                                 GAGCCCCAGGCT   GACA
                                       CCC
GAM1213  C14orf1  3'  GAAGACAACTAAACCCCGAG   24168       CTGA  AC
                                 CTCGGGGT    AG  TGTCTTC
                                 ||||||||    ||  |||||||
                                 GAGCCCCA    TC  ACAGAAG
                                     AA__  A_
GAM1213  HEM1     5'  GAAGACTTGTTCAGACCCC    19237         GACT
                                 GGGGTCTGAA    GTCTTC
                                 ||||||||||    ||||||
                                 CCCCAGACTT    CAGAAG
                                       GTT_
GAM1213  HTR4     3'  GAAGACAGCCATGCCTCCGA   7883      _   C  AAGA
                                 TCGG GGT TG    CTGTCTTC
                                 |||| ||| ||    ||||||||
                                 AGCC CCG AC    GACAGAAG
                                   T   T  C___
GAM1213  MYEOV    5'  GAAAGTTCATCTCAGACCCT   57848         A___    G
                                 GGGGTCTGA    GACT TC
                                 |||||||||    |||| ||
                                 TCCCAGACT    TTGA AG
                                       CTAC    A
GAM1213  PRX      3'  GGAAGGGTCCCCCAGCCCCGAG 40898        T   AA_   GT
                                 CTCGGGG CTG   GACT  CTTCC
                                 ||||||| |||   ||||  |||||
                                 GAGCCCC GAC   CTGG  GAAGG
                                     _   CCC    __
GAM1213  PTMA     3'  ACAATCTTATTCCGAG      12556         CTG    C
                                 CTCGGGGT   AAGA TGT
                                 ||||||||   |||| |||
                                 GAGCCTTA   TTCT ACA
                                      ___    A
GAM1213  TIMP3    5'  GAAAACAGTCTTCTATC     6286      CT       C
                                 GGT  GAAGACTGT TTC
                                 |||  ||||||||| |||
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                                CTA  CTTCTGACA AAG
                                  T_       A
GAM1213  TNFRSF14  3'  GAGGGCCCTTCAGACCCC    15113          ACT
                                GGGGTCTGAAG   GTCTTC
                                ||||||||||   ||||||
                                CCCCAGACTTC   CGGGAG
                                      C__
GAM1213  VDR       3'  GAAGAATTTTCAGACCCC    6344           CTG
                                GGGGTCTGAAGA   TCTTC
                                ||||||||||||   |||||
                                CCCCAGACTTTT   AGAAG
                                      A__
GAM1213  C20orf177 5'  AAGACAGTCCATCAAACCCGAG 62822       GTC   A_
                                CTCGGG   TGA  GACTGTCTT
                                ||||||   |||  |||||||||
                                GAGCCC   ACT  CTGACAGAA
                                   AA_   AC
GAM1213  DKFZp434O0320 3'  GGACTTCTCTCCAGGCCCCGA  84699          A   CT_
                                TCGGGGTCTG AGA   GTCT
                                ||||||||||  |||   ||||
                                AGCCCCGGAC TCT   CAGG
                                      C   CTT
GAM1213  FLJ20507  3'  GGCCCAACCTTCAAACCCTGAG 60849         C    ACT__
                                CTCGGGGT TGAAG    GTC
                                ||||||||  |||||    |||
                                GAGTCCCA ACTTC    CGG
                                     A    CAACC
GAM1213  FLJ20507  3'  GGCCCAACCTTCAAACCCTGAG 35745         C    ACT__
                                CTCGGGGT TGAAG    GTC
                                ||||||||  |||||    |||
                                GAGTCCCA ACTTC    CGG
                                     A    CAACC
GAM1213  FLJ21562  5'  GGAATAGCTCTCCAGACCCC   47794         A   _   CT
                                GGGGTCTG AGA CTGT  TCC
                                ||||||||  ||| ||||  |||
                                CCCCAGAC TCT GATA  AGG
                                     C   C    __
GAM1213  FLJ22938  3'  AGAAGTCCCAGACCCCG     45479         AA   G
                                CGGGGTCTG  GACT TCT
                                |||||||||  |||| |||
                                GCCCCAGAC  CTGA AGA
                                     C_   _
GAM1213  FLNC      3'  AGATACCCTCCTGACCCCGAG  9388          TGA  AC
                                CTCGGGGTC   AG  TGTCT
                                |||||||||   ||  |||||
                                GAGCCCCAG   TC  ATAGA
                                     TCC  CC
GAM1213  KIAA1819  3'  GGAAGACAATTTACAAACTCC  70253       C  A   C
                                GGGGT TG AGA TGTCTTCC
                                |||||  ||  |||  ||||||||
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                                CCTCA AC TTT ACAGAAGG
                                   A A   A
GAM1213  NXP-2    3'  GAAGACAGTCTTTCTC      71659     TCT
                                GGG   GAAGACTGTCTTC
                                |||   ||||||||||||||
                                CTC   TTTCTGACAGAAG
                                 ____
GAM1213  PRO2389  5'  GGGATCTCAGCCCCGAG     64481        T    A  CTG
                                CTCGGGG CTGA GA   TCTT
                                ||||||| |||| ||   ||||
                                GAGCCCC GACT CT   AGGG
                                  _   _ ____
GAM1213  SMARCF1  3'  GGACCTATCTCCATACCCCGAG 38042         C  A   CT_
                                CTCGGGGT TG AGA   GTCT
                                |||||||| || |||   ||||
                                GAGCCCCA AC TCT   CAGG
                                     T  C   ATC
GAM1213  TGFB1I1  3'  AAGCCGGGTCCTCCAGACCCCG 32495          AA_   _ T
            AG                    CTCGGGGTCTG   GACT G CTT
                                ||||||||||   |||| | |||
                                GAGCCCCAGAC   CTGG C GAA
                                      CTC    G C
GAM1213  LOC143677 3'  GAAGAGCCAGCCAGACCCC    83897        AAGA   __
                                GGGGTCTG    CTG  TCTTC
                                ||||||||    |||  |||||
                                CCCCAGAC    GAC  AGAAG
                                     C___   CG
GAM1213  LOC145694 5'  AGACGCCTGCCCCCAGCCCCGA 84438        T   AAGAC___
            G                     CTCGGGG CTG       TGTCT
                                ||||||| |||       |||||
                                GAGCCCC GAC       GCAGA
                                   _  CCCCGTCC
GAM1213  LOC148936 5'  GAAGAGGTCCTCCAGACCCC   85453        AA_   G
                                GGGGTCTG   GACT TCTTC
                                ||||||||   |||| |||||
                                CCCCAGAC   CTGG AGAAG
                                     CTC   _
GAM1213  LOC148938 5'  GAAGAGGTCCTCCAGACCCC   85436        AA_   G
                                GGGGTCTG   GACT TCTTC
                                ||||||||   |||| |||||
                                CCCCAGAC   CTGG AGAAG
                                     CTC   _
GAM1213  LOC152273 3'  GAAAACAAGTTAGACTCC    81374         AGAC   C
                                GGGGTCTGA    TGT TTC
                                |||||||||    ||| |||
                                CCTCAGATT    ACA AAG
                                      GA__   A
GAM1213  LOC158288 3'  GAAGACAGTCCCCCAGGCTGAG 88021     GG     AA_
                                CTC  GGTCTG   GACTGTCTTC
                                |||  ||||||   ||||||||||
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                                GAG  TCGGAC   CTGACAGAAG
                                  __     CCC
GAM1213  LOC201910 3'  AGATTTGTCCATTCAAACCCC  90549      C    __   T_
                                GGGGT TGAA  GAC  GTCT
                                ||||| ||||  |||  ||||
                                CCCCA ACTT  CTG  TAGA
                                   A    AC   TT
GAM1213  LOC220177 5'  GGATACTTCAAACCCC      95968      C     AC
                                GGGGT TGAAG  TGTCT
                                ||||| |||||  |||||
                                CCCCA ACTTC  ATAGG
                                   A    __
GAM1213  LOC255974 5'  GGAAGCTGCTCCTCAGACCCC  99343         A  CT_ T
                                GGGGTCTGA GA   G CTTCC
                                ||||||||| ||   | |||||
                                CCCCAGACT CT   C GAAGG
                                     C  CGT _
GAM1213  LOC257485 5'  GAAGAGTCAGACCTCGA     66210          AGACTG
                                TCGGGGTCTGA     TCTTC
                                ||||||||||      |||||
                                AGCTCCAGACT     AGAAG
                                      G_____
GAM1213  LOC64167  5'  GAAAATATTGTTCAGACCCC   42539         GAC   C
                                GGGGTCTGAA   TGT TTC
                                |||||||||   ||| |||
                                CCCCAGACTT   ATA AAG
                                     GTT   A
GAM1213  LOC90190  3'  GGAAGACTTGATCCTCAGCCCC 62428        T    A  CT__
            GAG                   CTCGGGG CTGA GA    GTCTTCC
                                |||||||  |||| ||    |||||||
                                GAGCCCC GACT CT    CAGAAGG
                                   _    C  AGTT
GAM1214  ACLY     5'  GGATGTCCTCGAAGCTACCGGC 65687        C__   A_______   ATGT
            TGCTG                 CAGCAGCC   AGC      GGG    CC
                                |||||||   |||      |||    ||
                                GTCGTCGG   TCG      TCC    GG
                                     CCA   AAG___C   TGTA
GAM1214  ALX4     3'  AGGCCCCGTGGACTGCTG    41919       C   G A   ATGT
                                CAGCAG CCA C GGG    CCT
                                |||||| ||| | |||    |||
                                GTCGTC GGT G CCC    GGA
                                   A   _ C   ____
GAM1214  ANAPC5   3'  GAGGACATCCCTGCTGGGCTGC 33180
            TG                   CAGCAGCCCAGCAGGGATGTCCTC
                                |||||||||||||||||||||||
                                GTCGTCGGGTCGTCCCTACAGGAG

GAM1214  ARNT2    3'  AGGTACCGTGGCTGCTG     30082         CA  A  GATGT
                                CAGCAGCC  GC GG    CCT
                                ||||||||  || ||    |||
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                                GTCGTCGG  TG CC    GGA
                                   __  _  AT___
GAM1214  ARVCF    3'  GAGGAGGCCGACTGGGCTGCTG 9804          CA  GATG
                                CAGCAGCCCAG  GG   TCCTC
                                ||||||||||  ||   |||||
                                GTCGTCGGGTC  CC   AGGAG
                                     AG  GG__
GAM1214  ATP6V1A1 3'  AGGACCAGCTGGGCTGT    9864          A  GATG
                                GCAGCCCAGC GG   TCCT
                                |||||||||| ||   ||||
                                TGTCGGGTCG CC   AGGA
                                     A  _____
GAM1214  CACNA1A  5'  AGATGTCCCGAGCTGCT    43782       CCAGCA       C
                                AGCAGC     GGGATGTC T
                                ||||||     |||||||| |
                                TCGTCG     CCCTGTAG A
                                   AG_____       A
GAM1214  CACNA1A  5'  AGATGTCCCGAGCTGCT    5352        CCAGCA       C
                                AGCAGC     GGGATGTC T
                                ||||||     |||||||| |
                                TCGTCG     CCCTGTAG A
                                   AG_____       A
GAM1214  CHST1    5'  GAGGATGCCGCCGCGGCTGCTG 14699        CA  AG_  A
                                CAGCAGCC  GC   GG TGTCCTC
                                ||||||||  ||   || |||||||
                                GTCGTCGG  CG   CC GTAGGAG
                                   __  CCG  _
GAM1214  CNN2     3'  AGGCTGAGCCACTGGGCTGT   16455        CAG  AT__ T
                                GCAGCCCAG   GG    G CCT
                                |||||||||   ||    | |||
                                TGTCGGGTC   CC    C GGA
                                     A__  GAGT _
GAM1214  CXorf6   3'  GATATTCCCCCTGAGCTGC    19706       C   CA
                                GCAGC CAG  GGGATGTC
                                ||||| |||  ||||||||
                                CGTCG GTC  CCTTATAG
                                   A   CC
GAM1214  EXTL1    5'  AGGCAGCTGCTGGGCTGC    16732          GGA  T
                                GCAGCCCAGCAG   TG CCT
                                ||||||||||||   || |||
                                CGTCGGGTCGTC   AC GGA
                                     G__  _
GAM1214  FAT2     3'  CCTTGCCCACAGGGCTGCTG   9347         A____
                                CAGCAGCCC    GCAGGG
                                |||||||||    ||||||
                                GTCGTCGGG    CGTTCC
                                     ACACC
GAM1214  GGT2     5'  AGGACATCCAGGCGGCTG    74084       CA  AG
                                CAGCC  GC  GGATGTCCT
                                |||||  ||  |||||||||
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                                GTCGG  CG  CCTACAGGA
                                  __  GA
GAM1214  GPR85    3'  GAGTGATCCTGCTGACTGC   39103     CC     GAT  _
                                GCAG  CAGCAGG  GTC CTC
                                ||||  |||||||  ||| |||
                                CGTC  GTCGTCC  TAG GAG
                                  A_     ___  T
GAM1214  IL10RA   3'  GAGGATAAGCCACTGGGCACTG 60380    CA    CA  GA
                                CAG  GCCCAG  GG  TGTCCTC
                                |||  ||||||  ||  |||||||
                                GTC  CGGGTC  CC  ATAGGAG
                                  A_    A_  GA
GAM1214  IMPA2    3'  AGGCCTCCCTGGGCTGCTG   96943        GCA   T T
                                CAGCAGCCCA  GGGA G CCT
                                ||||||||||  |||| | |||
                                GTCGTCGGGT  CCCT C GGA
                                     ___   C _
GAM1214  LIMD1    3'  GAGGACTGGGTGCTGGGCTGC  27261         GGGAT
                                GCAGCCCAGCA   GTCCTC
                                ||||||||||    ||||||
                                CGTCGGGTCGT   CAGGAG
                                      GGGT_
GAM1214  MLC1     3'  GACTGGTCCCCCATGGGCTGCT 58291        GCA   __
           G                     CAGCAGCCCA  GGGAT  GTC
                                ||||||||||  |||||  |||
                                GTCGTCGGGT  CCCTG  CAG
                                     ACC    GT
GAM1214  MLC1     3'  GACTGGTCCCCCATGGGCTGCT 31468        GCA   __
           G                     CAGCAGCCCA  GGGAT  GTC
                                ||||||||||  |||||  |||
                                GTCGTCGGGT  CCCTG  CAG
                                     ACC    GT
GAM1214  PPP1R12B 3'  GCAGCCTACTGGGCTGT    50390        C  GA
                                GCAGCCCAG AGG  TGT
                                ||||||||| |||  |||
                                TGTCGGGTC TCC  ACG
                                     A  G_
GAM1214  ROBO1    3'  AGAACATCCCTGTCTTAACTG  56898    CCC  _      C
                                CAG  AG CAGGGATGT CT
                                |||  || ||||||||| ||
                                GTC  TC GTCCCTACA GA
                                  AAT  T       A
GAM1214  ROBO1    3'  AGAACATCCCTGTCTTAACTG  12892    CCC  _      C
                                CAG  AG CAGGGATGT CT
                                |||  || ||||||||| ||
                                GTC  TC GTCCCTACA GA
                                  AAT  T       A
GAM1214  RPS9     3'  GTCCCTCCTGGGCTGCTG    8277          C
                                CAGCAGCCCAG AGGGAT
                                |||||||||| ||||||
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                                GTCGTCGGGTC TCCCTG
                                      C
GAM1214  RPS9     3'  GTCCCTCCTGGGCTGCTG    72526          C
                                CAGCAGCCCAG AGGGAT
                                |||||||||| ||||||
                                GTCGTCGGGTC TCCCTG
                                      C
GAM1214  SCA7     3'  GAAACCTGCCGGGCTGTTG   6192         A    GATG
                                CAGCAGCCC GCAGG   TC
                                ||||||||| |||||   ||
                                GTTGTCGGG CGTCC   AG
                                     C    AA__
GAM1214  SHANK2   3'  GAAATGCCTCTGGGCTGCTG  56553          C  G  G
                                CAGCAGCCCAG AGG AT TC
                                |||||||||| ||| || ||
                                GTCGTCGGGTC TCC TA AG
                                      _  G  A
GAM1214  SHANK2   3'  GAGGTCTCCTGGGCTGC     25528         CA    G
                                GCAGCCCAG  GGGAT TC
                                |||||||||  ||||| ||
                                CGTCGGGTC  CTCTG AG
                                     __    G
GAM1214  TNFSF6   3'  AGAACATAGAACTCTGGGCTGC 7167          C  GG__   C
                                GCAGCCCAG AG   ATGT CT
                                ||||||||| ||   |||| ||
                                CGTCGGGTC TC   TACA GA
                                      _ AAGA   A
GAM1214  WHN      3'  GAGGACATCACCTGGGGTGCTG 14578      G    CAGG
                                CAGCA CCCAG   GATGTCCTC
                                ||||| |||||   |||||||||
                                GTCGT GGGTC   CTACAGGAG
                                   G    CA__
GAM1214  ZNF147   3'  GAAATCTCCAGGCTGCTG    18680        CAGCA    G
                                CAGCAGCC    GGGAT TC
                                ||||||||    ||||| ||
                                GTCGTCGG    CTCTA AG
                                     AC___    A
GAM1214  ARHGEF4  3'  GACACCGCTGGCTGCTG     53371        C  AG  A
                                CAGCAGCC AGC  GG TGTC
                                |||||||| |||  || ||||
                                GTCGTCGG TCG  CC ACAG
                                      _  __  _
GAM1214  BMF      3'  AGGACATCGGGCAGGACTG   54277     C  A  AGG
                                CAG CC GC   GATGTCCT
                                ||| || ||   ||||||||
                                GTC GG CG   CTACAGGA
                                  A  A  GG_
GAM1214  C6orf26  3'  GACTCCGGTGGGCTGC      48270         G AG   T
                                GCAGCCCA C  GGA GTC
                                |||||||| |  ||| |||
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                                CGTCGGGT G  CCT CAG
                                     _ G_  _
GAM1214  CECR6    3'  AGGACATTGTGTCTGAGC    49930    C  _  G G
                                GC CAG CA G ATGTCCT
                                || ||| || | |||||||
                                CG GTC GT T TACAGGA
                                 A  T  G _
GAM1214  CLTH     5'  GTCCCCGCCGGCTGCTG     24132        CA  A
                                CAGCAGCC  GC GGGAT
                                ||||||||  || |||||
                                GTCGTCGG  CG CCCTG
                                     C_  C
GAM1214  DKFZP434B205 3'  AGGACATCGCCAGGCTCTG   75841    C   CA  AGG
                                CAG AGCC  GC   GATGTCCT
                                ||| ||||  ||   ||||||||
                                GTC TCGG  CG   CTACAGGA
                                  _    AC  ___
GAM1214  ETR101   3'  GAGAAGCCGCCGCCCGGGCTGC 72818         A_  A  GATGTC
            TG                    CAGCAGCCC  GC GG     CTC
                                |||||||||  || ||     |||
                                GTCGTCGGG  CG CC     GAG
                                     CC  _  GCCGAA
GAM1214  FBXO24   3'  AGGAGCTGCTGGGCTGC     25147          GGATG
                                GCAGCCCAGCAG    TCCT
                                ||||||||||||    ||||
                                CGTCGGGTCGTC    AGGA
                                      G____
GAM1214  FLJ10687 3'  GAGGATGTGCACTGAGCTGT   36946      C   CAGGG
                                GCAGC CAG    ATGTCCTC
                                ||||| |||    ||||||||
                                TGTCG GTC    TGTAGGAG
                                   A   ACG__
GAM1214  FLJ10774 3'  GAGGCTGCTGCTGGGCCGCTG  45417     A       GGAT T
                                CAGC GCCCAGCAG    G CCTC
                                |||| |||||||||    | ||||
                                GTCG CGGGTCGTC    C GGAG
                                   C       GT__ _
GAM1214  FLJ10853 5'  GAAGACATCCCAAAGGAAGTGC 37316      GC_  AGCA      C
            TG                    CAGCA   CC    GGGATGTC TC
                                |||||   ||    |||||||| ||
                                GTCGT   GG    CCCTACAG AG
                                   GAA  AAA_       A
GAM1214  FLJ11099 3'  GAGAACACTGCTGGGCT     37606          GGA   C
                                AGCCCAGCAG   TGT CTC
                                ||||||||||   ||| |||
                                TCGGGTCGTC   ACA GAG
                                      ___   A
GAM1214  FLJ13491 5'  GAGGCTGCTGCCAGGGCTGCTG 45218         A_    GGAT T
                                CAGCAGCCC  GCAG    G CCTC
                                |||||||||  ||||    | ||||
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                                GTCGTCGGG  CGTC   C GGAG
                                     AC   GT__ _
GAM1214  FLJ14596  5'  GGATGTCCTCGAGCTGCTGGGC 52517          _________  ATGT
              TGCT                  AGCAGCCCAGCAG      GG   CC
                                ||||||||||||       ||   ||
                                TCGTCGGGTCGTC      CC   GG
                                     GAG___CT  TGTA
GAM1214  FLJ20359  3'  GACATCCCCCGCAGGCCGC   35514   A   CA  A_
                                GC GCC  GC  GGGATGTC
                                || |||  ||  ||||||||
                                CG CGG  CG  CCCTACAG
                                 C   A_  CC
GAM1214  FLJ21432  3'  GCCTCCCTGCTGGCTACTG   44943    C   C      T
                                CAG AGCC AGCAGGGA GT
                                ||| |||| |||||||| ||
                                GTC TCGG TCGTCCCT CG
                                  A   _      C
GAM1214  FLJ21916  3'  GAAGCCTCACTGGGCTGCT   43896         CA   ATG
                                AGCAGCCCAG  GGG   TC
                                ||||||||||  |||   ||
                                TCGTCGGGTC  TCC   AG
                                     AC   GA_
GAM1214  FLJ22301  5'  GAGGACATCCCATGCGGCTACT 46177   C   CA   _
                                AG AGCC  GCA GGGATGTCCTC
                                || ||||  ||| ||||||||||
                                TC TCGG  CGT CCCTACAGGAG
                                 A   __  A
GAM1214  FLJ30927  5'  AGCGCGCCCTGGGCTGC     59081        GCA   A   C
                                GCAGCCCA   GGG TGT CT
                                ||||||||   ||| ||| ||
                                CGTCGGGT   CCC GCG GA
                                     ___   _   C
GAM1214  FOXO3A    5'  ACACCCGCTGGGCTGCTG    9379           A   A
                                CAGCAGCCCAGC GGG TGT
                                |||||||||||| ||| |||
                                GTCGTCGGGTCG CCC ACA
                                          _   _
GAM1214  FUK       5'  ATCCCTGCTGGGACGCTG    59623      AG
                                CAGC  CCCAGCAGGGAT
                                ||||  ||||||||||||
                                GTCG  GGGTCGTCCCTA
                                  CA
GAM1214  HBXIP     5'  AGGACGTGCCGTGCCGCTG   22153      CCA   G  _
                                CAGC   GCA GG ATGTCCT
                                ||||   ||| || |||||||
                                GTCG   CGT CC TGCAGGA
                                  C__   G  G
GAM1214  HSA250839 3'  CAGCCCTGCTGGCTACT     37849    C   C      A
                                AG AGCC AGCAGGG TG
                                || |||| ||||||| ||
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                                TC TCGG TCGTCCC AC
                                 A   _      G
GAM1214 IGSF9    5' AGGACATCCCTTGGCCCCT   40811    CA   CAGC
                                AG  GCC    AGGGATGTCCT
                                ||  |||    ||||||||||
                                TC  CGG    TCCCTACAGGA
                                 CC   T___
GAM1214 KIAA0179 3' GAGAGTGCCCGCAGGCTGCTG  65455        CA  A   A  TC
                                CAGCAGCC  GC GGG TG  CTC
                                ||||||||  || ||| ||  |||
                                GTCGTCGG  CG CCC GT  GAG
                                     A_ _  _  GA
GAM1214 KIAA0767 3' GAGAACATCCGCGAAGGCTGTT 61255        CA_  AG     C
             G                   CAGCAGCC   GC  GGATGT CTC
                                ||||||||   ||  |||||| |||
                                GTTGTCGG   CG  CCTACA GAG
                                     AAG  __     A
GAM1214 KIAA1115 3' GAGGACACCGAACTGGGCTGGC 30692    _      CAG  A
                                GC AGCCCAG   GG TGTCCTC
                                || |||||||   || |||||||
                                CG TCGGGTC   CC ACAGGAG
                                 G      AAG  _
GAM1214 KIAA1609 5' AGGAGCCCGTGGGCTGCTG   74707         G A   ATG
                                CAGCAGCCCA C GGG   TCCT
                                |||||||||| | |||   ||||
                                GTCGTCGGGT G CCC   AGGA
                                      _ _  G__
GAM1214 KIAA1656 5' GAGGCCACCCTGCTGGGCCACT 66369    CA         A  T
                                AG  GCCCAGCAGGG TG CCTC
                                ||  |||||||||| || ||||
                                TC  CGGGTCGTCCC AC GGAG
                                 AC          _ C
GAM1214 LRRN3    5' AGGACATCGGAGGTGGGCTAGC 69977    _     G AGG_
                                GC AGCCCA C    GATGTCCT
                                || |||||| |    ||||||||
                                CG TCGGGT G    CTACAGGA
                                 A     _ GAGG
GAM1214 MAP2K5   3' GAAGAGCTTTGCTGGGCCCTG  12327     CA         ATG_
                                CAG  GCCCAGCAGGG    TC
                                |||  ||||||||||    ||
                                GTC  CGGGTCGTTTC    AG
                                  C_          GAGA
GAM1214 MGC1842  3' GCACCTGCTGGCTGCTG     66256        C     GA
                                CAGCAGCC AGCAGG  TGT
                                |||||||| ||||||  |||
                                GTCGTCGG TCGTCC  ACG
                                      _     ___
GAM1214 MGC19604 3' GAGAACTCGCGGCTGGGCTGC  55612          AGG  T  C
                                GCAGCCCAGC   GA GT CTC
                                ||||||||||   || || |||
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                                CGTCGGGTCG   CT CA GAG
                                     GCG  _  A
GAM1214  MSH5     3'  GACTCCGGTGGGCTGC      11696         G AG   T
                                GCAGCCCA C  GGA GTC
                                |||||||| |  ||| |||
                                CGTCGGGT G  CCT CAG
                                    _ G_  _
GAM1214  PDE4DIP  5'  GACCCCACTGGGCTGT      28407         CA   AT
                                GCAGCCCAG  GGG  GTC
                                |||||||||  |||  |||
                                TGTCGGGTC  CCC  CAG
                                     A_  __
GAM1214  PTPRT    3'  GACCCACCCCCACTGGGCCTGC 56493        _    CA   AT__
            TG                    CAGCAG CCCAG  GGG    GTC
                                |||||| |||||  |||    |||
                                GTCGTC GGGTC  CCC    CAG
                                   C    AC   CACC
GAM1214  RASD2    3'  GCACCTACTGGGTGCTG     27462       G    C   GA
                                CAGCA CCCAG AGG  TGT
                                ||||| ||||| |||  |||
                                GTCGT GGGTC TCC  ACG
                                  _    A  __
GAM1214  SLC17A3  5'  GAGGAGCTTAACAAGCTGCTG 22791        CCAGC   GATG
                                CAGCAGC    AGG    TCCTC
                                |||||||    |||    |||||
                                GTCGTCG    TTC    AGGAG
                                    AACAA   G___
GAM1214  TUB      3'  GCACACTGCAGGGCTGCTG   13895         A    GGA
                                CAGCAGCCC GCAG   TGT
                                ||||||||| ||||   |||
                                GTCGTCGGG CGTC   ACG
                                     A   AC_
GAM1214  X123     3'  AGGACAGATCTGCCGGGCTGCT 70477        A    GA
                                AGCAGCCC GCAGG  TGTCCT
                                |||||||| |||||  ||||||
                                TCGTCGGG CGTCT  ACAGGA
                                    C    AG
GAM1214  ZNF313   3'  GCTCCCGCTGGGCTGT      38565         A   T
                                GCAGCCCAGC GGGA GT
                                |||||||||| |||| ||
                                TGTCGGGTCG CCCT CG
                                     _   _
GAM1214  LOC116411 5'  GAGGAGCGTCTCTGCCCGGCCG 74301    A   CA       _
            C                    GC GCC  GCAGGGATG TCCTC
                                || |||  ||||||||| |||||
                                CG CGG  CGTCTCTGC AGGAG
                                 C  CC       G
GAM1214  LOC123792 3'  AGGTGGTGCCCATGAACTGCTG 74703       CC  GCA  G  GT
                                CAGCAG  CA   GG AT  CCT
                                ||||||  ||   || ||  |||
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                                GTCGTC  GT   CC TG  GGA
                                   AA  AC_  G  GT
GAM1214  LOC128267 5'  GAGGACATATTCTGGGCACTG  75991    CA     C  GG
                                CAG  GCCCAG AG  ATGTCCTC
                                |||  ||||||  ||  ||||||||
                                GTC  CGGGTC TT  TACAGGAG
                                  A_     _  A_
GAM1214  LOC128916 5'  AGGACATCTCCAGGCCCTG   76295    CA   CAGCA
                                CAG  GCC    GGGATGTCCT
                                |||  |||    ||||||||||
                                GTC  CGG    CTCTACAGGA
                                  C_  AC___
GAM1214  LOC138128 5'  GAGCCGCAGCCTGCTGGGCT  76478         GA   C_
                                AGCCCAGCAGG  TGT  CTC
                                ||||||||||  |||  |||
                                TCGGGTCGTCC  ACG  GAG
                                      G_  CC
GAM1214  LOC145501 3'  GGACAGCCGGCTGCTG     77770        CAGCAG  A
                                CAGCAGCC     GG TGTCC
                                ||||||||     || |||||
                                GTCGTCGG     CC ACAGG
                                     _______  G
GAM1214  LOC147525 5'  GAGCTTCGTCCCTGCTAGCCGC 79006    A  CC        TC_
                                GC GC  AGCAGGGATG   CTC
                                || ||  ||||||||||   |||
                                CG CG  TCGTCCCTGC   GAG
                                 C  A_        TTC
GAM1214  LOC148413 3'  ATCCCTGCTGGGCTGCTG    79576
                                CAGCAGCCCAGCAGGGAT
                                ||||||||||||||||||
                                GTCGTCGGGTCGTCCCTA

GAM1214  LOC148775 5'  ACTCCCCACTGGGCTGGC    85378    _     CA    T
                                GC AGCCCAG  GGGA GT
                                || |||||||  |||| ||
                                CG TCGGGTC  CCCT CA
                                 G      AC   _
GAM1214  LOC153688 3'  AGGACATCTATGAGCTGT    87293      C  GCAG
                                GCAGC CA    GGATGTCCT
                                |||||  ||   |||||||||
                                TGTCG GT    TCTACAGGA
                                   A  A___
GAM1214  LOC157918 3'  AGGGAGCCGCTGGCTGCTG   87928        C   AG  ATG
                                CAGCAGCC AGC  GG   TCCT
                                |||||||| |||  ||   ||||
                                GTCGTCGG TCG  CC   GGGA
                                     _  __  GA_
GAM1214  LOC163782 3'  GAGGACATGGTTCAAGCGCTG  83036     A  CC_   AGGG
                                CAGC GC   AGC    ATGTCCTC
                                ||||  ||   |||    ||||||||
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                                GTCG CG   TTG    TACAGGAG
                                  _ AAC   G___
GAM1214  LOC164862 5'  AGGACATATATTTGGCTGCTG  88532        CAGCAGGG
                                CAGCAGCC       ATGTCCT
                                ||||||||       |||||||
                                GTCGTCGG       TACAGGA
                                    TTTATA__
GAM1214  LOC196510 5'  GCCGACCGCTGGGCTGCTG    89094          A  GAT
                                CAGCAGCCCAGC GG   GT
                                |||||||||||| ||   ||
                                GTCGTCGGGTCG CC   CG
                                      _ AGC
GAM1214  LOC196878 5'  AGGTCGGCCAGGCTGCTG     89176        CA  AGGGA  T
                                CAGCAGCC  GC     TG CCT
                                ||||||||  ||     || |||
                                GTCGTCGG  CG     GC GGA
                                    AC  _____  T
GAM1214  LOC199799 3'  GTCCCTCCTGGGCTGCTG     79253          C
                                CAGCAGCCCAG AGGGAT
                                |||||||||| ||||||
                                GTCGTCGGGTC TCCCTG
                                      C
GAM1214  LOC200220 5'  GAGCCGACCCCTGGGCTGCTG  90036          CA   A  TC
                                CAGCAGCCCAG  GGG TG  CTC
                                ||||||||||  ||| ||  |||
                                GTCGTCGGGTC  CCC GC  GAG
                                     __  A  C_
GAM1214  LOC201164 3'  GAGCCCTCCCTGCGGGCTGCTG 89495        A      TGTC
                                CAGCAGCCC GCAGGGA    CTC
                                |||||||| |||||||    |||
                                GTCGTCGGG CGTCCCT    GAG
                                    _      CCC_
GAM1214  LOC255057 3'  GAGGATGGCGCTGGTACTGCTG 97096       C_    AGGGA
                                CAGCAG  CCAGC     TGTCCTC
                                ||||||  |||||     |||||||
                                GTCGTC  GGTCG     GTAGGAG
                                   AT    CG___
GAM1214  LOC90362  5'  GGACAGCCGGCTGCTG      63115        CAGCAG  A
                                CAGCAGCC     GG TGTCC
                                ||||||||     || |||||
                                GTCGTCGG     CC ACAGG
                                     _______  G
GAM1214  LOC92697  5'  GAGGAGCGTCTCTGCCAGGCCG 70812    A   CA       _
            C                    GC GCC  GCAGGGATG TCCTC
                                 || |||  ||||||||| |||||
                                 CG CGG  CGTCTCTGC AGGAG
                                  C  AC       G
GAM1214  LOC92697  5'  GAGGAGCGTCTCTGCCCGGCCG 70813    A   CA       _
            C                    GC GCC  GCAGGGATG TCCTC
                                 || |||  ||||||||| |||||
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                                CG CGG  CGTCTCTGC AGGAG
                                 C  CC       G
GAM1214 LOC92715 3' GCTTCCCTGCTGGGCCCCTG  70900    CA         T
                                CAG  GCCCAGCAGGGA GT
                                |||  |||||||||||| ||
                                GTC  CGGGTCGTCCCT CG
                                  CC          T
GAM1215 PTPRC    5' ACGGCTGACTTCCAGATATGA  12603    CGGA    A
                                TCA    TGGAA GTCAGCCGT
                                |||    ||||| |||||||||
                                AGT    ACCTT CAGTCGGCA
                                  ATAG    _
GAM1215 PTPRC    5' ACGGCTGACTTCCAGATATGA  56052    CGGA    A
                                TCA    TGGAA GTCAGCCGT
                                |||    ||||| |||||||||
                                AGT    ACCTT CAGTCGGCA
                                  ATAG    _
GAM1215 PTPRC    5' ACGGCTGACTTCCAGATATGA  56053    CGGA    A
                                TCA    TGGAA GTCAGCCGT
                                |||    ||||| |||||||||
                                AGT    ACCTT CAGTCGGCA
                                  ATAG    _
GAM1215 ZNF261   3' ACGACTAACCTTCTGTCTCTGA 18730     C       A  C  C
             A                   TTCA GGATGGAA GT AG CGT
                                 |||| |||||||| || || |||
                                 AAGT TCTGTCTT CA TC GCA
                                   C       C  A  A
GAM1215 BIRC3    5' ACAGCAGAGCTTTCCACCATGA 67775     C  A     _  A  C
             A                   TTCA GG TGGAAAG TC GC GT
                                 |||| || ||||||| || || ||
                                 AAGT CC ACCTTTC AG CG CA
                                   A  _      G  A  A
GAM1215 FLJ10932 3' TGCCTTTCCATCCGTGAA    37433            T
                                 TTCACGGATGGAAAG CA
                                 |||||||||||||| ||
                                 AAGTGCCTACCTTTC GT
                                           C
GAM1215 G2       5' ACAGCCGACTTTCCCTCC    67239     T      A  C
                                 GGA GGAAAGTC GC GT
                                 ||| |||||||| || ||
                                 CCT CCTTTCAG CG CA
                                   C       C  A
GAM1215 KIAA1940 3' GGGACCTTCCATCCCTGAA   80789     C       A   AG
                                 TTCA GGATGGAA GTC  CC
                                 |||| |||||||| |||  ||
                                 AAGT CCTACCTT CAG  GG
                                   C       C  __
GAM1216 CDH12    3' CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                 TACACCACT    GAA  ATAAG
                                 |||||||||    |||  |||||
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                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM1216  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM1216  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090      T   AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                   _   GTCA_
GAM1216  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
            A                    TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM1216  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126        CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM1216  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
            TA                   TACA   TCC   GAAGAATAAG
                                ||||   |||   ||||||||||
                                ATGT   AGG   TTTCTTATTC
                                  AAA_  ATTG
GAM1216  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA  68742             _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                          G
GAM1216  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929    CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM1216  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748     CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM1216  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM1216  OSBPL11   3'  CTTAATTTCCCAAGAGTGGTG  43206        CCAA   AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
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                                GTGGTGAG   CTTT  ATTC
                                    AACC   A_
GAM1216 YME1L1   3' TCATTCTTGATGTGGTGTA   58438       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                    TA_     A
GAM1216 ZNF262   3' CTTATTTTGTTTGGGAGT    18723        A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                     G
GAM1216 LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_    AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
                                ATGTGGTG   GGTTC   TGT
                                    CAA    GG__
GAM1217 HRH1     3' CTCAAACATGTTTAGAGTGGA 7819      A    TGG
                                TCCA TCTGA   GCATGTTTGAG
                                ||||  |||||   ||||||||||
                                AGGT AGATT   TGTACAAACTC
                                  G    ___
GAM1217 TRIM37   3' CTCAAATTTGTCATCAG     31625       G  T
                                CTGATGG CA GTTTGAG
                                ||||||| ||  |||||||
                                GACTACT GT TAAACTC
                                    _  T
GAM1217 HTMP10   3' CTCAAAAAAGCCATCAGATCTG 53758    CA       G ATG
            A                    TC  ATCTGATGG C   TTTGAG
                                ||  |||||||||  |   ||||||
                                AG  TAGACTACC G   AAACTC
                                 TC       _ AAA
GAM1217 PAK2     5' CTCAAATATCACCAAACTAGA  67140     A__   GC
                                TCTG   TGG  ATGTTTGAG
                                ||||   |||  |||||||||
                                AGAT   ACC  TATAAACTC
                                  CAA   AC
GAM1217 SEMA6A   3' CTCGAGTACCCACCAGA     40818     A   CA
                                TCTG TGGG  TGTTTGAG
                                |||| ||||  ||||||||
                                AGAC ACCC  ATGAGCTC
                                  C   __
GAM1217 TTY7     3' TCAAACATGCAGGCTGGA    50019     AT  GATGG
                                TCCA  CT    GCATGTTTGA
                                ||||  ||    ||||||||||
                                AGGT  GA    CGTACAAACT
                                  CG  _____
GAM1217 LOC144766 3' CTCAAACATGAGAAGACTGGG  77481      A   GATGGG
                                TCCA TCT     CATGTTTGAG
                                |||| |||     ||||||||||
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                                GGGT AGA     GTACAAACTC
                                  C   AGA___
GAM1217  LOC201685 5'  TAAACACCCATCAGATGGA   91845      A       CA
                                TCCA TCTGATGGG  TGTTTG
                                |||| |||||||||  ||||||
                                AGGT AGACTACCC  ACAAAT
                                  _       __
GAM1217  LOC221596 5'  CTCAAACAAAACTCAGATT   93623       TG GCA
                                AATCTGA  G   TGTTTGAG
                                |||||||  |  ||||||||
                                TTAGACT  C   ACAAACTC
                                   __ AAA
GAM1217  LOC93622  3'  CTCTGCAGACCATCAGAT    57729        GCA   TT
                                ATCTGATGG   TGT  GAG
                                |||||||||   |||  |||
                                TAGACTACC   ACG  CTC
                                     AG_   T_
GAM1218  BAP1      3'  ACAGCCCCATGGCCTCTGC    17392      A   G   A
                                GCAGA GTTG TGG GCTGT
                                ||||| |||| ||| |||||
                                CGTCT CGGT ACC CGACA
                                   C    _  C
GAM1218  C14orf1   3'  ACAGCTCTCCTTCTATCT    24159     _  TT  T
                                AGA AG  GG GGAGCTGT
                                ||| ||  || ||||||||
                                TCT TC  CC TCTCGACA
                                  A  TT  _
GAM1218  RB1       5'  ACAGCTCGCTGGCTCCCGCCGC 92552    A  AGA   TG   G
                                GC GC   AGT  GTG AGCTGT
                                || ||   |||  ||| ||||||
                                CG CG   TCG  CGC TCGACA
                                 C  CCC   GT  _
GAM1218  SLC9A1    3'  CAGCTCCTCCCCTGCCGC    70919    A   AAGTT  T
                                GC GCAG    GG GGAGCTG
                                || ||||    || |||||||
                                CG CGTC    CC CCTCGAC
                                 C   C____  T
GAM1218  SNAP23    3'  ACAGTTTTGCAACCTCTGCTCC 56332    C     A   G TG
              A                  TG AGCAGA GTT G  GAGCTGT
                                || |||||| ||| |  |||||||
                                AC TCGTCT CAA C  TTTGACA
                                 C     C   _ GT
GAM1218  SNAP23    3'  ACAGTTTTGCAACCTCTGCTCC 15132    C     A   G TG
              A                  TG AGCAGA GTT G  GAGCTGT
                                || |||||| ||| |  |||||||
                                AC TCGTCT CAA C  TTTGACA
                                 C     C   _ GT
GAM1218  CDC14A    3'  ACAGGGTACAACCCCCTGCTGC 14780        AA_    GTGGAG
              A                  TGCAGCAG   GTTG     CTGT
                                ||||||||   ||||     ||||
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                                ACGTCGTC  CAAC     GACA
                                    CCC   ATGG__
GAM1218 FLJ10604 5' ACAGCCCCTGCCCCTGCTGC  36857       AAGTT  _ A
                                GCAGCAG    GGT GG GCTGT
                                |||||||    ||| || |||||
                                CGTCGTC    CCG CC CGACA
                                    C____   T  C
GAM1218 FLJ13154 3' ACAGCCCGGGTTCTCCTGCTGC 45101       A  TTGG  A
                                GCAGCAG AG    TGG GCTGT
                                ||||||| ||    ||| |||||
                                CGTCGTC TC    GCC CGACA
                                    C  TTGG  _
GAM1218 FLJ20171 3' ACATTTCCAGCTCCTGCTGCA 35172       A  TGG    C
                                TGCAGCAG AGT   TGGAG TGT
                                |||||||| |||   ||||| |||
                                ACGTCGTC TCG   ACCTT ACA
                                    C  ___    T
GAM1218 FLJ23047 3' AGAAAAACCAATTTCCACTGCA 44930      CA       GGAG
                                TGCAG  GAAGTTGGT   CT
                                |||||  |||||||||   ||
                                ACGTC  CTTTAACCA   GA
                                  AC       AAAA
GAM1218 HPCAL4   3' CAAGCAACTTTCTGCTACA   33205   C     _   G_
                                TG AGCAGAA GTTG  TG
                                || ||||||| ||||  ||
                                AC TCGTCTT CAAC  AC
                                 A      T   GA
GAM1218 KIAA1045 3' CCACCAACCTCTGGCA     71600     AG   A
                                TGC  CAGA GTTGGTGG
                                |||  |||| ||||||||
                                ACG  GTCT CAACCACC
                                  __   C
GAM1218 KIAA1061 3' ACAGAGTCAACTTCTGCAGCA  71714     A        TGGAG
                                TGC GCAGAAGTTGG    CTGT
                                ||| ||||||||||    ||||
                                ACG CGTCTTCAACT    GACA
                                  A         GA___
GAM1218 MGC5601  5' ACAGCTGGGAATCCCTGCTGCA 48258       AA  GGTGG
                                TGCAGCAG  GTT    AGCTGT
                                |||||||  |||    ||||||
                                ACGTCGTC  TAA    TCGACA
                                    CC   GGG__
GAM1218 MRPL35   3' TTCACCAACTTCTCTACA    34025    C  C
                                TG AG AGAAGTTGGTGGA
                                || || ||||||||||||
                                AC TC TCTTCAACCACTT
                                 A  _
GAM1218 RGS4     5' CAGCTCCTCCTGCCGCA     20044     A  GAAGTT  T
                                TGC GCA     GG GGAGCTG
                                ||| |||     || |||||||
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                                ACG CGT     CC CCTCGAC
                                  C  _______ T
GAM1218  LOC144110 3'  ACAACTCCATCTTCTGCTGC  77187         TTG     C
                                GCAGCAGAAG  GTGGAG TGT
                                ||||||||||  |||||| |||
                                CGTCGTCTTC  TACCTC ACA
                                      ___     A
GAM1218  LOC170127 3'  CAGGCAAGCTTCCACTGCA   83454      CA     G  GGAG
                                TGCAG  GAAGTT GT   CTG
                                |||||  |||||| ||   |||
                                ACGTC  CTTCGA CG   GAC
                                   AC     A ____
GAM1218  LOC196955 3'  CAGCTGGATCCTGCTGCA    77863        AAGTT   GG
                                TGCAGCAG    GGT  AGCTG
                                ||||||||    |||  |||||
                                ACGTCGTC    CTA  TCGAC
                                     _____  GG
GAM1218  LOC220776 3'  CAGCCCTCTTCTGCCGC    68918    A      TTGGT  A
                                GC GCAGAAG    GG GCTG
                                || |||||||    || ||||
                                CG CGTCTTC    CC CGAC
                                 C      T____ _
GAM1218  LOC84549  3'  ACAGACACACCCTCTGCCACA  51677    CA    AGTT    GAG
                                TG  GCAGA   GGTG   CTGT
                                ||  |||||   ||||   ||||
                                AC  CGTCT   CCAC   GACA
                                 AC    C___   ACA
GAM1219  FLJ12903  3'  TTACTTTTTTATTTGAA     43080         C
                                TTCAAATAA AAAAGTAG
                                ||||||||| ||||||||
                                AAGTTTATT TTTTCATT
                                     _
GAM1219  FLJ12934  3'  CAGACTGGCTTTTGTTACCTGA 43487     AA        AGAT
                                TCA  TAACAAAAGT    TCTG
                                |||  ||||||||||    ||||
                                AGT  ATTGTTTTCG    AGAC
                                  CC         GTC_
GAM1219  KIAA0825  3'  TTACTTTTGTTTTCTGAA    61693      AAT
                                TTCA   AACAAAAGTAG
                                ||||   ||||||||||
                                AAGT   TTGTTTTCATT
                                  CTT
GAM1219  METAP1   3'  TTACTTTTATTATTTGAA    73038         C
                                TTCAAATAA AAAAGTAG
                                ||||||||| ||||||||
                                AAGTTTATT TTTTCATT
                                      A
GAM1219  POFUT1   3'  TCACTATTGTTATTTGAA    70983           A   A
                                TTCAAATAACAA AGT GA
                                |||||||||||| ||| ||
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                                AAGTTTATTGTT TCA CT
                                      A  _
GAM1219  SAC2     3'  CAGAGCACTTTGCTTATTTGAA 30722        CA    AGA
                                TTCAAATAA  AAAGT   TTCTG
                                |||||||||  |||||   |||||
                                AAGTTTATT  TTTCA   GAGAC
                                     CG    C__
GAM1219  STK39    3'  CAGAATCTGAGTTTTACTTGAA 26010      A   CA  AG
                                TTCAA TAA  AA  TAGATTCTG
                                |||||  |||  ||  |||||||||
                                AAGTT ATT  TT  GTCTAAGAC
                                   C  __  GA
GAM1219  LOC122830 3'  CAGTGATGCTTTTGTTATTT   74629           GATT
                                AAATAACAAAAGTA    CTG
                                ||||||||||||||    |||
                                TTTATTGTTTTCGT    GAC
                                      AGT_
GAM1219  LOC92344  3'  CTGCGTTTTGTTATTTGAA    69576           _
                                TTCAAATAACAAAA GTAG
                                |||||||||||||| ||||
                                AAGTTTATTGTTTT CGTC
                                      G
GAM1220  NAV2     3'  AGACTTCCCTCCTGGGTCCAG  60789       ATGCCA
                                TTGGACC     GAGGGAAGTCT
                                |||||||     ||||||||||||
                                GACCTGG     CTCCCTTCAGA
                                    GTC___
GAM1220  RAB40A   5'  TTCCTTTGACATAATCCAA   82946      CC   C
                                TTGGA  ATG CAGAGGGA
                                |||||  ||| ||||||||
                                AACCT  TAC GTTTCCTT
                                   AA   A
GAM1220  SLC12A5  3'  AGACCTCCCTCTGAACACCA   40767     ACCATGC      A
                                TGG      CAGAGGGA GTCT
                                |||      |||||||| ||||
                                ACC      GTCTCCCT CAGA
                                  ACAA___       C
GAM1220  LOC131478 5'  AGACTTCCAGGACTGCAAACCC 76378     ACCA   C  AG__
            AA                    TTGG    TGC AG    GGAAGTCT
                                |||||   ||| ||   ||||||||
                                AACC    ACG TC    CCTTCAGA
                                  CAA_   _  AGGA
GAM1220  LOC152317 5'  CCTTCATGGCATGCCCCAA    86827      AC      _
                                TTGG  CATGCCA GAGGG
                                ||||  ||||||| |||||
                                AACC  GTACGGT CTTCC
                                  CC      A
GAM1220  LOC222112 3'  AGAATTTTATGGCATGGCCCAA 94377      A       GAGG   G
                                TTGG CCATGCCA    GAA TCT
                                |||| ||||||||    ||| |||
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                                AACC GGTACGGT    TTT AGA
                                  C       AT__   A
GAM1220  LOC257117 5'  AGACCTTTTTTGGATAGTCCAA 97954       C  G       AA
                                TTGGAC AT CCAGAGGG  GTCT
                                |||||| || ||||||||  ||||
                                AACCTG TA GGTTTTTT  CAGA
                                   A  _       C_
GAM1221  ABCA9    3'  AAAGGATGAGTTCATATTCTTC 55362         CG_   C
           ACA                    TGTGAAGAG   GAGC CATCCTTT
                                |||||||||   |||| ||||||||
                                ACACTTCTT   CTTG GTAGGAAA
                                     ATA   A
GAM1221  AP1S2    3'  GTGTTGCTCTCTTCACA     15350        GCG   C_
                                TGTGAAGA   GAGC  CAT
                                ||||||||   ||||  |||
                                ACACTTCT   CTCG  GTG
                                     ___    TT
GAM1221  DKFZP434F1735 5'  AAAGGATGGACTCTGTTACCCA 32109      AAG      C
           CA                     TGTG   AGCGGAG CCATCCTTT
                                ||||   ||||||| |||||||||
                                ACAC   TTGTCTC GGTAGGAAA
                                  CCA      A
GAM1221  DNAJA2   3'  ATGGGCTTTGCACACA      60487      AAGA
                                TGTG    GCGGAGCCCAT
                                ||||    ||||||||||
                                ACAC    CGTTTCGGGTA
                                  A___
GAM1221  DRIL2    3'  AAAGGATGGACTCTTCCCAC   22344     AA  GC    C
                                GTG  GA  GGAG CCATCCTTT
                                |||  ||  |||| |||||||||
                                CAC  CT  TCTC GGTAGGAAA
                                  C_  __    A
GAM1221  SLC26A9  3'  AAAGGATGAGCCTGGGGTCACA 54708       AGAG   A  C
                                TGTGA    CGG GC CATCCTTT
                                |||||    ||| || ||||||||
                                ACACT    GTC CG GTAGGAAA
                                   GGG_   _  A
GAM1221  LOC150837 3'  ATGAGGCTTCGCTCTCCACA   80800      A         _
                                TGTG AGAGCGGAGCC CAT
                                |||| |||||||||| |||
                                ACAC TCTCGCTTCGG GTA
                                  C         A
GAM1222  CBFA2T2  3'  CCACACCTGGCCTTGGCTG    18705      A___     A
                                CAGC    GCCGG GTGTGG
                                ||||    ||||| ||||||
                                GTCG    CGGTC CACACC
                                  GTTC    _
GAM1222  CD97     3'  CCACTGGTCCTGCTGCTG     55303        C   G _
                                CAGCAGC GGA T GTGG
                                ||||||| ||| | ||||
```

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                                GTCGTCG CCT G CACC
                                    T   G T
GAM1222  COLQ     3'  CCACACCTGGGCAGGCTGTTG  55419        _____  A
                                CAGCAGCC    GG GTGTGG
                                ||||||||    || ||||||
                                GTTGTCGG    TC CACACC
                                    ACGGG  _
GAM1222  COLQ     3'  CCACACCTGGGCAGGCTGTTG  55420        _____  A
                                CAGCAGCC    GG GTGTGG
                                ||||||||    || ||||||
                                GTTGTCGG    TC CACACC
                                    ACGGG  _
GAM1222  LETM1    3'  CCACACAGAGCTGGCTGCTG   25550         A___
                                CAGCAGCCGG   GTGTGG
                                ||||||||||   ||||||
                                GTCGTCGGTC   CACACC
                                     GAGA
GAM1222  MASP1    3'  CCACACTGTGTCCTGCTG    58211       C_  G
                                CAGCAG  CG AGTGTGG
                                ||||||  || |||||||
                                GTCGTC  GT TCACACC
                                   CT  G
GAM1222  MAT1A    3'  CCAGACGCCTGGCTGCTG    92497         A_  G
                                CAGCAGCCGG  GT TGG
                                ||||||||||  || |||
                                GTCGTCGGTC  CA ACC
                                     CG  G
GAM1222  PKD1     3'  CCACTGCTAAGGCTGCTG    6102         GG  _
                                CAGCAGCC  AGT GTGG
                                ||||||||  ||| ||||
                                GTCGTCGG  TCG CACC
                                    AA   T
GAM1222  RNMT     3'  CCACACCTGCAGGCGCTG    15050      A  ___  A
                                CAGC GCC   GG GTGTGG
                                ||||  |||   || ||||||
                                GTCG CGG   TC CACACC
                                  _   ACG  _
GAM1222  RPL30    5'  CCATCTTAGCGGCTGCTG    8271          __  T
                                CAGCAGCCG  GAG GTGG
                                |||||||||  ||| ||||
                                GTCGTCGGC  TTC TACC
                                     GA   _
GAM1222  TEM5     3'  CCACATATGCTGGCTGCTG   52298         A__
                                CAGCAGCCGG   GTGTGG
                                ||||||||||   ||||||
                                GTCGTCGGTC   TACACC
                                     GTA
GAM1222  XT3      3'  CCAGCTACTCTGGCTGCTG   39906           __
                                CAGCAGCCGGAGTG  TGG
                                ||||||||||||||  |||
```

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                                GTCGTCGGTCTCAT  ACC
                                       CG
GAM1222  AD034    3'  CCACAGTTCAGCTGGCTG    49747     _  C   G
                                CAGC AGC GGA TGTGG
                                |||| ||| ||| |||||
                                GTCG TCG CTT ACACC
                                  G   A   G
GAM1222  ALLC     5'  CCTAATTTCAGGCTGCTG    37980       _    GT
                                CAGCAGCC GGAGT  GG
                                |||||||| |||||  ||
                                GTCGTCGG CTTTA  CC
                                     A     AT
GAM1222  COLEC12  3'  CCACAGTTTTGGCCTCTG    56101     CA     _
                                CAG  GCCGGAG TGTGG
                                |||  ||||||| |||||
                                GTC  CGGTTTT ACACC
                                  TC      G
GAM1222  DKFZP564C186 3'  CCACAACTGTGGGCTGCTG    72841       _ G  _
                                CAGCAGCC G AGT GTGG
                                |||||||| | ||| ||||
                                GTCGTCGG T TCA CACC
                                     G G   A
GAM1222  FBXO26   5'  CCAGGACTCTGGCTACTG    46624     C       G_
                                CAG AGCCGGAGT  TGG
                                ||| |||||||||  |||
                                GTC TCGGTCTCA  ACC
                                  A       GG
GAM1222  FLJ21736 3'  CCACACTCTGTATCTGGCT    46780     _ C__
                                AGC AG   CGGAGTGTGG
                                ||| ||   ||||||||||
                                TCG TC   GTCTCACACC
                                  G  TAT
GAM1222  ITGB5    3'  CCATGTCACCTGGCTGCT    60215       A  ___
                                AGCAGCCGG GTG   TGG
                                ||||||||| |||   |||
                                TCGTCGGTC CAC   ACC
                                     _  TGT
GAM1222  KIAA0084 5'  CCACCGCTCCAGCGGCTG    68706     A  C     _
                                CAGC GC GGAGTG TGG
                                |||| || |||||| |||
                                GTCG CG CCTCGC ACC
                                  G A     C
GAM1222  KIAA1582 5'  CCACAGGCTCCAGCTCTG    65987     C   C    __
                                CAG AGC GGAGT  GTGG
                                ||| ||| |||||  ||||
                                GTC TCG CCTCG  CACC
                                  _  A    GA
GAM1222  KIAA1879 5'  CCACAGTGCTGCGGCTGCT    73933       G   ___
                                AGCAGCCG AGT   GTGG
                                |||||||| |||   ||||
```

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                                TCGTCGGC TCG   CACC
                                    G   TGA
GAM1222  LGI2     3'  GCCACACTCCAGGTCTGT    36926     _ _      ___
                                GCAG CC GGAGTGTGG   C
                                |||| || |||||||||   |
                                TGTC GG CCTCACACC   G
                                  T  A       ___
GAM1222  MAP-1    3'  CCACCTGCTTCGGCCTCTG   42437     CA      __
                                CAG  GCCGGAGT  GTGG
                                |||  ||||||||  ||||
                                GTC  CGGCTTCG  CACC
                                  TC       TC
GAM1222  MGC2647  3'  CCACAGGCTGTGGCTGCT    74076        G   __
                                AGCAGCCG AGT  GTGG
                                |||||||| |||  ||||
                                TCGTCGGT TCG  CACC
                                    G   GA
GAM1222  SCAM-1   3'  CCAGCACCCCAGCTTGCTG   20501      _ C  A  _
                                CAGCA GC GG GTG TGG
                                ||||| || || ||| |||
                                GTCGT CG CC CAC ACC
                                   T  A  C   G
GAM1222  XYLT1    5'  CCACAAGTTAGGGCTGCTG   78412        G_  G_
                                CAGCAGCC  GA  TGTGG
                                ||||||||  ||  |||||
                                GTCGTCGG  TT  ACACC
                                    GA  GA
GAM1222  LOC136120 3'  CCATCAACCTGGCTGCTG    76706         AG  _
                                CAGCAGCCGG  TG TGG
                                ||||||||||  || |||
                                GTCGTCGGTC  AC ACC
                                     CA  T
GAM1222  LOC144486 5'  CCACCGACGCCGGTTGCTG   84002          A  __
                                CAGCAGCCGG GT  GTGG
                                |||||||||| ||  ||||
                                GTCGTTGGCC CA  CACC
                                     G  GC
GAM1222  LOC200471 5'  CCAGGCTGCTGGCTGCTG    91634          _  G
                                CAGCAGCCGG AGT TGG
                                |||||||||| ||| |||
                                GTCGTCGGTC TCG ACC
                                     G   G
GAM1222  LOC256905 5'  CCACAGCTCTGGCTCCTG    98658     C      _
                                CAG AGCCGGAG TGTGG
                                ||| |||||||| |||||
                                GTC TCGGTCTC ACACC
                                  C       G
GAM1223  ADAM12   3'  CATGTTTCACAAGGTCTT    14423          TGGCT
                                AAGACTTTGTG    ACATG
                                ||||||||||     |||||
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                                TTCTGGAACAC    TGTAC
                                      TT___
GAM1223 CELSR1   3' TCATCCAGACACAAAGGTCTT 27278       G   G  AC
                                AAGACTTT TGTG CT  ATGA
                                |||||||| |||| ||  ||||
                                TTCTGGAA ACAC GA  TACT
                                     _   A  CC
GAM1223 GAN      3' GTCTGAAAGCACACAAAGTCTT 42121         G  ACAT
                                AAGACTTTGTGTG CT   GAC
                                |||||||||||| ||   |||
                                TTCTGAAACACAC GA   CTG
                                      _ AAGT
GAM1223 HFE      3' GTCATACAGATTTGCAAAGTTT 58121        TGG  AC
                                AGACTTTGTG   CT  ATGAC
                                ||||||||||   ||  |||||
                                TTTGAAACGT   GA  TACTG
                                      TTA  CA
GAM1223 HFE      3' GTCATACAGATTTGCAAAGTTT 6400         TGG  AC
                                AGACTTTGTG   CT  ATGAC
                                ||||||||||   ||  |||||
                                TTTGAAACGT   GA  TACTG
                                      TTA  CA
GAM1223 KCNS2    3' GTCATGTGAAAACAAAATCT   68851    C    GTGGC
                                AGA TTTGT    TACATGAC
                                ||| |||||    ||||||||
                                TCT AAACA    GTGTACTG
                                  A    AAA__
GAM1223 RAB38    3' GTCATGTAGCTGACCAAAATC  60926    C   TG
                                GA TTTG  TGGCTACATGAC
                                || ||||  ||||||||||||
                                CT AAAC  GTCGATGTACTG
                                 A   CA
GAM1223 RCN2     3' GCCATATGACAACAAAGTCTT  12798        _______
                                AAGACTTTGT     GTGGC
                                ||||||||||     |||||
                                TTCTGAAACA     TACCG
                                      ACAGTA
GAM1223 SLC26A3  5' CACATAGTTGCAAAGGTCTT   5470        G  TG   CA
                                AAGACTTT TG  GCTA  TG
                                |||||||| ||  ||||  ||
                                TTCTGGAA AC  TGAT  AC
                                     _ GT    AC
GAM1223 TCF2     3' GCCACACAGGAAGAAAGTCTT  22408       _______
                                AAGACTT     TGTGTGGC
                                |||||||     ||||||||
                                TTCTGAA     ACACACCG
                                    AGAAGG
GAM1223 ALK7     3' ATGGACCCGCACAAAATCT    76241     C       CTA
                                AGA TTTGTGTGG   CAT
                                ||| |||||||||   |||
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                                TCT AAACACGCC   GTA
                                  A        CAG
GAM1223  AQP10    3'  GTCTGCTCAACACAAAGCCT   55397    A      __   T_
                                AG CTTTGTGT  GGC  AC
                                || ||||||||  |||  ||
                                TC GAAACACA  TCG  TG
                                 C       AC   TC
GAM1223  DKFZP434P0721 3'  TCATGTAGACTAAAGTCTT    64466         T  GG
                                AAGACTTTG GT  CTACATGA
                                ||||||||| ||  ||||||||
                                TTCTGAAAT CA  GATGTACT
                                     _ __
GAM1223  DKFZP564D0462 3'  GCCACAGCACAAAGTTTT    71022           ___
                                AAGACTTTGTGT   GGC
                                ||||||||||||   |||
                                TTTTGAAACACG   CCG
                                       ACA
GAM1223  FLJ14936  3'  CAGGAGCCACTCAAAGTCT    51127        T     ACA
                                AGACTTTG GTGGCT   TG
                                |||||||| ||||||   ||
                                TCTGAAAC CACCGA   AC
                                     T     GG_
GAM1223  FLJ21551  3'  CACGTAGTTACCAAAACTCT   46031     C_   T      A
                                AGA  TTTG GTGGCTAC TG
                                |||  |||| |||||||| ||
                                TCT  AAAC CATTGATG AC
                                  CA   _       C
GAM1223  FLJ21709  3'  GTCTCACCGCACAAAGCCT    78482    A        CTACAT
                                AG CTTTGTGTGG     GAC
                                || ||||||||||     |||
                                TC GAAACACGCC     CTG
                                 C        ACT___
GAM1223  GRID1    3'  TCATGGAGAAATACAAAGTC   69027         GG  A
                                GACTTTGTGT  CT CATGA
                                ||||||||||  || |||||
                                CTGAAACATA  GA GTACT
                                       AA  G
GAM1223  KIAA0179  3'  GTCATATAGCCAAACGGG    65458      G     C
                                TTTGT TGGCTA ATGAC
                                ||||| |||||| |||||
                                GGGCA ACCGAT TACTG
                                   A     A
GAM1223  KRTAP1-1  3'  TCACACAGCCACATAAATTC   49046    C         ACA
                                GA TTTGTGTGGCT   TGA
                                || ||||||||||   |||
                                CT AAATACACCGA   ACT
                                 T         CAC
GAM1223  LOXL4    3'  CATGCCCTTCACAGAGTC    50857         T_  CTA
                                GACTTTGTG  GG   CATG
                                |||||||||  ||   ||||
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                                CTGAGACAC  CC   GTAC
                                     TT  C__
GAM1223  MISS     3'  GTCATACAGCACTAAAGTCT   58641        T   G  AC
                                AGACTTTG GTG CT  ATGAC
                                |||||||| ||| ||  |||||
                                TCTGAAAT CAC GA  TACTG
                                     _  _  CA
GAM1223  NXP-2    3'  TCACGGTTAAACACAAAGTGTT 71660    G       GGCT  A_
                                AA ACTTTGTGT    AC  TGA
                                || |||||||||    ||  |||
                                TT TGAAACACA    TG  ACT
                                 G        AAT_  GC
GAM1223  PTD011   3'  GTCACATAAAGGAAGTCTT   26760        ____
                                AAGACTTT    GTGTGGC
                                ||||||||    |||||||
                                TTCTGAAG    TACACTG
                                     GAAA
GAM1223  SDFR1    3'  GTCATGTAAATTCATAAATC   34359    C     TGGC
                                GA TTTGTG    TACATGAC
                                || ||||||    ||||||||
                                CT AAATAC    ATGTACTG
                                 _     TTAA
GAM1223  SDFR1    3'  GTCATGTAAATTCATAAATC   25793    C     TGGC
                                GA TTTGTG    TACATGAC
                                || ||||||    ||||||||
                                CT AAATAC    ATGTACTG
                                 _     TTAA
GAM1223  LOC124842 3'  GTCACAGGCTGCACAAAGACTT 76159     A      TG   ACA
                                AAG CTTTGTG  GCT   TGAC
                                ||| |||||||  |||   ||||
                                TTC GAAACAC  CGG   ACTG
                                  A      GT   AC_
GAM1223  LOC146310 5'  CATGCAGCCACATCTTCT    78350     CTTT       A
                                AGA    GTGTGGCT CATG
                                |||    |||||||| ||||
                                TCT    TACACCGA GTAC
                                  TC__       C
GAM1223  LOC147040 3'  CACGTAGCCAGGAGGGGCCT   78831    A   GTG      A
                                AG CTTT   TGGCTAC TG
                                || ||||   ||||||| ||
                                TC GGGG   ACCGATG AC
                                 C    AGG      C
GAM1223  LOC148534 3'  CATCAGTACCAAAGTCTT    79633         T   G  AC
                                AAGACTTTG GTG CT  ATG
                                ||||||||| ||| ||  |||
                                TTCTGAAAC CAT GA  TAC
                                     _  _  C_
GAM1223  LOC150112 3'  CATGTAGCCCCAGTCT      80388       TTGT T
                                AGACT    G GGCTACATG
                                |||||    | |||||||||
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                                TCTGA   C CCGATGTAC
                                  ____ C
GAM1223  LOC153894 3'  GTCATACAGCCCTAAAGTCT  81879       TGT   AC
                                AGACTTTG  GGCT  ATGAC
                                ||||||||  ||||  |||||
                                TCTGAAAT  CCGA  TACTG
                                    C__   CA
GAM1223  LOC253389 5'  CATGTTGCTCACACAAAGCCT  97646    A       _ T
                                AG CTTTGTGTG GC ACATG
                                || |||||||||| || |||||
                                TC GAAACACAC CG TGTAC
                                 C        T  T
GAM1223  LOC253681 3'  CACGTAGCCAGGAGGGGCCT  96836    A   GTG     A
                                AG CTTT   TGGCTAC TG
                                || ||||   ||||||| ||
                                TC GGGG   ACCGATG AC
                                 C   AGG      C
GAM1223  LOC253805 3'  TCATATATTTGTGCAAAGTTTT 98184          TG C  C
                                AAGACTTTGTG  G TA ATGA
                                ||||||||||  | || ||||
                                TTTTGAAACGT  T AT TACT
                                      GT T  A
GAM1223  LOC255349 3'  TCATGTAGCCAACTTCAAATC  97352    C   TG__
                                GA TTTG   TGGCTACATGA
                                || ||||   ||||||||||
                                CT AAAC   ACCGATGTACT
                                 _   TTCA
GAM1224  APM1     3'  ACTCCATCTCTAAGTGCTGAAC 17754       AG_    CAA
                                GTTCAGTG  AGAGA  AGT
                                ||||||||  |||||  |||
                                CAAGTCGT  TCTCT  TCA
                                    GAA   ACC
GAM1224  BCL7A    3'  GCTTCCTCTCACTGAACG    40987          A  CAA
                                CGTTCAGTGAGAG GA  AGT
                                |||||||||||| ||  |||
                                GCAAGTCACTCTC CT  TCG
                                          _ ___
GAM1224  COG5     3'  ACCCTGCCTTTTTCACTAAAT  22024    C       A  AA
                                GTT AGTGAGAGAG CA  GT
                                ||| |||||||||| ||  ||
                                TAA TCACTTTTTC GT  CA
                                  A        C  CC
GAM1224  DVL3     3'  TGACTTTACCCCACATTACTGA 16652       GAGAGAC_
            A                    TTCAGTGA      AAAGTCA
                                ||||||||      |||||||
                                AAGTCATT      TTTCAGT
                                    ACACCCCA
GAM1224  F8A      3'  TGACTTTGCCTGTTACCAAAC  25121    CA   G  AGA
                                GTT  GTGA AG   CAAAGTCA
                                |||  |||| ||   ||||||||
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                                CAA  CATT TC   GTTTCAGT
                                  AC    G  C__
GAM1224  LDHA     3'  ACTTCCTGGCTCCTTCACTGAA 19914          A   A  __
              C                    GTTCAGTGAG GAG CA  AAGT
                                   |||||||||| ||| ||  ||||
                                   CAAGTCACTT CTC GT  TTCA
                                        C   G  CC
GAM1224  LEP      3'  TGACCCATCTCCCCCTCACTGA 5871           A__    CAAA
              ATG                   CGTTCAGTGAG   GAGA    GTCA
                                   ||||||||||   ||||   ||||
                                   GTAAGTCACTC   CTCT    CAGT
                                         CCC    ACC_
GAM1224  PRKACB   3'  CTCTGTTCTCTCAGTAAAC   12274     CAG       A  A
                                   GTT   TGAGAGAG CA AG
                                   |||   |||||||| || ||
                                   CAA   ACTCTCTT GT TC
                                     ATG       _  C
GAM1224  TEAD2    3'  TGACTTTATCTCCGCTGCAC   14586    T    A    GAC
                                   GT CAGTG GAGA   AAAGTCA
                                   || ||||| ||||   |||||||
                                   CA GTCGC CTCT   TTTCAGT
                                    C     _    A__
GAM1224  WFDC1    3'  TGACTTTGTGGGAGCCACTTAA 41341     C    AGAGAG
              C                    GTT AGTG     ACAAAGTCA
                                   ||| ||||     |||||||||
                                   CAA TCAC     TGTTTCAGT
                                     T    CGAGGG
GAM1224  C20orf80  5'  TGACCCTGTCTGGGCTGGACG  65883        GAGAG    AA
                                   CGTTCAGT    AGACA  GTCA
                                   ||||||||    |||||  ||||
                                   GCAGGTCG    TCTGT  CAGT
                                        GG___     CC
GAM1224  CACNG4   3'  TGACTTTGTCCCCTCCCCGAA  27711     AGT   AGA
                                   TTC   GAG   GACAAAGTCA
                                   |||   |||   ||||||||||
                                   AAG   CTC   CTGTTTCAGT
                                     CCC   CC_
GAM1224  FLJ10803  3'  ACAGTGGCCTCTCACTAAATG  37190     C       AGA  AA
                                   CGTT AGTGAGAG   CA  GT
                                   |||| ||||||||   ||  ||
                                   GTAA TCACTCTC   GT  CA
                                     A       CG_  GA
GAM1224  FLJ20209  3'  TGACCCTGCCTCCCCTCTTCAC 86709       _  ___   A  AA
              TG                     CAGTGA GA   GAG CA  GTCA
                                   ||||||  ||   |||  ||  ||||
                                   GTCACT CT   CTC GT  CAGT
                                      T  CCC   C  CC
GAM1224  LOC151124 5'  TGACCCTACTGTCCTCACTGAA 86421          AGA    AA___
                                   TTCAGTGAG   GACA    GTCA
                                   |||||||||   ||||    ||||
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                                AAGTCACTC  CTGT    CAGT
                                    ___    CATCC
GAM1224  LOC199923 3'  TGACTCTGATTCCACTGAGCG  89878        A   AGA  A
                                CGTTCAGTG GAG   CA AGTCA
                                ||||||||| |||   || |||||
                                GCGAGTCAC CTT   GT TCAGT
                                     _  A__  C
GAM1224  LOC201669 5'  ACCTTGGGTTCTCACTAAGC   91829     C       AGA   A
                                GTT AGTGAGAG   CAA GT
                                ||| ||||||||   ||| ||
                                CGA TCACTCTT   GTT CA
                                  A       GG_   C
GAM1224  LOC201799 3'  ACTTCTAGCTCACTGAAC    90487          AG   CAA
                                GTTCAGTGAG  AGA   AGT
                                ||||||||||  |||   |||
                                CAAGTCACTC  TCT   TCA
                                     GA  ___
GAM1225  SCAMP1    3'  GCTAAATAAATATTCTCC    54500     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1225  SCAMP1    3'  GCTAAATAAATATTCTCC    54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1225  NX-17     3'  TGAATATCAGCCCCTAATA   40706         ATA_
                                TATTAGGG    ATATTCA
                                ||||||||    |||||||
                                ATAATCCC    TATAAGT
                                    CGAC
GAM1225  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
              TA                  TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM1226  DLEC1     3'  CATCTGGCCCTCCCTTG     24716       A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                   C    G  _
GAM1226  DLEC1     3'  CATCTGGCCCTCCCTTG     24728       A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                   C    G  _
GAM1226  PIP5K1A   3'  TATCCCACCCTGCCTTGATA   14520         A   CA  C
                                TATCAAGG AGGG  GG GTG
                                |||||||| ||||  || |||
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                                ATAGTTCC TCCC  CC TAT
                                    G   A_  C
GAM1226  SOX11    3'  ACCCACCCCCCCTTGGTA    13308        AA  CA  C
                                TATCAAGG  GGG  GG GT
                                ||||||||  |||  || ||
                                ATGGTTCC  CCC  CC CA
                                    CC   A_  _
GAM1226  CHL1     3'  TGTTACCTTTCCTCAATA    22768     CA       CA
                                TAT  AGGAAGGG  GGCG
                                |||  ||||||||  ||||
                                ATA  TCCTTTCC  TTGT
                                  AC       A_
GAM1226  EPB41L1  3'  CATTCTGCCCTTCCCTGA    71104     A         C
                                TCA GGAAGGGCAGG GTG
                                ||| ||||||||||| |||
                                AGT CCTTCCCGTCT TAC
                                  C         _
GAM1226  FLJ00060 3'  CATACCCCCTGCCCTCCTCTGA 61741     _   A      CGTG
                                TCA AGGA GGGCAGG    ATG
                                ||| |||| |||||||    |||
                                AGT TCCT CCCGTCC    TAC
                                  C   _      CCCA
GAM1226  FLJ10898 5'  CACCACAGCCCTTTCTCAATA  60126     CA       AGGC
                                TAT  AGGAAGGGC    GTG
                                |||  |||||||||    |||
                                ATA  TCTTTCCCG    CAC
                                  AC        ACAC
GAM1226  FLJ22557 3'  ATCATCCCATCCTTAATA    45581     C    A   CAGGC
                                TAT AAGGA GGG     GTGAT
                                ||| ||||| |||     |||||
                                ATA TTCCT CCC     TACTA
                                  A    A  _____
GAM1226  KIAA0574 3'  CATCCCCTGCCCTCCCCTGA   69808     A  A      CGT
                                TCA GG AGGGCAGG   GATG
                                ||| ||  ||||||||   ||||
                                AGT CC TCCCGTCC   CTAC
                                  C  C       C__
GAM1226  KIAA0632 3'  CACCTCAGAAACCCTTCCTTGA 32071          CA___  C
                                TCAAGGAAGGG     GG GTG
                                ||||||||||     || |||
                                AGTTCCTTCCC     CT CAC
                                      AAAGA  C
GAM1226  KIAA1045 3'  CATCACATGTCCTTCC      71599         GGC
                                GGAAGGGCA   GTGATG
                                |||||||||   ||||||
                                CCTTCCTGT   CACTAC
                                      A__
GAM1226  KIAA1354 5'  CAGTGACTGCCTTCCCTTGATA 61572        A      G  _
                                TATCAAGG AGGGCAG CG TG
                                |||||||| ||||||| || ||
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                                ATAGTTCC TTCCGTC GT AC
                                    C      A  G
GAM1226  MGC20460  5'  CACCGCCTCCTACCCTTCTT   54901        C___    _
                                AGGAAGGG    AGGCG TG
                                ||||||||    ||||| ||
                                TTCTTCCC    TCCGC AC
                                    ATCC     C
GAM1226  LOC158476 3'  CACGCCCGCCCCCCCCATTGA  88186     _ AA_   A
                                TCAA GG   GGGC GGCGTG
                                |||| ||   |||| ||||||
                                AGTT CC   CCCG CCGCAC
                                  A CCC    C
GAM1226  LOC90459  3'  CACACCCGCCTAATTTTTG    63550       A_   A  C
                                CAAGGA  GGGC GG GTG
                                ||||||  |||| || |||
                                GTTTTT  TCCG CC CAC
                                   AA    C  A
GAM1227  A1BG      3'  AACTCCTGAGCTCAGGTGATCC 56274           G
           A                     TGGATCACCTGAG TCAGGAGTT
                                ||||||||||||| |||||||||
                                ACCTAGTGGACTC AGTCCTCAA
                                       G
GAM1227  ADAMTS4   3'  AACTCCTGACCTCAGGTAATC  18737     C
                                GAT ACCTGAGGTCAGGAGTT
                                ||| ||||||||||||||||
                                CTA TGGACTCCAGTCCTCAA
                                  A
GAM1227  ADAMTS4   3'  AACTCCTGACCTTAGGTGATCC 18738
           A                     TGGATCACCTGAGGTCAGGAGTT
                                ||||||||||||||||||||||
                                ACCTAGTGGATTCCAGTCCTCAA

GAM1227  ALDH1B1   3'  AACTCCTGACCTCAGGTGATCC 7311
           A                     TGGATCACCTGAGGTCAGGAGTT
                                ||||||||||||||||||||||
                                ACCTAGTGGACTCCAGTCCTCAA

GAM1227  APM1      3'  AAACTCCTGACTTTGTGATCCA 17747        CT
                                TGGATCAC  GAGGTCAGGAGTTT
                                ||||||||  ||||||||||||||
                                ACCTAGTG  TTTCAGTCCTCAAA
                                      __
GAM1227  AQP6      3'  CCTGACCCCAGATGCCCA    54997     AT  C   A
                                TGG  CA CTG GGTCAGG
                                |||  || ||| |||||||
                                ACC  GT GAC CCAGTCC
                                  C_  A   C
GAM1227  AQP6      3'  CCTGACCCCAGATGCCCA    9729      AT  C   A
                                TGG  CA CTG GGTCAGG
                                |||  || ||| |||||||
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                                ACC  GT GAC CCAGTCC
                                  C_  A  C
GAM1227  ARSF     5'  AACTCCCGACCTCAAGTGATCC 65206        C      A
                                GGATCAC TGAGGTC GGAGTT
                                ||||||| ||||||| ||||||
                                CCTAGTG ACTCCAG CCTCAA
                                    A      C
GAM1227  ATP1B2   3'  AACTCCCGACCTCAGGTGATCC 9821              A
            A                    TGGATCACCTGAGGTC GGAGTT
                                ||||||||||||||| ||||||
                                ACCTAGTGGACTCCAG CCTCAA
                                        C
GAM1227  ATP7A    3'  AAACTCCTAACCTCAGGTGATC 5306             C
            CA                    TGGATCACCTGAGGT AGGAGTTT
                                ||||||||||||||| ||||||||
                                ACCTAGTGGACTCCA TCCTCAAA
                                        A
GAM1227  AXL      3'  AAACTCCTGACCTCAAGTGATC 9894         C
            T                    GGATCAC TGAGGTCAGGAGTTT
                                ||||||| ||||||||||||||||
                                TCTAGTG ACTCCAGTCCTCAAA
                                    A
GAM1227  AXL      3'  AAACTCCTGACCTCAAGTGATC 41867        C
            T                    GGATCAC TGAGGTCAGGAGTTT
                                ||||||| ||||||||||||||||
                                TCTAGTG ACTCCAGTCCTCAAA
                                    A
GAM1227  C7       3'  AACTCCTGACCTCAGGTAATCC 6973       C
                                GGAT ACCTGAGGTCAGGAGTT
                                |||| ||||||||||||||||
                                CCTA TGGACTCCAGTCCTCAA
                                  A
GAM1227  CASP10   3'  AAACTCCTGGGCTCAAGCGATC 53209      ACC    G
            C                    GGATC   TGAG TCAGGAGTTT
                                |||||   |||| ||||||||||
                                CCTAG   ACTC GGTCCTCAAA
                                   CGA    G
GAM1227  CASP10   3'  AAACTCCTGGGCTCAAGCGATC 53232      ACC    G
            C                    GGATC   TGAG TCAGGAGTTT
                                |||||   |||| ||||||||||
                                CCTAG   ACTC GGTCCTCAAA
                                   CGA    G
GAM1227  CBFA2T2  3'  AAACCCCGGACCTCAGGTGATC 18695            A  A
            C                    GGATCACCTGAGGTC GG GTTT
                                |||||||||||||| || ||||
                                CCTAGTGGACTCCAG CC CAAA
                                        G  C
GAM1227  CDH1     3'  AAACTCCTGGCCTCAAGCAATC 16393      CACC
            C                    GGAT    TGAGGTCAGGAGTTT
                                ||||    ||||||||||||||||
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                                CCTA   ACTCCGGTCCTCAAA
                                  ACGA
GAM1227  CDH1     3'  AAACTCCTGGGCTCAAGTGATC 16394       C   G
             C                   GGATCAC TGAG TCAGGAGTTT
                                 ||||||| |||| ||||||||||
                                 CCTAGTG ACTC GGTCCTCAAA
                                    A   G
GAM1227  CHRNB4   3'  AACTCCTGACCTCAGATGACCC 7444     A  C
             A                   TGG TCA CTGAGGTCAGGAGTT
                                 ||| ||| ||||||||||||||
                                 ACC AGT GACTCCAGTCCTCAA
                                   C  A
GAM1227  COX15    3'  AACTCCTGACCTCAGGTAATCC 55274     C
                                 GGAT ACCTGAGGTCAGGAGTT
                                 |||| ||||||||||||||||
                                 CCTA TGGACTCCAGTCCTCAA
                                   A
GAM1227  CRTAP    3'  AACTCTTGACTTCAGATGATCC 22071       C
             A                   TGGATCA CTGAGGTCAGGAGTT
                                 ||||||| ||||||||||||||
                                 ACCTAGT GACTTCAGTTCTCAA
                                    A
GAM1227  CYP1A2   3'  AAACTCCTGACCTCAAGTGATC 7487        C
             T                   GGATCAC TGAGGTCAGGAGTTT
                                 ||||||| |||||||||||||||
                                 TCTAGTG ACTCCAGTCCTCAAA
                                    A
GAM1227  CYP1A2   3'  AACTCCTGACCCCAAGTTATCC 7491      C  C  A
             A                   TGGAT AC TG GGTCAGGAGTT
                                 ||||| || || ||||||||||
                                 ACCTA TG AC CCAGTCCTCAA
                                   T  A  C
GAM1227  CYP2B6   3'  CCTGGCCTCAGGTGATCCA   7558
                                 TGGATCACCTGAGGTCAGG
                                 |||||||||||||||||||
                                 ACCTAGTGGACTCCGGTCC

GAM1227  CYP4F3   3'  AACTCCTAACCTCAGGTGATCC 7987             C
             A                   TGGATCACCTGAGGT AGGAGTT
                                 |||||||||||||| |||||||
                                 ACCTAGTGGACTCCA TCCTCAA
                                          A
GAM1227  DFFB     3'  AAACTCCTGACCTCAGGTGATC 88744
             C                   GGATCACCTGAGGTCAGGAGTTT
                                 |||||||||||||||||||||||
                                 CCTAGTGGACTCCAGTCCTCAAA

GAM1227  DIAPH2   3'  AACTCCTAGCCTCAAGCAATCC 22998      CACC    TC
             A                   TGGAT   TGAGG  AGGAGTT
                                 |||||   |||||  |||||||
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                                ACCTA   ACTCC  TCCTCAA
                                  ACGA    GA
GAM1227  DISC1    3'  AAACTCCTGACCTCAGGCGATC 38492       A
             CA                   TGGATC CCTGAGGTCAGGAGTTT
                                  |||||| ||||||||||||||||
                                  ACCTAG GGACTCCAGTCCTCAAA
                                     C
GAM1227  EPB72    3'  AACTCCTAACCTCAGGTGATCC 15863             C
             A                    TGGATCACCTGAGGT AGGAGTT
                                  ||||||||||||||| |||||||
                                  ACCTAGTGGACTCCA TCCTCAA
                                           A
GAM1227  F3       3'  AATTCCTGACCTCAGTTGATCC 67670        C
             A                    TGGATCA CTGAGGTCAGGAGTT
                                  ||||||| ||||||||||||||
                                  ACCTAGT GACTCCAGTCCTTAA
                                     T
GAM1227  FCAR     3'  AACTCCTGACCTCAGGTGATCC 56600
             A                    TGGATCACCTGAGGTCAGGAGTT
                                  ||||||||||||||||||||||
                                  ACCTAGTGGACTCCAGTCCTCAA

GAM1227  FCAR     3'  AACTCCTGACCTCAGGTGATCC 56612
             A                    TGGATCACCTGAGGTCAGGAGTT
                                  ||||||||||||||||||||||
                                  ACCTAGTGGACTCCAGTCCTCAA

GAM1227  FCAR     3'  AACTCCCGACCTCAGGTGATCC 56625             A
             A                    TGGATCACCTGAGGTC GGAGTT
                                  |||||||||||||||| ||||||
                                  ACCTAGTGGACTCCAG CCTCAA
                                           C
GAM1227  FCAR     3'  AACTCCTGACCTCAGGTGATCC 56556
             A                    TGGATCACCTGAGGTCAGGAGTT
                                  ||||||||||||||||||||||
                                  ACCTAGTGGACTCCAGTCCTCAA

GAM1227  FCAR     3'  AACTCCTGACCTCAGGTGATCC 56588
             A                    TGGATCACCTGAGGTCAGGAGTT
                                  ||||||||||||||||||||||
                                  ACCTAGTGGACTCCAGTCCTCAA

GAM1227  FCAR     3'  AACTCCTGACCTCAGGTGATCC 10579
             A                    TGGATCACCTGAGGTCAGGAGTT
                                  ||||||||||||||||||||||
                                  ACCTAGTGGACTCCAGTCCTCAA

GAM1227  G6PC     3'  AACTCCTGACCTCAAGTGATCC 5646         C
             A                    TGGATCAC TGAGGTCAGGAGTT
                                  ||||||||| ||||||||||||||
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                                ACCTAGTG ACTCCAGTCCTCAA
                                    A
GAM1227  GLTSCR1   5'  AAACTCTTTGGCTCAAGCCATC 32299      CAC  GA     _
             CA                   TGGAT   CT  GGTCAG GAGTTT
                                  ||||||   ||  |||||| |||||||
                                  ACCTA   GA  TCGGTT CTCAAA
                                     CC_  AC     T
GAM1227  GNE      3'  AACTCCTGACCTCAGGTGATCC 19656
                                  GGATCACCTGAGGTCAGGAGTT
                                  ||||||||||||||||||||||
                                  CCTAGTGGACTCCAGTCCTCAA

GAM1227  GPR81    3'  CCTGACCTCAGGTGATCC    51745
                                  GGATCACCTGAGGTCAGG
                                  ||||||||||||||||||
                                  CCTAGTGGACTCCAGTCC

GAM1227  HCS      3'  AAACTCCTGAGCTCAAGCAATC 38953      CACC    G
             C                    GGAT    TGAG TCAGGAGTTT
                                  ||||    |||| ||||||||||
                                  CCTA    ACTC AGTCCTCAAA
                                    ACGA    G
GAM1227  IL11     3'  AACTCCTGACCTCAGGTGATCC 7169
                                  GGATCACCTGAGGTCAGGAGTT
                                  ||||||||||||||||||||||
                                  CCTAGTGGACTCCAGTCCTCAA

GAM1227  JAK3     3'  AACTCCTAACCTCAAGTGATCC 5818         C     C
                                  GGATCAC TGAGGT AGGAGTT
                                  ||||||| |||||| |||||||
                                  CCTAGTG ACTCCA TCCTCAA
                                      A     A
GAM1227  LNK      3'  TCTGACCTCAGGTGATCCA   19653
                                  TGGATCACCTGAGGTCAGG
                                  ||||||||||||||||||
                                  ACCTAGTGGACTCCAGTCT

GAM1227  LZTS1    3'  AAACTTGTGGCCTCAAGCAATC 41018      CACC       G
             CA                   TGGAT    TGAGGTCA GAGTTT
                                  |||||    |||||||| ||||||
                                  ACCTA    ACTCCGGT TTCAAA
                                     ACGA       G
GAM1227  MAK      3'  AAACTCCTGACCTCAGGTGATC 20931
             CA                   TGGATCACCTGAGGTCAGGAGTTT
                                  |||||||||||||||||||||||
                                  ACCTAGTGGACTCCAGTCCTCAAA

GAM1227  MEFV     3'  AAACTCCTGACCTCAGGTGATG 5913     G
             CA                   TG ATCACCTGAGGTCAGGAGTTT
                                  || ||||||||||||||||||||
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                                AC TAGTGGACTCCAGTCCTCAAA
                                 G
GAM1227  MEFV     3'  AACTCCTGACCTCAGGTGATCC 5916
                A                TGGATCACCTGAGGTCAGGAGTT
                                 ||||||||||||||||||||||
                                 ACCTAGTGGACTCCAGTCCTCAA

GAM1227  MHC2TA   3'  AACTCTTGACCTCGGGTGATCC 5963
                A                TGGATCACCTGAGGTCAGGAGTT
                                 ||||||||||||||||||||||
                                 ACCTAGTGGGCTCCAGTTCTCAA

GAM1227  MICB     3'  AAACTCCTGACCTCAGGTGATC 21014
                T                GGATCACCTGAGGTCAGGAGTTT
                                 |||||||||||||||||||||||
                                 TCTAGTGGACTCCAGTCCTCAAA

GAM1227  MLANA    3'  AAACTCCTGACCTCAGGTGATC 19751
                T                GGATCACCTGAGGTCAGGAGTTT
                                 |||||||||||||||||||||||
                                 TCTAGTGGACTCCAGTCCTCAAA

GAM1227  MPL      3'  AACTCCTAACCTCGGGTGATCC 19334          C
                A                TGGATCACCTGAGGT AGGAGTT
                                 |||||||||||||| |||||||
                                 ACCTAGTGGGCTCCA TCCTCAA
                                       A
GAM1227  MRPL49   3'  AAACTCCTGACTCGAAGTGATC 70153       CTGA
                C                GGATCAC   GGTCAGGAGTTT
                                 |||||||   ||||||||||||
                                 CCTAGTG   TCAGTCCTCAAA
                                    AAGC
GAM1227  MYCL2    3'  CCTGACCTAGGTGATCCA    19373         G
                                 TGGATCACCT AGGTCAGG
                                 |||||||||| ||||||||
                                 ACCTAGTGGA TCCAGTCC
                                           _
GAM1227  NCOA6    5'  AAACTCCTGACCTCAAGTGATC 26815        C
                CA                TGGATCAC TGAGGTCAGGAGTTT
                                  |||||||| ||||||||||||||
                                  ACCTAGTG ACTCCAGTCCTCAAA
                                     A
GAM1227  NDRG3    3'  AAACTCCTGACCTCAGGTGATC 50111
                CA                TGGATCACCTGAGGTCAGGAGTTT
                                  |||||||||||||||||||||||
                                  ACCTAGTGGACTCCAGTCCTCAAA

GAM1227  NQO1     3'  AAACTCCTGACCTCAGGTGATC 8035
                C                 GGATCACCTGAGGTCAGGAGTTT
                                  |||||||||||||||||||||||
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                                CCTAGTGGACTCCAGTCCTCAAA

GAM1227  NT5C2    5'  CCTGACGTCAAGTGATCCA   25262        C   G
                                TGGATCAC TGA GTCAGG
                                |||||||| ||| ||||||
                                ACCTAGTG ACT CAGTCC
                                     A   G
GAM1227  PDE6B    3'  AACTCCTGACCTCAGGTGATC  6067
                                GATCACCTGAGGTCAGGAGTT
                                ||||||||||||||||||||
                                CTAGTGGACTCCAGTCCTCAA

GAM1227  PER2     3'  AACTCCTGACCTCAAGCGATCC 43336       ACC
                A                TGGATC   TGAGGTCAGGAGTT
                                ||||||   ||||||||||||||
                                ACCTAG   ACTCCAGTCCTCAA
                                   CGA
GAM1227  PIK3CD   3'  AACTCCTGACCTCAGGTGATCC 18480
                A                TGGATCACCTGAGGTCAGGAGTT
                                ||||||||||||||||||||||||
                                ACCTAGTGGACTCCAGTCCTCAA

GAM1227  PPEF2    3'  AACTCCCAACCTCAGGTGATCC 21769             CA
                A                TGGATCACCTGAGGT  GGAGTT
                                ||||||||||||||  ||||||
                                ACCTAGTGGACTCCA  CCTCAA
                                      AC
GAM1227  PRKR     3'  AAACTCCTGACCTCAAGTAATC 12333      C  C
                CA                TGGAT AC TGAGGTCAGGAGTTT
                                ||||| || ||||||||||||||||
                                ACCTA TG ACTCCAGTCCTCAAA
                                   A  A
GAM1227  PRKWNK3  3'  AAACTCCTAACCTTGTGATCC  62220       CT    C
                                GGATCAC  GAGGT AGGAGTTT
                                |||||||  ||||| ||||||||
                                CCTAGTG  TTCCA TCCTCAAA
                                   __    A
GAM1227  PTGES    3'  AACTCCTGGCCTCAAGTGATCC 18049        C
                A                TGGATCAC TGAGGTCAGGAGTT
                                ||||||||| ||||||||||||||
                                ACCTAGTG ACTCCGGTCCTCAA
                                     A
GAM1227  RBBP9    3'  AACTCCTGGCCTCAAGTGATCC 70674        C
                A                TGGATCAC TGAGGTCAGGAGTT
                                ||||||||| ||||||||||||||
                                ACCTAGTG ACTCCGGTCCTCAA
                                     A
GAM1227  RGS9     5'  AAACTCCTGGGCTCAAGCGATC 15165      ACC   G
                C                GGATC   TGAG TCAGGAGTTT
                                |||||   |||| ||||||||||
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                                CCTAG   ACTC GGTCCTCAAA
                                   CGA    G
GAM1227  RHD      3'  AAACTCCTGACCTCAAGTGATC 32795         C
                T                   GGATCAC TGAGGTCAGGAGTTT
                                    ||||||| ||||||||||||||||
                                    TCTAGTG ACTCCAGTCCTCAAA
                                       A
GAM1227  RHD      3'  AAACTCCTGACCTCAAGTGATC 33125         C
                T                   GGATCAC TGAGGTCAGGAGTTT
                                    ||||||| ||||||||||||||||
                                    TCTAGTG ACTCCAGTCCTCAAA
                                       A
GAM1227  RP2      3'  AACTCCTGACCTCAGGTGATCC 23594
                                    GGATCACCTGAGGTCAGGAGTT
                                    ||||||||||||||||||||||
                                    CCTAGTGGACTCCAGTCCTCAA

GAM1227  SAS      3'  AACTCCTGACCTCAGGTGATCC 21089
                A                   TGGATCACCTGAGGTCAGGAGTT
                                    ||||||||||||||||||||||
                                    ACCTAGTGGACTCCAGTCCTCAA

GAM1227  SCML2    3'  AAACTCCTGACCTCAGGTGATC 21416
                C                   GGATCACCTGAGGTCAGGAGTTT
                                    ||||||||||||||||||||||
                                    CCTAGTGGACTCCAGTCCTCAAA

GAM1227  SEDL     3'  AAACTCCTGACCTCAGTTGATC 28060         C
                CA                    TGGATCA CTGAGGTCAGGAGTTT
                                    ||||||| ||||||||||||||||
                                    ACCTAGT GACTCCAGTCCTCAAA
                                       T
GAM1227  SEPN1    3'  AACTTCTGACCTCAGGTGATCC 66956
                A                   TGGATCACCTGAGGTCAGGAGTT
                                    ||||||||||||||||||||||
                                    ACCTAGTGGACTCCAGTCTTCAA

GAM1227  SHOX     3'  AAACTCCTGGGCTCAAGCAATC 23507      CACC    G
                C                   GGAT    TGAG TCAGGAGTTT
                                    ||||    |||| ||||||||||
                                    CCTA    ACTC GGTCCTCAAA
                                       ACGA    G
GAM1227  SHOX     3'  AACTCCTGACCTCAGGTGATCC 23509
                A                   TGGATCACCTGAGGTCAGGAGTT
                                    ||||||||||||||||||||||
                                    ACCTAGTGGACTCCAGTCCTCAA

GAM1227  SIL      3'  AAACTCCCGACCTCAGGTGATC 13146              A
                C                   GGATCACCTGAGGTC GGAGTTT
                                    |||||||||||||| |||||||
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                                CCTAGTGGACTCCAG CCTCAAA
                                        C
GAM1227 SIL      5'  TCCTGACTTCAGGTGATCCA  13164
                                TGGATCACCTGAGGTCAGGA
                                ||||||||||||||||||||
                                ACCTAGTGGACTTCAGTCCT

GAM1227 SLA2     3'  AACTCCTGACCTCAGGTGATCC 50876
                A                TGGATCACCTGAGGTCAGGAGTT
                                 ||||||||||||||||||||||||
                                 ACCTAGTGGACTCCAGTCCTCAA

GAM1227 SLC14A2  5'  AACTTCTGACGTCAAGTGATCC 24103        C  G
                A                TGGATCAC TGA GTCAGGAGTT
                                 |||||||| ||| ||||||||||
                                 ACCTAGTG ACT CAGTCTTCAA
                                      A  G
GAM1227 SMAC     5'  AATTCCTGACCTCAAGTGATCC 58010        C
                A                TGGATCAC TGAGGTCAGGAGTT
                                 |||||||| ||||||||||||||
                                 ACCTAGTG ACTCCAGTCCTTAA
                                      A
GAM1227 SNX15    3'  AACTCCTGACCTCAAGTGATCC 74111        C
                A                TGGATCAC TGAGGTCAGGAGTT
                                 |||||||| ||||||||||||||
                                 ACCTAGTG ACTCCAGTCCTCAA
                                      A
GAM1227 SPN      3'  AAACTCCTGACCTCAGGTGATC 13360
                TA                TGGATCACCTGAGGTCAGGAGTTT
                                  |||||||||||||||||||||||||
                                  ATCTAGTGGACTCCAGTCCTCAAA

GAM1227 SULT2B1  5'  AAACTCCTGACCTCAGGTGATC 17216
                CA                TGGATCACCTGAGGTCAGGAGTTT
                                  |||||||||||||||||||||||||
                                  ACCTAGTGGACTCCAGTCCTCAAA

GAM1227 TAT      3'  AAACTCCTGACCTCAGGCAATC 6241       CA
                T                 GGAT  CCTGAGGTCAGGAGTTT
                                  ||||  ||||||||||||||||
                                  TCTA  GGACTCCAGTCCTCAAA
                                    AC
GAM1227 TBXA2R   3'  AACTCCTGACCTCAGGTGATTC 8334
                A                 TGGATCACCTGAGGTCAGGAGTT
                                  |||||||||||||||||||||||
                                  ACTTAGTGGACTCCAGTCCTCAA

GAM1227 TES      3'  AAACTCCTGACCTCAGATGATC 72453       C
                C                 GGATCA CTGAGGTCAGGAGTTT
                                  ||||||| ||||||||||||||||
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                                CCTAGT GACTCCAGTCCTCAAA
                                   A
GAM1227  TMPRSS3   3'  AAACCCCTGACCTCAAATGAT  51505      CC         A
                                ATCA  TGAGGTCAGG GTTT
                                ||||  |||||||||| ||||
                                TAGT  ACTCCAGTCC CAAA
                                  AA         C
GAM1227  TMPRSS3   3'  AAACCCCTGACCTCAAATGAT  51533      CC         A
                                ATCA  TGAGGTCAGG GTTT
                                ||||  |||||||||| ||||
                                TAGT  ACTCCAGTCC CAAA
                                  AA         C
GAM1227  TMPRSS3   3'  AAACCCCTGACCTCAAATGAT  44007      CC         A
                                ATCA  TGAGGTCAGG GTTT
                                ||||  |||||||||| ||||
                                TAGT  ACTCCAGTCC CAAA
                                  AA         C
GAM1227  TNFRSF10B 3'  AACTCCTGACCTCAGGTGATCC 15207
            A                    TGGATCACCTGAGGTCAGGAGTT
                                 ||||||||||||||||||||||
                                 ACCTAGTGGACTCCAGTCCTCAA

GAM1227  TNFRSF10B 3'  CCTGACCTCAGGTGATCCA   15222
                                TGGATCACCTGAGGTCAGG
                                ||||||||||||||||||
                                ACCTAGTGGACTCCAGTCC

GAM1227  TP53      3'  AAACTCCTGGGCTCAGGCGATC 6788        A      G
            CA                    TGGATC CCTGAG TCAGGAGTTT
                                  |||||| |||||| ||||||||||
                                  ACCTAG GGACTC GGTCCTCAAA
                                     C      G
GAM1227  TPMT      3'  AGCTCCTGACCTCAGGTGATCT 6305
            A                     TGGATCACCTGAGGTCAGGAGTT
                                  |||||||||||||||||||||||
                                  ATCTAGTGGACTCCAGTCCTCGA

GAM1227  TRAF5     3'  AAACTCCTGACCTCAAGTGATC 17261         C
            T                     GGATCAC TGAGGTCAGGAGTTT
                                  ||||||| ||||||||||||||
                                  TCTAGTG ACTCCAGTCCTCAAA
                                     A
GAM1227  TRPM6     3'  AAACTCCTGACCTCAGATGATC 35016         C
            CA                    TGGATCA CTGAGGTCAGGAGTTT
                                  ||||||| ||||||||||||||||
                                  ACCTAGT GACTCCAGTCCTCAAA
                                     A
GAM1227  TRPV1     3'  AACTCCTGACCTCAGGTGATCC 38680
                                GGATCACCTGAGGTCAGGAGTT
                                ||||||||||||||||||||||
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                                CCTAGTGGACTCCAGTCCTCAA

GAM1227  TRPV1    3'  AACTCCTGACCTCAGGTGATCC 55645
                                GGATCACCTGAGGTCAGGAGTT
                                ||||||||||||||||||||||
                                CCTAGTGGACTCCAGTCCTCAA

GAM1227  TRPV1    3'  AACTCCTGACCTCAGGTGATCC 55696
                                GGATCACCTGAGGTCAGGAGTT
                                ||||||||||||||||||||||
                                CCTAGTGGACTCCAGTCCTCAA

GAM1227  TRPV1    3'  AACTCCTGACCTCAGGTGATCC 55727
                                GGATCACCTGAGGTCAGGAGTT
                                ||||||||||||||||||||||
                                CCTAGTGGACTCCAGTCCTCAA

GAM1227  TUFT1    3'  AATTCCTGACCTCAGGTGATCC 39663
                A                TGGATCACCTGAGGTCAGGAGTT
                                ||||||||||||||||||||||
                                ACCTAGTGGACTCCAGTCCTTAA

GAM1227  VENTX2   3'  AAACTCCTGACCCTGTGATCC  27847        CTGA
                                GGATCAC    GGTCAGGAGTTT
                                |||||||    ||||||||||||
                                CCTAGTG    CCAGTCCTCAAA
                                    TC__
GAM1227  VHL      3'  AAACTCCTGACCTCAGGTGATC 6811
                C                GGATCACCTGAGGTCAGGAGTTT
                                ||||||||||||||||||||||
                                CCTAGTGGACTCCAGTCCTCAAA

GAM1227  XRCC2    3'  AACTCCTGACCTCAAGTGATCC 19481         C
                A                TGGATCAC TGAGGTCAGGAGTT
                                ||||||||| ||||||||||||||
                                ACCTAGTG ACTCCAGTCCTCAA
                                    A
GAM1227  ZNF133   5'  AACTGCTGACCTCAGGTGATCC 14289               G
                A                TGGATCACCTGAGGTCAG AGTT
                                ||||||||||||||||| ||||
                                ACCTAGTGGACTCCAGTC TCAA
                                          G
GAM1227  ZNF157   3'  AACTCCTGACCTCAGGTGATCC 14318
                A                TGGATCACCTGAGGTCAGGAGTT
                                ||||||||||||||||||||||
                                ACCTAGTGGACTCCAGTCCTCAA

GAM1227  AAK1     3'  AACTCCTGACCTCAGGTGATCC 30508
                                GGATCACCTGAGGTCAGGAGTT
                                ||||||||||||||||||||||
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                                CCTAGTGGACTCCAGTCCTCAA

GAM1227 ARHGAP5  5' AACTCCCAACCTCAGGTGATCC 77591            CA
                                GGATCACCTGAGGT GGAGTT
                                |||||||||||||| ||||||
                                CCTAGTGGACTCCA CCTCAA
                                      AC
GAM1227 ASB16    3' CTGACCTCAGGTGATCCA    55982
                                TGGATCACCTGAGGTCAG
                                ||||||||||||||||||
                                ACCTAGTGGACTCCAGTC

GAM1227 ATP1B4   3' AACTCCTGACCTCAAGTGATCC 24827       C
                                GGATCAC TGAGGTCAGGAGTT
                                ||||||| ||||||||||||||
                                CCTAGTG ACTCCAGTCCTCAA
                                     A
GAM1227 BA108L7.2 3' AACTCCTGACCTCAGGTGATCC 49057
             A                   TGGATCACCTGAGGTCAGGAGTT
                                ||||||||||||||||||||||
                                ACCTAGTGGACTCCAGTCCTCAA

GAM1227 C13orf1  3' AAACTCCTGACCTCATGATCCA 40340       CC
                                TGGATCA  TGAGGTCAGGAGTTT
                                |||||||  ||||||||||||||
                                ACCTAGT  ACTCCAGTCCTCAAA
                                      __
GAM1227 C1QTNF6  3' AACTCCTGACTTCAGGTGACCC 49980     A
             A                   TGG TCACCTGAGGTCAGGAGTT
                                ||| ||||||||||||||||||
                                ACC AGTGGACTTCAGTCCTCAA
                                  C
GAM1227 C20orf142 3' AAACTCCTGACCGCAGGTGATC 75265          A
             CA                   TGGATCACCTG GGTCAGGAGTTT
                                |||||||||| ||||||||||
                                ACCTAGTGGAC CCAGTCCTCAAA
                                      G
GAM1227 C21orf25 3' AACTCCTGACCTCAGGTGATCC 64277
             A                   TGGATCACCTGAGGTCAGGAGTT
                                ||||||||||||||||||||||
                                ACCTAGTGGACTCCAGTCCTCAA

GAM1227 C3F      3' AACTCCTGACCGCAAGTGATCC 20470       C  A
             A                   TGGATCAC TG GGTCAGGAGTT
                                |||||||| || ||||||||||
                                ACCTAGTG AC CCAGTCCTCAA
                                     A  G
GAM1227 CARD6    3' AACTCCCGACCTCAGGTGATCC 51834            A
                                GGATCACCTGAGGTC GGAGTT
                                |||||||||||||| ||||||
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                                  CCTAGTGGACTCCAG CCTCAA
                                        C
GAM1227  CHRAC1    3'  AAACTCCTAACCTCAACTGATC 34323        CC      C
            CA                   TGGATCA  TGAGGT AGGAGTTT
                                 |||||||  ||||||| ||||||||
                                 ACCTAGT  ACTCCA TCCTCAAA
                                    CA     A
GAM1227  CIP29     3'  AACTCCTGAGCTCAGGTGATCC 51364             G
            A                    TGGATCACCTGAG TCAGGAGTT
                                 |||||||||||||| ||||||||
                                 ACCTAGTGGACTC AGTCCTCAA
                                       G
GAM1227  COLEC12   3'  AAACTTCTGGCCTCAAGTGATC 48601         C
            CA                   TGGATCAC TGAGGTCAGGAGTTT
                                 |||||||| ||||||||||||||||
                                 ACCTAGTG ACTCCGGTCTTCAAA
                                    A
GAM1227  CPSF2     3'  AAACTCCCGACCTCAGGTGATC 62250              A
            C                    GGATCACCTGAGGTC GGAGTTT
                                 |||||||||||||| |||||||
                                 CCTAGTGGACTCCAG CCTCAAA
                                       C
GAM1227  CPSF2     3'  AAACTCCTGACCTCAAGCGATC 62251        ACC
            CA                   TGGATC   TGAGGTCAGGAGTTT
                                 ||||||   ||||||||||||||||
                                 ACCTAG   ACTCCAGTCCTCAAA
                                    CGA
GAM1227  DBR1      3'  AACTCCTGACCTCAGGCGATCC 33054       A
            A                    TGGATC CCTGAGGTCAGGAGTT
                                 |||||| ||||||||||||||||
                                 ACCTAG GGACTCCAGTCCTCAA
                                    C
GAM1227  DCOHM     3'  AAACTCCTGGCCTCAAGTGATC 50502        C
            C                    GGATCAC TGAGGTCAGGAGTTT
                                 ||||||| ||||||||||||||||
                                 CCTAGTG ACTCCGGTCCTCAAA
                                    A
GAM1227  DKFZp434A2417 3'  AAACTCCCAACCTCAGGTGATC 66670             CA
            T                    GGATCACCTGAGGT  GGAGTTT
                                 ||||||||||||||  |||||||
                                 TCTAGTGGACTCCA  CCTCAAA
                                       AC
GAM1227  DKFZP434B044 3'  AACTCCTTACCTCAGGTGATCC 49705             C
            A                    TGGATCACCTGAGGT AGGAGTT
                                 |||||||||||||||| |||||||
                                 ACCTAGTGGACTCCA TCCTCAA
                                       T
GAM1227  DKFZP434D146 3'  AACTCCTGCCCTCAAGTGATCC 32128         C    T
            A                    TGGATCAC TGAGG CAGGAGTT
                                 |||||||| ||||| ||||||||
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                                ACCTAGTG ACTCC GTCCTCAA
                                    A    C
GAM1227  DKFZP434J037 3'  AAACTCCCGACCTCAGGTGATC 48932              A
           CA                    TGGATCACCTGAGGTC GGAGTTT
                                 ||||||||||||||| |||||||
                                 ACCTAGTGGACTCCAG CCTCAAA
                                       C
GAM1227  DKFZp547H025 3'  AAACTCTTGACTTCAAGTGATC 39760        C
           CA                    TGGATCAC TGAGGTCAGGAGTTT
                                 |||||||| ||||||||||||||
                                 ACCTAGTG ACTTCAGTTCTCAAA
                                    A
GAM1227  DKFZP564K0322 3'  AAACTTCTGGCCTCAAGTGATC 50182       C
           C                     GGATCAC TGAGGTCAGGAGTTT
                                 ||||||| ||||||||||||||
                                 CCTAGTG ACTCCGGTCTTCAAA
                                    A
GAM1227  DKFZP564O0423 3'  AAACTCCTGGCCTCAGGCGATC 93333       A
           CA                    TGGATC CCTGAGGTCAGGAGTTT
                                 |||||| ||||||||||||||||
                                 ACCTAG GGACTCCGGTCCTCAAA
                                   C
GAM1227  DSCR6    3'  AACTCCTGACCTCAGGTGATCC 39051
           A                     TGGATCACCTGAGGTCAGGAGTT
                                 |||||||||||||||||||||
                                 ACCTAGTGGACTCCAGTCCTCAA

GAM1227  EVI5     3'  AAACTTCTGACCTCAGGTGATC 20184
           CA                    TGGATCACCTGAGGTCAGGAGTTT
                                 |||||||||||||||||||||||
                                 ACCTAGTGGACTCCAGTCTTCAAA

GAM1227  EVI5     3'  AACTCCTAACCTCAAGTGATCC 20185        C     C
           A                     TGGATCAC TGAGGT AGGAGTT
                                 |||||||| |||||| |||||||
                                 ACCTAGTG ACTCCA TCCTCAA
                                    A     A
GAM1227  FBP17    3'  AAACTCCTGACCTCAGGTGATC 73136
           C                     GGATCACCTGAGGTCAGGAGTTT
                                 |||||||||||||||||||||||
                                 CCTAGTGGACTCCAGTCCTCAAA

GAM1227  FER1L4   3'  AACCCCTGACCTCAAGTGATCC 48102         C        A
           A                     TGGATCAC TGAGGTCAGG GTT
                                 |||||||| |||||||||| |||
                                 ACCTAGTG ACTCCAGTCC CAA
                                    A        C
GAM1227  FLJ10232  3'  AACTCCTGACCTCAGGTGATCC 36369
           A                     TGGATCACCTGAGGTCAGGAGTT
                                 |||||||||||||||||||||||
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                                ACCTAGTGGACTCCAGTCCTCAA

GAM1227  FLJ10298  3'  AAACTCCTGACCTAGTGATCCA 36447        CTG
                                TGGATCAC   AGGTCAGGAGTTT
                                ||||||||   ||||||||||||||
                                ACCTAGTG   TCCAGTCCTCAAA
                                    A__
GAM1227  FLJ10607  3'  AAACTCCTGAGCTCAAGTGATC 77617        C    G
                C                GGATCAC TGAG TCAGGAGTTT
                                 ||||||| |||| ||||||||||
                                 CCTAGTG ACTC AGTCCTCAAA
                                    A    G
GAM1227  FLJ10713  3'  AAACTCCTGGACTCAAGTGATC 36991       C    GT
                                 GATCAC TGAG  CAGGAGTTT
                                 |||||| ||||  |||||||||
                                 CTAGTG ACTC  GTCCTCAAA
                                    A    AG
GAM1227  FLJ10718  3'  AAACTCTTAGGCTCAGGCGATC 37024      A     G  _
                C                GGATC CCTGAG TC AGGAGTTT
                                 |||||| |||||| || |||||||||
                                 CCTAG GGACTC GG TTCTCAAA
                                   C     _  A
GAM1227  FLJ10901  3'  AACTCCTGACCTCAAGTGATCC 37348         C
                A                TGGATCAC TGAGGTCAGGAGTT
                                 |||||||| ||||||||||||||
                                 ACCTAGTG ACTCCAGTCCTCAA
                                    A
GAM1227  FLJ11193  3'  AAACTCCTGGGCACAAGCAATC 37741      CAC  GAG  _
                CA                 TGGAT   CT   GTC AGGAGTTT
                                   |||||   ||   ||| ||||||||
                                   ACCTA   GA   CGG TCCTCAAA
                                     AC_  ACA   G
GAM1227  FLJ12363  3'  AAACTCCTGACCTCAGGTGATC 50621
                T                GGATCACCTGAGGTCAGGAGTTT
                                 ||||||||||||||||||||||||
                                 TCTAGTGGACTCCAGTCCTCAAA

GAM1227  FLJ12668  3'  AAACTCCTGACCTCAGGGGATC 47150       A
                CA                 TGGATC CCTGAGGTCAGGAGTTT
                                   |||||| ||||||||||||||||
                                   ACCTAG GGACTCCAGTCCTCAAA
                                      G
GAM1227  FLJ12687  3'  AAACTCCTGACCTCAAGTGATC 46735        C
                CA                 TGGATCAC TGAGGTCAGGAGTTT
                                   |||||||| ||||||||||||||
                                   ACCTAGTG ACTCCAGTCCTCAAA
                                      A
GAM1227  FLJ12747  3'  CCCGACCTCAGGTGATCC    50664           A
                                   GGATCACCTGAGGTC GG
                                   ||||||||||||||| ||
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                                CCTAGTGGACTCCAG CC
                                        C
GAM1227  FLJ12787  3'  AAACTCCTGACCTCAAGTGATC 50684        C
              TA                  TGGATCAC TGAGGTCAGGAGTTT
                                  |||||||| ||||||||||||||||
                                  ATCTAGTG ACTCCAGTCCTCAAA
                                      A
GAM1227  FLJ13072  5'  AACTCCTGACCTCAGGTAATCC 91377      C
                                  GGAT ACCTGAGGTCAGGAGTT
                                  |||| ||||||||||||||||||
                                  CCTA TGGACTCCAGTCCTCAA
                                    A
GAM1227  FLJ13197  3'  AACTCCTGACCTCAAGTGATCC 45168        C
              A                   TGGATCAC TGAGGTCAGGAGTT
                                  |||||||| ||||||||||||||||
                                  ACCTAGTG ACTCCAGTCCTCAA
                                      A
GAM1227  FLJ13305  5'  CCTGACCTCAAGTGACCCA   91708    A   C
                                  TGG TCAC TGAGGTCAGG
                                  ||| |||| ||||||||||
                                  ACC AGTG ACTCCAGTCC
                                    C   A
GAM1227  FLJ13590  5'  AACTCCTGACCTCAAGTGATCC 46201        C
                                  GGATCAC TGAGGTCAGGAGTT
                                  ||||||| |||||||||||||||
                                  CCTAGTG ACTCCAGTCCTCAA
                                      A
GAM1227  FLJ13952  3'  CCTGACGTCAGGTGATCCA   46011          G
                                  TGGATCACCTGA GTCAGG
                                  |||||||||||| ||||||
                                  ACCTAGTGGACT CAGTCC
                                         G
GAM1227  FLJ14950  3'  AACTCCTGACCGCAGGTAATCC 52775      C    A
              A                   TGGAT ACCTG GGTCAGGAGTT
                                  ||||| ||||| ||||||||||
                                  ACCTA TGGAC CCAGTCCTCAA
                                    A   G
GAM1227  FLJ14957  3'  AACTCCTGACCTCAGGTGATCC 52802
              A                   TGGATCACCTGAGGTCAGGAGTT
                                  ||||||||||||||||||||||
                                  ACCTAGTGGACTCCAGTCCTCAA

GAM1227  FLJ20034  3'  AAACTCCCGACCTCAGGTGATC 34825            A
              C                   GGATCACCTGAGGTC GGAGTTT
                                  |||||||||||||| |||||||
                                  CCTAGTGGACTCCAG CCTCAAA
                                         C
GAM1227  FLJ20344  3'  AACTCCTGACCTCAAGTGATCC 35471        C
                                  GGATCAC TGAGGTCAGGAGTT
                                  ||||||| ||||||||||||||
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                                CCTAGTG ACTCCAGTCCTCAA
                                    A
GAM1227  FLJ20452  3'  AACTCCTGACCTCAGGTGATCC 35640
              A                  TGGATCACCTGAGGTCAGGAGTT
                                 ||||||||||||||||||||||
                                 ACCTAGTGGACTCCAGTCCTCAA

GAM1227  FLJ20507  3'  AACTCCTAACCTCAGGTTATCC 35725      C       C
              A                  TGGAT ACCTGAGGT AGGAGTT
                                 ||||| ||||||||| |||||||
                                 ACCTA TGGACTCCA TCCTCAA
                                    T       A
GAM1227  FLJ20507  3'  AACTCCTAACCTCAGGTTATCC 60835      C       C
              A                  TGGAT ACCTGAGGT AGGAGTT
                                 ||||| ||||||||| |||||||
                                 ACCTA TGGACTCCA TCCTCAA
                                    T       A
GAM1227  FLJ20671  3'  AACTGCTGGCCTCAAGCGATCC 35930       ACC       G
              A                  TGGATC   TGAGGTCAG AGTT
                                 ||||||   ||||||||| ||||
                                 ACCTAG   ACTCCGGTC TCAA
                                    CGA       G
GAM1227  FLJ20813  3'  AAACTCCTGACCTCATGATCCA 36122       CC
                                 TGGATCA  TGAGGTCAGGAGTTT
                                 |||||||  |||||||||||||||
                                 ACCTAGT  ACTCCAGTCCTCAAA
                                    __
GAM1227  FLJ21324  5'  AAACTCCTGACCTCAAGTGATC 92835       C
              T                  GGATCAC TGAGGTCAGGAGTTT
                                 ||||||| |||||||||||||||
                                 TCTAGTG ACTCCAGTCCTCAAA
                                    A
GAM1227  FLJ21459  3'  AACTCCTGACCTCAGGTGATCC 44798
                                 GGATCACCTGAGGTCAGGAGTT
                                 ||||||||||||||||||||||
                                 CCTAGTGGACTCCAGTCCTCAA

GAM1227  FLJ22002  3'  AACCTCTGACCTCAGGTGATCC 46188              GA
              A                  TGGATCACCTGAGGTCAG  GTT
                                 ||||||||||||||||  |||
                                 ACCTAGTGGACTCCAGTC  CAA
                                       TC
GAM1227  FLJ22625  3'  AAACTGCTGACTTCAGGTGATC 45583              G
              CA                   TGGATCACCTGAGGTCAG AGTTT
                                 |||||||||||||||| |||||
                                 ACCTAGTGGACTTCAGTC TCAAA
                                       G
GAM1227  FLJ22684  3'  AAACTCCTGACCTCAGGTGATC 47458
              C                  GGATCACCTGAGGTCAGGAGTTT
                                 |||||||||||||||||||||||
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                                CCTAGTGGACTCCAGTCCTCAAA

GAM1227  FLJ23563  3'  CCTGACCTCAGGTGATCC    68214
                                GGATCACCTGAGGTCAGG
                                ||||||||||||||||||
                                CCTAGTGGACTCCAGTCC

GAM1227  FLJ30532  3'  AAGCTCCTGACCTCAGATGATC 59211        C
                TA                  TGGATCA CTGAGGTCAGGAGTTT
                                ||||||| ||||||||||||||||
                                ATCTAGT GACTCCAGTCCTCGAA
                                    A
GAM1227  FLJ32865  3'  AAACCCCTGACCTCAGGCAATC 58791      CA          A
                T                   GGAT  CCTGAGGTCAGG GTTT
                                ||||  |||||||||||| ||||
                                TCTA  GGACTCCAGTCC CAAA
                                  AC          C
GAM1227  GAL3ST-4  3'  AACTCCTCACCTCAGGTGATCC 45272              C
                A                   TGGATCACCTGAGGT AGGAGTT
                                |||||||||||||| |||||||
                                ACCTAGTGGACTCCA TCCTCAA
                                          C
GAM1227  GGA2      3'  AACTCCTGACCTCAGGTGATCC 57644
                                GGATCACCTGAGGTCAGGAGTT
                                ||||||||||||||||||||||
                                CCTAGTGGACTCCAGTCCTCAA

GAM1227  GGA2      3'  AACTCCTGACCTCAGGTGATCC 31150
                                GGATCACCTGAGGTCAGGAGTT
                                ||||||||||||||||||||||
                                CCTAGTGGACTCCAGTCCTCAA

GAM1227  GMPPB     5'  AATTCCTGACCTCAGGTGATCC 97427
                A                   TGGATCACCTGAGGTCAGGAGTT
                                ||||||||||||||||||||||
                                ACCTAGTGGACTCCAGTCCTTAA

GAM1227  GNG4      3'  AAACTCCTGACCTCGTGATCCA 16832         CT
                                TGGATCAC  GAGGTCAGGAGTTT
                                ||||||||  ||||||||||||||
                                ACCTAGTG  CTCCAGTCCTCAAA
                                          —
GAM1227  H2AV      3'  AAACTCCTGACCTCAGGCGATC 57622       A
                C                   GGATC CCTGAGGTCAGGAGTTT
                                |||||| ||||||||||||||||
                                CCTAG GGACTCCAGTCCTCAAA
                                  C
GAM1227  HRH4      3'  AAACTCCTGGGCTGAAACAATC 41516      CACCTG  G
                C                   GGAT     AG TCAGGAGTTT
                                ||||     || ||||||||||
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                                CCTA     TC GGTCCTCAAA
                                  ACAAAG  G
GAM1227  HSMPP8   3'  AACTCCTGACCTCAGGTGATCC 95121
                                GGATCACCTGAGGTCAGGAGTT
                                ||||||||||||||||||||||
                                CCTAGTGGACTCCAGTCCTCAA

GAM1227  JAM1     3'  AAACTCCTGACCTCTTGATCC  58500       CCT
                                GGATCA   GAGGTCAGGAGTTT
                                ||||||   |||||||||||||||
                                CCTAGT   CTCCAGTCCTCAAA
                                   T__
GAM1227  JAM1     3'  AAACTCCTGACCTCTTGATCC  58528       CCT
                                GGATCA   GAGGTCAGGAGTTT
                                ||||||   |||||||||||||||
                                CCTAGT   CTCCAGTCCTCAAA
                                   T__
GAM1227  JAM1     3'  AAACTCCTGACCTCTTGATCC  58555       CCT
                                GGATCA   GAGGTCAGGAGTTT
                                ||||||   |||||||||||||||
                                CCTAGT   CTCCAGTCCTCAAA
                                   T__
GAM1227  JAM1     3'  AAACTCCTGACCTCTTGATCC  34204       CCT
                                GGATCA   GAGGTCAGGAGTTT
                                ||||||   |||||||||||||||
                                CCTAGT   CTCCAGTCCTCAAA
                                   T__
GAM1227  KIAA0022 3'  AAACTCCTGACCTCAAGTGATC 30270         C
              CA                  TGGATCAC TGAGGTCAGGAGTTT
                                ||||||||| ||||||||||||||||
                                ACCTAGTG ACTCCAGTCCTCAAA
                                    A
GAM1227  KIAA0063 3'  AAACTCCCGACCTCAAGTGATC 30242         C       A
              T                   GGATCAC TGAGGTC GGAGTTT
                                ||||||| ||||||| |||||||
                                TCTAGTG ACTCCAG CCTCAAA
                                    A      C
GAM1227  KIAA0161 3'  AAACTCCTGACCTCAGGTGATC 29182
              T                   GGATCACCTGAGGTCAGGAGTTT
                                ||||||||||||||||||||||||
                                TCTAGTGGACTCCAGTCCTCAAA

GAM1227  KIAA0186 3'  AAACTCCTGACCTCAAGTGACC 41088     A    C
              CA                  TGG TCAC TGAGGTCAGGAGTTT
                                ||| |||| ||||||||||||||||
                                ACC AGTG ACTCCAGTCCTCAAA
                                  C    A
GAM1227  KIAA0186 3'  CCTGACCTCAAGTGACCCA    41104     A    C
                                TGG TCAC TGAGGTCAGG
                                ||| |||| ||||||||||
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                                ACC AGTG ACTCCAGTCC
                                  C    A
GAM1227  KIAA0210  5'  AACTGCTGACCTCAAGTAATCC 29141      C  C        G
                                GGAT AC TGAGGTCAG AGTT
                                |||| || ||||||||| ||||
                                CCTA TG ACTCCAGTC TCAA
                                  A  A        G
GAM1227  KIAA0391  3'  AAACTCCTGACCTCAGGTGATC 28593
                CA                TGGATCACCTGAGGTCAGGAGTTT
                                |||||||||||||||||||||||
                                ACCTAGTGGACTCCAGTCCTCAAA

GAM1227  KIAA0475  3'  ACTCCTGACCCCAGGTGATCCA 30107           A
                                TGGATCACCTG GGTCAGGAGT
                                |||||||||| |||||||||
                                ACCTAGTGGAC CCAGTCCTCA
                                       C
GAM1227  KIAA0513  5'  AACTCCTGACCTCAGGTGAGCC 29002     A
                A                TGG TCACCTGAGGTCAGGAGTT
                                ||| ||||||||||||||||||
                                ACC AGTGGACTCCAGTCCTCAA
                                  G
GAM1227  KIAA0513  3'  AACTCCTGACCTCAGGTGATCC 29003
                                GGATCACCTGAGGTCAGGAGTT
                                |||||||||||||||||||||
                                CCTAGTGGACTCCAGTCCTCAA

GAM1227  KIAA0544  3'  AACTCCTAAGGTCATCCA    71453       C    GAGGTC
                                TGGAT ACCT     AGGAGTT
                                ||||| ||||     |||||||
                                ACCTA TGGA     TCCTCAA
                                  C    A_____
GAM1227  KIAA0562  3'  AAACTCCTGACCTTGTGATCCA 28808         CT
                                TGGATCAC  GAGGTCAGGAGTTT
                                ||||||||  ||||||||||||||
                                ACCTAGTG  TTCCAGTCCTCAAA
                                          __
GAM1227  KIAA0599  3'  AACTTCTGACCTCAGGTGATCC 77682
                A                TGGATCACCTGAGGTCAGGAGTT
                                |||||||||||||||||||||||
                                ACCTAGTGGACTCCAGTCTTCAA

GAM1227  KIAA0682  3'  AACTCCCAACCTCAAGTGATCC 30004         C     CA
                A                TGGATCAC TGAGGT  GGAGTT
                                |||||||| ||||||  ||||||
                                ACCTAGTG ACTCCA  CCTCAA
                                     A     AC
GAM1227  KIAA0682  3'  AATTCCTGACCTCAAGTGATCC 30005         C
                A                TGGATCAC TGAGGTCAGGAGTT
                                |||||||| ||||||||||||||
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                                ACCTAGTG ACTCCAGTCCTTAA
                                    A
GAM1227  KIAA0828  3'  AAACTCCTGGGCTCAAGCAATC 82105     CACC    G
             C                   GGAT    TGAG TCAGGAGTTT
                                 ||||    |||| ||||||||||
                                 CCTA    ACTC GGTCCTCAAA
                                   ACGA    G
GAM1227  KIAA0889  3'  AACTCCCGACCTCAAGTGATCC 31744       C      A
                                 GGATCAC TGAGGTC GGAGTT
                                 |||||||| ||||||| ||||||
                                 CCTAGTG ACTCCAG CCTCAA
                                    A      C
GAM1227  KIAA0931  3'  AACTCTTGACCTCAGGTGATCC 67997
             A                   TGGATCACCTGAGGTCAGGAGTT
                                 ||||||||||||||||||||||
                                 ACCTAGTGGACTCCAGTTCTCAA

GAM1227  KIAA0961  3'  AACTCCTGACCTCAGGTGATCC 30381
             A                   TGGATCACCTGAGGTCAGGAGTT
                                 ||||||||||||||||||||||
                                 ACCTAGTGGACTCCAGTCCTCAA

GAM1227  KIAA1128  3'  AACTCCTGACCTCAAGTGATCC 68992        C
             A                   TGGATCAC TGAGGTCAGGAGTT
                                 |||||||| ||||||||||||||
                                 ACCTAGTG ACTCCAGTCCTCAA
                                    A
GAM1227  KIAA1161  5'  AAACTCCTGACCTAGTGATGCA 82632    G    CTG
                                 TG ATCAC   AGGTCAGGAGTTT
                                 || |||||   |||||||||||||
                                 AC TAGTG   TCCAGTCCTCAAA
                                  G    A__
GAM1227  KIAA1170  3'  AAACTCCTGACCTCAGGTGATC 70400
             C                   GGATCACCTGAGGTCAGGAGTTT
                                 |||||||||||||||||||||||
                                 CCTAGTGGACTCCAGTCCTCAAA

GAM1227  KIAA1198  3'  AAACTCCTGACCTCAGGTGATC 63964
             T                   GGATCACCTGAGGTCAGGAGTTT
                                 |||||||||||||||||||||||
                                 TCTAGTGGACTCCAGTCCTCAAA

GAM1227  KIAA1198  3'  AAACTCTTGACCTCAAATGATC 63965        CC
             CA                    TGGATCA  TGAGGTCAGGAGTTT
                                 |||||||  ||||||||||||||
                                 ACCTAGT  ACTCCAGTTCTCAAA
                                    AA
GAM1227  KIAA1198  3'  AACTCCTGACCTCAGGTAATCC 63969      C
             A                   TGGAT ACCTGAGGTCAGGAGTT
                                 ||||| ||||||||||||||||
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                                ACCTA TGGACTCCAGTCCTCAA
                                   A
GAM1227  KIAA1243  3'  CTTGACCTCAAGTAACCA    74025     ATC  C
                                TGG   AC TGAGGTCAGG
                                |||   || ||||||||||
                                ACC   TG ACTCCAGTTC
                                  AA_  A
GAM1227  KIAA1254  3'  TCCTGACCTCAAGTGATCCA   70567         C
                                TGGATCAC TGAGGTCAGGA
                                |||||||| ||||||||||
                                ACCTAGTG ACTCCAGTCCT
                                     A
GAM1227  KIAA1257  3'  AAACTCCCGACTTCAGGTGATC 63379              A
            C                    GGATCACCTGAGGTC GGAGTTT
                                |||||||||||||| |||||||
                                CCTAGTGGACTTCAG CCTCAAA
                                        C
GAM1227  KIAA1257  3'  AAACTCCTGGTCACAAGTAATC 63380      C  C  A GT
            C                    GGAT AC TG G  CAGGAGTTT
                                |||| || || |  |||||||||
                                CCTA TG AC C  GTCCTCAAA
                                  A  A  A TG
GAM1227  KIAA1320  5'  AATTCCTGACCTCAAGTGATCT 69829         C
            A                    TGGATCAC TGAGGTCAGGAGTT
                                |||||||| ||||||||||||||
                                ATCTAGTG ACTCCAGTCCTTAA
                                     A
GAM1227  KIAA1396  3'  AAACTCCTGTGCTCAAGTGACC 63665    A    C    GT
            C                    GG TCAC TGAG  CAGGAGTTT
                                || |||| ||||  |||||||||
                                CC AGTG ACTC  GTCCTCAAA
                                 C    A    GT
GAM1227  KIAA1465  3'  CTCTTGACCTCAGGTGATCCA  61493
                                TGGATCACCTGAGGTCAGGAG
                                |||||||||||||||||||||
                                ACCTAGTGGACTCCAGTTCTC

GAM1227  KIAA1467  3'  AACTCCTGACCTCAGATAATCC 72053       CAC
            A                    TGGAT   CTGAGGTCAGGAGTT
                                |||||   ||||||||||||||||
                                ACCTA   GACTCCAGTCCTCAA
                                   ATA
GAM1227  KIAA1493  3'  AAACTCCTGACCTCAGGTGATC 64826
            CA                    TGGATCACCTGAGGTCAGGAGTTT
                                |||||||||||||||||||||||||
                                ACCTAGTGGACTCCAGTCCTCAAA

GAM1227  KIAA1508  3'  AACTCCTGACCTCAGGTAATCC 62531       C
            A                    TGGAT ACCTGAGGTCAGGAGTT
                                ||||| ||||||||||||||||
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                                ACCTA TGGACTCCAGTCCTCAA
                                  A
GAM1227  KIAA1615  3'  AAACTCCCGACCTCAGGTGATC 69259              A
             CA                   TGGATCACCTGAGGTC GGAGTTT
                                  ||||||||||||||| |||||||
                                  ACCTAGTGGACTCCAG CCTCAAA
                                        C
GAM1227  KIAA1655  3'  AAACTCCTGACCTCCAGTGATC 67165         CT
             CA                   TGGATCAC  GAGGTCAGGAGTTT
                                  ||||||||  ||||||||||||||
                                  ACCTAGTG  CTCCAGTCCTCAAA
                                     AC
GAM1227  KIAA1712  3'  AAACTCCTGACCTCAGGTGATC 68141
             T                    GGATCACCTGAGGTCAGGAGTTT
                                  ||||||||||||||||||||||
                                  TCTAGTGGACTCCAGTCCTCAAA

GAM1227  KIAA1755  3'  AAACTCCTGGGCTCAAGTGATC 62001         C    G
             C                    GGATCAC TGAG TCAGGAGTTT
                                  ||||||| |||| ||||||||||
                                  CCTAGTG ACTC GGTCCTCAAA
                                     A    G
GAM1227  KIAA1821  3'  AGCTGCTGACCTCAAGTGATCC 72258         C        G
                                  GGATCAC TGAGGTCAG AGTT
                                  ||||||| ||||||||| ||||
                                  CCTAGTG ACTCCAGTC TCGA
                                     A        G
GAM1227  KIAA1922  5'  AACTCCTGACCTCAGGTGATCC 73978
                                  GGATCACCTGAGGTCAGGAGTT
                                  ||||||||||||||||||||||
                                  CCTAGTGGACTCCAGTCCTCAA

GAM1227  KIAA1987  5'  AACTTCTGACCTCAGGTGATCC 89375
             A                    TGGATCACCTGAGGTCAGGAGTT
                                  ||||||||||||||||||||||
                                  ACCTAGTGGACTCCAGTCTTCAA

GAM1227  KLK7      3'  AACGCCTGACCTCAGATGATCC 18533         C         A
             A                    TGGATCA CTGAGGTCAGG GTT
                                  ||||||| |||||||||| |||
                                  ACCTAGT GACTCCAGTCC CAA
                                     A         G
GAM1227  KLK7      3'  AACGCCTGACCTCAGATGATCC 58382         C         A
             A                    TGGATCA CTGAGGTCAGG GTT
                                  ||||||| |||||||||| |||
                                  ACCTAGT GACTCCAGTCC CAA
                                     A         G
GAM1227  LAMP3     3'  AACTCTTGACCTCAGGTGATCC 60189
             A                    TGGATCACCTGAGGTCAGGAGTT
                                  ||||||||||||||||||||||
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                                ACCTAGTGGACTCCAGTTCTCAA

GAM1227 MAP-1    3' AACTCCTGACCTCAAGTGATCC 42427         C
             A                   TGGATCAC TGAGGTCAGGAGTT
                                 |||||||| ||||||||||||||
                                 ACCTAGTG ACTCCAGTCCTCAA
                                      A
GAM1227 MCLC     3' AACTCCTGACCTCAAGTGACCC 31372    A    C
                                 GG TCAC TGAGGTCAGGAGTT
                                 || |||| ||||||||||||||
                                 CC AGTG ACTCCAGTCCTCAA
                                  C    A
GAM1227 MCM10    3' AAACTCCTGAGCACTAGCAATC 38170      CAC   AG _
             CA                    TGGAT   CTG  G TCAGGAGTTT
                                   |||||   |||  | ||||||||||
                                   ACCTA   GAT  C AGTCCTCAAA
                                      AC_   CA G
GAM1227 MEF-2    3' AAACTCCTGACCTCGTGATCCA 65010         CT
                                 TGGATCAC  GAGGTCAGGAGTTT
                                 ||||||||  ||||||||||||||
                                 ACCTAGTG  CTCCAGTCCTCAAA
                                           __
GAM1227 MGC10200 3' AGCTCCTGAGCTCAAACAATCC 59634      CACC    G
             A                   TGGAT    TGAG TCAGGAGTT
                                 |||||    |||| |||||||||
                                 ACCTA    ACTC AGTCCTCGA
                                    ACAA    G
GAM1227 MGC11386 3' AAACTCCTGGGCTCAAGCAATC 53048     CACC    G
             C                    GGAT    TGAG TCAGGAGTTT
                                  ||||    |||| ||||||||||
                                  CCTA    ACTC GGTCCTCAAA
                                    ACGA    G
GAM1227 MGC1842  3' AACCCCTGAGCTCAGGTGATCC 66242            G     A
             A                   TGGATCACCTGAG TCAGG GTT
                                 |||||||||||| ||||| |||
                                 ACCTAGTGGACTC AGTCC CAA
                                        G     C
GAM1227 MGC21675 3' AACTCCTGACCTCAGGTGATCC 54576
             A                   TGGATCACCTGAGGTCAGGAGTT
                                 |||||||||||||||||||||||
                                 ACCTAGTGGACTCCAGTCCTCAA

GAM1227 MGC21738 3' AACTCCTGACCTCAAGTGATCC 59573        C
                                 GGATCAC TGAGGTCAGGAGTT
                                 ||||||| ||||||||||||||
                                 CCTAGTG ACTCCAGTCCTCAA
                                      A
GAM1227 MGC2474  3' AACTCCTGCCCTCAGGTGATCC 43942             T
             A                   TGGATCACCTGAGG CAGGAGTT
                                 |||||||||||||| ||||||||
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                                ACCTAGTGGACTCC GTCCTCAA
                                       C
GAM1227  MKRN4     3'  AACTCCTGACCTCAGGTGATCC 48444
              A                 TGGATCACCTGAGGTCAGGAGTT
                                ||||||||||||||||||||||
                                ACCTAGTGGACTCCAGTCCTCAA

GAM1227  moblak    3'  AAACTCCTGACTTCAGGTGATC 56376
              C                 GGATCACCTGAGGTCAGGAGTTT
                                |||||||||||||||||||||||
                                CCTAGTGGACTTCAGTCCTCAAA

GAM1227  MRPL44    3'  AACTCCTGACCTCAGGTGATCC 43589
              A                 TGGATCACCTGAGGTCAGGAGTT
                                ||||||||||||||||||||||
                                ACCTAGTGGACTCCAGTCCTCAA

GAM1227  NFAT5     3'  AACTCCTAACCTCCAGTGATCC 57781        CT    C
              A                 TGGATCAC  GAGGT AGGAGTT
                                ||||||||  ||||| |||||||
                                ACCTAGTG  CTCCA TCCTCAA
                                     AC    A
GAM1227  NXN       3'  AACTCCTGACCTCAGGTGATCC 42658
              A                 TGGATCACCTGAGGTCAGGAGTT
                                ||||||||||||||||||||||
                                ACCTAGTGGACTCCAGTCCTCAA

GAM1227  NYD-SP11  5'  AAACTCCTCCTAAATGACACCA 50051    A_  CCTG  TC
                                TGG  TCA   AGG  AGGAGTTT
                                |||  |||   |||  ||||||||
                                ACC  AGT   TCC  TCCTCAAA
                                  AC   AAA_  __
GAM1227  PELI1     5'  AAACTCCCAACCTCAAGTGATC 40611       C     CA
              C                 GGATCAC TGAGGT  GGAGTTT
                                |||||||  ||||||  |||||||
                                CCTAGTG ACTCCA  CCTCAAA
                                     A     AC
GAM1227  PIP3-E    3'  AAACTCCTGACCTCAGGTGATC 67338
              T                 GGATCACCTGAGGTCAGGAGTTT
                                |||||||||||||||||||||||
                                TCTAGTGGACTCCAGTCCTCAAA

GAM1227  POLR2D    3'  AAACTCCTGGGCTCAAGTGATC 17836       C   G
              C                 GGATCAC TGAG TCAGGAGTTT
                                |||||||  ||||  ||||||||||
                                CCTAGTG ACTC GGTCCTCAAA
                                     A   G
GAM1227  PRO1992   3'  AACTCAACCTCAGGTGATCC   26891           CAG
                                GGATCACCTGAGGT   GAGTT
                                ||||||||||||||   |||||
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                                CCTAGTGGACTCCA   CTCAA
                                      A__
GAM1227  PRO2955   3'  AAACTCCTGACCTCAGGTGATC 38226
              CA                  TGGATCACCTGAGGTCAGGAGTTT
                                  ||||||||||||||||||||||
                                  ACCTAGTGGACTCCAGTCCTCAAA

GAM1227  PSTPIP2   3'  AAACTCCTGACCTCAGGTGATC 44642
              CA                  TGGATCACCTGAGGTCAGGAGTTT
                                  ||||||||||||||||||||||
                                  ACCTAGTGGACTCCAGTCCTCAAA

GAM1227  RES4-25   3'  AATTCCCGACCTCAGGTAATCC 65256      C        A
              A                   TGGAT ACCTGAGGTC GGAGTT
                                  ||||| |||||||||| ||||||
                                  ACCTA TGGACTCCAG CCTTAA
                                     A         C
GAM1227  RNF8      3'  AAATTCCTGACCTTAAGTGATC 15549        C
              CA                  TGGATCAC TGAGGTCAGGAGTTT
                                  ||||||||| ||||||||||||||
                                  ACCTAGTG ATTCCAGTCCTTAAA
                                      A
GAM1227  Rpo1-2    3'  AGACCCTGACCTCAAGTGATCC 50866        C        A
              A                   TGGATCAC TGAGGTCAGG GTTT
                                  ||||||||| |||||||||| ||||
                                  ACCTAGTG ACTCCAGTCC CAGA
                                      A        _
GAM1227  Rpo1-2    3'  AGACCCTGACCTCAAGTGATCC 39210        C        A
              A                   TGGATCAC TGAGGTCAGG GTTT
                                  ||||||||| |||||||||| ||||
                                  ACCTAGTG ACTCCAGTCC CAGA
                                      A        _
GAM1227  SCAMP-4   3'  AACTCCTGACCTCAAGTGATCC 55328        C
              A                   TGGATCAC TGAGGTCAGGAGTT
                                  ||||||||| ||||||||||||||
                                  ACCTAGTG ACTCCAGTCCTCAA
                                      A
GAM1227  SCYA22    3'  AAACTCCTGGGCTCAAGCGATC 92563      ACC    G
              C                   GGATC   TGAG TCAGGAGTTT
                                  |||||   |||| ||||||||||
                                  CCTAG   ACTC GGTCCTCAAA
                                     CGA    G
GAM1227  SCYA22    3'  AACTCCTGACCTCAAGTGATCC 92564        C
              A                   TGGATCAC TGAGGTCAGGAGTT
                                  ||||||||| |||||||||||||
                                  ACCTAGTG ACTCCAGTCCTCAA
                                      A
GAM1227  SCYA28    3'  AACTTCTGATCTCAAGTGATCC 39533        C
              A                   TGGATCAC TGAGGTCAGGAGTT
                                  ||||||||| |||||||||||||
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                                ACCTAGTG ACTCTAGTCTTCAA
                                    A
GAM1227  SFXN2    3'  AACTCCTGACCTCAGGTGATCC 74366
                                GGATCACCTGAGGTCAGGAGTT
                                ||||||||||||||||||||||
                                CCTAGTGGACTCCAGTCCTCAA

GAM1227  SIRPB1   3'  AACTCCCGACCTCAGGTGATCC 21350              A
              A                  TGGATCACCTGAGGTC GGAGTT
                                 ||||||||||||||| ||||||
                                 ACCTAGTGGACTCCAG CCTCAA
                                       C
GAM1227  SLC2A10  3'  AACTCCTGAGCTCAAGTGATCC 48540        C   G
              A                  TGGATCAC TGAG TCAGGAGTT
                                 |||||||| |||| |||||||||
                                 ACCTAGTG ACTC AGTCCTCAA
                                     A   G
GAM1227  STAF65(gamma) 3'  AAACTCCTGACCTCAAGTGATC 30053        C
              T                  GGATCAC TGAGGTCAGGAGTTT
                                 ||||||| ||||||||||||||
                                 TCTAGTG ACTCCAGTCCTCAAA
                                    A
GAM1227  TBCC     3'  AACTCCTGACCTCAGGTGATCC 13596
              A                  TGGATCACCTGAGGTCAGGAGTT
                                 ||||||||||||||||||||||
                                 ACCTAGTGGACTCCAGTCCTCAA

GAM1227  TCL6     3'  AAACTCCTGAGCTCAAGCGATC 40499      ACC   G
              C                  GGATC   TGAG TCAGGAGTTT
                                 |||||   |||| ||||||||||
                                 CCTAG   ACTC AGTCCTCAAA
                                    CGA   G
GAM1227  TCL6     3'  AAACTCCTGAGCTCAAGCGATC 40523      ACC   G
              C                  GGATC   TGAG TCAGGAGTTT
                                 |||||   |||| ||||||||||
                                 CCTAG   ACTC AGTCCTCAAA
                                    CGA   G
GAM1227  TRIM16   3'  AAACTCCTGACCTCGTGATGCA 22358    G    CT
                                 TG ATCAC  GAGGTCAGGAGTTT
                                 || |||||  ||||||||||||||
                                 AC TAGTG  CTCCAGTCCTCAAA
                                  G   __
GAM1227  TRIM5    3'  AACCTCTGACCTCAGGTGATCC 53456              GA
              A                  TGGATCACCTGAGGTCAG  GTT
                                 ||||||||||||||||||  |||
                                 ACCTAGTGGACTCCAGTC  CAA
                                       TC
GAM1227  TRIM5    3'  AACCTCTGACCTCAGGTGATCC 53534              GA
              A                  TGGATCACCTGAGGTCAG  GTT
                                 ||||||||||||||||||  |||
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                                ACCTAGTGGACTCCAGTC  CAA
                                           TC
GAM1227  TRIM6    3'  AACTCCTGACCGCAAGTGATCC 55170        C  A
             A                  TGGATCAC TG GGTCAGGAGTT
                                |||||||| || ||||||||||
                                ACCTAGTG AC CCAGTCCTCAA
                                    A  G
GAM1227  TUCAN    3'  AACTCCTGGCCTCAAGTGATCC 30957        C
             A                  TGGATCAC TGAGGTCAGGAGTT
                                |||||||| ||||||||||||||
                                ACCTAGTG ACTCCGGTCCTCAA
                                    A
GAM1227  TUSP     3'  AACTCCTGACCTCAGGTGATCC 40014
                                GGATCACCTGAGGTCAGGAGTT
                                ||||||||||||||||||||||
                                CCTAGTGGACTCCAGTCCTCAA

GAM1227  UBF-fl   3'  AAACTCCTGACCTCAAGTGATC 52611         C
             CA                   TGGATCAC TGAGGTCAGGAGTTT
                                |||||||| ||||||||||||||||
                                ACCTAGTG ACTCCAGTCCTCAAA
                                    A
GAM1227  VDU1     3'  AAACTCCTGACCTCAGGTGATC 31110
             CA                   TGGATCACCTGAGGTCAGGAGTTT
                                ||||||||||||||||||||||||
                                ACCTAGTGGACTCCAGTCCTCAAA

GAM1227  VPS33A   3'  AAACTCCTGACCTCAGGTGATC 43602
             CA                   TGGATCACCTGAGGTCAGGAGTTT
                                ||||||||||||||||||||||||
                                ACCTAGTGGACTCCAGTCCTCAAA

GAM1227  WBSCR23  3'  AAACTCCTGACCTCAGGTGATC 47403
             CA                   TGGATCACCTGAGGTCAGGAGTTT
                                ||||||||||||||||||||||||
                                ACCTAGTGGACTCCAGTCCTCAAA

GAM1227  ZNF177   5'  AAACTCCTGCTCTCAAGTGATC 14354        C   GT
             C                    GGATCAC TGAG  CAGGAGTTT
                                ||||||| ||||  |||||||||
                                CCTAGTG ACTC  GTCCTCAAA
                                    A   TC
GAM1227  LOC112687 3'  AAACTCCTGACCTCATGTAATC 73213      C  C
             CA                   TGGAT AC TGAGGTCAGGAGTTT
                                ||||| || ||||||||||||||
                                ACCTA TG ACTCCAGTCCTCAAA
                                   A  T
GAM1227  LOC112817 3'  AACTCCTGACCTCAGGTGATCC 57309
             A                    TGGATCACCTGAGGTCAGGAGTT
                                ||||||||||||||||||||||
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                                ACCTAGTGGACTCCAGTCCTCAA

GAM1227  LOC113026 3'  CCTGACCTCAAGTGATCC    56727        C
                                GGATCAC TGAGGTCAGG
                                ||||||| ||||||||||
                                CCTAGTG ACTCCAGTCC
                                    A
GAM1227  LOC115219 5'  AAACTCCTGACGTCGTGATCC  73678        CT  G
                                GGATCAC  GA GTCAGGAGTTT
                                |||||||  || ||||||||||
                                CCTAGTG  CT CAGTCCTCAAA
                                    __  G
GAM1227  LOC115648 3'  AACTCCTGACCTCAGGTGATCC 60009
              A                  TGGATCACCTGAGGTCAGGAGTT
                                ||||||||||||||||||||||
                                ACCTAGTGGACTCCAGTCCTCAA

GAM1227  LOC119392 3'  AACTCCTGACCTCAGGTGATCC 59807
              A                  TGGATCACCTGAGGTCAGGAGTT
                                ||||||||||||||||||||||
                                ACCTAGTGGACTCCAGTCCTCAA

GAM1227  LOC120114 3'  AAACTCCTGACCTCGTAATCCA 76030       C  CT
                                TGGAT AC  GAGGTCAGGAGTTT
                                ||||| ||  ||||||||||||||
                                ACCTA TG  CTCCAGTCCTCAAA
                                   A  __
GAM1227  LOC125194 5'  AAACTCCTGGCTTCAAGTGATC 74858        C
              C                  GGATCAC TGAGGTCAGGAGTTT
                                ||||||| ||||||||||||||||
                                CCTAGTG ACTTCGGTCCTCAAA
                                    A
GAM1227  LOC126669 3'  AAACTCCTGACCTCAAATGATC 75915        CC
              CA                   TGGATCA  TGAGGTCAGGAGTTT
                                |||||||  ||||||||||||||||
                                ACCTAGT  ACTCCAGTCCTCAAA
                                    AA
GAM1227  LOC130639 5'  AACTCCTGACCTCAAGTGATCC 75477        C
                                GGATCAC TGAGGTCAGGAGTT
                                ||||||| ||||||||||||||
                                CCTAGTG ACTCCAGTCCTCAA
                                    A
GAM1227  LOC130813 3'  AAACTCCCAACTTCAGGTGATC 76255             CA
              C                  GGATCACCTGAGGT  GGAGTTT
                                ||||||||||||||  |||||||
                                CCTAGTGGACTTCA  CCTCAAA
                                       AC
GAM1227  LOC132241 5'  AACGCCTGACCTCAAGTGATCC 75549        C        A
                                GGATCAC TGAGGTCAGG GTT
                                ||||||| |||||||||| |||
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                                CCTAGTG ACTCCAGTCC CAA
                                    A         G
GAM1227  LOC135154 3'  AACTCCTGACCTCAGTTGATCC 75712        C
              A                  TGGATCA CTGAGGTCAGGAGTT
                                 ||||||| ||||||||||||||||
                                 ACCTAGT GACTCCAGTCCTCAA
                                    T
GAM1227  LOC135293 3'  AAACTCCTGGGCTCAAGCAATC 76670      CACC    G
              C                  GGAT    TGAG TCAGGAGTTT
                                 ||||    |||| ||||||||||
                                 CCTA    ACTC GGTCCTCAAA
                                   ACGA    G
GAM1227  LOC135293 3'  AACTCCTGACCTCAGGTGATGC 76672    G
              A                  TG ATCACCTGAGGTCAGGAGTT
                                 || ||||||||||||||||||||
                                 AC TAGTGGACTCCAGTCCTCAA
                                  G
GAM1227  LOC142927 5'  AAACTCCTGGCCTCAAGTGATC 76936        C
              C                  GGATCAC TGAGGTCAGGAGTTT
                                 ||||||| ||||||||||||||||
                                 CCTAGTG ACTCCGGTCCTCAAA
                                    A
GAM1227  LOC143916 3'  AAACTTCTGACCTCAGGTGATC 77130
              CA                  TGGATCACCTGAGGTCAGGAGTTT
                                 |||||||||||||||||||||||||
                                 ACCTAGTGGACTCCAGTCTTCAAA

GAM1227  LOC144305 3'  AAACTCCTGGACCCAAGCGATC 83964      AC  GA   _
              C                  GGATC  CT  GGTC AGGAGTTT
                                 |||||  ||  |||| ||||||||
                                 CCTAG  GA  CCAG TCCTCAAA
                                   C_  AC    G
GAM1227  LOC144317 5'  AACTCCTGACCTCAGGTGATCC 77284
              A                  TGGATCACCTGAGGTCAGGAGTT
                                 |||||||||||||||||||||||||
                                 ACCTAGTGGACTCCAGTCCTCAA

GAM1227  LOC144524 5'  AAACTCCTGAACTCAGGTGATC 84043          G
              C                  GGATCACCTGAG TCAGGAGTTT
                                 |||||||||||| ||||||||||
                                 CCTAGTGGACTC AGTCCTCAAA
                                       A
GAM1227  LOC145082 5'  CCTAACCTAAGGTGATCCA    84185        G   C
                                 TGGATCACCT AGGT AGG
                                 |||||||||| |||| |||
                                 ACCTAGTGGA TCCA TCC
                                       A   A
GAM1227  LOC145268 5'  AACTCCTAACCTCGGGTGATCC 77565            C
              A                  TGGATCACCTGAGGT AGGAGTT
                                 |||||||||||||| |||||||
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                                ACCTAGTGGGCTCCA TCCTCAA
                                       A
GAM1227  LOC145453 5'  AAACTCCTGACCTCAAGGATCT 77648      ACC
                                GGATC   TGAGGTCAGGAGTTT
                                |||||   ||||||||||||||||
                                TCTAG   ACTCCAGTCCTCAAA
                                  GA_
GAM1227  LOC145873 5'  AACTCCTGAACTCAAGTAATCC 78008      C  C    G
           A                     TGGAT AC TGAG TCAGGAGTT
                                |||||  ||  ||||  |||||||||
                                ACCTA TG ACTC AGTCCTCAA
                                  A  A    A
GAM1227  LOC146050 3'  AAACTCCCGACCTCAGGTGATC 78092              A
           T                     GGATCACCTGAGGTC GGAGTTT
                                ||||||||||||||| |||||||
                                TCTAGTGGACTCCAG CCTCAAA
                                       C
GAM1227  LOC146108 3'  AAACTCCTGGCTTCAAGCAATC 78144      CACC
           C                     GGAT    TGAGGTCAGGAGTTT
                                ||||    ||||||||||||||||
                                CCTA    ACTTCGGTCCTCAAA
                                  ACGA
GAM1227  LOC146229 3'  AAACTCCTGACCTCAAGTGATC 78233         C
           CA                      TGGATCAC TGAGGTCAGGAGTTT
                                ||||||||  ||||||||||||||||
                                ACCTAGTG ACTCCAGTCCTCAAA
                                    A
GAM1227  LOC146229 3'  AAACTCCTGACCTCAGGTGATC 78234
           CA                      TGGATCACCTGAGGTCAGGAGTTT
                                |||||||||||||||||||||||||
                                ACCTAGTGGACTCCAGTCCTCAAA

GAM1227  LOC146229 3'  AAACTCCTGACTTCAAATGATC 78235        CC
           CA                      TGGATCA  TGAGGTCAGGAGTTT
                                |||||||  ||||||||||||||||
                                ACCTAGT  ACTTCAGTCCTCAAA
                                    AA
GAM1227  LOC146901 3'  AACTCCTGACCTCAGGTGATCC 84877
           A                     TGGATCACCTGAGGTCAGGAGTT
                                |||||||||||||||||||||||
                                ACCTAGTGGACTCCAGTCCTCAA

GAM1227  LOC146909 3'  AACTCCTGACCTCAGGTGATCC 78752
                                GGATCACCTGAGGTCAGGAGTT
                                |||||||||||||||||||||||
                                CCTAGTGGACTCCAGTCCTCAA

GAM1227  LOC146952 5'  AAACTCCTGACCTCAGATGATC 84916        C
           TA                      TGGATCA CTGAGGTCAGGAGTTT
                                |||||||  ||||||||||||||||
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                                ATCTAGT GACTCCAGTCCTCAAA
                                    A
GAM1227  LOC147276 3'  AACTCCTGACCTCAAGTGATCC 78945        C
             A                   TGGATCAC TGAGGTCAGGAGTT
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                                 ACCTAGTG ACTCCAGTCCTCAA
                                     A
GAM1227  LOC147817 3'  AAACTCCTGACCTTATAATCC  79158      CACC
                                 GGAT    TGAGGTCAGGAGTTT
                                 ||||    |||||||||||||||
                                 CCTA    ATTCCAGTCCTCAAA
                                   AT__
GAM1227  LOC147817 3'  AAACTCCTGGCTTCAAGTGATC 79159        C
             C                   GGATCAC TGAGGTCAGGAGTTT
                                 |||||||| ||||||||||||||
                                 CCTAGTG ACTTCGGTCCTCAAA
                                     A
GAM1227  LOC147841 3'  AACTCCTGACCTCAGGTGATCC 79217
             A                   TGGATCACCTGAGGTCAGGAGTT
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GAM1227  LOC147935 3'  AAACTCCTGGGCTCAAGTGATC 85201        C    G
             C                   GGATCAC TGAG TCAGGAGTTT
                                 |||||||| |||| ||||||||||
                                 CCTAGTG ACTC GGTCCTCAAA
                                     A    G
GAM1227  LOC148709 3'  AAACTCCCGACCTTAGGTGATG 79683    G          A
             CA                    TG ATCACCTGAGGTC GGAGTTT
                                   || |||||||||||| |||||||
                                   AC TAGTGGATTCCAG CCTCAAA
                                    G           C
GAM1227  LOC148918 5'  AACTCCTGACCTCAGGTGATCC 79811
             A                   TGGATCACCTGAGGTCAGGAGTT
                                 |||||||||||||||||||||||
                                 ACCTAGTGGACTCCAGTCCTCAA

GAM1227  LOC149577 3'  AACTCCTGACCTCAAGTGATCC 85659        C
             A                   TGGATCAC TGAGGTCAGGAGTT
                                 |||||||| ||||||||||||||
                                 ACCTAGTG ACTCCAGTCCTCAA
                                     A
GAM1227  LOC149577 3'  ACTCCTGACCTCAAGTGATCCA 85663        C
                                 TGGATCAC TGAGGTCAGGAGT
                                 |||||||| |||||||||||||
                                 ACCTAGTG ACTCCAGTCCTCA
                                     A
GAM1227  LOC149692 3'  AACTCCTGACCTCAGGTGATCC 85718
             A                   TGGATCACCTGAGGTCAGGAGTT
                                 |||||||||||||||||||||||
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                                ACCTAGTGGACTCCAGTCCTCAA

GAM1227  LOC149711 3'  AAACTCCTGACCTCAGGTGATC 85827
                 CA                TGGATCACCTGAGGTCAGGAGTTT
                                   ||||||||||||||||||||||||
                                   ACCTAGTGGACTCCAGTCCTCAAA

GAM1227  LOC150054 5'  AACTTATGACCTCAGGTGATCC 85965              G
                                   GGATCACCTGAGGTCA GAGTT
                                   |||||||||||||||| |||||
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                                              A
GAM1227  LOC150225 3'  AAACTCCTGACCTCAGATGATT 86173        C
                 CA                TGGATCA CTGAGGTCAGGAGTTT
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                                   ACTTAGT GACTCCAGTCCTCAAA
                                      A
GAM1227  LOC150282 5'  AACTCCTGACCTCAGGTGATCC 80528
                 A                 TGGATCACCTGAGGTCAGGAGTT
                                   |||||||||||||||||||||||
                                   ACCTAGTGGACTCCAGTCCTCAA

GAM1227  LOC150290 3'  AAACTCCTGGCCTCAAGCAATC 80580      CACC
                 C                  GGAT    TGAGGTCAGGAGTTT
                                    ||||    ||||||||||||||
                                    CCTA    ACTCCGGTCCTCAAA
                                      ACGA
GAM1227  LOC150397 3'  CCTGACCTCAGGTGATCC    80659
                                   GGATCACCTGAGGTCAGG
                                   ||||||||||||||||||
                                   CCTAGTGGACTCCAGTCC

GAM1227  LOC150407 3'  AAACTCCTGGGCTCAAGTAATC 80633      C  C    G
                 C                  GGAT AC TGAG TCAGGAGTTT
                                    |||| || |||| ||||||||||
                                    CCTA TG ACTC GGTCCTCAAA
                                      A  A    G
GAM1227  LOC150587 3'  AAACTCCTGGGCTCAAGCAATC 86236      CACC    G
                 C                  GGAT    TGAG TCAGGAGTTT
                                    ||||    |||| ||||||||||
                                    CCTA    ACTC GGTCCTCAAA
                                      ACGA    G
GAM1227  LOC150587 3'  AAACTCCTGGGCTCAAGCGATC 86237       ACC    G
                 C                  GGATC   TGAG TCAGGAGTTT
                                    |||||   |||| ||||||||||
                                    CCTAG   ACTC GGTCCTCAAA
                                      CGA    G
GAM1227  LOC150960 3'  AAATTCCTGACCTCAGGTGATC 80857
                 CA                TGGATCACCTGAGGTCAGGAGTTT
                                   |||||||||||||||||||||||
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                                ACCTAGTGGACTCCAGTCCTTAAA

GAM1227  LOC151826 3'  AACTCCTGACATCAGGTGATCC 81172          G
                A                TGGATCACCTGA GTCAGGAGTT
                                 |||||||||||| ||||||||||
                                 ACCTAGTGGACT CAGTCCTCAA
                                       A
GAM1227  LOC152137 3'  AACCCCTGACCTCAAGTGATCC 81303       C       A
                A                TGGATCAC TGAGGTCAGG GTT
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                                 ACCTAGTG ACTCCAGTCC CAA
                                      A        C
GAM1227  LOC152794 5'  AACTCCTGACCTCAGGTGATCC 81551
                                 GGATCACCTGAGGTCAGGAGTT
                                 ||||||||||||||||||||||
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GAM1227  LOC153077 3'  AACTCCTGACCTCAGGTGATCC 87099
                A                TGGATCACCTGAGGTCAGGAGTT
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GAM1227  LOC153443 3'  AAACTCCTGGGCTCAAGTGATC 81685       C   G
                C                GGATCAC TGAG TCAGGAGTTT
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                                 CCTAGTG ACTC GGTCCTCAAA
                                      A   G
GAM1227  LOC153688 3'  AACTCCCAACCTCAGGTGATCC 87279           CA
                                 GGATCACCTGAGGT  GGAGTT
                                 ||||||||||||||  ||||||
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                                           AC
GAM1227  LOC153811 3'  AAACTCCTGACCTCAAATGATC 81815       CC
                CA                 TGGATCA  TGAGGTCAGGAGTTT
                                   |||||||  ||||||||||||||||
                                   ACCTAGT  ACTCCAGTCCTCAAA
                                      AA
GAM1227  LOC153883 5'  AACTCCTGACCTCAAGTGATCC 81882       C
                A                TGGATCAC TGAGGTCAGGAGTT
                                 |||||||| ||||||||||||||
                                 ACCTAGTG ACTCCAGTCCTCAA
                                      A
GAM1227  LOC154007 3'  AAACTCCTAGGCTCAGGCGATC 81920      A    G  _
                C                GGATC CCTGAG TC AGGAGTTT
                                 ||||| |||||| || ||||||||
                                 CCTAG GGACTC GG TCCTCAAA
                                   C     _  A
GAM1227  LOC154726 3'  AAACTCCTGGGCTCAGATGATC 82001       C    G
                CA                 TGGATCA CTGAG TCAGGAGTTT
                                   ||||||| ||||| ||||||||||
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                                ACCTAGT GACTC GGTCCTCAAA
                                    A    G
GAM1227  LOC154877 3'  AAACTCCTGGGCTCAAGTGATC 87509       C   G
             C                   GGATCAC TGAG TCAGGAGTTT
                                 ||||||| |||| ||||||||||
                                 CCTAGTG ACTC GGTCCTCAAA
                                    A   G
GAM1227  LOC154877 3'  AACTCCCGACCTCAGGTGATCT 87511             A
             A                   TGGATCACCTGAGGTC GGAGTT
                                 |||||||||||||||| ||||||
                                 ATCTAGTGGACTCCAG CCTCAA
                                           C
GAM1227  LOC157247 5'  AACTCCTGACCTCAGGTGATCC 82278
             A                   TGGATCACCTGAGGTCAGGAGTT
                                 ||||||||||||||||||||||||
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GAM1227  LOC157623 3'  AAACTCCTGGGCTCAAGTGATC 82404       C   G
             C                   GGATCAC TGAG TCAGGAGTTT
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                                 CCTAGTG ACTC GGTCCTCAAA
                                    A   G
GAM1227  LOC157867 5'  AAACTCCTGGCTTCAAGCAATC 87870     CACC
             C                   GGAT   TGAGGTCAGGAGTTT
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                                 CCTA   ACTTCGGTCCTCAAA
                                   ACGA
GAM1227  LOC158310 5'  AACTCCTGACCTTAAGTGATCC 88069       C
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                                 ACCTAGTG ATTCCAGTCCTCAA
                                     A
GAM1227  LOC158476 3'  AACTCCTGACCCCAGGTGATCC 88171         A
                                 GGATCACCTG GGTCAGGAGTT
                                 |||||||||| ||||||||||
                                 CCTAGTGGAC CCAGTCCTCAA
                                       C
GAM1227  LOC160646 3'  AACTCCTGACCTTCAGGTGATC 83097          _
             CA                    TGGATCACCTGA GGTCAGGAGTT
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                                 ACCTAGTGGACT CCAGTCCTCAA
                                        T
GAM1227  LOC162427 3'  AAACTCCTGACCTCAAGTGAGC 83216    A   C
             T                   GG TCAC TGAGGTCAGGAGTTT
                                 || |||| ||||||||||||||
                                 TC AGTG ACTCCAGTCCTCAAA
                                  G   A
GAM1227  LOC169611 3'  AAACTCCTGACCTCAGGTGATC 83626
             CA                    TGGATCACCTGAGGTCAGGAGTTT
                                 |||||||||||||||||||||||||
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                                ACCTAGTGGACTCCAGTCCTCAAA

GAM1227  LOC196047 5'  AAACTCCTGACCTCAGGTGATC 91131
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GAM1227  LOC196529 3'  AACTCCTGATCTCAGGCAATCC 89115      CA
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                                    AC
GAM1227  LOC197358 3'  AACTCCTGACCTCAAGTGATCC 89403        C
                A                 TGGATCAC TGAGGTCAGGAGTT
                                  ||||||||| ||||||||||||||
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                                      A
GAM1227  LOC197358 3'  AACTCCTGACCTCAGGTGATCC 89404
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GAM1227  LOC199786 3'  AAACTCCTGGACTCAAGCAATC 89727     CACC   GT
                C                 GGAT   TGAG  CAGGAGTTT
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                                    ACGA   AG
GAM1227  LOC199906 3'  AAACTCCTGACCTCAGGCGATC 89836      A
                C                 GGATC CCTGAGGTCAGGAGTTT
                                  ||||| ||||||||||||||||
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                                    C
GAM1227  LOC200314 3'  AACTCCTGACCTCAGGTGATCC 91583
                A                 TGGATCACCTGAGGTCAGGAGTT
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GAM1227  LOC200339 3'  AACTCCTGGCCTCAAGCGATCC 91611       ACC
                A                 TGGATC   TGAGGTCAGGAGTT
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GAM1227  LOC200407 3'  AAACTCCTGACCTCAGGTGATC 91620
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                                  |||||||||||||||||||||||
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GAM1227  LOC200853 3'  AAACTCCTAGGCTCAAGCGATC 90322      AC  GA   _
                C                 GGATC  CT  GGTC AGGAGTTT
                                  |||||  ||  |||| ||||||||
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                                CCTAG  GA  TCGG TCCTCAAA
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GAM1227  LOC201164 3'  AAACTCCTGACCTCAAGTGATC 89479         C
                CA                   TGGATCAC TGAGGTCAGGAGTTT
                                     |||||||| ||||||||||||||||
                                     ACCTAGTG ACTCCAGTCCTCAAA
                                        A
GAM1227  LOC201510 3'  AAACTCCTGGTCTCAAGTGATC 89626        C    GT
                C                    GGATCAC TGAG  CAGGAGTTT
                                     ||||||| ||||  |||||||||
                                     CCTAGTG ACTC  GTCCTCAAA
                                        A    TG
GAM1227  LOC201626 3'  AACTCCTGACCTCAGGTGATCC 90421
                A                    TGGATCACCTGAGGTCAGGAGTT
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GAM1227  LOC201627 3'  AAACTCCCGACCTCAGGTGATC 90441              A
                C                    GGATCACCTGAGGTC GGAGTTT
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                                     CCTAGTGGACTCCAG CCTCAAA
                                              C
GAM1227  LOC203197 3'  AACTCCTGACCTCAGGTGATCC 90797
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GAM1227  LOC203197 3'  ACTCCTGACCTCAGGTGATCCA 90799
                                     TGGATCACCTGAGGTCAGGAGT
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GAM1227  LOC203378 3'  AAACTCCTCCACTCAGGTGATC 92264             GTC
                CA                   TGGATCACCTGAG   AGGAGTTT
                                     ||||||||||||   ||||||||
                                     ACCTAGTGGACTC   TCCTCAAA
                                              ACC
GAM1227  LOC204804 3'  AACTCCTGGCCTCAGGTGATCC 91027
                A                    TGGATCACCTGAGGTCAGGAGTT
                                     ||||||||||||||||||||||
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GAM1227  LOC219529 5'  AAACTCCTGAGCCCAGGTGATC 94559          A  _
                C                    GGATCACCTG GG TCAGGAGTTT
                                     |||||||||| || ||||||||||
                                     CCTAGTGGAC CC AGTCCTCAAA
                                           _  G
GAM1227  LOC219673 5'  AAACGCCTGACCTCAAGTAATC 94602       C  C         A
                CA                   TGGAT AC TGAGGTCAGG GTTT
                                     ||||| || |||||||||| ||||
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                                ACCTA TG ACTCCAGTCC CAAA
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GAM1227  LOC220074 3'  AAACTCCTGACCTCAGGTGATC 59945
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GAM1227  LOC220074 3'  AACTCCTGACCTCAGGTGATCC 59948
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                                    |||||||||||||||||||||
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GAM1227  LOC221060 3'  AACTCCTGACCTCAGGTGATCC 94823
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                                    |||||||||||||||||||||
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GAM1227  LOC221964 3'  AACTCCTGACCTCAGGTGATCC 95596
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GAM1227  LOC222031 3'  AACTCCTGACCTCAGGTGATCC 95662
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GAM1227  LOC222068 3'  ACTCCTGACCTCAGTTGATCCA 94265        C
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                                       T
GAM1227  LOC245771 5'  AACTCCTGACCTCAAGTGATCC 94462         C
                A                   TGGATCAC TGAGGTCAGGAGTT
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                                       A
GAM1227  LOC253805 3'  AACTCCTGACCTCAGATGATTC 98163        C
                A                   TGGATCA CTGAGGTCAGGAGTT
                                    ||||||| ||||||||||||||
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                                       A
GAM1227  LOC253981 3'  AACTCCTGACCTCAGGCGATCT 97525        A
                A                   TGGATC CCTGAGGTCAGGAGTT
                                    |||||| ||||||||||||||||
                                    ATCTAG GGACTCCAGTCCTCAA
                                       C
GAM1227  LOC254268 3'  AAACTCCTGACCTCAAGTGATC 97131        C
                C                   GGATCAC TGAGGTCAGGAGTTT
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GAM1227  LOC254351 5'  AAGCTCCTGACCTCGGGTGATC 96676
                 CA                  TGGATCACCTGAGGTCAGGAGTTT
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GAM1227  LOC254532 5'  AAACTCCTGACCTCAAGTGATC 98440         C
                 CA                  TGGATCAC TGAGGTCAGGAGTTT
                                     |||||||| ||||||||||||||
                                     ACCTAGTG ACTCCAGTCCTCAAA
                                        A
GAM1227  LOC254655 3'  AACTCCTGACCTCAGGTGATCC 97205
                 A                    TGGATCACCTGAGGTCAGGAGTT
                                      ||||||||||||||||||||||
                                      ACCTAGTGGACTCCAGTCCTCAA

GAM1227  LOC254778 3'  AAACTCCTGGGTTCAAGAGATC 97824       ACC    G
                 CA                  TGGATC   TGAG TCAGGAGTTT
                                     ||||||   |||| ||||||||||
                                     ACCTAG   ACTT GGTCCTCAAA
                                        AGA    G
GAM1227  LOC255065 5'  AAACTCCTGACCTCAAGTAATC 98366      C  C
                 CA                  TGGAT AC TGAGGTCAGGAGTTT
                                     ||||| || ||||||||||||||
                                     ACCTA TG ACTCCAGTCCTCAAA
                                        A  A
GAM1227  LOC255065 5'  CCTGACCTCAAGTAATCCA    98370      C  C
                                     TGGAT AC TGAGGTCAGG
                                     ||||| || ||||||||||
                                     ACCTA TG ACTCCAGTCC
                                        A  A
GAM1227  LOC255458 5'  AAACTCCTGGGCTCAAGCGATC 98929       ACC    G
                 C                    GGATC   TGAG TCAGGAGTTT
                                      |||||   |||| ||||||||||
                                      CCTAG   ACTC GGTCCTCAAA
                                         CGA    G
GAM1227  LOC256306 3'  CCTGACCTCAAATGATCC     98512       CC
                                     GGATCA  TGAGGTCAGG
                                     ||||||  ||||||||||
                                     CCTAGT  ACTCCAGTCC
                                        AA
GAM1227  LOC256364 5'  AAACTCCTGGCCTCAGGTGACC 96439     A
                 C                    GG TCACCTGAGGTCAGGAGTTT
                                      || ||||||||||||||||||||
                                      CC AGTGGACTCCGGTCCTCAAA
                                       C
GAM1227  LOC257127 5'  AACTCCTGACCTCAGGTGATCC 98492
                                     GGATCACCTGAGGTCAGGAGTT
                                     ||||||||||||||||||||||
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                                CCTAGTGGACTCCAGTCCTCAA

GAM1227  LOC51008  5'  AACTCCCGACCTCAGGTGATCC 32522              A
                 A                TGGATCACCTGAGGTC GGAGTT
                                  |||||||||||||||| ||||||
                                  ACCTAGTGGACTCCAG CCTCAA
                                           C
GAM1227  LOC51193  3'  AAACTCCTGGACTCAAGCAATC 33350     CACC    GT
                 C                GGAT   TGAG  CAGGAGTTT
                                  ||||   ||||  |||||||||
                                  CCTA   ACTC  GTCCTCAAA
                                    ACGA   AG
GAM1227  LOC51200  3'  AAACTCCCAACCTCAGGTGATC 33429            CA
                 T                GGATCACCTGAGGT  GGAGTTT
                                  ||||||||||||||  |||||||
                                  TCTAGTGGACTCCA  CCTCAAA
                                           AC
GAM1227  LOC57107  3'  AACTCCTGACCTCAGGTGATCC 40176
                                  GGATCACCTGAGGTCAGGAGTT
                                  ||||||||||||||||||||||
                                  CCTAGTGGACTCCAGTCCTCAA

GAM1227  LOC57146  3'  AAACTCCTGACCTCAGGTGCTC 40283     T
                 CA                 TGGA CACCTGAGGTCAGGAGTTT
                                  |||| ||||||||||||||||||
                                  ACCT GTGGACTCCAGTCCTCAAA
                                    C
GAM1227  LOC89932  3'  AACTCCCGACCTCAGGTAATCC 61435     C       A
                                  GGAT ACCTGAGGTC GGAGTT
                                  |||| |||||||||| ||||||
                                  CCTA TGGACTCCAG CCTCAA
                                    A        C
GAM1227  LOC90072  3'  AACTCCCGACCTCAAGTGATCC 61942       C      A
                                  GGATCAC TGAGGTC GGAGTT
                                  ||||||| ||||||| ||||||
                                  CCTAGTG ACTCCAG CCTCAA
                                       A      C
GAM1227  LOC90110  5'  AACTTCTGACCTCAAGTGGTCC 62174       C
                 A                TGGATCAC TGAGGTCAGGAGTT
                                  |||||||| ||||||||||||||
                                  ACCTGGTG ACTCCAGTCTTCAA
                                       A
GAM1227  LOC90288  3'  CTGACCTCAGCTGATCCA    62786       C
                                  TGGATCA CTGAGGTCAG
                                  ||||||| ||||||||||
                                  ACCTAGT GACTCCAGTC
                                       C
GAM1227  LOC90408  5'  AACTCCTGACTTCAAGTGATCC 63336       C
                 A                TGGATCAC TGAGGTCAGGAGTT
                                  |||||||| ||||||||||||||
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                                ACCTAGTG ACTTCAGTCCTCAA
                                    A
GAM1227  LOC90591  3'  AACTCCTGACCTCAGGTGATCC 64128
              A                  TGGATCACCTGAGGTCAGGAGTT
                                 ||||||||||||||||||||||
                                 ACCTAGTGGACTCCAGTCCTCAA

GAM1227  LOC90591  3'  AACTCCTGACCTGAAGTGATCC 64129       CTG
              A                  TGGATCAC   AGGTCAGGAGTT
                                 ||||||||   ||||||||||||
                                 ACCTAGTG   TCCAGTCCTCAA
                                    AAG
GAM1227  LOC91115  3'  AACTCCTGACCTCAGATGGTCC 65532       C
              A                  TGGATCA CTGAGGTCAGGAGTT
                                 |||||||  ||||||||||||||
                                 ACCTGGT GACTCCAGTCCTCAA
                                    A
GAM1227  LOC92267  3'  AAACTCCTGACCTCAAGTGATC 69157       C
              C                   GGATCAC TGAGGTCAGGAGTTT
                                 |||||||  ||||||||||||||
                                 CCTAGTG ACTCCAGTCCTCAAA
                                    A
GAM1227  LOC92303  3'  AATTCCAGACCTCAGGTGATCC 69379           A
              A                  TGGATCACCTGAGGTC GGAGTT
                                 ||||||||||||||| ||||||
                                 ACCTAGTGGACTCCAG CCTTAA
                                       A
GAM1227  LOC92697  5'  AACTCCCAACCTCAGGTGATCC 70800          CA
                                 GGATCACCTGAGGT  GGAGTT
                                 ||||||||||||||  ||||||
                                 CCTAGTGGACTCCA  CCTCAA
                                       AC
GAM1227  LOC92841  3'  AACTCCTGACCTCAAGTGATCC 71235       C
                                 GGATCAC TGAGGTCAGGAGTT
                                 |||||||  ||||||||||||||
                                 CCTAGTG ACTCCAGTCCTCAA
                                    A
GAM1227  LOC92876  5'  ACTCCTGACCTCAGGTGATCCA 71345
                                 TGGATCACCTGAGGTCAGGAGT
                                 ||||||||||||||||||||||
                                 ACCTAGTGGACTCCAGTCCTCA

GAM1227  LOC93408  5'  AAACTCCTGGCCTCAAGTGATC 57280       C
              C                   GGATCAC TGAGGTCAGGAGTTT
                                 |||||||  ||||||||||||||
                                 CCTAGTG ACTCCGGTCCTCAAA
                                    A
GAM1228  GNA11     3'  CGTCGTGGCCTGGATCCTCTG  76588        A  T  T
                                 TAGAGGATCCA GCT ACG ACG
                                 |||||||||||  ||| ||| |||
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                                GTCTCCTAGGT CGG TGC TGC
                                      C  _  _
GAM1228 KIAA0150 3' GCGCACAGGCCGGCTGGATCCT 71882       A  TAC__ A
                                AGGATCCA GCT    GT CGC
                                |||||||| |||    || |||
                                TCCTAGGT CGG    CA GCG
                                   _  CCGGA  C
GAM1228 KIAA1695 3' ACGCATTGACTTGGATCT    47830       C  ___
                                GGATCCAAG TTA   CGT
                                ||||||||| |||   |||
                                TCTAGGTTC AGT   GCA
                                   _  TAC
GAM1228 LOC152274 3' CGAAGCCTGGTCCTCTA    81339       T  A  A
                                TAGAGGA CCA GCTT CG
                                ||||||| ||| |||| ||
                                ATCTCCT GGT CGAA GC
                                   _  C   _
GAM1228 LOC93626 3' CGTCGTGGCCTGGATCCTCTG 73129        A  T  T
                                TAGAGGATCCA GCT ACG ACG
                                |||||||||||| ||| ||| |||
                                GTCTCCTAGGT CGG TGC TGC
                                      C  _  _
GAM1229 GNA11    3' CGTCGTGGCCTGGATCCTCTG  76588        A  T  T
                                TAGAGGATCCA GCT ACG ACG
                                |||||||||||| ||| ||| |||
                                GTCTCCTAGGT CGG TGC TGC
                                      C  _  _
GAM1229 KIAA0150 3' GCGCACAGGCCGGCTGGATCCT 71882       A  TAC__ A
                                AGGATCCA GCT    GT CGC
                                |||||||| |||    || |||
                                TCCTAGGT CGG    CA GCG
                                   _  CCGGA  C
GAM1229 KIAA1695 3' ACGCATTGACTTGGATCT    47830       C  ___
                                GGATCCAAG TTA   CGT
                                ||||||||| |||   |||
                                TCTAGGTTC AGT   GCA
                                   _  TAC
GAM1229 LOC152274 3' CGAAGCCTGGTCCTCTA    81339       T  A  A
                                TAGAGGA CCA GCTT CG
                                ||||||| ||| |||| ||
                                ATCTCCT GGT CGAA GC
                                   _  C   _
GAM1229 LOC93626 3' CGTCGTGGCCTGGATCCTCTG 73129        A  T  T
                                TAGAGGATCCA GCT ACG ACG
                                |||||||||||| ||| ||| |||
                                GTCTCCTAGGT CGG TGC TGC
                                      C  _  _
GAM1230 DLEC1    3' CATCTGGCCCTCCCTTG    24716      A   A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
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                                GTTCC TCCCG TC TAC
                                  C    G  _
GAM1230 DLEC1    3' CATCTGGCCCTCCCTTG    24728      A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                  C    G  _
GAM1230 PIP5K1A  3' TATCCCACCCTGCCTTGATA  14520       A   CA  C
                                TATCAAGG AGGG  GG GTG
                                |||||||| ||||  || |||
                                ATAGTTCC TCCC  CC TAT
                                    G   A_  C
GAM1230 SOX11    3' ACCCACCCCCCCTTGGTA    13308       AA   CA  C
                                TATCAAGG  GGG  GG GT
                                ||||||||  |||  || ||
                                ATGGTTCC  CCC  CC CA
                                    CC   A_  _
GAM1230 CHL1     3' TGTTACCTTTCCTCAATA    22768     CA      CA
                                TAT  AGGAAGGG  GGCG
                                |||  ||||||||  ||||
                                ATA  TCCTTTCC  TTGT
                                  AC       A_
GAM1230 EPB41L1  3' CATTCTGCCCTTCCCTGA    71104     A        C
                                TCA GGAAGGGCAGG GTG
                                ||| |||||||||| |||
                                AGT CCTTCCCGTCT TAC
                                  C         _
GAM1230 FLJ00060 3' CATACCCCCTGCCCTCCTCTGA 61741     _   A      CGTG
                                TCA AGGA GGGCAGG   ATG
                                ||| |||| |||||||   |||
                                AGT TCCT CCCGTCC   TAC
                                  C   _      CCCA
GAM1230 FLJ10898 5' CACCACAGCCCTTTCTCAATA  60126     CA       AGGC
                                TAT  AGGAAGGGC   GTG
                                |||  |||||||||   |||
                                ATA  TCTTTCCCG   CAC
                                  AC        ACAC
GAM1230 FLJ22557 3' ATCATCCCATCCTTAATA    45581     C    A  CAGGC
                                TAT AAGGA GGG    GTGAT
                                ||| ||||| |||    |||||
                                ATA TTCCT CCC    TACTA
                                  A    A  _____
GAM1230 KIAA0574 3' CATCCCCTGCCCTCCCCTGA  69808     A  A      CGT
                                TCA GG AGGGCAGG   GATG
                                ||| || ||||||||   ||||
                                AGT CC TCCCGTCC   CTAC
                                  C  C       C__
GAM1230 KIAA0632 3' CACCTCAGAAACCCTTCCTTGA 32071          CA___  C
                                TCAAGGAAGGG    GG GTG
                                ||||||||||    || |||
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                                AGTTCCTTCCC    CT CAC
                                      AAAGA  C
GAM1230  KIAA1045  3'  CATCACATGTCCTTCC      71599         GGC
                                GGAAGGGCA   GTGATG
                                |||||||||   ||||||
                                CCTTCCTGT   CACTAC
                                     A__
GAM1230  KIAA1354  5'  CAGTGACTGCCTTCCCTTGATA 61572        A      G  _
                                TATCAAGG AGGGCAG CG TG
                                |||||||| ||||||| || ||
                                ATAGTTCC TTCCGTC GT AC
                                     C      A  G
GAM1230  MGC20460  5'  CACCGCCTCCTACCCTTCTT   54901        C___    _
                                AGGAAGGG    AGGCG TG
                                ||||||||    ||||| ||
                                TTCTTCCC    TCCGC AC
                                     ATCC    C
GAM1230  LOC158476 3'  CACGCCCGCCCCCCCCATTGA  88186     _ AA_   A
                                TCAA GG   GGGC GGCGTG
                                |||| ||   |||| ||||||
                                AGTT CC   CCCG CCGCAC
                                  A  CCC    C
GAM1230  LOC90459  3'  CACACCCGCCTAATTTTTG    63550       A_   A  C
                                CAAGGA  GGGC GG GTG
                                ||||||  |||| || |||
                                GTTTTT  TCCG CC CAC
                                    AA    C  A
GAM1231  ELMO1     3'  ACGCCTTGGAACCGTCCTT    56152       G       TGCCA
                                AAGGA CGGTTCCA     GCGT
                                ||||| ||||||||     ||||
                                TTCCT GCCAAGGT     CGCA
                                  _       TC___
GAM1231  LOC206480 5'  CACGCTGGAGTGACCGGCCCT  92406     AG    TC   G
                                AGG  CGGT  CAT CCAGCGTG
                                |||  ||||  ||| ||||||||
                                TCC  GCCA  GTG GGTCGCAC
                                  CG   __   A
GAM1231  LOC220064 3'  CACGCTGGCTCTCCACACCCCT 95063     C   TCCAT__
            C                    GAG GGT      GCCAGCGTG
                                ||| |||      |||||||||
                                CTC CCA      CGGTCGCAC
                                  C   CACCTCT
GAM1232  DLEC1     3'  CATCTGGCCCTCCCTTG     24716       A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                  C    G  _
GAM1232  DLEC1     3'  CATCTGGCCCTCCCTTG     24717       A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
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                                GTTCC TCCCG TC TAC
                                  C    G  _
GAM1232 PIP5K1A  3' TATCCCACCCTGCCTTGATA  14520       A   CA  C
                                TATCAAGG AGGG  GG GTG
                                |||||||| ||||  || |||
                                ATAGTTCC TCCC  CC TAT
                                    G   A_  C
GAM1232 SOX11    3' ACCCACCCCCCCTTGGTA    13308       AA   CA  C
                                TATCAAGG  GGG  GG GT
                                ||||||||  |||  || ||
                                ATGGTTCC  CCC  CC CA
                                    CC   A_  _
GAM1232 CHL1     3' TGTTACCTTTCCTCAATA    22768     CA      CA
                                TAT  AGGAAGGG  GGCG
                                |||  ||||||||  ||||
                                ATA  TCCTTTCC  TTGT
                                  AC       A_
GAM1232 EPB41L1  3' CATTCTGCCCTTCCCTGA    71104     A        C
                                TCA GGAAGGGCAGG GTG
                                ||| ||||||||||| |||
                                AGT CCTTCCCGTCT TAC
                                  C         _
GAM1232 FLJ00060 3' CATACCCCCTGCCCTCCTCTGA 61741     _   A      CGTG
                                TCA AGGA GGGCAGG   ATG
                                ||| |||| |||||||   |||
                                AGT TCCT CCCGTCC   TAC
                                  C   _      CCCA
GAM1232 FLJ10898 5' CACCACAGCCCTTTCTCAATA  60126     CA       AGGC
                                TAT  AGGAAGGGC   GTG
                                |||  |||||||||   |||
                                ATA  TCTTTCCCG   CAC
                                  AC        ACAC
GAM1232 FLJ22557 3' ATCATCCCATCCTTAATA    45581     C    A   CAGGC
                                TAT AAGGA GGG    GTGAT
                                ||| ||||| |||    |||||
                                ATA TTCCT CCC    TACTA
                                  A    A  _____
GAM1232 KIAA0574 3' CATCCCCTGCCCTCCCCTGA   69808     A  A      CGT
                                TCA GG AGGGCAGG   GATG
                                ||| || ||||||||   ||||
                                AGT CC TCCCGTCC   CTAC
                                  C  C       C__
GAM1232 KIAA0632 3' CACCTCAGAAACCCTTCCTTGA 32071          CA___  C
                                TCAAGGAAGGG    GG GTG
                                ||||||||||    || |||
                                AGTTCCTTCCC    CT CAC
                                       AAAGA  C
GAM1232 KIAA1045 3' CATCACATGTCCTTCC      71599         GGC
                                GGAAGGGCA   GTGATG
                                |||||||||   ||||||
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                                CCTTCCTGT   CACTAC
                                    A__
GAM1232  KIAA1354  5'  CAGTGACTGCCTTCCCTTGATA 61572        A      G  _
                                TATCAAGG AGGGCAG CG TG
                                |||||||| ||||||| || ||
                                ATAGTTCC TTCCGTC GT AC
                                    C       A  G
GAM1232  MGC20460  5'  CACCGCCTCCTACCCTTCTT   54901        C___    _
                                AGGAAGGG    AGGCG TG
                                |||||||||    ||||| ||
                                TTCTTCCC    TCCGC AC
                                    ATCC     C
GAM1232  LOC158476 3'  CACGCCCGCCCCCCCCCATTGA  88186     _ AA_    A
                                TCAA GG   GGGC GGCGTG
                                |||| ||   |||| ||||||
                                AGTT CC   CCCG CCGCAC
                                  A  CCC    C
GAM1232  LOC90459  3'  CACACCCGCCTAATTTTTG    63550       A_    A  C
                                CAAGGA  GGGC GG GTG
                                ||||||  |||| || |||
                                GTTTTT  TCCG CC CAC
                                   AA    C  A
GAM1233  C18orf1   3'  CAGCCAAGTGAAGGACCT    60861      T       GTGCGT
                                AGGT CCTTCACT     GCTG
                                |||| ||||||||      ||||
                                TCCA GGAAGTGA     CGAC
                                  _       AC_____
GAM1233  CNR1      3'  GGGGTTTACAGTGAAGAAAGCC 32720      C_         CG G
                                GGTT  CTTCACTGTG  T CT
                                ||||  ||||||||||  | ||
                                CCGA  GAAGTGACAT  G GG
                                  AA         TT G
GAM1233  FACL2     3'  CAAAAACAATGAAGGAAACC   41208      _     C   GCG
                                GGTT CCTTCA TGT   TG
                                |||| |||||| |||   ||
                                CCAA GGAAGT ACA   AC
                                  A     A   AAA
GAM1233  FADD      3'  AGCACAGAAGGAATCT      15122          ACTGTGC
                                AGGTTCCTTC      GTGCT
                                ||||||||||      |||||
                                TCTAAGGAAG      CACGA
                                    A_______
GAM1233  HIS1      3'  CAGCTGAATGAGGAACC      22337        T  CTGTG  T
                                GGTTCCT CA     CG GCTG
                                ||||||| ||     || ||||
                                CCAAGGA GT     GT CGAC
                                   _ AA___  _
GAM1233  KMO       3'  TATCACAATGGAAGGAACCT   14847          AC_    C
                                AGGTTCCTTC   TGTG GTG
                                ||||||||||   |||| |||
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                                TCCAAGGAAG   ACAC TAT
                                      GTA   _
GAM1233  OGN      3'  TCAACAATGAGTAAAGGAACTT 26769        C   GTGCG  C
                                AGGTTCCTT ACT    TG TGA
                                ||||||||| |||    || |||
                                TTCAAGGAA TGA    AC ACT
                                      A   GTA__  A
GAM1233  OGN      3'  TCAACAATGTGTAAAGGAACTT 44591        CAC  TG   GC_
                                AGGTTCCTT   TG  CGT   TGA
                                |||||||||   ||  |||   |||
                                TTCAAGGAA   AT  GTA   ACT
                                      ___  GT   ACA
GAM1233  OGN      3'  TCAACAATGTGTAAAGGAACTT 53401        CAC  TG   GC_
                                AGGTTCCTT   TG  CGT   TGA
                                |||||||||   ||  |||   |||
                                TTCAAGGAA   AT  GTA   ACT
                                      ___  GT   ACA
GAM1233  DKFZP564M182 3'  TACTACAGTGAAGAAACCT    78641      C        C
                                AGGTT CTTCACTGTG GTG
                                ||||| |||||||||| |||
                                TCCAA GAAGTGACAT CAT
                                   A         _
GAM1233  FLJ12660  3'  TCAGCAATGTGGTGATGGAACC 47899        T    TG GCG
            T                    AGGTTCC TCAC  T   TGCTGA
                                 ||||||| ||||  |   ||||||
                                 TCCAAGG AGTG  G   ACGACT
                                     T   GT TA_
GAM1233  IMAGE3451454 5'  TCAGCACGGGTCGAAGGACCCT 54939     T     _   GTG
                                AGG TCCTTC ACT   CGTGCTGA
                                ||| |||||| |||   ||||||||
                                TCC AGGAAG TGG   GCACGACT
                                  C     C  ___
GAM1233  KIAA0930  3'  CAACACGCACACCTCCAACCT  71065      CCTTCAC       C
                                AGGTT      TGTGCGTG TG
                                |||||      |||||||| ||
                                TCCAA      ACACGCAC AC
                                   CCTCC__       A
GAM1233  KIAA0930  3'  CAGCACACAGGCACCAAGGAAC 71066        CACT   _____
            T                    GGTTCCTT   GTGC   GTGCTG
                                 ||||||||   ||||   ||||||
                                 TCAAGGAA   CACG   CACGAC
                                     C___    GACA
GAM1233  KIAA1247  3'  CAGCAGTTGGTATGAAGAACCT 62506       C   CTGT_  G
                                AGGTTC TTCA    GC TGCTG
                                |||||| ||||    || |||||
                                TCCAAG AAGT    TG ACGAC
                                   _   ATGGT  _
GAM1233  KIAA1737  3'  CAGCAAATGGAGGAACCT    67935          CTGTGCG
                                AGGTTCCTTCA      TGCTG
                                ||||||||||       |||||
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                                TCCAAGGAGGT      ACGAC
                                      AA_____
GAM1233  MGC10955  3'  TTGGCCAAAATAAAGGAACCT  52034        CAC   GCGT  TG
                                AGGTTCCTT   TGT    GC  A
                                |||||||||   |||    ||  |
                                TCCAAGGAA   ATA    CG  T
                                      ___   AAAC   GT
GAM1233  POLR3F    5'  CAACTCAGAATGAAGGAACC   60616         __   TGCG
                                GGTTCCTTCA  CTG    TG
                                ||||||||||  |||    ||
                                CCAAGGAAGT  GAC    AC
                                      AA   TCA_
GAM1233  LOC127534 3'  CAACACACACAGTGTGTGCC   75965     TCCTT      C   C
                                GGT     CACTGTG GTG TG
                                |||     ||||||| ||| ||
                                CCG     GTGACAC CAC AC
                                  TGT__      A   A
GAM1233  LOC144600 3'  CAACACGCACACCTCCAACCT  84083      CCTTCAC       C
                                AGGTT      TGTGCGTG TG
                                |||||      |||||||| ||
                                TCCAA      ACACGCAC AC
                                   CCTCC__       A
GAM1233  LOC150282 3'  CAGCACACACAGTGGGTACTT  80538      T  TT      C
                                AGGT CC  CACTGTG GTGCTG
                                |||| ||  ||||||| ||||||
                                TTCA GG  GTGACAC CACGAC
                                  T  __      A
GAM1233  LOC255231 3'  CAGCGGCTGAGCAGAGGAACC  97118        CA  GT  G
                                GGTTCCTT  CT  GC TGCTG
                                ||||||||  ||  || |||||
                                CCAAGGAG  GA  CG GCGAC
                                     AC  GT  _
GAM1233  LOC91748  5'  CAGCACGCAGGTGCCAGAACC  67636      CTT    G
                                GGTTC   CACT TGCGTGCTG
                                |||||   |||| |||||||||
                                CCAAG   GTGG ACGCACGAC
                                   ACC    _
GAM1234  ADAT1     3'  CTCCAGCCTGGGTGATAGA   24915    CC      TTTAT
                                TC  ATCACCC    TTGGAG
                                ||  |||||||    ||||||
                                AG  TAGTGGG    GACCTC
                                 A_      TCC__
GAM1234  ASH1      3'  CCAAAATGGAATCATGGGATA  38085        CAC_  TTTA
                                TATCCCAT    CC    TTTGG
                                ||||||||    ||    |||||
                                ATAGGGTA    GG    AAACC
                                     CTAA  TA__
GAM1234  EHD2      3'  CCAAAGTGATGGGAT       28217          CCTTTA
                                ATCCCATCAC     TTTGG
                                ||||||||||     |||||
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                                TAGGGTAGTG     AAACC
                                          ______
GAM1234 KCNK3    3' CTCCAGCCTGGGTGACAGGG  11174     A_     TTTAT
                                CCC  TCACCC    TTGGAG
                                |||  ||||||    ||||||
                                GGG  AGTGGG    GACCTC
                                  AC     TCC__
GAM1234 MS4A1    3' CCAAGATTAAAAGGTGACAGG  5546     CA    C   __
                                CC  TCACC TTTA  TTTGG
                                ||  ||||| ||||  |||||
                                GG  AGTGG AAAT  GAACC
                                 AC    A   TA
GAM1234 PART1    3' CTCCATTCCAGGTGACATGGAT 33900      CA_    CTTTATT
             A                   TATCC   TCACC      TGGAG
                                 |||||   |||||      |||||
                                 ATAGG   AGTGG      ACCTC
                                    TAC    ACCTT__
GAM1234 SNX5     3' CTAAGAAAGGGTGTAGGA    27787     CAT      A
                                TCC   CACCCTTT TTTGG
                                |||   |||||||| |||||
                                AGG   GTGGGAAA GAATC
                                  AT_      _
GAM1234 FADS1    3' CTCCAGCCTGGGGTGATAGA   26378    CC      TTAT
                                TC  ATCACCCT    TTGGAG
                                ||  ||||||||    ||||||
                                AG  TAGTGGGG    GACCTC
                                 A_      TCC_
GAM1234 FLJ10460 3' CTCCAACCTGGGTGATGG    36615        TTTAT
                                CCATCACCC    TTGGAG
                                |||||||||    ||||||
                                GGTAGTGGG    AACCTC
                                     TCC__
GAM1234 FLJ20220 3' TCTTAAAAGCAATGGGATG   35277       CACC    ATTT
                                TATCCCAT    CTTT    GGA
                                ||||||||    ||||    |||
                                GTAGGGTA    GAAA    TCT
                                     AC__    AT__
GAM1234 FLJ20312 3' CTCCAAATAAATCAAGATGAAG 35409     CC    ACCC
             TA                   TAT  CATC    TTTATTTGGAG
                                  |||  ||||    ||||||||||
                                  ATG  GTAG    AAATAAACCTC
                                    AA    AACT
GAM1234 FRAG1    3' CTCCTTTGCAAAGGTATGGGAT 27944        CAC     ATTT_
             A                    TATCCCAT   CCTTT    GGAG
                                  ||||||||   |||||    ||||
                                  ATAGGGTA   GGAAA    CCTC
                                     T__     CGTTT
GAM1234 JAM1     3' CCAAAGTGATGGGAT      58497          CCTTTA
                                ATCCCATCAC     TTTGG
                                ||||||||||     |||||
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                                TAGGGTAGTG     AAACC
                                          _______
GAM1234  JAM1     3'  CCAAAGTGATGGGAT      58512          CCTTTA
                                ATCCCATCAC     TTTGG
                                ||||||||||     |||||
                                TAGGGTAGTG     AAACC
                                          _______
GAM1234  JAM1     3'  CCAAAGTGATGGGAT      58540          CCTTTA
                                ATCCCATCAC     TTTGG
                                ||||||||||     |||||
                                TAGGGTAGTG     AAACC
                                          _______
GAM1234  JAM1     3'  CCAAAGTGATGGGAT      58568          CCTTTA
                                ATCCCATCAC     TTTGG
                                ||||||||||     |||||
                                TAGGGTAGTG     AAACC
                                          _______
GAM1234  JAM1     3'  CCAAAGTGATGGGAT      34221          CCTTTA
                                ATCCCATCAC     TTTGG
                                ||||||||||     |||||
                                TAGGGTAGTG     AAACC
                                          _______
GAM1234  KIAA1001 3'  CTCCAGCCTGGGTGATGG    31005          TTTAT
                                CCATCACCC    TTGGAG
                                |||||||||    ||||||
                                GGTAGTGGG    GACCTC
                                     TCC__
GAM1234  KIAA1877 3'  CCAAAGTGATGGGAT       66743          CCTTTA
                                ATCCCATCAC     TTTGG
                                ||||||||||     |||||
                                TAGGGTAGTG     AAACC
                                          _______
GAM1234  MESDC2   3'  CTCCAGCCTGGATGACGGGATG 72913        A   C  TTTAT
                                TATCCC TCA CC     TTGGAG
                                |||||| ||| ||     ||||||
                                GTAGGG AGT GG     GACCTC
                                   C   A  TCC__
GAM1234  MGC10612 3'  CCAGTGAGAAGGAAAATGGGAT 49521          CAC     AT_
            A                    TATCCCAT   CCTTT   TTGG
                                 ||||||||   |||||   ||||
                                 ATAGGGTA   GGAAG   GACC
                                      AAA     AGT
GAM1234  RNF8     3'  CCAAACAATGTACCAGTGATGG 15561         CCT____  A
            G                    CCCATCAC      TT TTTGG
                                 ||||||||      || |||||
                                 GGGTAGTG      AA AAACC
                                      ACCATGT  C
GAM1234  SEMA3C   3'  CTCCAAATAAAAATTAGATGG  22106       ACCC_
                                 CCATC    TTTATTTGGAG
                                 |||||    ||||||||||
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                                GGTAG    AAATAAACCTC
                                   ATTAA
GAM1234  WBSCR23   3' CTCCAGCCTGGGTGATAGA   47432    CC      TTTAT
                                TC  ATCACCC    TTGGAG
                                ||  |||||||    ||||||
                                AG  TAGTGGG    GACCTC
                                 A_      TCC__
GAM1234  LOC124145 3' GATAAAAAGTGATGGGGTA   74723          CC
                                TATCCCATCAC  TTTATT
                                ||||||||||  ||||||
                                ATGGGGTAGTG  AAATAG
                                       AA
GAM1234  LOC146280 5' CTCCTGGGAGGGTGATG     78348          ATTT
                                CATCACCCTTT    GGAG
                                ||||||||||    ||||
                                GTAGTGGGAGG    CCTC
                                       GT__
GAM1234  LOC147740 3' CCAAATAAAGAGCACAGGATA  79153      CATCACC
                                TATCC      CTTTATTTGG
                                |||||      ||||||||||
                                ATAGG      GAAATAAACC
                                   ACACGA_
GAM1234  LOC159110 5' CCAGGCGCGCGGCGATGGGATA 82987         A  CTTTA
                                TATCCCATC CC    TTTGG
                                |||||||| ||    |||||
                                ATAGGGTAG GG    GGACC
                                      C  CGCGC
GAM1234  LOC159116 5' CCAGGCGCGCGGCGATGGGATA 82970         A  CTTTA
                                TATCCCATC CC    TTTGG
                                |||||||| ||    |||||
                                ATAGGGTAG GG    GGACC
                                      C  CGCGC
GAM1234  LOC255328 3' CTCCAGCCTGGGTGATAAGA   98339    CC      TTTAT
                                TC  ATCACCC    TTGGAG
                                ||  |||||||    ||||||
                                AG  TAGTGGG    GACCTC
                                 AA      TCC__
GAM1234  LOC256980 3' CTCCACAAAGGTGAGGGGA    96928     A    C   ATT
                                TCCC TCACC TTT   TGGAG
                                |||| ||||| |||   |||||
                                AGGG AGTGG AAA   ACCTC
                                  G     _   C__
GAM1234  LOC90573  3' CTCCAGGCTGGGTGACAGAT   63957     CCA     TTTA
                                ATC   TCACCC    TTTGGAG
                                |||   ||||||   |||||||
                                TAG   AGTGGG   GGACCTC
                                  AC_     TC__
GAM1235  CRACC     3' ACCATAAAAAAAGTGCTT    41303          CTG  GAA
                                AAGCACTTTT   TA   GGT
                                ||||||||||   ||   |||
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                                TTCGTGAAAA  AT  CCA
                                     AA_  A__
GAM1235  GNB5     3'  ACCTTCCTCTGGAAGTGCTGA  22698     A      CTGTA
                                TCA GCACTTTT    GAAGGT
                                ||| ||||||||    ||||||
                                AGT CGTGAAGG    CTTCCA
                                  _      TCTC_
GAM1235  GNB5     3'  ACCTTCCTCTGGAAGTGCTGA  33001     A      CTGTA
                                TCA GCACTTTT    GAAGGT
                                ||| ||||||||    ||||||
                                AGT CGTGAAGG    CTTCCA
                                  _      TCTC_
GAM1235  NEUROD1  3'  ACCAGCAGAAAAGTGCTT    11777          AGAA
                                AAGCACTTTTCTGT   GGT
                                ||||||||||||||   |||
                                TTCGTGAAAAGACG   CCA
                                       A___
GAM1235  NGFR     3'  GACCTTCTGGGAAATGGCTTGA 11796      ACT    G
                                TCAAGC  TTTCT TAGAAGGTC
                                ||||||  ||||| |||||||||
                                AGTTCG  AAAGG GTCTTCCAG
                                   GT_    _
GAM1235  DKFZp547I224 5'  ACCAATACAGAGAAGTGCTT  39947           GAA
                                AAGCACTTTTCTGTA  GGT
                                ||||||||||||||  |||
                                TTCGTGAAGAGACAT  CCA
                                       AA_
GAM1235  FKBP5    3'  ACCTTTTAAAAAAAAATGCTT  15929     C   CTG
                                AAGCA TTTT   TAGAAGGT
                                ||||| ||||  ||||||||
                                TTCGT AAAA   ATTTTCCA
                                   A   AAA
GAM1235  FLJ10803 3'  ACTAAAGACAGAAAAAAGCTTG 37193      AC      AGAA
            A                    TCAAGC  TTTTCTGT   GGT
                                ||||||  ||||||||   |||
                                AGTTCG  AAAAGACA   TCA
                                   AA      GAAA
GAM1235  MGC11324 3'  ATAGAAAAAAGTGCTTGA    52148          __
                                TCAAGCACTTT  TCTGT
                                ||||||||||  |||||
                                AGTTCGTGAAA  AGATA
                                       AA
GAM1235  MGC3113  3'  ACCTCCCAAAAGTGCTGGA   44056   A      CTGTA  A
                                TC AGCACTTTT    GA GGT
                                || |||||||||    || |||
                                AG TCGTGAAAA    CT CCA
                                 G       CC___  _
GAM1235  MRPS18C  3'  ACCTTTGGATAGAAAAGTGTTT 32679           A_
            GA                    TCAAGCACTTTTCTGT  GAAGGT
                                ||||||||||||||||  ||||||
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                                AGTTTGTGAAAAGATA  TTTCCA
                                      GG
GAM1235  PDZD2    3'  ACCTGTCTTGATAAGTGCTTGA 81714          T  TGT   _
                                TCAAGCACTT TC   AGA AGGT
                                |||||||||| ||   ||| ||||
                                AGTTCGTGAA AG   TCT TCCA
                                      T  T__   G
GAM1235  PTPN21   3'  ACCTGGGAAAGGTGCT      23862          GTAGA
                                AGCACTTTTCT    AGGT
                                ||||||||||    ||||
                                TCGTGGAAAGG    TCCA
                                      G____
GAM1235  LOC133418 3'  ACCTTAAATAGGAAAAGTACT  75593    C       GTAG_
                                AG ACTTTTCT    AAGGT
                                || ||||||||    |||||
                                TC TGAAAAGG    TTCCA
                                 A       ATAAA
GAM1235  LOC134265 3'  ACCTTTTACAAACACTTGA    75651       CACTTTTC
                                TCAAG       TGTAGAAGGT
                                |||||       ||||||||||
                                AGTTC       ACATTTTCCA
                                   ACAA____
GAM1235  LOC144766 3'  ACCTTCCGGAAAAGTGCTGGA  77478    A          TA
                                TC AGCACTTTTCTG  GAAGGT
                                || ||||||||||||  ||||||
                                AG TCGTGAAAAGGC  CTTCCA
                                 G          __
GAM1235  LOC153603 5'  CTTAGACAGAAAATACTTGA   81776      CAC       AG
                                TCAAG   TTTTCTGT  AAG
                                |||||   ||||||||  |||
                                AGTTC   AAAAGACA  TTC
                                   AT_       GA
GAM1235  LOC204285 5'  ACCTCCTACAGAATTGTG    91011     TT       A
                                CAC  TTCTGTAG AGGT
                                |||  |||||||| ||||
                                GTG  AAGACATC TCCA
                                  TT       C
GAM1235  LOC256597 5'  ACCCCCTACAAGGCCTGA    98024     A  A  TTTC    AA
                                TCA GC CT    TGTAG  GGT
                                ||| || ||    |||||  |||
                                AGT CG GA    ACATC  CCA
                                  C  _  ____     CC
GAM1235  LOC89932  5'  GACCCTCTAGCCCCAAAAGTGC 61460    A       CT_ _   A
              CTG                    CA GCACTTTT   GT AGA GGTC
                                || ||||||||   || ||| ||||
                                GT CGTGAAAA   CG TCT CCAG
                                 C       CCC  A   C
GAM1236  AXUD1    3'  TGCCCCTTGCCCAGGAGGC    53446    G   AGATC
                                GC CTC     GGCAAGGGGCA
                                || |||     ||||||||||
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                              CG GAG    CCGTTCCCCGT
                               _  GAC__
GAM1236 HYOU1    3' GCCCCTTGCCTAAAAGCCT   60386   C  CAGATC
                              AG GCT    GGCAAGGGGC
                              || |||    ||||||||||
                              TC CGA    CCGTTCCCCG
                               _  AAAT__
GAM1236 LGALS3BP 3' GCCCTACTCACCTGAGCGCT  69859       ATC  CAA
                              AGCGCTCAG  GG  GGGGC
                              |||||||||  ||  |||||
                              TCGCGAGTC  TC  TCCCG
                                   CAC  A__
GAM1236 MFGE8    3' GCCCCTTGTCCTGAAGC    21007   GC   ATC
                              GC  TCAG  GGCAAGGGGC
                              ||  ||||  ||||||||||
                              CG  AGTC  CTGTTCCCCG
                               A_  ____
GAM1236 NUP62    3' CCCCTGTAATCTCAGCACTT  25645    C  C   CG  A
                              AAG GCT AGAT  GCA GGGG
                              ||| ||| ||||  ||| ||||
                              TTC CGA TCTA  TGT CCCC
                                A  C   A_  _
GAM1236 PEA15    5' GCCCGCGCCCTGAGCGCT   15009       ATC  AAG
                              AGCGCTCAG  GGC  GGGC
                              |||||||||  |||  ||||
                              TCGCGAGTC  CCG  CCCG
                                   ____  CG_
GAM1236 PLCB4    5' TGCCCCTTGTTCTCCCAAGC  8121    CA_ TC
                              GCT  GA  GGCAAGGGGCA
                              |||  ||  ||||||||||
                              CGA  CT  TTGTTCCCCGT
                                ACC  C_
GAM1236 TPS1     3' TGCCCCTTCCTGTCCTAAGC  61106   C  AT  C
                              GCT AG  CGG AAGGGGCA
                              ||| ||  ||| ||||||||
                              CGA TC  GTC TTCCCCGT
                                A  CT  C
GAM1236 TPSB1    3' TGCCCCTTCCTGTCCTAAGC  13838   C  AT  C
                              GCT AG  CGG AAGGGGCA
                              ||| ||  ||| ||||||||
                              CGA TC  GTC TTCCCCGT
                                A  CT  C
GAM1236 VPS41    3' CCTTCGAGTCTGAGCGCTT   27691        _  CA
                              AAGCGCTCAGA TCGG  AGG
                              |||||||||| ||||  |||
                              TTCGCGAGTCT AGCT  TCC
                                    G   __
GAM1236 BFAR     3' CCCCTGTAATCCCAGCACTT  61424   C  CA  CG  A
                              AAG GCT  GAT  GCA GGGG
                              ||| |||  |||  ||| ||||
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                                TTC CGA  CTA  TGT CCCC
                                  A   CC   A_  _
GAM1236 COLEC12  3' TGCTGGCCGCCCTGAGCGCT  56108        AT   AAGG
                                AGCGCTCAG  CGGC   GGCA
                                |||||||||  ||||   ||||
                                TCGCGAGTC  GCCG   TCGT
                                     CC   G___
GAM1236 FLJ12770 3' CCCCTTGCCCTCAGGCTT   50676     G  C  ATC
                                AAGC CT AG   GGCAAGGGG
                                |||| || ||   |||||||||
                                TTCG GA TC   CCGTTCCCC
                                  _ C  ___
GAM1236 FLJ20519 3' TGCCCTTTCAATCCTAGC   35799     CA   C  CA
                                GCT  GAT GG  AGGGGCA
                                |||  ||| ||  |||||||
                                CGA  CTA CT  TTCCCGT
                                  TC   A  __
GAM1236 GNG4     3' TGCCCCCAAGTCATCTGAGC  16856        C   AA_
                                GCTCAGAT GGC   GGGGCA
                                |||||||| |||   ||||||
                                CGAGTCTA CTG   CCCCGT
                                     _  AAC
GAM1236 MGC2705  3' CCCCCAGGGATCTGAGCCCT  52081    C       GGCAA
                                AG GCTCAGATC    GGGG
                                || |||||||||    ||||
                                TC CGAGTCTAG    CCCC
                                 C       GGAC_
GAM1236 NR4A3    5' CCTCTTGCCCTGAGCCCTT   23719    C     ATC
                                AAG GCTCAG   GGCAAGGGG
                                ||| ||||||   |||||||||
                                TTC CGAGTC   CCGTTCTCC
                                  C    ___
GAM1236 RNF36    5' TGCCCCTTGGTGGGCTGAAGCT 55800     GC   AT  G
             T                   AAGC  TCAG  CG CAAGGGGCA
                                ||||  ||||  || |||||||||
                                TTCG  AGTC  GT GTTCCCCGT
                                  A_   GG  G
GAM1236 SCYA17   3' GCCCCCACCCTGAGCGC    12973        ATC  CAA
                                GCGCTCAG   GG   GGGGC
                                ||||||||   ||   |||||
                                CGCGAGTC   CC   CCCCG
                                     ___  AC_
GAM1236 LOC138311 5' TGCCCCTTCTCCAAGCGC    76723      CA  TCG C
                                GCGCT  GA   G AAGGGGCA
                                |||||  ||   | ||||||||
                                CGCGA  CT   C TTCCCCGT
                                  AC  ___ _
GAM1236 LOC151534 5' CCCCAGATCCGGCCTGAGCGC  57481        AT   CAA_
                                GCGCTCAG  CGG   GGGG
                                ||||||||  |||   ||||
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                                CGCGAGTC GCC   CCCC
                                    CG  TAGA
GAM1236 LOC155060 3' TGCCCCTTAAATCTGAGC   87607       CGGC
                                GCTCAGAT   AAGGGGCA
                                ||||||||   ||||||||
                                CGAGTCTA   TTCCCCGT
                                    AA__
GAM1236 LOC254896 5' GCCCCTTTTCTGAGTGCTT  97861         TCGGC
                                AAGCGCTCAGA   AAGGGGC
                                ||||||||||    |||||||
                                TTCGTGAGTCT   TTCCCCG
                                     T____
GAM1236 LOC57228 3' CCCCCTAATCTGAGCCCTT   40400    C      CG CAA
                                AAG GCTCAGAT  G  GGGG
                                ||| ||||||||  |  ||||
                                TTC CGAGTCTA  C  CCCC
                                  C       AT ___
GAM1237 ACTR1B   3' GACACAGCCCCTTTCACACTCT 71380        CCCAA
                                AGAGTGTGA   GCTGTGTC
                                |||||||||   ||||||||
                                TCTCACACT   CGACACAG
                                    TTCCC
GAM1237 ASL     3' ACACAGCCTGGGCAACAC   72392     GA   A
                                GTGT  CCCA GCTGTGT
                                ||||  |||| |||||||
                                CACA  GGGT CGACACA
                                  AC   C
GAM1237 DSCR3   3' ACAGAGGCCACACTTTC    21299        A  CAAG
                                GAGAGTGTG CC   CTGT
                                ||||||||| ||   ||||
                                CTTTCACAC GG   GACA
                                    C  A___
GAM1237 HIRA    3' GGCAGGGCCACACTCTC    13907        A  AA
                                GAGAGTGTG CCC  GCT
                                ||||||||| |||  |||
                                CTCTCACAC GGG  CGG
                                    C  A_
GAM1237 LAMC3   3' ACATGAGTGCACACTCTC   21343        ACCCAA  _
                                GAGAGTGTG    GCT GTGT
                                |||||||||    ||| ||||
                                CTCTCACAC    TGA TACA
                                    G_____  G
GAM1237 PHKA2   3' ACATGATCACACTCTC     6088         CC  AGC
                                GAGAGTGTGA  CA  TGT
                                ||||||||||  ||  |||
                                CTCTCACACT  GT  ACA
                                    A_ ___
GAM1237 RAD52   3' ACACAGCTCTCTCCACAACCTC 12754    AG   ACCCA
                                GAG  TGTG   AGCTGTGT
                                |||  ||||   ||||||||
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                                CTC  ACAC    TCGACACA
                                  CA   CTCTC
GAM1237  RAD52    3'  ACACAGCTCTCTCCACAACCTC 57016    AG   ACCCA
                                GAG  TGTG    AGCTGTGT
                                |||  ||||    ||||||||
                                CTC  ACAC    TCGACACA
                                  CA   CTCTC
GAM1237  RAD52    3'  ACACAGCTCTCTCCACAACCTC 57040    AG   ACCCA
                                GAG  TGTG    AGCTGTGT
                                |||  ||||    ||||||||
                                CTC  ACAC    TCGACACA
                                  CA   CTCTC
GAM1237  RAD52    3'  ACACAGCTCTCTCCACAACCTC 57047    AG   ACCCA
                                GAG  TGTG    AGCTGTGT
                                |||  ||||    ||||||||
                                CTC  ACAC    TCGACACA
                                  CA   CTCTC
GAM1237  RRP22    3'  GACCTCAATGGGTCACAATC   22392    G      AGC  T_
                                GA TGTGACCCA   TG  GTC
                                || |||||||||   ||  |||
                                CT ACACTGGGT   AC  CAG
                                 A       A__  TC
GAM1237  WHSC1    3'  GACACACACCCATTGGGTCACA 24672         GC____
           C                     GTGTGACCCAA     TGTGTC
                                ||||||||||      ||||||
                                CACACTGGGTT     ACACAG
                                      ACCCAC
GAM1237  WNT7A    3'  GACACAGCCCAGGTCCCTCC   17317   A   TGT   CAA
                                G GAG   GACC   GCTGTGTC
                                | |||   ||||   ||||||||
                                C CTC   CTGG   CGACACAG
                                 _   C__    ACC
GAM1237  CREB-H   3'  GACACAGCCTGAAACAGACCT  51874    A  G  ACC  A
                                AG GT TG   CA GCTGTGTC
                                || || ||   || ||||||||
                                TC CA AC   GT CGACACAG
                                 _  G  AAA  C
GAM1237  CREB-H   3'  GACACAGCCTGAAACAGATCC  51875   A  G_   GACC  A
                                G GA  TGT    CA GCTGTGTC
                                | ||  |||    || ||||||||
                                C CT  ACA    GT CGACACAG
                                 _  AG   AA__  C
GAM1237  FBXO22   3'  ACTTCCTTGAGTCACATTCTC  25143          C    CT_
                                GAGAGTGTGAC CAAG   GT
                                |||||||||| ||||   ||
                                CTCTTACACTG GTTC   CA
                                      A    CTT
GAM1237  FLJ23519 3'  GACACAGCTTGGGTCCCCTCC  50950   A   TGT
                                G GAG   GACCCAAGCTGTGTC
                                | |||   ||||||||||||||
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                                C CTC   CTGGGTTCGACACAG
                                 _  CC_
GAM1237 IKKE     3' ACACAGCTCTCTCCACTC    26593      T  CCCA
                                GAGTG GA    AGCTGTGT
                                ||||| ||    ||||||||
                                CTCAC CT    TCGACACA
                                   _ CTC_
GAM1237 KIAA0356 3' GCCCGGGGTCACACTCTC    66775           AA_
                                GAGAGTGTGACCC   GC
                                ||||||||||||   ||
                                CTCTCACACTGGG   CG
                                       GCC
GAM1237 KIAA0544 3' GACACAGCCCAGGTGCGC    71466     G   CAA
                                GTGT ACC   GCTGTGTC
                                |||| |||   ||||||||
                                CGCG TGG   CGACACAG
                                   _   ACC
GAM1237 KIAA0557 3' GATGTGGCCAGGCCACACTCC  78566   A      A  CAA  TG
                                G GAGTGTG CC   GC  TGTC
                                | |||||||  ||   ||  ||||
                                C CTCACAC GG   CG  GTAG
                                 _      C  AC_  GT
GAM1237 KIAA1210 3' ACACAGCTGTTACACCTC    98055     A      CCA
                                GAG GTGTGAC   AGCTGTGT
                                ||| |||||||   ||||||||
                                CTC CACATTG   TCGACACA
                                  _     ____
GAM1237 KIAA1915 5' ACAGGGGTACACTCTC      73664         A   AAG
                                GAGAGTGTG CCC   CTGT
                                |||||||||  |||   ||||
                                CTCTCACAT GGG   GACA
                                      _  ____
GAM1237 MGC16279 5' GGCTCGGTCACACTCTC     52987           CA
                                GAGAGTGTGACC  AGCT
                                ||||||||||||  ||||
                                CTCTCACACTGG  TCGG
                                       C_
GAM1237 MGC16279 5' GGCTCGGTCACACTCTC     63542           CA
                                GAGAGTGTGACC  AGCT
                                ||||||||||||  ||||
                                CTCTCACACTGG  TCGG
                                       C_
GAM1237 MGC3178  3' ACACAGTTGGAGGTCACCTCTC 48714      T     CA_
                                GAGAG GTGACC   AGCTGTGT
                                ||||| ||||||   ||||||||
                                CTCTC CACTGG   TTGACACA
                                   _     AGG
GAM1237 PMVK     3' ACCTCTTGGAGCACACTCTC   22647         AC    CT
                                GAGAGTGTG  CCAAG  GT
                                |||||||||  |||||  ||
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                                CTCTCACAC  GGTTC  CA
                                     GA    TC
GAM1237  PMVK     3'  ACCTCTTGGAGCACACTCTC   96253        AC    CT
                                GAGAGTGTG  CCAAG  GT
                                |||||||||  |||||  ||
                                CTCTCACAC  GGTTC  CA
                                     GA    TC
GAM1237  TACTILE  3'  GACACAGGCATCAACACTCTC  20587        GACCCAAG
                                GAGAGTGT      CTGTGTC
                                ||||||||      |||||||
                                CTCTCACA      GACACAG
                                    ACTACG__
GAM1237  LOC145195 3'  GACACAGCCTGGCCTGCTC   84231      TGAC   A
                                GAGTG   CCA GCTGTGTC
                                |||||   ||| ||||||||
                                CTCGT   GGT CGACACAG
                                   CC__   C
GAM1237  LOC147054 5'  ACACGGAGTCACACTC      84997        CCAAG
                                GAGTGTGAC    CTGTGT
                                |||||||||    ||||||
                                CTCACACTG    GGCACA
                                     A____
GAM1237  LOC150358 5'  ACACAGCCCAGGGCACTC    86081      TGA   AA_
                                GAGTG   CCC   GCTGTGT
                                |||||   |||   |||||||
                                CTCAC   GGG   CGACACA
                                   ___   ACC
GAM1237  LOC158490 5'  GGCTCAGTCACACTCTC     82824         CCA
                                GAGAGTGTGAC   AGCT
                                ||||||||||   ||||
                                CTCTCACACTG   TCGG
                                      AC_
GAM1237  LOC195977 3'  GACACAGCCCGGAGTACTTTTC 88932      T   AC  AA
                                GAGAG GTG  CC  GCTGTGTC
                                ||||| |||  ||  ||||||||
                                CTTTT CAT  GG  CGACACAG
                                   _  GA  CC
GAM1237  LOC254182 5'  GATCACCTGGTCACACTC    97749        CA  C  T
                                GAGTGTGACC  AG TG GTC
                                ||||||||||  || || |||
                                CTCACACTGG  TC AC TAG
                                     __  C  _
GAM1237  LOC255598 5'  ACACAGCTCATGACTCACCTC  99345    T   CC  __
                                GAG GTGA  CA  AGCTGTGT
                                ||| ||||  ||  ||||||||
                                CTC CACT  GT  TCGACACA
                                  _   CA  AC
GAM1237  LOC255975 5'  ACTTCCTCAGGTCATACTCTC  97568         CA  CT_
                                GAGAGTGTGACC  AG   GT
                                ||||||||||||  ||   ||
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                                CTCTCATACTGG  TC   CA
                                      AC  CTT
GAM1237  LOC257486 3'  ACACAGCTGTTACACCTC    69756     A      CCA
                                GAG GTGTGAC   AGCTGTGT
                                ||| |||||||   ||||||||
                                CTC CACATTG   TCGACACA
                                  _     ____
GAM1238  PROK1     3'  CACCAACCTGCTGGCTTTAGAA 51567     TCAC  G    AGC
                                TTCT    GG CAGCA   TGGTG
                                ||||    || |||||   |||||
                                AAGA    TC GTCGT   ACCAC
                                  TT__  G    CCA
GAM1238  HSA404617 5'  CACCAGCTCGCCCTTCTGAGAA 73089      CAC_   AGCA
                                TTCTT    GGGC    AGCTGGTG
                                |||||    ||||    ||||||||
                                AAGAG    CCCG    TCGACCAC
                                   TCTT    C___
GAM1238  KIAA0431  3'  CACCAGCTTGGGCAACATAAGA 31546      CACGG  AG
              A                  TTCTT    GC  CAAGCTGGTG
                                 |||||    ||  ||||||||||
                                 AAGAA    CG  GTTCGACCAC
                                    TACAA  G_
GAM1238  PAK6      5'  ACCAGCCTGCAGTGGAGAA    39806       GG    CAA
                                TTCTTCAC  GCAG   GCTGGT
                                ||||||||  ||||   ||||||
                                AAGAGGTG  CGTC   CGACCA
                                     A_   ___
GAM1238  LOC90670  3'  TTTGCTGCCCTGAAGAA     64486       C
                                TTCTTCA GGGCAGCAAG
                                ||||||| ||||||||||
                                AAGAAGT CCCGTCGTTT
                                     _
GAM1239  ALDH3B1   3'  CTCCTTCGACACCTTCTCCC   93158       ATTGA
                                GGGAGAAG    GAAGGAG
                                ||||||||    |||||||
                                CCCTCTTC    CTTCCTC
                                     CACAG
GAM1239  AQP6      5'  CTCCTTTTCTCTCCCGGTA    55000        AGATT
                                TACCGGGAGA    GAGAAGGAG
                                ||||||||||    |||||||||
                                ATGGCCCTCT    CTTTTCCTC
                                     _____
GAM1239  DACH      5'  CTCCTTCTCGTTCTCTCCCGG  55822       A  T
                                CCGGGAGA GA TGAGAAGGAG
                                |||||||| || ||||||||||
                                GGCCCTCT CT GCTCTTCCTC
                                     _ T
GAM1239  EIF3S10   5'  CCTTCGTCTCCTCTCCCGG    72168       A  TTGA
                                CCGGGAGA GA    GAAGG
                                |||||||| ||    |||||
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                                GGCCCTCT CT    CTTCC
                                    C  CTG_
GAM1239  FOXD2    3'  CTCCTCAGCCTCTCCCGG    16788        A AT    A
                                CCGGGAGA G  TGAG AG
                                |||||||| |  |||| ||
                                GGCCCTCT C  ACTC TC
                                    _ CG    C
GAM1239  GTF2IRD1  5'  CTCCTTCCCCCATTCTCCCGG  33348        GATTGA
                                CCGGGAGAA     GAAGGAG
                                |||||||||     |||||||
                                GGCCCTCTT     CTTCCTC
                                    ACCCC_
GAM1239  PIAS3    3'  CTCCTTCCCAATCTTCTTTTTC 21446    ___         A
           AGG                    CC   GGGAGAAGATTG GAAGGAG
                                ||   |||||||||||| |||||||
                                GG   TTTTCTTCTAAC CTTCCTC
                                  ACT          C
GAM1239  SEDL     3'  CTCCTTCTTCAGCCTCCCGAGT 28093     _     AAGA    _
           A                     TAC CGGGAG    TTGA GAAGGAG
                                ||| ||||||    |||| |||||||
                                ATG GCCCTC    GACT CTTCCTC
                                  A     C___    T
GAM1239  SEDL     3'  CTCCTTCTTCAGCCTCCCGAGT 28094     _     AAGA    _
           A                     TAC CGGGAG    TTGA GAAGGAG
                                ||| ||||||    |||| |||||||
                                ATG GCCCTC    GACT CTTCCTC
                                  A     C___    T
GAM1239  ATP6V1B1  3'  TCCCCCTCGACTCCCGGTG    9881         AAGA    AA
                                TACCGGGAG    TTGAG  GGA
                                |||||||||    |||||  |||
                                GTGGCCCTC    AGCTC  CCT
                                    _____    CC
GAM1239  C6orf31   3'  CCCCTCCCTTTCTTCCGG    48383         ATT   AA
                                CCGGGAGAAG   GAG  GG
                                ||||||||||   |||  ||
                                GGCCTTCTTT   CTC  CC
                                    CC_   C_
GAM1239  CENTB5    3'  CTCCGGAGGCACCTTCTCCTGG 97233          AT  AGAA_
           TA                     TACCGGGAGAAG  TG    GGAG
                                ||||||||||||  ||    ||||
                                ATGGTCCTCTTC  AC    CCTC
                                    C_  GGAGG
GAM1239  FLJ10079  3'  CTCCTTCCCCTTCTCCCAGTG  60832     C       ATTGA
                                TAC GGGAGAAG    GAAGGAG
                                ||| ||||||||    |||||||
                                GTG CCCTCTTC    CTTCCTC
                                  A       CC___
GAM1239  FLJ31547  3'  CTCCTCCCATAATTTCTCCCG  59489         AT_  A  A
                                CGGGAGAAG   TG GA GGAG
                                |||||||||   || || ||||
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                                GCCCTCTTT  AC CT CCTC
                                     AAT  C  _
GAM1239  FOXJ1    3'  CCCCCTGGAGGCTTCTCCTGG  9376         A_  G  AA
                                CCGGGAGAAG  TT AG  GG
                                ||||||||||  || ||  ||
                                GGTCCTCTTC  AG TC  CC
                                     GG  G  CC
GAM1239  KIAA0561  5'  CTCCCCGACCCTCTCCCGG   66472        AGA   AGAA
                                CCGGGAGA   TTG   GGAG
                                ||||||||   |||   ||||
                                GGCCCTCT   AGC   CCTC
                                    CCC   C___
GAM1239  LR8      3'  CTCCTCCTTTCTTCTCCC    26701         TT   A
                                GGGAGAAGA  GAG AGGAG
                                |||||||||  ||| |||||
                                CCCTCTTCT  TTC TCCTC
                                     __   C
GAM1239  MGC10986  3'  TTCCTTCTTCCTTCTCCCG   48330         ATT
                                CGGGAGAAG   GAGAAGGAG
                                |||||||||   |||||||||
                                GCCCTCTTC   TTCTTCCTT
                                     C__
GAM1239  MGC5338   3'  CCTTCCTCTTTCTCCC      44151         ATT  _
                                GGGAGAAG   GAG AAGG
                                ||||||||   ||| ||||
                                CCCTCTTT   CTC TTCC
                                     ___   C
GAM1239  MSC      3'  CTCCTTCCCAAGCTCCCGG   76840        AAGA   A
                                CCGGGAG    TTG GAAGGAG
                                |||||||    ||| |||||||
                                GGCCCTC    AAC CTTCCTC
                                    G___   C
GAM1239  NIP30    3'  TCCTTTTCCCCTTCCAGTA   46900     C    AAGATT
                                TAC GGGAG     GAGAAGGA
                                ||| |||||     ||||||||
                                ATG CCTTC     CTTTTCCT
                                  A    CC____
GAM1239  RAB6B    5'  TCCTCCTCCTCTCCCGG     33877         AGATT   A
                                CCGGGAGA    GAG AGGA
                                ||||||||    ||| ||||
                                GGCCCTCT    CTC TCCT
                                     C____   C
GAM1239  STRN3    5'  CCTTCCCCGCCCCTCTCCCGG  28138         AGAT  A_
                                CCGGGAGA   TG  GAAGG
                                ||||||||   ||  |||||
                                GGCCCTCT   GC  CTTCC
                                     CCCC  CC
GAM1239  LOC145719 5'  CTCCCTCTTCTGCTTTTCCC   84462         ATT    A
                                GGGAGAAG   GAGA GGAG
                                ||||||||   |||| ||||
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                                CCCTTTTC  TTCT CCTC
                                    GTC   C
GAM1239  LOC145720 5'  CTCCCTCTTCTGCTTTTCCC  84448       ATT   A
                                GGGAGAAG  GAGA GGAG
                                ||||||||  |||| ||||
                                CCCTTTTC  TTCT CCTC
                                    GTC   C
GAM1239  LOC197114 5'  CTCCCTCTTCTGCTTTTCCC  91268       ATT   A
                                GGGAGAAG  GAGA GGAG
                                ||||||||  |||| ||||
                                CCCTTTTC  TTCT CCTC
                                    GTC   C
GAM1239  LOC197117 5'  CTCCCTCTTCTGCTTTTCCC  91280       ATT   A
                                GGGAGAAG  GAGA GGAG
                                ||||||||  |||| ||||
                                CCCTTTTC  TTCT CCTC
                                    GTC   C
GAM1239  LOC201911 3'  TCCCTCCCTCTCCCGG     91871       A ATT  AA
                                CCGGGAGA G  GAG  GGA
                                |||||||| |  |||  |||
                                GGCCCTCT C  CTC  CCT
                                   _ C__  __
GAM1239  LOC220932 3'  CTCCTTCCCATGCTTCTCCCGG 94754         AT  A
                                CCGGGAGAAG  TG GAAGGAG
                                ||||||||||  || |||||||
                                GGCCCTCTTC  AC CTTCCTC
                                     GT  C
GAM1239  LOC64744  3'  CCTTCCCTTCTCCCGGT     62440         ATTGA
                                ACCGGGAGAAG    GAAGG
                                ||||||||||     |||||
                                TGGCCCTCTTC    CTTCC
                                     C____
GAM1239  LOC64744  3'  CTCCCCAGTCCTCTCCTGG   62441       A    AGAA
                                CCGGGAGA GATTG   GGAG
                                |||||||| |||||   ||||
                                GGTCCTCT CTGAC   CCTC
                                    C    C___
GAM1239  LOC92249  3'  CCCTCTCCGCAGGTCTTTCTCC 69106       _  ____   A
            C                    GGGAGAA GATT   GAGA GG
                                |||||||  ||||   |||| ||
                                CCCTCTT CTGG   CTCT CC
                                   T   ACGC   C
GAM1240  SCAMP1    3'  GCTAAATAAATATTCTCC    54500    T    C
                                GGA AATATT ATTTAGC
                                |||  |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1240  SCAMP1    3'  GCTAAATAAATATTCTCC    54501    T    C
                                GGA AATATT ATTTAGC
                                |||  |||||| |||||||
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                                CCT TTATAA TAAATCG
                                  C     A
GAM1240 NX-17    3' TGAATATCAGCCCCTAATA   40706        ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM1240 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
             TA                   TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM1241 CDH12    3' CTTATCATTTAAAGTGGTGTA  15777        CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM1241 GOCAP1   3' ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM1241 DKFZp434N2435 5' CTTATTACTGTGGGGTGGT   98090      T   AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                   _   GTCA_
GAM1241 DKFZP564I122 3' CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
             A                   TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM1241 FLJ21791  3' CTTATTTGCAGAAGTGGTGTA  62126        CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM1241 HMP19    3' CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
             TA                   TACA   TCC   GAAGAATAAG
                                ||||   |||   ||||||||||
                                ATGT   AGG   TTTCTTATTC
                                  AAA_   ATTG
GAM1241 KIAA1719  3' TCTGTCTTGGGAGTGGTGTA  68742           _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                          G
GAM1241 KIAA1853  3' TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
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                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM1241  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748     CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM1241  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM1241  OSBPL11   3'  CTTAATTTCCCAAGAGTGGTG  43206       CCAA   AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                     AACC   A_
GAM1241  YME1L1    3'  TCATTCTTGATGTGGTGTA   58438       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                     TA_    A
GAM1241  ZNF262    3'  CTTATTTTGTTTGGGAGT    18723       A
                                ACTCCCAAG AGAATAAG
                                |||||||||  ||||||||
                                TGAGGGTTT TTTTATTC
                                      G
GAM1241  LOC91960  3'  TGTGGCTTGGAACGTGGTGTA  68294       TC_    AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
                                ATGTGGTG   GGTTC   TGT
                                     CAA    GG__
GAM1242  MHC2TA    3'  TGACATTGTTGGCCAA     5998       CAT
                                TTGGCCA   CAATGTCA
                                |||||||   ||||||||
                                AACCGGT   GTTACAGT
                                     T__
GAM1242  C3IP1     3'  TGACATCAATGTGGGAGTTCAG 41581       GG     CA
                                TTGAACTT  CCACAT  ATGTCA
                                ||||||||  ||||||  ||||||
                                GACTTGAG  GGTGTA  TACAGT
                                     __     AC
GAM1242  CIB1      3'  TGAGCTGTGGCCAAGGTCAA   22123     A       __
                                TTGA CTTGGCCACA  TCA
                                |||| ||||||||||  |||
                                AACT GAACCGGTGT  AGT
                                  G        CG
GAM1242  FLJ14054  5'  GACATTGATACAGGTCAA    44967       AC_
                                TTGGCC   ATCAATGTC
                                ||||||   |||||||||
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                                AACTGG   TAGTTACAG
                                   ACA
GAM1242  FLJ20097  5'  TGACATTAACCATTATACCAAG 35049       _   CCACATC___
             GTTCAA                  TTGAAC TTGG        AATGTCA
                                |||||| ||||        |||||||
                                AACTTG AACC        TTACAGT
                                   G   ATATTACCAA
GAM1242  KIAA0620  3'  ACACCAATGTGGCCATGGCAG  62807    AACT       CAA
                                TTG   TGGCCACAT   TGT
                                |||   |||||||||   |||
                                GAC   ACCGGTGTA   ACA
                                  GGT_       ACC
GAM1242  KIAA1001  5'  TGACATTGATGTCTAA     31015     CC
                                TTGG  ACATCAATGTCA
                                ||||  ||||||||||||
                                AATC  TGTAGTTACAGT
                                   __
GAM1242  MGC22014  3'  ACAGCATGACCAAGTTCGA   65103        CCA   CAA
                                TTGAACTTGG   CAT   TGT
                                ||||||||||   |||   |||
                                AGCTTGAACC   GTA   ACA
                                      A__   CG_
GAM1242  POPX1    3'  TGATGCATGGCCAAGTTCAG   30477          __
                                TTGAACTTGGCCA  CATCA
                                ||||||||||||  |||||
                                GACTTGAACCGGT  GTAGT
                                      AC
GAM1242  LOC150468 3'  GACAGATGGCCAAGTCAA    80685     A      CATCAA
                                TTGA CTTGGCCA     TGTC
                                |||| ||||||||     ||||
                                AACT GAACCGGT     ACAG
                                  _       AG_____
GAM1242  LOC160897 3'  TGACAAAGTTACCAAGTTCAA  83133         CC  ATCAA
                                TTGAACTTGG  AC    TGTCA
                                ||||||||||  ||    |||||
                                AACTTGAACC  TG    ACAGT
                                      AT  AA___
GAM1242  LOC200301 5'  GACATCTTTGACAAGTTCAA   90139        GC  CATCA
                                TTGAACTTG  CA    ATGTC
                                |||||||||  ||    |||||
                                AACTTGAAC  GT    TACAG
                                      A_  TTC__
GAM1242  LOC255147 3'  TGACATTGATATAGCTTGT   97409    TT   CAC
                                AC  GGC   ATCAATGTCA
                                ||  |||   ||||||||||
                                TG  TCG   TAGTTACAGT
                                  T_   ATA
GAM1243  AVPR1A   5'  GCACCGCATAAATACTTGAGT  7381         TCTTTCC   CA
                                ACTCAAGT     TGC  GTGC
                                ||||||||     |||  ||||
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                                TGAGTTCA     ACG  CACG
                                    TAAAT__   C_
GAM1243  IFNG     3'  GCATGTCAGACAGAACTTGA   7091         TTC   CCA
                                TCAAGTTCT   CTG   GTGC
                                |||||||||   |||   ||||
                                AGTTCAAGA   GAC   TACG
                                    CA_   TG_
GAM1243  IGFBP2   3'  CACCGGCAGAAAACGGAGAGT  6997      AAG  _  C    A
                                ACTC   TTC TTT CTGCC GTG
                                ||||   ||| ||| ||||| |||
                                TGAG   AGG AAA GACGG CAC
                                  ___  C  A    C
GAM1243  LY9      3'  CACTGCTGAAAAGAACCCAAG  72145    CAA      CCT  C
                                CT   GTTCTTT   GC AGTG
                                ||   |||||||   || ||||
                                GA   CAAGAAA   CG TCAC
                                 ACC      AGT  _
GAM1243  MYLK     3'  CACTCTCCAAAGAACTTGA    98792          CCTGCC
                                TCAAGTTCTTT     AGTG
                                ||||||||||     ||||
                                AGTTCAAGAAA     TCAC
                                     CCTC__
GAM1243  RLBP1    5'  GCAAGTGGAAGAGAAGAACTTG 6164          TC  G   G_
           A                     TCAAGTTCTT  CT CCA  TGC
                                ||||||||||  || |||  |||
                                AGTTCAAGAA  GA GGT  ACG
                                     GA  A   GA
GAM1243  TAF9     5'  CACTAGGCAAAGAACTTGCGT  13518    T       TCC   _
                                AC CAAGTTCTT   TGCC AGTG
                                || |||||||||   |||| ||||
                                TG GTTCAAGAA   ACGG TCAC
                                 C        ___    A
GAM1243  ZNF174   3'  GCACTGGGGCAAAGAGAACTTA 14353     C       CC   __
           AGT                    ACT AAGTTCTTT  TGCC  AGTGC
                                ||| |||||||||  ||||  |||||
                                TGA TTCAAGAGA  ACGG  TCACG
                                  A       A_   GG
GAM1243  ATP9A    3'  CACTGGCAAGTCTTAAG     62735    C   TT  TTCC
                                CT AAG  CT    TGCCAGTG
                                || |||  ||    ||||||||
                                GA TTC  GA    ACGGTCAC
                                 A  T_  _____
GAM1243  CDT6     3'  GCACCAGCAGGAGGTGGACAGA 41250      AA   _      CA
           GT                     ACTC  GTTC TTTCCTGC  GTGC
                                ||||  |||| ||||||||  ||||
                                TGAG  CAGG GGAGGACG  CACG
                                  A_   T       AC
GAM1243  COVA1    3'  GCACCAGCAGGAAGCTCAGGT  73641     CA  TCT     CA
                                ACT  AGT   TTCCTGC  GTGC
                                |||  |||   |||||||  ||||
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                                TGG  TCG   AAGGACG  CACG
                                  AC   ___      AC
GAM1243  CXYorf1   3'  CACCAATCAATAAAGAACTGAG 82903      A      CC  CCA_
                                CTCA GTTCTTT  TG    GTG
                                |||| |||||||  ||    |||
                                GAGT CAAGAAA  AC    CAC
                                  _      TA  TAAC
GAM1243  DKFZP434C0826 5'  GCACATTGCCAGAAAGAACCTG 85153     A       CT  CA_
           G                     TCA GTTCTTTC  GC   GTGC
                                ||| ||||||||  ||   ||||
                                GGT CAAGAAAG  CG   CACG
                                  C       AC  TTA
GAM1243  ELF1      3'  GCCAAGAAAGCAACTTGAG    71950         _    CT_
                                CTCAAGTT CTTTC   GC
                                |||||||| |||||   ||
                                GAGTTCAA GAAAG   CG
                                     C     AAC
GAM1243  FLJ11726  3'  GCAATGTAATAAAAACTTGAG  47022        C   CC   CAG
                                CTCAAGTT TTT  TGC   TGC
                                |||||||| |||  |||   |||
                                GAGTTCAA AAA  ATG   ACG
                                     _  TA   TA_
GAM1243  KIAA0826  3'  GCCTTTAGGAAAGAAACT    83527      _      CC  T
                                AGTT CTTTCCTG  AG GC
                                |||| ||||||||  || ||
                                TCAA GAAAGGAT  TC CG
                                  A       T_ _
GAM1243  KIAA0970  3'  CATGGAAAAGAATTGAGT    30616       G     _ _
                                ACTCAA TTCTTT CC TG
                                |||||| |||||| || ||
                                TGAGTT AAGAAA GG AC
                                     _     A  T
GAM1243  KIAA1940  3'  GCACCGGCAGGAAATGAAGGTG 80786    AG  _       A
                                CA  TTC TTTCCTGCC GTGC
                                ||  ||| |||||||||| ||||
                                GT  AAG AAAGGACGG CACG
                                 GG   T        C
GAM1243  MCLC      3'  GCAATTCAGGAAAGACTT    31384      T       CCAG
                                AAGT CTTTCCTG    TGC
                                |||| ||||||||    |||
                                TTCA GAAAGGAC    ACG
                                  _       TTA_
GAM1243  MGC33177  3'  GCACCAGATCTAGAACTTGA   58627         TTC_   CCA
                                TCAAGTTCT    CTG   GTGC
                                |||||||||    |||   ||||
                                AGTTCAAGA    GAC   CACG
                                     TCTA   ____
GAM1243  P38IP     3'  GCACTGAATCAAAAGAATTGAG 34532       G     CCTGC
           T                     ACTCAA TTCTTT    CAGTGC
                                |||||| ||||||     ||||||
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                                TGAGTT AAGAAA    GTCACG
                                   _     ACTAA
GAM1243  PINK1    3'  GCAAATGGAAGAACTTGAGT   51564          C__
                                ACTCAAGTTCTTTC   TGC
                                ||||||||||||||  |||
                                TGAGTTCAAGAAGG   ACG
                                      TAA
GAM1243  PNMA5    3'  CACTAACAGGGAACTTGA    73969       TTT   CC
                                TCAAGTTC   CCTG  AGTG
                                ||||||||   ||||  ||||
                                AGTTCAAG   GGAC  TCAC
                                   ___    AA
GAM1243  TBDN100  3'  CACCGTTGAAGAACTTGG    47639         CCT  CA
                                TCAAGTTCTTT   GC  GTG
                                ||||||||||   ||  |||
                                GGTTCAAGAAG   TG  CAC
                                      T__  C_
GAM1243  LOC121642 5'  GCACTGGGGATAGAACTTGAG  74563         T   TG
                                CTCAAGTTCT TCC  CCAGTGC
                                |||||||||| |||  |||||||
                                GAGTTCAAGA AGG  GGTCACG
                                      T   __
GAM1243  LOC129293 3'  GCACCAGGCTAAGAACCTGA   75369     A     T_   CCA
                                TCA GTTCTT  CCTG   GTGC
                                ||| ||||||  ||||   ||||
                                AGT CAAGAA  GGAC   CACG
                                  C     TC   ___
GAM1243  LOC133258 5'  CATCTGCAATGAACTTGAGT   76452         TTTCC   CA
                                ACTCAAGTTC    TGC  GTG
                                ||||||||||    |||  |||
                                TGAGTTCAAG    ACG  TAC
                                      TA___   TC
GAM1243  LOC144108 5'  GCATAGGAGAAAAAAACTTGAG 77189         C   C  G  A
                                CTCAAGTT TTT CT CC GTGC
                                |||||||| ||| || || ||||
                                GAGTTCAA AAA GA GG TACG
                                     A   A  _  A
GAM1243  LOC145826 5'  CACTGGCAGGAGCTAAACT    84527     CT_
                                AGTT   TTCCTGCCAGTG
                                ||||   ||||||||||||
                                TCAA   GAGGACGGTCAC
                                  ATC
GAM1243  LOC148709 3'  GCACCGGATTGTAGAACTTGG  79692         TTCCTG  A
                                TCAAGTTCT     CC GTGC
                                |||||||||     || ||||
                                GGTTCAAGA     GG CACG
                                      TGTTA_  C
GAM1243  LOC149319 3'  CACCGGCAGGAATTCTCCAGT  80067     CA  TTCT      A
                                ACT  AG    TTCCTGCC GTG
                                |||  ||    |||||||| |||
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                                TGA  TC    AAGGACGG CAC
                                  CC  TT__       C
GAM1243  LOC161829 5'  CATGCAGAAAGAACCTGG    83185     A       C   CA
                                TCA GTTCTTTC TGC  GTG
                                ||| |||||||| |||  |||
                                GGT CAAGAAAG ACG  TAC
                                  C       _  __
GAM1243  LOC200093 3'  CACCAATCAATAAAGAACTGAG 63761      A      CC  CCA_
                                CTCA GTTCTTT  TG    GTG
                                |||| |||||||  ||    |||
                                GAGT CAAGAAA  AC    CAC
                                  _      TA  TAAC
GAM1243  LOC254020 5'  GCACTGGCAGGAAAGGAC    97854
                                GTTCTTTCCTGCCAGTGC
                                ||||||||||||||||||
                                CAGGAAAGGACGGTCACG

GAM1243  LOC91040  3'  CACCAATCAATAAAGAACTGAG 65334      A      CC  CCA_
                                CTCA GTTCTTT  TG    GTG
                                |||| |||||||  ||    |||
                                GAGT CAAGAAA  AC    CAC
                                  _      TA  TAAC
GAM1244  BAX      3'  GGCCTCCTCTCCTACTTTGGG  16316         TC    A  A
                                CCCAAGGTG  AGAG AG CC
                                |||||||||  |||| || ||
                                GGGTTTCAT  TCTC TC GG
                                     CC    C  C
GAM1244  CASP8    5'  TGGTCACTTGAACCTTGGG    8770         GTCA   AA
                                CCCAAGGT    GAG  GACCA
                                ||||||||    |||  |||||
                                GGGTTCCA    TTC  CTGGT
                                    AG__    A_
GAM1244  CASP8    5'  TGGTCACTTGAACCTTGGG    54085        GTCA   AA
                                CCCAAGGT    GAG  GACCA
                                ||||||||    |||  |||||
                                GGGTTCCA    TTC  CTGGT
                                    AG__    A_
GAM1244  CD34     3'  TGGGGCCCTACACCTTGAGGA  10110     C       C  AGAAGA
                                TCC CAAGGTGT AG      CCA
                                ||| ||||||| ||      |||
                                AGG GTTCCACA TC      GGT
                                  A       _  CCGG__
GAM1244  ERBB4    3'  TGGTCTTCCTTCTACCCCAAGG 19111    CCAA    TC  A
                                CC    GGTG  AG GAAGACCA
                                ||    ||||  || ||||||||
                                GG    CCAT  TC CTTCTGGT
                                 AACC    CT  _
GAM1244  GRAF     3'  GTCTTCTCATGCACGGGA    31242      CAAG    CA
                                TCCC    GTGT  GAGAAGAC
                                ||||    ||||  ||||||||
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                                AGGG   CACG  CTCTTCTG
                                  ____   TA
GAM1244 ID3     3' TGGTCTTCTGGTCTCCTTGGAG 79807    C     TGTCAG
             A                    TC CCAAGG     AGAAGACCA
                                  || ||||||     |||||||||
                                  AG GGTTCC     TCTTCTGGT
                                   A     TCTGG_
GAM1244 IKBKG   3' GGTCCCCTCTTTTGGGG     14666       GTGTC   AA
                                  CCCCAAG    AGAG  GACC
                                  |||||||    ||||  ||||
                                  GGGGTTT    TCTC  CTGG
                                      _____   CC
GAM1244 MMP19   3' TGGTCTTCCCCAGGTTGAGGA  11645    C   GG  TCAGA
                                  TCC CAA  TG    GAAGACCA
                                  ||| |||  ||    ||||||||
                                  AGG GTT  AC    CTTCTGGT
                                    A   GG  CC___
GAM1244 MMP19   3' TGGTCTTCCCCAGGTTGAGGA  11646    C   GG  TCAGA
                                  TCC CAA  TG    GAAGACCA
                                  ||| |||  ||    ||||||||
                                  AGG GTT  AC    CTTCTGGT
                                    A   GG  CC___
GAM1244 PNUTL1  3' TGGCCCTCTCTGACCTTGGGGG 12194        TG      AGA
                                  TCCCCAAGG  TCAGAGA   CCA
                                  |||||||||  |||||||   |||
                                  GGGGGTTCC  AGTCTCT   GGT
                                      __      CCC
GAM1244 ROBO1   5' TCTCTGCCACCCCGGGGA   12894      AA   T
                                  TCCCC  GGTG CAGAGA
                                  |||||  |||| ||||||
                                  AGGGG  CCAC GTCTCT
                                     CC   C
GAM1244 SLC10A1  5' TGGTCTTCCACTGCCTCACAGG 13202    CCA_  TGT   A_
             A                    TCC    AGG   CAG  GAAGACCA
                                  |||    |||   |||  ||||||||
                                  AGG    TCC   GTC  CTTCTGGT
                                    ACAC   ___   AC
GAM1244 TRIM39   3' TCCTGAATCATCTTGGAGA   41452    C       __    A
                                  TC CCAAGGTG  TCAG GA
                                  || ||||||||  |||| ||
                                  AG GGTTCTAC  AGTC CT
                                   A       TA   _
GAM1244 XT3     3' TCCTAGCACCTTGGGGG     39919          TC  A
                                  TCCCCAAGGTG  AG GA
                                  ||||||||||  || ||
                                  GGGGGTTCCAC  TC CT
                                         GA  _
GAM1244 BRD1    5' TGGTTTTGGACACCTTGG    28145          AGAG
                                  CCAAGGTGTC    AAGACCA
                                  |||||||||    |||||||
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                                GGTTCCACAG    TTTTGGT
                                      G___
GAM1244  CDH26    3'  GTCTTCCTCTGCTTTGGG    41766       TGT    _
                                CCCAAGG   CAGAG AAGAC
                                |||||||   ||||| |||||
                                GGGTTTC   GTCTC TTCTG
                                   ___    C
GAM1244  CINP     3'  CTTCTCTGCCCCTCCTGGG   51926     __  T T
                                CCCA  AGG G CAGAGAAG
                                ||||  ||| | ||||||||
                                GGGT  TCC C GTCTCTTC
                                  CC   C _
GAM1244  DGS-A    3'  TCTTCTCTGGACAGGA      86056     CCAAGG   _
                                TCC      TGTC AGAGAAGA
                                |||      |||| ||||||||
                                AGG      ACAG TCTCTTCT
                                 _______   G
GAM1244  DJ37E16.5 3'  GTCTTCTCCCCCTTCCCTGGGG 40098       A  TGTCA_
                                CCCCA GG     GAGAAGAC
                                ||||| ||     ||||||||
                                GGGGT CC     CTCTTCTG
                                   C  TTCCCC
GAM1244  DKFZP761D0211 3'  TGGTCTCCCTGGCCACCTTGGG 50181          _   A  A
                                CCCAAGGTG TCAG GA GACCA
                                ||||||||| |||| || |||||
                                GGGTTCCAC GGTC CT CTGGT
                                     C   C  _
GAM1244  EPS8R1   3'  TGGTCTTCCCCCATCCCGGTGG 35303    _ AA   TCAGA
            A                    TCC CC  GGTG    GAAGACCA
                                ||| ||  ||||    ||||||||
                                AGG GG  CTAC    CTTCTGGT
                                  T  CC   CCC__
GAM1244  EPS8R3   5'  GGCCTTCACTGGCACCCAGGG  56531    AA      A   A
                                CCC  GGTGTCAG GAAG CC
                                |||  |||||||| |||| ||
                                GGG  CCACGGTC CTTC GG
                                  AC       A   C
GAM1244  FLJ10460 3'  TCCTAACACTTGGGGA     36624        G   C  A
                                TCCCCAAG TGT AG GA
                                |||||||| ||| || ||
                                AGGGGTTC ACA TC CT
                                     _   A  _
GAM1244  FLJ10688 5'  TGGTCCTCTCTGATGAAGAGG  36955    AAGG       A
                                CC    TGTCAGAGA GACCA
                                ||    ||||||||| |||||
                                GG    GTAGTCTCT CTGGT
                                 AGAA        C
GAM1244  FLJ12547 3'  TGGCCTTCTCACACCTTGGG   47137         CA     A
                                CCCAAGGTGT  GAGAAG CCA
                                ||||||||||  |||||| |||
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                                GGGTTCCACA  CTCTTC GGT
                                      __      C
GAM1244  FLJ20195  5'  TGGCCTTCTCTGAAGATGGG   35224      AGGTG        A
                                CCCA     TCAGAGAAG CCA
                                ||||     ||||||||| |||
                                GGGT     AGTCTCTTC GGT
                                  AGA__         C
GAM1244  FLJ22059  5'  GTCTGGACCAGCACCTTGGAGA 43058    C        CAGAGA
                                TC CCAAGGTGT      AGAC
                                || |||||||||      ||||
                                AG GGTTCCACG      TCTG
                                 A         ACCAGG
GAM1244  FZD9      3'  TGATCCTCTCTGGCTGGG    14510      AGGT       A  C
                                CCCA    GTCAGAGA GA CA
                                ||||    |||||||| || ||
                                GGGT    CGGTCTCT CT GT
                                  _____       C  A
GAM1244  GS3955    5'  GGTCCCCTCTTTTCTCTGGGGG 41625       AG TGTC    AA
                                TCCCCA  G    AGAG  GACC
                                ||||||  |    ||||  ||||
                                GGGGGT  C    TCTC  CTGG
                                   CT TTT_    CC
GAM1244  KIAA0377  3'  CTTCTCTGAGCATCCTAGG    28502     A  _ _
                                CC AGG TG TCAGAGAAG
                                || ||| || |||||||||
                                GG TCC AC AGTCTCTTC
                                 A   T  G
GAM1244  KIAA0522  3'  TGGCCCTCTCTCTGACCTCAGG 72428     AA  T       _  A_
              G                  CCC  GG GTCAGAGA AG  CCA
                                ||| || |||||||| ||  |||
                                GGG  TC CAGTCTCT TC  GGT
                                 AC  _       C  CC
GAM1244  KIAA0672  3'  CTTTTCACACTTGGGGA     30049         G   CA
                                TCCCCAAG TGT  GAGAAG
                                |||||||| |||  ||||||
                                AGGGGTTC ACA  CTTTTC
                                      _   __
GAM1244  KIAA1409  5'  TGGTCTCCTGCTTGACACC    61879        _ _  A
                                GGTGTCA G AG AGACCA
                                ||||||| | || ||||||
                                CCACAGT C TC TCTGGT
                                    T G  C
GAM1244  KREMEN2   3'  CTCTGGTCGCCTTGGGGA     44718           _
                                TCCCCAAGGTG TCAGAG
                                |||||||||||| ||||||
                                AGGGGTTCCGC GGTCTC
                                       T
GAM1244  LASP1     3'  TGGTCTTCTCTACAGTT     21583     G   C
                                AG TGT AGAGAAGACCA
                                || ||| ||||||||||
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                                TT ACA TCTCTTCTGGT
                                 G  _
GAM1244 LIMK2    5' TGGTCTTCCCGCGCCTGAGG  19925    CA     CAGA
                                CC  AGGTGT   GAAGACCA
                                ||  ||||||   ||||||||
                                GG  TCCGCG   CTTCTGGT
                                 AG     CC__
GAM1244 MGC20496 3' TGGCCCTCTTGAGCCTTGGG  54533        GTC    AAGA
                                CCCAAGGT   AGAG   CCA
                                ||||||||   ||||   |||
                                GGGTTCCG   TCTC   GGT
                                     AGT   CC__
GAM1244 MUC17    3' CTTCTCTGATAGAGGAGGA   95926     _ AAGG
                                TCC CC    TGTCAGAGAAG
                                ||| ||    ||||||||||
                                AGG GG    ATAGTCTCTTC
                                  A  AG__
GAM1244 NAV1     3' TGGCCTCCTCTAATGACTTTGG 40325          _ C    A  A
             GGA                    TCCCCAAGGT GT AGAG AG CCA
                                ||||||||| || |||| || |||
                                AGGGGTTTCA TA TCTC TC GGT
                                      G  A    C  C
GAM1244 SCYA13   3' TGGCCTCCTCTTCTATGCTTTG 19432         C__    A  A
             G                   CCAAGGTGT   AGAG AG CCA
                                |||||||||   |||| || |||
                                GGTTTCGTA   TCTC TC GGT
                                      TCT    C  C
GAM1244 SLC22A4  5' TTCTAACATCCTTGGGGA    13225         _  C
                                TCCCCAAGG TGT AGAG
                                ||||||||| ||| ||||
                                AGGGGTTCC ACA TCTT
                                      T   A
GAM1244 SNPH     3' TCTCTGACCTAGGGGA      28909       A   TG
                                TCCCC AGG  TCAGAGA
                                ||||| |||  |||||||
                                AGGGG TCC  AGTCTCT
                                   A  __
GAM1244 TAS1R1   3' CTTCTCTGCCCTGAGGG     57723     CA   T T
                                CCC  AGG G CAGAGAAG
                                |||  ||| | ||||||||
                                GGG  TCC C GTCTCTTC
                                  AG  _ _
GAM1244 TRIM15   3' TGGCCTTCTCTGCACCT     54473       T       A
                                AGGTG CAGAGAAG CCA
                                ||||| |||||||| |||
                                TCCAC GTCTCTTC GGT
                                   _       C
GAM1244 LOC144695 5' TCTTCCCTGACACTTAGG    84097    A        A
                                CC AGGTGTCAG GAAGA
                                || ||||||||| |||||
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                                GG TTCACAGTC CTTCT
                                 A       C
GAM1244  LOC145864 3'  TGGTCTCCCTCCCTTAAGGA  78017    CC   TGTCA  A_
                                TCC  AAGG    GAG  AGACCA
                                |||  ||||    |||  ||||||
                                AGG  TTCC    CTC  TCTGGT
                                 AA   _____  CC
GAM1244  LOC149837 3'  TGGTCTTCTGCTGCCTGGAGA  85910    C   A  TGT  _
                                TC CCA GG   CAG AGAAGACCA
                                || ||| ||   ||| |||||||||
                                AG GGT CC   GTC TCTTCTGGT
                                 A  _ ___   G
GAM1244  LOC150271 5'  TGGTCTTCTCCAGACTGGTGA  86150    C   AGGT   A_
                                TC CCA   GTC  GAGAAGACCA
                                || |||   |||  ||||||||||
                                AG GGT   CAG  CTCTTCTGGT
                                 T  ____  AC
GAM1244  LOC150311 5'  TCTTTTTTCCCTAAGGGA    80570     CA   TGTC
                                TCCC  AGG   AGAGAAGA
                                ||||  |||   ||||||||
                                AGGG  TCC   TTTTTTCT
                                  AA  C___
GAM1244  LOC151300 3'  TGGTGGGATCGATACCTTGGAG 86496    C       A  GAAG
           A                     TC CCAAGGTGTC GA   ACCA
                                || ||||||||| ||   ||||
                                AG GGTTCCATAG CT   TGGT
                                 A        _  AGGG
GAM1244  LOC152286 3'  TGGCCCCCTAAGGCACTTTGGG 86815          AG  AAGA
           GA                    TCCCCAAGGTGTC  AG   CCA
                                ||||||||||||  ||   |||
                                AGGGGTTTCACGG  TC   GGT
                                       AA  CCCC
GAM1244  LOC163412 5'  GGTCTTCCCACCCGGTGA   83018   C  AA   TCAGA
                                TC CC  GGTG   GAAGACC
                                || ||  ||||   |||||||
                                AG GG  CCAC   CTTCTGG
                                 T  C_   C____
GAM1244  LOC222493 5'  TGTCTTCTCTGCCCCCGGGG  96014    AA  T T      C
                                CCCC  GG G CAGAGAAGA CA
                                ||||  || | |||||||||| ||
                                GGGG  CC C GTCTCTTCT GT
                                  CC  _ _       A
GAM1244  LOC255314 5'  TCTCCGACTACCTCAGGGA   99472    CA   _  A
                                TCCC  AGGT GTC GAGA
                                ||||  |||| ||| ||||
                                AGGG  TCCA CAG CTCT
                                  AC   T  C
GAM1244  LOC256906 3'  TGGCCTCCTCAGGCTCAGGGGA 96981      AA  T  A  A A
                                TCCCC  GG GTC GAG AG CCA
                                |||||  || ||| ||| || |||
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                                AGGGG  CT CGG CTC TC GGT
                                  A_ _  A  C  C
GAM1244 LOC50999 3' TGGTCTTCTCCAAAATATTTTG 32640       CA__
                                CAAGGTGT   GAGAAGACCA
                                ||||||||   ||||||||||
                                GTTTTATA   CTCTTCTGGT
                                    AAAC
GAM1244 LOC84548 3' GTCTTCTCAGCCAGGAGA   71766   C  AA  GTCA     C
                                TC CC  GGT   GAGAAGA C
                                || ||  |||   ||||||| |
                                AG GG  CCG   CTCTTCT G
                                 A  A_  A___     A
GAM1244 LOC91445 3' GGTCTTCCCTCCTGTGGA   61172    CCA  TGTC  A
                                TCC   AGG   AG GAAGACC
                                |||   |||   || |||||||
                                AGG   TCC   TC CTTCTGG
                                  TG_  _____ C
GAM1245 CCNB3   3' GACCCTGCAGGAATACCA   54468     CG      TACCG
                                TGGTA  CCTGCAGG   GTC
                                |||||  ||||||||   |||
                                ACCAT  GGACGTCC   CAG
                                  AA      ______
GAM1245 D4ST-1   3' GGACCCAGCTCTGCAGGCACCC 56198    TAC      _ ACC
          A                      TGG   GCCTGCAG GT   GGTCC
                                |||   |||||||| ||   |||||
                                ACC   CGGACGTC CG   CCAGG
                                  CA_      T  AC_
GAM1245 HEYL    3' GCTTTAACCTGCAGGGCACCA  28131     ACG      ACC
                                TGGT   CCTGCAGGT   GGT
                                ||||   |||||||||   |||
                                ACCA   GGACGTCCA   TCG
                                  CG_       ATT
GAM1245 KIAA0971  3' GGAGCCTGCAGCACACCA   30674     AC  C     A
                                TGGT  GC TGCAGGT CC
                                ||||  || ||||||| ||
                                ACCA  CG ACGTCCG GG
                                  CA  _     A
GAM1245 KIAA1089  3' GGACCAGCACCTGTAGTCACCC 69431    TACGC      ACC
          CA                      TGG    CTGCAGGT   GGTCC
                                |||    ||||||||   |||||
                                ACC    GATGTCCA   CCAGG
                                  CCACT      CGA
GAM1245 LOC115073 3' CGTGACCTGCAGGCGTCCA   73580    T         AC
                                TGG ACGCCTGCAGGT  CG
                                ||| ||||||||||||  ||
                                ACC TGCGGACGTCCA  GC
                                  _         GT
GAM1246 ADH7    3' AAGATTAAGGGACGGGC    7268      ACA   G
                                GCCC   TCT TTTAATCTT
                                ||||   ||| |||||||||
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                                CGGG   AGG GAATTAGAA
                                  C__   _
GAM1246 ARAF1    5' GGAAGGACTTCAGATGTGAGC  64644    C       TTTAA
                                GC CACATCTG    TCTTCC
                                || ||||||||    ||||||
                                CG GTGTAGAC    GGAAGG
                                 A       TTCA_
GAM1246 CEACAM6  3' GGAAGACTGGCAGATTGGACCA 11756    C   C      TAA
                                TGG CCA ATCTGTT   TCTTCC
                                ||| ||| |||||||   ||||||
                                ACC GGT TAGACGG   AGAAGG
                                  A   _      TC_
GAM1246 CLECSF12 3' GGATTACAGATGTGAGCCA   77214     C        TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1246 CYP1A2   3' GGATTAACAGGTATGAACCA   7518     CC  C      T
                                TGG  CA ATCTGTT AATCT
                                |||  || ||||||| |||||
                                ACC  GT TGGACAA TTAGG
                                  AA  A      _
GAM1246 ENG      3' GAACTTGAAACAGATTCAGGCC 5496       CAC       AATC
                   A                 TGGCC   ATCTGTTT    TTC
                                |||||   ||||||||    |||
                                ACCGG   TAGACAAA    AAG
                                   ACT       GTTC
GAM1246 ERCC3    3' GAATAAACAGAATGGACCA   5506     C   CA      A
                                TGG CCA  TCTGTTTA TC
                                ||| |||  |||||||| ||
                                ACC GGT  AGACAAAT AG
                                  A  A_       A
GAM1246 HTLF     5' AAGATTGCAGGATTAAGCCA   10973     CCACA    TT
                                TGGC    TCTGT  AATCTT
                                ||||    |||||  ||||||
                                ACCG    GGACG  TTAGAA
                                  AATTA    __
GAM1246 MS4A8B   3' GATTTTAAACAGATGTTAACCA 49588     CCC          TCT
                                TGG   ACATCTGTTTAA   TC
                                |||   ||||||||||||   ||
                                ACC   TGTAGACAAATT   AG
                                  AAT          TT_
GAM1246 PRKAA2   3' GAAGATTAAAAAGTAAAGAACC 21811     CCCACAT  G
                   A                 TGG      CT TTTAATCTTC
                                |||      || ||||||||||
                                ACC      GA AAATTAGAAG
                                  AAGAAAT  A
GAM1246 ASE-1    3' GGATAACAGGTGTGAGCCA   24983     C        TA
                                TGGC CACATCTGTT  ATCT
                                |||| ||||||||||  ||||
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                                ACCG GTGTGGACAA  TAGG
                                  A       __
GAM1246  CITED2   3'  GGAAGATTAAACAGATGTGGGC 21403
                CA                TGGCCCACATCTGTTTAATCTTCC
                                  ||||||||||||||||||||||||
                                  ACCGGGTGTAGACAAATTAGAAGG

GAM1246  DKFZP564K0322 3'  GGATTACAGATGTGAGCCA   50188     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1246  DZIP1    3'  GAAGATTATTCCAGAAGCCA  30703     CCACA   TT_
                                TGGC    TCTG   TAATCTTC
                                ||||    ||||  ||||||||
                                ACCG    AGAC   ATTAGAAG
                                  A____   CTT
GAM1246  FLJ22969 3'  GGATTACAGATGTGAGCCA   69211     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1246  HSNOV1   3'  GGATTACAGATGTGAACCA   34437     CC       TT
                                TGG  CACATCTGT  AATCT
                                |||  |||||||||  |||||
                                ACC  GTGTAGACA  TTAGG
                                  AA       __
GAM1246  IMPACT   3'  GAATTACAGGTGTGAGCCA   38006     C       TTAATC
                                TGGC CACATCTGT     TTC
                                |||| |||||||||     |||
                                ACCG GTGTGGACA     AAG
                                  A       TT____
GAM1246  JAM1     3'  GGATTACAGATGTGAGCCA   34234     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1246  JAM1     3'  GGATTACAGATGTGAGCCA   58499     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1246  JAM1     3'  GGATTACAGATGTGAGCCA   58520     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1246  JAM1     3'  GGATTACAGATGTGAGCCA   58548     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
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                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1246  JAM1     3'  GGATTACAGATGTGAGCCA    58577      C        TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1246  KIAA0210 5'  GAATTACAGGTGTGAGCCA    29159      C        TTAATC
                                TGGC CACATCTGT     TTC
                                |||| |||||||||      |||
                                ACCG GTGTGGACA     AAG
                                  A       TT_____
GAM1246  KIAA0280 3'  GAGCATAAACAGATGTGGTCCA 93301     C           AT
                                TGG CCACATCTGTTTA  CTT
                                ||| ||||||||||||  |||
                                ACC GGTGTAGACAAAT  GAG
                                  T           AC
GAM1246  KIAA0285 5'  GAAGATTGAGCTTGACCGGACC 29684     C  ACA  T_
              A                  TGG CC   TC  GTTTAATCTTC
                                ||| ||   ||  ||||||||||
                                ACC GG   AG  CGAGTTAGAAG
                                  A  CC_  TT
GAM1246  KIAA0356 3'  GGAAGACCCTCAGATGTGGCCA 66778       C      TTTAA
                                TGGCC ACATCTG     TCTTCC
                                ||||| |||||||     ||||||
                                ACCGG TGTAGAC     AGAAGG
                                   _      TCCC_
GAM1246  KIAA1354 3'  GGAAGATTGTCAGCATGT    61576      _  TT
                                ACAT CTG  TAATCTTCC
                                |||| |||  |||||||||
                                TGTA GAC  GTTAGAAGG
                                  C   T_
GAM1246  KIAA1466 3'  ATTAAATAGTATGGGCCA    72406        CAT
                                TGGCCCA   CTGTTTAAT
                                |||||||   |||||||||
                                ACCGGGT   GATAAATTA
                                    AT_
GAM1246  KIAA1468 5'  AAGATCTTGTAGATGTGGCCA  93423       C      TTTA
                                TGGCC ACATCTG    ATCTT
                                ||||| |||||||    |||||
                                ACCGG TGTAGAT    TAGAA
                                   _      GTTC
GAM1246  MRPS26   3'  GGAAGATTACAGTCTGAGGGCC 48723        A  T_   TT
              A                  TGGCCC CA  CTGT  AATCTTCC
                                |||||| ||  ||||  ||||||||
                                ACCGGG GT  GACA  TTAGAAGG
                                   A  CT   __
GAM1246  PANX3    3'  AAGATTAATAAAGATGTAAACC 54765    CCC     GT_
                                GG   ACATCT   TTAATCTT
                                ||   ||||||   ||||||||
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                                CC   TGTAGA   AATTAGAA
                                 AAA     AAT
GAM1246  PLCL1    3'  AAGATTAAACAGATGATG    21714    _
                                CA CATCTGTTTAATCTT
                                || ||||||||||||||
                                GT GTAGACAAATTAGAA
                                 A
GAM1246  SPRY4    3'  GAAGACAGAACACAGATGTGGA 49013    GC        _  AA_
              CA                   TG  CCACATCTGT TT   TCTTC
                                ||  |||||||||| ||   |||||
                                AC  GGTGTAGACA AA   AGAAG
                                 A_         C  GAC
GAM1246  WNT10A   3'  GAAGAGGAGATTGGACCA    48170     C   C    G TTAA
                                TGG CCA ATCT T    TCTTC
                                ||| ||| |||| |    |||||
                                ACC GGT TAGA G    AGAAG
                                  A   _    G ____
GAM1246  LOC113523 5'  GGATTACAGATGTGAGCCA    73427      C        TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A        __
GAM1246  LOC124216 3'  GGATTACAGATGTGAGCCA    74736      C        TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A        __
GAM1246  LOC130639 5'  GGATTAAAGACGTGAGCCA    75480      C   A   GT
                                TGGC CAC TCT  TTAATCT
                                |||| ||| |||  |||||||
                                ACCG GTG AGA  AATTAGG
                                  A   C   __
GAM1246  LOC144202 5'  GGAAGATTCGATGGACATGGAC 77226    GC   CA     T
              A                   TG  CCA  TCTGTT AATCTTCC
                                ||  |||  ||||||| ||||||||
                                AC  GGT  AGGTAG TTAGAAGG
                                 A_   AC      C
GAM1246  LOC149171 5'  GAATTACAGGTGTGAGCCA    79967      C        TTAATC
                                TGGC CACATCTGT      TTC
                                |||| |||||||||      |||
                                ACCG GTGTGGACA      AAG
                                  A        TT____
GAM1246  LOC150245 3'  GAAGCAAGACAGATGTGGGCC  86112              AAT
                                GGCCCACATCTGTTT   CTTC
                                ||||||||||||||   ||||
                                CCGGGTGTAGACAGA   GAAG
                                          AC_
GAM1246  LOC152620 3'  AGATTACAGATGTGAGCCA    60703      C        TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
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                                ACCG GTGTAGACA  TTAGA
                                  A       __
GAM1246  LOC153577 3'  GAAGATTTTATGTGACCA    87239     CC    CTGTTT
                                TGG  CACAT     AATCTTC
                                |||  |||||     |||||||
                                ACC  GTGTA     TTAGAAG
                                  A_    TT____
GAM1246  LOC154930 3'  GAATAACAGGTGTGAGCCA    82091     C       TAATC
                                TGGC CACATCTGTT    TTC
                                |||| ||||||||||    |||
                                ACCG GTGTGGACAA    AAG
                                  A        T____
GAM1246  LOC157507 5'  AAGATTAAACCATGGATG    82376      ___
                                CATCT   GTTTAATCTT
                                |||||   ||||||||||
                                GTAGG   CAAATTAGAA
                                   TAC
GAM1246  LOC158014 5'  AGAATTACAGGTGTGAGCCA   82549     C       TTAA
                                TGGC CACATCTGT    TCT
                                |||| |||||||||    |||
                                ACCG GTGTGGACA    AGA
                                  A       TTA_
GAM1246  LOC158668 3'  AGATTACAGATGTGAGCCA    69892     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGA
                                  A       __
GAM1246  LOC170409 5'  GGATTACAGATGTGAGCCA    83745     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1246  LOC200282 5'  GAAATTACAGGTGTGAGCCA   90099     C       TTAA
                                TGGC CACATCTGT    TC
                                |||| |||||||||    ||
                                ACCG GTGTGGACA    AG
                                  A       TTAA
GAM1246  LOC220595 3'  GGAAGACCTCAGATGTGACCA  92778     CC      TTTAA
                                TGG  CACATCTG    TCTTCC
                                |||  ||||||||    ||||||
                                ACC  GTGTAGAC    AGAAGG
                                  A_       TCC__
GAM1246  LOC253805 3'  GGATTACAGATGTGAGCCA    98179     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1246  LOC56181  5'  GGATTACAGATGTGAGCCA    97278     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
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                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1246  LOC91547  3'  GGATTACAGATGTGAGCCA   67004     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1247  GPR48     3'  ATTTAAAAACTAGAATAACAGA 38093        GCAA    GG
                                TCTGTTATT    AGTT  TAAAT
                                |||||||||    ||||  |||||
                                AGACAATAA    TCAA  ATTTA
                                     GA__    AA
GAM1247  ZFP36L1   3'  TTACCATGCATAACAGA     18203       T   AAGT
                                TCTGTTAT GCA    TGGTAA
                                |||||||| |||    ||||||
                                AGACAATA CGT    ACCATT
                                  _  _____
GAM1247  AKAP6     3'  GCTAAGTTTGCAATAACAGA   16251           G
                                TCTGTTATTGCAAA TTGGT
                                |||||||||||||| |||||
                                AGACAATAACGTTT AATCG
                                         G
GAM1247  C11orf25  5'  TACCAACTTTTAGGAAATAA   49466      GC___
                                TTATT     AAAGTTGGTA
                                |||||     ||||||||||
                                AATAA     TTTCAACCAT
                                   AGGAT
GAM1247  DKFZP586B2420 3'  ACTTATTTACAATAACAGG    75488         C   GTT
                                TCTGTTATTG AAA   GGT
                                |||||||||| |||   |||
                                GGACAATAAC TTT   TCA
                                      A   AT_
GAM1247  DKFZp586H0623 3'  ATTTACCAATTAAATAACTGA  34496    T     GCAAA
                                TC GTTATT     GTTGGTAAAT
                                || ||||||     ||||||||||
                                AG CAATAA     TAACCATTTA
                                 T     AT___
GAM1247  KIAA0455  3'  GCTCACTTTCCAATAACAGA   72885         C     T
                                TCTGTTATTG AAAGT GGT
                                |||||||||| ||||| |||
                                AGACAATAAC TTTCA TCG
                                      C     C
GAM1247  MEIS3     3'  TTTACCAAAACAAAACAGA    78875       A   CAAAG
                                TCTGTT TTG     TTGGTAAA
                                |||||| |||     ||||||||
                                AGACAA AAC     AACCATTT
                                   _   AA___
GAM1247  MGC16291  3'  ATCGCTTTGCAAAAACAGA    52283       A       T
                                TCTGTT TTGCAAAGT GGT
                                |||||| ||||||||| |||
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                                AGACAA AACGTTTCG CTA
                                   A       _
GAM1247  mPA-PLA1  3'  ATCTAATTTGCAATAAGAGA   58356     G        GTT
                                TCT TTATTGCAAA   GGT
                                ||| ||||||||||   |||
                                AGA AATAACGTTT   CTA
                                  G         AAT
GAM1247  NUP54     3'  ATCTACTTTGCACATAACAGA  60723        _      T
                                TCTGTTAT TGCAAAGT GGT
                                |||||||| |||||||| |||
                                AGACAATA ACGTTTCA CTA
                                     C       T
GAM1247  PREI3     3'  ATTTACCGTTCTGCAACAACGG 66924       A    AAGT
               A                 TCTGTT TTGCA    TGGTAAAT
                                ||||||| |||||    ||||||||
                                AGGCAA AACGT    GCCATTTA
                                   C    CTT_
GAM1247  LOC145609 5'  ACTGACTTTGCAACAATAGA   84358       A       TG
                                TCTGTT TTGCAAAGT  GT
                                |||||| |||||||||  ||
                                AGATAA AACGTTTCA  CA
                                   C        GT
GAM1247  LOC148823 3'  ACTTTGTCTACATAACAGA    59891        T___
                                TCTGTTAT    GCAAAGT
                                ||||||||    |||||||
                                AGACAATA    TGTTTCA
                                     CATC
GAM1247  LOC151121 5'  ACTTCTCTTTATAATAACAGA  80932         C    TT_
                                TCTGTTATTG AAAG   GGT
                                |||||||||| ||||   |||
                                AGACAATAAT TTTC   TCA
                                      A   TCT
GAM1247  LOC152273 3'  ATTTACTTAAGTCAATAACAGA 81372         CAAAGTT
                                TCTGTTATTG      GGTAAAT
                                ||||||||||      |||||||
                                AGACAATAAC      TCATTTA
                                      TGAAT__
GAM1247  LOC92218  3'  TTAATAAACTCTCAATAACAGA 69033         CAA    GG_
                                TCTGTTATTG   AGTT   TAA
                                |||||||||   ||||  |||
                                AGACAATAAC   TCAA   ATT
                                      TC_    ATA
GAM1248  SCAMP1    3'  GCTAAATAAATATTCTCC    18014     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1248  SCAMP1    3'  GCTAAATAAATATTCTCC    54500     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
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                                CCT TTATAA TAAATCG
                                  C     A
GAM1248 NX-17    3' TGAATATCAGCCCCTAATA   40706        ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM1248 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
             TA                   TATTAGGGATAATATTCATTTAGC
                                  ||||||||||||||||||||||||
                                  ATAATCCCTATTATAAGTAAATCG

GAM1249 EHF      3' TCCAAAACCCAAGGTTGGCT  25127     AT   _   C
                                AGT  GCCT GGGT TTGGA
                                |||  |||| |||| |||||
                                TCG  TGGA CCCA AACCT
                                  GT   A   A
GAM1249 EPHA2    3' CCATCGGCCAAGAATACTTGAA 16675         GC  G   T_
             G                   CTTCAAGTAT  CT GGTC  TGG
                                 ||||||||||  || ||||  |||
                                 GAAGTTCATA  GA CCGG  ACC
                                      A_  A   CT
GAM1249 ITGA5    3' CCCAGAGACATACTTGAAG   61933          C__
                                CTTCAAGTATG   CTGGG
                                ||||||||||   |||||
                                GAAGTTCATAC   GACCC
                                     AGA
GAM1249 TREM2    3' TCCAAGACTGTCATATTT    39098       CCTG
                                AAGTATG   GGTCTTGGA
                                |||||||   |||||||||
                                TTTATAC   TCAGAACCT
                                    TG__
GAM1249 UQCRB    3' CCAACATAGGCATACTTAAG  21939     C        GGTC
                                CTT AAGTATGCCTG   TTGG
                                ||| ||||||||||   ||||
                                GAA TTCATACGGAT   AACC
                                  _        AC__
GAM1249 ATP10D   3' CAGAGACCACTTGAAG      73526        ATGCCTG   _
                                CTTCAAGT      GGTCT TG
                                ||||||||      ||||| ||
                                GAAGTTCA      CCAGA AC
                                    _______   G
GAM1249 B3GNT7   3' CCCTTCCAGGCAACCTGAA   71678     A  A      TCTT
                                TTCA GT TGCCTGGG   GG
                                ||||  ||  ||||||||   ||
                                AAGT CA ACGGACCT   CC
                                  C  _       TC__
GAM1249 DKFZp547I224 3' TCCAAAATTGACCACATACTTG 39963         CCTG   ____
             GA                   TTCAAGTATG   GGTC   TTGGA
                                  ||||||||||   ||||   |||||
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                                AGGTTCATAC   CCAG   AACCT
                                     A___    TTAA
GAM1249  FLJ22341  3'  CCAAGCTCAGGCACACCCAAG  45114    CAA  A      T
                                CTT   GT TGCCTGGG CTTGG
                                |||   || |||||||| |||||
                                GAA   CA ACGGACTC GAACC
                                  CC_  C      _
GAM1249  KIAA0779  3'  CCGAACAGCATACTTGAAG   86908          C  GGTC
                                CTTCAAGTATGC TG   TTGG
                                ||||||||||||| ||   ||||
                                GAAGTTCATACG AC   AGCC
                                       _  A___
GAM1249  LOC144233 3'  CCAAGGCACATAATTGAA    77246      G   CCTGG
                                TTCAA TATG    GTCTTGG
                                ||||| ||||    |||||||
                                AAGTT ATAC    CGGAACC
                                   A   A____
GAM1249  LOC147341 3'  ACCCAGGCATAACTGAAG    85116      AG
                                CTTCA  TATGCCTGGGT
                                |||||  ||||||||||
                                GAAGT  ATACGGACCCA
                                   CA
GAM1249  LOC221088 5'  TCCAAGGTGCTGGCCACTCGAA 94888     A   AT   TGGG
            G                    CTTC AGT  GCC   TCTTGGA
                                |||| |||  |||   |||||||
                                GAAG TCA  CGG   GGAACCT
                                  C   C_   TCGT
GAM1250  CPNE7    3'  CAGTCAGCCTCCTGTCCCTG   27789        TCTC
                                CAGGGACA   AGGCTGACTG
                                ||||||||   ||||||||||
                                GTCCCTGT   TCCGACTGAC
                                     CC__
GAM1250  FMR2     3'  GCTGACTGCAACAAGATGTCTC 10695          T_________   GCTGA
            TGTA                   TACAGGGACATC       CAG    C
                                ||||||||||||       |||    |
                                ATGTCTCTGTAG       GTC    G
                                       AACAAC___   AGTCG
GAM1250  LILRB2   3'  CAGTCAGCCTGGACCCCT    20804     ACA  T
                                AGGG   TC CAGGCTGACTG
                                ||||   || ||||||||||
                                TCCC   AG GTCCGACTGAC
                                  C__  _
GAM1250  LILRB3   3'  CAGTCAGCCTGGACCCCT    23424     ACA  T
                                AGGG   TC CAGGCTGACTG
                                ||||   || ||||||||||
                                TCCC   AG GTCCGACTGAC
                                  C__  _
GAM1250  LILRB5   3'  CAGCCAGCCTGGACCCCT    23370     ACA  T      A
                                AGGG   TC CAGGCTG CTG
                                ||||   || ||||||| |||
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                                TCCC   AG GTCCGAC GAC
                                  C__ _      C
GAM1250  TCTEL1   3'  CAGATGAGTATCCCTGTA    22533        CAT    GG
                                TACAGGGA   CTCA  CTG
                                ||||||||   ||||  |||
                                ATGTCCCT   GAGT  GAC
                                    AT_    A_
GAM1250  CDH22    3'  CACGCCGCTGAGATGCCC    41437     A      __   _
                                GGG CATCTCA  GGC TG
                                ||| |||||||  ||| ||
                                CCC GTAGAGT  CCG AC
                                  _      CG   C
GAM1250  CECR2    3'  CAGTCAGCCTGAGAGAGAACAC 49430    GACA___
              C                  GG       TCTCAGGCTGACTG
                                 ||       ||||||||||||||
                                 CC       AGAGTCCGACTGAC
                                  ACAAGAG
GAM1250  FAM8A1   3'  AGTTGAAATGTCCCTCA     33198    C       C    G
                                A AGGGACAT TCAG CT
                                | ||||||||  |||| ||
                                A TCCCTGTA AGTT GA
                                 C       A    _
GAM1250  FLJ11850 3'  CAGCTGCTTACTGAGATGCCCC 43020     A       _______
                                GGG CATCTCAG      GCTG
                                ||| ||||||||      ||||
                                CCC GTAGAGTC      CGAC
                                  C       ATTCGT
GAM1250  KIAA0161 3'  CAGTCACCATAGATGTCCACGT 29193     AG       CA  C
              A                  TAC  GGACATCT  GG TGACTG
                                 |||  ||||||||  || ||||||
                                 ATG  CCTGTAGA  CC ACTGAC
                                   CA       TA  _
GAM1250  KIAA0978 3'  CAGCCAGCCTGAGCTCTCCTG  70991      _ CAT        A
                                CAGG GA   CTCAGGCTG CTG
                                |||| ||   ||||||||| |||
                                GTCC CT   GAGTCCGAC GAC
                                  T  C__        C
GAM1250  KIAA1281 3'  CAGTGTAAAATGTTCCTGTA   90626          CTCAG
                                TACAGGGACAT     GCTG
                                ||||||||||     ||||
                                ATGTCCTTGTA     TGAC
                                      AAATG
GAM1250  LOC146520 3' CAGCAGAAATGTTCCTG     78516          C  AG
                                CAGGGACAT TC  GCTG
                                |||||||| ||  ||||
                                GTCCTTGTA AG  CGAC
                                      A  A_
GAM1250  LOC151568 5' AGCCAGCCTGAGGCTGTG    57491       GGACA         A
                                TACAG     TCTCAGGCTG CT
                                |||||     |||||||||| ||
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                                GTGTC    GGAGTCCGAC GA
                                  _____        C
GAM1250  LOC152274 5'  CAGTGAGGTGAGATTCCCTG  81336      C    GG  G
                                CAGGGA ATCTCA  CT ACTG
                                |||||| ||||||  || ||||
                                GTCCCT TAGAGT  GA TGAC
                                   _     G_  G
GAM1250  LOC221975 3'  AGTCAGCTTCATCCCTCA    94187   C    CATCTC
                                A AGGGA     AGGCTGACT
                                | |||||     |||||||||
                                A TCCCT     TTCGACTGA
                                 C    AC____
GAM1250  LOC253502 3'  CAGTCAGCTCCTGTCCCTG   96216       TCTCA
                                CAGGGACA    GGCTGACTG
                                ||||||||    |||||||||
                                GTCCCTGT    TCGACTGAC
                                     CC___
GAM1250  LOC256113 5'  CAGCCTGAAAGTCCCTGTA   98571        ATC
                                TACAGGGAC   TCAGGCTG
                                |||||||||   ||||||||
                                ATGTCCCTG   AGTCCGAC
                                     AA_
GAM1250  LOC256402 3'  CAGTCAGCCTGAAATATC    97542    C  C
                                GA AT TCAGGCTGACTG
                                || || ||||||||||||
                                CT TA AGTCCGACTGAC
                                 A  A
GAM1251  CYP4F3    3'  CTGTATTCACAGCTGCTT    8004         CGTAAAAC
                                GAGCAGCTG       ATACAG
                                |||||||||       ||||||
                                TTCGTCGAC       TATGTC
                                     ACT_____
GAM1251  EN2       5'  CTGCATGCGCGCAGCTCTC   9258      C      AAAA   A
                                GAG AGCTGCGT    CAT CAG
                                ||| ||||||||    ||| |||
                                CTC TCGACGCG    GTA GTC
                                  _       C___   C
GAM1251  GPR44     3'  CTGTATGCAACAGGCACTC   17697     CA   GC  AAAA
                                GAG  GCT  GT    CATACAG
                                |||  |||  ||    |||||||
                                CTC  CGG  CA    GTATGTC
                                  A_   A_  AC__
GAM1251  NUCB1     3'  CCTGTATGCCCACAGCTACT   21639    C    CGTAAAA
                                AG AGCTG      CATACAGG
                                || |||||      ||||||||
                                TC TCGAC      GTATGTCC
                                 A    ACCC___
GAM1251  SYNGR3    3'  CCTAGTACTCCACAAGCTGCTC 16118        GC  AAAACA  _
                                GAGCAGCT  GT     TAC AGG
                                ||||||||  ||     ||| |||
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                                CTCGTCGA  CA     ATG TCC
                                    A_  CCTC__   A
GAM1251  WBSCR14   3'  CCTGCTGCTCACTCAGCTGC   53094       C  AAAA  TA
                                GCAGCTG GT    CA  CAGG
                                ||||||| ||    ||  ||||
                                CGTCGAC CA    GT  GTCC
                                    T  CTC_  C_
GAM1251  WBSCR14   3'  CCTGCTGCTCACTCAGCTGC   53096       C  AAAA  TA
                                GCAGCTG GT    CA  CAGG
                                ||||||| ||    ||  ||||
                                CGTCGAC CA    GT  GTCC
                                    T  CTC_  C_
GAM1251  DKFZP434F1735 3'  ATGCTTTAGCAGCTGCTC    32114         G    A
                                GAGCAGCTGC TAAA CAT
                                |||||||||| |||| |||
                                CTCGTCGACG ATTT GTA
                                     _    C
GAM1251  ELL2      3'  CTGCATTTCGAAGCTGCTC   24893        G  T   ACATA
                                GAGCAGCT CG AAA     CAG
                                |||||||| || |||     |||
                                CTCGTCGA GC TTT     GTC
                                    A  _   AC___
GAM1251  FLJ20730  3'  CCTGTATGTTTACAGACT    36049    _   CGTA
                                AG CTG    AAACATACAGG
                                || |||    ||||||||||
                                TC GAC    TTTGTATGTCC
                                 A  A___
GAM1251  HSPB7     3'  CCAGGGTGTCAACAGCTGCTC  27783         CGTAAA    ACA
                                GAGCAGCTG     ACAT   GG
                                |||||||||     ||||   ||
                                CTCGTCGAC     TGTG   CC
                                     AAC___    GGA
GAM1251  KIAA0984  3'  TATGCTTTACGCAGTTGCTC   66143             A
                                GAGCAGCTGCGTAAA CATA
                                |||||||||||||| ||||
                                CTCGTTGACGCATTT GTAT
                                       C
GAM1251  LOC201627 3'  CCTACATGTTTCACAGTTCAGC 90451         C___  A     AC
            TGCT                   AGCAGCTG   GT AAACAT  AGG
                                |||||||   || ||||||  |||
                                TCGTCGAC   CA TTTGTA  TCC
                                    TTGA  C     CA
GAM1252  TERF1     3'  CCCAAATCCTGTTCCAATGA   34391        C   TA   C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                    _  C_   A
GAM1252  FLJ10159  3'  CCATGTCACGCCATCCAATGAC 36334         CA_   A   TC
                                GTCATTGGA   CGT GAT  GG
                                |||||||||   ||| |||  ||
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                                CAGTAACCT   GCA CTG  CC
                                     ACC  _   TA
GAM1252  FLJ14213  3'  CCGATGCTCCCAATGACG    46216        ACAC   GAT
                                CGTCATTGG   GTA   TCGG
                                |||||||||   |||  ||||
                                GCAGTAACC   CGT   AGCC
                                     CT__   ___
GAM1252  MGC10715  3'  ATTTACCAGACATCCAATGAC  44495        CAC___
                                GTCATTGGA     GTAGAT
                                |||||||||     ||||||
                                CAGTAACCT     CATTTA
                                     ACAGAC
GAM1252  MOST2     5'  CCAGGACTGCCCAATGAC    40059        ACAC   A  _
                                GTCATTGG   GTAG TTC GG
                                ||||||||   |||| ||| ||
                                CAGTAACC   CGTC AGG CC
                                     ____   _  A
GAM1252  LOC150370 3'  CCGGGTCTACGTGCCCATGAC  86123      T  A
                                GTCAT GG CACGTAGATTCGG
                                ||||| || ||||||||||||
                                CAGTA CC GTGCATCTGGGCC
                                   C  _
GAM1252  LOC152620 3'  CCCAAATCCTGTTCCAATGA   60707        C   TA   C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                     _  C_   A
GAM1252  LOC158668 3'  CCCAAATCCTGTTCCAATGA   69896        C   TA   C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                     _  C_   A
GAM1253  GRM3      3'  ACGTGCAGCTCCAGAATA     7743       A       G
                                TATT TGGAGCTG GCGT
                                |||| ||||||||  ||||
                                ATAA ACCTCGAC TGCA
                                   G       G
GAM1253  RORA      5'  ACCTTGGACTCCATAGTA     56957          _ TG  C
                                TATTATGGAG C  GG GT
                                |||||||||| |  || ||
                                ATGATACCTC G  TC CA
                                     A GT  _
GAM1253  IRX4      3'  ACACTCGACTCCATAATA     33450          C   C
                                TATTATGGAG TGGG GT
                                |||||||||| ||||  ||
                                ATAATACCTC GCTC CA
                                     A   A
GAM1253  KIAA1536  3'  ACACTGGGCTCCATGATA     40874          G  C
                                TATTATGGAGCT GG GT
                                ||||||||||| || ||
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                                ATAGTACCTCGG TC CA
                                      G  A
GAM1253  KIAA1944  5'  TACACCCAATGTCTGCTCCATA 76082        _______   C ___
                                TATGGAGC     TGGG GT   A
                                ||||||||     |||| ||   |
                                ATACCTCG     ACCC CA   T
                                     TCTGTA    A __
GAM1253  LOC135154 3'  ACGCCCAGCCTAGAAATG    75715     A_  A
                                TATT  TGG GCTGGGCGT
                                ||||  ||| |||||||||
                                GTAA  ATC CGACCCGCA
                                  AG   _
GAM1253  LOC220565 3'  ACACCTGTGTGCCATGATA   92438       A _   C
                                TATTATGG GC TGGG GT
                                |||||||| || |||| ||
                                ATAGTACC TG GTCC CA
                                     G  T    A
GAM1253  LOC64150  5'  ACACCTCGGGACTCCATAATA  67864        __  _ C
                                TATTATGGAG  CTG GG GT
                                ||||||||||  ||| || ||
                                ATAATACCTC  GGC CC CA
                                      AG   T  A
GAM1254  ARHC     5'  CTTGCTGTGAAGTGGTGTA    18969        _ C  AG
                                TACACCACT C CA  AAG
                                ||||||||| | ||  |||
                                ATGTGGTGA G GT  TTC
                                      A T  CG
GAM1254  BACH2    3'  CTTGCTCTTGGAAGTGGTGTG  41783        C     AGAA
                                TACACCACT CCAAGA    CAAG
                                ||||||||| ||||||    ||||
                                GTGTGGTGA GGTTCT    GTTC
                                      A     C___
GAM1254  GOCAP1   3'  TTGTTCTTGGGAGCAGTGTA   43009      CA        G
                                TACAC  CTCCCAAGAA AA
                                |||||  |||||||||| ||
                                ATGTG  GAGGGTTCTT TT
                                   AC         G
GAM1254  LAMC1    3'  TTGCTCTCCGGGGTGGTTA    11276   C      CAA  A  A
                                A ACCACTCC   GA GA CAA
                                | ||||||||   || || |||
                                A TGGTGGGG   CT CT GTT
                                 T       C__  _ C
GAM1254  MECP2    3'  TGTCTTTTGGGAGTGGT     18417           A  A
                                ACCACTCCCAAGA GA CA
                                |||||||||||| || ||
                                TGGTGAGGGTTTT CT GT
                                          _ _
GAM1254  TLL2     3'  TTGTTCTAGAGAAGTGTA    25886      CA   CCAAGA
                                TACAC  CTC     AGAACAA
                                |||||  |||     |||||||
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                                ATGTG  GAG     TCTTGTT
                                  AA   A_____
GAM1254  WISP1    3'  TGTCTGGCCCCTGAGAGTGGTG 15281        C  AGA___   A
                                CACCACTC CA     AGA CA
                                |||||||| ||     ||| ||
                                GTGGTGAG GT     TCT GT
                                    A  CCCCGG  _
GAM1254  APOL2    3'  TTGTCCTTCTGGGGGTG     48796        A    A
                                CACTCCCA GAAG ACAA
                                |||||||| |||| ||||
                                GTGGGGGT CTTC TGTT
                                    _   C
GAM1254  C22orf5  3'  CTTGGACAGGCCTCAGGAGTGG 25338    C       CA  AAGAA__
            TCA                   A ACCACTCC  AG      CAAG
                                | ||||||||  ||      ||||
                                A TGGTGAGG  TC      GTTC
                                 C       AC  CGGACAG
GAM1254  DKFZP586M1523 3'  CTTGTTCTGGGTTGGCAGT    89609     C    GA_
                                ACT CCAA   AGAACAAG
                                ||| ||||   ||||||||
                                TGA GGTT   TCTTGTTC
                                  C    GGG
GAM1254  FLJ10120  3'  CTTGTCAGGCTTTGGGAGTG   36307         _ AAGA
                                CACTCCCAA G    ACAAG
                                |||||||||  |    |||||
                                GTGAGGGTT C    TGTTC
                                    T GGAC
GAM1254  FLJ10656  3'  GTTCTTCTTTGGCTGTA     36910      _   CTCCC
                                TACA CCA     AAGAAGAAC
                                ||||  |||     |||||||||
                                ATGT GGT     TTCTTCTTG
                                  C   _____
GAM1254  FLJ14906  3'  CTTGTTGCTAAAGTGGTGTA   52761         CC__   G
                                TACACCACT    CAA AAG
                                |||||||||    ||| |||
                                ATGTGGTGA    GTT TTC
                                    AATC   G
GAM1254  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         _ C_   _
                                TACACCACT C  CAAG AAG
                                |||||||||  |  |||| |||
                                ATGTGGTGA G  GTTT TTC
                                    A AC    A
GAM1254  HSJ1     3'  CTTGGGGGAGGTGGTGTA    23080         ___
                                TACACCACT   CCCAAG
                                |||||||||   ||||||
                                ATGTGGTGG   GGGTTC
                                    AGG
GAM1254  HSU79274  5'  CTTGTTTTGGGGAGCATGTA  26147      CCA     AAGAA
                                TACA   CTCCC    GAACAAG
                                ||||   |||||    |||||||
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                                ATGT  GAGGG   TTTGTTC
                                  AC_   GT___
GAM1254 KIAA1219 3' CTTGTTCTAGTTGAAGTG   62027    CC  GA
                                CACT  CAA  AGAACAAG
                                ||||  |||  ||||||||
                                GTGA  GTT  TCTTGTTC
                                  A_  GA
GAM1254 KIAA1719 3' TCTGTCTTGGGAGTGGTGTA  68742          _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                         G
GAM1254 KIAA1853 3' TTTTTCTTGGAAGCAGTG   69929    CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM1254 KIAA1906 3' CTTATTCTTCTTGACTTTTGG  73571    CTCC_      C
                                CCA    CAAGAAGAA AAG
                                |||    ||||||||| |||
                                GGT    GTTCTTCTT TTC
                                  TTTCA       A
GAM1254 NOVA2    3' TGCTCCTCTTGGGATGG    11820    C      A  A
                                CCA TCCCAAGA GA CA
                                ||| |||||||| || ||
                                GGT AGGGTTCT CT GT
                                  _      C  C
GAM1254 SLC11A2  3' CTTGTTCTTCTTAAATGTG  7050     TCCC
                                CAC   AAGAAGAACAAG
                                |||   ||||||||||||
                                GTG   TTCTTCTTGTTC
                                  TAAA
GAM1254 YME1L1   3' TCATTCTTGATGTGGTGTA  27323       TCC    _
                                TACACCAC  CAAGAA GA
                                ||||||||  |||||| ||
                                ATGTGGTG  GTTCTT CT
                                     TA_    A
GAM1254 YME1L1   3' TCATTCTTGATGTGGTGTA  58438       TCC    _
                                TACACCAC  CAAGAA GA
                                ||||||||  |||||| ||
                                ATGTGGTG  GTTCTT CT
                                     TA_    A
GAM1254 ZNF262   3' CTTATTTTGTTTGGGAGT   18723        A   C
                                ACTCCCAAG AGAA AAG
                                ||||||||| |||| |||
                                TGAGGGTTT TTTT TTC
                                     G   A
GAM1254 LOC146136 5' CTTGTTCTTCTTCTGCAGT  73318    CCC_
                                ACT   AAGAAGAACAAG
                                |||   ||||||||||||
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                                TGA   TTCTTCTTGTTC
                                  CGTC
GAM1254  LOC147172 3'  CTTGTCAGGCTTTGGGAGTG  78901        _ AAGA
                                CACTCCCAA G   ACAAG
                                ||||||||| |   |||||
                                GTGAGGGTT C   TGTTC
                                     T GGAC
GAM1254  LOC149175 3'  GTTCCTCAGGCGAGTGGTG   79956       _  AA  A
                                CACCACTC CC  GA GAAC
                                |||||||| ||  || ||||
                                GTGGTGAG GG  CT CTTG
                                     C  A_  C
GAM1254  LOC150207 5'  GTTCCTTTGAGTGGTG     80597       CC   AA
                                CACCACTC  AAG  GAAC
                                ||||||||  |||  ||||
                                GTGGTGAG  TTC  CTTG
                                     T_   __
GAM1254  LOC199692 3'  CTTGTTCTTCTGCTGTAGTGTG 59926     C  TCCCA
                                TACAC AC    AGAAGAACAAG
                                ||||| ||    ||||||||||
                                GTGTG TG    TCTTCTTGTTC
                                   A  TCG__
GAM1254  LOC220565 3'  CTTGTTCTTCTTCTGCAGT   92443    CCC_
                                ACT   AAGAAGAACAAG
                                |||   ||||||||||
                                TGA   TTCTTCTTGTTC
                                  CGTC
GAM1254  LOC221297 3'  CTTGTTCTTCTTACTGTGGT  93481     TCCC
                                ACCAC   AAGAAGAACAAG
                                |||||   ||||||||||
                                TGGTG   TTCTTCTTGTTC
                                   TCA_
GAM1254  LOC90050  3'  CTTGTTCTTCTTGTTCTTTGTA 57186    CCACTCC
                                TACA     CAAGAAGAACAAG
                                ||||     ||||||||||||
                                ATGT     GTTCTTCTTGTTC
                                   TTCTT__
GAM1254  LOC91960  3'  TGTGGCTTGGAACGTGGTGTA  68294       TC_    AAGA
                                TACACCAC  CCAAG   ACA
                                ||||||||  |||||   |||
                                ATGTGGTG  GGTTC   TGT
                                     CAA    GG__
GAM1255  ACP2     3'  TGCCTGTCACTCAGCATTCCCA 9657        _ CACTT
            TG                   CATGGGAA GC    TGACAGGCA
                                ||||||||| ||    |||||||||
                                GTACCCTT CG    ACTGTCCGT
                                     A  ACTC_
GAM1255  CTSB     3'  CCTCCAAGCAAGTAGCTTTCCA 65360       C   TGAC__
                                TGGGAAGC ACTT     AGG
                                |||||||| ||||     |||
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                                ACCTTTCG TGAA     TCC
                                    A   CGAACC
GAM1255 DLG4     3' TGCCTCATCGTAATTCCCCATG 9091       A  CC  TT   CA
                                CATGGG AG  AC  TGA  GGCA
                                |||||| ||  ||  |||  ||||
                                GTACCC TT  TG  ACT  CCGT
                                   C  AA  CT  __
GAM1255 FLT1     3' TGCCATTTCAGTGGCTTCCCA  10665          TT  CA
                                TGGGAAGCCACT  GA  GGCA
                                ||||||||||||  ||  ||||
                                ACCCTTCGGTGA  TT  CCGT
                                      CT  A_
GAM1255 ITGB7    3' CCCAAGAGGGCTGCTTCCCATG 7961          CA_   GACA
                                CATGGGAAGC   CTTT   GG
                                |||||||||   ||||   ||
                                GTACCCTTCG   GGAG   CC
                                      TCG   AAC_
GAM1255 SLC12A7  3' GCCCATGGGGCTTCCTA     22742        A  T  ACA
                                TGGGAAGCC CT TG   GGC
                                |||||||| || ||   |||
                                ATCCTTCGG GG AC   CCG
                                     _ T  ___
GAM1255 DKFZp434E0519 5' CCTGCTGACTGAGTGGCTTCC  50988          TGA___
                                GGAAGCCACTT     CAGG
                                ||||||||||     ||||
                                CCTTCGGTGAG     GTCC
                                      TCAGTC
GAM1255 DKFZP434F0318 3' GCCCACCTTGGCTTCCCA    48760        CTT  ACA
                                TGGGAAGCCA   TG   GGC
                                |||||||||   ||   |||
                                ACCCTTCGGT   AC   CCG
                                      TCC  ___
GAM1255 DKFZp762A227 5'  TGCCTCTACCAGCTTCCCATG  26884         CACTTTGAC
                                CATGGGAAGC       AGGCA
                                |||||||||        |||||
                                GTACCCTTCG       TCCGT
                                      ACCATC___
GAM1255 FKBP5    3' TGAAGACAGCTTCCCATG    15933        CA_
                                CATGGGAAGC   CTTTG
                                |||||||||   |||||
                                GTACCCTTCG   GAAGT
                                      ACA
GAM1255 FLJ14146 3' TGCCCATCTGCTGAGCTTCTCA 45572        _ CTTT  CA
                                TGGGAAGC CA   GA  GGCA
                                |||||||| ||   ||  ||||
                                ACTCTTCG GT   CT  CCGT
                                    A  CGT_  AC
GAM1255 FLJ20195 3' CCTGGGGGTGGCCCGCCAT   35218     GAA      GA
                                ATGG   GCCACTTT  CAGG
                                ||||   ||||||||  ||||
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                                TACC  CGGTGGGG  GTCC
                                  GCC      __
GAM1255  FLJ20651  3'  CAAAATGGCGTTCCCATG   35920       _   C
                                CATGGGAA GCCA TTTG
                                |||||||| |||| ||||
                                GTACCCTT CGGT AAAC
                                    G   A
GAM1255  FLJ22056  3'  GCCTGCACGTGCCAGCCTCCCA 42834     A ___  TT  A
                                TGGGA GC  CAC  TG CAGGC
                                ||||| ||  |||  || |||||
                                ACCCT CG  GTG  AC GTCCG
                                  C  ACC  C_ _
GAM1255  FLJ32468  3'  TGCCCGTGAGAACATCTTCCCA 59715       CCAC  G  A
            TG                   CATGGGAAG   TTT AC GGCA
                                |||||||||   ||| || ||||
                                GTACCCTTC   AGA TG CCGT
                                     TACA  G  C
GAM1255  KIAA0140  3'  TGCCTGTCCTGTGCCCA    28521     AAGC  TTT
                                TGGG   CAC  GACAGGCA
                                ||||   |||  ||||||||
                                ACCC   GTG  CTGTCCGT
                                  ____  TC_
GAM1255  KIAA0140  3'  TGCCTGTCTGAGCAAGCTTCCC 28522      CA_  T
                                GGGAAGC  CTT GACAGGCA
                                |||||||  ||| ||||||||
                                CCCTTCG  GAG CTGTCCGT
                                    AAC  T
GAM1255  KIAA0161  3'  TGCCCACCTCGGCTTCCCA   29211       ACTT  ACA
                                TGGGAAGCC   TG  GGCA
                                |||||||||   ||  ||||
                                ACCCTTCGG   AC  CCGT
                                     CTCC  ___
GAM1255  KIAA1829  3'  TGCCCATCTCGGCTTCCCA   62659       ACTTT  CA
                                TGGGAAGCC    GA  GGCA
                                |||||||||    ||  ||||
                                ACCCTTCGG    CT  CCGT
                                     CT___  AC
GAM1255  MDS030   5'  GCCCAGTGTGGTTTCCCAT   38065        T  ACA
                                ATGGGAAGCCAC TTG  GGC
                                |||||||||||| |||  |||
                                TACCCTTTGGTG GAC  CCG
                                       T  ___
GAM1255  MGC3178  3'  CCATCGAGCTACTTCCCAT   48715       CCAC   CA
                                ATGGGAAG   TTTGA  GG
                                ||||||||   |||||  ||
                                TACCCTTC   GAGCT  CC
                                    ATC_    A_
GAM1255  SEMA4F   3'  TGCCTGATTCCTGATTCCCATG 16210       GC  CTTTGA
                                CATGGGAA  CA    CAGGCA
                                ||||||||  ||    ||||||
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                                GTACCCTT GT    GTCCGT
                                    A_ CCTTA_
GAM1255 XLKD1    3' CCTCCAAAGCTTCCCA     22924       CAC   AC
                                TGGGAAGC  TTTG AGG
                                ||||||||  |||| |||
                                ACCCTTCG  AAAC TCC
                                    ____  C_
GAM1255 LOC132241 3' TGCCTGTCTCGGCCTCCCA   75566     A  ACTTT
                                TGGGA GCC   GACAGGCA
                                ||||| |||   ||||||||
                                ACCCT CGG   CTGTCCGT
                                  C  CT___
GAM1255 LOC142820 5' TGCCTGCCTCGGCTTCCCA   76920       ACTTTGA
                                TGGGAAGCC     CAGGCA
                                |||||||||     ||||||
                                ACCCTTCGG     GTCCGT
                                    CTCC___
GAM1255 LOC146909 3' GCCTGCCTCAGCTTCCCA    78775       CACTT  __
                                TGGGAAGC    TGA CAGGC
                                ||||||||    ||| |||||
                                ACCCTTCG    ACT GTCCG
                                    _____  CC
GAM1255 LOC147990 3' TGCCTGTCTCAGCCTCCCA   85241     A CACTTT
                                TGGGA GC    GACAGGCA
                                ||||| ||    ||||||||
                                ACCCT CG    CTGTCCGT
                                  C ACT___
GAM1255 LOC149108 3' GCTTCAGAGCTTCCCATG    85511       CAC   CA
                                CATGGGAAGC  TTTGA GGC
                                ||||||||||  |||||  |||
                                GTACCCTTCG  AGACT TCG
                                    ___   __
GAM1255 LOC152316 3' GCCTTGGTAGCTTCCCA     86793       C  TTGAC
                                TGGGAAGC ACT    AGGC
                                |||||||| |||    ||||
                                ACCCTTCG TGG    TCCG
                                    A  T____
GAM1255 LOC154790 5' CCTGCCAGGCTTCCCA      82038       ACTT A
                                TGGGAAGCC   TG CAGG
                                |||||||||   || ||||
                                ACCCTTCGG   AC GTCC
                                    ____ C
GAM1255 LOC155435 3' TGCCCATCAGCAGGTTCCCATG 82275       G ACT   CA
                                CATGGGAA CC  TTGA GGCA
                                |||||||| ||  ||||  ||||
                                GTACCCTT GG  GACT CCGT
                                    _ AC_   AC
GAM1255 LOC157567 3' TGCCTGTTTCCTGGCTTCCAAT 82395    G      CTTT
            G                    CAT GGAAGCCA   GACAGGCA
                                ||| ||||||||   ||||||||
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                                GTA CCTTCGGT    TTGTCCGT
                                  A       CCT_
GAM1255  LOC164397 5'  GCCTGCACTTCTACCTTCCCAT 83409         CCACTT_  A
                 G                 CATGGGAAG      TG CAGGC
                                   |||||||||      || |||||
                                   GTACCCTTC      AC GTCCG
                                        CATCTTC  _
GAM1255  LOC170425 3'  CCTAATCTGGCTTCCCA     76885          CT  GAC
                                   TGGGAAGCCA  TT   AGG
                                   ||||||||||  ||   |||
                                   ACCCTTCGGT  AA   TCC
                                         CT  ___
GAM1255  LOC196746 3'  TGCCTGTCTGCGCCTCTCA    88904       A  _  CTTT
                                   TGGGA GC CA    GACAGGCA
                                   ||||| || ||    ||||||||
                                   ACTCT CG GT    CTGTCCGT
                                      C  C  _____
GAM1255  LOC203248 3'  TGCCTGTCCTGCAGAGTCCCCA 90847       AAGCC    _____
                 TG                  CATGGG    ACTTT    GACAGGCA
                                     ||||||    |||||    ||||||||
                                     GTACCC    TGAGA    CTGTCCGT
                                        C_____    CGTC
GAM1255  LOC221552 3'  GCCTGACATAGCTTCTCA    95451         CACTT  A
                                   TGGGAAGC    TG CAGGC
                                   ||||||||    || |||||
                                   ACTCTTCG    AC GTCCG
                                         AT___  A
GAM1255  LOC222224 5'  TGCCTGTCTCAGCCTCCCA    95878       A  CACTTT
                                   TGGGA GC     GACAGGCA
                                   ||||| ||     ||||||||
                                   ACCCT CG     CTGTCCGT
                                      C  ACT___
GAM1255  LOC254122 3'  TGCCTGTAATACCATGTCTTCC 96397         C  CTTTG__
                 CATG                  CATGGGAAG CA      ACAGGCA
                                       |||||||| ||      |||||||
                                       GTACCCTTC GT      TGTCCGT
                                            T  ACCATAA
GAM1255  LOC254228 3'  TGCCTAAGAATAAAGCTTCCCA 97654         CAC_   GAC
                 T                   ATGGGAAGC    TTT   AGGCA
                                     |||||||||    |||   |||||
                                     TACCCTTCG    AAG   TCCGT
                                          AAAT   AA_
GAM1255  LOC256277 3'  GCCTGGCAAGCTCCCCA     96350      A   CACT   A
                                   TGGG AGC    TTG CAGGC
                                   |||| |||    ||| |||||
                                   ACCC TCG    AAC GTCCG
                                     C   _____   G
GAM1255  LOC256337 3'  GCCTGGCAAGCTCCCCA     96344      A   CACT   A
                                   TGGG AGC    TTG CAGGC
                                   |||| |||    ||| |||||
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                                ACCC TCG    AAC GTCCG
                                  C  ____   G
GAM1255  LOC257493 3'  GCCTGACATAGCTTCTCA    99637        CACTT  A
                                TGGGAAGC    TG CAGGC
                                ||||||||    || |||||
                                ACTCTTCG    AC GTCCG
                                    AT___   A
GAM1255  LOC257609 3'  GCCTGACATAGCTTCTCA    99797        CACTT  A
                                TGGGAAGC    TG CAGGC
                                ||||||||    || |||||
                                ACTCTTCG    AC GTCCG
                                    AT___   A
GAM1255  LOC51107  3'  GCCTGTCCACTGCCCATG    32610       A  CCACTTT
                                CATGGG AG      GACAGGC
                                |||||| ||      |||||||
                                GTACCC TC      CTGTCCG
                                   G  AC_____
GAM1255  LOC91960  3'  GCCTGTCAGAACTCCCCA    68287     A  CCAC
                                TGGG AG    TTTGACAGGC
                                |||| ||    ||||||||||
                                ACCC TC    AGACTGTCCG
                                  C  A___
GAM1256  PCDH11X   5'  AGCACTATGAGGACTGAACG   28005    C_     A   TC
                                CG  CAGTCC TGT  AGTGCT
                                ||  |||||| |||  ||||||
                                GC  GTCAGG GTA  TCACGA
                                 AA     A  __
GAM1256  SORBS1    3'  AGCAAGTGCAACTAACTGGCGG 31802        CCAT   _  G_
                                CCGCCAGT    GTT CA  TGCT
                                ||||||||    ||| ||  ||||
                                GGCGGTCA    CAA GT  ACGA
                                    AT__    C  GA
GAM1256  ZNF236    3'  GCTGTCCACACGGGCTGGCG   24737        A   T__
                                CGCCAGTCC TGT   CAGT
                                ||||||||| |||   ||||
                                GCGGTCGGG ACA   GTCG
                                     C   CCT
GAM1256  CG012     5'  AGCAAACTTCATGGACTGGC   84141          TTCAG
                                GCCAGTCCATG     TGCT
                                ||||||||||     ||||
                                CGGTCAGGTAC     ACGA
                                    TTCAA
GAM1256  CGI-203   5'  AGCACCACTTGAGACTGGGGG  40276    G     _  T  TCA
                                CC CCAGTC CA GT   GTGCT
                                || |||||| || ||   |||||
                                GG GGTCAG GT CA   CACGA
                                 G     A  T  C__
GAM1256  KLHL8     3'  AGCACTTACTAGACTGGTG    63504        CAT  TC
                                CGCCAGTC   GT  AGTGCT
                                ||||||||   ||  ||||||
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                                GTGGTCAG   CA  TCACGA
                                    AT_  T_
GAM1256  SLC26A8   3'  ACTGGATACGAACTAGCAGTA  54767     C  C   CCA
                                TAC GC AGT   TGTTCAGT
                                ||| || |||   ||||||||
                                ATG CG TCA   ATAGGTCA
                                  A  A   AGC
GAM1256  LOC253044 5'  AGCAGCTGGACAAACCTGCG   98362     C  TCCA     _
                                CGC AG    TGTTCAG TGCT
                                ||| ||    ||||||| ||||
                                GCG TC    ACAGGTC ACGA
                                  _  CAA_      G
GAM1256  LOC256081 3'  AGCACTGGGAGACCAGCAGG   97647    _  CA   CATG
                                CC GC  GTC    TTCAGTGCT
                                || ||  |||    |||||||||
                                GG CG  CAG    GGGTCACGA
                                 A  AC   A___
GAM1256  LOC256339 5'  AGGGCTGAACACAGACCTGC   97151    CA   CA      G
                                GC  GTC  TGTTCAGT CT
                                ||  |||  |||||||| ||
                                CG  CAG  ACAAGTCG GA
                                 TC   AC       G
GAM1257  G6PT1     3'  GGTTCCGGAGCACCAT      9405          CTTCGTCC
                                ATGGTGTTCC       GAACC
                                ||||||||||       |||||
                                TACCACGAGG       CTTGG
                                     C________
GAM1257  LRAT      3'  GTTCAGATTTAAAGCACCAT   60731        CCCTTC   C
                                ATGGTGTT     GTC GAAC
                                ||||||||     ||| ||||
                                TACCACGA     TAG CTTG
                                    AATT__   A
GAM1257  XRCC4     3'  GACAAAGAAAACATCATT    14147         CC   C
                                AATGGTGTT  CTT GTC
                                |||||||||  ||| |||
                                TTACTACAA  GAA CAG
                                     AA   A
GAM1257  XRCC4     3'  GACAAAGAAAACATCATT    42599         CC   C
                                AATGGTGTT  CTT GTC
                                |||||||||  ||| |||
                                TTACTACAA  GAA CAG
                                     AA   A
GAM1257  XRCC4     3'  GACAAAGAAAACATCATT    42878         CC   C
                                AATGGTGTT  CTT GTC
                                |||||||||  ||| |||
                                TTACTACAA  GAA CAG
                                     AA   A
GAM1257  CHST3     3'  GTTCAAAGGAACACCA      16243         C  CGTCC
                                TGGTGTTCC TT     GAAC
                                |||||||| ||     ||||
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                                ACCACAAGG AA    CTTG
                                    A _____
GAM1257 DKFZP564I052 3' GACATGGAAGAGAACATCATT 67285        C   ___
                                AATGGTGTTC CTTC  GTC
                                |||||||||| ||||  |||
                                TTACTACAAG GAAG  CAG
                                    A   GTA
GAM1257 DKFZp564K142 3' GGTCTTCTGAAAATGGAACACC 50435        CTTCG  C __
          ATT                    AATGGTGTTCC    TC GA  ACC
                                |||||||||||    || ||  |||
                                TTACCACAAGG    AG CT  TGG
                                     TAAA_  T  TC
GAM1257 MCFP    3' GGTTCAACTTGGAACAACA   38736    G    CTTC  CC
                                TG TGTTCC   GT  GAACC
                                || ||||||   ||  |||||
                                AC ACAAGG   CA  CTTGG
                                 A     TT__  A_
GAM1257 STARD7   3' TCCGATTGTATAGAAAACACCA 39746       CC  TC___  C
          TT                    AATGGTGTT  CT    GTC GA
                                |||||||||  ||    ||| ||
                                TTACCACAA  GA    TAG CT
                                    AA  TATGT   C
GAM1257 STARD7   3' TCCGATTGTATAGAAAACACCA 58372       CC  TC___  C
          TT                    AATGGTGTT  CT    GTC GA
                                |||||||||  ||    ||| ||
                                TTACCACAA  GA    TAG CT
                                    AA  TATGT   C
GAM1257 LOC131368 3' GGTTCAGGTGAGAACACCA   76374       CCT  T  _
                                TGGTGTTC   TCG CC GAACC
                                ||||||||   ||| || |||||
                                ACCACAAG   AGT GG CTTGG
                                    ___   _  A
GAM1257 LOC143153 5' TCGGTGAAGGACCACCA    76984      TTC    T
                                TGGTG   CCTTCG CCGA
                                |||||   |||||| ||||
                                ACCAC   GGAAGT GGCT
                                   CA_     _
GAM1257 LOC157858 5' GGCCAAGAGACACCATT    87892       CC   C
                                AATGGTGTT  CTT GTC
                                |||||||||  ||| |||
                                TTACCACAG  GAA CGG
                                    A_   C
GAM1257 LOC200860 3' TGGAAGAGAGACACCAT    91762       CC   CG
                                ATGGTGTT  CTT  TCCG
                                ||||||||  |||  ||||
                                TACCACAG  GAG  AGGT
                                    A_   A_
GAM1257 LOC219406 5' GTTTTAACAATGGAAACACCAT 95207       C  TTC  CC
                                ATGGTGTT CC   GT  GAAC
                                |||||||| ||   ||  ||||
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                                TACCACAA GG   CA  TTTG
                                    A  TAA  AT
GAM1257  LOC256476 5'  TGGAAAGAAACACCATT     98626        CC   CG
                                AATGGTGTT  CTT  TCCG
                                |||||||||  |||  ||||
                                TTACCACAA  GAA  AGGT
                                    A_   __
GAM1257  LOC90092  3'  GGCTCGGACGAGCTGGCCCCAT 62068     T   CCC       A
                                ATGG GTT   TTCGTCCGA CC
                                |||| |||   |||||||||| ||
                                TACC CGG   GAGCAGGCT GG
                                  C  TC_       C
GAM1258  TERF1    3'  CCCAAATCCTGTTCCAATGA   34391        C   TA    C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                    _  C_    A
GAM1258  FLJ10159  3'  CCATGTCACGCCATCCAATGAC 36334         CA_   A   TC
                                GTCATTGGA   CGT GAT  GG
                                |||||||||   ||| |||  ||
                                CAGTAACCT   GCA CTG  CC
                                    ACC   _   TA
GAM1258  FLJ14213  3'  CCGATGCTCCCAATGACG    46216         ACAC   GAT
                                CGTCATTGG    GTA   TCGG
                                |||||||||    |||   ||||
                                GCAGTAACC    CGT   AGCC
                                    CT__   ____
GAM1258  MGC10715  3'  ATTTACCAGACATCCAATGAC  44495         CAC____
                                GTCATTGGA     GTAGAT
                                |||||||||     ||||||
                                CAGTAACCT     CATTTA
                                    ACAGAC
GAM1258  MOST2    5'  CCAGGACTGCCCAATGAC    40059        ACAC    A   _
                                GTCATTGG    GTAG TTC GG
                                ||||||||    |||| ||| ||
                                CAGTAACC    CGTC AGG CC
                                    _____    _   A
GAM1258  LOC150370 3'  CCGGGTCTACGTGCCCATGAC  86123      T  A
                                GTCAT GG CACGTAGATTCGG
                                ||||| || ||||||||||||||
                                CAGTA CC GTGCATCTGGGCC
                                  C  _
GAM1258  LOC152620 3'  CCCAAATCCTGTTCCAATGA   60707        C   TA    C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                    _  C_    A
GAM1258  LOC158668 3'  CCCAAATCCTGTTCCAATGA   69896        C   TA    C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
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                                AGTAACCT TGT  CTAA CCC
                                   _  C_   A
GAM1259  ELF3     3'  TGACCTTGACCTTGACCAA   16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                   _    AGT  ___
GAM1259  JAK2     3'  TGACCTTCATTCTGAGACCAA  18318      CAA      AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_      C_
GAM1259  SLC10A2  5'  ACTCTCTGTCTTGACCAA    6590       CAA      A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM1259  FLJ10803 3'  GTGACTTTCAGTTAAAGCCAA  37205      CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM1259  KIAA1958 5'  GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM1259  MARCKS   3'  ACTTTCCACCCTGCCCA     11411     TTCA   A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM1259  TUB      5'  GTGGGACCATCCCTTAAACC   13898     C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A       AG__
GAM1259  LOC80298 3'  ACTTTTACCTTGAACCA     48062         GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                     A___
GAM1260  INHBA    3'  TCTAGAAAGCCATGAGTTTGAA 11003       AGAGGT      C
                                TTCAGA     TGGCTTTC AGA
                                ||||||     |||||||| |||
                                AAGTTT     ACCGAAAG TCT
                                   GAGT__       A
GAM1260  MBNL     5'  TCTAAAAACCAAAACCTCTTTG 41072       A    __   C   CC
            AA                   TTCAGA GAGGT  TGG TTT  AGA
                                ||||||  |||||  ||| |||  |||
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                                AAGTTT CTCCA  ACC AAA  TCT
                                   _    AA  _  AA
GAM1260  NPEPPS   3'  TCTGAAAAGCCAGCTCTTGAA  63787     GA   G      C
                                TTCA  AGAG TTGGCTTT CAGA
                                |||| |||| |||||||| ||||
                                AAGT  TCTC GACCGAAA GTCT
                                  __  _      A
GAM1260  RPH3AL   3'  TCTGGAAAACCCTTCCCTGAA  23744      AA   TT  C
                                TTCAG  GAGG  GG TTTCCAGA
                                ||||| ||||  || ||||||||
                                AAGTC  CTTC  CC AAAGGTCT
                                   C_   __ A
GAM1260  TRPV3    3'  TCTGGAAACACCCTTCCGGA  96816    A   A  TGGC
                                TTC GAAG GGT   TTTCCAGA
                                ||| |||| |||   ||||||||
                                AGG CTTC CCA   AAAGGTCT
                                  C   _  C___
GAM1260  TYRO3    3'  TCTGAGCCCAACCCTTCT    21938      A    _ TTC
                                AGAAG GGTTGG CT   CAGA
                                ||||| |||||| ||   ||||
                                TCTTC CCAACC GA   GTCT
                                   _     C ___
GAM1260  ZNF146   3'  GAAATAATCCTTCTGAA     24075        A    GC
                                TTCAGAAG GGTTG  TTTC
                                |||||||| |||||  ||||
                                AAGTCTTC CTAAT  AAAG
                                   _    __
GAM1260  AKAP6    3'  CTAAAAAGCCAACATTTGAA  16248      AGAG       CC
                                TTCAGA   GTTGGCTTT  AG
                                ||||||   |||||||||  ||
                                AAGTTT   CAACCGAAA  TC
                                   A___       AA
GAM1260  DED      3'  CTGGAAAGATGCTGCGTTCCGA 25112    A  GA_  TGG
            A                    TTC GAA   GGT   CTTTCCAG
                                ||| |||   |||   ||||||||
                                AAG CTT   TCG   GAAAGGTC
                                  C   GCG   TA_
GAM1260  DKFZp434J0617 3'  CTGTGGCCACAACCTCTTCTG  50977          __    TTC
                                CAGAAGAGGT  TGGCT   CAG
                                ||||||||||  |||||   |||
                                GTCTTCTCCA  ACCGG   GTC
                                      AC    T__
GAM1260  DKFZp761G0313 3'  TCTGGAAAATAGACCCCTTCT  66394      A   GGC
                                AGAAG GGTT   TTTCCAGA
                                ||||| ||||   ||||||||
                                TCTTC CCAG   AAAGGTCT
                                   C    ATA
GAM1260  FLJ10483  3'  TCCGGAAAACTTTTAATCTTCT 36656       GGTT_  C    A
                                AGAAGA    GG TTTCC GA
                                ||||||    || ||||| ||
```

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                                TCTTCT    TC AAAGG CT
                                   AATTT  A    C
GAM1260 KIAA0280 3' CTAGAAAACTCCTCGTTTCTGA 93295       __   TT  C   C
             A                   TTCAGAA  GAGG  GG TTTC AG
                                 |||||||  ||||  || |||| ||
                                 AAGTCTT  CTCC  TC AAAG TC
                                    TG   __ A   A
GAM1260 KIAA0352 3' AGCTCACCCTCTTCTGAA    29824          T _
                                 TTCAGAAGAGG TG GCT
                                 |||||||||||| || |||
                                 AAGTCTTCTCC AC CGA
                                       C  T
GAM1260 KIAA0515 3' TCCAGAAAGCCAGCTCTCTTCT 64555          _        CA
             GAA                   TTCAGAAGAG GTTGGCTTTC  GA
                                 |||||||||| ||||||||||  ||
                                 AAGTCTTCTC CGACCGAAAG  CT
                                       T         AC
GAM1260 KIAA1102 3' CTGAAAGGCTCTTCTGAA    69583         GGTTG    C
                                 TTCAGAAGA    GCTTT CAG
                                 |||||||||    ||||| |||
                                 AAGTCTTCT    CGGAA GTC
                                      _____    A
GAM1260 MCPR     3' TCTGGCGGTGAACCTACCCTGA 42959      AAG    G   TT
             A                   TTCAG   AGGTT GCT  CCAGA
                                 |||||   ||||| |||  |||||
                                 AAGTC   TCCAA TGG  GGTCT
                                    CCA    G   C_
GAM1260 PADI1    3' CTGAAAATCCCCTTCTGGA   62701        A  TT GC   C
                                 TTCAGAAG GG  G  TTTC AG
                                 ||||||||  ||  |  |||| ||
                                 AGGTCTTC CC  C  AAAG TC
                                      _ __ TA   _
GAM1260 PRO2012  3' CTGAAAAGCAGACTTCTGAA  38389      AGA   G    C
                                 TTCAGA   GGTT GCTTT CAG
                                 ||||||   |||| ||||| |||
                                 AAGTCT   TCAG CGAAA GTC
                                    ___   A    A
GAM1260 SCYA18   3' CTGGAGGCCACCTCTTCT    12974         T    T
                                 AGAAGAGGT GGCTT CCAG
                                 |||||||| ||||| ||||
                                 TCTTCTCCA CCGGA GGTC
                                      _    _
GAM1260 SNX7     3' TCTGGAAAACCAACAACTTGAA 32563     GA  AG    C
                                 TTCA  AG  GTTGG TTTCCAGA
                                 ||||  ||  ||||| ||||||||
                                 AAGT  TC  CAACC AAAGGTCT
                                   __ AA    A
GAM1260 LOC159199 5' CTGGCTTTCCAGCCTCTCCTGA 83059      A       CTTT
             A                   TTCAG AGAGGTTGG    CCAG
                                 ||||| |||||||||    ||||
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                                AAGTC TCTCCGACC   GGTC
                                   C       TTTC
GAM1260 LOC256987 3' CTGGAAAGTGCCATCTTTTGAA 97641        _  TG
                                TTCAGAAGA GGT  GCTTTCCAG
                                ||||||||| |||  |||||||||
                                AAGTTTTCT CCG  TGAAAGGTC
                                     A  __
GAM1261 BCL2    3' AATGACAGCTGACAGGGTC   7232         A  ACTA
                                GACCCTGTTA CT   CGTT
                                |||||||||| ||   ||||
                                CTGGGACAGT GA   GTAA
                                     C  CA__
GAM1261 RBBP2   3' CAACTAGGAGTAACAGGG    18569       A  A   C
                                CCCTGTTA CT CTA GTTG
                                |||||||| || ||| ||||
                                GGGACAAT GA GAT CAAC
                                     _  G  _
GAM1261 ICK     3' CAACATGAAGGTTAACACAGTC 33679    CC      AC  C
                                GAC  TGTTAACT  TA GTTG
                                |||  |||||||||  || ||||
                                CTG  ACAATTGG  GT CAAC
                                  AC       AA  A
GAM1261 NR6A1   3' CAACGTAGTATTGAACAG    9443      AAC
                                CTGTT   TACTACGTTG
                                |||||   ||||||||||
                                GACAA   ATGATGCAAC
                                   GTT
GAM1261 LOC57399 5' CAACAGGTGAAACCAACAGGGT 40707        AAC__   AC
             T                   GACCCTGTT    TACT  GTTG
                                |||||||||    ||||  ||||
                                TTGGGACAA    GTGG  CAAC
                                     CCAAA   A_
GAM1262 HAL     5' GCCACTCCTGCATAAAGCTC   10903         TGAAAA
                                GAGCTTTATGC     GGTGGC
                                ||||||||||     ||||||
                                CTCGAAATACG     TCACCG
                                     TCC___
GAM1262 HMGN2   3' GGCCACCTTGGCACAAAAGC   19809      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _  GG
GAM1262 NMI     5' GGCCACCTCCTCAGGAAG    17436     ATG   AA
                                CTTT   CTGA  AGGTGGCC
                                ||||   ||||  ||||||||
                                GAAG   GACT  TCCACCGG
                                  ___    CC
GAM1262 PACE    3' GGCCACCTCTCCAAGGGCTT   11944       A  CT  AAA
                                GAGCTTT TG  GA   GGTGGCC
                                ||||||| ||  ||   |||||||
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                                TTCGGGA AC  CT   CCACCGG
                                   _ CT  ___
GAM1262 PYCR1    3' CCACCTTCCTCTAGAGCTC   70639       TGCT  A_
                                GAGCTTTA   GA  AAGGTGG
                                ||||||||   ||  |||||||
                                CTCGAGAT   CT  TTCCACC
                                   _____ CC
GAM1262 SDC1     3' GGCCACCTCCCCAGCATTCCAG 12991     TT_    AAA
             C                   GCT   ATGCTG   AGGTGGCC
                                 |||   ||||||   ||||||||
                                 CGA   TACGAC   TCCACCGG
                                   CCT     CCC
GAM1262 FLJ11560 5' GCCCAGGCCCAGCATAAAG   48008        AAAA  ___
                                CTTTATGCTG   GGT   GGC
                                ||||||||||   |||   |||
                                GAAATACGAC   CCG   CCG
                                     _____  GAC
GAM1262 KIAA0446 5' CCACCTTTTGAAGAGCTC    69446       ATGCTG
                                GAGCTTT     AAAAGGTGG
                                |||||||     |||||||||
                                CTCGAGA     TTTTCCACC
                                   AG_____
GAM1262 KIAA0971 3' GTTGTTCTCAGCATAAAGT   30677         AAA  TG
                                GCTTTATGCTGA   GG  GC
                                ||||||||||||   ||  ||
                                TGAAATACGACT   TT  TG
                                     C__  GT
GAM1262 KIAA1393 3' GGCCACCTTGGCACAAAAGC  72574      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                   _ _  GG
GAM1262 KIAA1656 3' GGCCACCTCCTCCTAGAAGCC 66377   A    ATGCT  AA
                                G GCTTT    GA  AGGTGGCC
                                | |||||    ||  ||||||||
                                C CGAAG    CT  TCCACCGG
                                _    ATC__  CC
GAM1262 KIAA1884 3' GCCACCTTCATCTACCAAGGCT 73728       ATGCT  A_
             C                   GAGCTTT    GA  AAGGTGGC
                                 |||||||    ||  ||||||||
                                 CTCGGAA    CT  TTCCACCG
                                    CCAT_  AC
GAM1262 PP3501   3' GGCCACCGTTGACAGCATAAAG 41683         AAAA_
                                CTTTATGCTG    GGTGGCC
                                ||||||||||    |||||||
                                GAAATACGAC    CCACCGG
                                     AGTTG
GAM1262 SDCCAG3  3' GGTGTTCTCAGCATGAAGCTC 22803           AAA  TG
                                GAGCTTTATGCTGA   GG  GCC
                                ||||||||||||||   ||  |||
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                                CTCGAAGTACGACT  CT  TGG
                                      ___  TG
GAM1262  SP140    3'  GGCCACCTCCATGCAGAAGC  24327      A  TGAAA
                                GCTTT TGC    AGGTGGCC
                                ||||| |||    ||||||||
                                CGAAG ACG    TCCACCGG
                                  _  TACC_
GAM1262  LOC148760 3'  GGCCACCTTCTCCAACAAGCTC 85364       TA  CT  A
                                GAGCTT  TG  GA AAGGTGGCC
                                ||||||  ||  || |||||||||
                                CTCGAA  AC  CT TTCCACCGG
                                   CA  __  C
GAM1262  LOC150170 5'  ACCTGTTTCACATAAAGC    80414        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                     _    G
GAM1262  LOC150175 5'  ACCTGTTTCACATAAAGC    80453        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                     _    G
GAM1262  LOC150215 5'  ACCTGTTTCACATAAAGC    80456        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                     _    G
GAM1262  LOC150218 5'  ACCTGTTTCACATAAAGC    80525        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                     _    G
GAM1262  LOC152065 3'  GGCCACCTTCTCCTTGGCAGGC 86737      TTA   ___  A
            TC                    GAGCT   TGCT   GA AAGGTGGCC
                                |||||   ||||   || |||||||||
                                CTCGG   ACGG   CT TTCCACCGG
                                  ___    TTC  C
GAM1262  LOC152267 3'  GGCCACCTTGGCACAAAAGC   61036      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _  GG
GAM1262  LOC158292 5'  CCTCTGGACCCAGCATAAGGCT 88046           AAAA_  T
            C                     GAGCTTTATGCTG     GG GG
                                ||||||||||||     || ||
                                CTCGGAATACGAC     TC CC
                                      CCAGG  T
GAM1262  LOC219997 3'  GCCACCTCTTCAGCCTC     93256     CTTTAT     A
                                GAG     GCTGAA AGGTGGC
                                |||     |||||| |||||||
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                                CTC     CGACTT TCCACCG
                                  _______     C
GAM1262  LOC256269 3'  GGCCACCTTGGCACAAAAGC   96608      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _ GG
GAM1262  LOC91963  5'  GGCCACCTCCTCTGAGAAGC   68321      ATGCT  AA
                                GCTTT    GA  AGGTGGCC
                                |||||    ||  ||||||||
                                CGAAG    CT  TCCACCGG
                                  AGT__  CC
GAM1263  ABL2      5'  TGTGAGTCGCCTGGAGGCAG   24611            A_
                                CTGCCTCCAGGTGAC  GCA
                                ||||||||||||||  |||
                                GACGGAGGTCCGCTG  TGT
                                         AG
GAM1263  DYRK1B    3'  TGATTGGGGCCTGGGGCAG    17517      T     GACAG
                                CTGCC CCAGGT    CAATCA
                                ||||| ||||||    ||||||
                                GACGG GGTCCG    GTTAGT
                                  _     GG___
GAM1263  GNAZ      3'  CTGCACCCCTGTCACCTGGAGG 10827            CAAT_
                                CCTCCAGGTGACAG    CAG
                                ||||||||||||||    |||
                                GGAGGTCCACTGTC    GTC
                                         CCCAC
GAM1263  GYPC      3'  GATAGCCACCTGGAAACA    10900    CC      ACA  A
                                TG  TCCAGGTG   GC ATC
                                ||  ||||||||   || |||
                                AC  AGGTCCAC   CG TAG
                                 AA       ___  A
GAM1263  GYPC      3'  GATAGCCACCTGGAAACA    34143    CC      ACA  A
                                TG  TCCAGGTG   GC ATC
                                ||  ||||||||   || |||
                                AC  AGGTCCAC   CG TAG
                                 AA       ___  A
GAM1263  IL1R1     3'  TGAGGTCACCTGGAATCAG   7928     CC       AG
                                CTG  TCCAGGTGAC  CA
                                |||  ||||||||||  ||
                                GAC  AGGTCCACTG  GT
                                  TA        GA
GAM1263  SLC21A9   3'  TGTGTCACCTGGGGCAG    24384      T       G
                                CTGCC CCAGGTGACA CA
                                ||||| |||||||||| ||
                                GACGG GGTCCACTGT GT
                                  _       _
GAM1263  ZNF138    5'  CTGATTACCTGTCTGGA    82099     GGT    C_
                                TCCA   GACAG  AATCAG
                                ||||   |||||  ||||||
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                                AGGT   CTGTC  TTAGTC
                                  ___    CA
GAM1263  C8orf13   3'  GTGGGTCTCCCGGAGGCAG   82482        A  T   A_
                                CTGCCTCC GG GAC  GC
                                |||||||| || |||  ||
                                GACGGAGG CC CTG  TG
                                    C  T   GG
GAM1263  CHST3     3'  TGTGGTCCCTGGAGGCA     16246         T   A
                                TGCCTCCAGG GAC GCA
                                |||||||||| ||| |||
                                ACGGAGGTCC CTG TGT
                                      _  G
GAM1263  CMG1      5'  TGCAATGCCACCTGGGACAG   47728     C T      A __
                                CTG C CCAGGTG CA  GCA
                                ||| | ||||||| ||  |||
                                GAC G GGTCCAC GT  CGT
                                  A _      C  AA
GAM1263  DKFZP434H132 3'  GATGGGCCCTGGAGGCAG    31932          TGACA  A_
                                CTGCCTCCAGG    GC  ATC
                                ||||||||||    ||  |||
                                GACGGAGGTCC    CG  TAG
                                      _____ GG
GAM1263  FLJ10036  3'  CTGATTGCCCTTATGGAG    96627      GG   CA
                                CTCCA  TGA  GCAATCAG
                                |||||  |||  ||||||||
                                GAGGT  ATT  CGTTAGTC
                                   __  CC
GAM1263  FLJ11053  3'  CTGACTATCTACCTGGAGATAG 90123     C       _  C  CAA
                                CTG CTCCAGGT GA AG   TCAG
                                ||| |||||||| || ||   ||||
                                GAT GAGGTCCA CT TC   AGTC
                                  A       T  A  ___
GAM1263  FLJ11767  3'  CTGATTGTAAGCACCTGAAGGC 45059       C     ACA
            A                    TGCCT CAGGTG   GCAATCAG
                                |||||  ||||||   ||||||||
                                ACGGA GTCCAC   TGTTAGTC
                                   A     GAA
GAM1263  FLJ12691  3'  CTGATTGGTATCTGGAGACAG  45001     C       ACAG
                                CTG CTCCAGGTG    CAATCAG
                                ||| |||||||||    |||||||
                                GAC GAGGTCTAT    GTTAGTC
                                  A       G___
GAM1263  GALNT6    3'  CTGATCACCAGCTTCTCTGGAG 24247         T  C   A____
            GC                    GCCTCCAGG GA AGC     ATCAG
                                |||||||||  || |||     |||||
                                CGGAGGTCT CT TCG     TAGTC
                                     _ _   ACCAC
GAM1263  H-plk     5'  CTGATTACCTGTCTGGAGCA   32381     C    GGT    C_
                                TGC TCCA   GACAG  AATCAG
                                ||| ||||   |||||  ||||||
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                                ACG AGGT   CTGTC  TTAGTC
                                  _   ___    CA
GAM1263  KIAA0781  3'  GCCACCGTGGAGGCAG     68058        _   ACA
                                CTGCCTCCA GGTG   GC
                                ||||||||| ||||   ||
                                GACGGAGGT CCAC   CG
                                    G   ___
GAM1263  KIAA0971  3'  CTGATTACTGTCATTACTAGAG 30670    C __     C
                                CTC AG  GTGACAG AATCAG
                                ||| ||  ||||||| ||||||
                                GAG TC  TACTGTC TTAGTC
                                  A  AT      A
GAM1263  KIAA1344  3'  CTGATTATTACCTGGATACA  72866    CC       CAGC
                                TG  TCCAGGTGA    AATCAG
                                ||  |||||||||    ||||||
                                AC  AGGTCCATT    TTAGTC
                                 AT        A___
GAM1263  MADCAM1   3'  CTGATTGCCTCTTTGGAG    56238       T  CA
                                CTCCAGG GA  GCAATCAG
                                |||||||  ||  ||||||||
                                GAGGTTT CT  CGTTAGTC
                                    _  C_
GAM1263  MADCAM1   3'  CTGATTGCCTCTTTGGAG    56241       T  CA
                                CTCCAGG GA  GCAATCAG
                                |||||||  ||  ||||||||
                                GAGGTTT CT  CGTTAGTC
                                    _  C_
GAM1263  MADCAM1   3'  CTGATTGCCTCTTTGGAG    56244       T  CA
                                CTCCAGG GA  GCAATCAG
                                |||||||  ||  ||||||||
                                GAGGTTT CT  CGTTAGTC
                                    _  C_
GAM1263  MGC10870  5'  CTGACCATGTCACCTGGAGGC  51178           GCAA
                                GCCTCCAGGTGACA    TCAG
                                ||||||||||||||    ||||
                                CGGAGGTCCACTGT    AGTC
                                        ACC_
GAM1263  MGC10924  3'  CTGTATGAACACCTGGAAGCA  48311    C      _____
                                TGC TCCAGGTG     ACAG
                                ||| ||||||||     ||||
                                ACG AGGTCCAC     TGTC
                                  A       AAGTA
GAM1263  MGC14436  5'  CTGACCACCTGGAGACAG    52926    C       A_
                                CTG CTCCAGGTG  CAG
                                ||| |||||||||  |||
                                GAC GAGGTCCAC  GTC
                                  A       CA
GAM1263  SYT12     3'  TGATCGCTGTGGGGGCAG    96390        AGGTG    A
                                CTGCCTCC     ACAGC ATCA
                                ||||||||     ||||| ||||
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                                GACGGGGG    TGTCG TAGT
                                     _____    C
GAM1263  TReP-132  3'  TGTGTGTCACTTAGAGACAG   54274    C  C     _
                                CTG CTC AGGTGACA GCA
                                ||| ||| |||||||| |||
                                GAC GAG TTCACTGT TGT
                                  A  A      G
GAM1263  TReP-132  3'  TGTGTGTCACTTAGAGACAG   54276    C  C     _
                                CTG CTC AGGTGACA GCA
                                ||| ||| |||||||| |||
                                GAC GAG TTCACTGT TGT
                                  A  A      G
GAM1263  TReP-132  3'  TGTGTGTCACTTAGAGACAG   37915    C  C     _
                                CTG CTC AGGTGACA GCA
                                ||| ||| |||||||| |||
                                GAC GAG TTCACTGT TGT
                                  A  A      G
GAM1263  ZFD25     5'  CTGATCACCTGTCTGGAGCA   33109    C   GGT   CA_
                                TGC TCCA   GACAG   ATCAG
                                ||| ||||   |||||   |||||
                                ACG AGGT   CTGTC   TAGTC
                                  _   ___    CAC
GAM1263  ZNF177    3'  CTGTTATGGTCACCTGGAAACA 14356    CC       AGCAAT
           G                     CTG  TCCAGGTGAC     CAG
                                ||| ||||||||||     |||
                                GAC  AGGTCCACTG     GTC
                                  AA        GTATT_
GAM1263  ZNF90     5'  CTGATCACCTGTCTGGAGCA   79467    C   GGT   CA_
                                TGC TCCA   GACAG   ATCAG
                                ||| ||||   |||||   |||||
                                ACG AGGT   CTGTC   TAGTC
                                  _   ___    CAC
GAM1263  LOC149606 3'  CTGAAGCACCACTGGAGGCA   80261        G  ACA  AA
                                TGCCTCCAG TG   GC  TCAG
                                ||||||||| ||   ||  ||||
                                ACGGAGGTC AC   CG  AGTC
                                     _ CA_  A_
GAM1263  LOC157663 3'  CTGAAAGTACTGTCATCTAAAA 82450    CTCC       CAA__
           GCA                    TGC    AGGTGACAG    TCAG
                                |||   |||||||||    ||||
                                ACG   TCTACTGTC    AGTC
                                  AAAA       ATGAA
GAM1263  LOC196527 3'  TGATTGTACTAGAGACAG    89102    C   CA   GACA
                                CTG CTC  GGT   GCAATCA
                                ||| |||  |||   |||||||
                                GAC GAG  TCA   TGTTAGT
                                  A  A_  _____
GAM1263  LOC221025 5'  CTGGCCACCTGGAGACAG    94785    C       A_
                                CTG CTCCAGGTG  CAG
                                ||| |||||||||  |||
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                                GAC GAGGTCCAC  GTC
                                  A        CG
GAM1263  LOC253943 3'  CTGATTGCTATCATGAAGTA  97845    C  CAG    C
                                TGC TC   GTGA AGCAATCAG
                                ||| ||   |||| |||||||||
                                ATG AG   TACT TCGTTAGTC
                                  A ___    A
GAM1263  LOC255180 3'  GATCACTGTCATCTAAAAGCAG 96732      CTCC        CA
                                CTGC    AGGTGACAG  ATC
                                ||||    |||||||||  |||
                                GACG    TCTACTGTC  TAG
                                   AAAA        AC
GAM1263  LOC256416 3'  CTGTCCACCTGGGGACAG    96059     C        _
                                CTG CTCCAGGTG ACAG
                                ||| ||||||||| ||||
                                GAC GGGGTCCAC TGTC
                                  A        C
GAM1263  LOC51673  3'  CTGTCCACCTGGGGACAG    96207     C        _
                                CTG CTCCAGGTG ACAG
                                ||| ||||||||| ||||
                                GAC GGGGTCCAC TGTC
                                  A        C
GAM1264  DDX19     5'  CATCCCTCGAATCCACCAG   24337         A   CCA
                                CTGGTGGAT TGG   GGATG
                                ||||||||| |||   |||||
                                GACCACCTA GCT   CCTAC
                                     A  C__
GAM1264  RUVBL2    3'  CCTGTTTTCCACCAGAGT    22863          TATGGC
                                ACTCTGGTGGA     CAGG
                                ||||||||||      ||||
                                TGAGACCACCT     GTCC
                                      TTT___
GAM1264  C20orf162 5'  CATCCTAGCCATGCTCAGT   55498    G  GA     C
                                G TG  TATGGC AGGATG
                                | ||  |||||| ||||||
                                T AC  GTACCG TCCTAC
                                 G  TC     A
GAM1264  DKFZP727G051 3'  ATCCCCAGACCCACCAGA    70001         ATA   CCA
                                TCTGGTGG   TGG   GGAT
                                ||||||||   |||   ||||
                                AGACCACC   ACC   CCTA
                                    CAG   ___
GAM1264  FLJ10404  5'  ATCCTCCACCCACCAGAG    39314         ATA   CC
                                CTCTGGTGG   TGG  AGGAT
                                |||||||||   |||  |||||
                                GAGACCACC   ACC  TCCTA
                                     C__   __
GAM1264  FLJ21324  5'  CATCCCATCACCCACCAGGGT  92847         ATA   CCA
                                ACTCTGGTGG   TGG   GGATG
                                ||||||||||   |||   |||||
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                                TGGGACCACC  ACT  CCTAC
                                     C__  AC_
GAM1264 MGC11287 3' ATCCCAGTCACCACCAGG   49611       ATA  CA
                                TCTGGTGG  TGGC GGAT
                                ||||||||  |||| ||||
                                GGACCACC  ACTG CCTA
                                   ___   AC
GAM1264 TEX27    3' CCTCCACCCACCAGAGT    41946       ATA  CC
                                ACTCTGGTGG  TGG AGG
                                ||||||||||  ||| |||
                                TGAGACCACC  ACC TCC
                                     C__  __
GAM1264 LOC145858 3' CATCCTGCAGGGGCTCCCACCA 78001       ATAT  _____
           GAG                   CTCTGGTGG   GGCC   AGGATG
                                ||||||||   ||||   ||||||
                                GAGACCACC   TCGG   TCCTAC
                                     C___   GGACG
GAM1264 LOC163231 5' CCACTTATTCACCAGAGT   83331          __
                                ACTCTGGTGGATA TGG
                                ||||||||||||| |||
                                TGAGACCACTTAT ACC
                                      TC
GAM1264 LOC165246 5' ATCCACCATCCACCAGA    83364       TA  CCA
                                TCTGGTGGA TGG  GGAT
                                |||||||| |||  ||||
                                AGACCACCT ACC  CCTA
                                   __  A__
GAM1264 LOC256032 5' GGTACCCATACCCACCAGG  99362       A   ___
                                TCTGGTGG TATGG  CC
                                |||||||| |||||  ||
                                GGACCACC ATACC  GG
                                    C   CAT
GAM1265 B4GALT5  3' GCAGGTTCCTGCCCTTGAA   17689       T   AC
                                TTCAAGGGCA GGAAC GT
                                |||||||||| ||||| ||
                                AAGTTCCCGT CCTTG CG
                                   _   GA
GAM1265 CNGB3    3' GACATGCTGGGACCCTTGAG  39389       CA_  AA C
                                TTCAAGGG  TGG CA GTC
                                ||||||||  ||| || |||
                                GAGTTCCC  GTC GT CAG
                                    AGG  __ A
GAM1265 ICA1     3' TGACGTGTCCTACAGCCTCAGA 18314    AA  AT__  A
                                TC GGGC   GGA CACGTCA
                                ||  ||||   ||| |||||||
                                AG TCCG   CCT GTGCAGT
                                 AC   ACAT  _
GAM1265 FLJ22625 3' TGACGTGTTGACTTGAA    45587      GG TGGA
                                TTCAAG CA   ACACGTCA
                                ||||||  ||   ||||||||
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                                AAGTTC  GT    TGTGCAGT
                                   A_ _____
GAM1265 KIAA1884 3' TGACATGCTGGCCTCAGA    73732    AA    A   AA  C
                                TC  GGGC TGG  CA GTCA
                                ||  |||| |||  || ||||
                                AG  TCCG GTC  GT CAGT
                                 AC    _  __  A
GAM1265 MGC14859 3' TGGCCCCATGCCCCTGTAG   62606    T  A      AACAC
                                CT CA GGGCATGG    GTCA
                                || || ||||||||    ||||
                                GA GT CCCGTACC    CGGT
                                 T  C       C____
GAM1265 OSBPL5   3' GTGTTCCACACCTTGAA     73065       GCA
                                TTCAAGG   TGGAACAC
                                |||||||   ||||||||
                                AAGTTCC   ACCTTGTG
                                    AC_
GAM1266 ASGR2    3' AGTTTAAGAGTCCCTGAC    56038     A     CC
                                GTCA GGACTC  AAGCT
                                |||| ||||||  |||||
                                CAGT CCTGAG  TTTGA
                                  C     AA
GAM1266 HDAC7A   3' AGAACAGCCTGCCTGCTTTGAC 31829        ACTCC  A    C
           A                     TGTCAAGG    CA GCTG TCT
                                ||||||||    || |||| |||
                                ACAGTTTC    GT CGAC AGA
                                     GTCC_  C    A
GAM1266 TRHDE    3' AGAGGTAAAATAGCCCTTGACA 26312        A  CCCAA  TG
                                TGTCAAGG CT    GC  CTCT
                                |||||||| ||    ||  ||||
                                ACAGTTCC GA    TG  GAGA
                                     C  TAAAA  __
GAM1266 ZFP93    3' AGAGCTTCAAAGAATCTTGACA 16173        AC  CCAAGCT
                                TGTCAAGG  TC      GCTCT
                                ||||||||  ||      |||||
                                ACAGTTCT  AG      CGAGA
                                     A_  AAACTT_
GAM1266 CFDP1    3' AGAGCAGCTTAATCCTGTTTAC 21986    CA__   CTCCC
           A                     TGT    AGGA    AAGCTGCTCT
                                |||    ||||    ||||||||||
                                ACA    TCCT    TTCGACGAGA
                                  TTTG    AA___
GAM1266 DKFZP434A0131 3' AGAGCAGCCTGGGCAACCT   39148    ACT    A
                                AGG   CCCA GCTGCTCT
                                |||   |||| ||||||||
                                TCC   GGGT CGACGAGA
                                  AAC    C
GAM1266 GLTP     3' AGAGCAGCCCAGGGTCCT    33579       CCAA
                                AGGACTC    GCTGCTCT
                                |||||||    ||||||||
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                                TCCTGGG   CGACGAGA
                                   ACC_
GAM1266 KIAA0847 3' GAGCAAGAGTTCTTAACA   78074    C      CCAAGC
                                TGT AAGGACTC    TGCTC
                                ||| ||||||||    |||||
                                ACA TTCTTGAG    ACGAG
                                  A      A_____
GAM1266 KIAA1237 3' AGCAGCTTGTTGAGCCCCTGCA 81297   T A A  C_
                                TG CA GG CTC  CAAGCTGCT
                                || || || |||  |||||||||
                                AC GT CC GAG  GTTCGACGA
                                 _ C C  TT
GAM1266 KIAA1393 5' AGCTTGGACATCCCTGACA   72567     A  CTC
                                TGTCA GGA  CCAAGCT
                                ||||| |||  |||||||
                                ACAGT CCT  GGTTCGA
                                   C  ACA
GAM1266 KIAA1887 3' AGCCTTGGGAGCCCCTGCCA  77276   T A A     CT
                                TG CA GG CTCCCAAG  GCT
                                || || || ||||||||  |||
                                AC GT CC GAGGGTTC  CGA
                                 C C C      __
GAM1266 NYD-SP14 3' AGCAGCTTTTCACTTAACA   50071    C  _ CTCCC
                                TGT AAG GA    AAGCTGCT
                                ||| ||| ||    ||||||||
                                ACA TTC CT    TTCGACGA
                                  A  A T____
GAM1266 OAZ3    3' AGGGGCTGGAAGCCTTGACA  32974       A C  A  G
                                TGTCAAGG CT CCA GCT CT
                                |||||||| || ||| ||| ||
                                ACAGTTCC GA GGT CGG GA
                                    _ A  _  G
GAM1266 LOC114926 3' AGTGGCTCAAAAGGCCTTGACA 57387       A  CCCA  TG
                                TGTCAAGG CT   AGC  CT
                                |||||||| ||   |||  ||
                                ACAGTTCC GA   TCG  GA
                                    G  AAAC  GT
GAM1266 LOC115219 3' AGAGCAGCCTGGACGGTCC   73687     C_  A
                                GGACT  CCA GCTGCTCT
                                |||||  ||| ||||||||
                                CCTGG  GGT CGACGAGA
                                   CA  C
GAM1266 LOC145439 5' AGAGCAGCCCTGGCACCCGACA 77723    AA  ACTC  A_
                                TGTC  GG   CCA  GCTGCTCT
                                ||||  ||   |||  ||||||||
                                ACAG  CC   GGT  CGACGAGA
                                  C_  AC__  CC
GAM1266 LOC151610 3' AGAGCAGCCTCATTCCTTCACA 81089    C    CTCCCAA
                                TGT AAGGA     GCTGCTCT
                                ||| |||||     ||||||||
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                                ACA TTCCT      CGACGAGA
                                  C    TACTC__
GAM1266  LOC152018 3'  AGGTTAGGAGACCCCTGACA   86726      A  A_   C  G
                                TGTCA GG  CTCC AA CT
                                ||||| ||  |||| || ||
                                ACAGT CC  GAGG TT GA
                                   C  CA    A  G
GAM1266  LOC158863 5'  GGTGATGAGAATGCCTTGACA  88298        AC_  C  A_
                                TGTCAAGG   TC CA  GCT
                                ||||||||   || ||  |||
                                ACAGTTCC   AG GT  TGG
                                     GTA  A  AG
GAM1266  LOC199796 5'  GAGCAGCTCAAAGCCGAC    74923     AA  A  CCCA
                                GTC  GG CT    AGCTGCTC
                                |||  || ||    ||||||||
                                CAG  CC GA    TCGACGAG
                                  __  _  AAC_
GAM1266  LOC254003 5'  AGAGCAGCTCAGGACAAGGACA 98026     AAGGAC   CA
                                TGTC     TCC  AGCTGCTCT
                                ||||     |||  |||||||||
                                ACAG     AGG  TCGACGAGA
                                  GAAC__   AC
GAM1266  LOC256300 5'  AGAGCAGCAGGACCCTTCACA  99445     C    AC   CAA
                                TGT AAGG  TCC   GCTGCTCT
                                ||| ||||  |||   ||||||||
                                ACA TTCC  AGG   CGACGAGA
                                  C   C_   A__
GAM1266  LOC92106  5'  AGAGCAGCTTAGCCTCCTCGAC 57225     A    CTCCC
                                GTC AGGA    AAGCTGCTCT
                                ||| ||||    ||||||||||
                                CAG TCCT    TTCGACGAGA
                                  C   CCGA_
GAM1267  CRYBA4    3'  CCTGTAACCTGTGTGAA     10304         AA   CACG
                                TTCACACAG  TTAC    AGG
                                |||||||||  ||||    |||
                                AAGTGTGTC  AATG    TCC
                                     C_   _____
GAM1267  IDS      3'  TGTGGTAATTCCAAGTGAA   21518      ACA
                                TTCAC   GAATTACCACG
                                |||||   ||||||||||||
                                AAGTG   CTTAATGGTGT
                                   AAC
GAM1267  IL1R1    3'  CCTCGCTGTCCTGCTGTGTGAA 7922         AATT  CA
                                TTCACACAG    AC  CGAGG
                                |||||||||    ||  |||||
                                AAGTGTGTC    TG  GCTCC
                                     GTCC  TC
GAM1267  PCDHB9   3'  CTCCTTTTAATTCTGT      39442         CCAC
                                ACAGAATTA    GAGGAG
                                |||||||||    ||||||
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                                TGTCTTAAT   TTCCTC
                                     T___
GAM1267 EIF4ENIF1 3' CTTTGGAGCACTCTGTGTGAA 39529        ATTACCA
                                TTCACACAGA     CGAGG
                                ||||||||||     |||||
                                AAGTGTGTCT     GTTTC
                                     CACGAG_
GAM1267 SFXN5   3' CTCAGCACAATTATGTGTGAA 58650       G   ACCAC
                                TTCACACA AATT    GAG
                                |||||||| ||||    |||
                                AAGTGTGT TTAA    CTC
                                     A   CACGA
GAM1267 LOC150084 5' CTCCCCATAATGGGAATGTGTG 80381       GAATTA  CGA___
            AG                    TTCACACA    CCA    GGAG
                                |||||||     |||    ||||
                                GAGTGTGT    GGT    CCTC
                                     AAG___  AATACC
GAM1267 LOC152860 3' CTCCTCGAGTCCCTGTGTGAG 81579        AATT CA
                                TTCACACAG   AC CGAGGAG
                                |||||||||   ||  |||||||
                                GAGTGTGTC   TG GCTCCTC
                                     CC__ A_
GAM1268 GPD1    3' TCATGCCACCACATTTG    60398      C      C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A      _
GAM1268 IL5RA   5' TCGCATGGCCACCGCATTT   6906         AT__
                                AAATGCGGTGGC   CGA
                                ||||||||||||   |||
                                TTTACGCCACCG   GCT
                                      GTAC
GAM1268 MYO1C   3' TGCCGATGCCAAATATTTG   61873      CGG      A
                                TAAATG  TGGCATCG CA
                                ||||||  |||||||| ||
                                GTTTAT  ACCGTAGC GT
                                   AA_      C
GAM1268 C6orf37  3' TGTCACACTGCATTTA     68097         GCATC
                                TAAATGCGGTG    GACA
                                ||||||||||     ||||
                                ATTTACGTCAC    CTGT
                                      A____
GAM1268 DNAJC6  3' TTGCAGAACCACCGCATT    29498        CA  GA
                                AATGCGGTGG  TC  CAA
                                |||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                      A_  AC
GAM1268 FLJ11210 3' GTCGATGTGCATGCTTTTA   60319     T  GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
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                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM1268  FLJ12476  3'  TCGATCTTCTGCATTTA     43270         T  C
                                TAAATGCGG GG ATCGA
                                ||||||||| || |||||
                                ATTTACGTC TC TAGCT
                                     T  _
GAM1268  KIAA1034  3'  TCGATGGCATCCGCATTTG    63134         _  G
                                TAAATGCGG TG CATCGA
                                ||||||||| || ||||||
                                GTTTACGCC AC GTAGCT
                                     T  G
GAM1268  KIAA1987  3'  TCATGTAACTGCATTTA     89391         G    C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                     A   _
GAM1268  MGC16063  3'  TGTCCTGGCCACTGCATT    54929          ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                      GTC
GAM1268  LOC147949 3'  TGTCAGATGTCCACATTGCA   79279      __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM1268  LOC150577 3'  GTCCTCACCGCATTTG      86258          CATC
                                TAAATGCGGTGG    GAC
                                ||||||||||||    |||
                                GTTTACGCCACT    CTG
                                      C___
GAM1268  LOC158219 3'  TGTGTGTCACCACATTT     82694       C       CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                   A       __
GAM1268  LOC202020 3'  TGTCTCACCACATTTA      90605       C    CATC
                                TAAATG GGTGG    GACA
                                |||||| |||||    ||||
                                ATTTAC CCACT    CTGT
                                   A    ____
GAM1268  LOC90826  5'  TGTCGATGCAGGTTTATTTG   64788       CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                    TTGGA
GAM1268  LOC93587  3'  TTGTCTTTACCTGCATTTA    73042        _    CATC
                                TAAATGC GGTGG    GACAA
                                ||||||| |||||    |||||
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                                ATTTACG CCATT    CTGTT
                                    T    T___
GAM1269  TERF1     3'  CCCAAATCCTGTTCCAATGA   34391        C   TA    C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                    _   C_    A
GAM1269  FLJ10159  3'  CCATGTCACGCCATCCAATGAC 36334        CA_   A   TC
                                GTCATTGGA   CGT GAT  GG
                                |||||||||   ||| |||  ||
                                CAGTAACCT   GCA CTG  CC
                                    ACC   _   TA
GAM1269  FLJ14213  3'  CCGATGCTCCCAATGACG    46216        ACAC   GAT
                                CGTCATTGG    GTA   TCGG
                                |||||||||    |||   ||||
                                GCAGTAACC    CGT   AGCC
                                    CT__   ___
GAM1269  MGC10715  3'  ATTTACCAGACATCCAATGAC  44495        CAC___
                                GTCATTGGA     GTAGAT
                                |||||||||     ||||||
                                CAGTAACCT     CATTTA
                                    ACAGAC
GAM1269  MOST2     5'  CCAGGACTGCCCAATGAC    40059        ACAC    A  _
                                GTCATTGG    GTAG TTC GG
                                ||||||||    |||| ||| ||
                                CAGTAACC    CGTC AGG CC
                                    _____    _   A
GAM1269  LOC150370 3'  CCGGGTCTACGTGCCCATGAC  86123      T  A
                                GTCAT GG CACGTAGATTCGG
                                ||||| || ||||||||||||
                                CAGTA CC GTGCATCTGGGCC
                                  C  _
GAM1269  LOC152620 3'  CCCAAATCCTGTTCCAATGA   60707        C   TA    C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                    _   C_    A
GAM1269  LOC158668 3'  CCCAAATCCTGTTCCAATGA   69896        C   TA    C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                    _   C_    A
GAM1270  DLG5      5'  CAGCAGCAGCAGGTGTTGA    83811        CG   TCGGAA
                                TCAACACC  GCT     GCTG
                                ||||||||  |||     ||||
                                AGTTGTGG  CGA     CGAC
                                    A_   CGA___
GAM1270  KCNK7     5'  CCAGCCCCTCCCAGGTGCCTGA 20345     A_    C  CTTC  AA
                                TCA  CACC GG    GG  GCTGG
                                |||  |||| ||    ||  |||||
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                                AGT  GTGG CC   CC  CGACC
                                  CC   A  CT__  C_
GAM1270  KCNK7    5'  CCAGCCCCTCCCAGGTGCCTGA 54055    A_   C  CTTC  AA
                                TCA  CACC GG   GG  GCTGG
                                |||  |||| ||   ||  |||||
                                AGT  GTGG CC   CC  CGACC
                                  CC   A  CT__  C_
GAM1270  KCNK7    5'  CCAGCCCCTCCCAGGTGCCTGA 54062    A_   C  CTTC  AA
                                TCA  CACC GG   GG  GCTGG
                                |||  |||| ||   ||  |||||
                                AGT  GTGG CC   CC  CGACC
                                  CC   A  CT__  C_
GAM1270  KCNK7    5'  CCAGCCCCTCCCAGGTGCCTGA 54232    A_   C  CTTC  AA
                                TCA  CACC GG   GG  GCTGG
                                |||  |||| ||   ||  |||||
                                AGT  GTGG CC   CC  CGACC
                                  CC   A  CT__  C_
GAM1270  TNFRSF6B 5'  CCAGCCAGTGCCGGGTGCTGG  33596    A      TTCGGAA
                                TCA CACCCGGC      GCTGG
                                |||  ||||||||      |||||
                                GGT GTGGGCCG      CGACC
                                  C       TGAC___
GAM1270  CARD9    3'  CCAGCCGGACTGCCGGGCATTG 42546     CA     __   GAA
           G                     TCAA  CCCGGC  TTCG   GCTGG
                                ||||  ||||||  ||||   |||||
                                GGTT  GGGCCG  AGGC   CGACC
                                  AC     TC   ___
GAM1270  CARD9    3'  CCAGCCGGACTGCCGGGCATTG 54474     CA     __   GAA
           G                     TCAA  CCCGGC  TTCG   GCTGG
                                ||||  ||||||  ||||   |||||
                                GGTT  GGGCCG  AGGC   CGACC
                                  AC     TC   ___
GAM1270  FLJ21438 3'  CTGGCTGGGCCGGGCACTGA   62192    ACA      CGGA   TG
                                TCA   CCCGGCTT    AGC  G
                                |||   ||||||||    |||  |
                                AGT   GGGCCGGG    TCG  C
                                  CAC       ____   GT
GAM1270  KIAA1560 3'  CCAGCTTCTGGCTCAAGAGTTG 64849      ACCC_   TT
           A                     TCAAC    GGC  CGGAAGCTGG
                                |||||    |||  ||||||||||
                                AGTTG    TCG  GTCTTCGACC
                                   AGAAC   __
GAM1270  MAPK11   3'  CCAGGGAAGCCTGGGTGT    58100       _     GGAAG
                                ACACCC GGCTTC    CTGG
                                ||||||  ||||||    ||||
                                TGTGGG CCGAAG    GACC
                                   T     G____
GAM1270  MAPK11   3'  CCAGGGAAGCCTGGGTGT    12313       _     GGAAG
                                ACACCC GGCTTC    CTGG
                                ||||||  ||||||    ||||
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                                TGTGGG CCGAAG    GACC
                                   T     G____
GAM1270  LOC130497 3'  CCAGCCAAGAGCCGGGCGTT  75446    A      CGGAA
                                AAC CCCGGCTT    GCTGG
                                ||| ||||||||    |||||
                                TTG GGGCCGAG    CGACC
                                  C       AAC__
GAM1270  LOC203052 3'  CCAGCTCTGTGCCGGGTG    92076       TT   A
                                CACCCGGC  CGGA GCTGG
                                ||||||||  |||| |||||
                                GTGGGCCG  GTCT CGACC
                                     T_   _
GAM1270  LOC256905 5'  CCAGGGATAGCCGGGTATTGA  98659     C      TCGGAAG
                                TCAA ACCCGGCT      CTGG
                                |||| ||||||||      ||||
                                AGTT TGGGCCGA      GACC
                                  A       TAGG___
GAM1270  LOC91409  3'  CAGCTTCCACTATGTTGA    66570      CCC  CTTC
                                TCAACA   GG   GGAAGCTG
                                ||||||   ||   ||||||||
                                AGTTGT   TC   CCTTCGAC
                                   A__  A___
GAM1271  ABCC1     3'  CCCTGGTAAACCAAGCCTC   39602    AAAA  CT_      A
                                GAG   GC   GTTTACCA GG
                                |||   ||   |||||||| ||
                                CTC   CG   CAAATGGT CC
                                  _____ AAC       C
GAM1271  ANKH      3'  TCCTCAGAGTGGCTTTTCCT   55076    A      TG   ACCA
                                AG GAAAAGCC  TTT   AGGA
                                || ||||||||  |||   ||||
                                TC CTTTTCGG  AGA   TCCT
                                 _      TG   C___
GAM1271  BAZ2A     3'  CCCCAGTTTTCAGATTTTCTCT 26507       GC   TTT  CAA
                                AGAGAAAA  CTG   AC   GG
                                ||||||||  |||   ||   ||
                                TCTCTTTT  GAC   TG   CC
                                     A_   TTT  ACC
GAM1271  DSG1      3'  TCCTTAGCATTCATAAACTTTT 10451       CC__  TTTACC
            CTCT                  AGAGAAAAG    TG     AAGGA
                                |||||||||    ||     |||||
                                TCTCTTTTC    AC     TTCCT
                                      AAAT  TTACGA
GAM1271  DUOX2     3'  CCCTGGGCAGGCCCCTCTCT   26865      AAA     TTA   A
                                AGAGA   GCCTGT   CCA GG
                                |||||   ||||||   ||| ||
                                TCTCT   CGGACG   GGT CC
                                   CCC      ___   C
GAM1271  EHD2      3'  TCCTCAGATGGGCCCCTC    28230     AAAA       ACCA
                                GAG   GCCTGTTT    AGGA
                                |||   ||||||||    ||||
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                                CTC   CGGGTAGA   TCCT
                                  CC__      C___
GAM1271 F9      3' TCCCCAAATCAGTTTTTCTCT 5530         C TTTACCAA
                                AGAGAAAAGC TG      GGA
                                |||||||||| ||      |||
                                TCTCTTTTTG AC      CCT
                                      _ TAAACC__
GAM1271 GBF1    5' TCCAGGAAACAGGCTCCTTCT 16093     A_      A AA
                                AGAA AGCCTGTTT CC GGA
                                ||||  |||||||| ||  |||
                                TCTT TCGGACAAA GG CCT
                                  CC       _ A_
GAM1271 GLUL    3' CCTCGTGGTGGAAACTTTTCTT 10808       CCTG     __
                                GAGAAAAG   TTTACCA AGG
                                ||||||||   |||||||  |||
                                TTCTTTTC   AGGTGGT TCC
                                     AA__     GC
GAM1271 HDAC4   3' TCCTTGGACCTTTAGCCTTTTT 21252      A CTGTTTA
             CT                   AGAGAAA GC     CCAAGGA
                                |||||||  ||     |||||||
                                TCTTTTT CG     GGTTCCT
                                   C ATTTCCA
GAM1271 IGF2    3' TCCCCGAAACAGGCTACTCTC 7038      AA       ACCAA
                                GAGA AGCCTGTTT    GGA
                                ||||  |||||||||    |||
                                CTCT TCGGACAAA    CCT
                                  CA       GCC__
GAM1271 JUP     3' CCTCTTTGCAGGCTTTTCCT  11108   A       TTACCA
                                AG GAAAAGCCTGT     AGG
                                || ||||||||||     |||
                                TC CTTTTCGGACG     TCC
                                 _        TTTC__
GAM1271 KCNH3   3' TCCCTGGGGCAGGCCTCTC   65214     AAA     TA  A
                                GAGA  GCCTGTT  CCA GGA
                                ||||  |||||||  ||| |||
                                CTCT  CGGACGG  GGT CCT
                                  C__      __  C
GAM1271 MAZ     3' CCTTGGTACAAGCTCCTCTC  73778     AA  C  TT
                                GAGA  AGC TGT  ACCAAGG
                                ||||  ||| |||  |||||||
                                CTCT  TCG ACA  TGGTTCC
                                  CC  A  __
GAM1271 PDE7A   3' CCTGGTTTGCCTTTTTCT    66135       A CTGTTT   A
                                AGAGAAA GC     ACCA GG
                                ||||||| ||     |||| ||
                                TCTTTTT CG     TGGT CC
                                    C TT_____    C
GAM1271 PIK3C2B 3' TCCTCGGCCAGAGCCCTCTCT 12112      AAA _  TTTA A
                                AGAGA  GC CTG   CC AGGA
                                |||||  || |||   || ||||
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                                TCTCT  CG GAC   GG TCCT
                                  CC_  A  C___  C
GAM1271  PKP2    3'  CCTTGGTTGTTTTTCTCT   17109        CTGTTT
                                AGAGAAAAGC    ACCAAGG
                                ||||||||||    |||||||
                                TCTCTTTTTG    TGGTTCC
                                     T_____
GAM1271  PPL     3'  TCCTTGGTGTCGTCCTCTC   12223     AAA  CTGTT
                                GAGA  GC    TACCAAGGA
                                ||||  ||    |||||||||
                                CTCT  TG    GTGGTTCCT
                                  CC_  CT___
GAM1271  PRKAR1A  3'  TCCTCTGGCAAACTTTTCTTT  12283        CC  TTTA  _
                                AGAGAAAAG  TG   CCA AGGA
                                |||||||||  ||   ||| ||||
                                TTTCTTTTC  AC   GGT TCCT
                                     AA  _____  C
GAM1271  RFNG    3'  TCCCACGGGAACAGGCTT    89563         A  AA_
                                AAGCCTGTTT CC   GGA
                                ||||||||||  ||   |||
                                TTCGGACAAG GG   CCT
                                     _  CAC
GAM1271  SREBF2   3'  TCCTCAGTTTTTATCAGGCTTT 17190       A    TTT___  CA
           CTCT                   AGAGAAA GCCTG     AC  AGGA
                                |||||||  |||||     ||  ||||
                                TCTCTTT CGGAC     TG  TCCT
                                   _    TATTTT  AC
GAM1271  TAF1    3'  CCTTGGTCAGCCTTCCCT    17230    AA   C   TTT
                                AG  AAG CTG   ACCAAGG
                                ||  |||  |||   |||||||
                                TC  TTC GAC   TGGTTCC
                                 CC   C  ___
GAM1271  TEAD3    3'  CCTTGGTGGGCACTGTTCCCT  13669    A   A  CC
                                AG GAA AG  TGTTTACCAAGG
                                || ||| ||  ||||||||||||
                                TC CTT TC  ACGGGTGGTTCC
                                 C   G  __
GAM1271  TMPRSS3   5'  CCTTGGTGGGTGGCCCTTTCCC 44022    A    A_   T TT
           T                    AG GAAA  GCC G  TACCAAGG
                                || ||||  ||| |  ||||||||
                                TC CTTT  CGG T  GTGGTTCC
                                 C    CC   _ GG
GAM1271  TNFRSF1A  3'  CCTCGATGTACATAGCTTTTCT 8377         C   T   CA__
           C                    GAGAAAAGC TGT TAC    AGG
                                |||||||||  ||| |||   |||
                                CTCTTTTCG ATA ATG    TCC
                                     _  C   TAGC
GAM1271  VDR     3'  CCTTTCCTGCGGGCTTTTC   6343          TTACC
                                GAAAAGCCTGT    AAGG
                                ||||||||||     ||||
```

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                                CTTTTCGGGCG    TTCC
                                      TCCT_
GAM1271 ZNF219   3' TCCCCAATAAACAGGTGTCTT 33557     AAA       CCAA
                                GAGA   GCCTGTTTA    GGA
                                ||||   |||||||||    |||
                                TTCT   TGGACAAAT    CCT
                                  G__       AACC
GAM1271 ALK7     3' CCTTGAATAGTGCTTTTCTC   76242         _    TAC
                                GAGAAAAGC CTGTT   CAAGG
                                ||||||||| |||||   |||||
                                CTCTTTTCG GATAA   GTTCC
                                      T    ___
GAM1271 C11orf11 3' TCCTGGGAGCAGGCCTTCCTC  94882     A  A      A   A
                                GAG AA GCCTGTTT CCA GGA
                                ||| || |||||||| ||| |||
                                CTC TT CGGACGAG GGT CCT
                                  C  C      _  _
GAM1271 DKFZP564O0463 3'  CCTTGGACTCCAGATCTTTCTC 27124        AGC   TTTA
             T                   AGAGAAA   CTG    CCAAGG
                                 |||||||   |||    ||||||
                                 TCTCTTT   GAC    GGTTCC
                                     CTA   CTCA
GAM1271 DPCR1    3' GTAAACAGGCTCATCTCT    55997      AA
                                 AGAGA  AGCCTGTTTAC
                                 |||||  ||||||||||
                                 TCTCT  TCGGACAAATG
                                    AC
GAM1271 FLJ10350 3' CCCTGGGGGTGGGTCCTCTCT  97247      AAA   TG   A   A
                                 AGAGA   GCC  TTT CCA GG
                                 |||||   |||  ||| ||| ||
                                 TCTCT   TGG  GGG GGT CC
                                    CC_   GT   _   C
GAM1271 FLJ12921 3' TCCTTGACATTTGTGCTTTTCT 46401         CTGTTTAC
             C                   GAGAAAAGC       CAAGGA
                                 |||||||||       ||||||
                                 CTCTTTTCG       GTTCCT
                                       TGTTTACA
GAM1271 FLJ14326 5' TCCTCCAGGGCAGGCTCCTTC  50787     A_       ACCA
                                 GAA  AGCCTGTTT    AGGA
                                 |||  |||||||||    ||||
                                 CTT  TCGGACGGG    TCCT
                                   CC        ACC_
GAM1271 FLJ23153 3' CCTTGACTTTGCTTTTCTT    45267         CT_  TTAC
                                 GAGAAAAGC   GT    CAAGG
                                 |||||||||   ||    |||||
                                 TTCTTTTCG   CA    GTTCC
                                       TTT  _____
GAM1271 GAB3     3'  TCCTCAGACCTGGCTTTTTCCT 55523     AG      T_    ACCA
                                 AG  AAAAGCC  GTTT    AGGA
                                 ||  |||||||  ||||    ||||
```

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                              TC  TTTTCGG  CAGA    TCCT
                               CT      TC    C___
GAM1271  GABBR1   3'  TGGGAAACAGACCTTTTTCT   9414        AGC     A
                              AGAGAAA   CTGTTT CCA
                              |||||||   |||||| |||
                              TCTTTTT   GACAAA GGT
                                  CCA     G
GAM1271  H2AV     3'  TCCCCAGTAAAAATAGGCCTTT 25763      A      __   CAA
           C                   GAAA GCCTGTT  TAC   GGA
                              |||| |||||||  |||   |||
                              CTTT CGGATAA  ATG   CCT
                                C      AA   ACC
GAM1271  HSPC195  5'  CCTCGGCAGTTGGCAGGCTCCC 81863     AAA       TA___  A
           TCT                   AGAG   AGCCTGTT    CC AGG
                              ||||   ||||||||    || |||
                              TCTC   TCGGACGG    GG TCC
                                CC_       TTGAC  C
GAM1271  KIAA0478 3'  TCCTCTGTAGCAGACAGGCCTC 30184     AAAA      ___   CA
           CCTC                  GAG    GCCTGTT   TAC  AGGA
                              |||    |||||||   |||  ||||
                              CTC    CGGACAG   ATG  TCCT
                                CCTC      ACG   TC
GAM1271  KIAA1016 5'  TCCTTGGTAAAGTTTGACTTTT 93389       CCTG__
           C                   GAAAAG     TTTACCAAGGA
                              ||||||     ||||||||||
                              CTTTTC     AAATGGTTCCT
                                 AGTTTG
GAM1271  KIAA1260 3'  TCCCCAACAAAAGAGGCTTTTC 60672          G   ACCAA_
           TT                   GAGAAAAGCCT TTT     GGA
                              ||||||||||| |||     |||
                              TTCTTTTCGGA AAA     CCT
                                    G   ACAACC
GAM1271  KIAA1327 3'  CCTAGGTGCAAGCTTTTTCT   72726       A  C   TT   A
                              AGAGAAA GC TGT  ACC AGG
                              ||||||| || |||  ||| |||
                              TCTTTTT CG ACG  TGG TCC
                                  _  A   __   A
GAM1271  KIAA1668 3'  CCTCACTTAGGCTTTCCTCT   67063     A       TTTACCA
                              AGAG AAAGCCTG      AGG
                              |||| ||||||||      |||
                              TCTC TTTCGGAT      TCC
                                C       TCAC___
GAM1271  KIAA1668 3'  CCTGGCAGGCTCCTTCT     67066     A_     TTTA   A
                              AGAA  AGCCTG    CCA GG
                              ||||  ||||||    ||| ||
                              TCTT  TCGGAC    GGT CC
                                CC      _____   C
GAM1271  KIAA1877 3'  TCCCCGGTTCTGGCTTTTCT   66763         TGTTT   AA
                              AGAAAAGCC    ACC  GGA
                              |||||||||    |||  |||
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                                TCTTTTCGG    TGG  CCT
                                     TCT__   CC
GAM1271  MAWBP    5'  TCCTTGGTAATTATTTCCTTT  42389     A   GCCTGT
                                AGAG AAA     TTACCAAGGA
                                |||| |||     ||||||||||
                                TTTC TTT     AATGGTTCCT
                                  C   ATT___
GAM1271  MGC24447 3'  CCCCGTGAAAGCTTTTCTT   57123        CTG    CAA
                                GAGAAAAGC   TTTAC   GG
                                |||||||||   |||||   ||
                                TTCTTTTCG   AAGTG   CC
                                     A__    CC_
GAM1271  MGC2628  3'  CCCTGGACCGGCTCTTCCT   44196    A   A    T  TTA   A
                                AG GAA AGCC GT   CCA GG
                                || ||| |||| ||   ||| ||
                                TC CTT TCGG CA   GGT CC
                                 _   C    C ___   C
GAM1271  MGC9753  5'  CCTTGAGATGATTTTCTCT   54188       GCCT    AC
                                AGAGAAAA   GTTT  CAAGG
                                ||||||||   ||||  |||||
                                TCTCTTTT   TAGA  GTTCC
                                     AG__   __
GAM1271  NDP52    3'  CCTTGGTGTTGCTTTCTC    20669       A  CTGTT
                                GAGAAA GC    TACCAAGG
                                |||||| ||    ||||||||
                                CTCTTT CG    GTGGTTCC
                                   _ TT___
GAM1271  NET-5    3'  CCCCGGCACTGATGGGCTTCT  22893     AA      TA__  AA
                                AGA  AGCCTGTT   CC  GG
                                |||  ||||||||   ||  ||
                                TCT  TCGGGTAG   GG  CC
                                  __      TCAC  CC
GAM1271  NICE-3   3'  CCCCAGTAGCGCTTTTTTCT  31883        CTGT   CAA
                                AGAGAAAAGC   TTAC   GG
                                ||||||||||   ||||   ||
                                TCTTTTTTCG   GATG   CC
                                     C___    ACC
GAM1271  p25      3'  CCAGCGGCCCTCAGGCTTTTCT 23826         TTTA  AA_
            C                    GAGAAAAGCCTG   CC   GG
                                 ||||||||||||   ||   ||
                                 CTCTTTTCGGAC   GG   CC
                                       TCCC  CGA
GAM1271  PDE8B    3'  CCTTGGACAAGCTTTTCTT   68201        C   TTA
                                GAGAAAAGC TGT   CCAAGG
                                ||||||||| |||   ||||||
                                TTCTTTTCG ACA   GGTTCC
                                     A  ___
GAM1271  TUSP     3'  CCGATGGAGGCACAGGCTTCTG 40021     GAA      _ TA   A_
            TCT                    AGA   AAGCCTGT T  CCA  GG
                                |||   |||||||| |  |||  ||
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                                TCT   TTCGGACA G  GGT  CC
                                  GTC       C GA   AG
GAM1271  ZNF262    3'  TCCCCAATGGCAGCTTTTCTC  18727         C    TACCAA
                                GAGAAAAGC TGTT     GGA
                                ||||||||| ||||     |||
                                CTCTTTTCG ACGG     CCT
                                      _   TAACC_
GAM1271  LOC115399 3'  TCCTTAGGGCCAGGCTTT    73817         TTTA  _
                                AAAGCCTG    CC AAGGA
                                ||||||||    || |||||
                                TTTCGGAC    GG TTCCT
                                     CG__  A
GAM1271  LOC127943 3'  TCCTTGGTCTCCTGCTTCCCCT 75192     AA_    CTGTTT
             C                   GAG   AAGC     ACCAAGGA
                                |||   ||||     ||||||||
                                CTC   TTCG     TGGTTCCT
                                  CCC    TCCTC_
GAM1271  LOC144742 5'  CCTAGGTCCTCACCTTTTCTCT 77456         CC  TTT   A
                                AGAGAAAAG  TG   ACC AGG
                                |||||||||  ||   ||| |||
                                TCTCTTTTC  AC   TGG TCC
                                     C_  TCC   A
GAM1271  LOC144747 5'  CCTTGGTAGCTTTTTCTC    77471         _  CTGTT
                                GAGAAAA GC     TACCAAGG
                                ||||||| ||     ||||||||
                                CTCTTTT CG     ATGGTTCC
                                    T  ______
GAM1271  LOC146958 5'  TCCTTAACACCAACAGGCTTTC 84949     A         TACC__
             CTC                   GAG AAAGCCTGTT     AAGGA
                                ||| ||||||||||     |||||
                                CTC TTTCGGACAA     TTCCT
                                  C         CCACAA
GAM1271  LOC147858 3'  CCTTCTGCAGAACGGGCCCCTC 79268     AAAA       ACC__
                                GAG    GCCTGTTT     AAGG
                                |||    ||||||||     ||||
                                CTC    CGGGCAAG     TTCC
                                  CC__       ACGTC
GAM1271  LOC150279 3'  CCTGCTTGAACAGGCCTCTC   80481      AAA       CCA
                                GAGA   GCCTGTTTA   AGG
                                ||||   |||||||||   |||
                                CTCT   CGGACAAGT   TCC
                                  C__        TCG
GAM1271  LOC154104 5'  TCCTTGGTGAAAACTCTC    88625      AAAGCCTG
                                GAGA       TTTACCAAGGA
                                ||||       ||||||||||
                                CTCT       AAGTGGTTCCT
                                  CAA_____
GAM1271  LOC155036 5'  CCTTGGGCTAGATTTTCTCT   87613         GC   TTTA
                                AGAGAAAA  CTG    CCAAGG
                                ||||||||  |||    ||||||
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                                TCTCTTTT  GAT    GGTTCC
                                    A_   CG__
GAM1271  LOC200010 3'  CCACAGAAACAGGCTCTCCTCT 91525      AAA       ACCAA
                                AGAG   AGCCTGTTT    GG
                                ||||   |||||||||    ||
                                TCTC   TCGGACAAA    CC
                                  CTC       GACA_
GAM1271  LOC203536 3'  TCCTTGGTTTATACTTTTTCT  90944       CC   TT
                                AGAAAAG  TGT  ACCAAGGA
                                |||||||  |||  ||||||||
                                TCTTTTT  ATA  TGGTTCCT
                                    C_   TT
GAM1271  LOC220776 3'  CCTCGTGTCCATGACTTTTCTC 68925        CC_  TT   CA
             T                   AGAGAAAAG   TG  TAC  AGG
                                |||||||||   ||  |||  |||
                                TCTCTTTTC   AC  GTG  TCC
                                     AGT  CT   C_
GAM1271  LOC255332 3'  CCTTAGCAAACAGGTTCATCTC 97948      AA       ACC
                                GAGA  AGCCTGTTT   AAGG
                                ||||  |||||||||   ||||
                                CTCT  TTGGACAAA   TTCC
                                  AC        CGA
GAM1271  LOC257364 5'  TCCCCGGTCTGGGCAGGACCCT 96648      AAAG      __   AA
             CTC                   GAGA    CCTGTTT  ACC  GGA
                                ||||    |||||||  |||  |||
                                CTCT    GGACGGG  TGG  CCT
                                  CCCA      TC   CC
GAM1271  LOC93624  3'  CCTGCCTACAAGTTTTTCTCT  73100         C   TTACCA
                                AGAGAAAAGC TGT      AGG
                                |||||||||| |||      |||
                                TCTCTTTTTG ACA      TCC
                                     A   TCCG__
GAM1272  EDNRA     3'  CCAAGAAGAAATGCTTTC     64799      T    GATT     C
                                GAGA CATT    TCTTC TGG
                                |||| ||||    ||||| |||
                                CTTT GTAA    AGAAG ACC
                                  C    _____     A
GAM1272  PRPH      3'  CCCGATAAGAAGCCAATGATC  21831        AT     CC
                                GATCATTG  TTCTT  TGGG
                                |||||||  |||||  ||||
                                CTAGTAAC  AAGAA  GCCC
                                    CG     TA
GAM1272  TMEM2     3'  CCCAGAAAGCTTAATGAT     26336        TTT   C
                                ATCATTGA   CTT CTGGG
                                ||||||||   ||| |||||
                                TAGTAATT   GAA GACCC
                                    C__   A
GAM1272  TNFSF4    3'  CCTTATGAAAAATAATGATCTC 13912          A_    TTCCT
             T                   AGAGATCATTG  TTTC     GG
                                ||||||||||  ||||    ||
```

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                                TCTCTAGTAAT  AAAG    CC
                                      AA   TATT_
GAM1272  DCLRE1A   3'  CCCAGGAAAAATATAAAACTCT 69683     ATCATTG   C
                                AGAG      ATTT TTCCTGGG
                                ||||      |||| ||||||||
                                TCTC      TAAA AAGGACCC
                                  AAAATA_   _
GAM1272  DKFZp434F2322 3'  CCCATCTGAATCAGTAATCCCT 70300    A  C      CTTCC
                                AG GAT ATTGATTT    TGGG
                                || ||| ||||||||    ||||
                                TC CTA TGACTAAG    ACCC
                                 C  A      TCT__
GAM1272  DKFZP566G1424 5'  CCTGGAAGAAACCCATAATCCC 85941    A  CAT  A_     T
            T                    AG GAT   TG  TTTCTTCC GG
                                || |||   ||  |||||||| ||
                                TC CTA   AC  AAAGAAGG CC
                                 C  AT_  CC       T
GAM1272  FLJ14326  3'  CCATGAGTCAATGACCTC    50764    A      TTCT  C
                                GAG TCATTGAT    TC TGG
                                ||| ||||||||    || |||
                                CTC AGTAACTG    AG ACC
                                  C       _____  T
GAM1272  FLJ20170  5'  CCAGGAAACCAGATCTC     35164       AT  ATTTC
                                GAGATC  TG    TTCCTGG
                                ||||||  ||    |||||||
                                CTCTAG  AC    AAGGACC
                                   __  CA___
GAM1272  FLJ20249  3'  CCCAGAAAGGAAACTGATCTCT 80220        TTGA     C
                                AGAGATCA    TTTCTT CTGGG
                                ||||||||    |||||| |||||
                                TCTCTAGT    AAGGAA GACCC
                                     CA__     A
GAM1272  KIAA0295  3'  CCCAGGAAGCTTTCCAGTGATC 68661          ATTT_
            TC                    GAGATCATTG    CTTCCTGGG
                                ||||||||||    |||||||||
                                CTCTAGTGAC    GAAGGACCC
                                      CTTTC
GAM1272  KIAA0825  3'  CCCAGGAAGACACTGACCTGCT 61683    _  A   T  ATT
                                AG AG TCA TG   TCTTCCTGGG
                                || || ||| ||   ||||||||||
                                TC TC AGT AC   AGAAGGACCC
                                 G  C   C  ___
GAM1272  KIAA1190  3'  CCCAAAAAAAAGTTGATCTCT   71644        TTG    C  CC
                                AGAGATCA   ATTT TT  TGGG
                                ||||||||   |||| ||  ||||
                                TCTCTAGT   TGAA AA  ACCC
                                     ___    A  A_
GAM1272  MGC4638   3'  CCAGAAAGCATGATTTC     49733         T ATTT   C
                                GAGATCAT G    CTT CTGG
                                |||||||| |    ||| ||||
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                                CTTTAGTA C    GAA GACC
                                  _ _____   A
GAM1272  PLPL     3'  CCAGGAAAAAGAGTCTC     39820       CATTGA   C
                                GAGAT      TTT TTCCTGG
                                |||||      ||| |||||||
                                CTCTG      AAA AAGGACC
                                  AG_____   _
GAM1272  RIN3     5'  CCCAGGAAAAAACGGATCTCT  46161        ATTGA   C
                                AGAGATC     TTT TTCCTGGG
                                |||||||     ||| ||||||||
                                TCTCTAG     AAA AAGGACCC
                                   GC___   A
GAM1272  SLC26A1  3'  CCCAAACACTCAGAAATCAAGA 42126      ATCA       TCC_____
              ACCTCT                AGAG    TTGATTTCT      TGGG
                                ||||   |||||||||      ||||
                                TCTC    AACTAAAGA      ACCC
                                  CAAG       CTCACAA
GAM1272  LOC121838 5'  CCAGGAAGGACAATCTCTC    76512      TC    AT
                                GAGA  ATTG  TTCTTCCTGG
                                ||||  ||||  ||||||||||
                                CTCT  TAAC  AGGAAGGACC
                                  C_   __
GAM1272  LOC200138 5'  CCCAGGAAAAAATCAATGATCT 91540             C
              C                  GAGATCATTGATTT TTCCTGGG
                                ||||||||||||| ||||||||
                                CTCTAGTAACTAAA AAGGACCC
                                     A
GAM1272  LOC220000 3'  CCAGGAAGATCTGGCCTCT   93231      AT  TT  TT
                                AGAG  CA  GA  TCTTCCTGG
                                ||||  ||  ||  |||||||||
                                TCTC  GT  CT  AGAAGGACC
                                  CG  __  __
GAM1272  LOC221550 5'  CCCAGGAAAAAGAATAGATC   93745      _  GA   C
                                GATC ATT  TTT TTCCTGGG
                                |||| |||  ||| ||||||||
                                CTAG TAA  AAA AAGGACCC
                                  A  G_  _
GAM1272  LOC255721 3'  CCAGGAAGATCTGGCCTCT   96487      AT  TT  TT
                                AGAG  CA  GA  TCTTCCTGG
                                ||||  ||  ||  |||||||||
                                TCTC  GT  CT  AGAAGGACC
                                  CG  __  __
GAM1272  LOC257495 5'  CCCAGGAAAAAGAATAGATC   99572      _  GA   C
                                GATC ATT  TTT TTCCTGGG
                                |||| |||  ||| ||||||||
                                CTAG TAA  AAA AAGGACCC
                                  A  G_  _
GAM1272  LOC257576 5'  CCCAGGAAAAAGAATAGATC   99709      _  GA   C
                                GATC ATT  TTT TTCCTGGG
                                |||| |||  ||| ||||||||
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                                CTAG TAA  AAA AAGGACCC
                                  A  G_  _
GAM1273  GUCY1A2  3'  CCGCTGTCAATAAAAAGCC   7802        C      _
                                GGCTTTT ATTGACA TGG
                                ||||||| ||||||| |||
                                CCGAAAA TAACTGT GCC
                                   A      C
GAM1273  MNT      3'  TCTACCAACAATAAACCA    40090     C  TC   ACA
                                TGG TTT  ATTG   TGGTAGA
                                ||| |||  ||||   |||||||
                                ACC AAA  TAAC   ACCATCT
                                  _  __    A__
GAM1273  SCA1     3'  ATCTGTCACAAAAAGCCA    6171         CAT    T
                                TGGCTTTT   TGACA GGT
                                ||||||||   ||||| |||
                                ACCGAAAA   ACTGT CTA
                                   AC_    _
GAM1273  TNNT2    3'  CTCCACACCAGTAATAAAAAGC 6293         C   A A   A__
              CA                  TGGCTTTT ATTG C TGGT   GAG
                                ||||||||| |||| | ||||   |||
                                ACCGAAAA TAAT G ACCA   CTC
                                   A   _ _   CAC
GAM1273  FLJ11113 3'  CTATGCCAATATAAAAGCCA   37632        C_   A
                                TGGCTTTT  ATTG CATGG
                                ||||||||  |||| |||||
                                ACCGAAAA  TAAC GTATC
                                   TA   C
GAM1273  FLJ14708 3'  CCACAGCGAAAAGCCA      52606         A   ACA
                                TGGCTTTTC TTG   TGG
                                |||||||||| |||   |||
                                ACCGAAAAG GAC   ACC
                                   C  ___
GAM1273  KIAA1399  3'  CTCCACAACAACAATGAAAACC 70792     C       ACATG  A
              A                   TGG TTTTCATTG    GT GAG
                                ||| |||||||||    || |||
                                ACC AAAAGTAAC    CA CTC
                                  _       AACAA  C
GAM1273  RPS6KB1   3'  CTACCTCACACAAGAAGCCA   61637        CAT_   CAT
                                TGGCTTTT   TGA   GGTAG
                                ||||||||   |||   |||||
                                ACCGAAGA   ACT   CCATC
                                   ACAC   ___
GAM1273  LOC127262 3'  CTCTACCAAACAGACAAAAAGC 76596       CA  GACA
                                GCTTTT  TT    TGGTAGAG
                                ||||||  ||    ||||||||
                                CGAAAA  AG    ACCATCTC
                                   AC  ACAA
GAM1273  LOC149692 3'  CTCTACCACCCCCAAAAAGCC  85733        CATTGACA
                                GGCTTTT       TGGTAGAG
                                |||||||       ||||||||
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                                CCGAAAA       ACCATCTC
                                    ACCCCC__
GAM1274  SLC24A1   3'  TCTACCCCTGACTCATGCAG   17568          ATTG_
                                CTGCATGGGTTA     AGA
                                ||||||||||||    |||
                                GACGTACTCAGT     TCT
                                      CCCCA
GAM1274  DJ328E19.C1.1 3'  CTATTCTCAAACCATGC     31797       GTTAA
                                GCATGG    TTGAGAATAG
                                ||||||    ||||||||||
                                CGTACC    AACTCTTATC
                                   A____
GAM1274  DKFZp434D177 3'  CTATTCTCAGACCATGC     51069       GTTAAT
                                GCATGG     TGAGAATAG
                                ||||||     |||||||||
                                CGTACC     ACTCTTATC
                                   AG____
GAM1274  FLJ13263  3'  TCTATTCTCAATCACTTCTCCA 47815      TTA___
                                TGGG     ATTGAGAATAGA
                                ||||     ||||||||||||
                                ACCT     TAACTCTTATCT
                                  CTTCAC
GAM1274  FLJ14213  3'  TCTATCCTCAACCTACATCCA  46217      TAA__    A
                                TGGGT    TTGAG ATAGA
                                |||||    ||||| |||||
                                ACCTA    AACTC TATCT
                                   CATCC    C
GAM1274  KIAA0618  3'  TCTCCGACCCATGCAG      29859          AATT
                                CTGCATGGGTT    GAGA
                                ||||||||||    ||||
                                GACGTACCCAG    CTCT
                                      C___
GAM1274  KIAA1376  3'  TCTATCCTGCCATTTAACCCCA 64389     CAT      T __  A
            CAG                    CTG   GGGTTAA TG  AG ATAGA
                                |||   ||||||| ||  || |||||
                                GAC   CCCAATT AC  TC TATCT
                                  AC_      T  CG  C
GAM1274  LOC149010 3'  CTATTCTCAGACCATGC     79853       GTTAAT
                                GCATGG     TGAGAATAG
                                ||||||     |||||||||
                                CGTACC     ACTCTTATC
                                   AG____
GAM1274  LOC149317 3'  CTATTCTCAAACCATGC     80060       GTTAA
                                GCATGG    TTGAGAATAG
                                ||||||    ||||||||||
                                CGTACC    AACTCTTATC
                                   A____
GAM1274  LOC152313 5'  CTACTCTCCCCACAGCAG    86850      A_   TTAATT   A
                                CTGC  TGGG     GAGA TAG
                                ||||  ||||     |||| |||
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                                GACG  ACCC     CTCT ATC
                                  AC   _______   C
GAM1274  LOC203636 3'  CTCGAAGCCCATGCAG      90977          AA
                                CTGCATGGGTT  TTGAG
                                ||||||||||  |||||
                                GACGTACCCGA  AGCTC
                                          __
GAM1274  LOC220638 3'  CTATTCTCAAACCATGC     74340       GTTAA
                                GCATGG    TTGAGAATAG
                                ||||||    ||||||||||
                                CGTACC    AACTCTTATC
                                   A____
GAM1274  LOC256581 3'  TCTATTCTCTCGGCGCCCACGC 99433     A    TAATT
            A                    TGC TGGGT    GAGAATAGA
                                ||| |||||    |||||||||
                                ACG ACCCG    CTCTTATCT
                                  C    CGGCT
GAM1275  SLC25A15  3'  CAAGTGGAAATGAGGAACGGAA 27289     ATCA  AG   CC
                                TTC    CC  TCA  TCCACTTG
                                |||    ||  |||  ||||||||
                                AAG    GG  AGT  AGGTGAAC
                                  GCAA  __   AA
GAM1275  FLJ12581  3'  CAAGTACGAATTGGTGATGAA  46331          CACC  C_
                                TTCATCACCAGT    TC  ACTTG
                                ||||||||||||    ||  |||||
                                AAGTAGTGGTTA    AG  TGAAC
                                      _____  CA
GAM1275  KIAA1193  3'  GAGGTGACTGATGAGAA     68272     A   C
                                TTC TCA CAGTCACCTC
                                ||| ||| ||||||||||
                                AAG AGT GTCAGTGGAG
                                  _   A
GAM1275  LOC113523 3'  CAAGTACATGGGACTGGTGAT  73412          A  TCC_
                                ATCACCAGTC CC    ACTTG
                                |||||||||| ||    |||||
                                TAGTGGTCAG GG    TGAAC
                                      _  TACA
GAM1275  LOC147976 3'  CAAGTAAAGGAGCAAGTGATGG 79286        CA  CA   CC
            A                    TTCATCAC  GT  CCT  ACTTG
                                ||||||||  ||  |||  |||||
                                AGGTAGTG  CG  GGA  TGAAC
                                     AA  A_   AA
GAM1275  LOC149705 3'  GGAGATGATAGTGATGAA    85784        CA    C
                                TTCATCAC  GTCA CTCC
                                ||||||||  |||| ||||
                                AAGTAGTG  TAGT GAGG
                                     A_    A
GAM1275  LOC149722 5'  CAAGTGGAGGGTGAGCAAGATG 85750       ACCAG    _
            AA                    TTCATC    TCACC TCCACTTG
                                ||||||    ||||| ||||||||
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                                AAGTAG    AGTGG AGGTGAAC
                                   AACG_    G
GAM1275  LOC153688 3'  CAAGTGGAGGTGGTCGTAAGTG 87297     CAG___
             A                     TCAC     TCACCTCCACTTG
                                   ||||     ||||||||||||
                                   AGTG     GGTGGAGGTGAAC
                                     AATGCT
GAM1275  LOC256021 3'  GTGAAGGTGACAGTGATGAA   98280       CA      C
                                   TTCATCAC  GTCACCT CAC
                                   ||||||||  ||||||| |||
                                   AAGTAGTG  CAGTGGA GTG
                                        A_      A
GAM1276  SCAMP1    3'  GCTAAATAAATATTCTCC    54500     T     C
                                   GGA AATATT ATTTAGC
                                   ||| |||||| |||||||
                                   CCT TTATAA TAAATCG
                                     C     A
GAM1276  SCAMP1    3'  GCTAAATAAATATTCTCC    54501     T     C
                                   GGA AATATT ATTTAGC
                                   ||| |||||| |||||||
                                   CCT TTATAA TAAATCG
                                     C     A
GAM1276  NX-17     3'  TGAATATCAGCCCCTAATA   40706       ATA_
                                   TATTAGGG   ATATTCA
                                   ||||||||   |||||||
                                   ATAATCCC   TATAAGT
                                        CGAC
GAM1276  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
             TA                      TATTAGGGATAATATTCATTTAGC
                                   ||||||||||||||||||||||||
                                   ATAATCCCTATTATAAGTAAATCG

GAM1277  SCAMP1    3'  GCTAAATAAATATTCTCC    54500     T     C
                                   GGA AATATT ATTTAGC
                                   ||| |||||| |||||||
                                   CCT TTATAA TAAATCG
                                     C     A
GAM1277  SCAMP1    3'  GCTAAATAAATATTCTCC    54501     T     C
                                   GGA AATATT ATTTAGC
                                   ||| |||||| |||||||
                                   CCT TTATAA TAAATCG
                                     C     A
GAM1277  NX-17     3'  TGAATATCAGCCCCTAATA   40706       ATA_
                                   TATTAGGG   ATATTCA
                                   ||||||||   |||||||
                                   ATAATCCC   TATAAGT
                                        CGAC
GAM1277  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
             TA                      TATTAGGGATAATATTCATTTAGC
                                   ||||||||||||||||||||||||
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                                ATAATCCCTATTATAAGTAAATCG

GAM1278 SCAMP1   3' GCTAAATAAATATTCTCC    18013    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1278 SCAMP1   3' GCTAAATAAATATTCTCC    54501    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1278 NX-17    3' TGAATATCAGCCCCTAATA   40706       ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                     CGAC
GAM1278 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
             TA                   TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM1279 CALU     3' CCCTCAGGTTACCAAGATAAA 8695        TTTG__
                                TTTATCTT    CTGAGGG
                                ||||||||    |||||||
                                AAATAGAA    GACTCCC
                                     CCATTG
GAM1279 DNM1     3' CCCTCGGCTGAGAATAAA    16612     C   T
                                TTTAT TTTT GCTGAGGG
                                ||||| |||| ||||||||
                                AAATA AGAG CGGCTCCC
                                   _   T
GAM1279 DPP4     3' CCCTGTTAAAAGATGAA     10422       T  TG
                                TTTATCTTTT GC  AGGG
                                |||||||||| ||  ||||
                                AAGTAGAAAA TG  TCCC
                                      T  __
GAM1279 FGF12    3' CCCTGGGGCAAAAATATAA   41060     C     _ G
                                TTAT TTTTTGC T AGGG
                                |||| ||||||| | ||||
                                AATA AAAAACG G TCCC
                                   T     G G
GAM1279 IRTA1    3' CCTTTAAAAAAAGATAAA    49239        GCT
                                TTTATCTTTTT  GAGG
                                ||||||||||  ||||
                                AAATAGAAAAA  TTCC
                                      AAT
GAM1279 OPCML    3' CCCTCAGTCTAAAAAATAA   11896     C   T_
                                TTAT TTTT  GCTGAGGG
                                |||| ||||  ||||||||
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                                AATA AAAA  TGACTCCC
                                  A    TC
GAM1279  P2RY2     3'  CCCCAGCCCAAGAGATGAA    11935          T_    A
                                TTTATCTTTT  GCTG GGG
                                ||||||||||  |||| |||
                                AAGTAGAGAA  CGAC CCC
                                     CC    _
GAM1279  PITX3     3'  CCCTCGTTTTCAAAGATAAA   18521         TT__  T
                                TTTATCTTT    GC GAGGG
                                |||||||||    || |||||
                                AAATAGAAA    TG CTCCC
                                     CTTT  _
GAM1279  RARB      3'  CCTAGGTTCAAAAAGATAA    32888           __  G
                                TTATCTTTTTG  CT AGG
                                ||||||||||  ||  |||
                                AATAGAAAAAC  GG TCC
                                      TT  A
GAM1279  RARB      3'  CCTAGGTTCAAAAAGATAA    8259            __  G
                                TTATCTTTTTG  CT AGG
                                ||||||||||  ||  |||
                                AATAGAAAAAC  GG TCC
                                      TT  A
GAM1279  RREB1     3'  CCCTCAGCACAGACAAA      12910      A   TTT
                                TTT TCT   TGCTGAGGG
                                |||  |||   |||||||||
                                AAA AGA   ACGACTCCC
                                  C   C__
GAM1279  SLC26A4   3'  CCCTGCCTAAAGATAGA      6526          TT  TG
                                TTTATCTTT  GC  AGGG
                                |||||||||  ||  ||||
                                AGATAGAAA  CG  TCCC
                                     TC  __
GAM1279  SRGAP2    3'  CCCTCTAAGAAAGTAAA      75109      T     GCT
                                TTTA CTTTTT   GAGGG
                                ||||  ||||||   |||||
                                AAAT GAAAGA   CTCCC
                                   _     AT_
GAM1279  DKFZP434J193 3'  CCCTCAGTTCAGATAGA     71561        TTTT
                                TTTATCT    GCTGAGGG
                                |||||||    ||||||||
                                AGATAGA    TGACTCCC
                                    CT__
GAM1279  DKFZP762D096 3'  CCCCAGTGAAGAGTAAA     66179      T    TG   A
                                TTTA CTTTT  CTG GGG
                                ||||  |||||  |||  |||
                                AAAT GAGAA  GAC CCC
                                   _    GT   _
GAM1279  FLJ13096  3'  CTTATGCAATAAGATAAA     47173         T   _
                                TTTATCTT TTGC TGAG
                                ||||||||  ||||  ||||
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                                AAATAGAA AACG ATTC
                                     T   T
GAM1279  FLJ22390  3'  CCCAGTGCAAAAAGTAAA    43031     T      TGA
                                TTTA CTTTTTGC   GGG
                                |||| ||||||||   |||
                                AAAT GAAAAACG   CCC
                                  _      TGA
GAM1279  KIAA1045  3'  CCCTCAGCAAAGAGTAGA    71601     T
                                TTTA CTTTTTGCTGAGGG
                                |||| ||||||||||||||
                                AGAT GAGAAACGACTCCC
                                  _
GAM1279  KIAA1405  3'  CCCTCAGCCCTGGGAAGA    61696       ___
                                TCTTTTT   GCTGAGGG
                                |||||||   ||||||||
                                AGAAGGG   CGACTCCC
                                     TCC
GAM1279  KIAA1789  5'  CCTAGAAAAAGATAAA      67699         G  G
                                TTTATCTTTTT CT AGG
                                |||||||||| || |||
                                AAATAGAAAAA GA TCC
                                      _ _
GAM1279  PP35      3'  CCTAGCTAAAAAGATAAA    23798         _  G
                                TTTATCTTTTT GCT AGG
                                |||||||||| ||| |||
                                AAATAGAAAAA CGA TCC
                                      T  _
GAM1279  PRO1992   5'  CCCAGTGAAAAGGATAAA    26901         _   A
                                TTTATCTTTTT GCTG GG
                                |||||||||| |||| ||
                                AAATAGGAAAA TGAC CC
                                      G   _
GAM1279  RRP46     3'  CCCCAGCAAGGATAA       39758       TT    A
                                TTATCT  TTGCTG GGG
                                ||||||  |||||| |||
                                AATAGG  AACGAC CCC
                                  __    _
GAM1279  TNKS2     3'  CCTGTGGCAAAAGGATAAA   48218           _
                                TTTATCTTTTTGCTG AGG
                                |||||||||||||| |||
                                AAATAGGAAAACGGT TCC
                                      G
GAM1279  TRIM29    3'  CCCTCTGCTGAGATAAA     25007        TTT  T
                                TTTATCTT   GC GAGGG
                                ||||||||   || |||||
                                AAATAGAG   CG CTCCC
                                     T__  T
GAM1279  LOC119548 3'  CCCTGGGACAAAAGATAA    74451         TG  G
                                TTATCTTTT  CT AGGG
                                |||||||||  || ||||
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                                AATAGAAAA  GG TCCC
                                     CA  G
GAM1279  LOC128077 3'  CCCAGGGACAAGATAAA     75210        T  G   A
                                TTTATCTT TT CTG GG
                                |||||||| || ||| ||
                                AAATAGAA AG GAC CC
                                     C  G  _
GAM1279  LOC148203 3'  CCCTTGTAGAAAGGCAAA    79459     AT      T
                                TTT  CTTTTTGC GAGGG
                                |||  |||||||| |||||
                                AAA  GAAAGATG TTCCC
                                  CG      _
GAM1279  LOC153346 5'  CCCTCAAGGCAAGATAAG    87204       TTT   __
                                TTTATCT   TGCT  GAGGG
                                |||||||   ||||  |||||
                                GAATAGA   ACGG  CTCCC
                                    ___    AA
GAM1279  LOC157624 5'  CCCCAGCAAGATTTTAAG    87792     TCT      A
                                TTTA   TTTTGCTG GGG
                                ||||   |||||||| |||
                                GAAT   AGAACGAC CCC
                                   TTT      _
GAM1279  LOC158156 3'  CCCTCCTGCTGAAGATAAA   82625        TT  T_
                                TTTATCTTT  GC  GAGGG
                                |||||||||  ||  |||||
                                AAATAGAAG  CG  CTCCC
                                     T_  TC
GAM1279  LOC203084 3'  CCCTCATAGGCAAAGATGAA  88876        TT   ___
                                TTTATCTT  TGCT   GAGGG
                                ||||||||  ||||   |||||
                                AAGTAGAA  ACGG   CTCCC
                                    __    ATA
GAM1279  LOC254243 3'  CCCTTGTTTAAAGATAAA    99257        TT  T
                                TTTATCTTT  GC GAGGG
                                |||||||||  || |||||
                                AAATAGAAA  TG TTCCC
                                     TT  _
GAM1279  LOC255019 3'  CCCTCAGCGGATGATAA     96777      TT
                                TTATC  TTTGCTGAGGG
                                |||||  ||||||||||
                                AATAG  AGGCGACTCCC
                                   T_
GAM1279  LOC255019 3'  CCCTCAGCGGATGATAA     96778      TT
                                TTATC  TTTGCTGAGGG
                                |||||  ||||||||||
                                AATAG  AGGCGACTCCC
                                   T_
GAM1279  LOC255019 3'  CCCTCAGCGGATGATAA     96779      TT
                                TTATC  TTTGCTGAGGG
                                |||||  ||||||||||
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                                AATAG  AGGCGACTCCC
                                  T_
GAM1279  LOC90038  3'  CCCTTGTTTAAAGATAAA    61800        TT  T
                                TTTATCTTT  GC GAGGG
                                |||||||||  || |||||
                                AAATAGAAA  TG TTCCC
                                     TT  _
GAM1280  SCAMP1    3'  GCTAAATAAATATTCTCC    54500    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1280  SCAMP1    3'  GCTAAATAAATATTCTCC    54501    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1280  NX-17     3'  TGAATATCAGCCCCTAATA   40706       ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                     CGAC
GAM1280  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
           TA                    TATTAGGGATAATATTCATTTAGC
                                 ||||||||||||||||||||||||
                                 ATAATCCCTATTATAAGTAAATCG

GAM1281  ABL2      5'  TGTGAGTCGCCTGGAGGCAG  24611           A_
                                CTGCCTCCAGGTGAC  GCA
                                ||||||||||||||  |||
                                GACGGAGGTCCGCTG  TGT
                                         AG
GAM1281  DYRK1B    3'  TGATTGGGGCCTGGGGCAG   17517     T    GACAG
                                CTGCC CCAGGT    CAATCA
                                ||||| ||||||    ||||||
                                GACGG GGTCCG    GTTAGT
                                  _     GG___
GAM1281  GNAZ      3'  CTGCACCCCTGTCACCTGGAGG 10827          CAAT_
                                CCTCCAGGTGACAG    CAG
                                ||||||||||||||    |||
                                GGAGGTCCACTGTC    GTC
                                      CCCAC
GAM1281  GYPC      3'  GATAGCCACCTGGAAACA    10900    CC      ACA  A
                                TG  TCCAGGTG   GC ATC
                                ||  ||||||||   || |||
                                AC  AGGTCCAC   CG TAG
                                 AA       ___  A
GAM1281  GYPC      3'  GATAGCCACCTGGAAACA    34143    CC      ACA  A
                                TG  TCCAGGTG   GC ATC
                                ||  ||||||||   || |||
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                                AC  AGGTCCAC   CG TAG
                                 AA       ___  A
GAM1281  IL1R1    3'  TGAGGTCACCTGGAATCAG   7928     CC        AG
                                CTG  TCCAGGTGAC  CA
                                |||  ||||||||||  ||
                                GAC  AGGTCCACTG  GT
                                  TA        GA
GAM1281  SLC21A9  3'  TGTGTCACCTGGGGCAG    24384      T        G
                                CTGCC CCAGGTGACA CA
                                |||||  ||||||||||  ||
                                GACGG GGTCCACTGT GT
                                   _        _
GAM1281  ZNF138   5'  CTGATTACCTGTCTGGA    82099     GGT    C_
                                TCCA   GACAG  AATCAG
                                ||||   |||||  ||||||
                                AGGT   CTGTC  TTAGTC
                                  ___     CA
GAM1281  C8orf13  3'  GTGGGTCTCCCGGAGGCAG   82482        A  T   A_
                                CTGCCTCC GG GAC  GC
                                ||||||||  ||  |||  ||
                                GACGGAGG CC CTG  TG
                                    C  T   GG
GAM1281  CHST3    3'  TGTGGTCCCTGGAGGCA     16246         T   A
                                TGCCTCCAGG GAC GCA
                                ||||||||||  ||| |||
                                ACGGAGGTCC CTG TGT
                                     _  G
GAM1281  CMG1     5'  TGCAATGCCACCTGGGACAG   47728     C T      A __
                                CTG C CCAGGTG CA  GCA
                                |||  |  |||||||  ||  |||
                                GAC G GGTCCAC GT  CGT
                                  A _      C  AA
GAM1281  DKFZP434H132 3'  GATGGGCCCTGGAGGCAG    31932          TGACA  A_
                                CTGCCTCCAGG    GC  ATC
                                ||||||||||     ||  |||
                                GACGGAGGTCC    CG  TAG
                                     _____  GG
GAM1281  FLJ10036 3'  CTGATTGCCCTTATGGAG    96627      GG   CA
                                CTCCA  TGA  GCAATCAG
                                |||||  |||  ||||||||
                                GAGGT  ATT  CGTTAGTC
                                   __   CC
GAM1281  FLJ11053 3'  CTGACTATCTACCTGGAGATAG 90123     C       _  C  CAA
                                CTG CTCCAGGT GA AG   TCAG
                                |||  ||||||||  ||  ||   ||||
                                GAT GAGGTCCA CT TC   AGTC
                                  A       T  A  ___
GAM1281  FLJ11767 3'  CTGATTGTAAGCACCTGAAGGC 45059       C     ACA
            A                    TGCCT CAGGTG   GCAATCAG
                                 |||||  ||||||   ||||||||
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                                ACGGA GTCCAC   TGTTAGTC
                                  A     GAA
GAM1281  FLJ12691  3'  CTGATTGGTATCTGGAGACAG  45001     C       ACAG
                                CTG CTCCAGGTG    CAATCAG
                                ||| |||||||||    |||||||
                                GAC GAGGTCTAT    GTTAGTC
                                  A       G___
GAM1281  GALNT6    3'  CTGATCACCAGCTTCTCTGGAG 24247         T  C   A____
           GC                     GCCTCCAGG GA AGC     ATCAG
                                |||||||||  || |||    |||||
                                CGGAGGTCT CT TCG     TAGTC
                                     _ _   ACCAC
GAM1281  H-plk     5'  CTGATTACCTGTCTGGAGCA   32381     C    GGT    C_
                                TGC TCCA   GACAG  AATCAG
                                ||| ||||   |||||  ||||||
                                ACG AGGT   CTGTC  TTAGTC
                                  _   ___    CA
GAM1281  KIAA0781  3'  GCCACCGTGGAGGCAG      68058         _   ACA
                                CTGCCTCCA GGTG   GC
                                |||||||||  ||||   ||
                                GACGGAGGT CCAC   CG
                                     G   ___
GAM1281  KIAA0971  3'  CTGATTACTGTCATTACTAGAG 30670     C  __      C
                                CTC AG  GTGACAG AATCAG
                                ||| ||  ||||||| ||||||
                                GAG TC  TACTGTC TTAGTC
                                  A  AT      A
GAM1281  KIAA1344  3'  CTGATTATTACCTGGATACA   72866    CC       CAGC
                                TG  TCCAGGTGA    AATCAG
                                ||  |||||||||    ||||||
                                AC  AGGTCCATT    TTAGTC
                                  AT       A___
GAM1281  MADCAM1   3'  CTGATTGCCTCTTTGGAG    56238       T  CA
                                CTCCAGG GA  GCAATCAG
                                |||||||  ||  ||||||||
                                GAGGTTT CT  CGTTAGTC
                                     _  C_
GAM1281  MADCAM1   3'  CTGATTGCCTCTTTGGAG    56241       T  CA
                                CTCCAGG GA  GCAATCAG
                                |||||||  ||  ||||||||
                                GAGGTTT CT  CGTTAGTC
                                     _  C_
GAM1281  MADCAM1   3'  CTGATTGCCTCTTTGGAG    56244       T  CA
                                CTCCAGG GA  GCAATCAG
                                |||||||  ||  ||||||||
                                GAGGTTT CT  CGTTAGTC
                                     _  C_
GAM1281  MGC10870  5'  CTGACCATGTCACCTGGAGGC  51178            GCAA
                                GCCTCCAGGTGACA    TCAG
                                ||||||||||||||    ||||
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                                CGGAGGTCCACTGT   AGTC
                                       ACC_
GAM1281 MGC10924 3' CTGTATGAACACCTGGAAGCA 48311    C     _____
                                TGC TCCAGGTG    ACAG
                                ||| ||||||||    ||||
                                ACG AGGTCCAC    TGTC
                                  A       AAGTA
GAM1281 MGC14436 5' CTGACCACCTGGAGACAG   52926    C       A_
                                CTG CTCCAGGTG  CAG
                                ||| |||||||||  |||
                                GAC GAGGTCCAC  GTC
                                  A       CA
GAM1281 SYT12    3' TGATCGCTGTGGGGGCAG   96390       AGGTG    A
                                CTGCCTCC    ACAGC ATCA
                                ||||||||    ||||| ||||
                                GACGGGGG    TGTCG TAGT
                                     _____    C
GAM1281 TReP-132 3' TGTGTGTCACTTAGAGACAG  54274    C  C     _
                                CTG CTC AGGTGACA GCA
                                ||| ||| |||||||| |||
                                GAC GAG TTCACTGT TGT
                                  A  A       G
GAM1281 TReP-132 3' TGTGTGTCACTTAGAGACAG  54276    C  C     _
                                CTG CTC AGGTGACA GCA
                                ||| ||| |||||||| |||
                                GAC GAG TTCACTGT TGT
                                  A  A       G
GAM1281 TReP-132 3' TGTGTGTCACTTAGAGACAG  37915    C  C     _
                                CTG CTC AGGTGACA GCA
                                ||| ||| |||||||| |||
                                GAC GAG TTCACTGT TGT
                                  A  A       G
GAM1281 ZFD25    5' CTGATCACCTGTCTGGAGCA  33109    C   GGT    CA_
                                TGC TCCA   GACAG   ATCAG
                                ||| ||||   |||||   |||||
                                ACG AGGT   CTGTC   TAGTC
                                  _   ___     CAC
GAM1281 ZNF177   3' CTGTTATGGTCACCTGGAAACA 14356    CC       AGCAAT
           G                     CTG  TCCAGGTGAC     CAG
                                ||| ||||||||||     |||
                                GAC  AGGTCCACTG     GTC
                                  AA        GTATT_
GAM1281 ZNF90    5' CTGATCACCTGTCTGGAGCA  79467    C   GGT    CA_
                                TGC TCCA   GACAG   ATCAG
                                ||| ||||   |||||   |||||
                                ACG AGGT   CTGTC   TAGTC
                                  _   ___     CAC
GAM1281 LOC149606 3' CTGAAGCACCACTGGAGGCA  80261        G  ACA  AA
                                TGCCTCCAG TG   GC  TCAG
                                |||||||| ||   ||  ||||
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                                ACGGAGGTC AC   CG  AGTC
                                     _ CA_  A_
GAM1281  LOC157663 3'  CTGAAAGTACTGTCATCTAAAA 82450     CTCC       CAA__
              GCA                    TGC    AGGTGACAG    TCAG
                                ||| |||||||||    ||||
                                ACG   TCTACTGTC    AGTC
                                  AAAA       ATGAA
GAM1281  LOC196527 3'  TGATTGTACTAGAGACAG    89102     C   CA   GACA
                                CTG CTC  GGT   GCAATCA
                                ||| |||  |||   |||||||
                                GAC GAG  TCA   TGTTAGT
                                  A  A_  _____
GAM1281  LOC221025 5'  CTGGCCACCTGGAGACAG    94785     C       A_
                                CTG CTCCAGGTG  CAG
                                ||| |||||||||  |||
                                GAC GAGGTCCAC  GTC
                                  A       CG
GAM1281  LOC253943 3'  CTGATTGCTATCATGAAGTA   97845     C  CAG    C
                                TGC TC   GTGA AGCAATCAG
                                ||| ||   |||| |||||||||
                                ATG AG   TACT TCGTTAGTC
                                  A ____   A
GAM1281  LOC255180 3'  GATCACTGTCATCTAAAAGCAG 96732      CTCC       CA
                                CTGC    AGGTGACAG  ATC
                                ||||    |||||||||  |||
                                GACG    TCTACTGTC  TAG
                                  AAAA       AC
GAM1281  LOC256416 3'  CTGTCCACCTGGGGACAG    96059     C       _
                                CTG CTCCAGGTG ACAG
                                ||| ||||||||| ||||
                                GAC GGGGTCCAC TGTC
                                  A       C
GAM1281  LOC51673  3'  CTGTCCACCTGGGGACAG    96207     C       _
                                CTG CTCCAGGTG ACAG
                                ||| ||||||||| ||||
                                GAC GGGGTCCAC TGTC
                                  A       C
GAM1282  CCRL2     3'  TCCACCAAATGCAAGAAGAAT  15584        CACTC_
                                GTTCTTTT     TGGTGGA
                                ||||||||     |||||||
                                TAAGAAGA     ACCACCT
                                     ACGTAA
GAM1282  HSPC228   3'  TAGAGAATGAAAAGAAGATA   33651      G       __
                                TATC TTCTTTTCA  CTCTG
                                |||| |||||||||  |||||
                                ATAG AAGAAAAGT  GAGAT
                                  _       AA
GAM1282  MGC10765  3'  CCATAGAGTGATAAGAAC    44557       T       G
                                GTTCTT TCACTCTG TGG
                                |||||| |||||||| |||
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                                CAAGAA AGTGAGAT ACC
                                   T      _
GAM1282  LOC158125 3'  CCACCAGAGCAGACAAC     82616     C   TCA
                                GTT TTT   CTCTGGTGG
                                ||| |||   |||||||||
                                CAA AGA   GAGACCACC
                                  C   C__
GAM1282  LOC202309 5'  CCACCAAAGTGAAAAAGAGGA  91940    G TC       C
                                TC T  TTTTCACT TGGTGG
                                || |  |||||||| ||||||
                                AG A  AAAAGTGA ACCACC
                                 G GA       A
GAM1282  LOC257464 5'  TCCACCAAAGTGAAACTGGGGT 91246    TT __      C
                                G  CT  TTTCACT TGGTGGA
                                |  ||  ||||||| |||||||
                                T  GG  AAAGTGA ACCACCT
                                 GG  TC      A
GAM1283  ALEX3    5'  ACTAGGGAAAAGAAGAAGGGG  33971           _ ATCC
                                CCCTTTCTTCTTT CC    AGT
                                |||||||||||| ||    |||
                                GGGGAAGAAGAAA GG    TCA
                                       A  GA__
GAM1283  C18orf1   3'  CTGAATAAAGAAGGAAG     60864          CC  C
                                CTTTCTTCTTT  AT CAG
                                ||||||||||  || |||
                                GAAGGAAGAAA  TA GTC
                                      __ A
GAM1283  CDH17    5'  CTGAATGGAAGAAAAGG     15784      CT    T    C
                                CCTTT  TCTT CCAT CAG
                                |||||  |||| |||| |||
                                GGAAA  AGAA GGTA GTC
                                   __   _    A
GAM1283  CNTNAP2   3'  ACTAGAATGAAAGAAGGAA   27087          CA  C
                                TTTCTTCTTTC  TC AGT
                                ||||||||||  || |||
                                AAGGAAGAAAG  AG TCA
                                       TA  A
GAM1283  DDX6     3'  CTGGTGAAGAGAAAAAGG     16564      C     C  T
                                CCTTT TTCTTT CA CCAG
                                ||||| |||||| || ||||
                                GGAAA AAGAGA GT GGTC
                                   _     A  _
GAM1283  DMD      5'  GGAGTGGAAGAAACAGGT     15685     CC       _
                                ACC  TTTCTTCT TTCC
                                |||  |||||||| ||||
                                TGG  AAAGAAGG GAGG
                                  AC       T
GAM1283  DMD      5'  GGAGTGGAAGAAACAGGT     15689     CC       _
                                ACC  TTTCTTCT TTCC
                                |||  |||||||| ||||
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                                TGG  AAAGAAGG GAGG
                                  AC       T
GAM1283  ENC1     3'  ACTGGACATGAAGGAAAGGGG  14646         TCT   CA_
                                CCCCTTTCT   TTC   TCCAGT
                                |||||||||   |||   ||||||
                                GGGGAAAGG   AAG   AGGTCA
                                     ___   TAC
GAM1283  FBXW7    3'  ACTAAGAAGGAAAAGAAGAAG  54408          _  A  C_
                                TTTCTTCTTT CC TC  AGT
                                |||||||||| || ||  |||
                                GAAGAAGAAA GG AG  TCA
                                      A  A  AA
GAM1283  FBXW7    3'  ACTAAGAAGGAAAAGAAGAAG  37590          _  A  C_
                                TTTCTTCTTT CC TC  AGT
                                |||||||||| || ||  |||
                                GAAGAAGAAA GG AG  TCA
                                      A  A  AA
GAM1283  HDAC8    3'  ACTGGACCTAGGGGAAGAAGGA 38079           A____
              G                  TTTCTTCTTTCC    TCCAGT
                                |||||||||||    ||||||
                                GAGGAAGAAGGG    AGGTCA
                                      GATCC
GAM1283  IL18R1   3'  ACTGGATGACTAAAAAGAG   15250       C  TC_
                                TTCTT TT   CATCCAGT
                                |||||  ||   ||||||||
                                GAGAA AA   GTAGGTCA
                                   A  TCA
GAM1283  IL2RA    5'  ACTGGATGGACCCACAAGGG   6445       TCTTCTT
                                CCCTT      TCCATCCAGT
                                |||||      ||||||||||
                                GGGAA      AGGTAGGTCA
                                   CACCC__
GAM1283  KCND3    5'  TGCAAGAAAAAGGGGT      18355        C    TCCATC
                                ACCCCTTT TTCTT     CA
                                |||||||| |||||     ||
                                TGGGGAAA AAGAA     GT
                                     _    C_____
GAM1283  MMP1     5'  ACTGAGAAAGAAGACAAAGG   11604      __       CATC
                                CCTT  TCTTCTTTC   CAGT
                                ||||  |||||||||   ||||
                                GGAA  AGAAGAAAG   GTCA
                                   AC       A___
GAM1283  OAS3     3'  ACTGGATATGGAAAAAAGAAGG 21649       C     __
                                CTTTCTT TTTCCA  TCCAGT
                                ||||||| ||||||  ||||||
                                GGAAGAA AAAGGT  AGGTCA
                                     A     AT
GAM1283  OCA2     3'  ACTGTTTGAAGAAGAAAAGG   60824    C       TC  TC
                                CC TTTCTTCTT  CA  CAGT
                                || |||||||||  ||  ||||
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                                GG AAAGAAGAA  GT  GTCA
                                 A        __ TT
GAM1283  PMX1     5'  CTGAGAAGGAAAAAGGAG    42961      C    A  _
                                TTCTT TTTCC TC CAG
                                ||||| ||||| || |||
                                GAGGA AAAGG AG GTC
                                   A    A  A
GAM1283  PMX1     5'  CTGAGAAGGAAAAAGGAG    23567      C    A  _
                                TTCTT TTTCC TC CAG
                                ||||| ||||| || |||
                                GAGGA AAAGG AG GTC
                                   A    A  A
GAM1283  SLC1A3   5'  ACTGAAGTGCAAAGAAGAGA   16058         C   C_
                                TTTCTTCTTT CAT  CAGT
                                |||||||||| |||  ||||
                                AGAGAAGAAA GTG  GTCA
                                      C   AA
GAM1283  SMP1     3'  GAAGGAAAGGAAAAAAGGG   27473       C_      A
                                CCCTTT  TTCTTTCC TC
                                ||||||  |||||||| ||
                                GGGAAA  AGGAAAGG AG
                                   AA       A
GAM1283  TES      3'  ACTGAATGGAAAGATGAG    72457     T       C
                                TTC TCTTTCCAT CAGT
                                ||| |||||||| ||||
                                GAG AGAAAGGTA GTCA
                                  T       A
GAM1283  TNFAIP2  3'  ACTGGAAGAGAAAGAAGGAA  21915         CA_
                                TTTCTTCTTTC   TCCAGT
                                ||||||||||   ||||||
                                AAGGAAGAAAG   AGGTCA
                                      AGA
GAM1283  ZNF38    5'  GGAGAAAGAAGAGAAAGG    96030    CC        CA
                                CC  TTTCTTCTTTC  TCC
                                ||  ||||||||||  |||
                                GG  AGAGAAGAAAG  AGG
                                 AA         __
GAM1283  ABCA10   5'  ACTGGACAAGGAGAAA      55360        TCCA
                                TTTCTTCTT    TCCAGT
                                |||||||||    ||||||
                                AAAGAGGAA    AGGTCA
                                     C___
GAM1283  ADAM9    3'  GCTGGAGAAAGAAGGAAG    15106          CA
                                CTTTCTTCTTTC  TCCAGT
                                ||||||||||||  ||||||
                                GAAGGAAGAAAG  AGGTCG
                                                __
GAM1283  AP3M2    3'  GGAAAAAGAAGTAAAGGAGT  23301    C    _     CCA
                                AC CCTTT CTTCTTT   TCC
                                || ||||| |||||||   |||
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                                TG GGAAA GAAGAAA   AGG
                                 A    T      A__
GAM1283  C11orf11  5'  ATGACAAGAAGAAAGTGGT   94873     C        TC
                                ACC CTTTCTTCTT  CAT
                                ||| ||||||||||  |||
                                TGG GAAAGAAGAA  GTA
                                  T         CA
GAM1283  C20orf60  3'  ACTGAACGGGTAAGAGAAGAGG 54803      CT    T  ATC_
                                CCTTT  TCTT CC    CAGT
                                |||||  |||| ||    ||||
                                GGAGA  AGAA GG    GTCA
                                   AG    T  GCAA
GAM1283  C7orf13   3'  ACTGGATCTAGAAGAAAAGG   51920    C       TTCC
                                CC TTTCTTCT    ATCCAGT
                                || ||||||||    |||||||
                                GG AAAGAAGA    TAGGTCA
                                 A       TC__
GAM1283  C8orf2    3'  ACTGTGGTGAAAAAGAAGAAA  24141          C_   _
                                TTTCTTCTTT  CATC CAGT
                                ||||||||||  |||| ||||
                                AAAGAAGAAA  GTGG GTCA
                                      AA    T
GAM1283  CREG      3'  ACTGGATTGCAAAAGAAAGAGG 15245    C      CTTTCC
                                CC CTTTCTT     ATCCAGT
                                || |||||||     |||||||
                                GG GAAAGAA     TAGGTCA
                                 A       AACGT_
GAM1283  DKFZP434C171 5'  ACTGGATGAGCAGCAAAGGG   32179       _  T  TTC
                                CCCTTT CT CT   CATCCAGT
                                |||||| || ||   ||||||||
                                GGGAAA GA GA   GTAGGTCA
                                   C  C  ___
GAM1283  DKFZP434F0318 3'  ACTGGGAGAAAAAAGAGAGGAG 48740    C       C    CA
              T                  AC CCTTTCTT TTTC  TCCAGT
                                || |||||||| ||||  ||||||
                                TG GGAGAGAA AAAG  GGGTCA
                                 A       A    A_
GAM1283  DKFZP564I052 5'  ACTGGATGATTGTGAGAAAAGG 67275     C     CTTTC
              G                  CCC TTTCTT     CATCCAGT
                                ||| ||||||     ||||||||
                                GGG AAAGAG     GTAGGTCA
                                  A      TGTTA
GAM1283  DKFZP566D193 3'  ACTGGAATAAAAAGGAAGAAA  86750          CCA__
                                TTTCTTCTTT     TCCAGT
                                ||||||||||     ||||||
                                AAAGAAGGAA     AGGTCA
                                      AAATA
GAM1283  EIF4G3    3'  GGGGAAAGAGAAAAAAAGGT   15001     CC__    T     AT
                                ACC    TTTCT CTTTCC  CC
                                |||    ||||| ||||||  ||
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                                TGG    AAAGA GAAAGG  GG
                                  AAAA    _     __
GAM1283  ETAA16    5'  GTGAAAAGAAGAAAGCGG    39170    C         C
                                CC CTTTCTTCTTT CAT
                                || |||||||||| |||
                                GG GAAAGAAGAAA GTG
                                 C          A
GAM1283  FLJ11996  3'  ACTGAAGTGTTGAAGAAGGAA  47048          C_   C_
                                TTTCTTCTTT  CAT  CAGT
                                ||||||||||  |||  ||||
                                AAGGAAGAAG  GTG  GTCA
                                      TT   AA
GAM1283  FLJ13782  3'  CAGATGGAAAGGGGGT      46698      TTTCTT       CA
                                ACCCC     CTTTCCATC  G
                                |||||     |||||||||  |
                                TGGGG     GAAAGGTAG  C
                                  _______        AC
GAM1283  FLJ13955  3'  GTGGAGAGAAGAAAGAGGT    45749     C
                                ACC CTTTCTTCTTTCCAT
                                ||| ||||||||||||||
                                TGG GAAAGAAGAGAGGTG
                                  A
GAM1283  FLJ21438  5'  GGCTGAAAGAGAAGAAAAAGG  62199    CC        C_  T
                                CC  TTTCTTCTTT  CA CC
                                ||  ||||||||||  || ||
                                GG  AAAGAAGAGA  GT GG
                                 AA         AA  C
GAM1283  KIAA0694  3'  ACTGAATGAACTAAGAAAGG   72960        CT   C  C
                                CCTTTCTT  TTC AT CAGT
                                ||||||||  ||| || ||||
                                GGAAAGAA  AAG TA GTCA
                                     TC   _  A
GAM1283  KIAA0794  3'  TTGGGAAAAGAAGAAA      81240          CCA
                                TTTCTTCTTT   TCCAG
                                ||||||||||   |||||
                                AAAGAAGAAA   GGGTT
                                      A__
GAM1283  KIAA0998  3'  ACTGAATGAATTTGAAAGGG   31255        TTCT   C  C
                                CCCTTTC    TTC AT CAGT
                                |||||||    ||| || ||||
                                GGGAAAG    AAG TA GTCA
                                    TTT_   _  A
GAM1283  KIAA1391  3'  GGAGAAAGAAGAAAATGG    67852    CC        CA
                                CC  TTTCTTCTTTC  TCC
                                ||  ||||||||||  |||
                                GG  AAAGAAGAAAG  AGG
                                 TA         __
GAM1283  KIAA1656  3'  ACTGAATGGAAAGCAGGAAG   66356       T       C
                                CTTTCT CTTTCCAT CAGT
                                |||||| |||||||| ||||
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                                GAAGGA GAAAGGTA GTCA
                                   C       A
GAM1283 LSM5     3' CTGGAAAAAGAAGAAA      25569          CCA
                                TTTCTTCTTT   TCCAG
                                ||||||||||  |||||
                                AAAGAAGAAA   AGGTC
                                     A__
GAM1283 MCJ      3' ACTGAAGGAAAAAAAAAGAGGG 26017     _   C  C    ATC
                                CCC CTTT TT TTTCC   CAGT
                                ||| |||| || |||||   ||||
                                GGG GAAA AA AAAGG   GTCA
                                  A   _ A    AA_
GAM1283 MGC15606 3' ACTGGCTATCTAAGAAGAATGG 59517    T       TCCAT_
                                CC TTCTTCTT     CCAGT
                                || ||||||||     |||||
                                GG AAGAAGAA     GGTCA
                                 T       TCTATC
GAM1283 MGC20460 5' CTGAAAGGAAAGAAGGAA    54907          ATC
                                TTTCTTCTTTCC   CAG
                                ||||||||||||  |||
                                AAGGAAGAAAGG   GTC
                                      AAA
GAM1283 ORMDL3   3' ACTGAAGACAGAAAGAAGAAG  74796          CA __
                                TTTCTTCTTTC  TC  CAGT
                                ||||||||||  ||  ||||
                                GAAGAAGAAAG  AG  GTCA
                                      AC  AA
GAM1283 PCDH10   5' CTGGAAGGAAAAAGAGA     53101       C    A
                                TTTCTT TTTCC TCCAG
                                |||||| ||||| |||||
                                AGAGAA AAAGG AGGTC
                                   _    A
GAM1283 PCDH10   5' CTGGAAGGAAAAAGAGA     40822       C    A
                                TTTCTT TTTCC TCCAG
                                |||||| ||||| |||||
                                AGAGAA AAAGG AGGTC
                                   _    A
GAM1283 PDCD10   5' CTGGAAGAAGGAAGAGA     24274          CA
                                TTTCTTCTTTC  TCCAG
                                ||||||||||  |||||
                                AGAGAAGGAAG  AGGTC
                                      A_
GAM1283 S164     5' CTGGAAGAAGAGAAAGG     61431       T   CCA
                                CCTTTCT CTTT   TCCAG
                                ||||||| ||||   |||||
                                GGAAAGA GAAG   AGGTC
                                   _   A__
GAM1283 SERHL    3' ACTGGATGGAAAATAAAAGG   97348      CTTC
                                CCTTT    TTTCCATCCAGT
                                |||||    ||||||||||||
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                                GGAAA   AAAGGTAGGTCA
                                  ATA_
GAM1283 SRCRB4D  5' GCTGTGGAAAGAAAAGAAG   55797     C_       TC
                                CTTT  TTCTTTCCA  CAGT
                                ||||  |||||||||  ||||
                                GAAG  AAGAAAGGT  GTCG
                                  AA       __
GAM1283 TED      3' CTGGACAAGAGAAGAGG     32267         CCA
                                TTTCTTCTTT   TCCAG
                                ||||||||||   |||||
                                GGAGAAGAGA   AGGTC
                                      AC_
GAM1283 LOC120105 5' ACTGAATACTGTTAAGAAGGAG 76025         TC  TC___
             G                   CTTTCTTCTT  CA    CAGT
                                ||||||||||  ||    ||||
                                GGAGGAAGAA  GT    GTCA
                                      TT  CATAA
GAM1283 LOC125270 3' ACTGGATGAATTAAAAAGAAA  74865       C  TC__
                                TTTCTT TT    CATCCAGT
                                ||||||  ||    ||||||||
                                AAAGAA AA    GTAGGTCA
                                   A  TTAA
GAM1283 LOC131870 3' ACCAGATGAAAAGAAGGAG    75506         C    CA
                                TTTCTTCTTT CATC  GT
                                |||||||||| ||||  ||
                                GAGGAAGAAA GTAG  CA
                                      A    AC
GAM1283 LOC135293 3' ACTGGGTGTAAGAAGAAA     76675         TC
                                TTTCTTCTT  CATCCAGT
                                |||||||||  ||||||||
                                AAAGAAGAA  GTGGGTCA
                                      T_
GAM1283 LOC135932 5' CGGAGGAAAGGAAAAG       76697      C       A   A
                                CTTT TTCTTTCC TCC G
                                |||| |||||||| ||| |
                                GAAA AGGAAAGG AGG C
                                  _       _   C
GAM1283 LOC143392 5' ACCGGATGGAAATGGGGAGA   83851         _       A
                                TTTCTTC TTTCCATCC GT
                                ||||||| ||||||||| ||
                                AGAGGGG AAAGGTAGG CA
                                     T       C
GAM1283 LOC144811 3' ACTAGATAATGGAAGTAAGAGG 84106     C   T    TTCC   C
             T                   ACC CTT CTTCT    ATC AGT
                                ||| ||| |||||    ||| |||
                                TGG GAA GAAGG    TAG TCA
                                  A   T    TAA_   A
GAM1283 LOC146774 5' GGAAAAGGAAGAAAGGGG    78697            CCA
                                CCCCTTTCTTCTTT   TCC
                                ||||||||||||||   |||
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                                GGGGAAAGAAGGAA   AGG
                                       A__
GAM1283  LOC153077 3'  ACTGAGGTCAGAAAAAAGG   87104      C   TT  ATC
                                CCTTT TTCT  CC   CAGT
                                ||||| ||||  ||   ||||
                                GGAAA AAGA  GG   GTCA
                                   A    CT  A__
GAM1283  LOC154760 5'  CGGAGGAAAGGAAAAG      87453      C       A   A
                                CTTT TTCTTTCC TCC G
                                |||| |||||||| ||| |
                                GAAA AGGAAAGG AGG C
                                  _       _  C
GAM1283  LOC157381 3'  ACTGGATGACAGAGAAAG    87730       T  TTC
                                CTTTCT CT   CATCCAGT
                                |||||| ||   ||||||||
                                GAAAGA GA   GTAGGTCA
                                   _  CA_
GAM1283  LOC166042 5'  ACTGGATGTCCAGAAAAAGAGG 83503    C    C    TTC
                                CC CTTT TTCT   CATCCAGT
                                || |||| ||||   ||||||||
                                GG GAAA AAGA   GTAGGTCA
                                 A    _    CCT
GAM1283  LOC170372 5'  ACTGGCTGGAAAAGAAAGGG   76857         CT    T
                                CCCTTTCTT  TTCCA CCAGT
                                |||||||||  ||||| |||||
                                GGGAAAGAA  AAGGT GGTCA
                                     __     C
GAM1283  LOC197358 3'  ACTGGTGGAGAAAACAAAG    89410      C  C     T
                                CTTT TT TTTCCA CCAGT
                                |||| || |||||| |||||
                                GAAA AA AGAGGT GGTCA
                                  C  A     _
GAM1283  LOC200138 3'  ACTGGATGGCGTTGAAATGAAA 91538      __   TTT_
                                TTTC  TTC    CCATCCAGT
                                ||||  |||    |||||||||
                                AAAG  AAG    GGTAGGTCA
                                  TA   TTGC
GAM1283  LOC200314 3'  ACTGGATGAGAGCAAAAGGG   91585       CTT    C
                                CCCTTT   CTTTC ATCCAGT
                                ||||||   ||||| |||||||
                                GGGAAA   GAGAG TAGGTCA
                                   AC_    _
GAM1283  LOC219287 3'  ACCGGATAACACCAGAAAGAGG 95216     _     TCTTTCC    A
            G                   CCC CTTTCT      ATCC GT
                                ||| ||||||      |||| ||
                                GGG GAAAGA      TAGG CA
                                  A     CCACAA_   C
GAM1283  LOC221814 5'  ACTGGATGTTGTTAGAAAAAG  95553      C    TTC__
                                CTTT TTCT    CATCCAGT
                                |||| ||||    ||||||||
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                                GAAA AAGA    GTAGGTCA
                                  _   TTGTT
GAM1283  LOC222414 3'  CTAGATAGGAGGAAGGAGT   95974    C       TTCC   C
                                AC CCTTTCTTCT   ATC AG
                                || ||||||||||   ||| ||
                                TG GGAAGGAGGA   TAG TC
                                 A       _____  A
GAM1283  LOC51075  3'  ACTGGAGCAAAGAAAGAGA   32553      _   CCA
                                TTTCTT CTTT   TCCAGT
                                |||||| ||||  ||||||
                                AGAGAA GAAA   AGGTCA
                                   A   CG_
GAM1283  LOC90917  3'  CTGGACAGGAGGAAAAGG    64985      CT    CA
                                CCTTT  TCTTTC  TCCAG
                                |||||  ||||||  |||||
                                GGAAA  AGGAGG  AGGTC
                                  __     AC
GAM1283  LOC92979  3'  ATGCCAGAAGAAAGGGG     57251          TTC
                                CCCCTTTCTTCT   CAT
                                ||||||||||||  |||
                                GGGGAAAGAAGA   GTA
                                       CC_
GAM1284  CDH12     3'  CTTATCATTTAAAGTGGTGTA  15777        CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM1284  GOCAP1    3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA       G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM1284  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090      T   AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                  _   GTCA_
GAM1284  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
            A                    TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM1284  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126        CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM1284  HMP19     3'  CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
            TA                    TACA   TCC   GAAGAATAAG
                                ||||   |||   ||||||||||
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                                ATGT   AGG   TTTCTTATTC
                                  AAA_  ATTG
GAM1284 KIAA1719 3' TCTGTCTTGGGAGTGGTGTA  68742           _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                         G
GAM1284 KIAA1853 3' TTTTTCTTGGAAGCAGTG   69929    CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM1284 KIAA1877 3' CTTATTCTTCTGCCATGAGT  66748    CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM1284 KIAA1906 3' CTTATTCTTCTTGACTTTTGG 73571    CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM1284 OSBPL11  3' CTTAATTTCCCAAGAGTGGTG 43206       CCAA   AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                     AACC   A_
GAM1284 YME1L1   3' TCATTCTTGATGTGGTGTA   58438       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   |||||| ||
                                ATGTGGTG   GTTCTT CT
                                     TA_    A
GAM1284 ZNF262   3' CTTATTTTGTTTGGGAGT    18723        A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                     G
GAM1284 LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_    AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
                                ATGTGGTG   GGTTC   TGT
                                     CAA    GG__
GAM1285 MUCDHL   3' CAACTCTGAGGCCACCAAC   41915   GA       A
                                GT  GTGGCCTCA AGTTG
                                ||  ||||||||| |||||
                                CA  CACCGGAGT TCAAC
                                  AC       C
GAM1285 MUCDHL   3' CAACTCTGAGGCCACCAAC   88636   GA       A
                                GT  GTGGCCTCA AGTTG
                                ||  ||||||||| |||||
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                                CA  CACCGGAGT TCAAC
                                 AC        C
GAM1285  FLJ14957  3'  AACCTTGGCTCACTGCA     52801          GGCCT   A
                                TGCAGTGAGT    CAA GTT
                                ||||||||||    ||| |||
                                ACGTCACTCG    GTT CAA
                                      _____  C
GAM1285  FYCO1     3'  TGAAGCCACTCACCAC      44776     CA       C
                                GTG  GTGAGTGGC TCA
                                |||  ||||||||| |||
                                CAC  CACTCACCG AGT
                                  __        A
GAM1285  KIAA1202  3'  TGAGACCACACCACTGCAC   72493        A_   C
                                GTGCAGTG  GTGG CTCA
                                ||||||||  |||| ||||
                                CACGTCAC  CACC GAGT
                                     CA    A
GAM1285  KIAA1784  3'  AACTCTGATGCCACCAC     65736     A    C   A
                                GTG GTGGC TCA AGTT
                                ||| ||||| ||| ||||
                                CAC CACCG AGT TCAA
                                  _    T   C
GAM1285  LANO      3'  GAGACCACGCCACTGCAC     47973        A_   C
                                GTGCAGTG  GTGG CTC
                                ||||||||  |||| |||
                                CACGTCAC  CACC GAG
                                     CG    A
GAM1285  MEGF10    3'  ACTTAGAACACTCACTGCAC   51604          GC  CA
                                GTGCAGTGAGTG  CT  AAGT
                                ||||||||||||  ||  ||||
                                CACGTCACTCAC  GA  TTCA
                                       AA  __
GAM1285  ZNF338    3'  CAACTTTGAGACCACCTCTG   42253     TGA    C
                                CAG   GTGG CTCAAAGTTG
                                |||   |||| ||||||||||
                                GTC   CACC GAGTTTCAAC
                                  TC_    A
GAM1285  LOC113675 5'  AACCTTGGCTCACTGCA     57377          GGCCT   A
                                TGCAGTGAGT    CAA GTT
                                ||||||||||    ||| |||
                                ACGTCACTCG    GTT CAA
                                      _____  C
GAM1286  SCAMP1    3'  GCTAAATAAATATTCTCC     54500     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1286  SCAMP1    3'  GCTAAATAAATATTCTCC     54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
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                                CCT TTATAA TAAATCG
                                  C     A
GAM1286 NX-17    3' TGAATATCAGCCCCTAATA   40706        ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM1286 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
              TA                  TATTAGGGATAATATTCATTTAGC
                                  ||||||||||||||||||||||||
                                  ATAATCCCTATTATAAGTAAATCG

GAM1287 DPYSL3   3' GCTGTCCTTTGCCATCTCA   9126       A      T__
                                TGAGA TGGCAAA   TAGT
                                ||||| |||||||   ||||
                                ACTCT ACCGTTT   GTCG
                                  _      CCT
GAM1287 KIF3C    3' AGGCAACTCCCCATTTTCA   11203        CAAATT   C
                                TGAGAATGG     AGT GCCT
                                |||||||||     ||| ||||
                                ACTTTTACC     TCA CGGA
                                     CC____   A
GAM1287 NR1I2    5' GCGGATATTTGCCACTCTC   15302      A       TAG
                                GAGA TGGCAAAT   TCGC
                                |||| ||||||||   ||||
                                CTCT ACCGTTTA   GGCG
                                  C       TA_
GAM1287 DKFZP434O125 3' ACTAACTTCCATTCTCA     65582         C  A
                                TGAGAATGG AA TTAGT
                                ||||||||| || |||||
                                ACTCTTACC TT AATCA
                                     _ C
GAM1287 KIAA0152  3' GCAGAACTCCATTCTCA     28976        CAAATT  _ _
                                TGAGAATGG     AGT C GC
                                |||||||||     ||| | ||
                                ACTCTTACC     TCA G CG
                                     _______  A A
GAM1287 KIAA1871  3' GCAAATAATTTACCATTTTCA  61904        C     GTC
                                TGAGAATGG AAATTA   GC
                                |||||||| ||||||   ||
                                ACTTTTACC TTTAAT   CG
                                     A     AAA
GAM1287 MAPKAPK3  3' AAGGCGACTGAGCCATGCTCA  17342     A    AAA
                                TGAG ATGGC   TTAGTCGCCTT
                                |||| |||||   ||||||||||
                                ACTC TACCG   AGTCAGCGGAA
                                  G    ___
GAM1287 LOC121457 3' TGACCCCAATTTGCCATTTTCA 74512             A__
                                TGAGAATGGCAAATT   GTCG
                                ||||||||||||||   ||||
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                                ACTTTTACCGTTTAA  CAGT
                                      CCC
GAM1287 LOC151196 5' AAGGTCATTAAATTTGCCACCT 86444     AA       _  C
          CA                    TGAG TGGCAAATT AGT GCCTT
                                |||| ||||||||| ||| |||||
                                ACTC ACCGTTTAA TTA TGGAA
                                  C_       A  C
GAM1287 LOC152343 3' AAGGCGAGTGCCACCATGCTCA 81412     A   CAAAT G
                                TGAG ATGG    TA TCGCCTT
                                |||| ||||    || |||||||
                                ACTC TACC    GT AGCGGAA
                                  G   ACC__ G
GAM1288 CDH12   3' CTTATCATTTAAAGTGGTGTA 15777        CCCAA  GA
                                TACACCACT    GAA ATAAG
                                |||||||||    ||| |||||
                                ATGTGGTGA    TTT TATTC
                                     AA___  AC
GAM1288 GOCAP1  3' ATTGTTCTTGGGAGCAGTGTA 43007     CA       G
                                TACAC CTCCCAAGAA AAT
                                ||||| |||||||||| |||
                                ATGTG GAGGGTTCTT TTA
                                   AC       G
GAM1288 DKFZp434N2435 5' CTTATTACTGTGGGGTGGT   98090      T   AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                  _   GTCA_
GAM1288 DKFZP564I122 3' CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
          A                     TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM1288 FLJ21791  3' CTTATTTGCAGAAGTGGTGTA  62126        CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM1288 HMP19   3' CTTATTCTTTGTTAGGAAAATG 88860     CCAC  CAA_
          TA                    TACA   TCC   GAAGAATAAG
                                ||||   |||   ||||||||||
                                ATGT   AGG   TTTCTTATTC
                                  AAA_  ATTG
GAM1288 KIAA1719  3' TCTGTCTTGGGAGTGGTGTA  68742           _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                          G
GAM1288 KIAA1853  3' TTTTTCTTGGAAGCAGTG   69929    CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
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                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM1288 KIAA1877 3' CTTATTCTTCTGCCATGAGT  66748     CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM1288 KIAA1906 3' CTTATTCTTCTTGACTTTTGG 73571    CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM1288 OSBPL11  3' CTTAATTTCCCAAGAGTGGTG 43206       CCAA   AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                     AACC   A_
GAM1288 YME1L1   3' TCATTCTTGATGTGGTGTA   58438       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                     TA_    A
GAM1288 ZNF262   3' CTTATTTTGTTTGGGAGT    18723        A
                                ACTCCCAAG AGAATAAG
                                |||||||||  ||||||||
                                TGAGGGTTT TTTTATTC
                                      G
GAM1288 LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_   AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
                                ATGTGGTG   GGTTC   TGT
                                     CAA    GG__
GAM1289 H4FB     3' CCTCTACAGTACACTACCG   14514     G  CT
                                CGGT AG  TGCTGTAGAGG
                                ||||  ||  ||||||||||
                                GCCA TC  ATGACATCTCC
                                  _ AC
GAM1289 NLGN2    5' CCTCTACGTGCCCACCGAGGA  89532     A    A  TT  T
                                TCC CGGTG GC  GC GTAGAGG
                                |||  |||||  ||  ||  |||||||
                                AGG GCCAC CG  TG CATCTCC
                                  A    C  __  _
GAM1289 VARS2    3' CAGCGGCTCACCATGGG     21941     C       T
                                TCCA GGTGAGCT GCTG
                                ||||  ||||||||  ||||
                                GGGT CCACTCGG CGAC
                                  A       _
GAM1289 ESPL1    5' CCTCTTGGAGCTCACCTTGGA  25437     C       GCTGT
                                TCCA GGTGAGCTT    AGAGG
                                ||||  |||||||||    |||||
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                                AGGT CCACTCGAG    TCTCC
                                  T       GT___
GAM1289 FLJ11807 3' CCTCCACAGCAGGTCCCTGTGG 46944       T G      A
            A                    TCCACGG GA CTTGCTGT GAGG
                                 ||||||| || |||||||| ||||
                                 AGGTGTC CT GGACGACA CTCC
                                    C _      C
GAM1289 KIAA0515 3' CCTCCCACACAGCTCATCGTG 64547          T C  A_
                                 CACGGTGAGCT G TGT  GAGG
                                 |||||||||| | |||  ||||
                                 GTGCTACTCGA C ACA  CTCC
                                       _ _  CC
GAM1289 KIAA1553 3' CCTCTTTGAGCTCACCATG  93565   C       GCTGT
                                 CA GGTGAGCTT    AGAGG
                                 || |||||||||    |||||
                                 GT CCACTCGAG    TCTCC
                                  A       TT___
GAM1289 KIAA1833 5' CCTCTACCTGGTCAGCACCACC 90752        A_  T  __
            GTGGA                  TCCACGGTG  GCT GCT  GTAGAGG
                                 |||||||||  ||| |||  |||||||
                                 AGGTGCCAC  CGA TGG  CATCTCC
                                      CA  C   TC
GAM1289 PRKWNK4  3' ACACCAGGGCCCACCATGGA  51501    C   A   GC_
                                 TCCA GGTG GCTT   TGT
                                 |||| |||| ||||   |||
                                 AGGT CCAC CGGG   ACA
                                   A   C   ACC
GAM1289 LOC219793 5' ACATCCAAGCTCACCGGGA  93017    A       C_
                                 TCC CGGTGAGCTTG  TGT
                                 ||| ||||||||||  |||
                                 AGG GCCACTCGAAC  ACA
                                   _        CT
GAM1290 ACHE    3' GTTCGACCACTACAGCA    32333    G        T
                                 TGC TGTAGTGGTTG GC
                                 ||| |||||||||| ||
                                 ACG ACATCACCAGC TG
                                   _        T
GAM1290 CARD15   5' CTGCACAAGGCCTACCCGCA  42467    T   TGG
                                 TGCG GTAG   TTGTGCAG
                                 |||| ||||   ||||||||
                                 ACGC CATC   AACACGTC
                                   C   CGG
GAM1290 CD2     3' CTGGGTCTCACTACAAGCA   10093    G      TTG G
                                 TGC TGTAGTGG   T CAG
                                 ||| ||||||||   | |||
                                 ACG ACATCACT   G GTC
                                   A       CT_ G
GAM1290 CXCL16   3' CACATCCAGCCTACACGTA   42162         __  T
                                 TGCGTGTAG  TGG TGTG
                                 |||||||||  ||| ||||
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                                ATGCACATC  ACC ACAC
                                     CG   T
GAM1290  MAPRE2   3'  CTGCACCATGCCACACAC    27332     A    T__
                                GTGT GTGGT   GTGCAG
                                |||| |||||   ||||||
                                CACA CACCG   CACGTC
                                  _    TAC
GAM1290  NBS1     3'  CTGCAATTTCTACTACAGGCA  70025     G      TTG_
                                TGC TGTAGTGG    TGCAG
                                ||| ||||||||    |||||
                                ACG ACATCATC    ACGTC
                                  G       TTTA
GAM1290  NLGN2    3'  CTGCACAACCTGCACACG     89534      A  _
                                CGTGT GT GGTTGTGCAG
                                ||||| || ||||||||||
                                GCACA CG CCAACACGTC
                                  _ T
GAM1290  PIP5K1B  3'  CTGAGCCCCACTACATACA    14525    CG      TT  G
                                TG  TGTAGTGG  GT CAG
                                ||  ||||||||  || |||
                                AC  ACATCACC  CG GTC
                                 AT       C_  A
GAM1290  PMM2     3'  CTGTGTTCACTACACTCA     72560    C       TT TG
                                TG GTGTAGTGG  G  CAG
                                || |||||||||  |  |||
                                AC CACATCACT  T  GTC
                                 T        __ GT
GAM1290  PPP2CA   3'  CTGCACAAGAGCACTGCA     12235       G__
                                TGTAGTG   TTGTGCAG
                                |||||||   ||||||||
                                ACGTCAC   AACACGTC
                                    GAG
GAM1290  RCV1     3'  CTGCACACAAGCCCACAGCAC  12802     A   T____
                                GTGT GTGG    TGTGCAG
                                |||| ||||    |||||||
                                CACG CACC    ACACGTC
                                  A   CGAAC
GAM1290  SLC12A7  3'  CTGCAGCCTCTGCACGCA    22739        T   TG
                                TGCGTGTAG GGT  TGCAG
                                ||||||||| |||  |||||
                                ACGCACGTC CCG  ACGTC
                                     T  __
GAM1290  SPAG6    3'  CACACACACTCGTACATGCA  25847       ___   GT
                                TGCGTGT   AGTG  TGTG
                                |||||||   ||||  ||||
                                ACGTACA   TCAC  ACAC
                                    TGC   AC
GAM1290  TLX1     3'  CTGTGACACACTACACCA    19822    C      _  GT
                                TG GTGTAGTG GTT  GCAG
                                || ||||||| |||  ||||
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                                AC CACATCAC CAG  TGTC
                                 _       A   __
GAM1290 WNT14    3' CTGCACATGGCACAGGCA    14135    G   A  G  T
                                TGC TGT GT GT GTGCAG
                                ||| ||| || || ||||||
                                ACG ACA CG TA CACGTC
                                  G   _  G  _
GAM1290 CUL4A    5' CTGCCCGACAACTACACGCA   14569         G    T
                                TGCGTGTAGT GTTG GCAG
                                |||||||||| |||| ||||
                                ACGCACATCA CAGC CGTC
                                      A    C
GAM1290 DCTD     3' CTGCTCTCCCACTGCACACA   10391    C        TTGT
                                TG GTGTAGTGG    GCAG
                                || |||||||||    ||||
                                AC CACGTCACC    CGTC
                                 A         CTCT
GAM1290 DKFZP564D0462 5' CTGTGTAACCACTTCACACA   71020    C   T      TG
                                TG GTG AGTGGTTG  CAG
                                || ||| ||||||||  |||
                                AC CAC TCACCAAT  GTC
                                 A   T       GT
GAM1290 FLJ20132 3' CTGCACGGCACCCACGCA    35087       TA   G
                                TGCGTG  GTG TTGTGCAG
                                ||||||  ||| ||||||||
                                ACGCAC  CAC GGCACGTC
                                   C_   _
GAM1290 FLJ22002 3' CTGCACACAACTGATACAC   46196      GT   __
                                GTGTA  GGT  TGTGCAG
                                |||||  |||  |||||||
                                CACAT  TCA  ACACGTC
                                   AG   AC
GAM1290 GREAT    3' CTGCACAGAGAGCACAGCA   56374    G   A  GG_
                                TGC TGT GT   TTGTGCAG
                                ||| ||| ||   ||||||||
                                ACG ACA CG   GACACGTC
                                  _   _  AGA
GAM1290 HN1L     3' CTGTGTGACTCTACACACA   58617    C     T   TG
                                TG GTGTAG GGT  TGCAG
                                || |||||| |||  |||||
                                AC CACATC TCA  GTGTC
                                 A     _   GT
GAM1290 KIAA0240 3' CTGTGTCCCACTACACACA   94040    C        TT TG
                                TG GTGTAGTGG  G  CAG
                                || |||||||||  |  |||
                                AC CACATCACC  T  GTC
                                 A        C_ GT
GAM1290 KIAA0998 3' TACAAACAACTACATGCA    31258          GG_
                                TGCGTGTAGT   TTGTG
                                ||||||||||   |||||
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                                ACGTACATCA  AACAT
                                     ACA
GAM1290 KIAA1357 3' CTGTGCAGCCACATACACACA 72432   C   _    TG
                                TG GTGTA GTGGTTG  CAG
                                || ||||| |||||||  |||
                                AC CACAT CACCGAC  GTC
                                 A   A     GT
GAM1290 LCE     3' CTGCATAGATCACACGCA   44259      AGTGG
                                TGCGTGT   TTGTGCAG
                                |||||||   ||||||||
                                ACGCACA   GATACGTC
                                    CTA__
GAM1290 MUC13   3' CTGTGGCCACCAACACACA  53509   C   A_    GT
                                TG GTGT  GTGGTT  GCAG
                                || ||||  ||||||  ||||
                                AC CACA  CACCGG  TGTC
                                 A   AC    __
GAM1290 P101-PI3K 3' CTGCAAACACCACACACACA  27457   C   A   TG_
                                TG GTGT GTGGT  TGCAG
                                || |||| |||||  |||||
                                AC CACA CACCA  ACGTC
                                 A   _    CAA
GAM1290 PAXIP1L  3' CTGCACAGAAGTGCACACA   70672   C   G GG
                                TG GTGTA T  TTGTGCAG
                                || ||||| |  ||||||||
                                AC CACGT G  GACACGTC
                                 A   _ AA
GAM1290 TRPV5   5' CTGCATGCACACACACACA   39523   C   A  GT
                                TG GTGT GTG  TGTGCAG
                                || |||| |||  |||||||
                                AC CACA CAC  GTACGTC
                                 A   _  AC
GAM1290 LOC148046 3' CTGCGTCAGCCACTCACGCA  85246      T     _
                                TGCGTG AGTGGTTG TGCAG
                                |||||| |||||||| |||||
                                ACGCAC TCACCGAC GCGTC
                                    _      T
GAM1290 LOC149134 5' CACACCCAGTGCACAGCA   85516   _   G  T
                                TGC GTGTA TGG TGTG
                                ||| ||||| ||| ||||
                                ACG CACGT ACC ACAC
                                  A   G  C
GAM1290 LOC150889 5' TACGCTCACTGACACGCA   80818      _  GT
                                TGCGTGT AGTG  TGTG
                                ||||||| ||||  ||||
                                ACGCACA TCAC  GCAT
                                    G   TC
GAM1290 LOC152275 3' CTGAATGCCCACTGCACACA  86797   C      TT  G
                                TG GTGTAGTGG  GT CAG
                                || |||||||||  || |||
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                                AC CACGTCACC  TA GTC
                                 A        CG  A
GAM1290  LOC153811 3'  GCATGCCACTACACCCA     81836    C        T
                                TG GTGTAGTGGT GTGC
                                || |||||||||| ||||
                                AC CACATCACCG TACG
                                 C        _
GAM1290  LOC219513 5'  CACACCCACCCACACGCA     95981        A_    T
                                TGCGTGT  GTGG TGTG
                                |||||||  |||| ||||
                                ACGCACA  CACC ACAC
                                    CC    C
GAM1290  LOC220021 5'  CTGCACACCTCACAAGCA     95021     G   AGT   T
                                TGC TGT   GGT GTGCAG
                                ||| |||   ||| ||||||
                                ACG ACA   CCA CACGTC
                                  A  CT_  _
GAM1290  LOC254557 5'  CTGCACAGTGCGCACGCGCA   97979        A  _
                                TGCGTGT GTG GTTGTGCAG
                                ||||||| ||| |||||||||
                                ACGCGCA CGC TGACACGTC
                                    _  G
GAM1290  LOC256346 5'  CTGCAACATCCTACATGCA    99321         T   TG
                                TGCGTGTAG GGT  TGCAG
                                ||||||||| |||  |||||
                                ACGTACATC CTA  ACGTC
                                      _  CA
GAM1290  LOC257200 3'  CTGCACCTTCACCACCACAC   97368      A    T___
                                GTGT GTGGT    GTGCAG
                                |||| |||||    ||||||
                                CACA CACCA    CACGTC
                                  C    CTTC
GAM1291  CD83     3'  GGTGAGATGCAGCTGGAAAA   16171       T   A    GG
                                TTTTCC AGCT CATCT  TACC
                                |||||| |||| |||||  ||||
                                AAAAGG TCGA GTAGA  GTGG
                                   _   C    __
GAM1291  DSPG3    3'  ACCAGATGAGTTAGGAA     60814         A
                                TTCCTAGCT CATCTGGT
                                ||||||||| ||||||||
                                AAGGATTGA GTAGACCA
                                      _
GAM1291  IL1RAP   3'  CCAAATGTAGCTAAAAAAA    57070      CC       C
                                TTTT  TAGCTACAT TGG
                                ||||  ||||||||| |||
                                AAAA  ATCGATGTA ACC
                                  AA        A
GAM1291  OAS3     3'  TACACACGCAATAGCTAGGAAA 21656           CATC_ _
            A                    TTTTCCTAGCTA     TG GTA
                                ||||||||||||     || |||
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                                AAAAGGATCGAT    AC CAT
                                     AACGC  A
GAM1291  PLS3     3'  TACATCGTAGCTAGAAGA    18526      C      ATCTG
                                TTTTC TAGCTAC    GTA
                                ||||| |||||||    |||
                                AGAAG ATCGATG    CAT
                                   _     CTA__
GAM1291  CED-6    3'  AGGTACATTTTCACTAGGAAAA 33316         CTACATCTG
                                TTTTCCTAG       GTACCT
                                |||||||||       ||||||
                                AAAAGGATC       CATGGA
                                     ACTTTTA__
GAM1291  DKFZP566F2124 3'  AGATTCATAGCTAGGAAA    32214          C__
                                TTTCCTAGCTA   ATCT
                                ||||||||||   ||||
                                AAAGGATCGAT   TAGA
                                     ACT
GAM1291  FBXO24   3'  AGATACGGGCAGCTAGGAA   25146        ACAT  G   C
                                TTCCTAGCT    CT GTA CT
                                |||||||||    || ||| ||
                                AAGGATCGA    GG CAT GA
                                     C___  G   A
GAM1291  FLJ10895 3'  GGTACCAGCACCAGGAAGA   39359       AGCTACAT
                                TTTTCCT       CTGGTACC
                                |||||||       ||||||||
                                AGAAGGA       GACCATGG
                                    CCAC____
GAM1291  FLJ11996 3'  AGGTGCCTACAGGTAGGAAAA  47055        G  ACATCT
                                TTTTCCTA CT     GGTACCT
                                |||||||| ||     |||||||
                                AAAAGGAT GA     CCGTGGA
                                     G  CAT___
GAM1291  KIAA0433 3'  AGGTACCAGATGTAAGAG    31499    AGC
                                CT   TACATCTGGTACCT
                                ||   ||||||||||||||
                                GA   ATGTAGACCATGGA
                                 GA_
GAM1291  KIAA1110 3'  CAGATGTAAGCAAGAAAA    62499      CTA   _
                                TTTTC   GCT ACATCTG
                                |||||   ||| |||||||
                                AAAAG   CGA TGTAGAC
                                   AA_   A
GAM1291  PSR      3'  CAGGTGTAACCAGGAAAA    65779       AGC
                                TTTTCCT   TACATCTG
                                |||||||   ||||||||
                                AAAAGGA   ATGTGGAC
                                    CCA
GAM1291  SYTL2    3'  AGATATTTGAACAAGCTAGGAA 53076          ACA  TG   C
             AA                   TTTTCCTAGCT   TC  GTA CT
                                ||||||||||   ||  ||| ||
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                                AAAAGGATCGA   AG  TAT GA
                                      ACA  TT   A
GAM1291  TA-KRP    3'  AGGTACCAGATGAATCAGGA   51670     AGCTA
                                TCCT    CATCTGGTACCT
                                ||||    ||||||||||||
                                AGGA    GTAGACCATGGA
                                  CTAA_
GAM1291  LOC139767 5'  AGGTACCAGATGCCATAG    76367     GCTA
                                CTA   CATCTGGTACCT
                                |||   ||||||||||||
                                GAT   GTAGACCATGGA
                                  ACC_
GAM1291  LOC147080 3'  GTATAAGCAGGTAGGAAAA   85048       G  ACAT  G
                                TTTTCCTA CT   CT GTAC
                                |||||||| ||   || ||||
                                AAAAGGAT GA   GA TATG
                                     G  C___  A
GAM1291  LOC199918 3'  ACCTTGTATAAATAGGAAAA  91474       GC__   TCT
                                TTTTCCTA   TACA  GGT
                                ||||||||   ||||  |||
                                AAAAGGAT   ATGT  CCA
                                     AAAT   T__
GAM1291  LOC257428 5'  ACAACGTGAAGCTAGGAAAA  95929         A  CTG
                                TTTTCCTAGCT CAT  GT
                                ||||||||||| |||  ||
                                AAAAGGATCGA GTG  CA
                                      A  CAA
GAM1292  CAMLG     3'  TCAGAATTGGAACTTTTTA   10007        G  TC
                                TAAGAAGTT TCA  ATTCTGA
                                ||||||||| |||  |||||||
                                ATTTTTCAA GGT  TAAGACT
                                          _  __
GAM1292  CCNT2     3'  ATTCAGAATGACACCATATTCT 55247      GT  TCA
            TA                    TAAGAA  TG   TCATTCTGAAT
                                ||||||  ||   ||||||||||
                                ATTCTT  AC   AGTAAGACTTA
                                   AT  CAC
GAM1292  E2F3      3'  TCAGGGAGACCACTTCT     10472       T  A  AT
                                AGAAGT GTC TC  TCTGA
                                |||||| ||| ||  |||||
                                TCTTCA CAG AG  GGACT
                                   C  _ __
GAM1292  GAS11     3'  TCGGGATGACACCCCTTA    9432      AA  T    ATT
                                TAAG  GT GTCATC   CTGA
                                ||||  || ||||||   ||||
                                ATTC  CA CAGTAG   GGCT
                                  CC  _     ____
GAM1292  SACS      3'  TCAAAATGGTGGCAGTTCTTA 96587       G        C
                                TAAGAA TTGTCATCATT TGA
                                |||||| |||||||||| |||
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                                ATTCTT GACGGTGGTAA ACT
                                  _        A
GAM1292 UTY      3' ATTCAGAATGATAACCTCTTTT 24063      TT  C
                                AGAAG  GT ATCATTCTGAAT
                                |||||  || ||||||||||||
                                TTTTC  CA TAGTAAGACTTA
                                   TC  A
GAM1292 KIAA0459 3' ATTCAGAATGACAAGTTTCCTT 61645     __ G     CAT
             A                   TAAG  AA TTGTCAT   TCTGAAT
                                ||||  || |||||||   |||||||
                                ATTC  TT AACAGTA   AGACTTA
                                  CT  G     ___
GAM1292 KIAA1344 3' TCAGAATGATATTTATATTTTA 72869      A  TGTC
                                TAAGA GT    ATCATTCTGA
                                |||||  ||    ||||||||||
                                ATTTT TA    TAGTAAGACT
                                   A  TTTA
GAM1292 KIAA1946 3' ATTCAATGTGAACAACTTTTTA 83356         CA   TC
                                TAAGAAGTTGT  TCAT  TGAAT
                                ||||||||||  ||||  |||||
                                ATTTTTCAACA  AGTG  ACTTA
                                      __    TA
GAM1292 RNF8     3' ATTCAGAGAAAGAAACTTC   15560      G  ATCA
                                GAAGTT TC    TTCTGAAT
                                ||||||  ||    ||||||||
                                CTTCAA AG    GAGACTTA
                                   _ AAA_
GAM1292 ST7L     3' CAGAATGACTAAAACATCTTA  35337      A   GTCA
                                TAAGA GTT    TCATTCTG
                                |||||  |||    ||||||||
                                ATTCT CAA    AGTAAGAC
                                   A   AATC
GAM1292 ST7L     3' CAGAATGACTAAAACATCTTA  57814      A   GTCA
                                TAAGA GTT    TCATTCTG
                                |||||  |||    ||||||||
                                ATTCT CAA    AGTAAGAC
                                   A   AATC
GAM1292 ST7L     3' CAGAATGACTAAAACATCTTA  58281      A   GTCA
                                TAAGA GTT    TCATTCTG
                                |||||  |||    ||||||||
                                ATTCT CAA    AGTAAGAC
                                   A   AATC
GAM1292 UGTREL7  3' TCAGAACACTGGCAGTTC    31397     G     TCA
                                GAA TTGTCA   TTCTGA
                                |||  ||||||   ||||||
                                CTT GACGGT   AAGACT
                                  _     CAC
GAM1292 LOC132235 5' ATTCAGAATGATGTTTCGGTTC 76661      GTTGT_
             TT                   AAGAA     CATCATTCTGAAT
                                |||||     ||||||||||||
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                                TTCTT     GTAGTAAGACTTA
                                   GGCTTT
GAM1292  LOC153856 3'  TCAGAACAGTATAACTTCT   81874         C  CA
                                AGAAGTTGT AT  TTCTGA
                                ||||||||| ||  ||||||
                                TCTTCAATA TG  AAGACT
                                      _  AC
GAM1293  DLEC1     3'  CATCTGGCCCTCCCTTG     96278       A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                   C    G  _
GAM1293  PIP5K1A   3'  TATCCCACCCTGCCTTGATA   14520         A   CA  C
                                TATCAAGG AGGG  GG GTG
                                |||||||| ||||  || |||
                                ATAGTTCC TCCC  CC TAT
                                     G   A_  C
GAM1293  SOX11     3'  ACCCACCCCCCCTTGGTA    13308         AA   CA  C
                                TATCAAGG  GGG  GG GT
                                ||||||||  |||  || ||
                                ATGGTTCC  CCC  CC CA
                                     CC   A_  _
GAM1293  CHL1      3'  TGTTACCTTTCCTCAATA    22768     CA       CA
                                TAT  AGGAAGGG  GGCG
                                |||  ||||||||  ||||
                                ATA  TCCTTTCC  TTGT
                                  AC       A_
GAM1293  EPB41L1   3'  CATTCTGCCCTTCCCTGA    71104     A         C
                                TCA GGAAGGGCAGG GTG
                                ||| ||||||||||| |||
                                AGT CCTTCCCGTCT TAC
                                  C         _
GAM1293  FLJ00060  3'  CATACCCCCTGCCCTCCTCTGA 61741     _   A      CGTG
                                TCA AGGA GGGCAGG    ATG
                                ||| |||| |||||||    |||
                                AGT TCCT CCCGTCC    TAC
                                  C   _      CCCA
GAM1293  FLJ10898  5'  CACCACAGCCCTTTCTCAATA  60126     CA       AGGC
                                TAT  AGGAAGGGC    GTG
                                |||  |||||||||    |||
                                ATA  TCTTTCCCG    CAC
                                  AC        ACAC
GAM1293  FLJ22557  3'  ATCATCCCATCCTTAATA    45581     C    A   CAGGC
                                TAT AAGGA GGG     GTGAT
                                ||| ||||| |||     |||||
                                ATA TTCCT CCC     TACTA
                                  A    A  _____
GAM1293  KIAA0574  3'  CATCCCCTGCCCTCCCCTGA   69808     A  A      CGT
                                TCA GG AGGGCAGG   GATG
                                ||| || ||||||||   ||||
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                                AGT CC TCCCGTCC   CTAC
                                  C  C       C__
GAM1293  KIAA0632  3'  CACCTCAGAAACCCTTCCTTGA 32071          CA___  C
                                TCAAGGAAGGG    GG GTG
                                ||||||||||    || |||
                                AGTTCCTTCCC    CT CAC
                                     AAAGA  C
GAM1293  KIAA1045  3'  CATCACATGTCCTTCC      71599         GGC
                                GGAAGGGCA   GTGATG
                                |||||||||   ||||||
                                CCTTCCTGT   CACTAC
                                     A__
GAM1293  KIAA1354  5'  CAGTGACTGCCTTCCCTTGATA 61572        A      G  _
                                TATCAAGG AGGGCAG CG TG
                                |||||||| ||||||| || ||
                                ATAGTTCC TTCCGTC GT AC
                                     C      A  G
GAM1293  MGC20460  5'  CACCGCCTCCTACCCTTCTT   54901        C___    _
                                AGGAAGGG    AGGCG TG
                                ||||||||    ||||| ||
                                TTCTTCCC    TCCGC AC
                                     ATCC     C
GAM1293  LOC158476 3'  CACGCCCGCCCCCCCCATTGA  88186     _ AA_   A
                                TCAA GG   GGGC GGCGTG
                                |||| ||   |||| ||||||
                                AGTT CC   CCCG CCGCAC
                                  A  CCC    C
GAM1293  LOC90459  3'  CACACCCGCCTAATTTTTG   63550       A_   A  C
                                CAAGGA  GGGC GG GTG
                                ||||||  |||| || |||
                                GTTTTT  TCCG CC CAC
                                   AA    C  A
GAM1294  ACATN     5'  GACTGGCTCCCGGCTTCAG   17596        AGTG   CA   A
                                TTGAAGCC    GGG  CCA TC
                                ||||||||    |||  ||| ||
                                GACTTCGG    CCC  GGT AG
                                     _____   TC   C
GAM1294  B3GALT2   3'  GTGTCTCAGGCTCAA       15032      A   AG
                                TTGA GCC  TGGGGCAC
                                |||| |||  ||||||||
                                AACT CGG  ACTCTGTG
                                  _   __
GAM1294  CD164     3'  GGACTAGTGCAGAGGCTTTAA  21197        AGTGGG    CAA
                                TTGAAGCC     GCAC   TCC
                                ||||||||     ||||   |||
                                AATTTCGG     CGTG   AGG
                                     AGA___    ATC
GAM1294  DRG2      3'  TGGTTAGTGGCTTCAA      9131          G  GGGC
                                TTGAAGCCA TG    ACCA
                                |||||||| ||    ||||
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                                AACTTCGGT AT    TGGT
                                     G _____
GAM1294  HPS4     3'  ATTGGTGCCACAAGCTTC    42226       CAG  G
                                GAAGC   TG GGCACCAAT
                                ||||||   || |||||||||
                                CTTCG   AC CCGTGGTTA
                                   A__  A
GAM1294  SDPR     5'  GACTGGTGCCCTGAGCTCCAA  17400     A   CAG         A
                                TTG AGC   TGGGGCACCA TC
                                ||| |||   |||||||||| ||
                                AAC TCG   GTCCCGTGGT AG
                                  C   A__         C
GAM1294  C5orf6   3'  GATTGGCTGTGCCAGCTTC    33954       CAG   G   _
                                GAAGC   TGG GCA CCAATC
                                ||||||   ||| ||| ||||||
                                CTTCG   ACC TGT GGTTAG
                                   ___   G   C
GAM1294  C8orf17  3'  GGACCACACTGGCTGCAA     39998     A       G  CA
                                TTG AGCCAGTG GG  CC
                                ||| ||||||||  ||  ||
                                AAC TCGGTCAC CC  GG
                                  G       A  A_
GAM1294  CABP5    5'  GACTGGTGCCCTGCGAGCTCCA 39562     A   CA TG       A
                                TG AGC  G  GGGCACCA TC
                                || |||  |  ||||||||  ||
                                AC TCG  C  CCCGTGGT AG
                                 C   AG GT       C
GAM1294  FLJ13940 3'  GGACTGGTGCCCCACAGGCTTT 47309          A         A
            AA                    TTGAAGCC GTGGGGCACCA TCC
                                ||||||||  ||||||||||  |||
                                AATTTCGG CACCCCGTGGT AGG
                                     A          C
GAM1294  KCNMB2   3'  ATTGGTGGACTGGTTTCAA   20684           GGGG
                                TTGAAGCCAGT    CACCAAT
                                ||||||||||    |||||||
                                AACTTTGGTCA    GTGGTTA
                                       G___
GAM1294  KIAA0530 3'  GATTGGTGTATAGCTTTAA   71431        CAGTGGG
                                TTGAAGC      GCACCAATC
                                |||||||      |||||||||
                                AATTTCG      TGTGGTTAG
                                    ATA_____
GAM1294  KIAA1522 3'  GGATTGGCCTTCCTGTGCCTCA 65607      A _   TG    AC
            A                     TTGA GC CAG  GGGC  CAATCC
                                ||||  ||  |||  ||||  ||||||
                                AACT CG GTC  TCCG  GTTAGG
                                  C  T   CT   __
GAM1294  KIAA1853 3'  GGATGCCCCACTAGTCCAA    69924     AA  C        _
                                TTG  GC AGTGGGGCA CC
                                |||  ||  |||||||||  ||
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                                AAC  TG TCACCCCGT GG
                                  C_  A       A
GAM1294  LOXL4    3'  GATTGGTCTAAACTTCAA    50859      CCAG   GGC
                                TTGAAG   TGG   ACCAATC
                                ||||||   |||   |||||||
                                AACTTC   ATC   TGGTTAG
                                   AA__   ___
GAM1294  LSR7     5'  GGACCGGCCCTGCCCCCGGCTT 38280        AGT    ___  AA
              CAA                  TTGAAGCC   GGGGCA   CC  TCC
                                |||||||   ||||||   ||  |||
                                AACTTCGG   CCCCGT   GG  AGG
                                    C__     CCC  CC
GAM1294  PLK      3'  GGACTGGTGCCCTCCTCACT   18525    CC  TG      A
                                AG  AG  GGGCACCA TCC
                                ||  ||  |||||||| |||
                                TC  TC  CCCGTGGT AGG
                                 AC  CT       C
GAM1294  STK22D   3'  GGTCCCCACTGGCCGCAA    50145     AA        C
                                TTG  GCCAGTGGGG ACC
                                |||  |||||||||| |||
                                AAC  CGGTCACCCC TGG
                                  GC        _
GAM1294  LOC124871 3'  TGCTGCCCCACCAGCTTCAG   74818        CA       C
                                TTGAAGC  GTGGGGCA CA
                                |||||||  |||||||| ||
                                GACTTCG  CACCCCGT GT
                                    AC       C
GAM1294  LOC157349 3'  GACTGGCTGCTGGCTCCGA   82341     A     TG GGCA   A
                                TTG AGCCAG  G    CCA TC
                                ||| ||||||  |    ||| ||
                                AGC TCGGTC  C    GGT AG
                                  C     GT _____   C
GAM1294  LOC222550 5'  GGATCAATATCGTGCTGGCTT  96018         G  CACCA
                                AAGCCAGTG GG     ATCC
                                |||||||||  ||     ||||
                                TTCGGTCGT CT     TAGG
                                     G  ATAAC
GAM1295  SCAMP1   3'  GCTAAATAAATATTCTCC    54500     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1295  SCAMP1   3'  GCTAAATAAATATTCTCC    54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1295  NX-17    3'  TGAATATCAGCCCCTAATA   40706         ATA_
                                TATTAGGG    ATATTCA
                                ||||||||    |||||||
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                                ATAATCCC    TATAAGT
                                    CGAC
GAM1295  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
             TA                   TATTAGGGATAATATTCATTTAGC
                                  ||||||||||||||||||||||
                                  ATAATCCCTATTATAAGTAAATCG

GAM1296  COL15A1   3'  AGGCCAGATTCTGCCACTGC   10257      AAGT  TT_
                                  GCAGT    GT   ATCTGGCCT
                                  |||||    ||   |||||||||
                                  CGTCA    CG   TAGACCGGA
                                     C___  TCT
GAM1296  CSN10     5'  AGGCCAACTCAACCTACTGCCA 19054        A T   TATC
                                  TGGCAGTA G GTT    TGGCCT
                                  |||||||| | |||    ||||||
                                  ACCGTCAT C CAA    ACCGGA
                                      _ _   CTCA
GAM1296  FBLN1     3'  GGCCAAATCATTGCTGCCA    22414        G  TTTATC
                                  TGGCAGTAA TG     TGGCC
                                  |||||||||  ||     |||||
                                  ACCGTCGTT AC     ACCGG
                                       _  TAA___
GAM1296  FMOD      3'  AGGCCAGACTTTGCTTACCATC 10670     CA      TTTA
             A                     TGG  GTAAGTG    TCTGGCCT
                                   |||  |||||||    ||||||||
                                   ACT  CATTCGT    AGACCGGA
                                     AC      TTC_
GAM1296  PTGES     3'  GGCCAGGGGACCCCTGCCA    18065       TAAGT    A
                                   TGGCAG     GTTT TCTGGCC
                                   ||||||     |||| |||||||
                                   ACCGTC     CAGG GGACCGG
                                      CC___    _
GAM1296  CPXCR1    3'  AGGCCAGACAAAGTTCTACCA  53505     C  TAAG_  TTTA
                                   TGG AG     TG    TCTGGCCT
                                   ||| ||     ||    ||||||||
                                   ACC TC     AC    AGACCGGA
                                     A  TTGAA  _____
GAM1296  DKFZp761A132 3'  AGGCCAGGTCAACCCACACCA  51164     CA  AAGT   T
                                   TGG  GT    GTT ATCTGGCCT
                                   |||  ||    ||| |||||||||
                                   ACC  CA    CAA TGGACCGGA
                                     A_  CC__   C
GAM1296  DKFZp761F2014 3'  AGAAAACAGTTACTGCCA    39935         G    A
                                   TGGCAGTAA TGTTT TCT
                                   |||||||||  ||||| |||
                                   ACCGTCATT ACAAA AGA
                                        G    _
GAM1296  FLJ14871  3'  CCAGATGGGCGTCACCCCA   52729     CA  AAG
                                   TGG  GT   TGTTTATCTGG
                                   |||  ||   ||||||||||
```

```
                                ACC  CA   GCGGGTAGACC
                                  C_  CT_
GAM1296  PMF1     3'  AGGCCAGAGCAAGCCTCACTGC 24283        A  T    A_
              CA                    TGGCAGT AG GTTT  TCTGGCCT
                                ||||||| || ||||  ||||||||
                                ACCGTCA TC CGAA  AGACCGGA
                                    C  _    CG
GAM1296  ZFP67    3'  AGGCCGGGGACACCCATGCCA 32425      GTAA    TA
                                TGGCA   GTGTT  TCTGGCCT
                                |||||   |||||  ||||||||
                                ACCGT   CACAG  GGGCCGGA
                                  ACC_    __
GAM1296  LOC151720 5'  GCCAAATACTTACAGCCA    81155     A       TATC
                                TGGC GTAAGTGTT   TGGC
                                |||| |||||||||   ||||
                                ACCG CATTCATAA   ACCG
                                  A       _____
GAM1296  LOC153577 5'  AGATAAAACATTTACCACCA   87235     CA       _
                                TGG  GTAAGTGTTT ATCT
                                |||  ||||||||||| ||||
                                ACC  CATTTACAAA TAGA
                                  AC        A
GAM1297  ACTB     3'  GTTACACCCTTTCTTGA     8466          CAGGC
                                TCAAGGAAGGG    GTGAT
                                ||||||||||    |||||
                                AGTTCTTTCCC    CATTG
                                      A_____
GAM1297  AF1Q     3'  GTCTCTTGCTTTTTTTTGAT   23333           CGT   G
                                ATCAAGGAAGGGCAGG   GAT
                                ||||||||||||||||   |||
                                TAGTTTTTTTTCGTTC   CTG
                                        T__
GAM1297  ARCN1    3'  TGTCACAGAGACATTCTTTGAT 9760          GGGCAGGC
              A                   TATCAAGGAA       GTGATG
                                ||||||||||       ||||||
                                ATAGTTTCTT       CACTGT
                                     ACAGAGA_
GAM1297  ATP8B2   3'  CTTTCCTCTTCTTTGATA    65834          _  C
                                TATCAAGGAAG GG AGG
                                |||||||||| || |||
                                ATAGTTTCTTC CC TTC
                                      T  T
GAM1297  BZRP     3'  CATCACGCTTGTGATGTGGTG  24601      AGGAAGG
                                TATCA      GCAGGCGTGATG
                                |||||      ||||||||||||
                                GTGGT      TGTTCGCACTAC
                                  GTAG___
GAM1297  C4orf1   3'  TTTCAAAGTCTGTCTTTCCTT  60228           G_   TG
                                AAGGAAGGGCAGGC  TGA
                                ||||||||||||| |||
```

```
                                TTCCTTTCTGTCTG ACT
                                      AA  TTG
GAM1297 C8orf1   3' CATTTTCTTTTCTTTTTTTGGT 16344          C  CGT
             A                    TATCAAGGAAGGG AGG  GATG
                                  ||||||||||||| |||  ||||
                                  ATGGTTTTTTTCT TTC  TTAC
                                        T  TT_
GAM1297 CETN1    3' TTTGTCACTTCTTTGGTG    96971          _
                                  TATCAAGGAAG GGCAGG
                                  |||||||||||| ||||||
                                  GTGGTTTCTTC CTGTTT
                                       A
GAM1297 CLN2     3' ATCTCGTTTCTTCTTGGTA   6363        G   CAG  T
                                  TATCAAG AAGGG  GCG GAT
                                  ||||||| |||||  ||| |||
                                  ATGGTTC TTCTT  TGC CTA
                                     _   ___  T
GAM1297 CNGB3    3' TATTGTGTTTAATTTCTTCTTT 39390          C__   TG
             GG                    TCAAGGAAGGG  AGGCG  ATG
                                  ||||||||||  |||||  |||
                                  GGTTTCTTCTT  TTTGT  TAT
                                       TAA   GT
GAM1297 CPD      3' TATTATGTCTGTCTTATC    8952    A
                                  GG AGGGCAGGCGTGATG
                                  || ||||||||||||||
                                  CT TTCTGTCTGTATTAT
                                   A
GAM1297 CXADR    3' CCTTTCCTTTTTTTGATA    9029          C_
                                  TATCAAGGAAGGG  AGG
                                  ||||||||||||  |||
                                  ATAGTTTTTTTCC  TCC
                                        TT
GAM1297 CXCL6    3' TGTCATGTTGGTTTTTGGTA  12980         AG  _
                                  TATCAAGGA  GGCA GGCG
                                  |||||||||  |||| ||||
                                  ATGGTTTTT  TTGT CTGT
                                      GG   A
GAM1297 DAPP1    3' CGTTGCTGCCCTTCCATGATG  27682      A       __
                                  TATCA GGAAGGGCAG  GCG
                                  ||||| ||||||||||  |||
                                  GTAGT CCTTCCCGTC  TGC
                                    A        GT
GAM1297 DCK      3' TTTTTTAGTTTGTTTTTGTTTG 7633        G       GTGATG
             GTA                   TATCAAG AAGGGCAGGC
                                  ||||||| ||||||||||
                                  ATGGTTT TTTTTGTTTG
                                     G        ATTTTTTT
GAM1297 DMD      3' CATTGCGTTATTTTCTTTTTCC 5462      C       CA____   TG
             TTTATA                 TAT AAGGAAGGG     GGCG  ATG
                                  ||| |||||||||     ||||  |||
```

```
                                ATA TTCCTTTTT     TTGC  TAC
                                  T       CTTTTA    GT
GAM1297  DMD     3'  CATTGCGTTATTTTCTTTTTCC 5463      C       CA____    TG
              TTTATA                  TAT AAGGAAGGG     GGCG  ATG
                                ||| |||||||||     ||||  |||
                                ATA TTCCTTTTT     TTGC  TAC
                                  T       CTTTTA    GT
GAM1297  DPP6    3'  CATCCTTGTCCTCCTTGGTA   56319         A      C
                                TATCAAGGA GGGCAGG GTG
                                ||||||||| ||||||| |||
                                ATGGTTCCT CCTGTTC TAC
                                      _      C
GAM1297  DSCR1   3'  TTTGTACTTGTTCTTTTCTGGT 16624       AG        CG   TG
              A                   TATCA  GAAGGGCAGG  TGA
                                |||||  ||||||||||  |||
                                ATGGT  TTTCTTGTTC  GTT
                                   CT        AT   TT
GAM1297  EIF4A2  3'  CATTGTGCTTCTTTCTTTGG   10503          CA    TG
                                TCAAGGAAGGG  GGCG  ATG
                                ||||||||||  ||||  |||
                                GGTTTCTTTCT  TCGT  TAC
                                      __    GT
GAM1297  EIF4E   3'  TATTATGTCCTCTTTTGTGGTG 10505       AG     CA
                                TATCA  GAAGGG  GGCGTGATG
                                |||||  ||||||  |||||||||
                                GTGGT  TTTCTC  CTGTATTAT
                                   GT     __
GAM1297  ELMO2    3'  TGCTTTTGTCTTTTTTGATG   42244        G      __
                                TATCAAG AAGGGCA  GGCG
                                |||||||  |||||||  ||||
                                GTAGTTT TTTCTGT  TCGT
                                      _      TT
GAM1297  EMP1    3'  TGTTATGCCATGATTTTTGGTA 9241          AGGG  _
                                TATCAAGGA    CA GGCGTGATG
                                |||||||||    ||  |||||||||
                                ATGGTTTTT    GT CCGTATTGT
                                      A___  A
GAM1297  ENTPD6   3'  AGTGTGTTTGCTCTTCCTTGG  8805              GT ATG
                                TCAAGGAAGGGCAGGC  G
                                ||||||||||||||||  |
                                GGTTCCTTCTCGTTTG  T
                                         TG GAG
GAM1297  F8      3'  CATCAGTCCTGCATTTCTTTGG 5526           G    CG
              TG                    TATCAAGGAAG GCAGG  TGATG
                                ||||||||||| |||||  |||||
                                GTGGTTTCTTT CGTCC  ACTAC
                                      A    TG    T
GAM1297  FCMD    3'  TCTAGCCTTTCCTAGATG    23046      A       _
                                TATC AGGAAGGGC AGG
                                |||| ||||||||| |||
```

```
                                GTAG TCCTTTCCG TCT
                                  A       A
GAM1297  FE65L2   3'  TGTCTTCTCTTTTCTTGATG   21297          _ C
                                TATCAAGGAAGG G AGGCG
                                |||||||||||| | |||||
                                GTAGTTCTTTTC C TCTGT
                                      T T
GAM1297  FE65L2   3'  TGTCTTCTCTTTTCTTGATG   56520          _ C
                                TATCAAGGAAGG G AGGCG
                                |||||||||||| | |||||
                                GTAGTTCTTTTC C TCTGT
                                      T T
GAM1297  FEZ1     3'  TGTTTTGTTTTGTTTTTTTTTG 18791            _ TGATG
            A                    TCAAGGAAGGGCAGG CG
                                |||||||||||||| ||
                                AGTTTTTTTTTGTTT GT
                                       T  TTTGT
GAM1297  FGF1     3'  CATTGTGCTTGGCCCCTGGTA  53639      A  AA  G     TG
                                TATCA GG  GG CAGGCG  ATG
                                ||||| ||  || ||||||  |||
                                ATGGT CC  CC GTTCGT  TAC
                                  _ __  G     GT
GAM1297  FGF1     3'  CATTGTGCTTGGCCCCTGGTA  53640      A  AA  G     TG
                                TATCA GG  GG CAGGCG  ATG
                                ||||| ||  || ||||||  |||
                                ATGGT CC  CC GTTCGT  TAC
                                  _ __  G     GT
GAM1297  FUT1     3'  CATTATGCCTGGCTAATTTTTG 5586        A_  G
                                CAAGGA  GG CAGGCGTGATG
                                ||||||  || ||||||||||
                                GTTTTT  TC GTCCGTATTAC
                                   AA  G
GAM1297  GCNT2    3'  GTCTTGCTGTTTCTTGATG   9456           G    _
                                TATCAAGGAA GGCAGG C
                                |||||||||| |||||| |
                                GTAGTTCTTT TCGTTC G
                                      G     T
GAM1297  GEMIN5   3'  TGTCATGCTTGTTTGAGATGGA 90647    AAGGAA
                                TC     GGGCAGGCGTGATG
                                ||     |||||||||||||
                                AG     TTTGTTCGTACTGT
                                 GTAGAG
GAM1297  GNA11    3'  TGTGTGTTTTTACCTTGGTG   10817        _     G
                                TATCAAGG AAGGGCA GCG
                                |||||||| ||||||| |||
                                GTGGTTCC TTTTTGT TGT
                                     A      G
GAM1297  GNRH2    5'  CATCCACAGCTCTTCCTTGA   9477           A__  C
                                TCAAGGAAGGGC   GG GTG
                                ||||||||||||   || |||
```

```
                                AGTTCCTTCTCG  CC TAC
                                      ACA  _
GAM1297  GRIA1    3'  CCTTTTCCTTTTTTGATG    7711            C_
                                TATCAAGGAAGGG  AGG
                                |||||||||||||  |||
                                GTAGTTTTTTCCT  TCC
                                      TT
GAM1297  HIF1A    3'  CATTAATGCTCTTTTTTAGTA  9514      C         GGC
                                TAT AAGGAAGGGCA  GTG
                                ||| ||||||||||  |||
                                ATG TTTTTTCTCGT  TAC
                                  A         AAT
GAM1297  HIS1     3'  GTTTTCTTTCTTGATG      22341           GC
                                TATCAAGGAAGG  AGGC
                                ||||||||||||  ||||
                                GTAGTTCTTTCT  TTTG
                                      __
GAM1297  HLCS     3'  TTGTCGTTTTCTTTGGTG    6423            __
                                TATCAAGGAAG  GGCAG
                                ||||||||||  |||||
                                GTGGTTTCTTT  CTGTT
                                      TG
GAM1297  HMGN1    3'  ATTTGCTGGTTGTTTATTTTTT 18301          _     G _ TG TG
            GGTA                    TATCAAGGAA GGGCAG C G  A
                                ||||||||| |||||| | |  |
                                ATGGTTTTTT TTTGTT G C  T
                                      A     G T GT TAC
GAM1297  HTR4     3'  CGTCCACTTGCTCTTCCTT    7881            CGT
                                AAGGAAGGGCAGG  GATG
                                ||||||||||||  ||||
                                TTCCTTCTCGTTC  CTGC
                                      AC_
GAM1297  IL12RB2  5'  TATCGCGCCTATCATATCTTGG 9563         AAG GC
            TG                    TATCAAGG  G  AGGCGTGATG
                                ||||||||  |  ||||||||||
                                GTGGTTCT  C  TCCGCGCTAT
                                     ATA TA
GAM1297  IL2RA    3'  CGTTGTGCTTGCCTGCGTTTTG 6451       AA_       TG
            G                     TCAAGG  GGGCAGGCG  ATG
                                ||||||  |||||||||  |||
                                GGTTTT  TCCGTTCGT  TGC
                                   GCG       GT
GAM1297  ITPR1    3'  TGTCACATGATTTCTTTTCTTG 11075          CAGGC_
            ATG                     TATCAAGGAAGGG     GTGATG
                                ||||||||||||     ||||||
                                GTAGTTCTTTTCT     CACTGT
                                      TTAGTA
GAM1297  JDP1     3'  TGTCATGTCTGTGAATTGCT  41725    G  GG_
                                AG AA  GCAGGCGTGATG
                                || ||  ||||||||||||
```

```
                                TC TT   TGTCTGTACTGT
                                 G  AAG
GAM1297  JMJ      3'  CATTCTGTTATTTTTTGGTG   18321          GG    C
                                TATCAAGGAA  GCAGG GTG
                                ||||||||||  ||||| |||
                                GTGGTTTTTT  TGTCT TAC
                                      AT    _
GAM1297  KCNJ1    5'  TGTCATGTCTTAGCATGTTGGT 5844        GGAAGG  __
              A                  TATCAA     GC  AGGCGTGATG
                                 ||||||     ||  ||||||||||
                                 ATGGTT     CG  TCTGTACTGT
                                    GTA___  AT
GAM1297  KDR      3'  CATTGTGTTTGCTCTGGTGG   11198     AGGA        TG
                                TCA   AGGGCAGGCG  ATG
                                |||   ||||||||||  |||
                                GGT   TCTCGTTTGT  TAC
                                  GG__        GT
GAM1297  LAMA3    3'  TGTTATGCACAGAATGTTTTTG 5854          AGGGCAG_
              GTA                   TATCAAGGA       GCGTGATG
                                    |||||||||       ||||||||
                                    ATGGTTTTT       CGTATTGT
                                         GTAAGACA
GAM1297  LARGE    3'  GTTTTGTTTTGTTTTTCTTTGG 56930             _  TGATG
                                TCAAGGAAGGGCAGG CG
                                |||||||||||||| ||
                                GGTTTCTTTTTGTTT GT
                                       T  TTTGT
GAM1297  LARGE    3'  TGTTTTGTTTTGTTTTTCTTTG 56933             _  TGATG
              G                  TCAAGGAAGGGCAGG CG
                                 |||||||||||||| ||
                                 GGTTTCTTTTTGTTT GT
                                       T  TTTGT
GAM1297  LASS1    3'  CATCTCCGTGCTCTTCTTTGA  41473           _  CGT
                                TCAAGGAAGGGCA GG   GATG
                                ||||||||||||  ||   ||||
                                AGTTTCTTCTCGT CC   CTAC
                                       G  T__
GAM1297  LCP1     3'  TATCAATGTTTACTTTTTTGGT 11285          GGCA    _
              A                  TATCAAGGAAG    GGCGT GATG
                                 ||||||||||    ||||| ||||
                                 ATGGTTTTTTC    TTGTA CTAT
                                       AT__     A
GAM1297  LILRB4   3'  CATTAGCTCTTTTTCCTGATG  23385      A      CA   G
                                TATCA GGAAGGG  GGC TGATG
                                ||||| |||||||  ||| |||||
                                GTAGT CCTTTTT  TCG ATTAC
                                   _      C_  _
GAM1297  LMO7     3'  TATGTGGCCTTTTTTGATG    32369           G AG
                                TATCAAGGAAGG C  GCGTG
                                ||||||||||| |  |||||
```

```
                                GTAGTTTTTTCC G  TGTAT
                                       G __
GAM1297  LMO7     3'  TATGTGGCCTTTTTTGATG   32370          G AG
                                TATCAAGGAAGG C  GCGTG
                                |||||||||||| |  |||||
                                GTAGTTTTTTCC G  TGTAT
                                       G __
GAM1297  MATN3    3'  TATCATGTCTATTTTTGATG  11469        AGGGC
                                TATCAAGGA    AGGCGTGATG
                                |||||||||    ||||||||||
                                GTAGTTTTT    TCTGTACTAT
                                      A____
GAM1297  MATN3    3'  TATCATGTCTATTTTTGATG  11470        AGGGC
                                TATCAAGGA    AGGCGTGATG
                                |||||||||    ||||||||||
                                GTAGTTTTT    TCTGTACTAT
                                      A____
GAM1297  MECP2    3'  CAAAGCTGTTCTTCCTGGTG  18388      A       GCG
                                TATCA GGAAGGGCAG  TG
                                ||||| ||||||||||  ||
                                GTGGT CCTTCTTGTC  AC
                                   _       GAA
GAM1297  MLLT3    3'  TATTGTGTTTTTTTTTTTTGGT 16962         C    TG
                                ATCAAGGAAGGG AGGCG  ATG
                                |||||||||||| |||||  |||
                                TGGTTTTTTTTT TTTGT  TAT
                                      _   GT
GAM1297  MOX2     3'  TTTGCCTTTCTGTTGATG    67476      _
                                TATCAA GGAAGGGCAGG
                                |||||| ||||||||||
                                GTAGTT TCTTTCCGTTT
                                   G
GAM1297  MYO6     3'  CAGATTTGCTTTTCTTTG    18441          CG
                                CAAGGAAGGGCAGG  TG
                                ||||||||||||||  ||
                                GTTTCTTTTCGTTT  AC
                                       AG
GAM1297  NAGA     5'  CGCCCCTCCGCTCTTTCTTGGT 6036          __  C  ATG
            G                    TATCAAGGAAGGGC  AGG GTG
                                ||||||||||||||  ||| |||
                                GTGGTTCTTTCTCG  TCC CGC
                                       CC  C
GAM1297  NFE2L1   3'  CGTCGTCTGCTTTCTTTTTTGG 13629        __      _ ATG
                                TCAAGGAAG  GGCAGGCG TG
                                |||||||||  |||||||| ||
                                GGTTTTTTC  TCGTCTGC GC
                                      TT       T
GAM1297  NONO     3'  TCACAGCTTTTCTTGATA    82893        GGGCA  _
                                TATCAAGGAA    GGC GTGA
                                ||||||||||    ||| ||||
```

```
                                ATAGTTCTTT    TCG CACT
                                      _____  A
GAM1297 NOV     3' TGGCTCCCTTTTTGGGTA   11815     A      C  G
                                TATC AGGAAGGG AG CG
                                |||| |||||||| || ||
                                ATGG TTTTTCCC TC GT
                                  G       _ G
GAM1297 NQO1    3' CATCATGCCTGACTAATTTTTG 8044       AG  _
                                CAAGGA  GG CAGGCGTGATG
                                ||||||  || ||||||||||
                                GTTTTT  TC GTCCGTACTAC
                                   AA  A
GAM1297 PAIP2   3' CAAATTGTCTTTTTTTGA   33643           GCG
                                TCAAGGAAGGGCAG   TG
                                ||||||||||||||   ||
                                AGTTTTTTTCTGTT   AC
                                      AA_
GAM1297 PAM     3' CATTGCCAGTGTCTTTCTTTGG 57841           __   TGATG
             TG                   TATCAAGGAAGGGCA  GGCG
                                ||||||||||||||  ||||
                                GTGGTTTCTTTCTGT  CCGT
                                      GA    TAC
GAM1297 PCDH15  3' CATTGTGCTTTCCCTTCC    53513       C    TG
                                GGAAGGG AGGCG  ATG
                                ||||||| |||||  |||
                                CCTTCCC TTCGT  TAC
                                   T    GT
GAM1297 PCDH15  3' TAGGTTCTGTTTTTTCTTGA  53514           _ G
                                TCAAGGAAGGGCAGG C TG
                                |||||||||||||| | ||
                                AGTTCTTTTTTGTCT G AT
                                      T G
GAM1297 PCDHB4  3' TGTTGTGCCTGTCTTTACC   38942   _       TG
                                GG AAGGGCAGGCG  ATG
                                || ||||||||||  |||
                                CC TTTCTGTCCGT  TGT
                                 A         GT
GAM1297 PDYN    3' TATCATGCTTCTACTCCATGGT 44589      A  AG  C
             G                   TATCA GGA  GG AGGCGTGATG
                                ||||| |||  || ||||||||||
                                GTGGT CCT  TC TTCGTACTAT
                                   A  CA  _
GAM1297 PEA15   3' TGCCATGTCTGCCCTTTTTTG  15015            ATG
                                CAAGGAAGGGCAGGCGTG
                                ||||||||||||||||||
                                GTTTTTTCCCGTCTGTAC
                                      CGTC
GAM1297 PFKFB3  3' GCTTTTGCACTTTTTTGATG  83752         G    C
                                TATCAAGGAAG GCAGG GT
                                |||||||||| ||||| ||
```

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                                GTAGTTTTTTC CGTTT CG
                                      A    T
GAM1297  PNUTL1   3'  CATTGTGTCTGTTTCCGAGGG  12188    AA_   GG      TG
                                TC   GGAA  GCAGGCG  ATG
                                ||   ||||  |||||||  |||
                                GG   CCTT  TGTCTGT  TAC
                                 GAG   __      GT
GAM1297  POLS     3'  TATCATGTTTCGATTTTTTTG  23781        GGC
                                CAAGGAAG   AGGCGTGATG
                                ||||||||   ||||||||||
                                GTTTTTTT   TTTGTACTAT
                                     AGC
GAM1297  PPAT     3'  AAACTGTTTGTCTTCCTTTGGT 12217         A        TGATG
              A                  TATCAAGG AGGGCAGGCG
                                 ||||||||| ||||||||||
                                 ATGGTTTC TTCTGTTTGT
                                      C         CAAAG
GAM1297  PPP2R1A  3'  CATCATTGGTTTTTTTTTG   27247          AGGC
                                CAAGGAAGGGC    GTGATG
                                ||||||||||    ||||||
                                GTTTTTTTTTG    TACTAC
                                      GT__
GAM1297  PPP2R2B  3'  GTCTGTTCTTTTTGGGTG    17123      A
                                TATC AGGAAGGGCAGGC
                                |||| ||||||||||||
                                GTGG TTTTTCTTGTCTG
                                  G
GAM1297  PPP3CB   3'  TGTTGAAACCTTTCTTTTGATA 41218        _     CA__
                                TATCAAG GAAGGG    GGCG
                                ||||||| ||||||    ||||
                                ATAGTTT CTTTCC    TTGT
                                     T     AAAG
GAM1297  PRKG1    3'  TGTTTGTTTTTTTTGATA    21822          G
                                TATCAAGGAAGG CAGGCG
                                |||||||||||| ||||||
                                ATAGTTTTTTTT GTTTGT
                                                _
GAM1297  RAB13    3'  TGTCATGGTCTTTCTTGGTA   12720          G  _
                                TATCAAGGAAGG CA GGCG
                                |||||||||||| || ||||
                                ATGGTTCTTTCT GT CTGT
                                      G  A
GAM1297  RARB     3'  TGTCTTTGCTCTTTCTGATG   32891      A       __
                                TATCA GGAAGGGCA  GGCG
                                ||||| |||||||||  ||||
                                GTAGT CTTTCTCGT  CTGT
                                  _       TT
GAM1297  RBM10    5'  TGTCTGGGAGCCCTTCCTTGA  20249          _____    TGATG
                                TCAAGGAAGGGC    AGGCG
                                ||||||||||||    |||||
```

```
                                AGTTCCTTCCCG   TCTGT
                                      AGGG      G
GAM1297 RECK    3' TGTCTGACTTTCTTTTTTGATA 41200         __ _
                                TATCAAGGAAG  GG CAGGCG
                                ||||||||||  || ||||||
                                ATAGTTTTTTC  TC GTCTGT
                                      TT  A
GAM1297 SCA1    3' GTCCCTTTCTTTGATG     6183           CA
                                TATCAAGGAAGGG  GGC
                                ||||||||||||  |||
                                GTAGTTTCTTTCC  CTG
                                       __
GAM1297 SCAP2   3' TATCATGCGAGTTTTTTTTGGT 15426          G AG
            A                    TATCAAGGAAGG C  GCGTGATG
                                ||||||||||| |  ||||||||
                                ATGGTTTTTTTT G  CGTACTAT
                                      _ AG
GAM1297 SDC4    3' TATTATTATTCTTCCTTGGT   12999          CAGGC
                                ATCAAGGAAGGG    GTGATG
                                ||||||||||||    ||||||
                                TGGTTCCTTCTT    TATTAT
                                      AT___
GAM1297 SDC4    3' TGTTGTCTGTTACTGATTTTTT 13000          _______     TGATG
            TTGATA                TATCAAGGAAGG     GCAGGCG
                                ||||||||||||    |||||||
                                ATAGTTTTTTTT    TGTCTGT
                                      AGTCAT     TGT
GAM1297 SERPINI1 3' ATTATGTTTGCAACTGGTA   18478      A GAAGG
                                TATCA G    GCAGGCGTGAT
                                ||||| |    ||||||||||
                                ATGGT C    CGTTTGTATTA
                                   _ AA___
GAM1297 SGK     3' CATCACACAACTTTTTTTG   20063        GCAGGC
                                CAAGGAAGG     GTGATG
                                |||||||||     ||||||
                                GTTTTTTTC     CACTAC
                                     AACA__
GAM1297 SHOC2   3' CATGAATGTCTTTCTTTGA   24782          GG
                                TCAAGGAAGGGCA  CGTG
                                ||||||||||||  ||||
                                AGTTTCTTTCTGT  GTAC
                                      AA
GAM1297 SLC19A1 3' TGCTGGTCATCCTTGGTG    13222        AG  A
                                TATCAAGGA  GGC GGCG
                                |||||||||  ||| ||||
                                GTGGTTCCT  CTG TCGT
                                     A_  G
GAM1297 SLC20A2 3' CATTGGAGTCTCTTCTTTTTTT 23116          C_   G_
            GATA                  TATCAAGGAAGGG  AGGC  TGATG
                                ||||||||||||  ||||  |||||
```

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                                ATAGTTTTTTTCT  TCTG  GTTAC
                                      TC    AG
GAM1297  SLC22A5   3'  CATTGTGTGTGTTCCTTTCTTG 13227          _ G   TG
              ATA                   TATCAAGGAAGGG CA GCG  ATG
                                ||||||||||||| || |||  |||
                                ATAGTTCTTTCCT GT TGT  TAC
                                      T  G   GT
GAM1297  SOCS5    3'  TGTTATGGCTGCTTTTTTT   26685          G
                                AGGAAGGGCAG CGTGATG
                                |||||||||||| |||||||
                                TTTTTTTCGTC GTATTGT
                                      G
GAM1297  SOD2     3'  TGTAGCATTTCTTGATG     7160          GG  AG
                                TATCAAGGAA  GC  GCG
                                ||||||||||  ||  |||
                                GTAGTTCTTT  CG  TGT
                                     A_  A_
GAM1297  SOX13    3'  TATTTCTCTCTTTCTTGGTG   20285          C   C
                                TATCAAGGAAGGG AGG GTG
                                |||||||||||| ||| |||
                                GTGGTTCTTTCTC TCT TAT
                                      _   T
GAM1297  SPAP1    3'  TATTGCAGCATTTGTTTTATTT 57837        A      __  _ TG
              TGGTA                  TATCAAGG AGGGCAG  GC G  ATG
                                |||||||| |||||||  || |  |||
                                ATGGTTTT TTTTGTT  CG C  TAT
                                     A      TA  A GT
GAM1297  SPG4     3'  TGTTGTTTAAGGCCTTGCCTTG 30812        A    ____    TGATG
              ATG                    TATCAAGG AGGGC   AGGCG
                                |||||||| |||||   |||||
                                GTAGTTCC TTCCG   TTTGT
                                     G    GAA    TGT
GAM1297  SPS2     3'  CGGCTGCCCTTTCTAGGTG   25312      A         G
                                TATC AGGAAGGGCAG CG
                                |||| |||||||||| ||
                                GTGG TCTTTCCCGTC GC
                                  A         G
GAM1297  SUDD     3'  TGTTGCGTCTTTCCTTGA    15162          A_
                                TCAAGGAAGGGC  GGCG
                                ||||||||||||  ||||
                                AGTTCCTTTCTG  TTGT
                                      CG
GAM1297  SWAP70   3'  CATCAGGTGTTTTCCTTAATA  71864     C       G AG  G
                                TAT AAGGAAGG C  GC TGATG
                                ||| |||||||| |  || |||||
                                ATA TTCCTTTT G  TG ACTAC
                                  A       _ __  G
GAM1297  TM4SF4   3'  TGTTATTTGTTGTCTTTTTTTG 17257          GC_
                                CAAGGAAGGGCAG   GTGATG
                                ||||||||||||   ||||||
```

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                                GTTTTTTTCTGTT  TATTGT
                                       GTT
GAM1297 TMOD3    3' CATCATGTAAAATTTTCCTGGG 28020     A     GCAG
             TA                  TATC AGGAAGG   GCGTGATG
                                 |||| |||||||   ||||||||
                                 ATGG TCCTTTT   TGTACTAC
                                   G      AAAA
GAM1297 TRIM9    3' CATCACAGAGCCCTTCTTGGTA 31446       G     AGGC
                                 TATCAAG AAGGGC   GTGATG
                                 ||||||| ||||||   ||||||
                                 ATGGTTC TTCCCG   CACTAC
                                     _     AGA_
GAM1297 UBL1     3' CATTGTGCTGATTTTTGGTGA 13974     AG    GCA   TG
                                 TCA GAAGG  GGCG ATG
                                 |||  |||||  ||||  |||
                                 AGT TTTTT  TCGT TAC
                                   GG    AG_   GT
GAM1297 ULBP2    3' TATTATGCAATTTTCTCTTGGT 48172       _    GCAG
             G                   TATCAAG GAAGG   GCGTGATG
                                 ||||||| |||||   ||||||||
                                 GTGGTTC CTTTT   CGTATTAT
                                     T    AA__
GAM1297 USP14    3' ATGTGTCTCTCTCTGATG    18929      AG  A  C    TG
                                 TATCA  GA GGG AGGCG  AT
                                 |||||  || ||| |||||  ||
                                 GTAGT  CT CTC TCTGT  TA
                                    __ _  _    GT
GAM1297 VBP1     3' TTTGTAAACTTGTTTTTCTTTG 14031             CG  ATG
             GTA                   TATCAAGGAAGGGCAGG  TG
                                 ||||||||||||||||  ||
                                 ATGGTTTCTTTTTGTTC  AT
                                        AA  GTTTA
GAM1297 ZNF217   3' TATTATGCTGGAATTTTTTGG  22547        GGGCA
                                 TCAAGGAA    GGCGTGATG
                                 ||||||||    |||||||||
                                 GGTTTTTT    TCGTATTAT
                                     AAGG_
GAM1297 ADG-90   3' AAAGGGCTTTTCTTTCTTGGTA 53523           C   GTGATG
                                 TATCAAGGAAGGG AGGC
                                 |||||||||||| ||||
                                 ATGGTTCTTTCTT TTCG
                                        _   GGAAAA
GAM1297 ALS2CR2  3' ATCAGACCCTTTTCTGGTA   38320      AG    CAGGCG
                                 TATCA  GAAGGG     TGAT
                                 |||||  ||||||     ||||
                                 ATGGT  TTTCCC     ACTA
                                    CT     AG____
GAM1297 AP1GBP1  3' TGTCATGTCTGATAGCTCTTTG 24357       AGGG_
             G                   TCAAGGA    CAGGCGTGATG
                                 |||||||    ||||||||||
```

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                                GGTTTCT    GTCTGTACTGT
                                    CGATA
GAM1297 ATP10D   3' TATTGCTTTGCCTTTTCTT   73529          C TG
                                AAGGAAGGGCAGG G  ATG
                                |||||||||||| |  |||
                                TTCTTTTCCGTTT C  TAT
                                      _ GT
GAM1297 B3GNT1   3' TATTGTGTAACATACTTTCTTG 22696        GGCAG_  TG
           A                     TCAAGGAAG     GCG  ATG
                                 |||||||||     |||  |||
                                 AGTTCTTTC     TGT  TAT
                                       ATACAA   GT
GAM1297 B3GNT1   3' TATTGTGTAACATACTTTCTTG 22697        GGCAG_  TG
           A                     TCAAGGAAG     GCG  ATG
                                 |||||||||     |||  |||
                                 AGTTCTTTC     TGT  TAT
                                       ATACAA   GT
GAM1297 BHLHB2   3' CCTGTTTTTATTTTGGTA    14762        _
                                TATCAAGG AAGGGCAGG
                                |||||||| |||||||||
                                ATGGTTTT TTTTTGTCC
                                    A
GAM1297 C17      3' TACTTTTATTCTTTCTTGATA  38487          C   C
                                TATCAAGGAAGGG AGG GTG
                                |||||||||||| ||| |||
                                ATAGTTCTTTCTT TTT CAT
                                      A   T
GAM1297 C20orf59 3' CGGGCTGTCCTCCTTGGTG   42232        A     G G
                                TATCAAGGA GGGCAG C TG
                                ||||||||| |||||| | ||
                                GTGGTTCCT CCTGTC G GC
                                    _     _ G
GAM1297 CAPS2    3' TGTCACATATCTTTTTCTTGG  71130          CAGGC
                                TCAAGGAAGGG    GTGATG
                                ||||||||||     ||||||
                                GGTTCTTTTTC    CACTGT
                                      TATA_
GAM1297 CGI-01   3' CATTATTTGACAGCTTTCCTTG 32504          GCAGGC_
           GTG                    TATCAAGGAAGG      GTGATG
                                  ||||||||||||      ||||||
                                  GTGGTTCCTTTC      TATTAC
                                        GACAGTT
GAM1297 CLSTN2   3' ATTTCTTTCTTTTTTTGATA  42399          C   C
                                TATCAAGGAAGGG AGG GT
                                |||||||||||| ||| ||
                                ATAGTTTTTTTCT TCT TA
                                      T   T
GAM1297 CNOT7    3' TATCAGAAAATTTGTTTTTTCT 26255            CG___
           TGAT                   ATCAAGGAAGGGCAGG    TGATG
                                  ||||||||||||||||    |||||
```

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                                TAGTTCTTTTTTGTTT    ACTAT
                                      AAAAG
GAM1297 COLEC10   3' CATCATCATGCTCTTTTGTGAT 22236      AG      GGC
           G                   TATCA GAAGGGCA  GTGATG
                               ||||| |||||||| ||||||
                               GTAGT TTTCTCGT  TACTAC
                                  GT      AC_
GAM1297 DDX33     3' CATTCTTGTATCTTTTTTGGTG 39783          _    C
                               TATCAAGGAAGG GCAGG GTG
                               |||||||||||| ||||| |||
                               GTGGTTTTTTCT TGTTC TAC
                                       A    T
GAM1297 DKFZP434A0225 3' CATTATCCAATTTGTATTTCCT 95522          G  ____  C
           TGGTA                    TATCAAGGAAG GCA   GG GTGATG
                               |||||||||||| |||   || ||||||
                               ATGGTTCCTTT TGT   CC TATTAC
                                       A  TTAA  _
GAM1297 DKFZp434C0328 3' GTTTGTTTTGTTTTGGTA    34548        A
                               TATCAAGG AGGGCAGGC
                               |||||||| |||||||||
                               ATGGTTTT TTTTGTTTG
                                    G
GAM1297 DKFZp547C176 3' GTTACATCTTGCCTTGATA   67805      AGGAA     C_
                               TATCA    GGGCAGG  GTGAT
                               |||||    |||||||  |||||
                               ATAGT    TCCGTTC  CATTG
                                  _____      TA
GAM1297 DKFZp566D234 3' TGTCGCATACATCCTTCTTTTG 62521     C       CAGGC
           TA                   TAT AAGGAAGGG    GTGATG
                               ||| |||||||||    ||||||
                               ATG TTTCTTCCT    CGCTGT
                                 T       ACATA
GAM1297 DKFZp761K1423 5' ATCACATTCTTTCTTG      37935         CAGGC
                               CAAGGAAGGG    GTGAT
                               ||||||||||    |||||
                               GTTCTTTCTT    CACTA
                                     A____
GAM1297 DMTF1     3' TGTTACCTATCCTTGATA    41247         A  CA
                               TATCAAGGA GGG  GGCG
                               ||||||||| |||  ||||
                               ATAGTTCCT TCC  TTGT
                                     A  A_
GAM1297 EIF3S1    3' CATTTTATCTTTTCTTGGTG  63867          GC  C
                               TATCAAGGAAGG  AGG GTG
                               ||||||||||||  ||| |||
                               GTGGTTCTTTTC  TTT TAC
                                      TA  _
GAM1297 EPSTI1    3' CATGAGATGCTTTTTCTT    53827          GG_
                               AAGGAAGGGCA   CGTG
                               ||||||||||   ||||
```

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                                TTCTTTTTCGT  GTAC
                                      AGA
GAM1297 FIBL-6   3' GTTTTGTGTGCCTTCCTTGGTA 73297          G G  TGATG
                                TATCAAGGAAGG CA GCG
                                |||||||||||| || |||
                                ATGGTTCCTTCC GT TGT
                                      _ G  TTTGT
GAM1297 FLJ10315 3' TGTTACGTACTGTTTCTTTGAT 36494         GG  _
           A                    TATCAAGGAA  GCAG GCGTGATG
                                |||||||||| |||| ||||||||
                                ATAGTTTCTT  TGTC TGCATTGT
                                      __  A
GAM1297 FLJ10546 5' CATTATGTCTGCAAAACTTG  60179     GAAGG
                                CAAG    GCAGGCGTGATG
                                ||||    ||||||||||||
                                GTTC    CGTCTGTATTAC
                                  AAAA_
GAM1297 FLJ10607 3' GCTTCCTTTCTTGGTA     77637           CA
                                TATCAAGGAAGGG  GGC
                                |||||||||||| |||
                                ATGGTTCTTTCCT  TCG
                                      __
GAM1297 FLJ10829 3' CGTTAGGTTTTCTTTTCTTGGT 37259          C   G
           G                    TATCAAGGAAGGG AGGC TGATG
                                |||||||||||| |||| |||||
                                GTGGTTCTTTTCT TTTG ATTGC
                                      _   G
GAM1297 FLJ10842 3' CATTAGCGCATGTTTTATTTTG 37269        A    G  _
           GTG                    TATCAAGG AGGGCA GCG TGATG
                                |||||||| |||||| ||| |||||
                                GTGGTTTT TTTTGT CGC ATTAC
                                    A    A  G
GAM1297 FLJ10849 3' CAAGAGTTTGCATTTTCTTGAT 37306          G    GTGATG
           G                    TATCAAGGAAG GCAGGC
                                |||||||||| ||||||
                                GTAGTTCTTTT CGTTTG
                                      A    AGAAC
GAM1297 FLJ11506 3' TGTCACCTTTCCTGGGTG   45438     A      CA
                                TATC AGGAAGGG  GGCG
                                |||| ||||||||  ||||
                                GTGG TCCTTTCC  CTGT
                                  G      A_
GAM1297 FLJ11608 3' TATCATGTATCCTTCCTGGTG  44962      A     CAG
                                TATCA GGAAGGG   GCGTGATG
                                ||||| |||||||   ||||||||
                                GTGGT CCTTCCT   TGTACTAT
                                  _     A__
GAM1297 FLJ13102 3' CACTCCCCTTCCTTTTCTTGGT 46527          C  C__  ATG
           G                    TATCAAGGAAGGG AGG  GTG
                                |||||||||||| |||  |||
```

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                                GTGGTTCTTTTCC TCC   CAC
                                      T  CCT
GAM1297  FLJ13910  3'  TACTTTTGTCATTTTCTTGATA 43252          _     C
                                TATCAAGGAAG GGCAGG GTG
                                |||||||||||  ||||||  |||
                                ATAGTTCTTTT CTGTTT CAT
                                      A     T
GAM1297  FLJ14084  3'  CATTACGTACTGTTGTTTTTCC 41592           ____
            TTG                   CAAGGAAGGGCAG   GCGTGATG
                                |||||||||||||    ||||||||
                                GTTCCTTTTTGTT    TGCATTAC
                                      GTCA
GAM1297  FLJ14641  5'  TATCATGTTTGCCTTCCCTGG  52567    A     G
                                TCA GGAAGG CAGGCGTGATG
                                |||  ||||||  ||||||||||
                                GGT CCTTCC GTTTGTACTAT
                                  C     _
GAM1297  FLJ14728  3'  TGTCTGTGTCCTTCCTTGA   52645          __
                                TCAAGGAAGG  GCAGGCG
                                ||||||||||  |||||||
                                AGTTCCTTCC  TGTCTGT
                                      TG
GAM1297  FLJ14824  3'  TATATCTTTTTTCCTTGATG   52718           C  GC
                                TATCAAGGAAGGG AG  GTG
                                ||||||||||||| ||  |||
                                GTAGTTCCTTTTT TC  TAT
                                      _  TA
GAM1297  FLJ14966  3'  ATCCATATTTGCCTTTTTTTG  52832           CG  ATG
                                CAAGGAAGGGCAGG  TG
                                ||||||||||||||  ||
                                GTTTTTTTCCGTTT  AC
                                        AT  CTAT
GAM1297  FLJ20010  3'  ATTATTCCTTTCTTTGG     39229          CAGGC
                                TCAAGGAAGGG    GTGAT
                                ||||||||||     |||||
                                GGTTTCTTTCC    TATTA
                                      T____
GAM1297  FLJ20081  3'  TATTTTTGCTTTTTCTTAGATA 34992      _          C
                                TATC AAGGAAGGGCAGG GTG
                                ||||  ||||||||||||| |||
                                ATAG TTCTTTTTCGTTT TAT
                                  A           T
GAM1297  FLJ20152  3'  TGATGTCCTTTATTGATA    39166       G       GG
                                TATCAA GAAGGGCA  CG
                                ||||||  ||||||||  ||
                                ATAGTT TTTCCTGT  GT
                                    A       A_
GAM1297  FLJ20485  3'  CGGGTTTTTTTTTCTTGATG  39291           C   G
                                TATCAAGGAAGGG AGGC TG
                                ||||||||||||| ||||  ||
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                                GTAGTTCTTTTTT TTTG GC
                                      _   G
GAM1297  FLJ20859  3'  TATCGTGCCTGCCAGGGCTGA  43005     AGGAAG
                                TCA     GGCAGGCGTGATG
                                |||     ||||||||||||
                                AGT     CCGTCCGTGCTAT
                                  CGGGA_
GAM1297  FLJ20984  3'  TGGCTGCTTTCTTTTGGTG   45250       GA      G
                                TATCAAG  AGGGCAG CG
                                |||||||  ||||||| ||
                                GTGGTTT  TTTCGTC GT
                                    TC      G
GAM1297  FLJ21596  3'  TGTCATAACTTTCTGTTTTTCC 46125     C          C____
                TTTATA                  TAT AAGGAAGGGCAGG    GTGATG
                                ||| ||||||||||||    ||||||
                                ATA TTCCTTTTTGTCT    TACTGT
                                  T          TTCAA
GAM1297  FLJ22029  3'  TTTGGTGTTTGGTTTTTTTTGG 46913          G      GATG
                TA                  TATCAAGGAAGG CAGGCGT
                                ||||||||||| |||||||
                                ATGGTTTTTTTT GTTTGTG
                                      G      GTTTT
GAM1297  FLJ22671  3'  TGTATGCCATTCCTTGGTG   46315         G   G
                                TATCAAGGAA GGCA GCG
                                |||||||||| |||| |||
                                GTGGTTCCTT CCGT TGT
                                     A   A
GAM1297  FLJ23047  3'  TGCCTTTGCTTTTTTTTGG   44936          __
                                TCAAGGAAGGGCA  GGCG
                                ||||||||||||  ||||
                                GGTTTTTTTTCGT  CCGT
                                      TT
GAM1297  FLJ23121  5'  ATGTGCCTTTCTTTGATA    45520           AG
                                TATCAAGGAAGGGC  GCGT
                                ||||||||||||  ||||
                                ATAGTTTCTTTCCG  TGTA
                                      __
GAM1297  FLJ23451  3'  GTCTTTGTTCTGTTTTGGTG   45789        A    __
                                TATCAAGG AGGGCA  GGC
                                |||||||| ||||||  |||
                                GTGGTTTT TCTTGT  CTG
                                    G     TT
GAM1297  FLJ25461  3'  TATCATGGGATAGTTTCCTTGA 59299         GGCAGG
                                TCAAGGAAG     CGTGATG
                                |||||||||     |||||||
                                AGTTCCTTT     GTACTAT
                                     GATAGG
GAM1297  GPA33     3'  TGCTATCTTTTCTGGATG    20574      A       CA
                                TATC AGGAAGGG  GGCG
                                ||||  ||||||||  ||||
```

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                                GTAG TCTTTTCT  TCGT
                                  G       A_
GAM1297  GPT2     3'  AGGCCCTGTCCTTTCTTGA   56767            C  GATG
                                TCAAGGAAGGGCAGG GT
                                ||||||||||||||| ||
                                AGTTCTTTCCTGTCC CG
                                       _  GAA
GAM1297  GRP3     3'  GTTTTGTTTTGTTCTTCTTGGT 31741        G       _  TGATG
              G                  TATCAAG AAGGGCAGG CG
                                 ||||||| ||||||||| ||
                                 GTGGTTC TTCTTGTTT GT
                                    _       T  TTTGT
GAM1297  H17739   3'  CACTTCCTTCCTTCTTTGGTG  55627           C   C_
                                 TATCAAGGAAGGG AGG  GTG
                                 |||||||||||| |||  |||
                                 GTGGTTTCTTCCT TCC  CAC
                                       _  TT
GAM1297  HCC-4    5'  CGTTTTGTCCTTCCTTTATA   57598     C          _
                                 TAT AAGGAAGGGCAGG CG
                                 ||| |||||||||||| ||
                                 ATA TTCCTTCCTGTTT GC
                                   T          T
GAM1297  HMGN4    5'  TATTATGCTATCTTTTTTGATA 22033           GCA
                                 TATCAAGGAAGG   GGCGTGATG
                                 ||||||||||||   |||||||||
                                 ATAGTTTTTTCT   TCGTATTAT
                                       A__
GAM1297  HNRPA3   3'  TGTTACTCCTTCTTTGGTA    20454           CA
                                 TATCAAGGAAGGG  GGCG
                                 ||||||||||||  ||||
                                 ATGGTTTCTTCCT  TTGT
                                       CA
GAM1297  HNT      3'  CATCGTGCAACCTCTTTGGTG  33698         A  GCAG
                                 TATCAAGGA GG    GCGTGATG
                                 |||||||||  ||    ||||||||
                                 GTGGTTTCT CC    CGTGCTAC
                                      _  AA__
GAM1297  HSPBAP1  3'  TGCCACCTTCTTTCATG     45157     C       GCA
                                 TAT AAGGAAGG   GGCG
                                 ||| ||||||||   ||||
                                 GTA TTTCTTCC   CCGT
                                   C       A__
GAM1297  HSPC039  3'  CATTACATTTCTATTTCTTGGT 32737          G  C   C
              G                  TATCAAGGAA GG AGG GTGATG
                                 ||||||||||  || ||| ||||||
                                 GTGGTTCTTT TC TTT CATTAC
                                       A  _   A
GAM1297  HSPC039  3'  TGTTGCTTCTCTTTTTTTAGAT 32739      __        C    TGATG
              A                  TATC  AAGGAAGGG AGGCG
                                 ||||  ||||||||| |||||
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                                ATAG  TTTTTTCTC TTCGT
                                  AT        _     TGT
GAM1297  JAM1     3'  GTCAAGGCTCTTTTTTG     34240          AGGCG
                                CAAGGAAGGGC    TGAT
                                ||||||||||     ||||
                                GTTTTTTCTCG    ACTG
                                      GA___
GAM1297  JAM1     3'  GTCAAGGCTCTTTTTTG     34241          AGGCG
                                CAAGGAAGGGC    TGAT
                                ||||||||||     ||||
                                GTTTTTTCTCG    ACTG
                                      GA___
GAM1297  KALI     3'  TTGACTCTCTCTTTGATA    54699          _   _
                                TATCAAGGA AGGG CAG
                                ||||||||| |||| |||
                                ATAGTTTCT TCTC GTT
                                     C   A
GAM1297  KIAA0210 5'  TATTTTGTATGTTCTTTTTTAG 29176    C        G   T
           TA                    TAT AAGGAAGGGCA GCG GATG
                                 ||| |||||||||| ||| ||||
                                 ATG TTTTTTCTTGT TGT TTAT
                                   A         A   T
GAM1297  KIAA0255 3'  TGTATGCCTTTTTTTGGT    29138            G
                                ATCAAGGAAGGGCA GCG
                                |||||||||||||| |||
                                TGGTTTTTTTCCGT TGT
                                       A
GAM1297  KIAA0261 3'  TGTCTTCCTATTTTTGATA   68745         A   C
                                TATCAAGGA GGG AGGCG
                                ||||||||| ||| |||||
                                ATAGTTTTT TCC TCTGT
                                     A   T
GAM1297  KIAA0365 3'  CGTCTTGATTTTCCCTTTCTTT 79367            CAGG__  T
           GATG                    TATCAAGGAAGGG     CG GATG
                                   |||||||||||||     || ||||
                                   GTAGTTTCTTTCC     GT CTGC
                                         CTTTTA  T
GAM1297  KIAA0449 3'  TCTGTTTCTTCTTTGATA    34640            _
                                TATCAAGGAAGGG CAGG
                                |||||||||||| ||||
                                ATAGTTTCTTCTT GTCT
                                       T
GAM1297  KIAA0570 3'  CATTATTGAAATTTCTTCCTGA 28849       A      CAGG  _
           TG                    TATCA GGAAGGG    CG TGATG
                                 ||||| |||||||    || |||||
                                 GTAGT CCTTCTT    GT ATTAC
                                   _      TAAA  T
GAM1297  KIAA0660 3'  CATCGTGTTTGCATTCTTG   25470       AGG
                                CAAGGA   GCAGGCGTGATG
                                ||||||   ||||||||||||
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                                GTTCTT   CGTTTGTGCTAC
                                   A__
GAM1297  KIAA0763  3'  TTGGCGTGGCATTTCTTTGGTG 30167          G  AG    GATG
                                TATCAAGGAAG GC  GCGT
                                |||||||||| ||  ||||
                                GTGGTTTCTTT CG  TGCG
                                      A  G_    GTTA
GAM1297  KIAA0971  3'  CAGTCTTGCCTTTCTCTTGGTG 30669        _        CG
                                TATCAAG GAAGGGCAGG  TG
                                ||||||| |||||||||  ||
                                GTGGTTC CTTTCCGTTC  AC
                                    T        TG
GAM1297  KIAA1058  3'  CGTCATCCCCTTCTTTGA    83137          CA_
                                TCAAGGAAGGG   GGCG
                                ||||||||||   ||||
                                AGTTTCTTCCC   CTGC
                                      CTA
GAM1297  KIAA1084  3'  TGTTGCAGCATCTTTTCTTTG  30505         CAG  _ TG
                                CAAGGAAGGG   GC G  ATG
                                ||||||||||   || |  |||
                                GTTTCTTTTC   CG C  TGT
                                      TA_  A GT
GAM1297  KIAA1102  3'  TGTTATTCTCTTCTTTGG    69586          CA_
                                TCAAGGAAGGG   GGCG
                                ||||||||||   ||||
                                GGTTTCTTCTC   TTGT
                                      TTA
GAM1297  KIAA1199  3'  TATCTAGGCATTTTCTTGGTA  72934          G  AGGCGT
                                TATCAAGGAAG GC     GATG
                                |||||||||| ||     ||||
                                ATGGTTCTTTT CG     CTAT
                                      A  GAT___
GAM1297  KIAA1205  3'  TGTCTCTTGCTCTTTCTTGG   70583            CGT
                                TCAAGGAAGGGCAGG   GATG
                                ||||||||||||||   ||||
                                GGTTCTTTCTCGTTC   CTGT
                                        T__
GAM1297  KIAA1280  5'  TATCATCGGGGAGTTTGTCTTT 70288         AG   AGG_  _
            GATG                  TATCAAGGA  GGC    CG TGATG
                                |||||||||  |||    || |||||
                                GTAGTTTCT  TTG    GC ACTAT
                                     GT   AGGG  T
GAM1297  KIAA1349  3'  CATTTATCTGTCTTTTCTT    71292          CGT
                                AAGGAAGGGCAGG   GATG
                                ||||||||||||   ||||
                                TTCTTTTCTGTCT   TTAC
                                      AT_
GAM1297  KIAA1391  3'  GTGTCCATATGCATCTTTTTTG 67854          _  _____   TGATG
            GTA                   TATCAAGGAAGG GCA    GGCG
                                |||||||||||| |||    ||||
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                                ATGGTTTTTTCT CGT    CTGT
                                      A   ATAC      GT
GAM1297  KIAA1497  5'  CATCTGCAGGCTTTTTCTTAGT 68117     C        AG   T
              G                   TAT AAGGAAGGGC  GCG GATG
                                  ||| ||||||||||  ||| ||||
                                  GTG TTCTTTTTCG  CGT CTAC
                                    A         GA  _
GAM1297  KIAA1751  3'  CATTTACAAGTTGTATCTTCTT 72151           GCA  __    TG
              TGGTG                 TATCAAGGAAGG   GGC  GTGA
                                  ||||||||||||   |||  ||||
                                  GTGGTTTCTTCT   TTG  CATT
                                        ATG   AA    TAC
GAM1297  KIAA1764  3'  CATTATGACCCCTTCTTTTATA 69826     C        CAGG
                                  TAT AAGGAAGGG    CGTGATG
                                  ||| |||||||||    |||||||
                                  ATA TTTCTTCCC    GTATTAC
                                    T        CA__
GAM1297  KIAA1789  5'  CATTTTCTGTTTTTCTTT     67698            C_
                                  AAGGAAGGGCAGG  GTG
                                  ||||||||||||  |||
                                  TTTCTTTTTGTCT  TAC
                                         TT
GAM1297  KIAA1817  3'  ATCCCTGCCCATCCTTGGTA   68773          A      C
                                  TATCAAGGA GGGCAGG GT
                                  ||||||||| ||||||| ||
                                  ATGGTTCCT CCCGTCC TA
                                        A      C
GAM1297  KIAA1922  3'  TCCACCATGTCCTTCTGTGGTA 74006       A        GGC   ATG
                                  TATCA GGAAGGGCA   GTG
                                  ||||| |||||||||   |||
                                  ATGGT TCTTCCTGT   CAC
                                     G        AC_   CTG
GAM1297  KIAA1944  5'  GCTCTGCCCTTCCTGGTA     76079       A         _
                                  TATCA GGAAGGGCAG GC
                                  ||||| |||||||||| ||
                                  ATGGT CCTTCCCGTC CG
                                     _         T
GAM1297  KLHL8     3'  TAAAATGTTTTTTCTTTGATG  63518           GGC     GATG
                                  TATCAAGGAAG   AGGCGT
                                  ||||||||||   ||||||
                                  GTAGTTTCTTT   TTTGTA
                                         ___      AAATT
GAM1297  KNSL6     5'  TTGCGCGTTTCTCTTCCTTG   23382          C      ATG
                                  CAAGGAAGGG AGGCGTG
                                  |||||||||| |||||||
                                  GTTCCTTCTC TTTGCGC
                                         _      GTTA
GAM1297  LBP-32    3'  CATTATGTTTGAATTTCCTGAT 28040       A     GG
              A                   TATCA GGAAG  CAGGCGTGATG
                                  ||||| |||||  ||||||||||
```

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                                ATAGT CCTTT  GTTTGTATTAC
                                  _    AA
GAM1297 MAGE-E1  3' CATTTTGTGCTTTTCCTTG   48673          AG   T
                                CAAGGAAGGGC  GCG GATG
                                |||||||||||  ||| ||||
                                GTTCCTTTTCG  TGT TTAC
                                     __   T
GAM1297 MAT2B    3' CATTATGTTTGTCCTGGCT   26127    GA
                                AG  AGGGCAGGCGTGATG
                                ||  ||||||||||||||
                                TC  TCCTGTTTGTATTAC
                                 GG
GAM1297 MGC11034 3' TATCTTTGTTTTTCCTTG    49576           C
                                CAAGGAAGGGCAGG GTG
                                |||||||||||||| |||
                                GTTCCTTTTTGTTT TAT
                                        C
GAM1297 MGC13125 3' CATTGACCAGGGTTTGTTCTTG 52165         AG   AGGC _
           GTA                    TATCAAGGA  GGC    GT GATG
                                |||||||||  |||    || ||||
                                ATGGTTCTT  TTG    CA TTAC
                                     GT   GGAC  G
GAM1297 MGC14258 3' TATGCATTGTCTTTCTTTTATA 52948     C          _
                                TAT AAGGAAGGGCAG GCGTG
                                ||| ||||||||||| |||||
                                ATA TTTCTTTCTGTT CGTAT
                                  T          A
GAM1297 MGC15437 3' CGTTTTGTTTGTTTTTCTATGA 52845       A           T
           TA                     TATCA GGAAGGGCAGGCG GATG
                                ||||| |||||||||||| ||||
                                ATAGT TCTTTTTGTTTGT TTGC
                                   A           T   T
GAM1297 MGC15606 3' GTTTGTTTGTTTGTTTTTTGGT 59526          _        TGATG
           A                     TATCAAGGAA GGGCAGGCG
                                |||||||||| |||||||||
                                ATGGTTTTTT TTTGTTTGT
                                     G        TTGT
GAM1297 MGC20255 3' TGCCTCTGTCTTTCTTGGTG   54545           GC_
                                TATCAAGGAAGG   AGGCG
                                ||||||||||||   |||||
                                GTGGTTCTTTCT   TCCGT
                                      GTC
GAM1297 MGC22014 3' GTGTTGTGTTGTATTGTTCTTC 65118         _      ____   TG
           CCTTGGTG                TATCAAGG AAGGGCAG    GCG  ATG   T
                                |||||||| ||||||||    |||  |||   |
                                GTGGTTCC TTCTTGTT    TGT  TGT   G
                                     C       ATGT   GT
GAM1297 MGC34869 3' TAGCCCTCTGTTTTTGTTTGAT 58718         G      ___   GTGATG
           G                     TATCAAG AAGGGCA   GGC
                                ||||||| |||||||   |||
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                                GTAGTTT TTTTTGT  CCG
                                   G     CTC  AT  G
GAM1297 MGC8407  3' TACCTCCTTGCTCTTCCTAGAT 44118     A        C__  ATG
           G                    TATC AGGAAGGGCAGG  GTG
                                |||| ||||||||||||  |||
                                GTAG TCCTTCTCGTTC  CAT
                                  A         CTC
GAM1297 MRG15   3' ATTTGTGCTTTTGTTTTTTTTT 23283         __   TG TG
                                AAGGAAGGGCA  GGCG  A
                                ||||||||||  ||||  |
                                TTTTTTTTTGT  TCGT  T
                                      TT   GT TAC
GAM1297 MTHFD2   3' AGCAGCTGCCTGCTTTTCTGTG 22793      A         TGATG
           ATG                    TATCA GGAAGGGCAGGCG
                                  ||||| ||||||||||||
                                  GTAGT TCTTTTCGTCCGT
                                     G          CGACGAC
GAM1297 OSBPL1A  3' TGTCATGCTTGAATGTTTTAGA 55491     A   AGGG
           TG                     TATC AGGA   CAGGCGTGATG
                                  |||| ||||   ||||||||||
                                  GTAG TTTT   GTTCGTACTGT
                                    A   GTAA
GAM1297 PABPC5   3' TGTCATTTTGTACTTTTTTTGA 55935          _   C
           TG                     TATCAAGGAAGG GCAGG GTGATG
                                  |||||||||||| ||||| ||||||
                                  GTAGTTTTTTTC TGTTT TACTGT
                                        A   _
GAM1297 PAPSS2   3' ATCAAGATTCTTCCTGATA   60337     A     CAGGCG
                                  TATCA GGAAGGG     TGAT
                                  ||||| |||||||     ||||
                                  ATAGT CCTTCTT     ACTA
                                    _      AGA___
GAM1297 PARG1    3' TATTGTGCTTGTTTTGTGA   17871    AGGAA       TG
                                  TCA    GGGCAGGCG  ATG
                                  |||    |||||||||  |||
                                  AGT    TTTGTTCGT  TAT
                                    GT___       GT
GAM1297 PC4     3' TGTTGTGGCCTTTTTTGAT   22972         G  _
                                  ATCAAGGAAGG CA GGCG
                                  |||||||||| || ||||
                                  TAGTTTTTTCC GT TTGT
                                        G  G
GAM1297 PGCP     3' TGTTATTATCTTTCTTGATA  32848          GCA_
                                  TATCAAGGAAGG   GGCG
                                  ||||||||||||   ||||
                                  ATAGTTCTTTCT   TTGT
                                        ATTA
GAM1297 PPP1R1B  3' TGTTGCGTTTTGTGCTTTGATG 50794      GGA  G    _  TG
                                  TATCAA   AG GCAGG CG  ATG
                                  ||||||   || ||||| ||  |||
```

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                                GTAGTT  TC TGTTT GC  TGT
                                   ___ G    T  GT
GAM1297 PRO0159  5' TGTCATAAATGGTCCTTTTTGG 26951     A       AGGC_
           ATG                   TATC AGGAAGGGC    GTGATG
                                 |||| |||||||||    ||||||
                                 GTAG TTTTTCCTG    TACTGT
                                   G       GTAAA
GAM1297 PRO0159  5' TGTCATAAATGGTCCTTTTTGG 26952     A       AGGC_
           ATG                   TATC AGGAAGGGC    GTGATG
                                 |||| |||||||||    ||||||
                                 GTAG TTTTTCCTG    TACTGT
                                   G       GTAAA
GAM1297 PRO2964  5' TATAACTGCTATCTTTTTTTGG 38263          ___   GC  ATG
           TA                    TATCAAGGAAGG  GCAG  GTG
                                 ||||||||||||  ||||  |||
                                 ATGGTTTTTTTC  CGTC  TAT
                                       TAT   AA
GAM1297 PTPRT    3' GTAACCCCTGTGTTTCTTTGGT 56507         G    C  GATG
           G                     TATCAAGGAAG GCAGG GT
                                 |||||||||| ||||| ||
                                 GTGGTTTCTTT TGTCC CA
                                       G    C  ATGT
GAM1297 RABEX5   3' CAAAACTTGCCCTTCTTTGGT  27959           CG_
                                 ATCAAGGAAGGGCAGG  TG
                                 |||||||||||||||  ||
                                 TGGTTTCTTCCCGTTC  AC
                                       AAA
GAM1297 RBM5     3' TGTTGTGATGTCTTTTCTTGG  20509          GG  TG
                                 TCAAGGAAGGGCA  CG  ATG
                                 ||||||||||||  ||  |||
                                 GGTTCTTTTCTGT  GT  TGT
                                       A_  GT
GAM1297 RNPS1    3' CATTGTGTTTGTACTTTGTTG  55486    G   GG    TG
                                 CAA GAAG  CAGGCG  ATG
                                 ||| ||||  ||||||  |||
                                 GTT TTTC  GTTTGT  TAC
                                   G   AT    GT
GAM1297 RYK      3' TATTGTGTCTGGTAAGTCTTTG 83510       AGG  _   TG
           A                     TCAAGGA   GC AGGCG  ATG
                                 |||||||   || |||||  |||
                                 AGTTTCT   TG TCTGT  TAT
                                     GAA  G    GT
GAM1297 SAC2     3' CATTATGTCGTTACTTTGATA  30724        AAG  A
                                 TATCAAGG   GGC GGCGTGATG
                                 ||||||||   ||| |||||||||
                                 ATAGTTTC   TTG CTGTATTAC
                                      A__   _
GAM1297 SAE1     3' TGTTGTGAATTTTCCTTGGT   19730          GCAGG  TG
                                 ATCAAGGAAGG    CG  ATG
                                 ||||||||||    ||  |||
```

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                                TGGTTCCTTTT    GT  TGT
                                      AA___  GT
GAM1297  SCAND2   3'  AAGATTGCTGCTTTTTTTTGAT 54411             G  TGATG
             A                   TATCAAGGAAGGGCAG CG
                                 |||||||||||||||| ||
                                 ATAGTTTTTTTTCGTC GT
                                       _  TAGAAA
GAM1297  SEC24A   3'  TATTTGTAGGTCCTTTCTTAGT 83567    C       AG   TGATG
             A                   TAT AAGGAAGGGC  GCG
                                 ||| ||||||||||  |||
                                 ATG TTCTTTCCTG  TGT
                                   A        GA   TTAT
GAM1297  SETBP1   3'  TGCCTTTTTTTTTTTCTTGGTA  32086          C__
                                 TATCAAGGAAGGG   AGGCG
                                 ||||||||||||   |||||
                                 ATGGTTCTTTTTT   TCCGT
                                       TTT
GAM1297  SFRS11   3'  TATTATGCACTAACCTTTTTTG 17674          GC  _
             GTG                   TATCAAGGAAGG  AG GCGTGATG
                                 ||||||||||||  || ||||||||
                                 GTGGTTTTTTCC  TC CGTATTAT
                                       AA  A
GAM1297  SKB1     3'  TCTGTTCTTGTTTTGATG    21473        _
                                 TATCAAGG AAGGGCAGG
                                 ||||||||  |||||||||
                                 GTAGTTTT TTCTTGTCT
                                    G
GAM1297  SLB      5'  CATCGTTAGGTATTTCTTTGAT 90260          G  A_   _  ATG
             G                    TATCAAGGAAG GC  GGCG TG
                                 ||||||||||| ||  |||| ||
                                 GTAGTTTCTTT TG  TTGC AC
                                       A  GA   T
GAM1297  SLC11A2  3'  CGTCATGTTTTTCTGATG    7049       AG      _
                                 TATCA  GAAGGGCA GGCG
                                 |||||  ||||||||  ||||
                                 GTAGT  CTTTTTGT CTGC
                                    __       A
GAM1297  SLC2A10  3'  CATCATGTTAGTCTTTGGTTG  48545    GG     AG
                                 CAA  AAGGGC  GCGTGATG
                                 |||  ||||||  ||||||||
                                 GTT  TTTCTG  TGTACTAC
                                   GG     AT
GAM1297  SOX7     3'  TTCACTGACGTCTTTTCTTGGT 49532           AGGC    TG
             A                    TATCAAGGAAGGGC    GTGA
                                 ||||||||||||||    ||||
                                 ATGGTTCTTTTCTG    CACT
                                       CAGT    TG
GAM1297  SPIN     3'  CGTTATTGCCTTTTTTGA    60327      G      __
                                 TCAAG AAGGGCAG  GCG
                                 |||||  ||||||||  |||
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                                AGTTT TTTCCGTT  TGC
                                  _       AT
GAM1297  SSR3     3'  CAATTCTTTACTTTTCTTTGGT 24028           C__   CG  ATG
                 G                 TATCAAGGAAGGG   AGG  TG
                                   ||||||||||||   |||  ||
                                   GTGGTTTCTTTTC   TCT  AC
                                         ATT   TA
GAM1297  SV2      3'  TGTGGCTGCTTTCTTTGGTG   29960          G   G GT
                                   TATCAAGGAAGG CAG C  G
                                   |||||||||||| ||| |  |
                                   GTGGTTTCTTTC GTC G  T
                                         _  G TG
GAM1297  SYPL     3'  CATCTTGCTGTTGCCTTATTTT 94501         _     __    T
                    TGATG                TATCAAGGA AGGGCA  GGCG GATG
                                   |||||||| ||||||  |||| ||||
                                   GTAGTTTTT TTCCGT  TCGT CTAC
                                         A     TG    T
GAM1297  TADA3L   3'  GTTTTTGTTTTGTTTTTTTTTG 22045            _  TGATG
                 A                  TCAAGGAAGGGCAGG CG
                                   ||||||||||||||| ||
                                   AGTTTTTTTTTGTTT GT
                                         T  TTTTGT
GAM1297  TADA3L   3'  TTTTTGTTTTGTTTTTTTTTGA 22048            _  TGATG
                                   TCAAGGAAGGGCAGG CG
                                   |||||||||||||| ||
                                   AGTTTTTTTTTGTTT GT
                                         T  TTTTG
GAM1297  TESK2    3'  TGTCTCTTGCCTTTTCTTGG   63887            CGT
                                   TCAAGGAAGGGCAGG   GATG
                                   ||||||||||||||   ||||
                                   GGTTCTTTTCCGTTC   CTGT
                                         T__
GAM1297  TOLLIP   3'  GCATTGTCCAGATTTTTCTTTG 39195         _______     GCGTGATG
                 AT                  ATCAAGGAA     GGGCAG
                                   |||||||||     ||||||
                                   TAGTTTCTT     CCTGTT
                                        TTTAGA     AC   GT
GAM1297  TOMM34   3'  TCGGGCCCTCCTTTGGTG    23315        A    A_
                                   TATCAAGG AGGGC  GG
                                   |||||||| |||||  ||
                                   GTGGTTTC TCCCG  CT
                                        C     GG
GAM1297  UBA2     3'  TATTATGCCTTTATTTTTGG   19726        AGGGC
                                   TCAAGGA    AGGCGTGATG
                                   |||||||    ||||||||||
                                   GGTTTTT    TCCGTATTAT
                                       ATT__
GAM1297  UBE1C    3'  TTGCCACGATTTGTCTTTTTTT 15604           _   ATG
                                   AAGGAAGGGCAGG CGTG
                                   |||||||||||| ||||
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                                TTTTTTTCTGTTT GCAC
                                      A   CGTTG
GAM1297 UBE3B    3' TGTGTGCTCTACTTTGATG   77449       A     G
                                TATCAAGG AGGGCA GCG
                                |||||||| |||||| |||
                                GTAGTTTC TCTCGT TGT
                                    A     G
GAM1297 UHRF1    3' TATTGTGTTTAGTTCTTTGA  26125       AGG _    TG
                                TCAAGGA  GC AGGCG  ATG
                                |||||||  || |||||  |||
                                AGTTTCT  TG TTTGT  TAT
                                   ___ A    GT
GAM1297 UHRF2    3' CATTGTGCTTTTTTCTGGTG  73830      AG       GGC
                                TATCA  GAAGGGCA  GTG
                                |||||  ||||||||  |||
                                GTGGT  TTTTTCGT  TAC
                                   CT       GT_
GAM1297 VPS28    3' TGTCTGGTGTCTGTCTTTGGTG 33036        A    ___
                                TATCAAGGA GGGCA  GGCG
                                ||||||||| |||||  ||||
                                GTGGTTTCT TCTGT  CTGT
                                     G    GGT
GAM1297 VRP      5' CACCTTGTCTGTCTTTGATA  23917        A     C
                                TATCAAGGA GGGCAGG GTG
                                ||||||||| ||||||| |||
                                ATAGTTTCT TCTGTTC CAC
                                     G     _
GAM1297 WBSCR20A 3' ATTGGGTCCCTTCCTTGG    50568         CAG  G
                                TCAAGGAAGGG  GC TGAT
                                ||||||||||  || ||||
                                GGTTCCTTCCC  TG GTTA
                                      ___ G
GAM1297 ZNF313   3' TGTCACAAATGTTTTCCTT   38567        G  GGC
                                AAGGAAGG CA  GTGATG
                                |||||||| ||  ||||||
                                TTCCTTTT GT  CACTGT
                                     _ AAA
GAM1297 ZWINT    3' TGTTGAGTCCTTTCTTTGTG  23909     C       A_
                                TAT AAGGAAGGGC  GGCG
                                ||| ||||||||||  ||||
                                GTG TTCTTTCCTG  TTGT
                                  T        AG
GAM1297 LOC112970 3' CATCTGCACCTGCCCTTTTTTC 57345     C          C _
           ATA                    TAT AAGGAAGGGCAGG GT GATG
                                ||| |||||||||||| || ||||
                                ATA TTTTTTCCCGTCC CG CTAC
                                  C          A  T
GAM1297 LOC116068 3' TGTTGACACCCTTCTTTGA   74109          CA__
                                TCAAGGAAGGG   GGCG
                                ||||||||||   ||||
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                                AGTTTCTTCCC    TTGT
                                      ACAG
GAM1297  LOC116349 3'  TATTATTTCAGTTTTTCCTTG  74280          A  C
                                CAAGGAAGGGC GG GTGATG
                                |||||||||||  ||  ||||||
                                GTTCCTTTTTG CT TATTAT
                                      A  T
GAM1297  LOC121838 5'  TGTTATTTCTCTTTTCCTTGAT 76520           C   C
                                ATCAAGGAAGGG AGG GTGATG
                                ||||||||||||  |||  ||||||
                                TAGTTCCTTTTC TCT TATTGT
                                      _   T
GAM1297  LOC124470 3'  CGTCATGTTTTCCTTTTC     76146        C
                                GGAAGGG AGGCGTGATG
                                |||||||  |||||||||
                                CTTTTCC TTTGTACTGC
                                    T
GAM1297  LOC126364 3'  CATCCCTGTTTTTTTTTG     76184             C
                                CAAGGAAGGGCAGG GTG
                                ||||||||||||||  |||
                                GTTTTTTTTTGTCC TAC
                                       C
GAM1297  LOC133088 5'  GTTTGTTTTTCCATGATG     75587       A
                                TATCA GGAAGGGCAGGC
                                |||||  ||||||||||||
                                GTAGT CCTTTTTGTTTG
                                   A
GAM1297  LOC133686 3'  GCTTTTTTTTTTTGATA      75617            C
                                TATCAAGGAAGGG AGGC
                                ||||||||||||  ||||
                                ATAGTTTTTTTTT TTCG
                                       _
GAM1297  LOC133686 3'  TATTGTGCTCCATTTGTGATA  75621       AG  A  GCA    TG
                                TATCA  GA GG   GGCG  ATG
                                |||||  ||  ||   ||||  |||
                                ATAGT  TT CC   TCGT  TAT
                                   GT  A  ___    GT
GAM1297  LOC135154 3'  CATTGCGCCTGGCTAATTTTTG 75725       A_  G     TG
                                CAAGGA  GG CAGGCG  ATG
                                ||||||  ||  ||||||  |||
                                GTTTTT  TC GTCCGC  TAC
                                    AA  G     GT
GAM1297  LOC143631 3'  CAGGCTGCCCTCCCTTGGTG   77097        A      G G
                                TATCAAGG AGGGCAG C TG
                                ||||||||  |||||||  |  ||
                                GTGGTTCC TCCCGTC G AC
                                     C      _ G
GAM1297  LOC143872 3'  TGTTGGCCATTCTTTTTTGGT  77156          ___   AG   TGATG
                                ATCAAGGAAG   GGC  GCG
                                ||||||||||   |||  |||
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                                TGGTTTTTTC  CCG  TGT
                                     TTA  GT    G
GAM1297  LOC144363 3'  TGTTGTGTATCAATTACCTTCT 77317          GCAG____  TG
             TTGATA                TATCAAGGAAGG      GCG  ATG
                                   ||||||||||||      |||  |||
                                   ATAGTTTCTTCC      TGT  TGT
                                      ATTAACTA   GT
GAM1297  LOC144558 3'  CATGAGTCTGCCTTTTCTTCAT 84075    C          GTGATG
             G                     TAT AAGGAAGGGCAGGC
                                   |||  ||||||||||||||
                                   GTA TTCTTTTCCGTCTG
                                     C           AGTAC
GAM1297  LOC144962 5'  TATCGTGCAGCAGTTTTTGGTG 77528        AGG  AG
                                   TATCAAGGA   GC  GCGTGATG
                                   |||||||||   ||  ||||||||
                                   GTGGTTTTT   CG  CGTGCTAT
                                        GA_  A_
GAM1297  LOC145333 3'  CATCAGAGGCCTTCTTCTTTGA 84293         GC   G__
                                   TCAAGGAAGG  AGGC   TGATG
                                   ||||||||||  ||||   |||||
                                   AGTTTCTTCT  TCCG   ACTAC
                                         __    GAG
GAM1297  LOC145608 5'  TATTATTTCCCCCTTTTTGGTA 84385       G    CA  C
                                   TATCAAG AAGGG  GG GTGATG
                                   |||||||  |||||  ||  ||||||
                                   ATGGTTT TTCCC  CT TATTAT
                                      _     C_  T
GAM1297  LOC145609 5'  TATTATTTCCCCCTTTTTGGTA 84369       G    CA  C
                                   TATCAAG AAGGG  GG GTGATG
                                   |||||||  |||||  ||  ||||||
                                   ATGGTTT TTCCC  CT TATTAT
                                      _     C_  T
GAM1297  LOC145725 3'  GTGTCTACTCAGTTTTTTTTTG 77888           _____    TGATG
             GTG                     TATCAAGGAAGGGC    AGGCG
                                     ||||||||||||||    |||||
                                     GTGGTTTTTTTTTG    TCTGT
                                           ACTCA       GT
GAM1297  LOC145732 3'  TGTCTACTCAGTTTTTTTTTGG 77901           _____    TGATG
             TG                      TATCAAGGAAGGGC    AGGCG
                                     ||||||||||||||    |||||
                                     GTGGTTTTTTTTTG    TCTGT
                                           ACTCA       G
GAM1297  LOC145781 3'  GTTCATGCATGCTCTACTTTGA 77959       A    G    TG
             TA                      TATCAAGG AGGGCA GCGTGA
                                     ||||||||  ||||||  ||||||
                                     ATAGTTTC TCTCGT CGTACT
                                        A     A     TGT
GAM1297  LOC145845 3'  CGCTTTGTTTTTCTTTTGTG  84546    C        _
                                   TAT AAGGAAGGGCAG GCG
                                   |||  ||||||||||| |||
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                                GTG TTTCTTTTTGTT CGC
                                  T         T
GAM1297  LOC145945 5'  CGTGTTTTCTTTTTTGATA   84565           CAG
                                TATCAAGGAAGGG  GCG
                                |||||||||||||  |||
                                ATAGTTTTTTCTT  TGC
                                     TTG
GAM1297  LOC146176 5'  CATCAATGCTTGTTTTTCCTGG 78192      A          _
                TG                TATCA GGAAGGGCAGGCGT GATG
                                |||||| |||||||||||||| ||||
                                GTGGT CCTTTTTGTTCGTA CTAC
                                  _          A
GAM1297  LOC146315 3'  TGTCACTGAAACCTTTTTTG  61559        GCAGGC
                                CAAGGAAGG     GTGATG
                                |||||||||     ||||||
                                GTTTTTTCC     CACTGT
                                     AAAGT_
GAM1297  LOC146455 3'  TCACAGCTTTTCTTGATA    78467         GGGCA  _
                                TATCAAGGAA    GGC GTGA
                                ||||||||||    ||| ||||
                                ATAGTTCTTT    TCG CACT
                                     _____  A
GAM1297  LOC146819 3'  CATTATGTCTTTTTTTCTTTG  78740         C
                                CAAGGAAGGG AGGCGTGATG
                                |||||||||| ||||||||||
                                GTTTCTTTTT TCTGTATTAC
                                     T
GAM1297  LOC146821 3'  CGTTATGTCTTTTTTTCTTTG  78730         C
                                CAAGGAAGGG AGGCGTGATG
                                |||||||||| ||||||||||
                                GTTTCTTTTT TCTGTATTGC
                                     T
GAM1297  LOC146901 3'  TGCCCCCATCTTTGGTG     84915         A  CA
                                TATCAAGGA GGG  GGCG
                                ||||||||| |||  ||||
                                GTGGTTTCT CCC  CCGT
                                     A  __
GAM1297  LOC147965 3'  CGTTTAAGGCTTTCCTTGGTA  79299          GC__
                                TATCAAGGAAGG   AGGCG
                                ||||||||||||   |||||
                                ATGGTTCCTTTC   TTTGC
                                     GGAA
GAM1297  LOC148446 3'  ACCCTTGTCCTTCTTGATA    79607        G       C
                                TATCAAG AAGGGCAGG GT
                                ||||||| ||||||||| ||
                                ATAGTTC TTCCTGTTC CA
                                  _       C
GAM1297  LOC149086 5'  ACTCCTGTCCTTCTTTGGT    85489            C
                                ATCAAGGAAGGGCAGG GT
                                |||||||||||||||| ||
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                                TGGTTTCTTCCTGTCC CA
                                          T
GAM1297  LOC149276 5'  GCCCTTGCCTGCCTTTCTTTTA 85536     C           TGATG
                TG                  TAT AAGGAAGGGCAGGCG
                                    ||| ||||||||||||||
                                    GTA TTTCTTTCCGTCCGT
                                      T           TCCCGT
GAM1297  LOC149332 5'  CATTGGGCCTCTTTTTCTGGTG 85545      A     C   G
                                    TATCA GGAAGGG AGGC TGATG
                                    ||||| ||||||| |||| |||||
                                    GTGGT CTTTTTC TCCG GTTAC
                                       _      _   G
GAM1297  LOC149603 3'  ATCGTGTCTCATCTTGCT    71172    G   GC
                                    AG AAGG  AGGCGTGAT
                                    || ||||  |||||||||
                                    TC TTCT  TCTGTGCTA
                                     G   AC
GAM1297  LOC150350 3'  CATCACAATATCTATTTTTGAT 80572         A   CAGGC
                A                    TATCAAGGA GGG    GTGATG
                                    ||||||||| |||    ||||||
                                    ATAGTTTTT TCT    CACTAC
                                          A   ATAA_
GAM1297  LOC151318 3'  TGTCGTGTCTAAGGTCTTTGAT 81032         AGGGC
                G                    TATCAAGGA    AGGCGTGATG
                                    |||||||||    ||||||||||
                                    GTAGTTTCT    TCTGTGCTGT
                                          GGAA_
GAM1297  LOC151742 3'  TGTTGTGTCCTCTCTTTG    58348       _     _
                                    CAAGGA AGGGCA GGCG
                                    |||||| |||||| ||||
                                    GTTTCT TCCTGT TTGT
                                       C     G
GAM1297  LOC151826 3'  TGTTATGTGATGTTTTGTTTTG 81190        A     G_
                ATA                    TATCAAGG AGGGCA  GCGTGATG
                                    |||||||| ||||||  ||||||||
                                    ATAGTTTT TTTTGT  TGTATTGT
                                          G     AG
GAM1297  LOC151963 3'  TGCTTTGCCCTCTTTGATA   81217         A     _
                                    TATCAAGGA GGGCAG GCG
                                    ||||||||| |||||| |||
                                    ATAGTTTCT CCCGTT CGT
                                          _     T
GAM1297  LOC151963 3'  TGGCTCCCTGTTTTGGTG    81218        A   C  G
                                    TATCAAGG AGGG AG CG
                                    |||||||| |||| || ||
                                    GTGGTTTT TCCC TC GT
                                          G   _  G
GAM1297  LOC152674 5'  TGTCATGTTCAGTTGCATTCCT 87006          GG   ____
                TGGTG                    TATCAAGGAA  GCAG   GCGTGATG
                                    ||||||||||  ||||   ||||||||
```

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                                GTGGTTCCTT  CGTT    TGTACTGT
                                      A_    GACT
GAM1297  LOC152972 5'  TATCAGTTCCTCTGTCTTTCTT 81637           ____  G
               T                    AAGGAAGGGCAG    GC TGATG
                                    ||||||||||||    || |||||
                                    TTTCTTTCTGTC    TG ACTAT
                                          TCCT  _
GAM1297  LOC153027 3'  CATTGTGTTTGTACTTTGTTG  68030     G    GG     TG
                                    CAA GAAG  CAGGCG  ATG
                                    ||| ||||  ||||||  |||
                                    GTT TTTC  GTTTGT  TAC
                                      G    AT     GT
GAM1297  LOC154089 3'  TGGCTGTACTTTTTTGATA    81947          GG   G
                                    TATCAAGGAAG  CAG CG
                                    ||||||||||  ||| ||
                                    ATAGTTTTTTC  GTC GT
                                          AT   G
GAM1297  LOC154865 3'  CATTATAAAGTGCTCTTTCTTG 82061           GGC_
               A                    TCAAGGAAGGGCA    GTGATG
                                    ||||||||||||    ||||||
                                    AGTTCTTTCTCGT    TATTAC
                                          GAAA
GAM1297  LOC155038 3'  TGTTATGCTGGTTTCCTGGGTG 82186      A     GG  A
                                    TATC AGGAA  GC GGCGTGATG
                                    |||| |||||  || |||||||||
                                    GTGG TCCTT  TG TCGTATTGT
                                      G    __  G
GAM1297  LOC157278 3'  GTCTGCCTTTTCTTCATG     87709     C
                                    TAT AAGGAAGGGCAGGC
                                    ||| ||||||||||||||
                                    GTA TTCTTTTCCGTCTG
                                      C
GAM1297  LOC157464 5'  CATTATGTTTTTTACTTGATA  87744        GAAGGGC
                                    TATCAAG      AGGCGTGATG
                                    |||||||      ||||||||||
                                    ATAGTTC      TTTGTATTAC
                                         ATTT___
GAM1297  LOC158332 3'  CGTTGTTGTTTTTTGGTA     82765          G    G
                                    TATCAAGGAA GGCAG CG
                                    |||||||||| ||||| ||
                                    ATGGTTTTTT TTGTT GC
                                          G    _
GAM1297  LOC158363 3'  CGCCTGTCTTTCTCTGGTA    88116       AG
                                    TATCA  GAAGGGCAGGCG
                                    |||||  ||||||||||||
                                    ATGGT  CTTTCTGTCCGC
                                       CT
GAM1297  LOC158714 3'  TGTCACTCCTCTTTCCCTTGGT 82869         A   C   C
               A                    TATCAAGG AGGG AGG GTGATG
                                    |||||||| |||| ||| ||||||
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                                ATGGTTCC TTTC TCC CACTGT
                                    C   _  T
GAM1297  LOC158956 3'  ATTTGCTGGTTGTTTATTTTTT 67211        _    G _ TG TG
             GGTA                  TATCAAGGAA GGGCAG C G  A
                                |||||||||| ||||||  | |  |
                                ATGGTTTTTT TTTGTT G C  T
                                     A     G T GT TAC
GAM1297  LOC162461 3'  TATTGGCTGTCTGTTTTTTGAT 83240        _    G  TGATG
             G                   TATCAAGGAA GGGCAG CG
                                |||||||||| ||||||  ||
                                GTAGTTTTTT TCTGTC GT
                                     G     G  TAT
GAM1297  LOC196074 3'  TGTTATGTCCCTGAATGTCTTG 88972       AA___   CA
             GTA                   TATCAAGG    GGG  GGCGTGATG
                                ||||||||    |||  |||||||||
                                ATGGTTCT    TCC  CTGTATTGT
                                    GTAAG  __
GAM1297  LOC196957 3'  GTGTCTACTCAGTTTTTTTTTG 89194          _____    TGATG
             GTG                   TATCAAGGAAGGGC    AGGCG
                                ||||||||||||||    |||||
                                GTGGTTTTTTTTTG    TCTGT
                                       ACTCA       GT
GAM1297  LOC196961 3'  GTGTCTACTCAGTTTTTTTTTG 89207          _____    TGATG
             GTG                   TATCAAGGAAGGGC    AGGCG
                                ||||||||||||||    |||||
                                GTGGTTTTTTTTTG    TCTGT
                                       ACTCA       GT
GAM1297  LOC197049 3'  TGTCCTGGGGTCCTTCTTTG  91262        ___  _
                                CAAGGAAGGGC   AGG CG
                                ||||||||||   ||| ||
                                GTTTCTTCCTG   TCC GT
                                      GGG   T
GAM1297  LOC197138 3'  TGTCTACTCAGTTTTTTTTTGG 89257          _____    TGATG
             TG                    TATCAAGGAAGGGC    AGGCG
                                ||||||||||||||    |||||
                                GTGGTTTTTTTTTG    TCTGT
                                       ACTCA       G
GAM1297  LOC199906 3'  CATCACGCCTGGCTAATTTTTG 89847      A_  G
                                CAAGGA  GG CAGGCGTGATG
                                ||||||  || ||||||||||
                                GTTTTT  TC GTCCGCACTAC
                                    AA  G
GAM1297  LOC199906 5'  CGTTGCCCTGTTCTTGGTG   89852        _    G
                                TATCAAGGA AGGGCAG CG
                                |||||||| ||||||| ||
                                GTGGTTCTT TCCCGTT GC
                                     G     _
GAM1297  LOC200609 5'  CATCACTACTCTTTTTTTG   91660        GC  GC
                                CAAGGAAGG  AG  GTGATG
                                |||||||||  ||  ||||||
```

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                                GTTTTTTTC  TC  CACTAC
                                     __  AT
GAM1297  LOC200918 3'  TATCATCTGCTTCCTTTCTGGA 90369      A      __    GC
                TG                    TATC AGGAAGG  GCAG  GTGATG
                                      ||||  |||||||  ||||  ||||||
                                      GTAG TCTTTCC  CGTC  TACTAT
                                        G      TT   __
GAM1297  LOC201252 3'  TGTTAGCTCTTTTCTTGA    89558          _  AG
                                      TCAAGGAAGG GC  GCG
                                      ||||||||||  ||  |||
                                      AGTTCTTTTC CG  TGT
                                            T  AT
GAM1297  LOC202934 5'  CATTAAACCTCTTTCTTTTGTA 92032     C       GC   CG
                                      TAT AAGGAAGG  AGG  TGATG
                                      |||  ||||||||  |||  |||||
                                      ATG TTTCTTTC  TCC  ATTAC
                                        T       __   AA
GAM1297  LOC203377 5'  TGTGCCTTTTTTGTTTTTCTTTG 92261            ____   GT ATG
                G                     TCAAGGAAGGGCA    GGC  G
                                      ||||||||||||||    |||  |
                                      GGTTTCTTTTTGT    CCG  T
                                            TTTT   TG
GAM1297  LOC203411 3'  ATGAGCTTGCTGTTTCTTTGAT 92312          _      GTGATG
                G                     TATCAAGGAAG GGCAGGC
                                      ||||||||||| |||||||
                                      GTAGTTTCTTT TCGTTCG
                                            G      AGTAT
GAM1297  LOC204084 5'  CATTGTATCTCCTTTCTTG    90994         GC  GC TG
                                      CAAGGAAGG  AG  G  ATG
                                      |||||||||  ||  |  |||
                                      GTTCTTTCC  TC  T  TAC
                                           __  TA GT
GAM1297  LOC219333 3'  TATAGGGTTTTTTCTTTCCTTG 95187           C_   GTGATG
                ATG                     TATCAAGGAAGGG  AGGC
                                      ||||||||||||||  ||||
                                      GTAGTTCCTTTCT  TTTG
                                            TT    GGATAT
GAM1297  LOC219672 5'  TATTACTACCCCTTTTTTGG   92972          CAGGC
                                      TCAAGGAAGGG    GTGATG
                                      ||||||||||     ||||||
                                      GGTTTTTTCCC    CATTAT
                                            CAT__
GAM1297  LOC220018 5'  GCCCCTTCTTTTCTTGGTG    95029           C   C
                                      TATCAAGGAAGGG AGG GT
                                      ||||||||||||| ||| ||
                                      GTGGTTCTTTTCT TCC CG
                                            _  C
GAM1297  LOC220045 3'  TGCCAAATTCTTTCTGATG    95038       A      CA_
                                      TATCA GGAAGGG   GGCG
                                      |||||  |||||||   ||||
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                                GTAGT CTTTCTT   CCGT
                                  _      AAA
GAM1297  LOC220692 5'  CGTTATGCCTGCCCTTTCCTG  92865    A
                                CA GGAAGGGCAGGCGTGATG
                                || ||||||||||||||||||
                                GT CTTTCCCGTCCGTATTGC
                                 C
GAM1297  LOC221191 3'  TTGATGTCTGTTTTTGATA    95222        AAGG       GATG
                                TATCAAGG    GCAGGCGT
                                ||||||||    ||||||||
                                ATAGTTTT    TGTCTGTA
                                     ____       GTTT
GAM1297  LOC221241 3'  CATTTATTTGTCTTCTTTGATA 95230           G    CGT
                                TATCAAGGAAGG CAGG   GATG
                                |||||||||||| ||||   ||||
                                ATAGTTTCTTCT GTTT   TTAC
                                      _    AT_
GAM1297  LOC221241 5'  TGTCAAGGTCCCTTTCTTG    95231          _ AGGCG
                                CAAGGAAGGG C     TGATG
                                |||||||||| |     |||||
                                GTTCTTTCCC G     ACTGT
                                      T GA___
GAM1297  LOC221296 3'  TATTGTGCTTTGTTTTTGCT   93618    G       _   TG
                                AG AAGGGCAG GCG  ATG
                                || |||||||| |||  |||
                                TC TTTTTGTT CGT  TAT
                                 G       T   GT
GAM1297  LOC221322 3'  ACTTCTGCTTTTCTTTGGT    93581             C
                                ATCAAGGAAGGGCAGG GT
                                |||||||||||||||| ||
                                TGGTTTCTTTTCGTCT CA
                                          T
GAM1297  LOC221395 3'  TCTGCATGTGTGCTTTTTTTTG 93663             G     ATG
           GTG                    TATCAAGGAAGGGCA GCGTG
                                |||||||||||||| |||||
                                GTGGTTTTTTTTCGT TGTAC
                                          G     GTCTA
GAM1297  LOC221395 3'  TGTGTGCTTTTTTTTGGTG    93664             G
                                TATCAAGGAAGGGCA GCG
                                |||||||||||||| |||
                                GTGGTTTTTTTTCGT TGT
                                          G
GAM1297  LOC221806 5'  TGTCAGCTTATCTTCTTTGATA 94112           GC    G
                                TATCAAGGAAGG  AGGC TGATG
                                ||||||||||||  |||| |||||
                                ATAGTTTCTTCT  TTCG ACTGT
                                      A_    _
GAM1297  LOC221962 3'  CATGAGTCTGCCTTTTCTTCAT 94238     C           GTGATG
           G                     TAT AAGGAAGGGCAGGC
                                ||| ||||||||||||||
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                                GTA TTCTTTTCCGTCTG
                                  C           AGTAC
GAM1297  LOC221979 5'  CGTCACTCCTCTTTCCCTTGGT 94219        A   C   C
                A                  TATCAAGG AGGG AGG GTGATG
                                   |||||||| |||| ||| ||||||
                                   ATGGTTCC TTTC TCC CACTGC
                                       C   _  T
GAM1297  LOC253128 3'  TATTACTCCTTCCTTTCTTGG  96578          C   C
                                   TCAAGGAAGGG AGG GTGATG
                                   |||||||||||| ||| ||||||
                                   GGTTCTTTCCT TCC CATTAT
                                          _  T
GAM1297  LOC253776 3'  CATCGTCCCCTCTTTTCTTGG  99293          CA  CG
                                   TCAAGGAAGGG  GG  TGATG
                                   ||||||||||  ||  |||||
                                   GGTTCTTTTCT  CC  GCTAC
                                          C_  CT
GAM1297  LOC253832 3'  ATTATGCACTTTCATGGTA   96588      A    GGCAG
                                   TATCA GGAAG    GCGTGAT
                                   ||||| |||||    |||||||
                                   ATGGT CTTTC    CGTATTA
                                      A    A____
GAM1297  LOC253951 5'  CGTCATGCCCATCTATTTTGGT 99413        A   GCA
                G                  TATCAAGG AGG   GGCGTGATG
                                   |||||||| |||   |||||||||
                                   GTGGTTTT TCT   CCGTACTGC
                                       A   AC_
GAM1297  LOC254100 5'  CATTAGGCTCTTCTTGGGTG   98151      A       AGGC
                                   TATC AGGAAGGGC    GTG
                                   |||| |||||||||    |||
                                   GTGG TTCTTCTCG    TAC
                                     G        GAT_
GAM1297  LOC254130 3'  TGCTTTTTCCCTTCTTTGATG  97382           C__
                                   TATCAAGGAAGGG   AGGCG
                                   ||||||||||||   |||||
                                   GTAGTTTCTTCCC   TTCGT
                                           TTT
GAM1297  LOC255223 3'  TGTCCTGGGGTCCTTCTTTG   98360          ___  _
                                   CAAGGAAGGGC   AGG CG
                                   ||||||||||   ||| ||
                                   GTTTCTTCCTG   TCC GT
                                         GGG   T
GAM1297  LOC255360 3'  ATCACAGCCTCTCTTGATG    98762      AGGA   C   _
                                   TATCA    AGGG AGGC GTGAT
                                   |||||    |||| |||| |||||
                                   GTAGT    TCTC TCCG CACTA
                                      _____   _   A
GAM1297  LOC255465 5'  CATTAAGCCTCTTTCTTTTGTA 99107     C       GC   G
                                   TAT AAGGAAGG  AGGC TGATG
                                   ||| ||||||||  |||| |||||
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                                ATG TTTCTTTC  TCCG ATTAC
                                  T       __    A
GAM1297  LOC255855 3'  TATGCTGCTCTCTCTTGATG   97960       GA      G
                                TATCAAG  AGGGCAG CGTG
                                |||||||  ||||||| ||||
                                GTAGTTC  TCTCGTC GTAT
                                    TC      _
GAM1297  LOC256447 3'  ATTGTTCCTGTCTTGATG    96977      AGGAA      C TG
                                TATCA    GGGCAGG G  AT
                                |||||    ||||||| |  ||
                                GTAGT    TCTGTCC T  TA
                                   _____      T GT
GAM1297  LOC51110  3'  CATAATTGCTTTGTCTTGATG  32625       GA      GC
                                TATCAAG  AGGGCAG  GTG
                                |||||||  |||||||  |||
                                GTAGTTC  TTTCGTT  TAC
                                    TG      AA
GAM1297  LOC51605  3'  TATTTTACTGCTCTTTTTTG   32512          GCGT
                                CAAGGAAGGGCAG   GATG
                                ||||||||||||    ||||
                                GTTTTTTCTCGTC    TTAT
                                       ATT_
GAM1297  LOC56920  3'  TGTCGCGCCGTGATATCTTGGT 39800        AAGGG  _
           G                     TATCAAGG    CA GGCGTGATG
                                |||||||     || |||||||||
                                GTGGTTCT    GT CCGCGCTGT
                                    ATA__  G
GAM1297  LOC90309  5'  TATTGTACTACTCTTCTTT   62876        C  GC TG
                                AAGGAAGGG AG  G  ATG
                                |||||||| ||  |  |||
                                TTTCTTCTC TC  T  TAT
                                     A  A_ GT
GAM1297  LOC90355  5'  TATTATGTCTGTGTTCCCTTGG 53768       A  G
                                TCAAGG AG GCAGGCGTGATG
                                |||||| || ||||||||||||
                                GGTTCC TT TGTCTGTATTAT
                                   C  G
GAM1297  LOC91115  3'  CATCATGTTTGCCAGACTGGT  65552      A GAAG
                                ATCA G   GGCAGGCGTGATG
                                |||| |   ||||||||||||
                                TGGT C   CCGTTTGTACTAC
                                  _ AGA_
GAM1297  LOC91963  5'  CATTTCTTCTTTCTTTGGTG   68317          C   C
                                TATCAAGGAAGGG AGG GTG
                                |||||||||||| ||| |||
                                GTGGTTTCTTTCT TCT TAC
                                       _  T
GAM1297  LOC92126  3'  CGTCGTCGTTTTTCCTTC    68772       C    _
                                GAAGGG AGGCG TGATG
                                |||||| ||||| |||||
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                                CTTCCT TTTGC GCTGC
                                   T    T
GAM1297 LOC92218 3' TGTTTGTCTGCACTTTCTTGAT 69032          G      TGATG
             A                    TATCAAGGAAG GCAGGCG
                                  |||||||||||| |||||||
                                  ATAGTTCTTTC CGTCTGT
                                        A      TTGT
GAM1297 LOC93444 3' CATTATGTTCTAGTTCTTGA  72824       AG  CA
                                  TCAAGGA  GG  GGCGTGATG
                                  |||||||  ||  |||||||||
                                  AGTTCTT  TC  TTGTATTAC
                                     GA  __
GAM1297 LOC93626 3' TGTGTGTTTTTACCTTGGTG  73131        _     G
                                  TATCAAGG AAGGGCA GCG
                                  |||||||| ||||||| |||
                                  GTGGTTCC TTTTTGT TGT
                                       A      G
GAM1297 LOC96597 5' CTTGTTTTTTCCTTGGTG    67458          _
                                  TATCAAGGAAGGG CAGG
                                  |||||||||||| ||||
                                  GTGGTTCCTTTTT GTTC
                                         T
GAM1298 ANPEP    3' GCTCCAGGGCCAGATGAGC   8565         _ AGGGG
                                  GCTCATTTG C    GGAGC
                                  ||||||||| |    |||||
                                  CGAGTAGAC G    CCTCG
                                       C GGA__
GAM1298 CLU      3' GCTCCCCCCAAGATGAGC    10213        GCA
                                  GCTCATTT   GGGGGGAGC
                                  ||||||||   |||||||||
                                  CGAGTAGA   CCCCCCTCG
                                     A__
GAM1298 F13A1    3' CTCAGCCTTGCAAATAGC    92710     C        GG
                                  GCT ATTTGCAGGG  GAG
                                  ||| ||||||||||  |||
                                  CGA TAAACGTTCC  CTC
                                    _        GA
GAM1298 HRH2     3' GCTCCCTTTTAAAAGGAGC   42510     A  GC
                                  GCTC TTT  AGGGGGGAGC
                                  |||| |||  ||||||||||
                                  CGAG AAA  TTTTCCCTCG
                                    G  A_
GAM1298 IFNGR2   3' CTTGACTTTGGCAAATGAGC  19848         _   GG
                                  GCTCATTTGC AGGG  GAG
                                  |||||||||| ||||  |||
                                  CGAGTAAACG TTTC  TTC
                                        G   AG
GAM1298 PAK4     3' TCCAGCCCCTGCAGCAAATGA  20829      ____      __
                                  TCATT   TGCAGGGG  GGA
                                  |||||   ||||||||  |||
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                                AGTAA  ACGTCCCC  CCT
                                  ACG       GA
GAM1298  PIM2     3'  CCCAATCCTACAAAGGAGC   60651     A   C   __
                                GCTC TTTG AGGG  GGG
                                |||| |||| ||||  |||
                                CGAG AAAC TCCT  CCC
                                  G   A   AA
GAM1298  PKHD1    5'  TTTGGCTGGGACACAAACGAGT 57721     A   CAGGGGGG
                                GCTC TTTG       AGCCAAA
                                |||| ||||       |||||||
                                TGAG AAAC       TCGGTTT
                                  C   ACAGGG__
GAM1298  PLAT     3'  CTCCTCAAAAGCAAATGAG   53395        AGG_
                                CTCATTTGC   GGGGAG
                                |||||||||   ||||||
                                GAGTAAACG   CTCCTC
                                     AAAA
GAM1298  RAI2     3'  TTTGACTTTTCACAAATGAGT  41717        CAGG GG   C
                                GCTCATTTG   G  GAG CAAA
                                |||||||||   |  ||| ||||
                                TGAGTAAAC   C  TTC GTTT
                                     A___ TT   A
GAM1298  TGFB3    3'  GGCTCCGGGCAAATGGC     13719    T     AGGGG
                                GC CATTTGC    GGAGCC
                                || |||||||    ||||||
                                CG GTAAACG    CCTCGG
                                 _     GG___
GAM1298  BTN2A2   3'  TCCAGCCTACAGATGAGC    23771        C   GG
                                GCTCATTTG AGG  GGA
                                ||||||||| |||  |||
                                CGAGTAGAC TCC  CCT
                                     A   GA
GAM1298  C20orf72 5'  TTCGACCGTTGCAAATAG    54609    C      G  G_
                                CT ATTTGCAG GG  GAG
                                || |||||||| ||  |||
                                GA TAAACGTT CC  CTT
                                 _      G  AG
GAM1298  DOC2A    3'  GCTAGTCCCTGCAAATATGC   14563    TC        GG
                                GC  ATTTGCAGGGG  AGC
                                ||  ||||||||||  |||
                                CG  TAAACGTCCCT  TCG
                                  TA         GA
GAM1298  FADS1    3'  GCTCCATAAGCAAGTGAGC   26382        AGGGG
                                GCTCATTTGC    GGAGC
                                ||||||||||    |||||
                                CGAGTGAACG    CCTCG
                                     AATA_
GAM1298  FLJ20413 3'  CTCAATCCCTGCAAATGA    35595          G_
                                TCATTTGCAGGGG  GAG
                                ||||||||||||  |||
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                                AGTAAACGTCCCT  CTC
                                      AA
GAM1298 HTATIP2  3' CTTATGACCGTGCAAATGAGC 22167         G  GG__
                                GCTCATTTGCA GG   GAG
                                |||||||||||  ||   |||
                                CGAGTAAACGT CC   TTC
                                     G  AGTA
GAM1298 KIAA1423 3' CCCAACCCACTAAATGAGC   62392        CA  __
                                GCTCATTTG  GGG  GGG
                                |||||||||  |||  |||
                                CGAGTAAAT  CCC  CCC
                                     CA   AA
GAM1298 MFN1     3' TTCAACTTGAAAATGAGC    54322        G   GG
                                GCTCATTT CAGG  GGA
                                ||||||||  ||||  |||
                                CGAGTAAA GTTC  CTT
                                    A    AA
GAM1298 MGC15619 3' GCCTTAATTGAAAATGAGC   51402        G   GG   A
                                GCTCATTT CAG  GGG GC
                                ||||||||  |||  ||| ||
                                CGAGTAAA GTT  TTC CG
                                    A   AA  _
GAM1298 MGEA6    5' GCTCCCCCCCGCAGCCGGC    21013     CAT   A
                                GCT   TTGC GGGGGGGAGC
                                |||   ||||  |||||||||
                                CGG   GACG CCCCCCTCG
                                  CC_   _
GAM1298 NMT1     3' GCTCCCCTTCTGAATCAGC    41147     C   TG   _
                                GCT ATT  CAGG GGGGAGC
                                ||| |||  ||||  |||||||
                                CGA TAA  GTCT CCCCTCG
                                  C   __   T
GAM1298 P114-RHO-GEF 3' CTCAGCCCCCGGGAAATGAGC 31669        GCA   __
                                GCTCATTT   GGGGG  GAG
                                ||||||||   |||||  |||
                                CGAGTAAA   CCCCC  CTC
                                     GGG    GA
GAM1298 TRPV5    5' CTCAGCTCTGCAAAGAGC    39522     A       GG
                                GCTC TTTGCAGGG  GAG
                                ||||  |||||||||  |||
                                CGAG AAACGTCTC  CTC
                                  _       GA
GAM1298 LOC126961 3' GGCTCCCCCCCGCGCGTGA    75121     T   A
                                TCAT TGC GGGGGGGAGCC
                                ||||  ||| ||||||||||
                                AGTG GCG CCCCCCTCGG
                                  C   _
GAM1298 LOC143915 3' CTCCCCTCGGGCAACAAGC   83906     CAT   A_
                                GCT   TTGC  GGGGGGAG
                                |||   ||||  ||||||||
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                                CGA  AACG  CTCCCCTC
                                  AC_   GG
GAM1298  LOC145623 5'  TTGGCAGCTCCAGCAAATGAGC 84398         AG   GA
                                GCTCATTTGC  GGGG  GCCAA
                                ||||||||||  ||||  |||||
                                CGAGTAAACG  CCTC  CGGTT
                                     A_   GA
GAM1298  LOC146268 3'  CCCGGGAATCTGCAAATGAGC  78335          _____
                                GCTCATTTGCAGG    GGG
                                ||||||||||||    |||
                                CGAGTAAACGTCT    CCC
                                       AAGGG
GAM1298  LOC148887 3'  GGCTCCCCCGCATGCGC    85405    T  TT   AG
                                GC CA  TGC  GGGGGAGCC
                                || ||  |||  |||||||||
                                CG GT  ACG  CCCCCTCGG
                                 C __  __
GAM1298  LOC207043 3'  GCTCCCCCCGGGTATCAGC   91078    CATT  A_
                                GCT   TGC  GGGGGGAGC
                                |||   |||  |||||||||
                                CGA   ATG  CCCCCCTCG
                                  CT__  GG
GAM1298  LOC253786 5'  TTAACTTTTGCAAATGAGC   98836           GG
                                GCTCATTTGCAGGGG  AG
                                ||||||||||||||  ||
                                CGAGTAAACGTTTTC  TT
                                       AA
GAM1298  LOC253974 3'  TTTGGCTCCCCCCTGCAAATGA 99286
            GC                   GCTCATTTGCAGGGGGGAGCCAAA
                                ||||||||||||||||||||||||||
                                CGAGTAAACGTCCCCCCTCGGTTT

GAM1298  LOC256905 3'  TCCATGTCCCTGCAAATGA   98663          ___
                                TCATTTGCAGGGG  GGA
                                ||||||||||||  |||
                                AGTAAACGTCCCT  CCT
                                       GTA
GAM1298  LOC257395 3'  GGCTCCCCCCCGCGCGTGA    97149     T  A
                                TCAT TGC GGGGGGAGCC
                                |||| ||| ||||||||||
                                AGTG GCG CCCCCCTCGG
                                  C  _
GAM1298  LOC90233  3'  CCCAGGTCCTGCAAAGGAGC  57193     A      ___
                                GCTC TTTGCAGGG  GGG
                                |||| |||||||||  |||
                                CGAG AAACGTCCT  CCC
                                  G       GGA
GAM1299  ASH1     3'  CCATCTATTCTCTGT      38086      A  ATAC
                                ACAGA GA   ATAGATGG
                                ||||| ||   ||||||||
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                              TGTCT CT    TATCTACC
                                 _ ____
GAM1299 ATP4A    3' GCCCCACCAGTATCTGCTTCTG 7373         A__   ATAGA  A
             TA                  TACAGAAG  ATAC    TGG GC
                              ||||||||  ||||    ||| ||
                              ATGTCTTC  TATG    ACC CG
                                  GTC   ACC__   C
GAM1299 BCAS1    3' GCTCCATGTATATATTCTTCTG 14713         C  G
                              CAGAAGAATA ATA ATGGAGC
                              |||||||||| ||| |||||||
                              GTCTTCTTAT TAT TACCTCG
                                    A  G
GAM1299 CHAC     3' CTCCATCTTTTTCTCTGTA   53953       A  TACAT
                              TACAGA GAA    AGATGGAG
                              |||||| |||    ||||||||
                              ATGTCT CTT    TCTACCTC
                                 _  TT___
GAM1299 CHC1L    5' GCAAATCATATATTCTTCTGTG 8856          C  A  GGA
                              TACAGAAGAATA AT GAT  GC
                              |||||||||||| || |||  ||
                              GTGTCTTCTTAT TA CTA  CG
                                    A  _  AA_
GAM1299 DFFB     3' GCTCCATCCTCTTGACTCTTCT 88773      ATA  TA__
                              AGAAGA  CA   GATGGAGC
                              ||||||  ||   ||||||||
                              TCTTCT  GT   CTACCTCG
                                 CA_  TCTC
GAM1299 DLG4     5' CCTAAGTGTATTCTTCTG    9080           AGAT
                              CAGAAGAATACAT   GG
                              ||||||||||||    ||
                              GTCTTCTTATGTG   CC
                                    AAT_
GAM1299 EIF2C1   3' CTCCATCCTTCCTCTGTG    25188      A  TACATA
                              TACAGA GAA     GATGGAG
                              |||||| |||     |||||||
                              GTGTCT CTT     CTACCTC
                                 C  C_____
GAM1299 GABRE    3' CTCCATCTTTCGTCTG      18282     A  TACAT
                              CAGA GAA    AGATGGAG
                              |||| |||    ||||||||
                              GTCT CTT    TCTACCTC
                                G  _____
GAM1299 GABRE    3' CTCCATCTTTCGTCTG      42057     A  TACAT
                              CAGA GAA    AGATGGAG
                              |||| |||    ||||||||
                              GTCT CTT    TCTACCTC
                                G  _____
GAM1299 GABRE    3' CTCCATCTTTCGTCTG      42061     A  TACAT
                              CAGA GAA    AGATGGAG
                              |||| |||    ||||||||
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                                GTCT CTT    TCTACCTC
                                  G  _____
GAM1299  GABRE    3'  CTCCATCTTTCGTCTG     42072     A  TACAT
                                CAGA GAA    AGATGGAG
                                |||| |||    ||||||||
                                GTCT CTT    TCTACCTC
                                  G  _____
GAM1299  MADH4    3'  CAGTAGTTGTATTCTTCTGTA  19306           TAGA_
                                TACAGAAGAATACA    TG
                                ||||||||||||||    ||
                                ATGTCTTCTTATGT    AC
                                        TGATG
GAM1299  NAT1     3'  CTATCATGTATCTTCTGTA   7260         A    A
                                TACAGAAGA TACAT GATGG
                                ||||||||| ||||| |||||
                                ATGTCTTCT ATGTA CTATC
                                          _    _
GAM1299  P53AIP1  3'  GCCTCATTTTGCATCCTTCTGT 42338       A  A  T    GA
           A                     TACAGAAG AT CA AGATG  GC
                                ||||||||  || || |||||  ||
                                ATGTCTTC TA GT TTTAC  CG
                                     C  C  _    TC
GAM1299  PRELP    3'  CCATCTATTCTTCTG      12256       ATAC
                                CAGAAGA   ATAGATGG
                                |||||||   ||||||||
                                GTCTTCT   TATCTACC
                                          ____
GAM1299  PTER     3'  CTATCTATATATTCTTCT    48408        C
                                AGAAGAATA ATAGATGG
                                ||||||||| ||||||||
                                TCTTCTTAT TATCTATC
                                     A
GAM1299  SLC30A3  3'  CTCCATCCATGTGTCTGT    14398      AGAA    A
                                ACAGA   TACAT GATGGAG
                                |||||   ||||| |||||||
                                TGTCT   GTGTA CTACCTC
                                  ____    C
GAM1299  TAL1     3'  GCCCCATCTGTGCATTCTCCTG 13529    A    A       A
                                CAG AGAAT CATAGATGG GC
                                ||| ||||| ||||||||| ||
                                GTC TCTTA GTGTCTACC CG
                                  C    C       C
GAM1299  USP1     3'  GCTCGTATTTGTATTCT     14019        TA   _
                                AGAATACA  GATG GAGC
                                ||||||||  |||| ||||
                                TCTTATGT  TTAT CTCG
                                     __   G
GAM1299  AB026190 3'  TCTTGTATATATTCCTCTGTA  27831       A    C   GAT
                                TACAGA GAATA ATA   GGA
                                |||||| ||||| |||   |||
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                                ATGTCT CTTAT TAT   TCT
                                   C    A  GT_
GAM1299 AKAP11   3' CTTCATTTATTCTTCT     33191         CATA
                                AGAAGAATA   GATGGAG
                                |||||||||   |||||||
                                TCTTCTTAT   TTACTTC
                                     ____
GAM1299 AP3M1    3' GCTCCATGCTCCATTCTCACTG 24937      A_    ACAT _
           TA                    TACAG  AGAAT   AG ATGGAGC
                                |||||  |||||   || |||||||
                                ATGTC  TCTTA   TC TACCTCG
                                   AC    CC__  G
GAM1299 ATIP1    3' GTCTATACATTCTCTGTA    40775       A   AC
                                TACAGA GAAT  ATAGAT
                                ||||||| ||||  ||||||
                                ATGTCT CTTA  TATCTG
                                   _   CA
GAM1299 BCAA     3' CTGTATATGTATTCCCTTGTA 33494      AA       G
                                TACAG  GAATACATA ATGG
                                |||||  ||||||||| ||||
                                ATGTT  CTTATGTAT TGTC
                                   CC       A
GAM1299 BOP      5' GCTCCATCTATTATTGCTTCT  86230      _   C
                                AGAAG AATA ATAGATGGAGC
                                ||||| |||| ||||||||||
                                TCTTC TTAT TATCTACCTCG
                                   G   _
GAM1299 FLJ20188 3' CTCAATTATATTTTCTGTA   35205        ATAC   ATG
                                TACAGAAGA   ATAG   GAG
                                |||||||||   ||||  |||
                                ATGTCTTTT   TATT   CTC
                                     A___   AA_
GAM1299 HSPCAL3  3' GCTCGAGTCACATTCTTCTTA 77066   C      ACATA  G_
                                A AGAAGAAT    GAT  GAGC
                                | ||||||||    |||  ||||
                                A TCTTCTTA    CTG  CTCG
                                 T      CA___   AG
GAM1299 IDN3     3' CCGTTTATACATCCTTTTGTA 31799       A  AC
                                TACAGAAG AT  ATAGATGG
                                |||||||| ||  ||||||||
                                ATGTTTTC TA  TATTTGCC
                                     C  CA
GAM1299 KIAA0256 3' TTGTCATGTATTTTCTGTA   65053       A    A  TG
                                TACAGAAGA TACAT GA  G
                                ||||||||| ||||| ||  |
                                ATGTCTTTT ATGTA CT  T
                                     _    _ GT
GAM1299 KIAA0894 3' CAATTACGTATTCTTCTG    30326         A  A
                                CAGAAGAATAC TAG TG
                                |||||||||| ||| ||
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                                GTCTTCTTATG ATT AC
                                      C   A
GAM1299 KIAA1157 3' GCCCCATCCCACTTTTCTGTA 72701        ATACATA    A
                                TACAGAAGA      GATGG GC
                                |||||||||      ||||| ||
                                ATGTCTTTT      CTACC CG
                                     CACC___    C
GAM1299 KIAA1719 3' CCCTCCTGCTTCTTCTGTA   68730        TACA   AT  A
                                TACAGAAGAA    TAG  GG G
                                ||||||||||    |||  || |
                                ATGTCTTCTT    GTC  CC C
                                      C___   CT  _
GAM1299 KIAA1817 3' CCAATGTTTCTTCTGTA     68774         T    AGA
                                TACAGAAGAA ACAT   TGG
                                |||||||||| ||||   |||
                                ATGTCTTCTT TGTA   ACC
                                      _   ___
GAM1299 MGC14156 3' CCAGTGTATGTATTCTTC    52956          G _
                                GAAGAATACATA A TGG
                                |||||||||||| | |||
                                CTTCTTATGTAT T ACC
                                       G G
GAM1299 MGC26651 3' CATTTGCATTCTTCTG      58949         ACA
                                CAGAAGAAT   TAGATG
                                |||||||||   ||||||
                                GTCTTCTTA   GTTTAC
                                     C__
GAM1299 MGC2941  3' CCATTTATTTTCTTCT      44413        TAC
                                AGAAGAA   ATAGATGG
                                |||||||   ||||||||
                                TCTTCTT   TATTTACC
                                    T__
GAM1299 PCBP3    5' GCCCCATCTGTCCTTCCTC   40444    A   TAC      A
                                GA GAA   ATAGATGG GC
                                || |||   |||||||| ||
                                CT CTT   TGTCTACC CG
                                 C   CC_       C
GAM1299 PFTK1    5' GCTCCCATTCTGTATTCTTCTG 25689           TAGAT
                                CAGAAGAATACA    GGAGC
                                ||||||||||||    |||||
                                GTCTTCTTATGT    CCTCG
                                       CTTAC
GAM1299 PRO1575  5' GCCCCATCTATTTTCATTCTGT 26872        _  TAC      A
             A                   TACAGAA GAA   ATAGATGG GC
                                 ||||||| |||   |||||||| ||
                                 ATGTCTT CTT   TATCTACC CG
                                     A  T__       C
GAM1299 SQV7L    5' GCTCCATCCATGTCCCTG    71097     AAGAAT    A
                                CAG      ACAT GATGGAGC
                                |||      |||| ||||||||
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                                GTC     TGTA CTACCTCG
                                  CC_____   C
GAM1299  TRIM4    3'  GCTCCATCCATGTTGCTG    53407     AAGAAT   A
                                CAG     ACAT GATGGAGC
                                |||     |||| ||||||||
                                GTC     TGTA CTACCTCG
                                  GT_____   C
GAM1299  LOC150319 3'  GCCCCAGTCTCCTCTTCTGTA  80474         ATACAT  _  A
                                TACAGAAGA     AGA TGG GC
                                |||||||||     ||| ||| ||
                                ATGTCTTCT     TCT ACC CG
                                      CC_____   G   C
GAM1299  LOC154866 3'  TCAGCATGTTTCTTCTGTA    82060          T   AGA
                                TACAGAAGAA ACAT   TGG
                                |||||||||| ||||   |||
                                ATGTCTTCTT TGTA   ACT
                                      _   CG_
GAM1299  LOC200081 3'  GCTCCATCCATGTCTAGACCTT 89976      AAT___   A
             C                   GAAG     ACAT GATGGAGC
                                ||||     |||| ||||||||
                                CTTC     TGTA CTACCTCG
                                  CAGATC    C
GAM1299  LOC221656 5'  CTCCTCAGAAATGTATTCCTC  93849    A       A___  T
                                GA GAATACAT    GA GGAG
                                || ||||||||    || ||||
                                CT CTTATGTA    CT CCTC
                                 C       AAGA  _
GAM1300  FLJ21438  5'  CAAAACGCTTCCCCCCATCCCA 62190      GAGATTATC
                                TGGGA        AAGCGTTTTG
                                |||||        ||||||||||
                                ACCCT        TTCGCAAAAC
                                   ACCCCCC__
GAM1300  FLJ32334  3'  AAAACGCTATTCCTTCCCA    58605       A  TTATCA
                                TGGGAG GA     AGCGTTTT
                                |||||| ||     ||||||||
                                ACCCTT CT     TCGCAAAA
                                   C  TA_____
GAM1300  HHLA2     3'  CAATGTACTTTGTAATCTCCCC 23953      A       C   CG T
             CA                   TGGG GAGATTAT AAG  T TTG
                                |||| |||||||| |||  | |||
                                ACCC CTCTAATG TTC  G AAC
                                  C       T   AT T
GAM1301  CDH12     3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                      AA___   AC
GAM1301  GOCAP1    3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
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                                ATGTG  GAGGGTTCTT TTA
                                  AC         G
GAM1301  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT    98090       T    AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||     ||||||
                                TGGTG GGGT     TTATTC
                                  _    GTCA_
GAM1301  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
           A                     TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                  TACTCCC_
GAM1301  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM1301  HMP19     3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
           TA                    TACA    TCC    GAAGAATAAG
                                ||||    |||    ||||||||||
                                ATGT    AGG    TTTCTTATTC
                                  AAA_   ATTG
GAM1301  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68742             _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                         G
GAM1301  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM1301  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748      CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM1301  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM1301  OSBPL11   3'  CTTAATTTCCCAAGAGTGGTG  43206        CCAA    AA
                                CACCACTC    GAAG  TAAG
                                ||||||||    ||||  ||||
                                GTGGTGAG    CTTT  ATTC
                                     AACC    A_
GAM1301  YME1L1    3'  TCATTCTTGATGTGGTGTA    58438         TCC     _
                                TACACCAC   CAAGAA GA
                                ||||||||   |||||| ||
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                                ATGTGGTG  GTTCTT CT
                                    TA_    A
GAM1301 ZNF262   3' CTTATTTTGTTTGGGAGT   18723       A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                    G
GAM1301 LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_   AAGA
                                TACACCAC  CCAAG   ATA
                                ||||||||  |||||   |||
                                ATGTGGTG  GGTTC   TGT
                                    CAA   GG__
GAM1302 DAG1     3' CAAGTGTTCACCAACCACTGA 16547       CAGC  A
                                TCAGTGGT  GGA ACTTG
                                ||||||||  ||| |||||
                                AGTCACCA  CTT TGAAC
                                    ACCA  G
GAM1302 LDHB     5' CAAGTTTCTGTGCCTCTGA   11287     T  CA
                                TCAG GGT  GCGGAAACTTG
                                |||| |||  ||||||||||
                                AGTC CCG  TGTCTTTGAAC
                                  T  __
GAM1302 SNRPN    5' CATCAAGTCTCCACACAGCT  43319     G  CAGC  A
                                AGT GT   GGA ACTTGATG
                                ||| ||   ||| ||||||||
                                TCG CA   CCT TGAACTAC
                                  A  CA__  C
GAM1302 SNRPN    5' CATCAAGTCTCCACACAGCT  43326     G  CAGC  A
                                AGT GT   GGA ACTTGATG
                                ||| ||   ||| ||||||||
                                TCG CA   CCT TGAACTAC
                                  A  CA__  C
GAM1302 SNRPN    5' CATCAAGTCTCCACACAGCT  43328     G  CAGC  A
                                AGT GT   GGA ACTTGATG
                                ||| ||   ||| ||||||||
                                TCG CA   CCT TGAACTAC
                                  A  CA__  C
GAM1302 SNRPN    5' CATCAAGTCTCCACACAGCT  43330     G  CAGC  A
                                AGT GT   GGA ACTTGATG
                                ||| ||   ||| ||||||||
                                TCG CA   CCT TGAACTAC
                                  A  CA__  C
GAM1302 DKFZP564O0423 3' TCAGCCGCCACCACTGA    93360       CA   AAAC
                                TCAGTGGT  GCGG   TTGA
                                ||||||||  ||||   ||||
                                AGTCACCA  CGCC   GACT
                                    C_   ____
GAM1302 FLJ10201 5' CATCAAAGAAACCGACCCTGA  36353     T   AGC  AAAC_
                                TCAG GGTC  GG    TTGATG
                                |||| ||||  ||    ||||||
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                                AGTC CCAG   CC    AACTAC
                                  _   ____ AAAGA
GAM1302  KIAA0040  3'  CAAGTTTCTGTGCCTCTGA   28488     T   CA
                                TCAG GGT  GCGGAAACTTG
                                |||| |||  ||||||||||
                                AGTC CCG  TGTCTTTGAAC
                                  T   __
GAM1302  KIAA0953  3'  CATCTCTCCCCTAACCACTGA  67324        C  C   AACTT
                                TCAGTGGT AG GGA    GATG
                                |||||||| || |||    ||||
                                AGTCACCA TC CCT    CTAC
                                     A  C   CT___
GAM1302  MGC20253  3'  CATCAAGCTCCACATCACTGA  58675        CAGC   AA
                                TCAGTGGT   GGA  CTTGATG
                                ||||||||   |||  |||||||
                                AGTCACTA   CCT  GAACTAC
                                     CA__   C_
GAM1302  MYH10     3'  CATCAAGTCTCCTAGACCACTG 69670        AGC   A
                                CAGTGGTC   GGA ACTTGATG
                                ||||||||   ||| ||||||||
                                GTCACCAG   CCT TGAACTAC
                                     AT_   C
GAM1302  RBM14     3'  CAAGTCCCTGCTGACCACT   21991          AA
                                AGTGGTCAGCGG  ACTTG
                                ||||||||||||  |||||
                                TCACCAGTCGTC  TGAAC
                                      CC
GAM1302  LOC150503 5'  CATCAAGTTCCCACTGAGAAT  80724    GG    C  A
                                GT  TCAG GG AACTTGATG
                                ||  |||| || |||||||||
                                TA  AGTC CC TTGAACTAC
                                 AG    A  C
GAM1302  LOC150504 5'  CATCAAGTTCCCACTGAGAAT  60070    GG    C  A
                                GT  TCAG GG AACTTGATG
                                ||  |||| || |||||||||
                                TA  AGTC CC TTGAACTAC
                                 AG    A  C
GAM1303  ITSN1     3'  CAATGAAAACACACTGGTGT   13091    TG    ACA
                                GC  TAGT   TGTTTTCATTG
                                ||  ||||   ||||||||||
                                TG  GTCA   ACAAAAGTAAC
                                 TG    C__
GAM1303  TMEFF2    3'  CAATGAAAACATGTACTACAGC 32996
              TA                  TAGCTGTAGTACATGTTTTCATTG
                                ||||||||||||||||||||||||
                                ATCGACATCATGTACAAAAGTAAC

GAM1303  DKFZp564I1922 3'  GAGTTACATACATACAGCTA   31850        GTAC    T_
                                TAGCTGTA    ATGT  TTC
                                ||||||||    ||||  |||
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                                ATCGACAT   TACA  GAG
                                    ACA_   TT
GAM1304  BMPR2    3'  GTCAACACAAGATGGCAAA   54049
                                TTTGCCATCTTGTGTTGAC
                                ||||||||||||||||||
                                AAACGGTAGAACACAACTG

GAM1304  CYLN2    5'  GTGAGTGAAGATGGCAGA    14094         TGTGT G
                                TTTGCCATCT    T ACTCAC
                                ||||||||||    | ||||||
                                AGACGGTAGA    A TGAGTG
                                      _____ G
GAM1304  KRAS2    3'  TGAGCAAAGATGGTAAA    54125         GTGT  A
                                TTTGCCATCTT   TG CTCA
                                ||||||||||   || ||||
                                AAATGGTAGAA   AC GAGT
                                     _____  _
GAM1304  SURF6    3'  AGTGAATGCAAGATACAAA   23132     CC        G
                                TTTG  ATCTTGTGTT ACT
                                ||||  |||||||||| |||
                                AAAC  TAGAACGTAA TGA
                                  A_        G
GAM1304  BC022889 3'  TGAGTCAACATTCGGACAAG  84628     _  ATCTT
                                TTTG CC    GTGTTGACTCA
                                |||| ||    ||||||||||
                                GAAC GG    TACAACTGAGT
                                  A  CT___
GAM1304  CAMKK2   3'  AGACAGCAAAATGGTAAA    22613        CTTG    A
                                TTTGCCAT   TGTTG CT
                                ||||||||   ||||| ||
                                AAATGGTA   ACGAC GA
                                     AA__    A
GAM1304  FLJ10701 3'  GGTAAAAAGCTGCAAGATGCCA 36964     C       _  GACTC
           AA                     TTTG CATCTTGT GTT    ACC
                                ||||  |||||||| |||    |||
                                AAAC GTAGAACG CGA    TGG
                                  C       T   AAAA_
GAM1304  KIAA0660 3'  AGTAAACCACAAGTATGGCAAA 25469        _    TTG_
                                TTTGCCAT CTTGTG    ACT
                                |||||||| ||||||    |||
                                AAACGGTA GAACAC    TGA
                                     T     CAAA
GAM1304  KIAA0716 3'  TGACATGCATAAGATAACAAA  28838     CC       TGAC
                                TTTG  ATCTTGTGT    TCA
                                ||||  |||||||||    |||
                                AAAC  TAGAATACG    AGT
                                  AA        TAC_
GAM1304  KIAA1199 3'  GTGAGCCCCCAAGATGGGAAA  72932     G       TGTTGA
                                TTT CCATCTTG     CTCAC
                                ||| ||||||||     |||||
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                                AAA GGTAGAAC     GAGTG
                                  G       CCCC__
GAM1304  KIAA1872  3'  AGCCAACACAAGATGACAAA   63590      C          A
                                TTTG CATCTTGTGTTG CT
                                |||| |||||||||||| ||
                                AAAC GTAGAACACAAC GA
                                  A          C
GAM1304  KIAA1958  3'  GGTAAGCCTGCTAAAATGGCAA 82786        C   T  TGA  C
            A                    TTTGCCAT TTG GT   CT ACC
                                |||||||| ||| ||   || |||
                                AAACGGTA AAT CG   GA TGG
                                     A   _  TCC  A
GAM1304  MGC26778  5'  GGCGAGTCAACGACGCTTAGCA 59405      CATCTTG        A
            A                    TTGC       TGTTGACTC CC
                                ||||       ||||||||| ||
                                AACG       GCAACTGAG GG
                                  ATTCGCA        C
GAM1304  PRPF4     3'  TGGGCAACATGGCAAA      17472        TCTTG     A
                                TTTGCCA     TGTTG CTCA
                                |||||||     ||||| ||||
                                AAACGGT     ACAAC GGGT
                                     _____    _
GAM1304  ST6GalNAcI 3'  GACTCTCTCAAGATGGCAAA   37913           TGTT  C
                                TTTGCCATCTTG    GA TC
                                ||||||||||||    || ||
                                AAACGGTAGAAC    CT AG
                                       TCT_  C
GAM1304  LOC126669 3'  GGTTGTGACACAAGCTGACAAA 75944      C  T       G  TC
                                TTTG CA CTTGTGTT AC  ACC
                                |||| || ||||||| ||  |||
                                AAAC GT GAACACAG TG  TGG
                                  A  C       _  T_
GAM1304  LOC144583 3'  AGTGAGCCAGGATGGCA     77411          T   G
                                TGCCATCTTG GTT ACT
                                |||||||||| ||| |||
                                ACGGTAGGAC CGA TGA
                                      _   G
GAM1304  LOC151723 5'  GATGAAACACAAACGGCAAA   83497        ATC      GAC
                                TTTGCC   TTGTGTT   TC
                                ||||||   |||||||   ||
                                AAACGG   AACACAA   AG
                                   CA_      AGT
GAM1304  LOC153205 3'  TTAACAACAGGATGGCAAA    87163           _
                                TTTGCCATCTTGT GTTGA
                                |||||||||||| |||||
                                AAACGGTAGGACA CAATT
                                      A
GAM1304  LOC219690 3'  GATCTAACACAAGACAAA    94663      CCA        AC
                                TTTG   TCTTGTGTTG  TC
                                ||||   ||||||||||  ||
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                                AAAC   AGAACACAAT  AG
                                  ___        CT
GAM1304  LOC221178 3'  GTGGCCAATATGGCAAA     95174        C   T   G
                                TTTGCCAT TTG GTT AC
                                |||||||| ||| ||| ||
                                AAACGGTA AAC CGG TG
                                    T  _  _
GAM1304  LOC253373 5'  GAGGGCACAAGACAGCAAG    99017      CA       GA
                                TTTGC  TCTTGTGTT  CTC
                                |||||  |||||||||  |||
                                GAACG  AGAACACGG  GAG
                                  AC        __
GAM1304  LOC91496  5'  GATTAAAACAAGATGGCAAA   66810           G    C
                                TTTGCCATCTTGT TTGA TC
                                |||||||||||| |||| ||
                                AAACGGTAGAACA AATT AG
                                       A   _
GAM1305  IMPG2     5'  ATAACTCTTTGTTATTGGA    33188       TC
                                TCTAGT  AACAAAGAGTTAT
                                ||||||  ||||||||||||
                                AGGTTA  TTGTTTCTCAATA
                                  __
GAM1305  BITE      3'  ATAACTCTTATAAACTAGA    61077        CAACA
                                TCTAGTT    AAGAGTTAT
                                |||||||    |||||||||
                                AGATCAA    TTCTCAATA
                                    ATA__
GAM1305  CEACAM8   3'  AACTCTTTGTTCAAATGTA    10172     TCTAG  C
                                TAC    TT AACAAAGAGTT
                                |||    || ||||||||||
                                ATG    AA TTGTTTCTCAA
                                  TA___  C
GAM1305  DKFZP564K0822 3'  ACTCATTGAACTGGAG      95696          CAAA
                                CTCTAGTTCAA   GAGT
                                ||||||||||   ||||
                                GAGGTCAAGTT   CTCA
                                       A___
GAM1305  FLJ00024  3'  AGGTCTTTGTTGCACTAAAG   64488    C   T       G
                                CT TAGT CAACAAAGA TT
                                || |||| ||||||||| ||
                                GA ATCA GTTGTTTCT GA
                                 A   C       G
GAM1305  KIAA0007  3'  TAACTACAAACTGGAGTA    80928         CAACAAAG
                                TACTCTAGTT       AGTTA
                                ||||||||||       |||||
                                ATGAGGTCAA       TCAAT
                                      ACA_____
GAM1305  KIAA1243  3'  ATAACTCTCTGTTAACCAGA   74021     A   C   A
                                TCT GTT AACA AGAGTTAT
                                ||| ||| |||| ||||||||
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                                AGA CAA TTGT TCTCAATA
                                  C  _   C
GAM1305  MGC12217  3'  ATAACTCTTTGTTGAACTAGAG 52286
                TA                TACTCTAGTTCAACAAAGAGTTAT
                                  ||||||||||||||||||||||
                                  ATGAGATCAAGTTGTTTCTCAATA

GAM1305  LOC255919 3'  ACTTTTTGTTAAACCAGA    96740    A  C
                                  TCT GTT AACAAAGAGT
                                  ||| ||| ||||||||||
                                  AGA CAA TTGTTTTTCA
                                    C  A
GAM1306  GNA11     3'  CGTCGTGGCCTGGATCCTCTG  76588         A  T  T
                                  TAGAGGATCCA GCT ACG ACG
                                  |||||||||||| ||| ||| |||
                                  GTCTCCTAGGT CGG TGC TGC
                                        C  _  _
GAM1306  KIAA0150  3'  GCGCACAGGCCGGCTGGATCCT 71882       A  TAC__  A
                                  AGGATCCA GCT    GT CGC
                                  |||||||| |||    || |||
                                  TCCTAGGT CGG    CA GCG
                                       _  CCGGA  C
GAM1306  KIAA1695  3'  ACGCATTGACTTGGATCT    47830        C  ___
                                  GGATCCAAG TTA   CGT
                                  ||||||||| |||   |||
                                  TCTAGGTTC AGT   GCA
                                       _  TAC
GAM1306  LOC152274 3'  CGAAGCCTGGTCCTCTA     81339       T  A  A
                                  TAGAGGA CCA GCTT CG
                                  ||||||| ||| |||| ||
                                  ATCTCCT GGT CGAA GC
                                       _  C   _
GAM1306  LOC93626  3'  CGTCGTGGCCTGGATCCTCTG  73129         A  T  T
                                  TAGAGGATCCA GCT ACG ACG
                                  |||||||||||| ||| ||| |||
                                  GTCTCCTAGGT CGG TGC TGC
                                        C  _  _
GAM1307  GNA11     3'  CGTCGTGGCCTGGATCCTCTG  76588         A  T  T
                                  TAGAGGATCCA GCT ACG ACG
                                  |||||||||||| ||| ||| |||
                                  GTCTCCTAGGT CGG TGC TGC
                                        C  _  _
GAM1307  KIAA0150  3'  GCGCACAGGCCGGCTGGATCCT 71882       A  TAC__  A
                                  AGGATCCA GCT    GT CGC
                                  |||||||| |||    || |||
                                  TCCTAGGT CGG    CA GCG
                                       _  CCGGA  C
GAM1307  KIAA1695  3'  ACGCATTGACTTGGATCT    47830        C  ___
                                  GGATCCAAG TTA   CGT
                                  ||||||||| |||   |||
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                                TCTAGGTTC AGT   GCA
                                     _  TAC
GAM1307  LOC152274 3'  CGAAGCCTGGTCCTCTA     81339       T  A   A
                                TAGAGGA CCA GCTT CG
                                ||||||| ||| |||| ||
                                ATCTCCT GGT CGAA GC
                                    _  C   _
GAM1307  LOC93626  3'  CGTCGTGGCCTGGATCCTCTG  73129         A  T  T
                                TAGAGGATCCA GCT ACG ACG
                                |||||||||| ||| ||| |||
                                GTCTCCTAGGT CGG TGC TGC
                                      C  _  _
GAM1308  BMP1      3'  CTGAATACCCCAATGGCT    21530         __ C
                                AGCCATTGGG  AT CAG
                                ||||||||||  || |||
                                TCGGTAACCC  TA GTC
                                     CA  A
GAM1308  ISGF3G    3'  GATGAGGGTCCCATGGC     21407      T     AGA
                                GCCAT GGGATCC   CATC
                                ||||| |||||||   ||||
                                CGGTA CCCTGGG   GTAG
                                  _      A__
GAM1308  NR5A2     5'  TCTGATGTGTCCTTCCCAAGGC 15118     A     TCCAG
                                GCC TTGGGA    ACATCAGA
                                ||| ||||||    ||||||||
                                CGG AACCCT    TGTAGTCT
                                  _     TCCTG
GAM1308  PKD2      3'  TCTGATGTCTGTGGGACTAA  33616     GA _
                                TTGG  TC CAGACATCAGA
                                ||||  || ||||||||||
                                AATC  GG GTCTGTAGTCT
                                   AG  T
GAM1308  SLA       3'  CTGATGTCTGCAGCCATGGCT  23112      TG  ATC
                                AGCCAT  GG   CAGACATCAG
                                ||||||  ||   ||||||||||
                                TCGGTA  CC   GTCTGTAGTC
                                   __  GAC
GAM1308  SPINT2    5'  CTGATCGCGAGACCCCAACGGC 63849     A    A  CAGAC
              T                  AGCC TTGGG TC    ATCAG
                                 |||| ||||| ||    |||||
                                 TCGG AACCC AG    TAGTC
                                   C    C  AGCGC
GAM1308  DKFZP434G1411 3'  CTGATGTCTAAATTGCAGTG  93731      G   CC
                                CATTG GAT  AGACATCAG
                                ||||| |||  |||||||||
                                GTGAC TTA  TCTGTAGTC
                                   G   AA
GAM1308  DKFZp434G179 3'  TCTGATGTCTTCAAACAAACAG 80893     CA_  GGATCC
              CT                  AGC   TTG     AGACATCAGA
                                  |||   |||     ||||||||||
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                                TCG  AAC    TCTGTAGTCT
                                  ACA  AAACT_
GAM1308 DUSP9    3' TCGTTGCACTGGATCCCAGTGG 9158           A_ TCA
            CT                    AGCCATTGGGATCCAG CA  GA
                                |||||||||||||||| ||  ||
                                TCGGTGACCCTAGGTC GT  CT
                                       AC TG_
GAM1308 FLJ10111 3' GATGAGGGTCCCATGGC    36302     T     AGA
                                GCCAT GGGATCC  CATC
                                ||||| |||||||  ||||
                                CGGTA CCCTGGG  GTAG
                                  _     A__
GAM1308 FLJ21135 5' ATGGCCCGGATCCCGACGGC  46347    A      AGA_
                                GCC TTGGGATCC   CAT
                                ||| |||||||||   |||
                                CGG AGCCCTAGG   GTA
                                  C       CCCG
GAM1308 FLJ21865 3' TGTCTGGACCCCACGGC    43115    AT   A
                                GCC  TGGG TCCAGACA
                                |||  |||| ||||||||
                                CGG  ACCC AGGTCTGT
                                  C_   C
GAM1308 KIAA0542 5' GTCAGGCCCGATGGCT     66666        AT  A
                                AGCCATTGGG  CC GAC
                                ||||||||||  || |||
                                TCGGTAGCCC  GG CTG
                                     __  A
GAM1308 KIAA0644 3' CTAATGCCTGGATCTGTG   29725    TG     A  C
                                CAT  GGATCCAG CAT AG
                                |||  |||||||| ||| ||
                                GTG  TCTAGGTC GTA TC
                                  __      C  A
GAM1308 MIG2     3' CTAATGCCTGGACTGGC    72858     TTGG A    A  C
                                GCCA   G TCCAG CAT AG
                                ||||   | ||||| ||| ||
                                CGGT   C AGGTC GTA TC
                                  _____ _    C  A
GAM1308 LOC126767 3' CTGATGTCCAGAGGACGTGGT  75959      T GGA  CA
                                GCCAT G   TC  GACATCAG
                                ||||| |   ||  ||||||||
                                TGGTG C   AG  CTGTAGTC
                                  _ AGG  AC
GAM1308 LOC146562 5' TCTGATGCCCGCGGTAGCCAAT 58256    _    GAT  AGA__
            GAGCT                  AGC CATTGG   CC    CATCAGA
                                ||| ||||||   ||    |||||||
                                TCG GTAACC   GG    GTAGTCT
                                  A     GAT  CGCCC
GAM1308 LOC146957 3' CTGATTTTGACCCCAGTGGC  78814        ATC   C
                                GCCATTGGG   CAGA ATCAG
                                |||||||||   |||| |||||
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                                CGGTGACCC   GTTT TAGTC
                                     CA_   _
GAM1308  LOC220980 5'  TCTGATGTCTATTGTGAATTGG 94774      __  G   CC
              CT                    AGCCA  TTG GAT  AGACATCAGA
                                    |||||  ||| |||  ||||||||||
                                    TCGGT  AGT TTA  TCTGTAGTCT
                                      TA   G   __
GAM1308  LOC221486 3'  TCTGATGTCCATTTGTCCCAAT 92662     C       CCA__
              AGCT                   AGC ATTGGGAT    GACATCAGA
                                    |||  ||||||||    |||||||||
                                    TCG TAACCCTG    CTGTAGTCT
                                      A       TTTAC
GAM1308  LOC221496 3'  TCTGATGTCTGGATGATCGGC  93644     _  GGG
                                    GCC ATT   ATCCAGACATCAGA
                                    |||  |||   ||||||||||||||
                                    CGG TAG   TAGGTCTGTAGTCT
                                      C   ____
GAM1308  LOC91050  3'  CTGAGACTAGATCCCAAAGCT  65374     CA      C  ACA
                                    AGC  TTGGGATC AG   TCAG
                                    |||  ||||||||  ||   ||||
                                    TCG  AACCCTAG TC   AGTC
                                      A_       A  AG_
GAM1309  APAF1    3'  CTGTGCCATATCTGGACT    25970    _    GT   AGA
                                    AG CCAGA  TGG   CACAG
                                    ||  |||||  |||   |||||
                                    TC GGTCT  ACC   GTGTC
                                     A     AT   ____
GAM1309  BCKDHA   3'  CTGCATCTCTGCGCCTGGCT   62941       A  _     CA
                                    AGCCAG GT TGGAGA  CAG
                                    ||||||  ||  ||||||  |||
                                    TCGGTC CG GTCTCT  GTC
                                       _  C      AC
GAM1309  CNK      3'  CTGTGCCTGTCAGGCTCTGGC  15803         _  _  A
                                    GCCAGAGT TGG AG CACAG
                                    ||||||||  |||  ||  |||||
                                    CGGTCTCG ACT TC GTGTC
                                         G   G  C
GAM1309  ESPN     3'  TGTGTCTCCAACTGCTGC    49704    C  _
                                    GC AG AGTTGGAGACACA
                                    ||  ||  ||||||||||||||
                                    CG TC TCAACCTCTGTGT
                                     _  G
GAM1309  F2RL3    3'  CTGGTCTCCAACTCCTGC    15512    CA         A
                                    GC  GAGTTGGAGAC CAG
                                    ||  ||||||||||  |||
                                    CG  CTCAACCTCTG GTC
                                     TC         _
GAM1309  GADD45G  5'  GTGCTGAGCTCTGGCT      22956          GG  A
                                    AGCCAGAGTT  AG CAC
                                    |||||||||  ||  |||
```

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                                TCGGTCTCGA  TC GTG
                                     G_  _
GAM1309  GRM4     3'  CTGTGTCTCCTTTCTGGCTCTT 7751      A       TT
              G                    TAA AGCCAGAG  GGAGACACAG
                                   ||| ||||||||  ||||||||||
                                   GTT TCGGTCTT  CCTCTGTGTC
                                     C       T_
GAM1309  GYS1     3'  GTGCCTTTCTCTGGCT      89785         TT    A
                                   AGCCAGAG  GGAG CAC
                                   ||||||||  |||| |||
                                   TCGGTCTC  TTTC GTG
                                        __    C
GAM1309  INHBB    3'  GTGTGCCCCGTGGCTTTTA    11011          GAGTT  AG
                                   TAAAAGCCA    GG  ACAC
                                   |||||||||    ||  ||||
                                   ATTTTCGGT    CC  TGTG
                                        GC___  CG
GAM1309  MUC4     3'  CTGAATTCCAACTCAGGC    37877     A        ACA
                                   GCC GAGTTGGAG   CAG
                                   ||| |||||||||   |||
                                   CGG CTCAACCTT   GTC
                                     A        AA_
GAM1309  NPTX1    3'  CTGTGTCTTGGAGCTGACTT   11834     C   AG  G
                                   AAG CAG  TT GAGACACAG
                                   ||| |||  || |||||||||
                                   TTC GTC  AG TTCTGTGTC
                                     A   G_  G
GAM1309  PLD2     3'  CTGTGCCCCACCACGTCTGGCT 12161         _ __   AGA
                                   AGCCAGA GT  TGG   CACAG
                                   ||||||| ||  |||   |||||
                                   TCGGTCT CA  ACC   GTGTC
                                       G  CC   CC_
GAM1309  POLA     3'  CTGTGCCTCCACTCTGGC    34197         T    A
                                   GCCAGAGT GGAG CACAG
                                   |||||||| |||| |||||
                                   CGGTCTCA CCTC GTGTC
                                        _    C
GAM1309  PPP1CB   3'  CTGTATCCCATTGTCTGGCTTT 12225           GT_   A  C
              TG                     TAAAAGCCAGA   TGG GA ACAG
                                   ||||||||||   ||| || ||||
                                   GTTTTCGGTCT   ACC CT TGTC
                                         GTT   _  A
GAM1309  SCD      5'  GTTGCCAGCTCTAGCCTTTA   18595      A  C       AG
                                   TAAA GC AGAGTTGG  AC
                                   |||| || ||||||||  ||
                                   ATTT CG TCTCGACC  TG
                                     C  A       GT
GAM1309  WEE1     5'  CTGCGTCCAGGCCGGCTTT   14108       AGA   GGA   A
                                   AAAGCC   GTT   GAC CAG
                                   ||||||   |||   ||| |||
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                                TTTCGG  CGG  CTG GTC
                                   C__  AC_  C
GAM1309 ZNF215   3' TGTCTCCGGGTGCTCCAGTTTC 26035   A   CA   ___
             A                   A AAGC  GAGT  TGGAGACA
                                 | ||||  ||||  ||||||||
                                 A TTTG  CTCG  GCCTCTGT
                                  C   AC   TGG
GAM1309 BIRC2    5' TGTGTGAACTTAGCTTTTA   67782       CA    GGAG
                                 TAAAAGC  GAGTT   ACACA
                                 |||||||  |||||   |||||
                                 ATTTTCG  TTCAA   TGTGT
                                     A_    G___
GAM1309 C20orf44 3' GTTGTCCCTCGGCTTT     37312       A   TT  _
                                 AAAGCC GAG  GGA GAC
                                 |||||| |||  ||| |||
                                 TTTCGG CTC  CCT TTG
                                    _  __  G
GAM1309 CBX6     3' CTGGGTGCCCACTCTGACCTTT 27414     C_     T  AG  A
                                 AAAG  CAGAGT GG  AC CAG
                                 ||||  |||||| ||  || |||
                                 TTTC  GTCTCA CC  TG GTC
                                   CA     C  G_  G
GAM1309 CGI-85   3' CTGTATCCCATCTCTAACTTCA 32628   A   CC    T   A  C
                                 A AAG  AGAG TGG GA ACAG
                                 | |||  |||| ||| || ||||
                                 A TTC  TCTC ACC CT TGTC
                                  C   AA    T   _ A
GAM1309 CPZ      3' TCCCGGGCTCCTGGCTCTTG   14692     A     _   _ A
                                 TAA AGCCAG AGTT GG GA
                                 ||| |||||| |||| || ||
                                 GTT TCGGTC TCGG CC CT
                                   C     C    G  _
GAM1309 dJ309H15.1 3' CTGTGCCCCCAGCTTCCGGCT  57568      A_      AGA
                                 AGCC  GAGTTGG   CACAG
                                 ||||  |||||||   |||||
                                 TCGG  TTCGACC   GTGTC
                                   CC      CCC
GAM1309 DNER     5' CTGCGTCCTGGCTCCGGCT   58189      A   TG A  A
                                 AGCC GAGT  G GAC CAG
                                 |||| ||||  | ||| |||
                                 TCGG CTCG  C CTG GTC
                                   C   GT _   C
GAM1309 FLJ12355 5' CTGCGTCTCCTAGCTCTG    47118        _     A
                                 CAGAGTT GGAGAC CAG
                                 ||||||| |||||| |||
                                 GTCTCGA CCTCTG GTC
                                     T     C
GAM1309 FLJ12975 3' CTGCGTCCGGTCCATCTGACTT 70193     C   GT   ___   A
                                 AAG CAGA  TGGA   GAC CAG
                                 ||| ||||  ||||   ||| |||
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                                TTC GTCT  ACCT   CTG GTC
                                  A   __   GGC   C
GAM1309  FLJ14721  3'  CTGTGTCTCCCCACACTGGCT  52640       A  T_
                                AGCCAG GT  GGAGACACAG
                                |||||| ||  ||||||||||
                                TCGGTC CA  CCTCTGTGTC
                                   A  CC
GAM1309  FLJ21313  3'  CTGTGCCTGGTGCACCTCTGGC 43931           T  G___  A
           TTTTA                   TAAAAGCCAGAG TG    AG CACAG
                                |||||||||||| ||    || |||||
                                ATTTTCGGTCTC AC    TC GTGTC
                                      C  GTGG  C
GAM1309  FLJ23375  3'  CTGTGTCTGTAGCCCAGGC   46948     AGA    G
                                GCC   GTTG AGACACAG
                                |||   |||| ||||||||
                                CGG   CGAT TCTGTGTC
                                  ACC    G
GAM1309  FLJ32356  3'  CTGTGTCTCCGTGGTGGCT   59021      GAGT
                                AGCCA    TGGAGACACAG
                                |||||    ||||||||||
                                TCGGT    GCCTCTGTGTC
                                   GGT_
GAM1309  GBTS1     3'  CTGTGCCCACTCCTCCGGTT   59724      A   T__   AGA
                                AGCC GAG   TGG   CACAG
                                |||| |||   |||   |||||
                                TTGG CTC   ACC   GTGTC
                                  C   CTC   C__
GAM1309  HHGP      3'  CTGTGTTTAATACTCTGAATTT 39888      GC     TGG
           TA                    TAAAA  CAGAGT   AGACACAG
                                |||||  ||||||   ||||||||
                                ATTTT  GTCTCA   TTTGTGTC
                                   AA     TAA
GAM1309  KIAA0303  3'  CTGTGTCTTGACTACCTTT    69990      CCAG   TG A
                                AAAG    AGT  G GACACAG
                                ||||    |||  | |||||||
                                TTTC    TCA  T CTGTGTC
                                  CA__   GT _
GAM1309  KIAA0939  3'  CTGCAACTCTAGGCTTTTA    62713         _      G
                                TAAAAGCC AGAGTTG AG
                                |||||||| ||||||| ||
                                ATTTTCGG TCTCAAC TC
                                     A      G
GAM1309  KIAA1271  3'  CTGCGTCCCAACCTGCCT    70137    C   A    A   A
                                AG CAG GTTGG GAC CAG
                                || ||| ||||| ||| |||
                                TC GTC CAACC CTG GTC
                                 C   _    _  C
GAM1309  KLHL4     3'  CTGTGACTCTGGATTTTA    55143       G       G
                                TAAAA CCAGAGTTG AG
                                ||||| ||||||||| ||
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                                ATTTT GGTCTCAGT TC
                                   A       G
GAM1309 KLHL4    3' CTGTGACTCTGGATTTTA    55144      G       G
                                TAAAA CCAGAGTTG AG
                                ||||| ||||||||| ||
                                ATTTT GGTCTCAGT TC
                                   A       G
GAM1309 LY6G6C   3' TGTATCCCCTGGCTTT     48274        AGTT  A  C
                                AAAGCCAG   GG GA ACA
                                ||||||||   || || |||
                                TTTCGGTC   CC CT TGT
                                     _____ _ A
GAM1309 MGC15668 3' CTGTGTCTCTCATTGGGCT   52243     AG   T
                                AGCC  AGT GGAGACACAG
                                ||||  ||| ||||||||||
                                TCGG  TTA TCTCTGTGTC
                                  G_   C
GAM1309 MGC20235 3' CTGTAGTTTTATCTGGCTTTTA 59552          GTTG    _
                                TAAAAGCCAGA    GAGAC ACAG
                                ||||||||||    ||||| ||||
                                ATTTTCGGTCT    TTTTG TGTC
                                      A___     A
GAM1309 MGC5242  3' CTGTGCCCTCTCCTGGCTCTTG 44053     A     AGTT    A_
                                TAA AGCCAG    GGAG  CACAG
                                ||| ||||||    ||||  |||||
                                GTT TCGGTC    TCTC  GTGTC
                                  C     C___    CC
GAM1309 MRPS18B  3' CTACCAACTCAGCTTTTA    26750       CA      _
                                TAAAAGC  GAGTTGG AG
                                |||||||  ||||||| ||
                                ATTTTCG  CTCAACC TC
                                    A_      A
GAM1309 MSTP028  5' TGCGTCCTCCGACTTTTC    50069    C        _ A
                                C AGAGTTGGAG AC CA
                                | ||||||||| || ||
                                C TTTCAGCCTC TG GT
                                 T        C  C
GAM1309 NY-REN-60 3' CTGCGTCTCCAATTTCAGCTTC 51815    A   CA        A
           TA                     TA AAGC  GAGTTGGAGAC CAG
                                || ||||  |||||||||||| |||
                                AT TTCG  TTTAACCTCTG GTC
                                 C    AC          C
GAM1309 SYT6     3' CTGCGTCTCCAGCAAGCT    79520     CAGA       A
                                AGC    GTTGGAGAC CAG
                                |||    ||||||||| |||
                                TCG    CGACCTCTG GTC
                                  AA__         C
GAM1309 TMG3     3' CTGTGTCTAGAGCTCTGG    44221         GG
                                CCAGAGTT  AGACACAG
                                ||||||||  ||||||||
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                                GGTCTCGA  TCTGTGTC
                                    GA
GAM1309  TTYH2    3'  CTGTGTGTTCTCTCTGGT    51977       TT   G
                                GCCAGAG  GGA ACACAG
                                |||||||  ||| ||||||
                                TGGTCTC  CTT TGTGTC
                                   T_   G
GAM1309  TXI1     5'  CTGTGAAGTTAACCCTGGCTCT 37970     A     A    AGA
            TA                   TAA AGCCAG GTTGG   CACAG
                                ||| |||||| |||||   |||||
                                ATT TCGGTC CAATT   GTGTC
                                  C     C    GAA
GAM1309  UBCE7IP5  3'  TGTGTGCCCCTGGCTTT     30857       AGTT  AG
                                AAAGCCAG    GG  ACACA
                                ||||||||    ||  |||||
                                TTTCGGTC    CC  TGTGT
                                    _____  CG
GAM1309  LOC122786 3'  TGTCTTCATTTTGGCTT     74625         T
                                AAGCCAGAGT GGAGACA
                                |||||||||| |||||||
                                TTCGGTTTTA CTTCTGT
                                    _
GAM1309  LOC131615 5'  CTGTGTGCCCTCCGGCT     76385     A   TT  AG
                                AGCC GAG  GG  ACACAG
                                |||| |||  ||  ||||||
                                TCGG CTC  CC  TGTGTC
                                  C   __  G_
GAM1309  LOC145813 3'  CTGTGTCTCAAAGCGGCTTT   84507      AGA   G_
                                AAAGCC   GTT  GAGACACAG
                                ||||||   |||  |||||||||
                                TTTCGG   CGA  CTCTGTGTC
                                    ___   AA
GAM1309  LOC146073 5'  CTGTGTTCCCCCAGCTTT    78134        A__
                                AGAGTTGG   GACACAG
                                ||||||||   |||||||
                                TTTCGACC   TTGTGTC
                                    CCC
GAM1309  LOC146287 5'  CTGTGTCTCTCTCCTCTGACTT 84632     C    TT _
                                AAG CAGAG  G GAGACACAG
                                ||| |||||  | |||||||||
                                TTC GTCTC  C CTCTGTGTC
                                  A    CT T
GAM1309  LOC150159 3'  CTGTGTTAGGTCCTCTGGCT   58260        TTGGA
                                AGCCAGAG    GACACAG
                                ||||||||    |||||||
                                TCGGTCTC    TTGTGTC
                                    CTGGA
GAM1309  LOC150538 3'  TGTGTTCTCTAGTCTTTCA    80742    C   _      _
                                C AGAG TTGGAGA CACA
                                | |||| ||||||| ||||
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                                A TTTC GATCTCT GTGT
                                 C   T     T
GAM1309  LOC152185 3'  CTGTGTGATTAGAGTCTGGCTT 59201        G  G  G_
              T                   AAAGCCAGA TT GA  ACACAG
                                  ||||||||| || ||  ||||||
                                  TTTCGGTCT AG TT  TGTGTC
                                       G  A  AG
GAM1309  LOC152762 3'  CTGTATCTTTGGGCCTGACTTT 81533     C   AG TG   C
                                  AAAG CAG  T  GAGA ACAG
                                  |||| |||  |  |||| ||||
                                  TTTC GTC  G  TTCT TGTC
                                    A   CG GT   A
GAM1309  LOC162333 5'  CTGTACCTCTCCGGTCAGCT   88492     CA  G      C__
                                  AGC  GA TTGGAGA   ACAG
                                  |||  || |||||||   ||||
                                  TCG  CT GGCCTCT   TGTC
                                    A_  _      CCA
GAM1309  LOC163915 5'  CTGTGTCTCCAACTGATGCT   88423     CAG
                                  AGC   AGTTGGAGACACAG
                                  |||   ||||||||||||||
                                  TCG   TCAACCTCTGTGTC
                                    TAG
GAM1309  LOC199982 3'  CTCCAACTGCTGACTTTTA    89900       C   _
                                  TAAAAG CAG AGTTGGAG
                                  |||||| ||| ||||||||
                                  ATTTTC GTC TCAACCTC
                                      A   G
GAM1309  LOC203952 5'  CTGTGTCTCCGTCAACTCT    92337       ____
                                  AGAGTT   GGAGACACAG
                                  ||||||   ||||||||||
                                  TCTCAA   CCTCTGTGTC
                                      CTG
GAM1309  LOC219743 3'  CTGTGCCTTCATTTTCCAGC   94745    CA   T_    A
                                  GC  GAG  TGGAG CACAG
                                  ||  |||  ||||| |||||
                                  CG  CTT  ACTTC GTGTC
                                   AC   TT    C
GAM1309  LOC219988 3'  CTGTACCTCCTTTTGGCT    93264         TT    AC
                                  AGCCAGAG  GGAG  ACAG
                                  ||||||||  ||||  ||||
                                  TCGGTTTT  CCTC  TGTC
                                       __    CA
GAM1309  LOC220074 3'  CTGCACCTGGCCAGCTCTAGTC 59976     _ C       AGACA__
              TT                    AAG C AGAGTTGG       CAG
                                  ||| | ||||||||       |||
                                  TTC G TCTCGACC       GTC
                                    T A       GGTCCAC
GAM1309  LOC221632 3'  CTGTGTCTCCTTGCTTCTG    95449      _  T_
                                  CAGA GT  GGAGACACAG
                                  |||| ||  ||||||||||
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                                GTCT CG  CCTCTGTGTC
                                  T  TT
GAM1309  LOC221692 3'  GTTTATGTCAACTCTGCCTTT  93857      C        ___
                                AAAG CAGAGTTGG   AGAC
                                |||| |||||||||   ||||
                                TTTC GTCTCAACT   TTTG
                                  C        GTA
GAM1309  LOC221954 5'  TGCTTCCAACTTCAACTTTTA  95656       CCA       GA
                                TAAAAG   GAGTTGGA  CA
                                ||||||   ||||||||  ||
                                ATTTTC   TTCAACCT  GT
                                   AAC       TC
GAM1309  LOC222057 3'  GCTGTGTCTCCAGGCCCGACTC 94358        _______         ___
            TGGC                  GCCAGAGT     TGGAGACACAG   C
                                |||||||||     ||||||||||||  |
                                CGGTCTCA     ACCTCTGTGTC   G
                                    GCCCGG          __
GAM1309  LOC222134 3'  CTGTGTCTCCTCACTTGGTTTC 95800    A     G   T_
            A                    A AAGCCA AGT  GGAGACACAG
                                | ||||||| |||  ||||||||||
                                A TTTGGT TCA  CCTCTGTGTC
                                C      _  CT
GAM1309  LOC253758 5'  TCCCAACTCCGGCTTTTG    98746        A      A
                                TAAAAGCC GAGTTGG GA
                                |||||||| ||||||| ||
                                GTTTTCGG CTCAACC CT
                                    C      _
GAM1309  LOC58504  3'  CTGGTCTCCAGCCTTGT     41405    C  A       A
                                GC AG GTTGGAGAC CAG
                                || || ||||||||| |||
                                TG TC CGACCTCTG GTC
                                 T  _       _
GAM1309  LOC91812  5'  TGGGCCAGCTCTGGCTT     67822           AGA
                                AAGCCAGAGTTGG   CA
                                ||||||||||||   ||
                                TTCGGTCTCGACC   GT
                                       GG_
GAM1309  LOC91813  5'  TGGGCCAGCTCTGGCTT     67849           AGA
                                AAGCCAGAGTTGG   CA
                                ||||||||||||   ||
                                TTCGGTCTCGACC   GT
                                       GG_
GAM1310  ADCY1     5'  ACGACAATGTGAGCATC     94336          AG
                                GATGCTCACAT  GTTGT
                                ||||||||||  |||||
                                CTACGAGTGTA  CAGCA
                                      A_
GAM1310  C8orf1    3'  ATAGCATGATGTGAGCATC    16343          AG_
                                GATGCTCACAT   GTTGT
                                ||||||||||   |||||
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                                CTACGAGTGTA   CGATA
                                      GTA
GAM1310  CDH12    3'  ATAGCTATGTGGCATCA     15776       T      G
                                TGATGC CACATAG TTGT
                                |||||| ||||||| ||||
                                ACTACG GTGTATC GATA
                                  _      _
GAM1310  HIP1     3'  ACAAACTTGTGAGCATCA     19242          T  G
                                TGATGCTCACA AG TTGT
                                |||||||||||| || ||||
                                ACTACGAGTGT TC AACA
                                      _ A
GAM1310  DKFZp547I224 5'  ATGGCCTATGTGAGATCA     39948      G         TG
                                TGAT CTCACATAGGT  T
                                |||| ||||||||||  |
                                ACTA GAGTGTATCCG  A
                                  _         GT
GAM1310  DKFZp761P1010 3'  GGCACAAATAAGCTCA      37943     T   CACA  GG
                                TGA GCT    TA  TTGTGCC
                                ||| |||    ||  |||||||
                                ACT CGA    AT  AACACGG
                                  _  _____  A_
GAM1310  FLJ13114  3'  ACAGGCCAGGTGAGCATCA    44889          ATA   _
                                TGATGCTCAC   GGT TGT
                                ||||||||||   ||| |||
                                ACTACGAGTG   CCG ACA
                                      GA_   G
GAM1310  FLJ23024  3'  TGGCACAACCTCAGCTCA     46851     T   CACAT
                                TGA GCT     AGGTTGTGCCA
                                ||| |||     ||||||||||||
                                ACT CGA     TCCAACACGGT
                                  _   C_____
GAM1310  HNK-1ST   5'  ACAGCAAGGAAATGTGAGCCCC 17946     AT       AG_____
              A                  TG  GCTCACAT      GTTGT
                                 ||  ||||||||      |||||
                                 AC  CGAGTGTA      CGACA
                                  CC       AAGGAA
GAM1310  KIAA0459  3'  ACAATCATGTGAGCTCA     61639     T      A
                                TGA GCTCACAT GGTTGT
                                ||| ||||||| ||||||
                                ACT CGAGTGTA CTAACA
                                  _      _
GAM1310  KIAA1466  3'  ATAACCTATGAAACATCA     72405      CTCA
                                TGATG    CATAGGTTGT
                                |||||    ||||||||||
                                ACTAC    GTATCCAATA
                                   AAA_
GAM1310  KIAA1954  5'  ACAGCTTACTGAGCATCA     78220         CA
                                TGATGCTCA  TAGGTTGT
                                |||||||||  ||||||||
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                                ACTACGAGT  ATTCGACA
                                     C_
GAM1310  PACSIN2   3'  ATGGCACAGATTGATGCGCACC 24296    A   T  _  TAGG
             A                    TG TGC CA CA    TTGTGCCAT
                                  || ||| || ||    |||||||||
                                  AC ACG GT GT    GACACGGTA
                                   C   C  A  TA__
GAM1310  PARVA     3'  GGCCCATGTGAGCATCA     37183          A  TTGT
                                  TGATGCTCACAT GG    GCC
                                  ||||||||||||| ||    |||
                                  ACTACGAGTGTA CC    CGG
                                        _  _____
GAM1310  RoXaN     3'  GCACACATGTGAGCACA     47292    A       AGGT
                                  TG TGCTCACAT    TGTGC
                                  || |||||||||    |||||
                                  AC ACGAGTGTA    ACACG
                                   _       C___
GAM1310  LOC148638 3'  ATGGCCATGTGAGCACA     79665    A       A   TG
                                  TG TGCTCACAT GGT  T
                                  || ||||||||| |||  |
                                  AC ACGAGTGTA CCG  A
                                   _       _  GT
GAM1310  LOC148696 5'  GGCCAGCATTGAGCATCA     85348         CATAG    T
                                  TGATGCTCA    GTTG GCC
                                  |||||||||    |||| |||
                                  ACTACGAGT    CGAC CGG
                                       TA___   _
GAM1310  LOC200609 5'  ATAACACTGTGCAATCATCA   91658      CTCA    _
                                  TGATG   CATAG GTTGT
                                  |||||   ||||| |||||
                                  ACTAC   GTGTC CAATA
                                     TAAC    A
GAM1310  LOC203235 3'  ATGACACAACCTGAGAGGCACC 92097    A   CACA       C
             A                    TG TGCT   TAGGTTGTG CAT
                                  || ||||   ||||||||| |||
                                  AC ACGG   GTCCAACAC GTA
                                   C   AGA_       A
GAM1310  LOC219667 3'  GCCAGCCTATGCAACATCA   92948      CTCA       T
                                  TGATG   CATAGGTTG GC
                                  |||||   ||||||||| ||
                                  ACTAC   GTATCCGAC CG
                                     AAC_       _
GAM1310  LOC220514 3'  ATGGCACAGATTGATGCGCACC 61072    A   T  _  TAGG
             A                    TG TGC CA CA    TTGTGCCAT
                                  || ||| || ||    |||||||||
                                  AC ACG GT GT    GACACGGTA
                                   C   C  A  TA__
GAM1310  LOC221463 3'  GGCATGGCACGTGAGCAGCA  93706    A      ATAG  TG
                                  TG TGCTCAC    GT  TGCC
                                  || |||||||    ||  ||||
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                                AC ACGAGTG   CG  ACGG
                                 G      CA__  GT
GAM1311  CDH12    3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM1311  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC         G
GAM1311  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090       T    AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||     ||||||
                                TGGTG GGGT     TTATTC
                                  _    GTCA_
GAM1311  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
            A                    TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM1311  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM1311  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
            TA                    TACA    TCC    GAAGAATAAG
                                ||||    |||    ||||||||||
                                ATGT    AGG    TTTCTTATTC
                                  AAA_   ATTG
GAM1311  KIAA1579  3'  TACTCTTAGTGGTGTA      37154         CCCAAG    A
                                TACACCACT     AAGA TA
                                |||||||||     |||| ||
                                ATGTGGTGA     TTCT AT
                                     _______   C
GAM1311  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68742              _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                          G
GAM1311  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM1311  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748      CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
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                                TGAG    TCTTCTTATTC
                                  TACCG
GAM1311 KIAA1906 3' CTTATTCTTCTTGACTTTTGG 73571    CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM1311 OSBPL11  3' CTTAATTTCCCAAGAGTGGTG 43206       CCAA   AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                     AACC   A_
GAM1311 YME1L1   3' TCATTCTTGATGTGGTGTA   58438       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                     TA_    A
GAM1311 YME1L1   3' TCATTCTTGATGTGGTGTA   27323       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                     TA_    A
GAM1311 ZNF262   3' CTTATTTTGTTTGGGAGT    18723        A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                      G
GAM1311 LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_    AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
                                ATGTGGTG   GGTTC   TGT
                                     CAA    GG__
GAM1312 CDH12    3' CTTATCATTTAAAGTGGTGTA  15777       CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM1312 GOCAP1   3' ATTGTTCTTGGGAGCAGTGTA  43007     CA       G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM1312 DKFZp434N2435 5' CTTATTACTGTGGGGTGGT   98090      T   AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT     TTATTC
                                   _   GTCA_
GAM1312 DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
            A                    TACAC       AGAAGAATAAG
                                |||||       ||||||||||
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                                ATGTG      TCTTCTTATTC
                                  TACTCCC_
GAM1312 FLJ21791 3' CTTATTTGCAGAAGTGGTGTA 62126        CCCAAGAA
                                TACACCACT      GAATAAG
                                |||||||||      |||||||
                                ATGTGGTGA      TTTATTC
                                    AGACG___
GAM1312 HMP19    3' CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
           TA                    TACA   TCC   GAAGAATAAG
                                ||||   |||   ||||||||||
                                ATGT   AGG   TTTCTTATTC
                                  AAA_  ATTG
GAM1312 KIAA1719 3' TCTGTCTTGGGAGTGGTGTA  68742             _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                          G
GAM1312 KIAA1853 3' TTTTTCTTGGAAGCAGTG    69929    CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM1312 KIAA1877 3' CTTATTCTTCTGCCATGAGT  66748     CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM1312 KIAA1906 3' CTTATTCTTCTTGACTTTTGG 73571    CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM1312 OSBPL11  3' CTTAATTTCCCAAGAGTGGTG 43206       CCAA   AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                    AACC   A_
GAM1312 YME1L1   3' TCATTCTTGATGTGGTGTA   58438       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   |||||| ||
                                ATGTGGTG   GTTCTT CT
                                    TA_     A
GAM1312 ZNF262   3' CTTATTTTGTTTGGGAGT    18723        A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                     G
GAM1312 LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_    AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
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                                ATGTGGTG  GGTTC   TGT
                                    CAA    GG__
GAM1313  IRO039700 3'  CAGGCCTGCCCCTCCA     38529     C  TT
                                TGGA GGG  CAGGCCTG
                                |||| |||  ||||||||
                                ACCT CCC  GTCCGGAC
                                  _  C_
GAM1313  MRPL11   3'  ATCAGGCCTGAATAAACATCC  32649    CGG__
                                GGA    GTTCAGGCCTGAT
                                |||    ||||||||||||
                                CCT    TAAGTCCGGACTA
                                 ACAAA
GAM1313  MYOZ2    5'  ATCAGGCCCAAGTGCCATCCAT 33938     CG  TCA__
                                ATGGA  GGT    GGCCTGAT
                                |||||  |||    ||||||||
                                TACCT  CCG    CCGGACTA
                                   A_  TGAAC
GAM1313  LOC145226 3'  TCAGGCCCAATCCATGCCA   77561    AC_   CA
                                TGG   GGGTT  GGCCTGA
                                |||   |||||  |||||||
                                ACC   CCTAA  CCGGACT
                                 GTA    C_
GAM1313  LOC146108 5'  ATCAGACCCAAGGGCCCGTTCA 78146         A__  C
                                TGGACGGGTTC   GG CTGAT
                                ||||||||||   || |||||
                                ACTTGCCCGGG   CC GACTA
                                      AAC  A
GAM1314  BECN1    5'  TGGAGGCCTCGCTCCGGGGCCG 15005    A  A   ACC  _
            A                    TC GC CCG   GG GAGGCCTCCA
                                || || |||   || ||||||||||
                                AG CG GGC   TC CTCCGGAGGT
                                 C  G   C__  G
GAM1314  CDC25B   3'  GGAGGCCTCAGGTGCTG     41855       GACCGG
                                CAGCACC     GAGGCCTCC
                                |||||||     |||||||||
                                GTCGTGG     CTCCGGAGG
                                   A_____
GAM1314  CDC25B   3'  GGAGGCCTCAGGTGCTG     41858       GACCGG
                                CAGCACC     GAGGCCTCC
                                |||||||     |||||||||
                                GTCGTGG     CTCCGGAGG
                                   A_____
GAM1314  CSNK1G2  3'  TGGAGGCCCCCCGGCCTGG   8992     A_    A
                                CCG  CCGGG GGCCTCCA
                                |||  ||||| ||||||||
                                GGT  GGCCC CCGGAGGT
                                  CC    C
GAM1314  DNAJB1   3'  TGGAGGCCAGTCCAGTGCT   21569      C_  CGGGA
                                AGCAC  GAC    GGCCTCCA
                                |||||  |||    ||||||||
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                              TCGTG CTG    CCGGAGGT
                                AC  A____
GAM1314 GPR44    3' TGAAGGCCTGGCCCACAGCAGG 17703       GACC__ __    C
           TGCTGA                TCAGCACC    GGG AGGCCT CA
                              ||||||||     |||  |||||| ||
                              AGTCGTGG     CCC  TCCGGA GT
                                   ACGACA  GG     A
GAM1314 HEXA     3' TGGAGAGAAAGGGGCCGGTGCT 6719         A GGGAGGC
           GG                  TCAGCACCG CC      CTCCA
                              |||||||||  ||      |||||
                              GGTCGTGGC GG      GAGGT
                                   C GGAAAGA
GAM1314 IL1F9    5' AGACCCTTTCTTGCCAGGTGCT 39511       GAC    ___ C
           GA                  TCAGCACC   CGGGA   GG CT
                              ||||||||   |||||   || ||
                              AGTCGTGG   GTTCT   CC GA
                                   ACC    TTC  A
GAM1314 POLR2E   3' GGAGGCCTCCTCTAGGTC    60599     ___
                              GACC   GGGAGGCCTCC
                              ||||   ||||||||||
                              CTGG   TCCTCCGGAGG
                                ATC
GAM1314 RHEB2    5' GAGGGGCGGTGCTGA      20046        A GGGAGG
                              TCAGCACCG CC     CCTC
                              |||||||| ||     ||||
                              AGTCGTGGC GG     GGAG
                                        _ _______
GAM1314 TNFSF9   3' GGAGACCCCTGGTGCTGG    15098       GACC   A  C
                              TCAGCACC    GGG GG CTCC
                              ||||||||    ||| || ||||
                              GGTCGTGG    TCC CC GAGG
                                   _____  _  A
GAM1314 XT3      3' GAGGCCTCCATAAAGGGTCGGT 39914         G_________  GGCC
           GCTGA                 TCAGCACCGACC       GGA   TC
                              ||||||||||||       |||   ||
                              AGTCGTGGCTGG       CCT   AG
                                    GAAAT___A  CCGG
GAM1314 CBCIP2   3' AGGCCTCCCAGCCGACACTGG  52648     CAC  ACC
                              TCAG   CG   GGGAGGCCT
                              ||||   ||   |||||||||
                              GGTC   GC   CCCTCCGGA
                                ACA  CGA
GAM1314 COE2     3' AGGCCTCCTCATGCTGG     64902       CCGACC
                              TCAGCA     GGGAGGCCT
                              ||||||     |||||||||
                              GGTCGT     TCCTCCGGA
                                 AC_____
GAM1314 FLJ13441 3' TGGAGGCCCTGCTGCAGGCT   43921     ACCGAC   G  _
                              AGC     CGG AGG CCTCCA
                              |||     ||| ||| ||||||
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                              TCG     GTC TCC GGAGGT
                                GAC___  G   C
GAM1314  FLJ14326  3'  GCCTCCCAGCCTCTCGTGCTGA 50773       C_  CC__
                              TCAGCAC  GA   GGGAGGC
                              |||||||  ||   |||||||
                              AGTCGTG  CT   CCCTCCG
                                  CT  CCGA
GAM1314  FLJ22202  3'  TGGAGGCCGGGAGGCCAATGCT 46500       ____  GA  GGGA
           GG                   TCAGCA   CC  CC   GGCCTCCA
                              ||||||   ||  ||   ||||||||
                              GGTCGT   GG  GG   CCGGAGGT
                                 AACC  AG  ____
GAM1314  KIAA0514  3'  GAGGCCTCCTGTGTGC     28746     CGAC
                              GCAC   CGGGAGGCCTC
                              ||||   ||||||||||
                              CGTG   GTCCTCCGGAG
                                T___
GAM1314  KIAA0542  3'  TGAAGGCCTCCCGGCAGCAGCT 66669     ACCGA        C
           G                   CAGC    CCGGGAGGCCT CA
                              ||||    |||||||||| ||
                              GTCG    GGCCCTCCGGA GT
                                ACGAC         A
GAM1314  MGC4737   5'  TGGAGGCCCGGGCCACACTGA  49653     CACCGA   GAG
                              TCAG    CCGG   GCCTCCA
                              ||||    ||||   |||||||
                              AGTC    GGCC   CGGAGGT
                                ACACCG   ___
GAM1314  MMP28     3'  GAGGGGGTCGATGCTGG     53092       C    GGGAGG
                              TCAGCA CGACC     CCTC
                              |||||| |||||     ||||
                              GGTCGT GCTGG     GGAG
                                 A    G_____
GAM1314  PRO2015   3'  AGGCAGGCGGTGCTGA      38154         A  GGGAG
                              TCAGCACCG CC    GCCT
                              ||||||||| ||    ||||
                              AGTCGTGGC GG    CGGA
                                   _  A____
GAM1314  RALY      5'  GAGGCAGGTGGTGCTGA     34116         G  GGGAG
                              TCAGCACC ACC    GCCTC
                              |||||||| |||    |||||
                              AGTCGTGG TGG    CGGAG
                                   _   A____
GAM1314  SLC5A6    5'  TGAAGGCCTCCCCCGTCGCCGC 41180    AC   C_      C
                              GC  CGAC  GGGAGGCCT CA
                              ||  ||||  ||||||||| ||
                              CG  GCTG  CCCTCCGGA GT
                               CC   CC       A
GAM1314  STAT5A    5'  GGGATTTCCCGGCAACGCCGA  13443    A  ACCGA      _
                              TC GC    CCGGGAGG CCT
                              || ||    |||||||| |||
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                                AG CG    GGCCCTTT GGG
                                 C  CAAC_       A
GAM1314  VPS33B   3'  TTTCCCGGCCAGTGTTGA    38525        CGA
                                TCAGCAC   CCGGGAGG
                                |||||||   ||||||||
                                AGTTGTG   GGCCCTTT
                                    ACC
GAM1314  LOC123242 5'  GAGGCCCAGCTGGTGCTGA   76117         ACCGGGA
                                TCAGCACCG      GGCCTC
                                |||||||||      ||||||
                                AGTCGTGGT      CCGGAG
                                     CGAC___
GAM1314  LOC125988 5'  GAGGCCTCTGCGGCGCCGC   74899    AC  A  _
                                GC  CG CCG GGAGGCCTC
                                ||  || ||| |||||||||
                                CG  GC GGC TCTCCGGAG
                                 CC  _   G
GAM1314  LOC143101 5'  GGAGGCCTCAGGCCTCGGTGT  83786        __  GG
                                GCACCGA  CC  GAGGCCTCC
                                |||||||  ||  |||||||||
                                TGTGGCT  GG  CTCCGGAGG
                                    CC  A_
GAM1314  LOC143666 5'  GGCTCCCGGTAGATGCTGA   83886       CCG       G
                                TCAGCA   ACCGGGAG CC
                                ||||||   |||||||| ||
                                AGTCGT   TGGCCCTC GG
                                   AGA       _
GAM1314  LOC146435 5'  GAGGCCTCAAGTTTCGGGCTGA 78452       A    CCGG_
                                TCAGC CCGA     GAGGCCTC
                                ||||| ||||     ||||||||
                                AGTCG GGCT     CTCCGGAG
                                   _    TTGAA
GAM1314  LOC146445 3'  GGAGGCCTCCACGGAGC     84683     A   ACCG
                                GC CCG    GGAGGCCTCC
                                || |||    ||||||||||
                                CG GGC    CCTCCGGAGG
                                 A   A___
GAM1314  LOC153205 3'  GAGGCCTCATGAGTGCT     87159       CGAC  G
                                AGCAC    CG GAGGCCTC
                                |||||    || ||||||||
                                TCGTG    GT CTCCGGAG
                                   A___  A
GAM1314  LOC155060 5'  TGGAGGCCCCCCGAGCCAGGCT 87608       ACCGAC    A
            GA                    TCAGC      CGGG GGCCTCCA
                                |||||      |||| ||||||||
                                AGTCG      GCCC CCGGAGGT
                                   GACCGA    C
GAM1314  LOC158055 3'  GAGGCCTCCACCCAGTGCTGG  82582        CGACCG
                                TCAGCAC     GGAGGCCTC
                                |||||||     |||||||||
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                                GGTCGTG     CCTCCGGAG
                                    ACCCA_
GAM1314  LOC253001 5'  GAGGCCCAGCTGGTGCTGA   97995        ACCGGGA
                                TCAGCACCG      GGCCTC
                                |||||||||      ||||||
                                AGTCGTGGT      CCGGAG
                                     CGAC___
GAM1314  LOC255187 5'  AGGCCTCCCTTGGCTCTCTGA  98974      CA__   CC
                                TCAG   CCGA  GGGAGGCCT
                                ||||   ||||  |||||||||
                                AGTC   GGTT  CCCTCCGGA
                                  TCTC   __
GAM1314  LOC93550  5'  GGCTTTCCCGACGGGTGCTGA  72978        GAC    _
                                TCAGCACC   CGGGAG GCC
                                ||||||||   |||||| |||
                                AGTCGTGG   GCCCTT CGG
                                     GCA     T
GAM1315  B3GALT2   3'  CAGCAGGTGTACACATGC    15030      AT    TG
                                GCAT  TGTAC  GCCTGCTG
                                ||||  |||||  ||||||||
                                CGTA  ACATG  TGGACGAC
                                  C_    __
GAM1315  FBN1      3'  CAGCATGTGCAATATGC     65037          TGGCC
                                GCATATTGTAC    TGCTG
                                ||||||||||    |||||
                                CGTATAACGTG    ACGAC
                                      T_____
GAM1315  GRLF1     3'  CAGCAGGCCAGCTGCAGTG   79256        _
                                TATTGTA CTGGCCTGCTG
                                ||||||| ||||||||||
                                GTGACGT GACCGGACGAC
                                    C
GAM1315  MAPRE1    3'  GCAGCAGGCAGGTGATCATGCT 25591       ATTG   G
             G                   CAGCAT    TACT GCCTGCTGC
                                ||||||    |||| |||||||||
                                GTCGTA    GTGG CGGACGACG
                                    CTA_    A
GAM1315  SMURF1    3'  CAGCAGGCCAATGTTCCTATGT 94044      TTGT  __
                                GCATA    AC  TGGCCTGCTG
                                |||||    ||  ||||||||||
                                TGTAT    TG  ACCGGACGAC
                                   CCT_  TA
GAM1315  UQCRC1    5'  GCCAGGCCAGCACAATAGACTG 14015     CA     A      _
                                CAG  TATTGT CTGGCCTG C
                                |||  |||||| |||||||| |
                                GTC  ATAACA GACCGGAC G
                                  AG     C       C
GAM1315  DKFZP434P211 5'  CAGCAAGCCAGTGCTGTGTG   28026       T       C
                                CATAT GTACTGGC TGCTG
                                ||||| |||||||| |||||
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                                GTGTG CGTGACCG ACGAC
                                  T       A
GAM1315  KIAA0063  3'  GCAGCGGTACAGCATGCTG   30259       A       GC
                                CAGCAT TTGTACTG  CTGC
                                |||||| ||||||||  ||||
                                GTCGTA GACATGGC  GACG
                                   C       __
GAM1315  KIAA0795  3'  CAGCAAGCCAGGTATGGTG   47228    G    TGTA    C
                                CA CATAT   CTGGC TGCTG
                                || |||||   ||||| |||||
                                GT GTATG   GACCG ACGAC
                                 G    _____    A
GAM1315  KIAA1817  3'  GCAGCAGGCCACATTGCCGTGC 68781     ATT   C__
                                GCAT   GTA   TGGCCTGCTGC
                                ||||   |||   ||||||||||
                                CGTG   CGT   ACCGGACGACG
                                  C__   TAC
GAM1315  MGC14156  3'  GCAACTAGAGTCAATATGCTG  52959         TA_   CC
                                CAGCATATTG   CTGG  TGC
                                ||||||||||   ||||  |||
                                GTCGTATAAC   GATC  ACG
                                     TGA   A_
GAM1315  MYH7B     3'  GCAGCAGGCCAACACCAACCTG 71057     CATAT   AC
                                CAG    TGT  TGGCCTGCTGC
                                |||    |||  ||||||||||||
                                GTC    ACA  ACCGGACGACG
                                 CAACC   __
GAM1315  NEK1      3'  CAGCTTCAATCACAATATGC   97561         AC_   CCT
                                GCATATTGT   TGG   GCTG
                                |||||||||   |||   ||||
                                CGTATAACA   ACT   CGAC
                                     CTA   T__
GAM1315  LOC146455 5'  GCAACAGGCCAGCAGCCAAAAT 78461     A   TA__      C
            G                    CAT TTG    CTGGCCTG TGC
                                ||| |||    |||||||| |||
                                GTA AAC    GACCGGAC ACG
                                  A   CGAC       A
GAM1315  LOC150174 5'  CAGCAAGCCAGTGCTGC     80433     TATT       C
                                GCA    GTACTGGC TGCTG
                                |||    |||||||| |||||
                                CGT    CGTGACCG ACGAC
                                  _____       A
GAM1315  LOC150213 5'  CAGCAAGCCAGTGCTGTGTG   75352       T       C
                                CATAT GTACTGGC TGCTG
                                ||||| |||||||| |||||
                                GTGTG CGTGACCG ACGAC
                                  T       A
GAM1315  LOC150271 5'  CAGCAAGCTCTGAAGATATGCT 86134         GTACT   C
            G                    CAGCATATT     GGC TGCTG
                                |||||||||     ||| |||||
```

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                                GTCGTATAG    TCG ACGAC
                                     AAGTC   A
GAM1315  LOC160646 3'  CAGCAGGCAGAAATGCTG    83108      ATTGTA   G
                                CAGCAT     CTG CCTGCTG
                                ||||||     ||| |||||||
                                GTCGTA     GAC GGACGAC
                                   AA____   _
GAM1315  LOC164714 5'  AGCAGGCAAGATGCTG      88579      ATTGTA  G
                                CAGCAT     CT GCCTGCT
                                ||||||     || |||||||
                                GTCGTA     GA CGGACGA
                                   _______ A
GAM1315  LOC256809 3'  CAGTGTGGAGTCAATATGCT   98130        T   GG  _
                                AGCATATTG ACT  CC TGCTG
                                ||||||||| |||  || |||||
                                TCGTATAAC TGA  GG GTGAC
                                     _  __  T
GAM1316  EMR1      3'  GAACACCTGGCTACCA      10517      C       CC
                                TGGT AGCCAGGTG  TTC
                                |||| |||||||||  |||
                                ACCA TCGGTCCAC  AAG
                                   _       __
GAM1316  POLS      3'  TGAATTGGCCTGGCTACCA    23783      C       GCC
                                TGGT AGCCAGGT   TTCA
                                |||| ||||||||   ||||
                                ACCA TCGGTCCG   AAGT
                                   _       GTT
GAM1316  SLC22A3   3'  AGGGACTAAGCTCCTAGCTGAC 42038        C   T  CT__  A
              CA                  TGGTCAGC AGG GC    TC CCT
                                ||||||||| ||| ||    || |||
                                ACCAGTCG TCC CG    AG GGA
                                     A   T  AATC  _
GAM1316  ARTN      3'  CAGGTGAAGGGACAACTGACTA 15610        CCAG  G
                                TGGTCAG    GT CCTTCACCTG
                                |||||||    || ||||||||||
                                ATCAGTC    CA GGAAGTGGAC
                                     AA__  G
GAM1316  ARTN      3'  CAGGTGAAGGGACAACTGACTA 55108        CCAG  G
                                TGGTCAG    GT CCTTCACCTG
                                |||||||    || ||||||||||
                                ATCAGTC    CA GGAAGTGGAC
                                     AA__  G
GAM1316  ARTN      3'  CAGGTGAAGGGACAACTGACTA 55111        CCAG  G
                                TGGTCAG    GT CCTTCACCTG
                                |||||||    || ||||||||||
                                ATCAGTC    CA GGAAGTGGAC
                                     AA__  G
GAM1316  ARTN      3'  CAGGTGAAGGGACAACTGACTA 55136        CCAG  G
                                TGGTCAG    GT CCTTCACCTG
                                |||||||    || ||||||||||
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                                ATCAGTC    CA GGAAGTGGAC
                                    AA__  G
GAM1316  FLJ10211  5'  CAGACAAAGGCACCGAGGCCA  36363      AGCCA      CAC
                                TGGTC    GGTGCCTT   CTG
                                |||||    ||||||||   |||
                                ACCGG    CCACGGAA   GAC
                                   AG___       ACA
GAM1316  FLJ13089  3'  CAGGCAAAAGCAACATCTGGTT 71427           C__   CA_
           GACCA                  TGGTCAGCCAGGTG   CTT   CCTG
                                |||||||||||||   |||   ||||
                                ACCAGTTGGTCTAC   GAA   GGAC
                                       AAC   AAC
GAM1316  KIAA1280  5'  GATTAACCTGGCTGACTA    70280           GCCT
                                TGGTCAGCCAGGT    TC
                                ||||||||||||    ||
                                ATCAGTCGGTCCA    AG
                                       ATT_
GAM1316  LRG      3'  CAGGTGAAACTCGGGGCTGTCC 54816     T    A_ _  GCC
           A                    TGG CAGCC  G GT   TTCACCTG
                                ||| |||||  | ||   ||||||||
                                ACC GTCGG  C CA   AAGTGGAC
                                  T    GG T  ___
GAM1316  LOC155434 3'  GGAGGCACCCGACTACCA    87691      C  CCA
                                TGGT AG   GGTGCCTTC
                                |||| ||   |||||||||
                                ACCA TC   CCACGGAGG
                                  _  AGC
GAM1316  LOC196484 5'  CAGGTCACCACCTGGCTGACC  63537           CCTTC
                                GGTCAGCCAGGTG    ACCTG
                                ||||||||||||    |||||
                                CCAGTCGGTCCAC    TGGAC
                                       CAC__
GAM1316  LOC256158 5'  AGGCATCCCCCGGCCGACCA   99478      A   A___
                                TGGTC GCC    GGTGCCT
                                ||||| |||    |||||||
                                ACCAG CGG    CTACGGA
                                   C   CCCC
GAM1316  LOC91069  3'  CAGGTCACCACCTGGCTGACC  65400           CCTTC
                                GGTCAGCCAGGTG    ACCTG
                                ||||||||||||    |||||
                                CCAGTCGGTCCAC    TGGAC
                                       CAC__
GAM1316  LOC93624  3'  CAGGCAAGAGCCGTCTGACC   73099      CCA   GC   CA
                                GGTCAG   GGT  CTT  CCTG
                                ||||||   |||  |||  ||||
                                CCAGTC   CCG  GAA  GGAC
                                   TG_   A_   C_
GAM1317  BMP1     3'  CTGAATACCCCAATGGCT    21530          __  C
                                AGCCATTGGG  AT CAG
                                ||||||||||  || |||
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                                TCGGTAACCC  TA GTC
                                      CA  A
GAM1317  NR5A2    5'  TCTGATGTGTCCTTCCCAAGGC 15118     A     TCCAG
                                GCC TTGGGA    ACATCAGA
                                ||| ||||||    ||||||||
                                CGG AACCCT    TGTAGTCT
                                  _     TCCTG
GAM1317  PKD2     3'  TCTGATGTCTGTGGGACTAA  33616      GA  _
                                TTGG  TC CAGACATCAGA
                                ||||  || ||||||||||
                                AATC  GG GTCTGTAGTCT
                                  AG  T
GAM1317  SLA      3'  CTGATGTCTGCAGCCATGGCT  23112       TG  ATC
                                AGCCAT  GG   CAGACATCAG
                                ||||||  ||   ||||||||||
                                TCGGTA  CC   GTCTGTAGTC
                                   __  GAC
GAM1317  SPINT2   5'  CTGATCGCGAGACCCCAACGGC 63849      A    A  CAGAC
             T                   AGCC TTGGG TC    ATCAG
                                ||||| ||||| ||    |||||
                                TCGG AACCC AG    TAGTC
                                  C    C  AGCGC
GAM1317  DKFZP434G1411 3'  CTGATGTCTAAATTGCAGTG   93731       G   CC
                                CATTG GAT  AGACATCAG
                                ||||| |||  |||||||||
                                GTGAC TTA  TCTGTAGTC
                                   G   AA
GAM1317  DKFZp434G179 3'  TCTGATGTCTTCAAACAAACAG 80893     CA_   GGATCC
             CT                   AGC   TTG     AGACATCAGA
                                |||   |||     ||||||||||
                                TCG   AAC     TCTGTAGTCT
                                  ACA   AAACT_
GAM1317  DUSP9    3'  TCGTTGCACTGGATCCCAGTGG 9158             A_  TCA
             CT                   AGCCATTGGGATCCAG  CA   GA
                                ||||||||||||||||  ||   ||
                                TCGGTGACCCTAGGTC  GT   CT
                                         AC  TG_
GAM1317  FLJ21135  5'  ATGGCCCGGATCCCGACGGC   46347     A       AGA_
                                GCC TTGGGATCC    CAT
                                ||| |||||||||    |||
                                CGG AGCCCTAGG    GTA
                                  C        CCCG
GAM1317  KIAA0644  3'  CTAATGCCTGGATCTGTG    29725     TG      A   C
                                CAT  GGATCCAG CAT AG
                                |||  |||||||| ||| ||
                                GTG  TCTAGGTC GTA TC
                                  __       C   A
GAM1317  LOC126767 3'  CTGATGTCCAGAGGACGTGGT  75959       T GGA  CA
                                GCCAT G   TC  GACATCAG
                                ||||| |   ||  ||||||||
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                                TGGTG C   AG  CTGTAGTC
                                  _ AGG  AC
GAM1317  LOC146562 5'  TCTGATGCCCGCGGTAGCCAAT 58256     _     GAT  AGA__
              GAGCT                  AGC CATTGG   CC     CATCAGA
                                ||| ||||||   ||    |||||||
                                TCG GTAACC   GG    GTAGTCT
                                  A     GAT  CGCCC
GAM1317  LOC146957 3'  CTGATTTTGACCCCAGTGGC   78814         ATC    C
                                GCCATTGGG   CAGA ATCAG
                                |||||||||   |||| |||||
                                CGGTGACCC   GTTT TAGTC
                                     CA_   _
GAM1317  LOC220980 5'  TCTGATGTCTATTGTGAATTGG 94774       __   G   CC
              CT                   AGCCA  TTG GAT  AGACATCAGA
                                |||||  ||| |||  ||||||||||
                                TCGGT  AGT TTA  TCTGTAGTCT
                                   TA   G   __
GAM1317  LOC221486 3'  TCTGATGTCCATTTGTCCCAAT 92662     C       CCA__
              AGCT                   AGC ATTGGGAT    GACATCAGA
                                ||| ||||||||    |||||||||
                                TCG TAACCCTG    CTGTAGTCT
                                  A       TTTAC
GAM1317  LOC221496 3'  TCTGATGTCTGGATGATCGGC  93644     _  GGG
                                GCC ATT   ATCCAGACATCAGA
                                ||| |||   ||||||||||||||
                                CGG TAG   TAGGTCTGTAGTCT
                                  C  ____
GAM1317  LOC91050  3'  CTGAGACTAGATCCCAAAGCT  65374     CA      C  ACA
                                AGC  TTGGGATC AG   TCAG
                                |||  |||||||| ||   ||||
                                TCG  AACCCTAG TC   AGTC
                                  A_       A  AG_
GAM1318  ADCY1     5'  ACGACAATGTGAGCATC     94336          AG
                                GATGCTCACAT  GTTGT
                                ||||||||||  |||||
                                CTACGAGTGTA  CAGCA
                                     A_
GAM1318  C8orf1    3'  ATAGCATGATGTGAGCATC    16343          AG_
                                GATGCTCACAT   GTTGT
                                ||||||||||   |||||
                                CTACGAGTGTA   CGATA
                                     GTA
GAM1318  CDH12     3'  ATAGCTATGTGGCATCA     15776       T      G
                                TGATGC CACATAG TTGT
                                |||||| ||||||| ||||
                                ACTACG GTGTATC GATA
                                   _     _
GAM1318  HIP1      3'  ACAAACTTGTGAGCATCA     19242          T  G
                                TGATGCTCACA AG TTGT
                                |||||||||| || ||||
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                                ACTACGAGTGT TC AACA
                                      _ A
GAM1318  DKFZp547I224 5'  ATGGCCTATGTGAGATCA    39948     G        TG
                                TGAT CTCACATAGGT  T
                                |||| ||||||||||  |
                                ACTA GAGTGTATCCG  A
                                  _        GT
GAM1318  DKFZp761P1010 3'  GGCACAAATAAGCTCA     37943    T  CACA  GG
                                TGA GCT   TA  TTGTGCC
                                ||| |||   ||  |||||||
                                ACT CGA   AT  AACACGG
                                  _  ____ A_
GAM1318  FLJ13114  3'  ACAGGCCAGGTGAGCATCA   44889         ATA  _
                                TGATGCTCAC  GGT TGT
                                ||||||||||  ||| |||
                                ACTACGAGTG  CCG ACA
                                      GA_  G
GAM1318  FLJ23024  3'  TGGCACAACCTCAGCTCA    46851    T  CACAT
                                TGA GCT    AGGTTGTGCCA
                                ||| |||    ||||||||||
                                ACT CGA    TCCAACACGGT
                                  _  C____
GAM1318  HNK-1ST   5'  ACAGCAAGGAAATGTGAGCCCC 17946   AT      AG____
           A                     TG  GCTCACAT     GTTGT
                                ||  ||||||||     |||||
                                AC  CGAGTGTA     CGACA
                                 CC       AAGGAA
GAM1318  KIAA0459  3'  ACAATCATGTGAGCTCA    61639    T      A
                                TGA GCTCACAT GGTTGT
                                ||| |||||||| ||||||
                                ACT CGAGTGTA CTAACA
                                  _      _
GAM1318  KIAA1466  3'  ATAACCTATGAAACATCA    72405      CTCA
                                TGATG   CATAGGTTGT
                                |||||   ||||||||||
                                ACTAC   GTATCCAATA
                                   AAA_
GAM1318  KIAA1954  5'  ACAGCTTACTGAGCATCA    78220        CA
                                TGATGCTCA  TAGGTTGT
                                |||||||||  ||||||||
                                ACTACGAGT  ATTCGACA
                                     C_
GAM1318  PACSIN2   3'  ATGGCACAGATTGATGCGCACC 24296   A  T  _  TAGG
           A                     TG TGC CA CA   TTGTGCCAT
                                || ||| || ||   |||||||||
                                AC ACG GT GT   GACACGGTA
                                 C  C  A  TA__
GAM1318  PARVA     3'  GGCCCATGTGAGCATCA     37183          A  TTGT
                                TGATGCTCACAT GG   GCC
                                ||||||||||| ||   |||
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                                ACTACGAGTGTA CC    CGG
                                          _ _____
GAM1318  RoXaN    3'  GCACACATGTGAGCACA     47292    A       AGGT
                                TG TGCTCACAT    TGTGC
                                || |||||||||    |||||
                                AC ACGAGTGTA    ACACG
                                  _       C___
GAM1318  LOC148638 3'  ATGGCCATGTGAGCACA     79665    A       A   TG
                                TG TGCTCACAT GGT  T
                                || ||||||||| |||  |
                                AC ACGAGTGTA CCG  A
                                  _       _  GT
GAM1318  LOC148696 5'  GGCCAGCATTGAGCATCA     85348         CATAG    T
                                TGATGCTCA     GTTG GCC
                                |||||||||     |||| |||
                                ACTACGAGT     CGAC CGG
                                      TA___   _
GAM1318  LOC200609 5'  ATAACACTGTGCAATCATCA   91658      CTCA    _
                                TGATG    CATAG GTTGT
                                |||||    ||||| |||||
                                ACTAC    GTGTC CAATA
                                   TAAC     A
GAM1318  LOC203235 3'  ATGACACAACCTGAGAGGCACC 92097    A    CACA       C
           A                     TG TGCT    TAGGTTGTG CAT
                                || ||||    ||||||||| |||
                                AC ACGG    GTCCAACAC GTA
                                 C    AGA_       A
GAM1318  LOC219667 3'  GCCAGCCTATGCAACATCA    92948      CTCA       T
                                TGATG    CATAGGTTG GC
                                |||||    ||||||||| ||
                                ACTAC    GTATCCGAC CG
                                   AAC_       _
GAM1318  LOC220514 3'  ATGGCACAGATTGATGCGCACC 61072    A   T  _  TAGG
           A                     TG TGC CA CA    TTGTGCCAT
                                || ||| || ||    |||||||||
                                AC ACG GT GT    GACACGGTA
                                 C   C  A  TA__
GAM1318  LOC221463 3'  GGCATGGCACGTGAGCAGCA   93706    A      ATAG  TG
                                TG TGCTCAC    GT  TGCC
                                || |||||||    ||  ||||
                                AC ACGAGTG    CG  ACGG
                                 G      CA__  GT
GAM1319  SCAMP1    3'  GCTAAATAAATATTCTCC     18013     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1319  SCAMP1    3'  GCTAAATAAATATTCTCC     54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
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                                CCT TTATAA TAAATCG
                                  C     A
GAM1319 NX-17    3' TGAATATCAGCCCCTAATA   40706       ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM1319 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
              TA                  TATTAGGGATAATATTCATTTAGC
                                  ||||||||||||||||||||||||
                                  ATAATCCCTATTATAAGTAAATCG

GAM1320 SCAMP1   3' GCTAAATAAATATTCTCC    54500    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1320 SCAMP1   3' GCTAAATAAATATTCTCC    54501    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1320 NX-17    3' TGAATATCAGCCCCTAATA   40706       ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM1320 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
              TA                  TATTAGGGATAATATTCATTTAGC
                                  ||||||||||||||||||||||||
                                  ATAATCCCTATTATAAGTAAATCG

GAM1321 CUBN     3' TACACTCCAGCCTGGGCGA   8423       GATCAA   CA__
                                TCGCCCA    GGCT   TGTA
                                |||||||    ||||   ||||
                                AGCGGGT    CCGA   ACAT
                                   _______  CCTC
GAM1321 DPT      3' ACATACCAAATCTGGGTGA   60073       CAA  CTC
                                TCGCCCAGAT  GG  ATGT
                                ||||||||||  ||  ||||
                                AGTGGGTCTA  CC  TACA
                                     AA_  A__
GAM1321 NAV2     3' CAGAAGCCCCGTCTGGACGA  60790    C    CAA   CA
                                TCG CCAGAT  GGCT  TG
                                ||| ||||||  ||||  ||
                                AGC GGTCTG  CCGA  AC
                                  A    CC_   AG
GAM1321 VHL      3' CTGCACTCTAACCTGGGCGA  6854       ATCA  CTCA
                                TCGCCCAG   AGG   TGTAG
                                ||||||||   |||   |||||
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                                AGCGGGTC   TCT   ACGTC
                                    CAA_  C___
GAM1321 ZNF91    3' CTGCACTCAAGCCTGGGCGA  14281      GATCAA   CA__
                                TCGCCCA    GGCT   TGTAG
                                |||||||    ||||   |||||
                                AGCGGGT    CCGA   ACGTC
                                   _______  ACTC
GAM1321 ARNTL2   3' CTGCACCCCAGCCTGGGCGA  39847      GATCAA   CA__
                                TCGCCCA    GGCT   TGTAG
                                |||||||    ||||   |||||
                                AGCGGGT    CCGA   ACGTC
                                   _______  CCCC
GAM1321 C20orf175 3' TACATTTCAGCCTGGGCGA  55929      GATCAA   C__
                                TCGCCCA    GGCT   ATGTA
                                |||||||    ||||   |||||
                                AGCGGGT    CCGA   TACAT
                                   _______  CTT
GAM1321 DKFZP586C1324 3' CTGCACTCAAGTCTGGGCGA  70357        CAA  CTCA
                                TCGCCCAGAT  GG   TGTAG
                                ||||||||||  ||   |||||
                                AGCGGGTCTG  TC   ACGTC
                                     AAC  _____
GAM1321 FLJ14768  3' GACCTTGATCTGGAGA    52675   GC       C
                                TC  CCAGATCAAGG TC
                                ||  ||||||||||| ||
                                AG  GGTCTAGTTCC AG
                                 A_       _
GAM1321 FLJ22692  3' CTGCACTTGAGCCTGGGCGA  47482      GATCAA    __
                                TCGCCCA    GGCTCA  TGTAG
                                |||||||    ||||||  |||||
                                AGCGGGT    CCGAGT  ACGTC
                                   _______   TC
GAM1321 KIAA1503  3' TACACTCCAGCCTGGGCGA  68899      GATCAA   CA__
                                TCGCCCA    GGCT   TGTA
                                |||||||    ||||   ||||
                                AGCGGGT    CCGA   ACAT
                                   _______  CCTC
GAM1321 MSC      3' CTACAGCTGCGCCGGATCTGGG 76839        AA   T __
           CGA                   TCGCCCAGATC  GGC CA  TGTAG
                                ||||||||||  ||| ||  |||||
                                AGCGGGTCTAG  CCG GT  ACATC
                                     G_  C  CG
GAM1321 LOC122704 3' CATTGCACTCCAACCTGGGCGA 74603       ATCA_ _  TC
                                TCGCCCAG    AG GC  ATG
                                ||||||||    || ||  |||
                                AGCGGGTC    TC CG  TAC
                                    CAACC  A  T_
GAM1321 LOC146229 3' TACACTCCAGCCTGGGCGA  78308      GATCAA   CA__
                                TCGCCCA    GGCT   TGTA
                                |||||||    ||||   ||||
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                                AGCGGGT    CCGA   ACAT
                                   _____   CCTC
GAM1321  LOC146475 5'  CTGCACTCAAGCCTGGGCGA  84690      GATCAA   CA__
                                TCGCCCA    GGCT   TGTAG
                                |||||||    ||||   |||||
                                AGCGGGT    CCGA   ACGTC
                                   _____   ACTC
GAM1321  LOC147837 3'  TGCACCCCAGCCTGGGCGA  79212      GATCAA   CA__
                                TCGCCCA    GGCT   TGTA
                                |||||||    ||||   ||||
                                AGCGGGT    CCGA   ACGT
                                   _____   CCCC
GAM1321  LOC154739 5'  CGTAGCCATCAATCTGGGC  87437      CAA_   C
                                GCCCAGAT   GGCT ATG
                                ||||||||   |||| |||
                                CGGGTCTA   CCGA TGC
                                    ACTA   _
GAM1321  LOC203276 3'  CATAGCCATCGATCTGGGC  92113      AA_   C
                                GCCCAGATC  GGCT ATG
                                |||||||||  |||| |||
                                CGGGTCTAG  CCGA TAC
                                    CTA    _
GAM1321  LOC203305 3'  CATAGCCATCGATCTGGGC  92166      AA_   C
                                GCCCAGATC  GGCT ATG
                                |||||||||  |||| |||
                                CGGGTCTAG  CCGA TAC
                                    CTA    _
GAM1321  LOC254243 3'  CATAGCCATCGATCTGGGC  99252      AA_   C
                                GCCCAGATC  GGCT ATG
                                |||||||||  |||| |||
                                CGGGTCTAG  CCGA TAC
                                    CTA    _
GAM1321  LOC90038  3'  CATAGCCATCGATCTGGGC  61795      AA_   C
                                GCCCAGATC  GGCT ATG
                                |||||||||  |||| |||
                                CGGGTCTAG  CCGA TAC
                                    CTA    _
GAM1322  FLRT2     3'  GGATGCTTCACTTGATCTCCGG 26002     A      CGT  _
                                CCGGA GATCAAGT  GC TCC
                                |||||  ||||||||  || |||
                                GGCCT CTAGTTCA  CG AGG
                                   _      CTT  T
GAM1322  NEDD4L    3'  GAGACTTGACTTGATCCTCTGA 31604    C   A       TG_
            GC                    GC CGGA GATCAAGTCG  CTC
                                || |||| ||||||||||  |||
                                CG GTCT CTAGTTCAGT  GAG
                                 A   C        TCA
GAM1322  NUP98     3'  GGAGGGATTGATCTTCAGGGC  33326     G       G  GTG
                                GCCC GAAGATCAA TC  CTCC
                                |||| |||||||| ||  ||||
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                                CGGG CTTCTAGTT AG   GAGG
                                  A       _ G__
GAM1322 PTGIS    3' ATGGTCTTGATCTCCTGAGC  8194     C  A      _
                                GC CGG AGATCAAG TCGT
                                || ||| |||||||| ||||
                                CG GTC TCTAGTTC GGTA
                                 A  C       T
GAM1322 B7-H1    3' GAACTTCTGATCTTCAAGC   27096    CCG      A TC  GC
                                GC   GAAGATCA G  GT  TC
                                ||   |||||||| |  ||  ||
                                CG   CTTCTAGT C  CA  AG
                                 AA_       _ TT  __
GAM1322 CIC      3' GGAGCGTGTGACCTTCAGAGC 31369    CCG    A   AGT
                                GC   GAAG TCA   CGTGCTCC
                                ||   |||| |||   ||||||||
                                CG   CTTC AGT   GTGCGAGG
                                 AGA   C  ___
GAM1322 DKFZP434C1715 3' GGAGCACGACTGTGTCCC    87354    AA   CA
                                GG  GAT  AGTCGTGCTCC
                                ||  |||  ||||||||||
                                CC  CTG  TCAGCACGAGG
                                 __   TG
GAM1322 FLJ10094  5' GAACACATTTGTCTTCTGAGC  36295    C      T    C  C
                                GC CGGAAGA CAAGT GTG TC
                                || ||||||| ||||| ||| ||
                                CG GTCTTCT GTTTA CAC AG
                                 A      _    _  A
GAM1322 ICAM4    3' GAGCACGACCCTGTCTCC    9541     A   CAA
                                GGA GAT   GTCGTGCTC
                                ||| |||   |||||||||
                                CCT CTG   CAGCACGAG
                                  _   TCC
GAM1322 ICAM4    3' GAGCACGACCCTGTCTCC    9542     A   CAA
                                GGA GAT   GTCGTGCTC
                                ||| |||   |||||||||
                                CCT CTG   CAGCACGAG
                                  _   TCC
GAM1322 KIAA0913  5' GGAGCACGACCTGTTTGCTGGG 69533       A   T  A
             C                   GCCCGG AGA CA GTCGTGCTCC
                                 |||||| ||| || ||||||||||
                                 CGGGTC TTT GT CAGCACGAGG
                                    G   _  C
GAM1322 KIAA1274  5' GGAGCACGGATGCCCCCCGGAG 93012    _   AAGATCAAG
             C                   GC CCGG        TCGTGCTCC
                                 || ||||        |||||||||
                                 CG GGCC        GGCACGAGG
                                  A   CCCCGTA__
GAM1322 KIAA1656  3' GGAGCAAGGCATGATCCCCAAG 66373     C_  AA    A  G
             GC                    GCC  GG  GATCA GTC TGCTCC
                                   |||  ||  ||||| ||| ||||||
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                                CGG  CC  CTAGT CGG ACGAGG
                                  AA  C_    A   A
GAM1322  SLC26A1   3'  GGAACAAGGGGTCTTCCGAGC  57054    C       AAGTCG  C
                                GC CGGAAGATC     TG TCC
                                || |||||||||     || |||
                                CG GCCTTCTGG     AC AGG
                                 A        GGA___  A
GAM1322  SRPK1     3'  GATCTTGATCTTCCAGGT    13407     C         _
                                GCC GGAAGATCAAG TC
                                ||| ||||||||||| ||
                                TGG CCTTCTAGTTC AG
                                  A         T
GAM1322  LOC158856 5'  GCGACTTGACTTTCCAGGC   88290     C    A
                                GCC GGAAG TCAAGTCGT
                                ||| ||||| |||||||||
                                CGG CCTTT AGTTCAGCG
                                  A    C
GAM1323  DLEC1     3'  CATCTGGCCCTCCCTTG     24716      A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                   C    G  _
GAM1323  DLEC1     3'  CATCTGGCCCTCCCTTG     24728      A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                   C    G  _
GAM1323  PIP5K1A   3'  TATCCCACCCTGCCTTGATA   14520        A   CA  C
                                TATCAAGG AGGG  GG GTG
                                |||||||| ||||  || |||
                                ATAGTTCC TCCC  CC TAT
                                     G   A_  C
GAM1323  SOX11     3'  ACCCACCCCCCCTTGGTA    13308        AA   CA  C
                                TATCAAGG  GGG  GG GT
                                ||||||||  |||  || ||
                                ATGGTTCC  CCC  CC CA
                                     CC   A_  _
GAM1323  CHL1      3'  TGTTACCTTTCCTCAATA    22768     CA      CA
                                TAT  AGGAAGGG  GGCG
                                |||  ||||||||  ||||
                                ATA  TCCTTTCC  TTGT
                                  AC       A_
GAM1323  EPB41L1   3'  CATTCTGCCCTTCCCTGA    71104     A        C
                                TCA GGAAGGGCAGG GTG
                                ||| |||||||||| |||
                                AGT CCTTCCCGTCT TAC
                                  C         _
GAM1323  FLJ00060  3'  CATACCCCCTGCCCTCCTCTGA 61741     _   A      CGTG
                                TCA AGGA GGGCAGG    ATG
                                ||| |||| |||||||    |||
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                                AGT TCCT CCCGTCC    TAC
                                  C    _      CCCA
GAM1323  FLJ10898  5'  CACCACAGCCCTTTCTCAATA  60126     CA       AGGC
                                TAT  AGGAAGGGC    GTG
                                |||  |||||||||    |||
                                ATA  TCTTTCCCG    CAC
                                  AC        ACAC
GAM1323  FLJ22557  3'  ATCATCCCATCCTTAATA    45581     C    A   CAGGC
                                TAT AAGGA GGG     GTGAT
                                ||| ||||| |||     |||||
                                ATA TTCCT CCC     TACTA
                                  A    A  _____
GAM1323  KIAA0574  3'  CATCCCCTGCCCTCCCCTGA   69808     A  A       CGT
                                TCA GG AGGGCAGG   GATG
                                ||| || ||||||||   ||||
                                AGT CC TCCCGTCC   CTAC
                                  C  C       C__
GAM1323  KIAA0632  3'  CACCTCAGAAACCCTTCCTTGA 32071          CA___  C
                                TCAAGGAAGGG     GG GTG
                                ||||||||||     || |||
                                AGTTCCTTCCC     CT CAC
                                      AAAGA  C
GAM1323  KIAA1045  3'  CATCACATGTCCTTCC      71599          GGC
                                GGAAGGGCA   GTGATG
                                |||||||||   ||||||
                                CCTTCCTGT   CACTAC
                                     A__
GAM1323  KIAA1354  5'  CAGTGACTGCCTTCCCTTGATA 61572         A      G  _
                                TATCAAGG AGGGCAG CG TG
                                |||||||| ||||||| || ||
                                ATAGTTCC TTCCGTC GT AC
                                     C      A  G
GAM1323  MGC20460  5'  CACCGCCTCCTACCCTTCTT   54901         C___    _
                                AGGAAGGG    AGGCG TG
                                ||||||||    ||||| ||
                                TTCTTCCC    TCCGC AC
                                     ATCC     C
GAM1323  LOC158476 3'  CACGCCCGCCCCCCCCCATTGA  88186      _ AA_   A
                                TCAA GG   GGGC GGCGTG
                                |||| ||   |||| ||||||
                                AGTT CC   CCCG CCGCAC
                                  A  CCC    C
GAM1323  LOC90459  3'  CACACCCGCCTAATTTTTG    63550       A_   A  C
                                CAAGGA  GGGC GG GTG
                                ||||||  |||| || |||
                                GTTTTT  TCCG CC CAC
                                   AA    C  A
GAM1324  KIAA1069  3'  TGACCTACATTCAACTGCAA   68535          _  C_
                                TTGCAGTTGAA GT  GTCG
                                ||||||||||| ||  ||||
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                                AACGTCAACTT CA  CAGT
                                      A  TC
GAM1324  NICN1    3'  TGGCGACTTCATCTGCAA    51261       T
                                TTGCAG TGAAGTCGTCG
                                |||||| ||||||||||
                                AACGTC ACTTCAGCGGT
                                   T
GAM1324  TEX27    3'  GCTGAACACCTGCAACTGCAA  41952         A  TC  CG
                                TTGCAGTTG AG  GT  TAGC
                                ||||||||| ||  ||  ||||
                                AACGTCAAC TC  CA  GTCG
                                      G  CA  A_
GAM1324  LOC142948 3'  TGGCCACCGGCCCAACTGCAG  83782         AA    TC  A
                                TTGCAGTTG  GTCG  GT GCCA
                                |||||||||  ||||  || ||||
                                GACGTCAAC  CGGC  CA CGGT
                                      C_   __  C
GAM1324  LOC146488 5'  GCTACAACCGCTTCAACAACAA 71359     CA       C  C
                                TTG  GTTGAAGT GT GTAGC
                                |||  |||||||| || |||||
                                AAC  CAACTTCG CA CATCG
                                  AA       C  A
GAM1324  LOC147080 3'  TGCACAACTTCAGCCACAA    85053     CA       C  C
                                TTG  GTTGAAGT GT GTA
                                |||  |||||||| || |||
                                AAC  CGACTTCA CA CGT
                                  AC       A  _
GAM1324  LOC152845 5'  GCGGTGACCTCAGCTGCAA    60958         A   GT
                                TTGCAGTTGA GTC  CGT
                                |||||||||| |||  |||
                                AACGTCGACT CAG  GCG
                                      C   TG
GAM1324  LOC203052 3'  ACCACCATTTCAACTGCA     92073          C  C
                                TGCAGTTGAAGT GT GT
                                |||||||||||| || ||
                                ACGTCAACTTTA CA CA
                                       C  C
GAM1324  LOC204084 5'  GGCCAGACCTCCAACTGCAG   91000         A  TC   GTA
                                TTGCAGTTG AG  GTC   GCC
                                ||||||||| ||  |||   |||
                                GACGTCAAC TC  CAG   CGG
                                      C  __   AC_
GAM1325  CDH12    3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                      AA___   AC
GAM1325  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007       CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
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                                ATGTG  GAGGGTTCTT TTA
                                   AC         G
GAM1325  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT    98090       T    AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||     ||||||
                                TGGTG GGGT     TTATTC
                                   _    GTCA_
GAM1325  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
           A                     TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM1325  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM1325  HMP19     3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
           TA                    TACA    TCC    GAAGAATAAG
                                ||||    |||    ||||||||||
                                ATGT    AGG    TTTCTTATTC
                                  AAA_   ATTG
GAM1325  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68742             _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                         G
GAM1325  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM1325  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748      CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM1325  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM1325  OSBPL11   3'  CTTAATTTCCCAAGAGTGGTG  43206         CCAA    AA
                                CACCACTC    GAAG  TAAG
                                ||||||||    ||||  ||||
                                GTGGTGAG    CTTT  ATTC
                                     AACC    A_
GAM1325  YME1L1    3'  TCATTCTTGATGTGGTGTA    58438         TCC     _
                                TACACCAC   CAAGAA GA
                                ||||||||   |||||| ||
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                                ATGTGGTG  GTTCTT CT
                                    TA_    A
GAM1325 ZNF262   3' CTTATTTTGTTTGGGAGT   18723       A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                     G
GAM1325 LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_   AAGA
                                TACACCAC  CCAAG   ATA
                                ||||||||  |||||   |||
                                ATGTGGTG  GGTTC   TGT
                                    CAA   GG__
GAM1326 DKFZp761J139 5' GGTGAGGTTCTCAGCCACCAA 51110       CA     T
                                TTGGTGGC  AGAATCTC TC
                                ||||||||  |||||||| ||
                                AACCACCG  TCTTGGAG GG
                                    AC      T
GAM1326 LOC162952 3' GAAGAGCTCTCGGCCACCAA  83263       A  AT
                                TTGGTGGCC AGA  CTCTTC
                                ||||||||| |||  ||||||
                                AACCACCGG TCT  GAGAAG
                                     C  C_
GAM1327 CHRNA3   3' CTGGGAGACTTCCTTGTGTCA 7433     TGT  CA  A
                                TGAC  AG  GAA TCTCCCAG
                                ||||  ||  ||| ||||||||
                                ACTG  TC  CTT AGAGGGTC
                                  TGT  __  C
GAM1327 MYO1D    3' CTGGGAGACTCCCTTTGCCAC  72246    A    AA___
                                GT GCAGA    TCTCCCAG
                                || |||||    ||||||||
                                CA CGTTT    AGAGGGTC
                                 C    CCCTC
GAM1327 OASL     3' CTGGGAGACTTCTCTGTACA   14956     G   AA__
                                TGTA CAGA   TCTCCCAG
                                |||| ||||   ||||||||
                                ACAT GTCT   AGAGGGTC
                                  _   CTTC
GAM1327 PAX5     3' TGGGAGATTCCTCAGCTAC    34136     __ A
                                GTAGC  AG AATCTCCCA
                                |||||  || |||||||||
                                CATCG  TC TTAGAGGGT
                                   AC  C
GAM1327 SWAP70   3' GGATTTCTGCCCAGCCAT    71870    A  TA
                                ATG CTG  GCAGAAATCT
                                ||| |||  ||||||||||
                                TAC GAC  CGTCTTTAGG
                                 C  C_
GAM1327 VIL2     3' CTGGACCTGCCTGCTGCAGTCA 14052          AAATCTC
                                TGACTGTAGCAG      CCAG
                                ||||||||||||      ||||
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                                ACTGACGTCGTC      GGTC
                                      CGTCCA_
GAM1327 ATP6V1D  3' GAGATTGCTGCAGCCAT     32590     A       GAA
                                ATG CTGTAGCA   ATCTC
                                ||| ||||||||   |||||
                                TAC GACGTCGT   TAGAG
                                  C       ___
GAM1327 C6orf26  3' GGAGCTGCTACAGCAT      48271     A       AAAT
                                ATG CTGTAGCAG    CTCC
                                ||| |||||||||    ||||
                                TAC GACATCGTC    GAGG
                                  _       _____
GAM1327 CLSTN2   3' CTGGGCACCTGCTGCAACCAT  42401     AC       AAATCT
                                ATG  TGTAGCAG     CCCAG
                                |||  ||||||||     |||||
                                TAC  ACGTCGTC     GGGTC
                                  CA       CAC___
GAM1327 COPS7A   3' AGAATCCTGTCACACTACAGTC 33321          _____   AAA
             AT                   ATGACTGTAG    CAG   TCT
                                ||||||||||    |||   |||
                                TACTGACATC    GTC   AGA
                                      ACACT   CTA
GAM1327 DKFZP564I1171 3' CTGGTTCCCTGCTGCAGCCA   72045    A       AAATCTC
                                TG CTGTAGCAG      CCAG
                                || |||||||||      ||||
                                AC GACGTCGTC      GGTC
                                 C        CCTT___
GAM1327 FLJ22393 3' CTGGGAGAAGGCTGCAGCCA   47777    A     AGAAA
                                TG CTGTAGC     TCTCCCAG
                                || |||||||     ||||||||
                                AC GACGTCG     AGAGGGTC
                                 C      GA___
GAM1327 HARC     3'  CTGGGAGGCATCTGCTACAGTC 35917           AA
                                GACTGTAGCAGA  TCTCCCAG
                                ||||||||||||  ||||||||
                                CTGACATCGTCT  GGAGGGTC
                                      AC
GAM1327 KIAA0831  3' CTGAGAGATGCACAACAGTCAT 30634        A__   GAAA   C
                                ATGACTGT   GCA    TCTC CAG
                                ||||||||   |||    |||| |||
                                TACTGACA   CGT    AGAG GTC
                                     ACA   _____    A
GAM1327 KIAA1219  3' TGGGAGACTTCCTCGTC     62030     T T  CA   A
                                GAC G AG  GAA TCTCCCA
                                ||| | ||  ||| |||||||
                                CTG C TC  CTT AGAGGGT
                                  _ _ __   C
GAM1327 MGC12679  3' AGAAAATCTACTGCAGTCGT   52181          C   AA_
                                ATGACTGTAG AGA   TCT
                                |||||||||| |||   |||
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                                TGCTGACGTC TCT   AGA
                                      A   AAA
GAM1327  MGC17303  3'  TGGGGCCTGCTGCAGCCA    58235    A       AAATC
                                TG CTGTAGCAG    TCCCA
                                || |||||||||    |||||
                                AC GACGTCGTC    GGGGT
                                 C       C____
GAM1327  TRIM11    3'  CTGGGAGACCCCTCCAGCCA   73191    A   T  CAGAAA
                                TG CTG AG     TCTCCCAG
                                || ||| ||     ||||||||
                                AC GAC TC     AGAGGGTC
                                 C   C  CCC___
GAM1327  LOC123591 5'  CTGGGAGATTCCTAAGGAATCA 76130      __  G   CAGA
              T                  ATGA  CT TAG    AATCTCCCAG
                                ||||  || |||   ||||||||||
                                TACT  GG ATC    TTAGAGGGTC
                                  AA  A   C___
GAM1327  LOC153474 3'  CTGGTTCCCTGCTGCAGCCA   81702    A       AAATCTC
                                TG CTGTAGCAG      CCAG
                                || |||||||||      ||||
                                AC GACGTCGTC      GGTC
                                 C       CCTT___
GAM1327  LOC163341 3'  CTGAAAGACCTGCTGCGTCA   83009     T     AAA   CC
                                TGAC GTAGCAG   TCT  CAG
                                |||| |||||||   |||  |||
                                ACTG CGTCGTC   AGA  GTC
                                  _      C__   AA
GAM1327  LOC197342 3'  AGACCTCACGCTACAGTCA    89349         A_  AA
                                TGACTGTAGC  GA  TCT
                                ||||||||||  ||  |||
                                ACTGACATCG  CT  AGA
                                      CA  CC
GAM1327  LOC219731 5'  CTGGCTTTTCTGCCTCAGCCA  94704    A   TA     TCTC
                                TG CTG  GCAGAAA    CCAG
                                || |||  |||||||    ||||
                                AC GAC  CGTCTTT    GGTC
                                 C   TC      TC__
GAM1327  LOC91565  5'  AGAAAGGCTGCTGCAGTCA    67050          AAA_
                                TGACTGTAGCAG    TCT
                                ||||||||||||    |||
                                ACTGACGTCGTC    AGA
                                      GGAA
GAM1328  DBH       3'  GACCTCGTCCATTTAAACCC   7627     AC         T
                                GG  TTGAATGGATGA GTC
                                ||  |||||||||||| |||
                                CC  AATTTACCTGCT CAG
                                 CA          C
GAM1328  FGF7      3'  ATATTTGTCATTCAAGTCC    10627           AT
                                GGACTTGAATGG  GATGT
                                ||||||||||||  |||||
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                                CCTGAACTTACT  TTATA
                                      GT
GAM1328 ITGA1    3' ACAGGGTTCATTCAAACCC   64268    AC       GA
                                GG  TTGAATGGAT  TGT
                                ||  ||||||||||  |||
                                CC  AACTTACTTG  ACA
                                 CA        GG
GAM1328 MAPK9    3' TGACATTTCATCCATGTCC   58177     TTGA      __
                                GGAC   ATGGATGA  TGTCA
                                ||||   ||||||||  |||||
                                CCTG   TACCTACT  ACAGT
                                  ____      TT
GAM1328 MAPK9    3' TGACATTTCATCCATGTCC   58180     TTGA      __
                                GGAC   ATGGATGA  TGTCA
                                ||||   ||||||||  |||||
                                CCTG   TACCTACT  ACAGT
                                  ____      TT
GAM1328 NRCAM    3' ACATCACCAACAGATCC     18453    C   AA   A
                                GGA TTG  TGG TGATGT
                                ||| |||  ||| ||||||
                                CCT GAC  ACC ACTACA
                                  A  A_  _
GAM1328 PLCG2    3' GTGACATCTTTTCTTCAAGCC  72882    A     TG  T
                                GG CTTGAA  GA GATGTCAC
                                || ||||||  || ||||||||
                                CC GAACTT  TT CTACAGTG
                                 _     CT  T
GAM1328 RPLP0    5' GTGACATCGTCTTTAAACCC   54975    AC    AT
                                GG  TTGA  GGATGATGTCAC
                                ||  ||||  ||||||||||||
                                CC  AATT  TCTGCTACAGTG
                                 CA   __
GAM1328 RPLP0    5' GTGACATCGTCTTTAAACCC   8275     AC    AT
                                GG  TTGA  GGATGATGTCAC
                                ||  ||||  ||||||||||||
                                CC  AATT  TCTGCTACAGTG
                                 CA   __
GAM1328 SLC13A3  3' TGGCCCACTCAAGTCC      61092        A   ATGAT
                                GGACTTGA TGG    GTCA
                                |||||||| |||    ||||
                                CCTGAACT ACC    CGGT
                                     C  _____
GAM1328 VNN1     3' ACAACATCATTTAAGCC     17420    A      G   A
                                GG CTTGAATG ATG TGT
                                || |||||||| ||| |||
                                CC GAATTTAC TAC ACA
                                 _      _  A
GAM1328 DKFZP434P0721 5' ACATCAGTACACTCAAAATCC  64452     C_   A  GA_
                                GGA  TTGA TG   TGATGT
                                |||  |||| ||   ||||||
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                                CCT  AACT AC   ACTACA
                                  AA    C  ATG
GAM1328  DNAM-1    3'  TGACATCACCAACAGTC     22689      TGAA   A
                                GACT    TGG TGATGTCA
                                ||||    ||| ||||||||
                                CTGA    ACC ACTACAGT
                                  CA__   _
GAM1328  HBXAP     3'  ACATCATACATAAGTC      33878      GA   G
                                GACTT  ATG ATGATGT
                                |||||  ||| |||||||
                                CTGAA  TAC TACTACA
                                   __   A
GAM1328  HNRPA3    3'  ACAATTTCATTCAAGTCC    20451           TGA
                                GGACTTGAATGGA   TGT
                                ||||||||||||   |||
                                CCTGAACTTACTT   ACA
                                        TA_
GAM1328  KIAA0174  3'  ACAAGGTGCCATTCAAGTCC   79293           _  GA
                                GGACTTGAATGG AT  TGT
                                ||||||||||| ||  |||
                                CCTGAACTTACC TG  ACA
                                       G  GA
GAM1328  KIAA0218  3'  TGAGTCATCTCAAGTCC     29296        ATG     G
                                GGACTTGA   GATGAT TCA
                                ||||||||   |||||| |||
                                CCTGAACT   CTACTG AGT
                                          ___     _
GAM1328  KIAA0286  3'  TGGATTATCCATTAAAGCC   68863    A   G        G
                                GG CTT AATGGATGAT TCA
                                || ||| |||||||||| |||
                                CC GAA TTACCTATTA GGT
                                 _   A         _
GAM1328  KIAA1854  3'  TGACGTCACCCTAGTCC     72215      TGAAT  A
                                GGACT     GG TGATGTCA
                                |||||     || ||||||||
                                CCTGA     CC ACTGCAGT
                                   TC___  _
GAM1328  MGC3067   3'  GATTCTCATTCAAGTCC     44408           AT  T
                                GGACTTGAATGG  GA GTC
                                ||||||||||||  || |||
                                CCTGAACTTACT  CT TAG
                                          __  _
GAM1328  MY014     5'  GTGACATCATGCAGGAATTCC  48880     C  GAA  G
                                GGA TT   TG ATGATGTCAC
                                ||| ||   || ||||||||||
                                CCT AA   AC TACTACAGTG
                                  T  GG_  G
GAM1328  PELI2     3'  ATTTTCCATTTCAAGTCC     41455         _   T
                                GGACTTGAA TGGA GAT
                                |||||||| |||| |||
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                                CCTGAACTT ACCT TTA
                                     T   T
GAM1328  TTTY12   3'  TGACACTCTCTATTCAACC   50029   AC      T _
                                GG  TTGAATGGA GA TGTCA
                                ||  ||||||||| || |||||
                                CC  AACTTATCT CT ACAGT
                                 __       _ C
GAM1328  ZNF31    3'  GTGACATCATTACAAAATC   65615   C  GAATG
                                GA TT    GATGATGTCAC
                                || ||    ||||||||||
                                CT AA    TTACTACAGTG
                                 A  ACA__
GAM1328  LOC124602 3'  TGACATCCGCCACATCC    74794    CT  AA  AT
                                GGA  TG  TGG  GATGTCA
                                |||  ||  |||  |||||||
                                CCT  AC  ACC  CTACAGT
                                  __ __  GC
GAM1328  LOC128344 3'  TGACATCATCCATTTAGTCT  75249     T
                                GGACT GAATGGATGATGTCA
                                ||||| ||||||||||||||
                                TCTGA TTTACCTACTACAGT
                                  _
GAM1328  LOC146901 3'  GATACCTATTCAAGTCC    84904         ATGA
                                GGACTTGAATGG   TGTC
                                ||||||||||||   ||||
                                CCTGAACTTATC   ATAG
                                       C___
GAM1328  LOC147219 5'  TGGCTTCTATTCAAGTCC   85114          TGAT
                                GGACTTGAATGGA   GTCA
                                ||||||||||||   ||||
                                CCTGAACTTATCT   CGGT
                                       T___
GAM1328  LOC150343 5'  GTGACATCATTAGCAAGCC   80496   A   AATG
                                GG CTTG   GATGATGTCAC
                                || ||||   ||||||||||
                                CC GAAC   TTACTACAGTG
                                 _   GA__
GAM1328  LOC157798 3'  ATATTTTCCCATTCAAGT    87853        AT_
                                ACTTGAATGG   GATGT
                                |||||||||   |||||
                                TGAACTTACC   TTATA
                                     CTT
GAM1328  LOC158116 3'  ATATTTGTCATTCAAGTCC   60947         AT
                                GGACTTGAATGG  GATGT
                                ||||||||||||  |||||
                                CCTGAACTTACT  TTATA
                                       GT
GAM1328  LOC196955 5'  GTGACATCACCCCCAGATCC  77870    C   AAT  A
                                GGA TTG   GG TGATGTCAC
                                ||| |||   || |||||||||
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                                CCT GAC   CC ACTACAGTG
                                  A  C__  C
GAM1328  LOC203397 3'  TGACATCCGCCACATCC     90907     CT  AA   AT
                                GGA  TG  TGG  GATGTCA
                                |||  ||  |||  |||||||
                                CCT  AC  ACC  CTACAGT
                                  __  __  GC
GAM1328  LOC220717 5'  GTGACATCGTCTTTAAACCC  92458    AC    AT
                                GG  TTGA  GGATGATGTCAC
                                ||  ||||  ||||||||||||
                                CC  AATT  TCTGCTACAGTG
                                 CA   __
GAM1328  LOC255027 3'  GTGACGGCACATTCAAGTC   96776          GATGA
                                GACTTGAATG    TGTCAC
                                ||||||||||    ||||||
                                CTGAACTTAC    GCAGTG
                                      ACG__
GAM1328  LOC255506 3'  TGACCCCATTCAGTCC      98825      T     ATGAT
                                GGACT GAATGG    GTCA
                                |||||  ||||||    ||||
                                CCTGA CTTACC    CAGT
                                  _     C____
GAM1329  DLEC1    3'  CATCTGGCCCTCCCTTG     24716      A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                  C    G  _
GAM1329  PIP5K1A   3'  TATCCCACCCTGCCTTGATA   14520        A    CA  C
                                TATCAAGG AGGG  GG GTG
                                |||||||| ||||  || |||
                                ATAGTTCC TCCC  CC TAT
                                     G   A_  C
GAM1329  SOX11    3'  ACCCACCCCCCCTTGGTA    13308        AA   CA  C
                                TATCAAGG  GGG  GG GT
                                ||||||||  |||  || ||
                                ATGGTTCC  CCC  CC CA
                                     CC   A_  _
GAM1329  CHL1     3'  TGTTACCTTTCCTCAATA    22768     CA      CA
                                TAT  AGGAAGGG  GGCG
                                |||  ||||||||  ||||
                                ATA  TCCTTTCC  TTGT
                                  AC       A_
GAM1329  EPB41L1   3'  CATTCTGCCCTTCCCTGA    71104     A         C
                                TCA GGAAGGGCAGG GTG
                                ||| |||||||||| |||
                                AGT CCTTCCCGTCT TAC
                                  C         _
GAM1329  FLJ00060  3'  CATACCCCCTGCCCTCCTCTGA 61741     _   A      CGTG
                                TCA AGGA GGGCAGG    ATG
                                ||| |||| |||||||    |||
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                                AGT TCCT CCCGTCC    TAC
                                  C    _      CCCA
GAM1329  FLJ10898  5'  CACCACAGCCCTTTCTCAATA  60126     CA       AGGC
                                TAT  AGGAAGGGC    GTG
                                |||  |||||||||    |||
                                ATA  TCTTTCCCG    CAC
                                  AC        ACAC
GAM1329  FLJ22557  3'  ATCATCCCATCCTTAATA    45581     C    A   CAGGC
                                TAT AAGGA GGG     GTGAT
                                ||| ||||| |||     |||||
                                ATA TTCCT CCC     TACTA
                                  A    A  _____
GAM1329  KIAA0574  3'  CATCCCCTGCCCTCCCCTGA   69808     A  A       CGT
                                TCA GG AGGGCAGG   GATG
                                ||| || ||||||||   ||||
                                AGT CC TCCCGTCC   CTAC
                                  C  C       C__
GAM1329  KIAA0632  3'  CACCTCAGAAACCCTTCCTTGA 32071          CA___  C
                                TCAAGGAAGGG     GG GTG
                                ||||||||||     || |||
                                AGTTCCTTCCC     CT CAC
                                      AAAGA  C
GAM1329  KIAA1045  3'  CATCACATGTCCTTCC      71599          GGC
                                GGAAGGGCA   GTGATG
                                |||||||||   ||||||
                                CCTTCCTGT   CACTAC
                                     A__
GAM1329  KIAA1354  5'  CAGTGACTGCCTTCCCTTGATA 61572         A      G  _
                                TATCAAGG AGGGCAG CG TG
                                |||||||| ||||||| || ||
                                ATAGTTCC TTCCGTC GT AC
                                     C      A  G
GAM1329  MGC20460  5'  CACCGCCTCCTACCCTTCTT   54901         C___    _
                                AGGAAGGG    AGGCG TG
                                ||||||||    ||||| ||
                                TTCTTCCC    TCCGC AC
                                     ATCC     C
GAM1329  LOC158476 3'  CACGCCCGCCCCCCCCCATTGA  88186      _ AA_   A
                                TCAA GG   GGGC GGCGTG
                                |||| ||   |||| ||||||
                                AGTT CC   CCCG CCGCAC
                                  A  CCC    C
GAM1329  LOC90459  3'  CACACCCGCCTAATTTTTG    63550       A_   A  C
                                CAAGGA  GGGC GG GTG
                                ||||||  |||| || |||
                                GTTTTT  TCCG CC CAC
                                   AA    C  A
GAM1330  APG5L     3'  GTTGGTCAAAGACCAGATA    17941           _ A
                                TATCTGGTCTTTG C AGC
                                |||||||||||| | |||
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                                ATAGACCAGAAAC G TTG
                                      T G
GAM1330  LOC118851 3'  AAGACCTCCCAAAGACCA    76012         CA  CA
                                TGGTCTTTG  AG  GTCTT
                                |||||||||  ||  |||||
                                ACCAGAAAC  TC  CAGAA
                                     CC  __
GAM1330  LOC201685 3'  AAGATATGACAAAGACCAG   91830          _  AGCA
                                CTGGTCTTTG CA   GTCTT
                                |||||||||| ||   |||||
                                GACCAGAAAC GT   TAGAA
                                      A  A___
GAM1331  CMAR     3'  CAGGTTGGGATGGCACCTGG   19028          G   TT
                                CCAGGTGCCAT CCTA  CCTG
                                |||||||||| ||||  ||||
                                GGTCCACGGTA GGGT  GGAC
                                      _   T_
GAM1331  IFRD2    3'  CAGACATGGGGTGGGTAGCTG  23149    G   ATG    TC
                                CAG TGCC   CCTAT  CTG
                                ||| ||||   |||||  |||
                                GTC ATGG   GGGTA  GAC
                                  G   GTG    CA
GAM1331  JPH2     3'  AGGAATGAGCACCTTGTG    96080    C    _  G
                                CAC AGGTGC CAT CCT
                                ||| |||||| ||| |||
                                GTG TCCACG GTA GGA
                                  T    A  A
GAM1331  KCNJ4    5'  CAGGAATAAACTTGGCCCTG   18356     T   TGCC
                                CAGG GCCA   TATTCCTG
                                |||| ||||   ||||||||
                                GTCC CGGT   ATAAGGAC
                                  _   TCAA
GAM1331  PTPN1    3'  CAGGAATAGGCATTTGCCT   12574     GCC
                                AGGT  ATGCCTATTCCTG
                                ||||  ||||||||||||
                                TCCG  TACGGATAAGGAC
                                  TT_
GAM1331  RGS14    3'  CAGGACAGCTGCATGGCACCCG 22397    A       CTAT_
           G                     CC GGTGCCATGC    TCCTG
                                || ||||||||||    |||||
                                GG CCACGGTACG    AGGAC
                                 C        TCGAC
GAM1331  CDK5RAP3 3'  CAGGAAGGAAGCGGCACCTG  48059       ATG_  AT
                                CAGGTGCC   CCT  TCCTG
                                ||||||||   |||  |||||
                                GTCCACGG   GGA  AGGAC
                                     CGAA  __
GAM1331  DKFZp434G171 5'  CAGGAAGTTTGGCACCTG    80237        T  CTA
                                CAGGTGCCA GC   TTCCTG
                                ||||||||| ||   ||||||
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                                GTCCACGGT TG   AAGGAC
                                     T ___
GAM1331  FLJ20195  3'  AGGAATCACCACCTGGT     35212        CCA  CCT
                                ACCAGGTG   TG   ATTCCT
                                |||||||   ||   ||||||
                                TGGTCCAC   AC   TAAGGA
                                     C__  ___
GAM1331  FLJ23476  3'  CAGGAAGGCCCAAGACCTGGTG 45312        GCCAT    AT
                                CACCAGGT    GCCT  TCCTG
                                ||||||||    ||||  |||||
                                GTGGTCCA    CGGA  AGGAC
                                     GAACC   __
GAM1331  MGC2562   3'  CAGGAGAATAGCATGAACCCGG 51432     A   GC    CTA_
           T                     ACC GGT  CATGC    TTCCTG
                                ||| |||  |||||    ||||||
                                TGG CCA  GTACG    GAGGAC
                                  C   A_    ATAA
GAM1331  LOC115219 5'  CAGGAATAGGGGGCACCTG    73690        ATG
                                CAGGTGCC   CCTATTCCTG
                                ||||||||   ||||||||||
                                GTCCACGG   GGATAAGGAC
                                     G__
GAM1331  LOC147136 3'  CAGGAAACCCGGTGGCACCTG  78860         GCCTA
                                CAGGTGCCAT    TTCCTG
                                ||||||||||    ||||||
                                GTCCACGGTG    AAGGAC
                                      GCCCA
GAM1331  LOC148562 5'  CAGGAACAGGGCTTCACTTGGT 79662         CCAT    A_
           G                     CACCAGGTG   GCCT  TTCCTG
                                |||||||||   ||||  ||||||
                                GTGGTTCAC   CGGG  AAGGAC
                                     TT__    AC
GAM1331  LOC149935 3'  CAGGAAGGAAGCGGCACCTG   60933        ATG_   AT
                                CAGGTGCC    CCT  TCCTG
                                ||||||||    |||  |||||
                                GTCCACGG    GGA  AGGAC
                                     CGAA   __
GAM1331  LOC200261 3'  CAGTGCCCAGCTCAGCACCTGG 90050         CAT  CTATTC
           TG                     CACCAGGTGC   GC     CTG
                                ||||||||||   ||     |||
                                GTGGTCCACG   CG     GAC
                                      ACT  ACCCGT
GAM1331  LOC202915 3'  CAGGGGGTCAGGGCACCTG    92015        A  _   ATT
                                CAGGTGCC TG CCT   CCTG
                                |||||||| || |||   ||||
                                GTCCACGG AC GGG   GGAC
                                     G  T  ___
GAM1331  LOC57109  3'  CAGGAACAGCCAGTGGCACT   40202        GC_  A
                                GGTGCCAT   CT TTCCTG
                                ||||||||   || ||||||
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                                TCACGGTG  GA AAGGAC
                                    ACC  C
GAM1332 ADA     3' CGCCACTCCTCCAAGCCTTC  62439       ATGC  ACC
                                GAAGGCTTG   AG  TGGCG
                                |||||||||   ||  |||||
                                CTTCCGAAC   TC  ACCGC
                                    C___  CTC
GAM1332 PAX2    3' CGGGGACCACATCAAGCTTC  15657     G     CAGA_
                                GAAG CTTGATG    CCTG
                                |||| |||||||    ||||
                                CTTC GAACTAC    GGGC
                                  _     ACCAG
GAM1332 RFP     5' GCCACTCCAAGCCTTCG     22509       ATGC  ACC
                                CGAAGGCTTG   AG  TGGC
                                ||||||||||   ||  ||||
                                GCTTCCGAAC   TC  ACCG
                                    C___  ___
GAM1332 CACNG4  3' CCAGAGCTCAAGGCCTTC    27706      _   T  AGAC
                                GAAGGC TTGA GC   CTGG
                                |||||| |||| ||   ||||
                                CTTCCG AACT CG   GACC
                                   G   _ A___
GAM1332 FLJ10120 3' CGCCATCTACACCAAGCCTTCG 36305        A  C   CC
                                CGAAGGCTTG TG AGA  TGGCG
                                |||||||||| || |||  |||||
                                GCTTCCGAAC AC TCT  ACCGC
                                    C  A  __
GAM1332 KIAA0747 3' CGTGGATTCTACTCAAGCCT  31619       TGC  __ TG
                                AGGCTTGA  AGA  CC  GCG
                                ||||||||  |||  ||  |||
                                TCCGAACT  TCT  GG  TGC
                                    CA_  TA  __
GAM1332 LOC92840 3' CGCCAGGCTCCCAGGCCT   57244       ATGC  A
                                AGGCTTG   AG CCTGGCG
                                |||||||   || |||||||
                                TCCGGAC   TC GGACCGC
                                    CC__  _
GAM1333 MPHOSPH1 3' ATGCCCATGAGGTCAATTGATT 33003          G  AAA
          T                      AAATCAATTGACT CA  GCAT
                                ||||||||||||| ||  ||||
                                TTTAGTTAACTGG GT  CGTA
                                      A  ACC
GAM1333 PCCA    3' ATGCTTTCACACACAATTGATT 71797       AC  CA
                                AATCAATTG  TG  AAAGCAT
                                |||||||||  ||  |||||||
                                TTAGTTAAC  AC  TTTCGTA
                                    AC  AC
GAM1333 SCN3A   3' TGCTTTTGCTTTTGATTT   23620       TTGACT
                                AAATCAA    GCAAAAGCA
                                |||||||    |||||||||
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                                TTTAGTT     CGTTTTCGT
                                   TT____
GAM1333  WHSC1    3'  ATGCTTTTAAAATCAATAGATT 56690      A    CTGC
                                AATC ATTGA    AAAAGCAT
                                |||| |||||    ||||||||
                                TTAG TAACT    TTTTCGTA
                                  A     AAAA
GAM1333  CTPS2    3'  ATGCTGAATAATTAATTGATTT 39564          CTGCAAA
            A                    TAAATCAATTGA      AGCAT
                                ||||||||||||      |||||
                                ATTTAGTTAATT      TCGTA
                                      AATAAG_
GAM1333  DKFZp547G183 3'  ATGCTTTTGTAGCAATTG    38639       A
                                CAATTG CTGCAAAAGCAT
                                |||||| ||||||||||||
                                GTTAAC GATGTTTTCGTA
                                _
GAM1333  FLJ21603  3'  TGCAGACAACCATTGATTTA   45782         ___  A
                                TAAATCAAT   TG CTGCA
                                |||||||||   || |||||
                                ATTTAGTTA   AC GACGT
                                     CCA  A
GAM1333  PRMT6    3'  ATGCTTTTGCCTTTTTAAT    36785      CT__
                                ATTGA    GCAAAAGCAT
                                |||||    ||||||||||
                                TAATT    CGTTTTCGTA
                                   TTTC
GAM1334  SLC21A2   3'  TGCTAATCAGGGTTCTCCA    20088        G     C
                                TGGAGAACC TGATTA CG
                                ||||||||| |||||| ||
                                ACCTCTTGG ACTAAT GT
                                     G     C
GAM1334  KIAA0418  5'  CATCCCGGAGCGTCAGTTTCCC 28292     AG   CG    TA_
            A                    TGG  AAC  TGAT   CCGGGATG
                                |||  |||  ||||   ||||||||
                                ACC  TTG  ACTG   GGCCCTAC
                                  CT   __    CGA
GAM1334  LOC138311 3'  CATCCCGGCAGGAGAGTCCTCC 76720       A  CGTGA  A
            A                    TGGAG AC     TT CCGGGATG
                                ||||| ||     || ||||||||
                                ACCTC TG     GA GGCCCTAC
                                   C  AGAG_  C
GAM1334  LOC151996 5'  CATCCCGGCCCATACCCCTCCA 86715       AACC   ATTA
                                TGGAG    GTG    CCGGGATG
                                |||||    |||    ||||||||
                                ACCTC    TAC    GGCCCTAC
                                   CCCA   CC__
GAM1334  LOC254556 3'  TGGACAATCAGGTTCTCCA    96263         G    A_
                                TGGAGAACC TGATT  CCG
                                ||||||||| |||||  |||
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                                ACCTCTTGG ACTAA  GGT
                                      _    CA
GAM1334 LOC57406 3' CTGGTATCCACGGTTCCCCA  40715    A      AT
                                TGG GAACCGTG  TACCGG
                                ||| ||||||||  ||||||
                                ACC CTTGGCAC  ATGGTC
                                  C       CT
GAM1335 DLEC1    3' CATCTGGCCCTCCCTTG    24716     A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                   C    G  _
GAM1335 DLEC1    3' CATCTGGCCCTCCCTTG    24717     A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                   C    G  _
GAM1335 PIP5K1A  3' TATCCCACCCTGCCTTGATA  14520       A   CA  C
                                TATCAAGG AGGG  GG GTG
                                |||||||| ||||  || |||
                                ATAGTTCC TCCC  CC TAT
                                     G   A_  C
GAM1335 SOX11    3' ACCCACCCCCCCTTGGTA    13308       AA   CA  C
                                TATCAAGG  GGG  GG GT
                                ||||||||  |||  || ||
                                ATGGTTCC  CCC  CC CA
                                     CC   A_  _
GAM1335 CHL1     3' TGTTACCTTTCCTCAATA    22768    CA      CA
                                TAT  AGGAAGGG  GGCG
                                |||  ||||||||  ||||
                                ATA  TCCTTTCC  TTGT
                                  AC       A_
GAM1335 EPB41L1  3' CATTCTGCCCTTCCCTGA    71104    A        C
                                TCA GGAAGGGCAGG GTG
                                ||| ||||||||||| |||
                                AGT CCTTCCCGTCT TAC
                                  C        _
GAM1335 FLJ00060 3' CATACCCCCTGCCCTCCTCTGA 61741    _   A     CGTG
                                TCA AGGA GGGCAGG   ATG
                                ||| |||| |||||||   |||
                                AGT TCCT CCCGTCC   TAC
                                  C   _     CCCA
GAM1335 FLJ10898 5' CACCACAGCCCTTTCTCAATA 60126    CA       AGGC
                                TAT  AGGAAGGGC   GTG
                                |||  |||||||||   |||
                                ATA  TCTTTCCCG   CAC
                                  AC       ACAC
GAM1335 FLJ22557 3' ATCATCCCATCCTTAATA    45581    C    A  CAGGC
                                TAT AAGGA GGG    GTGAT
                                ||| ||||| |||    |||||
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                                ATA TTCCT CCC     TACTA
                                  A     A  _____
GAM1335  KIAA0574  3'  CATCCCCTGCCCTCCCCTGA   69808      A  A       CGT
                                TCA GG AGGGCAGG   GATG
                                ||| || ||||||||   ||||
                                AGT CC TCCCGTCC   CTAC
                                  C  C       C__
GAM1335  KIAA0632  3'  CACCTCAGAAACCCTTCCTTGA 32071           CA___  C
                                TCAAGGAAGGG     GG GTG
                                ||||||||||     || |||
                                AGTTCCTTCCC     CT CAC
                                      AAAGA  C
GAM1335  KIAA1045  3'  CATCACATGTCCTTCC      71599          GGC
                                GGAAGGGCA   GTGATG
                                |||||||||   ||||||
                                CCTTCCTGT   CACTAC
                                     A__
GAM1335  KIAA1354  5'  CAGTGACTGCCTTCCCTTGATA 61572         A      G  _
                                TATCAAGG AGGGCAG CG TG
                                |||||||| ||||||| || ||
                                ATAGTTCC TTCCGTC GT AC
                                     C      A  G
GAM1335  MGC20460  5'  CACCGCCTCCTACCCTTCTT   54901         C___    _
                                AGGAAGGG    AGGCG TG
                                ||||||||    ||||| ||
                                TTCTTCCC    TCCGC AC
                                     ATCC     C
GAM1335  LOC158476 3'  CACGCCCGCCCCCCCCATTGA  88186      _ AA_    A
                                TCAA GG   GGGC GGCGTG
                                ||||  ||   ||||  ||||||
                                AGTT CC   CCCG CCGCAC
                                  A  CCC    C
GAM1335  LOC90459  3'  CACACCCGCCTAATTTTTG    63550       A_    A  C
                                CAAGGA  GGGC GG GTG
                                ||||||  ||||  ||  |||
                                GTTTTT  TCCG CC CAC
                                    AA    C  A
GAM1336  SCAMP1    3'  GCTAAATAAATATTCTCC     54500     T     C
                                GGA AATATT ATTTAGC
                                |||  ||||||  |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1336  SCAMP1    3'  GCTAAATAAATATTCTCC     54501     T     C
                                GGA AATATT ATTTAGC
                                |||  ||||||  |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1336  NX-17     3'  TGAATATCAGCCCCTAATA    40706         ATA_
                                TATTAGGG    ATATTCA
                                ||||||||    |||||||
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                                ATAATCCC   TATAAGT
                                    CGAC
GAM1336  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
             TA                   TATTAGGGATAATATTCATTTAGC
                                  ||||||||||||||||||||||
                                  ATAATCCCTATTATAAGTAAATCG

GAM1337  DLEC1    3'  CATCTGGCCCTCCCTTG     24716      A    A  C
                                  CAAGG AGGGC GG GTG
                                  ||||| ||||| || |||
                                  GTTCC TCCCG TC TAC
                                    C    G  _
GAM1337  DLEC1    3'  CATCTGGCCCTCCCTTG     96279      A    A  C
                                  CAAGG AGGGC GG GTG
                                  ||||| ||||| || |||
                                  GTTCC TCCCG TC TAC
                                    C    G  _
GAM1337  PIP5K1A  3'  TATCCCACCCTGCCTTGATA  14520        A   CA  C
                                  TATCAAGG AGGG  GG GTG
                                  |||||||| ||||  || |||
                                  ATAGTTCC TCCC  CC TAT
                                      G   A_  C
GAM1337  SOX11    3'  ACCCACCCCCCCTTGGTA    13308        AA  CA  C
                                  TATCAAGG  GGG  GG GT
                                  ||||||||  |||  || ||
                                  ATGGTTCC  CCC  CC CA
                                      CC   A_  _
GAM1337  CHL1     3'  TGTTACCTTTCCTCAATA    22768     CA      CA
                                  TAT  AGGAAGGG  GGCG
                                  |||  ||||||||  ||||
                                  ATA  TCCTTTCC  TTGT
                                    AC       A_
GAM1337  EPB41L1  3'  CATTCTGCCCTTCCCTGA    71104     A        C
                                  TCA GGAAGGGCAGG GTG
                                  ||| |||||||||| |||
                                  AGT CCTTCCCGTCT TAC
                                    C         _
GAM1337  FLJ00060 3'  CATACCCCCTGCCCTCCTCTGA 61741     _   A     CGTG
                                  TCA AGGA GGGCAGG   ATG
                                  ||| |||| |||||||   |||
                                  AGT TCCT CCCGTCC   TAC
                                    C   _      CCCA
GAM1337  FLJ10898 5'  CACCACAGCCCTTTCTCAATA  60126     CA       AGGC
                                  TAT  AGGAAGGGC   GTG
                                  |||  |||||||||   |||
                                  ATA  TCTTTCCCG   CAC
                                    AC       ACAC
GAM1337  FLJ22557 3'  ATCATCCCATCCTTAATA    45581     C    A  CAGGC
                                  TAT AAGGA GGG    GTGAT
                                  ||| ||||| |||    |||||
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                                ATA TTCCT CCC     TACTA
                                  A     A  _____
GAM1337  KIAA0574  3'  CATCCCCTGCCCTCCCCTGA   69808      A  A       CGT
                                TCA GG AGGGCAGG   GATG
                                ||| || ||||||||   ||||
                                AGT CC TCCCGTCC   CTAC
                                  C  C       C__
GAM1337  KIAA0632  3'  CACCTCAGAAACCCTTCCTTGA 32071           CA___  C
                                TCAAGGAAGGG     GG GTG
                                ||||||||||     || |||
                                AGTTCCTTCCC     CT CAC
                                      AAAGA  C
GAM1337  KIAA1045  3'  CATCACATGTCCTTCC      71599          GGC
                                GGAAGGGCA   GTGATG
                                |||||||||   ||||||
                                CCTTCCTGT   CACTAC
                                     A__
GAM1337  KIAA1354  5'  CAGTGACTGCCTTCCCTTGATA 61572         A      G  _
                                TATCAAGG AGGGCAG CG TG
                                |||||||| ||||||| || ||
                                ATAGTTCC TTCCGTC GT AC
                                     C      A  G
GAM1337  MGC20460  5'  CACCGCCTCCTACCCTTCTT   54901         C___    _
                                AGGAAGGG    AGGCG TG
                                ||||||||    ||||| ||
                                TTCTTCCC    TCCGC AC
                                     ATCC     C
GAM1337  LOC158476 3'  CACGCCCGCCCCCCCCATTGA  88186      _  AA_    A
                                TCAA GG   GGGC GGCGTG
                                ||||  ||   ||||  ||||||
                                AGTT CC   CCCG CCGCAC
                                  A  CCC    C
GAM1337  LOC90459  3'  CACACCCGCCTAATTTTTG    63550       A_    A  C
                                CAAGGA  GGGC GG GTG
                                ||||||  ||||  ||  |||
                                GTTTTT  TCCG CC CAC
                                    AA    C  A
GAM1338  SCAMP1    3'  GCTAAATAAATATTCTCC     54500     T     C
                                GGA AATATT ATTTAGC
                                |||  ||||||  |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1338  SCAMP1    3'  GCTAAATAAATATTCTCC     54501     T     C
                                GGA AATATT ATTTAGC
                                |||  ||||||  |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1338  NX-17     3'  TGAATATCAGCCCCTAATA    40706         ATA_
                                TATTAGGG    ATATTCA
                                ||||||||    |||||||
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                                ATAATCCC    TATAAGT
                                    CGAC
GAM1338  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
             TA                   TATTAGGGATAATATTCATTTAGC
                                  ||||||||||||||||||||||
                                  ATAATCCCTATTATAAGTAAATCG

GAM1339  BACH2     3'  CTGTCAAGCAATGGATAAACAG 41782          C     GGGA__
             CTCT                  AGAGTTGTT ATCCA      GACAG
                                  ||||||||| |||||      |||||
                                  TCTCGACAA TAGGT      CTGTC
                                      A    AACGAA
GAM1339  CHRNA1    3'  CTGTCTCCCTGAAGAGTGAAC  5375        C___
                                  GTTCAT    CAGGGAGACAG
                                  ||||||    ||||||||||
                                  CAAGTG    GTCCCTCTGTC
                                    AGAA
GAM1339  FZD8      3'  CCATGGATAACAACTCT     49873         C    G
                                  AGAGTTGTT ATCCA GG
                                  ||||||||| ||||| ||
                                  TCTCAACAA TAGGT CC
                                      _    A
GAM1339  HHIP      5'  CTGTCCCACCTAAACAACTC   42753         CATCCAG  A
                                  GAGTTGTT      GG GACAG
                                  ||||||||      || |||||
                                  CTCAACAA      CC CTGTC
                                      ATCCA__ _
GAM1339  MME       3'  TCCCTATGGAGGAACAACTCT  8034          A   __
                                  AGAGTTGTTC TCCA  GGGA
                                  |||||||||| ||||  ||||
                                  TCTCAACAAG AGGT  CCCT
                                      G    AT
GAM1339  MME       3'  TCCCTATGGAGGAACAACTCT  24437         A   __
                                  AGAGTTGTTC TCCA  GGGA
                                  |||||||||| ||||  ||||
                                  TCTCAACAAG AGGT  CCCT
                                      G    AT
GAM1339  MME       3'  TCCCTATGGAGGAACAACTCT  24439         A   __
                                  AGAGTTGTTC TCCA  GGGA
                                  |||||||||| ||||  ||||
                                  TCTCAACAAG AGGT  CCCT
                                      G    AT
GAM1339  MME       3'  TCCCTATGGAGGAACAACTCT  24441         A   __
                                  AGAGTTGTTC TCCA  GGGA
                                  |||||||||| ||||  ||||
                                  TCTCAACAAG AGGT  CCCT
                                      G    AT
GAM1339  MTCP1     5'  CTACATGGATAACAACTCT    27242         C    GGG
                                  AGAGTTGTT ATCCA   AG
                                  ||||||||| |||||   ||
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                                TCTCAACAA TAGGT   TC
                                     _    ACA
GAM1339  NR1D1    3'  TGTCTCCCCCACAACCCT    41672    A    TCATCCA
                                AG GTTGT      GGGAGACA
                                || |||||      ||||||||
                                TC CAACA      CCCTCTGT
                                 C    CC_____
GAM1339  NR1I2    3'  TGTCTCCCTAGGGAATTC    42088      GTTCA  _
                                GAGTT    TCC AGGGAGACA
                                |||||    ||| |||||||||
                                CTTAA    GGG TCCCTCTGT
                                   _____  A
GAM1339  NR1I2    3'  TGTCTCCCTAGGGAATTC    15304      GTTCA  _
                                GAGTT    TCC AGGGAGACA
                                |||||    ||| |||||||||
                                CTTAA    GGG TCCCTCTGT
                                   _____  A
GAM1339  PCOLN3   3'  CTGCCCTGTTGCCAAACAACTC 12411        ___  TC    _
                                GAGTTGTT   CA  CAGGG AG
                                ||||||||   ||  ||||| ||
                                CTCAACAA   GT  GTCCC TC
                                     ACC  T_    G
GAM1339  PFN2     3'  TGTCTTCATCAACAACCCT    12063    A    CATCCAG
                                AG GTTGTT      GGAGACA
                                || ||||||      |||||||
                                TC CAACAA      CTTCTGT
                                 C     CTA____
GAM1339  PFN2     3'  TGTCTTCATCAACAACCCT    54890    A    CATCCAG
                                AG GTTGTT      GGAGACA
                                || ||||||      |||||||
                                TC CAACAA      CTTCTGT
                                 C     CTA____
GAM1339  TNS      3'  CTGTCTCCCTAACTCAACTGCT 42950    _    TTCATCC
                                AG AGTTG      AGGGAGACAG
                                || |||||      ||||||||||
                                TC TCAAC      TCCCTCTGTC
                                 G    TCAA___
GAM1339  FLJ10511 3'  CCCTAGAAAAACAACTCT    36686        CA  C
                                AGAGTTGTT  TC AGGG
                                |||||||||  || ||||
                                TCTCAACAA  AG TCCC
                                     AA  A
GAM1339  FLJ20195 3'  CCCGATGAACACCTCT      35216      T      CA
                                AGAG TGTTCATC  GGG
                                |||| ||||||||  |||
                                TCTC ACAAGTAG  CCC
                                  C       __
GAM1339  HAAO     3'  TCCCTGCCAAACAACTCT    60173        CATC
                                AGAGTTGTT    CAGGGA
                                |||||||||    ||||||
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                                TCTCAACAA   GTCCCT
                                     ACC_
GAM1339  KIAA0843  3'  CTGAACAACCAGACAGACAACT 30801       CA  CA  GAGA_
            CT                   AGAGTTGTT  TC  GG    CAG
                                 |||||||||  ||  ||    |||
                                 TCTCAACAG  AG  CC    GTC
                                      AC  A_  AACAA
GAM1339  KIAA1497  5'  CTGTCCTTGTATGAGCAAC   68121       C     GA
                                 GTTGTTCAT CAGGGA  CAG
                                 |||||||||  ||||||  |||
                                 CAACGAGTA GTTCCT  GTC
                                      T     __
GAM1339  KIAA1710  3'  TCTCCATACATGAACAATCT   63181     G      CCAG
                                 AGA TTGTTCAT    GGAGA
                                 |||  ||||||||    |||||
                                 TCT AACAAGTA    CCTCT
                                   _       CATA
GAM1339  PDE7B    3'  CTGCCGAAATGAGCAACTC   38949         CCA  G
                                 GAGTTGTTCAT   GG AG
                                 ||||||||||   || ||
                                 CTCAACGAGTA   CC TC
                                       AAG  G
GAM1339  SEC24B   3'  CTGCATTGTTGGATGACAACTC 21984       T      G  GA
            T                    AGAGTTGT CATCCAG GA  CAG
                                 ||||||||  |||||||  ||  |||
                                 TCTCAACA GTAGGTT TT  GTC
                                      _      G  AC
GAM1339  LOC124753 5'  CTGCCTCCCTGGCTTCCATCTC 74803     T  TTCAT      A
                                 GAG TG     CCAGGGAG CAG
                                 |||  ||     ||||||||  |||
                                 CTC AC     GGTCCCTC GTC
                                   T  CTTC_       C
GAM1339  LOC142948 3'  CTACCGGGAGGAATGAATAACT 83777         _____  A  G
            C                     GAGTTGTTCA    TCC GG AG
                                  ||||||||||    |||  ||  ||
                                  CTCAATAAGT    AGG CC TC
                                        AAGG   G  A
GAM1339  LOC153914 5'  CCACTAAAGTGAACAACTC    81898         CC_  _
                                 GAGTTGTTCAT   AG GG
                                 ||||||||||   || ||
                                 CTCAACAAGTG   TC CC
                                       AAA  A
GAM1339  LOC219445 5'  CTCCCTGGTTCAAACAATTC   93202       CAT_
                                 GAGTTGTT    CCAGGGAG
                                 ||||||||    ||||||||
                                 CTTAACAA    GGTCCCTC
                                      ACTT
GAM1339  LOC219914 5'  CCACTGGGAGGAACGAACAACT 94967        A_____    _
            C                     GAGTTGTTC     TCCAG GG
                                  |||||||||     ||||| ||
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                                CTCAACAAG     GGGTC CC
                                     CAAGGA    A
GAM1340  BACH2    3'  CTGTCAAGCAATGGATAAACAG 41782        C    GGGA__
              CTCT                  AGAGTTGTT ATCCA     GACAG
                                |||||||||  |||||     |||||
                                TCTCGACAA TAGGT     CTGTC
                                     A    AACGAA
GAM1340  CHRNA1   3'  CTGTCTCCCTGAAGAGTGAAC  5375       C___
                                GTTCAT   CAGGGAGACAG
                                ||||||   ||||||||||
                                CAAGTG   GTCCCTCTGTC
                                   AGAA
GAM1340  FZD8     3'  CCATGGATAACAACTCT     49873        C    G
                                AGAGTTGTT ATCCA GG
                                |||||||||  |||||  ||
                                TCTCAACAA TAGGT CC
                                     _    A
GAM1340  HHIP     5'  CTGTCCCACCTAAACAACTC   42753       CATCCAG  A
                                GAGTTGTT      GG GACAG
                                ||||||||      ||  |||||
                                CTCAACAA      CC CTGTC
                                     ATCCA__  _
GAM1340  MME      3'  TCCCTATGGAGGAACAACTCT  24437         A   __
                                AGAGTTGTTC TCCA  GGGA
                                ||||||||||  ||||  ||||
                                TCTCAACAAG AGGT  CCCT
                                     G    AT
GAM1340  MME      3'  TCCCTATGGAGGAACAACTCT  24439         A   __
                                AGAGTTGTTC TCCA  GGGA
                                ||||||||||  ||||  ||||
                                TCTCAACAAG AGGT  CCCT
                                     G    AT
GAM1340  MME      3'  TCCCTATGGAGGAACAACTCT  24441         A   __
                                AGAGTTGTTC TCCA  GGGA
                                ||||||||||  ||||  ||||
                                TCTCAACAAG AGGT  CCCT
                                     G    AT
GAM1340  MME      3'  TCCCTATGGAGGAACAACTCT  8034          A   __
                                AGAGTTGTTC TCCA  GGGA
                                ||||||||||  ||||  ||||
                                TCTCAACAAG AGGT  CCCT
                                     G    AT
GAM1340  MTCP1    5'  CTACATGGATAACAACTCT   27242        C    GGG
                                AGAGTTGTT ATCCA   AG
                                |||||||||  |||||   ||
                                TCTCAACAA TAGGT   TC
                                     _    ACA
GAM1340  NR1D1    3'  TGTCTCCCCCACAACCCT    41672    A    TCATCCA
                                AG GTTGT      GGGAGACA
                                ||  |||||      ||||||||
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                                TC CAACA      CCCTCTGT
                                 C    CC_____
GAM1340 NR1I2    3' TGTCTCCCTAGGGAATTC    42088      GTTCA  _
                                GAGTT    TCC AGGGAGACA
                                |||||    ||| |||||||||
                                CTTAA    GGG TCCCTCTGT
                                   _____  A
GAM1340 NR1I2    3' TGTCTCCCTAGGGAATTC    15304      GTTCA  _
                                GAGTT    TCC AGGGAGACA
                                |||||    ||| |||||||||
                                CTTAA    GGG TCCCTCTGT
                                   _____  A
GAM1340 PCOLN3   3' CTGCCCTGTTGCCAAACAACTC 12411        ___ TC    _
                                GAGTTGTT   CA  CAGGG AG
                                ||||||||   ||  ||||| ||
                                CTCAACAA   GT  GTCCC TC
                                     ACC  T_    G
GAM1340 PFN2     3' TGTCTTCATCAACAACCCT   54890    A     CATCCAG
                                AG GTTGTT      GGAGACA
                                || ||||||      |||||||
                                TC CAACAA      CTTCTGT
                                 C     CTA____
GAM1340 PFN2     3' TGTCTTCATCAACAACCCT   12063    A     CATCCAG
                                AG GTTGTT      GGAGACA
                                || ||||||      |||||||
                                TC CAACAA      CTTCTGT
                                 C     CTA____
GAM1340 TNS      3' CTGTCTCCCTAACTCAACTGCT 42950    _    TTCATCC
                                AG AGTTG      AGGGAGACAG
                                || |||||      ||||||||||
                                TC TCAAC      TCCCTCTGTC
                                 G    TCAA___
GAM1340 FLJ10511 3' CCCTAGAAAAACAACTCT    36686        CA  C
                                AGAGTTGTT  TC AGGG
                                |||||||||  || ||||
                                TCTCAACAA  AG TCCC
                                     AA  A
GAM1340 FLJ20195 3' CCCGATGAACACCTCT      35216      T      CA
                                AGAG TGTTCATC  GGG
                                |||| ||||||||  |||
                                TCTC ACAAGTAG  CCC
                                  C      __
GAM1340 HAAO     3' TCCCTGCCAAACAACTCT    60173        CATC
                                AGAGTTGTT   CAGGGA
                                |||||||||   ||||||
                                TCTCAACAA   GTCCCT
                                     ACC_
GAM1340 KIAA0843 3' CTGAACAACCAGACAGACAACT 30801        CA  CA  GAGA_
             CT                   AGAGTTGTT  TC  GG    CAG
                                |||||||||  ||  ||    |||
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                                TCTCAACAG  AG  CC    GTC
                                     AC  A_  AACAA
GAM1340  KIAA1497  5'  CTGTCCTTGTATGAGCAAC   68121        C     GA
                                GTTGTTCAT CAGGGA  CAG
                                ||||||||| ||||||  |||
                                CAACGAGTA GTTCCT  GTC
                                     T     __
GAM1340  KIAA1710  3'  TCTCCATACATGAACAATCT   63181     G      CCAG
                                AGA TTGTTCAT    GGAGA
                                ||| ||||||||    |||||
                                TCT AACAAGTA    CCTCT
                                  _       CATA
GAM1340  PDE7B     3'  CTGCCGAAATGAGCAACTC   38949          CCA  G
                                GAGTTGTTCAT   GG AG
                                ||||||||||   || ||
                                CTCAACGAGTA   CC TC
                                      AAG  G
GAM1340  SEC24B    3'  CTGCATTGTTGGATGACAACTC 21984        T      G  GA
              T                  AGAGTTGT CATCCAG GA  CAG
                                 ||||||| ||||||| ||  |||
                                 TCTCAACA GTAGGTT TT  GTC
                                      _      G  AC
GAM1340  LOC124753 5'  CTGCCTCCCTGGCTTCCATCTC 74803     T  TTCAT       A
                                GAG TG     CCAGGGAG CAG
                                ||| ||     |||||||| |||
                                CTC AC     GGTCCCTC GTC
                                  T  CTTC_       C
GAM1340  LOC142948 3'  CTACCGGGAGGAATGAATAACT 83777          _____   A  G
              C                  GAGTTGTTCA    TCC GG AG
                                 ||||||||||    ||| || ||
                                 CTCAATAAGT    AGG CC TC
                                      AAGG   G  A
GAM1340  LOC153914 5'  CCACTAAAGTGAACAACTC    81898          CC_  _
                                GAGTTGTTCAT   AG GG
                                ||||||||||   || ||
                                CTCAACAAGTG   TC CC
                                      AAA  A
GAM1340  LOC219445 5'  CTCCCTGGTTCAAACAATTC   93202        CAT_
                                GAGTTGTT    CCAGGGAG
                                ||||||||    ||||||||
                                CTTAACAA    GGTCCCTC
                                     ACTT
GAM1340  LOC219914 5'  CCACTGGGAGGAACGAACAACT 94967         A_____    _
              C                  GAGTTGTTC     TCCAG GG
                                 |||||||||     ||||| ||
                                 CTCAACAAG     GGGTC CC
                                      CAAGGA    A
GAM1341  CCNF      3'  CCACTTGAGCCCCTGCCCACAT 10069    A  CCA   A  CTTT_
              CTG                  CA ATG   GCAG GGC    TGG
                                   || |||   |||| |||    |||
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                                GT TAC   CGTC CCG    ACC
                                 C  ACC   C  AGTTC
GAM1341  EZH1    3'  CACCCTCTCTGGCATTCA   10548   A     C    CCTTT
                                C AATGCCAG AGAGG    TG
                                | |||||||| |||||    ||
                                A TTACGGTC TCTCC    AC
                                 C       _    C____
GAM1341  FANCC   3'  CCAAAAGGCCCTTGGGACAT  71034    _  AGC  A
                                ATG CC   AG GGCCTTTTGG
                                ||| ||   || ||||||||||
                                TAC GG   TC CCGGAAAACC
                                  A  GT_ _
GAM1341  MYOM2   3'  CCAAATGAGCAGCTGGCAT   15606       AGAG  CT_
                                ATGCCAGC   GC   TTTGG
                                ||||||||   ||   |||||
                                TACGGTCG   CG   AAACC
                                     A___  AGT
GAM1341  PML     3'  CCACTAGGCCTCTGCCAGG   53807   A_       TT
                                CC  GCAGAGGCCT  TGG
                                ||  ||||||||||  |||
                                GG  CGTCTCCGGA  ACC
                                 AC        TC
GAM1341  PML     3'  CCACTAGGCCTCTGCCAGG   53809   A_       TT
                                CC  GCAGAGGCCT  TGG
                                ||  ||||||||||  |||
                                GG  CGTCTCCGGA  ACC
                                 AC        TC
GAM1341  PML     3'  CCACTAGGCCTCTGCCAGG   53815   A_       TT
                                CC  GCAGAGGCCT  TGG
                                ||  ||||||||||  |||
                                GG  CGTCTCCGGA  ACC
                                 AC        TC
GAM1341  PML     3'  CCACTAGGCCTCTGCCAGG   53823   A_       TT
                                CC  GCAGAGGCCT  TGG
                                ||  ||||||||||  |||
                                GG  CGTCTCCGGA  ACC
                                 AC        TC
GAM1341  REGL    3'  CCATCTCTCCTCTGCTAAATTT 22500      GCC      CCTTT
           G                     CAAAT   AGCAGAGG    TGG
                                |||||   ||||||||    |||
                                GTTTA   TCGTCTCC    ACC
                                   AA_      TCTCT
GAM1341  REV3L   5'  CTTTGGCCTCCTCTGCTGGCAT 12822    A        G_______  TTTT
           GTG                    CA ATGCCAGCAGAG     CC   G
                                || ||||||||||||     ||   |
                                GT TACGGTCGTCTC     GG   C
                                 G         CTCC___  TTTT
GAM1341  RGL     3'  CTTTGGCAACCTCTGCCTGCAT 31427    A   CA    G_______  TTTT
           CTG                    CA ATGC  GCAGAG     CC   G
                                || ||||  ||||||     ||   |
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                                GT TACG  CGTCTC      GG   C
                                 C   TC     CAAC___  TTTT
GAM1341  RPL10    3'  CCAAAAGGCCTCTGGTTTTTTG 21177     T_   GCA
                                CAAA  GCCA   GAGGCCTTTTGG
                                ||||  ||||   ||||||||||||
                                GTTT  TGGT   CTCCGGAAAACC
                                  TT   ___
GAM1341  SALL2    3'  CAAAAGGGCTGGCAGCTG    64588    AA     AGAGG    _
                                CA  TGCCAGC    CCTTTT G
                                ||  |||||||    |||||| |
                                GT  ACGGTCG    GGAAAA C
                                 CG      _____     A
GAM1341  TACC1    3'  CCAAAAAGGTTTGACTGGC   21867      _  AG     _
                                GCCAG CAG  GCCTTTT GG
                                ||||| |||  ||||||| ||
                                CGGTC GTT  TGGAAAA CC
                                   A  __      A
GAM1341  ARTN     5'  CCGAGGGGCCCCTCCCAGCAT  55115     CAGC  A
                                ATGC    AG GGCCTTTTGG
                                ||||    || ||||||||||
                                TACG    TC CCGGGGAGCC
                                  ACCC  C
GAM1341  BRDG1    3'  GCCAAAAAACCTAAGTTTTGCT 25042      _____  CC     ___
           G                     CAGCAG    AGG  TTTTGG   C
                                ||||||    |||  ||||||   |
                                GTCGTT    TCC  AAAACC   G
                                   TTGAA   AA     ___
GAM1341  CACNG4   3'  CCTCCCTCCAACTGGCATTTG  27707        CA_   CCTTTT
                                CAAATGCCAG   GAGG     GG
                                ||||||||||   ||||     ||
                                GTTTACGGTC   CTCC     CC
                                     AAC   CT____
GAM1341  FLJ10847 3'  CATGCCCAGCTGGCATTTG   37299         AGA   CTTT
                                CAAATGCCAGC   GGC   TG
                                ||||||||||   |||   ||
                                GTTTACGGTCG   CCG   AC
                                      AC_   T___
GAM1341  FLJ13215 3'  CAAGCTCCACTGGCATTT    47193        CA   GCCT
                                AAATGCCAG  GAG   TTTG
                                |||||||||  |||   ||||
                                TTTACGGTC  CTC   GAAC
                                     AC   ____
GAM1341  FLJ20374 5'  CCTTTTGGCCTTACCCCTGCTG 35550     AT      A G_________  TTTT
           GCCCTTG                CAA  GCCAGCAG G       CC    GG
                                |||  |||||||| |       ||    ||
                                GTT  CGGTCGTC C       GG    CC
                                  CC       C CATTCC___  TTTT
GAM1341  FLJ30473 3'  CTGGGAGGCCTCTGCTGG    59140            TG
                                CCAGCAGAGGCCTTT  G
                                ||||||||||||||  |
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                                GGTCGTCTCCGGAGG  C
                                      GT
GAM1341  HEMK     3'  CCATACCTCTGCTGGCA     32954          CCTTT
                                TGCCAGCAGAGG    TGG
                                ||||||||||||    |||
                                ACGGTCGTCTCC    ACC
                                      AT___
GAM1341  KIAA0892 3'  CCATGGCCTCTGCTAGC     71568    C       TTT
                                GC AGCAGAGGCC   TGG
                                || ||||||||||   |||
                                CG TCGTCTCCGG   ACC
                                 A        T__
GAM1341  LATS1    3'  CCAAAATGTTGTCCCTGCTGGC 60909        A   C___
            A                    TGCCAGCAG GGC    TTTTGG
                                ||||||||| |||    ||||||
                                ACGGTCGTC CTG    AAAACC
                                      C   TTGT
GAM1341  PPIL3    5'  CCAACAGACCTCTGCTGGCATC 51642    A         C  T
            TG                    CA ATGCCAGCAGAGG CT TTGG
                                || ||||||||||||| || ||||
                                GT TACGGTCGTCTCC GA AACC
                                 C          A  C
GAM1341  PPIL3    5'  CCAACAGACCTCTGCTGGCATC 56473    A         C  T
            TG                    CA ATGCCAGCAGAGG CT TTGG
                                || ||||||||||||| || ||||
                                GT TACGGTCGTCTCC GA AACC
                                 C          A  C
GAM1341  PPIL3    5'  CCAACAGACCTCTGCTGGCATC 56474    A         C  T
            TG                    CA ATGCCAGCAGAGG CT TTGG
                                || ||||||||||||| || ||||
                                GT TACGGTCGTCTCC GA AACC
                                 C          A  C
GAM1341  STK3     3'  CCAAAAGGCAGAATTGACAGTT 74101     A  C   CAGAG
            G                     CAA TG CAG     GCCTTTTGG
                                ||| || |||     |||||||||
                                GTT AC GTT     CGGAAAACC
                                  G  A   AAGA_
GAM1341  LOC147515 3'  CTTTGGCCTCCTTCTGCTGGCA 85149    A         G________  TTTT
            TCTG                    CA ATGCCAGCAGAG       CC    G
                                || ||||||||||||       ||    |
                                GT TACGGTCGTCTT       GG    C
                                 C          CCTCC___  TTTT
GAM1341  LOC148089 3'  CCAAAAAACATAGACTGCTGGC 79326         AGGCC___
            A                     TGCCAGCAG       TTTTGG
                                |||||||||       ||||||
                                ACGGTCGTC       AAAACC
                                      AGATACAA
GAM1341  LOC149461 5'  CCAAAGCCCCTGCTGGCA    80201         A   CT
                                TGCCAGCAG GGC  TTTGG
                                ||||||||| |||  |||||
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                                ACGGTCGTC CCG  AAACC
                                    C   __
GAM1341  LOC149995 3'  CTTTGGCCTCCTTCTGCTGGCA 85984    A         G_______  TTTT
             TCTG                   CA ATGCCAGCAGAG       CC    G
                                || ||||||||||||       ||    |
                                GT TACGGTCGTCTT       GG    C
                                 C          CCTCC___  TTTT
GAM1342  AQP6     5'  AGCCAGAAGACAGGACACCAGA 9723      C       GTGG   A
                                TCTG TGTCCTGT    TGG CT
                                |||| ||||||||    ||| ||
                                AGAC ACAGGACA    ACC GA
                                  C       GAAG  _
GAM1342  AQP6     5'  GCCAGAGACAGGACACCAGA   55005     C       G__
                                TCTG TGTCCTGT   TGGT
                                |||| ||||||||   ||||
                                AGAC ACAGGACA   ACCG
                                  C       GAG
GAM1342  COL19A1   3'  TAGCTTATCACAAGAAGCAGA  10264      GTCCTG      GA
                                TCTGCT     TGTGGTG  CTA
                                ||||||     |||||||  |||
                                AGACGA     ACACTAT  GAT
                                   AGA___      TC
GAM1342  DNAH9     5'  TCCGATCTCACAAAGCAGCAGA 17413        CC    T   _
                                TCTGCTGT  TGTG GGT GGA
                                ||||||||  |||| ||| |||
                                AGACGACG  ACAC CTA CCT
                                     AA    T   G
GAM1342  PARK2     3'  AGTTTGTCCACACAAGACAGCA 26539        C      _ GG
             GA                   TCTGCTGTC TGTGTGG T  ACT
                                |||||||||  |||||||  |  |||
                                AGACGACAG ACACACC G  TGA
                                     A       T TT
GAM1342  PARK2     3'  AGTTTGTCCACACAAGACAGCA 26543        C      _ GG
             GA                   TCTGCTGTC TGTGTGG T  ACT
                                |||||||||  |||||||  |  |||
                                AGACGACAG ACACACC G  TGA
                                     A       T TT
GAM1342  PARK2     3'  AGTTTGTCCACACAAGACAGCA 17075        C      _ GG
             GA                   TCTGCTGTC TGTGTGG T  ACT
                                |||||||||  |||||||  |  |||
                                AGACGACAG ACACACC G  TGA
                                     A       T TT
GAM1342  TFDP1     3'  AGCCCCAAGCAAACAGCAGA   24049       CC   G   T  A
                                TCTGCTGT  TGT TGG GG CT
                                ||||||||  ||| ||| || ||
                                AGACGACA  ACG ACC CC GA
                                     A_   A   _  _
GAM1342  C1orf34   3'  GTGTACCAGGACAGCAGA    61320          GTGT    G
                                TCTGCTGTCCT    GGTG AC
                                ||||||||||    |||| ||
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                                AGACGACAGGA    CCAT TG
                                      ____   G
GAM1342  CPR2     3'  GCCATACAGAACAGAGA     48832     G    C
                                TCT CTGT CTGTGTGGT
                                ||| |||| |||||||||
                                AGA GACA GACATACCG
                                  _    A
GAM1342  DKFZp434K1210 3'  AGCCCACCCGGGCAGCAGA    34685          TGT T     A
                                TCTGCTGTCC   G GGTGG CT
                                ||||||||||   | ||||| ||
                                AGACGACGGG   C CCACC GA
                                     ____ _    C
GAM1342  DKFZP547L112 3'  ATTACACAAGACAAAGA     67126     GC    C
                                TCT  TGTC TGTGTGGT
                                |||  |||| ||||||||
                                AGA  ACAG ACACATTA
                                  A_   A
GAM1342  FLJ22833  3'  CCAGATTATCGAGGACAGCAGA 43404           GT   __
                                TCTGCTGTCCT  GTGG  TGG
                                ||||||||||  ||||  |||
                                AGACGACAGGA  TATT  ACC
                                      GC    AG
GAM1342  FLJ30213  3'  ACCACAGAACAGCAGA      59400         C    GT
                                TCTGCTGT CTGT  GGT
                                |||||||| ||||  |||
                                AGACGACA GACA  CCA
                                     A   __
GAM1342  KIAA1530  3'  GTCTCAGGACAGCAGA      68570           TGTGGT
                                TCTGCTGTCCTG     GGAC
                                ||||||||||||     ||||
                                AGACGACAGGAC     TCTG
                                      _______
GAM1342  KOC1     3'  AGCCCACCACAGAGGCAG    92714     T   G       A
                                CTG CCT TGTGGTGG CT
                                ||| ||| |||||||| ||
                                GAC GGA ACACCACC GA
                                  _  G       C
GAM1342  LOC148114 3'  ACCACACAGACAGCAGA     79358          C
                                TCTGCTGTC TGTGTGGT
                                ||||||||| ||||||||
                                AGACGACAG ACACACCA
                                      _
GAM1342  LOC148343 5'  CCACCACACAGGTGGAGC    79539     GT_
                                GCT   CCTGTGTGGTGG
                                |||   ||||||||||||
                                CGA   GGACACACCACC
                                  GGT
GAM1342  LOC149276 3'  TATCACACAAAACACCAGA    85540      C   CC
                                TCTG TGT  TGTGTGGTG
                                |||| |||  |||||||||
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                                AGAC ACA  ACACACTAT
                                  C   AA
GAM1342  LOC151361 5'  TAGCTTTGGCACAAAGCAGCAG 86506        CC    GGT  A
             A                    TCTGCTGT  TGTGT   GG CTA
                                  |||||||| |||||   || |||
                                  AGACGACG  ACACG   TC GAT
                                      AA    GTT  _
GAM1342  LOC151438 3'  AGCCCGTGACAGGACACAGA   86553     C      GTGG   A
                                  TCTG TGTCCTGT    TGG CT
                                  |||| ||||||||    ||| ||
                                  AGAC ACAGGACA    GCC GA
                                    _       GT__   C
GAM1342  LOC157958 5'  CAGTCACAGGACAGAAGA    82529     G        TGG
                                  TCT CTGTCCTGTG   TG
                                  ||| ||||||||||   ||
                                  AGA GACAGGACAC   AC
                                    A         TG_
GAM1342  LOC203286 5'  TTTGCAGACAGGACAGCAGA   92152           G G TG
                                  TCTGCTGTCCTGT T G  GA
                                  |||||||||||| | |  ||
                                  AGACGACAGGACA A C  TT
                                         G _ GT
GAM1342  LOC222962 3'  CCACCCAGGACAGCAGA     94454           TGT
                                  TCTGCTGTCCTG   GGTGG
                                  ||||||||||||   |||||
                                  AGACGACAGGAC   CCACC
                                                 ____
GAM1342  LOC91963  5'  CAGTATTCCAGGACAGCA    68315          T_   G
                                  TGCTGTCCTG  GTG TG
                                  ||||||||||  ||| ||
                                  ACGACAGGAC  TAT AC
                                        CT   G
GAM1343  DPYSL2    3'  CAATGCCCACCCGCATCGCCA  9114       AGT    GA
                                  TGGC   GGTG  GGTGGGCATTG
                                  ||||   ||||  ||||||||||||
                                  ACCG   CTAC  CCACCCGTAAC
                                    ___    GC
GAM1343  EGLN2     5'  CCACCTCTACCACTGCCA    34518
                                  TGGCAGTGGTGGAGGTGG
                                  ||||||||||||||||||
                                  ACCGTCACCATCTCCACC

GAM1343  FMNL      5'  CCACCCCCGCCACCGCCA    20866      A      A
                                  TGGC GTGGTGG GGTGG
                                  |||| ||||||| |||||
                                  ACCG CACCGCC CCACC
                                    C      C
GAM1343  G6PD      3'  CCCACCTCCACCCCCGCCA   6386       AGT
                                  TGGC   GGTGGAGGTGGG
                                  ||||   ||||||||||||
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                                ACCG   CCACCTCCACCC
                                  CCC
GAM1343  MPP3     5'  CAATACCCACCTCCACCCCC   10409    CAGT         C
                                GG    GGTGGAGGTGGG ATTG
                                ||    |||||||||||| ||||
                                CC    CCACCTCCACCC TAAC
                                 C___          A
GAM1343  MYOZ1    5'  CTTCCCTCCCCCACTGCCA   41434         T    TG
                                TGGCAGTGG GGAGG  GG
                                ||||||||| |||||  ||
                                ACCGTCACC CCTCC  TC
                                      C    CT
GAM1343  SCA1     5'  TCTCCTCCTCCACTGCCA    6185          T    T
                                TGGCAGTGG GGAGG GG
                                ||||||||| ||||| ||
                                ACCGTCACC CCTCC CT
                                      T    T
GAM1343  STAR     5'  GCGACCCCACCACTGCCA    6238           A   GG
                                TGGCAGTGGTGG GGT  GC
                                |||||||||||| |||  ||
                                ACCGTCACCACC CCA  CG
                                       _  G_
GAM1343  BIKE     3'  CCACCACCACCACCACCA    34604     CA      A
                                TGG  GTGGTGG GGTGG
                                |||  ||||||| |||||
                                ACC  CACCACC CCACC
                                  AC      A
GAM1343  BIKE     3'  CCACCACCACCACCACCA    34605     CA      A
                                TGG  GTGGTGG GGTGG
                                |||  ||||||| |||||
                                ACC  CACCACC CCACC
                                  AC      A
GAM1343  CAPN6    3'  CCACCACCACCACCACCA    27399     CA      A
                                TGG  GTGGTGG GGTGG
                                |||  ||||||| |||||
                                ACC  CACCACC CCACC
                                  AC      A
GAM1343  DKFZP434N1817 5'  CTACCTCCACCACCACCA    68720     CA
                                TGG  GTGGTGGAGGTGG
                                |||  |||||||||||||
                                ACC  CACCACCTCCATC
                                  AC
GAM1343  KIAA1582  5'  CAATACCACCACCACCACCACC 65985     CA      A    GC
            A                    TGG  GTGGTGG GGTGG  ATTG
                                |||  ||||||| |||||  ||||
                                ACC  CACCACC CCACC  TAAC
                                  AC      A    A_
GAM1343  KIAA1582  5'  CCACCACCACCACTACCA    65988     C       A
                                TGG AGTGGTGG GGTGG
                                ||| |||||||| |||||
```

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                                ACC TCACCACC CCACC
                                  A       A
GAM1343  PEG10    3'  CCGCCTCCACCACCACCA    31203     CA
                                TGG  GTGGTGGAGGTGG
                                |||  ||||||||||||
                                ACC  CACCACCTCCGCC
                                  AC
GAM1343  PTPNS1   3'  CCACCACCACCACCACCA    55831     CA      A
                                TGG  GTGGTGG GGTGG
                                |||  ||||||| |||||
                                ACC  CACCACC CCACC
                                  AC      A
GAM1343  PTPNS1   3'  CCACCACCACCACCACCA    55832     CA      A
                                TGG  GTGGTGG GGTGG
                                |||  ||||||| |||||
                                ACC  CACCACC CCACC
                                  AC      A
GAM1343  PTPNS1   3'  CCACCACCACCACCACCA    55833     CA      A
                                TGG  GTGGTGG GGTGG
                                |||  ||||||| |||||
                                ACC  CACCACC CCACC
                                  AC      A
GAM1343  PTPNS1   3'  CCACCACCACCACCACCA    55834     CA      A
                                TGG  GTGGTGG GGTGG
                                |||  ||||||| |||||
                                ACC  CACCACC CCACC
                                  AC      A
GAM1343  PTPNS1   3'  CCACCACCACCACCACCA    55835     CA      A
                                TGG  GTGGTGG GGTGG
                                |||  ||||||| |||||
                                ACC  CACCACC CCACC
                                  AC      A
GAM1343  PTPNS1   3'  CCACCACCACCACTACCA    55836     C       A
                                TGG AGTGGTGG GGTGG
                                |||  |||||||| |||||
                                ACC TCACCACC CCACC
                                  A       A
GAM1343  PTPNS1   3'  CCACCTCCACCACCACCA    55837     CA
                                TGG  GTGGTGGAGGTGG
                                |||  ||||||||||||
                                ACC  CACCACCTCCACC
                                  AC
GAM1343  LOC138240 3'  CAATATCTCCCCCACCACCTCC 75829      CA      A  TG GC
           A                     TGG  GTGGTGG GG  G  ATTG
                                |||  ||||||| ||  |  ||||
                                ACC  CACCACC CC  C  TAAC
                                  TC       _  CT TA
GAM1343  LOC146237 3'  CCACCACCACCACCACCA    84605     CA      A
                                TGG  GTGGTGG GGTGG
                                |||  ||||||| |||||
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                                ACC  CACCACC CCACC
                                  AC      A
GAM1343  LOC146237 3'  TCACCACCACCACCACCA    84615     CA      A
                                TGG  GTGGTGG GGTGG
                                |||  ||||||| |||||
                                ACC  CACCACC CCACT
                                  AC      A
GAM1343  LOC148255 5'  CCACCACCACCACCACCA    79496     CA      A
                                TGG  GTGGTGG GGTGG
                                |||  ||||||| |||||
                                ACC  CACCACC CCACC
                                  AC      A
GAM1343  LOC149018 3'  CCCCACCACCACTGCCA     79861           A  T
                                TGGCAGTGGTGG GG GG
                                |||||||||||| || ||
                                ACCGTCACCACC CC CC
                                       A  _
GAM1343  LOC159121 5'  CAATGTTTGTGTCCACCACCAG 88383      A_       G TG
            CCA                   TGGC  GTGGTGGA G  GGCATTG
                                ||||  |||||||| |  |||||||
                                ACCG  CACCACCT T  TTGTAAC
                                  AC       G GT
GAM1343  LOC221477 3'  CCCACCTCCACCACCACA    93770    GCA
                                TG   GTGGTGGAGGTGGG
                                ||   ||||||||||||||
                                AC   CACCACCTCCACCC
                                 AC_
GAM1343  LOC90342  5'  CAATAAGCCCCACTACTACCA  63008     C       A   GGGC
                                TGG AGTGGTGG GGT    ATTG
                                ||| |||||||| |||    ||||
                                ACC TCATCACC CCG    TAAC
                                  A       _   AA__
GAM1344  EDNRA     3'  CCAAGAAGAAATGCTTTC     64799      T    GATT    C
                                GAGA CATT    TCTTC TGG
                                |||| ||||    ||||| |||
                                CTTT GTAA    AGAAG ACC
                                  C    _____     A
GAM1344  PRPH      3'  CCCGATAAGAAGCCAATGATC  21831         AT    CC
                                GATCATTG  TTCTT  TGGG
                                ||||||||  |||||  ||||
                                CTAGTAAC  AAGAA  GCCC
                                     CG     TA
GAM1344  TMEM2     3'  CCCAGAAAGCTTAATGAT     26336         TTT   C
                                ATCATTGA   CTT CTGGG
                                ||||||||   ||| |||||
                                TAGTAATT   GAA GACCC
                                     C__   A
GAM1344  TNFSF4    3'  CCTTATGAAAAATAATGATCTC 13912           A_   TTCCT
              T                  AGAGATCATTG  TTTC     GG
                                ||||||||||  ||||    ||
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                                TCTCTAGTAAT  AAAG    CC
                                      AA   TATT_
GAM1344  DCLRE1A   3'  CCCAGGAAAAATATAAAACTCT 69683     ATCATTG   C
                                AGAG      ATTT TTCCTGGG
                                ||||      |||| ||||||||
                                TCTC      TAAA AAGGACCC
                                  AAAATA_   _
GAM1344  DKFZp434F2322 3'  CCCATCTGAATCAGTAATCCCT 70300    A  C      CTTCC
                                AG GAT ATTGATTT    TGGG
                                || ||| ||||||||    ||||
                                TC CTA TGACTAAG    ACCC
                                 C  A      TCT__
GAM1344  DKFZP566G1424 5'  CCTGGAAGAAACCCATAATCCC 85941    A  CAT  A_     T
            T                    AG GAT   TG  TTTCTTCC GG
                                || |||   ||  |||||||| ||
                                TC CTA   AC  AAAGAAGG CC
                                 C  AT_  CC       T
GAM1344  FLJ14326  3'  CCATGAGTCAATGACCTC    50764    A      TTCT  C
                                GAG TCATTGAT    TC TGG
                                ||| ||||||||    || |||
                                CTC AGTAACTG    AG ACC
                                  C       _____  T
GAM1344  FLJ20170  5'  CCAGGAAACCAGATCTC     35164       AT  ATTTC
                                GAGATC  TG    TTCCTGG
                                ||||||  ||    |||||||
                                CTCTAG  AC    AAGGACC
                                   __  CA___
GAM1344  FLJ20249  3'  CCCAGAAAGGAAACTGATCTCT 80220        TTGA     C
                                AGAGATCA    TTTCTT CTGGG
                                ||||||||    |||||| |||||
                                TCTCTAGT    AAGGAA GACCC
                                     CA__     A
GAM1344  KIAA0295  3'  CCCAGGAAGCTTTCCAGTGATC 68661          ATTT_
            TC                    GAGATCATTG    CTTCCTGGG
                                ||||||||||    |||||||||
                                CTCTAGTGAC    GAAGGACCC
                                      CTTTC
GAM1344  KIAA0825  3'  CCCAGGAAGACACTGACCTGCT 61683    _  A   T  ATT
                                AG AG TCA TG   TCTTCCTGGG
                                || || ||| ||   ||||||||||
                                TC TC AGT AC   AGAAGGACCC
                                 G  C   C  ___
GAM1344  KIAA1190  3'  CCCAAAAAAAAGTTGATCTCT   71644        TTG    C  CC
                                AGAGATCA   ATTT TT  TGGG
                                ||||||||   |||| ||  ||||
                                TCTCTAGT   TGAA AA  ACCC
                                     ___    A  A_
GAM1344  MGC4638   3'  CCAGAAAGCATGATTTC     49733         T ATTT   C
                                GAGATCAT G    CTT CTGG
                                |||||||| |    ||| ||||
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                                CTTTAGTA C    GAA GACC
                                  _ _____  A
GAM1344  PLPL     3'  CCAGGAAAAAGAGTCTC     39820       CATTGA   C
                                GAGAT      TTT TTCCTGG
                                |||||      ||| |||||||
                                CTCTG      AAA AAGGACC
                                  AG_____  _
GAM1344  RIN3     5'  CCCAGGAAAAAACGGATCTCT  46161        ATTGA   C
                                AGAGATC    TTT TTCCTGGG
                                |||||||    ||| ||||||||
                                TCTCTAG    AAA AAGGACCC
                                   GC___   A
GAM1344  SLC26A1  3'  CCCAAACACTCAGAAATCAAGA 42126      ATCA       TCC_____
              ACCTCT                AGAG    TTGATTTCT      TGGG
                                ||||   |||||||||      ||||
                                TCTC    AACTAAAGA      ACCC
                                  CAAG       CTCACAA
GAM1344  LOC121838 5'  CCAGGAAGGACAATCTCTC    76512      TC    AT
                                GAGA  ATTG  TTCTTCCTGG
                                ||||  ||||  ||||||||||
                                CTCT  TAAC  AGGAAGGACC
                                  C_   __
GAM1344  LOC200138 5'  CCCAGGAAAAAATCAATGATCT 91540            C
              C                  GAGATCATTGATTT TTCCTGGG
                                ||||||||||||| ||||||||
                                CTCTAGTAACTAAA AAGGACCC
                                      A
GAM1344  LOC220000 3'  CCAGGAAGATCTGGCCTCT   93231      AT  TT  TT
                                AGAG  CA  GA  TCTTCCTGG
                                ||||  ||  ||  |||||||||
                                TCTC  GT  CT  AGAAGGACC
                                  CG  __  __
GAM1344  LOC221550 5'  CCCAGGAAAAAGAATAGATC   93745      _  GA   C
                                GATC ATT  TTT TTCCTGGG
                                |||| |||  ||| ||||||||
                                CTAG TAA  AAA AAGGACCC
                                  A  G_  _
GAM1344  LOC255721 3'  CCAGGAAGATCTGGCCTCT   96487      AT  TT  TT
                                AGAG  CA  GA  TCTTCCTGG
                                ||||  ||  ||  |||||||||
                                TCTC  GT  CT  AGAAGGACC
                                  CG  __  __
GAM1344  LOC257495 5'  CCCAGGAAAAAGAATAGATC   99572      _  GA   C
                                GATC ATT  TTT TTCCTGGG
                                |||| |||  ||| ||||||||
                                CTAG TAA  AAA AAGGACCC
                                  A  G_  _
GAM1344  LOC257576 5'  CCCAGGAAAAAGAATAGATC   99709      _  GA   C
                                GATC ATT  TTT TTCCTGGG
                                |||| |||  ||| ||||||||
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                                CTAG TAA  AAA AAGGACCC
                                  A  G_  _
GAM1345 CACNA1G  3' CCGCGAGCACATTGCAGCCCC 38775     A A      CA  T
                                GGGG CT CAATGTGC  CG CGG
                                |||| || ||||||||  || |||
                                CCCC GA GTTACACG  GC GCC
                                  _ C       A_ _
GAM1345 DDX3     3' TGGCACATTGCAATCCTC    9063       CTA
                                GGGGA   CAATGTGCCA
                                |||||   ||||||||||
                                CTCCT   GTTACACGGT
                                   AAC
GAM1345 PLOD     3' ATGAGAGCAAACCGTAGTCCCC 6113         AATG   CA_
                                GGGGACTAC    TGC   CGT
                                |||||||||    |||   |||
                                CCCCTGATG    ACG   GTA
                                     CCAA   AGA
GAM1345 LOC200138 5' CCGACGTGACCGTTGTAGCCC  91541     A       TGC
                                GGG CTACAATG   CACGTCGG
                                ||| ||||||||   ||||||||
                                CCC GATGTTGC   GTGCAGCC
                                  _      CA_
GAM1346 CHST1    3' CTCATCTTCGTGTCC       14697         GCAAAT
                                GGACACGAA     GATGAG
                                |||||||||     ||||||
                                CCTGTGCTT     CTACTC
                                              _______
GAM1346 CYBB     3' TACTCATCATTTACCACTGTG  76853      AAGC_
                                CACG     AAATGATGAGTA
                                ||||     ||||||||||||
                                GTGT     TTTACTACTCAT
                                  CACCA
GAM1346 DRIL1    3' ACTCACCACTCCCAGCTTCTCG 19075         __   AAA___  A
            TGTCC                  GGACACGA  AGC     TG TGAGT
                                |||||||  |||     || |||||
                                CCTGTGCT  TCG     AC ACTCA
                                     CT   ACCCTC  C
GAM1346 EIF2C1   3' ACAGTCTACTTCGTGTTC    25180          CAAAT   GA
                                GGACACGAAG    GAT  GT
                                ||||||||||    |||  ||
                                CTTGTGCTTC    CTG  CA
                                     AT___   A_
GAM1346 FN14     3' ACTCATCATTCATTCATCC   34041     CAC   GCA
                                GGA   GAA   AATGATGAGT
                                |||   |||   ||||||||||
                                CCT   CTT   TTACTACTCA
                                  A__   AC_
GAM1346 HFE      3' ACTTACTTCGTGTCC       58120          CAAATGA
                                GGACACGAAG      TGAGT
                                ||||||||||      |||||
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                                CCTGTGCTTC      ATTCA
                                        _______
GAM1346 HFE     3' ACTTACTTCGTGTCC      6397          CAAATGA
                                GGACACGAAG      TGAGT
                                ||||||||||      |||||
                                CCTGTGCTTC      ATTCA
                                        _______
GAM1346 KCNMB4  3' ACTCATCGGCACGCGTCC   27965     A  AA  AAA
                                GGAC CG  GC   TGATGAGT
                                |||| ||  ||   ||||||||
                                CCTG GC  CG   GCTACTCA
                                  C  A_  ___
GAM1346 KIF3C   3' ACTTGCCATTTGCTCCTGTCC 11201      C  A      AT
                                GGACA GA GCAAATG  GAGT
                                ||||| || |||||||  ||||
                                CCTGT CT CGTTTAC  TTCA
                                   C  _      CG
GAM1346 TAF10   3' TACTTATCTGTCCCCATGTCC 21883      CGAA_   AAT
                                GGACA    GCA   GATGAGTA
                                ||||||    |||  ||||||||
                                CCTGT    TGT   CTATTCAT
                                   ACCCC   ___
GAM1346 THBS1   3' TACTCATCACCTTGCAGTGGCC 13749    A   GAA    A_
                                GG CAC   GCAA  TGATGAGTA
                                || |||   ||||  |||||||||
                                CC GTG   CGTT  ACTACTCAT
                                 G   A__    CC
GAM1346 TPT     3' ACTTTGTTTGCTTCATGTGC  61024   G   C       TG TG
                                G ACA GAAGCAAA  A  AGT
                                | ||| ||||||||  |  |||
                                C TGT CTTCGTTT  T  TCA
                                 G   A       GT __
GAM1346 C17orf31 5' TACTCCTCGTTGCTTGTGTCC 34542       G     A   T
                                GGACAC AAGCAA TGA GAGTA
                                |||||| |||||| ||| |||||
                                CCTGTG TTCGTT GCT CTCAT
                                   _     _  C
GAM1346 C5orf8  3' CATTTTGCTTCTTGCC     23330    A  C      AT
                                GG CA GAAGCAA  GATG
                                || || |||||||  ||||
                                CC GT CTTCGTT  TTAC
                                 _  T      __
GAM1346 DDX34   3' GCTCCTCAGCTTCGTGTCC   28672          AAA   T
                                GGACACGAAGC   TGA GAGT
                                ||||||||||   ||| ||||
                                CCTGTGCTTCG   ACT CTCG
                                      ___   C
GAM1346 GRWD    3' CACAATTTGCTTCTGCC     49776    A  C       GA
                                GG CA GAAGCAAAT  TG
                                || || |||||||||  ||
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                                CC GT CTTCGTTTA  AC
                                 _ _       AC
GAM1346  GTPBP2   3'  ACTCATCAATTCTTCGTCCCC  39384    AC     C  A
                                GG  ACGAAG AA TGATGAGT
                                ||  |||||| || ||||||||
                                CC  TGCTTC TT ACTACTCA
                                 CC     _  A
GAM1346  KIAA0800 3'  ACTCAGCTCTTTGCTTCATGCC 28804    A  C       TGA_
                                GG CA GAAGCAAA    TGAGT
                                || || ||||||||    |||||
                                CC GT CTTCGTTT    ACTCA
                                 _ A       CTCG
GAM1346  KIAA1691 3'  CAACATTTGCTCCTGCC     94123    A  C  A      A
                                GG CA GA GCAAATG TG
                                || || || ||||||| ||
                                CC GT CT CGTTTAC AC
                                 _ C  _      A
GAM1346  P66      3'  ACTGATTGCCTTGTGTCC    40734         A   AATG  G
                                GGACACGA GCA    AT AGT
                                |||||||| |||    || |||
                                CCTGTGTT CGT    TA TCA
                                     C   ____  G
GAM1346  ZNF258   5'  CACATTGCCTCGTGTCC     24133         A    A  A
                                GGACACGA GCAA TG TG
                                |||||||| |||| || ||
                                CCTGTGCT CGTT AC AC
                                     C   _ _
GAM1346  LOC146227 5'  GCCATCTGCTCGTGTCC     78215         A   AAT    A
                                GGACACGA GCA   GATG GT
                                |||||||| |||   |||| ||
                                CCTGTGCT CGT   CTAC CG
                                    _   ___   _
GAM1346  LOC199920 3'  ACCCATCATTTTAAGAAGTGCC 89861    A   GAAGC_       A
                                GG CAC      AAATGATG GT
                                || |||     |||||||| ||
                                CC GTG      TTTACTAC CA
                                 _  AAGAAT       C
GAM1346  LOC203504 3'  CAGCATTTGCTCCTGTCC     92319      C  A      A
                                GGACA GA GCAAATG TG
                                ||||| || ||||||| ||
                                CCTGT CT CGTTTAC AC
                                   C  _      G
GAM1346  LOC90141  3'  TACTCACTCACTTCATTGTCC  62309      C_    CAAA  _
                                GGACA  GAAG    TGA TGAGTA
                                |||||  ||||    ||| ||||||
                                CCTGT  CTTC    ACT ACTCAT
                                   TA    _____  C
GAM1347  APBA2    3'  GGGCAGCCGTCACCCCTGCCTC 19741       CAAG__   C    A
              C                  GGAGGT      GAC GCTGC CC
                                ||||||      ||| ||||| ||
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                                CCTCCG     CTG CGACG GG
                                   TCCCCA  C    _
GAM1347  COL18A1  3'  GCAGCCTGGGGCTGGCCTCC  56161        A GA  __
                                GGAGGTCA G  CC  GCTGC
                                |||||||| |  ||  |||||
                                CCTCCGGT C  GG  CGACG
                                     _ GG  TC
GAM1347  DMD      5'  GGCGCCTCCTAGACCTCCT   5467         A   C_
                                AGGAGGTC AGGA  CGCT
                                |||||||| ||||  ||||
                                TCCTCCAG TCCT  GCGG
                                     A   CC
GAM1347  DMD      5'  GGCGCCTCCTAGACCTCCT   15725        A   C_
                                AGGAGGTC AGGA  CGCT
                                |||||||| ||||  ||||
                                TCCTCCAG TCCT  GCGG
                                     A   CC
GAM1347  DRD2     3'  TGCAGCCGCCTTCCTTGACCTT 7678          CC___
              C                  GGAGGTCAAGGA    GCTGCA
                                ||||||||||||    ||||||
                                CTTCCAGTTCCT    CGACGT
                                      TCCGC
GAM1347  EGLN2    5'  GGGTGCAGCACTGGACCCCT   54920    A   A  GACC
                                AGG GGTC AG   GCTGCACCC
                                ||| |||| ||   |||||||||
                                TCC CCAG TC   CGACGTGGG
                                  _   G  A___
GAM1347  GYPA     3'  GTACAAACTGCTTTGACCTCCT 88839          ACCGC  C
                                AGGAGGTCAAGG    TG AC
                                ||||||||||||    || ||
                                TCCTCCAGTTTC    AC TG
                                      GTCAA  A
GAM1347  JUND     3'  GGGTGCGGCCCTCCACCCCC  19301    A  CAA  CC
                                GG GGT   GGA  GCTGCACCC
                                || |||   |||  |||||||||
                                CC CCA   CCT  CGGCGTGGG
                                 C  ___   CC
GAM1347  KCNQ3    5'  GGATGTGACCCCCTGACCCCCT 16927    A    A  AC_  TGCA
                                AGG GGTCA GG   CGC   CC
                                ||| ||||| ||   |||   ||
                                TCC CCAGT CC   GTG   GG
                                  C    C  CCA   TA__
GAM1347  MAP4     3'  GGGCTCCCGGGTCCTTGGCCCC 11448    A        GCT__  A
              CT                  AGG GGTCAAGGACC    GC CC
                                ||| ||||||||||    || ||
                                TCC CCGGTTCCTGG    CG GG
                                  C         GCCCT  _
GAM1347  MAP4     3'  GGGCTCCCGGGTCCTTGGCCCC 11449    A        GCT__  A
              CT                  AGG GGTCAAGGACC    GC CC
                                ||| ||||||||||    || ||
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                                TCC CCGGTTCCTGG    CG GG
                                  C         GCCCT  _
GAM1347  MECP2    3'  AGCGCTCCCTTGACCTGCT   18382    G       AC_
                                AG AGGTCAAGG   CGCT
                                || |||||||||   ||||
                                TC TCCAGTTCC   GCGA
                                 G        CTC
GAM1347  MYCL2    3'  GGCTGGTCTTGACCTCCT    19379          G  _
                                AGGAGGTCAAG ACC GCT
                                |||||||||||| ||| |||
                                TCCTCCAGTTC TGG CGG
                                       _  T
GAM1347  NR2F6    5'  GGTGCAGCCCGTGCCCCC    19106    A  CAA  ACC
                                GG GGT   GG   GCTGCACC
                                || |||   ||   ||||||||
                                CC CCG   CC   CGACGTGG
                                 C  TG_  ___
GAM1347  PDGFRB   3'  GGGTGCAGGAAGCTCAACCCCT 66582     A  CA  GACCG
                                AGG GGT  AG    CTGCACCC
                                ||| |||  ||    ||||||||
                                TCC CCA  TC    GACGTGGG
                                  _  AC  GAAG_
GAM1347  PRPSAP1  3'  GGGTCTCGACCCTGGACCTCCT 12404        A  AC  CTGC
                                AGGAGGTC AGG  CG   ACCC
                                |||||||| |||  ||   ||||
                                TCCTCCAG TCC  GC   TGGG
                                     G  CA  TC__
GAM1347  TCF2     3'  GGATGGAATCCTACGACCTCCT 6616         A_   __  _
                                AGGAGGTC  AGGA  CCG CT
                                ||||||||  ||||  ||| ||
                                TCCTCCAG  TCCT  GGT GG
                                     CA   AA  A
GAM1347  TLR9     5'  GGTGCAGCCTAGCCTCCT    34309       CA  GACC
                                AGGAGGT  AG   GCTGCACC
                                |||||||  ||   ||||||||
                                TCCTCCG  TC   CGACGTGG
                                    A_  _____
GAM1347  XRCC3    3'  GGCACAGTGGTGACCCCCT   19519    A   AAGG     CA
                                AGG GGTC   ACCGCTG  CC
                                ||| ||||   |||||||  ||
                                TCC CCAG   TGGTGAC  GG
                                  C   ____      AC
GAM1347  AGPAT1   3'  GGATACAGCGCCACTCCTGCCC 22177    A  CA   C___    CA_
            CCT                  AGG GGT  AGGA   CGCTG  CC
                                ||| |||  ||||   |||||  ||
                                TCC CCG  TCCT   GCGAC  GG
                                  C  __   CACC    ATA
GAM1347  ASE-1    3'  GGTGGTCTCGATCTCCTGACCT 24988        A  C__  CT  AC_
            CCT                  AGGAGGTCA GGA   CG  GC   CC
                                |||||||| |||   ||  ||   ||
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                                TCCTCCAGT CCT   GC  TG   GG
                                     _  CTA  TC  GTA
GAM1347  C20orf162 5'  GGTGCAGCCCCAGCCCCCT   55502     A   CAA  ACC
                                AGG GGT   GG   GCTGCACC
                                ||| |||   ||   ||||||||
                                TCC CCG   CC   CGACGTGG
                                  C   A__  C__
GAM1347  DKFZp434F054 5'  GTAGCTCGGTCCTTGACGTCC  51048     G        __
                                GGA GTCAAGGACC  GCTGC
                                ||| ||||||||||  |||||
                                CCT CAGTTCCTGG  CGATG
                                  G         CT
GAM1347  DKFZp586H0623 3'  GGGTCTGCCTGGTCCTTGAGCC 34502     A  _        CT  __
            CCT                    AGG GG TCAAGGACCG  GC  ACCC
                                ||| || ||||||||||  ||  ||||
                                TCC CC AGTTCCTGGT  CG  TGGG
                                  _  G         C_  TC
GAM1347  DMWD     3'  GGACTCCTCGGTCCTTGCCTCC 61553       T       CTGCA_
            T                     AGGAGG CAAGGACCG     CC
                                ||||||| |||||||||      ||
                                TCCTCC GTTCCTGGC     GG
                                   _       TCCTCA
GAM1347  EDG2     5'  GCGAGGCTCCCCTGGCCTCC   9174         A_   _  GC
                                GGAGGTCA  GGA CC  TGC
                                ||||||||  ||| ||  |||
                                CCTCCGGT  CCT GG  GCG
                                     CC   C  A_
GAM1347  EDG2     5'  GCGAGGCTCCCCTGGCCTCC   9175         A_   _  GC
                                GGAGGTCA  GGA CC  TGC
                                ||||||||  ||| ||  |||
                                CCTCCGGT  CCT GG  GCG
                                     CC   C  A_
GAM1347  FLJ10640  5'  GGCGCACTGCAGCCTTGACCTC 39237           ACC  __   A
            CT                     AGGAGGTCAAGG   GC  TGC CC
                                ||||||||||||   ||  ||| ||
                                TCCTCCAGTTCC   CG  ACG GG
                                       GA_  TC   C
GAM1347  FLJ10737  3'  TGCAGCGGAGCTAGGACCCC   37055    A    AA  A_
                                GG GGTC  GG  CCGCTGCA
                                || ||||  ||  ||||||||
                                CC CCAG  TC  GGCGACGT
                                  _    GA  GA
GAM1347  FLJ14107  3'  GCGCTCCCACCCCTGACCTTCT 47346         A_____   C
                                AGGAGGTCA      GGA CGC
                                |||||||||      ||| |||
                                TCTTCCAGT      CCT GCG
                                     CCCCAC   C
GAM1347  FLJ20034  3'  GGTGCAGCCCCCGGCATTGACC 34851          GGA  ____     _
            TCCT                    AGGAGGTCAA   CC    GCTGCA CC
                                ||||||||||   ||    |||||| ||
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                                TCCTCCAGTT   GG    CGACGT GG
                                      AC_  CCCC     A
GAM1347  FLJ22378  3'  GGGCACTGGTGGGCCCTGACCT 47598        A  A     CA_
              CC                    GGAGGTCA GG CCGCTG   CCC
                                    |||||||| || ||||||   |||
                                    CCTCCAGT CC GGTGGT   GGG
                                        C  G     CAC
GAM1347  FLJ32452  3'  GGTTGCTCCCTGACCTCC    58633        A   CC  TGCA
                                    GGAGGTCA GGA  GC    CC
                                    |||||||| |||  ||    ||
                                    CCTCCAGT CCT  CG    GG
                                        C   __  TTA
GAM1347  FLJ32784  3'  AGCACAGTTCGGCCTCCT    58883        AA    C__
                                    AGGAGGTC  GGAC   GCT
                                    ||||||||  ||||   |||
                                    TCCTCCGG  CTTG   CGA
                                        __    ACA
GAM1347  FLJ32919  3'  GGTCCTGAAGCCCTTGACCCCT 58698     A       ACC   GC___
                                    AGG GGTCAAGG   GCT    ACC
                                    ||| ||||||||   |||    |||
                                    TCC CCAGTTCC   CGA    TGG
                                      _       ___   AGTCC
GAM1347  GOLGA3    3'  AGCTGGCCCTCAACTCTCCT   20879       _  CA   A  _
                                    AGGAG GT  AGG CC GCT
                                    ||||| ||  ||| || |||
                                    TCCTC CA  TCC GG CGA
                                       T  AC   C  T
GAM1347  KIAA0574  3'  GGGCTTGTCCTTGAGCTCC    69820      G       CGCT  A
                                    GGAG TCAAGGAC    GC CC
                                    |||| ||||||||    || ||
                                    CCTC AGTTCCTG    CG GG
                                      G       TT__
GAM1347  KIAA0620  3'  GGGCGCCCCCGCCTTGACCCCT 62812     A       ACCGCT  A
                                    AGG GGTCAAGG     GC CCC
                                    ||| ||||||||     || |||
                                    TCC CCAGTTCC     CG GGG
                                      _       GCCCC_  C
GAM1347  KIAA1052  5'  GCTGCGGCCTTGACCTCCT    30943          A   T
                                    AGGAGGTCAAGG CCGC GC
                                    |||||||||||| |||| ||
                                    TCCTCCAGTTCC GGCG CG
                                           _    T
GAM1347  KIAA1110  3'  GCGGGGCTCGCTGACCTCC    62501        A_ GA  G
                                    GGAGGTCA  G  CC CTGC
                                    ||||||||  |  || ||||
                                    CCTCCAGT  C  GG GGCG
                                        CG TC  _
GAM1347  KIAA1130  3'  GGACATGGTCCTTGACCCCC   63098    A         C  CA
                                    GG GGTCAAGGACCG TG  CC
                                    || ||||||||||| ||  ||
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                                CC CCAGTTCCTGGT AC  GG
                                 C          _  A_
GAM1347  KIAA1233  3'  CAGCAACCCATGACTTCCT   63754         A  ACC
                                AGGAGGTCA GG   GCTG
                                ||||||||| ||   ||||
                                TCCTTCAGT CC   CGAC
                                     A  CAA
GAM1347  KIAA1449  3'  GGTGCAGCAGTTTCACTCCT   40841      GTCAA    C
                                AGGAG    GGAC GCTGCACC
                                |||||    |||| ||||||||
                                TCCTC    TTTG CGACGTGG
                                   AC___   A
GAM1347  KIAA1522  3'  GCACCTGCCCCTTGCCTCCT   65606       T    ACC  ___
                                AGGAGG CAAGG   GC   TGC
                                |||||| |||||   ||   |||
                                TCCTCC GTTCC   CG   ACG
                                   _    C__  TCC
GAM1347  KIAA1813  5'  GGTGCCAGCCCCCTTGGCCCCC 70830     A       ACC   _
              T                  AGG GGTCAAGG   GCTG CACC
                                 ||| ||||||||   |||| ||||
                                 TCC CCGGTTCC   CGAC GTGG
                                   C       CC_    C
GAM1347  MGC11386  3'  GCTGCAGCCTTGACCTCCT   53070          ACC  T
                                AGGAGGTCAAGG   GC GC
                                ||||||||||||   || ||
                                TCCTCCAGTTCC   CG CG
                                     GA_  T
GAM1347  MGC2376   3'  GGTACAAAAGACTGACCTCTT  43941         A GACCGC  C
                                AGGAGGTCA G      TG ACC
                                ||||||||| |      || |||
                                TTCTCCAGT C      AC TGG
                                     _ AGAAA_  A
GAM1347  MRPS6     3'  GGTATTTTTAGCCCTTGATCCC 51645     A       ACC    C____
              CT                   AGG GGTCAAGG   GCTG    ACC
                                   ||| ||||||||   ||||    |||
                                   TCC CTAGTTCC   CGAT    TGG
                                     C        ___    TTTTA
GAM1347  NMT1      3'  AGAGGCCCTTGGACCTCCT   41143         _   A  G
                                AGGAGGTC AAGG CC CT
                                ||||||||| |||| || ||
                                TCCTCCAG TTCC GG GA
                                     G    C  A
GAM1347  PP1201    3'  AGCTTTGTCCCCGGCCTCCT   42454        AA    C__
                                AGGAGGTC  GGAC   GCT
                                ||||||||  ||||   |||
                                TCCTCCGG  CCTG   CGA
                                     CC    TTT
GAM1347  PSMD3     3'  GCAGCCACCCTGACCTCC    12517         A  ACC   _
                                GGAGGTCA GG   GCTG C
                                |||||||| ||   |||| |
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                                CCTCCAGT CC   CGAC G
                                     C  AC_    C
GAM1347  SCAND2    5'  GGTCACTAGCCCTTGACTCCT  54419      G     ACC    C__
                                AGGAG TCAAGG   GCTG   ACC
                                ||||| ||||||   ||||   |||
                                TCCTC AGTTCC   CGAT   TGG
                                  _     ___    CAC
GAM1347  TOR2A     3'  CACTGAGCCTTGACCTCC     56182          AC  C
                                GGAGGTCAAGG  CG TG
                                ||||||||||  || ||
                                CCTCCAGTTCC  GT AC
                                       GA  C
GAM1347  TU12B1-TY 3'  GGGTACAAAGGTCTGGCCTCCT 33857         AG    GC  C
                                AGGAGGTCA  GACC  TG ACCC
                                |||||||||  ||||  || ||||
                                TCCTCCGGT  CTGG  AC TGGG
                                     __    AA  A
GAM1347  LOC123792 3'  GGTGCAGCAGCTCACACCCT   74704    A   CAA  ACC
                                GG GGT   GG   GCTGCACC
                                || |||   ||   ||||||||
                                TC CCA   TC   CGACGTGG
                                 _   CAC  GA_
GAM1347  LOC138241 5'  AGCGATGCTCTTTGACCTCC   75832          C___
                                GGAGGTCAAGGA    CGCT
                                ||||||||||||    ||||
                                CCTCCAGTTTCT    GCGA
                                       CGTA
GAM1347  LOC143943 5'  GGTCAACAAGTCCTTGACTCCT 83920      G       CGC_  C
                                AGGAG TCAAGGAC    TG ACC
                                ||||| ||||||||    || |||
                                TCCTC AGTTCCTG    AC TGG
                                  _       AACA  _
GAM1347  LOC145826 5'  GGTATTTCCCTGACCTCTT    84531         A   CC_
                                AGGAGGTCA GGA   GCT
                                ||||||||| |||   |||
                                TTCTCCAGT CCT   TGG
                                     C   TTA
GAM1347  LOC146224 5'  GTAGCATCAGAGCCCTGACCTC 78204         A  ACC_____
            CT                    AGGAGGTCA GG       GCTGC
                                ||||||||| ||       |||||
                                TCCTCCAGT CC       CGATG
                                     C  GAGACTA
GAM1347  LOC148114 5'  GGGTGCAGGGGCCCCCGACCTC 79364       AA  A  G
                                GAGGTC  GG CC CTGCACCC
                                ||||||  || || ||||||||
                                CTCCAG  CC GG GACGTGGG
                                   CC  C  G
GAM1347  LOC148811 3'  AGTGCCTTTGACCCCCT     79768     A       AC
                                AGG GGTCAAGG  CGCT
                                ||| ||||||||  ||||
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                                TCC CCAGTTTC  GTGA
                                  C       C_
GAM1347  LOC149448 3'  GGTGCAGCGGCCAGCTTCT   85579       CAA  A      _
                                GGAGGT   GG CCGCTGCA CC
                                ||||||   || |||||||| ||
                                TCTTCG   CC GGCGACGT GG
                                   A__  _       A
GAM1347  LOC149837 3'  GGCTCTGTGTGCCTGACCTCCT 85902         A  AC   TGCA_
                                AGGAGGTCA GG  CGC    CC
                                ||||||||| ||  |||    ||
                                TCCTCCAGT CC  GTG    GG
                                      _ GT   TCTCA
GAM1347  LOC154222 3'  GCTGCATACCCTTGACTTCCT  87392          ACC_  T_
                                AGGAGGTCAAGG   GC  GC
                                ||||||||||||   ||  ||
                                TCCTTCAGTTCC   CG  CG
                                       CATA  TC
GAM1347  LOC199899 5'  GGTGCAGCCCTCGACCTCCT   91469        A   ACC    _
                                AGGAGGTC AGG   GCTGCA CC
                                |||||||| |||   |||||| ||
                                TCCTCCAG TCC   CGACGT GG
                                     C  ___     C
GAM1347  LOC201294 3'  GGATGGTCTCAATCTCTTGACC 89587          ________   _
           TCCT                  AGGAGGTCAAG      GACCG CT
                                ||||||||||       ||||| ||
                                TCCTCCAGTTC      CTGGT GG
                                      TCTAACT    A
GAM1347  LOC201952 5'  GGGCACAGCTGATTTGACCTCT 91878          GACC   CA
           T                   AGGAGGTCAAG   GCTG  CCC
                                ||||||||||   ||||  |||
                                TTCTCCAGTTT   CGAC  GGG
                                      AGT_   AC
GAM1347  LOC204285 5'  GGATGGTCCCTGACCTCCT   91021        A    _
                                AGGAGGTCA GGACCG CT
                                ||||||||| |||||| ||
                                TCCTCCAGT CCTGGT GG
                                     C     A
GAM1347  LOC205418 5'  CAGGGTCCTTGCCCTCCT    92369       T      G
                                AGGAGG CAAGGACC CTG
                                |||||| |||||||| |||
                                TCCTCC GTTCCTGG GAC
                                   C       _
GAM1347  LOC221501 3'  GGGTGTGGCCTCCCCGCCTCC  95435      CAA   CC  TG
                                GGAGGT   GGA  GC  CACCC
                                ||||||   |||  ||  |||||
                                CCTCCG   CCT  CG  GTGGG
                                   CC_   C_  GT
GAM1347  LOC221830 3'  GGTGCAGGCCAACCTCTT    94104       CAA  A  GC   _
                                AGGAGGT   GG CC  TGCA CC
                                |||||||   || ||  |||| ||
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                                TTCTCCA   CC GG  ACGT GG
                                   A__  _ __    A
GAM1347 LOC51205 5' GGACAGCGGTCCCTGCTTGCT 33466    G   T  A       CA
                                AG AGG CA GGACCGCTG  CC
                                || ||| || |||||||||  ||
                                TC TTC GT CCTGGCGAC  GG
                                 G   _  C        AC
GAM1347 LOC54550 3' GCAGCACCCCTGCCTCCT    78186       CA   ACC   _
                                AGGAGGT  AGG   GCTG C
                                |||||||  |||   |||| |
                                TCCTCCG  TCC   CGAC G
                                   __   CCA
GAM1347 LOC89932 5' GCCCTGGCCCTGACCTCC    61467        A  A   CT
                                GGAGGTCA GG CCG  GC
                                |||||||| || |||  ||
                                CCTCCAGT CC GGT  CG
                                    C  _   CC
GAM1347 LOC91010 5' GGGCCCTGCCCTTGACCTC   65223         ACC  TGCA
                                GAGGTCAAGG   GC    CCC
                                ||||||||||   ||    |||
                                CTCCAGTTCC   CG    GGG
                                     ___  TCCC
GAM1348 AKAP1    3' TGCCCAGGCAGGCTCCAA    14473          AGCCCCA
                                TTGGAGCCTGTC      GCA
                                ||||||||||||      |||
                                AACCTCGGACGG      CGT
                                     ACC_____
GAM1348 CAD      3' TGCTGGGGCCCAGTCTGCCCCA 16353    A ____   TCA
                                TGG GC   CTG   GCCCCAGCA
                                ||| ||   |||   |||||||||
                                ACC CG   GAC   CGGGGTCGT
                                  C  TCT   C__
GAM1348 CTSD     3' GTGCTGGGACTGAGCCAGTCCC 10342    AG CT _    C
              A                  TGG  C  G TCAG CCCAGCAC
                                 |||  |  | |||| ||||||||
                                 ACC  G  C AGTC GGGTCGTG
                                   CT AC G    A
GAM1348 DLG5     5' GCAGACTCTGAAGGCTCCAA   83816        G    CCCCA
                                TTGGAGCCT TCAG     GC
                                |||||||| ||||     ||
                                AACCTCGGA AGTC     CG
                                     _    TCAGA
GAM1348 ELAC2    3' GTGCCGAGGCTTGGGCTCC    36730        TC    CCA
                                GGAGCCTG  AGCC   GCAC
                                ||||||||  ||||   ||||
                                CCTCGGGT  TCGG   CGTG
                                     __    AGC
GAM1348 FCER2    5' GGAGGACAGACACAGGCTCCAA 10605          CAG___  _
                                TTGGAGCCTGT      CC CC
                                ||||||||||       || ||
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                                AACCTCGGACA     GG GG
                                      CAGACA  A
GAM1348  GBA     3'  GTGCCAGGGGCTGGAGGCCCC  76823    A   G      A_
                                GG GCCT TCAGCCCC  GCAC
                                || |||| ||||||||  ||||
                                CC CGGA GGTCGGGG  CGTG
                                 C   _       AC
GAM1348  HMGA1    5'  GCGCTGGCGCGGCTCCAA    77451        _     CCCA
                                TTGGAGCC TGTCAGC   GC
                                |||||||| |||||||   ||
                                AACCTCGG GCGGTCG   CG
                                     C     _____
GAM1348  MMP2     5'  GCGCCGCGGACCAGGCTCCAA  16966         _ A  CCCA
                                TTGGAGCCTG TC GC   GC
                                |||||||||| || ||   ||
                                AACCTCGGAC AG CG   CG
                                      C  G  CCG_
GAM1348  OA1      3'  GTGCTGGGGGTCCAGACCCCA  6057     AGC   TCAG
                                TGG   CTG   CCCCAGCAC
                                |||   |||   |||||||||
                                ACC   GAC   GGGGTCGTG
                                  CCA   CTG_
GAM1348  P53AIP1  3'  GTGCTGGGGTGACAAAGCCCCG 42339     A  C_    G
           A                     TTGG GC  TGTCA CCCCAGCAC
                                |||| ||  ||||| |||||||||
                                AGCC CG  ACAGT GGGGTCGTG
                                  C  AA    _
GAM1348  SCN4A    3'  CTGGGGCTGACACCCAG     6201      AGCC
                                TTGG    TGTCAGCCCCAG
                                ||||    ||||||||||||
                                GACC    ACAGTCGGGGTC
                                  C___
GAM1348  TCF1     3'  GTGCCAGAGCCTGGGGCTCTAA 6787         GT   _ CCCA
                                TTGGAGCCT  CAG C    GCAC
                                |||||||||  ||| |    ||||
                                AATCTCGGG  GTC G    CGTG
                                     __   C AGAC
GAM1348  ZFP36    3'  GCTGGGGCAGGTCCCCAA    14159     A_   GTCA
                                TTGG  GCCT   GCCCCAGC
                                ||||  ||||   ||||||||
                                AACC  TGGA   CGGGGTCG
                                  CC   _____
GAM1348  ADAMTS10 5'  GCGCGGCGCAGGCTCCAA    48980         CA   CCA
                                TTGGAGCCTGT  GCC   GC
                                ||||||||||  |||   ||
                                AACCTCGGACG  CGG   CG
                                     __   CG_
GAM1348  DIM1     3'  GTGCTGGGGGTTAGGACTTCAA 22948       _   TCAG
                                TTGGAG CCTG   CCCCAGCAC
                                ||||||  ||||   |||||||||
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                                AACTTC GGAT   GGGGTCGTG
                                   A   TG__
GAM1348  DKFZP564O0423 3'  GTGCCTATGTAATAGGCTCCAA 93357          CA  CCCA
                                TTGGAGCCTGT  GC   GCAC
                                ||||||||||  ||   ||||
                                AACCTCGGATA  TG   CGTG
                                     A_  TATC
GAM1348  FLJ10052  3'  TGAGGCTGACAAACTGCAA   36250    G  CC      C
                                TTG AG  TGTCAGCC CA
                                ||| ||  |||||||| ||
                                AAC TC  ACAGTCGG GT
                                  G  AA       A
GAM1348  FLJ14810  5'  CTGGGGCTGCCAGCGCCAA   52701     A  C  T
                                TTGG GC TG CAGCCCCAG
                                |||| || || |||||||||
                                AACC CG AC GTCGGGGTC
                                  G  _  C
GAM1348  FLJ23360  3'  CTGGGGCTGATGTTCCAG    43828       CT
                                TTGGAGC  GTCAGCCCCAG
                                |||||||  ||||||||||
                                GACCTTG  TAGTCGGGGTC
                                   __
GAM1348  KIAA0767  3'  GTGCTGGGATTCAGTCCCCAA  61258     AGC   TCAGC
                                TTGG   CTG    CCCAGCAC
                                ||||   |||    ||||||||
                                AACC   GAC    GGGTCGTG
                                  CCT   TTA__
GAM1348  MGC2752   5'  GCTGGGGCTGTCCAACTCCA   79082      CCTGT
                                TGGAG    CAGCCCCAGC
                                |||||    ||||||||||
                                ACCTC    GTCGGGGTCG
                                   AACCT
GAM1348  PPFIBP1   5'  GTGCTGGGGCTTTGAACTCCGA 14630       CCTGTC
                                TTGGAG     AGCCCCAGCAC
                                ||||||     ||||||||||
                                AGCCTC     TCGGGGTCGTG
                                   AAGTT_
GAM1348  SLC37A1   3'  CTGGGATTGGCGGGTCCAA   39089      G     GC
                                TTGGA CCTGTCA  CCCAG
                                ||||| |||||||  |||||
                                AACCT GGGCGGT  GGGTC
                                   _      TA
GAM1348  ST7L     3'  GTGCTGGGACTCTGGTGCC   35341    A   TGTC  C
                                GG GCC    AG CCCAGCAC
                                || |||    || ||||||||
                                CC TGG    TC GGGTCGTG
                                 G   TC__  A
GAM1348  LOC126520 3'  GTGCCAGGGACCCAGGCTCCA  75026         TCAG   CA
                                TGGAGCCTG    CCC  GCAC
                                |||||||||    |||  ||||
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                                ACCTCGGAC   GGG  CGTG
                                     CCA_   AC
GAM1348  LOC138241 5'  GTGCCAAAGCTGACCCCGGCTC 75836        T__     CCCA
             CAG                   TTGGAGCC   GTCAGC   GCAC
                                   ||||||||   ||||||   ||||
                                   GACCTCGG   CAGTCG   CGTG
                                        CCC     AAAC
GAM1348  LOC146774 3'  GCCGGGGCTGGAGTCCGA    78696      GC  G      A
                                   TTGGA  CT TCAGCCCC GC
                                   |||||  || ||||||||  ||
                                   AGCCT  GA GGTCGGGG CG
                                      __  _      C
GAM1348  LOC146856 5'  GCTTTGCTACAGGCTCCAA   83702          C   CCC
                                   TTGGAGCCTGT AGC   AGC
                                   ||||||||||| |||   |||
                                   AACCTCGGACA TCG   TCG
                                         _   TT_
GAM1348  LOC151124 5'  TGCTGGGGCCAGAACCCCAG   86422     AGC_   TCA
                                   TTGG   CTG   GCCCCAGCA
                                   ||||   |||   |||||||||
                                   GACC   GAC   CGGGGTCGT
                                     CCAA   ___
GAM1348  LOC158434 5'  CTGGGGTTAGGACTTCAA    88161       _    TCA
                                   TTGGAG CCTG   GCCCCAG
                                   ||||||  ||||   |||||||
                                   AACTTC GGAT   TGGGGTC
                                      A   ___
GAM1348  LOC202546 3'  GTGCTGGGGGAATGACCCCCA  91960     AGCCT   G__
                                   TGG    GTCA   CCCCAGCAC
                                   |||    ||||   |||||||||
                                   ACC    CAGT   GGGGTCGTG
                                     CC___    AAG
GAM1348  LOC91115  3'  GCCGCTTACAGGCTCCAA    65569          C   CCCA
                                   TTGGAGCCTGT AGC    GC
                                   |||||||||| |||    ||
                                   AACCTCGGACA TCG    CG
                                         T   C___
GAM1349  DDB2     3'  TAAATGACTTTTCTCCTCTCA  5457      A    CAGCAC
                                   TGA AGGGG     AGTCATTTA
                                   ||| |||||     |||||||||
                                   ACT TCCTC     TCAGTAAAT
                                     C    TTT___
GAM1349  PPP5C    3'  TGGCTGCCCTGCCCCCCTCA   21810     AA      CA
                                   TGA  GGGGCAG  CAGTCA
                                   |||  |||||||  ||||||
                                   ACT  CCCCGTC  GTCGGT
                                     CC      CC
GAM1349  ASB16    3'  ATGGTGTGTTCTGCCCCTCCCA 55972     AA       __    G
                                   TG  AGGGGCAG  CACA TCAT
                                   ||  ||||||||  |||| ||||
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                                AC  TCCCCGTC  GTGT GGTA
                                 CC       TT   _
GAM1349  ETR101    3'  GGCTGTGCTGGCCCTTTCA   72819        G
                                TGAAAGGG CAGCACAGTC
                                |||||||| ||||||||||
                                ACTTTCCC GTCGTGTCGG
                                     G
GAM1349  HSPC065   3'  AAAGGAATTCCTGCCCCTCCCA 27129    AA       CACAG  A
                                TG  AGGGGCAG    TC TTT
                                ||  ||||||||    || |||
                                AC  TCCCCGTC    AG AAA
                                 CC       CTTA_  G
GAM1349  MAD4      3'  GCTGCCTGCCCCTTCCA     22276    A       CA
                                TG AAGGGGCAG  CAGT
                                || |||||||||  ||||
                                AC TTCCCCGTC  GTCG
                                 C        C_
GAM1349  MRPL13    5'  TAAATAACTGCATTATATGCTC 26862          GCA____    C
              CTTTCA                  TGAAAGGGGCA      CAGT ATTTA
                                ||||||||||       |||| |||||
                                ACTTTCCTCGT      GTCA TAAAT
                                       ATATTAC    A
GAM1349  ZNF-U69274 3'  TAAATGACTGTACTGAATTT   27742     GG   C
                                AGG  CAG ACAGTCATTTA
                                |||  ||| ||||||||||
                                TTT  GTC TGTCAGTAAAT
                                  AA   A
GAM1349  LOC155032 3'  AAATGACCACTCCTCTCA    87588     A    CAGCACA
                                TGA AGGGG      GTCATTT
                                ||| |||||      |||||||
                                ACT TCCTC      CAGTAAA
                                  C    AC_____
GAM1350  CACNG3    5'  TGACTCTCCCCCTCCAACCCCC 22569      ACCCCA    A
              A                  TGGGG     AGGG GAGAGTCA
                                |||||     |||| ||||||||
                                ACCCC     TCCC CTCTCAGT
                                   CAACC_    C
GAM1350  DNMT3L    5'  CTCCCCACTGAGGTCCCCA    26287        C  A__
                                TGGGGACC CA   GGGAG
                                |||||||| ||   |||||
                                ACCCCTGG GT   CCCTC
                                     A  CAC
GAM1350  DPYSL2    3'  GGGTCCCCCTTGGGGCCCCA   9117       A       AGA  G
                                TGGGG CCCCAAGGG   GA TC
                                ||||| |||||||||   || ||
                                ACCCC GGGGTTCCC   CT GG
                                   _       C__  G
GAM1350  HS3ST4    3'  TCCCCTAGGGTCCCTA      73858         CA    A
                                TGGGGACCC  AGGG GA
                                |||||||||  |||| ||
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                                ATCCCTGGG  TCCC CT
                                    A_   _
GAM1350  MEF2D    3'  GACTCTTTGGAATCCCC     20983      CC   AGGGA
                                GGGGA  CCA    GAGAGTC
                                |||||  |||    |||||||
                                CCCCT  GGT    TTCTCAG
                                  AA  _____
GAM1350  MIC1     5'  GACCGCCCCCGGGGTCCCC   26188        AA   AGAGA
                                GGGGACCCC  GGG    GTC
                                |||||||||  |||    |||
                                CCCCTGGGG  CCC    CAG
                                    CC   GC___
GAM1350  MLF2     3'  ACCTCTTCCTCAGAGCCCCCA  19554      ACCCCA       A
                                TGGGG     AGGGAGAG GT
                                |||||     |||||||| ||
                                ACCCC     TCCTTCTC CA
                                  CGAGAC       _
GAM1350  POLE2    5'  TTTTCCCTCAGGGCCCCC    12200     A   CA
                                GGGG CCC  AGGGAGAG
                                ||||  |||  ||||||||
                                CCCC GGG  TCCCTTTT
                                  C   AC
GAM1350  WHSC1    3'  TCTCCCATCAGGGTCCCCA   24688        CAA_
                                TGGGGACCC   GGGAGA
                                |||||||||   ||||||
                                ACCCCTGGG   CCCTCT
                                    ACTA
GAM1350  WHSC1    3'  TCTCCCATCAGGGTCCCCA   24689        CAA_
                                TGGGGACCC   GGGAGA
                                |||||||||   ||||||
                                ACCCCTGGG   CCCTCT
                                    ACTA
GAM1350  WHSC1    3'  TCTCCCATCAGGGTCCCCA   24690        CAA_
                                TGGGGACCC   GGGAGA
                                |||||||||   ||||||
                                ACCCCTGGG   CCCTCT
                                    ACTA
GAM1350  ALTE     5'  GACCCCTACCCACCCCAGGGTC 61001         CAA  AG___  A_
          CCCA                    TGGGGACCC  GGG    AG  GTC
                                |||||||||  |||    ||  |||
                                ACCCCTGGG  CCC    TC  CAG
                                    AC_  ACCCA  CC
GAM1350  C1QR1    3'  ACTCTCTCCCTCCCC      24864      CCCCAA
                                GGGGA     GGGAGAGAGT
                                |||||     ||||||||||
                                CCCCT     CCCTCTCTCA
                                  _______
GAM1350  C22orf3  5'  TGACTCCCAGCCGGGGTCCCC  25351        AAG  AGA_
                                GGGGACCCC   GG   GAGTCA
                                |||||||||   ||   ||||||
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                                CCCCTGGGG  CC   CTCAGT
                                     ___ GACC
GAM1350 FLJ10748 5' GACCCTCTCCCGGCCCCTCCCC 37101     CCCCAA     A
                                GGGGA    GGGAGAG GTC
                                |||||    ||||||| |||
                                CCCCT    CCCTCTC CAG
                                   CCCCGG     C
GAM1350 FLJ10901 3' GACTCTCCCCCATTTCCCA  37362     CCCCAA  A
                                TGGGGA    GGG GAGAGTC
                                ||||||    ||| |||||||
                                ACCCTT    CCC CTCTCAG
                                   TAC___  _
GAM1350 FLJ13782 3' TGACTCTCCTTCGAGGCCACCA 46704    _ A CCAA GA
                                TGG GG CC   GG  GAGAGTCA
                                ||| || ||   ||  ||||||||
                                ACC CC GG   CT  CTCTCAGT
                                  A _ AG__  TC
GAM1350 FLJ32658 3' CTCTCTCCACTGGGATCCCCA 59077     C   AG
                                TGGGGA CCCA  GGAGAGAG
                                |||||| ||||  ||||||||
                                ACCCCT GGGT  CCTCTCTC
                                   A   CA
GAM1350 GOLGA3   3' CTCTCCTTGGTGCAGGGTTCCC 20888       CA____
            A                    TGGGGACCC    AGGGAGAG
                                 |||||||||    ||||||||
                                 ACCCTTGGG    TTCCTCTC
                                      ACGTGG
GAM1350 HIC2     3' GACTCTGGTGGGTCCCCA    65868       CAAGGGAG
                                TGGGGACCC      AGAGTC
                                |||||||||      ||||||
                                ACCCCTGGG      TCTCAG
                                      TGG_____
GAM1350 KIAA0821 3' TGACCCCCTCCCTTGGGGCGAC 30611    GA_       AGA
            TC                    GGG  CCCCAAGGGAG  GTCA
                                  |||  ||||||||||  ||||
                                  CTC  GGGGTTCCCTC  CAGT
                                    AGC         CCC
GAM1350 KIAA1881 3' GAGCCTTCCCTTGAAGTCCCCA 97085      CC     G  AG
                                TGGGGAC  CAAGGGA AG  TC
                                |||||||  ||||||| ||  ||
                                ACCCCTG  GTTCCCT TC  AG
                                   AA     _  CG
GAM1350 SARM     3' ACTCCCTCCTGAGGTCCCCA  31275       CCAA    A
                                TGGGGACC   GGGAG GAGT
                                ||||||||   ||||| ||||
                                ACCCCTGG   TCCTC CTCA
                                     AG__    C
GAM1350 LOC146958 5' TCTCCCTGGAGGCCCCCA   84950      A _  A
                                TGGGG CC CCA GGGAGA
                                ||||| || ||| ||||||
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                                ACCCC GG GGT CCCTCT
                                  C  A  _
GAM1350  LOC151816 5'  GACTGTCCCAGGTCCCCA    86686       CCAA   GAG
                                TGGGGACC   GGGA  AGTC
                                ||||||||   ||||  ||||
                                ACCCCTGG   CCCT  TCAG
                                    A___   G__
GAM1350  LOC152464 3'  GACCCCTTGGGATCCCTA    60647      C      AGAGA
                                TGGGGA CCCAAGGG    GTC
                                |||||| ||||||||    |||
                                ATCCCT GGGTTCCC    CAG
                                  A      _____
GAM1350  LOC158376 5'  TGACTCAAGGGCCCAGGATCCT 88137      C  CAA  AGA__
            CA                    TGGGGA CC   GGG    GAGTCA
                                |||||| ||  |||    ||||||
                                ACTCCT GG   CCC    CTCAGT
                                  A  A__   GGGAA
GAM1350  LOC169693 3'  GGCTGGCCTTGGGTCCCCA   88629       C   GAGAG
                                TGGGGACCC AAGG    AGTC
                                ||||||||| ||||    ||||
                                ACCCCTGGG TTCC    TCGG
                                    _   GG___
GAM1350  LOC204285 3'  ACCTCTCCCTGGGGTCCCCA  91012        A     A
                                TGGGGACCCCA GGGAGAG GT
                                |||||||||| ||||||| ||
                                ACCCCTGGGGT CCCTCTC CA
                                    _     _
GAM1350  LOC220020 5'  GGCTCTCTCAGGGCCCCCA   95050     A  CAAGG
                                TGGGG CCC    GAGAGAGTC
                                ||||| |||    |||||||||
                                ACCCC GGG    CTCTCTCGG
                                  C  A____
GAM1350  LOC221399 5'  TGACTCTCTCTAAGTAATCCC  95487    CCCCAAG
                                GGGA     GGAGAGAGTCA
                                ||||     ||||||||||
                                CCCT     TCTCTCTCAGT
                                  AATGAA_
GAM1350  LOC245771 5'  GACTCTCCCCCATTTCCCA   94475      CCCCAA  A
                                TGGGGA    GGG GAGAGTC
                                ||||||    ||| |||||||
                                ACCCTT    CCC CTCTCAG
                                  TAC___  _
GAM1350  LOC256032 5'  GACTCTCCGCAGGTACCCA   99361    G  CCAA  GAG
                                TGGG ACC   GG  AGAGTC
                                |||| |||   ||  ||||||
                                ACCC TGG   CC  TCTCAG
                                  A  ACG_ ___
GAM1350  LOC90190  3'  TGACTCTTCAGCCTCAAATCCC 62433     CCCCA  GA_
            CA                    TGGGGA   AGG  GAGAGTCA
                                ||||||   |||  ||||||||
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                                ACCCCT    TCC   TTCTCAGT
                                   AAAC_  GAC
GAM1351  KCNJ5    5'  CAGAAATTAATCTCTGGGGA  7969        A    ___
                                TCCCCAGA ATTGA   CTG
                                |||||||| |||||   |||
                                AGGGGTCT TAATT   GAC
                                    C    AAA
GAM1351  MFNG     3'  TGTCTCTCAGTCATTCCCCTGG 11548      AAAT_
            GG                    CCCCAG    TGACTGAGAGACA
                                |||||||   ||||||||||||||
                                GGGGTC    ACTGACTCTCTGT
                                   CCCTT
GAM1351  MGEA5    3'  GCTCTCAGTCTTAGGGGA    25219      AGAAATT       A
                                TCCCC      GACTGAGAG C
                                |||||      ||||||||| |
                                AGGGG      CTGACTCTC G
                                   ATT____
GAM1351  PRKAB1   3'  GTCTCTCGGCTCCAGGGA    21814     CA  AATTGA
                                TCCC  GA     CTGAGAGAC
                                ||||  ||     |||||||||
                                AGGG  CT     GGCTCTCTG
                                  AC  C_____
GAM1351  SNAI1    3'  TGTCTCCCAGAACTATTCTGGG 21126         ATTGA   A
            GG                    TCCCCAGAA    CTG GAGACA
                                |||||||||    ||| ||||||
                                GGGGGTCTT    GAC CTCTGT
                                     ATCAA   C
GAM1351  TEX14    3'  TTTTCAGTCAGATTTCTG    49228       _
                                CAGAAAT TGACTGAGAG
                                ||||||| ||||||||||
                                GTCTTTA ACTGACTTTT
                                   G
GAM1351  ZNF264   3'  GTCTTGTCTTTTTTAGGG    14227     A   TT   TGA
                                CCC GAAA  GAC   GAGAC
                                ||| ||||  |||   |||||
                                GGG TTTT  CTG   TTCTG
                                  A   TT  ___
GAM1351  DDX18    3'  GTCTCTCTTTTATTTCTGGG   23197         TGACT
                                CCCAGAAAT    GAGAGAC
                                |||||||||    |||||||
                                GGGTCTTTA    CTCTCTG
                                     TTTT_
GAM1351  DSCR6    3'  CTCACGTTCTCTTGGGGA    39065       _  AATT  _
                                TCCCCA GA    GAC TGAG
                                ||||||| ||   ||| ||||
                                AGGGGT CT    TTG ACTC
                                   T  C___   C
GAM1351  FLJ00001 3'  CTCTTGATTTCTGTGGA     82713     C       GACT
                                TCC CAGAAATT    GAGAG
                                ||| ||||||||    |||||
```

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                                AGG GTCTTTAG    TTCTC
                                  T      ____
GAM1351  FLJ00060  5'  CTCCACCTCACCTCTGGGGA  61747        AAT   C_  A
                                TCCCCAGA   TGA  TG GAG
                                ||||||||   |||  || |||
                                AGGGGTCT   ACT  AC CTC
                                     CC_   CC  _
GAM1351  FLJ14564  3'  TCTCTGCCTCATTTCTGGAGG  77018    _      T  CTG
                                CC CCAGAAAT GA   AGAGA
                                || ||||||||  ||   |||||
                                GG GGTCTTTA CT   TCTCT
                                 A       _  CCG
GAM1351  FYCO1     3'  CTCAGAGGCGGTGTCTGGGGA  44770        A    A__
                                TCCCCAGA ATTG   CTGAG
                                |||||||| ||||   |||||
                                AGGGGTCT TGGC   GACTC
                                     G    GGA
GAM1351  GT650     5'  TCTGTCAGTTTCTGAGGA    54554     C         T
                                TCC CAGAAATTGAC GA
                                ||| ||||||||||| ||
                                AGG GTCTTTGACTG CT
                                  A          T
GAM1351  ITM3      3'  TTCAGTCAGTCTCTGGGGA    48894         A
                                TCCCCAGA ATTGACTGAG
                                |||||||| ||||||||||
                                AGGGGTCT TGACTGACTT
                                     C
GAM1351  KIAA0652  3'  TCTCCCACAGTTTCTGCAGA   29124    CC        AC  A
                                TC  CAGAAATTG  TG GAGA
                                ||  |||||||||  || ||||
                                AG  GTCTTTGAC  AC CTCT
                                 AC         __  C
GAM1351  KIAA1328  3'  GTCTCTCCTTTCACGGGGA   62330      A_   TTGACT
                                TCCCC  GAAA     GAGAGAC
                                |||||  ||||     |||||||
                                AGGGG  CTTT     CTCTCTG
                                   CA    C_____
GAM1351  MEP50     3'  GTCTCTCAGCCTGAGGGA    44318     _  AAATTGA
                                TCCC CAG      CTGAGAGAC
                                |||| |||      |||||||||
                                AGGG GTC      GACTCTCTG
                                   A   C_______
GAM1351  NET-7     3'  CTCTCAGTCAACATCGTGGGG  25622      _ AA
                                CCCCA GA  TTGACTGAGAG
                                ||||| ||  ||||||||||
                                GGGGT CT  AACTGACTCTC
                                   G  AC
GAM1351  phospho1  3'  TGTCCCTCTGGGAATTTCTGG  83250        GA  _   A
                                CCAGAAATT  CT GAG GACA
                                |||||||||  || ||| ||||
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                                GGTCTTTAA  GG CTC CTGT
                                     G_  T   C
GAM1351  RAI17    3'  TCCCTCAGTCAGCTGGCAGGGA 92908      ___   AAA       A
                                TCCC   CAG   TTGACTGAG GA
                                ||||   |||   |||||||||| ||
                                AGGG   GTC   GACTGACTC CT
                                  ACG   ___       C
GAM1351  UBE3B    5'  CTCTTTTCACTTTGGGGA    77443        AAT   CT
                                TCCCCAGA   TGA  GAGAG
                                ||||||||   |||  |||||
                                AGGGGTTT   ACT  TTCTC
                                     C__   T_
GAM1351  LOC145314 3'  CTGTTGGCCAATTTCTGGG    77612          A TG G
                                CCCAGAAATTG C  A AG
                                |||||||||||  |  | ||
                                GGGTCTTTAAC G  T TC
                                       C GT G
GAM1351  LOC150606 5'  GTCTCTCACACTCAGGGGA    86272      A  AAT  AC
                                TCCCC GA   TG  TGAGAGAC
                                ||||| ||   ||  ||||||||
                                AGGGG CT   AC  ACTCTCTG
                                   A  C__  __
GAM1351  LOC161734 3'  TCTCTCAGAGATATTGTGAGGA 88470     C  G  _   GA
                                TCC CA AA ATT  CTGAGAGA
                                ||| || || |||  ||||||||
                                AGG GT TT TAG  GACTCTCT
                                  A  G  A   A_
GAM1351  LOC196746 3'  GTCCTGGCACCAATTTCTG    88902         A__  G  A
                                CAGAAATTG   CT AG GAC
                                |||||||||   || || |||
                                GTCTTTAAC   GG TC CTG
                                      CAC  _  _
GAM1351  LOC201229 3'  GTCTCTCCATGCCTAGGGA    89522      C  AAAT  ACT
                                TCCC AG    TG   GAGAGAC
                                |||| ||    ||   |||||||
                                AGGG TC    AC   CTCTCTG
                                  A  CGT_  ___
GAM1351  LOC219654 3'  TGCTCCCACCCACTCTGGGGG  92941         AAT  AC  A   A
                                TCCCCAGA   TG  TG GAG CA
                                ||||||||   ||  || ||| ||
                                GGGGGTCT   AC  AC CTC GT
                                     C__  CC  C   C
GAM1351  LOC219743 3'  TGCCTCTCAGTCAGAGTCAGGG 94750     A  AA        A
                                CCC GA  TTGACTGAGAG CA
                                ||| ||  |||||||||||  ||
                                GGG CT  GACTGACTCTC GT
                                  A  GA         C
GAM1351  LOC256364 5'  TCATGTCCAATTCTGGGGA    96449         ATT  _
                                TCCCCAGAA   GAC TGA
                                |||||||||   ||| |||
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                                AGGGGTCTT  CTG ACT
                                     AAC  T
GAM1352 ANKTM1   3' TTATTCCCTCACTACCCCCAGG 24703    AGAA_ _   TT
            A                    TCC    GT GTGA  GGGAATAA
                                 |||    || ||||  ||||||||
                                 AGG    CA CACT  CCCTTATT
                                   ACCCC  T   __
GAM1352 GPR85    3' TTATTGGAATATCACACTTT  39110        TGGG_
                                 GAAGTGTGAT    AATAA
                                 ||||||||||    |||||
                                 TTTCACACTA    TTATT
                                      TAAGG
GAM1352 ICMT     3' TCATTAGTCACTCTTCTGGAA 25738        T      _
                                 TTCCAGAAG GTGATTGG GA
                                 |||||||| |||||||| ||
                                 AAGGTCTTC CACTGATT CT
                                      T      A
GAM1352 NUCB1    3' TCCAAATACACTTTCTGGAA  21645       _    A
                                 TTCCAGAA GTGTG TTGGG
                                 |||||||| ||||| |||||
                                 AAGGTCTT CACAT AACCT
                                     T    A
GAM1352 OGT      5' TCATAGAACACACTTCCGGAA 14595     A      A  GG_
                                 TTCC GAAGTGTG TT   GA
                                 |||| |||||||| ||   ||
                                 AAGG CTTCACAC AG   CT
                                   C       A  ATA
GAM1352 XT3      3' CCCATCAGACCTTCTGGAA   39907       _ G   T
                                 TTCCAGAAG T TGAT GGG
                                 ||||||||| | |||| |||
                                 AAGGTCTTC A ACTA CCC
                                     C G   _
GAM1352 FLJ11016 3' TATTTGAGACACACTTTAGAA 37542    CA      A  GG
                                 TTC  GAAGTGTG TT  GAATA
                                 |||  |||||||| ||  |||||
                                 AAG  TTTCACAC AG  TTTAT
                                   A_       _ AG
GAM1352 FLJ21168 3' TTATTTTTCACATCTCTG   47585     AG    TTG
                                 CAGA  TGTGA   GGAATAA
                                 ||||  |||||   |||||||
                                 GTCT  ACACT   TTTTATT
                                   CT    ____
GAM1352 KIAA0828 3' TTATTCCCTCTACCCTTGGAA 82121      AA   T  TT
                                 TTCCAG  GTG GA  GGGAATAA
                                 ||||||  ||| ||  ||||||||
                                 AAGGTT  CAT CT  CCCTTATT
                                    CC   _ ___
GAM1352 KIAA1715 3' TTATTTGGCTCACAGTTCTGGA 68695       G    TTGG
            A                    TTCCAGAA TGTGA   GAATAA
                                 |||||||| |||||   ||||||
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                                AAGGTCTT ACACT    TTTATT
                                     G    CGG_
GAM1352  KIAA1786  3'  TATTCCCATGTCATTCTAGAA  66635     C   AGT    _
                                TTC AGA   GTGAT TGGGAATA
                                ||| |||   ||||| ||||||||
                                AAG TCT   TACTG ACCCTTAT
                                  A  ___    T
GAM1352  PRO1598   5'  TTATTCCCATTCCCATTCTGGA 38133         G  T  T
            A                    TTCCAGAA TG GA TGGGAATAA
                                ||||||||  ||  ||  |||||||||
                                AAGGTCTT AC CT ACCCTTATT
                                     _  C  T
GAM1352  SLC31A2   3'  TATTCCCAGCCCCTGGAA    60760       AA  GTGAT
                                TTCCAG  GT    TGGGAATA
                                ||||||  ||    ||||||||
                                AAGGTC  CG    ACCCTTAT
                                   CC  ______
GAM1352  LOC132203 3'  CCCATACACTTCAAGAA     75542     CA      AT
                                TTC  GAAGTGTG  TGGG
                                |||  ||||||||  ||||
                                AAG  CTTCACAT  ACCC
                                  AA      __
GAM1352  LOC143162 3'  TCCCAATCCCTTCCTGAA    77009     CA    TGT
                                TTC  GAAG   GATTGGGA
                                |||  ||||   ||||||||
                                AAG  CTTC   CTAACCCT
                                  TC    C__
GAM1352  LOC148293 3'  ATTCCCAACCTGTTTTCTTGAA 79527     C     TGTGA
                                TTC AGAAG    TTGGGAAT
                                ||| |||||    ||||||||
                                AAG TCTTT    AACCCTTA
                                  T    TGTCC
GAM1352  LOC153688 3'  TCCCCTTCAGACATTCCTGAA  87335     CA  _  G   TT
                                TTC  GAA GT TGA  GGGA
                                |||  ||| ||  |||  ||||
                                AAG  CTT CA ACT  CCCT
                                  TC   A  G   TC
GAM1352  LOC163782 3'  TCCCCACACTTCCTGAA     83037     CA      ATT
                                TTC  GAAGTGTG   GGGA
                                |||  ||||||||   ||||
                                AAG  CTTCACAC   CCCT
                                  TC      ____
GAM1352  LOC169245 5'  CTATCACCAACTTCTGGAA    88627          __    T
                                TTCCAGAAGT  GTGAT GG
                                ||||||||||  ||||| ||
                                AAGGTCTTCA  CACTA TC
                                      AC    _
GAM1352  LOC196738 3'  TCCCAATCCCTTCCTGAA    88894     CA    TGT
                                TTC  GAAG   GATTGGGA
                                |||  ||||   ||||||||
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                                AAG  CTTC   CTAACCCT
                                  TC    C__
GAM1352  LOC200853 5'  ATTCCTGAGACACTTTGAA   90323     CA      GA TG
                                TTC  GAAGTGT  T  GGAAT
                                |||  |||||||  |  |||||
                                AAG  TTTCACA  A  CCTTA
                                  __      G_ GT
GAM1352  LOC201973 5'  TTATTCTCTCCACACTTCTG   90576         ATT
                                CAGAAGTGTG   GGGAATAA
                                ||||||||||   ||||||||
                                GTCTTCACAC   CTCTTATT
                                      CT_
GAM1352  LOC220963 3'  CCACACTCAGACTTCTGGAA   93098         G   T  _
                                TTCCAGAAGT TGA TG GG
                                |||||||||| ||| || ||
                                AAGGTCTTCA ACT AC CC
                                      G   C  A
GAM1352  LOC221296 3'  TTATTCCCAGGGCCTCTG    93619      A T  GA
                                CAGA G GT  TTGGGAATAA
                                |||| | ||  ||||||||||
                                GTCT C CG  GACCCTTATT
                                  _ _  G_
GAM1353  B4GALT5   3'  ACCAGCTGGCTTCAGTGAT   17680       TT__  GG
                                ATCACT    CC  AGCTGGT
                                ||||||    ||  |||||||
                                TAGTGA    GG  TCGACCA
                                   CTTC  __
GAM1353  HRB       3'  ACCATTGCTACTGGAAAGT   16912         _   __
                                ACTTTCCGG AGC  TGGT
                                |||||||| |||  ||||
                                TGAAAGGTC TCG  ACCA
                                      A   TT
GAM1353  MS4A7     3'  ACTGAGCAGAAGGTGATA    41353         CGGA  _
                                TATCACTTTC    GCT GGT
                                ||||||||||    ||| |||
                                ATAGTGGAAG    CGA TCA
                                      A___   G
GAM1353  PPGB      3'  ACCAGCTCCACGGCCTGATG   6123       CTTT  __
                                TATCA   CC  GGAGCTGGT
                                |||||    ||  |||||||||
                                GTAGT   GG  CCTCGACCA
                                   CC__  CA
GAM1353  RORC      3'  ACCAGCTCTTTGGAAGTGA   18586        C_
                                TCACTTTC  GGAGCTGGT
                                ||||||||  |||||||||
                                AGTGAAGG  TCTCGACCA
                                      TT
GAM1353  SLC25A12  3'  ACCACTGAATAAGTGATA    14918        TC_  AGC
                                TATCACTT   CGG   TGGT
                                ||||||||   |||   ||||
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                                ATAGTGAA  GTC  ACCA
                                    TAA  ___
GAM1353 UTY      5' ACCAGCCTATGGAGGTGA   24061       C_ A
                                TCACTTTC  GG GCTGGT
                                ||||||||  || ||||||
                                AGTGGAGG  TC CGACCA
                                    TA  _
GAM1353 CASPR3   3' ACCAAAGGGAAGAGTGATA   54454        _ GGAGC
                                TATCACTTT CC    TGGT
                                ||||||||| ||    ||||
                                ATAGTGAGA GG    ACCA
                                     A  GAA__
GAM1353 DKFZP434I092 3' ACCAGCTTTACAAATTGA   68410    C  CC
                                TCA TTT  GGAGCTGGT
                                ||| |||  |||||||||
                                AGT AAA  TTTCGACCA
                                  T  CA
GAM1353 DKFZP564L2423 3' ACCAGCTCCAGGTTTGAT   63020     CTTT  _
                                ATCA   CC GGAGCTGGT
                                ||||   || |||||||||
                                TAGT   GG CCTCGACCA
                                  TT__  A
GAM1353 FLJ20464 5' ACCAGCTCCGGGAGGCGA   35678   A
                                TC CTTTCCGGAGCTGGT
                                || ||||||||||||||
                                AG GGAGGGCCTCGACCA
                                 C
GAM1353 FLJ23436 3' ACCAGGGTGGAGGAAGTGA   45461      __   GAG
                                TCACTT  TCCG  CTGGT
                                ||||||  ||||  |||||
                                AGTGAA  AGGT  GACCA
                                   GG   GG_
GAM1353 KIAA0323 3' ACCAATTATCTGGAAAATGA  63944    C      GC__
                                TCA TTTCCGGA   TGGT
                                ||| ||||||||   ||||
                                AGT AAAGGTCT   ACCA
                                  A       ATTA
GAM1353 KIAA0711 3' ACTGTCCCCGGAAAAGGATA  30146    AC     A_ T
                                TATC  TTTCCGG  GC GGT
                                ||||  |||||||  || |||
                                ATAG  AAAGGCC  TG TCA
                                  GA      CC  _
GAM1353 KIAA0976 3' ACCCTCTGACTAAAAGTGATA 30546       C___    CT
                                TATCACTTT   CGGAG  GGT
                                |||||||||   |||||  |||
                                ATAGTGAAA   GTCTC  CCA
                                     ATCA   __
GAM1353 KIAA1464 3' GGGTCCAGAGAAGTGATA   68821       _  C  G
                                TATCACT TTC GGA CT
                                ||||||| ||| ||| ||
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                                ATAGTGA GAG CCT GG
                                    A  A  G
GAM1353 KIAA1908 5' ACCAGCTCTCGGGCGATG   73779    ACTT  _
                                TATC   TCCG GAGCTGGT
                                ||||   |||| ||||||||
                                GTAG   GGGC CTCGACCA
                                  C___   T
GAM1353 KIAA1912 3' ACCACTGCCAGAAAGTGATA  73755       C _ C
                                TATCACTTTC GG AG TGGT
                                |||||||||| || || ||||
                                ATAGTGAAAG CC TC ACCA
                                     A  G  _
GAM1353 MGC20235 3' ACCATGTGAAAAAGTGATA   59545       CCGGA _
                                TATCACTTT    GC TGGT
                                |||||||||    || ||||
                                ATAGTGAAA    TG ACCA
                                     AAG__  T
GAM1353 MRP63    3' ACCAGCTTGGCCAAGGTGATA 44040       __  G
                                TATCACTTT  CCG AGCTGGT
                                |||||||||  ||| |||||||
                                ATAGTGGAA  GGT TCGACCA
                                     CC  _
GAM1353 TSARG1   3' ACCAGCCCCAGGAGTTGATA  58190     CT  _ A
                                TATCA  TTCC GG GCTGGT
                                |||||  |||| || ||||||
                                ATAGT  GAGG CC CGACCA
                                   T_   A  C
GAM1353 LOC144698 5' ACCAGCTCCGCGGGGATG   77430    A  TC
                                TATC CTT  CGGAGCTGGT
                                |||| |||  ||||||||||
                                GTAG GGG  GCCTCGACCA
                                  _  C_
GAM1353 LOC152992 5' ACCAGCTCCGGGGCGGGAT  81641    ACT
                                ATC   TTCCGGAGCTGGT
                                |||   ||||||||||||
                                TAG   GGGGCCTCGACCA
                                  GGC
GAM1353 LOC51716 3' ACCAGCCAGGGCAACAAAGTGA 33257       _____  GGA
           TA                    TATCACTT    TCC  GCTGGT
                                |||||||    |||  ||||||
                                ATAGTGAA    GGG  CGACCA
                                     ACAAC  AC_
GAM1354 ADAMTS13 3' AACAGCACGTGCAGCCCAC   58147    CT
                                GTG  GTTGCACGTGCTGTT
                                |||  |||||||||||||||
                                CAC  CGACGTGCACGACAA
                                  C_
GAM1354 MRC1     3' ACAGCACCACAGCACCA     11680       TGCAC
                                TGGTGCTGT    GTGCTGT
                                |||||||||    |||||||
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                                ACCACGACA    CACGACA
                                     C____
GAM1354 KIAA0841 3' AACAGCACATGCAAAGGCCC  71883   T  G   C
                                GG GCT TTGCA GTGCTGTT
                                || ||| ||||| ||||||||
                                CC CGG AACGT CACGACAA
                                 _  A   A
GAM1354 KREMEN   3' AACAGCACACAGCAAGCAACCA 50220    _  _   CAC
                                TGGT GCT GTTG  GTGCTGTT
                                |||| ||| ||||  ||||||||
                                ACCA CGA CGAC  CACGACAA
                                  A  A   A__
GAM1354 MGC2721  3' AACAGCACGCCCCAGGCCCA  52187    T  GTTGCA
                                TGG GCT     CGTGCTGTT
                                ||| |||     |||||||||
                                ACC CGG     GCACGACAA
                                 _  ACCCC_
GAM1354 POFUT1   3' AACAGCACGTGCAAAGGCCCC  70965   T  G
                                GG GCT TTGCACGTGCTGTT
                                || ||| ||||||||||||||
                                CC CGG AACGTGCACGACAA
                                 C  A
GAM1354 LOC92405 5' TAACAGCACGTGCAACAGCACC 69717   T              ___
           TG                    CA GGTGCTGTTGCACGTGCTGTT  A
                                || ||||||||||||||||||||  |
                                GT CCACGACAACGTGCACGACAA  T
                                _           ___
GAM1355 HRH1     3' AAATGTGCCCTTTTGGCCGG  7812    A     A  TCA
                                CC GGCCAAAA GGC  ACATTT
                                || |||||||| |||  ||||||
                                GG CCGGTTTT CCG  TGTAAA
                                 _      C  ___
GAM1355 POLD2    5' TTGAACCTCCTTGGCCTGG   21721        AA  C
                                CCAGGCCAA  AGG TCAA
                                |||||||||  ||| ||||
                                GGTCCGGTT  TCC AGTT
                                     CC  A
GAM1355 SCN7A    3' AAATGTTGAAAGCCTAAGCC  12947    CAAAA  __
                                GGC    AGGC  TCAACATTT
                                |||    ||||  |||||||||
                                CCG    TCCG  AGTTGTAAA
                                  AA___   AA
GAM1355 SHANK2   3' GTTGAACTTCTTCTTTGGCCTC 25531  C      _  C__
           A                     C AGGCCAAA AAGG  TCAAC
                                | |||||||| ||||  |||||
                                A TCCGGTTT TTCT  AGTTG
                                 C      C   TCA
GAM1355 SIAT8E   3' TGAGCCTCCTGGCCTGG    60552        AAA
                                CCAGGCCA  AGGCTCA
                                ||||||||  |||||||
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                                GGTCCGGT  TCCGAGT
                                    CC_
GAM1355 SLC7A8   3' GAGCCCTTCCTGGCCTGG   25304       AA  _
                                CCAGGCCA  AAGG CTC
                                |||||||| |||| |||
                                GGTCCGGT  TTCC GAG
                                    CC   C
GAM1355 TFAP2C   3' TGGGAACCCCTCCTGGCCTGG 13687       AAA  ____
                                CCAGGCCA  AGG   CTCA
                                |||||||| |||   ||||
                                GGTCCGGT  TCC   GGGT
                                    CC_  CCAA
GAM1355 TRPM2    3' GAGCCTTGCCTGGCCTGG   13864       AA_
                                CCAGGCCA  AAGGCTC
                                |||||||| |||||||
                                GGTCCGGT  TTCCGAG
                                    CCG
GAM1355 FLJ13189 3' TTGAACCTTTTTTGCCTGG  46498      C     C
                                CCAGGC AAAAAGG TCAA
                                |||||| ||||||| ||||
                                GGTCCG TTTTTCC AGTT
                                   T     A
GAM1355 FLJ20208 3' AAATGCAGGCTTTTTAGCC  35240    C    G  CAA
                                GGC AAAAAG CT  CATTT
                                ||| |||||| ||  |||||
                                CCG TTTTTC GA  GTAAA
                                  A    G  C__
GAM1355 FLJ22944 3' AAATGTTGGGATTTGAACCC  47866   CCAA  GG
                                GG   AAA  CTCAACATTT
                                ||   |||  ||||||||||
                                CC   TTT  GGGTTGTAAA
                                 CAAG  A_
GAM1355 HPRP8BP  3' AAATGTTGGATGTCCAGGCT  60060    AAAAA  __
                                GGCC    GGC  TCAACATTT
                                ||||    |||  |||||||||
                                TCGG    CTG  GGTTGTAAA
                                  AC___  TA
GAM1355 KIAA0872 3' AAATGTTAAGCCTTTTGTTATT 30731    GCCA     C
           G                     CAG   AAAAGGCT AACATTT
                                |||   |||||||| |||||||
                                GTT   TTTTCCGA TTGTAAA
                                  ATTG      A
GAM1355 KIAA1843 3' AAATGTTGACTGAACCTGACCT 62880    C  AAAA_  C
           G                     CAGG CA    GG TCAACATTT
                                |||| ||    || |||||||||
                                GTCC GT    TC AGTTGTAAA
                                  A  CCAAG  _
GAM1355 KIAA1975 3' AAATGTTGATTTTTCTGACC  74407   C  A    C
                                GG CA AAAGG TCAACATTT
                                || || ||||| |||||||||
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                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM1355  MRIP2    3'  AAATGTTGATTTTTCTGACC   56789    C  A    C
                                GG CA AAAGG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM1355  SLC26A10  5'  TTGAACCCCTTTGGCCTG    56851         AA  C
                                CAGGCCAAA  GG TCAA
                                |||||||||  || ||||
                                GTCCGGTTT  CC AGTT
                                      CC  A
GAM1355  THEG     3'  TGAGCTTTTTGGCCTGG     33892           G
                                CCAGGCCAAAAAG CTCA
                                |||||||||||| ||||
                                GGTCCGGTTTTTC GAGT
                                                _
GAM1355  LOC118704 3'  AAATGTTGATTTTTCTGACC   74359    C  A    C
                                GG CA AAAGG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM1355  LOC118706 3'  AAATGTTGATTTTTCTGACC   74361    C  A    C
                                GG CA AAAGG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM1355  LOC123036 3'  AAATGTTTGCAGTTTTGGCT   74645        AG  TC
                                GGCCAAAA  GC  AACATTT
                                ||||||||  ||  |||||||
                                TCGGTTTT  CG  TTGTAAA
                                     GA  T_
GAM1355  LOC123624 3'  AAATGTTGGGCTTCTGTGCCT  76134     _  AAA
                                AGGC CA   AGGCTCAACATTT
                                |||| ||   ||||||||||||
                                TCCG GT   TTCGGGTTGTAAA
                                  T  C__
GAM1355  LOC128338 3'  AAATATTGAGCCTTTTTAATAG 75250    AGGCC          C
            G                    CC     AAAAAGGCTCAA ATTT
                                 ||     |||||||||||| ||||
                                 GG     TTTTTCCGAGTT TAAA
                                  ATAA_          A
GAM1355  LOC143158 3'  AAATGTTGATTTTTCTGACC   76997    C  A    C
                                GG CA AAAGG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM1355  LOC195979 3'  AAATGTTGATTTTTCTGACC   88928    C  A    C
                                GG CA AAAGG TCAACATTT
                                || || ||||| |||||||||
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                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM1355  LOC219672 5'  AATGGTGCTTTTTGGCTGG   92963     G      G TCAA
                                CCAG CCAAAAAG C   CATT
                                |||| |||||||| |   ||||
                                GGTC GGTTTTTC G   GTAA
                                  _      _ TG__
GAM1355  LOC220466 3'  AAATGTTGATTTTTCTGACC  74398   C  A    C
                                GG CA AAAGG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM1355  LOC254105 3'  AGGTGTGGCCCCCTTGGCCTGG 96416        AAA   CA
                                CCAGGCCAA   GGCT  ACATTT
                                |||||||||   ||||  ||||||
                                GGTCCGGTT   CCGG  TGTGGA
                                     CCC   __
GAM1355  LOC255319 3'  AAATGTTGATTTTTCTGACC  96152   C  A    C
                                GG CA AAAGG TCAACATTT
                                || || ||||| |||||||||
                                CC GT TTTTT AGTTGTAAA
                                 A  C    _
GAM1355  LOC91300  5'  GTTGAGCTTTTCTGGCCCGG  96238   A    A
                                CC GGCCA AAAGGCTCAAC
                                || ||||| ||||||||||
                                GG CCGGT TTTTCGAGTTG
                                 C    C
GAM1355  LOC91300  5'  GTTGAGCTTTTCTGGCCCGG  57864   A    A
                                CC GGCCA AAAGGCTCAAC
                                || ||||| ||||||||||
                                GG CCGGT TTTTCGAGTTG
                                 C    C
GAM1355  LOC91660  5'  AAATGTTTATCTTCTTTTTGGC 67399          CTC__
            TT                   AGGCCAAAAAGG    AACATTT
                                ||||||||||||    |||||||
                                TTCGGTTTTTCT    TTGTAAA
                                      TCTAT
GAM1356  AQP7     5'  GACAGTCACGGAGGAACAAGAT 8605        A_
            CAA                   TTGATCTT  TCCTCCGTGACTGTC
                                |||||||  ||||||||||||||||
                                AACTAGAA  AGGAGGCACTGACAG
                                    CA
GAM1356  MMP14    5'  GACTAAGCAGAAGAAAGATCAA 18428       A  C  C  GACT
                                TTGATCTT TC TC GT   GTC
                                |||||||| || || ||   |||
                                AACTAGAA AG AG CG   CAG
                                    _ A  A  AAT_
GAM1356  KIAA0433  5'  ACAGTCATCATAATATCAA   31498     C   CCTCC
                                TTGAT TTAT    GTGACTGT
                                ||||| ||||    ||||||||
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                                AACTA AATA    TACTGACA
                                  T   C____
GAM1356  KIAA1915  5'  GACAGTATTTTAAAAATAAGGT 73667        CCTCCGTG_
             CAA                   TTGATCTTAT       ACTGTC
                                |||||||||         ||||||
                                AACTGGAATA       TGACAG
                                     AAAATTTTA
GAM1356  MGC5370   3'  CAGTTGAAAAGATCAA     52193        A  CTCCGT
                                TTGATCTT TC     GACTG
                                |||||||| ||     |||||
                                AACTAGAA AG     TTGAC
                                     A  ______
GAM1356  TREX1     5'  GACAGCTGGAGACAGAGATCAA 54382       ATC    TGA
                                TTGATCTT   CTCCG   CTGTC
                                |||||||   |||||   |||||
                                AACTAGAG   GAGGT   GACAG
                                     ACA    C__
GAM1356  TREX1     5'  GACAGCTGGAGACAGAGATCAA 54388       ATC    TGA
                                TTGATCTT   CTCCG   CTGTC
                                |||||||   |||||   |||||
                                AACTAGAG   GAGGT   GACAG
                                     ACA    C__
GAM1356  LOC127534 3'  ACAGCAGATAAGATCAA     75963         CTCCG  A  _
                                TTGATCTTATC     TG CTG T
                                ||||||||||     || ||| |
                                AACTAGAATAG     AC GAC A
                                      _____  _   T
GAM1356  LOC150480 5'  GACAGTCACGGAGGAAGAAGAT 61025        A_
             CAA                   TTGATCTT  TCCTCCGTGACTGTC
                                |||||||  ||||||||||||||
                                AACTAGAA  AGGAGGCACTGACAG
                                     GA
GAM1356  LOC158279 5'  GACAGTCACAGAGGAACAAGAT 60330        A_    C
             CAA                   TTGATCTT  TCCTC GTGACTGTC
                                |||||||  ||||| |||||||||
                                AACTAGAA  AGGAG CACTGACAG
                                     CA    A
GAM1356  LOC201522 3'  GACCTTCGGGAGAACGAGATCA 89637        ATC   G   CT
             A                    TTGATCTT   CTCC TGA  GTC
                                |||||||   |||| |||  |||
                                AACTAGAG   GAGG GCT  CAG
                                     CAA   _   TC
GAM1356  LOC220864 5'  GACAGTCACAGAGGAACAAGAT 92487        A_    C
             CAA                   TTGATCTT  TCCTC GTGACTGTC
                                |||||||  ||||| |||||||||
                                AACTAGAA  AGGAG CACTGACAG
                                     CA    A
GAM1356  LOC254381 5'  GACAGTCACGACAGCAGACCAA 99328     A   TATCCTC
                                TTG TCT      CGTGACTGTC
                                ||| |||      ||||||||||
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                                AAC AGA      GCACTGACAG
                                  C   CGACA__
GAM1357 LDLR     3' GGGATTGGCAATTGTCCCCA  6741      A  C       GT
                                TGGG AC ATTGCCAA  CT
                                |||| || ||||||||  ||
                                ACCC TG TAACGGTT  GG
                                  C  T       AG
GAM1357 NRIP1    3' TACCAAACTCAGGTGATTCC  60624     ACC  TG  A_   C
                                GGA   AT  CC  AGT TGGTA
                                |||   ||  ||  ||| |||||
                                CCT   TA  GG  TCA ACCAT
                                  ___  GT  AC   A
GAM1357 PSEN2    3' ACCAGACTTTGGCTCCC     25950      ACCATT    _
                                GGGA     GCCAA GTCTGGT
                                ||||     ||||| |||||||
                                CCCT     CGGTT CAGACCA
                                  _______    T
GAM1357 PSEN2    3' ACCAGACTTTGGCTCCC     6542       ACCATT    _
                                GGGA     GCCAA GTCTGGT
                                ||||     ||||| |||||||
                                CCCT     CGGTT CAGACCA
                                  _______    T
GAM1357 FLJ12604 3' ACATGGTAAAATGGTTCCCA  65059          __    A
                                TGGGAACCAT  TGCCA GT
                                ||||||||||  ||||| ||
                                ACCCTTGGTA  ATGGT CA
                                      AA    A
GAM1357 FLJ13081 3' ACATGGCAGTGGTTCCCA    46169            A
                                TGGGAACCATTGCCA GT
                                |||||||||||||| ||
                                ACCCTTGGTGACGGT CA
                                         A
GAM1357 FLJ23093 3' ACCAGACTCCTCAGGTTCC   45321       AT  CCA
                                GGAACC  TG   AGTCTGGT
                                ||||||  ||   ||||||||
                                CCTTGG  AC   TCAGACCA
                                   __  TCC
GAM1357 GP5      3' ACCAGACTCACGGTCTCCA   16857     GA   AT  CCA
                                TGG  ACC  TG   AGTCTGGT
                                |||  |||  ||   ||||||||
                                ACC  TGG  AC   TCAGACCA
                                  TC   C_  ___
GAM1357 KIAA0286 3' ACCAGACTTACTGGCTCACCA 68855    _ A   TTGCC
                                TGG GA CCA    AAGTCTGGT
                                ||| || |||    |||||||||
                                ACC CT GGT    TTCAGACCA
                                  A  C   CA___
GAM1357 MGC10540 3' ACCAGACTCAAAAGGACTCCA 51356     AA  A  GCCA
                                TGGG  CC TT   AGTCTGGT
                                ||||  || ||   ||||||||
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                                ACCT  GG AA    TCAGACCA
                                  CA  A  AC__
GAM1357  LOC157226 5'  TACCGCAGGCAAAGGTTCCCA  64640         A     AAGTC
                                TGGGAACC TTGCC     TGGTA
                                |||||||| |||||     |||||
                                ACCCTTGG AACGG     GCCAT
                                     A     AC___
GAM1358  ANGPT4    3'  GTACCTTGAATGGGCT      32572         GGCA
                                AGCCCATT    GGGGTAC
                                ||||||||    |||||||
                                TCGGGTAA    TTCCATG
                                     G___
GAM1358  ASS       5'  GGCACCCCTGCCAGTCCTGCTC 55026      CC_          A
                                GAGC   ATTGGCAGGGGT CC
                                ||||   |||||||||||| ||
                                CTCG   TGACCGTCCCCA GG
                                  TCC          C
GAM1358  BAK1      3'  TACCCTTGTGAGAGCCCA    93634    A  CCA  G
                                TG GC   TT GCAGGGGTA
                                || ||   || |||||||||
                                AC CG   GA TGTTCCCAT
                                 C  A__  G
GAM1358  DNASE1L1  3'  GGTACCGATATGCCAATGGGCC 23018    A        A________  GGTA
           A                     TG GCCCATTGGC       GG    C
                                || ||||||||||       ||    |
                                AC CGGGTAACCG       CC    G
                                 _        TATAG___  ATGG
GAM1358  DUSP6     3'  ACACCAAATCATGGGCTCA    66576         T  CAG  _
                                TGAGCCCAT GG   GG GT
                                ||||||||| ||   || ||
                                ACTCGGGTA CT   CC CA
                                     _  AAA  A
GAM1358  MN1       3'  ACACTTTGCCAATTAGCTCA   11647       CC         _
                                TGAGC  ATTGGCAGGG GT
                                |||||  |||||||||| ||
                                ACTCG  TAACCGTTTC CA
                                   AT         A
GAM1358  MPP2      3'  GCAGGGGCCAGTGGGCTCA    60520            AGGG
                                TGAGCCCATTGGC    GT
                                ||||||||||||    ||
                                ACTCGGGTGACCG    CG
                                       GGGA
GAM1358  SULT1A2   3'  CCCTGACCAATGGGCTCA    72672           _
                                TGAGCCCATTGG CAGGG
                                |||||||||||| |||||
                                ACTCGGGTAACC GTCCC
                                       A
GAM1358  SULT1A3   3'  CCCTGACCAATGGGCTCA    13483           _
                                TGAGCCCATTGG CAGGG
                                |||||||||||| |||||
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                                ACTCGGGTAACC GTCCC
                                       A
GAM1358 TRPM2    3' GGCACCCCTGCAGAGGCTC   13868      CATTG      A
                                GAGCC    GCAGGGGT CC
                                |||||    |||||||| ||
                                CTCGG    CGTCCCCA GG
                                   AGA__       C
GAM1358 XBP1     3' ACTTTTGCCAATGAACTC    18674     CC
                                GAG  CATTGGCAGGGGT
                                |||  ||||||||||||
                                CTC  GTAACCGTTTTCA
                                  AA
GAM1358 BMF      3' GGTACCGGTGCCATATGGGCTC 54286         _   A_____ GGTA
             A                   TGAGCCCAT TGGC     GG   C
                                |||||||| ||||     ||   |
                                ACTCGGGTA ACCG     CC   G
                                      T   TGG___ ATGG
GAM1358 DKFZP727M111 5' GCTTTTGCCAGTGAGCCCA   32061    A  C
                                TG GC CATTGGCAGGGGT
                                || || ||||||||||||
                                AC CG GTGACCGTTTTCG
                                 C  A
GAM1358 FLJ13162 5' GCACCCTCCATGGGCTCA    47185         T  C   _
                                TGAGCCCAT GG AGGG GT
                                |||||||| || |||| ||
                                ACTCGGGTA CC TCCC CG
                                      _ _   A
GAM1358 GMPPB    5' ACTTCTGCAATAAGCCCA    97429    A  CC   G
                                TG GC  ATTG CAGGGGT
                                || ||  |||| |||||||
                                AC CG  TAAC GTCTTCA
                                 C  AA   _
GAM1358 KIAA0444 3' TGCCCCATGGGCTCA       63006         TGGCA
                                TGAGCCCAT    GGGGTA
                                |||||||||    ||||||
                                ACTCGGGTA    CCCCGT
                                      _____
GAM1358 KIAA0963 3' GACCCACAAGGGCTCA      31033       A   GCAG   A
                                TGAGCCC TTG    GGGT C
                                ||||||| |||    |||| |
                                ACTCGGG AAC    CCCA G
                                    _  A___    C
GAM1358 KIAA1649 3' GCTTATGACCAATGGGCCA   67517    A       _ GG
                                TG GCCCATTGG CA  GGT
                                || |||||||| ||  |||
                                AC CGGGTAACC GT  TCG
                                 _       A  AT
GAM1358 KIAA1649 5' GCTTATGACCAATGGGCCA   51243    A       _ GG
                                TG GCCCATTGG CA  GGT
                                || |||||||| ||  |||
```

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                                AC CGGGTAACC GT  TCG
                                 _       A  AT
GAM1358 KIAA1813 3' GCTTCTGCCAAGAACTCA    70825     CCCA
                                TGAG    TTGGCAGGGGT
                                ||||    ||||||||||
                                ACTC    AACCGTCTTCG
                                  AAG_
GAM1358 KIAA1813 5' GGCTCCCCCCACCAATGGGC  70828        CA_   TA
                                GCCCATTGG   GGGG  CC
                                |||||||||   ||||  ||
                                CGGGTAACC   CCCC  GG
                                      ACC    TC
GAM1358 MAP1LC3A 3' ACCCCTGCTGTGTGGTTCA   51679       _  T
                                TGAGCC CAT GGCAGGGGT
                                |||||| ||| |||||||||
                                ACTTGG GTG TCGTCCCCA
                                    T  _
GAM1358 MGC11316 3' GGTGCATTGCCAAGGACTCA  53047     C  A     GG
                                TGAG CC TTGGCAG  GTACC
                                |||| || |||||||  |||||
                                ACTC GG AACCGTT  CGTGG
                                  A  _      A_
GAM1358 PDE8B    5' GGCACCCCTGCCCGGCCTC   68203     C  ATT       A
                                GAG CC   GGCAGGGGT CC
                                ||| ||   ||||||||| ||
                                CTC GG   CCGTCCCCA GG
                                  C  C__        C
GAM1358 PRO0529  3' TACTCACCAATGGGACCA    26857    AG      CAG
                                TG  CCCATTGG   GGGTA
                                ||  ||||||||   |||||
                                AC  GGGTAACC   CTCAT
                                 CA       A__
GAM1358 RAB17    3' CCCCTGCCTGGGCCA       42617    A    TT
                                TG GCCCA  GGCAGGGG
                                || |||||  ||||||||
                                AC CGGGT  CCGTCCCC
                                 _    __
GAM1358 UBE2G1   3' ACTCCTGCCAAGAGCCCA    13950    A  CCA
                                TG GC   TTGGCAGGGGT
                                || ||   ||||||||||
                                AC CG   AACCGTCCTCA
                                 C  AG_
GAM1358 LOC115708 3' GGTACCCCTACCCCTCA    73920     CCCATT  C
                                TGAG     GG AGGGGTACC
                                ||||     || |||||||||
                                ACTC     CC TCCCCATGG
                                  C_____  A
GAM1358 LOC150481 3' GCACCTAACAATGGGTCA   80705     G     GC   G
                                TGA CCCATTG  AGG GT
                                ||| |||||||  ||| ||
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                                ACT GGGTAAC  TCC CG
                                  _      AA   A
GAM1358  LOC153196 5'  GGCACTGCCTTGCCATCGGGCC 87171    A    AT       __ A
                CA                  TG GCCC  TGGCAGGG  GT CC
                                   || ||||  ||||||||  || ||
                                   AC CGGG  ACCGTTCC  CA GG
                                    C    CT       GT  C
GAM1358  LOC153711 5'  ACCTGTTAGCCGATGGGCCCA  87342    A        AG__
                                   TG GCCCATTGGC    GGGT
                                   || ||||||||||    ||||
                                   AC CGGGTAGCCG    TCCA
                                    C         ATTG
GAM1358  LOC157860 3'  GGCACCCCCTCCTGGGCTC    87878       TT  CA    A
                                   GAGCCCA  GG  GGGGT CC
                                   |||||||  ||  ||||| ||
                                   CTCGGGT  CC  CCCCA GG
                                       __ TC    C
GAM1358  LOC158014 5'  GTGCCACCCATGGGCTCA     82566        T  CAGG
                                   TGAGCCCAT GG    GGTAC
                                   |||||||||  ||    |||||
                                   ACTCGGGTA CC    CCGTG
                                         _ CA__
GAM1358  LOC158191 3'  GCACCTAACAATGGGTCA     82677     G      GC   G
                                   TGA CCCATTG  AGG GT
                                   ||| |||||||  ||| ||
                                   ACT GGGTAAC  TCC CG
                                     _      AA   A
GAM1358  LOC203378 5'  ATCTCTGCCAACAGTCTCA    92276      CCCA
                                   TGAG    TTGGCAGGGGT
                                   ||||    ||||||||||
                                   ACTC    AACCGTCTCTA
                                      TGAC
GAM1358  LOC203378 3'  GGTATTTTGCCCAAAGGCTCA  92295       CATT      G
                                   TGAGCC    GGCAGGG TACC
                                   ||||||    ||||||| ||||
                                   ACTCGG    CCGTTTT ATGG
                                       AAAC       _
GAM1358  LOC204970 3'  GGCACCCCTGCGGGCTCA     90964        ATTG      A
                                   TGAGCCC    GCAGGGGT CC
                                   |||||||    |||||||| ||
                                   ACTCGGG    CGTCCCCA GG
                                         ____        C
GAM1358  LOC219700 5'  GGCTTCCCTGCCATGGACTCA  94653      C    T       TA
                                   TGAG CCAT GGCAGGGG  CC
                                   |||| |||| ||||||||  ||
                                   ACTC GGTA CCGTCCCT  GG
                                     A    _       TC
GAM1358  LOC256126 3'  GCCCCTGCCATAGGCCCA     97015     A   CAT
                                   TG GCC   TGGCAGGGGT
                                   || |||   ||||||||||
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                                AC CGG   ACCGTCCCCG
                                 C  AT_
GAM1358 LOC51246 3' ACCTGGGCCAATGGGCCA    33636    A        AG
                                TG GCCCATTGGC  GGGT
                                || ||||||||||  ||||
                                AC CGGGTAACCG  TCCA
                                 _        GG
GAM1358 LOC90190 3' ACTGTTACCAATGGGCTC    62421          C  G
                                GAGCCCATTGG AG GGT
                                |||||||||||  || |||
                                CTCGGGTAACC TT TCA
                                      A  G
GAM1359 DPH2L1   3' CTGACAAAGTCATCCCCTCTCA 9112      C       _  CTCA
            GG                    CCT GAGAGGGGG GAT    TCAG
                                ||| |||||||| |||    ||||
                                GGA CTCTCCCCT CTG    AGTC
                                 _       A   AAAC
GAM1359 MEF2D    3' ATGGCCCTCCCCCTCCCCAGG  20979     CGA      ATC
                                CCT   GAGGGGGG   TCAT
                                |||   ||||||||   ||||
                                GGA   CTCCCCCT   GGTA
                                  CCC       CCC
GAM1359 SORCS2   3' ATGAGGGTCCCTCTCAGAG   40797     GA      AT
                                CTC  GAGGGGGG  CTCAT
                                |||  ||||||||  |||||
                                GAG  CTCTCCCT  GAGTA
                                  A_       GG
GAM1359 CACNG4   3' CTGACTTTGTCCCCTCCCCGA  27708     AGA      CTCA
                                TCG   GGGGGGAT    TCAG
                                |||   ||||||||    ||||
                                AGC   CTCCCCTG    AGTC
                                  CC_       TTTC
GAM1359 CYP2A7   5' TGGAGTCCCCCCTCCTGAG    7544      A        CT
                                CTCG GAGGGGGGAT  CA
                                |||| ||||||||||  ||
                                GAGT CTCCCCCCTG  GT
                                   C         AG
GAM1359 FLJ20457 3' GATGGCCTTCCCCTCTGA    35671    G       ATC
                                TC AGAGGGGGG   TCATC
                                || |||||||||   |||||
                                AG TCTCCCCTT   GGTAG
                                 _        CC_
GAM1359 HABP2    5' CTGACATTTTTCCCCCCTAAAG 15951     CGAG      TCTCA_
            G                    CCT    AGGGGGGA     TCAG
                                |||    ||||||||     ||||
                                GGA    TCCCCCCT     AGTC
                                  AA__       TTTTAC
GAM1359 KLF12    3' ATGAGATTCTCTCAGAGG    33276     GAGA
                                CCTC    GGGGGGATCTCAT
                                ||||    ||||||||||||
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                                GGAG   CTCTCTTAGAGTA
                                  A___
GAM1359 SDCCAG3  3' TGACGGCCCCCCTCAGAGG   22806     GA      A _
                                CCTC  GAGGGGGG TC TCA
                                |||| |||||||| || |||
                                GGAG  CTCCCCCC GG AGT
                                  A_      _ C
GAM1359 XPO5     3' CTGACAAGAGGGTTTCCCCGAG 92874     AGA   GG AT   A__
                                CTCG   GGG  G  CTC   TCAG
                                ||||   |||  |  |||   ||||
                                GAGC   CCC  T  GAG   AGTC
                                  ___   TT GG   AAC
GAM1359 LOC147599 3' AGGCTCCCCTCTCTCAAGG   85159     C        _
                                CCT GAGAGGGGGGA TCT
                                ||| |||||||||| |||
                                GGA CTCTCTCCCCT GGA
                                  A         C
GAM1359 LOC200314 3' TGTGACCCCCCCCCTCAAGG   91608     C   A     A  T
                                CCT GAG GGGGGG TC CA
                                ||| ||| |||||| || ||
                                GGA CTC CCCCCC AG GT
                                  A  _     C  T
GAM1359 LOC222414 3' TGTAATCCCCCCCCCTCAAGG   95975     C   A      CT
                                CCT GAG GGGGGGAT  CA
                                ||| ||| ||||||||  ||
                                GGA CTC CCCCCCTA  GT
                                  A   C       AT
GAM1360 LAMC1    3' TTGCAAAGTTTTCACGTCA   11275        C  CC_
                                TGACGTGGA AT   GCAA
                                |||||||| ||   ||||
                                ACTGCACTT TG   CGTT
                                      T  AAA
GAM1360 OPA1     3' TTGCGGGTGGAACAGTCA    56430     G  GA_
                                TGAC TG   CATCCGCAA
                                |||| ||   |||||||||
                                ACTG AC   GTGGGCGTT
                                  _ AAG
GAM1360 OPA1     3' TTGCGGGTGGAACAGTCA    56432     G  GA_
                                TGAC TG   CATCCGCAA
                                |||| ||   |||||||||
                                ACTG AC   GTGGGCGTT
                                  _ AAG
GAM1360 OPA1     3' TTGCGGGTGGAACAGTCA    56434     G  GA_
                                TGAC TG   CATCCGCAA
                                |||| ||   |||||||||
                                ACTG AC   GTGGGCGTT
                                  _ AAG
GAM1360 OPA1     3' TTGCGGGTGGAACAGTCA    56436     G  GA_
                                TGAC TG   CATCCGCAA
                                |||| ||   |||||||||
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                                ACTG AC   GTGGGCGTT
                                  _ AAG
GAM1360  OPA1     3'  TTGCGGGTGGAACAGTCA    56438      G  GA_
                                TGAC TG   CATCCGCAA
                                |||| ||   |||||||||
                                ACTG AC   GTGGGCGTT
                                  _ AAG
GAM1360  PITX2    5'  TTGCGGAGGGTGCGCTCA    6161      C   G  A_
                                TGA GTG AC  TCCGCAA
                                ||| ||| ||  |||||||
                                ACT CGC TG  AGGCGTT
                                  _  G  GG
GAM1360  TLR4     5'  TTGCGGGTTCTACATCA     57506     C    C
                                TGA GTGGA ATCCGCAA
                                ||| ||||| ||||||||
                                ACT CATCT TGGGCGTT
                                  A    _
GAM1360  KIAA1962 5'  TTGCGGATGCTGATGCA     82803     A  _  A
                                TG CGT GG CATCCGCAA
                                || ||| || |||||||||
                                AC GTA TC GTAGGCGTT
                                  _  G  _
GAM1360  MGC861   3'  TTGAGGATGTCCAGTCA     44134      G        G
                                TGAC TGGACATCC CAA
                                |||| ||||||||| |||
                                ACTG ACCTGTAGG GTT
                                  _        A
GAM1360  LOC132332 5'  TTGCGGATTGCCGTGCA     76669     A     AC
                                TG CGTGG  ATCCGCAA
                                || |||||  ||||||||
                                AC GTGCC  TAGGCGTT
                                  _    GT
GAM1360  LOC144848 3'  TGGAGGATGTCCACATCA     73961     C        G_
                                TGA GTGGACATCC  CA
                                ||| ||||||||||  ||
                                ACT CACCTGTAGG  GT
                                  A         AG
GAM1360  LOC165257 5'  TTGTGTGCCCCACGTCA     83373         A_  TC
                                TGACGTGG  CA  CGCAA
                                ||||||||  ||  |||||
                                ACTGCACC  GT  GTGTT
                                     CC  __
GAM1360  LOC200269 3'  TTGCAGTGTCCACTCA      90079     C       CC
                                TGA GTGGACAT  GCAA
                                ||| ||||||||  ||||
                                ACT CACCTGTG  CGTT
                                  _       A_
GAM1360  LOC221495 5'  TTGCAGGGGCATCACGTTA    95498         ACA  _
                                TGACGTGG   TCC GCAA
                                ||||||||   ||| ||||
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                                ATTGCACT   GGG CGTT
                                     ACG   A
GAM1360  LOC256520 3'  GCAGATTTTGTTCTACGTCA   97667          _ ___  C
                                TGACGTGGA CA   TC GC
                                |||||||||  ||   || ||
                                ACTGCATCT GT   AG CG
                                      T  TTT  A
GAM1361  CDH13     3'  TGAATCATCAAAGCTCACACCA 8841      CA       C   TCC
                                TGG  TGGGCTTT GTG   CA
                                |||  ||||||||  |||   ||
                                ACC  ACTCGAAA TAC   GT
                                  AC       C   TAA
GAM1361  FKBP1A    3'  ACACCCAGTGAAAGCCCAGCCA 55029      A        _____
                                TGGC TGGGCTTTC     GTGT
                                ||||  |||||||||     ||||
                                ACCG ACCCGAAAG     CACA
                                  _        TGACC
GAM1361  FZD1      3'  GTGAGATAACCAATGCCA     14501       G  CTTTCG    C
                                TGGCAT GG      TGTC CAC
                                ||||||  ||      ||||  |||
                                ACCGTA CC      ATAG GTG
                                    A  A_____    A
GAM1361  LRP4      5'  GCGACGAAAGCCCACAGC     65062     A_         _
                                GC  TGGGCTTTCGT GT
                                ||  ||||||||||| ||
                                CG  ACCCGAAAGCA CG
                                  AC          G
GAM1361  TP73      5'  GAAACCGGGGCCCGCGCCA    19471      A      TC  G
                                TGGC TGGGCTT  GT TC
                                ||||  |||||||  || ||
                                ACCG GCCCGGG  CA AG
                                   C      GC  A
GAM1361  FLJ12650  3'  AGCAGGACATCAGGCCCATCCC 44815     C       TC      CA
              A                  TGG ATGGGCTT  GTGTCC  CT
                                 |||  ||||||||  ||||||  ||
                                 ACC TACCCGGA  TACAGG  GA
                                   C       C_      AC
GAM1361  FLJ14641  3'  GCCCGAAACCCCATACCA     52561     C     C     T
                                TGG ATGGG TTTCG GT
                                |||  |||||  |||||  ||
                                ACC TACCC  AAAGC CG
                                   A    C    C
GAM1361  FLJ22056  3'  GTGAGAGAGCCCAGGCCA     42835      A       GTGTCC
                                TGGC TGGGCTTTC      CAC
                                ||||  |||||||||      |||
                                ACCG ACCCGAGAG      GTG
                                   G        A_____
GAM1361  HDCMA18P  5'  AGTGAAAAATAAGCCCATTCCA 34090     C       TCGTGTCC
                                TGG ATGGGCTT       CACT
                                |||  ||||||||       ||||
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                                ACC TACCCGAA       GTGA
                                  T       TAAAAA__
GAM1361  KIAA0738  3'  GCAGAGGAAACCCATGCCA   28886         C   G_
                                TGGCATGGG TTTC  TGT
                                ||||||||| ||||  |||
                                ACCGTACCC AAGG  ACG
                                     A    AG
GAM1361  KIAA0843  3'  TGGGACACACTGCCTGCCA   30806      TG   TTTC
                                TGGCA  GGC   GTGTCCCA
                                |||||  |||   ||||||||
                                ACCGT  CCG   CACAGGGT
                                   __   TCA_
GAM1361  KIAA0940  3'  TGGGAAGAGCCCATAACA    30536    GC       CGTG
                                TG  ATGGGCTTT    TCCCA
                                ||  |||||||||    |||||
                                AC  TACCCGAGA    AGGGT
                                 AA        _____
GAM1361  LOC126917 3'  AGTGGGGTTCGAAGCCACACCA 75083     CATG    T  TG
                                TGG    GGCTT CG  TCCCACT
                                |||    ||||| ||  |||||||
                                ACC    CCGAA GC  GGGGTGA
                                  ACA_     _ TT
GAM1361  LOC148696 5'  AGCAGGACAGAAAAACCAACGC 85342      A_   GC    G    CA
            CA                    TGGC  TGG  TTTC TGTCC  CT
                                |||| |||  |||| |||||  ||
                                ACCG  ACC  AAAG ACAGG  GA
                                  CA   AA   _    AC
GAM1362  ACT      5'  CCACAATCCAGGGGGCCAT   40420         CCG   AAC
                                ATGGCCCCT   GGA   TGTGG
                                |||||||||   |||   |||||
                                TACCGGGGG   CCT   ACACC
                                     A__   A__
GAM1362  ADAM11   3'  GCCACAGCTCAACTCGGGGGC  41490      TC   AAA__
                                GCCCC  CGGG    CTGTGGC
                                |||||  ||||    |||||||
                                CGGGG  GCTC    GACACCG
                                   __    AACTC
GAM1362  ADAM11   3'  GCCACAGCTCAACTCGGGGGC  11487      TC   AAA__
                                GCCCC  CGGG    CTGTGGC
                                |||||  ||||    |||||||
                                CGGGG  GCTC    GACACCG
                                   __    AACTC
GAM1362  CDC34    3'  GCCGCACCCCGGAGGAGCCA   16390      C       AAAC
                                TGGC CCTCCGGG    TGTGGC
                                |||| ||||||||    ||||||
                                ACCG GGAGGCCC    ACGCCG
                                  A       C___
GAM1362  CRI1     3'  GCCACAGTTATCAAAGGCTA   27537       CCTCCG  A
                                TGGCC     GG AACTGTGGC
                                |||||     || |||||||||
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                                ATCGG     CT TTGACACCG
                                   AAA___  A
GAM1362  FLII     3'  GCCACAGTCCCCAGTAGCC   10656     CC  CC   AA
                                GGC  CT  GGG  ACTGTGGC
                                |||  ||  |||  ||||||||
                                CCG  GA  CCC  TGACACCG
                                  AT  __   C_
GAM1362  FZD10    3'  GCCCACCCCCAGGAAGGCCA   24214      CC   _   AAAC  T
                                TGGCC  TCC GGG    TG GGC
                                |||||  ||| |||    || |||
                                ACCGG  AGG CCC    AC CCG
                                   A_   A   CC__  _
GAM1362  GNA11    5'  CCACAGCCCCGGGGGCCG    76585       TC    AAA
                                TGGCCCC  CGGG   CTGTGG
                                |||||||  ||||   ||||||
                                GCCGGGG  GCCC   GACACC
                                    __    C__
GAM1362  IGHMBP2  3'  GCCACAGAGGAGCGGAGGGGCC 10984          GGAAA
                                GGCCCCTCCG     CTGTGGC
                                ||||||||||     |||||||
                                CCGGGGAGGC     GACACCG
                                     GAGGA
GAM1362  MAGEA3   5'  CCAGAGGCCCCCGGAGGAGC   19315    C       AAA  G
                                GC CCTCCGGG   CT TGG
                                || ||||||||   || |||
                                CG GGAGGCCC   GA ACC
                                 A       CCG  G
GAM1362  PYGB     3'  CCAGGGGTCCCGGAGGAACC   12687    CC       AA  G
                                GG  CCTCCGGGA  CT TGG
                                ||  |||||||||  || |||
                                CC  GGAGGCCCT  GG ACC
                                 AA        G_  G
GAM1362  PYGB     3'  CCATGTTTCCAGGAGGGGCCAT 12689          G     T
                                ATGGCCCCTCC GGAAAC GTGG
                                |||||||||| |||||| ||||
                                TACCGGGGAGG CCTTTG TACC
                                     A     _
GAM1362  SLC6A6   3'  GCCACAGTCCTTCCTGGGGC   13183      TCC    __
                                GCCCC   GGGAA  ACTGTGGC
                                |||||   |||||  ||||||||
                                CGGGG   TCCTT  TGACACCG
                                   ___     CC
GAM1362  UBTF     3'  CCATTCCTTCCCAGAGGGGCC  27252        C    ACT
                                GGCCCCTC GGGAA   GTGG
                                |||||||| |||||   ||||
                                CCGGGGAG CCCTT   TACC
                                    A     CCT
GAM1362  CBCIP2   3'  GCCACACGGACTCAGAGGGGCC 52658         C   AAAC
              A                  TGGCCCCTC GGG    TGTGGC
                                 |||||||| |||    ||||||
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                                ACCGGGGAG CTC   ACACCG
                                     A  AGGC
GAM1362 FEM-2   3' GCCACAGTCCCATGAGGGCC  28316     C  C_   AA
                                GGCCC TC  GGGA  CTGTGGC
                                ||||| ||  ||||  |||||||
                                CCGGG AG  CCCT  GACACCG
                                  _ TA   __
GAM1362 FLJ10199 3' GCCACAGTTGAGAAGCGGAGGG 71755          GGA___
           GCCA                   TGGCCCCTCCG     AACTGTGGC
                                ||||||||||     |||||||||
                                ACCGGGGAGGC     TTGACACCG
                                     GAAGAG
GAM1362 FLJ11715 3' ACAGTGTCCCCAGGAGGCCAT  44972       _  CC   A
                                ATGGCC CCT  GGGA ACTGT
                                |||||| |||  |||| |||||
                                TACCGG GGA  CCCT TGACA
                                   A  C_   G
GAM1362 FLJ12505 5' CCCGGTCCCGGAGCAGCCA   45713     CC      AA  T
                                TGGC  CTCCGGGA  CTG GG
                                ||||  ||||||||  ||| ||
                                ACCG  GAGGCCCT  GGC CC
                                  AC       __  _
GAM1362 KIAA0828 3' GTTTCCCAGGAAGGCCAT    82119       CC  _
                                ATGGCC  TCC GGGAAAC
                                ||||||  ||| |||||||
                                TACCGG  AGG CCCTTTG
                                   A_  A
GAM1362 KIAA1190 3' CCACAGTTCTGGGAGCC     71643     CCC  G   A
                                GGC   TCC GGAA CTGTGG
                                |||   ||| |||| ||||||
                                CCG   AGG TCTT GACACC
                                  ___   G   _
GAM1362 KIAA1297 5' CCATGCCCAGAAGGCCA     72634      CC  C   AAAC
                                TGGCC  TC GGG   TGTGG
                                |||||  || |||   |||||
                                ACCGG  AG CCC   GTACC
                                  A_  A  ____
GAM1362 PASK    5' GCCACAGAGTTGGGGGGCCAT  31415        T   GAAA
                                ATGGCCCC CCGG   CTGTGGC
                                |||||||| ||||   |||||||
                                TACCGGGG GGTT   GACACCG
                                    _   GA__
GAM1362 PCDH17  3' GCCACAGTTCCCTGCAGCCA   27836     CCCTC   A
                                TGGC    CGGG AACTGTGGC
                                ||||    |||| |||||||||
                                ACCG    GTCC TTGACACCG
                                  AC___   C
GAM1362 RIL     3' CCATGCTGCCCTGAAGGGGCCA 14885        C   AAACT
                                TGGCCCCT CGGG   GTGG
                                |||||||| ||||   ||||
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                                ACCGGGGA GTCC    TACC
                                    A   CGTCG
GAM1362  SREC     3'  GCAGTGCTCCCGGAGGGGCC  14905          A_
                                GGCCCCTCCGGGA  ACTGT
                                ||||||||||||  |||||
                                CCGGGGAGGCCCT  TGACG
                                     CG
GAM1362  TRAF2    3'  GCCGGCTCACGGAGGGGCCA  41236         G  AACTG
                                TGGCCCCTCCG GA    TGGC
                                |||||||||| ||    ||||
                                ACCGGGGAGGC CT    GCCG
                                      A  CG___
GAM1362  LOC123242 5'  CCACAGCCCACCTGGAGGCCA  76111      CC     AAA_
                                TGGCC  TCCGGG   CTGTGG
                                |||||  ||||||   ||||||
                                ACCGG  AGGTCC   GACACC
                                  __     ACCC
GAM1362  LOC124460 5'  CCAAGAGCTCGAAGGGGCCAT  76559        C   AAA  G
                                ATGGCCCCT CGGG   CT TGG
                                |||||||| ||||   || |||
                                TACCGGGGA GCTC   GA ACC
                                     A   GA_  _
GAM1362  LOC132166 3'  GCCAGCGCCCGAGGGGGCCA  75537       TC   AAACTG
                                TGGCCCC  CGGG     TGGC
                                |||||||  ||||     ||||
                                ACCGGGG  GCCC     ACCG
                                    GA   GCG___
GAM1362  LOC146958 5'  GCCACAGTCTCAAGTGGACAT  84944     G  C  CC   AA
                                ATG CC CT  GGGA  CTGTGGC
                                ||| || ||  ||||  |||||||
                                TAC GG GA  CTCT  GACACCG
                                  A  T  A_   __
GAM1362  LOC149420 3'  GCCACAGTTTCCTAAGCGC   80155    CC  CC
                                GC  CT  GGGAAACTGTGGC
                                ||  ||  ||||||||||||||
                                CG  GA  TCCTTTGACACCG
                                 C_  A_
GAM1362  LOC152317 3'  GCCACAGTCTGGGAGAGCCA  86831     CC   G   AA
                                TGGC  CTCC GGA  CTGTGGC
                                ||||  |||| |||  |||||||
                                ACCG  GAGG TCT  GACACCG
                                  A_   G   __
GAM1362  LOC157450 3'  CCACAGCTTCCCGGGTCAT   71531       CTCC    A
                                ATGGCCC   GGGAA CTGTGG
                                |||||||   ||||| ||||||
                                TACTGGG   CCCTT GACACC
                                    _____    C
GAM1362  LOC157807 5'  GCCACAGTTTCAGCAGACCAT  82513     CCC  CCGG
                                ATGG   CT   GAAACTGTGGC
                                ||||   ||   ||||||||||
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                                TACC   GA    CTTTGACACCG
                                  A__  CGA_
GAM1362  LOC157923 5'  GCCACAGTCCAGAGAAGGCCA  82526      C_   C  GAA
                                TGGCC  CTC GG   ACTGTGGC
                                |||||  ||| ||   ||||||||
                                ACCGG  GAG CC   TGACACCG
                                   AA   A  ___
GAM1362  LOC158510 5'  CCAGAGGCCCCCGGAGGAGC   82833    C       AAA  G
                                GC CCTCCGGG   CT TGG
                                || ||||||||   || |||
                                CG GGAGGCCC   GA ACC
                                 A       CCG  G
GAM1362  LOC196860 3'  CCACAGTTCCCCGGAAAGTGCT 91214     CCC_     A
                                GGC    TCCGGG AACTGTGG
                                |||    |||||| ||||||||
                                TCG    AGGCCC TTGACACC
                                  TGAA     C
GAM1362  LOC203235 5'  GCCAGGGCCCCCAGAGGGGCC  92099        C   AAA  G
                                GGCCCCTC GGG   CT TGGC
                                |||||||| |||   || ||||
                                CCGGGGAG CCC   GG ACCG
                                     A   CC_  G
GAM1362  LOC220739 3'  GCCACAGTAGGAGGGGCCA    94521          GGGAA
                                TGGCCCCTCC     ACTGTGGC
                                ||||||||||     ||||||||
                                ACCGGGGAGG     TGACACCG
                                     A_____
GAM1362  LOC222166 5'  CCCGGCCCCGGAGGAGCC     95733     C       AAA   T
                                GGC CCTCCGGG   CTG GG
                                ||| ||||||||   ||| ||
                                CCG GGAGGCCC   GGC CC
                                  A       C__   _
GAM1362  LOC253001 5'  CCACAGCCCACCTGGAGGCCA  97990      CC     AAA_
                                TGGCC  TCCGGG    CTGTGG
                                |||||  ||||||    ||||||
                                ACCGG  AGGTCC    GACACC
                                   __      ACCC
GAM1362  LOC254057 3'  GCCCCTATCCCAGAGGGGCC   98782        C    AACTGT
                                GGCCCCTC GGGA      GGC
                                |||||||| ||||      |||
                                CCGGGGAG CCCT      CCG
                                     A    ATCC__
GAM1362  LOC92558  3'  GCCACCTCCCAGAGGGGCC    70312        C    AACT
                                GGCCCCTC GGGA    GTGGC
                                |||||||| ||||    |||||
                                CCGGGGAG CCCT    CACCG
                                     A    C___
GAM1362  LOC93626  5'  CCACAGCCCCGGGGGCCG     73128        TC    AAA
                                TGGCCCC  CGGG   CTGTGG
                                |||||||  ||||   ||||||
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                                GCCGGGG  GCCC   GACACC
                                   __    C__
GAM1363  BCAS2    3'  CTGTACAGTTATCATTATC   20797       A       G
                                GATAAT GTAATTGTG CAG
                                |||||| ||||||||| |||
                                CTATTA TATTGACAT GTC
                                   C       _
GAM1363  CHAC     3'  GCCACCAAGTTACTATTA    53956          __
                                TAATAGTAATT  GTGGC
                                ||||||||||  |||||
                                ATTATCATTGA  CACCG
                                      AC
GAM1363  IL13RA1  3'  GCCATTTTTACTGTTATC    9572           TT
                                GATAATAGTAA  GTGGC
                                ||||||||||  |||||
                                CTATTGTCATT  TACCG
                                      TT
GAM1363  PCDH11X  3'  GCTATGGTATTACTATATC   53136     A    __  TG
                                GATA TAGTA  AT  TGGC
                                |||| |||||  ||  ||||
                                CTAT ATCAT  TG  ATCG
                                   _    TA  GT
GAM1363  PCDH11X  3'  GCTATGGTATTACTATATC   53143     A    __  TG
                                GATA TAGTA  AT  TGGC
                                |||| |||||  ||  ||||
                                CTAT ATCAT  TG  ATCG
                                   _    TA  GT
GAM1363  PCDH11Y  3'  GCTATGGTATTACTATATC   53188     A    __  TG
                                GATA TAGTA  AT  TGGC
                                |||| |||||  ||  ||||
                                CTAT ATCAT  TG  ATCG
                                   _    TA  GT
GAM1363  RB1      3'  GCTATGTTACTATTTTC     92554    T       T
                                GA AATAGTAAT GTGGC
                                || ||||||||| |||||
                                CT TTATCATTG TATCG
                                 T       _
GAM1363  SFTPA2   3'  GCTGTCACAATTATTACCATC 23629     AA
                                GAT  TAGTAATTGTGGCAGC
                                |||  ||||||||||||||||
                                CTA  ATTATTAACACTGTCG
                                  CC
GAM1363  SLC21A3  5'  GCTATGTTACTATCATC     57060     A       T
                                GAT ATAGTAAT GTGGC
                                ||| |||||||| |||||
                                CTA TATCATTG TATCG
                                  C       _
GAM1363  SRRM1    3'  GCTGCCACAACCACATTA    20697     A  AA
                                TAAT GT  TTGTGGCAGC
                                |||| ||  ||||||||||
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                                ATTA CA  AACACCGTCG
                                  _ CC
GAM1363 UBL3    3' GCTGCCACAAAATTTTCATC  24024    AAT  AA
                                GAT  AGT  TTGTGGCAGC
                                |||  |||  ||||||||||
                                CTA  TTA  AACACCGTCG
                                  CTT  A_
GAM1363 AKT3    3' GCTACTGTCTTACTATTAT   19607       TT__
                                ATAATAGTAA   GTGGC
                                ||||||||||   |||||
                                TATTATCATT   CATCG
                                     CTGT
GAM1363 AMOT    3' GCTACACAGTCTCCTATTATC 56546       TA_    GC
                                GATAATAG  ATTGTG  AGC
                                ||||||||  ||||||  |||
                                CTATTATC  TGACAC  TCG
                                    CTC    A_
GAM1363 APOARGC 3' GCCGCGCCTCTGACTATTATC 44676       AAT___
                                GATAATAGT    TGTGGC
                                |||||||||    ||||||
                                CTATTATCA    GCGCCG
                                     GTCTCC
GAM1363 COP     3' CTCCCAATTACTATTTTC    54667    T       T  C
                                GA AATAGTAATTG GG AG
                                || ||||||||||| || ||
                                CT TTATCATTAAC CC TC
                                 T        _ _
GAM1363 FLJ12888 3' GCTAATTTATAATTACTATTAT 46890            C__
            T                    GATAATAGTAATTGTGG  AGC
                                 ||||||||||||||||  |||
                                 TTATTATCATTAATATT  TCG
                                          TAA
GAM1363 FLJ13940 3' GCTGCCATTGCTGCCATC   47308    AA   ATT
                                GAT  TAGTA  GTGGCAGC
                                |||  |||||  ||||||||
                                CTA  GTCGT  TACCGTCG
                                  CC   ___
GAM1363 FLJ21551 3' CTGCAGCTTTATTATTA    46037       TT  G
                                TAATAGTAA  GT GCAG
                                |||||||||  || ||||
                                ATTATTATT  CG CGTC
                                     T_  A
GAM1363 FLJ22009 5' CTACCACAATCTGTTGTC   60918       TA     C
                                GATAATAG  ATTGTGG AG
                                ||||||||  ||||||| ||
                                CTGTTGTC  TAACACC TC
                                    __      A
GAM1363 FLJ23309 3' GCTGCCATCTGGGCTATTCC  46590   T    AATT
                                A AATAGT   GTGGCAGC
                                | ||||||   ||||||||
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                                C TTATCG   TACCGTCG
                                 C     GGTC
GAM1363 HAPIP    3' GCTGAACATTTCTATTATC   15466       T T  GG
                                GATAATAG AA TGT  CAGC
                                |||||||| || |||  ||||
                                CTATTATC TT ACA  GTCG
                                     _ T   A_
GAM1363 HSPC155  3' GCTACGATACTATTTTC    33521    T     A
                                GA AATAGTA TTGTGGC
                                || ||||||| |||||||
                                CT TTATCAT AGCATCG
                                 T     _
GAM1363 KIAA1596 5' GCTGCCACATGTACTATT    71480       AT
                                AATAGTA  TGTGGCAGC
                                |||||||  |||||||||
                                TTATCAT  ACACCGTCG
                                    GT
GAM1363 KPNA6    3' GCTGCCTCTCCTATTATCTATT 25543       _   TGT___
             ATC                   GATAATAG TAAT     GGCAGC
                                |||||||| ||||     ||||||
                                CTATTATC ATTA     CCGTCG
                                     T   TCCTCT
GAM1363 PPM1A    3' CTGCCACATTTTTGCTAT    41007       T__
                                ATAGTAA   TGTGGCAG
                                |||||||   ||||||||
                                TATCGTT   ACACCGTC
                                    TTT
GAM1363 PRO2405  5' GCTGTGATTCACTATTATT   38417        _  TG
                                GATAATAGT AAT  TGGC
                                ||||||||| |||  ||||
                                TTATTATCA TTA  GTCG
                                     C   GT
GAM1363 SLC2A10  3' CTACCTGTTACTATTATC    48549         T_
                                GATAATAGTAAT  GTGG
                                ||||||||||||  ||||
                                CTATTATCATTG  CATC
                                       TC
GAM1363 SNX11    3' GCTGCCATATTGAACATC    26172     AATAG   T
                                GAT    TAAT GTGGCAGC
                                |||    |||| ||||||||
                                CTA    GTTA TACCGTCG
                                  CAA__   _
GAM1363 SYNJ2    3' GCCCTATCAATTACTATAATC  62419     A       T___
                                GAT ATAGTAATTG   GGC
                                ||| ||||||||||   |||
                                CTA TATCATTAAC   CCG
                                  A        TATC
GAM1363 USP15    3' GCTGCCGTATATACTACTAT   21963     A    AT
                                ATA TAGTA  TGTGGCAGC
                                ||| |||||  |||||||||
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                                TAT ATCAT  ATGCCGTCG
                                  C    AT
GAM1363  WNT2B    3'  GCTACCACATTCTATTATT   16083       TAAT    C
                                GATAATAG   TGTGG AGC
                                ||||||||   ||||| |||
                                TTATTATC   ACACC TCG
                                    TT__    A
GAM1363  WNT2B    3'  GCTACCACATTCTATTATT   44680       TAAT    C
                                GATAATAG   TGTGG AGC
                                ||||||||   ||||| |||
                                TTATTATC   ACACC TCG
                                    TT__    A
GAM1363  LOC124151 3'  CTGCCACAATTGCTTTGATTAT 74729      ___
              T                  GATAAT   AGTAATTGTGGCAG
                                ||||||  ||||||||||||||
                                TTATTA   TCGTTAACACCGTC
                                   GTT
GAM1363  LOC143916 3'  GCTGGGGTGATTACCCTTATC  77142      TA    TG GG
                                GATAA  GTAAT  T  CAGC
                                |||||  |||||  |  ||||
                                CTATT  CATTA  G  GTCG
                                  CC    GT GG
GAM1363  LOC152286 5'  GCTGCCACCGCTACCATC    86810    AA   AATT
                                GAT  TAGT   GTGGCAGC
                                |||  ||||   ||||||||
                                CTA  ATCG   CACCGTCG
                                  CC   C___
GAM1363  LOC152348 3'  GCTGATTACTGTTATC     86880          GT
                                GATAATAGTAATT  GGC
                                ||||||||||||  |||
                                CTATTGTCATTAG  TCG
                                       __
GAM1363  LOC160820 5'  GCCTCTGATTACTATTACC   88444   A       GT_
                                G TAATAGTAATT   GGC
                                | ||||||||||   |||
                                C ATTATCATTAG   CCG
                                 C         TCT
GAM1363  LOC203536 3'  GCTCAATTACTATTTTC    90943    T       T
                                GA AATAGTAATTG GGC
                                || ||||||||||| |||
                                CT TTATCATTAAC TCG
                                  T        _
GAM1363  LOC219294 3'  GCTGCCACAGTCCCACTTC   94596   T   A__
                                A AGT   ATTGTGGCAGC
                                | |||   ||||||||||
                                C TCA   TGACACCGTCG
                                 T   CCC
GAM1363  LOC219295 3'  GCTGCCACAGTCCCACTTC   94587   T   A__
                                A AGT   ATTGTGGCAGC
                                | |||   ||||||||||
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                                C TCA   TGACACCGTCG
                                 T   CCC
GAM1363  LOC219654 3'  GCTGCCACTGACAGTCATC    92937     A  A  AATT
                                GAT AT GT    GTGGCAGC
                                ||| || ||    ||||||||
                                CTA TG CA    CACCGTCG
                                  C  A  GT__
GAM1363  LOC253727 5'  GCTGCGCAATTACTACTAT    99277     A         G
                                ATA TAGTAATTGTG CAGC
                                ||| |||||||||| ||||
                                TAT ATCATTAACGC GTCG
                                  C         _
GAM1363  LOC255870 3'  GCTGCCACAACTGGCCATGTC  96312      ATA  AA_
                                GATA   GT   TTGTGGCAGC
                                ||||   ||   ||||||||||
                                CTGT   CG   AACACCGTCG
                                   AC_  GTC
GAM1363  LOC90120  5'  CTGCCACAAAGCTGCTTA    62213     _   AA
                                TAA TAGT  TTGTGGCAG
                                ||| ||||  |||||||||
                                ATT GTCG  AACACCGTC
                                  C   A_
GAM1363  LOC92095  3'  CTGCACAATTATACTATC    68653      ATA       G
                                GATA   GTAATTGTG CAG
                                ||||   ||||||||| |||
                                CTAT   TATTAACAC GTC
                                   CA_       _
GAM1363  LOC92096  3'  CTGCACAATTATACTATC    68655      ATA       G
                                GATA   GTAATTGTG CAG
                                ||||   ||||||||| |||
                                CTAT   TATTAACAC GTC
                                   CA_       _
GAM1364  FLJ22332  5'  GGAAAGAAAACTACATCACA   45637      G  A      _______
                                TGTG AT TAGTTTTC     CC
                                |||| || ||||||||     ||
                                ACAC TA ATCAAAAG     GG
                                  _  C       AAA___
GAM1365  AMACR     3'  TTGTATGCATGGAAACATGGA  69103      ATC        G
                                TCCAT   TCCATGCATG CGG
                                |||||   |||||||||| |||
                                AGGTA   AGGTACGTAT GTT
                                   CAA        _
GAM1365  BCL2L11   3'  TCGCCCAGAGATATGGA     57615         CA  CAT    G
                                TCCATATCTC  TG   GGCG A
                                ||||||||||  ||   |||| |
                                AGGTATAGAG  AC   CCGC T
                                      __  ____    G
GAM1365  BCL2L11   3'  TCGCCCAGAGATATGGA     57616         CA  CAT    G
                                TCCATATCTC  TG   GGCG A
                                ||||||||||  ||   |||| |
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                                AGGTATAGAG  AC   CCGC T
                                           __ ____   G
GAM1365  FGFR2   5' CGTCCACATGGAGATATGGA  5559          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                           __  T
GAM1365  FGFR2   5' CGTCCACATGGAGATATGGA  43633         CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                           __  T
GAM1365  FGFR2   5' CGTCCACATGGAGATATGGA  43638         CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                           __  T
GAM1365  FGFR2   5' CGTCCACATGGAGATATGGA  43642         CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                           __  T
GAM1365  FGFR2   5' CGTCCACATGGAGATATGGA  43652         CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                           __  T
GAM1365  FGFR2   5' CGTCCACATGGAGATATGGA  43665         CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                           __  T
GAM1365  FGFR2   5' CGTCCACATGGAGATATGGA  43674         CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                           __  T
GAM1365  FGFR2   5' CGTCCACATGGAGATATGGA  43678         CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                           __  T
GAM1365  FGFR2   5' CGTCCACATGGAGATATGGA  43763         CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                           __  T
GAM1365  FGFR2   5' CGTCCACATGGAGATATGGA  43767         CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
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                                AGGTATAGAGGTAC  ACC GC
                                       __   T
GAM1365  FGFR2    5'  CGTCCACATGGAGATATGGA   43771          CA  _
                                TCCATATCTCCATG  TGG CG
                                ||||||||||||||  ||| ||
                                AGGTATAGAGGTAC  ACC GC
                                       __   T
GAM1365  MAP3K14  3'  ATCCGCCACGTGAAGAGA    15541     CA  A
                                TCTC  TGC TGGCGGAT
                                ||||  ||| ||||||||
                                AGAG  GTG ACCGCCTA
                                  AA  C
GAM1365  KIAA0819  3'  CCCCAGCATCACAGGAGACATG 64330      A   _____   A  C
            GA                    TCCAT TCTCC   ATGC TGG GG
                                |||||  |||||   ||||  |||  ||
                                AGGTA  AGAGG   TACG ACC CC
                                   C    ACAC   _  _
GAM1365  PORIMIN  3'  CATACATGGAGTATGGA     54702       T     C
                                TCCATA CTCCATG ATG
                                ||||||  ||||||| |||
                                AGGTAT GAGGTAC TAC
                                   _     A
GAM1365  RDC1     3'  CCGGCACGGGATATGGA     72832        T  A  A
                                TCCATATC CC TGC TGG
                                ||||||||  ||  |||  |||
                                AGGTATAG  GG  ACG  GCC
                                     _  C  _
GAM1365  VEZATIN  3'  ATCCGCCACAACAGACAATG   34656    A_  CCA  CA
                                CAT  TCT   TG  TGGCGGAT
                                |||  |||   ||  ||||||||
                                GTA  AGA   AC  ACCGCCTA
                                  AC   CA_  __
GAM1365  LOC147645 5'  ATCCGCTGGTGGCAGAGACACG 79065    ATA   CA   AT__
            G                     CC   TCTC  TGC   GGCGGAT
                                ||   ||||  |||   |||||||
                                GG   AGAG  ACG   TCGCCTA
                                 CAC    __   GTGG
GAM1365  LOC199775 3'  TTGCTGCATCAGAGATATG   89726        C_    TG
                                CATATCTC  ATGCA  GCGG
                                ||||||||  |||||  ||||
                                GTATAGAG  TACGT  CGTT
                                     AC    __
GAM1365  LOC51279  3'  CCGCTATTAGAGTATGGA    33752       T  CATGC
                                TCCATA CTC    ATGGCGG
                                ||||||  |||    |||||||
                                AGGTAT GAG    TATCGCC
                                   _  AT___
GAM1366  BHLHB3   3'  GCCTACAAGGTGGCTCTT    48488      T      CAGCT
                                AAGAG CCACCTTG    GGT
                                |||||  ||||||||    |||
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                                TTCTC GGTGGAAC    CCG
                                  _       AT___
GAM1366  CDC20    5'  GCACCAACTGCAAGGACCCCTC 8833      TCCA       C
                                GAG    CCTTGCAG TGGTGC
                                |||    |||||||| ||||||
                                CTC    GGAACGTC ACCACG
                                  CCCA       A
GAM1366  FOXE1    5'  GCACCAGCGCGCAAGGGACCCT 16780     A    AC    A_
              T                  AAG GTCC  CTTGC  GCTGGTGC
                                ||| ||||  |||||  ||||||||
                                TTC CAGG  GAACG  CGACCACG
                                  C   __    CG
GAM1366  ITPKB    3'  GCCCTGTAAGATGGACTCTT   11065         C      CT
                                AAGAGTCCA CTTGCAG  GGT
                                |||||||| |||||||  |||
                                TTCTCAGGT GAATGTC  CCG
                                     A      __
GAM1366  LEP      3'  GCACCAGCTTCTCCAGGCTCTT 5862         CACCTTGC
                                AAGAGTC       AGCTGGTGC
                                |||||||       |||||||||
                                TTCTCGG       TCGACCACG
                                    ACCTCT__
GAM1366  RBP5     3'  CACCAGCTCACAGACGCTC    49797      CCAC  _  C
                                GAGT    CT TG AGCTGGTG
                                ||||    || || ||||||||
                                CTCG    GA AC TCGACCAC
                                  CA__  C  _
GAM1366  SHOX2    3'  GCAAAGCTACAACGATGGACTC 13125          CC_   C    GG
              TT                  AAGAGTCCA   TTG AGCT  TGC
                                |||||||||   ||| ||||  |||
                                TTCTCAGGT   AAC TCGA  ACG
                                     AGC   A    A_
GAM1366  SRR      3'  GCACCGGTAAGACAGAATCT   41967     G  CAC   GCA
                                AGA TC   CTT   GCTGGTGC
                                ||| ||   |||   ||||||||
                                TCT AG   GAA   TGGCCACG
                                  A  ACA   ___
GAM1366  C20orf150 3'  CACCAACTGTGCCGCTGGCTC  66005     T   CCTT_   C
                                GAG CCA     GCAG TGGTG
                                ||| |||     |||| |||||
                                CTC GGT     TGTC ACCAC
                                  _   CGCCG    A
GAM1366  CGRP-RCP  5'  GCTGGAAGGTGGACCCTT     27892      A        G
                                AAG GTCCACCTT CAGC
                                ||| ||||||||| ||||
                                TTC CAGGTGGAA GTCG
                                  C        G
GAM1366  DKFZP564O0823 3'  GCACCAGCCAGGCCAGAC    60258     CAC    CA
                                GTC   CTTG  GCTGGTGC
                                |||   ||||  ||||||||
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                                CAG   GGAC  CGACCACG
                                  ACC   __
GAM1366  FLJ14624  3'  CACCAGCAATATACTCTT    71844       CCACCT  CA
                                AAGAGT     TG  GCTGGTG
                                ||||||     ||  |||||||
                                TTCTCA     AT  CGACCAC
                                   T_____  AA
GAM1366  KIAA0063  5'  CACCAGAGAATAAGGTGGACCT 30253    A        CAG_
                                AG GTCCACCTTG    CTGGTG
                                || ||||||||||    ||||||
                                TC CAGGTGGAAT    GACCAC
                                 _        AAGA
GAM1366  KIAA0494  3'  CACCAGCTAGAAGTGGTCCCTC 29400     T__    C  GC
                                GAG   CCAC TT  AGCTGGTG
                                |||   |||| ||  ||||||||
                                CTC   GGTG AG  TCGACCAC
                                  CCT    A  A_
GAM1366  KIAA1303  3'  GCACCAGCATCCAGGTGCAC   66605    C     TGCA
                                GT CACCT    GCTGGTGC
                                || |||||    ||||||||
                                CA GTGGA    CGACCACG
                                 C    CCTA
GAM1366  MGC15476  3'  CACCTGGAAAGAAGGACTCTT  59605        AC   GCAGCT
                                AAGAGTCC  CTT     GGTG
                                ||||||||  |||     ||||
                                TTCTCAGG  GAA     CCAC
                                     AA   AGGT__
GAM1366  NYD-SP11  3'  GCACCAGTGTAATAAAGCTCT  50057      CCACC    G
                                AGAGT    TTGCA CTGGTGC
                                |||||    ||||| |||||||
                                TCTCG    AATGT GACCACG
                                   AAAT_    _
GAM1366  VAV3     3'  CACCTCAAAGTGTACTCTT   21476       C   C   CAGCT
                                AAGAGT CAC TTG    GGTG
                                |||||| ||| |||    ||||
                                TTCTCA GTG AAC    CCAC
                                   T   A   T____
GAM1366  WDF2     3'  CACTCGCAAGGGGACTCTT   54749        A     AGCT
                                AAGAGTCC CCTTGC   GGTG
                                |||||||| ||||||   ||||
                                TTCTCAGG GGAACG   TCAC
                                     _     C___
GAM1366  LOC113523 3'  CACCAAAATGTGGTGAACTCTT 73413       C    TT   GC_
                                AAGAGT CACC  GCA   TGGTG
                                |||||| ||||  |||   |||||
                                TTCTCA GTGG  TGT   ACCAC
                                   A   __   AAA
GAM1366  LOC124446 5'  GCACCAGCGGCGGCGGACCCT  74777    A   A  TT  A
                                AG GTCC CC  GC GCTGGTGC
                                || |||| ||  || ||||||||
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                                TC CAGG GG  CG CGACCACG
                                 C   C __  G
GAM1366  LOC132880 3'  GCACCAGCTGGAAAGACCCTT  75581     A  CACC  G
                                AAG GTC   TT CAGCTGGTGC
                                ||| |||   || ||||||||||
                                TTC CAG   AA GTCGACCACG
                                  C  A___  G
GAM1366  LOC143158 5'  GCACCAGCCAGGAGGACCCT  77000    A   A  TGCA
                                AG GTCC CCT   GCTGGTGC
                                || |||| |||   ||||||||
                                TC CAGG GGA   CGACCACG
                                 C   A  C___
GAM1366  LOC145757 3'  CACCAGTTTCCGATGGCTCT  77917     T  CC  C_
                                AGAG CCA  TTG  AGCTGGTG
                                |||| |||  |||  ||||||||
                                TCTC GGT  AGC  TTGACCAC
                                  _  __  CT
GAM1366  LOC205272 5'  GCACCAGCTAGAAAACCTCT  91065     TCCAC  TGC
                                AGAG   CT  AGCTGGTGC
                                ||||   ||  |||||||||
                                TCTC   GA  TCGACCACG
                                  CAAAA  ____
GAM1366  LOC90625  3'  CACCAGCTGACAATGGACT   64377      CC  _
                                AGTCCA  TTG CAGCTGGTG
                                ||||||  ||| |||||||||
                                TCAGGT  AAC GTCGACCAC
                                   __  A
GAM1366  LOC96652  3'  GCACCTCAGCAAGGTGAACCTC 66079     TC_     AGCT
            T                    AGAG  CACCTTGC   GGTGC
                                ||||  ||||||||   |||||
                                TCTC  GTGGAACG   CCACG
                                  CAA      ACT_
GAM1367  ABCC3    3'  CAGAACTGCACTCTTCAGGAA  39610       AG _  A
                                TTCCTGGA  G GTAG TTCTG
                                ||||||||  | |||| |||||
                                AAGGACTT  C CGTC AAGAC
                                     CT A   _
GAM1367  BCL6     3'  CAGAATCTACCCAAAGGA   58034     GGAA
                                TCCT   GGGTAGATTCTG
                                ||||   ||||||||||||
                                AGGA   CCCATCTAAGAC
                                  AA__
GAM1367  BCL6     3'  CAGAATCTACCCAAAGGA   9918      GGAA
                                TCCT   GGGTAGATTCTG
                                ||||   ||||||||||||
                                AGGA   CCCATCTAAGAC
                                  AA__
GAM1367  CASP7    5'  CAGAGAGCGCCCTCCAGGGA  8737        A  AGA
                                TTCCTGGA GGGT   TTCTG
                                |||||||| ||||  |||||
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                                AGGGACCT CCCG  GAGAC
                                    _   CGA
GAM1367  CASP7   5'  CAGAGAGCGCCCTCCAGGGA  54028       A   AGA
                                TTCCTGGA GGGT  TTCTG
                                |||||||| ||||  |||||
                                AGGGACCT CCCG  GAGAC
                                    _   CGA
GAM1367  CDC2    5'  CAGAGAGCGCCCTCCAGGGA  54132       A   AGA
                                TTCCTGGA GGGT  TTCTG
                                |||||||| ||||  |||||
                                AGGGACCT CCCG  GAGAC
                                    _   CGA
GAM1367  CFTR    3'  AATTTTTTCTCTAGGAA    6679        A  T
                                TTCCTGGA GGG AGATT
                                |||||||| ||| |||||
                                AAGGATCT CTT TTTAA
                                    _  T
GAM1367  CNGA3   3'  CAGAATCTGCTTCACAG    8939     GAA
                                CTG  GGGTAGATTCTG
                                |||  ||||||||||||
                                GAC  TTCGTCTAAGAC
                                  AC_
GAM1367  CRY2    3'  CAGAACACCATTCCTTCCAGGA 72657          TAGA__
           G                     TTCCTGGAAGGG    TTCTG
                                ||||||||||||    |||||
                                GAGGACCTTCCT    AAGAC
                                      TACCAC
GAM1367  DLEC1   3'  AGTCTCCCTCCAGGAA     24713       A  T
                                TTCCTGGA GGG AGATT
                                |||||||| ||| |||||
                                AAGGACCT CCC TCTGA
                                    _  _
GAM1367  DLEC1   3'  AGTCTCCCTCCAGGAA     24726       A  T
                                TTCCTGGA GGG AGATT
                                |||||||| ||| |||||
                                AAGGACCT CCC TCTGA
                                    _  _
GAM1367  EFNA1   3'  AGATGCCCCCTCCAGGAG   16662       A_   GAT
                                TTCCTGGA  GGGTA  TCT
                                ||||||||  |||||  |||
                                GAGGACCT  CCCGT  AGA
                                    CC   ___
GAM1367  HDAC5   3'  CAGAACCCAGGGATCCAGGAG  58297       A____   AGAT
                                TTCCTGGA   GGGT   TCTG
                                ||||||||   ||||   ||||
                                GAGGACCT   CCCA   AGAC
                                    AGGGA   ____
GAM1367  HSPA5   3'  CAGAATCTCCATCCCTGAA   19280    CT  AG  T
                                TTC  GGA  GG AGATTCTG
                                |||  |||  || ||||||||
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                                AAG  CCT  CC TCTAAGAC
                                  TC   A_  _
GAM1367 KNG     3' CAGAATCTTCACTCCAGG    7983       AG  T
                                CCTGGA  GG AGATTCTG
                                ||||||  || ||||||||
                                GGACCT  CT TCTAAGAC
                                   CA  _
GAM1367 MAP3K14  3' CAGAATGCCTCCCAGGA    15542      AA   AG
                                TCCTGG  GGGT  ATTCTG
                                ||||||  ||||  ||||||
                                AGGACC  TCCG  TAAGAC
                                   C_   __
GAM1367 MECP2    3' GGGGTCCCCTCCAGGAG    18410       A   TA
                                TTCCTGGA GGG  GATTCT
                                |||||||| |||  ||||||
                                GAGGACCT CCC  CTGGGG
                                   _   __
GAM1367 MJD     3' AATTAACCTTTCAGGAA    18420         GTA
                                TTCCTGGAAGG   GATT
                                ||||||||||   ||||
                                AAGGACTTTCC   TTAA
                                      AA_
GAM1367 MJD     3' AATTAACCTTTCAGGAA    48398         GTA
                                TTCCTGGAAGG   GATT
                                ||||||||||   ||||
                                AAGGACTTTCC   TTAA
                                      AA_
GAM1367 MTL5     5' CAGAATCTTCTTGCTCAGGAA 18197       AA   T
                                TTCCTGG  GGG AGATTCTG
                                |||||||  ||| ||||||||
                                AAGGACT  TTC TCTAAGAC
                                   CG   T
GAM1367 NXF2     5' CAGAATCCGGCTCCAGGAA   35599       AGG  A_
                                TTCCTGGA   GT  GATTCTG
                                ||||||||   ||  |||||||
                                AAGGACCT   CG  CTAAGAC
                                    ____  GC
GAM1367 SLC1A5   3' CAGAAACACTCCCAGGGA    20066       AA   AGA
                                TTCCTGG  GGGT   TTCTG
                                |||||||  ||||   |||||
                                AGGGACC  CTCA   AAGAC
                                    __    CA_
GAM1367 SLC1A5   3' CAGAAACACTCCCAGGGA    79236       AA   AGA
                                TTCCTGG  GGGT   TTCTG
                                |||||||  ||||   |||||
                                AGGGACC  CTCA   AAGAC
                                    __    CA_
GAM1367 TR2      5' CAGAAGCTCCTTCAGGAA    72777        A   AGA
                                TTCCTGGA GGGT   TTCTG
                                |||||||| ||||   |||||
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                                AAGGACTT CTCG   AAGAC
                                    C   ___
GAM1367 UGT2B15  3' AATTTATTTTCCAGGGA    60701         G
                                TTCCTGGAAGG TAGATT
                                |||||||||| ||||||
                                AGGGACCTTTT ATTTAA
                                                _
GAM1367 C20orf85 3' CAGCGTCACCCTTCCAG    75261         A  T
                                CTGGAAGGGT GAT CTG
                                ||||||||| ||| |||
                                GACCTTCCCA CTG GAC
                                      _  C
GAM1367 FLJ10539 5' CAGATTAACCCTTCCTGGAA  36760    T      A  T
                                TTCC GGAAGGGT GAT CTG
                                |||| |||||||| ||| |||
                                AAGG CCTTCCCA TTA GAC
                                  T       A  _
GAM1367 FLJ22160 5' CAGAATCTGAACCCAGGAA   45031       AAGGG
                                TTCCTGG    TAGATTCTG
                                |||||||    |||||||||
                                AAGGACC    GTCTAAGAC
                                    CAA__
GAM1367 FSCN3    3' AATCCAAATCCTCCAGGAA   40157       A   A__
                                TTCCTGGA GGGT   GATT
                                |||||||| ||||   ||||
                                AAGGACCT CCTA   CTAA
                                    _   AAC
GAM1367 FYCO1    3' CAGAACCACTCCTCCAGGAG  44767       A   AGA
                                TTCCTGGA GGGT   TTCTG
                                |||||||| ||||   |||||
                                GAGGACCT CTCA   AAGAC
                                    C   CC_
GAM1367 GFRA4    3' CAGAATCCCAGAATTCTAGGAA 42419       GGGTA_
                                TTCCTGGAA     GATTCTG
                                |||||||||     |||||||
                                AAGGATCTT     CTAAGAC
                                     AAGACC
GAM1367 KIAA0110 3' CAGAATTTTTACCAGGAA    28280       AAGGGT
                                TTCCTGG     AGATTCTG
                                |||||||     ||||||||
                                AAGGACC     TTTAAGAC
                                    ATT___
GAM1367 KIAA0337 3' GGAAGCCCCTTCAGGAA     29479       A   AGA
                                TTCCTGGA GGGT   TTCT
                                |||||||| ||||   ||||
                                AAGGACTT CCCG   AAGG
                                    C   ___
GAM1367 KIAA0889 3' CAGCATCCCCTCCAGGGA    31762       A  TA  T
                                TTCCTGGA GGG  GAT CTG
                                |||||||| |||  ||| |||
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                                AGGGACCT CCC  CTA GAC
                                   _  __  C
GAM1367 KIAA0998 3' CAGAATCATACTCTCCAGGAA 31256       A   _
                                TTCCTGGA GGGTA GATTCTG
                                |||||||| ||||| |||||||
                                AAGGACCT CTCAT CTAAGAC
                                   _    A
GAM1367 KIAA1036 3' CAGAATCTTGACCCAGGGA   30486      AAGGGT
                                TTCCTGG     AGATTCTG
                                |||||||     ||||||||
                                AGGGACC     TCTAAGAC
                                    CAGT__
GAM1367 KIAA1171 3' CAGAGGGAGCCCTCCAGGAG  89338       A   AGA
                                TTCCTGGA GGGT   TTCTG
                                |||||||| ||||   |||||
                                GAGGACCT CCCG   GAGAC
                                   _   AGG
GAM1367 KIAA1862 3' CAGAGGGCCCTCCAGGAA    69502       A   AGAT
                                TTCCTGGA GGGT   TCTG
                                |||||||| ||||   ||||
                                AAGGACCT CCCG   AGAC
                                   _   GG__
GAM1367 MGC2848  3' AGAATCTCTGCAGGAA      52997      GA  GGT
                                TTCCTG  AG   AGATTCT
                                ||||||  ||   |||||||
                                AAGGAC  TC   TCTAAGA
                                   G_  ___
GAM1367 MGC4309  3' CAGAATCTAAGCAGGAA     44367      GAAGGG
                                TTCCTG     TAGATTCTG
                                ||||||     |||||||||
                                AAGGAC     ATCTAAGAC
                                   GA____
GAM1367 NEUROD4  5' CAGAGTTCACTCCAGGAA    41332       AGG  AG
                                TTCCTGGA   GT  ATTCTG
                                ||||||||   ||  ||||||
                                AAGGACCT   CA  TGAGAC
                                    ___  CT
GAM1367 NYD-SP21 3' CAGAATCTACCCAATACCA   51862     AA__
                                TGG   GGGTAGATTCTG
                                |||   ||||||||||||
                                ACC   CCCATCTAAGAC
                                  ATAA
GAM1367 PRKRI    5' AATCACCCCTTCCAGGAA    21826         TA
                                TTCCTGGAAGGG  GATT
                                ||||||||||||  ||||
                                AAGGACCTTCCC  CTAA
                                      CA
GAM1367 SEC24D   3' CAGAATAACTTTCCAGGAA   29751         GTAG
                                TTCCTGGAAGG   ATTCTG
                                ||||||||||    ||||||
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                                AAGGACCTTTC    TAAGAC
                                      AA__
GAM1367  ZAP3     5'  CTACACCTCCTCCAGGAA    77734        __  _
                                TTCCTGGA  AGG GTAG
                                ||||||||  ||| ||||
                                AAGGACCT  TCC CATC
                                     CC   A
GAM1367  LOC122618 3'  CAGGGAGCCCTCCAGGAA    57901        A   AGA
                                TTCCTGGA GGGT   TTCTG
                                ||||||||| ||||   |||||
                                AAGGACCT CCCG   GGGAC
                                     _    A__
GAM1367  LOC147632 5'  CAGAATCTATATCCTCAGGAA  57469       AAGG
                                TTCCTGG    GTAGATTCTG
                                |||||||    ||||||||||
                                AAGGACT    TATCTAAGAC
                                     CCTA
GAM1367  LOC151701 3'  AGAGCACCTTCCGGAA      86665      T     _  AGAT
                                TTCC GGAAGG GT    TCT
                                |||| |||||| ||    |||
                                AAGG CCTTCC CG    AGA
                                   _      A  _____
GAM1367  LOC152300 5'  CAGAATCCAAGATCTGCCAGGA 81381        A   GTA__
              A                  TTCCTGG AGG     GATTCTG
                                 ||||||| |||     |||||||
                                 AAGGACC TCT     CTAAGAC
                                     G   AGAAC
GAM1367  LOC158267 3'  CAGATGCCCCTTCTAGGAA    82721          TAGAT
                                TTCCTGGAAGGG     TCTG
                                ||||||||||||     ||||
                                AAGGATCTTCCC     AGAC
                                       CGT__
GAM1367  LOC158969 3'  CGGGGGTCCTCCAGGAG     82934        A   TAGA
                                TTCCTGGA GGG    TTCTG
                                |||||||| |||    |||||
                                GAGGACCT CCT    GGGGC
                                     _   G___
GAM1367  LOC202266 3'  AATTGGCCTTCAGGAA      91935        AA   A
                                TTCCTGG  GGGT GATT
                                |||||||  |||| ||||
                                AAGGACT  TCCG TTAA
                                     __    G
GAM1367  LOC257418 5'  CAGAACATTTTCCAGGA     99423         GTAGA
                                TCCTGGAAGG     TTCTG
                                ||||||||||     |||||
                                AGGACCTTTT     AAGAC
                                       AC___
GAM1367  LOC90538  3'  CAGATGCTCTTTCCAG      63897        _   GAT
                                CTGGAAGG GTA   TCTG
                                |||||||| |||   ||||
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                                GACCTTTC CGT   AGAC
                                    T  ___
GAM1367 LOC91056 3' CAGAATCTCTGCCCAGGAG   96402       AA  GT
                                TTCCTGG  GG  AGATTCTG
                                |||||||  ||  ||||||||
                                GAGGACC  TC  TCTAAGAC
                                   CG  __
GAM1367 LOC93097 5' CAGAACACAGGTTCCAGGAG  71880        GG_  AGA
                                TTCCTGGAA  GT  TTCTG
                                |||||||||  ||  |||||
                                GAGGACCTT  CA  AAGAC
                                     GGA  C__
GAM1368 DSC1    3'  TGTTTATGGAGGTAAACTTTGT 18246    T    G_   G
            CA                    TG CAAAGT  ACTT CCATAAACA
                                || ||||||  |||| |||||||||
                                AC GTTTCA  TGGA GGTATTTGT
                                 T     AA   _
GAM1368 DSC1    3'  TGTTTATGGAGGTAAACTTTGT 44609    T    G_   G
            CA                    TG CAAAGT  ACTT CCATAAACA
                                || ||||||  |||| |||||||||
                                AC GTTTCA  TGGA GGTATTTGT
                                 T     AA   _
GAM1368 HIF1A   3'  TGTTTCTATAGTCACTTTGCCA 9515     T       TGCCAT
                                TG CAAAGTGACT     AAACA
                                || ||||||||||     |||||
                                AC GTTTCACTGA     TTTGT
                                 C        TATC__
GAM1368 HS2ST1  3'  TTTATGGCACAGTTTGGACA  25332     AAAGT   _
                                TGTC    GACT TGCCATAAA
                                ||||    |||| |||||||||
                                ACAG    TTGA ACGGTATTT
                                  GT___    C
GAM1368 TIMM17A  3'  TGTTTATAGTTTACTTTGA   22016        CTT  C
                                TCAAAGTGA   GC ATAAACA
                                |||||||||   || |||||||
                                AGTTTCATT   TG TATTTGT
                                     ___  A
GAM1368 ZNF215   3'  TGTTTATAGCAGGTCCTTGA  26036     A T     C
                                TCAA G GACTTGC ATAAACA
                                |||| | ||||||| |||||||
                                AGTT C CTGGACG TATTTGT
                                  _ _      A
GAM1368 C8orf4   3'  TTTATCCAGGGTCACTTTGTCA 39693    T        GCC
                                TG CAAAGTGACTT   ATAAA
                                || ||||||||||   |||||
                                AC GTTTCACTGGG   TATTT
                                 T         ACC
GAM1368 DKFZp761D0614 3'  TGTCTCAAAACACTTTGACA   88948         AC   CC
                                TGTCAAAGTG  TTG  ATA
                                |||||||||  |||  |||
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                                ACAGTTTCAC  AAC  TGT
                                      AA   TC
GAM1368  EAT2     3'  TTATGCATCAGTCATTTCAACA 80056     CA       __   C
                                TGT  AAGTGACT  TGC ATAA
                                |||  ||||||||  ||| ||||
                                ACA  TTTACTGA  ACG TATT
                                  AC       CT  _
GAM1368  FLJ14600 3'  TGTTTATGGTTTTATACTCTGA 52529     A    ACTT
                                TCA AGTG    GCCATAAACA
                                |||  ||||    ||||||||||
                                AGT TCAT    TGGTATTTGT
                                  C    ATTT
GAM1368  HMGN4    3'  GTGTCAGCCACTTTGGCA    22032          A  T C
                                TGTCAAAGTG CT G CAT
                                |||||||||| || | |||
                                ACGGTTTCAC GA C GTG
                                      C  _ T
GAM1368  KIAA1069 3'  TGACAATGTCACTTTAACA   68534     C       _   C
                                TGT AAAGTGAC TTG CA
                                |||  |||||||| ||| ||
                                ACA TTTCACTG AAC GT
                                  A       T   A
GAM1368  KIAA1253 3'  TGTTTGAAAGTCACTTTGA   93552           GCCA
                                TCAAAGTGACTT    TAAACA
                                ||||||||||||    ||||||
                                AGTTTCACTGAA    GTTTGT
                                      A___
GAM1368  KIAA1364 3'  TTTATGGCAGGTATGACA    64361       AAGTG
                                TGTCA    ACTTGCCATAAA
                                |||||    ||||||||||||
                                ACAGT    TGGACGGTATTT
                                   A____
GAM1368  MRPS10   3'  ATGAGCAAACCACTTTGAC    36813         AC   _
                                GTCAAAGTG  TTGC CAT
                                |||||||||  |||| |||
                                CAGTTTCAC  AACG GTA
                                      CA   A
GAM1368  PRO1430  3'  TTTATCCAGGGTCACTTTGTCA 38358    T         GCC
                                TG CAAAGTGACTT   ATAAA
                                || ||||||||||   |||||
                                AC GTTTCACTGGG   TATTT
                                  T         ACC
GAM1368  LOC128338 3'  TTTATGGCAAGTTATAATTACA 75254     CAAA
                                TGT    GTGACTTGCCATAAA
                                |||    |||||||||||||||
                                ACA    TATTGAACGGTATTT
                                  TTAA
GAM1368  LOC146159 5'  TGTGGCAAATCACTTTGCA    78182    T       C
                                TG CAAAGTGA TTGCCATA
                                || |||||||| ||||||||
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                                AC GTTTCACT AACGGTGT
                                 _       A
GAM1368  LOC154336 3'  TGTTTATGGCAAGCCACTTTGA 60099          A
                CA                    TGTCAAAGTG CTTGCCATAAACA
                                      |||||||||| ||||||||||||
                                      ACAGTTTCAC GAACGGTATTTGT
                                           C
GAM1368  LOC221474 5'  TTGGGGCAAGTCACTTTGAC   94005              A
                                      GTCAAAGTGACTTGCC TAA
                                      |||||||||||||||| |||
                                      CAGTTTCACTGAACGG GTT
                                               G
GAM1369  GPR81     3'  CCCAAGAAGAACAACAACAA   51741      GCTTA
                                      TTGT     TTCTTCTTGGG
                                      ||||     ||||||||||
                                      AACA     AAGAAGAACCC
                                        ACAAC
GAM1369  TMEFF2    3'  CAAAAGAATAAGACAAGAGA   32995        G       C
                                      TCTCTTGT CTTATTCTT TTG
                                      |||||||| ||||||||| |||
                                      AGAGAACA GAATAAGAA AAC
                                               _       _
GAM1369  FLJ20374  3'  CCAATAAAACAAGCACAA     35549        A  C  C
                                      TTGTGCTT TT TT TTGG
                                      |||||||| || || ||||
                                      AACACGAA AA AA AACC
                                           C  _  T
GAM1369  KIAA1560  3'  CCCTGCAGAAAATAAGCACAGA 64850     T       C    T__
                                      TCT GTGCTTATT TTCT   GGG
                                      ||| ||||||||| ||||   |||
                                      AGA CACGAATAA AAGA   CCC
                                        _       _    CGT
GAM1369  MGC2821   3'  CCCAAAGTAGAAAAAGCACAAG 44135          A    T   _
                AGA                      TCTCTTGTGCTT TTCT CTT GGG
                                         |||||||||||| |||| ||| |||
                                         AGAGAACACGAA AAGA GAA CCC
                                                A    T   A
GAM1369  MUC13     3'  CCCAAGAAGACTGGAAAGAGA  53508       GTG  TAT
                                      TCTCTT   CT   TCTTCTTGGG
                                      ||||||   ||   ||||||||||
                                      AGAGAA   GG   AGAAGAACCC
                                         A__  TC_
GAM1369  PCDH20    3'  CCCAAGAAAAACAGCCAGAAG  43419    CT  T   TATTC
                                      CT  TG GCT     TTCTTGGG
                                      ||  || |||     ||||||||
                                      GA  AC CGA     AAGAACCC
                                       AG  _   CAAA_
GAM1369  LOC168448 3'  CCCAAAAAGAATGACTCAAAGA 83582      GTGC       C
                                      TCTT    TTATTCTT TTGGG
                                      ||||    |||||||| |||||
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                                AGAA    AGTAAGAA AACCC
                                  ACTC       A
GAM1369  LOC254848 5'  CCCAAGAAGAACTTCCACAA   98881      CTTA
                                TTGTG    TTCTTCTTGGG
                                |||||    ||||||||||
                                AACAC    AAGAAGAACCC
                                   CTTC
GAM1369  LOC256401 3'  CCCAAAAAGAATGACTCAAAGA 97719      GTGC       C
                                TCTT    TTATTCTT TTGGG
                                ||||    |||||||| |||||
                                AGAA    AGTAAGAA AACCC
                                  ACTC       A
GAM1370  SCAMP1    3'  GCTAAATAAATATTCTCC    54500     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1370  SCAMP1    3'  GCTAAATAAATATTCTCC    54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1370  NX-17     3'  TGAATATCAGCCCCTAATA    40706        ATA_
                                TATTAGGG    ATATTCA
                                ||||||||    |||||||
                                ATAATCCC    TATAAGT
                                     CGAC
GAM1370  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
              TA                  TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM1371  KIAA0295  3'  CCAGGAAGCTTTCCAGTGATCT 68660     _    A
              C                   GAG TTACT GAAAGCTTCCTGG
                                ||| ||||| ||||||||||||
                                CTC AGTGA CTTTCGAAGGACC
                                  T    C
GAM1371  NYD-SP15  3'  CCAAAGCTTTCTAGTAATCA   48845     G          CC
                                TGA TTACTAGAAAGCTT  TGG
                                ||| ||||||||||||  |||
                                ACT AATGATCTTTCGAA  ACC
                                  _          __
GAM1371  UBN1      3'  CCAGGGTACAGCGCCCAGTAAC 34195        AGAAA  ___
              TCA                   TGAGTTACT    GCT   TCCTGG
                                |||||||||    |||  ||||||
                                ACTCAATGA    CGA   GGGACC
                                     CCCG_   CAT
GAM1371  LOC152445 3'  CCAGGAAGCTGAGAAAACTCA  86942       ACTAGAA
                                TGAGTT      AGCTTCCTGG
                                ||||||      ||||||||||
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                                ACTCAA      TCGAAGGACC
                                   AAGAG__
GAM1371  LOC153688 3'  TCCAGGAAGCCTTCTCAGCTT  87334      ACT   A
                                GAGTT   AGAA GCTTCCTGGA
                                |||||   |||| ||||||||||
                                TTCGA   TCTT CGAAGGACCT
                                   C__   C
GAM1371  LOC158263 3'  TCCAGGAAGCCTTCCTGCTC   82732     TACTA   A
                                GAGT    GAA GCTTCCTGGA
                                ||||    ||| ||||||||||
                                CTCG    CTT CGAAGGACCT
                                  TC___   C
GAM1371  LOC51161  3'  TCCAGGAGGTCTCCCAGCCACC 33045    A  TA  A_  AA
            CA                    TG GT  CT  GA  GCTTCCTGGA
                                || ||  ||  ||  ||||||||||
                                AC CA  GA  CT  TGGAGGACCT
                                 C  CC  CC  C_
GAM1372  BRF1     3'  CCCCGCCCAGAGCTCAGT    9503     C       AC  T A
                                AC GAGCTCTGG  GC G GG
                                || |||||||||  || | ||
                                TG CTCGAGACC  CG C CC
                                 A        __ _ C
GAM1372  CERD4    3'  TCCTCAGCATTAAAACTGGTG  24883      G  CTCTG  C
                                CACC AG    GA GCTGAGGA
                                |||| ||    || ||||||||
                                GTGG TC    TT CGACTCCT
                                  _  AAAA_  A
GAM1372  CNP      3'  TCTGCCCAGAGCTGGGTG    53625      G      AC  T
                                CACC AGCTCTGG  GC GA
                                |||| ||||||||  || ||
                                GTGG TCGAGACC  CG CT
                                  G       __ T
GAM1372  GARP     3'  CCAGGGCTCCAGAGCTCGG    19776          C   GA
                                CCGAGCTCTGGA GCT  GG
                                |||||||||||| |||  ||
                                GGCTCGAGACCT CGG  CC
                                       _  GA
GAM1372  IL13     3'  TCCAGGGCCCTGAGCTCGGTGG 10995          T  AC   GA
                                CCACCGAGCTC GG  GCT  GGA
                                |||||||||| ||  |||  |||
                                GGTGGCTCGAG CC  CGG  CCT
                                      T  __   GA
GAM1372  IRAK1    3'  TCCTCAGCACTCTGCCGG    9619      A  TCT   C_
                                CCG GC   GGA  GCTGAGGA
                                ||| ||   |||  ||||||||
                                GGC CG   TCT  CGACTCCT
                                  _ ____   CA
GAM1372  LHX1     5'  TCCTCGCAACCCGAGCTCGG   19919        T  AC  T
                                CCGAGCTC GG  GC GAGGA
                                |||||||| ||  || |||||
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                                GGCTCGAG CC  CG CTCCT
                                    C  AA  _
GAM1372 LTBP3    3'  CCTCGGCCCAGACCTCGGTG  41137       C    AC
                                CACCGAG TCTGG  GCTGAGG
                                ||||||| |||||  |||||||
                                GTGGCTC AGACC  CGGCTCC
                                    C    __
GAM1372 MAGEA3   5'  CGGCCCAGGCTCGGTG     19316        T   AC
                                CACCGAGC CTGG  GCTG
                                |||||||| ||||  ||||
                                GTGGCTCG GACC  CGGC
                                   _   __
GAM1372 MUS81    5'  TCCCGACTCCAGAACTGGCGG  47820    A  G  C     CGC  A
                                CC CC AG TCTGGA   TG GGA
                                || || || ||||||   || |||
                                GG GG TC AGACCT   GC CCT
                                 C  _  A     CA_  _
GAM1372 NAGLU    3'  TCCAGGGCCCAGAGCTGG    6042     G       AC   GA
                                CC AGCTCTGG  GCT  GGA
                                || ||||||||  |||  |||
                                GG TCGAGACC  CGG  CCT
                                 _       __   GA
GAM1372 PAEP     5'  CCTCTGGCTCCAGAGCTC    11954          C  _
                                GAGCTCTGGA GCT GAGG
                                |||||||||| ||| ||||
                                CTCGAGACCT CGG CTCC
                                     _  T
GAM1372 PSD      5'  CCGGGGCCCAGAGCTCTGTGG  12434     C       AC   GA
                                CCAC GAGCTCTGG  GCT  GG
                                |||| |||||||||  |||  ||
                                GGTG CTCGAGACC  CGG  CC
                                  T        __   GG
GAM1372 RRM2B    5'  CCTCAGCGCCCGTAGCTTCGGC 68432    A   _  C   A
              GG                    CC CCGA GCT TGG CGCTGAGG
                                || |||| ||| ||| ||||||||
                                GG GGCT CGA GCC GCGACTCC
                                 C   T  T  C
GAM1372 TNXB     5'  TCCTCTTCCAGAGCTCGCTG  51636    C        CGCT
                                CA CGAGCTCTGGA   GAGGA
                                || ||||||||||   |||||
                                GT GCTCGAGACCT   CTCCT
                                 C         T___
GAM1372 ZNF207   3'  CCCAACCTAGCTTGGTG     14373         CT  ACGC  A
                                CACCGAGCT  GG   TG GG
                                |||||||||  ||   || ||
                                GTGGTTCGA  CC   AC CC
                                     T_  A___  C
GAM1372 C22orf4  3'  TCCTCAGCGACCCACTGGTG  61276     G  CTC   A_
                                CACC AG   TGG  CGCTGAGGA
                                |||| ||   |||  |||||||||
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                                GTGG TC   ACC  GCGACTCCT
                                  _ ___   CA
GAM1372  CASPR3   3'  TCCTGGAATCCAGAGCCAAGTG 46416     CGA      CG  G
             G                   CCAC   GCTCTGGA  CT AGGA
                                 ||||   ||||||||  || ||||
                                 GGTG   CGAGACCT  GG TCCT
                                   AAC       AA  _
GAM1372  CCNB2    5'  TCCCCAGCGCTGCGGGCTCGG  17478        _  A    A
                                 CCGAGCTC TGG CGCTG GGA
                                 |||||||| ||| ||||| |||
                                 GGCTCGGG GTC GCGAC CCT
                                      C   _    C
GAM1372  CDCA4    5'  TCCTCAGCGGCGGGAAGCTGGC 36087    A  G   __   GA
             GG                    CC CC AGCT  CTG  CGCTGAGGA
                                   || || ||||  |||  |||||||||
                                   GG GG TCGA  GGC  GCGACTCCT
                                    C  _   AG   G_
GAM1372  DCNP1    3'  TCCTCAGCATCCACCCCGTG   56461    CGAGCTC    C
                                   CAC      TGGA GCTGAGGA
                                   |||      |||| ||||||||
                                   GTG      ACCT CGACTCCT
                                     CCCC___    A
GAM1372  DKFZP547L112 5'  CCTCAGCGCCCTGGACTGTGG  67127      CG  CT T  A
                                   CCAC  AG  C GG CGCTGAGG
                                   ||||  ||  | || ||||||||
                                   GGTG  TC  G CC GCGACTCC
                                     __  AG T  C
GAM1372  FGD3     3'  CCAACAGCCCAGAGCTCAGG   73278    _       AC    A_
                                   CC GAGCTCTGG  GCTG  GG
                                   || |||||||||  ||||  ||
                                   GG CTCGAGACC  CGAC  CC
                                    A        __    AA
GAM1372  FLJ10349  3'  TCCTCCCAGCCAGAGCTGGCGG 36535    A  G       ACGCT
                                   CC CC AGCTCTGG     GAGGA
                                   || || ||||||||     |||||
                                   GG GG TCGAGACC     CTCCT
                                    C  _       GACC_
GAM1372  FLJ12577  3'  TCCTCAGCATGGCCTCAGTGG  48887      C   CT TGGAC
                                   CCAC GAG  C     GCTGAGGA
                                   |||| |||  |     ||||||||
                                   GGTG CTC  G     CGACTCCT
                                     A   CG TA___
GAM1372  FLJ13842  5'  TCCTCAGCGTGCTCCAGC    45335     CT  _
                                   GCT  GG ACGCTGAGGA
                                   |||  || ||||||||||
                                   CGA  TC TGCGACTCCT
                                     CC  G
GAM1372  FLJ13941  3'  TCCCCGATTCTCCAGAGCCCCG 46273      CGA       CGC_  A
             TGG                     CCAC   GCTCTGGA    TG GGA
                                   ||||   ||||||||    || |||
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                                GGTG  CGAGACCT   GC CCT
                                  CCC      CTTA  C
GAM1372 FLJ22313 5' TCCACAGTCCGGAGCCCGGCGG 42581   A  A      GC  A
                                CC CCG GCTCTGGAC  TG GGA
                                || ||| |||||||||  || |||
                                GG GGC CGAGGCCTG  AC CCT
                                 C  C       __  A
GAM1372 FLJ22555 5' TCCTCAGCGCCATCCGCCCGG  44797    A  TC_  A
                                CCG GC   TGG CGCTGAGGA
                                ||| ||   ||| |||||||||
                                GGC CG   ACC GCGACTCCT
                                  C  CCT  _
GAM1372 GOLGA3   5' CCTCAGCGTCAGCTCAGCTGG  20886    CC_    CTG
                                CCA  GAGCT  GACGCTGAGG
                                |||  |||||  ||||||||||
                                GGT  CTCGA  CTGCGACTCC
                                  CGA   ____
GAM1372 IGF2AS   3'  TCCTCCCACACAGGCTCGGTGG 33533        T  GACGCT
                                CCACCGAGC CTG     GAGGA
                                ||||||||| |||     |||||
                                GGTGGCTCG GAC     CTCCT
                                     _  ACACC_
GAM1372 KCNT1    3'  CCCAGTCCCAGATCTCGGTG  62488       C    AC   A
                                CACCGAG TCTGG  GCTG GG
                                ||||||| |||||  |||| ||
                                GTGGCTC AGACC  TGAC CC
                                    T    C_   _
GAM1372 KIAA0042 5' TCCTCAGCATTCCAGGTCGGCG 30240    A   G T    C_
            G                    CC CCGA C CTGGA  GCTGAGGA
                                || |||| | |||||  ||||||||
                                GG GGCT G GACCT  CGACTCCT
                                 C   _ _    TA
GAM1372 KIAA0057 3' CCCCAGTTGCCAGGGCTCGACG 25406    AC       AC   A
            G                    CC  CGAGCTCTGG  GCTG GG
                                ||  ||||||||||  |||| ||
                                GG  GCTCGGGACC  TGAC CC
                                 CA        GT   C
GAM1372 KIAA0939 5' CCGCGGCTCCGAACTCGGTGG  62710       C  T   C   A
                                CCACCGAG TC GGA GCTG GG
                                |||||||| || ||| |||| ||
                                GGTGGCTC AG CCT CGGC CC
                                    A  _   _   G
GAM1372 KIAA1706 3' TCACGCCCAGGGCTCAGTGG   94371     C       A  C
                                CCAC GAGCTCTGG CG TGA
                                |||| ||||||||| || |||
                                GGTG CTCGGGACC GC ACT
                                  A       C  _
GAM1372 KIAA1853 5' CCTCGCGGTCCCAGAGCTCGG  69919         A__   T
                                CCGAGCTCTGG   CGC GAGG
                                ||||||||||   ||| ||||
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                                GGCTCGAGACC   GCG CTCC
                                      CTG  _
GAM1372 MGC10966 5' TCCTCAGCATCCGGCACCCCG 49686    AGCT_    C
                                CG    CTGGA GCTGAGGA
                                ||    ||||| ||||||||
                                GC    GGCCT CGACTCCT
                                 CCCAC    A
GAM1372 MGC11287 5' TCCTCAGCTCTCTCCAGAGCTC 49621         C___
                                GAGCTCTGGA   GCTGAGGA
                                ||||||||||   ||||||||
                                CTCGAGACCT   CGACTCCT
                                      CTCT
GAM1372 MGC3048  3' CCTCAGCCTTGGTGCTCAGTGG 44129     C   T TG AC
                                CCAC GAGC C  G  GCTGAGG
                                |||| |||| |  |  |||||||
                                GGTG CTCG G  T  CGACTCC
                                  A   T GT C_
GAM1372 MGC4293  5' TCCTGAGTCTCCAGAGCTCGGT 49345           C  G
            G                    CACCGAGCTCTGGA GCT AGGA
                                ||||||||||||| ||| ||||
                                GTGGCTCGAGACCT TGA TCCT
                                       C  G
GAM1372 PIP5K1C  3' CTGAGGCCCAGAGCTCGG    71300         AC  GA
                                CCGAGCTCTGG  GCT  GG
                                ||||||||||  |||  ||
                                GGCTCGAGACC  CGG  TC
                                      __  AG
GAM1372 SLC2A10  5' CCTCAGCGCCCCCAGCACG   48548   A  CT  A
                                CG GCT  GG CGCTGAGG
                                || |||  || ||||||||
                                GC CGA  CC GCGACTCC
                                 A  CC  C
GAM1372 UBE3B    3' TCCTCAGCACAGGGAACCCGG  77448    AG__    GAC
                                CCG   CTCTG   GCTGAGGA
                                |||   |||||  ||||||||
                                GGC   GGGAC   CGACTCCT
                                  CCAA    A__
GAM1372 UHRF2    5' CGGCGCCCAGAGCTCAGGGG   73831   A  _      A
                                CC CC GAGCTCTGG CGCTG
                                || || ||||||||| |||||
                                GG GG CTCGAGACC GCGGC
                                 _ A       C
GAM1372 UMP-CMPK 5' CCTCAGCGTCCGGCCGAGG   33311   GAGCT
                                CC    CTGGACGCTGAGG
                                ||    ||||||||||||
                                GG    GGCCTGCGACTCC
                                 AGCC_
GAM1372 WBSCR21  5' CCACAGCCAGAGCTGGTGG   49299     G     GAC   A
                                CCACC AGCTCTG   GCTG GG
                                ||||| |||||||   |||| ||
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                                GGTGG TCGAGAC   CGAC CC
                                  _     ___    A
GAM1372  YKT6     3'  TCCTGACCAGAGTCTCAGTGG  22644      C  _     A GCTG
                                CCAC GAG CTCTGG C    AGGA
                                |||| ||| |||||| |    ||||
                                GGTG CTC GAGACC G    TCCT
                                  A  T     A ____
GAM1372  LOC135398 5'  TCCCGCGCTTTCCGGAGCTC   76470          ___   T A
                                GAGCTCTGGA   CGC G GGA
                                ||||||||||   ||| | |||
                                CTCGAGGCCT   GCG C CCT
                                     TTC  _ _
GAM1372  LOC143719 5'  CCTGTGAATCCAGAGCTCAGTG 61251     C        __   TG
                                CAC GAGCTCTGGA  CGC  AGG
                                ||| ||||||||||  |||  |||
                                GTG CTCGAGACCT  GTG  TCC
                                  A        AA  __
GAM1372  LOC150577 3'  CCTCAGCGCAACCTGGTG    86254      AGCTCT  A__
                                CACCG     GG   CGCTGAGG
                                |||||     ||   ||||||||
                                GTGGT     CC   GCGACTCC
                                  _______  AAC
GAM1372  LOC152283 3'  TCCTCAGCACCTGGCATCGGAG 86876    A   _   CT  AC
           G                     CC CCGA GCT  GG  GCTGAGGA
                                || |||| |||  ||  ||||||||
                                GG GGCT CGG  CC  CGACTCCT
                                 A   A  T_  A_
GAM1372  LOC158510 5'  CGGCCCAGGCTCGGTG      82834         T    AC
                                CACCGAGC CTGG  GCTG
                                |||||||| ||||  ||||
                                GTGGCTCG GACC  CGGC
                                   _   __
GAM1372  LOC163682 5'  TCCCCACGTGTCAGGGCTC    88416         G   _  A
                                GAGCTCTG ACGC TG GGA
                                |||||||| |||| || |||
                                CTCGGGAC TGTG AC CCT
                                     _   C  C
GAM1372  LOC164537 5'  TCCTCAGCACCTTGTCTGTG   88577     C  G TCT  AC
                                CAC GA C   GG  GCTGAGGA
                                ||| || |   ||  ||||||||
                                GTG CT G   CC  CGACTCCT
                                  T  _ TT_  A_
GAM1372  LOC164538 5'  TCCTCAGCACCCGTGTCAGTGG 83414      C  G TC   AC
                                CCAC GA C  TGG  GCTGAGGA
                                |||| || |  |||  ||||||||
                                GGTG CT G  GCC  CGACTCCT
                                  A  _ T_   CA
GAM1372  LOC169611 3'  TCCTCAGCACCCAGTGGGT   83664     GAGCT   AC
                                ACC    CTGG  GCTGAGGA
                                |||    ||||  ||||||||
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                                TGG    GACC  CGACTCCT
                                  GT___    CA
GAM1372  LOC196738 3'  CCCCGGTCTCCTGAGCTCGGT  88887         T  C   A
                                ACCGAGCTC GGA GCTG GG
                                ||||||||| ||| |||| ||
                                TGGCTCGAG CCT TGGC CC
                                     T  C   C
GAM1372  LOC199936 3'  TCCCCAGCACGGGGCTCCATGG 91486     CC       GAC   A
                                CCA  GAGCTCTG   GCTG GGA
                                |||  ||||||||   |||| |||
                                GGT  CTCGGGGC   CGAC CCT
                                  AC       A__   C
GAM1372  LOC219700 3'  CCCCGGCTCCAGAGCTCAGGGG 94648    A  _        C   A
                                CC CC GAGCTCTGGA GCTG GG
                                || || |||||||||| |||| ||
                                GG GG CTCGAGACCT CGGC CC
                                 _  A         _   C
GAM1372  LOC253847 5'  CCTCAGCATCCCTTCAGTG   97715     C  CTCT  C
                                CAC GAG    GGA GCTGAGG
                                ||| |||    ||| |||||||
                                GTG CTT    CCT CGACTCC
                                  A  C___   A
GAM1372  LOC255328 3'  CCTGTAACCCAGAGCTGATGG  98337     C G       AC_  TG
                                CCA C AGCTCTGG   GC  AGG
                                ||| | ||||||||   ||  |||
                                GGT G TCGAGACC   TG  TCC
                                  A _       CAA  __
GAM1372  LOC257095 5'  CCCCAGCGTCCACACGTGG   98718      CGAGCTC       A
                                CCAC      TGGACGCTG GG
                                ||||      ||||||||| ||
                                GGTG      ACCTGCGAC CC
                                   CAC_____        C
GAM1372  LOC51668  5'  CGGCGCCCAGAGCTAACGG   32846     __      A
                                CCG  AGCTCTGG CGCTG
                                |||  |||||||| |||||
                                GGC  TCGAGACC GCGGC
                                  AA       C
GAM1373  DGKI     5'  CATCCTGGCTAACACGCGGTA  17526      AGGATG   _
                                TACC     GTTA CCAGGATG
                                ||||     |||| ||||||||
                                ATGG     CAAT GGTCCTAC
                                   CGCA__    C
GAM1373  IFITM2   5'  CTGAGAACCATCCCGGTA    22234      A      AC
                                TACC GGATGGTT  CAG
                                |||| ||||||||  |||
                                ATGG CCTACCAA  GTC
                                  C       GA
GAM1373  MAP1A    5'  TCATCCTGGTAAATCCCAGTG  11443     CA   GG
                                TAC  GGAT  TTACCAGGATGA
                                |||  ||||  ||||||||||||
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                                GTG  CCTA  AATGGTCCTACT
                                  AC   __
GAM1373  PYCR1    5'  TCATCCCCTTCATCCTGG    70644        TTACCA
                                CCAGGATGG     GGATGA
                                |||||||||     ||||||
                                GGTCCTACT     CCTACT
                                    TCC___
GAM1373  SLC26A4  3'  CATCCTGGCTAACATGGTA   6524       GGATG   _
                                TACCA    GTTA CCAGGATG
                                |||||    |||| ||||||||
                                ATGGT    CAAT GGTCCTAC
                                   A____   C
GAM1373  TYK2     3'  CATCTCCACCATCTGGTA    60562       G    TACCA
                                TACCAG ATGGT    GGATG
                                ||||||| |||||    |||||
                                ATGGTC TACCA    TCTAC
                                   _    CC___
GAM1373  ADPRTL3  3'  TCATCCTGCCCATCTCTGGTA  19693       _    TTAC
                                TACCAG GATGG    CAGGATGA
                                ||||||| |||||   ||||||||
                                ATGGTC CTACC    GTCCTACT
                                   T    C___
GAM1373  ARFGAP1  3'  CATCCTGGAACACCCTGG    37137      ATG   A
                                CCAGG   GTT CCAGGATG
                                |||||   ||| ||||||||
                                GGTCC   CAA GGTCCTAC
                                   CA_  _
GAM1373  CXYorf1  5'  CATCCCTTGGCCATCCTGG   82904          CCA
                                CCAGGATGGTTA   GGATG
                                ||||||||||||   |||||
                                GGTCCTACCGGT   CCTAC
                                      TC_
GAM1373  DKFZP566G1424 5'  CACCCTAGAATTCCTGGTA   85939        TG   ACC   A
                                TACCAGGA  GTT   AGG TG
                                ||||||||  |||   ||| ||
                                ATGGTCCT  TAA   TCC AC
                                    __  GA_   C
GAM1373  FLJ11286 3'  CCCAGTAGACACCATCCTGGTA 37793          ___   CA
                                TACCAGGATGGT   TAC  GG
                                ||||||||||||   |||  ||
                                ATGGTCCTACCA   ATG  CC
                                      CAG   AC
GAM1373  FLJ21551 3'  CACCCTGGCCAACCTGGTG   46030       A   TTA    A
                                TACCAGG TGG   CCAGG TG
                                ||||||| |||   ||||| ||
                                GTGGTCC ACC   GGTCC AC
                                   A  ____    C
GAM1373  KIAA1505 5'  CATCAAACCATTCCAGTA    95846     CA       ACCAG
                                TAC  GGATGGTT    GATG
                                |||  ||||||||    ||||
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                                ATG  CTTACCAA    CTAC
                                  AC       A____
GAM1373  MBD2     3'  GTCACAAATCATCCTAGTA   32335     C       ACCAG
                                TAC AGGATGGTT    GAT
                                ||| |||||||||    |||
                                ATG TCCTACTAA    CTG
                                  A        ACA__
GAM1373  LOC200093 5'  CATCCCTTGGCCATCCTGG   63762          CCA
                                CCAGGATGGTTA   GGATG
                                ||||||||||||   |||||
                                GGTCCTACCGGT   CCTAC
                                       TC_
GAM1373  LOC253926 5'  GTCATCCTGGTAATAACC    96596    ATG
                                GG   GTTACCAGGATGAC
                                ||   ||||||||||||||
                                CC   TAATGGTCCTACTG
                                 AA_
GAM1373  LOC253927 3'  CATCCTGGCAAACATGGTG   96727      GGA  GTTA
                                TACCA   TG    CCAGGATG
                                |||||   ||    ||||||||
                                GTGGT   AC    GGTCCTAC
                                   ____  AAAC
GAM1373  LOC51754  5'  TCATCCCGGGGCCCTGGTA   71583       ATG   A  A
                                TACCAGG   GTT CC GGATGA
                                |||||||   ||| || ||||||
                                ATGGTCC   CGG GG CCTACT
                                   ____   _ C
GAM1373  LOC91040  5'  CATCCTGGCCCTCCCAGG    65336    A_   T  TTA
                                CC  GGA GG   CCAGGATG
                                ||  ||| ||   ||||||||
                                GG  CCT CC   GGTCCTAC
                                 AC   C  ___
GAM1373  LOC91040  5'  CATCCCTTGGCCATCCTGG    65335          CCA
                                CCAGGATGGTTA   GGATG
                                ||||||||||||   |||||
                                GGTCCTACCGGT   CCTAC
                                       TC_
GAM1374  FLJ20312  3'  ATGGACCACTTATGCAAA    35408         GCATA  GA
                                TTTGCATAAG    GG  CAT
                                ||||||||||    ||  |||
                                AAACGTATTC    CC  GTA
                                      A_____  AG
GAM1374  KIAA0888  3'  TGATCTTGATCCTTATGCAAA  63927          C  AG   CA
                                TTTGCATAAGG AT  GGA  TCA
                                |||||||||||  ||  |||  |||
                                AAACGTATTCC TA  TCT  AGT
                                       _  GT   __
GAM1374  KIAA1695  5'  TGATGAGTATGCCTTAAACAAA 47834      CA        GGGA
                                TTTG  TAAGGCATA    CATCA
                                ||||  |||||||||    |||||
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                                AAAC  ATTCCGTAT   GTAGT
                                  AA       GA__
GAM1374  MYT1     3'  ATGTCCCTACCGTGTAAA    16974       AA  CA
                                TTTGCAT  GG  TAGGGACAT
                                |||||||  ||  |||||||||
                                AAATGTG  CC  ATCCCTGTA
                                   __  __
GAM1374  SCYA7    3'  TGATGTCCCTATGGAAGCA   21854     ATAAGG
                                TGC     CATAGGGACATCA
                                |||     ||||||||||||
                                ACG     GTATCCCTGTAGT
                                  AAG___
GAM1374  SLC22A4  3'  ATGTCCTTGCTTTACAAA    13224     CA      TA
                                TTTG  TAAGGCA  GGGACAT
                                ||||  |||||||  |||||||
                                AAAC  ATTTCGT  TCCTGTA
                                   __     __
GAM1374  SPRY4    3'  GATATCCTCCTTATGCA     49014        CATA    C
                                TGCATAAGG    GGGA ATC
                                |||||||||    |||| |||
                                ACGTATTCC    TCCT TAG
                                     _____   A
GAM1374  LOC146481 3'  TTCATATGCCTTTGCAAA    78488       T       G
                                TTTGCA AAGGCATA GGA
                                ||||||| |||||||| |||
                                AAACGT TTCCGTAT CTT
                                   _       A
GAM1375  KCNK3    3'  GCCCAGTGGGACCCCGCACAAC 11175     C  _    A   TG
            AT                    ATG TGT CGGGG TTC  CTGGGC
                                ||| ||| ||||| |||  ||||||
                                TAC ACA GCCCC AGG  GACCCG
                                  A  C    _  GT
GAM1375  PCDH9    3'  GCCCGGCACCTCCAACAACAT  83695     C   C    ATTC
                                ATG TGT GGGG    TGCTGGGC
                                ||| ||| ||||    ||||||||
                                TAC ACA CCTC    ACGGCCCG
                                  A  A   C___
GAM1375  RNF4     3'  GCCCAAGCTGCCCCTGACAGCA 12884          ATTCT  _
                                TGCTGTCGGGG     GCT GGGC
                                ||||||||||     ||| ||||
                                ACGACAGTCCC     CGA CCCG
                                     CGT__   A
GAM1375  SPRR2C   3'  GCCCATGATGATCCCCGACAGC 22530            CTGC
            A                    TGCTGTCGGGGATT    TGGGC
                                ||||||||||||||    |||||
                                ACGACAGCCCCTAG    ACCCG
                                       TAGT
GAM1375  DKFZP586J0619 3'  GCCCAGCAGGGACGACAG    82319       GGGAT
                                CTGTCG    TCTGCTGGGC
                                ||||||    ||||||||||
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                                GACAGC    GGACGACCCG
                                  AG___
GAM1375  GABARAPL3 3'  CCCAGCAGATGGAAGCA    51779     GT  GGGAT
                                TGCT  CG    TCTGCTGGG
                                ||||  ||    |||||||||
                                ACGA  GT    AGACGACCC
                                  AG  _____
GAM1375  KIAA1634  3'  GCCCAGCAAATGAGGACA    64125     GGGG   C
                                TGTC    ATT TGCTGGGC
                                ||||    ||| ||||||||
                                ACAG    TAA ACGACCCG
                                  GAG_  _
GAM1375  KIAA1765  3'  CCCAGCAGAAATTCAAGCAT   71132     GTCG   A
                                ATGCT    GGG TTCTGCTGGG
                                |||||    ||| ||||||||||
                                TACGA    CTT AAGACGACCC
                                  A___   A
GAM1375  RBPMS    5'  GCCCAACCCGAGCCCGACAGC  23430       GA   TGC_
                                GCTGTCGGG  TTC    TGGGC
                                |||||||||  |||    |||||
                                CGACAGCCC  GAG    ACCCG
                                     __   CCCA
GAM1375  SSR3     3'  CCCAGCAGAATGTAATTCAGTA 24031      TCGGGG
                T                ATGCTG     ATTCTGCTGGG
                                 ||||||     ||||||||||
                                 TATGAC     TAAGACGACCC
                                    TTAATG
GAM1375  TNFRSF19L 3'  GCCCAGCAGACGAGACAGCA   52836      GGGGAT
                                TGCTGTC     TCTGCTGGGC
                                |||||||     ||||||||||
                                ACGACAG     AGACGACCCG
                                   AGC___
GAM1375  LOC152580 5'  CCCAGCAGGCAACAGCA     86984      CGGGGAT
                                TGCTGT      TCTGCTGGG
                                ||||||      |||||||||
                                ACGACA      GGACGACCC
                                  AC_____
GAM1375  LOC222166 3'  GCAAAATCCCAAACAGCAT    95739      CG     C
                                ATGCTGT  GGGATT TGC
                                |||||||  |||||| |||
                                TACGACA  CCCTAA ACG
                                   AA     A
GAM1375  LOC253868 3'  CCCAGCAGATGCCAGCA     97319      T  GGGAT
                                TGCTG CG    TCTGCTGGG
                                ||||| ||    |||||||||
                                ACGAC GT    AGACGACCC
                                  C  _____
GAM1375  LOC254266 3'  CCCAGCAAAACCCGCAGT    99197     T   GATTC
                                GCTG CGGG    TGCTGGG
                                |||| ||||    |||||||
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                                TGAC GCCC     ACGACCC
                                  _   AAA__
GAM1375  LOC254556 3'  GCCCAAGCTGCCCCTGACAGCA 96261           ATTCT  _
                                TGCTGTCGGGG     GCT GGGC
                                ||||||||||     ||| ||||
                                ACGACAGTCCC     CGA CCCG
                                      CGT__   A
GAM1376  B3GALT3   3'  TAGGACCAAACAATTTGGACA  53718       A     CCAGA
                                TGTCCA GATTGT     CCTA
                                |||||| ||||||     ||||
                                ACAGGT TTAACA     GGAT
                                   _     AACCA
GAM1376  EDAR      3'  GGTAGGTCTGTGGCCCTTAGAC 42528      C   ATT  _
             A                   TGTC AAG   GTC CAGACCTACC
                                |||| |||   ||| ||||||||||
                                ACAG TTC   CGG GTCTGGATGG
                                  A  C__   T
GAM1376  MFGE8     3'  GTAGGTCTGGGATGGACA     21008       AGATTG
                                TGTCCA     TCCAGACCTAC
                                ||||||     ||||||||||
                                ACAGGT     GGGTCTGGATG
                                   A_____
GAM1376  NOLA1     3'  GTCTTGAAGATCTTGGTCA    39126    T      G  C
                                TG CCAAGATT TC AGAC
                                || |||||||| || ||||
                                AC GGTTCTAG AG TCTG
                                 T       A  T
GAM1376  BTN3A3    3'  TAGGTCTGTCCACTCCTGGTCA 23768    T   A  T  TC
                                TG CCA GA TG  CAGACCTA
                                || ||| || ||  ||||||||
                                AC GGT CT AC  GTCTGGAT
                                 T   C  C  CT
GAM1376  C1QTNF6   3'  AGGTCTGGGGAGCTAGAGCA   49987     CCA  A  G
                                TGT   AG TT TCCAGACCT
                                |||   || || |||||||||
                                ACG   TC GA GGGTCTGGA
                                  AGA  _  G
GAM1376  DKFZP564D166 3'  GGCAGGTCTGGACCAAATGACA 48018      CAAGATT         A
                                TGTC      GTCCAGACCT CC
                                ||||      |||||||||| ||
                                ACAG      CAGGTCTGGA GG
                                   TAAAC__         C
GAM1376  FLJ10921  5'  GGCAGATCTGGACAGTGGA   37394      AGA        C  A
                                TCCA   TTGTCCAGA CT CC
                                ||||   ||||||||| || ||
                                AGGT   GACAGGTCT GA GG
                                   ___        A  C
GAM1376  FLJ23142  3'  AGATCTGATTATTCTTGGATA  45027          T  TC    C
                                TGTCCAAGA TG  CAGA CT
                                |||||||| ||  |||| ||
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                                ATAGGTTCT AT  GTCT GA
                                     T  TA   A
GAM1376  KCNT1    3'  GGCTCTGTGGACAACCTGGACA 62493       A A     __ _
                                TGTCCA G TTGTCCA  GA CC
                                |||||| | |||||||  || ||
                                ACAGGT C AACAGGT  CT GG
                                   _ C      GT  C
GAM1376  PIP5K2B  3'  GGTAGGTCTGAACAACTGCCGC 57699    CCA  A   C
           A                     TGT   AG TTGT CAGACCTACC
                                |||   || |||| ||||||||||
                                ACG   TC AACA GTCTGGATGG
                                  CCG  _   A
GAM1376  PIP5K2B  3'  GGTAGGTCTGAACAACTGCCGC 57700    CCA  A   C
           A                     TGT   AG TTGT CAGACCTACC
                                |||   || |||| ||||||||||
                                ACG   TC AACA GTCTGGATGG
                                  CCG  _   A
GAM1376  PRC1     5'  GTAGGTCTGGACCTGGAC    15630      AGATT
                                GTCCA    GTCCAGACCTAC
                                |||||    ||||||||||||
                                CAGGT    CAGGTCTGGATG
                                  C____
GAM1376  RAI16    3'  AGGTCCACAGCACCTGGGCA  43043      AGA_   CCA
                                TGTCCA   TTGT   GACCT
                                ||||||   ||||  |||||
                                ACGGGT   GACA   CTGGA
                                   CCAC   C__
GAM1376  LOC124460 3'  GGTAGGTCCAGGACACACCCGG 76566     AAGAT    A_
           AC                    GTCC    TGTCC  GACCTACC
                                ||||    |||||  ||||||||
                                CAGG    ACAGG  CTGGATGG
                                  CCCAC    AC
GAM1376  LOC147093 3'  GGTAGGTCCCAGGCACGTTAGA 85058     CAAGAT    CA_
           CA                    TGTC     TGTC   GACCTACC
                                ||||     ||||   ||||||||
                                ACAG     ACGG   CTGGATGG
                                  ATTGC_   ACC
GAM1376  LOC203197 3'  GGTCCTAGGACACCCTTGGACA 90814        AT    A__
                                TGTCCAAG  TGTCC   GACC
                                ||||||||  |||||   ||||
                                ACAGGTTC  ACAGG   CTGG
                                    CC    ATC
GAM1376  LOC203339 5'  GGCAGATCTGAATTTTCTTCTT 92215        TT___  C   C  A
           GGACA                   TGTCCAAGA    GT CAGA CT CC
                                |||||||||    || |||| || ||
                                ACAGGTTCT    TA GTCT GA GG
                                     TCTTT  A   A  C
GAM1376  LOC255193 3'  GTTTGAGACCATCCTGGACA   97106      A   T   _
                                TGTCCA GAT GTC CAGAC
                                |||||| ||| ||| |||||
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                                ACAGGT CTA CAG GTTTG
                                   C  C  A
GAM1376 LOC256530 3' AGGTCAGGATCTGGACA    98621      A TTG  A
                                TGTCCA GA  TCC GACCT
                                |||||| ||  ||| |||||
                                ACAGGT CT  AGG CTGGA
                                   _ ___  A
GAM1376 LOC51213 3' GGTAGGTCTGCTTTCCCTGGA 33506     A_ TT TC
                                TCCA GA G CAGACCTACC
                                |||| || | ||||||||||
                                AGGT CT C GTCTGGATGG
                                  CC TT __
GAM1376 LOC90499 3' GAGGTCTGGAGATGACA    63742     CAAG G      A
                                TGTC   ATT TCCAGACCT C
                                ||||   ||| |||||||| |
                                ACAG   TAG AGGTCTGGA G
                                  ____ _       C
GAM1377 ETV5    3' TGATGACAATTTCCATTTC   16730    CG   C
                                GAA GGAAG TTGTCATCA
                                |||  ||||| |||||||||
                                CTT  CCTTT AACAGTAGT
                                  TA   _
GAM1377 HTRA3   3' TGAGCCGGCTTCCCCTTCCCA 90585   A  C      T CA
                                TG GAA GGGAAGCT GT  TCA
                                || ||| |||||||| ||  |||
                                AC CTT CCCTTCGG CG  AGT
                                 C  C      C __
GAM1377 KCNK5   3' TTGATGGCCTCTTCCCCCCTCA 14973    AAC    CTT
                                TGAG  GGGAAG  GTCATCAA
                                ||||  ||||||  ||||||||
                                ACTC  CCCTTC  CGGTAGTT
                                  CC_    TC_
GAM1377 MTM1    3' TGGTGTTGGCTTCCCCTC   6007     AAC      TGT
                                GAG  GGGAAGCT  CATCA
                                |||  ||||||||  |||||
                                CTC  CCCTTCGG  GTGGT
                                  ___      TT_
GAM1377 NFRKB   5' TGGTCCAGCTTCCCTTCCTCA 21608    AAC      T TC
                                TGAG  GGGAAGCT G  ATCA
                                ||||  |||||||| |  ||||
                                ACTC  CCCTTCGA C  TGGT
                                  CTT      _ C_
GAM1377 STX1A   3' GGCCTCAGCTTCCCTTCCCA  17213   A  C      T__
                                TG GAA GGGAAGCT  GTC
                                || ||| ||||||||  |||
                                AC CTT CCCTTCGA  CGG
                                 C  _      CTC
GAM1377 B3GNT7  3' TTGGTGTGAAACTTCCTGTTCC 71684   A       C  GT
            CA                    TG GAACGGGAAG TT  CATCAA
                                || |||||||||| ||  ||||||
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                                AC CTTGTCCTTC AA  GTGGTT
                                 C         A  GT
GAM1377  BA108L7.2 3'  TGACATCTGGCTTCCCTTCTCA 49082       C       ___
                                TGAGAA GGGAAGCT   TGTCA
                                |||||| ||||||||   |||||
                                ACTCTT CCCTTCGG   ACAGT
                                   _       TCT
GAM1377  BRPF3     3'  GGCAGCTTCCCCCTCTCA     93932       AC       T
                                TGAGA  GGGAAGCT GTC
                                |||||  |||||||| |||
                                ACTCT  CCCTTCGA CGG
                                  CC       _
GAM1377  C3orf4    3'  TGATATTTTCCCCACCTCTCA  39597       AC__     CT
                                TGAGA   GGGAAG  TGTCA
                                |||||   ||||||  |||||
                                ACTCT   CCCTTT  ATAGT
                                  CCAC     T_
GAM1377  EPB41L4   3'  ACAAGCTTCCCGCCTCA     42422      AA
                                TGAG  CGGGAAGCTTGT
                                ||||  ||||||||||||
                                ACTC  GCCCTTCGAACA
                                  C_
GAM1377  FLJ14457  5'  GAGCCGGGGCTTCCCCTTCTCA 52407       C        GTCA
                                TGAGAA GGGAAGCTT    TC
                                |||||| |||||||||    ||
                                ACTCTT CCCTTCGGG    AG
                                   C        GCCG
GAM1377  FLJ20254  3'  GCAGCCTCCTGTTCCCA     35297    A       A   T
                                TG GAACGGGA GCT GT
                                || |||||||| ||| ||
                                AC CTTGTCCT CGA CG
                                 C       C   _
GAM1377  HLA-DOA   3'  ACTAGCTTCCCTTCCCA     10929    A   C       T
                                TG GAA GGGAAGCT GT
                                || ||| |||||||| ||
                                AC CTT CCCTTCGA CA
                                 C   _       T
GAM1377  MGC29654  5'  TGACCCTCCTGTTCCCA     67210    A       A CTT
                                TG GAACGGGA G   GTCA
                                || |||||||| |   ||||
                                AC CTTGTCCT C   CAGT
                                 C       _ C__
GAM1377  RAB35     3'  TTGATGACTGCTCCCCG     23421      A   TT
                                CGGG AGC  GTCATCAA
                                ||||  |||  ||||||||
                                GCCC TCG  CAGTAGTT
                                  C   T_
GAM1377  LOC149386 5'  ATGACAAGCTTCCCGTTTTCA  85554
                                TGAGAACGGGAAGCTTGTCAT
                                |||||||||||||||||||||
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                                ACTTTTGCCCTTCGAACAGTA

GAM1377  LOC253974 3'  TTGATGACAAATTTCCCGTTCT 99285           C
              CA                  TGAGAACGGGAAG TTGTCATCAA
                                  |||||||||||| ||||||||||
                                  ACTCTTGCCCTTT AACAGTAGTT
                                        A
GAM1378  SCAMP1    3'  GCTAAATAAATATTCTCC    54500    T    C
                                  GGA AATATT ATTTAGC
                                  ||| |||||| |||||||
                                  CCT TTATAA TAAATCG
                                    C     A
GAM1378  SCAMP1    3'  GCTAAATAAATATTCTCC    54501    T    C
                                  GGA AATATT ATTTAGC
                                  ||| |||||| |||||||
                                  CCT TTATAA TAAATCG
                                    C     A
GAM1378  NX-17     3'  TGAATATCAGCCCCTAATA   40706       ATA_
                                  TATTAGGG   ATATTCA
                                  ||||||||   |||||||
                                  ATAATCCC   TATAAGT
                                       CGAC
GAM1378  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
              TA                  TATTAGGGATAATATTCATTTAGC
                                  ||||||||||||||||||||||||
                                  ATAATCCCTATTATAAGTAAATCG

GAM1379  ASNS      5'  CTGTAGACTGCAAGACTCATCA 56762       C  ATCACT
                                  TGATGAG TC     GTCTACAG
                                  ||||||| ||     ||||||||
                                  ACTACTC AG     CAGATGTC
                                     _  AACGT_
GAM1379  FCMD      3'  TGGAAGATGAGCTCACCA    23049    A       ACTG
                                  TG TGAGCTCATC    TCTA
                                  || ||||||||||    ||||
                                  AC ACTCGAGTAG    AGGT
                                   C        A___
GAM1379  PPARGC1   3'  CTGCAGACACTGTGGGTAGCCC 26077      A  CA   __    A
              ATCA                  TGATG GCT  TCAC  TGTCT CAG
                                    ||||| |||  ||||  ||||| |||
                                    ACTAC CGA  GGTG  ACAGA GTC
                                       C  TG   TC    C
GAM1379  FLJ20689  3'  CTGCAGAAACTCAGACAGCTCA 35961        CATCACTG_  A
              TCA                   TGATGAGCT       TCT CAG
                                    |||||||||       ||| |||
                                    ACTACTCGA       AGA GTC
                                         CAGACTCAA   C
GAM1379  FLJ20689  3'  CTGCAGAAACTCAGACAGCTCA 36210        CATCACTG_  A
              TCA                   TGATGAGCT       TCT CAG
                                    |||||||||       ||| |||
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                                ACTACTCGA        AGA GTC
                                     CAGACTCAA   C
GAM1379  FLJ31890  3'  CTGTAGACATCCAAAAGCTCAC 92985    A     CATCAC
              A                   TG TGAGCT     TGTCTACAG
                                  || ||||||     |||||||||
                                  AC ACTCGA     ACAGATGTC
                                   _     AAACCT
GAM1379  KIAA0342  3'  TGTCTACAGCTGCTTGCTGAGC 71144          T A_________   TCTA
              TCATCA                 TGATGAGCTCA C        CTG    CA
                                  |||||||||||| |        |||    ||
                                  ACTACTCGAGT G        GAC    GT
                                        C TTCGTCIII   ATCT
GAM1379  STK3     3'  ACTGTAATAAGCTCATCA     74100         C  C  T
                                  TGATGAGCT AT AC GT
                                  ||||||||| || || ||
                                  ACTACTCGA TA TG CA
                                        A  A  T
GAM1379  LOC146136 5'  CTGCAGACAGTGATGAAGGCCA 73317     A  __         A
              T                   ATG GC  TCATCACTGTCT CAG
                                  ||| ||  |||||||||||| |||
                                  TAC CG  AGTAGTGACAGA GTC
                                    _ GA          C
GAM1379  LOC146439 5'  GCAGGTGACATGAGCTCTCCA  78450    AT     __   _
                                  TG  GAGCTCA  TCAC TGT
                                  ||  |||||||  |||| |||
                                  AC  CTCGAGT  AGTG ACG
                                   CT      AC    G
GAM1379  LOC220565 3'  CTGCAGACAGTGATGAAGGCCA 92442     A  __         A
              T                   ATG GC  TCATCACTGTCT CAG
                                  ||| ||  |||||||||||| |||
                                  TAC CG  AGTAGTGACAGA GTC
                                    _ GA          C
GAM1379  LOC90520  3'  AGAACAGTGATAAAGCCACCA  63833    A  A   C_      _
                                  TG TG GCT  ATCACTGT CT
                                  || || |||  |||||||| ||
                                  AC AC CGA  TAGTGACA GA
                                   C  _   AA       A
GAM1380  ELF3     3'  TGACCTTGACCTTGACCAA    16685      T    GAT  AAA
                                  TTGGT CAAGG   GG   GTCA
                                  ||||| |||||   ||   ||||
                                  AACCA GTTCC   TC   CAGT
                                     _     AGT  ___
GAM1380  JAK2     3'  TGACCTTCATTCTGAGACCAA  18318       CAA       AA
                                  TTGGTT   GGGATGGA  GTCA
                                  ||||||   ||||||||  ||||
                                  AACCAG   TCTTACTT  CAGT
                                      AG_       C_
GAM1380  SLC10A2  5'  ACTCTCTGTCTTGACCAA    6590        CAA       A
                                  TTGGTT   GGGATGGA AGT
                                  ||||||   |||||||| |||
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                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM1380  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM1380  KIAA1958  5'  GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                GGTT   GGG   AAAGTCAC
                                ||||   |||   ||||||||
                                CCAA   CCC   TTTCAGTG
                                  A__   CAAG
GAM1380  MARCKS   3'  ACTTTCCACCCTGCCCA     11411     TTCA   A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM1380  TUB      5'  GTGGGACCATCCCTTAAACC   13898     C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A       AG__
GAM1380  LOC80298  3'  ACTTTTACCTTGAACCA     48062          GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                      A___
GAM1381  AQP6     5'  CAGCCCTAGGCAGCCAGATAAG 54988       G       ATGTA__
            GAA                    TTCCT TATCTGGCT      GCTG
                                |||||  |||||||||       ||||
                                AAGGA ATAGACCGA      CGAC
                                  _       CGGATCC
GAM1381  CD8A     3'  ACTAGCAGATACAGGGA     10094           G   T
                                TTCCTGTATCTG CTA GT
                                |||||||||||| ||| ||
                                AGGGACATAGAC GAT CA
                                      _   _
GAM1381  GPC6     3'  CAGCTACATTTTCAACA     20330     ATC   CT
                                TGT   TGG  ATGTAGCTG
                                |||   |||  |||||||||
                                ACA   ACT  TACATCGAC
                                  ___   TT
GAM1381  MHC2TA   3'  CAGGTAACAGGCAGATACAGGA 5970           G  ATG  G
            A                   TTCCTGTATCTG CT   TA CTG
                                ||||||||||||  ||   ||  |||
                                AAGGACATAGAC GA   AT GAC
                                      G  CA_  G
GAM1381  RAP1A    3'  CAGCTCTGAGCCAGATTACAGG 12765        _      ATGT
            AA                    TTCCTGTA TCTGGCT    AGCTG
                                ||||||||  |||||||    |||||
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                                AAGGACAT AGACCGA    TCGAC
                                     T      GTC_
GAM1381  KIAA1724  3'  CAGCCAAAAACAGATACAG   67608        GCTA  TA
                                CTGTATCTG    TG  GCTG
                                |||||||||    ||  ||||
                                GACATAGAC    AC  CGAC
                                     AAAA  __
GAM1381  MAL2      3'  CAGCTATACACAATACAG    54660       C  GCTA
                                CTGTAT TG    TGTAGCTG
                                ||||||  ||   ||||||||
                                GACATA AC    ATATCGAC
                                   _  AC__
GAM1381  LOC222302 5'  CAGAGAGCACAGATACAGGAA  95971           _   ATGTAG
                                TTCCTGTATCTG GCT      CTG
                                ||||||||||||  |||      |||
                                AAGGACATAGAC CGA      GAC
                                      A   GA_____
GAM1381  LOC56932  3'  CAGCTTGGAACTAGATACAG   70532          CTATGT
                                CTGTATCTGG      AGCTG
                                ||||||||||      |||||
                                GACATAGATC      TCGAC
                                     AAGGT_
GAM1381  LOC90550  3'  CAGCTGTACTACCAAATCAGGA 73479       T  C   CTA
              A                  TTCCTG AT TGG   TGTAGCTG
                                ||||||  ||  |||   ||||||||
                                AAGGAC TA ACC   ATGTCGAC
                                   _  A   ATC
GAM1382  CDH12     3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM1382  GOCAP1    3'  ATTGTTCTTGGGAGCAGTGTA  43007       CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC         G
GAM1382  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT    98090       T    AGAAG
                                ACCAC CCCA     AATAAG
                                |||||  ||||    ||||||
                                TGGTG GGGT     TTATTC
                                   _    GTCA_
GAM1382  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
              A                  TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM1382  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126          CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
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                                ATGTGGTGA      TTTATTC
                                     AGACG___
GAM1382 HMP19    3' CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
            TA                    TACA   TCC   GAAGAATAAG
                                  ||||   |||   ||||||||||
                                  ATGT   AGG   TTTCTTATTC
                                    AAA_   ATTG
GAM1382 KIAA1719 3' TCTGTCTTGGGAGTGGTGTA  68742           _
                                  TACACCACTCCCAAGA AGA
                                  |||||||||||||||| |||
                                  ATGTGGTGAGGGTTCT TCT
                                           G
GAM1382 KIAA1853 3' TTTTTCTTGGAAGCAGTG    69929    CA  C
                                  CAC  CT CCAAGAAGAA
                                  |||  || ||||||||||
                                  GTG  GA GGTTCTTTTT
                                    AC  A
GAM1382 KIAA1877 3' CTTATTCTTCTGCCATGAGT  66748    CCA__
                                  ACTC    AGAAGAATAAG
                                  ||||    ||||||||||
                                  TGAG    TCTTCTTATTC
                                    TACCG
GAM1382 KIAA1906 3' CTTATTCTTCTTGACTTTTGG 73571    CTCC_
                                  CCA    CAAGAAGAATAAG
                                  |||    ||||||||||||
                                  GGT    GTTCTTCTTATTC
                                    TTTCA
GAM1382 OSBPL11  3' CTTAATTTCCCAAGAGTGGTG 43206       CCAA   AA
                                  CACCACTC   GAAG  TAAG
                                  ||||||||   ||||  ||||
                                  GTGGTGAG   CTTT  ATTC
                                       AACC   A_
GAM1382 YME1L1   3' TCATTCTTGATGTGGTGTA   58438       TCC    _
                                  TACACCAC   CAAGAA GA
                                  ||||||||   |||||| ||
                                  ATGTGGTG   GTTCTT CT
                                       TA_     A
GAM1382 ZNF262   3' CTTATTTTGTTTGGGAGT    18723        A
                                  ACTCCCAAG AGAATAAG
                                  ||||||||| ||||||||
                                  TGAGGGTTT TTTTATTC
                                       G
GAM1382 LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_    AAGA
                                  TACACCAC   CCAAG   ATA
                                  ||||||||   |||||   |||
                                  ATGTGGTG   GGTTC   TGT
                                       CAA    GG__
GAM1383 CIAS1    5' AGGAATAGTGAAGAGTTTGTCC 18093       CCCT   GA_  C___
            AA                    TTGGACAA   GCTC   AT   CCT
                                  ||||||||   ||||   ||   |||
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                                AACCTGTT   TGAG  TG   GGA
                                    ____   AAG  ATAA
GAM1383 DYSF    5' AGAGATTCGAGCCGGCCTCGCC 14489   ACAAC  T      C
                                GG    CC GCTCGAATC CT
                                ||    || |||||||| ||
                                CC    GG CGAGCTTAG GA
                                 GCTCC  C       A
GAM1383 GIPR    3' AGAGAAGTGGGCAGGGGCACCC 5710     ACAA       AA  C
           AA                    TTGG   CCCTGCTCG  TC CT
                                ||||   |||||||||  || ||
                                AACC   GGGACGGGT  AG GA
                                  CACG       GA  A
GAM1383 ITGB1BP2 3' GGGGAGAACAAAATTGTCCAA 25380       CCC  C  GAA
                                TTGGACAA   TG TC   TCCCT
                                ||||||||   || ||   |||||
                                AACCTGTT   AC AG   AGGGG
                                    AAA  A  ___
GAM1383 RAD54B  3' GGAAAACTACAGGTGTTGTCCA 25768       _   CTCGAA
           A                    TTGGACAAC CCTG     TCC
                                |||||||||| ||||     |||
                                AACCTGTTG GGAC     AGG
                                     T    ATCAAA
GAM1383 SCTR    3' AGGCTGGAGCAGGGTCACCCA  12949    ACA       GAATC
                                TGG   ACCCTGCTC    CCT
                                |||   |||||||||    |||
                                ACC   TGGGACGAG    GGA
                                  CAC       GTC__
GAM1383 C22orf23 3' GAGACGGGCAGGGTAGCCCAA  51771     ACA       AA
                                TTGG   ACCCTGCTCG  TC
                                ||||   ||||||||||  ||
                                AACC   TGGGACGGGC  AG
                                  CGA        AG
GAM1383 DRIL2   3' GGACAGACAGCGTTGTCCAA   22352       C   C  GAA
                                TTGGACAAC CTG TC   TCC
                                ||||||||| ||| ||   |||
                                AACCTGTTG GAC AG   AGG
                                     C   _  AC_
GAM1383 FLJ12587 3' AGGGACTGGGCAGGGTGTCCAA 42774       A       AA
                                TTGGACA CCCTGCTCG  TCCCT
                                |||||||  |||||||||  |||||
                                AACCTGT GGGACGGGT  AGGGA
                                    _       C_
GAM1383 FLJ20085 3' AGGGATTCCAGAAGCTGCCCA  35002    A  ACC  G  C
                                TGG CA   CT CT GAATCCCT
                                ||| ||   || || ||||||||
                                ACC GT   GA GA CTTAGGGA
                                  C  C__  A  C
GAM1383 KCNJ14  3' GGGATACAGAGTTGTCCA    26243       C   CTCGA
                                TGGACAAC CTG    ATCCC
                                ||||||||  |||    |||||
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                                ACCTGTTG GAC    TAGGG
                                    A  A____
GAM1383 KIAA0677 3' GGGATTCTCAGCCATCCAG  28533     CAACC  CTC
                                TTGGA   CTG  GAATCCC
                                |||||    |||  |||||||
                                GACCT   GAC  CTTAGGG
                                   ACC__  T__
GAM1383 KIAA0889 3' GGACTGGGTGGGCTGTCC   31779     A  T   AA
                                GGACA CCC GCTCG  TCC
                                ||||| ||| |||||  |||
                                CCTGT GGG TGGGT  AGG
                                   C  _   C_
GAM1383 MGC4677  5' GGGACAGCAGGGTTCCCAA  54614     AC      CGAA
                                TTGG  AACCCTGCT   TCCC
                                ||||  |||||||||   ||||
                                AACC  TTGGGACGA   AGGG
                                  C_      C___
GAM1383 UNC5D    3' GACGTGAAACAGGGTTGCCAA 56004     A     C_  AA
                                TTGG CAACCCTG  TCG  TC
                                |||| ||||||||  |||  ||
                                AACC GTTGGGAC  AGT  AG
                                  _      AA  GC
GAM1383 LOC124977 5' GGGGACCACAGAGTTGTCCAG 76571       C  CTCGAA
                                TTGGACAAC CTG    TCCCT
                                ||||||||| |||    |||||
                                GACCTGTTG GAC    AGGGG
                                    A  ACC___
GAM1383 LOC149276 3' GGATCCCACCAGGTTGTCCAG 85538       C  CTCGA
                                TTGGACAACC TG    ATCC
                                |||||||||| ||    ||||
                                GACCTGTTGG AC    TAGG
                                     _ CACCC
GAM1383 LOC152426 5' AGGGTCAGCTGAATTGTCCAA 86889       CCCT  C  AT  _
                                TTGGACAA   GCT GA  CC CT
                                ||||||||   ||| ||  || ||
                                AACCTGTT   CGA CT  GG GA
                                    AAGT  _  __  A
GAM1383 LOC196337 5' AGGAAAGTCTTCAGGTGTTGTC 89020       _   CTC  ATC_
           CAA                  TTGGACAAC CCTG  GA   CCT
                                |||||||| ||||  ||   |||
                                AACCTGTTG GGAC  CT   GGA
                                    T   TT_  GAAA
GAM1383 LOC254266 3' AGGGATTCCTGTTGGTTACCCA 99193    AC   CT  TC
           G                    TTGG  AACC  GC  GAATCCCT
                                ||||  ||||  ||  ||||||||
                                GACC  TTGG  TG  CTTAGGGA
                                  CA   T_  TC
GAM1383 LOC51285  3' GGGACTGTAGGTTGTCCAG  33802       C  TCGAA
                                TTGGACAACC TGC    TCCC
                                |||||||||| |||    ||||
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                                GACCTGTTGG ATG    AGGG
                                      _  TC___
GAM1383 LOC90072 3' GGACTGGGTGGGCTGTCC   61960     A  T   AA
                                GGACA CCC GCTCG  TCC
                                ||||| ||| |||||  |||
                                CCTGT GGG TGGGT  AGG
                                   C  _    C_
GAM1384 ABCG2   5' TGCTTGGTGGTCTTGTTA   17894      AGG
                                TAACAA  TACTAAGCA
                                ||||||  |||||||||
                                ATTGTT  GTGGTTCGT
                                    CTG
GAM1384 AKAP13  3' TGTGCTTACATACCTTTGT  91260       C_
                                ACAAAGGTA  TAAGCACA
                                |||||||||  ||||||||
                                TGTTTCCAT  ATTCGTGT
                                      AC
GAM1384 ARHG    3' TGTGCCTTGGTGCCTTGT   77091     A      _
                                ACAA GGTACTAAG CACA
                                |||| ||||||||| ||||
                                TGTT CCGTGGTTC GTGT
                                  _       C
GAM1384 CEBPA   3' TGTGCCCAGCAGTGCCTTGT  16433    A    AA___
                                ACAA GGTACT    GCACA
                                |||| ||||||    |||||
                                TGTT CCGTGA    CGTGT
                                  _     CGACC
GAM1384 CHD2    3' TGTGCCTAGTAATTTTTGT   8871       _  A
                                ACAAAGGT ACTA GCACA
                                |||||||| |||| |||||
                                TGTTTTTA TGAT CGTGT
                                     A   C
GAM1384 CORO1C  3' TGTGCTTGGGAGCTGGTTA  27508    AAA  A_
                                TAAC  GGT  CTAAGCACA
                                ||||  |||  |||||||||
                                ATTG  TCG  GGTTCGTGT
                                  G__  AG
GAM1384 CSNK1G3 3' TGTGCTCCGCTTTTGTTG   16512       ACTA
                                TAACAAAGGT   AGCACA
                                ||||||||||   ||||||
                                GTTGTTTTCG   TCGTGT
                                      CC__
GAM1384 DRD3    3' TGTGCTTGGGGCCTTCATTG  7679    CA   TA
                                TAA  AAGG  CTAAGCACA
                                |||  ||||  |||||||||
                                GTT  TTCC  GGTTCGTGT
                                  AC   GG
GAM1384 DUSP4   3' TGTACTTGTCCCTTTGTTG   9155       T  T   C
                                TAACAAAGG AC AAG ACA
                                ||||||||| || ||| |||
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                                GTTGTTTCC TG TTC TGT
                                    C  _  A
GAM1384  DUSP5    3'  TGTGCTTATGTCTCTTGT    16633     AG T  _
                                ACAA  G AC TAAGCACA
                                ||||  | || ||||||||
                                TGTT  C TG ATTCGTGT
                                  CT _  T
GAM1384  GPM6A    3'  TGCTTCTTATCTTTGTTA    19178          CT
                                TAACAAAGGTA  AAGCA
                                ||||||||||  |||||
                                ATTGTTTCTAT  TTCGT
                                      TC
GAM1384  HDAC5    3'  TGTGCTTGTGTGTTTGTT    19623       GG   T
                                AACAAA  TAC AAGCACA
                                ||||||  ||| |||||||
                                TTGTTT  GTG TTCGTGT
                                   GT  _
GAM1384  MATN4    3'  TGCGCTCAGTTCTTTGTTG   48359         T   A   A
                                TAACAAAGG ACT AGC CA
                                |||||||||  ||| ||| ||
                                GTTGTTTCT TGA TCG GT
                                     _  C  C
GAM1384  NFIB     3'  TGCAACGTAGCCTTTGTTA   20010          _ TAA
                                TAACAAAGGT AC   GCA
                                ||||||||||  ||   |||
                                ATTGTTTCCG TG   CGT
                                      A  CAA
GAM1384  PER2     3'  TGTGCTTACACAGGTGTTA   43364      AAG  AC
                                TAACA   GT  TAAGCACA
                                |||||   ||  ||||||||
                                ATTGT   CA  ATTCGTGT
                                   GGA  C_
GAM1384  TARDBP   3'  TGTGCTTGGATGCTTTTTA   24791   C      _
                                A AAAGGTA CTAAGCACA
                                | |||||||  |||||||||
                                A TTTTCGT GGTTCGTGT
                                 T      A
GAM1384  ALS2CR3  3'  TGTGCCCCTATCTTTGTT    31186          CTAA
                                AACAAAGGTA    GCACA
                                ||||||||||    |||||
                                TTGTTTCTAT    CGTGT
                                     CCC_
GAM1384  BM-009   3'  TGTGTTTAACCTTTATTA    62373     C     AC
                                TAA AAAGGT  TAAGCACA
                                |||  ||||||  ||||||||
                                ATT TTTCCA  ATTTGTGT
                                  A     __
GAM1384  BTBD3    3'  TGTAATGAGATACCTTTGTT   31031          _ AAGC
                                AACAAAGGTA CT    ACA
                                ||||||||||  ||    |||
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                                TTGTTTCCAT GA   TGT
                                     A  GTAA
GAM1384  COL21A1   3'  TGTGCTTAATGCTTTTGT   48774        C
                                ACAAAGGTA TAAGCACA
                                ||||||||| ||||||||
                                TGTTTTCGT ATTCGTGT
                                     A
GAM1384  DIO2      3'  TGTGCTTATACAATTTGTT   7669       G_  C
                                AACAAA  GTA TAAGCACA
                                ||||||  ||| ||||||||
                                TTGTTT  CAT ATTCGTGT
                                   AA  _
GAM1384  DKFZP566M114 3'  TGTGCCTTAAAACTTTGTTA  50450        GTAC   _
                                TAACAAAG   TAAG CACA
                                ||||||||   |||| ||||
                                ATTGTTTC   ATTC GTGT
                                     AAA_   C
GAM1384  IMPACT    3'  TGTCAAGTGCCTTTGTTA   38010          AA
                                TAACAAAGGTACT  GCA
                                ||||||||||||  |||
                                ATTGTTTCCGTGA  TGT
                                      AC
GAM1384  KIAA0513  3'  TGTTTTTAGCCTTTGTTA   29056         ACT
                                TAACAAAGGT   AAGCA
                                |||||||||   |||||
                                ATTGTTTCCG   TTTGT
                                     ATT
GAM1384  MGC14433  3'  TGTCAGGATGCCTTTGTTA   52955          _ AA
                                TAACAAAGGTA CT  GCA
                                |||||||||| ||  |||
                                ATTGTTTCCGT GG  TGT
                                      A  AC
GAM1384  NAP1L1    3'  TGTGCCTTTCATTACTTTGTTA 58304        GTACT_  _
                                TAACAAAG     AAG CACA
                                ||||||||     ||| ||||
                                ATTGTTTC     TTC GTGT
                                     ATTACT   C
GAM1384  PLSCR4    3'  TGCCTAGTACACCTTTGT   40134        __   A
                                ACAAAGGT  ACTA GCA
                                ||||||||  |||| |||
                                TGTTTCCA  TGAT CGT
                                     CA   C
GAM1384  PRO0971   3'  TGTGCTTAGCCTTTTTGT   38319       TA
                                ACAAAGG  CTAAGCACA
                                |||||||  |||||||||
                                TGTTTTT  GATTCGTGT
                                     CC
GAM1384  RHOBTB1   3'  TGTGCATTTATCTTTGTTA   93096          CTAA
                                TAACAAAGGTA   GCACA
                                ||||||||||   |||||
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                                ATTGTTTCTAT   CGTGT
                                      TTA_
GAM1384  SIAT8C   5'  TGTGCTTAGATCGAACTGT   32454    AA__  A
                                ACA   GGT CTAAGCACA
                                |||   ||| |||||||||
                                TGT   CTA GATTCGTGT
                                  CAAG  _
GAM1384  LOC115219 5'  TGTGCTTATTAATTGTTA   73710      AGG  C
                                TAACAA   TA TAAGCACA
                                ||||||   || ||||||||
                                ATTGTT   AT ATTCGTGT
                                   A__  T
GAM1384  LOC221968 3'  TGTGTTCCCACCTTTGTT   94157        ACTA
                                AACAAAGGT   AGCACA
                                |||||||||   ||||||
                                TTGTTTCCA   TTGTGT
                                      CCC_
GAM1384  LOC253292 5'  TGTGCTTAATCTTTCTTA   98772    C    AC
                                TAA AAAGGT  TAAGCACA
                                ||| ||||||  ||||||||
                                ATT TTTCTA  ATTCGTGT
                                  C    __
GAM1384  LOC256965 5'  TGTGCCTTGGGGCTTTGTTG  99419       GTA   _
                                TAACAAAG   CTAAG CACA
                                ||||||||   ||||| ||||
                                GTTGTTTC   GGTTC GTGT
                                     GG_    C
GAM1384  LOC91660  5'  TGTGCTTAGAACTTTGTT   67405      GTA
                                AACAAAG   CTAAGCACA
                                |||||||   |||||||||
                                TTGTTTC   GATTCGTGT
                                   AA_
GAM1385  ADH5     3'  GCTTCTGTGATATTATCTTTAA 7267          T   TT_
                                TTAGGGATAATAT CAT   AGC
                                |||||||||||| |||   |||
                                AATTTCTATTATA GTG   TCG
                                       _   TCT
GAM1385  AES      3'  GTTAGGTGGATACCTGCCCTGA 8525       ATAA
                                TTAGGG    TATTCATTTAGC
                                ||||||    ||||||||||||
                                AGTCCC    ATAGGTGGATTG
                                   GTCC
GAM1385  AGL      3'  GCCATTTGGGGTTATCTCTAGT 7215          A    TTTA
            A                    TATTAGGGATAAT TTCA    GC
                                ||||||||||||| ||||    ||
                                ATGATCTCTATTG GGGT    CG
                                       _   TTAC
GAM1385  APAF1    3'  GTTGGATGAATAATATTAATG  25979    GG   A
                                TA  GATA TATTCATTTAGC
                                ||  |||| ||||||||||||
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                                GT  TTAT ATAAGTAGGTTG
                                 AA    A
GAM1385  APM1     3'  GCTAAATGGACATCATGTTTTC 17784       GG TA___  A
              TGGTG                   TATTAG  A     AT TTCATTTAGC
                                |||||| |    || ||||||||||
                                GTGGTC  T    TA AGGTAAATCG
                                   TT TGTAC  C
GAM1385  APXL     3'  CTAATGGTTGGCCCTGGTG   9713          A    ATTCAT
                                TATTAGGG TAAT     TTAG
                                |||||||| ||||     ||||
                                GTGGTCCC GTTG     AATC
                                     G   GT____
GAM1385  ARF3     3'  GTTGGATGGGTCATCTGTCCTT 9781          _ _
              GGT                    ATTAGGGATA AT ATTCATTTAGC
                                |||||||||| || ||||||||||
                                TGGTTCCTGT TA TGGGTAGGTTG
                                      C  C
GAM1385  BACE     3'  GAAGATGGGTGTTGTTTTCAAT 58086      AG            AGC
              G                   TATT  GGATAATATTCATTT
                                ||||  ||||||||||||||
                                GTAA  TTTGTTGTGGGTAGA
                                  CT            AG
GAM1385  BACE     3'  GCTAAGTGTGGAATTACCTGAT 58088        GATAATATT
              A                   TATTAGG        CATTTAGC
                                |||||||        ||||||||
                                ATAGTCC        GTGAATCG
                                    ATTAAGGT_
GAM1385  BACH2    3'  GCTGGATGTTCAGATTCCTAA  41786         AATATT
                                TTAGGGAT     CATTTAGC
                                ||||||||     ||||||||
                                AATCCTTA     GTAGGTCG
                                     GACTT_
GAM1385  BAZ2A    3'  GCTAGGTGGATTTTCTCT    26512       TAAT
                                AGGGA    ATTCATTTAGC
                                |||||    ||||||||||
                                TCTCT    TAGGTGGATCG
                                  TT__
GAM1385  BCL11A   3'  GCTAAATGTCTGTCTCTAA   43467          ATATT
                                TTAGGGATA    CATTTAGC
                                |||||||||    ||||||||
                                AATCTCTGT    GTAAATCG
                                     CT___
GAM1385  C11orf8  3'  GCTAGCACAAAATATTGTCGCT 9624         G        CAT__
              AATA                   TATTAG GATAATATT     TTAGC
                                |||||| |||||||||    |||||
                                ATAATC CTGTTATAA     GATCG
                                   G        AACAC
GAM1385  C4BPB    5'  GCTGGGTGAATTCCAGCCTGG  7389       GATAAT
                                TTAGG     ATTCATTTAGC
                                |||||     ||||||||||
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                                GGTCC     TAAGTGGGTCG
                                  GACCT_
GAM1385 CAMLG    3' GCTGAGTTTGTATTATTACTGA 10002      GG      TC
            TA                   TATTAG  ATAATAT  ATTTAGC
                                 ||||||  |||||||  |||||||
                                 ATAGTC  TATTATG  TGAGTCG
                                    AT      TT
GAM1385 CAT      3' GCTTAATGTTTATTCCTGATA  10021          TATT    T
                                 TATTAGGGATAA    CATT AGC
                                 ||||||||||||    |||| |||
                                 ATAGTCCTTATT    GTAA TCG
                                       T___    T
GAM1385 CDKN1A   3' GTTGAATGAGAGGTTCCTAA   55271        AATA
                                 TTAGGGAT    TTCATTTAGC
                                 ||||||||    ||||||||||
                                 AATCCTTG    GAGTAAGTTG
                                     GA__
GAM1385 CHC1L    3' GTATGAAGTATTATCTTTGA   8857            _   TTAGC
                                 TTAGGGATAATATT CAT
                                 |||||||||||||| |||
                                 AGTTTCTATTATGA GTA
                                        A   TG
GAM1385 CLN5     3' GCTAAGTGATCTTTCTCTGG   22431       TAATAT
                                 TTAGGGA     TCATTTAGC
                                 |||||||     |||||||||
                                 GGTCTCT     AGTGAATCG
                                     TTCT__
GAM1385 CTRL     3' CTGAGTGACTCCTTGA      10340        TAATAT
                                 TTAGGGA     TCATTTAG
                                 |||||||     ||||||||
                                 AGTTCCT     AGTGAGTC
                                     C_____
GAM1385 CUL4B    3' GTTGAGTGGACTTTTTCTC    14566      T  TA
                                 GGGA AA  TTCATTTAGC
                                 |||| ||  ||||||||||
                                 CTCT TT  AGGTGAGTTG
                                   T  TC
GAM1385 CXorf6   3' GTTGATTTGGGGTTTGTCTTTG 19709           TA    T_
            ATG                    TATTAGGGATAA  TTCA  TTAGC
                                   ||||||||||||  ||||  |||||
                                   GTAGTTTCTGTT  GGGT  AGTTG
                                         TG    TT
GAM1385 DAAM2    3' CTGAGCTGGTCCTTAATA    93902         AATATT  _
                                 TATTAGGGAT     CA TTTAG
                                 ||||||||||     || |||||
                                 ATAATTCCTG     GT GAGTC
                                        _______  C
GAM1385 DAG1     3' CTGGTGAGATTATTTCTGATG  16554       GG    A     TAGC
                                 TATTAG  ATAAT TTCATT
                                 ||||||  ||||| ||||||
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                                GTAGTC  TATTA GAGTGG
                                   TT    _     TCC
GAM1385  DNTT     3'  GCTGAAATACTGTCTATCTCTA 73663          _  TTCA
                ATA                  TATTAGGGATA ATA    TTTAGC
                                     |||||||||||| |||    ||||||
                                     ATAATCTCTAT TGT    AAGTCG
                                           C   CATA
GAM1385  EIF4G2   3'  GCTAGATTTTAATATCCTTGA  9219          A  TTC
                                     TTAGGGATA TA   ATTTAGC
                                     |||||||||  ||   |||||||
                                     AGTTCCTAT AT   TAGATCG
                                           A  TT_
GAM1385  EYA4     3'  GCTGAATGGAGTTAAACTTTAG 15885         ATAATA
                TG                   TATTAGGG     TTCATTTAGC
                                     ||||||||     ||||||||||
                                     GTGATTTC     AGGTAAGTCG
                                           AAATTG
GAM1385  EZH1     3'  GCTAAGTGAAGTGTGGTCCCTG 10552         A    _
                G                    TTAGGGAT ATATT CATTTAGC
                                     |||||||| ||||| ||||||||
                                     GGTCCCTG TGTGA GTGAATCG
                                           G    A
GAM1385  FBXL7    3'  GCTGGATGCTGTCGTCTCTG   25496       TA   TT
                                     TAGGGA  ATA  CATTTAGC
                                     ||||||  |||  ||||||||
                                     GTCTCT  TGT  GTAGGTCG
                                        GC   C_
GAM1385  FLRT2    3'  TTGAATGGAATTATTTTTGATA 26007           A       C
                                     TATTAGGGATAAT TTCATTTAG
                                     |||||||||||| |||||||||
                                     ATAGTTTTTATTA AGGTAAGTT
                                              _       A
GAM1385  FMR2     3'  GCTGTAGTGTTGTCTTTGATA  10696             CATT
                                     TATTAGGGATAATATT    TAGC
                                     ||||||||||||||||    ||||
                                     ATAGTTTCTGTTGTGA    GTCG
                                              T____
GAM1385  FZD3     3'  GCTAAATGAAGCATGATTAGTC 34258         GA    A_____
                TTAGTA                TATTAGG  TAAT    TTCATTTAGC
                                      |||||||  ||||    ||||||||||
                                      ATGATTC  ATTA    AAGTAAATCG
                                         TG    GTACG
GAM1385  FZD7     3'  GCTGGGTGGGGGCCTGTTTCTG 14504     GG   ATA_
                                     TAG  ATA    TTCATTTAGC
                                     |||  |||    ||||||||||
                                     GTC  TGT    GGGTGGGTCG
                                       TT   CCGG
GAM1385  GALNT3   3'  GCTAAATGTAACTTATTCCAAG 16826      A      TATT
                TG                    TATT GGGATAA    CATTTAGC
                                      ||||  |||||||    ||||||||
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                                GTGA CCTTATT    GTAAATCG
                                  A      CAAT
GAM1385  GAN      3'  GTTAGTCTCCATTTATTCCTAG 42122           TATTCAT
                TA                  TATTAGGGATAA      TTAGC
                                    ||||||||||||      |||||
                                    ATGATCCTTATT      GATTG
                                          TACCTCT
GAM1385  GPLD1    3'  GCTGGAGGCCATTATCCTTCAT 93660     T       AT  A
                A                   TAT AGGGATAAT  TC TTTAGC
                                    ||| |||||||||  || ||||||
                                    ATA TTCCTATTA  GG AGGTCG
                                      C        CC  _
GAM1385  GRINL1A  3'  GTTAGGTGAAAGTGTTTTTGA  70069         ATA
                                    TTAGGGATA   TTCATTTAGC
                                    |||||||||   ||||||||||
                                    AGTTTTTGT   AAGTGGATTG
                                          GA_
GAM1385  HSPG2    3'  TGGGAATTGTCTTTAGTG    19841           A
                                    TATTAGGGATAAT TTCA
                                    |||||||||||||| ||||
                                    GTGATTTCTGTTA GGGT
                                            A
GAM1385  KCND2    3'  GCTGAGTGTTCATGTTCCATGG 25383       _     ATATT
                TG                  TATTA GGGATA     CATTTAGC
                                    ||||| ||||||     ||||||||
                                    GTGGT CCTTGT     GTGAGTCG
                                      A      ACTT_
GAM1385  KCNK2    3'  AATGAATGAGAATTGTTTCTGG 27236       GG     A       GC
                TA                  TATTAG  ATAAT TTCATTTA
                                    ||||||  ||||| ||||||||
                                    ATGGTC  TGTTA GAGTAAGT
                                       TT     A       AAG
GAM1385  LMCD1    3'  GTTGGGTGGTGGTAGATCCTTG 28150         AATAT_
                A                   TTAGGGAT      TCATTTAGC
                                    ||||||||      |||||||||
                                    AGTTCCTA      GGTGGGTTG
                                          GATGGT
GAM1385  MGA      3'  CTAATAATTGTCCTTAG      63466           ATTCAT
                                    TTAGGGATAAT      TTAG
                                    ||||||||||      ||||
                                    GATTCCTGTTA      AATC
                                          AT____
GAM1385  NBS1     3'  GCTGGGTGGGTGTCTGTTTTGA 70026       ATA
                                    TTAGGG   ATATTCATTTAGC
                                    ||||||   ||||||||||||
                                    AGTTTT   TGTGGGTGGGTCG
                                       GTC
GAM1385  NDST2    3'  CTAGAAATGTCCTTAATA     14664          ATATTCA
                                    TATTAGGGATA      TTTAG
                                    ||||||||||       |||||
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                                ATAATTCCTGT      AGATC
                                      AA_____
GAM1385  NEB     3'  GCTAATGCTTATTATTTCTAAT 17008      GG     TT   T
                                ATTAG  ATAATA  CATT AGC
                                |||||  ||||||  |||| |||
                                TAATC  TATTAT  GTAA TCG
                                   TT     TC   _
GAM1385  NEB     3'  GCTTCTGCAATATTATTTCTG  17009     GG      _  TTT
                                TAG  ATAATATT CA   AGC
                                |||  |||||||| ||   |||
                                GTC  TATTATAA GT   TCG
                                  TT       C  CT_
GAM1385  NRXN1   5'  GCTAAATGGATTTACCTAGTG  17825       GATAAT
                                TATTAGG     ATTCATTTAGC
                                |||||||     ||||||||||
                                GTGATCC     TAGGTAAATCG
                                    ATT___
GAM1385  NSF     3'  GTTAAATGAGCTTAATGTCTTT 63750        A  __
            G                    TAGGGATA TA  TTCATTTAGC
                                |||||||| ||  |||||||||
                                GTTTCTGT AT  GAGTAAATTG
                                     A  TC
GAM1385  NTSR1   3'  GCTGGATGAGACTGTCCT    11858       ATA
                                GGGATA   TTCATTTAGC
                                ||||||   |||||||||
                                TCCTGT   GAGTAGGTCG
                                   CA_
GAM1385  OGG1    3'  CTAGATGGGGCACCCTGG    34156       ATAATA
                                TTAGGG     TTCATTTAG
                                ||||||     |||||||||
                                GGTCCC     GGGTAGATC
                                   ACG___
GAM1385  PCDH12  5'  GTTAAGTGACTTGTCCCAGATG 33888     A      TAT
                                TATT GGGATAA   TCATTTAGC
                                |||| |||||||   |||||||||
                                GTAG CCCTGTT   AGTGAATTG
                                  A      C__
GAM1385  PIN4    3'  GCTAAGTGAATGTCAACTGTAG 21711      G  ATA
            TA                   TATTA GG   ATATTCATTTAGC
                                |||||  ||   ||||||||||||
                                ATGAT TC   TGTAAGTGAATCG
                                   G  AAC
GAM1385  PMX1    3'  GTTAAAGATATTTGTTGTCTTT 23573          TTCA__
            GA                   TTAGGGATAATA     TTTAGC
                                ||||||||||||     ||||||
                                AGTTTCTGTTGT     AAATTG
                                       TTATAG
GAM1385  PMX1    3'  GTTAAAGATATTTGTTGTCTTT 42962          TTCA__
            GA                   TTAGGGATAATA     TTTAGC
                                ||||||||||||     ||||||
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                                AGTTTCTGTTGT      AAATTG
                                      TTATAG
GAM1385  PPARGC1   3'  GACCATGGTGTTGTTCTTGATG 26079              T   TTAGC
                                TATTAGGGATAATAT CAT
                                ||||||||||||||| |||
                                GTAGTTCTTGTTGTG GTA
                                      _   CCAGT
GAM1385  PPID      3'  GTCTATGAATATGATCCCTAAT 88828           A       TTAGC
              G                  TATTAGGGAT ATATTCAT
                                ||||||||||| ||||||||
                                GTAATCCCTA TATAAGTA
                                      G       TCTG
GAM1385  PTPN7     5'  GCTGAGTGAGCCTCCCCTGG   55463        ATAATA
                                TTAGGG      TTCATTTAGC
                                ||||||      ||||||||||
                                GGTCCC      GAGTGAGTCG
                                   CTCC__
GAM1385  QDPR      3'  GTTATTCAGAATGTTGTTCCTA 6147                ATT_
              ATA                  TATTAGGGATAATATTC    TAGC
                                |||||||||||||||||    ||||
                                ATAATCCTTGTTGTAAG    ATTG
                                      ACTT
GAM1385  RBL2      3'  GCTAAACATCCAATATTTTCTT 20041          T     CA___
              TAATG                 TATTAGGGA AATATT     TTTAGC
                                |||||||||  ||||||    ||||||
                                GTAATTTCT TTATAA     AAATCG
                                      T     CCTAC
GAM1385  RBM8A     3'  GCTGAAATGATTTTCCTGGTA  18810          TAATAT    _
                                TATTAGGGA      TCATT TAGC
                                |||||||||      ||||| ||||
                                ATGGTCCTT      AGTAA GTCG
                                      TT_____     A
GAM1385  RECK      3'  GTTAAAATGTGTTGTTCCAAAT 41199       A         TCA
              A                   TATT GGGATAATAT   TTTAGC
                                |||| ||||||||||   ||||||
                                ATAA CCTTGTTGTG   AAATTG
                                   A         TA_
GAM1385  RGL       3'  GTTAAGTGACACTTTTGTCTCT 31429      T       TAT__
              CATA                   TAT AGGGATAA     TCATTTAGC
                                ||| ||||||||     |||||||||
                                ATA TCTCTGTT     AGTGAATTG
                                   C        TTCAC
GAM1385  RHAG      3'  ATGAATATTATTCTTAAT     6153
                                ATTAGGGATAATATTCAT
                                ||||||||||||||||||
                                TAATTCTTATTATAAGTA

GAM1385  ROCK2     3'  GTTGGAACTAATATATCCTTGA 66624            A    CA_
              TG                   TATTAGGGATA TATT   TTTAGC
                                |||||||||||| ||||   ||||||
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                                GTAGTTCCTAT ATAA   AGGTTG
                                      _    TCA
GAM1385  RP42     3'  AGATGAAGATTATCTTTAGTG  40564           A
                                TATTAGGGATAAT TTCATTT
                                ||||||||||||| |||||||
                                GTGATTTCTATTA AAGTAGA
                                   G
GAM1385  SART2    3'  ATGAATGAATATTTCCTTGATG 26250         T         GC
                                TATTAGGGA AATATTCATTTA
                                ||||||||| ||||||||||||
                                GTAGTTCCT TTATAAGTAAGT
                                      _          AT
GAM1385  SDPR     3'  GTTAAAGCTGTATTTTTCTTAA 17401         T    TCA
                TA                  TATTAGGGA AATAT   TTTAGC
                                ||||||||| |||||   ||||||
                                ATAATTCTT TTATG   AAATTG
                                     T    TCG
GAM1385  SEL1L    3'  GCTGAATGAATCCAATTTTTTA 18603         TAAT_
                ATG                   TATTAGGGA    ATTCATTTAGC
                                |||||||||    ||||||||||
                                GTAATTTTT    TAAGTAAGTCG
                                     TAACC
GAM1385  SEL1L    3'  GCTGGATATTTTGTTTCTGA   18604     GG   TATTC
                                TTAG  ATAA    ATTTAGC
                                ||||  ||||    |||||||
                                AGTC  TGTT    TAGGTCG
                                  TT    TTA__
GAM1385  SERPINA3 3'  GCTGGATGCCTGGGTCTCTGG  61821       AATATT
                                TTAGGGAT     CATTTAGC
                                ||||||||     ||||||||
                                GGTCTCTG     GTAGGTCG
                                     GGTCC_
GAM1385  SERPINB5 3'  GTTGGGTGGATAAGCTATCCCT 12072        A__
                G                    TAGGGATA   TATTCATTTAGC
                                |||||||   ||||||||||||
                                GTCCCTAT   ATAGGTGGGTTG
                                     CGA
GAM1385  SLC12A7  3'  TGAAGCTGTCCCTGATG     22744          ATA
                                TATTAGGGATA   TTCA
                                ||||||||||   ||||
                                GTAGTCCCTGT   AAGT
                                      CG_
GAM1385  SLC20A2  3'  GCTGGATGGAGTATTTCTCTGA 23118        T     _
                                TTAGGGA AATATTC ATTTAGC
                                ||||||| ||||||| |||||||
                                AGTCTCT TTATGAG TAGGTCG
                                     _      G
GAM1385  SLC6A6   3'  GCTGAATGAGGAGGCCCTA   13184      ATAATA
                                TAGGG     TTCATTTAGC
                                |||||     ||||||||||
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                                ATCCC     GAGTAAGTCG
                                   GGAG__
GAM1385  SNX6     3'  GTTAGTGACAGTTATTCCTGA  41443          AT    T
                                TTAGGGATAAT  TCATT AGC
                                ||||||||||  ||||| |||
                                AGTCCTTATTG  AGTGA TTG
                                      AC    _
GAM1385  SOCS5    3'  GTTAAATGGAAATTGTTTTAAA 26684      AG      A
            TG                    TATT  GGATAAT TTCATTTAGC
                                ||||  ||||||| ||||||||||
                                GTAA  TTTGTTA AGGTAAATTG
                                   AT      A
GAM1385  SOX12    3'  CTGGATGGATGTTTCTGA    23685      GG  AAT
                                TTAG  AT   ATTCATTTAG
                                ||||  ||   ||||||||||
                                AGTC  TG   TAGGTAGGTC
                                   TT  ____
GAM1385  SPAP1    5'  GTTGAGAAAATTATCTCTAA   57835          A   AT
                                TTAGGGATAAT TTC  TTAGC
                                ||||||||||| |||  |||||
                                AATCTCTATTA AAG  AGTTG
                                      A   __
GAM1385  SPAP1    5'  GTTGAGAAAATTATCTCTAA   57836          A   AT
                                TTAGGGATAAT TTC  TTAGC
                                ||||||||||| |||  |||||
                                AATCTCTATTA AAG  AGTTG
                                      A   __
GAM1385  SSPN     3'  GCTGAATCTCTTTATTTTCCCT 18684         T    TTC__
            GGTA                    TATTAGGGA AATA     ATTTAGC
                                |||||||||  ||||     |||||||
                                ATGGTCCCT TTAT     TAAGTCG
                                      T    TTCTC
GAM1385  STK31    3'  TGAGTTGTATCTTTAGTA    53079          AT
                                TATTAGGGATA  ATTCA
                                ||||||||||  |||||
                                ATGATTTCTAT  TGAGT
                                      GT
GAM1385  SURF5    3'  GCTAGGTGGGACTCATTCCTAA 56915         AATA
            T                    ATTAGGGAT    TTCATTTAGC
                                |||||||||    ||||||||||
                                TAATCCTTA    GGGTGGATCG
                                     CTCA
GAM1385  SURF5    3'  GCTAGGTGGGACTCATTCCTAA 56916         AATA
            T                    ATTAGGGAT    TTCATTTAGC
                                |||||||||    ||||||||||
                                TAATCCTTA    GGGTGGATCG
                                     CTCA
GAM1385  SYT1     3'  GCTAAAGATTTATTTCTAGT   20113      GG   TAT  A
                                ATTAG  ATAA   TC TTTAGC
                                |||||  ||||   || ||||||
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                                TGATC  TATT   AG AAATCG
                                  TT   T__  _
GAM1385  TSN      3'  GCTTTCTGATGTTGCCTTAATA 17302        A     T  TTT
                                TATTAGGG TAATAT CA   AGC
                                |||||||| |||||| ||   |||
                                ATAATTCC GTTGTA GT   TCG
                                    _     _ CTT
GAM1385  UBL3     3'  GTTAAATGAAGTTTCCTCATA  24025     T    TAATA
                                TAT AGGGA    TTCATTTAGC
                                ||| |||||    ||||||||||
                                ATA TCCTT    AAGTAAATTG
                                  C    TG___
GAM1385  VBP1     3'  GCTGGGTGATACAGATTCTGAT 14030        ATAATAT
              A                  TATTAGGG      TCATTTAGC
                                |||||||      |||||||||
                                ATAGTCTT      AGTGGGTCG
                                    AGACAT_
GAM1385  WHSC1L1  3'  GCTGGATGGGTACAGCTTAA   35500      GATAA
                                TTAGG    TATTCATTTAGC
                                |||||    ||||||||||||
                                AATTC    ATGGGTAGGTCG
                                  GAC__
GAM1385  XPR1     3'  GCTGGGTGGGTGGGAAATATGA 17622      GGGATAA
              TG                  TATTA      TATTCATTTAGC
                                |||||      ||||||||||||
                                GTAGT      GTGGGTGGGTCG
                                  ATAAAGG
GAM1385  ZNF255   5'  TGAATAGTATTCCATGGTG    20499      _     A
                                TATTA GGGATA TATTCA
                                ||||| |||||| ||||||
                                GTGGT CCTTAT ATAAGT
                                  A     G
GAM1385  A4GALT   3'  GCTGGGTGGGGAGGCTCTTTAG 34301        TAATA
                                TTAGGGA    TTCATTTAGC
                                |||||||    ||||||||||
                                GATTTCT    GGGTGGGTCG
                                    CGGAG
GAM1385  AKAP8    3'  CTGAATCAGTTCTCTAATA    20734        TAAT   C
                                TATTAGGGA    ATT ATTTAG
                                |||||||||    ||| ||||||
                                ATAATCTCT    TGA TAAGTC
                                      ____   C
GAM1385  AKAP8    3'  GCTGAAGTACATTGTCCTTAG  20736         ATTCA
                                TTAGGGATAAT    TTTAGC
                                ||||||||||     ||||||
                                GATTCCTGTTA    AAGTCG
                                    CATG_
GAM1385  ALLC     5'  ATTTTGTGAATATTATCTTTTG 37978     T           TTAGC
              TA                  TAT AGGGATAATATTCAT
                                ||| ||||||||||||||
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                                ATG TTTCTATTATAAGTG
                                  T           TTTTAG
GAM1385  ARF4     3'  TGGAATTATTCCTAATA     83708           A
                                TATTAGGGATAAT TTCA
                                |||||||||||| ||||
                                ATAATCCTTATTA AGGT
                                          _
GAM1385  ARG99    3'  GCTAAGTGAGCTTTATCT    50012       TA
                                GGATAA  TTCATTTAGC
                                ||||||  ||||||||||
                                TCTATT  GAGTGAATCG
                                   TC
GAM1385  C1orf9   3'  TGGGTATTGTTTGTAATG    33162       G
                                TATTA GGATAATATTCA
                                ||||| ||||||||||||
                                GTAAT TTTGTTATGGGT
                                   G
GAM1385  C20orf126 3'  GCTGAATGAAGAACAGAATCTT 48734         ATAATA__
            GGTG                   TATTAGGG       TTCATTTAGC
                                |||||||||       ||||||||||
                                GTGGTTCT       AAGTAAGTCG
                                     AAGACAAG
GAM1385  C20orf142 3'  GTTAGGCACTTTTTGTCCCTGG 75287            TATTCA
            TA                   TATTAGGGATAA     TTTAGC
                                ||||||||||||     ||||||
                                ATGGTCCCTGTT     GGATTG
                                      TTTCAC
GAM1385  C20orf162 5'  CTGAATGGGCTCCTGAT     55499        ATAATA
                                ATTAGGG     TTCATTTAG
                                |||||||     |||||||||
                                TAGTCCT     GGGTAAGTC
                                   C_____
GAM1385  C6.1A    3'  GCTAGGTGACAAGTTCTTGG   44533         AATAT
                                TTAGGGAT    TCATTTAGC
                                ||||||||    |||||||||
                                GGTTCTTG    AGTGGATCG
                                     AAC__
GAM1385  C8orf4   3'  TGAGTATTGTCTATTGGTA    39692        _
                                TATTAG GGATAATATTCA
                                |||||| ||||||||||||
                                ATGGTT TCTGTTATGAGT
                                   A
GAM1385  CAMKK2   3'  CTAGATGTGGCTCCTAGTG    22619         ATAATATT
                                TATTAGGG       CATTTAG
                                ||||||||       |||||||
                                GTGATCCT       GTAGATC
                                     CGGT____
GAM1385  CBX8     3'  GTTGGAAAGATTATCTCTAG   40610           ATTCA
                                TTAGGGATAAT     TTTAGC
                                ||||||||||     ||||||
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                                GATCTCTATTA    AGGTTG
                                     GAA__
GAM1385  CDC14A   3'  ATGGTTTTGTCTCTAATG    53965          TAT
                                TATTAGGGATAA   TCAT
                                ||||||||||||  ||||
                                GTAATCTCTGTT   GGTA
                                     TT_
GAM1385  CLIC2    3'  ATGAGTTTATTTCTGATA    8914       GG   T
                                TATTAG  ATAA ATTCAT
                                ||||||  |||| ||||||
                                ATAGTC  TATT TGAGTA
                                   TT   _
GAM1385  CPR2     3'  GCTGAGTGAAAGGCACCCTGA  48834       ATAATA
                                TTAGGG     TTCATTTAGC
                                ||||||     ||||||||||
                                AGTCCC     AAGTGAGTCG
                                   ACGGA_
GAM1385  DCTD     3'  GCTGAATAATGAGTTGTTCCTA 10392          __  C
                 G                TTAGGGATAAT  ATT ATTTAGC
                                  ||||||||||  ||| |||||||
                                  GATCCTTGTTG  TAA TAAGTCG
                                       AG  _
GAM1385  DDM36    3'  GTTAGGGTCTTTACTCCCTAAT 40928         _  TATTCA
                 G                TATTAGGGA TAA     TTTAGC
                                  |||||||| |||     ||||||
                                  GTAATCCCT ATT     GGATTG
                                       C  TCTG__
GAM1385  DJ667H12.2 3'  GCTAGATGAAATGGCTTAATG  39478       GATA  A
                                TATTAGG    AT TTCATTTAGC
                                |||||||    || ||||||||||
                                GTAATTC    TA AAGTAGATCG
                                   GG__  _
GAM1385  DKFZP434A0225 3'  GCTAGGTGGAGTATGCTTGATA 95524       G  ATA
                                TATTAGG ATA   TTCATTTAGC
                                ||||||| |||   ||||||||||
                                ATAGTTC TAT   AGGTGGATCG
                                   G  G__
GAM1385  DKFZP434H0820 3'  GTTGGGTGGGCCCTCCCTGA   64585       TAATA
                                TTAGGGA    TTCATTTAGC
                                |||||||    ||||||||||
                                AGTCCCT    GGGTGGGTTG
                                   CCC__
GAM1385  DKFZP564O0523 3'  GCTAAGTTTTGTGTTTTTTTTA 50421         T    TC_
                 GTA                TATTAGGGA AATAT   ATTTAGC
                                    |||||||| |||||   |||||||
                                    ATGATTTTT TTGTG   TGAATCG
                                         T    TTT
GAM1385  DKFZP761E2110 3'  GAGTATTTATTCCTAATA    48963          _
                                TATTAGGGATAA TATTC
                                |||||||||||| |||||
```

```
                                ATAATCCTTATT ATGAG
                                       T
GAM1385  DKFZP761F241 3'  GCTGAGTAATTGTTTCTAATG  49582       GG    ATTC
                                TATTAG  ATAAT    ATTTAGC
                                ||||||  |||||    |||||||
                                GTAATC  TGTTA    TGAGTCG
                                   TT    A___
GAM1385  DKFZP761F241 3'  GCTGAGTAATTGTTTCTAATG  49583       GG    ATTC
                                TATTAG  ATAAT    ATTTAGC
                                ||||||  |||||    |||||||
                                GTAATC  TGTTA    TGAGTCG
                                   TT    A___
GAM1385  DKFZp761G0313 3'  AAATGAAATTATCTTTGATA   66390            A
                                TATTAGGGATAAT TTCATTT
                                |||||||||||||| |||||||
                                ATAGTTTCTATTA AAGTAAA
                                                _
GAM1385  DKFZp761O132 5'  GCTGGATGGATGTTTGTTGA   51170      G  TA
                                TTAG GA  ATATTCATTTAGC
                                ||||  ||  ||||||||||||||
                                AGTT TT  TGTAGGTAGGTCG
                                  G  __
GAM1385  EIF2S1    3'  GCTGAATATTTTTTATTTCTAA 15847      GG    TATTC
                                TTAG  ATAA    ATTTAGC
                                ||||  ||||    |||||||
                                AATC  TATT    TAAGTCG
                                  TT    TTTTA
GAM1385  ENPP4     3'  GTTAAGTGGCAGAATAGCCTTA 30718         ATAATAT_
            GTG                   TATTAGGG       TCATTTAGC
                                ||||||||       |||||||||
                                GTGATTCC       GGTGAATTG
                                     GATAAGAC
GAM1385  ERAP140   3'  GTTGAATGCAATTTTTATTTTT 75707           T_  _
            GGTA                   TATTAGGGATAA  ATT CATTTAGC
                                ||||||||||||  ||| ||||||||
                                ATGGTTTTTATT  TAA GTAAGTTG
                                       TT   C
GAM1385  FBX30     3'  CTAGATGGGTACCAGGTG    53745     TA  GATAA
                                TAT  GG    TATTCATTTAG
                                |||  ||    ||||||||||
                                GTG  CC    ATGGGTAGATC
                                  GA  _____
GAM1385  FLJ10300  3'  ATGAATATTTCTTTGGTA    36468          T
                                TATTAGGGA AATATTCAT
                                |||||||| |||||||||
                                ATGGTTTCT TTATAAGTA
                                                _
GAM1385  FLJ10375  5'  GTTGAATGAATGTCTGGCTC   36560     ATA_
                                GGG    ATATTCATTTAGC
                                |||    ||||||||||||
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                              CTC    TGTAAGTAAGTTG
                                GGTC
GAM1385  FLJ10656  3'  GTTAGGTGGATAGTCCTGTAGT 36909      _    AA
              G                  TATTA GGGAT  TATTCATTTAGC
                                 ||||| |||||  ||||||||||||
                                 GTGAT TCCTG  ATAGGTGGATTG
                                   G    __
GAM1385  FLJ10980  3'  GTGATGTTTGTCTCTAGTG   65254          TAT
                                 TATTAGGGATAA   TCAT
                                 ||||||||||||   ||||
                                 GTGATCTCTGTT   AGTG
                                        TGT
GAM1385  FLJ11149  3'  GCTAAATGCTATCTTTAG    37687         ATATT
                                 TTAGGGATA    CATTTAGC
                                 |||||||||    ||||||||
                                 GATTTCTAT    GTAAATCG
                                      C_____
GAM1385  FLJ12649  3'  GCTGTCAGATTGTTTCTAATA  45094       GG    ATTCATT
                                 TATTAG  ATAAT      TAGC
                                 ||||||  |||||      ||||
                                 ATAATC  TGTTA      GTCG
                                    TT    GACT____
GAM1385  FLJ12787  3'  ATCTGGGATGGATATTAATTTT 50689        A         AGC
              AATA                 TATTAGGG TAATATTCATTT
                                   ||||||||| ||||||||||||
                                   ATAATTTT ATTATAGGTAGG
                                      A          GTCTAT
GAM1385  FLJ12892  3'  GCTGAATGTTGTGTTATCACTA 68453       G       T_
              ATA                    TATTAG GATAATAT  CATTTAGC
                                     |||||| ||||||||  ||||||||
                                     ATAATC CTATTGTG  GTAAGTCG
                                        A       TT
GAM1385  FLJ13194  3'  GTTGGAACATTGTTATCCTTG  47873          TTCA
                                 TAGGGATAATA    TTTAGC
                                 ||||||||||    ||||||
                                 GTTCCTATTGT    AGGTTG
                                        TACA
GAM1385  FLJ13657  3'  GTTAGATGAGTATTTAGCTGTG 46140    G  AT_
                                 TA GG   AATATTCATTTAGC
                                 || ||   ||||||||||||||
                                 GT TC   TTATGAGTAGATTG
                                  G  GAT
GAM1385  FLJ13769  3'  GCTGGGTGGCCTGGCCCTGGTA 47257        ATAATAT
                                 TATTAGGG      TCATTTAGC
                                 ||||||||      |||||||||
                                 ATGGTCCC      GGTGGGTCG
                                      GGTCC__
GAM1385  FLJ14437  3'  GTGATATCCCTAGTA      51799          ATAT
                                 TATTAGGGATA    TCAT
                                 ||||||||||    ||||
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                                ATGATCCCTAT   AGTG
                                      ____
GAM1385 FLJ14600 3' TTAGGTGCTGGTTCCTAG   52530       AATATT
                                TTAGGGAT    CATTTAG
                                ||||||||    |||||||
                                GATCCTTG    GTGGATT
                                    GTC___
GAM1385 FLJ14668 3' GCTGTGATATATTTTCCTAGTG 52588        T   _   TT
                                TATTAGGGA AATAT TCAT  AGC
                                ||||||||| ||||| ||||  |||
                                GTGATCCTT TTATA AGTG  TCG
                                      _   T   __
GAM1385 FLJ14735 3' TTGAGTGGATTCCTGGGTA   52670    TA   TAAT
                                TAT  GGGA   ATTCATTTAG
                                |||  ||||   ||||||||||
                                ATG  TCCT   TAGGTGAGTT
                                  GG   ____
GAM1385 FLJ20127 3' GCTAAATGAGATGTTTCTAAT  35080     GG   ATA
                                ATTAG  ATA   TTCATTTAGC
                                |||||  |||   ||||||||||
                                TAATC  TGT   GAGTAAATCG
                                   TT   A__
GAM1385 FLJ20436 3' GCTAGGTGGGAGCTGTCTTTG  35626       ATA
                                TAGGGATA   TTCATTTAGC
                                ||||||||   ||||||||||
                                GTTTCTGT   GGGTGGATCG
                                    CGA
GAM1385 FLJ20986 5' GCTAGGTGGATGGATGTT    44837     A_
                                GATA  TATTCATTTAGC
                                ||||  ||||||||||||
                                TTGT  GTAGGTGGATCG
                                  AG
GAM1385 FLJ21596 3' GCTGAGTGGATGGTTGCTGA  46117     G   AA
                                TTAG GAT  TATTCATTTAGC
                                |||| |||  ||||||||||||
                                AGTC TTG  GTAGGTGAGTCG
                                  G   __
GAM1385 FLJ21615 3' AAACTTGAATTTATCTTTGATA 50805          T    TTTAGC
                                TATTAGGGATAA ATTCA
                                |||||||||||| |||||
                                ATAGTTTCTATT TAAGT
                                      _    TCAAAT
GAM1385 FLJ22969 3' GCTGAGTGTTTGTTTCTA    69210    GG    TATT
                                TAG  ATAA    CATTTAGC
                                |||  ||||    ||||||||
                                ATC  TGTT    GTGAGTCG
                                  TT   T___
GAM1385 FLJ23024 3' GTTGAATGAGTGAGATGTTTAG 46847      G  AA
                                TTAGG AT  TATTCATTTAGC
                                ||||| ||  ||||||||||||
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                                GATTT TA  GTGAGTAAGTTG
                                   G  GA
GAM1385  FLJ23058  3'  GCTGGGTTCCGCTTTGTCCCTG 45526          TATTC_
                 GT                  ATTAGGGATAA     ATTTAGC
                                     ||||||||||      |||||||
                                     TGGTCCCTGTT     TGGGTCG
                                           TCGCCT
GAM1385  FLJ23416  3'  GTTAAATGCTCTGGGTTTTCTC 50934         T   ATT___
                 TGATA                 TATTAGGGA AAT     CATTTAGC
                                     |||||||||  |||      ||||||||
                                     ATAGTCTCT TTG     GTAAATTG
                                           T   GGTCTC
GAM1385  FLJ23560  3'  GTTGAATAAAACAGTGTTATCT 45509            C____
                 TTAAT                 ATTAGGGATAATATT     ATTTAGC
                                     ||||||||||||||||     |||||||
                                     TAATTTCTATTGTGA     TAAGTTG
                                           CAAAA
GAM1385  GENX-3414 3'  GCTGAGTGAGGTGGCCTGAATG 15457      A   ATAATA
                                     TATT GGG     TTCATTTAGC
                                     ||||  |||     ||||||||||
                                     GTAA TCC     GAGTGAGTCG
                                        G   GGTG__
GAM1385  GMPPB    5'  GCTGCTCTGTACTGTCCCTGGT 26223          A   TCATT
                 G                   TATTAGGGATA TAT     TAGC
                                     ||||||||||  |||     ||||
                                     GTGGTCCCTGT ATG     GTCG
                                           C   TCTC_
GAM1385  HSJ1     3'  GCTGGGCTTTTGTGCCCTGGTA 23082         _    TATTCA
                                     TATTAGGG ATAA      TTTAGC
                                     ||||||||  ||||      ||||||
                                     ATGGTCCC TGTT      GGGTCG
                                          G    TTC___
GAM1385  HSPC228   3'  GTTAATAATTTATTTCCCTAAT 33649          T    TTCAT
                 A                    TATTAGGGA AATA     TTAGC
                                     |||||||||  ||||     |||||
                                     ATAATCCCT TTAT     AATTG
                                           _   TTAAT
GAM1385  IPLA2(GAMMA) 5'  GCTGAGTGGGTGGCGACCTAG  61341       GATAA
                                     TTAGG     TATTCATTTAGC
                                     |||||     ||||||||||||
                                     GATCC     GTGGGTGAGTCG
                                        AGCG_
GAM1385  ITGB8    3'  GCTAGATGAATAAATGATTCGT 11056     G    AA__
                 G                    TA GGAT    TATTCATTTAGC
                                     ||  ||||    ||||||||||||
                                     GT CTTA    ATAAGTAGATCG
                                      G    GTAA
GAM1385  KALI     3'  GTTGGATGGGCCCATCCTGATA 54696         ATAATA
                                     TATTAGGG      TTCATTTAGC
                                     ||||||||      ||||||||||
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                                ATAGTCCT     GGGTAGGTTG
                                     ACCC__
GAM1385  KIAA0161  3'  GTTGAGTGGACGGACTTATTCC 29208         TA___
              TG                   TAGGGATAA    TTCATTTAGC
                                   |||||||||    ||||||||||
                                   GTCCTTATT    AGGTGAGTTG
                                        CAGGC
GAM1385  KIAA0226  3'  CTGGGTCCTTCCCTGGTG    64258         TAATATTC
                                   TATTAGGGA       ATTTAG
                                   |||||||||       ||||||
                                   GTGGTCCCT       TGGGTC
                                        TCC_____
GAM1385  KIAA0321  3'  GCTGAAGTCAGTGTCTCTGGTG 63055          ATATTCA
                                   TATTAGGGATA      TTTAGC
                                   ||||||||||       ||||||
                                   GTGGTCTCTGT      AAGTCG
                                         GACTG__
GAM1385  KIAA0416  3'  CTGAGTGACTCTTTAATA    32091         TAATAT
                                   TATTAGGGA     TCATTTAG
                                   |||||||||     ||||||||
                                   ATAATTTCT     AGTGAGTC
                                        C_____
GAM1385  KIAA0459  3'  GTTAGGTGGATGTGAACTTAA  61658      GATA
                                   TTAGG    ATATTCATTTAGC
                                   |||||    ||||||||||||
                                   AATTC    TGTAGGTGGATTG
                                      AAG_
GAM1385  KIAA0711  3'  GTTAGATGAGGCTATTGCCTTG 30153        A    __
              ATG                    TATTAGGG TAATA  TTCATTTAGC
                                   |||||||| |||||  ||||||||||
                                   GTAGTTCC GTTAT  GAGTAGATTG
                                        _    CG
GAM1385  KIAA0769  3'  GCTAGCCAAATTGTCCTTGA   29757          ATTCAT
                                   TTAGGGATAAT     TTAGC
                                   ||||||||||     |||||
                                   AGTTCCTGTTA     GATCG
                                         AACC__
GAM1385  KIAA0794  3'  GTTATAGGATATGGTTTCTAAT 81237       GG  A     ATT
              G                     TATTAG  AT ATATTC   TAGC
                                   ||||||  || ||||||   ||||
                                   GTAATC  TG TATAGG   ATTG
                                      TT  G     AT_
GAM1385  KIAA0820  3'  GTTGAATGAAGTCTGAAACTCT 69591        ATAATA__
              AGTA                    TATTAGGG       TTCATTTAGC
                                   ||||||||       ||||||||||
                                   ATGATCTC       AAGTAAGTTG
                                        AAAGTCTG
GAM1385  KIAA0841  3'  GCTTTCCCATGTAGTCCTTAGT 71897          A    TCATTT
              G                     TATTAGGGAT ATAT      AGC
                                   |||||||||| ||||      |||
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                                GTGATTCCTG TGTA      TCG
                                     A    CCCTT_
GAM1385  KIAA1116  3'  GTTGGGTGAATTTTGTTTTTAG 30304          T
                                TTAGGGATAA ATTCATTTAGC
                                |||||||||| ||||||||||
                                GATTTTTGTT TAAGTGGGTTG
                                     T
GAM1385  KIAA1165  3'  GCTAAAACAATATTATTTCCAG 67994      A GG       CA
           TA                     TATT G  ATAATATT  TTTAGC
                                |||| |  ||||||||  ||||||
                                ATGA C  TATTATAA  AAATCG
                                  C TT       CA
GAM1385  KIAA1229  3'  GCTAAATGAATGTATATT    62755      _
                                GATA ATATTCATTTAGC
                                |||| ||||||||||||
                                TTAT TGTAAGTAAATCG
                                  A
GAM1385  KIAA1350  3'  GCTAAATGGATAAACCTCATA  73087     T   GATAA
                                TAT AGG     TATTCATTTAGC
                                ||| |||     ||||||||||||
                                ATA TCC     ATAGGTAAATCG
                                  C   AA___
GAM1385  KIAA1372  3'  GTTGGGTGAAGTGCCCTGA    93321       ATAATA
                                TTAGGG      TTCATTTAGC
                                ||||||      ||||||||||
                                AGTCCC      AAGTGGGTTG
                                    GTG___
GAM1385  KIAA1486  3'  TGAATATTGATGTCCTTA     67981         ___
                                TAGGGATA   ATATTCA
                                ||||||||   |||||||
                                ATTCCTGT   TATAAGT
                                     AGT
GAM1385  KIAA1546  3'  GCTAAGAAAATGGTGTCTTTAA 68499          A    CA
           TA                     TATTAGGGATA TATT  TTTAGC
                                |||||||||| ||||  ||||||
                                ATAATTTCTGT GTAA  GAATCG
                                     G    AA
GAM1385  KIAA1554  3'  GTTAGAGGCAGTATCCTTAATA 96860          ATATTCA
                                TATTAGGGATA       TTTAGC
                                ||||||||||       ||||||
                                ATAATTCCTAT       AGATTG
                                     GACGG__
GAM1385  KIAA1557  3'  GCTTTAATGTTATCTTTGA    61786           CATTT
                                TTAGGGATAATATT     AGC
                                ||||||||||||||     |||
                                AGTTTCTATTGTAA     TCG
                                     TT___
GAM1385  KIAA1822  3'  GTTGAGTGGGCATCTTCCT    68196      TA  A
                                GGGA  AT TTCATTTAGC
                                ||||  || ||||||||||
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                                TCCT  TA GGGTGAGTTG
                                  TC  C
GAM1385  KIAA1854  3'  TGATTTGTTCCTAGTA      72216          TAT
                                TATTAGGGATAA   TCA
                                ||||||||||||  |||
                                ATGATCCTTGTT   AGT
                                       T__
GAM1385  KIAA1867  3'  GCTGAGTGCGCTGTGCTTAGTG 96483       G   ATATT
                                TATTAGG ATA    CATTTAGC
                                ||||||| |||    ||||||||
                                GTGATTC TGT    GTGAGTCG
                                    G   CGC__
GAM1385  KIAA1878  3'  GCTGAGTGAGAAGTCTTTTGTA 93369     T     AATA
                                TAT AGGGAT    TTCATTTAGC
                                ||| ||||||    ||||||||||
                                ATG TTTCTG    GAGTGAGTCG
                                  T     AA__
GAM1385  KIAA1957  3'  GCTGACTGGAGTATTATTTTTC 76215     T          AT_
            ATG                   TAT AGGGATAATATTC   TTAGC
                                ||| ||||||||||||  |||||
                                GTA TTTTTATTATGAG   AGTCG
                                  C           GTC
GAM1385  KREMEN    3'  GCTAGATGGATGTGTACCTGGT 50235       GATA
            G                    TATTAGG    ATATTCATTTAGC
                                |||||||    ||||||||||||
                                GTGGTCC    TGTAGGTAGATCG
                                    ATG_
GAM1385  LANO      3'  TAAATGATGTCTCTGATG    37162          ATAT
                                TATTAGGGATA    TCATTTA
                                ||||||||||    |||||||
                                GTAGTCTCTGT    AGTAAAT
                                      ____
GAM1385  LCHN      3'  GCTGGGCTGCCCTGTTGTTCCT 87473          TT_ _
            GA                    TTAGGGATAATA   CA TTTAGC
                                ||||||||||||  || ||||||
                                AGTCCTTGTTGT   GT GGGTCG
                                       CCC  C
GAM1385  LGP2      5'  GTTAAGTGGGACTGCCCTGG   44380       ATAATA
                                TTAGGG     TTCATTTAGC
                                ||||||     ||||||||||
                                GGTCCC     GGGTGAATTG
                                   GTCA__
GAM1385  LRMP      5'  GCTGGATGCCTTATCTCTGG   21586         TATT
                                TTAGGGATAA    CATTTAGC
                                ||||||||||    ||||||||
                                GGTCTCTATT    GTAGGTCG
                                      CC__
GAM1385  LY6G6C    3'  GCTTCTGTGTTGTCCCCAGTG  48273      A        TCATTT
                                TATT GGGATAATAT     AGC
                                |||| ||||||||||     |||
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                                GTGA CCCTGTTGTG     TCG
                                  C        TCT___
GAM1385  MARK2    5'  GCTGAATGGAAGTCGCTGGTA  66222      G   AATA
                                TATTAG GAT    TTCATTTAGC
                                ||||||| |||    ||||||||||
                                ATGGTC CTG    AGGTAAGTCG
                                   G   A___
GAM1385  MGC10981 3'  GCTGAGTGTCTCATGTCTTAAT 51986       ATAATATT
             G                   TATTAGGG      CATTTAGC
                                ||||||||       ||||||||
                                GTAATTCT       GTGAGTCG
                                     GTACTCT_
GAM1385  MGC12217 5'  GTTGAATGAATGTCTGGCTC   52288     ATA_
                                GGG    ATATTCATTTAGC
                                |||    ||||||||||||
                                CTC    TGTAAGTAAGTTG
                                  GGTC
GAM1385  MGC12921 5'  CTGAGTTCCTGTCCCTGA     64514        ATATTC
                                TTAGGGATA      ATTTAG
                                |||||||||      ||||||
                                AGTCCCTGT      TGAGTC
                                     CCT___
GAM1385  MGC12945 5'  GCTAAGTGGTCGGTTCCTGG   51267       AATAT
                                TTAGGGAT     TCATTTAGC
                                ||||||||     |||||||||
                                GGTCCTTG     GGTGAATCG
                                     GCT__
GAM1385  MGC16142 5'  GCTAAATGGGTCGTGTGTTTCT 52265     GG   AT__
             GA                   TTAG  ATA    ATTCATTTAGC
                                ||||  |||    ||||||||||||
                                AGTC  TGT    TGGGTAAATCG
                                  TT   GTGC
GAM1385  MGC4268  3'  GCTGAGTGTTTCCTTTGTCCTT 49544         TATT__
             GG                   TTAGGGATAA      CATTTAGC
                                ||||||||||      ||||||||
                                GGTTCCTGTT      GTGAGTCG
                                     TCCTTT
GAM1385  MGC4643  3'  GTTGAAGGAATATTGTTTCTAA 52146      GG        A
                                TTAG  ATAATATTC TTTAGC
                                ||||  ||||||||| ||||||
                                AATC  TGTTATAAG AAGTTG
                                  TT        G
GAM1385  NCKX3    3'  GTTGAATGTTTCTGTCTGTGGT 40727       G     ATATT
             G                    TATTA GGATA     CATTTAGC
                                ||||| |||||     ||||||||
                                GTGGT TCTGT     GTAAGTTG
                                  G    CTTT_
GAM1385  NEK1     3'  ATGTATATTATTTCTAATA   97560        GG      T
                                TATTAG  ATAATAT CAT
                                ||||||  ||||||| |||
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                                ATAATC  TATTATA GTA
                                   TT      T
GAM1385  POLYDOM   3'  GCTAGCATTGTTGTTCTTGGT  44687           TTCAT
                                ATTAGGGATAATA    TTAGC
                                ||||||||||||    |||||
                                TGGTTCTTGTTGT    GATCG
                                      TAC__
GAM1385  PPM1A     3'  GCTGGGCCTGCTGCTGTTCCTA 41009          ATATTCA_
           GTA                    TATTAGGGATA       TTTAGC
                                ||||||||||       ||||||
                                ATGATCCTTGT       GGGTCG
                                      CGTCGTCC
GAM1385  PPP1R10   3'  GCTAAGTTCATTATTCCTCATG 12231     T       ATTC
                                TAT AGGGATAAT    ATTTAGC
                                ||| |||||||||    |||||||
                                GTA TCCTTATTA    TGAATCG
                                  C        CT__
GAM1385  PRAX-1    3'  CTAAATGGCTCCTTAA      17655        TAATAT
                                TTAGGGA     TCATTTAG
                                |||||||     ||||||||
                                AATTCCT     GGTAAATC
                                    C_____
GAM1385  PRO0159   5'  GCTGGGTGGGTATAGGCT    26947    ATA
                                GG   ATATTCATTTAGC
                                ||   ||||||||||||
                                TC   TATGGGTGGGTCG
                                 GGA
GAM1385  PRO1430   3'  TGAGTATTGTCTATTGGTA    38357       _
                                TATTAG GGATAATATTCA
                                ||||||| ||||||||||||
                                ATGGTT TCTGTTATGAGT
                                   A
GAM1385  PSMD10    3'  GTGTTGTTGTCCCCAGTG     12533      A       TT
                                TATT GGGATAATA  CAT
                                |||| |||||||||  |||
                                GTGA CCCTGTTGT  GTG
                                  C        T_
GAM1385  RAB40A    5'  GTTGGGTGAATATTATTTATGA 82945     GG
                                TTA  GATAATATTCATTTAGC
                                |||  ||||||||||||||||
                                AGT  TTATTATAAGTGGGTTG
                                  AT
GAM1385  RBM11     3'  TGCATATTGTTCCTAATG    59239            T
                                TATTAGGGATAATAT CA
                                |||||||||||||| ||
                                GTAATCCTTGTTATA GT
                                          C
GAM1385  SCDGF-B   3'  GTTAGATGAGTGACCTAA    53634       GATAA
                                TTAGG    TATTCATTTAGC
                                |||||    ||||||||||||
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                                AATCC    GTGAGTAGATTG
                                  A____
GAM1385 SEMA7A   3' GCTGGGTGGCTGGTGTTCCTGA 14610        A  TT
                                TTAGGGATA TA  CATTTAGC
                                ||||||||| ||  ||||||||
                                AGTCCTTGT GT  GTGGGTCG
                                    G  CG
GAM1385 SGK2    3' GCTGGGTACGTGACTATCCCTA 33252         A_  TC
           ATA                   TATTAGGGATA  TAT  ATTTAGC
                                ||||||||||  |||  |||||||
                                ATAATCCCTAT  GTG  TGGGTCG
                                      CA   CA
GAM1385 ShrmL   3' GTTATTGGTGTTTGTTCCTGAT 40851          TAT   TT
           G                    TATTAGGGATAA   TCA  TAGC
                                ||||||||||||   |||  ||||
                                GTAGTCCTTGTT   GGT  ATTG
                                      TGT   T_
GAM1385 SLC38A4  3' GCTTTTTCATGTTATTCCTAA  36343          TCATTT
                                TTAGGGATAATAT     AGC
                                ||||||||||||      |||
                                AATCCTTATTGTA     TCG
                                      CTTTT_
GAM1385 SPTLC2   3' GCTAGTTCTCTTTTATTCTTGA 17997          TATTCAT
           TG                   TATTAGGGATAA      TTAGC
                                ||||||||||||      |||||
                                GTAGTTCTTATT      GATCG
                                      TTCTCTT
GAM1385 ST13    3' TGGATATGTGGTTCCTGATG   15434         A__
                                TATTAGGGAT   ATATTCA
                                ||||||||||   |||||||
                                GTAGTCCTTG   TATAGGT
                                     GTG
GAM1385 STRIN    3' GTTAAAATTGGGTATGTTCTTA 33232          A    __
           ATA                    TATTAGGGATA TATTCA  TTTAGC
                                ||||||||||| ||||||  ||||||
                                ATAATTCTTGT ATGGGT  AAATTG
                                     _     TA
GAM1385 SWAP2    3' GCTGCTGGTTTTATCTCTAGTG 23901          TAT   TT
                                TATTAGGGATAA   TCA  TAGC
                                ||||||||||||   |||  ||||
                                GTGATCTCTATT   GGT  GTCG
                                      TT_   C_
GAM1385 TEB4    3' GCTAGGTGAGGAAATTATTTTT 61284          A__
           AAT                    ATTAGGGATAAT   TTCATTTAGC
                                ||||||||||||   ||||||||||
                                TAATTTTTATTA   GAGTGGATCG
                                      AAG
GAM1385 TTC2    3' GTTGGATGCCCTGTGTCTCTG  13877        ATATT
                                TAGGGATA    CATTTAGC
                                ||||||||    ||||||||
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                                GTCTCTGT    GTAGGTTG
                                    GTCCC
GAM1385 UBE3B    5' GCTGGGTGATTTGTTCCTG   77446        TAT
                                TAGGGATAA   TCATTTAGC
                                |||||||||   |||||||||
                                GTCCTTGTT   AGTGGGTCG
                                     T__
GAM1385 VEST1    3' GTTAAGTGAATGGATCTAA   54764      GATAA
                                TTAGG    TATTCATTTAGC
                                |||||    ||||||||||||
                                AATCT    GTAAGTGAATTG
                                  AG___
GAM1385 WBSCR20A 5' GCTGGATGGAGTGCCCTGG   50572      ATAATA
                                TTAGGG     TTCATTTAGC
                                ||||||     ||||||||||
                                GGTCCC     AGGTAGGTCG
                                   GTG___
GAM1385 XYLT1    3' TGAACTATTCTCCTTAGTA   78416        T   _
                                TATTAGGGA AATA TTCA
                                ||||||||| |||| ||||
                                ATGATTCCT TTAT AAGT
                                     C   C
GAM1385 ZFP95    3' GCTGGATGGTATGTGTTTCTG 28120    GG   ATAT
                                TAG  ATA    TCATTTAGC
                                |||  |||    |||||||||
                                GTC  TGT    GGTAGGTCG
                                  TT   GTAT
GAM1385 ZNF197   3' GTTAAGTGAAAGGATCTTTG  23759      AATA
                                TAGGGAT    TTCATTTAGC
                                |||||||    ||||||||||
                                GTTTCTA    AAGTGAATTG
                                   GGA_
GAM1385 ZNF225   5' GCTGCAGTTTTGTCCCTGGTA 26273         T   CATT
                                TATTAGGGATAA ATT    TAGC
                                |||||||||||| |||    ||||
                                ATGGTCCCTGTT TGA    GTCG
                                       T   C___
GAM1385 ZNF33A   3' CTAACATTATCCTTGATG    92994          ATTCAT
                                TATTAGGGATAAT     TTAG
                                ||||||||||||      ||||
                                GTAGTTCCTATTA     AATC
                                       C_____
GAM1385 LOC115219 5' GCTGGGTGAGTGTGCACTTGGT 73697      GATA
                                ATTAGG    ATATTCATTTAGC
                                ||||||    ||||||||||||
                                TGGTTC    TGTGAGTGGGTCG
                                   ACG_
GAM1385 LOC122830 5' CTGAGTGAGAACCTTGG     74630      ATAATA
                                TTAGGG     TTCATTTAG
                                ||||||     |||||||||
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                                GGTTCC     GAGTGAGTC
                                   AA____
GAM1385  LOC127703 3'  GCTGAGGCTATTGTCCCTGATG 75178            TTCA
                                TATTAGGGATAATA    TTTAGC
                                |||||||||||||    ||||||
                                GTAGTCCCTGTTAT    GAGTCG
                                      CG__
GAM1385  LOC130502 3'  GTTGAATGGGTTTTTTTTAATG 75444         TAAT
                                TATTAGGGA    ATTCATTTAGC
                                |||||||||    ||||||||||
                                GTAATTTTT    TGGGTAAGTTG
                                     TT__
GAM1385  LOC137221 5'  GCTGGCTGAGTTTTATTTCTGA 76475       GG    T    T
            TG                    TATTAG  ATAA ATTCA TTAGC
                                |||||||  |||| ||||| |||||
                                GTAGTC  TATT TGAGT GGTCG
                                   TT    T    C
GAM1385  LOC137221 5'  TGAGTTTTATTTCTGATG    76476       GG    T
                                TATTAG  ATAA ATTCA
                                |||||||  |||| |||||
                                GTAGTC  TATT TGAGT
                                   TT    T
GAM1385  LOC143381 3'  GTTGAATGAAAAGCCTTGA    77062       ATAATA
                                TTAGGG     TTCATTTAGC
                                |||||||     ||||||||||
                                AGTTCC     AAGTAAGTTG
                                   GAA___
GAM1385  LOC144809 3'  ATGACAGTGAATAATTTCTAAT 84103       GG  AA       TAGC
            A                    TATTAG  AT  TATTCATT
                                |||||||  ||  ||||||||
                                ATAATC  TA  ATAAGTGA
                                   TT  __       CAGTAA
GAM1385  LOC145231 3'  AATGGGTATTGTCCCTAG    84234
                                TTAGGGATAATATTCATT
                                ||||||||||||||||||
                                GATCCCTGTTATGGGTAA

GAM1385  LOC146455 3'  TATTTGATTTGTCTCTGATA   78466          TAT   TT
                                TATTAGGGATAA   TCA  TA
                                ||||||||||||   |||  ||
                                ATAGTCTCTGTT   AGT  AT
                                      T__   TT
GAM1385  LOC146723 3'  GCTAAAGACCTTATCCTTG    78681         TAT  A
                                TAGGGATAA   TC TTTAGC
                                |||||||||   || ||||||
                                GTTCCTATT   AG AAATCG
                                     CC_  _
GAM1385  LOC146990 5'  GTTGTTTTTGTGTTGTTCCTG  84956          TCATT
                                TAGGGATAATAT    TAGC
                                ||||||||||||    ||||
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                                GTCCTTGTTGTG    GTTG
                                      TTTTT
GAM1385  LOC149832 5' GTGATTTTGTCTCTAGTG    85869          TAT
                                TATTAGGGATAA   TCAT
                                ||||||||||||  ||||
                                GTGATCTCTGTT   AGTG
                                      TT_
GAM1385  LOC149844 3' GTTGAATGGGCTGATCCT    80347      AATA
                                GGGAT   TTCATTTAGC
                                |||||   ||||||||||
                                TCCTA   GGGTAAGTTG
                                   GTC_
GAM1385  LOC149911 3' GCTAAGTGAGTGAAGAGTC   85874    AA__
                                GAT   TATTCATTTAGC
                                |||   ||||||||||||
                                CTG   GTGAGTGAATCG
                                  AGAA
GAM1385  LOC150271 3' CTGGGTGACTCCCTGA      86137       TAATAT
                                TTAGGGA     TCATTTAG
                                |||||||     ||||||||
                                AGTCCCT     AGTGGGTC
                                    C_____
GAM1385  LOC150372 3' GCTGAATGAATGGGCCTGG   80617     GATAA
                                TTAGG    TATTCATTTAGC
                                |||||    ||||||||||||
                                GGTCC    GTAAGTAAGTCG
                                   GG___
GAM1385  LOC150933 3' GTTGATTTTTGTTGTTCCTGA 86339          TTCAT
                                TTAGGGATAATA    TTAGC
                                ||||||||||||    |||||
                                AGTCCTTGTTGT    AGTTG
                                      TTTT_
GAM1385  LOC151516 3' GCTAGAAATGCTTGTCTTTGA 81067         _   CA
                                TTAGGGATAA TATT  TTTAGC
                                |||||||||| ||||  ||||||
                                AGTTTCTGTT GTAA  AGATCG
                                      C   __
GAM1385  LOC152185 3' CTCACTGAGTTTGTTCTTAATA 59200          T    TTTAGC
                                TATTAGGGATAA ATTCA
                                |||||||||||| |||||
                                ATAATTCTTGTT TGAGT
                                      _    CACTCT
GAM1385  LOC152245 5' GTTGGGTGGGCACCCCCTGAT 86784       ATAATA
                                ATTAGGG     TTCATTTAGC
                                |||||||     ||||||||||
                                TAGTCCC     GGGTGGGTTG
                                    CCAC__
GAM1385  LOC152674 5' GTTGAGTGGAAGATGTCTTAGT 87005       ATAATA
            A                    TATTAGGG     TTCATTTAGC
                                |||||||     ||||||||||
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                                ATGATTCT     AGGTGAGTTG
                                     GTAGA_
GAM1385  LOC153205 3'  GCTAACAATGGTTATCTCTGA  87160          ATTCAT
                                TTAGGGATAAT     TTAGC
                                ||||||||||      |||||
                                AGTCTCTATTG     AATCG
                                      GTAAC_
GAM1385  LOC157798 5'  CTGGATGAAACCTTAGTA    87857        ATAATA
                                TATTAGGG     TTCATTTAG
                                ||||||||     |||||||||
                                ATGATTCC     AAGTAGGTC
                                     A_____
GAM1385  LOC157858 5'  GTTAAATGAGGGGCTCTCTGA  87895       TAATA
                                TTAGGGA     TTCATTTAGC
                                |||||||     ||||||||||
                                AGTCTCT     GAGTAAATTG
                                     CGGG_
GAM1385  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83158
                   TA                  TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG
                                                    G
GAM1385  LOC164971 5'  GCTAATATATTATCCTTTGGTG 83349       _       TCAT
                                TATTAG GGATAATAT    TTAGC
                                |||||| |||||||||    |||||
                                GTGGTT CCTATTATA    AATCG
                                     T       T___
GAM1385  LOC170127 3'  GCTGAGTGCCTGCCCTTGATG  83460        ATAATATT
                                TATTAGGG       CATTTAGC
                                ||||||||       ||||||||
                                GTAGTTCC       GTGAGTCG
                                     CGTCC___
GAM1385  LOC196394 3'  GTTGGATGAGTCATTATTTTTG 89032          _
                   A                 TTAGGGATAAT ATTCATTTAGC
                                ||||||||||| ||||||||||
                                AGTTTTTATTA TGAGTAGGTTG
                                      C
GAM1385  LOC199704 5'  GCTCCTATGAGTGTTAACCTTG 89697        A       TT_
                   ATG                  TATTAGGG TAATATTCAT   AGC
                                |||||||| ||||||||||   |||
                                GTAGTTCC ATTGTGAGTA   TCG
                                     A        TCC
GAM1385  LOC199953 3'  TTGGGTGAGGGTCCTGGT    89887        ATAATA
                                ATTAGGG     TTCATTTAG
                                |||||||     |||||||||
                                TGGTCCT     GAGTGGGTT
                                     GG____
GAM1385  LOC200311 3'  CTGGGTGACTCCCTGA      91576        TAATAT
                                TTAGGGA     TCATTTAG
                                |||||||     ||||||||
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                                AGTCCCT     AGTGGGTC
                                   C_____
GAM1385  LOC200352 3'  CTAGATGCATTCCTGA     90233        AATATT
                                TTAGGGAT     CATTTAG
                                ||||||||     |||||||
                                AGTCCTTA     GTAGATC
                                   C_____
GAM1385  LOC200399 3'  GTTGGGCTGATGTTGTTGTTGG 90241       G       CA
                TG                  TATTAG GATAATATT  TTTAGC
                                ||||||| |||||||||  |||||||
                                GTGGTT TTGTTGTAG  GGGTTG
                                   G        TC
GAM1385  LOC200734 3'  GCTGGAAAAGAGTATTTTTCTA 90280       GG T      A__
                ATA                 TATTAG  A AATATTC   TTTAGC
                                ||||||  | |||||||   |||||||
                                ATAATC  T TTATGAG   AGGTCG
                                   TT _      AAA
GAM1385  LOC200830 3'  TGAATTGTAATTCCTGATG    91731         A   _
                                TATTAGGGAT ATA TTCA
                                |||||||||| ||| ||||
                                GTAGTCCTTA TGT AAGT
                                     A   T
GAM1385  LOC200942 3'  GTTAGGGGAGCCTTTGTCTTTA 90379           TA_   A
                GTG                 TATTAGGGATAA   TTC TTTAGC
                                ||||||||||||   ||| |||||||
                                GTGATTTCTGTT   GAG GGATTG
                                      TCC   G
GAM1385  LOC201736 5'  TGGGTATGTGCCTAGTG     90482        G   A
                                TATTAGG ATA TATTCA
                                ||||||| ||| |||||||
                                GTGATCC TGT ATGGGT
                                   G   _
GAM1385  LOC202460 5'  GCTGAGAGATATTATTCTTAG  90673            CA
                                TTAGGGATAATATT  TTTAGC
                                ||||||||||||||  |||||||
                                GATTCTTATTATAG  GAGTCG
                                      A_
GAM1385  LOC203286 3'  GCTGGATGTCCAAGTCCCTG   92146        AATATT
                                TAGGGAT     CATTTAGC
                                |||||||     ||||||||
                                GTCCCTG     GTAGGTCG
                                   AACCT_
GAM1385  LOC219902 5'  GCTAACATGTTATCTCTGA    93129           TCAT
                                TTAGGGATAATAT    TTAGC
                                ||||||||||||    |||||
                                AGTCTCTATTGTA    AATCG
                                      C___
GAM1385  LOC221496 3'  GCTGGATGAATAAACTATTT   93642       A__
                                GGATA   TATTCATTTAGC
                                |||||   ||||||||||||
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                              TTTAT  ATAAGTAGGTCG
                                 CAA
GAM1385  LOC221687 3'  GTTGAATGTATATATTTCTAA  93871     GG  A  T
                              TTAG  ATA TAT CATTTAGC
                              ||||  ||| ||| ||||||||
                              AATC  TAT ATA GTAAGTTG
                                 TT  _  T
GAM1385  LOC221895 3'  GTTAGATGAGTAAACCTCTA  94106      ATAA
                              TAGGG  TATTCATTTAGC
                              |||||  ||||||||||||
                              ATCTC  ATGAGTAGATTG
                                 CAA_
GAM1385  LOC221931 3'  GCTGGGTGATGTTAGGTTTCTG 95631     GG  AATAT_
            G                  TTAG  AT    TCATTTAGC
                              ||||  ||    |||||||||
                              GGTC  TG    AGTGGGTCG
                                 TT  GATTGT
GAM1385  LOC222662 3'  GCTAAATGGGTCCATCTCTAG  94414       AAT
                              TTAGGGAT  ATTCATTTAGC
                              ||||||||  ||||||||||
                              GATCTCTA  TGGGTAAATCG
                                   CC_
GAM1385  LOC253698 3'  GCTGAAAATGTCATTTCTAGTA 96546      GG  A   CA
                              TATTAG  AT ATATT  TTTAGC
                              ||||||  || |||||  ||||||
                              ATGATC  TA TGTAA  AAGTCG
                                 TT  C   __
GAM1385  LOC255391 5'  GTTGGGTGGGTTTCTCTGG  99458       TAAT
                              TTAGGGA  ATTCATTTAGC
                              |||||||  ||||||||||
                              GGTCTCT  TGGGTGGGTTG
                                   T___
GAM1385  LOC255465 5'  GCTGGATGAAATATTCT    99118       ATA
                              GGGATA  TTCATTTAGC
                              ||||||  |||||||||
                              TCTTAT  AAGTAGGTCG
                                 A__
GAM1385  LOC257481 3'  GCTGTTCCGATGGTGTCTTTGA 61763         A   CATT
            TG                  TATTAGGGATA TATT   TAGC
                              ||||||||||| ||||  ||||
                              GTAGTTTCTGT GTAG   GTCG
                                    G   CCTT
GAM1385  LOC51316  3'  TAAATGAATGTTGTCCCTGA  60248             GC
                              TTAGGGATAATATTCATTTA
                              ||||||||||||||||||||
                              AGTCCCTGTTGTAAGTAAAT
                                          A
GAM1385  LOC83468  3'  TCTTTATGAATATTACCTTTGA 49344       A       TT  C
            TA                  TATTAGGG TAATATTCAT  AG
                              ||||||||  |||||||||  ||
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                                ATAGTTTC ATTATAAGTA  TC
                                    C        TT  TT
GAM1385  LOC90190  3'  GCTAACTTTTGTGTTGACTCTG 62427        A     TCAT_
            GTG                   TATTAGGG TAATAT    TTAGC
                                  |||||||| ||||||    |||||
                                  GTGGTCTC GTTGTG    AATCG
                                     A     TTTTC
GAM1385  LOC90246  3'  GCTAAATGGATGTTGCTTGA   62587      GA
                                  TTAGG  TAATATTCATTTAGC
                                  |||||  ||||||||||||||
                                  AGTTC  GTTGTAGGTAAATCG
                                    __
GAM1385  LOC91137  3'  TGGTATAGTATCCTTAATA    57860          A  _
                                  TATTAGGGATA TAT TCA
                                  |||||||||| ||| |||
                                  ATAATTCCTAT ATA GGT
                                        G   T
GAM1385  LOC92140  3'  GCTTATGAAGTTATTTTTGATA 68826           A     TT
                                  TATTAGGGATAAT TTCAT  AGC
                                  |||||||||||| ||||||  |||
                                  ATAGTTTTTATTG AAGTA  TCG
                                        _    T_
GAM1385  LOC92283  3'  TGAAGTTGTTTCTAATG     69306       GG    A
                                  TATTAG  ATAAT TTCA
                                  ||||||  ||||| ||||
                                  GTAATC  TGTTG AAGT
                                     TT    _
GAM1385  LOC92344  3'  GTTTGAGGGTATTATCTTCTGG 69578        _        ATTTAGC
            TA                    TATTAGG GATAATATTC
                                  ||||||| ||||||||||
                                  ATGGTCT CTATTATGGG
                                     T        AGTTTG
GAM1385  LOC92379  3'  GTTAAATGTTTGATTGTTTTTG 69677          ATT_
            G                     TTAGGGATAAT    CATTTAGC
                                  ||||||||||    ||||||||
                                  GGTTTTTGTTA    GTAAATTG
                                        GTTT
GAM1385  LOC92421  3'  GCTGAATGAGAATCTCCTGG   69726      _  AATA
                                  TTAGG GAT    TTCATTTAGC
                                  ||||| |||    ||||||||||
                                  GGTCC CTA    GAGTAAGTCG
                                     T   A___
GAM1385  LOC93070  3'  CTGAATGGAAGTCTTGA     71806       ATAATA
                                  TTAGGG     TTCATTTAG
                                  ||||||     |||||||||
                                  AGTTCT     AGGTAAGTC
                                     GA____
GAM1386  EPHB4     3'  TGTAAATGCCCCTCCCCCAGCT 16711      CA   T  CC     C
                                  AGCT  GGG GG  GGCATT ACA
                                  ||||  ||| ||  |||||| |||
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                                TCGA  CCC CC  CCGTAA TGT
                                  CC   T __     A
GAM1386  HPCAL1   3'  TGTGGCCCGCAGCCCCCTGAGC 10970        T  __  CAT
                                GCTCAGGG GGC  CGG   TCACA
                                |||||||| |||  |||   |||||
                                CGAGTCCC CCG  GCC   GGTGT
                                     _   AC   C__
GAM1386  HPCAL1   3'  TGTGGCCCGCAGCCCCCTGAGC 57012        T  __  CAT
                                GCTCAGGG GGC  CGG   TCACA
                                |||||||| |||  |||   |||||
                                CGAGTCCC CCG  GCC   GGTGT
                                     _   AC   C__
GAM1386  IL1RL1LG 3'  TGTAAATGTGCCTTAGCCTAAG 23409     C   G __   CG    C
             C                   GCT AGG T  GGC  GCATT ACA
                                ||| ||| |  |||  ||||| |||
                                CGA TCC A  CCG  TGTAA TGT
                                  A   G TT   __     A
GAM1386  IMMP2L   5'  TGCGGCGGCCACCCCAGC    51709     CA       __
                                GCT  GGGTGGCCG  GCA
                                |||  |||||||||  |||
                                CGA  CCCACCGGC  CGT
                                  C_        GG
GAM1386  MTCP1    5'  GAACGCCGGCCTCTTGAGC    27243        T      A
                                GCTCAGGG GGCCGGC TTC
                                |||||||| ||||||| |||
                                CGAGTTCT CCGGCCG AAG
                                     _      C
GAM1386  NFE2L1   3'  GTGCTCCAGCCACCCCTGAGCT 13634         _   C__
                                AGCTCAGGG TGGC   GGCAT
                                |||||||||| ||||   |||||
                                TCGAGTCCC ACCG   TCGTG
                                     C    ACC
GAM1386  NR1D1    5'  TGCAGTCCGGCCACCCCAAG   41671    CA        C  _
                                CT  GGGTGGCCGG ATT CA
                                ||  |||||||||| ||| ||
                                GA  CCCACCGGCC TGA GT
                                 AC         _  C
GAM1386  RNF14    5'  ATGAACTCCACTCTGAGCT    16271           CCGG
                                AGCTCAGGGTGG    CAT
                                ||||||||||||    |||
                                TCGAGTCTCACC    GTA
                                       TCAA
GAM1386  AF9Q34   3'  TGCGTCCACCCTGAGCT     51725           C  G
                                AGCTCAGGGTGG CG CA
                                |||||||||||| || ||
                                TCGAGTCCCACC GC GT
                                       T  _
GAM1386  AFAP     3'  GGGGCCGACACCCTGAGCT   41610           GC   A
                                AGCTCAGGGTG  CGGC TTC
                                ||||||||||  |||| |||
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                                TCGAGTCCCAC  GCCG GGG
                                      A_   _
GAM1386 AMOTL1   3' TGCGAGCCACCCCCTGAGCT  74015      __     CG
                                AGCTCA  GGGTGGC  GCA
                                ||||||  |||||||  |||
                                TCGAGT  CCCACCG  CGT
                                   CC      AG
GAM1386 ARGBP2   5' GTAAATGCTCCCTAGGCT    41134    TC   TGGCC    C
                                AGC  AGGG    GGCATT AC
                                |||  ||||    |||||| ||
                                TCG  TCCC    TCGTAA TG
                                  GA   _____     A
GAM1386 ARHGAP5  3' TGTGAATACCAGTTTATTTAAG 77610     C  GT  C  C
             CT                   AGCT AGG  GGC GG ATTCACA
                                ||||  |||  ||| || |||||||
                                TCGA TTT  TTG CC TAAGTGT
                                  A   AT   A  A
GAM1386 ATP10B   3' ATGATAGGGCAACCCTGAGCT  64102        G  GG__
                                AGCTCAGGGT GCC    CAT
                                ||||||||||  |||    |||
                                TCGAGTCCCA CGG    GTA
                                      A   GATA
GAM1386 BTBD2    3' GTGCCCGAGGCCACCCAAGC   35566     CA      ___
                                GCT  GGGTGGCC   GGCAT
                                |||  ||||||||   |||||
                                CGA  CCCACCGG   CCGTG
                                  A_       AGC
GAM1386 CYP2E    3' GTGGAGGACACCCTGA      7580         G  GGCA
                                TCAGGGTG CC    TTCAC
                                ||||||||  ||    |||||
                                AGTCCCAC GG    AGGTG
                                     A  ____
GAM1386 FLJ20421 3' TGGTTAAGGCCATCCCGAACT  35615    C  A      GGCAT
                                AG TC GGGTGGCC     TCA
                                ||  ||  ||||||||     |||
                                TC AG CCTACCGG     GGT
                                 A  C       AATT_
GAM1386 GGA2     3' TGACCAGCTACCCTGAGC     31175          C  _
                                GCTCAGGGTGGC GG CA
                                ||||||||||||  ||  ||
                                CGAGTCCCATCG CC GT
                                      A  A
GAM1386 GGA2     3' TGACCAGCTACCCTGAGC     57687          C  _
                                GCTCAGGGTGGC GG CA
                                ||||||||||||  ||  ||
                                CGAGTCCCATCG CC GT
                                      A  A
GAM1386 KIAA0057 3' TGTAAATGCCAAGGCATTTGGC 25427     T  GGTG  __     C
             T                    AGC CAG    GCC  GGCATT ACA
                                ||| |||    |||  |||||| |||
```

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                                TCG GTT   CGG  CCGTAA TGT
                                  _  TA__   AA     A
GAM1386  KIAA0342  3'  TGCCACTGGCCACCCCGAGC   71142     A     ___
                                GCTC GGGTGGCC   GGCA
                                |||| ||||||||   ||||
                                CGAG CCCACCGG   CCGT
                                  C       TCA
GAM1386  KIAA1259  3'  GCCCGGCCAGCCTGAGCT    50799       G     _
                                AGCTCAGG TGGCCGG C
                                |||||||| ||||||| |
                                TCGAGTCC ACCGGCC G
                                    G      C
GAM1386  KIAA1822  3'  TGTAAATACTTGTTCCCCGATG 68197    TCA  TG  C  C   C
            CT                    AGC   GGG  GC GG ATT ACA
                                |||   |||  || || ||| |||
                                TCG   CCC  TG TC TAA TGT
                                  TAG   CT  T  A   A
GAM1386  MADCAM1   3'  GTGCCCTGACCACCCTGGGC   56240         CC__
                                GCTCAGGGTGG   GGCAT
                                ||||||||||   |||||
                                CGGGTCCCACC   CCGTG
                                      AGTC
GAM1386  MADCAM1   3'  GTGCCCTGACCACCCTGGGC   56243         CC__
                                GCTCAGGGTGG   GGCAT
                                ||||||||||   |||||
                                CGGGTCCCACC   CCGTG
                                      AGTC
GAM1386  MADCAM1   3'  GTGCCCTGACCACCCTGGGC   56246         CC__
                                GCTCAGGGTGG   GGCAT
                                ||||||||||   |||||
                                CGGGTCCCACC   CCGTG
                                      AGTC
GAM1386  OSBPL3    3'  TGCAGGTAACCACCCTGCACT  32079    CT      ___  G
                                AG  CAGGGTGG   CC GCA
                                ||  ||||||||   || |||
                                TC  GTCCCACC   GG CGT
                                 AC       AAT  A
GAM1386  PSMD3     3'  TGGGAGCCAGCCACCCTGACCT 12518    C       C   A
                                AG TCAGGGTGGC GGC TTCA
                                || ||||||||||  ||| ||||
                                TC AGTCCCACCG CCG GGGT
                                 C        A   A
GAM1386  TMLHE     3'  TGAATACACCTGGCACCCTGGC 37049     T     G    C___
              T                   AGC CAGGGTG CCGG    ATTCA
                                ||| ||||||| ||||    |||||
                                TCG GTCCCAC GGTC    TAAGT
                                  _      _    CACA
GAM1386  ZNF213    5'  TGAAGCCGACCAACCCTGAGC  65701         _ C    A
                                GCTCAGGGT GG CGGC TTCA
                                ||||||||| || |||| ||||
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                                CGAGTCCCA CC GCCG AAGT
                                     A  A   _
GAM1386  LOC115708 3'  TGTGAATGCCAGCCTGTGAGT  73922      G GT   C
                                GCTCA G  GGC GGCATTCACA
                                ||||| |  ||| ||||||||||
                                TGAGT T  CCG CCGTAAGTGT
                                   G __   A
GAM1386  LOC138515 5'  GTGAACACCCTGAACT      76484    C      GCCGGCA
                                AG TCAGGGTG      TTCAC
                                || ||||||||      |||||
                                TC AGTCCCAC      AAGTG
                                 A      ________
GAM1386  LOC139709 5'  TGCTCCAGCCCCCTGAGC    75900        T   C__
                                GCTCAGGG GGC   GGCA
                                |||||||| |||   ||||
                                CGAGTCCC CCG   TCGT
                                     _   ACC
GAM1386  LOC143146 5'  TGAATGCGGGCCCCGGCT    60766     CAG  T    G
                                AGCT   GG GGCC GCATTCA
                                ||||   || |||| |||||||
                                TCGG   CC CCGG CGTAAGT
                                  ___ _   G
GAM1386  LOC145783 5'  GCTGGACGCCACCCTAAGCT   77950     C      ___
                                AGCT AGGGTGGC   CGGC
                                |||| ||||||||   ||||
                                TCGA TCCCACCG   GTCG
                                  A       CAG
GAM1386  LOC157381 3'  TGTGAATACCACATGCCCTGGG 87736          GCC  C
             CT                   AGCTCAGGGTG   GG ATTCACA
                                ||||||||||   || |||||||
                                TCGGGTCCCGT   CC TAAGTGT
                                      ACA  A
GAM1386  LOC158056 3'  GTGAATAAACACCCTGGC    82593    T     GCCGGC
                                GC CAGGGTG     ATTCAC
                                || |||||||     ||||||
                                CG GTCCCAC     TAAGTG
                                 _      AAA___
GAM1386  LOC158204 3'  TGCAAATGGTCACCCTGA    67713          ___
                                TCAGGGTGGCCG   GCA
                                ||||||||||||   |||
                                AGTCCCACTGGT   CGT
                                       AAA
GAM1386  LOC200583 5'  GTGCTCTGGCCACCATGAACT  90253    C   G       CATT
                                AG TCA GGTGGCCGG    CAC
                                || ||| |||||||||    |||
                                TC AGT CCACCGGTC    GTG
                                 A  A        TC__
GAM1386  LOC201245 3'  TGTGAACAGCCATCCTGAACT  88738    C        CGGCA
                                AG TCAGGGTGGC     TTCACA
                                || ||||||||||     ||||||
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                                TC AGTCCTACCG    AAGTGT
                                 A        AC___
GAM1386  LOC202899 5'  TGCGGCGGCCACCCCAGC    92014    CA      __
                                GCT  GGGTGGCCG  GCA
                                |||  |||||||||  |||
                                CGA  CCCACCGGC  CGT
                                  C_       GG
GAM1386  LOC221576 3'  TGCCCGCCACCCTGAGCT    95324          C
                                AGCTCAGGGTGGC GGCA
                                |||||||||||| ||||
                                TCGAGTCCCACCG CCGT
                                        C
GAM1386  LOC221749 3'  TGCCCCCCAGCCACCCTGACT  93650    C       C____
                                AG TCAGGGTGGC    GGCA
                                || ||||||||||    ||||
                                TC AGTCCCACCG    CCGT
                                 _        ACCCC
GAM1386  LOC257515 3'  TGCCCGCCACCCTGAGCT    99624          C
                                AGCTCAGGGTGGC GGCA
                                |||||||||||| ||||
                                TCGAGTCCCACCG CCGT
                                        C
GAM1386  LOC257572 3'  TGCCCGCCACCCTGAGCT    99744          C
                                AGCTCAGGGTGGC GGCA
                                |||||||||||| ||||
                                TCGAGTCCCACCG CCGT
                                        C
GAM1386  LOC51074  3'  TGCAAATGGTCACCCTGA    32552          ___
                                TCAGGGTGGCCG   GCA
                                ||||||||||||   |||
                                AGTCCCACTGGT   CGT
                                       AAA
GAM1386  LOC85414  5'  TGCCTGAACGGCCCCCTGAGC  53554       T   _____
                                GCTCAGGG GGCC    GGCA
                                |||||||| ||||    ||||
                                CGAGTCCC CCGG    CCGT
                                     _   CAAGT
GAM1387  LAMC1     3'  TCCCCTGTCTCATCGATCCAG  11271         GT  T  A
                                CTGGATCGATG  AC GG GA
                                ||||||||||  || || ||
                                GACCTAGCTAC  TG CC CT
                                       TC  T  C
GAM1387  MYO15A    3'  CTCCAGTACCTTCTGCCAGA   33182      ATC  T
                                TCTGG   GA GGTACTGGAG
                                |||||   || ||||||||||
                                AGACC   CT CCATGACCTC
                                   GT_  T
GAM1387  PPP2R2B   3'  TCCCAGTTGAGGATCCAGAT   17124        GATGGT    A
                                ATCTGGATC     ACTGG GA
                                |||||||||     ||||| ||
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                                TAGACCTAG     TGACC CT
                                     GAGT__    C
GAM1387  PRDM4    3'  TCTCCAGTAAACATCCAG    25743       CGATGG
                                CTGGAT     TACTGGAGA
                                ||||||     |||||||||
                                GACCTA     ATGACCTCT
                                   CAA___
GAM1387  ABLIM    3'  TCTCCATCCCAATCCAGTATA  22986    _     CGA   TAC
                                TAT CTGGAT   TGG   TGGAGA
                                ||| ||||||   |||   ||||||
                                ATA GACCTA   ACC   ACCTCT
                                  T     ____  CT_
GAM1387  LOC161734 5'  TCCCCAGCAAAGATCCAGA   88469        GA  GTA    A
                                TCTGGATC  TG   CTGG GA
                                ||||||||  ||   |||| ||
                                AGACCTAG  AC   GACC CT
                                     AA  ___    C
GAM1387  LOC256940 5'  TCCCCAGTGGTCCAGA      98248         A   TACT
                                TCTGGATCG TGG    GGA
                                |||||||||| |||    |||
                                AGACCTGGT ACC    CCT
                                     G  _____
GAM1388  ADH7     3'  AAGATTAAGGGACGGGC     7268       ACA   G
                                GCCC   TCT TTTAATCTT
                                ||||   ||| |||||||||
                                CGGG   AGG GAATTAGAA
                                  C__   _
GAM1388  ARAF1    5'  GGAAGGACTTCAGATGTGAGC  64644    C       TTTAA
                                GC CACATCTG     TCTTCC
                                || ||||||||     ||||||
                                CG GTGTAGAC     GGAAGG
                                 A       TTCA_
GAM1388  CEACAM6  3'  GGAAGACTGGCAGATTGGACCA 11756     C   C      TAA
                                TGG CCA ATCTGTT   TCTTCC
                                ||| ||| |||||||   ||||||
                                ACC GGT TAGACGG   AGAAGG
                                  A   _       TC_
GAM1388  CLECSF12 3'  GGATTACAGATGTGAGCCA    77214      C        TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A        __
GAM1388  CYP1A2   3'  GGATTAACAGGTATGAACCA   7518      CC  C      T
                                TGG  CA ATCTGTT AATCT
                                |||  || ||||||| |||||
                                ACC  GT TGGACAA TTAGG
                                  AA  A      _
GAM1388  ENG      3'  GAACTTGAAACAGATTCAGGCC 5496       CAC       AATC
             A                   TGGCC   ATCTGTTT    TTC
                                |||||   ||||||||    |||
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                                ACCGG  TAGACAAA   AAG
                                  ACT      GTTC
GAM1388 ERCC3    3' GAATAAACAGAATGGACCA   5506     C  CA      A
                                TGG CCA  TCTGTTTA TC
                                ||| |||  |||||||| ||
                                ACC GGT  AGACAAAT AG
                                  A  A_      A
GAM1388 HTLF     5' AAGATTGCAGGATTAAGCCA  10973     CCACA    TT
                                TGGC    TCTGT  AATCTT
                                ||||    |||||  ||||||
                                ACCG    GGACG  TTAGAA
                                  AATTA   __
GAM1388 MS4A8B   3' GATTTTAAACAGATGTTAACCA 49588     CCC         TCT
                                TGG  ACATCTGTTTAA  TC
                                |||  ||||||||||||  ||
                                ACC  TGTAGACAAATT  AG
                                  AAT         TT_
GAM1388 PRKAA2   3' GAAGATTAAAAAGTAAAGAACC 21811     CCCACAT  G
              A                  TGG      CT TTTAATCTTC
                                |||      || ||||||||||
                                ACC      GA AAATTAGAAG
                                  AAGAAAT  A
GAM1388 ASE-1    3' GGATAACAGGTGTGAGCCA   24983     C        TA
                                TGGC CACATCTGTT  ATCT
                                |||| ||||||||||  ||||
                                ACCG GTGTGGACAA  TAGG
                                  A        __
GAM1388 CITED2   3' GGAAGATTAAACAGATGTGGGC 21403
              CA                  TGGCCCACATCTGTTTAATCTTCC
                                |||||||||||||||||||||||||
                                ACCGGGTGTAGACAAATTAGAAGG

GAM1388 DKFZP564K0322 3' GGATTACAGATGTGAGCCA   50188     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1388 DZIP1    3' GAAGATTATTCCAGAAGCCA   30703     CCACA   TT_
                                TGGC    TCTG   TAATCTTC
                                ||||    ||||   ||||||||
                                ACCG    AGAC   ATTAGAAG
                                  A____    CTT
GAM1388 FLJ22969 3' GGATTACAGATGTGAGCCA   69211     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1388 HSNOV1   3' GGATTACAGATGTGAACCA   34437     CC       TT
                                TGG  CACATCTGT  AATCT
                                |||  |||||||||  |||||
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                                ACC  GTGTAGACA  TTAGG
                                  AA       __
GAM1388  IMPACT   3'  GAATTACAGGTGTGAGCCA   38006     C       TTAATC
                                TGGC CACATCTGT     TTC
                                |||| |||||||||      |||
                                ACCG GTGTGGACA     AAG
                                  A       TT_____
GAM1388  JAM1     3'  GGATTACAGATGTGAGCCA   34234     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1388  JAM1     3'  GGATTACAGATGTGAGCCA   58499     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1388  JAM1     3'  GGATTACAGATGTGAGCCA   58520     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1388  JAM1     3'  GGATTACAGATGTGAGCCA   58548     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1388  JAM1     3'  GGATTACAGATGTGAGCCA   58577     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1388  KIAA0210 5'  GAATTACAGGTGTGAGCCA   29159     C       TTAATC
                                TGGC CACATCTGT     TTC
                                |||| |||||||||      |||
                                ACCG GTGTGGACA     AAG
                                  A       TT_____
GAM1388  KIAA0280 3'  GAGCATAAACAGATGTGGTCCA 93301     C          AT
                                TGG CCACATCTGTTTA  CTT
                                |||  ||||||||||||  |||
                                ACC GGTGTAGACAAAT  GAG
                                  T          AC
GAM1388  KIAA0285 5'  GAAGATTGAGCTTGACCGGACC 29684     C  ACA  T_
            A                    TGG CC   TC  GTTTAATCTTC
                                ||| ||   ||  ||||||||||
                                ACC GG   AG  CGAGTTAGAAG
                                  A  CC_  TT
GAM1388  KIAA0356 3'  GGAAGACCCTCAGATGTGGCCA 66778      C      TTTAA
                                TGGCC ACATCTG    TCTTCC
                                ||||| |||||||    ||||||
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                                ACCGG TGTAGAC    AGAAGG
                                  _      TCCC_
GAM1388 KIAA1354 3' GGAAGATTGTCAGCATGT    61576     _  TT
                                ACAT CTG  TAATCTTCC
                                |||| |||  |||||||||
                                TGTA GAC  GTTAGAAGG
                                  C   T_
GAM1388 KIAA1466 3' ATTAAATAGTATGGGCCA    72406       CAT
                                TGGCCCA   CTGTTTAAT
                                |||||||   |||||||||
                                ACCGGGT   GATAAATTA
                                    AT_
GAM1388 KIAA1468 5' AAGATCTTGTAGATGTGGCCA 93423      C     TTTA
                                TGGCC ACATCTG    ATCTT
                                ||||| |||||||    |||||
                                ACCGG TGTAGAT    TAGAA
                                  _      GTTC
GAM1388 MRPS26   3' GGAAGATTACAGTCTGAGGGCC 48723       A  T_   TT
            A                    TGGCCC CA  CTGT  AATCTTCC
                                ||||||| ||  ||||  ||||||||
                                ACCGGG GT  GACA  TTAGAAGG
                                   A  CT   __
GAM1388 PANX3    3' AAGATTAATAAAGATGTAAACC 54765    CCC     GT_
                                GG   ACATCT   TTAATCTT
                                ||   ||||||   ||||||||
                                CC   TGTAGA   AATTAGAA
                                 AAA     AAT
GAM1388 PLCL1    3' AAGATTAAACAGATGATG    21714    _
                                CA CATCTGTTTAATCTT
                                || ||||||||||||||
                                GT GTAGACAAATTAGAA
                                 A
GAM1388 SPRY4    3' GAAGACAGAACACAGATGTGGA 49013    GC        _  AA_
            CA                    TG  CCACATCTGT TT   TCTTC
                                ||  |||||||||| ||   |||||
                                AC  GGTGTAGACA AA   AGAAG
                                 A_         C  GAC
GAM1388 WNT10A   3' GAAGAGGAGATTGGACCA    48170     C   C    G TTAA
                                TGG CCA ATCT T    TCTTC
                                ||| ||| |||| |    |||||
                                ACC GGT TAGA G    AGAAG
                                  A   _    G _____
GAM1388 LOC113523 5' GGATTACAGATGTGAGCCA   73427      C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A        __
GAM1388 LOC124216 3' GGATTACAGATGTGAGCCA   74736      C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
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                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1388  LOC130639 5'  GGATTAAAGACGTGAGCCA    75480      C   A   GT
                                TGGC CAC TCT  TTAATCT
                                |||| ||| |||  |||||||
                                ACCG GTG AGA  AATTAGG
                                  A  C  __
GAM1388  LOC144202 5'  GGAAGATTCGATGGACATGGAC 77226    GC   CA     T
             A                   TG  CCA  TCTGTT AATCTTCC
                                ||  |||  |||||| ||||||||
                                AC  GGT  AGGTAG TTAGAAGG
                                 A_  AC     C
GAM1388  LOC149171 5'  GAATTACAGGTGTGAGCCA    79967      C       TTAATC
                                TGGC CACATCTGT     TTC
                                |||| |||||||||      |||
                                ACCG GTGTGGACA     AAG
                                  A       TT____
GAM1388  LOC150245 3'  GAAGCAAGACAGATGTGGGCC  86112             AAT
                                GGCCCACATCTGTTT   CTTC
                                ||||||||||||||   ||||
                                CCGGGTGTAGACAGA   GAAG
                                         AC_
GAM1388  LOC152620 3'  AGATTACAGATGTGAGCCA    60703      C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGA
                                  A       __
GAM1388  LOC153577 3'  GAAGATTTTATGTGACCA    87239     CC    CTGTTT
                                TGG  CACAT     AATCTTC
                                |||  |||||     |||||||
                                ACC  GTGTA     TTAGAAG
                                  A_    TT____
GAM1388  LOC154930 3'  GAATAACAGGTGTGAGCCA    82091      C       TAATC
                                TGGC CACATCTGTT    TTC
                                |||| ||||||||||    |||
                                ACCG GTGTGGACAA    AAG
                                  A       T____
GAM1388  LOC157507 5'  AAGATTAAACCATGGATG    82376      ___
                                CATCT   GTTTAATCTT
                                |||||   ||||||||||
                                GTAGG   CAAATTAGAA
                                   TAC
GAM1388  LOC158014 5'  AGAATTACAGGTGTGAGCCA   82549      C       TTAA
                                TGGC CACATCTGT    TCT
                                |||| |||||||||    |||
                                ACCG GTGTGGACA    AGA
                                  A       TTA_
GAM1388  LOC158668 3'  AGATTACAGATGTGAGCCA    69892      C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
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                                ACCG GTGTAGACA  TTAGA
                                  A       __
GAM1388  LOC170409 5'  GGATTACAGATGTGAGCCA   83745     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1388  LOC200282 5'  GAAATTACAGGTGTGAGCCA  90099     C       TTAA
                                TGGC CACATCTGT   TC
                                |||| |||||||||   ||
                                ACCG GTGTGGACA   AG
                                  A       TTAA
GAM1388  LOC220595 3'  GGAAGACCTCAGATGTGACCA 92778     CC      TTTAA
                                TGG  CACATCTG    TCTTCC
                                |||  ||||||||    ||||||
                                ACC  GTGTAGAC    AGAAGG
                                  A_      TCC__
GAM1388  LOC253805 3'  GGATTACAGATGTGAGCCA   98179     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1388  LOC56181  5'  GGATTACAGATGTGAGCCA   97278     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1388  LOC91547  3'  GGATTACAGATGTGAGCCA   67004     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1389  BGN       3'  CCCAAGTGTCCAAGGCTC    9924      CGAA      _
                                GAGCT   TGGGCATT GGG
                                |||||   |||||||| |||
                                CTCGG   ACCTGTGA CCC
                                   A___      A
GAM1389  CRMP5     3'  AGCCCAATGCATAGAGCCCTG  39700     A   GAATGG
                                TAG GCTC     GCATTGGGCT
                                ||| ||||     ||||||||||
                                GTC CGAG     CGTAACCCGA
                                  C   ATA___
GAM1389  LOC158427 3'  CCCAATGCATACTCAAGT    58353     C  A  G
                                GCT GA TG GCATTGGG
                                ||| || || ||||||||
                                TGA CT AT CGTAACCC
                                  A  C  A
GAM1389  LOC90550  3'  GCACCCCACTCGACTCTA    73481      C   A   CATTGG
                                TAGAG TCGA TGGG     GC
                                ||||| |||| ||||     ||
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                                ATCTC AGCT ACCC     CG
                                  _   C   CA____
GAM1390  FBXL7    3'  TTGGCCAAAGCACTTCAC    25502       ACC
                                GTGAAGT   TTTTGGCTAA
                                |||||||   ||||||||||
                                CACTTCA   GAAACCGGTT
                                    C__
GAM1390  MSR1     3'  TCTCATTAAAAGGCCCTTCAC  11705       TA      CTAA
                                GTGAAG  CCTTTTGG   AGA
                                ||||||  ||||||||   |||
                                CACTTC  GGAAAATT   TCT
                                   CC       AC__
GAM1390  NCAM2    3'  GTCTTTAGTGTTCAAATACTTC 17003       CCT   ___
             A                   TGAAGTA   TTTG   GCTAAAGAC
                                 |||||||   ||||   |||||||||
                                 ACTTCAT   AAAC   TGATTTCTG
                                    ___   TTG
GAM1390  PCDHB13  3'  TCTTTAGCTGAACTTCAC    38936       ACCTT TG
                                GTGAAGT    T  GCTAAAGA
                                |||||||    |  ||||||||
                                CACTTCA    A  CGATTTCT
                                   _____ GT
GAM1390  PON1     3'  GTCTTTAGAACTCCAGTACTCA 6537      A    CTTTTGG
             C                   GTGA GTAC      CTAAAGAC
                                 |||| ||||      ||||||||
                                 CACT CATG      GATTTCTG
                                   _   ACCTCAA
GAM1390  PYCS     3'  TTTTCCAAAAGGTCTTCAC    12680       T       CT
                                GTGAAG ACCTTTTGG  AA
                                |||||| |||||||||  ||
                                CACTTC TGGAAAACC  TT
                                   _       TT
GAM1390  TNFAIP6  5'  GCCCCTAACAGGCTGTTACTTC 60167       _____   T ___
             AC                    GTGAAGTA    CCT TT   GGC
                                   ||||||||    ||| ||   |||
                                   CACTTCAT    GGA AA   CCG
                                       TGTC   C  TCC
GAM1390  ZNF146   5'  TCTTCAGCCAAAAGTAAATC   24078    AG   C      A
                                GA  TAC TTTTGGCT AAGA
                                ||  ||| |||||||| ||||
                                CT  ATG AAAACCGA TTCT
                                 AA  _       C
GAM1390  ATIP1    3'  GTCTTTAACTTCCAATACTTCA 40776       CCTT    C___
             T                   GTGAAGTA    TTGG    TAAAGAC
                                 ||||||||    ||||    |||||||
                                 TACTTCAT    AACC    ATTTCTG
                                      _____   TTCA
GAM1390  DKFZP434N1817 5'  TCTCTAGCTACAAAAGGTCCCC 68722     AAGT      __   A
             AC                    GTG    ACCTTTTG  GCTA AGA
                                   |||    ||||||||  |||| |||
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                                CAC   TGGAAAAC  CGAT TCT
                                  CCC_      AT   C
GAM1390  TED     3'  GTCCCCAGCCTACCAAAGGTAT 32274      G     T___   AAA
             TCAC                  GTGAA TACCTTT   GGCT   GAC
                                |||||| |||||||   ||||  |||
                                CACTT ATGGAAA   CCGA   CTG
                                  _     CCAT   CCC
GAM1390  LOC145608 5'  GGACAAAAGGTACCCCAC    84384     AA       G
                                GTG  GTACCTTTTG CT
                                |||  |||||||||| ||
                                CAC  CATGGAAAAC GG
                                  CC        A
GAM1390  LOC149464 5'  GTCTCCAGCTGGTTGGGACCCC 85598     AA  A  TT TG   AA
             AC                   GTG  GT CC  T  GCT  AGAC
                                |||  || ||  |  |||  ||||
                                CAC  CA GG  G  CGA  TCTG
                                  CC  G  TT GT   CC
GAM1390  LOC152245 3'  GCCCTGCAAAAGGACCTCAC   86779      A  A    ____
                                GTGA GT CCTTTT    GGC
                                |||| || ||||||    |||
                                CACT CA GGAAAA    CCG
                                  C  _     CGTC
GAM1390  LOC157909 5'  TCTTCTTCAGAAGGCACCTCAC 82520      A  A       CTA
                                GTGA GT CCTTTTGG   AAGA
                                |||| || ||||||||   ||||
                                CACT CA GGAAGACT   TTCT
                                  C  C       TC_
GAM1391  ABCA3    3'  CCCTCAGGAAGTCGCCCGCCCC 8443      AACAA  TC  A
             A                    TGG    GT  GC TCCTGAGGG
                                |||    ||  || |||||||||
                                ACC    CG  TG AGGACTCCC
                                  CCGCC  C_  A
GAM1391  PRPH     3'  CCCTCAGGACAAATCTACTCCA 21832      ACA  TTCGCA
                                TGGA   AG     TCCTGAGGG
                                ||||   ||     |||||||||
                                ACCT   TC     AGGACTCCC
                                  CA_  TAAAC_
GAM1391  PXN      3'  CCCTCAGGAGCCTCTTGCTCC  12670     A   TTC  A
                                GGA CAAG   GC TCCTGAGGG
                                ||| ||||   || |||||||||
                                CCT GTTC   CG AGGACTCCC
                                  C    TC_  _
GAM1391  BCL2L1    3'  CCCCACCCCACACTTGTTCCA  57590          TCGCATCC  A
                                TGGAACAAGT       TG GGG
                                ||||||||||       || |||
                                ACCTTGTTCA       AC CCC
                                      CACCCC__  _
GAM1391  FLJ21736  3'  CCCTCAGGACGCTGGATGCCA  46781     AACAA   _  A
                                TGG    GTTC GC TCCTGAGGG
                                |||    |||| || |||||||||
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                                ACC    TAGG CG AGGACTCCC
                                  G____   T  C
GAM1391  FLJ31762  3'  CCCTCAGGACAGTGAACTTCCA 58763     ACA     A_
                                TGGA  AGTTCGC  TCCTGAGGG
                                ||||  |||||||  |||||||||
                                ACCT  TCAAGTG  AGGACTCCC
                                  ___     AC
GAM1391  MMP24    3'  CCCTCAGGAAACCTGCTCCA  22917     A  A  CGCA
                                TGGA CA GTT   TCCTGAGGG
                                |||| || |||   |||||||||
                                ACCT GT CAA   AGGACTCCC
                                  C  C  ____
GAM1391  NEUROG3  3'  CCCTCAAAAGCACTTGTTCC  41002       TC  ATCC
                                GGAACAAGT  GC   TGAGGG
                                |||||||||  ||   ||||||
                                CCTTGTTCA  CG   ACTCCC
                                     __ AAA_
GAM1391  RGS11    3'  CCTCGCCAAACGCGTTCCA   15163      AA  C_  ATCCT
                                TGGAAC  GTT  GC   GAGG
                                ||||||  |||  ||   ||||
                                ACCTTG  CAA  CG   CTCC
                                   CG   AC  _____
GAM1391  RTBDN    3'  CCCTCAGGACACCCAGAACCCC 49496    AACAA   GCA___
           A                     TGG    GTTC    TCCTGAGGG
                                |||    ||||    |||||||||
                                ACC    CAAG    AGGACTCCC
                                  C____   ACCCAC
GAM1391  LOC165741 3'  CAGGAGACCCGAACTTGTTCCA 88602          CA__
                                TGGAACAAGTTCG   TCCTG
                                ||||||||||||   |||||
                                ACCTTGTTCAAGC   AGGAC
                                       CCAG
GAM1392  GPD1     3'  TCATGCCACCACATTTG     60398      C      C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A      _
GAM1392  IL5RA    5'  TCGCATGGCCACCGCATTT   6906         AT__
                                AAATGCGGTGGC   CGA
                                ||||||||||||   |||
                                TTTACGCCACCG   GCT
                                      GTAC
GAM1392  MYO1C    3'  TGCCGATGCCAAATATTTG   61873      CGG      A
                                TAAATG  TGGCATCG CA
                                ||||||  |||||||| ||
                                GTTTAT  ACCGTAGC GT
                                   AA_      C
GAM1392  C6orf37  3'  TGTCACACTGCATTTA     68097         GCATC
                                TAAATGCGGTG    GACA
                                ||||||||||    ||||
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                                ATTTACGTCAC    CTGT
                                      A____
GAM1392 DNAJC6   3' TTGCAGAACCACCGCATT    29498        CA  GA
                                AATGCGGTGG  TC  CAA
                                ||||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                      A_  AC
GAM1392 FLJ11210 3' GTCGATGTGCATGCTTTTA   60319     T   GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM1392 FLJ12476 3' TCGATCTTCTGCATTTA     43270        T  C
                                TAAATGCGG GG ATCGA
                                ||||||||| || |||||
                                ATTTACGTC TC TAGCT
                                      T  _
GAM1392 KIAA1034 3' TCGATGGCATCCGCATTTG   63134        _  G
                                TAAATGCGG TG CATCGA
                                ||||||||| || ||||||
                                GTTTACGCC AC GTAGCT
                                      T  G
GAM1392 KIAA1987 3' TCATGTAACTGCATTTA     89391        G   C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                      A   _
GAM1392 MGC16063 3' TGTCCTGGCCACTGCATT    54929         ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                       GTC
GAM1392 LOC147949 3' TGTCAGATGTCCACATTGCA  79279     __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM1392 LOC150577 3' GTCCTCACCGCATTTG      86258         CATC
                                TAAATGCGGTGG   GAC
                                ||||||||||||   |||
                                GTTTACGCCACT   CTG
                                       C___
GAM1392 LOC158219 3' TGTGTGTCACCACATTT     82694      C      CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                  A       __
GAM1392 LOC202020 3' TGTCTCACCACATTTA      90605      C    CATC
                                TAAATG GGTGG   GACA
                                |||||| |||||   ||||
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                                ATTTAC CCACT    CTGT
                                   A    ____
GAM1392 LOC90826 5' TGTCGATGCAGGTTTATTTG  64788       CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                   TTGGA
GAM1392 LOC93587 3' TTGTCTTTACCTGCATTTA   73042       _    CATC
                                TAAATGC GGTGG   GACAA
                                ||||||| |||||   |||||
                                ATTTACG CCATT   CTGTT
                                    T    T___
GAM1393 CDC6     3' TGACCTTTTTTACTTGAAGCCA 8831       _   GGAT    A
             A                   TTGGTT CAAG   GGAAA GTCA
                                ||||||| ||||   ||||| ||||
                                AACCGA GTTC    TTTTT CAGT
                                   A   AT__    C
GAM1393 ELF3     3' GACCTTGACCTTGACCAA    16682      T    GAT  AAAA
                                TTGGT CAAGG   GG   GTC
                                ||||| |||||   ||   |||
                                AACCA GTTCC   TC    CAG
                                  _    AGT  _____
GAM1393 SLC10A2  5' ACTCTCTGTCTTGACCAA    6591       CAA      AA
                                TTGGTT   GGGATGGA  AGT
                                ||||||   ||||||||  |||
                                AACCAG   TTCTGTCT  TCA
                                   ___       C_
GAM1393 FLJ10829 3' ACTTTTCCACCAAAGCTA    37252      CAAG  A
                                TGGTT    GG TGGAAAAGT
                                |||||    || |||||||||
                                ATCGA    CC ACCTTTTCA
                                  AA__  _
GAM1393 HEAB     3' TGACTCTTCTAATCTTGAACCA 23363          GA    A
             A                   TTGGTTCAAGG  TGGAA AGTCA
                                ||||||||||  ||||| |||||
                                AACCAAGTTCT  ATCTT TCAGT
                                      A_    C
GAM1393 HEMK     5' TGACCTCTCCATCTCCACC    32966     TCAA      AAA
                                GGT    GGGATGGA   GTCA
                                |||    ||||||||   ||||
                                CCA    CTCTACCT   CAGT
                                  C___       CTC
GAM1393 KIAA0298 3' TCCAAGTTCATGAGCCAA    77080        A   A_
                                TTGGTTCA GGG  TGGA
                                |||||||| |||  ||||
                                AACCGAGT CTT  ACCT
                                    A   GA
GAM1393 KIAA1228 3' ACTTTTCTACCTTGAGCCAA  65664          GA
                                TTGGTTCAAGG  TGGAAAAGT
                                ||||||||||  |||||||||
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                                AACCGAGTTCC  ATCTTTTCA
                                          __
GAM1393  KIAA1486  3'  TGACTTTTCTCTCTTATACCAA 67982      TC     TG
                                TTGGT  AAGGGA  GAAAAGTCA
                                |||||  ||||||  |||||||||
                                AACCA  TTCTCT  CTTTTCAGT
                                   TA     __
GAM1393  MGC21854  3'  ACTTTTCAATTTGATCCAA   54601     T    GGATG
                                TTGG TCAAG    GAAAAGT
                                |||| |||||    |||||||
                                AACC AGTTT    CTTTTCA
                                  T    AA___
GAM1393  LOC148697 3'  ACTTTTCCTGCTCAAACC    79671     CAA   AT
                                GGTT   GGG  GGAAAAGT
                                ||||   |||  ||||||||
                                CCAA   CTC  CCTTTTCA
                                  A__   GT
GAM1393  LOC80298  3'  ACTTTTACCTTGAACCA     48063         GATGG
                                TGGTTCAAGG    AAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                     A____
GAM1394  CARKL    3'  TAAGATGAGAGCAAATGCCTGA 26108     CG       G_  AC_
            TCA                   TGA  AGGCATTTG  CT   CTTA
                                |||  |||||||||  ||   ||||
                                ACT  TCCGTAAAC  GA   GAAT
                                  AG        GA  GTA
GAM1394  CHRNA2   5'  GGGAAGCCAAATGCCTCTCA   7430     C          A
                                TGA GAGGCATTTGGCT CCT
                                ||| ||||||||||||| |||
                                ACT CTCCGTAAACCGA GGG
                                  _          A
GAM1394  HLF      3'  TAAGGTAGCCCTCTCATC    10935    C    CATTT
                                GA GAGG    GGCTACCTTA
                                || ||||    ||||||||||
                                CT CTCT    CCGATGGAAT
                                 A   C____
GAM1394  FLJ10997  3'  TTAAGATGTGGCAAATGCCT   37516         G   __
                                AGGCATTTG CTAC  CTTAA
                                ||||||||| ||||  |||||
                                TCCGTAAAC GGTG  GAATT
                                     _   TA
GAM1394  LOC255452 3'  AAGGCAGCCACGGTGTCTC   99382         _    A
                                GAGGCATT TGGCT CCTT
                                |||||||| ||||| ||||
                                CTCTGTGG ACCGA GGAA
                                     C    C
GAM1394  LOC51291  3'  GTGGCCAAACACCCCGCCA   33812    A  A  CA
                                TG CG GG  TTTGGCTAC
                                || || ||  |||||||||
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                                AC GC CC  AAACCGGTG
                                 C  C  AC
GAM1395  GJA1     3'  ATACAGGCTTGAAAGCATCAAG 5712     C  C       TTGACA
                A                 TC TG TGCTTTCA     GTAT
                                  || || ||||||||     ||||
                                  AG AC ACGAAAGT     CATA
                                   A  T       TCGGA_
GAM1395  SLC1A3   3'  ACTGTCAATGAGGTTATGAGA  16059    CT CT    T
                                  TC  G  GCTT CATTGACAGT
                                  ||  |  |||| ||||||||||
                                  AG  T  TGGA GTAACTGTCA
                                   AG AT    _
GAM1395  AMOT     3'  ATACCTTTGGGAAGCAGCAGGA 56534            ATTGACA
                                  TCCTGCTGCTTTC      GTAT
                                  ||||||||||||       ||||
                                  AGGACGACGAAGG      CATA
                                           GTTTC__
GAM1395  DKFZP586B2420 3'  ACTGCCACGAAGCAGCAAGG   75487     _      CAT  A
                                  CCT GCTGCTTT   TG CAGT
                                  ||| ||||||||   || ||||
                                  GGA CGACGAAG   AC GTCA
                                    A       C__  C
GAM1395  KIAA0793  3'  ACTACAAAGAACAGCAGGA   29692         CT   A   AC
                                  TCCTGCTG  TTC TTG  AGT
                                  ||||||||  ||| |||  |||
                                  AGGACGAC  AAG AAC  TCA
                                       __   A   A_
GAM1395  KIAA1577  5'  ATACATTAAGACGACAGCAGCA 65099         T  A  GACA_
                G                  CTGCTGCT TC TT     GTAT
                                   |||||||| || ||     ||||
                                   GACGACGA AG AG     CATA
                                       C  C  AATTA
GAM1395  KIAA1946  3'  TACATCAAAAGCAGCATGA   83357    C       CAT   CA
                                  TC TGCTGCTTT   TGA  GTA
                                  || |||||||||   |||  |||
                                  AG ACGACGAAA   ACT  CAT
                                   T         ____   A_
GAM1395  MGC5139   5'  ATACTTTCTCTGAAAGTAACAG 74566     C       TT  C
                                  CTG TGCTTTCA  GA AGTAT
                                  ||| ||||||||  || |||||
                                  GAC ATGAAAGT  CT TCATA
                                    A       CT  T
GAM1395  PTPN4    3'  CTGTATCATGAAAGCAAAAAG  12590    GC_       TG_
                                  CT   TGCTTTCAT   ACAG
                                  ||   |||||||||   ||||
                                  GA   ACGAAAGTA   TGTC
                                   AAA        CTA
GAM1395  LOC147057 3'  ACTGAGATAAAGCAGCAG    84973          C   GA
                                  CTGCTGCTTT ATT  CAGT
                                  |||||||||| |||  ||||
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                                GACGACGAAA TAG  GTCA
                                      _  A_
GAM1395  LOC220177 5'  TCAGAATTGAAAGCAGCAAGA  95969    C        ___
                                TC TGCTGCTTTCA   TTGA
                                || ||||||||||   ||||
                                AG ACGACGAAAGT   GACT
                                 A         TAA
GAM1395  LOC90593  3'  GCTGAACAAAAGGCAGCAG   64204         CA  A_
                                CTGCTGCTTT  TTG  CAGT
                                ||||||||||  |||  ||||
                                GACGACGGAA  AAC  GTCG
                                      __  AA
GAM1395  LOC91664  5'  TGTAATGAATGCAGCAGGA   67407        T     A
                                TCCTGCTGC TTCATTG CA
                                ||||||||| ||||||| ||
                                AGGACGACG AAGTAAT GT
                                      T     _
GAM1396  VEGFB     3'  ATCATCAAACAGGACAGA    14047     G  A_
                                TTTG CC  TTTGATGAT
                                |||| ||  |||||||||
                                AGAC GG  AAACTACTA
                                  A  AC
GAM1396  acmsd     5'  CAAAAGAATGGCCAGATCTA  57168           GA_
                                TAGATTTGGCCATTT   TG
                                ||||||||||||||   ||
                                ATCTAGACCGGTAAG   AC
                                      AAA
GAM1396  CTSO      3'  CAAGAATGGCCAACCTA     9026      AT       GA
                                TAG  TTGGCCATTT  TG
                                |||  ||||||||||  ||
                                ATC  AACCGGTAAG  AC
                                  C_        A_
GAM1396  LOC204301 3'  CATCATCAAACAGCTGCTCAAG 91022     A  TTT   CA
            A                    TCT GA   GGC  TTTGATGATG
                                ||| ||   |||  ||||||||||
                                AGA CT   TCG  AAACTACTAC
                                  A  CG_   AC
GAM1396  LOC254358 3'  CATCATCAAACAGCTGCTCAAG 96653     A  TTT   CA
            A                    TCT GA   GGC  TTTGATGATG
                                ||| ||   |||  ||||||||||
                                AGA CT   TCG  AAACTACTAC
                                  A  CG_   AC
GAM1396  LOC90918  5'  CATCTGACCAAATCTA      64996         C  TTT
                                TAGATTTGG CA   GATG
                                ||||||||| ||   ||||
                                ATCTAAACC GT   CTAC
                                      A  ___
GAM1397  ARHD      3'  CCTAATGTTCTTAGGTCCCTCT 28146       A       GTAT_
                                AGAGG ACTTAAGAA    GG
                                ||||| |||||||||    ||
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                                TCTCC TGGATTCTT    CC
                                  C       GTAAT
GAM1397 BLTR2    5' ACTCCATACCCTGACCCCCTT 39517     AACTTA  AA
                                GAGG     AG  GTATGGAGT
                                ||||     ||  |||||||||
                                TTCC     TC  CATACCTCA
                                  CCCAG_  C_
GAM1397 CTSK     3' ACTTCTCACTTCCTAAGTTCCC 6371     A      A    AT
             T                   AG GGAACTTA GAAGT  GGAGT
                                || ||||||| |||||  |||||
                                TC CCTTGAAT CTTCA  CTTCA
                                 _      C    CT
GAM1397 FLJ23071 3' ACTCCCTTCCCAAGTTCCTTT  48046        AA   TAT
                                AGAGGAACTT  GAAG   GGAGT
                                ||||||||||  ||||   |||||
                                TTTCCTTGAA  CTTC   CCTCA
                                      CC   ___
GAM1397 NPC1L1   5' ACTTTTCCCTTCTCAGTTCCTC 26331        TA    TAT
             T                   AGAGGAACT  AGAAG   GGAGT
                                |||||||||  |||||   |||||
                                TCTCCTTGA  TCTTC   TTTCA
                                     C_    CCT
GAM1397 NPC1L1   3' ACTTTTCCCTTCTCAGTTCCTC 26331        TA    TAT
             T                   AGAGGAACT  AGAAG   GGAGT
                                |||||||||  |||||   |||||
                                TCTCCTTGA  TCTTC   TTTCA
                                     C_    CCT
GAM1397 SCYA28   3' CTCCATACTCCTTTCCTTT   39540       CTTA  A
                                AGAGGAA    AG AGTATGGAG
                                |||||||    || |||||||||
                                TTTCCTT    TC TCATACCTC
                                    ____  C
GAM1397 SCYA28   5' CTCCATACTCCTTTCCTTT   39540       CTTA  A
                                AGAGGAA    AG AGTATGGAG
                                |||||||    || |||||||||
                                TTTCCTT    TC TCATACCTC
                                    ____  C
GAM1397 SV2      3' ACCCTGCCTCCCACAGTTCCTC 29955        TAA_  A   T  A
                                GAGGAACT    GA GTA GG GT
                                ||||||||    || ||| || ||
                                CTCCTTGA    CT CGT CC CA
                                     CACC  C   _  _
GAM1397 LOC147669 5' CCACCTCTCAGGTCCCTC    85179     A    A   A  AT
                                GAGG ACTT AGA GT  GG
                                |||| |||| ||| ||  ||
                                CTCC TGGA TCT CA  CC
                                  C   C   C  __
GAM1397 LOC196337 3' CCCTGCCTTCAGTTCCTC    89022        TAA    TAT  A
                                GAGGAACT   GAAG   GG G
                                ||||||||   ||||   || |
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                              CTCCTTGA  CTTC  CC C
                                  ___   CGT  _
GAM1397 LOC196337 5' CCCTGCCTTCAGTTCCTC   89022       TAA   TAT  A
                              GAGGAACT  GAAG  GG G
                              ||||||||  ||||  || |
                              CTCCTTGA  CTTC  CC C
                                  ___   CGT  _
GAM1397 LOC51226 3' CTCTGTATCCCCAGGTCCCTC 33573     A   AAGAA
                              GAGG ACTT    GTATGGAG
                              |||| ||||    ||||||||
                              CTCC TGGA    TATGTCTC
                                C   CCCC_
GAM1398 SCAMP1   3' GCTAAATAAATATTCTCC    54500     T    C
                              GGA AATATT ATTTAGC
                              ||| |||||| |||||||
                              CCT TTATAA TAAATCG
                                C    A
GAM1398 SCAMP1   3' GCTAAATAAATATTCTCC    54501     T    C
                              GGA AATATT ATTTAGC
                              ||| |||||| |||||||
                              CCT TTATAA TAAATCG
                                C    A
GAM1398 NX-17    3' TGAATATCAGCCCCTAATA   40706       ATA_
                              TATTAGGG   ATATTCA
                              ||||||||   |||||||
                              ATAATCCC   TATAAGT
                                   CGAC
GAM1398 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
            TA                  TATTAGGGATAATATTCATTTAGC
                              ||||||||||||||||||||||||
                              ATAATCCCTATTATAAGTAAATCG

GAM1399 ANP32A   3' AATACTATTTTTACTGCCA   21945      GTAT      A
                              TGGCAG   TAGGGATA TATT
                              ||||||   |||||||| ||||
                              ACCGTC   ATTTTTAT ATAA
                                  ____       C
GAM1399 EEF1A1   3' ATATTATCCCTAATACCTGCCA 9180
                              TGGCAGGTATTAGGGATAATAT
                              |||||||||||||||||||||
                              ACCGTCCATAATCCCTATTATA

GAM1399 WNT14    3' AATGGGCCTACACCTGCCA   14131       AT   GATAA
                              TGGCAGGT  TAGG    TATT
                              ||||||||  ||||    ||||
                              ACCGTCCA  ATCC    GTAA
                                   C_   GG___
GAM1399 FLJ14075 3' AATACCATCCCTGTTTTACCT  46580     T__     AA
                              AGGTA   TAGGGAT  TATT
                              |||||   |||||||  ||||
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                                TCCAT   GTCCCTA  ATAA
                                   TTT      CC
GAM1399  GPR105    3'  AATATCATCTCTAGCACTGCCA 30267       GTA       A
                                TGGCAG   TTAGGGAT ATATT
                                |||||||  |||||||| |||||
                                ACCGTC   GATCTCTA TATAA
                                   AC_       C
GAM1399  KIAA1034  3'  ATTATCCCAGTTACCTACA    63128    GC    TTA
                                TG  AGGTA   GGGATAAT
                                ||  |||||   ||||||||
                                AC  TCCAT   CCCTATTA
                                 A_    TGA
GAM1399  LOC145678 5'  GAATATTACCCCCGCCTGCT   84434        ATTA   A
                                GGCAGGT    GGG TAATATTC
                                |||||||    ||| ||||||||
                                TCGTCCG    CCC ATTATAAG
                                   C___   C
GAM1399  LOC148371 3'  ATATTATCCCTAATACCTGCCA 79551
                                TGGCAGGTATTAGGGATAATAT
                                |||||||||||||||||||||
                                ACCGTCCATAATCCCTATTATA

GAM1399  LOC161589 3'  GAATATTATCCCTAATACCTGC 83157
            CA                    TGGCAGGTATTAGGGATAATATTC
                                |||||||||||||||||||||||
                                ACCGTCCATAATCCCTATTATAAG

GAM1399  LOC202108 3'  ATATTATCCCTAATACCTGCCA 90629
                                TGGCAGGTATTAGGGATAATAT
                                |||||||||||||||||||||
                                ACCGTCCATAATCCCTATTATA

GAM1399  LOC221838 3'  ATATTATCCCTAATACCTGCCA 94118
                                TGGCAGGTATTAGGGATAATAT
                                |||||||||||||||||||||
                                ACCGTCCATAATCCCTATTATA

GAM1399  LOC221839 3'  ATATTATCCCTAATACCTGCCA 94098
                                TGGCAGGTATTAGGGATAATAT
                                |||||||||||||||||||||
                                ACCGTCCATAATCCCTATTATA

GAM1400  SCAMP1    3'  GCTAAATAAATATTCTCC    54500     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1400  SCAMP1    3'  GCTAAATAAATATTCTCC    54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
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                                CCT TTATAA TAAATCG
                                  C     A
GAM1400 NX-17    3' TGAATATCAGCCCCTAATA   40706        ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM1400 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
             TA                   TATTAGGGATAATATTCATTTAGC
                                  ||||||||||||||||||||||||
                                  ATAATCCCTATTATAAGTAAATCG

GAM1401 APP      3' CCAAGAATTCTCCAAAACA   6660       AC        AC
                                TGTT  TGGAGAATTC  TGG
                                ||||  ||||||||||  |||
                                ACAA  ACCTCTTAAG  ACC
                                  A_        A_
GAM1401 SF3B1    3' ATGCCAGTAGTGACCAAGAACA 25817      AC   AGA   C
                                TGTT  TGG   ATT ACTGGCAT
                                ||||  |||   ||| ||||||||
                                ACAA  ACC   TGA TGACCGTA
                                  GA   AG_  _
GAM1401 DKFZP434C171 5' CCAGAATTCTCCAGCAACA   32187      A         AC
                                TGTT CTGGAGAATTC  TGG
                                |||| ||||||||||  |||
                                ACAA GACCTCTTAAG  ACC
                                  C         __
GAM1401 DKFZp434F1719 3' ATGCCAGTGAACTTATTGCTGA 51011       CT  A  A
             CA                   TGTTA  GG GA TTCACTGGCAT
                                  |||||  || || ||||||||||
                                  ACAGT  TT TT AAGTGACCGTA
                                     CG  A  C
GAM1401 FLJ11259  3' TGCCAGTAAATGTGGCA     37774        TGGAGA   C
                                TGTTAC     ATT ACTGGCA
                                ||||||     ||| |||||||
                                ACGGTG     TAA TGACCGT
                                   _______  A
GAM1401 VEST1    5' CTGGGGAATTTCCAGTAACA   54763           A   A TG
                                TGTTACTGGAGA TTC C  G
                                |||||||||||| ||| |  |
                                ACAATGACCTTT AGG G  C
                                      A   _ GT
GAM1401 LOC151996 5' ATGTGGTAAAATTCTCCATCAA 86714      AC        C_    G
             CA                   TGTT  TGGAGAATT  ACTG CAT
                                  ||||  |||||||||  |||| |||
                                  ACAA  ACCTCTTAA  TGGT GTA
                                    CT        AA   _
GAM1401 LOC152122 3' GCAAGACTCTCCAGTAACA    86740           AT  ACTG
                                TGTTACTGGAGA  TC    GC
                                ||||||||||||  ||    ||
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                                ACAATGACCTCT  AG   CG
                                      C_  AA__
GAM1401  LOC152845 5'  GTGAGGAATTCTCAATAACA  60959      CTG      A  G
                                TGTTA  GAGAATTC CT GC
                                |||||  |||||||| || ||
                                ACAAT  CTCTTAAG GA TG
                                   AA_      _ G
GAM1401  LOC255762 3'  GCCAAATTCCCAGTAACA    96733        A    CAC
                                TGTTACTGG GAATT  TGGC
                                ||||||||| |||||  ||||
                                ACAATGACC CTTAA  ACCG
                                      _   ___
GAM1402  ELF3      3'  TGACCTTGACCTTGACCAA   16685      T    GAT  AAA
                                TTGGT CAAGG  GG  GTCA
                                ||||| |||||  ||  ||||
                                AACCA GTTCC  TC  CAGT
                                   _    AGT  ___
GAM1402  JAK2      3'  TGACCTTCATTCTGAGACCAA  18318      CAA      AA
                                TTGGTT  GGGATGGA  GTCA
                                ||||||  ||||||||  ||||
                                AACCAG  TCTTACTT  CAGT
                                   AG_      C_
GAM1402  SLC10A2   5'  ACTCTCTGTCTTGACCAA    6590       CAA      A
                                TTGGTT  GGGATGGA AGT
                                ||||||  |||||||| |||
                                AACCAG  TTCTGTCT TCA
                                   ___       C
GAM1402  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA  37205      CAAGG  G
                                TTGGTT   GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA   TTG CTTTCAGTG
                                   AA___  A
GAM1402  KIAA1958  5'  GTGACTTTGAACCCCAAACC  82788     CAA  ATGG
                                GGTT  GGG   AAAGTCAC
                                ||||  |||   ||||||||
                                CCAA  CCC   TTTCAGTG
                                  A__  CAAG
GAM1402  MARCKS    3'  ACTTTCCACCCTGCCCA    11411    TTCA  A
                                TGG   AGGG TGGAAAGT
                                |||   |||| ||||||||
                                ACC   TCCC ACCTTTCA
                                  CG__  _
GAM1402  TUB       5'  GTGGGACCATCCCTTAAACC  13898     C       AAAG
                                GGTT AAGGGATGG   TCAC
                                |||| |||||||||   ||||
                                CCAA TTCCCTACC   GGTG
                                  A       AG__
GAM1402  LOC80298  3'  ACTTTTACCTTGAACCA    48062         GATG
                                TGGTTCAAGG   GAAAGT
                                ||||||||||   ||||||
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                                ACCAAGTTCC    TTTTCA
                                     A___
GAM1403 ADAMTS13 5' TCAGCCGAGGTCCTGGC     58143      CA  CC
                                GCCAGG  GCT  CGGCTGA
                                ||||||  |||  |||||||
                                CGGTCC  TGG  GCCGACT
                                   __   A_
GAM1403 ADAMTS13 5' TCAGCCGAGGTCCTGGC     58146      CA  CC
                                GCCAGG  GCT  CGGCTGA
                                ||||||  |||  |||||||
                                CGGTCC  TGG  GCCGACT
                                   __   A_
GAM1403 ADAMTS13 5' TCAGCCGAGGTCCTGGC     58157      CA  CC
                                GCCAGG  GCT  CGGCTGA
                                ||||||  |||  |||||||
                                CGGTCC  TGG  GCCGACT
                                   __   A_
GAM1403 AK1      3' TCGAGAGCAGCCTGGCCA    6642         A   C
                                TGGCCAGGC GCTC CGG
                                ||||||||| |||| |||
                                ACCGGTCCG CGAG GCT
                                     A    A
GAM1403 ASB2     5' GCAGGGATCTGCCTGGCCA   32875          C   G
                                TGGCCAGGCAG TCCC GC
                                |||||||||||| |||| ||
                                ACCGGTCCGTC AGGG CG
                                      T    A
GAM1403 ATM      3' GCCAAGAGACCAGCCTGGCCA 5296         AG__  CC
                                TGGCCAGGC   CTC  GGC
                                |||||||||   |||  |||
                                ACCGGTCCG   GAG  CCG
                                     ACCA   AA
GAM1403 ATM      3' GCCAAGAGACCAGCCTGGCCA 57133        AG__  CC
                                TGGCCAGGC   CTC  GGC
                                |||||||||   |||  |||
                                ACCGGTCCG   GAG  CCG
                                     ACCA   AA
GAM1403 AXIN1    3' CAGTTCAAGGAGCTGCTGACCA 61534    CCA      C__
                                TGG  GGCAGCTCC  GGCTG
                                |||  |||||||||  |||||
                                ACC  TCGTCGAGG  TTGAC
                                  AG_       AAC
GAM1403 CAPN1    3' GCCGACCAGGAGCTGCCCAGCC 19009    CA       ____
                                GGC  GGCAGCTCC   CGGC
                                |||  |||||||||   ||||
                                CCG  CCGTCGAGG   GCCG
                                  AC       ACCA
GAM1403 COPA     3' TCGAGACCTGCCTGGCCA    16481         C  C
                                TGGCCAGGCAG TC CGG
                                |||||||||| || |||
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                                ACCGGTCCGTC AG GCT
                                      C  A
GAM1403  CYP1A2   3'  TTGGAAAGCAGCCTGGCCA   7532         A   C_
                                TGGCCAGGC GCT  CCGG
                                ||||||||| |||  ||||
                                ACCGGTCCG CGA  GGTT
                                     A   AA
GAM1403  DAPK1    3'  GTCAGCCAGGAGCTGTCACCA  18228     CCA       C
                                TGG   GGCAGCTCC GGCTGAC
                                |||   ||||||||| |||||||
                                ACC   CTGTCGAGG CCGACTG
                                  A__       A
GAM1403  FLRT2    3'  GCTTGATGCTGCCTGGCCA   26001          _ CC
                                TGGCCAGGCAGC TC  GGC
                                |||||||||||| ||  |||
                                ACCGGTCCGTCG AG  TCG
                                      T  T_
GAM1403  FOXD2    3'  CCGGGAGAGATGCCTGGCCA  16786         G__
                                TGGCCAGGCA  CTCCCGG
                                ||||||||||  |||||||
                                ACCGGTCCGT  GAGGGCC
                                     AGA
GAM1403  FZD1     5'  CAGCCGGGAGCCAGCGAGCC  14496     CAG  A_
                                GGC  GC  GCTCCCGGCTG
                                |||  ||  ||||||||||
                                CCG  CG  CGAGGGCCGAC
                                  AG_  AC
GAM1403  G22P1    3'  GCCAGGCTGCCTGGCC     9407          CCC
                                GGCCAGGCAGCT  GGC
                                ||||||||||||  |||
                                CCGGTCCGTCGG  CCG
                                      A__
GAM1403  GUCY1A3  5'  GCCTGAGCTGCCTGACA    64227    GC       CC
                                TG  CAGGCAGCTC  GGC
                                ||  ||||||||||  |||
                                AC  GTCCGTCGAG  CCG
                                 A_        T_
GAM1403  HTRA3    3'  GCCAGGGCTGCTGCCTGCCA  90581     C     T_  _
                                TGGC AGGCAGC  CCC GGC
                                |||| |||||||  ||| |||
                                ACCG TCCGTCG  GGG CCG
                                  _     TC  A
GAM1403  IL17R    3'  GTCAGGAGTTTGAGCCAGCCTG 27560        A_   CCGG__
            GCCA                  TGGCCAGGC  GCTC     CTGAC
                                |||||||||  ||||     |||||
                                ACCGGTCCG  CGAG     GACTG
                                     AC    TTTGAG
GAM1403  INMT     3'  CAGCCAGAGGTCTGGTCA    23210        AG   CC
                                TGGCCAGGC  CTC  GGCTG
                                |||||||||  |||  |||||
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                                ACTGGTCTG  GAG  CCGAC
                                    __   A_
GAM1403  INPP5B   3'  GTCTGGGAACTACCTGCCCA  97259    C   C  C    _
                                TGG CAGG AG TCCCGG C
                                ||| |||| || |||||| |
                                ACC GTCC TC AGGGTC G
                                  C   A  A     T
GAM1403  LATS2    5'  GCCCGGGAGCCGCCGGCCA   28134     A   A     _
                                TGGCC GGC GCTCCCGG C
                                ||||| ||| |||||||| |
                                ACCGG CCG CGAGGGCC G
                                   _  C       C
GAM1403  LNK      3'  CAGCCACCATGCCTGGCTA   19634        GCTCCC
                                TGGCCAGGCA     GGCTG
                                ||||||||||     |||||
                                ATCGGTCCGT     CCGAC
                                     ACCA__
GAM1403  NTSR1    3'  CAGCCAGGAGCTGGGAGCCA  11852     CAGG     C
                                TGGC   CAGCTCC GGCTG
                                ||||   ||||||| |||||
                                ACCG   GTCGAGG CCGAC
                                  AGG_     A
GAM1403  OVOL1    3'  GCCTCCCAGCTGCCTGGCCA  17070          CCC_
                                TGGCCAGGCAGCT   GGC
                                ||||||||||||   |||
                                ACCGGTCCGTCGA   CCG
                                      CCCT
GAM1403  PFKL     3'  CAGCCCTTGCTCTACCTGGCC  12053       C__  TCCC
                                GGCCAGG  AGC   GGCTG
                                |||||||  |||   |||||
                                CCGGTCC  TCG   CCGAC
                                   ATC  TTC_
GAM1403  PODXL    3'  GCAGGAGTGCCTGGCCA     19417        G   CG
                                TGGCCAGGCA CTCC  GC
                                |||||||||| ||||  ||
                                ACCGGTCCGT GAGG  CG
                                     _   A_
GAM1403  PPP2R2C  5'  CGGGAGAGCTGCTGGCCA    62418       G   __
                                TGGCCAG CAGC  TCCCG
                                ||||||| ||||  |||||
                                ACCGGTC GTCG  AGGGC
                                   _   AG
GAM1403  PRKWNK3  3'  CAGCCACCATGCCTGGCTA   62228         GCTCCC
                                TGGCCAGGCA     GGCTG
                                ||||||||||     |||||
                                ATCGGTCCGT     CCGAC
                                     ACCA__
GAM1403  RNF4     3'  TCAGAAGCTTCCTGGCCA    12885        C   CCCGG
                                TGGCCAGG AGCT    CTGA
                                |||||||| ||||    ||||
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                                ACCGGTCC TCGA     GACT
                                     T    A____
GAM1403  SCNN1A    3'  CAGCCCCCGACTGGCCTGGCCA 8295          _  C  CC_
                                TGGCCAGGC AG TC   GGCTG
                                ||||||||| || ||   |||||
                                ACCGGTCCG TC AG   CCGAC
                                     G  _  CCC
GAM1403  SLC12A4   3'  CAGCCCTGCTTGCCTGGCC    18626         _  TCCC
                                GGCCAGGCA GC    GGCTG
                                ||||||||| ||    |||||
                                CCGGTCCGT CG    CCGAC
                                     T  TC__
GAM1403  SLC19A1   3'  TCAGGGCAGCTGCCTGGCCA   13220           _  GGC
                                TGGCCAGGCAGCT CCC   TGA
                                |||||||||||| |||   |||
                                ACCGGTCCGTCGA GGG   ACT
                                       C  ___
GAM1403  SLC24A1   3'  GTCAGCCACCGCGCCTGGCC   17564         A  TCCC
                                GGCCAGGC GC    GGCTGAC
                                |||||||| ||    |||||||
                                CCGGTCCG CG    CCGACTG
                                     _  CCA_
GAM1403  SURF4     3'  CTGCAAGCCAGCCTGGCCA    53708         A_  CC
                                TGGCCAGGC  GCT  CGG
                                |||||||||  |||  |||
                                ACCGGTCCG  CGA  GTC
                                     AC   AC
GAM1403  SURF5     3'  GCAGAGCTCCTGGCCA      23127         C    CCG
                                TGGCCAGG AGCTC   GC
                                |||||||| |||||   ||
                                ACCGGTCC TCGAG   CG
                                     _    A__
GAM1403  SWAP70    3'  GTTCAAGAGCAGCCTGGCCA   71873         A   CC_
                                TGGCCAGGC GCTC   GGC
                                ||||||||| ||||   |||
                                ACCGGTCCG CGAG   TTG
                                     A    AAC
GAM1403  TCAP      3'  TGGAGGGGAGCTGCTGGCCA   14790        G      GG
                                TGGCCAG CAGCTCCC  CTG
                                ||||||| ||||||||  |||
                                ACCGGTC GTCGAGGG  GGT
                                     _      GA
GAM1403  TCIRG1    5'  CAGCCCAGAACCCCTGGCCA   21329         CAGC  CC
                                TGGCCAGG   TC  GGCTG
                                ||||||||   ||  |||||
                                ACCGGTCC   AG  CCGAC
                                     CCA_  AC
GAM1403  TRPM2     3'  GCCTGGGGCTGCCTGGCCA    13867            C
                                TGGCCAGGCAGCTCC GGC
                                ||||||||||||||| |||
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                                ACCGGTCCGTCGGGG CCG
                                         T
GAM1403  TSSC4    3'  GTCAGGGGGCAGCCTGGCCA  20327        A    _
                                TGGCCAGGC GCTCCC GGC
                                ||||||||| |||||| |||
                                ACCGGTCCG CGGGGG CTG
                                     A     A
GAM1403  AKAP10   5'  GCTGGAGCTGCCTGGGCA   24221    G        C
                                TG CCAGGCAGCTCC GGC
                                || ||||||||||| |||
                                AC GGTCCGTCGAGG TCG
                                 G         _
GAM1403  C20orf106 3'  GTTTGAGAACAGCCTGGCCA  55912        AG__  CC
                                TGGCCAGGC   CTC  GGC
                                |||||||||   |||  |||
                                ACCGGTCCG   GAG  TTG
                                     ACAA   T_
GAM1403  C20orf43  3'  GTCATAAAGCTGTCCTGGCCA 60613        _    CCC_
                                TGGCCAGG CAGCT   GGC
                                |||||||| |||||   |||
                                ACCGGTCC GTCGA   CTG
                                     T    AATA
GAM1403  CECR7    5'  GCCAAGCTGACCTGGCCA    80449        _    CCC
                                TGGCCAGG CAGCT   GGC
                                |||||||| |||||  |||
                                ACCGGTCC GTCGA   CCG
                                     A    A__
GAM1403  CLDN7    5'  GCCCGGAGGGAACCGCCTGGCC 96226        AG__  _   _
                                GGCCAGGC   CTC CCGG C
                                ||||||||   ||| |||| |
                                CCGGTCCG   GGG GGCC G
                                     CCAA  A   C
GAM1403  CLDN7    5'  GCCCGGAGGGAACCGCCTGGCC 8963         AG__  _   _
                                GGCCAGGC   CTC CCGG C
                                ||||||||   ||| |||| |
                                CCGGTCCG   GGG GGCC G
                                     CCAA  A   C
GAM1403  DKFZP434K1172 5'  CAGCCGACCTGGACCTGGCCA  49264        __  CTCC
                                TGGCCAGG  CAG   CGGCTG
                                ||||||||  |||   ||||||
                                ACCGGTCC  GTC   GCCGAC
                                     AG   CA__
GAM1403  DKFZP566C243 3'  GCCAAGAACTCCTGGCCA   31810        C  C  CC
                                TGGCCAGG AG TC  GGC
                                |||||||| || ||  |||
                                ACCGGTCC TC AG  CCG
                                     _ A  AA
GAM1403  EPI64    3'  GCCAAGCTGCCTGGCCA     50035           CCC
                                TGGCCAGGCAGCT   GGC
                                ||||||||||||   |||
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                                ACCGGTCCGTCGA  CCG
                                      A__
GAM1403 FGD3    5' TCAGGAAGCCCCTGGCCA   73281       CA  _ C
                                TGGCCAGG  GCT CC GG
                                ||||||||  ||| || ||
                                ACCGGTCC  CGA GG CT
                                    C_  A  A
GAM1403 FLJ10232 3' TCAGCCGGGAACTCTGATTGC 36385   CAGG  C__
                                GC   CAG  TCCCGGCTGA
                                ||   |||  ||||||||||
                                CG   GTC  AGGGCCGACT
                                 TTA_  TCA
GAM1403 FLJ10261 3' CAGCCGGGCATCCTGACCG  36417    C   CAGCT
                                TGG CAGG    CCCGGCTG
                                ||| ||||    ||||||||
                                GCC GTCC    GGGCCGAC
                                  A   TAC__
GAM1403 FLJ11151 3' GTTTGAGAACAGCCTGGCCA  68481       AG__  CC
                                TGGCCAGGC   CTC  GGC
                                |||||||||   |||  |||
                                ACCGGTCCG   GAG  TTG
                                     ACAA  T_
GAM1403 FLJ11526 5' CGGGGGAGCTGCCCGGC    45253    A       GG
                                GCC GGCAGCTCCC  CTG
                                ||| ||||||||||  |||
                                CGG CCGTCGAGGG  GGC
                                  C        __
GAM1403 FLJ12985 3' TTGAGAGCAGCCTGGCCA   46802       A   C
                                TGGCCAGGC GCTC CGG
                                ||||||||| |||| |||
                                ACCGGTCCG CGAG GTT
                                     A   A
GAM1403 FLJ13262 3' GTCGGAGCTGCCCAGCC    46694    CA       C
                                GGC  GGCAGCTCC GGC
                                |||  ||||||||| |||
                                CCG  CCGTCGAGG CTG
                                  AC       _
GAM1403 FLJ14154 3' GCAAGGAGCTGCCAGCCA   46232    CA       CG
                                TGGC  GGCAGCTCC  GC
                                ||||  |||||||||  ||
                                ACCG  CCGTCGAGG  CG
                                  A_       AA
GAM1403 FLJ14154 3' GCCTCCAGAGCTGCCCAGCCA 46234    CA      CC__
                                TGGC  GGCAGCTC   GGC
                                ||||  ||||||||   |||
                                ACCG  CCGTCGAG   CCG
                                  AC       ACCT
GAM1403 FLJ14810 3' GTCAGCCTTGGGGAGCTGCCTA 52703   C        ___
            GC                    GC AGGCAGCTCCC   GGCTGAC
                                || ||||||||||   |||||||
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                                CG TCCGTCGAGGG   CCGACTG
                                 A          GTT
GAM1403  FLJ20359  3'  GTTGGGGAGCGCCTGGCCA   35520         A     _
                                TGGCCAGGC GCTCCC GGC
                                ||||||||| |||||| |||
                                ACCGGTCCG CGAGGG TTG
                                      _     G
GAM1403  FLJ20548  3'  GTCAGCCGTGGCCCCACCTACC 35821     CC   CAGCT  _
              A                  TGG  AGG     CC CGGCTGAC
                                 |||  |||     || ||||||||
                                 ACC  TCC     GG GCCGACTG
                                   A_   ACCCC  T
GAM1403  FLJ21687  3'  GTTCAAGAGCAGCCTGGCCA   46302         A    CC_
                                TGGCCAGGC GCTC   GGC
                                ||||||||| ||||   |||
                                ACCGGTCCG CGAG   TTG
                                      A    AAC
GAM1403  FLJ22349  3'  GTCACAGAGCTGCCTGGC    46109           CC_
                                GCCAGGCAGCTC   GGC
                                ||||||||||||   |||
                                CGGTCCGTCGAG   CTG
                                       ACA
GAM1403  FLJ22593  5'  CAGCCAGATGCCTGGCC     45549         G  CCC
                                GGCCAGGCA CT   GGCTG
                                ||||||||| ||   |||||
                                CCGGTCCGT GA   CCGAC
                                      A  ___
GAM1403  FLJ23058  3'  CAGCCAAATCTGCCTGGCC    45522         CTCCC
                                GGCCAGGCAG     GGCTG
                                ||||||||||     |||||
                                CCGGTCCGTC     CCGAC
                                      TAAA_
GAM1403  GNB1L     3'  CAGCCAGAGCCCTGGCC     54863        CA    CC
                                GGCCAGG  GCTC  GGCTG
                                |||||||  ||||  |||||
                                CCGGTCC  CGAG  CCGAC
                                     __    A_
GAM1403  GP5       3'  GTCTTGAACTCCTGGCCA    16879         C  C  CC
                                TGGCCAGG AG TC  GGC
                                |||||||| || ||  |||
                                ACCGGTCC TC AG  CTG
                                     _  A  TT
GAM1403  GRIN3A    3'  TTGGAGGAACTACCTGGCCA   56788         C  C   CGG TG
                                TGGCCAGG AG TCC   C  A
                                |||||||| || |||   |  |
                                ACCGGTCC TC AGG   G  T
                                     A  A   A__ GT
GAM1403  HGC6.1.1  3'  GCTGAAAGGAGCTGCCTGGGCA 27613     G          ___
                                TG CCAGGCAGCTCC   CGGC
                                || ||||||||||||   ||||
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                                AC GGTCCGTCGAGG   GTCG
                                 G          AAA
GAM1403 HSU84971 5' GCCAGGGGCCACCGCGGCCA  26154      A_  CA    C
                                TGGCC  GG  GCTCC GGC
                                ||||||  ||  |||||| |||
                                ACCGG  CC  CGGGG CCG
                                   CG  AC    A
GAM1403 KIAA0280 3' GCTCAGAAGCTGTCTAGCCA  93305      C       _ CC
                                TGGC AGGCAGCT C  GGC
                                |||| |||||||| |  |||
                                ACCG TCTGTCGA G  TCG
                                  A       A AC
GAM1403 KIAA0322 3' TCAGCCGGAACTAGCCTAGACA 94332    GCC    _  CTC
                                TG   AGGC AG   CCGGCTGA
                                ||   |||| ||   ||||||||
                                AC   TCCG TC   GGCCGACT
                                 AGA    A  AA_
GAM1403 KIAA0472 3' GTTCAAGAGCAGCCTGGCCA  72363         A    CC_
                                TGGCCAGGC GCTC   GGC
                                |||||||||| ||||   |||
                                ACCGGTCCG CGAG   TTG
                                     A    AAC
GAM1403 KIAA0556 3' GTCAGCTGGGCCACCCGCCA  69651      CA  CAGCT
                                TGGC  GG    CCCGGCTGAC
                                ||||  ||    ||||||||||
                                ACCG  CC    GGGTCGACTG
                                  C_  ACC__
GAM1403 KIAA0662 3' GCCGAGCTGCCTCACCA     82738     CC       CC
                                TGG  AGGCAGCTC  GGC
                                |||  |||||||||  |||
                                ACC  TCCGTCGAG  CCG
                                  AC        __
GAM1403 KIAA1045 3' GTCAGCAGAAGCTGCCTGGC  71608          CCCG
                                GCCAGGCAGCT    GCTGAC
                                ||||||||||    ||||||
                                CGGTCCGTCGA    CGACTG
                                      AGA_
GAM1403 KIAA1255 3' CAGCCAAGGGCCCTGGCCA   67742        CA    CC
                                TGGCCAGG  GCTC  GGCTG
                                ||||||||  ||||  |||||
                                ACCGGTCC  CGGG  CCGAC
                                    __    AA
GAM1403 KIAA1464 3' GTGGGGACTGCCTGGCCA    68823          C    G
                                TGGCCAGGCAG TCCC GC
                                |||||||||||| |||| ||
                                ACCGGTCCGTC AGGG TG
                                      _    G
GAM1403 KIAA1582 5' GCCAACCCAGCTGCCTGGCC  65989          CCC__
                                GGCCAGGCAGCT    GGC
                                ||||||||||||    |||
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                                CCGGTCCGTCGA    CCG
                                      CCCAA
GAM1403 KIAA1719 5' CAGCCATGCCACCGCCCTGGCC 68726       _ A___  TCCC
             A                   TGGCCAGG C   GC   GGCTG
                                 |||||||| |   ||   |||||
                                 ACCGGTCC G   CG   CCGAC
                                     C CCAC  TA__
GAM1403 KIAA1872 3' GTTTGAGAACAGCCTGGCCA  63618        AG__  CC
                                 TGGCCAGGC   CTC  GGC
                                 |||||||||   |||  |||
                                 ACCGGTCCG   GAG  TTG
                                       ACAA  T_
GAM1403 KIAA1872 3' TCAGCCGAGATTGCACCA   63619    CCAG   C  C
                                 TGG   GCAG TC CGGCTGA
                                 |||   |||| || |||||||
                                 ACC   CGTT AG GCCGACT
                                   A___   _ A
GAM1403 KIAA1932 3' GCCTTGAGTGCCTGGCCA   73824        G   CC
                                 TGGCCAGGCA CTC  GGC
                                 |||||||||| |||  |||
                                 ACCGGTCCGT GAG  CCG
                                       _  TT
GAM1403 KIAA1940 3' GTCAGCCAAAAGCTGGGGGC  80791    AGG    CCC
                                 GCC   CAGCT   GGCTGAC
                                 |||   |||||   |||||||
                                 CGG   GTCGA   CCGACTG
                                   GG_    AAA
GAM1403 LANO    5' CAGCTCCGCGAGCTGCCCGAGC 37161    CA_      C __
                                 GC   GGCAGCTC CG  GCTG
                                 ||   |||||||| ||  ||||
                                 CG   CCGTCGAG GC  CGAC
                                  AGC       C  CT
GAM1403 MAP2K7   3' GCCACCCAGCTGCCTGCCA   18531     C      CCC_
                                 TGGC AGGCAGCT   GGC
                                 |||| ||||||||   |||
                                 ACCG TCCGTCGA   CCG
                                   _       CCCA
GAM1403 MGC10814 5' GTTTGAGAACAGCCTGGCCA  52024        AG__  CC
                                 TGGCCAGGC   CTC  GGC
                                 |||||||||   |||  |||
                                 ACCGGTCCG   GAG  TTG
                                       ACAA  T_
GAM1403 MGC13204 3' CAGCCACCATGCCTGGCTA   49627        GCTCCC
                                 TGGCCAGGCA     GGCTG
                                 ||||||||||     |||||
                                 ATCGGTCCGT     CCGAC
                                       ACCA__
GAM1403 MGC15737 5' CAGCTGTCTGAGCTGCCCGGGC 53031    G  A      C__
             A                   TG CC GGCAGCTC   CGGCTG
                                 || || ||||||||   ||||||
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                                AC GG CCGTCGAG   GTCGAC
                                 G  C       TCT
GAM1403  MGC22014  5'  GCCGAGCTGCCCAGCCA     65112      CA       CC
                                TGGC  GGCAGCTC  GGC
                                ||||  ||||||||  |||
                                ACCG  CCGTCGAG  CCG
                                  AC       __
GAM1403  ORCTL3    3'  CAGCAGGGAGCTGCCTAAACA  16190    GCC         G
                                TG   AGGCAGCTCCC GCTG
                                ||   |||||||||| ||||
                                AC   TCCGTCGAGGG CGAC
                                 AAA          A
GAM1403  R32184_3  3'  CACTACGAGCTGCCTGCCA    54199      C        CC  C
                                TGGC AGGCAGCTC  GG TG
                                |||| |||||||||  || ||
                                ACCG TCCGTCGAG  TC AC
                                  _        CA  _
GAM1403  SC65      3'  GTTCAAGACCTGCCTGGCCA   22301           C  CC_
                                TGGCCAGGCAG TC   GGC
                                ||||||||||| ||   |||
                                ACCGGTCCGTC AG   TTG
                                      C  AAC
GAM1403  SIMRP7    5'  CAGCCGGGGCGGGCCCAGC    93966    CA   A_  T
                                GC  GGC  GC CCCGGCTG
                                ||  |||  || ||||||||
                                CG  CCG  CG GGGCCGAC
                                 AC   GG  _
GAM1403  STMN4     3'  GTCAGCCGGACAGCTCCAGC   48651    CA  C    C_
                                GC  GG AGCT  CCGGCTGAC
                                ||  || ||||  |||||||||
                                CG  CC TCGA  GGCCGACTG
                                 A_  _    CA
GAM1403  THEA      3'  GTTCAAGAGCAGCCTGGCCA   66893         A    CC_
                                TGGCCAGGC GCTC   GGC
                                ||||||||| ||||   |||
                                ACCGGTCCG CGAG   TTG
                                      A    AAC
GAM1403  LOC128402 3'  GCCAGGACAGCCCCTGGCCA   76287         CA  __   C
                                TGGCCAGG  GC  TCC GGC
                                ||||||||  ||  ||| |||
                                ACCGGTCC  CG  AGG CCG
                                     C_  AC   A
GAM1403  LOC145453 3'  TCGAGAGCAGCCTGGCCA     77671         A   C
                                TGGCCAGGC GCTC CGG
                                ||||||||| |||| |||
                                ACCGGTCCG CGAG GCT
                                      A   A
GAM1403  LOC146733 3'  GCTGGAGCCGCCAGGCCA     84785       A  A    C
                                TGGCC GGC GCTCC GGC
                                ||||| ||| ||||| |||
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                                ACCGG CCG CGAGG TCG
                                  A  C    _
GAM1403  LOC146895 3'  GTTTGAGAACAGCCTGGCCA  84873       AG__  CC
                                TGGCCAGGC   CTC  GGC
                                |||||||||   |||  |||
                                ACCGGTCCG   GAG  TTG
                                     ACAA   T_
GAM1403  LOC147804 5'  GCTCAGGAGCGCCTGGCCA   79157       A    C _
                                TGGCCAGGC GCTCC G GC
                                ||||||||| ||||| | ||
                                ACCGGTCCG CGAGG C CG
                                     _    A T
GAM1403  LOC148479 3'  CAGCCAGAGCTGCTGCCA    79609     CA      CC
                                TGGC  GGCAGCTC  GGCTG
                                ||||  ||||||||  |||||
                                ACCG  TCGTCGAG  CCGAC
                                  __       A_
GAM1403  LOC149267 3'  GCAGAGCTCCTGGCCA      57479       C    CCG
                                TGGCCAGG AGCTC   GC
                                |||||||| |||||   ||
                                ACCGGTCC TCGAG   CG
                                     _    A__
GAM1403  LOC149372 3'  GGCAAGGAGCTGCCTGGCC   80103          CG
                                GGCCAGGCAGCTCC  GCT
                                ||||||||||||||  |||
                                CCGGTCCGTCGAGG  CGG
                                      AA
GAM1403  LOC150685 5'  GCCCTGAGCTGCCTGCCA    88535     C       CC
                                TGGC AGGCAGCTC  GGC
                                |||| |||||||||  |||
                                ACCG TCCGTCGAG  CCG
                                  _       TC
GAM1403  LOC153196 3'  TTAGTAGCTGCCTGACCA    87175     C       CCCG
                                TGG CAGGCAGCT   GCTGA
                                ||| |||||||||   |||||
                                ACC GTCCGTCGA   TGATT
                                  A       _____
GAM1403  LOC153688 3'  GCCCAGAGCAGCCTGGCCA   87320       A   CC
                                TGGCCAGGC GCTC  GGC
                                ||||||||| ||||  |||
                                ACCGGTCCG CGAG  CCG
                                     A    AC
GAM1403  LOC196510 3'  GCCACAGCTACCTGGTCA    89093       C   CCC
                                TGGCCAGG AGCT   GGC
                                |||||||| ||||   |||
                                ACTGGTCC TCGA   CCG
                                     A   CA_
GAM1403  LOC197342 3'  GCCAAGGCTGCCTGGCC     89367         CCC
                                GGCCAGGCAGCT   GGC
                                ||||||||||||   |||
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                                CCGGTCCGTCGG  CCG
                                      AA_
GAM1403  LOC200220 3'  GCCACAGCTACCTGGTCA    90037       C   CCC
                                TGGCCAGG AGCT  GGC
                                |||||||| ||||  |||
                                ACTGGTCC TCGA  CCG
                                    A   CA_
GAM1403  LOC203232 3'  CAGCCGGGGCAGCCAGC    71915    CA  A  T
                                GC  GGC GC CCCGGCTG
                                ||  ||| || ||||||||
                                CG  CCG CG GGGCCGAC
                                 A_  A  _
GAM1403  LOC203668 5'  GCTTCGGAAACCCGCCTGGCCA 90984        AGC__  C_
                                TGGCCAGGC    TCC  GGC
                                |||||||||    |||  |||
                                ACCGGTCCG    AGG  TCG
                                     CCCAA  CT
GAM1403  LOC219513 5'  GCCAGCGCTGCCTGGCCA    95984          TCCC
                                TGGCCAGGCAGC   GGC
                                ||||||||||||   |||
                                ACCGGTCCGTCG   CCG
                                      CGA_
GAM1403  LOC221463 3'  GCTGGAGGAGCTGCCCGGCC  93705     A       __
                                GGCC GGCAGCTCC  CGGC
                                |||| |||||||||  ||||
                                CCGG CCGTCGAGG  GTCG
                                  C       AG
GAM1403  LOC221632 3'  GTCAGAGCTGGCTGCCTGACA 95450    GC       CCCGG
                                TG  CAGGCAGCT    CTGAC
                                ||  |||||||||    |||||
                                AC  GTCCGTCGG    GACTG
                                 A_       TCGA_
GAM1403  LOC221935 3'  CAGAGAGAGCTGCCAGGCCA  94198      A      CCGG
                                TGGCC GGCAGCTC   CTG
                                ||||| ||||||||   |||
                                ACCGG CCGTCGAG   GAC
                                   A       AGA_
GAM1403  LOC222057 3'  TCAGCCGGTCCAGGCCA     94360      A  CAGCTC
                                TGGCC GG     CCGGCTGA
                                ||||| ||     ||||||||
                                ACCGG CC     GGCCGACT
                                   A  T_____
GAM1403  LOC253936 3'  CAGCCGGGGCAGCCAGC     96317    CA  A  T
                                GC  GGC GC CCCGGCTG
                                ||  ||| || ||||||||
                                CG  CCG CG GGGCCGAC
                                 A_  A  _
GAM1403  LOC254876 5'  GTCGGACAAGCTATCTGGCCA 97767       GC   C__
                                TGGCCAG  AGCT  CCGGC
                                |||||||  ||||  |||||
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                                ACCGGTC  TCGA   GGCTG
                                   TA    ACA
GAM1403  LOC255042 3'  GCCCAGGCCGCCTGGCCA    97047         A   CCC
                                TGGCCAGGC GCT   GGC
                                ||||||||| |||   |||
                                ACCGGTCCG CGG   CCG
                                     C   AC_
GAM1403  LOC255624 3'  TTGAGAGCAGCCTGGCCA    96169         A    C
                                TGGCCAGGC GCTC CGG
                                ||||||||| |||| |||
                                ACCGGTCCG CGAG GTT
                                     A    A
GAM1403  LOC255975 5'  TCAGCCGGTCCAGGCCA     97589       A  CAGCTC
                                TGGCC GG     CCGGCTGA
                                ||||| ||     ||||||||
                                ACCGG CC     GGCCGACT
                                   A  T_____
GAM1403  LOC256286 3'  TCTCCCAGGAGCTGCCCAGCCA 96897      CA        C  CT
                                TGGC  GGCAGCTCC GG  GA
                                ||||  ||||||||| ||  ||
                                ACCG  CCGTCGAGG CC  CT
                                  AC        A  CT
GAM1403  LOC256715 3'  CAGCCTTGCTGCCCGGCC    99092      A     TCCC
                                GGCC GGCAGC    GGCTG
                                |||| ||||||    |||||
                                CCGG CCGTCG    CCGAC
                                  C     TT__
GAM1403  LOC257309 5'  GTCAGCTACCGCGCCTGGCCA  96287         A  TCCC
                                TGGCCAGGC GC    GGCTGAC
                                ||||||||| ||    |||||||
                                ACCGGTCCG CG    TCGACTG
                                     _  CCA_
GAM1403  LOC92148  5'  GTCAGCTGTGCCCCTGACCA   68887     C    CA  TCC
                                TGG CAGG  GC   CGGCTGAC
                                ||| ||||  ||   ||||||||
                                ACC GTCC  CG   GTCGACTG
                                  A   C_  T__
GAM1404  MASP2     3'  GAGATGGCTGTGCCCCAACTCC 58306       CTC  AT G
            CA                    TGGGAG   GG  G GGCCATCTC
                                ||||||   ||  | |||||||||
                                ACCCTC   CC  T TCGGTAGAG
                                   AAC  CG G
GAM1404  TEM7      3'  ATGGTTGGCCGAGCTCCCA    40246          ATGG
                                TGGGAGCTCGG    GGCCAT
                                ||||||||||    ||||||
                                ACCCTCGAGCC    TTGGTA
                                      GG__
GAM1404  C14orf4   5'  GAGACAGCCCCTTTCGAGCTTC 67917           T    CA
            CA                    TGGGAGCTCGGA GGGGC  TCTC
                                ||||||||||| |||||  ||||
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                                ACCTTCGAGCTT CCCCG  AGAG
                                       T    AC
GAM1404  DKFZP586M1120 3'  GAGATGGCCCCGGGAACCCCA  49281     AG_  GGAT
                                TGGG  CTC   GGGGCCATCTC
                                ||||  |||   ||||||||||
                                ACCC  GGG   CCCCGGTAGAG
                                  CAA  ____
GAM1404  FLJ12547  3'  AGATGGTTTGACCAAGTCTCCC 47127       _  C  ATG
             A                   TGGGAG CT GG  GGGCCATCT
                                 |||||| || ||  |||||||||
                                 ACCCTC GA CC  TTTGGTAGA
                                    T  A  AG_
GAM1404  FLJ32384  5'  AGACGGCCCCTGAATCCCA   58786      GC  GAT    A
                                TGGGA  TCG  GGGGCC TCT
                                |||||  |||  |||||| |||
                                ACCCT  AGT  CCCCGG AGA
                                   A_  ___    C
GAM1404  KIAA0417  3'  GAGATGGCCCTTTTAACCCTC  71760    CTCG  T
                                GAG   GA GGGGCCATCTC
                                |||   || ||||||||||
                                CTC   TT TCCCGGTAGAG
                                  CCAA  T
GAM1404  KIAA0447  3'  GCCTCTGAGGCTCCCA     72124       _    TGG
                                TGGGAGC TCGGA  GGC
                                ||||||| |||||  |||
                                ACCCTCG AGTCT  CCG
                                    G   ___
GAM1404  KR19    5'  GAGATGGTAGCCAAACGCCCA  82059     AGCT  GA  G_
                                TGGG   CG  TGG  GCCATCTC
                                ||||   ||  |||  ||||||||
                                ACCC   GC  ACC  TGGTAGAG
                                  ____  AA  GA
GAM1404  MGC15854  5'  GATGGCCACGCCCCCA     59501     AGCTC  A  G
                                TGGG    GG TG GGCCATC
                                ||||    || || |||||||
                                ACCC    CC GC CCGGTAG
                                  _____  _  A
GAM1404  TED     3'  GTGACCCCTCCCAAGCTCCCA  32275       C  AT   C
                                TGGGAGCT GG  GGGG CAT
                                |||||||| ||  |||| |||
                                ACCCTCGA CC  CCCC GTG
                                    A  CT   A
GAM1404  LOC116113 3'  AGAACTCTCCACCCCAGCTCCC 93830       C  A    CCA
             A                   TGGGAGCT GG TGGGG  TCT
                                 |||||||| || |||||  |||
                                 ACCCTCGA CC ACCTC  AGA
                                    C  C    TCA
GAM1404  LOC130612 3'  GAAAGCCCCCTCCCAAGCTCCC 75468       C_  T    CA
             A                   TGGGAGCT  GGA GGGGC  TC
                                 ||||||||  ||| |||||  ||
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                                ACCCTCGA  CCT CCCCG  AG
                                    AC  C    AA
GAM1404  LOC144583 3'  GCCCTCCATCCAAGCTCCCA  77417       C    __
                                TGGGAGCT GGATGG  GGC
                                |||||||| ||||||  |||
                                ACCCTCGA CCTACC  CCG
                                    A     TC
GAM1404  LOC158147 3'  AGACAGCAGTTTCAAGCCCCA  70077     A  C  TGGG  CA
                                TGGG GCT GGA   GC  TCT
                                |||| ||| |||   ||  |||
                                ACCC CGA CTT   CG  AGA
                                  _  A  TGA_  AC
GAM1404  LOC169933 5'  AGATGGCCAAGAGCACCCA   83431     A   GGATGG
                                TGGG GCTC    GGCCATCT
                                |||| ||||    ||||||||
                                ACCC CGAG    CCGGTAGA
                                  A   AA____
GAM1404  LOC202759 5'  GAGATGGTAGCCAAACGCCCA  73888     AGCT  GA  G_
                                TGGG   CG  TGG  GCCATCTC
                                ||||   ||  |||  ||||||||
                                ACCC   GC  ACC  TGGTAGAG
                                  ____  AA  GA
GAM1404  LOC203197 3'  AGATGGCCAATGGGGAGCCCCA 90802     A   GGATGG
                                TGGG GCTC    GGCCATCT
                                |||| ||||    ||||||||
                                ACCC CGAG    CCGGTAGA
                                  _   GGGTAA
GAM1404  LOC51029  3'  AGATGGCTCTCCCCCAAATCCC 32694     GCTC  AT
            A                    TGGGA   GG  GGGGCCATCT
                                |||||   ||  ||||||||||
                                ACCCT   CC  TCTCGGTAGA
                                  AAAC  CC
GAM1405  ATF5     3'  GCTAAAGGCGGCCAGGTTTGC  24822     ACTTA   T    C__
                                GCAA   GCCT GCTGCC  AGC
                                ||||   |||| ||||||  |||
                                CGTT   TGGA CGGCGG  TCG
                                  _____  C    AAA
GAM1405  EGFL5    5'  AGCCTGGCTAGAGTTTGC    87904       _  TT
                                GCAAACTT AGCC  GCT
                                |||||||| ||||  |||
                                CGTTTGAG TCGG  CGA
                                    A   TC
GAM1405  FE65L2   3'  GCTGGATGCGGTAAGCCAAGCT 56516    AA  A  C    __
            GC                    GCA  CTT GC TTGCTGC  CCAGC
                                ||| ||| || |||||||  |||||
                                CGT  GAA CG AATGGCG  GGTCG
                                  C_  C  _     TA
GAM1405  FE65L2   3'  GCTGGATGCGGTAAGCCAAGCT 56518    AA  A  C    __
            GC                    GCA  CTT GC TTGCTGC  CCAGC
                                ||| ||| || |||||||  |||||
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                                CGT  GAA CG AATGGCG  GGTCG
                                  C_  C _      TA
GAM1405  IRF6     3'  GTACAAGGCTAAACTGC     21570     AAC       C
                                GCA   TTAGCCTTG TGC
                                |||   ||||||||| |||
                                CGT   AATCGGAAC ATG
                                  CA_       _
GAM1405  MAP4     3'  GCTGGGCAGCCCGCTAGGCTCG 11447    AAA     CTT
              C                  GC   CTTAGC   GCTGCCCAGC
                                ||   ||||||   ||||||||||
                                CG   GGATCG   CGACGGGTCG
                                 CTC     CC_
GAM1405  MAP4     3'  GCTGGGCAGCCCGCTAGGCTCG 48798    AAA     CTT
              C                  GC   CTTAGC   GCTGCCCAGC
                                ||   ||||||   ||||||||||
                                CG   GGATCG   CGACGGGTCG
                                 CTC     CC_
GAM1405  MPHOSPH1  5'  GCTAGTCAGGCGAAGTTTGC   33005        A   T   _
                                GCAAACTT GCCT GCT GC
                                |||||||| |||| ||| ||
                                CGTTTGAA CGGA TGA CG
                                     G   C   T
GAM1405  TIMP3    5'  TCCCAGCGCCGGAGGCCAAGGT 6292       A  A   T_______   GCCC
              TGC                  GCAA CTT GCCT       GCT   A
                                |||| ||| ||||       |||   |
                                CGTT GAA CGGA       CGA   T
                                  G   C   GGCCG___   CCCG
GAM1405  AKAP6    3'  GCTGGAGAAAATAAGCTAAGTT 16252          CTTGCTGC_
              TGC                  GCAAACTTAGC       CCAGC
                                ||||||||||        |||||
                                CGTTTGAATCG       GGTCG
                                      AATAAAAGA
GAM1405  CXYorf1   3'  CGGCAAGGCCAAGCTGC     82911     AA   A
                                GCA  CTT GCCTTGCTG
                                |||  ||| |||||||||
                                CGT  GAA CGGAACGGC
                                  C_   C
GAM1405  DCNP1     3'  CTGAGCAGCAAGGCTGCAG    56458    _         C
                                CT TAGCCTTGCTGC CAG
                                || |||||||||||| |||
                                GA GTCGGAACGACG GTC
                                 C          A
GAM1405  DKFZP564O0463 3'  GCTGTCCTGAAGGCTAAGCTAG 27125    AAA       GCTGCC
              C                  GC   CTTAGCCTT     CAGC
                                ||   |||||||||     ||||
                                CG   GAATCGGAA     GTCG
                                 ATC       GTCCT_
GAM1405  FLJ00007  3'  TAGCAAAGGCTAAGCCTGC   71782     AA       _
                                GCA  CTTAGCCTT GCTG
                                |||  ||||||||| ||||
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                                CGT  GAATCGGAA CGAT
                                  CC        A
GAM1405  FLJ12691  3'  CTGGGCAGCAAGCAGCCTGC   45002     AA  TA  C
                                GCA  CT  GC TTGCTGCCCAG
                                |||  ||  || ||||||||||
                                CGT  GA  CG AACGACGGGTC
                                  CC  __  _
GAM1405  FLJ23556  3'  GCTGGGCAACAAAGCAAG    46445     A  C   C
                                CTT GC TTG TGCCCAGC
                                ||| || ||| ||||||||
                                GAA CG AAC ACGGGTCG
                                  _ A  A
GAM1405  KIAA1464  3'  GCTGGGCAACAAGAAAAATGTT 68820      TTAGC_   C
              TG                  CAAAC     CTTG TGCCCAGC
                                |||||     |||| ||||||||
                                GTTTG     GAAC ACGGGTCG
                                   TAAAAA    A
GAM1405  MAP-1    3'  GCTGAGATTGGTTAAGTTTGC  42444          TTG  GCC
                                GCAAACTTAGCC   CT   CAGC
                                ||||||||||||   ||   ||||
                                CGTTTGAATTGG   GA   GTCG
                                       TTA  ____
GAM1405  MGC4618   3'  GCTGGGCAGGGGAAGCCAAGT  51300      A  C_  G
                                ACTT GC  TT CTGCCCAGC
                                |||| ||  || |||||||||
                                TGAA CG  GG GACGGGTCG
                                  C  AA  G
GAM1405  MGC4796   3'  GCTGGACAGCAAGGAATCCACA 62166    AAACTTAG      C
              GC                  GC       CCTTGCTG CCAGC
                                ||       |||||||| |||||
                                CG       GGAACGAC GGTCG
                                 ACACCTAA       A
GAM1405  PRO0611   5'  GCTAACAAGAACTAAGTTTGC  26860         C_   CT_
                                GCAAACTTAG  CTTG   GC
                                ||||||||||  ||||   ||
                                CGTTTGAATC  GAAC   CG
                                      AA    AAT
GAM1405  RTVP1     5'  GCTGAAGTCGGCTAGGTTTGC  23395          TT   GCC
                                GCAAACTTAGCC  GCT   CAGC
                                ||||||||||||  |||   ||||
                                CGTTTGGATCGG  TGA   GTCG
                                       C_   A__
GAM1405  ZNF185    3'  GCTGGGCAGATGTAAGCCTG   24095     C    ____
                                TAG CTTGC   TGCCCAGC
                                ||| |||||   ||||||||
                                GTC GAATG   ACGGGTCG
                                  C    TAG
GAM1405  LOC150382 5'  CTGGGTGGGCCAGGTT      80629       A    TGCT
                                AACTT GCCT    GCCCAG
                                ||||| ||||    ||||||
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                                TTGGA CGGG    TGGGTC
                                  C   ____
GAM1405  LOC166341 3'  GCTGAAAGGAGCCAAGTTTGC  83517        A  _   GCTGCC
                                GCAAACTT GC CTT     CAGC
                                |||||||| || |||     ||||
                                CGTTTGAA CG GGA     GTCG
                                    C  A   AA____
GAM1405  LOC200093 3'  CGGCAAGGCCAAGCTGC     63770     AA   A
                                GCA  CTT GCCTTGCTG
                                |||  ||| |||||||||
                                CGT  GAA CGGAACGGC
                                  C_   C
GAM1405  LOC245744 3'  GCTGGGCAGAAGCCTAGGCCCG 92786    AAA    C   G
              C                  GC   CTTAG CTT CTGCCCAGC
                                ||   ||||| ||| |||||||||
                                CG   GGATC GAA GACGGGTCG
                                 CCC    C   _
GAM1405  LOC255718 5'  GCCGGGCAGCAACCGCCGTGC  99408     AACTTA  C_       A
                                GCA     GC  TTGCTGCCC GC
                                |||     ||  |||||||||  ||
                                CGT     CG  AACGACGGG CG
                                  GC____  CC        C
GAM1405  LOC90639  3'  TCCCAGCGCCAGAGGTTAAGTC 64417     A       T_______  GCCC
              TGC                 GCA ACTTAGCCT       GCT    A
                                ||| |||||||||       |||    |
                                CGT TGAATTGGA       CGA    T
                                  C        GACCG___   CCCG
GAM1405  LOC91040  3'  CGGCAAGGCCAAGCTGC     65344     AA   A
                                GCA  CTT GCCTTGCTG
                                |||  ||| |||||||||
                                CGT  GAA CGGAACGGC
                                  C_   C
GAM1405  LOC91286  5'  CTAAGCAGCATCTTAAGTTT   66058        CCT     CC
                                AAACTTAG   TGCTGC  AG
                                ||||||||   ||||||  ||
                                TTTGAATT   ACGACG  TC
                                     CT_     AA
GAM1405  LOC93259  5'  GCTGGGCAAAGTTAAGACTTGC 72288      A_     CTTGC
                                GCAA  CTTAGC     TGCCCAGC
                                ||||  ||||||     ||||||||
                                CGTT  GAATTG     ACGGGTCG
                                  CA     AA___
GAM1406  ADAR     3'  CTGCAGGGCGGGCAAGG     8483     A    CAG  T
                                CC TGCCC   GC CCTGCAG
                                || |||||   || |||||||
                                GG ACGGG   CG GGACGTC
                                 A    ___  _
GAM1406  ADAR     3'  CTGCAGGGCGGGCAAGG     32351    A    CAG  T
                                CC TGCCC   GC CCTGCAG
                                || |||||   || |||||||
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                                GG ACGGG   CG GGACGTC
                                 A    ___  _
GAM1406  ADAR     3'  CTGCAGGGCGGGCAAGG     32361    A    CAG  T
                                CC TGCCC   GC CCTGCAG
                                || |||||   || |||||||
                                GG ACGGG   CG GGACGTC
                                 A    ___  _
GAM1406  AIRE     3'  TGGGAGCCTGAGGCATGAGAA  6354      C     C
                                TTC CATGCC CAGGCTCCTG
                                ||| |||||| ||||||||||
                                AAG GTACGG GTCCGAGGGT
                                  A     A
GAM1406  ANG      5'  GCAGGAGCCTGTGTTGG     8557      T  CC
                                CCA GC  CAGGCTCCTGC
                                ||| ||  ||||||||||
                                GGT TG  GTCCGAGGACG
                                  _  T_
GAM1406  BCAS1    3'  CTCGGGAGCCCAACGCACGAGA 14711     CCA   CCCA      C
              A                  TTC   TGC    GGCTCCTG AG
                                |||   |||    |||||||| ||
                                AAG   ACG    CCGAGGGC TC
                                  AGC   CAAC       _
GAM1406  DAG1     3'  CTGCAGGATGTAACATGG    16553       CCCCAG  _
                                CCATG     GC TCCTGCAG
                                |||||     || ||||||||
                                GGTAC     TG AGGACGTC
                                   AA_____  T
GAM1406  GPRK7    3'  CGGGAGCCTGAGGCAGGAGAA  58313     _  A    C
                                TTC CC TGCC CAGGCTCCTG
                                ||| || |||| ||||||||||
                                AAG GG ACGG GTCCGAGGGC
                                  A  _    A
GAM1406  KIF1B    3'  TGGGAGCCTGAGGCAGGAGAA  31273     _  A    C
                                TTC CC TGCC CAGGCTCCTG
                                ||| || |||| ||||||||||
                                AAG GG ACGG GTCCGAGGGT
                                  A  _    A
GAM1406  NCAM1    5'  CTGCAGGGGGGGGGGCACAGAA 7040      CCA     AGG
                                TTC   TGCCCC   CTCCTGCAG
                                |||   ||||||   |||||||||
                                AAG   ACGGGG   GGGGACGTC
                                  AC_     GG_
GAM1406  NOS1     3'  CTGCAGGGTCCCCAAGGATGG  7095       G  CCA_  CT
                                CCAT CC    GG  CCTGCAG
                                |||| ||    ||  |||||||
                                GGTA GG    CC  GGACGTC
                                  _  AACC  TG
GAM1406  PDGFRB   3'  TGCCCCAGGGACATGGGAA   66584         _   CA  CTCCT
                                TTCCCATG CCC  GG    GCA
                                |||||||| |||  ||    |||
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                                AAGGGTAC GGG  CC    CGT
                                    A  AC _____
GAM1406  RAB31    3'  CTGCAGGGGGCGGGGCAGGAA  23440     CA    AGG
                                TTCC  TGCCCC  CTCCTGCAG
                                ||||  ||||||  |||||||||
                                AAGG  ACGGGG  GGGGACGTC
                                  __    CG_
GAM1406  SCN4A    3'  CTGCGTTCCCAGACCATGGGAA 6200        CCCCA  CTCC
                                TTCCCATG    GG   TGCAG
                                ||||||||    ||   |||||
                                AAGGGTAC    CC   GCGTC
                                    CAGAC  TT__
GAM1406  WHSC1    3'  CTGCAATGACTGCAGGGCTGGG 56669      T  __  GCTCC
           AA                     TTCCCA GCCC  CAG    TGCAG
                                ||||||| ||||  |||    |||||
                                AAGGGT CGGG  GTC    ACGTC
                                  _   AC   AGTA_
GAM1406  WHSC1    3'  CTGCAATGACTGCAGGGCTGGG 56680      T  __  GCTCC
           AA                     TTCCCA GCCC  CAG    TGCAG
                                ||||||| ||||  |||    |||||
                                AAGGGT CGGG  GTC    ACGTC
                                  _   AC   AGTA_
GAM1406  WHSC1    3'  CTGCAATGACTGCAGGGCTGGG 30582      T  __  GCTCC
           AA                     TTCCCA GCCC  CAG    TGCAG
                                ||||||| ||||  |||    |||||
                                AAGGGT CGGG  GTC    ACGTC
                                  _   AC   AGTA_
GAM1406  ZFP36L1  3'  CTGCAGGAAGGAAGGCTG    18201    T  __  AGGC
                                CA GCC  CC    TCCTGCAG
                                || |||  ||    ||||||||
                                GT CGG  GG    AGGACGTC
                                 _  AA  A___
GAM1406  C20orf64  5'  CAAGAGCCCTTCCTGCAGGGAA 54334      A  CCCA__    C
                                TTCCC TGC     GGCTC TG
                                ||||| |||     ||||| ||
                                AAGGG ACG     CCGAG AC
                                  _  TCCTTC    A
GAM1406  DRIL2    3'  CTGCAGGGTGTGGGCAGAGAA  22350    CCA    C G  T
                                TTC   TGCCC A GC CCTGCAG
                                |||   ||||| | || |||||||
                                AAG   ACGGG T TG GGACGTC
                                  AG_    _ G  _
GAM1406  FEM-2    3'  CTGCAGGGCCAAGCCACAGGAA 28312     CAT_  CCCA   T
                                TTCC    GC    GGC CCTGCAG
                                ||||    ||    ||| |||||||
                                AAGG    CG    CCG GGACGTC
                                  ACAC  AA__   _
GAM1406  FLJ10737  3'  CTGCAGTCCAAGCTGAACATGG 37054        CCCCA   C___
           GAA                    TTCCCATG    GGCT    CTGCAG
                                ||||||||    ||||    ||||||
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                                AAGGGTAC    TCGA   GACGTC
                                    AAG__   ACCT
GAM1406  FLJ10898  5' CTGCCAAACCTGCAACATGGGA 60133       CCC   CTCCT
           A                     TTCCCATG   CAGG    GCAG
                                 ||||||||   ||||    ||||
                                 AAGGGTAC   GTCC    CGTC
                                     AAC    AAAC_
GAM1406  FLJ11618  3' CTGCAGGGGGGAAGAGCCGGGAA 42624     AT  CCCAGG
                                 TTCCC  GC     CTCCTGCAG
                                 |||||  ||     |||||||||
                                 AAGGG  CG     GGGGACGTC
                                   C_   AGAAG_
GAM1406  FLJ12287  5' TGCCTCTGGGGCCTGGGAA   42564      T      CTCCT
                                 TTCCCA GCCCCAGG    GCA
                                 ||||||| ||||||||    |||
                                 AAGGGT CGGGGTCT    CGT
                                     C       C____
GAM1406  FLJ14129  3' TGGGAGCCTGGGGCAGGAGAA  48814    _ A
                                 TTC CC TGCCCCAGGCTCCTG
                                 ||| || ||||||||||||||||
                                 AAG GG ACGGGGTCCGAGGGT
                                   A  _
GAM1406  KIAA0187  3' CTGCAGGAGGAGGAACAGAGAA 29250    CCA  CC  AGG
                                 TTC   TG  CC   CTCCTGCAG
                                 |||   ||  ||   |||||||||
                                 AAG   AC  GG   GAGGACGTC
                                   AG_  AA  AG_
GAM1406  KIAA0416  5' GGAAAGCCTGGGACACAGAA   32093    CCA  C     __
                                 TTC   TG CCCAGGC  TCC
                                 |||   || |||||||  |||
                                 AAG   AC GGGTCCG  AGG
                                   AC_  A      AA
GAM1406  KIAA1266  3' CTGCAAGGGCGAGCATGGGA   66695       CCCAG    C
                                 TCCCATGC    GCTC TGCAG
                                 ||||||||    |||| |||||
                                 AGGGTACG    CGGG ACGTC
                                     AG___    A
GAM1406  KIAA1483  3' CTGCAGGGAAAAGGATATAGGA 70434     C   C  CAGG T
           A                     TTCC ATG CC    C CCTGCAG
                                 |||| ||| ||    | |||||||
                                 AAGG TAT GG    G GGACGTC
                                   A   A  AAAA _
GAM1406  KIAA1706  3' TGCAGTGAGAGCATGGGA    94372       CCCAGG  _
                                 TCCCATGC     CTC CTGCA
                                 ||||||||     ||| |||||
                                 AGGGTACG     GAG GACGT
                                     A_____   T
GAM1406  KIAA1715  3' CTCAGGAGCCTGAGGCAGGAGA 68684    _ A   C       C
           A                     TTC CC TGCC CAGGCTCCTG AG
                                 ||| || |||| |||||||||| ||
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                                AAG GG ACGG GTCCGAGGAC TC
                                  A _   A       _
GAM1406 KIAA1981 3' CAGGAGCCAAGGTCACAGAA  89710    CCA  C  CA
                                TTC   TG CC  GGCTCCTG
                                |||   || ||  ||||||||
                                AAG   AC GG  CCGAGGAC
                                  AC_  T  AA
GAM1406 MCAM     3' CAGGAACCTGGGGGCCTGTGAA 22457    C  T    _   C
                                TTC CA GCCCC AGG TCCTG
                                ||| || ||||| ||| |||||
                                AAG GT CGGGG TCC AGGAC
                                  T  C    G   A
GAM1406 MRPS24   3' CTGCAGAGAATGGAAACGTGGG 50130       CC_  GG   C
             AA                   TTCCCATG   CCA  CTC TGCAG
                                ||||||||   |||  ||| |||||
                                AAGGGTGC   GGT  GAG ACGTC
                                     AAA   AA  _
GAM1406 MSE55    3' TGCAGGACAGACATGGGAG   23916       CCCCAGGC
                                TTCCCATG      TCCTGCA
                                ||||||||      |||||||
                                GAGGGTAC      AGGACGT
                                     AGAC____
GAM1406 OS4      3' CTGCTTTGTGCTAAAAGCATGG 20388        CCCA   TCCT_
             GAA                    TTCCCATGC   GGC    GCAG
                                |||||||||   |||    ||||
                                AAGGGTACG   TCG    CGTC
                                     AAAA   TGTTT
GAM1406 PASK     5' CAGGGTCTCGCCTGGGGCATTA 31405     CC        ____
             GAA                    TTC  ATGCCCCAGGC   TCCTG
                                |||  ||||||||||   |||||
                                AAG  TACGGGGTCCG   GGGAC
                                  AT         CTCT
GAM1406 PRO1163  3' CTGAATGAGCCTGGGGCA    38323          CTG
                                TGCCCCAGGCTC   CAG
                                ||||||||||||   |||
                                ACGGGGTCCGAG   GTC
                                       TAA
GAM1406 THEA     3' CTCAGGAAGCTGAGGCACAAGA 66887     CCA   C   GC    C
             A                    TTC   TGCC CAG  TCCTG AG
                                |||   |||| |||  ||||| ||
                                AAG   ACGG GTC  AGGAC TC
                                  AAC    A   GA    _
GAM1406 WFDC3    3' GCTGACCAGAGCATGGGAA   98702        CCCA  C  CT
                                TTCCCATGC    GG TC  GC
                                |||||||||    || ||  ||
                                AAGGGTACG    CC AG  CG
                                     AGA_  _  T_
GAM1406 LOC122726 5' CTGCAGGAAACACTGAGGCTTG 76103       T   C   GC__
             GGAA                   TTCCCA GCC CAG    TCCTGCAG
                                ||||||  ||| |||    ||||||||
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                                AAGGGT CGG GTC   AGGACGTC
                                   T  A  ACAA
GAM1406  LOC129303 3'  CTGCAGGAATTGGGGGCTGGGA 75373      T    AG C
             A                    TTCCCA GCCCC  G TCCTGCAG
                                  |||||| |||||  | ||||||||
                                  AAGGGT CGGGG  T AGGACGTC
                                     _    GT A
GAM1406  LOC132617 5'  CTGCAGATCGAGGCATGGGA  76415       CCA  CTC
                                  TCCCATGCC  GG  CTGCAG
                                  |||||||||  ||  ||||||
                                  AGGGTACGG  CT  GACGTC
                                       AG_ A__
GAM1406  LOC145945 5'  AGGGCCTGGACCATAGAA   84563    CC  CC    T
                                  TTC  ATG  CCAGGC CCT
                                  |||  |||  |||||| |||
                                  AAG  TAC  GGTCCG GGA
                                    A_  CA    _
GAM1406  LOC146332 3'  CAGGAGCCTGGGGCCTGTGGA  78353    _ T
                                  TCC CA GCCCCAGGCTCCTG
                                  ||| || ||||||||||||||
                                  AGG GT CGGGGTCCGAGGAC
                                    T  C
GAM1406  LOC146714 5'  TGCAGGGCAGGCACAGGGA   84754    A_   CCAG  T
                                  TCCC  TGCC   GC CCTGCA
                                  ||||  ||||   || ||||||
                                  AGGG  ACGG   CG GGACGT
                                    AC   A___ _
GAM1406  LOC147958 3'  CTGCAGGGCAGGCAGCAGAA  88523    CCA   CCAG  T
                                  TTC   TGCC   GC CCTGCAG
                                  |||   ||||   || |||||||
                                  AAG   ACGG   CG GGACGTC
                                    ACG   A___ _
GAM1406  LOC149501 3'  CTGCAAGAGCCTGGCTGGGAA  75800      T  CC    C
                                  TTCCCA GCC  AGGCTC TGCAG
                                  |||||| |||  |||||| |||||
                                  AAGGGT CGG  TCCGAG ACGTC
                                     _  __     A
GAM1406  LOC150397 3'  CAGGAGCCTGAGTGAAGGA   80655    CA  CC
                                  TCC  TGC  CAGGCTCCTG
                                  |||  |||  ||||||||||
                                  AGG  GTG  GTCCGAGGAC
                                    AA  A_
GAM1406  LOC150397 3'  GCAGGAGCCTGCAGGAGA   80664   _ A  CCC
                                  TC CC TGC   AGGCTCCTGC
                                  || || |||   ||||||||||
                                  AG GG ACG   TCCGAGGACG
                                   A  _  ___
GAM1406  LOC150517 5'  CTGCAGGTAGGAGCACAGAA  80725    CCA  C  AGGCT
                                  TTC   TGC CC    CCTGCAG
                                  |||   ||| ||    |||||||
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                                AAG   ACG GG    GGACGTC
                                  AC_   A  AT___
GAM1406  LOC153688 3'  TGGGAGGCTGGGGCATGAGAA  87341     C        G
                                TTC CATGCCCCAG CTCCTG
                                ||| |||||||||| ||||||
                                AAG GTACGGGGTC GAGGGT
                                  A         G
GAM1406  LOC154849 3'  CTGCAGGAGGTGGAAGATG   60941     GCC   GG
                                CAT   CCA  CTCCTGCAG
                                |||   |||  |||||||||
                                GTA   GGT  GAGGACGTC
                                  GAA   G_
GAM1406  LOC162137 3'  GCAGGAGCTTCCCATAAAGAA  88480     CC_   CCCC
                                TTC   ATG    AGGCTCCTGC
                                |||   |||    ||||||||||
                                AAG   TAC    TTCGAGGACG
                                  AAA   CC__
GAM1406  LOC219654 3'  CAGGAGCCCAGGGGATGGGAA  92925       G   CA
                                TTCCCAT CCC  GGCTCCTG
                                ||||||| |||  ||||||||
                                AAGGGTA GGG  CCGAGGAC
                                    G   AC
GAM1406  LOC254552 5'  CAGGAGCCCGGGGCTGG     96422     T    A
                                CCA GCCCC GGCTCCTG
                                ||| ||||| ||||||||
                                GGT CGGGG CCGAGGAC
                                  _     C
GAM1406  LOC255042 3'  CTCGGGAGCCTGAGGCAGGAGA 97042     _ A    C        C
            A                    TTC CC TGCC CAGGCTCCTG AG
                                ||| || |||| |||||||||| ||
                                AAG GG ACGG GTCCGAGGGC TC
                                  A  _    A         _
GAM1406  LOC257000 3'  CTGCAGGACTCAGAGCATGG   98587       CCCA  C
                                CCATGC    GG TCCTGCAG
                                ||||||    || ||||||||
                                GGTACG    TC AGGACGTC
                                    AGAC  _
GAM1406  LOC91750  3'  TGGGGGCCTGAGGCACGAGAA  67659     CCA    C
                                TTC   TGCC CAGGCTCCTG
                                |||   |||| ||||||||||
                                AAG   ACGG GTCCGGGGGT
                                  AGC    A
GAM1407  TERF1    3'  CCCAAATCCTGTTCCAATGA   34391        C   TA    C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                     _  C_    A
GAM1407  FLJ10159  3'  CCATGTCACGCCATCCAATGAC 36334         CA_   A   TC
                                GTCATTGGA   CGT GAT  GG
                                |||||||||   ||| |||  ||
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                                CAGTAACCT   GCA CTG  CC
                                     ACC  _   TA
GAM1407  FLJ14213  3'  CCGATGCTCCCAATGACG    46216        ACAC   GAT
                                CGTCATTGG   GTA   TCGG
                                |||||||||   |||  ||||
                                GCAGTAACC   CGT   AGCC
                                     CT__   ___
GAM1407  MGC10715  3'  ATTTACCAGACATCCAATGAC  44495        CAC___
                                GTCATTGGA     GTAGAT
                                |||||||||     ||||||
                                CAGTAACCT     CATTTA
                                     ACAGAC
GAM1407  MOST2     5'  CCAGGACTGCCCAATGAC    40059        ACAC   A  _
                                GTCATTGG   GTAG TTC GG
                                ||||||||   |||| ||| ||
                                CAGTAACC   CGTC AGG CC
                                     ____   _  A
GAM1407  LOC150370 3'  CCGGGTCTACGTGCCCATGAC  86123      T  A
                                GTCAT GG CACGTAGATTCGG
                                ||||| || ||||||||||||||
                                CAGTA CC GTGCATCTGGGCC
                                   C  _
GAM1407  LOC152620 3'  CCCAAATCCTGTTCCAATGA   60707        C   TA   C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                     _  C_   A
GAM1407  LOC158668 3'  CCCAAATCCTGTTCCAATGA   69896        C   TA   C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                     _  C_   A
GAM1408  ELF3      3'  TGACCTTGACCTTGACCAA    16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                   _    AGT  ___
GAM1408  JAK2      3'  TGACCTTCATTCTGAGACCAA  18318      CAA      AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_       C_
GAM1408  SLC10A2   5'  ACTCTCTGTCTTGACCAA    6590       CAA      A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM1408  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA  37205      CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
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                                AACCGA    TTG CTTTCAGTG
                                   AA___  A
GAM1408 KIAA1958 5' GTGACTTTGAACCCCAAACC  82788     CAA  ATGG
                                GGTT  GGG   AAAGTCAC
                                ||||  |||   ||||||||
                                CCAA  CCC   TTTCAGTG
                                  A__  CAAG
GAM1408 MARCKS   3' ACTTTCCACCCTGCCCA    11411    TTCA   A
                                TGG   AGGG TGGAAAGT
                                |||   |||| ||||||||
                                ACC   TCCC ACCTTTCA
                                 CG__  _
GAM1408 TUB      5' GTGGGACCATCCCTTAAACC  13898     C       AAAG
                                GGTT AAGGGATGG   TCAC
                                |||| |||||||||   ||||
                                CCAA TTCCCTACC   GGTG
                                  A       AG__
GAM1408 LOC80298 3' ACTTTTACCTTGAACCA    48062         GATG
                                TGGTTCAAGG   GAAAGT
                                ||||||||||   ||||||
                                ACCAAGTTCC   TTTTCA
                                     A___
GAM1409 TERF1    3' CCCAAATCCTGTTCCAATGA  34391       C  TA   C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                    _  C_   A
GAM1409 FLJ10159 3' CCATGTCACGCCATCCAATGAC 36334       CA_  A  TC
                                GTCATTGGA  CGT GAT  GG
                                |||||||||  ||| |||  ||
                                CAGTAACCT  GCA CTG  CC
                                     ACC  _  TA
GAM1409 FLJ14213 3' CCGATGCTCCCAATGACG   46216        ACAC  GAT
                                CGTCATTGG   GTA  TCGG
                                |||||||||   |||  ||||
                                GCAGTAACC   CGT  AGCC
                                     CT__  ___
GAM1409 MGC10715 3' ATTTACCAGACATCCAATGAC 44495       CAC___
                                GTCATTGGA    GTAGAT
                                |||||||||    ||||||
                                CAGTAACCT    CATTTA
                                     ACAGAC
GAM1409 MOST2    5' CCAGGACTGCCCAATGAC    40059       ACAC   A  _
                                GTCATTGG   GTAG TTC GG
                                ||||||||   |||| ||| ||
                                CAGTAACC   CGTC AGG CC
                                    ____   _  A
GAM1409 LOC150370 3' CCGGGTCTACGTGCCCATGAC 86123     T  A
                                GTCAT GG CACGTAGATTCGG
                                ||||| || ||||||||||||
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                                CAGTA CC GTGCATCTGGGCC
                                   C  _
GAM1409  LOC152620 3'  CCCAAATCCTGTTCCAATGA   60707        C   TA   C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                     _  C_   A
GAM1409  LOC158668 3'  CCCAAATCCTGTTCCAATGA   69896        C   TA   C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                     _  C_   A
GAM1410  GPD1      3'  TCATGCCACCACATTTG     60398       C      C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A      _
GAM1410  IL5RA     5'  TCGCATGGCCACCGCATTT    6906          AT__
                                AAATGCGGTGGC   CGA
                                ||||||||||||   |||
                                TTTACGCCACCG   GCT
                                      GTAC
GAM1410  MYO1C     3'  TGCCGATGCCAAATATTTG   61873       CGG      A
                                TAAATG  TGGCATCG CA
                                ||||||  |||||||| ||
                                GTTTAT  ACCGTAGC GT
                                   AA_      C
GAM1410  C6orf37   3'  TGTCACACTGCATTTA      68097         GCATC
                                TAAATGCGGTG    GACA
                                ||||||||||     ||||
                                ATTTACGTCAC    CTGT
                                      A____
GAM1410  DNAJC6    3'  TTGCAGAACCACCGCATT    29498         CA  GA
                                AATGCGGTGG  TC  CAA
                                ||||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                      A_  AC
GAM1410  FLJ11210  3'  GTCGATGTGCATGCTTTTA   60319     T   GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM1410  FLJ12476  3'  TCGATCTTCTGCATTTA     43270         T  C
                                TAAATGCGG GG ATCGA
                                ||||||||| || |||||
                                ATTTACGTC TC TAGCT
                                      T  _
GAM1410  KIAA1034  3'  TCGATGGCATCCGCATTTG   63134          _  G
                                TAAATGCGG TG CATCGA
                                ||||||||| || ||||||
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                                GTTTACGCC AC GTAGCT
                                     T  G
GAM1410  KIAA1987  3'  TCATGTAACTGCATTTA     89391          G    C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                     A   _
GAM1410  MGC16063  3'  TGTCCTGGCCACTGCATT    54929           ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                      GTC
GAM1410  LOC147949 3'  TGTCAGATGTCCACATTGCA   79279      __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T    A
GAM1410  LOC150577 3'  GTCCTCACCGCATTTG      86258           CATC
                                TAAATGCGGTGG    GAC
                                ||||||||||||    |||
                                GTTTACGCCACT    CTG
                                      C___
GAM1410  LOC158219 3'  TGTGTGTCACCACATTT     82694       C       CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                   A       __
GAM1410  LOC202020 3'  TGTCTCACCACATTTA      90605       C    CATC
                                TAAATG GGTGG    GACA
                                ||||||| |||||    ||||
                                ATTTAC CCACT    CTGT
                                   A    _____
GAM1410  LOC90826  5'  TGTCGATGCAGGTTTATTTG   64788       CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                    TTGGA
GAM1410  LOC93587  3'  TTGTCTTTACCTGCATTTA    73042       _    CATC
                                TAAATGC GGTGG    GACAA
                                ||||||| |||||    |||||
                                ATTTACG CCATT    CTGTT
                                     T    T___
GAM1411  ABP1      5'  GCAGAGCGAACTGGGAGCAGAG 63799          CCGC    C
                                CTCTGTTCTT    CGCTC GC
                                ||||||||||    ||||| ||
                                GAGACGAGGG    GCGAG CG
                                      TCAA    A
GAM1411  AHCY      3'  GGCAACTGAGAAAGAACAGAG  7304          _ _ _____
                                CTCTGTTCTT C C    GCC
                                |||||||||| | |    |||
```

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                                GAGACAAGAA G G   CGG
                                    A A TCAA
GAM1411  BSN     3'  GGCAGAGGCAAGAGCAGAG   14387         CC  G  _
                                CTCTGTTCTT  GCC CT CC
                                ||||||||||  ||| || ||
                                GAGACGAGAA  CGG GA GG
                                    __   A  C
GAM1411  CSE1L   5'  GCGGAGCGGCGGCAGGAGC   62513       _
                                GTTCTT CCGCCGCTCCGC
                                |||||| ||||||||||||
                                CGAGGA GGCGGCGAGGCG
                                   C
GAM1411  EHD4    3'  AGTGGCAAAAAAATAGAG    58362        C  CC
                                CTCTGTT TT  GCCGCT
                                |||||||  ||  ||||||
                                GAGATAA AA  CGGTGA
                                    A  AA
GAM1411  EIF2C1  3'  AGCCCAGCTGAAGAACAGA   25181         C  C__
                                TCTGTTCTTC GC   GCT
                                |||||||||| ||   |||
                                AGACAAGAAG CG   CGA
                                    T  ACC
GAM1411  KCNK4   3'  GCGAGCAGCAGAGCAGG     33986        TCC  C    C
                                TCTGTTCT   GC GCTC GC
                                ||||||||   || |||| ||
                                GGACGAGA   CG CGAG CG
                                    ___  A    A
GAM1411  MYO1D   3'  GCGGAACAGCCCATCCAGCAGA 72249        CTTCC_  CGC
           GT                    ACTCTGTT     GC   TCCGC
                                ||||||||     ||   |||||
                                TGAGACGA     CG   AGGCG
                                    CCTACC  ACA
GAM1411  NUP62   3'  GGCAAAGCAGCACAGTGTGAAT 25650        TTCC___  C   CC
           AGA                   TCTGTTC      GC GCT  GCC
                                |||||||      || |||  |||
                                AGATAAG      CG CGA  CGG
                                    TGTGACA  A   AA
GAM1411  RABIF   3'  GGCATGTGCAGAAAAACAGAGT 12728        C   C  C  TCC
                                ACTCTGTT TTC GC GC   GCC
                                |||||||| ||| || ||   |||
                                TGAGACAA AAG CG TG   CGG
                                    A   A  _  TA_
GAM1411  RAX     3'  GCAGGGGAGGCGGAAAAATAGA 26466        C      G   _
           GT                    ACTCTGTT TTCCGCC CTCC GC
                                |||||||| ||||||| |||| ||
                                TGAGATAA AAGGCGG GGGG CG
                                    A      A   A
GAM1411  RBM10   3'  GGCAGGGAAGGACAGAGT    20247           __
                                ACTCTGTTCTTCC  GCC
                                ||||||||||||  |||
```

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                                TGAGACAGGAAGG  CGG
                                       GA
GAM1411  RGS16    3'  GGCAGGGCCCAGGAGAACAAAG 12869     C     T  GCC    C
              T                  ACT TGTTCT CC   GCTC GCC
                                 ||| |||||| ||   |||| |||
                                 TGA ACAAGA GG   CGGG CGG
                                   A     _ ACC    A
GAM1411  ROM1     3'  GGAACAGCAAAGAACAGAGT   6165          CC  CGC
                                 ACTCTGTTCTT  GC   TCC
                                 ||||||||||  ||   |||
                                 TGAGACAAGAA  CG   AGG
                                       A_  ACA
GAM1411  SLC21A2  3'  GCAAAGCAAGTGATGAAGCAGA 20084        _ TTC   C_   CC
              GT                   ACTCTGTT C   CGC  GCT  GC
                                 |||||||| |   |||  |||  ||
                                 TGAGACGA G   GTG  CGA  CG
                                     A TA_   AA   AA
GAM1411  SMARCA5  5'  AGCCCCGCGGAAGAGCAGA    14588           C__
                                 TCTGTTCTTCCGC   GCT
                                 ||||||||||||   |||
                                 AGACGAGAAGGCG   CGA
                                       CCC
GAM1411  SYNGR1   3'  GGCAGAGCGGCAAGGACAGGG  17507          CC      C
                                 CTCTGTTCTT  GCCGCTC GCC
                                 ||||||||||  ||||||| |||
                                 GGGACAGGAA  CGGCGAG CGG
                                       __       A
GAM1411  TRAM     5'  AGCAGCTGGGAAGAGCAGA   27451           __ C
                                 TCTGTTCTTCC  GC GCT
                                 ||||||||||  || |||
                                 AGACGAGAAGG  CG CGA
                                       GT  A
GAM1411  VAT1     3'  AGCAGGGAAGTACAGAGT    22088        T    GCC
                                 ACTCTGT CTTCC   GCT
                                 ||||||| |||||   |||
                                 TGAGACA GAAGG   CGA
                                     T    GA_
GAM1411  CBX1     3'  AGCAATGGAAAAGAACAGA   23308         __   CC
                                 TCTGTTCT  TCCG  GCT
                                 ||||||||  ||||  |||
                                 AGACAAGA  AGGT  CGA
                                      AA    AA
GAM1411  CDC14A   5'  GGCGGAGCAGCAGCTGCAGCAG 53966    _   TCTTCC  C
                                 CT CTGT     GC GCTCCGCC
                                 || ||||     || ||||||||
                                 GA GACG     CG CGAGGCGG
                                  C   TCGA__  A
GAM1411  CDC14A   5'  GGCGGAGCAGCAGCTGCAGCAG 53967    _   TCTTCC  C
                                 CT CTGT     GC GCTCCGCC
                                 || ||||     || ||||||||
```

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                                GA GACG     CG CGAGGCGG
                                 C   TCGA__ A
GAM1411 DKFZp547I224 5' GATGGGGAAAAAACAGAG    39956       C_   G  C
                                CTCTGTT  TTCC CCG TC
                                |||||||  |||| ||| ||
                                GAGACAA  AAGG GGT AG
                                   AA   _  _
GAM1411 ECE2     3'  GCAGGGAAAAGGAAGAACAGAG 28732          GCCG  C
          T                      ACTCTGTTCTTCC   CTC GC
                                 ||||||||||||    ||| ||
                                 TGAGACAAGAAGG   GGG CG
                                       AAAA  A
GAM1411 FLJ10648 3'  CGAAGCAAACCAAGAACAGAG  36890        CCGCC  C
                                CTCTGTTCTT    GCT CG
                                ||||||||||    ||| ||
                                GAGACAAGAA    CGA GC
                                      CCAAA  A
GAM1411 GRIN3A   3'  GCGGAGCAAGTGCCAAGCAGA  56783      CTTC  C_
                                TCTGTT   CGC  GCTCCGC
                                ||||||   |||  |||||||
                                AGACGA   GTG  CGAGGCG
                                   ACC_  AA
GAM1411 INE1     3'  GCAGGTGTTAGACGAAAGAACA 14757       C  CC__  T  _
          GA                     TCTGTTCTT CG   GC CC GC
                                 |||||||| ||   || || ||
                                 AGACAAGAA GC   TG GG CG
                                      A  AGAT  T  A
GAM1411 KIAA0410 3'  GCAGAGCTTAAGAATAGA    29426       CCGCC   C
                                TCTGTTCTT    GCTC GC
                                |||||||||    |||| ||
                                AGATAAGAA    CGAG CG
                                      TT___   A
GAM1411 KIAA0964  5' GCGGAACGGCAGAGCGGG    30448       TCC   C
                                TCTGTTCT   GCCG TCCGC
                                ||||||||   |||| |||||
                                GGGCGAGA   CGGC AGGCG
                                   ___   A
GAM1411 KIAA1218  5' AGCAGCACAAAAGAAACAGAGT 95958       _  CC__  C
                                ACTCTGTT CTT   GC GCT
                                ||||||| |||   || |||
                                TGAGACAA GAA   CG CGA
                                   A   AACA  A
GAM1411 KIAA1322  3' GGCAGCCGAGAAGAACAGA   73112        _ CC  _
                                TCTGTTCTTC CG  GCT CC
                                |||||||||| ||  ||| ||
                                AGACAAGAAG GC  CGA GG
                                      A  __  C
GAM1411 KIAA1391  3' AGTGGAGAAAAAACAGAGT    67851       C  CG
                                ACTCTGTT TTC  CCGCT
                                |||||||| |||  |||||
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                                TGAGACAA AAG  GGTGA
                                    A   A_
GAM1411  MGC13251  3'  AGCAGCCATAGAAAGGACAGA  52134        _ C___  C
                                TCTGTTCTT C    GC GCT
                                ||||||||| |    || |||
                                AGACAGGAA G    CG CGA
                                     A ATAC  A
GAM1411  MYH7B     3'  GGCGGAGCAGCAGGCCAACA   71058     CTT  _  C
                                TGTT   CC GC GCTCCGCC
                                ||||   || || ||||||||
                                ACAA   GG CG CGAGGCGG
                                  CC_  A  A
GAM1411  NCOA2     3'  GGCAAGGAGAAGAGCAAAGT   22572     C      CG  GCT
                                ACT TGTTCTTC  CC   CC
                                ||| ||||||||  ||   ||
                                TGA ACGAGAAG  GG   GG
                                  A       A_  AAC
GAM1411  PTRF      3'  GGCAGTGGGGAAGACAGAG    64242      T    G    _
                                CTCTGT CTTCC CCGCT CC
                                |||||| ||||| ||||| ||
                                GAGACA GAAGG GGTGA GG
                                   _    _    C
GAM1411  RHOBTB2   3'  AGCAGGAGGAAAAGCAGAGT   61593       C   G  _
                                ACTCTGTT TTCC CC GCT
                                |||||||| |||| || |||
                                TGAGACGA AAGG GG CGA
                                     A   A  A
GAM1411  TAGAP     3'  AGACTGCAAGGAACAGAGT    55099         CC  CG_
                                ACTCTGTTCTT  GC   CT
                                ||||||||||  ||   ||
                                TGAGACAAGGA  CG   GA
                                      A_  TCA
GAM1411  VELI1     3'  AGTGTAAGAAGAATAAAGT    17417     C      CGC
                                ACT TGTTCTTC   CGCT
                                ||| ||||||||   ||||
                                TGA ATAAGAAG   GTGA
                                  A       AAT
GAM1411  LOC145783 5'  GCGGAGCGACGGAGACACAG   77949     TC    C
                                CTGT  TTCCG CGCTCCGC
                                ||||  ||||| ||||||||
                                GACA  GAGGC GCGAGGCG
                                  CA    A
GAM1411  LOC150157 3'  AGCAAATGGAAAAGAACAGA   86020        __   CC_
                                TCTGTTCT  TCCG   GCT
                                ||||||||  ||||   |||
                                AGACAAGA  AGGT   CGA
                                     AA    AAA
GAM1411  LOC151516 5'  GGCGGAGCTTCCAGAACAAAG  81068    C     TCCGCC
                                CT TGTTCT     GCTCCGCC
                                || ||||||     ||||||||
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                                GA ACAAGA     CGAGGCGG
                                 A     CCTT__
GAM1411  LOC153769 3'  GGCGGAGCAGCATGAGAAAGA  81807     G    CC  C
                                TCT TTCTT  GC GCTCCGCC
                                ||| |||||  || ||||||||
                                AGA AAGAG  CG CGAGGCGG
                                  _    TA  A
GAM1411  LOC161734 3'  GATGGGGAAAAAACAGAG    88467       C_   G   C
                                CTCTGTT  TTCC CCG TC
                                |||||||  |||| ||| ||
                                GAGACAA  AAGG GGT AG
                                    AA   _  _
GAM1411  LOC167026 5'  GGCGGAGCGGCGGGCGGA    88620      TCTT
                                TCTGT   CCGCCGCTCCGCC
                                |||||   ||||||||||||
                                AGGCG   GGCGGCGAGGCGG
                                  _____
GAM1411  LOC196890 3'  AGCAAATGGAAAAGAACAGA   91222        __   CC_
                                TCTGTTCT  TCCG   GCT
                                ||||||||  ||||   |||
                                AGACAAGA  AGGT   CGA
                                    AA    AAA
GAM1411  LOC200731 5'  AGCACTGAAGAACAGAGT    91688          CGCC
                                ACTCTGTTCTTC    GCT
                                ||||||||||||   |||
                                TGAGACAAGAAG    CGA
                                      TCA_
GAM1411  LOC221504 5'  CGGAGCGGCGGGGCAGGAG   94020     GTTC
                                CTCT    TTCCGCCGCTCCG
                                ||||    ||||||||||||
                                GAGG    GGGGCGGCGAGGC
                                  AC__
GAM1411  LOC221663 5'  GCAAGCCCAGAACAGAGT    95463         TCCGCC   CC
                                ACTCTGTTCT     GCT  GC
                                ||||||||||     |||  ||
                                TGAGACAAGA     CGA  CG
                                     CC_____   AA
GAM1411  LOC256310 3'  GGCAGAGCAGCGGGAGCAGGAG 98102      GTT      C    C
                                CTCT   CTTCCGC GCTC GCC
                                ||||   ||||||| |||| |||
                                GAGG   GAGGGCG CGAG CGG
                                  AC_      A    A
GAM1411  LOC51762  3'  GGCCTAGCAAAAGAACAGA   33708        CCGCC   CC
                                TCTGTTCTT    GCT  GCC
                                |||||||||    |||  |||
                                AGACAAGAA    CGA  CGG
                                     AA___   TC
GAM1411  LOC91266  5'  GGCTGAGGAAAAACAGAGT   66024        ___     C
                                ACTCTGT   TCTTC GCC
                                |||||||   ||||| |||
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                                TGAGACA   AGGAG CGG
                                   AAA    T
GAM1412 ELF3     3' TGACCTTGACCTTGACCAA   16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                   _    AGT  ___
GAM1412 JAK2     3' TGACCTTCATTCTGAGACCAA 18318      CAA      AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_      C_
GAM1412 SLC10A2  5' ACTCTCTGTCTTGACCAA    6590       CAA      A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM1412 FLJ10803 3' GTGACTTTCAGTTAAAGCCAA 37205      CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM1412 KIAA1958 5' GTGACTTTGAACCCCAAACC  82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM1412 MARCKS   3' ACTTTCCACCCTGCCCA     11411     TTCA    A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM1412 TUB      5' GTGGGACCATCCCTTAAACC   13898     C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A       AG__
GAM1412 LOC80298 3' ACTTTTACCTTGAACCA     48062         GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                     A___
GAM1413 ABCC3    3' CCATCATCCCGCAGGACCCCA 39611     AA        CCAA
                                TGG  TCTTGCGGGAT   GG
                                |||  ||||||||||   ||
                                ACC  AGGACGCCCTA   CC
                                  CC         CTA_
GAM1413 ABCC3    3' CCATCATCCCGCAGGACCCCA 39612     AA        CCAA
                                TGG  TCTTGCGGGAT   GG
                                |||  ||||||||||   ||
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                                ACC  AGGACGCCCTA    CC
                                  CC         CTA_
GAM1413  ATF4     5'  CCCGAGCCCCGCAAGGTCCCA  9810      A        A_  CAA
                                TGG ATCTTGCGGG  TC   GG
                                ||| ||||||||||  ||   ||
                                ACC TGGAACGCCC  AG   CC
                                  C        CG  C__
GAM1413  CHC1     5'  CTCCTTGGATTTGTTAAGGATT 8860          GCG_
             CCA                   TGGAATCTT    GGATCCAAGGAG
                                ||||||||||   ||||||||||||
                                ACCTTAGGA    TTTAGGTTCCTC
                                     ATTG
GAM1413  MAP3K10  5'  CTCCCTAGACCCCGCAGGG   68581         A  CAA
                                TCTTGCGGG TC   GGAG
                                ||||||||| ||   ||||
                                GGGACGCCC AG   CCTC
                                     C  ATC
GAM1413  SLC16A2  3'  CTCCTTGGAGTCAAAGCTCCA  22523     ATCTT  GG_ _
                                TGGA    GC   GA TCCAAGGAG
                                ||||    ||   || |||||||||
                                ACCT    CG   CT AGGTTCCTC
                                  _____  AAA  G
GAM1413  FLJ12587 3'  CTCCTTGGACCCTGTAGACCCA 42777     AA   T    A
                                TGG  TCT GCGGG TCCAAGGAG
                                |||  ||| ||||| |||||||||
                                ACC  AGA TGTCC AGGTTCCTC
                                  C_  _    C
GAM1413  FLJ12700 3'  TCCTTGCAGGAAGATTCCA   46660         GCGGGATC
                                TGGAATCTT       CAAGGA
                                |||||||||       ||||||
                                ACCTTAGAA       GTTCCT
                                     GGAC_____
GAM1413  LSR68    5'  CTCCTTGGATGGTGGAGACC   38556    AA   G  GG
                                GG  TCTT CG  ATCCAAGGAG
                                ||  |||| ||  ||||||||||
                                CC  AGAG GT  TAGGTTCCTC
                                 __   _ GG
GAM1413  NKX2B    3'  CTCCTTGGAGTGGCAGATTCCA 11810         T  GGGA
                                TGGAATCT GC    TCCAAGGAG
                                |||||||| ||    |||||||||
                                ACCTTAGA CG    AGGTTCCTC
                                    _ GTG_
GAM1413  LOC151610 3'  CTCCTTGGACTCCAGACCCC   81092    AA   TGC  GA
                                GG  TCT   GG  TCCAAGGAG
                                ||  |||   ||  |||||||||
                                CC  AGA   CC  AGGTTCCTC
                                 CC   ___  TC
GAM1413  LOC256158 5'  CCCTGGATCCCAGGAGCCCCA  99487     AA_   GC      A
                                TGG   TCTT  GGGATCCA GG
                                |||   ||||  |||||||| ||
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                                ACC   AGGA  CCCTAGGT CC
                                  CCG    __       C
GAM1413  LOC51312  3'  CTCCCTGGATCCTTAGATCCCA 33992     A    TGC       A
                                TGG ATCT   GGGATCCA GGAG
                                ||| ||||   |||||||| ||||
                                ACC TAGA   TCCTAGGT CCTC
                                  C    T__       C
GAM1414  CYP7B1    3'  GTCACAAAGCCCATATAA    17875      GA    C
                                TTATG  GGCT TGTGAC
                                |||||  |||| ||||||
                                AATAT  CCGA ACACTG
                                   AC    A
GAM1414  F8        3'  TCACAATCCACAAATGATG    5529          A    GGCTC
                                TATCATTT TGGA     TGTGA
                                |||||||| ||||     |||||
                                GTAGTAAA ACCT     ACACT
                                     C    A____
GAM1414  DCTN4     3'  GTCACAGATGAAACTTAAATGA 68396          TGGAGGC
              TA                  TATCATTTA      TCTGTGAC
                                |||||||||      ||||||||
                                ATAGTAAAT      AGACACTG
                                     TCAAAGT
GAM1414  DIS3      3'  CACATTTGCCCCATAGAT    30910         A   TC_
                                ATTTATGG GGC   TGTG
                                |||||||| |||   ||||
                                TAGATACC CCG   ACAC
                                   _  TTT
GAM1414  FLJ10261  3'  ACCAAGTCTCATAAATGATA   36415          G    CT
                                TATCATTTATG AGGCT  GT
                                |||||||||||| |||||  ||
                                ATAGTAAATAC TCTGA  CA
                                     _    AC
GAM1414  FLJ20344  3'  GTCACAGAACATAAATGCATA  35485     _       GAGGC
                                TAT CATTTATG     TCTGTGAC
                                ||| ||||||||     ||||||||
                                ATA GTAAATAC     AGACACTG
                                  C       A____
GAM1414  PRO2714   5'  TCACAGAGAAGGTCAAATGA   38195      TA   AGG_
                                TCATT  TGG    CTCTGTGA
                                |||||  |||    ||||||||
                                AGTAA  ACT    GAGACACT
                                   __   GGAA
GAM1414  LOC115265 3'  TCACAGAATCATACTAAATGAT 73742          TGGA GC
              A                   TATCATTTA    G  TCTGTGA
                                |||||||||    |  |||||||
                                ATAGTAAAT    C  AGACACT
                                     CATA TA
GAM1414  LOC159053 3'  CACAGAGCTAGTAAGT      88363       GGA
                                ATTTAT   GGCTCTGTG
                                ||||||   |||||||||
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                                TGAATG   TCGAGACAC
                                   A__
GAM1414  LOC221718 3'  GTCACAGAGACTGGAATAAAT  95283       GGA  _
                                ATTTAT   GG CTCTGTGAC
                                ||||||   || |||||||||
                                TAAATA   TC GAGACACTG
                                   AGG  A
GAM1414  LOC51141  3'  GTCACAAAAGTGCAAAGTGATA 69149        A  GAG   C_
                                TATCATTT TG   GCT  TGTGAC
                                |||||||| ||   |||  ||||||
                                ATAGTGAA AC   TGA  ACACTG
                                     _ G__   AA
GAM1414  LOC90139  3'  GCAACCCCATAAATGA      56270          A  CTC
                                TCATTTATGG GG   TGT
                                |||||||||| ||   |||
                                AGTAAATACC CC   ACG
                                     _  A__
GAM1415  ELF3      3'  TGACCTTGACCTTGACCAA    16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                   _    AGT  ____
GAM1415  JAK2      3'  TGACCTTCATTCTGAGACCAA  18318       CAA       AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_       C_
GAM1415  SLC10A2   5'  ACTCTCTGTCTTGACCAA    6590        CAA       A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ____       C
GAM1415  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM1415  KIAA1958  5'  GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM1415  MARCKS    3'  ACTTTCCACCCTGCCCA     11411     TTCA   A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM1415  TUB       5'  GTGGGACCATCCCTTAAACC   13898      C        AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
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                                CCAA TTCCCTACC    GGTG
                                  A       AG__
GAM1415 LOC80298 3' ACTTTTACCTTGAACCA     48062          GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                      A___
GAM1416 IRAK1    3' GTCAAAGTTCTCATGGTCA    9617         C    CTCAAC
                                TGACCATG AGAAC     GAC
                                |||||||| |||||     |||
                                ACTGGTAC TCTTG     CTG
                                    _    AAA___
GAM1416 FLJ11413 3' GTCACGGCTCTTTGCATGATCA 44957     C       A__  TCAAC
                                TGA CATGCAGA   CC    GAC
                                ||| ||||||||   ||    |||
                                ACT GTACGTTT   GG    CTG
                                  A       CTC  CA___
GAM1416 GGA2     3' GTCATGTTTCTGCATGTCA    57675     C       CCT  AC
                                TGAC ATGCAGAA   CA  GAC
                                |||| ||||||||   ||  |||
                                ACTG TACGTCTT   GT  CTG
                                  _       T__  A_
GAM1416 GGA2     3' GTCATGTTTCTGCATGTCA    57676     C       CCT  AC
                                TGAC ATGCAGAA   CA  GAC
                                |||| ||||||||   ||  |||
                                ACTG TACGTCTT   GT  CTG
                                  _       T__  A_
GAM1416 KIAA0446 5' GTCTCTGGGCATCTGCATGGCC 69458    A       AC    AC
             A                   TG CCATGCAGA  CTCA  GAC
                                || |||||||||  ||||  |||
                                AC GGTACGTCT  GGGT  CTG
                                 C        AC    CT
GAM1416 MAP3K3   3' GGTCGCCCTTTGCTGCATGGCA 11544    A       AACCTCAA
                                TG CCATGCAG       CGACC
                                || ||||||||       |||||
                                AC GGTACGTC       GCTGG
                                 _       GTTTCCC_
GAM1416 RABEX5   3' TTGAGGTTCTATATAGTCA    27964     C   C
                                TGAC ATG AGAACCTCAA
                                |||| ||| ||||||||||
                                ACTG TAT TCTTGGAGTT
                                  A   A
GAM1416 ShrmL    5' TGAATTCTGCATGGCA      40853    A       CC
                                TG CCATGCAGAA  TCA
                                || ||||||||||  |||
                                AC GGTACGTCTT  AGT
                                 _        A_
GAM1416 LOC124446 5' GTTGAATTCCTGCATGGCCA   74778    A       AACC
                                TG CCATGCAG    TCAAC
                                || ||||||||    |||||
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                                AC GGTACGTC    AGTTG
                                 C       CTTA
GAM1416  LOC144289 5'  GTCTCAGAGGTTCTGGACAGTC 83960      CATG       AAC
              A                   TGAC    CAGAACCTC   GAC
                                  ||||    |||||||||   |||
                                  ACTG    GTCTTGGAG   CTG
                                    ACAG        ACT
GAM1416  LOC144747 5'  GTCGTTGAGTCCCACAGTCA   77473      CA  CA  AC
                                  TGAC  TG  GA  CTCAACGAC
                                  ||||  ||  ||  |||||||||
                                  ACTG  AC  CT  GAGTTGCTG
                                    AC  C_  __
GAM1417  B4GALT4   3'  CACACATTAAGAACCTGTTACA 15025         C  G  __
              GCT                   AGCTGTAAC GG TC  AATGTGTG
                                  |||||||||  ||  ||  ||||||||
                                  TCGACATTG CC AG  TTACACAC
                                       T  A  AA
GAM1417  CRACC    3'  CACACATATTAATGACAGC    41307      AACCG   CA
                                  GCTGT    GGT  ATGTGTG
                                  |||||    |||  |||||||
                                  CGACA    TTA  TACACAC
                                    GTAA_   __
GAM1417  DRD2     3'  CACCTCACCCCGTTACAGCT   7673         C    CAAT
                                  AGCTGTAAC GGGT    GTG
                                  |||||||||  ||||    |||
                                  TCGACATTG CCCA    CAC
                                       C    CTC_
GAM1417  RNF4     3'  CACACATTGACCAAGCCAG    12879     TAACCG
                                  CTG     GGTCAATGTGTG
                                  |||     ||||||||||||
                                  GAC     CCAGTTACACAC
                                    CGAA__
GAM1417  SDC3     3'  ACACATTGTCTCCAGCTT     28461       TAACC   T
                                  AAGCTG    GGG CAATGTGT
                                  ||||||    ||| ||||||||
                                  TTCGAC    CTC GTTACACA
                                      _____   T
GAM1417  LOC163724 5'  ACACACCAGCTGCAGCTT    83031        ACCG   CAAT
                                  AAGCTGTA   GGT   GTGT
                                  ||||||||   |||   ||||
                                  TTCGACGT   CCA   CACA
                                       CGA_   ____
GAM1417  LOC254556 3'  CACACATTGACCAAGCCAG    96255     TAACCG
                                  CTG     GGTCAATGTGTG
                                  |||     ||||||||||||
                                  GAC     CCAGTTACACAC
                                    CGAA__
GAM1418  DNA2L    3'  TGTAAAACAAAATTGTCTC    92950    _  C
                                  GA ATA TTTTGTTTTACA
                                  || ||| ||||||||||||
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```
                                CT TGT AAAACAAAATGT
                                 C  T
GAM1418 HDAC4    3' GTAAAACAAAACCTTG     21248     AATAC
                                CAAG    TTTTGTTTTAC
                                ||||    ||||||||||
                                GTTC    AAAACAAAATG
                                  C____
GAM1418 OTP      3' TGTAGATAAAGCATTCTTGT  50408       A   TGT
                                ACAAGAAT CTTT  TTTACA
                                |||||||| ||||  ||||||
                                TGTTCTTA GAAA  AGATGT
                                     C   T__
GAM1418 PRG4     3' TAAAACTGTTGGGTATTCT   20552       TT__
                                AGAATACTT   GTTTTA
                                |||||||||   ||||||
                                TCTTATGGG   CAAAAT
                                      TTGT
GAM1418 KIAA1724 3' AGATAAAAGTACCTTGTAA   67606       AA
                                TTACAAG  TACTTTTGTTT
                                |||||||  ||||||||||
                                AATGTTC  ATGAAAATAGA
                                    C_
GAM1418 MLLT10   3' GCAAGGACATTCTTGTAA    17352        AC
                                TTACAAGAAT  TTTTGT
                                ||||||||||  ||||||
                                AATGTTCTTA  GGAACG
                                      CA
GAM1418 PTPNS1   3' GCAAAATATTTTTGTAA     55841         C
                                TTACAAGAATA TTTTGT
                                |||||||||||| ||||||
                                AATGTTTTTAT AAAACG
                                          _
GAM1418 SDF1     3' TGCAAGGGAAAAGTCTCTTGTA 92521       AT     G    A
           A                     TTACAAGA  ACTTTT TTTT CA
                                |||||||||  |||||| |||| ||
                                AATGTTCT  TGAAAA GGAA GT
                                    C_     G    C
GAM1418 SYTL2    3' TGTAAAATTTTCGTATTTTGTA 53078       A   TTTT
           A                     TTACAAGA TAC    GTTTTACA
                                |||||||| |||    ||||||||
                                AATGTTTT ATG    TAAAATGT
                                     _  CTTT
GAM1418 SYTL2    3' TGTAAAATTTTCGTATTTTGTA 51480       A   TTTT
           A                     TTACAAGA TAC    GTTTTACA
                                |||||||| |||    ||||||||
                                AATGTTTT ATG    TAAAATGT
                                     _  CTTT
GAM1418 VEGFC    3' GCAAAAGGCCTCTTGTAA     19473       ATA
                                TTACAAGA   CTTTTGT
                                ||||||||   |||||||
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                                AATGTTCT  GAAAACG
                                    CCG
GAM1418 VIT1     3' ATGTAAAACAAAAGTATTCTTG 38600                  ___
             TAA                  TTACAAGAATACTTTTGTTTTACA  T
                                  ||||||||||||||||||||||||  |
                                  AATGTTCTTATGAAAACAAAATGT  A
                                                  ___
GAM1418 LOC148760 3' ACAAAATGTCATTCTTGTGA  85360        _ _
                                  TTACAAGAAT AC TTTTGT
                                  |||||||||| || ||||||
                                  AGTGTTCTTA TG AAAACA
                                      C  T
GAM1418 LOC152343 5' TGTATCTAAATGTATTCTTGTA 81442          T   TTT
             A                    TTACAAGAATAC TTTG  TACA
                                  |||||||||||| ||||  ||||
                                  AATGTTCTTATG AAAT  ATGT
                                        T   CT_
GAM1418 LOC157247 3' AACAAAAGCATTCTGTAA   82276     A   A
                                  TTACA GAAT CTTTTGTT
                                  ||||| |||| ||||||||
                                  AATGT CTTA GAAAACAA
                                    _   C
GAM1419 ATP5J   5' CTCCTCCCCGGCGGCCGC   9855       GA  AA  A
                                  GCGGTCGC  TGG  GA GAG
                                  ||||||||  |||  || |||
                                  CGCCGGCG  GCC  CT CTC
                                      __  C_  C
GAM1419 CEP2    3' TCCCTTCCCCACGTGACCGGG  23249   G     A  AA   A
                                  C CGGTCGCG TGG  GAAG GA
                                  | ||||||||| |||  |||| ||
                                  G GCCAGTGC ACC  CTTC CT
                                   G      _  C_   C
GAM1419 CLN5    5' CCTTCTTCCTCACTGC     22430      CGC  T      A
                                  GCGGT  GA GGAAGAAG G
                                  |||||  || |||||||| |
                                  CGTCA  CT CCTTCTTC C
                                    ____ _      C
GAM1419 FKRP    3' CTCCCCTTCTTTTGGACTGCG  44434       G  T   AA
                                  CGCGGTC CGA GGAAG  GAG
                                  ||||||| ||| |||||  |||
                                  GCGTCAG GTT TCTTC  CTC
                                      _  T   CC
GAM1419 GBF1    5' TCTCTTCTCCCATCTGCTACC  16094    C  _   A
                                  GGT GC GATGG AGAAGAGA
                                  ||| || ||||| ||||||||
                                  CCA CG CTACC TCTTCTCT
                                    T  T   C
GAM1419 GUCY1A2  5' CTCCCCGCCCCGCCGACCGCG  7803        _ AT  AAGAA
                                  CGCGGTCG CG  GG   GAG
                                  |||||||| ||  ||   |||
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                              GCGCCAGC GC  CC    CTC
                                  C  C_  GCCC_
GAM1419 HNRPDL   5' TCTCTTCTCCCAAGCCCGCG  19604     TC  GA   A
                              CGCGG  GC  TGG AGAAGAGA
                              |||||  ||  ||| ||||||||
                              GCGCC  CG  ACC TCTTCTCT
                                 __  A_   C
GAM1419 RENT1    3' CTTCTTCCGGTAGGCCGCG   12812       GCGA
                              CGCGGTC   TGGAAGAAG
                              |||||||   |||||||||
                              GCGCCGG   GCCTTCTTC
                                  ATG_
GAM1419 TNFRSF14 5' TCTCTTCTGGCCCACAGCCGC 15114      CGCGAT  A_
                              GCGGT     GG  AGAAGAGA
                              |||||     ||  ||||||||
                              CGCCG     CC  TCTTCTCT
                                 ACAC__  GG
GAM1419 WNT10B   5' TCCCTTCCTCCCGGCGGCCGCG 14130        GAT   A    A
                              CGCGGTCGC   GGA GAAG GA
                              |||||||||   ||| |||| ||
                              GCGCCGGCG   CCT CTTC CT
                                   GC_   C    C
GAM1419 ZFP103   5' CTCCCCCTTGAGATCGCG    20225       G   T  AAGAA
                              CGCGGTC CGA GG    GAG
                              ||||||| ||| ||    |||
                              GCGCTAG GTT CC    CTC
                                  A   C  C____
GAM1419 ZFP103   5' CTCCTGACCCGCGGCCGCG   20226        AT  A_  AA
                              CGCGGTCGCG  GG  AG  GAG
                              ||||||||||  ||  ||  |||
                              GCGCCGGCGC  CC  TC  CTC
                                   __  AG  __
GAM1419 FBXO27   3' TCTCTTCTCCTCCCAACC    75017     CGC  T   A
                              GGT   GA GGA GAAGAGA
                              |||   || ||| |||||||
                              CCA   CT CCT CTTCTCT
                                ACC  _   _
GAM1419 FKBP4    3' TCCCTTCCTCCATTGCAC    10644    C      A   A
                              GT GCGATGGA GAAG GA
                              || |||||||| |||| ||
                              CA CGTTACCT CTTC CT
                               _       C    C
GAM1419 FLJ20257 5' TCTCCCCTTCCATCTGCTCTGC 39492     TC  _      AA
                              GCGG  GC GATGGAAG  GAGA
                              ||||  || ||||||||  ||||
                              CGTC  CG CTACCTTC  CTCT
                                T_  T       CC
GAM1419 FLJ22215 3' CTCTCCCTGCGGCCGC      43397        AT   AGAA
                              GCGGTCGCG  GGA   GAG
                              |||||||||  |||   |||
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                                CGCCGGCGT  CCT   CTC
                                     C_  ____
GAM1419 HSRNAFEV 5' TCTCCTCCTTGTCACCCGCG  34454     TC_   T  AGAA
                                CGCGG  GCGA GGA   GAGA
                                |||||  |||| |||   ||||
                                GCGCC  TGTT CCT   CTCT
                                  CAC   _  C___
GAM1419 KIAA0084 5' CTCAGGGAGCCCGCGACCGCG 68707        AT  AAGAA_
                                CGCGGTCGCG  GG    GAG
                                ||||||||||  ||    |||
                                GCGCCAGCGC  CC    CTC
                                     __  GAGGGA
GAM1419 KIAA0561 3' CTCCTTCCATCCTGGAGC   66473   GG  C     AA
                                GC  TCG GATGGAAG  GAG
                                ||  ||| ||||||||  |||
                                CG  GGT CTACCTTC  CTC
                                 A_  C      __
GAM1419 KIAA1041 5' TCTTCCAGCCGCAGCCGCG   30832     C  A_
                                CGCGGT GCG  TGGAAGA
                                |||||| |||  |||||||
                                GCGCCG CGC  ACCTTCT
                                   A  CG
GAM1419 KIAA1676 3' TCTCTTCTTATTGAACAACC  94743    CG__   GA
                                GGT   CGATG  AGAAGAGA
                                |||   |||||  ||||||||
                                CCA   GTTAT  TCTTCTCT
                                  ACAA   __
GAM1419 LHFPL2   3' CTCTTCTTCTGGAGATC    70497    GCGA
                                GGTC   TGGAAGAAGAG
                                ||||   ||||||||||
                                CTAG   GTCTTCTTCTC
                                  AG__
GAM1419 POFUT1   5' CTCCCCGACTGTGCGCCGCG  70975     T  G   AAGAA
                                CGCGG CGC ATGG    GAG
                                ||||| ||| ||||    |||
                                GCGCC GCG TGTC    CTC
                                   _  _   AGCCC
GAM1419 RBPMS    5' CTCCTTCCAGCGGCTGC    23429       GA    AA
                                GCGGTCGC  TGGAAG  GAG
                                ||||||||  ||||||  |||
                                CGTCGGCG  ACCTTC  CTC
                                     __    __
GAM1419 LOC201102 3' TCCCTTCTTCCCTCCACC   89471    CGC  T     A
                                GGT   GA GGAAGAAG GA
                                |||   || ||||||| ||
                                CCA   CT CCTTCTTC CT
                                  C__  C      C
GAM1419 LOC203954 5' CTCTCCTTCGTGACCCCG   92338    C      T  AGAA
                                CG GGTCGCGA GGA   GAG
                                || |||||||| |||   |||
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                                GC CCAGTGCT CCT    CTC
                                 C       T  _____
GAM1419  LOC219513 3'  CTCTTCCTCCACGGGAACCGC  95982       _ G  A    A
                                GCGGT C CG TGGA GAAGAG
                                |||||| | || |||| ||||||
                                CGCCA G GC ACCT CTTCTC
                                   A G  _    C
GAM1419  LOC221510 3'  TCCCTTCTTCTTAGCACC    92705     C  GAT       A
                                GGT GC   GGAAGAAG GA
                                ||| ||   |||||||| ||
                                CCA CG   TCTTCTTC CT
                                  _ AT_       C
GAM1419  LOC56902  3'  TCCCTTCTTCCATTCTCAGCC  39718     CGC_         A
                                GGT    GATGGAAGAAG GA
                                |||    |||||||||||| ||
                                CCG    TTACCTTCTTC CT
                                  ACTC          C
GAM1420  GASC1     5'  TCACCTAGTGCGGAACAAGTCT 64898       AAT  AC_   T__     C
            CCCA                   TGGGA   CT   TCC   TTGGG GA
                                |||||   ||   |||   ||||| ||
                                ACCCT   GA   AGG   GATCC CT
                                   CT_  ACA   CGT    A
GAM1420  GCK       3'  CGCTGGAATCAATTTCCCA   5683         CTAC   TTTG
                                TGGGAAAT    TCC    GGCG
                                ||||||||    |||    ||||
                                ACCCTTTA    AGG    TCGC
                                     ACTA  _____
GAM1420  HDAC4     5'  CGCCCGAACAGCCTCCCA    21243       AAT  ACTCC
                                TGGGA   CT    TTTGGGCG
                                |||||   ||    ||||||||
                                ACCCT   GA    AAGCCCGC
                                   CC_  C_____
GAM1420  ZNF274    3'  TCATTTGGAAAAAAGATTTCCC 33341          AC__   TT_
            A                   TGGGAAATCT    TCC   TGG
                                ||||||||||    |||   |||
                                ACCCTTTAGA    AGG   ACT
                                      AAAA   TTT
GAM1420  IMAGE145052 3'  TCTAAATAAAGAGCAGTTTCCC 27330        T  A   C___
            A                   TGGGAAA CT CTC    TTTGGG
                                ||||||| || |||    ||||||
                                ACCCTTT GA GAG    AAATCT
                                   _  C   AAAT
GAM1420  NX-17     3'  CCTAAGGAAAAATAAATTTTCC 40704         C  C___    T
            A                   TGGGAAAT TA    TCCTT GG
                                |||||||| ||    ||||| ||
                                ACCTTTTA AT    AGGAA CC
                                     A  AAAA    T
GAM1420  LOC145463 3'  TCTAAATAAAGAGCAGTTTCCC 71484        T  A   C___
            A                   TGGGAAA CT CTC    TTTGGG
                                ||||||| || |||    ||||||
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                                ACCCTTT GA GAG    AAATCT
                                    _ C   AAAT
GAM1420  LOC149668 5'  TGCCTGGGCACAGACCTCCCA  85704      AA   ACT   TT
                                TGGGA  TCT   CCT  GGGCG
                                |||||  |||   |||  |||||
                                ACCCT  AGA   GGG  TCCGT
                                   CC   CAC   __
GAM1420  LOC219672 5'  CCAAGGAAAGTGGATTCCCCA  92966      A       C_
                                TGGG AATCTACT  CTTTGG
                                ||||  ||||||||  ||||||
                                ACCC TTAGGTGA  GGAACC
                                  C       AA
GAM1420  LOC257095 5'  TCCCCAAAGGAAGATTTC    98723        AC        C
                                GAAATCT  TCCTTTGGG GA
                                |||||||  |||||||||  ||
                                CTTTAGA  AGGAAACCC CT
                                    __        A
GAM1420  LOC90462  5'  CAAAACAGCAGATTTCCCA    63569          A  CC
                                TGGGAAATCT CT  TTTG
                                ||||||||||  ||  ||||
                                ACCCTTTAGA GA  AAAC
                                      C  CA
GAM1421  GPD1      3'  TCATGCCACCACATTTG      60398       C       C
                                TAAATG GGTGGCAT GA
                                ||||||  ||||||||  ||
                                GTTTAC CCACCGTA CT
                                   A       _
GAM1421  IL5RA     5'  TCGCATGGCCACCGCATTT    6906           AT__
                                AAATGCGGTGGC    CGA
                                ||||||||||||    |||
                                TTTACGCCACCG    GCT
                                      GTAC
GAM1421  MYO1C     3'  TGCCGATGCCAAATATTTG    61873       CGG       A
                                TAAATG   TGGCATCG CA
                                ||||||   ||||||||  ||
                                GTTTAT   ACCGTAGC GT
                                   AA_       C
GAM1421  C6orf37   3'  TGTCACACTGCATTTA      68097          GCATC
                                TAAATGCGGTG     GACA
                                ||||||||||     ||||
                                ATTTACGTCAC     CTGT
                                      A____
GAM1421  DNAJC6    3'  TTGCAGAACCACCGCATT     29498          CA  GA
                                AATGCGGTGG  TC  CAA
                                ||||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                      A_  AC
GAM1421  FLJ11210  3'  GTCGATGTGCATGCTTTTA    60319      T   GTG
                                TAAA GCG   GCATCGAC
                                ||||  |||   ||||||||
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                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM1421  FLJ12476  3'  TCGATCTTCTGCATTTA     43270         T  C
                                TAAATGCGG GG ATCGA
                                ||||||||| || |||||
                                ATTTACGTC TC TAGCT
                                     T  _
GAM1421  KIAA1034  3'  TCGATGGCATCCGCATTTG    63134         _  G
                                TAAATGCGG TG CATCGA
                                ||||||||| || ||||||
                                GTTTACGCC AC GTAGCT
                                     T  G
GAM1421  KIAA1987  3'  TCATGTAACTGCATTTA     89391         G    C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                     A   _
GAM1421  MGC16063  3'  TGTCCTGGCCACTGCATT    54929          ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                      GTC
GAM1421  LOC147949 3'  TGTCAGATGTCCACATTGCA   79279      __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM1421  LOC150577 3'  GTCCTCACCGCATTTG      86258          CATC
                                TAAATGCGGTGG   GAC
                                ||||||||||||   |||
                                GTTTACGCCACT   CTG
                                      C___
GAM1421  LOC158219 3'  TGTGTGTCACCACATTT     82694       C       CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                   A       __
GAM1421  LOC202020 3'  TGTCTCACCACATTTA      90605       C    CATC
                                TAAATG GGTGG   GACA
                                |||||| |||||   ||||
                                ATTTAC CCACT   CTGT
                                   A   ____
GAM1421  LOC90826  5'  TGTCGATGCAGGTTTATTTG  64788       CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                    TTGGA
GAM1421  LOC93587  3'  TTGTCTTTACCTGCATTTA   73042       _    CATC
                                TAAATGC GGTGG   GACAA
                                ||||||| |||||   |||||
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                                ATTTACG CCATT   CTGTT
                                   T    T___
GAM1422 ELF3     3' TGACCTTGACCTTGACCAA   16685     T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                   _    AGT  ___
GAM1422 JAK2     3' TGACCTTCATTCTGAGACCAA 18318      CAA      AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_      C_
GAM1422 SLC10A2  5' ACTCTCTGTCTTGACCAA    6590      CAA      A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM1422 FLJ10803 3' GTGACTTTCAGTTAAAGCCAA 37205      CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM1422 KIAA1958 5' GTGACTTTGAACCCCAAACC  82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM1422 MARCKS   3' ACTTTCCACCCTGCCCA     11411     TTCA    A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM1422 TUB      5' GTGGGACCATCCCTTAAACC   13898     C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A       AG__
GAM1422 LOC80298 3' ACTTTTACCTTGAACCA     48062         GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                     A___
GAM1423 KRTHA8   3' AACTTTCCTTGTATCAAATCCT 23191    C       T  A
                                AG ATTTGATAC GG GAAAGTT
                                || ||||||||| || |||||||
                                TC TAAACTATG TC CTTTCAA
                                 C       T _
GAM1423 NR5A2    3' ACTTTCAAAGCAAATGCT    15116        ATA  GGA
                                AGCATTTG   CT   GAAAGT
                                ||||||||   ||   ||||||
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                                TCGTAAAC  GA  CTTTCA
                                   ___  AA_
GAM1423  PRM2     3'  TTCCCCTACATCAAATGCT   12398         ACT  A
                                AGCATTTGAT  GG GAA
                                ||||||||||  || |||
                                TCGTAAACTA  CC CTT
                                     CAT  C
GAM1423  SIRT1    3'  AACTTTCTCAGCTGCAAAAGCT 25287     A   ATA  G
              T                  AAGC TTTG  CTG AGAAAGTT
                                 |||| ||||  ||| ||||||||
                                 TTCG AAAC  GAC TCTTTCAA
                                   A   GTC  _
GAM1423  EFA6R    3'  AACTTTCTCCTAAAAATACTT  31630     C   GATACT
                                 AAG ATTT    GGAGAAAGTT
                                 ||| ||||    ||||||||||
                                 TTC TAAA    CCTCTTTCAA
                                   A   AAT___
GAM1423  KIAA1726 3'  AACTTTCTCTCTAACCAAATCT 67823     C    ATACT
              T                  AAG ATTTG   GGAGAAAGTT
                                 ||| |||||   ||||||||||
                                 TTC TAAAC   TCTCTTTCAA
                                  _    CAATC
GAM1423  ZER6     3'  AACTCTTGGCCTATCAAGTGCT 64112         CT  A_  A
                                 AGCATTTGATA  GG  GA AGTT
                                 ||||||||||  ||  || ||||
                                 TCGTGAACTAT  CC  TT TCAA
                                      __  GG  C
GAM1423  LOC153856 3'  AACTTCTGACACACACAAATGC 81871        ATAC  G_   A
              TT                  AAGCATTTG   TG  AGAA GTT
                                  |||||||||   ||  |||| |||
                                  TTCGTAAAC   AC  TCTT CAA
                                      ACAC  AG   _
GAM1423  LOC203427 3'  AACTTTCTAAAAATCAAATCT  90917    C     ACTGG
                                 AG ATTTGAT    AGAAAGTT
                                 || |||||||    ||||||||
                                 TC TAAACTA    TCTTTCAA
                                  _     AAAA_
GAM1424  ANXA7    3'  ACCTTCATTCTTACTA     15743    _     ATA
                                 TAG AAGAATGA  AGGT
                                 ||| ||||||||  ||||
                                 ATC TTCTTACT  TCCA
                                   A      ___
GAM1424  GTF2H1   3'  GTAGACCTTAAGTATTCCTC  19210   A   AA   TG
                                 GA GAATG  TAAGG  TCTAC
                                 || |||||  |||||  |||||
                                 CT CTTAT  ATTCC  AGATG
                                  C    GA   __
GAM1424  HAP1     3'  TAGACACCTCTGATCCCCTTC  15478     AAT  A  _
                                 GAAG  GA TA AGGTGTCTA
                                 ||||  || || |||||||||
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                                CTTC   CT GT TCCACAGAT
                                  CC_  A  C
GAM1424  IL22RA2   3'  ACCTTCATTCTTCTA      54771          ATA
                                TAGAAGAATGA   AGGT
                                ||||||||||   ||||
                                ATCTTCTTACT   TCCA
                                      ___
GAM1424  MEP1B     3'  AGCCACCTCATTCTTCTA    20996          ATAA    T
                                TAGAAGAATGA    GGTG CT
                                ||||||||||    |||| ||
                                ATCTTCTTACT    CCAC GA
                                      ____   C
GAM1424  SCML1     3'  TAGAAAATTCATTCTTT     23110          AAGGTG
                                GAAGAATGAAT     TCTA
                                ||||||||||     ||||
                                TTTCTTACTTA     AGAT
                                      AA____
GAM1424  TOP3B     3'  AGACACCTCATGGCACTTC    15440      AA  A_  A
                                GAAG  TG  AT AGGTGTCT
                                ||||  ||  || ||||||||
                                CTTC  AC  TA TCCACAGA
                                  __ GG  C
GAM1424  UNC13     3'  GTAGACACCTCTCCACTCCTC  22100     A  A  AATA
                                GA GA TG    AGGTGTCTAC
                                || || ||   ||||||||||
                                CT CT AC    TCCACAGATG
                                 C  C  CTC_
GAM1424  DKFZp761A132 3'  AGAAACTTCTTTTCATTCTTC  51163          TA_   G
                                GAAGAATGAA   AGGT TCT
                                ||||||||||   |||| |||
                                CTTCTTACTT   TTCA AGA
                                      TTC    A
GAM1424  FLJ13769  3'  GCCTTGTTCATTCCTCTA    47254      A
                                TAGA GAATGAATAAGGT
                                |||| ||||||||||||
                                ATCT CTTACTTGTTCCG
                                  C
GAM1424  KIAA0993  3'  GTAGTTTGTTCATTCATC    64822    A        GTGT
                                GA GAATGAATAAG    CTAC
                                || ||||||||||    ||||
                                CT CTTACTTGTTT    GATG
                                 A         ____
GAM1424  KIAA1210  3'  ACCTAGCTCATTTTTCTA    98058          ATA
                                TAGAAGAATGA   AGGT
                                ||||||||||   ||||
                                ATCTTTTTACT   TCCA
                                      CGA
GAM1424  KIAA1373  3'  TAGACCATTCATTCTTC     71512          AAGGT
                                GAAGAATGAAT    GTCTA
                                ||||||||||     |||||
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                                CTTCTTACTTA    CAGAT
                                      C____
GAM1424 KIAA1870 5' GGCTATTCGTTCTTC      50585          AGGT
                                GAAGAATGAATA   GTC
                                ||||||||||||  |||
                                CTTCTTGCTTAT   CGG
                                     ____
GAM1424 LEPROTL1 3' ACATTACCATTCTTCTA    31698         AATAA
                                TAGAAGAATG   GGTGT
                                ||||||||||   |||||
                                ATCTTCTTAC   TTACA
                                      CA___
GAM1424 MGC20253 3' AGACACCTCTTTCCTTT    58673    AAT  TA
                                GAAG  GAA  AGGTGTCT
                                ||||  |||  ||||||||
                                TTTC  CTT  TCCACAGA
                                  ___  TC
GAM1424 NSG-X    3' GCATCCATTCTTCTG      27728         AATAA
                                TAGAAGAATG   GGTGT
                                ||||||||||   |||||
                                GTCTTCTTAC   CTACG
                                     _____
GAM1424 PRSS22   3' ATATCTTATTTATTCCTC   42349   A
                                GA GAATGAATAAGGTGT
                                || ||||||||||||||
                                CT CTTATTTATTCTATA
                                 C
GAM1424 RAB35    3' GGACACCTCATTCCCCT    23417   AA    ATAA
                                AG  GAATGA   GGTGTCT
                                ||  ||||||   |||||||
                                TC  CTTACT   CCACAGG
                                 CC    ____
GAM1424 LOC124152 3' ACATTTTATTCATTCATC   74727   A
                                GA GAATGAATAAGGTGT
                                || ||||||||||||||
                                CT CTTACTTATTTTACA
                                 A
GAM1424 LOC196337 3' GCACCTTTCACCCTTCTA   89024      AA   TA
                                TAGAAG  TGAA  AGGTGT
                                ||||||  ||||  ||||||
                                ATCTTC  ACTT  TCCACG
                                   CC   __
GAM1424 LOC220662 3' GCAGTTTCATTCATTTTTC  92821         _  G
                                GAAGAATGAAT AAG TGT
                                |||||||||||| ||| |||
                                CTTTTTACTTA TTT ACG
                                      C  G
GAM1424 LOC257463 3' ACACTTTATCCATTATTCTA  71616     G   A
                                TAGAA AATG ATAAGGTGT
                                ||||| |||| |||||||||
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                                ATCTT TTAC TATTTCACA
                                   A    C
GAM1424  LOC257486 3'  ACCTAGCTCATTTTTCTA    69759          ATA
                                TAGAAGAATGA   AGGT
                                ||||||||||   ||||
                                ATCTTTTTACT   TCCA
                                     CGA
GAM1424  LOC51218  3'  GTAAACAAAATTCATTCTT   33534         AAGG   C
                                AAGAATGAAT    TGT TAC
                                ||||||||||    ||| |||
                                TTCTTACTTA    ACA ATG
                                     AA__   A
GAM1424  LOC91149  3'  ACAAATTATTTATCCATTCTTC 65689         ____    GG
           TG                     TAGAAGAATG    AATAA  TGT
                                ||||||||||    |||||  |||
                                GTCTTCTTAC    TTATT  ACA
                                     CTAT     AA
GAM1425  ELF3      3'  TGACCTTGACCTTGACCAA    16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                   _    AGT  ___
GAM1425  JAK2      3'  TGACCTTCATTCTGAGACCAA  18318       CAA       AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_       C_
GAM1425  SLC10A2   5'  ACTCTCTGTCTTGACCAA    6590        CAA       A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM1425  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM1425  KIAA1958  5'  GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM1425  MARCKS    3'  ACTTTCCACCCTGCCCA     11411     TTCA    A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM1425  TUB       5'  GTGGGACCATCCCTTAAACC   13898      C        AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
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                                CCAA TTCCCTACC    GGTG
                                  A       AG__
GAM1425 LOC80298 3' ACTTTTACCTTGAACCA     48062         GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                     A___
GAM1426 ELF3     3' TGACCTTGACCTTGACCAA    16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                  _    AGT  ___
GAM1426 JAK2     3' TGACCTTCATTCTGAGACCAA  18318      CAA       AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_       C_
GAM1426 SLC10A2  5' ACTCTCTGTCTTGACCAA    6590       CAA       A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM1426 FLJ10803 3' GTGACTTTCAGTTAAAGCCAA 37205      CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM1426 KIAA1958 5' GTGACTTTGAACCCCAAACC  82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM1426 MARCKS   3' ACTTTCCACCCTGCCCA     11411     TTCA    A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM1426 TUB      5' GTGGGACCATCCCTTAAACC   13898     C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A       AG__
GAM1426 LOC80298 3' ACTTTTACCTTGAACCA     48062         GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                     A___
GAM1427 ARHGAP6  3' GCGATTGAGCTTCCCAGAG   21519     CAA       CCTGG
                                CTC   GGAGCTCAA    TGC
                                |||   |||||||||    |||
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                                GAG  CTTCGAGTT   GCG
                                  ACC       A____
GAM1427 ARHGAP6  3' GCGATTGAGCTTCCCAGAG  26429    CAA      CCTGG
                                CTC  GGAGCTCAA   TGC
                                |||  |||||||||   |||
                                GAG  CTTCGAGTT   GCG
                                  ACC       A____
GAM1427 ENTPD6   3' AGTGTCGGGGCTGAGCCCCTTG 8804      A   A_   TG
                                CAAGG GCTCA  CCTGG  CT
                                ||||| |||||  |||||  ||
                                GTTCC CGAGT  GGGCT  GA
                                   C    CG    GT
GAM1427 LGALS3BP 3' AGCACCAGGACGCCCTCGAG  69856    CA  A  TCAA
                                CTC  AGG GC   CCTGGTGCT
                                |||  ||| ||   |||||||||
                                GAG  TCC CG   GGACCACGA
                                  C_  _ CA__
GAM1427 PLCG1    3' GCCGAAGCCCCTTGGAG    12158       A  CAACC
                                CTCCAAGG GCT   TGGT
                                |||||||| |||    ||||
                                GAGGTTCC CGA   GCCG
                                    C  A____
GAM1427 ZNF157   3' ATTGGATCAAGCTCCTTGGGG  14327         CAAC TG
                                CTCCAAGGAGCT   C  GT
                                ||||||||||||   |  ||
                                GGGGTTCCTCGA   G  TA
                                       ACTA GT
GAM1427 BLR1     3' GCAGCCAAGCTCCTTGGG    9939         CAACC  _
                                TCCAAGGAGCT    TGG TGC
                                ||||||||||     ||| |||
                                GGGTTCCTCGA    ACC ACG
                                      _____  G
GAM1427 BLR1     3' GCAGCCAAGCTCCTTGGG    53115        CAACC  _
                                TCCAAGGAGCT    TGG TGC
                                ||||||||||     ||| |||
                                GGGTTCCTCGA    ACC ACG
                                      _____  G
GAM1427 DKFZP434F0318 3' CACCAAGCTGGGTTAGGAG   48746     AAGG    ACC
                                CTCC   AGCTCA  TGGTG
                                ||||   ||||||  |||||
                                GAGG   TTGGGT  ACCAC
                                  A___     CGA
GAM1427 DKFZP434H132 5' GCACCAGGCTTGCCTGGGG   31933      A  AGCT  _
                                CTCCA GG   CAA CCTGGTGC
                                ||||| ||   ||| ||||||||
                                GGGGT CC   GTT GGACCACG
                                  _ ____  C
GAM1427 DKFZp434K1210 3' AGCTTGACTCCTTGGAG    34686        C   C
                                CTCCAAGGAG TCAA CT
                                |||||||||| |||| ||
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                                GAGGTTCCTC AGTT GA
                                      _   C
GAM1427  FLJ11726  3'  GCAGCAAGCTCCTTAGAG    47024    C      CAACC  G
                                CTC AAGGAGCT    TG TGC
                                ||| ||||||||    || |||
                                GAG TTCCTCGA    AC ACG
                                  A       _____  G
GAM1427  FLJ21839  3'  GCCGTTAAGTCCTTGGA     41835        G  C   CT
                                TCCAAGGA CT AAC  GGT
                                |||||||| || |||  |||
                                AGGTTCCT GA TTG  CCG
                                     _ A  __
GAM1427  FLJ23476  3'  AGCACTGTAGACCAAGCCCTTG 45311        A   CAAC  __
             GAG                   CTCCAAGG GCT    CT  GGTGCT
                                |||||||| |||    ||  ||||||
                                GAGGTTCC CGA    GA  TCACGA
                                     _   ACCA  TG
GAM1427  KIAA1925  5'  GGGTCTGAGCTCCTCAGAG   93715     CA       _
                                CTC  AGGAGCTCA ACCT
                                |||  |||||||||| ||||
                                GAG  TCCTCGAGT TGGG
                                  AC        C
GAM1427  KIAA1958  3'  CAGCTGGAGCTCCTTGGAG   82779           AAC
                                CTCCAAGGAGCTC   CTG
                                ||||||||||||   |||
                                GAGGTTCCTCGAG   GAC
                                       GTC
GAM1427  LMOD1     3'  ACCCTGGGCTCCCTGGAG    25097      A      ACCT
                                CTCCA GGAGCTCA    GGT
                                ||||| ||||||||    |||
                                GAGGT CCTCGGGT    CCA
                                   C       C___
GAM1427  OVCOV1    5'  AGCACCAGCCACCAGCCCCTTA 32516    _    A   CAAC_
             GG                    CC AAGG GCT     CTGGTGCT
                                || |||| |||     ||||||||
                                GG TTCC CGA     GACCACGA
                                 A   C   CCACC
GAM1427  OVCOV1    3'  GCACCAGGCCAGCCTGGGA   32519     AA  A   CAA
                                TCC  GG GCT   CCTGGTGC
                                |||  || |||   ||||||||
                                AGG  TC CGA   GGACCACG
                                  G_  _   CC_
GAM1427  PRO0611   3'  ACCTGAGCTCCTAGAG      26858     CA       ACCT
                                CTC  AGGAGCTCA    GGT
                                |||  |||||||||    |||
                                GAG  TCCTCGAGT    CCA
                                  A_        _____
GAM1427  PTPRT     3'  GCACCTAGCACCTTGGAG    56496         A   CAACCT
                                CTCCAAGG GCT     GGTGC
                                |||||||| |||     |||||
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                                GAGGTTCC CGA     CCACG
                                    A  T_____
GAM1427  RASGRP4   3'  AGCACCAAGGCCCTCCTGGAG  54742      A   CTCAA  _
                                CTCCA GGAG    CCT GGTGCT
                                ||||| ||||    ||| ||||||
                                GAGGT CCTC    GGA CCACGA
                                  _   CC___   A
GAM1427  RNF40     3'  AGCACTTGACTGAGCTTCCCGG 29361     AA       ACCT
             A                   TCC  GGAGCTCA   GGTGCT
                                 |||  ||||||||   ||||||
                                 AGG  CTTCGAGT   TCACGA
                                   CC       CAGT
GAM1427  THTPA     5'  AGCACCAGGCTTTGCATCCTTG 44509        _  TCAA
             GG                    TCCAAGGA GC   CCTGGTGCT
                                 |||||||| ||   |||||||||
                                 GGGTTCCT CG   GGACCACGA
                                     A  TTTC
GAM1427  LOC112868 3'  CACCAGGTTGGGGCCCTGG   73266     A  AG
                                CCA GG  CTCAACCTGGTG
                                ||| ||  ||||||||||||
                                GGT CC  GGGTTGGACCAC
                                  C  G_
GAM1427  LOC118738 3'  AGGTCAGCTCCTTAGAG     76000     C       CA
                                CTC AAGGAGCT  ACCT
                                ||| ||||||||  ||||
                                GAG TTCCTCGA  TGGA
                                  A       C_
GAM1427  LOC139221 5'  CGTGTTCAAGCATCCTTGGA   76327        _  C_  C
                                TCCAAGGA GCT  AAC TG
                                |||||||| |||  ||| ||
                                AGGTTCCT CGA  TTG GC
                                     A  AC   T
GAM1427  LOC145833 5'  AGTACATTGAGCTCCACAGAG  60939     CAA       CCTG
                                CTC   GGAGCTCAA   GTGCT
                                |||   |||||||||   |||||
                                GAG   CCTCGAGTT   CATGA
                                  ACA       A___
GAM1427  LOC148147 5'  AGTGTGGTGATCAAGCTCTTTG 79389          CA___   TG TG
             GAG                   CTCCAAGGAGCT    ACC  G  CT
                                |||||||||||    |||  |  ||
                                GAGGTTTCTCGA    TGG  T  GA
                                       ACTAG   __ GT
GAM1427  LOC149767 5'  AGTACATTGAGCTCCATAGAG  80311     CAA       CCTG
                                CTC   GGAGCTCAA   GTGCT
                                |||   |||||||||   |||||
                                GAG   CCTCGAGTT   CATGA
                                  ATA       A___
GAM1427  LOC151126 5'  AGCACCAGGTTGAGATGATGGA 80936      AGGAG
                                TCCA    CTCAACCTGGTGCT
                                ||||    ||||||||||||||
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                                AGGT    GAGTTGGACCACGA
                                  AGTA_
GAM1427  LOC151446 5'  GCTGCCCAGCTCCTTGGAG   86572          CAACCT  _
                                CTCCAAGGAGCT     GGT GC
                                ||||||||||||    ||| ||
                                GAGGTTCCTCGA     CCG CG
                                       C_____   T
GAM1427  LOC153205 5'  AGCACCAGGCTGCTCCT     87151       TCAA
                                AGGAGC   CCTGGTGCT
                                ||||||   |||||||||
                                TCCTCG   GGACCACGA
                                   TC__
GAM1427  LOC196214 3'  AGCTGTCATTGAGCCTCTTGGA 91171       GA     CCTGGT
              G                  CTCCAAG  GCTCAA     GCT
                                |||||||  ||||||     |||
                                GAGGTTC  CGAGTT     CGA
                                    TC     ACTGT_
GAM1427  LOC196337 5'  AGCACCAGCTCGTCTCCCTAGA 89019     CAA    CTCAAC
              G                  CTC   GGAG     CTGGTGCT
                                |||   ||||     ||||||||
                                GAG   CCTC     GACCACGA
                                  ATC    TGCTC_
GAM1427  LOC206795 5'  AGGCTGTCAGCTCCTTGGAG   92409          __  A
                                CTCCAAGGAGCT  CA CCT
                                ||||||||||||  || |||
                                GAGGTTCCTCGA  GT GGA
                                       CT  C
GAM1427  LOC221370 5'  GCACCAGGCTCCCCGGA     93654     AA    TCAAC
                                TCC  GGAGC    CTGGTGC
                                |||  |||||    |||||||
                                AGG  CCTCG    GACCACG
                                  CC    ______
GAM1427  LOC93259  5'  GCCTTGAGTTCCTTGGAG    72286           CCT
                                CTCCAAGGAGCTCAA   GGT
                                ||||||||||||||   |||
                                GAGGTTCCTTGAGTT   CCG
                                          ___
GAM1428  ITGAL     3'  CTCAGGATGCCCAGGGCCAC   11043      GA       C
                                GTGGT  TGGGCATCC GAG
                                |||||  ||||||||| |||
                                CACCG  ACCCGTAGG CTC
                                   GG       A
GAM1428  BIRC1     3'  GCTCAAGAAATAAATCATCACC 16993        GGGCA  CC
                                GGTGGTGAT    TC  GAGC
                                |||||||||    ||  ||||
                                CCACTACTA    AG  CTCG
                                     AATAA  AA
GAM1428  MGC15476  3'  CTCCCCCACCACCACCGA    59610         A    CATCCC
                                TCGGTGGTG TGGG     GAG
                                |||||||| ||||     |||
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                                AGCCACCAC ACCC     CTC
                                     C   C_____
GAM1428 THG-1    5' CTCGGGACACCCACTCGC    48912     _   CA
                                GTGA TGGG  TCCCGAG
                                |||| ||||  |||||||
                                CGCT ACCC  AGGGCTC
                                  C   AC
GAM1428 LOC245771 5' GCTGGTCGCCCACCACCCC   94483    T   A    AT  CG
                                GG GGTG TGGGC  CC  AGC
                                || |||| |||||  ||  |||
                                CC CCAC ACCCG  GG  TCG
                                 _   C    CT  __
GAM1429 ABCD4    3' TCTCAGGTCCTAGAGTCAGGG  40103       T  CCC   CC
                                CCCTGACT CT   GCT  GAGA
                                |||||||| ||   |||  ||||
                                GGGACTGA GA   TGG  CTCT
                                     _ TCC   A_
GAM1429 CBS     5' TCCCGAAGCAAGAAGTTA    5365        CCC   C  A
                                TGACTTCT   GCT CG GA
                                ||||||||   ||| || ||
                                ATTGAAGA   CGA GC CT
                                     A__   A  C
GAM1429 EFNB1    5' CGAAGCGTCTCGGGAAGTCG   16668        C___    C
                                TGACTTCTC    CGCT CG
                                |||||||||    |||| ||
                                GCTGAAGGG    GCGA GC
                                     CTCT    A
GAM1429 FBXW1B   3' CTCAAAGTTGCTGGAGTCAGGG 25473         TCCC   CC
                                CCCTGACTTC    GCT  GAG
                                ||||||||||    |||  |||
                                GGGACTGAGG    TGA  CTC
                                     TCGT   AA
GAM1429 FBXW1B   3' CTCAAAGTTGCTGGAGTCAGGG 54443         TCCC   CC
                                CCCTGACTTC    GCT  GAG
                                ||||||||||    |||  |||
                                GGGACTGAGG    TGA  CTC
                                     TCGT   AA
GAM1429 FBXW1B   3' CTCAAAGTTGCTGGAGTCAGGG 54446         TCCC   CC
                                CCCTGACTTC    GCT  GAG
                                ||||||||||    |||  |||
                                GGGACTGAGG    TGA  CTC
                                     TCGT   AA
GAM1429 PER2     3' CTCGGAGCAGCTTCAGG     43350      CTT  CCC
                                CCTGA  CT   GCTCCGAG
                                |||||  ||   ||||||||
                                GGACT  GA   CGAGGCTC
                                  TC_  ____
GAM1429 RNTRE    3' TCTCAGAGCAGGAGAAGTTGCA 28716     __       C   C
             G                   CTG  ACTTCTCC GCTC GAGA
                                 |||  |||||||| |||| ||||
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                                GAC  TGAAGAGG CGAG CTCT
                                  GT       A   A
GAM1429  SH3BP4   3'  CTCGGAAGGAAGTCATAGT   28000    CC      CCCGC
                                AC  TGACTTCT    TCCGAG
                                ||  ||||||||    ||||||
                                TG  ACTGAAGG    AGGCTC
                                 AT       A____
GAM1429  SORCS2   3'  TCTCAGAGCGGGAGAACGCCAG 40807    AC_        C
                                CTG   TTCTCCCGCTC GAGA
                                |||   |||||||||||| ||||
                                GAC   AAGAGGGCGAG CTCT
                                  CGC         A
GAM1429  CAP350   5'  CGGAGCGGGGAGGCCAGG    29705     A   T
                                CCTG CTTC CCCGCTCCG
                                |||| |||| |||||||||
                                GGAC GGAG GGGCGAGGC
                                  C   _
GAM1429  CEP3     3'  TCTGAGCAAGAGGAAGTCA   22251       _ CC   C
                                TGACTTC TC  GCTC GA
                                ||||||| ||  |||| ||
                                ACTGAAG AG  CGAG CT
                                    G  AA   T
GAM1429  CMG1     5'  CTCAGAAAGAAGTCAAGG    47726    C      CCCGC  C
                                CC TGACTTCT    TC GAG
                                || ||||||||    || |||
                                GG ACTGAAGA    AG CTC
                                 A       A____  A
GAM1429  CNR2     3'  CTCTTGGGAAGTCAGGGT    10233        TC    CTCC
                                ACCCTGACT  TCCCG   GAG
                                |||||||||  |||||   |||
                                TGGGACTGA  AGGGT   CTC
                                     __     T___
GAM1429  DUSP9    3'  TCTCAGAGCGAGAGCTGCGGAG 9159     GACTT_  C    C
            GG                    CCCT     CTC CGCTC GAGA
                                ||||     ||| ||||| ||||
                                GGGA     GAG GCGAG CTCT
                                  GGCGTC   A    A
GAM1429  FLJ20730 3'  TCTCGTAGATAGAGAAGTCAGG 36052         CCG  C
                                CCTGACTTCTC   CT CGAGA
                                ||||||||||   || |||||
                                GGACTGAAGAG   GA GCTCT
                                      ATA  T
GAM1429  HSA249128 3'  CTTGAAGGGAAGTCAGAGT   34560    C     TC    GCTC
                                AC CTGACT  TCCC   CGAG
                                || ||||||  ||||   ||||
                                TG GACTGA  AGGG   GTTC
                                 A     __    AA__
GAM1429  IRX4     3'  TCTCGGAGCAGAAGAGGCCAG  33452     A    CCC
                                CTG CTTCT   GCTCCGAGA
                                ||| |||||   |||||||||
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                                GAC GGAGA   CGAGGCTCT
                                  C     AGA
GAM1429  KIAA0391  3'  CTCAAAGTAAGTTAGGGT    28608         CTCCC   CC
                                ACCCTGACTT    GCT  GAG
                                ||||||||||    |||  |||
                                TGGGATTGAA    TGA  CTC
                                      _____   AA
GAM1429  KIAA1036  3'  GAGCGGGACAAACCAGAGG   30491    _   AC  C
                                CC CTG  TT TCCCGCTC
                                || |||  || ||||||||
                                GG GAC  AA AGGGCGAG
                                 A   CA  C
GAM1429  KIAA1582  5'  TGGAGATGGGAGAAGTCAG   65994           _
                                CTGACTTCTCCCG CTCCG
                                |||||||||||| |||||
                                GACTGAAGAGGGT GAGGT
                                       A
GAM1429  PCTAIRE2BP 5'  CTCGAAGCGGGGCGGGG     71123      ACTTC      C
                                CCCTG     TCCCGCT CGAG
                                |||||     ||||||| ||||
                                GGGGC     GGGGCGA GCTC
                                  _____       A
GAM1429  RHOBTB2   3'  CTCACTGGAGAAGTCAGGGT   61596           CGCTCC
                                ACCCTGACTTCTCC     GAG
                                ||||||||||||||     |||
                                TGGGACTGAAGAGG     CTC
                                       TCA___
GAM1429  TEX27     5'  CTCAGAGCGGGGCCCGGG    41947      ACTTC      C
                                CCTG     TCCCGCTC GAG
                                ||||     |||||||| |||
                                GGGC     GGGGCGAG CTC
                                  CC___       A
GAM1429  LOC144308 5'  TCCCGGAGCTGTCAGCCAGGG  83987      A  TCTCCC     A
                                CCCTG CT     GCTCCG GA
                                ||||| ||     |||||| ||
                                GGGAC GA     CGAGGC CT
                                   C  CTGT__     C
GAM1429  LOC150889 3'  AGCGTGAGAAGCCAGAGT    80809    C   A     C
                                AC CTG CTTCTC CGCT
                                || ||| |||||| ||||
                                TG GAC GAAGAG GCGA
                                 A   C     T
GAM1429  LOC152765 5'  TCTAAGAGAGGAAGTCAG    81545         CCCG   CG
                                CTGACTTCT    CTC  AGA
                                |||||||||    |||  |||
                                GACTGAAGG    GAG  TCT
                                      A___   AA
GAM1429  LOC152915 3'  CGGAGCAGGGTCAGGGT     67584         TTCT  C
                                ACCCTGAC    CC GCTCCG
                                ||||||||    || ||||||
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                                TGGGACTG   GG CGAGGC
                                    _____  A
GAM1429  LOC199745 3'  CTCAGAGCAGAGCAAGGGT   89718     GACTT  CC   C
                                ACCCT    CTC  GCTC GAG
                                |||||    |||  |||| |||
                                TGGGA    GAG  CGAG CTC
                                  AC___   A_   A
GAM1429  LOC219743 3'  CTCAGTCAGAGTCAGGG    94744       T  CCC  CC
                                CCCTGACT CT   GCT  GAG
                                |||||||| ||   |||  |||
                                GGGACTGA GA   TGA  CTC
                                    _ C__   __
GAM1429  LOC219793 5'  TGGAGAAGAAGTCAGGG    93022         CCCG
                                CCCTGACTTCT   CTCCG
                                ||||||||||    |||||
                                GGGACTGAAGA   GAGGT
                                      A___
GAM1429  LOC221496 3'  GAGGGGGAGAAGCCAGGGT   93639      A      G
                                ACCCTG CTTCTCCC CTC
                                |||||| |||||||| |||
                                TGGGAC GAAGAGGG GAG
                                   C       G
GAM1429  LOC255328 3'  TGGAGGAAAAGCCAGGG    98350      A  C  CGC
                                CCCTG CTT TCC   TCCG
                                ||||| ||| |||   ||||
                                GGGAC GAA AGG   AGGT
                                  C  A  ___
GAM1429  LOC256158 5'  CCGGAGCGGGGCAGGTT    99488      C       A
                                GACTT TCCCGCTCCG G
                                ||||| |||||||||| |
                                TTGGA GGGGCGAGGC C
                                  C        C
GAM1429  LOC256598 3'  CGGAGCAGGGTCAGGGT    98104       TTCT  C
                                ACCCTGAC   CC GCTCCG
                                ||||||||   || ||||||
                                TGGGACTG   GG CGAGGC
                                    _____  A
GAM1429  LOC257438 3'  TCTCAAATGCCGGAAGTCAGGG 95595         CCC  TCC_
                                CCCTGACTTCT   GC   GAGA
                                ||||||||||   ||   ||||
                                GGGACTGAAGG   CG   CTCT
                                      C__  TAAA
GAM1429  LOC51725  3'  TCTCGGAGTTCCTGAAGTAGG  70428    A   TCCC
                                CCTG CTTC   GCTCCGAGA
                                |||| ||||   |||||||||
                                GGAT GAAG   TGAGGCTCT
                                  _   TCCT
GAM1429  LOC54518  5'  CTCGGAGCAAAGCAGCTCGG   39298    _  T  CCC
                                CTGA CT CT   GCTCCGAG
                                |||| || ||   ||||||||
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                                GGCT GA GA   CGAGGCTC
                                  C  C  AA_
GAM1429  LOC55924  3'  AGCGGGGAGAAGCCAGAGT   39391    C   A      _
                                AC CTG CTTCTCCC GCT
                                || ||| |||||||| |||
                                TG GAC GAAGAGGG CGA
                                 A   C       G
GAM1429  LOC90957  3'  TCGACTGAGAGAAGTCAG    65090          C  CTC
                                CTGACTTCTC CG   CGA
                                |||||||||| ||   |||
                                GACTGAAGAG GT   GCT
                                      A  CA_
GAM1430  LAMC1     3'  TTGCAAAGTTTTCACGTCA   11275          C  CC_
                                TGACGTGGA AT   GCAA
                                ||||||||| ||   ||||
                                ACTGCACTT TG   CGTT
                                      T  AAA
GAM1430  OPA1      3'  TTGCGGGTGGAACAGTCA    56430      G  GA_
                                TGAC TG   CATCCGCAA
                                |||| ||   |||||||||
                                ACTG AC   GTGGGCGTT
                                  _  AAG
GAM1430  PITX2     5'  TTGCGGAGGGTGCGCTCA    6161      C   G  A_
                                TGA GTG AC  TCCGCAA
                                ||| ||| ||  |||||||
                                ACT CGC TG  AGGCGTT
                                  _   G  GG
GAM1430  LOC144848 3'  TGGAGGATGTCCACATCA    73961     C        G_
                                TGA GTGGACATCC  CA
                                ||| ||||||||||  ||
                                ACT CACCTGTAGG  GT
                                  A         AG
GAM1430  LOC221495 5'  TTGCAGGGGCATCACGTTA   95498         ACA  _
                                TGACGTGG   TCC GCAA
                                ||||||||   ||| ||||
                                ATTGCACT   GGG CGTT
                                     ACG   A
GAM1430  LOC256520 3'  GCAGATTTTGTTCTACGTCA  97667          _ ___  C
                                TGACGTGGA CA   TC GC
                                ||||||||| ||   || ||
                                ACTGCATCT GT   AG CG
                                      T  TTT  A
GAM1431  ALDH3B2   3'  GCAGCTCCATCCACTGGG    7343           TAT
                                TCCAGTGGATG   GGCTGC
                                ||||||||||   ||||||
                                GGGTCACCTAC   TCGACG
                                       C__
GAM1431  DGSI      3'  CAGCTGTACACCCAGCAGAG  42963     CAG   A
                                CTC   TGG TGTATGGCTG
                                |||   ||| ||||||||||
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                                GAG   ACC ACATGTCGAC
                                  ACG   C
GAM1431  DSCR3    3'  CGCAAAGTGCTAGCCACTGGA  21310        AT_   GGC
                                TCCAGTGG   GTAT   TGCG
                                ||||||||   ||||   ||||
                                AGGTCACC   CGTG   ACGC
                                    GAT    AA_
GAM1431  ENG      5'  CGCAGCCCTGCCACTGGA    5494         ATGTAT
                                TCCAGTGG     GGCTGCG
                                ||||||||     |||||||
                                AGGTCACC     CCGACGC
                                    GTC___
GAM1431  ENPP3    3'  CAGCACATCCACTGGAG     18469           ATG
                                CTCCAGTGGATGT   GCTG
                                ||||||||||||   ||||
                                GAGGTCACCTACA   CGAC
                                              ___
GAM1431  FBXL7    5'  CGCAGCACCCCCTCCCACTGGA 25491         ATGTATG_
                  G              CTCCAGTGG       GCTGCG
                                 |||||||||       ||||||
                                 GAGGTCACC       CGACGC
                                     CTCCCCCA
GAM1431  GRIN2A   5'  CGCAGCCATCAGCCCTGGAG   7722        T  A  T
                                CTCCAG GG TG ATGGCTGCG
                                |||||| || || |||||||||
                                GAGGTC CC AC TACCGACGC
                                   _  G  _
GAM1431  IGFBP4   3'  CAGCCATGAAGTCACCGGG    9551      A    ATG
                                TCC GTGG   TATGGCTG
                                |||  ||||   ||||||||
                                GGG CACT   GTACCGAC
                                  C    GAA
GAM1431  INSR     5'  CGCAGCCATGGGCACCGGGG   71538     A   GATG
                                CTCC GTG    TATGGCTGCG
                                ||||  |||    ||||||||||
                                GGGG CAC    GTACCGACGC
                                  C   GG__
GAM1431  MGAT3    5'  CGCAGCCGCTGCCGCCGGAG   11561     A    ATGTA
                                CTCC GTGG     TGGCTGCG
                                ||||  ||||     ||||||||
                                GAGG CGCC     GCCGACGC
                                  C    GTC__
GAM1431  MYLK2    3'  CGCAGCCACACAGTGGCCGGGG 53583      A  GGA   A
                                CTCC GT   TGT TGGCTGCG
                                ||||  ||   |||  ||||||||
                                GGGG CG   ACA ACCGACGC
                                  C  GTG   C
GAM1431  NYX      3'  CACACGGGCATCCATTGGA    42904          A  GC
                                TCCAGTGGATGT TG  TG
                                ||||||||||||  ||  ||
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                                AGGTTACCTACG GC  AC
                                      G  AC
GAM1431  RPS6KA1   5'  CGCAGCCGGGGCCGCCGGAG   60042     A   ATGTA
                                CTCC GTGG    TGGCTGCG
                                |||| ||||    ||||||||
                                GAGG CGCC    GCCGACGC
                                  C   GGG__
GAM1431  SLC13A3   3'  CAGTTACAACCCACTGGGG   61089       A_   TG
                                CTCCAGTGG  TGTA  GCTG
                                |||||||||  ||||  ||||
                                GGGGTCACC  ACAT  TGAC
                                     CA   __
GAM1431  SLC6A5    5'  CGCAGCCCCCTCCCGCTGGAG  16140       ATGTAT
                                CTCCAGTGG     GGCTGCG
                                |||||||||     |||||||
                                GAGGTCGCC     CCGACGC
                                     CTCCC_
GAM1431  USP9Y     5'  CAGATACTTCCACTGGAG    64736        T   GG
                                CTCCAGTGGA GTAT  CTG
                                |||||||||| ||||  |||
                                GAGGTCACCT CATA  GAC
                                      T   __
GAM1431  VBP1      5'  CGCAGCCAATCAGCACCTAGAG 14029    CA_   GA  TA
                                CTC   GTG  TG  TGGCTGCG
                                |||   |||  ||  ||||||||
                                GAG   CAC  AC  ACCGACGC
                                  ATC   G_  TA
GAM1431  C20orf130 3'  CGCAGCCATCAGGACTAGG   62414    _   GGA  T
                                CC AGT   TG ATGGCTGCG
                                || |||   || |||||||||
                                GG TCA   AC TACCGACGC
                                 A  GG_  _
GAM1431  C20orf150 3'  CAGCCACTCACTGGGG     66007        ATGTA
                                CTCCAGTGG    TGGCTG
                                |||||||||    ||||||
                                GGGGTCACT    ACCGAC
                                     C_____
GAM1431  CAMK2G    3'  CGCAGCCAGTGGCTCTGGAG   69536      T  ATGTA
                                CTCCAG GG    TGGCTGCG
                                |||||| ||    ||||||||
                                GAGGTC TC    ACCGACGC
                                   _  GGTG_
GAM1431  CST7      3'  CAGCCATGACAAACACCAGG   14682    A_   GA  _
                                CC  GTG  TGT ATGGCTG
                                ||  |||  ||| |||||||
                                GG  CAC  ACA TACCGAC
                                 AC   AA   G
GAM1431  FLJ10432  3'  AGATCTACATCCACCGAG    39347     CA       T  _
                                CTC  GTGGATGTA GG CT
                                |||  ||||||||| || ||
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                                GAG  CACCTACAT CT GA
                                  C_       _ A
GAM1431  FLJ20127  5'  CAGCTGCACATCCTACTGGAG  35078       _    AT
                                CTCCAGT GGATGT  GGCTG
                                ||||||| ||||||  |||||
                                GAGGTCA CCTACA  TCGAC
                                    T     CG
GAM1431  FLJ23584  3'  CAGACCACGCCCACTGGAG   45037        AT TA  _
                                CTCCAGTGG  G  TGG CTG
                                |||||||||  |  ||| |||
                                GAGGTCACC  C  ACC GAC
                                     __ GC   A
GAM1431  FLJ25422  5'  CAGCCATACTGCTAGGA    59391    _   GAT
                                TCC AGTG   GTATGGCTG
                                ||| ||||   |||||||||
                                AGG TCGT   CATACCGAC
                                  A   ___
GAM1431  KIAA0420  3'  CTGTATACCCCACTGGAG   64088        A_
                                CTCCAGTGG  TGTATGG
                                |||||||||  |||||||
                                GAGGTCACC  ATATGTC
                                     CC
GAM1431  KIAA0649  3'  CAGCCGTCCGCTGGA      29711         GTAT
                                TCCAGTGGAT   GGCTG
                                ||||||||||   |||||
                                AGGTCGCCTG   CCGAC
                                     _____
GAM1431  KIAA1576  5'  CGCAGCCACCGCAGCCAC   66492     A  A_
                                GTGG TGT  TGGCTGCG
                                |||| |||  ||||||||
                                CACC ACG  ACCGACGC
                                  G   CC
GAM1431  KIAA1855  3'  CGCAGCCGGCCACACTGGAG  93950       GA  TA
                                CTCCAGTG  TG  TGGCTGCG
                                |||||||  ||  ||||||||
                                GAGGTCAC  AC  GCCGACGC
                                    __  CG
GAM1431  KIAA1913  5'  CGCAGCCACGCCCCTGGA   74316     T  AT TA
                                TCCAG GG  G  TGGCTGCG
                                ||||| ||  |  ||||||||
                                AGGTC CC  C  ACCGACGC
                                  _ __ GC
GAM1431  MGC12760  5'  CGCAGCCATAGACAACTAGAG  52158    C  GGATG
                                CTC AGT    TATGGCTGCG
                                ||| |||    ||||||||||
                                GAG TCA    ATACCGACGC
                                  A  ACAG_
GAM1431  PTPRT    3'  CATCTTCACATCCACTGG    56489         AT  C
                                CCAGTGGATGT  GG TG
                                ||||||||||  || ||
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                                GGTCACCTACA  TC AC
                                      CT  T
GAM1431  RGS20    3'  CAGGTACATCCACAGAG     14915     CA        GG
                                CTC  GTGGATGTAT  CTG
                                |||  ||||||||||  |||
                                GAG  CACCTACATG  GAC
                                  A_         __
GAM1431  SIAT8C   5'  CATTGTCCATCCACTGGA     32443          T TG C
                                TCCAGTGGATG A  G TG
                                ||||||||||| |  | ||
                                AGGTCACCTAC T  T AC
                                      C GT _
GAM1431  SMCR7    3'  CAGCTGGGGCATCTCACTGGAG 58236         _    A_
                                CTCCAGTG GATGT  TGGCTG
                                |||||||| |||||  ||||||
                                GAGGTCAC CTACG  GTCGAC
                                     T    GG
GAM1431  SULT1C2  5'  CGCAGCCATATGCTGACTG    22712     _ A
                                CAGT GG TGTATGGCTGCG
                                |||| || ||||||||||||
                                GTCA TC GTATACCGACGC
                                  G  _
GAM1431  ZNF339   3'  CGCAGTTGCTCACATTCAC    41391        A__
                                GTGGATGT   TGGCTGCG
                                ||||||||   ||||||||
                                CACTTACA   GTTGACGC
                                     CTC
GAM1431  LOC123855 3'  CGCTTGGAATACCCACTGGA   76144        AT   GGCT_
                                TCCAGTGG  GTAT    GCG
                                ||||||||  ||||    |||
                                AGGTCACC  CATA    CGC
                                     __   AGGTT
GAM1431  LOC149992 5'  CGCAGCCATTTTCTCCCTGGAG 80374       T   TGT_
                                CTCCAG GGA    ATGGCTGCG
                                ||||||| |||   |||||||||
                                GAGGTC CCT    TACCGACGC
                                   _  CTTT
GAM1431  LOC150185 3'  CAGACCACATCCACTAGG     86064    _       AT  _
                                CC AGTGGATGT  GG CTG
                                || |||||||||  || |||
                                GG TCACCTACA  CC GAC
                                 A        __  A
GAM1431  LOC200958 3'  GCTCACATCCACCGGAG      66506      A       AT
                                CTCC GTGGATGT  GGC
                                |||| ||||||||  |||
                                GAGG CACCTACA  TCG
                                  C       C_
GAM1431  LOC222031 3'  CGCAGCTCTGTCTCACTGGA   95677        _    TAT
                                TCCAGTG GATG   GGCTGCG
                                ||||||| ||||   |||||||
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                                AGGTCAC CTGT   TCGACGC
                                    T   C__
GAM1431  LOC253626 5'  CAGCTCCACATCACTGGA    99013       G   AT
                                TCCAGTG ATGT  GGCTG
                                ||||||| ||||  |||||
                                AGGTCAC TACA  TCGAC
                                    _   CC
GAM1431  LOC253805 5'  CGCAGCCACACGGCCCGGC   98171   _ A_  A
                                GT GG  TGT TGGCTGCG
                                || ||  ||| ||||||||
                                CG CC  GCA ACCGACGC
                                 G  CG   C
GAM1431  LOC257354 3'  CTGTATACCCCACTGGAG    96790       A_
                                CTCCAGTGG  TGTATGG
                                |||||||||  |||||||
                                GAGGTCACC  ATATGTC
                                     CC
GAM1431  LOC91300  5'  CGCAGCCGCATCCCCATGGA  96235    GT_    AT
                                TCCA   GGATGT  GGCTGCG
                                ||||   ||||||  |||||||
                                AGGT   CCTACG  CCGACGC
                                  ACC    __
GAM1431  LOC91300  5'  CGCAGCCGCATCCCCATGGA  57862    GT_    AT
                                TCCA   GGATGT  GGCTGCG
                                ||||   ||||||  |||||||
                                AGGT   CCTACG  CCGACGC
                                  ACC    __
GAM1431  LOC93259  5'  GGCTCACATCCACTGAG    72289    C      AT
                                CTC AGTGGATGT  GGCT
                                ||| |||||||||  ||||
                                GAG TCACCTACA  TCGG
                                  _       C_
GAM1432  BCAT2     3'  GCGACACTCCCAAAGCCGTAAG 8650         ___  AA__
                                CTTACGGTTT   GAG   GC
                                ||||||||||   |||   ||
                                GAATGCCGAA   CTC   CG
                                     ACC   ACAG
GAM1432  NPY2R     3'  GCGGAAGGCTTCACCACAAG   8066     AC   TTGA
                                CTT  GGT   GAAGCCTTCCGC
                                |||  |||   ||||||||||||
                                GAA  CCA   CTTCGGAAGGCG
                                  CA   ____
GAM1432  KIAA0972  3'  GCAGAAAGCTTCTGTGTAAGCC 30681      ___    C   C
                                GGTTTG   AGAAGC TTC GC
                                ||||||   |||||| ||| ||
                                CCGAAT   TCTTCG AAG CG
                                   GTG     A  A
GAM1432  KRT6      3'  GCAGAAGGCTTCCCAACTC   83095   GT   A      C
                                G  TTG GAAGCCTTC GC
                                |  ||| |||||||| ||
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                                C  AAC CTTCGGAAG CG
                                 TC  C       A
GAM1432  LRMP     5'  CGGAACCTTCAAACTATAA   21584     CG     AAGCC
                                TTA  GTTTGAG    TTCCG
                                |||  |||||||    |||||
                                AAT  CAAACTT    AAGGC
                                  AT      CC___
GAM1432  MGC16291  3'  GCGGAAAACTGCTCAAACC   52285        A  CC
                                GGTTTGAG AG  TTCCGC
                                ||||||||  ||  ||||||
                                CCAAACTC TC  AAGGCG
                                     G  AA
GAM1432  LOC142820 3'  GAGGATTCAAACCGCAAG    76914     A      GAAG
                                CTT CGGTTTGA    CCTT
                                |||  ||||||||    ||||
                                GAA GCCAAACT    GGAG
                                  C       TA__
GAM1432  LOC152317 3'  GCAGAAGGCTTCTCTGGACACC 86830     TT___         C
                                GGT    GAGAAGCCTTC GC
                                |||    ||||||||||| ||
                                CCA    CTCTTCGGAAG CG
                                  CAGGT         A
GAM1433  ABR      3'  CTCCTGTGGCCTTGGGCAG   42001          ATGAC
                                CTGCCCAAGG    CAGGAG
                                ||||||||||    ||||||
                                GACGGGTTCC    GTCCTC
                                     GGT__
GAM1433  APLP1    3'  TCCCAGCCTAGGGCAGCA    18968        A  A  ACCA
                                TGCTGCCC AGG TG   GGA
                                ||||||||  ||| ||   |||
                                ACGACGGG TCC AC   CCT
                                     A  G  ____
GAM1433  BARX2    3'  TCCTGACCTCTGGGCAGC    14717        _  ATGAC
                                GCTGCCCA AGG    CAGGA
                                ||||||||  |||    |||||
                                CGACGGGT TCC    GTCCT
                                     C  A____
GAM1433  CYLN2    3'  CTCCCACCGTGACCTTGGGCA  14090         __  ACCA
                                TGCCCAAGG  ATG   GGAG
                                |||||||||  |||   ||||
                                ACGGGTTCC  TGC   CCTC
                                     AG  CAC_
GAM1433  EBAF     5'  CTCCTGCTCCCCCAGGGCAGCA 66028         AA  AT  C
              C                   GTGCTGCCC  GG  GA CAGGAG
                                |||||||||  ||  || ||||||
                                CACGACGGG  CC  CT GTCCTC
                                     AC  C_  C
GAM1433  HMGA2    5'  CTCCCGAAAGGTGCTGGGCAGC 14452        A  G  GACCA_
                                GCTGCCC AG AT     GGAG
                                |||||||  ||  ||     ||||
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                                CGACGGG TC TG     CCTC
                                   _ G  GAAAGC
GAM1433  KLHL3    3'  CTTGACATCCCCAGGCAGCAC  88846        CAA    AC
                                GTGCTGCC   GGATG  CAGG
                                ||||||||   |||||  ||||
                                CACGACGG   CCTAC  GTTC
                                     ACC    A_
GAM1433  L1CAM    3'  CTCCCAGCATCGCACTCTGGCA 43989        CA ___   ACCA
              GCAC                 GTGCTGCC  AG   GATG   GGAG
                                ||||||||  ||   ||||   ||||
                                CACGACGG  TC   CTAC   CCTC
                                     TC  ACG   GAC_
GAM1433  MAPK1    3'  CTCCGGAATCCTTGGGGAGCAC 12296      G       GA  A
                                GTGCT CCCAAGGAT  CC GGAG
                                |||||  |||||||||  ||  ||||
                                CACGA GGGTTCCTA  GG CCTC
                                   G        A_  _
GAM1433  MAPK4    5'  CCTGTGTTACCTGGGCAGC   12301        A  A   _
                                GCTGCCCA GG TGAC CAGG
                                ||||||||  ||  ||||  ||||
                                CGACGGGT CC ATTG GTCC
                                     _  _    T
GAM1433  MEOX1    3'  TCCTGGTCTGGACACCAC    16954     C  C   AGGAT
                                GTG TG CCA    GACCAGGA
                                |||  ||  |||    ||||||||
                                CAC AC GGT    CTGGTCCT
                                  C  A  _____
GAM1433  MEOX1    3'  TCCTGGTCTGGACACCAC    16955     C  C   AGGAT
                                GTG TG CCA    GACCAGGA
                                |||  ||  |||    ||||||||
                                CAC AC GGT    CTGGTCCT
                                  C  A  _____
GAM1433  OGDH     3'  TCCTGGGCCCAGGCAGCAC   92752        CAA  ATGA
                                GTGCTGCC   GG   CCAGGA
                                ||||||||   ||   ||||||
                                CACGACGG   CC   GGTCCT
                                     A__  CG__
GAM1433  SLC2A6   3'  CCTGGCTCGGGACAGGTAGCAC 34569        CAAGGA  _
                                GTGCTGCC     TGA CCAGG
                                ||||||||     |||  |||||
                                CACGATGG     GCT GGTCC
                                     ACAGG_   C
GAM1433  C14orf4  5'  CTCCCCACGCCCTGGGCAGC   67914        A  A  ACCA
                                GCTGCCCA GG TG   GGAG
                                ||||||||  ||  ||   ||||
                                CGACGGGT CC GC    CCTC
                                     C  _  ACC_
GAM1433  C20orf58 3'  CCAGGCGGCCGGCAGCAC    75260        CAA  A  A  A
                                GTGCTGCC   GG TG CC GG
                                ||||||||   ||  ||  ||  ||
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                                CACGACGG   CC GC GG CC
                                    ___  G  _  A
GAM1433  DJ159A19.3 5'  CTGAGTCATCCTCCGACAGCAC 32282       CCCA      _
                                GTGCTG    AGGATGAC CAG
                                ||||||    |||||||| |||
                                CACGAC    TCCTACTG GTC
                                   AGCC       A
GAM1433  HCNGP    3'  CCACAGCAGCCCCTGGGCAGCA 26072         A  A_  ACCA
           C                     GTGCTGCCCA GG  TG    GG
                                ||||||||||  ||  ||    ||
                                CACGACGGGT CC  AC    CC
                                      C  CG  GACA
GAM1433  KIAA0210  3'  CCTGGCCATCCCTGGGCAGCA  29156         A     A
                                TGCTGCCCA GGATG CCAGG
                                |||||||||  |||||  |||||
                                ACGACGGGT CCTAC GGTCC
                                      C     C
GAM1433  RNASE6PL  5'  CTCCCGGAAGTCTTCCTCGGGC 14953        A    T  ___  A
           AGCA                    TGCTGCCC AGGA GA   CC GGAG
                                |||||||| ||||  ||   ||  ||||
                                ACGACGGG TCCT CT   GG CCTC
                                     C    T  GAA  C
GAM1433  UPK3     3'  CCAGCACCACCCCTGGGCAGCA 23706         A  A  ACCA_
                                TGCTGCCCA GG TG     GG
                                |||||||||  || ||     ||
                                ACGACGGGT CC AC     CC
                                      C  C  CACGA
GAM1433  LOC127534 3'  CTCCTGGTTCCCCAGGCAGACA 75968     _    CAA  AT
           C                     GTG CTGCC   GG  GACCAGGAG
                                |||  |||||   ||  |||||||||
                                CAC GACGG   CC  TTGGTCCTC
                                  A     A__  CC
GAM1433  LOC130985 3'  CCCCGTTGCCGAGGCAGCAC   75491        CAA  A    CA
                                GTGCTGCC   GG TGAC  GG
                                ||||||||   || ||||  ||
                                CACGACGG   CC GTTG  CC
                                     AG_  _    CC
GAM1433  LOC145989 5'  CCTGACTAGGCGGGCAGCGC   60291         AAGGA  AC
                                GTGCTGCCC     TG  CAGG
                                |||||||||     ||  ||||
                                CGCGACGGG     AT  GTCC
                                      CGG__  CA
GAM1433  LOC146108 5'  TCCTGGGCCCGGGCAGCA    78152        AA  ATGA
                                TGCTGCCC  GG    CCAGGA
                                ||||||||  ||    ||||||
                                ACGACGGG  CC    GGTCCT
                                     __  CG__
GAM1433  LOC151174 5'  CTCCTCACGGCTCCCTGGGCAG 86436         A   TGA  ___
           CA                      TGCTGCCCA GGA   CC   AGGAG
                                |||||||||  |||   ||   |||||
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                                ACGACGGGT CCT   GG   TCCTC
                                     C   C__  CAC
GAM1433  LOC151512 5'  CTCCTGGTCACCCTCACCTGTC 86616    T  CCA__   A
              GC                   GC GC    AGG TGACCAGGAG
                                || ||    ||| ||||||||||
                                CG TG    TCC ACTGGTCCTC
                                 C  TCCAC   C
GAM1433  LOC151742 5'  CCAGACCATCCTTGAACAGCA  58344      CC       ACCA
                                TGCTG  CAAGGATG    GG
                                |||||  ||||||||    ||
                                ACGAC  GTTCCTAC    CC
                                   AA       CAGA
GAM1433  LOC205143 5'  CTGAGCTCCCCTGGGCAGCAC  92349         A_   TGAC
                                GTGCTGCCCA  GGA    CAG
                                ||||||||||  |||    |||
                                CACGACGGGT  CCT    GTC
                                      CC   CGA_
GAM1433  LOC219920 5'  CTCCCGAGGGTGCTGGGCAGC  94948        A G  GA  A__
                                GCTGCCCA G AT  CC   GGAG
                                |||||||| | ||  ||   ||||
                                CGACGGGT C TG  GG   CCTC
                                     _ G  __  AGC
GAM1433  LOC253983 3'  CTCCTGGTCATGAGCAGCAT   98430        C  AGGA
                                GTGCTGC CA    TGACCAGGAG
                                |||||||  ||    ||||||||||
                                TACGACG GT    ACTGGTCCTC
                                   A  _____
GAM1433  LOC255193 5'  CCGAACACCAGGGCAGCAC    97102         AA  A  ACCA
                                GTGCTGCCC  GG TG    GG
                                |||||||||  || ||    ||
                                CACGACGGG  CC AC    CC
                                     A_  _  AAG_
GAM1433  LOC91450  5'  CTCCTCTACCCTCGGGCAGCAC 66656         A   A  ACC
                                GTGCTGCCC AGG TG   AGGAG
                                |||||||||  ||| ||   |||||
                                CACGACGGG TCC AT   TCCTC
                                     C   C  C__
GAM1434  AIPL1    3'  GCCCACAGCCACCCAGGCA    60535         A    CA__
                                TGCCTGGG TGGC    GGC
                                ||||||||  ||||    |||
                                ACGGACCC ACCG    CCG
                                     _    ACAC
GAM1434  AK3      3'  GCCCAGGCTTTGTCCCAGGC   26398          __   A_
                                GCCTGGGAT  GGCC  GGC
                                |||||||||  ||||  |||
                                CGGACCCTG  TCGG  CCG
                                     TT    AC
GAM1434  AOC3     3'  GCCTGGCCTGGTCCAGGC    14960         AT_
                                GCCTGGG   GGCCAGGC
                                |||||||   ||||||||
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                                CGGACCT   CCGGTCCG
                                    GGT
GAM1434  APBA2    3'  CCCGGCTGCATACCCGGGCA  19739        _  __  A
                                TGCCTGGG ATG  GCC GG
                                |||||||| |||  ||| ||
                                ACGGGCCC TAC  CGG CC
                                    A  GT  C
GAM1434  APOC3    3'  GCCTGGCCCCCCTCCAGGCA  5266        AT__
                                TGCCTGGG   GGCCAGGC
                                ||||||||   ||||||||
                                ACGGACCT   CCGGTCCG
                                    CCCC
GAM1434  ARG2     3'  GCCTGGCTATACAGTGCA   8607     _  GG
                                TGC CTG  ATGGCCAGGC
                                ||| |||  ||||||||||
                                ACG GAC  TATCGGTCCG
                                  T  A_
GAM1434  ATP11B   3'  CCTGAGCCACACCCAGGC   81125      A_  _
                                GCCTGGG  TGGC CAGG
                                |||||||  |||| ||||
                                CGGACCC  ACCG GTCC
                                    AC   A
GAM1434  BAK1     5'  GCCCAGGTCCTCCCAGGCA   93630       T   A_
                                TGCCTGGGA GGCC  GGC
                                ||||||||| ||||  |||
                                ACGGACCCT CTGG  CCG
                                     C   AC
GAM1434  CAPN10   3'  GCCCAGCGAGCATCCCGGGCA  43870         ___  CA
                                TGCCTGGGATG   GC  GGC
                                ||||||||||   ||  |||
                                ACGGGCCCTAC   CG  CCG
                                      GAG  AC
GAM1434  CDK3     5'  GCCTTCTGTTTCCCAGGCA   8842        T  C__
                                TGCCTGGGA GGC   AGGC
                                ||||||||| |||   ||||
                                ACGGACCCT TTG   TCCG
                                    _  TCT
GAM1434  CLDN14   5'  GCCCGGCTGGCCTAGGCA   25095       AT   A
                                TGCCTGGG  GGCC GGC
                                ||||||||  |||| |||
                                ACGGATCC  TCGG CCG
                                    GG   C
GAM1434  CLDN14   5'  GCCCGGCTGGCCTAGGCA   58471       AT   A
                                TGCCTGGG  GGCC GGC
                                ||||||||  |||| |||
                                ACGGATCC  TCGG CCG
                                    GG   C
GAM1434  COL4A6   3'  GCCCACTGTGTCTAGGCA   10246       _   CCA
                                TGCCTGGG ATGG   GGC
                                |||||||| ||||   |||
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                                ACGGATCT TGTC   CCG
                                    G    AC_
GAM1434  CRK      3'  GCCTCCTTTCTCTCAGGCA   60544        T___  CC
                                TGCCTGGGA   GG  AGGC
                                |||||||||   ||  ||||
                                ACGGACTCT   CC  TCCG
                                    CTTT  __
GAM1434  CSF2RB   3'  GCCTGACCTTCCTCAGTCA   6370    C  _  T  C
                                TG CTG GGA GG CAGGC
                                || ||| ||| || |||||
                                AC GAC CCT CC GTCCG
                                 T   T   T  A
GAM1434  DNAI2    5'  CCTGGAGCTGTCCTGGCA    43785     T      __
                                TGCC GGGATGGC  CAGG
                                |||| ||||||||  ||||
                                ACGG TCCTGTCG  GTCC
                                  _       AG
GAM1434  DRD2     5'  GCCTGGCCACCCAGTGGC    7677      __    A
                                GCC  TGGG TGGCCAGGC
                                |||  |||| |||||||||
                                CGG  ACCC ACCGGTCCG
                                  TG   _
GAM1434  EHD2     3'  GCCCAGCCCTGTTCTAGGCA   28223          __   CA
                                TGCCTGGGAT  GGC  GGC
                                ||||||||||  |||  |||
                                ACGGATCTTG  CCG  CCG
                                     TC   AC
GAM1434  GRM7     5'  CCTGGCTGACTCCAGGCA    7784         _ A
                                TGCCTGG G TGGCCAGG
                                ||||||| | ||||||||
                                ACGGACC C GTCGGTCC
                                    T A
GAM1434  GUCY1A3  5'  GCCTGGAACAGACCCAGGC   64228        A_  G_
                                GCCTGGG  TG  CCAGGC
                                |||||||  ||  ||||||
                                CGGACCC  AC  GGTCCG
                                    AG  AA
GAM1434  IL1RL1LG 3'  GCCCGGCCAAAGTCTAGGCA  23408        A__    A
                                TGCCTGGG   TGGCC GGC
                                ||||||||   ||||| |||
                                ACGGATCT   ACCGG CCG
                                    GAA    C
GAM1434  IL2RB    3'  CCTGGGAGCCCTCAGGCA    7936         AT   ___
                                TGCCTGGG  GGC   CAGG
                                ||||||||  |||   ||||
                                ACGGACTC  CCG   GTCC
                                    __   AGG
GAM1434  LTB4R    3'  GCCTGGCTCCCACAGGCA    7466        _  AT
                                TGCCTG GG  GGCCAGGC
                                ||||||  ||  ||||||||
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                                ACGGAC CC  TCGGTCCG
                                   A  C_
GAM1434  MATK     5'  GCCTGGCCTGTGGCAGGC    11464      GG  _
                                GCCTG  AT GGCCAGGC
                                |||||  || ||||||||
                                CGGAC  TG CCGGTCCG
                                   GG  T
GAM1434  NFIL3    5'  CGCCTGACGGATTTATCCCAG  19389        C_____    ___
                                CTGGGATGG    CAGGC  G
                                |||||||||    |||||  |
                                GACCCTATT    GTCCG  C
                                     TAGGCA   __
GAM1434  NGFR     3'  GCCTGTCCCTCTCAGGCA    11798        T  C
                                TGCCTGGGA GG CAGGC
                                ||||||||| || |||||
                                ACGGACTCT CC GTCCG
                                     C  T
GAM1434  PBP      5'  GCCTGGCCTACCGCGGCA    11939     _  GAT
                                TGCC TGG   GGCCAGGC
                                |||| |||   ||||||||
                                ACGG GCC   CCGGTCCG
                                  C   AT_
GAM1434  PC       3'  GCCTGGCCATCCCCAAGC    8089     CT_
                                GC   GGGATGGCCAGGC
                                ||   ||||||||||||
                                CG   CCCTACCGGTCCG
                                 AAC
GAM1434  PDYN     3'  GCTCTCTCATTCCCAGGCA   44588        _  CCA
                                TGCCTGGGA TGG   GGC
                                ||||||||| |||   |||
                                ACGGACCCT ACT   TCG
                                     T   CTC
GAM1434  PLXNA2   3'  CCTGGAATTATCCCGGCA    48002     T     __
                                TGCC GGGATGG  CCAGG
                                |||| |||||||  |||||
                                ACGG CCCTATT  GGTCC
                                  _     AA
GAM1434  PTPN6    3'  GCCCAGCCAGGCCCCAGGCA  55433       A__   CA
                                TGCCTGGG   TGGC  GGC
                                ||||||||   ||||  |||
                                ACGGACCC   ACCG  CCG
                                    CGG   AC
GAM1434  PTPN6    3'  GCCCAGCCAGGCCCCAGGCA  55434       A__   CA
                                TGCCTGGG   TGGC  GGC
                                ||||||||   ||||  |||
                                ACGGACCC   ACCG  CCG
                                    CGG   AC
GAM1434  RALBP1   3'  GCCTGGCTTGGCCCCAGGCA  23276       AT__
                                TGCCTGGG    GGCCAGGC
                                ||||||||    ||||||||
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                                ACGGACCC   TCGGTCCG
                                    CGGT
GAM1434 RBP1    3' GTCCAGCCACCCCTAGGCA   12793       A_   CA
                                TGCCTGGG TGGC GGC
                                |||||||| |||| |||
                                ACGGATCC ACCG CTG
                                    CC   AC
GAM1434 RFNG    3' GCCTGGCTCTGTCCCAGGC   89561        __
                                GCCTGGGAT GGCCAGGC
                                ||||||||| ||||||||
                                CGGACCCTG TCGGTCCG
                                     TC
GAM1434 SIRT7   3' GCCTGGCCATCGAGGACA    33737   _  G G
                                TG CCT G ATGGCCAGGC
                                || ||| | ||||||||||
                                AC GGA C TACCGGTCCG
                                 A  G _
GAM1434 SLC12A7 3' GCCCAGAGCGTGTCCCAGACA 22741   C      _ CA__
                                TG CTGGGATG GC   GGC
                                || |||||||| ||   |||
                                AC GACCCTGT CG   CCG
                                 A       G AGAC
GAM1434 STXBP1  3' GCCCTTCTGTCCCCAGGCA   13477       _   CCA
                                TGCCTGGG ATGG  GGC
                                |||||||| ||||  |||
                                ACGGACCC TGTC  CCG
                                    C   TTC
GAM1434 TCTA    3' GCCTGCTCCCTCACCCAGGCA 42499       AT_ C__
                                TGCCTGGG  GG  CAGGC
                                ||||||||  ||  |||||
                                ACGGACCC  CC  GTCCG
                                    ACT CTC
GAM1434 TNFAIP2 3' GCCCTTCGATCTCAGGCA    21922       _ CCA
                                TGCCTGGGAT GG  GGC
                                |||||||||| ||  |||
                                ACGGACTCTA CT  CCG
                                     G TC_
GAM1434 TRPM2   3' GCCTGGCCAGGACTCAGGC   13866      A__
                                GCCTGGG  TGGCCAGGC
                                |||||||  |||||||||
                                CGGACTC  ACCGGTCCG
                                   AGG
GAM1434 WBSCR1  3' GCCTGGTGAGTCCCCGGGCA  42482       _ G_
                                TGCCTGGG AT GCCAGGC
                                |||||||| ||  |||||||
                                ACGGGCCC TG  TGGTCCG
                                    C  AG
GAM1434 ACAS2L  3' CCTGGACATGGTCCCGGGCA  68645       GG___
                                TGCCTGGGAT   CCAGG
                                ||||||||||   |||||
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                                ACGGGCCCTG    GGTCC
                                      GTACA
GAM1434  AF9Q34   3'  GCCCCGGTCCCCCAGAGCA   51717    _    AT   A_
                                TGC CTGGG  GGCC  GGC
                                ||| |||||  ||||  |||
                                ACG GACCC  CTGG  CCG
                                  A    C_   CC
GAM1434  ASTN2    3'  GCTGTCAATCCCGAGGCA    73561      _    _  CA
                                TGCCT GGGAT GGC  GGC
                                ||||| ||||| |||  |||
                                ACGGA CCCTA CTG  TCG
                                   G    A  __
GAM1434  CCR1     3'  GCCTGGCTCTCCCAGCCA    8929     C     T
                                TG CTGGGA GGCCAGGC
                                || |||||| ||||||||
                                AC GACCCT TCGGTCCG
                                 C     C
GAM1434  CETN2    3'  CCTGTGTTGCCACAAGCA    16354     C  _  A   _
                                TGC TG GG TGGC CAGG
                                ||| || || |||| ||||
                                ACG AC CC GTTG GTCC
                                  A  A  _   T
GAM1434  DAPK3    3'  GCCTGTGGACGCCTAGGCA   9047         A  GC__
                                TGCCTGGG TG   CAGGC
                                |||||||| ||   |||||
                                ACGGATCC GC   GTCCG
                                     _ AGGT
GAM1434  DKFZP434C131 3'  GCCTACAGTTTCCTCAGGCA  69639        AT   C__
                                TGCCTGGG  GGC   AGGC
                                ||||||||  |||   ||||
                                ACGGACTC  TTG   TCCG
                                     CT   ACA
GAM1434  DKFZP434F0318 3'  GCCTGGCCAGATGCTAGCA   48761     C   GA__
                                TGC TGG   TGGCCAGGC
                                ||| |||   |||||||||
                                ACG ATC   ACCGGTCCG
                                  _  GTAG
GAM1434  DKFZp434I1117 5'  GCCTGGCTCCCTCCCAGGC   62846        T__
                                GCCTGGGA  GGCCAGGC
                                ||||||||  ||||||||
                                CGGACCCT  TCGGTCCG
                                     CCC
GAM1434  DKFZp547I224 5'  GCCCGCCATTGCCCAGGC    39957        __    CA
                                GCCTGGG  ATGGC  GGC
                                |||||||  |||||  |||
                                CGGACCC  TACCG  CCG
                                     GT    C_
GAM1434  DKFZP564J157 3'  GCCTGGCCATCTTGTTGC    38055    CT_
                                GC   GGGATGGCCAGGC
                                ||   ||||||||||||
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                                CG  TTCTACCGGTCCG
                                 TTG
GAM1434 DOCK3    3' GCCCAGCCAGGCTTCCAGGC  67096       ___   CA
                                GCCTGGGA  TGGC  GGC
                                ||||||||  ||||  |||
                                CGGACCTT  ACCG  CCG
                                    CGG   AC
GAM1434 DXS1357E 3' GCCTGGCCAGGCCTGGCA   20434     T  GA
                                TGCC GG  TGGCCAGGC
                                ||||  ||  |||||||||
                                ACGG CC  ACCGGTCCG
                                  T  GG
GAM1434 FEM-2    3' GCCTAGCCTCGTCCCAAGC   28317   C    __  C
                                GC TGGGAT  GGC AGGC
                                ||  ||||||  ||| ||||
                                CG ACCCTG  CCG TCCG
                                 A     CT  A
GAM1434 FEM-2    3' GCCTGGCTGGATCCCAGGCA  28318        __
                                TGCCTGGGAT  GGCCAGGC
                                ||||||||||  ||||||||
                                ACGGACCCTA  TCGGTCCG
                                      GG
GAM1434 FLJ10044 3' GCCTGGCCCTCCCCAGGC   36242       AT_
                                GCCTGGG   GGCCAGGC
                                |||||||   ||||||||
                                CGGACCC   CCGGTCCG
                                    CTC
GAM1434 FLJ11186 5' GCCTGGCCGCCGCGGGCA   37728      _ A
                                TGCCTG GG TGGCCAGGC
                                ||||||  ||  |||||||||
                                ACGGGC CC GCCGGTCCG
                                   G  _
GAM1434 FLJ12649 3' GCCTCCTCATCTCAAGCA   45093    C      CC
                                TGC TGGGATGG  AGGC
                                |||  ||||||||  ||||
                                ACG ACTCTACT  TCCG
                                  A       CC
GAM1434 FLJ12691 3' GCCTGCAACCACCTCAGACA  45003   C    A  C__
                                TG CTGGG TGG   CAGGC
                                ||  |||||  |||   |||||
                                AC GACTC ACC   GTCCG
                                 A    C   AAC
GAM1434 FLJ12770 3' GCCTGGCCTTCTAGAGCA   50679    _    T
                                TGC CTGGGA GGCCAGGC
                                |||  ||||||  ||||||||
                                ACG GATCTT CCGGTCCG
                                  A    _
GAM1434 FLJ14126 3' CCTGTGCATATCCCAGGTA  46276        _ _
                                TGCCTGGGATG GC CAGG
                                ||||||||||  ||  ||||
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                                ATGGACCCTAT CG GTCC
                                      A  T
GAM1434  FLJ14397  3'  GCCTGGCTTGCCCTCAGGCA   52330        AT__
                                TGCCTGGG    GGCCAGGC
                                ||||||||    ||||||||
                                ACGGACTC    TCGGTCCG
                                    CCGT
GAM1434  FLJ14490  3'  GCCTGGGCTGGGCTCAGGCA   52444        A_    _
                                TGCCTGGG  TGGCC AGGC
                                ||||||||  ||||| ||||
                                ACGGACTC  GTCGG TCCG
                                    GG    G
GAM1434  FLJ20254  3'  GCCTGAGTTCTCTCCTAGGCA  35298        T__   _
                                TGCCTGGGA   GGC CAGGC
                                |||||||||   ||| |||||
                                ACGGATCCT   TTG GTCCG
                                     CTC   A
GAM1434  FLJ22690  3'  CCTTGTTATTCTCAGGCA    45573        _     C
                                TGCCTG GGATGGC AGG
                                |||||| ||||||| |||
                                ACGGAC CTTATTG TCC
                                   T      T
GAM1434  FLJ23056  3'  CCTGTGGGCACCCAGGCA    45022        A  G  __
                                TGCCTGGG TG CCA  GG
                                |||||||| || |||  ||
                                ACGGACCC AC GGT  CC
                                    _  G   GT
GAM1434  FLJ23185  3'  GCCTGGCCGTGTGGAGCA    47517     _  GGG
                                TGC CT   ATGGCCAGGC
                                ||| ||   ||||||||||
                                ACG GG   TGCCGGTCCG
                                  A  TG_
GAM1434  FLJ23360  3'  GCCTGGCCACATGGTGCA    43832     _   GGA
                                TGC CTG   TGGCCAGGC
                                ||| |||   |||||||||
                                ACG GGT   ACCGGTCCG
                                  T   AC_
GAM1434  FLJ32786  3'  CCTGGCCATGGGTCCAGC    58964    C    ___
                                GC TGGG   ATGGCCAGG
                                || ||||   |||||||||
                                CG ACCT   TACCGGTCC
                                  _    GGG
GAM1434  FOXH1     5'  GCCTGGCCACCCAAAGGC    15379     __   A
                                GCCT  GGG TGGCCAGGC
                                ||||  ||| |||||||||
                                CGGA  CCC ACCGGTCCG
                                  AA  _
GAM1434  GIT2      3'  GCCTGGCTTCCCCGGACA    29412    C    AT
                                TG CTGGG  GGCCAGGC
                                || |||||  ||||||||
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                                AC GGCCC  TCGGTCCG
                                 A    CT
GAM1434  HEY2     3'  GCCTGCAGGCCCCCAGGCA   25322        AT   ___
                                TGCCTGGG  GGCC   AGGC
                                ||||||||  ||||   ||||
                                ACGGACCC  CCGG   TCCG
                                     __    ACG
GAM1434  HPCAL4   3'  CCTGGCCACTGTTTAGGCA   33206        A__
                                TGCCTGGG   TGGCCAGG
                                ||||||||   ||||||||
                                ACGGATTT   ACCGGTCC
                                     GTC
GAM1434  HRD1     3'  GCCCAGCCGCACTCCAGGCA   70150        A__   CA
                                TGCCTGGG   TGGC  GGC
                                ||||||||   ||||  |||
                                ACGGACCT   GCCG  CCG
                                     CAC    AC
GAM1434  IGSF9    3'  GCCCCTTTGGTGCCCAGGCA   40812        ATG   ____
                                TGCCTGGG   GCCA   GGC
                                ||||||||   ||||   |||
                                ACGGACCC   TGGT   CCG
                                     G__    TTCC
GAM1434  KIAA0150 3'  GCCTGGCCATCATCCGGC    71881     T  _
                                GCC GG GATGGCCAGGC
                                ||| || ||||||||||
                                CGG CT CTACCGGTCCG
                                  C  A
GAM1434  KIAA0210 3'  CCTGGCCATCCCTGGGCA    29155      _
                                TGCCT GGGATGGCCAGG
                                ||||| ||||||||||||
                                ACGGG CCCTACCGGTCC
                                   T
GAM1434  KIAA0227 3'  CGCCTGACCGGGGACTTCCAGG 61346        _____  C    ___
              CA                  TGCCTGGGA    TGG CAGGC   G
                                |||||||||    ||| |||||  |
                                ACGGACCTT    GCC GTCCG   C
                                     CAGGG   A    __
GAM1434  KIAA0350 3'  GCCAGCTGTCCCGGCA      61829      T       CA
                                TGCC GGGATGGC  GGC
                                |||| ||||||||  |||
                                ACGG CCCTGTCG  CCG
                                  _       A_
GAM1434  KIAA0415 3'  GCCTTTTGCTCCCAGGCA    94164        TG  C__
                                TGCCTGGGA  GC   AGGC
                                |||||||||  ||   ||||
                                ACGGACCCT  CG   TCCG
                                     __ TTT
GAM1434  KIAA0939 3'  GCCTGGCCCCCTCAGCCA    62717    C    AT
                                TG CTGGG  GGCCAGGC
                                || |||||  ||||||||
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                                AC GACTC  CCGGTCCG
                                 C    CC
GAM1434 KIAA1145 3' CCTTCTCATACCCAGGCA   66236       _   CC
                                TGCCTGGG ATGG  AGG
                                |||||||| ||||  |||
                                ACGGACCC TACT  TCC
                                    A   CT
GAM1434 KIAA1169 3' GCCTGGCCCCACCCAGCA   35882    C   AT_
                                TGC TGGG  GGCCAGGC
                                ||| ||||  ||||||||
                                ACG ACCC  CCGGTCCG
                                  _   ACC
GAM1434 KIAA1185 3' GCCTGGCCCACCCCAGCA   63287    C   AT_
                                TGC TGGG  GGCCAGGC
                                ||| ||||  ||||||||
                                ACG ACCC  CCGGTCCG
                                  _   CAC
GAM1434 KIAA1210 3' GCCTGGCTGTAGCGAGCA   98074    C  GG
                                TGC TG  ATGGCCAGGC
                                ||| ||  ||||||||||
                                ACG GC  TGTCGGTCCG
                                  A  GA
GAM1434 KIAA1344 5' GCCCGCAGGTCCCGGGCA   72867        G_  CA
                                TGCCTGGGAT  GC  GGC
                                ||||||||||  ||  |||
                                ACGGGCCCTG  CG  CCG
                                     GA  C_
GAM1434 KIAA1364 3' GCCTAGTCCGTCCCCCAGGCA 64352     __     _ C
                                TGCCT  GGGATGG C AGGC
                                |||||  ||||||| | ||||
                                ACGGA  CCCTGCC G TCCG
                                   CC      T A
GAM1434 MED8    5' CCTGGCCATCTGTCCTGGACA  54626   _ T ___
                                TG CC GG  GATGGCCAGG
                                || || ||  ||||||||||
                                AC GG CC  CTACCGGTCC
                                 A  T  TGT
GAM1434 NR6A1   5' CCCGGCGCGGACCCTAGGCA  9444      _  A_ _  A
                                TGCCT GGG  TG GCC GG
                                ||||| |||  || ||| ||
                                ACGGA CCC  GC CGG CC
                                   T   AG  G   C
GAM1434 NR6A1   5' CCCGGCGCGGACCCTAGGCA  9445      _  A_ _  A
                                TGCCT GGG  TG GCC GG
                                ||||| |||  || ||| ||
                                ACGGA CCC  GC CGG CC
                                   T   AG  G   C
GAM1434 NTKL    3' GCCCGGCCGGCCCAGCCA   40720   C   A   A
                                TG CTGGG TGGCC GGC
                                || ||||| ||||| |||
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                                AC GACCC GCCGG CCG
                                 C    G    C
GAM1434  OS4     3'  GCCTTTGGGTACTCCAGGCA  20391       GA  G  __
                                TGCCTGG  TG CCA  GGC
                                |||||||  || |||  |||
                                ACGGACC  AT GGT  CCG
                                    TC  G   TT
GAM1434  P2RXL1  3'  CCTCCCTATCCCCCAGGCA   19558      __     CC
                                TGCCT  GGGATGG  AGG
                                |||||  |||||||  |||
                                ACGGA  CCCTATC  TCC
                                   CC      CC
GAM1434  PALM    3'  GCCCCCCAATCTCAGGCA    11966         _  CCA
                                TGCCTGGGAT GG   GGC
                                ||||||||||  ||   |||
                                ACGGACTCTA CC   CCG
                                      A  CC_
GAM1434  PEPP3   3'  GCCTATCCCCCTATCCCAGGCA 30709          CC____
                                TGCCTGGGATGG     AGGC
                                ||||||||||||     ||||
                                ACGGACCCTATC     TCCG
                                      CCCCTA
GAM1434  PIPPIN  3'  GCCATTCACTCCCAGGCA    80509        _   CCA
                                TGCCTGGGA TGG   GGC
                                |||||||||  |||   |||
                                ACGGACCCT ACT   CCG
                                      C   TA_
GAM1434  POLR2D  3'  GCCTGTGTACTTCCCAGGC   17842       TG_  _
                                GCCTGGGA   GC CAGGC
                                ||||||||   || |||||
                                CGGACCCT   TG GTCCG
                                     TCA  T
GAM1434  PPIE    3'  GCCTGGACTATTCCCAGGCA  21474        _   _
                                TGCCTGGGA TGG CCAGGC
                                |||||||||  ||| ||||||
                                ACGGACCCT ATC GGTCCG
                                      T   A
GAM1434  PPP1R16B 3'  GCCCAGCCCATCTCAGCCA   62038    C       _ CA
                                TG CTGGGATGG C  GGC
                                ||  |||||||| |  |||
                                AC GACTCTACC G  CCG
                                  C        C AC
GAM1434  PRO0641  5'  GCCCAACTGTCTCAGGTA    27065          CCA
                                TGCCTGGGATGG   GGC
                                ||||||||||||   |||
                                ATGGACTCTGTC   CCG
                                      AAC
GAM1434  RHOBTB3  5'  GCCCGGCGATGTTCCCGGGCA  30428         ___ G   A
                                TGCCTGGGA   T GCC GGC
                                |||||||||   | ||| |||
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                                ACGGGCCCT  A CGG CCG
                                     TGT G  C
GAM1434 SEF      3' GCCATTTCATCCTAGGCA   69996          CCA
                                TGCCTGGGATGG  GGC
                                ||||||||||||  |||
                                ACGGATCCTACT  CCG
                                    TTA
GAM1434 SMARCF1  5' GCCCCCCTCATTCCCAGGCA  21190        _  CCA_
                                TGCCTGGGA TGG   GGC
                                ||||||||| |||   |||
                                ACGGACCCT ACT   CCG
                                     T  CCCC
GAM1434 SMCR5    3' GCCTCGATGTTCCAGGCA   59249         GCC
                                TGCCTGGGATG  AGGC
                                ||||||||||  ||||
                                ACGGACCTTGT  TCCG
                                    AGC
GAM1434 TP53TG3  3' CCAGGCTGCTTCCCAGGC   31728        __   A
                                GCCTGGGA  TGGCC GG
                                ||||||||  ||||| ||
                                CGGACCCT  GTCGG CC
                                     TC   A
GAM1434 LOC115708 3' GCCTGGGTTTCTGCCCAGGCA  73916        AT__  _
                                TGCCTGGG   GGCC AGGC
                                ||||||||   |||| ||||
                                ACGGACCC   TTGG TCCG
                                     GTCT   G
GAM1434 LOC128209 3' GTCTGACCATCTCAAGCA   75236    C      C
                                TGC TGGGATGG CAGGC
                                ||| |||||||| |||||
                                ACG ACTCTACC GTCTG
                                  A       A
GAM1434 LOC131870 3' GCCTGGTAACCCCCAGGCA  75509        ATG_
                                TGCCTGGG   GCCAGGC
                                ||||||||   |||||||
                                ACGGACCC   TGGTCCG
                                     CCAA
GAM1434 LOC139221 3' GCCTGGCCACTCTAGACA   76329   C   GA
                                TG CTGG  TGGCCAGGC
                                || ||||  |||||||||
                                AC GATC  ACCGGTCCG
                                 A   TC
GAM1434 LOC139941 5' GCCTCTAGCTTCCCAGGC   75910        T  C__
                                GCCTGGGA GGC  AGGC
                                |||||||| |||  ||||
                                CGGACCCT TCG  TCCG
                                     _  ATC
GAM1434 LOC144308 3' GCCTGAGGCCTCCTAGCA   83981    C   T   __
                                TGC TGGGA GGCC  AGGC
                                ||| ||||| ||||  ||||
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                                ACG ATCCT CCGG  TCCG
                                  _   _   AG
GAM1434  LOC144583 3'  GTCTGACCATCTCAAGCA   77420    C      C
                                TGC TGGGATGG CAGGC
                                ||| |||||||| |||||
                                ACG ACTCTACC GTCTG
                                  A       A
GAM1434  LOC145748 3'  GCCTTGTGTCCCCAGGCA   84473       AT  _ _
                                TGCCTGGG  GGC CA GGC
                                ||||||||  ||| || |||
                                ACGGACCC  CTG GT CCG
                                     __   T  T
GAM1434  LOC146728 5'  CCTGGGGCCATCCAGCCA   84764    C   G    __
                                TG CTGG ATGGCC  AGG
                                || |||| ||||||  |||
                                AC GACC TACCGG  TCC
                                 C   _     GG
GAM1434  LOC146733 3'  GCCTAGGGCAGTCCAGGCA   84784       GA  G  _
                                TGCCTGG  TG CC AGGC
                                |||||||  || || ||||
                                ACGGACC  AC GG TCCG
                                    TG  G  A
GAM1434  LOC148918 5'  CCTCCTAGATCCTCAGGCA   79822       _   ___  CC
                                TGCCTG GGAT   GG  AGG
                                |||||| ||||   ||  |||
                                ACGGAC CCTA   CC  TCC
                                   T   GAT  __
GAM1434  LOC149478 5'  GCCTGGCCAGGCCTCCCAGGC  80171         ____
                                GCCTGGGA   TGGCCAGGC
                                ||||||||   |||||||||
                                CGGACCCT   ACCGGTCCG
                                    CCGG
GAM1434  LOC150150 5'  GCCTGGTGCTGTCCCAGGC   86012          __
                                GCCTGGGATGGC  CAGGC
                                ||||||||||||  |||||
                                CGGACCCTGTCG  GTCCG
                                       TG
GAM1434  LOC150998 3'  GCCTGGCCGGCTGGAGGC   86360     G_  A
                                GCCT  GG TGGCCAGGC
                                ||||  || |||||||||
                                CGGA  TC GCCGGTCCG
                                  GG  G
GAM1434  LOC151178 3'  CCTGCGTCAGCTCAGGCA   80956       A   _
                                TGCCTGGG TGGC CAGG
                                |||||||| |||| ||||
                                ACGGACTC ACTG GTCC
                                     G   C
GAM1434  LOC151438 5'  GCCTGGGCTATCCCTGGCA   86558     T       _
                                TGCC GGGATGGCC AGGC
                                |||| |||||||| ||||
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                                ACGG CCCTATCGG TCCG
                                  T       G
GAM1434  LOC152195 5'  GCCTGGTAACCCCCAGGCA   86749        ATG_
                                TGCCTGGG   GCCAGGC
                                ||||||||   |||||||
                                ACGGACCC   TGGTCCG
                                    CCAA
GAM1434  LOC153196 3'  CGCCTGACCATCTTCCTCCCAG 87167        _______  C    ___
             GC                   GCCTGGGA    TGG CAGGC  G
                                  ||||||||    ||| |||||  |
                                  CGGACCCT    ACC GTCCG  C
                                      CCTTCT  A   __
GAM1434  LOC154442 3'  GCCCAGATTCACTCCCAGGCA  87423         _  CCA__
                                TGCCTGGGA TGG    GGC
                                ||||||||| |||    |||
                                ACGGACCCT ACT    CCG
                                     C  TAGAC
GAM1434  LOC158158 3'  GCCCGCCATTGCCCAGGC    82621        __   CA
                                GCCTGGG  ATGGC  GGC
                                |||||||  |||||  |||
                                CGGACCC  TACCG  CCG
                                    GT   C_
GAM1434  LOC158235 5'  CCTGCTATGCGCCAGGCA    88003        G__   C
                                TGCCTGG  ATGGC AGG
                                |||||||  ||||| |||
                                ACGGACC  TATCG TCC
                                    GCG   _
GAM1434  LOC158308 3'  CGCCTGGCCCCAGTGTGCCCAG 88066        AT_______      ___
             GCA                  TGCCTGGG      GGCCAGGC  G
                                  ||||||||      ||||||||  |
                                  ACGGACCC      CCGGTCCG  C
                                      GTGTGACC      __
GAM1434  LOC158377 3'  GCCTGGCTGGTCACAGGC    88133      _ GA
                                GCCTG G  TGGCCAGGC
                                ||||| |  |||||||||
                                CGGAC C  GTCGGTCCG
                                   A TG
GAM1434  LOC159228 5'  GCAGGCCACCCTCAGGCA    88427       _ A    AG
                                TGCCTG GG TGGCC  GC
                                |||||| || |||||  ||
                                ACGGAC CC ACCGG  CG
                                    T  C    A_
GAM1434  LOC162333 5'  GCCTGGCTGTCCCCAGGCA   88496        _
                                TGCCTGGG ATGGCCAGGC
                                |||||||| ||||||||||
                                ACGGACCC TGTCGGTCCG
                                     C
GAM1434  LOC166867 5'  GCCCAGGCCGTCCCCAGG    83554       _    A_
                                CCTGGG ATGGCC  GGC
                                |||||| ||||||  |||
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                                GGACCC TGCCGG  CCG
                                   C     AC
GAM1434  LOC197336 3'  GCCTGGTCATGCCAGGCA    59922       G
                                TGCCTGG ATGGCCAGGC
                                ||||||| ||||||||||
                                ACGGACC TACTGGTCCG
                                    G
GAM1434  LOC200301 3'  GCCCAGCTCTCTGTCCCGGGCA 90141         ____  CA
                                TGCCTGGGAT   GGC  GGC
                                ||||||||||   |||  |||
                                ACGGGCCCTG   TCG  CCG
                                      TCTC   AC
GAM1434  LOC200844 5'  GCCCGGAGTCCGTCCAGGCA  90321       G   ___ A
                                TGCCTGG ATGG   CC GGC
                                ||||||| ||||   || |||
                                ACGGACC TGCC   GG CCG
                                   _   TGA  C
GAM1434  LOC202775 3'  CCGGGTCACACCCAGGTA    91963       A_    A
                                TGCCTGGG  TGGCC GG
                                ||||||||  ||||| ||
                                ATGGACCC  ACTGG CC
                                     AC    G
GAM1434  LOC220595 5'  GCCTGGTCTCCACAGGCA    92777       _  T
                                TGCCTG GGA GGCCAGGC
                                |||||| ||| ||||||||
                                ACGGAC CCT CTGGTCCG
                                   A  _
GAM1434  LOC221399 5'  GCCTGGCTAGGCAGAGCA    95486    _  GGA
                                TGC CTG   TGGCCAGGC
                                ||| |||   |||||||||
                                ACG GAC   ATCGGTCCG
                                  A  GG_
GAM1434  LOC221479 3'  GCCCTTTGGTTCCCGAGCA   93844    C    TG   ___
                                TGC TGGGA  GCCA   GGC
                                ||| |||||  ||||   |||
                                ACG GCCCT  TGGT   CCG
                                  A    __    TTC
GAM1434  LOC221496 5'  GCCCGGCGCAACTCAGGC    93640       A  _  A
                                GCCTGGG TG GCC GGC
                                ||||||| || ||| |||
                                CGGACTC AC CGG CCG
                                    A  G   C
GAM1434  LOC253792 5'  GCCTGTGTGTCCCGGGCA    99024         GC
                                TGCCTGGGATG  CAGGC
                                ||||||||||  |||||
                                ACGGGCCCTGT  GTCCG
                                      GT
GAM1434  LOC254778 5'  GCCTCCAGTTCCCAGGCA    97832        __  CC
                                TGCCTGGGA  TGG  AGGC
                                |||||||||  |||  ||||
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                                ACGGACCCT  ACC  TCCG
                                     TG  __
GAM1434  LOC255481 3'  CCTGGCCACTGAGACAGCA   96079    ___  G  A
                                TGC  CT GG TGGCCAGG
                                |||  || || ||||||||
                                ACG  GA TC ACCGGTCC
                                  ACA  G  _
GAM1434  LOC255714 5'  GCCTGGCTGTCACCCAGCCA  98197   C   __
                                TG CTGGG  ATGGCCAGGC
                                || |||||  ||||||||||
                                AC GACCC  TGTCGGTCCG
                                 C    AC
GAM1434  LOC255736 3'  GCCTGGCCATCTTGTTGC   97076   CT_
                                GC  GGGATGGCCAGGC
                                ||  ||||||||||||
                                CG  TTCTACCGGTCCG
                                 TTG
GAM1434  LOC256230 5'  GCCCGCGACAACCCGGGCA  99316       A  __  CA
                                TGCCTGGG TG  GC  GGC
                                |||||||| ||  ||  |||
                                ACGGGCCC AC  CG  CCG
                                     A  AG  C_
GAM1434  LOC256231 5'  GCCCGCGACAACCCGGGCA  99319       A  __  CA
                                TGCCTGGG TG  GC  GGC
                                |||||||| ||  ||  |||
                                ACGGGCCC AC  CG  CCG
                                     A  AG  C_
GAM1434  LOC257309 5'  CCTGGAGCTGTCCTGGCA   96286    T     __
                                TGCC GGGATGGC  CAGG
                                |||| ||||||||  ||||
                                ACGG TCCTGTCG  GTCC
                                  _      AG
GAM1434  LOC257486 3'  GCCTGGCTGTAGCGAGCA   69774    C  GG
                                TGC TG  ATGGCCAGGC
                                ||| ||  ||||||||||
                                ACG GC  TGTCGGTCCG
                                  A  GA
GAM1434  LOC51112  5'  GCCCGCGAGGTCCCAGGCA  32630       G__  CA
                                TGCCTGGGAT  GC  GGC
                                |||||||||  ||  |||
                                ACGGACCCTG  CG  CCG
                                     GAG  C_
GAM1434  LOC85414  5'  GCCTGGCTGATTCCTAGGCA  53551       __
                                TGCCTGGGA  TGGCCAGGC
                                |||||||||  |||||||||
                                ACGGATCCT  GTCGGTCCG
                                     TA
GAM1434  LOC91759  3'  GCCTGGCCAACTCACACA   67692   CC   A
                                TG  TGGG TGGCCAGGC
                                ||  |||| |||||||||
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                                AC  ACTC ACCGGTCCG
                                 AC    A
GAM1434  LOC92578  5'  GCCTGGCCATCCCCCAGC    70395    CT_
                                GC   GGGATGGCCAGGC
                                ||   |||||||||||||
                                CG   CCCTACCGGTCCG
                                 ACC
GAM1434  LOC93259  5'  GCCTGGCTTATTTCAGGC    72285      GG  _
                                GCCTG  ATG GCCAGGC
                                |||||  ||| |||||||
                                CGGAC  TAT CGGTCCG
                                   TT   T
GAM1435  CDH12     3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                      AA___   AC
GAM1435  GOCAP1    3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC         G
GAM1435  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT    98090       T    AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT     TTATTC
                                   _    GTCA_
GAM1435  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
              A                    TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM1435  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                      AGACG___
GAM1435  HMP19     3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
              TA                    TACA    TCC    GAAGAATAAG
                                ||||    |||    ||||||||||
                                ATGT    AGG    TTTCTTATTC
                                   AAA_   ATTG
GAM1435  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68742             _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                           G
GAM1435  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
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                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM1435 KIAA1877 3' CTTATTCTTCTGCCATGAGT  66748     CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM1435 KIAA1906 3' CTTATTCTTCTTGACTTTTGG 73571    CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM1435 OSBPL11  3' CTTAATTTCCCAAGAGTGGTG 43206       CCAA   AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                     AACC   A_
GAM1435 YME1L1   3' TCATTCTTGATGTGGTGTA   58438       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                     TA_    A
GAM1435 ZNF262   3' CTTATTTTGTTTGGGAGT    18723        A
                                ACTCCCAAG AGAATAAG
                                |||||||||  ||||||||
                                TGAGGGTTT TTTTATTC
                                     G
GAM1435 LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_    AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
                                ATGTGGTG   GGTTC   TGT
                                     CAA    GG__
GAM1436 APM1     3' CGGGGTTTCACCACATTCGTCA 17779       _ CA    AG
                                TGACGAATG GG  AAATT  TCG
                                |||||||||  ||  |||||  |||
                                ACTGCTTAC CC  TTTGG  GGC
                                     A  AC   __
GAM1436 OSF-2    3' ACTAATTTTGTACTCTCA    22391     C  ATGG
                                TGA GA   GCAAAATTAGT
                                |||  ||   ||||||||||
                                ACT CT   TGTTTTAATCA
                                  _  CA__
GAM1436 VAV3     3' ATTTGTTTTGCCCAGCCATCA  21475     CGAA       T
                                TGA   TGGGCAAAAT AGT
                                |||   |||||||||| |||
                                ACT   ACCCGTTTTG TTA
                                  ACCG       T
GAM1437 AKAP1    3' ACTATGGGTTCTCTTCGCAAA  14472      A  CTT      C
                                TTTGT GA   GGAACCCA AGT
                                |||||  ||   |||||||  |||
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                                AAACG CT   TCTTGGGT TCA
                                  _ TC_       A
GAM1437  AKAP1    3'  ACTATGGGTTCTCTTCGCAAA  58373      A  CTT       C
                                TTTGT GA   GGAACCCA AGT
                                ||||| ||   |||||||| |||
                                AAACG CT   TCTTGGGT TCA
                                  _ TC_       A
GAM1437  EGF      3'  ACTATAGGTTTTGGTTCCACAA 10488      A  C TG    CAC
                                TTGT GA T  GAACC   AGT
                                |||| || |  |||||   |||
                                AACA CT G  TTTGG   TCA
                                  C  T GT    ATA
GAM1437  EZH1     3'  GACTGTGGGTTCCAAATTAC   10551      AC
                                GTAG  TTGGAACCCACAGTC
                                ||||  ||||||||||||||
                                CATT  AACCTTGGGTGTCAG
                                  A_
GAM1437  STAC     3'  GACTGTGGAGTAATAGCCACAA 13427      AGA  TGGA  _
              A                  TTTGT   CT    AC CCACAGTC
                                |||||   ||    || ||||||||
                                AAACA   GA    TG GGTGTCAG
                                  CC_  TAA_  A
GAM1437  CCR1     3'  GACTGTGGGCTCCATTC     8927     CT    A
                                GA  TGGA CCCACAGTC
                                ||  |||| |||||||||
                                CT  ACCT GGGTGTCAG
                                 T_    C
GAM1437  FLJ10483 3'  GACTGTGGAAGAGATTACAAA  36652       A   GGAAC
                                TTTGTAG CTT     CCACAGTC
                                ||||||| |||     ||||||||
                                AAACATT GAG     GGTGTCAG
                                   A   AA___
GAM1437  KIAA1871 3'  ACTGTAAGAGTCTACAAA    61890         GGAACCC
                                TTTGTAGACTT      ACAGT
                                ||||||||||       |||||
                                AAACATCTGAG      TGTCA
                                      AA_____
GAM1437  LOC150821 3'  GGGTTCCACATCCACAAA    60944      A  CT
                                TTTGT GA  TGGAACCC
                                ||||| ||  ||||||||
                                AAACA CT  ACCTTGGG
                                  C  AC
GAM1437  LOC151057 3'  ACTGTGGGTACACCTATAAA   86379       ACT  GA
                                TTTGTAG   TG  ACCCACAGT
                                |||||||   ||  |||||||||
                                AAATATC   AC  TGGGTGTCA
                                   C__  A_
GAM1437  LOC157507 5'  ACTGTAAAAGTCTGCAAA    82377         GGAACCC
                                TTTGTAGACTT      ACAGT
                                ||||||||||       |||||
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                                AAACGTCTGAA      TGTCA
                                      AA_____
GAM1437  LOC203339 5'  GGATTCCCAGTCTACAAA    92214         T   C
                                TTTGTAGACT GGAA CC
                                |||||||||| |||| ||
                                AAACATCTGA CCTT GG
                                     C   A
GAM1437  LOC51030  3'  ACTGTAAATTAAACCAATCTAC 32695        C   AACCC___
           AAA                    TTTGTAGA TTGG       ACAGT
                                |||||||| ||||       |||||
                                AAACATCT AACC       TGTCA
                                   _   AAATTAAA
GAM1437  LOC90906  3'  GACTGTGGATCCCAAACTTTGC 64951       C_   AAC
           A                     TGTAGA  TTGG   CCACAGTC
                                ||||||  ||||   ||||||||
                                ACGTTT  AACC   GGTGTCAG
                                   CA   CTA
GAM1438  ADH1B    3'  ATGGGGGCTTTCCAAAG     73039     C   CTGCT
                                CTT TGGA    GCCCCCAT
                                ||| ||||    ||||||||
                                GAA ACCT    CGGGGGTA
                                  _   TT___
GAM1438  CAPN10   3'  ATGGAGGCCTCACACCCAGAGG 43868         AC_  CT   C
           GT                    ACCTTCTGG   TG  GCC CCAT
                                |||||||||   ||  ||| ||||
                                TGGGAGACC   AC  CGG GGTA
                                     CAC  TC   A
GAM1438  CAPN10   3'  ATGGAGGCCTCACACCCAGAGG 41445         AC_  CT   C
           GT                    ACCTTCTGG   TG  GCC CCAT
                                |||||||||   ||  ||| ||||
                                TGGGAGACC   AC  CGG GGTA
                                     CAC  TC   A
GAM1438  CAPN10   3'  ATGGAGGCCTCACACCCAGAGG 43857         AC_  CT   C
           GT                    ACCTTCTGG   TG  GCC CCAT
                                |||||||||   ||  ||| ||||
                                TGGGAGACC   AC  CGG GGTA
                                     CAC  TC   A
GAM1438  CAPN10   3'  ATGGAGGCCTCACACCCAGAGG 43859         AC_  CT   C
           GT                    ACCTTCTGG   TG  GCC CCAT
                                |||||||||   ||  ||| ||||
                                TGGGAGACC   AC  CGG GGTA
                                     CAC  TC   A
GAM1438  CAPN10   3'  ATGGAGGCCTCACACCCAGAGG 43862         AC_  CT   C
           GT                    ACCTTCTGG   TG  GCC CCAT
                                |||||||||   ||  ||| ||||
                                TGGGAGACC   AC  CGG GGTA
                                     CAC  TC   A
GAM1438  CAPN10   3'  ATGGAGGCCTCACACCCAGAGG 43865         AC_  CT   C
           GT                    ACCTTCTGG   TG  GCC CCAT
                                |||||||||   ||  ||| ||||
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                                TGGGAGACC  AC  CGG GGTA
                                     CAC  TC  A
GAM1438  CSNK1E   3'  ATGGAGACTGCTTCCAGAAGG  97355       CT  TGCCC
                                CCTTCTGGA  GC    CCAT
                                |||||||||  ||    ||||
                                GGAAGACCT  CG    GGTA
                                     T_  TCAGA
GAM1438  DTNBP1   5'  GGCAGCAGCAGCCCGAGG    50439     T  A     CC
                                CTTC GG CTGCTGC  CC
                                |||| || |||||||  ||
                                GGAG CC GACGACG  GG
                                  C  _      AC
GAM1438  IPP      3'  GGGCTATACAGTCCAGCAGG  20906     T      CT__
                                CCT CTGGACTG   GCCC
                                ||| ||||||||   ||||
                                GGA GACCTGAC   CGGG
                                  C       ATAT
GAM1438  LILRB4   3'  ATGGAGACTCAGGACCCCAGAA 23384       ACTG  CCC__
            GG                    CCTTCTGG   CTG    CCAT
                                |||||||||  |||    ||||
                                GGAAGACC   GAC    GGTA
                                     CCAG  TCAGA
GAM1438  MECP2    3'  ATGGAGGCAGTAGGACAAGGTG 18384      TC  GA      C
                                CACCT  TG  CTGCTGCC CCAT
                                |||||  ||  |||||||| ||||
                                GTGGA  AC  GATGACGG GGTA
                                  __  AG       A
GAM1438  MEL      3'  GGAAGCGAGGTCCCAGAAGG   19330        _  GC  CC
                                CCTTCTGG ACT  TGC  CC
                                |||||||| |||  |||  ||
                                GGAAGACC TGG  GCG  GG
                                     C  A_  AA
GAM1438  PPP2R2C  3'  ATGAGGACAGCTGCAGAGGTG  62417      T  GACT   C  C
                                CACCT CTG   GCTG CC CAT
                                ||||| |||   |||| || |||
                                GTGGA GAC   CGAC GG GTA
                                  _  GT__   A  A
GAM1438  RXRB     3'  ATGGGGAACTCCCCCAGAGGTG 42028      T   ACTGCTGC
                                CACCT CTGG       CCCCAT
                                ||||| ||||       ||||||
                                GTGGA GACC       GGGGTA
                                  _   CCCTCAA_
GAM1438  SP3      5'  ATGGGGGTATAAATCAAGAA   83381      G  CTGC
                                TTCT GA   TGCCCCCAT
                                |||| ||   |||||||||
                                AAGA CT   ATGGGGGTA
                                  A  AAAT
GAM1438  TCF1     3'  ATGAGGGCAGCAGCCAG     6782       A       C
                                CTGG CTGCTGCCC CAT
                                |||| ||||||||| |||
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                                GACC GACGACGGG GTA
                                  _       A
GAM1438  TRAF1    3'  GGCAAAGGGTCCAGAAGG    20176          GC_
                                CCTTCTGGACT   TGCC
                                ||||||||||   ||||
                                GGAAGACCTGG   ACGG
                                      GAA
GAM1438  WNT5A    3'  GGTACACATCCAGAAGGT    14124          C_  C
                                ACCTTCTGGA  TG TGCC
                                |||||||||  || ||||
                                TGGAAGACCT  AC ATGG
                                      AC  _
GAM1438  ATF3     3'  ATGGGAGGACTCCAGAAG    15730        CTGCTG  _
                                CTTCTGGA     CC CCCAT
                                ||||||||     || |||||
                                GAAGACCT     GG GGGTA
                                     CA_____  A
GAM1438  C20orf16 5'  GGAGCGGTTCCTAGAAGGTG  39241         _  _    G
                                CACCTTCT GGA CTGCT CC
                                |||||||| ||| ||||| ||
                                GTGGAAGA CCT GGCGA GG
                                     T  T    _
GAM1438  C21orf41 3'  ATGGAGCGTGAAACCCAGAAGG 57170         ACTGC_   CC
                                CCTTCTGG     TGC  CCAT
                                ||||||||     |||  ||||
                                GGAAGACC     GCG  GGTA
                                     CAAAGT   A_
GAM1438  FBX30    5'  GGAGGGTGTCCAGAAG      53747         TGCT   _
                                CTTCTGGAC    GCCC CC
                                |||||||||    |||| ||
                                GAAGACCTG    TGGG GG
                                     _____    A
GAM1438  FLJ10468 3'  GGGTAGGTCCAGAAGGTG    36633          TG
                                CACCTTCTGGAC  CTGCCC
                                ||||||||||||  ||||||
                                GTGGAAGACCTG  GATGGG
                                              __
GAM1438  FLJ14442 3'  GGGGGGAGTACAGAAGGT    52387         GAC   G
                                ACCTTCTG   TGCT CCCCC
                                ||||||||   |||| |||||
                                TGGAAGAC   ATGA GGGGG
                                     ___    G
GAM1438  FLJ20651 3'  GGGCACCTGCACCCCAGAAGGT 35922          AC  ___
            G                    CACCTTCTGG  TGC   TGCCC
                                 ||||||||||  |||   |||||
                                 GTGGAAGACC  ACG   ACGGG
                                       CC   TCC
GAM1438  FLJ21195 3'  CAGCAGGCCCAGAAGGTG    42701          A_
                                CACCTTCTGG  CTGCTG
                                ||||||||||  ||||||
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                                GTGGAAGACC  GACGAC
                                     CG
GAM1438  FLJ22169  3'  TGGGGGCTTCCAGAGG     44235       CTGCT
                                CTTCTGGA    GCCCCCA
                                ||||||||    |||||||
                                GGAGACCT    CGGGGGT
                                     T_____
GAM1438  FLJ30663  3'  ATGGAGGAAACAATCTAGAAG  79356       C  CTG  C
                                CTTCTGGA TG   CC CCAT
                                |||||||| ||   || ||||
                                GAAGATCT AC   GG GGTA
                                     A  AAA  A
GAM1438  GIT2      3'  ATGAAGGCGCACCAGAAGG   58286       AC   T   CC
                                CCTTCTGG  TGC GCC  CAT
                                ||||||||  ||| |||  |||
                                GGAAGACC  ACG CGG  GTA
                                     __  _  AA
GAM1438  H11       5'  GGCTTGCAGCCCAGAAGG    27636       A   T_
                                CCTTCTGG CTGC  GCC
                                |||||||| ||||  |||
                                GGAAGACC GACG  CGG
                                     C   TT
GAM1438  HM74      3'  GGGGATTAGCCCCAGAAGG   21202       ACT   C_
                                CCTTCTGG   GCTG  CCCC
                                ||||||||   ||||  ||||
                                GGAAGACC   CGAT  GGGG
                                     C__   TA
GAM1438  KIAA0280  3'  ATGAGGATGAGGCCCAGGAG  93289       ACT   GCC_ _
                                CTTCTGG   GCT   CC CAT
                                |||||||   |||   || |||
                                GAGGACC   CGG   GG GTA
                                    ___   AGTA  A
GAM1438  KIAA0547  3'  ATGGGGGCAAAAAGAAGAGTG  29588    _    GGACTGC
                                CAC CTTCT      TGCCCCCAT
                                ||| |||||      |||||||||
                                GTG GAAGA      ACGGGGGTA
                                  A    AAA____
GAM1438  KIAA0945  3'  ATGAAGGCCCTCCTCCCAGGAG 30898        ACTGCT_  CC
            GT                    ACCTTCTGG      GCC  CAT
                                |||||||||      |||  |||
                                TGGAGGACC      CGG  GTA
                                     CTCCTCC   AA
GAM1438  KIAA1364  3'  GGAGGGCAGCACAGAA      64353      GAC      _
                                TTCTG   TGCTGCCC CC
                                |||||   |||||||| ||
                                AAGAC   ACGACGGG GG
                                   ___      A
GAM1438  KIAA1505  5'  GGCTGTTGCACCCAGAGGTG   95848      T   AC   T  CC
                                CACCT CTGG  TGC GC  CC
                                ||||| ||||  ||| ||  ||
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                                GTGGA GACC  ACG TG  GG
                                  _   C_   T  TC
GAM1438  MGC10715  3'  GGGGACAACTCCAGAAGGT   44500        CTGC  C
                                ACCTTCTGGA   TG CCCC
                                ||||||||||   || ||||
                                TGGAAGACCT   AC GGGG
                                     CA__  A
GAM1438  RASSF2   3'  ATGGAGTGGAAGCCCAGAAGG  29090       A  G TG CC
                                CCTTCTGG CT C  C  CCAT
                                |||||||| || |  |  ||||
                                GGAAGACC GA G  G  GGTA
                                     C  A GT A_
GAM1438  RDH-E2   3'  GGGGCAGCAGTCTCAGGGGGTG 58071         _
                                CACCTTCTG GACTGCTGCCCC
                                ||||||||| ||||||||||||
                                GTGGGGGAC CTGACGACGGGG
                                     T
GAM1438  SNRK     3'  GGGCCTAGTACAGAAGGTG   35279        G   CT
                                CACCTTCTG ACTG  GCCC
                                ||||||||| ||||  ||||
                                GTGGAAGAC TGAT  CGGG
                                     A   C_
GAM1438  SRCAP    5'  GGGGTGTGGCCCGGAAGGTG  22846        ACT  TG _
                                CACCTTCTGG   GC  C CCCC
                                ||||||||||   ||  | ||||
                                GTGGAAGGCC   CG  G GGGG
                                     ____  GT T
GAM1438  LOC134265 3'  ATGGGTTAGAAATCCAGGAGG  75652        CTG   CC
                                CCTTCTGGA   CTG  CCCAT
                                |||||||||   |||  |||||
                                GGAGGACCT   GAT  GGGTA
                                     AAA   T_
GAM1438  LOC148293 3'  GCAGAGAGCAGAATGGTG    79529     _    GA  G
                                CACC TTCTG  CT CTGC
                                |||| |||||  || ||||
                                GTGG AAGAC  GA GACG
                                  T    GA  _
GAM1438  LOC150397 3'  ATGAAAGCCACAGATCCAGAAG 80653        _  CT  CCC
                                CTTCTGGA CTG  GC   CAT
                                |||||||| |||  ||   |||
                                GAAGACCT GAC  CG   GTA
                                     A   AC  AAA
GAM1438  LOC151657 5'  ATGAAAGCAGAGGACAGAAGGT 86653        GA  G    CCC
           G                     CACCTTCTG  CT CTGC   CAT
                                |||||||||  || ||||   |||
                                GTGGAAGAC  GA GACG   GTA
                                     AG  _    AAA
GAM1438  LOC153057 5'  ATGGGAACAGCTCTGGAAG   87097     TG  CT   CC
                                CTTC  GA  GCTG  CCCAT
                                ||||  ||  ||||  |||||
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                                GAAG  CT  CGAC  GGGTA
                                  GT  __   AA
GAM1438  LOC158263 5'  ATGGAAGAGTTGGTCCAGGA  82725        _ GCCC
                                TTCTGGACTG CT   CCAT
                                |||||||||| ||   ||||
                                AGGACCTGGT GA   GGTA
                                     T  GAA_
GAM1438  LOC204823 5'  TATGGAGACAGCAACCCAAAGA 91059      ____ AC   CCC   ___
           GAAGG                 CCTTCT   GG  TGCTG   CCAT   A
                                ||||||   ||  |||||  ||||  |
                                GGAAGA   CC  ACGAC   GGTA   T
                                   GAAA  CA    AGA   ___
GAM1438  LOC220021 3'  ATGGAAGCAGCAGTTCCTGAA  95017    T  _     CC
                                TTC GGA CTGCTGC  CCAT
                                ||| ||| |||||||  ||||
                                AAG CCT GACGACG  GGTA
                                  T   T      AA
GAM1438  LOC221474 5'  GGTGAGGTCCAAAGGTG     93999       C     GC
                                CACCTT TGGACT  TGCC
                                |||||| ||||||  ||||
                                GTGGAA ACCTGG  GTGG
                                   _     A_
GAM1438  LOC255294 5'  GGAAGTAGACAATCCAGAAG   96108        C  _   CC
                                CTTCTGGA TG CTGC  CC
                                |||||||| || ||||  ||
                                GAAGACCT AC GATG  GG
                                     A  A    AA
GAM1438  LOC257471 5'  ATGGGGGTATAAATCAAGAA   97387     G  CTGC
                                TTCT GA    TGCCCCCAT
                                |||| ||    |||||||||
                                AAGA CT    ATGGGGGTA
                                  A  AAAT
GAM1438  LOC92497  5'  GGCAGCAGTGACAAGGAG    70096      _ G_
                                CTTCT G  ACTGCTGCC
                                ||||| |  |||||||||
                                GAGGA C  TGACGACGG
                                   A AG
GAM1439  AP2B1    3'  GCTCTTCACATATTCCA     8893          A   AAT
                                TGGAATATG GAA   AGC
                                ||||||||| |||   |||
                                ACCTTATAC CTT   TCG
                                     A   C__
GAM1439  ATRX     3'  TTCTGCCATTTTTTATTTTCA  6673       TATG      A
                                TGGAA    AGAAAAT GCAGAA
                                |||||    ||||||| ||||||
                                ACTTT    TTTTTTA CGTCTT
                                   TA__      C
GAM1439  ATRX     3'  TTCTGCCATTTTTTATTTTCA  57080      TATG      A
                                TGGAA    AGAAAAT GCAGAA
                                |||||    ||||||| ||||||
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                                ACTTT    TTTTTTA CGTCTT
                                   TA__      C
GAM1439 BAI2     3'  TCTCTATTTTCACACTCCA    9915       ATA  A       C
                                TGGA   TG GAAAATAG AGA
                                ||||   || |||||||| |||
                                ACCT   AC CTTTTATC TCT
                                  C__  A       _
GAM1439 CLASP2   3'  CTGCTATTCTCTCCCA      65202     AATAT    A
                                TGG    GAGA AATAGCAG
                                |||    |||| ||||||||
                                ACC    CTCT TTATCGTC
                                  _____   C
GAM1439 CNR1     3'  TTCTGCCATTTCATGTCCA    32725      A      AAATA
                                TGGA TATGAGA    GCAGAA
                                |||| |||||||    ||||||
                                ACCT GTACTTT    CGTCTT
                                  _      AC___
GAM1439 INPP5B   3'  TTTCTACTCTCCCCATATTCCA 97260         A_  AAAT  C
                                TGGAATATG  GA    AG AGAAA
                                |||||||||  ||    || |||||
                                ACCTTATAC  CT    TC TCTTT
                                     CC  C___  A
GAM1439 MAB21L1  3'  TTCTGTTCAATTCCTAATATTC 19971        GA_   AAT
            CA                   TGGAATAT   GAA   AGCAGAA
                                |||||||   |||   |||||||
                                ACCTTATA   CTT   TTGTCTT
                                    ATC   AAC
GAM1439 PDE1A    3'  TTCTGCCATTTTTTTCCCTCCA 18461      ATAT       A
                                TGGA    GAGAAAAT GCAGAA
                                ||||    |||||||| ||||||
                                ACCT    TTTTTTTA CGTCTT
                                  CCC_       C
GAM1439 PXN      3'  TCTCTTCCTCATATTTCA     12675          AAAAT  C
                                TGGAATATGAG     AG AGA
                                ||||||||||     || |||
                                ACTTTATACTC     TC TCT
                                      CT___  _
GAM1439 RBBP9    3'  TTTCTGCTATTTTGCATCCCA  70706     AAT   AG
                                TGG   ATG  AAAATAGCAGAAA
                                |||   |||  |||||||||||||
                                ACC   TAC  TTTTATCGTCTTT
                                  C__   G_
GAM1439 RBM3     3'  TTTCTGCTGCCCTCATACC    71015    AA     AAAA
                                GG  TATGAG    TAGCAGAAA
                                ||  ||||||    |||||||||
                                CC  ATACTC    GTCGTCTTT
                                  __     CC__
GAM1439 STAT1    3'  CTGCTACTCTGTTCC       24612       T   AAAA
                                GGAATA GAG    TAGCAG
                                |||||| |||    ||||||
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                              CCTTGT CTC    ATCGTC
                                 _  ____
GAM1439  TMEM2    3'  TCTCTTATTCCTCACTTTCCA  26340      TA   AA    C
                              TGGAA  TGAG  AATAG AGA
                              |||||  ||||  ||||| |||
                              ACCTT  ACTC  TTATT TCT
                                 TC   C_    C
GAM1439  TPMT     3'  TCTGCCATCGATGTATTCTA   6319        GA_  AAATA
                              TGGAATAT   GA    GCAGA
                              ||||||||   ||    |||||
                              ATCTTATG   CT    CGTCT
                                   TAG  AC___
GAM1439  WIG1     3'  TTTCTGCCATTTTCTTTTGCA  96107    G  TAT      A
                              TG AA   GAGAAAAT GCAGAAA
                              || ||   |||||||| |||||||
                              AC TT   TTCTTTTA CGTCTTT
                               G  ___       C
GAM1439  ERF      3'  CTAGGTTTCTCATACCCCA   22438     AA       A_
                              TGG  TATGAGAAA  TAG
                              |||  |||||||||  |||
                              ACC  ATACTCTTT  ATC
                                CC        GG
GAM1439  FLJ10379 3'  TTATTTTCTCATTTCCA     36570      T
                              TGGAA ATGAGAAAATAG
                              ||||| ||||||||||||
                              ACCTT TACTCTTTTATT
                                 _
GAM1439  FLJ10989 3'  TTCTGCTATTCCGGAGCCCA  37510     AATA  A  AA
                              TGG    TG GA  ATAGCAGAA
                              |||    || ||  |||||||||
                              ACC    GC CT  TATCGTCTT
                                CGAG  _  __
GAM1439  FLJ13081 3'  TTATTTTCTCCTATCCCA    46171     A   T
                              TGG ATA GAGAAAATAG
                              ||| ||| ||||||||||
                              ACC TAT CTCTTTTATT
                                C   C
GAM1439  FLJ13385 3'  CTGCTATTTCGTTCC       46282      ATGA    A
                              GGAAT    GAAA TAGCAG
                              |||||    |||| ||||||
                              CCTTG    CTTT ATCGTC
                                 ____   _
GAM1439  FLJ20502 3'  TGTCTTTCTCATATTTCA    35718            ATA
                              TGGAATATGAGAAA   GCA
                              ||||||||||||||   |||
                              ACTTTATACTCTTT   TGT
                                       C__
GAM1439  FLJ20701 3'  TTCTTATTTTTCTCATTTCC   36028      T       TAGC
                              GGAA ATGAGAAAA    AGAA
                              |||| |||||||||    ||||
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                                CCTT TACTCTTTT   TCTT
                                  _       TAT_
GAM1439 GMFB     3' TCTGCTAGTTCATATTGCA  15942   G     GAAAA
                                TG AATATGA    TAGCAGA
                                || |||||||    |||||||
                                AC TTATACT    ATCGTCT
                                 G      TG___
GAM1439 HERC3    3' TCTACCATTTTCTCCTTCC  28237    TAT      AGC
                                GGAA  GAGAAAAT  AGA
                                ||||  ||||||||  |||
                                CCTT  CTCTTTTA  TCT
                                  C__      CCA
GAM1439 HNOEL-iso 3' TTTGCATCTTTCTCACTCC  39881    ATA     ATA
                                GGA  TGAGAAA  GCAGA
                                |||  |||||||  |||||
                                CCT  ACTCTTT  CGTTT
                                  C__     CTA
GAM1439 KIAA0237 3' CTCCTAATACCTCATATTCC  29219        AAAA  C
                                GGAATATGAG   TAG AG
                                ||||||||||   ||| ||
                                CCTTATACTC   ATC TC
                                     CATA  C
GAM1439 KIAA0547 3' TCTGCTATTCTGTTGCCA   29602    AAT  G  AA
                                TGG  AT AGA  ATAGCAGA
                                |||  || |||  ||||||||
                                ACC  TG TCT  TATCGTCT
                                  GT_ _  __
GAM1439 KIAA0759 3' TTTCTGCTATCTCCCATCTCC 67893    ATAT_   AAA
                                GGA   GAGA  TAGCAGAAA
                                |||   ||||  |||||||||
                                CCT   CTCT  ATCGTCTTT
                                  CTACC   ___
GAM1439 KIAA1046 3' TTCTGTTTCCCATATCTCA  30665   GA   A  AATA
                                TG  ATATG GAA   GCAGAA
                                ||  ||||| |||   ||||||
                                AC  TATAC CTT   TGTCTT
                                 TC    C  ____
GAM1439 KIAA1719 3' TCTGCTATCTTGGATTCC   68738     A   AAA
                                GGAAT TGAGA  TAGCAGA
                                ||||| |||||  |||||||
                                CCTTA GTTCT  ATCGTCT
                                   G   ___
GAM1439 KIAA1786 3' CTGGTTTTCTCCACTCCA   66632    ATAT     AG
                                TGGA   GAGAAAAT  CAG
                                ||||   ||||||||  |||
                                ACCT   CTCTTTTG  GTC
                                  CAC_      __
GAM1439 KLF12    3' TTTCTGCTAATTTCATGCTCCA 24366     A     AAA
                                TGGA TATGAGA  TAGCAGAAA
                                |||| |||||||  |||||||||
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                                ACCT GTACTTT   ATCGTCTTT
                                  C      A__
GAM1439  PFTK1    3'  TTGTACTTTTCTCATACACCA  25691     AA        TA
                                TGG  TATGAGAAAA  GCAG
                                |||  ||||||||||  ||||
                                ACC  ATACTCTTTT  TGTT
                                  AC         CA
GAM1439  TCEA3    3'  TCTGCTATTCCCTGTTC     89895     ATG  AA
                                GAAT   AG  AATAGCAGA
                                ||||   ||  |||||||||
                                CTTG   TC  TTATCGTCT
                                   ___ CC
GAM1439  USP15    3'  TCTGTTTTTCTCTACCCCA   21965     AA  T      TA
                                TGG  TA GAGAAAA  GCAGA
                                |||  || |||||||  |||||
                                ACC  AT CTCTTTT  TGTCT
                                  CC  _      __
GAM1439  LOC112476 5'  TCTGCTATTTCCATCCTCC   59789     AT   A    A
                                GGA  ATG GAAA TAGCAGA
                                |||  ||| |||| |||||||
                                CCT  TAC CTTT ATCGTCT
                                  CC   _    _
GAM1439  LOC126669 3'  TTCTGTATTCTCATTTCCA   75955      T      AATA
                                TGGAA ATGAGAA    GCAGAA
                                |||||| |||||||    ||||||
                                ACCTT TACTCTT    TGTCTT
                                   _      A___
GAM1439  LOC131544 3'  TTATTTTCTCTCATATCCA   75501      A      __
                                TGGA TATGAGA  AAATAG
                                |||| |||||||  ||||||
                                ACCT ATACTCT  TTTATT
                                   _      CT
GAM1439  LOC150368 3'  CTGCTATTTAGGCATTCTCCA  80515      AT   AGA
                                TGGA  ATG   AAATAGCAG
                                ||||  |||   |||||||||
                                ACCT  TAC   TTTATCGTC
                                  CT   GGA
GAM1439  LOC155072 3'  TTGTTTTCTCCCATGTTCCA   87675         __
                                TGGAATAT  GAGAAAATAG
                                ||||||||  ||||||||||
                                ACCTTGTA  CTCTTTTGTT
                                     CC
GAM1439  LOC201324 3'  TTTCTGCAGTTCCCTCATATTC 69098         AA   A
                                GAATATGAG  AAT GCAGAAA
                                |||||||||  ||| |||||||
                                CTTATACTC  TTG CGTCTTT
                                     CC   A
GAM1439  LOC202868 3'  TTGTTTTCTCCCATGTTCCA   92012         __
                                TGGAATAT  GAGAAAATAG
                                ||||||||  ||||||||||
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                                ACCTTGTA  CTCTTTTGTT
                                    CC
GAM1439  LOC257235 3'  TTTGAAGTCTTTCTCATTTCC  98843     T      _  AG
                                GGAA ATGAGAAA AT  CAGA
                                |||| |||||||| ||  ||||
                                CCTT TACTCTTT TG  GTTT
                                  _      C  AA
GAM1439  LOC51605  3'  TTGTTTTTTCATATCCCA    32513     A
                                TGG ATATGAGAAAATAG
                                ||| ||||||||||||||
                                ACC TATACTTTTTTGTT
                                  C
GAM1440  HAL      5'  GCCACTCCTGCATAAAGCTC   10903          TGAAAA
                                GAGCTTTATGC     GGTGGC
                                ||||||||||     ||||||
                                CTCGAAATACG     TCACCG
                                      TCC___
GAM1440  HMGN2    3'  GGCCACCTTGGCACAAAAGC   19809      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _  GG
GAM1440  NMI      5'  GGCCACCTCCTCAGGAAG    17436     ATG   AA
                                CTTT   CTGA  AGGTGGCC
                                ||||   ||||  ||||||||
                                GAAG   GACT  TCCACCGG
                                  ___    CC
GAM1440  PACE     3'  GGCCACCTCTCCAAGGGCTT   11944       A  CT  AAA
                                GAGCTTT TG  GA   GGTGGCC
                                ||||||| ||  ||   |||||||
                                TTCGGGA AC  CT   CCACCGG
                                   _ CT  ___
GAM1440  PYCR1    3'  CCACCTTCCTCTAGAGCTC   70639       TGCT  A_
                                GAGCTTTA   GA  AAGGTGG
                                ||||||||   ||  |||||||
                                CTCGAGAT   CT  TTCCACC
                                    _____  CC
GAM1440  SDC1     3'  GGCCACCTCCCCAGCATTCCAG 12991     TT_     AAA
            C                    GCT   ATGCTG   AGGTGGCC
                                |||   ||||||   ||||||||
                                CGA   TACGAC   TCCACCGG
                                  CCT     CCC
GAM1440  FLJ11560 5'  GCCCAGGCCCAGCATAAAG   48008         AAAA  ___
                                CTTTATGCTG   GGT   GGC
                                ||||||||||   |||   |||
                                GAAATACGAC   CCG   CCG
                                      _____  GAC
GAM1440  KIAA0446 5'  CCACCTTTTGAAGAGCTC    69446       ATGCTG
                                GAGCTTT     AAAAGGTGG
                                |||||||     |||||||||
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                                CTCGAGA     TTTTCCACC
                                    AG____
GAM1440  KIAA0971  3'  GTTGTTCTCAGCATAAAGT   30677          AAA  TG
                                GCTTTATGCTGA   GG  GC
                                ||||||||||||   ||  ||
                                TGAAATACGACT   TT  TG
                                       C__  GT
GAM1440  KIAA1393  3'  GGCCACCTTGGCACAAAAGC   72574      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                   _ _ GG
GAM1440  KIAA1656  3'  GGCCACCTCCTCCTAGAAGCC  66377   A    ATGCT  AA
                                G GCTTT    GA  AGGTGGCC
                                | |||||    ||  ||||||||
                                C CGAAG    CT  TCCACCGG
                                _    ATC__  CC
GAM1440  KIAA1884  3'  GCCACCTTCATCTACCAAGGCT 73728       ATGCT  A_
              C                  GAGCTTT    GA  AAGGTGGC
                                 |||||||    ||  ||||||||
                                 CTCGGAA    CT  TTCCACCG
                                     CCAT_  AC
GAM1440  PP3501    3'  GGCCACCGTTGACAGCATAAAG 41683         AAAA_
                                CTTTATGCTG    GGTGGCC
                                ||||||||||    |||||||
                                GAAATACGAC    CCACCGG
                                      AGTTG
GAM1440  SDCCAG3   3'  GGTGTTCTCAGCATGAAGCTC  22803           AAA  TG
                                GAGCTTTATGCTGA   GG  GCC
                                ||||||||||||||   ||  |||
                                CTCGAAGTACGACT   CT  TGG
                                         ___  TG
GAM1440  SP140     3'  GGCCACCTCCATGCAGAAGC   24327      A  TGAAA
                                GCTTT TGC    AGGTGGCC
                                ||||| |||    ||||||||
                                CGAAG ACG    TCCACCGG
                                   _  TACC_
GAM1440  LOC148760 3'  GGCCACCTTCTCCAACAAGCTC 85364       TA  CT  A
                                GAGCTT  TG  GA AAGGTGGCC
                                ||||||  ||  || |||||||||
                                CTCGAA  AC  CT TTCCACCGG
                                    CA  __  C
GAM1440  LOC150170 5'  ACCTGTTTCACATAAAGC    80414        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                     _    G
GAM1440  LOC150175 5'  ACCTGTTTCACATAAAGC    80453        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
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                                CGAAATAC ACTTT TCCA
                                    _    G
GAM1440  LOC150215 5'  ACCTGTTTCACATAAAGC    80456        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                    _    G
GAM1440  LOC150218 5'  ACCTGTTTCACATAAAGC    80525        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                    _    G
GAM1440  LOC152065 3'  GGCCACCTTCTCCTTGGCAGGC 86737      TTA   ___  A
            TC                   GAGCT   TGCT   GA AAGGTGGCC
                                |||||   ||||   || |||||||||
                                CTCGG   ACGG   CT TTCCACCGG
                                  ___   TTC  C
GAM1440  LOC152267 3'  GGCCACCTTGGCACAAAAGC   61036      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _  GG
GAM1440  LOC158292 5'  CCTCTGGACCCAGCATAAGGCT 88046           AAAA_  T
            C                    GAGCTTTATGCTG    GG GG
                                ||||||||||||    || ||
                                CTCGGAATACGAC    TC CC
                                      CCAGG  T
GAM1440  LOC219997 3'  GCCACCTCTTCAGCCTC    93256    CTTTAT    A
                                GAG     GCTGAA AGGTGGC
                                |||     |||||| |||||||
                                CTC     CGACTT TCCACCG
                                  _______     C
GAM1440  LOC256269 3'  GGCCACCTTGGCACAAAAGC   96608      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _  GG
GAM1440  LOC91963  5'  GGCCACCTCCTCTGAGAAGC   68321      ATGCT  AA
                                GCTTT    GA  AGGTGGCC
                                |||||    ||  ||||||||
                                CGAAG    CT  TCCACCGG
                                   AGT__  CC
GAM1441  CCND2    3'  TCCCAGCAAATCATCGGGCCA  10055          CCACA  _  A
                                TGGCCTGATGAT    GC GG GA
                                ||||||||||||    || || ||
                                ACCGGGCTACTA    CG CC CT
                                      AA___  A  C
GAM1441  GCN5L2   5'  CTCCGCTGCGGGGGAGGCC   60529      GATGA   A
                                GGCCT    TCC CAGCGGAG
                                |||||    ||| ||||||||
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                                CCGGA    GGG GTCGCCTC
                                  GG___  C
GAM1441  GJA5     3'  CTGACCAGATCATCAGCCA   19164     C      CACAG
                                TGGC TGATGATC    CGG
                                |||| ||||||||    |||
                                ACCG ACTACTAG    GTC
                                  _      ACCA_
GAM1441  HIVEP3   3'  TCCCCGCTGTGGTTGGCAGCCA 44702     C  ATGAT       A
                                TGGC TG    CCACAGCGG GA
                                |||| ||    ||||||||| ||
                                ACCG AC    GGTGTCGCC CT
                                  _ GGTT_       C
GAM1441  HOXD1    5'  CCGCCGGTATATTAGGCCA   44696         AT  ACA
                                TGGCCTGATG  CC   GCGG
                                ||||||||||  ||   ||||
                                ACCGGATTAT  GG   CGCC
                                      AT  C__
GAM1441  SUFU     3'  CCTTGTGACCCATCAGGCCA   32934         ATC    C
                                TGGCCTGATG   CACAG GG
                                ||||||||||   ||||| ||
                                ACCGGACTAC   GTGTT CC
                                      CCA    _
GAM1441  DKFZP586J1624 3'  CTCCGCCCAGTCACCATCAGGC 32043          ATCCACA_
           CA                   TGGCCTGATG       GCGGAG
                                ||||||||||       ||||||
                                ACCGGACTAC       CGCCTC
                                      CACTGACC
GAM1441  KIAA1671  3'  CTTTGCTTATGAATCATCAGAC 66282    C       C  C_
           C                    GG CTGATGAT CA  AGCGGAG
                                || ||||||||  ||  |||||||
                                CC GACTACTA GT  TCGTTTC
                                 A       A  AT
GAM1441  LOC159110 5'  TCTCCGCTGCCCCGGTCAACCA 82995     CCTGA    CA__
                                TGG    TGATC    CAGCGGAGA
                                |||    |||||   |||||||||
                                ACC    ACTGG    GTCGCCTCT
                                  A____     CCCC
GAM1441  LOC159116 5'  TCTCCGCTGCCCCGGTCAACCA 82978     CCTGA    CA__
                                TGG    TGATC    CAGCGGAGA
                                |||    |||||   |||||||||
                                ACC    ACTGG    GTCGCCTCT
                                  A____     CCCC
GAM1441  LOC165476 5'  CTCCGCTGCCTGCTCAGCCA   88550     C   TGATCCA
                                TGGC TGA      CAGCGGAG
                                |||| |||      ||||||||
                                ACCG ACT      GTCGCCTC
                                  _  CGTCC__
GAM1441  LOC200032 5'  CTGACCAGATCATCAGCCA    85475      C       CACAG
                                TGGC TGATGATC    CGG
                                |||| ||||||||    |||
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                                ACCG ACTACTAG    GTC
                                  _      ACCA_
GAM1441  LOC219654 5'  CTCCGCTGCGGAGGGGGGCC  92932      GATGA  A
                                GGCCT    TCC CAGCGGAG
                                |||||    ||| ||||||||
                                CCGGG    AGG GTCGCCTC
                                   GGG__  C
GAM1441  LOC255862 3'  TCAAATGTAGACTATCAGGCCA 96115         A  C  GCG
                                TGGCCTGATG TC ACA  GA
                                |||||||||| || |||  ||
                                ACCGGACTAT AG TGT  CT
                                      C  A  AAA
GAM1442  ACATN    5'  GACTGGCTCCCGGCTTCAG   17596       AGTG  CA  A
                                TTGAAGCC   GGG  CCA TC
                                ||||||||   |||  ||| ||
                                GACTTCGG   CCC  GGT AG
                                     ____  TC  C
GAM1442  B3GALT2  3'  GTGTCTCAGGCTCAA      15032     A  AG
                                TTGA GCC  TGGGGCAC
                                |||| |||  ||||||||
                                AACT CGG  ACTCTGTG
                                  _  __
GAM1442  CD164    3'  GGACTAGTGCAGAGGCTTTAA  21197       AGTGGG   CAA
                                TTGAAGCC    GCAC  TCC
                                ||||||||    ||||  |||
                                AATTTCGG    CGTG  AGG
                                     AGA___   ATC
GAM1442  DRG2     3'  TGGTTAGTGGCTTCAA     9131         G  GGGC
                                TTGAAGCCA TG   ACCA
                                |||||||||  ||   ||||
                                AACTTCGGT AT   TGGT
                                     G  ____
GAM1442  HPS4     3'  ATTGGTGCCACAAGCTTC   42226      CAG  G
                                GAAGC  TG GGCACCAAT
                                |||||  ||  |||||||||
                                CTTCG  AC CCGTGGTTA
                                   A__  A
GAM1442  SDPR     5'  GACTGGTGCCCTGAGCTCCAA  17400    A  CAG       A
                                TTG AGC  TGGGGCACCA TC
                                ||| |||  ||||||||||  ||
                                AAC TCG  GTCCCGTGGT AG
                                  C  A__       C
GAM1442  C5orf6   3'  GATTGGCTGTGCCAGCTTC   33954     CAG  G  _
                                GAAGC  TGG GCA CCAATC
                                |||||  ||| ||| ||||||
                                CTTCG  ACC TGT GGTTAG
                                   ___  G  C
GAM1442  C8orf17  3'  GGACCACACTGGCTGCAA    39998    A      G  CA
                                TTG AGCCAGTG GG  CC
                                ||| ||||||||  ||  ||
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                                AAC TCGGTCAC CC  GG
                                  G       A  A_
GAM1442  CABP5    5'  GACTGGTGCCCTGCGAGCTCCA 39562    A   CA TG      A
                                TG AGC  G  GGGCACCA TC
                                || |||  |  |||||||| ||
                                AC TCG  C  CCCGTGGT AG
                                 C   AG GT       C
GAM1442  FLJ13940  3'  GGACTGGTGCCCCACAGGCTTT 47309        A        A
             AA                   TTGAAGCC GTGGGGCACCA TCC
                                |||||||| |||||||||| |||
                                AATTTCGG CACCCCGTGGT AGG
                                     A         C
GAM1442  KCNMB2   3'  ATTGGTGGACTGGTTTCAA   20684          GGGG
                                TTGAAGCCAGT   CACCAAT
                                ||||||||||   |||||||
                                AACTTTGGTCA   GTGGTTA
                                      G___
GAM1442  KIAA0530  3'  GATTGGTGTATAGCTTTAA   71431       CAGTGGG
                                TTGAAGC      GCACCAATC
                                |||||||      |||||||||
                                AATTTCG      TGTGGTTAG
                                   ATA____
GAM1442  KIAA1522  3'  GGATTGGCCTTCCTGTGCCTCA 65607     A _  TG   AC
             A                   TTGA GC CAG  GGGC  CAATCC
                                |||| || |||  ||||  ||||||
                                AACT CG GTC  TCCG  GTTAGG
                                  C  T   CT   __
GAM1442  KIAA1853  3'  GGATGCCCCACTAGTCCAA   69924     AA  C       _
                                TTG  GC AGTGGGGCA CC
                                |||  || |||||||| ||
                                AAC  TG TCACCCCGT GG
                                  C_  A       A
GAM1442  LOXL4    3'  GATTGGTCTAAACTTCAA    50859       CCAG   GGC
                                TTGAAG   TGG   ACCAATC
                                ||||||   |||   |||||||
                                AACTTC   ATC   TGGTTAG
                                   AA__  ____
GAM1442  LSR7     5'  GGACCGGCCCTGCCCCCGGCTT 38280        AGT     ___  AA
             CAA                   TTGAAGCC   GGGGCA   CC  TCC
                                |||||||   ||||||   ||  |||
                                AACTTCGG   CCCCGT   GG  AGG
                                     C__     CCC  CC
GAM1442  PLK      3'  GGACTGGTGCCCTCCTCACT   18525    CC  TG      A
                                AG  AG  GGGCACCA TCC
                                ||  ||  |||||||| |||
                                TC  TC  CCCGTGGT AGG
                                 AC  CT      C
GAM1442  STK22D   3'  GGTCCCCACTGGCCGCAA    50145     AA        C
                                TTG  GCCAGTGGGG ACC
                                |||  |||||||||| |||
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                                AAC  CGGTCACCCC TGG
                                  GC        _
GAM1442  LOC124871 3'  TGCTGCCCCACCAGCTTCAG   74818        CA       C
                                TTGAAGC  GTGGGGCA CA
                                |||||||  |||||||| ||
                                GACTTCG  CACCCCGT GT
                                    AC       C
GAM1442  LOC157349 3'  GACTGGCTGCTGGCTCCGA    82341     A     TG GGCA   A
                                TTG AGCCAG  G    CCA TC
                                ||| ||||||  |    ||| ||
                                AGC TCGGTC  C    GGT AG
                                  C     GT _____   C
GAM1442  LOC222550 5'  GGATCAATATCGTGCTGGCTT  96018         G  CACCA
                                AAGCCAGTG GG     ATCC
                                |||||||||| ||     ||||
                                TTCGGTCGT CT     TAGG
                                     G  ATAAC
GAM1443  CDH12    3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM1443  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC         G
GAM1443  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT    98090      T    AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||     ||||||
                                TGGTG GGGT     TTATTC
                                   _    GTCA_
GAM1443  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
            A                    TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM1443  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM1443  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
            TA                   TACA   TCC    GAAGAATAAG
                                ||||   |||    ||||||||||
                                ATGT   AGG    TTTCTTATTC
                                  AAA_   ATTG
GAM1443  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68742              _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
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                                ATGTGGTGAGGGTTCT TCT
                                       G
GAM1443 KIAA1853 3' TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM1443 KIAA1877 3' CTTATTCTTCTGCCATGAGT   66748      CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM1443 KIAA1906 3' CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM1443 OSBPL11  3' CTTAATTTCCCAAGAGTGGTG  43206        CCAA   AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                     AACC   A_
GAM1443 YME1L1   3' TCATTCTTGATGTGGTGTA    58438        TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   |||||| ||
                                ATGTGGTG   GTTCTT CT
                                     TA_    A
GAM1443 ZNF262   3' CTTATTTTGTTTGGGAGT     18723         A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                     G
GAM1443 LOC91960 3' TGTGGCTTGGAACGTGGTGTA  68294        TC_    AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
                                ATGTGGTG   GGTTC   TGT
                                     CAA    GG__
GAM1444 GALNT2   3' CCGCACACACAGATGCTCAGT   16814        C   _   AA
                                ACTGAGCA CTG GTG  TGG
                                ||||||||| ||| |||  |||
                                TGACTCGT GAC CAC  GCC
                                     A   A   AC
GAM1444 NCSTN    3' CGCCCACAGTGCTCAGT      74135         CTG   AAT   C
                                ACTGAGCAC   GTG   GGC G
                                |||||||||   |||   ||| |
                                TGACTCGTG   CAC   CCG C
                                     A__   ___   A
GAM1444 PPP1R11  3' CCGGCAGCCCAGATGTTCAGT  41986        C    TGAATG
                                ACTGAGCA CTGG     GCCGG
                                |||||||| ||||     |||||
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                                TGACTTGT GACC     CGGCC
                                    A   CGA___
GAM1444  GP5      3'  CCTTCCCTCCAGGTGCCCAGT  16873     A      T__  T
                                ACTG GCACCTGG   GAA GG
                                |||| ||||||||   ||| ||
                                TGAC CGTGGACC   CTT CC
                                  C       TCC  _
GAM1444  HRH3     3'  CCGGCCACTCTGTTTGCTCA  24316      CCTGGT  A
                                TGAGCA     GA TGGCCGG
                                ||||||     || |||||||
                                ACTCGT     CT ACCGGCC
                                   TTGT__  C
GAM1444  KIAA0574  3'  CCAGCCACCCAGTGGACTCGGT 69809      __  CT   AA
                                ACTGAG  CAC  GGTG  TGG
                                ||||||  |||  ||||  |||
                                TGGCTC  GTG  CCAC  ACC
                                   AG   AC   CG
GAM1444  LOC145622 5'  CCATCACCCAGGTGCTCAGT   77807          _  A
                                ACTGAGCACCTGG TGA TGG
                                |||||||||||| ||| |||
                                TGACTCGTGGACC ACT ACC
                                       C  _
GAM1444  LOC145622 5'  CCATCAGCCAGGTGCTCAG   77808          GA
                                CTGAGCACCTGGT  ATGG
                                ||||||||||||  ||||
                                GACTCGTGGACCG  TACC
                                       AC
GAM1444  LOC145622 5'  CCATCAGCCAGGTGCTCAG   77809          GA
                                CTGAGCACCTGGT  ATGG
                                ||||||||||||  ||||
                                GACTCGTGGACCG  TACC
                                       AC
GAM1444  LOC145622 5'  CCATCAGCCAGGTGCTCAG   77810          GA
                                CTGAGCACCTGGT  ATGG
                                ||||||||||||  ||||
                                GACTCGTGGACCG  TACC
                                       AC
GAM1444  LOC145622 5'  CCATCATCCAGGTGCTCAG   77811          _  A
                                CTGAGCACCTGG TGA TGG
                                |||||||||||| ||| |||
                                GACTCGTGGACC ACT ACC
                                       T  _
GAM1444  LOC145622 5'  TGTACGTCAGCCAGGTGCTCAG 77827          GA  GC
                                CTGAGCACCTGGT  ATG  CG
                                ||||||||||||  |||  ||
                                GACTCGTGGACCG  TGC  GT
                                       AC  AT
GAM1444  LOC145622 5'  TGTCTGTCAGCCAGGTGCTCAG 77828          GA   C
                                CTGAGCACCTGGT  ATGG CG
                                ||||||||||||  |||| ||
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                                GACTCGTGGACCG  TGTC GT
                                       AC    T
GAM1444  LOC154995 5'  CGGCCTCCAGGTGCTCA     82104          TGAAT
                                TGAGCACCTGG     GGCCG
                                ||||||||||     |||||
                                ACTCGTGGACC     CCGGC
                                       T_____
GAM1444  LOC155036 5'  CCAGCTGGCCAAGTGTTCAG   87611        C    GAA    C
                                CTGAGCAC TGGT   TGGC GG
                                |||||||| ||||   |||| ||
                                GACTTGTG ACCG   GTCG CC
                                     A    ___    A
GAM1444  LOC203248 3'  CCAGCCATTCATCGACAGTCAG 90842      G ACC          C
                                CTGA C   TGGTGAATGGC GG
                                |||| |   |||||||||| ||
                                GACT G   GCTACTTACCG CC
                                  _ ACA          A
GAM1444  LOC221362 3'  CCAAAAGACACCAATGCTCAGT 95398         CC     AA___
                                ACTGAGCA  TGGTG     TGG
                                ||||||||  |||||     |||
                                TGACTCGT  ACCAC     ACC
                                     A_     AGAAA
GAM1444  LOC57821  5'  CCGGCCATCTCTGTGATCCCAG 41301     AG__   CT  T  A
                                CTG    CAC  GG GA TGGCCGG
                                |||    |||  || || |||||||
                                GAC    GTG  TC CT ACCGGCC
                                  CCTA   __  T  _
GAM1445  A1BG     3'  TCGGCCTGGTCCCAGCAGGTA  56299      C  C     AGATCT
                                TACC GC GGGAC      GCTGG
                                |||| || |||||      |||||
                                ATGG CG CCCTG      CGGCT
                                  A  A    GTC___
GAM1445  CLCN6    3'  CATGGTATCAGTCCCAGCAGG  8901     C  C     A  _  C
                                CC GC GGGAC GAT CTG TG
                                || || ||||| ||| ||| ||
                                GG CG CCCTG CTA GGT AC
                                 A  A    A  T  _
GAM1445  CLCN6    3'  CATGGTATCAGTCCCAGCAGG  41693    C  C     A  _  C
                                CC GC GGGAC GAT CTG TG
                                || || ||||| ||| ||| ||
                                GG CG CCCTG CTA GGT AC
                                 A  A    A  T  _
GAM1445  CLCN6    3'  CATGGTATCAGTCCCAGCAGG  41700    C  C     A  _  C
                                CC GC GGGAC GAT CTG TG
                                || || ||||| ||| ||| ||
                                GG CG CCCTG CTA GGT AC
                                 A  A    A  T  _
GAM1445  ERBB4    3'  CCAGCAGTTTCTGTCCTAGCAA 19108     CC  CG      T_
            GTA                   TAC  GC  GGACAGA  CTGCTGG
                                |||  ||  |||||||  |||||||
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                                ATG  CG  CCTGTCT  GACGACC
                                 AA  AT      TT
GAM1445  IDH1     5'  CCAGCATATCATCCCGGCAGG  62096    C      CA   C
                                CC GCCGGGA  GAT TGCTGG
                                || |||||||  ||| ||||||
                                GG CGGCCCT  CTA ACGACC
                                 A      A_  T
GAM1445  ITGA2    3'  CCAGCAGACCTACCTGCAGTG  11024     __    AC  A
                                CGC  CGGG  AG TCTGCTGG
                                |||  ||||  || ||||||||
                                GTG  GTCC  TC AGACGACC
                                  AC   A_  C
GAM1445  JAM3     3'  CCAGCAGCGCATCCCGGCGGG  52486          CAGAT
                                CCCGCCGGGA    CTGCTGG
                                ||||||||||    |||||||
                                GGGCGGCCCT    GACGACC
                                      ACGC_
GAM1445  NUP155   5'  CCAGCGTTGGTCCCGGCGAGG  16285    _       AGATC
                                CC CGCCGGGAC    TGCTGG
                                || |||||||||    ||||||
                                GG GCGGCCCTG    GCGACC
                                 A        GTT__
GAM1445  OXTR     5'  CCAGCAGATCCGTCCGTGGAGT 8076     _   CG    A
                                AC CCGC  GGAC GATCTGCTGG
                                || ||||  |||| ||||||||||
                                TG GGTG  CCTG CTAGACGACC
                                 A   __   C
GAM1445  PKIB     5'  CCAGCCCAGGGCACCGGCAGG  51637    C    GACAGA  __
                                CC GCCGG     TCT  GCTGG
                                || |||||     |||  |||||
                                GG CGGCC     GGA  CGACC
                                 A    ACG___   CC
GAM1445  PPOX     5'  CCAGCAGAGCGCCGGCGGG   6127         GACAGA
                                CCCGCCGG     TCTGCTGG
                                ||||||||     ||||||||
                                GGGCGGCC     AGACGACC
                                     GCG___
GAM1445  RANBP3   5'  CCAGCAGACTGCACGGGGG   24637    G   GGA   A
                                CCC CCG   CAG TCTGCTGG
                                ||| |||   ||| ||||||||
                                GGG GGC   GTC AGACGACC
                                  _   AC_   _
GAM1445  ST7      5'  CCGGTGAATCATCCCGGC    37911       CA   CT
                                GCCGGGA  GAT  GCTGG
                                |||||||  |||  |||||
                                CGGCCCT  CTA  TGGCC
                                    A_   AG
GAM1445  ST7      5'  CCGGTGAATCATCCCGGC    41864       CA   CT
                                GCCGGGA  GAT  GCTGG
                                |||||||  |||  |||||
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                                CGGCCCT  CTA  TGGCC
                                   A_   AG
GAM1445  STAU     3'  CCAGCAGATCCACACCCTGGGC 34349     __   ACA_
                                GCC  GGG   GATCTGCTGG
                                |||  |||   ||||||||||
                                CGG  CCC   CTAGACGACC
                                  GT   ACAC
GAM1445  STAU     3'  CCAGCAGATCCACACCCTGGGC 34352     __   ACA_
                                GCC  GGG   GATCTGCTGG
                                |||  |||   ||||||||||
                                CGG  CCC   CTAGACGACC
                                  GT   ACAC
GAM1445  STAU     3'  CCAGCAGATCCACACCCTGGGC 34355     __   ACA_
                                GCC  GGG   GATCTGCTGG
                                |||  |||   ||||||||||
                                CGG  CCC   CTAGACGACC
                                  GT   ACAC
GAM1445  STAU     3'  CCAGCAGATCCACACCCTGGGC 17194     __   ACA_
                                GCC  GGG   GATCTGCTGG
                                |||  |||   ||||||||||
                                CGG  CCC   CTAGACGACC
                                  GT   ACAC
GAM1445  DDA3     3'  CCAGCAGACCCTGACTCCAGC  51948    C  _ A   A_
                                GC GG G CAG  TCTGCTGG
                                || || | |||  ||||||||
                                CG CC C GTC  AGACGACC
                                 A  T A   CC
GAM1445  DDA3     3'  CCAGCAGATTCTGGCCCAGGG  51949     GCC   A   _
                                CCC   GGG CAGA TCTGCTGG
                                |||   ||| |||| ||||||||
                                GGG   CCC GTCT AGACGACC
                                  A__   G   T
GAM1445  DKFZP434N178 3'  CGCTCTGTCCCGAGGG      72399     GC       TCT  T
                                CCC  CGGGACAGA   GC G
                                |||  |||||||||   || |
                                GGG  GCCCTGTCT   CG C
                                  A_        ___  T
GAM1445  FLJ10774  3'  CCAGCAGACCCACTGTCCC    45415       A___
                                GGGACAG    TCTGCTGG
                                |||||||    ||||||||
                                CCCTGTC    AGACGACC
                                   ACCC
GAM1445  HEYL     3'  CCAGCAGTCGTTCCCAGC     28124     C    CA  T
                                GC GGGA  GA CTGCTGG
                                || ||||  || |||||||
                                CG CCCT  CT GACGACC
                                 A   TG  _
GAM1445  KIAA1115  3'  CGTTCCGTCCCAGCGGG     30690      C     A  TCT  T
                                CCCGC GGGAC GA   GC G
                                ||||| ||||| ||   || |
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                                GGGCG CCCTG CT   TG C
                                  A    C ___  T
GAM1445 KIAA1656 3' CAGCAGACCTGCTGGC     66360      GA  A
                                GCCGG  CAG TCTGCTG
                                ||||| ||| |||||||
                                CGGTC  GTC AGACGAC
                                  __  C
GAM1445 STX3A    5' CCAGCTCCTTCGCCCCGGCGGG 16067        ACA  TCT_
                                CCCGCCGGG  GA   GCTGG
                                |||||||||  ||   |||||
                                GGGCGGCCC  CT   CGACC
                                     CG_  TCCT
GAM1445 TOB2     3' CCAGCTCTACCTCCCCCGGCAG 97353    C     AC  ATCT_
            G                    CC GCCGGG  AG    GCTGG
                                || ||||||  ||    |||||
                                GG CGGCCC  TC    CGACC
                                 A     CC  CATCT
GAM1445 LOC135892 3' CCACAGGCCCATCCCGGCGGG  75759         CAGA   C
                                CCCGCCGGGA   TCTG TGG
                                ||||||||||   |||| |||
                                GGGCGGCCCT   GGAC ACC
                                     ACCC   _
GAM1445 LOC203292 3' CCAGCAGATCTGCCTGTGC   92154   _   A
                                GC CGGG CAGATCTGCTGG
                                || |||| ||||||||||||
                                CG GTCC GTCTAGACGACC
                                 T   _
GAM1445 LOC253650 3' CCAGCAGATCTGCCTGTGC   97871   _   A
                                GC CGGG CAGATCTGCTGG
                                || |||| ||||||||||||
                                CG GTCC GTCTAGACGACC
                                 T   _
GAM1445 LOC257458 5' CCAGCTCTGGTCCCGGCAGG  68400   C      _  TCT
                                CC GCCGGGAC AGA   GCTGG
                                || |||||||| |||   |||||
                                GG CGGCCCTG TCT   CGACC
                                 A       G  ___
GAM1445 LOC91263  5' CCAGCAGATCTACACTAGAGGT 65998     CGCC  GAC
            A                    TACC   GG   AGATCTGCTGG
                                ||||   ||   ||||||||||||
                                ATGG   TC   TCTAGACGACC
                                  AGA_  ACA
GAM1446 BLAME    3' GCCTCAATCCAGTCTTGATA   39653      _    A    _
                                TATCA GACTG GATTG GGC
                                ||||| ||||| ||||| |||
                                ATAGT CTGAC CTAAC CCG
                                   T    _    T
GAM1446 KCNJ16   5' GCCCAATCTCTGCTGGT     38485      ACT
                                ATCAG   GAGATTGGGC
                                |||||   ||||||||||
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                                TGGTC  CTCTAACCCG
                                  GT_
GAM1446 LRPAP1   3' GCTGTCAGGTCTGATA     11367        GA  TG
                                TATCAGACT  GAT  GGC
                                |||||||||  |||  |||
                                ATAGTCTGG  CTG  TCG
                                    A_  __
GAM1446 MHC2TA   3' GCCCACAGGATCAGTCTGAT  5987         GAT__
                                ATCAGACTGA    TGGGC
                                ||||||||||    |||||
                                TAGTCTGACT    ACCCG
                                    AGGAC
GAM1446 NPHP1    3' CTTAATTCAGTCTGATA     63142          A
                                TATCAGACTGAG TTGGG
                                |||||||||||| |||||
                                ATAGTCTGACTT AATTC
                                    _
GAM1446 PROCR    3' GCTGAATTAGTCTGATA     22157        GA   G
                                TATCAGACT  GATT GGC
                                |||||||||  |||| |||
                                ATAGTCTGA  TTAA TCG
                                    __   G
GAM1446 PROK1    3' GTTCAATCTAATCTGATA    51569       CTG
                                TATCAGA   AGATTGGGC
                                |||||||   |||||||||
                                ATAGTCT   TCTAACTTG
                                   AA_
GAM1446 RUNX1    3' CCCAAGGTCATCTGATA     10029       C  GA
                                TATCAGA TGA  TTGGG
                                ||||||| |||  |||||
                                ATAGTCT ACT  AACCC
                                   _  GG
GAM1446 TMEM2    3' CCATTTTCCAGTTTGATA    26335         _  T
                                TATCAGACTG AGA TGG
                                |||||||||| ||| |||
                                ATAGTTTGAC TTT ACC
                                    C  T
GAM1446 UBE4A    3' CCCAATCTAGTAGGATG     17731     AG  G
                                TATC  ACT AGATTGGG
                                ||||  ||| ||||||||
                                GTAG  TGA TCTAACCC
                                  GA  _
GAM1446 FLJ10330 3' CCCAATTGTTAAGTTTGATA  36504        GA__
                                TATCAGACT   GATTGGG
                                |||||||||   |||||||
                                ATAGTTTGA   TTAACCC
                                    ATTG
GAM1446 FLJ10852 3' CCCAAAACTCTCAATCTGAT  39251       C   ___
                                ATCAGA TGAGA  TTGGG
                                |||||| |||||  |||||
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                              TAGTCT ACTCT   AACCC
                                 A     CAA
GAM1446  FLJ20511  3'  GCCCAATCTCTGATG      35776       CTGA
                              TATCAGA    GATTGGGC
                              |||||||    ||||||||
                              GTAGTCT    CTAACCCG
                                     ____
GAM1446  KIAA0194  3'  GCCCCCTCAGTCTGATG     66591          ATT
                              TATCAGACTGAG   GGGC
                              ||||||||||||   ||||
                              GTAGTCTGACTC   CCCG
                                     C__
GAM1446  KIAA0326  3'  GCCCAATCTCAGCCTTGA    64962      A_
                              TCAG  CTGAGATTGGGC
                              ||||  ||||||||||||
                              AGTT  GACTCTAACCCG
                                CC
GAM1446  KIAA0844  5'  GCCCGGCTCAGTCTGAT     30894          A
                              ATCAGACTGAG TTGGGC
                              |||||||||||| ||||||
                              TAGTCTGACTC GGCCCG
                                      _
GAM1446  KIAA1878  3'  GCCCAAATCGCAGTTTGA    93368        A   _
                              TCAGACTG GATT GGGC
                              |||||||| |||| ||||
                              AGTTTGAC CTAA CCCG
                                    G   A
GAM1446  KIAA1906  3'  CCCAAATTATTAGTCTTGATA  73570      _     GA__
                              TATCA GACTGA    TTGGG
                              ||||| ||||||    |||||
                              ATAGT CTGATT    AACCC
                                 T     ATTA
GAM1446  NICE-3    3'  GCCCAATGCACTGGTCTGA    31885       G ___
                              TCAGACT AG   ATTGGGC
                              ||||||| ||   |||||||
                              AGTCTGG TC   TAACCCG
                                   _ ACG
GAM1446  OGFR      3'  GCTTTTCTTAGTCTGATA     62000          TT
                              TATCAGACTGAGA  GGGC
                              ||||||||||||  ||||
                              ATAGTCTGATTCT  TTCG
                                      T_
GAM1446  PRO0902   3'  GCCTAATTCAATTGATA     54967       AC   A
                              TATCAG  TGAG TTGGGC
                              ||||||  |||| ||||||
                              ATAGTT  ACTT AATCCG
                                 A_   _
GAM1446  PRPF4     3'  GCCCAATCCCTAGGTGATG    17467       GA  A_
                              TATCA  CTG  GATTGGGC
                              |||||  |||  ||||||||
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                                GTAGT  GAT  CTAACCCG
                                   G_   CC
GAM1446  SS18L1   3'  GCCCAATTCTAAGTTGATA   65956       A  G  _
                                TATCAG CT AGA TTGGGC
                                |||||| || ||| ||||||
                                ATAGTT GA TCT AACCCG
                                   _ A   T
GAM1446  TRIM7    3'  GCTCAGTCACTCTGATA     54042       CTGA
                                TATCAGA    GATTGGGC
                                |||||||    ||||||||
                                ATAGTCT    CTGACTCG
                                    CA__
GAM1446  LOC145828 3'  GCCCAATCCAGTATTTGAT   84538       __   A
                                ATCAG  ACTG GATTGGGC
                                |||||  |||| ||||||||
                                TAGTT  TGAC CTAACCCG
                                   TA   _
GAM1446  LOC146481 5'  GCCTTCTACAGTTTGATA    78487         _  TT
                                TATCAGACTG AGA  GGGC
                                |||||||||| |||  ||||
                                ATAGTTTGAC TCT  TCCG
                                      A  __
GAM1446  LOC147343 3'  GCCCTCAATTTCTATCTAATA  85129     C   CT    __
                                TAT AGA  GAGATT  GGGC
                                ||| |||  ||||||  ||||
                                ATA TCT  CTTTAA  CCCG
                                  A  AT     CT
GAM1446  LOC204804 3'  GCCCTCTCAGCCTGAT      91045      A     TT
                                ATCAG CTGAGA  GGGC
                                |||||  ||||||  ||||
                                TAGTC GACTCT  CCCG
                                   C     __
GAM1446  LOC257194 3'  GCTGGATCCAATCTGGTA    97242       C  A   G
                                TATCAGA TG GATT GGC
                                ||||||| || |||| |||
                                ATGGTCT AC CTAG TCG
                                    A  _   G
GAM1447  ARF3     3'  CCAGGCCCTCAGACCATC    9772      A   CCAGC
                                GAT GTCT    AGGGCCTGG
                                |||  ||||    |||||||||
                                CTA CAGA    TCCCGGACC
                                  C   C____
GAM1447  CACNA1C   5'  CCATTAATTCACTGGAGATATC 7398       G      CA  GCC_
             A                   TGATA TCTCCAG  GG   TGG
                                 |||||  |||||||  ||   |||
                                 ACTAT AGAGGTC  TT   ACC
                                    _      AC  AATT
GAM1447  CLTCL1   3'  TCCAGGCCAGTTTGAAGACTAC 64423    A     C   CAG
             A                   TG TAGTCT CAG   GGCCTGGA
                                 || |||||| |||   ||||||||
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                                AC ATCAGA GTT   CCGGACCT
                                 _     A   TGA
GAM1447  DAAM2    5'  TCCAGACCCTGCTGAACGAGCT 93906     T  ___      C
              A                   TAG CTC   CAGCAGGG CTGGA
                                  ||| |||   |||||||| |||||
                                  ATC GAG   GTCGTCCC GACCT
                                   _  CAA       A
GAM1447  HDAC7A   5'  CCAGGCCCTGTGCAGAC     31830      CCA
                                  GTCT   GCAGGGCCTGG
                                  ||||   ||||||||||
                                  CAGA   TGTCCCGGACC
                                    CG_
GAM1447  HDAC7A   5'  CCAGGCCCTGTGCAGAC     33923      CCA
                                  GTCT   GCAGGGCCTGG
                                  ||||   ||||||||||
                                  CAGA   TGTCCCGGACC
                                    CG_
GAM1447  MPZ      3'  CCAGGCCCTGCCAGAGC     6749    T   CA
                                  G CTC  GCAGGGCCTGG
                                  | |||  ||||||||||
                                  C GAG  CGTCCCGGACC
                                   _  AC
GAM1447  NEUROD1   5'  CCAGGGTTATGAGACTATCA   11778          CAGCA  G
                                  TGATAGTCTC    GG CCTGG
                                  ||||||||||    || |||||
                                  ACTATCAGAG    TT GGACC
                                        TA___  G
GAM1447  PC       3'  CCTCACTGGAGACTACA     42507    A        CA
                                  TG TAGTCTCCAG  GGG
                                  || ||||||||||  |||
                                  AC ATCAGAGGTC  TCC
                                   _         AC
GAM1447  PC       3'  CCTCACTGGAGACTACA     8088     A        CA
                                  TG TAGTCTCCAG  GGG
                                  || ||||||||||  |||
                                  AC ATCAGAGGTC  TCC
                                   _         AC
GAM1447  PPT2     3'  CCAGGCCCTCTTTTAACTA   57800      CTCC  C
                                  TAGT    AG AGGGCCTGG
                                  ||||    || |||||||||
                                  ATCA    TC TCCCGGACC
                                    ATTT  _
GAM1447  PPT2     3'  CCAGGCCCTCTTTTAACTA   18948      CTCC  C
                                  TAGT    AG AGGGCCTGG
                                  ||||    || |||||||||
                                  ATCA    TC TCCCGGACC
                                    ATTT  _
GAM1447  SLC2A4   5'  TCCAGGCCGGAGTCAGAGACT  8309        CA  AG_
                                  AGTCTC  GC   GGCCTGGA
                                  ||||||  ||   ||||||||
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                              TCAGAG  TG   CCGGACCT
                                 AC  AGG
GAM1447  TRIM37   3'  TCCAGGCCCTGCATGCCGTCA  31627     TA  CTCCA
                              TGA  GT    GCAGGGCCTGGA
                              |||  ||    ||||||||||||
                              ACT  CG    CGTCCCGGACCT
                                GC  TA___
GAM1447  DKFZP434P0111 3'  TCCAGGCCCTGCCCGACCCCAT 67962      A__   TCCA
           CA                   TGAT   GTC    GCAGGGCCTGGA
                              ||||   |||    ||||||||||||
                              ACTA   CAG    CGTCCCGGACCT
                                CCC   CC__
GAM1447  DOCK3    3'  TCCAGGCCATGGGGAC      67099        GCAG
                              GTCTCCA    GGCCTGGA
                              |||||||    ||||||||
                              CAGGGGT    CCGGACCT
                                 A___
GAM1447  FLJ10759  3'  CCGTGGCCACTGGAGACCTCA  37122     TA      CAG   _
                              TGA  GTCTCCAG   GGCC TGG
                              |||  ||||||||   |||| |||
                              ACT  CAGAGGTC   CCGG GCC
                                C_       A__    T
GAM1447  FLJ21916  3'  CCAGGCCCTGCTGGATGTGGGC 43892     ____
                              GTC    TCCAGCAGGGCCTGG
                              |||    |||||||||||||||
                              CGG    AGGTCGTCCCGGACC
                                GTGT
GAM1447  KIAA0298  3'  CCAGCACAGCCAAAGACTGTCA 77075         CCA  AGG  C
                              TGATAGTCT   GC   GC TGG
                              |||||||||   ||   || |||
                              ACTGTCAGA   CG   CG ACC
                                   AAC  ACA  _
GAM1447  KIAA0802  3'  TCCAGGCCCGAGAGACCAGCA  63251    ATA    CAGCA
                              TG   GTCTC    GGGCCTGGA
                              ||   |||||    |||||||||
                              AC   CAGAG    CCCGGACCT
                               GAC    AG___
GAM1447  KIAA1464  3'  CCAGAAGTTGGAGACATCA    68817     A       AGGGC
                              TGAT GTCTCCAGC    CTGG
                              |||| |||||||||    ||||
                              ACTA CAGAGGTTG    GACC
                                _       AA___
GAM1447  KIAA1978  3'  CCAGGCCCTGCTGGCCAGA    74891     __
                              TCT  CCAGCAGGGCCTGG
                              |||  ||||||||||||||
                              AGA  GGTCGTCCCGGACC
                                CC
GAM1447  MYT1     3'  CCAGGCCCCCGACCCATCA    16976     A_   TCCAGCA
                              TGAT  GTC      GGGCCTGG
                              ||||  |||      ||||||||
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                                ACTA  CAG      CCCGGACC
                                  CC   CC_____
GAM1447  NKX2C    3'  TCCAGGCCCTACCGATCCTC   59909    TA   TCCAGC
                                GA  GTC     AGGGCCTGGA
                                ||  |||     ||||||||||
                                CT  TAG     TCCCGGACCT
                                 CC   CCA___
GAM1447  NTSR2    3'  CCTGCTCTGCTGAGAACCATCA 25634      AG_   C      CT
                                TGAT   TCTC AGCAGGGC  GG
                                ||||   |||| ||||||||  ||
                                ACTA   AGAG TCGTCTCG  CC
                                  CCA    _       T_
GAM1447  SIRPB1   3'  TCCAAGCCTGCTGCTGGAAACC 21368     TA  C      __   C
             TCA                   TGA  GT TCCAGCAG  GGC TGGA
                                |||  || ||||||||  ||| ||||
                                ACT  CA AGGTCGTC  CCG ACCT
                                  C_  A       GT   A
GAM1447  SMCR7    3'  TCCAGGCCCCACTGGAGA    58241        CA
                                TCTCCAG  GGGCCTGGA
                                |||||||  |||||||||
                                AGAGGTC  CCCGGACCT
                                    AC
GAM1447  LOC123792 3'  TCCAGGCCAACAAGACCATC   74706     A    CCAGCAG
                                GAT GTCT      GGCCTGGA
                                ||| ||||      ||||||||
                                CTA CAGA      CCGGACCT
                                  C    ACAA___
GAM1447  LOC124751 5'  CCAGGCCCCAAGACTAT     76155        CCAGCA
                                ATAGTCT     GGGCCTGG
                                |||||||     ||||||||
                                TATCAGA     CCCGGACC
                                    AC_____
GAM1447  LOC145676 5'  CCAAACTGGAGGCTATCA     77846            CAG
                                TGATAGTCTCCAG   GG
                                ||||||||||||   ||
                                ACTATCGGAGGTC   CC
                                       AAA
GAM1447  LOC146802 3'  CCTACCAGCAGACTATCA     78725         CCA  A  GCCT
                                TGATAGTCT   GC GG    GG
                                |||||||||   || ||    ||
                                ACTATCAGA   CG CC    CC
                                     ___  A  AT__
GAM1447  LOC148293 5'  CCAGGCCTGAGAAGCCATCA   79528      A TC  CAGCA
                                TGAT G  TC    GGGCCTGG
                                |||| |  ||    ||||||||
                                ACTA C  AG    TCCGGACC
                                  C GA  AG___
GAM1447  LOC148894 5'  CCAGTGGCTGGAGACTTCA    85419     T        AGGGC
                                TGA AGTCTCCAGC    CTGG
                                ||| ||||||||||    ||||
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                                ACT TCAGAGGTCG    GACC
                                  _       GT___
GAM1447  LOC149603 3'  TCCAGGCCCTGCCATCGTGTC  71176     GTCTCCA
                                GATA      GCAGGGCCTGGA
                                ||||      ||||||||||||
                                CTGT      CGTCCCGGACCT
                                  GCTAC__
GAM1447  LOC152845 5'  CCAGGCCCTGCTAGAGCAC   60956    _  C
                                GT CTC AGCAGGGCCTGG
                                || ||| ||||||||||||
                                CA GAG TCGTCCCGGACC
                                 C   A
GAM1447  LOC199988 5'  TCCAGGCTTCATCCTAGAGACT 91501         C  CA__
            GTCA                   TGATAGTCTC AG   GGGCCTGGA
                                |||||||||| ||   |||||||||
                                ACTGTCAGAG TC   TTCGGACCT
                                      A  CTAC
GAM1447  LOC220766 5'  TCCAGGCTACTGAAAAGCATCA 92476     A  CTCCAG  _
                                TGAT GT     CAG GGCCTGGA
                                |||| ||     ||| ||||||||
                                ACTA CG     GTC TCGGACCT
                                  _ AAAA__   A
GAM1447  LOC222662 5'  CCAAACCCCGCTGGGGAGTG   94409    G      A   CC
                                TA TCTCCAGC GGG  TGG
                                || |||||||| |||  |||
                                GT AGGGGTCG CCC  ACC
                                 G       C   AA
GAM1447  LOC254532 5'  TCCAGGCCCCGCCACCTCTGTT 98463      TCTCCA  A
                                GATAG     GC GGGCCTGGA
                                |||||     || |||||||||
                                TTGTC     CG CCCGGACCT
                                   TCCAC_  C
GAM1447  LOC254873 5'  TCCAGGCCGGAGTCAGAGACT  96213      CA  AG_
                                AGTCTC  GC   GGCCTGGA
                                ||||||  ||   ||||||||
                                TCAGAG  TG   CCGGACCT
                                    AC  AGG
GAM1447  LOC90049  3'  CCAGGCCTGAGAAGCCATCA   61875     A TC  CAGCA
                                TGAT G  TC    GGGCCTGG
                                |||| |  ||    ||||||||
                                ACTA C  AG    TCCGGACC
                                  C GA  AG___
GAM1447  LOC90379  5'  TCCATCAGACTGGAAACTCCCA 63204    AT   C    CAG  CC
                                TG  AGT TCCAG   GG  TGGA
                                ||  ||| |||||   ||  ||||
                                AC  TCA AGGTC   CT  ACCT
                                 CC   A    AGA  __
GAM1448  EDNRA     3'  AAGTCACTTTTATTTGAAA    64795      T       AAT
                                TTTC AATAAAAGT   GGCTT
                                |||| |||||||||   |||||
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                                AAAG TTATTTTCA   CTGAA
                                  T       ___
GAM1448 MAB21L1  3' CAAAGCCACTAGTATTAGAAG 19953        AA   AAT
                                TTTCTAATA  AGT   GGCTTTG
                                |||||||||  |||   |||||||
                                GAAGATTAT  TCA   CCGAAAC
                                    GA   ___
GAM1448 PACE4    3' CAAAGCCACCACATTTAGAA   57167      TAAAA  AA
                                TTCTAA    GT  TGGCTTTG
                                ||||||    ||  ||||||||
                                AAGATT    CA  ACCGAAAC
                                   TA___  CC
GAM1448 API5     3' CAAAGCCATTTCAAGTACAGAA 22733      AATAAAAGT
             A                   TTTCT        AATGGCTTTG
                                 |||||        ||||||||||
                                 AAAGA        TTACCGAAAC
                                    CATGAACT_
GAM1448 ATP10D   3' CAAAGCATGCCTTTTACCAGAA 73525     AA     TA   G
                                TTCT  TAAAAG  ATG CTTTG
                                ||||  ||||||  ||| |||||
                                AAGA  ATTTTC  TAC GAAAC
                                  CC     CG  _
GAM1448 KIAA0826 3' AGCTATTCTCATTAGAAA    83524        AAA  T
                                TTTCTAAT   AG AATGGCT
                                ||||||||   || |||||||
                                AAAGATTA   TC TTATCGA
                                    C__  _
GAM1448 KIAA1323 3' AGAGCTTTTACTTTTCTTAGAA 63720       T       T
             A                   TTTCTAA AAAAGTAA GGCTTT
                                 ||||||| |||||||| ||||||
                                 AAAGATT TTTTCATT TCGAGA
                                    C       T
GAM1448 NTPBP    3' CAAAGTTTCTCTTATTAGAGA  24391         A  TAAT
                                TTTCTAATAA AG    GGCTTTG
                                |||||||||| ||    |||||||
                                AGAGATTATT TC    TTGAAAC
                                      C  T___
GAM1448 LOC200107 3' CTATTACTTCTACTAGAGA    89984       A  A
                                TTTCTA TA AAGTAATGG
                                |||||| || |||||||||
                                AGAGAT AT TTCATTATC
                                   C  C
GAM1449 SCAMP1   3' GCTAAATAAATATTCTCC     18013     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1449 SCAMP1   3' GCTAAATAAATATTCTCC     54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
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                                CCT TTATAA TAAATCG
                                  C     A
GAM1449  NX-17    3'  TGAATATCAGCCCCTAATA   40706        ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM1449  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
              TA                  TATTAGGGATAATATTCATTTAGC
                                  ||||||||||||||||||||||||
                                  ATAATCCCTATTATAAGTAAATCG

GAM1450  SCAMP1   3'  GCTAAATAAATATTCTCC    54500     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1450  SCAMP1   3'  GCTAAATAAATATTCTCC    54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1450  NX-17    3'  TGAATATCAGCCCCTAATA   40706        ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM1450  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
              TA                  TATTAGGGATAATATTCATTTAGC
                                  ||||||||||||||||||||||||
                                  ATAATCCCTATTATAAGTAAATCG

GAM1451  BACH2    3'  CTGTCAAGCAATGGATAAACAG 41782          C     GGGA__
              CTCT                  AGAGTTGTT ATCCA     GACAG
                                ||||||||| |||||     |||||
                                TCTCGACAA TAGGT     CTGTC
                                    A     AACGAA
GAM1451  CHRNA1   3'  CTGTCTCCCTGAAGAGTGAAC  5375        C___
                                GTTCAT    CAGGGAGACAG
                                ||||||    ||||||||||||
                                CAAGTG    GTCCCTCTGTC
                                  AGAA
GAM1451  HHIP     5'  CTGTCCCACCTAAACAACTC   42753        CATCCAG  A
                                GAGTTGTT      GG GACAG
                                ||||||||      || |||||
                                CTCAACAA      CC CTGTC
                                    ATCCA__  _
GAM1451  MME      3'  TCCCTATGGAGGAACAACTCT  8034           A   __
                                AGAGTTGTTC TCCA  GGGA
                                |||||||||| ||||  ||||
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                                TCTCAACAAG AGGT  CCCT
                                      G    AT
GAM1451  MTCP1    5'  CTACATGGATAACAACTCT   27242        C    GGG
                                AGAGTTGTT ATCCA   AG
                                ||||||||| |||||   ||
                                TCTCAACAA TAGGT   TC
                                      _    ACA
GAM1451  NR1D1    3'  TGTCTCCCCCACAACCCT    41672    A    TCATCCA
                                AG GTTGT      GGGAGACA
                                || |||||      ||||||||
                                TC CAACA      CCCTCTGT
                                 C    CC_____
GAM1451  NR1I2    3'  TGTCTCCCTAGGGAATTC    15304      GTTCA  _
                                GAGTT    TCC AGGGAGACA
                                |||||    ||| |||||||||
                                CTTAA    GGG TCCCTCTGT
                                   _____  A
GAM1451  PCOLN3   3'  CTGCCCTGTTGCCAAACAACTC 12411        ___  TC    _
                                GAGTTGTT   CA  CAGGG AG
                                ||||||||   ||  ||||| ||
                                CTCAACAA   GT  GTCCC TC
                                     ACC  T_    G
GAM1451  PFN2     3'  TGTCTTCATCAACAACCCT   54889    A    CATCCAG
                                AG GTTGTT      GGAGACA
                                || ||||||      |||||||
                                TC CAACAA      CTTCTGT
                                 C     CTA____
GAM1451  PFN2     3'  TGTCTTCATCAACAACCCT   54890    A    CATCCAG
                                AG GTTGTT      GGAGACA
                                || ||||||      |||||||
                                TC CAACAA      CTTCTGT
                                 C     CTA____
GAM1451  TNS      3'  CTGTCTCCCTAACTCAACTGCT 42950    _    TTCATCC
                                AG AGTTG      AGGGAGACAG
                                || |||||      ||||||||||
                                TC TCAAC      TCCCTCTGTC
                                 G    TCAA___
GAM1451  FLJ10511 3'  CCCTAGAAAAACAACTCT    36686        CA  C
                                AGAGTTGTT  TC AGGG
                                |||||||||  || ||||
                                TCTCAACAA  AG TCCC
                                     AA  A
GAM1451  FLJ20195 3'  CCCGATGAACACCTCT      35216      T      CA
                                AGAG TGTTCATC  GGG
                                |||| ||||||||  |||
                                TCTC ACAAGTAG  CCC
                                  C       __
GAM1451  HAAO     3'  TCCCTGCCAAACAACTCT    60173        CATC
                                AGAGTTGTT    CAGGGA
                                |||||||||    ||||||
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                                TCTCAACAA   GTCCCT
                                     ACC_
GAM1451  KIAA0843  3'  CTGAACAACCAGACAGACAACT 30801       CA  CA  GAGA_
           CT                   AGAGTTGTT  TC  GG    CAG
                                |||||||||  ||  ||    |||
                                TCTCAACAG  AG  CC    GTC
                                     AC  A_  AACAA
GAM1451  KIAA1497  5'  CTGTCCTTGTATGAGCAAC   68121        C     GA
                                GTTGTTCAT CAGGGA  CAG
                                |||||||||| ||||||  |||
                                CAACGAGTA GTTCCT  GTC
                                     T     __
GAM1451  KIAA1710  3'  TCTCCATACATGAACAATCT   63181     G      CCAG
                                AGA TTGTTCAT    GGAGA
                                ||| ||||||||    |||||
                                TCT AACAAGTA    CCTCT
                                  _       CATA
GAM1451  PDE7B    3'  CTGCCGAAATGAGCAACTC   38949         CCA  G
                                GAGTTGTTCAT   GG AG
                                ||||||||||   || ||
                                CTCAACGAGTA   CC TC
                                     AAG  G
GAM1451  SEC24B   3'  CTGCATTGTTGGATGACAACTC 21984        T      G  GA
           T                    AGAGTTGT CATCCAG GA  CAG
                                |||||||| |||||||  ||  |||
                                TCTCAACA GTAGGTT TT  GTC
                                     _      G  AC
GAM1451  LOC124753 5'  CTGCCTCCCTGGCTTCCATCTC 74803     T  TTCAT       A
                                GAG TG     CCAGGGAG CAG
                                ||| ||     |||||||| |||
                                CTC AC     GGTCCCTC GTC
                                  T  CTTC_       C
GAM1451  LOC142948 3'  CTACCGGGAGGAATGAATAACT 83777          ____   A  G
           C                     GAGTTGTTCA    TCC GG AG
                                ||||||||||    ||| || ||
                                CTCAATAAGT    AGG CC TC
                                     AAGG   G  A
GAM1451  LOC153914 5'  CCACTAAAGTGAACAACTC   81898          CC_  _
                                GAGTTGTTCAT   AG GG
                                ||||||||||   || ||
                                CTCAACAAGTG   TC CC
                                     AAA  A
GAM1451  LOC219445 5'  CTCCCTGGTTCAAACAATTC   93202        CAT_
                                GAGTTGTT    CCAGGGAG
                                ||||||||    ||||||||
                                CTTAACAA    GGTCCCTC
                                     ACTT
GAM1451  LOC219914 5'  CCACTGGGAGGAACGAACAACT 94967         A_____    _
           C                     GAGTTGTTC     TCCAG GG
                                |||||||||     ||||| ||
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                                CTCAACAAG     GGGTC CC
                                     CAAGGA    A
GAM1452 CDH12    3' CTTATCATTTAAAGTGGTGTA 15777        CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM1452 GOCAP1   3' ATTGTTCTTGGGAGCAGTGTA 43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC         G
GAM1452 DKFZp434N2435 5' CTTATTACTGTGGGGTGGT    98090       T    AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT     TTATTC
                                   _    GTCA_
GAM1452 DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
             A                   TACAC       AGAAGAATAAG
                                 |||||       ||||||||||
                                 ATGTG       TCTTCTTATTC
                                    TACTCCC_
GAM1452 FLJ21791  3' CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                 TACACCACT       GAATAAG
                                 |||||||||       |||||||
                                 ATGTGGTGA       TTTATTC
                                      AGACG___
GAM1452 HMP19    3' CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
             TA                    TACA    TCC    GAAGAATAAG
                                   ||||    |||    ||||||||||
                                   ATGT    AGG    TTTCTTATTC
                                     AAA_   ATTG
GAM1452 KIAA1719  3' TCTGTCTTGGGAGTGGTGTA   68742             _
                                 TACACCACTCCCAAGA AGA
                                 |||||||||||||||| |||
                                 ATGTGGTGAGGGTTCT TCT
                                           G
GAM1452 KIAA1853  3' TTTTTCTTGGAAGCAGTG    69929     CA  C
                                 CAC  CT CCAAGAAGAA
                                 |||  || ||||||||||
                                 GTG  GA GGTTCTTTTT
                                   AC  A
GAM1452 KIAA1877  3' CTTATTCTTCTGCCATGAGT   66748      CCA__
                                 ACTC    AGAAGAATAAG
                                 ||||    ||||||||||
                                 TGAG    TCTTCTTATTC
                                   TACCG
GAM1452 KIAA1906  3' CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                                 CCA    CAAGAAGAATAAG
                                 |||    ||||||||||||
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                              GGT    GTTCTTCTTATTC
                                TTTCA
GAM1452 OSBPL11  3' CTTAATTTCCCAAGAGTGGTG 43206       CCAA   AA
                              CACCACTC   GAAG  TAAG
                              ||||||||   ||||  ||||
                              GTGGTGAG   CTTT  ATTC
                                  AACC   A_
GAM1452 YME1L1   3' TCATTCTTGATGTGGTGTA   58438       TCC    _
                              TACACCAC   CAAGAA GA
                              ||||||||   ||||||  ||
                              ATGTGGTG   GTTCTT CT
                                  TA_    A
GAM1452 ZNF262   3' CTTATTTTGTTTGGGAGT    18723        A
                              ACTCCCAAG AGAATAAG
                              ||||||||| ||||||||
                              TGAGGGTTT TTTTATTC
                                  G
GAM1452 LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_    AAGA
                              TACACCAC   CCAAG   ATA
                              ||||||||   |||||   |||
                              ATGTGGTG   GGTTC   TGT
                                  CAA    GG__
GAM1453 SCAMP1   3' GCTAAATAAATATTCTCC    54500    T    C
                              GGA AATATT ATTTAGC
                              ||| |||||| |||||||
                              CCT TTATAA TAAATCG
                                C    A
GAM1453 SCAMP1   3' GCTAAATAAATATTCTCC    54501    T    C
                              GGA AATATT ATTTAGC
                              ||| |||||| |||||||
                              CCT TTATAA TAAATCG
                                C    A
GAM1453 NX-17    3' TGAATATCAGCCCCTAATA   40706       ATA_
                              TATTAGGG   ATATTCA
                              ||||||||   |||||||
                              ATAATCCC   TATAAGT
                                  CGAC
GAM1453 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
          TA                    TATTAGGGATAATATTCATTTAGC
                              ||||||||||||||||||||||||
                              ATAATCCCTATTATAAGTAAATCG

GAM1454 SCAMP1   3' GCTAAATAAATATTCTCC    54500    T    C
                              GGA AATATT ATTTAGC
                              ||| |||||| |||||||
                              CCT TTATAA TAAATCG
                                C    A
GAM1454 SCAMP1   3' GCTAAATAAATATTCTCC    54501    T    C
                              GGA AATATT ATTTAGC
                              ||| |||||| |||||||
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                                CCT TTATAA TAAATCG
                                  C     A
GAM1454  NX-17    3'  TGAATATCAGCCCCTAATA   40706        ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM1454  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
                TA                  TATTAGGGATAATATTCATTTAGC
                                    ||||||||||||||||||||||||
                                    ATAATCCCTATTATAAGTAAATCG

GAM1455  SCAMP1   3'  GCTAAATAAATATTCTCC    18014     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1455  SCAMP1   3'  GCTAAATAAATATTCTCC    54500     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1455  NX-17    3'  TGAATATCAGCCCCTAATA   40706        ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM1455  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
                TA                  TATTAGGGATAATATTCATTTAGC
                                    ||||||||||||||||||||||||
                                    ATAATCCCTATTATAAGTAAATCG

GAM1456  ADAMTS13  5'  CAAGGCCCAGCTTGCAGCAGG  58149          A   CTTT
                                CTTGCTGCAA CTG    TCTTG
                                |||||||||| |||    |||||
                                GGACGACGTT GAC    GGAAC
                                      C   CC__
GAM1456  BLAME     3'  CAAGAAAAGCAGCTCAGCTCAG 39650     T_   CAAA
                G                    CCT  GCTG    CTGCTTTTCTTG
                                     |||  ||||    ||||||||||||
                                     GGA  CGAC    GACGAAAAGAAC
                                       CT    TC__
GAM1456  FHL1      3'  AAAAGCAACCCTGCAGCAA    9359        AAC_
                                TTGCTGCA    TGCTTTT
                                ||||||||    |||||||
                                AACGACGT    ACGAAAA
                                    CCCA
GAM1456  MRPL49    3'  CAAGTGTACAGCCACAGCAAGG 70163        CAAA   CTTTT
                                CCTTGCTG    CTG     CTTG
                                ||||||||    |||     ||||
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                                GGAACGAC   GAC    GAAC
                                    ACC_  ATGT_
GAM1456  PTPRA    5'  CAAGAATGAGTTTGCAGCCAAG 55948     _      GCTT
                                CTTG CTGCAAACT   TTCTTG
                                |||| |||||||||   ||||||
                                GAAC GACGTTTGA   AAGAAC
                                  C       GT__
GAM1456  TBX3     3'  AGAGCAACTTCCAGCAAGG   21145       C  AC
                                CCTTGCTG AA  TGCTTT
                                |||||||| ||  ||||||
                                GGAACGAC TT  ACGAGA
                                    C  CA
GAM1456  C12orf2  3'  CAAGAAAAGCAAAAATGAACAA 83679     CTG  AAC_
           G                     CTTG   CA   TGCTTTTCTTG
                                ||||  ||   ||||||||||
                                GAAC  GT   ACGAAAAGAAC
                                  AA_  AAAA
GAM1456  C5orf4   5'  CAAGGTTAGCCTGCAGCAG   33423       AACT   TT
                                TTGCTGCA   GCT  TCTTG
                                ||||||||   |||  |||||
                                GACGACGT   CGA  GGAAC
                                    C___   TT
GAM1456  C8orf4   3'  AAAATGCTTTCAGCAAGG    39689       C   CT  _
                                CCTTGCTG AAA  GC TTTT
                                |||||||| |||  || ||||
                                GGAACGAC TTT  CG AAAA
                                    _   __  T
GAM1456  EIF3S1   3'  CAAGAAAAGCAGTTTGCAGCAA 63866
           GG                     CCTTGCTGCAAACTGCTTTTCTTG
                                ||||||||||||||||||||||||
                                GGAACGACGTTTGACGAAAAGAAC

GAM1456  FLJ10512 3'  CAAGAAAATGTACAGCAA    36692       CAAAC  _
                                TTGCTG    TGC TTTTCTTG
                                ||||||    ||| ||||||||
                                AACGAC    ATG AAAAGAAC
                                   ______  T
GAM1456  FLJ23441 3'  CAAGAAGAGGTACTTATAGCAA 45491        CAAACTG
           GG                     CCTTGCTG     CTTTTCTTG
                                ||||||||     |||||||||
                                GGAACGAT     GAGAAGAAC
                                    ATTCATG
GAM1456  KIAA0033 3'  CAAGAAAGGACCCTTCAGCAAG 77083        CAAACTG
           G                     CCTTGCTG     CTTTTCTTG
                                ||||||||     |||||||||
                                GGAACGAC     GGAAAGAAC
                                    TTCCCA_
GAM1456  KIAA1202 3'  AAGGGAGCTGCAGCAAGG    72479         AACT  T TT
                                CCTTGCTGCA   GC T  CTT
                                ||||||||||   || |  |||
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                                GGAACGACGT   CG A  GAA
                                     _____  _ GG
GAM1456  PCDH20   3'  CAAGAAAAACAGCCAGAAGCAA 43418      GCAAA  C
                                TTGCT    CTG TTTTCTTG
                                ||||||    ||| ||||||||
                                AACGA    GAC AAAAGAAC
                                   AGACC   A
GAM1456  PDZD2    5'  AGAACAGCCTGCAGGAAGG   81715     G    AACT  T
                                CCTT CTGCA   GCT TTCT
                                |||| ||||||   ||| ||||
                                GGAA GACGT   CGA AAGA
                                  G    C___  C
GAM1456  PRO1430  3'  AAAATGCTTTCAGCAAGG    38353       C  CT  _
                                CCTTGCTG AAA  GC TTTT
                                |||||||| |||  || ||||
                                GGAACGAC TTT  CG AAAA
                                     _  __  T
GAM1456  SLB      5'  CAAGAAAGTCATCTGCAACAAG 90259     C   AAC  C
                                CTTG TGCA   TG TTTTCTTG
                                |||| ||||   || ||||||||
                                GAAC ACGT   AC GAAAGAAC
                                  A   CT_  T
GAM1456  LOC129228 5'  AAAGGCCGTCTCAGCAAGG   76319       CAA  T
                                CCTTGCTG   AC GCTTTT
                                ||||||||   || ||||||
                                GGAACGAC   TG CGGAAA
                                     TC_  C
GAM1456  LOC143310 5'  AAAGGCAGATTCACAGGAAG   77028    G   CA  _
                                CTT CTG  AA CTGCTTTT
                                ||| |||  || ||||||||
                                GAA GAC  TT GACGGAAA
                                  G   AC  A
GAM1456  LOC157737 5'  AAAGCAGCCTGACAGCAAGG   87840       _  AA
                                CCTTGCTG CA  CTGCTTT
                                |||||||| ||  |||||||
                                GGAACGAC GT  GACGAAA
                                     A  CC
GAM1456  LOC200010 3'  AAGAAAAGGAGCAGGAAG    91523    G   AAAC G
                                CTT CTGC    T CTTTTCTT
                                ||| ||||    | ||||||||
                                GAA GACG    A GAAAAGAA
                                  G    ____ G
GAM1456  LOC202134 3'  CAAGAAAAGTAACAGGCAAGG  91916       GCAAAC
                                CCTTGCT     TGCTTTTCTTG
                                |||||||     ||||||||||
                                GGAACGG     ATGAAAAGAAC
                                     ACA___
GAM1456  LOC219578 5'  AGAAAAGCAACTCCAGCAAGG  96025       CAAAC
                                CCTTGCTG    TGCTTTTCT
                                ||||||||    |||||||||
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                                GGAACGAC    ACGAAAAGA
                                    CTCA_
GAM1456  LOC257096 5'  AGAGGTAAATTTGCAGCAA   97625         C_
                                TTGCTGCAAA  TGCTTTT
                                ||||||||||  |||||||
                                AACGACGTTT  ATGGAGA
                                     AA
GAM1456  LOC257096 3'  CAAGAAAAGCAGGTTGTA    97626      A
                                TGCAA CTGCTTTTCTTG
                                ||||| ||||||||||||
                                ATGTT GACGAAAAGAAC
                                   G
GAM1456  LOC257485 3'  CAAGAAAACCAGCTTGCAGCAA 66209          A   C
            GG                    CCTTGCTGCAA CTG TTTTCTTG
                                ||||||||||| ||| ||||||||
                                GGAACGACGTT GAC AAAAGAAC
                                     C   C
GAM1457  GPD1     3'  TCATGCCACCACATTTG     60398      C      C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A       _
GAM1457  IL5RA    5'  TCGCATGGCCACCGCATTT    6906          AT__
                                AAATGCGGTGGC   CGA
                                ||||||||||||   |||
                                TTTACGCCACCG   GCT
                                     GTAC
GAM1457  MYO1C    3'  TGCCGATGCCAAATATTTG   61873      CGG      A
                                TAAATG   TGGCATCG CA
                                ||||||   |||||||| ||
                                GTTTAT   ACCGTAGC GT
                                   AA_      C
GAM1457  C6orf37  3'  TGTCACACTGCATTTA     68097         GCATC
                                TAAATGCGGTG    GACA
                                ||||||||||    ||||
                                ATTTACGTCAC    CTGT
                                     A____
GAM1457  DNAJC6   3'  TTGCAGAACCACCGCATT    29498         CA  GA
                                AATGCGGTGG  TC  CAA
                                |||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                     A_  AC
GAM1457  FLJ11210 3'  GTCGATGTGCATGCTTTTA   60319     T   GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM1457  FLJ12476 3'  TCGATCTTCTGCATTTA     43270         T  C
                                TAAATGCGG GG ATCGA
                                ||||||||| || |||||
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                                ATTTACGTC TC TAGCT
                                      T  _
GAM1457  KIAA1034  3'  TCGATGGCATCCGCATTTG   63134        _  G
                                TAAATGCGG TG CATCGA
                                |||||||||  ||  ||||||
                                GTTTACGCC AC GTAGCT
                                      T  G
GAM1457  KIAA1987  3'  TCATGTAACTGCATTTA    89391         G   C
                                TAAATGCGGT GCAT GA
                                ||||||||||  ||||  ||
                                ATTTACGTCA TGTA CT
                                      A   _
GAM1457  MGC16063  3'  TGTCCTGGCCACTGCATT   54929          ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                       GTC
GAM1457  LOC147949 3'  TGTCAGATGTCCACATTGCA  79279     __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  ||||  ||||  ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM1457  LOC150577 3'  GTCCTCACCGCATTTG     86258          CATC
                                TAAATGCGGTGG   GAC
                                ||||||||||||   |||
                                GTTTACGCCACT   CTG
                                       C___
GAM1457  LOC158219 3'  TGTGTGTCACCACATTT    82694      C       CG
                                AAATG GGTGGCAT  ACA
                                |||||  ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                   A       __
GAM1457  LOC202020 3'  TGTCTCACCACATTTA     90605       C    CATC
                                TAAATG GGTGG   GACA
                                ||||||  |||||   ||||
                                ATTTAC CCACT   CTGT
                                    A    _____
GAM1457  LOC90826  5'  TGTCGATGCAGGTTTATTTG  64788       CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                    TTGGA
GAM1457  LOC93587  3'  TTGTCTTTACCTGCATTTA   73042       _    CATC
                                TAAATGC GGTGG   GACAA
                                |||||||  |||||   |||||
                                ATTTACG CCATT   CTGTT
                                     T    T___
GAM1458  LOC204285 3'  ACCAGTACCTGCAGGTCACCCA 91010     TAC          C
                                TGG   GCCTGCAGGTAC GGT
                                |||   ||||||||||| |||
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                                ACC   TGGACGTCCATG CCA
                                  CAC          A
GAM1459  IRS1     3'  CCATAGATGGTTCTCAATTGTA 19874      C        TGAAC
                                TACA ATTGAGAACC     ATGG
                                |||| ||||||||||     ||||
                                ATGT TAACTCTTGG     TACC
                                  _         TAGA_
GAM1459  SERPINF1  3'  CCTGTAAGGTTTCAATG     12038        A   GA   T
                                CATTGAGA CCT  ACA GG
                                |||||||| |||  ||| ||
                                GTAACTTT GGA  TGT CC
                                     _   A_   _
GAM1459  HSA243396 3'  CCATGTTCAGCAATGTCAATG  37844       GAAC_
                                CATTGA     CTGAACATGG
                                ||||||     ||||||||||
                                GTAACT     GACTTGTACC
                                   GTAAC
GAM1459  KIAA1387  3'  CAGGAATTTTCAATATGTA    71444      C       __
                                TACA ATTGAGAA  CCTG
                                |||| ||||||||  ||||
                                ATGT TAACTTTT  GGAC
                                  A       AA
GAM1459  MGC16063  3'  TTCAAATTCCAATGTGTA     54930         A   CC
                                TACACATTG GAA  TGAA
                                |||||||||| |||  ||||
                                ATGTGTAAC CTT  ACTT
                                     _   AA
GAM1459  SMCR8     3'  CCATGCTCAGGTTTGACTATGT 59253      TGA_       A
                                ACAT    GAACCTGA CATGG
                                ||||    |||||||| |||||
                                TGTA    TTTGGACT GTACC
                                  TCAG       C
GAM1459  UPLC1     3'  CCATGCTAGGCCCCAATGT    35227       AGAA    AA
                                ACATTG    CCTG  CATGG
                                ||||||    ||||  |||||
                                TGTAAC    GGAT  GTACC
                                   CCC_    C_
GAM1459  ZNF334    3'  CCATAAGTCAACCCTCAATGT  36637        AACC   AC_
                                ACATTGAG    TGA   ATGG
                                ||||||||    |||   ||||
                                TGTAACTC    ACT   TACC
                                    CCA_   GAA
GAM1459  LOC145082 3'  TATGGAATGCCCTTAATGTGTA 84196          AACCTGAA
                                TACACATTGAG       CATG
                                ||||||||||        ||||
                                ATGTGTAATTC       GTAT
                                      CCGTAAG_
GAM1459  LOC157723 3'  CCAAGTAAGGTTCTCAAATGT  82465       _       GA  A
                                ACATT GAGAACCT  AC TGG
                                ||||| ||||||||  || |||
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                                TGTAA CTCTTGGA  TG ACC
                                   A       A_  A
GAM1459  LOC219988 5'  CCATGTTCGGCCCCCAATG   93262      AGAAC
                                CATTG    CTGAACATGG
                                |||||    ||||||||||
                                GTAAC    GGCTTGTACC
                                   CCCC_
GAM1460  CCBL1    3'  CATCCCAGCTCTGCATGGC   15769          TCTA
                                GCCATGCGGAGCT   GATG
                                ||||||||||||   ||||
                                CGGTACGTCTCGA   CTAC
                                       CC__
GAM1460  CD209L   3'  GCATCCAGAGAGGGCATGG   27307      GGAG    A__
                                CCATGC   CTTCT   GATGC
                                ||||||   |||||  |||||
                                GGTACG   GGAGA   CTACG
                                   ____    GAC
GAM1460  INHBA    3'  GCATCTAGAAAGCCATG     11002     CGGA   _
                                CATG   GCTT CTAGATGC
                                ||||   |||| ||||||||
                                GTAC   CGAA GATCTACG
                                  ____   A
GAM1460  OLFM1    3'  CTGAGGCTCCACATAGC     27344    C  C      T
                                GC ATG GGAGCTTC AG
                                || ||| |||||||| ||
                                CG TAC CCTCGGAG TC
                                 A  A      _
GAM1460  PODXL    3'  CACTAGAAGCTCAGCATG    19413      G       A
                                CATGC GAGCTTCTAG TG
                                ||||| |||||||||| ||
                                GTACG CTCGAAGATC AC
                                   A       _
GAM1460  RAMP3    3'  GCATCCTGTGCTCCGCAGGC  20727     A      TTCTA
                                GCC TGCGGAGC    GATGC
                                ||| ||||||||    |||||
                                CGG ACGCCTCG    CTACG
                                  _      TGTC_
GAM1460  ZNF80    3'  CATCTAGAAGTATAAGCAT   24069     GGA_
                                ATGC   GCTTCTAGATG
                                ||||   ||||||||||
                                TACG   TGAAGATCTAC
                                  AATA
GAM1460  FLJ11125 5'  GCATCTAGAGCAGAGCCTGGC 60324     T  GGA  T
                                GCCA GC   GCT CTAGATGC
                                |||| ||   ||| ||||||||
                                CGGT CG   CGA GATCTACG
                                  C  AGA  _
GAM1460  FLJ14249 3'  GCACCCAGAACTGCATGGT   42642        AGC   AGA
                                GCCATGCGG   TTCT   TGC
                                |||||||||   ||||   |||
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                                TGGTACGTC  AAGA  ACG
                                     ___   CCC
GAM1460 KIAA1023 3' GCATCTAGACCCCTGCACAGC 34681   CA   AGCT
                                GC TGCGG   TCTAGATGC
                                || |||||   |||||||||
                                CG ACGTC   AGATCTACG
                                 AC   CCC_
GAM1460 KIAA1453 5' CATTCAGGAGCTCCGCGTAGC 47659   C        AG
                                GC ATGCGGAGCTTCT ATG
                                || ||||||||||||| |||
                                CG TGCGCCTCGAGGA TAC
                                 A          CT
GAM1460 PEPP3   3' CTGTGAAGCTCCACAGAGC   30707   CA C     _
                                GC TG GGAGCTTC TAG
                                ||  || |||||||| |||
                                CG  AC CCTCGAAG GTC
                                 AG A       T
GAM1460 RAB35   3' CTAGAAGCCCCCATGGC    23413      C A
                                GCCATG GG GCTTCTAG
                                |||||| || ||||||||
                                CGGTAC CC CGAAGATC
                                   _ C
GAM1460 SCAND1  5' GCAGGTAAGCTCCGCA     33796        _ AGA
                                TGCGGAGCTT CT  TGC
                                |||||||||| ||  |||
                                ACGCCTCGAA GG  ACG
                                     T ____
GAM1460 LOC148426 5' CATCCAGAAGCTTCGGCAGG  85305   A _      A
                                CC TGC GGAGCTTCT GATG
                                || ||| ||||||||| ||||
                                GG ACG CTTCGAAGA CTAC
                                 _  G       C
GAM1460 LOC155179 3' GCATCTAGACCCCTGCACAGC 82231   CA   AGCT
                                GC TGCGG   TCTAGATGC
                                || |||||   |||||||||
                                CG ACGTC   AGATCTACG
                                 AC   CCC_
GAM1461 CDH12   3' CTTATCATTTAAAGTGGTGTA 15777       CCCAA  GA
                                TACACCACT   GAA ATAAG
                                |||||||||   ||| |||||
                                ATGTGGTGA   TTT TATTC
                                     AA___  AC
GAM1461 GOCAP1  3' ATTGTTCTTGGGAGCAGTGTA 43007     CA       G
                                TACAC CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG GAGGGTTCTT TTA
                                   AC       G
GAM1461 DKFZp434N2435 5' CTTATTACTGTGGGGTGGT   98090     T   AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
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                                TGGTG GGGT     TTATTC
                                  _    GTCA_
GAM1461  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
           A                       TACAC       AGAAGAATAAG
                                   |||||       ||||||||||
                                   ATGTG       TCTTCTTATTC
                                     TACTCCC_
GAM1461  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                   TACACCACT       GAATAAG
                                   |||||||||       |||||||
                                   ATGTGGTGA       TTTATTC
                                        AGACG___
GAM1461  HMP19     3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
           TA                        TACA    TCC    GAAGAATAAG
                                   ||||    |||    ||||||||||
                                   ATGT    AGG    TTTCTTATTC
                                     AAA_   ATTG
GAM1461  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68742              _
                                   TACACCACTCCCAAGA AGA
                                   |||||||||||||||| |||
                                   ATGTGGTGAGGGTTCT TCT
                                              G
GAM1461  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                   CAC  CT CCAAGAAGAA
                                   |||  || ||||||||||
                                   GTG  GA GGTTCTTTTT
                                     AC  A
GAM1461  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748      CCA__
                                   ACTC    AGAAGAATAAG
                                   ||||    ||||||||||
                                   TGAG    TCTTCTTATTC
                                     TACCG
GAM1461  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                                   CCA    CAAGAAGAATAAG
                                   |||    ||||||||||||
                                   GGT    GTTCTTCTTATTC
                                     TTTCA
GAM1461  OSBPL11   3'  CTTAATTTCCCAAGAGTGGTG  43206         CCAA    AA
                                   CACCACTC    GAAG  TAAG
                                   ||||||||    ||||  ||||
                                   GTGGTGAG    CTTT  ATTC
                                        AACC    A_
GAM1461  YME1L1    3'  TCATTCTTGATGTGGTGTA    58438         TCC     _
                                   TACACCAC   CAAGAA GA
                                   ||||||||   |||||| ||
                                   ATGTGGTG   GTTCTT CT
                                        TA_     A
GAM1461  ZNF262    3'  CTTATTTTGTTTGGGAGT     18723          A
                                   ACTCCCAAG AGAATAAG
                                   ||||||||| ||||||||
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                                TGAGGGTTT TTTTATTC
                                     G
GAM1461 LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_    AAGA
                                TACACCAC  CCAAG   ATA
                                ||||||||  |||||   |||
                                ATGTGGTG  GGTTC   TGT
                                     CAA    GG__
GAM1462 DJ971N18.2 3' GCCCTGTGAAATGAAAGCCAAG 41263     AT     AA _  A
                                CTTG  TTTCATT  TC CAG GC
                                ||||  |||||||  || ||| ||
                                GAAC  AAAGTAA  AG GTC CG
                                  CG      __ T  C
GAM1462 FLJ10498 3' GCTCTGAAAATTGGTAAATCAA 36677       _  TTAATC
             G                   CTTGATTT TCA     CAGAGC
                                ||||||||| |||     ||||||
                                GAACTAAA GGT     GTCTCG
                                     T   TAAAA_
GAM1462 GRSF1    3' GCTCTAGATAGGAAAAAAATCA 10880       CA  A_  C
             G                   TTGATTTT  TT  ATC AGAGC
                                ||||||||  ||  ||| |||||
                                GACTAAAA  AG  TAG TCTCG
                                     AA  GA   A
GAM1462 KIAA1046 3' CTGATTTTAATGAAAATCA   30661          TC_
                                TGATTTTCATTAA   CAG
                                ||||||||||||   |||
                                ACTAAAAGTAATT   GTC
                                       TTA
GAM1462 KIAA1107 5' CTCTGGTGATATAAAAATCAA 64690       C  TAAT
                                TTGATTTT AT    CCAGAG
                                ||||||||  ||    ||||||
                                AACTAAAA TA    GGTCTC
                                     A  TAGT
GAM1462 KIAA1145 3' CTCAGGAAATGAAAACAA    66237     A      AA   A
                                TTG TTTTCATT  TCC GAG
                                ||| ||||||||  ||| |||
                                AAC AAAAGTAA  AGG CTC
                                  _       __   A
GAM1462 LCE      3' GCTCTGGAACTCAAAATCAA   44260       CATTAA
                                TTGATTTT     TCCAGAGC
                                ||||||||     ||||||||
                                AACTAAAA     AGGTCTCG
                                     CTCA__
GAM1462 MGC16175 3' CTCTGAATTAATGACTGT    52278    TT      C
                                AT  TCATTAAT CAGAG
                                ||  |||||||| |||||
                                TG  AGTAATTA GTCTC
                                 TC       A
GAM1462 SPANXB1  3' CTTCGGCAATGAAAATAAAGT  51624     G       AAT  AG
                                ACTT ATTTTCATT   CC  AG
                                |||| |||||||||   ||  ||
```

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                                TGAA TAAAAGTAA   GG  TC
                                  A        C__  CT
GAM1462  TRAG3    3'  TGGTGATGAAAATAAAGT    68134      G         AT
                                ACTT ATTTTCATTA  CCA
                                |||| ||||||||||  |||
                                TGAA TAAAAGTAGT  GGT
                                  A         __
GAM1462  LOC221688 5'  GCTCCATATAGTATGAAAATCA 95309             TAATCCA_
           AGT                    ACTTGATTTTCAT       GAGC
                                |||||||||||||       ||||
                                TGAACTAAAAGTA       CTCG
                                       TGATATAC
GAM1463  DHCR24   3'  CCCCCAGCCACCACTGA     29299        AGACTCT  _    C
                                TCAGTG      TGG TGGGG G
                                ||||||      ||| ||||| |
                                AGTCAC      ACC ACCCC C
                                   C_______  G    A
GAM1463  KCNS2    3'  CCCCTAAAGTCTCACT      68845          C   T
                                AGTGAGACT TTGG GGG
                                ||||||||| |||| |||
                                TCACTCTGA AATC CCC
                                          _   _
GAM1463  LHX2     5'  CCACCCCACCAGGCAACCCCTG 17735      TGAGACT         C
           A                     TCAG      CTTGGTGGGG GG
                                ||||      |||||||||| ||
                                AGTC      GGACCACCCC CC
                                  CCCAAC_         A
GAM1463  LHX5     3'  CCGCCCCGAAGCAGCCTCCTGA 42560      T  A  _   GG
                                TCAG GAG CT CTT  TGGGGCGG
                                |||| ||| || |||  ||||||||
                                AGTC CTC GA GAA  GCCCCGCC
                                  _  C  C   __
GAM1463  PACSIN1  3'  CCACCAAAGAGTCTCCTGA    93879      T        _
                                TCAG GAGACTCTT GGTGG
                                |||| |||||||| |||||
                                AGTC CTCTGAGAA CCACC
                                  _        A
GAM1463  SLC25A15 3'  CTGACCAAAAATTCACTGA    27294         ACTC    G
                                TCAGTGAG    TTGGT GG
                                ||||||||    ||||| ||
                                AGTCACTT    AACCA TC
                                     AAA_    G
GAM1463  FLJ14075 3'  CCAGATCTCCAAGAACTCACT  46581        AC     T  GGC
                                AGTGAG  TCTTGG GG   GG
                                ||||||  |||||| ||   ||
                                TCACTC  AGAACC CT   CC
                                   A_     T  AGA
GAM1463  HSGP25L2G 3'  CCACCCTGGGAACCTCACTG   62867        A__   TT
                                CAGTGAG   CTC  GGTGG
                                |||||||   |||  |||||
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                                GTCACTC  GGG  CCACC
                                    CAA  TC
GAM1463 HSRNAFEV 3' CCCCCGCAGTCCCCTGA    34446     TGA   CTTG    C
                                TCAG  GACT   GTGGGG G
                                ||||  ||||   |||||| |
                                AGTC  CTGA   CGCCCC C
                                  CC_  _____    A
GAM1463 KIAA0972 5' CCAGGAACAGGAGTCCCACCGA 30679    A  A      GTG__
                                TC GTG GACTCTTG    GG
                                || ||| ||||||||    ||
                                AG CAC CTGAGGAC    CC
                                 C  C       AAGGA
GAM1463 KIAA1205 3' CCGCCCCACCCCCTGCTCCCAC 70582     A  CTCTT_
             T                   AGTG GA     GGTGGGGCGG
                                ||||  ||     ||||||||||
                                TCAC CT     CCACCCCGCC
                                  C  CGTCCC
GAM1463 KIAA1856 3' CCACCCCACCAAGTGTACTG  94227      AGACT       C
                                CAGTG    CTTGGTGGGG GG
                                |||||    |||||||||| ||
                                GTCAT    GAACCACCCC CC
                                  GT___        A
GAM1463 MGC29654 5' CCGCCCCGTGCAACCTCAC   67206      ACTC  _
                                GTGAG   TTG GTGGGGCGG
                                |||||   ||| |||||||||
                                CACTC   AAC TGCCCCGCC
                                  C___  G
GAM1463 RAI     3' CCGCCCCACCAAGCTCTGTCTC 22852      T___
                                GAGAC   CTTGGTGGGGCGG
                                |||||   ||||||||||||
                                CTCTG   GAACCACCCCGCC
                                  TCTC
GAM1463 TOR2A   3' CCCCAGAACCTCACTGA    56183       AC  TGGT
                                TCAGTGAG  TCT   GGGG
                                ||||||||  |||   ||||
                                AGTCACTC  AGA   CCCC
                                    CA  _____
GAM1463 LOC144108 5' CCACCCATGAACTTCACTGA  77188       AC  TT_
                                TCAGTGAG  TC  GGTGG
                                ||||||||  ||  |||||
                                AGTCACTT  AG  CCACC
                                    CA  TAC
GAM1463 LOC149076 3' CCGCCCCACCCGGCCCACTGG  79875      AGACT  T
                                TCAGTG    CT GGTGGGGCGG
                                ||||||    || ||||||||||
                                GGTCAC    GG CCACCCCGCC
                                  CC___  C
GAM1463 LOC149670 3' CCACCCAAGACCCACTGA    80302      AGAC    _
                                TCAGTG   TCTTGG TGG
                                ||||||   |||||| |||
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                                AGTCAC    AGAACC ACC
                                   CC__      C
GAM1463  LOC150384 5'  CCACCCACGGCAAAGTGTCACT 86225       G   C   G _   C
                                AGTGA ACT TTG TG GGG GG
                                ||||| ||| ||| || ||| ||
                                TCACT TGA AAC GC CCC CC
                                   G   _   G A   A
GAM1463  LOC197342 3'  CCACCCCTCCCAGCCTCACTG  89354        A  CTT  T    C
                                CAGTGAG CT   GG GGGG GG
                                ||||||| ||   || |||| ||
                                GTCACTC GA   CC CCCC CC
                                    C  C__  T    A
GAM1463  LOC203504 5'  CCACCCCACCTGGAGCTTCAC  92320      GA    T      C
                                GTGA  CTCT GGTGGGG GG
                                ||||  |||| ||||||| ||
                                CACT  GAGG CCACCCC CC
                                   TC    T      A
GAM1463  LOC203636 3'  CCCCCAGGGCCTCACCGG    90976    A    A   TGGT    C
                                TC GTGAG CTCT    GGGG G
                                || ||||| ||||    |||| |
                                GG CACTC GGGA    CCCC C
                                 C    C    ____    A
GAM1463  LOC90019  5'  CCGCCCCACCTTCCTTCCCAC  57526     A  CTCTT
                                GTG GA    GGTGGGGCGG
                                ||| ||    ||||||||||
                                CAC CT    CCACCCCGCC
                                  C  TCCTT
GAM1463  LOC90917  3'  CCACCCAAAGAGTCTGACTGA  64982       G       __
                                TCAGT AGACTCTT  GGTGG
                                ||||| ||||||||  |||||
                                AGTCA TCTGAGAA  CCACC
                                   G       AC
GAM1463  LOC91421  5'  CCACCCCAGTGGCAGAGCCTAC 66594     G  A    __  G    C
              T                    AGT AG CTCT  TG TGGGG GG
                                ||| || ||||  || ||||| ||
                                TCA TC GAGA  GT ACCCC CC
                                  _  C    CG  G    A
GAM1464  DLEC1    3'  CATCTGGCCCTCCCTTG     24716       A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                   C    G  _
GAM1464  DLEC1    3'  CATCTGGCCCTCCCTTG     24717       A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                   C    G  _
GAM1464  PIP5K1A   3'  TATCCCACCCTGCCTTGATA   14520         A   CA  C
                                TATCAAGG AGGG  GG GTG
                                |||||||| ||||  || |||
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                                ATAGTTCC TCCC  CC TAT
                                    G   A_  C
GAM1464  SOX11    3'  ACCCACCCCCCCTTGGTA    13308        AA  CA  C
                                TATCAAGG  GGG  GG GT
                                ||||||||  |||  || ||
                                ATGGTTCC  CCC  CC CA
                                    CC   A_  _
GAM1464  CHL1     3'  TGTTACCTTTCCTCAATA    22768     CA       CA
                                TAT  AGGAAGGG  GGCG
                                |||  ||||||||  ||||
                                ATA  TCCTTTCC  TTGT
                                  AC       A_
GAM1464  EPB41L1  3'  CATTCTGCCCTTCCCTGA    71104     A         C
                                TCA GGAAGGGCAGG GTG
                                ||| ||||||||||| |||
                                AGT CCTTCCCGTCT TAC
                                  C         _
GAM1464  FLJ00060 3'  CATACCCCCTGCCCTCCTCTGA 61741     _   A      CGTG
                                TCA AGGA GGGCAGG    ATG
                                ||| |||| |||||||    |||
                                AGT TCCT CCCGTCC    TAC
                                  C   _      CCCA
GAM1464  FLJ10898 5'  CACCACAGCCCTTTCTCAATA  60126     CA       AGGC
                                TAT  AGGAAGGGC    GTG
                                |||  |||||||||    |||
                                ATA  TCTTTCCCG    CAC
                                  AC        ACAC
GAM1464  FLJ22557 3'  ATCATCCCATCCTTAATA    45581     C    A   CAGGC
                                TAT AAGGA GGG     GTGAT
                                ||| ||||| |||     |||||
                                ATA TTCCT CCC     TACTA
                                  A    A  _____
GAM1464  KIAA0574 3'  CATCCCCTGCCCTCCCCTGA   69808     A  A      CGT
                                TCA GG AGGGCAGG   GATG
                                ||| ||  ||||||||   ||||
                                AGT CC TCCCGTCC   CTAC
                                  C  C       C__
GAM1464  KIAA0632 3'  CACCTCAGAAACCCTTCCTTGA 32071          CA___  C
                                TCAAGGAAGGG     GG GTG
                                ||||||||||     || |||
                                AGTTCCTTCCC     CT CAC
                                      AAAGA  C
GAM1464  KIAA1045 3'  CATCACATGTCCTTCC      71599         GGC
                                GGAAGGGCA   GTGATG
                                |||||||||   ||||||
                                CCTTCCTGT   CACTAC
                                    A__
GAM1464  KIAA1354 5'  CAGTGACTGCCTTCCCTTGATA 61572         A      G  _
                                TATCAAGG AGGGCAG CG TG
                                |||||||| ||||||| || ||
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                                ATAGTTCC TTCCGTC GT AC
                                    C      A  G
GAM1464  MGC20460  5'  CACCGCCTCCTACCCTTCTT   54901        C___    _
                                AGGAAGGG    AGGCG TG
                                ||||||||    ||||| ||
                                TTCTTCCC    TCCGC AC
                                    ATCC     C
GAM1464  LOC158476 3'  CACGCCCGCCCCCCCCATTGA  88186     _ AA_   A
                                TCAA GG   GGGC GGCGTG
                                |||| ||   |||| ||||||
                                AGTT CC   CCCG CCGCAC
                                  A CCC    C
GAM1464  LOC90459  3'  CACACCCGCCTAATTTTTG    63550       A_   A  C
                                CAAGGA  GGGC GG GTG
                                ||||||  |||| || |||
                                GTTTTT  TCCG CC CAC
                                   AA    C  A
GAM1465  ADAR      3'  CTGCAGGGCGGGCAAGG     32361    A    CAG  T
                                CC TGCCC   GC CCTGCAG
                                || |||||   || |||||||
                                GG ACGGG   CG GGACGTC
                                 A    ___ _
GAM1465  AIRE      3'  TGGGAGCCTGAGGCATGAGAA  7247     C     C
                                TTC CATGCC CAGGCTCCTG
                                ||| |||||| ||||||||||
                                AAG GTACGG GTCCGAGGGT
                                  A     A
GAM1465  ANG       5'  GCAGGAGCCTGTGTTGG     8557      T  CC
                                CCA GC  CAGGCTCCTGC
                                ||| ||  ||||||||||
                                GGT TG  GTCCGAGGACG
                                  _  T_
GAM1465  BCAS1     3'  CTCGGGAGCCCAACGCACGAGA 14711     CCA   CCCA       C
              A                  TTC   TGC    GGCTCCTG AG
                                 |||   |||    |||||||| ||
                                 AAG   ACG    CCGAGGGC TC
                                   AGC   CAAC       _
GAM1465  DAG1      3'  CTGCAGGATGTAACATGG    16553       CCCCAG  _
                                CCATG     GC TCCTGCAG
                                |||||     || ||||||||
                                GGTAC     TG AGGACGTC
                                   AA____  T
GAM1465  GPRK7     3'  CGGGAGCCTGAGGCAGGAGAA  58313     _  A   C
                                TTC CC TGCC CAGGCTCCTG
                                ||| || |||| ||||||||||
                                AAG GG ACGG GTCCGAGGGC
                                  A  _    A
GAM1465  KIF1B     3'  TGGGAGCCTGAGGCAGGAGAA  31273     _  A   C
                                TTC CC TGCC CAGGCTCCTG
                                ||| || |||| ||||||||||
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                                AAG GG ACGG GTCCGAGGGT
                                  A _   A
GAM1465 NCAM1    5' CTGCAGGGGGGGGGGCACAGAA 7040     CCA     AGG
                                TTC  TGCCCC  CTCCTGCAG
                                |||  ||||||  |||||||||
                                AAG  ACGGGG  GGGGACGTC
                                  AC_    GG_
GAM1465 NOS1     3' CTGCAGGGTCCCCAAGGATGG  7095      G  CCA_  CT
                                CCAT CC   GG  CCTGCAG
                                |||| ||   ||  |||||||
                                GGTA GG   CC  GGACGTC
                                  _ AACC  TG
GAM1465 PDGFRB   3' TGCCCCAGGGACATGGGAA   66584        _   CA  CTCCT
                                TTCCCATG CCC  GG    GCA
                                |||||||| |||  ||    |||
                                AAGGGTAC GGG  CC    CGT
                                    A  AC  _____
GAM1465 RAB31    3' CTGCAGGGGGGCGGGGCAGGAA  23440     CA     AGG
                                TTCC  TGCCCC  CTCCTGCAG
                                ||||  ||||||  |||||||||
                                AAGG  ACGGGG  GGGGACGTC
                                  __     CG_
GAM1465 SCN4A    3' CTGCGTTCCCAGACCATGGGAA 6200        CCCCA  CTCC
                                TTCCCATG    GG   TGCAG
                                ||||||||    ||   |||||
                                AAGGGTAC    CC   GCGTC
                                    CAGAC  TT__
GAM1465 WHSC1    3' CTGCAATGACTGCAGGGCTGGG 24667      T   __  GCTCC
           AA                    TTCCCA GCCC  CAG    TGCAG
                                ||||||| ||||  |||    |||||
                                AAGGGT CGGG  GTC    ACGTC
                                  _   AC   AGTA_
GAM1465 WHSC1    3' CTGCAATGACTGCAGGGCTGGG 24668      T   __  GCTCC
           AA                    TTCCCA GCCC  CAG    TGCAG
                                ||||||| ||||  |||    |||||
                                AAGGGT CGGG  GTC    ACGTC
                                  _   AC   AGTA_
GAM1465 WHSC1    3' CTGCAATGACTGCAGGGCTGGG 24669      T   __  GCTCC
           AA                    TTCCCA GCCC  CAG    TGCAG
                                ||||||| ||||  |||    |||||
                                AAGGGT CGGG  GTC    ACGTC
                                  _   AC   AGTA_
GAM1465 ZFP36L1  3' CTGCAGGAAGGAAGGCTG    18201    T  __ AGGC
                                CA GCC  CC    TCCTGCAG
                                || |||  ||    ||||||||
                                GT CGG  GG    AGGACGTC
                                 _  AA  A___
GAM1465 C20orf64 5' CAAGAGCCCTTCCTGCAGGGAA 54334      A  CCCA__    C
                                TTCCC TGC     GGCTC TG
                                ||||| |||     ||||| ||
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                                AAGGG ACG     CCGAG AC
                                  _  TCCTTC    A
GAM1465 DRIL2    3' CTGCAGGGTGTGGGCAGAGAA 22350    CCA    C G  T
                                TTC  TGCCC A GC CCTGCAG
                                |||  ||||| | || |||||||
                                AAG  ACGGG T TG GGACGTC
                                  AG_    _ G  _
GAM1465 FEM-2    3' CTGCAGGGCCAAGCCACAGGAA 28312     CAT_  CCCA  T
                                TTCC   GC   GGC CCTGCAG
                                ||||   ||   ||| |||||||
                                AAGG   CG   CCG GGACGTC
                                  ACAC  AA__  _
GAM1465 FLJ10737 3' CTGCAGTCCAAGCTGAACATGG 37054       CCCCA   C___
            GAA                  TTCCCATG    GGCT   CTGCAG
                                ||||||||    ||||   ||||||
                                AAGGGTAC    TCGA   GACGTC
                                     AAG__   ACCT
GAM1465 FLJ10898 5' CTGCCAAACCTGCAACATGGGA 60133       CCC   CTCCT
            A                   TTCCCATG   CAGG    GCAG
                                ||||||||  ||||    ||||
                                AAGGGTAC  GTCC    CGTC
                                     AAC   AAAC_
GAM1465 FLJ11618 3' CTGCAGGGGGGAAGAGCCGGGAA 42624      AT  CCCAGG
                                TTCCC  GC     CTCCTGCAG
                                |||||  ||     |||||||||
                                AAGGG  CG     GGGGACGTC
                                  C_  AGAAG_
GAM1465 FLJ12287 5' TGCCTCTGGGGCCTGGGAA   42564      T      CTCCT
                                TTCCCA GCCCCAGG    GCA
                                |||||| ||||||||    |||
                                AAGGGT CGGGGTCT    CGT
                                   C       C_____
GAM1465 FLJ14129 3' TGGGAGCCTGGGGCAGGAGAA  48814    _ A
                                TTC CC TGCCCCAGGCTCCTG
                                ||| || ||||||||||||||
                                AAG GG ACGGGGTCCGAGGGT
                                  A  _
GAM1465 KIAA0187 3' CTGCAGGAGGAGGAACAGAGAA 29250    CCA  CC  AGG
                                TTC   TG  CC   CTCCTGCAG
                                |||   ||  ||   |||||||||
                                AAG   AC  GG   GAGGACGTC
                                  AG_  AA  AG_
GAM1465 KIAA0416 5' GGAAAGCCTGGGACACAGAA   32093    CCA  C     __
                                TTC   TG CCCAGGC  TCC
                                |||   || |||||||  |||
                                AAG   AC GGGTCCG  AGG
                                  AC_  A      AA
GAM1465 KIAA1266 3' CTGCAAGGGCGAGCATGGGA   66695       CCCAG   C
                                TCCCATGC    GCTC TGCAG
                                ||||||||    |||| |||||
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                                AGGGTACG    CGGG ACGTC
                                    AG___   A
GAM1465 KIAA1483 3' CTGCAGGGAAAAGGATATAGGA 70434     C  C  CAGG T
            A                    TTCC ATG CC   C CCTGCAG
                                 |||| ||| ||   | |||||||
                                 AAGG TAT GG   G GGACGTC
                                   A  A  AAAA _
GAM1465 KIAA1706 3' TGCAGTGAGAGCATGGGA    94372       CCCAGG  _
                                 TCCCATGC    CTC CTGCA
                                 ||||||||    ||| |||||
                                 AGGGTACG    GAG GACGT
                                    A_____   T
GAM1465 KIAA1715 3' CTCAGGAGCCTGAGGCAGGAGA 68684    _ A   C       C
            A                    TTC CC TGCC CAGGCTCCTG AG
                                 ||| || |||| |||||||||| ||
                                 AAG GG ACGG GTCCGAGGAC TC
                                   A _   A       _
GAM1465 KIAA1981 3' CAGGAGCCAAGGTCACAGAA  89710    CCA  C  CA
                                 TTC   TG CC  GGCTCCTG
                                 |||   || ||  ||||||||
                                 AAG   AC GG  CCGAGGAC
                                   AC_  T  AA
GAM1465 MCAM     3' CAGGAACCTGGGGGCCTGTGAA 22457    C  T   _  C
                                 TTC CA GCCCC AGG TCCTG
                                 ||| || ||||| ||| |||||
                                 AAG GT CGGGG TCC AGGAC
                                   T  C    G   A
GAM1465 MRPS24   3' CTGCAGAGAATGGAAACGTGGG 50130       CC_  GG  C
            AA                     TTCCCATG   CCA  CTC TGCAG
                                   ||||||||   |||  ||| |||||
                                   AAGGGTGC   GGT  GAG ACGTC
                                      AAA   AA  _
GAM1465 MSE55    3' TGCAGGACAGACATGGGAG   23916       CCCCAGGC
                                   TTCCCATG      TCCTGCA
                                   ||||||||      |||||||
                                   GAGGGTAC      AGGACGT
                                      AGAC____
GAM1465 OS4      3' CTGCTTTGTGCTAAAAGCATGG 20388       CCCA  TCCT_
            GAA                      TTCCCATGC   GGC    GCAG
                                     |||||||||   |||    ||||
                                     AAGGGTACG   TCG    CGTC
                                        AAAA   TGTTT
GAM1465 PASK     5' CAGGGTCTCGCCTGGGGCATTA 31405    CC        ____
            GAA                      TTC  ATGCCCCAGGC   TCCTG
                                     |||  ||||||||||   |||||
                                     AAG  TACGGGGTCCG   GGGAC
                                       AT         CTCT
GAM1465 PRO1163  3' CTGAATGAGCCTGGGGCA   38323          CTG
                                   TGCCCCAGGCTC   CAG
                                   ||||||||||||   |||
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                                ACGGGGTCCGAG  GTC
                                      TAA
GAM1465 THEA     3' CTCAGGAAGCTGAGGCACAAGA 66887    CCA   C  GC    C
            A                  TTC  TGCC CAG  TCCTG AG
                               |||  |||| |||  ||||| ||
                               AAG  ACGG GTC  AGGAC TC
                                 AAC   A  GA   _
GAM1465 WFDC3    3' GCTGACCAGAGCATGGGAA   98702       CCCA  C  CT
                               TTCCCATGC   GG TC  GC
                               |||||||||   || ||  ||
                               AAGGGTACG   CC AG  CG
                                     AGA_ _  T_
GAM1465 LOC122726 5' CTGCAGGAAACACTGAGGCTTG 76103      T  C  GC__
            GGAA                   TTCCCA GCC CAG   TCCTGCAG
                               ||||||| ||| |||   ||||||||
                               AAGGGT CGG GTC   AGGACGTC
                                  T  A  ACAA
GAM1465 LOC129303 3' CTGCAGGAATTGGGGGCTGGGA 75373      T    AG C
            A                  TTCCCA GCCCC  G TCCTGCAG
                               |||||| |||||  | ||||||||
                               AAGGGT CGGGG  T AGGACGTC
                                  _   GT A
GAM1465 LOC132617 5' CTGCAGATCGAGGCATGGGA  76415       CCA  CTC
                               TCCCATGCC  GG  CTGCAG
                               |||||||||  ||  ||||||
                               AGGGTACGG  CT  GACGTC
                                     AG_ A__
GAM1465 LOC145945 5' AGGGCCTGGACCATAGAA   84563    CC  CC    T
                               TTC  ATG  CCAGGC CCT
                               |||  |||  |||||| |||
                               AAG  TAC  GGTCCG GGA
                                 A_  CA    _
GAM1465 LOC146332 3' CAGGAGCCTGGGGCCTGTGGA  78353    _ T
                               TCC CA GCCCCAGGCTCCTG
                               ||| || ||||||||||||||
                               AGG GT CGGGGTCCGAGGAC
                                 T  C
GAM1465 LOC146714 5' TGCAGGGCAGGCACAGGGA   84754    A_   CCAG  T
                               TCCC  TGCC   GC CCTGCA
                               ||||  ||||   || ||||||
                               AGGG  ACGG   CG GGACGT
                                 AC   A___  _
GAM1465 LOC147958 3' CTGCAGGGCAGGCAGCAGAA  88523    CCA   CCAG  T
                               TTC   TGCC   GC CCTGCAG
                               |||   ||||   || |||||||
                               AAG   ACGG   CG GGACGTC
                                 ACG   A___  _
GAM1465 LOC149501 3' CTGCAAGAGCCTGGCTGGGAA  75800      T  CC    C
                               TTCCCA GCC  AGGCTC TGCAG
                               |||||| |||  |||||| |||||
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                                AAGGGT CGG  TCCGAG ACGTC
                                   _  __     A
GAM1465  LOC150397 3'  CAGGAGCCTGAGTGAAGGA   80655    CA   CC
                                TCC  TGC  CAGGCTCCTG
                                |||  |||  ||||||||||
                                AGG  GTG  GTCCGAGGAC
                                  AA   A_
GAM1465  LOC150397 3'  GCAGGAGCCTGCAGGAGA    80664    _ A   CCC
                                TC CC TGC   AGGCTCCTGC
                                || || |||   ||||||||||
                                AG GG ACG   TCCGAGGACG
                                 A  _  ___
GAM1465  LOC150517 5'  CTGCAGGTAGGAGCACAGAA   80725    CCA   C  AGGCT
                                TTC   TGC CC    CCTGCAG
                                |||   ||| ||    |||||||
                                AAG   ACG GG    GGACGTC
                                  AC_   A  AT___
GAM1465  LOC153688 3'  TGGGAGGCTGGGGCATGAGAA  87341     C        G
                                TTC CATGCCCCAG CTCCTG
                                ||| |||||||||| ||||||
                                AAG GTACGGGGTC GAGGGT
                                  A         G
GAM1465  LOC154849 3'  CTGCAGGAGGTGGAAGATG    60941    GCC   GG
                                CAT   CCA  CTCCTGCAG
                                |||   |||  |||||||||
                                GTA   GGT  GAGGACGTC
                                  GAA   G_
GAM1465  LOC162137 3'  GCAGGAGCTTCCCATAAAGAA  88480     CC_   CCCC
                                TTC   ATG    AGGCTCCTGC
                                |||   |||    ||||||||||
                                AAG   TAC    TTCGAGGACG
                                  AAA   CC__
GAM1465  LOC219654 3'  CAGGAGCCCAGGGGATGGGAA  92925        G   CA
                                TTCCCAT CCC  GGCTCCTG
                                ||||||| |||  ||||||||
                                AAGGGTA GGG  CCGAGGAC
                                    G   AC
GAM1465  LOC254552 5'  CAGGAGCCCGGGGCTGG     96422     T    A
                                CCA GCCCC GGCTCCTG
                                ||| ||||| ||||||||
                                GGT CGGGG CCGAGGAC
                                  _    C
GAM1465  LOC255042 3'  CTCGGGAGCCTGAGGCAGGAGA 97042     _ A   C        C
            A                    TTC CC TGCC CAGGCTCCTG AG
                                ||| || |||| |||||||||| ||
                                AAG GG ACGG GTCCGAGGGC TC
                                  A  _   A        _
GAM1465  LOC257000 3'  CTGCAGGACTCAGAGCATGG   98587       CCCA  C
                                CCATGC    GG TCCTGCAG
                                ||||||    || ||||||||
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                                GGTACG    TC AGGACGTC
                                   AGAC  _
GAM1465  LOC91750  3'  TGGGGGCCTGAGGCACGAGAA  67659     CCA    C
                                TTC   TGCC CAGGCTCCTG
                                |||   |||| ||||||||||
                                AAG   ACGG GTCCGGGGGT
                                  AGC    A
GAM1466  CDKN2C    5'  CAAAGGCTCTTCTGGAGA    8845     G  G   TAAA
                                TC TT GGA    AGCCTTTG
                                || || |||    ||||||||
                                AG AG TCT    TCGGAAAC
                                 _  G   TC__
GAM1466  CYP1B1    3'  GTCAAAGACTTAAAGGGCCCAA 5447          ATAA__   C
            TGA                    TCGTTGGG     AAG CTTTGAC
                                |||||||||     ||| |||||||
                                AGTAACCC     TTC GAAACTG
                                     GGGAAA   A
GAM1466  RAD50     3'  CAAGATATTTTTATCCCAAGA  20405    G         CC_
                                TC TTGGGATAAAAG   TTTG
                                || ||||||||||||   ||||
                                AG AACCCTATTTTT   GAAC
                                 _          ATA
GAM1466  RAD50     3'  CAAGATATTTTTATCCCAAGA  56820    G         CC_
                                TC TTGGGATAAAAG   TTTG
                                || ||||||||||||   ||||
                                AG AACCCTATTTTT   GAAC
                                 _          ATA
GAM1466  DKFZP434A043 3'  GTCAAAGGCTTCGCAAC     31822      G  TAAA
                                GTTG GA    AGCCTTTGAC
                                ||||  ||    ||||||||||
                                CAAC CT    TCGGAAACTG
                                  G  _____
GAM1466  KIAA0476  3'  GTCAAAGGCTCCAAGCGA    30042       G   TAAAA
                                TCGTT GGA    GCCTTTGAC
                                ||||| |||    |||||||||
                                AGCGA CCT    CGGAAACTG
                                   A  ______
GAM1466  LOC146177 3'  CAAAGGCTTCATCAATGA    78189        GATAA
                                TCGTTGG    AAGCCTTTG
                                |||||||    |||||||||
                                AGTAACT    TTCGGAAAC
                                    AC___
GAM1467  DKFZp761H039 3'  CCGAGGCTGGTCTTTGAGGCTG 77383     A       _   _______ GCGA
            CAGA                   TCT CAGCCTCAA GACC      C    G
                                ||| ||||||||| ||||     |   |
                                AGA GTCGGAGTT CTGG     G    C
                                  C        T    TCIIIG AGCG
GAM1467  DNAJC5    3'  CCGAGGCCCAGCCTTGAGGCTG 62135    A        AC________  GCGA
            CAG                    CT CAGCCTCAAG       CC    G
                                || ||||||||||        ||    |
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                                GA GTCGGAGTTC       GG   C
                                 C        CGACCCIII  AGCG
GAM1467  FLJ20972  3'  CCGAGGCTGGTCTTGACACTGC 47386     A   CC      _______ GCGA
              AGA                  TCT CAG  TCAAGACC     C   G
                                |||  |||  ||||||||     |   |
                                AGA GTC  AGTTCTGG     G   C
                                  C   AC       TCIIIG AGCG
GAM1467  G10       5'  CTTTGGACCTTGAGGCCGGAGA 92713     ACA       AC   C
                                TCT   GCCTCAAG  CCG GAG
                                |||   ||||||||  ||| |||
                                AGA   CGGAGTTC  GGT TTC
                                  GGC       CA  _
GAM1467  ICB-1     3'  CCTTATGGAGACCTGAGGCTGC 17931     A       AGAC_   CG
              AGA                  TCT CAGCCTCA     CCG  AGG
                                ||| ||||||||     |||  |||
                                AGA GTCGGAGT     GGT  TCC
                                  C       CCAGA   AT
GAM1467  KIAA1522  3'  CCTGCTGGCCCTGAGGCTGCAG 65605     A       AGA  C  G
              A                    TCT CAGCCTCA   CC GC AGG
                                ||| ||||||||   || || |||
                                AGA GTCGGAGT   GG CG TCC
                                  C       CCC  T  _
GAM1467  KIAA1674  3'  CTCTCCTGAGGCTGTGGA     69338           A  CCCGC
                                TCTACAGCCTCA GA     GAG
                                ||||||||||||| ||     |||
                                AGGTGTCGGAGT CT     CTC
                                       C  _____
GAM1467  STK22D    5'  CCATGCGCCTCGGGGCTGTAGA 50143           A  ACC    A
                                TCTACAGCCTC AG   CGCG GG
                                |||||||||||| ||   |||| ||
                                AGATGTCGGGG TC   GCGT CC
                                       C  C__    A
GAM1467  LOC127281 3'  GGCAAGTCTGAAGCTGTAGA   75136         C   A   _______
                                TCTACAGC TCA GAC      CC
                                |||||||| ||| |||      ||
                                AGATGTCG AGT CTG      GG
                                     A   _   AACIII
GAM1467  LOC145135 5'  CCTCGCGGGAGGCCGGCTCAGA 84202     AC    TCAAGA
                                TCT  AGCC     CCCGCGAGG
                                |||  ||||     |||||||||
                                AGA  TCGG     GGGCGCTCC
                                  C_    CCGGA_
GAM1467  LOC149464 3'  GGCCATCTTGAGGTTACAGA   85594     AC        C_____
                                TCT  AGCCTCAAGA     CC
                                |||  ||||||||||     ||
                                AGA  TTGGAGTTCT     GG
                                  CA         ACCIII
GAM1467  LOC151429 3'  GTGGACCCTTAGGCTGTAGA   86546         C   AC_
                                TCTACAGCCT AAG   CCGC
                                |||||||||| |||   ||||
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                                AGATGTCGGA TTC   GGTG
                                      _  CCA
GAM1467  LOC55908  5'  CCTCGCGGGTAAATTCACTGCA 38570    A   CCTCAAG
              G                    CT CAG      ACCCGCGAGG
                                   || |||      ||||||||||
                                   GA GTC      TGGGCGCTCC
                                    C   ACTTAAA
GAM1468  CASP7    5'  GCGGGGACACGGGTCGCTT   54029     A      _  GG  A
                                   AAGC GACCCGTG CC  CC GC
                                   |||| |||||||| ||  || ||
                                   TTCG CTGGGCAC GG  GG CG
                                     _       A  __  _
GAM1468  CASP7    5'  GCGGGGACACGGGTCGCTT   8738      A      _  GG  A
                                   AAGC GACCCGTG CC  CC GC
                                   |||| |||||||| ||  || ||
                                   TTCG CTGGGCAC GG  GG CG
                                     _       A  __  _
GAM1468  CHGB     5'  CGCTGGTTTTCCGGGGCCGCT  10194    AGA   TGCC
                                   AGC   CCCG   GGCCAGCG
                                   |||   ||||   ||||||||
                                   TCG   GGGC   TTGGTCGC
                                     CCG   CTT_
GAM1468  GDI1     5'  GCGCTGGCACCGAGGCCTG   60642    A  _  TGCCG
                                   CAG CC CG    GCCAGCGC
                                   ||| || ||    ||||||||
                                   GTC GG GC    CGGTCGCG
                                     C  A  CA___
GAM1468  HK1      3'  CGCTGGCGCCAGGGCCTGC   54259     A  GT  CG
                                   GCAG CCC  GC  GCCAGCG
                                   |||| |||  ||  |||||||
                                   CGTC GGG  CG  CGGTCGC
                                     C   AC  __
GAM1468  HK1      3'  CGCTGGCGCCAGGGCCTGC   54262     A  GT  CG
                                   GCAG CCC  GC  GCCAGCG
                                   |||| |||  ||  |||||||
                                   CGTC GGG  CG  CGGTCGC
                                     C   AC  __
GAM1468  HK1      3'  CGCTGGCGCCAGGGCCTGC   54265     A  GT  CG
                                   GCAG CCC  GC  GCCAGCG
                                   |||| |||  ||  |||||||
                                   CGTC GGG  CG  CGGTCGC
                                     C   AC  __
GAM1468  HK1      3'  CGCTGGCGCCAGGGCCTGC   54268     A  GT  CG
                                   GCAG CCC  GC  GCCAGCG
                                   |||| |||  ||  |||||||
                                   CGTC GGG  CG  CGGTCGC
                                     C   AC  __
GAM1468  HK1      3'  CGCTGGCGCCAGGGCCTGC   5746      A  GT  CG
                                   GCAG CCC  GC  GCCAGCG
                                   |||| |||  ||  |||||||
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                                CGTC GGG  CG  CGGTCGC
                                  C  AC  __
GAM1468 INPP5A   3' GCGGTTCAACACGGAGTCCGC 19866   A  _   CC_  A
                                GC GAC CCGTG  GGCC GC
                                || ||| |||||  |||| ||
                                CG CTG GGCAC  TTGG CG
                                 C  A   AAC  _
GAM1468 OSCAR    3' GCACCCCACCAGAGTCTGCTT 56250      CC__  CC  CCA
                                AAGCAGAC  GTG  GG  GC
                                ||||||||  |||  ||  ||
                                TTCGTCTG  CAC  CC  CG
                                    AGAC  __ CA_
GAM1468 OSCAR    3' GCACCCCACCAGAGTCTGCTT 56478      CC__  CC  CCA
                                AAGCAGAC  GTG  GG  GC
                                ||||||||  |||  ||  ||
                                TTCGTCTG  CAC  CC  CG
                                    AGAC  __ CA_
GAM1468 OSCAR    3' GCACCCCACCAGAGTCTGCTT 56481      CC__  CC  CCA
                                AAGCAGAC  GTG  GG  GC
                                ||||||||  |||  ||  ||
                                TTCGTCTG  CAC  CC  CG
                                    AGAC  __ CA_
GAM1468 PYCR1    5' GCGCTGGCCAGCTGGCTTTTGC 70642     C_  T  C
                                GCAGA  CCG GC GGCCAGCGC
                                |||||  ||| || |||||||||
                                CGTTT  GGT CG CCGGTCGCG
                                   TC  _ A
GAM1468 SH3GL1   3' CTGGCCGGCACCCCCTGCT  13095     ACCC
                                AGCAG  GTGCCGGCCAG
                                |||||  ||||||||||
                                TCGTC  CACGGCCGGTC
                                   CCC_
GAM1468 SLC7A6   3' GCACGGACAGAGTCTGCTT  15641      CCG  _  ____
                                AAGCAGAC  TG CCG  GC
                                ||||||||  || |||  ||
                                TTCGTCTG  AC GGC  CG
                                    AG_  A  A___
GAM1468 CASP9    3' GCAGCCGGCACAGGGTCTGCT 8772       _     CA
                                AGCAGACCC GTGCCGGC  GC
                                ||||||||| ||||||||  ||
                                TCGTCTGGG CACGGCCG  CG
                                     A      A_
GAM1468 CPZ      5' GCGCTGGCCGTCCAAGGTCCGC 14691   A   CG  C_
                                GC GACC  TG  CGGCCAGCGC
                                || ||||  ||  ||||||||||
                                CG CTGG  AC  GCCGGTCGCG
                                 C   A_  CT
GAM1468 DKFZP434N1511 3' GCACTGGCCCCCAAGGTCAGCT 93061    A   CG  CC    C
                                AGC GACC  TG  GGCCAG GC
                                ||| ||||  ||  |||||| ||
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                                TCG CTGG  AC  CCGGTC CG
                                  A   A_  CC     A
GAM1468  DKFZP586J1624 3'  CTGGCCGAGTCTCTGGGTCTGT 32045         T__ _
                                GCAGACCCG   GC CGGCCAG
                                |||||||||   || |||||||
                                TGTCTGGGT   TG GCCGGTC
                                     CTC  A
GAM1468  EHM2     5'  GCGCTGGCCGGGCCGGCGC   39418    AGAC   TG
                                GC   CCG  CCGGCCAGCGC
                                ||   |||  ||||||||||
                                CG   GGC  GGCCGGTCGCG
                                 C___   CG
GAM1468  FLJ10748  5'  CCTGGCCGGGGTCTGGCT    37100     _     GTGC      C
                                AGC AGACCC    CGGCCAG G
                                ||| ||||||    ||||||| |
                                TCG TCTGGG    GCCGGTC C
                                  G     _____      A
GAM1468  FLJ10751  3'  CGCTGGCCCCACCTGC     37111      ACCC   CC
                                GCAG   GTG  GGCCAGCG
                                ||||   |||  ||||||||
                                CGTC   CAC  CCGGTCGC
                                  _____  C_
GAM1468  FLJ10751  3'  CGCTGGCCCCACCTGC     37274      ACCC   CC
                                GCAG   GTG  GGCCAGCG
                                ||||   |||  ||||||||
                                CGTC   CAC  CCGGTCGC
                                  _____  C_
GAM1468  FLJ14810  5'  CGCTGGCCGACCAGCTGC    52700      ACCC  GC
                                GCAG   GT  CGGCCAGCG
                                ||||   ||  |||||||||
                                CGTC   CA  GCCGGTCGC
                                  GAC_  __
GAM1468  FLJ23519  3'  GCACCTCCAGGCAGGGTCTGCT 50952          G   _  CCA_
              T                  AAGCAGACCC TGCC GG    GC
                                 |||||||||| |||| ||    ||
                                 TTCGTCTGGG ACGG CC    CG
                                       _    A  TCCA
GAM1468  HSPC133   5'  GCACCGGCCGAGGTGCGGGTCG 27184    A     TG  __    A__
              C                  GC GACCCG  CC  GGCC   GC
                                 || ||||||  ||  ||||   ||
                                 CG CTGGGC  GG  CCGG   CG
                                  _     GT  AG    CCA
GAM1468  KIAA0562  5'  GCAGAGGCGGCCGGGTCTGCTT 28824           T    G  A__
                                 AAGCAGACCCG GCCG CC   GC
                                 |||||||||||| |||| ||   ||
                                 TTCGTCTGGGC CGGC GG   CG
                                       _    _  AGA
GAM1468  KIAA1185  3'  GCGCTGACGCCAGGGCCGC   63288    AGA   G  C  GC
                                 GC   CCC TG CG  CAGCGC
                                 ||   ||| || ||  ||||||
```

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                                CG  GGG AC GC  GTCGCG
                                 CC_  _ C  A_
GAM1468 KIAA1862 3' CGCTGGCAGGCCTGGCTC   69509   C  T  G
                                GA CCG GCC GCCAGCG
                                || ||| ||| |||||||
                                CT GGT CGG CGGTCGC
                                 C  C  A
GAM1468 KIAA1872 3' GCGCTGGCCGCAGCCACCTGC 63612    ACCCG  C
                                GCAG   TGC GGCCAGCGC
                                ||||    ||| |||||||||
                                CGTC    ACG CCGGTCGCG
                                  CACCG  _
GAM1468 KIAA1893 5' GCGCCGAGTCTGCGGGTC   73588      __ _   CA
                                GACCCGT  GC CGGC  GC
                                |||||||  || ||||  ||
                                CTGGGCG  TG GCCG  CG
                                    TC  A   __
GAM1468 MGC2594  3' GCGCCTCCTGCCAGGTCTGCT 44127      CGT  C  CCA
                                AGCAGACC   GC GG   GCGC
                                ||||||||   || ||   ||||
                                TCGTCTGG   CG CC   CGCG
                                    AC_  T  TC_
GAM1468 SLC26A10 5' CGCTGGCCACCACCAATCTACT 56843   C  CCC  CC
                                AG AGA   GTG  GGCCAGCG
                                || |||   |||  ||||||||
                                TC TCT   CAC  CCGGTCGC
                                 A  AAC   CA
GAM1468 TRAF3   3' GCGCTGGCCACCTGGGCCAGC  60455   AGA   TGCC
                                GC   CCCG   GGCCAGCGC
                                ||   ||||   |||||||||
                                CG   GGGT   CCGGTCGCG
                                 ACC   CCA_
GAM1468 TU3A    5' CGCCAGCTTGGCACGAGGCTGC 24183    A _    _ CA
                                GCAG CC CGTGCCG GC  GCG
                                |||| || ||||||| ||  |||
                                CGTC GG GCACGGT CG  CGC
                                  _ A     T  AC
GAM1468 LOC124222 5' GCAGGAGCACGGGCTGC    74751    A    CGG  A
                                GCAG CCCGTGC   CC GC
                                |||| |||||||   || ||
                                CGTC GGGCACG   GG CG
                                  _     A__  A
GAM1468 LOC157349 5' GCGCTGGTTCCCAGCCTGC   82346    ACCC  GCC_
                                GCAG   GT   GGCCAGCGC
                                ||||   ||   |||||||||
                                CGTC   CG   TTGGTCGCG
                                  ____ ACCC
GAM1468 LOC163412 5' GCTGCGGCCACGGGTCTGC   83015        _  GC
                                GCAGACCCGTG CCG  CAGC
                                |||||||||| |||  ||||
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                                CGTCTGGGCAC GGC  GTCG
                                      C   __
GAM1468  LOC165721 3'  GCGCTGGCCACCCGGCCCTGC  83494     AC   TGCC
                                GCAG  CCG   GGCCAGCGC
                                |||| |||   |||||||||
                                CGTC  GGC   CCGGTCGCG
                                  CC   CCA_
GAM1468  LOC220143 3'  GCATCAGCACGGGTCTGGCT   95234     _       C  CCA
                                AGC AGACCCGTGC GG   GC
                                ||| |||||||||| ||   ||
                                TCG TCTGGGCACG CT   CG
                                  G        A  A__
GAM1468  LOC221491 5'  GCGCCGGCACGGGTCCACGC   93657    A__          CA
                                GC   GACCCGTGCCGGC  GC
                                ||   ||||||||||||  ||
                                CG   CTGGGCACGGCCG  CG
                                 CAC          __
GAM1468  LOC256537 5'  CGCTGGCCGGACAGGGCCGC   96937    AGA   GTG
                                GC   CCC   CCGGCCAGCG
                                ||   |||   ||||||||||
                                CG   GGG   GGCCGGTCGC
                                 CC_   ACA
GAM1468  LOC84548  5'  GCGCTGGCGCCATGAACCCGCT 71763     ACC___   C  G
           GT                    GCAG     CGTG CG CCAGCGC
                                ||||     |||| || |||||||
                                TGTC     GTAC GC GGTCGCG
                                  GCCCAA    C  _
GAM1468  LOC90459  5'  CGCCGGCTCACTGCGCCTGC   63554     ACCC   C___   A
                                GCAG   GTGC   GGCC GCG
                                ||||   ||||   |||| |||
                                CGTC   CGCG   TCGG CGC
                                  _____   TCAC   C
GAM1468  LOC91561  5'  GCGCTGGCCACCACACCTGGTT 67045    G   ACCC   CC
                                AA CAG   GTG  GGCCAGCGC
                                || |||   |||  |||||||||
                                TT GTC   CAC  CCGGTCGCG
                                 G   CA__   CA
GAM1468  LOC92140  5'  GCGCTGGCGCCGAGACGCCGCT 68825     AGACC   GC   __
           T                     AAGC    CGT  CGGC  CAGCGC
                                ||||    |||  ||||  ||||||
                                TTCG    GCA  GCCG  GTCGCG
                                  CC___   GA   CG
GAM1469  ALPL     3'  CCTCTGGAACCCCCCAGGCCCT 6646      A  AAGAGCAT
                                AGG CC       GTTCCAGAGG
                                ||| ||       ||||||||||
                                TCC GG       CAAGGTCTCC
                                 C  ACCCCC__
GAM1469  ARNT2    3'  CCTCTGGGAAAGCCCTTGTGTC 30085     _   A  ATG
           C                     GGAC CAAG GC   TTCCAGAGG
                                |||| |||| ||   |||||||||
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                                CCTG GTTC CG   AGGGTCTCC
                                  T   C  AA_
GAM1469 B3GALT5  3' CCTCCACCTCAGCTCCCAGTCC 21338     CAA   A  TTCCA
            T                    AGGAC   GAGC TG    GAGG
                                 |||||   |||| ||    ||||
                                 TCCTG   CTCG AC    CTCC
                                   ACC   _  TCCAC
GAM1469 B3GALT5  3' CCTCCACCTCAGCTCCCAGTCC 53721     CAA   A  TTCCA
            T                    AGGAC   GAGC TG    GAGG
                                 |||||   |||| ||    ||||
                                 TCCTG   CTCG AC    CTCC
                                   ACC   _  TCCAC
GAM1469 B3GALT5  3' CCTCCACCTCAGCTCCCAGTCC 53725     CAA   A  TTCCA
            T                    AGGAC   GAGC TG    GAGG
                                 |||||   |||| ||    ||||
                                 TCCTG   CTCG AC    CTCC
                                   ACC   _  TCCAC
GAM1469 B3GALT5  3' CCTCCACCTCAGCTCCCAGTCC 53729     CAA   A  TTCCA
            T                    AGGAC   GAGC TG    GAGG
                                 |||||   |||| ||    ||||
                                 TCCTG   CTCG AC    CTCC
                                   ACC   _  TCCAC
GAM1469 B3GALT5  3' CCTCCACCTCAGCTCCCAGTCC 53733     CAA   A  TTCCA
            T                    AGGAC   GAGC TG    GAGG
                                 |||||   |||| ||    ||||
                                 TCCTG   CTCG AC    CTCC
                                   ACC   _  TCCAC
GAM1469 CLN3    5' CCTTTGGACACTCTATGACCCT 72709    AC  _   CA   T
                                 AGG  CA AGAG  TGT CCAGAGG
                                 |||  || ||||  ||| |||||||
                                 TCC  GT TCTC  ACA GGTTTCC
                                   CA  A   __  _
GAM1469 CLN3    5' CCTTTGGACACTCTATGACCCT 5388     AC  _   CA   T
                                 AGG  CA AGAG  TGT CCAGAGG
                                 |||  || ||||  ||| |||||||
                                 TCC  GT TCTC  ACA GGTTTCC
                                   CA  A   __  _
GAM1469 CTRL    3' CCTCCAGGGCAACCCCTTGGTC 10339       AGCA    CA
            CT                   AGGACCAAG   TGTTC  GAGG
                                 |||||||||   |||||  ||||
                                 TCCTGGTTC   ACGGG  CTCC
                                      CCCA    AC
GAM1469 EIF1A   5' CCTCCAGCACCTACTTGGTCC  90006       _ CA   CCA
                                 GGACCAAG AG  TGTT   GAGG
                                 ||||||||  ||  ||||   ||||
                                 CCTGGTTC TC  ACGA   CTCC
                                      A  C_    C__
GAM1469 GEM     5' CCCTGGAACGTGCGCTCAGCAC 19151    GACCA  A        A
            T                    AG    AG GCATGTTCCAG GG
                                 ||    || ||||||||||| ||
```

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                                TC    TC CGTGCAAGGTC CC
                                 ACGAC  G        _
GAM1469 ITPR2   5' CCTCCGCCGTGGCTCTTGGCC 11080   A     _  TTCCA
                                GG CCAAGAGC ATG    GAGG
                                || |||||||| |||    ||||
                                CC GGTTCTCG TGC    CTCC
                                 _      G  CGC__
GAM1469 KIAA0857 3' CCTAAAGTTAATCTCTTGGTCT 67251         C GTTCCAG
                                GGACCAAGAG AT      AGG
                                |||||||||| ||      |||
                                TCTGGTTCTC TA      TCC
                                      _ ATTGAAA
GAM1469 LZTR1   3' CCCTGCACTATGCTCTTGGCTC 23167    _        TTC  A
            C                    GGA CCAAGAGCATG  CAG GG
                                ||| ||||||||||  ||| ||
                                CCT GGTTCTCGTAT  GTC CC
                                  C         CAC  _
GAM1469 NOS1    3' CCTCTGGGACCCCCTGTGGCCC 7093     A  AG  CAT
            T                    AGG CCA  AG  GTTCCAGAGG
                                ||| |||  ||  ||||||||||
                                TCC GGT  TC  CAGGGTCTCC
                                  C  G_  CCC
GAM1469 PFKFB4  3' CCCTGAGTTCTTTTGGTCC   17083        C GTTC  A
                                GGACCAAGAG AT   CAG GG
                                |||||||||| ||   ||| ||
                                CCTGGTTTTC TG   GTC CC
                                      T  A___  _
GAM1469 POR     3' CCTCTGGAGGCCTCTGGCCCT  95841    A  A  CATG
                                AGG CCA GAG   TTCCAGAGG
                                ||| ||| |||   |||||||||
                                TCC GGT CTC   GAGGTCTCC
                                  C  _  CG__
GAM1469 POU2F2  3' CCTCTGGTCCCTGCCTTGGTCC 12213       A  TGTT
                                GGACCAAG GCA   CCAGAGG
                                |||||||| |||   |||||||
                                CCTGGTTC CGT   GGTCTCC
                                     _  CCCT
GAM1469 RNH     3' CCCTGCCATGCTCTCACCCT  12889    ACCA     TTC  A
                                AGG   AGAGCATG  CAG GG
                                |||   ||||||||  ||| ||
                                TCC   TCTCGTAC  GTC CC
                                  CAC_      C__  _
GAM1469 RNH     3' CCCTGCCATGCTCTCACCCT  60368    ACCA     TTC  A
                                AGG   AGAGCATG  CAG GG
                                |||   ||||||||  ||| ||
                                TCC   TCTCGTAC  GTC CC
                                  CAC_      C__  _
GAM1469 SCAMP3  3' CCTGACTGGGATGCCCTGGCCC 54517    A  A A  TG   __
            T                    AGG CCA G GCA  TTCCAG  AGG
                                ||| ||| | |||  ||||||  |||
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                                TCC GGT C CGT  AGGGTC  TCC
                                  C  _ C  __     AG
GAM1469 SCAMP3   3' CCTGACTGGGATGCCCTGGCCC 20305    A  A A  TG    __
             T                   AGG CCA G GCA  TTCCAG  AGG
                                ||| ||| | |||  ||||||  |||
                                TCC GGT C CGT  AGGGTC  TCC
                                  C  _ C  __     AG
GAM1469 TCF20    3' CTCTGGGGCCCCCTGTCCT   67502      CAAG  CAT
                                AGGAC   AG  GTTCCAGAG
                                ||||||   ||  |||||||||
                                TCCTG   TC  CGGGGTCTC
                                   _____ CCC
GAM1469 TLR9     5' CCTCTGGAGAAGCCCCTGCCCC 34306    AC  AGA  ATG
                                GG  CA  GC  TTCCAGAGG
                                ||  ||  ||  |||||||||
                                CC  GT  CG  GAGGTCTCC
                                 CC  CCC  AA_
GAM1469 ARHU     5' GGAACGTGTGTTCCAGGTCCT  41362       AA  __
                                AGGACC  GA  GCATGTTCC
                                ||||||  ||  |||||||||
                                TCCTGG  CT  TGTGCAAGG
                                   AC  TG
GAM1469 C21orf18 3' CCTCTAAGCATGCTCCTGGCCT 34304     A  A       CC
                                AGG CCA GAGCATGTT  AGAGG
                                ||| ||| |||||||||  |||||
                                TCC GGT CTCGTACGA  TCTCC
                                  _  C       A_
GAM1469 CLSTN3   3' CCTCTGGAGTCCGCCCTGCCCC 28876     ACCA  A  ATG
             T                   AGG   AG GC   TTCCAGAGG
                                |||   || ||  |||||||||
                                TCC   TC CG   GAGGTCTCC
                                  CCG_  C  CCT
GAM1469 DKFZP434J037 3' CCTCTGGACTCCACCTTGGACC 48945     A    AGCAT  T
             T                   AGG CCAAG    GT CCAGAGG
                                ||| |||||    || |||||||
                                TCC GGTTC    CA GGTCTCC
                                  A    CACCT  _
GAM1469 DKFZP434L0117 3' CCACTTCACACCTTGGTCCT   43241         AGCA   TCC  A
                                AGGACCAAG   TGT   AG GG
                                |||||||||   |||   || ||
                                TCCTGGTTC   ACA   TC CC
                                     C___   CT_  A
GAM1469 DLAT     5' CCTCTGGAACACTCCTGCCCC  68085    AC  A   CA
                                GG  CA GAG  TGTTCCAGAGG
                                ||  || |||  ||||||||||
                                CC  GT CTC  ACAAGGTCTCC
                                 CC  C  __
GAM1469 FLJ10044 3' CCTCTGGGAGCCACCTCCAATC 36239     CCAA   CAT    _
             C                   GGA   GAG   GTTCC AGAGG
                                |||   |||   ||||| |||||
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                              CCT   CTC  CGAGG TCTCC
                                AAC_  CAC   G
GAM1469 FLJ20195 3' CCTCTGGAAGCTTCCCTACC  35217   ACCAA   ATG
                              GG   GAGC  TTCCAGAGG
                              ||   ||||  |||||||||
                              CC   TTCG  AAGGTCTCC
                               ATCCC  ___
GAM1469 FLJ23519 3' CCCTGCCATGCTCTCACCCT  69720    ACCA     TTC  A
                              AGG  AGAGCATG  CAG GG
                              |||  ||||||||  ||| ||
                              TCC  TCTCGTAC  GTC CC
                                CAC_     C__  _
GAM1469 FYCO1   3' CCTCCAGTCATGCTCTTGTCCC 44769    AC       TTCCA
           T                   AGG CAAGAGCATG   GAGG
                              |||  ||||||||||   ||||
                              TCC  GTTCTCGTAC   CTCC
                                CT       TGAC_
GAM1469 HMT-1   3' CCTCTGCAGAACTCCTCATCCT 39409    CCAA  CAT   __
                              AGGA   GAG  GTTC  CAGAGG
                              ||||   |||  ||||  ||||||
                              TCCT   CTC  CAAG  GTCTCC
                                A___   CT_   AC
GAM1469 KCND1   5' CCTCTGGATGCCCCAGTCT   18342    CAAGA  TGT
                              GGAC   GCA  TCCAGAGG
                              ||||   |||  ||||||||
                              TCTG   CGT  AGGTCTCC
                                ACCC_  ___
GAM1469 KIAA0450 5' CTGCCATGCTCTCGGGCC   28351   A A     TTC
                              GG CC AGAGCATG   CAG
                              || || ||||||||  |||
                              CC GG TCTCGTAC   GTC
                               G  C      C__
GAM1469 KIAA0493 3' CCTCTGAAAATGCTTCTTGGTA 64933   G    _   G  C
           CT                   AG ACCAAGA GCAT TTC AGAGG
                              || ||||||| |||| ||| |||||
                              TC TGGTTCT CGTA AAG TCTCC
                               A     T   A  _
GAM1469 KIAA1354 3' CCTCTGGAACACTATGGTCTT  61574       AG  CA
                              AGGACCA  AG  TGTTCCAGAGG
                              |||||||  ||  ||||||||||||
                              TTCTGGT  TC  ACAAGGTCTCC
                                 A_  __
GAM1469 LHPP    3' CCTCTGGGAATCTCCCAAATCC 42365    CCAA_  CATG
                              GGA   GAG   TTCCAGAGG
                              |||   |||   |||||||||
                              CCT   CTC   AGGGTCTCC
                                AAACC  TA__
GAM1469 MGC2541  3' CCTAGAGACATGCTCCCTGCCC 55622    ACCAA      CCAG
           T                   AGG   GAGCATGTT   AGG
                              |||   |||||||||   |||
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                                TCC    CTCGTACAG   TCC
                                  CGTCC       AGA_
GAM1469  N4BP3    3'  CTCTGGGGCCTCCAGTCCT   66850      CAA   CAT
                                AGGAC   GAG   GTTCCAGAG
                                ||||||  |||  |||||||||
                                TCCTG   CTC   CGGGGTCTC
                                  AC_   ___
GAM1469  NTPBP    3'  CTTCTTGCTCTTGACCCT    24392     AC      TGTTCC
                                AGG  CAAGAGCA     AGAGG
                                |||  ||||||||     |||||
                                TCC  GTTCTCGT     TCTTC
                                  CA       _______
GAM1469  UBXD1    3'  CCTCTGGAAATACTTGGCTCT  48229    GA    AGCATG
                                AG  CCAAG     TTCCAGAGG
                                ||  |||||     |||||||||
                                TC  GGTTC     AAGGTCTCC
                                  TC    ATA___
GAM1469  LOC126549 5'  CCTCTGGGAGGCCCTTGGTC   76208       A  ATG
                                GACCAAG GC   TTCCAGAGG
                                |||||||  ||   |||||||||
                                CTGGTTC CG   AGGGTCTCC
                                    C  G__
GAM1469  LOC126964 3'  CCTCCCTGCTGTGCTCTCTGCC 75113    ACCA      _  TCCA
                                GG    AGAGCAT GT    GAGG
                                ||    |||||||  ||    ||||
                                CC    TCTCGTG CG    CTCC
                                  GTC_      T  TCC_
GAM1469  LOC129011 3'  CCTCTGGCCACACCGCCAGCCC 75366    ACCAAGA  A_   T_
              T                    AGG      GC  TGT  CCAGAGG
                                |||      ||  |||  |||||||
                                TCC      CG  ACA  GGTCTCC
                                  CGAC___  CC   CC
GAM1469  LOC139522 5'  CCCTGAAGCCACAAGCCTTGGT 76363        A  A   TC___   A
              CC                    GGACCAAG GC TGT     CAG GG
                                |||||||| || |||     ||| ||
                                CCTGGTTC CG ACA     GTC CC
                                    _  A   CCGAA   _
GAM1469  LOC146237 3'  CCTCTCCCGTGCTCTCTGCCCT 84607     AC  _      TTCC
                                AGG  CA AGAGCATG    AGAGG
                                |||  || ||||||||    |||||
                                TCC  GT TCTCGTGC    TCTCC
                                  C_  C       CC__
GAM1469  LOC149050 3'  CCTCTGAGAGTGCCCCTTGGTC 61061         A_   GT  _
              CT                    AGGACCAAG  GCAT  TC CAGAGG
                                |||||||||  ||||  || ||||||
                                TCCTGGTTC  CGTG  AG GTCTCC
                                     CC    __  A
GAM1469  LOC149267 3'  CCTCTGGGCCATCCCTGGCCCT 57476     A   A AGC   TT
                                AGG CCA G   ATG  CCAGAGG
                                ||| ||| |   |||  |||||||
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                                TCC GGT C   TAC  GGTCTCC
                                  C   _ CC_   CG
GAM1469  LOC149422 3'  CCCTAAAATATGCTCCTACCCC 80133     ACCAA       CC  A
                T                  AGG     GAGCATGTT  AG GG
                                   |||     |||||||||  || ||
                                   TCC     CTCGTATAA  TC CC
                                     CCATC        AA  _
GAM1469  LOC149668 5'  CCTCTGGAACCCCACCTCAGTC 85699      CAA   CAT__
                T                  GGAC   GAG    GTTCCAGAGG
                                   ||||   |||    ||||||||||
                                   TCTG   CTC    CAAGGTCTCC
                                     A__   CACCC
GAM1469  LOC151121 5'  CTCTTTTGTCTTGGTCC     80934          G  TGTTCC
                                   GGACCAAGA CA     AGAG
                                   |||||||||  ||     ||||
                                   CCTGGTTCT GT     TCTC
                                         _ TT_____
GAM1469  LOC151475 3'  CCTCTGTGGTTATGCTCTTGGC 86590    A_         TT _
                ACC                  GG  CCAAGAGCATG  C CAGAGG
                                   ||  ||||||||||||  | ||||||
                                   CC  GGTTCTCGTAT  G GTCTCC
                                    AC          TG T
GAM1469  LOC152286 3'  CCTCCAGTCCAGACTTTGGTCC 86806        A   CA  TTCCA
                T                  AGGACCA GAG  TG    GAGG
                                   |||||||  |||  ||    ||||
                                   TCCTGGT TTC  AC    CTCC
                                      _  AG  CTGAC
GAM1469  LOC158056 5'  CCTCTGGAGGTGCACCCTGGAC 82588    A   AGA_   G
                C                  GG CCA    GCAT TTCCAGAGG
                                   || |||    |||| |||||||||
                                   CC GGT    CGTG GAGGTCTCC
                                    A  CCCA    _
GAM1469  LOC158117 3'  CCTCCATGTTGCTCTTGAGCCT 82611     AC       TGTTCCA
                                   AGG  CAAGAGCA      GAGG
                                   |||  ||||||||      ||||
                                   TCC  GTTCTCGT      CTCC
                                     GA       TGTAC__
GAM1469  LOC196890 3'  CCCTGGGGCACCCCTGACCCT  91225     ACCA  AGCA      A
                                   AGG    AG    TGTTCCAG GG
                                   |||    ||    |||||||| ||
                                   TCC    TC    ACGGGGTC CC
                                     CAG_  CCC_       _
GAM1469  LOC199883 3'  CCTCTGGAGGTCCTCCCGGTCC 91463       AA   C  G
                T                  AGGACC  GAG AT TTCCAGAGG
                                   ||||||  ||| || |||||||||
                                   TCCTGG  CTC TG GAGGTCTCC
                                      CC   C  _
GAM1469  LOC200020 3'  CCTCTGGAGGTCCTCCCGGTCC 91534       AA   C  G
                T                  AGGACC  GAG AT TTCCAGAGG
                                   ||||||  ||| || |||||||||
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                                TCCTGG  CTC TG GAGGTCTCC
                                   CC   C  _
GAM1469  LOC203275 3'  CCTCCATGTTGCTCTTGAGCCT 90853     AC       TGTTCCA
                                AGG  CAAGAGCA      GAGG
                                |||  ||||||||      ||||
                                TCC  GTTCTCGT      CTCC
                                  GA       TGTAC__
GAM1469  LOC221416 3'  CCTCTGGGACTGCCCCTCAGTC 95405      CA  A_   T
              C                  GGAC  AG  GCA GTTCCAGAGG
                                ||||  ||  ||| ||||||||||
                                CCTG  TC  CGT CAGGGTCTCC
                                  AC  CC   _
GAM1469  LOC223073 5'  CCTCTGGATCACCTCTCAATCT 96037     CCA    CA  T
                                GGA   AGAG  TG TCCAGAGG
                                |||   ||||  || ||||||||
                                TCT   TCTC  AC AGGTCTCC
                                  AAC    C_  T
GAM1469  LOC255017 3'  CCTGACTGGGATGCCCTGGCCC 96270     A   A A   TG     __
              T                  AGG CCA G GCA  TTCCAG  AGG
                                ||| ||| | |||  ||||||  |||
                                TCC GGT C CGT  AGGGTC  TCC
                                  C   _ C   __     AG
GAM1469  LOC91960  3'  CCGATTAACATGCTTTTAGCC  68281    ACC         CCAGA
                                GG   AAGAGCATGTT    GG
                                ||   ||||||||||    ||
                                CC   TTTTCGTACAA    CC
                                 GA_         TTAG_
GAM1469  LOC96597  5'  CTGGGCCATGCTCTTAGCCCT  67457    ACC       TT
                                AGG   AAGAGCATG  CCAG
                                |||   |||||||||  ||||
                                TCC   TTCTCGTAC  GGTC
                                  CGA       CG
GAM1470  CDH12     3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                      AA___   AC
GAM1470  GOCAP1    3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM1470  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT    98090       T    AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT     TTATTC
                                   _    GTCA_
GAM1470  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
              A                  TACAC       AGAAGAATAAG
                                |||||       ||||||||||
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                              ATGTG      TCTTCTTATTC
                                 TACTCCC_
GAM1470 FLJ21791 3' CTTATTTGCAGAAGTGGTGTA 62126        CCCAAGAA
                              TACACCACT      GAATAAG
                              |||||||||      |||||||
                              ATGTGGTGA      TTTATTC
                                   AGACG___
GAM1470 HMP19    3' CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
           TA                   TACA   TCC   GAAGAATAAG
                              ||||   |||   ||||||||||
                              ATGT   AGG   TTTCTTATTC
                                AAA_  ATTG
GAM1470 KIAA1719 3' TCTGTCTTGGGAGTGGTGTA  68742             _
                              TACACCACTCCCAAGA AGA
                              |||||||||||||||| |||
                              ATGTGGTGAGGGTTCT TCT
                                        G
GAM1470 KIAA1853 3' TTTTTCTTGGAAGCAGTG    69929    CA  C
                              CAC  CT CCAAGAAGAA
                              |||  || ||||||||||
                              GTG  GA GGTTCTTTTT
                                AC  A
GAM1470 KIAA1877 3' CTTATTCTTCTGCCATGAGT  66748     CCA__
                              ACTC    AGAAGAATAAG
                              ||||    ||||||||||
                              TGAG    TCTTCTTATTC
                                TACCG
GAM1470 KIAA1906 3' CTTATTCTTCTTGACTTTTGG 73571    CTCC_
                              CCA    CAAGAAGAATAAG
                              |||    ||||||||||||
                              GGT    GTTCTTCTTATTC
                                TTTCA
GAM1470 OSBPL11  3' CTTAATTTCCCAAGAGTGGTG 43206       CCAA   AA
                              CACCACTC   GAAG  TAAG
                              ||||||||   ||||  ||||
                              GTGGTGAG   CTTT  ATTC
                                   AACC   A_
GAM1470 YME1L1   3' TCATTCTTGATGTGGTGTA   58438       TCC    _
                              TACACCAC   CAAGAA GA
                              ||||||||   |||||| ||
                              ATGTGGTG   GTTCTT CT
                                   TA_     A
GAM1470 ZNF262   3' CTTATTTTGTTTGGGAGT    18723        A
                              ACTCCCAAG AGAATAAG
                              ||||||||| ||||||||
                              TGAGGGTTT TTTTATTC
                                   G
GAM1470 LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_    AAGA
                              TACACCAC   CCAAG   ATA
                              ||||||||   |||||   |||
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                                ATGTGGTG  GGTTC   TGT
                                    CAA   GG__
GAM1471  CDC42    5'  GCAGTGCTGCCAACGC     10139   A      GA
                                GC TTGGCAGT  ATTGC
                                || ||||||||  |||||
                                CG AACCGTCG  TGACG
                                 C      __
GAM1471  FOSB     3'  TCTGACTGTCCCTGCCAATGCT 23059          T  ATTG
           C                     GAGCATTGGCAG GA   CAGA
                                ||||||||||||| ||   ||||
                                CTCGTAACCGTC CT   GTCT
                                       C  GTCA
GAM1471  HSD11B2  3'  TGCCCACTGCCGATGC      5772           AATT
                                GCATTGGCAGTG   GCA
                                ||||||||||||   |||
                                CGTAGCCGTCAC   CGT
                                       C___
GAM1471  LDHA     3'  TCTGACGCACCACTGCCAATGC 19915          AAT  _
           T                     AGCATTGGCAGTG  TG CAGA
                                ||||||||||||   || ||||
                                TCGTAACCGTCAC  GC GTCT
                                       CAC  A
GAM1471  PRG2     5'  CTGGCCATGCCAATGCTC    12261          G  AATTG
                                GAGCATTGGCA TG    CAG
                                |||||||||| ||    |||
                                CTCGTAACCGT AC    GTC
                                      _  CG___
GAM1471  ALTE     3'  TCTGCTTGGGAACTGCCAACGC 17584     A      GAATT_
           TT                     GAGC TTGGCAGT     GCAGA
                                |||| ||||||||     |||||
                                TTCG AACCGTCA     CGTCT
                                  C       AGGGTT
GAM1471  C20orf39 3'  TCTGCAGCCTGCCAGTGC    46577          TGAA
                                GCATTGGCAG   TTGCAGA
                                ||||||||||   |||||||
                                CGTGACCGTC   GACGTCT
                                      C___
GAM1471  FLJ10687 3'  TCTGCATAATGTTCACTGCCAA 36952     CA         ____
           ACTC                    GAG  TTGGCAGTGAAT   TGCAGA
                                |||  ||||||||||||   ||||||
                                CTC  AACCGTCACTTG   ACGTCT
                                  A_          TAAT
GAM1471  FLJ21615 3'  CTGCCTGCCAGTACTC      50808     C      TGAATT
                                GAG ATTGGCAG     GCAG
                                ||| ||||||||     ||||
                                CTC TGACCGTC     CGTC
                                  A      _______
GAM1471  HBP17    5'  CTGCAATTCACTCCCACTGC   18887     T  C
                                GCA TGG AGTGAATTGCAG
                                ||| ||| ||||||||||||
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                                CGT ACC TCACTTAACGTC
                                  C   C
GAM1471 KIAA1210 3' GTAGTCACTGCCAGC      98079    AT       A
                                GC  TGGCAGTGA TTGC
                                ||  ||||||||| ||||
                                CG  ACCGTCACT GATG
                                 __       _
GAM1471 MGC3123  3' TGATTCACTGCCACCGCTC   44348     AT
                                GAGC  TGGCAGTGAATTG
                                ||||  ||||||||||||
                                CTCG  ACCGTCACTTAGT
                                  CC
GAM1471 MGC3248  3' TCCACAATTCACACCAAAATGT 51652     __  CA      CA
                                GCAT  TGG  GTGAATTG  GA
                                ||||  |||  ||||||||  ||
                                TGTA  ACC  CACTTAAC  CT
                                  AA  A_      AC
GAM1471 RMP      3' TCTGAATACTGTCAACACTC   57065    CA       AATTG
                                GAG  TTGGCAGTG    CAGA
                                |||  |||||||||    ||||
                                CTC  AACTGTCAT    GTCT
                                  AC       AA___
GAM1471 RMP      3' TCTGAATACTGTCAACACTC   15045    CA       AATTG
                                GAG  TTGGCAGTG    CAGA
                                |||  |||||||||    ||||
                                CTC  AACTGTCAT    GTCT
                                  AC       AA___
GAM1471 TTTY11   3' TCTGCAAAACAGCCAATGCT   50026        A  GAA
                                AGCATTGGC GT   TTGCAGA
                                |||||||||  ||   |||||||
                                TCGTAACCG CA   AACGTCT
                                     A  A__
GAM1471 LOC125268 3' TCTGAAGAACTGCCAATGC   76583          GAA  G
                                GCATTGGCAGT   TT CAGA
                                ||||||||||   || ||||
                                CGTAACCGTCA   AA GTCT
                                      AG_  _
GAM1471 LOC157807 3' CTGAGTCACCCCAATGCTC   82512        CA    ATTG
                                GAGCATTGG  GTGA    CAG
                                |||||||||  ||||    |||
                                CTCGTAACC  CACT    GTC
                                     C_    GA__
GAM1471 LOC257486 3' GTAGTCACTGCCAGC      69779    AT       A
                                GC  TGGCAGTGA TTGC
                                ||  ||||||||| ||||
                                CG  ACCGTCACT GATG
                                 __       _
GAM1472 HAL      5' GCCACTCCTGCATAAAGCTC   10903          TGAAAA
                                GAGCTTTATGC     GGTGGC
                                ||||||||||      ||||||
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                                CTCGAAATACG     TCACCG
                                      TCC___
GAM1472 HMGN2    3' GGCCACCTTGGCACAAAAGC  19809      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _ GG
GAM1472 NMI      5' GGCCACCTCCTCAGGAAG    17436     ATG   AA
                                CTTT   CTGA  AGGTGGCC
                                ||||   ||||  ||||||||
                                GAAG   GACT  TCCACCGG
                                  ___   CC
GAM1472 PACE     3' GGCCACCTCTCCAAGGGCTT   11944       A  CT  AAA
                                GAGCTTT TG  GA   GGTGGCC
                                ||||||| ||  ||   |||||||
                                TTCGGGA AC  CT   CCACCGG
                                   _ CT  ___
GAM1472 PYCR1    3' CCACCTTCCTCTAGAGCTC   70639       TGCT  A_
                                GAGCTTTA   GA  AAGGTGG
                                ||||||||   ||  |||||||
                                CTCGAGAT   CT  TTCCACC
                                     _____ CC
GAM1472 SDC1     3' GGCCACCTCCCCAGCATTCCAG 12991     TT_     AAA
          C                      GCT   ATGCTG   AGGTGGCC
                                 |||   ||||||   ||||||||
                                 CGA   TACGAC   TCCACCGG
                                   CCT     CCC
GAM1472 FLJ11560 5' GCCCAGGCCCAGCATAAAG   48008         AAAA  ___
                                CTTTATGCTG   GGT   GGC
                                ||||||||||   |||   |||
                                GAAATACGAC   CCG   CCG
                                     _____  GAC
GAM1472 KIAA0446 5' CCACCTTTTGAAGAGCTC    69446       ATGCTG
                                GAGCTTT     AAAAGGTGG
                                |||||||     |||||||||
                                CTCGAGA     TTTTCCACC
                                   AG_____
GAM1472 KIAA0971 3' GTTGTTCTCAGCATAAAGT   30677          AAA  TG
                                GCTTTATGCTGA   GG  GC
                                ||||||||||||   ||  ||
                                TGAAATACGACT   TT  TG
                                      C__  GT
GAM1472 KIAA1393 3' GGCCACCTTGGCACAAAAGC  72574      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _ GG
GAM1472 KIAA1656 3' GGCCACCTCCTCCTAGAAGCC 66377   A    ATGCT  AA
                                G GCTTT    GA  AGGTGGCC
                                | |||||    ||  ||||||||
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                                C CGAAG    CT  TCCACCGG
                                _    ATC__  CC
GAM1472  KIAA1884  3'  GCCACCTTCATCTACCAAGGCT 73728       ATGCT  A_
             C                   GAGCTTT    GA  AAGGTGGC
                                 |||||||    ||  ||||||||
                                 CTCGGAA    CT  TTCCACCG
                                     CCAT_  AC
GAM1472  PP3501    3'  GGCCACCGTTGACAGCATAAAG 41683         AAAA_
                                 CTTTATGCTG    GGTGGCC
                                 ||||||||||    |||||||
                                 GAAATACGAC    CCACCGG
                                       AGTTG
GAM1472  SDCCAG3   3'  GGTGTTCTCAGCATGAAGCTC  22803           AAA  TG
                                 GAGCTTTATGCTGA   GG  GCC
                                 ||||||||||||||   ||  |||
                                 CTCGAAGTACGACT   CT  TGG
                                          ___  TG
GAM1472  SP140     3'  GGCCACCTCCATGCAGAAGC   24327      A   TGAAA
                                 GCTTT TGC    AGGTGGCC
                                 ||||| |||    ||||||||
                                 CGAAG ACG    TCCACCGG
                                    _  TACC_
GAM1472  LOC148760 3'  GGCCACCTTCTCCAACAAGCTC 85364       TA  CT  A
                                 GAGCTT  TG  GA AAGGTGGCC
                                 ||||||  ||  || |||||||||
                                 CTCGAA  AC  CT TTCCACCGG
                                     CA  __  C
GAM1472  LOC150170 5'  ACCTGTTTCACATAAAGC    80414         C    _
                                 GCTTTATG TGAAA AGGT
                                 |||||||| ||||| ||||
                                 CGAAATAC ACTTT TCCA
                                      _    G
GAM1472  LOC150175 5'  ACCTGTTTCACATAAAGC    80453         C    _
                                 GCTTTATG TGAAA AGGT
                                 |||||||| ||||| ||||
                                 CGAAATAC ACTTT TCCA
                                      _    G
GAM1472  LOC150215 5'  ACCTGTTTCACATAAAGC    80456         C    _
                                 GCTTTATG TGAAA AGGT
                                 |||||||| ||||| ||||
                                 CGAAATAC ACTTT TCCA
                                      _    G
GAM1472  LOC150218 5'  ACCTGTTTCACATAAAGC    80525         C    _
                                 GCTTTATG TGAAA AGGT
                                 |||||||| ||||| ||||
                                 CGAAATAC ACTTT TCCA
                                      _    G
GAM1472  LOC152065 3'  GGCCACCTTCTCCTTGGCAGGC 86737       TTA   ___  A
             TC                    GAGCT   TGCT   GA AAGGTGGCC
                                   |||||   ||||   || |||||||||
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                                CTCGG  ACGG  CT TTCCACCGG
                                  ___   TTC  C
GAM1472  LOC152267 3'  GGCCACCTTGGCACAAAAGC  61036     A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _  GG
GAM1472  LOC158292 5'  CCTCTGGACCCAGCATAAGGCT 88046          AAAA_  T
           C                     GAGCTTTATGCTG    GG GG
                                ||||||||||||    || ||
                                CTCGGAATACGAC    TC CC
                                      CCAGG  T
GAM1472  LOC219997 3'  GCCACCTCTTCAGCCTC    93256    CTTTAT    A
                                GAG    GCTGAA AGGTGGC
                                |||    |||||| |||||||
                                CTC    CGACTT TCCACCG
                                  _______    C
GAM1472  LOC256269 3'  GGCCACCTTGGCACAAAAGC  96608     A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _  GG
GAM1472  LOC91963  5'  GGCCACCTCCTCTGAGAAGC  68321     ATGCT  AA
                                GCTTT    GA  AGGTGGCC
                                |||||    ||  ||||||||
                                CGAAG    CT  TCCACCGG
                                   AGT__  CC
GAM1473  CCND2    3'  TCCCAGCAAATCATCGGGCCA  10055         CCACA  _  A
                                TGGCCTGATGAT    GC GG GA
                                ||||||||||||    || || ||
                                ACCGGGCTACTA    CG CC CT
                                      AA___  A  C
GAM1473  GCN5L2   5'  CTCCGCTGCGGGGGAGGCC   60529     GATGA  A
                                GGCCT    TCC CAGCGGAG
                                |||||    ||| ||||||||
                                CCGGA    GGG GTCGCCTC
                                   GG___  C
GAM1473  GJA5     3'  CTGACCAGATCATCAGCCA   19164     C      CACAG
                                TGGC TGATGATC    CGG
                                |||| ||||||||    |||
                                ACCG ACTACTAG    GTC
                                  _       ACCA_
GAM1473  HIVEP3   3'  TCCCCGCTGTGGTTGGCAGCCA 44702     C  ATGAT       A
                                TGGC TG    CCACAGCGG GA
                                |||| ||    ||||||||| ||
                                ACCG AC    GGTGTCGCC CT
                                  _ GGTT_       C
GAM1473  HOXD1    5'  CCGCCGGTATATTAGGCCA   44696         AT  ACA
                                TGGCCTGATG  CC   GCGG
                                ||||||||||  ||   ||||
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                                ACCGGATTAT  GG   CGCC
                                      AT  C__
GAM1473  SUFU     3'  CCTTGTGACCCATCAGGCCA   32934          ATC    C
                                TGGCCTGATG   CACAG GG
                                ||||||||||   ||||| ||
                                ACCGGACTAC   GTGTT CC
                                      CCA    _
GAM1473  DKFZP586J1624 3'  CTCCGCCCAGTCACCATCAGGC 32043          ATCCACA_
           CA                    TGGCCTGATG       GCGGAG
                                ||||||||||       ||||||
                                ACCGGACTAC       CGCCTC
                                      CACTGACC
GAM1473  KIAA1671  3'  CTTTGCTTATGAATCATCAGAC 66282    C       C  C_
           C                     GG CTGATGAT CA  AGCGGAG
                                || ||||||||  ||  |||||||
                                CC GACTACTA GT  TCGTTTC
                                 A       A  AT
GAM1473  LOC159110 5'  TCTCCGCTGCCCCGGTCAACCA 82995     CCTGA    CA__
                                TGG    TGATC    CAGCGGAGA
                                |||    |||||    |||||||||
                                ACC    ACTGG    GTCGCCTCT
                                  A____     CCCC
GAM1473  LOC159116 5'  TCTCCGCTGCCCCGGTCAACCA 82978     CCTGA    CA__
                                TGG    TGATC    CAGCGGAGA
                                |||    |||||    |||||||||
                                ACC    ACTGG    GTCGCCTCT
                                  A____     CCCC
GAM1473  LOC165476 5'  CTCCGCTGCCTGCTCAGCCA   88550     C   TGATCCA
                                TGGC TGA      CAGCGGAG
                                |||| |||      ||||||||
                                ACCG ACT      GTCGCCTC
                                  _   CGTCC__
GAM1473  LOC200032 5'  CTGACCAGATCATCAGCCA    85475      C       CACAG
                                TGGC TGATGATC     CGG
                                |||| ||||||||     |||
                                ACCG ACTACTAG     GTC
                                  _       ACCA_
GAM1473  LOC219654 5'  CTCCGCTGCGGAGGGGGGCC   92932      GATGA   A
                                GGCCT     TCC CAGCGGAG
                                |||||     ||| ||||||||
                                CCGGG     AGG GTCGCCTC
                                   GGG__   C
GAM1473  LOC255862 3'  TCAAATGTAGACTATCAGGCCA 96115          A  C   GCG
                                TGGCCTGATG TC ACA   GA
                                |||||||||| || |||   ||
                                ACCGGACTAT AG TGT   CT
                                      C  A   AAA
GAM1474  JAG2     3'  CACCAAAAACAAAAACCAA    11093       GC__
                                TTGGTT    TTTTTGGTG
                                ||||||    |||||||||
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                                AACCAA    AAAAACCAC
                                   AAAC
GAM1474  RPLP0    3'  TCACCAAAAAGCAACCAACTTA 54976
                                TAAGTTGGTTGCTTTTTGGTGA
                                ||||||||||||||||||||||
                                ATTCAACCAACGAAAAACCACT

GAM1474  FIGN     3'  ACCAACCAACAAACCAACTTA  36573          GCTTT_
                                TAAGTTGGTT     TTGGT
                                ||||||||||     |||||
                                ATTCAACCAA     AACCA
                                      ACAACC
GAM1474  FLJ11136  3'  AATCTGCATAAAAACAACCAAC 37661         C     _ _
                                GTTGGTTG TTTTTG GT GATT
                                |||||||| |||||| || ||||
                                CAACCAAC AAAAAT CG CTAA
                                     _     A  T
GAM1474  LOC220717 3'  TCACCAAAAAGCAACCAACTTA 92459
                                TAAGTTGGTTGCTTTTTGGTGA
                                ||||||||||||||||||||||
                                ATTCAACCAACGAAAAACCACT

GAM1475  CDKN1A   5'  AGGCCGAGCCAAGCGTGCC    55266        CGAA  TC    C
                                GGCACGCT    CT  CGGC CT
                                ||||||||    ||  |||| ||
                                CCGTGCGA    GA  GCCG GA
                                     ACC_ ___    A
GAM1475  DKFZp761A052 5'  GGCCGGAACAAGCGTAGC    73377    _    CGAAC
                                GC ACGCT    TTCCGGCC
                                || |||||    ||||||||
                                CG TGCGA    AAGGCCGG
                                 A    AC____
GAM1475  KIAA0415  3'  GGCTCAGCCCGGCGTGCCA   94167        T  AA  TCC
                                TGGCACGC CG  CT   GGCC
                                |||||||| ||  ||   ||||
                                ACCGTGCG GC  GA   TCGG
                                     _  CC  C__
GAM1475  PDE4DIP   5'  AGGCCGGAAGCCCGCTGACC   97173    _ C  TCGAA      C
                                GG CA GC     CTTCCGGC CT
                                || || ||     |||||||| ||
                                CC GT CG     GAAGGCCG GA
                                 A  _  CCC__       A
GAM1475  LOC144100 3'  AGGGCCGGAGCAGGAGCATGCT 77183      C    GAAC
              A                  TGGCA GCTC    TTCCGGCCCT
                                 ||||| ||||    ||||||||||
                                 ATCGT CGAG    GAGGCCGGGA
                                    A    GAC_
GAM1475  LOC145934 5'  AGGGCCGGAGAAGCGAGCGGCC 84558      A     AAC
              A                  TGGC CGCTCG   TTCCGGCCCT
                                 |||| ||||||   ||||||||||
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                                ACCG GCGAGC   GAGGCCGGGA
                                  _     GAA
GAM1475  LOC148696 5'  AGGGCCGAGAAGGCGCGTGCCA 85344        TCGAA   _
                                TGGCACGC    CTTC CGGCCCT
                                ||||||||    |||| |||||||
                                ACCGTGCG    GAAG GCCGGGA
                                    CG___   A
GAM1475  LOC253263 3'  AGGGCCGGCTCGTGAACAGCCA 98813     ACGCT_  ACTT
                                TGGC    CGA   CCGGCCCT
                                ||||    |||   ||||||||
                                ACCG    GCT   GGCCGGGA
                                  ACAAGT  C___
GAM1475  LOC254559 5'  AGGGCGCGTGGTTCGGCGTGCC 98380        T     TC  _
            A                    TGGCACGC CGAACT  CG GCCCT
                                ||||||| ||||||  || |||||
                                ACCGTGCG GCTTGG  GC CGGGA
                                    _     T_  G
GAM1475  LOC256444 5'  AGGGCCGGAGAAGCGAGCGGCC 98382     A     AAC
            A                    TGGC CGCTCG   TTCCGGCCCT
                                |||| ||||||   ||||||||||
                                ACCG GCGAGC   GAGGCCGGGA
                                  _     GAA
GAM1476  ELF3    3'  TGACCTTGACCTTGACCAA   16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                  _     AGT  ___
GAM1476  JAK2    3'  TGACCTTCATTCTGAGACCAA  18318      CAA      AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_      C_
GAM1476  SLC10A2  5'  ACTCTCTGTCTTGACCAA    6590       CAA      A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM1476  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM1476  KIAA1958  5'  GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                GGTT   GGG   AAAGTCAC
                                ||||   |||   ||||||||
                                CCAA   CCC   TTTCAGTG
                                  A__   CAAG
GAM1476  MARCKS   3'  ACTTTCCACCCTGCCCA     11411     TTCA   A
                                TGG   AGGG TGGAAAGT
                                |||   |||| ||||||||
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                                ACC   TCCC ACCTTTCA
                                  CG__   _
GAM1476 TUB     5' GTGGGACCATCCCTTAAACC  13898     C       AAAG
                                GGTT AAGGGATGG   TCAC
                                |||| |||||||||   ||||
                                CCAA TTCCCTACC   GGTG
                                  A       AG__
GAM1476 LOC80298 3' ACTTTTACCTTGAACCA    48062         GATG
                                TGGTTCAAGG   GAAAGT
                                ||||||||||   ||||||
                                ACCAAGTTCC   TTTTCA
                                     A___
GAM1477 ACT     5' CCACAATCCAGGGGGCCAT   40420        CCG  AAC
                                ATGGCCCCT  GGA  TGTGG
                                |||||||||  |||  |||||
                                TACCGGGGG  CCT  ACACC
                                     A__  A__
GAM1477 ADAM11   3' GCCACAGCTCAACTCGGGGGC 41490     TC   AAA__
                                GCCCC  CGGG   CTGTGGC
                                |||||  ||||   |||||||
                                CGGGG  GCTC   GACACCG
                                  __   AACTC
GAM1477 ADAM11   3' GCCACAGCTCAACTCGGGGGC 11487     TC   AAA__
                                GCCCC  CGGG   CTGTGGC
                                |||||  ||||   |||||||
                                CGGGG  GCTC   GACACCG
                                  __   AACTC
GAM1477 CDC34    3' GCCGCACCCCGGAGGAGCCA  16390     C      AAAC
                                TGGC CCTCCGGG   TGTGGC
                                |||| ||||||||   ||||||
                                ACCG GGAGGCCC   ACGCCG
                                  A      C___
GAM1477 CRI1     3' GCCACAGTTATCAAAGGCTA  27537     CCTCCG  A
                                TGGCC     GG AACTGTGGC
                                |||||     || |||||||||
                                ATCGG     CT TTGACACCG
                                  AAA___  A
GAM1477 FLII     3' GCCACAGTCCCCAGTAGCC   10656    CC  CC   AA
                                GGC  CT  GGG  ACTGTGGC
                                |||  ||  |||  ||||||||
                                CCG  GA  CCC  TGACACCG
                                  AT  __   C_
GAM1477 FZD10    3' GCCCACCCCCAGGAAGGCCA  24214     CC  _  AAAC  T
                                TGGCC  TCC GGG   TG GGC
                                |||||  ||| |||   || |||
                                ACCGG  AGG CCC   AC CCG
                                  A_   A  CC__  _
GAM1477 GNA11    5' CCACAGCCCCGGGGGCCG    76585       TC   AAA
                                TGGCCCC  CGGG  CTGTGG
                                |||||||  ||||  ||||||
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                                GCCGGGG  GCCC   GACACC
                                   __    C__
GAM1477  IGHMBP2   3'  GCCACAGAGGAGCGGAGGGGCC 10984          GGAAA
                                GGCCCCTCCG     CTGTGGC
                                ||||||||||     |||||||
                                CCGGGGAGGC     GACACCG
                                     GAGGA
GAM1477  MAGEA3    5'  CCAGAGGCCCCCGGAGGAGC   19315    C       AAA  G
                                GC CCTCCGGG   CT TGG
                                || ||||||||   || |||
                                CG GGAGGCCC   GA ACC
                                 A       CCG  G
GAM1477  PYGB      3'  CCAGGGGTCCCGGAGGAACC   12687    CC        AA  G
                                GG  CCTCCGGGA  CT TGG
                                ||  |||||||||  || |||
                                CC  GGAGGCCCT  GG ACC
                                 AA        G_  G
GAM1477  PYGB      3'  CCATGTTTCCAGGAGGGGCCAT 12689           G     T
                                ATGGCCCCTCC GGAAAC GTGG
                                |||||||||||| |||||| ||||
                                TACCGGGGAGG CCTTTG TACC
                                      A     _
GAM1477  SLC6A6    3'  GCCACAGTCCTTCCTGGGGC   13183      TCC    __
                                GCCCC   GGGAA  ACTGTGGC
                                |||||   |||||  ||||||||
                                CGGGG   TCCTT  TGACACCG
                                   ___     CC
GAM1477  UBTF      3'  CCATTCCTTCCCAGAGGGGCC  27252        C    ACT
                                GGCCCCTC GGGAA   GTGG
                                |||||||| |||||   ||||
                                CCGGGGAG CCCTT   TACC
                                     A    CCT
GAM1477  CBCIP2    3'  GCCACACGGACTCAGAGGGGCC 52658         C   AAAC
              A                  TGGCCCCTC GGG    TGTGGC
                                 |||||||| |||    ||||||
                                 ACCGGGGAG CTC    ACACCG
                                      A   AGGC
GAM1477  FEM-2     3'  GCCACAGTCCCATGAGGGCC   28316      C  C_   AA
                                GGCCC TC  GGGA  CTGTGGC
                                ||||| ||  ||||  |||||||
                                CCGGG AG  CCCT  GACACCG
                                   _  TA   __
GAM1477  FLJ10199  3'  GCCACAGTTGAGAAGCGGAGGG 71755          GGA___
              GCCA                  TGGCCCCTCCG     AACTGTGGC
                                    ||||||||||     |||||||||
                                    ACCGGGGAGGC     TTGACACCG
                                         GAAGAG
GAM1477  FLJ11715  3'  ACAGTGTCCCCAGGAGGCCAT  44972       _  CC    A
                                ATGGCC CCT  GGGA ACTGT
                                |||||| |||  |||| |||||
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                                TACCGG GGA  CCCT TGACA
                                   A  C_   G
GAM1477  FLJ12505  5'  CCCGGTCCCGGAGCAGCCA   45713     CC      AA  T
                                TGGC  CTCCGGGA  CTG GG
                                ||||  ||||||||  ||| ||
                                ACCG  GAGGCCCT  GGC CC
                                  AC       __  _
GAM1477  KIAA0828  3'  GTTTCCCAGGAAGGCCAT    82119      CC  _
                                ATGGCC  TCC GGGAAAC
                                ||||||  ||| |||||||
                                TACCGG  AGG CCCTTTG
                                   A_  A
GAM1477  KIAA1190  3'  CCACAGTTCTGGGAGCC     71643    CCC  G   A
                                GGC   TCC GGAA CTGTGG
                                |||   ||| |||| ||||||
                                CCG   AGG TCTT GACACC
                                  ___   G   _
GAM1477  KIAA1297  5'  CCATGCCCAGAAGGCCA     72634     CC  C   AAAC
                                TGGCC  TC GGG   TGTGG
                                |||||  || |||   |||||
                                ACCGG  AG CCC   GTACC
                                   A_  A  _____
GAM1477  PASK     5'  GCCACAGAGTTGGGGGGCCAT  31415       T   GAAA
                                ATGGCCCC CCGG   CTGTGGC
                                |||||||| ||||   |||||||
                                TACCGGGG GGTT   GACACCG
                                    _   GA__
GAM1477  PCDH17   3'  GCCACAGTTCCCTGCAGCCA  27836     CCCTC   A
                                TGGC    CGGG AACTGTGGC
                                ||||    |||| |||||||||
                                ACCG    GTCC TTGACACCG
                                  AC___   C
GAM1477  RIL      3'  CCATGCTGCCCTGAAGGGGCCA 14885       C   AAACT
                                TGGCCCCT CGGG    GTGG
                                |||||||| ||||    ||||
                                ACCGGGGA GTCC    TACC
                                    A   CGTCG
GAM1477  SREC     3'  GCAGTGCTCCCGGAGGGGCC  14905         A_
                                GGCCCCTCCGGGA  ACTGT
                                ||||||||||||  |||||
                                CCGGGGAGGCCCT  TGACG
                                      CG
GAM1477  TRAF2    3'  GCCGGCTCACGGAGGGGCCA  41236         G  AACTG
                                TGGCCCCTCCG GA    TGGC
                                |||||||||| ||    ||||
                                ACCGGGGAGGC CT    GCCG
                                    A  CG___
GAM1477  LOC123242 5'  CCACAGCCCACCTGGAGGCCA  76111      CC    AAA_
                                TGGCC  TCCGGG   CTGTGG
                                |||||  ||||||   ||||||
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                                ACCGG  AGGTCC    GACACC
                                  __      ACCC
GAM1477  LOC124460 5'  CCAAGAGCTCGAAGGGGCCAT  76559         C    AAA  G
                                ATGGCCCCT CGGG   CT TGG
                                ||||||||| ||||   || |||
                                TACCGGGGA GCTC   GA ACC
                                    A    GA_  _
GAM1477  LOC132166 3'  GCCAGCGCCCGAGGGGGCCA   75537        TC    AAACTG
                                TGGCCCC  CGGG     TGGC
                                |||||||  ||||     ||||
                                ACCGGGG  GCCC     ACCG
                                   GA    GCG___
GAM1477  LOC146958 5'  GCCACAGTCTCAAGTGGACAT  84944     G  C  CC    AA
                                ATG CC CT  GGGA  CTGTGGC
                                ||| || ||  ||||  |||||||
                                TAC GG GA  CTCT  GACACCG
                                  A  T  A_    __
GAM1477  LOC149420 3'  GCCACAGTTTCCTAAGCGC    80155    CC  CC
                                GC  CT  GGGAAACTGTGGC
                                ||  ||  ||||||||||||||
                                CG  GA  TCCTTTGACACCG
                                 C_  A_
GAM1477  LOC152317 3'  GCCACAGTCTGGGAGAGCCA   86831      CC    G   AA
                                TGGC  CTCC GGA  CTGTGGC
                                ||||  |||| |||  |||||||
                                ACCG  GAGG TCT  GACACCG
                                  A_    G   __
GAM1477  LOC157450 3'  CCACAGCTTCCCGGGTCAT    71531        CTCC     A
                                ATGGCCC    GGGAA CTGTGG
                                |||||||    ||||| ||||||
                                TACTGGG    CCCTT GACACC
                                    _____     C
GAM1477  LOC157807 5'  GCCACAGTTTCAGCAGACCAT  82513      CCC  CCGG
                                ATGG   CT    GAAACTGTGGC
                                ||||   ||    ||||||||||||
                                TACC   GA    CTTTGACACCG
                                  A__  CGA_
GAM1477  LOC157923 5'  GCCACAGTCCAGAGAAGGCCA  82526       C_   C  GAA
                                TGGCC  CTC GG   ACTGTGGC
                                |||||  ||| ||   ||||||||
                                ACCGG  GAG CC   TGACACCG
                                   AA   A  ___
GAM1477  LOC158510 5'  CCAGAGGCCCCCGGAGGAGC   82833    C       AAA  G
                                GC CCTCCGGG   CT TGG
                                || ||||||||   || |||
                                CG GGAGGCCC   GA ACC
                                 A       CCG  G
GAM1477  LOC196860 3'  CCACAGTTCCCCGGAAAGTGCT 91214      CCC_      A
                                GGC    TCCGGG AACTGTGG
                                |||    |||||| ||||||||
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                                TCG    AGGCCC TTGACACC
                                  TGAA     C
GAM1477  LOC203235 5'  GCCAGGGCCCCCAGAGGGGCC  92099        C   AAA  G
                                GGCCCCTC GGG   CT TGGC
                                |||||||| |||   || ||||
                                CCGGGGAG CCC   GG ACCG
                                    A   CC_  G
GAM1477  LOC220739 3'  GCCACAGTAGGAGGGGCCA   94521         GGGAA
                                TGGCCCCTCC    ACTGTGGC
                                ||||||||||    ||||||||
                                ACCGGGGAGG    TGACACCG
                                     A_____
GAM1477  LOC222166 5'  CCCGGCCCCGGAGGAGCC    95733     C       AAA   T
                                GGC CCTCCGGG   CTG GG
                                ||| ||||||||   ||| ||
                                CCG GGAGGCCC   GGC CC
                                  A       C__   _
GAM1477  LOC253001 5'  CCACAGCCCACCTGGAGGCCA  97990      CC     AAA_
                                TGGCC  TCCGGG   CTGTGG
                                |||||  ||||||   ||||||
                                ACCGG  AGGTCC   GACACC
                                   __     ACCC
GAM1477  LOC254057 3'  GCCCCTATCCCAGAGGGGCC   98782        C    AACTGT
                                GGCCCCTC GGGA     GGC
                                |||||||| ||||     |||
                                CCGGGGAG CCCT     CCG
                                    A    ATCC__
GAM1477  LOC92558  3'  GCCACCTCCCAGAGGGGCC   70312        C    AACT
                                GGCCCCTC GGGA    GTGGC
                                |||||||| ||||   |||||
                                CCGGGGAG CCCT    CACCG
                                    A    C___
GAM1477  LOC93626  5'  CCACAGCCCCGGGGGCCG    73128        TC    AAA
                                TGGCCCC  CGGG   CTGTGG
                                |||||||  ||||   ||||||
                                GCCGGGG  GCCC   GACACC
                                   __    C__
GAM1478  ATP10C    3'  GCATGAGTGGACGTCAGAAG   44668    C       _   GA
                                CT CTGACGTCC CTCA  TGC
                                || |||||||| ||||  |||
                                GA GACTGCAGG GAGT  ACG
                                  A       T   __
GAM1478  BLVRB     3'  GCATTCTGGACATGAGGAGCAA 7387         GAC    CTCA
                                TTGCTCCT   GTCC    GATGC
                                ||||||||   ||||    |||||
                                AACGAGGA   CAGG    TTACG
                                    GTA    TC__
GAM1478  EGFL5     5'  GCATCTGAAATTTTCAGGTACA 87913     CT    CGTCCC
              A                  TTG  CCTGA     TCAGATGC
                                 |||  |||||     ||||||||
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                                AAC  GGACT     AGTCTACG
                                  AT    TTTAA_
GAM1478  GATM     3'  CACCTAAGAAGCTTAGGGGCAA 9434          C  CC  C  A
                                TTGCTCCTGA GT  CT AG TG
                                |||||||||| ||  || || ||
                                AACGGGGATT CG  GA TC AC
                                      _  AA  A  C
GAM1478  KCNK7    3'  CACCTGAGGAGGAAGCAG    20344      _  GACGTC     A
                                TTGCT CCT     CCTCAG TG
                                ||||| |||     |||||| ||
                                GACGA GGA     GGAGTC AC
                                   A  _______     C
GAM1478  KCNK7    3'  CACCTGAGGAGGAAGCAG    54054      _  GACGTC     A
                                TTGCT CCT     CCTCAG TG
                                ||||| |||     |||||| ||
                                GACGA GGA     GGAGTC AC
                                   A  _______     C
GAM1478  KCNK7    3'  CACCTGAGGAGGAAGCAG    54061      _  GACGTC     A
                                TTGCT CCT     CCTCAG TG
                                ||||| |||     |||||| ||
                                GACGA GGA     GGAGTC AC
                                   A  _______     C
GAM1478  KCNK7    3'  CACCTGAGGAGGAAGCAG    54231      _  GACGTC     A
                                TTGCT CCT     CCTCAG TG
                                ||||| |||     |||||| ||
                                GACGA GGA     GGAGTC AC
                                   A  _______     C
GAM1478  LYL1     3'  TGAAGACGTCAGGGGCAA    19951           CC
                                TTGCTCCTGACGTC  TCA
                                ||||||||||||||  |||
                                AACGGGGACTGCAG  AGT
                                      A_
GAM1478  TMOD2    3'  CATTTGCAAACGTCAGGAG   28022         CCCT
                                CTCCTGACGT    CAGATG
                                ||||||||||    ||||||
                                GAGGACTGCA    GTTTAC
                                     AAC_
GAM1478  UBE2A    3'  GCATCTGAGAACCTTAAAGC   13927     CC   C  CC
                                GCT  TGA GT  CTCAGATGC
                                |||  ||| ||  |||||||||
                                CGA  ATT CA  GAGTCTACG
                                  A_   C  A_
GAM1478  CGB1     5'  ATCTGAGAGAGAGCAG      54128       CTGACG  C
                                TTGCTC     TC CTCAGAT
                                ||||||     || |||||||
                                GACGAG     AG GAGTCTA
                                     _______  A
GAM1478  DKFZp547N157 3'  CACCTGAGACCAGCAGGACAA  69524     C    AC_  CC   A
                                TTG TCCTG   GTC  TCAG TG
                                ||| |||||   |||  |||| ||
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                                AAC AGGAC   CAG  AGTC AC
                                  _    GAC   __    C
GAM1478  DNAJB11   3'  GCAAGAGGACTCCAGGAGCAA  33306         AC    C  AGA
                                TTGCTCCTG  GTCC TC   TGC
                                |||||||||  |||| ||   |||
                                AACGAGGAC  CAGG AG   ACG
                                     CT    _  A__
GAM1478  KIAA1951  3'  CTGGAGACCCAGGAGCAA    74154         AC   C T
                                TTGCTCCTG  GTC C CAG
                                |||||||||  ||| | |||
                                AACGAGGAC  CAG G GTC
                                     C_   A _
GAM1478  OBTP      3'  GCACCCAAAGGGCAGGAGCAA  34665         ACGT    CAGA_
                                TTGCTCCTG    CCCT    TGC
                                |||||||||    ||||    |||
                                AACGAGGAC    GGGA    ACG
                                     _____    AACCC
GAM1478  TROAP     5'  GCACCCGAGAGGGTCAGGAG   19692         GT  _   AGA
                                CTCCTGAC  CC CTC   TGC
                                ||||||||  || |||   |||
                                GAGGACTG  GG GAG   ACG
                                     __  A   CCC
GAM1478  LOC146515 3'  GCATCTGAGAATTGGAGAGCAG 78518        _ TG CGTCC
                                TTGCTC C  A     CTCAGATGC
                                ||||||  |  |    |||||||||
                                GACGAG G  T     GAGTCTACG
                                    A GT AA___
GAM1478  LOC149426 3'  GCATCTGAGAAACACATGGGC  85574      C  AC  CC
                                GCTC TG  GT  CTCAGATGC
                                ||||  ||  ||  |||||||||
                                CGGG AC  CA  GAGTCTACG
                                   T  A_  AA
GAM1478  LOC153577 3'  GCATCCAAGGGTGGGGAGCAG  87240         GA  T    CA
                                TTGCTCCT  CG CCCT  GATGC
                                ||||||||  || ||||  |||||
                                GACGAGGG  GT GGGA  CTACG
                                     __  _    AC
GAM1478  LOC220021 3'  GCAAGGGAGGAGCCAGGAGCAA 95023          AC TC    AGA
                                TTGCTCCTG  G  CCTC   TGC
                                |||||||||  |  ||||   |||
                                AACGAGGAC  C  GGAG   ACG
                                     __ GA    GGA
GAM1479  TERF1     3'  CCCAAATCCTGTTCCAATGA   34391         C   TA    C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                     _  C_    A
GAM1479  FLJ10159  3'  CCATGTCACGCCATCCAATGAC 36334         CA_   A   TC
                                GTCATTGGA   CGT GAT  GG
                                |||||||||   ||| |||  ||
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                                CAGTAACCT   GCA CTG  CC
                                     ACC  _   TA
GAM1479  FLJ14213  3'  CCGATGCTCCCAATGACG    46216        ACAC   GAT
                                CGTCATTGG   GTA   TCGG
                                |||||||||   |||  ||||
                                GCAGTAACC   CGT   AGCC
                                     CT__   ___
GAM1479  MGC10715  3'  ATTTACCAGACATCCAATGAC  44495        CAC___
                                GTCATTGGA     GTAGAT
                                |||||||||     ||||||
                                CAGTAACCT     CATTTA
                                     ACAGAC
GAM1479  MOST2     5'  CCAGGACTGCCCAATGAC    40059        ACAC   A  _
                                GTCATTGG   GTAG TTC GG
                                ||||||||   |||| ||| ||
                                CAGTAACC   CGTC AGG CC
                                     ____   _  A
GAM1479  LOC150370 3'  CCGGGTCTACGTGCCCATGAC  86123      T  A
                                GTCAT GG CACGTAGATTCGG
                                ||||| || ||||||||||||||
                                CAGTA CC GTGCATCTGGGCC
                                   C  _
GAM1479  LOC152620 3'  CCCAAATCCTGTTCCAATGA   60707        C   TA   C
                                TCATTGGA ACG  GATT GGG
                                ||||||||  |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                     _  C_   A
GAM1479  LOC158668 3'  CCCAAATCCTGTTCCAATGA   69896        C   TA   C
                                TCATTGGA ACG  GATT GGG
                                ||||||||  |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                     _  C_   A
GAM1480  DNASE1L1  3'  GTCCCGGAAAGGGGCTGCAGGA 23019      A  TT  A    _
              C                  GTCC GT  GT CCCTT CCGGGAC
                                 |||| ||  ||  ||||| |||||||
                                 CAGG CG  CG GGGAA GGCCCTG
                                   A  T_  _    A
GAM1480  FABP2     3'  TCCAAAATACAAATTGGAC    5537           CCCTTCCG
                                GTCCAGTTTGTA       GGA
                                ||||||||||||       |||
                                CAGGTTAAACAT       CCT
                                     AAAA_____
GAM1480  FHOD1     3'  TCCCGGAAATCTATCTGGAC   60827       TTT   CCC
                                GTCCAG   GTA   TTCCGGGA
                                ||||||   |||   ||||||||
                                CAGGTC   TAT   AAGGCCCT
                                   ___   CTA
GAM1480  HDAC8     3'  CCCAGAGTCCTCAACTGGAC   38080        T TACCC   C
                                GTCCAGTT G     TTC GGG
                                |||||||| |     ||| |||
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                                CAGGTCAA C     GAG CCC
                                    _ TCCT_   A
GAM1480 JUND     3'  CCCGGACTCGACAAGCTGGAC  19294          ACCCT
                                GTCCAGTTTGT     TCCGGG
                                ||||||||||     ||||||
                                CAGGTCGAACA     AGGCCC
                                     GCTC_
GAM1480 LDHB     5'  TCCCAAGGACACACACTG    11293      T   AC    CC
                                CAGT TGT  CCTT  GGGA
                                |||| |||  ||||  ||||
                                GTCA ACA  GGAA  CCCT
                                  C   CA   __
GAM1480 MPP3     3'  TCCCAGAACATCCAAGCTGGAC 10411          TACCC   C
                                GTCCAGTTTG     TTC GGGA
                                |||||||||     ||| ||||
                                CAGGTCGAAC     AAG CCCT
                                     CTAC_   A
GAM1480 MUC5B    3'  CCCAGAAGGGTGAGGGGC    67396      AGTTTG       C
                                GTCC      TACCCTTC GGG
                                ||||      |||||||| |||
                                CGGG      GTGGGAAG CCC
                                  GA_____       A
GAM1480 SLC16A2  3'  TCCCAAAAAGGTACAGGC    22528         C  CC
                                GTTTGTACC TT  GGGA
                                ||||||||| ||  ||||
                                CGGACATGG AA  CCCT
                                     A  AA
GAM1480 FLJ20195 3'  CCCAGGAGCACAGACTGGAC   35215          ACC    C
                                GTCCAGTTTGT   CTTC GGG
                                ||||||||||   |||| |||
                                CAGGTCAGACA   GAGG CCC
                                     C__    A
GAM1480 KIAA0040 5'  TCCCAAGGACACACACTG    28495      T   AC    CC
                                CAGT TGT  CCTT  GGGA
                                |||| |||  ||||  ||||
                                GTCA ACA  GGAA  CCCT
                                  C   CA   __
GAM1480 KIAA1954 3'  CCAATTTGGGCACAACTGGAC  78223        T  A   TTCCG
                                GTCCAGTT GT CCC     GG
                                |||||||| || |||     ||
                                CAGGTCAA CA GGG     CC
                                     _ C   TTTAA
GAM1480 MSP      3'  CCCAGAAGAGCAAGCTGGA    50242         ACC    C
                                TCCAGTTTGT   CTTC GGG
                                ||||||||||   |||| |||
                                AGGTCGAACG   GAAG CCC
                                     A__    A
GAM1480 UBCE7IP5 3'  CCTGAAAGGACACAAACTGGA  30845          AC    C
                                TCCAGTTTGT  CCTT CGGG
                                ||||||||||  |||| ||||
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                                AGGTCAAACA  GGAA GTCC
                                      CA    A
GAM1480  LOC119587 3'  GTCCCAAAAGGGAAGGCTGGA  74456        GTA    CC
                                TCCAGTTT   CCCTT  GGGAC
                                ||||||||   |||||  |||||
                                AGGTCGGA   GGGAA  CCCTG
                                     A__     AA
GAM1480  LOC155060 3'  GTCCCGGAAGGGCCTGGGCTGG 87605      TT TA
                                CCAGT  G  CCCTTCCGGGAC
                                |||||  |  ||||||||||||
                                GGTCG  T  GGGAAGGCCCTG
                                   GG CC
GAM1480  LOC197259 3'  CTGGGAGAGGCACAAACTGGAC 89299          A  _
                                GTCCAGTTTGT CC CTTCCGG
                                |||||||||||| || |||||||
                                CAGGTCAAACA GG GAGGGTC
                                      C  A
GAM1480  LOC222697 3'  TCTCTGAGTACAAACTGGA   96020          CCT  C
                                TCCAGTTTGTAC   TC GGGA
                                ||||||||||||   || ||||
                                AGGTCAAACATG   AG CTCT
                                       ___  T
GAM1480  LOC255620 5'  CCCTGAACAAAACTGGAC    98873         GTACCC   C
                                GTCCAGTTT     TTC GGG
                                |||||||||     ||| |||
                                CAGGTCAAA     AAG CCC
                                     AC____   T
GAM1480  LOC51093  5'  TCCCGGAAAGGCAGCGTCGGA  32593     AGTT   A_  C
                                TCC    TGT  CC TTCCGGGA
                                |||    |||  || ||||||||
                                AGG    GCG  GG AAGGCCCT
                                  CT__   AC  A
GAM1480  LOC51149  5'  CCCAGAAGGGACAGGCTGG    32972         A     C
                                CCAGTTTGT CCCTTC GGG
                                ||||||||| |||||| |||
                                GGTCGGACA GGGAAG CCC
                                     _     A
GAM1481  ARNT2    3'  GGTCTCCCCACTCCCGGCAGC  30088      G ATC    C
                                GCTG T   GGAG GGGGAGACC
                                |||| |   |||| |||||||||
                                CGAC G   CCTC CCCCTCTGG
                                  _ GC_    A
GAM1481  ATP11A   3'  GTCTCCCCATCACCGGC     77557       ATCG  GC
                                GCTGGT    GA  GGGGAGAC
                                ||||||    ||  ||||||||
                                CGGCCA    CT  CCCCTCTG
                                   _____  A_
GAM1481  CAPNS1   3'  GGTCTCCCCATTCCCACCAG   10016      ATC    C
                                CTGGT   GGAG GGGGAGACC
                                |||||   |||| |||||||||
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                                GACCA  CCTT CCCCTCTGG
                                  C__   A
GAM1481  CAPS     5'  GTCTCCCCAGGCACAACACAGC 15768      GTATCGGA __
                T                  AGCTG      GC  GGGGAGAC
                                   |||||      ||  ||||||||
                                   TCGAC      CG  CCCCTCTG
                                     ACAACA__  GA
GAM1481  FGFR4    3'  CTCCTGCCTCCCAATACCAGC  10636       C_   CG
                                   GCTGGTAT  GGAG  GGGAG
                                   ||||||||  ||||  |||||
                                   CGACCATA  CCTC  TCCTC
                                        AC   CG
GAM1481  FGFR4    3'  CTCCTGCCTCCCAATACCAGC  43628       C_   CG
                                   GCTGGTAT  GGAG  GGGAG
                                   ||||||||  ||||  |||||
                                   CGACCATA  CCTC  TCCTC
                                        AC   CG
GAM1481  LPIN1    3'  GGTCTCCCCGGAGTGCACAGCT 67990      _   CGGAG
                                   AGCTG GTAT    CGGGGAGACC
                                   ||||| ||||    ||||||||||
                                   TCGAC CGTG    GCCCCTCTGG
                                     A   AG___
GAM1481  MGAT1    3'  CTCCCCGCCCGCTCCCAG    11552     TAT   A
                                   CTGG   CGG GCGGGGAG
                                   ||||   ||| ||||||||
                                   GACC   GCC CGCCCCTC
                                     CTC  _
GAM1481  NID      3'  CCTTTTCCCAATACTAGC    11807       C_   C
                                   GCTGGTAT  GGAG GGG
                                   ||||||||  |||| |||
                                   CGATCATA  CCTT TCC
                                        AC   T
GAM1481  PACE4    3'  TCTCCCCGGCCCAGCT     11953       TATCG AG
                                   AGCTGG    G  CGGGGAGA
                                   ||||||    |  ||||||||
                                   TCGACC    C  GCCCCTCT
                                     _____ G_
GAM1481  PACE4    3'  TCTCCCCGGCCCAGCT     57164       TATCG AG
                                   AGCTGG    G  CGGGGAGA
                                   ||||||    |  ||||||||
                                   TCGACC    C  GCCCCTCT
                                     _____ G_
GAM1481  PPFIA3   3'  GGCCTCCCCGCCCCAGGCGTCA 61671    C   TA  _  A      A
                CT                   AG TGG  TC GG GCGGGGAG CC
                                     || |||  || || |||||||| ||
                                     TC ACT  GG CC CGCCCCTC GG
                                      _  GC  A  C       C
GAM1481  RELA     3'  GAGACCAACGCCCCAGATACCA 42026         _  A  _____  GAGA
                GC                   GCTGGTATC GG GCG    GG   C
                                     |||||||| || |||    ||   |
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                                CGACCATAG CC CGC    CC   G
                                     A  C   AA___  AGAG
GAM1481  RFX1     3'  GGCCTCCCCGCCCCACCCGC  12851   T  ATC  A      A
                                GC GGT   GG GCGGGGAG CC
                                || |||   || |||||||| ||
                                CG CCA   CC CGCCCCTC GG
                                 C  C__  _      C
GAM1481  TGFB1    5'  GGCCTCCCCACCACACCAGC  7259       ATC  AGC    A
                                GCTGGT   GG   GGGGAG CC
                                ||||||   ||   |||||| ||
                                CGACCA   CC   CCCCTC GG
                                   CA_  A__     C
GAM1481  C20orf18 3'  CTCCCCGCCTTCAGCT     49171       TATC  A
                                AGCTGG    GG GCGGGGAG
                                ||||||    || ||||||||
                                TCGACT    TC CGCCCCTC
                                     ____  _
GAM1481  C20orf18 3'  CTCCCCGCCTTCAGCT     49177       TATC  A
                                AGCTGG    GG GCGGGGAG
                                ||||||    || ||||||||
                                TCGACT    TC CGCCCCTC
                                     ____  _
GAM1481  C20orf19 5'  GAGACCAGTCTCTCCGATACCA 38071            C _______  GAGA
           GTT                    AGCTGGTATCGGAG G     GG    C
                                ||||||||||||| |     ||    |
                                TTGACCATAGCCTC C     CC    G
                                       T TGA___  AGAG
GAM1481  DKFZP434K1772 3'  GGTCTCCCCACCAACTCCAGTT 68338       TATC  AGC
                                AGCTGG    GG   GGGGAGACC
                                ||||||    ||   |||||||||
                                TTGACC    CC   CCCCTCTGG
                                   TCAA  A__
GAM1481  FLJ22555 5'  GTCTCTTTCTCCGACACCGCT  44796     T   A     C
                                AGC GGT TCGGAG GGGGAGAC
                                ||| ||| |||||| ||||||||
                                TCG CCA AGCCTC TTTCTCTG
                                  _  C     _
GAM1481  FLJ23322 3'  CTCCCCGCCCCATTTTCAGC   90215      TATC  A
                                GCTGG    GG GCGGGGAG
                                |||||    || ||||||||
                                CGACT    CC CGCCCCTC
                                   TTTA  C
GAM1481  KIAA0125 3'  GGCCTCCCCGCCTTCCCCACT  29571    C   TATC  __      A
                                AG TGG    GGA  GCGGGGAG CC
                                || |||    |||  |||||||| ||
                                TC ACC    CCT  CGCCCCTC GG
                                 _  _____  TC       C
GAM1481  KIAA1036 3'  CTCCCCGCTCCCTCAAGCT   30488     GGTATC
                                AGCT     GGAGCGGGGAG
                                ||||     ||||||||||
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                                TCGA     CCTCGCCCCTC
                                  ACTC__
GAM1481 KIAA1043 3' GTCCCCCCACAGCCACCAGC  66351      ATC  AGC_   A
                                GCTGGT   GG    GGGG GAC
                                ||||||   ||    |||| |||
                                CGACCA   CC    CCCC CTG
                                   ___  GACA    C
GAM1481 KIAA1163 3' GTCTCCCCGCTTGGCACCATCT 79654    C    AT  G
                                AG TGGT  CG AGCGGGGAGAC
                                || ||||  || ||||||||||
                                TC ACCA  GT TCGCCCCTCTG
                                 T    CG  _
GAM1481 KIAA1463 3' GTCTCCCCAGTACCAAGT    72741     _    CGGAGC
                                GCT GGTAT     GGGGAGAC
                                ||| |||||     ||||||||
                                TGA CCATG     CCCCTCTG
                                  A    A_____
GAM1481 KIAA1855 3' CTCCCCGCGAGGGTCCAGC   93951      T   GGA
                                GCTGG ATC   GCGGGGAG
                                ||||| |||   ||||||||
                                CGACC TGG   CGCCCCTC
                                   _  GAG
GAM1481 MESDC2   3' GGCCCACCTGCTCCAACCCCAG 72919       TATC       GAGA
            CT                   AGCTGG    GGAGCGGG    CC
                                ||||||    ||||||||    ||
                                TCGACC    CCTCGTCC    GG
                                   CCAA       ACCC
GAM1481 MGC14425 5' TCCTGCTCCGACACCACCT   52951    C    A
                                AG TGGT TCGGAGCGGGG
                                || |||| ||||||||||
                                TC ACCA AGCCTCGTCCT
                                 C    C
GAM1481 MGC16063 3' GCTCCCCGCCTGCCCGC     54928    T   ATC  A      A
                                GC GGT   GG GCGGGGAG C
                                || |||   || |||||||| |
                                CG CCG   TC CGCCCCTC G
                                 C   ___  _       C
GAM1481 OSBPL2   3' GGCCTATGAGCTCCGTACCAGC 58487       T     GGGG  A
                                GCTGGTA CGGAGC    AG CC
                                |||||||  ||||||    || ||
                                CGACCAT GCCTCG    TC GG
                                   _     AGTA  C
GAM1481 OSBPL2   3' GGCCTATGAGCTCCGTACCAGC 29901       T     GGGG  A
                                GCTGGTA CGGAGC    AG CC
                                |||||||  ||||||    || ||
                                CGACCAT GCCTCG    TC GG
                                   _     AGTA  C
GAM1481 LOC148530 5' GCTCCACCGACACCTGCT    85316    T   A   AGCGG   A
                                AGC GGT TCGG     GGAG C
                                ||| ||| ||||     |||| |
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                                TCG CCA AGCC    CCTC G
                                  T  C   A____   C
GAM1481  LOC150290 3'  CCACTGTACCCCGATACCACT  80586   C      A__  _
                                AG TGGTATCGG  GCGG GG
                                || |||||||||  |||| ||
                                TC ACCATAGCC  TGTC CC
                                 _      CCA   A
GAM1481  LOC165693 5'  CCTGCCTGCAATACCAGCT   83487        __  A
                                AGCTGGTAT  CGG GCGGG
                                |||||||||  ||| |||||
                                TCGACCATA  GTC CGTCC
                                     AC  _
GAM1481  LOC197003 3'  CCCTGCTCCAACACCAGC    89214      ATC
                                GCTGGT  GGAGCGGGG
                                ||||||  |||||||||
                                CGACCA  CCTCGTCCC
                                   CAA
GAM1481  LOC219908 5'  CTCCCCGCCCCAGTCCAGGCT  95976    _  T  C  A
                                AGC TGG AT GG GCGGGGAG
                                ||| ||| || || ||||||||
                                TCG ACC TG CC CGCCCCTC
                                  G  _ A  C
GAM1481  LOC220758 5'  GAGACCAGTATACTCCATACCA 92465       C   CG_______  GAGA
           GC                    GCTGGTAT GGAG       GG   C
                                |||||||| ||||       ||   |
                                CGACCATA CCTC       CC   G
                                     _   ATATGA___  AGAG
GAM1481  LOC91351  3'  GGGAGACCAATTAAACTCAGAT 66300        G  CG_________  GAGA
           ACCAGCT                 AGCTGGTATC GAG        GG   CC
                                |||||||||| |||        ||   ||
                                TCGACCATAG CTC        CC   GG
                                     A  AAATTAA___  AGAG
GAM1482  KCNK9    5'  GCCTGCGGGACATGC      33940    C  CT
                                GCA TG  TCCCGCAGGC
                                ||| ||  ||||||||||
                                CGT AC  AGGGCGTCCG
                                 _ __
GAM1482  TIMELESS  5'  CCCGCAGGGAGCGGGCCTCATC 15364    A  CA     C  A
                                GAT AG  CTGCTTCC GC GG
                                ||| ||  |||||||| || ||
                                CTA TC  GGCGAGGG CG CC
                                  C  CG      A  C
GAM1482  C22orf23  5'  CTGTAAAGCAGTGGTC     51770    AAG     CCC
                                GAT   CACTGCTT   GCAG
                                |||   ||||||||   ||||
                                CTG   GTGACGAA   TGTC
                                  ____      A__
GAM1482  ELA3A    3'  GCCCAGCTGGCAGTGCTGATCG 20436     A      TCCC  A_
                                CGAT AGCACTGCT    GC  GGC
                                |||| |||||||||    ||  |||
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                                GCTA TCGTGACGG   CG  CCG
                                  G       T___  AC
GAM1482 ELA3B   3' GCCCAGCTGGCAGTGCTGATCG 24741     A      TCCC  A_
                                CGAT AGCACTGCT   GC  GGC
                                |||| |||||||||   ||  |||
                                GCTA TCGTGACGG   CG  CCG
                                  G       T___  AC
GAM1482 ESPL1   5' GCCTGCTTGGTGCAGTGCTCTC 25440    TA      TT  C_
            G                    CGA  AGCACTGC  CC  GCAGGC
                                |||  ||||||||  ||  ||||||
                                GCT  TCGTGACG  GG  CGTCCG
                                  C_      T_  TT
GAM1482 FLJ10466 5' GCCCGCGAACACTGCTTGTCG  36630        C  C   CC  A
                                CGATAAGCA TG TTC  GC GGC
                                ||||||||| || |||  || |||
                                GCTGTTCGT AC AAG  CG CCG
                                     C  _   __  C
GAM1482 FLJ32884 5' CTGCCGGAGCAGTCCTATC   59135     A C     T  C
                                GATA G ACTGCT CC GCAG
                                |||| | |||||| || ||||
                                CTAT C TGACGA GG CGTC
                                  _ C     _  C
GAM1482 KIAA0774  3' GCCTGCGGGAGCTCCGGCTTCT 93407     T   ACT_  T
            CG                    CGA AAGC   GCT CCCGCAGGC
                                ||| ||||   ||| |||||||||
                                GCT TTCG   CGA GGGCGTCCG
                                  C   GCCT  _
GAM1482 KIAA1023  3' CCTGCTGGCAGTGCCTACG   34678    A  A      TCCC
                                CG TA GCACTGCT   GCAGG
                                || || ||||||||   |||||
                                GC AT CGTGACGG   CGTCC
                                 _  C       T___
GAM1482 MGC16291  3' CCTATAGAAACAATGCTTATC  52284        C  C   CCGC
                                GATAAGCA TG TTC   AGG
                                |||||||| || |||   |||
                                CTATTCGT AC AAG   TCC
                                     A  A   ATA_
GAM1482 NEIL2   5' GCCTGCGGAGGTGCTGC    59569     CT     C
                                GCA  GCTTCC GCAGGC
                                |||  |||||| ||||||
                                CGT  TGGAGG CGTCCG
                                  CG    _
GAM1482 PKNOX2   3' CCTGCGGGGATGCCCATC    92528     AA   CTGC
                                GAT  GCA   TTCCCGCAGG
                                |||  |||   ||||||||||
                                CTA  CGT   AGGGGCGTCC
                                  CC  _____
GAM1482 SNRK    3' GTCTTAAAAGCAGTGCTTA   35280          CCCGC
                                TAAGCACTGCTT    AGGC
                                ||||||||||||    ||||
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                                ATTCGTGACGAA    TCTG
                                      AAT__
GAM1482  LOC145439 5'  GCCTACGCTGCAGTGCTTTC  77727    T       TTCC  C
                                GA AAGCACTGC    CG AGGC
                                || |||||||||    || ||||
                                CT TTCGTGACG    GC TCCG
                                 _       TC__  A
GAM1482  LOC147700 5'  GCCTGCGGGACGCGACTGATCG 59883      A  CAC   T
                                CGAT AG   TGC TCCCGCAGGC
                                |||| ||   ||| ||||||||||
                                GCTA TC   GCG AGGGCGTCCG
                                  G  A__   C
GAM1482  LOC150197 3'  GCCTGCGAGGGGCAGTCATCG  80425      AAGC       C
                                CGAT    ACTGCTTC CGCAGGC
                                ||||    |||||||| |||||||
                                GCTA    TGACGGGG GCGTCCG
                                  C___       A
GAM1482  LOC155179 3'  CCTGCTGGCAGTGCCTACG    82227    A  A      TCCC
                                CG TA GCACTGCT    GCAGG
                                || || ||||||||    |||||
                                GC AT CGTGACGG    CGTCC
                                 _ C       T___
GAM1482  LOC91300  5'  GCGGAAACAGCACTTCATC    96237    _  CA   C    C
                                GAT AAG  CTG TTCC GC
                                ||| |||  ||| |||| ||
                                CTA TTC  GAC AAGG CG
                                  C   AC   A   _
GAM1482  LOC91300  5'  GCGGAAACAGCACTTCATC    57863    _  CA   C    C
                                GAT AAG  CTG TTCC GC
                                ||| |||  ||| |||| ||
                                CTA TTC  GAC AAGG CG
                                  C   AC   A   _
GAM1483  GPD1      3'  TCATGCCACCACATTTG     60398       C       C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                    A       _
GAM1483  IL5RA     5'  TCGCATGGCCACCGCATTT    6906           AT__
                                AAATGCGGTGGC    CGA
                                ||||||||||||    |||
                                TTTACGCCACCG    GCT
                                      GTAC
GAM1483  MYO1C     3'  TGCCGATGCCAAATATTTG    61873       CGG       A
                                TAAATG   TGGCATCG CA
                                ||||||   |||||||| ||
                                GTTTAT   ACCGTAGC GT
                                    AA_       C
GAM1483  C6orf37   3'  TGTCACACTGCATTTA      68097           GCATC
                                TAAATGCGGTG    GACA
                                ||||||||||     ||||
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                                ATTTACGTCAC    CTGT
                                     A____
GAM1483  DNAJC6   3'  TTGCAGAACCACCGCATT    29498        CA  GA
                                AATGCGGTGG  TC  CAA
                                ||||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                     A_  AC
GAM1483  FLJ11210 3'  GTCGATGTGCATGCTTTTA   60319     T   GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM1483  FLJ12476 3'  TCGATCTTCTGCATTTA     43270        T  C
                                TAAATGCGG GG ATCGA
                                ||||||||| || |||||
                                ATTTACGTC TC TAGCT
                                     T  _
GAM1483  KIAA1034  3'  TCGATGGCATCCGCATTTG   63134        _  G
                                TAAATGCGG TG CATCGA
                                ||||||||| || ||||||
                                GTTTACGCC AC GTAGCT
                                     T  G
GAM1483  KIAA1987  3'  TCATGTAACTGCATTTA     89391        G   C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                     A   _
GAM1483  MGC16063  3'  TGTCCTGGCCACTGCATT    54929         ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                     GTC
GAM1483  LOC147949 3'  TGTCAGATGTCCACATTGCA  79279     __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM1483  LOC150577 3'  GTCCTCACCGCATTTG      86258         CATC
                                TAAATGCGGTGG   GAC
                                ||||||||||||   |||
                                GTTTACGCCACT   CTG
                                     C___
GAM1483  LOC158219 3'  TGTGTGTCACCACATTT     82694      C      CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                  A       __
GAM1483  LOC202020 3'  TGTCTCACCACATTTA      90605       C    CATC
                                TAAATG GGTGG   GACA
                                |||||| |||||   ||||
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                                ATTTAC CCACT    CTGT
                                   A    ____
GAM1483 LOC90826 5' TGTCGATGCAGGTTTATTTG  64788      CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                   TTGGA
GAM1483 LOC93587 3' TTGTCTTTACCTGCATTTA   73042       _    CATC
                                TAAATGC GGTGG    GACAA
                                ||||||| |||||    |||||
                                ATTTACG CCATT    CTGTT
                                   T    T___
GAM1484 ELF3     3' TGACCTTGACCTTGACCAA   16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                  _    AGT  ___
GAM1484 JAK2     3' TGACCTTCATTCTGAGACCAA  18318      CAA      AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_      C_
GAM1484 SLC10A2  5' ACTCTCTGTCTTGACCAA    6590       CAA      A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                  ___       C
GAM1484 FLJ10803 3' GTGACTTTCAGTTAAAGCCAA 37205      CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM1484 KIAA1958 5' GTGACTTTGAACCCCAAACC  82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM1484 MARCKS   3' ACTTTCCACCCTGCCCA     11411     TTCA   A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM1484 TUB      5' GTGGGACCATCCCTTAAACC   13898     C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A       AG__
GAM1484 LOC80298 3' ACTTTTACCTTGAACCA     48062         GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
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                                ACCAAGTTCC    TTTTCA
                                     A___
GAM1485  GPD1     3'  TCATGCCACCACATTTG     60398       C       C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A      _
GAM1485  IL5RA    5'  TCGCATGGCCACCGCATTT    6906           AT__
                                AAATGCGGTGGC    CGA
                                ||||||||||||    |||
                                TTTACGCCACCG    GCT
                                      GTAC
GAM1485  MYO1C    3'  TGCCGATGCCAAATATTTG    61873       CGG       A
                                TAAATG   TGGCATCG CA
                                ||||||   |||||||| ||
                                GTTTAT   ACCGTAGC GT
                                   AA_       C
GAM1485  C6orf37  3'  TGTCACACTGCATTTA      68097          GCATC
                                TAAATGCGGTG     GACA
                                ||||||||||     ||||
                                ATTTACGTCAC     CTGT
                                      A_____
GAM1485  DNAJC6   3'  TTGCAGAACCACCGCATT    29498          CA  GA
                                AATGCGGTGG  TC  CAA
                                |||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                      A_  AC
GAM1485  FLJ11210 3'  GTCGATGTGCATGCTTTTA   60319     T   GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM1485  FLJ12476 3'  TCGATCTTCTGCATTTA     43270         T  C
                                TAAATGCGG GG ATCGA
                                ||||||||| || |||||
                                ATTTACGTC TC TAGCT
                                      T  _
GAM1485  KIAA1034 3'  TCGATGGCATCCGCATTTG   63134          _  G
                                TAAATGCGG TG CATCGA
                                ||||||||| || ||||||
                                GTTTACGCC AC GTAGCT
                                      T  G
GAM1485  KIAA1987 3'  TCATGTAACTGCATTTA     89391         G   C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                      A   _
GAM1485  MGC16063 3'  TGTCCTGGCCACTGCATT    54929          ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
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                                TTACGTCACCG  CTGT
                                     GTC
GAM1485  LOC147949 3'  TGTCAGATGTCCACATTGCA  79279     __  _  _
                                TGCG  GTGG CATC GACA
                                |||| |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM1485  LOC150577 3'  GTCCTCACCGCATTTG     86258          CATC
                                TAAATGCGGTGG   GAC
                                ||||||||||||   |||
                                GTTTACGCCACT   CTG
                                      C___
GAM1485  LOC158219 3'  TGTGTGTCACCACATTT    82694      C      CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                   A       __
GAM1485  LOC202020 3'  TGTCTCACCACATTTA     90605      C    CATC
                                TAAATG GGTGG   GACA
                                |||||| |||||   ||||
                                ATTTAC CCACT   CTGT
                                   A    ____
GAM1485  LOC90826  5'  TGTCGATGCAGGTTTATTTG  64788      CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                    TTGGA
GAM1485  LOC93587  3'  TTGTCTTTACCTGCATTTA  73042      _    CATC
                                TAAATGC GGTGG   GACAA
                                ||||||| |||||   |||||
                                ATTTACG CCATT   CTGTT
                                    T    T___
GAM1486  TERF1     3'  CCCAAATCCTGTTCCAATGA  34391       C  TA   C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                     _  C_   A
GAM1486  FLJ10159  3'  CCATGTCACGCCATCCAATGAC 36334       CA_  A  TC
                                GTCATTGGA   CGT GAT  GG
                                |||||||||   ||| |||  ||
                                CAGTAACCT   GCA CTG  CC
                                     ACC  _  TA
GAM1486  FLJ14213  3'  CCGATGCTCCCAATGACG   46216       ACAC  GAT
                                CGTCATTGG   GTA  TCGG
                                |||||||||   |||  ||||
                                GCAGTAACC   CGT  AGCC
                                     CT__  ___
GAM1486  MGC10715  3'  ATTTACCAGACATCCAATGAC  44495       CAC___
                                GTCATTGGA    GTAGAT
                                |||||||||    ||||||
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                                CAGTAACCT     CATTTA
                                     ACAGAC
GAM1486  MOST2     5'  CCAGGACTGCCCAATGAC    40059        ACAC   A  _
                                GTCATTGG    GTAG TTC GG
                                ||||||||    |||| ||| ||
                                CAGTAACC    CGTC AGG CC
                                     _____   _   A
GAM1486  LOC150370 3'  CCGGGTCTACGTGCCCATGAC  86123      T  A
                                GTCAT GG CACGTAGATTCGG
                                ||||| || ||||||||||||
                                CAGTA CC GTGCATCTGGGCC
                                   C  _
GAM1486  LOC152620 3'  CCCAAATCCTGTTCCAATGA   60707        C   TA   C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                     _  C_   A
GAM1486  LOC158668 3'  CCCAAATCCTGTTCCAATGA   69896        C   TA   C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                     _  C_   A
GAM1487  ADAR      3'  CTGCAGGGCGGGCAAGG     8483     A    CAG  T
                                CC TGCCC   GC CCTGCAG
                                || |||||   || |||||||
                                GG ACGGG   CG GGACGTC
                                 A    ___ _
GAM1487  ADAR      3'  CTGCAGGGCGGGCAAGG     32351    A    CAG  T
                                CC TGCCC   GC CCTGCAG
                                || |||||   || |||||||
                                GG ACGGG   CG GGACGTC
                                 A    ___ _
GAM1487  ADAR      3'  CTGCAGGGCGGGCAAGG     32361    A    CAG  T
                                CC TGCCC   GC CCTGCAG
                                || |||||   || |||||||
                                GG ACGGG   CG GGACGTC
                                 A    ___ _
GAM1487  AIRE      3'  TGGGAGCCTGAGGCATGAGAA  6354     C     C
                                TTC CATGCC CAGGCTCCTG
                                ||| |||||| ||||||||||
                                AAG GTACGG GTCCGAGGGT
                                  A     A
GAM1487  ANG       5'  GCAGGAGCCTGTGTTGG     8557     T  CC
                                CCA GC  CAGGCTCCTGC
                                ||| ||  ||||||||||
                                GGT TG  GTCCGAGGACG
                                  _  T_
GAM1487  BCAS1     3'  CTCGGGAGCCCAACGCACGAGA 14711     CCA   CCCA      C
              A                  TTC   TGC    GGCTCCTG AG
                                 |||   |||    |||||||| ||
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                                AAG  ACG   CCGAGGGC TC
                                  AGC  CAAC      _
GAM1487  DAG1    3'  CTGCAGGATGTAACATGG   16553      CCCCAG  _
                                CCATG    GC TCCTGCAG
                                |||||    || ||||||||
                                GGTAC    TG AGGACGTC
                                   AA____  T
GAM1487  GPRK7   3'  CGGGAGCCTGAGGCAGGAGAA  58313    _ A   C
                                TTC CC TGCC CAGGCTCCTG
                                ||| || |||| ||||||||||
                                AAG GG ACGG GTCCGAGGGC
                                  A _   A
GAM1487  KIF1B   3'  TGGGAGCCTGAGGCAGGAGAA  31273    _ A   C
                                TTC CC TGCC CAGGCTCCTG
                                ||| || |||| ||||||||||
                                AAG GG ACGG GTCCGAGGGT
                                  A _   A
GAM1487  NCAM1   5'  CTGCAGGGGGGGGGGCACAGAA 7040     CCA    AGG
                                TTC  TGCCCC  CTCCTGCAG
                                |||  ||||||  |||||||||
                                AAG  ACGGGG  GGGGACGTC
                                  AC_    GG_
GAM1487  NOS1    3'  CTGCAGGGTCCCCAAGGATGG  7095     G  CCA_  CT
                                CCAT CC   GG  CCTGCAG
                                |||| ||   ||  |||||||
                                GGTA GG   CC  GGACGTC
                                  _ AACC  TG
GAM1487  PDGFRB  3'  TGCCCCAGGGACATGGGAA   66584       _  CA  CTCCT
                                TTCCCATG CCC  GG   GCA
                                |||||||| |||  ||   |||
                                AAGGGTAC GGG  CC   CGT
                                    A  AC  _____
GAM1487  RAB31   3'  CTGCAGGGGGCGGGGCAGGAA  23440    CA    AGG
                                TTCC  TGCCCC  CTCCTGCAG
                                ||||  ||||||  |||||||||
                                AAGG  ACGGGG  GGGGACGTC
                                  __    CG_
GAM1487  SCN4A   3'  CTGCGTTCCCAGACCATGGGAA 6200       CCCCA  CTCC
                                TTCCCATG   GG   TGCAG
                                ||||||||   ||   |||||
                                AAGGGTAC   CC   GCGTC
                                    CAGAC  TT__
GAM1487  WHSC1   3'  CTGCAATGACTGCAGGGCTGGG 30582      T   __  GCTCC
            AA                  TTCCCA GCCC  CAG    TGCAG
                                ||||||  ||||  |||    |||||
                                AAGGGT CGGG  GTC    ACGTC
                                  _   AC   AGTA_
GAM1487  WHSC1   3'  CTGCAATGACTGCAGGGCTGGG 56669      T   __  GCTCC
            AA                  TTCCCA GCCC  CAG    TGCAG
                                ||||||  ||||  |||    |||||
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                                AAGGGT CGGG  GTC    ACGTC
                                   _   AC   AGTA_
GAM1487  WHSC1    3'  CTGCAATGACTGCAGGGCTGGG 56680      T   __  GCTCC
              AA                  TTCCCA GCCC  CAG    TGCAG
                                |||||| ||||  |||    |||||
                                AAGGGT CGGG  GTC    ACGTC
                                   _   AC   AGTA_
GAM1487  ZFP36L1  3'  CTGCAGGAAGGAAGGCTG    18201    T  __  AGGC
                                CA GCC  CC    TCCTGCAG
                                || |||  ||    ||||||||
                                GT CGG  GG    AGGACGTC
                                 _   AA  A___
GAM1487  C20orf64  5'  CAAGAGCCCTTCCTGCAGGGAA 54334      A   CCCA__    C
                                TTCCC TGC     GGCTC TG
                                ||||| |||     ||||| ||
                                AAGGG ACG     CCGAG AC
                                   _   TCCTTC     A
GAM1487  DRIL2    3'  CTGCAGGGTGTGGGCAGAGAA  22350     CCA     C G  T
                                TTC   TGCCC A GC CCTGCAG
                                |||   ||||| | || |||||||
                                AAG   ACGGG T TG GGACGTC
                                  AG_     _ G  _
GAM1487  FEM-2    3'  CTGCAGGGCCAAGCCACAGGAA 28312      CAT_  CCCA   T
                                TTCC    GC    GGC CCTGCAG
                                ||||    ||    ||| |||||||
                                AAGG    CG    CCG GGACGTC
                                   ACAC  AA__   _
GAM1487  FLJ10737  3'  CTGCAGTCCAAGCTGAACATGG 37054        CCCCA    C___
              GAA                   TTCCCATG    GGCT    CTGCAG
                                |||||||||     ||||    ||||||
                                AAGGGTAC    TCGA    GACGTC
                                     AAG__    ACCT
GAM1487  FLJ10898  5'  CTGCCAAACCTGCAACATGGGA 60133        CCC    CTCCT
              A                   TTCCCATG   CAGG    GCAG
                                |||||||||   ||||    ||||
                                AAGGGTAC   GTCC    CGTC
                                     AAC    AAAC_
GAM1487  FLJ11618  3'  CTGCAGGGGGAAGAGCCGGGAA 42624      AT  CCCAGG
                                TTCCC  GC     CTCCTGCAG
                                |||||  ||     |||||||||
                                AAGGG  CG     GGGGACGTC
                                   C_  AGAAG_
GAM1487  FLJ12287  5'  TGCCTCTGGGGCCTGGGAA    42564       T       CTCCT
                                TTCCCA GCCCCAGG     GCA
                                |||||| ||||||||     |||
                                AAGGGT CGGGGTCT     CGT
                                   C       C_____
GAM1487  FLJ14129  3'  TGGGAGCCTGGGGCAGGAGAA  48814     _ A
                                TTC CC TGCCCCAGGCTCCTG
                                ||| || ||||||||||||||
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                                AAG GG ACGGGGTCCGAGGGT
                                  A  _
GAM1487  KIAA0187  3'  CTGCAGGAGGAGGAACAGAGAA 29250    CCA  CC  AGG
                                TTC   TG  CC   CTCCTGCAG
                                |||   ||  ||   |||||||||
                                AAG   AC  GG   GAGGACGTC
                                  AG_  AA  AG_
GAM1487  KIAA0416  5'  GGAAAGCCTGGGACACAGAA   32093    CCA  C     __
                                TTC   TG CCCAGGC  TCC
                                |||   || |||||||  |||
                                AAG   AC GGGTCCG  AGG
                                  AC_  A      AA
GAM1487  KIAA1266  3'  CTGCAAGGGCGAGCATGGGA   66695       CCCAG    C
                                TCCCATGC    GCTC TGCAG
                                ||||||||    |||| |||||
                                AGGGTACG    CGGG ACGTC
                                     AG___    A
GAM1487  KIAA1483  3'  CTGCAGGGAAAAGGATATAGGA 70434     C   C  CAGG T
              A                  TTCC ATG CC    C CCTGCAG
                                 |||| ||| ||    | |||||||
                                 AAGG TAT GG    G GGACGTC
                                   A   A  AAAA _
GAM1487  KIAA1706  3'  TGCAGTGAGAGCATGGGA    94372       CCCAGG   _
                                TCCCATGC     CTC CTGCA
                                ||||||||     ||| |||||
                                AGGGTACG     GAG GACGT
                                     A_____   T
GAM1487  KIAA1715  3'  CTCAGGAGCCTGAGGCAGGAGA 68684     _ A   C       C
              A                  TTC CC TGCC CAGGCTCCTG AG
                                 ||| || |||| |||||||||| ||
                                 AAG GG ACGG GTCCGAGGAC TC
                                   A  _    A        _
GAM1487  KIAA1981  3'  CAGGAGCCAAGGTCACAGAA   89710    CCA  C  CA
                                TTC   TG CC  GGCTCCTG
                                |||   || ||  ||||||||
                                AAG   AC GG  CCGAGGAC
                                  AC_  T  AA
GAM1487  MCAM      3'  CAGGAACCTGGGGGCCTGTGAA 22457    C  T    _  C
                                TTC CA GCCCC AGG TCCTG
                                ||| || ||||| ||| |||||
                                AAG GT CGGGG TCC AGGAC
                                  T  C    G   A
GAM1487  MRPS24    3'  CTGCAGAGAATGGAAACGTGGG 50130       CC_  GG   C
              AA                  TTCCCATG   CCA  CTC TGCAG
                                  ||||||||   |||  ||| |||||
                                  AAGGGTGC   GGT  GAG ACGTC
                                       AAA   AA  _
GAM1487  MSE55     3'  TGCAGGACAGACATGGGAG   23916       CCCCAGGC
                                TTCCCATG       TCCTGCA
                                ||||||||       |||||||
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                                GAGGGTAC       AGGACGT
                                    AGAC____
GAM1487  OS4      3'  CTGCTTTGTGCTAAAAGCATGG 20388         CCCA   TCCT_
             GAA                    TTCCCATGC    GGC    GCAG
                                    |||||||||    |||    ||||
                                    AAGGGTACG    TCG    CGTC
                                        AAAA   TGTTT
GAM1487  PASK     5'  CAGGGTCTCGCCTGGGGCATTA 31405     CC         ____
             GAA                    TTC  ATGCCCCAGGC    TCCTG
                                    |||  ||||||||||    |||||
                                    AAG  TACGGGGTCCG    GGGAC
                                      AT         CTCT
GAM1487  PRO1163  3'  CTGAATGAGCCTGGGGCA    38323           CTG
                                    TGCCCCAGGCTC   CAG
                                    ||||||||||||   |||
                                    ACGGGGTCCGAG   GTC
                                           TAA
GAM1487  THEA     3'  CTCAGGAAGCTGAGGCACAAGA 66887     CCA    C   GC     C
             A                      TTC   TGCC CAG  TCCTG AG
                                    |||   |||| |||  ||||| ||
                                    AAG   ACGG GTC  AGGAC TC
                                      AAC    A   GA    _
GAM1487  WFDC3    3'  GCTGACCAGAGCATGGGAA    98702         CCCA  C  CT
                                    TTCCCATGC    GG TC  GC
                                    |||||||||    || ||  ||
                                    AAGGGTACG    CC AG  CG
                                        AGA_  _  T_
GAM1487  LOC122726 5'  CTGCAGGAAACACTGAGGCTTG 76103        T   C   GC__
             GGAA                     TTCCCA GCC CAG    TCCTGCAG
                                    ||||||| ||| |||    |||||||||
                                    AAGGGT CGG GTC    AGGACGTC
                                       T   A   ACAA
GAM1487  LOC129303 3'  CTGCAGGAATTGGGGGCTGGGA 75373        T     AG C
             A                      TTCCCA GCCCC  G TCCTGCAG
                                    |||||| |||||  | |||||||||
                                    AAGGGT CGGGG  T AGGACGTC
                                       _    GT A
GAM1487  LOC132617 5'  CTGCAGATCGAGGCATGGGA   76415         CCA  CTC
                                    TCCCATGCC   GG   CTGCAG
                                    |||||||||   ||   ||||||
                                    AGGGTACGG   CT   GACGTC
                                        AG_  A__
GAM1487  LOC145945 5'  AGGGCCTGGACCATAGAA    84563     CC   CC     T
                                    TTC  ATG  CCAGGC CCT
                                    |||  |||  |||||| |||
                                    AAG  TAC  GGTCCG GGA
                                      A_   CA     _
GAM1487  LOC146332 3'  CAGGAGCCTGGGGCCTGTGGA  78353     _  T
                                    TCC CA GCCCCAGGCTCCTG
                                    ||| || ||||||||||||||
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                                AGG GT CGGGGTCCGAGGAC
                                  T  C
GAM1487  LOC146714 5'  TGCAGGGCAGGCACAGGGA   84754     A_   CCAG  T
                                TCCC  TGCC    GC CCTGCA
                                ||||  ||||    || ||||||
                                AGGG  ACGG    CG GGACGT
                                  AC    A___  _
GAM1487  LOC147958 3'  CTGCAGGGCAGGCAGCAGAA   88523     CCA    CCAG  T
                                TTC   TGCC    GC CCTGCAG
                                |||   ||||    || |||||||
                                AAG   ACGG    CG GGACGTC
                                  ACG   A___  _
GAM1487  LOC149501 3'  CTGCAAGAGCCTGGCTGGGAA  75800       T   CC     C
                                TTCCCA GCC  AGGCTC TGCAG
                                |||||| |||  |||||| |||||
                                AAGGGT CGG  TCCGAG ACGTC
                                   _  __     A
GAM1487  LOC150397 3'  CAGGAGCCTGAGTGAAGGA   80655     CA   CC
                                TCC  TGC  CAGGCTCCTG
                                |||  |||  ||||||||||
                                AGG  GTG  GTCCGAGGAC
                                  AA   A_
GAM1487  LOC150397 3'  GCAGGAGCCTGCAGGAGA    80664    _ A   CCC
                                TC CC TGC   AGGCTCCTGC
                                || || |||   ||||||||||
                                AG GG ACG   TCCGAGGACG
                                 A  _  ____
GAM1487  LOC150517 5'  CTGCAGGTAGGAGCACAGAA   80725     CCA   C  AGGCT
                                TTC   TGC CC     CCTGCAG
                                |||   ||| ||     |||||||
                                AAG   ACG GG     GGACGTC
                                  AC_   A  AT____
GAM1487  LOC153688 3'  TGGGAGGCTGGGGCATGAGAA  87341     C         G
                                TTC CATGCCCCAG CTCCTG
                                ||| |||||||||| ||||||
                                AAG GTACGGGGTC GAGGGT
                                  A         G
GAM1487  LOC154849 3'  CTGCAGGAGGTGGAAGATG    60941     GCC   GG
                                CAT   CCA  CTCCTGCAG
                                |||   |||  |||||||||
                                GTA   GGT  GAGGACGTC
                                  GAA   G_
GAM1487  LOC162137 3'  GCAGGAGCTTCCCATAAAGAA  88480     CC_   CCCC
                                TTC   ATG    AGGCTCCTGC
                                |||   |||    ||||||||||
                                AAG   TAC    TTCGAGGACG
                                  AAA   CC__
GAM1487  LOC219654 3'  CAGGAGCCCAGGGGATGGGAA  92925        G   CA
                                TTCCCAT CCC  GGCTCCTG
                                ||||||| |||  ||||||||
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                                AAGGGTA GGG  CCGAGGAC
                                    G   AC
GAM1487  LOC254552 5'  CAGGAGCCCGGGGCTGG     96422     T    A
                                CCA GCCCC GGCTCCTG
                                ||| ||||| ||||||||
                                GGT CGGGG CCGAGGAC
                                  _     C
GAM1487  LOC255042 3'  CTCGGGAGCCTGAGGCAGGAGA 97042     _ A    C        C
              A                  TTC CC TGCC CAGGCTCCTG AG
                                ||| || |||| |||||||||| ||
                                AAG GG ACGG GTCCGAGGGC TC
                                  A _    A        _
GAM1487  LOC257000 3'  CTGCAGGACTCAGAGCATGG   98587       CCCA  C
                                CCATGC    GG TCCTGCAG
                                ||||||    || ||||||||
                                GGTACG    TC AGGACGTC
                                    AGAC  _
GAM1487  LOC91750  3'  TGGGGGCCTGAGGCACGAGAA  67659     CCA    C
                                TTC   TGCC CAGGCTCCTG
                                |||   |||| ||||||||||
                                AAG   ACGG GTCCGGGGGT
                                  AGC    A
GAM1488  EHF      3'  TCCAAAACCCAAGGTTGGCT   25127     AT   _    C
                                AGT  GCCT GGGT TTGGA
                                |||  |||| |||| |||||
                                TCG  TGGA CCCA AACCT
                                  GT    A    A
GAM1488  EPHA2    3'  CCATCGGCCAAGAATACTTGAA 16675          GC  G    T_
              G                  CTTCAAGTAT  CT GGTC  TGG
                                ||||||||||  || ||||  |||
                                GAAGTTCATA  GA CCGG  ACC
                                      A_  A    CT
GAM1488  ITGA5    3'  CCCAGAGACATACTTGAAG    61933          C__
                                CTTCAAGTATG   CTGGG
                                ||||||||||   |||||
                                GAAGTTCATAC   GACCC
                                      AGA
GAM1488  TREM2    3'  TCCAAGACTGTCATATTT     39098        CCTG
                                AAGTATG    GGTCTTGGA
                                |||||||    |||||||||
                                TTTATAC    TCAGAACCT
                                    TG__
GAM1488  UQCRB    3'  CCAACATAGGCATACTTAAG   21939     C         GGTC
                                CTT AAGTATGCCTG    TTGG
                                ||| ||||||||||    ||||
                                GAA TTCATACGGAT    AACC
                                  _         AC__
GAM1488  ATP10D   3'  CAGAGACCACTTGAAG      73526         ATGCCTG    _
                                CTTCAAGT      GGTCT TG
                                ||||||||      ||||| ||
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                                GAAGTTCA      CCAGA AC
                                   _______    G
GAM1488 B3GNT7   3' CCCTTCCAGGCAACCTGAA   71678     A  A      TCTT
                                TTCA GT TGCCTGGG   GG
                                |||| || ||||||||   ||
                                AAGT CA ACGGACCT   CC
                                  C  _       TC__
GAM1488 DKFZp547I224 3'  TCCAAAATTGACCACATACTTG 39963          CCTG   ____
          GA                     TTCAAGTATG   GGTC   TTGGA
                                |||||||||   ||||   |||||
                                AGGTTCATAC   CCAG   AACCT
                                     A___    TTAA
GAM1488 FLJ22341  3' CCAAGCTCAGGCACACCCAAG  45114    CAA  A      T
                                CTT   GT TGCCTGGG CTTGG
                                |||   || |||||||| |||||
                                GAA   CA ACGGACTC GAACC
                                  CC_  C       _
GAM1488 KIAA0779  3' CCGAACAGCATACTTGAAG   86908          C  GGTC
                                CTTCAAGTATGC TG   TTGG
                                |||||||||||| ||   ||||
                                GAAGTTCATACG AC   AGCC
                                      _  A___
GAM1488 LOC144233 3'  CCAAGGCACATAATTGAA   77246      G   CCTGG
                                TTCAA TATG    GTCTTGG
                                ||||| ||||    |||||||
                                AAGTT ATAC    CGGAACC
                                   A   A____
GAM1488 LOC147341 3'  ACCCAGGCATAACTGAAG   85116      AG
                                CTTCA  TATGCCTGGGT
                                |||||  ||||||||||
                                GAAGT  ATACGGACCCA
                                   CA
GAM1488 LOC221088 5'  TCCAAGGTGCTGGCCACTCGAA 94888     A   AT   TGGG
          G                     CTTC AGT  GCC    TCTTGGA
                                |||| |||  |||   |||||||
                                GAAG TCA  CGG    GGAACCT
                                  C   C_   TCGT
GAM1489 ELF3     3'  TGACCTTGACCTTGACCAA   16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                   _    AGT  ___
GAM1489 JAK2     3'  TGACCTTCATTCTGAGACCAA  18318       CAA      AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_       C_
GAM1489 SLC10A2   5'  ACTCTCTGTCTTGACCAA    6590       CAA      A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
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                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM1489  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM1489  KIAA1958  5'  GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM1489  MARCKS   3'  ACTTTCCACCCTGCCCA     11411     TTCA    A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM1489  TUB      5'  GTGGGACCATCCCTTAAACC   13898     C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A        AG__
GAM1489  LOC80298  3'  ACTTTTACCTTGAACCA     48062          GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                      A___
GAM1490  GLDC     3'  TCTGTAATCACATTTCTGA   64897     A   CA
                                TCA AAA  TGATTACAGG
                                ||| |||  ||||||||||
                                AGT TTT  ACTAATGTCT
                                  C   AC
GAM1490  IDH3A    3'  ATGTCCCTAGGTCTGTTTT    19843       T    AC
                                AAAACA GATT  AGGGACAT
                                |||||| ||||  ||||||||
                                TTTTGT CTGG  TCCCTGTA
                                   _    A_
GAM1490  LYAAT1   3'  ATGTCCCCCACCTCATGTTTT  55308         TTACA
                                AAAACATGA    GGGACAT
                                |||||||||    |||||||
                                TTTTGTACT    CCCTGTA
                                     CCACC
GAM1490  PDGFRA   3'  ATGCCCCTGTTCATGTTTTTG  21694           TT     A
                                CAAAAACATGA  ACAGGG CAT
                                ||||||||||||  |||||| |||
                                GTTTTTGTACT  TGTCCC GTA
                                      __     C
GAM1490  RPL10    3'  ATGTCTTTGTATCTACATTCTT 21176      A  CA  AT
            GA                    TCAA AA  TG  TACAGGGACAT
                                ||||  ||  ||  ||||||||||
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                                AGTT TT  AT  ATGTTTCTGTA
                                  C  AC  CT
GAM1490  WHSC1L1   3'  ATGTCTCTGCAACCATATTT   35495     C   A  A
                                AAA ATG TT CAGGGACAT
                                ||| ||| || |||||||||
                                TTT TAC AA GTCTCTGTA
                                  A   C  C
GAM1490  ZNF9      3'  TTGCTGTAATCAGTTTTT     14238       A       G
                                AAAAAC TGATTACAG GA
                                |||||| ||||||||| ||
                                TTTTTG ACTAATGTC TT
                                   _       G
GAM1490  BM046     3'  TTTCTGTAAACATATTTCTGA  38060     A   C   A     GG
                                TCA AAA ATG TTACAG  A
                                ||| ||| ||| ||||||  |
                                AGT TTT TAC AATGTC  T
                                  C   A   A     TT
GAM1490  DKFZp547I224 5'  ATGTCCCTGTCTGACAGCTTTG 39950       AACA  ATT_
           A                     TCAAA    TG    ACAGGGACAT
                                |||||    ||    ||||||||||
                                AGTTT    AC    TGTCCCTGTA
                                   CG__  AGTC
GAM1490  DKFZP566K1924 3'  CCTGTAATCAACTTTTGA    74196       ACA
                                TCAAAA   TGATTACAGG
                                ||||||   ||||||||||
                                AGTTTT   ACTAATGTCC
                                   CA_
GAM1490  KIAA0937  3'  ATGTCCCTGCACTCTGTTTT   93222       T  TTA
                                AAAACA GA   CAGGGACAT
                                |||||| ||   |||||||||
                                TTTTGT CT   GTCCCTGTA
                                   _ CAC
GAM1490  KIAA1668  3'  ATGTCCCTGAGCCGGCCCTTGA 67059      AAACA  AT A
                                TCAA    TG  T CAGGGACAT
                                ||||    ||  | |||||||||
                                AGTT    GC  A GTCCCTGTA
                                  CCCG_  CG _
GAM1490  MGC20398  3'  TTTGTGTAACATGTTTTTGA   67164          A    G
                                TCAAAAACATG TTACA GGA
                                |||||||||| ||||| |||
                                AGTTTTTGTAC AATGT TTT
                                      _    G
GAM1490  PP35      3'  TCCTAATCATGTTTTT      23800           ACA
                                AAAAACATGATT   GGGA
                                ||||||||||||   ||||
                                TTTTTGTACTAA   TCCT
                                       ____
GAM1490  PPFIA1    3'  TCCTTTCAAATCATGTTCTT   14635    A       AC_
                                AA AACATGATT   AGGGA
                                || |||||||||   |||||
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                                TT TTGTACTAA   TTCCT
                                 C        ACT
GAM1490  ZNF323    3'  TCTAACTCATGTTTTTGA    48820          TTACAG
                                TCAAAAACATGA     GGA
                                ||||||||||||     |||
                                AGTTTTTGTACT     TCT
                                       CAA___
GAM1490  LOC158549 5'  ATGTTGTAATAATCATGTTTTG 88215       A       CAGG
                A                TCAAAA CATGATTA    GACAT
                                 |||||| ||||||||    |||||
                                 AGTTTT GTACTAAT    TTGTA
                                    _       AATG
GAM1490  LOC161734 3'  ATGTCCCTGTCTGACAGCTTTG 88460      AACA  ATT_
                A                TCAAA    TG    ACAGGGACAT
                                 |||||    ||    ||||||||||
                                 AGTTT    AC    TGTCCCTGTA
                                    CG__  AGTC
GAM1490  LOC203276 3'  CTTGATAATTATGTTTCTGA   92123     A         _
                                TCA AAACATGATTA CAGG
                                ||| |||||||||| ||||
                                AGT TTTGTATTAAT GTTC
                                  C          A
GAM1490  LOC203305 3'  CTTGATAATTATGTTTCTGA   92176     A         _
                                TCA AAACATGATTA CAGG
                                ||| |||||||||| ||||
                                AGT TTTGTATTAAT GTTC
                                  C          A
GAM1490  LOC203339 5'  CCCTGTGATACTGTTCTT    92208    A    TG
                                AA AACA  ATTACAGGG
                                || ||||  |||||||||
                                TT TTGT  TAGTGTCCC
                                 C    CA
GAM1490  LOC220758 3'  TCTGTAATCACATTTCTGA    92469     A   CA
                                TCA AAA  TGATTACAGG
                                ||| |||  ||||||||||
                                AGT TTT  ACTAATGTCT
                                  C   AC
GAM1490  LOC221975 5'  ATGTCAGGTGGATCTATGTTTC 94188     A     _   _ AGG
                TGA                TCA AAACAT GATT AC   GACAT
                                ||| |||||| |||| ||   |||||
                                AGT TTTGTA CTAG TG   CTGTA
                                  C     T    G  GA_
GAM1490  LOC254243 3'  CTTGATAATTATGTTTCTGA   99262     A         _
                                TCA AAACATGATTA CAGG
                                ||| |||||||||| ||||
                                AGT TTTGTATTAAT GTTC
                                  C          A
GAM1490  LOC90038  3'  CTTGATAATTATGTTTCTGA   61806     A         _
                                TCA AAACATGATTA CAGG
                                ||| |||||||||| ||||
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                                AGT TTTGTATTAAT GTTC
                                  C         A
GAM1490 LOC90593 3' ATGTCCCTGTCTGACAGCTTTG 64201      AACA  ATT_
             A                   TCAAA    TG    ACAGGGACAT
                                 |||||    ||    ||||||||||
                                 AGTTT    AC    TGTCCCTGTA
                                   CG__  AGTC
GAM1490 LOC92181 3' TTGTAACATCATGTTTCTGA   68950     A       __
                                 TCA AAACATGAT  TACAG
                                 ||| |||||||||  |||||
                                 AGT TTTGTACTA  ATGTT
                                  C        CA
GAM1491 ELF3     3' TGACCTTGACCTTGACCAA    16685      T    GAT  AAA
                                 TTGGT CAAGG   GG   GTCA
                                 ||||| |||||   ||   ||||
                                 AACCA GTTCC   TC   CAGT
                                   _    AGT  ____
GAM1491 JAK2     3' TGACCTTCATTCTGAGACCAA  18318       CAA       AA
                                 TTGGTT   GGGATGGA  GTCA
                                 ||||||   ||||||||  ||||
                                 AACCAG   TCTTACTT  CAGT
                                    AG_       C_
GAM1491 SLC10A2  5' ACTCTCTGTCTTGACCAA    6590        CAA       A
                                 TTGGTT   GGGATGGA AGT
                                 ||||||   |||||||| |||
                                 AACCAG   TTCTGTCT TCA
                                    ___         C
GAM1491 FLJ10803 3' GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                 TTGGTT    GAT GAAAGTCAC
                                 ||||||    ||| |||||||||
                                 AACCGA    TTG CTTTCAGTG
                                    AA___   A
GAM1491 KIAA1958 5' GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                 GGTT   GGG    AAAGTCAC
                                 ||||   |||    ||||||||
                                 CCAA   CCC    TTTCAGTG
                                   A__   CAAG
GAM1491 MARCKS   3' ACTTTCCACCCTGCCCA     11411     TTCA    A
                                 TGG    AGGG TGGAAAGT
                                 |||    |||| ||||||||
                                 ACC    TCCC ACCTTTCA
                                   CG__   _
GAM1491 TUB      5' GTGGGACCATCCCTTAAACC   13898      C        AAAG
                                 GGTT AAGGGATGG    TCAC
                                 |||| |||||||||    ||||
                                 CCAA TTCCCTACC    GGTG
                                   A        AG__
GAM1491 LOC80298 3' ACTTTTACCTTGAACCA     48062          GATG
                                 TGGTTCAAGG    GAAAGT
                                 ||||||||||    ||||||
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                                ACCAAGTTCC    TTTTCA
                                     A___
GAM1492 ELF3     3' TGACCTTGACCTTGACCAA   16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                   _    AGT  ___
GAM1492 JAK2     3' TGACCTTCATTCTGAGACCAA 18318       CAA       AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_       C_
GAM1492 SLC10A2  5' ACTCTCTGTCTTGACCAA    6590       CAA       A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM1492 FLJ10803 3' GTGACTTTCAGTTAAAGCCAA 37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM1492 KIAA1958 5' GTGACTTTGAACCCCAAACC  82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM1492 MARCKS   3' ACTTTCCACCCTGCCCA     11411     TTCA    A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                 CG__    _
GAM1492 TUB      5' GTGGGACCATCCCTTAAACC   13898      C        AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A        AG__
GAM1492 LOC80298 3' ACTTTTACCTTGAACCA     48062          GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                     A___
GAM1493 GPD1     3' TCATGCCACCACATTTG      60398       C       C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A       _
GAM1493 IL5RA    5' TCGCATGGCCACCGCATTT    6906           AT__
                                AAATGCGGTGGC    CGA
                                ||||||||||||    |||
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                                TTTACGCCACCG   GCT
                                      GTAC
GAM1493 MYO1C    3' TGCCGATGCCAAATATTTG   61873      CGG      A
                                TAAATG  TGGCATCG CA
                                ||||||  |||||||| ||
                                GTTTAT  ACCGTAGC GT
                                   AA_      C
GAM1493 C6orf37  3' TGTCACACTGCATTTA     68097         GCATC
                                TAAATGCGGTG    GACA
                                ||||||||||    ||||
                                ATTTACGTCAC    CTGT
                                      A____
GAM1493 DNAJC6   3' TTGCAGAACCACCGCATT    29498        CA  GA
                                AATGCGGTGG  TC  CAA
                                |||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                      A_  AC
GAM1493 FLJ11210 3' GTCGATGTGCATGCTTTTA   60319     T   GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM1493 FLJ12476 3' TCGATCTTCTGCATTTA     43270        T  C
                                TAAATGCGG GG ATCGA
                                |||||||| || |||||
                                ATTTACGTC TC TAGCT
                                      T  _
GAM1493 KIAA1034 3' TCGATGGCATCCGCATTTG   63134        _  G
                                TAAATGCGG TG CATCGA
                                |||||||| || ||||||
                                GTTTACGCC AC GTAGCT
                                      T  G
GAM1493 KIAA1987 3' TCATGTAACTGCATTTA     89391        G   C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                      A   _
GAM1493 MGC16063 3' TGTCCTGGCCACTGCATT    54929         ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                      GTC
GAM1493 LOC147949 3' TGTCAGATGTCCACATTGCA  79279     __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM1493 LOC150577 3' GTCCTCACCGCATTTG      86258          CATC
                                TAAATGCGGTGG   GAC
                                ||||||||||||   |||
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                                GTTTACGCCACT   CTG
                                      C___
GAM1493  LOC158219 3'  TGTGTGTCACCACATTT    82694      C      CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                   A      __
GAM1493  LOC202020 3'  TGTCTCACCACATTTA     90605      C    CATC
                                TAAATG GGTGG   GACA
                                |||||| |||||   ||||
                                ATTTAC CCACT   CTGT
                                   A    _____
GAM1493  LOC90826  5'  TGTCGATGCAGGTTTATTTG  64788      CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                    TTGGA
GAM1493  LOC93587  3'  TTGTCTTTACCTGCATTTA   73042      _    CATC
                                TAAATGC GGTGG   GACAA
                                ||||||| |||||   |||||
                                ATTTACG CCATT   CTGTT
                                    T    T___
GAM1494  GPD1      3'  TCATGCCACCACATTTG     60398      C      C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A      _
GAM1494  IL5RA     5'  TCGCATGGCCACCGCATTT   6906         AT__
                                AAATGCGGTGGC   CGA
                                ||||||||||||   |||
                                TTTACGCCACCG   GCT
                                      GTAC
GAM1494  MYO1C     3'  TGCCGATGCCAAATATTTG   61873      CGG      A
                                TAAATG   TGGCATCG CA
                                ||||||   |||||||| ||
                                GTTTAT   ACCGTAGC GT
                                   AA_      C
GAM1494  C6orf37   3'  TGTCACACTGCATTTA     68097         GCATC
                                TAAATGCGGTG    GACA
                                ||||||||||    ||||
                                ATTTACGTCAC    CTGT
                                      A_____
GAM1494  DNAJC6    3'  TTGCAGAACCACCGCATT    29498        CA  GA
                                AATGCGGTGG  TC  CAA
                                ||||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                      A_  AC
GAM1494  FLJ11210  3'  GTCGATGTGCATGCTTTTA   60319     T  GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
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                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM1494  FLJ12476  3'  TCGATCTTCTGCATTTA     43270         T  C
                                TAAATGCGG GG ATCGA
                                ||||||||| || |||||
                                ATTTACGTC TC TAGCT
                                     T  _
GAM1494  KIAA1034  3'  TCGATGGCATCCGCATTTG    63134         _  G
                                TAAATGCGG TG CATCGA
                                ||||||||| || ||||||
                                GTTTACGCC AC GTAGCT
                                     T  G
GAM1494  KIAA1987  3'  TCATGTAACTGCATTTA     89391         G    C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                     A   _
GAM1494  MGC16063  3'  TGTCCTGGCCACTGCATT    54929          ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                      GTC
GAM1494  LOC147949 3'  TGTCAGATGTCCACATTGCA   79279      __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM1494  LOC150577 3'  GTCCTCACCGCATTTG      86258          CATC
                                TAAATGCGGTGG   GAC
                                ||||||||||||   |||
                                GTTTACGCCACT   CTG
                                      C___
GAM1494  LOC158219 3'  TGTGTGTCACCACATTT     82694       C       CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                   A       __
GAM1494  LOC202020 3'  TGTCTCACCACATTTA      90605       C    CATC
                                TAAATG GGTGG   GACA
                                |||||| |||||   ||||
                                ATTTAC CCACT   CTGT
                                   A   ____
GAM1494  LOC90826  5'  TGTCGATGCAGGTTTATTTG  64788       CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                    TTGGA
GAM1494  LOC93587  3'  TTGTCTTTACCTGCATTTA   73042       _    CATC
                                TAAATGC GGTGG   GACAA
                                ||||||| |||||   |||||
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                                ATTTACG CCATT   CTGTT
                                   T    T___
GAM1495 TERF1    3' CCCAAATCCTGTTCCAATGA  34391       C  TA   C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                   _  C_   A
GAM1495 FLJ10159 3' CCATGTCACGCCATCCAATGAC 36334       CA_  A  TC
                                GTCATTGGA  CGT GAT  GG
                                |||||||||  ||| |||  ||
                                CAGTAACCT  GCA CTG  CC
                                   ACC  _  TA
GAM1495 FLJ14213 3' CCGATGCTCCCAATGACG   46216       ACAC  GAT
                                CGTCATTGG   GTA  TCGG
                                |||||||||   |||  ||||
                                GCAGTAACC   CGT  AGCC
                                   CT__  ___
GAM1495 MGC10715 3' ATTTACCAGACATCCAATGAC 44495       CAC___
                                GTCATTGGA    GTAGAT
                                |||||||||    ||||||
                                CAGTAACCT    CATTTA
                                   ACAGAC
GAM1495 MOST2    5' CCAGGACTGCCCAATGAC   40059       ACAC   A  _
                                GTCATTGG   GTAG TTC GG
                                ||||||||   |||| ||| ||
                                CAGTAACC   CGTC AGG CC
                                   ____   _  A
GAM1495 LOC150370 3' CCGGGTCTACGTGCCCATGAC 86123     T  A
                                GTCAT GG CACGTAGATTCGG
                                ||||| || ||||||||||||
                                CAGTA CC GTGCATCTGGGCC
                                  C  _
GAM1495 LOC152620 3' CCCAAATCCTGTTCCAATGA  60707       C  TA   C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                   _  C_   A
GAM1495 LOC158668 3' CCCAAATCCTGTTCCAATGA  69896       C  TA   C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                   _  C_   A
GAM1496 ELF3     3' TGACCTTGACCTTGACCAA   16685     T   GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                  _    AGT  ___
GAM1496 JAK2     3' TGACCTTCATTCTGAGACCAA 18318      CAA      AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
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                                AACCAG   TCTTACTT  CAGT
                                   AG_      C_
GAM1496 SLC10A2  5' ACTCTCTGTCTTGACCAA    6590       CAA      A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM1496 FLJ10803 3' GTGACTTTCAGTTAAAGCCAA 37205      CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM1496 KIAA1958 5' GTGACTTTGAACCCCAAACC  82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM1496 MARCKS   3' ACTTTCCACCCTGCCCA     11411     TTCA   A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                 CG__   _
GAM1496 TUB      5' GTGGGACCATCCCTTAAACC   13898     C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A       AG__
GAM1496 LOC80298 3' ACTTTTACCTTGAACCA     48062         GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                      A___
GAM1497 FLRT1    5' ACCCCAGTCAAACCCAGA    60363     A  AGACCAC
                                TCTG GG      GACTGGGGT
                                |||| ||      |||||||||
                                AGAC CC      CTGACCCCA
                                  _  AAA____
GAM1497 JAM2     5' ACCCTCGACCTCCTCAGA    41383        ACCA   CTG
                                TCTGAGGAG    CGA   GGGT
                                |||||||||    |||   ||||
                                AGACTCCTC    GCT   CCCA
                                     CA__    ___
GAM1497 LPXN     3' GATCCATAGCCTCTTCAGA   17866        ACCACGA  _
                                TCTGAGGAG      CTG GGGTC
                                |||||||||      ||| |||||
                                AGACTTCTC      GAT CCTAG
                                     C_______   A
GAM1497 PBX2     3' CCATCTGATCCCCTCAGA    11978       A  C  C  C
                                TCTGAGG GA CA GA TGG
                                ||||||| || || || |||
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                                AGACTCC CT GT CT ACC
                                    C  A  _  _
GAM1497  SYNGR1   3'  ACCCCTTCGTGGTCTCTCA   17493     G       CT
                                TGAG AGACCACGA  GGGGT
                                |||| |||||||||  |||||
                                ACTC TCTGGTGCT  CCCCA
                                  _       T_
GAM1497  TJP1     3'  GGTTCCATGGCCTCTTCAGA   13765        A   CGAC   GG
                                TCTGAGGAG CCA    TGG  TC
                                ||||||||| |||    |||  ||
                                AGACTTCTC GGT    ACC  GG
                                     C   ____   TT
GAM1497  C20orf42 3'  AGTCATTGGTCTCCTCAGA   35061          C_
                                TCTGAGGAGACCA  GACT
                                ||||||||||||  ||||
                                AGACTCCTCTGGT  CTGA
                                       TA
GAM1497  C9orf5   3'  ACCTTGCAGTCTCCTCTGA   50098    T      CA  ACTG
                                TC GAGGAGAC  CG    GGGT
                                || ||||||||  ||    ||||
                                AG CTCCTCTG  GT    TCCA
                                 T       AC  _____
GAM1497  FGD3     5'  GACCCTCAGCATCCTCCTCAGA 73279         ACCACGA   _
                                TCTGAGGAG      CTG GGGTC
                                |||||||||      ||| |||||
                                AGACTCCTC      GAC CCCAG
                                     CTAC___   T
GAM1497  FLJ12587 3'  GACCCCAGGGTGTCCCCTGCAG 42778     _   A   C  GA
            A                    TCTG AGG GAC AC  CTGGGGTC
                                |||| ||| ||| ||  ||||||||
                                AGAC TCC CTG TG  GACCCCAG
                                  G   C   _  G_
GAM1497  FLJ21276 3'  GGCCCCATGTCTCCTCAGA   45261          CACGAC
                                TCTGAGGAGAC     TGGGGTC
                                ||||||||||     |||||||
                                AGACTCCTCTG     ACCCCGG
                                      T_____
GAM1497  KIAA0280 3'  GACCCCAGCCTTTCTCCTCAGG 93300          CCACGA
                                TCTGAGGAGA     CTGGGGTC
                                |||||||||     ||||||||
                                GGACTCCTCT     GACCCCAG
                                     TTCC__
GAM1497  KIAA0337 3'  GGGCCCATGATCTCCTCA    29480        C  CGAC   G
                                TGAGGAGA CA    TGGG TC
                                |||||||| ||    |||| ||
                                ACTCCTCT GT    ACCC GG
                                    A  _____   G
GAM1497  KIAA0700 3'  GACCCCAGCCAGTATTCCCTCA 72521        A  CC  GA_
            GA                     TCTGAGG GA  AC   CTGGGGTC
                                |||||||  ||  ||   ||||||||
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                                AGACTCC CT  TG   GACCCCAG
                                    _  TA  ACC
GAM1497  KIAA1318  3'  GACCTCTGGGTGACCCCCTCAG 67875       AGAC   GACT
                                CTGAGG    CAC    GGGGTC
                                ||||||    |||    ||||||
                                GACTCC    GTG    CTCCAG
                                   CCCA   GGT_
GAM1497  MGC14141  3'  GACCCCAGCCCGACCCTCCCCA 53042    A    ACCA  A_
                                TG GGAG    CG  CTGGGGTC
                                || ||||    ||  ||||||||
                                AC CCTC    GC  GACCCCAG
                                 C    CCA_  CC
GAM1497  MGC16385  5'  GACCCGCGCGGCCTCCTCGGA  59535         A  A  ACTG
                                TCTGAGGAG CC CG    GGGTC
                                ||||||||| || ||    |||||
                                AGGCTCCTC GG GC    CCCAG
                                     C  C  G___
GAM1497  MGC26766  3'  ACCCTCCTTAGTCTCCTAGA   59465     G      CAC  CT
                                TCT AGGAGAC   GA  GGGGT
                                ||| |||||||   ||  |||||
                                AGA TCCTCTG   TT  TCCCA
                                  _      A__  CC
GAM1497  OSBPL5    3'  ACCCCAGGCCTCCTGCAGA    73060      _    A  ACGAC
                                TCTG AGGAG CC     TGGGGT
                                |||| ||||| ||     ||||||
                                AGAC TCCTC GG     ACCCCA
                                  G    C  _____
GAM1497  SCYA22    3'  ACCCTAGTCACAGTCTCCGCAG 92567      A     CAC
            A                    TCTG GGAGAC   GACTGGGGT
                                ||||  ||||||   |||||||||
                                AGAC CCTCTG   CTGATCCCA
                                  G     ACA
GAM1497  TEX27     5'  GCCGCCACCGCCTCCTCAGA   41950         ACCA  AC  _
                                TCTGAGGAG    CG  TGG GGT
                                |||||||||    ||  ||| |||
                                AGACTCCTC    GC  ACC CCG
                                     C___  C_   G
GAM1497  XPO5      3'  GACCCCTCAGTCTGGCCTCCCC 92875     A   A  C   __
            AG                    CTG GGAG CCA GACT  GGGGTC
                                ||| |||| ||| ||||  ||||||
                                GAC CCTC GGT CTGA  CCCCAG
                                  C    C   _    CT
GAM1497  LOC135892 3'  GACCCCAGTCCCTTTCCCCTCA 75760       A  CCAC
            G                     CTGAGG GA    GACTGGGGTC
                                ||||||  ||    ||||||||||
                                GACTCC CT    CTGACCCCAG
                                   C  TTCC
GAM1497  LOC147700 3'  ATCCCACAGTCCCCCAGA     59876      A  A   CACGAC
                                TCTG GG GAC      TGGGGT
                                |||| || |||      ||||||
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                                AGAC CC CTG     ACCCTA
                                  _ C  AC____
GAM1497  LOC148089 3'  ACCCCAGCAGCTCCCAGA   79324     A   ACCACGA
                                TCTG GGAG     CTGGGGT
                                |||| ||||     |||||||
                                AGAC CCTC     GACCCCA
                                  _   GAC____
GAM1497  LOC148638 3'  ACCCCAGTACACCTCAGA   79664       AGACCACG
                                TCTGAGG      ACTGGGGT
                                |||||||      ||||||||
                                AGACTCC      TGACCCCA
                                    ACA_____
GAM1497  LOC149271 3'  GACCCTAGTGACCTCCCCA  80004   A   AC   GAC
                                TG GGAG  CAC   TGGGGTC
                                || ||||  |||   |||||||
                                AC CCTC  GTG   ATCCCAG
                                 C   CA  ___
GAM1497  LOC152065 3'  TGGTTTGTGGTCCCCCCA   86738   A  A      _
                                TG GG GACCACGA CTG
                                || || |||||||| |||
                                AC CC CTGGTGTT GGT
                                 C  C       T
GAM1497  LOC160414 3'  AGTCACAGTCTTCCTCAGA   88441        _   CAC
                                TCTGAGGA GAC   GACT
                                |||||||| |||   ||||
                                AGACTCCT CTG   CTGA
                                     T   ACA
GAM1497  LOC162333 5'  GACCCCAGCGAACCCTCTCCAG 88493     AG   ACCA  A
            A                    TCTG  GAG    CG CTGGGGTC
                                ||||  |||    || ||||||||
                                AGAC  CTC    GC GACCCCAG
                                  CT   CCAA  _
GAM1497  LOC163682 5'  GACCCATCTGAGCCTCCTCAGA 88404         AC_  C  CTG
                                TCTGAGGAG   CA GA   GGGTC
                                |||||||||   || ||   |||||
                                AGACTCCTC   GT CT   CCCAG
                                     CGA  _  A__
GAM1497  LOC220431 5'  GACCCCAGTTTATTCACCTCTT 95995         ACCAC__
            CAGA                 TCTGAGGAG      GACTGGGGTC
                                |||||||||      ||||||||||
                                AGACTTCTC      TTGACCCCAG
                                     CACTTAT
GAM1497  LOC220980 5'  TCATCGTGGCATCCTCAGA   94772        GA     C
                                TCTGAGGA  CCACGA TGG
                                ||||||||  |||||| |||
                                AGACTCCT  GGTGCT ACT
                                     AC     _
GAM1498  DXS1283E  3'  CTTAGGTGATAAGGAATCATT  71387      C  __     _
                                AATGA TCC  GTCACC AAG
                                ||||| |||  |||||| |||
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                                TTACT AGG  TAGTGG TTC
                                   A  AA     A
GAM1498  EGFL4    3'  GTGACGGTGACGGAGCCGT   62473    A       AAGA
                                ATG CTCCGTCACC   GC
                                ||| ||||||||||   ||
                                TGC GAGGCAGTGG   TG
                                  C        CAG_
GAM1498  GYG2     3'  ACTGCTCTTGGCTTGGTCTC  15359   CT  TCA
                                GA  CCG   CCAAGAGCAGT
                                ||  |||   ||||||||||
                                CT  GGT   GGTTCTCGTCA
                                 CT   TC_
GAM1498  CRNKL1   3'  CTTAGTGGACAATGGAGTCATT 34095         CA_  A_
                                AATGACTCCGT   CCA  GAG
                                ||||||||||   |||  |||
                                TTACTGAGGTA   GGT  TTC
                                      ACA   GA
GAM1498  KIAA0528 3'  CTGCCCTTAAGAGTCATT    72823       CGTCACC   A
                                AATGACTC      AAG GCAG
                                ||||||||      ||| ||||
                                TTACTGAG      TTC CGTC
                                    AA_____   C
GAM1498  KIAA1956 3'  TGCCTTATGACGGAGCCAT   79081    A      CC   A
                                ATG CTCCGTCA  AAG GCA
                                ||| ||||||||  ||| |||
                                TAC GAGGCAGT  TTC CGT
                                  C       A_  _
GAM1498  LOC51193 3'  ACCACTCTTGGTGACTGTCAT  33355     TCC        CA
                                ATGAC   GTCACCAAGAG  GT
                                |||||   ||||||||||  ||
                                TACTG   CAGTGGTTCTC  CA
                                   T__          AC
GAM1499  ABCC5    3'  CACAGAGCTCTCCAGCTCCA   20294     A  AT     C
                                TGGA TTG  AGAGCTC GTG
                                |||| |||  ||||||| |||
                                ACCT GAC  TCTCGAG CAC
                                  C  C_      A
GAM1499  ATP11A   3'  CACGGAGCCGTCAGTCCA    77553     A    AGA
                                TGGA TTGAT   GCTCCGTG
                                |||| |||||   ||||||||
                                ACCT GACTG   CGAGGCAC
                                   _    C__
GAM1499  CABC1    3'  CACAGGTGTCACCAGTTCCA   40039       ATA  G T  _
                                TGGAATTG   GA C CC GTG
                                ||||||||   || | || |||
                                ACCTTGAC   CT G GG CAC
                                    CA_  _ T  A
GAM1499  CPS1     3'  CACACTGCACTATTAATTCCA  10286          A  TCC
                                TGGAATTGATAG GC   GTG
                                ||||||||||| ||   |||
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                                ACCTTAATTATC CG   CAC
                                      A  TCA
GAM1499  ICAM1    3'  CACGGAGCTCCCAGTCC     72033     A   ATA
                                GGA TTG   GAGCTCCGTG
                                ||| |||   ||||||||||
                                CCT GAC   CTCGAGGCAC
                                  _  C__
GAM1499  KLHL3    3'  CACAGAAGCTCTCAATTTCA   88843         TA    _ C
                                TGGAATTGA  GAGCT C GTG
                                |||||||||  ||||| | |||
                                ACTTTAACT  CTCGA G CAC
                                     __    A A
GAM1499  KLK10    5'  ACGGAAGCCAGTTCCA      12427         ATAGA  _
                                TGGAATTG    GCT CCGT
                                ||||||||    ||| ||||
                                ACCTTGAC    CGA GGCA
                                     _____  A
GAM1499  NLGN2    3'  CACGGAGCTCTTCACCACCA   89529     AAT   T
                                TGG   TGA AGAGCTCCGTG
                                |||   ||| ||||||||||
                                ACC   ACT TCTCGAGGCAC
                                  ACC   _
GAM1499  NTRK2    3'  CACAGAACCTTTGTCAACTTCA 21634      A        C_  C
                                TGGA TTGATAGAG  TC GTG
                                |||| |||||||||  || |||
                                ACTT AACTGTTTC  AG CAC
                                   C        CA  A
GAM1499  PDYN     3'  CACGTGACTCCTCAATTCCA   44582         TA   C  _
                                TGGAATTGA  GAG TC CGTG
                                |||||||||  ||| || ||||
                                ACCTTAACT  CTC AG GCAC
                                     C_   _  T
GAM1499  SLC21A9  3'  CATGTATCTATCAACGCCA   24379     AA       GCTC
                                TGG  TTGATAGA    CGTG
                                |||  ||||||||    ||||
                                ACC  AACTATCT    GTAC
                                  GC       AT__
GAM1499  TCF7     3'  CACAGAGCCTTTTTCACAATTC 13615         AT_____ A    C
            CA                    TGGAATTG     AG GCTC GTG
                                |||||||      || |||| |||
                                ACCTTAAC     TC CGAG CAC
                                     ACTTTT  _    A
GAM1499  BCL2L12  5'  CACAGAACTTCCATTCAATTCC 57641         TA__   C  C
                                GGAATTGA    GAG TC GTG
                                ||||||||    ||| || |||
                                CCTTAACT    TTC AG CAC
                                     TACC   A  A
GAM1499  C11orf11 5'  CACGGAGCCCCGTGACTCCA   94874      A   ATAGA
                                TGGA TTG    GCTCCGTG
                                |||| |||    ||||||||
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                                ACCT AGT    CGAGGCAC
                                  C  GCCC_
GAM1499 CRA     3' CACAGATACTACAATTCCA   22933       A  AGC  C
                                TGGAATTG TAG  TC GTG
                                |||||||| |||  || |||
                                ACCTTAAC ATC  AG CAC
                                     _  AT_  A
GAM1499 DKFZP564J102 5' CACAGAGCTCTACCACCG    66649    AAT  A      C
                                TGG  TG TAGAGCTC GTG
                                |||  || |||||||| |||
                                GCC  AC ATCTCGAG CAC
                                  ___ C       A
GAM1499 DKFZp761F2014 3' CACAGGGATTTATCAGTTCCA  39939          G  C
                                TGGAATTGATAGA CTC GTG
                                |||||||||||| ||| |||
                                ACCTTGACTATTT GGG CAC
                                        A  A
GAM1499 FEM-2    3' CACGGAGCTCTGCCATTCC    28310      T A
                                GGAAT G TAGAGCTCCGTG
                                ||||| | ||||||||||||
                                CCTTA C GTCTCGAGGCAC
                                  _ C
GAM1499 KIAA0870  3' CACGGAGCTCCAGCTTCT    82381     _  ATA
                                GGAA TTG  GAGCTCCGTG
                                |||| |||  ||||||||||
                                TCTT GAC  CTCGAGGCAC
                                  C  ___
GAM1499 LMOD1    3' CACCTGCTCACCAATTCCA   25099       ATA   TCC
                                TGGAATTG  GAGC  GTG
                                ||||||||  ||||  |||
                                ACCTTAAC  CTCG  CAC
                                    CA_   TC_
GAM1499 MGC9753   5' CACAAAGTGCCTCAGTTCCA  54185        TAGA  CC
                                TGGAATTGA   GCT  GTG
                                |||||||||   |||  |||
                                ACCTTGACT   TGA  CAC
                                     CCG_  AA
GAM1499 RHOBTB1   3' CACGGAAAGGAATCTAATTCCA 93091       _  AGAGC
                                TGGAATT GAT    TCCGTG
                                ||||||| |||    ||||||
                                ACCTTAA CTA    AGGCAC
                                    T  AGGAA
GAM1499 LOC134265 3' CACAGAGCTCTAATGTCCA   75653     ATTGA      C
                                TGGA    TAGAGCTC GTG
                                ||||    |||||||| |||
                                ACCT    ATCTCGAG CAC
                                  GTA__       A
GAM1499 LOC145231 3' CACGAGACTAGTCCCAATTCCA 84242        ATAG_ _  C
                                TGGAATTG    AG CTC GTG
                                ||||||||    || ||| |||
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                                ACCTTAAC    TC GAG CAC
                                    CCTGA  A  _
GAM1499  LOC147160 5'  CACGGAGCCCTCGGACCA    85068    AA   TA A
                                TGG  TTGA  G GCTCCGTG
                                |||  ||||  | ||||||||
                                ACC  GGCT  C CGAGGCAC
                                  A_   __ C
GAM1499  LOC149830 3'  CACATCTCTATTAACTCCA    85885     A       CTCC
                                TGGA TTGATAGAG   GTG
                                |||| |||||||||   |||
                                ACCT AATTATCTC   CAC
                                  C       TA__
GAM1499  LOC202025 5'  CACGGAACTTGCAGTTCCA    91884       ATA   C
                                TGGAATTG   GAG TCCGTG
                                ||||||||   ||| ||||||
                                ACCTTGAC   TTC AGGCAC
                                     G__   A
GAM1499  LOC253841 3'  CACGGGGCACCAATCCA     98092     A   ATAGA
                                TGGA TTG    GCTCCGTG
                                |||| |||    ||||||||
                                ACCT AAC    CGGGGCAC
                                  _   CA___
GAM1499  LOC254057 3'  CACAGGTTCTATTAATTCCA   98777            CC
                                TGGAATTGATAGAGCT  GTG
                                ||||||||||||||||  |||
                                ACCTTAATTATCTTGG  CAC
                                          A_
GAM1500  ELF3     3'  TGACCTTGACCTTGACCAA    16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                   _    AGT  ____
GAM1500  JAK2     3'  TGACCTTCATTCTGAGACCAA  18318      CAA       AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                    AG_       C_
GAM1500  SLC10A2  5'  ACTCTCTGTCTTGACCAA    6590       CAA       A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                    ___       C
GAM1500  FLJ10803 3'  GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                    AA___   A
GAM1500  KIAA1958 5'  GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
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                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM1500 MARCKS   3' ACTTTCCACCCTGCCCA     11411     TTCA   A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM1500 TUB      5' GTGGGACCATCCCTTAAACC   13898     C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A       AG__
GAM1500 LOC80298 3' ACTTTTACCTTGAACCA     48062         GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                     A___
GAM1501 GPD1     3' TCATGCCACCACATTTG     60398       C       C
                                TAAATG GGTGGCAT GA
                                ||||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A       _
GAM1501 IL5RA    5' TCGCATGGCCACCGCATTT    6906          AT__
                                AAATGCGGTGGC    CGA
                                ||||||||||||    |||
                                TTTACGCCACCG    GCT
                                     GTAC
GAM1501 MYO1C    3' TGCCGATGCCAAATATTTG    61873      CGG      A
                                TAAATG   TGGCATCG CA
                                ||||||   |||||||| ||
                                GTTTAT   ACCGTAGC GT
                                   AA_       C
GAM1501 C6orf37  3' TGTCACACTGCATTTA      68097         GCATC
                                TAAATGCGGTG     GACA
                                ||||||||||     ||||
                                ATTTACGTCAC     CTGT
                                     A____
GAM1501 DNAJC6   3' TTGCAGAACCACCGCATT    29498         CA  GA
                                AATGCGGTGG  TC  CAA
                                ||||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                     A_  AC
GAM1501 FLJ11210 3' GTCGATGTGCATGCTTTTA   60319     T   GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM1501 FLJ12476 3' TCGATCTTCTGCATTTA     43270         T  C
                                TAAATGCGG GG ATCGA
                                ||||||||| || |||||
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                                ATTTACGTC TC TAGCT
                                     T  _
GAM1501  KIAA1034  3'  TCGATGGCATCCGCATTTG   63134        _  G
                                TAAATGCGG TG CATCGA
                                ||||||||| || ||||||
                                GTTTACGCC AC GTAGCT
                                     T  G
GAM1501  KIAA1987  3'  TCATGTAACTGCATTTA    89391        G   C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                     A   _
GAM1501  MGC16063  3'  TGTCCTGGCCACTGCATT   54929         ATC
                                AATGCGGTGGC  GACA
                                ||||||||||  ||||
                                TTACGTCACCG  CTGT
                                      GTC
GAM1501  LOC147949 3'  TGTCAGATGTCCACATTGCA  79279    __  _  _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM1501  LOC150577 3'  GTCCTCACCGCATTTG     86258         CATC
                                TAAATGCGGTGG   GAC
                                ||||||||||||   |||
                                GTTTACGCCACT   CTG
                                      C___
GAM1501  LOC158219 3'  TGTGTGTCACCACATTT    82694      C      CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                   A       __
GAM1501  LOC202020 3'  TGTCTCACCACATTTA     90605      C    CATC
                                TAAATG GGTGG   GACA
                                |||||| |||||   ||||
                                ATTTAC CCACT   CTGT
                                   A    _____
GAM1501  LOC90826  5'  TGTCGATGCAGGTTTATTTG  64788      CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                    TTGGA
GAM1501  LOC93587  3'  TTGTCTTTACCTGCATTTA   73042       _   CATC
                                TAAATGC GGTGG   GACAA
                                ||||||| |||||   |||||
                                ATTTACG CCATT   CTGTT
                                    T    T___
GAM1502  CDC6      3'  TGACCTTTTTTACTTGAAGCCA 8831       _   GGAT    A
            A                    TTGGTT CAAG   GGAAA GTCA
                                ||||||| ||||   ||||| ||||
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                                AACCGA GTTC    TTTTT CAGT
                                   A    AT__     C
GAM1502  ELF3     3'  GACCTTGACCTTGACCAA     16682       T     GAT  AAAA
                                TTGGT CAAGG   GG    GTC
                                ||||| |||||   ||    |||
                                AACCA GTTCC   TC    CAG
                                   _     AGT  _____
GAM1502  SLC10A2  5'  ACTCTCTGTCTTGACCAA     6591        CAA       AA
                                TTGGTT   GGGATGGA  AGT
                                ||||||   ||||||||  |||
                                AACCAG   TTCTGTCT  TCA
                                   ___        C_
GAM1502  FLJ10829 3'  ACTTTTCCACCAAAGCTA     37252       CAAG  A
                                TGGTT    GG TGGAAAAGT
                                |||||    || |||||||||
                                ATCGA    CC ACCTTTTCA
                                   AA__  _
GAM1502  HEAB     3'  TGACTCTTCTAATCTTGAACCA 23363           GA    A
                 A                TTGGTTCAAGG  TGGAA AGTCA
                                |||||||||||  ||||| |||||
                                AACCAAGTTCT  ATCTT TCAGT
                                      A_    C
GAM1502  HEMK     5'  TGACCTCTCCATCTCCACC    32966     TCAA       AAA
                                GGT    GGGATGGA   GTCA
                                |||    ||||||||   ||||
                                CCA    CTCTACCT   CAGT
                                  C___       CTC
GAM1502  KIAA0298 3'  TCCAAGTTCATGAGCCAA     77080         A   A_
                                TTGGTTCA GGG  TGGA
                                |||||||| |||  ||||
                                AACCGAGT CTT  ACCT
                                     A   GA
GAM1502  KIAA1228 3'  ACTTTTCTACCTTGAGCCAA   65664           GA
                                TTGGTTCAAGG  TGGAAAAGT
                                ||||||||||  |||||||||
                                AACCGAGTTCC  ATCTTTTCA
                                             __
GAM1502  KIAA1486 3'  TGACTTTTCTCTCTTATACCAA 67982       TC     TG
                                TTGGT  AAGGGA  GAAAAGTCA
                                |||||  ||||||  |||||||||
                                AACCA  TTCTCT  CTTTTCAGT
                                   TA     __
GAM1502  MGC21854 3'  ACTTTTCAATTTGATCCAA    54601      T    GGATG
                                TTGG TCAAG     GAAAAGT
                                |||| |||||     |||||||
                                AACC AGTTT     CTTTTCA
                                  T    AA___
GAM1502  LOC148697 3'  ACTTTTCCTGCTCAAACC     79671      CAA   AT
                                GGTT   GGG  GGAAAAGT
                                ||||   |||  ||||||||
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                                CCAA  CTC  CCTTTTCA
                                  A__  GT
GAM1502 LOC80298 3' ACTTTTACCTTGAACCA    48063        GATGG
                                TGGTTCAAGG    AAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                     A____
GAM1503 ITGA1    3' CCAATGAGACAGTCCCTGA   64271     A  CAT  CA
                                TCAGG GAC   TG  TCATTGG
                                ||||| |||   ||  |||||||
                                AGTCC CTG   AC  AGTAACC
                                  _  ___ AG
GAM1503 SH3GL3   5' GCCAATATGGTCTCGATCTCCT 13111       CCATT  ATC
            GA                   TCAGGAGA    GC   ATTGGC
                                ||||||||    ||  ||||||
                                AGTCCTCT    TG   TAACCG
                                     AGCTC  GTA
GAM1503 ARHGEF15 3' GCCAATGAAAACGGCCGCCTGA 30954     AGA  ATTGCA
                                TCAGG   CC     TCATTGGC
                                |||||   ||     ||||||||
                                AGTCC   GG     AGTAACCG
                                   GCC  CAAA__
GAM1503 DKFZp434F2322 3' CCACCGACGATCTCCTGA    70299       CCA   CA  AT
                                TCAGGAGA   TTG  TC  TGG
                                ||||||||   |||  ||  |||
                                AGTCCTCT   AGC  AG  ACC
                                     ___   __ CC
GAM1503 FLJ10716 3' GCCACGTATCAACAATCTTCTG 37018       CCA   C  CAT
            A                    TCAGGAGA   TTG AT   TGGC
                                ||||||||   ||| ||   ||||
                                AGTCTTCT   AAC TA   ACCG
                                     AAC   _  TGC
GAM1503 KIAA0527  3' GCCACCTGCAATAGTCTCCTG  97499       C     TCAT
                                CAGGAGAC ATTGCA    TGGC
                                |||||||| ||||||    ||||
                                GTCCTCTG TAACGT    ACCG
                                     A     CC__
GAM1503 KIAA1111  3' GCCAATGACGCAGATAACCCTG 97946     AGACCA   A
            G                    TCAGG     TTGC TCATTGGC
                                |||||     |||| ||||||||
                                GGTCC     GACG AGTAACCG
                                   CAATA_   C
GAM1503 Kv6.3    3' GCCAATGATGCAAAGGTCCCC  56855    A   A
                                GG GACC TTGCATCATTGGC
                                || |||| ||||||||||||
                                CC CTGG AACGTAGTAACCG
                                 C   A
GAM1503 LOC145547 3' GCCAATGGAGACAATTCCTGA  77782      GACC   CA_
                                TCAGGA   ATTG   TCATTGGC
                                ||||||   ||||   ||||||||
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                                AGTCCT    TAAC   GGTAACCG
                                    _____    AGA
GAM1503  LOC162333 5'  GCCAATGACTGAGAACGCCCCT 88494       AGACCATTG  _
              GA                     TCAGG        CA TCATTGGC
                                |||||        || ||||||||
                                AGTCC        GT AGTAACCG
                                   CCGCAAGA_  C
GAM1504  HMGA2     3'  CACCTCAAATACCACCC     14450      CGT       A
                                GGGT   GTGTTTGA GTG
                                ||||   |||||||| |||
                                CCCA   CATAAACT CAC
                                  C__       C
GAM1504  SLC13A4   3'  CACCAGGAGCACACAACCCCAG 25859     AA    C       GAA
              A                      TC  GGGT GTGTGTTT   GTG
                                ||  |||| ||||||||   |||
                                AG  CCCA CACACGAG   CAC
                                 AC    A       GAC
GAM1504  ATP10B    3'  CACTGGTCCACATAACCCTTGA 64104         CG    TTTGA
                                TCAAGGGT  TGTG    AGTG
                                ||||||||  ||||    ||||
                                AGTTCCCA  ACAC    TCAC
                                     AT    CTGG_
GAM1504  DKFZP761G1913 3'  CACCCCAAACACAACTC     49693      CG       AA
                                GGGT  TGTGTTTG  GTG
                                ||||  ||||||||  |||
                                CTCA  ACACAAAC  CAC
                                  __       CC
GAM1504  FLJ12076  3'  CACATTGCCACATGACCCTT   48021           TTT  A
                                AAGGGTCGTGTG   GA GTG
                                ||||||||||||   || |||
                                TTCCCAGTACAC   TT CAC
                                       CG_  A
GAM1504  KIAA0750  5'  CACTGCCGCACACGACTCCTGA 28304      A          TTGA
                                TCA GGGTCGTGTGT    AGTG
                                ||| ||||||||||    ||||
                                AGT CTCAGCACACG    TCAC
                                  C          CCG_
GAM1504  KIAA1485  3'  TAGACACACACCCCCTGA    90771     A   TC
                                TCA GGG  GTGTGTTTG
                                ||| |||  |||||||||
                                AGT CCC  CACACAGAT
                                  C   CA
GAM1504  SFXN5     3'  CACTTCAAACATGCCCT     58646       CGT
                                AGGGT   GTGTTTGAAGTG
                                |||||   ||||||||||||
                                TCCCG   TACAAACTTCAC
                                    ___
GAM1504  LOC145608 5'  CACCCCAAATTACTGACCCTTG 84374          T   _    AA
              A                      TCAAGGGTCG GTG TTTG  GTG
                                |||||||||| ||| ||||  |||
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                                AGTTCCCAGT CAT AAAC  CAC
                                      _  T   CC
GAM1505  DEDD     3'  TACAGCTACCTTACCACTG   53380    A  C   A
                                CA TG TAA GTAGCTGTG
                                || || ||| |||||||||
                                GT AC ATT CATCGACAT
                                 C  C   C
GAM1505  ENAM     3'  CCTAGCACAGTGTCTTCAACAT 49927     CTA   TA
                                ATG   AAG  GCTGTGCTAGG
                                |||   |||  ||||||||||
                                TAC   TTC  TGACACGATCC
                                  AAC   TG
GAM1505  MAP3K14  3'  CCAGAGCACAGCTCAGCATCA  15544   A    AAAGT       A_
                                C ATGCT    AGCTGTGCT  GG
                                | |||||    |||||||||  ||
                                A TACGA    TCGACACGA  CC
                                 C    C____        GA
GAM1505  MYH11    3'  CCCAGCAGACTGTACTTAGCAT 43430         A   GCTG_   A
              TG                  CAATGCTAA GTA     TGCT GG
                                |||||||||  |||     ||||  ||
                                GTTACGATT CAT     ACGA CC
                                      _  GTCAG    C
GAM1505  MYH11    3'  CCCAGCAGACTGTACTTAGCAT 11739         A   GCTG_   A
              TG                  CAATGCTAA GTA     TGCT GG
                                |||||||||  |||     ||||  ||
                                GTTACGATT CAT     ACGA CC
                                      _  GTCAG    C
GAM1505  USP11    5'  CCCAGCACGTGCTTGGCATT   17384       AAGT   _     A
                                AATGCTA    AGC TGTGCT GG
                                |||||||    ||| ||||||  ||
                                TTACGGT    TCG GCACGA CC
                                     ____   T     C
GAM1505  FLJ20086 3'  CCTAGCACAACAGAGGCA    35012     AAA  AGC
                                TGCT   GT   TGTGCTAGG
                                ||||   ||   |||||||||
                                ACGG   CA   ACACGATCC
                                  AGA  ___
GAM1505  KIAA0397 3'  CCCAGCACAGCCTGCCCAGC   62346     AAA   _     A
                                GCT   GTAG CTGTGCT GG
                                |||   |||| |||||||  ||
                                CGA   CGTC GACACGA CC
                                  CC_   C      C
GAM1505  KIAA0945 3'  CCCAGCACAGCTCTGAGCTTG  30901     T   AA  T       A
                                CAA GCT  AG AGCTGTGCT GG
                                ||| |||  ||  |||||||||  ||
                                GTT CGA  TC TCGACACGA CC
                                  _  G_  _       C
GAM1505  KIAA1184 3'  CCTAGCACGGTGCCTAGCA   42925      AAGTA
                                TGCTA    GCTGTGCTAGG
                                |||||    ||||||||||
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                                ACGAT    TGGCACGATCC
                                  CCG__
GAM1505  KIAA1434  3'  TACAGCTACCTCAGTACTG   70212    A   AAA
                                CA TGCT   GTAGCTGTG
                                || ||||   |||||||||
                                GT ATGA   CATCGACAT
                                 C    CTC
GAM1505  KIAA1656  3'  CCCAGCATGCCCTTGGCA    66363      AGTA  T    A
                                TGCTAA    GC GTGCT GG
                                ||||||    || ||||| ||
                                ACGGTT    CG TACGA CC
                                   CC__  _    C
GAM1505  LIMK2     3'  AGCACAGTTCAGCATTG     34118      AAAGT
                                CAATGCT    AGCTGTGCT
                                |||||||    |||||||||
                                GTTACGA    TTGACACGA
                                    C____
GAM1505  LIMK2     3'  AGCACAGTTCAGCATTG     19920      AAAGT
                                CAATGCT    AGCTGTGCT
                                |||||||    |||||||||
                                GTTACGA    TTGACACGA
                                    C____
GAM1505  LOC134957 3'  CTAGCACAGTCATGCACTG   58342    A   TAAA  AG
                                CA TGC    GT  CTGTGCTAG
                                || |||    ||  |||||||||
                                GT ACG    TA  GACACGATC
                                 C  _____  CT
GAM1505  LOC147639 5'  CCTAGCACAGGTTAATTAG   79008     AG   _
                                CTAA  TAGC TGTGCTAGG
                                ||||  |||| |||||||||
                                GATT  ATTG ACACGATCC
                                  A_   G
GAM1505  LOC150350 3'  CCAAGACTTACGTTAGCATTG  80573        A   CT  G  A
                                CAATGCTAA GTAG  GT CT GG
                                ||||||||| ||||  || || ||
                                GTTACGATT CATT  CA GA CC
                                      G   __  _  A
GAM1505  LOC151778 3'  CCTAGCACGCGCCCCAGC    71947     AAA  A  T
                                GCT   GT GC GTGCTAGG
                                |||   || || ||||||||
                                CGA   CG CG CACGATCC
                                  CCC  _  _
GAM1505  LOC152915 3'  CCTAGCACGCGCCCCAGC    67583     AAA  A  T
                                GCT   GT GC GTGCTAGG
                                |||   || || ||||||||
                                CGA   CG CG CACGATCC
                                  CCC  _  _
GAM1505  LOC256598 3'  CCTAGCACGCGCCCCAGC    98103     AAA  A  T
                                GCT   GT GC GTGCTAGG
                                |||   || || ||||||||
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                                CGA   CG CG CACGATCC
                                  CCC  _ _
GAM1505 LOC90625 3' CACAGCTACCTTATCACTG   64376    A C   A
                                CA TG TAA GTAGCTGTG
                                || || ||| |||||||||
                                GT AC ATT CATCGACAC
                                 C  T   C
GAM1506 ELF3     3' TGACCTTGACCTTGACCAA   16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                   _    AGT  ___
GAM1506 JAK2     3' TGACCTTCATTCTGAGACCAA  18318      CAA       AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                    AG_       C_
GAM1506 SLC10A2  5' ACTCTCTGTCTTGACCAA    6590       CAA       A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM1506 FLJ10803 3' GTGACTTTCAGTTAAAGCCAA 37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM1506 KIAA1958 5' GTGACTTTGAACCCCAAACC  82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM1506 MARCKS   3' ACTTTCCACCCTGCCCA     11411     TTCA    A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM1506 TUB      5' GTGGGACCATCCCTTAAACC   13898     C        AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A        AG__
GAM1506 LOC80298 3' ACTTTTACCTTGAACCA     48062          GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                     A___
GAM1507 GPD1     3' TCATGCCACCACATTTG     60398       C       C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
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                                GTTTAC CCACCGTA CT
                                   A      _
GAM1507 IL5RA    5' TCGCATGGCCACCGCATTT   6906          AT__
                                AAATGCGGTGGC   CGA
                                ||||||||||||  |||
                                TTTACGCCACCG   GCT
                                     GTAC
GAM1507 MYO1C    3' TGCCGATGCCAAATATTTG   61873      CGG      A
                                TAAATG  TGGCATCG CA
                                ||||||  |||||||| ||
                                GTTTAT  ACCGTAGC GT
                                   AA_      C
GAM1507 C6orf37  3' TGTCACACTGCATTTA     68097         GCATC
                                TAAATGCGGTG    GACA
                                ||||||||||    ||||
                                ATTTACGTCAC    CTGT
                                     A____
GAM1507 DNAJC6   3' TTGCAGAACCACCGCATT    29498        CA  GA
                                AATGCGGTGG  TC  CAA
                                ||||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                     A_  AC
GAM1507 FLJ11210 3' GTCGATGTGCATGCTTTTA   60319     T  GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM1507 FLJ12476 3' TCGATCTTCTGCATTTA     43270        T  C
                                TAAATGCGG GG ATCGA
                                ||||||||| || |||||
                                ATTTACGTC TC TAGCT
                                     T  _
GAM1507 KIAA1034 3' TCGATGGCATCCGCATTTG   63134        _  G
                                TAAATGCGG TG CATCGA
                                ||||||||| || ||||||
                                GTTTACGCC AC GTAGCT
                                     T  G
GAM1507 KIAA1987 3' TCATGTAACTGCATTTA     89391        G   C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                     A   _
GAM1507 MGC16063 3' TGTCCTGGCCACTGCATT    54929         ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                     GTC
GAM1507 LOC147949 3' TGTCAGATGTCCACATTGCA  79279     __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
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                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM1507  LOC150577 3'  GTCCTCACCGCATTTG      86258          CATC
                                TAAATGCGGTGG   GAC
                                ||||||||||||   |||
                                GTTTACGCCACT   CTG
                                       C___
GAM1507  LOC158219 3'  TGTGTGTCACCACATTT     82694      C      CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                  A       __
GAM1507  LOC202020 3'  TGTCTCACCACATTTA      90605       C    CATC
                                TAAATG GGTGG   GACA
                                |||||| |||||   ||||
                                ATTTAC CCACT   CTGT
                                   A    _____
GAM1507  LOC90826  5'  TGTCGATGCAGGTTTATTTG  64788       CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                   TTGGA
GAM1507  LOC93587  3'  TTGTCTTTACCTGCATTTA   73042       _    CATC
                                TAAATGC GGTGG   GACAA
                                ||||||| |||||   |||||
                                ATTTACG CCATT   CTGTT
                                    T   T___
GAM1508  SCAMP1    3'  GCTAAATAAATATTCTCC    54500     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1508  SCAMP1    3'  GCTAAATAAATATTCTCC    54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1508  NX-17     3'  TGAATATCAGCCCCTAATA   40706        ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM1508  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
            TA                   TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM1509  CCR2      3'  GTAAAGCAGGTGCCCAGGAACC 7222      CTG   AC  AA
            T                    AGG   CCTG  CA  TGCTTTAC
                                |||   ||||  ||  ||||||||
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                                TCC  GGAC  GT  ACGAAATG
                                  AA_   CC  GG
GAM1509  CMA1     5'  GCATTTGCTCAGGCAGCCT   10219          C
                                AGGCTGCCTGA CAAATGC
                                |||||||||||  |||||||
                                TCCGACGGACT GTTTACG
                                      C
GAM1509  GFRA2    3'  AAGCAGGCAGGCAGCCT    9461          A  AAA
                                AGGCTGCCTG CC   TGCTT
                                ||||||||||  ||   |||||
                                TCCGACGGAC GG   ACGAA
                                      _  ____
GAM1509  GOT1     3'  GCTCTGGTGAGGCAGCCT    10853         G    AAT
                                AGGCTGCCT ACCA   GC
                                |||||||||  ||||   ||
                                TCCGACGGA TGGT   CG
                                     G   CT_
GAM1509  MECP2    3'  GCCTTTCAGCAGGCAGCCT   18406          ACC   T
                                AGGCTGCCTG   AAA GC
                                ||||||||||   ||| ||
                                TCCGACGGAC   TTT CG
                                     GAC   C
GAM1509  POLR2C   3'  AAAGCAGTTAATTAGGCAGCCT 12203           CCAAA
                                AGGCTGCCTGA    TGCTTT
                                ||||||||||     ||||||
                                TCCGACGGATT    ACGAAA
                                      AATTG
GAM1509  RAB11A   3'  GCAATGATCAGGCAGCC     17414          C  AA
                                GGCTGCCTGA CA  TGC
                                ||||||||||  ||  |||
                                CCGACGGACT GT  ACG
                                     A  A_
GAM1509  SUFU     3'  GTGAAGCACCTGGTCAGCAACC 32940     C   C     AA
            T                    AGG TGC TGACCA  TGCTTTAC
                                |||  ||| ||||||  ||||||||
                                TCC ACG ACTGGT  ACGAAGTG
                                  A  _     CC
GAM1509  TP53BP2  3'  TAAAGCATCTACGTCAGCAGGC 19468     GC    CAA_
            C                    GGCT  CTGAC    ATGCTTTA
                                ||||  |||||    ||||||||
                                CCGG  GACTG    TACGAAAT
                                  AC    CATC
GAM1509  CYYR1    3'  AAAGCATTCAAGAGTTTCAGCC 54757      CCT   CA___
                                GGCTG   GAC    AATGCTTT
                                |||||   |||    ||||||||
                                CCGAC   TTG    TTACGAAA
                                   T__   AGAAC
GAM1509  DKFZp586H0623 3'  GTAATACAGTCAAGGCAGCC   34503        _   CAAA  CT
                                GGCTGCCT GAC    TG  TTAC
                                ||||||||  |||    ||  ||||
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                                CCGACGGA CTG   AC  AATG
                                    A  ____  AT
GAM1509  FLJ11117  3'  TAAAACATCTAGGGTCAGGC  37637       AA__  C
                                GCCTGACC   ATG TTTA
                                ||||||||   ||| ||||
                                CGGACTGG   TAC AAAT
                                    GATC   A
GAM1509  FLJ11383  5'  TAAAGCATGAGACAGCCT   46856      C  GACCAA
                                AGGCTG CT    ATGCTTTA
                                |||||| ||    ||||||||
                                TCCGAC GA    TACGAAAT
                                   A  G_____
GAM1509  FLJ12875  3'  GCAGTTGGTCAGGCAGGCC   44918    _        A
                                GGC TGCCTGACCAA TGC
                                ||| ||||||||||| |||
                                CCG ACGGACTGGTT ACG
                                  G         G
GAM1509  FLJ12891  3'  GCACTGATCATGGCAGCCT   46925       _  C  AA
                                AGGCTGCC TGA CA  TGC
                                |||||||| ||| ||  |||
                                TCCGACGG ACT GT  ACG
                                    T  A  C_
GAM1509  FLJ23185  3'  GCACGCCTGGCAGGCAGCCT  47515        A  AA__
                                AGGCTGCCTG CCA   TGC
                                |||||||||| |||   |||
                                TCCGACGGAC GGT   ACG
                                    _  CCGC
GAM1509  GRP3     3'  GTAAAGCACTCAGAAGGCAGCC 31740       GACCAAA
                                GGCTGCCT     TGCTTTAC
                                ||||||||     ||||||||
                                CCGACGGA     ACGAAATG
                                    AGACTC_
GAM1509  KIAA0427  3'  GCCATCGTGGCCAGGCAGCCT  29383        A  AAT__
                                AGGCTGCCTG CCA    GC
                                |||||||||| |||    ||
                                TCCGACGGAC GGT    CG
                                    C  GCTAC
GAM1509  KLF12    3'  AGGGCACTCAGGCAGCC     24359        CCAAA
                                GGCTGCCTGA    TGCTTT
                                ||||||||||    ||||||
                                CCGACGGACT    ACGGGA
                                    C____
GAM1509  MGC16025  3'  GTCCTTGCTCAGGCAGCC    53027        C  AT
                                GGCTGCCTGA CAA  GC
                                |||||||||| |||  ||
                                CCGACGGACT GTT  TG
                                    C  CC
GAM1509  PIP5K1C  3'  GCACCCCGGTCGGCAGCCT   71303       T   AAA_
                                AGGCTGCC GACC   TGC
                                |||||||| ||||   |||
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                                TCCGACGG CTGG   ACG
                                    _   CCCC
GAM1509  SFXN2    3'  GCCCCCTGGTCAGGCAGCTT   74378          AAT_
                                AGGCTGCCTGACCA   GC
                                ||||||||||||||  ||
                                TTCGACGGACTGGT   CG
                                      CCCC
GAM1509  STAM2    3'  TAAAGCATTTAGTCAGTCCCCC 20708   CTGC    C
                                GG   CTGAC AAATGCTTTA
                                ||   ||||| ||||||||||
                                CC   GACTG TTTACGAAAT
                                 CCCT    A
GAM1509  SYNPO2   3'  TAAAGCATTTATGACAGCT   72390     CCTGACC
                                GGCTG     AAATGCTTTA
                                |||||     ||||||||||
                                TCGAC     TTTACGAAAT
                                   AGTA___
GAM1509  TACTILE  3'  AAGTAAACAGGCAGCCT    20577        ACCAAA
                                AGGCTGCCTG    TGCTT
                                ||||||||||    |||||
                                TCCGACGGAC    ATGAA
                                     AA____
GAM1509  THEA     3'  GTAAAGCATCCCGGGCAACCT  66892    C     ACCAA
                                AGG TGCCTG    ATGCTTTAC
                                ||| ||||||    |||||||||
                                TCC ACGGGC    TACGAAATG
                                  A     CC___
GAM1509  TOMM34   3'  AAAGCATTTGGCTTTGTCCT   23312    CT  CTGA
                                AGG  GC   CCAAATGCTTT
                                |||  ||   ||||||||||
                                TCC  TG   GGTTTACGAAA
                                  __  TTTC
GAM1509  LOC144845 3'  GTAAAGCATGTGAAGACAGGC  57463      AC__  A
                                GCCTG   CA ATGCTTTAC
                                |||||   || |||||||||
                                CGGAC   GT TACGAAATG
                                   AGAA  G
GAM1509  LOC150212 5'  TAAAGCATCTCCGGCAGAGCCT 80521      __   T  CCAA
                                AGGCT  GCC GA   ATGCTTTA
                                |||||  ||| ||   ||||||||
                                TCCGA  CGG CT   TACGAAAT
                                   GA   C  C___
GAM1509  LOC220020 3'  GCAGTGCTGGGCAGGCAGCCT  95048        A   AA__
                                AGGCTGCCTG CCA   TGC
                                |||||||||| |||   |||
                                TCCGACGGAC GGT   ACG
                                     G   CGTG
GAM1509  LOC221421 3'  GCAAGTGTGTCAGGCAGCC   93893         _  AA
                                GGCTGCCTGAC CA  TGC
                                |||||||||| ||  |||
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                                CCGACGGACTG GT  ACG
                                      T  GA
GAM1509  LOC51337  3'  GCATCTGCCAGGCAGCC     34082         AC  A
                                GGCTGCCTG  CA ATGC
                                |||||||||  || ||||
                                CCGACGGAC  GT TACG
                                     C_  C
GAM1510  EHF      3'  TCCAAAACCCAAGGTTGGCT   25127     AT   _   C
                                AGT  GCCT GGGT TTGGA
                                |||  |||| |||| |||||
                                TCG  TGGA CCCA AACCT
                                  GT   A   A
GAM1510  EPHA2    3'  CCATCGGCCAAGAATACTTGAA 16675          GC  G   T_
             G                   CTTCAAGTAT  CT GGTC  TGG
                                 ||||||||||  || ||||  |||
                                 GAAGTTCATA  GA CCGG  ACC
                                       A_  A   CT
GAM1510  ITGA5    3'  CCCAGAGACATACTTGAAG    61933          C__
                                CTTCAAGTATG   CTGGG
                                ||||||||||   |||||
                                GAAGTTCATAC   GACCC
                                       AGA
GAM1510  TREM2    3'  TCCAAGACTGTCATATTT    39098        CCTG
                                AAGTATG   GGTCTTGGA
                                |||||||   |||||||||
                                TTTATAC   TCAGAACCT
                                    TG__
GAM1510  UQCRB    3'  CCAACATAGGCATACTTAAG   21939     C         GGTC
                                CTT AAGTATGCCTG   TTGG
                                ||| ||||||||||   ||||
                                GAA TTCATACGGAT   AACC
                                  _         AC__
GAM1510  ATP10D   3'  CAGAGACCACTTGAAG      73526        ATGCCTG   _
                                CTTCAAGT      GGTCT TG
                                ||||||||      ||||| ||
                                GAAGTTCA      CCAGA AC
                                    ________    G
GAM1510  B3GNT7   3'  CCCTTCCAGGCAACCTGAA   71678     A  A      TCTT
                                TTCA GT TGCCTGGG   GG
                                |||| || ||||||||   ||
                                AAGT CA ACGGACCT   CC
                                  C  _       TC__
GAM1510  DKFZp547I224 3'  TCCAAAATTGACCACATACTTG 39963          CCTG   ____
             GA                   TTCAAGTATG   GGTC   TTGGA
                                  ||||||||||   ||||   |||||
                                  AGGTTCATAC   CCAG   AACCT
                                       A___    TTAA
GAM1510  FLJ22341 3'  CCAAGCTCAGGCACACCCAAG  45114     CAA  A      T
                                CTT   GT TGCCTGGG CTTGG
                                |||   || |||||||| |||||
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                                GAA   CA ACGGACTC GAACC
                                  CC_  C       _
GAM1510  KIAA0779  3'  CCGAACAGCATACTTGAAG   86908          C  GGTC
                                CTTCAAGTATGC TG    TTGG
                                |||||||||||| ||    ||||
                                GAAGTTCATACG AC    AGCC
                                       _  A___
GAM1510  LOC144233 3'  CCAAGGCACATAATTGAA    77246      G    CCTGG
                                TTCAA TATG     GTCTTGG
                                ||||| ||||    |||||||
                                AAGTT ATAC     CGGAACC
                                   A    A____
GAM1510  LOC147341 3'  ACCCAGGCATAACTGAAG    85116       AG
                                CTTCA  TATGCCTGGGT
                                |||||  ||||||||||
                                GAAGT  ATACGGACCCA
                                   CA
GAM1510  LOC221088 5'  TCCAAGGTGCTGGCCACTCGAA 94888      A   AT   TGGG
             G                   CTTC AGT  GCC    TCTTGGA
                                |||| |||  |||    |||||||
                                GAAG TCA  CGG    GGAACCT
                                  C   C_   TCGT
GAM1511  SCAMP1    3'  GCTAAATAAATATTCTCC    54500     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1511  SCAMP1    3'  GCTAAATAAATATTCTCC    54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1511  NX-17     3'  TGAATATCAGCCCCTAATA   40706         ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                     CGAC
GAM1511  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
             TA                   TATTAGGGATAATATTCATTTAGC
                                |||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM1512  ACATN     5'  GATGGCTCCCGGCTTCAG    17597        AGTG   CA   A
                                TTGAAGCC   GGG  CCA TC
                                ||||||||   |||  ||| ||
                                GACTTCGG   CCC  GGT AG
                                     ____  TC   C
GAM1512  B3GALT2   3'  GTGTCTCAGGCTCAA       15032      A   AG
                                TTGA GCC  TGGGGCAC
                                |||| |||  ||||||||
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                                AACT CGG  ACTCTGTG
                                  _  __
GAM1512 CD164    3' GGACTAGTGCAGAGGCTTTAA 21197       AGTGGG   CAA
                                TTGAAGCC    GCAC  TCC
                                ||||||||    ||||  |||
                                AATTTCGG    CGTG  AGG
                                    AGA___   ATC
GAM1512 HPS4     3' ATTGGTGCCACAAGCTTC   42226     CAG  G
                                GAAGC  TG GGCACCAAT
                                |||||  || |||||||||
                                CTTCG  AC CCGTGGTTA
                                  A__  A
GAM1512 SDPR     5' GACTGGTGCCCTGAGCTCCAA 17400    A  CAG       A
                                TTG AGC  TGGGGCACCA TC
                                ||| |||  |||||||||| ||
                                AAC TCG  GTCCCGTGGT AG
                                  C  A__       C
GAM1512 C5orf6   3' GATTGGCTGTGCCAGCTTC   33954     CAG  G  _
                                GAAGC  TGG GCA CCAATC
                                |||||  ||| ||| ||||||
                                CTTCG  ACC TGT GGTTAG
                                  ___  G  C
GAM1512 C8orf17  3' GGACCACACTGGCTGCAA    39998    A      G  CA
                                TTG AGCCAGTG GG  CC
                                ||| ||||||| ||  ||
                                AAC TCGGTCAC CC  GG
                                  G      A  A_
GAM1512 CABP5    5' GACTGGTGCCCTGCGAGCTCCA 39562    A  CA TG      A
                                TG AGC  G  GGGCACCA TC
                                || |||  |  ||||||| ||
                                AC TCG  C  CCCGTGGT AG
                                 C  AG GT       C
GAM1512 FLJ13940 3' GGACTGGTGCCCCACAGGCTTT 47309        A        A
            AA                   TTGAAGCC GTGGGGCACCA TCC
                                ||||||| |||||||||| |||
                                AATTTCGG CACCCCGTGGT AGG
                                    A         C
GAM1512 KCNMB2   3' ATTGGTGGACTGGTTTCAA   20684         GGGG
                                TTGAAGCCAGT   CACCAAT
                                ||||||||||   |||||||
                                AACTTTGGTCA   GTGGTTA
                                      G___
GAM1512 KIAA0530 3' GATTGGTGTATAGCTTTAA   71431       CAGTGGG
                                TTGAAGC     GCACCAATC
                                |||||||     |||||||||
                                AATTTCG     TGTGGTTAG
                                   ATA_____
GAM1512 KIAA1522 3' GGATTGGCCTTCCTGTGCCTCA 65607    A  _  TG   AC
            A                    TTGA GC CAG  GGGC  CAATCC
                                |||| || |||  ||||  ||||||
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                                AACT CG GTC  TCCG  GTTAGG
                                  C  T   CT   __
GAM1512 KIAA1853 3' GGATGCCCCACTAGTCCAA   69924     AA  C       _
                                TTG  GC AGTGGGGCA CC
                                |||  || |||||||| ||
                                AAC  TG TCACCCCGT GG
                                  C_  A       A
GAM1512 LOXL4    3' GATTGGTCTAAACTTCAA    50859       CCAG   GGC
                                TTGAAG   TGG   ACCAATC
                                ||||||   |||  |||||||
                                AACTTC   ATC   TGGTTAG
                                   AA__  ___
GAM1512 LSR7     5' GGACCGGCCCTGCCCCCGGCTT 38280         AGT     ___ AA
             CAA                   TTGAAGCC   GGGGCA   CC  TCC
                                |||||||   ||||||  ||  |||
                                AACTTCGG   CCCCGT   GG  AGG
                                    C__     CCC  CC
GAM1512 PLK      3' GGACTGGTGCCCTCCTCACT   18525    CC  TG      A
                                AG  AG  GGGCACCA TCC
                                ||  ||  |||||||| |||
                                TC  TC  CCCGTGGT AGG
                                 AC  CT       C
GAM1512 STK22D   3' GGTCCCCACTGGCCGCAA    50145     AA        C
                                TTG  GCCAGTGGGG ACC
                                |||  |||||||||| |||
                                AAC  CGGTCACCCC TGG
                                  GC        _
GAM1512 LOC124871 3' TGCTGCCCCACCAGCTTCAG   74818        CA       C
                                TTGAAGC  GTGGGGCA CA
                                |||||||  |||||||| ||
                                GACTTCG  CACCCCGT GT
                                    AC       C
GAM1512 LOC157349 3' GACTGGCTGCTGGCTCCGA    82341     A     TG GGCA   A
                                TTG AGCCAG  G    CCA TC
                                ||| ||||||  |    ||| ||
                                AGC TCGGTC  C    GGT AG
                                  C     GT _____   C
GAM1512 LOC222550 5' GGATCAATATCGTGCTGGCTT  96018         G  CACCA
                                AAGCCAGTG GG     ATCC
                                |||||||| ||     ||||
                                TTCGGTCGT CT     TAGG
                                     G  ATAAC
GAM1513 ADH7     3' AAGATTAAGGGACGGGC     7268       ACA   G
                                GCCC   TCT TTTAATCTT
                                ||||   ||| |||||||||
                                CGGG   AGG GAATTAGAA
                                  C__   _
GAM1513 ARAF1    5' GGAAGGACTTCAGATGTGAGC  64644    C       TTTAA
                                GC CACATCTG     TCTTCC
                                || ||||||||     ||||||
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                                CG GTGTAGAC    GGAAGG
                                 A      TTCA_
GAM1513 CEACAM6  3' GGAAGACTGGCAGATTGGACCA 11756    C  C     TAA
                                TGG CCA ATCTGTT  TCTTCC
                                ||| ||| |||||||  ||||||
                                ACC GGT TAGACGG  AGAAGG
                                  A  _     TC_
GAM1513 CLECSF12 3' GGATTACAGATGTGAGCCA   77214     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1513 CYP1A2   3' GGATTAACAGGTATGAACCA  7518     CC  C     T
                                TGG  CA ATCTGTT AATCT
                                |||  || ||||||| |||||
                                ACC  GT TGGACAA TTAGG
                                  AA  A     _
GAM1513 ENG      3' GAACTTGAAACAGATTCAGGCC 5496      CAC      AATC
                A                TGGCC  ATCTGTTT   TTC
                                |||||  ||||||||   |||
                                ACCGG  TAGACAAA   AAG
                                   ACT      GTTC
GAM1513 ERCC3    3' GAATAAACAGAATGGACCA   5506     C  CA      A
                                TGG CCA  TCTGTTTA TC
                                ||| |||  |||||||| ||
                                ACC GGT  AGACAAAT AG
                                  A  A_      A
GAM1513 HTLF     5' AAGATTGCAGGATTAAGCCA  10973     CCACA    TT
                                TGGC    TCTGT  AATCTT
                                ||||    |||||  ||||||
                                ACCG    GGACG  TTAGAA
                                  AATTA    __
GAM1513 MS4A8B   3' GATTTTAAACAGATGTTAACCA 49588     CCC         TCT
                                TGG   ACATCTGTTTAA   TC
                                |||   ||||||||||||   ||
                                ACC   TGTAGACAAATT   AG
                                  AAT         TT_
GAM1513 PRKAA2   3' GAAGATTAAAAAGTAAAGAACC 21811     CCCACAT  G
                A                TGG      CT TTTAATCTTC
                                |||      || ||||||||||
                                ACC      GA AAATTAGAAG
                                  AAGAAAT  A
GAM1513 ASE-1    3' GGATAACAGGTGTGAGCCA   24983     C       TA
                                TGGC CACATCTGTT  ATCT
                                |||| ||||||||||  ||||
                                ACCG GTGTGGACAA  TAGG
                                  A       __
GAM1513 CITED2   3' GGAAGATTAAACAGATGTGGGC 21403
                CA                TGGCCCACATCTGTTTAATCTTCC
                                |||||||||||||||||||||||||
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                                ACCGGGTGTAGACAAATTAGAAGG

GAM1513 DKFZP564K0322 3' GGATTACAGATGTGAGCCA  50188    C      TT
                           TGGC CACATCTGT  AATCT
                           |||| |||||||||  |||||
                           ACCG GTGTAGACA  TTAGG
                             A      __
GAM1513 DZIP1    3' GAAGATTATTCCAGAAGCCA  30703    CCACA   TT_
                           TGGC   TCTG  TAATCTTC
                           ||||   ||||  ||||||||
                           ACCG   AGAC  ATTAGAAG
                             A____  CTT
GAM1513 FLJ22969 3' GGATTACAGATGTGAGCCA  69211    C      TT
                           TGGC CACATCTGT  AATCT
                           |||| |||||||||  |||||
                           ACCG GTGTAGACA  TTAGG
                             A      __
GAM1513 HSNOV1   3' GGATTACAGATGTGAACCA  34437    CC      TT
                           TGG  CACATCTGT  AATCT
                           |||  |||||||||  |||||
                           ACC  GTGTAGACA  TTAGG
                             AA      __
GAM1513 IMPACT   3' GAATTACAGGTGTGAGCCA  38006    C      TTAATC
                           TGGC CACATCTGT    TTC
                           |||| |||||||||    |||
                           ACCG GTGTGGACA    AAG
                             A      TT____
GAM1513 JAM1     3' GGATTACAGATGTGAGCCA  34234    C      TT
                           TGGC CACATCTGT  AATCT
                           |||| |||||||||  |||||
                           ACCG GTGTAGACA  TTAGG
                             A      __
GAM1513 JAM1     3' GGATTACAGATGTGAGCCA  58499    C      TT
                           TGGC CACATCTGT  AATCT
                           |||| |||||||||  |||||
                           ACCG GTGTAGACA  TTAGG
                             A      __
GAM1513 JAM1     3' GGATTACAGATGTGAGCCA  58520    C      TT
                           TGGC CACATCTGT  AATCT
                           |||| |||||||||  |||||
                           ACCG GTGTAGACA  TTAGG
                             A      __
GAM1513 JAM1     3' GGATTACAGATGTGAGCCA  58548    C      TT
                           TGGC CACATCTGT  AATCT
                           |||| |||||||||  |||||
                           ACCG GTGTAGACA  TTAGG
                             A      __
GAM1513 JAM1     3' GGATTACAGATGTGAGCCA  58577    C      TT
                           TGGC CACATCTGT  AATCT
                           |||| |||||||||  |||||
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                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1513  KIAA0210  5'  GAATTACAGGTGTGAGCCA   29159     C       TTAATC
                                TGGC CACATCTGT     TTC
                                |||| |||||||||     |||
                                ACCG GTGTGGACA     AAG
                                  A       TT____
GAM1513  KIAA0280  3'  GAGCATAAACAGATGTGGTCCA 93301     C          AT
                                TGG CCACATCTGTTTA  CTT
                                ||| ||||||||||||  |||
                                ACC GGTGTAGACAAAT  GAG
                                  T          AC
GAM1513  KIAA0285  5'  GAAGATTGAGCTTGACCGGACC 29684     C  ACA  T_
            A                    TGG CC   TC  GTTTAATCTTC
                                ||| ||   ||  ||||||||||
                                ACC GG   AG  CGAGTTAGAAG
                                  A  CC_  TT
GAM1513  KIAA0356  3'  GGAAGACCCTCAGATGTGGCCA 66778      C      TTTAA
                                TGGCC ACATCTG    TCTTCC
                                ||||| |||||||    ||||||
                                ACCGG TGTAGAC    AGAAGG
                                   _      TCCC_
GAM1513  KIAA1354  3'  GGAAGATTGTCAGCATGT    61576     _  TT
                                ACAT CTG  TAATCTTCC
                                |||| |||  |||||||||
                                TGTA GAC  GTTAGAAGG
                                  C   T_
GAM1513  KIAA1466  3'  ATTAAATAGTATGGGCCA    72406       CAT
                                TGGCCCA   CTGTTTAAT
                                |||||||   |||||||||
                                ACCGGGT   GATAAATTA
                                    AT_
GAM1513  KIAA1468  5'  AAGATCTTGTAGATGTGGCCA  93423      C      TTTA
                                TGGCC ACATCTG    ATCTT
                                ||||| |||||||    |||||
                                ACCGG TGTAGAT    TAGAA
                                   _      GTTC
GAM1513  MRPS26    3'  GGAAGATTACAGTCTGAGGGCC 48723       A  T_   TT
            A                    TGGCCC CA  CTGT  AATCTTCC
                                |||||| ||  ||||  ||||||||
                                ACCGGG GT  GACA  TTAGAAGG
                                   A  CT   __
GAM1513  PANX3     3'  AAGATTAATAAAGATGTAAACC 54765    CCC     GT_
                                GG   ACATCT   TTAATCTT
                                ||   ||||||   ||||||||
                                CC   TGTAGA   AATTAGAA
                                 AAA     AAT
GAM1513  PLCL1     3'  AAGATTAAACAGATGATG    21714    _
                                CA CATCTGTTTAATCTT
                                || ||||||||||||||
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                                GT GTAGACAAATTAGAA
                                 A
GAM1513  SPRY4    3'  GAAGACAGAACACAGATGTGGA 49013    GC        _  AA_
             CA                   TG  CCACATCTGT TT   TCTTC
                                ||  |||||||||| ||   |||||
                                AC  GGTGTAGACA AA   AGAAG
                                 A_        C  GAC
GAM1513  WNT10A   3'  GAAGAGGAGATTGGACCA    48170     C   C    G TTAA
                                TGG CCA ATCT T    TCTTC
                                ||| ||| |||| |    |||||
                                ACC GGT TAGA G    AGAAG
                                 A   _    G ____
GAM1513  LOC113523 5'  GGATTACAGATGTGAGCCA    73427      C        TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A        __
GAM1513  LOC124216 3'  GGATTACAGATGTGAGCCA    74736      C        TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A        __
GAM1513  LOC130639 5'  GGATTAAAGACGTGAGCCA    75480      C   A   GT
                                TGGC CAC TCT  TTAATCT
                                |||| ||| |||  |||||||
                                ACCG GTG AGA  AATTAGG
                                  A   C   __
GAM1513  LOC144202 5'  GGAAGATTCGATGGACATGGAC 77226    GC   CA     T
             A                   TG  CCA  TCTGTT AATCTTCC
                                ||  |||  |||||| ||||||||
                                AC  GGT  AGGTAG TTAGAAGG
                                 A_   AC     C
GAM1513  LOC149171 5'  GAATTACAGGTGTGAGCCA    79967      C        TTAATC
                                TGGC CACATCTGT     TTC
                                |||| |||||||||      |||
                                ACCG GTGTGGACA     AAG
                                  A        TT_____
GAM1513  LOC150245 3'  GAAGCAAGACAGATGTGGGCC  86112             AAT
                                GGCCCACATCTGTTT   CTTC
                                ||||||||||||||   ||||
                                CCGGGTGTAGACAGA   GAAG
                                         AC_
GAM1513  LOC152620 3'  AGATTACAGATGTGAGCCA    60703      C        TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGA
                                  A        __
GAM1513  LOC153577 3'  GAAGATTTTATGTGACCA    87239     CC    CTGTTT
                                TGG  CACAT     AATCTTC
                                |||  |||||     |||||||
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                                ACC  GTGTA     TTAGAAG
                                  A_    TT____
GAM1513  LOC154930 3'  GAATAACAGGTGTGAGCCA   82091     C       TAATC
                                TGGC CACATCTGTT    TTC
                                |||| ||||||||||    |||
                                ACCG GTGTGGACAA    AAG
                                  A        T____
GAM1513  LOC157507 5'  AAGATTAAACCATGGATG    82376     ___
                                CATCT   GTTTAATCTT
                                |||||   ||||||||||
                                GTAGG   CAAATTAGAA
                                   TAC
GAM1513  LOC158014 5'  AGAATTACAGGTGTGAGCCA  82549     C       TTAA
                                TGGC CACATCTGT    TCT
                                |||| |||||||||    |||
                                ACCG GTGTGGACA    AGA
                                  A        TTA_
GAM1513  LOC158668 3'  AGATTACAGATGTGAGCCA    69892     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGA
                                  A       __
GAM1513  LOC170409 5'  GGATTACAGATGTGAGCCA    83745     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1513  LOC200282 5'  GAAATTACAGGTGTGAGCCA   90099     C       TTAA
                                TGGC CACATCTGT    TC
                                |||| |||||||||    ||
                                ACCG GTGTGGACA    AG
                                  A        TTAA
GAM1513  LOC220595 3'  GGAAGACCTCAGATGTGACCA  92778     CC      TTTAA
                                TGG  CACATCTG    TCTTCC
                                |||  ||||||||    ||||||
                                ACC  GTGTAGAC    AGAAGG
                                  A_       TCC__
GAM1513  LOC253805 3'  GGATTACAGATGTGAGCCA    98179     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1513  LOC56181  5'  GGATTACAGATGTGAGCCA    97278     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1513  LOC91547  3'  GGATTACAGATGTGAGCCA    67004     C       TT
                                TGGC CACATCTGT  AATCT
                                |||| |||||||||  |||||
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                                ACCG GTGTAGACA  TTAGG
                                  A       __
GAM1514  SCAMP1   3'  GCTAAATAAATATTCTCC    54500    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1514  SCAMP1   3'  GCTAAATAAATATTCTCC    54501    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1514  NX-17    3'  TGAATATCAGCCCCTAATA   40706        ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                     CGAC
GAM1514  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
              TA                  TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM1515  CDH12    3'  CTTATCATTTAAAGTGGTGTA  15777        CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM1515  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM1515  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090      T   AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                   _   GTCA_
GAM1515  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
              A                  TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM1515  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126        CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM1515  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
              TA                  TACA   TCC   GAAGAATAAG
                                ||||   |||   ||||||||||
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                              ATGT   AGG   TTTCTTATTC
                                AAA_  ATTG
GAM1515 KIAA1719 3' TCTGTCTTGGGAGTGGTGTA  68742          _
                              TACACCACTCCCAAGA AGA
                              |||||||||||||||| |||
                              ATGTGGTGAGGGTTCT TCT
                                       G
GAM1515 KIAA1853 3' TTTTTCTTGGAAGCAGTG   69929    CA  C
                              CAC  CT CCAAGAAGAA
                              |||  || ||||||||||
                              GTG  GA GGTTCTTTTT
                                AC  A
GAM1515 KIAA1877 3' CTTATTCTTCTGCCATGAGT  66748    CCA__
                              ACTC    AGAAGAATAAG
                              ||||    ||||||||||
                              TGAG    TCTTCTTATTC
                                TACCG
GAM1515 KIAA1906 3' CTTATTCTTCTTGACTTTTGG 73571    CTCC_
                              CCA    CAAGAAGAATAAG
                              |||    ||||||||||||
                              GGT    GTTCTTCTTATTC
                                TTTCA
GAM1515 OSBPL11  3' CTTAATTTCCCAAGAGTGGTG 43206       CCAA   AA
                              CACCACTC   GAAG  TAAG
                              ||||||||   ||||  ||||
                              GTGGTGAG   CTTT  ATTC
                                   AACC   A_
GAM1515 YME1L1   3' TCATTCTTGATGTGGTGTA   58438       TCC    _
                              TACACCAC   CAAGAA GA
                              ||||||||   ||||||  ||
                              ATGTGGTG   GTTCTT CT
                                   TA_    A
GAM1515 ZNF262   3' CTTATTTTGTTTGGGAGT    18723        A
                              ACTCCCAAG AGAATAAG
                              ||||||||| ||||||||
                              TGAGGGTTT TTTTATTC
                                   G
GAM1515 LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_    AAGA
                              TACACCAC   CCAAG   ATA
                              ||||||||   |||||   |||
                              ATGTGGTG   GGTTC   TGT
                                   CAA    GG__
GAM1516 ACVRL1   5' TTTATTAGGAGGGAGTGGTG  5240        AAGAAG
                              CACCACTCCC     AATAAG
                              ||||||||||     ||||||
                              GTGGTGAGGG     TTATTT
                                   AGGA__
GAM1516 BCL11B   3' TTTGTTTTTGGGGTGGGGGGTG 57582      A_ __      G  TAAG
           TG                   TACACC  CT  CCCAAGAA AA
                              ||||||  ||  |||||||| ||
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                                GTGTGG  GG  GGGTTTTT TT
                                   GG  TG      G  T
GAM1516  C18orf1   3'  CTTCGTGTGGGAGTGGTGTG  60865          A__
                                TACACCACTCCCA  GAAG
                                ||||||||||||  ||||
                                GTGTGGTGAGGGT  CTTC
                                     GTG
GAM1516  ITPR3     3'  CTTGTTTTTCTCCTTTTGGTGT 11085       CTCCCA
            A                    TACACCA     AGAAGAATAAG
                                |||||||     ||||||||||
                                ATGTGGT     TCTTTTTGTTC
                                   TTTCC_
GAM1516  KCNAB1    3'  GTTTGTTTTTTTTTTGAAGGGGG 61585          ____
            TGGTGTG                TACACCACTCCC    AAGAAGAATAAG   T
                                ||||||||||||  ||||||||||||  |
                                GTGTGGTGGGGG   TTTTTTTTGTTT  G
                                     AAGT
GAM1516  KRAS2     3'  CTTATTTTTCTTACCAAGTGTG 54123    C   CCC_
                                CAC ACT   AAGAAGAATAAG
                                ||| |||   ||||||||||||
                                GTG TGA   TTCTTTTTATTC
                                  _  ACCA
GAM1516  KRAS2     3'  CTTATTTTTCTTACCAAGTGTG 18375    C   CCC_
                                CAC ACT   AAGAAGAATAAG
                                ||| |||   ||||||||||||
                                GTG TGA   TTCTTTTTATTC
                                  _  ACCA
GAM1516  LIFR      3'  TTTGTTTTTTTTGGTTGGTTG  11315   C   CTC
                                A ACCA  CCAAGAAGAATAAG
                                | ||||  ||||||||||||||
                                G TGGT  GGTTTTTTTTGTTT
                                 T   T__
GAM1516  MEN1      5'  CTTGTTTTTTTCCTTTTGGTG  56348      CTCCCA
                                CACCA     AGAAGAATAAG
                                |||||     ||||||||||
                                GTGGT     TTTTTTTGTTC
                                   TTTCC_
GAM1516  MLLT7     3'  TTGTGCCTGGGAGTGTGTG   21043    _      AGAAGA
                                CAC CACTCCCA     ATAA
                                ||| ||||||||     ||||
                                GTG GTGAGGGT     TGTT
                                  T       CCG___
GAM1516  SIAH1     3'  TTTGTTTTTGCCGTGGGAGTGT 13128     _      AG__
            GTG                   CAC CACTCCCA    AAGAATAAG
                                ||| ||||||||    |||||||||
                                GTG GTGAGGGT    TTTTTGTTT
                                  T       GCCG
GAM1516  SLC7A6    3'  TTTGTTTTTGTGGTGGGTGCTG 15646     C    _   AG
            TG                    TACA CACTC CCA  AAGAATAAG
                                |||| ||||| |||  |||||||||
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                                GTGT GTGGG GGT  TTTTTGTTT
                                  C    T  G_
GAM1516 STAT6    5'  TTTTTCTTTTTGGTGGTGGTG  13453       TC        TAAG
                                CACCAC  CCAAGAAGAA
                                ||||||  ||||||||||
                                GTGGTG  GGTTTTTCTT
                                   GT         TTTA
GAM1516 TCF8     3'  CTTGTTTTTTTAAGAGTGTGTG 48429     _    CCA
                                CAC CACTC   AGAAGAATAAG
                                ||| |||||   ||||||||||
                                GTG GTGAG   TTTTTTTGTTC
                                  T    AA_
GAM1516 B3GNT7   3'  TTGTTCTTGGCTGGTGGGTG   71685     A    C_      G
                                TAC CCACT  CCAAGAA AA
                                ||| |||||  ||||||| ||
                                GTG GGTGG  GGTTCTT TT
                                  _    TC      G
GAM1516 BCDO     3'  TTATTCTTTCTGTGGGTG    34287      C  AG
                                CACTC CA  AAGAATAA
                                ||||| ||  ||||||||
                                GTGGG GT  TTCTTATT
                                   T  CT
GAM1516 DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
             A                   TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM1516 EPN2     3'  TTTATTTTTCTTTGACTCGTGT 31046       CAC  CC
             G                   TACAC   TC  AAGAAGAATAAG
                                |||||   ||  ||||||||||||
                                GTGTG   AG  TTCTTTTTATTT
                                   CTC  T_
GAM1516 FLJ13855 3'  GGGTATTTTTCTTGGGGGTGGA 43853     A              AG
             GTA                   TAC CCACTCCCAAGAAGAATA
                                ||| ||||||||||||||||||
                                ATG GGTGGGGGTTCTTTTTAT
                                  A              GGGA
GAM1516 FLJ21791 3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM1516 FLJ32865 3'  TTTGTTGGGGGTGGGGTG    58824     A        G
                                TAC CCACTCCCAA AAG
                                ||| |||||||||| |||
                                GTG GGTGGGGGTT TTT
                                  G        G
GAM1516 HAND1    3'  TTTGTTCTTCGAATCGTGGTG  17880       TCCCAA
                                CACCAC     GAAGAATAAG
                                ||||||     ||||||||||
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                                GTGGTG     CTTCTTGTTT
                                   CTAAG_
GAM1516  KIAA0562  3'  TTTGTTTTGCGGGGGTGGTG   28834          AAGA
                                CACCACTCCC    AGAATAAG
                                ||||||||||    ||||||||
                                GTGGTGGGGG    TTTTGTTT
                                     CG__
GAM1516  KIAA0871  5'  TTATTTTTTTGGTGTGTGTGTG 31022       _  TC        ATAAG
                                TACAC CAC  CCAAGAAGA
                                ||||| |||  |||||||||
                                GTGTG GTG  GGTTTTTTT
                                   T  T_       ATTT
GAM1516  KIAA0970  3'  TTTGTTTTTTTTGTTAGGGTG  30622      A  CC
                                CACC CT  CAAGAAGAATAAG
                                |||| ||  ||||||||||||
                                GTGG GA  GTTTTTTTTGTTT
                                  _  TT
GAM1516  KIAA1240  3'  TTTATTTTTAGGGAGTGGGTA  67297      A       AAG
                                TAC CCACTCCC   AAGAATAAG
                                ||| ||||||||   |||||||||
                                ATG GGTGAGGG   TTTTTATTT
                                  _       A__
GAM1516  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68742             _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                        G
GAM1516  KIAA1750  3'  TTTATTTTTTTGTTCTAGGTGT 68815        ACTCCCA
              G                  TACACC      AGAAGAATAAG
                                ||||||      ||||||||||
                                GTGTGG      TTTTTTTATTT
                                   ATCTTG_
GAM1516  MAP2K3    3'  CTTGTTTTTCTTGCATGGT    59686      CTCC
                                ACCA    CAAGAAGAATAAG
                                ||||    ||||||||||||
                                TGGT    GTTCTTTTTGTTC
                                  AC__
GAM1516  MLN64     3'  CTTGTTGGGGAGTGGGTG     96062      A       _  G
                                TAC CCACTCCC AA AAG
                                ||| |||||||| || |||
                                GTG GGTGAGGG TT TTC
                                  _       G  G
GAM1516  NY-REN-41 3'  TTTGTTTTTCTATCCTGGTGG  55564       CCCA_
                                CCACT     AGAAGAATAAG
                                |||||     ||||||||||
                                GGTGG     TCTTTTTGTTT
                                   TCCTA
GAM1516  PRO1489   5'  TTTGTTTTTCGTGTGTGTGTG  38334       _  TCCCAA
                                TACAC CAC     GAAGAATAAG
                                ||||| |||     ||||||||||
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                                GTGTG GTG     CTTTTTGTTT
                                  T   TG____
GAM1516  SEC15L   3'  TTTGTTCTACTTGGGTGGT   72731     CT     A
                                ACCA  CCCAAG AGAATAAG
                                ||||  |||||| ||||||||
                                TGGT  GGGTTC TCTTGTTT
                                  __     A
GAM1516  SHAPY    3'  TTTGTTCTTTTTGGAACTGTG  57915     TC__
                                CAC    CCAAGAAGAATAAG
                                |||    ||||||||||||||
                                GTG    GGTTTTTCTTGTTT
                                 TCAA
GAM1516  STAM2    3'  GTTTTTCTTCCTGCAATGTGGT 20707        TCC_  A     TAAG
            GTG                   TACACCAC    CA GAAGAA
                                |||||||||    || ||||||
                                GTGTGGTG    GT CTTCTT
                                     TAAC  C     TTTGT
GAM1516  TUBGCP3  3'  TTTATTTTTTTTTAGTGTTGTA 21982     C    CCC
                                TACA CACT   AAGAAGAATAAG
                                |||| ||||   ||||||||||||
                                ATGT GTGA   TTTTTTTTATTT
                                  T    T__
GAM1516  ZNF220   3'  CTTGTTTTTTTACCACCTGGTG 23157      CTCCCA
                                CACCA     AGAAGAATAAG
                                |||||     ||||||||||
                                GTGGT     TTTTTTTGTTC
                                  CCACCA
GAM1516  LOC121219 5'  TTGTTCTATGGGTGGGTG    74493     ACT    AGA
                                CACC   CCCA   AGAATAA
                                ||||   ||||   |||||||
                                GTGG   GGGT   TCTTGTT
                                  GT_    A__
GAM1516  LOC143146 3'  TTTGTTGGAGGTGGTGTA    60767        TC    G
                                TACACCAC  CCAA AAG
                                |||||||||  |||| |||
                                ATGTGGTG  GGTT TTT
                                     GA    G
GAM1516  LOC146445 3'  TTGTTCTTTGTGTGGTTG    84687    C    TCCCAA
                                A ACCAC     GAAGAATAA
                                | |||||     |||||||||
                                G TGGTG     TTTCTTGTT
                                 T    TG____
GAM1516  LOC150174 3'  TTTATTTTTTTTTACAATGGTG 80444      CTCCC
                                CACCA     AAGAAGAATAAG
                                |||||     ||||||||||||
                                GTGGT     TTTTTTTTATTT
                                  AACAT
GAM1516  LOC150213 3'  TTTATTTTTTTTACAATGGTG  75363      CTCCC
                                CACCA     AAGAAGAATAAG
                                |||||     ||||||||||||
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                                GTGGT    TTTTTTTTATTT
                                   AACA_
GAM1516  LOC150236 3'  TTTATTTTTTTTACAATGGTG  80505      CTCCC
                                CACCA    AAGAAGAATAAG
                                |||||    ||||||||||||
                                GTGGT    TTTTTTTTATTT
                                   AACA_
GAM1516  LOC154084 3'  CTTGTTTTTTTAGTAGGTGTG  87378      _  CCCA
                                TACACC ACT    AGAAGAATAAG
                                |||||| |||    ||||||||||
                                GTGTGG TGA    TTTTTTTGTTC
                                   A  ____
GAM1516  LOC170261 3'  TTTATTCTTTGTGAAAGTGGT  83472      CC  A
                                ACCACT  CA GAAGAATAAG
                                ||||||  || ||||||||||
                                TGGTGA  GT TTTCTTATTT
                                   AA  G
GAM1516  LOC199692 3'  CTTGTTCTTCTGCTGTAGTGTG 59926      C  TCCCA
                                TACAC AC     AGAAGAATAAG
                                ||||| ||     ||||||||||
                                GTGTG TG     TCTTCTTGTTC
                                   A  TCG__
GAM1516  LOC203414 3'  CTTGTCAACTGGGGGTGATGTG 90913      C       A AA  A
                                TACA CACTCCCA G  GA TAAG
                                |||| |||||||| |  || ||||
                                GTGT GTGGGGGT C  CT GTTC
                                  A       _ AA  _
GAM1516  LOC257051 3'  TTTATTCTTTGTGAAAGTGGT  98054      CC  A
                                ACCACT  CA GAAGAATAAG
                                ||||||  || ||||||||||
                                TGGTGA  GT TTTCTTATTT
                                   AA  G
GAM1516  LOC92303  3'  TTATTTTTTTTGAGGTGG    69400      CC
                                CCACT  CAAGAAGAATAA
                                |||||  ||||||||||||
                                GGTGG  GTTTTTTTTATT
                                   A_
GAM1517  DMRT2     3'  GCCACCACCTCAGTTC      22653    C  C       TT T
                                GA AC GAGGTGGT  G GC
                                || || ||||||||  | ||
                                CT TG CTCCACCA  C CG
                                 _  A      __ _
GAM1517  FKBP1B    3'  GGAGCCACGGGCCACCCCGGTG 55084        A        _
              TC                   GACACCG GGTGGTTTGTG CTCC
                                |||||||| |||||||||| ||||
                                CTGTGGC CCACCGGGCAC GAGG
                                    C         C
GAM1517  MTMR3     3'  GAGCACTGCCCTGGGCATC    41162    CA  G   TG  TT
                                GA  CC AGG  GT  GTGCTC
                                ||  || |||  ||  ||||||
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                                CT  GG TCC  CG  CACGAG
                                 AC  G   __  T_
GAM1517  NCOA6    5'  AGCACAACTATCTATGTC    26824      CCG       T
                                GACA   AGGTGGTT GTGCT
                                ||||   |||||||| |||||
                                CTGT   TCTATCAA CACGA
                                  A__       _
GAM1517  NKX3A    3'  AGCACAAGGGGCCAAGGTCA   21610    C   GA   GG
                                A ACC  GGT  TTTGTGCT
                                | |||  |||  ||||||||
                                A TGG  CCG  GAACACGA
                                 C   AA   GG
GAM1517  POLS     3'  GAGCACAGCCCAGCGTTG    23778     G _   T
                                CGA G TGG TTGTGCTC
                                ||| | ||| ||||||||
                                GTT C ACC GACACGAG
                                  G G   C
GAM1517  TNFRSF6B 5'  GGAGCACAAAGCAACGG     53083     AGG  G
                                CCG   TG TTTGTGCTCC
                                |||   || ||||||||||
                                GGC   AC AAACACGAGG
                                  A__  G
GAM1517  ZNF236   3'  AGCACAAGCCATACATCG     24735     G__
                                CGA   GTGGTTTGTGCT
                                |||   ||||||||||||
                                GCT   TACCGAACACGA
                                  ACA
GAM1517  C20orf59 3'  GAACACAAACCACTGTGG     42233     A         C
                                CCG GGTGGTTTGTG TC
                                ||| |||||||||| ||
                                GGT TCACCAAACAC AG
                                  G         A
GAM1517  FLJ13433 3'  AGCACAAATTTAACGGCTTC   42858    CA   AGGT
                                GA  CCG    GGTTTGTGCT
                                ||  |||    ||||||||||
                                CT  GGC    TTAAACACGA
                                 TC   AAT_
GAM1517  FLJ14840 5'  GAGCACAGCCACTCGGCGCG   52725    ACA    G    T
                                CG   CCGAG TGGTT GTGCTC
                                ||   ||||| ||||| ||||||
                                GC   GGCTC ACCGA CACGAG
                                 GC_    _    _
GAM1517  FLJ32865 5'  GAAGCGAGCGGCACCCCGG   58810     A   __     GC
                                CCG GGTG  GTTTGT  TC
                                ||| ||||  ||||||  ||
                                GGC CCAC  CGAGCG  AG
                                  C   GG     A_
GAM1517  MGC2835  3'  GAGCACAAACCAGGTG      44175      GAGG
                                CACC    TGGTTTGTGCTC
                                ||||    ||||||||||||
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                                GTGG   ACCAAACACGAG
                                  ____
GAM1517 NR6A1    3' GGAACATTACTCCTCAATGCCG 9447    A CC   T  TT  C
                                CG CA  GAGG GGT  GTG TCC
                                || ||  |||| |||  ||| |||
                                GC GT  CTCC TCA  TAC AGG
                                 C  AA   _  T_  A
GAM1517 PLP1     3' GAGCACTGACCCCGATGG    6758     A_ T   T
                                CCG  GG GGTT GTGCTC
                                |||  || |||| ||||||
                                GGT  CC CCAG CACGAG
                                  AG  _   T
GAM1517 SEC61A1  3' AGCACAAACACTGAAATGTC  26227     CCGA   G
                                GACA   GGTG TTTGTGCT
                                ||||   |||| ||||||||
                                CTGT   TCAC AAACACGA
                                  AAAG   _
GAM1517 SECP43   5' AGCCCCACCCCGGTGCG    35719    A    A    TTTGT
                                CG CACCG GGTGG    GCT
                                || ||||| |||||    |||
                                GC GTGGC CCACC    CGA
                                 _    C    C____
GAM1517 LOC115574 3' GGAGCCCTTGGCCACCTCG   73854         TGT_
                                CGAGGTGGTT   GCTCC
                                ||||||||||   |||||
                                GCTCCACCGG   CGAGG
                                      TTCC
GAM1517 LOC144395 3' AGCATGACAGCCACCTTGG   77319         __ TG
                                CCGAGGTGGT  T  TGCT
                                ||||||||||  |  ||||
                                GGTTCCACCG  A  ACGA
                                      AC GT
GAM1517 LOC167994 5' GGAGCACAAACTGCACATCATC 83573     CACCGAG TG
           G                     CGA      G  GTTTGTGCTCC
                                |||      |  ||||||||||||
                                GCT      C  CAAACACGAGG
                                  ACTACA_ GT
GAM1517 LOC254753 3' GAGCCCCACCTCGGGGTC    97857    A       TTTGT
                                GAC CCGAGGTGG    GCTC
                                ||| |||||||||    ||||
                                CTG GGCTCCACC    CGAG
                                  G        C____
GAM1517 LOC256015 5' CACAGATCCTGGTGCCG    99453    A   G   TG
                                CG CACC AGG  GTTTGTG
                                || |||| |||  |||||||
                                GC GTGG TCC  TAGACAC
                                 C   _  __
GAM1518 ASH1     3' GCAAGGGGAATGGGGCCAT   38088         G     A_
                                ATGGCCCCA TTCCCC  GC
                                ||||||||| ||||||  ||
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                                TACCGGGGT AAGGGG  CG
                                      _     AA
GAM1518 BSG     3'  GGTTTGCTGGGGAACTGGCGCC 9958       C
             AT                   ATGGC CCAGTTCCCCAGCAAACC
                                  ||||| ||||||||||||||||||
                                  TACCG GGTCAAGGGGTCGTTTGG
                                    C
GAM1518 IGFBP3  3'  GTTGCTGGGGAGCCCAT     7004      CCCCA         A
                                  ATGG    GTTCCCCAGCAA C
                                  ||||    |||||||||||| |
                                  TACC    CGAGGGGTCGTT G
                                    _____          C
GAM1518 SFN     3'  CTGGCAGAGCTGAGGCCA    75070      C     C_
                                  TGGCC CAGTTC  CCAG
                                  ||||| ||||||  ||||
                                  ACCGG GTCGAG  GGTC
                                     A     AC
GAM1518 SP1     3'  GTTTGCTGCCACTGGGGCC   61919        TCCC
                                  GGCCCCAGT   CAGCAAAC
                                  |||||||||   ||||||||
                                  CCGGGGTCA   GTCGTTTG
                                       CC__
GAM1518 UBE2I   5'  GGTCTGCCGGGGACTGGGCC  13962      C  T   A  A
                                  GGCCC AGT CCCC GCA ACC
                                  ||||| ||| |||| ||| |||
                                  CCGGG TCA GGGG CGT TGG
                                    _  _   C  C
GAM1518 ATP6V0A1 3'  GGTTTGCTGTTTGGAAGCCAT  18988     CCCAG   C__
                                  ATGGC    TTCC   CAGCAAACC
                                  |||||    ||||   |||||||||
                                  TACCG    AAGG   GTCGTTTGG
                                    _____   TTT
GAM1518 DCAMKL1  3'  GGTTTGCTGGGCTCTGGGATCC 17603    C_    TTC
             A                    TGG  CCCAG   CCCAGCAAACC
                                  |||  |||||   ||||||||||
                                  ACC  GGGTC   GGGTCGTTTGG
                                    TA    TC_
GAM1518 DNAJA3   3'  GCTGCCTTGGGAACTGAAGCC  61099    CC      ____
                                  GGC  CAGTTCCC    CAGC
                                  |||  ||||||||    ||||
                                  CCG  GTCAAGGG    GTCG
                                    AA       TTCC
GAM1518 FLJ14627 5'  CTGGGGAACTGGGGGCCAT   52545        _
                                  ATGGCCCC AGTTCCCCAG
                                  |||||||| ||||||||||
                                  TACCGGGG TCAAGGGGTC
                                       G
GAM1518 FLJ20294 3'  GGCCTGCCTCGGGGAACTAGAA 35356    CCCC      A__   AA
             CC                     GG   AGTTCCCC   GCA  CC
                                  ||   ||||||||   |||  ||
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                                CC   TCAAGGGG  CGT  GG
                                 AAGA      CTC  CC
GAM1518 FLJ20297 5' GTTTGCTAAGAAGGCCAT   35374      CCAG  CCC
                                ATGGCC   TTC  AGCAAAC
                                ||||||   |||  |||||||
                                TACCGG   AAG  TCGTTTG
                                   ____  AA_
GAM1518 FLJ20445 5' GTCACTGGGGAAGGCCGT   35632      CCAG      CAA
                                ATGGCC   TTCCCCAG  AC
                                ||||||   ||||||||  ||
                                TGCCGG   AAGGGGTC  TG
                                   ____      ACC
GAM1518 FLJ22173 5' TTTGCTGGGGCAAAAGGCCA  47401      CCAG  _
                                TGGCC   TT CCCCAGCAAA
                                |||||   || ||||||||||
                                ACCGG   AA GGGGTCGTTT
                                   AA__  C
GAM1518 FLJ22724 5' GGCTGCTGGGGGTGGGGGCC  44852      AGT       AA
                                GGCCCC  TCCCCAGCA  CC
                                ||||||  |||||||||  ||
                                CCGGGG  GGGGGTCGT  GG
                                   GT_       CC
GAM1518 HEMK     3' GTTGGGGAAACTGAGGCC    32961     C    _
                                GGCC CAGTT CCCCAGC
                                |||| ||||| |||||||
                                CCGG GTCAA GGGGTTG
                                  A    A
GAM1518 JFC1     5' TGCCAGGGGAGCTGGAGCCA  52840     C        A_
                                TGGC CCAGTTCCCC  GCA
                                |||| ||||||||||  |||
                                ACCG GGTCGAGGGG  CGT
                                  A        AC
GAM1518 KDELR3   5' GTTTGCTGGGCGCGGGCGC   23398   _  A  TC
                                GC CCC GT  CCCAGCAAAC
                                || ||| ||  ||||||||||
                                CG GGG CG  GGGTCGTTTG
                                 C  _  C_
GAM1518 KIAA0275 3' GTAGGGGAATTAGGGCCAT   29332       C       A
                                ATGGCCC AGTTCCCC GC
                                ||||||| |||||||| ||
                                TACCGGG TTAAGGGG TG
                                   A       A
GAM1518 KIAA0450 5' GGCTTGCTGAGGGCTGGGCCA 28367       C  TT  _     A
                                TGGCCC AG  CCC CAGCAA CC
                                |||||| ||  ||| |||||| ||
                                ACCGGG TC  GGG GTCGTT GG
                                   _ __  A     C
GAM1518 KIAA0552 3' GGTTTGCTGAAACTGACAGAGC 28995     CC___     CCC
            C                    GGC    CAGTT   CAGCAAACC
                                |||    |||||  |||||||||
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                              CCG    GTCAA  GTCGTTTGG
                                AGACA    A__
GAM1518 KIAA1198 3' GGTTTGCTGGCAGATGAGGCC 64054     CCA  CC
                              GGCC   GTT  CCAGCAAACC
                              ||||   |||  ||||||||||
                              CCGG   TAG  GGTCGTTTGG
                                AG_   AC
GAM1518 KIAA1281 5' GTTTGCTACATGGGATCAT   90628    GC   _ TCCCC
                              ATG  CCCA GT    AGCAAAC
                              |||  |||| ||    |||||||
                              TAC  GGGT CA    TCGTTTG
                                TA   A _____
GAM1518 KIAA1655 5' GGCCTGCTGGATTTGGGGAAGC 67191      ___    TTCC     AA
            CAT                   ATGGC   CCCAG   CCAGCA  CC
                              |||||   |||||   ||||||  ||
                              TACCG   GGGTT   GGTCGT  GG
                                 AAG    TA__    CC
GAM1518 KIAA1981 3' GCCACGGGAGCTGAGGCCA   89714      C      CA_
                              TGGCC CAGTTCCC   GC
                              ||||| ||||||||   ||
                              ACCGG GTCGAGGG   CG
                                 A       CAC
GAM1518 MGC11102 5' CTGGTGGGAACTGGGAACA   51299    GC       __
                              TG  CCCAGTTCCC  CAG
                              ||  ||||||||||  |||
                              AC  GGGTCAAGGG  GTC
                               AA         TG
GAM1518 MGC2628  3'  GGTTTGCTAACCTGAGGGGTCA 44202       AGTTCCCC
                              TGGCCCC       AGCAAACC
                              |||||||       ||||||||
                              ACTGGGG       TCGTTTGG
                                  AGTCCAA_
GAM1518 PLCL2    5'  GTCTGCTGGGGCGCCCAT    68697     CCCCA  T      A
                              ATGG    GT CCCCAGCA AC
                              ||||    || |||||||| ||
                              TACC    CG GGGGTCGT TG
                                _____  C       C
GAM1518 PMF1     3'  TTTGCTGGAGGACTAGGCCA   24288      CC    C
                              TGGCC  AGTTC CCAGCAAA
                              |||||  ||||| ||||||||
                              ACCGG  TCAGG GGTCGTTT
                                 A_    A
GAM1518 PPI5PIV  3'  GTTTGCTGAACGAGGACTCA   39585   T  C  CA   CCC
                              A GG CC  GTTC   AGCAAAC
                              | || ||  ||||   |||||||
                              A TC GG  CAAG   TCGTTTG
                               C  A  AG   ___
GAM1518 PTPRT    3'  GCTGGGGAAATGGAACCAT   56500     CC   G
                              ATGG  CCA TTCCCCAGC
                              ||||  ||| |||||||||
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                                TACC  GGT AAGGGGTCG
                                  AA  A
GAM1518  RBX1     3'  GTTTGCTGTTTCTGTAGCCAT  27285      CC   TTCCC
                                ATGGC  CAG    CAGCAAAC
                                |||||  |||    ||||||||
                                TACCG  GTC    GTCGTTTG
                                  AT   TTT__
GAM1518  RODH-4   3'  TGTTGGGACTGGAACCAT    14927      CC    TC
                                ATGG  CCAGT  CCCAGCA
                                ||||  |||||  |||||||
                                TACC  GGTCA  GGGTTGT
                                  AA    __
GAM1518  SEC31B-1 3'  GTTCTGGAATTGGAGCCAT   31928       C      CC
                                ATGGC CCAGTTCC  AGC
                                ||||| ||||||||  |||
                                TACCG GGTTAAGG  TTG
                                   A       TC
GAM1518  SEPT3    3'  TGCACACAAACTGGGGCTAT   39406           CCCCA
                                ATGGCCCCAGTT    GCA
                                ||||||||||||    |||
                                TATCGGGGTCAA    CGT
                                      ACACA
GAM1518  STMN3    3'  GTCTGCTGGGGAGTGGGC    32469      CAG         A
                                GCCC   TTCCCCAGCA AC
                                ||||   |||||||||| ||
                                CGGG   GAGGGGTCGT TG
                                  T__         C
GAM1518  TOR2A    3'  GCTGAGGGAACTGAGGCCA   56188       C       _
                                TGGCC CAGTTCCC CAGC
                                ||||| |||||||| ||||
                                ACCGG GTCAAGGG GTCG
                                   A       A
GAM1518  LOC115123 5'  GGTCCACTGGGCCGTGAGCAGC 73594      CCCA   ____    CAA
            CA                   TGGC    GTTC    CCCAG   ACC
                                ||||    ||||    |||||   |||
                                ACCG    CGAG    GGGTC   TGG
                                  A___    TGCC    ACC
GAM1518  LOC118470 3'  GCCGGAAGAGGAACTGGGGGCA 74347    G        ____  A
                                TG CCCCAGTTCC    CC GC
                                || ||||||||||    || ||
                                AC GGGGTCAAGG    GG CG
                                 G         AGAA  C
GAM1518  LOC143785 5'  TGCTGGGGACTGGGGGCCA    77103        _  T
                                TGGCCCC AGT CCCCAGCA
                                ||||||| ||| ||||||||
                                ACCGGGG TCA GGGGTCGT
                                    G  _
GAM1518  LOC145314 3'  GCTGGGGCTGGGCACAT     77613     GC     TT
                                ATG  CCCAG  CCCCAGC
                                |||  |||||  |||||||
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                                TAC  GGGTC  GGGGTCG
                                  AC    __
GAM1518  LOC148530 5'  GCCGGAGGAACTGGGGCC    85315          _  A
                                GGCCCCAGTTCC CC GC
                                |||||||||||| || ||
                                CCGGGGTCAAGG GG CG
                                       A  C
GAM1518  LOC151201 3'  TTTACTGGGGAAAATCCAT   86494     CCCCAG      C
                                ATGG     TTCCCCAG AAA
                                ||||     |||||||| |||
                                TACC     AAGGGGTC TTT
                                  TAA___       A
GAM1518  LOC152286 3'  TTTGCTGTGGGTGGGGTCAT  86817        GTT  _
                                ATGGCCCCA   CCC CAGCAAA
                                |||||||||   ||| |||||||
                                TACTGGGGT   GGG GTCGTTT
                                     ___   T
GAM1518  LOC158656 5'  GTTTGCTGCTGCCACTGGAGCC 73401     C    TCCC_
            A                    TGGC CCAGT    CAGCAAAC
                                |||| |||||    ||||||||
                                ACCG GGTCA    GTCGTTTG
                                  A    CCGTC
GAM1518  LOC163682 3'  GCACAAGGAGCTGGGGCCA   88406          CCA_
                                TGGCCCCAGTTCC   GC
                                ||||||||||||   ||
                                ACCGGGGTCGAGG   CG
                                       AACA
GAM1518  LOC196500 3'  GCTGTGGGGAGCTGGGGCCA  89085            __
                                TGGCCCCAGTTCCCCA  GC
                                ||||||||||||||||  ||
                                ACCGGGGTCGAGGGGT  CG
                                         GT
GAM1518  LOC256306 5'  GCTCAGTGAGCTGGGGCCAT  98517          CCC_
                                ATGGCCCCAGTTC   AGC
                                ||||||||||||   |||
                                TACCGGGGTCGAG   TCG
                                       TGAC
GAM1518  LOC51128  5'  GCTGATGCGAACTGGGGCCA  32752          CC__
                                TGGCCCCAGTTC   CAGC
                                ||||||||||||   ||||
                                ACCGGGGTCAAG   GTCG
                                       CGTA
GAM1518  LOC51337  3'  GCTGGGGAAACTGAGGCC    34084     C    _
                                GGCC CAGTT CCCCAGC
                                |||| ||||| |||||||
                                CCGG GTCAA GGGGTCG
                                  A    A
GAM1518  LOC58525  3'  GGCCTGCTGGGGCCTGGGAGCC 79346    _    TT      AA
                                GGC CCCAG  CCCCAGCA  CC
                                ||| |||||  ||||||||  ||
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                                CCG GGGTC  GGGGTCGT  GG
                                  A    C_      CC
GAM1519 ATP8A2   3' GGCGCCCCTCACCCCCAC   95156    CAGT     CTT
                                GTG   GGGTGAG  GTGCT
                                |||   |||||||  |||||
                                CAC   CCCACTC  CGCGG
                                  C___     CC_
GAM1519 BMP4     3' CATCCACTCACCCACACAC   8660     CA       CTT
                                GTG  GTGGGTGAG  GTG
                                |||  |||||||||  |||
                                CAC  CACCCACTC  TAC
                                  A_       ACC
GAM1519 BMP4     3' CATCCACTCACCCACACAC   56462    CA       CTT
                                GTG  GTGGGTGAG  GTG
                                |||  |||||||||  |||
                                CAC  CACCCACTC  TAC
                                  A_       ACC
GAM1519 BMP4     3' CATCCACTCACCCACACAC   56465    CA       CTT
                                GTG  GTGGGTGAG  GTG
                                |||  |||||||||  |||
                                CAC  CACCCACTC  TAC
                                  A_       ACC
GAM1519 ABLIM    3' CAGCAGCACTCACTGCAC    11322          AGCTTG
                                GTGCAGTGGGTG    TGCTG
                                ||||||||||||    |||||
                                CACGTCACTCAC    ACGAC
                                     G_____
GAM1519 ABLIM    3' CAGCAGCACTCACTGCAC    22979          AGCTTG
                                GTGCAGTGGGTG    TGCTG
                                ||||||||||||    |||||
                                CACGTCACTCAC    ACGAC
                                     G_____
GAM1519 CAC-1    3' CACCACCCAGCCCACTGCAC  54294          GAGCTT  C
                                GTGCAGTGGGT    GTG TG
                                ||||||||||    ||| ||
                                CACGTCACCCG    CAC AC
                                     ACC___  C
GAM1519 DCTD     3' CATTCCTGCTCTCCCACTGCAC 10390         T   TT__
                                GTGCAGTGGG GAGC   GTG
                                |||||||||| ||||   |||
                                CACGTCACCC CTCG   TAC
                                     T   TCCT
GAM1519 KIAA0169 3' CAGCCACCACCCACTG     73176        AGCT  T
                                CAGTGGGTG   TG GCTG
                                |||||||||   || ||||
                                GTCACCCAC   AC CGAC
                                     C___  _
GAM1519 KIAA0453 3' CAGCACTCACGCACTGCAC  69603        G   GCTT
                                GTGCAGTG GTGA   GTGCTG
                                |||||||| ||||   ||||||
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                                CACGTCAC CACT    CACGAC
                                     G   ____
GAM1519  KIAA1396  3'  CAGCTCTTCCTCACCCACTACA 63667     C        CTTGT
              T                   GTG AGTGGGTGAG     GCTG
                                  ||| ||||||||||     ||||
                                  TAC TCACCCACTC     CGAC
                                    A         CTTCT
GAM1519  KIAA1727  3'  CAGGACCCCACCACTGCAC    64753         G  AGCTT  G
                                  GTGCAGTGG TG     GT CTG
                                  ||||||||| ||     || |||
                                  CACGTCACC AC     CA GAC
                                        _  CC___  G
GAM1519  MGC10960  3'  CACATGTCACCCACCCACCGCA 51981     A      A___  T
                                  TGC GTGGGTG    GC TGTG
                                  ||| |||||||    || ||||
                                  ACG CACCCAC    TG ACAC
                                    C       CCAC  T
GAM1519  LOC144509 5'  CAGCCTGTGTCACCCACCCAC  77358     CA       _  TTGT
                                  GTG  GTGGGTGA GC    GCTG
                                  |||  |||||||| ||    ||||
                                  CAC  CACCCACT TG    CGAC
                                    C_       G  TC__
GAM1519  LOC148709 5'  TCAGAAATGTAACTCACCCACT 79702     C        CTTGTG__
               CAC                  GTG AGTGGGTGAG       CTGA
                                  ||| ||||||||||       ||||
                                  CAC TCACCCACTC       GACT
                                    _        AATGTAAA
GAM1519  LOC151959 5'  ACGACCCTCACCCACTGC     86710           C_
                                  GCAGTGGGTGAG  TTGT
                                  ||||||||||||  ||||
                                  CGTCACCCACTC  AGCA
                                          CC
GAM1519  LOC155054 3'  CATGCTCACACCACTGCAC    82203          _     T
                                  GTGCAGTGG GTGAGC TG
                                  ||||||||| |||||| ||
                                  CACGTCACC CACTCG AC
                                        A     T
GAM1519  LOC196880 3'  TCAGCACCAGGACCCACTAAAC 91218    GC      GAG  T
                                  GT  AGTGGGT   CT GTGCTGA
                                  ||  |||||||   || |||||||
                                  CA  TCACCCA   GA CACGACT
                                   AA      G__  C
GAM1519  LOC219319 5'  GGCGCCCCTCACCCCCAC     95150     CAGT      CTT
                                  GTG    GGGTGAG   GTGCT
                                  |||    |||||||   |||||
                                  CAC    CCCACTC   CGCGG
                                    C____      CC_
GAM1519  LOC254057 3'  CAGGGTTCCCACCCACCCAC   98780     CA     __     TGTG
                                  GTG  GTGGGT  GAGCT    CTG
                                  |||  ||||||  |||||    |||
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                                CAC  CACCCA  CTTGG   GAC
                                  C_    CC   _____
GAM1519  LOC254532 5'  CAGCACAAGCTCTGGAGGCCAC 98447     GT____
                                GTGG    GAGCTTGTGCTG
                                ||||    ||||||||||||
                                CACC    CTCGAACACGAC
                                  GGAGGT
GAM1519  LOC254944 3'  TCAGCTGTCCCCACCCACTACA 99004    C      AGCTTGT
           C                     GTG AGTGGGTG     GCTGA
                                ||| ||||||||     |||||
                                CAC TCACCCAC     CGACT
                                  A      CCCTGT_
GAM1520  CTNS     5'  CCGGGGGACTGAGCAGCACGAG 18217     ATC       ACAG
           A                     TCTC   GCTGCTCAGT   CGG
                                ||||   ||||||||||   |||
                                AGAG   CGACGAGTCA   GCC
                                  CA_       GGGG
GAM1520  ELSPBP1   3'  CCGCCATACTGAGGCTGAG   42424     TC  TG     CA
                                CTCA  GC  CTCAGTA  GCGG
                                ||||  ||  |||||||  ||||
                                GAGT  CG  GAGTCAT  CGCC
                                  __  __     AC
GAM1520  SIMRP7   3'  CCGCACTGAGTACCTGGAGA   93969     ATCGC      ACA
                                TCTC    TGCTCAGT   GCGG
                                ||||    ||||||||  ||||
                                AGAG    ATGAGTCA   CGCC
                                  GTCC_      ___
GAM1520  LOC200933 5'  CCGCTGCCTGCACGGCGATGAG 91791          CT   TA
           A                     TCTCATCGCTG  CAG  CAGCGG
                                ||||||||||  |||  ||||||
                                AGAGTAGCGGC  GTC  GTCGCC
                                      AC   C_
GAM1521  CNTN2    3'  GAAGAACTGGAGCGAAGTG   18661     CAA  GG
                                CAC   CG  TCCAGTTCTTC
                                |||   ||  ||||||||||
                                GTG   GC  AGGTCAAGAAG
                                  AA_  G_
GAM1521  HERC2    3'  AGAAGGCCATTTGGTGTC    17425       CG   CAG
                                GACACCAA  GGTC   TTCT
                                ||||||||  ||||   ||||
                                CTGTGGTT  CCGG   AAGA
                                    TA    ___
GAM1521  HRH2     5'  AACTGGACACATTTTGGATCT  42508     CA   CGG__
                                AGA  CCAA    GTCCAGTT
                                |||  ||||    ||||||||
                                TCT  GGTT    CAGGTCAA
                                  A_   TTACA
GAM1521  AKL3L    3'  AAGAACTCTATTGGTGTC    33267       CG GTCC
                                GACACCAA  G    AGTTCTT
                                ||||||||  |    |||||||
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                                CTGTGGTT  C    TCAAGAA
                                     AT ____
GAM1521  B3GNT5    3'  AAGAACTAGGTGGTGTCT    50247        ACGGGT  _
                                AGACACCA     CC AGTTCTT
                                ||||||||     || |||||||
                                TCTGTGGT     GG TCAAGAA
                                     _______  A
GAM1521  CDT6      3'  GAACTATTTAAACCCACTGGGT 41249     A   AC    CC____
              C                  GAC CCA  GGGT     AGTTC
                                 ||| |||  ||||     |||||
                                 CTG GGT  CCCA     TCAAG
                                   _  CA    AATTTA
GAM1521  DKFZP434B103 5'  GAAAAACCCAGTGTTGGTGTC  32224          ___    CCAG
                                 GACACCAAC   GGGT    TTC
                                 |||||||||   ||||    |||
                                 CTGTGGTTG   CCCA    AAG
                                      TGA    AA__
GAM1521  FLJ13920  3'  AAGAACTGAGATATTGTCT    44963      CCAACGG   _
                                 AGACA      GTC CAGTTCTT
                                 |||||      ||| ||||||||
                                 TCTGT      TAG GTCAAGAA
                                    TA_____   A
GAM1521  FLJ22490  3'  ACTGGACCCAGTAGTGCCT    45960    A   CA  _
                                 AG CAC  AC GGGTCCAGT
                                 || |||  || |||||||||
                                 TC GTG  TG CCCAGGTCA
                                  C   A_  A
GAM1521  HU-K4     5'  AAGAAAGCCCGCTGGGTC     25357     A   A     CCAG
                                 GAC CCA CGGGT    TTCTT
                                 ||| ||| |||||    |||||
                                 CTG GGT GCCCG    AAGAA
                                   _   C     A___
GAM1521  KIAA0410  3'  AAGAACTGGACATGTGTTT    29420       CAACGG
                                 AGACAC     GTCCAGTTCTT
                                 ||||||     ||||||||||||
                                 TTTGTG     CAGGTCAAGAA
                                    TA____
GAM1521  KIAA0556  3'  GAAGAACTCACCCCAGTG     69649     CAAC    CC
                                 CAC    GGGT  AGTTCTTC
                                 |||    ||||  ||||||||
                                 GTG    CCCA  TCAAGAAG
                                   AC__    C_
GAM1521  KIAA1096  3'  AAGAACTGAAGATAACTGGTGC 69057    A     ACGG   __
              T                   AG CACCA    GTC  CAGTTCTT
                                  || |||||    |||  ||||||||
                                  TC GTGGT    TAG  GTCAAGAA
                                   _    CAA_   AA
GAM1521  KIAA1297  5'  GAAGAGCTGCCCTCAGTG    72640     CAAC   TC
                                 CAC    GGG  CAGTTCTTC
                                 |||    |||  |||||||||
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                                GTG   CCC  GTCGAGAAG
                                  ACT_  __
GAM1521  KIAA1580  5'  AAGAACTGGTGTGGTGGTGTTT 69980        A  G T
                                AGACACCA CG G CCAGTTCTT
                                |||||||| || | |||||||||
                                TTTGTGGT GT T GGTCAAGAA
                                    G  G _
GAM1521  PEGASUS   3'  GAACAGTTAGACACATTGGTGT 42690        CGG   CA___
           CT                    AGACACCAA   GTC    GTTC
                                |||||||||   |||    ||||
                                TCTGTGGTT   CAG    CAAG
                                    ACA   ATTGA
GAM1521  TTTY9    3'  ATTGGACCTATTAGTGCCT   50020    A   C  CG
                                AG CAC AA  GGTCCAGT
                                || ||| ||  ||||||||
                                TC GTG TT  CCAGGTTA
                                 C   A  AT
GAM1521  LOC151201 3'  GAAAAACTGTATCTGTTGGTGT 86475          C    C
                                ACACCAACGGGT CAGTT TTC
                                |||||||||||| ||||| |||
                                TGTGGTTGTCTA GTCAA AAG
                                      T    A
GAM1521  LOC165614 5'  AAGAACTGAAGGGACACTGGTG 83481        ACGG   ____
           TCT                   AGACACCA   GTCC   AGTTCTT
                                |||||||    ||||   |||||||
                                TCTGTGGT   CAGG   TCAAGAA
                                    CA__   GAAG
GAM1521  LOC170425 5'  GAATGATCCCATTGGTGTC   76886        C   TCCA
                                GACACCAA GGG   GTTC
                                |||||||| |||   ||||
                                CTGTGGTT CCC   TAAG
                                    A   TAG_
GAM1521  LOC219347 5'  GAAAAACTGGCTGGACAGTCT  94577     ACCAA   GT     C
                                AGAC    CGG  CCAGTT TTC
                                ||||    |||  |||||| |||
                                TCTG    GTC  GGTCAA AAG
                                  ACAG_  __     A
GAM1521  LOC51308  3'  GAAGAGGGTGCCCATTGG    33967     C   _ AG
                                CCAA GGGT CC  TTCTTC
                                |||| |||| ||  ||||||
                                GGTT CCCG GG  GAGAAG
                                  A   T  __
GAM1522  CDH12    3'  CTTATCATTTAAAGTGGTGTA  15777        CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM1522  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA       G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
```

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                                ATGTG  GAGGGTTCTT TTA
                                   AC         G
GAM1522  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT    98090       T    AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||     ||||||
                                TGGTG GGGT     TTATTC
                                   _    GTCA_
GAM1522  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
            A                    TACAC       AGAAGAATAAG
                                ||||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM1522  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM1522  HMP19     3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
            TA                    TACA    TCC    GAAGAATAAG
                                ||||    |||    ||||||||||
                                ATGT    AGG    TTTCTTATTC
                                   AAA_   ATTG
GAM1522  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68742             _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                        G
GAM1522  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM1522  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748      CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM1522  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM1522  OSBPL11   3'  CTTAATTTCCCAAGAGTGGTG  43206        CCAA    AA
                                CACCACTC    GAAG  TAAG
                                ||||||||    ||||  ||||
                                GTGGTGAG    CTTT  ATTC
                                     AACC    A_
GAM1522  YME1L1    3'  TCATTCTTGATGTGGTGTA    58438         TCC     _
                                TACACCAC   CAAGAA GA
                                ||||||||   |||||| ||
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                                ATGTGGTG  GTTCTT CT
                                    TA_    A
GAM1522 ZNF262   3' CTTATTTTGTTTGGGAGT   18723       A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                    G
GAM1522 LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_   AAGA
                                TACACCAC  CCAAG   ATA
                                ||||||||  |||||   |||
                                ATGTGGTG  GGTTC   TGT
                                    CAA   GG__
GAM1523 ARAF1    5' CGGCGTGACAGTGAAGCTG   64642       CAC   G
                                CAGCTTCAC  CACG CCG
                                |||||||||  |||| |||
                                GTCGAAGTG  GTGC GGC
                                    ACA   _
GAM1523 CDK10    5' GCTCGGCATGGCGGAGC    54834     A  CCACG
                                GCTTC CCA   GCCGAGC
                                ||||| |||   |||||||
                                CGAGG GGT   CGGCTCG
                                  C  A____
GAM1523 COL19A1  3' GGTGCTTGGTGGTGAAGC   10263         CG_
                                GCTTCACCACCA  GCC
                                ||||||||||||  |||
                                CGAAGTGGTGGT  TGG
                                    TCG
GAM1523 FOLH1    5' GCTGTGGTGGAGAAACTG   16802    C  A
                                CAG TTC CCACCACGGC
                                ||| ||| ||||||||||
                                GTC AAG GGTGGTGTCG
                                 A  A
GAM1523 CECR7    5' CGCTTTCTTTGCGGATGGTGAA 80448         _ A  CC_
           GCTG                    CAGCTTCACCA CC CGG  GAGCG
                                ||||||||||| || |||  |||||
                                GTCGAAGTGGT GG GTT  TTCGC
                                    A C  TCT
GAM1523 CLPTM1   3' CTGGGAATCATGGTGAAGCTG 8924         CCACGG G
                                CAGCTTCACCA    CC AG
                                ||||||||||     || ||
                                GTCGAAGTGGT    GG TC
                                    ACTAA_ G
GAM1523 DGCR6L   5' CGCTCGGGATGTCGTGAAGCTG 53830       CACC  G_
                                CAGCTTCAC   ACG CCGAGCG
                                |||||||||   ||| |||||||
                                GTCGAAGTG   TGT GGCTCGC
                                    C___  AG
GAM1523 FLJ10244 5' CGGCCGTGGCGGTGAAGC   36400       A
                                GCTTCACC CCACGGCCG
                                |||||||| |||||||||
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                                CGAAGTGG GGTGCCGGC
                                     C
GAM1523  FLJ21870  3'  CGTGGAGGTGGTGAAGCTG   43743          ___
                                CAGCTTCACCACC   ACG
                                ||||||||||||   |||
                                GTCGAAGTGGTGG   TGC
                                      AGG
GAM1523  FLJ22059  5'  CGAGCTGCGCAATGGTGAAGC  43055        CCA__   _
                                GCTTCACCA    CGGC CG
                                |||||||||    |||| ||
                                CGAAGTGGT    GTCG GC
                                     AACGC   A
GAM1523  FLJ22795  3'  CTTGAACCAAAATGGTGAAGCT 47634         CCAC  C_
           G                     CAGCTTCACCA   GG  CGAG
                                ||||||||||    ||  ||||
                                GTCGAAGTGGT   CC  GTTC
                                      AAAA  AA
GAM1523  FREQ     3'  CGCCCCCTGGTGGTGGTAAGC  27369     __       C  CCGA
                                GCT  TCACCACCA GG   GCG
                                |||  |||||||||  ||   |||
                                CGA  GGTGGTGGT CC   CGC
                                  AT       C  C___
GAM1523  GRIN3A   5'  CCGAGTGGAGTGAAGCTG    56780         CA   __
                                CAGCTTCAC  CCAC  GG
                                |||||||||  ||||  ||
                                GTCGAAGTG  GGTG  CC
                                     A_   AG
GAM1523  HN1L     3'  CTCAGCTAATGGGATGGCAAAG 58616    G   CA   _  AC__   C
           GTG                    CA CTT  CCA CC    GGC GAG
                                || |||  ||| ||    ||| |||
                                GT GAA  GGT GG    TCG CTC
                                 G   AC   A  GTAA   A
GAM1523  KIAA1303  3'  CGCCTGCTGTACATAGTGAAGC 66603         CACC_    CGA
           TG                     CAGCTTCAC    ACGGC   GCG
                                |||||||||    |||||   |||
                                GTCGAAGTG    TGTCG   CGC
                                     ATACA    TC_
GAM1523  SFXN5    3'  CTCAGCACAATTATGTGTGAAG 58651         _  CCACG__  C
           CTG                    CAGCTTCAC CA      GC GAG
                                |||||||||  ||      || |||
                                GTCGAAGTG GT      CG CTC
                                     T  ATTAACA  A
GAM1523  TFIP11   5'  GCGCGGATGGTGAAGCTG    25119          CCACGG   A
                                CAGCTTCACCA     CCG GC
                                ||||||||||     ||| ||
                                GTCGAAGTGGT     GGC CG
                                      A_____   G
GAM1523  VPS4A    3'  TTGGGCAATGGTGAAGGTG   26023    G      CCACG   G
                                CA CTTCACCA    GCC AG
                                || ||||||||    ||| ||
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                                GT GAAGTGGT    CGG TT
                                 G       AA___  G
GAM1523  LOC145717 3'  CTTGAACCAAAATGGTGAAGCT 67374         CCAC  C_
                                AGCTTCACCA   GG  CGAG
                                ||||||||||   ||  ||||
                                TCGAAGTGGT   CC  GTTC
                                     AAAA  AA
GAM1523  LOC220537 3'  CTTGAACCAAAATGGTGAAGCT 92423         CCAC  C_
              G                  CAGCTTCACCA   GG  CGAG
                                 ||||||||||||  ||  ||||
                                 GTCGAAGTGGT   CC  GTTC
                                      AAAA  AA
GAM1523  LOC90874  5'  GCTCGGACTTGGTGAAGC    64917        CCAC  _
                                GCTTCACCA   GG CCGAGC
                                |||||||||   || ||||||
                                CGAAGTGGT   TC GGCTCG
                                     ____  A
GAM1523  LOC91531  5'  CTCAGCTAGTAAGTACTGAAGC 66941       CC  C_ _  C
              TG                   CAGCTTCA  AC  AC GGC GAG
                                   ||||||||  ||  || ||| |||
                                   GTCGAAGT  TG  TG TCG CTC
                                      CA  AA  A   A
GAM1524  ABP1     5'  GCAGAGCGAACTGGGAGCAGAG 63799         CCGC    C
                                CTCTGTTCTT   CGCTC GC
                                ||||||||||   ||||| ||
                                GAGACGAGGG   GCGAG CG
                                     TCAA    A
GAM1524  AHCY     3'  GGCAACTGAGAAAGAACAGAG  7304         _ _ _____
                                CTCTGTTCTT C C   GCC
                                |||||||||| | |   |||
                                GAGACAAGAA G G   CGG
                                     A A TCAA
GAM1524  BSN      3'  GGCAGAGGCAAGAGCAGAG   14387        CC   G  _
                                CTCTGTTCTT  GCC CT CC
                                ||||||||||  ||| || ||
                                GAGACGAGAA  CGG GA GG
                                     __   A  C
GAM1524  CSE1L    5'  GCGGAGCGGCGGCAGGAGC   62513       _
                                GTTCTT CCGCCGCTCCGC
                                |||||| ||||||||||||
                                CGAGGA GGCGGCGAGGCG
                                   C
GAM1524  EHD4     3'  AGTGGCAAAAAAATAGAG    58362       C  CC
                                CTCTGTT TT  GCCGCT
                                ||||||| ||  ||||||
                                GAGATAA AA  CGGTGA
                                    A  AA
GAM1524  EIF2C1   3'  AGCCCAGCTGAAGAACAGA   25181         C  C__
                                TCTGTTCTTC GC   GCT
                                |||||||||| ||   |||
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                                AGACAAGAAG CG   CGA
                                     T  ACC
GAM1524  KCNK4    3'  GCAGAGCAGCAGAGCAGG    33985        TCC  C    C
                                TCTGTTCT   GC GCTC GC
                                ||||||||   || |||| ||
                                GGACGAGA   CG CGAG CG
                                     ___  A    A
GAM1524  MYO1D    3'  GCGGAACAGCCCATCCAGCAGA 72249        CTTCC_  CGC
           GT                    ACTCTGTT     GC   TCCGC
                                 ||||||||     ||   |||||
                                 TGAGACGA     CG   AGGCG
                                     CCTACC  ACA
GAM1524  NUP62    3'  GGCAAAGCAGCACAGTGTGAAT 25650        TTCC___  C   CC
           AGA                    TCTGTTC      GC GCT  GCC
                                  |||||||      || |||  |||
                                  AGATAAG      CG CGA  CGG
                                     TGTGACA  A   AA
GAM1524  RABIF    3'  GGCATGTGCAGAAAAACAGAGT 12728        C   C  C  TCC
                                ACTCTGTT TTC GC GC   GCC
                                |||||||| ||| || ||   |||
                                TGAGACAA AAG CG TG   CGG
                                     A   A  _  TA_
GAM1524  RAX      3'  GCAGGGGAGGCGGAAAAATAGA 26466        C      G   _
           GT                    ACTCTGTT TTCCGCC CTCC GC
                                 |||||||| ||||||| |||| ||
                                 TGAGATAA AAGGCGG GGGG CG
                                     A      A   A
GAM1524  RBM10    3'  GGCAGGGAAGGACAGAGT    20247          __
                                ACTCTGTTCTTCC  GCC
                                ||||||||||||  |||
                                TGAGACAGGAAGG  CGG
                                      GA
GAM1524  RGS16    3'  GGCAGGGCCCAGGAGAACAAAG 12869     C     T  GCC   C
           T                     ACT TGTTCT CC   GCTC GCC
                                 ||| |||||| ||   |||| |||
                                 TGA ACAAGA GG   CGGG CGG
                                   A     _  ACC   A
GAM1524  ROM1     3'  GGAACAGCAAAGAACAGAGT   6165          CC  CGC
                                ACTCTGTTCTT  GC   TCC
                                ||||||||||  ||   |||
                                TGAGACAAGAA  CG   AGG
                                     A_  ACA
GAM1524  SLC21A2  3'  GCAAAGCAAGTGATGAAGCAGA 20084        _ TTC   C_   CC
           GT                    ACTCTGTT C   CGC  GCT  GC
                                 |||||||| |   |||  |||  ||
                                 TGAGACGA G   GTG  CGA  CG
                                     A TA_   AA   AA
GAM1524  SMARCA5  5'  AGCCCCGCGGAAGAGCAGA   14588          C__
                                TCTGTTCTTCCGC   GCT
                                ||||||||||||   |||
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                                AGACGAGAAGGCG  CGA
                                      CCC
GAM1524 SYNGR1   3' GGCAGAGCGGCAAGGACAGGG 17507        CC     C
                                CTCTGTTCTT GCCGCTC GCC
                                |||||||||| ||||||| |||
                                GGGACAGGAA CGGCGAG CGG
                                     __     A
GAM1524 TRAM     5' AGCAGCTGGGAAGAGCAGA  27451         __ C
                                TCTGTTCTTCC GC GCT
                                |||||||||||  || |||
                                AGACGAGAAGG CG CGA
                                      GT A
GAM1524 VAT1     3' AGCAGGGAAGTACAGAGT   22088       T   GCC
                                ACTCTGT CTTCC  GCT
                                ||||||| |||||  |||
                                TGAGACA GAAGG  CGA
                                    T   GA_
GAM1524 CBX1     3' AGCAATGGAAAAGAACAGA  23308       __  CC
                                TCTGTTCT TCCG GCT
                                |||||||| ||||  |||
                                AGACAAGA AGGT CGA
                                     AA  AA
GAM1524 CDC14A   5' GGCGGAGCAGCAGCTGCAGCAG 14786   _  TCTTCC C
                                CT CTGT    GC GCTCCGCC
                                || ||||    || ||||||||
                                GA GACG    CG CGAGGCGG
                                 C  TCGA__ A
GAM1524 CDC14A   5' GGCGGAGCAGCAGCTGCAGCAG 53966   _  TCTTCC C
                                CT CTGT    GC GCTCCGCC
                                || ||||    || ||||||||
                                GA GACG    CG CGAGGCGG
                                 C  TCGA__ A
GAM1524 DKFZp547I224 5' GATGGGGAAAAAACAGAG  39956      C_  G  C
                                CTCTGTT TTCC CCG TC
                                ||||||| |||| ||| ||
                                GAGACAA AAGG GGT AG
                                     AA  _  _
GAM1524 ECE2     3' GCAGGGAAAAGGAAGAACAGAG 28732         GCCG  C
           T                     ACTCTGTTCTTCC  CTC GC
                                ||||||||||||   ||| ||
                                TGAGACAAGAAGG  GGG CG
                                      AAAA  A
GAM1524 FLJ10648 3' CGAAGCAAACCAAGAACAGAG 36890        CCGCC  C
                                CTCTGTTCTT    GCT CG
                                ||||||||||    ||| ||
                                GAGACAAGAA    CGA GC
                                      CCAAA  A
GAM1524 GRIN3A   3' GCGGAGCAAGTGCCAAGCAGA 56783      CTTC  C_
                                TCTGTT   CGC GCTCCGC
                                ||||||   |||  |||||||
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                                AGACGA   GTG  CGAGGCG
                                   ACC_   AA
GAM1524  INE1     3'  GCAGGTGTTAGACGAAAGAACA 14757        C  CC__  T  _
              GA                    TCTGTTCTT CG    GC CC GC
                                    ||||||||| ||    || || ||
                                    AGACAAGAA GC    TG GG CG
                                       A  AGAT  T  A
GAM1524  KIAA0410 3'  GCAGAGCTTAAGAATAGA    29426        CCGCC    C
                                    TCTGTTCTT    GCTC GC
                                    |||||||||    |||| ||
                                    AGATAAGAA    CGAG CG
                                       TT___    A
GAM1524  KIAA0964  5'  GCGGAACGGCAGAGCGGG    30448        TCC    C
                                    TCTGTTCT   GCCG TCCGC
                                    ||||||||   |||| |||||
                                    GGGCGAGA   CGGC AGGCG
                                       ___    A
GAM1524  KIAA1218  5'  AGCAGCACAAAAGAAACAGAGT 95958        _   CC__  C
                                    ACTCTGTT CTT    GC GCT
                                    |||||||| |||    || |||
                                    TGAGACAA GAA    CG CGA
                                       A   AACA  A
GAM1524  KIAA1322  3'  GGCAGCCGAGAAGAACAGA    73112         _ CC   _
                                    TCTGTTCTTC CG  GCT CC
                                    |||||||||| ||  ||| ||
                                    AGACAAGAAG GC  CGA GG
                                       A  __   C
GAM1524  KIAA1391  3'  AGTGGAGAAAAACAGAGT    67851        C   CG
                                    ACTCTGTT TTC  CCGCT
                                    |||||||| |||  |||||
                                    TGAGACAA AAG  GGTGA
                                       A   A_
GAM1524  MGC13251  3'  AGCAGCCATAGAAAGGACAGA  52134         _ C___  C
                                    TCTGTTCTT C    GC GCT
                                    ||||||||| |    || |||
                                    AGACAGGAA G    CG CGA
                                       A ATAC  A
GAM1524  MYH7B    3'  GGCGGAGCAGCAGGCCAACA   71058      CTT  _  C
                                    TGTT   CC GC GCTCCGCC
                                    ||||   || || ||||||||
                                    ACAA   GG CG CGAGGCGG
                                      CC_  A  A
GAM1524  NCOA2    3'  GGCAAGGAGAAGAGCAAAGT   22572     C       CG  GCT
                                    ACT TGTTCTTC  CC   CC
                                    ||| ||||||||  ||   ||
                                    TGA ACGAGAAG  GG   GG
                                      A       A_  AAC
GAM1524  PTRF     3'  GGCAGTGGGGAAGACAGAG   64242       T    G    _
                                    CTCTGT CTTCC CCGCT CC
                                    |||||| ||||| ||||| ||
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                                GAGACA GAAGG GGTGA GG
                                  _    _    C
GAM1524  RHOBTB2  3'  AGCAGGAGGAAAAGCAGAGT  61593       C   G  _
                                ACTCTGTT TTCC CC GCT
                                |||||||| |||| || |||
                                TGAGACGA AAGG GG CGA
                                    A   A  A
GAM1524  TAGAP    3'  AGACTGCAAGGAACAGAGT   55099        CC  CG_
                                ACTCTGTTCTT  GC   CT
                                ||||||||||  ||   ||
                                TGAGACAAGGA  CG   GA
                                      A_  TCA
GAM1524  VELI1    3'  AGTGTAAGAAGAATAAAGT   17417    C      CGC
                                ACT TGTTCTTC   CGCT
                                ||| ||||||||   ||||
                                TGA ATAAGAAG   GTGA
                                  A       AAT
GAM1524  LOC145783 5'  GCGGAGCGACGGAGACACAG   77949     TC    C
                                CTGT  TTCCG CGCTCCGC
                                ||||  ||||| ||||||||
                                GACA  GAGGC GCGAGGCG
                                  CA    A
GAM1524  LOC150157 3'  AGCAAATGGAAAAGAACAGA   86020       __   CC_
                                TCTGTTCT  TCCG   GCT
                                ||||||||  ||||   |||
                                AGACAAGA  AGGT   CGA
                                    AA    AAA
GAM1524  LOC151516 5'  GGCGGAGCTTCCAGAACAAAG  81068    C     TCCGCC
                                CT TGTTCT     GCTCCGCC
                                || ||||||     ||||||||
                                GA ACAAGA     CGAGGCGG
                                 A     CCTT__
GAM1524  LOC153769 3'  GGCGGAGCAGCATGAGAAAGA  81807     G    CC  C
                                TCT TTCTT  GC GCTCCGCC
                                ||| |||||  || ||||||||
                                AGA AAGAG  CG CGAGGCGG
                                  _    TA  A
GAM1524  LOC161734 3'  GATGGGGAAAAAACAGAG    88467       C_   G   C
                                CTCTGTT  TTCC CCG TC
                                |||||||  |||| ||| ||
                                GAGACAA  AAGG GGT AG
                                    AA   _  _
GAM1524  LOC167026 5'  GGCGGAGCGGCGGGCGGA    88620      TCTT
                                TCTGT   CCGCCGCTCCGCC
                                |||||   |||||||||||||
                                AGGCG   GGCGGCGAGGCGG
                                  _____
GAM1524  LOC196890 3'  AGCAAATGGAAAAGAACAGA   91222       __   CC_
                                TCTGTTCT  TCCG   GCT
                                ||||||||  ||||   |||
```

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                                AGACAAGA  AGGT   CGA
                                    AA    AAA
GAM1524  LOC200731 5'  AGCACTGAAGAACAGAGT    91688          CGCC
                                ACTCTGTTCTTC    GCT
                                ||||||||||||   |||
                                TGAGACAAGAAG    CGA
                                      TCA_
GAM1524  LOC221504 5'  CGGAGCGGCGGGGCAGGAG   94020     GTTC
                                CTCT    TTCCGCCGCTCCG
                                ||||    ||||||||||||
                                GAGG    GGGGCGGCGAGGC
                                  AC__
GAM1524  LOC221663 5'  GCAAAGCCCAGAACAGAGT   95462         TCCGCC   CC
                                ACTCTGTTCT     GCT  GC
                                ||||||||||     |||  ||
                                TGAGACAAGA     CGA  CG
                                      CC_____   AA
GAM1524  LOC256310 3'  GGCAGAGCAGCGGGAGCAGGAG 98102      GTT      C    C
                                CTCT   CTTCCGC GCTC GCC
                                ||||   ||||||| |||| |||
                                GAGG   GAGGGCG CGAG CGG
                                  AC_      A    A
GAM1524  LOC51762  3'  GGCCTAGCAAAAGAACAGA   33708         CCGCC   CC
                                TCTGTTCTT    GCT  GCC
                                |||||||||    |||  |||
                                AGACAAGAA    CGA  CGG
                                     AA___   TC
GAM1524  LOC91266  5'  GGCTGAGGAAAAACAGAGT   66024        ___     C
                                ACTCTGT   TCTTC GCC
                                |||||||   ||||| |||
                                TGAGACA   AGGAG CGG
                                    AAA    T
GAM1525  C21orf2   3'  CGACCTTCCTAGTGCCCCCCAA 18204         CAA__   AT___    A   ___
           AACCAAGG                CCTTGGTT    GGG    GGAA GTC   G
                                |||||||||    |||    |||| |||   |
                                GGAACCAA    CCC    CCTT CAG   C
                                    AACCC   GTGAT    C   __
GAM1525  FBXW7    3'  GACTTTCTAAATCAAACCAGG  54409       CAA  GA
                                CTTGGTT   GG  TGGAAAGTC
                                |||||||   ||  |||||||||
                                GGACCAA   CT  ATCTTTCAG
                                    A__  AA
GAM1525  GPX3     3'  CCTCCCTGAGATCAACCAAGG  10868        ___  A_    T
                                CCTTGGT   TC  AGGGA GG
                                |||||||   ||  ||||| ||
                                GGAACCA   AG  TCCCT CC
                                    ACT  AG    _
GAM1525  HSPC126   3'  GACTTTCTTTTTAAAGCCAA   27176       CAAG   T
                                TTGGTT    GGA GGAAAGTC
                                ||||||    ||| ||||||||
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                                AACCGA   TTT TCTTTCAG
                                   AA__  T
GAM1525 JAK2    3' GACCTTCATTCTGAGACCAA  18316      CAA      AA
                                TTGGTT  GGGATGGA GTC
                                ||||||  |||||||| |||
                                AACCAG  TCTTACTT CAG
                                   AG_      C_
GAM1525 KLK4    3' TCCTCCCTCAAACCAAGG   63532       CA   T
                                CCTTGGTT AGGGA GGA
                                |||||||| ||||| |||
                                GGAACCAA TCCCT CCT
                                    AC   _
GAM1525 RPE65   3' ACTTTTTCTCAAACCAGGG  6167        CAA  TG
                                CCTTGGTT  GGGA GAAAGT
                                |||||||  ||||  ||||||
                                GGGACCAA  CTCT TTTTCA
                                    A__   __
GAM1525 FLJ11186 3' ACTTCCAACTCTGAACCAAG  37723       A  A   A
                                CTTGGTTCA GGG TGGAA GT
                                ||||||||| ||| ||||| ||
                                GAACCAAGT CTC ACCTT CA
                                    _  A   _
GAM1525 FLJ20085 3' CTGTCCTTAAACCTAGG    35007    T  CA
                                CCT GGTT  AGGGATGG
                                ||| ||||  ||||||||
                                GGA CCAA  TTCCTGTC
                                  T  A_
GAM1525 FLJ20986 5' GACATGCCCCCCCGAATCAAGG 44836       AA  AT  AAA
                                CCTTGGTTC  GGG  GG  GTC
                                |||||||||  |||  ||  |||
                                GGAACTAAG  CCC  CC  CAG
                                    __  CC  GTA
GAM1525 FLJ23142 5' ACTTTCCATAACAACCAAG   45026      CAAGGG
                                CTTGGTT    ATGGAAAGT
                                |||||||    |||||||||
                                GAACCAA    TACCTTTCA
                                   CAA___
GAM1525 KIAA0793 3' GACCTTCCATCTGGTGAACCAA 29694       AG      A
          G                      CTTGGTTCA  GGATGGAA GTC
                                |||||||||  |||||||| |||
                                GAACCAAGT  TCTACCTT CAG
                                    GG      C
GAM1525 KIAA1775 3' CCAGGAACTTGGACCAAGG   53543         GGA_
                                CCTTGGTTCAAG   TGG
                                ||||||||||||   |||
                                GGAACCAGGTTC   ACC
                                      AAGG
GAM1525 KIAA1843 3' GACTCTCCAGAAGGGAGCCAAG 62883       AAGGGA   A
                                CTTGGTTC    TGGA AGTC
                                ||||||||    |||| ||||
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                                GAACCGAG     ACCT TCAG
                                    GGAAG_   C
GAM1525  KIAA1940  3'  GACCTTCCATCCCTGAATACAA 80784      _    A       A
              GG                    CCTTG GTTCA GGGATGGAA GTC
                                    ||||| ||||| ||||||||| |||
                                    GGAAC TAAGT CCCTACCTT CAG
                                      A    _       C
GAM1525  MGC12837  3'  ACTTCCTCAAAGCCCAAAGCCA 52167       CAA   AT____   A
              AGG                   CCTTGGTT   GGG     GGAA GT
                                    ||||||||   |||     |||| ||
                                    GGAACCGA   CCC     CCTT CA
                                        AA_   GAAACT   _
GAM1525  MGC19556  5'  GACTTCATGTCTCAAACCAAGG 54340       CAA     GA
                                    CCTTGGTT   GGGATG  AAGTC
                                    ||||||||   ||||||  |||||
                                    GGAACCAA   CTCTGT  TTCAG
                                        A__     AC
GAM1525  MGC22014  3'  ACTTCAACATACCCTGGACCAA 65109       A   _   GA_
                                    TTGGTTCA GGG ATG   AAGT
                                    |||||||| ||| |||   ||||
                                    AACCAGGT CCC TAC   TTCA
                                        _   A   AAC
GAM1525  MGC32104  3'  CCCCCCAAGATTGAACCAAG   59066         ____   AT
                                    CTTGGTTCAA    GGG  GG
                                    ||||||||||    |||  ||
                                    GAACCAAGTT    CCC  CC
                                          AGAA   C_
GAM1525  PDZ-      3'  ACTCCCTTTGGCCCTGAACCAG 65627         A   AT__  AA
              GG                    CCTTGGTTCA GGG    GG  AGT
                                    |||||||||| |||    ||  |||
                                    GGGACCAAGT CCC    TC  TCA
                                          _   GGTT  CC
GAM1525  LOC147645 3'  GACTCTCTCTCTAAACTAAGG  79069       CA    T   AA
                                    CCTTGGTT  AGGGA GGA  GTC
                                    ||||||||  ||||| |||  |||
                                    GGAATCAA  TCTCT TCT  CAG
                                        A_    C   __
GAM1525  LOC153688 3'  GACCCTGCCCCCAAACCAAGG  87314       CAA   AT  AAA
                                    CCTTGGTT   GGG  GG   GTC
                                    ||||||||   |||  ||   |||
                                    GGAACCAA   CCC  TC   CAG
                                        AC_   CG  C__
GAM1525  LOC196812 3'  ACTTTTGTTCCCACACCAAGG  91122       TCAA    TG
                                    CCTTGGT    GGGA  GAAAGT
                                    |||||||    ||||  ||||||
                                    GGAACCA    CCCT  TTTTCA
                                        CA__    TG
GAM1526  MAP3K7IP2 3'  ACCAGCAACAGCAGCAGT    31354        A  CA_
                                    ACTGCTGC TG   CTGGT
                                    |||||||| ||   |||||
```

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                                TGACGACG AC   GACCA
                                    _ AAC
GAM1526  PMSCL1    5'  AGTCACCGCAGCAGTTGTC   18527          A_  C
                                GACAACTGCTGC  TG ACT
                                ||||||||||||  || |||
                                CTGTTGACGACG  AC TGA
                                    CC  _
GAM1526  RAD52     3'  ACCTGCCTCAGCAATTGTCTA  57017       C    CAT   CT
                                TAGACAA TGCTG   GCA  GGT
                                |||||||  |||||   |||  |||
                                ATCTGTT ACGAC   CGT  CCA
                                    A    TC_  __
GAM1526  RAD52     3'  ACCTGCCTCAGCAATTGTCTA  57041       C    CAT   CT
                                TAGACAA TGCTG   GCA  GGT
                                |||||||  |||||   |||  |||
                                ATCTGTT ACGAC   CGT  CCA
                                    A    TC_  __
GAM1526  RAD52     3'  ACCTGCCTCAGCAATTGTCTA  57048       C    CAT   CT
                                TAGACAA TGCTG   GCA  GGT
                                |||||||  |||||   |||  |||
                                ATCTGTT ACGAC   CGT  CCA
                                    A    TC_  __
GAM1526  RAD52     3'  ACCTGCCTCAGCAATTGTCTA  12755       C    CAT   CT
                                TAGACAA TGCTG   GCA  GGT
                                |||||||  |||||   |||  |||
                                ATCTGTT ACGAC   CGT  CCA
                                    A    TC_  __
GAM1526  BHC80     3'  ACCAGTGTGTGCCTGCAG    34012      T_
                                CTGC  GCATGCACTGGT
                                ||||  ||||||||||||
                                GACG  CGTGTGTGACCA
                                  TC
GAM1526  KIAA1364  3'  ACCAGTGCACCGGGCCGTCT   64341     AACT   GCA
                                AGAC    GCT   TGCACTGGT
                                ||||    |||   |||||||||
                                TCTG    CGG   ACGTGACCA
                                  C___   GCC
GAM1526  KIAA1750  3'  ACCAGTGCATGAGACACACACC 68805     ACAAC  _  G
            TA                    TAG    TG CT CATGCACTGGT
                                |||    || || ||||||||||||
                                ATC    AC GA GTACGTGACCA
                                  CACAC  A  _
GAM1526  SARM      3'  ACCAGTGCATACCACCATGCCT 31274     A  AC  C  C_
            G                     TAG CA  TG TG  ATGCACTGGT
                                ||| ||  || ||  ||||||||||
                                GTC GT  AC AC  TACGTGACCA
                                  C  __  C  CA
GAM1526  LOC145786 5'  ACCATATACAACCAGTTGTCTA 84489          C_  C   CAC
                                TAGACAACTG  TG ATG   TGGT
                                |||||||||  || |||   ||||
```

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                                ATCTGTTGAC  AC TAT   ACCA
                                      CA  A  ___
GAM1526 LOC90806 3' ACCAGTGCCTGCCAGTGTCTA 58611       A   CT   T
                                TAGACA CTG  GCA GCACTGGT
                                |||||| |||  ||| ||||||||
                                ATCTGT GAC  CGT CGTGACCA
                                   _  __  C
GAM1526 LOC91301 5' GCACACAGCAGTTGCCTA    66147     A       CA
                                TAG CAACTGCTG  TGC
                                ||| |||||||||  |||
                                ATC GTTGACGAC  ACG
                                  C        AC
GAM1527 ATP8B2   5' GTAAGCTTGCCAAGTTTGA   65843      G      G_
                                TCAAA TTGGCAAG  TGC
                                ||||| ||||||||  |||
                                AGTTT AACCGTTC  ATG
                                   G       GA
GAM1527 EGLN1    5' GCCACCTTGCAACCTTGA    42149     A   G     _
                                TCAA GTTG CAAGGTG C
                                |||| |||| ||||||| |
                                AGTT CAAC GTTCCAC G
                                  C   _      C
GAM1527 GCH1     3' AGTCCCATCTCTGCCACTTTGA 5678         T   _    C
           T                     ATCAAAGT GGCA AGGTG GGACT
                                |||||||| |||| ||||| |||||
                                TAGTTTCA CCGT TCTAC CCTGA
                                   _   C   _
GAM1527 PRKAR2A  3' CCACACCTCCACTTTG      16037       T  CA    C
                                CAAAGT GG  AGGTG GG
                                |||||| ||  ||||| ||
                                GTTTCA CC  TCCAC CC
                                   _ __    A
GAM1527 SON      3' AGCCCAGCTTTGCCAGC     55225          GC  A
                                GTTGGCAAGGT  GG CT
                                ||||||||||  || ||
                                CGACCGTTTCG  CC GA
                                      A_  C
GAM1527 SON      3' AGCCCAGCTTTGCCAGC     57986          GC  A
                                GTTGGCAAGGT  GG CT
                                ||||||||||  || ||
                                CGACCGTTTCG  CC GA
                                      A_  C
GAM1527 SON      3' AGCCCAGCTTTGCCAGC     57989          GC  A
                                GTTGGCAAGGT  GG CT
                                ||||||||||  || ||
                                CGACCGTTTCG  CC GA
                                      A_  C
GAM1527 COE2     5' AGTCCGCACCTCGCCAGTGA  64904     AAG    A
                                TCA   TTGGC AGGTGCGGACT
                                |||   ||||| ||||||||||
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                                AGT   GACCG TCCACGCCTGA
                                  ___     C
GAM1527  DIS3     3'  TCTCCTTTGCCATCTTT     30923      T       TGC
                                AAAG TGGCAAGG   GGA
                                |||| |||||||   |||
                                TTTC ACCGTTTC   TCT
                                  T       C__
GAM1527  FBXO29   3'  AGTCCCACGTGCTGCCAACT   77262        AG__   C
                                AGTTGGCA    GTG GGACT
                                ||||||||    ||| |||||
                                TCAACCGT    CAC CCTGA
                                     CGTG   _
GAM1527  FLJ11722 3'  CCTTCTCCCGGCAACTTTGAT  46999         G AA  TGC_
                                ATCAAAGTTG C  GG    GG
                                |||||||||| |  ||    ||
                                TAGTTTCAAC G  CC    CC
                                      _ GC  TCTT
GAM1527  FLJ32894 3'  GCTTCTTGCCAACTCTGGT    58999      A         T
                                ATCA AGTTGGCAAGG GC
                                |||| ||||||||||| ||
                                TGGT TCAACCGTTCT CG
                                  C         T
GAM1527  KIAA0337 3'  AGCCCACACGCAGACTTTGA   29475        G  AAG   C  A
                                TCAAAGTT GC   GTG GG CT
                                |||||||| ||   ||| || ||
                                AGTTTCAG CG   CAC CC GA
                                     A  CA_   _ _
GAM1527  PEX16    3'  AGCCCGCACCTTGTCACT     55155     T         A
                                AGT GGCAAGGTGCGG CT
                                ||| ||||||||||| ||
                                TCA CTGTTCCACGCC GA
                                  _         C
GAM1527  LOC163682 5'  GCCACCTTTGCCAACCTCGAT  88408     AAA       _   _
                                ATC   GTTGGCAA GGTG C
                                |||   |||||||| |||| |
                                TAG   CAACCGTT CCAC G
                                  CTC       T   C
GAM1527  LOC221025 5'  GCCTACACCAACTTTGAT     94788          CA_
                                ATCAAAGTTGG   AGGT
                                ||||||||||   ||||
                                TAGTTTCAACC   TCCG
                                      ACA
GAM1528  SCAMP1   3'  GCTAAATAAATATTCTCC     18013     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1528  SCAMP1   3'  GCTAAATAAATATTCTCC     54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
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                                CCT TTATAA TAAATCG
                                  C     A
GAM1528 NX-17    3' TGAATATCAGCCCCTAATA   40706        ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM1528 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
              TA                  TATTAGGGATAATATTCATTTAGC
                                  ||||||||||||||||||||||||
                                  ATAATCCCTATTATAAGTAAATCG

GAM1529 GPD1     3' TCATGCCACCACATTTG     60398       C       C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A      _
GAM1529 IL5RA    5' TCGCATGGCCACCGCATTT    6906           AT__
                                AAATGCGGTGGC   CGA
                                ||||||||||||   |||
                                TTTACGCCACCG   GCT
                                     GTAC
GAM1529 MYO1C    3' TGCCGATGCCAAATATTTG   61873       CGG       A
                                TAAATG   TGGCATCG CA
                                ||||||   |||||||| ||
                                GTTTAT   ACCGTAGC GT
                                   AA_       C
GAM1529 C6orf37  3' TGTCACACTGCATTTA      68097          GCATC
                                TAAATGCGGTG    GACA
                                ||||||||||     ||||
                                ATTTACGTCAC    CTGT
                                     A____
GAM1529 DNAJC6   3' TTGCAGAACCACCGCATT    29498         CA  GA
                                AATGCGGTGG  TC  CAA
                                ||||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                     A_  AC
GAM1529 FLJ11210 3' GTCGATGTGCATGCTTTTA   60319     T   GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM1529 FLJ12476 3' TCGATCTTCTGCATTTA     43270         T  C
                                TAAATGCGG GG ATCGA
                                ||||||||| || |||||
                                ATTTACGTC TC TAGCT
                                     T  _
GAM1529 KIAA1034 3' TCGATGGCATCCGCATTTG   63134          _  G
                                TAAATGCGG TG CATCGA
                                ||||||||| || ||||||
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                                GTTTACGCC AC GTAGCT
                                     T  G
GAM1529  KIAA1987  3'  TCATGTAACTGCATTTA     89391          G    C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                     A   _
GAM1529  MGC16063  3'  TGTCCTGGCCACTGCATT    54929           ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                     GTC
GAM1529  LOC147949 3'  TGTCAGATGTCCACATTGCA   79279      __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T    A
GAM1529  LOC150577 3'  GTCCTCACCGCATTTG      86258           CATC
                                TAAATGCGGTGG    GAC
                                ||||||||||||    |||
                                GTTTACGCCACT    CTG
                                     C___
GAM1529  LOC158219 3'  TGTGTGTCACCACATTT     82694       C       CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                  A       __
GAM1529  LOC202020 3'  TGTCTCACCACATTTA      90605       C    CATC
                                TAAATG GGTGG    GACA
                                ||||||| |||||    ||||
                                ATTTAC CCACT    CTGT
                                   A    _____
GAM1529  LOC90826  5'  TGTCGATGCAGGTTTATTTG   64788       CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                   TTGGA
GAM1529  LOC93587  3'  TTGTCTTTACCTGCATTTA    73042        _    CATC
                                TAAATGC GGTGG    GACAA
                                ||||||| |||||    |||||
                                ATTTACG CCATT    CTGTT
                                    T    T___
GAM1530  B4GALT4   5'  CAGTGAAGCAGAGAGATAGATA 15026         GG_  CA
           TTA                    TAGTATTTG   CTC  CTTCACTG
                                |||||||||   |||  ||||||||
                                ATTATAGAT   GAG  GAAGTGAC
                                     AGA   AC
GAM1530  SLC17A2   3'  TGGGGTGGAACCCAGATACTA  20693          C
                                TAGTATTTGGG TCCACTTCA
                                |||||||||| |||||||||
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                                ATCATAGACCC AGGTGGGGT
                                      A
GAM1530  TNF      3'  CAGTGAAGTGCTGGCAACCA   92706     __   C_
                                TGG  GCT  CACTTCACTG
                                |||  |||  ||||||||||
                                ACC  CGG  GTGAAGTGAC
                                  AA   TC
GAM1530  FLJ11132  3'  CAGTGAAGTGGAGTCAGATCCT 37659     T     G
           A                     TAG ATTTGG CTCCACTTCACTG
                                |||  ||||||  ||||||||||||
                                ATC TAGACT GAGGTGAAGTGAC
                                  C     _
GAM1530  FLJ11155  3'  CAGTGAAGTGAGGCAGAAATAC 37692       GG  TC
                                GTATTT  GC  CACTTCACTG
                                ||||||  ||  ||||||||||
                                CATAAA  CG  GTGAAGTGAC
                                    GA  GA
GAM1530  FLJ14768  3'  AGGGGAGCCCAAATCTA     52673     T         A
                                TAG ATTTGGGCTCC CTT
                                |||  ||||||||||| |||
                                ATC TAAACCCGAGG GGA
                                  _         _
GAM1530  FLJ20436  5'  CAGTGAAGCCAGCCGAATACTA 35624          G  CCA
                                TAGTATTTGG CT   CTTCACTG
                                ||||||||||  ||   ||||||||
                                ATCATAAGCC GA   GAAGTGAC
                                      _  CC_
GAM1530  LOC145447  3'  TGAAGACTTGGCCCAAACAC   77721     A       CCA_
                                GT TTTGGGCT    CTTCA
                                ||  ||||||||    |||||
                                CA AAACCCGG    GAAGT
                                 C       TTCA
GAM1530  LOC150135  3'  AGTGAAATGCAAATGCTA    80389         GGCTC  C
                                TAGTATTTG     CA TTCACT
                                |||||||||     ||  ||||||
                                ATCGTAAAC     GT AAGTGA
                                      _____  A
GAM1530  LOC257551  3'  CAGTGAAGTGCTGGCAACCA   99555     __   C_
                                TGG  GCT  CACTTCACTG
                                |||  |||  ||||||||||
                                ACC  CGG  GTGAAGTGAC
                                  AA   TC
GAM1530  LOC257601  3'  CAGTGAAGTGCTGGCAACCA   99649     __   C_
                                TGG  GCT  CACTTCACTG
                                |||  |||  ||||||||||
                                ACC  CGG  GTGAAGTGAC
                                  AA   TC
GAM1531  ADCY6    3'  GCCCCAGTGCTCCATGCCA   40956         T  CCATCG   A
                                TGGCATGG GC     TGG GC
                                ||||||||  ||     |||  ||
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                                ACCGTACC CG     ACC CG
                                    T  TG____   C
GAM1531  AVP      5'  CTCCACGACGGCGGCTGCC   6674      TGG   CA
                                GGCA   TGCC  TCGTGGAG
                                ||||   ||||  ||||||||
                                CCGT   GCGG  AGCACCTC
                                  CG_   C_
GAM1531  CDH17    3'  GGGTTTACAGGCACCCACCA  15786    CAT    CATC   G
                                TGG   GGTGCC   GTGGA CC
                                |||   ||||||   ||||| ||
                                ACC   CCACGG   CATTT GG
                                  AC_     A___    G
GAM1531  IGF1     3'  CTGGGATTACAGGCACCCACCA 7072     CAT    C___   G
                                TGG   GGTGCC   ATC TGG
                                |||   ||||||   ||| |||
                                ACC   CCACGG   TAG GTC
                                  AC_     ACAT   G
GAM1531  KLF1     5'  GGCCCAGGGTGGGCACCAGCCA 22671     A       G   A
                                TGGC TGGTGCCCATC TGG GCC
                                |||| ||||||||||| ||| |||
                                ACCG ACCACGGGTGG ACC CGG
                                  _        G   _
GAM1531  LNK      3'  CTGGGATTACAAGCACCAGCCA 19643     A     CC___   G
                                TGGC TGGTGC    ATC TGG
                                |||| ||||||    ||| |||
                                ACCG ACCACG    TAG GTC
                                  _     AACAT   G
GAM1531  STARD5   3'  CTCGGCCTGGACACCATGC   48316       C   TC  G
                                GCATGGTG CCA  GT GAG
                                |||||||| |||  || |||
                                CGTACCAC GGT  CG CTC
                                    A   C_  G
GAM1531  TAP2     3'  GCTCCACGACAAACTTTCTGCC 6779      T__   GCCCA
                                GGCA   GGT    TCGTGGAGC
                                ||||   |||    |||||||||
                                CCGT   TCA    AGCACCTCG
                                  CTT   AAC__
GAM1531  AP3S2    3'  CTGGGATTACAGGCACCCACCA 20650     CAT    C___   G
                                TGG   GGTGCC   ATC TGG
                                |||   ||||||   ||| |||
                                ACC   CCACGG   TAG GTC
                                  AC_     ACAT   G
GAM1531  C11orf17 3'  GCACTACAGGCACCCGCCA   40582     AT     CATC   A
                                TGGC  GGTGCC   GTGG GC
                                ||||  ||||||   |||| ||
                                ACCG  CCACGG   CATC CG
                                  C_     A___    A
GAM1531  CST7     5'  GGCTCGGCACGGGCACCAACCA 14684     CA      ATC  G
                                TGG  TGGTGCCC   GT GAGCC
                                |||  ||||||||   || |||||
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                                ACC  ACCACGGG   CG CTCGG
                                  A_       CA_  G
GAM1531  DKFZP434K028 3'  GCCCCCGGCCCCATGCCA    94861        T   CATC T  A
                                TGGCATGG GCC    G GG GC
                                |||||||| |||    | || ||
                                ACCGTACC CGG    C CC CG
                                    C   _____ _  C
GAM1531  DOCK3    3'  CACCATGGACTCCATGCCA    67091        TGC    C
                                TGGCATGG   CCAT GTG
                                ||||||||   |||| |||
                                ACCGTACC   GGTA CAC
                                    TCA    C
GAM1531  FLJ20045  3'  CTGGGATTACAGGCACATGCCA 34883        G   C___   G
                                TGGCATG TGCC    ATC TGG
                                ||||||| ||||    ||| |||
                                ACCGTAC ACGG    TAG GTC
                                   _    ACAT   G
GAM1531  FLJ20257  5'  GGCCCCACGGTGCCACCGCACC 39488     CA    CC       A
              A                    TGG  TGGTG  CATCGTGG GCC
                                ||| |||||  |||||||| |||
                                ACC  GCCAC  GTGGCACC CGG
                                  AC    C_       C
GAM1531  FLJ30532  3'  CTGGGATTACAGGCACCCACCA 59219     CAT     C___   G
                                TGG   GGTGCC    ATC TGG
                                |||   ||||||    ||| |||
                                ACC   CCACGG    TAG GTC
                                  AC_     ACAT   G
GAM1531  GIT2     3'  GCTCCACGCACATCACCACCCA 29413     CA     CCCAT
                                TGG  TGGTG    CGTGGAGC
                                |||  |||||    ||||||||
                                ACC  ACCAC    GCACCTCG
                                  C_    TACAC
GAM1531  IKKE     3'  GCTGAGACTGGGCACCAGGCCA 26594      A       _  GTGG
                                TGGC TGGTGCCCA TC    AGC
                                |||| ||||||||| ||    |||
                                ACCG ACCACGGGT AG    TCG
                                   G       C  AG__
GAM1531  JM11     3'  CTGGGATTACAGGCACACGCCA 54357      ATG    C___   G
                                TGGC   GTGCC    ATC TGG
                                ||||   |||||    ||| |||
                                ACCG   CACGG    TAG GTC
                                   CA_    ACAT   G
GAM1531  KIAA0089  3'  GGCCCCATGGCATCCACACCA  70510     CA  _   CATC    A
                                TGG  TGG TGCC    GTGG GCC
                                |||  ||| ||||    |||| |||
                                ACC  ACC ACGG    TACC CGG
                                  AC   T    _____    C
GAM1531  KIAA0831  3'  CTGGGATTATAGGCACCTGCCA 30635       T     C___   G
                                TGGCA GGTGCC    ATC TGG
                                ||||| ||||||    ||| |||
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                                ACCGT CCACGG   TAG GTC
                                  _     ATAT   G
GAM1531 KIAA0931 3' CTGGGATTACAGGCACCTGCCA 68010      T     C___   G
                                TGGCA GGTGCC   ATC TGG
                                ||||| ||||||   ||| |||
                                ACCGT CCACGG   TAG GTC
                                  _     ACAT   G
GAM1531 KIAA1032 3' GGCTCGGGGGGCTCCACGCCA 66727     A   T   AT GTG
                                TGGC TGG GCCC  C   GAGCC
                                |||| ||| ||||  |   |||||
                                ACCG ACC CGGG  G   CTCGG
                                  C   T   GG ___
GAM1531 KIAA1548 3' GCACTCACAGGCACCACACA  40880    GCA     CATC   _ A
                                TG   TGGTGCC   GTG G GC
                                ||   |||||||   ||| | ||
                                AC   ACCACGG   CAC C CG
                                 AC_     A___   T A
GAM1531 KIAA1617 3' CTGGGATTACAGGCACCCACCA 93076    CAT     C___   G
                                TGG   GGTGCC   ATC TGG
                                |||   ||||||   ||| |||
                                ACC   CCACGG   TAG GTC
                                  AC_     ACAT   G
GAM1531 KIAA1814 3' CTACAGGACGGGCACCAGCCA  70877     A      A  G  G
                                TGGC TGGTGCCC TC TG AG
                                |||| |||||||| || || ||
                                ACCG ACCACGGG AG AC TC
                                  _      C  G  A
GAM1531 MGC13204 3' CTGGGATTACAGGCACCAGCCA 49629     A     C___   G
                                TGGC TGGTGCC   ATC TGG
                                |||| |||||||   ||| |||
                                ACCG ACCACGG   TAG GTC
                                  _     ACAT   G
GAM1531 SEEK1    5' ACCGTGGGCTCCATGCCA    26806        T     C
                                TGGCATGG GCCCAT GT
                                |||||||| |||||| ||
                                ACCGTACC CGGGTG CA
                                     T     C
GAM1531 SYNE-1   3' CTCCCAAGCACCATGTCA    31621          CCATCGT
                                TGGCATGGTGC      GGAG
                                ||||||||||       ||||
                                ACTGTACCACG      CCTC
                                      AAC_____
GAM1531 TGIF2    3' CTGGGATTATAGGCACCCGCCA 41748     AT     C___   G
                                TGGC  GGTGCC   ATC TGG
                                ||||  ||||||   ||| |||
                                ACCG  CCACGG   TAG GTC
                                  C_     ATAT   G
GAM1531 TRIM6    3' CTGGGATTACAGGCACCCACCA 55178     CAT     C___   G
                                TGG   GGTGCC   ATC TGG
                                |||   ||||||   ||| |||
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                                ACC   CCACGG    TAG GTC
                                  AC_     ACAT   G
GAM1531  VDU1     3'  CTGGGATTACAGGCACCTGCCA 31123      T     C___   G
                                TGGCA GGTGCC    ATC TGG
                                ||||| ||||||    ||| |||
                                ACCGT CCACGG    TAG GTC
                                   _     ACAT   G
GAM1531  LOC149670 5'  GCTTTCTGGACACCATGCC    80307        C   TCGT
                                GGCATGGTG CCA    GGAGC
                                ||||||||| |||    |||||
                                CCGTACCAC GGT    TTTCG
                                     A   C___
GAM1531  LOC150271 3'  GGCTGCCACAGCACCATGCCA  86144          CCATC   _
                                TGGCATGGTGC    GTGG AGCC
                                ||||||||||     |||| ||||
                                ACCGTACCACG    CACC TCGG
                                      A____    G
GAM1531  LOC152300 3'  ACTGTAGGCACCTGCCA     81377      T     C  C
                                TGGCA GGTGCC AT GT
                                ||||| |||||| || ||
                                ACCGT CCACGG TG CA
                                   _     A  T
GAM1531  LOC154092 3'  GCCTGCAGCACCATGCCA     87369          CCATC TG A
                                TGGCATGGTGC    G  G GC
                                ||||||||||     |  | ||
                                ACCGTACCACG    C  C CG
                                      A____ GT _
GAM1531  LOC166341 3'  GCTGCCCAGGACCATGCCA    83518        G  CATCG  __
                                TGGCATGGT CC    TGG  AGC
                                ||||||||| ||    |||  |||
                                ACCGTACCA GG    ACC  TCG
                                     _ _____   CG
GAM1531  LOC197358 3'  GGAATACAGGCACCCGCCA    89437     AT     CATC   GAG
                                TGGC  GGTGCC    GTG   CC
                                ||||  ||||||    |||   ||
                                ACCG  CCACGG    CAT   GG
                                  C_     A___   AA_
GAM1531  LOC200014 3'  CTGGGATTACAGGCACCCACCA 89932     CAT     C___   G
                                TGG   GGTGCC    ATC TGG
                                |||   ||||||    ||| |||
                                ACC   CCACGG    TAG GTC
                                  AC_     ACAT   G
GAM1531  LOC253866 3'  CTCCACCTGGCACCTATGCCA  97333       _     CATC
                                TGGCAT GGTGCC    GTGGAG
                                ||||||  ||||||   ||||||
                                ACCGTA CCACGG    CACCTC
                                   T     TC__
GAM1531  LOC253974 3'  CTCCACGACGTACTCAGCACCA 99282     CA_  _   CCA
                                TGG   TG GTGC   TCGTGGAG
                                |||   || ||||   ||||||||
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                                ACC   AC CATG   AGCACCTC
                                  ACG  T    C__
GAM1531  LOC57146  3'  CTGGGATTACAGGCACCCGCCA 40295      AT     C___   G
                                TGGC  GGTGCC    ATC TGG
                                ||||  ||||||    ||| |||
                                ACCG  CCACGG    TAG GTC
                                  C_     ACAT   G
GAM1531  LOC93082  3'  GCTCCCAACACCCATGCCA    57256         _ CCCATCGT
                                TGGCATGG TG       GGAGC
                                |||||||| ||       |||||
                                ACCGTACC AC       CCTCG
                                     C  AAC_____
GAM1532  ABCG1     3'  CACCGTACGTGGACACCATCTC 18189         ___    _____ GACC
             C                   GGAGATGG   CCATG    GC    G
                                 ||||||||   |||||    ||    |
                                 CCTCTACC   GGTGC    TG    C
                                      ACA     A___  CCAG
GAM1532  ANXA2     3'  ACAGTCCCCGTGGCCATCCC   15746    A         C   C
                                GG GATGGCCATGG GAC GT
                                || ||||||||||| ||| ||
                                CC CTACCGGTGCC CTG CA
                                 _         C   A
GAM1532  APOBEC3B  3'  CGTTCACCACCATCTCC      18117         CCA   C  C
                                GGAGATGG   TGG GA CG
                                ||||||||   ||| || ||
                                CCTCTACC   ACC CT GC
                                     ___   A  T
GAM1532  AVP       5'  GCGACCGTACAGGGCTAACCCT 6676       A__     A _____  GACC
             CC                    GGAG   TGGCC TG    GC    GT
                                   ||||   ||||| ||    ||    ||
                                   CCTC   ATCGG AC    TG    CG
                                     CCA    G  A___  CCAG
GAM1532  DUSP7     5'  ACGGCCATCAACCTGGCCATCC 66038    A       T  C_  ___
             C                     GG GATGGCCA GG  GA   CCGT
                                   || |||||||| ||  ||   ||||
                                   CC CTACCGGT CC  CT   GGCA
                                    _       _  AA  ACC
GAM1532  IL5RA     5'  ACGGTCCTCGCCATCTTC     6904          CAT  C
                                GGAGATGGC   GG GACCGT
                                |||||||||   || ||||||
                                CTTCTACCG   TC CTGGCA
                                     C__  _
GAM1532  ITGAL     3'  ACGGGCCCGGACATCCC      11038    A    G  AT   GA
                                GG GATG CC  GGC  CCGT
                                || |||| ||  |||  ||||
                                CC CTAC GG  CCG  GGCA
                                 _   A  C_  __
GAM1532  KCNQ1     3'  CGTCTCACCATTTCC       5840          CCA   C   C
                                GGAGATGG   TGG GAC G
                                ||||||||   ||| ||| |
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                                CCTTTACC   ACT CTG C
                                   ___  _  A
GAM1532 MS4A4A   3' CACCGTATGCATGGCCATCTCC 44002          _______ GACC
                                GGAGATGGCCATG     GC   G
                                ||||||||||||     ||   |
                                CCTCTACCGGTAC     TG   C
                                   GTA___ CCAG
GAM1532 MUCDHL   3' CACCGTACATACTGCCATCTCC 49201        C__  _____ GACC
                                GGAGATGGC  ATG   GC   G
                                |||||||||  |||   ||   |
                                CCTCTACCG  TAC   TG   C
                                     TCA  A___ CCAG
GAM1532 MUCDHL   3' CACCGTACATACTGCCATCTCC 88637        C__  _____ GACC
                                GGAGATGGC  ATG   GC   G
                                |||||||||  |||   ||   |
                                CCTCTACCG  TAC   TG   C
                                     TCA  A___ CCAG
GAM1532 ROR2     3' CACCGTACACATGGTCATCCC 17059    A       _______ GACC
                                GG GATGGCCATG     GC   G
                                || ||||||||||     ||   |
                                CC CTACTGGTAC     TG   C
                                 _       ACA___ CCAG
GAM1532 APOBEC3G 3' TGTTCACCACCATCTCC     41823       CCA  C  C
                                GGAGATGG   TGG GA CG
                                ||||||||   ||| || ||
                                CCTCTACC   ACC CT GT
                                   ___  A  T
GAM1532 ATP6V1F  3' GGAAGCCTGACCATCTCC    16165       C  T  GA
                                GGAGATGG CA GGC  CC
                                |||||||| || |||  ||
                                CCTCTACC GT CCG  GG
                                    A  _  AA
GAM1532 C22orf4  3' ACGAGGTAGTGGCCATCTC   61268         G  GAC
                                GAGATGGCCAT GC   CGT
                                |||||||||||  ||   |||
                                CTCTACCGGTG TG   GCA
                                      A  GA_
GAM1532 EFNA2    3' ACCGTGGCCAGGCCATCTCC  9182         A   G  C
                                GGAGATGGCC TGGC AC GT
                                |||||||||| |||| || ||
                                CCTCTACCGG ACCG TG CA
                                     _   G  C
GAM1532 FLJ22055 3' ATGGAATATGGCCATTCC    45846     A      GCGA
                                GGAG TGGCCATG    CCGT
                                ||||  ||||||||   ||||
                                CCTT ACCGGTAT    GGTA
                                  _      AA__
GAM1532 HPCAL4   3' GGGGCATGGCCACCTCC     33211     A      G GA
                                GGAG TGGCCATG C  CC
                                ||||  |||||||| |  ||
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                                CCTC ACCGGTAC G  GG
                                  C      _ G_
GAM1532  KIAA0350  3'  ACGACCACCGTGGCCATCTGC  61823   G        CGAC
                                G AGATGGCCATGG   CGT
                                | ||||||||||||   |||
                                C TCTACCGGTGCC   GCA
                                 G         ACCA
GAM1532  KIAA0882  3'  ACAGTCAACTTTACCATTTCC  83532       CCAT  C_  C
                                GGAGATGG   GG  GAC GT
                                ||||||||   ||  ||| ||
                                CCTTTACC   TC  CTG CA
                                     ATT_  AA   A
GAM1532  KIAA1634  3'  ACAGTCACCATTACCCCCATCT 64121       CC___   C  C
            TC                    GGAGATGG    ATGG GAC GT
                                ||||||||    |||| ||| ||
                                CTTCTACC    TACC CTG CA
                                     CCCAT   A  A
GAM1532  KIAA1819  5'  GGTAGTTAACCTATCTCC    70254       CCA   G
                                GGAGATGG   TGGC ACC
                                ||||||||   |||| |||
                                CCTCTATC   ATTG TGG
                                     CA_   A
GAM1532  phorbolin-1 3'  CGTTCACCACCATCTCC    90209       CCA   C  C
                                GGAGATGG   TGG GA CG
                                ||||||||   ||| || ||
                                CCTCTACC   ACC CT GC
                                     ___   A  T
GAM1532  PKNOX2   3'  GGTCGCCACGGCCATCCC    92530    A     A
                                GG GATGGCC TGGCGACC
                                || ||||||| ||||||||
                                CC CTACCGG ACCGCTGG
                                 _      C
GAM1532  LOC150295 3'  ACGGCCGTCGCTCCGTCTCC   86152       CCA    A
                                GGAGATGG   TGGCG CCGT
                                ||||||||   ||||| ||||
                                CCTCTGCC   GCTGC GGCA
                                     TC_    C
GAM1532  LOC153364 5'  ACGGTCGCCACCTGAGTCTCC  81678      GGCCA
                                GGAGAT    TGGCGACCGT
                                ||||||    ||||||||||
                                CCTCTG    ACCGCTGGCA
                                    AGTCC
GAM1532  LOC196872 3'  GCGACCGTACAGGCATGGCCAC 89157     A      _________  GACC
            CTCC                   GGAG TGGCCATG       GC    GT
                                |||| ||||||||       ||    ||
                                CCTC ACCGGTAC       TG    CG
                                  C       GGACA___  CCAG
GAM1532  LOC203069 5'  ACGGTCCTCGGCCCATCTCC   90758        _  AT  C
                                GGAGATGG CC  GG GACCGT
                                |||||||| ||  || ||||||
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                                CCTCTACC GG  TC CTGGCA
                                     C  C_  _
GAM1532  LOC220070 3'  TGGCTCCATGGCCTCCC     59944    A  T      CGA
                                GG GA GGCCATGG   CCG
                                || || ||||||||   |||
                                CC CT CCGGTACC   GGT
                                 _ _       TC_
GAM1532  LOC222128 5'  ACAGTCGCCATGACGACC    94284    AGA  GC       C
                                GG   TG  CATGGCGAC GT
                                ||   ||  ||||||||| ||
                                CC   GC  GTACCGCTG CA
                                 A__  A_       A
GAM1532  LOC254057 3'  ACGGGCCCAGCCACCTGCC    98776    _ A    CAT   GA
                                GG AG TGGC   GGC  CCGT
                                || || ||||   |||  ||||
                                CC TC ACCG   CCG  GGCA
                                 G  C    AC_  __
GAM1533  ELF3     3'  TGACCTTGACCTTGACCAA    16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                   _    AGT  ____
GAM1533  JAK2     3'  TGACCTTCATTCTGAGACCAA  18318      CAA      AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_       C_
GAM1533  SLC10A2  5'  ACTCTCTGTCTTGACCAA    6590       CAA      A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ____       C
GAM1533  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM1533  KIAA1958  5'  GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM1533  MARCKS   3'  ACTTTCCACCCTGCCCA     11411     TTCA   A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                 CG__   _
GAM1533  TUB      5'  GTGGGACCATCCCTTAAACC   13898     C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
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                                CCAA TTCCCTACC    GGTG
                                  A       AG__
GAM1533  LOC80298  3'  ACTTTTACCTTGAACCA     48062          GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                     A___
GAM1534  AP2M1     3'  CTTCCCACCCCTGTGGCC     15799          A   A
                                GGTCACAGGG TGG AAG
                                |||||||||| ||| |||
                                CCGGTGTCCC ACC TTC
                                     C   C
GAM1534  AVP       5'  GGTGACCCCCCAGTCTGTCC   6677     TC    GA   AAA
                                GG  ACAGG  TGG   GTCACC
                                ||  |||||  |||   ||||||
                                CC  TGTCT  ACC   CAGTGG
                                 __    G_   CCC
GAM1534  BAX       3'  GTGACCCCTGACCTCACTGTGA 16319        G  T  AAA___
              CC                  GGTCACAG GA GG     GTCAC
                                ||||||||| || ||     |||||
                                CCAGTGTC CT CC     CAGTG
                                     A  _  AGTCCC
GAM1534  BSN       3'  TGACCCGAGTCCTCCACATGAC 14391      CAG   T   AA___
              C                   GGTCA   GGA GGA    GTCA
                                |||||   ||| |||    ||||
                                CCAGT   CCT CCT    CAGT
                                   ACA   _   GAGCC
GAM1534  CFL1      3'  TGACCCCTCCCTGTGCC     19748    T      T  AAA
                                GG CACAGGGA GG   GTCA
                                || ||||||||  ||   ||||
                                CC GTGTCCCT CC   CAGT
                                 _       C  ___
GAM1534  CRY2      3'  GTGACTTTCAGCTGAGACC    72666     A   GGATG
                                GGTC CAG    GAAAGTCAC
                                |||| |||    |||||||||
                                CCAG GTC    CTTTCAGTG
                                  A   GA___
GAM1534  ELF3      3'  GTGACCTTGACCTTGACC     16684      C   GAT  AAA
                                GGTCA AGG   GG   GTCAC
                                ||||| |||   ||   |||||
                                CCAGT TCC   TC   CAGTG
                                   _   AGT  ___
GAM1534  GRLF1     3'  GATGGGGGCATCCCTGTGCC   79259    T       GAAA_
                                GG CACAGGGATG    GTC
                                || ||||||||||    |||
                                CC GTGTCCCTAC    TAG
                                 _        GGGGG
GAM1534  HOXC6     5'  GATTGGAGCCGTCCCTATAACC 16909     CAC       AA__
                                GGT   AGGGATGG    AGTC
                                |||   ||||||||    ||||
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                                CCA  TCCCTGCC   TTAG
                                  ATA      GAGG
GAM1534 IRTA2    3' TGACTTTTAAGCCCCACGGCC 49235     ACA  ATG
                                GGTC  GGG  GAAAGTCA
                                ||||  |||  ||||||||
                                CCGG  CCC  TTTTCAGT
                                  CAC  GAA
GAM1534 JAK2     3' TGACCTTCATTCTGAGACC   18317     ACA      AA
                                GGTC  GGGATGGA GTCA
                                ||||  |||||||| ||||
                                CCAG  TCTTACTT CAGT
                                  AG_      C_
GAM1534 PRKCSH   3' TGACTTGACCTGTGACC     12294        GATGGA
                                GGTCACAGG     AAGTCA
                                |||||||||     ||||||
                                CCAGTGTCC     TTCAGT
                                     AG____
GAM1534 PRODH    3' GGCCCCCACCTCTGTGACC   33396         A  AAA
                                GGTCACAGGG TGG  GTC
                                |||||||||| |||  |||
                                CCAGTGTCTC ACC  CGG
                                     C  CC_
GAM1534 SOX10    3' TGACCCTCTATCCCAGGACC  23679     ACA      AA
                                GGTC  GGGATGGA GTCA
                                ||||  |||||||| ||||
                                CCAG  CCCTATCT CAGT
                                  GA_      CC
GAM1534 TBL1X    3' GGTAGAGTCATCCCTGTAATC 20137     C        AAAGTC
                                GGT ACAGGGATGG     ACC
                                ||| ||||||||||     |||
                                CTA TGTCCCTACT     TGG
                                  A        GAGA__
GAM1534 UBL1     3' TGACTTTCCAATTGGCC     13977      CAGGGA
                                GGTCA     TGGAAAGTCA
                                |||||     ||||||||||
                                CCGGT     ACCTTTCAGT
                                   TA____
GAM1534 XT3      3' GACATTCCATCCCTGTACC   39913     C         A
                                GGT ACAGGGATGGAA GTC
                                ||| |||||||||||| |||
                                CCA TGTCCCTACCTT CAG
                                  _         A
GAM1534 C22orf20 3' GTGACCCCTGCCTGTGAC    48199       GAT  AAA
                                GTCACAGG  GG  GTCAC
                                ||||||||  ||  |||||
                                CAGTGTCC  CC  CAGTG
                                     GT_  C__
GAM1534 CASP9    3' GTGACTTGTGTCCCATGATC  8776      CA     GA
                                GGTCA  GGGATG  AAGTCAC
                                |||||  ||||||  |||||||
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                                CTAGT  CCCTGT  TTCAGTG
                                  A_     G_
GAM1534  DKFZP564D0462 5'  GCGTATCATCCCTGTTACC    71023     C        AAA
                                GGT ACAGGGATGG   GT
                                ||| ||||||||||   ||
                                CCA TGTCCCTACT   CG
                                  T         ATG
GAM1534  FLJ10178 3'  GTAACTTTCCATGGAC      36340     A  GGGA       C
                                GTC CA    TGGAAAGT AC
                                ||| ||    |||||||| ||
                                CAG GT    ACCTTTCA TG
                                  _ _____       A
GAM1534  FLJ12443 5'  GACGCCATCCCTGTGACC    46145            AAA
                                GGTCACAGGGATGG   GTC
                                ||||||||||||||   |||
                                CCAGTGTCCCTACC   CAG
                                       G__
GAM1534  FLJ12517 3'  GACCGCCCTCCCTGTGACC    43720          T  AAA
                                GGTCACAGGGA GG   GTC
                                ||||||||||| ||   |||
                                CCAGTGTCCCT CC   CAG
                                      C  GC_
GAM1534  FLJ21415 3'  TGACTCAGCCCTGGGACC    45691      A    A  GAA
                                GGTC CAGGG TG   AGTCA
                                |||| ||||| ||   |||||
                                CCAG GTCCC AC   TCAGT
                                  G    G  ___
GAM1534  FLJ30791 5'  GGCCCCGTCCCTGTGACC    59116            AAA
                                GGTCACAGGGATGG   GTC
                                ||||||||||||||   |||
                                CCAGTGTCCCTGCC   CGG
                                       C__
GAM1534  GMEB2    5'  TGACTCCATCCCTGTGCC    25669    T         AA
                                GG CACAGGGATGGA  GTCA
                                || ||||||||||||  ||||
                                CC GTGTCCCTACCT  CAGT
                                  _         ___
GAM1534  KIAA0794 3'  GGTGACTTTCATTGTCCTAACC 81235     CAC    ATG_
                                GGT   AGGG    GAAAGTCACC
                                |||   ||||    ||||||||||
                                CCA   TCCT    CTTTCAGTGG
                                  A__    GTTA
GAM1534  KIAA0907 3'  GGTGACCATTGACCCTGTGACC 30881          ATGGAAA
                                GGTCACAGGG      GTCACC
                                ||||||||||      ||||||
                                CCAGTGTCCC      CAGTGG
                                      AGTTAC_
GAM1534  KIAA1171 3'  ACTTTCCATCCCCACACC    89335     CACA
                                GGT    GGGATGGAAAGT
                                |||    ||||||||||||
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                                CCA   CCCTACCTTTCA
                                  CAC_
GAM1534 KIAA1691 3' ACTACTCCATCCCATGACC   94122      CA      A_
                                GGTCA GGGATGGA AGT
                                ||||| |||||||| |||
                                CCAGT CCCTACCT TCA
                                   A_      CA
GAM1534 MGC29761 3' ACTGCATCACCTCCTGTGACC 58975        _ A  AA_
                                GGTCACAGG G TGG  AGT
                                ||||||||| | |||  |||
                                CCAGTGTCC C ACT  TCA
                                      T C  ACG
GAM1534 MGC3079  3' GGTGACTTGCACCTGTAATC  51946    C    GATGGA
                                GGT ACAGG     AAGTCACC
                                ||| |||||     ||||||||
                                CTA TGTCC     TTCAGTGG
                                  A    ACG___
GAM1534 MGC8407  5' GATCACTTCCTCCCTGTGACC 44114         T   A__
                                GGTCACAGGGA GGAA  GTC
                                |||||||||| ||||  |||
                                CCAGTGTCCCT CCTT  TAG
                                      _   CAC
GAM1534 PP1665   5' GGCCCGTACCCATCCTTGTGAC 48639          AAA___
             C                   GGTCACAGGGATGG     GTC
                                 ||||||||||||||     |||
                                 CCAGTGTTCCTACC     CGG
                                       CATGCC
GAM1534 PRO0456  3' GGCATACATCCCTGTAACT   27008    C       GAAA
                                GGT ACAGGGATG   GTC
                                ||| |||||||||   |||
                                TCA TGTCCCTAC   CGG
                                  A       ATA_
GAM1534 SP192    3' GGCACTCACCCCTGTGATC   41617         A  AAA
                                GGTCACAGGG TGG  GTC
                                |||||||||| |||  |||
                                CTAGTGTCCC ACT  CGG
                                      C  CA_
GAM1534 SS-56    3' GGTGACTTTCCCACTGTGCC  60357   T    GGAT
                                GG CACAG   GGAAAGTCACC
                                || |||||   ||||||||||
                                CC GTGTC   CCTTTCAGTGG
                                  _    AC__
GAM1534 STRAIT11499 5' GGCCGACCATCCCCGTGCC   41430   T  A     AAA
                                GG CAC GGGATGG  GTC
                                || ||| |||||||  |||
                                CC GTG CCCTACC  CGG
                                  _  C      AGC
GAM1534 ZNF317   3' GACCCTGGCCTCCCCTGTGGCC 72477         AT  AAA__
                                GGTCACAGGG  GG    GTC
                                ||||||||||  ||    |||
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                                CCGGTGTCCC CC    CAG
                                     CT GGTCC
GAM1534 LOC113444 3' GTGACTTGTCCTGCTACC   57365    CA   ATGGA
                                GGT CAGGG   AAGTCAC
                                ||| |||||   |||||||
                                CCA GTCCT   TTCAGTG
                                  TC   G____
GAM1534 LOC120939 5' GGTGACTTTCACCCTGCAAC  76767   CA   ATG
                                GT CAGGG  GAAAGTCACC
                                || |||||  ||||||||||
                                CA GTCCC  CTTTCAGTGG
                                 AC   A__
GAM1534 LOC124997 3' GACTTAAGCATCCCTGCGACC 74847     A     GA_
                                GGTC CAGGGATG  AAGTC
                                |||| ||||||||  |||||
                                CCAG GTCCCTAC  TTCAG
                                   C      GAA
GAM1534 LOC128954 5' GGCCCATCCCTGCACC     76305    CA      AAA
                                GGT CAGGGATGG  GTC
                                |||  |||||||||  |||
                                CCA GTCCCTACC  CGG
                                  C_       ___
GAM1534 LOC129198 3' GTGACTCCCCAGGCCCTGTGAC 76615        A_  AA
             C                   GGTCACAGGG TGG AGTCAC
                                ||||||||||  |||  ||||||
                                CCAGTGTCCC  ACC  TCAGTG
                                     GG   CC
GAM1534 LOC136319 3' TGACTCTCCTGTGGCC     75773        ATGGAA
                                GGTCACAGGG     AGTCA
                                ||||||||||     |||||
                                CCGGTGTCCT     TCAGT
                                     C_____
GAM1534 LOC147639 3' GATTTCCATCCCCAAGACC   79011     ACA       G
                                GGTC   GGGATGGAAA TC
                                ||||   |||||||||| ||
                                CCAG   CCCTACCTTT AG
                                  AAC        _
GAM1534 LOC152441 3' TGACTCATGCCTGTGATC    86920        G   GAA
                                GGTCACAGG ATG   AGTCA
                                |||||||| |||   |||||
                                CTAGTGTCC TAC   TCAGT
                                     G  ___
GAM1534 LOC152762 3' TGACCCAGGGTCCCTGTGACC 81538          GGAAA
                                GGTCACAGGGAT    GTCA
                                ||||||||||||    ||||
                                CCAGTGTCCCTG    CAGT
                                       GGACC
GAM1534 LOC162333 5' GTGAATTCATCCTATAACC   88500    CACA      AAG
                                GGT   GGGATGGA  TCAC
                                |||   ||||||||  ||||
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                                CCA   TCCTACTT  AGTG
                                  ATA_      A__
GAM1534  LOC170221 3'  CTTTCCATCCCCATGCC    83468    T  CA
                                GG CA  GGGATGGAAAG
                                || ||  ||||||||||
                                CC GT  CCCTACCTTTC
                                 _  AC
GAM1534  LOC196485 5'  GACGACCCCCTGTGGCC    89073         AT  AAA
                                GGTCACAGGG  GG   GTC
                                ||||||||||  ||   |||
                                CCGGTGTCCC  CC   CAG
                                      __  AG_
GAM1534  LOC196955 5'  GTGACTCCGTCCCCCACACC  77871    CACA      AA
                                GGT   GGGATGGA  GTCAC
                                |||   ||||||||  |||||
                                CCA   CCCTGCCT  CAGTG
                                  CACC      __
GAM1534  LOC200014 3'  GTGACTTTTTTCCCCATGAGC  89944   G   CA   T
                                G TCA  GGGA GGAAAGTCAC
                                | |||  |||| ||||||||||
                                C AGT  CCCT TTTTTCAGTG
                                 G   AC   _
GAM1534  LOC200301 5'  GTGACATTTCACTGTGACC   90151       GGA    A
                                GGTCACAG   TGGAA GTCAC
                                ||||||||   ||||| |||||
                                CCAGTGTC   ACTTT CAGTG
                                     ___    A
GAM1534  LOC202986 5'  GACGACCCCCTGTGGCC    92067         AT  AAA
                                GGTCACAGGG  GG   GTC
                                ||||||||||  ||   |||
                                CCGGTGTCCC  CC   CAG
                                      __  AG_
GAM1534  LOC56270  3'  GGTAACTCAGTGGCTGTGACC  39509       GG  GGAA   C
                                GGTCACAG  AT    AGT ACC
                                ||||||||  ||    ||| |||
                                CCAGTGTC  TG    TCA TGG
                                    GG  AC__   A
GAM1534  LOC90362  5'  GACAGCATTCCTGTGACC    63112          GAAA
                                GGTCACAGGGATG    GTC
                                ||||||||||||    |||
                                CCAGTGTCCTTAC    CAG
                                      GA__
GAM1534  LOC92421  3'  TGACGTGTATCCCTGTACC   69732     C       GAAA
                                GGT ACAGGGATG    GTCA
                                ||| |||||||||    ||||
                                CCA TGTCCCTAT    CAGT
                                  _       GTG_
GAM1535  TERF1     3'  CCCAAATCCTGTTCCAATGA   34391        C   TA   C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
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                                AGTAACCT TGT  CTAA CCC
                                    _  C_   A
GAM1535  FLJ10159  3'  CCATGTCACGCCATCCAATGAC 36334        CA_  A  TC
                                GTCATTGGA  CGT GAT  GG
                                |||||||||  ||| |||  ||
                                CAGTAACCT  GCA CTG  CC
                                    ACC  _  TA
GAM1535  FLJ14213  3'  CCGATGCTCCCAATGACG   46216        ACAC  GAT
                                CGTCATTGG   GTA  TCGG
                                |||||||||   |||  ||||
                                GCAGTAACC   CGT  AGCC
                                    CT__  ___
GAM1535  MGC10715  3'  ATTTACCAGACATCCAATGAC  44495        CAC___
                                GTCATTGGA    GTAGAT
                                |||||||||    ||||||
                                CAGTAACCT    CATTTA
                                    ACAGAC
GAM1535  MOST2    5'  CCAGGACTGCCCAATGAC    40059        ACAC   A  _
                                GTCATTGG   GTAG TTC GG
                                ||||||||   |||| ||| ||
                                CAGTAACC   CGTC AGG CC
                                    ____   _  A
GAM1535  LOC150370 3'  CCGGGTCTACGTGCCCATGAC  86123      T  A
                                GTCAT GG CACGTAGATTCGG
                                ||||| || ||||||||||||
                                CAGTA CC GTGCATCTGGGCC
                                  C  _
GAM1535  LOC152620 3'  CCCAAATCCTGTTCCAATGA   60707        C  TA   C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                    _  C_   A
GAM1535  LOC158668 3'  CCCAAATCCTGTTCCAATGA   69896        C  TA   C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                    _  C_   A
GAM1536  ELF3     3'  TGACCTTGACCTTGACCAA   16685      T   GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                  _    AGT  ___
GAM1536  JAK2     3'  TGACCTTCATTCTGAGACCAA  18318      CAA      AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                  AG_      C_
GAM1536  SLC10A2  5'  ACTCTCTGTCTTGACCAA    6590       CAA      A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
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                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM1536  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM1536  KIAA1958  5'  GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM1536  MARCKS   3'  ACTTTCCACCCTGCCCA     11411     TTCA    A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM1536  TUB      5'  GTGGGACCATCCCTTAAACC   13898     C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A       AG__
GAM1536  LOC80298  3'  ACTTTTACCTTGAACCA     48062         GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                     A___
GAM1537  ACRV1    3'  AAAAGCCTCCATCACT      39640       CTAA   _
                                AGTGA    TGG GGCTTTT
                                |||||    ||| |||||||
                                TCACT    ACC CCGAAAA
                                   _____   T
GAM1537  PRIM2A   3'  CTCTTAATCACTTTGTA     8141          C   T
                                TACAAAGTGA TAA GGG
                                |||||||||| ||| |||
                                ATGTTTCACT ATT CTC
                                     A   _
GAM1537  CBX3     3'  AAAAGCCAGGAAGAACAACTTT 24406        GACTAATGG_
            GTA                   TACAAAGT        GGCTTTT
                                |||||||         |||||||
                                ATGTTTCA        CCGAAAA
                                    ACAAGAAGGA
GAM1537  KIAA0063  3'  AAAGCCCCACTTCCTTT     30243      T  CTAA
                                AAAG GA    TGGGGCTTT
                                |||| ||    |||||||||
                                TTTC CT    ACCCCGAAA
                                  _  TC__
GAM1537  KIAA0630  5'  CTACCAGTCAGCTTTGTA    90950        _     AA
                                TACAAAG TGACT  TGG
                                ||||||| |||||  |||
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                                ATGTTTC ACTGA  ATC
                                   G    CC
GAM1537  PCDH17   3'  CCTTTGGTCATTTGTA     27835       G     T
                                TACAAA TGACTAA GGG
                                |||||| ||||||| |||
                                ATGTTT ACTGGTT TCC
                                  _     _
GAM1537  LOC146159 5'  AAAAACCTTGTGGCAAATCACT 78170        CTA___ TG   C
           TTG                   CAAAGTGA     A  GGG TTTT
                                |||||||      |  ||| ||||
                                GTTTCACT     T  TCC AAAA
                                   AAACGG GT   A
GAM1537  LOC157621 3'  AAAAGCCATCCCAGTCATTT   87787        AATGG
                                AAGTGACT    GGCTTTT
                                ||||||||    |||||||
                                TTTACTGA    CCGAAAA
                                   CCCTA
GAM1537  LOC157622 3'  AAAAGCCATCCCAGTCATTT   87794        AATGG
                                AAGTGACT    GGCTTTT
                                ||||||||    |||||||
                                TTTACTGA    CCGAAAA
                                   CCCTA
GAM1538  FUT4     5'  CTCCTGTACCTTCCCAGGGATG 10721      A   A      TTTTC
                                CATC CTG GAAGGTG    GAG
                                |||| ||| |||||||    |||
                                GTAG GAC CTTCCAT    CTC
                                  G   C     GTC__
GAM1538  GPR61    3'  CTCAAAATTAGCTTCAGTGA   79659        AAGGT    C
                                TCACTGAG    GTTTT GAG
                                ||||||||    ||||| |||
                                AGTGACTT    TAAAA CTC
                                   CGAT_    _
GAM1538  MPZ      3'  CTCAAAAACGCCCTCA      6750       AA       C
                                TGAG  GGTGTTTT GAG
                                ||||  |||||||| |||
                                ACTC  CCGCAAAA CTC
                                  __       A
GAM1538  PIGR     3'  TCAAAGGCCCTCAGTGA     73012        AA   G   TC
                                TCACTGAG  GGT TTT  GA
                                ||||||||  ||| |||  ||
                                AGTGACTC  CCG AAA  CT
                                   __   G   __
GAM1538  AKL3L    3'  TCAAAAACATCAGCGATG    33270      A    GAAGG     C
                                CATC CTGA    TGTTTT GA
                                |||| ||||    |||||| ||
                                GTAG GACT    ACAAAA CT
                                  C   _____     A
GAM1538  ASB13    3'  CTCAAAGGCACTCTCAGGA   45545    A     AG      C
                                TC CTGAGA  GTGTTTT GAG
                                || ||||||  ||||||| |||
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                                AG GACTCT  CACGGAA CTC
                                 _    __      A
GAM1538  CXorf1    3'  CTCAAAAATACCACTTCTCAGT 17486     C      __      C
              ATG                   CAT ACTGAGAA  GGTGTTTT GAG
                                    ||| ||||||||  |||||||| |||
                                    GTA TGACTCTT  CCATAAAA CTC
                                     _      CA       A
GAM1538  DKFZP434F0318 3'  GCACCCTTCCCAGTGATG    48759        A    _
                                    CATCACTG GAAGG TGT
                                    |||||||| ||||| |||
                                    GTAGTGAC CTTCC ACG
                                         C    C
GAM1538  FKBP5     3'  AAAACACCCTTCAGCAATG    15928     CA    AA
                                    CAT  CTGAG  GGTGTTTT
                                    |||  |||||  ||||||||
                                    GTA  GACTT  CCACAAAA
                                      AC    C_
GAM1538  FLJ12934  3'  CTCATAAACTCCCCAGTGATG  43488        AGAA  T    TC
                                    CATCACTG   GG GTTT  GAG
                                    ||||||||   || ||||  |||
                                    GTAGTGAC   CC CAAA  CTC
                                         C___  T    TA
GAM1538  GOLPH2    5'  CTCGAAAAGAGATTCTCAG   33770       GGTG
                                    CTGAGAA    TTTTCGAG
                                    |||||||    ||||||||
                                    GACTCTT    AAAAGCTC
                                         AGAG
GAM1538  KIAA0318  3'  CTCAAAATGCTTGCCTCA    69528     A_       C
                                    TGAG  AGGTGTTTT GAG
                                    ||||  ||||||||| |||
                                    ACTC  TTCGTAAAA CTC
                                      CG       _
GAM1538  KIAA1900  3'  CTCGTCACCCTTCTCAGTG   73634          T  TTT
                                    CACTGAGAAGG GT   CGAG
                                    |||||||||| ||   ||||
                                    GTGACTCTTCC CA   GCTC
                                           _ CT_
GAM1538  MFN2      3'  AGGACACTTTCAGCGA      30222    A    AA
                                    TC CTGAG  GGTGTTTT
                                    || |||||  ||||||||
                                    AG GACTT  TCACAGGA
                                     C    __
GAM1538  SEC24B    5'  CGGGTGACACCCTCAGTGA   21983        AA    _
                                    TCACTGAG  GGTGTT TTCG
                                    ||||||||  |||||| ||||
                                    AGTGACTC  CCACAG GGGC
                                         __      T
GAM1538  TUCAN     3'  CACCTTCATTCTCAGTGATG  30968          _____
                                    CATCACTGAGA    AGGTG
                                    ||||||||||    |||||
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                                GTAGTGACTCT    TCCAC
                                      TACT
GAM1538  LOC138199 3'  CTCAAAATCAACTATCAGTGAT 75824        GA  G  T   C
              G                 CATCACTGA  AG TG TTT GAG
                                |||||||||  || || ||| |||
                                GTAGTGACT  TC AC AAA CTC
                                     A_  A  T   A
GAM1538  LOC147077 5'  CTCACCACCCCTTCTCAGTAAT 78848     C         T  TTTC
              G                 CAT ACTGAGAAGG GT    GAG
                                ||| |||||||||| ||    |||
                                GTA TGACTCTTCC CA    CTC
                                  A        C  CCA_
GAM1538  LOC153205 3'  CTCATTCTGTCTTCTCAGTGA  87155          GT TTTTC
                                TCACTGAGAAG  G    GAG
                                ||||||||||  |    |||
                                AGTGACTCTTC  T    CTC
                                      TG CTTA_
GAM1538  LOC154007 3'  CTCAAAAACATAATGCTCAGTG 81924        AAG_      C
              A                 TCACTGAG   GTGTTTT GAG
                                ||||||||   ||||||| |||
                                AGTGACTC   TACAAAA CTC
                                     GTAA      A
GAM1538  LOC83985  5'  CGGGTCCCTTCTCAGTGGTG   50174           TGTT
                                CATCACTGAGAAGG   TTCG
                                ||||||||||||||   ||||
                                GTGGTGACTCTTCC   GGGC
                                       CT__
GAM1539  ABCB8     3'  TCCCTCCCTCCCCTCCCCA   24205    AA       AA
                                TG  GAGGGGGG  GAGGGG
                                ||  ||||||||  ||||||
                                AC  CTCCCCTC  CTCCCT
                                 CC       C_
GAM1539  AKAP1     3'  TTCCCCTCTTCTTCCTTCT   14474
                                AGAGGGGGGAAGAGGGGAA
                                ||||||||||||||||||||
                                TCTTCCTTCTTCTCCCCTT

GAM1539  AKAP1     3'  TTCCCCTCTTCTTCCTTCT   58374
                                AGAGGGGGGAAGAGGGGAA
                                ||||||||||||||||||||
                                TCTTCCTTCTTCTCCCCTT

GAM1539  ALMS1     5'  TCCCTCCCCCCCTCCTC     31366    A       AA
                                GA GAGGGGGG  GAGGGG
                                || ||||||||  ||||||
                                CT CTCCCCCC  CTCCCT
                                 C       __
GAM1539  ALPL      3'  TCCCCTCTGGAATCTTCCC    6650         ____
                                GGGGGGA    AGAGGGGA
                                |||||||    ||||||||
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                                CCCTTCT   TCTCCCCT
                                   AAGG
GAM1539  ANGPT4   3'  CCCCTCTTCTCTCCCTCCCCCT 32570     ____     _
             TCA                  TGAA   GAGGGGG GAAGAGGGG
                                |||||   ||||||| |||||||||
                                ACTT   CTCCCTC CTTCTCCCC
                                  CCCC      T
GAM1539  ANP32A   3'  TCCCCTCTCCCCCCCCCCTC  21947       A___
                                GAGGGGGG   AGAGGGGA
                                ||||||||   ||||||||
                                CTCCCCCC   TCTCCCCT
                                     CCCC
GAM1539  AOC2     3'  TCCCCAGATTCCCACCCCCTC  64126       ___  GA_
                                GAGGGGG  GAA  GGGGA
                                |||||||  |||  |||||
                                CTCCCCC  CTT  CCCCT
                                     ACC  AGA
GAM1539  ASNS     5'  CCTTCAACTGCCCCCCTCCTCA 56761     A      AA___
                                TGA GAGGGGGG    GAGGG
                                ||| ||||||||    |||||
                                ACT CTCCCCCC    CTTCC
                                  C       GTCAA
GAM1539  ATF4     5'  TTTCCCTCCTCCCCCGCCCTC  9813      ___   A
                                GAGGG  GGGA GAGGGGAA
                                |||||  |||| ||||||||
                                CTCCC  CCCT CTCCCTTT
                                   GCC   C
GAM1539  AXIN1    3'  CCCTCCCACCTCTTCA     61536       G   AGA
                                TGAAGAGG GGGA  GGG
                                |||||||| ||||  |||
                                ACTTCTCC CCCT  CCC
                                     A   ___
GAM1539  CALR     3'  TGTTCCCCTCCTCCACTCTC  63658     G  A
                                GAGGG GGA GAGGGGAACA
                                ||||| ||| ||||||||||
                                CTCTC CCT CTCCCCTTGT
                                   A  C
GAM1539  CARP     5'  TCCCTCCCCTCCCTCTTCA   27669         AA
                                TGAAGAGGGGGG  GAGGGG
                                ||||||||||||  ||||||
                                ACTTCTCCCTCC  CTCCCT
                                       C_
GAM1539  CASQ1    5'  TTCCCCAATCCCCCCTC     8779        AGA
                                GAGGGGGGA  GGGGAA
                                |||||||||  ||||||
                                CTCCCCCCT  CCCCTT
                                     AA_
GAM1539  CDK4     3'  TTCCCCTCCCACCTCTC     5369       _ AA
                                GAGGGG GG  GAGGGGAA
                                ||||||  ||  ||||||||
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                                CTCTCC CC  CTCCCCTT
                                   A  __
GAM1539  CDK4     3'  TTCCCCTCCCACCTCTC     54831       _  AA
                                GAGGGG GG  GAGGGGAA
                                |||||| ||  ||||||||
                                CTCTCC CC  CTCCCCTT
                                   A  __
GAM1539  CELSR2   3'  CCTCTCCTCCCCTCTCCTCA  9193      A       A
                                TGA GAGGGGGGA GAGGGG
                                ||| ||||||||| ||||||
                                ACT CTCTCCCCT CTCTCC
                                  C       C
GAM1539  CEP2     3'  CCTCTCCCTCCCTCTCCA    23244    A       A
                                TG AGAGGGGGG AGAGG
                                || ||||||||| |||||
                                AC TCTCCCTCC TCTCC
                                 C       C
GAM1539  CRY1     5'  TTCCCCTCCGGTTCTCCTC    15809        AA_
                                GAGGGGGG   GAGGGGAA
                                ||||||||   ||||||||
                                CTCCTCTT   CTCCCCTT
                                     GGC
GAM1539  DCK      3'  TTCCCCTCTTTTGTCTTCCTCA 7632      A    G
                                TGA GAGGG GGAAGAGGGGAA
                                ||| ||||| ||||||||||||
                                ACT CTTCT TTTTCTCCCCTT
                                  C    G
GAM1539  DDB1     3'  CCCTCCCCCTCCTCTCCA    10397    A       AA
                                TG AGAGGGGGG  GAGGG
                                || |||||||||  |||||
                                AC TCTCCTCCC  CTCCC
                                 C       C_
GAM1539  DDX26    5'  TCCCCTCTTCGCCAGCTC    25114     G_  G
                                GAG  GG GAAGAGGGGA
                                |||  || ||||||||||
                                CTC  CC CTTCTCCCCT
                                  GA  G
GAM1539  DDX3     5'  TCCCCTCTTTTCCCTCCCTCT  9061        _   __
                                AGAGGG GGGA  AGAGGGGA
                                |||||| ||||  ||||||||
                                TCTCCC CCCT  TCTCCCCT
                                   T   TT
GAM1539  DDX3     5'  TCCCCTCTTTTCCCTCCCTCT  43992       _   __
                                AGAGGG GGGA  AGAGGGGA
                                |||||| ||||  ||||||||
                                TCTCCC CCCT  TCTCCCCT
                                   T   TT
GAM1539  EGFL5    3'  TCCCCTCTCGCTCCCTCT    87922        GA
                                AGAGGGGG  AGAGGGGA
                                ||||||||  ||||||||
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                                TCTCCCTC  TCTCCCCT
                                    GC
GAM1539  EGR4     3'  GTTCCCCTCCCCGCTCTTC   10496       G    AGA
                                GAAGAG GGGGA   GGGGAAC
                                |||||| |||||   |||||||
                                CTTCTC CCCCT   CCCCTTG
                                   G    ___
GAM1539  ELF3     3'  TTCCCCTCCCCACTCCTCT   16687       _  AA
                                AGAGGGG GG  GAGGGGAA
                                ||||||| ||  ||||||||
                                TCTCCTC CC  CTCCCCTT
                                    A  C_
GAM1539  ESRRA    3'  TCCTACCCCCTCTTCA      16725          GAAG
                                TGAAGAGGGGG   AGGG
                                ||||||||||    ||||
                                ACTTCTCCCCC   TCCT
                                      A___
GAM1539  GFAP     3'  TCCCCTCCCTCCTCT       10784          AGA
                                AGAGGGGGGA   GGGGA
                                ||||||||||   |||||
                                TCTCCTCCCT   CCCCT
                                      ___
GAM1539  GPR86    3'  TCCCCCTGCCCCACCCTCCTCA 43905     A   _  A_ A
                                TGA GAGGG GGG  AG GGGGA
                                ||| ||||| |||  || |||||
                                ACT CTCCC CCC  TC CCCCT
                                  C    A  CG _
GAM1539  GRB7     3'  CTCCTGACCCCTCTCCTCA   19191     A      AAG
                                TGA GAGGGGGG   AGGGG
                                ||| ||||||||   |||||
                                ACT CTCTCCCC   TCCTC
                                  C       AG_
GAM1539  GRM6     5'  TCTCCTTCCCCCGCCCTC    7773       _  AA
                                GAGGG GGG  GAGGGGA
                                ||||| |||  |||||||
                                CTCCC CCC  TTCCTCT
                                   G  CC
GAM1539  HOXB5    3'  TTCTCCTCCTCCTCCCTCCTCA 10961     A       A
                                TGA GAGGGGGGA GAGGGGAA
                                ||| |||||||| ||||||||
                                ACT CTCCCTCCT CTCCTCTT
                                  C        C
GAM1539  HR       3'  TGTTCCCCTCCCCCTT      18920        GAAG
                                GAGGGGG   AGGGGAACA
                                |||||||   |||||||||
                                TTCCCCC   TCCCCTTGT
                                     ____
GAM1539  IRS1     5'  TCCCCTCCCCTCCTCCCCA   19880    AA      AA
                                TG  GAGGGGGG  GAGGGGA
                                ||  ||||||||  |||||||
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                                AC  CTCCTCCC  CTCCCCT
                                 CC      __
GAM1539  MAP4     3'  TGTTCCCCTCTCCCTTCCCTCC 11455        ____
                TC                  GAGGGGGGA   AGAGGGGAACA
                                    |||||||||   ||||||||||
                                    CTCCTCCCT   TCTCCCCTTGT
                                        TCCC
GAM1539  MAP4     3'  TGTTCCCCTCTTGTCTCCCCT  11456       __
                                    AGGGGGGA  AGAGGGGAACA
                                    ||||||||  ||||||||||
                                    TCCCCTCT  TCTCCCCTTGT
                                        GT
GAM1539  MNT      3'  TGGGCCCCCCCCCCCCTCCCCA  40092    AA      AAGA   AA
                                    TG  GAGGGGGG   GGGG  CA
                                    ||  ||||||||   ||||  ||
                                    AC  CTCCCCCC   CCCC  GT
                                     CC      C___   GG
GAM1539  PAFAH1B1 5'  TCCCCTCCCCTCCCCCTC    6478        AA_
                                    GAGGGGGG  GAGGGGA
                                    ||||||||  |||||||
                                    CTCCCCCT  CTCCCCT
                                        CCC
GAM1539  PAX7     5'  CCACCTCACCCCCCTCCCCA  11972    AA      AA   _
                                    TG  GAGGGGGG  GAGG GG
                                    ||  ||||||||  |||| ||
                                    AC  CTCCCCCC  CTCC CC
                                     CC      A_   A
GAM1539  PAX7     5'  CCACCTCACCCCCCTCCCCA  26527    AA      AA   _
                                    TG  GAGGGGGG  GAGG GG
                                    ||  ||||||||  |||| ||
                                    AC  CTCCCCCC  CTCC CC
                                     CC      A_   A
GAM1539  PAX7     5'  GTTCCCCCGGCCCCCCTC    26529        AAGA
                                    GAGGGGGG   GGGGAAC
                                    ||||||||   |||||||
                                    CTCCCCCC   CCCCTTG
                                        GGC_
GAM1539  PAX7     5'  GTTCCCCCGGCCCCCCTC    11975        AAGA
                                    GAGGGGGG   GGGGAAC
                                    ||||||||   |||||||
                                    CTCCCCCC   CCCCTTG
                                        GGC_
GAM1539  PCDH7    3'  TTTCTCTTCCCCACCCCTCTCC 51622    A     ___     GG
                A                    TG AGAGGGG   GGAAGAG  G
                                    ||  |||||||  |||||||  |
                                    AC TCTCCCC   CCTTCTC  T
                                     C      ACC      TT
GAM1539  PCOLN3   3'  TCCCCGCCCCTCTTCA      12416         GGAAGA
                                    TGAAGAGGGG     GGGGA
                                    ||||||||||     |||||
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                                ACTTCTCCCC     CCCCT
                                     G_____
GAM1539  PDE4A    3'  TCCCCTCCCCCCTTCTCCA   21687    A       AA
                                TG AGAGGGGGG  GAGGGGA
                                || |||||||||  |||||||
                                AC TCTTCCCCC  CTCCCCT
                                 C       __
GAM1539  PDE4A    3'  TGTTCCCCTCCACTCCTCCCCT 21689       _  A__
             C                   GAGGGG GGA   GAGGGGAACA
                                |||||| |||   ||||||||||
                                CTCCCC CCT   CTCCCCTTGT
                                   T   CAC
GAM1539  PKD2L1   5'  TCCCCTCTCCCCTCTTCA    32769         GGA
                                TGAAGAGGGG   AGAGGGGA
                                ||||||||||   ||||||||
                                ACTTCTCCCC   TCTCCCCT

                                     ___
GAM1539  PPP1R12B 3'  TTCCCTTCCCCACCCCCTC   50400       GAA_
                                GAGGGGG    GAGGGGAA
                                |||||||    ||||||||
                                CTCCCCC    CTTCCCTT
                                    ACCC
GAM1539  PPP2R5E  5'  TCCCTTCCCCCCCTCCCCA   21807    AA      AA
                                TG  GAGGGGGG  GAGGGGA
                                ||  ||||||||  |||||||
                                AC  CTCCCCCC  CTTCCCT
                                 CC       __
GAM1539  RAD23A   3'  TGTCCCCCCGTCCTCCTCCCC  18567     _  A _   A_
                                GGGG GGA GA GGGG  ACA
                                |||| ||| || ||||  |||
                                CCCC CCT CT CCCC  TGT
                                  T  C  G   CC
GAM1539  RARB     5'  TCCCAAGCCCCCCCATCTCCA   32890    A  _     AAGAG
                                TG AGA GGGGGGG     GGGA
                                || ||| |||||||     ||||
                                AC TCT CCCCCC     CCCT
                                 C  A     GAA__
GAM1539  RASGRP2  5'  TCCCCACAGGTCCCTCTCCCCA 20633    AA       AAGA_
                                TG  GAGGGGGGG    GGGGA
                                ||  ||||||||     |||||
                                AC  CTCTCCCT     CCCCT
                                 CC       GGACA
GAM1539  RHCG     3'  CCCCTGCCCTCCCCTTCA    33330       A     AAG
                                TGAAG GGGGGGG   AGGGG
                                |||||  ||||||   |||||
                                ACTTC CCCTCC   TCCCC
                                   _     CG_
GAM1539  SCN4A    3'  TCCCCTCTCCTCCCCCTTC    6207       A      A
                                GAAG GGGGGGA GAGGGGA
                                |||| ||||||| |||||||
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                                CTTC CCCTCCT CTCCCCT
                                  _     _
GAM1539 SIX3     5'  TCCCCCCTCCTTTCCTTC    19445      A GG   A A
                                GAAG G  GGGA G GGGGA
                                |||| |  |||| | |||||
                                CTTC C  TCCT C CCCCT
                                  _ TT   _ C
GAM1539 SLC16A2  3'  TCCCCTCTTCCCTTCCTTC   22529      A
                                GAAG GGGGGGAAGAGGGGA
                                |||| ||||||||||||||
                                CTTC CTTCCCTTCTCCCCT
                                  _
GAM1539 SPTBN4   3'  TGTTTTCCTCTCTCCTCCCCCC 48161         ____    GG
             TC                   GAGGGGGGA   AGAGG  AACA
                                |||||||||   |||||  ||||
                                CTCCCCCCT   TCTCC  TTGT
                                     CCTC    TT
GAM1539 TBR1     3'  TTCCCCTCCCCCTCGTCTTC   22731      _     AA
                                GAAGA GGGGGG  GAGGGGAA
                                ||||| ||||||  ||||||||
                                CTTCT CTCCCC  CTCCCCTT
                                  G    __
GAM1539 TCFL4    3'  CCCAGCCTTCCCCCCACTCCA  64209    A  A       AG_
                                TG AG GGGGGGAAG   GGG
                                || || |||||||||   |||
                                AC TC CCCCCCTTC   CCC
                                 C  A        CGA
GAM1539 TFAP4    3'  CCCCCTCCCCCTTCCCCA    13690    AA       A A
                                TG  GAGGGGGGA G GGGG
                                ||  |||||||||| | ||||
                                AC  CTTCCCCCT C CCCC
                                 CC       _ _
GAM1539 TNFRSF1B 3'  CCTCTTCCCCACTCCCCA    8391     AA   G
                                TG  GAG GGGGAAGAGG
                                ||  ||| ||||||||||
                                AC  CTC CCCCTTCTCC
                                 CC   A
GAM1539 UBE2V1   3'  CTTTTTCTCCCTCCTCCTCA   13968     A       AG
                                TGA GAGGGGGGA  AGGGG
                                ||| |||||||||  |||||
                                ACT CTCCTCCCT  TTTTC
                                  C        CT
GAM1539 UBE2V1   3'  CTTTTTCTCCCTCCTCCTCA   42064     A       AG
                                TGA GAGGGGGGA  AGGGG
                                ||| |||||||||  |||||
                                ACT CTCCTCCCT  TTTTC
                                  C        CT
GAM1539 UBE2V1   3'  CTTTTTCTCCCTCCTCCTCA   42604     A       AG
                                TGA GAGGGGGGA  AGGGG
                                ||| |||||||||  |||||
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                                ACT CTCCTCCCT  TTTTC
                                  C       CT
GAM1539  VGF      5'  CCCCGACCCTCCTCTCCA    14049    A       AAGA
                                TG AGAGGGGGG   GGGG
                                || |||||||||   ||||
                                AC TCTCCTCCC   CCCC
                                 C       AG__
GAM1539  WFS1     3'  TCTCCTCCCCCACCTTCA    21169      AG     AGA
                                TGAAG  GGGGGA  GGGGA
                                |||||  ||||||  |||||
                                ACTTC  CCCCCT  CCTCT
                                   CA    ___
GAM1539  ZNF278   3'  CCTTTTCCCCCCTTTCA     50280     A
                                TGA GAGGGGGGAAGAGG
                                ||| ||||||||||||||
                                ACT TTCCCCCCTTTTCC
                                 _
GAM1539  AAMP     3'  TCCCCTCTCCTTTTCTTC    8436          GA
                                GAAGAGGGGG  AGAGGGGA
                                ||||||||||  ||||||||
                                CTTCTTTTCC  TCTCCCCT
                                     __
GAM1539  ACTL6    3'  CCCCTCCTCCTTTCCCTCT   32994       __   A
                                AGAGGG  GGGA GAGGGG
                                ||||||  |||| ||||||
                                TCTCCC  TCCT CTCCCC
                                   TT   C
GAM1539  ARHGAP10 3'  CCCCCCCCCCCCTTCA      40829      A     AAGA
                                TGAAG GGGGGG   GGGG
                                ||||| ||||||   ||||
                                ACTTC CCCCCC   CCCC
                                  _    C___
GAM1539  ATP6V0A1 3'  CCCCTAGTGCCCCCTCCTCA  18984     A      GAAG
                                TGA GAGGGGG   AGGGG
                                ||| |||||||   |||||
                                ACT CTCCCCC   TCCCC
                                  C     GTGA
GAM1539  C11orf11 3'  TGTTCCCCTCAGCTTTCCCTCC 94885         ____
            TC                  GAGGGGGGAA   GAGGGGAACA
                                ||||||||||   ||||||||||
                                CTCCTCCCTT   CTCCCCTTGT
                                     TCGA
GAM1539  C11orf25 3'  TCCCCCCCCCTCCTTA     49467     A      AAGAG
                                TGA GAGGGGGG    GGGA
                                ||| ||||||||    ||||
                                ATT CTCCCCCC    CCCT
                                  C      _____
GAM1539  C19orf7  3'  CCCCTTCCCTCCTCCTCA    61779     A        A
                                TGA GAGGGGGGAAG GGG
                                ||| |||||||||| |||
```

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                                ACT CTCCTCCCTTC CCC
                                  C        _
GAM1539  C20orf149 3'  TCCCTCGCCCCCCTCCCCA   44428    AA       AA
                                TG  GAGGGGGGG  GAGGGG
                                ||  ||||||||  ||||||
                                AC  CTCCCCCC  CTCCCT
                                 CC       G_
GAM1539  C20orf98  3'  TGGATCCTTCCCCCCTTCTCA  72010     AG       AGA    AA
                                TGA  AGGGGGGA   GGGG  CA
                                |||  ||||||||   ||||  ||
                                ACT  TCCCCCCT   TCCT  GT
                                  CT        ___    AG
GAM1539  CAMTA2    3'  TGTAGGCCTCCTCCCTCCTCCC 61886    AA        A    GGA
              CA                  TG  GAGGGGGGA GAGG   ACA
                                ||  |||||||| ||||   |||
                                AC  CTCCTCCCT CTCC   TGT
                                 CC        C    GGA
GAM1539  CASKIN1   3'  TGTCCCCCCAGGCCTCTCCTC  40785       _  AAGA    A
                                GAGGGG GG    GGGG ACA
                                ||||||  ||    |||| |||
                                CTCCTC CC    CCCC TGT
                                   T  GGAC    C
GAM1539  CCNG2     3'  CCCTCCCCCCTTCTCA      16376     A       AA
                                TGA GAGGGGGG  GAGGG
                                |||  ||||||||  |||||
                                ACT CTTCCCCC  CTCCC
                                  _       __
GAM1539  CCNI      5'  CCCCTCCCCCCCTTTCA     23366     A       AA
                                TGA GAGGGGGG  GAGGGG
                                |||  ||||||||  ||||||
                                ACT TTCCCCCC  CTCCCC
                                  _       __
GAM1539  CNOT3     3'  CCCCTCCTCCCCTCCCCA    27983    AA       AA
                                TG  GAGGGGGG  GAGGGG
                                ||  ||||||||  ||||||
                                AC  CTCCCCTC  CTCCCC
                                 CC        __
GAM1539  CNOT7     3'  CCTTTCCCCCCCCTTTCA    26254      A     A
                                TGAAG GGGGGG AGAGG
                                |||||  ||||||  |||||
                                ACTTT  CCCCCC  TTTCC
                                   C      C
GAM1539  DDM36     3'  CCTCCTCCCCCTCCTTCA    40919      AG     A
                                TGAAG  GGGGGA GAGG
                                |||||  ||||||  ||||
                                ACTTC  CCCCCT CTCC
                                   CT      C
GAM1539  DGS-A     3'  TCCCTGCCCCCCCTCTTCA    86055          AAGA
                                TGAAGAGGGGGG    GGGGA
                                ||||||||||||    |||||
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                                ACTTCTCCCCCC   TCCCT
                                      G___
GAM1539  DKFZP434O047 5'  TGTTCCCACCCCTCCTCCCCA  32126    AA      AAGAG
                                TG  GAGGGGGG    GGGAACA
                                ||  ||||||||    |||||||
                                AC  CTCCTCCC    CCCTTGT
                                 CC       CA___
GAM1539  DKFZP434P1750 3'  GTTCCCTTCCACCCCTC     32028       GGAA
                                GAGGGG   GAGGGGAAC
                                ||||||   |||||||||
                                CTCCCC   CTTCCCTTG
                                   AC__
GAM1539  DKFZp547F072 5'  CCCCAAGACCCCTCCTTCA   51087      A     AAGA
                                TGAAG GGGGGG   GGGG
                                ||||| ||||||   ||||
                                ACTTC CTCCCC   CCCC
                                   _     AGAA
GAM1539  DKFZp761G2113 3'  CTGCTTCCACCCCCTTCA    70465      A   _    A
                                TGAAG GGGG GGAAG GG
                                ||||| |||| ||||| ||
                                ACTTC CCCC CCTTC TC
                                   _   A    G
GAM1539  EZF-2    3'  TCTCCTCCTTCCCCCCTCTTC  37680            _
                                GAAGAGGGGGGAAG AGGGGA
                                |||||||||||||| ||||||
                                CTTCTCCCCCCTTC TCCTCT
                                      C
GAM1539  FLJ10074  5'  TCCCCGGTCCCTCCCCTCCCCA 36284    AA    __   AGA
                                TG  GAGGGG  GGA   GGGGA
                                ||  ||||||  |||   |||||
                                AC  CTCCCC  CCT   CCCCT
                                 CC     TC   GG_
GAM1539  FLJ10700  3'  CCCCCTTCCCCTCCCTCCA   36961    A  A       A
                                TG AG GGGGGGAAG GGGG
                                || || ||||||||| ||||
                                AC TC CTCCCCTTC CCCC
                                 C  C       _
GAM1539  FLJ10706  5'  TTCAGAGTCTCCCCTCCTCA   36986     A       AGAGG
                                TGA GAGGGGGGA    GGA
                                ||| |||||||||    |||
                                ACT CTCCCCTCT    CTT
                                  C        GAGA_
GAM1539  FLJ10932  3'  TGTTCCTGCTGTCCCCTCCCCT 37434      A  _    _  AG
            TCA                   TGAAG GG GGGGA AG  GGGAACA
                                ||||| || ||||| ||  |||||||
                                ACTTC CC CCCCT TC  TCCTTGT
                                   C  T    G  G_
GAM1539  FLJ11320  3'  TCCCCCCTCCCTCTCCA     37831     A       AAGA
                                TG AGAGGGGGG   GGGGA
                                || |||||||||   |||||
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                                AC TCTCCCTCC    CCCCT
                                 C       ____
GAM1539  FLJ12587  3'  CCCCTCCCCTCCCCTCCTCA   42776     A       AA
                                TGA GAGGGGGG  GAGGGG
                                ||| ||||||||  ||||||
                                ACT CTCCCCTC  CTCCCC
                                  C       CC
GAM1539  FLJ13055  3'  CCCCTTTCCTGCCCCCTCCTCA 43015     A      GA__
                                TGA GAGGGGG    AGAGGGG
                                ||| |||||||    |||||||
                                ACT CTCCCCC    TTTCCCC
                                  C      GTCC
GAM1539  FLJ13612  3'  TTCCCCCAGTCCCTCCCTCTTC 48090         _    AGA
                  A                  TGAAGAGGG GGGA   GGGGAA
                                |||||||||| ||||   ||||||
                                ACTTCTCCC CCCT   CCCCTT
                                      T    GAC
GAM1539  FLJ14299  3'  CCTCCTCCTCCCTCCCCA    47550    AA       A
                                TG  GAGGGGGGA GAGG
                                ||  ||||||||| ||||
                                AC  CTCCCTCCT CTCC
                                 CC        C
GAM1539  FLJ14442  3'  CCCTCCTCCTCCCTCCTCA    52379     A       A
                                TGA GAGGGGGGA GAGGG
                                ||| ||||||||| |||||
                                ACT CTCCCTCCT CTCCC
                                  C        C
GAM1539  FLJ14525  3'  CCCAACTTTCCCCCTCCTCA   52479     A        AG
                                TGA GAGGGGGGAAG  GGG
                                ||| ||||||||||  |||
                                ACT CTCCCCCTTTC  CCC
                                  C         AA
GAM1539  FLJ14525  3'  TTCCCCCTCCCCCCTC      52484         A A
                                GAGGGGGGA G GGGGAA
                                ||||||||| | ||||||
                                CTCCCCCCT C CCCCTT
                                      _ _
GAM1539  FLJ21477  3'  GTTCCCCTCCCCACCCCCCC   47903       AA___
                                GGGGGG    GAGGGGAAC
                                ||||||    |||||||||
                                CCCCCC    CTCCCCTTG
                                   CACCC
GAM1539  FOXH1     5'  TCCCCTCCCCCACAGCCTCTTC 15380       ____   AA
                                GAAGAGG   GGGG  GAGGGGA
                                |||||||   ||||  |||||||
                                CTTCTCC   CCCC  CTCCCCT
                                    GACA   __
GAM1539  GTF2A1    5'  CCCCTCCTCCTCCTCTCTCCG  32401    A     _   A
                                TG AGAGGGG GGA GAGGGG
                                || ||||||| ||| ||||||
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                                GC TCTCTCC CCT CTCCCC
                                 C      T  C
GAM1539 H17      3' CCTTCTCCCCCTCCCCA     34514    AA      GA
                                TG  GAGGGGGG  AGAGGG
                                ||  |||||||  ||||||
                                AC  CTCCCCC  TCTTCC
                                 CC      __
GAM1539 HCNP     3' TCCCCCATCCCCCCTCCCCA  71543    AA       AGA
                                TG  GAGGGGGGA  GGGGA
                                ||  |||||||||  |||||
                                AC  CTCCCCCCT  CCCCT
                                 CC       AC_
GAM1539 HSA243666 3' CCCTTCCTCCCTCCCCA     34557    AA        A
                                TG  GAGGGGGGAAG GG
                                ||  |||||||||| ||
                                AC  CTCCCTCCTTC CC
                                 CC        _
GAM1539 HSPC166  3' TGTTCCCTGAGCCCCCTC    27198       GAAGA
                                GAGGGGG    GGGGAACA
                                |||||||    ||||||||
                                CTCCCCC    TCCCTTGT
                                    GAG__
GAM1539 ING4     3' TCCCTTCTCCTCCCCTCT    60432        A
                                AGAGGGGGG AGAGGGGA
                                ||||||||| |||||||
                                TCTCCCCTC TCTTCCCT
                                     C
GAM1539 KIAA0293 3' CCCCCTGCTCCTCTTCA     61236         GGA  A
                                TGAAGAGGGG   AG GGGG
                                ||||||||||   || ||||
                                ACTTCTCCTC   TC CCCC
                                     G__  _
GAM1539 KIAA0574 3' CCTTCCCCCCCTCCTC      69811    A       AA
                                GA GAGGGGGG  GAGGG
                                || ||||||||  |||||
                                CT CTCCCCCC  CTTCC
                                 C       __
GAM1539 KIAA0731 3' TCCCCTTCCCCCTCCTCT    67483        AA
                                AGAGGGGGG  GAGGGGA
                                |||||||||  |||||||
                                TCTCCTCCC  TTCCCCT
                                     CC
GAM1539 KIAA1183 3' GTTCCCCTCTCGGGCCCTC   63199      GGGA
                                GAGGG    AGAGGGGAAC
                                |||||    ||||||||||
                                CTCCC    TCTCCCCTTG
                                   GGGC
GAM1539 KIAA1337 3' CCCCGCAACCCTCCCCTTCA  73057      A     AAGA
                                TGAAG GGGGGG    GGGG
                                ||||| ||||||    ||||
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                                ACTTC CCTCCC    CCCC
                                  C     AACG
GAM1539  KIAA1536  3'  CCCCCCTCCCTCTCCA     40876    A       AAGA
                                TG AGAGGGGGG    GGGG
                                || |||||||||    ||||
                                AC TCTCCCTCC    CCCC
                                 C       _____
GAM1539  KIAA1576  3'  TTCCCCTCTCCCCTGTATCA   66494     AGAG     A
                                TGA    GGGGGA GAGGGGAA
                                |||    |||||| ||||||||
                                ACT    TCCCCT CTCCCCTT
                                  ATG_     _
GAM1539  KIAA1580  5'  TGTTCCCCTCCCCCCCCC    69983       AA
                                GGGGGG  GAGGGGAACA
                                ||||||  ||||||||||
                                CCCCCC  CTCCCCTTGT
                                   CC
GAM1539  KIAA1706  3'  TCACCTCCTCCCTCCTCCCCA  94370    AA       A    G
                                TG  GAGGGGGGA GAGG GA
                                ||  ||||||||| |||| ||
                                AC  CTCCTCCCT CTCC CT
                                 CC       C    A
GAM1539  KIAA1811  3'  TCCCCAACCCCCTCTTC     65421          GAAGA
                                GAAGAGGGGG    GGGGA
                                ||||||||||    |||||
                                CTTCTCCCCC    CCCCT
                                      AA___
GAM1539  MAP2K5    5'  TCCCCTCTTCCCTCCCCCTC   12329        ___
                                GAGGGGG   GAAGAGGGGA
                                |||||||   ||||||||||
                                CTCCCCC   CTTCTCCCCT
                                   TCC
GAM1539  MGC13090  3'  CCCTTCTTCCCACCCCCTC    52119        ___
                                GAGGGGG   GAAGAGGGG
                                |||||||   |||||||||
                                CTCCCCC   CTTCTTCCC
                                   ACC
GAM1539  MGC21854  3'  TCCTCTCCCCTCTTCA      54604          GGA
                                TGAAGAGGGG   AGAGGG
                                ||||||||||   ||||||
                                ACTTCTCCCC   TCTCCT
                                      ___
GAM1539  MGC2803   3'  TGTCCCCCCCTTCTCACCTCCT 44087     A   G     A   A
            CA                    TGA GAGG GGGAAG GGGG ACA
                                ||| |||| |||||| |||| |||
                                ACT CTCC CTCTTC CCCC TGT
                                  C   A     C   C
GAM1539  MGC33630  3'  TTTCCCTCCCCCCTCTCA    59005     A       AGA
                                TGA GAGGGGGGA   GGGGAA
                                ||| |||||||||   ||||||
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                                ACT CTCCCCCCT   CCCTTT
                                  _      ___
GAM1539  NFKBIE   5'  TTCCCCGGTTCCCCCTC    93661        AGA
                                GAGGGGGGA   GGGGAA
                                |||||||||   ||||||
                                CTCCCCCTT   CCCCTT
                                    GG_
GAM1539  PALM     5'  GTCCCCCTCCCCTCCCCTC   11967        AA     A
                                GAGGGGGG  GAGGGG AC
                                ||||||||  |||||| ||
                                CTCCCCTC  CTCCCC TG
                                    CC     C
GAM1539  PGS1     5'  TGTTCCCCAGGTCACCTCCCC  44596       AA ___
                                GGGGGG  GA   GGGGAACA
                                ||||||  ||   ||||||||
                                CCCCTC  CT   CCCCTTGT
                                   CA  GGA
GAM1539  PILB     3'  GTTCCCTTGCCACCCCTTC   25249        GAAG
                                GAGGGGG    AGGGGAAC
                                |||||||    ||||||||
                                CTTCCCC    TTCCCTTG
                                   ACCG
GAM1539  PMX2B    3'  CTCCTACCCCCTTCCTCA    15383     A      AAG
                                TGA GAGGGGGG   AGGGG
                                ||| ||||||||   |||||
                                ACT CTTCCCCC   TCCTC
                                  C       A__
GAM1539  PP1665   5'  TGTTCCCCTCTTTGGCCCTCTC 48643         __
                                GAGGGGG  GAAGAGGGGAACA
                                |||||||  ||||||||||||
                                CTCTCCC  TTTCTCCCCTTGT
                                   GG
GAM1539  PTPRU    3'  CCCCTCTTCCTTTAATCTTC   56523      GG_
                                GAAGA   GGGGAAGAGGGG
                                |||||   ||||||||||||
                                CTTCT   TTCCTTCTCCCC
                                   AAT
GAM1539  PTPRU    3'  CCCCTCTTCCTTTAATCTTC   56527      GG_
                                GAAGA   GGGGAAGAGGGG
                                |||||   ||||||||||||
                                CTTCT   TTCCTTCTCCCC
                                   AAT
GAM1539  PTPRU    3'  CCCCTCTTCCTTTAATCTTC   20321      GG_
                                GAAGA   GGGGAAGAGGGG
                                |||||   ||||||||||||
                                CTTCT   TTCCTTCTCCCC
                                   AAT
GAM1539  SENP7    5'  CCTCCCCCTCCCTCTCCA    40672    A       AA
                                TG AGAGGGGGG  GAGG
                                || |||||||||  ||||
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                                AC TCTCCCTCC  CTCC
                                 C        CC
GAM1539  SEPT6    5'  GTTAAATCCGCCCCCTCTCCA  31393    A       GAA  GGGG
                                TG AGAGGGGGG   GA    AAC
                                || ||||||||   ||    |||
                                AC TCTCCCCC   CT    TTG
                                 C       GC_  AAA_
GAM1539  THG-1    5'  TCCCCCCTCCCGCCACCTC   48915      _ _  A  A
                                GAGG GG GG AG GGGGA
                                |||| || || || |||||
                                CTCC CC CC TC CCCCT
                                  A  G  C  C
GAM1539  U2AF65   3'  CCCCCCTTATCCCCCTCT    24411          _   A
                                AGAGGGGGG AAG GGGG
                                ||||||||| ||| ||||
                                TCTCCCCCT TTC CCCC
                                      A   C
GAM1539  LOC113521 5'  CCTCTCCGCCCCCTCCCCA   73405    AA      GAA
                                TG  GAGGGGG   GAGGGG
                                ||  |||||||   ||||||
                                AC  CTCCCCC   CTCTCC
                                 CC      GC_
GAM1539  LOC126526 3'  TCCCTTCCCCCACTCCCCA   75039    AA  _       A
                                TG  GAG GGGGGAAG GGG
                                ||  ||| |||||||| |||
                                AC  CTC CCCCCTTC CCT
                                 CC   A       _
GAM1539  LOC127829 3'  GTCCCCCTAAGCCCACCCCTCC 57916     A     _  AAG_    A
            TCA                    TGA GAGGGG GG    AGGGG AC
                                ||| |||||| ||    ||||| ||
                                ACT CTCCCC CC    TCCCC TG
                                  C     A  CGAA    C
GAM1539  LOC143879 3'  TCTCCTCCCCCCCCTCTCA    77161     A       AA
                                TGA GAGGGGGG  GAGGGGA
                                ||| ||||||||  |||||||
                                ACT CTCCCCCC  CTCCTCT
                                  _      __
GAM1539  LOC145468 3'  TCCCTTCCCTCCCCCCTC    74257          A_
                                GAGGGGGGA  GAGGGGA
                                |||||||||  |||||||
                                CTCCCCCCT  CTTCCCT
                                      CC
GAM1539  LOC146756 3'  CCCCCAGTCCCTCTCCTCA   84797     A       AAGA
                                TGA GAGGGGGG    GGGG
                                ||| ||||||||    ||||
                                ACT CTCTCCCT    CCCC
                                  C       GAC_
GAM1539  LOC146958 5'  TGTTCCACCTCCCCCCCTCCCCA 84952     AA        AGA  _
                                TG  GAGGGGGGA   GG GGAACA
                                ||  |||||||||   || ||||||
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                                AC  CTCCCCCCT   CC CCTTGT
                                 CC        ___  A
GAM1539  LOC147353 3'  TTCCCCTCCTTCCCCTGCTTCA 85137      A      A
                                TGAAG GGGGGGA GAGGGGAA
                                ||||| ||||||| ||||||||
                                ACTTC TCCCCTT CTCCCCTT
                                   G      C
GAM1539  LOC148195 5'  TGTCCCCCTCTCCTTTTTTTC  85296          GA      A
                                GAAGAGGGGG  AGAGGGG ACA
                                ||||||||||  ||||||| |||
                                CTTTTTTTCC  TCTCCCC TGT
                                      __      C
GAM1539  LOC148758 3'  TTTTTCTTCCCTCCCCTTCA   79731       A
                                TGAAG GGGGGGAAGAGGGG
                                ||||| ||||||||||||||
                                ACTTC CCTCCCTTCTTTTT
                                   C
GAM1539  LOC150155 3'  TCCCTTCCCTCCCCCCTC     71418         A_
                                GAGGGGGGA  GAGGGGA
                                |||||||||  |||||||
                                CTCCCCCCT  CTTCCCT
                                     CC
GAM1539  LOC152414 5'  TCCCCTTTCCCTCCTCT     88610          A
                                AGAGGGGGGA GAGGGGA
                                |||||||||| |||||||
                                TCTCCTCCCT TTCCCCT
                                      _
GAM1539  LOC157531 5'  TTCCCCCCTGCCTCTCTC     87768         A  A
                                GAGGGGGG AG GGGGAA
                                |||||||| || ||||||
                                CTCTCTCC TC CCCCTT
                                     G  C
GAM1539  LOC158062 3'  TCCCCTCTGTCCCTCCCCTCCA 87967     A  A      _
                                TG AG GGGGGGA AGAGGGGA
                                || || ||||||| ||||||||
                                AC TC CCTCCCT TCTCCCCT
                                 C  C      G
GAM1539  LOC168544 3'  CCCCTCCACTTCCCCTTCT    83592          A__
                                AGAGGGGGGA   GAGGGG
                                ||||||||||   ||||||
                                TCTTCCCCTT   CTCCCC
                                      CAC
GAM1539  LOC196500 3'  CCCTTTCCCCCTCCTCA     89082     A         A
                                TGA GAGGGGGGAAG GG
                                ||| ||||||||||| ||
                                ACT CTCCCCCTTTC CC
                                  C         _
GAM1539  LOC199986 5'  TCAGCCTCCCTCCCCTCTC    91511         A_   G_
                                GAGGGGGGA  GAGG  GA
                                |||||||||  ||||  ||
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                                CTCTCCCCT  CTCC  CT
                                     CC    GA
GAM1539  LOC200261 5'  TCCCCCTCCCTTCCCTTC    90053     A     A  A
                                GAAG GGGGGG AG GGGGA
                                |||| |||||| || |||||
                                CTTC CCTTCC TC CCCCT
                                  _     C  _
GAM1539  LOC200734 5'  TCTCTAGCCGCCCCCCCTCCCC 90283    AA       AAGA__
            A                    TG  GAGGGGGG     GGGGA
                                ||  ||||||||     |||||
                                AC  CTCCCCCC     TCTCT
                                 CC       CGCCGA
GAM1539  LOC219688 5'  CCCCTCCTCCTCCTCTTC    94639          AA
                                GAAGAGGGGGG  GAGGGG
                                ||||||||||  ||||||
                                CTTCTCCTCCT  CTCCCC
                                       C_
GAM1539  LOC222815 5'  TCTCCTCCCCCTTCTCCA    96024    A        AGA
                                TG AGAGGGGGGA   GGGGA
                                || ||||||||||   |||||
                                AC TCTTCCCCCT   CCTCT
                                 C        ___
GAM1539  LOC254428 3'  TGTTCCCCTGTCCCTCCTC    97201         AG
                                GAGGGGGGA  AGGGGAACA
                                |||||||||  |||||||||
                                CTCCTCCCT  TCCCCTTGT
                                      G_
GAM1539  LOC256901 3'  CCACTTCCCCCTTCTCCA    98420    A         A
                                TG AGAGGGGGGAAG GG
                                || ||||||||||| ||
                                AC TCTTCCCCCTTC CC
                                 C          A
GAM1539  LOC51031  3'  CCCCTCTTACTTGCTTTCA   32707     A  G  G
                                TGA GAG GGG AAGAGGGG
                                ||| ||| ||| ||||||||
                                ACT TTC TTC TTCTCCCC
                                  _  G  A
GAM1539  LOC58486  5'  TTCCCCTCCCTCTCTCCCCTC  41364         A___
                                GAGGGGGGA   GAGGGGAA
                                |||||||||   ||||||||
                                CTCCCCTCT   CTCCCCTT
                                     CTCC
GAM1539  LOC90719  5'  CCCCCTCCCTCCTCTCCG    64607    A        A A
                                TG AGAGGGGGGA G GGGG
                                || ||||||||||| | ||||
                                GC TCTCCTCCCT C CCCC
                                 C        _ _
GAM1539  LOC91947  3'  TTCCCCTCTTGCTCTTCT    68227        G  A
                                AGAGGGG GA GAGGGGAA
                                ||||||| || ||||||||
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                                TCTTCTC TT CTCCCCTT
                                   G  _
GAM1539 LOC92230 5' TTTGCCTCCCCCTCTTCA    69088          GAAG  G
                                TGAAGAGGGGG   AGG GAA
                                ||||||||||   ||| |||
                                ACTTCTCCCCC   TCC TTT
                                      ____  G
GAM1540 ADAMTS13 3' TGACAGTTACCCCCAACCTG  58158        AA  TGGA
                                CAGGTTGG  GTG   GTCA
                                ||||||||  |||   ||||
                                GTCCAACC  CAT   CAGT
                                    CC  TGA_
GAM1540 ASGR2    3' ACCCATACCCCACACCTG    56028      _  AA    A
                                CAGGT TGG  GTGTGG GT
                                ||||| |||  |||||| ||
                                GTCCA ACC  CATACC CA
                                  C  C_    _
GAM1540 ASGR2    3' ACCCATACCCCACACCTG    56033      _  AA    A
                                CAGGT TGG  GTGTGG GT
                                ||||| |||  |||||| ||
                                GTCCA ACC  CATACC CA
                                  C  C_    _
GAM1540 ASGR2    3' ACCCATACCCCACACCTG    56037      _  AA    A
                                CAGGT TGG  GTGTGG GT
                                ||||| |||  |||||| ||
                                GTCCA ACC  CATACC CA
                                  C  C_    _
GAM1540 ASGR2    3' ACCCATACCCCACACCTG    8628       _  AA    A
                                CAGGT TGG  GTGTGG GT
                                ||||| |||  |||||| ||
                                GTCCA ACC  CATACC CA
                                  C  C_    _
GAM1540 CNR1     3' CAAATTCCCAACCTGCTC    32719    A      A  G
                                GA CAGGTTGG AGT TG
                                || |||||||| ||| ||
                                CT GTCCAACC TTA AC
                                 C       C  A
GAM1540 DXF68S1E 3' ACTCTTCAATCCCAACCTG   60663        AAG  T
                                CAGGTTGG   TG GGAGT
                                ||||||||   || |||||
                                GTCCAACC   AC TCTCA
                                    CTA  T
GAM1540 EVA1     3' TGACCCGTTTTCCAACCAGTTC 20533     A       TGT  A
                                GAAC GGTTGGAAG   GG GTCA
                                |||| |||||||||   || ||||
                                CTTG CCAACCTTT   CC CAGT
                                  A       TG_  _
GAM1540 HPRT1    3' TGACTGTATTTTCCAACTTGTT 5760            T  G
            C                    GAACAGGTTGGAAG GTG AGTCA
                                ||||||||||||| ||| |||||
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                                  CTTGTTCAACCTTT TAT TCAGT
                                        _  G
GAM1540  HTR6     5'  CAAACTTCCAACCCGTTT    7889       A        G
                                  GAAC GGTTGGAAGT TG
                                  |||| |||||||||| ||
                                  TTTG CCAACCTTCA AC
                                    C         A
GAM1540  IL1RN    3'  CCACCTGCCCAACCTGCTC   6957     A       A_  T
                                  GA CAGGTTGG  AG GTGG
                                  || ||||||||  || ||||
                                  CT GTCCAACC  TC CACC
                                   C       CG  _
GAM1540  IRTA2    3'  TGACTCTGCTGCCCCAACCTTT 49234     C       AAGT TG
               C                   GAA AGGTTGG    G  GAGTCA
                                  ||| |||||||    |  ||||||
                                  CTT TCCAACC    C  CTCAGT
                                   _      CCGT GT
GAM1540  PDYN     5'  CCACCTCCGACCTGCTC     44586    A       A T
                                  GA CAGGTTGGA G GTGG
                                  || |||||||||  | ||||
                                  CT GTCCAGCCT C CACC
                                   C       _ _
GAM1540  PLOD     3'  TGACTCGTGCTCTCCAACCTGT 6117          _  TG  G
                                  ACAGGTTGGA AG  TG AGTCA
                                  ||||||||||  ||  || |||||
                                  TGTCCAACCT TC  GC TCAGT
                                        C  GT  _
GAM1540  RARA     3'  GCCCCCCACCCCCAACCTGT   8253          AA   T  A
                                  ACAGGTTGG  GTG GG GT
                                  |||||||||  ||| || ||
                                  TGTCCAACC  CAC CC CG
                                        CC   C  C
GAM1540  SLC9A1   3'  TGGCCACCACCCAACCTGT    70933         AAGT    A_
                                  ACAGGTTGG    GTGG  GTCA
                                  |||||||||    ||||  ||||
                                  TGTCCAACC    CACC  CGGT
                                        _____    AC
GAM1540  C20orf16 3'  ACTCGTGACCTCCAGCCTG   39239         A  GTG
                                  CAGGTTGGA GT   GAGT
                                  |||||||||  ||   ||||
                                  GTCCGACCT CA   CTCA
                                        C  GTG
GAM1540  C20orf4  3'  TCACCTCCCACCTGTTC     31949         T   A T
                                  GAACAGGT GGA G GTGG
                                  |||||||| ||| | ||||
                                  CTTGTCCA CCT C CACT
                                        C   _ _
GAM1540  FLJ13769 3'  ACCCCACACCCCTCCACTTCC  47236   C    T   A__      A
                                  A AGGT GGA   GTGTGG GT
                                  | |||| |||   |||||| ||
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                                C TTCA CCT   CACACC CA
                                 C   _   CCC     C
GAM1540 KIAA0450 5' TGACTCCACACCCAGCATGT  28373    G    AA
                                ACA GTTGG  GTGTGGAGTCA
                                ||| |||||  ||||||||||
                                TGT CGACC  CACACCTCAGT
                                  A    __
GAM1540 KIAA1271 3' GACTCCACAAGACCTGCCT   70139     T  AAG
                                AGGT GG   TGTGGAGTC
                                |||| ||   |||||||||
                                TCCG CC   ACACCTCAG
                                  T  AGA
GAM1540 KIAA1317 3' TGACTCCACACTCAGCCT    87215      GA
                                AGGTTG  AGTGTGGAGTCA
                                ||||||  ||||||||||||
                                TCCGAC  TCACACCTCAGT

                                  __
GAM1540 KIAA1784 3' GACCCCACCCCAACCTG     65750       AA   T  A
                                CAGGTTGG  GTG GG GTC
                                ||||||||  ||| || |||
                                GTCCAACC  CAC CC CAG
                                     C_   _ _
GAM1540 MGC35558 3' TGACTGAGTTTCCCAACCTG  59421       A  TGTGG
                                CAGGTTGG AG    AGTCA
                                |||||||| ||    |||||
                                GTCCAACC TT    TCAGT
                                     C  TGAG_
GAM1540 NBR2     3' ACTCCACAAGGACCCTTC    20614     CA    GGAAG
                                GAA  GGTT    TGTGGAGT
                                |||  ||||    ||||||||
                                CTT  CCAG    ACACCTCA
                                  C_   GA___
GAM1540 phospho1 3' GACCCCACACTATTTCTGT   83247      TTGGA      A
                                ACAGG    AGTGTGG GTC
                                |||||    ||||||| |||
                                TGTCT    TCACACC CAG
                                   TTA__      C
GAM1540 SLC26A10 5' TGACTGTGGACCCCAACC    56849       AA  G  G
                                GGTTGG  GT TG AGTCA
                                ||||||  || || |||||
                                CCAACC  CA GT TCAGT
                                   C_  G  G
GAM1540 TPC2     3' GACTCCACAGGGACCTTTC    58195     C    GGAAG
                                GAA AGGTT    TGTGGAGTC
                                ||| |||||    |||||||||
                                CTT TCCAG    ACACCTCAG
                                  _    GG___
GAM1540 LOC145790 3' GACCAGTTTCCAACCTTTC  77954     C        _  TGGA
                                GAA AGGTTGGAAG TG    GTC
                                ||| ||||||||| ||    |||
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                                CTT TCCAACCTTT AC    CAG
                                  _        G _____
GAM1540  LOC151361 3'  TGACCCTCCTTCCTCCAGCCTG 86508         AGTGT  __
                                CAGGTTGGA    GGA  GTCA
                                |||||||||    |||  ||||
                                GTCCGACCT    CCT  CAGT
                                     CCTT_   CC
GAM1540  LOC202038 5'  CCACCCCAACCTGTTC      90619          AAGT
                                GAACAGGTTGG    GTGG
                                ||||||||||    ||||
                                CTTGTCCAACC    CACC
                                      C___
GAM1540  LOC219405 3'  TGAAGCCCCAGCCTGCTC    92451    A      AAGTGT  AG
                                GA CAGGTTGG     GG  TCA
                                || ||||||||     ||  |||
                                CT GTCCGACC     CC  AGT
                                 C       _______  GA
GAM1541  CELL      3'  CTGCCATCAACAAGGGCAA    10169         CT_   A
                                TTGCCCTTG   ATGG GG
                                |||||||||   |||| ||
                                AACGGGAAC   TACC TC
                                     AAC    G
GAM1541  EFNB2     3'  CTCCTCCAGCCGCTGGCAA    15842      CTT  TA_
                                TTGCC   GC   TGGAGGAG
                                |||||   ||   ||||||||
                                AACGG   CG   ACCTCCTC
                                   T__  CCG
GAM1541  MECP2     3'  CTCCCCTTCCCAGGGCAATA   18400         TGCTAT  A
                                TATTGCCCT     GG GGAG
                                |||||||||     || ||||
                                ATAACGGGA     CC CCTC
                                     CCCTT_ _
GAM1541  PKDREJ    3'  CTCCCCGTACAAGGGCAA     21383         C    A
                                TTGCCCTTG TATGG GGAG
                                ||||||||| ||||| ||||
                                AACGGGAAC ATGCC CCTC
                                     _    _
GAM1541  RXRB      3'  CTCTCCTCCAGCCCTGGGCA   42030      TT_  AT
                                TGCCC   GCT  GGAGGAGAG
                                |||||   |||  |||||||||
                                ACGGG   CGA  CCTCCTCTC
                                   TCC  __
GAM1541  FLJ20519  3'  TCTCCTCAAAAGGGCAATG    35798         GCTATG
                                TATTGCCCTT     GAGGAGA
                                ||||||||||     |||||||
                                GTAACGGGAA     CTCCTCT
                                     AA_____
GAM1541  HAIK1     5'  CTCCCACAGCAAAGGCCATA   31955     T  C    A  AG
                                TAT GCC TTGCT TGG  GAG
                                ||| ||| ||||| |||  |||
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                                ATA CGG AACGA ACC  CTC
                                  C  A    C  __
GAM1541  KIAA1184  3'  CTCCTCCAGGAAGGCAA    42926      CTTG  A
                                TTGCC   CT TGGAGGAG
                                |||||   || ||||||||
                                AACGG   GG ACCTCCTC
                                   AA__  _
GAM1541  KIAA1432  3'  CTCCCCTTGGTAAAGGGCAATA 67301         _   T  A
                                TATTGCCCTT GCTA GG GGAG
                                |||||||||| |||| || ||||
                                ATAACGGGAA TGGT CC CCTC
                                      A   T  _
GAM1541  SH3BGRL3  3'  CTCTCCTCCATGTAAAGGCAA  49260      C   T
                                TTGCC TTGC ATGGAGGAGAG
                                ||||| |||| ||||||||||
                                AACGG AATG TACCTCCTCTC
                                   A   _
GAM1541  LOC122330 5'  CCTCCATGGGAGGAAGGGCAAT 76773         G___
            A                    TATTGCCCTT   CTATGGAGG
                                |||||||||   |||||||||
                                ATAACGGGAA   GGTACCTCC
                                      GGAG
GAM1541  LOC145623 3'  CTCCCCTCCAGAAAGGGCAG   84390       GCTA    A
                                TTGCCCTT   TGGAGG GAG
                                ||||||||   |||||| |||
                                GACGGGAA   ACCTCC CTC
                                     AG__     C
GAM1541  LOC220776 3'  CTCCCCTCTGTAAAAGACAA   68926    CC   GC      A
                                TTG  CTT  TATGGAGG GAG
                                |||  |||  |||||||| |||
                                AAC  GAA  ATGTCTCC CTC
                                  A_  A_       C
GAM1541  LOC255057 3'  CTCCCCCAACCCAAGGGCAA   97093       CTA   A
                                TTGCCCTTG   TGG GGAG
                                |||||||||   ||| ||||
                                AACGGGAAC   ACC CCTC
                                     CCA   C
GAM1541  LOC255649 3'  CTCTCCTCCCTAAAGCAAGGG  98195       AT__
                                CCCTTGCT   GGAGGAGAG
                                ||||||||   |||||||||
                                GGGAACGA   CCTCCTCTC
                                     AATC
GAM1542  B4GALT1   5'  GGCGGGTCGCCTCCCCTCCTG  9471       AA  T   GT  _
                                CAGGAG  GA GGCG  CT CC
                                ||||||  || ||||  || ||
                                GTCCTC  CT CCGC  GG GG
                                   CC  _   TG  C
GAM1542  BCRP2     3'  TGTACTTTTTGCCATCTCACCC 63072     AGA       TCTCC
            TG                   CAGG   AGATGGCGG    ACA
                                ||||   |||||||||    |||
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                                GTCC  TCTACCGTT   TGT
                                  CAC       TTTCA
GAM1542 CFL1    3' TGTGGAGATGACCCCTCCCTG 19749    A AGAT CG
                                CAGG GA   GG GTCTCCACA
                                |||| ||   ||  |||||||||
                                GTCC CT   CC TAGAGGTGT
                                  _ CC__  AG
GAM1542 EDAR    5' AGACCCATCTTCTGCTG    42520    G      CG
                                CAG AGAAGATGG GTCT
                                ||| |||||||||  ||||
                                GTC TCTTCTACC CAGA
                                 G       __
GAM1542 EP300   5' GCCCCGGCCGTCTTCTCC    9285          ___
                                GGAGAAGATGGC  GGT
                                ||||||||||||  |||
                                CCTCTTCTGCCG  CCG
                                       GCC
GAM1542 GCN1L1  3' GTGGGTTCCTCTTCTCCTG   70313        TGGC TC
                                CAGGAGAAGA   GG TCCAC
                                ||||||||||   ||  |||||
                                GTCCTCTTCT   CC GGGTG
                                      ____ TT
GAM1542 GLP1R   3' GGACACATTTTCTCCT     10797         GCG
                                AGGAGAAGATG  GTCT
                                ||||||||||  ||||
                                TCCTCTTTTAC  CAGG
                                      A__
GAM1542 HTRA3   3' TGGAGGTCCCCTCCTCTCCT  90586      A T C GT
                                AGGAGA GA GG G  CTCCA
                                |||||| || || |  |||||
                                TCCTCT CT CC C  GAGGT
                                   C  C  _ TG
GAM1542 KCNC4   5' GGGGGCCGCCACCGCCTCCTG 18334      AAGA
                                CAGGAG   TGGCGGTCTCC
                                ||||||   ||||||||||
                                GTCCTC   ACCGCCGGGGG
                                   CGCC
GAM1542 MAD1L1  3' TGTGAAATAAAATCTTCTCC  88873       GGCG CTC
                                GGAGAAGAT   GT  CACA
                                |||||||||   ||  ||||
                                CCTCTTCTA   TA  GTGT
                                     AAA_  AA_
GAM1542 MRPL49  3' TGGAAACCCTCACTCCTG    70175      AAGA  C  C
                                CAGGAG   TGG GGT TCCA
                                ||||||   ||| ||| ||||
                                GTCCTC   ACT CCA AGGT
                                   ____  C  A
GAM1542 NLGN1   5' GTAGAGACCGTCTCCT     30700      AAGATG      C
                                AGGAG    GCGGTCTC AC
                                |||||    |||||||| ||
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                                TCCTC     TGCCAGAG TG
                                  _______      A
GAM1542 OLIG2    5' GACGACTATCTTCCCCTG    20547     A      CG
                                CAGG GAAGATGG  GTC
                                |||| ||||||||  |||
                                GTCC CTTCTATC  CAG
                                  C       AG
GAM1542 PAFAH1B1 5' TGTGAAAGAATCATTTTCCCCT 6481      A      CGG   C_
           G                     CAGG GAAGATGG   TCT  CACA
                                |||| ||||||||   |||  ||||
                                GTCC CTTTTACT   AGA  GTGT
                                  C       A__   AA
GAM1542 PYGB     3' TGTGGAGGAGGCCATACTCCCC 12693     A  AG    GG
           T                     AGG GA  ATGGC  TCTCCACA
                                ||| ||  |||||  ||||||||
                                TCC CT  TACCG  GGAGGTGT
                                  C  CA    GA
GAM1542 SLC1A3   3' TGTGGGGAGCCCATCCTCTC   16065     A    CGG
                                GAGA GATGG   TCTCCACA
                                |||| |||||   ||||||||
                                CTCT CTACC   AGGGGTGT
                                  C    CG_
GAM1542 SLC24A1  5' TGGAGAAATCTTCTCT      17570         GGCGG
                                GGAGAAGAT    TCTCCA
                                |||||||||    ||||||
                                TCTCTTCTA    AGAGGT
                                     A_____
GAM1542 SMARCD2  3' GGCCGCCATCATCTCCTG    13263        A
                                CAGGAGA GATGGCGGTC
                                ||||||| ||||||||||
                                GTCCTCT CTACCGCCGG
                                    A
GAM1542 STK11    3' GTGGAGACCAGGCTCCTG    6601         AAGATGGC
                                CAGGAG       GGTCTCCAC
                                ||||||       |||||||||
                                GTCCTC       CCAGAGGTG
                                   GGA_____
GAM1542 SUV39H2  5' TGCGGACGCCTATCCTCC    45460     AA  _   GTC   A
                                GGAG  GAT GGCG   TCC CA
                                ||||  ||| ||||   ||| ||
                                CCTC  CTA CCGC   AGG GT
                                  __   T   ___   C
GAM1542 TAL1     3' GTGAGCCCCATCTTCACC    13531    A      C  T   C
                                GG GAAGATGG GG CTC AC
                                || |||||||| || ||| ||
                                CC CTTCTACC CC GAG TG
                                 A       _ _  _
GAM1542 UBE2H    3' TGCAGATTTCATCTTCACCT   13955     A      C    C
                                AGG GAAGATGG GGTCT CA
                                ||| |||||||| ||||| ||
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                                TCC CTTCTACT TTAGA GT
                                  A       _    C
GAM1542  ACYP2    5'  TGTGGAGACAGCATCCTCCCC  57407    A  A    G G
                                GG GA GATG C GTCTCCACA
                                || || |||| | |||||||||
                                CC CT CTAC G CAGAGGTGT
                                 C  C    _ A
GAM1542  AP1GBP1   5'  TGTGATTTCGCCATCTTCTCC  55449            TCTC
                                GGAGAAGATGGCGG    CACA
                                ||||||||||||||    ||||
                                CCTCTTCTACCGCT    GTGT
                                         TTA_
GAM1542  B3GNT7   3'  GAGACCACCACTTCTCCTG   71679         A   C
                                CAGGAGAAG TGG GGTCTC
                                ||||||||| ||| ||||||
                                GTCCTCTTC ACC CCAGAG
                                      _   A
GAM1542  CGI-127   3'  GAGAAATCCATCTTTTCC    32674          CGG
                                GGAGAAGATGG   TCTC
                                ||||||||||   ||||
                                CCTTTTCTACC   AGAG
                                       TAA
GAM1542  DKFZP434B205 3'  GGCCTCGCACCTTCTTCTCCTG 75845          TG__  __
                                CAGGAGAAGA    GC  GGTC
                                |||||||||    ||  ||||
                                GTCCTCTTCT    CG  CCGG
                                      TCCA  CT
GAM1542  DKFZP434H0820 3'  TGGGTGCTGCCATCCTTCCTG  64587       AA       CT
                                CAGGAG  GATGGCGGT  CCA
                                ||||||  |||||||||  |||
                                GTCCTT  CTACCGTCG  GGT
                                   C_       TG
GAM1542  DKFZP564G202 3'  TGTGGAGACTTTTCTTCCCC   65887    A    TGGC
                                GG GAAGA    GGTCTCCACA
                                || |||||    ||||||||||
                                CC CTTCT    TCAGAGGTGT
                                 C    TT__
GAM1542  DKFZP564O043 5'  GGGAGACCGTCCGCCTG     94093      AGAAGAT        A
                                CAGG      GGCGGTCTCC C
                                ||||      |||||||||| |
                                GTCC      CTGCCAGAGG G
                                  GC_____         C
GAM1542  DKFZP566H073 5'  GAGCTCCGCCACCCTTCCC    32031    A   A_     T_
                                GG GAAG  TGGCGG  CTC
                                || ||||  ||||||  |||
                                CC CTTC  ACCGCC  GAG
                                 _   CC     TC
GAM1542  E46L     3'  TGGATTTTTCATCTTCTACC   26014    _       CG TC
                                GG AGAAGATGG  G  TCCA
                                || |||||||||  |  ||||
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                                CC TCTTCTACT  T  AGGT
                                 A        TT T_
GAM1542  FIGN     3'  AGAACCTCTCCATCTCCTCC   97362      A     C__  _
                                GGAG AGATGG   GGT CT
                                |||| ||||||   ||| ||
                                CCTC TCTACC   CCA GA
                                  C     TCT   A
GAM1542  FLJ12517 3'  TGTGGAGACTGGCACTCTCC   43721      A A  G
                                GGAGA G TG CGGTCTCCACA
                                ||||| | || ||||||||||
                                CCTCT C AC GTCAGAGGTGT
                                  _ _  G
GAM1542  FLJ14437 5'  GTGAAGAATTTCCCTCTTCTCC 51798         T  CGG_   C
            TG                    CAGGAGAAGA GG    TCT CAC
                                |||||||||| ||    ||| |||
                                GTCCTCTTCT CC    AGA GTG
                                      C  TTTA   A
GAM1542  FLJ14936 3'  GTGAAGACCAGCTGCCCTG    52773     AGAAGAT  _    C
                                CAGG      GGC GGTCT CAC
                                ||||      ||| ||||| |||
                                GTCC      TCG CCAGA GTG
                                  CG_____   A     A
GAM1542  GENX-3414 3'  TGTAGGACCATCTCTCTCC    15458      _     CGGTC  _
                                GGAGA AGATGG     TCC ACA
                                ||||| ||||||     ||| |||
                                CCTCT TCTACC     AGG TGT
                                  C      _____   A
GAM1542  HGC6.1.1  3'  GTGGAAAGTCCTCTTCTCC    27615        T   GGTC
                                GGAGAAGA GGC    TCCAC
                                |||||||| |||    |||||
                                CCTCTTCT CTG    AGGTG
                                     C   AA__
GAM1542  HGC6.1.1  3'  TGGGGACCACCCTCCT      27616      AAGAT  C
                                AGGAG     GG GGTCTCCA
                                |||||     || ||||||||
                                TCCTC     CC CCAGGGGT
                                  _____  A
GAM1542  KIAA0293  3'  TGTGGCCACCATCTTCCCCT   61240     A       C  TCT
                                AGG GAAGATGG GG   CCACA
                                ||| |||||||| ||   |||||
                                TCC CTTCTACC CC   GGTGT
                                  C       A  ___
GAM1542  KIAA0322  3'  TGAAGAACTGCCTTCTTCT    94333       T     _  C
                                AGAAGA GGCGGT CT CA
                                |||||| |||||| || ||
                                TCTTCT CCGTCA GA GT
                                   T     A  A
GAM1542  KIAA0545  3'  GTGATGCCATCTTCTCC     63847           GTCTC
                                GGAGAAGATGGCG     CAC
                                ||||||||||||     |||
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                                CCTCTTCTACCGT    GTG
                                      A____
GAM1542 KIAA1045 3' GTGGCAGCATCCTCTCCTG   71609       A   G GGTCT
                                CAGGAGA GATG C    CCAC
                                ||||||| |||| |    ||||
                                GTCCTCT CTAC G    GGTG
                                   C   _ AC___
GAM1542 KIAA1196 3' TGTGGAGACCCGGACTCC    62156     AAGA  CG
                                GGAG   TGG  GTCTCCACA
                                ||||   |||  |||||||||
                                CCTC   GCC  CAGAGGTGT
                                  AG__  __
GAM1542 KIAA1679 3' TGCAGAAAACCTTTCTCCT   70717       AT  CGG  C
                                AGGAGAAG  GG   TCT CA
                                ||||||||  ||   ||| ||
                                TCCTCTTT  CC   AGA GT
                                     __  AAA   C
GAM1542 KIAA1853 3' TGTGGAGACAGTTCTTCTCCT 69928        TG  G
                                AGGAGAAGA  GC GTCTCCACA
                                |||||||||  || |||||||||
                                TCCTCTTCT  TG CAGAGGTGT
                                     __  A
GAM1542 KLF12    3' TGTGAATTATTGCATCTTCTTC 24365        G   CTC_
                                GGAGAAGATG CGGT   CACA
                                |||||||||| ||||   ||||
                                CTTCTTCTAC GTTA   GTGT
                                     _   TTAA
GAM1542 L3MBTL   3' GAGAGCCATCTTCCCC     70085    A      GG
                                GG GAAGATGGC  TCTC
                                || |||||||||  ||||
                                CC CTTCTACCG  AGAG
                                 C       __
GAM1542 LASP1    3' TGAAGAGCTGTCTTCCCCTG  21579     A       GG   C
                                CAGG GAAGATGGC  TCT CA
                                |||| |||||||||  ||| ||
                                GTCC CTTCTGTCG  AGA GT
                                  C       __  A
GAM1542 MGC14376 5' TGTGCCTCTGCCATCTTCACC  52918    A        TCTC
                                GG GAAGATGGCGG   CACA
                                || ||||||||||   ||||
                                CC CTTCTACCGTC   GTGT
                                 A         TCC_
GAM1542 MGC2605  5' TGTGGAGAGCGGGCCCCGCCCT 51186     AGAAGAT  __ G
           G                     CAGG      GGC  G TCTCCACA
                                ||||      |||  | |||||||||
                                GTCC      CCG  C AGAGGTGT
                                  CGCC___   GG G
GAM1542 MGC33901 3' TGGAGACCTTCTTCTACC    59362    _     TGGC
                                GG AGAAGA   GGTCTCCA
                                || ||||||   ||||||||
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                                CC TCTTCT    CCAGAGGT
                                 A     T___
GAM1542  NY-REN-60 3'  ACATGCCATCTCTTCCTG    67707      GA      _
                                CAGGA  AGATGGCG GT
                                ||||||  |||||||| ||
                                GTCCT  TCTACCGT CA
                                   TC       A
GAM1542  PP1665   3'  TGTGGAGACACGTCCTCCTCCC 48642    A  A  T   _
            C                    GG GA GA GGCG GTCTCCACA
                                || || || |||| |||||||||
                                CC CT CT CTGC CAGAGGTGT
                                 C  C  C    A
GAM1542  PRRG1    3'  TGGAGAATTTTCCCCT     8154     A     GGCGG
                                AGG GAAGAT    TCTCCA
                                ||| ||||||    ||||||
                                TCC CTTTTA    AGAGGT
                                  C     _____
GAM1542  SDCBP    3'  TGTGAAAACCAGTCACCTTTCT 20059        A_   _  CTC
            CCT                   AGGAGAAG  TGGC GGT   CACA
                                |||||||  |||| |||   ||||
                                TCCTCTTT  ACTG CCA   GTGT
                                    CC    A   AAA
GAM1542  SP140    3'  AGGCTCTTACCTCTTCTCCTG  24325         T  C___
                                CAGGAGAAGA GG    GGTCT
                                |||||||||| ||    |||||
                                GTCCTCTTCT CC    TCGGA
                                     _ ATTC
GAM1542  SV2B     3'  GAGATCTACTTTTCTCCT    29950         TGGC
                                AGGAGAAGA    GGTCTC
                                |||||||||    ||||||
                                TCCTCTTTT    CTAGAG
                                    CAT_
GAM1542  TUSP     3'  TGTAGAGAAATATTTCTTTTCC 40036         TGGCGG    C
            TG                    CAGGAGAAGA     TCTC ACA
                                ||||||||||     |||| |||
                                GTCCTTTTCT     AGAG TGT
                                     TTATAA    A
GAM1542  ZFP91    3'  TGGGGACCACCTCCCCCT    54880     AGAA  T  C
                                AGG    GA GG GGTCTCCA
                                |||    || || ||||||||
                                TCC    CT CC CCAGGGGT
                                  CC__  _  A
GAM1542  ZNF263   3'  TGTGGAGAATGAGATTCCCC   20429    A   GATGG  G
                                GG GAA     CG TCTCCACA
                                || |||     || ||||||||
                                CC CTT     GT AGAGGTGT
                                 C   AGA__  A
GAM1542  LOC123591 3'  GGAGACCACCATCTGAGCCT   76131     AGA     C
                                AGG   AGATGG GGTCTCC
                                |||   |||||| |||||||
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                                TCC   TCTACC CCAGAGG
                                  GAG     A
GAM1542  LOC143524 3'  GAGACCACCACTTCTCCTG   77095        A   C
                                CAGGAGAAG TGG GGTCTC
                                ||||||||| ||| ||||||
                                GTCCTCTTC ACC CCAGAG
                                     _  A
GAM1542  LOC144559 3'  TGTGAGGCCACCACTTCTCCTG 77386        A   C     C
                                CAGGAGAAG TGG GGTCTC ACA
                                ||||||||| ||| |||||| |||
                                GTCCTCTTC ACC CCGGAG TGT
                                     _  A     _
GAM1542  LOC145968 3'  TGAAGACGGCTTCTTCTCC   84578        T   G   C
                                GGAGAAGA GGC GTCT CA
                                |||||||| ||| |||| ||
                                CCTCTTCT TCG CAGA GT
                                     _  G   A
GAM1542  LOC146268 3'  GAAACCCCTCTTCTCC      78340        T  C   C
                                GGAGAAGA GG GGT TC
                                |||||||| || ||| ||
                                CCTCTTCT CC CCA AG
                                     _ _  A
GAM1542  LOC147976 3'  TGCGAAGCCTCATCTTCTCT   79292         C  TC  _
                                GGAGAAGATGG GG  TC CA
                                |||||||||| ||  || ||
                                TCTCTTCTACT CC  AG GT
                                     _ GA  C
GAM1542  LOC150935 3'  GAAAGTCACATCCTTCTCCTG  80827        A___   GG
                                CAGGAGAAG   TGGC  TC
                                |||||||||   ||||  ||
                                GTCCTCTTC   ACTG  AG
                                     CTAC   AA
GAM1542  LOC158777 3'  TGTGAAAACCAGTCACCTTTCT 82873        A_   _  CTC
            CCT                   AGGAGAAG  TGGC GGT   CACA
                                |||||||  |||| |||  ||||
                                TCCTCTTT  ACTG CCA   GTGT
                                     CC   A  AAA
GAM1542  LOC199678 3'  TGGGTTCCGCCACCTTCTCCTG 91373        A    TC
                                CAGGAGAAG TGGCGG  TCCA
                                |||||||| ||||||  ||||
                                GTCCTCTTC ACCGCC  GGGT
                                     C     TT
GAM1542  LOC219918 3'  GAGACCACCACTTCTCCTG   93172        A   C
                                CAGGAGAAG TGG GGTCTC
                                ||||||||| ||| ||||||
                                GTCCTCTTC ACC CCAGAG
                                     _  A
GAM1542  LOC220071 3'  GAGACCACCACTTCTCCTG   95081        A   C
                                CAGGAGAAG TGG GGTCTC
                                ||||||||| ||| ||||||
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                                GTCCTCTTC ACC CCAGAG
                                     _  A
GAM1542  LOC221927 5'  TGCGGTCGACACCATCTTCTCC 94222          CG  T_ A
                                GGAGAAGATGG  GTC  CC CA
                                ||||||||||  |||  || ||
                                CCTCTTCTACC  CAG  GG GT
                                     A_  CT  C
GAM1542  LOC255146 3'  TGTGAAATAAAATCTTCTCC  97347         GGCG  CTC
                                GGAGAAGAT   GT   CACA
                                |||||||||   ||   ||||
                                CCTCTTCTA   TA   GTGT
                                     AAA_  AA_
GAM1542  LOC255338 5'  GACTCATGCCATCTTCCCCT  97631     A       ___
                                AGG GAAGATGGC   GGTC
                                ||| |||||||||   ||||
                                TCC CTTCTACCG   TCAG
                                  C        TAC
GAM1542  LOC255360 3'  TGTGGACACCTCCTCCTCCTG  98765       AA  T  C   C
                                CAGGAG  GA GG GGT TCCACA
                                ||||||  || || ||| ||||||
                                GTCCTC  CT CC CCA AGGTGT
                                   __ _  T   C
GAM1542  LOC255515 3'  GAGACCACCACTTCTCCTG   97812         A   C
                                CAGGAGAAG TGG GGTCTC
                                |||||||||| ||| ||||||
                                GTCCTCTTC ACC CCAGAG
                                     _  A
GAM1542  LOC257289 5'  TGGAGACCGGCTCCTG      99356       AAGATGG
                                CAGGAG      CGGTCTCCA
                                ||||||      |||||||||
                                GTCCTC      GCCAGAGGT
                                   G_______
GAM1542  LOC51279  3'  TGCAGAGACTGTGCTCTTCCC  33766    A    TG      CA
                                GG GAAGA  GCGGTCTC  CA
                                || |||||  ||||||||  ||
                                CC CTTCT  TGTCAGAG  GT
                                 _    CG       AC
GAM1542  LOC81558  3'  TGTAGAGACTCTATTTTCTCC  48680          C     C
                                GGAGAAGATGG GGTCTC ACA
                                |||||||||| |||||| |||
                                CCTCTTTTATC TCAGAG TGT
                                      _     A
GAM1542  LOC90520  5'  GTGGGGTTGCCTCCCCCTCCTG 63839       AA_  T    T
                                CAGGAG   GA GGCGG CTCCAC
                                ||||||   || ||||| ||||||
                                GTCCTC   CT CCGTT GGGGTG
                                   CCC  _    _
GAM1542  LOC90906  3'  GAGGTCGCCACTTCTCCTG   64952         A    GT
                                CAGGAGAAG TGGCG  CTC
                                ||||||||| |||||  |||
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                                GTCCTCTTC ACCGC  GAG
                                      _    TG
GAM1542  LOC91263  3'  TGGAGACCAGCCCCCATCCTG  66003      GAAGAT  _
                                CAGGA     GGC GGTCTCCA
                                |||||     ||| ||||||||
                                GTCCT     CCG CCAGAGGT
                                   ACCC__   A
GAM1542  LOC92335  3'  GGACCGCCACCTCTTCCC    69545    A    __
                                GG GAAGA  TGGCGGTCT
                                || |||||  |||||||||
                                CC CTTCT  ACCGCCAGG
                                 _    CC
GAM1543  ABCE1     5'  GGGGATCGTTTTCTCCAGA   60261         C  CTG
                                TCTGGAGAAA TG   CCTC
                                |||||||||| ||   ||||
                                AGACCTCTTT GC   GGGG
                                      T  TA_
GAM1543  AKAP13    3'  TGAGGCAGCTGCCTCCTGA   91257    T   AAACT
                                TC GGAG    GCTGCCTCA
                                || ||||    |||||||||
                                AG CCTC    CGACGGAGT
                                 T   CGT__
GAM1543  ALOX12B   5'  GGGCAGCAGCTTTTCCAGA   8537          A
                                TCTGGAGAA CTGCTGCCT
                                ||||||||| |||||||||
                                AGACCTTTT GACGACGGG
                                      C
GAM1543  BCL7A     3'  GAGGCGGCGTTACCTCCAGA  40984        A_  T
                                TCTGGAG  AAC GCTGCCTC
                                |||||||  ||| ||||||||
                                AGACCTC  TTG CGGCGGAG
                                    CA  _
GAM1543  CLDN3     3'  TGGGGCAGCTTCCCCAG     8961       A  ACT
                                CTGG GAA   GCTGCCTCA
                                |||| |||   |||||||||
                                GACC CTT   CGACGGGGT
                                  C  ___
GAM1543  CUTL1     3'  GAGCCCCAGTCTCTTCAGA   10348        A   CT  C
                                TCTGGAGA ACTG  GC TC
                                |||||||| ||||  || ||
                                AGACTTCT TGAC  CG AG
                                    C   CC  _
GAM1543  EFNA1     3'  TGGGGCAGCACTCCCCAGA   16666      A  AAC
                                TCTGG GA   TGCTGCCTCA
                                ||||| ||   ||||||||||
                                AGACC CT   ACGACGGGGT
                                  C  C__
GAM1543  EGR1      3'  TGAGCTTCGGTTCTCCAGA   10493        A  CT  C
                                TCTGGAGAA CTG  GC TCA
                                ||||||||| |||  || |||
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                                AGACCTCTT GGC  CG AGT
                                     _  TT  _
GAM1543  FLT1    3'  TGAGGAGAGTTTTCTCCA    10664       _ G  G
                                TGGAGAAA CT CT CCTCA
                                |||||||| || || |||||
                                ACCTCTTT GA GA GGAGT
                                    T  _ _
GAM1543  FRK     5'  AGCCGGTAAGTCTCTCCAGG  10715       A  _   C
                                TCTGGAGA ACT GCTG CT
                                |||||||| ||| |||| ||
                                GGACCTCT TGA TGGC GA
                                    C  A   C
GAM1543  GAB2    3'  GAGGCAGCATCTCCAGA    25458       AAC
                                TCTGGAGA  TGCTGCCTC
                                ||||||||  |||||||||
                                AGACCTCT  ACGACGGAG
                                     ___
GAM1543  GPC6    5'  AGGCAGCAGCCTTCCCAG   20329     A  A_
                                CTGG GAA  CTGCTGCCT
                                |||| |||  |||||||||
                                GACC CTT  GACGACGGA
                                  _  CC
GAM1543  GUCA2B  3'  TGAGGCAGCCCAGCTCCTGA  24020   T   AAACT
                                TC GGAG    GCTGCCTCA
                                || ||||    |||||||||
                                AG CCTC    CGACGGAGT
                                 T   GACC_
GAM1543  MGAM    3'  GGGGCAGTTTCTCCAGG    72812          G
                                TCTGGAGAAACTGCT CC
                                |||||||||||||| ||
                                GGACCTCTTTGACGG GG
                                     _
GAM1543  MYO7A   3'  GAGGCAGCAGTGGGTTCAGG  6032       GAA
                                TCTGGA  ACTGCTGCCTC
                                ||||||  ||||||||||
                                GGACTT  TGACGACGGAG
                                   GGG
GAM1543  NEUROD2 3'  AGGAGTGCTTCTCCAGG    21592       ACT  G
                                TCTGGAGAA  GCT CCT
                                |||||||||  ||| |||
                                GGACCTCTT  TGA GGA
                                     CG_  _
GAM1543  NPY2R   3'  TGAACAGAAATTTCTCCAGG  8067        CTG  CC
                                TCTGGAGAAA  CTG  TCA
                                ||||||||||  |||  |||
                                GGACCTCTTT  GAC  AGT
                                      AAA  A_
GAM1543  OXTR    3'  TGAATAGACATTTCTCCA    8083        C  _  CC
                                TGGAGAAA TG CTG  TCA
                                |||||||| || |||  |||
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                                ACCTCTTT AC GAT  AGT
                                     _ A   A_
GAM1543  PPP2R4   3'  TGAGGCATGTCTTTCCAGA   61184        A  TGC
                                TCTGGAGA AC   TGCCTCA
                                |||||||| ||   |||||||
                                AGACCTTT TG   ACGGAGT
                                    C  T__
GAM1543  REV3L    5'  TGAGGAAGATTTCTCTCA    12825   _     CTG  G
                                TG GAGAAA   CT CCTCA
                                || ||||||   || |||||
                                AC CTCTTT   GA GGAGT
                                 T     A__  A
GAM1543  RXRA     3'  TGAGGCAGCAGCCTTC      12925      AAA
                                GGAG   CTGCTGCCTCA
                                ||||   ||||||||||
                                CTTC   GACGACGGAGT
                                  C__
GAM1543  SURF5    3'  TGAGGCAGCATTTCCTCCA   56919      A  C
                                TGGAG AA TGCTGCCTCA
                                ||||| || ||||||||||
                                ACCTC TT ACGACGGAGT
                                   C  T
GAM1543  VANGL2   3'  TGAGACATCGGACTCTCCGGA  72095        AA   C  C
                                TCTGGAGA  CTG TG CTCA
                                ||||||||  ||| || ||||
                                AGGCCTCT  GGC AC GAGT
                                     CA   T  A
GAM1543  WARS     3'  GAGGCAGCAGCCCTCGAGG   67865     G   AAA
                                TCT GAG   CTGCTGCCTC
                                ||| |||   ||||||||||
                                GGA CTC   GACGACGGAG
                                  G   CC_
GAM1543  ZNF45    5'  GACTTGGCACTTCTCCAGA   14250        AC    CC
                                TCTGGAGAA  TGCTG  TC
                                |||||||||  |||||  ||
                                AGACCTCTT  ACGGT  AG
                                     C_    TC
GAM1543  BLR1     3'  TGAGGCAGGGAAGTCCCCAGG  53119      A  AA_  G
                                TCTGG GA   CT CTGCCTCA
                                ||||| ||   || ||||||||
                                GGACC CT   GG GACGGAGT
                                   C  GAA  _
GAM1543  C20orf150 3'  TGAAGCCGAGCTCCTCCAGA   66017       AAACT   __  C
                                TCTGGAG    GCT  GC TCA
                                |||||||    |||  || |||
                                AGACCTC    CGA  CG AGT
                                    CT___   GC  A
GAM1543  C20orf4  3'  GGGCAGCAATCTCTCCAGG   31948        AAC
                                TCTGGAGA   TGCTGCCT
                                ||||||||   ||||||||
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                                GGACCTCT   ACGACGGG
                                    CTA
GAM1543  C20orf7   3'  TGAATATGCACCTTCTCCAGA  44383        AC   TGCC
                                TCTGGAGAA  TGC    TCA
                                |||||||||  |||    |||
                                AGACCTCTT  ACG    AGT
                                    CC   TATA
GAM1543  C6orf26   3'  AGAAAGCAGCTTTCTCCA    48268        _    GC
                                TGGAGAAA CTGCT  CT
                                |||||||| |||||  ||
                                ACCTCTTT GACGA  GA
                                    C     AA
GAM1543  CASKIN1   3'  TGAGGCGGATTTCCCCAGA   40784      A    CTG
                                TCTGG GAAA   CTGCCTCA
                                ||||| ||||   ||||||||
                                AGACC CTTT   GGCGGAGT
                                   C    A__
GAM1543  CCR8      3'  TGAGGCAGATGCCTCTAGA   19041       AAACTG
                                TCTGGAG     CTGCCTCA
                                |||||||     ||||||||
                                AGATCTC     GACGGAGT
                                    CGTA__
GAM1543  CPGL2     5'  GAAGCCGCTTTGTTCTCCAGA  74884        ACT_  T  C
                                TCTGGAGAA    GC GC TC
                                |||||||||    || || ||
                                AGACCTCTT    CG CG AG
                                    GTTT  C  A
GAM1543  CSRP2BP   5'  TGAAGCAGCAGTGGGACCAG   70657     AGAA      C
                                CTGG    ACTGCTGC TCA
                                ||||    |||||||| |||
                                GACC    TGACGACG AGT
                                  AGGG       A
GAM1543  DGKD      3'  TGAAACAACACTTTCTCCAG   60113        C  C  CC
                                CTGGAGAAA TG TG  TCA
                                ||||||||| || ||  |||
                                GACCTCTTT AC AC  AGT
                                    C  A  AA
GAM1543  DKFZP434A043 3'  TGAGGTAGTAATTTCCTCAGA  31823      GA    C
                                TCTG  GAAA TGCTGCCTCA
                                ||||  |||| ||||||||||
                                AGAC  CTTT ATGATGGAGT
                                  TC    A
GAM1543  DKFZP434P0111 3'  TGAGGGTGTCTTTCCAGA    67963        A  T  TG
                                TCTGGAGA AC GC  CCTCA
                                |||||||| || ||  |||||
                                AGACCTTT TG TG  GGAGT
                                    C  _  __
GAM1543  DKFZP586M1120 3'  TGAGGCAGCAGCTCCCAG    49287      A  AA
                                CTGG GA  CTGCTGCCTCA
                                |||| ||  ||||||||||
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                                GACC CT  GACGACGGAGT
                                  _  C_
GAM1543  ERG-1    3'  TGAGACATGTTTCTCCAGG   42102          TGC  C
                                TCTGGAGAAAC   TG CTCA
                                ||||||||||   || ||||
                                GGACCTCTTTG   AC GAGT
                                      T__  A
GAM1543  FASTK    3'  TGAGGCAGAAGCTCCAGG    47690       AAACTG
                                TCTGGAG     CTGCCTCA
                                |||||||     ||||||||
                                GGACCTC     GACGGAGT
                                   GAA___
GAM1543  FLJ14855 5'  GGTTCCCAGTTTTCCAGA    53766        A   CT_
                                TCTGGAGAA CTG   GCC
                                ||||||||| |||   |||
                                AGACCTTTT GAC   TGG
                                      _  CCT
GAM1543  FLJ20249 3'  TGAGGAGTCCCTCCCAGA    80223      A  AACT   G
                                TCTGG GA    GCT CCTCA
                                ||||| ||    ||| |||||
                                AGACC CT    TGA GGAGT
                                  _  CCC_  _
GAM1543  FLJ20730 3'  TGAAGAAGCAGTTTCTCAGA   36053     G        GCC
                                TCTG AGAAACTGCT   TCA
                                |||| ||||||||||   |||
                                AGAC TCTTTGACGA   AGT
                                  _        AGA
GAM1543  FLJ21007 5'  TGAAGCTTGCACAAGCTCTCCA 48648        AAC__   T_  C
            GA                   TCTGGAGA    TGC  GC TCA
                                ||||||||    |||  || |||
                                AGACCTCT    ACG  CG AGT
                                     CGAAC   TT  A
GAM1543  GPT2     3'  TGAGGCAGCAGCCTCTA     56772      AAA
                                TGGAG   CTGCTGCCTCA
                                |||||   ||||||||||||
                                ATCTC   GACGACGGAGT
                                  C__
GAM1543  KIAA0542 3'  GGGGCAGCTCCTCCAGG     66665       AAACT
                                TCTGGAG    GCTGCCTC
                                |||||||    ||||||||
                                GGACCTC    CGACGGGG
                                   CT___
GAM1543  KIAA0652 3'  TGAGGCAGCAATCTTTGG    29125   TG   AAC
                                C  GAGA   TGCTGCCTCA
                                |  ||||   ||||||||||
                                G  TTCT   ACGACGGAGT
                                 GT   A__
GAM1543  KIAA1026 3'  GAGACGGCTTTTTCCA      71738        CT   C
                                TGGAGAAA  GCTG CTC
                                ||||||||  |||| |||
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                                ACCTTTTT  CGGC GAG
                                    __    A
GAM1543  KIAA1030  3'  GAGGCAGCAGTGAGCCGAGA   94981     _  AGAA
                                TCT GG    ACTGCTGCCTC
                                ||| ||    ||||||||||
                                AGA CC    TGACGACGGAG
                                  G  GAG_
GAM1543  KIAA1086  3'  TGAGGCAGGGGGTCCCCA    71291     A  AA  G
                                TGG GA  CT CTGCCTCA
                                ||| ||  || ||||||||
                                ACC CT  GG GACGGAGT
                                  C  GG  _
GAM1543  KIAA1322  3'  TGAGATAGTTTTTCCAGA    73118           CTGC
                                TCTGGAGAAACTG    CTCA
                                ||||||||||||    ||||
                                AGACCTTTTTGAT    GAGT
                                       A___
GAM1543  KIAA1634  3'  GCATCAGTCTCTTCTCCAGA   64124         ___    C
                                TCTGGAGAA   ACTG TGC
                                |||||||||   |||| |||
                                AGACCTCTT   TGAC ACG
                                     CTC    T
GAM1543  KIAA1638  3'  TGAAACAACGGTGACCTCTCCA 47824         A___    C  CC
           GG                     TCTGGAGA    ACTG TG  TCA
                                |||||||    |||| ||  |||
                                GGACCTCT    TGGC AC  AGT
                                    CCAG    A  AA
GAM1543  KIAA1771  5'  GGGTTACCAGACCTCTCCAGA  79866         AA_   CT_
                                TCTGGAGA   CTG   GCCT
                                ||||||||   |||   ||||
                                AGACCTCT   GAC   TGGG
                                    CCA   CAT
GAM1543  KIAA1894  3'  GAGGCAACCTTTGCCTTCTTCA 74285         ACT  _______
           GA                     TCTGGAGAA   GC     TGCCTC
                                |||||||||   ||     ||||||
                                AGACTTCTT   CG     ACGGAG
                                    C__  TTTCCA
GAM1543  KIAA1937  3'  GAGGCAGTGTCCCCCAGG    74071      AGAA  T
                                TCTGG    AC GCTGCCTC
                                |||||    || ||||||||
                                GGACC    TG TGACGGAG
                                  CCC_  _
GAM1543  KIAA1985  3'  TGAAAAGCACTTTCTCCA    45018        C   GCC
                                TGGAGAAA TGCT   TCA
                                |||||||| ||||   |||
                                ACCTCTTT ACGA   AGT
                                    C    AA_
GAM1543  LCHN      3'  TGAGATGCTTTCTCCAGA    87480          CT  TGC
                                TCTGGAGAAA  GC   CTCA
                                ||||||||||  ||   ||||
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                                AGACCTCTTT  CG   GAGT
                                      __  TA_
GAM1543  MGC13007  3'  CAGTTCAGTTATCTCCAGA   51277        _    __
                                TCTGGAGA AACTG  CTG
                                |||||||| |||||  |||
                                AGACCTCT TTGAC  GAC
                                     A     TT
GAM1543  MGC16385  5'  TGAAGCAGCAGCTGGGCTAGG  59543      AGAAA      C
                                TCTGG    CTGCTGC TCA
                                |||||    ||||||| |||
                                GGATC    GACGACG AGT
                                   GGGTC      A
GAM1543  MGC26914  3'  TGAATAGACATTTCTCCA    59332        C  _   CC
                                TGGAGAAA TG CTG  TCA
                                |||||||| || |||  |||
                                ACCTCTTT AC GAT  AGT
                                     _  A   A_
GAM1543  PPP1R13B  3'  TGAGGCCCTTTCTCCAG     31660        CTGCT
                                CTGGAGAAA    GCCTCA
                                |||||||||    ||||||
                                GACCTCTTT    CGGAGT
                                     CC___
GAM1543  PSKH1     3'  AGGCTCCAGCCTCTCCAGA   68791        AA   CT
                                TCTGGAGA  CTG  GCCT
                                ||||||||  |||  ||||
                                AGACCTCT  GAC  CGGA
                                     CC   CT
GAM1543  SPAF      3'  TGAAGCGATTTCTTTTTCCAGA 83521         CTGC_   C
                                TCTGGAGAAA    TGC TCA
                                ||||||||||    ||| |||
                                AGACCTTTTT    GCG AGT
                                      CTTTA   A
GAM1543  SUN1      3'  TGAGTTTCCCAGTTTCTACAGA 47926      G       CTGC_
                                TCTG AGAAACTG    CTCA
                                |||| ||||||||    ||||
                                AGAC TCTTTGAC    GAGT
                                   A       CCTTT
GAM1543  USP24     3'  TGAAAATGCTGTGTTCTCCAGA 92795         _  T  TGCC
                                TCTGGAGAA AC GC    TCA
                                ||||||||| || ||    |||
                                AGACCTCTT TG CG    AGT
                                     G  T  TAAA
GAM1543  LOC123096 3'  TGAGGCAGACACTCCAG     74654       AAAC  _
                                CTGGAG    TG CTGCCTCA
                                ||||||    || ||||||||
                                GACCTC    AC GACGGAGT
                                    ____  A
GAM1543  LOC129831 5'  TGAGACAGCAGCGGTGGCAGA  75398      GAGAA      ___
                                TCTG    ACTGCTGC   CTCA
                                ||||    ||||||||   ||||
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                                AGAC    TGGCGACG   GAGT
                                  GG___      ACA
GAM1543  LOC134637 3'  TGAGAACACCTTCTCCAGG   75693        AC  CTGC
                                TCTGGAGAA  TG   CTCA
                                |||||||||  ||   ||||
                                GGACCTCTT  AC   GAGT
                                     CC  AA__
GAM1543  LOC146420 3'  TGAACTTCCAGATTCTCCAGA  84653        A   CTGCC
                                TCTGGAGAA CTG    TCA
                                ||||||||| |||    |||
                                AGACCTCTT GAC    AGT
                                     A   CTTCA
GAM1543  LOC147711 5'  TGAGCAGGCAAGTCTCTTCAGA 79117        A   _   GC
                                TCTGGAGA ACT GCT  CTCA
                                |||||||| ||| |||  ||||
                                AGACTTCT TGA CGG  GAGT
                                     C   A   AC
GAM1543  LOC148753 3'  TGAGACTCCATTTTCTCCAGG  85373        C  CTGC
                                TCTGGAGAAA TG   CTCA
                                |||||||||| ||   ||||
                                GGACCTCTTT AC   GAGT
                                      T  CTCA
GAM1543  LOC150290 3'  TGAGGCAGATGGTGCCCAGA   80592      AGAA   _
                                TCTGG   ACTG CTGCCTCA
                                |||||   |||| ||||||||
                                AGACC   TGGT GACGGAGT
                                  CG__   A
GAM1543  LOC153218 5'  TGAAATAGAACTTTTCCAGA   81658        ACTG   CC
                                TCTGGAGAA   CTG  TCA
                                |||||||||   |||  |||
                                AGACCTTTT   GAT  AGT
                                     CAA_   AA
GAM1543  LOC157570 5'  TGAGGCTTTTTCTTCAGA    82397         CTGCT
                                TCTGGAGAAA    GCCTCA
                                ||||||||||    ||||||
                                AGACTTCTTT    CGGAGT
                                      TT___
GAM1543  LOC197259 5'  TGAGGCAGTGGCCTCCGGA   89304        AAA TG
                                TCTGGAG   C  CTGCCTCA
                                |||||||   |  ||||||||
                                AGGCCTC   G  GACGGAGT
                                    C__ GT
GAM1543  LOC199923 3'  TGAGTTAGCCAGTTTCTTCAGA 89879           _  C
                                TCTGGAGAAACTG CTG CTCA
                                |||||||||||||| ||| ||||
                                AGACTTCTTTGAC GAT GAGT
                                       C   T
GAM1543  LOC200940 3'  TGAGGCAGGCGGATCTCCTGA  90398    T    AA   _
                                TC GGAGA  CTGC TGCCTCA
                                || |||||  |||| |||||||
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                                AG CCTCT  GGCG ACGGAGT
                                 T    A_   G
GAM1543  LOC201685 3'  AGGAGCTATTTTCCAGA     91834        ACT   G
                                TCTGGAGAA   GCT CCT
                                |||||||||   ||| |||
                                AGACCTTTT   CGA GGA
                                     AT_  _
GAM1543  LOC205327 3'  AGTCAATGTTTCTCCAGA    91067         TGC  C
                                TCTGGAGAAAC   TG CT
                                ||||||||||   || ||
                                AGACCTCTTTG   AC GA
                                      TA_  T
GAM1543  LOC221288 3'  TGAAGCAGCAGTATCTAGA   95264       GAA       C
                                TCTGGA   ACTGCTGC TCA
                                ||||||   |||||||| |||
                                AGATCT   TGACGACG AGT
                                   A__       A
GAM1543  LOC222057 3'  AGGTCAGCCTCTCCAGG     94345        AACT   _
                                TCTGGAGA    GCTG CCT
                                ||||||||    |||| |||
                                GGACCTCT    CGAC GGA
                                     C___    T
GAM1543  LOC253254 5'  TGAGAAGAACTTCTTCAGA   98908         ACTG  GC
                                TCTGGAGAA    CT  CTCA
                                |||||||||    ||  ||||
                                AGACTTCTT    GA  GAGT
                                     CAA_  A_
GAM1543  LOC256789 3'  TGAGGCTGTACTCTCTAGA   99312        AAC   T
                                TCTGGAGA   TGC GCCTCA
                                ||||||||   ||| ||||||
                                AGATCTCT   ATG CGGAGT
                                     C__   T
GAM1543  LOC257336 5'  GGGCCCTAGTCCTCCAGA    97900       AA    CT
                                TCTGGAG  ACTG  GCCT
                                |||||||  ||||  ||||
                                AGACCTC  TGAT  CGGG
                                   C_    CC
GAM1543  LOC91923  5'  AGAGTTCCAGTTTCTCCA    68169         CT  _
                                TGGAGAAACTG  GC CT
                                ||||||||||  || ||
                                ACCTCTTTGAC  TG GA
                                      CT  A
GAM1543  LOC92876  5'  AGAGTTCCAGTTTCTCCA    71346         CT  _
                                TGGAGAAACTG  GC CT
                                ||||||||||  || ||
                                ACCTCTTTGAC  TG GA
                                      CT  A
GAM1543  LOC93496  3'  TGAAACAGACTTACACTTCTTC 72863        ACTG____   CC
            AGA                   TCTGGAGAA       CTG  TCA
                                |||||||||       |||  |||
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                                AGACTTCTT      GAC  AGT
                                     CACATTCA   AA
GAM1544  HAL     5'  GCCACTCCTGCATAAAGCTC  10903         TGAAAA
                                GAGCTTTATGC     GGTGGC
                                ||||||||||     ||||||
                                CTCGAAATACG     TCACCG
                                      TCC___
GAM1544  HMGN2   3'  GGCCACCTTGGCACAAAAGC  19809      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                   _ _ GG
GAM1544  NMI     5'  GGCCACCTCCTCAGGAAG   17436     ATG   AA
                                CTTT   CTGA  AGGTGGCC
                                ||||   ||||  ||||||||
                                GAAG   GACT  TCCACCGG
                                   ___    CC
GAM1544  PACE    3'  GGCCACCTCTCCAAGGGCTT  11944       A  CT  AAA
                                GAGCTTT TG  GA   GGTGGCC
                                |||||||  ||  ||   |||||||
                                TTCGGGA AC  CT   CCACCGG
                                    _  CT  ___
GAM1544  PYCR1   3'  CCACCTTCCTCTAGAGCTC   70639       TGCT  A_
                                GAGCTTTA   GA  AAGGTGG
                                ||||||||   ||  |||||||
                                CTCGAGAT   CT  TTCCACC
                                     _____  CC
GAM1544  SDC1    3'  GGCCACCTCCCCAGCATTCCAG 12991    TT_    AAA
            C                    GCT   ATGCTG   AGGTGGCC
                                |||   ||||||   ||||||||
                                CGA   TACGAC   TCCACCGG
                                  CCT     CCC
GAM1544  FLJ11560 5' GCCCAGGCCCAGCATAAAG   48008        AAAA  ___
                                CTTTATGCTG   GGT   GGC
                                ||||||||||   |||   |||
                                GAAATACGAC   CCG   CCG
                                     _____   GAC
GAM1544  KIAA0446 5' CCACCTTTTGAAGAGCTC    69446       ATGCTG
                                GAGCTTT     AAAAGGTGG
                                |||||||     |||||||||
                                CTCGAGA     TTTTCCACC
                                    AG_____
GAM1544  KIAA0971 3' GTTGTTCTCAGCATAAAGT   30677          AAA  TG
                                GCTTTATGCTGA   GG  GC
                                ||||||||||||   ||  ||
                                TGAAATACGACT   TT  TG
                                      C__   GT
GAM1544  KIAA1393 3' GGCCACCTTGGCACAAAAGC  72574      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
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                                CGAAA AC AC  TTCCACCGG
                                   _ _ GG
GAM1544 KIAA1656 3' GGCCACCTCCTCCTAGAAGCC 66377   A    ATGCT  AA
                                G GCTTT    GA  AGGTGGCC
                                | |||||    ||  ||||||||
                                C CGAAG    CT  TCCACCGG
                                _    ATC__  CC
GAM1544 KIAA1884 3' GCCACCTTCATCTACCAAGGCT 73728       ATGCT  A_
             C                   GAGCTTT    GA  AAGGTGGC
                                |||||||    ||  ||||||||
                                CTCGGAA    CT  TTCCACCG
                                    CCAT_  AC
GAM1544 PP3501   3' GGCCACCGTTGACAGCATAAAG 41683         AAAA_
                                CTTTATGCTG    GGTGGCC
                                ||||||||||    |||||||
                                GAAATACGAC    CCACCGG
                                      AGTTG
GAM1544 SDCCAG3  3' GGTGTTCTCAGCATGAAGCTC  22803           AAA  TG
                                GAGCTTTATGCTGA   GG  GCC
                                ||||||||||||||   ||  |||
                                CTCGAAGTACGACT   CT  TGG
                                       ___  TG
GAM1544 SP140    3' GGCCACCTCCATGCAGAAGC   24327      A   TGAAA
                                GCTTT TGC    AGGTGGCC
                                ||||| |||    ||||||||
                                CGAAG ACG    TCCACCGG
                                   _  TACC_
GAM1544 LOC148760 3' GGCCACCTTCTCCAACAAGCTC 85364       TA  CT  A
                                GAGCTT  TG  GA AAGGTGGCC
                                ||||||  ||  || |||||||||
                                CTCGAA  AC  CT TTCCACCGG
                                   CA  __  C
GAM1544 LOC150170 5' ACCTGTTTCACATAAAGC    80414         C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                     _    G
GAM1544 LOC150175 5' ACCTGTTTCACATAAAGC    80453         C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                     _    G
GAM1544 LOC150215 5' ACCTGTTTCACATAAAGC    80456         C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                     _    G
GAM1544 LOC150218 5' ACCTGTTTCACATAAAGC    80525         C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
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                                CGAAATAC ACTTT TCCA
                                   _    G
GAM1544  LOC152065 3'  GGCCACCTTCTCCTTGGCAGGC 86737      TTA   ___  A
            TC                    GAGCT  TGCT  GA AAGGTGGCC
                                  ||||| ||||  || |||||||||
                                  CTCGG  ACGG  CT TTCCACCGG
                                    ___   TTC  C
GAM1544  LOC152267 3'  GGCCACCTTGGCACAAAAGC  61036      A  C  AA
                                  GCTTT TG TG  AAGGTGGCC
                                  ||||| || ||  |||||||||
                                  CGAAA AC AC  TTCCACCGG
                                    _ _ GG
GAM1544  LOC158292 5'  CCTCTGGACCCAGCATAAGGCT 88046           AAAA_  T
            C                     GAGCTTTATGCTG    GG GG
                                  ||||||||||||    || ||
                                  CTCGGAATACGAC    TC CC
                                        CCAGG  T
GAM1544  LOC219997 3'  GCCACCTCTTCAGCCTC    93256    CTTTAT    A
                                  GAG    GCTGAA AGGTGGC
                                  |||    |||||| |||||||
                                  CTC    CGACTT TCCACCG
                                   _______    C
GAM1544  LOC256269 3'  GGCCACCTTGGCACAAAAGC  96608      A  C  AA
                                  GCTTT TG TG  AAGGTGGCC
                                  ||||| || ||  |||||||||
                                  CGAAA AC AC  TTCCACCGG
                                    _ _ GG
GAM1544  LOC91963  5'  GGCCACCTCCTCTGAGAAGC  68321     ATGCT  AA
                                  GCTTT    GA  AGGTGGCC
                                  |||||    ||  ||||||||
                                  CGAAG    CT  TCCACCGG
                                    AGT__  CC
GAM1545  CDH12     3'  CTTATCATTTAAAGTGGTGTA  15777        CCCAA   GA
                                  TACACCACT    GAA  ATAAG
                                  |||||||||    |||  |||||
                                  ATGTGGTGA    TTT  TATTC
                                       AA___   AC
GAM1545  GOCAP1    3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA       G
                                  TACAC  CTCCCAAGAA AAT
                                  |||||  |||||||||| |||
                                  ATGTG  GAGGGTTCTT TTA
                                    AC        G
GAM1545  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090      T   AGAAG
                                  ACCAC CCCA    AATAAG
                                  ||||| ||||    ||||||
                                  TGGTG GGGT    TTATTC
                                    _   GTCA_
GAM1545  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
            A                     TACAC       AGAAGAATAAG
                                  |||||       ||||||||||
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                                ATGTG      TCTTCTTATTC
                                  TACTCCC_
GAM1545 FLJ21791 3' CTTATTTGCAGAAGTGGTGTA 62126        CCCAAGAA
                                TACACCACT      GAATAAG
                                |||||||||      |||||||
                                ATGTGGTGA      TTTATTC
                                    AGACG___
GAM1545 HMP19    3' CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
           TA                    TACA   TCC   GAAGAATAAG
                                ||||   |||   ||||||||||
                                ATGT   AGG   TTTCTTATTC
                                  AAA_  ATTG
GAM1545 KIAA1719 3' TCTGTCTTGGGAGTGGTGTA  68742             _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                          G
GAM1545 KIAA1853 3' TTTTTCTTGGAAGCAGTG    69929    CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM1545 KIAA1877 3' CTTATTCTTCTGCCATGAGT  66748     CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM1545 KIAA1906 3' CTTATTCTTCTTGACTTTTGG 73571    CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM1545 OSBPL11  3' CTTAATTTCCCAAGAGTGGTG 43206        CCAA   AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                    AACC   A_
GAM1545 YME1L1   3' TCATTCTTGATGTGGTGTA   58438       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   |||||| ||
                                ATGTGGTG   GTTCTT CT
                                    TA_     A
GAM1545 ZNF262   3' CTTATTTTGTTTGGGAGT    18723        A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                     G
GAM1545 LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294        TC_    AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
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                                ATGTGGTG  GGTTC   TGT
                                    CAA   GG__
GAM1546 ATP10C   3' GCATGAGTGGACGTCAGAAG  44668   C      _   GA
                                CT CTGACGTCC CTCA  TGC
                                || ||||||||| ||||  |||
                                GA GACTGCAGG GAGT  ACG
                                 A       T   __
GAM1546 BLVRB    3' GCATTCTGGACATGAGGAGCAA 7387       GAC   CTCA
                                TTGCTCCT  GTCC   GATGC
                                ||||||||  ||||   |||||
                                AACGAGGA  CAGG   TTACG
                                    GTA   TC__
GAM1546 EGFL5    5' GCATCTGAAATTTTCAGGTACA 87913    CT    CGTCCC
           A                     TTG  CCTGA     TCAGATGC
                                |||  |||||     ||||||||
                                AAC  GGACT     AGTCTACG
                                 AT    TTTAA_
GAM1546 GATM     3' CACCTAAGAAGCTTAGGGGCAA 9434       C  CC  C  A
                                TTGCTCCTGA GT  CT AG TG
                                |||||||||| ||  || || ||
                                AACGGGGATT CG  GA TC AC
                                    _ AA  A  C
GAM1546 KCNK7    3' CACCTGAGGAGGAAGCAG   54054     _  GACGTC     A
                                TTGCT CCT     CCTCAG TG
                                ||||| |||     |||||| ||
                                GACGA GGA     GGAGTC AC
                                   A _______     C
GAM1546 KCNK7    3' CACCTGAGGAGGAAGCAG   54061     _  GACGTC     A
                                TTGCT CCT     CCTCAG TG
                                ||||| |||     |||||| ||
                                GACGA GGA     GGAGTC AC
                                   A _______     C
GAM1546 KCNK7    3' CACCTGAGGAGGAAGCAG   54231     _  GACGTC     A
                                TTGCT CCT     CCTCAG TG
                                ||||| |||     |||||| ||
                                GACGA GGA     GGAGTC AC
                                   A _______     C
GAM1546 KCNK7    3' CACCTGAGGAGGAAGCAG   20344     _  GACGTC     A
                                TTGCT CCT     CCTCAG TG
                                ||||| |||     |||||| ||
                                GACGA GGA     GGAGTC AC
                                   A _______     C
GAM1546 LYL1     3' TGAAGACGTCAGGGGCAA    19951          CC
                                TTGCTCCTGACGTC  TCA
                                ||||||||||||||  |||
                                AACGGGGACTGCAG  AGT
                                      A_
GAM1546 TMOD2    3' CATTTGCAAACGTCAGGAG   28022        CCCT
                                CTCCTGACGT   CAGATG
                                ||||||||||   ||||||
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                                GAGGACTGCA   GTTTAC
                                     AAC_
GAM1546 UBE2A    3' GCATCTGAGAACCTTAAAGC  13927    CC  C CC
                                GCT  TGA GT  CTCAGATGC
                                |||  ||| ||  |||||||||
                                CGA  ATT CA  GAGTCTACG
                                  A_   C  A_
GAM1546 CGB1     5' ATCTGAGAGAGAGCAG     54128      CTGACG  C
                                TTGCTC     TC CTCAGAT
                                ||||||     || |||||||
                                GACGAG     AG GAGTCTA
                                   _______ A
GAM1546 DKFZp547N157 3' CACCTGAGACCAGCAGGACAA 69524    C    AC_  CC   A
                                TTG TCCTG   GTC  TCAG TG
                                ||| |||||   |||  |||| ||
                                AAC AGGAC   CAG  AGTC AC
                                  _    GAC   __    C
GAM1546 DNAJB11  3' GCAAGAGGACTCCAGGAGCAA 33306       AC   C  AGA
                                TTGCTCCTG  GTCC TC   TGC
                                |||||||||  |||| ||   |||
                                AACGAGGAC  CAGG AG   ACG
                                     CT    _ A__
GAM1546 KIAA1951 3' CTGGAGACCCAGGAGCAA    74154       AC   C T
                                TTGCTCCTG  GTC C CAG
                                |||||||||  ||| | |||
                                AACGAGGAC  CAG G GTC
                                     C_   A _
GAM1546 OBTP     3' GCACCCAAAGGGCAGGAGCAA 34665       ACGT   CAGA_
                                TTGCTCCTG   CCCT    TGC
                                |||||||||   ||||    |||
                                AACGAGGAC   GGGA    ACG
                                     _____   AACCC
GAM1546 TROAP    5' GCACCCGAGAGGGTCAGGAG  19692       GT  _  AGA
                                CTCCTGAC  CC CTC   TGC
                                |||||||  || |||   |||
                                GAGGACTG  GG GAG   ACG
                                     __  A   CCC
GAM1546 LOC146515 3' GCATCTGAGAATTGGAGAGCAG 78518      _ TG CGTCC
                                TTGCTC C  A    CTCAGATGC
                                ||||||  |  |    |||||||||
                                GACGAG G  T    GAGTCTACG
                                   A GT AA___
GAM1546 LOC149426 3' GCATCTGAGAAACACATGGGC  85574     C  AC  CC
                                GCTC TG  GT  CTCAGATGC
                                ||||  ||  ||  |||||||||
                                CGGG AC  CA  GAGTCTACG
                                  T  A_  AA
GAM1546 LOC153577 3' GCATCCAAGGGTGGGGAGCAG  87240       GA  T   CA
                                TTGCTCCT  CG CCCT  GATGC
                                ||||||||  || ||||  |||||
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                                GACGAGGG  GT GGGA  CTACG
                                   __ _    AC
GAM1546  LOC220021 3'  GCAAGGGAGGAGCCAGGAGCAA 95023         AC TC    AGA
                                TTGCTCCTG  G  CCTC   TGC
                                |||||||||  |  ||||   |||
                                AACGAGGAC  C  GGAG   ACG
                                   __ GA    GGA
GAM1547  CDH12    3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                   AA___   AC
GAM1547  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                  AC        G
GAM1547  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090      T    AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                  _   GTCA_
GAM1547  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
           A                     TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                  TACTCCC_
GAM1547  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                   AGACG___
GAM1547  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
           TA                    TACA   TCC   GAAGAATAAG
                                ||||   |||   ||||||||||
                                ATGT   AGG   TTTCTTATTC
                                  AAA_  ATTG
GAM1547  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA  68742              _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                          G
GAM1547  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM1547  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748     CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
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                                TGAG    TCTTCTTATTC
                                  TACCG
GAM1547 KIAA1906 3' CTTATTCTTCTTGACTTTTGG 73571    CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM1547 OSBPL11  3' CTTAATTTCCCAAGAGTGGTG 43206       CCAA   AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                     AACC   A_
GAM1547 YME1L1   3' TCATTCTTGATGTGGTGTA   58438       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                     TA_    A
GAM1547 ZNF262   3' CTTATTTTGTTTGGGAGT    18723        A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                     G
GAM1547 LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_    AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
                                ATGTGGTG   GGTTC   TGT
                                     CAA    GG__
GAM1548 SCAMP1   3' GCTAAATAAATATTCTCC    18013    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1548 SCAMP1   3' GCTAAATAAATATTCTCC    54501    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1548 NX-17    3' TGAATATCAGCCCCTAATA   40706       ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                     CGAC
GAM1548 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
             TA                   TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM1549 ABCG1    3' TCCAACCCCTAGAACCGCGT   18191      CCAA  T   C
                                ACGCGG    TG GGG TGGA
                                ||||||    || ||| ||||
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                                TGCGCC   AT CCC ACCT
                                   AAG_  C   A
GAM1549 AGPAT2   3' TCCAGCCCACAAGCTGC    22183     CAA
                                GCGGC   TGTGGGCTGGA
                                |||||   ||||||||||
                                CGTCG   ACACCCGACCT
                                  A__
GAM1549 BHMT2    3' TCCAGCCCACAAGTGTGTGC  34739    GC  A_
                                GCG  CA  TGTGGGCTGGA
                                |||  ||  ||||||||||
                                CGT  GT  ACACCCGACCT
                                 GT  GA
GAM1549 CD44     5' TCCAGCTCCTTTCGCCCGCG  7027      _ C  TGT
                                CGCGG C AA   GGGCTGGA
                                ||||| | ||   ||||||||
                                GCGCC G TT   CTCGACCT
                                   C C  TC_
GAM1549 DNASE1L1 5' TCCAGCCTTCTATTACCACGT 23020    C  CC    T_
                                ACG GG  AATG  GGGCTGGA
                                ||| ||  ||||  ||||||||
                                TGC CC  TTAT  TCCGACCT
                                 A  A_   CT
GAM1549 ENG      5' TCCAGCCCAGCCCCGCGT    5500       CCAATG
                                ACGCGG     TGGGCTGGA
                                ||||||     |||||||||
                                TGCGCC     ACCCGACCT
                                   CCG___
GAM1549 GGT2     5' TCCAGCCCAGCATCCAGC    74089    _ CCA  _
                                GC GG   ATG TGGGCTGGA
                                || ||   ||| |||||||||
                                CG CC   TAC ACCCGACCT
                                 A ____  G
GAM1549 GUCY1A2  5' CCAGCCCGGCGCCGCCGC    7801       CAA  _
                                GCGGC   TGT GGGCTGG
                                |||||   ||| |||||||
                                CGCCG   GCG CCCGACC
                                   CC_  G
GAM1549 HLCS     5' TCCATGGCTCATGGACCACG   6420    C  _  ATG     __
                                CG GG CCA   TGGGCT  GGA
                                || || |||   ||||||  |||
                                GC CC GGT   ACTCGG  CCT
                                 A  A  ____     TA
GAM1549 HSF4     5' CCAGCCCACACCAGGTCGCG   60480       AA_
                                CGCGGCC   TGTGGGCTGG
                                |||||||   ||||||||||
                                GCGCTGG   ACACCCGACC
                                    ACC
GAM1549 IDH3G    3' TCCAGCACCCCAGCCAGC    15956    _  CAA  T  _
                                GC GGC   TG GG GCTGGA
                                || |||   || || ||||||
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                                CG CCG   AC CC CGACCT
                                 A  ___  C  A
GAM1549  IGSF3    3'  CCAGCGGATGTTGGCCACG   9524     C       GG
                                CG GGCCAATGT  GCTGG
                                || |||||||||  |||||
                                GC CCGGTTGTA  CGACC
                                 A        GG
GAM1549  MAB21L1  5'  TCCAGCTCTAGCAGCCGC    19970      CAA  T
                                GCGGC   TG GGGCTGGA
                                |||||   || ||||||||
                                CGCCG   AT CTCGACCT
                                   ACG  _
GAM1549  MADH6    5'  TCCATGTAGCCGCTGGCCGCG  19978        AT   __  _
                                CGCGGCCA  GTGG  GC TGGA
                                ||||||||  ||||  || ||||
                                GCGCCGGT  CGCC  TG ACCT
                                     __   GA  T
GAM1549  NCSTN    3'  TCCAGCCCACAGTGCTCAGT   74138    GC   CAA
                                AC  GGC   TGTGGGCTGGA
                                ||  |||   ||||||||||
                                TG  TCG   ACACCCGACCT
                                 AC   TG_
GAM1549  NGB      5'  TCCACCTACGACTGGCCGCG   41466        A_     C
                                CGCGGCCA  TGTGGG TGGA
                                ||||||||  |||||| ||||
                                GCGCCGGT  GCATCC ACCT
                                     CA     _
GAM1549  PABPC4   5'  TCCAGCTCGTCCTCGCCGCG   15111       CAATG
                                CGCGGC    TGGGCTGGA
                                ||||||    |||||||||
                                GCGCCG    GCTCGACCT
                                   CTCCT
GAM1549  PDGFB    5'  CCAGCCCCCCACCCTGGCCGCG 12021        AT  ___
                                CGCGGCCA  GT   GGGCTGG
                                ||||||||  ||   |||||||
                                GCGCCGGT  CA   CCCGACC
                                     CC  CCC
GAM1549  PDPK1    3'  CCAGCGCGGCTTGGCCGC    12032        TG  G
                                GCGGCCAA  TG GCTGG
                                ||||||||  || |||||
                                CGCCGGTT  GC CGACC
                                     CG  G
GAM1549  PMM2     3'  CCAGCCCACAGCCAGGTG    72557     __  CAA
                                CGC  GGC   TGTGGGCTGG
                                |||  |||   ||||||||||
                                GTG  CCG   ACACCCGACC
                                  GA  ___
GAM1549  PMX1     3'  TCCAATGTAATTGGCTGCGT  23574          GTGGGC
                                ACGCGGCCAAT     TGGA
                                ||||||||||     ||||
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                                TGCGTCGGTTA     ACCT
                                      ATGTA_
GAM1549  PMX1     3'  TCCAATGTAATTGGCTGCGT  23575          GTGGGC
                                ACGCGGCCAAT     TGGA
                                ||||||||||      ||||
                                TGCGTCGGTTA     ACCT
                                      ATGTA_
GAM1549  PRX      3'  TCCAGCTGCCTCGGCTGCGT  40902        AAT TG G
                                ACGCGGCC   G  G CTGGA
                                ||||||||   |  | |||||
                                TGCGTCGG   C  C GACCT
                                     CTC GT _
GAM1549  RAB7     5'  CCAGCGCAGCGGCCGCGT    17346        AA   GG
                                ACGCGGCC  TGT  GCTGG
                                ||||||||  |||  |||||
                                TGCGCCGG  ACG  CGACC
                                     CG   __
GAM1549  RAMP3    3'  TCCAGCCTAGCCTTAGCCGC  20729       C  T _
                                GCGGC AA G TGGGCTGGA
                                ||||| || | |||||||||
                                CGCCG TT C ATCCGACCT
                                   A  C G
GAM1549  TIMP3    5'  CCAGCCCACCCACTCGCGT   6282        CCAAT
                                ACGCGG    GTGGGCTGG
                                ||||||    |||||||||
                                TGCGCT    CACCCGACC
                                   CACC_
GAM1549  WSX1     3'  CCAGCACAGTGGCTCACG    17914    C _   A   GG
                                CG G GCCA TGT  GCTGG
                                || | |||| |||  |||||
                                GC C CGGT ACA  CGACC
                                 A T   G   __
GAM1549  ACRBP    3'  CCAGCCCAACCTGCCCACGT  51653     C  C  ATG
                                ACG GG CA   TGGGCTGG
                                ||| || ||   ||||||||
                                TGC CC GT   ACCCGACC
                                  A  C  CCA
GAM1549  APCL     3'  TCCAGCCCTGATGGCGCGCG  20821      _   ATGT
                                CGCG GCCA    GGGCTGGA
                                ||||  ||||   ||||||||
                                GCGC CGGT    CCCGACCT
                                   G    AGT_
GAM1549  C20orf100 3'  CCAGCCCAGGTGGGCCGC    52877       A  G
                                GCGGCC AT TGGGCTGG
                                |||||| || ||||||||
                                CGCCGG TG ACCCGACC
                                   G  G
GAM1549  CHODL    5'  TCCAGCCCCGCACATCCACG  46886    C  CCAA     _
                                CG GG    TGTGGG CTGGA
                                || ||    |||||| |||||
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                                GC CC    ACGCCC GACCT
                                 A  TAC_     C
GAM1549  CTCF     3'  TCCAGCCCACGGAGCCAGC   22679    _  CAA
                                GC GGC   TGTGGGCTGGA
                                || |||   ||||||||||
                                CG CCG   GCACCCGACCT
                                 A   AG_
GAM1549  DC-TM4F2  3'  CCAGCCCAAGATGGCCAGC   48897    _    ATG
                                GC GGCCA   TGGGCTGG
                                || |||||   ||||||||
                                CG CCGGT   ACCCGACC
                                 A    AGA
GAM1549  DHODH    3'  CCAGCCTGGCATGGCTGC    9067        A  _
                                GCGGCCA TGT GGGCTGG
                                ||||||| ||| |||||||
                                CGTCGGT ACG TCCGACC
                                    _  G
GAM1549  DIO2     3'  TCCAGCTTCTAGCCATGT    26556     C   CAA  TG
                                ACG GGC   TG  GGCTGGA
                                ||| |||   ||  |||||||
                                TGT CCG   AT  TCGACCT
                                  A  ___  CT
GAM1549  DKFZP434N093 3'  TCCAGGTTAGATTGACCGGT   80745    G   C    G   G
                                AC CGG CAAT TGG CTGGA
                                || ||| |||| ||| |||||
                                TG GCC GTTA ATT GACCT
                                 _  A   G   G
GAM1549  DKFZP434P0721 3'  TCCAGCCGTACACCAACTGC   64468      CCAA   _
                                GCGG    TGTG GGCTGGA
                                ||||    |||| |||||||
                                CGTC    ACAT CCGACCT
                                  AACC    G
GAM1549  DKFZp727G131 3'  TCCAGCCTGGGCAACAGCGT   59697      G___   AATG
                                ACGC    GCC    TGGGCTGGA
                                ||||    |||    |||||||||
                                TGCG    CGG    GTCCGACCT
                                  ACAA   ____
GAM1549  FASTK    5'  TCCAGCCGCGGAGCCCGCGT   47688       CCAA    G
                                ACGCGG    TGTGG CTGGA
                                ||||||    ||||| |||||
                                TGCGCC    GCGCC GACCT
                                   CGAG    _
GAM1549  FLJ10661  3'  TCCAGCCCACAGCCTGTGT    36918     _  CAA
                                ACGC GGC   TGTGGGCTGGA
                                |||| |||   ||||||||||
                                TGTG CCG   ACACCCGACCT
                                  T  ___
GAM1549  FLJ11336  5'  TCCAGCCTAGGCCCGCGT    37834       _  AATG
                                ACGCGG CC    TGGGCTGGA
                                |||||| ||    |||||||||
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                                TGCGCC GG   ATCCGACCT
                                   C ____
GAM1549 FLJ12587 3' CCAGCAGGAGCCTGGCCGCG  42775       AT  GG__
                                CGCGGCCA GT   GCTGG
                                |||||||| ||   |||||
                                GCGCCGGT CG   CGACC
                                    C_ AGGA
GAM1549 FLJ12592 3' TCCAGCCTGGGTGACCGAGT  50654   G  CCA  G
                                AC CGG  AT TGGGCTGGA
                                || |||  || |||||||||
                                TG GCC  TG GTCCGACCT
                                 A  AG_ G
GAM1549 FLJ13842 5' TCCAGCCCACAGCTTCGC    45334     CCAA
                                GCGG   TGTGGGCTGGA
                                ||||   ||||||||||
                                CGCT   ACACCCGACCT
                                  TCG_
GAM1549 FLJ14596 5' TCCAGCCCCACAGCCGCGT   52521       CAA    _
                                ACGCGGC  TGTGGG CTGGA
                                |||||||  |||||| |||||
                                TGCGCCG  ACACCC GACCT
                                   ___    C
GAM1549 FLJ20297 5' TCCAGCCCAGGGGGGACCAGC 35375   _ _ AATG
                                GC GG CC   TGGGCTGGA
                                || || ||   |||||||||
                                CG CC GG   ACCCGACCT
                                 A  A  GGGG
GAM1549 FLJ20321 3' TCCAGGCCGTCACTGGCCTGC 35432   _   A _  G
                                GC GGCCA TG TGG CTGGA
                                || ||||| || ||| |||||
                                CG CCGGT AC GCC GACCT
                                 T   C  T  G
GAM1549 FLJ20984 5' TCCAGCCCGACACGCCGC    45249     CAA  _
                                GCGGC  TGT GGGCTGGA
                                |||||  ||| ||||||||
                                CGCCG  ACA CCCGACCT
                                   C__  G
GAM1549 FLJ21687 3' TCCAGCCGGCTAGCCTGCG   46303    _  CAAT  G
                                CGC GGC   GT GGCTGGA
                                ||| |||   || |||||||
                                GCG CCG   CG CCGACCT
                                  T  AT__  G
GAM1549 FLJ22477 3' CCAGCCCACAGCCAGC     45670   _  CAA
                                GC GGC  TGTGGGCTGG
                                || |||  ||||||||||
                                CG CCG  ACACCCGACC
                                 A  ___
GAM1549 FLJ22578 3' CCAGCCCAGGGGACCCGT   46323    C  _  AATG
                                ACG GG CC   TGGGCTGG
                                ||| || ||   ||||||||
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                                TGC CC GG    ACCCGACC
                                  _ A  GG__
GAM1549  FLJ25193  5'  CCAGCCAGCTCATGGGCCACGT 59355     C    A   TG__
                                ACG GGCC ATG    GGCTGG
                                ||| |||| |||    ||||||
                                TGC CCGG TAC    CCGACC
                                  A    G   TCGA
GAM1549  HEMK      3'  CCAGCAGGGCTGGCCCGT    32953     C    AT  GG_
                                ACG GGCCA  GT   GCTGG
                                ||| |||||  ||   |||||
                                TGC CCGGT  CG   CGACC
                                  _    __  GGA
GAM1549  HSA249128 5'  CCGAGGCCTTGGCCGCGT    34559          TGT  G  _
                                ACGCGGCCAA   GG CT GG
                                ||||||||||   || || ||
                                TGCGCCGGTT   CC GA CC
                                      ___  G  G
GAM1549  IMAGE3451454 3'  CCAGCTCACTTAGCCAGC    54938    _   C  T
                                GC GGC AA GTGGGCTGG
                                || ||| || |||||||||
                                CG CCG TT CACTCGACC
                                 A   A  _
GAM1549  IRX4      5'  TCCGGAGCAGTGGCCGCG    33451         A   GGG
                                CGCGGCCA TGT   CTGGA
                                |||||||| |||   |||||
                                GCGCCGGT ACG   GGCCT
                                     G   A__
GAM1549  KIAA0133  3'  TCCAGAGGCTTTGGCTGC    29417         T  GGG
                                GCGGCCAA GT   CTGGA
                                |||||||| ||   |||||
                                CGTCGGTT CG   GACCT
                                     T  GA_
GAM1549  KIAA0633  5'  CCGGAGCACCGCCCGCGT    95701        CCAAT   _  __
                                ACGCGG    GTGG GCT  GG
                                ||||||    |||| |||  ||
                                TGCGCC    CGCC CGA  CC
                                   ______   A   GG
GAM1549  KIAA0819  3'  TCCAGCCCCGGCAGAGCCGC   64336      CAA   __
                                GCGGC   TGT  GGGCTGGA
                                |||||   |||  ||||||||
                                CGCCG   ACG  CCCGACCT
                                   AG_   GC
GAM1549  KIAA1808  3'  CCAGCCCACCTTCCCAGCGT   87048     _  CCAAT
                                ACGC GG    GTGGGCTGG
                                |||| ||    |||||||||
                                TGCG CC    CACCCGACC
                                  A  CTTC_
GAM1549  KIAA1884  3'  CCGAGTCCATTGGCCGC     73722        AT      _
                                GCGGCCA  GTGGGCT GG
                                |||||||  ||||||| ||
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                                CGCCGGT  TACCTGA CC
                                   __      G
GAM1549 KIAA1949 3' CCAGGTTTACAAGCCACG    99693    C   CAA     _
                                CG GGC   TGTGGGC TGG
                                || |||   ||||||| |||
                                GC CCG   ACATTTG ACC
                                 A  A__      G
GAM1549 MAP1LC3A 5' CCAGAGCCCCGGCCTGCG    51681    _   AAT T   __
                                CGC GGCC   G GGGCT  GG
                                ||| ||||   | |||||  ||
                                GCG CCGG   C CCCGA  CC
                                  T   ___ _    GA
GAM1549 MCF2L    3' CCAGAGCGCCTGGCCGTG    61526       AT   GG
                                CGCGGCCA  GTG  CTGG
                                ||||||||  |||  ||||
                                GTGCCGGT  CGC  GACC
                                     C_   GA
GAM1549 MCF2L    3' CCAGCGGCTTGTAGCCGTCA   61527   C    __   T  GG
                                A GCGGC  CAA GT  GCTGG
                                | |||||  ||| ||  |||||
                                A TGCCG  GTT CG  CGACC
                                 C    AT   _ G_
GAM1549 MGC10500 3' TCCAGCCCGGCCTGGCCGC   49727       ATG
                                GCGGCCA   TGGGCTGGA
                                |||||||   |||||||||
                                CGCCGGT   GCCCGACCT
                                    CCG
GAM1549 MGC11352 5' CCAGCCCAAGATGGCCAGC   65428   _    ATG
                                GC GGCCA   TGGGCTGG
                                || |||||   ||||||||
                                CG CCGGT   ACCCGACC
                                 A    AGA
GAM1549 MGC14839 3' CCAGGGATGTTGTCCACGT   55587    C  C     GGG
                                ACG GG CAATGT   CTGG
                                ||| || ||||||   ||||
                                TGC CC GTTGTA   GACC
                                  A  T     GG_
GAM1549 MGC15875 5' CCAGCCCGCGCGGCGACGT   53013    CG   AA
                                ACG  GCC  TGTGGGCTGG
                                |||  |||  ||||||||||
                                TGC  CGG  GCGCCCGACC
                                  AG   C_
GAM1549 MGC16279 3' TCCAGCCCACAGCCTGTGT   52996     _  CAA
                                ACGC GGC   TGTGGGCTGGA
                                |||| |||   ||||||||||
                                TGTG CCG   ACACCCGACCT
                                  T   ___
GAM1549 MGC2668  3' TCCAGCCCCAGAGCCAGCGT  61197     _  CAA  T
                                ACGC GGC   TG GGGCTGGA
                                |||| |||   || ||||||||
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                                TGCG CCG   AC CCCGACCT
                                  A  AG_  _
GAM1549  MGC2865   3'  TCCAGCCCACGACCTGCCGCG  51462       CAA_
                                CGCGGC   TGTGGGCTGGA
                                ||||||   ||||||||||
                                GCGCCG   GCACCCGACCT
                                   TCCA
GAM1549  MGC3123   3'  CCAGCCCGCACACTGCGT    44342       CCAA
                                ACGCGG   TGTGGGCTGG
                                ||||||   |||||||||
                                TGCGTC   ACGCCCGACC
                                   AC__
GAM1549  OR2C3     3'  CCAGCCCTCAGGCCTGCG    75973     _   AA  T
                                CGC GGCC  TG GGGCTGG
                                ||| ||||  || |||||||
                                GCG CCGG  AC CCCGACC
                                  T   __  T
GAM1549  PABPC5    5'  CCAGCCCATCGGTCTGCG    55932      _ AAT
                                CGCGG CC   GTGGGCTGG
                                ||||| ||   |||||||||
                                GCGTC GG   TACCCGACC
                                   T  C__
GAM1549  PP1665    3'  TCCAGCCCCTTGTCAGCCGC  48641      CA  T_
                                GCGGC  ATG  GGGCTGGA
                                |||||  |||  ||||||||
                                CGCCG  TGT  CCCGACCT
                                   AC   TC
GAM1549  PPM1A     5'  CCAGCCTGACCTGGCCCG    41004    C    ATG
                                CG GGCCA   TGGGCTGG
                                || |||||   ||||||||
                                GC CCGGT   GTCCGACC
                                 _    CCA
GAM1549  PRO0097   3'  CCAGCCCACAGGCAGC      26933    G   AA
                                GC GCC  TGTGGGCTGG
                                || |||  ||||||||||
                                CG CGG  ACACCCGACC
                                 A  __
GAM1549  PTDSS1    3'  CCCACAGACCTGGCCGCGT   29251        A___
                                ACGCGGCCA   TGTGGG
                                |||||||||   ||||||
                                TGCGCCGGT   ACACCC
                                     CCAG
GAM1549  PV1       3'  CCAGCCCTGCCTGTGGCCCGT  49373    C    AT_ _
                                ACG GGCCA   GT GGGCTGG
                                ||| |||||   || |||||||
                                TGC CCGGT   CG CCCGACC
                                  _    GTC  T
GAM1549  RBPMS     5'  TCCAGCCCCACAGCCCGC    23437     CCAA    _
                                GCGG   TGTGGG CTGGA
                                ||||   |||||| |||||
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                                CGCC   ACACCC GACCT
                                  CG__     C
GAM1549  RRP4     3'  TCCAGCCCACAGGCCTGC    27362    _   AA
                                GC GGCC  TGTGGGCTGGA
                                || ||||  ||||||||||
                                CG CCGG  ACACCCGACCT
                                 T   __
GAM1549  SMCR7    3'  CCAGCCCACAGCTGGGGC    58238    GG  A_
                                GC  CCA  TGTGGGCTGG
                                ||  |||  ||||||||||
                                CG  GGT  ACACCCGACC
                                 G_  CG
GAM1549  TRPM3    5'  TCCAGAGACTTTGGCCAGC   65527    _    T  GGG
                                GC GGCCAA GT   CTGGA
                                || |||||| ||   |||||
                                CG CCGGTT CA   GACCT
                                 A     T  GA_
GAM1549  WNT10A   5'  CCAGCCCGTCAGGGCCTGCG  48169    _   AA  _
                                CGC GGCC  TG TGGGCTGG
                                ||| ||||  || ||||||||
                                GCG CCGG  AC GCCCGACC
                                  T   G_  T
GAM1549  LOC112885 5'  CCAGCCCGGAGGCCGCGT    57337        AATG
                                ACGCGGCC    TGGGCTGG
                                ||||||||    ||||||||
                                TGCGCCGG    GCCCGACC
                                     AG__
GAM1549  LOC129880 3'  TCCAGCTCCTAACCGCG     75408      CCAA  T
                                CGCGG    TG GGGCTGGA
                                |||||    || ||||||||
                                GCGCC    AT CTCGACCT
                                   A___  C
GAM1549  LOC139065 5'  TCTGGAACACATTGGCCGTGT  76325            GG TG
                                ACGCGGCCAATGTG  C  GA
                                |||||||||||||  |  ||
                                TGTGCCGGTTACAC  G  CT
                                         AA GT
GAM1549  LOC139522 5'  TCCAGCCCAGATCCGGCCACG  76364    C    A_  G
                                CG GGCC  AT TGGGCTGGA
                                || ||||  || |||||||||
                                GC CCGG  TA ACCCGACCT
                                 A   CC  G
GAM1549  LOC143666 5'  TCCAGCCCAGCCCCGCGT    83889       CCAATG
                                ACGCGG     TGGGCTGGA
                                ||||||     |||||||||
                                TGCGCC     ACCCGACCT
                                   CCG____
GAM1549  LOC144108 3'  TCCAAGAATATCATTAGCCGGT 77191    G   C   _  GG  _
                                AC CGGC AATG TG  CT GGA
                                || |||| |||| ||  || |||
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                                TG GCCG TTAC AT  GA CCT
                                 _   A   T  AA  A
GAM1549  LOC146957 3'  CCAGCCTGCCTTTGGCCGC   78812       T_ TG
                                GCGGCCAA  G  GGCTGG
                                |||||||| |  ||||||
                                CGCCGGTT  C  CCGACC
                                    TC GT
GAM1549  LOC148753 3'  CCAGCCCACCACGCCGAGT   85370   G   CAAT
                                AC CGGC   GTGGGCTGG
                                || ||||   |||||||||
                                TG GCCG   CACCCGACC
                                 A   CAC_
GAM1549  LOC149319 5'  TCCAGCCCAGCATCCAGC    80077   _ CCA  _
                                GC GG  ATG TGGGCTGGA
                                || ||  ||| |||||||||
                                CG CC  TAC ACCCGACCT
                                 A ___  G
GAM1549  LOC150197 3'  CCAGCCTGGCAGCCGC     80420     CAA  _
                                GCGGC  TGT GGGCTGG
                                |||||  ||| |||||||
                                CGCCG  ACG TCCGACC
                                   ___  G
GAM1549  LOC151781 3'  TCCAGCCCACAGCCTGTGT   81163    _  CAA
                                ACGC GGC  TGTGGGCTGGA
                                |||| |||  ||||||||||
                                TGTG CCG  ACACCCGACCT
                                  T  ___
GAM1549  LOC152048 3'  TCCAGCCCCGGGAGCCGCG   86734      CAA  T
                                CGCGGC  TG GGGCTGGA
                                ||||||  || ||||||||
                                GCGCCG  GC CCCGACCT
                                   AGG  _
GAM1549  LOC152447 3'  TCCAGGCGCCGGCCGCGT   81459       AAT  GG
                                ACGCGGCC  GTG  CTGGA
                                ||||||||  |||  |||||
                                TGCGCCGG  CGC  GACCT
                                    C__  G_
GAM1549  LOC158490 3'  TCCAGCCCACAGCCTGTGT   82825    _  CAA
                                ACGC GGC  TGTGGGCTGGA
                                |||| |||  ||||||||||
                                TGTG CCG  ACACCCGACCT
                                  T  ___
GAM1549  LOC167606 5'  TCCAGCCGTAATATTGGC    88623       G__
                                GCCAATGT  GGCTGGA
                                ||||||||  |||||||
                                CGGTTATA  CCGACCT
                                    ATG
GAM1549  LOC203504 5'  CCAGCCCTGGCCCTGGCCGCG  92322       AT __
                                CGCGGCCA  GT  GGGCTGG
                                ||||||||  ||  |||||||
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                                GCGCCGGT  CG  CCCGACC
                                    CC  GT
GAM1549  LOC219688 5'  TCCGAGTCGTTGGCCGCGT   94644         GTG   _
                                ACGCGGCCAAT   GGCT GGA
                                ||||||||||   |||| |||
                                TGCGCCGGTTG   CTGA CCT
                                      ___   G
GAM1549  LOC219743 3'  TCCAGCCCACAGCCTGGGT   94749    G _   CAA
                                AC C GGC   TGTGGGCTGGA
                                || | |||   ||||||||||
                                TG G CCG   ACACCCGACCT
                                 G T  ___
GAM1549  LOC220073 5'  TCCAGCCCACAGCCTGTGT   95075     _   CAA
                                ACGC GGC   TGTGGGCTGGA
                                |||| |||   ||||||||||
                                TGTG CCG   ACACCCGACCT
                                  T  ___
GAM1549  LOC221477 5'  TCCAGTTCTCAGCCGC      93777      CAA  T
                                GCGGC   TG GGGCTGGA
                                |||||   || ||||||||
                                CGCCG   AC CTTGACCT
                                   ___  T
GAM1549  LOC253258 5'  TCCAGCCCAGCCCCGCGT    98233       CCAATG
                                ACGCGG     TGGGCTGGA
                                ||||||     |||||||||
                                TGCGCC     ACCCGACCT
                                   CCG___
GAM1549  LOC254263 3'  CCAGCCCTGCCCCTTGGCCGC  96366        T__  _
                                GCGGCCAA   GT GGGCTGG
                                ||||||||   || |||||||
                                CGCCGGTT   CG CCCGACC
                                     CCC  T
GAM1549  LOC254659 5'  TCTGCCCACATCAGCAGC    96823    G  CA      T
                                GC GC  ATGTGGGC GGA
                                || ||  |||||||| |||
                                CG CG  TACACCCG TCT
                                 A  AC       _
GAM1549  LOC255251 5'  CCAGCCCGCGCGGCGACGT   97619     CG   AA
                                ACG  GCC  TGTGGGCTGG
                                |||  |||  ||||||||||
                                TGC  CGG  GCGCCCGACC
                                  AG   C_
GAM1549  LOC255330 3'  TCCAGCCCACATTCAAGG    97503    ___
                                CC   AATGTGGGCTGGA
                                ||   ||||||||||||
                                GG   TTACACCCGACCT
                                 AAC
GAM1549  LOC255704 5'  CCACAACCACGTGGCCGCG   96990        A    GC_
                                CGCGGCCA TGTGG   TGG
                                |||||||| |||||   |||
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                                GCGCCGGT GCACC   ACC
                                     _    AAC
GAM1549  LOC256211 5'  TCCAGCCCTGCGCAGCCGC   98524      CAA  _
                                GCGGC   TGT GGGCTGGA
                                |||||   ||| ||||||||
                                CGCCG   GCG CCCGACCT
                                   AC_   T
GAM1549  LOC256364 5'  TCCAGCCGCTTTGGCCGC    96450        T   G
                                GCGGCCAA GTGG CTGGA
                                |||||||| |||| |||||
                                CGCCGGTT CGCC GACCT
                                     T   _
GAM1549  LOC256710 5'  CCAGCCGTTACTGGTCCGCG  96563      _  A  TG
                                CGCGG CCA TG  GGCTGG
                                ||||| ||| ||  ||||||
                                GCGCC GGT AT  CCGACC
                                   T   C  TG
GAM1549  LOC51107  3'  CCAGCCCGGGGTCCATTGCCC  32608    C    _____
                                GG CAATG    TGGGCTGG
                                || |||||    ||||||||
                                CC GTTAC    GCCCGACC
                                 C    CTGGG
GAM1549  LOC51336  3'  TCCAGCCTGGGTGACAGCGT   34078     GGCCA  G
                                ACGC    AT TGGGCTGGA
                                ||||    || |||||||||
                                TGCG    TG GTCCGACCT
                                  ACAG_  G
GAM1549  LOC51667  3'  TCCAGCCCCAGGACCGC     32779     _  AA  T
                                GCGG CC  TG GGGCTGGA
                                |||| ||  || ||||||||
                                CGCC GG  AC CCCGACCT
                                  A  __  _
GAM1549  LOC91069  3'  TCCAGCCCACAGCCTGTGT    65405     _  CAA
                                ACGC GGC   TGTGGGCTGGA
                                |||| |||   ||||||||||
                                TGTG CCG   ACACCCGACCT
                                  T   ___
GAM1550  ELF3      3'  TGACCTTGACCTTGACCAA    16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                   _    AGT  ___
GAM1550  JAK2      3'  TGACCTTCATTCTGAGACCAA  18318       CAA      AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_       C_
GAM1550  SLC10A2   5'  ACTCTCTGTCTTGACCAA    6590        CAA      A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
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                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM1550  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM1550  KIAA1958  5'  GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM1550  MARCKS   3'  ACTTTCCACCCTGCCCA     11411     TTCA    A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM1550  TUB      5'  GTGGGACCATCCCTTAAACC   13898     C        AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A        AG__
GAM1550  LOC80298  3'  ACTTTTACCTTGAACCA     48062          GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                     A___
GAM1551  GPD1     3'  TCATGCCACCACATTTG     60398       C       C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A       _
GAM1551  IL5RA    5'  TCGCATGGCCACCGCATTT    6906           AT__
                                AAATGCGGTGGC    CGA
                                ||||||||||||    |||
                                TTTACGCCACCG    GCT
                                      GTAC
GAM1551  MYO1C    3'  TGCCGATGCCAAATATTTG   61873       CGG       A
                                TAAATG   TGGCATCG CA
                                ||||||   |||||||| ||
                                GTTTAT   ACCGTAGC GT
                                   AA_       C
GAM1551  C6orf37   3'  TGTCACACTGCATTTA      68097          GCATC
                                TAAATGCGGTG     GACA
                                ||||||||||     ||||
                                ATTTACGTCAC     CTGT
                                      A____
GAM1551  DNAJC6   3'  TTGCAGAACCACCGCATT    29498          CA  GA
                                AATGCGGTGG  TC  CAA
                                ||||||||||  ||  |||
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                                TTACGCCACC  AG  GTT
                                     A_  AC
GAM1551  FLJ11210  3'  GTCGATGTGCATGCTTTTA   60319     T   GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM1551  FLJ12476  3'  TCGATCTTCTGCATTTA     43270        T  C
                                TAAATGCGG GG ATCGA
                                ||||||||| || |||||
                                ATTTACGTC TC TAGCT
                                     T  _
GAM1551  KIAA1034  3'  TCGATGGCATCCGCATTTG   63134        _  G
                                TAAATGCGG TG CATCGA
                                ||||||||| || ||||||
                                GTTTACGCC AC GTAGCT
                                     T  G
GAM1551  KIAA1987  3'  TCATGTAACTGCATTTA     89391        G   C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                     A   _
GAM1551  MGC16063  3'  TGTCCTGGCCACTGCATT    54929         ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                      GTC
GAM1551  LOC147949 3'  TGTCAGATGTCCACATTGCA   79279     __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM1551  LOC150577 3'  GTCCTCACCGCATTTG      86258         CATC
                                TAAATGCGGTGG   GAC
                                ||||||||||||   |||
                                GTTTACGCCACT   CTG
                                      C___
GAM1551  LOC158219 3'  TGTGTGTCACCACATTT     82694      C      CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                   A      __
GAM1551  LOC202020 3'  TGTCTCACCACATTTA      90605      C    CATC
                                TAAATG GGTGG   GACA
                                |||||| |||||   ||||
                                ATTTAC CCACT   CTGT
                                   A    ____
GAM1551  LOC90826  5'  TGTCGATGCAGGTTTATTTG  64788      CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
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                                GTTTAT    CGTAGCTGT
                                   TTGGA
GAM1551  LOC93587  3'  TTGTCTTTACCTGCATTTA   73042       _    CATC
                                TAAATGC GGTGG   GACAA
                                ||||||| |||||   |||||
                                ATTTACG CCATT   CTGTT
                                    T   T___
GAM1552  ABCC1     3'  CCCTGGTAAACCAAGCCTC   18435    AAAA  CT_     A
                                GAG   GC   GTTTACCA GG
                                |||   ||   |||||||| ||
                                CTC   CG   CAAATGGT CC
                                  ____  AAC      C
GAM1552  ABCC1     3'  CCCTGGTAAACCAAGCCTC   39599    AAAA  CT_     A
                                GAG   GC   GTTTACCA GG
                                |||   ||   |||||||| ||
                                CTC   CG   CAAATGGT CC
                                  ____  AAC      C
GAM1552  ABCC1     3'  CCCTGGTAAACCAAGCCTC   39602    AAAA  CT_     A
                                GAG   GC   GTTTACCA GG
                                |||   ||   |||||||| ||
                                CTC   CG   CAAATGGT CC
                                  ____  AAC      C
GAM1552  ANKH      3'  TCCTCAGAGTGGCTTTTCCT   55076    A     TG   ACCA
                                AG GAAAAGCC  TTT   AGGA
                                || ||||||||  |||   ||||
                                TC CTTTTCGG  AGA   TCCT
                                 _      TG   C___
GAM1552  BAZ2A     3'  CCCCAGTTTTCAGATTTTCTCT 26507       GC   TTT  CAA
                                AGAGAAAA  CTG   AC   GG
                                ||||||||  |||   ||   ||
                                TCTCTTTT  GAC   TG   CC
                                    A_   TTT  ACC
GAM1552  DSG1      3'  TCCTTAGCATTCATAAACTTTT 10451       CC__  TTTACC
            CTCT                   AGAGAAAAG   TG    AAGGA
                                |||||||||   ||    |||||
                                TCTCTTTTC   AC    TTCCT
                                     AAAT  TTACGA
GAM1552  DUOX2     3'  CCCTGGGCAGGCCCCTCTCT   26865     AAA    TTA   A
                                AGAGA   GCCTGT   CCA GG
                                |||||   ||||||   ||| ||
                                TCTCT   CGGACG   GGT CC
                                  CCC     ___   C
GAM1552  EHD2      3'  TCCTCAGATGGGCCCCTC    28230     AAAA      ACCA
                                GAG   GCCTGTTT   AGGA
                                |||   ||||||||   ||||
                                CTC   CGGGTAGA   TCCT
                                  CC__      C___
GAM1552  F9        3'  TCCCCAAATCAGTTTTTCTCT  5530         C  TTTACCAA
                                AGAGAAAAGC TG      GGA
                                |||||||||| ||      |||
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                                TCTCTTTTTG AC       CCT
                                      _ TAAACC__
GAM1552 GBF1     5' TCCAGGAAACAGGCTCCTTCT 16093     A_       A AA
                                AGAA AGCCTGTTT CC GGA
                                |||| ||||||||| || |||
                                TCTT TCGGACAAA GG CCT
                                  CC       _ A_
GAM1552 GLUL     3' CCTCGTGGTGGAAACTTTTCTT 10808       CCTG     __
                                GAGAAAAG   TTTACCA AGG
                                |||||||| |||||||  |||
                                TTCTTTTC   AGGTGGT TCC
                                    AA__     GC
GAM1552 HDAC4    3' TCCTTGGACCTTTAGCCTTTTT 21252       A CTGTTTA
              CT                  AGAGAAA GC     CCAAGGA
                                |||||||  ||     |||||||
                                TCTTTTT CG     GGTTCCT
                                   C ATTTCCA
GAM1552 IGF2     3' TCCCCGAAACAGGCTACTCTC 7038      AA       ACCAA
                                GAGA AGCCTGTTT    GGA
                                |||| |||||||||    |||
                                CTCT TCGGACAAA    CCT
                                  CA       GCC__
GAM1552 JUP      3' CCTCTTTGCAGGCTTTTCCT  11108    A        TTACCA
                                AG GAAAAGCCTGT     AGG
                                || ||||||||||     |||
                                TC CTTTTCGGACG     TCC
                                _         TTTC__
GAM1552 KCNH3    3' TCCCTGGGGCAGGCCTCTC   65214     AAA      TA  A
                                GAGA  GCCTGTT  CCA GGA
                                ||||  |||||||  ||| |||
                                CTCT  CGGACGG  GGT CCT
                                  C__      __  C
GAM1552 MAZ      3' CCTTGGTACAAGCTCCTCTC  73778     AA  C   TT
                                GAGA  AGC TGT  ACCAAGG
                                ||||  ||| |||  |||||||
                                CTCT  TCG ACA  TGGTTCC
                                  CC  A  __
GAM1552 PDE7A    3' CCCTGGTTTGCCTTTTTCT   66134       A CTGTTT   A
                                AGAGAAA GC     ACCA GG
                                ||||||| ||     |||| ||
                                TCTTTTT CG     TGGT CC
                                   C TT____    C
GAM1552 PIK3C2B  3' TCCTCGGCCAGAGCCCTCTCT 12112      AAA _   TTTA A
                                AGAGA  GC CTG   CC AGGA
                                |||||  || |||   || ||||
                                TCTCT  CG GAC   GG TCCT
                                  CC_ A  C___ C
GAM1552 PKP2     3' CCTTGGTTGTTTTTCTCT    17109         CTGTTT
                                AGAGAAAAGC     ACCAAGG
                                ||||||||||     |||||||
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                                TCTCTTTTTG     TGGTTCC
                                      T_____
GAM1552 PPL     3' TCCTTGGTGTCGTCCTCTC   12223     AAA  CTGTT
                                GAGA   GC    TACCAAGGA
                                ||||   ||    |||||||||
                                CTCT   TG    GTGGTTCCT
                                  CC_  CT___
GAM1552 PRKAR1A  3' TCCTCTGGCAAACTTTTCTTT  12283         CC  TTTA  _
                                AGAGAAAAG  TG    CCA AGGA
                                |||||||||  ||    ||| ||||
                                TTTCTTTTC  AC    GGT TCCT
                                     AA  ____   C
GAM1552 RFNG     3' TCCCACGGGAACAGGCTT    89563          A  AA_
                                AAGCCTGTTT CC   GGA
                                ||||||||||  ||   |||
                                TTCGGACAAG GG   CCT
                                     _  CAC
GAM1552 SLC2A3   3' CTTGGAGCTTTTTTCT      23640          CTGTTTA
                                AGAGAAAAGC      CCAAG
                                ||||||||||      |||||
                                TCTTTTTTCG      GGTTC
                                     A_______
GAM1552 SREBF2   3' TCCTCAGTTTTTATCAGGCTTT 17190        A    TTT___  CA
             CTCT                  AGAGAAA GCCTG     AC  AGGA
                                |||||||  |||||     ||  ||||
                                TCTCTTT CGGAC     TG  TCCT
                                   _    TATTTT  AC
GAM1552 TAF1     3' CCTTGGTCAGCCTTCCCT    17230    AA   C   TTT
                                AG  AAG CTG   ACCAAGG
                                ||  |||  |||   |||||||
                                TC  TTC GAC   TGGTTCC
                                 CC   C  ___
GAM1552 TAF1     3' CCTTGGTCAGCCTTCCCT    57982    AA   C   TTT
                                AG  AAG CTG   ACCAAGG
                                ||  |||  |||   |||||||
                                TC  TTC GAC   TGGTTCC
                                 CC   C  ___
GAM1552 TEAD3    3' CCTTGGTGGGCACTGTTCCCT  13669    A   A  CC
                                AG GAA AG  TGTTTACCAAGG
                                || ||| ||  ||||||||||||
                                TC CTT TC  ACGGGTGGTTCC
                                 C   G  __
GAM1552 TMPRSS3  5' CCTTGGTGGGTGGCCCTTTCCC 51515    A    A_   T TT
             T                   AG GAAA  GCC G  TACCAAGG
                                || ||||  ||| |  ||||||||
                                TC CTTT  CGG T  GTGGTTCC
                                 C    CC   _ GG
GAM1552 TNFRSF1A 3' CCTCGATGTACATAGCTTTTCT 8377          C   T   CA__
             C                   GAGAAAAGC TGT TAC    AGG
                                |||||||| ||| |||    |||
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                                CTCTTTTCG ATA ATG   TCC
                                     _  C  TAGC
GAM1552 VDR     3' CCTTTCCTGCGGGCTTTTC  6343         TTACC
                                GAAAAGCCTGT   AAGG
                                ||||||||||    ||||
                                CTTTTCGGGCG   TTCC
                                      TCCT_
GAM1552 ZNF219  3' TCCCCAATAAACAGGTGTCTT 33557    AAA      CCAA
                                GAGA  GCCTGTTTA   GGA
                                ||||  |||||||||   |||
                                TTCT  TGGACAAAT   CCT
                                  G__       AACC
GAM1552 ALK7    3' CCTTGAATAGTGCTTTTCTC  76242       _    TAC
                                GAGAAAAGC CTGTT  CAAGG
                                ||||||||| |||||  |||||
                                CTCTTTTCG GATAA  GTTCC
                                     T   ____
GAM1552 C11orf11 3' TCCTGGGAGCAGGCCTTCCTC 94882    A A      A  A
                                GAG AA GCCTGTTT CCA GGA
                                ||| || |||||||| ||| |||
                                CTC TT CGGACGAG GGT CCT
                                  C C      _  _
GAM1552 DKFZP564O0463 3' CCTTGGACTCCAGATCTTTCTC 27124       AGC  TTTA
           T                     AGAGAAA  CTG   CCAAGG
                                 |||||||  |||   ||||||
                                 TCTCTTT  GAC   GGTTCC
                                     CTA  CTCA
GAM1552 DPCR1   3' GTAAACAGGCTCATCTCT   55997     AA
                                AGAGA  AGCCTGTTTAC
                                |||||  ||||||||||
                                TCTCT  TCGGACAAATG
                                   AC
GAM1552 FLJ10350 3' CCCTGGGGGTGGGTCCTCTCT 97247     AAA  TG  A  A
                                AGAGA  GCC  TTT CCA GG
                                |||||  |||  ||| ||| ||
                                TCTCT  TGG  GGG GGT CC
                                   CC_  GT  _  C
GAM1552 FLJ12921 3' TCCTTGACATTTGTGCTTTTCT 46401       CTGTTTAC
           C                     GAGAAAAGC      CAAGGA
                                 |||||||||      ||||||
                                 CTCTTTTCG      GTTCCT
                                      TGTTTACA
GAM1552 FLJ14326 5' TCCTCCAGGGCAGGCTCCTTC  50787    A_      ACCA
                                GAA  AGCCTGTTT   AGGA
                                |||  |||||||||   ||||
                                CTT  TCGGACGGG   TCCT
                                  CC       ACC_
GAM1552 FLJ23153 3' CCTTGACTTTGCTTTTCTT   45267       CT_  TTAC
                                GAGAAAAGC  GT   CAAGG
                                |||||||||  ||   |||||
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                                TTCTTTTCG  CA   GTTCC
                                     TTT  ____
GAM1552  GAB3     3'  TCCTCAGACCTGGCTTTTTCCT 55523   AG     T_   ACCA
                                AG  AAAAGCC  GTTT   AGGA
                                ||  |||||||  ||||   ||||
                                TC  TTTTCGG  CAGA   TCCT
                                 CT      TC   C___
GAM1552  GABBR1   3'  TGGGAAACAGACCTTTTTCT  41862       AGC     A
                                AGAGAAA  CTGTTT CCA
                                |||||||  |||||| |||
                                TCTTTTT  GACAAA GGT
                                    CCA     G
GAM1552  GABBR1   3'  TGGGAAACAGACCTTTTTCT  9414        AGC     A
                                AGAGAAA  CTGTTT CCA
                                |||||||  |||||| |||
                                TCTTTTT  GACAAA GGT
                                    CCA     G
GAM1552  H2AV     3'  TCCCCAGTAAAAATAGGCCTTT 57637     A     __  CAA
             C                   GAAA GCCTGTT  TAC  GGA
                                ||||  |||||||  |||  |||
                                CTTT CGGATAA  ATG  CCT
                                  C      AA   ACC
GAM1552  HSPC195  5'  CCTCGGCAGTTGGCAGGCTCCC 81863     AAA      TA___  A
             TCT                  AGAG  AGCCTGTT    CC AGG
                                ||||  ||||||||    || |||
                                TCTC  TCGGACGG    GG TCC
                                  CC_      TTGAC  C
GAM1552  KIAA0478 3'  TCCTCTGTAGCAGACAGGCCTC 30184    AAAA     ___  CA
             CCTC                  GAG   GCCTGTT   TAC  AGGA
                                |||   |||||||  |||  ||||
                                CTC   CGGACAG   ATG  TCCT
                                 CCTC     ACG   TC
GAM1552  KIAA1016 5'  TCCTTGGTAAAGTTTGACTTTT 93389      CCTG__
             C                   GAAAAG     TTTACCAAGGA
                                ||||||     ||||||||||
                                CTTTTC     AAATGGTTCCT
                                   AGTTTG
GAM1552  KIAA1260 3'  TCCCCAACAAAAGAGGCTTTTC 60672         G   ACCAA_
             TT                   GAGAAAAGCCT TTT     GGA
                                ||||||||||| |||     |||
                                TTCTTTTCGGA AAA     CCT
                                      G   ACAACC
GAM1552  KIAA1327 3'  CCTAGGTGCAAGCTTTTTCT  72726       A  C   TT   A
                                AGAGAAA GC TGT  ACC AGG
                                ||||||| || |||  ||| |||
                                TCTTTTT CG ACG  TGG TCC
                                    _ A   __   A
GAM1552  KIAA1668 3'  CCCTGGCAGGCTCCTTCT    67062     A_     TTTA   A
                                AGAA  AGCCTG    CCA GG
                                ||||  ||||||    ||| ||
```

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                                TCTT  TCGGAC    GGT CC
                                  CC      _____   C
GAM1552 KIAA1668 3' CCTCACTTAGGCTTTCCTCT  67063     A       TTTACCA
                                AGAG AAAGCCTG      AGG
                                |||| ||||||||      |||
                                TCTC TTTCGGAT      TCC
                                  C       TCAC___
GAM1552 KIAA1877 3' TCCCCGGTTCTGGCTTTTCT  66763         TGTTT   AA
                                AGAAAAGCC    ACC  GGA
                                |||||||||    |||  |||
                                TCTTTTCGG    TGG  CCT
                                     TCT__   CC
GAM1552 MAWBP    5' TCCTTGGTAATTATTTCCTTT 42389     A  GCCTGT
                                AGAG AAA     TTACCAAGGA
                                |||| |||     ||||||||||
                                TTTC TTT     AATGGTTCCT
                                  C  ATT___
GAM1552 MGC24447 3' CCCCGTGAAAGCTTTTCTT   57123         CTG    CAA
                                GAGAAAAGC   TTTAC   GG
                                |||||||||   |||||   ||
                                TTCTTTTCG   AAGTG   CC
                                     A__    CC_
GAM1552 MGC2628  3' CCCTGGACCGGCTCTTCCT   44196    A  A   T  TTA  A
                                AG GAA AGCC GT   CCA GG
                                || ||| |||| ||   ||| ||
                                TC CTT TCGG CA   GGT CC
                                 _  C   C  ___   C
GAM1552 MGC9753  5' CCTTGAGATGATTTTCTCT   54188       GCCT   AC
                                AGAGAAAA   GTTT  CAAGG
                                ||||||||   ||||  |||||
                                TCTCTTTT   TAGA  GTTCC
                                     AG__   __
GAM1552 MRF2     5' CTTGGCGACTTTTTCT     77027       CCT   TA
                                AGAAAAG   GTT  CCAAG
                                |||||||   |||  |||||
                                TCTTTTT   CAG  GGTTC
                                    ___   C_
GAM1552 NDP52    3' CCTTGGTGTTGCTTTCTC    20669      A  CTGTT
                                GAGAAA GC    TACCAAGG
                                |||||| ||    ||||||||
                                CTCTTT CG    GTGGTTCC
                                   _  TT___
GAM1552 NET-5    3' CCCCGGCACTGATGGGCTTCT  22893     AA      TA__  AA
                                AGA  AGCCTGTT   CC  GG
                                |||  ||||||||   ||  ||
                                TCT  TCGGGTAG   GG  CC
                                  __      TCAC  CC
GAM1552 NICE-3   3' CCCCAGTAGCGCTTTTTTCT  31883        CTGT   CAA
                                AGAGAAAAGC   TTAC   GG
                                ||||||||||   ||||   ||
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                                TCTTTTTTCG   GATG  CC
                                     C___    ACC
GAM1552 p25     3'  CCAGCGGCCCTCAGGCTTTTCT 23826          TTTA  AA_
            C                    GAGAAAAGCCTG   CC  GG
                                 ||||||||||||   ||  ||
                                 CTCTTTTCGGAC   GG  CC
                                      TCCC  CGA
GAM1552 PDE8B   3'  CCTTGGACAAGCTTTTCTT   68201        C   TTA
                                 GAGAAAAGC TGT   CCAAGG
                                 |||||||||  |||   ||||||
                                 TTCTTTTCG ACA   GGTTCC
                                      A  ____
GAM1552 TUSP    3'  CCGATGGAGGCACAGGCTTCTG 40021    GAA      _ TA   A_
            TCT                    AGA   AAGCCTGT T  CCA  GG
                                 |||   ||||||||  |  |||  ||
                                 TCT   TTCGGACA G  GGT  CC
                                   GTC       C GA   AG
GAM1552 ZNF262  3'  TCCCCAATGGCAGCTTTTCTC  18727        C    TACCAA
                                 GAGAAAAGC TGTT     GGA
                                 |||||||||  ||||     |||
                                 CTCTTTTCG ACGG     CCT
                                      _   TAACC_
GAM1552 LOC115399 3'  TCCTTAGGGCCAGGCTTT    73817        TTTA  _
                                 AAAGCCTG    CC AAGGA
                                 ||||||||    || |||||
                                 TTTCGGAC    GG TTCCT
                                      CG__  A
GAM1552 LOC127943 3'  TCCTTGGTCTCCTGCTTCCCCT 75192     AA_    CTGTTT
            C                     GAG   AAGC     ACCAAGGA
                                 |||   ||||     ||||||||
                                 CTC   TTCG     TGGTTCCT
                                   CCC    TCCTC_
GAM1552 LOC144742 5'  CCTAGGTCCTCACCTTTTCTCT 77456         CC  TTT   A
                                 AGAGAAAAG  TG   ACC AGG
                                 |||||||||  ||   ||| |||
                                 TCTCTTTTC  AC   TGG TCC
                                      C_  TCC   A
GAM1552 LOC144747 5'  CCTTGGTAGCTTTTTCTC    77471        _  CTGTT
                                 GAGAAAA GC     TACCAAGG
                                 |||||||  ||    ||||||||
                                 CTCTTTT CG     ATGGTTCC
                                     T  ______
GAM1552 LOC146958 5'  TCCTTAACACCAACAGGCTTTC 84949     A         TACC__
            CTC                    GAG AAAGCCTGTT     AAGGA
                                 |||  ||||||||||     |||||
                                 CTC TTTCGGACAA     TTCCT
                                   C         CCACAA
GAM1552 LOC147858 3'  CCTTCTGCAGAACGGGCCCCTC 79268     AAAA       ACC__
                                 GAG    GCCTGTTT    AAGG
                                 |||    ||||||||    ||||
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                                CTC   CGGGCAAG    TTCC
                                  CC__      ACGTC
GAM1552  LOC150279 3'  CCTGCTTGAACAGGCCTCTC   80481     AAA       CCA
                                GAGA   GCCTGTTTA   AGG
                                ||||   |||||||||   |||
                                CTCT   CGGACAAGT   TCC
                                  C__       TCG
GAM1552  LOC154104 5'  TCCTTGGTGAAAACTCTC    88625     AAAGCCTG
                                GAGA      TTTACCAAGGA
                                ||||      ||||||||||
                                CTCT      AAGTGGTTCCT
                                  CAA_____
GAM1552  LOC155036 5'  CCTTGGGCTAGATTTTCTCT   87613       GC   TTTA
                                AGAGAAAA  CTG   CCAAGG
                                ||||||||  |||   ||||||
                                TCTCTTTT  GAT   GGTTCC
                                    A_   CG__
GAM1552  LOC200010 3'  CCACAGAAACAGGCTCTCCTCT 91525     AAA       ACCAA
                                AGAG   AGCCTGTTT    GG
                                ||||   |||||||||    ||
                                TCTC   TCGGACAAA    CC
                                  CTC       GACA_
GAM1552  LOC203536 3'  TCCTTGGTTTATACTTTTTCT  90944      CC   TT
                                AGAAAAG  TGT  ACCAAGGA
                                |||||||  |||  ||||||||
                                TCTTTTT  ATA  TGGTTCCT
                                    C_   TT
GAM1552  LOC220776 3'  CCTCGTGTCCATGACTTTTCTC 68925        CC_  TT   CA
            T                   AGAGAAAAG   TG  TAC  AGG
                                |||||||||   ||  |||  |||
                                TCTCTTTTC   AC  GTG  TCC
                                     AGT  CT   C_
GAM1552  LOC255332 3'  CCTTAGCAAACAGGTTCATCTC 97948     AA       ACC
                                GAGA  AGCCTGTTT   AAGG
                                ||||  |||||||||   ||||
                                CTCT  TTGGACAAA   TTCC
                                  AC        CGA
GAM1552  LOC257364 5'  TCCCCGGTCTGGGCAGGACCCT 96648     AAAG      __   AA
            CTC                   GAGA   CCTGTTT  ACC  GGA
                                ||||   |||||||  |||  |||
                                CTCT   GGACGGG  TGG  CCT
                                  CCCA      TC   CC
GAM1552  LOC92305  3'  CTTGGTGCCTTTTTCT     57233        A  CTGTTT
                                AGAGAAA GC     ACCAAG
                                |||||||  ||     ||||||
                                TCTTTTT CG     TGGTTC
                                    C  _______
GAM1552  LOC93624  3'  CCTGCCTACAAGTTTTTCTCT  73100          C   TTACCA
                                AGAGAAAAGC TGT     AGG
                                |||||||||| |||     |||
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                                TCTCTTTTTG ACA     TCC
                                     A  TCCG__
GAM1553 DLG5     5' CAGCAGCAGCAGGTGTTGA  83811       CG  TCGGAA
                                TCAACACC GCT     GCTG
                                |||||||| |||     ||||
                                AGTTGTGG CGA     CGAC
                                    A_  CGA___
GAM1553 KCNK7    5' CCAGCCCCTCCCAGGTGCCTGA 54055    A_   C CTTC AA
                                TCA CACC GG   GG GCTGG
                                ||| |||| ||   || |||||
                                AGT GTGG CC   CC CGACC
                                  CC   A CT__ C_
GAM1553 TNFRSF6B 5' CCAGCCAGTGCCGGGTGCTGG 53082    A      TTCGGAA
                                TCA CACCCGGC      GCTGG
                                ||| ||||||||      |||||
                                GGT GTGGGCCG      CGACC
                                  C       TGAC___
GAM1553 CARD9    3' CCAGCCGGACTGCCGGGCATTG 42545     CA    __   GAA
             G                   TCAA  CCCGGC  TTCG   GCTGG
                                 ||||  ||||||  ||||   |||||
                                 GGTT  GGGCCG  AGGC   CGACC
                                   AC     TC   ___
GAM1553 CARD9    3' CCAGCCGGACTGCCGGGCATTG 42546     CA    __   GAA
             G                   TCAA  CCCGGC  TTCG   GCTGG
                                 ||||  ||||||  ||||   |||||
                                 GGTT  GGGCCG  AGGC   CGACC
                                   AC     TC   ___
GAM1553 FLJ21438 3' CTGGCTGGGCCGGGCACTGA  62192    ACA     CGGA   TG
                                TCA   CCCGGCTT   AGC  G
                                |||   ||||||||   |||  |
                                AGT   GGGCCGGG   TCG  C
                                  CAC       _____  GT
GAM1553 KIAA1560 3' CCAGCTTCTGGCTCAAGAGTTG 64849      ACCC_  TT
             A                   TCAAC    GGC  CGGAAGCTGG
                                 |||||    |||  ||||||||||
                                 AGTTG    TCG  GTCTTCGACC
                                    AGAAC  __
GAM1553 MAPK11   3' CCAGGGAAGCCTGGGTGT    58101       _    GGAAG
                                ACACCC GGCTTC    CTGG
                                |||||| ||||||    ||||
                                TGTGGG CCGAAG    GACC
                                   T     G_____
GAM1553 MAPK11   3' CCAGGGAAGCCTGGGTGT    12312       _    GGAAG
                                ACACCC GGCTTC    CTGG
                                |||||| ||||||    ||||
                                TGTGGG CCGAAG    GACC
                                   T     G_____
GAM1553 LOC130497 3' CCAGCCAAGAGCCGGGCGTT  75446     A      CGGAA
                                AAC CCCGGCTT    GCTGG
                                ||| ||||||||    |||||
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                                TTG GGGCCGAG    CGACC
                                  C       AAC__
GAM1553  LOC203052 3'  CCAGCTCTGTGCCGGGTG    92076        TT    A
                                CACCCGGC  CGGA GCTGG
                                ||||||||  |||| |||||
                                GTGGGCCG  GTCT CGACC
                                    T_   _
GAM1553  LOC256905 5'  CCAGGGATAGCCGGGTATTGA  98659     C       TCGGAAG
                                TCAA ACCCGGCT      CTGG
                                |||| ||||||||      ||||
                                AGTT TGGGCCGA      GACC
                                  A       TAGG___
GAM1553  LOC91409  3'  CAGCTTCCACTATGTTGA    66570       CCC  CTTC
                                TCAACA   GG    GGAAGCTG
                                ||||||   ||    ||||||||
                                AGTTGT   TC    CCTTCGAC
                                   A__  A___
GAM1554  ADAM12    3'  TTCGTAGATATTGGACAAA    14427      G        GT
                                TTTGT CCAATATCTG  TGGA
                                ||||| ||||||||||  ||||
                                AAACA GGTTATAGAT  GCTT
                                  _        __
GAM1554  C20orf106 3'  TCCACAGATATTGGGACAAA   55913      G        GT
                                TTTGT CCAATATCTG  TGGA
                                ||||| ||||||||||  ||||
                                AAACA GGTTATAGAC  ACCT
                                  G         __
GAM1554  FLJ10352  3'  TTCCAACTCTCTGGACAAA    50474      G   ATATCT
                                TTTGT CCA     GGTTGGAA
                                ||||| |||     ||||||||
                                AAACA GGT     TCAACCTT
                                  _  CTC___
GAM1554  GIT1      3'  CCAACAGAGCCACTGGCACAAG 26718        ATA__    G
                                TTTGTGCCA    TCTG TTGG
                                |||||||||    |||| ||||
                                GAACACGGT    AGAC AACC
                                     CACCG   _
GAM1554  KIAA0140  3'  CCAGCCACCGGCACAAA     28508        AATATC
                                TTTGTGCC     TGGTTGG
                                ||||||||     |||||||
                                AAACACGG     ACCGACC
                                     CC_____
GAM1554  SLC38A1   5'  AGCCAGACCTTGACACAAA    48420       C   TA
                                TTTGTG CAA  TCTGGTT
                                |||||| |||  |||||||
                                AAACAC GTT  AGACCGA
                                   A   CC
GAM1554  TSLRP     5'  CTATGAAGATACAGCACAAA   25930        CAA    GGT
                                TTTGTGC   TATCT   TGG
                                |||||||   |||||   |||
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                                AAACACG  ATAGA  ATC
                                   AC_    AGT
GAM1554  LOC145773 3'  TTCCAAAATTGGCACAAA    77964         ATCTGG
                                TTTGTGCCAAT    TTGGAA
                                ||||||||||     ||||||
                                AAACACGGTTA    AACCTT
                                     A_____
GAM1554  LOC220573 3'  TTCAAGACTGGCACAAA    70208        ATA  GGT
                                TTTGTGCCA  TCT  TGGA
                                |||||||||  |||  ||||
                                AAACACGGT  AGA  ACTT
                                   C__  ___
GAM1554  LOC222160 3'  CCAGAAAAGATTCTGACACAAA 95777       C  AT   GG_
                                TTTGTG CA  ATCT  TTGG
                                ||||||  ||  ||||  ||||
                                AAACAC GT  TAGA  GACC
                                   A  CT   AAA
GAM1555  ELF3     3'  TGACCTTGACCTTGACCAA   16685      T   GAT  AAA
                                TTGGT CAAGG  GG  GTCA
                                ||||| |||||  ||  ||||
                                AACCA GTTCC  TC  CAGT
                                  _    AGT  ___
GAM1555  JAK2     3'  TGACCTTCATTCTGAGACCAA  18318      CAA      AA
                                TTGGTT  GGGATGGA  GTCA
                                ||||||  ||||||||  ||||
                                AACCAG  TCTTACTT  CAGT
                                   AG_      C_
GAM1555  SLC10A2  5'  ACTCTCTGTCTTGACCAA    6590       CAA      A
                                TTGGTT  GGGATGGA AGT
                                ||||||  |||||||| |||
                                AACCAG  TTCTGTCT TCA
                                   ___      C
GAM1555  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA  37205      CAAGG  G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___  A
GAM1555  KIAA1958  5'  GTGACTTTGAACCCCAAACC  82788     CAA  ATGG
                                GGTT  GGG   AAAGTCAC
                                ||||  |||   ||||||||
                                CCAA  CCC   TTTCAGTG
                                  A__  CAAG
GAM1555  MARCKS   3'  ACTTTCCACCCTGCCCA    11411    TTCA  A
                                TGG   AGGG TGGAAAGT
                                |||   |||| ||||||||
                                ACC   TCCC ACCTTTCA
                                  CG__  _
GAM1555  TUB      5'  GTGGGACCATCCCTTAAACC  13898     C       AAAG
                                GGTT AAGGGATGG   TCAC
                                |||| |||||||||   ||||
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                                CCAA TTCCCTACC    GGTG
                                  A       AG__
GAM1555 LOC80298 3' ACTTTTACCTTGAACCA     48062         GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                     A___
GAM1556 ELF3     3' TGACCTTGACCTTGACCAA    16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                  _    AGT  ___
GAM1556 JAK2     3' TGACCTTCATTCTGAGACCAA  18318       CAA       AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_       C_
GAM1556 SLC10A2  5' ACTCTCTGTCTTGACCAA    6590        CAA       A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM1556 FLJ10803 3' GTGACTTTCAGTTAAAGCCAA 37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM1556 KIAA1958 5' GTGACTTTGAACCCCAAACC  82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM1556 MARCKS   3' ACTTTCCACCCTGCCCA     11411     TTCA    A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM1556 TUB      5' GTGGGACCATCCCTTAAACC   13898     C        AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A       AG__
GAM1556 LOC80298 3' ACTTTTACCTTGAACCA     48062         GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                     A___
GAM1557 ADH1C    5' CACCAGCCTCCTGGTC      7263          ACCTACC   _
                                GACCAGGAG      GCTG TG
                                |||||||||      |||| ||
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                                CTGGTCCTC      CGAC AC
                                        _______   C
GAM1557 ARHGDIA  3'  CACAGGCCCAGCCTCCTCGGTC 16292     _    AC  ACCG
                                GACC AGGAG  CT   CTGTG
                                |||| |||||  ||   |||||
                                CTGG TCCTC  GA   GACAC
                                  C    C_  CCCG
GAM1557 GALNT1   3'  TTCACAGCAATAAATCTTC   40402      CC  CC
                                GGAGA  TA  GCTGTGAA
                                |||||  ||  ||||||||
                                CTTCT  AT  CGACACTT
                                   AA  AA
GAM1557 HPGD     3'  TTCACAGTTCAGCCTCCT    7811       AC  ACC
                                AGGAG  CT   GCTGTGAA
                                |||||  ||   ||||||||
                                TCCTC  GA   TGACACTT
                                   C_  CT_
GAM1557 MIF      5'  GCGCGGGTCTCCTGGTC     11583           AC
                                GACCAGGAGACCT  CGC
                                ||||||||||||  |||
                                CTGGTCCTCTGGG  GCG
                                       C_
GAM1557 NFIX     3'  CACAGCAGTCTCAGTCCTGGTT 11780        GACCT  C
                                GACCAGGA    AC GCTGTG
                                ||||||||    || ||||||
                                TTGGTCCT    TG CGACAC
                                     GACTC  A
GAM1557 PML      3'  TCACAGCGAGCCTCCTGATC   53813    C     AC  AC
                                GA CAGGAG  CT  CGCTGTGA
                                || ||||||  ||  ||||||||
                                CT GTCCTC  GA  GCGACACT
                                 A     C_  __
GAM1557 PML      3'  TCACAGCGAGCCTCCTGATC   53819    C     AC  AC
                                GA CAGGAG  CT  CGCTGTGA
                                || ||||||  ||  ||||||||
                                CT GTCCTC  GA  GCGACACT
                                 A     C_  __
GAM1557 POU2F2   3'  TCCAGCAAGTCTCCTGG     12215        CTACC   T
                                CCAGGAGAC    GCTG GA
                                |||||||||    |||| ||
                                GGTCCTCTG    CGAC CT
                                     AA___   _
GAM1557 PTGIS    3'  TCACAGCGCCTCCTGG      8227        ACCTAC
                                CCAGGAG     CGCTGTGA
                                |||||||     ||||||||
                                GGTCCTC     GCGACACT
                                    C_____
GAM1557 PYCR1    5'  TTCACAGCAGCAGGCGTCTTGG 70645       GA  ACC
                                CCAGGA  CCT   GCTGTGAA
                                ||||||  |||   ||||||||
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                                GGTTCT  GGA   CGACACTT
                                   GC   CGA
GAM1557  RAD9     3'  CACAGCGGTCGGGCCTGG    17157      AGA  T
                                CCAGG   CC ACCGCTGTG
                                |||||   || |||||||||
                                GGTCC   GG TGGCGACAC
                                   G__  C
GAM1557  CALN1    3'  TTCACATAAGATCTTCTGG   49672        C  ACCGC
                                CCAGGAGA CT    TGTGAA
                                |||||||| ||    ||||||
                                GGTCTTCT GA    ACACTT
                                     A  AT___
GAM1557  CLDN7    3'  CGGACAAAGGCCTCCTGGTC  8962         A   ACCG
                                GACCAGGAG CCT    CTG
                                ||||||||| |||    |||
                                CTGGTCCTC GGA    GGC
                                      C   AACA
GAM1557  CLDN7    3'  CGGACAAAGGCCTCCTGGTC  96225        A   ACCG
                                GACCAGGAG CCT    CTG
                                ||||||||| |||    |||
                                CTGGTCCTC GGA    GGC
                                      C   AACA
GAM1557  DIO2     3'  TCACATTGGGTCTCTGGTC   7667       G      CCGC
                                GACCAG AGACCTA    TGTGA
                                |||||| |||||||    |||||
                                CTGGTC TCTGGGT    ACACT
                                   _      T____
GAM1557  DIO2     3'  TCACATTGGGTCTCTGGTC   26555      G      CCGC
                                GACCAG AGACCTA    TGTGA
                                |||||| |||||||    |||||
                                CTGGTC TCTGGGT    ACACT
                                   _      T____
GAM1557  DKFZp434F142 3'  TCACAGTGCACCTTCCAGTC  51035     CA    ACCTAC
                                GAC  GGAG     CGCTGTGA
                                |||  ||||     ||||||||
                                CTG  CCTT     GTGACACT
                                  A_    CCAC__
GAM1557  DKFZP564I1171 5'  CACAGACGAGGTCTCCGG    72043    A      ACCG
                                CC GGAGACCT    CTGTG
                                || ||||||||    |||||
                                GG CCTCTGGA    GACAC
                                  _       GCA_
GAM1557  FLJ14549  3'  TTCACAGCTGTCCTTCCCTGG  52499      A  CCT  C
                                CCAGG GA   AC GCTGTGAA
                                ||||| ||   || ||||||||
                                GGTCC CT   TG CGACACTT
                                   _ TCC  T
GAM1557  FLJ20974  3'  TTCACAGCAGTAAACCAGCTCT 50795      ACC___   C
                                GGAG     TAC GCTGTGAA
                                ||||     ||| ||||||||
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                                TCTC     ATG CGACACTT
                                  GACCAA   A
GAM1557 HRH3     3' CAGCCCAGGTCTCCTGG     24314          ACC
                                CCAGGAGACCT   GCTG
                                ||||||||||   ||||
                                GGTCCTCTGGA   CGAC
                                      CC_
GAM1557 KIAA0007 3' TTCACAGCAGTGGATCCC    80929    A  C    C
                                GG GA CTAC GCTGTGAA
                                || || |||| ||||||||
                                CC CT GGTG CGACACTT
                                 _ A   A
GAM1557 KIAA0449 3' CATAGCCTCCTGGTC       34635         ACCTACC
                                GACCAGGAG      GCTGTG
                                |||||||||      ||||||
                                CTGGTCCTC      CGATAC

                                ________
GAM1557 KIAA1719 3' CAGACACAGGCCTCCTGGTC  68725         A   ACCG
                                GACCAGGAG CCT    CTG
                                ||||||||| |||    |||
                                CTGGTCCTC GGA    GAC
                                     C   CACA
GAM1557 KIAA1944 3' TTCATGGCAGATCTCCTGTC  76084     C     C  ACC
                                GAC AGGAGA CT   GCTGTGAA
                                ||| |||||| ||   ||||||||
                                CTG TCCTCT GA   CGGTACTT
                                  _     A  ___
GAM1557 KIAA1950 3' ACAGCAGGCTCCTGGTC     94173         A   ACC
                                GACCAGGAG CCT   GCTGT
                                ||||||||| |||   |||||
                                CTGGTCCTC GGA   CGACA

                                      _  ____
GAM1557 NSE1     3' TCCAGCCCCAGGTCTCCTG   59737         ACC    T
                                CAGGAGACCT   GCTG GA
                                ||||||||||   |||| ||
                                GTCCTCTGGA   CGAC CT
                                     CCC    _
GAM1557 OPN4     3' TTCACAGCCCCAGCCCCATGG 53856     _ AGAC  ACC
                                CCA GG    CT   GCTGTGAA
                                ||| ||    ||   ||||||||
                                GGT CC    GA   CGACACTT
                                  A  CC__  CCC
GAM1557 PSKH1    3' TTCACAGCATTAACCTTCCAGT 68804     CA    ACCTACC
             C                   GAC  GGAG      GCTGTGAA
                                ||| ||||      ||||||||
                                CTG  CCTT      CGACACTT
                                  A_    CCAATTA
GAM1557 SUI1     3' TGGTGGTAGATCCCCTGGT   20540       A  C
                                ACCAGG GA CTACCGCTG
                                |||||| || |||||||||
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                                TGGTCC CT GATGGTGGT
                                   C  A
GAM1557  LOC134265 3'  TTCACAGCATCGCACTCCCAGT 75659     CA    ACCTACC
              C                    GAC  GGAG      GCTGTGAA
                                   |||  ||||      ||||||||
                                   CTG  CCTC      CGACACTT
                                     AC    ACGCTA_
GAM1557  LOC150311 5'  TTCACAGTATCAACCTCCCCGT 80571     CA    ACCTACC
              C                    GAC  GGAG      GCTGTGAA
                                   |||  ||||      ||||||||
                                   CTG  CCTC      TGACACTT
                                     CC    CAACTA_
GAM1557  LOC158747 3'  TTCACAGCAGAGTTTCCTAATC 82871    CC      _  ACC
                                   GA  AGGAGAC CT   GCTGTGAA
                                   ||  ||||||| ||   ||||||||
                                   CT  TCCTTTG GA   CGACACTT
                                    AA      A  ___
GAM1557  LOC196812 3'  TCATAGTGACTGGCCTCCT    91128      A  TAC
                                   AGGAG CC   CGCTGTGA
                                   |||||  ||   ||||||||
                                   TCCTC GG   GTGATACT
                                      C  TCA
GAM1557  LOC91948  3'  TCATGTAGGTCTTCTGGTC    68246           CGCT
                                   GACCAGGAGACCTAC    GTGA
                                   ||||||||||||||    ||||
                                   CTGGTCTTCTGGATG    TACT
                                                 ____
GAM1558  TERF1     3'  CCCAAATCCTGTTCCAATGA   34391       C   TA    C
                                   TCATTGGA ACG  GATT GGG
                                   ||||||||  |||  ||||  |||
                                   AGTAACCT TGT  CTAA CCC
                                        _  C_    A
GAM1558  FLJ10159  3'  CCATGTCACGCCATCCAATGAC 36334        CA_   A   TC
                                   GTCATTGGA   CGT GAT  GG
                                   |||||||||   |||  |||  ||
                                   CAGTAACCT   GCA CTG  CC
                                         ACC  _   TA
GAM1558  FLJ14213  3'  CCGATGCTCCCAATGACG    46216        ACAC   GAT
                                   CGTCATTGG    GTA   TCGG
                                   |||||||||    |||   ||||
                                   GCAGTAACC    CGT   AGCC
                                         CT__   ___
GAM1558  MGC10715  3'  ATTTACCAGACATCCAATGAC  44495        CAC___
                                   GTCATTGGA     GTAGAT
                                   |||||||||     ||||||
                                   CAGTAACCT     CATTTA
                                         ACAGAC
GAM1558  MOST2     5'  CCAGGACTGCCCAATGAC    40059        ACAC    A   _
                                   GTCATTGG    GTAG TTC GG
                                   ||||||||    |||| ||| ||
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                                CAGTAACC    CGTC AGG CC
                                    _____   _  A
GAM1558  LOC150370 3'  CCGGGTCTACGTGCCCATGAC  86123      T  A
                                GTCAT GG CACGTAGATTCGG
                                ||||| || ||||||||||||
                                CAGTA CC GTGCATCTGGGCC
                                   C  _
GAM1558  LOC152620 3'  CCCAAATCCTGTTCCAATGA   60707        C   TA    C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                     _  C_   A
GAM1558  LOC158668 3'  CCCAAATCCTGTTCCAATGA   69896        C   TA    C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                     _  C_   A
GAM1559  BRCA1     3'  GTGACTCTTCTGCCCTTGAG   24572        A    _
                                TTCAAGGG TGGAA AGTCAC
                                |||||||| ||||| ||||||
                                GAGTTCCC GTCTT TCAGTG
                                     _    C
GAM1559  CA12      3'  TGACCCAATCTGCCTTTGAA   8692         A   AA__
                                TTCAAGGG TGGA   GTCA
                                |||||||| ||||   ||||
                                AAGTTTCC GTCT   CAGT
                                     _   AACC
GAM1559  DLG5      3'  GGTGACTTTGGCATTCTT    83820        G_
                                AGGGATG  AAAGTCACC
                                |||||||  |||||||||
                                TTCTTAC  TTTCAGTGG
                                    GG
GAM1559  FOXE1     3'  ACTCTCCCCCTTTCCCTTGAG  16775        T____  A
                                TTCAAGGGA    GGA AGT
                                |||||||||    ||| |||
                                GAGTTCCCT    CCT TCA
                                     TTCCC   C
GAM1559  FTH1      3'  GGTGACTTCCCTGGTCACC    68714    _  __  A
                                GG GAT  GG AAGTCACC
                                || |||  || ||||||||
                                CC CTG  CC TTCAGTGG
                                 A  GT  C
GAM1559  GFAP      3'  GTGACTCATCCTCTTGAA     10783      _    GAA
                                TTCAAG GGATG   AGTCAC
                                |||||| |||||   ||||||
                                AAGTTC CCTAC   TCAGTG
                                   T    ___
GAM1559  GRINL1A   3'  GGTGACTTTCATGTGCTTGAA  70064      GGATG
                                TTCAAG    GAAAGTCACC
                                ||||||    ||||||||||
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                                AAGTTC    CTTTCAGTGG
                                   GTGTA
GAM1559 JDP1    3' GATTCCTCCATCCTTGAA    41724       G    A_
                                TTCAAGG ATGGA  AGTC
                                ||||||| |||||  ||||
                                AAGTTCC TACCT  TTAG
                                   _    CC
GAM1559 KCND2   3' GTGACTTTCCTACTTTTG    25385       AT
                                CAAGGG  GGAAAGTCAC
                                ||||||  ||||||||||
                                GTTTTC  CCTTTCAGTG
                                   AT
GAM1559 LECT2   5' GACTTGCTCCATCCTCTT    11296    _     __
                                AAG GGATGGA  AAGTC
                                ||| |||||||  |||||
                                TTC CCTACCT  TTCAG
                                  T      CG
GAM1559 MASP1   3' GGTGACTTCATCTCTTCGAA  58216    _       AA
                                TTC AAGGGATGG  AGTCACC
                                ||| |||||||||  |||||||
                                AAG TTCTCTACT  TCAGTGG
                                  C       __
GAM1559 NOTCH2  3' GGTGACTCTCTGCCCTTGGA  44577        A   A
                                TTCAAGGG TGGA AGTCACC
                                |||||||| |||| |||||||
                                AGGTTCCC GTCT TCAGTGG
                                   _   C
GAM1559 Nrap    3' TGACCTCCACCCTCCTTGGA  56311        A__   AA
                                TTCAAGGG   TGGA  GTCA
                                ||||||||   ||||  ||||
                                AGGTTCCT   ACCT  CAGT
                                     CCC   C_
GAM1559 NT5C3   3' GGTATCACCATCTCTTGAA   33660          AAA  C
                                TTCAAGGGATGG   GT ACC
                                ||||||||||||   || |||
                                AAGTTCTCTACC   TA TGG
                                       AC_  _
GAM1559 PITX2   3' GGCAACTCCGCCCTTGAA    6157         A   AA_
                                TTCAAGGG TGGA   GTC
                                ||||||| ||||   |||
                                AAGTTCCC GCCT   CGG
                                   _   CAA
GAM1559 PML     3' GTGACCCTTCTGTCCCTAGA  53804    A       A_
                                TC AGGGATGGAA  GTCAC
                                || ||||||||||  |||||
                                AG TCCCTGTCTT  CAGTG
                                  A        CC
GAM1559 RAB36   3' GGTAACTCACTCTGCAGCCCTT 18173        AT__  A__  C
             GAA                   TTCAAGGG   GGA   AGT ACC
                                ||||||||   |||   ||| |||
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                                AAGTTCCC   TCT   TCA TGG
                                    GACG   CAC   A
GAM1559  TIMP4    3'  GTGACCATCACATCCCTT    13757        _  AA
                                AAGGGATG GA  GTCAC
                                |||||||| ||  |||||
                                TTCCCTAC CT  CAGTG
                                    A  AC
GAM1559  AKL3L    3'  TGACTTGTTTCCTTTGAA    33271        TGGA
                                TTCAAGGGA   AAGTCA
                                |||||||||   ||||||
                                AAGTTTCCT   TTCAGT
                                    TTG_
GAM1559  C20orf72 3'  GGTGACTCTTGTACTCCCTTGA 54607        _  G  _
           G                     TTCAAGGGA TG AA AGTCACC
                                |||||||||| || || |||||||
                                GAGTTCCCT AT TT TCAGTGG
                                    C  G  C
GAM1559  FLJ10008 3'  GGCAACCTGTCCCTTGAG    36190          AAA
                                TTCAAGGGATGG  GTC
                                ||||||||||||  |||
                                GAGTTCCCTGTC  CGG
                                    CAA
GAM1559  FLJ11726 3'  GTGACCCAGGCTCTTTGAA   47027       _ A_  AAA
                                TTCAAGG G  TGG  GTCAC
                                ||||||| |  |||  |||||
                                AAGTTTC C  ACC  CAGTG
                                    T GG  ____
GAM1559  FLJ12847 3'  GGTGACTTTCTGATGACTGAA  45078     A GG  _
                                TTCA G  AT GGAAAGTCACC
                                |||| |  || ||||||||||
                                AAGT C  TA TCTTTCAGTGG
                                  _ AG  G
GAM1559  FLJ12891 3'  GGTGACCGCAGCCCCTTGGA  46929       A_  GAAA
                                TTCAAGGG  TG   GTCACC
                                ||||||||  ||   ||||||
                                AGGTTCCC  AC   CAGTGG
                                    CG  GC__
GAM1559  FLJ12891 3'  GGTGACTTCTCAGAGCCTGAA  46930     A  GA_  GA
                                TTCA GG   TG  AAGTCACC
                                |||| ||   ||  ||||||||
                                AAGT CC   AC  TTCAGTGG
                                  _  GAG  TC
GAM1559  FLJ20498 3'  TGACCCTCCACTCCTTGAA   39282       GA   AA
                                TTCAAGG  TGGA  GTCA
                                |||||||  ||||  ||||
                                AAGTTCC  ACCT  CAGT
                                    TC   CC
GAM1559  GFR      3'  TGACTTCTTATCCCTGGA    25451     A    GA
                                TTCA GGGATG  AAGTCA
                                |||| ||||||  ||||||
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                                AGGT CCCTAT  TTCAGT
                                  _     TC
GAM1559 HSNOV1   3' GGTGGGTCAGCCCTTGAA    34439        ATG  AAG
                                TTCAAGGG   GA   TCACC
                                ||||||||   ||   |||||
                                AAGTTCCC   CT   GGTGG
                                    GA_  G__
GAM1559 KIAA0731 3' GACCTTTCCATCCTTGAA    67479        G      _
                                TTCAAGG ATGGAAAG TC
                                ||||||| |||||||| ||
                                AAGTTCC TACCTTTC AG
                                    _      C
GAM1559 KIAA1046 3' GGTGACTTTCTTTTTTTG    30662        T
                                CAAGGGA GGAAAGTCACC
                                ||||||| ||||||||||
                                GTTTTTT TCTTTCAGTGG
                                    _
GAM1559 KIAA1276 5' GGTGATTTATGCCCTGAA    67032     A   ATGGA
                                TTCA GGG    AAGTCACC
                                |||| |||    ||||||||
                                AAGT CCC    TTTAGTGG
                                  _  GTA__
GAM1559 KIAA1495 5' GGTTATTTGCACCCCTTGAA   73566        A  G   GTC
                                TTCAAGGG TG AAA   ACC
                                |||||||| || |||   |||
                                AAGTTCCC AC TTT   TGG
                                    C  G   AT_
GAM1559 KIAA1755 5' GGTACCCTCCATCCCTCGA    62018    A       AA  C
                                TC AGGGATGGA  GT ACC
                                || |||||||||  || |||
                                AG TCCCTACCT  CA TGG
                                 C       CC  _
GAM1559 MGC4737  5' TGACTTTCTGTGGCTTGGA    49652       GG
                                TTCAAG  ATGGAAAGTCA
                                ||||||  ||||||||||
                                AGGTTC  TGTCTTTCAGT
                                   GG
GAM1559 P2RXL1   3' CGGTGACCCCCCAGCCCAACCC 19559        A_______   AAA     ___
           CTTGGA                TTCAAGGG      TGG   GTCACC   G
                                ||||||||      |||   ||||||   |
                                AGGTTCCC      ACC   CAGTGG   C
                                    CAACCCG   CCC     __
GAM1559 PRO1600  5' GGCAACCCTATCTCTTGAG    26877          AAA_
                                TTCAAGGGATGG    GTC
                                ||||||||||||    |||
                                GAGTTCTCTATC    CGG
                                      CCAA
GAM1559 SLC5A7   3' ACTTCAGTCACTCCCTTGAA   41802         _   A__
                                TTCAAGGGA TGG   AAGT
                                ||||||||| |||   ||||
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                                AAGTTCCCT ACT   TTCA
                                     C   GAC
GAM1559  ZNF297B   3'  GTGACTTTCTAAATATGAA   26670     AGGGA
                                TTCA    TGGAAAGTCAC
                                ||||    ||||||||||
                                AAGT    ATCTTTCAGTG
                                  ATAA_
GAM1559  LOC116113 3'  GTGCCTCCATCCCCAGAA    93841     AA       AA T
                                TTC  GGGATGGA  G CAC
                                |||  ||||||||  | |||
                                AAG  CCCTACCT  C GTG
                                  AC       C_ _
GAM1559  LOC138855 3'  GGTGACTTCCCTGGTCACC   75893    _  __  A
                                GG GAT  GG AAGTCACC
                                || |||  || ||||||||
                                CC CTG  CC TTCAGTGG
                                 A   GT  C
GAM1559  LOC143943 3'  GGCTACCCCCACCCCTTGGA   83919        A   AA__
                                TTCAAGGG TGG    AGTC
                                |||||||| |||    ||||
                                AGGTTCCC ACC    TCGG
                                     C   CCCA
GAM1559  LOC145231 3'  GGCTTGTCCATCCCTTGA    84253          _
                                TCAAGGGATGGA AAGTC
                                |||||||||||| |||||
                                AGTTCCCTACCT TTCGG
                                       G
GAM1559  LOC146337 5'  GGCAACTCTAGCCTTTGAA   84643        A    AA_
                                TTCAAGGG TGGA   GTC
                                |||||||| ||||   |||
                                AAGTTTCC ATCT   CGG
                                     G    CAA
GAM1559  LOC146499 5'  GGTGACTTTGAAGACTTGGA   71367       GGATGG
                                TTCAAG     AAAGTCACC
                                ||||||     |||||||||
                                AGGTTC     TTTCAGTGG
                                   AGAAG_
GAM1559  LOC147176 5'  GGTGACTTTGAAGACTTGGA   61147       GGATGG
                                TTCAAG     AAAGTCACC
                                ||||||     |||||||||
                                AGGTTC     TTTCAGTGG
                                   AGAAG_
GAM1559  LOC147463 3'  TGACTTTGAGGTCCTTGGA    79005        ATGG
                                TTCAAGGG    AAAGTCA
                                ||||||||    |||||||
                                AGGTTCCT    TTTCAGT
                                     GGAG
GAM1559  LOC151057 3'  GGTGACCCTACCCTTGAG    86393        A   AAA
                                TTCAAGGG TGG   GTCACC
                                |||||||| |||   ||||||
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                                GAGTTCCC ATC   CAGTGG
                                     _  C__
GAM1559  LOC152018 3'  GACCTCCACCCCCTTGAA    86728        A_   AA
                                TTCAAGGG  TGGA  GTC
                                |||||||| ||||  |||
                                AAGTTCCC  ACCT  CAG
                                     CC    C_
GAM1559  LOC152179 5'  GGTGACTTGAAACCCTGAG   86743     A   ATGGA
                                TTCA GGG    AAGTCACC
                                |||| |||    ||||||||
                                GAGT CCC    TTCAGTGG
                                  _  AAAG_
GAM1559  LOC153565 3'  GGTGACTTCCCTGGTCACC   81758    _  __ A
                                GG GAT  GG AAGTCACC
                                || |||  || ||||||||
                                CC CTG  CC TTCAGTGG
                                 A   GT  C
GAM1559  LOC155435 3'  GGTGACTTTGGTAGCCCTTGAG 82270        ATGG_
                                TTCAAGGG    AAAGTCACC
                                ||||||||    |||||||||
                                GAGTTCCC    TTTCAGTGG
                                     GATGG
GAM1559  LOC253336 3'  GTAACTTTCTTCATCCCTTGAA 99181          __     C
                                TTCAAGGGATG  GAAAGT AC
                                ||||||||||  |||||| ||
                                AAGTTCCCTAC  CTTTCA TG
                                       TT     A
GAM1559  LOC256714 3'  TGACCTTTTCTTCTTTGAA   98046         T    _
                                TTCAAGGGA GGAAAG TCA
                                ||||||||| |||||| |||
                                AAGTTTCTT CTTTTC AGT
                                     _    C
GAM1559  LOC51696  3'  TGGCTTTCTACCCCCTGAA   33093     A   A
                                TTCA GGG TGGAAAGTCA
                                |||| ||| ||||||||||
                                AAGT CCC ATCTTTCGGT
                                  C   C
GAM1559  LOC96610  5'  GGTGACTTTGAAGACTTGGA   56054       GGATGG
                                TTCAAG     AAAGTCACC
                                ||||||     |||||||||
                                AGGTTC     TTTCAGTGG
                                   AGAAG_
GAM1560  ELF3      3'  TGACCTTGACCTTGACCAA   16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                  _    AGT  ____
GAM1560  JAK2      3'  TGACCTTCATTCTGAGACCAA  18318       CAA       AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
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                                AACCAG   TCTTACTT  CAGT
                                   AG_      C_
GAM1560 SLC10A2  5' ACTCTCTGTCTTGACCAA    6590       CAA      A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM1560 FLJ10803 3' GTGACTTTCAGTTAAAGCCAA 37205      CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM1560 KIAA1958 5' GTGACTTTGAACCCCAAACC  82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM1560 MARCKS   3' ACTTTCCACCCTGCCCA     11411     TTCA    A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                 CG__   _
GAM1560 TUB      5' GTGGGACCATCCCTTAAACC   13898     C        AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A        AG__
GAM1560 LOC80298 3' ACTTTTACCTTGAACCA     48062         GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                     A___
GAM1561 ELF3     3' TGACCTTGACCTTGACCAA    16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                   _     AGT  ____
GAM1561 JAK2     3' TGACCTTCATTCTGAGACCAA  18318       CAA       AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_      C_
GAM1561 SLC10A2  5' ACTCTCTGTCTTGACCAA    6590       CAA      A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM1561 FLJ10803 3' GTGACTTTCAGTTAAAGCCAA 37205      CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
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                                AACCGA    TTG CTTTCAGTG
                                   AA___  A
GAM1561 KIAA1958 5' GTGACTTTGAACCCCAAACC  82788     CAA  ATGG
                                GGTT  GGG   AAAGTCAC
                                ||||  |||   ||||||||
                                CCAA  CCC   TTTCAGTG
                                  A__  CAAG
GAM1561 MARCKS   3' ACTTTCCACCCTGCCCA    11411    TTCA   A
                                TGG   AGGG TGGAAAGT
                                |||   |||| ||||||||
                                ACC   TCCC ACCTTTCA
                                 CG__  _
GAM1561 TUB      5' GTGGGACCATCCCTTAAACC  13898     C       AAAG
                                GGTT AAGGGATGG   TCAC
                                |||| |||||||||   ||||
                                CCAA TTCCCTACC   GGTG
                                  A       AG__
GAM1561 LOC80298 3' ACTTTTACCTTGAACCA    48062        GATG
                                TGGTTCAAGG   GAAAGT
                                ||||||||||   ||||||
                                ACCAAGTTCC   TTTTCA
                                     A___
GAM1562 GPD1     3' TCATGCCACCACATTTG    60398      C      C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A      _
GAM1562 IL5RA    5' TCGCATGGCCACCGCATTT   6906         AT__
                                AAATGCGGTGGC   CGA
                                ||||||||||||   |||
                                TTTACGCCACCG   GCT
                                       GTAC
GAM1562 MYO1C    3' TGCCGATGCCAAATATTTG   61873     CGG      A
                                TAAATG  TGGCATCG CA
                                ||||||  |||||||| ||
                                GTTTAT  ACCGTAGC GT
                                   AA_      C
GAM1562 C6orf37  3' TGTCACACTGCATTTA     68097        GCATC
                                TAAATGCGGTG    GACA
                                ||||||||||     ||||
                                ATTTACGTCAC    CTGT
                                      A____
GAM1562 DNAJC6   3' TTGCAGAACCACCGCATT   29498        CA  GA
                                AATGCGGTGG  TC  CAA
                                |||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                      A_  AC
GAM1562 FLJ11210 3' GTCGATGTGCATGCTTTTA  60319     T  GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
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                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM1562  FLJ12476  3'  TCGATCTTCTGCATTTA     43270         T  C
                                TAAATGCGG GG ATCGA
                                ||||||||| || |||||
                                ATTTACGTC TC TAGCT
                                     T  _
GAM1562  KIAA1034  3'  TCGATGGCATCCGCATTTG    63134         _  G
                                TAAATGCGG TG CATCGA
                                ||||||||| || ||||||
                                GTTTACGCC AC GTAGCT
                                     T  G
GAM1562  KIAA1987  3'  TCATGTAACTGCATTTA     89391         G    C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                     A   _
GAM1562  MGC16063  3'  TGTCCTGGCCACTGCATT    54929          ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                      GTC
GAM1562  LOC147949 3'  TGTCAGATGTCCACATTGCA   79279      __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM1562  LOC150577 3'  GTCCTCACCGCATTTG      86258          CATC
                                TAAATGCGGTGG   GAC
                                ||||||||||||   |||
                                GTTTACGCCACT   CTG
                                      C___
GAM1562  LOC158219 3'  TGTGTGTCACCACATTT     82694       C       CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                   A       __
GAM1562  LOC202020 3'  TGTCTCACCACATTTA      90605       C    CATC
                                TAAATG GGTGG   GACA
                                |||||| |||||   ||||
                                ATTTAC CCACT   CTGT
                                   A   ____
GAM1562  LOC90826  5'  TGTCGATGCAGGTTTATTTG  64788       CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                    TTGGA
GAM1562  LOC93587  3'  TTGTCTTTACCTGCATTTA   73042       _    CATC
                                TAAATGC GGTGG   GACAA
                                ||||||| |||||   |||||
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                                ATTTACG CCATT   CTGTT
                                   T    T___
GAM1563 ELF3    3' TGACCTTGACCTTGACCAA   16685     T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                   _    AGT  ___
GAM1563 JAK2    3' TGACCTTCATTCTGAGACCAA 18318      CAA      AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_      C_
GAM1563 SLC10A2  5' ACTCTCTGTCTTGACCAA    6590      CAA      A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM1563 FLJ10803 3' GTGACTTTCAGTTAAAGCCAA 37205      CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM1563 KIAA1958 5' GTGACTTTGAACCCCAAACC  82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM1563 MARCKS   3' ACTTTCCACCCTGCCCA     11411     TTCA    A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM1563 TUB     5' GTGGGACCATCCCTTAAACC   13898     C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A       AG__
GAM1563 LOC80298 3' ACTTTTACCTTGAACCA     48062         GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                     A___
GAM1564 EHF     3' TCCAAAACCCAAGGTTGGCT   25127     AT   _   C
                                AGT  GCCT GGGT TTGGA
                                |||  |||| |||| |||||
                                TCG  TGGA CCCA AACCT
                                  GT   A   A
GAM1564 EPHA2    3' CCATCGGCCAAGAATACTTGAA 16675         GC  G   T_
            G                    CTTCAAGTAT  CT GGTC  TGG
                                ||||||||||  || ||||  |||
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                                GAAGTTCATA  GA CCGG  ACC
                                     A_  A    CT
GAM1564  ITGA5    3'  CCCAGAGACATACTTGAAG   61933          C__
                                CTTCAAGTATG  CTGGG
                                ||||||||||  |||||
                                GAAGTTCATAC  GACCC
                                     AGA
GAM1564  TREM2    3'  TCCAAGACTGTCATATTT   39098        CCTG
                                AAGTATG   GGTCTTGGA
                                |||||||   |||||||||
                                TTTATAC   TCAGAACCT
                                   TG__
GAM1564  UQCRB    3'  CCAACATAGGCATACTTAAG  21939    C         GGTC
                                CTT AAGTATGCCTG   TTGG
                                ||| ||||||||||   ||||
                                GAA TTCATACGGAT   AACC
                                  _        AC__
GAM1564  ATP10D   3'  CAGAGACCACTTGAAG     73526        ATGCCTG   _
                                CTTCAAGT     GGTCT TG
                                ||||||||     ||||| ||
                                GAAGTTCA     CCAGA AC
                                     ________   G
GAM1564  B3GNT7   3'  CCCTTCCAGGCAACCTGAA   71678     A  A      TCTT
                                TTCA GT TGCCTGGG   GG
                                |||| || ||||||||   ||
                                AAGT CA ACGGACCT   CC
                                  C  _      TC__
GAM1564  DKFZp547I224 3'  TCCAAAATTGACCACATACTTG 39963          CCTG   _____
           GA                    TTCAAGTATG   GGTC   TTGGA
                                ||||||||||   ||||   |||||
                                AGGTTCATAC   CCAG   AACCT
                                     A___   TTAA
GAM1564  FLJ22341 3'  CCAAGCTCAGGCACACCCAAG  45114    CAA  A      T
                                CTT   GT TGCCTGGG CTTGG
                                |||   || |||||||| |||||
                                GAA   CA ACGGACTC GAACC
                                  CC_  C       _
GAM1564  KIAA0779 3'  CCGAACAGCATACTTGAAG   86908          C  GGTC
                                CTTCAAGTATGC TG   TTGG
                                |||||||||||| ||   ||||
                                GAAGTTCATACG AC   AGCC
                                     _  A___
GAM1564  LOC144233 3'  CCAAGGCACATAATTGAA   77246      G   CCTGG
                                TTCAA TATG    GTCTTGG
                                ||||| ||||    |||||||
                                AAGTT ATAC    CGGAACC
                                  A   A_____
GAM1564  LOC147341 3'  ACCCAGGCATAACTGAAG   85116      AG
                                CTTCA  TATGCCTGGGT
                                |||||  ||||||||||
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                                GAAGT  ATACGGACCCA
                                   CA
GAM1564  LOC221088 5'  TCCAAGGTGCTGGCCACTCGAA 94888      A   AT   TGGG
              G                     CTTC AGT  GCC    TCTTGGA
                                    |||| |||  |||    |||||||
                                    GAAG TCA  CGG    GGAACCT
                                      C   C_   TCGT
GAM1565  ELF3     3'  TGACCTTGACCTTGACCAA    16685      T    GAT  AAA
                                    TTGGT CAAGG   GG   GTCA
                                    ||||| |||||   ||   ||||
                                    AACCA GTTCC   TC   CAGT
                                       _    AGT  ___
GAM1565  JAK2     3'  TGACCTTCATTCTGAGACCAA  18318       CAA       AA
                                    TTGGTT   GGGATGGA  GTCA
                                    ||||||   ||||||||  ||||
                                    AACCAG   TCTTACTT  CAGT
                                       AG_       C_
GAM1565  SLC10A2   5'  ACTCTCTGTCTTGACCAA    6590       CAA       A
                                    TTGGTT   GGGATGGA AGT
                                    ||||||   |||||||| |||
                                    AACCAG   TTCTGTCT TCA
                                       ___       C
GAM1565  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                    TTGGTT    GAT GAAAGTCAC
                                    ||||||    ||| |||||||||
                                    AACCGA    TTG CTTTCAGTG
                                       AA___   A
GAM1565  KIAA1958  5'  GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                    GGTT   GGG    AAAGTCAC
                                    ||||   |||    ||||||||
                                    CCAA   CCC    TTTCAGTG
                                      A__   CAAG
GAM1565  MARCKS   3'  ACTTTCCACCCTGCCCA     11411     TTCA    A
                                    TGG    AGGG TGGAAAGT
                                    |||    |||| ||||||||
                                    ACC    TCCC ACCTTTCA
                                      CG__   _
GAM1565  TUB      5'  GTGGGACCATCCCTTAAACC   13898     C        AAAG
                                    GGTT AAGGGATGG    TCAC
                                    |||| |||||||||    ||||
                                    CCAA TTCCCTACC    GGTG
                                      A        AG__
GAM1565  LOC80298  3'  ACTTTTACCTTGAACCA     48062          GATG
                                    TGGTTCAAGG    GAAAGT
                                    ||||||||||    ||||||
                                    ACCAAGTTCC    TTTTCA
                                          A___
GAM1566  ELF3     3'  TGACCTTGACCTTGACCAA    16685      T    GAT  AAA
                                    TTGGT CAAGG   GG   GTCA
                                    ||||| |||||   ||   ||||
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                                AACCA GTTCC   TC   CAGT
                                  _    AGT  ___
GAM1566 JAK2     3'  TGACCTTCATTCTGAGACCAA  18318       CAA       AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_       C_
GAM1566 SLC10A2  5'  ACTCTCTGTCTTGACCAA    6590        CAA       A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___        C
GAM1566 FLJ10803 3'  GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM1566 KIAA1958 5'  GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM1566 MARCKS   3'  ACTTTCCACCCTGCCCA     11411     TTCA    A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM1566 TUB      5'  GTGGGACCATCCCTTAAACC   13898     C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A        AG__
GAM1566 LOC80298 3'  ACTTTTACCTTGAACCA     48062         GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                     A___
GAM1567 GPD1     3'  TCATGCCACCACATTTG      60398       C       C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A       _
GAM1567 IL5RA    5'  TCGCATGGCCACCGCATTT    6906          AT__
                                AAATGCGGTGGC    CGA
                                ||||||||||||    |||
                                TTTACGCCACCG    GCT
                                      GTAC
GAM1567 MYO1C    3'  TGCCGATGCCAAATATTTG    61873       CGG       A
                                TAAATG   TGGCATCG CA
                                ||||||   |||||||| ||
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                                GTTTAT   ACCGTAGC GT
                                   AA_       C
GAM1567  C6orf37   3'  TGTCACACTGCATTTA      68097          GCATC
                                TAAATGCGGTG    GACA
                                ||||||||||    ||||
                                ATTTACGTCAC    CTGT
                                      A____
GAM1567  DNAJC6    3'  TTGCAGAACCACCGCATT    29498          CA  GA
                                AATGCGGTGG  TC  CAA
                                |||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                      A_  AC
GAM1567  FLJ11210  3'  GTCGATGTGCATGCTTTTA   60319      T   GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                   T   ACG
GAM1567  FLJ12476  3'  TCGATCTTCTGCATTTA     43270         T  C
                                TAAATGCGG GG ATCGA
                                |||||||||  || |||||
                                ATTTACGTC TC TAGCT
                                      T  _
GAM1567  KIAA1034  3'  TCGATGGCATCCGCATTTG   63134          _  G
                                TAAATGCGG TG CATCGA
                                |||||||||  || ||||||
                                GTTTACGCC AC GTAGCT
                                      T  G
GAM1567  KIAA1987  3'  TCATGTAACTGCATTTA     89391          G    C
                                TAAATGCGGT GCAT GA
                                ||||||||||  ||||  ||
                                ATTTACGTCA TGTA CT
                                      A   _
GAM1567  MGC16063  3'  TGTCCTGGCCACTGCATT    54929          ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                      GTC
GAM1567  LOC147949 3'  TGTCAGATGTCCACATTGCA   79279      __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  ||||  ||||  ||||
                                ACGT  CACC GTAG CTGT
                                   TA   T   A
GAM1567  LOC150577 3'  GTCCTCACCGCATTTG      86258          CATC
                                TAAATGCGGTGG    GAC
                                ||||||||||||    |||
                                GTTTACGCCACT    CTG
                                      C___
GAM1567  LOC158219 3'  TGTGTGTCACCACATTT     82694       C       CG
                                AAATG GGTGGCAT  ACA
                                |||||  ||||||||  |||
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                                TTTAC CCACTGTG  TGT
                                   A       __
GAM1567  LOC202020 3'  TGTCTCACCACATTTA      90605       C     CATC
                                TAAATG GGTGG    GACA
                                |||||| |||||    ||||
                                ATTTAC CCACT    CTGT
                                   A    ____
GAM1567  LOC90826  5'  TGTCGATGCAGGTTTATTTG   64788       CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                   TTGGA
GAM1567  LOC93587  3'  TTGTCTTTACCTGCATTTA    73042       _     CATC
                                TAAATGC GGTGG    GACAA
                                ||||||| |||||    |||||
                                ATTTACG CCATT    CTGTT
                                    T    T___
GAM1568  ELF3      3'  TGACCTTGACCTTGACCAA    16685       T     GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                   _    AGT  ___
GAM1568  JAK2      3'  TGACCTTCATTCTGAGACCAA  18318       CAA       AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_       C_
GAM1568  SLC10A2   5'  ACTCTCTGTCTTGACCAA    6590        CAA       A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM1568  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM1568  KIAA1958  5'  GTGACTTTGAACCCCAAACC   82788      CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM1568  MARCKS    3'  ACTTTCCACCCTGCCCA     11411     TTCA    A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM1568  TUB       5'  GTGGGACCATCCCTTAAACC   13898      C        AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
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                                CCAA TTCCCTACC   GGTG
                                  A       AG__
GAM1568 LOC80298 3' ACTTTTACCTTGAACCA    48062        GATG
                                TGGTTCAAGG   GAAAGT
                                ||||||||||   ||||||
                                ACCAAGTTCC   TTTTCA
                                     A___
GAM1569 ELF3     3' TGACCTTGACCTTGACCAA   16685     T   GAT  AAA
                                TTGGT CAAGG  GG  GTCA
                                ||||| |||||  ||  ||||
                                AACCA GTTCC  TC  CAGT
                                  _    AGT  ___
GAM1569 JAK2     3' TGACCTTCATTCTGAGACCAA 18318     CAA      AA
                                TTGGTT  GGGATGGA GTCA
                                ||||||  |||||||| ||||
                                AACCAG  TCTTACTT CAGT
                                   AG_      C_
GAM1569 SLC10A2  5' ACTCTCTGTCTTGACCAA   6590      CAA      A
                                TTGGTT  GGGATGGA AGT
                                ||||||  |||||||| |||
                                AACCAG  TTCTGTCT TCA
                                   ___      C
GAM1569 FLJ10803 3' GTGACTTTCAGTTAAAGCCAA 37205     CAAGG  G
                                TTGGTT   GAT GAAAGTCAC
                                ||||||   ||| |||||||||
                                AACCGA   TTG CTTTCAGTG
                                   AA___  A
GAM1569 KIAA1958 5' GTGACTTTGAACCCCAAACC  82788    CAA  ATGG
                                GGTT  GGG   AAAGTCAC
                                ||||  |||   ||||||||
                                CCAA  CCC   TTTCAGTG
                                  A__  CAAG
GAM1569 MARCKS   3' ACTTTCCACCCTGCCCA    11411    TTCA   A
                                TGG   AGGG TGGAAAGT
                                |||   |||| ||||||||
                                ACC   TCCC ACCTTTCA
                                  CG__  _
GAM1569 TUB      5' GTGGGACCATCCCTTAAACC  13898    C       AAAG
                                GGTT AAGGGATGG   TCAC
                                |||| |||||||||   ||||
                                CCAA TTCCCTACC   GGTG
                                  A       AG__
GAM1569 LOC80298 3' ACTTTTACCTTGAACCA    48062        GATG
                                TGGTTCAAGG   GAAAGT
                                ||||||||||   ||||||
                                ACCAAGTTCC   TTTTCA
                                     A___
GAM1570 EHF      3' TCCAAAACCCAAGGTTGGCT  25127    AT   _   C
                                AGT  GCCT GGGT TTGGA
                                |||  |||| |||| |||||
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                                TCG  TGGA CCCA AACCT
                                  GT   A   A
GAM1570  EPHA2    3'  CCATCGGCCAAGAATACTTGAA 16675        GC  G   T_
              G                   CTTCAAGTAT  CT GGTC  TGG
                                  ||||||||||  || ||||  |||
                                  GAAGTTCATA  GA CCGG  ACC
                                        A_  A   CT
GAM1570  ITGA5    3'  CCCAGAGACATACTTGAAG   61933         C__
                                  CTTCAAGTATG  CTGGG
                                  ||||||||||   |||||
                                  GAAGTTCATAC  GACCC
                                        AGA
GAM1570  TREM2    3'  TCCAAGACTGTCATATTT    39098       CCTG
                                  AAGTATG   GGTCTTGGA
                                  |||||||   |||||||||
                                  TTTATAC   TCAGAACCT
                                      TG__
GAM1570  UQCRB    3'  CCAACATAGGCATACTTAAG  21939    C        GGTC
                                  CTT AAGTATGCCTG   TTGG
                                  ||| ||||||||||   ||||
                                  GAA TTCATACGGAT   AACC
                                    _        AC__
GAM1570  ATP10D   3'  CAGAGACCACTTGAAG     73526        ATGCCTG   _
                                  CTTCAAGT     GGTCT TG
                                  ||||||||     ||||| ||
                                  GAAGTTCA     CCAGA AC
                                       _______   G
GAM1570  B3GNT7   3'  CCCTTCCAGGCAACCTGAA   71678     A  A      TCTT
                                  TTCA GT TGCCTGGG   GG
                                  |||| || ||||||||   ||
                                  AAGT CA ACGGACCT   CC
                                    C  _      TC__
GAM1570  DKFZp547I224 3'  TCCAAAATTGACCACATACTTG 39963         CCTG  ____
              GA                    TTCAAGTATG   GGTC   TTGGA
                                    ||||||||||   ||||   |||||
                                    AGGTTCATAC   CCAG   AACCT
                                         A___   TTAA
GAM1570  FLJ22341 3'  CCAAGCTCAGGCACACCCAAG  45114    CAA  A      T
                                  CTT   GT TGCCTGGG CTTGG
                                  |||   || |||||||| |||||
                                  GAA   CA ACGGACTC GAACC
                                    CC_  C       _
GAM1570  KIAA0779 3'  CCGAACAGCATACTTGAAG   86908          C  GGTC
                                  CTTCAAGTATGC TG   TTGG
                                  |||||||||||| ||   ||||
                                  GAAGTTCATACG AC   AGCC
                                         _  A___
GAM1570  LOC144233 3'  CCAAGGCACATAATTGAA    77246      G   CCTGG
                                  TTCAA TATG    GTCTTGG
                                  ||||| ||||    |||||||
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                                AAGTT ATAC    CGGAACC
                                  A   A____
GAM1570 LOC147341 3' ACCCAGGCATAACTGAAG   85116      AG
                                CTTCA TATGCCTGGGT
                                ||||| ||||||||||
                                GAAGT ATACGGACCCA
                                  CA
GAM1570 LOC221088 5' TCCAAGGTGCTGGCCACTCGAA 94888     A  AT  TGGG
          G                      CTTC AGT GCC   TCTTGGA
                                |||| ||| ||| |||||||
                                GAAG TCA CGG   GGAACCT
                                  C  C_  TCGT
GAM1571 GPD1    3' TCATGCCACCACATTTG    60398      C      C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A      _
GAM1571 IL5RA   5' TCGCATGGCCACCGCATTT   6906          AT__
                                AAATGCGGTGGC   CGA
                                ||||||||||||   |||
                                TTTACGCCACCG   GCT
                                     GTAC
GAM1571 MYO1C   3' TGCCGATGCCAAATATTTG   61873      CGG      A
                                TAAATG  TGGCATCG CA
                                ||||||  |||||||| ||
                                GTTTAT  ACCGTAGC GT
                                   AA_      C
GAM1571 C6orf37  3' TGTCACACTGCATTTA     68097         GCATC
                                TAAATGCGGTG    GACA
                                ||||||||||    ||||
                                ATTTACGTCAC    CTGT
                                     A____
GAM1571 DNAJC6  3' TTGCAGAACCACCGCATT    29498        CA  GA
                                AATGCGGTGG  TC  CAA
                                |||||||||  ||  |||
                                TTACGCCACC  AG  GTT
                                     A_  AC
GAM1571 FLJ11210 3' GTCGATGTGCATGCTTTTA   60319     T  GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM1571 FLJ12476 3' TCGATCTTCTGCATTTA     43270        T  C
                                TAAATGCGG GG ATCGA
                                ||||||||| || |||||
                                ATTTACGTC TC TAGCT
                                     T  _
GAM1571 KIAA1034 3' TCGATGGCATCCGCATTTG   63134         _  G
                                TAAATGCGG TG CATCGA
                                ||||||||| || ||||||
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                                GTTTACGCC AC GTAGCT
                                     T  G
GAM1571  KIAA1987  3'  TCATGTAACTGCATTTA     89391          G    C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                     A   _
GAM1571  MGC16063  3'  TGTCCTGGCCACTGCATT    54929           ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                      GTC
GAM1571  LOC147949 3'  TGTCAGATGTCCACATTGCA   79279      __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T    A
GAM1571  LOC150577 3'  GTCCTCACCGCATTTG      86258           CATC
                                TAAATGCGGTGG    GAC
                                ||||||||||||    |||
                                GTTTACGCCACT    CTG
                                      C___
GAM1571  LOC158219 3'  TGTGTGTCACCACATTT     82694       C       CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                   A       __
GAM1571  LOC202020 3'  TGTCTCACCACATTTA      90605       C    CATC
                                TAAATG GGTGG    GACA
                                |||||| |||||    ||||
                                ATTTAC CCACT    CTGT
                                   A    _____
GAM1571  LOC90826  5'  TGTCGATGCAGGTTTATTTG  64788       CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
                                GTTTAT    CGTAGCTGT
                                    TTGGA
GAM1571  LOC93587  3'  TTGTCTTTACCTGCATTTA   73042        _    CATC
                                TAAATGC GGTGG    GACAA
                                ||||||| |||||    |||||
                                ATTTACG CCATT    CTGTT
                                     T    T___
GAM1572  ELF3      3'  TGACCTTGACCTTGACCAA   16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                   _    AGT  ____
GAM1572  JAK2      3'  TGACCTTCATTCTGAGACCAA 18318       CAA       AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
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                                AACCAG   TCTTACTT  CAGT
                                   AG_      C_
GAM1572 SLC10A2  5' ACTCTCTGTCTTGACCAA    6590       CAA      A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM1572 FLJ10803 3' GTGACTTTCAGTTAAAGCCAA 37205      CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM1572 KIAA1958 5' GTGACTTTGAACCCCAAACC  82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM1572 MARCKS   3' ACTTTCCACCCTGCCCA     11411     TTCA    A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                 CG__   _
GAM1572 TUB      5' GTGGGACCATCCCTTAAACC   13898     C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A       AG__
GAM1572 LOC80298 3' ACTTTTACCTTGAACCA     48062         GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                      A___
GAM1573 FLJ12949 5' CCGCATTTATCAGAAAGATGCC 43725     C    GA  _
            A                    TGGC ATCT  TCT ATAAATGCGG
                                ||||  ||||  |||  ||||||||||
                                ACCG TAGA  AGA TATTTACGCC
                                  _   A_   C
GAM1573 MAN1     3' TTGCATAGATCAAACAGCCA   27484     CATC      TAAA
                                TGGC    TGATCTA    TGCGG
                                ||||    |||||||    |||||
                                ACCG    ACTAGAT    ACGTT
                                  ACAA      _____
GAM1573 LOC143188 5' CCATTCCACAGGTGGCCA    83791         ATCTATA    C
                                TGGCCATCTG      AATG G
                                ||||||||||      |||| |
                                ACCGGTGGAC      TTAC C
                                      ACC_____    A
GAM1574 ELF3     3' TGACCTTGACCTTGACCAA    16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
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                                AACCA GTTCC   TC   CAGT
                                  _    AGT  ___
GAM1574 JAK2     3' TGACCTTCATTCTGAGACCAA 18318      CAA      AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_      C_
GAM1574 SLC10A2  5' ACTCTCTGTCTTGACCAA    6590       CAA      A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM1574 FLJ10803 3' GTGACTTTCAGTTAAAGCCAA 37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM1574 KIAA1958 5' GTGACTTTGAACCCCAAACC  82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM1574 MARCKS   3' ACTTTCCACCCTGCCCA     11411     TTCA    A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                 CG__   _
GAM1574 TUB      5' GTGGGACCATCCCTTAAACC   13898     C        AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A        AG__
GAM1574 LOC80298 3' ACTTTTACCTTGAACCA     48062         GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                     A___
GAM1575 ELF3     3' TGACCTTGACCTTGACCAA    16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                  _    AGT  ___
GAM1575 JAK2     3' TGACCTTCATTCTGAGACCAA 18318      CAA      AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_      C_
GAM1575 SLC10A2  5' ACTCTCTGTCTTGACCAA    6590       CAA      A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
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                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM1575 FLJ10803 3' GTGACTTTCAGTTAAAGCCAA 37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___  A
GAM1575 KIAA1958 5' GTGACTTTGAACCCCAAACC  82788     CAA   ATGG
                                GGTT   GGG   AAAGTCAC
                                ||||   |||   ||||||||
                                CCAA   CCC   TTTCAGTG
                                  A__  CAAG
GAM1575 MARCKS   3' ACTTTCCACCCTGCCCA     11411     TTCA   A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM1575 TUB      5' GTGGGACCATCCCTTAAACC   13898     C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A       AG__
GAM1575 LOC80298 3' ACTTTTACCTTGAACCA     48062         GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                     A___
GAM1576 GPD1     3' TCATGCCACCACATTTG     60398       C       C
                                TAAATG GGTGGCAT GA
                                |||||| |||||||| ||
                                GTTTAC CCACCGTA CT
                                   A      _
GAM1576 IL5RA    5' TCGCATGGCCACCGCATTT    6906           AT__
                                AAATGCGGTGGC    CGA
                                ||||||||||||    |||
                                TTTACGCCACCG    GCT
                                      GTAC
GAM1576 MYO1C    3' TGCCGATGCCAAATATTTG   61873       CGG       A
                                TAAATG   TGGCATCG CA
                                ||||||   |||||||| ||
                                GTTTAT   ACCGTAGC GT
                                   AA_       C
GAM1576 C6orf37  3' TGTCACACTGCATTTA      68097          GCATC
                                TAAATGCGGTG     GACA
                                ||||||||||||    ||||
                                ATTTACGTCAC     CTGT
                                      A____
GAM1576 DNAJC6   3' TTGCAGAACCACCGCATT    29498         CA  GA
                                AATGCGGTGG  TC  CAA
                                ||||||||||  ||  |||
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                                TTACGCCACC  AG  GTT
                                     A_  AC
GAM1576  FLJ11210  3'  GTCGATGTGCATGCTTTTA   60319     T   GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM1576  FLJ12476  3'  TCGATCTTCTGCATTTA     43270         T  C
                                TAAATGCGG GG ATCGA
                                ||||||||| || |||||
                                ATTTACGTC TC TAGCT
                                     T  _
GAM1576  KIAA1034  3'  TCGATGGCATCCGCATTTG   63134         _  G
                                TAAATGCGG TG CATCGA
                                ||||||||| || ||||||
                                GTTTACGCC AC GTAGCT
                                     T  G
GAM1576  KIAA1987  3'  TCATGTAACTGCATTTA     89391         G   C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                     A   _
GAM1576  MGC16063  3'  TGTCCTGGCCACTGCATT    54929          ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                      GTC
GAM1576  LOC147949 3'  TGTCAGATGTCCACATTGCA   79279     __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM1576  LOC150577 3'  GTCCTCACCGCATTTG      86258          CATC
                                TAAATGCGGTGG   GAC
                                ||||||||||||   |||
                                GTTTACGCCACT   CTG
                                      C___
GAM1576  LOC158219 3'  TGTGTGTCACCACATTT     82694      C       CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                   A       __
GAM1576  LOC202020 3'  TGTCTCACCACATTTA      90605       C    CATC
                                TAAATG GGTGG   GACA
                                |||||| |||||   ||||
                                ATTTAC CCACT   CTGT
                                   A    _____
GAM1576  LOC90826  5'  TGTCGATGCAGGTTTATTTG  64788       CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
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                                GTTTAT    CGTAGCTGT
                                   TTGGA
GAM1576 LOC93587 3' TTGTCTTTACCTGCATTTA   73042       _    CATC
                                TAAATGC GGTGG   GACAA
                                ||||||| |||||   |||||
                                ATTTACG CCATT   CTGTT
                                    T   T___
GAM1577 ELF3     3' TGACCTTGACCTTGACCAA   16685     T   GAT  AAA
                                TTGGT CAAGG  GG  GTCA
                                ||||| |||||  ||  ||||
                                AACCA GTTCC  TC  CAGT
                                   _    AGT  ___
GAM1577 JAK2     3' TGACCTTCATTCTGAGACCAA 18318      CAA      AA
                                TTGGTT  GGGATGGA  GTCA
                                ||||||  ||||||||  ||||
                                AACCAG  TCTTACTT  CAGT
                                   AG_      C_
GAM1577 SLC10A2  5' ACTCTCTGTCTTGACCAA    6590      CAA      A
                                TTGGTT  GGGATGGA AGT
                                ||||||  |||||||| |||
                                AACCAG  TTCTGTCT TCA
                                   ___      C
GAM1577 FLJ10803 3' GTGACTTTCAGTTAAAGCCAA 37205      CAAGG  G
                                TTGGTT   GAT GAAAGTCAC
                                ||||||   ||| |||||||||
                                AACCGA   TTG CTTTCAGTG
                                   AA___  A
GAM1577 KIAA1958 5' GTGACTTTGAACCCCAAACC  82788    CAA  ATGG
                                GGTT  GGG   AAAGTCAC
                                ||||  |||   ||||||||
                                CCAA  CCC   TTTCAGTG
                                  A__  CAAG
GAM1577 MARCKS   3' ACTTTCCACCCTGCCCA     11411    TTCA   A
                                TGG   AGGG TGGAAAGT
                                |||   |||| ||||||||
                                ACC   TCCC ACCTTTCA
                                  CG__  _
GAM1577 TUB      5' GTGGGACCATCCCTTAAACC   13898    C      AAAG
                                GGTT AAGGGATGG   TCAC
                                |||| |||||||||   ||||
                                CCAA TTCCCTACC   GGTG
                                  A       AG__
GAM1577 LOC80298 3' ACTTTTACCTTGAACCA     48062        GATG
                                TGGTTCAAGG   GAAAGT
                                ||||||||||   ||||||
                                ACCAAGTTCC   TTTTCA
                                      A___
GAM1578 ELF3     3' TGACCTTGACCTTGACCAA   16685     T   GAT  AAA
                                TTGGT CAAGG  GG  GTCA
                                ||||| |||||  ||  ||||
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                                AACCA GTTCC   TC   CAGT
                                  _    AGT  ___
GAM1578 JAK2     3'  TGACCTTCATTCTGAGACCAA  18318      CAA      AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_      C_
GAM1578 SLC10A2  5'  ACTCTCTGTCTTGACCAA    6590       CAA      A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM1578 FLJ10803 3'  GTGACTTTCAGTTAAAGCCAA  37205      CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM1578 KIAA1958 5'  GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM1578 MARCKS   3'  ACTTTCCACCCTGCCCA     11411     TTCA    A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM1578 TUB      5'  GTGGGACCATCCCTTAAACC   13898     C        AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A        AG__
GAM1578 LOC80298 3'  ACTTTTACCTTGAACCA     48062          GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                     A___
GAM1579 ELF3     3'  TGACCTTGACCTTGACCAA    16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                  _    AGT  ___
GAM1579 JAK2     3'  TGACCTTCATTCTGAGACCAA  18318      CAA      AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_      C_
GAM1579 SLC10A2  5'  ACTCTCTGTCTTGACCAA    6590       CAA      A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
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                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM1579  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM1579  KIAA1958  5'  GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM1579  MARCKS   3'  ACTTTCCACCCTGCCCA     11411     TTCA   A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM1579  TUB      5'  GTGGGACCATCCCTTAAACC   13898     C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A       AG__
GAM1579  LOC80298  3'  ACTTTTACCTTGAACCA     48062          GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
                                ACCAAGTTCC    TTTTCA
                                      A___
GAM1580  ABCD1    3'  CCCATGCACGCACCCCGCCC   5259     A   A   G  CGG  _
                                GG GCGG GTG GT   GCG GGG
                                || |||| ||| ||   ||| |||
                                CC CGCC CAC CA   CGT CCC
                                 _   C   G  ___   A
GAM1580  ADD1     3'  CCCCACCCCACCCTGCCC    27203    A  GAGT   C   C
                                GG GCG    GGGT GGG GGGG
                                || |||    |||| ||| ||||
                                CC CGT    CCCA CCC CCCC
                                 _  _____    C   A
GAM1580  ADD1     3'  CCCCACCCCACCCTGCCC    27204    A  GAGT   C   C
                                GG GCG    GGGT GGG GGGG
                                || |||    |||| ||| ||||
                                CC CGT    CCCA CCC CCCC
                                 _  _____    C   A
GAM1580  AK1      3'  CCCCGCCCCACCCCGTCC    6636     GT    C
                                GGA  GGGT GGGCGGGG
                                |||  |||| ||||||||
                                CCT  CCCA CCCGCCCC
                                  GC    C
GAM1580  ALDH3A1  3'  GCCCCAGCCCAGCCCCACTCC  7309          TC_   _
                                GGAGTGGG   GGGC GGGGC
                                ||||||||   |||| |||||
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                                CCTCACCC  CCCG CCCCG
                                    CGA   A
GAM1580 AP2S1   3' CCCCACCCCGGCCCCGGCCC  41485   A GGAGT     C_
                                GG GC    GGGTCGGG GGGG
                                || ||    |||||||| ||||
                                CC CG    CCCGGCCC CCCC
                                 _ GC___      CA
GAM1580 ARVCF   3' CCCCCCCACCCCACTCC    9802        TC  C
                                GGAGTGGG GGG GGGG
                                |||||||| ||| ||||
                                CCTCACCC CCC CCCC
                                    CA  _
GAM1580 ATP1A2  3' CCCCACCCTGCCCACTCC   7362         C  C
                                GGAGTGGGT GGG GGGG
                                ||||||||| ||| ||||
                                CCTCACCCG CCC CCCC
                                     T  A
GAM1580 AXUD1   3' CCCCACCCTGCCCCCTCC   53439    T   C  C
                                GGAG GGGT GGG GGGG
                                |||| |||| ||| ||||
                                CCTC CCCG CCC CCCC
                                  C   T  A
GAM1580 BARHL1  3' GCCCACCCACCCCGACCC   39637   AG  A    C
                                GG  CGG GTGGGT GGGC
                                ||  ||| |||||| ||||
                                CC  GCC CACCCA CCCG
                                 CA  C    _
GAM1580 BLK     3' CCCCGCCCTGCCCCGCT    9938      AGTG  C
                                AGCGG   GGT GGGCGGGG
                                |||||   ||| ||||||||
                                TCGCC   CCG CCCGCCCC
                                   _____  T
GAM1580 BMP2    5' GCCCCACCGCCCCTCCACTCC 8656     C   T  T  GC
                                GGAG GGAG GGG CGG  GGGGC
                                |||| |||| ||| |||  |||||
                                CCTC CCTC CCC GCC  CCCCG
                                  A   _  _  A_
GAM1580 BSN     3' CCCCTCCCCACCCCACCCCT  14381   C A   TC_  C
                                AG GG GTGGG   GGG GGGG
                                || || |||||   ||| ||||
                                TC CC CACCC   CCC CCCC
                                 _ _    CAC  T
GAM1580 CA3     5' GCCCCTTCGCCCACCTCCGCCC 18997   A    _   T   C
                                GG GCGGAG TGGG CGGG GGGGC
                                || |||||| |||| |||| |||||
                                CC CGCCTC ACCC GCTT CCCCG
                                 _    C   _  _
GAM1580 CACNA2D2 3' GCCCCCACCCCACCTCCACTCC 21223    C  GTG  C  C
                                GGAG GGA   GGT GGG GGGGC
                                |||| |||   ||| ||| |||||
```

```
                                CCTC CCT   CCA CCC CCCCG
                                  A  ___   C  A
GAM1580  CHST1    3'  GCCCCCAGCTCACCCCACTCC  14700        TC   __
                                GGAGTGGG  GGGC  GGGGC
                                ||||||||  ||||  |||||
                                CCTCACCC  CTCG  CCCCG
                                    CA    AC
GAM1580  DNMT3L   5'  CCCCACCCCTCACTCCACCC   26285    AGC      TC   C
                                GG   GGAGTGGG  GGG GGGG
                                ||   ||||||||  ||| ||||
                                CC   CCTCACTC  CCC CCCC
                                 CA_       __   A
GAM1580  DNMT3L   5'  GCCCCGCCCCCGCCCCTCCCCG 26288    A __    T   C_
            CCC                   GG GC  GGAG GGGT  GGGCGGGGC
                                || ||  |||| ||||  |||||||||
                                CC CG  CCTC CCCG  CCCGCCCCG
                                 _ CC   _   CC
GAM1580  ECM1     3'  CCCCACCCTGCCCCACCC    16656    A    T _  C
                                GG GTGGG C GGG GGGG
                                || ||||| | ||| ||||
                                CC CACCC G CCC CCCC
                                 _    C T   A
GAM1580  EGR1     5'  GCCCCGGGCTGCACCCCCCCGC 10492    A   AGT   _  G_
            CC                    GG GCGG   GGGT CGG  CGGGGC
                                || ||||   |||| |||  ||||||
                                CC CGCC   CCCA GTC  GCCCCG
                                 _   CC_   C   GG
GAM1580  F2R      5'  GCCCCAGTCCCGCCCCGCCC   10567    A    T   _ _
                                GG GTGGG CGGG C GGGGC
                                || ||||| |||| | |||||
                                CC CGCCC GCCC G CCCCG
                                 _    C    T A
GAM1580  FOXD2    5'  CCCCGCCCAGGGAGCTCCGCCC 16785    A      GGGTC
                                GG GCGGAGT    GGGCGGGG
                                || |||||||    ||||||||
                                CC CGCCTCG    CCCGCCCC
                                 _      AGGGA
GAM1580  GALNT2   3'  GCCCCGCCCGCAGCTCCCTCC  16817     C    GG T
                                GGAG GGAGT  G CGGGCGGGGC
                                |||| |||||  | ||||||||||
                                CCTC CCTCG  C GCCCGCCCCG
                                  _    A_ _
GAM1580  GNB1     3'  CCCCGCCCCCCGCACTCC    10835       _ TC
                                GGAGTG GG  GGGCGGGG
                                ||||||  ||  ||||||||
                                CCTCAC CC  CCCGCCCC
                                   G  C_
GAM1580  HCN2     3'  GCCCCGCCCGCCCCCCACCC   8652     A    T__
                                GG GTGGG   CGGGCGGGGC
                                || |||||   ||||||||||
```

```
                                CC CACCC   GCCCGCCCCG
                                 _    CCC
GAM1580 HSD11B2  5' CCCCGCCCCGCCCCAGCCC   5768    A  GGAGT   C
                                GG GC    GGGT GGGCGGGG
                                || ||    |||| ||||||||
                                CC CG    CCCG CCCGCCCC
                                 _ AC___   C
GAM1580 HSD11B2  5' CCCCGCCCCGCCCCGCCC    5769    A   AGTG   C
                                GG GCGG   GGT GGGCGGGG
                                || ||||   ||| ||||||||
                                CC CGCC   CCG CCCGCCCC
                                 _  _____  C
GAM1580 HSF4     5' CCCCACCCCACCCCACTCC    60481       TC_   C
                                GGAGTGGG   GGG GGGG
                                ||||||||   ||| ||||
                                CCTCACCC   CCC CCCC
                                     CAC   A
GAM1580 HSF4     5' CCCCACCCCACTCCACCC    60482    A   _ C   C
                                GG GTGG GT GGG GGGG
                                || |||| || ||| ||||
                                CC CACC CA CCC CCCC
                                 _   T  C   A
GAM1580 HSF4     5' CCCCACCCCTCCACTCCACTCC 60483      C       TC   C
                                GGAG GGAGTGGG  GGG GGGG
                                |||| ||||||||  ||| ||||
                                CCTC CCTCACCT  CCC CCCC
                                  A       C_   A
GAM1580 HSF4     5' CCCCACTCCACCCCACCCCACC 60484    AGC  A    TC  _ C
            CC                    GG   GG GTGGG  GG G GGGG
                                ||   || |||||  || | ||||
                                CC   CC CACCC  CC C CCCC
                                 CCA  C    CA  T A
GAM1580 INHBB    5' CCCCGCCCGGCGCGCCC     11006    A   G
                                GG GTG GTCGGGCGGGG
                                || ||| ||||||||||
                                CC CGC CGGCCCGCCCC
                                 _  G
GAM1580 KCNC3    5' CCCCTCCCGCCCCGCCC     18329    A    T   C
                                GG GTGGG CGGG GGGG
                                || ||||| |||| ||||
                                CC CGCCC GCCC CCCC
                                 _    C   T
GAM1580 KCNK7    5' CCCCGCCCTGCCCAGCCC    54056    AG    C
                                GG  TGGGT GGGCGGGG
                                ||  ||||| ||||||||
                                CC  ACCCG CCCGCCCC
                                 CG    T
GAM1580 KIP2     3' CCCCGCCCCATGCCCCAGTCC  22120     G   T ___
                                GGA TGGG C   GGGCGGGG
                                ||| |||| |   ||||||||
```

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                                CCT ACCC G   CCCGCCCC
                                  G    C TAC
GAM1580 KLF7     5' CCCCACTCACTCGCTCC     14928       G      C
                                GGAGCG AGTGGGT GGG
                                |||||| ||||||| |||
                                CCTCGC TCACTCA CCC
                                   _      C
GAM1580 KPNB1    5' CCCTCCCTTCCCACCCGACCC 11219    AG  A    TC  C
                                GG  CGG GTGGG  GGG GGG
                                ||  ||| |||||  ||| |||
                                CC  GCC CACCC  CCC CCC
                                 CA  _    TT  T
GAM1580 LU       3' CCCCGCCCCTGGTCCCACTCC  19942        _ __
                                GGAGTGGG TC  GGGCGGGG
                                |||||||| ||  ||||||||
                                CCTCACCC GG  CCCGCCCC
                                     T  TC
GAM1580 LU       3' CCCCTGGTCCCACTCCTGCCC  19943    A _      _    C
                                GG GC GGAGTGGG TCGGG GG
                                || || |||||||| ||||| ||
                                CC CG CCTCACCC GGTCC CC
                                 _ T      T    _
GAM1580 MAP3K10  5' CCCCGCCCCGCCCCGCCC    68580    A   AGTG  C
                                GG GCGG    GGT GGGCGGGG
                                || ||||    ||| ||||||||
                                CC CGCC    CCG CCCGCCCC
                                 _   _____  C
GAM1580 MAP3K10  5' GCCCCACTCCCACCCCGCCCC 68582    A   A    TCG  C
                                GG GCGG GTGGG   GG GGGGC
                                || |||| |||||   || |||||
                                CC CGCC CACCC   TC CCCCG
                                 C   C    ___  A
GAM1580 MYO5A    5' GCCCCGCCCCGCCCCGCCCC  60472    A   AGTG  C
                                GG GCGG    GGT GGGCGGGGC
                                || ||||    ||| |||||||||
                                CC CGCC    CCG CCCGCCCCG
                                 C   _____  C
GAM1580 NGB      3' CCCCGCCCGGCAGCCCCCATCC 41461     GC  A  GG
                                GGA  GG GT  GTCGGGCGGGG
                                |||  || ||  ||||||||||
                                CCT  CC CG  CGGCCCGCCCC
                                  AC  C  A_
GAM1580 NRG2     3' GCCCCGCCGCGCGCCCCTCCGC 18082    A     T   _ _
             CC                   GG GCGGAG GGGT CG GGCGGGGC
                                || |||||| |||| || ||||||||
                                CC CGCCTC CCCG GC CCGCCCCG
                                 _     _   C  G
GAM1580 NRG2     3' GCCCCGCCGCGCGCCCCTCCGC 18083    A     T   _ _
             CC                   GG GCGGAG GGGT CG GGCGGGGC
                                || |||||| |||| || ||||||||
```

```
                                CC CGCCTC CCCG GC CCGCCCCG
                                 _    _   C  G
GAM1580  OTP     3'  GCCCCGGCCCGCTCCGCCC   50406    A          _
                                GG GCGGAGTGGGTCGGG C
                                || |||||||||||||| |
                                CC CGCCTCGCCCGGCCC G
                                 _           C
GAM1580  PAX2    3'  CCCCTCCCCCTCCGCCC    15653    A    T  TC  C
                                GG GCGGAG GGG  GGG GGG
                                || |||||| |||  ||| |||
                                CC CGCCTC CCC  CTC CCC
                                 _    _  __  _
GAM1580  PAX2    3'  CCCCTCCCCCTCCGCCC    15654    A    T  TC  C
                                GG GCGGAG GGG  GGG GGG
                                || |||||| |||  ||| |||
                                CC CGCCTC CCC  CTC CCC
                                 _    _  __  _
GAM1580  PCM1    5'  CCCCGCCCTCTTCTCCACC   21672    AGC   T  TC
                                GG   GGAG GGG  GGGCGGGG
                                ||   |||| |||  ||||||||
                                CC   CCTC TCT  CCCGCCCC
                                 A__   T  __
GAM1580  PNUTL1  5'  GCCCCGCCCGCGAGCCCGCCCC 12191    A    ___
           G                     CGG GTGGGT  CGGGCGGGGC
                                ||| ||||||  ||||||||||
                                GCC CGCCCG  GCCCGCCCCG
                                  C    AGC
GAM1580  RAB3B   5'  CCCCGCCCCGGCCCCCTCC   12702     T     _
                                GGAG GGGTCGGG CGGGG
                                |||| |||||||| |||||
                                CCTC CCCGGCCC GCCCC
                                  C      C
GAM1580  RAD54L  5'  CCCCCAATCCCACCCCGCCCC  14551   A   A   TCG  C
                                GG GCGG GTGGG  GG GGG
                                || |||| |||||  || |||
                                CC CGCC CACCC  CC CCC
                                 C   C    TAA _
GAM1580  S100A1  3'  CCCCACCCTTGCCCACCCCACC 21847   AGC  A    C_  C
           CC                    GG  GG GTGGGT  GGG GGGG
                                ||  || ||||||  ||| ||||
                                CC  CC CACCCG  CCC CCCC
                                 CCA  C    TT  A
GAM1580  SBF1    3'  CCCCGTCCCCGCCCCCGCCC   66068   A   A   TCG
                                GG GCGG GTGGG  GGCGGGG
                                || |||| |||||  |||||||
                                CC CGCC CGCCC  CTGCCCC
                                 _   C   ___
GAM1580  SFN     3'  CCCCGCCCTGCCCCCTCC    75069     T   C
                                GGAG GGGT GGGCGGGG
                                |||| |||| ||||||||
```

```
                                CCTC CCCG CCCGCCCC
                                  C   T
GAM1580 SLC13A2  3' GCCCAGGAAGACCCACCCCATT 15647     C  A     GGGCG
             CC                   GGAG GG GTGGGTC    GGGC
                                ||||  ||  |||||||    ||||
                                CCTT CC CACCCAG    CCCG
                                  A  C      AAGGA
GAM1580 SLC21A2  5' CCCCGCGCCACTCCGCGCC   20080    A       GTCGG
                                GG GCGGAGTGG    GCGGGG
                                ||  |||||||||    ||||||
                                CC CGCCTCACC    CGCCCC
                                 G       G____
GAM1580 SLC6A9   5' GCCCACACACCCCACTCC    23654     C  A   G  C
                                GGAG GG GTG GT GGGC
                                ||||  ||  |||  ||  ||||
                                CCTC CC CAC CA CCCG
                                  A  C   A  _
GAM1580 SLC8A2   3' CCCCCCCCCCCACTTCACCC   66933    AGC      TC   C
                                GG   GGAGTGGG  GGG GGGG
                                ||   ||||||||  |||  ||||
                                CC   CTTCACCC  CCC CCCC
                                 CA_      __  _
GAM1580 SMT3H1   3' CCCCTCCCACCCCACTCC    60628        TC   C
                                GGAGTGGG  GGG GGGG
                                ||||||||  |||  ||||
                                CCTCACCC  CCC CCCC
                                     CA   T
GAM1580 SOX10    3' GCCCTGATGACCCACCCGCCC  23677    A   A      GG
                                GG GCGG GTGGGTCG  CGGGGC
                                ||  ||||  ||||||||  ||||||
                                CC CGCC CACCCAGT  GTCCCG
                                 _   _      A_
GAM1580 SRC      3' GCCCCGCCTGCCTGCCACCCTG 19450    A   A   GT__
             CCC                   GG GCGG GTGG    CGGGCGGGGC
                                ||  ||||  ||||    ||||||||||
                                CC CGTC CACC    GTCCGCCCCG
                                 _   C    GTCC
GAM1580 TCF20    3' GCCCCGCCCCGCCCCGCCCGC  67503     A    T   _
                                GCGG GTGGG CGGG CGGGGC
                                ||||  |||||  ||||  ||||||
                                CGCC CGCCC GCCC GCCCCG
                                  _    C   C
GAM1580 TGFB1    3' CCCCGCCCCGCCCCCGCTGCC  7253     _    AGT   C
                                GG AGCGG   GGGT GGGCGGGG
                                ||  |||||   ||||  ||||||||
                                CC TCGCC   CCCG CCCGCCCC
                                 G    ____   C
GAM1580 TGFB1    3' GCCCCACCCCGCCCCGCCCC   7254     A   AGTG   C   C
                                GG GCGG    GGT GGG GGGGC
                                ||  ||||    |||  |||  |||||
```

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                                CC CGCC   CCG CCC CCCCG
                                 C  ____  C  A
GAM1580 TGFB1   3' GCCCCGCCCCGCCCCGCCCC  7255    A  AGTG  C
                                GG GCGG   GGT GGGCGGGGC
                                || ||||   ||| |||||||||
                                CC CGCC   CCG CCCGCCCCG
                                 C  ____  C
GAM1580 TNFRSF12 3' CCCCACCCCTGCTCGCCC   15039   A  G  TG  TCG  C
                                GG GCG AG  GG  GG GGGG
                                || ||| ||  ||  || ||||
                                CC CGC TC  CC  CC CCCC
                                 _  _ GT  ___  A
GAM1580 UBE2A   5' GCCCCACCCCTGACCCCGCTC 13928      A  G  TC  C
                                GAGCGG GT GG  GGG GGGGC
                                |||||| || ||  ||| |||||
                                CTCGCC CA TC  CCC CCCCG
                                   C  G  __  A
GAM1580 VIPR1   3' CCCCTTCCCACTCACCC    17311   A    C  C_
                                GG GTGGGT GGG  GGGG
                                || |||||| |||  ||||
                                CC CACTCA CCC  CCCC
                                 _    _  TT
GAM1580 APCL    3' GCCCCGCCTCCCACCCCCACCC 20816   AGC  A   TC
                                GG  GG GTGGG  GGGCGGGGC
                                ||  || |||||  |||||||||
                                CC  CC CACCC  TCCGCCCCG
                                 CAC  C   __
GAM1580 ATPW    5' GCCCCGCCCCCGCCCCCGCTCC 32260      AGT   C_
                                GGAGCGG  GGGT  GGGCGGGGC
                                |||||||  ||||  |||||||||
                                CCTCGCC  CCCG  CCCGCCCCG
                                   ___   CC
GAM1580 ATPW    5' GCCCCGCCCTCGCCCCGCCCC  32261   A  A  GTC
                                GG GCGG GTGG  GGGCGGGGC
                                || |||| ||||  |||||||||
                                CC CGCC CGCT  CCCGCCCCG
                                 C  C  ___
GAM1580 BCKDK   5' GCCCCTACCCACCCACACC   60495   A   C  C_
                                GG GTGGGT GGG  GGGGC
                                || |||||| |||  |||||
                                CC CACCCA CCC  CCCCG
                                 A   _  AT
GAM1580 BRUNOL6 5' GCCCCGCCCCCGGCCCCCGCCCC  54522   A  AGTG   _
                                GG GCGG   GGTCGGG CGGGGC
                                || ||||   ||||||| ||||||
                                CC CGCC   CCGGCCC GCCCCG
                                 C  ____    C
GAM1580 C1orf25 5' CCCCGCCGTGAGCCCCGCTCC  72939      AGT  G  _
                                GGAGCGG  GG TCG GGCGGGG
                                |||||||  || ||| |||||||
```

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                                CCTCGCC   CC AGT CCGCCCC
                                   ___ G   G
GAM1580  C20orf108 3'  GCCCCAACCCCACTCCACTCC  55881      C       TCG GC
                                GGAG GGAGTGGG   G  GGGGC
                                |||| ||||||||   |  |||||
                                CCTC CCTCACCC   C  CCCCG
                                  A       ___ AA
GAM1580  CBX6     3'  CCCCACCCTTGCCCCCAGCCC  27409    A  _  AGT    C_   C
                                GG GC GG   GGGT  GGG GGGG
                                || || ||   ||||  ||| ||||
                                CC CG CC   CCCG  CCC CCCC
                                 _  A  ___    TT   A
GAM1580  CDC42BPB  3'  CCCCGCCCCGCCCTGCCC    21239    A   GAGT    C
                                GG GCG    GGGT GGGCGGGG
                                || |||    |||| ||||||||
                                CC CGT    CCCG CCCGCCCC
                                 _  ____    C
GAM1580  CDC42BPB  3'  GCCCCGCCCTGCCCCCCCC    21240    AGT    C
                                GG   GGGT GGGCGGGGC
                                ||   |||| |||||||||
                                CC   CCCG CCCGCCCCG
                                 CCC    T
GAM1580  CECR2     5'  GCCCCGCGTCCGGCCCCTCCGC 49433    A     T      __
              CC                  GG GCGGAG GGGTCGG  GCGGGGC
                                || |||||| |||||||  |||||||
                                CC CGCCTC CCCGGCC  CGCCCCG
                                 _     _       TG
GAM1580  CENTA1    3'  GCCCCGCCCTCCCCCCACCTCC 23444      C_  AGT   TC
                                GGAG  GG   GGG  GGGCGGGGC
                                ||||  ||   |||  |||||||||
                                CCTC  CC   CCC  CCCGCCCCG
                                  CA  ___   CT
GAM1580  CENTG2    3'  GCCCACCCACTCTCACCC    30538    AGC       C
                                GG   GGAGTGGGT GGGC
                                ||   ||||||||| ||||
                                CC   TCTCACCCA CCCG
                                 CAC       _
GAM1580  CLSTN1    3'  CCCCGCCCAGCCCCGCCCC   30786    A   AGTG   C
                                GG GCGG    GGT GGGCGGGG
                                || ||||    ||| ||||||||
                                CC CGCC    CCG CCCGCCCC
                                 C   ____   A
GAM1580  CPLX1     3'  GCCCCGCGGAGCCCCCGCCC   22823    A   AGT    CGG
                                GG GCGG   GGGT   GCGGGGC
                                || ||||   ||||   |||||||
                                CC CGCC   CCCG   CGCCCCG
                                 _   ___    AGG
GAM1580  DDX8      3'  GCCCCACTTCCCACCCCGTCTC 18231      _   A    TC   C
              C                   GGAG CGG GTGGG  GGG GGGGC
                                |||| ||| |||||  ||| |||||
```

```
                                  CCTC GCC CACCC  TTC CCCCG
                                    T  C    __  A
GAM1580  DGKD     3'  CGGGCGACCCATCCCACTCC  60103     C  AG     GG
                                  GGAG GG  TGGGTCG  CG
                                  |||| ||  |||||||  ||
                                  CCTC CC  ACCCAGC  GC
                                    A  CT     GG
GAM1580  dJ309H15.1 3'  CCCCACCCCACCCCCGCCC   57567    A   AGT   C  C
                                  GG GCGG   GGGT GGG GGGG
                                  || ||||   |||| ||| ||||
                                  CC CGCC   CCCA CCC CCCC
                                   _   ___   C  A
GAM1580  DKFZP434J037 3'  CCCCCCCACACTCCACTCC    48944     C     GGTC  C
                                  GGAG GGAGTG    GGG GGG
                                  |||| ||||||    ||| |||
                                  CCTC CCTCAC    CCC CCC
                                    A     A___   _
GAM1580  DKFZP434P0111 3'  CCCCACCCCACTCCATCC    67954     GC       TCGG C
                                  GGA  GGAGTGGG    G GGGG
                                  |||  ||||||||    | ||||
                                  CCT  CCTCACCC    C CCCC
                                   A_       _____ A
GAM1580  DKFZp434P0531 3'  GCCCCACCCCACCCCCACTCC  93827     C  AGT   C  C
                                  GGAG GG   GGGT GGG GGGGC
                                  |||| ||   |||| ||| |||||
                                  CCTC CC   CCCA CCC CCCCG
                                    A ___    C  A
GAM1580  DKFZP564C196 3'  CCCCACCCGCGTACTCCCTCC  70602     C     G T   C
                                  GGAG GGAGTG G CGGG GGGG
                                  |||| |||||| | |||| ||||
                                  CCTC CCTCAT C GCCC CCCC
                                    _     G _   A
GAM1580  DKFZP564C196 3'  GCCCCCAATCACCCGCCCCGCC 70603    A   A     C  GC_
            C                      GG GCGG GTGGGT GG   GGGGC
                                  || |||| |||||| ||   |||||
                                  CC CGCC CGCCCA CT   CCCCG
                                   _   C     _ AAC
GAM1580  DKFZp762K222 5'  CCCCGCCCGCCCCCTCC     71667     T  T
                                  GGAG GGG CGGGCGGGG
                                  |||| ||| |||||||||
                                  CCTC CCC GCCCGCCCC
                                    _  C
GAM1580  EFNA5    3'  CCCCACCCCGCCCCACCCC   10485    A   T   C_
                                  GG GTGGG CGGG  GGGG
                                  || ||||| ||||  ||||
                                  CC CACCC GCCC  CCCC
                                   C    C   CA
GAM1580  EFNA5    3'  CCCCGCCCCACCCCCAGCCC   10486    A _ AGT   C
                                  GG GC GG   GGGT GGGCGGGG
                                  || || ||   |||| ||||||||
```

```
                                CC CG CC   CCCA CCCGCCCC
                                 _ A ___    C
GAM1580 EFS2     5' CCCCGGCCCGCCCCGCTCC   20770        T    _
                                GGAGTGGG CGGGC GGGG
                                |||||||| ||||| ||||
                                CCTCGCCC GCCCG CCCC
                                     C    G
GAM1580 EPB41L1  5' CCCCGCGCCGCCCCGCCC    71105    A    T  _
                                GG GTGGG CGG GCGGGG
                                || ||||| ||| ||||||
                                CC CGCCC GCC CGCCCC
                                 _    C  G
GAM1580 FBXO26   3' CCCCTGATTTCCCACTCC    46626        ___    C
                                GGAGTGGG   TCGGG GG
                                ||||||||   ||||| ||
                                CCTCACCC   AGTCC CC
                                     TTT    _
GAM1580 FLJ10110 5' CCCCGCCCTACCCCCTCC    36300     T   C
                                GGAG GGGT GGGCGGGG
                                |||| |||| ||||||||
                                CCTC CCCA CCCGCCCC
                                  C   T
GAM1580 FLJ11743 5' GCCTGGGACCCCTCCGCCC   44843    A     T    __
                                GG GCGGAG GGGTC  GGGC
                                || |||||| |||||  ||||
                                CC CGCCTC CCCAG  TCCG
                                 _     _    GG
GAM1580 FLJ14154 3' CCCCACCCTGCCCCACACC   46227    A    T _  C
                                GG GTGGG C GGG GGGG
                                || ||||| | ||| ||||
                                CC CACCC G CCC CCCC
                                 A    C T  A
GAM1580 FLJ14249 5' GCCCCGCCCGGAGTCCCCGCCG 42643     AGT   ___
             C                   GCGG   GGG   TCGGGCGGGGC
                                ||||   |||   ||||||||||
                                CGCC   CCC   GGCCCGCCCCG
                                  GC_   TGA
GAM1580 FLJ20359 3' GCCCCGCCCACTCTCCCACCCC 35516    C  A    TC___
             T                   AG GG GTGGG    GGGCGGGGC
                                || || |||||    |||||||||
                                TC CC CACCC    CCCGCCCCG
                                 _ _    TCTCA
GAM1580 FLJ21125 3' GCCCCACCCTCTCTGCTCC   45225        T   C
                                GGAGCGGAG GGGT GGGC
                                ||||||||| |||| ||||
                                CCTCGTCTC CCCA CCCG
                                     T   C
GAM1580 FLJ21162 3' CCCCCTACCCACCCACTCC   46370        C  C__
                                GGAGTGGGT GGG   GGGG
                                ||||||||| |||   ||||
```

```
                                CCTCACCCA CCC   CCCC
                                     _  ATC
GAM1580  FLJ21438  3'  GCCCCACCCTGGCCCCGCCCC  62195    A   AGTG   _  C
                                GG GCGG   GGTC GGG GGGGC
                                || ||||   |||| ||| |||||
                                CC CGCC   CCGG CCC CCCCG
                                 C   ____   T  A
GAM1580  GDBR1    5'  GCCCCGCCCCCTCCCCGCCCGC 32947     A    TC__
                                GCGG GTGGG   GGGCGGGGC
                                |||| |||||   |||||||||
                                CGCC CGCCC   CCCGCCCCG
                                  _   CTCC
GAM1580  GGA2     3'  GCCCCGCCCGACCAGGAGGCCC 57671    A  GGAGTG
                                GG GC     GGTCGGGCGGGGC
                                || ||     ||||||||||||
                                CC CG     CCAGCCCGCCCCG
                                 _ GAGGA_
GAM1580  HCGIV.9  5'  GCCCCGCCCACCGAGCCCCGCC 39133    A   A  G_  C
             C                   GG GCGG GT  GGT GGGCGGGGC
                                || |||| ||  ||| |||||||||
                                CC CGCC CG  CCA CCCGCCCCG
                                 _   C  AG  _
GAM1580  HEYL     3'  GCCCCTTCACCACCCCGCCC  28128    A   A   GTC  C
                                GG GCGG GTGG   GGG GGGGC
                                || |||| ||||   ||| |||||
                                CC CGCC CACC   CTT CCCCG
                                 _   C   A__  _
GAM1580  HSPBAP1  5'  CCCCACCCCAGCTCCGCTCC  45156         GGGTC  C
                                GGAGCGGAGT    GGG GGGG
                                ||||||||||    ||| ||||
                                CCTCGCCTCG    CCC CCCC
                                     AC___   A
GAM1580  INSM2    5'  GCCCCGCCCCCGGCGCCCGCTC 51856        A_  G  TC
             C                   GGAGCGG  GT GG  GGGCGGGGC
                                |||||||  || ||  |||||||||
                                CCTCGCC  CG CC  CCCGCCCCG
                                    CG  G  __
GAM1580  KHSRP    3'  CCCCGCCCGTCCCCCCTCC   14879     C  AGT   T
                                GGAG GG   GGG CGGGCGGGG
                                |||| ||   ||| |||||||||
                                CCTC CC   CCC GCCCGCCCC
                                  _ ___   T
GAM1580  KIAA0152 3'  CCCCTTCCATGTCCCACCCCAC 28971     C  A    T __  C
             TCC                  GGAG GG GTGGG C  GGG GGGG
                                |||| || ||||| |  ||| ||||
                                CCTC CC CACCC G  CCT CCCC
                                  A  C    T TA   T
GAM1580  KIAA0240 3'  CCCCGCCCCGAGACCCCACCCC 94037     A    _ ___
             G                   CGG GTGGG TC   GGGCGGGG
                                ||| ||||| ||   ||||||||
```

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                                GCC CACCC AG   CCCGCCCC
                                  C    C  AGC
GAM1580 KIAA0415 3' CCCCGCCCACCTCCCCTCC   94159     C  AGT   C
                                GGAG GG   GGGT GGGCGGGG
                                |||| ||   |||| ||||||||
                                CCTC CC   TCCA CCCGCCCC
                                  _  C__   _
GAM1580 KIAA0450 3' GCCCCACACCACCCTGCCC   28358    A   A   _ C
                                GG GCGG GTGG GT GGGC
                                || |||| |||| || ||||
                                CC CGTC CACC CA CCCG
                                 _   C   A C
GAM1580 KIAA0545 3' GCCCCTGCCCCCACCCTCACC  63844    AGC  A    TCG  _
                                GG   GG GTGGG   GGC GGGGC
                                ||   || |||||   ||| |||||
                                CC   CC CACCC   CCG CCCCG
                                 ACT  _    ____   T
GAM1580 KIAA0561 5' CCCCGCCTCCGACCCCGCTCT  66468       A  G  TC
                                GGAGCGG GT GG  GGGCGGGG
                                ||||||| || ||  ||||||||
                                TCTCGCC CA CC  TCCGCCCC
                                   C  G  __
GAM1580 KIAA0861 3' CCCCATCCTCCACCCCGCCCC  90344    A   A    TC  GC
                                GG GCGG GTGGG  GG  GGGG
                                || |||| |||||  ||  ||||
                                CC CGCC CACCT  CC  CCCC
                                 C   C    __ TA
GAM1580 KIAA1029 3' GCCCCACCCCCGACCCCACCCC 24429    A    _    C__
            G                    CGG GTGGG TCGGG   GGGGC
                                ||| ||||| |||||   |||||
                                GCC CACCC AGCCC   CCCCG
                                  C    C    CCA
GAM1580 KIAA1140 5' CCCCGCCCGCGAGTGCGCCC   63442    A   GAGTGG T
                                GG GCG     G CGGGCGGGGG
                                || |||     | ||||||||||
                                CC CGC     C GCCCGCCCC
                                 _  GTGAG_ _
GAM1580 KIAA1184 3' GCCCCCAGCCCAGCCCACTCC  42931        C   __
                                GGAGTGGGT GGGC  GGGGC
                                ||||||||| ||||  |||||
                                CCTCACCCG CCCG  CCCCG
                                     A   AC
GAM1580 KIAA1465 3' CCCCGCCCCACCCGCCC     61488    A     C
                                GG GTGGGT GGGCGGGG
                                || |||||| ||||||||
                                CC CGCCCA CCCGCCCC
                                 _     C
GAM1580 KIAA1762 3' CCCCACCCCCTGGCCCCGCCC  64530    A   A  G  TC   C
                                GG GCGG GT GG  GGG GGGG
                                || |||| || ||  ||| ||||
```

```
                                CC CGCC CG TC  CCC CCCC
                                 _   C  G  C_  A
GAM1580 LIECG3   3' GCCCCACTACCCCACCCCACTC 88801     C  A    TC  GC
             C                   GGAG GG GTGGG  GG  GGGGC
                                 |||| || |||||  ||  |||||
                                 CCTC CC CACCC  TC  CCCCG
                                   A  C    CA  A_
GAM1580 LRN      3' CCTCTGACCCACCCAGCCC   11354    A _ A       C
                                 GG GC GG GTGGGTCGGG GG
                                 || || || |||||||||| ||
                                 CC CG CC CACCCAGTCT CC
                                  _ A  _       _
GAM1580 MGC10882 3' GCCCCCACCCCATCCCACTCC  52030       TC   C__
                                 GGAGTGGG  GGG   GGGGC
                                 ||||||||  |||   |||||
                                 CCTCACCC  CCC   CCCCG
                                      TA   CAC
GAM1580 MGC10966 5' GCCCCAGCCGCCACCCGACCC  49685    AG   A   GTCG  _
                                 GG  CGG GTGG    GGC GGGGC
                                 ||  ||| ||||    ||| |||||
                                 CC  GCC CACC    CCG CCCCG
                                  CA  _   G___   A
GAM1580 N4BP3    3' GCCCCACCCTCTACCCCATTCC 66854        TC___   C
                                 GGAGTGGG    GGG GGGGC
                                 ||||||||    ||| |||||
                                 CCTTACCC    CCC CCCCG
                                      CATCT   A
GAM1580 NR5A1    3' GCCCCGCCCCCTCCCTGCTCC  18275       AGT   TC
                                 GGAGCGG   GGG  GGGCGGGGC
                                 |||||||   |||  |||||||||
                                 CCTCGTC   CCT  CCCGCCCCG
                                      ___   CC
GAM1580 PIGPC1   5' GCTCCTCCGACCCGCTCCGCTC 42350              C
             C                   GGAGCGGAGTGGGTCGGG GGGGC
                                 |||||||||||||||| |||||
                                 CCTCGCCTCGCCCAGCCT CCTCG
                                                  _
GAM1580 PNKP     3' CCCCGCCCAGCTCCCCTCC   24376     C    GGGTC
                                 GGAG GGAGT    GGGCGGGG
                                 |||| |||||    ||||||||
                                 CCTC CCTCG    CCCGCCCC
                                   C    A____
GAM1580 PRIC285  3' CCCCGCCCCACCCCACCCC   62112    A    TC_
                                 GG GTGGG   GGGCGGGG
                                 || |||||   ||||||||
                                 CC CACCC   CCCGCCCC
                                  C    CAC
GAM1580 PRIC285  3' GCCAGGGGCCCACCCCGCCC  62116    A   A     G__
                                 GG GCGG GTGGGTC   GGC
                                 || |||| |||||||   |||
```

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                                CC CGCC CACCCGG   CCG
                                 _   C      GGA
GAM1580  PRKCZ    5'  GCCCCACCTGGAGCCCCCGCCC 72167    A   AGT   __   C
                                GG GCGG   GGGT  CGGG GGGGC
                                || ||||   ||||  |||| |||||
                                CC CGCC   CCCG  GTCC CCCCG
                                 _   ___   AG   A
GAM1580  PRO0899  3'  CCCCACCCAGCCCACTCCG   38307         C   C
                                CGGAGTGGGT GGG GGGG
                                |||||||||| ||| ||||
                                GCCTCACCCG CCC CCCC
                                      A   A
GAM1580  REG-IV   3'  CCCCACCCCAGCCACTCAACTC 50217     CG     GTC   C
             C                   GGAG  GAGTGG   GGG GGGG
                                ||||  ||||||   ||| ||||
                                CCTC  CTCACC   CCC CCCC
                                  AA     GAC   A
GAM1580  RHO6     3'  CCCCAGTGCCCCCCCCCGCTCC  27874        TC   ___
                                GGAGTGGG  GGGC   GGGG
                                ||||||||  ||||   ||||
                                CCTCGCCC  CCCG   CCCC
                                     CC    TGA
GAM1580  SBBI54   3'  GCCCCGCCCCCTCCCCACACC  57174    A    TC__
                                GG GTGGG    GGGCGGGGC
                                || |||||    |||||||||
                                CC CACCC    CCCGCCCCG
                                 A    CTCC
GAM1580  SEMA3C   5'  CCCCGCCCGGTCCGCCCC    22103    A   GT
                                GG GTGG  CGGGCGGGG
                                || ||||  |||||||||
                                CC CGCC  GCCCGCCCC
                                 C   TG
GAM1580  SHANK3   3'  GCCCCACCCCCACTCCCGCCC  66109    A   _     TCG  C
                                GG GCGG AGTGGG   GG GGGGC
                                || |||| ||||||   || |||||
                                CC CGCC TCACCC   CC CCCCG
                                 _   C      ___  A
GAM1580  SHAPY    3'  CCCCGACCCCCACCCTCACTCC 57906      C__  A    TC  G
                                GGAG   GG GTGGG  GG CGGGG
                                ||||   || |||||  || |||||
                                CCTC   CC CACCC  CC GCCCC
                                  ACT  _    __  A
GAM1580  SLC5A7   5'  CCCGACCCACCCCGCACC    41804    A   A
                                GG GCGG GTGGGTCGGG
                                || |||| ||||||||||
                                CC CGCC CACCCAGCCC
                                 A   C
GAM1580  STAG3    3'  GCCCCTCCCCAGCTCCACTCC  25854      C    GGGTC   C
                                GGAG GGAGT    GGG GGGGC
                                |||| |||||    ||| |||||
```

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                                CCTC CCTCG    CCC CCCCG
                                  A    AC___   T
GAM1580  STK39    3'  GCCCCACCGCCACCCCTACTCC 26011        TCG  ___
                                GGAGTGGG  GGC  GGGGC
                                ||||||||  |||  |||||
                                CCTCATCC  CCG  CCCCG
                                    CCA  CCA
GAM1580  TBC1D1   5'  CCCCGCCCCAACCCGCCC    65288    A    C_
                                GG GTGGGT  GGGCGGGG
                                || ||||||  ||||||||
                                CC CGCCCA  CCCGCCCC
                                 _    AC
GAM1580  TLN1     3'  CCCCAGCCCACTCCACCC    21903    A   _ C   _
                                GG GTGG GT GGGC GGGG
                                || |||| || |||| ||||
                                CC CACC CA CCCG CCCC
                                 _   T _   A
GAM1580  TOB2     3'  CCCCACCCACTCCATCC     33235     GC       C
                                GGA  GGAGTGGGT GGG
                                |||  |||||||||| |||
                                CCT  CCTCACCCA CCC
                                  A_       C
GAM1580  YKT6     3'  GCCCCACCCACAGATCCCCTGC 22640        AGT    ___  C
           TCC                    GGAGCGG   GGGTC   GGG GGGGC
                                |||||||   |||||   ||| |||||
                                CCTCGTC   CCTAG   CCC CCCCG
                                    C__    ACA   A
GAM1580  ZNF213   3'  GCCCCACTCGGCGCCCCACTCC 65698         ___    C
                                GGAGTGGG   TCGGG GGGGC
                                ||||||||   ||||| |||||
                                CCTCACCC   GGCTC CCCCG
                                    CGC    A
GAM1580  LOC124987 5'  GCCCCACCGCCCTCGCCCCGCC 76165    A   A  _ T  GC
           C                     GG GCGG GTG GG CGG  GGGGC
                                || |||| ||| || |||  |||||
                                CC CGCC CGC CC GCC  CCCCG
                                 _   C  T  C   A_
GAM1580  LOC129138 3'  CCCCACCCTGCCCCACTGC   57922     AGT   C   C
                                GCGG   GGGT GGG GGGG
                                ||||   |||| ||| ||||
                                CGTC   CCCG CCC CCCC
                                  AC_   T   A
GAM1580  LOC136015 5'  CCCCGCCCCGCCCCACCC    76703    A    T   _
                                GG GTGGG CGGG CGGGG
                                || ||||| |||| |||||
                                CC CACCC GCCC GCCCC
                                 _    C   C
GAM1580  LOC137492 5'  CGGACGTCCCACCCCGCTCC   75792       A    T  GG
                                GGAGCGG GTGGG CG  CG
                                ||||||| ||||| ||  ||
```

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                                CCTCGCC CACCC GC  GC
                                    C    T  AG
GAM1580  LOC145468 3'  GCCCCGCCCACTTTCCCACCTC 74253     CGGA    TC___
             C                   GGAG   GTGGG    GGGCGGGGC
                                 ||||   |||||    |||||||||
                                 CCTC   CACCC    CCCGCCCCG
                                   ____    TTTCA
GAM1580  LOC145988 5'  GCCCCGCCTCCCTCCCCACCC  78068    A    TC___
                                 GG GTGGG    GGGCGGGGC
                                 || |||||    |||||||||
                                 CC CACCC    TCCGCCCCG
                                  _    CTCCC
GAM1580  LOC146562 3'  CCCCACCCGACCCCACTCC   58253        _    C
                                 GGAGTGGG TCGGG GGGG
                                 |||||||| ||||| ||||
                                 CCTCACCC AGCCC CCCC
                                      C    A
GAM1580  LOC147958 3'  GCCCCACGCACTCGGCCC    88524    A  G    G  C
                                 GG GC GAGTG GT GGGC
                                 || || ||||| || ||||
                                 CC CG CTCAC CA CCCG
                                  _ G    G  C
GAM1580  LOC149668 3'  GCCCCACCCTTGTCTCCACCTC 85700     C_   TGGGTC   C
             C                   GGAG  GGAG     GGG GGGGC
                                 ||||  ||||     ||| |||||
                                 CCTC  CCTC     CCC CCCCG
                                   CA   TGTT__   A
GAM1580  LOC150155 3'  GCCCCGCCCACTTTCCCACCTC 71412     CGGA    TC___
             C                   GGAG   GTGGG    GGGCGGGGC
                                 ||||   |||||    |||||||||
                                 CCTC   CACCC    CCCGCCCCG
                                   ____    TTTCA
GAM1580  LOC151521 3'  CCCCACCCCCACACTTCCACTC 86622     C  _  _ TC   C
             C                   GGAG GGA GTG GG  GGG GGGG
                                 |||| ||| ||| ||  ||| ||||
                                 CCTC CCT CAC CC  CCC CCCC
                                   A  T   A __   A
GAM1580  LOC157349 5'  GCCCCTGCCCCCACCCGCACC  82342    A   A    TCG  _
                                 GG GCGG GTGGG   GGC GGGGC
                                 || |||| |||||   ||| |||||
                                 CC CGCC CACCC   CCG CCCCG
                                  A   _    ___   T
GAM1580  LOC164633 3'  GCCCCACCCTGTCCCCACCC   83424    A    TC__   C
                                 GG GTGGG    GGG GGGGC
                                 || |||||    ||| |||||
                                 CC CACCC    CCC CCCCG
                                  _    CTGT   A
GAM1580  LOC201229 3'  GCCCCGCCCCCTCCTCTGCTCC 89519         TG  TC
                                 GGAGCGGAG  GG  GGGCGGGGC
                                 |||||||||  ||  |||||||||
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                                CCTCGTCTC  CC  CCCGCCCCG
                                     CT  __
GAM1580  LOC207043 3'  GCCCCGCCCACAGTGCCCGGCT 91077      _  A   G_  C
              CC                    GGAGC GG GTG  GT GGGCGGGGC
                                    ||||| || |||  || |||||||||
                                    CCTCG CC CGT  CA CCCGCCCCG
                                      G  _   GA  _
GAM1580  LOC220776 3'  CCCCGCCCCTCCCCACCC    68923    A    TC_
                                    GG GTGGG   GGGCGGGG
                                    || |||||   ||||||||
                                    CC CACCC   CCCGCCCC
                                     _    CTC
GAM1580  LOC221424 5'  CCCCCGGCCCCACTCCGCCC   95267    A       _    C
                                    GG GCGGAGTGGG TCGGG GG
                                    || |||||||||| ||||| ||
                                    CC CGCCTCACCC GGCCC CC
                                     _        C    _
GAM1580  LOC253181 5'  CCCCTGCCCACCCAGCTCC    99415      GGAG    C   _
                                    GGAGC    TGGGT GGGC GGGG
                                    |||||    ||||| |||| ||||
                                    CCTCG    ACCCA CCCG CCCC
                                       ____    _   T
GAM1580  LOC253822 5'  GCCCCGCCCGTCGGCCTCGCTC 96585       GA  G  T
              C                     GGAGCG  GT GG CGGGCGGGGC
                                    ||||||  || || ||||||||||
                                    CCTCGC  CG CT GCCCGCCCCG
                                       TC  G  _
GAM1580  LOC254532 5'  CCCCACCCCGCCCCTCC     98450      T   C   C
                                    GGAG GGGT GGG GGGG
                                    |||| |||| ||| ||||
                                    CCTC CCCG CCC CCCC
                                      _   C   A
GAM1580  LOC254532 5'  GCCAGCTTGCCCCACCCCGCCC 98455    A   A    T    GG
                                    GG GCGG GTGGG CGGGC  GGC
                                    || |||| ||||| |||||  |||
                                    CC CGCC CACCC GTTCG  CCG
                                     _   C    C    A_
GAM1580  LOC254552 5'  CCCCGCCCCGCCTCGCCC    96423    A   GAGT    C
                                    GG GCG    GGGT GGGCGGGG
                                    || |||    |||| ||||||||
                                    CC CGC    TCCG CCCGCCCC
                                     _  ____    C
GAM1580  LOC51308  3'  GCCCCGCCCTGCCCCACCC    33968    A    T _
                                    GG GTGGG C GGGCGGGGC
                                    || ||||| | |||||||||
                                    CC CACCC G CCCGCCCCG
                                     _    C T
GAM1580  LOC91517  3'  GCCCCCAGCCCACCCCTGCCC  66912    A   AGT    C   __
                                    GG GCGG   GGGT GGGC  GGGGC
                                    || ||||   |||| ||||  |||||
```

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                                CC CGTC   CCCA CCCG  CCCCG
                                 _   ___   _   AC
GAM1580  LOC95633  3'  GCCCCACCTTGGCCCCCACCC  60559    A __    _ C
                                GG GT  GGGTCG GG GGGGC
                                || ||  |||||| || |||||
                                CC CA  CCCGGT CC CCCCG
                                 _ CC     T  A
GAM1581  ADAMTS8   3'  GGTGACTGGGTCCCTTGGC   23854         GGAA
                                GTCAAGGGAT   AGTCACC
                                ||||||||||   |||||||
                                CGGTTCCCTG   TCAGTGG
                                      GG__
GAM1581  AXIN1     3'  GGTGACCCCCCCCCCATCCCCCG 61543     AA      AAA___
               GC                   GTC  GGGATGG     GTCACC
                                ||| |||||||     ||||||
                                CGG  CCCTACC     CAGTGG
                                  CC      CCCCCC
GAM1581  CLPS      3'  GGCTGGCCACCTCCTTGAC   10214       _ A   AA
                                GTCAAGG G TGG  AGTC
                                ||||||| | |||  ||||
                                CAGTTCC C ACC  TCGG
                                    T C   GG
GAM1581  DLG5      3'  GGTGACTTTGGCATTCTT    83820       G_
                                AGGGATG  AAAGTCACC
                                |||||||  |||||||||
                                TTCTTAC  TTTCAGTGG
                                    GG
GAM1581  EN2       3'  GGGACCCTCCTTTTGGC     9262         AT  AAA   A
                                GTCAAGGG  GG   GTC CC
                                ||||||||  ||   ||| ||
                                CGGTTTTC  CC   CAG GG
                                    CT  ___   C
GAM1581  ENC1      3'  GTGACTTTAAACTTTCCCTTGG 14650         T  ___
               C                    GTCAAGGGA GG   AAAGTCAC
                                ||||||||| ||   ||||||||
                                CGGTTCCCT TC   TTTCAGTG
                                     T  AAA
GAM1581  FOSB      3'  ACTTCTCCCACCCCTTGGC    23052        A   A__
                                GTCAAGGG TGG   AAGT
                                |||||||| |||   ||||
                                CGGTTCCC ACC   TTCA
                                    C   CTC
GAM1581  FTH1      3'  GGTGACTTCCCTGGTCACC    68714    _   __  A
                                GG GAT  GG AAGTCACC
                                || |||  || ||||||||
                                CC CTG  CC TTCAGTGG
                                 A   GT  C
GAM1581  GPR56     5'  GGTGACTTCCAAGAGTGAC    20275      AGGGA    A
                                GTCA    TGGAA GTCACC
                                ||||    ||||| ||||||
```

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                                CAGT    ACCTT CAGTGG
                                  GAGA_   _
GAM1581 GRINL1A  3' GGTGACTTTCATGTGCTTGA  70063      GGATG
                                TCAAG    GAAAGTCACC
                                |||||    ||||||||||
                                AGTTC    CTTTCAGTGG
                                   GTGTA
GAM1581 KNG      5' GGTTGAAACCATCCCTCAGC  7984     CA      AAAG  _
                                GT  AGGGATGG    TCA CC
                                ||  ||||||||    ||| ||
                                CG  TCCCTACC    AGT GG
                                 AC       AA__   T
GAM1581 NUMB     3' GGTGAGAACATCCCCTTGAC  14980        _  GAAAG
                                GTCAAGGG ATG    TCACC
                                |||||||| |||    |||||
                                CAGTTCCC TAC    AGTGG
                                     C   AAG__
GAM1581 OXCT     3' TGACTTTATATTCTTGAT    6490        G   G
                                GTCAAGG ATG AAAGTCA
                                ||||||| ||| |||||||
                                TAGTTCT TAT TTTCAGT
                                   _   A
GAM1581 PCDH1    3' TGACTGGGCTCCTTCCCTTGAC 51580        T   A___
                                GTCAAGGGA GGA    AGTCA
                                ||||||||| |||    |||||
                                CAGTTCCCT CCT    TCAGT
                                     T   CGGG
GAM1581 PFKFB4   3' GGTGACTTTTGTCACCTGGAC  17089     A  _  TG   A
                                GTC AGG GA  GAA GTCACC
                                ||| ||| ||  ||| ||||||
                                CAG TCC CT  TTT CAGTGG
                                  G   A  GT   _
GAM1581 PXF      3' GGTGAACCCAGCCCCTGAC   12655     A   A   AAAG
                                GTCA GGG TGG    TCACC
                                |||| ||| |||    |||||
                                CAGT CCC ACC    AGTGG
                                  C   G   CA__
GAM1581 RAB38    3' TGACCTCCATTCTCGGC     60927     AA      AA
                                GTC  GGGATGGA  GTCA
                                |||  ||||||||  ||||
                                CGG  TCTTACCT  CAGT
                                  C_       C_
GAM1581 WHSC1L1  5' GGCGACCCCCGTCCCTCGGC  35502     A      AAA   A
                                GTC AGGGATGG   GTC CC
                                ||| ||||||||   ||| ||
                                CGG TCCCTGCC   CAG GG
                                  C       CC_   C
GAM1581 ZK1      3' GTACAGTCATCCCTTGAT    20576          AAA  C
                                GTCAAGGGATGG   GT AC
                                ||||||||||||   || ||
```

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                                TAGTTCCCTACT   CA TG
                                      GA_ _
GAM1581 ZNF180   3' GACTTTTCAACCTGGC      26044      A  GA
                                GTCA GG  TGGAAAGTC
                                |||| ||  |||||||||
                                CGGT CC  ACTTTTCAG
                                  _ A_
GAM1581 C16orf5  3' GGCGACCTCTGGCCCTGGC   26353      A   AT   AA   A
                                GTCA GGG  GGA  GTC CC
                                |||| |||  |||  ||| ||
                                CGGT CCC  TCT  CAG GG
                                  _  GG   C_   C
GAM1581 C20orf72 3' GGTGACTCTTGTACTCCCTTGA 54606         _ G  _
                                TCAAGGGA TG AA AGTCACC
                                |||||||| || || |||||||
                                AGTTCCCT AT TT TCAGTGG
                                     C  G  C
GAM1581 CALN1    3' GGTGACTTGCACCCTGGC    49669      A   A  GA
                                GTCA GGG TG  AAGTCACC
                                |||| ||| ||  ||||||||
                                CGGT CCC AC  TTCAGTGG
                                  _  _ G_
GAM1581 FLJ10535 3' GATTGTCTCCATCTCTTGAC  36749           A__
                                GTCAAGGGATGGA   AGTC
                                ||||||||||||   ||||
                                CAGTTCTCTACCT   TTAG
                                       CTG
GAM1581 FLJ10726 3' GGTGCCCTATCCCTTAAC    37043    C       AAA T
                                GT AAGGGATGG   G CACC
                                || |||||||||   | ||||
                                CA TTCCCTATC   C GTGG
                                 A        C__ _
GAM1581 KIAA0453 3' GCTACCCAGTCCCTTGAC    69607         _  AA
                                GTCAAGGGA TGG  AGT
                                ||||||||| |||  |||
                                CAGTTCCCT ACC  TCG
                                     G   CA
GAM1581 KIAA1671 3' GGTGACCTTTGCCCCTTGGC  66286        AT   AA
                                GTCAAGGG  GGA  GTCACC
                                ||||||||  |||  ||||||
                                CGGTTCCC  TTT  CAGTGG
                                     CG   C_
GAM1581 KIAA1691 3' ACTACTCCATCCCATGAC    94121      A      A_
                                GTCA GGGATGGA  AGT
                                |||| ||||||||  |||
                                CAGT CCCTACCT  TCA
                                  A       CA
GAM1581 KIAA1755 5' GGTACCCTCCATCCCTCGAC  62019     A       AA  C
                                GTC AGGGATGGA  GT ACC
                                ||| |||||||||  || |||
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                                CAG TCCCTACCT  CA TGG
                                  C        CC  _
GAM1581  LMOD1    3'  GGTGCTGCCACCCCTTGGC   25104        A   AA  T
                                GTCAAGGG TGG  AG CACC
                                |||||||| |||  || ||||
                                CGGTTCCC ACC  TC GTGG
                                    C   G_  _
GAM1581  MAFB     3'  GGCTTAGCCATCCCTGAC    19592      A      A_
                                GTCA GGGATGG  AAGTC
                                |||| |||||||  |||||
                                CAGT CCCTACC  TTCGG
                                  _      GA
GAM1581  MG61     3'  GACCCCCTCCATCCTTGAC   43380        G     AA__
                                GTCAAGG ATGGA   GTC
                                ||||||| |||||   |||
                                CAGTTCC TACCT   CAG
                                    _   CCCC
GAM1581  N4BP3    3'  GATAACCCATCCCCCTTGGC  66851       __      AAA
                                GTCAA  GGGATGG  GTC
                                |||||  |||||||  |||
                                CGGTT  CCCTACC  TAG
                                   CC      CAA
GAM1581  SARM     3'  GGTGACTCCTAGTTCTTGGC  31300        AT_  AA
                                GTCAAGGG  GGA  GTCACC
                                ||||||||  |||  ||||||
                                CGGTTCTT  CCT  CAGTGG
                                    GAT  __
GAM1581  SLC5A7   3'  ACTTCAGTCACTCCCTTGA   41801        _  A__
                                TCAAGGGA TGG  AAGT
                                |||||||| |||  ||||
                                AGTTCCCT ACT  TTCA
                                    C  GAC
GAM1581  SNAP91   3'  GTGTTCTTCCATCCTTCAAC  29938    CA        AGT
                                GT  AGGGATGGAA  CAC
                                ||  ||||||||||  |||
                                CA  TTCCTACCTT  GTG
                                 AC        CTT
GAM1581  SRPK2    3'  GGTGACTCTCATTCTTTAAC  13413    C       AA
                                GT AAGGGATGG  AGTCACC
                                || |||||||||  |||||||
                                CA TTTCTTACT  TCAGTGG
                                 A       C_
GAM1581  ZNF282   3'  TGACTTTCCCTGCCCTTG    90698       AT_
                                CAAGGG  GGAAAGTCA
                                ||||||  |||||||||
                                GTTCCC  CCTTTCAGT
                                   GTC
GAM1581  ZNF304   3'  GGTAACTTTCAGTTTTTGGC  40682        ATG     C
                                GTCAAGGG  GAAAGT ACC
                                ||||||||  |||||| |||
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                                CGGTTTTT   CTTTCA TGG
                                    GA_     A
GAM1581  LOC115297 3'  TGACTTAGAACCATCCTTGAC  73262       G    A___
                                GTCAAGG ATGG    AAGTCA
                                ||||||| ||||    ||||||
                                CAGTTCC TACC    TTCAGT
                                   _    AAGA
GAM1581  LOC138855 3'  GGTGACTTCCCTGGTCACC    75893    _  __  A
                                GG GAT  GG AAGTCACC
                                || |||  || ||||||||
                                CC CTG  CC TTCAGTGG
                                 A   GT  C
GAM1581  LOC145231 3'  GGCTTGTCCATCCCTTGAC    84254          _
                                GTCAAGGGATGGA AAGTC
                                |||||||||||| |||||
                                CAGTTCCCTACCT TTCGG
                                       G
GAM1581  LOC148137 3'  GGCCTGCCCATCCCTGAC     59105      A      AA  _
                                GTCA GGGATGG  AG TC
                                |||| |||||||  || ||
                                CAGT CCCTACC  TC GG
                                  _      CG  C
GAM1581  LOC153020 3'  GGCAACTTCAACTCCTTGAT   81647       _ A    AA_
                                GTCAAGG G TGGA   GTC
                                ||||||| | ||||   |||
                                TAGTTCC C ACTT   CGG
                                    T A    CAA
GAM1581  LOC153565 3'  GGTGACTTCCCTGGTCACC    81758    _  __  A
                                GG GAT  GG AAGTCACC
                                || |||  || ||||||||
                                CC CTG  CC TTCAGTGG
                                 A   GT  C
GAM1581  LOC155435 3'  GGTGACTTTGGTAGCCCTTGA  82269       ATGG_
                                TCAAGGG     AAAGTCACC
                                |||||||     |||||||||
                                AGTTCCC     TTTCAGTGG
                                    GATGG
GAM1581  LOC162048 5'  GGTGAAGACGCCCTTGAC     83201        A  GAAAG
                                GTCAAGGG TG     TCACC
                                |||||||| ||     |||||
                                CAGTTCCC GC     AGTGG
                                    _  AGA__
GAM1581  LOC222865 3'  GGTTACCACCCCCTTGAC     94448        AT  AAA  C
                                GTCAAGGG  GG   GT ACC
                                ||||||||  ||   || |||
                                CAGTTCCC  CC   CA TGG
                                    __  AC_  T
GAM1581  LOC253336 3'  GTAACTTTCTTCATCCCTTGA  99180          __     C
                                TCAAGGGATG  GAAAGT AC
                                ||||||||||  |||||| ||
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                                AGTTCCCTAC  CTTTCA TG
                                      TT     A
GAM1581  LOC90576  3'  GTACAGTCATCCCTTGAT    64079          AAA  C
                                GTCAAGGGATGG   GT AC
                                ||||||||||||   || ||
                                TAGTTCCCTACT   CA TG
                                       GA_  _
GAM1581  LOC90917  3'  GTGACTTTAAATCCTGGC    64988     AG   GG
                                GTCA  GGAT  AAAGTCAC
                                ||||  ||||  ||||||||
                                CGGT  CCTA  TTTCAGTG
                                  __   AA
GAM1582  EPB41     5'  GGCCGAAAATTCACAGCACCA  16691     AT        ATAA
                                TGGT  CTGTGAATTTT   GCT
                                ||||  ||||||||||   |||
                                ACCA  GACACTTAAAA   CGG
                                  C_        GC__
GAM1582  ITGA2     3'  CTTAGATTAAAATTCACAGACA 11025     A         ___
              CTA                  TGGT TCTGTGAATTTTA   TAAG
                                ||||  ||||||||||||   ||||
                                ATCA AGACACTTAAAAT   ATTC
                                  C          TAG
GAM1582  KIAA1486  3'  CTTATAAAACACTGATGATACC 67974      T___   AA
                                GGTATC   GTG  TTTTATAAG
                                ||||||   |||  |||||||||
                                CCATAG   CAC  AAAATATTC
                                   TAGT  __
GAM1582  KIAA1804  3'  CTCTTCACAGATATCA     70348          TTTTATA
                                TGGTATCTGTGAA      AG
                                ||||||||||||      ||
                                ACTATAGACACTT      TC
                                       C_______
GAM1582  LOC129198 3'  AGCTTATCTTCACAGATGCCA  76612          TTTT
                                TGGTATCTGTGAA   ATAAGCT
                                ||||||||||||   |||||||
                                ACCGTAGACACTT   TATTCGA
                                       C___
GAM1582  LOC149372 5'  AGCTCTCCTTCACAGACACC   80097     A      TTTTATA
                                GGT TCTGTGAA      AGCT
                                ||| ||||||||      ||||
                                CCA AGACACTT      TCGA
                                  C       CCTC___
GAM1582  LOC157627 3'  GCTTAAACCACAGGTACCA   82419         AATTTTA
                                TGGTATCTGTG      TAAGC
                                ||||||||||      |||||
                                ACCATGGACAC      ATTCG
                                       CAA____
GAM1583  ALMS1     3'  GCTTATTCTTTGTCCATGTGTA 31365      CATCCCAA
                                TACAC       GAAGAATAAGC
                                |||||       ||||||||||
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                                ATGTG      TTTCTTATTCG
                                   TACCTG__
GAM1583  CCR9     3'  GCTTATTCCTTGGTATGGTG  22797      C    AA
                                CACCAT CCAAG  GAATAAGC
                                |||||| |||||  ||||||||
                                GTGGTA GGTTC  CTTATTCG
                                   T    __
GAM1583  CCR9     3'  GCTTATTCCTTGGTATGGTG  49125      C    AA
                                CACCAT CCAAG  GAATAAGC
                                |||||| |||||  ||||||||
                                GTGGTA GGTTC  CTTATTCG
                                   T    __
GAM1583  DIAPH2   3'  TCTGCTCTCGGGATGGTG    23013       A  __
                                CACCATCCC AGA  AGA
                                ||||||||| |||  |||
                                GTGGTAGGG TCT  TCT
                                      C   CG
GAM1583  GALNT3   3'  GCTTATTCCTCTTTTGGG    16827     __  A
                                CCCA  AGA GAATAAGC
                                ||||  ||| ||||||||
                                GGGT  TCT CTTATTCG
                                  TT   C
GAM1583  IL1F9    3'  GCTTTATTCCCTCTTGGGATG  39512        A_    _
                                CATCCCAAGA  GAATAA GC
                                ||||||||||  |||||| ||
                                GTAGGGTTCT  CTTATT CG
                                      CC     T
GAM1583  MKKS     5'  GCTCATACATTTGGGGTGGT  38750         AAGA  A
                                ACCATCCCAAG    AT AGC
                                ||||||||||    || |||
                                TGGTGGGGTTT    TA TCG
                                       ACA_  C
GAM1583  MLANA    3'  GTTCTCCTTTGGAATGGTGTA  19767       _  C   A
                                TACACCAT CC AAG AGAAT
                                |||||||| || ||| |||||
                                ATGTGGTA GG TTC TCTTG
                                     A  T   C
GAM1583  OGN      3'  GCTCATTCTTCTTTTATG    44590     CCC       A
                                CAT   AAGAAGAAT AGC
                                |||   |||||||||| |||
                                GTA   TTCTTCTTA TCG
                                  TT_       C
GAM1583  OGN      3'  GCTCATTCTTCTTTTATG    53399     CCC       A
                                CAT   AAGAAGAAT AGC
                                |||   |||||||||| |||
                                GTA   TTCTTCTTA TCG
                                  TT_       C
GAM1583  PRSS8    3'  CCATTCTTCTGGGTGTG     12420     CAT   A     AA
                                CAC   CCCA GAAGAAT  G
                                |||   |||| |||||||  |
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                                GTG   GGGT CTTCTTA  C
                                  T__   _      CC
GAM1583  TOP2B    3'  GCTTATTTTAATGTGATGATGT 8409      C    C  AGA
                A                  TACA CATC CA   AGAATAAGC
                                   |||| |||| ||   |||||||||
                                   ATGT GTAG GT   TTTTATTCG
                                     A   T  AA_
GAM1583  BRD4     3'  GCTTATCTCCGAAATGGTGTG  55252        CCCAA  A  A
                                   TACACCAT    GA GA TAAGC
                                   ||||||||    || || |||||
                                   GTGTGGTA    CT CT ATTCG
                                        AAGC_  _  _
GAM1583  C5orf4   3'  GCTTATTCTGATGCAGATGGTC 51493   C     CCAAGA
                A                   A ACCATC     AGAATAAGC
                                    | ||||||     |||||||||
                                    A TGGTAG     TCTTATTCG
                                     C     ACGTAG
GAM1583  C5orf4   5'  GCTTATTCTGATGCAGATGGTC 33427   C     CCAAGA
                A                   A ACCATC     AGAATAAGC
                                    | ||||||     |||||||||
                                    A TGGTAG     TCTTATTCG
                                     C     ACGTAG
GAM1583  CHIC1    3'  CTTATTCTTTATAATGGT    82899      CCCAA
                                   ACCAT    GAAGAATAAG
                                   |||||    ||||||||||
                                   TGGTA    TTTCTTATTC
                                      ATA__
GAM1583  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98089         AGAAG
                                   ACCATCCCA    AATAAG
                                   |||||||||    ||||||
                                   TGGTGGGGT    TTATTC
                                        GTCA_
GAM1583  DKFZP564I122 3'  GCTTATTCTTCTCCCTCATGTG 63879      CATCCCA
                TA                   TACAC      AGAAGAATAAGC
                                   |||||      ||||||||||||
                                   ATGTG      TCTTCTTATTCG
                                      TACTCCC
GAM1583  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62125        CCCAAGAA
                                   TACACCAT       GAATAAG
                                   ||||||||       |||||||
                                   ATGTGGTG       TTTATTC
                                        AAGACG__
GAM1583  FLJ22794  5'  CTTATTCTGGGACAGTG     93245     CA    AGAA
                                   CAC  TCCCA    GAATAAG
                                   |||  |||||    |||||||
                                   GTG  AGGGT    CTTATTC
                                     AC    _____
GAM1583  HN1L     3'  GCTCACTCAGCTAATGGGATGG 58618        __  AA  ATA
                                   CCATCCCA  AG  GA   AGC
                                   ||||||||  ||  ||   |||
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                              GGTAGGGT  TC  CT   TCG
                                  AA  GA  CAC
GAM1583  HYPH     3'  CTTATTCTATTGACAGACATGG 96567        CC____   GA
             TGTA                  TACACCAT     CAA  AGAATAAG
                              ||||||||     |||  ||||||||
                              ATGTGGTA     GTT  TCTTATTC
                                  CAGACA   A_
GAM1583  ITGB8    3'  GCTTATTTTTGCAAGATGG   11057      CCAAG
                              CCATC    AAGAATAAGC
                              |||||    ||||||||||
                              GGTAG    TTTTTATTCG
                                 AACG_
GAM1583  KIAA0342  3'  GCTCATCACTGTGGGATGGTG  71141          AGAA  ATA
                              CACCATCCCA   GA   AGC
                              ||||||||||   ||   |||
                              GTGGTAGGGT   CT   TCG
                                   GTCA  AC_
GAM1583  KIAA1579  3'  CTTACTCTTAGTGGTGTA    37149        CCCAAG    A
                              TACACCAT     AAGA TAAG
                              ||||||||     |||| ||||
                              ATGTGGTG     TTCT ATTC
                                  A_____    C
GAM1583  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68741        _      _
                              TACACCA TCCCAAGA AGA
                              ||||||| |||||||| |||
                              ATGTGGT AGGGTTCT TCT
                                  G       G
GAM1583  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66747    _   CCCA
                              AC CAT    AGAAGAATAAG
                              || |||    ||||||||||
                              TG GTA    TCTTCTTATTC
                               A   CCG_
GAM1583  MLZE     5'  GCTTATTTTTCCAGGATACTG  49452    CC    CAA
                              CA  ATCC   GAAGAATAAGC
                              ||  ||||   ||||||||||
                              GT  TAGG   CTTTTTATTCG
                               CA    AC_
GAM1583  POLD3    3'  GCTTCTTTTGCCTCAAGATGGT 93314         CCA  A_   T
             GTA                   TACACCATC   AG  AGAA AAGC
                              |||||||||   ||  |||| ||||
                              ATGTGGTAG   TC  TTTT TTCG
                                   AAC  CG   C
GAM1583  LOC145946 3'  CTAGTCCTGGAATGGTGTA   84560        C   A  AGAATA
                              TACACCAT CCA GA     AG
                              |||||||| ||| ||     ||
                              ATGTGGTA GGT CT     TC
                                  A   C  GA_____
GAM1583  LOC149322 3'  CTTATACCCAGGATGGTGTG   60287          CAAGAAGA
                              TACACCATCC       ATAAG
                              ||||||||||       |||||
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                                GTGTGGTAGG       TATTC
                                     ACCCA___
GAM1583  LOC149910 3'  CTTACATTCAGATGGTGTA   80355         CCAA   GAA
                                TACACCATC    GAA   TAAG
                                |||||||||    |||   ||||
                                ATGTGGTAG    CTT   ATTC
                                     A___    AC_
GAM1583  LOC220635 3'  CTTATACCCAGGATGGTGTG   92454          CAAGAAGA
                                TACACCATCC       ATAAG
                                ||||||||||       |||||
                                GTGTGGTAGG       TATTC
                                     ACCCA___
GAM1583  LOC253868 3'  GCTTATTCAGTGGGGGAGGTG  97323      A    AAGAA
                                CACC TCCC     GAATAAGC
                                |||| ||||     ||||||||
                                GTGG AGGG     CTTATTCG
                                  _    GGTGA
GAM1583  LOC256979 3'  GCTTATTCTCTTAGATG     97760      CC    A
                                CATC  AAGA GAATAAGC
                                ||||  |||| ||||||||
                                GTAG  TTCT CTTATTCG
                                  A_   _
GAM1583  LOC90826  5'  GCTTATTCTTCTGTAGAT    64786     CCA
                                ATC   AGAAGAATAAGC
                                |||   ||||||||||||
                                TAG   TCTTCTTATTCG
                                  ATG
GAM1584  ARF3      3'  AAGGCCTGAGGTTTTCCATCTT 9766      GA        AGTC
              CA                  TGA  ATGGAAAATT    GCCTT
                                |||  ||||||||||    |||||
                                ACT  TACCTTTTGG    CGGAA
                                  TC         AGTC
GAM1584  ENAM      3'  AAGGCAGATTAACTTTCCATTC 49924          A     _
              T                   AGAATGGAAA TTAGTC GCCTT
                                |||||||||| |||||| |||||
                                TCTTACCTTT AATTAG CGGAA
                                     C      A
GAM1584  ITGA1     3'  GACAATTTTCCATTTCA     64274       A       A
                                TGAGA TGGAAAATT GTC
                                ||||| ||||||||| |||
                                ACTTT ACCTTTTAA CAG
                                  _       _
GAM1584  KIF3C     3'  AGGCAACTCCCCATTTTCA    11203         AAAATT   C
                                TGAGAATGG      AGT GCCT
                                |||||||||      ||| ||||
                                ACTTTTACC      TCA CGGA
                                     CC_____   A
GAM1584  PCSK1     3'  ATTACTTTTCCATTCCCA     6513     A        T
                                TG GAATGGAAAA TAGT
                                || |||||||||| ||||
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                                AC CTTACCTTTT ATTA
                                 C        C
GAM1584 SLC6A12  3' GGGCCACCCTCCATTCTCA   13196         AAATTA  C
                                TGAGAATGGA     GT GCCT
                                ||||||||||     || ||||
                                ACTCTTACCT     CA CGGG
                                      CC_____  C
GAM1584 SOX15    5' GACCTTTCCATTTTCA     23680          ATTA
                                TGAGAATGGAAA   GTC
                                ||||||||||||   |||
                                ACTTTTACCTTT   CAG
                                       C___
GAM1584 DKFZP434O125 3' ACTAACTTCCATTCTCA     65582          AA
                                TGAGAATGGAA  TTAGT
                                ||||||||||  |||||
                                ACTCTTACCTT  AATCA
                                       C_
GAM1584 KIAA1906  3' GGTCTCAATTTTCCATTTCA   73573      A       _  TC
                                TGAGA TGGAAAATT AG  GCC
                                ||||| |||||||| ||  |||
                                ACTTT ACCTTTTAA TC  TGG
                                   _       C  __
GAM1584 MAPKAPK3  3' AAGGCGACTGAGCCATGCTCA  17342     A   AAAA
                                TGAG ATGG    TTAGTCGCCTT
                                |||| ||||    ||||||||||
                                ACTC TACC    AGTCAGCGGAA
                                  G   G___
GAM1584 MGC1127   3' AAGGCAACATCCCCATTCCA   54329    A     AAAATTA  C
                                TG GAATGG      GT GCCTT
                                || ||||||      || |||||
                                AC CTTACC      CA CGGAA
                                 _     CCTA___  A
GAM1584 PFTK1     3' GCAATCTTCTATTCTCA     25688          A   A
                                TGAGAATGGAA ATT GT
                                |||||||||| ||| ||
                                ACTCTTATCTT TAA CG
                                       C  _
GAM1584 SS18L1    3' AAGACGACTGTTTTCCATTTCC 65941    AG        T    C
             A                   TG  AATGGAAAAT AGTCG CTT
                                ||  |||||||||| ||||| |||
                                AC  TTACCTTTTG TCAGC GAA
                                 CT        _    A
GAM1584 LOC90538  3' AAGGTCCATAATTTTCCATTCC 63890    A          GTC
             A                   TG GAATGGAAAATTA   GCCTT
                                || ||||||||||||   |||||
                                AC CTTACCTTTTAAT   TGGAA
                                 _          ACC
GAM1584 LOC92293  3' AAGAGACATTTTCCATTCT   69315          TA   GC
                                AGAATGGAAAAT  GTC  CTT
                                ||||||||||||  |||  |||
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                                TCTTACCTTTTA  CAG  GAA
                                      __  A_
GAM1585 BAPX1    3'  TTCCTTCTCTGAAGTCCA    8648       GTCC  TAC
                                TGGACT   TC   AGAAGGAA
                                ||||||   ||   ||||||||
                                ACCTGA   AG   TCTTCCTT
                                   _____  TC_
GAM1585 CNTNAP2  5'  CTTCCTCGCGTATTTGAGGACA 27091     A      ___  A_  A
            GCCCA                   TGG CTGTCCTC   TAC  GA GGAAG
                                ||| ||||||||  |||  || |||||
                                ACC GACAGGAG   ATG  CT CCTTC
                                  C       TTT   CG  _
GAM1585 EBAF     5'  CCTCCCTAGAGGACAGCC    66027    A        CA  A
                                GG CTGTCCTCTA  GA GG
                                || ||||||||||  || ||
                                CC GACAGGAGAT  CT CC
                                 _        CC  _
GAM1585 PLP2     3'  TCCTTCTGCACGATCCA     12177     C   CCTCTA
                                TGGA TGT     CAGAAGGA
                                |||| |||     ||||||||
                                ACCT GCA     GTCTTCCT
                                  A  C_____
GAM1585 SYNGR1   3'  CTTCTGTTGGCAGAGGACAGCC 17503    A       ____
                                GG CTGTCCTCT    ACAGAAG
                                || |||||||||    |||||||
                                CC GACAGGAGA    TGTCTTC
                                 _        CGGT
GAM1585 SYNGR1   3'  TCCTCCCCTGGGGACAGCC    17514    A      TACA  A
                                GG CTGTCCTC    GA GGA
                                || ||||||||    || |||
                                CC GACAGGGG    CT CCT
                                 _       TCCC  _
GAM1585 AFAP     3'  CTTCCTTCTGTCCACTGTCCA  41606      T  CCTCT
                                TGGAC GT    ACAGAAGGAAG
                                ||||| ||    ||||||||||
                                ACCTG CA    TGTCTTCCTTC
                                   T  CC___
GAM1585 ARGBP2   3'  TCCTTCTGTAGAGGCCGCC    41135    ACT T
                                GG   G CCTCTACAGAAGGA
                                ||   | ||||||||||||||
                                CC   C GGAGATGTCTTCCT
                                 GC_ _
GAM1585 ARGBP2   3'  TCCTTCTGTAGAGGGCGCC    14591    AC
                                GG  TGTCCTCTACAGAAGGA
                                ||  ||||||||||||||||
                                CC  GCGGGAGATGTCTTCCT
                                  __
GAM1585 CEGP1    3'  CTTCCTTCTGCATGTCAGCACA 40936    GA   TCCTCTA
                                TG  CTG      CAGAAGGAAG
                                ||  |||      ||||||||||
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                                AC  GAC      GTCTTCCTTC
                                 AC   TGTAC__
GAM1585  DKFZP564D0478 3'  CTTCCCTCTGTAGAGCTGCTCC 50443     CTGTC        A
                                GGA    CTCTACAGA GGAAG
                                |||    ||||||||| |||||
                                CCT    GAGATGTCT CCTTC
                                  CGTC_       C
GAM1585  FLJ10374  3'  CTTCCTTCCACAAACTGTCTA  36554       T  CCTCTACA
                                TGGAC GT       GAAGGAAG
                                ||||| ||       ||||||||
                                ATCTG CA       CTTCCTTC
                                   T  AACAC___
GAM1585  FLJ12700  3'  TCCTCCTACCTGGCAGTCCA   46659        T  TCTAC  A
                                TGGACTG CC     AG AGGA
                                ||||||| ||     || ||||
                                ACCTGAC GG     TC TCCT
                                    _  TCCA_  C
GAM1585  KIAA0255  3'  TCCTTTTGGGGACACCCA    29137     AC     CTA
                                TGG  TGTCCT   CAGAAGGA
                                |||  ||||||   ||||||||
                                ACC  ACAGGG   GTTTTCCT
                                  C_     ____
GAM1585  KIAA0256  3'  CCTCTAGAGGACAACCCA    65050     AC       AC   A
                                TGG  TGTCCTCT  AGA GG
                                |||  ||||||||  ||| ||
                                ACC  ACAGGAGA  TCT CC
                                  CA       __  _
GAM1585  SSB-3     3'  CTTCCTTCCAGCCACACTCCA  55958      C   CCT  ACA
                                TGGA TGT   CT   GAAGGAAG
                                |||| |||   ||   ||||||||
                                ACCT ACA   GA   CTTCCTTC
                                  C   CC_  C__
GAM1585  TIP120B   3'  CTTCCTTAACTCAGGACAGTC  72851         CTACAG
                                GACTGTCCT     AAGGAAG
                                |||||||||     |||||||
                                CTGACAGGA     TTCCTTC
                                     CTCAA_
GAM1585  LOC122792 5'  CTTCCTTCCGCCGCCGCAGCCA 59824     A   CCTCTACA
                                TGG CTGT       GAAGGAAG
                                ||| ||||       ||||||||
                                ACC GACG       CTTCCTTC
                                  _    CCGCCGC_
GAM1585  LOC154141 5'  CCAGAGCTGCAGAGACAGTCCA 87386         C   A   AA__
                                TGGACTGTC TCT CAG    GG
                                ||||||||| ||| |||    ||
                                ACCTGACAG AGA GTC    CC
                                     _  C   GAGA
GAM1585  LOC154790 5'  CTTCCTTCCCAGAAAAGTCCA  82041       GTCC   ACA
                                TGGACT    TCT   GAAGGAAG
                                ||||||    |||   ||||||||
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                                ACCTGA   AGA  CTTCCTTC
                                   AA__  CC_
GAM1585 LOC170037 5' CTTCTTTTAAAAGACGGTCCA 88594        CTCTACA
                                TGGACTGTC     GAAGGAAG
                                |||||||||     ||||||||
                                ACCTGGCAG     TTTTCTTC
                                     AAAA___
GAM1585 LOC91050 3' TTCCTTCTGTCCCAGCC    65380    A   TCCTCT
                                GG CTG    ACAGAAGGAA
                                || |||    ||||||||||
                                CC GAC    TGTCTTCCTT
                                 _  CC____
GAM1585 LOC92465 5' TCCTCCTGGGCTGAAGCAGTCC 69957        CC  TA__   A
             A                   TGGACTGT  TC   CAG AGGA
                                 ||||||||  ||   ||| ||||
                                 ACCTGACG  AG   GTC TCCT
                                     A_  TCGG   C
GAM1586 ATRX    3'  CTTTAGGAATCAATGACTTAAC 6672     C      GAGTC
             A                   TGT TAAGTCA    TCCTAAAG
                                 ||| |||||||    ||||||||
                                 ACA ATTCAGT    AGGATTTC
                                  _      AACTA
GAM1586 ATRX    3'  CTTTAGGAATCAATGACTTAAC 57077    C      GAGTC
             A                   TGT TAAGTCA    TCCTAAAG
                                 ||| |||||||    ||||||||
                                 ACA ATTCAGT    AGGATTTC
                                  _      AACTA
GAM1586 EZH1    3'  AGGAATCAACTTAGGCA    10546        CA  GTC
                                TGTCTAAGT  GA   TCCT
                                |||||||||  ||   ||||
                                ACGGATTCA  CT   AGGA
                                     A_  A__
GAM1586 RAB26   3'  TAGGAGGCTCTGGCTCAAACA  27606    CTA
                                TGT   AGTCAGAGTCTCCTA
                                |||   ||||||||||||||||
                                ACA   TCGGTCTCGGAGGAT
                                  AAC
GAM1586 RCN2    3'  TTTAGAAGGACTTAGAC    12799        AGAGT  C
                                GTCTAAGTC    CT CTAAA
                                |||||||||    || |||||
                                CAGATTCAG    GA GATTT
                                     _____  A
GAM1586 CRMP5   3'  TTAGGAGACGCTGCACTTGACA 39708     T   _   A
                                TGTC AAGT CAG GTCTCCTAA
                                |||| |||| ||| |||||||||
                                ACAG TTCA GTC CAGAGGATT
                                  _   C   G
GAM1586 FLJ32356 3' CTTTAGGACCATGTGACCCAGA 59023    AA   GAGTC
                                TCT  GTCA    TCCTAAAG
                                |||  ||||    ||||||||
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                                AGA  CAGT    AGGATTTC
                                  CC   GTACC
GAM1586  LCHN     3'  CTTTAGGAGGCAGACTTGACA  87471     T    AGA
                                TGTC AAGTC   GTCTCCTAAAG
                                |||| |||||   ||||||||||
                                ACAG TTCAG   CGGAGGATTTC
                                  _    A__
GAM1586  MGC11287 3'  CTTCAGGAGACTGAGACAGAGA 49616     AA   AG      A
                                TCT  GTC  AGTCTCCT AAG
                                |||  |||  |||||||| |||
                                AGA  CAG  TCAGAGGA TTC
                                  GA   AG       C
GAM1586  LOC152078 3'  TAGGAAGTTAAATGACTTAGAC 81289          GA__ TC
             A                   TGTCTAAGTCA    G  TCCTA
                                ||||||||||    |  |||||
                                ACAGATTCAGT    T  AGGAT
                                      AAAT GA
GAM1587  EN2      5'  GCTCTGTTGAATCTCTCAT   9259         CCA    CCA
                                ATGAGAGAT   AACA   AGC
                                |||||||||   ||||   |||
                                TACTCTCTA   TTGT   TCG
                                     AG_    C__
GAM1587  LOXL2    5'  GCTTGGTGCTTGCTTTCTC   11352       TC   A
                                GAGAGA  CAA CACCAAGC
                                ||||||  ||| ||||||||
                                CTCTTT  GTT GTGGTTCG
                                   C_   C
GAM1587  PTMS     3'  GCCTGATCCCTGGATCTCCCTC 12564     __       AACAC  A
             A                   TGA  GAGATCCA     CA GC
                                |||  ||||||||     || ||
                                ACT  CTCTAGGT     GT CG
                                  CC       CCCTA  C
GAM1587  TCFL4    3'  CTTGGTGTTTGGTTTTTC    64211       T
                                GAGAGA CCAAACACCAAG
                                |||||| ||||||||||||
                                CTTTTT GGTTTGTGGTTC
                                       _
GAM1587  AD-020   3'  GCTTGGTGTTTAGAGCTGCTTC 39714   T  _  A  C
             A                   A GAG AG TC AAACACCAAGC
                                | ||| || || ||||||||||
                                A TTC TC AG TTTGTGGTTCG
                                 C   G  G  A
GAM1587  AD-020   3'  GCTTGGTGTTTAGAGCTGCTTC 60092   T  _  A  C
             A                   A GAG AG TC AAACACCAAGC
                                | ||| || || ||||||||||
                                A TTC TC AG TTTGTGGTTCG
                                 C   G  G  A
GAM1587  COVA1    3'  GCTCACTGATGCATCTCTCAT  73642        C  AA  CCA
                                ATGAGAGAT CA  CA   AGC
                                ||||||||| ||  ||   |||
```

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                                TACTCTCTA GT  GT   TCG
                                     C  A_  CAC
GAM1587  CXYorf1   3'  CTTGATGTCGGATCTCTTCA   82912   T       AA   C
                                A GAGAGATCC  ACA CAAG
                                | |||||||||  ||| ||||
                                A TTCTCTAGG  TGT GTTC
                                 C       C_   A
GAM1587  DKFZp434E0519 3'  GCTTGGTGCACACTCTCATT   50994        ATCCAAA
                                AATGAGAG      CACCAAGC
                                ||||||||      ||||||||
                                TTACTCTC      GTGGTTCG
                                     ACAC___
GAM1587  FLJ14054  3'  GTTTGTTCAAATTTCTCATTA  44970          C____
                                TAATGAGAGAT    CAAAC
                                ||||||||||     |||||
                                ATTACTCTTTA    GTTTG
                                      AACTT
GAM1587  FLJ23416  3'  GCCTGGTGTTTGGCAAACTCA  50933     AGAT        A
                                TGAG    CCAAACACCA GC
                                ||||    |||||||||| ||
                                ACTC    GGTTTGTGGT CG
                                  AAAC        C
GAM1587  KIAA0628  3'  CTTGGCATTGTCAGTCTCTTA  29529        C__   ACA
                                TGAGAGAT   CAA   CCAAG
                                ||||||||   |||   |||||
                                ATTCTCTG   GTT   GGTTC
                                     ACT   AC_
GAM1587  KIAA1726  3'  CTTGGTGTTTGTCTATCA    67831     G   TC
                                TGA AGA  CAAACACCAAG
                                ||| |||  ||||||||||
                                ACT TCT  GTTTGTGGTTC
                                  A  __
GAM1587  P2RX1     3'  GCTTCTCTCTCCGGACTCTCAT 67751         A   AAACACC_
            TA                    TAATGAGAG TCC       AAGC
                                ||||||||| |||       ||||
                                ATTACTCTC AGG       TTCG
                                     _   CCTCTCTC
GAM1587  PDZD2     3'  GCTTGTCTGAGTCCAGATTTCT 81727         CAAA__  C_
            CAT                    ATGAGAGATC     CA  CAAGC
                                ||||||||||     ||  |||||
                                TACTCTTTAG     GT  GTTCG
                                     ACCTGA  CT
GAM1587  TOR1B     3'  CTTGGGTCAATCTCTCA     27972        CCAA  A
                                TGAGAGAT    AC CCAAG
                                ||||||||    || |||||
                                ACTCTCTA    TG GGTTC
                                     AC__  _
GAM1587  LOC149773 5'  CGCTTGGTACTTAAATGAAACA 80292        GA__  CAAAC___      ___
            TCTTATTA                TAATGAGA    TC       ACCAAGC   G
                                ||||||||    ||       |||||||  |
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                                ATTATTCT   AG      TGGTTCG  C
                                    ACAA  TAAATTCA     ___
GAM1587  LOC152920 5'  GCTTCATTTGGATTTCTCAT  81624          CACC
                                ATGAGAGATCCAAA   AAGC
                                ||||||||||||||  ||||
                                TACTCTTTAGGTTT   TTCG
                                      AC__
GAM1587  LOC158983 3'  CTCAGTGACTTATTTCTCATTA 82949         CCAAA  CA
                                TAATGAGAGAT    CAC  AG
                                ||||||||||    |||  ||
                                ATTACTCTTTA    GTG  TC
                                      TTCA_  AC
GAM1587  LOC199993 3'  GCTTGGTCACTGTCTCTCA   72142       CCAAAC
                                TGAGAGAT     ACCAAGC
                                ||||||||     |||||||
                                ACTCTCTG     TGGTTCG
                                    TCAC__
GAM1587  LOC200093 3'  CTTGATGTCGGATCTCTTCA  63772  T      AA  C
                                A GAGAGATCC  ACA CAAG
                                | |||||||||  ||| ||||
                                A TTCTCTAGG  TGT GTTC
                                 C       C_  A
GAM1587  LOC91040  3'  CTTGATGTCGGATCTCTTCA  65346  T      AA  C
                                A GAGAGATCC  ACA CAAG
                                | |||||||||  ||| ||||
                                A TTCTCTAGG  TGT GTTC
                                 C       C_  A
GAM1588  ARF1      3'  GGGCACCTGGCCTCCAGGAGTC 71197      CAA  A
                                GATTCT   AG CCAGGTGCCC
                                ||||||   || ||||||||||
                                CTGAGG   TC GGTCCACGGG
                                   ACC  C
GAM1588  BCL6      3'  ACACGGATCTGAGAATCT    58032        AA  _  AG
                                AGATTCTCA  GA CC  GT
                                |||||||||  || ||  ||
                                TCTAAGAGT  CT GG  CA
                                     __  A  CA
GAM1588  BCL6      3'  ACACGGATCTGAGAATCT    9916         AA  _  AG
                                AGATTCTCA  GA CC  GT
                                |||||||||  || ||  ||
                                TCTAAGAGT  CT GG  CA
                                     __  A  CA
GAM1588  CLCN6     3'  GGCACCCAAAGTGAGCATCTG  8905       T   AAGACCA
                                CAGAT CTCA      GGTGCC
                                ||||| ||||      ||||||
                                GTCTA GAGT      CCACGG
                                  C   GAAAC__
GAM1588  CLCN6     3'  GGCACCCAAAGTGAGCATCTG  41697      T   AAGACCA
                                CAGAT CTCA      GGTGCC
                                ||||| ||||      ||||||
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                                GTCTA GAGT      CCACGG
                                  C   GAAAC__
GAM1588 CLCN6   3' GGCACCCAAAGTGAGCATCTG 41704      T   AAGACCA
                                CAGAT CTCA      GGTGCC
                                |||||  ||||      ||||||
                                GTCTA GAGT      CCACGG
                                  C   GAAAC__
GAM1588 CYBB    3' GGTATTGAATCTTTTAAAATCT 76851      CTC    CCA
            G                    CAGATT   AAAGA   GGTGCC
                                |||||||  |||||  ||||||
                                GTCTAA   TTTCT   TTATGG
                                   AAT    AAG
GAM1588 DGUOK   3' CACCTTTGTAAAGAATCTG   56047       CAAAG  C_
                                CAGATTCT    AC  AGGTG
                                ||||||||    ||  |||||
                                GTCTAAGA    TG  TCCAC
                                    AA___  TT
GAM1588 DGUOK   3' CACCTTTGTAAAGAATCTG   56048       CAAAG  C_
                                CAGATTCT    AC  AGGTG
                                ||||||||    ||  |||||
                                GTCTAAGA    TG  TCCAC
                                    AA___  TT
GAM1588 DGUOK   3' CACCTTTGTAAAGAATCTG   10408       CAAAG  C_
                                CAGATTCT    AC  AGGTG
                                ||||||||    ||  |||||
                                GTCTAAGA    TG  TCCAC
                                    AA___  TT
GAM1588 FCMD    3' GCCTTCTCTAGAATCTG    23039       CAA   CC
                                CAGATTCT   AGA  AGGT
                                ||||||||   |||  ||||
                                GTCTAAGA   TCT  TCCG
                                    ___   CT
GAM1588 GAD2    3' ACTTCCTTTGAGAATT     7698          ACC
                                GATTCTCAAAG   AGGT
                                ||||||||||   ||||
                                TTAAGAGTTTC   TTCA
                                     C__
GAM1588 KCNK3   3' ACACTGCCCTTAGAATCTG   11167       CA   AC   _
                                CAGATTCT  AAG  CAG GT
                                ||||||||  |||  ||| ||
                                GTCTAAGA  TTC  GTC CA
                                    __   CC   A
GAM1588 KLHL3   3' GGACACCCTCCCTACTTTGAGA 88848         ACCA___   _
            ATC                   GATTCTCAAAG      GGTG CC
                                ||||||||||      |||| ||
                                CTAAGAGTTTC      CCAC GG
                                     ATCCCTC    A
GAM1588 MADH2   3' GCACCTTGTGGAATCTG    20915       CAAAG  C
                                CAGATTCT    AC AGGTGC
                                ||||||||    || ||||||
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                                GTCTAAGG    TG TCCACG
                                     _____  T
GAM1588  MASP1    3'  CACCTGGTTCTAGAACT     10295    A   CAAA
                                AG TTCT    GACCAGGTG
                                || ||||    |||||||||
                                TC AAGA    TTGGTCCAC
                                 _    TC__
GAM1588  NPC1     3'  GCTTGGTCTCCAAAAATCTG   6054        CTCAA
                                CAGATT     AGACCAGGT
                                ||||||     |||||||||
                                GTCTAA     TCTGGTTCG
                                    AAACC
GAM1588  NTSR1    3'  GGACACCTGGTCTTGGGCTG   11861     ATT    A       _
                                CAG   CTCAA GACCAGGTG CC
                                |||   ||||| ||||||||| ||
                                GTC   GGGTT CTGGTCCAC GG
                                  ____    _       A
GAM1588  PHB      3'  GGGCACAGATTGAAGAATCTG  12069        _  AGACCAG
                                CAGATTCT CAA      GTGCCC
                                |||||||| |||      ||||||
                                GTCTAAGA GTT      CACGGG
                                     A   AGA_____
GAM1588  PIK3CD   3'  ACCATCACCTTTGGGAACCTG  18481     A       ACCA_
                                CAG TTCTCAAAG     GGT
                                ||| |||||||||     |||
                                GTC AAGGGTTTC     CCA
                                  C        CACTA
GAM1588  PLD2     3'  GGGCAGTGCCCTTTGAGATCTG 12164      T      AC  GG
                                CAGAT CTCAAAG  CA  TGCCC
                                ||||| |||||||  ||  |||||
                                GTCTA GAGTTTC  GT  ACGGG
                                   _      CC  G_
GAM1588  PRKCN    3'  GGCACTGTCAGAGAATCTG    20563         AAA   CA
                                CAGATTCTC   GAC  GGTGCC
                                |||||||||   |||  ||||||
                                GTCTAAGAG   CTG  TCACGG
                                     A__   __
GAM1588  SUOX     5'  GGCATTTTGCCCCCAGAATCTG 6603         CAAAGACC
                                CAGATTCT       AGGTGCC
                                ||||||||       |||||||
                                GTCTAAGA       TTTACGG
                                     CCCCCGT_
GAM1588  TRDN     3'  GGGTCTAAGTCTCAAGAATCTG 21385        CAA    CA  T
                                CAGATTCT   AGAC  GG GCCC
                                ||||||||   ||||  || ||||
                                GTCTAAGA   TCTG  TC TGGG
                                     AC_    AA  _
GAM1588  UNG      3'  GGTGGCCTTTGAGAAGCTG    56025     A       A  AGGT
                                CAG TTCTCAAAG CC    GCC
                                ||| |||||||| ||    |||
```

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                                GTC AAGAGTTTC GG    TGG
                                  G        C _____
GAM1588 UNG      3' GGTGGCCTTTGAGAAGCTG   14014     A       A  AGGT
                                CAG TTCTCAAAG CC    GCC
                                ||| ||||||||| ||    |||
                                GTC AAGAGTTTC GG    TGG
                                  G        C _____
GAM1588 APOL4    3' GGACCAGGTGTCTCTGAGAATC 48379        A    CA__   G
                                GATTCTCA AGAC    GGT CC
                                |||||||| ||||    ||| ||
                                CTAAGAGT TCTG    CCA GG
                                     C    TGGA   _
GAM1588 B3GNT5   3' GGCACCTGTTAGGGAAAATC   50249      C  AAA   C
                                GATT TC   GAC AGGTGCC
                                |||| ||   ||| |||||||
                                CTAA AG   TTG TCCACGG
                                  A  GGA   _
GAM1588 CALN1    3' GGCAATTACCCTTAAAGAATCT 49666        CA   ACCAGG
                  G                CAGATTCT  AAG     TGCC
                                |||||||  |||     ||||
                                GTCTAAGA  TTC     ACGG
                                     AA   CCATTA
GAM1588 DDA3     3' GGCACCTGGTCTTCAGAAATTG 51951     A    CA
                                CAG TTCT  AAGACCAGGTGCC
                                ||| ||||  ||||||||||||
                                GTT AAGA  TTCTGGTCCACGG
                                  A    C_
GAM1588 DDM36    3' GCCTGGTTTTGAAAATC     40925      C    A
                                GATT TCAA GACCAGGT
                                |||| |||| ||||||||
                                CTAA AGTT TTGGTCCG
                                  A    _
GAM1588 FLJ10094 5' GCAGTTTTGAGAATCTG     36296           GACCA G
                                CAGATTCTCAAA    G TGC
                                ||||||||||||    | |||
                                GTCTAAGAGTTT    T ACG
                                      _____ G
GAM1588 FLJ12610 3' GCCAGTCTCTGAGAATC     45859        A    CA
                                GATTCTCA AGAC  GGT
                                |||||||| ||||  |||
                                CTAAGAGT TCTG  CCG
                                     C    A_
GAM1588 FLJ14627 5' GGCGTCTTTGAGAGTCTG    52546            CAGGT
                                CAGATTCTCAAAGAC    GCC
                                ||||||||||||||    |||
                                GTCTGAGAGTTTCTG    CGG
                                                  _____
GAM1588 FLJ23375 3' GGGCAGGGAACCTTTGAGGATC 46952           A__  AGG
                  TG                CAGATTCTCAAAG   CC   TGCCC
                                ||||||||||||||   ||   |||||
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                                GTCTAGGAGTTTC  GG  ACGGG
                                       CAA  G__
GAM1588  FLJ32468  3'  GCACCTGGCCGTGGGAAT   59710       AAGA
                                ATTCTCA   CCAGGTGC
                                |||||||   ||||||||
                                TAAGGGT   GGTCCACG
                                   GCC_
GAM1588  GREB1    3'  CACCTTTGAGAATTT      72837         AGACC
                                AGATTCTCAA    AGGTG
                                ||||||||||    |||||
                                TTTAAGAGTT    TCCAC
                                      _____
GAM1588  HIF1AN   3'  GCTTGCCTTTGAGAGCCT    62670    AT      AC
                                AG  TCTCAAAG  CAGGT
                                ||  ||||||||  |||||
                                TC  AGAGTTTC  GTTCG
                                 CG       C_
GAM1588  HSD17B12  3'  GCACCCTACTGGTTTTGAAAAT 32862      C   A   ____
            CTG                   CAGATT TCAA GACCA   GGTGC
                                |||||| |||| |||||   |||||
                                GTCTAA AGTT TTGGT   CCACG
                                   A   _    CATC
GAM1588  HSPC189  3'  CACCTGGTGAGAGCCTG    96986    AT   AAAG
                                CAG  TCTC   ACCAGGTG
                                |||  ||||   ||||||||
                                GTC  AGAG   TGGTCCAC
                                 CG   ____
GAM1588  KCNJ9    3'  GGACCACACTTTGAGAACCTG  18367    A      ACCA   G
                                CAG TTCTCAAAG   GGT CC
                                ||| |||||||||   ||| ||
                                GTC AAGAGTTTC   CCA GG
                                 C       ACA_  _
GAM1588  KIAA0321  3'  GGACTTCCTCTTTGAGAGTCTG 63056           CC   G
                                CAGATTCTCAAAGA  AGGT CC
                                ||||||||||||||  |||| ||
                                GTCTGAGAGTTTCT  TTCA GG
                                       CC   _
GAM1588  KIAA0376  3'  ACCTGTACCTTTGAGAAT    66211         AC_
                                ATTCTCAAAG   CAGGT
                                |||||||||   |||||
                                TAAGAGTTTC   GTCCA
                                     CAT
GAM1588  MGC11287  3'  GCCTCTGGTCTCTGAAAAGCTG 49618    A  C   A      T
                                CAG TT TCA AGACCAGG GC
                                ||| || ||| ||||||||| ||
                                GTC AA AGT TCTGGTCT CG
                                 G  A   C       C
GAM1588  MGC14128  3'  GGGCAGAAGCTTTGAGAGCCTG 52946    AT      ACCAGG
                                CAG  TCTCAAAG     TGCCC
                                |||  ||||||||     |||||
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                                GTC  AGAGTTTC     ACGGG
                                  CG       GAAG__
GAM1588  NET-7    3'  GCAGCTCTGGAATCTG      25623         CAA   CCA G
                                CAGATTCT   AGA   G TGC
                                ||||||||   |||   | |||
                                GTCTAAGG   TCT   C ACG
                                     ___   ___ G
GAM1588  PMF1     5'  GGTCGTCTTCGGAATCTG    24287         CA    CAGGT
                                CAGATTCT  AAGAC    GCC
                                ||||||||  |||||    |||
                                GTCTAAGG  TTCTG    TGG
                                     C_    C____
GAM1588  PPP1R16B 3'  GCCTTTCCTTGGGAATCTG   62039          A  CC
                                CAGATTCTCAA GA  AGGT
                                ||||||||||| ||  ||||
                                GTCTAAGGGTT CT  TCCG
                                      C  T_
GAM1588  SEC3     3'  GCAACTGTTTTGAGAA      37340         AC   G
                                TTCTCAAAG  CAG TGC
                                |||||||||  ||| |||
                                AAGAGTTTT  GTC ACG
                                     __  A
GAM1588  SEPW1    3'  GGACACCTGGTCTTTCCCTG   13014     ATTCTC         _
                                CAG     AAAGACCAGGTG CC
                                |||     |||||||||||| ||
                                GTC     TTTCTGGTCCAC GG
                                  CC____          A
GAM1588  TCL6     5'  GGGCACCGTAGCTCTGGAATCT 40532       T  A  ACCA
           G                     CAGATTC CA AG    GGTGCCC
                                |||||||  || ||    |||||||
                                GTCTAAG GT TC    CCACGGG
                                   _  C  GATG
GAM1588  TCL6     5'  GGGCACCGTAGCTCTGGAATCT 40539       T  A  ACCA
           G                     CAGATTC CA AG    GGTGCCC
                                |||||||  || ||    |||||||
                                GTCTAAG GT TC    CCACGGG
                                   _  C  GATG
GAM1588  VPS39    3'  GCACCTGGCCTTAGGAATC    63500       CA   A
                                GATTCT  AAG CCAGGTGC
                                ||||||  ||| ||||||||
                                CTAAGG  TTC GGTCCACG
                                   A_   C
GAM1588  YR-29    5'  GGGCTTGTGGGTCTTTGAGA   30300          AGGT_
                                TCTCAAAGACC     GCCC
                                ||||||||||     ||||
                                AGAGTTTCTGG     CGGG
                                      GTGTT
GAM1588  ZNF220   5'  GGTTCCCAGCCTCCGAGAATCT 23160         AA  ACCA  T
                                AGATTCTC  AG    GG GCC
                                ||||||||  ||    || |||
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                                TCTAAGAG  TC    CC TGG
                                     CC  CGAC  T
GAM1588  LOC127281 3'  GGCCCTGGCCTCCGAGGATCTG 75137         AA  A    T
                                CAGATTCTC  AG CCAGG GCC
                                |||||||||  || ||||| |||
                                GTCTAGGAG  TC GGTCC CGG
                                     CC  C    _
GAM1588  LOC129530 3'  GGGCACCTGTAACTGGGAATCT 75384         AAGAC
              G                  CAGATTCTCA    CAGGTGCCC
                                ||||||||||    |||||||||
                                GTCTAAGGGT    GTCCACGGG
                                      CAAT_
GAM1588  LOC143338 3'  CACCTGGTCAGGAATGTG    77057    G    CAAA
                                CA ATTCT    GACCAGGTG
                                || |||||    |||||||||
                                GT TAAGG    CTGGTCCAC
                                 G    A___
GAM1588  LOC145990 3'  ACTTCTTTGAGATCT       78055      T      CCA
                                AGAT CTCAAAGA   GGT
                                |||| ||||||||   |||
                                TCTA GAGTTTCT   TCA
                                  _      ___
GAM1588  LOC146475 5'  GCCTCAGTCTTTGAGATCCTG  84692     AT        C_
                                CAG  TCTCAAAGAC  AGGT
                                |||  ||||||||||  ||||
                                GTC  AGAGTTTCTG  TCCG
                                  CT         AC
GAM1588  LOC146499 3'  CACCTGGTCAGGAATGTG    71366    G    CAAA
                                CA ATTCT    GACCAGGTG
                                || |||||    |||||||||
                                GT TAAGG    CTGGTCCAC
                                 G    A___
GAM1588  LOC147176 3'  CACCTGGTCAGGAATGTG    61146    G    CAAA
                                CA ATTCT    GACCAGGTG
                                || |||||    |||||||||
                                GT TAAGG    CTGGTCCAC
                                 G    A___
GAM1588  LOC150372 5'  GCATCCTTCAGAATCTG     80613        CA   ACCA
                                CAGATTCT  AAG    GGTGC
                                ||||||||  |||    |||||
                                GTCTAAGA  TTC    CTACG
                                     C_   _____
GAM1588  LOC158276 3'  CACCTGGTCAGGAATGTG    82736    G    CAAA
                                CA ATTCT    GACCAGGTG
                                || |||||    |||||||||
                                GT TAAGG    CTGGTCCAC
                                 G    A___
GAM1588  LOC162918 5'  ACATTGTGTCTTTGAACATC   88514     TC       _   _
                                GAT  TCAAAGAC CAG GT
                                |||  |||||||| ||| ||
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                                CTA  AGTTTCTG GTT CA
                                  CA       T   A
GAM1588  LOC165721 5'  GGGCCCCTCCAGTCCCTGAGAA 83495        AA   C__   T
             TT                    GATTCTCA  GAC   AGG GCCC
                                   |||||||  |||   ||| ||||
                                   TTAAGAGT  CTG   TCC CGGG
                                       CC   ACC   C
GAM1588  LOC199678 3'  GCCTTAACCTCTGAGAGTCTG  91367          A  ACC_
                                   CAGATTCTCA AG    AGGT
                                   |||||||||| ||    ||||
                                   GTCTGAGAGT TC    TCCG
                                         C  CAAT
GAM1588  LOC221763 3'  GGATATTTAATCTTTGAGAAAC 95438    A        CC    _
             T                     AG TTCTCAAAGA  AGGTG CC
                                   || ||||||||||  ||||| ||
                                   TC AAGAGTTTCT  TTTAT GG
                                    A         AA    A
GAM1588  LOC254251 3'  ATTTGGTCTCTGAGATCT    97597      T    A
                                   AGAT CTCA AGACCAGGT
                                   |||| |||| |||||||||
                                   TCTA GAGT TCTGGTTTA
                                     _    C
GAM1588  LOC254848 5'  GGCACCTGGTCCCCAAGAA    98883      CAAA
                                   TTCT    GACCAGGTGCC
                                   ||||    ||||||||||
                                   AAGA    CTGGTCCACGG
                                     ACCC
GAM1588  LOC255131 5'  ATCAGTCTTTGAGAACT     97690    A         CA
                                   AG TTCTCAAAGAC  GGT
                                   || ||||||||||  |||
                                   TC AAGAGTTTCTG  CTA
                                    _         A_
GAM1588  LOC256339 5'  GCACCTGGAGAGGAACCTG    97152     A_    AAAGA
                                   CAG  TTCTC    CCAGGTGC
                                   |||  |||||    ||||||||
                                   GTC  AGGAG    GGTCCACG
                                     CA    A____
GAM1588  LOC51285  3'  GGACACACCTTTGAGATC    33801     T      ACCAG  _
                                   GAT CTCAAAG     GTG CC
                                   ||| |||||||     ||| ||
                                   CTA GAGTTTC     CAC GG
                                    _      CA___   A
GAM1589  BDKRB2    3'  TGAGCCAGCCTGCTCCTT    7116          A  AT
                                   AAGGAGCAG CT  TTTA
                                   |||||||||  ||  ||||
                                   TTCCTCGTC GA  GAGT
                                         C  CC
GAM1589  GDF5      5'  TTTTGAAAGTCCACTCCTTT   6900         CA    AT
                                   AAAGGAG  GACT  TTTAAAA
                                   |||||||  ||||  |||||||
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                                TTTCCTC  CTGA  AAGTTTT
                                   AC   __
GAM1589  KCNS2    3'  AAAATGCTCCTGCTCCTCTTG  68842     A       AC_
                                TAA AGGAGCAG   TATTTT
                                ||| ||||||||   ||||||
                                GTT TCCTCGTC   GTAAAA
                                  C       CTC
GAM1589  RRM2B    3'  TTTTGAGAAGTCTGCCCCT   68440     A      A
                                AGG GCAGACT TTTTAAAA
                                ||| ||||||| ||||||||
                                TCC CGTCTGA AGAGTTTT
                                  C      _
GAM1589  RUNX3    3'  AAAATAGTTGCTGACTCC    16363      _   __
                                GGAG CAG  ACTATTTT
                                |||| |||  ||||||||
                                CCTC GTC  TGATAAAA
                                  A  GT
GAM1589  SACM1L   3'  TTTTAAAAACCTAGCTCCTTT  26697         _  ACTA
                                AAAGGAGC AG    TTTTAAAA
                                |||||||| ||    ||||||||
                                TTTCCTCG TC    AAAATTTT
                                    A  CA__
GAM1589  SET      3'  TTTTAAAATAAATTCTCTCCT  13023       C   C__
                                AGGAG AGA   TATTTTAAAA
                                ||||| |||   ||||||||||
                                TCCTC TCT   ATAAAATTTT
                                  _   TAA
GAM1589  SPG4     3'  TTAAAATAGTAATTTCTCCT   30813      CAG__
                                AGGAG    ACTATTTTAA
                                |||||    ||||||||||
                                TCCTC    TGATAAAATT
                                   TTTAA
GAM1589  CNOT3    5'  TTTAAAATAAAGACGCTCCT   27990       AGAC_
                                AGGAGC    TATTTTAAA
                                ||||||    |||||||||
                                TCCTCG    ATAAAATTT
                                   CAGAA
GAM1589  EREG     3'  TAAAATAGTTAGATCTTT    9317       GCA
                                AAGGA   GACTATTTTA
                                |||||   ||||||||||
                                TTTCT   TTGATAAAAT
                                   AGA
GAM1589  FHOD2    3'  TTTTAAAATGAGCTCTCCTTT  74266        C  AC
                                AAAGGAG AG  TATTTTAAAA
                                ||||||| ||  ||||||||||
                                TTTCCTC TC  GTAAAATTTT
                                    _  GA
GAM1589  FLJ22195 3'  AATAGTCCCTGCTCCTCTTA   43105     A      __
                                TAA AGGAGCA  GACTATT
                                ||| |||||||  |||||||
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                                ATT TCCTCGT  CTGATAA
                                  C      CC
GAM1589  KIAA0237  3'  TTTAAAATGCTGCTTCTT    29235        AC
                                AAGGAGCAG  TATTTTAAA
                                |||||||||  |||||||||
                                TTCTTCGTC  GTAAAATTT
                                          __
GAM1589  KIAA0285  3'  TGGAACAGGCTGCTCCTT    29690        A  A
                                AAGGAGCAG CT TTTTA
                                |||||||||  || |||||
                                TTCCTCGTC GA AAGGT
                                     G  C
GAM1589  KIAA0446  5'  TTTTAGGAGCAGCCTGCCCCTT 69464       A    A  A_
              TT                  AAAAGG GCAG CT  TTTTAAAA
                                |||||| |||| ||  ||||||||
                                TTTTCC CGTC GA  AGGATTTT
                                   C    C  CG
GAM1589  KIAA0472  3'  TTATTGTGGTCTGTCCTT    72376      G       TT
                                AAGGA CAGACTAT  TAA
                                |||||  ||||||||  |||
                                TTCCT GTCTGGTG  ATT
                                  _       TT
GAM1589  KIAA1546  3'  TTTTAAAATATTTTTGCTTTT  68501        C_
                                AGGAGCAGA  TATTTTAAAA
                                |||||||||  ||||||||||
                                TTTTCGTTT  ATAAAATTTT
                                     TT
GAM1589  MEGF10    3'  AAAATAGAGTTCCTTTTG    51602        AGA
                                TAAAAGGAGC   CTATTTT
                                ||||||||||   |||||||
                                GTTTTCCTTG   GATAAAA
                                     A__
GAM1589  MGC15875  3'  TTTAAAGTGCTCCTGCTT    53018       AC_
                                GAGCAG   TATTTTAAA
                                ||||||   |||||||||
                                TTCGTC   GTGAAATTT
                                   CTC
GAM1589  MGC2560   3'  TTTTAAAATAGAAAATGCTTTT 49568       GA__
                                AGGAGCA    CTATTTTAAAA
                                |||||||    ||||||||||
                                TTTTCGT    GATAAAATTTT
                                    AAAA
GAM1589  MYNN      3'  TTTTAAAATTTTCCTGCCCTCA 38482   A   A   ACT_
                                A AGG GCAG    ATTTTAAAA
                                | ||| ||||    |||||||||
                                A TCC CGTC    TAAAATTTT
                                 C   _    CTTT
GAM1589  PREI3     3'  TTAAAATAGTTTGACTCTT    66929      _
                                AGGAG CAGACTATTTTAA
                                ||||| ||||||||||||
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                                TTCTC GTTTGATAAAATT
                                   A
GAM1589  PROL2    3'  TTTTAAAATAGTCTTGACTCTT 23324       _ _
                T                AAGGAG CA GACTATTTTAAAA
                                 |||||| || ||||||||||||
                                 TTTCTC GT CTGATAAAATTTT
                                    A  T
GAM1589  LOC148293 5'  TTTTAAGAAACCTGCCACTTTT 79531       GA    ACTA
                A                 TAAAAG  GCAG    TTTTAAAA
                                  ||||||  ||||    ||||||||
                                  ATTTTC  CGTC    AGAATTTT
                                     AC    CAA_
GAM1589  LOC199907 3'  TTTTAAAAGTGTGCCACCTTTT 89834       A_   G   AT
                A                 TAAAAGG  GCA ACT  TTTAAAA
                                  |||||||  ||| |||  |||||||
                                  ATTTTCC  CGT TGA  AAATTTT
                                      AC   G   __
GAM1589  LOC219790 3'  TTTTATTGTCCCTGCTCTTTT  93006         ACT  TT
                                  AAAGGAGCAG   AT  TAAAA
                                  ||||||||||   ||  |||||
                                  TTTTCTCGTC   TG  ATTTT
                                       CC_  TT
GAM1589  LOC90049  3'  TTTTAAGAAACCTGCCACTTTT 61878       GA    ACTA
                A                 TAAAAG  GCAG    TTTTAAAA
                                  ||||||  ||||    ||||||||
                                  ATTTTC  CGTC    AGAATTTT
                                     AC    CAA_
GAM1590  GPD1     3'  TCATGCCACCACATTTG     60398       C       C
                                  TAAATG GGTGGCAT GA
                                  |||||| |||||||| ||
                                  GTTTAC CCACCGTA CT
                                     A       _
GAM1590  IL5RA    5'  TCGCATGGCCACCGCATTT    6906           AT__
                                  AAATGCGGTGGC    CGA
                                  ||||||||||||    |||
                                  TTTACGCCACCG    GCT
                                        GTAC
GAM1590  MYO1C    3'  TGCCGATGCCAAATATTTG   61873       CGG       A
                                  TAAATG   TGGCATCG CA
                                  ||||||   |||||||| ||
                                  GTTTAT   ACCGTAGC GT
                                     AA_       C
GAM1590  C6orf37   3'  TGTCACACTGCATTTA      68097          GCATC
                                  TAAATGCGGTG     GACA
                                  ||||||||||||    ||||
                                  ATTTACGTCAC     CTGT
                                        A_____
GAM1590  DNAJC6   3'  TTGCAGAACCACCGCATT    29498          CA  GA
                                  AATGCGGTGG  TC  CAA
                                  ||||||||||  ||  |||
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                                TTACGCCACC  AG  GTT
                                     A_  AC
GAM1590  FLJ11210  3'  GTCGATGTGCATGCTTTTA   60319     T   GTG
                                TAAA GCG   GCATCGAC
                                |||| |||   ||||||||
                                ATTT CGT   TGTAGCTG
                                  T   ACG
GAM1590  FLJ12476  3'  TCGATCTTCTGCATTTA     43270         T  C
                                TAAATGCGG GG ATCGA
                                ||||||||| || |||||
                                ATTTACGTC TC TAGCT
                                     T  _
GAM1590  KIAA1034  3'  TCGATGGCATCCGCATTTG   63134         _  G
                                TAAATGCGG TG CATCGA
                                ||||||||| || ||||||
                                GTTTACGCC AC GTAGCT
                                     T  G
GAM1590  KIAA1987  3'  TCATGTAACTGCATTTA     89391         G   C
                                TAAATGCGGT GCAT GA
                                |||||||||| |||| ||
                                ATTTACGTCA TGTA CT
                                     A   _
GAM1590  MGC16063  3'  TGTCCTGGCCACTGCATT    54929          ATC
                                AATGCGGTGGC   GACA
                                ||||||||||   ||||
                                TTACGTCACCG   CTGT
                                      GTC
GAM1590  LOC147949 3'  TGTCAGATGTCCACATTGCA   79279     __   _   _
                                TGCG  GTGG CATC GACA
                                ||||  |||| |||| ||||
                                ACGT  CACC GTAG CTGT
                                  TA   T   A
GAM1590  LOC150577 3'  GTCCTCACCGCATTTG      86258          CATC
                                TAAATGCGGTGG   GAC
                                ||||||||||||   |||
                                GTTTACGCCACT   CTG
                                      C___
GAM1590  LOC158219 3'  TGTGTGTCACCACATTT     82694      C       CG
                                AAATG GGTGGCAT  ACA
                                ||||| ||||||||  |||
                                TTTAC CCACTGTG  TGT
                                   A       __
GAM1590  LOC202020 3'  TGTCTCACCACATTTA      90605       C    CATC
                                TAAATG GGTGG   GACA
                                |||||| |||||   ||||
                                ATTTAC CCACT   CTGT
                                   A    _____
GAM1590  LOC90826  5'  TGTCGATGCAGGTTTATTTG  64788       CGGTG
                                TAAATG    GCATCGACA
                                ||||||    |||||||||
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                                GTTTAT    CGTAGCTGT
                                   TTGGA
GAM1590 LOC93587 3' TTGTCTTTACCTGCATTTA   73042       _    CATC
                                TAAATGC GGTGG   GACAA
                                ||||||| |||||   |||||
                                ATTTACG CCATT   CTGTT
                                    T   T___
GAM1591 CAPZA1   5' GAAATGAGGGTCACCTTTCACA 73024      _    GAG_
                                TGTGAA GGTGAT   ATTTC
                                |||||| ||||||   |||||
                                ACACTT CCACTG   TAAAG
                                   T    GGAG
GAM1591 CASP10   3' GGAAACCTCCCTTTACA    53204       TGAT  A
                                TGTGAAGG   GAG TTTCC
                                ||||||||   ||| |||||
                                ACATTTCC   CTC AAAGG
                                    _____  C
GAM1591 FMR1     3' GAAATTGGTACCTTGCACA   10678    _    ATGA
                                TGTG AAGGTG   GATTTC
                                |||| ||||||   ||||||
                                ACAC TTCCAT   TTAAAG
                                  G    GG__
GAM1591 FZD8     3' GAGGTTCCCACCCCTTCACA  49874       TGA  A_
                                TGTGAAGG  TG  GATTTC
                                |||||||  ||  ||||||
                                ACACTTCC  AC  TTGGAG
                                     CC_  CC
GAM1591 SPINK2   3' GATGGAGAGACCACCTTCAC  41201       ATGAGA
                                GTGAAGGTG    TTTCCATC
                                |||||||||    ||||||||
                                CACTTCCAC    AGAGGTAG
                                     CAG___
GAM1591 TRAM     3' AAATTTTTACTTTCACA    27450         TG
                                TGTGAAGGTGA  AGATTT
                                ||||||||||  ||||||
                                ACACTTTCATT  TTTAAA
                                          __
GAM1591 BC008967 3' ATGGAAACCACGTTCACA   61414      G  ATGAGA
                                TGTGAA GTG    TTTCCAT
                                |||||| |||    |||||||
                                ACACTT CAC    AAAGGTA
                                   G  C_____
GAM1591 FLJ12650 3' ATCCCCATCACCTCCACA   44817    A     A_
                                TGTG AGGTGATG  GAT
                                |||| ||||||||  |||
                                ACAC TCCACTAC  CTA
                                  C      CC
GAM1591 KIAA0993 3' GATAGGCCTTCACACCTTCACA 64819        A   ATTT _
                                TGTGAAGGTG TGAG   CC ATC
                                |||||||||| ||||   || |||
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                                ACACTTCCAC ACTT   GG TAG
                                      _   CC__  A
GAM1591  KIAA1361  3'  GGAAACACCACTTCCACA    62886     A    A  AGA
                                TGTG AGGTG TG   TTTCC
                                |||| ||||| ||   |||||
                                ACAC TTCAC AC   AAAGG
                                  C    C ___
GAM1591  KIAA1724  3'  GATAAAAATAAGTCACCTTCAC 67616          GAG   CC
                                GTGAAGGTGAT   ATTT  ATC
                                ||||||||||   ||||  |||
                                CACTTCCACTG   TAAA  TAG
                                      AA_   AA
GAM1591  PAFAH2   3'  ATGAAAATCCCTACCTTCA   6495        ATGA    C
                                TGAAGGTG   GATTT CAT
                                ||||||||   ||||| |||
                                ACTTCCAT   CTAAA GTA
                                     CC__    A
GAM1591  SPS      3'  AAATCTCATTGTGTCTACA   25308    _  AG TG
                                TGT GA  G  ATGAGATTT
                                ||| ||  |  |||||||||
                                ACA CT  T  TACTCTAAA
                                  T  G_ GT
GAM1591  LOC118987 3'  ATGGAAATAAACCTCCAC    74392    A   GATGAG
                                GTG AGGT     ATTTCCAT
                                ||| ||||     ||||||||
                                CAC TCCA     TAAAGGTA
                                  C   AA____
GAM1591  LOC127428 3'  GAAACATCACCTTCA      75158          AGA
                                TGAAGGTGATG   TTTC
                                ||||||||||   ||||
                                ACTTCCACTAC   AAAG
                                      ___
GAM1591  LOC138046 3'  ATGGAAGAAACCATCTTCACA  75808         ATGAGA
                                TGTGAAGGTG     TTTCCAT
                                ||||||||||     |||||||
                                ACACTTCTAC     GAAGGTA
                                      CAAA__
GAM1591  LOC138399 3'  GATGGAAATCTGGATCCACACA 75849     AA  TGATG
                                TGTG  GG    AGATTTCCATC
                                ||||  ||    ||||||||||
                                ACAC  CC    TCTAAAGGTAG
                                  A_  TAGG_
GAM1591  LOC143279 5'  GAAGTTCACCTGCACA     77020     A     TGAG
                                TGTG AGGTGA    ATTTC
                                |||| ||||||    |||||
                                ACAC TCCACT    TGAAG
                                  G     ____
GAM1591  LOC144079 5'  AAGTCTCATCCACCCCCACA   77178     AA   _
                                TGTG  GGTG ATGAGATTT
                                ||||  |||| |||||||||
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                                ACAC  CCAC TACTCTGAA
                                  CC    C
GAM1591  LOC149271 3'  GAAAGCACATCACTTCACA    80003        G     AGA
                                TGTGAAG TGATG   TTTC
                                ||||||| |||||   ||||
                                ACACTTC ACTAC   AAAG
                                    _    ACG
GAM1591  LOC196214 3'  ATGGAACGGTCACCTTCCA    91172    T       GAGAT
                                TG GAAGGTGAT    TTCCAT
                                || |||||||||    ||||||
                                AC CTTCCACTG    AAGGTA
                                 _       GC___
GAM1591  LOC257319 3'  GATGGAAATCTTATTACTACCA 97472      AA
            CA                    TGTG  GGTGATGAGATTTCCATC
                                ||||  ||||||||||||||||||
                                ACAC  TCATTATTCTAAAGGTAG
                                  CA
GAM1591  LOC91266  5'  GATGCCGTCACCTCCACA    66021      A       AG
                                TGTG AGGTGATG  ATT
                                |||| ||||||||  |||
                                ACAC TCCACTGC  TAG
                                  C       CG
GAM1592  APAF1     3'  AGCCTTGAATGGCCCTTG    8580         TGTAC
                                CAAGGGCC    CAAGGCT
                                ||||||||    |||||||
                                GTTCCCGG    GTTCCGA
                                    TAA__
GAM1592  APAF1     3'  AGCCTTGAATGGCCCTTG    25961        TGTAC
                                CAAGGGCC    CAAGGCT
                                ||||||||    |||||||
                                GTTCCCGG    GTTCCGA
                                    TAA__
GAM1592  APG5L     3'  CCAGTGTCAGGCCTTTG     17938          _  CAA
                                CAAGGGCCTG TAC   GG
                                |||||||||| |||   ||
                                GTTTCCGGAC GTG   CC
                                     T   A__
GAM1592  BIN3      3'  AGCCCTGGCAGGCCCTCA    38572    A      TA   A
                                C AGGGCCTG  CCA GGCT
                                | ||||||||  ||| ||||
                                A TCCCGGAC  GGT CCGA
                                 C       __   C
GAM1592  CNN2      3'  AGCCACCGTGCCCAGGCCCTCA 16454    A     __    CAA
                                C AGGGCCT  GTAC   GGCT
                                | |||||||  ||||   ||||
                                A TCCCGGA  CGTG   CCGA
                                 C      CC    CCA
GAM1592  ENTPD5    3'  AGCCCAGGGACAGGTCCCT    8809      _    A  AA
                                AGGG CCTGT CC  GGCT
                                |||| ||||| ||  ||||
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                                TCCC GGACA GG  CCGA
                                  T    G  AC
GAM1592  ESR1     3'  AGCCTTCCCTGGGCCTTTG   5508         GTACC
                                CAAGGGCCT    AAGGCT
                                |||||||||    ||||||
                                GTTTCCGGG    TTCCGA
                                     TCCC_
GAM1592  ESRRA    3'  AGCCCCTGGGAACAGGCCC   16717        A_  A_
                                GGGCCTGT  CCA  GGCT
                                ||||||||  |||  ||||
                                CCCGGACA  GGT  CCGA
                                    AG   CC
GAM1592  FAT2     3'  AGCCTCTGTGGCCTTTG     9346         TGT  CA
                                CAAGGGCC   AC  AGGCT
                                ||||||||   ||  |||||
                                GTTTCCGG   TG  TCCGA
                                    ___  TC
GAM1592  GSPT1    5'  AGCCCCCGGGCCGGGCCCTTG  10881         TA  AA_
                                CAAGGGCCTG  CC   GGCT
                                ||||||||||  ||   ||||
                                GTTCCCGGGC  GG   CCGA
                                     CG  CCC
GAM1592  MEL      3'  AGCCAGTGTCAGGCCTCTG   19325    AG    _  CAA
                                CA  GGCCTG TAC   GGCT
                                ||  |||||| |||   ||||
                                GT  CCGGAC GTG   CCGA
                                 CT     T  A__
GAM1592  MNT      3'  AGCCCTGGGCTTGGCTCTTG  40085        TGTA  A
                                CAAGGGCC    CCA GGCT
                                ||||||||    ||| ||||
                                GTTCTCGG    GGT CCGA
                                    TTCG   C
GAM1592  NFIB     3'  GGTCCTTCAGGCCCTTG     20008         TACC   _
                                CAAGGGCCTG    AAGG CT
                                ||||||||||    |||| ||
                                GTTCCCGGAC    TTCC GG
                                     _____   T
GAM1592  NUP62    3'  AGCCCTGGGGCCCGCAGGTCCC 33779      _    A____  A
           T                     AGGG CCTGT    CCA GGCT
                                 |||| |||||    ||| ||||
                                 TCCC GGACG    GGT CCGA
                                   T    CCCGG   C
GAM1592  NUP62    3'  AGCCCTGGGGCCCGCAGGTCCC 25642      _    A____  A
           T                     AGGG CCTGT    CCA GGCT
                                 |||| |||||    ||| ||||
                                 TCCC GGACG    GGT CCGA
                                   T    CCCGG   C
GAM1592  PDYN     5'  AGCCTTGGACCAGCCACT    44581    _  C  TA
                                AG GGC TG  CCAAGGCT
                                || ||| ||  ||||||||
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                                TC CCG AC  GGTTCCGA
                                 A  _  CA
GAM1592  PLAG1    5'  AGCCCCGCGGTTGCCTCTTG  12146     _  __   ACCAA
                                CAAG GGC  CTGT    GGCT
                                |||| |||  ||||    ||||
                                GTTC CCG  GGCG    CCGA
                                  T  TT   CC___
GAM1592  PRKRA    3'  AGCACTAACAGGCCTTT    14891         ACCA  _
                                AAGGGCCTGT   AG GCT
                                ||||||||||   || |||
                                TTTCCGGACA   TC CGA
                                      A___  A
GAM1592  PSAP     3'  AGCCCTGACATGTGCTTG    69880     G  C   AC  A
                                CAAG GC TGT  CA GGCT
                                |||| || |||  || ||||
                                GTTC TG ACA  GT CCGA
                                  G  T  __  C
GAM1592  PTHLH    3'  AGCCTCAGCGGGGTGCTCTCA  12543   A    ___   ACCA
                                C AGGGC   CTGT   AGGCT
                                | |||||   ||||   |||||
                                A TCTCG   GGCG   TCCGA
                                 C    TGG   AC__
GAM1592  RAD50    3'  AGCCTCTGTCAGGCCTTCA   20403   A      T  CA
                                C AGGGCCTG AC  AGGCT
                                | |||||||| ||  |||||
                                A TTCCGGAC TG  TCCGA
                                 C       _  TC
GAM1592  RAD50    3'  AGCCTCTGTCAGGCCTTCA   56818   A      T  CA
                                C AGGGCCTG AC  AGGCT
                                | |||||||| ||  |||||
                                A TTCCGGAC TG  TCCGA
                                 C       _  TC
GAM1592  RARA     3'  AGCCCTGAAAGGACAGGCTCCT 8249     _     AC___  A
                                AGG GCCTGT    CA GGCT
                                ||| ||||||    || ||||
                                TCC CGGACA    GT CCGA
                                  T     GGAAA  C
GAM1592  RBM8A    3'  AGCCTTGAAGCTGCCTTTG   18804       CT  AC
                                CAAGGGC  GT  CAAGGCT
                                |||||||  ||  |||||||
                                GTTTCCG  CG  GTTCCGA
                                    T_  AA
GAM1592  SLC29A1  5'  AGTCTCAGCAGGCCCCTG   18260   A      ACCA
                                CA GGGCCTGT   AGGCT
                                || ||||||||   |||||
                                GT CCCGGACG   TCTGA
                                 C       AC__
GAM1592  SYNGR2   3'  AGCCGGACCAGGCTCTTG   17490         TA  AA
                                CAAGGGCCTG  CC  GGCT
                                ||||||||||  ||  ||||
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                                GTTCTCGGAC  GG  CCGA
                                      CA  __
GAM1592  TGFA     3'  AGCCTTTTGTGGGCCTTCA   13702   A     TG  CC
                                C AGGGCC  TA  AAGGCT
                                | ||||||  ||  ||||||
                                A TTCCGG  GT  TTCCGA
                                 C     GT  T_
GAM1592  THBD     3'  AGCCTTAATCAGGTCCTCA   6275    A      TACC
                                C AGGGCCTG    AAGGCT
                                | ||||||||    ||||||
                                A TCCTGGAC    TTCCGA
                                 C       TAA_
GAM1592  ABLIM    3'  AGCCTTGGCACAATGCCT    11320     C_   A
                                GGGC  TGT CCAAGGCT
                                ||||  ||| ||||||||
                                TCCG  ACA GGTTCCGA
                                   TA   C
GAM1592  ABLIM    3'  AGCCTTGGCACAATGCCT    22976     C_   A
                                GGGC  TGT CCAAGGCT
                                ||||  ||| ||||||||
                                TCCG  ACA GGTTCCGA
                                   TA   C
GAM1592  ASE-1    3'  AGCTGGGACTACAGGCCCCTG  24968    A       __  AA
                                CA GGGCCTGTA  CC  GGCT
                                || |||||||||  ||  ||||
                                GT CCCGGACAT  GG  TCGA
                                 C        CA  G_
GAM1592  BHC80    3'  AGCCCGGGCCACTGGCCCTTG  34013        T  A_  AA
                                CAAGGGCC GT  CC  GGCT
                                |||||||| ||  ||  ||||
                                GTTCCCGG CA  GG  CCGA
                                     T  CC  GC
GAM1592  BLCAP    5'  AGCCTTGGTGAAGGCCCT    22940        G
                                AGGGCCT TACCAAGGCT
                                ||||||| ||||||||||
                                TCCCGGA GTGGTTCCGA
                                    A
GAM1592  C1orf34  3'  AGCCCTGTGGAGGCCTTTG   61295         G   CAA
                                CAAGGGCCT TAC   GGCT
                                ||||||||| |||   ||||
                                GTTTCCGGA GTG   CCGA
                                      G   TC_
GAM1592  C1QR1    3'  AGCCAGGGCAGGCCTCA     24865   A      A  AA
                                A GGGCCTGT CC  GGCT
                                | ||||||||  ||  ||||
                                A TCCGGACG GG  CCGA
                                 C       _  A_
GAM1592  C1QTNF6  3'  AGCCCCAGGCTTTAGAGCCCTC 49985   A    _   TA_  AA_
            A                    C AGGGC CTG   CC   GGCT
                                | |||||  |||   ||   ||||
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                                A TCCCG GAT   GG   CCGA
                                 C    A   TTC  ACC
GAM1592  C22orf5   3'  AGCCCTTGGACAGGCCTCA   25335   A      A    _
                                A GGGCCTGT CCAAGG CT
                                | |||||||| |||||| ||
                                A TCCGGACA GGTTCC GA
                                 C       _     C
GAM1592  CBX6      3'  AGCCTTAGGCCAGGCCCT    27404        TA  _
                                AGGGCCTG  CC AAGGCT
                                ||||||||  || ||||||
                                TCCCGGAC  GG TTCCGA
                                     C_  A
GAM1592  CHST8     3'  AGCCTTGGATGGGGACCCC   42691     ___     A
                                GGG   CCTGT CCAAGGCT
                                |||   ||||| ||||||||
                                CCC   GGGTA GGTTCCGA
                                  CAG    _
GAM1592  CLDN4     5'  AGCCTTCCAGGTCCTCA     8953    A      TACC
                                C AGGGCCTG    AAGGCT
                                | ||||||||    ||||||
                                A TCCTGGAC    TTCCGA
                                 C       C___
GAM1592  CLSTN2    3'  AGCCTTGGGCACTCCCT     42396     CC   A
                                AGGG  TGT CCAAGGCT
                                ||||  ||| ||||||||
                                TCCC  ACG GGTTCCGA
                                  TC   _
GAM1592  DGS-A     3'  AGCCCTACTGGCAGGCCCTTG  86049          ACCAA_
                                CAAGGGCCTGT     GGCT
                                ||||||||||      ||||
                                GTTCCCGGACG     CCGA
                                       GTCATC
GAM1592  DKFZp434F142 3'  AGCCTCTGCAGGCCCT      51029          CCA
                                AGGGCCTGTA   AGGCT
                                ||||||||||   |||||
                                TCCCGGACGT   TCCGA
                                       C__
GAM1592  DKFZP434J037 3'  AGCCCGGTCAGGCTCTCA    48939   A      T   AA
                                C AGGGCCTG ACC  GGCT
                                | |||||||| |||  ||||
                                A TCTCGGAC TGG  CCGA
                                 C       _   C_
GAM1592  DKFZP566G1424 5'  AGCCGGTTGGCAGGGCCCTTG  85938         GTA   __
                                CAAGGGCCT   CCAA  GGCT
                                |||||||||   ||||  ||||
                                GTTCCCGGG   GGTT  CCGA
                                      AC_    GG
GAM1592  DKFZP586M1120 3'  AGCCTTCATGCAGGCCCCTG   49274    A       CC
                                CA GGGCCTGTA  AAGGCT
                                || |||||||||  ||||||
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                                GT CCCGGACGT  TTCCGA
                                 C       AC
GAM1592  DKFZp762A227 3'  AGCCTTGGCAGACCCTTG    34697      C   TA
                                CAAGGG CTG  CCAAGGCT
                                |||||| |||  ||||||||
                                GTTCCC GAC  GGTTCCGA
                                   A  __
GAM1592  DKFZp762M136 3'  AGCCACGGCCAGGCCCTT    65323        TA  AA
                                AAGGGCCTG  CC  GGCT
                                |||||||||  ||  ||||
                                TTCCCGGAC  GG  CCGA
                                     C_  CA
GAM1592  DNAJA3   3'  AGCCTCTGGACGGCCTT     61098       T  A  _
                                AGGGCC GT CCA AGGCT
                                |||||| || ||| |||||
                                TTCCGG CA GGT TCCGA
                                   _ _  C
GAM1592  FLJ10300  5'  AGTCGGACTCAGGCCCTT    36467        TA_  AA
                                AAGGGCCTG   CC  GGCT
                                |||||||||   ||  ||||
                                TTCCCGGAC   GG  CTGA
                                     TCA  __
GAM1592  FLJ11280  5'  AGCACTAACGGCCCTTG     37784        T  ACCA  _
                                CAAGGGCC GT    AG GCT
                                |||||||| ||    || |||
                                GTTCCCGG CA    TC CGA
                                    _ A___  A
GAM1592  FLJ11722  3'  AGCCTTGGGCTCCAGCCCT   46990      C  TA__
                                AGGGC TG    CCAAGGCT
                                ||||| ||    ||||||||
                                TCCCG AC    GGTTCCGA
                                  _ CTCG
GAM1592  FLJ13215  5'  AGCCGGAGCAGGCCTCG     47192   A      A  AA
                                A GGGCCTGT CC  GGCT
                                | ||||||||  ||  ||||
                                G TCCGGACG GG  CCGA
                                 C       A  __
GAM1592  FLJ13868  3'  AGCGGGTGGGCCAGGCCCTCA  43027   A      TA  AG_
                                C AGGGCCTG  CCA   GCT
                                | ||||||||  |||   |||
                                A TCCCGGAC  GGT   CGA
                                 C       CG   GGG
GAM1592  KIAA0057  3'  AGCCCCATGCTGGTCCCTTG   25399      _  T   CCAA
                                CAAGGG CC GTA    GGCT
                                |||||| || |||    ||||
                                GTTCCC GG CGT    CCGA
                                   T  T   ACC_
GAM1592  KIAA0179  3'  AGCCTTCTGCTGAGGTCCTTG  65453        __   CC
                                CAAGGGCCT  GTA  AAGGCT
                                |||||||||  |||  ||||||
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                                GTTCCTGGA CGT  TTCCGA
                                     GT  C_
GAM1592 KIAA0194 3' AGCCATAGTAAGGCCCTTG  66588       G  CAA
                                CAAGGGCCT TAC  GGCT
                                ||||||||| |||  ||||
                                GTTCCCGGA ATG  CCGA
                                     _  ATA
GAM1592 KIAA0239 5' AGCGGTAACCAGGCCCTTG  31614        __  AAG
                                CAAGGGCCTG TACC  GCT
                                |||||||||| ||||  |||
                                GTTCCCGGAC ATGG  CGA
                                     CA  ___
GAM1592 KIAA0323 3' GGCCTCAGGCCCTTG      63950        TACCA
                                CAAGGGCCTG   AGGCT
                                ||||||||||   |||||
                                GTTCCCGGAC   TCCGG
                                     _____
GAM1592 KIAA0399 5' AGCCTAAATGACAGGTCCTTG 31361        ACCA_
                                CAAGGGCCTGT   AGGCT
                                ||||||||||   |||||
                                GTTCCTGGACA   TCCGA
                                     GTAAA
GAM1592 KIAA0677 5' AGCCCTGGCGGGGCTTTG   28527     G  TA  A
                                CAAGG CCTG  CCA GGCT
                                ||||| ||||  ||| ||||
                                GTTTC GGGC  GGT CCGA
                                   G  __  C
GAM1592 KIAA0914 3' AGCCTTGGGGCTGGCCCT   30291      T TA
                                AGGGCC G  CCAAGGCT
                                |||||| |  ||||||||
                                TCCCGG C  GGTTCCGA
                                    T GG
GAM1592 KIAA1029 3' AGCCTGGCTGCAGGCCCTCA  24423  A       _  A
                                C AGGGCCTGTA CCA GGCT
                                | |||||||||| ||| ||||
                                A TCCCGGACGT GGT CCGA
                                 C        C  _
GAM1592 KIAA1535 3' AGCCTCTGTGGTCCTTG    80207       TGT  CA
                                CAAGGGCC  AC  AGGCT
                                ||||||||  ||  |||||
                                GTTCCTGG  TG  TCCGA
                                     ___  TC
GAM1592 KIAA1608 5' AGCCTCGAGCGGGCGGGCCC  46104       A  A____
                                GGGCCTGT CC    AGGCT
                                |||||||| ||    |||||
                                CCCGGGCG GG    TCCGA
                                     _ CGAGC
GAM1592 KIAA1922 5' AGCCCTGGAGAAGCAGGCCCT 73983        A___  A
                                AGGGCCTGT   CCA GGCT
                                |||||||||   ||| ||||
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                                TCCCGGACG   GGT CCGA
                                     AAGA  C
GAM1592 MAFB    3' AGCCCTGAGACACAGGCCCTCA 19586   A      AC__ A
                                C AGGGCCTGT   CA GGCT
                                | |||||||||   || ||||
                                A TCCCGGACA   GT CCGA
                                 C       CAGA  C
GAM1592 MGC12992 3' AGCCTTGGCTTTGGTAGCCTCC 51342   A  __  TGTA
                                C AGG  GCC   CCAAGGCT
                                | |||  |||   ||||||||
                                C TCC  TGG   GGTTCCGA
                                 C   GA   TTTC
GAM1592 MGC13170 3' AGCCTTGGGCACTACCCTCC  52128   A   CC_  A
                                C AGGG   TGT CCAAGGCT
                                | ||||   ||| ||||||||
                                C TCCC   ACG GGTTCCGA
                                 C   ATC  _
GAM1592 MGC15429 3' AGCCCTTGCAGGAGGCCCTT  52208       GTAC   _
                                AAGGGCCT   CAAGG CT
                                ||||||||   ||||| ||
                                TTCCCGGA   GTTCC GA
                                     GGAC   C
GAM1592 MGC2454  3' AGCCGGGTTCAGGCCCTTG   48282        T  AA
                                CAAGGGCCTG ACC  GGCT
                                |||||||||| |||  ||||
                                GTTCCCGGAC TGG  CCGA
                                      T  G_
GAM1592 MGC3113  3' AGCCTTGGAGCTGAGCCCT   44058     CT_  A
                                AGGGC  GT CCAAGGCT
                                |||||  || ||||||||
                                TCCCG  CG GGTTCCGA
                                   AGT  A
GAM1592 MGC8407  3' AGCCTTACTGGGTCCTT     44109       _  CCA
                                AAGGGCCT GTA  AGGCT
                                |||||||| |||  |||||
                                TTCCTGGG CAT  TCCGA
                                     T  ___
GAM1592 PGR1    3' AGATTGGCAAAGGCCCTTG   53904       GTA   GG
                                CAAGGGCCT  CCAA  CT
                                |||||||||  ||||  ||
                                GTTCCCGGA  GGTT  GA
                                     AAC   A_
GAM1592 PSKH1   3' AGCCTGGGCCAGGCCCTT   68788       TA  A
                                AAGGGCCTG  CCA GGCT
                                |||||||||  ||| ||||
                                TTCCCGGAC  GGT CCGA
                                     CG  _
GAM1592 RPP14   5' AGCCTTGGCGGGTCCTTG   60220       TA
                                CAAGGGCCTG  CCAAGGCT
                                ||||||||||  ||||||||
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                                GTTCCTGGGC  GGTTCCGA
                                    __
GAM1592  SCAMP-4   3'  AGCCCTGCAGGAGAGGCCTTTG 55337         GTAC__  A
                                CAAGGGCCT     CA GGCT
                                |||||||||     || ||||
                                GTTTCCGGA     GT CCGA
                                     GAGGAC  C
GAM1592  SEC14L1   3'  AGCCCTTGAGGTCCTT      13003        GTAC    _
                                AAGGGCCT    CAAGG CT
                                ||||||||    ||||| ||
                                TTCCTGGA    GTTCC GA
                                    _____    C
GAM1592  SEMA4G    3'  GTCCTCACAGGCCCTTG     35861          ACCA   _
                                CAAGGGCCTGT    AGG C
                                ||||||||||    ||| |
                                GTTCCCGGACA    TCC G
                                     C___   T
GAM1592  SEMA4G    3'  GTCCTCACAGGCCCTTG     96331          ACCA   _
                                CAAGGGCCTGT    AGG C
                                ||||||||||    ||| |
                                GTTCCCGGACA    TCC G
                                     C___   T
GAM1592  SNPH      3'  AGCCCTGGGACAGGCCCT    28898         A   A
                                AGGGCCTGT CCA GGCT
                                ||||||||| ||| ||||
                                TCCCGGACA GGT CCGA
                                     G   C
GAM1592  TU3A      3'  AGCCCTGGGCCCCAGGCCCT   24176         TA__   A
                                AGGGCCTG    CCA GGCT
                                ||||||||    ||| ||||
                                TCCCGGAC    GGT CCGA
                                    CCCG   C
GAM1592  WBSCR16   3'  AGCCTTTGGTGGGCCGCT    96146    _    GT     _
                                AG GGCCT  ACCAA GGCT
                                || |||||  ||||| ||||
                                TC CCGGG  TGGTT CCGA
                                 G     __     T
GAM1592  LOC124460 5'  AGCCCTGGAGACTGGAGCCTTG 76554       G_  T  A_   A
                                CAAGG  CC GT  CCA GGCT
                                |||||  || ||  ||| ||||
                                GTTCC  GG CA  GGT CCGA
                                   GA  T  GA   C
GAM1592  LOC130074 3'  AGCCTTGGGGTGGGCACCT    76621     _    TA
                                AGG GCCTG  CCAAGGCT
                                ||| |||||  ||||||||
                                TCC CGGGT  GGTTCCGA
                                  A    GG
GAM1592  LOC138428 3'  AGCCTTGGTATCTACTTT     75853      GCCT
                                AAGG    GTACCAAGGCT
                                ||||    ||||||||||
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                                TTTC    TATGGTTCCGA
                                  ATC_
GAM1592  LOC145693 5'  AGCCTTGGACAAGACCCTCA   77852    A    C  _  A
                                C AGGG CT GT CCAAGGCT
                                | |||| || || ||||||||
                                A TCCC GA CA GGTTCCGA
                                 C    A  A  _
GAM1592  LOC146818 5'  AGCCTGGGGCAGGCCCT     78735        TA   A
                                AGGGCCTG  CCA GGCT
                                |||||||||  ||| ||||
                                TCCCGGAC  GGT CCGA
                                     GG   _
GAM1592  LOC147160 5'  AGCCTACAGTCAGGCCCT    85066        T  CA_
                                AGGGCCTG AC   AGGCT
                                |||||||| ||   |||||
                                TCCCGGAC TG   TCCGA
                                     _  ACA
GAM1592  LOC147949 5'  AGCCCTGGCCCGGGCCCT    79276         TA   A
                                AGGGCCTG  CCA GGCT
                                |||||||||  ||| ||||
                                TCCCGGGC  GGT CCGA
                                     CC   C
GAM1592  LOC149134 5'  AGCCTTGGCAAGCTCTCG    85514    A    C  TA
                                C AGGGC TG  CCAAGGCT
                                | ||||| ||  ||||||||
                                G TCTCG AC  GGTTCCGA
                                 C    A  __
GAM1592  LOC150208 5'  AGCCTTGGAGATTAGCCCTT   86075       CT  A_
                                AAGGGC  GT  CCAAGGCT
                                ||||||  ||  ||||||||
                                TTCCCG  TA  GGTTCCGA
                                   AT  GA
GAM1592  LOC150372 3'  AGCCCCTGCAGGCCCCTG    80602    A       CCAA
                                CA GGGCCTGTA    GGCT
                                || |||||||||    ||||
                                GT CCCGGACGT    CCGA
                                 C        CC__
GAM1592  LOC151178 5'  AGCCCTGGAAGGGCTCTTG    80950         GTA   A
                                CAAGGGCCT   CCA GGCT
                                |||||||||   ||| ||||
                                GTTCTCGGG   GGT CCGA
                                     AA_   C
GAM1592  LOC151512 5'  AGCCTTGGTGGCTCCT      86610     _   TGT
                                AGG GCC   ACCAAGGCT
                                ||| |||   |||||||||
                                TCC CGG   TGGTTCCGA
                                  T   ____
GAM1592  LOC153894 5'  AGCCTCAACTGTGCCAGGCCCT 81876         _   CA____
                                AGGGCCTG TAC     AGGCT
                                |||||||| |||     |||||
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                                TCCCGGAC GTG    TCCGA
                                    C   TCAAC
GAM1592  LOC154881 3'  AGCCCCAAAACATGGCTCTTG  82067       _   ACCAA
                                CAAGGGCC TGT    GGCT
                                |||||||| |||    ||||
                                GTTCTCGG ACA    CCGA
                                    T   AAACC
GAM1592  LOC154990 5'  AGCCTCTGCAGGCCCT     82146         CCA
                                AGGGCCTGTA   AGGCT
                                ||||||||||   |||||
                                TCCCGGACGT   TCCGA
                                     C__
GAM1592  LOC196477 3'  CCTCATTTGCAGGCTCTTG   89064          CCA_
                                CAAGGGCCTGTA   AGG
                                ||||||||||||   |||
                                GTTCTCGGACGT   TCC
                                      TTAC
GAM1592  LOC196707 3'  CCTTGGGTACACCACAGGCCCT 88924         A_______
           T                     AAGGGCCTGT     CCAAGG
                                ||||||||||      ||||||
                                TTCCCGGACA     GGTTCC
                                     CCACATG
GAM1592  LOC197083 3'  AGCCCCTTGCAGAAGCACTTG  89223     G  __    CCAA
                                CAAG GC  CTGTA   GGCT
                                |||| ||  |||||   ||||
                                GTTC CG  GACGT   CCGA
                                  A  AA    TCC_
GAM1592  LOC199704 3'  AGCCTCACGGGCCCTCA     89695   A       ACCA
                                C AGGGCCTGT   AGGCT
                                | |||||||||   |||||
                                A TCCCGGGCA   TCCGA
                                 C       C___
GAM1592  LOC200197 3'  AGCCCTGTTGGAGGCTCTTG   90011         G  C  A
                                CAAGGGCCT TA CA GGCT
                                ||||||||| || || ||||
                                GTTCTCGGA GT GT CCGA
                                     G  T  C
GAM1592  LOC203276 3'  AGCTTTCACAAGCCCTT     92108       C   ACC
                                AAGGGC TGT   AAGGCT
                                |||||| |||   ||||||
                                TTCCCG ACA   TTTCGA
                                   A   C__
GAM1592  LOC203305 3'  AGCTTTCACAAGCCCTT     92161       C   ACC
                                AAGGGC TGT   AAGGCT
                                |||||| |||   ||||||
                                TTCCCG ACA   TTTCGA
                                   A   C__
GAM1592  LOC221424 3'  AGCCTTGGGGGGCACTTG    95266      G    GTA
                                CAAG GCCT   CCAAGGCT
                                |||| ||||   ||||||||
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                                GTTC CGGG   GGTTCCGA
                                  A   G__
GAM1592  LOC222031 3'  AGCAGGGACAGGCTCTT     95668          A  AAG
                                AAGGGCCTGT CC   GCT
                                |||||||||| ||   |||
                                TTCTCGGACA GG   CGA
                                     _  GA_
GAM1592  LOC222865 3'  AGCCCTGACAGGTTCT      94436          AC  A
                                AGGGCCTGT  CA GGCT
                                |||||||||  || ||||
                                TCTTGGACA  GT CCGA
                                     __  C
GAM1592  LOC255975 5'  AGCCTCTGCAGGCCCT      97570          CCA
                                AGGGCCTGTA   AGGCT
                                ||||||||||   |||||
                                TCCCGGACGT   TCCGA
                                     C__
GAM1592  LOC51014  3'  AGTTTATACAGGCCTT      66424          CCA
                                AGGGCCTGTA   AGGCT
                                ||||||||||   |||||
                                TTCCGGACAT   TTTGA
                                     A__
GAM1592  LOC56181  5'  AGCCCAGGAAGGCTCTTG    97269          GTA  AA
                                CAAGGGCCT   CC  GGCT
                                |||||||||   ||  ||||
                                GTTCTCGGA   GG  CCGA
                                     A__  AC
GAM1592  LOC90038  3'  AGCTTTCACAAGCCCTT     61791        C   ACC
                                AAGGGC TGT   AAGGCT
                                ||||||| |||   ||||||
                                TTCCCG ACA   TTTCGA
                                   A   C__
GAM1592  LOC90183  3'  AGCCCTGAGACACAGGCCTCA  62401    A       AC__  A
                                A GGGCCTGT    CA GGCT
                                | ||||||||    || ||||
                                A TCCGGACA    GT CCGA
                                 C       CAGA  C
GAM1592  LOC90625  5'  AGCCTTGGGGCTGGCCCT    64375        T TA
                                AGGGCC G  CCAAGGCT
                                |||||| |  ||||||||
                                TCCCGG C  GGTTCCGA
                                   T GG
GAM1592  LOC91012  5'  AGCAGTACAGGTCCTTG     65243           CAAG
                                CAAGGGCCTGTAC    GCT
                                ||||||||||||    |||
                                GTTCCTGGACATG    CGA
                                      A___
GAM1592  LOC91179  5'  AGCCCTGGCGTCCACGGGCCC  65762         A_____  A
                                GGGCCTGT    CCA GGCT
                                ||||||||    ||| ||||
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                                CCCGGGCA    GGT CCGA
                                    CCTGC   C
GAM1593  CSPG3    3'  AAATCCAGAAGTCAGAGCCAA  16515       CGG   ATC
                                TTGGCTC   GGC   CTGGATTT
                                |||||||   |||   ||||||||
                                AACCGAG   CTG   GACCTAAA
                                   A__   AA_
GAM1593  EXT2     3'  CCAGAATTCGGTGCAAAAGCCA 6379       CCGGG   _____
              A                  TTGGCT    GCATC    CTGG
                                 ||||||    |||||    ||||
                                 AACCGA    CGTGG    GACC
                                    AAA__    CTTAA
GAM1593  LOC152860 5'  AGGACGCCCCGAAGCCGA    81574       C     A
                                TTGGCT CGGGGC TCCT
                                |||||| |||||| ||||
                                AGCCGA GCCCCG AGGA
                                   A     C
GAM1593  LOC154092 3'  AATCCAGGATAGCAGC      87367     CCGGG  _
                                GCT    GC ATCCTGGATT
                                |||    || ||||||||||
                                CGA    CG TAGGACCTAA
                                 _____  A
GAM1594  TERF1    3'  CCCAAATCCTGTTCCAATGA   34391       C   TA   C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                    _  C_   A
GAM1594  FLJ10159  3'  CCATGTCACGCCATCCAATGAC 36334        CA_   A   TC
                                GTCATTGGA   CGT GAT  GG
                                |||||||||   ||| |||  ||
                                CAGTAACCT   GCA CTG  CC
                                    ACC  _   TA
GAM1594  FLJ14213  3'  CCGATGCTCCCAATGACG    46216        ACAC   GAT
                                CGTCATTGG    GTA   TCGG
                                |||||||||    |||   ||||
                                GCAGTAACC    CGT   AGCC
                                    CT__   ___
GAM1594  MGC10715  3'  ATTTACCAGACATCCAATGAC  44495        CAC___
                                GTCATTGGA     GTAGAT
                                |||||||||     ||||||
                                CAGTAACCT     CATTTA
                                    ACAGAC
GAM1594  MOST2    5'  CCAGGACTGCCCAATGAC    40059       ACAC   A  _
                                GTCATTGG    GTAG TTC GG
                                ||||||||    |||| ||| ||
                                CAGTAACC    CGTC AGG CC
                                    _____   _  A
GAM1594  LOC150370 3'  CCGGGTCTACGTGCCCATGAC  86123      T  A
                                GTCAT GG CACGTAGATTCGG
                                ||||| || ||||||||||||
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                                CAGTA CC GTGCATCTGGGCC
                                   C  _
GAM1594  LOC152620 3'  CCCAAATCCTGTTCCAATGA   60707        C   TA   C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                     _  C_   A
GAM1594  LOC158668 3'  CCCAAATCCTGTTCCAATGA   69896        C   TA   C
                                TCATTGGA ACG  GATT GGG
                                |||||||| |||  |||| |||
                                AGTAACCT TGT  CTAA CCC
                                     _  C_   A
GAM1595  ELF3      3'  TGACCTTGACCTTGACCAA    16685      T    GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                   _    AGT  ___
GAM1595  JAK2      3'  TGACCTTCATTCTGAGACCAA  18318       CAA      AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_      C_
GAM1595  SLC10A2   5'  ACTCTCTGTCTTGACCAA     6590        CAA      A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM1595  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA  37205       CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM1595  KIAA1958  5'  GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||   ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM1595  MARCKS    3'  ACTTTCCACCCTGCCCA     11411     TTCA   A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
                                ACC    TCCC ACCTTTCA
                                  CG__   _
GAM1595  TUB       5'  GTGGGACCATCCCTTAAACC   13898      C       AAAG
                                GGTT AAGGGATGG    TCAC
                                |||| |||||||||    ||||
                                CCAA TTCCCTACC    GGTG
                                  A        AG__
GAM1595  LOC80298  3'  ACTTTTACCTTGAACCA      48062          GATG
                                TGGTTCAAGG    GAAAGT
                                ||||||||||    ||||||
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                                ACCAAGTTCC    TTTTCA
                                     A___
GAM1596  FLJ21438  5'  CAAAACGCTTCCCCCCATCCCA 62190      GAGATTATC
                                TGGGA        AAGCGTTTTG
                                |||||        ||||||||||
                                ACCCT        TTCGCAAAAC
                                   ACCCCCC__
GAM1596  FLJ32334  3'  AAAACGCTATTCCTTCCCA   58605       A  TTATCA
                                TGGGAG GA     AGCGTTTT
                                |||||| ||     ||||||||
                                ACCCTT CT     TCGCAAAA
                                   C  TA____
GAM1596  HHLA2     3'  CAATGTACTTTGTAATCTCCCC 23953      A       C   CG T
              CA                   TGGG GAGATTAT AAG  T TTG
                                |||| |||||||| |||  | |||
                                ACCC CTCTAATG TTC  G AAC
                                   C       T   AT T
GAM1597  ADAT1     3'  CCAGCAAAGAATGAAGGC    24914     __        C
                                GTC  CATTCTTTGC GG
                                |||  |||||||||| ||
                                CGG  GTAAGAAACG CC
                                  AA         A
GAM1597  M17S2     5'  CCGGTAGCGGACGGTCCTT   20910          ATTCT
                                AAGGACCGTCC    TTGCCGG
                                ||||||||||     |||||||
                                TTCCTGGCAGG    GATGGCC
                                      C_____
GAM1597  ST14      5'  CCGGCAGGGACGACGCCT    42042     AC    CAT
                                AGG  CGTC   TCTTTGCCGG
                                |||  ||||   ||||||||||
                                TCC  GCAG   AGGGACGGCC
                                  __    C__
GAM1597  HTGN29    5'  GCCAACTGTGTGGCGGTCC    39885        _   TC  T
                                GGACCGTC CAT  TT GC
                                |||||||| |||  || ||
                                CCTGGCGG GTG  AA CG
                                     T   TC  C
GAM1597  PMAIP1    3'  GCAAGAATGGAAGACCCTT    41211      ACCG       T
                                AAGG    TCCATTCTT GC
                                ||||    ||||||||| ||
                                TTCC    AGGTAAGAA CG
                                  CAGA       _
GAM1597  LOC144278 3'  GCCAGCAAAGACTGCTCGATGG 77274          ___  T      C
              TCCT                   AGGACCGTC   CA TCTTTGC GGC
                                |||||||||   || ||||||| |||
                                TCCTGGTAG   GT AGAAACG CCG
                                     CTC  C      A
GAM1597  LOC147976 3'  CCGGTGAATGAAGACCCT    79287     ACC   CA   _  TG
                                AGG   GTC  TTC TT  CCGG
                                |||   |||  ||| ||  ||||
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                                TCC   CAG  AAG AA  GGCC
                                 ___   __   T  GT
GAM1597  LOC254263 5'  GCCGGCAGCGGACGCGCC    96367    AC     ATTCT
                                GG  CGTCC    TTGCCGGC
                                ||  |||||    ||||||||
                                CC  GCAGG    GACGGCCG
                                 GC    C____
GAM1598  ADCY8    5'  GCTCACAGCGCTGCGGCTCCT  8501      A  AT   CAA
                                AGGA CC  GGC   CTGTGAGC
                                ||||  ||  |||   ||||||||
                                TCCT GG  TCG   GACACTCG
                                  C  CG   C__
GAM1598  CIT      5'  GCTCACAGAGCTACAGCTCTCC 70304     ACCA__    CAA
                                GGA     TGGC   CTGTGAGC
                                |||     ||||   ||||||||
                                CCT     ATCG   GACACTCG
                                  CTCGAC   A__
GAM1598  FAAH     5'  GCGGTCTCCGGCCATGGCCCC  9341     AA       A___
                                GG  CCATGGCC    ACTGT
                                ||  ||||||||    |||||
                                CC  GGTACCGG    TGGCG
                                 CC       CCTC
GAM1598  GSTM3    5'  GCTCACAGTTTCCCTAGTCCT  68638     ACCAT  CC
                                AGGA    GG  AACTGTGAGC
                                ||||    ||  ||||||||||
                                TCCT    CC  TTGACACTCG
                                  GAT__  CT
GAM1598  HSD11B2  3'  GCTCCGTGAGCCTTGGTTCCT  5771         T   CA  T T
                                AGGAACCA GGC  AC G GAGC
                                |||||||| |||  || | ||||
                                TCCTTGGT CCG  TG C CTCG
                                    T   AG  _ _
GAM1598  HYAL1    5'  CTCCAGTGGCCATGCTCC    53703     AC       A   T
                                GGA  CATGGCCA CTG GAG
                                |||  |||||||| ||| |||
                                CCT  GTACCGGT GAC CTC
                                  C_       _   _
GAM1598  NPTX2    3'  GCTGGAGTGGCCATGTCCCTT  94085      AAC       A  G G
                                AAGG   CATGGCCA CT T AGC
                                ||||   |||||||| || | |||
                                TTCC   GTACCGGT GA G TCG
                                  CT_       _  G _
GAM1598  RFX2     3'  GCCCCACCAGACCATGGGTTCC 7158          _    CCAA   _  A_
            TT                   AAGGAACC ATGG    CTG TG  GC
                                ||||||||  ||||    ||| ||  ||
                                TTCCTTGG TACC    GAC AC  CG
                                    G    A___   C  CC
GAM1598  SMAP     5'  GCCCCACAGAGCCATGGTCC   22932     A      CAA     A_
                                GGA CCATGGC   CTGTG  GC
                                ||| |||||||   |||||  ||
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                                CCT GGTACCG  GACAC  CG
                                  _     A__    CC
GAM1598 SMURF1   3' GCTCACAGCCCTGAGCTCTTT 94049      AC_ T  CAAC
                                AAGGA  CA GGC   TGTGAGC
                                |||||  || |||   |||||||
                                TTTCT  GT CCG   ACACTCG
                                   CGA  C  ____
GAM1598 DC-TM4F2 3' ACTGTTGGCCAGGGCTCCT  48895     A  A      T
                                AGGA CC TGGCCAAC GT
                                |||| || |||||||| ||
                                TCCT GG ACCGGTTG CA
                                  C  G       T
GAM1598 DKFZp566H0824 5' GCTCACAAACCCCATAGTTGCC 34488     _  C   CCAAC
             T                   AGG AAC ATGG    TGTGAGC
                                ||| ||| ||||    |||||||
                                TCC TTG TACC    ACACTCG
                                  G  A   CCAA_
GAM1598 FLJ10292 3' GCCCACAGTTGTTGGTTGTTCC 36432       C  GGC      A
             T                   AGGAAC AT   CAACTGTG GC
                                |||||| ||   |||||||| ||
                                TCCTTG TG   GTTGACAC CG
                                   T  GTT      C
GAM1598 FLJ20085 3' GCTCATGGTGCCACAGCCCCT  35009     AACCA   CA
                                AGG    TGGC  ACTGTGAGC
                                |||    ||||  |||||||||
                                TCC    ACCG  TGGTACTCG
                                  CCGAC   __
GAM1598 FLJ22690 3' GCTCACAGCCGACCTGTGGCCT 45575     AA    CCAA_
                                AGG  CCATGG    CTGTGAGC
                                |||  ||||||    ||||||||
                                TCC  GGTGTC    GACACTCG
                                  __     CAGCC
GAM1598 FLJ32449 3' GCATTTGGCCATGGTTCCTT   59378            C
                                AAGGAACCATGGCCAA TGT
                                |||||||||||||||| |||
                                TTCCTTGGTACCGGTT ACG
                                          T
GAM1598 HPIP     3' GCTCACAGCTGCCTTGGCCCC  40425    AA  T   CAA
                                GG  CCA GGC   CTGTGAGC
                                ||  ||| |||   ||||||||
                                CC  GGT CCG   GACACTCG
                                  CC   T   TC_
GAM1598 ILF3     3' GCTCACAGTCGAACTACAGCTC 25234     ACCA   CCA_
             C                   GGA   TGG   ACTGTGAGC
                                |||   |||   |||||||||
                                CCT   ATC   TGACACTCG
                                  CGAC   AAGC
GAM1598 KIAA1190 3' GCTCACAGAGCACCCCAGTTCC 71651       CAT  CCAA
             T                   AGGAAC   GG   CTGTGAGC
                                ||||||   ||   ||||||||
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                                TCCTTG  CC   GACACTCG
                                   ACC  ACGA
GAM1598  MGC11266  3'  GCTCACAGTGGTCAGGGCCC  44488   AA  A    A
                                GG  CC TGGCCA CTGTGAGC
                                ||  || |||||| ||||||||
                                CC  GG ACTGGT GACACTCG
                                 CG  _    _
GAM1598  MGC11352  5'  ACTGTTGGCCAGGGCTCCT   65424    A  A     T
                                AGGA CC TGGCCAAC GT
                                |||| || |||||||| ||
                                TCCT GG ACCGGTTG CA
                                  C  G      T
GAM1598  MKP-7     3'  GCTTCTCTTGGCCATGGTCCC  67015   A       CTGT
                                GG ACCATGGCCAA   GAGC
                                || ||||||||||   ||||
                                CC TGGTACCGGTT   TTCG
                                 C         CTC_
GAM1598  MSP       3'  GCTCAGGCAGGCCATGGCC   50245   AA      AA  G
                                GG  CCATGGCC  CT TGAGC
                                ||  ||||||||  || |||||
                                CC  GGTACCGG  GG ACTCG
                                 __       AC  _
GAM1598  PGR1      3'  CTCACAGTTGGAGTTCTCC   53905   A    CATGG
                                A GGAAC    CCAACTGTGAG
                                | |||||    ||||||||||
                                C TCTTG    GGTTGACACTC
                                 C    A____
GAM1598  PTPRT     3'  GCTTCGTGTTGGCCAAGACTCC 56502      ACCA      TGT
            TT                   AAGGA   TGGCCAAC  GAGC
                                |||||   ||||||||  ||||
                                TTCCT   ACCGGTTG  TTCG
                                   CAGA      TGC
GAM1598  TRF4-2    3'  CTCAAACAAGCCATGGTTCCTT 42611          CAACTG
                                AAGGAACCATGGC     TGAG
                                ||||||||||||     ||||
                                TTCCTTGGTACCG     ACTC
                                       AACAA_
GAM1598  LOC122786 3'  GCCTTTGGCCATGATTCT    74622     C       CT
                                GGAA CATGGCCAA  GT
                                |||| |||||||||  ||
                                TCTT GTACCGGTT  CG
                                  A       TC
GAM1598  LOC138428 3'  TAGTGGCCATGGCTGCCT    75862    AA_      A
                                AGG   CCATGGCCA CTG
                                |||   ||||||||| |||
                                TCC   GGTACCGGT GAT
                                  GTC       _
GAM1598  LOC145581 3'  GCTCCATTAGACCATGGTTC   77794        CCAAC  T
                                GAACCATGG    TG GAGC
                                |||||||||    || ||||
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                                CTTGGTACC     AC CTCG
                                     AGATT  _
GAM1598  LOC146268 5'  GCTCACAGTCGGCTTGCTGCCT 78342      AAC  T    A
                                AGG   CA GGCC ACTGTGAGC
                                |||   || |||| |||||||||
                                TCC   GT TCGG TGACACTCG
                                  GTC  _    C
GAM1598  LOC147299 3'  GCTGTGAGCCGCCATGGTCCC  78981     A       CAA  GTG
                                GG ACCATGGC   CT   AGC
                                || ||||||||   ||   |||
                                CC TGGTACCG   GA   TCG
                                 C       CC_  GTG
GAM1598  LOC159199 3'  GCTCACAGCTGGCGGCCCT    83062     AA  ATG    A
                                AGG  CC   GCCA CTGTGAGC
                                |||  ||   |||| ||||||||
                                TCC  GG   CGGT GACACTCG
                                  C_  ____    C
GAM1598  LOC200982 5'  AGTTGGCCATGGCTCTTT     91807       A
                                AAGGA CCATGGCCAACT
                                ||||| ||||||||||||
                                TTTCT GGTACCGGTTGA
                                   C
GAM1598  LOC253842 3'  GCTCATAGAAGCCTGGTCCCT  99238     A    T   CAA
                                AGG ACCA GGC   CTGTGAGC
                                ||| |||| |||   ||||||||
                                TCC TGGT CCG   GATACTCG
                                  C    _   AA_
GAM1598  LOC254778 3'  GCCCTGTGTTGGCCAAGGTTCC 97831        A       TGTGA
                                GGAACC TGGCCAAC     GC
                                |||||| ||||||||     ||
                                CCTTGG ACCGGTTG     CG
                                    A       TGTCC
GAM1598  LOC255231 3'  CTCACAGTTAGCCAGCTGACC  97119    AACCA    C
                                GG     TGGC AACTGTGAG
                                ||     |||| |||||||||
                                CC     ACCG TTGACACTC
                                 AGTCG    A
GAM1598  LOC257358 5'  GCTCGTGAAGAGCATGGTTCCT 98900           G CAACTG
           T                     AAGGAACCATG C      TGAGC
                                ||||||||||| |      |||||
                                TTCCTTGGTAC G      GCTCG
                                      _ AGAAGT
GAM1598  LOC90190  3'  CGCCCACAGAGCAATTGGCCAT 62422     AC       _____     A ___
           GCCTCC                  GGA  CATGGCCAA     CTGTG GC   G
                                |||  |||||||||     ||||| ||   |
                                CCT  GTACCGGTT     GACAC CG   C
                                  CC        AACGA     C __
GAM1598  LOC90495  3'  GCTCACAGTCAACTGCTTTCTT 63737       CCAT   CA___
           T                     AAGGAA    GGC     ACTGTGAGC
                                ||||||    |||     |||||||||
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                                TTTCTT   TCG    TGACACTCG
                                   ____  TCAAC
GAM1598 LOC90750 3' GCTCACAGCCCTGCCCTGCCCC 64630   AAC  T  CAA_
             C                   GG  CA GGC   CTGTGAGC
                                 ||  || |||   ||||||||
                                 CC  GT CCG   GACACTCG
                                  CCC  C  TCCC
GAM1599 ARHA    3' CTCTGCACTCCCACCTGA    71232   T_   A
                                 TC  GTGG GAGTGCAGAG
                                 ||  |||| ||||||||||
                                 AG  CACC CTCACGTCTC
                                  TC   _
GAM1599 ASGR2   5' CTCCACACCTTTCACAGATC   56046    T      A  CA
                                 GAT CTGTGGAG GTG  GAG
                                 ||| |||||||| |||  |||
                                 CTA GACACTTT CAC  CTC
                                   _      C  AC
GAM1599 GZMM    3' CTCGCTGTCTCCACAGGA    19213         GT  A
                                 TTCTGTGGAGA  GC GAG
                                 ||||||||||  || |||
                                 AGGACACCTCT  CG CTC
                                       GT  _
GAM1599 IFNAR2  3' CTCTGCCACCTCTACAGAATC  7899          A  _
                                 GATTCTGTGGAG GTG CAGAG
                                 |||||||||||| ||| |||||
                                 CTAAGACATCTC CAC GTCTC
                                      _  C
GAM1599 KAL1    3' CTCTGCATAGATACAAAAT   5835    C   GAGA
                                 ATT TGTG   GTGCAGAG
                                 ||| ||||   ||||||||
                                 TAA ACAT   TACGTCTC
                                   A   AGA_
GAM1599 LIF     3' CTGCACAGCATCACTGAATC  11303     T   AGA_
                                 GATTC GTGG   GTGCAG
                                 ||||| ||||   ||||||
                                 CTAAG CACT   CACGTC
                                    T   ACGA
GAM1599 MTMR1   5' CTGGACAGTCCCACAGGATC  70724         A __ G
                                 GATTCTGTGG GA  GT CAG
                                 |||||||||| ||  || |||
                                 CTAGGACACC CT  CA GTC
                                       _ GA  G
GAM1599 PKIG    3' CTCATGGAGCTCCACAGATC  23927    T      AGTG _
                                 GAT CTGTGGAG   CA GAG
                                 ||| ||||||||   || |||
                                 CTA GACACCTC   GT CTC
                                   _      GAG_  A
GAM1599 PPP1R3C 3' CTCTGCAGTGACAGAATT    19423        GGAGAG
                                 GATTCTGT     TGCAGAG
                                 ||||||||     |||||||
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                                TTAAGACA     ACGTCTC
                                     GTG___
GAM1599  RFX2     3'  CTCTGCACTCAACTGGAACC  7156    A   _  GGA
                                G TTCT GT   GAGTGCAGAG
                                | |||| ||   ||||||||||
                                C AAGG CA   CTCACGTCTC
                                 C    T  A__
GAM1599  SHMT2    3'  CTCCTTATTCCCTACAGAATC  19435         A    CA
                                GATTCTGTGG GAGTG  GAG
                                |||||||||| |||||  |||
                                CTAAGACATC CTTAT  CTC
                                      C     TC
GAM1599  STK4     3'  CTCTGTCGTCTCTCCACAG   21864          _  _
                                CTGTGGAGAG TG CAGAG
                                |||||||||| || |||||
                                GACACCTCTC GC GTCTC
                                      T  T
GAM1599  TEM8     3'  CTCTAGCTTTCCACAAATC   50826     C        GC
                                GATT TGTGGAGAGT  AGAG
                                |||| ||||||||||  ||||
                                CTAA ACACCTTTCG  TCTC
                                  _        A_
GAM1599  USH3A    3'  CTGCACTCTTATTGGATTC   54842    T   GTG
                                GA TCT   GAGAGTGCAG
                                || |||   ||||||||||
                                CT AGG   TTCTCACGTC
                                 T   TTA
GAM1599  ASB13    3'  CTGCGCTGTTCTACAGAA    45546          _
                                TTCTGTGGAG AGTGCAG
                                |||||||||| |||||||
                                AAGACATCTT TCGCGTC
                                      G
GAM1599  Di-Ras2  3'  CTCTGGAGTCACAGAATC    34611          AGAGTG
                                GATTCTGTGG     CAGAG
                                ||||||||||     |||||
                                CTAAGACACT     GTCTC
                                      GAG___
GAM1599  DKFZP434N014 3'  CTCTGCACCCCCAGCCTATC   61229     T__   T  AGA
                                GAT   CTG GG   GTGCAGAG
                                |||   ||| ||   ||||||||
                                CTA   GAC CC   CACGTCTC
                                  TCC   _  C__
GAM1599  FLJ10432 3'  CTCTGCACTCCATGATGAA   39351     T__    GA
                                TTC   GTGGA  GTGCAGAG
                                |||   |||||  ||||||||
                                AAG   TACCT  CACGTCTC
                                  TAG     __
GAM1599  FLJ12505 3'  CTCTGCACTTTACCCAGCATC  45714     T   T  _
                                GAT CTG GG AGAGTGCAGAG
                                ||| ||| || ||||||||||
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                                CTA GAC CC TTTCACGTCTC
                                  C  _ A
GAM1599 KIAA1854 3' CTCCGACCTCCCTACAGAATC 72205          A  TGCA
                                GATTCTGTGG GAG   GAG
                                |||||||||| |||   |||
                                CTAAGACATC CTC   CTC
                                     C  CAGC
GAM1599 KIF13B   3' CTTTCTCTCCACAAAGTC   83716     C       TGC
                                GATT TGTGGAGAG  AG
                                |||| |||||||||  ||
                                CTGA ACACCTCTC  TC
                                  A       TT_
GAM1599 KIF13B   3' CTTTCTCTCCACAAAGTC   31562     C       TGC
                                GATT TGTGGAGAG  AG
                                |||| |||||||||  ||
                                CTGA ACACCTCTC  TC
                                  A       TT_
GAM1599 MAP      3' CTCTTCAGGTTCACAGAA   43367        GAG  C
                                TTCTGTGGA  TG AGAG
                                |||||||||  || ||||
                                AAGACACTT  AC TCTC
                                     GG_  T
GAM1599 PRKRI    5' CTCTTCCCTCCACAGATC   21828     T      AGTGC
                                GAT CTGTGGAG    AGAG
                                ||| ||||||||    ||||
                                CTA GACACCTC    TCTC
                                  _      CCT__
GAM1599 PRO0650  5' CTGTGACGCTCCACAGAA   27071         A  _
                                TTCTGTGGAG GT GCAG
                                |||||||||| || ||||
                                AAGACACCTC CA TGTC
                                     G  G
GAM1599 RASSF2   3' CTCCACCTTCTCTCCACAGAAT 29096           TGCA__
                                ATTCTGTGGAGAG    GAG
                                ||||||||||||     |||
                                TAAGACACCTCTC    CTC
                                       TTCCAC
GAM1599 TRIM26   3' CTCTGCACTCTCTGGAAT   14347     GT
                                ATTCT  GGAGAGTGCAGAG
                                |||||  ||||||||||||
                                TAAGG  TCTCTCACGTCTC
                                  __
GAM1599 LOC143326 3' CTCTGCCAACACAGGATC   77055        GAGAGT
                                GATTCTGTG    GCAGAG
                                |||||||||    ||||||
                                CTAGGACAC    CGTCTC
                                     AAC___
GAM1599 LOC144058 5' CTCTGAGGGCCACAGAATT  77181         AGAGTG
                                GATTCTGTGG    CAGAG
                                ||||||||||    |||||
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                                TTAAGACACC      GTCTC
                                      GGGA__
GAM1599  LOC146443 3'  CTCTTGGACCCCACAGAAT    78446          AGA  G  _
                                ATTCTGTGG   GT CA GAG
                                |||||||||   || || |||
                                TAAGACACC   CA GT CTC
                                      C__  G  T
GAM1599  LOC146756 3'  CTCTGAGAAGCCTCCACAGAAT 84801           A  G___
               C                 GATTCTGTGGAG GT    CAGAG
                                ||||||||||||| ||    |||||
                                CTAAGACACCTC CG    GTCTC
                                      _  AAGA
GAM1599  LOC165246 5'  CTCCCACTGCCCACAGAA     83365         AG    CA
                                TTCTGTGG  AGTG  GAG
                                ||||||||  ||||  |||
                                AAGACACC  TCAC  CTC
                                     CG    C_
GAM1599  LOC202052 3'  CTCTGCAGGCATTCCACAGAGT 91898           A  __
               C                 GATTCTGTGGAG GT  GCAGAG
                                ||||||||||||| ||  ||||||
                                CTGAGACACCTT CG  CGTCTC
                                      A  GA
GAM1599  LOC206426 3'  CTCCATCCTCTCCACAGCATC  91098     T        TGCA
                                GAT CTGTGGAGAG    GAG
                                ||| ||||||||||    |||
                                CTA GACACCTCTC    CTC
                                  C         CTAC
GAM1599  LOC219920 5'  CTCCGCACTCTCCTGGGTC    94949      TGT        A
                                GATTC   GGAGAGTGC GAG
                                |||||   ||||||||| |||
                                CTGGG   CCTCTCACG CTC
                                   T__        C
GAM1599  LOC221354 3'  CTCCAGAACCTCACACAGAATC 94012          _   A  GCA_
                                GATTCTGTG GAG GT    GAG
                                ||||||||| ||| ||    |||
                                CTAAGACAC CTC CA    CTC
                                      A   _  AGAC
GAM1599  LOC255423 5'  CTCTTACTGCCCACAGAA     99439         AG    C
                                TTCTGTGG  AGTG AGAG
                                ||||||||  |||| ||||
                                AAGACACC  TCAT TCTC
                                     CG    _
GAM1599  LOC257464 5'  CTCTTGCTTTCCCCAAAATC   91242      C  T       C
                                GATT TG GGAGAGTG AGAG
                                |||| || |||||||| ||||
                                CTAA AC CCTTTCGT TCTC
                                  A  C       _
GAM1599  LOC257494 3'  CTCTGCACTCTCTGGAAT     99632       GT
                                ATTCT  GGAGAGTGCAGAG
                                |||||  ||||||||||||
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                                TAAGG  TCTCTCACGTCTC
                                  __
GAM1599 LOC92840 3' CTCCCAGGCCTCCACAGAGTC  57246          A  GCA_
                                GATTCTGTGGAG GT    GAG
                                |||||||||||| ||    |||
                                CTGAGACACCTC CG    CTC
                                      _  GACC
GAM1600 APPBP2   3' ATGCCCAAAAATAAGTCTTAGA 22117      A    GATGG
                                TCTGA GACT    TTTGGGCAT
                                ||||| ||||    |||||||||
                                AGATT CTGA    AAACCCGTA
                                   _   ATAA_
GAM1600 APTX     3' CCTGACCCACCATCTTCAGA   35150        C  A   T TG
                                TCTGAAGA TG TGG T  GG
                                |||||||| || ||| |  ||
                                AGACTTCT AC ACC A  CC
                                     _ C   C GT
GAM1600 RPS6KA1  3' CCCGCCCAGTCATCAGA     60041      A    AT   TT
                                TCTGA GACTG  GGT  GGG
                                ||||| |||||  |||  |||
                                AGACT CTGAC  CCG  CCC
                                   A    __  __
GAM1600 SLC26A2  5' CTGAACCATCTATCTCCAGA   5475      A  CT     TG
                                TCTG AGA  GATGGTT  G
                                |||| |||  |||||||  |
                                AGAC TCT  CTACCAA  C
                                  C   AT      GT
GAM1600 SUV39H1  3' CAAACCCCCACCCACCTTCAGA 13493        AC___  AT
                                TCTGAAG    TG  GGTTTG
                                |||||||    ||  ||||||
                                AGACTTC    AC  CCAAAC
                                    CACCC  CC
GAM1600 DKFZP566K1924 3' GCTTCCATAGTCTTCAGA    74199          A  TTT
                                TCTGAAGACTG TGG   GGGC
                                |||||||||| |||   ||||
                                AGACTTCTGAT ACC   TTCG
                                      _  ___
GAM1600 FLJ20079 5' TCTCACCATCAGCTTCAGA   34979        A      TT
                                TCTGAAG CTGATGGT  GG
                                ||||||| ||||||||  ||
                                AGACTTC GACTACCA  CT
                                   _       CT
GAM1600 FLJ20291 3' ATGTCAAACCACCAGTGTTCA  35345     G   A      G
                                TGAA ACTG TGGTTTGG CAT
                                |||| |||| |||||||| |||
                                ACTT TGAC ACCAAACT GTA
                                  G   C      _
GAM1600 KIAA1784 3' TGTTACCAGCAGTCTCCA    65757    A    A   TTG
                                TG AGACTG TGGT   GGCA
                                || |||||| ||||   ||||
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                                AC TCTGAC ACCA   TTGT
                                 C     G   ___
GAM1600  MGC955   3'  CCCAAGTCAGTCAGTTTCAGA  44280      A     _  GT
                                TCTGA GACTGA TG  TTGGG
                                ||||| |||||| ||  |||||
                                AGACT TTGACT AC  AACCC
                                   _     G  TG
GAM1600  MYLE     3'  ATGCCCTGGACCAGCCGCCCAG 26691      AAGACTGA     _
              A                  TCTG       TGGTTT GGGCAT
                                ||||       |||||| ||||||
                                AGAC       ACCAGG CCCGTA
                                  CCGCCG__     T
GAM1600  LOC122704 3'  GTTCCCCATCTGTCTTCAGA   74610        T    TTT
                                TCTGAAGAC GATGG   GGGC
                                ||||||||| |||||   ||||
                                AGACTTCTG CTACC   CTTG
                                      T    C__
GAM1600  LOC126528 5'  CCCACTGCTCAGTCCCCAGA   75028     AA     TG  T_
                                TCTG  GACTGA  GT  TGGG
                                ||||  ||||||  ||  ||||
                                AGAC  CTGACT  CG  ACCC
                                  CC      __  TC
GAM1600  LOC146783 5'  TGTGCACCTGTCTTCAGA    84824        TGAT   TT G
                                TCTGAAGAC    GGT  G GCA
                                |||||||||    |||  | |||
                                AGACTTCTG    CCA  C TGT
                                      T___   __ G
GAM1600  LOC146823 3'  ATGGTTACCATCAGCATCCAGA 84826     AAGA       TT  G
                                TCTG    CTGATGGT  GG CAT
                                ||||    ||||||||  || |||
                                AGAC    GACTACCA  TT GTA
                                  CTAC       __  G
GAM1600  LOC150577 3'  CCCACATCAATGCTCCAGA    86252     A  AC_    GTT
                                TCTG AG   TGATG   TGGG
                                |||| ||   |||||   ||||
                                AGAC TC   ACTAC   ACCC
                                  C  GTA    ___
GAM1600  LOC92017  3'  ATGCCCAGGTTTCAGCCCT    68487    A_    T  TT
                                AG  CTGA GG  TGGGCAT
                                ||  |||| ||  |||||||
                                TC  GACT TT  ACCCGTA
                                 CC    _  GG
GAM1601  GPC4     3'  TACCAAATGATAGCTCATAA   9356       A     GGGGA
                                TTAT AGCTAT    GTTTGGTA
                                |||| ||||||    ||||||||
                                AATA TCGATA    TAAACCAT
                                  C     G____
GAM1601  NHLH1    3'  ACCAAACTCCTAGCT       20014      ATG
                                AGCT   GGGAGTTTGGT
                                ||||   ||||||||||
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                                TCGA   TCCTCAAACCA
                                       ___
GAM1601  KIAA1553  3'  AGCCCCTCACAGCTTATAA   93561          A    A
                                TTATAAGCT TGGGG GTT
                                ||||||||| ||||| |||
                                AATATTCGA ACTCC CGA
                                      C    C
GAM1602  ADAM17    3'  TCCAGCCTGGGTGACAGAGTGA 13511          TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                        GT
GAM1602  ADAM17    3'  TCCAGCCTGGGTGACAGAGTGA 41848          TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                        GT
GAM1602  ADAT1     3'  TCCAGCCTGGGTGATAGAGCAA 24919     C      TG
                GA                TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGATA  GGGTCCGACCT
                                    A      GT
GAM1602  ADCY2     3'  CCTGGGCAACATAGCAAGA   65646     C   C
                                  TCT GCT TGTTGCCCAGG
                                  ||| ||| ||||||||||
                                  AGA CGA ACAACGGGTCC
                                    A   T
GAM1602  ADCY2     3'  TCCAGCCTGGGTGACAGAGCGA 65655          TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GT
GAM1602  AICDA     3'  TCCAGCCTGGGCGACAAGAGC  40698       _
                                  GCTCT GTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||
                                  CGAGA CAGCGGGTCCGACCT
                                     A
GAM1602  AK1       3'  TCCAGCCTGGGTGACAGAGCAA 6641      C      TG
                GA                TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A      GT
GAM1602  ALDH3A2   3'  TCAGCTTGGGCAACAGAGCAAG 69803     C
                A                  TCT GCTCTGTTGCCCAGGCTGG
                                   ||| ||||||||||||||||||
                                   AGA CGAGACAACGGGTTCGACT
                                     A
GAM1602  ALPP      3'  CCTGGGCGACAGAGCGAGA   69415
                                   TCTCGCTCTGTTGCCCAGG
                                   ||||||||||||||||||
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                                AGAGCGAGACAGCGGGTCC

GAM1602 ANKH    3' TCCAGCCTGGGTGACAAGAGC 55074      _ TG
                                GCTCT GT CCCAGGCTGGA
                                ||||| || ||||||||||
                                CGAGA CA GGGTCCGACCT
                                  A GT
GAM1602 ANKH    3' TCCAGCCTGAGCAACAGAGC 39550        C
                                GCTCTGTTGC CAGGCTGGA
                                |||||||||| |||||||||
                                CGAGACAACG GTCCGACCT
                                     A
GAM1602 APAF1   3' TCCAGCCTGGGTGACATAGCAA 25984    C  C  TG
            GA                    TCT GCT TGT CCCAGGCTGGA
                                ||| ||| ||| ||||||||||
                                AGA CGA ACA GGGTCCGACCT
                                  A  T  GT
GAM1602 APAF1   3' TCCAGCCTGGGTGACATAGCAA 8593     C  C  TG
            GA                    TCT GCT TGT CCCAGGCTGGA
                                ||| ||| ||| ||||||||||
                                AGA CGA ACA GGGTCCGACCT
                                  A  T  GT
GAM1602 APOC4   3' CCTGGGCAACACAGCGAGA  9705       C
                                TCTCGCT TGTTGCCCAGG
                                ||||||| ||||||||||
                                AGAGCGA ACAACGGGTCC
                                    C
GAM1602 APOL1   3' TCCAGCCTGGGTGACAGAGCGA 14745        TG
            GA                    TCTCGCTCTGT CCCAGGCTGGA
                                |||||||||| ||||||||||
                                AGAGCGAGACA GGGTCCGACCT
                                     GT
GAM1602 ARHGEF6 3' CCAACCTAGGTAACAGAG   68754        C  C
                                CTCTGTTGCC AGG TGG
                                |||||||||| ||| |||
                                GAGACAATGG TCC ACC
                                     A  A
GAM1602 ARSD    3' TCCAGCCTGGGCCACATAGCAA 24812    C  C  T
            GA                    TCT GCT TGT GCCCAGGCTGGA
                                ||| ||| ||| ||||||||||||
                                AGA CGA ACA CGGGTCCGACCT
                                  A  T  C
GAM1602 ATM     3' TCCAGCCTGGGTGACAAGAGCG 5304       _ TG
            A                     TCGCTCT GT CCCAGGCTGGA
                                ||||||| || ||||||||||
                                AGCGAGA CA GGGTCCGACCT
                                    A GT
GAM1602 ATM     3' TCCAGCCTGGGTGACAAGAGCG 57138      _ TG
            A                     TCGCTCT GT CCCAGGCTGGA
                                ||||||| || ||||||||||
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                                AGCGAGA CA  GGGTCCGACCT
                                   A  GT
GAM1602  ATM     3'  TCCAGCCTGGGAGACAGAGCGA 57149          TG
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                     GA
GAM1602  BCAS1   3'  CCTGGGCGACAGAGCAAGA   14710    C
                                  TCT GCTCTGTTGCCCAGG
                                  ||| ||||||||||||||
                                  AGA CGAGACAGCGGGTCC
                                    A
GAM1602  BPHL    3'  TCCAACCTGGGCAACAGAGTAA 16336    CG          C
              GA                  TCT  CTCTGTTGCCCAGG TGGA
                                  |||  |||||||||||||| ||||
                                  AGA  GAGACAACGGGTCC ACCT
                                    AT           A
GAM1602  BRCA1   3'  TCCAGCCTGGGTGACAGTGAGA 24450       CT  TG
                                  TCTCGCT  GT  CCCAGGCTGGA
                                  |||||||  ||  ||||||||||
                                  AGAGTGA  CA  GGGTCCGACCT
                                     __  GT
GAM1602  BRCA1   5'  TCCAGCCTGGGCGACAGAGCGA 24462
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCCGACCT

GAM1602  BRCA1   3'  TCCAGCCTGGGTGACAGTGAGA 24463       CT  TG
                                  TCTCGCT  GT  CCCAGGCTGGA
                                  |||||||  ||  ||||||||||
                                  AGAGTGA  CA  GGGTCCGACCT
                                     __  GT
GAM1602  BRCA1   3'  TCCAGCCTGGGTGACAGTGAGA 24473       CT  TG
                                  TCTCGCT  GT  CCCAGGCTGGA
                                  |||||||  ||  ||||||||||
                                  AGAGTGA  CA  GGGTCCGACCT
                                     __  GT
GAM1602  BRCA1   3'  TCCAGCCTGGGTGACAGTGAGA 24481       CT  TG
                                  TCTCGCT  GT  CCCAGGCTGGA
                                  |||||||  ||  ||||||||||
                                  AGAGTGA  CA  GGGTCCGACCT
                                     __  GT
GAM1602  BRCA1   3'  TCCAGCCTGGGTGACAGTGAGA 24489       CT  TG
                                  TCTCGCT  GT  CCCAGGCTGGA
                                  |||||||  ||  ||||||||||
                                  AGAGTGA  CA  GGGTCCGACCT
                                     __  GT
GAM1602  BRCA1   3'  TCCAGCCTGGGTGACAGTGAGA 24498       CT  TG
                                  TCTCGCT  GT  CCCAGGCTGGA
                                  |||||||  ||  ||||||||||
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                                AGAGTGA  CA  GGGTCCGACCT
                                   __  GT
GAM1602  BRCA1    3'  TCCAGCCTGGGTGACAGTGAGA 24508       CT  TG
                                TCTCGCT  GT  CCCAGGCTGGA
                                |||||||  ||  ||||||||||||
                                AGAGTGA  CA  GGGTCCGACCT
                                   __  GT
GAM1602  BRCA1    3'  TCCAGCCTGGGTGACAGTGAGA 24516       CT  TG
                                TCTCGCT  GT  CCCAGGCTGGA
                                |||||||  ||  ||||||||||||
                                AGAGTGA  CA  GGGTCCGACCT
                                   __  GT
GAM1602  BRCA1    3'  TCCAGCCTGGGTGACAGTGAGA 24524       CT  TG
                                TCTCGCT  GT  CCCAGGCTGGA
                                |||||||  ||  ||||||||||||
                                AGAGTGA  CA  GGGTCCGACCT
                                   __  GT
GAM1602  BRCA1    3'  TCCAGCCTGGGTGACAGTGAGA 24532       CT  TG
                                TCTCGCT  GT  CCCAGGCTGGA
                                |||||||  ||  ||||||||||||
                                AGAGTGA  CA  GGGTCCGACCT
                                   __  GT
GAM1602  BRCA1    3'  TCCAGCCTGGGTGACAGTGAGA 24580       CT  TG
                                TCTCGCT  GT  CCCAGGCTGGA
                                |||||||  ||  ||||||||||||
                                AGAGTGA  CA  GGGTCCGACCT
                                   __  GT
GAM1602  C1orf1   3'  TCCAGCCTAGGCGACAGAGTGA 8683             C
           GA                     TCTCGCTCTGTTGCC AGGCTGGA
                                  ||||||||||||||| ||||||||
                                  AGAGTGAGACAGCGG TCCGACCT
                                            A
GAM1602  CARKL    3'  TCCAGCCTGGGTGACAGAGCAA 26109     C      TG
           GA                     TCT GCTCTGT  CCCAGGCTGGA
                                  |||  |||||||  ||||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A      GT
GAM1602  CASP10   3'  TCCAGCTTGGGCAACAGGGCGA 53225
           GA                     TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGGGACAACGGGTTCGACCT

GAM1602  CASP10   3'  TCCAGCTTGGGCAACAGGGCGA 53264
           GA                     TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGGGACAACGGGTTCGACCT

GAM1602  CASP6    3'  TCCAGCCTGGGCAACGAGTGA  53366       T
                                TCGCTC GTTGCCCAGGCTGGA
                                ||||||  ||||||||||||||||
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                                AGTGAG CAACGGGTCCGACCT
                                      _
GAM1602  CASP6    3'  TCCAGCCTGGGCAACGAGTGA  8735        T
                                TCGCTC GTTGCCCAGGCTGGA
                                |||||| ||||||||||||||||
                                AGTGAG CAACGGGTCCGACCT
                                      _
GAM1602  CD28     3'  TCCAGCCTGGGCGACAGAGTGA 21558
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||||
                                AGAGTGAGACAGCGGGTCCGACCT

GAM1602  CD68     3'  TCCAGCCTGGGCGACAGAGCCA 60508     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGAGACAGCGGGTCCGACCT
                                  C
GAM1602  CEACAM5  3'  TCCAGTCTGGCAACAGAGCAAG 16425     C         C
                A                 TCT GCTCTGTTGCC AGGCTGGA
                                ||| |||||||||| ||||||||
                                AGA CGAGACAACGG TCTGACCT
                                  A         _
GAM1602  CENPB    3'  TCCAGCCTAGGCCCCCTGCAAG 70119     C  TCTGTT   C
                G                 TCT GC      GCC AGGCTGGA
                                ||| ||      ||| ||||||||
                                GGA CG      CGG TCCGACCT
                                  A  TCCCC_   A
GAM1602  CNGB1    3'  CTGGGCAACATAGCGAGA    8935        C
                                TCTCGCT TGTTGCCCAG
                                ||||||| |||||||||
                                AGAGCGA ACAACGGGTC
                                    T
GAM1602  COPA     3'  TCCAGCCTGGGTGACAGAGCAA 16480     C      TG
                GA                TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM1602  CPM      3'  TCCAGCTTGGGCAACAGAGTAA 60411     CG
                GA                TCT  CTCTGTTGCCCAGGCTGGA
                                |||  |||||||||||||||||
                                AGA  GAGACAACGGGTTCGACCT
                                  AT
GAM1602  CPT2     3'  CCTGGGCGACAGAGCGAGA   5424
                                TCTCGCTCTGTTGCCCAGG
                                |||||||||||||||||
                                AGAGCGAGACAGCGGGTCC

GAM1602  CTMP     3'  TCCAACCTGGGCAACAGAACAA 54954     CGC         C
                GA                TCT   TCTGTTGCCCAGG TGGA
                                |||   |||||||||||| ||||
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                                AGA   AGACAACGGGTCC ACCT
                                  ACA           A
GAM1602  CUBN     3'  TCCAGCCTGGGCGAGACGGCAA 8425      C   CTG
                GA                  TCT GCT   TTGCCCAGGCTGGA
                                    ||| |||   ||||||||||||||
                                    AGA CGG   AGCGGGTCCGACCT
                                      A   CAG
GAM1602  CYP4F3   3'  TCCAGCCTGGGTGAAAGAGCTA 8015      C     G TG
                GA                  TCT GCTCT T  CCCAGGCTGGA
                                    ||| ||||| |  ||||||||||
                                    AGA CGAGA A  GGGTCCGACCT
                                      T     A GT
GAM1602  DBT      3'  TCCAGCCTGGGCGACAGAGCAA 10379     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||
                                    AGA CGAGACAGCGGGTCCGACCT
                                      A
GAM1602  DBT      3'  TCCAGCCTGGGTGGCAGAGC   10380        TG
                                    GCTCTGT  CCCAGGCTGGA
                                    |||||||  ||||||||||
                                    CGAGACG  GGGTCCGACCT
                                       GT
GAM1602  DCLRE1C  3'  TCCAGCCTGGGCAACAAGAGC  42822       _
                                    GCTCT GTTGCCCAGGCTGGA
                                    ||||| ||||||||||||||
                                    CGAGA CAACGGGTCCGACCT
                                      A
GAM1602  DDOST    3'  TCCAGCCTGGGCAACAGTGT   19066    T
                                    GC CTGTTGCCCAGGCTGGA
                                    || ||||||||||||||||
                                    TG GACAACGGGTCCGACCT
                                     T
GAM1602  DFFA     3'  TCCAGCCTGGGCAACAGAGCGA 16598
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACAACGGGTCCGACCT

GAM1602  DGKI     5'  TCCAGCCTGGGCGACAAAGCAA 17529     C   C
                GA                  TCT GCT TGTTGCCCAGGCTGGA
                                    ||| ||| ||||||||||||||||
                                    AGA CGA ACAGCGGGTCCGACCT
                                      A   A
GAM1602  DMC1     3'  TCCAGCCTAGGTGACAGAGTGA 23947           TG  C
                GA                  TCTCGCTCTGT  CC AGGCTGGA
                                    ||||||||||  || ||||||||
                                    AGAGTGAGACA  GG TCCGACCT
                                          GT  A
GAM1602  DSC1     3'  TCCAGCCTGGGCAACAAGAGCG 44606        _
                A                    TCGCTCT GTTGCCCAGGCTGGA
                                    ||||||| ||||||||||||||||
```

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                                AGCGAGA CAACGGGTCCGACCT
                                   A
GAM1602  DSC1     3'  TCCAGCCTGGGCAACAAGAGCG 18243        _
                 A                TCGCTCT GTTGCCCAGGCTGGA
                                  ||||||| ||||||||||||||||
                                  AGCGAGA CAACGGGTCCGACCT
                                     A
GAM1602  DVL3     3'  TCCAGCCTGGGTGACAGAGTGA 16651           TG
                 GA                 TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          GT
GAM1602  EGFL4    3'  TCCAACCTGGGTGACAGAGCGA 62475          TG     C
                 GA                 TCTCGCTCTGT  CCCAGG TGGA
                                    ||||||||||  |||||| ||||
                                    AGAGCGAGACA  GGGTCC ACCT
                                          GT     A
GAM1602  EGFL5    3'  TCCAGCCTGGGCGACAGAGCAA 87921     C
                 GA                 TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAGCGGGTCCGACCT
                                      A
GAM1602  F2R      3'  TCCAGCCTGGGCAACAGAGCAA 10573     C
                 GA                 TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAACGGGTCCGACCT
                                      A
GAM1602  F2RL3    3'  TCCAGCCTGGGCAACAGAGCAA 15527     C
                 GA                 TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAACGGGTCCGACCT
                                      A
GAM1602  FANCC    3'  TCCAGCCTGGGCAACAGAGCGA 71049
                 GA                 TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACAACGGGTCCGACCT

GAM1602  FCAR     3'  TCCAGCCTGGGTGACAGAACGA 56640       C    TG
                 GA                 TCTCG TCTGT  CCCAGGCTGGA
                                    ||||| |||||  ||||||||||
                                    AGAGC AGACA  GGGTCCGACCT
                                      A    GT
GAM1602  FCAR     3'  TCCAGCCTGGGTGACAGAACGA 56648       C    TG
                 GA                 TCTCG TCTGT  CCCAGGCTGGA
                                    ||||| |||||  ||||||||||
                                    AGAGC AGACA  GGGTCCGACCT
                                      A    GT
GAM1602  FGF2     3'  TCCAGCCTAGGCAACAGAGTGA 10622            C
                 GA                 TCTCGCTCTGTTGCC AGGCTGGA
                                    |||||||||||||| ||||||||
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                                AGAGTGAGACAACGG TCCGACCT
                                       A
GAM1602  FGFR2    3'  TCCAGCCTTGGCGACAGAGCGA 43655            C
                GA                TCTCGCTCTGTTGCC AGGCTGGA
                                  ||||||||||||||| ||||||||
                                  AGAGCGAGACAGCGG TCCGACCT
                                       T
GAM1602  FGFR2    3'  TCCAGCCTTGGCGACAGAGCGA 43668            C
                GA                TCTCGCTCTGTTGCC AGGCTGGA
                                  ||||||||||||||| ||||||||
                                  AGAGCGAGACAGCGG TCCGACCT
                                       T
GAM1602  FLRT2    5'  TCCAGCCTAAGCAACAGAGCAA 26004     C        CC
                GA                TCT GCTCTGTTGC  AGGCTGGA
                                  ||| ||||||||||  ||||||||
                                  AGA CGAGACAACG  TCCGACCT
                                    A         AA
GAM1602  FUT6     3'  TCCAACCTGGACGACAGAGCAA 5644      C        C    C
                GA                TCT GCTCTGTTG CCAGG TGGA
                                  ||| ||||||||| ||||| ||||
                                  AGA CGAGACAGC GGTCC ACCT
                                    A        A    A
GAM1602  GALNT7   3'  TCCAACCTGGGTGACAGAGTGA 55090          TG     C
                GA                TCTCGCTCTGT  CCCAGG TGGA
                                  ||||||||||  |||||| ||||
                                  AGAGTGAGACA  GGGTCC ACCT
                                        GT     A
GAM1602  GAMT     3'  CCTGGGCTACAGAGCAAGA    57984     C      T
                                  TCT GCTCTGT GCCCAGG
                                  ||| ||||||| |||||||
                                  AGA CGAGACA CGGGTCC
                                    A      T
GAM1602  GGCX     3'  CCTGGGCAACAGAGCAAGA    7703      C
                                  TCT GCTCTGTTGCCCAGG
                                  ||| ||||||||||||||
                                  AGA CGAGACAACGGGTCC
                                    A
GAM1602  GM2A     3'  TCCAGCCTGGTGACAGAGTGAG 68390          TG  C
                A                  TCTCGCTCTGT  CC AGGCTGGA
                                  ||||||||||  || ||||||||
                                  AGAGTGAGACA  GG TCCGACCT
                                        GT  _
GAM1602  GP2      3'  TCCAGCCTGGGCAACAGAGCAA 9483      C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAACGGGTCCGACCT
                                    A
GAM1602  GRAF     3'  TCCAGCCTGGGTGACAGAGCCA 31248     C      TG
                GA                TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
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                                AGA CGAGACA  GGGTCCGACCT
                                  C      GT
GAM1602  GRM3     3'  TCCAGAATATGGAAACAGAGC  7746         GC   GG__
                                GCTCTGTT  CCA    CTGGA
                                |||||||  |||    |||||
                                CGAGACAA  GGT    GACCT
                                    A_   ATAA
GAM1602  GRM6     3'  TCCAGCCTGGGTGACAGAGCGA 7772           TG
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GT
GAM1602  GTF2F1   3'  TCCAGCCTGGGTGACAGAATGA 10893     C     TG
                                  TCG TCTGT  CCCAGGCTGGA
                                  |||  |||||  ||||||||||
                                  AGT AGACA  GGGTCCGACCT
                                    A     GT
GAM1602  GTF2F1   3'  TCCAGCCTGGGTGACAGTGAGA 10894        CT  TG
                                  TCTCGCT  GT  CCCAGGCTGGA
                                  |||||||  ||  ||||||||||
                                  AGAGTGA  CA  GGGTCCGACCT
                                     __  GT
GAM1602  HIP1     3'  TCCAGCCTGAGTGACAGAGCGA 19264          TG C
              GA                  TCTCGCTCTGT  C CAGGCTGGA
                                  ||||||||||  | |||||||||
                                  AGAGCGAGACA  G GTCCGACCT
                                        GT A
GAM1602  HIP1     3'  TCCAGCCTGGGCAACAAGAGC  19265       _
                                  GCTCT GTTGCCCAGGCTGGA
                                  |||||  ||||||||||||||
                                  CGAGA CAACGGGTCCGACCT
                                     A
GAM1602  HRH1     3'  TCCAGCCTGGGCAACAGAGCAA 7828      C
              GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                  |||  ||||||||||||||||||
                                  AGA CGAGACAACGGGTCCGACCT
                                    A
GAM1602  HSPA5    3'  TCCAGCCTGGCGACAAGAGTGA 19290          _     C
              GA                  TCTCGCTCT GTTGCC AGGCTGGA
                                  |||||||| ||||||  ||||||||
                                  AGAGTGAGA CAGCGG TCCGACCT
                                       A     _
GAM1602  HTR2A    3'  TCCTCCTGGGCAACAGAGTGAG 7107                 CT
              A                    TCTCGCTCTGTTGCCCAGG  GGA
                                  ||||||||||||||||||  |||
                                  AGAGTGAGACAACGGGTCC  CCT
                                           T_
GAM1602  IAPP     3'  TCCAGCCTGGGTGGCAGAGTGA 6443           TG
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
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                                AGAGTGAGACG  GGGTCCGACCT
                                      GT
GAM1602  ICA1     3'  CCAGCCTGGGCAACAAAGTGAG 42517        C
                A                      TCTCGCT TGTTGCCCAGGCTGG
                                       ||||||| ||||||||||||||
                                       AGAGTGA ACAACGGGTCCGACC
                                          A
GAM1602  IFIT4    3'  TCCAGCCTGGGCAACAGAGCAA 71497     C
                GA                       TCT GCTCTGTTGCCCAGGCTGGA
                                         ||| ||||||||||||||||||||
                                         AGA CGAGACAACGGGTCCGACCT
                                           A
GAM1602  IFRD1    3'  CCTGGGCAACATAGCGAGA    60753        C
                                         TCTCGCT TGTTGCCCAGG
                                         ||||||| ||||||||||
                                         AGAGCGA ACAACGGGTCC
                                            T
GAM1602  IL10     3'  TCCAGCCTGGGTGACAGAGCAA 6929      C      TG
                GA                       TCT GCTCTGT  CCCAGGCTGGA
                                         ||| |||||||  ||||||||||
                                         AGA CGAGACA  GGGTCCGACCT
                                           A      GT
GAM1602  IL1R1    3'  TCTAGCCTGGCAACAGAGCAAG 7925      C         C
                A                        TCT GCTCTGTTGCC AGGCTGGA
                                         ||| |||||||||| ||||||||
                                         AGA CGAGACAACGG TCCGATCT
                                           A        _
GAM1602  IL2RA    3'  TCCAGCCTGGGCAACAGAGCAA 6453      C
                GA                       TCT GCTCTGTTGCCCAGGCTGGA
                                         ||| ||||||||||||||||||||
                                         AGA CGAGACAACGGGTCCGACCT
                                           A
GAM1602  IL6R     3'  TCCAGCCTGGGGTGACAGAGC  6915         TG  _
                                         GCTCTGT  CCC AGGCTGGA
                                         |||||||  ||| ||||||||
                                         CGAGACA  GGG TCCGACCT
                                            GT   G
GAM1602  IPP      3'  TCCACTCTGGGCAACAGAATGA 20907       C          GC
                GA                       TCTCG TCTGTTGCCCAG  TGGA
                                         ||||| ||||||||||||  ||||
                                         AGAGT AGACAACGGGTC  ACCT
                                            A          TC
GAM1602  IRAK1    3'  TCCAGCCTGGGTGACAGAGCAA 9618      C      TG
                GA                       TCT GCTCTGT  CCCAGGCTGGA
                                         ||| |||||||  ||||||||||
                                         AGA CGAGACA  GGGTCCGACCT
                                           A      GT
GAM1602  IRAK4    3'  TCCAGCCTGGGTGACAGAGTGA 61847           TG
                GA                       TCTCGCTCTGT  CCCAGGCTGGA
                                         ||||||||||  ||||||||||
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                                AGAGTGAGACA  GGGTCCGACCT
                                      GT
GAM1602  ITGAL    3'  TCCAGCCTGGGCAACACAGCGA 11050        C
                GA                  TCTCGCT TGTTGCCCAGGCTGGA
                                    ||||||| ||||||||||||||||
                                    AGAGCGA ACAACGGGTCCGACCT
                                       C
GAM1602  KAI1     3'  TCCAGCCTGGGGGACAGAAAGA 11130      GC     G
                GA                  TCTC  TCTGTT CCCAGGCTGGA
                                    ||||  |||||| ||||||||||
                                    AGAG  AGACAG GGGTCCGACCT
                                      AA     G
GAM1602  KCNA7    3'  TCCAGCCTGGGCAACAGAGGGA 49905     G
                G                    CTC CTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||
                                    GAG GAGACAACGGGTCCGACCT
                                      G
GAM1602  KCNA7    3'  TCCAGCCTGGGCAGCAGAGC   49906
                                    GCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||
                                    CGAGACGACGGGTCCGACCT

GAM1602  KCNJ5    3'  TCCAGCCTGGGCGACAGAGCGA 7978
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACAGCGGGTCCGACCT

GAM1602  KCNK3    3'  TCCAGCCTGGGTGACAGGGCAA 11178     C      TG
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGGGACA  GGGTCCGACCT
                                      A      GT
GAM1602  KCNK6    3'  TCCAGCCTGCGGGACAGAGTGA 17885           G _
                GA                  TCTCGCTCTGTT CC CAGGCTGGA
                                    |||||||||||| || |||||||||
                                    AGAGTGAGACAG GG GTCCGACCT
                                          _ C
GAM1602  KIF1B    3'  TCCAGCCTGGGTGACAGAGCAA 31271     C      TG
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGAGACA  GGGTCCGACCT
                                      A      GT
GAM1602  KIF3B    3'  TCCAGCCTGGGTGACAGAGTGA 17810          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          GT
GAM1602  KLRG1    3'  TCCAGCCTGGGAGATAGAGCAA 20557     C      TG
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
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                                AGA CGAGATA  GGGTCCGACCT
                                  A      GA
GAM1602  KNSL1    3'  TCCAGCCTGGGCAACAGAGCAA 16949     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAACGGGTCCGACCT
                                      A
GAM1602  LAMC2    3'  TCCAGCCTGGGGAACAGAGCAA 38770     C       G
                GA                  TCT GCTCTGTT CCCAGGCTGGA
                                    ||| |||||||| ||||||||||
                                    AGA CGAGACAA GGGTCCGACCT
                                      A       G
GAM1602  LDLR     3'  CCTGGGCGACAGAGCGAGA    6733
                                    TCTCGCTCTGTTGCCCAGG
                                    |||||||||||||||||||
                                    AGAGCGAGACAGCGGGTCC

GAM1602  LDLR     3'  TCCAGCCTGGGCAACAGATGAA 6744      _  C
                GA                  TCT CG TCTGTTGCCCAGGCTGGA
                                    ||| || ||||||||||||||||||
                                    AGA GT AGACAACGGGTCCGACCT
                                      A  _
GAM1602  LDLR     3'  TCCAGCCTGGGCAACATAGTAA 6745      CG  C
                GA                  TCT  CT TGTTGCCCAGGCTGGA
                                    |||  || ||||||||||||||||
                                    AGA  GA ACAACGGGTCCGACCT
                                      AT  T
GAM1602  LILRB1   3'  TCCAGCCTGGCGACAGAGGGAG 22877      G        C
                A                    TCTC CTCTGTTGCC AGGCTGGA
                                    |||| |||||||||| ||||||||
                                    AGAG GAGACAGCGG TCCGACCT
                                      G        _
GAM1602  LPIN1    3'  TCCAGCCTGGGTGACAGAGTAA 67992     CG     TG
                GA                  TCT  CTCTGT  CCCAGGCTGGA
                                    |||  ||||||  ||||||||||||
                                    AGA  GAGACA  GGGTCCGACCT
                                      AT     GT
GAM1602  LRRC2    3'  TCCAGCCTGGGCAACAGAGTGA 44759
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAACGGGTCCGACCT

GAM1602  LRRC2    3'  TCCAGCCTGGGTGACAGAGCCA 44760     C      TG
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||||
                                    AGA CGAGACA  GGGTCCGACCT
                                      C      GT
GAM1602  LRRC2    3'  TCCAGCCTGGGTGACAGAGTGA 44761          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||||
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                                AGAGTGAGACA  GGGTCCGACCT
                                      GT
GAM1602  LUZP1    3'  TCCAGCCTGGGCAACAAGAGTG 54405        _
                A                  TCGCTCT GTTGCCCAGGCTGGA
                                   ||||||| |||||||||||||||
                                   AGTGAGA CAACGGGTCCGACCT
                                      A
GAM1602  LY94     3'  CCTGGGCGACAGAGCGAGA   17897
                                   TCTCGCTCTGTTGCCCAGG
                                   ||||||||||||||||||
                                   AGAGCGAGACAGCGGGTCC

GAM1602  MAFF     3'  TCCAGCCTGGGCAACATAGC  25583     C
                                   GCT TGTTGCCCAGGCTGGA
                                   ||| ||||||||||||||||
                                   CGA ACAACGGGTCCGACCT
                                     T
GAM1602  MDM4     3'  TCCAGCCTGGGTGACAGCGCGA 11514       T   TG
                GA                   TCTCGC CTGT  CCCAGGCTGGA
                                   |||||| ||||  ||||||||||
                                   AGAGCG GACA  GGGTCCGACCT
                                      C   GT
GAM1602  MEN1     5'  TCCAGCCTGGGCGAAAGAGAAA 56369     CG   G
                GA                   TCT  CTCT TTGCCCAGGCTGGA
                                   |||  |||| ||||||||||||||
                                   AGA  GAGA AGCGGGTCCGACCT
                                     AA   A
GAM1602  MEN1     5'  TCCAGCCTGGGCGAAAGAGAAA 56371     CG   G
                GA                   TCT  CTCT TTGCCCAGGCTGGA
                                   |||  |||| ||||||||||||||
                                   AGA  GAGA AGCGGGTCCGACCT
                                     AA   A
GAM1602  MSH3     3'  TCCAGCTTGGGCAACAGAGCAA 11693     C
                GA                   TCT GCTCTGTTGCCCAGGCTGGA
                                   ||| ||||||||||||||||||||
                                   AGA CGAGACAACGGGTTCGACCT
                                     A
GAM1602  MTMR8    3'  TCCAGCCTGAGCAACAGAGCGA 31917           C
                GA                   TCTCGCTCTGTTGC CAGGCTGGA
                                   |||||||||||||| |||||||||
                                   AGAGCGAGACAACG GTCCGACCT
                                         A
GAM1602  MTMR8    3'  TCCAGCCTGGGCGAAAGGGCAA 31918     C    G
                GA                   TCT GCTCT TTGCCCAGGCTGGA
                                   ||| ||||| ||||||||||||||
                                   AGA CGGGA AGCGGGTCCGACCT
                                     A    A
GAM1602  MYH11    3'  TCCAGCCTGGGCAACAGAG   11744
                                   CTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||
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                              GAGACAACGGGTCCGACCT

GAM1602  MYH11    3'  TCCAGCCTGGGCAACGTAGT   11746     C
                              GCT TGTTGCCCAGGCTGGA
                              ||| ||||||||||||||||
                              TGA GCAACGGGTCCGACCT
                                T
GAM1602  MYH11    3'  TCCAGCCTGGGCAACAGAG    43432
                              CTCTGTTGCCCAGGCTGGA
                              ||||||||||||||||||
                              GAGACAACGGGTCCGACCT

GAM1602  MYH11    3'  TCCAGCCTGGGCAACGTAGT   43433     C
                              GCT TGTTGCCCAGGCTGGA
                              ||| ||||||||||||||||
                              TGA GCAACGGGTCCGACCT
                                T
GAM1602  MYO1B    3'  TCCAGCCCGGGTGACAATACAA 25247     CGCTC   TG   A
                GA              TCT     TGT  CCC GGCTGGA
                              |||     |||  ||| |||||||
                              AGA     ACA  GGG CCGACCT
                                ACATA   GT   C
GAM1602  MYO1C    3'  TCCAGCCTGGGCAACAGAGCGA 61870
                GA              TCTCGCTCTGTTGCCCAGGCTGGA
                              |||||||||||||||||||||||
                              AGAGCGAGACAACGGGTCCGACCT

GAM1602  NCOA6    5'  TCCAGCCCAGGCAACAGAGCGT 26849     T          CA
                GA              TC CGCTCTGTTGCC  GGCTGGA
                              || ||||||||||||  |||||||
                              AG GCGAGACAACGG  CCGACCT
                               T          AC
GAM1602  NESG1    5'  CCAGCCCAGGGCCAGAGCGA   25619         TT    A_
                              TCGCTCTG  GCCC  GGCTGG
                              ||||||||  ||||  ||||||
                              AGCGAGAC  CGGG  CCGACC
                                   __    AC
GAM1602  NFKBIL2  3'  TCCAGCCTGGGCGACAGACCGA 26455       C
                GA              TCTCG TCTGTTGCCCAGGCTGGA
                              |||||| |||||||||||||||||
                              AGAGC AGACAGCGGGTCCGACCT
                                C
GAM1602  NKX3A    3'  TCCAGCCTGGGCAACGAGCAAG 21617     C    T
                A              TCT GCTC GTTGCCCAGGCTGGA
                              ||| |||| ||||||||||||||
                              AGA CGAG CAACGGGTCCGACCT
                                A   _
GAM1602  NPHP1    3'  TCCAGCCTAGGCAACAAGAGTG 63150         _     C
                A              TCGCTCT GTTGCC AGGCTGGA
                              ||||||| |||||| ||||||||
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                                AGTGAGA CAACGG TCCGACCT
                                   A     A
GAM1602  NPHS1    3'  TCCAGCCTGGGCGACAGAGCGA 17374
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACAGCGGGTCCGACCT

GAM1602  NT5C2    3'  TCCAGCCTGGGCAACAAGA   25268    _
                                    TCT GTTGCCCAGGCTGGA
                                    ||| ||||||||||||||
                                    AGA CAACGGGTCCGACCT
                                      A
GAM1602  NUP62    3'  TCCAGCCTAGGCAACAGAG   33788          C
                                    CTCTGTTGCC AGGCTGGA
                                    |||||||||| ||||||||
                                    GAGACAACGG TCCGACCT
                                       A
GAM1602  OGG1     5'  TCCAGCCTAGGCGACAGAGTGA 34160            C
                GA                  TCTCGCTCTGTTGCC AGGCTGGA
                                    |||||||||||||| ||||||||
                                    AGAGTGAGACAGCGG TCCGACCT
                                          A
GAM1602  OGG1     5'  TCCAGCCTAGGCGACAGAGTGA 34165            C
                GA                  TCTCGCTCTGTTGCC AGGCTGGA
                                    |||||||||||||| ||||||||
                                    AGAGTGAGACAGCGG TCCGACCT
                                          A
GAM1602  OGG1     5'  TCCAGCCTAGGCGACAGAGTGA 11891            C
                GA                  TCTCGCTCTGTTGCC AGGCTGGA
                                    |||||||||||||| ||||||||
                                    AGAGTGAGACAGCGG TCCGACCT
                                          A
GAM1602  OPA3     3'  CTAGCCTGGGCAACAGAGCAAG 47843     C
                A                    TCT GCTCTGTTGCCCAGGCTGG
                                    ||| ||||||||||||||||||
                                    AGA CGAGACAACGGGTCCGATC
                                      A
GAM1602  OPA3     3'  TCCAGCCCGGGTGACAGAGCAA 47848     C      TG   A
                GA                  TCT GCTCTGT  CCC GGCTGGA
                                    ||| |||||||  ||| |||||||
                                    AGA CGAGACA  GGG CCGACCT
                                      A      GT   C
GAM1602  OPTN     3'  TCCAGCCTGGGTGACAGAGGGA 42053      G     TG
                GA                  TCTC CTCTGT  CCCAGGCTGGA
                                    |||| ||||||  ||||||||||
                                    AGAG GAGACA  GGGTCCGACCT
                                      G     GT
GAM1602  P53AIP1  3'  TCCAGCCTGGGCGACAGAGAGA 42340      G
                GA                  TCTC CTCTGTTGCCCAGGCTGGA
                                    |||| ||||||||||||||||||
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                                AGAG GAGACAGCGGGTCCGACCT
                                  A
GAM1602  PA2G4    3'  TCCAGCCTGGGTGACAGAATGA 71831       C     TG
                GA                TCTCG TCTGT  CCCAGGCTGGA
                                  ||||| |||||  ||||||||||
                                  AGAGT AGACA  GGGTCCGACCT
                                    A     GT
GAM1602  PAICS    3'  TCCAACCTGGGCAGCAGAGCAA 22268     C            C
                GA                TCT GCTCTGTTGCCCAGG TGGA
                                  ||| |||||||||||||| ||||
                                  AGA CGAGACGACGGGTCC ACCT
                                    A             A
GAM1602  PCDH11X  3'  TCCAGCCTGGGTGACAGAGCAA 53133     C      TG
                GA                TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A       GT
GAM1602  PCDH11Y  3'  TCCAGCCTGGGTGACAGAGCAA 53169     C      TG
                GA                TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A       GT
GAM1602  PCDH11Y  3'  TCCAGCCTGGGTGACAGAGCAA 53186     C      TG
                GA                TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A       GT
GAM1602  PCDHB9   3'  TCCAGCCTGGGCAATAAGAGC  39451       _
                                  GCTCT GTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||
                                  CGAGA TAACGGGTCCGACCT
                                    A
GAM1602  PDCL     3'  CCAACCTGGGCGACAGAG     19395             C
                                  CTCTGTTGCCCAGG TGG
                                  |||||||||||||| |||
                                  GAGACAGCGGGTCC ACC
                                           A
GAM1602  PDE4C    3'  CCTGGGCAACATAGCAAGA    8101      C   C
                                  TCT GCT TGTTGCCCAGG
                                  ||| ||| ||||||||||
                                  AGA CGA ACAACGGGTCC
                                    A   T
GAM1602  PDE4C    3'  TCCAGCCTGGGCAACACAGCAA 8107      C   C
                GA                TCT GCT TGTTGCCCAGGCTGGA
                                  ||| ||| ||||||||||||||||
                                  AGA CGA ACAACGGGTCCGACCT
                                    A   C
GAM1602  PDE4C    3'  TCCAGCCTGGGGCTGACAGAGC 8108      C       _   _
                AAGA                  TCT GCTCTGTT GCCC AGGCTGGA
                                  ||| |||||||| |||| ||||||||
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                                AGA CGAGACAG CGGG TCCGACCT
                                  A       T   G
GAM1602  PIK3CD   3'  TCCAAAACTCAACAGAGCCAGA 18501     C       CCC  GC_
                                TCT GCTCTGTTG   AG   TGGA
                                ||| |||||||||   ||   ||||
                                AGA CGAGACAAC   TC   ACCT
                                  C        ___  AAA
GAM1602  PIK3CG   3'  TCCAGCCTGGATAACAGAGCGA 12125           C
            GA                    TCTCGCTCTGTTG CCAGGCTGGA
                                ||||||||||||| ||||||||||
                                AGAGCGAGACAAT GGTCCGACCT
                                        A
GAM1602  PLA2G2D  3'  TCCAGCCTGGGCAACAGAGTGA 25723
                                TCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||
                                AGTGAGACAACGGGTCCGACCT

GAM1602  POLH     3'  TCCAGCCTGGGCAACAGAGCGA 22484
            GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGCGAGACAACGGGTCCGACCT

GAM1602  POLH     3'  TCCAGCCTGGGCAACAGAGCGA 22485
            GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGCGAGACAACGGGTCCGACCT

GAM1602  POLK     3'  CCAGCCTGAAGAGCGAGA     33100          GTTGCC
                                TCTCGCTCT     CAGGCTGG
                                |||||||||     ||||||||
                                AGAGCGAGA     GTCCGACC
                                     A_____
GAM1602  PPP1R12B 3'  TCCAGCCTGGGTGACAGAGCAA 50395     C       TG
            GA                    TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM1602  PRKY     3'  TCCAGCCTGGGTGACAGAGTGA 12384           TG
            GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                       GT
GAM1602  PRKY     3'  TCCAGGCTGGACGACAGAGCAA 12385     C       C    G
            GA                    TCT GCTCTGTTG CCAG CTGGA
                                ||| ||||||||| |||| |||||
                                AGA CGAGACAGC GGTC GACCT
                                  A        A   G
GAM1602  PSMB2    3'  TCCAGCCTGGCAACAGAGTGAG 12478             C
            A                     TCTCGCTCTGTTGCC AGGCTGGA
                                ||||||||||||||| ||||||||
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                                AGAGTGAGACAACGG TCCGACCT
                                        _
GAM1602  PSMB2    3'  TCCAGCCTGGCTGACAGAGCAA 12479     C       GC
                GA                TCT GCTCTGTT  CCAGGCTGGA
                                  ||| ||||||||  ||||||||||
                                  AGA CGAGACAG  GGTCCGACCT
                                    A       TC
GAM1602  PSMB9    3'  TCCAGCCTGGGAAACAGAGCGA 12509          G
                                  TCGCTCTGTT CCCAGGCTGGA
                                  |||||||||| ||||||||||
                                  AGCGAGACAA GGGTCCGACCT
                                       A
GAM1602  PSMB9    3'  TCCAGCCTGGGCGACAAAGCGA 12510        C
                GA                TCTCGCT TGTTGCCCAGGCTGGA
                                  ||||||| ||||||||||||||||
                                  AGAGCGA ACAGCGGGTCCGACCT
                                     A
GAM1602  PSMD5    3'  CCTGGGCAACACAGCAAGA   18557     C  C
                                  TCT GCT TGTTGCCCAGG
                                  ||| ||| ||||||||||
                                  AGA CGA ACAACGGGTCC
                                    A  C
GAM1602  PTAFR    3'  TCTAGCCTGGCAACAGAGCGAG 8168              C
                A                  TCTCGCTCTGTTGCC AGGCTGGA
                                   |||||||||||||| ||||||||
                                   AGAGCGAGACAACGG TCCGATCT
                                           _
GAM1602  PTGIS    3'  TCCAGCCTGGGCGACAGAGCAA 8229      C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM1602  RABIF    3'  TCCAGCCTGGGCAACAGAGTGA 12730
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAACGGGTCCGACCT

GAM1602  RAD1     3'  TCCAGCCTAGGCAATAAGAGC  12647      _     C
                                  GCTCT GTTGCC AGGCTGGA
                                  ||||| |||||| ||||||||
                                  CGAGA TAACGG TCCGACCT
                                     A     A
GAM1602  RAD1     3'  TCCAGCCTAGGCAATAAGAGC  56655      _     C
                                  GCTCT GTTGCC AGGCTGGA
                                  ||||| |||||| ||||||||
                                  CGAGA TAACGG TCCGACCT
                                     A     A
GAM1602  RAD1     3'  TCCAGCCTAGGCAATAAGAGC  56752      _     C
                                  GCTCT GTTGCC AGGCTGGA
                                  ||||| |||||| ||||||||
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                                CGAGA TAACGG TCCGACCT
                                  A     A
GAM1602 RANBP2L1 3' TCCAGCTCGGGGAACAGAGCGA 18568          G   AG
            GA                    TCTCGCTCTGTT CCC  GCTGGA
                                  |||||||||||| |||  ||||||
                                  AGAGCGAGACAA GGG  CGACCT
                                        G   CT
GAM1602 RBBP5   3' TCCAGCCTAGGTGACAGAATGA 18579      C    TG  C
            GA                    TCTCG TCTGT  CC AGGCTGGA
                                  ||||| |||||  || ||||||||
                                  AGAGT AGACA  GG TCCGACCT
                                    A    GT  A
GAM1602 RBBP9   3' CCAGGGCAACACAGCAAGA   70687    C  C      A
                                  TCT GCT TGTTGCCC GG
                                  ||| ||| |||||||| ||
                                  AGA CGA ACAACGGG CC
                                    A  C       A
GAM1602 RBL1    3' TCCAGCCTGGGCAACAAGAGT  12789      _
                                  GCTCT GTTGCCCAGGCTGGA
                                  ||||| |||||||||||||||
                                  TGAGA CAACGGGTCCGACCT
                                    A
GAM1602 RBM3    3' TCCAGCCTGGGCAACAGCGAGA 71013        CT
                                  TCTCGCT  GTTGCCCAGGCTGGA
                                  |||||||  |||||||||||||||
                                  AGAGCGA  CAACGGGTCCGACCT
                                          __
GAM1602 RFC2    3' CCAGCCTGGGCGACAGAG    12839
                                  CTCTGTTGCCCAGGCTGG
                                  ||||||||||||||||||
                                  GAGACAGCGGGTCCGACC

GAM1602 ROCK2   3' TCCAGCCTGGGCAGCTGAACAA 66625    CGC  T
            GA                    TCT   TC GTTGCCCAGGCTGGA
                                  |||   || ||||||||||||||||
                                  AGA   AG CGACGGGTCCGACCT
                                    ACA  T
GAM1602 SCAP2   3' TCCAGCCTGGGCGACAGAGTGA 15427
            GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAGCGGGTCCGACCT

GAM1602 SFRS2IP  5' TCCAGCCTGGGTGACAGAGTGA 17547          TG
            GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                        GT
GAM1602 SIGLEC11 3' TCCAGCCTGGGCAACAGAGTGA 54657
            GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
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                                AGAGTGAGACAACGGGTCCGACCT

GAM1602  SIGLEC6   3'  CCAGCCTGGGCAACAGAGCGAG 60605
                A                TCTCGCTCTGTTGCCCAGGCTGG
                                 ||||||||||||||||||||||
                                 AGAGCGAGACAACGGGTCCGACC

GAM1602  SIM2      3'  TCCAGCCTGGGTAACAGAGTGA 24804
                GA                 TCTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGTGAGACAATGGGTCCGACCT

GAM1602  SLC14A2   3'  TCCAGCCTGGGCAACGGATTGA 24128       C
                GA                 TCTCG TCTGTTGCCCAGGCTGGA
                                   ||||| |||||||||||||||||
                                   AGAGT AGGCAACGGGTCCGACCT
                                     T
GAM1602  SLC17A5   3'  TCCAGCCTGGGCGATGGAGCGA 25835
                GA                 TCTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGCGAGGTAGCGGGTCCGACCT

GAM1602  SLC26A4   3'  TCCAGCCTGGGCGACAGAGCAA 6530      C
                GA                 TCT GCTCTGTTGCCCAGGCTGGA
                                   ||| ||||||||||||||||||
                                   AGA CGAGACAGCGGGTCCGACCT
                                     A
GAM1602  SLC28A2   3'  TCCAGCCTGGGTGACAGAGCGA 16154          TG
                GA                 TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   AGAGCGAGACA  GGGTCCGACCT
                                         GT
GAM1602  SLC2A6    3'  TCCAGCCTGGGCAACGAGAGTG 34577         _
                A                  TCGCTCT GTTGCCCAGGCTGGA
                                   ||||||| ||||||||||||||
                                   AGTGAGA CAACGGGTCCGACCT
                                       G
GAM1602  SLC31A1   3'  CCAGCCTGGGTGACAAG     10276    C   TG
                                   CT TGT  CCCAGGCTGG
                                   || |||  ||||||||||
                                   GA ACA  GGGTCCGACC
                                    _  GT
GAM1602  SMG1      3'  TCCAGCCTGGGCAACAGAGCTA 31352     C
                GA                 TCT GCTCTGTTGCCCAGGCTGGA
                                   ||| ||||||||||||||||||
                                   AGA CGAGACAACGGGTCCGACCT
                                     T
GAM1602  SRGAP1    5'  TCCAGCCTGGGCAACAGAGCGA 72721
                GA                 TCTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||||
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                                AGAGCGAGACAACGGGTCCGACCT

GAM1602  STK38    5'  TCCAGCCTGGGCAACAAGAGCG 24401        _
                A                TCGCTCT GTTGCCCAGGCTGGA
                                 ||||||| ||||||||||||||||
                                 AGCGAGA CAACGGGTCCGACCT
                                    A
GAM1602  SULT2A1  3'  TCCAGCCTGGGTGACAGAGCGA 72232          TG
                GA                 TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   AGAGCGAGACA  GGGTCCGACCT
                                         GT
GAM1602  SWAP70   3'  TCCAGCTTGGGCAACAGAGTGA 71874
                GA                 TCTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGTGAGACAACGGGTTCGACCT

GAM1602  TADA2L   3'  TCCAGCCTGGGCAACAAAGTGA 9439         C
                GA                 TCTCGCT TGTTGCCCAGGCTGGA
                                   ||||||| ||||||||||||||||
                                   AGAGTGA ACAACGGGTCCGACCT
                                      A
GAM1602  TBX1     3'  TCCAGCCTGGGTGACAGAGTGA 21141          TG
                GA                 TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   AGAGTGAGACA  GGGTCCGACCT
                                         GT
GAM1602  TBX6     3'  TCCAGCCTAGGCAACACGAGC  55817     _     C
                                   GCTC TGTTGCC AGGCTGGA
                                   |||| ||||||| ||||||||
                                   CGAG ACAACGG TCCGACCT
                                     C      A
GAM1602  TCF1     3'  CCAGCCTGGGCCTATGGAG   6783       T_
                                   CTCTGT  GCCCAGGCTGG
                                   ||||||  ||||||||||
                                   GAGGTA  CGGGTCCGACC
                                      TC
GAM1602  TCTA     3'  TCCAGCCTGGGCAACAGAGCAA 42503     C
                GA                 TCT GCTCTGTTGCCCAGGCTGGA
                                   ||| ||||||||||||||||||||
                                   AGA CGAGACAACGGGTCCGACCT
                                     A
GAM1602  TEM7     3'  TCCAGCCTGGGTGACAGAGCGA 40269          TG
                GA                 TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   AGAGCGAGACA  GGGTCCGACCT
                                         GT
GAM1602  TEM7     3'  TCCAGCCTGGGTGACAGAGTGA 40270          TG
                GA                 TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
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                                AGAGTGAGACA  GGGTCCGACCT
                                      GT
GAM1602  TNFAIP6   3'  CTGGGCAACATAGCAAGA    60165     C   C
                                TCT GCT TGTTGCCCAG
                                ||| ||| ||||||||||
                                AGA CGA ACAACGGGTC
                                  A   T
GAM1602  TNFRSF1B  3'  TCCAGCCTGAGCAACAGAGTGA 8402              C
           GA                    TCTCGCTCTGTTGC CAGGCTGGA
                                ||||||||||||| |||||||||
                                AGAGTGAGACAACG GTCCGACCT
                                      A
GAM1602  TNFRSF1B  3'  TCCAGCCTGGGCGACAGAGCGA 8403
           GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGCGAGACAGCGGGTCCGACCT

GAM1602  TNFSF10   3'  TCCAGCCTGGCGACAGAGCGAG 15094              C
           A                     TCTCGCTCTGTTGCC AGGCTGGA
                                ||||||||||||||| ||||||||
                                AGAGCGAGACAGCGG TCCGACCT
                                          _
GAM1602  TNFSF15   3'  TCCAGCCTGGGTAACAAGAGC  18870       _
                                GCTCT GTTGCCCAGGCTGGA
                                ||||| ||||||||||||||
                                CGAGA CAATGGGTCCGACCT
                                   A
GAM1602  TPM4      3'  TCCAGCCTGGTCGACAGAGTGA 13834           C
           GA                    TCTCGCTCTGTTG CCAGGCTGGA
                                |||||||||||| ||||||||||
                                AGAGTGAGACAGC GGTCCGACCT
                                      T
GAM1602  TPMT      3'  CCAGCCTGGGCAACAGAGCAAG 6307      C
           A                     TCT GCTCTGTTGCCCAGGCTGG
                                ||| ||||||||||||||||||
                                AGA CGAGACAACGGGTCCGACC
                                  A
GAM1602  TRIM14    3'  TCCAGCCTGGGCAATAGAGTGA 53778
           GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGATAACGGGTCCGACCT

GAM1602  TRIM14    3'  TCCAGCCTGGGGACAGAGCAAG 29517     C       G
           A                     TCT GCTCTGTT CCCAGGCTGGA
                                ||| |||||||| ||||||||||
                                AGA CGAGACAG GGGTCCGACCT
                                  A       _
GAM1602  TSN       3'  CCAGCCTGGGCAACAAAGTGAG 17297        C
           A                     TCTCGCT TGTTGCCCAGGCTGG
                                ||||||| |||||||||||||||
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                                AGAGTGA ACAACGGGTCCGACC
                                    A
GAM1602  TSNAX    3'  TCCAGCCTGGGTAACAGAGCAA 21160     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAATGGGTCCGACCT
                                      A
GAM1602  UBE2B    3'  TCCAGCCTGGGTGACAGAGC   13938        TG
                                    GCTCTGT  CCCAGGCTGGA
                                    |||||||  ||||||||||
                                    CGAGACA  GGGTCCGACCT
                                        GT
GAM1602  UBE2G2   3'  TCCAGCCTGGGCAACAGAGCGA 65495
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACAACGGGTCCGACCT

GAM1602  UBE2G2   3'  TCCAGCCTGGGCAACAGAGTGA 65496
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAACGGGTCCGACCT

GAM1602  UC28     3'  TCCAGCCTGGGCAACAGGAGT  41590      _
                                    GCTC TGTTGCCCAGGCTGGA
                                    |||| ||||||||||||||||
                                    TGAG ACAACGGGTCCGACCT
                                      G
GAM1602  USP14    3'  TCCAGCCTGGGTGACAGAGAGA 18940    G     TG
                                    TC CTCTGT  CCCAGGCTGGA
                                    || ||||||  ||||||||||
                                    AG GAGACA  GGGTCCGACCT
                                     A     GT
GAM1602  VHL      3'  CCAGCCTGGGAAACAAGAG    6841       _  G
                                    CTCT GTT CCCAGGCTGG
                                    |||| ||| ||||||||||
                                    GAGA CAA GGGTCCGACC
                                      A  A
GAM1602  VHL      3'  TCCAGCCTGGGGGACAGAGCAA 6876      C       G
                GA                  TCT GCTCTGTT CCCAGGCTGGA
                                    ||| |||||||| ||||||||||
                                    AGA CGAGACAG GGGTCCGACCT
                                      A       G
GAM1602  VHL      3'  TCCAGCCTGTGTGACAGAGC   6877         TG C
                                    GCTCTGT  C CAGGCTGGA
                                    |||||||  | |||||||||
                                    CGAGACA  G GTCCGACCT
                                        GT T
GAM1602  VPS41    3'  TCCAGCCTGGGCAACAAGAGC  27697       _
                                    GCTCT GTTGCCCAGGCTGGA
                                    ||||| ||||||||||||||||
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                                CGAGA CAACGGGTCCGACCT
                                  A
GAM1602  WIG1     3'  TCCAGCCTGGGTGACAGAGCGA 96105          TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                      GT
GAM1602  XT3      3'  TCCAGTCTGGGCGACAGAGCAA 39918     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGCGGGTCTGACCT
                                    A
GAM1602  ZNF14    3'  TCCAGCCTGTGCGACAGAATGA 41058       C       C
                GA                TCTCG TCTGTTGC CAGGCTGGA
                                  ||||| |||||||| |||||||||
                                  AGAGT AGACAGCG GTCCGACCT
                                    A       T
GAM1602  ZNF264   3'  TCCAGCCTGGGCAACAGAGCGA 14232
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAACGGGTCCGACCT

GAM1602  ZNF264   3'  TCCAGCCTGGGCAGCAGAGCGA 14233
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACGACGGGTCCGACCT

GAM1602  ZNF36    3'  TCCAGCCTGGGTGACTAGC   95587     CT  TG
                                  GCT  GT  CCCAGGCTGGA
                                  |||  ||  ||||||||||
                                  CGA  CA  GGGTCCGACCT
                                    T_  GT
GAM1602  ZNF91    3'  CCTGGGCGACAGAGCGAGA   14280
                                  TCTCGCTCTGTTGCCCAGG
                                  |||||||||||||||||
                                  AGAGCGAGACAGCGGGTCC

GAM1602  AF020591 3'  TCCAGCCTGGGCAACAGAGCAA 27916     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAACGGGTCCGACCT
                                    A
GAM1602  ALTE     3'  TCCAGCCTGGGCGACAAGAGCG 61007          _
                AGA                 TCTCGCTCT GTTGCCCAGGCTGGA
                                  |||||||||  ||||||||||||||
                                  AGAGCGAGA CAGCGGGTCCGACCT
                                      A
GAM1602  ALTE     3'  TCCAGCCTGGAGGCCAGAGTGA 17582          _  GC
                GA                TCTCGCTCTG TT  CCAGGCTGGA
                                  ||||||||||  ||  ||||||||||
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                                AGAGTGAGAC GG  GGTCCGACCT
                                     C  A_
GAM1602  ALTE     3'  TCCAGCCTGGGCGACAAGAGCG 17583         _
            AGA                   TCTCGCTCT GTTGCCCAGGCTGGA
                                  ||||||||| ||||||||||||||||
                                  AGAGCGAGA CAGCGGGTCCGACCT
                                       A
GAM1602  AP1GBP1   3'  TCTGAGCGACAGAGCAAGA   55447     C        C
                                  TCT GCTCTGTTGC CAGG
                                  ||| |||||||||| ||||
                                  AGA CGAGACAGCG GTCT
                                    A         A
GAM1602  AP4S1     3'  TCCAATCTGGCAACAGAGCGAG 23965              C  GC
            A                      TCTCGCTCTGTTGCC AG  TGGA
                                  |||||||||||||| ||  ||||
                                  AGAGCGAGACAACGG TC  ACCT
                                         _  TA
GAM1602  APOF     3'  TCCAGCCTGGGTGACAGAGCGA 9696           TG
            GA                     TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                       GT
GAM1602  APXL2     3'  TCCAGCCTGGGCGACAGAGCAA 75686     C
            GA                     TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM1602  ARNTL2    3'  CCAGCCTGGGCGACAGAGCGAG 39843
            A                      TCTCGCTCTGTTGCCCAGGCTGG
                                  ||||||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCCGACC

GAM1602  ARNTL2    3'  TCCAGTCTGGGCAACAGAGTGA 39858
            GA                     TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||
                                  AGAGTGAGACAACGGGTCTGACCT

GAM1602  ASAHL     3'  TCTAGCCTGGGCAACAGAGCGA 64321
            GA                     TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||
                                  AGAGCGAGACAACGGGTCCGATCT

GAM1602  ATP1B4    3'  TCCAGCCTGGGTGACAGAGTGA 24852           TG
            GA                     TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                       GT
GAM1602  BANP      3'  TCCAGACTGTGCGACAGAGCGA 66805           C   G
            GA                     TCTCGCTCTGTTGC CAG CTGGA
                                  |||||||||||||| ||| |||||
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                                AGAGCGAGACAGCG GTC GACCT
                                       T   A
GAM1602  BIRC1    3'  TCCAGCCTGGGCAACAGAGCAA 16995     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAACGGGTCCGACCT
                                    A
GAM1602  BIVM     3'  TCCAGCCTGGGCAACAGGGCAA 35160     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGGGACAACGGGTCCGACCT
                                    A
GAM1602  BLOV1    3'  TCCAGCCTGGGCAACAAGAGCG 76799        _
                A                  TCGCTCT GTTGCCCAGGCTGGA
                                  ||||||| ||||||||||||||||
                                  AGCGAGA CAACGGGTCCGACCT
                                      A
GAM1602  BLOV1    3'  TCCAGCCTGGGCGACAGAGCAA 76800     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM1602  BTN3A2   3'  TCCAGCCTGGGAGACAGAGCGA 23880          TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  |||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GA
GAM1602  C12orf2  3'  TCCAGCCTGGGTAACAGAGTGA 83688
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAATGGGTCCGACCT

GAM1602  C13orf1  3'  TCCAGCCTAGGCAACAGAGTGA 40372            C
                GA                TCTCGCTCTGTTGCC AGGCTGGA
                                  |||||||||||||| ||||||||
                                  AGAGTGAGACAACGG TCCGACCT
                                        A
GAM1602  C1orf33  3'  TCCAGCCTGGGCAACAGAGT  32987
                                  GCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||
                                  TGAGACAACGGGTCCGACCT

GAM1602  C1orf34  3'  CCTGGGCGACAGAGCGAGA   61304
                                  TCTCGCTCTGTTGCCCAGG
                                  |||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCC

GAM1602  C1QTNF2  3'  TCCAGCCTGGGCAACAGAGTGA 49977
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
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                                AGAGTGAGACAACGGGTCCGACCT

GAM1602  C20orf106 3'  TCCAGCCCAGGTGACAGAGTGA 55914          TG  CA
              GA                  TCTCGCTCTGT  CC  GGCTGGA
                                  ||||||||||  ||  |||||||
                                  AGAGTGAGACA  GG  CCGACCT
                                        GT  AC
GAM1602  C20orf108 3'  TCCAGCCTGGGCGACAGAGGGA 55883      G
              GA                  TCTC CTCTGTTGCCCAGGCTGGA
                                  |||| ||||||||||||||||||
                                  AGAG GAGACAGCGGGTCCGACCT
                                    G
GAM1602  C20orf12  3'  TCCAGCCTGGGCAACAAGAGC  36850       _
                                  GCTCT GTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||
                                  CGAGA CAACGGGTCCGACCT
                                     A
GAM1602  C20orf142 3'  TCCAGCCTGAGCGACAGAGTGA 75289            C
              GA                  TCTCGCTCTGTTGC CAGGCTGGA
                                  |||||||||||||| |||||||||
                                  AGAGTGAGACAGCG GTCCGACCT
                                        A
GAM1602  C20orf154 3'  CTTGGGCAACATAGCAAGA   90049     C   C
                                  TCT GCT TGTTGCCCAGG
                                  ||| ||| ||||||||||
                                  AGA CGA ACAACGGGTTC
                                    A   T
GAM1602  C20orf172 3'  TCCAGCCTGAGCGACAGAGTGA 46768            C
              GA                  TCTCGCTCTGTTGC CAGGCTGGA
                                  |||||||||||||| |||||||||
                                  AGAGTGAGACAGCG GTCCGACCT
                                        A
GAM1602  C20orf177 3'  TCCAGCCTGGGCAACAAGAGGG 62841    G   _
              A                    TC CTCT GTTGCCCAGGCTGGA
                                  || |||| ||||||||||||||
                                  AG GAGA CAACGGGTCCGACCT
                                    G   A
GAM1602  C20orf183 3'  TCCAGGCTGGGCGACAGAGCGA 48537                G
              GA                  TCTCGCTCTGTTGCCCAG CTGGA
                                  |||||||||||||||| |||||
                                  AGAGCGAGACAGCGGGTC GACCT
                                           G
GAM1602  C20orf29  3'  TCCAGCCTGGGCAACAGAGTGA 37712
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAACGGGTCCGACCT

GAM1602  C21orf108 3'  TCCAGCCTAGGTGACAGAGCAA 90121     C      TG  C
              GA                  TCT GCTCTGT  CC AGGCTGGA
                                  ||| |||||||  || ||||||||
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                                AGA CGAGACA  GG TCCGACCT
                                  A      GT  A
GAM1602  C22orf19  3'  TCTGGACAACAGAGCAAGA   14831     C       C
                                TCT GCTCTGTTG CCAGG
                                ||| ||||||||| |||||
                                AGA CGAGACAAC GGTCT
                                  A        A
GAM1602  C22orf20  3'  TCCAGCCTGGGCAACATGAGTG 48200       _
             A                   TCGCTC TGTTGCCCAGGCTGGA
                                ||||||| ||||||||||||||||
                                AGTGAG ACAACGGGTCCGACCT
                                   T
GAM1602  C6orf5    3'  TCCAGCCTGGGCAATAGAGTGA 32004
             GA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGATAACGGGTCCGACCT

GAM1602  C8orf17   3'  CAGCCTGGGCAACAGAATGAGA 39990       C
                                TCTCG TCTGTTGCCCAGGCTG
                                ||||| ||||||||||||||||
                                AGAGT AGACAACGGGTCCGAC
                                   A
GAM1602  C9orf5    3'  TCCAGCCTGGGTGAGAGAGTGA 50108          G TG
             GA                   TCTCGCTCT T  CCCAGGCTGGA
                                ||||||||| |  ||||||||||
                                AGAGTGAGA A  GGGTCCGACCT
                                     G GT
GAM1602  CAMKK2    5'  TCCAGCGTGGGCGACAGAGCGA 22631                G
             GA                   TCTCGCTCTGTTGCCCA GCTGGA
                                |||||||||||||||| ||||||
                                AGAGCGAGACAGCGGGT CGACCT
                                          G
GAM1602  CAMKK2    5'  TCCAGCCTGGGCAACACAGAGA 22630      G  C
             GA                   TCTC CT TGTTGCCCAGGCTGGA
                                |||| || ||||||||||||||||
                                AGAG GA ACAACGGGTCCGACCT
                                  A  C
GAM1602  CBCIP2    3'  TCCAGCCTGGGCGACAGAGCCA 52661     C
             GA                   TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGAGACAGCGGGTCCGACCT
                                  C
GAM1602  CCR6      3'  TCCAGCCTGGGTGACAGAGCGA 16448           TG
             GA                   TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      GT
GAM1602  CCR6      3'  TCCAGCCTGGGTGACAGAGCGA 49408           TG
             GA                   TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
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                                AGAGCGAGACA  GGGTCCGACCT
                                      GT
GAM1602  CDT1     3'  TCCAGCCTGGGTGACAGAGCGA 78166          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      GT
GAM1602  CENTA2   3'  TCCAGCCTGGGTGACAGAGCGA 37868          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      GT
GAM1602  cerk     3'  TCCAGCCTGGGCAACAGAGGGA 43169      G
                GA                  TCTC CTCTGTTGCCCAGGCTGGA
                                    |||| ||||||||||||||||||
                                AGAG GAGACAACGGGTCCGACCT
                                  G
GAM1602  CG012    5'  TCCAGCCCAGGTGACAGAGGGA 84166      G     TG  CA
                GA                  TCTC CTCTGT  CC  GGCTGGA
                                    |||| ||||||  ||  |||||||
                                AGAG GAGACA  GG  CCGACCT
                                  G     GT  AC
GAM1602  CG012    3'  TCCAGCCTCGCCGACAAAGCGA 84167        C     CCC
                GA                  TCTCGCT TGTTG   AGGCTGGA
                                    |||||||  |||||   ||||||||
                                AGAGCGA ACAGC   TCCGACCT
                                    A     CGC
GAM1602  CG012    5'  TCCAGCCTGGGCAACAGAACGA 84168      C
                GA                  TCTCG TCTGTTGCCCAGGCTGGA
                                    |||||  ||||||||||||||||||
                                AGAGC AGACAACGGGTCCGACCT
                                   A
GAM1602  CGI-203  3'  TCCAGCCTGGGTGACAGAGTGA 40277          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      GT
GAM1602  CHRFAM7A 3'  CCTGGGCGACAAAGCAAGA   96717    C   C
                                TCT GCT TGTTGCCCAGG
                                ||| ||| ||||||||||
                                AGA CGA ACAGCGGGTCC
                                  A   A
GAM1602  CNNM1    3'  CCTAGGCAACAGAGCGAGA   40117            C
                                TCTCGCTCTGTTGCC AGG
                                |||||||||||||| |||
                                AGAGCGAGACAACGG TCC
                                        A
GAM1602  CPR2     3'  TCCAGCCATACAGAACAGAGA  48838     GC_    TGCCCA
                                TCTC   TCTGT     GGCTGGA
                                ||||   |||||     |||||||
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                                AGAG   AGACA     CCGACCT
                                  ACA    TA____
GAM1602  CPR2     3'  TCCAGCCTGGGCGACAGAGTGA 48839
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAGCGGGTCCGACCT

GAM1602  CPR2     3'  TCCAGCCTGGGTAACAGAGCAA 48840     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAATGGGTCCGACCT
                                      A
GAM1602  CRTAM    3'  TCCAGCCTGGGCGACAGAGGGA 39476      G
                GA                  TCTC CTCTGTTGCCCAGGCTGGA
                                    |||| ||||||||||||||||||||
                                    AGAG GAGACAGCGGGTCCGACCT
                                      G
GAM1602  CSAD     3'  TCCAGGCTGGGCAACAGTACGA 32585       CT         G
                GA                  TCTCG  CTGTTGCCCAG CTGGA
                                    |||||  |||||||||| |||||
                                    AGAGC  GACAACGGGTC GACCT
                                       AT          G
GAM1602  CXYorf1   3'  CCAGCCCAAACTGTGACAGGAG 82906      GCT    TG CCA___
                A                    TCTC   CTGT  C     GGCTGG
                                    ||||   ||||  |     ||||||
                                    AGAG   GACA  G     CCGACC
                                      ___    GT TCAAAC
GAM1602  CYB5-M   3'  CCTGGGCAACATAGCGAGA    48334        C
                                    TCTCGCT TGTTGCCCAGG
                                    |||||||  ||||||||||
                                    AGAGCGA ACAACGGGTCC
                                         T
GAM1602  CYB5-M   3'  CCTGGGCAACATAGCGAGA    96201        C
                                    TCTCGCT TGTTGCCCAGG
                                    |||||||  ||||||||||
                                    AGAGCGA ACAACGGGTCC
                                         T
GAM1602  D21S2056E 3'  TCCAGCCTGGGCAACGAGAGGG 14873      G   T
                A                    TCTC CTC GTTGCCCAGGCTGGA
                                    |||| ||| ||||||||||||||
                                    AGGG GAG CAACGGGTCCGACCT
                                      A  _
GAM1602  DCOHM    3'  TCCAGCCTGGGTGACGGAACGG 50537       C     TG
                GA                  TCTCG TCTGT  CCCAGGCTGGA
                                    |||||  |||||  ||||||||||
                                    AGGGC AGGCA  GGGTCCGACCT
                                      A     GT
GAM1602  DDX34    3'  TCCAGCCTGGTTGACAGAGCAA 28678     C        GC
                GA                  TCT GCTCTGTT  CCAGGCTGGA
                                    |||  ||||||||  ||||||||||
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                                AGA CGAGACAG  GGTCCGACCT
                                  A       TT
GAM1602  DEGS     3'  TCCACCCTGGGCAACAGAGCAA 59270     C           C
                GA                  TCT GCTCTGTTGCCCAGG TGGA
                                    ||| |||||||||||||| ||||
                                    AGA CGAGACAACGGGTCC ACCT
                                      A            C
GAM1602  DEGS     3'  TCCACCCTGGGCAACAGAGCAA 14805     C           C
                GA                  TCT GCTCTGTTGCCCAGG TGGA
                                    ||| |||||||||||||| ||||
                                    AGA CGAGACAACGGGTCC ACCT
                                      A            C
GAM1602  DIS3     3'  TCCAGCCTGGGTGACAGAACAA 30922     CGC     TG
                GA                  TCT   TCTGT  CCCAGGCTGGA
                                    |||   |||||  ||||||||||
                                    AGA   AGACA  GGGTCCGACCT
                                      ACA     GT
GAM1602  dJ383J4.3 3'  TCCAGCCTGGGCAACAAAGTGA 67498        C
                GA                  TCTCGCT TGTTGCCCAGGCTGGA
                                    ||||||| ||||||||||||||||
                                    AGAGTGA ACAACGGGTCCGACCT
                                       A
GAM1602  DKFZP434A0131 3'  TCCAGCCTGGGTGACAGAGCAA 39154     C      TG
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGAGACA  GGGTCCGACCT
                                      A      GT
GAM1602  DKFZP434B168 3'  TCCAGCCTGGGCGACAGAGCGA 31872
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    |||||||||||||||||||||||||
                                    AGAGCGAGACAGCGGGTCCGACCT

GAM1602  DKFZP434C171 3'  TCCAGCCCGGGTGACAGAGCAA 32199     C      TG   A
                GA                  TCT GCTCTGT  CCC GGCTGGA
                                    ||| |||||||  ||| |||||||
                                    AGA CGAGACA  GGG CCGACCT
                                      A      GT   C
GAM1602  DKFZp434E0519 3'  TCTGGGCAACACAGCAAGA    51001     C   C
                                    TCT GCT TGTTGCCCAGG
                                    ||| ||| ||||||||||
                                    AGA CGA ACAACGGGTCT
                                      A   C
GAM1602  DKFZp434E169 3'  CCTGGGCGACAGAGCGAGA    51076
                                    TCTCGCTCTGTTGCCCAGG
                                    ||||||||||||||||||
                                    AGAGCGAGACAGCGGGTCC

GAM1602  DKFZP434F1735 3'  TCCAGCCTGGGCAGTATAGCAA 32117     C   C
                GA                  TCT GCT TGTTGCCCAGGCTGGA
                                    ||| ||| ||||||||||||||||
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                                AGA CGA ATGACGGGTCCGACCT
                                  A   T
GAM1602  DKFZp434G171 3'  TCCAGCCTGGGAGACACAGCGA 80247        C   TG
            GA                    TCTCGCT TGT  CCCAGGCTGGA
                                  ||||||| |||  ||||||||||
                                  AGAGCGA ACA  GGGTCCGACCT
                                     C   GA
GAM1602  DKFZp434G171 3'  TCCAGCCTGGGCAACAAGAGGG 80248    G   _
            A                     TC CTCT GTTGCCCAGGCTGGA
                                  || |||| ||||||||||||||
                                  AG GAGA CAACGGGTCCGACCT
                                   G   A
GAM1602  DKFZP434I1735 3'  TCCAGCCTGGGCGACAGAGTGA 89173
            GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAGCGGGTCCGACCT

GAM1602  DKFZP434K1421 3'  TCCAACCTGGGCAACAGAATGA 50468      C          C
            GA                    TCTCG TCTGTTGCCCAGG TGGA
                                  ||||| |||||||||||| ||||
                                  AGAGT AGACAACGGGTCC ACCT
                                    A          A
GAM1602  DKFZP434N1511 3'  TCCAGCCTGGGCAACAGAGCAA 93063    C
            GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||
                                  AGA CGAGACAACGGGTCCGACCT
                                    A
GAM1602  DKFZP434N161 3'  CCTGGGCAACACAGCAAGA   79214    C   C
                                  TCT GCT TGTTGCCCAGG
                                  ||| ||| ||||||||||
                                  AGA CGA ACAACGGGTCC
                                    A   C
GAM1602  DKFZp547C176 3'  TCCAGCCTGGCGACAGAGCAAG 67806    C         C
            A                     TCT GCTCTGTTGCC AGGCTGGA
                                  ||| |||||||||| ||||||||
                                  AGA CGAGACAGCGG TCCGACCT
                                    A        _
GAM1602  DKFZp547G183 3'  TCCAGCCTGGGCGACAAGAGC  38649       _
                                  GCTCT GTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||
                                  CGAGA CAGCGGGTCCGACCT
                                     A
GAM1602  DKFZp547I094 3'  TCCAGCCTGGGCGGCAGAGTGA 50566
            GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACGGCGGGTCCGACCT

GAM1602  DKFZP564A022 3'  TCCAGCCTGGGCAACAGAGTGA 48975
            GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
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                                AGAGTGAGACAACGGGTCCGACCT

GAM1602  DKFZP564B1023 3'  TCCAGCCTGGACAACAGATTGA 49368      C      C
            GA                  TCTCG TCTGTTG CCAGGCTGGA
                                ||||| ||||||| ||||||||||
                                AGAGT AGACAAC GGTCCGACCT
                                   T      A
GAM1602  DKFZP564B1023 3'  TCCAGCCTGGGCAACAAGAGTG 49369       _
            A                   TCGCTCT GTTGCCCAGGCTGGA
                                ||||||| ||||||||||||||||
                                AGTGAGA CAACGGGTCCGACCT
                                    A
GAM1602  DKFZP564I0422 5'  TCCAGCCTCTGCCAGAAGA   49518   GC   TT  CC
                                TC  TCTG  GC  AGGCTGGA
                                ||  ||||  ||  ||||||||
                                AG  AGAC  CG  TCCGACCT
                                 A_   __  TC
GAM1602  DKFZP564I0422 3'  TCCAGCCTGGGCAATGGAGTGA 49519
            GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||||
                                AGAGTGAGGTAACGGGTCCGACCT

GAM1602  DKFZP564I052 3'  TCCAGGCTGGGCAACAGAGTGA 67286              G
            GA                  TCTCGCTCTGTTGCCCAG CTGGA
                                |||||||||||||||| |||||
                                AGAGTGAGACAACGGGTC GACCT
                                       G
GAM1602  DKFZp564K142 3'  TCCAGCCTGAGTGATAGAGTGA 50436          TG C
            GA                  TCTCGCTCTGT  C CAGGCTGGA
                                |||||||||||  | |||||||||
                                AGAGTGAGATA  G GTCCGACCT
                                      GT A
GAM1602  DKFZp564K142 3'  TCCAGCCTGGCAACAGAGCGAG 50437             C
            A                   TCTCGCTCTGTTGCC AGGCTGGA
                                |||||||||||||| ||||||||
                                AGAGCGAGACAACGG TCCGACCT
                                              _
GAM1602  DKFZP564M182 3'  TCCAGCCTGATGACAGAGCAAG 78642     C       CC
            A                   TCT GCTCTGTTG  CAGGCTGGA
                                ||| |||||||||  |||||||||
                                AGA CGAGACAGT  GTCCGACCT
                                   A        A_
GAM1602  DKFZP564M182 3'  TCCAGCCTGGGCAACAGAGAGA 78643     G
            GA                  TCTC CTCTGTTGCCCAGGCTGGA
                                |||| ||||||||||||||||||
                                AGAG GAGACAACGGGTCCGACCT
                                   A
GAM1602  DKFZP564M182 3'  TCCAGCCTGGGCGGCAGAGC   78644
                                GCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||
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                                CGAGACGGCGGGTCCGACCT

GAM1602  DKFZp566H0824 3'  TCCAGCCTGGGCAACAGAGCAA 34492     C
            GG                  TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                GGA CGAGACAACGGGTCCGACCT
                                  A
GAM1602  DKFZp566H0824 5'  TCCAGCCTGGGCGACAGAGCGA 34493
            GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGCGAGACAGCGGGTCCGACCT

GAM1602  DKFZP586D2223 3'  CCTGGGCAACATAGCGAGA    38288        C
                                TCTCGCT TGTTGCCCAGG
                                ||||||| ||||||||||
                                AGAGCGA ACAACGGGTCC
                                     T
GAM1602  DKFZP586D2223 3'  TCTAGCCTGGGCAACAGAGTGA 38297
            GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGACAACGGGTCCGATCT

GAM1602  DKFZP586M1120 3'  TCCAGCCTGGGCAACAGAGTGA 49286
                                TCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||
                                AGTGAGACAACGGGTCCGACCT

GAM1602  DKFZP667O116 3'  CCTGGGCAACATAGCGAGA    95940        C
                                TCTCGCT TGTTGCCCAGG
                                ||||||| ||||||||||
                                AGAGCGA ACAACGGGTCC
                                     T
GAM1602  DKFZp727G131 3'  TCCAGCCTGGGCAACAGCGTGA 59698        T
            GA                  TCTCGC CTGTTGCCCAGGCTGGA
                                |||||| ||||||||||||||||
                                AGAGTG GACAACGGGTCCGACCT
                                   C
GAM1602  DKFZP761G1913 3'  TCCAGCCTGGGTGAAGGAGTGA 49699          G TG
            GA                  TCTCGCTCT T  CCCAGGCTGGA
                                ||||||||| |  ||||||||||
                                AGAGTGAGG A  GGGTCCGACCT
                                     A GT
GAM1602  DRF1     3'  TCCAGCCTGGGCGATAGAGCTA 47757     C
            GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGAGATAGCGGGTCCGACCT
                                  T
GAM1602  DRF1     3'  TCCAGCCTGGGTGACAGAGCGA 47758           TG
            GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
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                                AGAGCGAGACA  GGGTCCGACCT
                                      GT
GAM1602  DSCR6    3'  TCCAGCCTGGGCAACAAGAGCG 39076        _
                A                TCGCTCT GTTGCCCAGGCTGGA
                                 ||||||| ||||||||||||||
                                 AGCGAGA CAACGGGTCCGACCT
                                    A
GAM1602  ET       3'  CCAGCCTGGATGACAAG     44467    C   GC
                                 CT TGTT  CCAGGCTGG
                                 || ||||  |||||||||
                                 GA ACAG  GGTCCGACC
                                  _   TA
GAM1602  EVI5     3'  TCCAACCTGGGCAACATGGCAA 20218     C  C         C
                GA                 TCT GCT TGTTGCCCAGG TGGA
                                   ||| ||| |||||||||| ||||
                                   AGA CGG ACAACGGGTCC ACCT
                                     A  T         A
GAM1602  FADS1    3'  TCCAGCCTGGGCGACAGAGCAA 26386     C
                GA                 TCT GCTCTGTTGCCCAGGCTGGA
                                   ||| ||||||||||||||||||||
                                   AGA CGAGACAGCGGGTCCGACCT
                                     A
GAM1602  FADS1    3'  TCCAGCCTGGGGTGATAGAACA 26387     CGC    TG  _
                AGA                  TCT   TCTGT  CCC AGGCTGGA
                                     |||   |||||  ||| ||||||||
                                     AGA   AGATA  GGG TCCGACCT
                                       ACA     GT   G
GAM1602  FBXO26   3'  TCCAGCCTGGGTGAGAAAGCAA 46631     C   CTG TG
                GA                 TCT GCT   T  CCCAGGCTGGA
                                   ||| |||   |  ||||||||||
                                   AGA CGA   A  GGGTCCGACCT
                                     A   AAG GT
GAM1602  FBXO27   3'  TCCAGCCTGGGCAACACAGCGA 75014        C
                GA                 TCTCGCT TGTTGCCCAGGCTGGA
                                   ||||||| ||||||||||||||||
                                   AGAGCGA ACAACGGGTCCGACCT
                                      C
GAM1602  FBXO27   3'  TCCAGCCTGGGTGACAGAGCGA 75015          TG
                GA                 TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   AGAGCGAGACA  GGGTCCGACCT
                                         GT
GAM1602  FBXO6    3'  TCCAGCCTGGGTGACAGAGCGA 37997          TG
                GA                 TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   AGAGCGAGACA  GGGTCCGACCT
                                         GT
GAM1602  FBXO9    3'  CCTGGACAACATAGCAAGA   54244     C  C    C
                                   TCT GCT TGTTG CCAGG
                                   ||| ||| ||||| |||||
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                                AGA CGA ACAAC GGTCC
                                  A  T    A
GAM1602  FBXO9    3'  TCCAGCATGGGCAACATAACAA 54254     CGCTC       G
                GA                  TCT    TGTTGCCCA GCTGGA
                                    |||    ||||||||| |||||||
                                    AGA    ACAACGGGT CGACCT
                                      ACAAT       A
GAM1602  FBXO9    3'  TCCAGCCTGAGCAACACAGTGA 54255       C     C
                GA                  TCTCGCT TGTTGC CAGGCTGGA
                                    ||||||| |||||| |||||||||
                                    AGAGTGA ACAACG GTCCGACCT
                                       C     A
GAM1602  FKBP14   3'  TCCAGCCTGGGTGACAGAGCAA 36070     C      TG
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGAGACA  GGGTCCGACCT
                                      A      GT
GAM1602  FKSG17   3'  TCCAGCCTGGGTGACAGAGTGA 50159          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          GT
GAM1602  FKSG43   5'  TCCAGCCTGGGTGACAGAGCAA 50163     C      TG
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGAGACA  GGGTCCGACCT
                                      A      GT
GAM1602  FKSG44   5'  TCCAGCCTGGGCGACAGAGCGA 49963
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    |||||||||||||||||||||||||
                                    AGAGCGAGACAGCGGGTCCGACCT

GAM1602  FKSG83   3'  TCCAGCCTGGGAGACAGCAAGA 50146    GCT   TG
                                    TC   CTGT  CCCAGGCTGGA
                                    ||   ||||  ||||||||||
                                    AG   GACA  GGGTCCGACCT
                                     AAC    GA
GAM1602  FLJ00060 3'  TCCAGCCTGGGCGATAGAGCAA 61755     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGATAGCGGGTCCGACCT
                                      A
GAM1602  FLJ10008 3'  TCCAGCCTGGGCGACACAGCAA 36193     C   C
                GA                  TCT GCT TGTTGCCCAGGCTGGA
                                    ||| ||| ||||||||||||||||
                                    AGA CGA ACAGCGGGTCCGACCT
                                      A   C
GAM1602  FLJ10043 3'  TCCAGCCTGGGTGACAGAGCGA 36237          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
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                                AGAGCGAGACA  GGGTCCGACCT
                                      GT
GAM1602  FLJ10058  3'  TCCAGCCTGGGCAACACAGTGA 36264        C
                GA                  TCTCGCT TGTTGCCCAGGCTGGA
                                    ||||||| ||||||||||||||||
                                    AGAGTGA ACAACGGGTCCGACCT
                                       C
GAM1602  FLJ10139  3'  TCCAGCCTGGGTGACAAAGTAA 36317     CG  C   TG
                GA                  TCT  CT TGT  CCCAGGCTGGA
                                    |||  || |||  ||||||||||
                                    AGA  GA ACA  GGGTCCGACCT
                                      AT  A   GT
GAM1602  FLJ10157  5'  CCAGCCTGGACCAGAAGA    36329    GC    TTGC
                                    TC  TCTG    CCAGGCTGG
                                    ||  ||||    |||||||||
                                    AG  AGAC    GGTCCGACC
                                     A_    CA__
GAM1602  FLJ10159  3'  CCATTTGGGAACAGAGCAAGA  36335     C       G     C
                                    TCT GCTCTGTT CCCAGG TGG
                                    ||| |||||||| |||||| |||
                                    AGA CGAGACAA GGGTTT ACC
                                      A       _     _
GAM1602  FLJ10244  3'  TCCAGCCTGGGCAAAAAGAGC  36406       G_
                                    GCTCT  TTGCCCAGGCTGGA
                                    |||||  ||||||||||||||
                                    CGAGA  AACGGGTCCGACCT
                                       AA
GAM1602  FLJ10314  3'  CCAGCCTGCACAACAAG     36485    C    CC
                                    CT TGTTG  CAGGCTGG
                                    || |||||  ||||||||
                                    GA ACAAC  GTCCGACC
                                     _    AC
GAM1602  FLJ10460  3'  TCCAACCTGGGTGATGGAGCAA 36623     C       TG      C
                GA                  TCT GCTCTGT  CCCAGG TGGA
                                    ||| |||||||  |||||| ||||
                                    AGA CGAGGTA  GGGTCC ACCT
                                      A      GT     A
GAM1602  FLJ10520  3'  TCCAGCCTCGGTGACAGAGCAA 36710     C       TG  C
                GA                  TCT GCTCTGT  CC AGGCTGGA
                                    ||| |||||||  || ||||||||
                                    AGA CGAGACA  GG TCCGACCT
                                      A      GT  C
GAM1602  FLJ10547  3'  TCCAGCCTGGGCTACAGAGCGA 36779           T
                GA                  TCTCGCTCTGT GCCCAGGCTGGA
                                    |||||||||||| ||||||||||||
                                    AGAGCGAGACA CGGGTCCGACCT
                                           T
GAM1602  FLJ10597  3'  CCAGCCTGGGCTGACAGG    36835        _
                                    TCTGTT GCCCAGGCTGG
                                    |||||| ||||||||||
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                                GGACAG CGGGTCCGACC
                                   T
GAM1602  FLJ10607  3'  TCCAGCCTGGCGACAGAGAGAG 77646      G        C
                A                   TCTC CTCTGTTGCC AGGCTGGA
                                    |||| |||||||||| ||||||||
                                    AGAG GAGACAGCGG TCCGACCT
                                      A       _
GAM1602  FLJ10613  3'  TCTAGCCTGGGCAACAACACGA 39341     CTC
                                    TCG   TGTTGCCCAGGCTGGA
                                    |||   ||||||||||||||||
                                    AGC   ACAACGGGTCCGATCT
                                      ACA
GAM1602  FLJ10650  3'  TCCAGCCTGGGCGACAGAATGA 36903       C
                GA                  TCTCG TCTGTTGCCCAGGCTGGA
                                    ||||| ||||||||||||||||||
                                    AGAGT AGACAGCGGGTCCGACCT
                                      A
GAM1602  FLJ10704  3'  TCCAGCCTGGACGACAGAGTGA 36984            C
                GA                  TCTCGCTCTGTTG CCAGGCTGGA
                                    |||||||||||| ||||||||||
                                    AGAGTGAGACAGC GGTCCGACCT
                                          A
GAM1602  FLJ10781  3'  TCCAGCCTGGGCAGCAGAGTGA 37176
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACGACGGGTCCGACCT

GAM1602  FLJ10803  3'  TCCAGCCTGGGCAACAGAGCAA 37209     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||
                                    AGA CGAGACAACGGGTCCGACCT
                                      A
GAM1602  FLJ10826  3'  TCCAGCCTGGGCAACAAGAGTG 37250         _
                A                   TCGCTCT GTTGCCCAGGCTGGA
                                    ||||||| ||||||||||||||
                                    AGTGAGA CAACGGGTCCGACCT
                                       A
GAM1602  FLJ10830  3'  TCCAGCCTGGGCGACAGAACGA 37267       C
                GA                  TCTCG TCTGTTGCCCAGGCTGGA
                                    ||||| ||||||||||||||||||
                                    AGAGC AGACAGCGGGTCCGACCT
                                      A
GAM1602  FLJ10901  3'  CCAGCCTGGGCTGGGGGAGA  37355      G  TGTT
                                    TCTC CTC    GCCCAGGCTGG
                                    |||| |||    ||||||||||
                                    AGAG GGG    CGGGTCCGACC
                                      G  T___
GAM1602  FLJ10936  3'  TCCAGCCTGGGCAACAGAGGGA 37450      G
                GA                  TCTC CTCTGTTGCCCAGGCTGGA
                                    |||| ||||||||||||||||||
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                                AGAG GAGACAACGGGTCCGACCT
                                  G
GAM1602  FLJ10989  3'  TCCAGCCTGGGTGACAAAGCAA 37507     C   C   TG
                GA                  TCT GCT TGT  CCCAGGCTGGA
                                    ||| ||| |||  ||||||||||
                                    AGA CGA ACA  GGGTCCGACCT
                                      A   A   GT
GAM1602  FLJ10998  3'  TCCAGCCTGGGTGACAGTGA  37523       CT  TG
                                    TCGCT  GT  CCCAGGCTGGA
                                    |||||  ||  ||||||||||
                                    AGTGA  CA  GGGTCCGACCT
                                       __  GT
GAM1602  FLJ11016  3'  CCTGGGCAACACAGCAAGA   37540     C   C
                                    TCT GCT TGTTGCCCAGG
                                    ||| ||| ||||||||||
                                    AGA CGA ACAACGGGTCC
                                      A   C
GAM1602  FLJ11036  3'  TCCAGCCTGGGCGACAGAGCAA 37556     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAGCGGGTCCGACCT
                                      A
GAM1602  FLJ11126  3'  TCCAGCCTGGGTAACAGAGCGA 37655
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACAATGGGTCCGACCT

GAM1602  FLJ11149  3'  TCTGGGCAACATAGCGAGA   37689        C
                                    TCTCGCT TGTTGCCCAGG
                                    ||||||| ||||||||||
                                    AGAGCGA ACAACGGGTCT
                                        T
GAM1602  FLJ11151  3'  TCCAGCCTGGGCAACAGAGCAA 68482     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAACGGGTCCGACCT
                                      A
GAM1602  FLJ11259  3'  TCCAGTCTGGGCAACAGAGTGA 37772
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAACGGGTCTGACCT

GAM1602  FLJ11301  3'  TCCAGCCTGGGCGACAGAGTGA 37810
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAGCGGGTCCGACCT

GAM1602  FLJ11577  3'  TCCAGCCTGGGCAACAAGAGTG 47960          _
                AGA                   TCTCGCTCT GTTGCCCAGGCTGGA
                                    |||||||| ||||||||||||||
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                                AGAGTGAGA CAACGGGTCCGACCT
                                    A
GAM1602  FLJ11700  3'  TCCAGCCTGGGCAACAGAACAA 46567     CGC
                GA                  TCT   TCTGTTGCCCAGGCTGGA
                                    |||   ||||||||||||||||||
                                    AGA   AGACAACGGGTCCGACCT
                                      ACA
GAM1602  FLJ11710  5'  TCCAGCCTGGGCAACAGAGCAA 46252     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAACGGGTCCGACCT
                                      A
GAM1602  FLJ11715  3'  TCCAGCCTGGGTGATAGAGTGA 44983          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGATA  GGGTCCGACCT
                                          GT
GAM1602  FLJ11722  3'  TCCAGCCTGGCAACAGAGCAAG 47008     C         C
                G                    TCT GCTCTGTTGCC AGGCTGGA
                                    ||| |||||||||| ||||||||
                                    GGA CGAGACAACGG TCCGACCT
                                      A         _
GAM1602  FLJ11722  3'  TCCAGCCTGGCCACAGAGCGAG 47009          T   C
                A                    TCTCGCTCTGT GCC AGGCTGGA
                                    |||||||||| ||| ||||||||
                                    AGAGCGAGACA CGG TCCGACCT
                                          C  _
GAM1602  FLJ11726  3'  TCCAGCCTGGGCGACAGAGCAG 47031    TC
                GA                  TC  GCTCTGTTGCCCAGGCTGGA
                                    ||  ||||||||||||||||||||
                                    AG  CGAGACAGCGGGTCCGACCT
                                     GA
GAM1602  FLJ11800  3'  TCCAGCCTGGGCAACAGAG    47042
                                    CTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||
                                    GAGACAACGGGTCCGACCT


GAM1602  FLJ11827  3'  CCTGGGCAACATAGCAAGA    47681     C   C
                                    TCT GCT TGTTGCCCAGG
                                    ||| ||| ||||||||||
                                    AGA CGA ACAACGGGTCC
                                      A   T
GAM1602  FLJ11996  3'  TCCAACCTGGGCAACAGAGTAA 47069     CG          C
                GA                  TCT  CTCTGTTGCCCAGG TGGA
                                    |||  |||||||||||||| ||||
                                    AGA  GAGACAACGGGTCC ACCT
                                      AT           A
GAM1602  FLJ12056  3'  TCAGCCCGGGCAACAAGAGCGA 46823          _      A
                GA                  TCTCGCTCT GTTGCCC GGCTGG
                                    |||||||| ||||||| ||||||
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                                AGAGCGAGA CAACGGG CCGACT
                                    A      C
GAM1602  FLJ12078  3'  TCCAGCCTGGGTGGCAGAGAGA 47086     G     TG
              GA                  TCTC CTCTGT  CCCAGGCTGGA
                                  |||| ||||||  ||||||||||
                                  AGAG GAGACG  GGGTCCGACCT
                                    A     GT
GAM1602  FLJ12190  3'  TCCAGCCTGGGCAACAGAGC   47572
                                  GCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||
                                  CGAGACAACGGGTCCGACCT

GAM1602  FLJ12294  3'  TCCAGCCTGGGTGACAGAGAGA 47721     G     TG
              GA                  TCTC CTCTGT  CCCAGGCTGGA
                                  |||| ||||||  ||||||||||
                                  AGAG GAGACA  GGGTCCGACCT
                                    A     GT
GAM1602  FLJ12298  3'  TCCAGCCTGGGCAACAGAGCGA 50600
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                  |||||||||||||||||||||||||
                                  AGAGCGAGACAACGGGTCCGACCT

GAM1602  FLJ12331  3'  TCCAGCCTGAGCTACAGAGCAA 47114     C     T  C
              GA                  TCT GCTCTGT GC CAGGCTGGA
                                  ||| ||||||| || |||||||||
                                  AGA CGAGACA CG GTCCGACCT
                                    A      T  A
GAM1602  FLJ12363  3'  TCCAGCCTGGGCAACAAGAGAG 50643     G  C
              A                    TCTC CT TGTTGCCCAGGCTGGA
                                  |||| || ||||||||||||||||
                                  AGAG GA ACAACGGGTCCGACCT
                                    A  _
GAM1602  FLJ12586  3'  TCCAGCCTGGGTGACAGAGCGA 45212          TG
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GT
GAM1602  FLJ12592  3'  CCTGGGCAACATAGCGAGA   50650        C
                                  TCTCGCT TGTTGCCCAGG
                                  |||||||  ||||||||||
                                  AGAGCGA ACAACGGGTCC
                                      T
GAM1602  FLJ12592  3'  TCCAGCCTGGGTGACCGAGTGA 50655        T  TG
              GA                  TCTCGCTC GT  CCCAGGCTGGA
                                  ||||||||  ||  ||||||||||
                                  AGAGTGAG CA  GGGTCCGACCT
                                      C  GT
GAM1602  FLJ12618  3'  TCCAGCCTGGGTGACAGAGCAA 46508     C     TG
              GA                  TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
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                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM1602  FLJ12666  3'  TCCAGCCTGGGCAACAAAACGA 45072       CTC
                GA                  TCTCG   TGTTGCCCAGGCTGGA
                                    |||||   ||||||||||||||||
                                    AGAGC   ACAACGGGTCCGACCT
                                      AAA
GAM1602  FLJ12671  3'  TCCAGCCTGGGTGACAAGAGTG 49112          _  TG
                AGA                  TCTCGCTCT GT  CCCAGGCTGGA
                                     |||||||||  ||  ||||||||||
                                     AGAGTGAGA CA  GGGTCCGACCT
                                         A  GT
GAM1602  FLJ12687  3'  TCCAGCCTGGGTGACAGAGTGA 46759           TG
                GA                   TCTCGCTCTGT  CCCAGGCTGGA
                                     ||||||||||  ||||||||||
                                     AGAGTGAGACA  GGGTCCGACCT
                                           GT
GAM1602  FLJ12847  3'  TCCAGCCTGGGCAACAGAGT   45079
                                     GCTCTGTTGCCCAGGCTGGA
                                     ||||||||||||||||||||
                                     TGAGACAACGGGTCCGACCT

GAM1602  FLJ12921  3'  TCCAGCCTGGGCGACGGAGCGA 46400
                GA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                     ||||||||||||||||||||||||
                                     AGAGCGAGGCAGCGGGTCCGACCT

GAM1602  FLJ12949  3'  TCCAGCCTGGGCAACAAAGCAA 43727     C   C
                GA                   TCT GCT TGTTGCCCAGGCTGGA
                                     ||| ||| ||||||||||||||||
                                     AGA CGA ACAACGGGTCCGACCT
                                       A   A
GAM1602  FLJ13117  3'  TCCAGCCTGGGAGACAGAGCAA 43811     C      TG
                GA                   TCT GCTCTGT  CCCAGGCTGGA
                                     ||| |||||||  ||||||||||
                                     AGA CGAGACA  GGGTCCGACCT
                                       A      GA
GAM1602  FLJ13193  3'  TCCAGCCTGGCGACAGAGCGAG 50736             C
                A                     TCTCGCTCTGTTGCC AGGCTGGA
                                      ||||||||||||||| ||||||||
                                      AGAGCGAGACAGCGG TCCGACCT
                                                 _
GAM1602  FLJ13241  3'  TCCAGCCTGGGTGGCAGAGCCA 47656     C      TG
                GA                   TCT GCTCTGT  CCCAGGCTGGA
                                     ||| |||||||  ||||||||||
                                     AGA CGAGACG  GGGTCCGACCT
                                       C      GT
GAM1602  FLJ13352  3'  CTGGCCTGGGCAACAGAGCAAG 45053     C            TG
                A                     TCT GCTCTGTTGCCCAGGC  G
                                      ||| ||||||||||||||  |
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                                AGA CGAGACAACGGGTCCG  C
                                  A             GT
GAM1602  FLJ13448  3'  TCCAGCCTGGGCAACAGAGGGA 47885      G
                GA                TCTC CTCTGTTGCCCAGGCTGGA
                                  |||| ||||||||||||||||||
                                  AGAG GAGACAACGGGTCCGACCT
                                    G
GAM1602  FLJ13456  3'  CCTGGGAAACAGAGCGAGA   66542           G
                                  TCTCGCTCTGTT CCCAGG
                                  |||||||||||| ||||||
                                  AGAGCGAGACAA GGGTCC
                                         A
GAM1602  FLJ13456  3'  TCCAGCCTGGACAACGGAGTGA 66563           C
                GA                TCTCGCTCTGTTG CCAGGCTGGA
                                  |||||||||||| |||||||||
                                  AGAGTGAGGCAAC GGTCCGACCT
                                         A
GAM1602  FLJ13456  3'  TCCAGCCTGGGTGACAGAGTAA 66564     CG     TG
                GA                TCT  CTCTGT  CCCAGGCTGGA
                                  |||  ||||||  ||||||||||
                                  AGA  GAGACA  GGGTCCGACCT
                                    AT     GT
GAM1602  FLJ13544  3'  TCCAGCCTGGATGACAGAGTGA 47210           GC
                GA                TCTCGCTCTGTT  CCAGGCTGGA
                                  ||||||||||  |||||||||
                                  AGAGTGAGACAG  GGTCCGACCT
                                         TA
GAM1602  FLJ13621  3'  TCCAGCCTGGGCGACAGAGCGA 47226
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCCGACCT

GAM1602  FLJ13659  3'  TCCAGCCTGGGCAACAAGAGTG 48036        _
                G                  TCGCTCT GTTGCCCAGGCTGGA
                                   ||||||| ||||||||||||||
                                   GGTGAGA CAACGGGTCCGACCT
                                      A
GAM1602  FLJ13769  3'  TCCAGCCTGGGTGACAGAGCGA 47264          TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GT
GAM1602  FLJ13848  3'  TCCAGCCTAGGCGACAGAGTGA 45831           C
                GA                TCTCGCTCTGTTGCC AGGCTGGA
                                  |||||||||||||| ||||||||
                                  AGAGTGAGACAGCGG TCCGACCT
                                         A
GAM1602  FLJ13902  3'  CCTGGGCAATAGAGCGAGA   45380
                                  TCTCGCTCTGTTGCCCAGG
                                  |||||||||||||||||||
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                                AGAGCGAGATAACGGGTCC

GAM1602  FLJ13952  3'  TCCAGCCTGGGCAACAAGAGTG 46021        _
                 A                TCGCTCT GTTGCCCAGGCTGGA
                                  ||||||| ||||||||||||||||
                                  AGTGAGA CAACGGGTCCGACCT
                                     A
GAM1602  FLJ14011  3'  TCCAGTCTGGGCAACAGAGCAA 42320     C
                 GA                 TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAACGGGTCTGACCT
                                      A
GAM1602  FLJ14100  3'  TCCAGCCTGGGCGACAAAGCAA 47340     C   C
                 GA                 TCT GCT TGTTGCCCAGGCTGGA
                                    ||| ||| ||||||||||||||||
                                    AGA CGA ACAGCGGGTCCGACCT
                                      A   A
GAM1602  FLJ14117  3'  TCCAGCCTGGGCAACAGA     43233
                                    TCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||
                                    AGACAACGGGTCCGACCT

GAM1602  FLJ14117  3'  TCCAGCTTGGGCAACAGAGCAA 43235     C
                 GA                 TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAACGGGTTCGACCT
                                      A
GAM1602  FLJ14154  3'  CCAGCCTGAGGAGGAGGGAGA  46226      G    GTTG  _
                                    TCTC CTCT    CC CAGGCTGG
                                    |||| ||||    || ||||||||
                                    AGAG GAGG    GG GTCCGACC
                                      G    A___  A
GAM1602  FLJ14251  3'  TCCAGCCTGGGTAACAGAGCGA 46491
                 GA                 TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACAATGGGTCCGACCT

GAM1602  FLJ14326  3'  TCCAGCTTGGGCAACGAGC    50784      T
                                    GCTC GTTGCCCAGGCTGGA
                                    |||| ||||||||||||||
                                    CGAG CAACGGGTTCGACCT
                                      _
GAM1602  FLJ14327  3'  TCCAGCCTGGACAACAGAGCTA 46688     C        C
                 GA                 TCT GCTCTGTTG CCAGGCTGGA
                                    ||| ||||||||| ||||||||||
                                    AGA CGAGACAAC GGTCCGACCT
                                      T        A
GAM1602  FLJ14327  3'  TCCAGCCTGGATAATAGAGTGA 46689            C
                 GA                 TCTCGCTCTGTTG CCAGGCTGGA
                                    |||||||||||| ||||||||||
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                                AGAGTGAGATAAT GGTCCGACCT
                                       A
GAM1602  FLJ14345  3'  TCCAGCCTGGGCAACAAGAGTG 45662       _
              A                 TCGCTCT GTTGCCCAGGCTGGA
                                ||||||| ||||||||||||||||
                                AGTGAGA CAACGGGTCCGACCT
                                   A
GAM1602  FLJ14346  3'  CCTGGGCAACATAGCAAGA   47362    C   C
                                TCT GCT TGTTGCCCAGG
                                ||| ||| ||||||||||
                                AGA CGA ACAACGGGTCC
                                  A   T
GAM1602  FLJ14346  3'  TCCAGCCTGGGCAACAGAGCAA 47372    C
              GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAACGGGTCCGACCT
                                    A
GAM1602  FLJ14346  3'  TCCAGCCTGGGGGACAGAGCGA 47373          G
              GA                  TCTCGCTCTGTT CCCAGGCTGGA
                                  |||||||||||| ||||||||||
                                  AGAGCGAGACAG GGGTCCGACCT
                                         G
GAM1602  FLJ14397  3'  TCCAGCCTGGGCAACAAGGGC  52333      _
                                GCTCT GTTGCCCAGGCTGGA
                                ||||| ||||||||||||||
                                CGGGA CAACGGGTCCGACCT
                                   A
GAM1602  FLJ14397  3'  TCCAGCCTGGGTGACAGAGCAA 52335    C     TG
              GA                  TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A      GT
GAM1602  FLJ14431  3'  CCTGAGCAACATAGCAAGA   52367    C   C    C
                                TCT GCT TGTTGC CAGG
                                ||| ||| |||||| ||||
                                AGA CGA ACAACG GTCC
                                  A   T     A
GAM1602  FLJ14457  3'  TCCAGCCTGGGAGACAGAGTGA 52413          TG
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                         GA
GAM1602  FLJ14466  3'  TCCAACCTGGGCAACAGAGGGA 52431     G          C
              GA                  TCTC CTCTGTTGCCCAGG TGGA
                                  |||| |||||||||||||| ||||
                                  AGAG GAGACAACGGGTCC ACCT
                                    G           A
GAM1602  FLJ14466  3'  TCCAGCCTGGGCAACAACAGTG 52432      C_
              A                   TCGCT  TGTTGCCCAGGCTGGA
                                  |||||  ||||||||||||||||
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                                AGTGA  ACAACGGGTCCGACCT
                                  CA
GAM1602  FLJ14490  3'  TCCAGCCTGGGCAACAGAGCAA 52448     C
             GA                   TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAACGGGTCCGACCT
                                    A
GAM1602  FLJ14621  3'  TCCAGCCTGGGCAACAGAGC   52540
                                  GCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||
                                  CGAGACAACGGGTCCGACCT

GAM1602  FLJ14888  3'  CCTGGGCAACATAGCAAGA    52747     C   C
                                  TCT GCT TGTTGCCCAGG
                                  ||| ||| ||||||||||
                                  AGA CGA ACAACGGGTCC
                                    A   T
GAM1602  FLJ20004  3'  TCCAGCCTGGGCAACAGAGGGA 34767      G
             GA                   TCTC CTCTGTTGCCCAGGCTGGA
                                  |||| ||||||||||||||||||||
                                  AGAG GAGACAACGGGTCCGACCT
                                    G
GAM1602  FLJ20004  3'  TCCAGCCTAGGCAACAAGAGTG 97010        _     C
             A                     TCGCTCT GTTGCC AGGCTGGA
                                   ||||||| |||||| ||||||||
                                   AGTGAGA CAACGG TCCGACCT
                                       A     A
GAM1602  FLJ20004  3'  TCCAGCCTGGCAACAGAGCAAG 97011     C         C
             A                     TCT GCTCTGTTGCC AGGCTGGA
                                   ||| |||||||||| ||||||||
                                   AGA CGAGACAACGG TCCGACCT
                                     A         _
GAM1602  FLJ20004  3'  TCCAGCCTGGGTGACAGAGTGA 97013           TG
             GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                   |||||||||||  ||||||||||
                                   AGAGTGAGACA  GGGTCCGACCT
                                         GT
GAM1602  FLJ20006  3'  TCCAGCCTGGGCGATAGAGTGA 34788
             GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGTGAGATAGCGGGTCCGACCT

GAM1602  FLJ20013  3'  TCCAGCCTCGGTGACAGAGCAA 34803     C      TG  C
             GA                    TCT GCTCTGT  CC AGGCTGGA
                                   ||| |||||||  || ||||||||
                                   AGA CGAGACA  GG TCCGACCT
                                     A      GT  C
GAM1602  FLJ20019  3'  TCCAGCCTAGGTGACAGGGCAA 34816     C      TG  C
             GA                    TCT GCTCTGT  CC AGGCTGGA
                                   ||| |||||||  || ||||||||
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                                AGA CGGGACA  GG TCCGACCT
                                  A      GT  A
GAM1602  FLJ20045  3'  TCCAGCCTGGGTGAGAAGAGCG 34893        G_ TG
              A                    TCGCTCT  T  CCCAGGCTGGA
                                   |||||||  |  ||||||||||
                                   AGCGAGA  A  GGGTCCGACCT
                                      AG GT
GAM1602  FLJ20055  3'  TCCAGCTGGGCAACACAGCAAG 34914     C   C         G
              A                    TCT GCT TGTTGCCCAG CTGGA
                                   ||| ||| |||||||||| |||||
                                   AGA CGA ACAACGGGTC GACCT
                                     A  C        _
GAM1602  FLJ20059  3'  TCCAGCCTGGACAGCAGGAGCG 34930        _     C
              A                    TCGCTC TGTTG CCAGGCTGGA
                                   ||||||| ||||| ||||||||||
                                   AGCGAG ACGAC GGTCCGACCT
                                      G    A
GAM1602  FLJ20069  3'  TCCAGCCTGGGGGACAGAGCAA 34957     C       G
              GA                   TCT GCTCTGTT CCCAGGCTGGA
                                   ||| |||||||| ||||||||||
                                   AGA CGAGACAG GGGTCCGACCT
                                     A       G
GAM1602  FLJ20084  3'  TCCAGCCTGGGCAACAGAGCGA 34999
              GA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                   |||||||||||||||||||||||||
                                   AGAGCGAGACAACGGGTCCGACCT

GAM1602  FLJ20139  3'  TCCAGCCTGCGTGACAAAGTGA 35122        C   TG C
              GA                   TCTCGCT TGT  C CAGGCTGGA
                                   ||||||| |||  | |||||||||
                                   AGAGTGA ACA  G GTCCGACCT
                                      A  GT C
GAM1602  FLJ20139  3'  TTGGGCAACAAAGCAAGA    35124     C   C
                                   TCT GCT TGTTGCCCAG
                                   ||| ||| ||||||||||
                                   AGA CGA ACAACGGGTT
                                     A  A
GAM1602  FLJ20170  3'  TCCAGCCTGGGTGACAGAGTGA 35166          TG
              GA                   TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   AGAGTGAGACA  GGGTCCGACCT
                                        GT
GAM1602  FLJ20211  3'  TCCAGCCTGGGCAACAGAGTGA 35266
              GA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                   |||||||||||||||||||||||||
                                   AGAGTGAGACAACGGGTCCGACCT

GAM1602  FLJ20211  3'  TCCAGCCTGGGCGACAGAGTGA 35267
              GA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                   |||||||||||||||||||||||||
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                                AGAGTGAGACAGCGGGTCCGACCT

GAM1602  FLJ20241  3'  TCCAGCCTGGACAACAGAGCGA 35291          C
                GA                TCTCGCTCTGTTG CCAGGCTGGA
                                  ||||||||||||| ||||||||||
                                  AGAGCGAGACAAC GGTCCGACCT
                                        A
GAM1602  FLJ20280  3'  TCCAGCCTGGGTGACAGAGCGA 35334          TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GT
GAM1602  FLJ20306  3'  TCCAGCCTGGACGACTGAGTGA 35399        T   C
                GA                TCTCGCTC GTTG CCAGGCTGGA
                                  ||||||||  ||||  ||||||||||
                                  AGAGTGAG CAGC GGTCCGACCT
                                       T   A
GAM1602  FLJ20306  3'  TCCAGCCTGGCGACAGAGCAAG 35400     C        C
                A                  TCT GCTCTGTTGCC AGGCTGGA
                                   |||  ||||||||||| ||||||||
                                   AGA CGAGACAGCGG TCCGACCT
                                     A        _
GAM1602  FLJ20340  3'  TCCAGCCTGGTGACAGAGCGAG 35460          TG  C
                A                  TCTCGCTCTGT  CC AGGCTGGA
                                   ||||||||||  ||  ||||||||
                                   AGAGCGAGACA  GG TCCGACCT
                                         GT  _
GAM1602  FLJ20456  3'  TCCAGCCTGGGTAACAGAGCTA 35666     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  |||  ||||||||||||||||||||
                                  AGA CGAGACAATGGGTCCGACCT
                                    T
GAM1602  FLJ20546  3'  TCCAGCCTGGGCAACGAGCGA  35814       T
                                  TCGCTC GTTGCCCAGGCTGGA
                                  ||||||  ||||||||||||||||
                                  AGCGAG CAACGGGTCCGACCT
                                       _
GAM1602  FLJ20671  3'  TCCAGCCTGGGTGACAGAGCGA 35945          TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GT
GAM1602  FLJ20694  3'  TCCAGCCTGGCGACAGAGCAAG 35979     C        C
                A                  TCT GCTCTGTTGCC AGGCTGGA
                                   |||  ||||||||||| ||||||||
                                   AGA CGAGACAGCGG TCCGACCT
                                     A        _
GAM1602  FLJ20700  3'  TCCAGCCTGGGCGACACAGCGA 36020        C
                GA                TCTCGCT TGTTGCCCAGGCTGGA
                                  |||||||  ||||||||||||||||
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                                AGAGCGA ACAGCGGGTCCGACCT
                                   C
GAM1602  FLJ20802  3'  TCCAGCCTGGGCGACAGAGCGA 36114
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    |||||||||||||||||||||||
                                    AGAGCGAGACAGCGGGTCCGACCT

GAM1602  FLJ20825  3'  TCCAGCCTGGCCCACAGAGTGA 36148          TGC
                GA                  TCTCGCTCTGT  CCAGGCTGGA
                                    ||||||||||| ||||||||||
                                    AGAGTGAGACA  GGTCCGACCT
                                          CCC
GAM1602  FLJ20825  3'  TCCAGCCTGGGCAACAAGAGCG 36149       _
                A                   TCGCTCT GTTGCCCAGGCTGGA
                                    ||||||| ||||||||||||||
                                    AGCGAGA CAACGGGTCCGACCT
                                       A
GAM1602  FLJ20972  3'  TCCAGCCTGGGCAACAAGAGAA 47389     CG  _
                GA                  TCT  CTCT GTTGCCCAGGCTGGA
                                    |||  |||| ||||||||||||||
                                    AGA  GAGA CAACGGGTCCGACCT
                                     A_   A
GAM1602  FLJ21144  3'  TCCAGCCTGGGCAACAGAGTGA 43194
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    |||||||||||||||||||||||
                                    AGAGTGAGACAACGGGTCCGACCT

GAM1602  FLJ21240  3'  TCCAGCCTGGGCAAAAAGAGC  46268      G_
                                    GCTCT  TTGCCCAGGCTGGA
                                    |||||  ||||||||||||||
                                    CGAGA  AACGGGTCCGACCT
                                       AA
GAM1602  FLJ21369  3'  TCCAGCCTGGGTGACAGAGCAA 46056     C     TG
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGAGACA  GGGTCCGACCT
                                     A      GT
GAM1602  FLJ21687  3'  TCCAGCCTGGGTGACAGAGCGA 46304          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||| ||||||||||
                                    AGAGCGAGACA  GGGTCCGACCT
                                          GT
GAM1602  FLJ21870  3'  TCCAGCCTGGGCAACGGAG   43750
                                    CTCTGTTGCCCAGGCTGGA
                                    |||||||||||||||||||
                                    GAGGCAACGGGTCCGACCT

GAM1602  FLJ22009  3'  TCCAGCTTGGGCGACAGAGCGA 60921
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    |||||||||||||||||||||||
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                                AGAGCGAGACAGCGGGTTCGACCT

GAM1602  FLJ22054  3'  TCCAGCCTGGGCAACAGAGCAA 96053     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAACGGGTCCGACCT
                                    A
GAM1602  FLJ22316  3'  TCCAGCCTGGGCAACAGAGCCA 47619     C
                GG                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  GGA CGAGACAACGGGTCCGACCT
                                    C
GAM1602  FLJ22415  3'  TCCAGCCTGGGTGACAAAGCAA 93121     C   C   TG
                GA                TCT GCT TGT  CCCAGGCTGGA
                                  ||| ||| |||  ||||||||||
                                  AGA CGA ACA  GGGTCCGACCT
                                    A   A   GT
GAM1602  FLJ22474  3'  TCCAGCCTGGGCAACAGAGTGA 45618
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAACGGGTCCGACCT

GAM1602  FLJ22644  3'  TCCAGCCTGGGCTACAGAGCGA 47703          T
                GA                TCTCGCTCTGT GCCCAGGCTGGA
                                  |||||||||| ||||||||||
                                  AGAGCGAGACA CGGGTCCGACCT
                                        T
GAM1602  FLJ22814  3'  TCCAACCTGGGTGACGAGTGAG 46731        T  TG     C
                A                  TCTCGCTC GT  CCCAGG TGGA
                                   |||||||| ||  |||||| ||||
                                   AGAGTGAG CA  GGGTCC ACCT
                                       _ GT     A
GAM1602  FLJ22814  3'  TCCAGCCTGGGTGACAGAGGGA 46732     G     TG
                                  TC CTCTGT  CCCAGGCTGGA
                                  || ||||||  ||||||||||
                                  AG GAGACA  GGGTCCGACCT
                                   G     GT
GAM1602  FLJ23022  3'  TCCAGCCTGGGCGACAAGAGC  47499       _
                                  GCTCT GTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||
                                  CGAGA CAGCGGGTCCGACCT
                                     A
GAM1602  FLJ23040  3'  TCCAGCCTGGGCAATAGAGCAA 47992     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGATAACGGGTCCGACCT
                                    A
GAM1602  FLJ23042  3'  CCTGAGCAACAGATCAAGA   47941     CGC       C
                                  TCT   TCTGTTGC CAGG
                                  |||   |||||||| ||||
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                                AGA   AGACAACG GTCC
                                  ACT       A
GAM1602  FLJ23042  3'  TCCAGCCTGGGCAACAAGAGTG 47949        _
              A                    TCGCTCT GTTGCCCAGGCTGGA
                                   ||||||| |||||||||||||||
                                   AGTGAGA CAACGGGTCCGACCT
                                      A
GAM1602  FLJ23120  3'  TCCAGCCTGGGTGACGGAGAAA 86330     CG     TG
              GA                   TCT  CTCTGT  CCCAGGCTGGA
                                   |||  ||||||  ||||||||||
                                   AGA  GAGGCA  GGGTCCGACCT
                                     AA     GT
GAM1602  FLJ23185  3'  TCCAGCCTTGGCAACAAAGCAA 47522     C   C      C
              GA                   TCT GCT TGTTGCC AGGCTGGA
                                   ||| ||| ||||||| ||||||||
                                   AGA CGA ACAACGG TCCGACCT
                                     A   A      T
GAM1602  FLJ23185  3'  TCCAGCCTTGGCAACAGAGTGA 47523             C
              GA                   TCTCGCTCTGTTGCC AGGCTGGA
                                   |||||||||||||| ||||||||
                                   AGAGTGAGACAACGG TCCGACCT
                                            T
GAM1602  FLJ23209  3'  CCTGGGCAACATAGCAAGA    46586     C   C
                                   TCT GCT TGTTGCCCAGG
                                   ||| ||| ||||||||||
                                   AGA CGA ACAACGGGTCC
                                     A   T
GAM1602  FLJ23229  3'  TCCAGCCTGGACAACAGAGCAA 47532     C       C
              GA                   TCT GCTCTGTTG CCAGGCTGGA
                                   ||| ||||||||| ||||||||||
                                   AGA CGAGACAAC GGTCCGACCT
                                     A        A
GAM1602  FLJ23360  3'  TCCAGCCCGGGTGACAGAGCGA 43835           TG   A
              GA                   TCTCGCTCTGT  CCC GGCTGGA
                                   ||||||||||  ||| |||||||
                                   AGAGCGAGACA  GGG CCGACCT
                                         GT   C
GAM1602  FLJ23447  3'  CTGGGCAACAGAGCAAGA     46132     C
                                   TCT GCTCTGTTGCCCAG
                                   ||| ||||||||||||||
                                   AGA CGAGACAACGGGTC
                                     A
GAM1602  FLJ23499  3'  CCTGGGCAACATAGCAAGA    43132     C   C
                                   TCT GCT TGTTGCCCAGG
                                   ||| ||| ||||||||||
                                   AGA CGA ACAACGGGTCC
                                     A   T
GAM1602  FLJ23499  3'  TCCAGCCTGGGCGACAAGAGCG 43140        _
              A                    TCGCTCT GTTGCCCAGGCTGGA
                                   ||||||| |||||||||||||||
```

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                                AGCGAGA CAGCGGGTCCGACCT
                                    A
GAM1602  FLJ23537  3'  TCCAGCCTGGGCAACAAGAGGA 46545    G   _
                                TC CTCT GTTGCCCAGGCTGGA
                                || |||| ||||||||||||||||
                                AG GAGA CAACGGGTCCGACCT
                                 _   A
GAM1602  FLJ23556  3'  CTGGGCAACAAAGCAAGA    46439     C   C
                                TCT GCT TGTTGCCCAG
                                ||| ||| ||||||||||
                                AGA CGA ACAACGGGTC
                                  A   A
GAM1602  FLJ23556  3'  TCCAGCCTGGGCGACTGTGAGA 46455       TCT
                                TCTCGC   GTTGCCCAGGCTGGA
                                ||||||   ||||||||||||||||
                                AGAGTG   CAGCGGGTCCGACCT
                                   T__
GAM1602  FLJ23878  3'  TCCAGCCTGGGTGACAGGGCGA 59373          TG
           GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGGGACA  GGGTCCGACCT
                                      GT
GAM1602  FLJ25006  3'  TCCAGCCTGAGCAACAGAGTGA 58789            C
           GA                    TCTCGCTCTGTTGC CAGGCTGGA
                                |||||||||||||| |||||||||
                                AGAGTGAGACAACG GTCCGACCT
                                       A
GAM1602  FLJ30092  3'  TCCAGCCTGGGCAACAGAGTGA 59342
           G                     CTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                GAGTGAGACAACGGGTCCGACCT

GAM1602  FLJ30681  3'  TCCAGCCTAGGCAACAGAGGGA 93440      G        C
           GA                    TCTC CTCTGTTGCC AGGCTGGA
                                |||| |||||||||| ||||||||
                                AGAG GAGACAACGG TCCGACCT
                                  G         A
GAM1602  FLJ31168  3'  TCCAGCCTGGGCGACAGAGCGA 59186
           GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGCGAGACAGCGGGTCCGACCT

GAM1602  FLJ31455  3'  TCCAGCCTGGGCGACAGAGCCA 59291     C
           GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGAGACAGCGGGTCCGACCT
                                  C
GAM1602  FLJ31455  3'  TCCAGCCTGGGTGACAGAGCAA 59292     C      TG
           GA                    TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
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                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM1602  FLJ31952  3'  TCCAGCCTGGGCAACAGAGTGA 59050
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAACGGGTCCGACCT

GAM1602  FLJ32499  5'  TCCAGTGACCGACAGAGCAAGA 58782     C        CCCAG
                                    TCT GCTCTGTTG     GCTGGA
                                    ||| |||||||||     |||||||
                                    AGA CGAGACAGC     TGACCT
                                      A        CAG__
GAM1602  FLJ32915  5'  TCCAGCCTGGGCGACAAGAGCG 59437          _
                AGA                   TCTCGCTCT GTTGCCCAGGCTGGA
                                    ||||||||| ||||||||||||||||
                                    AGAGCGAGA CAGCGGGTCCGACCT
                                         A
GAM1602  FRSB     3'  TCCAGCCTGGGTGACAGAGTGA 20293            TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          GT
GAM1602  FUSIP1    3'  TCCAGCCTGGGCAACAGAGTGA 55043
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAACGGGTCCGACCT

GAM1602  GALNT6   3'  CCAGCCTGAGCAACAAGAGCGA 24244         _    C
                                    TCGCTCT GTTGC CAGGCTGG
                                    ||||||| ||||| ||||||||
                                    AGCGAGA CAACG GTCCGACC
                                       A    A
GAM1602  GALNT6   3'  TCCAGCCTGGGCAACAGGTAAG 24252     CG T
                A                    TCT  C CTGTTGCCCAGGCTGGA
                                    |||  | ||||||||||||||||
                                    AGA  G GACAACGGGTCCGACCT
                                      AT _
GAM1602  GCN2     3'  CCAGCCTGAGCAACAAAGCAAG 63437     C   C     C
                A                    TCT GCT TGTTGC CAGGCTGG
                                    ||| ||| |||||| ||||||||
                                    AGA CGA ACAACG GTCCGACC
                                      A  A     A
GAM1602  GCN2     3'  TCCAGTCTGGGACAACAGAGCA 63440     C        _
                AGA                   TCT GCTCTGTTG CCCAGGCTGGA
                                    ||| ||||||||| ||||||||||
                                    AGA CGAGACAAC GGGTCTGACCT
                                      A        A
GAM1602  GGA2     3'  TCCAGCCTGGGCTACATAGTGA 57683         C   T
                GA                  TCTCGCT TGT GCCCAGGCTGGA
                                    ||||||| ||| ||||||||||||
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                                AGAGTGA ACA CGGGTCCGACCT
                                   T   T
GAM1602  GGA2     3'  TCCAGCCTGGGCTACATAGTGA 31172        C   T
                GA                  TCTCGCT TGT GCCCAGGCTGGA
                                    ||||||| ||| ||||||||||||
                                    AGAGTGA ACA CGGGTCCGACCT
                                       T   T
GAM1602  GLTP     3'  TCCAGCCTGGGCAACAAGAGCG 33588        _
                A                    TCGCTCT GTTGCCCAGGCTGGA
                                    ||||||| ||||||||||||||||
                                    AGCGAGA CAACGGGTCCGACCT
                                       A
GAM1602  GNB4     3'  TCCAGCCTAGGCGACAGAGTGA 41570              C
                GA                  TCTCGCTCTGTTGCC AGGCTGGA
                                    |||||||||||||| ||||||||
                                    AGAGTGAGACAGCGG TCCGACCT
                                          A
GAM1602  GP5      3'  CCTGGGCGACAGAGCGAGA    16872
                                    TCTCGCTCTGTTGCCCAGG
                                    ||||||||||||||||||
                                    AGAGCGAGACAGCGGGTCC

GAM1602  GTPBP5   3'  TCCAGCCTGAGCGACAGAGCAA 65981     C        C
                GA                  TCT GCTCTGTTGC CAGGCTGGA
                                    ||| |||||||||| |||||||||
                                    AGA CGAGACAGCG GTCCGACCT
                                      A         A
GAM1602  GTPBP5   3'  TCCAGCCTGAGTGACAGAGCGA 65982           TG C
                GA                  TCTCGCTCTGT  C CAGGCTGGA
                                    ||||||||||| | |||||||||
                                    AGAGCGAGACA  G GTCCGACCT
                                          GT A
GAM1602  HCGIX    3'  TCCAGCCTGGGTGACAGCAAGA 20716     GCT    TG
                G                    CTC   CTGT  CCCAGGCTGGA
                                    |||   ||||  ||||||||||||
                                    GAG   GACA  GGGTCCGACCT
                                      AAC    GT
GAM1602  HEI10    3'  TCCAGCCTGGGCAACAGAGTGA 41299
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAACGGGTCCGACCT

GAM1602  HES2     3'  TCCAGGCTGGGCGACAGAGCGA 39378               G
                GA                  TCTCGCTCTGTTGCCCAG CTGGA
                                    |||||||||||||||| |||||
                                    AGAGCGAGACAGCGGGTC GACCT
                                          G
GAM1602  HIC      3'  TCCAGCCTGGGCAACAGAGCGA 68052
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
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                                AGAGCGAGACAACGGGTCCGACCT

GAM1602  HIG2     3'  CCAGCCTGGGCCACAGTGCAAG 26198     C  T    T
                A                TCT GC CTGT GCCCAGGCTGG
                                 ||| || |||| ||||||||||
                                 AGA CG GACA CGGGTCCGACC
                                   A  T    C
GAM1602  HRH4     3'  CCAGCCTGGCAACAGAGCAAGA 41530     C         C
                                 TCT GCTCTGTTGCC AGGCTGG
                                 ||| |||||||||| |||||||
                                 AGA CGAGACAACGG TCCGACC
                                   A         _
GAM1602  HSA250303 3'  TCCAGCCTGGGCTACAGAGTGA 38023           T
                GA               TCTCGCTCTGT GCCCAGGCTGGA
                                 |||||||||| ||||||||||
                                 AGAGTGAGACA CGGGTCCGACCT
                                        T
GAM1602  HSD17B7   3'  TCCAGCCTGGGTGACAGCGAGA 33484        CT  TG
                                 TCTCGCT  GT  CCCAGGCTGGA
                                 |||||||  ||  ||||||||||
                                 AGAGCGA  CA  GGGTCCGACCT
                                     __  GT
GAM1602  HSH2     3'  TCCAGCCTGGATGACAGAGTGA 52744           GC
                GA               TCTCGCTCTGTT  CCAGGCTGGA
                                 ||||||||||  |||||||||
                                 AGAGTGAGACAG  GGTCCGACCT
                                       TA
GAM1602  HSMPP8    3'  TCCAGCCTGAGTGACAGAATGA 95141      C     TG C
                GA               TCTCG TCTGT  C CAGGCTGGA
                                 ||||| |||||  | |||||||||
                                 AGAGT AGACA  G GTCCGACCT
                                    A     GT A
GAM1602  HSU79252  5'  TCCAGCCTGGGTGACAGAGTGA 26143           TG
                GA               TCTCGCTCTGT  CCCAGGCTGGA
                                 ||||||||||  ||||||||||
                                 AGAGTGAGACA  GGGTCCGACCT
                                       GT
GAM1602  HSU79266  3'  CCAGCCTGAGGAGGGAGCGTGA 26144    T     GTTG  _
                                 TC CGCTCT    CC CAGGCTGG
                                 || ||||||    || ||||||||
                                 AG GCGAGG    GG GTCCGACC
                                   T     GA__  A
GAM1602  HYPK     3'  TCCAGCCTGGGGGAAAGAGTGA 33516        G  G
                                 TCGCTCT TT CCCAGGCTGGA
                                 ||||||| || ||||||||||
                                 AGTGAGA AG GGGTCCGACCT
                                     A  G
GAM1602  ICAM4    3'  TCCAGCCTGGGGGACAGAGC   9545          G
                                 GCTCTGTT CCCAGGCTGGA
                                 |||||||| ||||||||||
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                                CGAGACAG GGGTCCGACCT
                                    G
GAM1602  ICAM4    3'  TCCAGCCTGGGGGACAGAGC   42596        G
                                GCTCTGTT CCCAGGCTGGA
                                |||||||| ||||||||||
                                CGAGACAG GGGTCCGACCT
                                    G
GAM1602  IGF2AS   3'  TCCAGGGTGCAACAGAG     33532         _ AGG
                                CTCTGTTGC CC   CTGGA
                                ||||||||| ||   |||||
                                GAGACAACG GG   GACCT
                                     T ___
GAM1602  IL-23R   3'  TCCAGCCTGGGCAACAAGAGC  59132       _
                                GCTCT GTTGCCCAGGCTGGA
                                ||||| ||||||||||||||
                                CGAGA CAACGGGTCCGACCT
                                   A
GAM1602  IL10RB   3'  TCCAGCCTGGGTGACAAAGTGA 7129        C   TG
             GA                   TCTCGCT TGT  CCCAGGCTGGA
                                  ||||||| |||  ||||||||||
                                  AGAGTGA ACA  GGGTCCGACCT
                                     A   GT
GAM1602  IMAGE:4907098 3'  TCCAGCCTGGGCGACAGAGCAA 93328     C
             GA                   TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM1602  KBRAS2   3'  TCCAGCCTGGTCAACAGAGCAA 34628     C       C
             GA                   TCT GCTCTGTTG CCAGGCTGGA
                                  ||| ||||||||| ||||||||||
                                  AGA CGAGACAAC GGTCCGACCT
                                    A        T
GAM1602  KCNH6    3'  TCCAGCCTGGGTGACAGAGTGA 48576          TG
             GA                   TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                       GT
GAM1602  KIAA0042  3'  TCCAGTCTGAGCAACAGAACGA 30239       C       C
             GA                   TCTCG TCTGTTGC CAGGCTGGA
                                  ||||| |||||||| |||||||||
                                  AGAGC AGACAACG GTCTGACCT
                                    A       A
GAM1602  KIAA0057  3'  TCCAGCCTGGACAACAAGAGCG 25424        _   C
             A                     TCGCTCT GTTG CCAGGCTGGA
                                   ||||||| |||| ||||||||||
                                   AGCGAGA CAAC GGTCCGACCT
                                      A   A
GAM1602  KIAA0184  3'  TCCAGCCTGGGTGACAGCACGA 65815       CT    TG
             GA                   TCTCG  CTGT  CCCAGGCTGGA
                                  |||||  ||||  ||||||||||
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                                AGAGC  GACA  GGGTCCGACCT
                                  AC    GT
GAM1602  KIAA0186  3'  TCCAGCCTGGGTGACAAAGTGA 41119       C   TG
                GA                  TCTCGCT TGT  CCCAGGCTGGA
                                    ||||||| |||  ||||||||||
                                    AGAGTGA ACA  GGGTCCGACCT
                                       A   GT
GAM1602  KIAA0226  3'  TCCAGCCTGGGTGACAGAGTGA 64264         TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          GT
GAM1602  KIAA0336  3'  TCCAGCTCGGGGAACAGAGCGA 28324          G   AG
                GA                  TCTCGCTCTGTT CCC  GCTGGA
                                    ||||||||||| |||  ||||||
                                    AGAGCGAGACAA GGG  CGACCT
                                          G   CT
GAM1602  KIAA0355  3'  TCCAGCCTGGGTGACAGAGTGA 28710         TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          GT
GAM1602  KIAA0391  3'  CCTGGGCAACATAGCAAGA   28605    C   C
                                    TCT GCT TGTTGCCCAGG
                                    ||| ||| ||||||||||
                                    AGA CGA ACAACGGGTCC
                                      A   T
GAM1602  KIAA0391  3'  TCCAGCCTAGGTGACAGAGTGA 28621         TG  C
                GA                  TCTCGCTCTGT  CC AGGCTGGA
                                    ||||||||||  ||  ||||||||
                                    AGAGTGAGACA  GG TCCGACCT
                                          GT  A
GAM1602  KIAA0408  3'  TCCAGCCTGGGTGACAGAGTGA 28802         TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          GT
GAM1602  KIAA0409  3'  TCCAGCCTGGCTGTGAGCCAAG 31682    C_   TGTT   C
                A                    TCT  GCTC   GCC AGGCTGGA
                                    |||  ||||   ||| ||||||||
                                    AGA  CGAG   CGG TCCGACCT
                                      AC   TGT_  _
GAM1602  KIAA0427  3'  CCAGCCTGGGAACACAGA    29375      TG_
                                    TCTGT   CCCAGGCTGG
                                    |||||   ||||||||||
                                    AGACA   GGGTCCGACC
                                       CAA
GAM1602  KIAA0431  3'  TCCAACCTGGGTAACAGGGCAA 31554    C          C
                GA                  TCT GCTCTGTTGCCCAGG TGGA
                                    ||| |||||||||||||| ||||
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                                AGA CGGGACAATGGGTCC ACCT
                                  A             A
GAM1602  KIAA0445  5'  TCCAGCCTGTGTGACAGAGCAA 28642     C      TG C
                GA                  TCT GCTCTGT  C CAGGCTGGA
                                    ||| |||||||  | |||||||||
                                    AGA CGAGACA  G GTCCGACCT
                                      A       GT T
GAM1602  KIAA0446  5'  TCCAGCCTGGGCGACAGAGCGA 69460
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    |||||||||||||||||||||||||
                                    AGAGCGAGACAGCGGGTCCGACCT

GAM1602  KIAA0447  3'  TCCAGCCTGGGCAACAGGGCAA 72129     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGGGACAACGGGTCCGACCT
                                      A
GAM1602  KIAA0451  5'  TCAGCCTGGGCAACAGAGCAAG 29781     C
                A                    TCT GCTCTGTTGCCCAGGCTGG
                                    ||| ||||||||||||||||||
                                    AGA CGAGACAACGGGTCCGACT
                                      A
GAM1602  KIAA0472  3'  TCCAGCCTGGGCAACAGAGCGA 72367
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    |||||||||||||||||||||||||
                                    AGAGCGAGACAACGGGTCCGACCT

GAM1602  KIAA0472  3'  TCCAGCCTGGGCAGCAGAGCAA 72368     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACGACGGGTCCGACCT
                                      A
GAM1602  KIAA0472  3'  TCCAGCCTGGGCGACAGAGTGA 72369
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    |||||||||||||||||||||||||
                                    AGAGTGAGACAGCGGGTCCGACCT

GAM1602  KIAA0475  3'  TCCAGCCTGGGAGACAGAGCGA 30130          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    |||||||||||  ||||||||||
                                    AGAGCGAGACA  GGGTCCGACCT
                                          GA
GAM1602  KIAA0514  3'  TCCAGCCTGGATGACGGAGCCA 28755     C       GC
                GA                  TCT GCTCTGTT  CCAGGCTGGA
                                    ||| ||||||||  ||||||||||
                                    AGA CGAGGCAG  GGTCCGACCT
                                      C       TA
GAM1602  KIAA0547  3'  TCCAGCCTGGCAACAGAGCAAG 29600     C         C
                A                    TCT GCTCTGTTGCC AGGCTGGA
                                    ||| |||||||||| ||||||||
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                                AGA CGAGACAACGG TCCGACCT
                                  A        _
GAM1602  KIAA0557  3'  TCCAGCCTGGTGATAGAACGAG 78576      C    TG  C
                A                  TCTCG TCTGT  CC AGGCTGGA
                                   ||||| |||||  || ||||||||
                                   AGAGC AGATA  GG TCCGACCT
                                     A    GT  _
GAM1602  KIAA0563  3'  TCCAGCCTGGGCGACAGAGCAA 29890     C
                GA                   TCT GCTCTGTTGCCCAGGCTGGA
                                   ||| ||||||||||||||||||||
                                   AGA CGAGACAGCGGGTCCGACCT
                                     A
GAM1602  KIAA0565  3'  TCCAACCTGGGCGACAGAGCAA 67441     C            C
                GA                   TCT GCTCTGTTGCCCAGG TGGA
                                   ||| |||||||||||||| ||||
                                   AGA CGAGACAGCGGGTCC ACCT
                                     A             A
GAM1602  KIAA0565  3'  TCCAATCTGGGCAACATAGCAA 67442     C   C        GC
                GA                   TCT GCT TGTTGCCCAG  TGGA
                                   ||| ||| ||||||||||  ||||
                                   AGA CGA ACAACGGGTC  ACCT
                                     A   T         TA
GAM1602  KIAA0643  3'  TCCAGCCTGGGTGACAGAGTGA 45980           TG
                GA                   TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   AGAGTGAGACA  GGGTCCGACCT
                                         GT
GAM1602  KIAA0694  3'  TCCAGCCTGGGCAACAGAGTGA 72974
                GA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGTGAGACAACGGGTCCGACCT

GAM1602  KIAA0701  5'  CAGTGAGCAACAGGACGAGA   70094       CT      C AG
                                   TCTCG  CTGTTGC C  GCTG
                                   |||||  ||||||| |  ||||
                                   AGAGC  GACAACG G  TGAC
                                     AG      A __
GAM1602  KIAA0738  3'  TCCAGCCTGGGGGACAGAGTGA 28887           G
                GA                   TCTCGCTCTGTT CCCAGGCTGGA
                                   |||||||||||| ||||||||||
                                   AGAGTGAGACAG GGGTCCGACCT
                                         G
GAM1602  KIAA0752  3'  TCCAGCCTGGGCAACGAGCGA  67635       T
                                   TCGCTC GTTGCCCAGGCTGGA
                                   |||||| ||||||||||||||
                                   AGCGAG CAACGGGTCCGACCT
                                      _
GAM1602  KIAA0794  3'  TCCAGCCTGGGCGACAAAGCGA 81238      C
                                   TCGCT TGTTGCCCAGGCTGGA
                                   ||||| ||||||||||||||||
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                                AGCGA ACAGCGGGTCCGACCT
                                  A
GAM1602  KIAA0795  3'  TCCAGCCTGGTTGACAGAGTGA 47232          GC
            GA                  TCTCGCTCTGTT  CCAGGCTGGA
                                ||||||||||||  ||||||||||
                                AGAGTGAGACAG  GGTCCGACCT
                                   TT
GAM1602  KIAA0798  3'  TCCAGCCTGGGCAACAAGAGCG 28455       _
            A                   TCGCTCT GTTGCCCAGGCTGGA
                                |||||||  ||||||||||||||||
                                AGCGAGA CAACGGGTCCGACCT
                                  A
GAM1602  KIAA0831  3'  TCCAGCCTGGGCAACAAGAGCG 30655       _
            AGG                  TCTCGCTCT GTTGCCCAGGCTGGA
                                |||||||||  ||||||||||||||||
                                GGAGCGAGA CAACGGGTCCGACCT
                                   A
GAM1602  KIAA0853  3'  TCCAACCTAGGTGACAGAGCAA 31215    C     TG  C   C
            GA                  TCT GCTCTGT  CC AGG TGGA
                                |||  |||||||  ||  |||  ||||
                                AGA CGAGACA  GG TCC ACCT
                                  A      GT  A   A
GAM1602  KIAA0872  3'  TCCAGCCTGGGTGACAGAGTGA 30762          TG
            GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                   GT
GAM1602  KIAA0876  3'  TCCAGCCTGGGCAACAGAGCGA 65319
            GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||||
                                AGAGCGAGACAACGGGTCCGACCT

GAM1602  KIAA0884  3'  TCCAACCTGGGTAACAGAGTGA 70758              C
            GA                  TCTCGCTCTGTTGCCCAGG TGGA
                                ||||||||||||||||||  ||||
                                AGAGTGAGACAATGGGTCC ACCT
                                      A
GAM1602  KIAA0889  3'  TCCAGCCTGGGTGACAGAGTGA 31786          TG
            GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                   GT
GAM1602  KIAA0894  3'  TCCAGCCTGGGTGACAGAGCGA 30342          TG
            GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                   GT
GAM1602  KIAA0907  3'  TCCAGCCTGGGCAATAGAGCAA 30882    C
            GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                |||  ||||||||||||||||||||
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                                AGA CGAGATAACGGGTCCGACCT
                                  A
GAM1602  KIAA0907  3'  TCCAGCCTGGGCACTAGAGTGA 30883          T
                GA                TCTCGCTCTG TGCCCAGGCTGGA
                                  |||||||||| ||||||||||||
                                  AGAGTGAGAT ACGGGTCCGACCT
                                       C
GAM1602  KIAA0924  3'  TCCAGCCTGGGCAACAGAGCGA 30376
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAACGGGTCCGACCT

GAM1602  KIAA0961  3'  TCCAGCCTGGGCAACAAGAGC  30409       _
                                  GCTCT GTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||
                                  CGAGA CAACGGGTCCGACCT
                                     A
GAM1602  KIAA0981  3'  TCCAGCCTGGGCAACAGAGCAA 62093     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAACGGGTCCGACCT
                                    A
GAM1602  KIAA1001  3'  TCCAGCCTGGGTGATGGAGCAA 31012     C      TG
                GA                TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGGTA  GGGTCCGACCT
                                    A      GT
GAM1602  KIAA1032  3'  TCCAGCCTGGGCAACAGA    66732
                                  TCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||
                                  AGACAACGGGTCCGACCT

GAM1602  KIAA1086  3'  CCAGCCCAGACAACAGAGTGAG 71284            CCCA
                A                  TCTCGCTCTGTTG    GGCTGG
                                   ||||||||||||    ||||||
                                   AGAGTGAGACAAC    CCGACC
                                          AGAC
GAM1602  KIAA1086  3'  TCCAGCCTGGGCAACAGAAGAA 71289     _ GC
                GA                TCT C  TCTGTTGCCCAGGCTGGA
                                  ||| |  ||||||||||||||||||
                                  AGA G  AGACAACGGGTCCGACCT
                                    A A_
GAM1602  KIAA1086  3'  TCCAGCCTGGGTTACAGAGCGA 71290          T
                GA                TCTCGCTCTGT GCCCAGGCTGGA
                                  |||||||||| ||||||||||||
                                  AGAGCGAGACA TGGGTCCGACCT
                                         T
GAM1602  KIAA1130  3'  CCTGGGCAACATAGCAAGA   63085     C   C
                                  TCT GCT TGTTGCCCAGG
                                  ||| ||| ||||||||||
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                                AGA CGA ACAACGGGTCC
                                  A   T
GAM1602  KIAA1143  3'  CCAGCCTGGGCGACAAAGC    69233     C
                                GCT TGTTGCCCAGGCTGG
                                ||| ||||||||||||||
                                CGA ACAGCGGGTCCGACC
                                  A
GAM1602  KIAA1143  3'  TCCAGCCTGGGCAACAGAGTAA 69251     CG
              GA                  TCT  CTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||
                                AGA  GAGACAACGGGTCCGACCT
                                  AT
GAM1602  KIAA1160  3'  TCCAGCCTGGCGACAGAGTGAG 40762             C
              A                   TCTCGCTCTGTTGCC AGGCTGGA
                                |||||||||||||| ||||||||
                                AGAGTGAGACAGCGG TCCGACCT

                                      _
GAM1602  KIAA1164  3'  CCTGGGCAATAGAGCGAGA    70041
                                TCTCGCTCTGTTGCCCAGG
                                ||||||||||||||||||
                                AGAGCGAGATAACGGGTCC

GAM1602  KIAA1164  3'  TCCAGCCTGGGTGACAGAGGGA 70051      G     TG
              GA                  TCTC CTCTGT  CCCAGGCTGGA
                                |||| ||||||  ||||||||||
                                AGAG GAGACA  GGGTCCGACCT
                                  G     GT
GAM1602  KIAA1191  3'  TCCAGCCTGGGCGACAGAACGA 40336      C
              GA                  TCTCG TCTGTTGCCCAGGCTGGA
                                ||||| ||||||||||||||||||
                                AGAGC AGACAGCGGGTCCGACCT
                                   A
GAM1602  KIAA1202  3'  TCCATCCTGGGCAACAGAGTGA 72492               C
              GA                  TCTCGCTCTGTTGCCCAGG TGGA
                                |||||||||||||||||| ||||
                                AGAGTGAGACAACGGGTCC ACCT
                                           T
GAM1602  KIAA1204  3'  CCTGGGCAACACAGCGAGA    69738       C
                                TCTCGCT TGTTGCCCAGG
                                ||||||| ||||||||||
                                AGAGCGA ACAACGGGTCC
                                    C
GAM1602  KIAA1228  3'  TCCAGCCTGGGCAACAGAGTGA 65678
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGACAACGGGTCCGACCT

GAM1602  KIAA1253  3'  TCTAGCCTGGGCAACAGAGTAA 93550     CG
              GA                  TCT  CTCTGTTGCCCAGGCTGGA
                                |||  ||||||||||||||||||
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                                AGA  GAGACAACGGGTCCGATCT
                                  AT
GAM1602  KIAA1257  3'  TCCAGCCTGGGCAGCAGAGCAA 63419     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACGACGGGTCCGACCT
                                      A
GAM1602  KIAA1271  3'  TCCAACCTGGGTGAGAGAGCGA 70145          G TG     C
                GA                  TCTCGCTCT T  CCCAGG TGGA
                                    |||||||||| |  |||||| ||||
                                    AGAGCGAGA A  GGGTCC ACCT
                                         G GT     A
GAM1602  KIAA1277  3'  TCCAGCCTGGACAACAGAGCAA 65086     C        C
                GA                  TCT GCTCTGTTG CCAGGCTGGA
                                    ||| ||||||||| ||||||||||
                                    AGA CGAGACAAC GGTCCGACCT
                                      A         A
GAM1602  KIAA1328  3'  TCCAGCCTGGGTGACAGAGCAA 62334     C       TG
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGAGACA  GGGTCCGACCT
                                      A       GT
GAM1602  KIAA1340  3'  TCCAGCCTGGGCGACAGTGCAA 69699     C  T
                GA                  TCT GC CTGTTGCCCAGGCTGGA
                                    ||| || ||||||||||||||||
                                    AGA CG GACAGCGGGTCCGACCT
                                      A  T
GAM1602  KIAA1348  3'  TCCAGCCTGGGCAACAAGAGTG 69129          _
                A                    TCGCTCT GTTGCCCAGGCTGGA
                                    |||||||  ||||||||||||||||
                                    AGTGAGA CAACGGGTCCGACCT
                                         A
GAM1602  KIAA1364  3'  TCCAGCCTGTGTGACAGAATGA 64359       C     TG C
                GA                  TCTCG TCTGT  C CAGGCTGGA
                                    |||||  |||||  | |||||||||
                                    AGAGT AGACA  G GTCCGACCT
                                      A     GT T
GAM1602  KIAA1423  3'  TCCAGCCTGGGTGTCAGAGCGA 62398           T
                GA                  TCTCGCTCTG TGCCCAGGCTGGA
                                    ||||||||||  ||||||||||||
                                    AGAGCGAGAC GTGGGTCCGACCT
                                          T
GAM1602  KIAA1456  3'  CCTGGGCAACATAGCAAGA    67546     C   C
                                    TCT GCT TGTTGCCCAGG
                                    ||| ||| ||||||||||
                                    AGA CGA ACAACGGGTCC
                                      A   T
GAM1602  KIAA1456  3'  CCTGGGCAACATAGCAAGA    67547     C   C
                                    TCT GCT TGTTGCCCAGG
                                    ||| ||| ||||||||||
```

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                                AGA CGA ACAACGGGTCC
                                  A   T
GAM1602  KIAA1456  3'  TCCAACCTGGGCAACAAGAGTG 67568        _        C
             A                   TCGCTCT GTTGCCCAGG TGGA
                                 ||||||| |||||||||| ||||
                                 AGTGAGA CAACGGGTCC ACCT
                                    A         A
GAM1602  KIAA1456  5'  TCCAGCCTGGGTGACTGAGGGA 67569      G   T  TG
             GA                    TCTC CTC GT  CCCAGGCTGGA
                                   |||| ||| ||  ||||||||||
                                   AGAG GAG CA  GGGTCCGACCT
                                     G   T  GT
GAM1602  KIAA1486  3'  TCCAGCCTGGGTGACAGAGCGA 67979           TG
             GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   AGAGCGAGACA  GGGTCCGACCT
                                         GT
GAM1602  KIAA1497  5'  TCCAGCCTGGGCGACAGAGCGA 68132
             GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGCGAGACAGCGGGTCCGACCT

GAM1602  KIAA1508  3'  TCCAGCCTGGGTGACAGAGCGA 62564           TG
             GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   AGAGCGAGACA  GGGTCCGACCT
                                         GT
GAM1602  KIAA1554  3'  TCCAACCTGGGTGACAGAGTGA 96862           TG     C
             GA                    TCTCGCTCTGT  CCCAGG TGGA
                                   ||||||||||  |||||| ||||
                                   AGAGTGAGACA  GGGTCC ACCT
                                         GT     A
GAM1602  KIAA1559  3'  TCCAGCCTGGGTAACAGAGCAA 73461     C
             GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                   ||| ||||||||||||||||||||
                                   AGA CGAGACAATGGGTCCGACCT
                                     A
GAM1602  KIAA1559  3'  TCCAGCCTGGGTGACAGAGTGA 73462           TG
             GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   AGAGTGAGACA  GGGTCCGACCT
                                         GT
GAM1602  KIAA1586  5'  CCTGGGCAACAGAGCAAGA   93938     C
                                   TCT GCTCTGTTGCCCAGG
                                   ||| ||||||||||||||
                                   AGA CGAGACAACGGGTCC
                                     A
GAM1602  KIAA1614  3'  TCCAGCCTGGGCAACAAGAGC  70668      _
                                   GCTCT GTTGCCCAGGCTGGA
                                   ||||| ||||||||||||||||
```

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                                CGAGA CAACGGGTCCGACCT
                                  A
GAM1602  KIAA1630  3'  TCCAGCCTGGGTGACAGAGCAA 38657     C      TG
                GA                TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A      GT
GAM1602  KIAA1641  3'  TCCAGCCTGAGCAACAGAGTGA 81022            C
                                  TCGCTCTGTTGC CAGGCTGGA
                                  |||||||||||| |||||||||
                                  AGTGAGACAACG GTCCGACCT
                                         A
GAM1602  KIAA1644  3'  TCCAGCCTGGGCAACAGAGTGA 86223
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAACGGGTCCGACCT

GAM1602  KIAA1649  3'  TCCAGCCTGTGCAACAGAGCGA 51248             C
                GG                TCTCGCTCTGTTGC CAGGCTGGA
                                  |||||||||||||| |||||||||
                                  GGAGCGAGACAACG GTCCGACCT
                                         T
GAM1602  KIAA1656  5'  TCCAGCCTGGCAACAGAGTGAG 66385              C
                A                 TCTCGCTCTGTTGCC AGGCTGGA
                                  |||||||||||||| ||||||||
                                  AGAGTGAGACAACGG TCCGACCT
                                                _
GAM1602  KIAA1674  3'  TCCAGCCTGGGCGACAGAGCGA 69348
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCCGACCT

GAM1602  KIAA1715  3'  TCCAGCCTGGGCAACAAGAGTG 68691          _
                A                 TCGCTCT GTTGCCCAGGCTGGA
                                  ||||||| ||||||||||||||
                                  AGTGAGA CAACGGGTCCGACCT
                                     A
GAM1602  KIAA1727  3'  TCCAGCCTGGATGACAGAGTGA 64765           GC
                GA                TCTCGCTCTGTT  CCAGGCTGGA
                                  ||||||||||||  ||||||||||
                                  AGAGTGAGACAG  GGTCCGACCT
                                        TA
GAM1602  KIAA1771  3'  TCCAGCCTGGACAACAGAGT   79867         C
                                  GCTCTGTTG CCAGGCTGGA
                                  ||||||||| ||||||||||
                                  TGAGACAAC GGTCCGACCT
                                     A
GAM1602  KIAA1786  3'  CCAGCCCGGGTGACAGAGCGAG 66630           TG   A
                A                 TCTCGCTCTGT  CCC GGCTGG
                                  ||||||||||  ||| ||||||
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                                AGAGCGAGACA  GGG CCGACC
                                      GT   C
GAM1602  KIAA1829  3'  TCCAGCCTGGGCAACAAGAGCG 62656       _
             A                   TCGCTCT GTTGCCCAGGCTGGA
                                 ||||||| ||||||||||||||||
                                 AGCGAGA CAACGGGTCCGACCT
                                    A
GAM1602  KIAA1871  3'  TCCAGCCTGGGCAACAAGTGCG 61911      T  _
             A                   TCGC CT GTTGCCCAGGCTGGA
                                 |||| || ||||||||||||||||
                                 AGCG GA CAACGGGTCCGACCT
                                   T  A
GAM1602  KIAA1872  3'  TCCAGCCTGGGAGACAGAGCAA 63620     C      TG
             GA                    TCT GCTCTGT  CCCAGGCTGGA
                                   ||| |||||||  ||||||||||
                                   AGA CGAGACA  GGGTCCGACCT
                                     A       GA
GAM1602  KIAA1872  3'  TCCAGCCTGGGCAACAAGAGC  63621       _
                                   GCTCT GTTGCCCAGGCTGGA
                                   ||||| ||||||||||||||||
                                   CGAGA CAACGGGTCCGACCT
                                     A
GAM1602  KIAA1872  3'  TCCAGCCTGGGCGACAGAGCAA 63623     C
             GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                   ||| ||||||||||||||||||||
                                   AGA CGAGACAGCGGGTCCGACCT
                                     A
GAM1602  KIAA1879  3'  TCCAGCCTGGGAGACAGAGCAA 73946     C      TG
             GA                    TCT GCTCTGT  CCCAGGCTGGA
                                   ||| |||||||  ||||||||||
                                   AGA CGAGACA  GGGTCCGACCT
                                     A       GA
GAM1602  KIAA1948  3'  TCCAGCCTGGGTGACAGACCGA 83306      C     TG
             GA                    TCTCG TCTGT  CCCAGGCTGGA
                                   ||||| |||||  ||||||||||
                                   AGAGC AGACA  GGGTCCGACCT
                                     C    GT
GAM1602  KIAA1948  5'  TCCAGCCTGGGTGACAGAGTGA 83307          TG
             GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   AGAGTGAGACA  GGGTCCGACCT
                                        GT
GAM1602  KIAA1951  3'  TCCAGCCTGGGCGACAGAGTGA 74165
             GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGTGAGACAGCGGGTCCGACCT

GAM1602  KIAA1951  3'  TCCAGTCTGGGCAACAGTGCAA 74166     C  T
             GA                    TCT GC CTGTTGCCCAGGCTGGA
                                   ||| || ||||||||||||||||
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                                AGA CG GACAACGGGTCTGACCT
                                  A  T
GAM1602  KIAA1954  3'  TCCAGCCTGAGCAACAGAGCAA 78231     C         C
                GA                  TCT GCTCTGTTGC CAGGCTGGA
                                    ||| |||||||||| |||||||||
                                    AGA CGAGACAACG GTCCGACCT
                                      A         A
GAM1602  KIAA1958  3'  TCCAGCCTGGGCAACAAAGCTA 82792     C   C
                GA                  TCT GCT TGTTGCCCAGGCTGGA
                                    ||| ||| ||||||||||||||||
                                    AGA CGA ACAACGGGTCCGACCT
                                      T   A
GAM1602  KIAA1969  3'  TCCAGTTTGGCAACAGAGTGAG 79482              C
                A                    TCTCGCTCTGTTGCC AGGCTGGA
                                    |||||||||||||| ||||||||
                                    AGAGTGAGACAACGG TTTGACCT
                                                 _
GAM1602  KR18      3'  TCCAGCCTGGGCAACAAGA    53896     _
                                    TCT GTTGCCCAGGCTGGA
                                    ||| ||||||||||||||
                                    AGA CAACGGGTCCGACCT
                                      A
GAM1602  KR18      3'  TCCAGCCTGGGCACCAGGAACG 53898     C_   T
                A                    TCG  TCTG TGCCCAGGCTGGA
                                    |||  |||| ||||||||||||
                                    AGC  GGAC ACGGGTCCGACCT
                                      AA   C
GAM1602  KREMEN    3'  TCCAGCCTGAGCAGCAGAGCGG 50237              C
                GA                  TCTCGCTCTGTTGC CAGGCTGGA
                                    |||||||||||||| |||||||||
                                    AGGGCGAGACGACG GTCCGACCT
                                            A
GAM1602  KREMEN    3'  TCCAGTGTAGGCAACAGAGTGA 50238              CAG
                GA                  TCTCGCTCTGTTGCC   GCTGGA
                                    ||||||||||||||   ||||||
                                    AGAGTGAGACAACGG   TGACCT
                                             ATG
GAM1602  LANO      3'  TCCAGCCCGGGTGACAGAGCGA 47977           TG   A
                GA                  TCTCGCTCTGT  CCC GGCTGGA
                                    ||||||||||  ||| |||||||
                                    AGAGCGAGACA  GGG CCGACCT
                                          GT   C
GAM1602  LIAS      3'  TCCAGCCTGGGTGACAAGAGC  71169       _  TG
                                    GCTCT GT  CCCAGGCTGGA
                                    ||||| ||  ||||||||||
                                    CGAGA CA  GGGTCCGACCT
                                      A  GT
GAM1602  LIM       3'  TCCAGCCTGGGTGACAGAGTGA 22334           TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
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                                AGAGTGAGACA  GGGTCCGACCT
                                      GT
GAM1602  LIM      3'  TCCAGCCTGGTGACAGAGCAAG 22335     C      TG  C
              A                    TCT GCTCTGT  CC AGGCTGGA
                                   ||| |||||||  || ||||||||
                                   AGA CGAGACA  GG TCCGACCT
                                     A      GT  _
GAM1602  LIN-28   3'  TCCAGCCTGGTTACAGAGCGAG 45471           TGC
              A                    TCTCGCTCTGT   CCAGGCTGGA
                                   ||||||||||   ||||||||||
                                   AGAGCGAGACA   GGTCCGACCT
                                         TT_
GAM1602  LRG      3'  CCTGGGCGACAGAGCAAGA   54817     C
                                   TCT GCTCTGTTGCCCAGG
                                   ||| ||||||||||||||
                                   AGA CGAGACAGCGGGTCC
                                     A
GAM1602  LRRFIP1  3'  TCCAGCCTGGACAACAAGAGCG 17617        _   C
              A                    TCGCTCT GTTG CCAGGCTGGA
                                   ||||||| |||| ||||||||||
                                   AGCGAGA CAAC GGTCCGACCT
                                       A   A
GAM1602  LSR68    3'  TCCAGCCTGGGCGACAGAATGA 38559       C
              GA                     TCTCG TCTGTTGCCCAGGCTGGA
                                   ||||| ||||||||||||||||||
                                   AGAGT AGACAGCGGGTCCGACCT
                                     A
GAM1602  MACF1    3'  TCCAACTTGGGCAACAGACAGA 53497           ____       C
              GCGAGA                   TCTCGCTCTGT   TGCCCAGG TGGA
                                   ||||||||||   |||||||| ||||
                                   AGAGCGAGACA   ACGGGTTC ACCT
                                         GACA       A
GAM1602  MACF1    3'  TCCAGCCTGGGCAACAGACAGA 53498           ____
              GTGAGA                   TCTCGCTCTGT   TGCCCAGGCTGGA
                                   ||||||||||   ||||||||||||
                                   AGAGTGAGACA   ACGGGTCCGACCT
                                         GACA
GAM1602  MAWBP    3'  CCTGGGCAACACAGCGAGA   42382       C
                                   TCTCGCT TGTTGCCCAGG
                                   ||||||| ||||||||||
                                   AGAGCGA ACAACGGGTCC
                                       C
GAM1602  MAWBP    3'  TCCAGCCTGGGCAACAGAGTAA 42388     CG
              GA                     TCT  CTCTGTTGCCCAGGCTGGA
                                   |||  ||||||||||||||||||
                                   AGA  GAGACAACGGGTCCGACCT
                                     AT
GAM1602  MCAM     3'  TCCAGCCTGGGCAACACAGCGA 22466       C
              GA                     TCTCGCT TGTTGCCCAGGCTGGA
                                   ||||||| ||||||||||||||||
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                                AGAGCGA ACAACGGGTCCGACCT
                                   C
GAM1602  METL     3'  TCCAGCCTGGGCAAAATAGCGA 37841        CTG
                GA                 TCTCGCT   TTGCCCAGGCTGGA
                                   |||||||   ||||||||||||||
                                   AGAGCGA   AACGGGTCCGACCT
                                      TAA
GAM1602  MGC10200  3'  TCCAGTCTGGGCAACAGAGCGA 59649
                GA                 TCTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGCGAGACAACGGGTCTGACCT

GAM1602  MGC10765  3'  TCCAGCCTAGGCGACAGAGCGA 44567              C
                GA                 TCTCGCTCTGTTGCC AGGCTGGA
                                   |||||||||||||| ||||||||
                                   AGAGCGAGACAGCGG TCCGACCT
                                            A
GAM1602  MGC10814  3'  TCCAGCCTGGGCAACAAGAGC  52025       _
                                   GCTCT GTTGCCCAGGCTGGA
                                   ||||| ||||||||||||||||
                                   CGAGA CAACGGGTCCGACCT
                                      A
GAM1602  MGC10814  5'  TCCAGCCTGGGCAACAGAGTGA 52027
                GG                 TCTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   GGAGTGAGACAACGGGTCCGACCT

GAM1602  MGC10999  3'  CCAGCCTCAGCAACAAG     51191    C     CC
                                   CT TGTTGC  AGGCTGG
                                   || ||||||  |||||||
                                   GA ACAACG  TCCGACC
                                    _     AC
GAM1602  MGC11386  3'  TCCAGCCTGGGCAACAGAGCGA 53072
                GA                 TCTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGCGAGACAACGGGTCCGACCT

GAM1602  MGC12972  3'  CCTGGGCAACATAGCAAGA    52052     C   C
                                   TCT GCT TGTTGCCCAGG
                                   ||| ||| ||||||||||
                                   AGA CGA ACAACGGGTCC
                                     A   T
GAM1602  MGC13008  3'  TCCAGCCTGGGCAACAGAATGA 52059       C
                GA                 TCTCG TCTGTTGCCCAGGCTGGA
                                   ||||| ||||||||||||||||||
                                   AGAGT AGACAACGGGTCCGACCT
                                      A
GAM1602  MGC13017  3'  TCCAGCCTAGGCAATAAGAGC  55578       _     C
                                   GCTCT GTTGCC AGGCTGGA
                                   ||||| |||||| ||||||||
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                                CGAGA TAACGG TCCGACCT
                                  A     A
GAM1602  MGC13053  3'  TCCAGCCTGGGCGACAGAGTGA 52114
             GA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAGCGGGTCCGACCT

GAM1602  MGC13053  3'  TCCAGCCTGGGCGACAGCAAGA 52115    GCT
                                  TC   CTGTTGCCCAGGCTGGA
                                  ||   ||||||||||||||||
                                  AG   GACAGCGGGTCCGACCT
                                   AAC
GAM1602  MGC14126  3'  TCCAGCCTGGGCGATGAGC    52942      T
                                  GCTC GTTGCCCAGGCTGGA
                                  |||| ||||||||||||||
                                  CGAG TAGCGGGTCCGACCT

                                   _
GAM1602  MGC14407  3'  TCCAGCCTGGGTGACAGAGCAA 52977     C      TG
             GA                   TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A      GT
GAM1602  MGC14436  3'  TCCAGCCTGGGTGACAGAACGA 52931      C    TG
             GA                   TCTCG TCTGT  CCCAGGCTGGA
                                  ||||| |||||  ||||||||||
                                  AGAGC AGACA  GGGTCCGACCT
                                     A    GT
GAM1602  MGC14799  3'  TCCAGCCTGGGTGACAGTGAGA 51332       CT  TG
                                  TCTCGCT  GT  CCCAGGCTGGA
                                  |||||||  ||  ||||||||||
                                  AGAGTGA  CA  GGGTCCGACCT
                                      __  GT
GAM1602  MGC15397  3'  TCCAGCCTGGGTGATAGAGTGA 55556          TG
             GA                   TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGATA  GGGTCCGACCT
                                        GT
GAM1602  MGC15631  3'  TCCAGCCTGTGCAACAGAGCCA 52235    C       C
             GA                   TCT GCTCTGTTGC CAGGCTGGA
                                  ||| |||||||||| |||||||||
                                  AGA CGAGACAACG GTCCGACCT
                                    C         T
GAM1602  MGC16037  3'  TCCAGCCTGGACAACAGAGTGG 52894           C
             GA                   TCTCGCTCTGTTG CCAGGCTGGA
                                  |||||||||||| ||||||||||
                                  AGGGTGAGACAAC GGTCCGACCT
                                        A
GAM1602  MGC16175  3'  TCCAGCCTGGGCAATAGAGCAA 52279    C
             GA                   TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
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                                AGA CGAGATAACGGGTCCGACCT
                                  A
GAM1602  MGC16332  3'  TCCAGCCTGGTCAACAAAGCAA 57545     C   C     C
                GA                  TCT GCT TGTTG CCAGGCTGGA
                                    ||| ||| ||||| ||||||||||
                                    AGA CGA ACAAC GGTCCGACCT
                                      A   A     T
GAM1602  MGC16703  3'  TCCAGCCTGGGCAACAGAGCGA 73498
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACAACGGGTCCGACCT

GAM1602  MGC20235  3'  TCCAGCCTGGGCAAAAGAGC   59562       G
                                    GCTCT TTGCCCAGGCTGGA
                                    ||||| ||||||||||||||
                                    CGAGA AACGGGTCCGACCT
                                       A
GAM1602  MGC22805  3'  CCAGGGCAACACAGCGAGA    58699        C       A
                                    TCTCGCT TGTTGCCC GG
                                    ||||||| |||||||| ||
                                    AGAGCGA ACAACGGG CC
                                        C       A
GAM1602  MGC23244  3'  TCCAGCCTGGGCGACAGAGTGA 58838
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAGCGGGTCCGACCT

GAM1602  MGC2396   3'  CCAGCCTGGGCAATAAGAG    54558      _
                                    CTCT GTTGCCCAGGCTGG
                                    |||| ||||||||||||||
                                    GAGA TAACGGGTCCGACC
                                      A
GAM1602  MGC2562   3'  CCACTAGGCAACAGAGCCAGA  51434     C         C  GC
                                    TCT GCTCTGTTGCC AG  TGG
                                    ||| |||||||||| ||  |||
                                    AGA CGAGACAACGG TC  ACC
                                      C         A __
GAM1602  MGC2562   3'  TCCAGCCTGACGACAAAGCGAG 51449        C     CC
                A                    TCTCGCT TGTTG  CAGGCTGGA
                                    ||||||| |||||  |||||||||
                                    AGAGCGA ACAGC  GTCCGACCT
                                        A    A_
GAM1602  MGC2562   3'  TCCAGCCTGGAAGACCAAACGA 51450       CTCT   GC
                GA                  TCTCG   GTT  CCAGGCTGGA
                                    |||||   |||  ||||||||||
                                    AGAGC   CAG  GGTCCGACCT
                                      AAAC   AA
GAM1602  MGC2562   3'  TCCAGCCTGGGCGACAGAGC   51451
                                    GCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||
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                                CGAGACAGCGGGTCCGACCT

GAM1602  MGC2663   3'  TCCAGCCTGGGCGATGGAGTGA 44338
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGGTAGCGGGTCCGACCT

GAM1602  MGC26641  3'  TCCAGCCTGGGCAATAGGGCAA 59326     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGGGATAACGGGTCCGACCT
                                    A
GAM1602  MGC26877  5'  CCAGCCTGGGTGACAGAGCGAG 58890          TG
                A                 TCTCGCTCTGT  CCCAGGCTGG
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACC
                                        GT
GAM1602  MGC2731   3'  TCCAGCCTGGGCAATAAGAGCG 44164        _
                A                 TCGCTCT GTTGCCCAGGCTGGA
                                  |||||||  ||||||||||||||
                                  AGCGAGA TAACGGGTCCGACCT
                                      A
GAM1602  MGC29762  3'  TCCAGCCTGGGCAACAAGAGC  59148       _
                                  GCTCT GTTGCCCAGGCTGGA
                                  |||||  ||||||||||||||
                                  CGAGA CAACGGGTCCGACCT
                                     A
GAM1602  MGC29891  3'  TCCAGCCTGGGCAACAGAGCCA 58871     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAACGGGTCCGACCT
                                    C
GAM1602  MGC29937  3'  TCCAGCCTGGGCAACAAGAGTG 58734        _
                A                 TCGCTCT GTTGCCCAGGCTGGA
                                  |||||||  ||||||||||||||
                                  AGTGAGA CAACGGGTCCGACCT
                                      A
GAM1602  MGC3101   5'  TCCAGCCTGGGTGACAGAGCGA 44105          TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GT
GAM1602  MGC3207   3'  TCCAGCCTGGGCAACAGAGCGA 63242
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAACGGGTCCGACCT

GAM1602  MGC4368   3'  CCTGGGCAACACAGCAAGA   44725     C   C
                                  TCT GCT TGTTGCCCAGG
                                  ||| ||| ||||||||||
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                                AGA CGA ACAACGGGTCC
                                  A   C
GAM1602  MGC4400   3'  CCTGGGCAACATAGCGAGA    52037        C
                                TCTCGCT TGTTGCCCAGG
                                ||||||| ||||||||||
                                AGAGCGA ACAACGGGTCC
                                    T
GAM1602  MGC4562   3'  TCCAGCCTGGGCAACAGAGCGA 56743
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAACGGGTCCGACCT

GAM1602  MGC4663   3'  TCCAGCCTGGGCAACAGAGCCA 44791     C
              GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAACGGGTCCGACCT
                                    C
GAM1602  MGC4771   3'  TCCAGCCTGGGCAACAGAGTGA 52006
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAACGGGTCCGACCT

GAM1602  MGC4840   3'  TCCAGCCTGGCTGACAGAGCGA 72029           GC
              GA                  TCTCGCTCTGTT  CCAGGCTGGA
                                  ||||||||||||  ||||||||||
                                  AGAGCGAGACAG  GGTCCGACCT
                                        TC
GAM1602  MGC5384   3'  TCCAGCCTGGGCGACAGAGTGA 49094
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAGCGGGTCCGACCT

GAM1602  MGC5457   3'  TCCAGCCTGGGTGACAGAGCGA 51943           TG
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GT
GAM1602  MKRN4     3'  CCAGCCTGGGTGACAGAGCGAG 48455           TG
              A                    TCTCGCTCTGT  CCCAGGCTGG
                                  ||||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACC
                                        GT
GAM1602  MOST2     5'  TCCAGCCTGGGCACCACAGCAA 40072     C   C  T
              GA                  TCT GCT TG TGCCCAGGCTGGA
                                  ||| ||| || ||||||||||||
                                  AGA CGA AC ACGGGTCCGACCT
                                    A   C  C
GAM1602  MRPL48    5'  TCCAGCCTGCGCAACAGAGCGA 32662            C
              GA                  TCTCGCTCTGTTGC CAGGCTGGA
                                  |||||||||||||| |||||||||
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                                AGAGCGAGACAACG GTCCGACCT
                                       C
GAM1602  MRPS10    3'  TCCAGCCTGGCGACAGAGCGAG 36822            C
                A                TCTCGCTCTGTTGCC AGGCTGGA
                                 ||||||||||||||| ||||||||
                                 AGAGCGAGACAGCGG TCCGACCT
                                                 _
GAM1602  MRPS18B   3'  TCCAGCCTGGGTGACAGCTAGA 26755     C   CT  TG
                                 TCT GCT  GT  CCCAGGCTGGA
                                 ||| |||  ||  ||||||||||
                                 AGA CGA  CA  GGGTCCGACCT
                                   T  __  GT
GAM1602  My015     3'  TCCAGCCTGGGAGACAGAGCAA 67235     C      TG
                GA               TCT GCTCTGT  CCCAGGCTGGA
                                 ||| |||||||  ||||||||||
                                 AGA CGAGACA  GGGTCCGACCT
                                   A      GA
GAM1602  NCBP2     3'  CTGGGCAACATAGCAAGA    24767     C   C
                                 TCT GCT TGTTGCCCAG
                                 ||| ||| ||||||||||
                                 AGA CGA ACAACGGGTC
                                   A   T
GAM1602  NDUFC2    3'  TCCAGCCTGGGTGACAAAGGAG 17038      G  C   TG
                A                TCTC CT TGT  CCCAGGCTGGA
                                 |||| || |||  ||||||||||
                                 AGAG GA ACA  GGGTCCGACCT
                                   _ A   GT
GAM1602  NMNAT     3'  TCCAGCCTGGCGACAGAGCAAG 43292     C         C
                A                TCT GCTCTGTTGCC AGGCTGGA
                                 ||| |||||||||| ||||||||
                                 AGA CGAGACAGCGG TCCGACCT
                                   A        _
GAM1602  NMNAT     3'  TCCAGCCTGGGCAAAAAAGC   43293     CTG
                                 GCT   TTGCCCAGGCTGGA
                                 |||   ||||||||||||||
                                 CGA   AACGGGTCCGACCT
                                   AAA
GAM1602  NMNAT     3'  TCCAGCCTGGGTGACAGAGCGA 43295          TG
                GA               TCTCGCTCTGT  CCCAGGCTGGA
                                 ||||||||||  ||||||||||
                                 AGAGCGAGACA  GGGTCCGACCT
                                       GT
GAM1602  NMT2      3'  TCCAGCCTGGGTGACAGAGCGT 17859     T       TG
                GA               TC CGCTCTGT  CCCAGGCTGGA
                                 || ||||||||  ||||||||||
                                 AG GCGAGACA  GGGTCCGACCT
                                  T       GT
GAM1602  NPTXR     3'  TCCAGCCTGGGCAACAGAGCAA 55218     C
                GA               TCT GCTCTGTTGCCCAGGCTGGA
                                 ||| ||||||||||||||||||||
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                                AGA CGAGACAACGGGTCCGACCT
                                  A
GAM1602  NPTXR    3'  TCCAGCCTGGGCAACAGAGCAA 27445     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                AGA CGAGACAACGGGTCCGACCT
                                  A
GAM1602  Nup43    3'  TCCAGCCTGGGCAAAAGAGC   45355       G
                                GCTCT TTGCCCAGGCTGGA
                                ||||| |||||||||||||
                                CGAGA AACGGGTCCGACCT
                                  A
GAM1602  NY-BR-1  3'  TCCAGCCTAGGTGACAGAGTGA 54853           TG  C
                GA                TCTCGCTCTGT  CC AGGCTGGA
                                  |||||||||||  || ||||||||
                                AGAGTGAGACA  GG TCCGACCT
                                      GT  A
GAM1602  OR51E2   3'  TCCAGCCTGGGCAACGGAGCAA 48521     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                AGA CGAGGCAACGGGTCCGACCT
                                  A
GAM1602  ORC6L    3'  TCCAGCCTGGGTGACAGAGCGA 27494           TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  |||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      GT
GAM1602  ORC6L    3'  TCCAGCCTGGGTGACAGAGCGA 27495           TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  |||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      GT
GAM1602  PAFAH2   3'  TCCAGCCTGGGTGACAGAGCAA 6508      C      TG
                GA                TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM1602  PB1      3'  TCCAGCCTGGGCAACAAGAGCG 37581          _
                A                  TCGCTCT GTTGCCCAGGCTGGA
                                   ||||||| |||||||||||||||
                                AGCGAGA CAACGGGTCCGACCT
                                     A
GAM1602  PB1      3'  TCCAGCCTGGGCAACAGAGTGA 37582
                G                  CTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||
                                GAGTGAGACAACGGGTCCGACCT

GAM1602  PDCD7    3'  TCCAGCCTGGGAGACAGAGCAA 72611     C      TG
                GA                TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
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                                AGA CGAGACA  GGGTCCGACCT
                                  A      GA
GAM1602  PIWIL2   3'  TCCAGCCTGTTGACAAAGCAAG 36547     C   C    GCC
             A                     TCT GCT TGTT   CAGGCTGGA
                                   ||| ||| ||||   |||||||||
                                   AGA CGA ACAG   GTCCGACCT
                                     A  A    TT_
GAM1602  POFUT1   3'  TCCAGCCTGGGCAACAGAGCGA 70984
             GA                      TCTCGCTCTGTTGCCCAGGCTGGA
                                     ||||||||||||||||||||||||
                                     AGAGCGAGACAACGGGTCCGACCT

GAM1602  POLYDOM  3'  TCCAGCCTGGGCAATGGAGAGA 44691     G
             G                       CTC CTCTGTTGCCCAGGCTGGA
                                     ||| ||||||||||||||||||
                                     GAG GAGGTAACGGGTCCGACCT
                                       A
GAM1602  PPP1R3B  3'  CCCGCCTGGGCAGCAGAGCGAG 45138                 T
             A                       TCTCGCTCTGTTGCCCAGGC GG
                                     |||||||||||||||||| ||
                                     AGAGCGAGACGACGGGTCCG CC
                                                  C
GAM1602  PRIC285  3'  TCCAGCCTGGGTGACAGAGCGA 62120           TG
             GA                      TCTCGCTCTGT  CCCAGGCTGGA
                                     |||||||||||  ||||||||||
                                     AGAGCGAGACA  GGGTCCGACCT
                                           GT
GAM1602  PRO0038  3'  TCCAGCCTGGGTGACAGACCGA 26931       C     TG
             GA                      TCTCG TCTGT  CCCAGGCTGGA
                                     |||||| |||||  ||||||||||
                                     AGAGC AGACA  GGGTCCGACCT
                                       C    GT
GAM1602  PRO0478  5'  TCCAGCCTAGGCAACAAGAGCG 27035         _     C
             A                       TCGCTCT GTTGCC AGGCTGGA
                                     |||||||| |||||| ||||||||
                                     AGCGAGA CAACGG TCCGACCT
                                        A     A
GAM1602  PRO0478  5'  TCCAGCCTGGACAACAGAGTGA 27036             C
             GA                      TCTCGCTCTGTTG CCAGGCTGGA
                                     |||||||||||| ||||||||||
                                     AGAGTGAGACAAC GGTCCGACCT
                                             A
GAM1602  PRO0478  3'  TCCAGCCTGGCAACAGAGCGAG 27037               C
             A                       TCTCGCTCTGTTGCC AGGCTGGA
                                     |||||||||||||| ||||||||
                                     AGAGCGAGACAACGG TCCGACCT
                                                _
GAM1602  PRO0478  3'  TCCAGCCTGGGGGACAGAGCAA 27038     C       G
             GG                      TCT GCTCTGTT CCCAGGCTGGA
                                     ||| |||||||| ||||||||||
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                                GGA CGAGACAG GGGTCCGACCT
                                  A       G
GAM1602  PRO1048   5'  TCCAGCCTGGGTGACAGAGCGA 38119          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGCGAGACA  GGGTCCGACCT
                                          GT
GAM1602  PRO1386   3'  TCCAGCCTGGGCAACAGAGTGA 49218
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAACGGGTCCGACCT

GAM1602  PRO1496   3'  TCCAACCTGGGTGACAGACCGA 38368      C    TG     C
                GA                  TCTCG TCTGT  CCCAGG TGGA
                                    |||||  |||||  ||||||  ||||
                                    AGAGC AGACA  GGGTCC ACCT
                                      C    GT     A
GAM1602  PRO1942   5'  TCCAGCCTGGACAACAGAAAGA 38384      GC      C
                GA                  TCTC  TCTGTTG CCAGGCTGGA
                                    ||||  |||||||  ||||||||||
                                    AGAG  AGACAAC GGTCCGACCT
                                      AA      A
GAM1602  PRO2015   3'  TCCAGCCTGGGCCACACAGTGA 38166        C   T
                GA                  TCTCGCT TGT GCCCAGGCTGGA
                                    |||||||  |||  ||||||||||||
                                    AGAGTGA ACA CGGGTCCGACCT
                                       C   C
GAM1602  PRO2859   3'  TCCAGCCTGGGGAGACAGAGCG 38214          G_
                AGA                   TCTCGCTCTGTT  CCCAGGCTGGA
                                      ||||||||||||  ||||||||||
                                      AGAGCGAGACAG  GGGTCCGACCT
                                            AG
GAM1602  PRO2893   3'  TCCAACCTGGGCAATAAGAGC  38435      _       C
                                    GCTCT GTTGCCCAGG TGGA
                                    |||||  ||||||||||  ||||
                                    CGAGA TAACGGGTCC ACCT
                                      A         A
GAM1602  PRO2964   3'  CCAGCCTGGGCAAAAAGAG   38255     G_
                                    CTCT  TTGCCCAGGCTGG
                                    ||||  ||||||||||||
                                    GAGA  AACGGGTCCGACC
                                      AA
GAM1602  PSR       3'  TCCAGCCTGGGTGACAGACCGA 65794      C    TG
                GA                  TCTCG TCTGT  CCCAGGCTGGA
                                    |||||  |||||  ||||||||||
                                    AGAGC AGACA  GGGTCCGACCT
                                      C    GT
GAM1602  PTD012    3'  CCAGCTTGGGCAACATAGCAAG 26736    C   C
                A                    TCT GCT TGTTGCCCAGGCTGG
                                     |||  |||  ||||||||||||||
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                                AGA CGA ACAACGGGTTCGACC
                                  A   T
GAM1602  PTK6     3'  TCCAGCCTGGGCGACAGAGCGA 21082
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    |||||||||||||||||||||||||
                                    AGAGCGAGACAGCGGGTCCGACCT

GAM1602  PTRF     3'  TCCAGCCTGGGTGACAGAGTGA 64245          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          GT
GAM1602  PTRF     3'  TCCATCCTAGGCAACAGAGTGA 64246            C   C
                GA                  TCTCGCTCTGTTGCC AGG TGGA
                                    |||||||||||||| ||| ||||
                                    AGAGTGAGACAACGG TCC ACCT
                                          A   T
GAM1602  Rabip4R  3'  TCCAACCTGGGTGACAGAGCAA 36279     C      TG      C
                GA                  TCT GCTCTGT  CCCAGG TGGA
                                    ||| |||||||  ||||||| ||||
                                    AGA CGAGACA  GGGTCC ACCT
                                      A      GT      A
GAM1602  RHOBTB3  3'  TCCAGCCTGGGTGACAAGAGCG 30432        _  TG
                A                    TCGCTCT GT  CCCAGGCTGGA
                                    |||||||  ||  ||||||||||
                                    AGCGAGA CA  GGGTCCGACCT
                                       A  GT
GAM1602  RNO2     5'  TCCAGCCTAGACAACAGGGCAA 53941     C        CCC
                GG                  TCT GCTCTGTTG   AGGCTGGA
                                    ||| |||||||||   ||||||||
                                    GGA CGGGACAAC   TCCGACCT
                                      A        AGA
GAM1602  RNO2     5'  TCCAGCCTGGGCAACAAGAGCG 53942         _
                A                    TCGCTCT GTTGCCCAGGCTGGA
                                    |||||||  ||||||||||||||
                                    AGCGAGA CAACGGGTCCGACCT
                                       A
GAM1602  RoXaN    3'  TCCAGCCTGAGAGACAGAATGA 47303       C     GCC
                GA                  TCTCG TCTGTT   CAGGCTGGA
                                    |||||  ||||||   |||||||||
                                    AGAGT AGACAG   GTCCGACCT
                                      A      AGA
GAM1602  RoXaN    3'  TCCAGCCTGGGCTACAGAGTGA 47304           T
                GA                  TCTCGCTCTGT GCCCAGGCTGGA
                                    ||||||||||| ||||||||||||
                                    AGAGTGAGACA CGGGTCCGACCT
                                          T
GAM1602  Rpo1-2   3'  TCCAGCCTGGGCGACAGAATGA 39225       C
                GA                  TCTCG TCTGTTGCCCAGGCTGGA
                                    ||||| ||||||||||||||||||
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                                AGAGT AGACAGCGGGTCCGACCT
                                  A
GAM1602  Rpo1-2   3'  TCCAGCCTGGGTGACAGAGCAG 39226    TC      TG
                GA                TC  GCTCTGT  CCCAGGCTGGA
                                  ||  |||||||  ||||||||||
                                  AG  CGAGACA  GGGTCCGACCT
                                   GA      GT
GAM1602  RRP4     3'  TCCAGCCTGGGTGACAGAGCGA 27363          TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GT
GAM1602  SAC2     3'  TCCAGCCTGGGGGACAGAGCAA 30728     C       G
                GA                TCT GCTCTGTT CCCAGGCTGGA
                                  |||  ||||||||  ||||||||||
                                  AGA CGAGACAG GGGTCCGACCT
                                    A       G
GAM1602  SAMHD1   3'  TCCAGCCTGGGTGACAGAGTGA 61991          TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                        GT
GAM1602  SC65     3'  TCCAGCCTGGGCGACAGAGCGA 22302
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  |||||||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCCGACCT

GAM1602  SC65     3'  TCCAGCCTGGGCGACAGAGTGA 22303
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  |||||||||||||||||||||||
                                  AGAGTGAGACAGCGGGTCCGACCT

GAM1602  SCAND2   3'  TCCAGCCTGGGCGACAGAGTGA 54436
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  |||||||||||||||||||||||
                                  AGAGTGAGACAGCGGGTCCGACCT

GAM1602  SCAND2   3'  TCCAGCCTGGGCGACAGAGTGA 42146
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  |||||||||||||||||||||||
                                  AGAGTGAGACAGCGGGTCCGACCT

GAM1602  SCIN     3'  TCCAGCCTGGGCAACAGAG   53605
                                  CTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||
                                  GAGACAACGGGTCCGACCT

GAM1602  SCN12A   3'  TCCAGCCTGGTGACAGAGTGAG 27083          TG  C
                A                 TCTCGCTCTGT  CC AGGCTGGA
                                  ||||||||||  ||  ||||||||
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                                AGAGTGAGACA  GG TCCGACCT
                                      GT  _
GAM1602  SCYA5    3'  TCCAGCCTGGGCGACAGAGCGA 12971
                GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                      ||||||||||||||||||||||||
                                      AGAGCGAGACAGCGGGTCCGACCT

GAM1602  SCYA5    3'  TCCAGCCTGGGTGACAAAGTGA 12972        C   TG
                GA                    TCTCGCT TGT  CCCAGGCTGGA
                                      |||||||  |||  ||||||||||
                                      AGAGTGA ACA  GGGTCCGACCT
                                         A   GT
GAM1602  SEMA3E   3'  CCTGGGCGACAGAGCGAGA   25806
                                      TCTCGCTCTGTTGCCCAGG
                                      |||||||||||||||||||
                                      AGAGCGAGACAGCGGGTCC

GAM1602  SMA3     3'  TCCAGGAGATACAACAGAGGAG 23263      G       CCCAGG
                A                      TCTC CTCTGTTG     CTGGA
                                       |||| ||||||||     ||||||
                                       AGAG GAGACAAC     GACCT
                                         _       ATAGAG
GAM1602  SMCR5    3'  TCTGGGCGACAGAGCAAGA   59251     C
                                      TCT GCTCTGTTGCCCAGG
                                      |||  ||||||||||||||
                                      AGA CGAGACAGCGGGTCT
                                        A
GAM1602  SNAPC1   3'  TCCAGCCTGGGCAACAGAGTGA 13279
                GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                      ||||||||||||||||||||||||
                                      AGAGTGAGACAACGGGTCCGACCT

GAM1602  SPRY4    3'  TCCAGCCTGGGTGACAGAGCAA 49032     C      TG
                GA                    TCT GCTCTGT  CCCAGGCTGGA
                                      |||  |||||||  ||||||||||
                                      AGA CGAGACA  GGGTCCGACCT
                                        A      GT
GAM1602  SPRY4    3'  TCCAGCCTGGGTGACAGAGTGA 49033          TG
                GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                      ||||||||||  ||||||||||
                                      AGAGTGAGACA  GGGTCCGACCT
                                            GT
GAM1602  SPTLC2   3'  CCTGGGCAACACAGCAAGA   17989     C   C
                                      TCT GCT TGTTGCCCAGG
                                      |||  |||  ||||||||||
                                      AGA CGA ACAACGGGTCC
                                        A   C
GAM1602  SPTLC2   3'  TCCAGCCTGGGTGACAGAGTGA 18001          TG
                GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                      ||||||||||  ||||||||||
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                                AGAGTGAGACA  GGGTCCGACCT
                                      GT
GAM1602  SYAP1    3'  TCCAGCCTGGGTGATAGAGTGA 52475          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGATA  GGGTCCGACCT
                                      GT
GAM1602  SYT12    3'  CCAGCCTGAGCAATGGCAGGA  96376    TC   CT    C
                                    TC  GCT  GTTGC CAGGCTGG
                                    ||  |||  ||||| ||||||||
                                    AG  CGG  TAACG GTCCGACC
                                     GA  __    A
GAM1602  TADA3L   3'  TCCAGCCTGGGCAACAAGAGTG 56815        _
                A                    TCGCTCT GTTGCCCAGGCTGGA
                                    |||||||  ||||||||||||||
                                    AGTGAGA CAACGGGTCCGACCT
                                       A
GAM1602  TBPL1    5'  CCGGAACAACAAAGCAAGG   18009     C  C    CCCAGG
                                    TCT GCT TGTTG     CTGG
                                    ||| ||| |||||     ||||
                                    GGA CGA ACAAC     GGCC
                                      A  A    AA____
GAM1602  THEA     3'  TCCAGCCCAGGCAATAGAGTAA 66896     CG        CA
                GA                  TCT  CTCTGTTGCC  GGCTGGA
                                    |||  ||||||||||  |||||||
                                    AGA  GAGATAACGG  CCGACCT
                                      AT         AC
GAM1602  TIP47    3'  TCCAGCCTGGGGGACAAGAGTG 20608         _  G
                AGA                   TCTCGCTCT GTT CCCAGGCTGGA
                                    |||||||||  ||| ||||||||||
                                    AGAGTGAGA CAG GGGTCCGACCT
                                         A  G
GAM1602  TMG4     3'  TCCAGCCTGGGCGACAGAGCAA 44217     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAGCGGGTCCGACCT
                                      A
GAM1602  TOMM70A  3'  TCCAGCCTGGGCAATATAGCAA 29739     C  C
                GA                  TCT GCT TGTTGCCCAGGCTGGA
                                    ||| ||| ||||||||||||||||
                                    AGA CGA ATAACGGGTCCGACCT
                                      A  T
GAM1602  TRIAD3   3'  TCCAGCCTGAGCAACAAAAGC  96138     C_     C
                                    GCT  TGTTGC CAGGCTGGA
                                    |||  |||||| |||||||||
                                    CGA  ACAACG GTCCGACCT
                                      AA     A
GAM1602  TSGA2    3'  TCCAGCCTGGGTGGCAGAGCGA 55956          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
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                                AGAGCGAGACG  GGGTCCGACCT
                                      GT
GAM1602  Ubc6p    5'  CCAGCCCAGGCAGGCGG     55191      CTGT   CA
                                TCGCT   TGCC  GGCTGG
                                ||||||   ||||  ||||||
                                GGCGG   ACGG  CCGACC
                                   ____   AC
GAM1602  UBCE7IP5  3'  TCCAGCCTGGGCGACGGAGTGA 30856
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGGCAGCGGGTCCGACCT

GAM1602  UST      3'  TCCAGCCTGGGTGACAGAGTGA 20354          TG
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                      GT
GAM1602  VIT1     5'  TCCAGCCTGGGTGGCAGAGTGA 38606          TG
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACG  GGGTCCGACCT
                                      GT
GAM1602  VPS4B    3'  TCCAGCCTGGGCGACTGA    18024    T
                                  TC GTTGCCCAGGCTGGA
                                  || ||||||||||||||
                                  AG CAGCGGGTCCGACCT
                                   T
GAM1602  WBSCR21  3'  TCCAGCCTAGGCAACAGAGCAA 49306     C         C
              GA                  TCT GCTCTGTTGCC AGGCTGGA
                                  ||| |||||||||| ||||||||
                                  AGA CGAGACAACGG TCCGACCT
                                    A         A
GAM1602  WBSCR23  3'  TCCAGCCTGGGCGACAAAGTGA 47443        C
              GA                  TCTCGCT TGTTGCCCAGGCTGGA
                                  ||||||| ||||||||||||||||
                                  AGAGTGA ACAGCGGGTCCGACCT
                                      A
GAM1602  WBSCR23  3'  TCCAGCCTGGGCGACAGAGCAA 47444     C
              GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM1602  WBSCR23  5'  TCCAGCCTGGGCGACAGAGCCA 47445     C
              GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    C
GAM1602  WBSCR23  3'  TCCAGCCTGGGTGATAGAGCAA 47446     C      TG
              GA                  TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
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                                AGA CGAGATA  GGGTCCGACCT
                                  A      GT
GAM1602  WIRE     3'  TCCAGCCTGGGCGACAGAGCCA 78907     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAGCGGGTCCGACCT
                                      C
GAM1602  WSB1     3'  TCCAACCTGGACAACAGAGCGA 56979           C    C
                GA                  TCTCGCTCTGTTG CCAGG TGGA
                                    |||||||||||| ||||| ||||
                                    AGAGCGAGACAAC GGTCC ACCT
                                          A    A
GAM1602  WSB1     3'  TCCAACCTGGACAACAGAGCGA 56994           C    C
                GA                  TCTCGCTCTGTTG CCAGG TGGA
                                    |||||||||||| ||||| ||||
                                    AGAGCGAGACAAC GGTCC ACCT
                                          A    A
GAM1602  YME1L1   3'  TCCAGCCTGGGCAACAGAGCAA 58439     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAACGGGTCCGACCT
                                      A
GAM1602  YME1L1   3'  TCCAGCCTGGGTGACAGAGTGA 58440          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          GT
GAM1602  YME1L1   3'  TCCAGCCTGGGCAACAGAGCAA 27324     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAACGGGTCCGACCT
                                      A
GAM1602  YME1L1   3'  TCCAGCCTGGGTGACAGAGTGA 27325          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          GT
GAM1602  ZAK      3'  CCTGGGCAAGAGAACAAGA   56941     CGC   G
                                    TCT   TCT TTGCCCAGG
                                    |||   ||| |||||||||
                                    AGA   AGA AACGGGTCC
                                      ACA   G
GAM1602  ZAK      3'  TCCAGCCTGGATGACAGAGTGA 56947           GC
                GA                  TCTCGCTCTGTT  CCAGGCTGGA
                                    ||||||||||||  ||||||||||
                                    AGAGTGAGACAG  GGTCCGACCT
                                          TA
GAM1602  ZFP106   3'  CCAGCCTGGGCGACAAGAG   42720      _
                                    CTCT GTTGCCCAGGCTGG
                                    |||| ||||||||||||||
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                                GAGA CAGCGGGTCCGACC
                                  A
GAM1602  ZFP106   3'  TCCAGCCTGGTGACAGAGTGAG 42742          TG  C
                 A                TCTCGCTCTGT  CC AGGCTGGA
                                  |||||||||||  ||  ||||||||
                                  AGAGTGAGACA  GG TCCGACCT
                                        GT  _
GAM1602  ZNF197   3'  TCCAGCCTGGGCAACAAGAGCG 23760        _
                 A                TCGCTCT GTTGCCCAGGCTGGA
                                  |||||||  ||||||||||||||
                                  AGCGAGA CAACGGGTCCGACCT
                                     A
GAM1602  ZNF271   3'  TCCAGCCTGGGCAACAGAGTGA 96968
                 GA                 TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAACGGGTCCGACCT

GAM1602  ZNF271   3'  TCCAGTCTGGGCAACAGAGCAA 96969     C
                 GA                 TCT GCTCTGTTGCCCAGGCTGGA
                                    |||  ||||||||||||||||||||
                                    AGA CGAGACAACGGGTCTGACCT
                                      A
GAM1602  ZNF297B  3'  TCCAGCCTGCGCGACAGATCGA 26672       C       C
                 GA                 TCTCG TCTGTTGC CAGGCTGGA
                                    |||||  ||||||||  |||||||||
                                    AGAGC AGACAGCG GTCCGACCT
                                       T       C
GAM1602  ZNF297B  5'  TCCAGCCTGGGCAACAAGAGC  26673       _
                                    GCTCT GTTGCCCAGGCTGGA
                                    |||||  ||||||||||||||
                                    CGAGA CAACGGGTCCGACCT
                                       A
GAM1602  ZNF297B  5'  TCCAGCCTGGGCAACAGAGCAA 26675     C
                 GA                 TCT GCTCTGTTGCCCAGGCTGGA
                                    |||  ||||||||||||||||||||
                                    AGA CGAGACAACGGGTCCGACCT
                                      A
GAM1602  ZNF297B  5'  TCCAGCCTGGGTAAAAGAGTGA 26676          G
                 GA                 TCTCGCTCT TTGCCCAGGCTGGA
                                    |||||||||  ||||||||||||||
                                    AGAGTGAGA AATGGGTCCGACCT
                                         A
GAM1602  ZNF333   3'  TCCAGCCTGGGCAACAGAGTGA 51595
                                    TCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||
                                    AGTGAGACAACGGGTCCGACCT

GAM1602  ZNF339   3'  TCCAGCCTGGGCAACAGAGTGG 41398
                                    TCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||
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                                GGTGAGACAACGGGTCCGACCT

GAM1602  LOC112687 3'  TCCAGCCTGGGCAACAGAGTGG 73243
                 GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGGGTGAGACAACGGGTCCGACCT

GAM1602  LOC112868 3'  TCCAGCCTGACCCCAGAGCAGA 73271     C     TTGCC
                                   TCT GCTCTG    CAGGCTGGA
                                   ||| ||||||    |||||||||
                                   AGA CGAGAC    GTCCGACCT
                                     _     CCCA_
GAM1602  LOC113201 3'  TCCAGCTTGGGCACCAGAGCAA 57357     C     T
                 GA                TCT GCTCTG TGCCCAGGCTGGA
                                   ||| |||||| ||||||||||||
                                   AGA CGAGAC ACGGGTTCGACCT
                                     A     C
GAM1602  LOC113523 3'  TCCAGCCTGGGCGACAGGGCAA 73434     C
                 GA                TCT GCTCTGTTGCCCAGGCTGGA
                                   ||| ||||||||||||||||||||
                                   AGA CGGGACAGCGGGTCCGACCT
                                     A
GAM1602  LOC114987 3'  TCCAGCCTGGGCAACAAGAGCG 59800         _
                 A                 TCGCTCT GTTGCCCAGGCTGGA
                                   |||||||| ||||||||||||||
                                   AGCGAGA CAACGGGTCCGACCT
                                        A
GAM1602  LOC115129 3'  TCCAGCCTGAGCGACAGAGTAA 73629     CG        C
                 GA                TCT  CTCTGTTGC CAGGCTGGA
                                   |||  ||||||||| |||||||||
                                   AGA  GAGACAGCG GTCCGACCT
                                     AT        A
GAM1602  LOC115196 3'  TCCAGCCTGGGAGACAGAGCGA 73661           TG
                 GA                TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   AGAGCGAGACA  GGGTCCGACCT
                                         GA
GAM1602  LOC115273 3'  TCCAGCCTGGGCAACAGAGTGA 73754
                 GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGTGAGACAACGGGTCCGACCT

GAM1602  LOC115761 3'  TCCAGTCTGGGCAACAGAGTGA 93398
                 GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGTGAGACAACGGGTCTGACCT

GAM1602  LOC116113 3'  CCAGCCTGGGGGAAGGAG    93832      G  G
                                   CTCT TT CCCAGGCTGG
                                   |||| || ||||||||||
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                                GAGG AG GGGTCCGACC
                                  A  G
GAM1602  LOC116143 3'  TCCAGCCTGGGCAACTGAGCAA 74194     C    T
                GA                TCT GCTC GTTGCCCAGGCTGGA
                                  ||| |||| ||||||||||||||||
                                  AGA CGAG CAACGGGTCCGACCT
                                    A    T
GAM1602  LOC116236 3'  TCCAGCCTGGGCGACAGAGTAA 74248     CG
                GA                TCT  CTCTGTTGCCCAGGCTGGA
                                  |||  ||||||||||||||||||
                                  AGA  GAGACAGCGGGTCCGACCT
                                    AT
GAM1602  LOC116349 3'  TCCAGCCTGGGCAACAGAGCGA 74281
                GG                TCTCGCTCTGTTGCCCAGGCTGGA
                                  |||||||||||||||||||||||||
                                  GGAGCGAGACAACGGGTCCGACCT

GAM1602  LOC119504 5'  TCCAGCCTGGGCAACAAGAGGG 74449    G   _
                A                  TC CTCT GTTGCCCAGGCTGGA
                                   || |||| ||||||||||||||||
                                   AG GAGA CAACGGGTCCGACCT
                                    G   A
GAM1602  LOC120406 3'  TCCAGCCTGGGTGACAGAGCGA 76066          TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GT
GAM1602  LOC122704 3'  TCCAACCTGGGCGACAGGGCGA 74611               C
                GA                TCTCGCTCTGTTGCCCAGG TGGA
                                  |||||||||||||||||| ||||
                                  AGAGCGGGACAGCGGGTCC ACCT
                                             A
GAM1602  LOC124225 5'  CCAGCCTGAGAAACAAGC    74758     C   GCC
                                  GCT TGTT   CAGGCTGG
                                  ||| ||||   ||||||||
                                  CGA ACAA   GTCCGACC
                                    _   AGA
GAM1602  LOC126282 3'  TCCAGCCTGGGTGACAGAGCAA 74967     C      TG
                GA                TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A      GT
GAM1602  LOC126669 3'  TCCAGCCTGAGTGACAGAGTGA 75951          TG C
                GA                TCTCGCTCTGT  C CAGGCTGGA
                                  ||||||||||  | |||||||||
                                  AGAGTGAGACA  G GTCCGACCT
                                        GT A
GAM1602  LOC127262 3'  TCCAGCCCGGGCGACAGAGCGA 76605              A
                GA                TCTCGCTCTGTTGCCC GGCTGGA
                                  |||||||||||||||| |||||||
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                                AGAGCGAGACAGCGGG CCGACCT
                                        C
GAM1602  LOC127428 3'  TCCAGCCTGGGCAACAGAGTGA 75163
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAACGGGTCCGACCT

GAM1602  LOC129880 3'  TCCAGCTTGGGCAACAGAGCAA 75409     C
              GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAACGGGTTCGACCT
                                    A
GAM1602  LOC130026 3'  TCCAGCCTAGGCAACAGAGCAA 57441     C          C
              GA                  TCT GCTCTGTTGCC AGGCTGGA
                                  ||| |||||||||| ||||||||
                                  AGA CGAGACAACGG TCCGACCT
                                    A          A
GAM1602  LOC130535 3'  TCCAGCCTGGGCAACAAGAATG 76655     C  _
              A                    TCG TCT GTTGCCCAGGCTGGA
                                  ||| ||| ||||||||||||||||
                                  AGT AGA CAACGGGTCCGACCT
                                    A  A
GAM1602  LOC130535 3'  TCCAGCCTGGGTGACAGAGCAA 76656     C      TG
              GA                  TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A      GT
GAM1602  LOC131965 3'  TCCAGCCTGGGCGACAGAGTGA 75528
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAGCGGGTCCGACCT

GAM1602  LOC133926 3'  TCCAGCCTGGGCGACAGAGCGA 75634
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCCGACCT

GAM1602  LOC134147 3'  TCCAGCCTGGACAACAGAGGGA 57967      G       C
              GA                  TCTC CTCTGTTG CCAGGCTGGA
                                  |||| |||||||| ||||||||||
                                  AGAG GAGACAAC GGTCCGACCT
                                    G       A
GAM1602  LOC134265 3'  TCCAGCCTAAGCAAATAGCAAG 75657     C  CTG    CC
              A                    TCT GCT   TTGC  AGGCTGGA
                                  ||| |||   ||||  ||||||||
                                  AGA CGA   AACG  TCCGACCT
                                    A  TA_    AA
GAM1602  LOC135154 3'  TCCAGCCTGGGCAACAAGAGCG 75736        _
              A                    TCGCTCT GTTGCCCAGGCTGGA
                                  ||||||| ||||||||||||||||
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                                AGCGAGA CAACGGGTCCGACCT
                                   A
GAM1602  LOC135818 3'  TCCAGCCTGGGCAATAGGGTAA 75749     CG
                GA                  TCT  CTCTGTTGCCCAGGCTGGA
                                    |||  ||||||||||||||||||
                                    AGA  GGGATAACGGGTCCGACCT
                                      AT
GAM1602  LOC137362 3'  TCCAGCCTGGGCAACAAGAGC  75787      _
                                    GCTCT GTTGCCCAGGCTGGA
                                    |||||| ||||||||||||||
                                    CGAGA CAACGGGTCCGACCT
                                       A
GAM1602  LOC138389 3'  TCCAGCCTGGGCAACAAGAGTG 76744       _
                A                    TCGCTCT GTTGCCCAGGCTGGA
                                     |||||||| ||||||||||||||
                                     AGTGAGA CAACGGGTCCGACCT
                                        A
GAM1602  LOC142937 3'  TCCAGCCTGGGCCACAGAACGA 57447      C    T
                GA                  TCTCG TCTGT GCCCAGGCTGGA
                                    |||||| ||||| ||||||||||||
                                    AGAGC AGACA CGGGTCCGACCT
                                       A    C
GAM1602  LOC142948 3'  TCCAGCCTGGGTGACAGAGCGA 83780          TG
                GG                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    GGAGCGAGACA  GGGTCCGACCT
                                          GT
GAM1602  LOC143196 3'  TCCAGCTTGGCAACAGAGCGAG 83805            C
                A                    TCTCGCTCTGTTGCC AGGCTGGA
                                     ||||||||||||||| ||||||||
                                     AGAGCGAGACAACGG TTCGACCT
                                                 _
GAM1602  LOC143310 3'  CCAGCCTGGGTGACAGAGCGAG 77040          TG
                A                    TCTCGCTCTGT  CCCAGGCTGG
                                     ||||||||||  |||||||||
                                     AGAGCGAGACA  GGGTCCGACC
                                           GT
GAM1602  LOC143465 3'  TCCAGCCTGGGTGACGGAGTGA 83878          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGGCA  GGGTCCGACCT
                                          GT
GAM1602  LOC143888 3'  TCCAGCCTGGGTGACAGAGTGA 77175          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          GT
GAM1602  LOC143943 3'  TCCAGCCTGGGTGACAGAGCGA 83921          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
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                                AGAGCGAGACA  GGGTCCGACCT
                                      GT
GAM1602  LOC144289 3'  TCCAGCCTGGGTGACAGAGTGA 83962          TG
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                  |||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                      GT
GAM1602  LOC144308 5'  TCCAGCCTGGGTGACAGAGC   83985       TG
                                  GCTCTGT  CCCAGGCTGGA
                                  |||||||  ||||||||||
                                  CGAGACA  GGGTCCGACCT
                                     GT
GAM1602  LOC144465 3'  TCCAGCCTGGGCAACAAGAGC  77350       _
                                  GCTCT GTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||
                                  CGAGA CAACGGGTCCGACCT
                                     A
GAM1602  LOC144465 3'  TCCAGCCTGGGCAACAAGAGTG 77352        _
              A                    TCGCTCT GTTGCCCAGGCTGGA
                                   |||||||  ||||||||||||||
                                   AGTGAGA CAACGGGTCCGACCT
                                      A
GAM1602  LOC144481 3'  CCATCTTGGGCAACAGAATGAG 84015       C          C
              A                    TCTCG TCTGTTGCCCAGG TGG
                                   ||||| |||||||||||| |||
                                   AGAGT AGACAACGGGTTC ACC
                                      A          T
GAM1602  LOC144519 5'  TCCAGCCTGGGCGACAGAGTGA 77380
              GA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGTGAGACAGCGGGTCCGACCT

GAM1602  LOC144563 3'  TCCAGCTTGGGCAACAGAGTAA 77405     CG
              GA                   TCT  CTCTGTTGCCCAGGCTGGA
                                   |||  ||||||||||||||||||
                                   AGA  GAGACAACGGGTTCGACCT
                                     AT
GAM1602  LOC144845 3'  TCCAGCCCGGGCGACAGAGCAA 57464     C          A
              GA                   TCT GCTCTGTTGCCC GGCTGGA
                                   ||| |||||||||||| |||||||
                                   AGA CGAGACAGCGGG CCGACCT
                                     A          C
GAM1602  LOC145216 3'  CCAGCCTAGCGACAGAGCAAGA 84219     C         CC
                                   TCT GCTCTGTTGC  AGGCTGG
                                   ||| ||||||||||  |||||||
                                   AGA CGAGACAGCG  TCCGACC
                                     A         A_
GAM1602  LOC145231 3'  TCCAGCCTGAACAACATAACAA 84259     CGCTC     CC
              GA                   TCT    TGTTG  CAGGCTGGA
                                   |||    |||||  |||||||||
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                                AGA    ACAAC  GTCCGACCT
                                  ACAAT    AA
GAM1602  LOC145299 3'  CCTGGGCGACAGAGCGAGA   84275
                                TCTCGCTCTGTTGCCCAGG
                                ||||||||||||||||||
                                AGAGCGAGACAGCGGGTCC

GAM1602  LOC145333 3'  TCCAGCCTGGGCGACAGAGCGA 84304
                  GA              TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCCGACCT

GAM1602  LOC145387 3'  TCCAGCCTGGGCGACAGAGAGA 84344      G
                  GA              TCTC CTCTGTTGCCCAGGCTGGA
                                  |||| ||||||||||||||||||
                                  AGAG GAGACAGCGGGTCCGACCT
                                    A
GAM1602  LOC145387 3'  TCCAGCCTGGGTGGCAGAGTGA 84345           TG
                  GA              TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACG  GGGTCCGACCT
                                        GT
GAM1602  LOC145438 3'  TCCAGCCTGGGCGACAGAGCGA 84316
                  GA              TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCCGACCT

GAM1602  LOC145453 3'  TCAGCCTGGGCAACAGAGTGAG 77670
                  A                TCTCGCTCTGTTGCCCAGGCTGG
                                   |||||||||||||||||||||||
                                   AGAGTGAGACAACGGGTCCGACT

GAM1602  LOC145482 3'  CCAGCCTGGGCGACAAGAG   77741      _
                                CTCT GTTGCCCAGGCTGG
                                |||| ||||||||||||||
                                GAGA CAGCGGGTCCGACC
                                  A
GAM1602  LOC145483 3'  TCCAGCCTGGGCAGCAGAGC   77758
                                GCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||
                                CGAGACGACGGGTCCGACCT

GAM1602  LOC145608 5'  TCCAGCCTGGGTGACAGAGCAA 84386     C      TG
                  GA              TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A      GT
GAM1602  LOC145609 3'  TCCAGCCTGGGTGACAGAGCAA 84370     C      TG
                  GA              TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
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                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM1602  LOC145663 3'  TCCAGCCTGGGCGACAGAGCTA 84430     C
              GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    T
GAM1602  LOC145757 3'  TCCAGCCTAGGTGACAGAGCGA 77942          TG  C
              GA                  TCTCGCTCTGT  CC AGGCTGGA
                                  ||||||||||  || ||||||||
                                  AGAGCGAGACA  GG TCCGACCT
                                        GT  A
GAM1602  LOC145820 3'  TCCAGCCTGGGCGACAGAGCAA 77980     C
              GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM1602  LOC145945 5'  TCCAGCCTGAGCAACAGAGCAA 84571     C        C
              GA                  TCT GCTCTGTTGC CAGGCTGGA
                                  ||| |||||||||| |||||||||
                                  AGA CGAGACAACG GTCCGACCT
                                    A         A
GAM1602  LOC145988 5'  TCCAGCCTGGAAGGCAGAGAGA 78072      G      GC
              GA                  TCTC CTCTGTT  CCAGGCTGGA
                                  |||| |||||||  ||||||||||
                                  AGAG GAGACGG  GGTCCGACCT
                                    A      AA
GAM1602  LOC146059 3'  TCCAGTCTGGGTAACAGAGCGA 78090
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAATGGGTCTGACCT

GAM1602  LOC146229 3'  TCCAGCCTGGGCGACAGAGCGA 78317
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCCGACCT

GAM1602  LOC146540 3'  TCCAGCCTGGGCTACAAAGCAG 78530    TC   C   T
              GA                  TC  GCT TGT GCCCAGGCTGGA
                                  ||  ||| ||| ||||||||||||
                                  AG  CGA ACA CGGGTCCGACCT
                                   GA   A   T
GAM1602  LOC146713 3'  TCCAGCCTGGGCAACAGAGC   84739
                                  GCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||
                                  CGAGACAACGGGTCCGACCT

GAM1602  LOC146713 3'  TCCAGCCTGGTCAACAGAGCAA 84741     C        C
              GA                  TCT GCTCTGTTG CCAGGCTGGA
                                  ||| ||||||||| ||||||||||
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                                AGA CGAGACAAC GGTCCGACCT
                                  A        T
GAM1602  LOC146728 5'  TCCAGACTGGACAACAGAGC   84772         C    G
                                GCTCTGTTG CCAG CTGGA
                                ||||||||| |||| |||||
                                CGAGACAAC GGTC GACCT
                                     A    A
GAM1602  LOC146728 3'  TCCAGCCTGGGAAGCAGAGTGA 84774           G
              GA                  TCTCGCTCTGTT CCCAGGCTGGA
                                  |||||||||||| ||||||||||
                                  AGAGTGAGACGA GGGTCCGACCT
                                        A
GAM1602  LOC146756 3'  TCCAGCCTGGGCGACAGAGCGA 84813
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCCGACCT

GAM1602  LOC146839 5'  TCCAGCCTGGGCAACATAGC   84853     C
                                GCT TGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||
                                CGA ACAACGGGTCCGACCT
                                  T
GAM1602  LOC146895 3'  TCCAGCCTGGGTGACAAGAGC  84874       _  TG
                                GCTCT GT  CCCAGGCTGGA
                                ||||| ||  ||||||||||
                                CGAGA CA  GGGTCCGACCT
                                   A  GT
GAM1602  LOC146901 3'  CAGCCTAGACAACAGAGCAAGA 84894     C        CCC
                                TCT GCTCTGTTG   AGGCTG
                                ||| |||||||||   ||||||
                                AGA CGAGACAAC   TCCGAC
                                  A        AGA
GAM1602  LOC146923 3'  TCCAGCCTGGGCGACAGAGTGA 78804
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAGCGGGTCCGACCT

GAM1602  LOC146958 3'  TCCAGCCTGGGTGACACAGCGA 84946         C   TG
              GA                  TCTCGCT TGT  CCCAGGCTGGA
                                  ||||||| |||  ||||||||||
                                  AGAGCGA ACA  GGGTCCGACCT
                                     C   GT
GAM1602  LOC146958 3'  TCCAGCCTGGGTGACAGAGCGA 84948           TG
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GT
GAM1602  LOC147063 5'  CCAGCCTGGGCAACAGAGTGAG 85016
              A                    TCTCGCTCTGTTGCCCAGGCTGG
                                  ||||||||||||||||||||||
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                                AGAGTGAGACAACGGGTCCGACC

GAM1602  LOC147071 3'  TCCAGCCTGGGCGACAGAGCAA 73373     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM1602  LOC147180 5'  TCCAGCCCGGGTGACAGAGTGA 85105          TG   A
                                  TCGCTCTGT  CCC GGCTGGA
                                  |||||||||  ||| |||||||
                                  AGTGAGACA  GGG CCGACCT
                                       GT   C
GAM1602  LOC147599 3'  TCCAGCCTGGGCAACAGAGAGA 85166    G
                                  TC CTCTGTTGCCCAGGCTGGA
                                  || ||||||||||||||||||
                                  AG GAGACAACGGGTCCGACCT
                                    A
GAM1602  LOC147622 3'  TCCAGCCTGGGTGACAGAGCTA 85172     C      TG
                GA                TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    T      GT
GAM1602  LOC147649 3'  CCTGGGCGACAGAGCGAGA    79060
                                  TCTCGCTCTGTTGCCCAGG
                                  |||||||||||||||||
                                  AGAGCGAGACAGCGGGTCC

GAM1602  LOC147664 3'  TCCAGCCTGGGCAACGAGAG   79049      _
                                  CTCT GTTGCCCAGGCTGGA
                                  |||| ||||||||||||||
                                  GAGA CAACGGGTCCGACCT
                                    G
GAM1602  LOC147700 3'  TCCAGCCTGTGCAACAAGCGA  59886      C     C
                                  TCGCT TGTTGC CAGGCTGGA
                                  ||||| |||||| |||||||||
                                  AGCGA ACAACG GTCCGACCT
                                     _      T
GAM1602  LOC147727 5'  TCCAGCCTGGGCGATAGAGTGA 79139
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGATAGCGGGTCCGACCT

GAM1602  LOC147727 5'  TCCAGTCTGGGCGACAGAGCGA 79140
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCTGACCT

GAM1602  LOC147837 3'  CCAGCCTGGGCGACAGAGCCAG 79204     C
                A                  TCT GCTCTGTTGCCCAGGCTGG
                                   ||| |||||||||||||||||
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                                AGA CGAGACAGCGGGTCCGACC
                                  C
GAM1602  LOC147837 3'  TCCAGCCTGGGCAGCAAGAGC  79209      _
                                GCTCT GTTGCCCAGGCTGGA
                                ||||| ||||||||||||||||
                                CGAGA CGACGGGTCCGACCT
                                   A
GAM1602  LOC147990 3'  TCCAGCCTGGGCAACAGAGC   85235
                                GCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||
                                CGAGACAACGGGTCCGACCT

GAM1602  LOC148166 3'  TCCAGCCTAGGCGACGGGGCAA 79424     C         C
            GA                    TCT GCTCTGTTGCC AGGCTGGA
                                ||| |||||||||| ||||||||
                                AGA CGGGGCAGCGG TCCGACCT
                                  A         A
GAM1602  LOC148206 3'  TCCAGCCTGGGCCACAAGGCAA 79466     C  TC   T
            GA                    TCT GC  TGT GCCCAGGCTGGA
                                ||| ||  ||| ||||||||||||
                                AGA CG  ACA CGGGTCCGACCT
                                  A  GA   C
GAM1602  LOC148397 3'  CCAGCCTGGGCAACAAGAGT   79565      _
                                GCTCT GTTGCCCAGGCTGG
                                ||||| |||||||||||||
                                TGAGA CAACGGGTCCGACC
                                   A
GAM1602  LOC148534 3'  TCCAGCCTGGGCGACAGAGCAA 79640     C
            GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGAGACAGCGGGTCCGACCT
                                  A
GAM1602  LOC148758 5'  TCCAGCCTGGGCAACAAGAGC  79726      _
                                GCTCT GTTGCCCAGGCTGGA
                                ||||| |||||||||||||||
                                CGAGA CAACGGGTCCGACCT
                                   A
GAM1602  LOC148809 3'  TCCAGCCTGGGCGACAGAGCAA 79762     C
            GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGAGACAGCGGGTCCGACCT
                                  A
GAM1602  LOC148809 5'  TCCAGCCTGGGTGACAGAGCAA 79763     C      TG
            GA                    TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM1602  LOC148823 3'  TCCAGCTTGGGCAACAGAGTGA 59896
            GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
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                                AGAGTGAGACAACGGGTTCGACCT

GAM1602  LOC148936 3'  TCCAGGTTGGGCAACAGAGCAA 85459     C           G
                GA                TCT GCTCTGTTGCCCAG CTGGA
                                  ||| |||||||||||||| |||||
                                  AGA CGAGACAACGGGTT GACCT
                                    A           G
GAM1602  LOC148938 3'  TCCAGGCTGGGCAACACAGCAA 85441     C   C       G
                GA                TCT GCT TGTTGCCCAG CTGGA
                                  ||| ||| |||||||||| |||||
                                  AGA CGA ACAACGGGTC GACCT
                                    A   C       G
GAM1602  LOC148946 5'  CCAACGGAAAACAGAGCGAGA  85465          GC  AGGC
                                  TCTCGCTCTGTT  CC    TGG
                                  ||||||||||||  ||    |||
                                  AGAGCGAGACAA  GG    ACC
                                        AA  CA__
GAM1602  LOC149073 3'  TCCAGCCTGGGCAACAGTGTGA 85487       T
                GA                TCTCGC CTGTTGCCCAGGCTGGA
                                  |||||| ||||||||||||||||
                                  AGAGTG GACAACGGGTCCGACCT
                                     T
GAM1602  LOC149113 5'  CCAGCCTGGGCTACAAGAG    79905      _  T
                                  CTCT GT GCCCAGGCTGG
                                  |||| || ||||||||||
                                  GAGA CA CGGGTCCGACC
                                    A  T
GAM1602  LOC149157 5'  TCCAGCCTGGTCCAGAGAGAAA 79943     CG    G   C_
                GA                TCT  CTCT TTG  CCAGGCTGGA
                                  |||  |||| |||  ||||||||||
                                  AGA  GAGA GAC  GGTCCGACCT
                                    AA    _   CT
GAM1602  LOC149175 3'  TCCAGCCTGGGCGACAGAGCGA 79957
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCCGACCT

GAM1602  LOC149194 5'  TCCAGCCTGGGCAACAAGAGC  79990       _
                                  GCTCT GTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||
                                  CGAGA CAACGGGTCCGACCT
                                     A
GAM1602  LOC149271 3'  TCCAGCCTGGGCAACAAGAGTG 80012        _
                A                  TCGCTCT GTTGCCCAGGCTGGA
                                  ||||||| |||||||||||||||
                                  AGTGAGA CAACGGGTCCGACCT
                                      A
GAM1602  LOC149464 3'  CCAGCCTGGGCAACAAGAG    85588      _
                                  CTCT GTTGCCCAGGCTGG
                                  |||| ||||||||||||
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                                GAGA CAACGGGTCCGACC
                                  A
GAM1602  LOC149579 5'  TCCAGCCTGTGTGACAGAGCAA 71695     C      TG C
                  GA                TCT GCTCTGT  C CAGGCTGGA
                                    ||| |||||||  | |||||||||
                                    AGA CGAGACA  G GTCCGACCT
                                      A       GT T
GAM1602  LOC149606 3'  CCTGGGCAACATAGCGAGA    80258        C
                                    TCTCGCT TGTTGCCCAGG
                                    ||||||| ||||||||||
                                    AGAGCGA ACAACGGGTCC
                                        T
GAM1602  LOC149628 3'  TCCAGCCTGGGTGACAGAGCGA 80281           TG
                  GA                TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGCGAGACA  GGGTCCGACCT
                                          GT
GAM1602  LOC149672 5'  TCCAGCCTGGGCAACAGAGTGA 80339
                  GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAACGGGTCCGACCT

GAM1602  LOC149705 3'  TCCAGCCTGGGTGACGAGTGA  85787       T  TG
                                    TCGCTC GT  CCCAGGCTGGA
                                    |||||| ||  ||||||||||
                                    AGTGAG CA  GGGTCCGACCT
                                       _  GT
GAM1602  LOC149711 3'  TCCAGCCTGGGTGACAGAGTGA 85856           TG
                  GA                TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          GT
GAM1602  LOC149952 3'  TCCAGCCTGGGCAATAGAGTGA 80372
                  GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGATAACGGGTCCGACCT

GAM1602  LOC150095 3'  TCCAGCCTGGGCAACAGAGCGA 85996
                  GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACAACGGGTCCGACCT

GAM1602  LOC150139 3'  CCTGAGCAACATAGCGAGA    80410        C     C
                                    TCTCGCT TGTTGC CAGG
                                    ||||||| |||||| ||||
                                    AGAGCGA ACAACG GTCC
                                        T     A
GAM1602  LOC150139 3'  TCCAGCCTGGGTGACAGAGAGA 80413    G     TG
                                    TC CTCTGT  CCCAGGCTGGA
                                    || ||||||  ||||||||||
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                                AG GAGACA  GGGTCCGACCT
                                 A     GT
GAM1602  LOC150142 5'  CCAGCCTGGGCAACAAAGTAAG 80404     CG  C
                 A                TCT  CT TGTTGCCCAGGCTGG
                                 |||  || ||||||||||||||||
                                 AGA  GA ACAACGGGTCCGACC
                                   AT  A
GAM1602  LOC150174 3'  TCCAGCCTGGTCAACAGAGTGA 80441           C
                 GA                TCTCGCTCTGTTG CCAGGCTGGA
                                 |||||||||||||| ||||||||||
                                 AGAGTGAGACAAC GGTCCGACCT
                                          T
GAM1602  LOC150185 3'  TCCAGCCTGGGTGACAGAGCGA 86070          TG
                 GA                TCTCGCTCTGT  CCCAGGCTGGA
                                 ||||||||||||  ||||||||||
                                 AGAGCGAGACA  GGGTCCGACCT
                                        GT
GAM1602  LOC150213 3'  TCCAGCCTGGTCAACAGAGTGA 75360           C
                 GA                TCTCGCTCTGTTG CCAGGCTGGA
                                 |||||||||||||| ||||||||||
                                 AGAGTGAGACAAC GGTCCGACCT
                                          T
GAM1602  LOC150225 3'  TCCAGCCTGGGCGTCAGAGTGA 86206          T
                 GA                TCTCGCTCTG TGCCCAGGCTGGA
                                 ||||||||||| ||||||||||||
                                 AGAGTGAGAC GCGGGTCCGACCT
                                         T
GAM1602  LOC150236 3'  TCCAGCCTGGTCAACAGAGTGA 80503           C
                 GA                TCTCGCTCTGTTG CCAGGCTGGA
                                 |||||||||||||| ||||||||||
                                 AGAGTGAGACAAC GGTCCGACCT
                                          T
GAM1602  LOC150244 3'  TCCAGCCTGGGCGACAGAGCGA 80552
                 GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                 ||||||||||||||||||||||||
                                 AGAGCGAGACAGCGGGTCCGACCT

GAM1602  LOC150245 3'  TCCAGCCTGGGTGACAGAATAA 86119     CGC    TG
                 GA                TCT   TCTGT  CCCAGGCTGGA
                                 |||   |||||  ||||||||||||
                                 AGA   AGACA  GGGTCCGACCT
                                   ATA     GT
GAM1602  LOC150299 3'  TCCAGCCTGGCGACAGAGCAAG 86170     C         C
                 A                 TCT GCTCTGTTGCC AGGCTGGA
                                 ||| ||||||||||| ||||||||
                                 AGA CGAGACAGCGG TCCGACCT
                                   A         _
GAM1602  LOC150319 3'  TCCAGCCTGGGCAACAAGAGCG 80477         _
                 A                 TCGCTCT GTTGCCCAGGCTGGA
                                 |||||||| ||||||||||||||||
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                                AGCGAGA CAACGGGTCCGACCT
                                   A
GAM1602  LOC150358 3'  TCCAGCCTGGGCGACAGAGCGA 86101
                 GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                   |||||||||||||||||||||||||
                                   AGAGCGAGACAGCGGGTCCGACCT

GAM1602  LOC150481 3'  TCCAGCCTGGTGACAGAGCAAG 80714     C      TG  C
                 A                 TCT GCTCTGT  CC AGGCTGGA
                                   ||| |||||||  || ||||||||
                                   AGA CGAGACA  GG TCCGACCT
                                     A      GT  _
GAM1602  LOC150577 3'  TCCAGCCTGGATGACAGAGTGA 86260          GC
                                   TCGCTCTGTT  CCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   AGTGAGACAG  GGTCCGACCT
                                         TA
GAM1602  LOC150622 3'  TCCAGCCTGGGCAACAAGAGC  80768       _
                                   GCTCT GTTGCCCAGGCTGGA
                                   ||||| ||||||||||||||||
                                   CGAGA CAACGGGTCCGACCT
                                      A
GAM1602  LOC150630 5'  TCCAGCCTGGGCAGCAGAGTGA 86307
                 GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                   |||||||||||||||||||||||||
                                   AGAGTGAGACGACGGGTCCGACCT

GAM1602  LOC150889 3'  TCCAGCCTGCGGGACAGAGTGA 80819           G  _
                 GA                TCTCGCTCTGTT CC CAGGCTGGA
                                   |||||||||||| || ||||||||
                                   AGAGTGAGACAG GG GTCCGACCT
                                         _  C
GAM1602  LOC150960 3'  TCCAGCTTGGGCAACAAAGTGA 80879         C
                 GA                TCTCGCT TGTTGCCCAGGCTGGA
                                   ||||||| ||||||||||||||||
                                   AGAGTGA ACAACGGGTTCGACCT
                                      A
GAM1602  LOC151196 3'  TCCAGCCTGGGCAACACAGCAA 86456     C   C
                 GA                TCT GCT TGTTGCCCAGGCTGGA
                                   ||| ||| ||||||||||||||||
                                   AGA CGA ACAACGGGTCCGACCT
                                     A   C
GAM1602  LOC151248 5'  CCTGGGCGACAGAGCGAGA    80992
                                   TCTCGCTCTGTTGCCCAGG
                                   |||||||||||||||||||
                                   AGAGCGAGACAGCGGGTCC

GAM1602  LOC151248 3'  TCCAGCCCAGGTAACAGAGTGA 80998              CA
                 GA                TCTCGCTCTGTTGCC  GGCTGGA
                                   ||||||||||||||  |||||||
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                                AGAGTGAGACAATGG  CCGACCT
                                       AC
GAM1602  LOC151248 3'  TCCAGCCTGGTGACAGAGCGAG 80999          TG  C
              A                 TCTCGCTCTGT  CC AGGCTGGA
                                |||||||||||  || ||||||||
                                AGAGCGAGACA  GG TCCGACCT
                                      GT  _
GAM1602  LOC151429 3'  TCCAGCCTGGGCGACAGAGCAA 86549     C
              GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM1602  LOC151429 3'  TCCAGCCTGGGTGACAGAGCAA 86550     C      TG
              GA                  TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A       GT
GAM1602  LOC151438 3'  CCTGGGCAACACAGCAAGA    86555     C   C
                                  TCT GCT TGTTGCCCAGG
                                  ||| ||| ||||||||||
                                  AGA CGA ACAACGGGTCC
                                    A   C
GAM1602  LOC151446 3'  TCTGAACAACAGAGCAAGA    86575     C        CC
                                  TCT GCTCTGTTG  CAGG
                                  ||| |||||||||  ||||
                                  AGA CGAGACAAC  GTCT
                                    A         AA
GAM1602  LOC151556 3'  TCCAGCCTGAGCAACAGAGCAA 81085     C         C
              GA                  TCT GCTCTGTTGC CAGGCTGGA
                                  ||| |||||||||| |||||||||
                                  AGA CGAGACAACG GTCCGACCT
                                    A          A
GAM1602  LOC151632 3'  TCCAGCCTGGGCAACAGAGTAA 86651     CG
              GA                  TCT  CTCTGTTGCCCAGGCTGGA
                                  |||  ||||||||||||||||||
                                  AGA  GAGACAACGGGTCCGACCT
                                    AT
GAM1602  LOC151720 3'  TCCAGCCTGGGCGACAGAGCGA 81158
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                  |||||||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCCGACCT

GAM1602  LOC151904 3'  TCCAGCCTGGGCAACAGAGCGA 81210
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                  |||||||||||||||||||||||
                                  AGAGCGAGACAACGGGTCCGACCT

GAM1602  LOC152002 3'  TCCAGCCTGGACGACAGAGTGA 81268          C
              GA                  TCTCGCTCTGTTG CCAGGCTGGA
                                  |||||||||||| ||||||||||
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                                AGAGTGAGACAGC GGTCCGACCT
                                      A
GAM1602  LOC152106 3'  TCCAGCCTGGTCGACAGAGTGA 70598            C
                GA                TCTCGCTCTGTTG CCAGGCTGGA
                                  |||||||||||| ||||||||||
                                  AGAGTGAGACAGC GGTCCGACCT
                                        T
GAM1602  LOC152271 3'  TCCAGCCTGGGCAACAGAGTAA 81365     CG
                GA                TCT  CTCTGTTGCCCAGGCTGGA
                                  |||  ||||||||||||||||||
                                  AGA  GAGACAACGGGTCCGACCT
                                    AT
GAM1602  LOC152283 3'  TCCAGCCTGGGCAACAAGAGTG 86875          _
                AGA                TCTCGCTCT GTTGCCCAGGCTGGA
                                   ||||||||| ||||||||||||||||
                                   AGAGTGAGA CAACGGGTCCGACCT
                                         A
GAM1602  LOC152313 3'  TCCAGCCTGGGTGACAGAGCGA 86853           TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GT
GAM1602  LOC152316 3'  TCCAGCCTAGGCAACAGAGCGA 86794             C
                GA                TCTCGCTCTGTTGCC AGGCTGGA
                                  |||||||||||||| ||||||||
                                  AGAGCGAGACAACGG TCCGACCT
                                         A
GAM1602  LOC152317 3'  TCCAGCCTGAGTGACAGA    86837      TG C
                                  TCTGT  C CAGGCTGGA
                                  |||||  | |||||||||
                                  AGACA  G GTCCGACCT
                                     GT A
GAM1602  LOC152426 3'  TCCAGCCTGGGCGACAGAGTGA 86902
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAGCGGGTCCGACCT


GAM1602  LOC152445 3'  TCCAGCCTGAGTGAGGAAGC   86964    _  G TG C
                                  GCT CT T  C CAGGCTGGA
                                  ||| || |  | |||||||||
                                  CGA GG A  G GTCCGACCT
                                    A  _ GT A
GAM1602  LOC152453 3'  TCCAGCCTGGGCAACAAGAGCG 81480          _
                A                  TCGCTCT GTTGCCCAGGCTGGA
                                   ||||||| ||||||||||||||||
                                   AGCGAGA CAACGGGTCCGACCT
                                      A
GAM1602  LOC152627 5'  TCCAGCCTGGATAAAAGAGCAA 81515     C     G   C
                GA                TCT GCTCT TTG CCAGGCTGGA
                                  ||| ||||| ||| ||||||||||
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                                AGA CGAGA AAT GGTCCGACCT
                                  A   A  A
GAM1602  LOC152627 3'  TCCAGCCTGGGCCACAGAGTGA 81516          T
                GA                TCTCGCTCTGT GCCCAGGCTGGA
                                  |||||||||| |||||||||||
                                  AGAGTGAGACA CGGGTCCGACCT
                                        C
GAM1602  LOC152804 3'  TCCAGCCTGGGCAACAGAGCGA 87088
                GG                TCTCGCTCTGTTGCCCAGGCTGGA
                                  |||||||||||||||||||||||
                                  GGAGCGAGACAACGGGTCCGACCT

GAM1602  LOC152860 3'  CCAGCCTGGGCAGCAAGAG   81578     _
                                  CTCT GTTGCCCAGGCTGG
                                  |||| ||||||||||||||
                                  GAGA CGACGGGTCCGACC
                                    A
GAM1602  LOC152897 3'  CCAGCCTGGGAGACAGAGTGAG 81603          TG
                A                  TCTCGCTCTGT  CCCAGGCTGG
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACC
                                        GA
GAM1602  LOC153077 3'  TCCAGCCTGGGCTACAGAGCAA 87133     C      T
                GA                TCT GCTCTGT GCCCAGGCTGGA
                                  ||| ||||||| ||||||||||||
                                  AGA CGAGACA CGGGTCCGACCT
                                    A      T
GAM1602  LOC153146 3'  TCCAGCCTGGGTGACAGAGGGA 87148      G     TG
                GA                TCTC CTCTGT  CCCAGGCTGGA
                                  |||| ||||||  ||||||||||||
                                  AGAG GAGACA  GGGTCCGACCT
                                    G     GT
GAM1602  LOC153243 5'  CCTGGAGCAGCAGAACAAGA   81662     CGC      _
                                  TCT   TCTGTTGC CCAGG
                                  |||   |||||||| |||||
                                  AGA   AGACGACG GGTCC
                                    ACA       A
GAM1602  LOC153338 3'  TCCAGCCTGGGTGACAGAGCAA 87198     C      TG
                GA                TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A      GT
GAM1602  LOC153561 3'  AGCCTGGGCAACAGAGTGAGA  81748
                                  TCTCGCTCTGTTGCCCAGGCT
                                  |||||||||||||||||||||
                                  AGAGTGAGACAACGGGTCCGA

GAM1602  LOC153579 3'  CCAGCCTGGGCCCGCAGA    81767      T_
                                  TCTGT  GCCCAGGCTGG
                                  |||||  ||||||||||
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                                AGACG  CGGGTCCGACC
                                  CC
GAM1602  LOC153579 3'  TCCAGCCTGGGCGACAGAGCGA 81774
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCCGACCT

GAM1602  LOC153642 3'  TCCAGCCTGGCAACAGAGTGAG 81793              C
                A                 TCTCGCTCTGTTGCC AGGCTGGA
                                  |||||||||||||| ||||||||
                                  AGAGTGAGACAACGG TCCGACCT
                                                _
GAM1602  LOC153682 3'  TCCAGCCTGAGCGACAGAGCAA 87276     C        C
                GA                TCT GCTCTGTTGC CAGGCTGGA
                                  ||| |||||||||| |||||||||
                                  AGA CGAGACAGCG GTCCGACCT
                                    A         A
GAM1602  LOC153688 3'  TCCAGCCTGGGCGACAGAGGGA 87333      G
                GA                TCTC CTCTGTTGCCCAGGCTGGA
                                  |||| ||||||||||||||||||
                                  AGAG GAGACAGCGGGTCCGACCT
                                    G
GAM1602  LOC154403 5'  CCAGCCTGGGCTACAAGAG    81971      _  T
                                  CTCT GT GCCCAGGCTGG
                                  |||| || ||||||||||
                                  GAGA CA CGGGTCCGACC
                                    A  T
GAM1602  LOC154739 5'  TCCAGCCTGGGCAACAGGTGAG 87443        T
                A                 TCTCGC CTGTTGCCCAGGCTGGA
                                  |||||| ||||||||||||||||
                                  AGAGTG GACAACGGGTCCGACCT
                                                _
GAM1602  LOC154739 3'  TCCAGCCTGGGTGACAGAGTGA 87444            TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                        GT
GAM1602  LOC154791 3'  TCCAGCCTGGGCAACAAGAGC  82055       _
                                  GCTCT GTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||
                                  CGAGA CAACGGGTCCGACCT
                                    A
GAM1602  LOC154877 3'  TCCAGCCTAGGTGATAGAGCAA 87576     C      TG  C
                GA                TCT GCTCTGT  CC AGGCTGGA
                                  ||| |||||||  || ||||||||
                                  AGA CGAGATA  GG TCCGACCT
                                    A      GT  A
GAM1602  LOC155006 3'  TCCAGCCTGGGCGGCAGAGCAA 82176     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
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                                AGA CGAGACGGCGGGTCCGACCT
                                  A
GAM1602  LOC155054 3'  TCCAGCCTGGGTGACAGAGCAA 82206     C      TG
                  GA                TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A       GT
GAM1602  LOC155072 3'  TCCAACCTGGGTGACAGAGCGA 87672          TG      C
                                TCGCTCTGT  CCCAGG TGGA
                                |||||||||  |||||| ||||
                                AGCGAGACA  GGGTCC ACCT
                                     GT      A
GAM1602  LOC155072 3'  TCCAGCCTGGGTGACTGAGCGA 87673          T  TG
                  GA                TCTCGCTC GT  CCCAGGCTGGA
                                |||||||| ||  ||||||||||
                                AGAGCGAG CA  GGGTCCGACCT
                                     T  GT
GAM1602  LOC155376 3'  TCCAGCCTGGGTGACAAAGCAA 82251     C   C   TG
                  GA                TCT GCT TGT  CCCAGGCTGGA
                                ||| ||| |||  ||||||||||
                                AGA CGA ACA  GGGTCCGACCT
                                  A   A   GT
GAM1602  LOC157247 5'  CCTGGGCAACATAGCAAGA    82294     C   C
                                TCT GCT TGTTGCCCAGG
                                ||| ||| ||||||||||
                                AGA CGA ACAACGGGTCC
                                  A   T
GAM1602  LOC157464 5'  TCCAGCCTGGGCAACGGGCGAG 87752        T
                  A                 TCTCGC CTGTTGCCCAGGCTGGA
                                |||||| ||||||||||||||||
                                AGAGCG GGCAACGGGTCCGACCT
                                      _
GAM1602  LOC157562 5'  TCCAGCCTGGGCAACATAGTGA 87776         C
                  GA                TCTCGCT TGTTGCCCAGGCTGGA
                                ||||||| ||||||||||||||||
                                AGAGTGA ACAACGGGTCCGACCT
                                     T
GAM1602  LOC157657 3'  TCCAGCCTGGACAACACAGTGA 82437         C    C
                  GA                TCTCGCT TGTTG CCAGGCTGGA
                                ||||||| ||||| ||||||||||
                                AGAGTGA ACAAC GGTCCGACCT
                                     C    A
GAM1602  LOC157660 3'  TCCAGCGTGGGCAACAGAGTGA 87807              G
                  GA                TCTCGCTCTGTTGCCCA GCTGGA
                                |||||||||||||||| ||||||
                                AGAGTGAGACAACGGGT CGACCT
                                          G
GAM1602  LOC157737 3'  TCCAGCCTGGGCAACAGAGAGA 87846      G
                  GA                TCTC CTCTGTTGCCCAGGCTGGA
                                |||| ||||||||||||||||||
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                                AGAG GAGACAACGGGTCCGACCT
                                  A
GAM1602  LOC157983 3'  TCCAGCCTGGCGACAGAGC    82543          C
                                GCTCTGTTGCC AGGCTGGA
                                |||||||||| ||||||||
                                CGAGACAGCGG TCCGACCT
                                          _
GAM1602  LOC158088 3'  TCCAGCCTGGCGACAGAGCAAG 87978     C         C
           A                     TCT GCTCTGTTGCC AGGCTGGA
                                ||| |||||||||| ||||||||
                                AGA CGAGACAGCGG TCCGACCT
                                  A        _
GAM1602  LOC158160 3'  TCCAGCCTGGGTGACAGCGAGA 73476       CT  TG
                                TCTCGCT  GT  CCCAGGCTGGA
                                |||||||  ||  ||||||||||
                                AGAGCGA  CA  GGGTCCGACCT
                                   __  GT
GAM1602  LOC158187 3'  TCCAGCCTGGGTGACAGAGCAA 87998     C      TG
           GA                     TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM1602  LOC158191 3'  TCCAGCCTGGCGACAGAGCTAG 82682     C         C
           A                     TCT GCTCTGTTGCC AGGCTGGA
                                ||| |||||||||| ||||||||
                                AGA CGAGACAGCGG TCCGACCT
                                  T        _
GAM1602  LOC158235 3'  TCCAGCCTGGGCAACACAGAGA 88008      G  C
           GA                     TCTC CT TGTTGCCCAGGCTGGA
                                |||| || ||||||||||||||||
                                AGAG GA ACAACGGGTCCGACCT
                                  A  C
GAM1602  LOC158292 5'  TCCAGCCTGGGCAACAGAGCAA 88056     C
           GA                     TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGAGACAACGGGTCCGACCT
                                  A
GAM1602  LOC158292 5'  TCCAGCCTGGGCGACAGAGCGA 88057
           GA                     TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||||
                                AGAGCGAGACAGCGGGTCCGACCT

GAM1602  LOC158337 3'  TCCAGCCTGGGTGACAGAGCGA 88112          TG
           GA                     TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      GT
GAM1602  LOC158677 5'  TCCAGCCTGGGTGACAGAGCAA 88252     C      TG
           GA                     TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
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                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM1602  LOC158819 3'  TCCAGCCTGGGTGACAGAGCGA 88286          TG
                  GA                TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGCGAGACA  GGGTCCGACCT
                                          GT
GAM1602  LOC158987 3'  TCCAGCCTGGGCAACAGAGGGA 88334     G
                  G                 CTC CTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||
                                    GAG GAGACAACGGGTCCGACCT
                                      G
GAM1602  LOC158987 3'  TCCAGCCTGGGCAACATAGTGA 88335        C
                  GA                TCTCGCT TGTTGCCCAGGCTGGA
                                    |||||||  ||||||||||||||||
                                    AGAGTGA ACAACGGGTCCGACCT
                                       T
GAM1602  LOC158987 3'  TCCAGCCTGGGTGACAGAGCGA 88337          TG
                  GA                TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGCGAGACA  GGGTCCGACCT
                                          GT
GAM1602  LOC159053 3'  TCCAGCCTGGGCAACAGTGAGA 88377        CT
                                    TCTCGCT  GTTGCCCAGGCTGGA
                                    |||||||  ||||||||||||||||
                                    AGAGTGA  CAACGGGTCCGACCT
                                          __
GAM1602  LOC159110 3'  CCAGCCTGGGCAACAGAACAGG 82986     CGC
                  A                  TCT   TCTGTTGCCCAGGCTGG
                                     |||   ||||||||||||||||||
                                     AGG   AGACAACGGGTCCGACC
                                       ACA
GAM1602  LOC159116 3'  CCAGCCTGGGCAACAGAACAGG 82969     CGC
                  A                  TCT   TCTGTTGCCCAGGCTGG
                                     |||   ||||||||||||||||||
                                     AGG   AGACAACGGGTCCGACC
                                       ACA
GAM1602  LOC161823 3'  TCCAGCCTGGGCAACAGAGTGA 83176
                                    TCGCTCTGTTGCCCAGGCTGGA
                                    |||||||||||||||||||||||
                                    AGTGAGACAACGGGTCCGACCT

GAM1602  LOC162962 3'  TCCAGCCTGGGTGACAGCGAGA 83260        CT  TG
                                    TCTCGCT  GT  CCCAGGCTGGA
                                    |||||||  ||  ||||||||||
                                    AGAGCGA  CA  GGGTCCGACCT
                                         __ GT
GAM1602  LOC170395 3'  TCAAGCCTGGGCAACAGAGTGA 76876                 G
                  GA                TCTCGCTCTGTTGCCCAGGCT GA
                                    |||||||||||||||||||||| ||
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                                AGAGTGAGACAACGGGTCCGA CT
                                      A
GAM1602  LOC170395 3'  TCCAGCCTGGGCAACAAGAGC  76877      _
                                GCTCT GTTGCCCAGGCTGGA
                                ||||| ||||||||||||||||
                                CGAGA CAACGGGTCCGACCT
                                   A
GAM1602  LOC196047 5'  TCCAGCCTGGGTGACAGAGCGA 91167          TG
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      GT
GAM1602  LOC196540 3'  TCCAGCCTGGGTGACAGAGTGA 91208          TG
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      GT
GAM1602  LOC196761 3'  TCCAGCCTGGGCGATAGAGGGA 91121     G
              GA                  TCTC CTCTGTTGCCCAGGCTGGA
                                ||||| ||||||||||||||||||
                                AGAG GAGATAGCGGGTCCGACCT
                                   G
GAM1602  LOC197196 3'  TCCAGCCTGGGCGACAAGAGCG 91306       _
              A                   TCGCTCT GTTGCCCAGGCTGGA
                                ||||||| ||||||||||||||||
                                AGCGAGA CAGCGGGTCCGACCT
                                   A
GAM1602  LOC197201 3'  TCCAGCCTGGGCAACACAGCAA 89288     C   C
              GA                  TCT GCT TGTTGCCCAGGCTGGA
                                ||| ||| ||||||||||||||||
                                AGA CGA ACAACGGGTCCGACCT
                                   A   C
GAM1602  LOC197319 3'  TCCAGCCTGGCAACAGAGTGAG 89329            C
              A                   TCTCGCTCTGTTGCC AGGCTGGA
                                ||||||||||||||| ||||||||
                                AGAGTGAGACAACGG TCCGACCT
                                               _
GAM1602  LOC197362 3'  TCCAGCCTGGGTGACAGAGTGA 91312          TG
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      GT
GAM1602  LOC199729 3'  TCCAGCCAGGGCAACAGAGTGA 73397             A
              GA                  TCTCGCTCTGTTGCCC GGCTGGA
                                ||||||||||||||| |||||||
                                AGAGTGAGACAACGGG CCGACCT
                                      A
GAM1602  LOC199733 3'  TCCAACCTGGGCAACAGAGCCA 91443     C           C
              GA                  TCT GCTCTGTTGCCCAGG TGGA
                                ||| |||||||||||||| ||||
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                                AGA CGAGACAACGGGTCC ACCT
                                  C           A
GAM1602  LOC199786 3'  TCCAGCCTGGGTGATGGGAGTG 89767        _  TG
                  AGA                TCTCGCTCT GT  CCCAGGCTGGA
                                |||||||||  ||  ||||||||||
                                AGAGTGAGG TA  GGGTCCGACCT
                                     G  GT
GAM1602  LOC199858 3'  TCCAGCCTGGGCGACAGAGCGA 89803
                  GA                 TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||
                                AGAGCGAGACAGCGGGTCCGACCT

GAM1602  LOC199923 3'  TCCAGCCTGGACGACAGAGCAA 89874     C       C
                  GA                 TCT GCTCTGTTG CCAGGCTGGA
                                ||| |||||||| ||||||||||
                                AGA CGAGACAGC GGTCCGACCT
                                  A       A
GAM1602  LOC199923 3'  TCCAGCCTGGGCAACTGAGC   89875      T
                                GCTC GTTGCCCAGGCTGGA
                                |||| ||||||||||||||
                                CGAG CAACGGGTCCGACCT
                                  T
GAM1602  LOC200014 3'  TCCAGCCTGGGCGACAGAGCAA 89948     C
                  GA                 TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||
                                AGA CGAGACAGCGGGTCCGACCT
                                  A
GAM1602  LOC200251 3'  TCCAGCCTAGGCAACAAGAGC  90066      _     C
                                GCTCT GTTGCC AGGCTGGA
                                ||||| |||||| ||||||||
                                CGAGA CAACGG TCCGACCT
                                   A     A
GAM1602  LOC200316 3'  TCCAGTTTGAGCAACAGATCAA 90194     CGC       C
                  GA                 TCT   TCTGTTGC CAGGCTGGA
                                |||   |||||||| |||||||||
                                AGA   AGACAACG GTTTGACCT
                                  ACT       A
GAM1602  LOC200317 3'  TCCAGCCTGGGCAACAAGAGTG 90229        _
                  A                  TCGCTCT GTTGCCCAGGCTGGA
                                |||||||  ||||||||||||||
                                AGTGAGA CAACGGGTCCGACCT
                                    A
GAM1602  LOC200853 3'  TCCAGCCTGGGAGACAGAGCGA 90335         TG
                                TCGCTCTGT  CCCAGGCTGGA
                                |||||||||  ||||||||||
                                AGCGAGACA  GGGTCCGACCT
                                     GA
GAM1602  LOC200904 3'  TCTAGCCTGGGCAACAGAGTAA 91785     CG
                  GA                 TCT  CTCTGTTGCCCAGGCTGGA
                                |||  ||||||||||||||||||
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                                AGA  GAGACAACGGGTCCGATCT
                                  AT
GAM1602  LOC200918 3'  CCAGCCTGGGCGACAAGAG    90366      _
                                CTCT GTTGCCCAGGCTGG
                                |||| ||||||||||||||
                                GAGA CAGCGGGTCCGACC
                                  A
GAM1602  LOC200940 3'  TCCAGCCTGGGCGACAGAGTGA 90396
                  GA              TCTCGCTCTGTTGCCCAGGCTGGA
                                  |||||||||||||||||||||||||
                                  AGAGTGAGACAGCGGGTCCGACCT

GAM1602  LOC201173 3'  TCCAGCCTGGGCGACAGAGCAA 88694     C
                  GA              TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM1602  LOC201182 5'  TCCAGCCTGGTCAACAGAGCAA 91338     C        C
                  GA              TCT GCTCTGTTG CCAGGCTGGA
                                  ||| ||||||||| ||||||||||
                                  AGA CGAGACAAC GGTCCGACCT
                                    A         T
GAM1602  LOC201220 3'  TCCAGCCTGGGTGACAGAGCAA 88727     C       TG
                  GA              TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A      GT
GAM1602  LOC201564 3'  TCCAGCCTGGGCAACAAGAGC  81276      _
                                GCTCT GTTGCCCAGGCTGGA
                                ||||| ||||||||||||||
                                CGAGA CAACGGGTCCGACCT
                                  A
GAM1602  LOC201685 3'  TCAAGCCTGGACAACAGGGCAA 91846     C        C       G
                  GA              TCT GCTCTGTTG CCAGGCT GA
                                  ||| ||||||||| ||||||| ||
                                  AGA CGGGACAAC GGTCCGA CT
                                    A         A       A
GAM1602  LOC201868 5'  CCAGCCTGGGCTACAAGAG    90518      _  T
                                CTCT GT GCCCAGGCTGG
                                |||| || ||||||||||
                                GAGA CA CGGGTCCGACC
                                  A  T
GAM1602  LOC201895 3'  TCCAGCCTAAGCAATAGAGCGA 90548              CC
                  GA              TCTCGCTCTGTTGC  AGGCTGGA
                                  ||||||||||||||  ||||||||
                                  AGAGCGAGATAACG  TCCGACCT
                                            AA
GAM1602  LOC201911 3'  TCCAGCCTGGGCAACAAGAGC  91869      _
                                GCTCT GTTGCCCAGGCTGGA
                                ||||| ||||||||||||||
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                                CGAGA CAACGGGTCCGACCT
                                  A
GAM1602  LOC201931 3'  TCCAGCCTGGGCGACAGAGCGA 90569
                GA               TCTCGCTCTGTTGCCCAGGCTGGA
                                 ||||||||||||||||||||||||
                                 AGAGCGAGACAGCGGGTCCGACCT

GAM1602  LOC202020 3'  TCCAGCCCGGGCGACAGAGTGA 90603              A
                GA               TCTCGCTCTGTTGCCC GGCTGGA
                                 |||||||||||||||| |||||||
                                 AGAGTGAGACAGCGGG CCGACCT
                                           C
GAM1602  LOC202781 3'  TCCAGCCTGGACGATATAGCCA 91975    C   C    C
                GA               TCT GCT TGTTG CCAGGCTGGA
                                 ||| ||| ||||| ||||||||||
                                 AGA CGA ATAGC GGTCCGACCT
                                   C  T    A
GAM1602  LOC202781 3'  TCCAGCCTGGGCGACAGAGCGA 91976
                GA               TCTCGCTCTGTTGCCCAGGCTGGA
                                 ||||||||||||||||||||||||
                                 AGAGCGAGACAGCGGGTCCGACCT

GAM1602  LOC202868 3'  TCCAACCTGGGTGACAGAGCGA 92009         TG     C
                                 TCGCTCTGT  CCCAGG TGGA
                                 |||||||||  |||||| ||||
                                 AGCGAGACA  GGGTCC ACCT
                                       GT     A
GAM1602  LOC202868 3'  TCCAGCCTGGGTGACAGAGCGA 92010          TG
                GA               TCTCGCTCTGT  CCCAGGCTGGA
                                 ||||||||||  ||||||||||
                                 AGAGCGAGACA  GGGTCCGACCT
                                       GT
GAM1602  LOC203025 3'  TCCAGCCTGGGCAACAAGAGC  90749      _
                                 GCTCT GTTGCCCAGGCTGGA
                                 |||||  ||||||||||||||
                                 CGAGA CAACGGGTCCGACCT
                                   A
GAM1602  LOC203083 3'  TCCAGCCTGGGCAACAGAGTAA 92095    CG
                GA               TCT  CTCTGTTGCCCAGGCTGGA
                                 |||  ||||||||||||||||||
                                 AGA  GAGACAACGGGTCCGACCT
                                   AT
GAM1602  LOC203246 3'  CCTGGGCGACAGAACGAGA   90830      C
                                 TCTCG TCTGTTGCCCAGG
                                 |||||  ||||||||||||
                                 AGAGC AGACAGCGGGTCC
                                   A
GAM1602  LOC203276 3'  TCCAGCCTGGGCAACAGAGTGA 92130
                GA               TCTCGCTCTGTTGCCCAGGCTGGA
                                 ||||||||||||||||||||||||
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                                AGAGTGAGACAACGGGTCCGACCT

GAM1602  LOC203289 3'  TCCAGCCTGGCGACAGAGC    90870          C
                                GCTCTGTTGCC AGGCTGGA
                                |||||||||| ||||||||
                                CGAGACAGCGG TCCGACCT
                                        _
GAM1602  LOC203305 3'  TCCAGCCTGGGCAACAGAGTGA 92183
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAACGGGTCCGACCT

GAM1602  LOC203350 3'  CCTGGGGCAACATAGCGAGA   92235       C      _
                                TCTCGCT TGTTGCCC AGG
                                ||||||| |||||||| |||
                                AGAGCGA ACAACGGG TCC
                                    T       G
GAM1602  LOC203350 3'  TCCAGCCTGGATGACAGAGTGA 92250           GC
                GA                TCTCGCTCTGTT  CCAGGCTGGA
                                  ||||||||||||  ||||||||||
                                  AGAGTGAGACAG  GGTCCGACCT
                                        TA
GAM1602  LOC203378 3'  TCCAGCCTGGGCGACAGAACAA 92303     CGC
                GA                TCT   TCTGTTGCCCAGGCTGGA
                                  |||   ||||||||||||||||||
                                  AGA   AGACAGCGGGTCCGACCT
                                    ACA
GAM1602  LOC205327 3'  TCCAACCTGGGCAACATAGTGG 91072       C         C
                GA                TCTCGCT TGTTGCCCAGG TGGA
                                  ||||||| |||||||||| ||||
                                  AGGGTGA ACAACGGGTCC ACCT
                                     T         A
GAM1602  LOC219347 3'  TCCAGCCTGGGCAACAGAGTGA 94581
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAACGGGTCCGACCT

GAM1602  LOC219540 3'  TCCAGCCTGGGCGACAGAGCGA 95247
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCCGACCT

GAM1602  LOC219627 3'  TCCAGCCTGGGCAACAAGCGA  93812       C
                                TCGCT TGTTGCCCAGGCTGGA
                                ||||| ||||||||||||||||
                                AGCGA ACAACGGGTCCGACCT
                                   _
GAM1602  LOC219627 3'  TCCAGCTGGGCGACAGAGCGAG 93813                G
                A                 TCTCGCTCTGTTGCCCAG CTGGA
                                  |||||||||||||||| |||||
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                                AGAGCGAGACAGCGGGTC GACCT

                                                 _
GAM1602  LOC219649 3'  TCCAGCCTAGGCAACAAGAGC  94557      _     C
                                GCTCT GTTGCC AGGCTGGA
                                ||||| |||||| ||||||||
                                CGAGA CAACGG TCCGACCT
                                   A     A
GAM1602  LOC219649 3'  TCCAGCCTGGGCGACAGAGTGA 94558
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAGCGGGTCCGACCT

GAM1602  LOC219672 5'  TCCAGCCTGGGCAACAAGAGTG 92973       _
              A                   TCGCTCT GTTGCCCAGGCTGGA
                                  ||||||| ||||||||||||||||
                                  AGTGAGA CAACGGGTCCGACCT
                                     A
GAM1602  LOC219722 5'  CCAGCCTGGGCAACAGAACAAG 94677     CGC
              A                   TCT   TCTGTTGCCCAGGCTGG
                                  |||   ||||||||||||||||||
                                  AGA   AGACAACGGGTCCGACC
                                    ACA
GAM1602  LOC219722 5'  TCAGCCTGGACAACAGAGTGAG 94685           C
              A                   TCTCGCTCTGTTG CCAGGCTGG
                                  |||||||||||| |||||||||
                                  AGAGTGAGACAAC GGTCCGACT
                                           A
GAM1602  LOC219919 3'  TCCAGCCTGGGCAACAGAGTAA 94933     CG
              GA                  TCT  CTCTGTTGCCCAGGCTGGA
                                  |||  ||||||||||||||||||
                                  AGA  GAGACAACGGGTCCGACCT
                                    AT
GAM1602  LOC220038 3'  TCCAGCCTGGGCGATGGAGTGA 93377
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGGTAGCGGGTCCGACCT

GAM1602  LOC220506 3'  TCCAGCCTGGGCAACAGAACAA 74521     CGC
              GA                  TCT   TCTGTTGCCCAGGCTGGA
                                  |||   ||||||||||||||||||
                                  AGA   AGACAACGGGTCCGACCT
                                    ACA
GAM1602  LOC220549 3'  TCCAGCCTGGGTGACAGAATGA 94511       C     TG
              GA                  TCTCG TCTGT  CCCAGGCTGGA
                                  ||||| |||||  ||||||||||
                                  AGAGT AGACA  GGGTCCGACCT
                                     A    GT
GAM1602  LOC220662 3'  TCCAGCCTGGGCAACACGAGCG 92831       _
              A                   TCGCTC TGTTGCCCAGGCTGGA
                                  |||||| ||||||||||||||||
```

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                                AGCGAG ACAACGGGTCCGACCT
                                   C
GAM1602  LOC220692 3'  TCCAGCTCGGGGAACAGAGCGA 92866          G   AG
                GA                TCTCGCTCTGTT CCC  GCTGGA
                                  |||||||||||| |||  ||||||
                                  AGAGCGAGACAA GGG  CGACCT
                                        G   CT
GAM1602  LOC220776 3'  CCAGCCCAGAGTAAGAGAGCAG 68920     C    G    CCA_
                A                 TCT GCTCT TTGC    GGCTGG
                                  ||| ||||| ||||    ||||||
                                  AGA CGAGA AATG    CCGACC
                                    _    G    AGAC
GAM1602  LOC220906 3'  TCCAGCCTGGGCAACAAGCGA  93037      C
                                  TCGCT TGTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||||
                                  AGCGA ACAACGGGTCCGACCT
                                    _
GAM1602  LOC220906 3'  TCCAGCTGGGCGACAGAGCGAG 93038              G
                A                 TCTCGCTCTGTTGCCCAG CTGGA
                                  |||||||||||||||| |||||
                                  AGAGCGAGACAGCGGGTC GACCT
                                                 _
GAM1602  LOC220992 3'  TCCAGCCTGGGCAACATAGCAA 93110     C   C
                GA                TCT GCT TGTTGCCCAGGCTGGA
                                  ||| ||| ||||||||||||||||
                                  AGA CGA ACAACGGGTCCGACCT
                                    A   T
GAM1602  LOC221042 3'  TCCAGCCTGGGTGACAGAGCAA 94807     C      TG
                GA                TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A       GT
GAM1602  LOC221069 3'  TCCAGCCTGGGCGACAGAGCAA 94821     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM1602  LOC221178 3'  TCCAGCCTGGGAGATACAGCGA 95176        C   TG
                GA                TCTCGCT TGT  CCCAGGCTGGA
                                  ||||||| |||  ||||||||||
                                  AGAGCGA ATA  GGGTCCGACCT
                                     C   GA
GAM1602  LOC221271 3'  TCCAGCCTGGGCAACAGAGGGA 93530      G
                GA                TCTC CTCTGTTGCCCAGGCTGGA
                                  |||| ||||||||||||||||||||
                                  AGAG GAGACAACGGGTCCGACCT
                                    G
GAM1602  LOC221271 3'  TCCAGCCTGGGTGACAGAGCGA 93532          TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
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                                AGAGCGAGACA  GGGTCCGACCT
                                      GT
GAM1602  LOC221288 3'  TCCAGCCTGGGCGACAGAGTGA 95263
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAGCGGGTCCGACCT

GAM1602  LOC221337 3'  TCCAGCCTGGGCAACAAGAGTG 93738       _
              A                   TCGCTCT GTTGCCCAGGCTGGA
                                  ||||||| ||||||||||||||||
                                  AGTGAGA CAACGGGTCCGACCT
                                     A
GAM1602  LOC221410 3'  TCCAGCCTGGGTGACAGAGCGA 93699          TG
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GT
GAM1602  LOC221477 3'  TCCAGCCTGGGCGACAGAGCGA 93776
                                  TCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||
                                  AGCGAGACAGCGGGTCCGACCT

GAM1602  LOC221490 3'  CCTAGGCGACAGAGCAAGA    95304     C         C
                                  TCT GCTCTGTTGCC AGG
                                  ||| |||||||||| |||
                                  AGA CGAGACAGCGG TCC
                                    A          A
GAM1602  LOC221543 3'  TCCAGCCTGGGCAACAAGAGTA 95386     CG    _
              AG                  CT  CTCT GTTGCCCAGGCTGGA
                                  ||  |||| ||||||||||||||||
                                  GA  GAGA CAACGGGTCCGACCT
                                   AT    A
GAM1602  LOC221543 5'  TCCAGCCTGGGCGACAGAGCAA 95388     C
              GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM1602  LOC221641 5'  TCCAGCCTGGGTGGCAGAGCGA 95348          TG
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACG  GGGTCCGACCT
                                        GT
GAM1602  LOC221795 3'  TCCAGCCTGGGCAACAGAGTAA 94081     CG
              GA                  TCT  CTCTGTTGCCCAGGCTGGA
                                  |||  ||||||||||||||||||
                                  AGA  GAGACAACGGGTCCGACCT
                                    AT
GAM1602  LOC221931 3'  CCAGAGCAACAGAGTGAGA    95630           CCAGG
                                  TCTCGCTCTGTTGC    CTGG
                                  ||||||||||||||    ||||
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                                AGAGTGAGACAACG    GACC
                                      A____
GAM1602  LOC221943 5'  TCCAGCCTGGGCGACAGAGCAA 95625    C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM1602  LOC221954 5'  TCCAGCCTGGGCAACAGAGCGA 95651
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  |||||||||||||||||||||||||
                                  AGAGCGAGACAACGGGTCCGACCT

GAM1602  LOC221954 5'  TCCAGCCTGGGTGACAGAGTAA 95652    CG    TG
                GA                TCT  CTCTGT  CCCAGGCTGGA
                                  |||  ||||||  ||||||||||
                                  AGA  GAGACA  GGGTCCGACCT
                                    AT     GT
GAM1602  LOC221954 5'  TCCAGCTTGGGCGACAGAGCAA 95653    C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGCGGGTTCGACCT
                                    A
GAM1602  LOC222008 5'  TCCAGCCTGGGCTCCGCAGG   95659      T__
                                  TCTGT   GCCCAGGCTGGA
                                  |||||   ||||||||||||
                                  GGACG   CGGGTCCGACCT
                                     CCT
GAM1602  LOC222060 5'  TCCAGCCTGGGCGACAGAGCAA 95758    C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM1602  LOC222160 3'  TCCAGCCTGGGCAGCAGAGGAA 95791    CG
                GA                TCT  CTCTGTTGCCCAGGCTGGA
                                  |||  ||||||||||||||||||
                                  AGA  GAGACGACGGGTCCGACCT
                                    AG
GAM1602  LOC222160 5'  TCCAGCCTGGGCGACAGAGCAA 95792    C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM1602  LOC222182 3'  TCCAGCCTGGGCAATAGAGTGA 95862
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  |||||||||||||||||||||||||
                                  AGAGTGAGATAACGGGTCCGACCT

GAM1602  LOC222865 3'  TCCAGCCTGAGTGACAGAGCGA 94450          TG C
                GA                TCTCGCTCTGT  C CAGGCTGGA
                                  ||||||||||  | |||||||||
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                                AGAGCGAGACA  G GTCCGACCT
                                      GT A
GAM1602  LOC245771 5'  CCAGCCTGGGCTGGGGGAGA   94469      G   TGTT
                                TCTC CTC    GCCCAGGCTGG
                                |||| |||    ||||||||||
                                AGAG GGG    CGGGTCCGACC
                                  G   T___
GAM1602  LOC253039 3'  TCCAGCCTGGGCGACAGAGCAA 97867     C
              GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM1602  LOC253532 3'  TCCAGCCTGGGTGACAAAGCAA 97740     C   C   TG
              GA                  TCT GCT TGT  CCCAGGCTGGA
                                  ||| ||| |||  ||||||||||
                                  AGA CGA ACA  GGGTCCGACCT
                                    A   A   GT
GAM1602  LOC253612 5'  TCCAGCCTAGGCAACAGAGTGA 98559              C
              GA                  TCTCGCTCTGTTGCC AGGCTGGA
                                  |||||||||||||| ||||||||
                                  AGAGTGAGACAACGG TCCGACCT
                                          A
GAM1602  LOC253639 3'  TCCAGCCTGGGCGACAGAGTGA 97517
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAGCGGGTCCGACCT

GAM1602  LOC253778 5'  TCCAGCCTGGGCGACAGAGTGA 96527
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAGCGGGTCCGACCT

GAM1602  LOC253786 3'  TCCAGCCTGGGCAATAGAGCAA 98834     C
              GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||
                                  AGA CGAGATAACGGGTCCGACCT
                                    A
GAM1602  LOC253832 3'  TCCAGCCTGGGCGACGAGTGA  96593       T
                                TCGCTC GTTGCCCAGGCTGGA
                                ||||||| ||||||||||||||
                                AGTGAG CAGCGGGTCCGACCT
                                  _
GAM1602  LOC253840 5'  TCCAGCCTGGGCAACAGAGCAA 97914     C
              GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||
                                  AGA CGAGACAACGGGTCCGACCT
                                    A
GAM1602  LOC253906 3'  CAGCCTGGGCAACAAAGTGAGA 98299        C
                                TCTCGCT TGTTGCCCAGGCTG
                                ||||||| |||||||||||||
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                                AGAGTGA ACAACGGGTCCGAC
                                   A
GAM1602  LOC254041 5'  CCTGGACGACAGAGCAAGA   96554     C       C
                                TCT GCTCTGTTG CCAGG
                                ||| ||||||||| |||||
                                AGA CGAGACAGC GGTCC
                                  A       A
GAM1602  LOC254045 3'  CCATCTTGGGCAACAGAATGAG 98265      C          C
            A                    TCTCG TCTGTTGCCCAGG TGG
                                ||||| |||||||||||| |||
                                AGAGT AGACAACGGGTTC ACC
                                   A          T
GAM1602  LOC254100 3'  TCCAGCCTGGGCAACAGAGTGA 98160
            GA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGACAACGGGTCCGACCT

GAM1602  LOC254176 3'  TCCAGCCTGGGCAACAGAGTAA 99176     CG
            GA                   TCT  CTCTGTTGCCCAGGCTGGA
                                |||  ||||||||||||||||||
                                AGA  GAGACAACGGGTCCGACCT
                                  AT
GAM1602  LOC254243 3'  TCCAGCCTGGGCAACAGAGTGA 99269
            GA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGACAACGGGTCCGACCT

GAM1602  LOC254531 5'  TCCAGCCTGGGTGACAGAGCAA 96673     C      TG
            GA                   TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM1602  LOC254659 3'  TCCAGAGTGGGAAACAGAGCAA 96822     C       G    GG
            GA                   TCT GCTCTGTT CCCA  CTGGA
                                ||| |||||||| ||||  |||||
                                AGA CGAGACAA GGGT  GACCT
                                  A       A   GA
GAM1602  LOC254756 3'  TCCAGCCTGGGCAATAGAGTAA 99212     CG
            GA                   TCT  CTCTGTTGCCCAGGCTGGA
                                |||  ||||||||||||||||||
                                AGA  GAGATAACGGGTCCGACCT
                                  AT
GAM1602  LOC254808 3'  TCCAGCCTGGGCAACAGAGCAA 98810     C
            GA                   TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGAGACAACGGGTCCGACCT
                                  A
GAM1602  LOC254875 3'  TCCAGCCTGGGTGACAAAGCAA 97785     C  C   TG
            GA                   TCT GCT TGT  CCCAGGCTGGA
                                ||| ||| |||  ||||||||||
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                                AGA CGA ACA  GGGTCCGACCT
                                  A   A   GT
GAM1602  LOC255030 5'  TCCAGCCTGGGTGACAGAGCGA 99086          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGCGAGACA  GGGTCCGACCT
                                          GT
GAM1602  LOC255031 3'  TCCAGCCTGGCTACAGAGTGAG 99044          T   C
                A                   TCTCGCTCTGT GCC AGGCTGGA
                                    ||||||||||| ||| ||||||||
                                    AGAGTGAGACA CGG TCCGACCT
                                          T  _
GAM1602  LOC255042 3'  TCCAGCCTGGGCAACAAGAGCG 97056        _
                A                   TCGCTCT GTTGCCCAGGCTGGA
                                    |||||||  ||||||||||||||
                                    AGCGAGA CAACGGGTCCGACCT
                                       A
GAM1602  LOC255042 3'  TCCAGCCTGGGCGACGAGC    97057      T
                                    GCTC GTTGCCCAGGCTGGA
                                    ||||  ||||||||||||||
                                    CGAG CAGCGGGTCCGACCT
                                     _
GAM1602  LOC255177 3'  TCCAGCCTAGGCAACAGAGTGA 98401            C
                GA                  TCTCGCTCTGTTGCC AGGCTGGA
                                    ||||||||||||||  ||||||||
                                    AGAGTGAGACAACGG TCCGACCT
                                          A
GAM1602  LOC255196 3'  CCTGGGCAACAGAGCCAGA    98952     C
                                    TCT GCTCTGTTGCCCAGG
                                    |||  ||||||||||||||
                                    AGA CGAGACAACGGGTCC
                                      C
GAM1602  LOC255196 5'  TCCAACCTGGGCAGCACGAAGA 98966     _  CTC          C
                                    TCT CG   TGTTGCCCAGG TGGA
                                    |||  ||   ||||||||||  ||||
                                    AGA GC   ACGACGGGTCC ACCT
                                      A  ___          A
GAM1602  LOC255231 3'  TCCAGCCTGGGTGACAGAGTGA 97123          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          GT
GAM1602  LOC255326 3'  TCCAGCCTGGGTGACAGAGCAA 98124     C      TG
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    |||  |||||||  ||||||||||
                                    AGA CGAGACA  GGGTCCGACCT
                                      A      GT
GAM1602  LOC255328 3'  TCCAGCCTGGGTGATAAGAGC  98347      _  TG
                                    GCTCT GT  CCCAGGCTGGA
                                    |||||  ||  ||||||||||
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                                CGAGA TA  GGGTCCGACCT
                                  A  GT
GAM1602  LOC255463 3'  TCCAGCCTGGACAACATAGTGA 96543        C    C
                  GA                TCTCGCT TGTTG CCAGGCTGGA
                                    ||||||| ||||| ||||||||||
                                    AGAGTGA ACAAC GGTCCGACCT
                                       T    A
GAM1602  LOC255523 3'  TCCAGCCTGGGCAACAGAGCAA 96737     C
                  GA                TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAACGGGTCCGACCT
                                      A
GAM1602  LOC255565 5'  CCAGCCTGAGAAACAAGC    96802     C    GCC
                                    GCT TGTT   CAGGCTGG
                                    ||| ||||   ||||||||
                                    CGA ACAA   GTCCGACC
                                     _    AGA
GAM1602  LOC255671 3'  TCCAGCCTGGGTAACAGAGCAA 99076     C
                  GA                TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAATGGGTCCGACCT
                                      A
GAM1602  LOC255671 5'  TCCAGCCTGGGTGACAGAGTGA 99077          TG
                  GA                TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          GT
GAM1602  LOC255792 5'  CCAGCCCAAGGCTAGAAGA   98469    GC   TT   CA_
                                    TC  TCTG  GCC   GGCTGG
                                    ||  ||||  |||   ||||||
                                    AG  AGAT  CGG   CCGACC
                                     A_   __   AAC
GAM1602  LOC256073 3'  CCTGGGCAACATAGCGAGA   98485       C
                                    TCTCGCT TGTTGCCCAGG
                                    ||||||| ||||||||||
                                    AGAGCGA ACAACGGGTCC
                                       T
GAM1602  LOC256207 3'  TCCAACCTGGGCGACAGAGCAA 96880     C           C
                  GA                TCT GCTCTGTTGCCCAGG TGGA
                                    ||| |||||||||||||| ||||
                                    AGA CGAGACAGCGGGTCC ACCT
                                      A            A
GAM1602  LOC256267 3'  CCAGCCTGGAAAACAAGT    98608     C    GC
                                    GCT TGTT  CCAGGCTGG
                                    ||| ||||  |||||||||
                                    TGA ACAA  GGTCCGACC
                                      _    AA
GAM1602  LOC256267 5'  TCCAGCCTGGGAGACAGAGTGA 98613          TG
                  GA                TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
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                                AGAGTGAGACA  GGGTCCGACCT
                                      GA
GAM1602  LOC256515 3'  TCCAGCCTGGGCAACAGAGTAA 98218     CG
              GA                  TCT  CTCTGTTGCCCAGGCTGGA
                                  |||  ||||||||||||||||||
                                  AGA  GAGACAACGGGTCCGACCT
                                    AT
GAM1602  LOC256520 3'  TCCAGCCTGGGCGACAGAGCCA 97670     C
              GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    C
GAM1602  LOC256544 3'  TCCAGCCTGGCGACAGAGC    97934          C
                                  GCTCTGTTGCC AGGCTGGA
                                  |||||||||||| ||||||||
                                  CGAGACAGCGG TCCGACCT
                                              _
GAM1602  LOC256594 3'  TCCAGCCTGGGCAACAGAGTAA 98868     CG
              GA                  TCT  CTCTGTTGCCCAGGCTGGA
                                  |||  ||||||||||||||||||
                                  AGA  GAGACAACGGGTCCGACCT
                                    AT
GAM1602  LOC256980 3'  TCCAGCCTGGTCGACAAGAGAG 96933      G  C     C
              A                    TCTC CT TGTTG CCAGGCTGGA
                                  |||| || ||||| ||||||||||
                                  AGAG GA ACAGC GGTCCGACCT
                                    A _    T
GAM1602  LOC257282 5'  TCAAGCCTGGGCAACAGAGCAA 98136     C              G
              GA                  TCT GCTCTGTTGCCCAGGCT GA
                                  ||| |||||||||||||||| ||
                                  AGA CGAGACAACGGGTCCGA CT
                                    A              A
GAM1602  LOC257397 3'  TCCAGCCTGGACAGCAGAACAA 97953     CGC      C
              GA                  TCT   TCTGTTG CCAGGCTGGA
                                  |||   ||||||| ||||||||||
                                  AGA   AGACGAC GGTCCGACCT
                                    ACA      A
GAM1602  LOC257596 3'  TCCAGCCTGGGCAACAAGAGTA 99789     CG   _
              AG                  CT  CTCT GTTGCCCAGGCTGGA
                                  ||  |||| ||||||||||||||||
                                  GA  GAGA CAACGGGTCCGACCT
                                   AT   A
GAM1602  LOC257596 5'  TCCAGCCTGGGCGACAGAGCAA 99791     C
              GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM1602  LOC51145  3'  TCCAGCCTGGGCGACAGAGTGA 32928
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                  |||||||||||||||||||||||||
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                                AGAGTGAGACAGCGGGTCCGACCT

GAM1602 LOC51212 3' TCCAGCCTGGGTGACAGAGCAA 33501     C      TG
             GA                   TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A      GT
GAM1602 LOC51279 3' TCCAGCCTAAGCAACATAGTGA 33763      C     CC
                                  TCGCT TGTTGC  AGGCTGGA
                                  ||||| ||||||  ||||||||
                                  AGTGA ACAACG  TCCGACCT
                                    T     AA
GAM1602 LOC51279 3' TCCAGCCTGCGGACAGACCAAG 33764     CGC    TG _
             A                    TCT   TCTGT  CC CAGGCTGGA
                                  |||   |||||  || |||||||||
                                  AGA   AGACA  GG GTCCGACCT
                                    ACC    __  C
GAM1602 LOC51333 3' TCCGGCCTGGGCAACAGAGGAA 34057     CG
             GA                   TCT  CTCTGTTGCCCAGGCTGGA
                                  |||  ||||||||||||||||||||
                                  AGA  GAGACAACGGGTCCGGCCT
                                    AG
GAM1602 LOC51336 3' TCCAGCCTGGGTGACAGCGT   34078    T    TG
                                  GC CTGT  CCCAGGCTGGA
                                  || ||||  ||||||||||
                                  TG GACA  GGGTCCGACCT
                                   C    GT
GAM1602 LOC51652 3' CCTGGGCAACATAGCAAGA    32700     C   C
                                  TCT GCT TGTTGCCCAGG
                                  ||| ||| ||||||||||
                                  AGA CGA ACAACGGGTCC
                                    A   T
GAM1602 LOC51759 3' TCCAGCCTGGGCAACGAGC    73172      T
                                  GCTC GTTGCCCAGGCTGGA
                                  |||| ||||||||||||||
                                  CGAG CAACGGGTCCGACCT
                                     _
GAM1602 LOC57107 5' CCAGCCTGGGCTGCTAGA     40182     _  T
                                  TCT GT GCCCAGGCTGG
                                  ||| || ||||||||||
                                  AGA CG CGGGTCCGACC
                                    T  T
GAM1602 LOC63929 3' TCCAGCCTGGGTGACTGAGCAA 42285     C    T  TG
             GA                   TCT GCTC GT  CCCAGGCTGGA
                                  ||| |||| ||  ||||||||||
                                  AGA CGAG CA  GGGTCCGACCT
                                    A    T  GT
GAM1602 LOC64167 3' TCCAGCCTGGGTGACTGAGCGA 42543         T  TG
             GA                   TCTCGCTC GT  CCCAGGCTGGA
                                  |||||||| ||  ||||||||||
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                                AGAGCGAG CA  GGGTCCGACCT
                                    T  GT
GAM1602  LOC85479  5'  TCCAGCCTGGGCGACAGAGCAA 53571     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAGCGGGTCCGACCT
                                      A
GAM1602  LOC89890  3'  TCCAGCCTGGATGACAGAGTGA 61209           GC
                GA                  TCTCGCTCTGTT  CCAGGCTGGA
                                    ||||||||||||  ||||||||||
                                    AGAGTGAGACAG  GGTCCGACCT
                                          TA
GAM1602  LOC90038  3'  TCCAGCCTGGGCAACAGAGTGA 61813
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAACGGGTCCGACCT

GAM1602  LOC90072  3'  TCCAGCCTGGGGAACAGAGCAA 61963     C       G
                GA                  TCT GCTCTGTT CCCAGGCTGGA
                                    ||| |||||||| ||||||||||
                                    AGA CGAGACAA GGGTCCGACCT
                                      A       G
GAM1602  LOC90072  5'  TCCAGCCTGGGTGACAGAACAA 61964     CGC     TG
                GA                  TCT   TCTGT  CCCAGGCTGGA
                                    |||   |||||  ||||||||||
                                    AGA   AGACA  GGGTCCGACCT
                                      ACA     GT
GAM1602  LOC90092  3'  TCCAGCCTGGCGACAAGAGCGA 62075          _     C
                GA                  TCTCGCTCT GTTGCC AGGCTGGA
                                    |||||||| |||||| ||||||||
                                    AGAGCGAGA CAGCGG TCCGACCT
                                         A     _
GAM1602  LOC90110  5'  TCCAGCCTGGGCAACGGAGTGA 62182
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGGCAACGGGTCCGACCT

GAM1602  LOC90141  3'  TCCAGCCTGGATGATAGAGCAA 62310     C       GC
                GA                  TCT GCTCTGTT  CCAGGCTGGA
                                    ||| ||||||||  ||||||||||
                                    AGA CGAGATAG  GGTCCGACCT
                                      A       TA
GAM1602  LOC90155  5'  TCCAGCCTGGGCAACAAGAGTG 62368        _
                A                    TCGCTCT GTTGCCCAGGCTGGA
                                    |||||||| ||||||||||||||
                                    AGTGAGA CAACGGGTCCGACCT
                                        A
GAM1602  LOC90233  3'  TCCAGCCCAGGCAACAGAGTGA 57197             CA
                GA                  TCTCGCTCTGTTGCC  GGCTGGA
                                    ||||||||||||||  |||||||
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                                AGAGTGAGACAACGG  CCGACCT
                                      AC
GAM1602  LOC90321  3'  TCCAACCTGGGTGACAGAGCGA 62938          TG     C
             GA                   TCTCGCTCTGT  CCCAGG TGGA
                                  |||||||||||  |||||| ||||
                                  AGAGCGAGACA  GGGTCC ACCT
                                        GT     A
GAM1602  LOC90393  5'  TCCAGCCTGGGTGACAGAGTGA 63309          TG
             GA                   TCTCGCTCTGT  CCCAGGCTGGA
                                  |||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                        GT
GAM1602  LOC90538  3'  TCTGGGCAAAAAAGCGAGA   63902        CTG
                                  TCTCGCT   TTGCCCAGG
                                  |||||||   |||||||||
                                  AGAGCGA   AACGGGTCT
                                      AAA
GAM1602  LOC90573  5'  TCCAGCCTGGGCGACAGAGTGA 63962
             GA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAGCGGGTCCGACCT

GAM1602  LOC90624  3'  TCCAGCCTGGGGGGACAGAGTGA 64373           G
             GA                   TCTCGCTCTGTT CCCAGGCTGGA
                                  |||||||||||| ||||||||||
                                  AGAGTGAGACAG GGGTCCGACCT
                                        G
GAM1602  LOC90639  3'  TCCAGCCTGAGCAACAGAGCCG 64416     C        C
             GA                   TCT GCTCTGTTGC CAGGCTGGA
                                  ||| |||||||||| |||||||||
                                  AGG CGAGACAACG GTCCGACCT
                                    C         A
GAM1602  LOC90784  5'  TCCAGCCTGGGCAACAGAGTGA 64700
             GA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAACGGGTCCGACCT

GAM1602  LOC90785  3'  TCCAGCCTGGGTGACAGAGCGA 64720          TG
             GA                   TCTCGCTCTGT  CCCAGGCTGGA
                                  |||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GT
GAM1602  LOC90918  5'  TCCAGCCTAGGCAACAAGAGTG 65005        _     C
             A                     TCGCTCT GTTGCC AGGCTGGA
                                  |||||||  ||||||  ||||||||
                                  AGTGAGA CAACGG TCCGACCT
                                      A     A
GAM1602  LOC91035  3'  TCCAGCCTGGACAACAAGAGC  65306       _   C
                                  GCTCT GTTG CCAGGCTGGA
                                  |||||  ||||  ||||||||||
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                                CGAGA CAAC GGTCCGACCT
                                  A   A
GAM1602  LOC91056  3'  TCCAGCCTGGGCGACAGAGCAA 96410     C
                GG                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  GGA CGAGACAGCGGGTCCGACCT
                                    A
GAM1602  LOC91064  3'  TCCAGCGTGGGCGACAGAGCAA 65391     C          G
                GA                TCT GCTCTGTTGCCCA GCTGGA
                                  ||| |||||||||||| ||||||
                                  AGA CGAGACAGCGGGT CGACCT
                                    A          G
GAM1602  LOC91250  5'  TCCAGCCTGAGTGACAGAGTGA 65921          TG C
                GA                TCTCGCTCTGT  C CAGGCTGGA
                                  ||||||||||  | |||||||||
                                  AGAGTGAGACA  G GTCCGACCT
                                        GT A
GAM1602  LOC91250  5'  TCCAGCCTGGGCAACAGAGTGA 65922
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAACGGGTCCGACCT

GAM1602  LOC91286  3'  TCCAGCCTGGACAACAGA    66061       C
                                  TCTGTTG CCAGGCTGGA
                                  ||||||| |||||||||
                                  AGACAAC GGTCCGACCT
                                     A
GAM1602  LOC91380  3'  TCCAGCCTGGGTGACAGAGTGA 66454          TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                        GT
GAM1602  LOC91442  3'  TCCAGCCTGGGCACCAGAGCGA 66648          T
                GA                TCTCGCTCTG TGCCCAGGCTGGA
                                  |||||||||| ||||||||||||
                                  AGAGCGAGAC ACGGGTCCGACCT
                                        C
GAM1602  LOC91547  3'  TCCAGCCTGGGCGACAGAGCGA 67006
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCCGACCT

GAM1602  LOC91750  3'  TCCAGCCTGGGCAACAGAGTGA 67657
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAACGGGTCCGACCT

GAM1602  LOC91812  3'  TCCAGCCTGGGCAACAGAACGA 67821      C
                GA                TCTCG TCTGTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||||||
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                                AGAGC AGACAACGGGTCCGACCT
                                  A
GAM1602 LOC91813 3' TCCAGCCTGGGCAACAGAACGA 67848      C
                GA                TCTCG TCTGTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||||||
                                AGAGC AGACAACGGGTCCGACCT
                                  A
GAM1602 LOC91862 3' TCCAGCCCAGGTGACAGAGCGA 54574          TG  CA
                GA                TCTCGCTCTGT  CC  GGCTGGA
                                  |||||||||||  ||  |||||||
                                AGAGCGAGACA  GG  CCGACCT
                                     GT  AC
GAM1602 LOC91963 5' TCCAGCCTGGGCAACAGAGTGA 68327
                                  TCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||
                                  AGTGAGACAACGGGTCCGACCT

GAM1602 LOC92078 3' TCCAGCCTGGGTGACAGAGTGA 68612          TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                     GT
GAM1602 LOC92223 3' TCCAGCCTGGGCAACAAGAGTG 69055       _
                A                  TCGCTCT GTTGCCCAGGCTGGA
                                  ||||||| ||||||||||||||
                                AGTGAGA CAACGGGTCCGACCT
                                    A
GAM1602 LOC92228 3' CCAGCCTGGGCAACGGAGTGAG 69073
                A                  TCTCGCTCTGTTGCCCAGGCTGG
                                  ||||||||||||||||||||||
                                AGAGTGAGGCAACGGGTCCGACC

GAM1602 LOC92267 3' TCCAGCCTGGGCAACAAGAGAG 69179     G  C
                A                  TCTC CT TGTTGCCCAGGCTGGA
                                  |||| || ||||||||||||||||
                                AGAG GA ACAACGGGTCCGACCT
                                  A _
GAM1602 LOC92299 3' TCCAGCCTGGCGACAAAGCGAG 69373       C      C
                A                  TCTCGCT TGTTGCC AGGCTGGA
                                  ||||||| ||||||| ||||||||
                                AGAGCGA ACAGCGG TCCGACCT
                                    A     _
GAM1602 LOC92340 3' TCCAGCCTAGTAATGGAGCAAG 69568     C        CC
                A                  TCT GCTCTGTTGC  AGGCTGGA
                                  ||| ||||||||||  ||||||||
                                AGA CGAGGTAATG  TCCGACCT
                                  A        A_
GAM1602 LOC92360 3' TCCAGCCTGGGTGACAGAGCAA 69626     C      TG
                GG                 TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
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                                GGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM1602  LOC92405  3'  TCTAGCCTGGGCAACAGAGCAA 69718     C
                GG                 TCT GCTCTGTTGCCCAGGCTGGA
                                   ||| ||||||||||||||||||||
                                   GGA CGAGACAACGGGTCCGATCT
                                     A
GAM1602  LOC92421  3'  TCCAGACTGGGCAACAGAGGGA 69729      G          G
                GA                 TCTC CTCTGTTGCCCAG CTGGA
                                   |||| |||||||||||| |||||
                                   AGAG GAGACAACGGGTC GACCT
                                     G          A
GAM1602  LOC92465  5'  TCCAGCCTGGGCGACAGAGCGA 69955
                GA                 TCTCGCTCTGTTGCCCAGGCTGGA
                                   |||||||||||||||||||||||||
                                   AGAGCGAGACAGCGGGTCCGACCT

GAM1602  LOC92465  5'  TCCAGTCTGGGCAACAGAGCAA 69956     C
                GA                 TCT GCTCTGTTGCCCAGGCTGGA
                                   ||| ||||||||||||||||||||
                                   AGA CGAGACAACGGGTCTGACCT
                                     A
GAM1602  LOC92466  3'  CCAGCCTGGAAAACAAGT    69964     C    GC
                                   GCT TGTT  CCAGGCTGG
                                   ||| ||||  |||||||||
                                   TGA ACAA  GGTCCGACC
                                     _    AA
GAM1602  LOC92466  5'  TCCAGCCTGGGAGACAGAGTGA 69969          TG
                GA                 TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   AGAGTGAGACA  GGGTCCGACCT
                                         GA
GAM1602  LOC92482  3'  CCAGCCTGGGCAACAGAGCAAG 70019     C
                A                   TCT GCTCTGTTGCCCAGGCTGG
                                   ||| ||||||||||||||||||
                                   AGA CGAGACAACGGGTCCGACC
                                     A
GAM1602  LOC92492  3'  TCCAGCCTGGATGACAGCGAGA 70083        CT   GC
                                   TCTCGCT  GTT  CCAGGCTGGA
                                   |||||||  |||  ||||||||||
                                   AGAGCGA  CAG  GGTCCGACCT
                                      __   TA
GAM1602  LOC92499  5'  CCTGGACGACAGAGCAAGA   70105     C        C
                                   TCT GCTCTGTTG CCAGG
                                   ||| ||||||||| |||||
                                   AGA CGAGACAGC GGTCC
                                     A        A
GAM1602  LOC92568  3'  TCCAGCCTGGGTGACAGAGTGA 70331          TG
                GA                 TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
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                                AGAGTGAGACA  GGGTCCGACCT
                                      GT
GAM1602  LOC92573  3'  TCCAGCCTGGGTGACAGAGCGA 70379          TG
             GA                   TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                      GT
GAM1602  LOC92659  3'  CCAGCCTGGGCGACAGAG    70609
                                  CTCTGTTGCCCAGGCTGG
                                  ||||||||||||||||||
                                  GAGACAGCGGGTCCGACC

GAM1602  LOC92771  3'  CCTGAGCAACATAGCGAGA   54210       C     C
                                  TCTCGCT TGTTGC CAGG
                                  |||||||  ||||||  ||||
                                  AGAGCGA ACAACG GTCC
                                      T     A
GAM1602  LOC92771  3'  TCCAGCCTGGGCCACAGAATGA 54215      C     T
             GA                   TCTCG TCTGT GCCCAGGCTGGA
                                  |||||  |||||  ||||||||||||
                                  AGAGT AGACA CGGGTCCGACCT
                                    A     C
GAM1602  LOC92973  5'  TCCAGCCTGGGCAACAGAGTGA 71594
             GG                   TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  GGAGTGAGACAACGGGTCCGACCT

GAM1602  LOC93070  3'  TCCAGCCTGGGCAACAGAGGGA 71815      G
             GA                   TCTC CTCTGTTGCCCAGGCTGGA
                                  ||||  ||||||||||||||||||
                                  AGAG GAGACAACGGGTCCGACCT
                                    G
GAM1602  LOC93132  3'  TCCAGCTCGGGCAACAAAGTGA 72000        C       AG
             GA                   TCTCGCT TGTTGCCC  GCTGGA
                                  |||||||  ||||||||  ||||||
                                  AGAGTGA ACAACGGG  CGACCT
                                     A       CT
GAM1602  LOC93613  3'  TCCAACCTGGGCGGCAGAGTGA 73082               C
             GA                   TCTCGCTCTGTTGCCCAGG TGGA
                                  ||||||||||||||||||  ||||
                                  AGAGTGAGACGGCGGGTCC ACCT
                                              A
GAM1602  LOC96597  5'  CCAGCCTGGGCGACAAGAG   67449      _
                                  CTCT GTTGCCCAGGCTGG
                                  ||||  ||||||||||||||
                                  GAGA CAGCGGGTCCGACC
                                    A
GAM1603  SCAMP1    3'  GCTAAATAAATATTCTCC    54500     T     C
                                  GGA AATATT ATTTAGC
                                  |||  ||||||  |||||||
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                                CCT TTATAA TAAATCG
                                  C     A
GAM1603  SCAMP1   3'  GCTAAATAAATATTCTCC    54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1603  NX-17    3'  TGAATATCAGCCCCTAATA   40706        ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM1603  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
             TA                   TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM1604  BAP1     3'  TTTCTGGGCTCCAACCCAACA  17399     CA  ATCTCA
                                TGTT  GT     AGCCCAGAAA
                                ||||  ||     ||||||||||
                                ACAA  CA     TCGGGTCTTT
                                  CC  ACC___
GAM1604  CD8A     3'  TCTGAATTTGAGATACAAACA  10097     CA        CC
                                TGTT  GTATCTCAAG  CAGA
                                ||||  ||||||||||  ||||
                                ACAA  CATAGAGTTT  GTCT
                                  A_        AA
GAM1604  ETF1     3'  TCTGCAGAGAGATACTAAGCA  17594     C       AAGCC
                                TGTT AGTATCTC    CAGA
                                |||| ||||||||    ||||
                                ACGA TCATAGAG    GTCT
                                  A       AGAC_
GAM1604  KTN1     3'  TTTCTACTTTGTCAGAAACACT 18376        A__  __   CCC
             GAACA                 TGTTCAGT   TCT  CAAG   AGAAA
                                ||||||||   |||  ||||   |||||
                                ACAAGTCA   AGA  GTTT   TCTTT
                                    CAA   CT    CA_
GAM1604  MTL5     3'  TCTCTAGAGAACTACTGAACA  18200         __   A  CCC
                                TGTTCAGTA  TCTC AG   AGA
                                |||||||||  |||| ||   |||
                                ACAAGTCAT  AGAG TC   TCT
                                    CA    A  ___
GAM1604  PAX2     3'  TCCGGCAGGAACTGAACA    15661        A   CAA   CA
                                TGTTCAGT TCT   GCC  GA
                                |||||||| |||   |||  ||
                                ACAAGTCA AGG   CGG  CT
                                    _   A__   C_
GAM1604  PAX2     3'  TCCGGCAGGAACTGAACA    15668        A   CAA   CA
                                TGTTCAGT TCT   GCC  GA
                                |||||||| |||   |||  ||
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                                ACAAGTCA AGG   CGG  CT
                                    _  A__   C_
GAM1604  PEA15    3'  CTGGGCTTGTGAACA       15007       GTATCT
                                TGTTCA     CAAGCCCAG
                                ||||||     |||||||||
                                ACAAGT     GTTCGGGTC
                                  _______
GAM1604  SLC13A3  3'  TCTGGGCTCCTGAGCA      61091        TATCTCA
                                TGTTCAG      AGCCCAGA
                                |||||||      ||||||||
                                ACGAGTC      TCGGGTCT
                                   C_______
GAM1604  USP9Y    5'  TTTCTGGGCTCAGAGGTG    64737       A_
                                TATCTC  AGCCCAGAAA
                                ||||||  ||||||||||
                                GTGGAG  TCGGGTCTTT
                                   AC
GAM1604  AGTRL2   3'  TCTGAGGCCAAAGACACTGAGC 18959        A   CAA   _
             A                   TGTTCAGT TCT   GCC CAGA
                                ||||||||| |||   ||| ||||
                                ACGAGTCA AGA   CGG GTCT
                                    C   AAC   A
GAM1604  C12orf22 3'  TTCTGGGCCACTGGAACA    48713       _   ATCTCAA
                                TGTTC AGT      GCCCAGAA
                                ||||| |||      ||||||||
                                ACAAG TCA      CGGGTCTT
                                  G   C_______
GAM1604  C20orf21 3'  TCTCTTGAAAATACTGAA    35573        C_    CCC
                                TTCAGTAT  TCAAG   AGA
                                ||||||||  |||||   |||
                                AAGTCATA  AGTTC   TCT
                                    AA    ____
GAM1604  D2S448   3'  TCTGGGCTCTCTGTAACA    73893      _   TATCTCA
                                TGTT CAG      AGCCCAGA
                                |||| |||      ||||||||
                                ACAA GTC      TCGGGTCT
                                  T   TC_____
GAM1604  FLJ12484 3'  CTTAGCTTTGAGATACTAAGCA 43173      C         _  CC
                                TGTT AGTATCTCAA GC  AG
                                |||| |||||||||| ||  ||
                                ACGA TCATAGAGTT CG  TC
                                  A        T  AT
GAM1604  FLJ13611 3'  TTTCTGTCACAAATACTGAAC  46870         CTCAAGCC
                                GTTCAGTAT       CAGAAA
                                |||||||||       ||||||
                                CAAGTCATA       GTCTTT
                                     AACACT__
GAM1604  FLJ20294 5'  CTGGGCCTGGTGTGACA     35354     T  G    TCAA
                                TGT CA TATC    GCCCAG
                                ||| || ||||    ||||||
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                                ACA GT GTGG   CGGGTC
                                  _ _   TC__
GAM1604 ITGB5   3' TCCGAGCTTGGGATAAAGCA  60217    TCAG       CCA
                                TGT   TATCTCAAGC  GA
                                |||   ||||||||||  ||
                                ACG   ATAGGGTTCG  CT
                                  AA__       AGC
GAM1604 KIAA0057 3' TCCAAGCTTGAGAGCTCAGCA 25423     C  A      CCA
                                TGTT AGT TCTCAAGC  GA
                                |||| ||| ||||||||  ||
                                ACGA TCG AGAGTTCG  CT
                                  C  _      AAC
GAM1604 KIAA0210 5' TTTCTGAGTGAGATACTGAA  29181          AGCC
                                TTCAGTATCTCA   CAGAAA
                                ||||||||||||   ||||||
                                AAGTCATAGAGT   GTCTTT
                                       GA__
GAM1604 KIAA1317 5' TTCTGGGCTTTCTGAA     87219      TATCTC
                                TTCAG     AAGCCCAGAA
                                |||||     ||||||||||
                                AAGTC     TTCGGGTCTT
                                  T_____
GAM1604 KPNA6   3' CTAAGCTTGAGATAGGGGGC  25540     AG       CC
                                GTTC  TATCTCAAGC  AG
                                ||||  ||||||||||  ||
                                CGGG  ATAGAGTTCG  TC
                                  GG        AA
GAM1604 LHPP    3' TTTCTGGACCCACTGCTGGACA 42368        TCTCAAGC
                                TGTTCAGTA      CCAGAAA
                                |||||||||      |||||||
                                ACAGGTCGT      GGTCTTT
                                     CACCCA__
GAM1604 MGC29891 3' TCCAGGCTTGAGTGACAGAGCA 58872      A  AT      CA
                                TGTTC GT  CTCAAGCC  GA
                                ||||| ||  ||||||||  ||
                                ACGAG CA  GAGTTCGG  CT
                                  A  GT       AC
GAM1604 P2RX1   3' TTCAGGTGCAGACACTGAACA  67754       A  CAA  _  A
                                TGTTCAGT TCT   GC CC GAA
                                |||||||| |||   || || |||
                                ACAAGTCA AGA   CG GG CTT
                                     C   ___  T  A
GAM1604 TCL6    5' TTTGGGCTGAGCACCAAACA  40498     CA  AT   A
                                TGTT  GT  CTCA GCCCAGA
                                ||||  ||  |||| |||||||
                                ACAA  CA  GAGT CGGGTTT
                                  AC  C_   _
GAM1604 TCL6    5' TTTGGGCTGAGCACCAAACA  40522     CA  AT   A
                                TGTT  GT  CTCA GCCCAGA
                                ||||  ||  |||| |||||||
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                                ACAA  CA  GAGT CGGGTTT
                                  AC  C_   _
GAM1604  TCL6     5'  TTTGGGCTGAGCACCAAACA  25921     CA  AT    A
                                TGTT  GT  CTCA GCCCAGA
                                ||||  ||  |||| |||||||
                                ACAA  CA  GAGT CGGGTTT
                                  AC  C_   _
GAM1604  TCL6     5'  TTTGGGCTGAGCACCAAACA  27773     CA  AT    A
                                TGTT  GT  CTCA GCCCAGA
                                ||||  ||  |||| |||||||
                                ACAA  CA  GAGT CGGGTTT
                                  AC  C_   _
GAM1604  TRAP-1   3'  TTCTGAGCCTGCTGGACA    16195        TCTCAA  C
                                TGTTCAGTA     GC CAGAA
                                |||||||||     || |||||
                                ACAGGTCGT     CG GTCTT
                                     C_____  A
GAM1604  LOC147184 5'  TCTGGGCTTGCCCTGAA     59872      TATCT
                                TTCAG    CAAGCCCAGA
                                |||||    ||||||||||
                                AAGTC    GTTCGGGTCT
                                  CC___
GAM1604  LOC158230 3'  TTTGTAAGATGCTGAACA    82703          __
                                TGTTCAGTATCT  CAAG
                                ||||||||||||  ||||
                                ACAAGTCGTAGA  GTTT
                                      AT
GAM1604  LOC200830 3'  CTGGGATGATGATACTGAATA  91726          _  AG
                                TGTTCAGTATC TCA  CCCAG
                                |||||||||||| |||  |||||
                                ATAAGTCATAG AGT  GGGTC
                                      T  A_
GAM1604  LOC221002 3'  TTCTGGGCTGTGACTGAA    93112       ATCTCA
                                TTCAGT     AGCCCAGAA
                                ||||||     |||||||||
                                AAGTCA     TCGGGTCTT
                                   GTG___
GAM1604  LOC221632 3'  CTGGGTTACTACTGAACA    95448        TCTCA
                                TGTTCAGTA    AGCCCAG
                                |||||||||    |||||||
                                ACAAGTCAT    TTGGGTC
                                     CA___
GAM1604  LOC222233 5'  CTAGGCTTGAGAATTGA     95904      A       C
                                TCAGT TCTCAAGCC AG
                                ||||| ||||||||| ||
                                AGTTA AGAGTTCGG TC
                                  _       A
GAM1604  LOC253044 3'  TCTGGGCTTTGTCCTGAGACA  98363     _   T  CTC
                                TGT TCAG AT   AAGCCCAGA
                                ||| |||| ||   |||||||||
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                                ACA AGTC TG   TTCGGGTCT
                                  G   C  T__
GAM1604  LOC256032 5'  CTGAGCCTGCTGCTGAAC    99360        TCT  A  C
                                GTTCAGTA   CA GC CAG
                                ||||||||   || || |||
                                CAAGTCGT   GT CG GTC
                                    C__  C  A
GAM1604  LOC51580  3'  TTCTGATAAGTACTGAACA   32431         CTCAAGCC
                                TGTTCAGTAT       CAGAA
                                ||||||||||       |||||
                                ACAAGTCATG       GTCTT
                                     AATA____
GAM1604  LOC90826  5'  TTCTGTAGATACTGAA      64789         CAAGCC
                                TTCAGTATCT     CAGAA
                                ||||||||||     |||||
                                AAGTCATAGA     GTCTT
                                     T_____
GAM1605  MFAP4     3'  AGAACACAGCTACCGCACACCA 69786    A      C  C  CCC
                                TG TGTGCGGT GC TG   TTCT
                                || |||||||| || ||   ||||
                                AC ACACGCCA CG AC   AAGA
                                 C       T  _  AC_
GAM1605  SLC22A7   3'  AGAAGGGCAGGCCCTGCAACTC 22883     TG    TC
           A                     TGA  TGCGG  GCCTGCCCTTCT
                                |||  |||||  ||||||||||||
                                ACT  ACGTC  CGGACGGGAAGA
                                  CA    C_
GAM1605  SLC22A7   3'  AGAAGGGCAGGCCCTTCAACTC 22884     TG  C  TC
           A                     TGA  TG GG  GCCTGCCCTTCT
                                |||  ||  ||  ||||||||||||
                                ACT  AC TC  CGGACGGGAAGA
                                  CA  T  C_
GAM1605  KIAA0295  3'  AGAAGAGCAGGTGAAAGCCACC 68657    A  T  GG      C
           A                     TG TG GC  TCGCCTGC CTTCT
                                || || ||  |||||||| |||||
                                AC AC CG  AGTGGACG GAAGA
                                 C  _  AA       A
GAM1606  AIRE      3'  TGGGAGCCTGAGGCATGAGAA  7247      C     C
                                TTC CATGCC CAGGCTCCTG
                                ||| |||||| ||||||||||
                                AAG GTACGG GTCCGAGGGT
                                  A     A
GAM1606  BCAS1     3'  CTCGGGAGCCCAACGCACGAGA 14711     CCA   CCCA      C
           A                     TTC   TGC    GGCTCCTG AG
                                |||   |||    |||||||| ||
                                AAG   ACG    CCGAGGGC TC
                                  AGC   CAAC       _
GAM1606  DAG1      3'  CTGCAGGATGTAACATGG    16553       CCCCAG  _
                                CCATG     GC TCCTGCAG
                                |||||     || ||||||||
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                                GGTAC     TG AGGACGTC
                                  AA____  T
GAM1606  GPRK7    3'  CGGGAGCCTGAGGCAGGAGAA  58313     _ A   C
                                TTC CC TGCC CAGGCTCCTG
                                ||| || |||| ||||||||||
                                AAG GG ACGG GTCCGAGGGC
                                  A _   A
GAM1606  KIF1B    3'  TGGGAGCCTGAGGCAGGAGAA  31273     _ A   C
                                TTC CC TGCC CAGGCTCCTG
                                ||| || |||| ||||||||||
                                AAG GG ACGG GTCCGAGGGT
                                  A _   A
GAM1606  NCAM1    5'  CTGCAGGGGGGGGGGCACAGAA 7040      CCA     AGG
                                TTC   TGCCCC   CTCCTGCAG
                                |||   ||||||   |||||||||
                                AAG   ACGGGG   GGGGACGTC
                                  AC_     GG_
GAM1606  NOS1     3'  CTGCAGGGTCCCCAAGGATGG  7095      G  CCA_  CT
                                CCAT CC    GG  CCTGCAG
                                |||| ||    ||  |||||||
                                GGTA GG    CC  GGACGTC
                                  _ AACC  TG
GAM1606  PDGFRB   3'  TGCCCCAGGGACATGGGAA   66584        _   CA  CTCCT
                                TTCCCATG CCC  GG    GCA
                                |||||||| |||  ||    |||
                                AAGGGTAC GGG  CC    CGT
                                     A   AC  ____
GAM1606  RAB31    3'  CTGCAGGGGGGCGGGGCAGGAA  23440     CA     AGG
                                TTCC  TGCCCC   CTCCTGCAG
                                ||||  ||||||   |||||||||
                                AAGG  ACGGGG   GGGGACGTC
                                  __      CG_
GAM1606  SCN4A    3'  CTGCGTTCCCAGACCATGGGAA 6200         CCCCA  CTCC
                                TTCCCATG    GG    TGCAG
                                ||||||||    ||    |||||
                                AAGGGTAC    CC    GCGTC
                                     CAGAC  TT__
GAM1606  WHSC1    3'  CTGCAATGACTGCAGGGCTGGG 24667       T   __   GCTCC
             AA                   TTCCCA GCCC  CAG    TGCAG
                                ||||||  ||||  |||    |||||
                                AAGGGT CGGG  GTC    ACGTC
                                  _    AC   AGTA_
GAM1606  WHSC1    3'  CTGCAATGACTGCAGGGCTGGG 24668       T   __   GCTCC
             AA                   TTCCCA GCCC  CAG    TGCAG
                                ||||||  ||||  |||    |||||
                                AAGGGT CGGG  GTC    ACGTC
                                  _    AC   AGTA_
GAM1606  WHSC1    3'  CTGCAATGACTGCAGGGCTGGG 24669       T   __   GCTCC
             AA                   TTCCCA GCCC  CAG    TGCAG
                                ||||||  ||||  |||    |||||
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                                AAGGGT CGGG  GTC    ACGTC
                                   _   AC   AGTA_
GAM1606  ZFP36L1   3'  CTGCAGGAAGGAAGGCTG    18201    T  __  AGGC
                                CA GCC  CC    TCCTGCAG
                                || |||  ||    ||||||||
                                GT CGG  GG    AGGACGTC
                                 _   AA  A___
GAM1606  C20orf64  5'  CAGAGCCCTTCCTGCAGGGAA  54335      A   CCCA__    C
                                TTCCC TGC     GGCTC TG
                                ||||| |||     ||||| ||
                                AAGGG ACG     CCGAG AC
                                   _  TCCTTC
GAM1606  DRIL2     3'  CTGCAGGGTGTGGGCAGAGAA  22350     CCA    C G  T
                                TTC   TGCCC A GC CCTGCAG
                                |||   ||||| | || |||||||
                                AAG   ACGGG T TG GGACGTC
                                  AG_    _ G  _
GAM1606  FEM-2     3'  CTGCAGGGCCAAGCCACAGGAA 28312     CAT_  CCCA   T
                                TTCC    GC    GGC CCTGCAG
                                ||||    ||    ||| |||||||
                                AAGG    CG    CCG GGACGTC
                                   ACAC  AA__   _
GAM1606  FLJ10737  3'  CTGCAGTCCAAGCTGAACATGG 37054        CCCCA    C___
            GAA                   TTCCCATG    GGCT    CTGCAG
                                |||||||     ||||    ||||||
                                AAGGGTAC    TCGA    GACGTC
                                     AAG__    ACCT
GAM1606  FLJ10898  5'  CTGCCAAACCTGCAACATGGGA 60133        CCC    CTCCT
            A                    TTCCCATG   CAGG    GCAG
                                |||||||   ||||    ||||
                                AAGGGTAC   GTCC    CGTC
                                     AAC    AAAC_
GAM1606  FLJ11618  3'  CTGCAGGGGGAAGAGCCGGGAA 42624      AT  CCCAGG
                                TTCCC  GC     CTCCTGCAG
                                |||||  ||     |||||||||
                                AAGGG  CG     GGGGACGTC
                                   C_  AGAAG_
GAM1606  FLJ12287  5'  TGCCTCTGGGGCCTGGGAA    42564       T       CTCCT
                                TTCCCA GCCCCAGG     GCA
                                ||||||  ||||||||     |||
                                AAGGGT CGGGGTCT     CGT
                                    C       C_____
GAM1606  FLJ14129  3'  TGGGAGCCTGGGGCAGGAGAA  48814     _ A
                                TTC CC TGCCCCAGGCTCCTG
                                ||| || ||||||||||||||
                                AAG GG ACGGGGTCCGAGGGT
                                  A  _
GAM1606  KIAA0187  3'  CTGCAGGAGGAGGAACAGAGAA 29250     CCA  CC  AGG
                                TTC   TG  CC   CTCCTGCAG
                                |||   ||  ||   |||||||||
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                                AAG   AC  GG   GAGGACGTC
                                  AG_  AA  AG_
GAM1606  KIAA0416  5'  GGAAAGCCTGGGACACAGAA   32093     CCA  C      __
                                TTC   TG CCCAGGC  TCC
                                |||   || |||||||  |||
                                AAG   AC GGGTCCG  AGG
                                  AC_  A      AA
GAM1606  KIAA1266  3'  CTGCAAGGGCGAGCATGGGA   66695        CCCAG    C
                                TCCCATGC    GCTC TGCAG
                                ||||||||    |||| |||||
                                AGGGTACG    CGGG ACGTC
                                     AG___    A
GAM1606  KIAA1483  3'  CTGCAGGGAAAAGGATATAGGA 70434      C   C  CAGG T
             A                   TTCC ATG CC    C CCTGCAG
                                |||| ||| ||    | |||||||
                                AAGG TAT GG    G GGACGTC
                                  A   A  AAAA _
GAM1606  KIAA1706  3'  TGCAGTGAGAGCATGGGA    94372        CCCAGG   _
                                TCCCATGC     CTC CTGCA
                                ||||||||     ||| |||||
                                AGGGTACG     GAG GACGT
                                     A_____   T
GAM1606  KIAA1715  3'  CTCAGGAGCCTGAGGCAGGAGA 68684     _ A    C        C
             A                   TTC CC TGCC CAGGCTCCTG AG
                                ||| || |||| |||||||||| ||
                                AAG GG ACGG GTCCGAGGAC TC
                                  A  _    A         _
GAM1606  KIAA1981  3'  CAGGAGCCAAGGTCACAGAA   89710     CCA  C  CA
                                TTC   TG CC  GGCTCCTG
                                |||   || ||  ||||||||
                                AAG   AC GG  CCGAGGAC
                                  AC_  T  AA
GAM1606  MCAM      3'  CAGGAACCTGGGGGCCTGTGAA 22457     C  T    _   C
                                TTC CA GCCCC AGG TCCTG
                                ||| || ||||| ||| |||||
                                AAG GT CGGGG TCC AGGAC
                                  T  C    G   A
GAM1606  MRPS24    3'  CTGCAGAGAATGGAAACGTGGG 50130         CC_   GG   C
             AA                    TTCCCATG   CCA  CTC TGCAG
                                |||||||   |||  ||| |||||
                                AAGGGTGC   GGT  GAG ACGTC
                                     AAA   AA   _
GAM1606  MSE55     3'  TGCAGGACAGACATGGGAG    23916        CCCCAGGC
                                TTCCCATG       TCCTGCA
                                ||||||||       |||||||
                                GAGGGTAC       AGGACGT
                                     AGAC_____
GAM1606  OS4       3'  CTGCTTTGTGCTAAAAGCATGG 20388         CCCA   TCCT_
             GAA                    TTCCCATGC    GGC    GCAG
                                |||||||||   |||    ||||
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                                AAGGGTACG   TCG    CGTC
                                     AAAA   TGTTT
GAM1606  PASK     5'  CAGGGTCTCGCCTGGGGCATTA 31405     CC        ____
              GAA                   TTC  ATGCCCCAGGC   TCCTG
                                |||  ||||||||||   |||||
                                AAG  TACGGGGTCCG   GGGAC
                                  AT         CTCT
GAM1606  PRO1163   3'  CTGAATGAGCCTGGGGCA    38323          CTG
                                TGCCCCAGGCTC   CAG
                                ||||||||||||  |||
                                ACGGGGTCCGAG   GTC
                                       TAA
GAM1606  THEA     3'  CTCAGGAAGCTGAGGCACAAGA 66887     CCA   C   GC    C
              A                    TTC   TGCC CAG  TCCTG AG
                                |||   |||| |||  ||||| ||
                                AAG   ACGG GTC  AGGAC TC
                                  AAC    A   GA    _
GAM1606  WFDC3    3'  GCTGACCAGAGCATGGGAA   98702        CCCA  C  CT
                                TTCCCATGC    GG TC  GC
                                |||||||||    || ||  ||
                                AAGGGTACG    CC AG  CG
                                     AGA_  _  T_
GAM1606  LOC122726 5'  CTGCAGGAAACACTGAGGCTTG 76103       T   C   GC__
              GGAA                   TTCCCA GCC CAG    TCCTGCAG
                                |||||| ||| |||    ||||||||
                                AAGGGT CGG GTC    AGGACGTC
                                    T   A   ACAA
GAM1606  LOC129303 3'  CTGCAGGAATTGGGGGCTGGGA 75373       T     AG C
              A                    TTCCCA GCCCC  G TCCTGCAG
                                |||||| |||||  | ||||||||
                                AAGGGT CGGGG  T AGGACGTC
                                    _    GT A
GAM1606  LOC132617 5'  CTGCAGATCGAGGCATGGGA   76415        CCA  CTC
                                TCCCATGCC   GG   CTGCAG
                                |||||||||   ||   ||||||
                                AGGGTACGG   CT   GACGTC
                                     AG_  A__
GAM1606  LOC145945 5'  AGGGCCTGGACCATAGAA    84563     CC   CC     T
                                TTC  ATG  CCAGGC CCT
                                |||  |||  |||||| |||
                                AAG  TAC  GGTCCG GGA
                                  A_   CA     _
GAM1606  LOC146332 3'  CAGGAGCCTGGGGCCTGTGGA  78353     _  T
                                TCC CA GCCCCAGGCTCCTG
                                ||| || ||||||||||||||
                                AGG GT CGGGGTCCGAGGAC
                                  T  C
GAM1606  LOC146714 5'  TGCAGGGCAGGCACAGGGA   84754      A_   CCAG  T
                                TCCC  TGCC    GC CCTGCA
                                ||||  ||||    || ||||||
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                                AGGG  ACGG    CG GGACGT
                                  AC    A___  _
GAM1606  LOC147958 3'  CTGCAGGGCAGGCAGCAGAA   88523     CCA    CCAG  T
                                TTC   TGCC    GC CCTGCAG
                                |||   ||||    || |||||||
                                AAG   ACGG    CG GGACGTC
                                  ACG    A___  _
GAM1606  LOC149501 3'  CTGCAAGAGCCTGGCTGGGAA  75800       T   CC     C
                                TTCCCA GCC  AGGCTC TGCAG
                                |||||| |||  |||||| |||||
                                AAGGGT CGG  TCCGAG ACGTC
                                   _  __     A
GAM1606  LOC150397 3'  CAGGAGCCTGAGTGAAGGA    80655     CA   CC
                                TCC  TGC  CAGGCTCCTG
                                |||  |||  ||||||||||
                                AGG  GTG  GTCCGAGGAC
                                  AA   A_
GAM1606  LOC150397 3'  GCAGGAGCCTGCAGGAGA     80664    _ A   CCC
                                TC CC TGC   AGGCTCCTGC
                                || || |||   ||||||||||
                                AG GG ACG   TCCGAGGACG
                                 A  _  ____
GAM1606  LOC150517 5'  CTGCAGGTAGGAGCACAGAA   80725     CCA   C  AGGCT
                                TTC   TGC CC    CCTGCAG
                                |||   ||| ||    |||||||
                                AAG   ACG GG    GGACGTC
                                  AC_   A  AT___
GAM1606  LOC153688 3'  TGGGAGGCTGGGGCATGAGAA  87341     C        G
                                TTC CATGCCCCAG CTCCTG
                                ||| |||||||||| ||||||
                                AAG GTACGGGGTC GAGGGT
                                  A         G
GAM1606  LOC154849 3'  CTGCAGGAGGTGGAAGATG    60941     GCC   GG
                                CAT   CCA  CTCCTGCAG
                                |||   |||  |||||||||
                                GTA   GGT  GAGGACGTC
                                  GAA   G_
GAM1606  LOC162137 3'  GCAGGAGCTTCCCATAAAGAA  88480     CC_   CCCC
                                TTC   ATG    AGGCTCCTGC
                                |||   |||    ||||||||||
                                AAG   TAC    TTCGAGGACG
                                  AAA   CC__
GAM1606  LOC219654 3'  CAGGAGCCCAGGGGATGGGAA  92925        G   CA
                                TTCCCAT CCC  GGCTCCTG
                                ||||||| |||  ||||||||
                                AAGGGTA GGG  CCGAGGAC
                                    G   AC
GAM1606  LOC255042 3'  CTCGGGAGCCTGAGGCAGGAGA 97042     _ A    C        C
            A                    TTC CC TGCC CAGGCTCCTG AG
                                ||| || |||| |||||||||| ||
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                                AAG GG ACGG GTCCGAGGGC TC
                                  A _   A       _
GAM1606 LOC257000 3' CTGCAGGACTCAGAGCATGG  98587      CCCA  C
                                CCATGC   GG TCCTGCAG
                                ||||||   || ||||||||
                                GGTACG   TC AGGACGTC
                                   AGAC  _
GAM1606 LOC91750  3' TGGGGGCCTGAGGCACGAGAA 67659    CCA   C
                                TTC   TGCC CAGGCTCCTG
                                |||   |||| ||||||||||
                                AAG   ACGG GTCCGGGGGT
                                  AGC   A
GAM1607 HAL      5' GCCACTCCTGCATAAAGCTC  10903        TGAAAA
                                GAGCTTTATGC     GGTGGC
                                ||||||||||     ||||||
                                CTCGAAATACG     TCACCG
                                      TCC___
GAM1607 HMGN2    3' GGCCACCTTGGCACAAAAGC  19809     A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _  GG
GAM1607 NMI      5' GGCCACCTCCTCAGGAAG    17436     ATG   AA
                                CTTT   CTGA  AGGTGGCC
                                ||||   ||||  ||||||||
                                GAAG   GACT  TCCACCGG
                                  ___    CC
GAM1607 PACE     3' GGCCACCTCTCCAAGGGCTT  11944       A  CT  AAA
                                GAGCTTT TG  GA   GGTGGCC
                                ||||||| ||  ||   |||||||
                                TTCGGGA AC  CT   CCACCGG
                                   _ CT  ___
GAM1607 PYCR1    3' CCACCTTCCTCTAGAGCTC   70639       TGCT  A_
                                GAGCTTTA   GA  AAGGTGG
                                ||||||||   ||  |||||||
                                CTCGAGAT   CT  TTCCACC
                                    _____  CC
GAM1607 SDC1     3' GGCCACCTCCCCAGCATTCCAG 12991    TT_    AAA
           C                     GCT   ATGCTG   AGGTGGCC
                                |||   ||||||   ||||||||
                                CGA   TACGAC   TCCACCGG
                                  CCT     CCC
GAM1607 FLJ11560 5' GCCCAGGCCCAGCATAAAG   48008        AAAA  ___
                                CTTTATGCTG   GGT   GGC
                                ||||||||||   |||   |||
                                GAAATACGAC   CCG   CCG
                                      _____  GAC
GAM1607 KIAA0446 5' CCACCTTTTGAAGAGCTC    69446       ATGCTG
                                GAGCTTT     AAAAGGTGG
                                |||||||     |||||||||
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                                CTCGAGA     TTTTCCACC
                                    AG____
GAM1607 KIAA0971 3' GTTGTTCTCAGCATAAAGT   30677          AAA  TG
                                GCTTTATGCTGA   GG  GC
                                ||||||||||||   ||  ||
                                TGAAATACGACT   TT  TG
                                       C__  GT
GAM1607 KIAA1393 3' GGCCACCTTGGCACAAAAGC  72574      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                   _ _ GG
GAM1607 KIAA1656 3' GGCCACCTCCTCCTAGAAGCC 66377   A    ATGCT  AA
                                G GCTTT    GA  AGGTGGCC
                                | |||||    ||  ||||||||
                                C CGAAG    CT  TCCACCGG
                                _    ATC__  CC
GAM1607 KIAA1884 3' GCCACCTTCATCTACCAAGGCT 73728       ATGCT  A_
             C                   GAGCTTT    GA  AAGGTGGC
                                 |||||||    ||  ||||||||
                                 CTCGGAA    CT  TTCCACCG
                                     CCAT_  AC
GAM1607 PP3501   3' GGCCACCGTTGACAGCATAAAG 41683         AAAA_
                                CTTTATGCTG    GGTGGCC
                                ||||||||||    |||||||
                                GAAATACGAC    CCACCGG
                                      AGTTG
GAM1607 SDCCAG3  3' GGTGTTCTCAGCATGAAGCTC  22803           AAA  TG
                                GAGCTTTATGCTGA   GG  GCC
                                ||||||||||||||   ||  |||
                                CTCGAAGTACGACT   CT  TGG
                                       ___  TG
GAM1607 SP140    3' GGCCACCTCCATGCAGAAGC   24327      A  TGAAA
                                GCTTT TGC    AGGTGGCC
                                ||||| |||    ||||||||
                                CGAAG ACG    TCCACCGG
                                   _  TACC_
GAM1607 LOC148760 3' GGCCACCTTCTCCAACAAGCTC 85364       TA  CT  A
                                GAGCTT  TG  GA AAGGTGGCC
                                ||||||  ||  || |||||||||
                                CTCGAA  AC  CT TTCCACCGG
                                    CA  __  C
GAM1607 LOC150170 5' ACCTGTTTCACATAAAGC    80414        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                     _    G
GAM1607 LOC150175 5' ACCTGTTTCACATAAAGC    80453        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
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                                CGAAATAC ACTTT TCCA
                                     _    G
GAM1607  LOC150215 5'  ACCTGTTTCACATAAAGC    80456        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                     _    G
GAM1607  LOC150218 5'  ACCTGTTTCACATAAAGC    80525        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                     _    G
GAM1607  LOC152065 3'  GGCCACCTTCTCCTTGGCAGGC 86737      TTA   ___  A
           TC                    GAGCT   TGCT   GA AAGGTGGCC
                                |||||   ||||   || |||||||||
                                CTCGG   ACGG   CT TTCCACCGG
                                  ___   TTC  C
GAM1607  LOC152267 3'  GGCCACCTTGGCACAAAAGC   61036      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _  GG
GAM1607  LOC158292 5'  CCTCTGGACCCAGCATAAGGCT 88046           AAAA_  T
           C                     GAGCTTTATGCTG    GG GG
                                ||||||||||||    || ||
                                CTCGGAATACGAC    TC CC
                                      CCAGG  T
GAM1607  LOC219997 3'  GCCACCTCTTCAGCCTC    93256    CTTTAT    A
                                GAG     GCTGAA AGGTGGC
                                |||     |||||| |||||||
                                CTC     CGACTT TCCACCG
                                  _______     C
GAM1607  LOC256269 3'  GGCCACCTTGGCACAAAAGC   96608      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _  GG
GAM1607  LOC91963  5'  GGCCACCTCCTCTGAGAAGC   68321      ATGCT  AA
                                GCTTT    GA  AGGTGGCC
                                |||||    ||  ||||||||
                                CGAAG    CT  TCCACCGG
                                   AGT__  CC
GAM1608  BCL2     3'  AATGACAGCTGACAGGGTC    7148          A  ACTA
                                GACCCTGTTA CT    CGTT
                                |||||||||| ||   ||||
                                CTGGGACAGT GA    GTAA
                                      C  CA__
GAM1608  DMP1     3'  ACGTAGCTAACAGAGTT     16610     C     ACTA
                                GAC CTGTTA    CTACGT
                                ||| ||||||    ||||||
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                                TTG GACAAT    GATGCA
                                  A     C___
GAM1608  RBBP2    3'  CAACTAGGAGTAACAGGG    18569        A  A   C
                                CCCTGTTA CT CTA GTTG
                                |||||||| || ||| ||||
                                GGGACAAT GA GAT CAAC
                                    _  G   _
GAM1608  ICK      3'  CAACATGAAGGTTAACACAGTC 30593     CC       AC  C
                                GAC  TGTTAACT  TA GTTG
                                |||  ||||||||  || ||||
                                CTG  ACAATTGG  GT CAAC
                                  AC       AA  A
GAM1608  NR6A1    3'  CAACGTAGTATTGAACAG    54016      AAC
                                CTGTT   TACTACGTTG
                                |||||   ||||||||||
                                GACAA   ATGATGCAAC
                                   GTT
GAM1608  NR6A1    3'  CAACGTAGTATTGAACAG    54022      AAC
                                CTGTT   TACTACGTTG
                                |||||   ||||||||||
                                GACAA   ATGATGCAAC
                                   GTT
GAM1608  NR6A1    3'  CAACGTAGTATTGAACAG    9443       AAC
                                CTGTT   TACTACGTTG
                                |||||   ||||||||||
                                GACAA   ATGATGCAAC
                                   GTT
GAM1608  LOC57399 5'  CAACAGGTGAAACCAACAGGGT 40707         AAC__    AC
              T                  GACCCTGTT    TACT  GTTG
                                |||||||||    ||||  ||||
                                TTGGGACAA    GTGG  CAAC
                                     CCAAA    A_
GAM1609  CTGF     3'  AGTTGTTCCTTAAGTCAG    10337         CT
                                CTGACTTGG  GGCAACT
                                |||||||||  |||||||
                                GACTGAATT  TTGTTGA
                                     CC
GAM1609  LANCL1   3'  GTTTTCAATCAGCGAT     21334         C    CT
                                ATCGCTGA TTGG  GGC
                                |||||||| ||||  |||
                                TAGCGACT AACT  TTG
                                     _    T_
GAM1609  NPTX1    3'  AGCTGCCACTGGCCGGCGA   11831       AC TG C     A
                                TCGCTG  T  G TGGCA CT
                                ||||||  |  | ||||| ||
                                AGCGGC  G  C ACCGT GA
                                   C_ GT _     C
GAM1609  PPP2R2B  3'  AGCTGCCAGCTAACAGT     17116      AC         A
                                GCTG  TTGGCTGGCA CT
                                ||||  |||||||||| ||
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                                TGAC  AATCGACCGT GA
                                  __        C
GAM1609 SGK     3' GAGCCGCCAGCTGACAGGA   20064    G   AC TG     AA
                                TC CTG  T  GCTGGC  CTC
                                || |||  |  ||||||  |||
                                AG GAC  A  CGACCG  GAG
                                 _  __ GT     CC
GAM1609 CDC14B  3' AGTCGCCAGCCAGAAACGTG  54000    TGAC       A
                                CGC    TTGGCTGGC ACT
                                |||    ||||||||| |||
                                GTG    GACCGACCG TGA
                                  CAAA        C
GAM1609 GMPPB   5' GAGCTGCCAGCCAAAGGC    97448    GAC        A
                                GCT   TTGGCTGGCA CTC
                                |||   |||||||||| |||
                                CGG   AACCGACCGT GAG
                                  A__         C
GAM1609 KIAA0436 3' GAGCTGTTGCCAAATCAGTGAT 60686        C    T    A
                                ATCGCTGA TTGGC GGCA CTC
                                |||||||| ||||| |||| |||
                                TAGTGACT AACCG TTGT GAG
                                     A    _   C
GAM1609 KIAA1024 3' AGCTGCCTGCTAACGATG    69614      CTGAC    T    A
                                CATCG    TTGGC GGCA CT
                                |||||    ||||| |||| ||
                                GTAGC    AATCG CCGT GA
                                   _____    T   C
GAM1609 KIAA1266 3' CAGCCAAACCAGCTGATG    66692     _    AC
                                CATC GCTG  TTGGCTG
                                |||| ||||  |||||||
                                GTAG CGAC  AACCGAC
                                  T   CA
GAM1609 MGC20486 5' AGTTGCCAGACGGCCAGC    54524     A  TGG
                                GCTG CT   CTGGCAACT
                                |||| ||   |||||||||
                                CGAC GG   GACCGTTGA
                                  C  CA_
GAM1609 RTBDN   3' AGTCGCCAGCTAGAGC     49495     GAC       A
                                GCT   TTGGCTGGC ACT
                                |||   ||||||||| |||
                                CGA   GATCGACCG TGA
                                  ___        C
GAM1609 SQV7L   5' CCATGCCCAGCCAGAGATG   71093     G   A  T   _
                                CATC CTG CT GGC TGG
                                |||| ||| || ||| |||
                                GTAG GAC GA CCG ACC
                                  A   C  C   T
GAM1609 LOC121036 3' AGTTGCCAGCTTGAGTGATG   74479        GACTT
                                CATCGCT    GGCTGGCAACT
                                |||||||    ||||||||||
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                                GTAGTGA    TCGACCGTTGA
                                   GT___
GAM1609  LOC144512 5'  GCCACCAGGATACAGTGATG   84037        A__    C
                                CATCGCTG   CTTGG TGGC
                                ||||||||   ||||| ||||
                                GTAGTGAC   GGACC ACCG
                                    ATA    _
GAM1609  LOC147042 3'  AGTTGCCAACTTCAGGA     84991    G   CTT  C
                                TC CTGA   GG TGGCAACT
                                || ||||   || ||||||||
                                AG GACT   TC ACCGTTGA
                                 _   ___  A
GAM1609  LOC157653 5'  GAGTTGCCTTTCAACCAGC    82445     AC   CT
                                GCTG  TTGG  GGCAACTC
                                ||||  ||||  ||||||||
                                CGAC  AACT  CCGTTGAG
                                  C_   TT
GAM1609  LOC158237 5'  CCAACCAAGTCAGAAATG    61081     CG       C
                                CAT  CTGACTTGG TGG
                                |||  |||||||||| |||
                                GTA  GACTGAACC ACC
                                  AA        A
GAM1609  LOC254143 5'  GCCACCAGGATACAGTGATG   98252        A__    C
                                CATCGCTG   CTTGG TGGC
                                ||||||||   ||||| ||||
                                GTAGTGAC   GGACC ACCG
                                    ATA    _
GAM1609  LOC256286 3'  AGCTGCCCAGCCAGCGCG    96894     TGAC      _ A
                                CGC    TTGGCTGG CA CT
                                |||    |||||||| || ||
                                GCG    GACCGACC GT GA
                                  C___       C  C
GAM1610  ORC1L     3'  AGGGCTTCACCATGTTGC     15980         CT
                                GCAACATGG  GAGCCTT
                                |||||||||  |||||||
                                CGTTGTACC  TTCGGGA
                                     AC
GAM1610  KIAA1164  3'  TGAAAGACTATTGCTGCTGC   70053     A  TG  TG_  C
                                GCA CA  GC   AG CTTTCA
                                ||| ||  ||   || ||||||
                                CGT GT  CG   TC GAAAGT
                                  C  __  TTA  A
GAM1610  KIAA1804  3'  AAAAGCTGTGGCCATGTTCCTA 70344      C        _  C
              A                  TTAG AACATGGCTG AGC TTT
                                 |||| |||||||||| ||| |||
                                 AATC TTGTACCGGT TCG AAA
                                   C         G   A
GAM1610  LRRN3     3'  GAAAGACTGCAGTTGTGCTAA  69978       A  TG    _  C
                                TTAGCA CA  GCTG AG CTTTC
                                ||||||  ||  ||||  ||  |||||
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                                AATCGT GT  TGAC TC GAAAG
                                   _ __    G  A
GAM1610  PRO2289   3'  TGAAAGGTGTGCACACGTTAGT 38414    _   A  _  TGA
                                GC AAC TG GC   GCCTTTCA
                                || ||| || ||   ||||||||
                                TG TTG AC CG   TGGAAAGT
                                 A   C  A  TG_
GAM1610  RALGPS1A  3'  AAAGGCTCAACAGACTGA    28326      CAACA  GC
                                TTAG    TG  TGAGCCTTT
                                ||||    ||  |||||||||
                                AGTC    AC  ACTCGGAAA
                                  AG___  A_
GAM1610  LOC121441 3'  TGAAAGCTTTAGCCATCCACTA 74504      CAAC        C
            A                    TTAG    ATGGCTGAG CTTTCA
                                ||||    ||||||||| ||||||
                                AATC    TACCGATTT GAAAGT
                                  ACC_        C
GAM1610  LOC153603 5'  TGAATTTCAGCCACATCCCTAA 81778      CAACA       CCT
                                TTAG    TGGCTGAG   TTCA
                                ||||    ||||||||   ||||
                                AATC    ACCGACTT   AAGT
                                  CCTAC       T__
GAM1610  LOC158450 5'  TGAAAGGCCCAACCCATGT    82816       C_  A
                                ACATGG  TG GCCTTTCA
                                ||||||  || ||||||||
                                TGTACC  AC CGGAAAGT
                                   CA  C
GAM1610  LOC158504 5'  TGAAAGGCCCAACCCATGT    82830       C_  A
                                ACATGG  TG GCCTTTCA
                                ||||||  || ||||||||
                                TGTACC  AC CGGAAAGT
                                   CA  C
GAM1611  ADH5      3'  GCTTCTGTGATATTATCTTTAA 7267            T   TT_
                                TTAGGGATAATAT CAT   AGC
                                |||||||||||| |||   |||
                                AATTTCTATTATA GTG   TCG
                                       _   TCT
GAM1611  AES       3'  GTTAGGTGGATACCTGCCCTGA 8525        ATAA
                                TTAGGG    TATTCATTTAGC
                                ||||||    ||||||||||||
                                AGTCCC    ATAGGTGGATTG
                                   GTCC
GAM1611  AGL       3'  GCCATTTGGGGTTATCTCTAGT 7215            A    TTTA
            A                    TATTAGGGATAAT TTCA    GC
                                |||||||||||| ||||    ||
                                ATGATCTCTATTG GGGT    CG
                                       _    TTAC
GAM1611  APAF1     3'  GTTGGATGAATAATATTAATG  25979    GG    A
                                TA  GATA TATTCATTTAGC
                                ||  |||| ||||||||||||
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                                GT  TTAT ATAAGTAGGTTG
                                 AA    A
GAM1611  APM1     3'  GCTAAATGGACATCATGTTTTC 17784       GG TA___  A
              TGGTG                   TATTAG  A     AT TTCATTTAGC
                                |||||| |    || ||||||||||
                                GTGGTC  T    TA AGGTAAATCG
                                   TT TGTAC  C
GAM1611  APXL     3'  CTAATGGTTGGCCCTGGTG   9713         A   ATTCAT
                                TATTAGGG TAAT     TTAG
                                |||||||| ||||     ||||
                                GTGGTCCC GTTG     AATC
                                     G   GT____
GAM1611  ARF3     3'  GTTGGATGGGTCATCTGTCCTT 9781          _ _
              GGT                    ATTAGGGATA AT ATTCATTTAGC
                                |||||||||| || ||||||||||
                                TGGTTCCTGT TA TGGGTAGGTTG
                                      C  C
GAM1611  BACE     3'  GAAGATGGGTGTTGTTTTCAAT 58086      AG           AGC
              G                   TATT  GGATAATATTCATTT
                                ||||  ||||||||||||||
                                GTAA  TTTGTTGTGGGTAGA
                                  CT           AG
GAM1611  BACE     3'  GCTAAGTGTGGAATTACCTGAT 58088       GATAATATT
              A                   TATTAGG       CATTTAGC
                                |||||||       ||||||||
                                ATAGTCC       GTGAATCG
                                    ATTAAGGT_
GAM1611  BACH2    3'  GCTGGATGTTCAGATTCCTAA  41786        AATATT
                                TTAGGGAT     CATTTAGC
                                ||||||||     ||||||||
                                AATCCTTA     GTAGGTCG
                                     GACTT_
GAM1611  BAZ2A    3'  GCTAGGTGGATTTTCTCT    26512      TAAT
                                AGGGA   ATTCATTTAGC
                                |||||   ||||||||||
                                TCTCT   TAGGTGGATCG
                                  TT__
GAM1611  BCL11A   3'  GCTAAATGTCTGTCTCTAA   43467         ATATT
                                TTAGGGATA    CATTTAGC
                                |||||||||    ||||||||
                                AATCTCTGT    GTAAATCG
                                     CT___
GAM1611  C11orf8  3'  GCTAGCACAAAATATTGTCGCT 9624       G       CAT__
              AATA                   TATTAG GATAATATT    TTAGC
                                |||||| |||||||||    |||||
                                ATAATC CTGTTATAA    GATCG
                                   G       AACAC
GAM1611  C4BPB    5'  GCTGGGTGAATTCCAGCCTGG  7389       GATAAT
                                TTAGG     ATTCATTTAGC
                                |||||     ||||||||||
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                                GGTCC     TAAGTGGGTCG
                                  GACCT_
GAM1611 CAMLG    3' GCTGAGTTTGTATTATTACTGA 10002      GG      TC
           TA                    TATTAG  ATAATAT  ATTTAGC
                                 ||||||  |||||||  |||||||
                                 ATAGTC  TATTATG  TGAGTCG
                                    AT      TT
GAM1611 CAT      3' GCTTAATGTTTATTCCTGATA  10021          TATT    T
                                 TATTAGGGATAA    CATT AGC
                                 ||||||||||||    |||| |||
                                 ATAGTCCTTATT    GTAA TCG
                                       T___    T
GAM1611 CDKN1A   3' GTTGAATGAGAGGTTCCTAA   55271        AATA
                                 TTAGGGAT    TTCATTTAGC
                                 ||||||||    ||||||||||
                                 AATCCTTG    GAGTAAGTTG
                                     GA__
GAM1611 CHC1L    3' GTATGAAGTATTATCTTTGA   8857            _   TTAGC
                                 TTAGGGATAATATT CAT
                                 |||||||||||||| |||
                                 AGTTTCTATTATGA GTA
                                       A   TG
GAM1611 CLN5     3' GCTAAGTGATCTTTCTCTGG   22431       TAATAT
                                 TTAGGGA     TCATTTAGC
                                 |||||||     |||||||||
                                 GGTCTCT     AGTGAATCG
                                     TTCT__
GAM1611 CTRL     3' CTGAGTGACTCCTTGA      10340        TAATAT
                                 TTAGGGA     TCATTTAG
                                 |||||||     ||||||||
                                 AGTTCCT     AGTGAGTC
                                     C_____
GAM1611 CUL4B    3' GTTGAGTGGACTTTTTCTC    14566      T  TA
                                 GGGA AA  TTCATTTAGC
                                 |||| ||  ||||||||||
                                 CTCT TT  AGGTGAGTTG
                                   T  TC
GAM1611 CXorf6   3' GTTGATTTGGGGTTTGTCTTTG 19709           TA   T_
           ATG                     TATTAGGGATAA  TTCA  TTAGC
                                 ||||||||||||  ||||  |||||
                                 GTAGTTTCTGTT  GGGT  AGTTG
                                       TG    TT
GAM1611 DAAM2    3' CTGAGCTGGTCCTTAATA    93902         AATATT  _
                                 TATTAGGGAT     CA TTTAG
                                 ||||||||||     || |||||
                                 ATAATTCCTG     GT GAGTC
                                       _______  C
GAM1611 DAG1     3' CCTGGTGAGATTATTTCTGATG 16550       GG     A     TAGC
                                 TATTAG  ATAAT TTCATT
                                 ||||||  ||||| ||||||
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                                GTAGTC  TATTA GAGTGG
                                   TT    _    TCCA
GAM1611  DNTT    3'  GCTGAAATACTGTCTATCTCTA 73663          _  TTCA
            ATA                   TATTAGGGATA ATA   TTTAGC
                                  |||||||||||| |||   ||||||
                                  ATAATCTCTAT TGT   AAGTCG
                                        C  CATA
GAM1611  EIF4G2   3'  GCTAGATTTTAATATCCTTGA  9219         A  TTC
                                  TTAGGGATA TA  ATTTAGC
                                  ||||||||| ||  |||||||
                                  AGTTCCTAT AT  TAGATCG
                                        A  TT_
GAM1611  EYA4     3'  GCTGAATGGAGTTAAACTTTAG 15885        ATAATA
            TG                    TATTAGGG    TTCATTTAGC
                                  ||||||||    ||||||||||
                                  GTGATTTC    AGGTAAGTCG
                                       AAATTG
GAM1611  EZH1     3'  GCTAAGTGAAGTGTGGTCCCTG 10552        A   _
            G                     TTAGGGAT ATATT CATTTAGC
                                  |||||||| ||||| ||||||||
                                  GGTCCCTG TGTGA GTGAATCG
                                       G    A
GAM1611  FACL4    3'  TGAATTTATCTTTGATA     16747          T
                                  TATTAGGGATAA ATTCA
                                  |||||||||||| |||||
                                  ATAGTTTCTATT TAAGT
                                                _
GAM1611  FBXL7    3'  GCTGGATGCTGTCGTCTCTG  25496      TA  TT
                                  TAGGGA  ATA  CATTTAGC
                                  ||||||  |||  ||||||||
                                  GTCTCT  TGT  GTAGGTCG
                                     GC  C_
GAM1611  FLRT2    3'  TTGAATGGAATTATTTTTGATA 26007          A       C
                                  TATTAGGGATAAT TTCATTTAG
                                  |||||||||||| |||||||||
                                  ATAGTTTTTATTA AGGTAAGTT
                                           _       A
GAM1611  FMR2     3'  GCTGTAGTGTTGTCTTTGATA  10696           CATT
                                  TATTAGGGATAATATT   TAGC
                                  ||||||||||||||||   ||||
                                  ATAGTTTCTGTTGTGA   GTCG
                                           T___   T
GAM1611  FZD3     3'  GCTAAATGAAGCATGATTAGTC 34258       GA   A____
            TTAGTA                TATTAGG  TAAT   TTCATTTAGC
                                  |||||||  ||||   ||||||||||
                                  ATGATTC  ATTA   AAGTAAATCG
                                     TG   GTACG
GAM1611  FZD7     3'  GCTGGGTGGGGGCCTGTTTCTG 14504    GG  ATA_
                                  TAG  ATA   TTCATTTAGC
                                  |||  |||   ||||||||||
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                                GTC  TGT    GGGTGGGTCG
                                  TT   CCGG
GAM1611  GALNT3    3'  GCTAAATGTAACTTATTCCAAG 16826      A      TATT
             TG                    TATT GGGATAA    CATTTAGC
                                   |||| |||||||    ||||||||
                                   GTGA CCTTATT    GTAAATCG
                                     A      CAAT
GAM1611  GAN       3'  GTTAGTCTCCATTTATTCCTAG 42122           TATTCAT
             TA                    TATTAGGGATAA      TTAGC
                                   ||||||||||||      |||||
                                   ATGATCCTTATT      GATTG
                                         TACCTCT
GAM1611  GPLD1     3'  GCTGGAGGCCATTATCCTTCAT 93660     T       AT  A
             A                      TAT AGGGATAAT  TC TTTAGC
                                   ||| |||||||||  || ||||||
                                   ATA TTCCTATTA  GG AGGTCG
                                     C        CC  _
GAM1611  GRINL1A   3'  GTTAGGTGAAAGTGTTTTTGA  70069         ATA
                                   TTAGGGATA   TTCATTTAGC
                                   |||||||||   ||||||||||
                                   AGTTTTTGT   AAGTGGATTG
                                        GA_
GAM1611  HSPG2     3'  TGGGAATTGTCTTTAGTG     19841            A
                                   TATTAGGGATAAT TTCA
                                   |||||||||||| ||||
                                   GTGATTTCTGTTA GGGT
                                          A
GAM1611  KCND2     3'  GCTGAGTGTTCATGTTCCATGG 25383       _     ATATT
             TG                    TATTA GGGATA     CATTTAGC
                                   ||||| ||||||     ||||||||
                                   GTGGT CCTTGT     GTGAGTCG
                                     A     ACTT_
GAM1611  KCNK2     3'  AATGAATGAGAATTGTTTCTGG 27236       GG     A       GC
             TA                    TATTAG  ATAAT TTCATTTA
                                   ||||||  ||||| ||||||||
                                   ATGGTC  TGTTA GAGTAAGT
                                      TT     A       AAG
GAM1611  LMCD1     3'  GTTGGGTGGTGGTAGATCCTTG 28150         AATAT_
             A                      TTAGGGAT     TCATTTAGC
                                   ||||||||     |||||||||
                                   AGTTCCTA     GGTGGGTTG
                                        GATGGT
GAM1611  MGA       3'  CTAATAATTGTCCTTAG     63466           ATTCAT
                                   TTAGGGATAAT     TTAG
                                   ||||||||||     ||||
                                   GATTCCTGTTA     AATC
                                         AT____
GAM1611  NBS1      3'  GCTGGGTGGGTGTCTGTTTTGA 70026       ATA
                                   TTAGGG   ATATTCATTTAGC
                                   ||||||   ||||||||||||
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                                AGTTTT   TGTGGGTGGGTCG
                                   GTC
GAM1611  NDST2    3'  CTAGAAATGTCCTTAATA    14664          ATATTCA
                                TATTAGGGATA      TTTAG
                                ||||||||||       |||||
                                ATAATTCCTGT      AGATC
                                     AA_____
GAM1611  NEB      3'  GCTAATGCTTATTATTTCTAAT 17008      GG     TT    T
                                ATTAG  ATAATA  CATT AGC
                                |||||  ||||||  |||| |||
                                TAATC  TATTAT  GTAA TCG
                                   TT     TC   _
GAM1611  NEB      3'  GCTTCTGCAATATTATTTCTG  17009     GG       _  TTT
                                TAG  ATAATATT CA   AGC
                                |||  ||||||||  ||   |||
                                GTC  TATTATAA GT   TCG
                                  TT       C  CT_
GAM1611  NRXN1    5'  GCTAAATGGATTTACCTAGTG  17825       GATAAT
                                TATTAGG     ATTCATTTAGC
                                |||||||     ||||||||||
                                GTGATCC     TAGGTAAATCG
                                    ATT___
GAM1611  NSF      3'  GTTAAATGAGCTTAATGTCTTT 63750        A  __
            G                    TAGGGATA TA  TTCATTTAGC
                                 ||||||||  ||  ||||||||||
                                 GTTTCTGT AT  GAGTAAATTG
                                      A  TC
GAM1611  NTSR1    3'  GCTGGATGAGACTGTCCT    11858       ATA
                                GGGATA   TTCATTTAGC
                                ||||||   ||||||||||
                                TCCTGT   GAGTAGGTCG
                                   CA_
GAM1611  OGG1     3'  CTAGATGGGGCACCCTGG    34156       ATAATA
                                TTAGGG     TTCATTTAG
                                ||||||     |||||||||
                                GGTCCC     GGGTAGATC
                                   ACG___
GAM1611  PCDH12   5'  GTTAAGTGACTTGTCCCAGATG 33888      A      TAT
                                TATT GGGATAA   TCATTTAGC
                                |||| |||||||   |||||||||
                                GTAG CCCTGTT   AGTGAATTG
                                  A      C__
GAM1611  PIN4     3'  GCTAAGTGAATGTCAACTGTAG 21711       G  ATA
            TA                    TATTA GG   ATATTCATTTAGC
                                  |||||  ||   ||||||||||||
                                  ATGAT TC   TGTAAGTGAATCG
                                     G  AAC
GAM1611  PMX1     3'  GTTAAAGATATTTGTTGTCTTT 23572           TTCA__
            GA                    TTAGGGATAATA     TTTAGC
                                  ||||||||||||     ||||||
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                                AGTTTCTGTTGT     AAATTG
                                      TTATAG
GAM1611  PMX1     3'  GTTAAAGATATTTGTTGTCTTT 23573          TTCA__
              GA                  TTAGGGATAATA     TTTAGC
                                  ||||||||||||     ||||||
                                  AGTTTCTGTTGT     AAATTG
                                        TTATAG
GAM1611  PPARGC1  3'  ACCATGGTGTTGTTCTTGATG  26075            T   TTAGC
                                  TATTAGGGATAATAT CAT
                                  ||||||||||||||| |||
                                  GTAGTTCTTGTTGTG GTA
                                        _  CCAG
GAM1611  PPID     3'  GTCTATGAATATGATCCCTAAT 88828          A       TTAGC
              G                   TATTAGGGAT ATATTCAT
                                  |||||||||| ||||||||
                                  GTAATCCCTA TATAAGTA
                                        G       TCTG
GAM1611  PTPN7    5'  GCTGAGTGAGCCTCCCCTGG   55463       ATAATA
                                  TTAGGG     TTCATTTAGC
                                  ||||||     ||||||||||
                                  GGTCCC     GAGTGAGTCG
                                     CTCC__
GAM1611  QDPR     3'  GTTATTCAGAATGTTGTTCCTA 6147               ATT_
              ATA                   TATTAGGGATAATATTC    TAGC
                                  ||||||||||||||||    ||||
                                  ATAATCCTTGTTGTAAG    ATTG
                                        ACTT
GAM1611  RBL2     3'  GCTAAACATCCAATATTTTCTT 20041          T     CA___
              TAATG                   TATTAGGGA AATATT     TTTAGC
                                  |||||||||| ||||||    ||||||
                                  GTAATTTCT TTATAA     AAATCG
                                        T     CCTAC
GAM1611  RBM8A    3'  GCTGAAATGATTTTCCTGGTA  18810          TAATAT    _
                                  TATTAGGGA     TCATT TAGC
                                  |||||||||     ||||| ||||
                                  ATGGTCCTT     AGTAA GTCG
                                        TT_____     A
GAM1611  RECK     3'  GTTAAAATGTGTTGTTCCAAAT 41199      A         TCA
              A                    TATT GGGATAATAT   TTTAGC
                                  |||| ||||||||||   ||||||
                                  ATAA CCTTGTTGTG   AAATTG
                                     A         TA_
GAM1611  RGL      3'  GTTAAGTGACACTTTTGTCTCT 31429     T       TAT__
              CATA                    TAT AGGGATAA     TCATTTAGC
                                  |||  ||||||||     |||||||||
                                  ATA TCTCTGTT     AGTGAATTG
                                     C       TTCAC
GAM1611  RHAG     3'  ATGAATATTATTCTTAAT     6153
                                  ATTAGGGATAATATTCAT
                                  ||||||||||||||||||
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                                TAATTCTTATTATAAGTA

GAM1611 ROCK2    3' GTTGGAACTAATATATCCTTGA 66624          A   CA_
           TG                    TATTAGGGATA TATT   TTTAGC
                                 |||||||||| ||||  ||||||
                                 GTAGTTCCTAT ATAA  AGGTTG
                                       _   TCA
GAM1611 RP42     3' AGATGAAGATTATCTTTAGTG 40564           A
                                 TATTAGGGATAAT TTCATTT
                                 ||||||||||||| |||||||
                                 GTGATTTCTATTA AAGTAGA
                                       G
GAM1611 SART2    3' ATGAATGAATATTTCCTTGATG 26250         T         GC
                                 TATTAGGGA AATATTCATTTA
                                 ||||||||| ||||||||||||
                                 GTAGTTCCT TTATAAGTAAGT
                                       _         AT
GAM1611 SDPR     3' GTTAAAGCTGTATTTTTCTTAA 17401         T    TCA
           TA                    TATTAGGGA AATAT   TTTAGC
                                 ||||||||| |||||   ||||||
                                 ATAATTCTT TTATG   AAATTG
                                       T    TCG
GAM1611 SEL1L    3' GCTGAATGAATCCAATTTTTTA 18603         TAAT_
           ATG                     TATTAGGGA    ATTCATTTAGC
                                 |||||||||    ||||||||||
                                 GTAATTTTT    TAAGTAAGTCG
                                       TAACC
GAM1611 SEL1L    3' GCTGGATATTTTGTTTCTGA  18604     GG   TATTC
                                 TTAG  ATAA    ATTTAGC
                                 ||||  ||||    |||||||
                                 AGTC  TGTT    TAGGTCG
                                   TT   TTA__
GAM1611 SERPINA3 3' GCTGGATGCCTGGGTCTCTGG 61821        AATATT
                                 TTAGGGAT     CATTTAGC
                                 ||||||||     ||||||||
                                 GGTCTCTG     GTAGGTCG
                                      GGTCC_
GAM1611 SERPINB5 3' GTTGGGTGGATAAGCTATCCCT 12072        A__
           G                      TAGGGATA   TATTCATTTAGC
                                 ||||||||   ||||||||||||
                                 GTCCCTAT   ATAGGTGGGTTG
                                      CGA
GAM1611 SLC12A7  3' TGAAGCTGTCCCTGATG     22744          ATA
                                 TATTAGGGATA   TTCA
                                 ||||||||||||  ||||
                                 GTAGTCCCTGT   AAGT
                                       CG_
GAM1611 SLC20A2  3' GCTGGATGGAGTATTTCTCTGA 23118        T     _
                                 TTAGGGA AATATTC ATTTAGC
                                 ||||||| ||||||| |||||||
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                                AGTCTCT TTATGAG TAGGTCG
                                   _     G
GAM1611  SLC6A6   3'  GCTGAATGAGGAGGCCCTA   13184      ATAATA
                                TAGGG     TTCATTTAGC
                                |||||     ||||||||||
                                ATCCC     GAGTAAGTCG
                                   GGAG__
GAM1611  SNX6     3'  GTTAGTGACAGTTATTCCTGA  41443          AT    T
                                TTAGGGATAAT  TCATT AGC
                                ||||||||||  ||||| |||
                                AGTCCTTATTG  AGTGA TTG
                                      AC    _
GAM1611  SOCS5    3'  GTTAAATGGAAATTGTTTTAAA 26684      AG      A
            TG                    TATT  GGATAAT TTCATTTAGC
                                ||||  ||||||| ||||||||||
                                GTAA  TTTGTTA AGGTAAATTG
                                   AT      A
GAM1611  SOX12    3'  CTGGATGGATGTTTCTGA    23685     GG  AAT
                                TTAG  AT   ATTCATTTAG
                                ||||  ||   ||||||||||
                                AGTC  TG   TAGGTAGGTC
                                   TT  ___
GAM1611  SPAP1    5'  GTTGAGAAAATTATCTCTAA   57835          A   AT
                                TTAGGGATAAT TTC  TTAGC
                                ||||||||||| |||  |||||
                                AATCTCTATTA AAG  AGTTG
                                      A  __
GAM1611  SPAP1    5'  GTTGAGAAAATTATCTCTAA   57836          A   AT
                                TTAGGGATAAT TTC  TTAGC
                                ||||||||||| |||  |||||
                                AATCTCTATTA AAG  AGTTG
                                      A  __
GAM1611  SSPN     3'  GCTGAATCTCTTTATTTTCCCT 18684         T    TTC__
            GGTA                    TATTAGGGA AATA     ATTTAGC
                                ||||||||| ||||    |||||||
                                ATGGTCCCT TTAT     TAAGTCG
                                      T    TTCTC
GAM1611  STK31    3'  TGAGTTGTATCTTTAGTA    53079          AT
                                TATTAGGGATA  ATTCA
                                ||||||||||  |||||
                                ATGATTTCTAT  TGAGT
                                      GT
GAM1611  SURF5    3'  GCTAGGTGGGACTCATTCCTAA 56915         AATA
            T                    ATTAGGGAT    TTCATTTAGC
                                |||||||||    ||||||||||
                                TAATCCTTA    GGGTGGATCG
                                      CTCA
GAM1611  SURF5    3'  GCTAGGTGGGACTCATTCCTAA 56916         AATA
            T                    ATTAGGGAT    TTCATTTAGC
                                |||||||||    ||||||||||
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                                TAATCCTTA   GGGTGGATCG
                                     CTCA
GAM1611  SYT1    3'  GCTAAAGATTTATTTCTAGT  20113      GG   TAT  A
                                ATTAG  ATAA   TC TTTAGC
                                |||||  ||||   || ||||||
                                TGATC  TATT   AG AAATCG
                                   TT   T__  _
GAM1611  TSN     3'  GCTTTCTGATGTTGCCTTAATA 17302        A     T  TTT
                                TATTAGGG TAATAT CA   AGC
                                |||||||| |||||| ||   |||
                                ATAATTCC GTTGTA GT   TCG
                                     _     _ CTT
GAM1611  UBL3    3'  GTTAAATGAAGTTTCCTCATA  24025     T    TAATA
                                TAT AGGGA    TTCATTTAGC
                                ||| |||||    ||||||||||
                                ATA TCCTT    AAGTAAATTG
                                  C    TG___
GAM1611  VBP1    3'  GCTGGGTGATACAGATTCTGAT 14030        ATAATAT
            A                    TATTAGGG      TCATTTAGC
                                |||||||      |||||||||
                                ATAGTCTT      AGTGGGTCG
                                     AGACAT_
GAM1611  WHSC1L1  3'  GCTGGATGGGTACAGCTTAA   35500      GATAA
                                TTAGG    TATTCATTTAGC
                                |||||    ||||||||||||
                                AATTC    ATGGGTAGGTCG
                                   GAC__
GAM1611  XPR1    3'  GCTGGGTGGGTGGGAAATATGA 17622      GGGATAA
            TG                    TATTA      TATTCATTTAGC
                                |||||      ||||||||||||
                                GTAGT      GTGGGTGGGTCG
                                   ATAAAGG
GAM1611  ZNF255   5'  TGAATAGTATTCCATGGTG   20499      _     A
                                TATTA GGGATA TATTCA
                                ||||| |||||| ||||||
                                GTGGT CCTTAT ATAAGT
                                   A     G
GAM1611  A4GALT   3'  GCTGGGTGGGGAGGCTCTTTAG 34301        TAATA
                                TTAGGGA    TTCATTTAGC
                                |||||||    ||||||||||
                                GATTTCT    GGGTGGGTCG
                                     CGGAG
GAM1611  AKAP8    3'  CTGAATCAGTTCTCTAATA   20734        TAAT   C
                                TATTAGGGA   ATT ATTTAG
                                |||||||||   ||| ||||||
                                ATAATCTCT   TGA TAAGTC
                                      _____  C
GAM1611  AKAP8    3'  GCTGAAGTACATTGTCCTTAG  20736         ATTCA
                                TTAGGGATAAT    TTTAGC
                                ||||||||||    ||||||
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                                GATTCCTGTTA    AAGTCG
                                     CATG_
GAM1611 ALLC    5' ATTTTGTGAATATTATCTTTTG 37978    T          TTAGC
           TA                   TAT AGGGATAATATTCAT
                                ||| ||||||||||||||
                                ATG TTTCTATTATAAGTG
                                  T           TTTTAG
GAM1611 ARG99   3' GCTAAGTGAGCTTTATCT    50012      TA
                                GGATAA  TTCATTTAGC
                                ||||||  ||||||||||
                                TCTATT  GAGTGAATCG
                                   TC
GAM1611 C12orf5  3' CTAGATGTCATCTCTGG    40169       AATATT
                                TTAGGGAT    CATTTAG
                                ||||||||    |||||||
                                GGTCTCTA    GTAGATC
                                     CT____
GAM1611 C1orf9   3' TGGGTATTGTTTGTAATG    33162      G
                                TATTA GGATAATATTCA
                                ||||| ||||||||||||
                                GTAAT TTTGTTATGGGT
                                   G
GAM1611 C20orf126 3' GCTGAATGAAGAACAGAATCTT 48734        ATAATA__
           GGTG                  TATTAGGG      TTCATTTAGC
                                 ||||||||      ||||||||||
                                 GTGGTTCT      AAGTAAGTCG
                                      AAGACAAG
GAM1611 C20orf142 3' GTTAGGCACTTTTTGTCCCTGG 75287          TATTCA
           TA                    TATTAGGGATAA    TTTAGC
                                 ||||||||||||    ||||||
                                 ATGGTCCCTGTT    GGATTG
                                       TTTCAC
GAM1611 C20orf162 5' CTGAATGGGCTCCTGAT    55499       ATAATA
                                 ATTAGGG    TTCATTTAG
                                 |||||||    |||||||||
                                 TAGTCCT    GGGTAAGTC
                                     C_____
GAM1611 C6.1A    3' GCTAGGTGACAAGTTCTTGG   44533       AATAT
                                 TTAGGGAT    TCATTTAGC
                                 ||||||||    |||||||||
                                 GGTTCTTG    AGTGGATCG
                                      AAC__
GAM1611 C8orf4   3' TGAGTATTGTCTATTGGTA   39692      _
                                 TATTAG GGATAATATTCA
                                 |||||| ||||||||||||
                                 ATGGTT TCTGTTATGAGT
                                    A
GAM1611 CAMKK2   3' CTAGATGTGGCTCCTAGTG   22619       ATAATATT
                                 TATTAGGG      CATTTAG
                                 ||||||||      |||||||
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                                GTGATCCT      GTAGATC
                                    CGGT____
GAM1611  CBX8     3'  GTTGGAAAGATTATCTCTAG  40610         ATTCA
                                TTAGGGATAAT    TTTAGC
                                ||||||||||    ||||||
                                GATCTCTATTA    AGGTTG
                                    GAA__
GAM1611  CDC14A   3'  ATGGTTTTGTCTCTAATG    53965         TAT
                                TATTAGGGATAA   TCAT
                                ||||||||||||  ||||
                                GTAATCTCTGTT   GGTA
                                    TT_
GAM1611  CLIC2    3'  ATGAGTTTATTTCTGATA    8914       GG   T
                                TATTAG  ATAA ATTCAT
                                ||||||  |||| ||||||
                                ATAGTC  TATT TGAGTA
                                   TT   _
GAM1611  CPR2     3'  GCTGAGTGAAAGGCACCCTGA  48834      ATAATA
                                TTAGGG     TTCATTTAGC
                                ||||||     ||||||||||
                                AGTCCC     AAGTGAGTCG
                                   ACGGA_
GAM1611  DCTD     3'  GCTGAATAATGAGTTGTTCCTA 10392         __  C
            G                   TTAGGGATAAT  ATT ATTTAGC
                                ||||||||||  ||| |||||||
                                GATCCTTGTTG  TAA TAAGTCG
                                    AG  _
GAM1611  DDM36    3'  GTTAGGGTCTTTACTCCCTAAT 40928        _  TATTCA
            G                    TATTAGGGA TAA     TTTAGC
                                |||||||||  |||     ||||||
                                GTAATCCCT ATT     GGATTG
                                    C  TCTG__
GAM1611  DJ667H12.2 3'  GCTAGATGAAATGGCTTAATG  39478       GATA  A
                                TATTAGG    AT TTCATTTAGC
                                |||||||    || ||||||||||
                                GTAATTC    TA AAGTAGATCG
                                    GG__  _
GAM1611  DKFZP434A0225 3'  GCTAGGTGGAGTATGCTTGATA 95524       G   ATA
                                TATTAGG ATA   TTCATTTAGC
                                ||||||| |||   ||||||||||
                                ATAGTTC TAT   AGGTGGATCG
                                    G  G__
GAM1611  DKFZP434H0820 3'  GTTGGGTGGGCCCTCCCTGA   64585       TAATA
                                TTAGGGA    TTCATTTAGC
                                |||||||    ||||||||||
                                AGTCCCT    GGGTGGGTTG
                                    CCC__
GAM1611  DKFZP564O0523 3'  GCTAAGTTTTGTGTTTTTTTTA 50421        T    TC_
            GTA                   TATTAGGGA AATAT   ATTTAGC
                                |||||||| |||||   |||||||
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                                ATGATTTTT TTGTG   TGAATCG
                                     T    TTT
GAM1611  DKFZP761E2110 3'  GAGTATTTATTCCTAATA    48963          _
                                TATTAGGGATAA TATTC
                                |||||||||||| |||||
                                ATAATCCTTATT ATGAG
                                      T
GAM1611  DKFZP761F241 3'  GCTGAGTAATTGTTTCTAATG  49582      GG    ATTC
                                TATTAG  ATAAT    ATTTAGC
                                ||||||  |||||   |||||||
                                GTAATC  TGTTA    TGAGTCG
                                   TT    A___      T
GAM1611  DKFZP761F241 3'  GCTGAGTAATTGTTTCTAATG  49583      GG    ATTC
                                TATTAG  ATAAT    ATTTAGC
                                ||||||  |||||   |||||||
                                GTAATC  TGTTA    TGAGTCG
                                   TT    A___
GAM1611  DKFZp761G0313 3'  AAATGAAATTATCTTTGATA   66390          A
                                TATTAGGGATAAT TTCATTT
                                |||||||||||| |||||||
                                ATAGTTTCTATTA AAGTAAA
                                      _
GAM1611  DKFZp761O132 5'  GCTGGATGGATGTTTGTTGA   51170     G  TA
                                TTAG GA  ATATTCATTTAGC
                                |||| ||  ||||||||||||
                                AGTT TT  TGTAGGTAGGTCG
                                  G  __
GAM1611  EIF2S1    3'  GCTGAATATTTTTTATTTCTAA 15847     GG    TATTC
                                TTAG  ATAA    ATTTAGC
                                ||||  ||||    |||||||
                                AATC  TATT    TAAGTCG
                                  TT   TTTTA
GAM1611  ENPP4     3'  GTTAAGTGGCAGAATAGCCTTA 30718        ATAATAT_
            GTG                   TATTAGGG       TCATTTAGC
                                |||||||       |||||||||
                                GTGATTCC       GGTGAATTG
                                     GATAAGAC
GAM1611  ERAP140   3'  GTTGAATGCAATTTTTATTTTT 75707          T_  _
            GGTA                  TATTAGGGATAA  ATT CATTTAGC
                                ||||||||||||  ||| ||||||||
                                ATGGTTTTTATT  TAA GTAAGTTG
                                      TT   C
GAM1611  FBX30     3'  CTAGATGGGTACCAGGTG    53745     TA  GATAA
                                TAT  GG    TATTCATTTAG
                                |||  ||    ||||||||||
                                GTG  CC    ATGGGTAGATC
                                  GA  _____
GAM1611  FLJ10300  3'  ATGAATATTTCTTTGGTA    36468         T
                                TATTAGGGA AATATTCAT
                                ||||||||| |||||||||
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                                ATGGTTTCT TTATAAGTA
                                        _
GAM1611  FLJ10375  5'  GTTGAATGAATGTCTGGCTC  36560    ATA_
                                GGG   ATATTCATTTAGC
                                |||   ||||||||||||
                                CTC   TGTAAGTAAGTTG
                                  GGTC
GAM1611  FLJ10656  3'  GTTAGGTGGATAGTCCTGTAGT 36909     _   AA
           G                    TATTA GGGAT  TATTCATTTAGC
                                ||||| |||||  ||||||||||||
                                GTGAT TCCTG  ATAGGTGGATTG
                                   G   __
GAM1611  FLJ10936  3'  CTGAATGGAAGTCTTGA    37442      ATAATA
                                TTAGGG    TTCATTTAG
                                ||||||    |||||||||
                                AGTTCT    AGGTAAGTC
                                   GA____
GAM1611  FLJ10980  3'  GTGATGTTTGTCTCTAGTG   65254         TAT
                                TATTAGGGATAA  TCAT
                                ||||||||||||  ||||
                                GTGATCTCTGTT  AGTG
                                      TGT
GAM1611  FLJ11149  3'  GCTAAATGCTATCTTTAG   37687       ATATT
                                TTAGGGATA   CATTTAGC
                                |||||||||   ||||||||
                                GATTTCTAT   GTAAATCG
                                    C____
GAM1611  FLJ12649  3'  GCTGTCAGATTGTTTCTAATA  45094      GG   ATTCATT
                                TATTAG  ATAAT     TAGC
                                ||||||  |||||     ||||
                                ATAATC  TGTTA     GTCG
                                   TT   GACT___
GAM1611  FLJ12787  3'  TCTGGGATGGATATTAATTTTA 50698       A        AGC
           ATA                    TATTAGGG TAATATTCATTT
                                  ||||||||| ||||||||||||
                                  ATAATTTT ATTATAGGTAGG
                                       A         GTCTA
GAM1611  FLJ12892  3'  GCTGAATGTTGTGTTATCACTA 68453      G     T_
           ATA                    TATTAG GATAATAT  CATTTAGC
                                  |||||| ||||||||  ||||||||
                                  ATAATC CTATTGTG  GTAAGTCG
                                     A      TT
GAM1611  FLJ13194  3'  GTTGGAACATTGTTATCCTTG  47873         TTCA
                                TAGGGATAATA   TTTAGC
                                ||||||||||||  ||||||
                                GTTCCTATTGT   AGGTTG
                                      TACA
GAM1611  FLJ13657  3'  GTTAGATGAGTATTTAGCTGTG 46140   G  AT_
                                TA GG   AATATTCATTTAGC
                                || ||   ||||||||||||||
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                              GT TC   TTATGAGTAGATTG
                               G  GAT
GAM1611  FLJ13769  3' GCTGGGTGGCCTGGCCCTGGTA 47257        ATAATAT
                              TATTAGGG      TCATTTAGC
                              ||||||||      |||||||||
                              ATGGTCCC      GGTGGGTCG
                                  GGTCC__
GAM1611  FLJ14437  3' GTGATATCCCTAGTA      51799          ATAT
                              TATTAGGGATA   TCAT
                              ||||||||||    ||||
                              ATGATCCCTAT   AGTG
                                    ____
GAM1611  FLJ14600  3' TTAGGTGCTGGTTCCTAG    52530        AATATT
                              TTAGGGAT     CATTTAG
                              ||||||||     |||||||
                              GATCCTTG     GTGGATT
                                  GTC___
GAM1611  FLJ14668  3' GCTGTGATATATTTTCCTAGTG 52588         T   _   TT
                              TATTAGGGA AATAT TCAT  AGC
                              ||||||||| ||||| ||||  |||
                              GTGATCCTT TTATA AGTG  TCG
                                  _    T   __
GAM1611  FLJ14735  3' TTGAGTGGATTCCTGGGTA   52670    TA   TAAT
                              TAT  GGGA   ATTCATTTAG
                              |||  ||||   ||||||||||
                              ATG  TCCT   TAGGTGAGTT
                               GG   _____
GAM1611  FLJ20127  3' GCTAAATGAGATGTTTCTAAT  35080     GG   ATA
                              ATTAG  ATA   TTCATTTAGC
                              |||||  |||   ||||||||||
                              TAATC  TGT   GAGTAAATCG
                                 TT  A__
GAM1611  FLJ20436  3' GCTAGGTGGGAGCTGTCTTTG  35626       ATA
                              TAGGGATA   TTCATTTAGC
                              ||||||||   ||||||||||
                              GTTTCTGT   GGGTGGATCG
                                  CGA
GAM1611  FLJ20986  5' GCTAGGTGGATGGATGTT    44837     A_
                              GATA  TATTCATTTAGC
                              ||||  ||||||||||||
                              TTGT  GTAGGTGGATCG
                                AG
GAM1611  FLJ21596  3' GCTGAGTGGATGGTTGCTGA   46117     G   AA
                              TTAG GAT  TATTCATTTAGC
                              |||| |||  ||||||||||||
                              AGTC TTG  GTAGGTGAGTCG
                                G   __
GAM1611  FLJ21615  3' AAACTTGAATTTATCTTTGATA 50805          T    TTTAGC
                              TATTAGGGATAA ATTCA
                              |||||||||||| |||||
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                                ATAGTTTCTATT TAAGT
                                      _    TCAAAT
GAM1611  FLJ22969  3'  GCTGAGTGTTTGTTTCTA   69210    GG   TATT
                                TAG  ATAA   CATTTAGC
                                |||  ||||   ||||||||
                                ATC  TGTT   GTGAGTCG
                                  TT   T___
GAM1611  FLJ23024  3'  GTTGAATGAGTGAGATGTTTAG 46847      G  AA
                                TTAGG AT  TATTCATTTAGC
                                ||||| ||  ||||||||||||
                                GATTT TA  GTGAGTAAGTTG
                                   G  GA
GAM1611  FLJ23058  3'  GCTGGGTTCCGCTTTGTCCCTG 45526          TATTC_
            GT                   ATTAGGGATAA     ATTTAGC
                                ||||||||||     |||||||
                                TGGTCCCTGTT     TGGGTCG
                                      TCGCCT
GAM1611  FLJ23416  3'  GTTAAATGCTCTGGGTTTTCTC 50934         T   ATT___
            TGATA                 TATTAGGGA AAT     CATTTAGC
                                |||||||||  |||     ||||||||
                                ATAGTCTCT TTG     GTAAATTG
                                     T   GGTCTC
GAM1611  FLJ23560  3'  GTTGAATAAAACAGTGTTATCT 45509             C____
            TTAAT                 ATTAGGGATAATATT    ATTTAGC
                                ||||||||||||||    |||||||
                                TAATTTCTATTGTGA    TAAGTTG
                                      CAAAA
GAM1611  GENX-3414 3'  GCTGAGTGAGGTGGCCTGAATG 15457      A   ATAATA
                                TATT GGG     TTCATTTAGC
                                ||||  |||     ||||||||||
                                GTAA TCC     GAGTGAGTCG
                                  G   GGTG__
GAM1611  GMPPB    5'  GCTGCTCTGTACTGTCCCTGGT 26223          A   TCATT
            G                   TATTAGGGATA TAT     TAGC
                                ||||||||||  |||     ||||
                                GTGGTCCCTGT ATG    GTCG
                                      C   TCTC_
GAM1611  HSJ1     3'  GCTGGGCTTTTGTGCCCTGGTA 23082         _   TATTCA
                                TATTAGGG ATAA     TTTAGC
                                ||||||||  ||||     ||||||
                                ATGGTCCC TGTT     GGGTCG
                                     G    TTC___
GAM1611  HSPC228   3'  GTTAATAATTTATTTCCCTAAT 33649         T   TTCAT
            A                    TATTAGGGA AATA     TTAGC
                                |||||||||  ||||    |||||
                                ATAATCCCT TTAT     AATTG
                                      _   TTAAT
GAM1611  IPLA2(GAMMA) 5'  GCTGAGTGGGTGGCGACCTAG  61341       GATAA
                                TTAGG    TATTCATTTAGC
                                |||||    ||||||||||||
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                                GATCC    GTGGGTGAGTCG
                                  AGCG_
GAM1611 ITGB8    3' GCTAGATGAATAAATGATTCGT 11056    G   AA__
            G                   TA GGAT   TATTCATTTAGC
                                || ||||   ||||||||||||
                                GT CTTA   ATAAGTAGATCG
                                 G   GTAA
GAM1611 KALI     3' GTTGGATGGGCCCATCCTGATA 54696       ATAATA
                                TATTAGGG    TTCATTTAGC
                                ||||||||    ||||||||||
                                ATAGTCCT    GGGTAGGTTG
                                    ACCC__
GAM1611 KIAA0161 3' GTTGAGTGGACGGACTTATTCC 29208       TA___
            TG                    TAGGGATAA   TTCATTTAGC
                                ||||||||||  ||||||||||
                                GTCCTTATT   AGGTGAGTTG
                                    CAGGC
GAM1611 KIAA0226 3' CTGGGTCCTTCCCTGGTG   64258       TAATATTC
                                TATTAGGGA      ATTTAG
                                |||||||||      ||||||
                                GTGGTCCCT      TGGGTC
                                    TCC_____
GAM1611 KIAA0321 3' GCTGAAGTCAGTGTCTCTGGTG 63055         ATATTCA
                                TATTAGGGATA     TTTAGC
                                ||||||||||     ||||||
                                GTGGTCTCTGT     AAGTCG
                                   GACTG__
GAM1611 KIAA0365 3' GCTAAGTGGTATTTCTG    79370    GG  ATAT
                                TAG  ATA   TCATTTAGC
                                |||  |||   |||||||||
                                GTC  TAT   GGTGAATCG
                                  TT  ____
GAM1611 KIAA0416 3' CTGAGTGACTCTTTAATA   32091       TAATAT
                                TATTAGGGA    TCATTTAG
                                |||||||||    ||||||||
                                ATAATTTCT    AGTGAGTC
                                    C_____
GAM1611 KIAA0459 3' GTTAGGTGGATGTGAACTTAA 61658     GATA
                                TTAGG   ATATTCATTTAGC
                                |||||   ||||||||||||||
                                AATTC   TGTAGGTGGATTG
                                  AAG_
GAM1611 KIAA0711 3' GTTAGATGAGGCTATTGCCTTG 30153       A   __
            ATG                   TATTAGGG TAATA  TTCATTTAGC
                                ||||||||| |||||  ||||||||||
                                GTAGTTCC GTTAT  GAGTAGATTG
                                    _   CG
GAM1611 KIAA0769 3' GCTAGCCAAATTGTCCTTGA  29757        ATTCAT
                                TTAGGGATAAT    TTAGC
                                ||||||||||    |||||
```

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                                AGTTCCTGTTA     GATCG
                                      AACC__
GAM1611  KIAA0794  3'  GTTATAGGATATGGTTTCTAAT 81237       GG  A     ATT
             G                   TATTAG  AT ATATTC   TAGC
                                 ||||||  || ||||||   ||||
                                 GTAATC  TG TATAGG   ATTG
                                    TT  G     AT_
GAM1611  KIAA0820  3'  GTTGAATGAAGTCTGAAACTCT 69591        ATAATA__
             AGTA                  TATTAGGG       TTCATTTAGC
                                 ||||||||       ||||||||||
                                 ATGATCTC       AAGTAAGTTG
                                      AAAGTCTG
GAM1611  KIAA0841  3'  GCTTTCCCATGTAGTCCTTAGT 71897          A    TCATTT
             G                   TATTAGGGAT ATAT      AGC
                                 |||||||||| ||||      |||
                                 GTGATTCCTG TGTA      TCG
                                       A    CCCTT_
GAM1611  KIAA1116  3'  GTTGGGTGAATTTTGTTTTTAG 30304          T
                                 TTAGGGATAA ATTCATTTAGC
                                 |||||||||| ||||||||||
                                 GATTTTTGTT TAAGTGGGTTG
                                       T
GAM1611  KIAA1165  3'  GCTAAAACAATATTATTTCCAG 67994      A GG       CA
             TA                    TATT G  ATAATATT  TTTAGC
                                   |||| |  ||||||||  ||||||
                                   ATGA C  TATTATAA  AAATCG
                                     C TT       CA
GAM1611  KIAA1229  3'  GCTAAATGAATGTATATT     62755      _
                                 GATA ATATTCATTTAGC
                                 |||| ||||||||||||
                                 TTAT TGTAAGTAAATCG
                                   A
GAM1611  KIAA1350  3'  GCTAAATGGATAAACCTCATA  73087     T   GATAA
                                 TAT AGG     TATTCATTTAGC
                                 ||| |||     ||||||||||||
                                 ATA TCC     ATAGGTAAATCG
                                   C   AA___
GAM1611  KIAA1372  3'  GTTGGGTGAAGTGCCCTGA    93321       ATAATA
                                 TTAGGG      TTCATTTAGC
                                 ||||||      ||||||||||
                                 AGTCCC      AAGTGGGTTG
                                    GTG___
GAM1611  KIAA1486  3'  TGAATATTGATGTCCTTA     67981         ___
                                 TAGGGATA   ATATTCA
                                 ||||||||   |||||||
                                 ATTCCTGT   TATAAGT
                                      AGT
GAM1611  KIAA1546  3'  GCTAAGAAAATGGTGTCTTTAA 68499          A    CA
             TA                    TATTAGGGATA TATT  TTTAGC
                                   |||||||||| ||||  ||||||
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                                ATAATTTCTGT GTAA  GAATCG
                                      G    AA
GAM1611  KIAA1554  3'  GTTAGAGGCAGTATCCTTAATA 96860          ATATTCA
                                TATTAGGGATA      TTTAGC
                                ||||||||||       ||||||
                                ATAATTCCTAT      AGATTG
                                      GACGG__
GAM1611  KIAA1557  3'  GCTTTAATGTTATCTTTGA   61786            CATTT
                                TTAGGGATAATATT    AGC
                                ||||||||||||||    |||
                                AGTTTCTATTGTAA    TCG
                                        TT___
GAM1611  KIAA1822  3'  GTTGAGTGGGCATCTTCCT   68196      TA  A
                                GGGA  AT TTCATTTAGC
                                ||||  || ||||||||||
                                TCCT  TA GGGTGAGTTG
                                  TC  C
GAM1611  KIAA1867  3'  GCTGAGTGCGCTGTGCTTAGTG 96483        G   ATATT
                                TATTAGG ATA     CATTTAGC
                                ||||||| |||     ||||||||
                                GTGATTC TGT     GTGAGTCG
                                    G   CGC__
GAM1611  KIAA1878  3'  GCTGAGTGAGAAGTCTTTTGTA 93369      T     AATA
                                TAT AGGGAT    TTCATTTAGC
                                ||| ||||||    ||||||||||
                                ATG TTTCTG    GAGTGAGTCG
                                  T     AA__
GAM1611  KIAA1957  3'  GCTGACTGGAGTATTATTTTTC 76215      T          AT_
            ATG                   TAT AGGGATAATATTC   TTAGC
                                ||| ||||||||||||||  |||||
                                GTA TTTTTATTATGAG   AGTCG
                                  C           GTC
GAM1611  KREMEN    3'  GCTAGATGGATGTGTACCTGGT 50235        GATA
            G                    TATTAGG    ATATTCATTTAGC
                                |||||||    ||||||||||||||
                                GTGGTCC    TGTAGGTAGATCG
                                    ATG_
GAM1611  LANO      3'  TAAATGATGTCTCTGATG    47975           ATAT
                                TATTAGGGATA    TCATTTA
                                ||||||||||    |||||||
                                GTAGTCTCTGT    AGTAAAT
                                      ____
GAM1611  LCHN      3'  GCTGGGCTGCCCTGTTGTTCCT 87473           TT_ _
            GA                    TTAGGGATAATA   CA TTTAGC
                                ||||||||||||  || ||||||
                                AGTCCTTGTTGT   GT GGGTCG
                                      CCC  C
GAM1611  LGP2      5'  GTTAAGTGGGACTGCCCTGG   44380        ATAATA
                                TTAGGG     TTCATTTAGC
                                ||||||     ||||||||||
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                                GGTCCC     GGGTGAATTG
                                   GTCA__
GAM1611 LRMP     5' GCTGGATGCCTTATCTCTGG  21586        TATT
                                TTAGGGATAA    CATTTAGC
                                ||||||||||    ||||||||
                                GGTCTCTATT    GTAGGTCG
                                     CC__
GAM1611 LY6G6C   3' GCTTCTGTGTTGTCCCCAGTG 48273     A       TCATTT
                                TATT GGGATAATAT     AGC
                                |||| ||||||||||     |||
                                GTGA CCCTGTTGTG     TCG
                                  C        TCT___
GAM1611 MARK2    5' GCTGAATGGAAGTCGCTGGTA 66222      G   AATA
                                TATTAG GAT    TTCATTTAGC
                                |||||| |||    ||||||||||
                                ATGGTC CTG    AGGTAAGTCG
                                   G   A___
GAM1611 MGC10981 3' GCTGAGTGTCTCATGTCTTAAT 51986       ATAATATT
             G                   TATTAGGG       CATTTAGC
                                 ||||||||       ||||||||
                                 GTAATTCT       GTGAGTCG
                                      GTACTCT_
GAM1611 MGC12217 5' GTTGAATGAATGTCTGGCTC  52288    ATA_
                                GGG    ATATTCATTTAGC
                                |||    ||||||||||||
                                CTC    TGTAAGTAAGTTG
                                  GGTC
GAM1611 MGC12921 5' CTGAGTTCCTGTCCCTGA    64514       ATATTC
                                TTAGGGATA     ATTTAG
                                |||||||||     ||||||
                                AGTCCCTGT     TGAGTC
                                     CCT___
GAM1611 MGC12945 5' GCTAAGTGGTCGGTTCCTGG  51267       AATAT
                                TTAGGGAT    TCATTTAGC
                                ||||||||    |||||||||
                                GGTCCTTG    GGTGAATCG
                                     GCT__
GAM1611 MGC16142 5' GCTAAATGGGTCGTGTGTTTCT 52265     GG   AT__
             GA                   TTAG  ATA    ATTCATTTAGC
                                  ||||  |||    ||||||||||
                                  AGTC  TGT    TGGGTAAATCG
                                    TT   GTGC
GAM1611 MGC4268  3' GCTGAGTGTTTCCTTTGTCCTT 49544        TATT__
             GG                   TTAGGGATAA     CATTTAGC
                                  ||||||||||     ||||||||
                                  GGTTCCTGTT     GTGAGTCG
                                       TCCTTT
GAM1611 MGC4643  3' GTTGAAGGAATATTGTTTCTAA 52146     GG       A
                                TTAG  ATAATATTC TTTAGC
                                ||||  ||||||||| ||||||
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                                AATC  TGTTATAAG AAGTTG
                                  TT        G
GAM1611  NCKX3    3'  GTTGAATGTTTCTGTCTGTGGT 40727       G     ATATT
                G                  TATTA GGATA     CATTTAGC
                                   |||||| |||||     |||||||||
                                   GTGGT TCTGT     GTAAGTTG
                                     G     CTTT_
GAM1611  NEK1     3'  ATGTATATTATTTCTAATA    97560        GG      T
                                   TATTAG  ATAATAT CAT
                                   ||||||  ||||||| |||
                                   ATAATC  TATTATA GTA
                                      TT      T
GAM1611  POLYDOM  3'  GCTAGCATTGTTGTTCTTGGT  44687             TTCAT
                                   ATTAGGGATAATA     TTAGC
                                   ||||||||||||||    |||||
                                   TGGTTCTTGTTGT     GATCG
                                           TAC__
GAM1611  PPM1A    3'  GCTGGGCCTGCTGCTGTTCCTA 41009           ATATTCA_
                GTA                   TATTAGGGATA       TTTAGC
                                      ||||||||||        ||||||
                                      ATGATCCTTGT       GGGTCG
                                            CGTCGTCC
GAM1611  PPP1R10  3'  GCTAAGTTCATTATTCCTCATG 12231     T        ATTC
                                   TAT AGGGATAAT    ATTTAGC
                                   ||| |||||||||    |||||||
                                   GTA TCCTTATTA    TGAATCG
                                     C        CT__
GAM1611  PRO0159  5'  GCTGGGTGGGTATAGGCT    26947    ATA
                                   GG   ATATTCATTTAGC
                                   ||   ||||||||||||||
                                   TC   TATGGGTGGGTCG
                                    GGA
GAM1611  PRO1430  3'  TGAGTATTGTCTATTGGTA    38357       _
                                   TATTAG GGATAATATTCA
                                   |||||| ||||||||||||
                                   ATGGTT TCTGTTATGAGT
                                      A
GAM1611  PSKH1    3'  CTGGGTGGAGTGTCCT      68797       ATA
                                   GGGATA   TTCATTTAG
                                   ||||||   |||||||||
                                   TCCTGT   AGGTGGGTC
                                      G__
GAM1611  PSMD10   3'  GTGTTGTTGTCCCCAGTG    12533      A       TT
                                   TATT GGGATAATA  CAT
                                   |||| |||||||||  |||
                                   GTGA CCCTGTTGT  GTG
                                     C        T_
GAM1611  RAB40A   5'  GTTGGGTGAATATTATTTATGA 82945     GG
                                   TTA  GATAATATTCATTTAGC
                                   |||  ||||||||||||||||
```

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                                AGT  TTATTATAAGTGGGTTG
                                  AT
GAM1611  RBM11    3'  TGCATATTGTTCCTAATG    59239            T
                                TATTAGGGATAATAT CA
                                |||||||||||||||| ||
                                GTAATCCTTGTTATA GT
                                        C
GAM1611  SCDGF-B  3'  GTTAGATGAGTGACCTAA    53634      GATAA
                                TTAGG    TATTCATTTAGC
                                |||||    ||||||||||||
                                AATCC    GTGAGTAGATTG
                                  A____
GAM1611  SEMA7A   3'  GCTGGGTGGCTGGTGTTCCTGA 14610        A  TT
                                TTAGGGATA TA  CATTTAGC
                                ||||||||| ||  ||||||||
                                AGTCCTTGT GT  GTGGGTCG
                                      G  CG
GAM1611  SGK2     3'  GCTGGGTACGTGACTATCCCTA 33252         A_  TC
            ATA                   TATTAGGGATA  TAT  ATTTAGC
                                ||||||||||  |||  |||||||
                                ATAATCCCTAT  GTG  TGGGTCG
                                      CA   CA
GAM1611  ShrmL    3'  GTTATTGGTGTTTGTTCCTGAT 40851          TAT   TT
            G                    TATTAGGGATAA   TCA  TAGC
                                ||||||||||||   |||  ||||
                                GTAGTCCTTGTT   GGT  ATTG
                                      TGT   T_
GAM1611  SLC38A4  3'  GCTTTTTCATGTTATTCCTAA  36343          TCATTT
                                TTAGGGATAATAT     AGC
                                ||||||||||||     |||
                                AATCCTTATTGTA     TCG
                                      CTTTT_
GAM1611  SPTLC2   3'  GCTAGTTCTCTTTTATTCTTGA 17997          TATTCAT
            TG                   TATTAGGGATAA      TTAGC
                                ||||||||||||      |||||
                                GTAGTTCTTATT      GATCG
                                      TTCTCTT
GAM1611  ST13     3'  TGGATATGTGGTTCCTGATG   15434         A__
                                TATTAGGGAT   ATATTCA
                                |||||||||   |||||||
                                GTAGTCCTTG   TATAGGT
                                     GTG
GAM1611  STRIN    3'  GTTAAAATTGGGTATGTTCTTA 33232          A    __
            ATA                   TATTAGGGATA TATTCA  TTTAGC
                                ||||||||||| ||||||  ||||||
                                ATAATTCTTGT ATGGGT  AAATTG
                                      _    TA
GAM1611  SWAP2    3'  GCTGCTGGTTTTATCTCTAGTG 23901          TAT   TT
                                TATTAGGGATAA   TCA  TAGC
                                ||||||||||||   |||  ||||
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                              GTGATCTCTATT  GGT  GTCG
                                    TT_  C_
GAM1611  TEB4    3'  GCTAGGTGAGGAAATTATTTTT 61284          A__
           AAT                  ATTAGGGATAAT  TTCATTTAGC
                              ||||||||||||  ||||||||||
                              TAATTTTTATTA  GAGTGGATCG
                                    AAG
GAM1611  TTC2    3'  GTTGGATGCCCTGTGTCTCTG  13877        ATATT
                              TAGGGATA    CATTTAGC
                              ||||||||    ||||||||
                              GTCTCTGT    GTAGGTTG
                                  GTCCC
GAM1611  UBE3B   5'  GCTGGGTGATTTGTTCCTG   77446        TAT
                              TAGGGATAA   TCATTTAGC
                              |||||||||   |||||||||
                              GTCCTTGTT   AGTGGGTCG
                                   T__
GAM1611  VEST1   3'  GTTAAGTGAATGGATCTAA   54764      GATAA
                              TTAGG    TATTCATTTAGC
                              |||||    ||||||||||||
                              AATCT    GTAAGTGAATTG
                                 AG___
GAM1611  WBSCR20A 5'  GCTGGATGGAGTGCCCTGG   50572      ATAATA
                              TTAGGG     TTCATTTAGC
                              ||||||     ||||||||||
                              GGTCCC     AGGTAGGTCG
                                 GTG___
GAM1611  XYLT1   3'  TGAACTATTCTCCTTAGTA   78416        T   _
                              TATTAGGGA AATA TTCA
                              ||||||||| |||| ||||
                              ATGATTCCT TTAT AAGT
                                   C   C
GAM1611  ZFP95   3'  GCTGGATGGTATGTGTTTCTG  28120    GG   ATAT
                              TAG  ATA   TCATTTAGC
                              |||  |||   |||||||||
                              GTC  TGT   GGTAGGTCG
                                TT   GTAT
GAM1611  ZNF197  3'  GTTAAGTGAAAGGATCTTTG   23759       AATA
                              TAGGGAT    TTCATTTAGC
                              |||||||    ||||||||||
                              GTTTCTA    AAGTGAATTG
                                 GGA_
GAM1611  ZNF225  5'  GCTGCAGTTTTGTCCCTGGTA  26273          T  CATT
                              TATTAGGGATAA ATT    TAGC
                              |||||||||||| |||    ||||
                              ATGGTCCCTGTT TGA    GTCG
                                     T  C___
GAM1611  ZNF33A  3'  CTAACATTATCCTTGATG    92994          ATTCAT
                              TATTAGGGATAAT     TTAG
                              ||||||||||||      ||||
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                                GTAGTTCCTATTA     AATC
                                      C_____
GAM1611  LOC115219 5'  GCTGGGTGAGTGTGCACTTGGT 73697       GATA
                                ATTAGG    ATATTCATTTAGC
                                ||||||    ||||||||||||
                                TGGTTC    TGTGAGTGGGTCG
                                   ACG_
GAM1611  LOC122830 5'  CTGAGTGAGAACCTTGG     74630       ATAATA
                                TTAGGG     TTCATTTAG
                                ||||||     |||||||||
                                GGTTCC     GAGTGAGTC
                                   AA____
GAM1611  LOC123643 5'  TTAGATGAAGCCCCTGA     76529       ATAATA
                                TTAGGG     TTCATTTAG
                                ||||||     |||||||||
                                AGTCCC     AAGTAGATT
                                   CG____
GAM1611  LOC127703 3'  GCTGAGGCTATTGTCCCTGATG 75178            TTCA
                                TATTAGGGATAATA    TTTAGC
                                ||||||||||||||    ||||||
                                GTAGTCCCTGTTAT    GAGTCG
                                      CG__
GAM1611  LOC130502 3'  GTTGAATGGGTTTTTTTTAATG 75444         TAAT
                                TATTAGGGA    ATTCATTTAGC
                                |||||||||    ||||||||||
                                GTAATTTTT    TGGGTAAGTTG
                                   TT__
GAM1611  LOC137221 5'  GCTGGCTGAGTTTTATTTCTGA 76475       GG    T    T
            TG                    TATTAG  ATAA ATTCA TTAGC
                                ||||||  |||| ||||| |||||
                                GTAGTC  TATT TGAGT GGTCG
                                   TT    T    C
GAM1611  LOC137221 5'  TGAGTTTTATTTCTGATG    76476       GG    T
                                TATTAG  ATAA ATTCA
                                ||||||  |||| |||||
                                GTAGTC  TATT TGAGT
                                   TT    T
GAM1611  LOC143381 3'  GTTGAATGAAAAGCCTTGA    77062       ATAATA
                                TTAGGG     TTCATTTAGC
                                ||||||     ||||||||||
                                AGTTCC     AAGTAAGTTG
                                   GAA___
GAM1611  LOC144809 3'  TGACAGTGAATAATTTCTAATA 84105       GG  AA       TAGC
                                TATTAG  AT  TATTCATT
                                ||||||  ||  ||||||||
                                ATAATC  TA  ATAAGTGA
                                   TT  __       CAGTA
GAM1611  LOC145231 3'  AATGGGTATTGTCCCTAG    84234
                                TTAGGGATAATATTCATT
                                ||||||||||||||||||
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                                GATCCCTGTTATGGGTAA

GAM1611  LOC146455 3'  TATTTGATTTGTCTCTGATA  78466          TAT  TT
                                TATTAGGGATAA  TCA  TA
                                ||||||||||||  |||  ||
                                ATAGTCTCTGTT  AGT  AT
                                      T__  TT
GAM1611  LOC146723 3'  GCTAAAGACCTTATCCTTG  78681        TAT  A
                                TAGGGATAA  TC TTTAGC
                                |||||||||  || ||||||
                                GTTCCTATT  AG AAATCG
                                     CC_ _
GAM1611  LOC146990 5'  GTTGTTTTTGTGTTGTTCCTG  84956          TCATT
                                TAGGGATAATAT    TAGC
                                ||||||||||||    ||||
                                GTCCTTGTTGTG    GTTG
                                      TTTTT
GAM1611  LOC149832 5'  GTGATTTTGTCTCTAGTG    85869          TAT
                                TATTAGGGATAA  TCAT
                                ||||||||||||  ||||
                                GTGATCTCTGTT  AGTG
                                      TT_
GAM1611  LOC149844 3'  GTTGAATGGGCTGATCCT    80347      AATA
                                GGGAT   TTCATTTAGC
                                |||||   ||||||||||
                                TCCTA   GGGTAAGTTG
                                  GTC_
GAM1611  LOC149911 3'  GCTAAGTGAGTGAAGAGTC   85874    AA__
                                GAT   TATTCATTTAGC
                                |||   ||||||||||||
                                CTG   GTGAGTGAATCG
                                  AGAA
GAM1611  LOC150271 3'  CTGGGTGACTCCCTGA     86137       TAATAT
                                TTAGGGA     TCATTTAG
                                |||||||     ||||||||
                                AGTCCCT     AGTGGGTC
                                    C_____
GAM1611  LOC150372 3'  GCTGAATGAATGGGCCTGG   80617     GATAA
                                TTAGG    TATTCATTTAGC
                                |||||    ||||||||||||
                                GGTCC    GTAAGTAAGTCG
                                  GG___
GAM1611  LOC150933 3'  GTTGATTTTTGTTGTTCCTGA  86339          TTCAT
                                TTAGGGATAATA    TTAGC
                                ||||||||||||    |||||
                                AGTCCTTGTTGT    AGTTG
                                      TTTT_
GAM1611  LOC151516 3'  GCTAGAAATGCTTGTCTTTGA  81067          _   CA
                                TTAGGGATAA TATT  TTTAGC
                                |||||||||| ||||  ||||||
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                                AGTTTCTGTT GTAA  AGATCG
                                      C   __
GAM1611  LOC152185 3'  CTCACTGAGTTTGTTCTTAATA 59200          T    TTTAGC
                                TATTAGGGATAA ATTCA
                                |||||||||||| |||||
                                ATAATTCTTGTT TGAGT
                                       _    CACTCT
GAM1611  LOC152245 5'  GTTGGGTGGGCACCCCCTGAT  86784       ATAATA
                                ATTAGGG     TTCATTTAGC
                                |||||||     ||||||||||
                                TAGTCCC     GGGTGGGTTG
                                    CCAC__
GAM1611  LOC152674 5'  GTTGAGTGGAAGATGTCTTAGT 87005       ATAATA
              A                  TATTAGGG     TTCATTTAGC
                                 ||||||||     ||||||||||
                                 ATGATTCT     AGGTGAGTTG
                                     GTAGA_
GAM1611  LOC153205 3'  GCTAACAATGGTTATCTCTGA  87160         ATTCAT
                                TTAGGGATAAT     TTAGC
                                ||||||||||      |||||
                                AGTCTCTATTG     AATCG
                                      GTAAC_
GAM1611  LOC157657 3'  TGGAATTATTCCTGATA     82439           A
                                TATTAGGGATAAT TTCA
                                |||||||||||| ||||
                                ATAGTCCTTATTA AGGT
                                      _
GAM1611  LOC157798 5'  CTGGATGAAACCTTAGTA     87857       ATAATA
                                TATTAGGG     TTCATTTAG
                                ||||||||     |||||||||
                                ATGATTCC     AAGTAGGTC
                                    A_____
GAM1611  LOC157858 5'  GTTAAATGAGGGGCTCTCTGA  87895       TAATA
                                TTAGGGA     TTCATTTAGC
                                |||||||     ||||||||||
                                AGTCTCT     GAGTAAATTG
                                    CGGG_
GAM1611  LOC161589 3'  GGCTAAATGAATATTATCCCTA 83160
              ATA                  TATTAGGGATAATATTCATTTAGC
                                   ||||||||||||||||||||||||
                                   ATAATCCCTATTATAAGTAAATCG
                                         GA
GAM1611  LOC164971 5'  GCTAATATATTATCCTTTGGTG 83349      _       TCAT
                                TATTAG GGATAATAT    TTAGC
                                |||||| |||||||||    |||||
                                GTGGTT CCTATTATA    AATCG
                                   T       T___
GAM1611  LOC170127 3'  GCTGAGTGCCTGCCCTTGATG  83460       ATAATATT
                                TATTAGGG       CATTTAGC
                                ||||||||       ||||||||
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                                GTAGTTCC       GTGAGTCG
                                     CGTCC___
GAM1611  LOC196394 3'  GTTGGATGAGTCATTATTTTTG 89032          _
                A                    TTAGGGATAAT ATTCATTTAGC
                                     |||||||||||  ||||||||||
                                     AGTTTTTATTA TGAGTAGGTTG
                                           C
GAM1611  LOC199704 5'  GCTCCTATGAGTGTTAACCTTG 89697        A        TT_
                ATG                    TATTAGGG TAATATTCAT   AGC
                                     ||||||||  ||||||||||   |||
                                     GTAGTTCC ATTGTGAGTA   TCG
                                          A         TCC
GAM1611  LOC199953 3'  TTGGGTGAGGGTCCTGGT    89887        ATAATA
                                     ATTAGGG     TTCATTTAG
                                     |||||||     |||||||||
                                     TGGTCCT     GAGTGGGTT
                                          GG____
GAM1611  LOC200352 3'  CTAGATGCATTCCTGA      90233         AATATT
                                     TTAGGGAT     CATTTAG
                                     ||||||||     |||||||
                                     AGTCCTTA     GTAGATC
                                          C_____
GAM1611  LOC200399 3'  GTTGGGCTGATGTTGTTGTTGG 90241        G        CA
                TG                     TATTAG GATAATATT  TTTAGC
                                     ||||||  |||||||||  ||||||
                                     GTGGTT TTGTTGTAG  GGGTTG
                                        G        TC
GAM1611  LOC200734 3'  GCTGGAAAAGAGTATTTTTCTA 90280        GG T      A__
                ATA                    TATTAG  A AATATTC   TTTAGC
                                     ||||||  | |||||||   ||||||
                                     ATAATC  T TTATGAG   AGGTCG
                                        TT _      AAA
GAM1611  LOC200830 3'  TGAATTGTAATTCCTGATG    91731          A  _
                                     TATTAGGGAT ATA TTCA
                                     ||||||||||  |||  ||||
                                     GTAGTCCTTA TGT AAGT
                                           A   T
GAM1611  LOC200942 3'  GTTAGGGGAGCCTTTGTCTTTA 90379           TA_   A
                GTG                    TATTAGGGATAA   TTC TTTAGC
                                     ||||||||||||   |||  ||||||
                                     GTGATTTCTGTT   GAG GGATTG
                                           TCC   G
GAM1611  LOC201736 5'  TGGGTATGTGCCTAGTG     90482        G   A
                                     TATTAGG ATA TATTCA
                                     |||||||  |||  ||||||
                                     GTGATCC TGT ATGGGT
                                        G   _
GAM1611  LOC202460 5'  GCTGAGAGATATTATTCTTAG  90673            CA
                                     TTAGGGATAATATT  TTTAGC
                                     ||||||||||||||  ||||||
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                                GATTCTTATTATAG  GAGTCG
                                      A_
GAM1611  LOC202934 5'  GCTGGATGAAATATTCT     92042       ATA
                                GGGATA   TTCATTTAGC
                                ||||||   ||||||||||
                                TCTTAT   AAGTAGGTCG
                                   A__
GAM1611  LOC203286 3'  GCTGGATGTCCAAGTCCCTG   92146        AATATT
                                TAGGGAT     CATTTAGC
                                |||||||     ||||||||
                                GTCCCTG     GTAGGTCG
                                    AACCT_
GAM1611  LOC219902 5'  GCTAACATGTTATCTCTGA    93129           TCAT
                                TTAGGGATAATAT    TTAGC
                                ||||||||||||    |||||
                                AGTCTCTATTGTA    AATCG
                                       C___
GAM1611  LOC221496 3'  GCTGGATGAATAAACTATTT   93642       A__
                                GGATA   TATTCATTTAGC
                                |||||   ||||||||||||
                                TTTAT   ATAAGTAGGTCG
                                   CAA
GAM1611  LOC221687 3'  GTTGAATGTATATATTTCTAA  93871      GG   A   T
                                TTAG  ATA TAT CATTTAGC
                                ||||  ||| ||| ||||||||
                                AATC  TAT ATA GTAAGTTG
                                  TT   _   T
GAM1611  LOC221895 3'  GTTAGATGAGTAAACCTCTA   94106      ATAA
                                TAGGG    TATTCATTTAGC
                                |||||    ||||||||||||
                                ATCTC    ATGAGTAGATTG
                                   CAA_
GAM1611  LOC221931 3'  GCTGGGTGATGTTAGGTTTCTG 95631      GG  AATAT_
            G                    TTAG  AT     TCATTTAGC
                                ||||  ||     |||||||||
                                GGTC  TG     AGTGGGTCG
                                  TT  GATTGT
GAM1611  LOC222662 3'  GCTAAATGGGTCCATCTCTAG  94414        AAT
                                TTAGGGAT   ATTCATTTAGC
                                ||||||||   ||||||||||
                                GATCTCTA   TGGGTAAATCG
                                    CC_
GAM1611  LOC253698 3'  GCTGAAAATGTCATTTCTAGTA 96546       GG  A    CA
                                TATTAG  AT ATATT  TTTAGC
                                ||||||  || |||||  ||||||
                                ATGATC  TA TGTAA  AAGTCG
                                   TT  C    __
GAM1611  LOC255391 5'  GTTGGGTGGGTTTCTCTGG   99458        TAAT
                                TTAGGGA    ATTCATTTAGC
                                |||||||    ||||||||||
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                                GGTCTCT    TGGGTGGGTTG
                                   T___
GAM1611  LOC255465 5'  GCTGGATGAAATATTCT     99118       ATA
                                GGGATA   TTCATTTAGC
                                ||||||   ||||||||||
                                TCTTAT   AAGTAGGTCG
                                   A__
GAM1611  LOC257481 3'  GCTGTTCCGATGGTGTCTTTGA 61763          A    CATT
           TG                     TATTAGGGATA TATT    TAGC
                                ||||||||||| ||||    ||||
                                GTAGTTTCTGT GTAG    GTCG
                                      G    CCTT
GAM1611  LOC51316  3'  ATAAATGAATGTTGTCCCTGA  60247               GC
                                TTAGGGATAATATTCATTTA
                                ||||||||||||||||||||
                                AGTCCCTGTTGTAAGTAAAT
                                            AT
GAM1611  LOC83468  3'  TCTTTATGAATATTACCTTTGA 49344         A        TT  C
           TA                     TATTAGGG TAATATTCAT  AG
                                |||||||| ||||||||||  ||
                                ATAGTTTC ATTATAAGTA  TC
                                   C         TT  TT
GAM1611  LOC90190  3'  GCTAACTTTTGTGTTGACTCTG 62427         A     TCAT_
           GTG                      TATTAGGG TAATAT     TTAGC
                                |||||||| ||||||     |||||
                                GTGGTCTC GTTGTG     AATCG
                                   A     TTTTC
GAM1611  LOC90246  3'  GCTAAATGGATGTTGCTTGA   62587       GA
                                TTAGG  TAATATTCATTTAGC
                                |||||  ||||||||||||||
                                AGTTC  GTTGTAGGTAAATCG
                                   __
GAM1611  LOC91137  3'  TGGTATAGTATCCTTAATA    57860          A  _
                                TATTAGGGATA TAT TCA
                                |||||||||| ||| |||
                                ATAATTCCTAT ATA GGT
                                      G   T
GAM1611  LOC91548  5'  CTGGGTGAGACCCCTGG     67008       ATAATA
                                TTAGGG     TTCATTTAG
                                ||||||     |||||||||
                                GGTCCC     GAGTGGGTC
                                   CA____
GAM1611  LOC92140  3'  GCTTATGAAGTTATTTTTGATA 68826           A    TT
                                TATTAGGGATAAT TTCAT  AGC
                                |||||||||||| |||||  |||
                                ATAGTTTTTATTG AAGTA  TCG
                                      _    T_
GAM1611  LOC92283  3'  TGAAGTTGTTTCTAATG     69306       GG    A
                                TATTAG  ATAAT TTCA
                                ||||||  ||||| ||||
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                                GTAATC  TGTTG AAGT
                                   TT    _
GAM1611  LOC92344  3'  GTTTGAGGGTATTATCTTCTGG 69578       _       ATTTAGC
             TA                    TATTAGG GATAATATTC
                                   ||||||| ||||||||||
                                   ATGGTCT CTATTATGGG
                                      T        AGTTTG
GAM1611  LOC92379  3'  GTTAAATGTTTGATTGTTTTTG 69677          ATT_
             G                     TTAGGGATAAT   CATTTAGC
                                   ||||||||||    ||||||||
                                   GGTTTTTGTTA   GTAAATTG
                                         GTTT
GAM1611  LOC92421  3'  GCTGAATGAGAATCTCCTGG   69726     _  AATA
                                   TTAGG GAT   TTCATTTAGC
                                   ||||| |||   ||||||||||
                                   GGTCC CTA   GAGTAAGTCG
                                      T  A___
GAM1612  RAB3A    3'  GCCTGCCAGGCTCCTCTC    12698     AA    A
                                   GAGA  AGCCTG TAGGT
                                   ||||  |||||| |||||
                                   CTCT  TCGGAC GTCCG
                                     CC     C
GAM1612  RAMP1    3'  ACGTGACCTTGACTTACCTCT  20724     AA  CCTGAT
                                   AGAG  AAG     AGGTCACGT
                                   ||||  |||     |||||||||
                                   TCTC  TTC     TCCAGTGCA
                                     CA  AGT___
GAM1612  RUNX1    3'  ACATGGTTTGTCAGCCTTTCTC 10025       A  C     GT  C
                                   GAGAAA GC TGATAG  CA GT
                                   |||||| || ||||||  || ||
                                   CTCTTT CG ACTGTT  GT CA
                                      C  _     TG  A
GAM1612  SLC25A1  3'  ACGTGACCCTGTGCCCCGCCTC 21115     AAAA_  CTG    _
                                   GAG    GC   ATAGG TCACGT
                                   |||    ||   ||||| ||||||
                                   CTC    CG   TGTCC AGTGCA
                                     CGCCC  ___    C
GAM1612  ZNF264   3'  ATCTTTTCAGGCTTCTCT    14197      AA     T_
                                   AGAGA  AGCCTGA  AGGT
                                   |||||  |||||||  ||||
                                   TCTCT  TCGGACT  TCTA
                                      __      TT
GAM1612  CAPN6    3'  ACTCCTCAGACTTTTCTCT   27388         C   TA
                                   AGAGAAAAG CTGA  GGT
                                   ||||||||| ||||  |||
                                   TCTCTTTTC GACT  TCA
                                         A   CC
GAM1612  DNAM-1   3'  TCTCATGCAGGCTTTCCTCT  22688     A      AT__
                                   AGAG AAAGCCTG   AGG
                                   |||| ||||||||   |||
```

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                                TCTC TTTCGGAC    TCT
                                  C       GTAC
GAM1612 GFR      3'  ACATGACCTGCATTCACTTTTT 25442          CC__  A      C
              TCT                   AGAGAAAAG    TG TAGGTCA GT
                                |||||||||    || ||||||| ||
                                TCTTTTTTC    AC GTCCAGT CA
                                     ACTT  _      A
GAM1612 HSC3     3'  ATGAGACCTGTCCTCT      59729      AAAAGCCT       A
                                AGAG       GATAGGTC CGT
                                ||||       |||||||| |||
                                TCTC       CTGTCCAG GTA
                                  _________       A
GAM1612 KIAA0322 3'  ACCTTCAGGCTTCTCTC     94328      A       T
                                GAGA AAGCCTGA AGGT
                                |||| |||||||| ||||
                                CTCT TTCGGACT TCCA
                                  C       _
GAM1612 KIAA0662 3'  TGGACATCAAGCTGTTCTCT   82740       A   C    AG   A
                                AGAGAA AGC TGAT  GTC CG
                                |||||| ||| ||||  ||| ||
                                TCTCTT TCG ACTA  CAG GT
                                   G   A   __  _
GAM1612 KIAA1877 3'  ATGTACAGACTTTTTTCT    66740         C   A  G
                                AGAGAAAAG CTG TA GT
                                ||||||||| ||| || ||
                                TCTTTTTTC GAC AT TA
                                     A  _  G
GAM1612 PL6      5'  GCCTACCAGACCCTTTTCT    23814        C__   A
                                AGAAAAG   CTG TAGGT
                                |||||||   ||| |||||
                                TCTTTTC   GAC ATCCG
                                    CCA   C
GAM1612 SEMA4F   3'  ACATGACCCCATCCTTTTCTTT 16204          CCT   A_    C
                                AGAGAAAAG   GAT  GGTCA GT
                                |||||||||   |||  ||||| ||
                                TTTCTTTTC   CTA  CCAGT CA
                                     ___  CC    A
GAM1612 SEZ6     3'  ACTTGTCAGGCTCTCCTCT    74827      AAA
                                AGAG   AGCCTGATAGGT
                                ||||   ||||||||||||
                                TCTC   TCGGACTGTTCA
                                  CTC
GAM1612 TPRA40   3'  ACATGGCCCAGGCTTTCCTT   33485     A       ATA    C
                                GAG AAAGCCTG   GGTCA GT
                                ||| ||||||||   ||||| ||
                                TTC TTTCGGAC   CCGGT CA
                                  C       ___     A
GAM1612 LOC146176 3'  ACATGACCAAGAGCTTTTCTCT 78191           _ GATA    C
                                AGAGAAAAGC CT    GGTCA GT
                                |||||||||| ||    ||||| ||
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                                TCTCTTTTCG GA    CCAGT CA
                                      A  A___     A
GAM1612  LOC149373 3'  ACGTGACCTAGTTTCTTGCCCT 80089      AA_   CCTGA
           CT                    AGAG   AAG     TAGGTCACGT
                                ||||   |||    ||||||||||
                                TCTC   TTC    ATCCAGTGCA
                                  CCG   TTTG_
GAM1612  LOC255000 3'  GATCATCTGGCTTTTCTCT    98633          T   A
                                AGAGAAAAGCC GAT GGTC
                                |||||||||||| ||| ||||
                                TCTCTTTTCGG CTA CTAG
                                      T   _
GAM1612  LOC90525  3'  ACGTGATCTTTCAAACCTTTCT 63856       AGCC   T
           T                     GAGAAA    TGA AGGTCACGT
                                ||||||    ||| |||||||||
                                TTCTTT    ACT TCTAGTGCA
                                   CCAA   T
GAM1612  LOC91138  5'  ATCTATTAGGCCTTTCCCT    65657    A    A
                                AG GAAA GCCTGATAGGT
                                || |||| ||||||||||
                                TC CTTT CGGATTATCTA
                                 C    C
GAM1613  ALX3     3'  CTACCACAAACTGAGTC     22424        CCTA
                                GACTCAG    TGTGGTGG
                                |||||||    ||||||||
                                CTGAGTC    ACACCATC
                                    AA__
GAM1613  ATP7B    3'  TCACCACAAGCTGAGCA     5336     A     CTA
                                TG CTCAGC   TGTGGTGG
                                || ||||||   ||||||||
                                AC GAGTCG   ACACCACT
                                 _     A__
GAM1613  DSCR4    3'  TCACCAAGGCTGAGT       20791         ATG
                                ACTCAGCCT   TGGTGG
                                |||||||||   ||||||
                                TGAGTCGGA   ACCACT
                                      ___
GAM1613  NDRG3    3'  TGCCACCATACCCAGCTAAGTT 50128       C   CTA_
           A                     TGACT AGC    TGTGGTGGCA
                                ||||| |||    ||||||||||
                                ATTGA TCG    ATACCACCGT
                                   A   ACCC
GAM1613  NDST1    3'  CCACCACACGCTGAGCCA    9528     A     CTA
                                TG CTCAGC   TGTGGTGG
                                || ||||||   ||||||||
                                AC GAGTCG   ACACCACC
                                 C     C__
GAM1613  PLIN     3'  GCCGCTTCACAGGCTGAGTC   12173          A  T
                                GACTCAGCCT TG GGTGGC
                                |||||||||| || ||||||
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                                CTGAGTCGGA AC TCGCCG
                                      C  T
GAM1613 SCGB2A2  5' CTTGCCACCCGCGACTGA    11572     CCTA    _
                                TCAG    TGTGG TGGCAAG
                                ||||    ||||| |||||||
                                AGTC    GCGCC ACCGTTC
                                  A___     C
GAM1613 ZNF217   3' TGTTCACAAGCTGAGCCA    22548    A     CTA    TG
                                TG CTCAGC   TGTGG  GCA
                                || ||||||   |||||  |||
                                AC GAGTCG   ACACT  TGT
                                 C     A__    __
GAM1613 C21orf25 3' CTTGCCACCAGATGCT      64292     CT  G
                                AGC  AT TGGTGGCAAG
                                |||  || ||||||||||
                                TCG  TA ACCACCGTTC
                                  __  G
GAM1613 FLJ12484 3' TGAGTCCACAGGCTGAGCA   43178    A      AT    TGG
                                TG CTCAGCCT  GTGG   CA
                                || ||||||||  ||||   ||
                                AC GAGTCGGA  CACC   GT
                                 _       __    TGA
GAM1613 FLJ20343 3' GTCACACAACTGAGTCA     35469        CCTA    G
                                TGACTCAG    TGTG TGGC
                                ||||||||    |||| ||||
                                ACTGAGTC    ACAC ACTG
                                    A___    _
GAM1613 HSPC065  3' CCACCCAGGCTGAGT       27145         AT T
                                ACTCAGCCT  G GGTGG
                                |||||||||  | |||||
                                TGAGTCGGA  C CCACC
                                      __ _
GAM1613 KIAA0326 3' TCACCACAACTGAGTC      64969        CCTA
                                GACTCAG    TGTGGTGG
                                |||||||    ||||||||
                                CTGAGTC    ACACCACT
                                    A___
GAM1613 KIAA0690 5' TCGCCACGGCTTAGTCA     31475      C    TAT
                                TGACT AGCC   GTGGTGG
                                ||||| ||||   |||||||
                                ACTGA TCGG   CACCGCT
                                   T   ___
GAM1613 KIAA1821 3' GTTACACAGCCTGAGTCA    72272        CCTA    G
                                TGACTCAG    TGTG TGGC
                                ||||||||    |||| ||||
                                ACTGAGTC    ACAC ATTG
                                    CG__    _
GAM1613 KIAA1908 5' CCGCCAGCTCCAGGCTGAG   73785         AT_ _
                                CTCAGCCT   G TGGTGG
                                ||||||||   | ||||||
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                                GAGTCGGA  C ACCGCC
                                     CCT G
GAM1613 NICE-3   3' CTTGCCGTAGATTAAGCCAGTC 31884     CA  C  TGTG
                                GACT  GC TA   GTGGCAAG
                                ||||  || ||   ||||||||
                                CTGA  CG AT   TGCCGTTC
                                  C_  A  TAGA
GAM1613 OSRF     3' TTACCACAAATGAGTCA     60271       GCCTA
                                TGACTCA    TGTGGTGG
                                |||||||    ||||||||
                                ACTGAGT    ACACCATT
                                    AA___
GAM1613 LOC253128 3' TCACTATAGGCAGAGCCA    96579    A  A    _
                                TG CTC GCCTAT GTGG
                                || ||| |||||| ||||
                                AC GAG CGGATA CACT
                                 C  A     T
GAM1613 LOC51754  5' CCCCGCAAGCTGAGTC      71580       CTA    T
                                GACTCAGC   TGTGG GG
                                ||||||||   ||||| ||
                                CTGAGTCG   ACGCC CC
                                    A__    _
GAM1613 LOC92078  5' CCATAGCACAGGCTGAGTC   68594         A  G
                                GACTCAGCCT TGT GTGG
                                |||||||||| ||| ||||
                                CTGAGTCGGA ACG TACC
                                      C  A
GAM1614 CYLN2    3' ATGCAGCCCATCGGGGA     14088         CCCA
                                TCCCCGATGG   CTGCGT
                                ||||||||||   ||||||
                                AGGGGCTACC   GACGTA
                                      C___
GAM1614 GADD45B  3' CACGAGGACCATCGGGGG    32246         C  ACTG
                                TCCCCGATGG CC   CGTG
                                |||||||||| ||   ||||
                                GGGGGCTACC GG   GCAC
                                      A  A___
GAM1614 ITGA3    3' CACGCAGTGCGGATCCGGGA  11028     C  GG  _
                                TCCC GAT  CC CACTGCGTG
                                |||| |||  || |||||||||
                                AGGG CTA  GG GTGACGCAC
                                  C  __  C
GAM1614 LEP      3' TCACACAGTGGGTGGTGG    5869     G  G      C
                                CC AT GCCCACTG GTGA
                                || || |||||||| ||||
                                GG TG TGGGTGAC CACT
                                 _  G       A
GAM1614 LOXL2    5' ACTGCGTGATCCAGCCATCGGA 11350    C      C________   TGC
            GA                    TC CCGATGGC       CAC   GT
                                || ||||||||       |||   ||
```

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                                AG GGCTACCG       GTG   CA
                                 A       ACCT___A   CGT
GAM1614  SFRS7    3'  TCACGCAGCAGGAGCAGGGGA  60151       GATGG  CA
                                TCCCC    CC  CTGCGTGA
                                |||||    ||  ||||||||
                                AGGGG    GG  GACGCACT
                                   ACGA_  AC
GAM1614  SIRT7    3'  ACTGCGTGACCTGGCCATCGAG 33735     C       ________  TGC
            GA                    TCC CGATGGCC      CAC   GT
                                ||| ||||||||      |||   ||
                                AGG GCTACCGG      GTG   CA
                                 A       TCC___A   CGT
GAM1614  TBL1X    3'  ACTGCGTGACCCAGCCATCGGG 20128          C________  TGC
            GA                    TCCCCGATGGC       CAC   GT
                                ||||||||||       |||   ||
                                AGGGGCTACCG       GTG   CA
                                      ACCC___A   CGT
GAM1614  CTRP5    5'  CGAAGGAGGCCATCGGGGA   32230          CA  G
                                TCCCCGATGGCC  CT CG
                                ||||||||||||  || ||
                                AGGGGCTACCGG  GA GC
                                      AG  A
GAM1614  CXYorf1  5'  GGTGCAGGCCATTGGAGA    82918    C       __
                                TC CCGATGGCC  CACT
                                || |||||||||  ||||
                                AG GGTTACCGG  GTGG
                                 A        AC
GAM1614  DKFZP434J1813 5'  CGCGGCTGGGCCGTCGGAGA   62437    C        _
                                TC CCGATGGCCCA CTGCG
                                || ||||||||||| |||||
                                AG GGCTGCCGGGT GGCGC
                                 A          C
GAM1614  DKFZP727M111 5'  ACTGCGTGACCAGGACCATCGG 32051         _ ________  TGC
            G                     CCCGATGG CC       CAC   GT
                                |||||||| ||      |||   ||
                                GGGCTACC GG       GTG   CA
                                     A  ACC___A   CGT
GAM1614  FLJ11506 3'  TGTATGGGCCATGGAGA     45437    C  G      C
                                TC CC ATGGCCCA TGCG
                                || || |||||||| ||||
                                AG GG TACCGGGT ATGT
                                 A  _       _
GAM1614  FLJ20552 3'  CACGTCGGCCGTCGGG      35826          CACT
                                CCCGATGGCC    GCGTG
                                ||||||||||    |||||
                                GGGCTGCCGG    TGCAC
                                      C___
GAM1614  FLJ22160 3'  CACGAGGGCATCAGGGA     45030      C   G   ACTG
                                TCCC GATG CCC    CGTG
                                |||| |||| |||    ||||
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                                AGGG CTAC GGG    GCAC
                                  A   _  A___
GAM1614  FLJ22169  5'  CATGTATGCTCATCGGGGA   44230        _ CCAC
                                TCCCCGATG GC   TGCGTG
                                ||||||||| ||   ||||||
                                AGGGGCTAC CG   ATGTAC
                                     T  T___
GAM1614  FLJ23598  3'  CACACAAGCACTTCATCGGGGG 45863        CCCAC_  C
                                TCCCCGATGG     TG GTG
                                ||||||||||     || |||
                                GGGGGCTACT     AC CAC
                                     TCACGA  A
GAM1614  FOXP1     3'  CACGCAGCAGTATTGGGGG   52043        G CCA
                                TCCCCGATG C   CTGCGTG
                                ||||||||| |   |||||||
                                GGGGGTTAT G   GACGCAC
                                     _ AC_
GAM1614  HSBP1     5'  CAAGCTGGGCATCGGGGA    9519         G   CT  G
                                TCCCCGATG CCCA  GC TG
                                ||||||||| ||||  || ||
                                AGGGGCTAC GGGT  CG AC
                                     _   __ A
GAM1614  HSH2      3'  TCAGAGCAAGGCCCTCAGGGA 52743     C  T   CAC   G_
                                TCCC GA GGCC   TGC  TGA
                                |||| || ||||   |||  |||
                                AGGG CT CCGG   ACG  ACT
                                  A  C   A__   AG
GAM1614  KIAA1904  3'  CGGGGCAAGCCGTCGGGGA   73865         CCA  G
                                TCCCCGATGGC   CT CG
                                ||||||||||   || ||
                                AGGGGCTGCCG   GG GC
                                     AAC  G
GAM1614  SIAT4A    5'  CACACAGCCGTGTCTGGGA   13134     C  __  CCAC  C
                                TCCC GAT  GGC    TG GTG
                                |||| |||  |||    || |||
                                AGGG CTG  CCG    AC CAC
                                  T   TG  _____  A
GAM1614  STC2      3'  CACACAGTGGGTGCTGGG    14933     ATG      C
                                CCCG   GCCCACTG GTG
                                ||||   |||||||| |||
                                GGGT   TGGGTGAC CAC
                                  CG_       A
GAM1614  ZDHHC3    3'  ACTGCGTGATATTGACCATCGG 33927         CC_________  TGC
           GGA                    TCCCCGATGG        CAC   GT
                                ||||||||||         |||   ||
                                AGGGGCTACC         GTG   CA
                                     AGTTAT___A   CGT
GAM1614  LOC128916 5'  CACACAGTGGTGGGGA      76297       ATGGC     C
                                TCCCCG    CCACTG GTG
                                ||||||    |||||| |||
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                                AGGGGT    GGTGAC CAC
                                   _____     A
GAM1614  LOC149111 3'  TCACGCAGCAGCTGGGA    79932     CGAT   CCA
                                TCCC   GGC   CTGCGTGA
                                ||||   |||   ||||||||
                                AGGG   TCG   GACGCACT
                                  ____  AC_
GAM1614  LOC149837 5'  CAGAGGGGCCATCAGGGA    85890     C      A_
                                TCCC GATGGCCC  CTG
                                |||| ||||||||  |||
                                AGGG CTACCGGG  GAC
                                  A       GA
GAM1614  LOC152313 5'  CACACTGGGCCATGAGGGA   86845     CG      CTGC
                                TCCC  ATGGCCCA   GTG
                                ||||  ||||||||   |||
                                AGGG  TACCGGGT   CAC
                                  AG       CA__
GAM1614  LOC166983 5'  TGGAGCAGGCCATCGGGGA   88619          CA  G
                                TCCCCGATGGCC  CT CG
                                ||||||||||||  || ||
                                AGGGGCTACCGG  GA GT
                                       AC  G
GAM1614  LOC196500 3'  ACTGCGTGATCAAGGCCATCGG 89080         _________  TGC
           G                     CCCGATGGCC       CAC   GT
                                ||||||||||       |||   ||
                                GGGCTACCGG       GTG   CA
                                      AACT___A   CGT
GAM1614  LOC199958 3'  TCACGTAGGGAGCCCCAGG   91493    GAT   _  A
                                CC   GGC CC CTGCGTGA
                                ||   ||| || ||||||||
                                GG   CCG GG GATGCACT
                                 ACC   A  _
GAM1614  LOC200093 5'  GGTGCAGGCCATTGGAGA    63775    C       __
                                TC CCGATGGCC  CACT
                                || |||||||||  ||||
                                AG GGTTACCGG  GTGG
                                 A        AC
GAM1614  LOC90342  5'  CACGCAGTGGACAGTAAGGG   63009     GA__  GC
                                CCC    TG  CCACTGCGTG
                                |||    ||  ||||||||||
                                GGG    AC  GGTGACGCAC
                                  AATG  A_
GAM1614  LOC91040  5'  GGTGCAGGCCATTGGAGA    65349    C       __
                                TC CCGATGGCC  CACT
                                || |||||||||  ||||
                                AG GGTTACCGG  GTGG
                                 A        AC
GAM1614  LOC91828  5'  CGGGGTGGGCCTTCGGGGA   67858       T      G
                                TCCCCGA GGCCCACT CG
                                ||||||| |||||||| ||
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                                AGGGGCT CCGGGTGG GC
                                    T       G
GAM1615 CHAD    3' GGAAGGCTGAGCCTCTC     8855       TA  CTGC
                                GAGAG  CTC   GTCTTCC
                                |||||  |||   |||||||
                                CTCTC  GAG   CGGAAGG
                                  C_   T___
GAM1615 DSG1    5' AGGAAGGCAGAAACACCTC   10449     A  ACTC   GT
                                GAG GT   CTGC  CTTCCT
                                ||| ||   ||||  ||||||
                                CTC CA   GACG  GAAGGA
                                  _ CAAA   __
GAM1615 MID1    3' AAGATGTAGAAGTCCCTC    6351      T_  C
                                GAG  ACT CTGCGTCTT
                                |||  ||| |||||||||
                                CTC  TGA GATGTAGAA
                                  CC   A
GAM1615 OTOF    3' AGGAAGACTCCTGAAACCCTC 17828     A  AC  CTGC
                                GAG GT  TC   GTCTTCCT
                                ||| ||  ||   ||||||||
                                CTC CA  AG   CAGAAGGA
                                  C  A_  TCCT
GAM1615 RNMT    3' AGGACATCCAAGGGTACTCTC 15047        T   GCGTCT
                                GAGAGTAC CCT     TCCT
                                |||||||| |||     ||||
                                CTCTCATG GGA     AGGA
                                     _  ACCTAC
GAM1615 SCN3A   5' AGGAAGACACGTTATACCCT  23612    A  CTCC  C
                                AG GTA   TG GTCTTCCT
                                || |||   || ||||||||
                                TC CAT   GC CAGAAGGA
                                 C  ATT_  A
GAM1615 SFRS7   3' GGAAGGCGATACTCTC      60148       CTCCTG
                                GAGAGTA     CGTCTTCC
                                |||||||     ||||||||
                                CTCTCAT     GCGGAAGG
                                    A_____
GAM1615 SLC13A4 5' AAGACGAAGGAGGACTCTC   25857      A   G
                                GAGAGT CTCCT CGTCTT
                                |||||| ||||| ||||||
                                CTCTCA GAGGA GCAGAA
                                   G    A
GAM1615 SSX2    3' AGGAAGATGACGAGTAACTC  97962     _   CTG
                                GAGT ACTC   CGTCTTCCT
                                |||| ||||   |||||||||
                                CTCA TGAG   GTAGAAGGA
                                  A   CA_
GAM1615 TGFBR2  3' AAGATTCAAGAGTATTCTC   13725        C  C
                                GAGAGTACTC TG GTCTT
                                |||||||||| || |||||
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                                CTCTTATGAG AC TAGAA
                                      A  T
GAM1615  TNFRSF11A 3'  AGGAAGACCACCCGGCATTCTC 15187       A  CC_  C
                                GAGAGT CT   TG GTCTTCCT
                                |||||| ||   || ||||||||
                                CTCTTA GG   AC CAGAAGGA
                                   C  CCC  _
GAM1615  AP3M2    3'  AGGAAGACCCGTACTCTC    23299        TCCT C
                                GAGAGTAC    G GTCTTCCT
                                |||||||||   | ||||||||
                                CTCTCATG    C CAGAAGGA
                                     _____ C
GAM1615  CALN1    3'  AGGAAGACACAGAATTCTTTC  49658      TACTC   C
                                GAGAG     CTG GTCTTCCT
                                |||||     ||| ||||||||
                                CTTTC     GAC CAGAAGGA
                                   TTAA_   A
GAM1615  DAMS     5'  AGGAAATTCAAGTACTCT    42084        CC  C  C
                                AGAGTACT  TG GT TTCCT
                                ||||||||  || || |||||
                                TCTCATGA  AC TA AAGGA
                                     __  T  _
GAM1615  DKFZP727M111 5'  AGGCCAGGAGGACCCTC     32055     A  A     C
                                GAG GT CTCCTG GTCT
                                ||| || |||||| ||||
                                CTC CA GAGGAC CGGA
                                  C  G     _
GAM1615  FLJ14486 5'  AGGAAGGTTCAAGTCTCTC   52434      T   CC  CG
                                GAGAG ACT  TG  TCTTCCT
                                ||||| |||  ||  |||||||
                                CTCTC TGA  AC  GGAAGGA
                                   _  __  TT
GAM1615  FUSIP1   3'  AGGAAGACAGCCATAGTCTC   22780     T   CCT  _
                                GAG ACT   GC GTCTTCCT
                                ||| |||   || ||||||||
                                CTC TGA   CG CAGAAGGA
                                  _   TAC  A
GAM1615  HIC      3'  GAAGATTGAGTACTCT      68048          CTGC
                                AGAGTACTC    GTCTTC
                                |||||||||    ||||||
                                TCTCATGAG    TAGAAG
                                     T____
GAM1615  IL22R    3'  AGGAAATGCAGGGAAACTC   41467      AC       C
                                GAGT  TCCTGCGT TTCCT
                                ||||  |||||||| |||||
                                CTCA  GGGACGTA AAGGA
                                  AA       _
GAM1615  KIAA0472 3'  AGGAGGGGTAAGTACTCTC   72334         CC   G
                                GAGAGTACT  TGC TCTTCCT
                                |||||||||  ||| |||||||
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                                CTCTCATGA  ATG GGGAGGA
                                     __  _
GAM1615 KIAA1229 3' AGGATGTAAAAGTTCTCTC   62750      T  CC
                                GAGAG ACT  TGCGTCTT
                                ||||| |||  ||||||||
                                CTCTC TGA  ATGTAGGA
                                   T   AA
GAM1615 LAK-4P   3' AGGAAGACAGTTTCGCCTCTC  24394      TACTCCT  _
                                GAGAG      GC GTCTTCCT
                                |||||      || ||||||||
                                CTCTC      TG CAGAAGGA
                                   CGCTT__  A
GAM1615 MRPS35   3' AGGTCCTCAGGAGTATTCTC   41819           CGTCTT
                                GAGAGTACTCCTG     CCT
                                ||||||||||||      |||
                                CTCTTATGAGGAC     GGA
                                        TCCT__
GAM1615 OBTP     5' AGGATCTGCAAGGAGGACCCTC 34663     A  A    _   TCT
                                GAG GT CTCCT GCG   TCCT
                                ||| || ||||| |||   ||||
                                CTC CA GAGGA CGT   AGGA
                                  C  G    A  CT_
GAM1615 RI58     3' AGATCAGGAATACTCTT     25774        C    C
                                GAGAGTA TCCTG GTCT
                                ||||||| ||||| ||||
                                TTCTCAT AGGAC TAGA
                                    A    _
GAM1615 SMBP     3' AAGACAGAAGTGTACTCTC   72620        TC  GC_
                                GAGAGTAC  CT   GTCTT
                                ||||||||  ||   |||||
                                CTCTCATG  GA   CAGAA
                                     T_  AGA
GAM1615 SNTG1    5' AGGACTCTGAGGAGTACTCTT  39099           G  TCT
                                GAGAGTACTCCT CG   TCCT
                                ||||||||||| ||   ||||
                                TTCTCATGAGGA GT   AGGA
                                        _  CTC
GAM1615 SNX11    3' AGGACCAGGAGTATCTC     26169      G       C
                                GAGA TACTCCTG GTCTT
                                |||| |||||||| |||||
                                CTCT ATGAGGAC CAGGA
                                   _       _
GAM1615 TTY7     3' AGGAAGACACAGGTAGCT    50015     ACT    C
                                AGT   CCTG GTCTTCCT
                                |||   |||| ||||||||
                                TCG   GGAC CAGAAGGA
                                  AT_    A
GAM1615 LOC123872 5' GGAAAGAGGGTACTCTC     74710          _  GCGTC
                                GAGAGTACTC CT     TTCC
                                |||||||||| ||     ||||
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                                CTCTCATGGG GA     AAGG
                                     A ______
GAM1615  LOC138389 3'  AGGAAGACTTGCAAGTCTCTC  76725      T   CC  __
                                GAGAG ACT  TGC  GTCTTCCT
                                ||||| |||  |||  ||||||||
                                CTCTC TGA  ACG  CAGAAGGA
                                   _  __   TT
GAM1615  LOC143943 3'  AGGAAGATCAGCAGCCTCTC   83911      TA  C   C
                                GAGAG  CT CTG GTCTTCCT
                                |||||  || ||| ||||||||
                                CTCTC  GA GAC TAGAAGGA
                                   C_  C   _
GAM1615  LOC145009 5'  AAGAAACAAAGGAGTACTTTC  60965          GCG__
                                GAGAGTACTCCT     TCTT
                                ||||||||||||     ||||
                                CTTTCATGAGGA     AGAA
                                      AACAA
GAM1615  LOC147976 5'  AGGAAGACTGGGGTACCCTC   79285     A      TGC
                                GAG GTACTCC   GTCTTCCT
                                ||| |||||||   ||||||||
                                CTC CATGGGG   CAGAAGGA
                                  C      T__
GAM1615  LOC151512 3'  AGGAAGACAATGCTTGTACCTC 86611     A    TCCT  ___
                                GAG GTAC    GC   GTCTTCCT
                                ||| ||||    ||   ||||||||
                                CTC CATG    CG   CAGAAGGA
                                  _    TT__  TAA
GAM1615  LOC158801 3'  GAAAACACAAGAAGTATTCT   88255        _ C  C  C
                                AGAGTACT C TG GT TTC
                                |||||||| | || || |||
                                TCTTATGA G AC CA AAG
                                     A A  A  A
GAM1615  LOC206426 3'  GAAGCGAGGTGCACTCTC    91099       ACT   G  T
                                GAGAGT   CCT CG CTTC
                                ||||||   ||| || ||||
                                CTCTCA   GGA GC GAAG
                                   CGT   _  _
GAM1615  LOC254337 5'  GGAAAGGGGAGTATCTC     98012      G      GCGTC
                                GAGA TACTCCT     TTCC
                                |||| |||||||     ||||
                                CTCT ATGAGGG     AAGG
                                  _      GA___
GAM1615  LOC256790 5'  AGTGCAGGAGTGCCCTC     96489     A         T
                                GAG GTACTCCTGCG CT
                                ||| ||||||||||| ||
                                CTC CGTGAGGACGT GA
                                  C         _
GAM1615  LOC256946 3'  AGGAAGACAGCCATAGTCTC   96182     T   CCT  _
                                GAG ACT   GC GTCTTCCT
                                ||| |||   || ||||||||
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                                CTC TGA   CG CAGAAGGA
                                  _  TAC  A
GAM1615  LOC257396 5'  GAAATGTAGGAGCATCTC    98922     GTA       C
                                GAGA   CTCCTGCGT TTC
                                ||||   ||||||||| |||
                                CTCT   GAGGATGTA AAG
                                  AC_       _
GAM1615  LOC257408 3'  AGGGCACCAGGAGTACCTC    97797     A       C  CT
                                GAG GTACTCCTG GT  TCCT
                                ||| ||||||||| ||  ||||
                                CTC CATGAGGAC CA  GGGA
                                  _       _ C_
GAM1615  LOC257453 3'  AGGAAGATGACGAGTAACTC   82927     _   CTG
                                GAGT ACTC   CGTCTTCCT
                                |||| ||||   |||||||||
                                CTCA TGAG   GTAGAAGGA
                                  A   CA_
GAM1615  LOC51066  3'  AGGAAGATGGCCGACACTCTC  32500      AC  CTG
                                GAGAGT  TC   CGTCTTCCT
                                ||||||  ||   |||||||||
                                CTCTCA  AG   GTAGAAGGA
                                   C_  CCG
GAM1616  CHRNE     3'  GGCTGCCGCCACCACGG     5380        AC    TT
                                CCGTGGTG  GTGGT  CC
                                ||||||||  |||||  ||
                                GGCACCAC  CGCCG  GG
                                    __    TC
GAM1616  EN2       5'  TGGGATTTCGCCCCACGGTA   9274        TGAC   TT
                                TACCGTGG    GTGG  TCCCA
                                ||||||||    ||||  |||||
                                ATGGCACC    CGCT  AGGGT
                                    C___    TT
GAM1616  GPRC5B    3'  GGAAGGCAGGCACCACGG    33177        ACG  G
                                CCGTGGTG   TG TTTCC
                                ||||||||   || |||||
                                GGCACCAC   AC GAAGG
                                    GG_  G
GAM1616  NIPSNAP1  3'  AAACCTCGTCACCACGGT    14655          T
                                ACCGTGGTGACG GGTTT
                                |||||||||||| |||||
                                TGGCACCACTGC CCAAA
                                      T
GAM1616  PPARA     5'  TGAGAAGCTGTCACCAC     18528        GT     C
                                GTGGTGAC  GGTTTC CA
                                ||||||||  ||||||  ||
                                CACCACTG  TCGAAG GT
                                    __     A
GAM1616  PTPRO     3'  GAAACCACATCTGGT       48410      T   GAC
                                ACCG GGT   GTGGTTTC
                                |||| |||   ||||||||
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                              TGGT CTA   CACCAAAG
                                _  ___
GAM1616 PTPRO    3' GAAACCACATCTGGT      48411     T   GAC
                              ACCG GGT   GTGGTTTC
                              |||| |||   ||||||||
                              TGGT CTA   CACCAAAG
                                _  ___
GAM1616 TGFBI    3' GGAGGAATGCACCACGG     6270         A   GG
                              CCGTGGTG CGT  TTTCC
                              |||||||| |||  |||||
                              GGCACCAC GTA  GGAGG
                                   _  A_
GAM1616 AMOTL1   3' TGGGAAGGAGTCACACGGTA  74016       G   GTGG
                              TACCGTG TGAC    TTTCCCA
                              ||||||| ||||    |||||||
                              ATGGCAC ACTG    GAAGGGT
                                   _   AG__
GAM1616 B3GALT1  3' TGGGAAACTGAAACTCACAGTA 40943     C  _  GACG
                              TAC GTG GT    TGGTTTCCCA
                              ||| ||| ||    ||||||||||
                              ATG CAC CA    GTCAAAGGGT
                                A   T  AA__
GAM1616 C8orf17  3' GGAATAGTCTGTTACCACGG  39996          TGGT_
                              CCGTGGTGACG    TTCC
                              ||||||||||     ||||
                              GGCACCATTGT    AAGG
                                    CTGAT
GAM1616 DDM36    3' TGGGAAACCGTGGCCCAGG   40930    GT   G  GT
                              CC  GGT AC  GGTTTCCCA
                              ||  ||| ||  |||||||||
                              GG  CCG TG  CCAAAGGGT
                               AC   G  __
GAM1616 FLJ11726 3' TGGAGGAGTCACCACCCG    47033    T   AC   GT  _
                              CG GGTG  GTG  TTC CCA
                              || ||||  |||  ||| |||
                              GC CCAC  CAC  AGG GGT
                               _   __   TG   A
GAM1616 KBRAS2   3' GGAAGCAGAGTCACCACG    34624         GTG
                              CGTGGTGAC   GTTTCC
                              |||||||||   ||||||
                              GCACCACTG   CGAAGG
                                   AGA
GAM1616 KIAA0285 5' TGGGACCAGCAGCCACCATGG 29691        AC_ _  TT
                              CCGTGGTG   G TGG  TCCCA
                              ||||||||   | |||  |||||
                              GGTACCAC   C ACC  AGGGT
                                   CGA G   __
GAM1616 MGC11349 5' TGGGAAATCATTCACCA     47791       C
                              TGGTGA GTGGTTTCCCA
                              |||||| ||||||||||
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                                ACCACT TACTAAAGGGT
                                      _
GAM1616 MGC2477   5' GGCGCCCGCCACCACGG     44307        A  T   TTC
                                CCGTGGTG CG GGT   CC
                                |||||||| || |||   ||
                                GGCACCAC GC CCG   GG
                                     C  _   C__
GAM1616 MGC26610  5' GAAAAAGCTCACCACGG     58961        C  GG
                                CCGTGGTGA GT  TTTC
                                ||||||||| ||  ||||
                                GGCACCACT CG  AAAG
                                      _ AA
GAM1616 MGC3248   3' GGAACAGCCTGTCACCAC    51649        T  __
                                GTGGTGACG GGT  TTCC
                                ||||||||| |||  ||||
                                CACCACTGT CCG  AAGG
                                      _  AC
GAM1616 PTDSS1    5' TGGGGCCGCCGCCACCGCGG   29255        AC    T_
                                CCGTGGTG  GTGGT  TCCCA
                                ||||||||  |||||  |||||
                                GGCGCCAC  CGCCG  GGGGT
                                     __    CC
GAM1616 STHM      3' GGATGATGTCACCAGGTA     22307      G       G
                                TACC TGGTGACGT GTTT
                                |||| ||||||||| ||||
                                ATGG ACCACTGTA TAGG
                                  _       G
GAM1616 LOC148137 3' GGTGCCCGCCACCACGGT     59109        A  T   TT
                                ACCGTGGTG CG GGT  CC
                                ||||||||| || |||  ||
                                TGGCACCAC GC CCG  GG
                                     C  _   T_
GAM1616 LOC150299 3' GAGATCGCACCACGG        86167        GAC
                                CCGTGGT   GTGGTTTC
                                |||||||   ||||||||
                                GGCACCA   CGCTAGAG
                                     ____
GAM1616 LOC152059 3' GAAGTTGGTCACCACAGTG    81281     C      G GG
                                TAC GTGGTGAC T  TTTC
                                ||| |||||||| |  ||||
                                GTG CACCACTG G  GAAG
                                  A       _ TT
GAM1616 LOC157958 3' TGAGAAGCCAGTCACCACG    82532        G     C
                                CGTGGTGAC TGGTTTC CA
                                ||||||||| ||||||| ||
                                GCACCACTG ACCGAAG GT
                                     _      A
GAM1616 LOC254173 3' TGGGAAGCCATCGCCCCAC    98647      TGA  _
                                GTGG   CG TGGTTTCCCA
                                ||||   || ||||||||||
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                                CACC   GC ACCGAAGGGT
                                  CC_  T
GAM1617 CD58     3' CAAGCATTAGTTTTGGCTG   10113      A      CCA
                                TAGC GAGATTA   ATGCTTG
                                |||| |||||||   |||||||
                                GTCG TTTTGAT   TACGAAC
                                  G      ____
GAM1617 FOXO1A   3' AGCAAACATTATGTGGCCTCTG 10646    G    AT   C_   C
           GTA                    TA CAGAG  TAC  AATG TTGCT
                                || |||||  |||  |||| |||||
                                AT GTCTC  GTG  TTAC AACGA
                                 G    CG   TA    A
GAM1617 MFAP4    3' AGCAGAGGACAATCTCTGC   69787         A_  AA
                                GCAGAGATT  CC  TGCT
                                |||||||||  ||  ||||
                                CGTCTCTAA  GG  ACGA
                                     CA  AG
GAM1617 PRKACB   3' GCAAGCATTGTCTGTGC     12277     G   TTAC
                                GCA AGA    CAATGCTTGC
                                ||| |||    ||||||||||
                                CGT TCT    GTTACGAACG
                                  G  _____
GAM1617 SMARCA2  5' GCAAGCATTACTCTACTG    13242     C    ATTACC
                                TAG AGAG      AATGCTTGC
                                ||| ||||      |||||||||
                                GTC TCTC      TTACGAACG
                                  A   A_____
GAM1617 DKFZp547E052 3'  AGCATTTGGTAATTCTGCTA   51090         A      _
                                TAGCAGAG TTACCAA TGCT
                                |||||||| ||||||| ||||
                                ATCGTCTT AATGGTT ACGA
                                     _      T
GAM1617 FLJ12331 3' AGTTTTTGGTAATCTTGC    47109     G        T_
                                GCA AGATTACCAA  GCT
                                ||| ||||||||||  |||
                                CGT TCTAATGGTT  TGA
                                  _         TT
GAM1617 FLJ20294 3' CAAGTGGGTATCTCTGC     35346        T   AAT
                                GCAGAGAT ACC   GCTTG
                                |||||||| |||   |||||
                                CGTCTCTA TGG   TGAAC
                                     _   G__
GAM1617 MGC15937 3' AGCTGCTTAGTAATCTCTGC   55599          C  T  TT
                                GCAGAGATTAC AA GC  GCT
                                |||||||||||| || ||  |||
                                CGTCTCTAATG TT CG  CGA
                                       A  _  T_
GAM1617 SCYB5    3' AGCATAGTACCTCTGCTA    12982        AT   CA
                                TAGCAGAG  TAC  ATGCT
                                ||||||||  |||  |||||
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                                ATCGTCTC  ATG  TACGA
                                    C_   A_
GAM1617  ZNF185   3'  AGCAAGCATTGATTTTGTGCT  24091     G   TTAC
                                AGCA AGA    CAATGCTTGCT
                                |||| |||    ||||||||||
                                TCGT TTT    GTTACGAACGA
                                  G   TA__
GAM1617  ZNF262   3'  AGCAAGTGTAATAGTCCCCACT 18722     CAGA    CCA
             A                   TAG    GATTA   ATGCTTGCT
                                |||    |||||   |||||||||
                                ATC    CTGAT   TGTGAACGA
                                  ACCC    AA_
GAM1617  LOC147817 3'  AGCTTACGGCAATCTCTGCT   79167         A  AAT_
                                AGCAGAGATT CC    GCT
                                |||||||||| ||    |||
                                TCGTCTCTAA GG    CGA
                                      C  CATT
GAM1617  LOC149351 5'  AGCAAGCACTAAATTACTGT   80084      A    ACCAA
                                GCAG GATT     TGCTTGCT
                                |||| ||||     ||||||||
                                TGTC TTAA     ACGAACGA
                                  A    ATC__
GAM1617  LOC200251 3'  GTGCCTGTAATCTCCGCTA    90065      A       CAAT  TT
                                TAGC GAGATTAC    GC  GC
                                |||| ||||||||    ||  ||
                                ATCG CTCTAATG    CG  TG
                                  C       TC__  __
GAM1617  LOC201853 5'  CAAGAGTGAAGATAATCTCTCC 90506     C       C___  ATG
             TA                   TAG AGAGATTA    CA   CTTG
                                ||| ||||||||    ||   ||||
                                ATC TCTCTAAT    GT   GAAC
                                  C       AGAA  GA_
GAM1617  LOC221893 3'  AGCCACTGATAGTCTCTGCTA  94094           C  A  CTT
                                TAGCAGAGATTA CA TG   GCT
                                |||||||||||| || ||   |||
                                ATCGTCTCTGAT GT AC   CGA
                                      A  C  ____
GAM1617  LOC256940 5'  AGCAAGCATCATGGTTTC     98244     TT    __
                                GA  ACCA  ATGCTTGCT
                                ||  ||||  |||||||||
                                CT  TGGT  TACGAACGA
                                 T_    AC
GAM1618  HAL      5'  GCCACTCCTGCATAAAGCTC   10903          TGAAAA
                                GAGCTTTATGC     GGTGGC
                                ||||||||||     ||||||
                                CTCGAAATACG     TCACCG
                                      TCC___
GAM1618  HMGN2    3'  GGCCACCTTGGCACAAAAGC   19809       A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
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                                CGAAA AC AC  TTCCACCGG
                                  _ _ GG
GAM1618 NMI     5' GGCCACCTCCTCAGGAAG    17436     ATG   AA
                                CTTT  CTGA  AGGTGGCC
                                ||||  ||||  ||||||||
                                GAAG  GACT  TCCACCGG
                                  ___   CC
GAM1618 PACE    3' GGCCACCTCTCCAAGGGCTT   11944       A  CT  AAA
                                GAGCTTT TG  GA  GGTGGCC
                                ||||||| ||  ||  |||||||
                                TTCGGGA AC  CT  CCACCGG
                                   _ CT  ___
GAM1618 PYCR1   3' CCACCTTCCTCTAGAGCTC   70639       TGCT  A_
                                GAGCTTTA   GA  AAGGTGG
                                ||||||||   ||  |||||||
                                CTCGAGAT   CT  TTCCACC
                                   _____ CC
GAM1618 SDC1    3' GGCCACCTCCCCAGCATTCCAG 12991    TT_    AAA
            C                    GCT   ATGCTG   AGGTGGCC
                                |||   ||||||   ||||||||
                                CGA   TACGAC   TCCACCGG
                                  CCT     CCC
GAM1618 FLJ11560 5' GCCCAGGCCCAGCATAAAG   48008        AAAA  ___
                                CTTTATGCTG   GGT   GGC
                                ||||||||||   |||   |||
                                GAAATACGAC   CCG   CCG
                                   _____  GAC
GAM1618 KIAA0446 5' CCACCTTTTGAAGAGCTC    69446      ATGCTG
                                GAGCTTT     AAAAGGTGG
                                |||||||     |||||||||
                                CTCGAGA     TTTTCCACC
                                   AG_____
GAM1618 KIAA0971 3' GTTGTTCTCAGCATAAAGT   30677         AAA  TG
                                GCTTTATGCTGA   GG  GC
                                ||||||||||||   ||  ||
                                TGAAATACGACT   TT  TG
                                      C__  GT
GAM1618 KIAA1393 3' GGCCACCTTGGCACAAAAGC  72574      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _ GG
GAM1618 KIAA1656 3' GGCCACCTCCTCCTAGAAGCC 66377   A    ATGCT  AA
                                G GCTTT    GA  AGGTGGCC
                                | |||||    ||  ||||||||
                                C CGAAG    CT  TCCACCGG
                                 _    ATC__  CC
GAM1618 KIAA1884 3' GCCACCTTCATCTACCAAGGCT 73728       ATGCT  A_
            C                    GAGCTTT    GA  AAGGTGGC
                                |||||||    ||  ||||||||
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                                CTCGGAA    CT  TTCCACCG
                                    CCAT_  AC
GAM1618  PP3501    3'  GGCCACCGTTGACAGCATAAAG 41683          AAAA_
                                CTTTATGCTG    GGTGGCC
                                ||||||||||    |||||||
                                GAAATACGAC    CCACCGG
                                     AGTTG
GAM1618  SDCCAG3   3'  GGTGTTCTCAGCATGAAGCTC  22803           AAA  TG
                                GAGCTTTATGCTGA   GG  GCC
                                ||||||||||||||   ||  |||
                                CTCGAAGTACGACT   CT  TGG
                                       ___  TG
GAM1618  SP140     3'  GGCCACCTCCATGCAGAAGC   24327      A   TGAAA
                                GCTTT TGC    AGGTGGCC
                                ||||| |||    ||||||||
                                CGAAG ACG    TCCACCGG
                                  _  TACC_
GAM1618  LOC148760 3'  GGCCACCTTCTCCAACAAGCTC 85364       TA  CT  A
                                GAGCTT  TG  GA AAGGTGGCC
                                ||||||  ||  || |||||||||
                                CTCGAA  AC  CT TTCCACCGG
                                   CA  __  C
GAM1618  LOC150170 5'  ACCTGTTTCACATAAAGC    80414         C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                     _    G
GAM1618  LOC150175 5'  ACCTGTTTCACATAAAGC    80453         C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                     _    G
GAM1618  LOC150215 5'  ACCTGTTTCACATAAAGC    80456         C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                     _    G
GAM1618  LOC150218 5'  ACCTGTTTCACATAAAGC    80525         C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                     _    G
GAM1618  LOC152065 3'  GGCCACCTTCTCCTTGGCAGGC 86737       TTA   ___  A
            TC                    GAGCT   TGCT   GA AAGGTGGCC
                                |||||   ||||   || |||||||||
                                CTCGG   ACGG   CT TTCCACCGG
                                   ___    TTC  C
GAM1618  LOC152267 3'  GGCCACCTTGGCACAAAAGC   61036       A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
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                                CGAAA AC AC  TTCCACCGG
                                  _ _ GG
GAM1618  LOC158292 5'  CCTCTGGACCCAGCATAAGGCT 88046           AAAA_  T
              C                   GAGCTTTATGCTG    GG GG
                                  ||||||||||||    || ||
                                  CTCGGAATACGAC    TC CC
                                        CCAGG  T
GAM1618  LOC219997 3'  GCCACCTCTTCAGCCTC    93256    CTTTAT    A
                                  GAG    GCTGAA AGGTGGC
                                  |||    |||||| |||||||
                                  CTC    CGACTT TCCACCG
                                   _______    C
GAM1618  LOC256269 3'  GGCCACCTTGGCACAAAAGC  96608     A  C  AA
                                  GCTTT TG TG  AAGGTGGCC
                                  ||||| || ||  |||||||||
                                  CGAAA AC AC  TTCCACCGG
                                    _ _ GG
GAM1618  LOC91963  5'  GGCCACCTCCTCTGAGAAGC  68321     ATGCT  AA
                                  GCTTT    GA  AGGTGGCC
                                  |||||    ||  ||||||||
                                  CGAAG    CT  TCCACCGG
                                     AGT__  CC
GAM1619  ATP1A1   3'  CGCCGTGGAGCATCAGGCCA  7352        A    A
                                  TGGCCTGATG TCCAC GCG
                                  |||||||||| ||||| |||
                                  ACCGGACTAC AGGTG CGC
                                        G    C
GAM1619  AVPR1A   5'  CCGCTGTGAATACAGGC    7378      ATG  C
                                  GCCTG   AT CACAGCGG
                                  |||||   || ||||||||
                                  CGGAC   TA GTGTCGCC
                                     A__  A
GAM1619  CCND2    3'  CCAGCAAATCATCGGGCCA   10048         CCACA  _
                                  TGGCCTGATGAT    GC GG
                                  ||||||||||||    || ||
                                  ACCGGGCTACTA    CG CC
                                        AA___  A
GAM1619  GCN5L2   5'  TCCGCTGCGGGGGAGGCC    60530     GATGA   A
                                  GGCCT    TCC CAGCGGA
                                  |||||    ||| |||||||
                                  CCGGA    GGG GTCGCCT
                                     GG___   C
GAM1619  GJA5     3'  CCCTGACCAGATCATCAGCCA  19163     C      CA__   C
                                  TGGC TGATGATC    CAG GG
                                  |||| ||||||||    ||| ||
                                  ACCG ACTACTAG    GTC CC
                                    _       ACCA  _
GAM1619  HIVEP3   3'  CCGCTGTGGTTGGCAGCCA   44701     C  ATGAT
                                  TGGC TG    CCACAGCGG
                                  |||| ||    |||||||||
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                                ACCG AC    GGTGTCGCC
                                  _ GGTT_
GAM1619 HOXD1    5' CCGCCGGTATATTAGGCCA   44697        AT  ACA
                                TGGCCTGATG  CC   GCGG
                                ||||||||||  ||   ||||
                                ACCGGATTAT  GG   CGCC
                                     AT  C__
GAM1619 NGFR     3' CCGTCACCATCTCAGGCCA   11790       T   CCACA
                                TGGCCTGA GAT    GCGG
                                ||||||||  |||    ||||
                                ACCGGACT CTA    TGCC
                                    _  CCAC_
GAM1619 SUFU     3' TTGTGACCCATCAGGCCA    32942        ATC
                                TGGCCTGATG   CACAG
                                ||||||||||   |||||
                                ACCGGACTAC   GTGTT
                                     CCA
GAM1619 DKFZP586J1624 3'  CTCCGCCCAGTCACCATCAGGC 32044         ATCCACA_
              CA                  TGGCCTGATG      GCGGAG
                                ||||||||||      ||||||
                                ACCGGACTAC      CGCCTC
                                     CACTGACC
GAM1619 FBXO9    5' CTCCGCTGCAGAGACAGGC   54245     ATGA  CA
                                GCCTG   TC  CAGCGGAG
                                |||||   ||  ||||||||
                                CGGAC   AG  GTCGCCTC
                                  AG__  AC
GAM1619 SLC26A9  3' CCCTTAGGACCTCAGGCCA   54710       TGA   AC  C
                                TGGCCTGA   TCC  AG GG
                                ||||||||   |||  || ||
                                ACCGGACT   AGG  TC CC
                                    CC_   AT  _
GAM1619 SLC26A9  3' CCCTTAGGACCTCAGGCCA   54711       TGA   AC  C
                                TGGCCTGA   TCC  AG GG
                                ||||||||   |||  || ||
                                ACCGGACT   AGG  TC CC
                                    CC_   AT  _
GAM1619 LOC130074 3'  CTGGGCCAGATCTCAGGCCA   76625       T   CACAG
                                TGGCCTGA GATC    CGG
                                ||||||||  ||||    |||
                                ACCGGACT CTAG    GTC
                                    _   ACCGG
GAM1619 LOC159110 5'  CTCCGCTGCCCCGGTCAACCA  82989    CCTGA    CA__
                                TGG    TGATC    CAGCGGAG
                                |||    |||||    ||||||||
                                ACC    ACTGG    GTCGCCTC
                                  A_____    CCCC
GAM1619 LOC159116 5'  CTCCGCTGCCCCGGTCAACCA  82972    CCTGA    CA__
                                TGG    TGATC    CAGCGGAG
                                |||    |||||    ||||||||
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                                ACC    ACTGG   GTCGCCTC
                                  A____    CCCC
GAM1619  LOC165476 5'  CTCCGCTGCCTGCTCAGCCA  88551     C  TGATCCA
                                TGGC TGA      CAGCGGAG
                                |||| |||      ||||||||
                                ACCG ACT      GTCGCCTC
                                  _  CGTCC__
GAM1619  LOC200032 5'  CCCTGACCAGATCATCAGCCA 85474     C      CA__  C
                                TGGC TGATGATC   CAG GG
                                |||| ||||||||   ||| ||
                                ACCG ACTACTAG   GTC CC
                                  _      ACCA  _
GAM1619  LOC219654 5'  CTCCGCTGCGGAGGGGGGCC  92933     GATGA  A
                                GGCCT    TCC CAGCGGAG
                                |||||    ||| ||||||||
                                CCGGG    AGG GTCGCCTC
                                   GGG__  C
GAM1619  LOC220002 3'  CTCCTGGCAACATCAGGCCA  93271       AT_  CAGC
                                TGGCCTGATG  CCA   GGAG
                                ||||||||||  |||   ||||
                                ACCGGACTAC  GGT   CCTC
                                      AAC  ____
GAM1620  COL12A1  3'  ACCAAATGGAATCTCCTCA   55532    A   CGAATG
                                TGA GGAGA     TATTTGGT
                                ||| |||||     ||||||||
                                ACT CCTCT     GTAAACCA
                                  _    AAG___
GAM1620  FENS-1   3'  CACCAAATGAAGTCCCTCTCA 40830    _  A  GAATG
                                TGA AGG GAC    TATTTGGTG
                                ||| ||| |||    |||||||||
                                ACT TCC CTG    GTAAACCAC
                                  C  _  AA___
GAM1620  KIAA0914 3'  CACCAAATCCTCCATCTCTTCA 30292     G  CGAATGT
                                TGAAG AGA      ATTTGGTG
                                ||||| |||      ||||||||
                                ACTTC TCT      TAAACCAC
                                  _  ACCTCC_
GAM1620  MOST2    3'  CAGGACTCTCACCTCCTTCA  40057       AC  AT  A
                                TGAAGGAG  GA  GT TTTG
                                ||||||||  ||  || ||||
                                ACTTCCTC  CT  CA GGAC
                                     CA  CT  _
GAM1620  RODH-4   3'  ACCAATCCCACTCCTTCA    14921       ACGAA  TAT
                                TGAAGGAG    TG   TTGGT
                                ||||||||    ||   |||||
                                ACTTCCTC    AC   AACCA
                                     _____  CCT
GAM1621  KCNJ8    3'  CACCAAGTGGAGGATTCAT   18360       CA   A  C
                                ATGAATCCT  CCAT TG TG
                                |||||||||  |||| || ||
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                                TACTTAGGA  GGTG AC AC
                                     __    A  C
GAM1621  LUM      5'  AGACAGTAAGGATTCA      11378         CACCATA    _
                                TGAATCCT      TGCTG CT
                                ||||||||      ||||| ||
                                ACTTAGGA      ATGAC GA
                                     ________    A
GAM1621  PODXL    3'  AGTGGGCATGGTGAGGTTTCAT 19412       T       ATG TG
                                ATGAA CCTCACCAT   C  CT
                                ||||| |||||||||   |  ||
                                TACTT GGAGTGGTA   G  GA
                                   T       CG_ GT
GAM1621  POLA     3'  TAGGGGTTACGGTGAGGATCAT 34200      A       ATAT   G
                                ATGA TCCTCACC    GCT CTA
                                |||| ||||||||    ||| |||
                                TACT AGGAGTGG    TGG GAT
                                  _       CAT_   G
GAM1621  SFRP1    3'  TAGCATGGGAGGTGAGGATTC  13026           A__
                                GAATCCTCACC   TATGCTG
                                ||||||||||   |||||||
                                CTTAGGAGTGG   GTACGAT
                                      AGG
GAM1621  C4ST     3'  CAGCATAGTGAGAATT      60813     C     CA
                                AAT CTCAC  TATGCTG
                                ||| |||||  |||||||
                                TTA GAGTG  ATACGAC
                                  A    __
GAM1621  DKFZP564F0522 3'  CAGTTTTGAAAATGAGGATTCA 69137          C___  TAT
                                TGAATCCTCA    CA   GCTG
                                ||||||||||    ||   ||||
                                ACTTAGGAGT    GT   TGAC
                                      AAAA  TT_
GAM1621  FLJ20511  5'  AGGAGTGACAGTGAGGATTCA  35765          CATAT   G
                                TGAATCCTCAC     GCT CT
                                ||||||||||     ||| ||
                                ACTTAGGAGTG     TGA GA
                                      ACAG_   G
GAM1621  FLJ20758  3'  CAGACACATGGTGAGGTCCAT  36079     AAT       A  _
                                ATG   CCTCACCAT TG CTG
                                |||   ||||||||| || |||
                                TAC   GGAGTGGTA AC GAC
                                  CT_       C  A
GAM1621  GT650    5'  CAGTTATATGAGGATTCA    54549          CC   T
                                TGAATCCTCA  ATA GCTG
                                ||||||||||  ||| ||||
                                ACTTAGGAGT  TAT TGAC
                                      A_  _
GAM1621  KIAA0247  3'  CAGAATATGGTGAAAATCA   29064     ATCC       G
                                TGA    TCACCATAT CTG
                                |||    ||||||||| |||
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                                ACT   AGTGGTATA GAC
                                  AAA_       A
GAM1621 KIAA1084 3' GTAGTAAGGATTCAT      30503        CACCATA    _
                                ATGAATCCT     TGCTG C
                                |||||||||     |||||| |
                                TACTTAGGA     ATGAT G
                                    ________    A
GAM1621 KIAA1511 3' TAGCAAGTGTGTGAATTCA   70730     CC   _  A
                                TGAAT  TCAC CAT TGCTG
                                |||||  |||| ||| |||||
                                ACTTA  AGTG GTG ACGAT
                                   __   T  A
GAM1621 KIAA1765 3' GGCAGTGTAATGGGACTCAT  71134     A  T  CCA
                                ATGA TCC CA   TATGCTGCT
                                |||| ||| ||   |||||||||
                                TACT AGG GT   ATGTGACGG
                                  C  _ A__
GAM1621 SLC26A7  3' TAGCAAATGTGTGGTAAACATT 54512      CCTC     GC_
           CAT                    ATGAAT   ACCATAT   TGCTA
                                |||||||   |||||||  |||||
                                TACTTA   TGGTGTG   ACGAT
                                   CAAA     TAA
GAM1622 ADAT1    3' TGAGGCAGGAGAATTGCTTGAA 24920      TG     C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622 AICDA    3' TGAGGCAGGAGAATCGCTTGAA 40700           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                          A
GAM1622 AIRE     3' TGAGGCATGAGAATCACTTGAA 6353           CC
                                TTCAAGTGATTCTC  GCCTCA
                                ||||||||||||  ||||||
                                AAGTTCACTAAGAG  CGGAGT
                                          TA
GAM1622 AK1      3' TGAGGCAGGAGGATCACCTGAG 6643      A       C
                                TTCA GTGATTCTCC GCCTCA
                                |||| ||||||||| ||||||
                                GAGT CACTAGGAGG CGGAGT
                                  C        A
GAM1622 ALDH3B1  3' AGGCAGGAGAATCGCTTGAA  93150           C
                                TTCAAGTGATTCTCC GCCT
                                |||||||||||||| ||||
                                AAGTTCGCTAAGAGG CGGA
                                          A
GAM1622 ALPP     3' TGAAGCAGGATAATCGCTTGAA 69422         C  C  C
                                TTCAAGTGATT TCC GC TCA
                                |||||||||| ||| || |||
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                                AAGTTCGCTAA AGG CG AGT
                                      T  A  A
GAM1622  ANKH     3'  TGAGGCAGGAGAATTTGCTTGA 55077      TG _     C
                                TCAAG  A TTCTCC GCCTCA
                                |||||  | |||||| ||||||
                                AGTTC  T AAGAGG CGGAGT
                                   GT T     A
GAM1622  ANKH     3'  TGAGGCAGGAGGATCGCTT   39551          C
                                AAGTGATTCTCC GCCTCA
                                |||||||||||| ||||||
                                TTCGCTAGGAGG CGGAGT
                                      A
GAM1622  APAF1    3'  TGAGACAGGAGGATTCCTTGAG 25986      TG      CGC
                                TTCAAG  ATTCTCC   CTCA
                                ||||||  |||||||   ||||
                                GAGTTC  TAGGAGG   GAGT
                                   CT      ACA
GAM1622  APAF1    3'  TGAGACAGGAGGATTCCTTGAG 8594       TG      CGC
                                TTCAAG  ATTCTCC   CTCA
                                ||||||  |||||||   ||||
                                GAGTTC  TAGGAGG   GAGT
                                   CT      ACA
GAM1622  ATM      3'  TGAGGCAGGAGAATCTCTTGAA 5305       T       C
                                TTCAAG GATTCTCC GCCTCA
                                |||||| |||||||| ||||||
                                AAGTTC CTAAGAGG CGGAGT
                                   T       A
GAM1622  ATM      3'  TGAGGCAGGAGAATCTCTTGAA 57139      T       C
                                TTCAAG GATTCTCC GCCTCA
                                |||||| |||||||| ||||||
                                AAGTTC CTAAGAGG CGGAGT
                                   T       A
GAM1622  ATP1A2   3'  TGAGGCAGGAGAATTGCTTGAA 7371       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  BHMT2    3'  GAGGCGGGCGGATCACCTGAG  34734     A       T
                                TTCA GTGATTC CCCGCCTC
                                |||| ||||||| ||||||||
                                GAGT CACTAGG GGGCGGAG
                                  C      C
GAM1622  BHMT2    3'  TGAGGCAGGAGAATCGCTTGAA 34741          C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  BRCA1    5'  TGAGGCAGGAGAATCGCTAGAA 24464     A        C
                                TTC AGTGATTCTCC GCCTCA
                                ||| |||||||||| ||||||
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                                AAG TCGCTAAGAGG CGGAGT
                                  A         A
GAM1622  C21orf5   3'  AGGCAGGCAGATCACTTGAG   18881          CT  C
                                TTCAAGTGATT  CC GCCT
                                ||||||||||  || ||||
                                GAGTTCACTAG  GG CGGA
                                      AC  A
GAM1622  CARKL     3'  TGAGGCAGGAAAATCACTTGAA 26110           C   C
                                TTCAAGTGATT TCC GCCTCA
                                ||||||||||| ||| ||||||
                                AAGTTCACTAA AGG CGGAGT
                                      A   A
GAM1622  CASP10    3'  AGGCAGGCAGATCACTTGAG   53215          CT  C
                                TTCAAGTGATT  CC GCCT
                                ||||||||||  || ||||
                                GAGTTCACTAG  GG CGGA
                                      AC  A
GAM1622  CASP10    3'  TGAGACAGGAGAATCTCTTGAA 53229       T      CGC
                                TTCAAG GATTCTCC   CTCA
                                ||||||| ||||||||   ||||
                                AAGTTC CTAAGAGG   GAGT
                                   T       ACA
GAM1622  CASP10    3'  AGGCAGGCAGATCACTTGAG   53242          CT  C
                                TTCAAGTGATT  CC GCCT
                                ||||||||||  || ||||
                                GAGTTCACTAG  GG CGGA
                                      AC  A
GAM1622  CASP10    3'  TGAGACAGGAGAATCTCTTGAA 53268       T      CGC
                                TTCAAG GATTCTCC   CTCA
                                ||||||| ||||||||   ||||
                                AAGTTC CTAAGAGG   GAGT
                                   T       ACA
GAM1622  CASP6     3'  TGAGGCAGGAGAATCACTTGAA 53367            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  CASP6     3'  TGAGGCAGGAGAATCACTTGAA 8736             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  CD28      3'  TGAGGCATGAGAATCGCTTGAA 21560           CC
                                TTCAAGTGATTCTC  GCCTCA
                                ||||||||||||  ||||||
                                AAGTTCGCTAAGAG  CGGAGT
                                      TA
GAM1622  CD68      3'  TGAGGCAGAACTGCTTGAA   60509       GA   CCC
                                TTCAAGT  TTCT   GCCTCA
                                |||||||  ||||   ||||||
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                                AAGTTCG  AAGA   CGGAGT
                                   TC   ___
GAM1622  CEACAM5   3'  TGAGGCAGGAGAATCGCTTGAA 16426              C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                         A
GAM1622  CHST5     3'  TGAGGCGGGTGGATCACCTGAG 25091      A      T
                                TTCA GTGATTC CCCGCCTCA
                                |||| ||||||| |||||||||
                                GAGT CACTAGG GGGCGGAGT
                                  C      T
GAM1622  CHST5     3'  TGAGGTGGGAGAATCACTTGGA 25092
                                TTCAAGTGATTCTCCCGCCTCA
                                |||||||||||||||||||||
                                AGGTTCACTAAGAGGGTGGAGT

GAM1622  CNGB1     3'  GAAGCAGGAGGATCACTGGA   8936      A        C  C
                                TTCA GTGATTCTCC GC TC
                                |||| |||||||||| || ||
                                AGGT CACTAGGAGG CG AG
                                  _        A  A
GAM1622  COPA      3'  TGAGGCATGAGAATCGCTTGAA 16482            CC
                                TTCAAGTGATTCTC  GCCTCA
                                ||||||||||||  ||||||
                                AAGTTCGCTAAGAG  CGGAGT
                                         TA
GAM1622  CPM       3'  TGAGACAGGAGAATCGCTTGAA 60412            CGC
                                TTCAAGTGATTCTCC   CTCA
                                ||||||||||||||   ||||
                                AAGTTCGCTAAGAGG   GAGT
                                         ACA
GAM1622  CPT2      3'  TGAAGCAGAATTGCTTGAA    5430       TG    CCC  C
                                TTCAAG  ATTCT   GC TCA
                                ||||||  |||||   || |||
                                AAGTTC  TAAGA   CG AGT
                                   GT    ___  A
GAM1622  CPT2      3'  TGAGGCGGGTGGATCACTTGAG 5431           T
                                TTCAAGTGATTC CCCGCCTCA
                                |||||||||||| |||||||||
                                GAGTTCACTAGG GGGCGGAGT
                                      T
GAM1622  CRACC     3'  AGGCATGAGAATCGCTTGAA   41305           CC
                                TTCAAGTGATTCTC  GCCT
                                ||||||||||||||  ||||
                                AAGTTCGCTAAGAG  CGGA
                                         TA
GAM1622  CTMP      3'  TGAGGCAGGAGAATTGCTTGAA 54956       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
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                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  CUBN     3'  TGAGGCAGGAGAATTGCTTGAA 8426       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  CYP3A4   3'  TGAGGCAGGAGAATCACTTGAA 34367           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                         A
GAM1622  CYP4F3   3'  TGAGGCAGGAGAATCGCTTGAA 8019            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                         A
GAM1622  CYP4F3   3'  TGATGCAGGAGAATCACTTGAA 8020            C  C
                                TTCAAGTGATTCTCC GC TCA
                                |||||||||||||| || |||
                                AAGTTCACTAAGAGG CG AGT
                                         A  T
GAM1622  DAPP1    3'  TGAGGCAGGAGAATTGCTTGAA 27684       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  DBT      3'  TGAAGCAGGAGGATCACTTGAG 10383           C  C
                                TTCAAGTGATTCTCC GC TCA
                                |||||||||||||| || |||
                                GAGTTCACTAGGAGG CG AGT
                                         A  A
GAM1622  DBT      3'  TGAGGCAGGAGAATCGCTTGAA 10384           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                         A
GAM1622  DBT      3'  TGAGGCAGGAGAATTGCTTGAG 10385       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                GAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  DCLRE1C  3'  AGGCAGGAGAATCACTTGAA  42818           C
                                TTCAAGTGATTCTCC GCCT
                                |||||||||||||| ||||
                                AAGTTCACTAAGAGG CGGA
                                         A
GAM1622  DHFR     3'  AGGCAGGCAGATCACTTGAG  7641          CT  C
                                TTCAAGTGATT  CC GCCT
                                ||||||||||  || ||||
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                                GAGTTCACTAG  GG CGGA
                                      AC  A
GAM1622  DLG5     5'  TGAGGCGGGAGAATGGGC    83824    G_
                                GT  ATTCTCCCGCCTCA
                                ||  ||||||||||||||
                                CG  TAAGAGGGCGGAGT
                                 GG
GAM1622  DMC1     3'  GAGGCAGGTGGATCACTTGAG  23944          T  C
                                TTCAAGTGATTC CC GCCTC
                                |||||||||||| || |||||
                                GAGTTCACTAGG GG CGGAG
                                      T  A
GAM1622  DMC1     3'  TGAGGCAGGAGAATTGCTTGAA 23948       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  DNASE2   3'  AGGAGGGAGGATCACTTGAA   9098             G
                                TTCAAGTGATTCTCCC CCT
                                |||||||||||||||| |||
                                AAGTTCACTAGGAGGG GGA
                                         A
GAM1622  DNASE2   3'  TGAGGCAGGAGAATCGCTTGAA 9101              C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                         A
GAM1622  DSC1     3'  TGAGGCAGGAGAATCGCTTGAA 18245             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                         A
GAM1622  DSC1     3'  TGAGGCAGGAGAATCGCTTGAA 44608             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                         A
GAM1622  DVL3     3'  TGAGACAGGTGGATCACTTGAG 16653          T  CGC
                                TTCAAGTGATTC CC   CTCA
                                |||||||||||  ||   ||||
                                GAGTTCACTAGG GG   GAGT
                                      T  ACA
GAM1622  DVL3     3'  TGAGGCACAAGAATCGCTTGAA 16654          CCC
                                TTCAAGTGATTCT   GCCTCA
                                ||||||||||||   ||||||
                                AAGTTCGCTAAGA   CGGAGT
                                         ACA
GAM1622  EGFL4    3'  TGAGGCAGAAGAATCGCTTGAA 62476           CCC
                                TTCAAGTGATTCT   GCCTCA
                                ||||||||||||   ||||||
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                                AAGTTCGCTAAGA  CGGAGT
                                      AGA
GAM1622  EGFL5    3'  TGAGGCAGGAGAATCACTTGAA 87923            C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  ENPP3    3'  TGAGGCAGGAGACTCGCTTGAA 18472        T   C
                                TTCAAGTGA TCTCC GCCTCA
                                ||||||||| ||||| ||||||
                                AAGTTCGCT AGAGG CGGAGT
                                    C   A
GAM1622  EPHA2    3'  GGCCAAGAATACTTGAA    16678        A   CCC
                                TTCAAGTG TTCT  GCC
                                |||||||| ||||  |||
                                AAGTTCAT AAGA  CGG
                                    _   AC_
GAM1622  ERBB3    3'  TGAGGCAGAAGGATTACCTGAG 10538     A      CCC
                                TTCA GTGATTCT  GCCTCA
                                |||| ||||||||  ||||||
                                GAGT CATTAGGA  CGGAGT
                                  C      AGA
GAM1622  F2RL3    3'  AGGCGGATGGATCACTTGAG  15494          TC
                                TTCAAGTGATTC  CCGCCT
                                ||||||||||||  ||||||
                                GAGTTCACTAGG  GGCGGA
                                      TA
GAM1622  F2RL3    3'  TGAGGCAGAAGGATCGCTTGAA 15529           CCC
                                TTCAAGTGATTCT  GCCTCA
                                ||||||||||||  ||||||
                                AAGTTCGCTAGGA  CGGAGT
                                      AGA
GAM1622  FCAR     3'  TGAGGCAGGAGAATCACTTGAA 56642            C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  FCMD     3'  AGGCAGGTGGATCACTTGAG  23024          T  C
                                TTCAAGTGATTC CC GCCT
                                |||||||||||| || ||||
                                GAGTTCACTAGG GG CGGA
                                      T  A
GAM1622  FCMD     3'  TGAGGCAGGAGAATCACTTGAA 23047            C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  FGF2     3'  GCAGGAGGATCGCTTGAG    10619            C
                                TTCAAGTGATTCTCC GC
                                |||||||||||||| ||
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                                GAGTTCGCTAGGAGG CG
                                       A
GAM1622  FGFR2    3'  TGAGGCAGGAGAGTCACTTGAA 43656            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTGAGAGG CGGAGT
                                       A
GAM1622  FGFR2    3'  TGAGGCAGGAGAGTCACTTGAA 43669            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTGAGAGG CGGAGT
                                       A
GAM1622  FLRT2    5'  GAGGCAGAAGAATCATTT    25999         CCC
                                AAGTGATTCT   GCCTC
                                ||||||||||   |||||
                                TTTACTAAGA   CGGAG
                                      AGA
GAM1622  GALNT3   3'  TGAGGCAGAAGCATTGCTTGAG 16828       TG  T  CCC
                                TTCAAG  AT CT   GCCTCA
                                ||||||  || ||   ||||||
                                GAGTTC  TA GA   CGGAGT
                                   GT  C  AGA
GAM1622  GALNT7   3'  TGAGGCAAGAGAATCGCTTGAA 55091            CC
                                TTCAAGTGATTCTC  GCCTCA
                                ||||||||||||||  ||||||
                                AAGTTCGCTAAGAG  CGGAGT
                                       AA
GAM1622  GAS7     3'  TGAGGCAGTAGAATCGCTTGAA 20862           CCC
                                TTCAAGTGATTCT   GCCTCA
                                ||||||||||||   ||||||
                                AAGTTCGCTAAGA   CGGAGT
                                       TGA
GAM1622  GP2      3'  AGGCAGGAGAATTGCTCGAA   9478     A  TG      C
                                TTC AG  ATTCTCC GCCT
                                ||| ||  ||||||| ||||
                                AAG TC  TAAGAGG CGGA
                                  C  GT      A
GAM1622  GP6      3'  AGGCAGGAGGATCGCTTGAG   33469            C
                                TTCAAGTGATTCTCC GCCT
                                |||||||||||||| ||||
                                GAGTTCGCTAGGAGG CGGA
                                       A
GAM1622  GPRK7    3'  TGAGGCAGGAGAATTGCTTGAA 58316       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  GRM6     3'  TGAGGCAGGAGAATCGCTTGAA 7775             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
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                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  GTF2F1   3'  TGAGGCACGAGATTCACTTGAA 10895        T   CC
                                TTCAAGTGA TCTC  GCCTCA
                                ||||||||| ||||  ||||||
                                AAGTTCACT AGAG  CGGAGT
                                     T   CA
GAM1622  HCS      3'  AGGCAGGCAGATCACTTGAG  38965         CT  C
                                TTCAAGTGATT  CC GCCT
                                |||||||||||  || ||||
                                GAGTTCACTAG  GG CGGA
                                      AC  A
GAM1622  HCS      3'  TGAGGCACAAGAATCACTTGAA 38994          CCC
                                TTCAAGTGATTCT   GCCTCA
                                ||||||||||||   ||||||
                                AAGTTCACTAAGA   CGGAGT
                                      ACA
GAM1622  HIP1     3'  TGAGACAGGAGAATCACCTGAA 19267      A        CGC
                                TTCA GTGATTCTCC   CTCA
                                |||| ||||||||||   ||||
                                AAGT CACTAAGAGG   GAGT
                                  C         ACA
GAM1622  HRH1     3'  GAGGCACGAGAATCGCTTGAA  7822           CC
                                TTCAAGTGATTCTC  GCCTC
                                ||||||||||||||  |||||
                                AAGTTCGCTAAGAG  CGGAG
                                      CA
GAM1622  HSPA5    3'  TGAGGCAGGAGAATCACTCGAA 19291     A         C
                                TTC AGTGATTCTCC GCCTCA
                                ||| ||||||||||| ||||||
                                AAG TCACTAAGAGG CGGAGT
                                  C         A
GAM1622  HUNK     3'  TGAGGTGGGAGGATCACTTGAA 28195
                                TTCAAGTGATTCTCCCGCCTCA
                                ||||||||||||||||||||||
                                AAGTTCACTAGGAGGGTGGAGT

GAM1622  IAPP     3'  AGGCAGGAGAATCGCTTGAA  6436            C
                                TTCAAGTGATTCTCC GCCT
                                |||||||||||||| ||||
                                AAGTTCGCTAAGAGG CGGA
                                      A
GAM1622  ICA1     3'  AGGCAGGAGGATCACTTGGA  42515           C
                                TTCAAGTGATTCTCC GCCT
                                |||||||||||||| ||||
                                AGGTTCACTAGGAGG CGGA
                                      A
GAM1622  IFNAR1   3'  TGAGGCAGGAGAATCGCTTGAA 7143            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
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                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  IL10     3'  TGAGGCAAGAGAATTGCTTGAA 6930        TG     CC
                                TTCAAG  ATTCTC  GCCTCA
                                ||||||  ||||||  ||||||
                                AAGTTC  TAAGAG  CGGAGT
                                   GT      AA
GAM1622  IL10     3'  TGAGGCGGGTGGATCACTTGAG 6931            T
                                TTCAAGTGATTC CCCGCCTCA
                                |||||||||||| |||||||||
                                GAGTTCACTAGG GGGCGGAGT
                                       T
GAM1622  IL11     3'  GAAGCGAGTGGATCACTGAA   7184       A      TCC   C
                                TTCA GTGATTC   CGC TC
                                |||| |||||||   ||| ||
                                AAGT CACTAGG   GCG AG
                                  _      TGA   A
GAM1622  IL12B    3'  TGAGGCAGGAGGATCTCTTGAG 10992       T       C
                                TTCAAG GATTCTCC GCCTCA
                                |||||| |||||||| ||||||
                                GAGTTC CTAGGAGG CGGAGT
                                   T       A
GAM1622  IL13RA1  3'  GAGGCGGGCGGATCACTCGAG  9569      A       T
                                TTC AGTGATTC CCCGCCTC
                                ||| |||||||| ||||||||
                                GAG TCACTAGG GGGCGGAG
                                  C       C
GAM1622  IL17R    3'  TGAGGCAGGAGAATTGCTTGAA 27561       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  IL18     3'  TGAGGCAGGAGAATCACTTG   9597            C
                                CAAGTGATTCTCC GCCTCA
                                |||||||||||| ||||||
                                GTTCACTAAGAGG CGGAGT
                                      A
GAM1622  IL1R1    3'  TGAGGCAGGAGAATTGCTTGAA 7927        TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  IL2RA    3'  AGGCGGGAGCATCTCTTGAG   6446       T   T
                                TTCAAG GAT CTCCCGCCT
                                |||||| ||| |||||||||
                                GAGTTC CTA GAGGGCGGA
                                   T   C
GAM1622  IL2RA    3'  TGAGGCAGGAGGATTGCTTGAG 6454        TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
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                                GAGTTC  TAGGAGG CGGAGT
                                   GT      A
GAM1622  IL4R     5'  TGAGGCGGGCAGATCACTTGAG 6459          CT
                                TTCAAGTGATT  CCCGCCTCA
                                ||||||||||  |||||||||
                                GAGTTCACTAG  GGGCGGAGT
                                      AC
GAM1622  IL6R     3'  GAGGCAGGAGGATCACTTGAG  6911            C
                                TTCAAGTGATTCTCC GCCTC
                                |||||||||||||| |||||
                                GAGTTCACTAGGAGG CGGAG
                                        A
GAM1622  IRAK1    3'  AGGCAGGAGGATCGCTGGA   9609      A       C
                                TTCA GTGATTCTCC GCCT
                                |||| |||||||||| ||||
                                AGGT CGCTAGGAGG CGGA
                                  _       A
GAM1622  KCNK1    3'  AGGAGGAGAATACTTGAA    11162       A     CG
                                TTCAAGTG TTCTCC  CCT
                                |||||||| ||||||  |||
                                AAGTTCAT AAGAGG  GGA
                                   _     A_
GAM1622  KIF1B    3'  TGAGGCAGGAGAACTGCTTGAA 31272       GA     C
                                TTCAAGT  TTCTCC GCCTCA
                                |||||||  |||||| ||||||
                                AAGTTCG  AAGAGG CGGAGT
                                    TC     A
GAM1622  KLF8     5'  TGAGGCAGGAGGATTGCTTGAG 24374       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                GAGTTC  TAGGAGG CGGAGT
                                   GT      A
GAM1622  KNSL1    3'  TGAGGCACGAGAATCACTTGAA 16950           CC
                                TTCAAGTGATTCTC  GCCTCA
                                ||||||||||||||  ||||||
                                AAGTTCACTAAGAG  CGGAGT
                                      CA
GAM1622  LAMC2    3'  TGAGGCAGGAGAATCGCTTGAA 38771            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                        A
GAM1622  LAMP2    3'  TGAGGCAGGAGAATCACTTGAA 26579            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                        A
GAM1622  LDLR     3'  TGAGGCAGGAGGATCGCCTGAG 6747       A       C
                                TTCA GTGATTCTCC GCCTCA
                                |||| |||||||||| ||||||
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                                  GAGT CGCTAGGAGG CGGAGT
                                    C         A
GAM1622  LEP      3'  TGAGACAGGAGAATCGCTT    5872            CGC
                                  AAGTGATTCTCC   CTCA
                                  ||||||||||||   ||||
                                  TTCGCTAAGAGG   GAGT
                                         ACA
GAM1622  LILRB1   3'  TGAGGCAGGAGAATCGCTTGAA 22878              C
                                  TTCAAGTGATTCTCC GCCTCA
                                  |||||||||||||||| ||||||
                                  AAGTTCGCTAAGAGG CGGAGT
                                         A
GAM1622  LRRC2    3'  TGAGGCAGGAGAATCGCTTGAA 44762              C
                                  TTCAAGTGATTCTCC GCCTCA
                                  |||||||||||||||| ||||||
                                  AAGTTCGCTAAGAGG CGGAGT
                                         A
GAM1622  LRRC2    3'  TGAGGCAGGAGAATTGCTTGAA 44763        TG      C
                                  TTCAAG  ATTCTCC GCCTCA
                                  ||||||  ||||||| ||||||
                                  AAGTTC  TAAGAGG CGGAGT
                                     GT      A
GAM1622  LRRC2    3'  TGAGGTGGGAAAATCACTTGAG 44764           C
                                  TTCAAGTGATT TCCCGCCTCA
                                  |||||||||| |||||||||
                                  GAGTTCACTAA AGGGTGGAGT
                                         A
GAM1622  LUZP1    3'  TGAGGCAGGAGAATCACTTGAA 54406              C
                                  TTCAAGTGATTCTCC GCCTCA
                                  |||||||||||||||| ||||||
                                  AAGTTCACTAAGAGG CGGAGT
                                         A
GAM1622  MAFF     3'  TGAGGCAGGAGGATCACTT    25585           C
                                  AAGTGATTCTCC GCCTCA
                                  |||||||||||| ||||||
                                  TTCACTAGGAGG CGGAGT
                                         A
GAM1622  MCM4     3'  TGAGGCAGGAGAATCGCTT    62584           C
                                  AAGTGATTCTCC GCCTCA
                                  |||||||||||| ||||||
                                  TTCGCTAAGAGG CGGAGT
                                         A
GAM1622  MIR16    3'  TGAGGCAGGAGGATTACTTGAG 34044              C
                                  TTCAAGTGATTCTCC GCCTCA
                                  |||||||||||||||| ||||||
                                  GAGTTCATTAGGAGG CGGAGT
                                         A
GAM1622  MMP19    3'  TGAAGCAGGAGGATCACTTGAG 43306              C  C
                                  TTCAAGTGATTCTCC GC TCA
                                  |||||||||||||||| || |||
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                                GAGTTCACTAGGAGG CG AGT
                                      A  A
GAM1622  MMP19    3'  TGAAGCAGGAGGATCACTTGAG 11642            C  C
                                TTCAAGTGATTCTCC GC TCA
                                |||||||||||||| || |||
                                GAGTTCACTAGGAGG CG AGT
                                      A  A
GAM1622  MOG      3'  TGAGGCAGGAGAATCGCTTGAA 11678             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  MS4A1    3'  TGAGGCAGGAGAATCGCTTGAA 5552              C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  MSH3     3'  TGAGGCAGGAGAATCTCTTGAA 11694       T      C
                                TTCAAG GATTCTCC GCCTCA
                                |||||| |||||||| ||||||
                                AAGTTC CTAAGAGG CGGAGT
                                    T       A
GAM1622  MYO1B    3'  TGAGGCAGGAGAATCGCTTGGA 25248             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AGGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  MYO1C    3'  TGAGGCAGGAGAATCACTTGAA 61872             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  NPHS1    3'  TGAGGCGGGTGGATCACCTGAG 17375      A      T
                                TTCA GTGATTC CCCGCCTCA
                                |||| ||||||| |||||||||
                                GAGT CACTAGG GGGCGGAGT
                                  C      T
GAM1622  NR1I2    5'  AGGCAAGCATCCACTTGAG    15295        _  T  CCC
                                TTCAAGTG AT CT   GCCT
                                |||||||| || ||   ||||
                                GAGTTCAC TA GA   CGGA
                                     C  C  A__
GAM1622  NT5C2    3'  TGAGGCAGGAGAATTGCTTGAA 25271       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  NUP62    3'  TGAGGCAGGAGAATCACTTGAA 33789             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
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                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  OPA3     3'  GAGGCGGGCGGATCACTTGAG  47845          T
                                TTCAAGTGATTC CCCGCCTC
                                |||||||||||| ||||||||
                                GAGTTCACTAGG GGGCGGAG
                                      C
GAM1622  OPA3     3'  TGAGGCAGGAGAATTGCTTGAA 47849       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  OPA3     3'  TGAGGCAGGAGAATTGCTTGAA 47850       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  OPTN     3'  TGAGGCAGGAGAATTGCTTGAA 42054       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  P2RX7    3'  TGAGGCACAAGAATCACTTGAA 11929           CCC
                                TTCAAGTGATTCT   GCCTCA
                                ||||||||||||   ||||||
                                AAGTTCACTAAGA   CGGAGT
                                      ACA
GAM1622  PA2G4    3'  TGAGGCAGGAGAGTTGCTTGGA 71832       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AGGTTC  TGAGAGG CGGAGT
                                   GT      A
GAM1622  PA2G4    3'  TGAGGCGGGTGGATCACCTGAG 71833      A       T
                                TTCA GTGATTC CCCGCCTCA
                                ||||  ||||||| |||||||||
                                GAGT CACTAGG GGGCGGAGT
                                  C      T
GAM1622  PACE4    3'  TGAGGCAGGAGGATTGCTTGAG 57166       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                GAGTTC  TAGGAGG CGGAGT
                                   GT      A
GAM1622  PAICS    3'  TGAAGCAAGCAGATCACTTGAG 22269          CTCCC  C
                                TTCAAGTGATT     GC TCA
                                ||||||||||     || |||
                                GAGTTCACTAG     CG AGT
                                      ACGAA  A
GAM1622  PCDH11Y  3'  GAGGCGGGTGGATCACCTGAG  53162      A       T
                                TTCA GTGATTC CCCGCCTC
                                |||| ||||||| ||||||||
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                                GAGT CACTAGG GGGCGGAG
                                  C      T
GAM1622  PCDH11Y   3'  GAGGCGGGTGGATCACCTGAG  53181      A      T
                                TTCA GTGATTC CCCGCCTC
                                |||| ||||||| ||||||||
                                GAGT CACTAGG GGGCGGAG
                                  C      T
GAM1622  PCDHA9    3'  TGAGGCGAGAGAATCGCTTGAG 26627            C
                                TTCAAGTGATTCTC CGCCTCA
                                ||||||||||||| |||||||
                                GAGTTCGCTAAGAG GCGGAGT
                                         A
GAM1622  PCDHB9    3'  TGAGGCAGGAGAATCGCTTGAA 39454            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                         A
GAM1622  PDE4C     3'  TGAGGCAGGAGAATCACTTGAA 8109             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                         A
GAM1622  PHKB      3'  TGAGGCAGGTGGATCACTTGAG 6101           T  C
                                TTCAAGTGATTC CC GCCTCA
                                |||||||||||| || ||||||
                                GAGTTCACTAGG GG CGGAGT
                                       T  A
GAM1622  PIK3CG    3'  TGAGGCAGGAGGATTGCCTGAG 12127     A TG      C
                                TTCA G  ATTCTCC GCCTCA
                                |||| |  ||||||| ||||||
                                GAGT C  TAGGAGG CGGAGT
                                  C GT      A
GAM1622  PKD2      3'  AGGCGAATCACTTGAG      60715          TCCC
                                TTCAAGTGATTC    GCCT
                                ||||||||||||    ||||
                                GAGTTCACTAAG    CGGA
                                                ____
GAM1622  PLA2G2D   3'  TGAGGCAGGAGAATCACTTGGA 25724            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AGGTTCACTAAGAGG CGGAGT
                                         A
GAM1622  POLH      3'  AGGCAGGAGAATCACTTGAA   22470           C
                                TTCAAGTGATTCTCC GCCT
                                |||||||||||||| ||||
                                AAGTTCACTAAGAGG CGGA
                                         A
GAM1622  POLK      3'  TGAGGCAGGAGAACTACTTGAA 33102        A     C
                                TTCAAGTG TTCTCC GCCTCA
                                |||||||| |||||| ||||||
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                                AAGTTCAT AAGAGG CGGAGT
                                    C     A
GAM1622  PRKY    3'  TGAAGCAGAAAGATTGCTTGAG 12387      TG  C_  CC  C
                                TTCAAG  ATT  TC  GC TCA
                                ||||||  |||  ||  || |||
                                GAGTTC  TAG  AG  CG AGT
                                   GT   AA  A_  A
GAM1622  PSMB2   3'  TGAGACGGGAGAATCGGTCGAA 12480    AAG        C
                                TTC   TGATTCTCCCG CTCA
                                |||   |||||||||||| ||||
                                AAG   GCTAAGAGGGC GAGT
                                  CTG         A
GAM1622  PSMB2   3'  TGAGGCAGGAGAATTGCTTGAG 12481      TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                GAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  PSMB9   3'  TGAGACAGAAGAATCACTTGAG 12513          CCCGC
                                TTCAAGTGATTCT    CTCA
                                ||||||||||||     ||||
                                GAGTTCACTAAGA    GAGT
                                      AGACA
GAM1622  PSMB9   3'  TGAGGCAGGAGAATTGCTTGAA 12514      TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  PTAFR   3'  TGAGGCAGGAGAATCGCTTGAA 8169           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  RAB7L1  3'  GAGGCAGGAGAATCACTTGAA  15406          C
                                TTCAAGTGATTCTCC GCCTC
                                |||||||||||||| |||||
                                AAGTTCACTAAGAGG CGGAG
                                      A
GAM1622  RAB7L1  3'  TGAGGCAGGAGAATCACTTGAA 15414          C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  RAD1    3'  TGAGGCAGGAAAATTGCTTGAA 12649      TG  C  C
                                TTCAAG  ATT TCC GCCTCA
                                ||||||  ||| ||| ||||||
                                AAGTTC  TAA AGG CGGAGT
                                   GT   A  A
GAM1622  RAD1    3'  TGAGGCAGGAAAATTGCTTGAA 56656      TG  C  C
                                TTCAAG  ATT TCC GCCTCA
                                ||||||  ||| ||| ||||||
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                                AAGTTC  TAA AGG CGGAGT
                                   GT   A   A
GAM1622  RAD1     3'  TGAGGCAGGAAAATTGCTTGAA 56753       TG   C   C
                                TTCAAG  ATT TCC GCCTCA
                                ||||||  ||| ||| ||||||
                                AAGTTC  TAA AGG CGGAGT
                                   GT   A   A
GAM1622  RBBP5    3'  TGAGTCAGGAGAATCACTTGAA 18580             CGC
                                TTCAAGTGATTCTCC   CTCA
                                ||||||||||||||   ||||
                                AAGTTCACTAAGAGG   GAGT
                                      ACT
GAM1622  RBBP9    3'  TGAGGCAGGATTGCTTGAG   70703       TG    CCC
                                TTCAAG  ATTCT   GCCTCA
                                ||||||  |||||   ||||||
                                GAGTTC  TAGGA   CGGAGT
                                   GT    ___
GAM1622  RBL1     3'  TGAGGCAGAATTGCTTGAA   12791       TG    CCC
                                TTCAAG  ATTCT   GCCTCA
                                ||||||  |||||   ||||||
                                AAGTTC  TAAGA   CGGAGT
                                   GT    ___
GAM1622  RBM3     3'  TGAGGCAGGAGAATCGCTTGAA 71014             C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  ROCK2    3'  TGAGACAGGAGAATCGCTTGAA 66626             CGC
                                TTCAAGTGATTCTCC   CTCA
                                ||||||||||||||   ||||
                                AAGTTCGCTAAGAGG   GAGT
                                      ACA
GAM1622  RPN1     5'  TGAGGCAGGAGAATTGCTTGAA 12907       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  SERPINE1 3'  AGGCGGGAGGATTGCTTGAG   7008        TG
                                TTCAAG  ATTCTCCCGCCT
                                ||||||  ||||||||||||
                                GAGTTC  TAGGAGGGCGGA
                                   GT
GAM1622  SFRS2IP  5'  GAGGCAGGCAGATCACTTGAA  17541          CT  C
                                TTCAAGTGATT  CC GCCTC
                                ||||||||||  || |||||
                                AAGTTCACTAG  GG CGGAG
                                      AC  A
GAM1622  SIM2     3'  TGAGATAGGAGGATCACTTGAA 24805             CGC
                                TTCAAGTGATTCTCC   CTCA
                                ||||||||||||||   ||||
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                                AAGTTCACTAGGAGG  GAGT
                                      ATA
GAM1622 SLC17A5  3' TGAGGTAGGAGAATCACTTGAA 25836          CG
                                TTCAAGTGATTCTCC  CCTCA
                                |||||||||||||||  |||||
                                AAGTTCACTAAGAGG  GGAGT
                                      AT
GAM1622 SLC25A15 3' TGAGGCAGGAGAATCGCTTGAA 27298           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622 SLC2A3   3' TGAGGCGGGAGAATCATGTGAA 23648     A
                                TTCA GTGATTCTCCCGCCTCA
                                |||| |||||||||||||||||
                                AAGT TACTAAGAGGGCGGAGT
                                   G
GAM1622 SLC31A1  3' TGAGGCAGGAGAATCACTTGAA 10280           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622 SRGAP1   5' TGAGGCAGGAGAATCACTTGAA 72723           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622 STAT3    3' TGAGGCAGGAGAATCGCTTGAA 58380           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622 STAT3    3' TGAGGCAGGAGAATCGCTTGAA 13440           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622 SUDD     3' AGGCGGGTGGATCACTTGAG  15151          T
                                TTCAAGTGATTC CCCGCCT
                                |||||||||||| |||||||
                                GAGTTCACTAGG GGGCGGA
                                      T
GAM1622 SUDD     3' TGAGACAGGAGAATCGCTTGAA 15161           CGC
                                TTCAAGTGATTCTCC  CTCA
                                ||||||||||||||  ||||
                                AAGTTCGCTAAGAGG  GAGT
                                      ACA
GAM1622 SUV39H2  3' TGAGGCAGGAGAATCACTTGAA 45459           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
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                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  SWAP70   3'  GAGGCGGGTGGATCACCTGAG  71868     A      T
                                TTCA GTGATTC CCCGCCTC
                                |||| ||||||| ||||||||
                                GAGT CACTAGG GGGCGGAG
                                  C      T
GAM1622  SWAP70   3'  TGAGGCAGGAGAATCACTTGAA 71875            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  TACC1    3'  GAGGCAGGAGGATCACTTGAG  21875            C
                                TTCAAGTGATTCTCC GCCTC
                                |||||||||||||| |||||
                                GAGTTCACTAGGAGG CGGAG
                                      A
GAM1622  TBX1     3'  TGAGGCAGGAGGATCACTTGAG 21142            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                GAGTTCACTAGGAGG CGGAGT
                                      A
GAM1622  TBX6     3'  TGAGGCAGGAGAATCTCTTGAA 55819      T     C
                                TTCAAG GATTCTCC GCCTCA
                                |||||| |||||||| ||||||
                                AAGTTC CTAAGAGG CGGAGT
                                   T       A
GAM1622  TBX6     3'  TGAGGCGGGCAGATCACCTGAG 55820     A     CT
                                TTCA GTGATT  CCCGCCTCA
                                |||| ||||||  |||||||||
                                GAGT CACTAG  GGGCGGAGT
                                  C     AC
GAM1622  TCF7     3'  TGAGGCGGAAGAATCACTTGAA 13626          C
                                TTCAAGTGATTCT CCGCCTCA
                                |||||||||||| ||||||||
                                AAGTTCACTAAGA GGCGGAGT
                                      A
GAM1622  TCTA     3'  TGAAGCAGGAGATTTGCTTGAA 42506      TG T    C  C
                                TTCAAG  A TCTCC GC TCA
                                ||||||  | ||||| || |||
                                AAGTTC  T AGAGG CG AGT
                                   GT T    A  A
GAM1622  TEM7     3'  TGAGACACGAGAATCACTTGAA 40272           CCGC
                                TTCAAGTGATTCTC   CTCA
                                ||||||||||||||   ||||
                                AAGTTCACTAAGAG   GAGT
                                      CACA
GAM1622  TEM7     3'  TGAGGCAGGAGGATTGCTTGAG 40273      TG     C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
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                                GAGTTC  TAGGAGG CGGAGT
                                   GT      A
GAM1622  TFE3     3'  AGGCAGAAGCTTGGA      22537       GA   CCC
                                TTCAAGT  TTCT   GCCT
                                |||||||  ||||   ||||
                                AGGTTCG  AAGA   CGGA
                                   __    ___
GAM1622  TNFRSF10A 3'  TGAGGCGGGTGGATCACTTGAG 15240          T
                                TTCAAGTGATTC CCCGCCTCA
                                |||||||||||| |||||||||
                                GAGTTCACTAGG GGGCGGAGT
                                      T
GAM1622  TNFRSF1B  3'  TGAGGCGGGTGGATCACCTGAG 8404      A     T
                                TTCA GTGATTC CCCGCCTCA
                                |||| ||||||| |||||||||
                                GAGT CACTAGG GGGCGGAGT
                                  C      T
GAM1622  TNFSF10   3'  TGAGGCAGGAGAATCGTTTGAA 15095           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTTGCTAAGAGG CGGAGT
                                         A
GAM1622  TNFSF15   3'  GAGGCAGAAGAATTGCTTGAA  18866      TG    CCC
                                TTCAAG  ATTCT   GCCTC
                                ||||||  |||||   |||||
                                AAGTTC  TAAGA   CGGAG
                                   GT     AGA
GAM1622  TPM4      3'  TGAGGCAGGAGGATCGCTTGAA 13835           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAGGAGG CGGAGT
                                         A
GAM1622  TPMT      3'  TGAGGCGGGAGAATCACTTGGA 6320
                                TTCAAGTGATTCTCCCGCCTCA
                                |||||||||||||||||||||
                                AGGTTCACTAAGAGGGCGGAGT

GAM1622  TRIM14    3'  TGAGGCAAGAGAGTTGCTTGAA 29520      TG     CC
                                TTCAAG  ATTCTC  GCCTCA
                                ||||||  ||||||  ||||||
                                AAGTTC  TGAGAG  CGGAGT
                                   GT     AA
GAM1622  TRIM14    3'  TGAGGAAGGAGAATCACTTGAA 53779           CG
                                TTCAAGTGATTCTCC  CCTCA
                                ||||||||||||||  |||||
                                AAGTTCACTAAGAGG  GGAGT
                                         AA
GAM1622  TRIM9     5'  TGAGGCAGGAGAATCGCTTGAA 31464           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
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                                  AAGTTCGCTAAGAGG CGGAGT
                                        A
GAM1622  TSNAX    3'  TGAGGCAGGAGACTCGCTTGAA 21161         T    C
                                  TTCAAGTGA TCTCC GCCTCA
                                  ||||||||| ||||| ||||||
                                  AAGTTCGCT AGAGG CGGAGT
                                      C    A
GAM1622  UBE2G2   3'  TGAGGCAGGAGAATCGCTTGAA 65499             C
                                  TTCAAGTGATTCTCC GCCTCA
                                  |||||||||||||| ||||||
                                  AAGTTCGCTAAGAGG CGGAGT
                                        A
GAM1622  VHL      3'  TGAGGCAGGAGAATCACTTGA  6880            C
                                  TCAAGTGATTCTCC GCCTCA
                                  |||||||||||||| ||||||
                                  AGTTCACTAAGAGG CGGAGT
                                        A
GAM1622  VPS41    3'  TGAGGCAGGAGAATCACTTGA  27699           C
                                  TCAAGTGATTCTCC GCCTCA
                                  |||||||||||||| ||||||
                                  AGTTCACTAAGAGG CGGAGT
                                        A
GAM1622  XRCC2    3'  GAGGCAGGAGAATTGCTGGAA  19502    A  TG     C
                                  TTC AG  ATTCTCC GCCTC
                                  ||| ||  ||||||| |||||
                                  AAG TC  TAAGAGG CGGAG
                                    G  GT      A
GAM1622  XT3      3'  TGAGGCACAAGAATCATTTGAA 39921          CCC
                                  TTCAAGTGATTCT   GCCTCA
                                  ||||||||||||   ||||||
                                  AAGTTTACTAAGA   CGGAGT
                                        ACA
GAM1622  ZNF136   3'  TGAGGCAGGAGGATCACTTGAG 60570             C
                                  TTCAAGTGATTCTCC GCCTCA
                                  |||||||||||||| ||||||
                                  GAGTTCACTAGGAGG CGGAGT
                                        A
GAM1622  ZNF14    3'  AGGCAGGAGAATCACTTGAA  41054            C
                                  TTCAAGTGATTCTCC GCCT
                                  |||||||||||||| ||||
                                  AAGTTCACTAAGAGG CGGA
                                        A
GAM1622  ZNF264   3'  TGAGGCAGGAGGATCAGTTGAA 14235      G       C
                                  TTCAA TGATTCTCC GCCTCA
                                  ||||| ||||||||| ||||||
                                  AAGTT ACTAGGAGG CGGAGT
                                     G        A
GAM1622  ZNF36    3'  TGAGGCAGGAGAATCACTTGAA 95589            C
                                  TTCAAGTGATTCTCC GCCTCA
                                  |||||||||||||| ||||||
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                                AAGTTCACTAAGAGG CGGAGT
                                       A
GAM1622 ZNF74    3' AGGCAAGGGGATCACTTGAG  14255          CC
                                TTCAAGTGATTCTC  GCCT
                                ||||||||||||||  ||||
                                GAGTTCACTAGGGG  CGGA
                                       AA
GAM1622 AAK1     3' TGAGACGGAAGATCACTTTGA 30527    _   T C  C
                                TCAA GTGAT CT CCG CTCA
                                |||| ||||| || ||| ||||
                                AGTT CACTA GA GGC GAGT
                                  T   _ A  A
GAM1622 AF020591 3' GAGGCAGGTGGATCACTTGAG 27911         T C
                                TTCAAGTGATTC CC GCCTC
                                |||||||||||| || |||||
                                GAGTTCACTAGG GG CGGAG
                                       T A
GAM1622 AGMAT    3' TGAGGCAGGAGAATCGCTT   45745          C
                                AAGTGATTCTCC GCCTCA
                                |||||||||||| ||||||
                                TTCGCTAAGAGG CGGAGT
                                       A
GAM1622 AKAP11   3' AGGCAGGAGAATTGCTTGAA  58456       TG     C
                                TTCAAG  ATTCTCC GCCT
                                ||||||  ||||||| ||||
                                AAGTTC  TAAGAGG CGGA
                                   GT      A
GAM1622 AKR1B10  5' TGAGGCAGGAGAATTGCTTGAA 40081      TG     C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622 ALTE     3' TGAGGCCAGAGAATCGCTTGAA 61008          CC
                                TTCAAGTGATTCTC  GCCTCA
                                ||||||||||||||  ||||||
                                AAGTTCGCTAAGAG  CGGAGT
                                       AC
GAM1622 ALTE     3' TGAGGCCAGAGAATCGCTTGAA 17585          CC
                                TTCAAGTGATTCTC  GCCTCA
                                ||||||||||||||  ||||||
                                AAGTTCGCTAAGAG  CGGAGT
                                       AC
GAM1622 ALTE     3' TGAGGCGGAAGATTCGCTTGAG 17586        T  C
                                TTCAAGTGA TCT CCGCCTCA
                                ||||||||| ||| ||||||||
                                GAGTTCGCT AGA GGCGGAGT
                                      T  A
GAM1622 AP1GBP1  3' TGAGGCAGGAGAATTGCTTGAA 55448      TG     C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
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                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  AP4S1    3'  TGAAGCAGGAGGATTGCTTGAG 23966       TG      C  C
                                TTCAAG  ATTCTCC GC TCA
                                ||||||  ||||||| || |||
                                GAGTTC  TAGGAGG CG AGT
                                   GT      A  A
GAM1622  APOF     3'  TGAGGCGGGAGAATCACCTGAG 9697       A
                                TTCA GTGATTCTCCCGCCTCA
                                |||| ||||||||||||||||
                                GAGT CACTAAGAGGGCGGAGT
                                  C
GAM1622  APOF     3'  TGAGGCGGGAGAATCACCTGAG 9698       A
                                TTCA GTGATTCTCCCGCCTCA
                                |||| ||||||||||||||||
                                GAGT CACTAAGAGGGCGGAGT
                                  C
GAM1622  APOF     3'  TGAGGCGGGATGATCACCTGAG 9699       A     C
                                TTCA GTGATT TCCCGCCTCA
                                |||| |||||| ||||||||||
                                GAGT CACTAG AGGGCGGAGT
                                  C     T
GAM1622  ARNTL2   3'  TGAGACGGGCAGATCACTTGAG 39859          CT    C
                                TTCAAGTGATT  CCCG CTCA
                                ||||||||||  |||| ||||
                                GAGTTCACTAG  GGGC GAGT
                                      AC    A
GAM1622  ARNTL2   3'  TGAGGCGAGAGGATTGCTTGAA 39860       TG     C
                                TTCAAG  ATTCTC CGCCTCA
                                ||||||  |||||| |||||||
                                AAGTTC  TAGGAG GCGGAGT
                                   GT     A
GAM1622  ASAHL    3'  AGGCGGGTGGATCACTTGAG   64312          T
                                TTCAAGTGATTC CCCGCCT
                                |||||||||||| |||||||
                                GAGTTCACTAGG GGGCGGA
                                      T
GAM1622  ATP1B4   3'  AGGCAGGAGGATCACTTGAG   24834            C
                                TTCAAGTGATTCTCC GCCT
                                |||||||||||||| ||||
                                GAGTTCACTAGGAGG CGGA
                                        A
GAM1622  BFAR     3'  TGAGGCAGGCGGATCACTTGAA 61426          T  C
                                TTCAAGTGATTC CC GCCTCA
                                |||||||||||| || ||||||
                                AAGTTCACTAGG GG CGGAGT
                                      C  A
GAM1622  BIRC3    3'  TGAGGCAAGAGAATTACTTGAG 67777            CC
                                TTCAAGTGATTCTC  GCCTCA
                                ||||||||||||||  ||||||
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                                  GAGTTCATTAAGAG  CGGAGT
                                        AA
GAM1622  BLOV1     3'  TGAGGCAGGAGAATCACTTGAA 76801            C
                                  TTCAAGTGATTCTCC GCCTCA
                                  |||||||||||||| ||||||
                                  AAGTTCACTAAGAGG CGGAGT
                                        A
GAM1622  C12orf2   3'  TGAGGCAGAAGGATTGTTTGAA 83689      TG    CCC
                                  TTCAAG  ATTCT   GCCTCA
                                  ||||||  |||||   ||||||
                                  AAGTTT  TAGGA   CGGAGT
                                     GT    AGA
GAM1622  C1orf33   3'  TGAGGCAGGAGAATCACTTGAA 32989            C
                                  TTCAAGTGATTCTCC GCCTCA
                                  |||||||||||||| ||||||
                                  AAGTTCACTAAGAGG CGGAGT
                                        A
GAM1622  C1orf34   3'  TGAGGCAACAAGAATCGCTTGA 61325           CCC_
               A                   TTCAAGTGATTCT    GCCTCA
                                  ||||||||||||    ||||||
                                  AAGTTCGCTAAGA    CGGAGT
                                        ACAA
GAM1622  C1QTNF2   3'  TGAGGCGGGAGAATCGCTTGAA 49978
                                  TTCAAGTGATTCTCCCGCCTCA
                                  |||||||||||||||||||||
                                  AAGTTCGCTAAGAGGGCGGAGT

GAM1622  C20orf106 3'  GAGACGGGCAGATCACTTGAG  55905         CT    C
                                  TTCAAGTGATT  CCCG CTC
                                  ||||||||||  |||| |||
                                  GAGTTCACTAG  GGGC GAG
                                        AC    A
GAM1622  C20orf106 3'  TGAGGCAGGAGAATCACTTGAA 55915            C
                                  TTCAAGTGATTCTCC GCCTCA
                                  |||||||||||||| ||||||
                                  AAGTTCACTAAGAGG CGGAGT
                                        A
GAM1622  C20orf108 3'  TGAGGCAGGCGTGTCACTTGAG 55884         TCT  C
                                  TTCAAGTGAT   CC GCCTCA
                                  |||||||||   || ||||||
                                  GAGTTCACTG   GG CGGAGT
                                        TGC  A
GAM1622  C20orf12  3'  TGAGGCAGGAAAATCGCTTGAA 36852         C   C
                                  TTCAAGTGATT TCC GCCTCA
                                  |||||||||| ||| ||||||
                                  AAGTTCGCTAA AGG CGGAGT
                                        A   A
GAM1622  C20orf175 3'  TGAGGCAGGAGAATCACTCGGA 55930     A        C
                                  TTC AGTGATTCTCC GCCTCA
                                  ||| |||||||||| ||||||
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                                  AGG TCACTAAGAGG CGGAGT
                                    C         A
GAM1622  C20orf28  3'  TGAGGCGGAAGGTTTGAA    31848       TGAT   C
                                  TTCAAG    TCT CCGCCTCA
                                  ||||||    ||| ||||||||
                                  AAGTTT    GGA GGCGGAGT
                                     ____   A
GAM1622  C21orf108 3'  AGGCAGGGGAATCGCTTGAA   90108             C
                                  TTCAAGTGATTCTCC GCCT
                                  |||||||||||||| ||||
                                  AAGTTCGCTAAGGGG CGGA
                                           A
GAM1622  C22orf19  3'  AGGCGGGAGGATCCCTTGAG   14813       T
                                  TTCAAG GATTCTCCCGCCT
                                  |||||| ||||||||||||
                                  GAGTTC CTAGGAGGGCGGA
                                     C
GAM1622  C22orf19  3'  AGGCGGGTGGATCACTTGAG   14814           T
                                  TTCAAGTGATTC CCCGCCT
                                  |||||||||||| |||||||
                                  GAGTTCACTAGG GGGCGGA
                                        T
GAM1622  C22orf19  3'  TGAGGCAGAATTGCTTGAA    14834       TG    CCC
                                  TTCAAG  ATTCT   GCCTCA
                                  ||||||  |||||   ||||||
                                  AAGTTC  TAAGA   CGGAGT
                                     GT    ___
GAM1622  C22orf19  3'  TGAGGCAGGAGAATTGCTTGAA 14835       TG      C
                                  TTCAAG  ATTCTCC GCCTCA
                                  ||||||  ||||||| ||||||
                                  AAGTTC  TAAGAGG CGGAGT
                                     GT      A
GAM1622  C22orf20  3'  TGAGGCAGGAGAATCACTTGAA 48201             C
                                  TTCAAGTGATTCTCC GCCTCA
                                  |||||||||||||| ||||||
                                  AAGTTCACTAAGAGG CGGAGT
                                           A
GAM1622  C6orf29   3'  TGAGGCGGGCGGATCACCTGAG 48267      A      T
                                  TTCA GTGATTC CCCGCCTCA
                                  |||| ||||||| |||||||||
                                  GAGT CACTAGG GGGCGGAGT
                                    C      C
GAM1622  C6orf29   3'  TGAGGCAGGAGAATCGCTTGAA 52461             C
                                  TTCAAGTGATTCTCC GCCTCA
                                  |||||||||||||| ||||||
                                  AAGTTCGCTAAGAGG CGGAGT
                                           A
GAM1622  C6orf29   3'  TGAGGCGGGCGGATCACCTGAG 52462      A      T
                                  TTCA GTGATTC CCCGCCTCA
                                  |||| ||||||| |||||||||
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                                    GAGT CACTAGG GGGCGGAGT
                                      C      C
GAM1622  C6orf5   3'  TGAGGCAGGAGAATCACTTGAA 32007              C
                                    TTCAAGTGATTCTCC GCCTCA
                                    ||||||||||||||| ||||||
                                    AAGTTCACTAAGAGG CGGAGT
                                              A
GAM1622  C8orf2   3'  TGAGGCAGGAGAATTGCTTGAA 24158        TG      C
                                    TTCAAG  ATTCTCC GCCTCA
                                    ||||||  ||||||| ||||||
                                    AAGTTC  TAAGAGG CGGAGT
                                       GT      A
GAM1622  CCR6     3'  TGAGGCAAGAGAATCGCTTGAA 16449             CC
                                    TTCAAGTGATTCTC  GCCTCA
                                    ||||||||||||||  ||||||
                                    AAGTTCGCTAAGAG  CGGAGT
                                              AA
GAM1622  CCR6     3'  TGAGGCAAGAGAATCGCTTGAA 49409             CC
                                    TTCAAGTGATTCTC  GCCTCA
                                    ||||||||||||||  ||||||
                                    AAGTTCGCTAAGAG  CGGAGT
                                              AA
GAM1622  cerk     3'  TGAGGCAGGAGAATCGCTTGAA 43170              C
                                    TTCAAGTGATTCTCC GCCTCA
                                    ||||||||||||||| ||||||
                                    AAGTTCGCTAAGAGG CGGAGT
                                               A
GAM1622  CG012    5'  TGAGGCACGAGAATCATTTGAA 84169             CC
                                    TTCAAGTGATTCTC  GCCTCA
                                    ||||||||||||||  ||||||
                                    AAGTTTACTAAGAG  CGGAGT
                                              CA
GAM1622  CG012    3'  TGAGGCAGGAGAATCACTT    84170            C
                                    AAGTGATTCTCC GCCTCA
                                    |||||||||||| ||||||
                                    TTCACTAAGAGG CGGAGT
                                              A
GAM1622  CLONE24922 3'  TGAGGCAGGAGAATTGCTTGAG 32251        TG      C
                                    TTCAAG  ATTCTCC GCCTCA
                                    ||||||  ||||||| ||||||
                                    GAGTTC  TAAGAGG CGGAGT
                                       GT      A
GAM1622  CNNM1    3'  GAGGCGGGTGGATCACTTGAA  40121            T
                                    TTCAAGTGATTC CCCGCCTC
                                    |||||||||||| ||||||||
                                    AAGTTCACTAGG GGGCGGAG
                                              T
GAM1622  CNNM1    3'  TGAGGCAGGAGAATCGCTTGAA 40125              C
                                    TTCAAGTGATTCTCC GCCTCA
                                    ||||||||||||||| ||||||
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                                    AAGTTCGCTAAGAGG CGGAGT
                                           A
GAM1622  COE2     3'  TGAGGCAGGAAAATCGCTTGAA 64912          C   C
                                    TTCAAGTGATT TCC GCCTCA
                                    |||||||||||  ||| ||||||
                                    AAGTTCGCTAA AGG CGGAGT
                                           A   A
GAM1622  CPR2     3'  TGAGGCAGGTGAATCACTTGAA 48842           T  C
                                    TTCAAGTGATTC CC GCCTCA
                                    ||||||||||||  || ||||||
                                    AAGTTCACTAAG GG CGGAGT
                                           T  A
GAM1622  CRTAM    3'  TGAGGGTGGAGAATCGCTTGAA 39477              CG
                                    TTCAAGTGATTCTCC  CCTCA
                                    ||||||||||||||  |||||
                                    AAGTTCGCTAAGAGG  GGAGT
                                           TG
GAM1622  CSAD     3'  GAGGCGGGTGGATCACTTGAG  32580           T
                                    TTCAAGTGATTC CCCGCCTC
                                    ||||||||||||  ||||||||
                                    GAGTTCACTAGG GGGCGGAG
                                           T
GAM1622  D21S2056E 3'  TGAGGCAGGAGAATTGCTTGAA 14875       TG      C
                                    TTCAAG  ATTCTCC GCCTCA
                                    ||||||  ||||||| ||||||
                                    AAGTTC  TAAGAGG CGGAGT
                                       GT      A
GAM1622  DCOHM    3'  TGAGGCAGGAGAATCCCTT   50538     T      C
                                    AAG GATTCTCC GCCTCA
                                    ||| ||||||||  ||||||
                                    TTC CTAAGAGG CGGAGT
                                      C       A
GAM1622  DIS3     3'  GAGGCGGGTGGATCACTCGA   30918    A      T
                                    TC AGTGATTC CCCGCCTC
                                    ||  ||||||||  ||||||||
                                    AG TCACTAGG GGGCGGAG
                                     C       T
GAM1622  DIS3     3'  TGAGGCAGGAGAATCGCTTGAA 30924             C
                                    TTCAAGTGATTCTCC GCCTCA
                                    ||||||||||||||  ||||||
                                    AAGTTCGCTAAGAGG CGGAGT
                                           A
GAM1622  DIS3     3'  TGAGGCAGGAGAATCGCTTGAA 30925             C
                                    TTCAAGTGATTCTCC GCCTCA
                                    ||||||||||||||  ||||||
                                    AAGTTCGCTAAGAGG CGGAGT
                                           A
GAM1622  DJ122O8.2 3'  TGAGGCAGGAGAATCACTTGAA 40397             C
                                    TTCAAGTGATTCTCC GCCTCA
                                    ||||||||||||||  ||||||
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                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  DKFZP434C1715 3'  AGGCAGAAGGATCACTTGAG   87348           CCC
                                TTCAAGTGATTCT   GCCT
                                ||||||||||||   ||||
                                GAGTTCACTAGGA   CGGA
                                      AGA
GAM1622  DKFZp434E0519 3'  AGGCAGGAGGATCACTTGAG   50982            C
                                TTCAAGTGATTCTCC GCCT
                                |||||||||||||| ||||
                                GAGTTCACTAGGAGG CGGA
                                      A
GAM1622  DKFZp434E0519 3'  TGAGGCAGGAGAATTGCTTGAA 51002       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  DKFZp434E2220 5'  TGAGGCAGGAGAATCCCTTGAA 34722       T       C
                                TTCAAG GATTCTCC GCCTCA
                                |||||| |||||||| ||||||
                                AAGTTC CTAAGAGG CGGAGT
                                   C       A
GAM1622  DKFZP434F091 3'  TGAGGCTAGAGAATCACTTGAA 31898           CC
                                TTCAAGTGATTCTC  GCCTCA
                                ||||||||||||  ||||||
                                AAGTTCACTAAGAG  CGGAGT
                                      AT
GAM1622  DKFZP434F1735 3'  AGGTAGAAGAATCACTTGAG   32112           CCC
                                TTCAAGTGATTCT   GCCT
                                ||||||||||||   ||||
                                GAGTTCACTAAGA   TGGA
                                      AGA
GAM1622  DKFZP434F1735 3'  TGAGGCGGGATTGCTTGAG    32118       TG TTC
                                TTCAAG  A   TCCCGCCTCA
                                ||||||  |   ||||||||||
                                GAGTTC  T   AGGGCGGAGT
                                   GT ____
GAM1622  DKFZp434G171 3'  AGGCAGGCAGATCACTTGAG   80231          CT  C
                                TTCAAGTGATT  CC GCCT
                                ||||||||||  || ||||
                                GAGTTCACTAG  GG CGGA
                                      AC  A
GAM1622  DKFZp434G171 3'  TGAGGCAGGAGAATTGCTT    80249     TG      C
                                AAG  ATTCTCC GCCTCA
                                |||  ||||||| ||||||
                                TTC  TAAGAGG CGGAGT
                                  GT      A
GAM1622  DKFZp434G171 3'  TGAGGCAGGAGCATTGCTTGAA 80250       TG  T    C
                                TTCAAG  AT CTCC GCCTCA
                                ||||||  || |||| ||||||
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                                AAGTTC  TA GAGG CGGAGT
                                   GT  C    A
GAM1622  DKFZP434I1735 3'  GAGGCAGGAAAATCGCTTGAA  89170          C   C
                                TTCAAGTGATT TCC GCCTC
                                |||||||||||  ||| |||||
                                AAGTTCGCTAA AGG CGGAG
                                      A   A
GAM1622  DKFZP434K1421 3'  TGAGGCAAGAAGATCACTTGAG 50469          TC  CC
                                TTCAAGTGAT  TC  GCCTCA
                                ||||||||||  ||  ||||||
                                GAGTTCACTA  AG  CGGAGT
                                      GA  AA
GAM1622  DKFZP434P0721 3'  AGGCAGGCGGATCACTTGAG   64455          T  C
                                TTCAAGTGATTC CC GCCT
                                ||||||||||||  ||  ||||
                                GAGTTCACTAGG GG CGGA
                                      C  A
GAM1622  DKFZp547C176 3'  TGAGGCAGGAGAATCGCTTGAA 67808            C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||  ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  DKFZp547G183 3'  TGAGGCAGGAGAATCACTTGAA 38651            C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||  ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  DKFZp547I094 3'  TGAGGCAGGAGGATTGCTTGAG 50567       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  |||||||  ||||||
                                GAGTTC  TAGGAGG CGGAGT
                                   GT      A
GAM1622  DKFZP564I052 3'  TGAGGCAGGAGAATTGCTTGAA 67287       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  |||||||  ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  DKFZP564I122 3'  TGAGGCAGTAGAATCATTTGAA 63882           CCC
                                TTCAAGTGATTCT   GCCTCA
                                ||||||||||||   ||||||
                                AAGTTTACTAAGA   CGGAGT
                                      TGA
GAM1622  DKFZp564K142 3'  TGAGGCACGAGAATCACTTGAA 50438            CC
                                TTCAAGTGATTCTC  GCCTCA
                                ||||||||||||||  ||||||
                                AAGTTCACTAAGAG  CGGAGT
                                      CA
GAM1622  DKFZP564M182 3'  TGAAGCAGGAGAATCACTT    78646          C  C
                                AAGTGATTCTCC GC TCA
                                ||||||||||||  ||  |||
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                                  TTCACTAAGAGG CG AGT
                                        A  A
GAM1622  DKFZP564M182 3'  TGAGGCAGGAGAATTGCTTGAA 78647       TG      C
                                  TTCAAG  ATTCTCC GCCTCA
                                  ||||||  ||||||| ||||||
                                  AAGTTC  TAAGAGG CGGAGT
                                     GT      A
GAM1622  DKFZp566H0824 3'  TGAGGGAGAAGAATCACTT    34494          CCCG
                                  AAGTGATTCT    CCTCA
                                  ||||||||||    |||||
                                  TTCACTAAGA    GGAGT
                                        AGAG
GAM1622  DKFZP566J2046 3'  TGAGGCAGGAGAATCAATTGAA 49141       G       C
                                  TTCAA TGATTCTCC GCCTCA
                                  ||||| |||||||| ||||||
                                  AAGTT ACTAAGAGG CGGAGT
                                     A        A
GAM1622  DKFZP586C1324 3'  TGAGGCAGAAGAATCGCTTGAA 70362            CCC
                                  TTCAAGTGATTCT   GCCTCA
                                  ||||||||||||   ||||||
                                  AAGTTCGCTAAGA   CGGAGT
                                           AGA
GAM1622  DKFZP586D2223 3'  TGAGGCAGGAGAATCGCTTGAA 38298             C
                                  TTCAAGTGATTCTCC GCCTCA
                                  |||||||||||||| ||||||
                                  AAGTTCGCTAAGAGG CGGAGT
                                            A
GAM1622  DKFZP586M1120 3'  TGAGGCGGGAGGATCGCTTGAG 49288
                                  TTCAAGTGATTCTCCCGCCTCA
                                  |||||||||||||||||||||
                                  GAGTTCGCTAGGAGGGCGGAGT

GAM1622  DKFZp727G131 3'  TGAGGCAGGAGAATCTCTT    59699     T       C
                                  AAG GATTCTCC GCCTCA
                                  ||| |||||||| ||||||
                                  TTC CTAAGAGG CGGAGT
                                    T       A
GAM1622  DKFZP761L0424 3'  TGAGACAGGAGAATTGTCTT   92979     _       CGC
                                  AAG TGATTCTCC   CTCA
                                  ||| |||||||||   ||||
                                  TTC GTTAAGAGG   GAGT
                                    T        ACA
GAM1622  DRF1     3'  TGAAGCAGAAGAATCACTTGAA 47760            CCC  C
                                  TTCAAGTGATTCT   GC TCA
                                  ||||||||||||   || |||
                                  AAGTTCACTAAGA   CG AGT
                                           AGA  A
GAM1622  DRF1     3'  TGAGGCAGGAGAATCACTTGAA 47761              C
                                  TTCAAGTGATTCTCC GCCTCA
                                  ||||||||||||||| ||||||
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                                  AAGTTCACTAAGAGG CGGAGT
                                        A
GAM1622  EIF2S1    3'  AGGCAGGAGGATCACTTGAG   15846            C
                                  TTCAAGTGATTCTCC GCCT
                                  ||||||||||||||| ||||
                                  GAGTTCACTAGGAGG CGGA
                                        A
GAM1622  ERAP140   3'  TGAGGCAGGAGAATTGCTTGAA 75708       TG      C
                                  TTCAAG  ATTCTCC GCCTCA
                                  ||||||  ||||||| ||||||
                                  AAGTTC  TAAGAGG CGGAGT
                                     GT      A
GAM1622  FADS1     3'  TGAGGCAGGAGAATCGCTTGAA 26389             C
                                  TTCAAGTGATTCTCC GCCTCA
                                  ||||||||||||||| ||||||
                                  AAGTTCGCTAAGAGG CGGAGT
                                        A
GAM1622  FBXO27    3'  TGAGGCAGGAGAATTGCTTGAG 75018       TG      C
                                  TTCAAG  ATTCTCC GCCTCA
                                  ||||||  ||||||| ||||||
                                  GAGTTC  TAAGAGG CGGAGT
                                     GT      A
GAM1622  FBXO9     3'  AGGCAGGAGGATTGCTTGAG   54238       TG      C
                                  TTCAAG  ATTCTCC GCCT
                                  ||||||  ||||||| ||||
                                  GAGTTC  TAGGAGG CGGA
                                     GT      A
GAM1622  FKBP14    3'  TGAGACAGGAGATTTGCTTGAA 36071       TG T    CGC
                                  TTCAAG  A TCTCC   CTCA
                                  ||||||  | |||||   ||||
                                  AAGTTC  T AGAGG   GAGT
                                     GT T    ACA
GAM1622  FKBP14    3'  TGAGGCGGCAGAATCACTTGAA 36072             C
                                  TTCAAGTGATTCT CCGCCTCA
                                  |||||||||||| ||||||||
                                  AAGTTCACTAAGA GGCGGAGT
                                        C
GAM1622  FKBP14    3'  TGAGGCGGGCGGATCACCTGAG 36073      A      T
                                  TTCA GTGATTC CCCGCCTCA
                                  |||| ||||||| |||||||||
                                  GAGT CACTAGG GGGCGGAGT
                                    C      C
GAM1622  FKSG17    3'  TGAGGCAGGAGAATCACTTGAA 50160             C
                                  TTCAAGTGATTCTCC GCCTCA
                                  |||||||||||||| ||||||
                                  AAGTTCACTAAGAGG CGGAGT
                                        A
GAM1622  FLJ10043  3'  TGAGGCAGGTGGATCACTTGAG 36238           T  C
                                  TTCAAGTGATTC CC GCCTCA
                                  |||||||||||| || ||||||
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                                GAGTTCACTAGG GG CGGAGT
                                      T  A
GAM1622  FLJ10058  3'  TGAGGCAAGTGGATCACTTGAG 36266          TCCC
                                TTCAAGTGATTC    GCCTCA
                                ||||||||||||    ||||||
                                GAGTTCACTAGG    CGGAGT
                                      TGAA
GAM1622  FLJ10058  3'  TGAGGCAGGAGAATCGCTTGAA 36267            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                       A
GAM1622  FLJ10244  3'  GAGGCGGGTGGATCACTTGAG  36402          T
                                TTCAAGTGATTC CCCGCCTC
                                |||||||||||| ||||||||
                                GAGTTCACTAGG GGGCGGAG
                                      T
GAM1622  FLJ10244  3'  TGAGGCAGGAGAATCACTTGAA 36408            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                       A
GAM1622  FLJ10439  5'  TGAGGCAGAAGAATCGCTTGAA 36599          CCC
                                TTCAAGTGATTCT   GCCTCA
                                ||||||||||||   ||||||
                                AAGTTCGCTAAGA   CGGAGT
                                       AGA
GAM1622  FLJ10460  3'  TGAGGCAGAATAATCGCTTGAA 36625         C_  CC
                                TTCAAGTGATT  TC  GCCTCA
                                ||||||||||  ||  ||||||
                                AAGTTCGCTAA  AG  CGGAGT
                                      TA  A_
GAM1622  FLJ10460  3'  TGAGGCGGGCAGATCACTT   36626        CT
                                AAGTGATT  CCCGCCTCA
                                ||||||||  |||||||||
                                TTCACTAG  GGGCGGAGT
                                     AC
GAM1622  FLJ10486  3'  TGAGGCAGGAGGATCTCTTGAG 36661       T       C
                                TTCAAG GATTCTCC GCCTCA
                                |||||| |||||||| ||||||
                                GAGTTC CTAGGAGG CGGAGT
                                    T       A
GAM1622  FLJ10520  3'  TGAGGCAGGAGAATTGCTTGAA 36712       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                    GT      A
GAM1622  FLJ10547  3'  TGAGACAGGAGAATCGCTTGAA 36780            CGC
                                TTCAAGTGATTCTCC   CTCA
                                ||||||||||||||   ||||
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                                AAGTTCGCTAAGAGG   GAGT
                                      ACA
GAM1622  FLJ10607  3'  TGAGGCGAGAGAATCGCTTGAA 77647            C
                                TTCAAGTGATTCTC CGCCTCA
                                ||||||||||||| |||||||
                                AAGTTCGCTAAGAG GCGGAGT
                                      A
GAM1622  FLJ10613  3'  AGGCAGGAGAATCGCCTGAA  39333     A       C
                                TTCA GTGATTCTCC GCCT
                                |||| |||||||||| ||||
                                AAGT CGCTAAGAGG CGGA
                                  C        A
GAM1622  FLJ10613  3'  TGAGGCAGGAGAATCGCCTGAA 39342     A       C
                                TTCA GTGATTCTCC GCCTCA
                                |||| |||||||||| ||||||
                                AAGT CGCTAAGAGG CGGAGT
                                  C        A
GAM1622  FLJ10650  3'  TGAGGCAAAAGAATTGCTTGAA 36905      TG    CCC
                                TTCAAG  ATTCT   GCCTCA
                                ||||||  |||||   ||||||
                                AAGTTC  TAAGA   CGGAGT
                                   GT    AAA
GAM1622  FLJ10704  3'  TGAGGCAGGAGATTCGCTTGAA 36985        T    C
                                TTCAAGTGA TCTCC GCCTCA
                                ||||||||| ||||| ||||||
                                AAGTTCGCT AGAGG CGGAGT
                                      T    A
GAM1622  FLJ10803  3'  TGAGGCACGAGAATTACTTGAA 37211           CC
                                TTCAAGTGATTCTC  GCCTCA
                                ||||||||||||||  ||||||
                                AAGTTCATTAAGAG  CGGAGT
                                      CA
GAM1622  FLJ10811  3'  AGGCAGGAGGATCACTTGAG  37219           C
                                TTCAAGTGATTCTCC GCCT
                                |||||||||||||| ||||
                                GAGTTCACTAGGAGG CGGA
                                      A
GAM1622  FLJ10830  3'  TGAGGCAGGAGGATCGCTTGAG 37268           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                GAGTTCGCTAGGAGG CGGAGT
                                      A
GAM1622  FLJ10932  3'  TGAGGCAGGAGAATCGTTTGAA 37432           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTTGCTAAGAGG CGGAGT
                                      A
GAM1622  FLJ10936  3'  TGAGGCAGGAGAATCGCTGGAA 37451     A       C
                                TTC AGTGATTCTCC GCCTCA
                                ||| |||||||||| ||||||
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                                AAG TCGCTAAGAGG CGGAGT
                                  G          A
GAM1622  FLJ10989  3'  TGAGGCAGGAGAATCACTTGAA 37508             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                       A
GAM1622  FLJ11036  3'  TGAGGCAGGAGGACTGCTTGAG 37557        GA     C
                                TTCAAGT  TTCTCC GCCTCA
                                |||||||  |||||| ||||||
                                GAGTTCG  AGGAGG CGGAGT
                                    TC      A
GAM1622  FLJ11136  3'  TGAGGCAGGAGAATCACTTGAA 37670             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                       A
GAM1622  FLJ11259  3'  TGAGGTGGGAGAATCACCTGAG 37773      A
                                TTCA GTGATTCTCCCGCCTCA
                                |||| ||||||||||||||||
                                GAGT CACTAAGAGGGTGGAGT
                                  C
GAM1622  FLJ11301  3'  TGAGGCAGGAGAATCACTTGAA 37811             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                       A
GAM1622  FLJ11370  3'  TGAGGCAGGAGAATCACTTGAA 46970             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                       A
GAM1622  FLJ11577  3'  TGAGGCAGGAGAATCTCTTGAA 47961        T       C
                                TTCAAG GATTCTCC GCCTCA
                                |||||| |||||||| ||||||
                                AAGTTC CTAAGAGG CGGAGT
                                    T       A
GAM1622  FLJ11700  3'  TGAGGCAGGAGAATTGCTTGAA 46568        TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                    GT      A
GAM1622  FLJ11715  3'  GAGGCAGGAGTATTGCTTGAG  44980       TG  T    C
                                TTCAAG  AT CTCC GCCTC
                                ||||||  || |||| |||||
                                GAGTTC  TA GAGG CGGAG
                                    GT  T    A
GAM1622  FLJ11722  3'  TGAGGCGGGAGAATCCCTTGAA 47010       T
                                TTCAAG GATTCTCCCGCCTCA
                                |||||| |||||||||||||||
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                                AAGTTC CTAAGAGGGCGGAGT
                                   C
GAM1622  FLJ11726  3'  TGAGGCAGGAGAATTGTTTGAA 47032      TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTT  TAAGAGG CGGAGT
                                   GT      A
GAM1622  FLJ11996  3'  GAGGCATGAGAGTCACTTGAA  47064          CC
                                TTCAAGTGATTCTC  GCCTC
                                ||||||||||||||  |||||
                                AAGTTCACTGAGAG  CGGAG
                                      TA
GAM1622  FLJ11996  3'  TGAGGCAAGAGAATTGCTTGGA 47071      TG     CC
                                TTCAAG  ATTCTC  GCCTCA
                                ||||||  ||||||  ||||||
                                AGGTTC  TAAGAG  CGGAGT
                                   GT     AA
GAM1622  FLJ11996  3'  TGAGGCGAGTGGATCACTTGAG 47072          TCC
                                TTCAAGTGATTC   CGCCTCA
                                ||||||||||||   |||||||
                                GAGTTCACTAGG   GCGGAGT
                                     TGA
GAM1622  FLJ12056  3'  TGAGGCAGGAGAATTGCTTGAA 46826      TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  FLJ12078  3'  GAGGCAGGAGAATTGCTTGAA  47081      TG      C
                                TTCAAG  ATTCTCC GCCTC
                                ||||||  ||||||| |||||
                                AAGTTC  TAAGAGG CGGAG
                                   GT      A
GAM1622  FLJ12078  5'  TGAGGCCGGAGGATCACTTGAA 47087           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAGGAGG CGGAGT
                                      C
GAM1622  FLJ12132  3'  GAGGCAGGAGCATCGCTTGAG  47101         T   C
                                TTCAAGTGAT CTCC GCCTC
                                |||||||||| |||| |||||
                                GAGTTCGCTA GAGG CGGAG
                                     C   A
GAM1622  FLJ12190  3'  TGAGGCAGGAGAATCTCTTGAA 47574      T      C
                                TTCAAG GATTCTCC GCCTCA
                                |||||| |||||||| ||||||
                                AAGTTC CTAAGAGG CGGAGT
                                   T      A
GAM1622  FLJ12294  5'  TGAGGCAGGAAGATCGCTT   47722       TC   C
                                AAGTGAT  TCC GCCTCA
                                |||||||  ||| ||||||
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                                TTCGCTA  AGG CGGAGT
                                   GA   A
GAM1622  FLJ12294  3'  TGAGGCAGGAGAATCGCTTGAA 47723            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                         A
GAM1622  FLJ12298  3'  TGAGGTAGGAGAATCACTTGAA 50602            CG
                                TTCAAGTGATTCTCC  CCTCA
                                |||||||||||||  |||||
                                AAGTTCACTAAGAGG  GGAGT
                                         AT
GAM1622  FLJ12331  3'  TGAGACAAGAATCACTTGAA  47116          CCCGC
                                TTCAAGTGATTCT    CTCA
                                ||||||||||||    ||||
                                AAGTTCACTAAGA    GAGT
                                         ACA__
GAM1622  FLJ12363  3'  TGAGGCAGGAGAATCGCTTGAA 50644            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                         A
GAM1622  FLJ12387  5'  TGAAGCGGGAGGCAGCCAGA  43377    AA  GAT      C
                                TC  GT   TCTCCCGC TCA
                                ||  ||   |||||||| |||
                                AG  CG   GGAGGGCG AGT
                                 AC  AC_      A
GAM1622  FLJ12448  3'  TGAGGTGGGAGAATCGCTTGAA 43482
                                TTCAAGTGATTCTCCCGCCTCA
                                ||||||||||||||||||||||
                                AAGTTCGCTAAGAGGGTGGAGT

GAM1622  FLJ12586  3'  TGAGGCAGGAGAATTGCTTGAA 45213       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  FLJ12592  3'  TGAGGCAGGAGGATTGCTTGAG 50656       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                GAGTTC  TAGGAGG CGGAGT
                                   GT      A
GAM1622  FLJ12618  3'  TGAGGCAGGAGAATCAATTGAA 46510      G       C
                                TTCAA TGATTCTCC GCCTCA
                                |||||  ||||||||| ||||||
                                AAGTT ACTAAGAGG CGGAGT
                                   A       A
GAM1622  FLJ12660  3'  TGAGGCAGGAGAATCATTT   47901          C
                                AAGTGATTCTCC GCCTCA
                                |||||||||||| ||||||
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                                TTTACTAAGAGG CGGAGT
                                      A
GAM1622  FLJ12666  3'  GAGGCATGCGGATCACTTGAG  45069          TCCC
                                TTCAAGTGATTC    GCCTC
                                ||||||||||||    |||||
                                GAGTTCACTAGG    CGGAG
                                      CGTA
GAM1622  FLJ12666  3'  TGAGGCAGTAGAATCACTTGAA 45073           CCC
                                TTCAAGTGATTCT   GCCTCA
                                ||||||||||||||  ||||||
                                AAGTTCACTAAGA   CGGAGT
                                      TGA
GAM1622  FLJ12671  3'  GAGGCGGGCGGATCACCTGAG  49109     A      T
                                TTCA GTGATTC CCCGCCTC
                                ||||| ||||||| ||||||||
                                GAGT CACTAGG GGGCGGAG
                                  C      C
GAM1622  FLJ12671  3'  TGAGGCAGGAGAATCGCTTGAG 49113            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||||| ||||||
                                GAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  FLJ12800  3'  TGAGGCTGGAAGATCACTTGAA 43535         TC   C
                                TTCAAGTGAT  TCC GCCTCA
                                ||||||||||  ||| ||||||
                                AAGTTCACTA  AGG CGGAGT
                                     GA   T
GAM1622  FLJ12985  3'  AGGTAGATCACTTGAG      46794          T  CCC
                                TTCAAGTGAT CT   GCCT
                                |||||||||| ||   ||||
                                GAGTTCACTA GA   TGGA
                                      _  ___
GAM1622  FLJ13117  3'  TGAGGCAGGAGAATCGCTTGAA 43812            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  FLJ13193  3'  AGGCGGGCAGATCACTTGAG   50707          CT
                                TTCAAGTGATT  CCCGCCT
                                ||||||||||  |||||||
                                GAGTTCACTAG  GGGCGGA
                                      AC
GAM1622  FLJ13193  3'  TGAGGCAGGAGAATCACCTGAA 50737     A        C
                                TTCA GTGATTCTCC GCCTCA
                                |||| |||||||||| ||||||
                                AAGT CACTAAGAGG CGGAGT
                                  C        A
GAM1622  FLJ13193  3'  TGAGGCAGGAGAATCACTTGAA 50738            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||||| ||||||
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                                  AAGTTCACTAAGAGG CGGAGT
                                        A
GAM1622  FLJ13315  3'  TGAGGCGGCAGGATCACTTGAA 47200          C
                                  TTCAAGTGATTCT CCGCCTCA
                                  |||||||||||| ||||||||
                                  AAGTTCACTAGGA GGCGGAGT
                                        C
GAM1622  FLJ13390  3'  TGAGGCAGGACGATTACTTGAG 42841        C  C
                                  TTCAAGTGATT TCC GCCTCA
                                  |||||||||| ||| ||||||
                                  GAGTTCATTAG AGG CGGAGT
                                        C  A
GAM1622  FLJ13448  3'  TGAGGCACAAGAATCGCTTGAA 47886         CCC
                                  TTCAAGTGATTCT  GCCTCA
                                  ||||||||||||  ||||||
                                  AAGTTCGCTAAGA  CGGAGT
                                        ACA
GAM1622  FLJ13456  3'  GAGGCGGGCAGATCACTTGAG  66548         CT
                                  TTCAAGTGATT  CCCGCCTC
                                  ||||||||||  ||||||||
                                  GAGTTCACTAG  GGGCGGAG
                                        AC
GAM1622  FLJ13456  3'  TGAAGCAGGAGGATTGCTTGAG 66565      TG     C  C
                                  TTCAAG  ATTCTCC GC TCA
                                  ||||||  ||||||| || |||
                                  GAGTTC  TAGGAGG CG AGT
                                     GT      A  A
GAM1622  FLJ13456  3'  TGAGGCACGAGAATCACTTGAA 66567          CC
                                  TTCAAGTGATTCTC  GCCTCA
                                  ||||||||||||||  ||||||
                                  AAGTTCACTAAGAG  CGGAGT
                                        CA
GAM1622  FLJ13456  3'  TGAGGCAGGAGAATCGCTTGAA 66568          C
                                  TTCAAGTGATTCTCC GCCTCA
                                  |||||||||||||| ||||||
                                  AAGTTCGCTAAGAGG CGGAGT
                                        A
GAM1622  FLJ13544  3'  AGGCAGGAGAAGCGCTTGAG  47205      A    C
                                  TTCAAGTG TTCTCC GCCT
                                  |||||||| |||||| ||||
                                  GAGTTCGC AAGAGG CGGA
                                     G     A
GAM1622  FLJ13611  3'  TGAGGCAGGAGAATCACTTGAA 46869          C
                                  TTCAAGTGATTCTCC GCCTCA
                                  |||||||||||||| ||||||
                                  AAGTTCACTAAGAGG CGGAGT
                                        A
GAM1622  FLJ13621  3'  GAGGCGGGTGGATCACTTGAG  47223          T
                                  TTCAAGTGATTC CCCGCCTC
                                  |||||||||||| ||||||||
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                                GAGTTCACTAGG GGGCGGAG
                                       T
GAM1622  FLJ13659  3'  TGAGGCAGGAGAATTGCTTGAA 48037       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  FLJ13769  3'  TGAGCCAGGAGAATCACTTGAA 47265             CGC
                                TTCAAGTGATTCTCC   CTCA
                                ||||||||||||||   ||||
                                AAGTTCACTAAGAGG   GAGT
                                       ACC
GAM1622  FLJ13769  3'  TGAGGCAGGAGAATTGCTTGAG 47266       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                GAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  FLJ13848  3'  TGAGGCAGGAGACTCGCTTGAA 45832         T    C
                                TTCAAGTGA TCTCC GCCTCA
                                |||||||| |||||| ||||||
                                AAGTTCGCT AGAGG CGGAGT
                                      C    A
GAM1622  FLJ13952  3'  AGGCAGGAGAATCTCTTGAA   46004       T       C
                                TTCAAG GATTCTCC GCCT
                                |||||| |||||||| ||||
                                AAGTTC CTAAGAGG CGGA
                                   T       A
GAM1622  FLJ14011  3'  TGAGGCAGGAGAATCGCTTGAA 42321             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                       A
GAM1622  FLJ14107  3'  AGGCAGGCAGATCACTTGAG   47344          CT  C
                                TTCAAGTGATT  CC GCCT
                                ||||||||||  || ||||
                                GAGTTCACTAG  GG CGGA
                                      AC  A
GAM1622  FLJ14117  3'  TGAGGCAGAATTGCCTGAA    43236      A TG    CCC
                                TTCA G  ATTCT   GCCTCA
                                |||| |  |||||  ||||||
                                AAGT C  TAAGA   CGGAGT
                                  C GT    ___
GAM1622  FLJ14117  3'  TGAGGCGGGCGGATCACTTGAG 43237           T
                                TTCAAGTGATTC CCCGCCTCA
                                |||||||||||| |||||||||
                                GAGTTCACTAGG GGGCGGAGT
                                       C
GAM1622  FLJ14129  3'  TGGGGCAGGAGAATCACTTGAA 48815             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
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                                AAGTTCACTAAGAGG CGGGGT
                                       A
GAM1622  FLJ14251  3'  TGAGGCAGGAGAATCACTTGAG 46493          C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                GAGTTCACTAAGAGG CGGAGT
                                       A
GAM1622  FLJ14326  3'  GAGGCAGGAAGATCACTTGAG  50772       TC  C
                                TTCAAGTGAT  TCC GCCTC
                                ||||||||||  ||| |||||
                                GAGTTCACTA  AGG CGGAG
                                      GA  A
GAM1622  FLJ14326  3'  TGAGGCGGGTGGATCACTTGAG 50788         T
                                TTCAAGTGATTC CCCGCCTCA
                                |||||||||||| |||||||||
                                GAGTTCACTAGG GGGCGGAGT
                                       T
GAM1622  FLJ14327  3'  GAGGCAGGTGGAACACTTGAG  46682      A  TC  _
                                TTCAAGTG TTC  CC GCCTC
                                |||||||| |||  || |||||
                                GAGTTCAC AAG  GG CGGAG
                                     _  GT  A
GAM1622  FLJ14345  3'  GAGGCAGGGGGATCACCTGAG  45657    A       C
                                TTCA GTGATTCTCC GCCTC
                                |||| |||||||||| |||||
                                GAGT CACTAGGGGG CGGAG
                                  C        A
GAM1622  FLJ14345  3'  TGAGGCAGGAGAATCACTTGAA 45663          C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                       A
GAM1622  FLJ14397  3'  TGAGGCAGGAGAATCGCTTGAA 52336          C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                       A
GAM1622  FLJ14466  3'  AGGCAGGAGGATCTCTTGAG   52417      T      C
                                TTCAAG GATTCTCC GCCT
                                |||||| |||||||| ||||
                                GAGTTC CTAGGAGG CGGA
                                    T       A
GAM1622  FLJ14466  3'  AGGCGGGCAGATCACTTGAG   52418        CT
                                TTCAAGTGATT  CCCGCCT
                                |||||||||||  |||||||
                                GAGTTCACTAG  GGGCGGA
                                       AC
GAM1622  FLJ14466  3'  TGAGGCAGGAGAATCGCTTGAA 52433          C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
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                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  FLJ14621  3'  TGAGGCAGGAAGAATCGCTTGA 52544          _  C
              A                  TTCAAGTGATTCT CC GCCTCA
                                 ||||||||||||| || ||||||
                                 AAGTTCGCTAAGA GG CGGAGT
                                       A  A
GAM1622  FLJ14641  3'  TGAGGCAGGAGAATCGCTTGAA 52569            C
                                 TTCAAGTGATTCTCC GCCTCA
                                 |||||||||||||| ||||||
                                 AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  FLJ20004  3'  GAGGCGGGCAGATCACTTGAG  34761          CT
                                 TTCAAGTGATT  CCCGCCTC
                                 ||||||||||  ||||||||
                                 GAGTTCACTAG  GGGCGGAG
                                       AC
GAM1622  FLJ20004  3'  TGAGGCAGGAGAATCGCTTGAA 34769            C
                                 TTCAAGTGATTCTCC GCCTCA
                                 |||||||||||||| ||||||
                                 AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  FLJ20004  3'  AGGCAGGAGGATTGCTTGAG  96996       TG     C
                                 TTCAAG  ATTCTCC GCCT
                                 ||||||  ||||||| ||||
                                 GAGTTC  TAGGAGG CGGA
                                    GT      A
GAM1622  FLJ20004  3'  AGGCGGGAGAATCACTTGAA  96997
                                 TTCAAGTGATTCTCCCGCCT
                                 ||||||||||||||||||||
                                 AAGTTCACTAAGAGGGCGGA

GAM1622  FLJ20004  3'  TGAGGCAGGAGAATCACTTGAA 97014            C
                                 TTCAAGTGATTCTCC GCCTCA
                                 |||||||||||||| ||||||
                                 AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  FLJ20006  3'  TGAGGCAGGAAAATCGCTTGAA 34789          C  C
                                 TTCAAGTGATT TCC GCCTCA
                                 |||||||||||  ||| ||||||
                                 AAGTTCGCTAA AGG CGGAGT
                                       A  A
GAM1622  FLJ20019  3'  TGAGGATGGAAAATCACTTGAG 34817          C  CG
                                 TTCAAGTGATT TCC  CCTCA
                                 |||||||||||  |||  |||||
                                 GAGTTCACTAA AGG  GGAGT
                                       A  TA
GAM1622  FLJ20038  3'  TGAGGCAAGGAATCATTGAA  34867       G     CCC
                                 TTCAA TGATTCT   GCCTCA
                                 |||||  |||||||   ||||||
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                                AAGTT ACTAAGG   CGGAGT
                                  _      AA_
GAM1622  FLJ20045  3'  TGAGGCTGGAGAATCGCTTGAA 34896            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                       T
GAM1622  FLJ20055  3'  TGAGGCAAGAGAATCACTTGAA 34915           CC
                                TTCAAGTGATTCTC  GCCTCA
                                |||||||||||||  ||||||
                                AAGTTCACTAAGAG  CGGAGT
                                       AA
GAM1622  FLJ20069  3'  TGAGGCAGGAGAATTGCTTGA  34958      TG      C
                                TCAAG  ATTCTCC GCCTCA
                                |||||  ||||||| ||||||
                                AGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  FLJ20071  3'  TGAGGCAGGAGAATCGCTTGAA 34962            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                       A
GAM1622  FLJ20211  3'  TGAAGCAGGAGAATTGCCTGAA 35269     A TG      C  C
                                TTCA G  ATTCTCC GC TCA
                                |||| |  ||||||| || |||
                                AAGT C  TAAGAGG CG AGT
                                  C GT      A  A
GAM1622  FLJ20280  3'  TGAAACAGGAGAATCACTTGAA 35335           CGCC
                                TTCAAGTGATTCTCC    TCA
                                ||||||||||||||    |||
                                AAGTTCACTAAGAGG    AGT
                                       ACAA
GAM1622  FLJ20306  3'  AGGCAGGAGGATTGCTTGAG   35383      TG      C
                                TTCAAG  ATTCTCC GCCT
                                ||||||  ||||||| ||||
                                GAGTTC  TAGGAGG CGGA
                                   GT      A
GAM1622  FLJ20306  3'  TGAGGCAGGGAGAATCGCTTGA 35401                _
            A                    TTCAAGTGATTCTCCC GCCTCA
                                |||||||||||||||| ||||||
                                AAGTTCGCTAAGAGGG CGGAGT
                                       A
GAM1622  FLJ20340  3'  TGAAGCAGGAGAATCGCTTGAA 35462           C  C
                                TTCAAGTGATTCTCC GC TCA
                                |||||||||||||| || |||
                                AAGTTCGCTAAGAGG CG AGT
                                       A  A
GAM1622  FLJ20456  3'  TGAGGCAGAAGAATCGCTTGAG 35667           CCC
                                TTCAAGTGATTCT   GCCTCA
                                ||||||||||||   ||||||
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                                  GAGTTCGCTAAGA  CGGAGT
                                        AGA
GAM1622  FLJ20464  3'  TGAGGCAGGAGAATCACTTGAA 35701          C
                                  TTCAAGTGATTCTCC GCCTCA
                                  |||||||||||||| ||||||
                                  AAGTTCACTAAGAGG CGGAGT
                                        A
GAM1622  FLJ20464  3'  TGAGGCAGGAGAATCGCTTGAA 35702          C
                                  TTCAAGTGATTCTCC GCCTCA
                                  |||||||||||||| ||||||
                                  AAGTTCGCTAAGAGG CGGAGT
                                        A
GAM1622  FLJ20464  3'  TGAGGCGGGCGGATCACCTGAG 35703     A    T
                                  TTCA GTGATTC CCCGCCTCA
                                  |||| ||||||| |||||||||
                                  GAGT CACTAGG GGGCGGAGT
                                    C     C
GAM1622  FLJ20546  3'  TGAGGCAGGAGAATCATTTGAA 35816          C
                                  TTCAAGTGATTCTCC GCCTCA
                                  |||||||||||||| ||||||
                                  AAGTTTACTAAGAGG CGGAGT
                                        A
GAM1622  FLJ20627  3'  TGAGGCAGGAGAATCTCTTGAA 35912      T    C
                                  TTCAAG GATTCTCC GCCTCA
                                  |||||| |||||||| ||||||
                                  AAGTTC CTAAGAGG CGGAGT
                                     T      A
GAM1622  FLJ20686  3'  TGAGGCAGGAGAATCGCTTGAA 35959          C
                                  TTCAAGTGATTCTCC GCCTCA
                                  |||||||||||||| ||||||
                                  AAGTTCGCTAAGAGG CGGAGT
                                        A
GAM1622  FLJ20694  3'  TGAGGCAGGAGAATCACCTGAA 35981     A    C
                                  TTCA GTGATTCTCC GCCTCA
                                  |||| |||||||||| ||||||
                                  AAGT CACTAAGAGG CGGAGT
                                    C       A
GAM1622  FLJ20802  3'  AGGCAGGAGAATTGCTTGAA  36105     TG   C
                                  TTCAAG  ATTCTCC GCCT
                                  ||||||  ||||||| ||||
                                  AAGTTC  TAAGAGG CGGA
                                     GT     A
GAM1622  FLJ20825  3'  TGAGGCAGGAGAATCGCTTGAA 36150          C
                                  TTCAAGTGATTCTCC GCCTCA
                                  |||||||||||||| ||||||
                                  AAGTTCGCTAAGAGG CGGAGT
                                        A
GAM1622  FLJ20972  3'  TGAGGCAGGAGAATCACTTGAA 47390          C
                                  TTCAAGTGATTCTCC GCCTCA
                                  |||||||||||||| ||||||
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                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  FLJ21162  3'  TGAGGCGGGAGGATCACTTGAG 46378
                                TTCAAGTGATTCTCCCGCCTCA
                                |||||||||||||||||||||
                                GAGTTCACTAGGAGGGCGGAGT

GAM1622  FLJ21240  3'  TGAGGCAGGAGAATTGCTTGAA 46270       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  FLJ21551  3'  TGAGACAGGAGAATCGCTTGAA 46043             CGC
                                TTCAAGTGATTCTCC   CTCA
                                ||||||||||||||   ||||
                                AAGTTCGCTAAGAGG   GAGT
                                      ACA
GAM1622  FLJ21657  3'  GAGGCAGGCAGGTCACTTGAG  42800          CT  C
                                TTCAAGTGATT  CC GCCTC
                                ||||||||||  || |||||
                                GAGTTCACTGG  GG CGGAG
                                      AC  A
GAM1622  FLJ21870  3'  GAGGCAGGTGGATCACTTGAG  43746           T  C
                                TTCAAGTGATTC CC GCCTC
                                ||||||||||| || |||||
                                GAGTTCACTAGG GG CGGAG
                                      T  A
GAM1622  FLJ21870  3'  TGAGGCATGAGAATCACTT    43751          CC
                                AAGTGATTCTC  GCCTCA
                                ||||||||||  ||||||
                                TTCACTAAGAG  CGGAGT
                                      TA
GAM1622  FLJ22009  3'  TGAGGCAGGAGGATCACTTGAG 60923             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                GAGTTCACTAGGAGG CGGAGT
                                      A
GAM1622  FLJ22054  3'  TGAGGCCGGAGAATCGCTTGAA 96054             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      C
GAM1622  FLJ22167  3'  TGAGGCGGGTGGATCACCTGAG 44879      A      T
                                TTCA GTGATTC CCCGCCTCA
                                |||| ||||||| |||||||||
                                GAGT CACTAGG GGGCGGAGT
                                  C      T
GAM1622  FLJ22167  3'  TGAGGTGGGAGAATCACTTGGA 44880
                                TTCAAGTGATTCTCCCGCCTCA
                                |||||||||||||||||||||
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                                AGGTTCACTAAGAGGGTGGAGT

GAM1622  FLJ22389  3'  AGGCAGGAAGATCACTTGAG   46789          TC   C
                                TTCAAGTGAT  TCC GCCT
                                ||||||||||  ||| ||||
                                GAGTTCACTA  AGG CGGA
                                      GA   A
GAM1622  FLJ22474  3'  TGAGGCACGAGAATCACTTGAA 45619             CC
                                TTCAAGTGATTCTC  GCCTCA
                                ||||||||||||||  ||||||
                                AAGTTCACTAAGAG  CGGAGT
                                          CA
GAM1622  FLJ22814  3'  AGGCGGGAGGATCACTTGAG   46711
                                TTCAAGTGATTCTCCCGCCT
                                ||||||||||||||||||||
                                GAGTTCACTAGGAGGGCGGA

GAM1622  FLJ22814  3'  TGAGGCAGGAGGATCACTTGAA 46733             C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||| ||||||
                                AAGTTCACTAGGAGG CGGAGT
                                          A
GAM1622  FLJ23022  3'  TGAGGCAGGAGAATCGCTTGAA 47501             C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                          A
GAM1622  FLJ23040  3'  TGAGGCAGGAAAATTGCTTGAA 47993          TG   C   C
                                TTCAAG  ATT TCC GCCTCA
                                ||||||  ||| ||| ||||||
                                AAGTTC  TAA AGG CGGAGT
                                    GT   A   A
GAM1622  FLJ23042  3'  GAGGCGGGCGGATCACCTGAG  47944       A       T
                                TTCA GTGATTC CCCGCCTC
                                ||||  |||||||  ||||||||
                                GAGT CACTAGG GGGCGGAG
                                   C       C
GAM1622  FLJ23042  3'  TGAGGCAAGAGGATCGCTTGAG 47950             CC
                                TTCAAGTGATTCTC  GCCTCA
                                ||||||||||||||  ||||||
                                GAGTTCGCTAGGAG  CGGAGT
                                          AA
GAM1622  FLJ23042  3'  TGAGGCAGGAGAATCACTTGAA 47951             C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                          A
GAM1622  FLJ23112  3'  GAGGCGGGTGGATCACCTGAG  46812       A       T
                                TTCA GTGATTC CCCGCCTC
                                ||||  |||||||  ||||||||
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                                GAGT CACTAGG GGGCGGAG
                                  C      T
GAM1622  FLJ23209  3'  TGAAGCAGCAAGATCACTTGAG 46587          CTCCC  C
                                TTCAAGTGATT    GC TCA
                                ||||||||||    || |||
                                GAGTTCACTAG    CG AGT
                                      AACGA  A
GAM1622  FLJ23235  3'  TGAGGCAGGAGAATCACTTGAA 46882             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  FLJ23360  3'  TGAGGCAGGAGAATCGCTTGAA 43836             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  FLJ23447  3'  TGAGGCAGGAGGATCGCTTGAG 46133             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                GAGTTCGCTAGGAGG CGGAGT
                                      A
GAM1622  FLJ23499  3'  TGAGGCAGGAGAATTGCTTGAA 43142       TG    C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  FLJ23499  3'  TGAGGCAGGGGAATCGCTTGAA 43143             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGGGG CGGAGT
                                      A
GAM1622  FLJ23537  3'  TGGGGCAGGAGAATCACTAGAA 46546     A       C
                                TTC AGTGATTCTCC GCCTCA
                                ||| |||||||||| ||||||
                                AAG TCACTAAGAGG CGGGGT
                                  A         A
GAM1622  FLJ23556  3'  TGAGGCAGAAGGATCACTTGAG 46460           CCC
                                TTCAAGTGATTCT   GCCTCA
                                ||||||||||||   ||||||
                                GAGTTCACTAGGA   CGGAGT
                                      AGA
GAM1622  FLJ23556  3'  TGAGGCGGGAGGATCGCTTGAG 46461
                                TTCAAGTGATTCTCCCGCCTCA
                                ||||||||||||||||||||||
                                GAGTTCGCTAGGAGGGCGGAGT

GAM1622  FLJ25179  3'  AGGCAGGAGGATTGCTTGAG   59011       TG    C
                                TTCAAG  ATTCTCC GCCT
                                ||||||  ||||||| ||||
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                                GAGTTC  TAGGAGG CGGA
                                   GT      A
GAM1622  FLJ30681  3'  TGAGGCAGGAGAATTACTT   93441          C
                                AAGTGATTCTCC GCCTCA
                                |||||||||||| ||||||
                                TTCATTAAGAGG CGGAGT
                                       A
GAM1622  FLJ31168  3'  TGAGGCAGGAGAATCGCTTGAG 59187            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                GAGTTCGCTAAGAGG CGGAGT
                                       A
GAM1622  FLJ31455  3'  TGAGGCAGGAGAATCACTTGAA 59293            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                       A
GAM1622  FLJ31455  3'  TGAGGCAGGAGAATCGCCTGAA 59294     A      C
                                TTCA GTGATTCTCC GCCTCA
                                |||| |||||||||| ||||||
                                AAGT CGCTAAGAGG CGGAGT
                                  C        A
GAM1622  FLJ31952  3'  TGAAGCATGAGAATCACTTGAA 59051          CC  C
                                TTCAAGTGATTCTC  GC TCA
                                |||||||||||||  || |||
                                AAGTTCACTAAGAG  CG AGT
                                       TA  A
GAM1622  FLJ32915  5'  TGAGGCAGGAGAGTCACTTGAA 59438            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTGAGAGG CGGAGT
                                       A
GAM1622  FUSIP1    3'  TGAGGCAAGAGAATCGCTTGAA 55044          CC
                                TTCAAGTGATTCTC  GCCTCA
                                |||||||||||||  ||||||
                                AAGTTCGCTAAGAG  CGGAGT
                                       AA
GAM1622  GADD45A   5'  AGGCGGGAGGGGTGGCCGGA   10403    AA  G   _
                                TC  GT ATTC TCCCGCCT
                                ||  || |||| ||||||||
                                AG  CG TGGG AGGGCGGA
                                  GC  G    G
GAM1622  GALNT6    3'  TGAGGCAGGAGAATCACTCGAA 24253     A      C
                                TTC AGTGATTCTCC GCCTCA
                                ||| |||||||||| ||||||
                                AAG TCACTAAGAGG CGGAGT
                                  C        A
GAM1622  GCN2      3'  AGGCAGGAAGACTGCTTGAA   63434       GA TC   C
                                TTCAAGT  T  TCC GCCT
                                |||||||  |  ||| ||||
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                                  AAGTTCG  A  AGG CGGA
                                      TC GA   A
GAM1622  GLTP     3'  TGAGGCAGGAGAATCGCTTGAA 33589            C
                                  TTCAAGTGATTCTCC GCCTCA
                                  ||||||||||||||| ||||||
                                  AAGTTCGCTAAGAGG CGGAGT
                                           A
GAM1622  GLTP     3'  TGAGGCGGGTGGATCACCTGAG 33590     A      T
                                  TTCA GTGATTC CCCGCCTCA
                                  |||| ||||||| |||||||||
                                  GAGT CACTAGG GGGCGGAGT
                                    C      T
GAM1622  GP5      3'  GAGGCAGGAGAATCACTTGAA  16875           C
                                  TTCAAGTGATTCTCC GCCTC
                                  ||||||||||||||| |||||
                                  AAGTTCACTAAGAGG CGGAG
                                           A
GAM1622  GSG2     3'  TGAGGCAGGAGGATCGCTTGAG 50075            C
                                  TTCAAGTGATTCTCC GCCTCA
                                  |||||||||||||| ||||||
                                  GAGTTCGCTAGGAGG CGGAGT
                                           A
GAM1622  HIC      3'  TGAGGCAGGAGAATTGCTTGAA 68053       TG     C
                                  TTCAAG  ATTCTCC GCCTCA
                                  ||||||  ||||||| ||||||
                                  AAGTTC  TAAGAGG CGGAGT
                                     GT      A
GAM1622  HIG2     3'  TGAGGCGGGAGAATTGCTTGAA 26206       TG
                                  TTCAAG  ATTCTCCCGCCTCA
                                  ||||||  ||||||||||||||
                                  AAGTTC  TAAGAGGGCGGAGT
                                     GT
GAM1622  HSA250303 3'  TGAGGCAGGAGGATCGCTTGAA 38024            C
                                  TTCAAGTGATTCTCC GCCTCA
                                  |||||||||||||| ||||||
                                  AAGTTCGCTAGGAGG CGGAGT
                                           A
GAM1622  HSD17B7  3'  AGGCAGAAGGATCACTTGAG  33479          CCC
                                  TTCAAGTGATTCT  GCCT
                                  ||||||||||||  ||||
                                  GAGTTCACTAGGA  CGGA
                                           AGA
GAM1622  HSH2     3'  TGAGGCGGGAGAATTGCTTGAA 52745       TG
                                  TTCAAG  ATTCTCCCGCCTCA
                                  ||||||  ||||||||||||||
                                  AAGTTC  TAAGAGGGCGGAGT
                                     GT
GAM1622  HSPC031  3'  AGGCGGACGGATCACTTGAG  32746          TC
                                  TTCAAGTGATTC  CCGCCT
                                  ||||||||||||  ||||||
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                                GAGTTCACTAGG  GGCGGA
                                      CA
GAM1622  HSPC043   3'  AGGCGGGCAGATCACTTGAG   68346          CT
                                TTCAAGTGATT  CCCGCCT
                                ||||||||||  |||||||
                                GAGTTCACTAG  GGGCGGA
                                      AC
GAM1622  HSPC043   3'  TGAGGCAGGAGAATCGCTTGAA 68354             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                       A
GAM1622  HYPK      3'  TGAGGCAGGAATCGCTTGAA   33518           CCC
                                TTCAAGTGATTCT   GCCTCA
                                ||||||||||||   ||||||
                                AAGTTCGCTAAGG   CGGAGT
                                      A__
GAM1622  ICAM4     3'  GAGGCAGGAGAATCGCTTGAG  9543             C
                                TTCAAGTGATTCTCC GCCTC
                                |||||||||||||| |||||
                                GAGTTCGCTAAGAGG CGGAG
                                       A
GAM1622  ICAM4     3'  GAGGCAGGAGAATCGCTTGAG  42594            C
                                TTCAAGTGATTCTCC GCCTC
                                |||||||||||||| |||||
                                GAGTTCGCTAAGAGG CGGAG
                                       A
GAM1622  IL-23R    3'  TGAGGCAGGAGAATCACTTGAA 59134            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                       A
GAM1622  IL10RB    3'  GAGGCAGGCGGATCACTTGAG  7127           T  C
                                TTCAAGTGATTC CC GCCTC
                                |||||||||||  || |||||
                                GAGTTCACTAGG GG CGGAG
                                      C  A
GAM1622  IL10RB    3'  TGAGGCAGGAGAATTGCATGAA 7130       A TG      C
                                TTCA G  ATTCTCC GCCTCA
                                ||||  |  ||||||| ||||||
                                AAGT C  TAAGAGG CGGAGT
                                   A GT      A
GAM1622  IMAGE:4907098 3'  TGAGGCAGGAGAATCACTTGAA 93329             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                       A
GAM1622  JDD1      3'  AGGTGGGAGGATCACTTGAA   63909
                                TTCAAGTGATTCTCCCGCCT
                                ||||||||||||||||||||
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                                AAGTTCACTAGGAGGGTGGA

GAM1622  KALI     3'  TGAGGCAGGAGAATCGCTTGAA 54698              C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                          A
GAM1622  KBRAS2    3'  TGAGGCAGGAGAATTGCTTGAA 34630       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  KIAA0042  3'  TGAGGCAGGAGGATCGCTTGAA 30241             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAGGAGG CGGAGT
                                          A
GAM1622  KIAA0057  3'  TGAGGCAGGAGAATCGCTTGAA 25425             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                          A
GAM1622  KIAA0062  3'  TGAGGCAAGGTTCATCCTGAA  70788     A_   TT  CCC
                                TTCA  GTGA  CT   GCCTCA
                                ||||  ||||  ||   ||||||
                                AAGT  TACT  GA   CGGAGT
                                  CC    TG  A__
GAM1622  KIAA0159  3'  TGAGGCAGGAGAATCGCCTGAA 30144      A        C
                                TTCA GTGATTCTCC GCCTCA
                                |||| |||||||||| ||||||
                                AAGT CGCTAAGAGG CGGAGT
                                  C         A
GAM1622  KIAA0186  3'  TGAGGTGGGAGGATCACTTGAA 41122
                                TTCAAGTGATTCTCCCGCCTCA
                                |||||||||||||||||||||
                                AAGTTCACTAGGAGGGTGGAGT

GAM1622  KIAA0226  3'  TGAGGCAGGAGAATCGCTTGAA 64265             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                          A
GAM1622  KIAA0252  3'  TGAGACAGGAGAATCCCTTGAA 63460       T       CGC
                                TTCAAG GATTCTCC   CTCA
                                |||||| ||||||||   ||||
                                AAGTTC CTAAGAGG   GAGT
                                   C       ACA
GAM1622  KIAA0266  3'  TGAGGCAGGAGAATTGCTTGAA 41646       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
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                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  KIAA0355  3'  TGAAGCAGAAGAATCGCTTGAA 28712          CCC  C
                                TTCAAGTGATTCT   GC TCA
                                |||||||||||||   || |||
                                AAGTTCGCTAAGA   CG AGT
                                      AGA  A
GAM1622  KIAA0420  3'  TGAGGCAGAAGGATTGCTTGGA 64095      TG    CCC
                                TTCAAG  ATTCT   GCCTCA
                                ||||||  |||||   ||||||
                                AGGTTC  TAGGA   CGGAGT
                                   GT    AGA
GAM1622  KIAA0431  3'  GCAGGACGATCACTTGAG    31549        C   C
                                TTCAAGTGATT TCC GC
                                |||||||||| ||| ||
                                GAGTTCACTAG AGG CG
                                      C   A
GAM1622  KIAA0441  3'  TGAGACAGGAGAATCACTTGAG 29645          CGC
                                TTCAAGTGATTCTCC   CTCA
                                ||||||||||||||   ||||
                                GAGTTCACTAAGAGG   GAGT
                                      ACA
GAM1622  KIAA0445  5'  TGAGGCAGGAGAATTGCTTGAA 28643      TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  KIAA0447  3'  TGAGGCAGGAGAATTGTTTGAA 72134      TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTT  TAAGAGG CGGAGT
                                   GT      A
GAM1622  KIAA0472  3'  TGAGGCAGGAGAATCACTTGAA 72372          C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  KIAA0472  3'  TGAGGCAGGAGAATCGCTTGAA 72373          C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  KIAA0475  3'  TGAGGCAGGAGAATCACTTGAA 30132          C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  KIAA0547  3'  AGGCTGGCAGATCACTTGAA   29586         CT  C
                                TTCAAGTGATT  CC GCCT
                                ||||||||||  || ||||
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                                AAGTTCACTAG  GG CGGA
                                      AC  T
GAM1622  KIAA0547  3'  TGAGGCAAGAGAATCACTTGAA 29603           CC
                                TTCAAGTGATTCTC  GCCTCA
                                |||||||||||||  ||||||
                                AAGTTCACTAAGAG  CGGAGT
                                      AA
GAM1622  KIAA0557  3'  TGAGGCAAGAGAATCACTTGAA 78578           CC
                                TTCAAGTGATTCTC  GCCTCA
                                |||||||||||||  ||||||
                                AAGTTCACTAAGAG  CGGAGT
                                      AA
GAM1622  KIAA0565  3'  TGAGGCAGGAAGATCACTTGAA 67443         TC  C
                                TTCAAGTGAT  TCC GCCTCA
                                ||||||||||  ||| ||||||
                                AAGTTCACTA  AGG CGGAGT
                                      GA  A
GAM1622  KIAA0565  3'  TGAGGCAGGAGAATTGCTTGAA 67444       TG     C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT     A
GAM1622  KIAA0596  3'  GAGGCGGGTGGATCACCTGAG  63491     A     T
                                TTCA GTGATTC CCCGCCTC
                                ||||  ||||||| ||||||||
                                GAGT CACTAGG GGGCGGAG
                                  C     T
GAM1622  KIAA0628  3'  TGAGGCAGGAGAATTGCTTGAG 29538       TG     C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                GAGTTC  TAAGAGG CGGAGT
                                   GT     A
GAM1622  KIAA0635  3'  TGAGGCAGGAGAATTGCTTGAA 28423       TG     C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT     A
GAM1622  KIAA0643  3'  TGAGGCAGGAGAATCACTTGAG 45981           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                GAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  KIAA0752  3'  AGGCAGGAGAATCACTTGAA   67629          C
                                TTCAAGTGATTCTCC GCCT
                                |||||||||||||| ||||
                                AAGTTCACTAAGAGG CGGA
                                      A
GAM1622  KIAA0825  3'  TGAGGCAGGAGAATCACTTGAA 61691           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
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                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  KIAA0831  3'  GAGGCAGGCGGATCACTTGAG  30638          T  C
                                TTCAAGTGATTC CC GCCTC
                                |||||||||||| || |||||
                                GAGTTCACTAGG GG CGGAG
                                      C  A
GAM1622  KIAA0872  3'  GAGGCGGGTGGGTCACCTGAG  30756     A      T
                                TTCA GTGATTC CCCGCCTC
                                |||| ||||||| ||||||||
                                GAGT CACTGGG GGGCGGAG
                                  C      T
GAM1622  KIAA0872  3'  TGAGGCAGGAGAATCACTTGAA 30763            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  KIAA0884  3'  TGAGGCAGGAAAATTACTT    70759        C   C
                                AAGTGATT TCC GCCTCA
                                |||||||| ||| ||||||
                                TTCATTAA AGG CGGAGT
                                     A   A
GAM1622  KIAA0889  3'  TGAGGCAGGAGAATCACTTGAA 31791            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  KIAA0889  3'  TGAGGCAGGAGAATCGCGTGAA 31792     A        C
                                TTCA GTGATTCTCC GCCTCA
                                |||| |||||||||| ||||||
                                AAGT CGCTAAGAGG CGGAGT
                                  G         A
GAM1622  KIAA0892  3'  TGAGGCAGGAGGATCACTTGAG 71574            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                GAGTTCACTAGGAGG CGGAGT
                                      A
GAM1622  KIAA0894  3'  GAGGCAAGTGGATCACTTGAG  30333          TCCC
                                TTCAAGTGATTC    GCCTC
                                ||||||||||||    |||||
                                GAGTTCACTAGG    CGGAG
                                      TGAA
GAM1622  KIAA0894  3'  TGAGGCAGGAGAATCGCTTGAA 30343            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  KIAA0907  3'  TGAGGCAGGAGAATCACTTGAA 30884            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
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                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  KIAA0907  3'  TGAGGCAGGAGAATCGCTT   30885          C
                                AAGTGATTCTCC GCCTCA
                                |||||||||||| ||||||
                                TTCGCTAAGAGG CGGAGT
                                      A
GAM1622  KIAA0930  3'  TGAGGAAGGAGAATCACTTGAA 71077             CG
                                TTCAAGTGATTCTCC  CCTCA
                                |||||||||||||||  |||||
                                AAGTTCACTAAGAGG  GGAGT
                                      AA
GAM1622  KIAA0953  3'  TGAGGCAGGAGGACTGCTTGAG 67333       GA     C
                                TTCAAGT  TTCTCC GCCTCA
                                |||||||  |||||| ||||||
                                GAGTTCG  AGGAGG CGGAGT
                                    TC     A
GAM1622  KIAA0953  3'  TGAGGTGGGAGAATCACCTGAG 67334     A
                                TTCA GTGATTCTCCCGCCTCA
                                |||| ||||||||||||||||
                                GAGT CACTAAGAGGGTGGAGT
                                  C
GAM1622  KIAA0961  3'  TGAGACAGGAGAATCACTTGG  30412           CGC
                                TCAAGTGATTCTCC   CTCA
                                ||||||||||||||   ||||
                                GGTTCACTAAGAGG   GAGT
                                      ACA
GAM1622  KIAA0981  3'  TGAGGCAGGAGAATTGTTTGAA 62094       TG     C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTT  TAAGAGG CGGAGT
                                   GT     A
GAM1622  KIAA1001  3'  TGAGGCAGGAGAGAATCGCTTG 31016          _ _
            AA                    TTCAAGTGATTCTC CC GCCTCA
                                |||||||||||||| || ||||||
                                AAGTTCGCTAAGAG GG CGGAGT
                                      A  A
GAM1622  KIAA1032  3'  TGAGGCGGGAGAATTGTTTGAA 66734       TG
                                TTCAAG  ATTCTCCCGCCTCA
                                ||||||  ||||||||||||||
                                AAGTTT  TAAGAGGGCGGAGT
                                   GT
GAM1622  KIAA1130  3'  AGGTGGATCACTTGAG      63077          TCTC
                                TTCAAGTGAT    CCGCCT
                                ||||||||||    ||||||
                                GAGTTCACTA    GGTGGA
                                                ____
GAM1622  KIAA1130  3'  TGAGACAGGAGAATCGCTTGAA 63101             CGC
                                TTCAAGTGATTCTCC   CTCA
                                ||||||||||||||   ||||
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                                AAGTTCGCTAAGAGG   GAGT
                                      ACA
GAM1622  KIAA1160  3'  TGAGGCAGGAGAATCACTTGAA 40763            C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  KIAA1164  3'  TGAGGCAGGAGAATCGCTTGAA 70054            C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  KIAA1164  3'  TGAGGCAGGAGAATTGCTTGAA 70055       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  KIAA1191  3'  TGAGGCAGGAGAATCGCCTGAA 40337      A        C
                                TTCA GTGATTCTCC GCCTCA
                                ||||| |||||||||| ||||||
                                AAGT CGCTAAGAGG CGGAGT
                                  C         A
GAM1622  KIAA1202  3'  TGAGGCAGGAGAATTGCTTGAA 72494       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  KIAA1228  3'  TGAGGCAGGAGAATTGCTTGAA 65679       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  KIAA1244  3'  GAGACAGGAGAATCGCTCGAA  72444     A         CGC
                                TTC AGTGATTCTCC   CTC
                                ||| ||||||||||   |||
                                AAG TCGCTAAGAGG   GAG
                                  C         ACA
GAM1622  KIAA1266  5'  GAGGCGGGAAGCACCCGGAA   66697     AA_   ATTC
                                TTC   GTG    TCCCGCCTC
                                |||   |||    |||||||||
                                AAG   CAC    AGGGCGGAG
                                  GCC   GA__
GAM1622  KIAA1276  3'  TGAGGCGGGAGGATCACTTGAA 67033
                                TTCAAGTGATTCTCCCGCCTCA
                                ||||||||||||||||||||||
                                AAGTTCACTAGGAGGGCGGAGT

GAM1622  KIAA1277  3'  TGAGGCAGAAGAATCGCTTGAA 65087            CCC
                                TTCAAGTGATTCT   GCCTCA
                                ||||||||||||   ||||||
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                                AAGTTCGCTAAGA  CGGAGT
                                      AGA
GAM1622  KIAA1328  3'  TGAGGCAGGAGAATCACTTGAA 62336            C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  KIAA1348  3'  TGAGGCAGGAAAATCACTTGAA 69130          C  C
                                TTCAAGTGATT TCC GCCTCA
                                |||||||||||  ||| ||||||
                                AAGTTCACTAA AGG CGGAGT
                                      A  A
GAM1622  KIAA1377  3'  TGAGGCGGGAGGATTACTTGAG 67761
                                TTCAAGTGATTCTCCCGCCTCA
                                |||||||||||||||||||||
                                GAGTTCATTAGGAGGGCGGAGT

GAM1622  KIAA1404  3'  TGAGGCAGAAGAATCGCTT   62695        CCC
                                AAGTGATTCT  GCCTCA
                                ||||||||||  ||||||
                                TTCGCTAAGA  CGGAGT
                                      AGA
GAM1622  KIAA1456  5'  AGGCAAGAGAATTGCTTGAA  67528      TG    CC
                                TTCAAG  ATTCTC  GCCT
                                ||||||  ||||||  ||||
                                AAGTTC  TAAGAG  CGGA
                                   GT     AA
GAM1622  KIAA1456  3'  AGGCAGAAGGATCACTTGAA  67529          CCC
                                TTCAAGTGATTCT  GCCT
                                ||||||||||||  ||||
                                AAGTTCACTAGGA  CGGA
                                      AGA
GAM1622  KIAA1456  3'  TGAGGCAGGAGAATCGCTTGAA 67571            C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  KIAA1473  3'  TGAGGCAGGAGAATCACTTGAA 71214            C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  KIAA1559  3'  AGGCAGGAGAATCACTTGAA  73444            C
                                TTCAAGTGATTCTCC GCCT
                                ||||||||||||||| ||||
                                AAGTTCACTAAGAGG CGGA
                                      A
GAM1622  KIAA1559  3'  TGAGGTGGGAGGATCACTTGAA 73463
                                TTCAAGTGATTCTCCCGCCTCA
                                |||||||||||||||||||||
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                                AAGTTCACTAGGAGGGTGGAGT

GAM1622  KIAA1614  3'  TGAGGCAGGAGAATTGCTTGAA 70670      TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  KIAA1630  3'  TGAGGCAAGAGAATCGCTTGAA 38658           CC
                                TTCAAGTGATTCTC  GCCTCA
                                ||||||||||||||  ||||||
                                AAGTTCGCTAAGAG  CGGAGT
                                         AA
GAM1622  KIAA1641  3'  TGAGGTGGGAGAATCACTTGAA 81023
                                TTCAAGTGATTCTCCCGCCTCA
                                |||||||||||||||||||||
                                AAGTTCACTAAGAGGGTGGAGT

GAM1622  KIAA1649  3'  TGAGGCAGGAGAATCACTTGAA 51255           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                         A
GAM1622  KIAA1656  5'  TGAGGCAGGAGAATCACTTGAA 66388           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                         A
GAM1622  KIAA1674  3'  TGAGGCGGGAGAATGGCGTGAA 69350     A  G
                                TTCA GT ATTCTCCCGCCTCA
                                |||| || ||||||||||||||
                                AAGT CG TAAGAGGGCGGAGT
                                  G  G
GAM1622  KIAA1715  3'  TGAGGCAGGAGAATTGCTTGAA 68692      TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  KIAA1724  3'  TGAGGCAGGAGAATCACTTGAA 67624           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                         A
GAM1622  KIAA1735  3'  GAGGCAGGAAGACTGCTTGAG  89006      GA TC   C
                                TTCAAGT  T  TCC GCCTC
                                |||||||  |  ||| |||||
                                GAGTTCG  A  AGG CGGAG
                                   TC GA   A
GAM1622  KIAA1751  3'  GAGGCAGGAGGATCACTTGAG  72158           C
                                TTCAAGTGATTCTCC GCCTC
                                |||||||||||||| |||||
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                                GAGTTCACTAGGAGG CGGAG
                                      A
GAM1622  KIAA1751  3'  TGAGGCAAGAGAATTGCTTGAA 72166      TG     CC
                                TTCAAG  ATTCTC  GCCTCA
                                ||||||  ||||||  ||||||
                                AAGTTC  TAAGAG  CGGAGT
                                   GT     AA
GAM1622  KIAA1771  3'  AGACGGGAGGATTGCTTGAA  79863      TG       C
                                TTCAAG  ATTCTCCCG CT
                                ||||||  ||||||||| ||
                                AAGTTC  TAGGAGGGC GA
                                   GT       A
GAM1622  KIAA1829  3'  TGAGGCAGGAGAATCACTTGAA 62658           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  KIAA1841  3'  GAGGCGGGCAGATCACCTGAG  80852     A     CT
                                TTCA GTGATT  CCCGCCTC
                                ||||  ||||||  ||||||||
                                GAGT CACTAG  GGGCGGAG
                                  C     AC
GAM1622  KIAA1871  3'  GGGCAGGAGAATCACTTGAA   61910          C
                                TTCAAGTGATTCTCC GCCT
                                |||||||||||||| ||||
                                AAGTTCACTAAGAGG CGGG
                                      A
GAM1622  KIAA1872  3'  TGAGGCAGGAGAACTGCTTGAA 63625       GA     C
                                TTCAAGT  TTCTCC GCCTCA
                                |||||||  |||||| ||||||
                                AAGTTCG  AAGAGG CGGAGT
                                   TC     A
GAM1622  KIAA1872  3'  TGAGGCATGAGAATCACTT    63626         CC
                                AAGTGATTCTC  GCCTCA
                                ||||||||||  ||||||
                                TTCACTAAGAG  CGGAGT
                                      TA
GAM1622  KIAA1879  3'  TGAGGCGGGAGGATTGCTTGAG 73948       TG
                                TTCAAG  ATTCTCCCGCCTCA
                                ||||||  ||||||||||||||
                                GAGTTC  TAGGAGGGCGGAGT
                                   GT
GAM1622  KIAA1941  3'  TGAGGCAGGAGAATCACTTGAA 75345           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  KIAA1948  5'  TGAGGCAGGAGAATCGCTTGAA 83308           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
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                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622 KIAA1951 3' TGAGGCAGGAGGATCACTCGAG 74167     A         C
                                TTC AGTGATTCTCC GCCTCA
                                ||| |||||||||| ||||||
                                GAG TCACTAGGAGG CGGAGT
                                  C          A
GAM1622 KIAA1951 3' TGAGGCAGGAGGATCACTT    74168           C
                                AAGTGATTCTCC GCCTCA
                                |||||||||||| ||||||
                                TTCACTAGGAGG CGGAGT
                                      A
GAM1622 KIAA1958 3' TGAAGCAGGAGAATTGCTTGAA 82795       TG      C  C
                                TTCAAG  ATTCTCC GC TCA
                                ||||||  ||||||| || |||
                                AAGTTC  TAAGAGG CG AGT
                                    GT       A  A
GAM1622 KIAA1969 3' AGGCAGGATAATCACTTGAA   79470          C   C
                                TTCAAGTGATT TCC GCCT
                                |||||||||| ||| ||||
                                AAGTTCACTAA AGG CGGA
                                      T   A
GAM1622 KIAA1979 3' TGAGGCAGGGGAATCTCTTGAA 89656       T       C
                                TTCAAG GATTCTCC GCCTCA
                                |||||| |||||||| ||||||
                                AAGTTC CTAAGGGG CGGAGT
                                    T       A
GAM1622 KLHL8    3' TGAGGCAGGAGAATTGCTTGAA 63520       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                    GT      A
GAM1622 KR18     3' TGAGGCAGGAGAATTGCTTGAG 53899       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                GAGTTC  TAAGAGG CGGAGT
                                    GT      A
GAM1622 KR18     3' TGAGGCAGGAGAGTGCTTGAA  53900       G       C
                                TTCAAGT ATTCTCC GCCTCA
                                ||||||| ||||||| ||||||
                                AAGTTCG TGAGAGG CGGAGT
                                    _       A
GAM1622 LANO     3' TGAGGCAAGAGAATTGCCTGAA 47978      A TG      CC
                                TTCA G  ATTCTC  GCCTCA
                                |||| |  ||||||  ||||||
                                AAGT C  TAAGAG  CGGAGT
                                  C GT      AA
GAM1622 LAP1B    3' TGAGGCAGGAGAATTGCTTGAA 65197       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
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                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  LENEP    3'  GTTTGAGAATCACTGAA     38479      A       CC
                                TTCA GTGATTCTC  GC
                                |||| |||||||||  ||
                                AAGT CACTAAGAG  TG
                                  _       TT
GAM1622  LIAS     3'  AGGCAGGAGAATCACTTGAA   71162            C
                                TTCAAGTGATTCTCC GCCT
                                |||||||||||||| ||||
                                AAGTTCACTAAGAGG CGGA
                                          A
GAM1622  LIM      3'  TGAGGCACGAGAATCACTTGAA 22336            CC
                                TTCAAGTGATTCTC  GCCTCA
                                ||||||||||||  ||||||
                                AAGTTCACTAAGAG  CGGAGT
                                          CA
GAM1622  LRRFIP1  3'  TGAGGCAGGAGAATCGCTTGAA 17618             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                          A
GAM1622  LSR68    3'  GAGGCGGGTGGACCACCTGAG  38557     A  A  T
                                TTCA GTG TTC CCCGCCTC
                                |||| ||| ||| ||||||||
                                GAGT CAC AGG GGGCGGAG
                                  C  C  T
GAM1622  LSR68    3'  TGAGGCAGGAGAATTCTT    38560     T      C
                                AAG GATTCTCC GCCTCA
                                ||| ||||||| ||||||
                                TTC TTAAGAGG CGGAGT
                                  _      A
GAM1622  MAWBP    3'  AGGCAGGAGGATCACTTGAA  42375            C
                                TTCAAGTGATTCTCC GCCT
                                |||||||||||||| ||||
                                AAGTTCACTAGGAGG CGGA
                                          A
GAM1622  MAWBP    3'  TGAGGCATGGAGAATCGCTTGA 42390            C_
            A                    TTCAAGTGATTCTCC  GCCTCA
                                ||||||||||||||  ||||||
                                AAGTTCGCTAAGAGG  CGGAGT
                                          TA
GAM1622  MEGF10   3'  TGAAAGTGGGAATCACTGAA  51610     A    TC    C_
                                TTCA GTGAT  TCCCGC  TCA
                                |||| |||||  ||||||  |||
                                AAGT CACTA  AGGGTG  AGT
                                  _    __     AA
GAM1622  MGC10765 3'  TGAGGCAAGAGAATCACTTGAA 44569            CC
                                TTCAAGTGATTCTC  GCCTCA
                                ||||||||||||||  ||||||
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                                AAGTTCACTAAGAG  CGGAGT
                                      AA
GAM1622  MGC10814  3'  TGAGGCAGGAGAATTGCTTGAA 52028       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  MGC10814  5'  TGAGGTGGGAGAATCGCTTGAA 52029
                                TTCAAGTGATTCTCCCGCCTCA
                                ||||||||||||||||||||||
                                AAGTTCGCTAAGAGGGTGGAGT

GAM1622  MGC10999  3'  AGGCAGGAGGATTGCTTGAG   51188       TG      C
                                TTCAAG  ATTCTCC GCCT
                                ||||||  ||||||| ||||
                                GAGTTC  TAGGAGG CGGA
                                   GT      A
GAM1622  MGC10999  3'  TGAGGCAAGAGAATCGCTTGAA 51201            CC
                                TTCAAGTGATTCTC  GCCTCA
                                ||||||||||||||  ||||||
                                AAGTTCGCTAAGAG  CGGAGT
                                      AA
GAM1622  MGC11287  5'  GAGGCAGACGGATCACTTGAG  49617           _ CC
                                TTCAAGTGATTC TC  GCCTC
                                ||||||||||||| ||  |||||
                                GAGTTCACTAGG AG  CGGAG
                                      C  A_
GAM1622  MGC13017  3'  TGAAGCAGAAGAACTGCTTGAA 55581        GA   CCC  C
                                TTCAAGT  TTCT   GC TCA
                                |||||||  ||||   || |||
                                AAGTTCG  AAGA   CG AGT
                                    TC    AGA  A
GAM1622  MGC13053  3'  TGAGGCAGGGGAATCACTTGAA 52116             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGGGG CGGAGT
                                      A
GAM1622  MGC13198  5'  GCAGGAGAATTGCTTGAA    52070       TG      C
                                TTCAAG  ATTCTCC GC
                                ||||||  ||||||| ||
                                AAGTTC  TAAGAGG CG
                                   GT      A
GAM1622  MGC14126  3'  TGAGGCAGGAGATTCGCTTGAA 52944         T    C
                                TTCAAGTGA TCTCC GCCTCA
                                |||||||||  ||||| ||||||
                                AAGTTCGCT AGAGG CGGAGT
                                      T    A
GAM1622  MGC15397  3'  TGAGGCAGGAGAATTGCTTGAA 55557       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
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                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  MGC15631  3'  TGAGGCAAGAGGATCACTTGAG 52237            CC
                                TTCAAGTGATTCTC  GCCTCA
                                |||||||||||||  ||||||
                                GAGTTCACTAGGAG  CGGAGT
                                      AA
GAM1622  MGC16037  3'  TGAGGCAGGAGAATCGCTTGAA 52895             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  MGC16142  3'  TGAGGCATGAGAATTACTTGAA 52268            CC
                                TTCAAGTGATTCTC  GCCTCA
                                |||||||||||||  ||||||
                                AAGTTCATTAAGAG  CGGAGT
                                      TA
GAM1622  MGC16385  3'  GCAGGAGAATTGCTTGAA    59536       TG     C
                                TTCAAG  ATTCTCC GC
                                ||||||  ||||||| ||
                                AAGTTC  TAAGAGG CG
                                   GT      A
GAM1622  MGC20235  3'  TGAGGCAGCAGAATCACTTGAA 59564           CCC
                                TTCAAGTGATTCT   GCCTCA
                                ||||||||||||   ||||||
                                AAGTTCACTAAGA   CGGAGT
                                      CGA
GAM1622  MGC22805  3'  TGAGGTGGGAGGATCACTTGAA 58700
                                TTCAAGTGATTCTCCCGCCTCA
                                ||||||||||||||||||||||
                                AAGTTCACTAGGAGGGTGGAGT

GAM1622  MGC23244  3'  GAGGCGGGTGGAACACTTGAG  58833        A   T
                                TTCAAGTG TTC CCCGCCTC
                                |||||||| ||| ||||||||
                                GAGTTCAC AGG GGGCGGAG
                                     A   T
GAM1622  MGC2562   3'  AGGCAAGCAAATCACTTGAG   51418          CTCCC
                                TTCAAGTGATT    GCCT
                                ||||||||||    ||||
                                GAGTTCACTAA    CGGA
                                      ACGAA
GAM1622  MGC2562   3'  GAGGCGGGTGGATCACTTGAG  51442           T
                                TTCAAGTGATTC CCCGCCTC
                                |||||||||||| ||||||||
                                GAGTTCACTAGG GGGCGGAG
                                      T
GAM1622  MGC2562   3'  TGAGGCACGAGAATCACTTGAA 51453            CC
                                TTCAAGTGATTCTC  GCCTCA
                                ||||||||||||||  ||||||
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                                AAGTTCACTAAGAG  CGGAGT
                                      CA
GAM1622  MGC2562   3'  TGAGGCGGGAGAATAGCATGAA 51454      A  G
                                TTCA GT ATTCTCCCGCCTCA
                                |||| || ||||||||||||||
                                AAGT CG TAAGAGGGCGGAGT
                                  A  A
GAM1622  MGC2663   3'  TGAGGCAAGTGAATCACTTGAA 44339           TCCC
                                TTCAAGTGATTC    GCCTCA
                                ||||||||||||    ||||||
                                AAGTTCACTAAG    CGGAGT
                                      TGAA
GAM1622  MGC2731   3'  TGAGGCAGGAGAATCTCTTGAA 44166       T       C
                                TTCAAG GATTCTCC GCCTCA
                                |||||| |||||||| ||||||
                                AAGTTC CTAAGAGG CGGAGT
                                   T       A
GAM1622  MGC29762  3'  TGAGGAAGGAGAATCGCTTGAA 59150            CG
                                TTCAAGTGATTCTCC  CCTCA
                                ||||||||||||||  |||||
                                AAGTTCGCTAAGAGG  GGAGT
                                      AA
GAM1622  MGC29891  3'  TGAGGCAGGAGAATTGCTTGAA 58876       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  MGC29891  3'  TGAGGCAGGAGAATCGCTTGAA 58875            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  MGC29937  3'  TGAGGCAGGAGAATCACTTGAA 58735            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  MGC3169   3'  GAGGCGGGCAGATCACCTGAG  44186      A     CT
                                TTCA GTGATT  CCCGCCTC
                                |||| ||||||  ||||||||
                                GAGT CACTAG  GGGCGGAG
                                  C     AC
GAM1622  MGC3169   3'  TGAGGCAGGAGAATCACATGAA 44190      A       C
                                TTCA GTGATTCTCC GCCTCA
                                |||| |||||||||| ||||||
                                AAGT CACTAAGAGG CGGAGT
                                  A        A
GAM1622  MGC4248   3'  TGAGGCAGGAGAATCACTTGAA 51320            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
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                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  MGC4400   3'  AGGCAGGAAGATCACTTGAG   52036          TC   C
                                TTCAAGTGAT  TCC GCCT
                                ||||||||||  ||| ||||
                                GAGTTCACTA  AGG CGGA
                                    GA   A
GAM1622  MGC4562   3'  TGAAGCAGGAGAATTGCCTGAA 56745      A TG      C  C
                                TTCA G  ATTCTCC GC TCA
                                |||| |  ||||||| || |||
                                AAGT C  TAAGAGG CG AGT
                                  C GT      A  A
GAM1622  MGC4771   3'  TGAGACAGGAGAATCGCTTGAA 52007             CGC
                                TTCAAGTGATTCTCC   CTCA
                                ||||||||||||||   ||||
                                AAGTTCGCTAAGAGG   GAGT
                                      ACA
GAM1622  MGC4840   3'  GAGGCGAGTGGATCACTT    72023         TCC
                                AAGTGATTC   CGCCTC
                                |||||||||   ||||||
                                TTCACTAGG   GCGGAG
                                    TGA
GAM1622  MKRN4     3'  TGAGGCGGGAGAATGGTGTGAA 48477      AG G
                                TTCA  T ATTCTCCCGCCTCA
                                ||||  | ||||||||||||||
                                AAGT  G TAAGAGGGCGGAGT
                                  GT G
GAM1622  MOST2     5'  AGGCAGGCAGATCACTTGAG   40050          CT  C
                                TTCAAGTGATT  CC GCCT
                                ||||||||||  || ||||
                                GAGTTCACTAG  GG CGGA
                                    AC  A
GAM1622  MOST2     5'  TGAGGCAGGAGAATCACTTG   40073           C
                                CAAGTGATTCTCC GCCTCA
                                |||||||||||| ||||||
                                GTTCACTAAGAGG CGGAGT
                                      A
GAM1622  MRP63     3'  AGGCGGGCGGATCACTTGAG   44041           T
                                TTCAAGTGATTC CCCGCCT
                                |||||||||||| |||||||
                                GAGTTCACTAGG GGGCGGA
                                      C
GAM1622  MRPL48    5'  GAGGCGGGCGGATCACCTGAG  32660      A      T
                                TTCA GTGATTC CCCGCCTC
                                |||| ||||||| ||||||||
                                GAGT CACTAGG GGGCGGAG
                                  C      C
GAM1622  MRPL56    3'  TGAGGCAGGAGAATCGCTTGAA 52758             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
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                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  MRPS10   3'  TGAGGCAGGAGAATCGCGTGAA 36823      A        C
                                TTCA GTGATTCTCC GCCTCA
                                |||| |||||||||| ||||||
                                AAGT CGCTAAGAGG CGGAGT
                                  G        A
GAM1622  My015    3'  TGAACAGGAGAATCGCTTGAA  67236            CGCC
                                TTCAAGTGATTCTCC   TCA
                                ||||||||||||||   |||
                                AAGTTCGCTAAGAGG   AGT
                                      ACA_
GAM1622  MYO5C    3'  CGAGATGAATCATTTGAA    38717          _  C
                                TTCAAGTGATTC TC CG
                                |||||||||||| || ||
                                AAGTTTACTAAG AG GC
                                       T  A
GAM1622  NMNAT    3'  TGAGGCAGGAGAATCACTTGA  43296           C
                                TCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  NMNAT    3'  TGAGGCAGGAGAATCGCTTGAA 43297           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  NMNAT    3'  TGAGGCAGGAGAATCGCTTGAA 43298           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  NMT2     3'  TGAGGCAGGAGAATCGCTTGAA 17861           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  NPTXR    3'  TGAGACAGGCAGATCACTTGAG 55220        T  C  GC_
                                TTCAAGTGAT CT CC   CTCA
                                |||||||||| || ||   ||||
                                GAGTTCACTA GA GG   GAGT
                                      _  C  ACA
GAM1622  NPTXR    3'  TGAGACAGGCAGATCACTTGAG 27447        T  C  GC_
                                TTCAAGTGAT CT CC   CTCA
                                |||||||||| || ||   ||||
                                GAGTTCACTA GA GG   GAGT
                                      _  C  ACA
GAM1622  Nup43    3'  TGAGGCAGGAGAATTGCT    45359    TG     C
                                AG  ATTCTCC GCCTCA
                                ||  ||||||| ||||||
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                                TC  TAAGAGG CGGAGT
                                 GT      A
GAM1622  ORC6L    3'  TGAGACAGGAGCATCACTTGAA 27496         T   CGC
                                TTCAAGTGAT CTCC   CTCA
                                |||||||||| ||||   ||||
                                AAGTTCACTA GAGG   GAGT
                                      C    ACA
GAM1622  PAFAH2   3'  TGAAGCAGAAGAATCACTTGAA 6510           CCC  C
                                TTCAAGTGATTCT   GC TCA
                                ||||||||||||   || |||
                                AAGTTCACTAAGA   CG AGT
                                       AGA  A
GAM1622  PB1      3'  TGAGGCAGGAGAATCGCTTGAA 37583           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                       A
GAM1622  PIWIL2   3'  AGGCAGGAGAATCGCTTGAA   36538          C
                                TTCAAGTGATTCTCC GCCT
                                |||||||||||||| ||||
                                AAGTTCGCTAAGAGG CGGA
                                       A
GAM1622  PNPASE   3'  TGAGGCAGAAGAATCACTT   71441         CCC
                                AAGTGATTCT   GCCTCA
                                |||||||||   ||||||
                                TTCACTAAGA   CGGAGT
                                      AGA
GAM1622  POLM     3'  GAGGCAGAAGCACTGAG     92729      A  A   CCC
                                TTCA GTG TTCT   GCCTC
                                |||| ||| ||||   |||||
                                GAGT CAC AAGA   CGGAG
                                  _  G   ___
GAM1622  POLYDOM  3'  TGAGGCAGGAGAATCGCTTGAA 44694           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                       A
GAM1622  PP591    5'  TGAGGCAGGAGGATCACTTGAG 48151           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                GAGTTCACTAGGAGG CGGAGT
                                       A
GAM1622  PPP1R3B  3'  TGAGGCAGGAGAATCACTTGAA 45146           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                       A
GAM1622  PRIC285  3'  GAGGCGGGCAGATCACCTGAG  62115      A    CT
                                TTCA GTGATT  CCCGCCTC
                                |||| ||||||  ||||||||
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                                GAGT CACTAG  GGGCGGAG
                                  C     AC
GAM1622  PRIC285   3'  TGAGGCAGGAGAATCGCTTGA  62121          C
                                TCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AGTTCGCTAAGAGG CGGAGT
                                       A
GAM1622  PRO0255   3'  GAGGCGGGCAGATCACCTGAG  26969     A    CT
                                TTCA GTGATT  CCCGCCTC
                                |||| ||||||  ||||||||
                                GAGT CACTAG  GGGCGGAG
                                  C     AC
GAM1622  PRO0255   3'  TGAGGCAGGAGAATCGCTTGAG 26972          C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                GAGTTCGCTAAGAGG CGGAGT
                                       A
GAM1622  PRO0478   5'  TGAAGCAGGAGAATCGCTTGAG 27041          C  C
                                TTCAAGTGATTCTCC GC TCA
                                |||||||||||||| || |||
                                GAGTTCGCTAAGAGG CG AGT
                                       A  A
GAM1622  PRO0618   3'  TGAGGCAGGAGAATCGCTTGAA 27056          C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                       A
GAM1622  PRO1777   3'  TGAGGCAGGAGGCTCACTTGAG 38376        TT   C
                                TTCAAGTGA  CTCC GCCTCA
                                |||||||||  |||| ||||||
                                GAGTTCACT  GAGG CGGAGT
                                     CG   A
GAM1622  PRO2015   3'  TGAGGCAGGAGAATCGCTTGAA 38167          C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                       A
GAM1622  PRO2037   3'  AGGCAAGAGGATTGCTTGAG   38394      TG    CC
                                TTCAAG  ATTCTC  GCCT
                                ||||||  ||||||  ||||
                                GAGTTC  TAGGAG  CGGA
                                   GT     AA
GAM1622  PRO2730   3'  TGAGGCAGGAGAATTGCTTGAA 48189       TG     C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT     A
GAM1622  PRO2859   3'  TGAAGCAGGAGAATCACTTGAA 38216          C  C
                                TTCAAGTGATTCTCC GC TCA
                                |||||||||||||| || |||
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                                AAGTTCACTAAGAGG CG AGT
                                      A  A
GAM1622  PSR      3'  AGGCAGGAGAATCACTTGAA   65774            C
                                TTCAAGTGATTCTCC GCCT
                                |||||||||||||| ||||
                                AAGTTCACTAAGAGG CGGA
                                      A
GAM1622  PTRF     3'  TGAGGCGGGAGGATCGCCAGA  64248    AA
                                TC  GTGATTCTCCCGCCTCA
                                ||  ||||||||||||||||
                                AG  CGCTAGGAGGGCGGAGT
                                 AC
GAM1622  PXMP4    3'  TGAGGCAGGTGGATCACTTGAG 24336          T  C
                                TTCAAGTGATTC CC GCCTCA
                                |||||||||||| || ||||||
                                GAGTTCACTAGG GG CGGAGT
                                      T  A
GAM1622  RAB4B    5'  TGAGGCAGGAGAATTGCTTGAA 32906       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  Rabip4R  3'  TGAGGCAGGAGAATCGCTTGAA 36280            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  RAD51    3'  TGAGGTGGGAGAATCACTT   12749
                                AAGTGATTCTCCCGCCTCA
                                ||||||||||||||||||
                                TTCACTAAGAGGGTGGAGT

GAM1622  RAD51    3'  TGAGGTGGGAGAATCACTT   56834
                                AAGTGATTCTCCCGCCTCA
                                ||||||||||||||||||
                                TTCACTAAGAGGGTGGAGT

GAM1622  RBPMS    3'  TGAGGCAGGCGGATCACTTGA  23439          T  C
                                TCAAGTGATTC CC GCCTCA
                                |||||||||| || ||||||
                                AGTTCACTAGG GG CGGAGT
                                      C  A
GAM1622  RES4-25  3'  TGAAGCAGGAGGACTGCTTGAG 65277       GA     C  C
                                TTCAAGT  TTCTCC GC TCA
                                |||||||  |||||| || |||
                                GAGTTCG  AGGAGG CG AGT
                                   TC      A  A
GAM1622  RHOBTB3  3'  TGAGGCAGGAAAATCGCTTGAA 30433          C   C
                                TTCAAGTGATT TCC GCCTCA
                                |||||||||| ||| ||||||
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                                AAGTTCGCTAA AGG CGGAGT
                                      A   A
GAM1622  RNO2     5'  TGAGGCGGGAGAATCGCTTGAA 53943
                                TTCAAGTGATTCTCCCGCCTCA
                                |||||||||||||||||||||
                                AAGTTCGCTAAGAGGGCGGAGT

GAM1622  RoXaN    3'  AGGCGGGTGGATCATTTGAA   47273           T
                                TTCAAGTGATTC CCCGCCT
                                |||||||||||| |||||||
                                AAGTTTACTAGG GGGCGGA
                                      T
GAM1622  RoXaN    3'  GAGATTAGAGAATCACTTGAA  47291            CCGC
                                TTCAAGTGATTCTC    CTC
                                ||||||||||||||    |||
                                AAGTTCACTAAGAG    GAG
                                      ATTA
GAM1622  RoXaN    3'  TGAGGCAGGAGAATCACTTGAA 47305             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  RRP4     3'  TGAGGTGGGAGAATCACTTGAA 27364
                                TTCAAGTGATTCTCCCGCCTCA
                                |||||||||||||||||||||
                                AAGTTCACTAAGAGGGTGGAGT

GAM1622  SAMHD1   3'  TGAGGCAGGAGAATCGCTTGAA 61992             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  SAMHD1   3'  TGAGGCAGGAGGATTGCTCGAA 61993     A  TG      C
                                TTC AG  ATTCTCC GCCTCA
                                ||| ||  ||||||| ||||||
                                AAG TC  TAGGAGG CGGAGT
                                  C  GT      A
GAM1622  SC65     3'  TGAGGCAGGAGAATCGCCTGAA 22305      A        C
                                TTCA GTGATTCTCC GCCTCA
                                |||| |||||||||| ||||||
                                AAGT CGCTAAGAGG CGGAGT
                                   C        A
GAM1622  SC65     3'  TGAGGCAGGAGAATCGCTTGAA 22306             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  SCIN     3'  TGAGACAGGAAAATTGCTTGAA 53606       TG   C   CGC
                                TTCAAG  ATT TCC   CTCA
                                ||||||  ||| |||   ||||
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                                AAGTTC  TAA AGG   GAGT
                                   GT   A   ACA
GAM1622  SCN12A   3'  TGAGGCAGGAGAATCGCTT   27084          C
                                AAGTGATTCTCC GCCTCA
                                |||||||||||| ||||||
                                TTCGCTAAGAGG CGGAGT
                                       A
GAM1622  SCYA5    3'  AGGCAGGAAAATTGTTTGAA   12957       TG   C   C
                                TTCAAG  ATT TCC GCCT
                                ||||||  ||| ||| ||||
                                AAGTTT  TAA AGG CGGA
                                   GT   A   A
GAM1622  SDS3     3'  TGAGGCAGGACTTCCCTCGCTT 69753         TTC___   C
            GAA                    TTCAAGTGA     TCC GCCTCA
                                |||||||||      ||| ||||||
                                AAGTTCGCT     AGG CGGAGT
                                      CCCTTC   A
GAM1622  SGKL     3'  AGGCAGGAGAATCGCTTGAA   26051            C
                                TTCAAGTGATTCTCC GCCT
                                |||||||||||||| ||||
                                AAGTTCGCTAAGAGG CGGA
                                       A
GAM1622  SGKL     3'  AGGCAGGAGGATCACTTGAG   26052            C
                                TTCAAGTGATTCTCC GCCT
                                |||||||||||||| ||||
                                GAGTTCACTAGGAGG CGGA
                                       A
GAM1622  SGKL     3'  TGAGGCGGGCAGATCACCTGAG 26063      A     CT
                                TTCA GTGATT  CCCGCCTCA
                                |||| ||||||  |||||||||
                                GAGT CACTAG  GGGCGGAGT
                                  C     AC
GAM1622  SIAT4A   3'  GAGGCGGGAGGATCACTTGAG  13138
                                TTCAAGTGATTCTCCCGCCTC
                                |||||||||||||||||||||
                                GAGTTCACTAGGAGGGCGGAG

GAM1622  SLC7A11  3'  TGAGGCAGGAGAATTGCTTGAA 27534       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  SMA3     3'  TGAGGCAGGCGGATCACTTGAG 23264          T  C
                                TTCAAGTGATTC CC GCCTCA
                                |||||||||||| || ||||||
                                GAGTTCACTAGG GG CGGAGT
                                       C  A
GAM1622  SMCR5    3'  AGGCAGGAGGATTGCTTGAG   59243       TG      C
                                TTCAAG  ATTCTCC GCCT
                                ||||||  ||||||| ||||
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                                  GAGTTC  TAGGAGG CGGA
                                     GT      A
GAM1622  SPRY4    3'  TGAGGCAGAAGAATCACTTGAA 49035           CCC
                                  TTCAAGTGATTCT   GCCTCA
                                  ||||||||||||   ||||||
                                  AAGTTCACTAAGA   CGGAGT
                                        AGA
GAM1622  SPTLC2   3'  TGAGGCAGGAGAATCGCTTGAA 18005            C
                                  TTCAAGTGATTCTCC GCCTCA
                                  |||||||||||||| ||||||
                                  AAGTTCGCTAAGAGG CGGAGT
                                        A
GAM1622  SPTLC2   3'  TGAGGCAGGTGGCTCACTTGAG 18006         TT T  C
                                  TTCAAGTGA  C CC GCCTCA
                                  |||||||||  | || ||||||
                                  GAGTTCACT  G GG CGGAGT
                                     CG T  A
GAM1622  SUN1     3'  TGAGGCGGGTGGATCACTTGAG 47925           T
                                  TTCAAGTGATTC CCCGCCTCA
                                  |||||||||||| |||||||||
                                  GAGTTCACTAGG GGGCGGAGT
                                        T
GAM1622  TACTILE  3'  TGAGGCAGGAGAAGGGTGGGAA 20596     AAGTGA     C
                                  TTC     TTCTCC GCCTCA
                                  |||     |||||| ||||||
                                  AAG     AAGAGG CGGAGT
                                    GGTGGG     A
GAM1622  TADA3L   3'  TGAGGCAGGAGAATCAGTTGAA 56816      G        C
                                  TTCAA TGATTCTCC GCCTCA
                                  ||||| |||||||||| ||||||
                                  AAGTT ACTAAGAGG CGGAGT
                                     G        A
GAM1622  TDP1     5'  GAGGCGGCTGAATCACTTGAG  37602          TC
                                  TTCAAGTGATTC  CCGCCTC
                                  ||||||||||||  |||||||
                                  GAGTTCACTAAG  GGCGGAG
                                        TC
GAM1622  THEA     3'  TGAGGCAGGAGAATTGGTTGAA 66900      G        C
                                  TTCAA TGATTCTCC GCCTCA
                                  ||||| |||||||||| ||||||
                                  AAGTT GTTAAGAGG CGGAGT
                                     G        A
GAM1622  TIP47    3'  TGAGGCGGGCGGAACACCTGAG 20609      A   A   T
                                  TTCA GTG TTC CCCGCCTCA
                                  |||| ||| ||| |||||||||
                                  GAGT CAC AGG GGGCGGAGT
                                    C   A   C
GAM1622  TMG4     3'  TGAAGCAGGAGAATTGCTCGAA 44219     A  TG      C  C
                                  TTC AG  ATTCTCC GC TCA
                                  ||| ||  ||||||| || |||
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                                AAG TC  TAAGAGG CG AGT
                                  C GT      A A
GAM1622  TRIAD3   3'  TGAGGCAGGAGAATCACTTGAA 96142            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                          A
GAM1622  TRIM38   3'  AGGCAGGAGAATTGCTTGAG  22050      TG     C
                                TTCAAG  ATTCTCC GCCT
                                ||||||  ||||||| ||||
                                GAGTTC  TAAGAGG CGGA
                                   GT      A
GAM1622  TRIM38   3'  TGAGGCAGGTGGATCACTTGAG 22057          T  C
                                TTCAAGTGATTC CC GCCTCA
                                |||||||||||| || ||||||
                                GAGTTCACTAGG GG CGGAGT
                                         T  A
GAM1622  TSGA2    3'  TGAGGCAGGAGGATTGCTTGAG 55957      TG     C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                GAGTTC  TAGGAGG CGGAGT
                                   GT      A
GAM1622  VIT1     5'  TGAAGCAGGAGAATTGCTTGAA 38608      TG     C  C
                                TTCAAG  ATTCTCC GC TCA
                                ||||||  ||||||| || |||
                                AAGTTC  TAAGAGG CG AGT
                                   GT      A  A
GAM1622  VPS4B    3'  TGAGGCGGGAGAATCACTTGAA 18027
                                TTCAAGTGATTCTCCCGCCTCA
                                ||||||||||||||||||||||
                                AAGTTCACTAAGAGGGCGGAGT

GAM1622  WBSCR21  3'  AGGCGGGAGGATGACTTGAG  49293      G
                                TTCAAGT ATTCTCCCGCCT
                                ||||||| ||||||||||||
                                GAGTTCA TAGGAGGGCGGA
                                    G
GAM1622  WBSCR21  3'  TGAGGCAGGAGAATCACTTGAA 49308            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                          A
GAM1622  WBSCR23  5'  TGAGACAGGAGGATCACTTGAG 47448           CGC
                                TTCAAGTGATTCTCC   CTCA
                                ||||||||||||||   ||||
                                GAGTTCACTAGGAGG   GAGT
                                          ACA
GAM1622  WBSCR23  3'  TGAGGCAGAAGAATCGCTTGAA 47449          CCC
                                TTCAAGTGATTCT   GCCTCA
                                ||||||||||||   ||||||
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                                AAGTTCGCTAAGA   CGGAGT
                                      AGA
GAM1622  WBSCR23   3'  TGAGGCAGGAGGATCACTTGAG 47450             C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||| ||||||
                                GAGTTCACTAGGAGG CGGAGT
                                      A
GAM1622  WBSCR23   3'  TGAGGGAGGAGAATCCCTTGAA 47451       T       CG
                                TTCAAG GATTCTCC  CCTCA
                                |||||| ||||||||  |||||
                                AAGTTC CTAAGAGG  GGAGT
                                   C       AG
GAM1622  WSB1      3'  TGAGGCAGGAGAATTGCTTGAA 56995       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  WSB1      3'  TGAGGCGGGCAAATCACCTGAG 56997      A     CT
                                TTCA GTGATT  CCCGCCTCA
                                |||| ||||||  |||||||||
                                GAGT CACTAA  GGGCGGAGT
                                  C     AC
GAM1622  WSB1      3'  TGAGGCAGGAGAATTGCTTGAA 56983       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  WSB1      3'  TGAGGCGGGCAAATCACCTGAG 56985      A     CT
                                TTCA GTGATT  CCCGCCTCA
                                |||| ||||||  |||||||||
                                GAGT CACTAA  GGGCGGAGT
                                  C     AC
GAM1622  YME1L1    3'  AGGCAGGAGAATTGCTTGAG  27316       TG      C
                                TTCAAG  ATTCTCC GCCT
                                ||||||  ||||||| ||||
                                GAGTTC  TAAGAGG CGGA
                                   GT      A
GAM1622  YME1L1    3'  AGGCAGGAGAATTGCTTGAG  58422       TG      C
                                TTCAAG  ATTCTCC GCCT
                                ||||||  ||||||| ||||
                                GAGTTC  TAAGAGG CGGA
                                   GT      A
GAM1622  ZAK       3'  AGGCAGGAGGATTGCTTGAG  56938       TG      C
                                TTCAAG  ATTCTCC GCCT
                                ||||||  ||||||| ||||
                                GAGTTC  TAGGAGG CGGA
                                   GT      A
GAM1622  ZAK       3'  TGAGGCAGGAGAATCACTTGAA 56949             C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||| ||||||
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                                AAGTTCACTAAGAGG CGGAGT
                                       A
GAM1622 ZF      5' TGAGGCGGGAGGCGACTCGGA 41371    A  GAT
                                TTC AGT  TCTCCCGCCTCA
                                ||| |||  ||||||||||||
                                AGG TCA  GGAGGGCGGAGT
                                  C  GC_
GAM1622 ZFP106  3' TGAGACAGGAGAATCACTTGAA 42744           CGC
                                TTCAAGTGATTCTCC  CTCA
                                ||||||||||||||  ||||
                                AAGTTCACTAAGAGG  GAGT
                                       ACA
GAM1622 ZFP106  3' TGAGGCAGGAGAATCGCTTGAA 42745           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                       A
GAM1622 ZIM3    3' TGAGGCAGGAGAATTGCTTGAA 54640      TG    C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT     A
GAM1622 ZNF197  3' TGAGACAGGAGAGTCGCTTGAA 23761           CGC
                                TTCAAGTGATTCTCC  CTCA
                                ||||||||||||||  ||||
                                AAGTTCGCTGAGAGG  GAGT
                                       ACA
GAM1622 ZNF271  3' TGAGGCATGAGAATCACTTGAA 96970           CC
                                TTCAAGTGATTCTC  GCCTCA
                                ||||||||||||||  ||||||
                                AAGTTCACTAAGAG  CGGAGT
                                       TA
GAM1622 ZNF297B 5' AGGCAGGAGAATCGCTCGAA  26641    A       C
                                TTC AGTGATTCTCC GCCT
                                ||| |||||||||| ||||
                                AAG TCGCTAAGAGG CGGA
                                  C         A
GAM1622 ZNF297B 3' GAGGCAGGAGAATCACTTGAA  26657           C
                                TTCAAGTGATTCTCC GCCTC
                                |||||||||||||| |||||
                                AAGTTCACTAAGAGG CGGAG
                                       A
GAM1622 ZNF297B 5' TGAGGCTGGTGGATCACTTGAA 26677          T  C
                                TTCAAGTGATTC CC GCCTCA
                                |||||||||||| || ||||||
                                AAGTTCACTAGG GG CGGAGT
                                      T  T
GAM1622 ZNF333  3' TGAGGCAGGAGAATTCTTTGAA 51596      T      C
                                TTCAAG GATTCTCC GCCTCA
                                |||||| |||||||| ||||||
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                                  AAGTTT TTAAGAGG CGGAGT
                                     C       A
GAM1622  ZNF339    3'  TGAGGCAAGAGAATCGCTTGAA 41400            CC
                                  TTCAAGTGATTCTC  GCCTCA
                                  ||||||||||||||  ||||||
                                  AAGTTCGCTAAGAG  CGGAGT
                                        AA
GAM1622  ZNF33A    3'  TGAGGCAGAAGAATCACTTGAA 93001            CCC
                                  TTCAAGTGATTCT   GCCTCA
                                  ||||||||||||   ||||||
                                  AAGTTCACTAAGA   CGGAGT
                                        AGA
GAM1622  ZNF347    3'  TGAGGCAGGAGAATCACTTGAA 51831             C
                                  TTCAAGTGATTCTCC GCCTCA
                                  ||||||||||||||| ||||||
                                  AAGTTCACTAAGAGG CGGAGT
                                        A
GAM1622  LOC114987 3'  TGAGGCGGGAGAATCGCTTGAA 59801
                                  TTCAAGTGATTCTCCCGCCTCA
                                  |||||||||||||||||||||
                                  AAGTTCGCTAAGAGGGCGGAGT

GAM1622  LOC115129 3'  TGAGGCAGGAGAATCACTTGAA 73630              C
                                  TTCAAGTGATTCTCC GCCTCA
                                  ||||||||||||||| ||||||
                                  AAGTTCACTAAGAGG CGGAGT
                                        A
GAM1622  LOC115129 5'  TGAGGCAGGAGAATCATCTGAA 73631      AG       C
                                  TTCA  TGATTCTCC GCCTCA
                                  ||||  ||||||||| ||||||
                                  AAGT  ACTAAGAGG CGGAGT
                                     CT       A
GAM1622  LOC115129 5'  TGAGGCAGGAGATTTGCTTGAA 73632       TG T    C
                                  TTCAAG  A TCTCC GCCTCA
                                  ||||||  | ||||| ||||||
                                  AAGTTC  T AGAGG CGGAGT
                                     GT T    A
GAM1622  LOC115273 3'  AGGCAGGAGAATTGCTTGAA  73745       TG      C
                                  TTCAAG  ATTCTCC GCCT
                                  ||||||  ||||||| ||||
                                  AAGTTC  TAAGAGG CGGA
                                     GT      A
GAM1622  LOC115761 3'  TGAGGCAGGAGAATCGCTTGAG 93399              C
                                  TTCAAGTGATTCTCC GCCTCA
                                  ||||||||||||||| ||||||
                                  GAGTTCGCTAAGAGG CGGAGT
                                        A
GAM1622  LOC115861 3'  AGGCGGGAGGATCGCTTGAG  57416
                                  TTCAAGTGATTCTCCCGCCT
                                  ||||||||||||||||||||
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                                GAGTTCGCTAGGAGGGCGGA

GAM1622  LOC116143 3'  TGAGGCAGGAGAATCACTTGAA 74195            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                          A
GAM1622  LOC116228 3'  TGAGGCAGGAGAATCACTTGAA 74232            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                          A
GAM1622  LOC119504 5'  TGAAGCAGGAGAATCGCTT   74450          C  C
                                AAGTGATTCTCC GC TCA
                                |||||||||||| || |||
                                TTCGCTAAGAGG CG AGT
                                          A  A
GAM1622  LOC122704 3'  TGAGGCAGGAGAATCGCTT   74613          C
                                AAGTGATTCTCC GCCTCA
                                |||||||||||| ||||||
                                TTCGCTAAGAGG CGGAGT
                                          A
GAM1622  LOC126282 3'  GAGGCAGGAAGATTGCTTGAA  74958       TG  TC   C
                                TTCAAG  AT  TCC GCCTC
                                ||||||  ||  ||| |||||
                                AAGTTC  TA  AGG CGGAG
                                    GT  GA   A
GAM1622  LOC126282 3'  TGAGGCAGGAGAATCGCTTGAA 74969            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                          A
GAM1622  LOC126282 3'  TGAGGCAGGATAATCACTTGAA 74970          C   C
                                TTCAAGTGATT TCC GCCTCA
                                |||||||||| ||| ||||||
                                AAGTTCACTAA AGG CGGAGT
                                         T   A
GAM1622  LOC126669 3'  TGAGGCACGAGAATCACTTGAG 75953            CC
                                TTCAAGTGATTCTC  GCCTCA
                                ||||||||||||||  ||||||
                                GAGTTCACTAAGAG  CGGAGT
                                          CA
GAM1622  LOC127428 3'  TGAGGTATGAGAATCGCTTGAA 75164            CC
                                TTCAAGTGATTCTC  GCCTCA
                                ||||||||||||||  ||||||
                                AAGTTCGCTAAGAG  TGGAGT
                                          TA
GAM1622  LOC129563 5'  AGGCGGGAACTCTGAG      75391      _  GATTC
                                TTCA AGT     TCCCGCCT
                                |||| |||     ||||||||
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                                GAGT TCA     AGGGCGGA
                                  C  _____
GAM1622  LOC130162 3'  GAGGCAGGAGGATCGCTTGAG  75419              C
                                TTCAAGTGATTCTCC GCCTC
                                ||||||||||||||| |||||
                                GAGTTCGCTAGGAGG CGGAG
                                        A
GAM1622  LOC130535 3'  TGAGGCAGGAGGATTGCCTGAG 76657      A TG       C
                                TTCA G  ATTCTCC GCCTCA
                                |||| |  ||||||| ||||||
                                GAGT C  TAGGAGG CGGAGT
                                  C GT       A
GAM1622  LOC130535 3'  TGAGGTAGGAGAATCGCTTGAA 76658              CG
                                TTCAAGTGATTCTCC  CCTCA
                                ||||||||||||||  |||||
                                AAGTTCGCTAAGAGG  GGAGT
                                        AT
GAM1622  LOC130589 3'  TGAAGCAGGAGAATCGCTTGAA 57936              C  C
                                TTCAAGTGATTCTCC GC TCA
                                |||||||||||||| || |||
                                AAGTTCGCTAAGAGG CG AGT
                                        A  A
GAM1622  LOC131965 3'  TGAGGCAAGAGAATCGCTTGAA 75529             CC
                                TTCAAGTGATTCTC  GCCTCA
                                ||||||||||||  ||||||
                                AAGTTCGCTAAGAG  CGGAGT
                                        AA
GAM1622  LOC134147 3'  TGAGGAGGAGAATCACTTGAA  57969             CG
                                TTCAAGTGATTCTCC  CCTCA
                                ||||||||||||||  |||||
                                AAGTTCACTAAGAGG  GGAGT
                                        A_
GAM1622  LOC135818 3'  TGAGGCAAGAGGATCACTTGAG 75752              CC
                                TTCAAGTGATTCTC  GCCTCA
                                ||||||||||||  ||||||
                                GAGTTCACTAGGAG  CGGAGT
                                        AA
GAM1622  LOC137362 3'  GAGGCGGGTGGGTCACCTGAG  75786      A       T
                                TTCA GTGATTC CCCGCCTC
                                |||| ||||||| ||||||||
                                GAGT CACTGGG GGGCGGAG
                                  C       T
GAM1622  LOC137362 3'  TGAGGCAGGAGAATCGCTTGAA 75789              C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                        A
GAM1622  LOC138428 3'  TGAGGCAGGAGAATCACTTGAA 75863              C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
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                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  LOC142779 3'  TGAGGCAGGAGAATCGCTTGAA 76909            C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  LOC142927 3'  TGAGGCGGGAGACTCGCTTGAA 76954         T
                                TTCAAGTGA TCTCCCGCCTCA
                                ||||||||| ||||||||||||
                                AAGTTCGCT AGAGGGCGGAGT
                                     C
GAM1622  LOC143888 3'  TGAGGCAGGAGAATCACTTGAA 77176            C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  LOC144289 3'  TGAGGCAGGAGAATCATTTGAA 83963            C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||| ||||||
                                AAGTTTACTAAGAGG CGGAGT
                                      A
GAM1622  LOC144465 3'  TGAGGCAGGAGAATCACTTGAA 77355            C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  LOC144465 3'  TGAGGCAGGAGAATCACTTGAA 77356            C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  LOC144465 3'  TGAGGCGGGTTGATCACCTGAG 77357      A     CT
                                TTCA GTGATT  CCCGCCTCA
                                |||| ||||||  |||||||||
                                GAGT CACTAG  GGGCGGAGT
                                  C     TT
GAM1622  LOC144481 3'  TGAGACAGGAGAATCACTTGAA 84024            CGC
                                TTCAAGTGATTCTCC   CTCA
                                |||||||||||||||   ||||
                                AAGTTCACTAAGAGG   GAGT
                                      ACA
GAM1622  LOC144524 3'  TGAGGCAGGAGAACTGCTTGAA 84069       GA     C
                                TTCAAGT  TTCTCC GCCTCA
                                |||||||  |||||| ||||||
                                AAGTTCG  AAGAGG CGGAGT
                                     TC     A
GAM1622  LOC144524 5'  TGAGGCAGGAGAATCTTTCGAG 84070     A  T      C
                                TTC AG GATTCTCC GCCTCA
                                ||| || |||||||| ||||||
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                                GAG TT CTAAGAGG CGGAGT
                                  C T       A
GAM1622  LOC144563 3'  TGAGACACGAGAATCACTTGAG 77406            CCGC
                                TTCAAGTGATTCTC    CTCA
                                |||||||||||||    ||||
                                GAGTTCACTAAGAG    GAGT
                                     CACA
GAM1622  LOC144583 3'  TGAGGCAGGATAATCACTTGAA 77423          C   C
                                TTCAAGTGATT TCC GCCTCA
                                |||||||||||| ||| ||||||
                                AAGTTCACTAA AGG CGGAGT
                                     T   A
GAM1622  LOC144817 3'  TGAGGCAGGAGAATCCCTTGAA 77523       T       C
                                TTCAAG GATTCTCC GCCTCA
                                |||||| |||||||| ||||||
                                AAGTTC CTAAGAGG CGGAGT
                                   C       A
GAM1622  LOC144845 3'  AGGCGGGCAGATCACTTGAG   57450          CT
                                TTCAAGTGATT  CCCGCCT
                                ||||||||||  |||||||
                                GAGTTCACTAG  GGGCGGA
                                     AC
GAM1622  LOC144845 3'  TGAGGCAGGAAAATCACTTGAA 57465          C   C
                                TTCAAGTGATT TCC GCCTCA
                                |||||||||| ||| ||||||
                                AAGTTCACTAA AGG CGGAGT
                                     A   A
GAM1622  LOC145082 3'  TGAGGCAGAAGGATTGCTTGGA 84200       TG    CCC
                                TTCAAG  ATTCT   GCCTCA
                                ||||||  |||||   ||||||
                                AGGTTC  TAGGA   CGGAGT
                                   GT    AGA
GAM1622  LOC145082 5'  TGAGGCAGGAGAATCATTTGGA 84201            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AGGTTTACTAAGAGG CGGAGT
                                     A
GAM1622  LOC145216 3'  TGAGGCAGGAGAATCACTTGAA 84227            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                     A
GAM1622  LOC145216 3'  TGAGGCGGGCGGATCACCTGAG 84228      A      T
                                TTCA GTGATTC CCCGCCTCA
                                |||| ||||||| |||||||||
                                GAGT CACTAGG GGGCGGAGT
                                  C      C
GAM1622  LOC145231 3'  TGAGGCAGGAGAATTGCTTGAA 84262       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
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                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  LOC145387 3'  AGGCAAAAGGATTGCTTGAG   84327       TG    CCC
                                TTCAAG  ATTCT   GCCT
                                ||||||  |||||   ||||
                                GAGTTC  TAGGA   CGGA
                                   GT    AAA
GAM1622  LOC145387 3'  TGAGGCAGGAGAATTGCTTGAA 84346       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  LOC145453 3'  TGAGGCACGAGAATCGCTTGAA 77672           CC
                                TTCAAGTGATTCTC  GCCTCA
                                ||||||||||||||  ||||||
                                AAGTTCGCTAAGAG  CGGAGT
                                          CA
GAM1622  LOC145482 3'  TGAGGCTGGAGAATCATTTGAA 77748           C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||| ||||||
                                AAGTTTACTAAGAGG CGGAGT
                                          T
GAM1622  LOC145483 3'  TGAGGCAGGAGAATCACTTGAA 77761           C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                          A
GAM1622  LOC145662 3'  TGAGGCACCAGAATCACTTGAA 77839          CCC
                                TTCAAGTGATTCT   GCCTCA
                                ||||||||||||   ||||||
                                AAGTTCACTAAGA   CGGAGT
                                          CCA
GAM1622  LOC145757 3'  AGGCAGGTGGATCACTTGAG   77915          T  C
                                TTCAAGTGATTC CC GCCT
                                ||||||||||| || ||||
                                GAGTTCACTAGG GG CGGA
                                          T  A
GAM1622  LOC145757 3'  TGAGGCAGGAGAATCGCTGGAA 77943     A        C
                                TTC AGTGATTCTCC GCCTCA
                                ||| |||||||||| ||||||
                                AAG TCGCTAAGAGG CGGAGT
                                  G         A
GAM1622  LOC145945 5'  TGAGGCAGGAGGATCGCTTGAG 84574           C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||| ||||||
                                GAGTTCGCTAGGAGG CGGAGT
                                          A
GAM1622  LOC146059 3'  TGAGGCAGGAGACCTGCTTGAA 78091        AT    C
                                TTCAAGTG  TCTCC GCCTCA
                                ||||||||  ||||| ||||||
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                                AAGTTCGT  AGAGG CGGAGT
                                    CC     A
GAM1622  LOC146159 3'  TGAGGCAGGAGGATCACTTGAA 78181              C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAGGAGG CGGAGT
                                       A
GAM1622  LOC146336 5'  GAGGCGGGTGGATCACCTGAG  78373      A       T
                                TTCA GTGATTC CCCGCCTC
                                |||| ||||||| ||||||||
                                GAGT CACTAGG GGGCGGAG
                                  C       T
GAM1622  LOC146512 3'  TGAGGCAGAGGATCACTTGAG  78502             CC
                                TTCAAGTGATTCTC  GCCTCA
                                ||||||||||||||  ||||||
                                GAGTTCACTAGGAG  CGGAGT
                                       A_
GAM1622  LOC146540 3'  AGGCAAGAGGATCACTTGAG   78524             CC
                                TTCAAGTGATTCTC  GCCT
                                ||||||||||||||  ||||
                                GAGTTCACTAGGAG  CGGA
                                       AA
GAM1622  LOC146713 3'  GAGGCAGGAGAATCACTTGAA  84731              C
                                TTCAAGTGATTCTCC GCCTC
                                |||||||||||||| |||||
                                AAGTTCACTAAGAGG CGGAG
                                       A
GAM1622  LOC146713 3'  TGAGGCACGAGAATCACTTGAA 84742              CC
                                TTCAAGTGATTCTC  GCCTCA
                                ||||||||||||||  ||||||
                                AAGTTCACTAAGAG  CGGAGT
                                       CA
GAM1622  LOC146723 3'  TGAGGCAGGAGAATCGCCTGAA 78687      A       C
                                TTCA GTGATTCTCC GCCTCA
                                |||| |||||||||| ||||||
                                AAGT CGCTAAGAGG CGGAGT
                                  C         A
GAM1622  LOC146728 5'  TGAGGCAAGAGAATCATTTGAA 84776              CC
                                TTCAAGTGATTCTC  GCCTCA
                                ||||||||||||||  ||||||
                                AAGTTTACTAAGAG  CGGAGT
                                       AA
GAM1622  LOC146728 3'  TGAGGCAGGAGGATCGCTTGAG 84777              C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                GAGTTCGCTAGGAGG CGGAGT
                                       A
GAM1622  LOC146780 5'  AGGCAAGAGGATCGCTTGAG   84816              CC
                                TTCAAGTGATTCTC  GCCT
                                ||||||||||||||  ||||
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                                GAGTTCGCTAGGAG  CGGA
                                      AA
GAM1622  LOC146895 3'  TGAGGCAGGAGAATTGCTTGAA 84876       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                |||||| ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  LOC146901 3'  GAGGCAGGTGGATCACTTGAG  84902           T  C
                                TTCAAGTGATTC CC GCCTC
                                |||||||||||| || |||||
                                GAGTTCACTAGG GG CGGAG
                                      T  A
GAM1622  LOC146901 3'  GAGGTGGGAGAATCACTTGAA  84903
                                TTCAAGTGATTCTCCCGCCTC
                                |||||||||||||||||||||
                                AAGTTCACTAAGAGGGTGGAG

GAM1622  LOC147057 3'  TGAGGCAGGAGAATCGCTTGAA 84990             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  LOC147063 5'  AGGCGGGAGGATGGCTTGAG   85014       G
                                TTCAAGT ATTCTCCCGCCT
                                ||||||| ||||||||||||
                                GAGTTCG TAGGAGGGCGGA
                                   G
GAM1622  LOC147180 5'  GAGGCGGGCGGATCACCTGAG  85099     A      T
                                TTCA GTGATTC CCCGCCTC
                                |||| ||||||| ||||||||
                                GAGT CACTAGG GGGCGGAG
                                  C      C
GAM1622  LOC147180 5'  TGAGGCAGGAGAATCGCTTGAA 85108             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  LOC147599 3'  GAGGCAGGTGGATCACTTGAG  85162           T  C
                                TTCAAGTGATTC CC GCCTC
                                |||||||||||| || |||||
                                GAGTTCACTAGG GG CGGAG
                                      T  A
GAM1622  LOC147599 3'  TGAGGCAGAAGTATTGCTTGAA 85167       TG  T  CCC
                                TTCAAG  AT CT   GCCTCA
                                ||||||  || ||   ||||||
                                AAGTTC  TA GA   CGGAGT
                                   GT  T  AGA
GAM1622  LOC147664 3'  TGAGGCAGGAGAATCGCTTGAA 79051             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
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                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  LOC147727 5'  TGAGACAGGAGGATCGCTTGAA 79141            CGC
                                TTCAAGTGATTCTCC  CTCA
                                |||||||||||||||  ||||
                                AAGTTCGCTAGGAGG  GAGT
                                      ACA
GAM1622  LOC147727 5'  TGAGGCAGGAGAATTGTTTGA  79142      TG     C
                                TCAAG  ATTCTCC GCCTCA
                                |||||  ||||||| ||||||
                                AGTTT  TAAGAGG CGGAGT
                                   GT      A
GAM1622  LOC147837 3'  TGAGGCAGGATAATCACTTGAA 79211         C  C
                                TTCAAGTGATT TCC GCCTCA
                                |||||||||| ||| ||||||
                                AAGTTCACTAA AGG CGGAGT
                                       T  A
GAM1622  LOC147990 3'  GAGGCGGGCAGATCACTTGAA  85223         CT
                                TTCAAGTGATT  CCCGCCTC
                                ||||||||||  ||||||||
                                AAGTTCACTAG  GGGCGGAG
                                       AC
GAM1622  LOC147990 3'  TGAGGCACAAGAATCACTTGAA 85240          CCC
                                TTCAAGTGATTCT  GCCTCA
                                ||||||||||||  ||||||
                                AAGTTCACTAAGA  CGGAGT
                                      ACA
GAM1622  LOC148137 3'  TGAGGCAAGAGAATTGCTTGAA 59113      TG    CC
                                TTCAAG  ATTCTC  GCCTCA
                                ||||||  ||||||  ||||||
                                AAGTTC  TAAGAG  CGGAGT
                                   GT     AA
GAM1622  LOC148198 3'  TGAGGCAGGAGAATCACTTGAA 71229           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  LOC148206 3'  GAGGCAGGAGAATCATTTGAA  79464           C
                                TTCAAGTGATTCTCC GCCTC
                                |||||||||||||| |||||
                                AAGTTTACTAAGAGG CGGAG
                                      A
GAM1622  LOC148254 3'  TGAGACAGGAGAAGTGCTTGAA 79504       GA    CGC
                                TTCAAGT  TTCTCC  CTCA
                                |||||||  ||||||  ||||
                                AAGTTCG  AAGAGG  GAGT
                                    TG     ACA
GAM1622  LOC148534 3'  TGAGGCAGGAGAATCGCTTGAA 79641           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
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                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  LOC148758 5'  TGAGGCAGGAGAATTGCTTGAA 79729       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  LOC148809 5'  TGAGGCAGGAGAATTGCTTGAA 79765       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  LOC148809 5'  TGAGGCGGGTGGATCACTTGAA 79766          T
                                TTCAAGTGATTC CCCGCCTCA
                                |||||||||||| |||||||||
                                AAGTTCACTAGG GGGCGGAGT
                                      T
GAM1622  LOC148918 5'  TGAGGCAGGAGAATTGCTTGAA 79833       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  LOC148936 3'  GAGGCAGGAGGATCACTTGAG  85454           C
                                TTCAAGTGATTCTCC GCCTC
                                ||||||||||||||| |||||
                                GAGTTCACTAGGAGG CGGAG
                                      A
GAM1622  LOC148938 3'  GAGGCAGGAGGATCACTTGAG  85437           C
                                TTCAAGTGATTCTCC GCCTC
                                ||||||||||||||| |||||
                                GAGTTCACTAGGAGG CGGAG
                                      A
GAM1622  LOC149073 3'  AGGCAGATGGAACACTTGAG   85480        A  _  CC
                                TTCAAGTG TTC TC  GCCT
                                |||||||| ||| ||  ||||
                                GAGTTCAC AGG AG  CGGA
                                     A  T  A_
GAM1622  LOC149113 5'  GAGGCAGGAGAATTGCTTGAA  79912       TG      C
                                TTCAAG  ATTCTCC GCCTC
                                ||||||  ||||||| |||||
                                AAGTTC  TAAGAGG CGGAG
                                   GT      A
GAM1622  LOC149113 5'  TGAGGCACATGGACCACTTGAG 79919         A   TCCC
                                TTCAAGTG TTC    GCCTCA
                                |||||||| |||    ||||||
                                GAGTTCAC AGG    CGGAGT
                                     C   TACA
GAM1622  LOC149194 5'  AGGCGGGAGAATCACTTGAA   79977
                                TTCAAGTGATTCTCCCGCCT
                                ||||||||||||||||||||
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                                AAGTTCACTAAGAGGGCGGA

GAM1622  LOC149271 3'  TGAGGCAGGAGAATCACTTGAA 80014              C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                          A
GAM1622  LOC149460 3'  TGAGGCAGGAGAATCGCTTGAA 85617              C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                          A
GAM1622  LOC149464 3'  TGAGGCAGGAGAATCACTTGAA 85601              C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                          A
GAM1622  LOC149579 5'  TGAGGCAGGAGAATTGCTTGAA 71696       TG     C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  LOC149672 5'  AGGCAGGGAGAATCGCTTGAA  80335              _
                                TTCAAGTGATTCTCCC GCCT
                                |||||||||||||| ||||
                                AAGTTCGCTAAGAGGG CGGA
                                          A
GAM1622  LOC149705 3'  TGAAGCAGGAGAATCACTT    85788          C  C
                                AAGTGATTCTCC GC TCA
                                |||||||||||| || |||
                                TTCACTAAGAGG CG AGT
                                         A  A
GAM1622  LOC149705 3'  TGAGGCAGGAGAATCGCTTGAA 85789              C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                          A
GAM1622  LOC149711 5'  TGAGGCAAGAGGATCACTTGAG 85858             CC
                                TTCAAGTGATTCTC  GCCTCA
                                ||||||||||||||  ||||||
                                GAGTTCACTAGGAG  CGGAGT
                                          AA
GAM1622  LOC150142 5'  TGAGGCAGGAGGATCGCTTGAG 80408              C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                GAGTTCGCTAGGAGG CGGAGT
                                          A
GAM1622  LOC150174 3'  AGGCGGGAGGCAGCTGA     80428     A  GAT
                                TCA GT   TCTCCCGCCT
                                ||| ||   ||||||||||
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                                AGT CG   GGAGGGCGGA
                                  _ AC_
GAM1622  LOC150185 3'  TGAGGCAGGAGAATTGCTTGAA 86071       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                    GT      A
GAM1622  LOC150213 3'  AGGCGGGAGGCAGCTGA     75347     A  GAT
                                TCA GT   TCTCCCGCCT
                                ||| ||   ||||||||||
                                AGT CG   GGAGGGCGGA
                                  _ AC_
GAM1622  LOC150225 3'  TGAGGCGTGAGAATCGCTTGAA 86208             C
                                TTCAAGTGATTCTC CGCCTCA
                                |||||||||||||| |||||||
                                AAGTTCGCTAAGAG GCGGAGT
                                         T
GAM1622  LOC150245 3'  AGGCAAAAGGATCGCTTGAG   86108           CCC
                                TTCAAGTGATTCT   GCCT
                                ||||||||||||   ||||
                                GAGTTCGCTAGGA   CGGA
                                       AAA
GAM1622  LOC150245 3'  TGAGGCAGGAAGATTGCTTGAG 86120       TG  TC   C
                                TTCAAG  AT  TCC GCCTCA
                                ||||||  ||  ||| ||||||
                                GAGTTC  TA  AGG CGGAGT
                                    GT  GA   A
GAM1622  LOC150299 3'  TGAAGCAGGAGAATCGCTGGAA 86172     A         C  C
                                TTC AGTGATTCTCC GC TCA
                                ||| |||||||||| || |||
                                AAG TCGCTAAGAGG CG AGT
                                  G          A  A
GAM1622  LOC150319 3'  TGAGGCAGGAGAACCGCTTGAA 80478         A     C
                                TTCAAGTG TTCTCC GCCTCA
                                |||||||| |||||| ||||||
                                AAGTTCGC AAGAGG CGGAGT
                                     C     A
GAM1622  LOC150319 3'  TGAGGCGGACGGAACACCTGAG 80479      A  A    C_
                                TTCA GTG TTCT  CCGCCTCA
                                |||| ||| ||||  ||||||||
                                GAGT CAC AAGG  GGCGGAGT
                                  C   _    CA
GAM1622  LOC150343 3'  GAGGCAGGTGGATCACTTGAG  80491           T  C
                                TTCAAGTGATTC CC GCCTC
                                |||||||||||| || |||||
                                GAGTTCACTAGG GG CGGAG
                                       T  A
GAM1622  LOC150358 3'  TGAGGCAGGAGAATCGCTTGAA 86104             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
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                                AAGTTCGCTAAGAGG CGGAGT
                                       A
GAM1622  LOC150372 3'  AGGCAGGAGAATCTCTTGAA   80604       T       C
                                TTCAAG GATTCTCC GCCT
                                |||||| |||||||| ||||
                                AAGTTC CTAAGAGG CGGA
                                   T       A
GAM1622  LOC150372 3'  GAGGCGGGTGGATCACTTGAG  80612           T
                                TTCAAGTGATTC CCCGCCTC
                                |||||||||||| ||||||||
                                GAGTTCACTAGG GGGCGGAG
                                       T
GAM1622  LOC150481 3'  TGAGGCGGGAGAACTGCTTGAA 80716        GA
                                TTCAAGT  TTCTCCCGCCTCA
                                |||||||  |||||||||||||
                                AAGTTCG  AAGAGGGCGGAGT
                                   TC
GAM1622  LOC150577 3'  AGGCAAGAGGATCACTTGAG   86249           CC
                                TTCAAGTGATTCTC  GCCT
                                ||||||||||||||  ||||
                                GAGTTCACTAGGAG  CGGA
                                       AA
GAM1622  LOC150630 3'  AGGCAGGAGAATCGCTTGAA   86288           C
                                TTCAAGTGATTCTCC GCCT
                                |||||||||||||| ||||
                                AAGTTCGCTAAGAGG CGGA
                                       A
GAM1622  LOC150630 5'  AGGCAGGAGGACTGCTTGAG   86289       GA     C
                                TTCAAGT  TTCTCC GCCT
                                |||||||  |||||| ||||
                                GAGTTCG  AGGAGG CGGA
                                   TC     A
GAM1622  LOC151068 3'  TGAGGCAGGCAGTTCACTTGAG 86406         TT  _  C
                                TTCAAGTGA  CT CC GCCTCA
                                |||||||||  || || ||||||
                                GAGTTCACT  GA GG CGGAGT
                                      T_  C  A
GAM1622  LOC151196 3'  TGAGGCAGGAGAATCACTTGAA 86457           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                       A
GAM1622  LOC151248 3'  TGAAGCAAGAGAATCGCTTGAA 81001           CC  C
                                TTCAAGTGATTCTC  GC TCA
                                ||||||||||||||  || |||
                                AAGTTCGCTAAGAG  CG AGT
                                       AA  A
GAM1622  LOC151446 3'  TGAGACACAAGAATCACTTGAA 86576           CCCGC
                                TTCAAGTGATTCT     CTCA
                                ||||||||||||     ||||
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                                AAGTTCACTAAGA    GAGT
                                      ACACA
GAM1622  LOC151556 3'  TGAGGCAGGAGAATCGCTTGAA 81087            C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  LOC151602 3'  TGAGGCAAGAGAATTGCTTGAA 81115       TG    CC
                                TTCAAG  ATTCTC  GCCTCA
                                ||||||  ||||||  ||||||
                                AAGTTC  TAAGAG  CGGAGT
                                   GT     AA
GAM1622  LOC151632 3'  TGAGGCAGGAGAATCACTTGAG 86652            C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||| ||||||
                                GAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  LOC152106 3'  TGAGGCAGGAGGATCGCTTGAA 70599            C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||| ||||||
                                AAGTTCGCTAGGAGG CGGAGT
                                      A
GAM1622  LOC152271 3'  TGAGGCAGGAGAATCACTTGAG 81366            C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||| ||||||
                                GAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  LOC152271 5'  TGAGGCAGGAGAATCCCTTGAA 81367       T    C
                                TTCAAG GATTCTCC GCCTCA
                                |||||| |||||||| ||||||
                                AAGTTC CTAAGAGG CGGAGT
                                   C       A
GAM1622  LOC152283 3'  TGAAACAGGAGAATTGCTTGAA 86878       TG    CGCC
                                TTCAAG  ATTCTCC    TCA
                                ||||||  |||||||    |||
                                AAGTTC  TAAGAGG    AGT
                                   GT      ACAA
GAM1622  LOC152445 5'  TGAAGCAGGAGGTGGCATTTGA 86968        AT_    C  C
            A                   TTCAAGTG   TCTCC GC TCA
                                ||||||||   ||||| || |||
                                AAGTTTAC   GGAGG CG AGT
                                     GGT    A  A
GAM1622  LOC152445 3'  TGAGGCAGGAGAATCGCTTGAA 86971            C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  LOC152445 3'  TGAGGCAGGAGACTCGCTTGAA 86972         T    C
                                TTCAAGTGA TCTCC GCCTCA
                                ||||||||| ||||| ||||||
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                                AAGTTCGCT AGAGG CGGAGT
                                    C     A
GAM1622  LOC152453 3'  GAGGCGGGAGGATCACCTGAG  81474      A
                                TTCA GTGATTCTCCCGCCTC
                                |||| ||||||||||||||||
                                GAGT CACTAGGAGGGCGGAG
                                  C
GAM1622  LOC152453 3'  TGAGGCAGGAGAATTGCTTGAA 81483       TG       C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT       A
GAM1622  LOC152453 3'  TGAGGCAGGAGGATTGCTTGAG 81484       TG       C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                GAGTTC  TAGGAGG CGGAGT
                                   GT       A
GAM1622  LOC152627 5'  AGGCAGGAGAATTGCTGGAA   81501     A  TG       C
                                TTC AG  ATTCTCC GCCT
                                ||| ||  ||||||| ||||
                                AAG TC  TAAGAGG CGGA
                                  G  GT       A
GAM1622  LOC152804 3'  TGAGGCAGGAGAATCACTTGAA 87090              C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  LOC152860 3'  TGAGGCAGGAGAATCCCTTGAA 81583       T       C
                                TTCAAG GATTCTCC GCCTCA
                                |||||| |||||||| ||||||
                                AAGTTC CTAAGAGG CGGAGT
                                   C       A
GAM1622  LOC153146 3'  AGGCAGGCATATCACTTGAG   87140          TCT  C
                                TTCAAGTGAT   CC GCCT
                                ||||||||||   || ||||
                                GAGTTCACTA   GG CGGA
                                     TAC  A
GAM1622  LOC153146 3'  TGAGGCAGGAGAATCCCTTGAA 87149       T       C
                                TTCAAG GATTCTCC GCCTCA
                                |||||| |||||||| ||||||
                                AAGTTC CTAAGAGG CGGAGT
                                   C       A
GAM1622  LOC153260 3'  TGAGGCAGGAGAAATGCTTGAA 81675        A     C
                                TTCAAGTG TTCTCC GCCTCA
                                |||||||| |||||| ||||||
                                AAGTTCGT AAGAGG CGGAGT
                                     A     A
GAM1622  LOC153338 3'  TGAAGCAGTAGAATCGCTT    87200          CCC  C
                                AAGTGATTCT   GC TCA
                                ||||||||||   || |||
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                                TTCGCTAAGA   CG AGT
                                      TGA  A
GAM1622  LOC153642 3'  TGAGGCAGGAGGATCGCTTGAA 81796             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAGGAGG CGGAGT
                                       A
GAM1622  LOC154092 3'  TGAAGCAGGAGGATCACTTGAG 87373             C  C
                                TTCAAGTGATTCTCC GC TCA
                                |||||||||||||| || |||
                                GAGTTCACTAGGAGG CG AGT
                                       A  A
GAM1622  LOC154403 5'  GAGGCAGGAGAATTGCTTGAA  81977       TG      C
                                TTCAAG  ATTCTCC GCCTC
                                ||||||  ||||||| |||||
                                AAGTTC  TAAGAGG CGGAG
                                    GT      A
GAM1622  LOC154403 5'  TGAGGCACATGGACCACTTGAG 81984         A   TCCC
                                TTCAAGTG TTC    GCCTCA
                                |||||||| |||    ||||||
                                GAGTTCAC AGG    CGGAGT
                                      C   TACA
GAM1622  LOC154739 5'  TGAGGCAGGAGAATCACTTGAA 87447             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                       A
GAM1622  LOC154877 3'  TGAGGCAGGAGAATCACTTGAA 87581             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                       A
GAM1622  LOC154881 3'  TGAGGCAGGAGGATCACTTGAG 82079             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                GAGTTCACTAGGAGG CGGAGT
                                       A
GAM1622  LOC154992 3'  TGAGGCAGAGAATCACTTGAA  82143            CC
                                TTCAAGTGATTCTC  GCCTCA
                                ||||||||||||  ||||||
                                AAGTTCACTAAGAG  CGGAGT
                                       A_
GAM1622  LOC154992 5'  TGAGGCAGGAGAATTGCTTGAA 82144       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                    GT      A
GAM1622  LOC155006 3'  GAGGCAGGAGAATCTCTTGAA  82171       T       C
                                TTCAAG GATTCTCC GCCTC
                                |||||| |||||||| |||||
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                                AAGTTC CTAAGAGG CGGAG
                                   T       A
GAM1622  LOC155054 3'  TGAGGCAGGAGGATCGCTTGAG 82207              C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                GAGTTCGCTAGGAGG CGGAGT
                                          A
GAM1622  LOC155376 3'  AGGCAGGCGGATCACTTGAG   82239            T  C
                                TTCAAGTGATTC CC GCCT
                                |||||||||||| || ||||
                                GAGTTCACTAGG GG CGGA
                                      C  A
GAM1622  LOC157247 5'  GTGGGAGAATCACTTGAG    82306
                                TTCAAGTGATTCTCCCGC
                                ||||||||||||||||||
                                GAGTTCACTAAGAGGGTG

GAM1622  LOC157278 3'  TGAGACGGGAAGACTGCTTGAA 87710        GA TC     C
                                TTCAAGT  T  TCCCG CTCA
                                |||||||  |  ||||| ||||
                                AAGTTCG  A  AGGGC GAGT
                                   TC GA     A
GAM1622  LOC157278 3'  TGAGGTGGGAGGATCACTTGAA 87711
                                TTCAAGTGATTCTCCCGCCTCA
                                ||||||||||||||||||||||
                                AAGTTCACTAGGAGGGTGGAGT

GAM1622  LOC157292 5'  TGAGGCGGGTGGATCACTTGAA 87702             T
                                TTCAAGTGATTC CCCGCCTCA
                                |||||||||||| |||||||||
                                AAGTTCACTAGG GGGCGGAGT
                                      T
GAM1622  LOC157464 5'  TGAGGCGGGTGAATCACTTGA  87753            T
                                TCAAGTGATTC CCCGCCTCA
                                |||||||||| |||||||||
                                AGTTCACTAAG GGGCGGAGT
                                      T
GAM1622  LOC157660 3'  TGAGGCAGGAGAATCGCTTGAA 87808              C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                          A
GAM1622  LOC157983 3'  TGAGGCAGGGGAATCACTTGAA 82545              C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGGGG CGGAGT
                                          A
GAM1622  LOC158160 3'  AGGCAGAAGGATCACTTGAG   73469            CCC
                                TTCAAGTGATTCT   GCCT
                                ||||||||||||   ||||
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                                GAGTTCACTAGGA  CGGA
                                       AGA
GAM1622  LOC158191 3'  TGAGGCGGGAGAACTGCTTGAA 82685       GA
                                TTCAAGT  TTCTCCCGCCTCA
                                |||||||  |||||||||||||
                                AAGTTCG  AAGAGGGCGGAGT
                                   TC
GAM1622  LOC158292 5'  TGAGGCAGAAGAATCACTTGAA 88058          CCC
                                TTCAAGTGATTCT  GCCTCA
                                ||||||||||||  ||||||
                                AAGTTCACTAAGA  CGGAGT
                                       AGA
GAM1622  LOC158677 5'  TGAGGTAGCAGACTCACTTGAA 88253        T  CCC
                                TTCAAGTGA TCT  GCCTCA
                                |||||||| |||  ||||||
                                AAGTTCACT AGA  TGGAGT
                                      C  CGA
GAM1622  LOC158819 5'  AGGCACAAGAATCGCTTGAA  88267          CCC
                                TTCAAGTGATTCT  GCCT
                                ||||||||||||  ||||
                                AAGTTCGCTAAGA  CGGA
                                       ACA
GAM1622  LOC159036 3'  TGAGGCAGGAGAATCGCTTGAA 88352           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                        A
GAM1622  LOC159053 3'  TGAGGCAGGAGAATCACTTGAA 88380           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                        A
GAM1622  LOC159110 3'  TGAGGCAGGTGAATCGCTTGAA 82996         T  C
                                TTCAAGTGATTC CC GCCTCA
                                |||||||||||  || ||||||
                                AAGTTCGCTAAG GG CGGAGT
                                       T  A
GAM1622  LOC159116 3'  TGAGGCAGGTGAATCGCTTGAA 82979         T  C
                                TTCAAGTGATTC CC GCCTCA
                                |||||||||||  || ||||||
                                AAGTTCGCTAAG GG CGGAGT
                                       T  A
GAM1622  LOC164295 3'  AGGCGGGAGGACTGAA      83394      A  GAT
                                TTCA GT   TCTCCCGCCT
                                ||||  ||   ||||||||||
                                AAGT CA   GGAGGGCGGA
                                  _  ___
GAM1622  LOC169166 3'  TGAGAAATGGAATCACTGAA   83607      A       CCCGC
                                TTCA GTGATTCT    CTCA
                                ||||  ||||||||    ||||
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                                AAGT CACTAAGG     GAGT
                                  _       TAAA_
GAM1622  LOC170395 3'  TGAGGCAGGAGGATCCCTTGAG 76880       T       C
                                TTCAAG GATTCTCC GCCTCA
                                |||||| |||||||| ||||||
                                GAGTTC CTAGGAGG CGGAGT
                                   C       A
GAM1622  LOC170395 3'  TGAGGCAGGAGAATCACTTGAA 76879             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                         A
GAM1622  LOC196027 3'  TGAGGCAAGGGGATCACTTGAA 88942             CC
                                TTCAAGTGATTCTC  GCCTCA
                                |||||||||||||  ||||||
                                AAGTTCACTAGGGG  CGGAGT
                                         AA
GAM1622  LOC196047 5'  TGAGGCAAGAGAATCGCTTGAA 91168             CC
                                TTCAAGTGATTCTC  GCCTCA
                                |||||||||||||  ||||||
                                AAGTTCGCTAAGAG  CGGAGT
                                         AA
GAM1622  LOC196528 3'  TGAGGCAGAAGGATCACTGGA  89110      A       CCC
                                TTCA GTGATTCT   GCCTCA
                                |||| ||||||||   ||||||
                                AGGT CACTAGGA   CGGAGT
                                  _       AGA
GAM1622  LOC196529 3'  TGAGGCAGGAGAATCTCTTGAA 89145       T       C
                                TTCAAG GATTCTCC GCCTCA
                                |||||| |||||||| ||||||
                                AAGTTC CTAAGAGG CGGAGT
                                   T       A
GAM1622  LOC196540 3'  TGAGGCAGGAGAATCACTTGAG 91209             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                GAGTTCACTAAGAGG CGGAGT
                                         A
GAM1622  LOC196761 3'  AGGCAGGAGAATCACTTGAA   91115             C
                                TTCAAGTGATTCTCC GCCT
                                |||||||||||||| ||||
                                AAGTTCACTAAGAGG CGGA
                                         A
GAM1622  LOC197196 3'  TGAGGCAGGAGAATCACTTGAA 91307             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                         A
GAM1622  LOC197319 3'  TGAGGCAGGAGAATTGCTTGAA 89330       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
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                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  LOC197408 5'  TGAGGTGGGAGAATCACTTGAG 91320
                                TTCAAGTGATTCTCCCGCCTCA
                                |||||||||||||||||||||
                                GAGTTCACTAAGAGGGTGGAGT

GAM1622  LOC199676 3'  TGAGGCACGAGAATCACTTGAA 91363           CC
                                TTCAAGTGATTCTC  GCCTCA
                                |||||||||||||  ||||||
                                AAGTTCACTAAGAG  CGGAGT
                                      CA
GAM1622  LOC199786 3'  TGAGGCGGGCAGATCACTTGAG 89770         CT
                                TTCAAGTGATT  CCCGCCTCA
                                ||||||||||  |||||||||
                                GAGTTCACTAG  GGGCGGAGT
                                    AC
GAM1622  LOC199923 3'  TGAAGCGGGAGGATCGCTTGAG 89877             C
                                TTCAAGTGATTCTCCCGC TCA
                                |||||||||||||||||| |||
                                GAGTTCGCTAGGAGGGCG AGT
                                         A
GAM1622  LOC200251 5'  TGAGGCAGGAGAATTGCTTGAA 90068      TG     C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  LOC200251 3'  TGAGGCAGGAGAATTGCTTGAA 90069      TG     C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  LOC200317 3'  TGAGGCAAGAGAATTGCTTGGA 90231      TG    CC
                                TTCAAG  ATTCTC  GCCTCA
                                ||||||  ||||||  ||||||
                                AGGTTC  TAAGAG  CGGAGT
                                   GT     AA
GAM1622  LOC200470 3'  TGAGGCGGGAGGATCACTTGAG 91642
                                TTCAAGTGATTCTCCCGCCTCA
                                |||||||||||||||||||||
                                GAGTTCACTAGGAGGGCGGAGT

GAM1622  LOC200731 3'  TGAAGCAGGAGAATCCCTTGAA 91700      T      C  C
                                TTCAAG GATTCTCC GC TCA
                                |||||| |||||||| || |||
                                AAGTTC CTAAGAGG CG AGT
                                   C       A  A
GAM1622  LOC200803 3'  TGAGGCATGAGAATCGCTTGAA 90300           CC
                                TTCAAGTGATTCTC  GCCTCA
                                ||||||||||||||  ||||||
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                                AAGTTCGCTAAGAG  CGGAGT
                                      TA
GAM1622  LOC200904 5'  TGAGGCAGGAGAATCCCTTGAA 91786       T       C
                                TTCAAG GATTCTCC GCCTCA
                                |||||| |||||||| ||||||
                                AAGTTC CTAAGAGG CGGAGT
                                   C       A
GAM1622  LOC200918 3'  TGAGGCAGGAGAATCACTTGAA 90371             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  LOC200940 3'  TGAGGCAGGAGAATCACTAGAA 90397     A       C
                                TTC AGTGATTCTCC GCCTCA
                                ||| |||||||||| ||||||
                                AAG TCACTAAGAGG CGGAGT
                                  A         A
GAM1622  LOC201182 5'  TGAGGCAGGAGAATTGCTTGAA 91339       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  LOC201252 3'  TGAGGCATGAGAATCACTTGAA 89557            CC
                                TTCAAGTGATTCTC  GCCTCA
                                ||||||||||||  ||||||
                                AAGTTCACTAAGAG  CGGAGT
                                      TA
GAM1622  LOC201564 3'  GAGGCAGGAGAATTGCTTGAA  81275       TG      C
                                TTCAAG  ATTCTCC GCCTC
                                ||||||  ||||||| |||||
                                AAGTTC  TAAGAGG CGGAG
                                   GT      A
GAM1622  LOC201627 3'  TGAGATGTGAGAATCACTTGAA 90464            C  C
                                TTCAAGTGATTCTC CG CTCA
                                |||||||||||||| || ||||
                                AAGTTCACTAAGAG GT GAGT
                                      T  A
GAM1622  LOC201868 5'  GAGGCAGGAGAATTGCTTGAA  90526       TG      C
                                TTCAAG  ATTCTCC GCCTC
                                ||||||  ||||||| |||||
                                AAGTTC  TAAGAGG CGGAG
                                   GT      A
GAM1622  LOC201868 5'  TGAGGCACATGGACCACTTGAG 90533         A   TCCC
                                TTCAAGTG TTC    GCCTCA
                                |||||||| |||    ||||||
                                GAGTTCAC AGG    CGGAGT
                                     C   TACA
GAM1622  LOC201895 3'  GCAGGAGAATTGCTTGAA    90546       TG      C
                                TTCAAG  ATTCTCC GC
                                ||||||  ||||||| ||
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                                AAGTTC  TAAGAGG CG
                                   GT      A
GAM1622  LOC201931 3'  TGAGGCAGGAGGATCACT    90570          C
                                AGTGATTCTCC GCCTCA
                                |||||||||| ||||||
                                TCACTAGGAGG CGGAGT
                                      A
GAM1622  LOC203025 3'  GAGGCGGGTGGGTCACCTGAG  90748     A      T
                                TTCA GTGATTC CCCGCCTC
                                |||| ||||||| ||||||||
                                GAGT CACTGGG GGGCGGAG
                                  C      T
GAM1622  LOC203025 3'  TGAGGCAGGAGAATCGCTTGAA 90751            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  LOC203083 3'  TGAGGCAGGAGAATCACTTGAG 92096            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                GAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  LOC203276 3'  TGAGGCAGGAGAATCACTTGAA 92134            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  LOC203276 3'  TGAGGCAGGAGGATCCCTTGAG 92135       T      C
                                TTCAAG GATTCTCC GCCTCA
                                |||||| |||||||| ||||||
                                GAGTTC CTAGGAGG CGGAGT
                                   C       A
GAM1622  LOC203289 3'  TGAGGCAGGGGAATCACTTGAA 90872            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGGGG CGGAGT
                                      A
GAM1622  LOC203305 3'  TGAGGCAGGAGAATCACTTGAA 92187            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  LOC203305 3'  TGAGGCAGGAGGATCCCTTGAG 92188       T      C
                                TTCAAG GATTCTCC GCCTCA
                                |||||| |||||||| ||||||
                                GAGTTC CTAGGAGG CGGAGT
                                   C       A
GAM1622  LOC203350 3'  GAGGCAGGAAGATCACTTGAG  92241         TC   C
                                TTCAAGTGAT  TCC GCCTC
                                |||||||||  ||| |||||
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                                GAGTTCACTA  AGG CGGAG
                                      GA   A
GAM1622  LOC203378 3'  TGAGGCAGGAGAATCACATGAA 92306      A         C
                                TTCA GTGATTCTCC GCCTCA
                                |||| |||||||||| ||||||
                                AAGT CACTAAGAGG CGGAGT
                                  A         A
GAM1622  LOC203378 3'  TGAGGCAGGAGAATTGCGTGAA 92307      A TG      C
                                TTCA G  ATTCTCC GCCTCA
                                |||| |  ||||||| ||||||
                                AAGT C  TAAGAGG CGGAGT
                                  G GT      A
GAM1622  LOC203536 3'  TGAAAGTGGAAAGCACTTGAA  90945        ATTCTC    C_
                                TTCAAGTG     CCGC  TCA
                                ||||||||     ||||  |||
                                AAGTTCAC     GGTG  AGT
                                     GAAA__    AA
GAM1622  LOC205327 3'  AGGCAGGAGGATTGCTTGAG   91066       TG      C
                                TTCAAG  ATTCTCC GCCT
                                ||||||  ||||||| ||||
                                GAGTTC  TAGGAGG CGGA
                                   GT      A
GAM1622  LOC219406 3'  TGAGGCAGGAGAATCGCTTGAA 95208             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                          A
GAM1622  LOC219627 3'  AGGCAGGAAAATCGCTTGAA   93796          C   C
                                TTCAAGTGATT TCC GCCT
                                |||||||||| ||| ||||
                                AAGTTCGCTAA AGG CGGA
                                      A   A
GAM1622  LOC219627 3'  TGAGGCAGGAGAATCGCTTGAA 93814             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                          A
GAM1622  LOC219672 5'  TGAGGCAGAAGAATCGTTTGAA 92974           CCC
                                TTCAAGTGATTCT   GCCTCA
                                ||||||||||||   ||||||
                                AAGTTTGCTAAGA   CGGAGT
                                      AGA
GAM1622  LOC219672 3'  TGAGGCGGGAGGATTGCTTGAG 92975       TG
                                TTCAAG  ATTCTCCCGCCTCA
                                ||||||  ||||||||||||||
                                GAGTTC  TAGGAGGGCGGAGT
                                   GT
GAM1622  LOC219722 5'  TGAAGCAGAAGAATCACTTGAA 94688           CCC  C
                                TTCAAGTGATTCT   GC TCA
                                ||||||||||||   || |||
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                                AAGTTCACTAAGA   CG AGT
                                      AGA  A
GAM1622  LOC219919 3'  TGAGGCAGGAGAATCACTTGAG 94934             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                GAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  LOC219919 5'  TGAGGCAGGAGAATCCCTTGAA 94935       T       C
                                TTCAAG GATTCTCC GCCTCA
                                |||||| |||||||| ||||||
                                AAGTTC CTAAGAGG CGGAGT
                                   C       A
GAM1622  LOC220370 3'  GAGGCGGGAAGATCACTTGAG  94399          TC
                                TTCAAGTGAT  TCCCGCCTC
                                ||||||||||  |||||||||
                                GAGTTCACTA  AGGGCGGAG
                                      GA
GAM1622  LOC220370 3'  TGAGGCAGTAGAATCGCTTGAA 94403            CCC
                                TTCAAGTGATTCT   GCCTCA
                                ||||||||||||   ||||||
                                AAGTTCGCTAAGA   CGGAGT
                                      TGA
GAM1622  LOC220506 3'  TGAGGCAGGAGAATTGCTTGAA 74523       TG       C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT       A
GAM1622  LOC220662 3'  TGAGGCACAACAATCACTTGAG 92832          CTCCC
                                TTCAAGTGATT     GCCTCA
                                ||||||||||     ||||||
                                GAGTTCACTAA     CGGAGT
                                      CAACA
GAM1622  LOC220662 3'  TGAGGCAGGAGAATCGCTTGAA 92833             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  LOC220662 3'  TGAGGCAGGAGAATTCCTTGAA 92834       TG       C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   CT       A
GAM1622  LOC220906 3'  AGGCAGGAAAATCGCTTGAA   93028          C   C
                                TTCAAGTGATT TCC GCCT
                                |||||||||| ||| ||||
                                AAGTTCGCTAA AGG CGGA
                                      A   A
GAM1622  LOC220906 3'  TGAGGCAGGAGAATCGCTTGGA 93039             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
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                                AGGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  LOC221042 3'  TGAGGCAGGAGAATCGCTTGAA 94809            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  LOC221069 3'  TGAGGCAGGAGAATTGATTGAA 94822      GT      C
                                TTCAA  GATTCTCC GCCTCA
                                |||||  |||||||| ||||||
                                AAGTT  TTAAGAGG CGGAGT
                                   AG       A
GAM1622  LOC221410 3'  TGAGGCAGAAGAATCGCTTGAA 93700          CCC
                                TTCAAGTGATTCT   GCCTCA
                                ||||||||||||   ||||||
                                AAGTTCGCTAAGA   CGGAGT
                                      AGA
GAM1622  LOC221474 3'  TGAGACAGGAGAATCACTTGAA 94002            CGC
                                TTCAAGTGATTCTCC   CTCA
                                ||||||||||||||   ||||
                                AAGTTCACTAAGAGG   GAGT
                                      ACA
GAM1622  LOC221477 3'  TGAGGCAGGAAAATTGCTTGAA 93779      TG   C   C
                                TTCAAG  ATT TCC GCCTCA
                                ||||||  ||| ||| ||||||
                                AAGTTC  TAA AGG CGGAGT
                                    GT   A   A
GAM1622  LOC221477 3'  TGAGGCAGGCAGATCACTTGAG 93780         CT  C
                                TTCAAGTGATT  CC GCCTCA
                                ||||||||||  || ||||||
                                GAGTTCACTAG  GG CGGAGT
                                      AC  A
GAM1622  LOC221489 3'  TGAGGCGAGATAATCGCTTGAA 95291          C  C
                                TTCAAGTGATT TC CGCCTCA
                                ||||||||||| || |||||||
                                AAGTTCGCTAA AG GCGGAGT
                                      T  A
GAM1622  LOC221490 3'  TGAGGCAGGAGAATCGCTTGAA 95308            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  LOC221543 3'  TGAGGCAGGAGAATTGCTTGAA 95389      TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                    GT      A
GAM1622  LOC221795 3'  TGAGGCAGGAGAATCACTTGAG 94082            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
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                                  GAGTTCACTAAGAGG CGGAGT
                                        A
GAM1622  LOC221943 5'  TGAGGCAGGAGAATCGTTTGAA 95626            C
                                  TTCAAGTGATTCTCC GCCTCA
                                  ||||||||||||||| ||||||
                                  AAGTTTGCTAAGAGG CGGAGT
                                        A
GAM1622  LOC221954 5'  TGAGGCAGGAGAATCGCTTGAA 95654            C
                                  TTCAAGTGATTCTCC GCCTCA
                                  ||||||||||||||| ||||||
                                  AAGTTCGCTAAGAGG CGGAGT
                                        A
GAM1622  LOC221954 5'  TGAGGCAGGCGGACACTTGAG  95655        A   T  C
                                  TTCAAGTG TTC CC GCCTCA
                                  |||||||| ||| || ||||||
                                  GAGTTCAC AGG GG CGGAGT
                                       _  C  A
GAM1622  LOC221962 3'  TGAGACGGGAAAATTGCTTGAA 94245       TG   C     C
                                  TTCAAG  ATT TCCCG CTCA
                                  ||||||  ||| ||||| ||||
                                  AAGTTC  TAA AGGGC GAGT
                                     GT   A     A
GAM1622  LOC222066 3'  TGAGGCAGGAAAATCACTTGAA 94325          C   C
                                  TTCAAGTGATT TCC GCCTCA
                                  |||||||||| ||| ||||||
                                  AAGTTCACTAA AGG CGGAGT
                                        A   A
GAM1622  LOC222160 3'  TGAGATGGGAGGATCACTTGAA 95794             C
                                  TTCAAGTGATTCTCCCG CTCA
                                  |||||||||||||||| ||||
                                  AAGTTCACTAGGAGGGT GAGT
                                        A
GAM1622  LOC222182 3'  TGAGGCAGGAGAATCACTTGAA 95863            C
                                  TTCAAGTGATTCTCC GCCTCA
                                  ||||||||||||||| ||||||
                                  AAGTTCACTAAGAGG CGGAGT
                                        A
GAM1622  LOC253532 3'  AGGCAGGCGGATCACTTGAG   97728          T  C
                                  TTCAAGTGATTC CC GCCT
                                  |||||||||||| || ||||
                                  GAGTTCACTAGG GG CGGA
                                        C  A
GAM1622  LOC253612 5'  TGAGGCAAGAGAATCACTGGAA 98561     A        CC
                                  TTC AGTGATTCTC  GCCTCA
                                  ||| ||||||||||  ||||||
                                  AAG TCACTAAGAG  CGGAGT
                                    G         AA
GAM1622  LOC253639 3'  TGAGGCAGGAGAATCACTTGAA 97519            C
                                  TTCAAGTGATTCTCC GCCTCA
                                  ||||||||||||||| ||||||
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                                  AAGTTCACTAAGAGG CGGAGT
                                        A
GAM1622  LOC253778 5'  TGAGGCAGGAGAGTCACTTGAA 96528            C
                                  TTCAAGTGATTCTCC GCCTCA
                                  ||||||||||||||| ||||||
                                  AAGTTCACTGAGAGG CGGAGT
                                        A
GAM1622  LOC253786 3'  TGAGGCAGGAGAATCGCTTGAA 98835            C
                                  TTCAAGTGATTCTCC GCCTCA
                                  ||||||||||||||| ||||||
                                  AAGTTCGCTAAGAGG CGGAGT
                                        A
GAM1622  LOC253906 3'  TGAGGCAGAAGGATTGCTTGAG 98300       TG    CCC
                                  TTCAAG  ATTCT   GCCTCA
                                  ||||||  |||||   ||||||
                                  GAGTTC  TAGGA   CGGAGT
                                     GT    AGA
GAM1622  LOC254041 5'  TGAGGCAGGAGAATCGCTTGAA 96558            C
                                  TTCAAGTGATTCTCC GCCTCA
                                  ||||||||||||||| ||||||
                                  AAGTTCGCTAAGAGG CGGAGT
                                        A
GAM1622  LOC254045 3'  TGAGACAGGAGAATCACTTGAA 98274            CGC
                                  TTCAAGTGATTCTCC   CTCA
                                  ||||||||||||||   ||||
                                  AAGTTCACTAAGAGG   GAGT
                                        ACA
GAM1622  LOC254176 3'  TGAGGCAGGAGAATCACTTGAG 99177            C
                                  TTCAAGTGATTCTCC GCCTCA
                                  ||||||||||||||| ||||||
                                  GAGTTCACTAAGAGG CGGAGT
                                        A
GAM1622  LOC254243 3'  TGAGGCAGGAGAATCACTTGAA 99273            C
                                  TTCAAGTGATTCTCC GCCTCA
                                  ||||||||||||||| ||||||
                                  AAGTTCACTAAGAGG CGGAGT
                                        A
GAM1622  LOC254243 3'  TGAGGCAGGAGGATCCCTTGAG 99274       T    C
                                  TTCAAG GATTCTCC GCCTCA
                                  |||||| |||||||| ||||||
                                  GAGTTC CTAGGAGG CGGAGT
                                     C     A
GAM1622  LOC254351 3'  TGAGGCAAGAAAATCGCTTGAA 96696          C  CC
                                  TTCAAGTGATT TC  GCCTCA
                                  |||||||||| ||  ||||||
                                  AAGTTCGCTAA AG  CGGAGT
                                        A  AA
GAM1622  LOC254531 5'  TGAGGCAGGAGAATTGCTTGAA 96675       TG    C
                                  TTCAAG  ATTCTCC GCCTCA
                                  ||||||  ||||||| ||||||
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                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  LOC254875 3'  AGGCAGGCGGATCACTTGAG   97772          T  C
                                TTCAAGTGATTC CC GCCT
                                |||||||||||| || ||||
                                GAGTTCACTAGG GG CGGA
                                      C  A
GAM1622  LOC255030 5'  TGAGTCAGGAGAATCACTTGAA 99087             CGC
                                TTCAAGTGATTCTCC   CTCA
                                ||||||||||||||   ||||
                                AAGTTCACTAAGAGG   GAGT
                                      ACT
GAM1622  LOC255031 3'  GAGGCAGGAGGATCACTTGAG  99035             C
                                TTCAAGTGATTCTCC GCCTC
                                |||||||||||||| |||||
                                GAGTTCACTAGGAGG CGGAG
                                      A
GAM1622  LOC255031 3'  TGAGGCAGGAGAATTACTTGAA 99045             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCATTAAGAGG CGGAGT
                                      A
GAM1622  LOC255042 3'  TGAGGCAGGAGAATCACTTGAA 97059             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  LOC255042 3'  TGAGGCAGGAGAATCGCTTGAA 97060             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  LOC255042 3'  TGAGGCGGGTGGATCACCTGAG 97061      A      T
                                TTCA GTGATTC CCCGCCTCA
                                |||| ||||||| |||||||||
                                GAGT CACTAGG GGGCGGAGT
                                  C      T
GAM1622  LOC255177 3'  TGAGGCAGGAGAATCACTT    98402           C
                                AAGTGATTCTCC GCCTCA
                                |||||||||||| ||||||
                                TTCACTAAGAGG CGGAGT
                                      A
GAM1622  LOC255196 3'  GAGGCGAGTGAATCACTTGAG  98958            TCC
                                TTCAAGTGATTC   CGCCTC
                                ||||||||||||   ||||||
                                GAGTTCACTAAG   GCGGAG
                                      TGA
GAM1622  LOC255196 5'  TGAGGCAGGAGGATTGCTGGA  98969      A TG      C
                                TTCA G  ATTCTCC GCCTCA
                                |||| |  ||||||| ||||||
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                                AGGT C  TAGGAGG CGGAGT
                                  _ GT      A
GAM1622  LOC255252 3'  AGGCGGGTGGCTCACTTGAG   96705        TT T
                                TTCAAGTGA  C CCCGCCT
                                |||||||||  | |||||||
                                GAGTTCACT  G GGGCGGA
                                   CG T
GAM1622  LOC255252 3'  TGAGGCAGGAGAATCGCTTGAA 96711             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                          A
GAM1622  LOC255328 3'  TGAGGCAGGAGAATCACTTGAA 98349             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                          A
GAM1622  LOC255461 3'  TGAGACGGGAAGACTGCTTGAA 99143       GA TC    C
                                TTCAAGT  T  TCCCG CTCA
                                |||||||  |  ||||| ||||
                                AAGTTCG  A  AGGGC GAGT
                                   TC GA    A
GAM1622  LOC255461 3'  TGAGGTGGGAGGATCACTTGAA 99144
                                TTCAAGTGATTCTCCCGCCTCA
                                ||||||||||||||||||||
                                AAGTTCACTAGGAGGGTGGAGT

GAM1622  LOC255516 3'  TGAGACGGGAAGACTGCTTGAA 99157       GA TC    C
                                TTCAAGT  T  TCCCG CTCA
                                |||||||  |  ||||| ||||
                                AAGTTCG  A  AGGGC GAGT
                                   TC GA    A
GAM1622  LOC255516 3'  TGAGGTGGGAGGATCACTTGAA 99158
                                TTCAAGTGATTCTCCCGCCTCA
                                ||||||||||||||||||||
                                AAGTTCACTAGGAGGGTGGAGT

GAM1622  LOC255624 3'  AGGTAGATCACTTGAG      96161          T  CCC
                                TTCAAGTGAT CT   GCCT
                                |||||||||| ||   ||||
                                GAGTTCACTA GA   TGGA
                                   _  ___
GAM1622  LOC255937 3'  GAGGCAGGCGGATCACTTGAG  97682           T  C
                                TTCAAGTGATTC CC GCCTC
                                |||||||||||| || |||||
                                GAGTTCACTAGG GG CGGAG
                                      C  A
GAM1622  LOC255971 3'  GAGGCGGGCGGATCACTTGAG  98312           T
                                TTCAAGTGATTC CCCGCCTC
                                |||||||||||| ||||||||
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                                GAGTTCACTAGG GGGCGGAG
                                      C
GAM1622  LOC255971 3'  TGAGGCAGGAGAATCGCTTGAA 98314            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  LOC256207 3'  TGAGGCAGGAAGATCACTTGAA 96881          TC  C
                                TTCAAGTGAT  TCC GCCTCA
                                ||||||||||  ||| ||||||
                                AAGTTCACTA  AGG CGGAGT
                                      GA  A
GAM1622  LOC256207 3'  TGAGGCAGGAGAATCGCTTGAA 96882            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  LOC256267 3'  TGAGACAGGAGAATCTCTTGAA 98616       T      CGC
                                TTCAAG GATTCTCC   CTCA
                                |||||| ||||||||  ||||
                                AAGTTC CTAAGAGG   GAGT
                                    T       ACA
GAM1622  LOC256277 3'  TGAAGCGGGTAGATCACTTGAG 96356          CT    C
                                TTCAAGTGATT  CCCGC TCA
                                ||||||||||  ||||| |||
                                GAGTTCACTAG  GGGCG AGT
                                      AT    A
GAM1622  LOC256515 3'  TGAGGCAGGAGAATCACTTGAG 98219            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                GAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  LOC256515 5'  TGAGGCAGGAGAATCCCTTGAA 98220       T      C
                                TTCAAG GATTCTCC GCCTCA
                                |||||| |||||||| ||||||
                                AAGTTC CTAAGAGG CGGAGT
                                    C       A
GAM1622  LOC256520 3'  TGAGGCACAAGAATCGCTTGAA 97671           CCC
                                TTCAAGTGATTCT   GCCTCA
                                ||||||||||||   ||||||
                                AAGTTCGCTAAGA   CGGAGT
                                      ACA
GAM1622  LOC256544 3'  TGAGGCAGGGGAATCACTTGAA 97936            C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGGGG CGGAGT
                                      A
GAM1622  LOC256594 3'  TGAGGCAGGAGAATCACTT   98869            C
                                AAGTGATTCTCC GCCTCA
                                |||||||||||| ||||||
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                                TTCACTAAGAGG CGGAGT
                                      A
GAM1622  LOC256594 5'  TGAGGCAGGAGAATTGCTTGAA 98870       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  LOC256658 3'  TGAGGCAGGAGAATCGTTTG   99148           C
                                CAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                GTTTGCTAAGAGG CGGAGT
                                      A
GAM1622  LOC256980 3'  GGCAGAAGGATCACCTGAA    96931      A       CCC
                                TTCA GTGATTCT   GCC
                                |||| ||||||||   |||
                                AAGT CACTAGGA   CGG
                                  C       AGA
GAM1622  LOC257282 5'  TGAGGCAGAAGTATTGCTTGAA 98138       TG  T  CCC
                                TTCAAG  AT CT   GCCTCA
                                ||||||  || ||   ||||||
                                AAGTTC  TA GA   CGGAGT
                                   GT  T  AGA
GAM1622  LOC257354 3'  TGAGGCAGAAGGATTGCTTGGA 96797       TG    CCC
                                TTCAAG  ATTCT   GCCTCA
                                ||||||  |||||   ||||||
                                AGGTTC  TAGGA   CGGAGT
                                   GT    AGA
GAM1622  LOC257489 3'  AGGCAAGAATCACTGAA     66227      A       CCC
                                TTCA GTGATTCT   GCCT
                                |||| ||||||||   ||||
                                AAGT CACTAAGA   CGGA
                                  _       A__
GAM1622  LOC257596 3'  TGAGGCAGGAGAATTGCTTGAA 99792       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  LOC51003  3'  GGCTTTAAGAATCACTGAA    32671      A       CCC_
                                TTCA GTGATTCT    GCC
                                |||| ||||||||   |||
                                AAGT CACTAAGA    CGG
                                  _       ATTT
GAM1622  LOC51145  3'  TGAGGCAGGAGAATCACTTG   32929           C
                                CAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                GTTCACTAAGAGG CGGAGT
                                      A
GAM1622  LOC51279  3'  TGAGGCAGGAGAATCACTTGAA 33765             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
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                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  LOC51333  3'  TGAGGCATGAGAATCACTTGAA 34058          CC
                                TTCAAGTGATTCTC  GCCTCA
                                |||||||||||||  ||||||
                                AAGTTCACTAAGAG  CGGAGT
                                      TA
GAM1622  LOC51336  3'  GAGGCAGGCGGATCACTTGAG  34071         T  C
                                TTCAAGTGATTC CC GCCTC
                                ||||||||||| || |||||
                                GAGTTCACTAGG GG CGGAG
                                      C  A
GAM1622  LOC51336  3'  TGAGGCAGGAGAATCACTTGAA 34080          C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  LOC51759  3'  TGAGGCAGGAGAATTGCTTGAA 73174       TG     C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  LOC54518  3'  TGAGGCAGGAGGATCACTTGAG 39301          C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||| ||||||
                                GAGTTCACTAGGAGG CGGAGT
                                      A
GAM1622  LOC55974  3'  TGAGGCAGGAGAATTGCTTGAA 38749       TG     C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  LOC57118  3'  TGAGGCAGGAGAATCACTTGAA 40229          C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  LOC89890  3'  TGAGGCAGGAGAATTGCTGAA  61210     A TG     C
                                TTCA G  ATTCTCC GCCTCA
                                |||| |  ||||||| ||||||
                                AAGT C  TAAGAGG CGGAGT
                                  _ GT      A
GAM1622  LOC90038  3'  TGAGGCAGGAGAATCACTTGAA 61817          C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  LOC90038  3'  TGAGGCAGGAGGATCCCTTGAG 61818       T     C
                                TTCAAG GATTCTCC GCCTCA
                                |||||| |||||||| ||||||
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                                GAGTTC CTAGGAGG CGGAGT
                                   C       A
GAM1622  LOC90072  5'  TGAGACAGGAGAATCTCTTGAA 61968       T       CGC
                                TTCAAG GATTCTCC   CTCA
                                |||||| ||||||||   ||||
                                AAGTTC CTAAGAGG   GAGT
                                   T       ACA
GAM1622  LOC90072  3'  TGAGGCACAAGAATCACTTGAA 61969           CCC
                                TTCAAGTGATTCT   GCCTCA
                                ||||||||||||   ||||||
                                AAGTTCACTAAGA   CGGAGT
                                       ACA
GAM1622  LOC90072  3'  TGAGGCAGGAGGATCGCTTGAG 61970            C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||| ||||||
                                GAGTTCGCTAGGAGG CGGAGT
                                       A
GAM1622  LOC90092  3'  TGAGGCAGAAGAATCGCTTGAA 62077           CCC
                                TTCAAGTGATTCT   GCCTCA
                                ||||||||||||   ||||||
                                AAGTTCGCTAAGA   CGGAGT
                                       AGA
GAM1622  LOC90141  3'  GCAGGAGGATCACTTGAG    62305           C
                                TTCAAGTGATTCTCC GC
                                ||||||||||||||| ||
                                GAGTTCACTAGGAGG CG
                                       A
GAM1622  LOC90233  3'  TGAGGCAGGAGAATCGCTTGAA 57198           C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                       A
GAM1622  LOC90321  3'  TGAGGCAGGAGAATTGCTTGAA 62940       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  LOC90580  3'  TGAGGCAAGAGAATCGCTTGAG 64111           CC
                                TTCAAGTGATTCTC  GCCTCA
                                ||||||||||||||  ||||||
                                GAGTTCGCTAAGAG  CGGAGT
                                       AA
GAM1622  LOC90591  3'  AGGCAGGTGGATCACTTGAG   64145          T  C
                                TTCAAGTGATTC CC GCCT
                                |||||||||||| || ||||
                                GAGTTCACTAGG GG CGGA
                                       T  A
GAM1622  LOC90591  3'  TGAGGCAGGAGAATCACTTGAA 64195           C
                                TTCAAGTGATTCTCC GCCTCA
                                ||||||||||||||| ||||||
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                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  LOC90591  3'  TGAGGCAGGAGAATTGCTTGAA 64196       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  LOC90624  3'  TGAGGCAGGAAAATCACTTGAA 64374         C   C
                                TTCAAGTGATT TCC GCCTCA
                                |||||||||||  ||| ||||||
                                AAGTTCACTAA AGG CGGAGT
                                      A  A
GAM1622  LOC90639  3'  TGAGGCAGGAGGATCACTTGAG 64418           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                GAGTTCACTAGGAGG CGGAGT
                                      A
GAM1622  LOC90777  3'  TGAGGCAGGAGGATCACTTGAA 64670           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAGGAGG CGGAGT
                                      A
GAM1622  LOC90784  5'  GAGGCAGGAGAATCACTTGAA  64697           C
                                TTCAAGTGATTCTCC GCCTC
                                |||||||||||||| |||||
                                AAGTTCACTAAGAGG CGGAG
                                      A
GAM1622  LOC90784  5'  TGAGGCAGGAGAATCACTTGAA 64703           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  LOC90785  3'  AGGCAGGAGAATCACTTGAA   64708           C
                                TTCAAGTGATTCTCC GCCT
                                |||||||||||||| ||||
                                AAGTTCACTAAGAGG CGGA
                                      A
GAM1622  LOC90841  5'  TGAGGCAGGAGAATCGCTTGAA 64874           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  LOC90918  5'  TGAGGGAGGAGAATCTCTTGAA 65007       T       CG
                                TTCAAG GATTCTCC  CCTCA
                                |||||| ||||||||  |||||
                                AAGTTC CTAAGAGG  GGAGT
                                   T       AG
GAM1622  LOC90979  3'  TGAGGCAGGAGAATTGCTTGAA 65140       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
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                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  LOC91035  3'  TGAGGCAGGAGAATCACTAGAA 65309     A         C
                                TTC AGTGATTCTCC GCCTCA
                                ||| |||||||||| ||||||
                                AAG TCACTAAGAGG CGGAGT
                                  A         A
GAM1622  LOC91056  3'  TGAGGCAGGAGAATTACTTGAA 96411             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCATTAAGAGG CGGAGT
                                          A
GAM1622  LOC91064  3'  TGAGGCAGGAGGATTGCTTGAA 65392       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAGGAGG CGGAGT
                                   GT      A
GAM1622  LOC91250  5'  AGGCAGGAGAATCGCTTGAA   65906            C
                                TTCAAGTGATTCTCC GCCT
                                |||||||||||||| ||||
                                AAGTTCGCTAAGAGG CGGA
                                          A
GAM1622  LOC91286  3'  TGAGGCAGGAGAATCGCTTGAA 66063             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                          A
GAM1622  LOC91380  3'  AGGCAGGAGAATTGCTTGAA   66434       TG      C
                                TTCAAG  ATTCTCC GCCT
                                ||||||  ||||||| ||||
                                AAGTTC  TAAGAGG CGGA
                                   GT      A
GAM1622  LOC91380  3'  TGAGGCAGGAGAATCACTTGAA 66456             C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                          A
GAM1622  LOC91380  3'  TGAGGCGGGTGGATCACCTGAG 66457      A      T
                                TTCA GTGATTC CCCGCCTCA
                                |||| ||||||| |||||||||
                                GAGT CACTAGG GGGCGGAGT
                                  C      T
GAM1622  LOC91442  3'  GAGGCATGAGAATCACTTGAA  66644            CC
                                TTCAAGTGATTCTC  GCCTC
                                ||||||||||||||  |||||
                                AAGTTCACTAAGAG  CGGAG
                                          TA
GAM1622  LOC91574  3'  GAGGCGGGCGGATCACTTGAG  67112            T
                                TTCAAGTGATTC CCCGCCTC
                                |||||||||||| ||||||||
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                                GAGTTCACTAGG GGGCGGAG
                                      C
GAM1622  LOC91750  3'  TGAGGCACGAGAATCGCTTGAA 67658          CC
                                TTCAAGTGATTCTC  GCCTCA
                                |||||||||||||  ||||||
                                AAGTTCGCTAAGAG  CGGAGT
                                      CA
GAM1622  LOC91862  3'  TGAGGCAGGAGAATCGCTTGAA 54575           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  LOC91947  3'  AGGAAAGATTCACTTGAA    68222        T  CCCG
                                TTCAAGTGA TCT    CCT
                                ||||||||| |||    |||
                                AAGTTCACT AGA    GGA
                                     T  AA__
GAM1622  LOC92223  3'  TGAGGCAGGAGAATCACTTGAA 69056           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCACTAAGAGG CGGAGT
                                      A
GAM1622  LOC92228  3'  GAGGCGGGGAGATCACCTGAG  69077     A     CT
                                TTCA GTGATT  CCCGCCTC
                                |||| ||||||  ||||||||
                                GAGT CACTAG  GGGCGGAG
                                  C     AG
GAM1622  LOC92228  3'  TGAGGCAGGAGAATCGCTTGAA 69081           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  LOC92267  3'  TGAGGCAGGAGAATCGCTTGAA 69180           C
                                TTCAAGTGATTCTCC GCCTCA
                                |||||||||||||| ||||||
                                AAGTTCGCTAAGAGG CGGAGT
                                      A
GAM1622  LOC92270  5'  TGAGACAGGAGAATTGCTTGAA 69191       TG      CGC
                                TTCAAG  ATTCTCC   CTCA
                                ||||||  |||||||   ||||
                                AAGTTC  TAAGAGG   GAGT
                                   GT      ACA
GAM1622  LOC92299  3'  TGAGGCAGGAGAATTGCTTGAA 69374       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622  LOC92405  3'  GAGGCAGGCGGATCACTT    69713        T  C
                                AAGTGATTC CC GCCTC
                                ||||||||| || |||||
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                                  TTCACTAGG GG CGGAG
                                        C  A
GAM1622  LOC92405  3'  TGAGGAAGGAGAATCGCTTGAA 69719            CG
                                  TTCAAGTGATTCTCC  CCTCA
                                  ||||||||||||||  |||||
                                  AAGTTCGCTAAGAGG  GGAGT
                                        AA
GAM1622  LOC92465  5'  GGCAGGAAAATCACTTGAA    69951          C   C
                                  TTCAAGTGATT TCC GCC
                                  |||||||||| ||| |||
                                  AAGTTCACTAA AGG CGG
                                        A   A
GAM1622  LOC92465  5'  TGAGGCAGGAGAAATCACTTGA 69958          _   C
               A                   TTCAAGTGATT CTCC GCCTCA
                                  |||||||||| |||| ||||||
                                  AAGTTCACTAA GAGG CGGAGT
                                        A   A
GAM1622  LOC92466  3'  TGAGACAGGAGAATCTCTTGAA 69972       T       CGC
                                  TTCAAG GATTCTCC   CTCA
                                  |||||| ||||||||   ||||
                                  AAGTTC CTAAGAGG   GAGT
                                     T       ACA
GAM1622  LOC92499  5'  TGAGGCAGGAGAATCGCTTGAA 70109            C
                                  TTCAAGTGATTCTCC GCCTCA
                                  |||||||||||||| ||||||
                                  AAGTTCGCTAAGAGG CGGAGT
                                        A
GAM1622  LOC92573  3'  TGAGGCAGGAGAATTGCTTGAA 70383       TG      C
                                  TTCAAG  ATTCTCC GCCTCA
                                  ||||||  ||||||| ||||||
                                  AAGTTC  TAAGAGG CGGAGT
                                     GT       A
GAM1622  LOC92771  3'  TGAGGCAGGAGAATTGCTTGAA 54216       TG      C
                                  TTCAAG  ATTCTCC GCCTCA
                                  ||||||  ||||||| ||||||
                                  AAGTTC  TAAGAGG CGGAGT
                                     GT       A
GAM1622  LOC92771  3'  TGAGGCAGGAGGATTGCCTGAG 54217      A TG      C
                                  TTCA G  ATTCTCC GCCTCA
                                  |||| |  ||||||| ||||||
                                  GAGT C  TAGGAGG CGGAGT
                                    C GT       A
GAM1622  LOC93070  3'  TGAGGCAGGAGAATCGCTGGAA 71816     A         C
                                  TTC AGTGATTCTCC GCCTCA
                                  ||| |||||||||| ||||||
                                  AAG TCGCTAAGAGG CGGAGT
                                    G          A
GAM1622  LOC93132  5'  TGAGGCAGGAGAATCACTTGAA 72002            C
                                  TTCAAGTGATTCTCC GCCTCA
                                  |||||||||||||| ||||||
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                                AAGTTCACTAAGAGG CGGAGT
                                       A
GAM1622 LOC93132 5' TGAGGCAGGAGAATTGCTTGAA 72003       TG      C
                                TTCAAG  ATTCTCC GCCTCA
                                ||||||  ||||||| ||||||
                                AAGTTC  TAAGAGG CGGAGT
                                   GT      A
GAM1622 LOC93259 5' TGAGTATCAGAATCACCTGGA  72297     A      CCCGC
                                TTCA GTGATTCT    CTCA
                                |||| ||||||||    ||||
                                AGGT CACTAAGA    GAGT
                                  C       CTAT_
GAM1622 LOC93613 3' GAGGCGGGCAGATCACTTGAG  73075          CT
                                TTCAAGTGATT  CCCGCCTC
                                ||||||||||  ||||||||
                                GAGTTCACTAG  GGGCGGAG
                                       AC
GAM1622 LOC93613 3' TGAGGCAGAAGGATTGCTGGA  73085     A TG    CCC
                                TTCA G  ATTCT   GCCTCA
                                |||| |  |||||   ||||||
                                AGGT C  TAGGA   CGGAGT
                                  _ GT    AGA
GAM1623 SCAMP1   3' GCTAAATAAATATTCTCC    18014     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1623 SCAMP1   3' GCTAAATAAATATTCTCC    54500     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1623 NX-17    3' TGAATATCAGCCCCTAATA    40706         ATA_
                                TATTAGGG    ATATTCA
                                ||||||||    |||||||
                                ATAATCCC    TATAAGT
                                     CGAC
GAM1623 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
              TA                  TATTAGGGATAATATTCATTTAGC
                                  |||||||||||||||||||||||
                                  ATAATCCCTATTATAAGTAAATCG

GAM1624 ABCD3    3' ACTACATGAAATAATGCACTGA 12661     ACAC    C_
                                TCA    CGTT  TTCATGTAGT
                                |||    ||||  ||||||||||
                                AGT    GTAA  AAGTACATCA
                                  CAC_    TA
GAM1624 MYO10    3' TGAAAAACACGTGTTGAC     25616         C_   C
                                GTCAACAC  GTT TTCA
                                ||||||||  ||| ||||
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                                CAGTTGTG  CAA AAGT
                                     CA   A
GAM1624  CCNB3    3'  ACATGAAGACACTGAC      54466      ACACC  _
                                GTCA    GT TCTTCATGT
                                ||||    || |||||||||
                                CAGT    CA AGAAGTACA
                                  _____  C
GAM1624  CGI-127  3'  ACCACATAATTGGTGTTGAT  32673          TTCTTC    A
                                GTCAACACCG     ATGT GT
                                ||||||||||     |||| ||
                                TAGTTGTGGT     TACA CA
                                     TAA___    C
GAM1624  KIAA1913  3'  TACATGAAGACAATGTTGAC  74321        CC  T
                                GTCAACA  GT CTTCATGTA
                                |||||||  || |||||||||
                                CAGTTGT  CA GAAGTACAT
                                     AA  _
GAM1624  LOC146733 5'  ACCTGAAAAGGGTGTTGAC   84779         G  C    T
                                GTCAACACC TT TTCA GT
                                ||||||||| || |||| ||
                                CAGTTGTGG AA AAGT CA
                                     G  _    C
GAM1624  LOC256520 3'  ACATTGTAAAGAAAGTGTTGAC 97660         CG     C___
                                GTCAACAC  TTCTT    ATGT
                                ||||||||  |||||    ||||
                                CAGTTGTG  AAGAA    TACA
                                     A_     ATGT
GAM1625  FGFR1    3'  GACCTGTCCATGCCCCTGGACC 43887         CC         A
              AG                    TTGGTTCA  GGCATGGACA GTC
                                ||||||||  |||||||||| |||
                                GACCAGGT  CCGTACCTGT CAG
                                     CC         C
GAM1625  PAPPA    3'  GACTCACATTGGGGCGAATGAA 11970         CCG  _____  GACA
              CCAA                   TTGGTTCA   GC    ATG    AGTC
                                ||||||||   ||    |||    ||||
                                AACCAAGT   CG    TAC    TCAG
                                     AAG  GGGT   AC__
GAM1625  FLJ10640  5'  GACTTGTCCACAAGAACTCAA  39235     _   ACCGGCA
                                TTG GTTC       TGGACAAGTC
                                ||| ||||       ||||||||||
                                AAC CAAG       ACCTGTTCAG
                                  T    AAC_____
GAM1625  MGC13090  5'  ACTTGTCCGCCAAGTAAACCA  52118      C  C_   AT
                                TGGTT AC  GGC  GGACAAGT
                                ||||| ||  |||  ||||||||
                                ACCAA TG  CCG  CCTGTTCA
                                  A  AA   __
GAM1625  LOC92340  3'  ACTTGCCCACAGCCACCAA    69555      TCACC   A_   A
                                TTGGT     GGC  TGG CAAGT
                                |||||     |||  ||| |||||
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                                AACCA    CCG  ACC GTTCA
                                  _____  AC   C
GAM1626  CBFA2T1   3'  CATTCTGGCAGTTTTGACA   16360        A __
                                TGTCAAGACT CC  GATG
                                |||||||||| ||  ||||
                                ACAGTTTTGA GG  TTAC
                                     C  TC
GAM1626  ERBB4     3'  GCCAGTAGTTTTGACA     19109         CGA
                                TGTCAAGACTAC   TGGT
                                ||||||||||||   ||||
                                ACAGTTTTGATG   ACCG
                                       ___
GAM1626  STAT1     5'  TAACCTCGACAGTCTTGGCA  24615        AC   T
                                TGTCAAGACT  CGA GGTTA
                                ||||||||||  ||| |||||
                                ACGGTTCTGA  GCT CCAAT
                                     CA  _
GAM1626  STAT1     5'  TAACCTCGACAGTCTTGGCA  58367        AC   T
                                TGTCAAGACT  CGA GGTTA
                                ||||||||||  ||| |||||
                                ACGGTTCTGA  GCT CCAAT
                                     CA  _
GAM1626  DKFZp434F1719 3'  ACCTTGGACAGTAGTCTTGAC  51008        ____   T
                                GTCAAGACTA   CCGA GGT
                                ||||||||||   |||| |||
                                CAGTTCTGAT   GGTT CCA
                                     GACA  _
GAM1626  FLJ10038  3'  TAACCATCAGCTTTGATA   36216      GA  ACC
                                TGTCAA  CT   GATGGTTA
                                ||||||  ||   ||||||||
                                ATAGTT  GA   CTACCAAT
                                   TC  ___
GAM1626  GW112     3'  GTAACCATCGTTATAGACA   22215     AAGAC  C
                                TGTC    TA CGATGGTTAC
                                ||||    || ||||||||||
                                ACAG    AT GCTACCAATG
                                  AT___  T
GAM1626  KIAA0157  5'  TAACCATCAGCCTTGTTCA   50752    T_   A  ACC
                                TG  CAAG CT   GATGGTTA
                                ||  |||| ||   ||||||||
                                AC  GTTC GA   CTACCAAT
                                 TT   C  ___
GAM1626  KIAA0844  3'  GTCTCCAGTAATCTTGGCA   30895       C   CGA   TT
                                TGTCAAGA TAC   TGG  AC
                                |||||||| |||   |||  ||
                                ACGGTTCT ATG   ACC  TG
                                     A  ___   TC
GAM1626  KIAA1894  3'  TAACTCTGTGAACAGTCTTGAC 74286        AC_  AT_
                                GTCAAGACT   CG   GGTTA
                                |||||||||   ||   |||||
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                                CAGTTCTGA  GT  TCAAT
                                     CAA  GTC
GAM1626  MGC1136   3'  TGGCTGGCAGTCTTGA     44038        A  GAT
                                TCAAGACT CC  GGTTA
                                |||||||| ||  |||||
                                AGTTCTGA GG  TCGGT
                                     C  ___
GAM1626  TRIM29    3'  ACCTCTCAGTGTCTTGACA   25003        T  C  T_
                                TGTCAAGAC AC GA  GGT
                                ||||||||| || ||  |||
                                ACAGTTCTG TG CT  CCA
                                     _  A  CT
GAM1626  LOC130813 3'  AATCATTGTAGCCTTGA     76258      A   C
                                TCAAG CTAC GATGGTT
                                ||||| |||| |||||||
                                AGTTC GATG TTACTAA
                                   C   _
GAM1626  LOC144266 5'  TAATTATGGTAATTTTGACA   77270       C   G
                                TGTCAAGA TACC ATGGTTA
                                |||||||| |||| |||||||
                                ACAGTTTT ATGG TATTAAT
                                     A   _
GAM1626  LOC151602 3'  CATTTTAATGGTCTTGACA    81105         CC__
                                TGTCAAGACTA   GATG
                                ||||||||||   ||||
                                ACAGTTCTGGT   TTAC
                                      AATT
GAM1626  LOC152179 5'  TAATCATTGTAGTCCATGACA  86744      A_    C
                                TGTCA  GACTAC GATGGTTA
                                |||||  |||||| ||||||||
                                ACAGT  CTGATG TTACTAAT
                                   AC    _
GAM1627  ITGA6     3'  TCACAAGACTATGCCA      5793         A   ACCC
                                TGGCATGG TCTT   GTGA
                                |||||||| ||||   ||||
                                ACCGTATC AGAA   CACT
                                     _  _____
GAM1627  TGM4      3'  CACCATAGAGACCCATGTCA   13721        A   ACCC
                                TGGCATGG TCTT   GTG
                                |||||||| ||||   |||
                                ACTGTACC AGAG   CAC
                                     C   ATAC
GAM1627  FLJ22615  3'  TGTCACCTGAGATCCAGCCA  69041     A       CCC
                                TGGC TGGATCTTA  GTGACA
                                |||| |||||||||  ||||||
                                ACCG ACCTAGAGT  CACTGT
                                   _       C__
GAM1627  KIAA0451  3'  TGTCACAAAAGACTCCTCACCA 29784    CAT  _   ACCC
                                TGG  GGA TCTT   GTGACA
                                |||  ||| ||||   ||||||
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                                ACC   CCT AGAA    CACTGT
                                  ACT   C    AA__
GAM1627  LOC118611 5'  TGTCACGCCAGCGATCATGCCA 75997       G   TTACC
                                TGGCATG ATC     CGTGACA
                                ||||||| |||     |||||||
                                ACCGTAC TAG     GCACTGT
                                   _   CGACC
GAM1627  LOC143914 5'  CACCAGGCCAAGCCCATGCCA  77109       AT   A_  C_
                                TGGCATGG  CTT  CC  GTG
                                ||||||||  |||  ||  |||
                                ACCGTACC  GAA  GG  CAC
                                     C_   CC  AC
GAM1627  LOC146434 3'  GGGATGCAAAATCCATGTCA   78455         C  A___
                                TGGCATGGAT TT    CCC
                                |||||||||| ||    |||
                                ACTGTACCTA AA    GGG
                                      A  CGTA
GAM1627  LOC152048 3'  TGTCACGAGGGATCCAGCCA   86736     A     TTA  _
                                TGGC TGGATC   CC CGTGACA
                                |||| ||||||   || |||||||
                                ACCG ACCTAG   GG GCACTGT
                                  _     ____ A
GAM1627  LOC157567 5'  CATAATAAGATCCTTGCCA    82390      T      CCC
                                TGGCA GGATCTTA   GTG
                                ||||| ||||||||   |||
                                ACCGT CCTAGAAT   TAC
                                   T       AA_
GAM1627  LOC158709 5'  TACCAGTAAATCCATGC     82866        C    CC
                                GCATGGAT TTAC  GTG
                                |||||||| ||||  |||
                                CGTACCTA AATG  CAT
                                     _   AC
GAM1627  LOC90841  3'  TGGATAAAATCCAAGCCA    64875     A    C  C
                                TGGC TGGAT TTA CCG
                                |||| ||||| ||| |||
                                ACCG ACCTA AAT GGT
                                  A    A  A
GAM1628  ADAM17    3'  TCCAGCCTGGGTGACAGAGTGA 41847          TG
            GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                       GT
GAM1628  ADAM17    3'  TCCAGCCTGGGTGACAGAGTGA 41848          TG
            GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                       GT
GAM1628  ADAT1     3'  TCCAGCCTGGGTGATAGAGCAA 24919     C      TG
            GA                    TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
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                                AGA CGAGATA  GGGTCCGACCT
                                  A      GT
GAM1628  ADCY2    3'  CCTGGGCAACATAGCAAGA   65646     C   C
                                TCT GCT TGTTGCCCAGG
                                ||| ||| ||||||||||
                                AGA CGA ACAACGGGTCC
                                  A   T
GAM1628  ADCY2    3'  TCCAGCCTGGGTGACAGAGCGA 65655           TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      GT
GAM1628  AICDA    3'  TCCAGCCTGGGCGACAAGAGC  40698       _
                                GCTCT GTTGCCCAGGCTGGA
                                ||||| ||||||||||||||
                                CGAGA CAGCGGGTCCGACCT
                                   A
GAM1628  AK1      3'  TCCAGCCTGGGTGACAGAGCAA 6641      C      TG
                GA                TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM1628  ALDH3A2  3'  TCAGCTTGGGCAACAGAGCAAG 69803     C
                A                 TCT GCTCTGTTGCCCAGGCTGG
                                ||| ||||||||||||||||||
                                AGA CGAGACAACGGGTTCGACT
                                  A
GAM1628  ALPP     3'  CCTGGGCGACAGAGCGAGA   69415
                                TCTCGCTCTGTTGCCCAGG
                                ||||||||||||||||||
                                AGAGCGAGACAGCGGGTCC

GAM1628  ANKH     3'  TCCAGCCTGAGCAACAGAGC   55072          C
                                GCTCTGTTGC CAGGCTGGA
                                |||||||||| |||||||||
                                CGAGACAACG GTCCGACCT
                                      A
GAM1628  ANKH     3'  TCCAGCCTGGGTGACAAGAGC  55074       _  TG
                                GCTCT GT  CCCAGGCTGGA
                                ||||| ||  ||||||||||
                                CGAGA CA  GGGTCCGACCT
                                   A  GT
GAM1628  APAF1    3'  TCCAGCCTGGGTGACATAGCAA 25984     C   C   TG
                GA                TCT GCT TGT  CCCAGGCTGGA
                                ||| ||| |||  ||||||||||
                                AGA CGA ACA  GGGTCCGACCT
                                  A   T   GT
GAM1628  APOC4    3'  CCTGGGCAACACAGCGAGA   9705         C
                                TCTCGCT TGTTGCCCAGG
                                ||||||| ||||||||||
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                                AGAGCGA ACAACGGGTCC
                                   C
GAM1628 APOL1    3' TCCAGCCTGGGTGACAGAGCGA 14745          TG
           GA                    TCTCGCTCTGT CCCAGGCTGGA
                                 |||||||||||  ||||||||||
                                 AGAGCGAGACA  GGGTCCGACCT
                                      GT
GAM1628 ARHGEF6  3' CCAACCTAGGTAACAGAG    68754         C  C
                                 CTCTGTTGCC AGG TGG
                                 |||||||||| ||| |||
                                 GAGACAATGG TCC ACC
                                      A  A
GAM1628 ARSD     3' TCCAGCCTGGGCCACATAGCAA 9800     C  C  T
           GA                    TCT GCT TGT GCCCAGGCTGGA
                                 ||| ||| ||| ||||||||||||
                                 AGA CGA ACA CGGGTCCGACCT
                                   A  T  C
GAM1628 ATM      3' TCCAGCCTGGGAGACAGAGCGA 5303          TG
           GA                    TCTCGCTCTGT CCCAGGCTGGA
                                 |||||||||||  ||||||||||
                                 AGAGCGAGACA  GGGTCCGACCT
                                      GA
GAM1628 ATM      3' TCCAGCCTGGGTGACAAGAGCG 5304        _ TG
           A                     TCGCTCT GT  CCCAGGCTGGA
                                 |||||||  ||  ||||||||||
                                 AGCGAGA CA  GGGTCCGACCT
                                    A  GT
GAM1628 BCAS1    3' CCTGGGCGACAGAGCAAGA   14710    C
                                 TCT GCTCTGTTGCCCAGG
                                 ||| ||||||||||||||
                                 AGA CGAGACAGCGGGTCC
                                   A
GAM1628 BPHL     3' TCCAACCTGGGCAACAGAGTAA 16336    CG          C
           GA                    TCT  CTCTGTTGCCCAGG TGGA
                                 |||  |||||||||||||| ||||
                                 AGA  GAGACAACGGGTCC ACCT
                                   AT           A
GAM1628 BRCA1    5' TCCAGCCTGGGCGACAGAGCGA 24576
           GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                 ||||||||||||||||||||||||
                                 AGAGCGAGACAGCGGGTCCGACCT

GAM1628 BRCA1    3' TCCAGCCTGGGTGACAGTGAGA 24577       CT  TG
                                 TCTCGCT  GT  CCCAGGCTGGA
                                 |||||||  ||  ||||||||||
                                 AGAGTGA  CA  GGGTCCGACCT
                                     __  GT
GAM1628 BRCA1    3' TCCAGCCTGGGTGACAGTGAGA 24578       CT  TG
                                 TCTCGCT  GT  CCCAGGCTGGA
                                 |||||||  ||  ||||||||||
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                                AGAGTGA  CA  GGGTCCGACCT
                                   __  GT
GAM1628  BRCA1    3'  TCCAGCCTGGGTGACAGTGAGA 24579       CT  TG
                                TCTCGCT  GT  CCCAGGCTGGA
                                |||||||  ||  ||||||||||||
                                AGAGTGA  CA  GGGTCCGACCT
                                   __  GT
GAM1628  BRCA1    3'  TCCAGCCTGGGTGACAGTGAGA 24580       CT  TG
                                TCTCGCT  GT  CCCAGGCTGGA
                                |||||||  ||  ||||||||||||
                                AGAGTGA  CA  GGGTCCGACCT
                                   __  GT
GAM1628  C1orf1   3'  TCCAGCCTAGGCGACAGAGTGA 8683             C
            GA                    TCTCGCTCTGTTGCC AGGCTGGA
                                ||||||||||||||| ||||||||
                                AGAGTGAGACAGCGG TCCGACCT
                                         A
GAM1628  CARKL    3'  TCCAGCCTGGGTGACAGAGCAA 26109     C      TG
            GA                    TCT GCTCTGT  CCCAGGCTGGA
                                |||  |||||||  ||||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM1628  CASP10   3'  TCCAGCTTGGGCAACAGGGCGA 53264
            GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGCGGGACAACGGGTTCGACCT

GAM1628  CASP10   3'  TCCAGCTTGGGCAACAGGGCGA 53265
            GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGCGGGACAACGGGTTCGACCT

GAM1628  CASP6    3'  TCCAGCCTGGGCAACGAGTGA  53366       T
                                TCGCTC GTTGCCCAGGCTGGA
                                ||||||  ||||||||||||||||
                                AGTGAG CAACGGGTCCGACCT
                                   _
GAM1628  CASP6    3'  TCCAGCCTGGGCAACGAGTGA  8735        T
                                TCGCTC GTTGCCCAGGCTGGA
                                ||||||  ||||||||||||||||
                                AGTGAG CAACGGGTCCGACCT
                                   _
GAM1628  CD28     3'  TCCAGCCTGGGCGACAGAGTGA 21558
            GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGACAGCGGGTCCGACCT

GAM1628  CD68     3'  TCCAGCCTGGGCGACAGAGCCA 60508     C
            GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                |||  ||||||||||||||||||
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                                AGA CGAGACAGCGGGTCCGACCT
                                  C
GAM1628 CEACAM5  3'  TCCAGTCTGGCAACAGAGCAAG 16425     C         C
             A                   TCT GCTCTGTTGCC AGGCTGGA
                                 ||| |||||||||| ||||||||
                                 AGA CGAGACAACGG TCTGACCT
                                  A         _
GAM1628 CENPB    3'  TCCAGCCTAGGCCCCCTGCAAG 70119     C  TCTGTT   C
             G                   TCT GC      GCC AGGCTGGA
                                 ||| ||      ||| ||||||||
                                 GGA CG      CGG TCCGACCT
                                  A  TCCCC_   A
GAM1628 CNGB1    3'  CTGGGCAACATAGCGAGA     8935         C
                                 TCTCGCT TGTTGCCCAG
                                 ||||||| ||||||||||
                                 AGAGCGA ACAACGGGTC
                                     T
GAM1628 COPA     3'  TCCAGCCTGGGTGACAGAGCAA 16480     C      TG
             GA                    TCT GCTCTGT  CCCAGGCTGGA
                                   ||| |||||||  ||||||||||
                                   AGA CGAGACA  GGGTCCGACCT
                                    A       GT
GAM1628 CPM      3'  TCCAGCTTGGGCAACAGAGTAA 60411     CG
             GA                    TCT  CTCTGTTGCCCAGGCTGGA
                                   |||  ||||||||||||||||||
                                   AGA  GAGACAACGGGTTCGACCT
                                    AT
GAM1628 CPT2     3'  CCTGGGCGACAGAGCGAGA    5424
                                 TCTCGCTCTGTTGCCCAGG
                                 ||||||||||||||||||
                                 AGAGCGAGACAGCGGGTCC

GAM1628 CTMP     3'  TCCAACCTGGGCAACAGAACAA 54954      CGC          C
             GA                    TCT   TCTGTTGCCCAGG TGGA
                                   |||   |||||||||||| ||||
                                   AGA   AGACAACGGGTCC ACCT
                                    ACA           A
GAM1628 CUBN     3'  TCCAGCCTGGGCGAGACGGCAA 8425      C   CTG
             GA                    TCT GCT   TTGCCCAGGCTGGA
                                   ||| |||   ||||||||||||||
                                   AGA CGG   AGCGGGTCCGACCT
                                    A   CAG
GAM1628 CYP4F3   3'  TCCAGCCTGGGTGAAAGAGCTA 8015      C     G TG
             GA                    TCT GCTCT T  CCCAGGCTGGA
                                   ||| ||||| |  ||||||||||
                                   AGA CGAGA A  GGGTCCGACCT
                                    T     A GT
GAM1628 DBT      3'  TCCAGCCTGGGCGACAGAGCAA 10379     C
             GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                   ||| ||||||||||||||||||||
```

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                                AGA CGAGACAGCGGGTCCGACCT
                                  A
GAM1628 DBT     3' TCCAGCCTGGGTGGCAGAGC  10380       TG
                                GCTCTGT  CCCAGGCTGGA
                                |||||||  ||||||||||
                                CGAGACG  GGGTCCGACCT
                                    GT
GAM1628 DCLRE1C  3' TCCAGCCTGGGCAACAAGAGC 42822      _
                                GCTCT GTTGCCCAGGCTGGA
                                ||||| ||||||||||||||
                                CGAGA CAACGGGTCCGACCT
                                   A
GAM1628 DDOST    3' TCCAGCCTGGGCAACAGTGT  19066    T
                                GC CTGTTGCCCAGGCTGGA
                                || ||||||||||||||||
                                TG GACAACGGGTCCGACCT
                                 T
GAM1628 DFFA    3' TCCAGCCTGGGCAACAGAGCGA 16598
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAACGGGTCCGACCT

GAM1628 DGKI    5' TCCAGCCTGGGCGACAAAGCAA 17529     C  C
                GA                TCT GCT TGTTGCCCAGGCTGGA
                                  ||| ||| ||||||||||||||||
                                  AGA CGA ACAGCGGGTCCGACCT
                                    A  A
GAM1628 DMC1    3' TCCAGCCTAGGTGACAGAGTGA 23947          TG  C
                GA                TCTCGCTCTGT  CC AGGCTGGA
                                  ||||||||||  || ||||||||
                                  AGAGTGAGACA  GG TCCGACCT
                                       GT  A
GAM1628 DSC1    3' TCCAGCCTGGGCAACAAGAGCG 44606      _
                A                 TCGCTCT GTTGCCCAGGCTGGA
                                  ||||||| |||||||||||||||
                                  AGCGAGA CAACGGGTCCGACCT
                                     A
GAM1628 DSC1    3' TCCAGCCTGGGCAACAAGAGCG 44607      _
                A                 TCGCTCT GTTGCCCAGGCTGGA
                                  ||||||| |||||||||||||||
                                  AGCGAGA CAACGGGTCCGACCT
                                     A
GAM1628 DVL3    3' TCCAGCCTGGGTGACAGAGTGA 16651          TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                       GT
GAM1628 EGFL4   3' TCCAACCTGGGTGACAGAGCGA 62475          TG    C
                GA                TCTCGCTCTGT  CCCAGG TGGA
                                  ||||||||||  ||||||  ||||
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                                AGAGCGAGACA  GGGTCC ACCT
                                      GT     A
GAM1628  EGFL5    3'  TCCAGCCTGGGCGACAGAGCAA 87921     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAGCGGGTCCGACCT
                                      A
GAM1628  F2R      3'  TCCAGCCTGGGCAACAGAGCAA 10573     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAACGGGTCCGACCT
                                      A
GAM1628  F2RL3    3'  TCCAGCCTGGGCAACAGAGCAA 15527     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAACGGGTCCGACCT
                                      A
GAM1628  FANCC    3'  TCCAGCCTGGGCAACAGAGCGA 71049
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    |||||||||||||||||||||||||
                                    AGAGCGAGACAACGGGTCCGACCT

GAM1628  FCAR     3'  TCCAGCCTGGGTGACAGAACGA 56582       C     TG
                GA                  TCTCG TCTGT  CCCAGGCTGGA
                                    ||||| |||||  ||||||||||
                                    AGAGC AGACA  GGGTCCGACCT
                                      A     GT
GAM1628  FCAR     3'  TCCAGCCTGGGTGACAGAACGA 10594       C     TG
                GA                  TCTCG TCTGT  CCCAGGCTGGA
                                    ||||| |||||  ||||||||||
                                    AGAGC AGACA  GGGTCCGACCT
                                      A     GT
GAM1628  FGF2     3'  TCCAGCCTAGGCAACAGAGTGA 10622              C
                GA                  TCTCGCTCTGTTGCC AGGCTGGA
                                    |||||||||||||| ||||||||
                                    AGAGTGAGACAACGG TCCGACCT
                                          A
GAM1628  FGFR2    3'  TCCAGCCTTGGCGACAGAGCGA 5566               C
                GA                  TCTCGCTCTGTTGCC AGGCTGGA
                                    |||||||||||||| ||||||||
                                    AGAGCGAGACAGCGG TCCGACCT
                                          T
GAM1628  FLRT2    5'  TCCAGCCTAAGCAACAGAGCAA 26004     C         CC
                GA                  TCT GCTCTGTTGC  AGGCTGGA
                                    ||| ||||||||||  ||||||||
                                    AGA CGAGACAACG  TCCGACCT
                                      A         AA
GAM1628  FUT6     3'  TCCAACCTGGACGACAGAGCAA 5644      C        C     C
                GA                  TCT GCTCTGTTG CCAGG TGGA
                                    ||| ||||||||| ||||| ||||
```

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                                AGA CGAGACAGC GGTCC ACCT
                                  A       A    A
GAM1628  GALNT7   3'  TCCAACCTGGGTGACAGAGTGA 55090          TG    C
                GA                  TCTCGCTCTGT  CCCAGG TGGA
                                    ||||||||||  |||||| ||||
                                    AGAGTGAGACA  GGGTCC ACCT
                                          GT     A
GAM1628  GAMT     3'  CCTGGGCTACAGAGCAAGA   5672      C      T
                                    TCT GCTCTGT GCCCAGG
                                    ||| ||||||| |||||||
                                    AGA CGAGACA CGGGTCC
                                      A      T
GAM1628  GGCX     3'  CCTGGGCAACAGAGCAAGA   7703      C
                                    TCT GCTCTGTTGCCCAGG
                                    ||| ||||||||||||||
                                    AGA CGAGACAACGGGTCC
                                      A
GAM1628  GM2A     3'  TCCAGCCTGGTGACAGAGTGAG 68390          TG  C
                A                    TCTCGCTCTGT  CC AGGCTGGA
                                    ||||||||||  || ||||||||
                                    AGAGTGAGACA  GG TCCGACCT
                                          GT  _
GAM1628  GP2      3'  TCCAGCCTGGGCAACAGAGCAA 9483      C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAACGGGTCCGACCT
                                      A
GAM1628  GRAF     3'  TCCAGCCTGGGTGACAGAGCCA 31248     C      TG
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGAGACA  GGGTCCGACCT
                                      C      GT
GAM1628  GRM3     3'  TCCAGAATATGGAAACAGAGC  7746         GC   GG__
                                    GCTCTGTT  CCA    CTGGA
                                    ||||||||  |||    |||||
                                    CGAGACAA  GGT    GACCT
                                         A_   ATAA
GAM1628  GRM6     3'  TCCAGCCTGGGTGACAGAGCGA 7772          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGCGAGACA  GGGTCCGACCT
                                          GT
GAM1628  GTF2F1   3'  TCCAGCCTGGGTGACAGAATGA 10893     C     TG
                                    TCG TCTGT  CCCAGGCTGGA
                                    ||| |||||  ||||||||||
                                    AGT AGACA  GGGTCCGACCT
                                      A    GT
GAM1628  GTF2F1   3'  TCCAGCCTGGGTGACAGTGAGA 10894        CT  TG
                                    TCTCGCT  GT  CCCAGGCTGGA
                                    |||||||  ||  ||||||||||
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                                AGAGTGA  CA  GGGTCCGACCT
                                   __  GT
GAM1628  HIP1     3'  TCCAGCCTGAGTGACAGAGCGA 19264          TG C
                GA                  TCTCGCTCTGT  C CAGGCTGGA
                                    ||||||||||  | |||||||||
                                    AGAGCGAGACA  G GTCCGACCT
                                          GT A
GAM1628  HIP1     3'  TCCAGCCTGGGCAACAAGAGC  19265       _
                                    GCTCT GTTGCCCAGGCTGGA
                                    ||||| ||||||||||||||||
                                    CGAGA CAACGGGTCCGACCT
                                      A
GAM1628  HRH1     3'  TCCAGCCTGGGCAACAGAGCAA 7828      C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAACGGGTCCGACCT
                                      A
GAM1628  HSPA5    3'  TCCAGCCTGGCGACAAGAGTGA 19290          _     C
                GA                  TCTCGCTCT GTTGCC AGGCTGGA
                                    |||||||||  ||||||  ||||||||
                                    AGAGTGAGA CAGCGG TCCGACCT
                                         A     _
GAM1628  HTR2A    3'  TCCTCCTGGGCAACAGAGTGAG 7107                CT
                A                    TCTCGCTCTGTTGCCCAGG  GGA
                                    ||||||||||||||||||  |||
                                    AGAGTGAGACAACGGGTCC  CCT
                                              T_
GAM1628  IAPP     3'  TCCAGCCTGGGTGGCAGAGTGA 6443          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACG  GGGTCCGACCT
                                          GT
GAM1628  ICA1     3'  CCAGCCTGGGCAACAAAGTGAG 18310        C
                A                    TCTCGCT TGTTGCCCAGGCTGG
                                    |||||||  |||||||||||||||
                                    AGAGTGA ACAACGGGTCCGACC
                                       A
GAM1628  IFIT4    3'  TCCAGCCTGGGCAACAGAGCAA 71497     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAACGGGTCCGACCT
                                      A
GAM1628  IFRD1    3'  CCTGGGCAACATAGCGAGA   60753        C
                                    TCTCGCT TGTTGCCCAGG
                                    |||||||  ||||||||||
                                    AGAGCGA ACAACGGGTCC
                                       T
GAM1628  IL10     3'  TCCAGCCTGGGTGACAGAGCAA 6929      C      TG
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    |||  |||||||  ||||||||||
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                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM1628  IL1R1    3'  TCTAGCCTGGCAACAGAGCAAG 7925      C         C
                A                  TCT GCTCTGTTGCC AGGCTGGA
                                   ||| |||||||||| ||||||||
                                   AGA CGAGACAACGG TCCGATCT
                                     A        _
GAM1628  IL2RA    3'  TCCAGCCTGGGCAACAGAGCAA 6453      C
                GA                   TCT GCTCTGTTGCCCAGGCTGGA
                                     ||| ||||||||||||||||||
                                     AGA CGAGACAACGGGTCCGACCT
                                       A
GAM1628  IL6R     3'  TCCAGCCTGGGGTGACAGAGC  6915         TG  _
                                     GCTCTGT  CCC AGGCTGGA
                                     |||||||  ||| ||||||||
                                     CGAGACA  GGG TCCGACCT
                                        GT   G
GAM1628  IPP      3'  TCCACTCTGGGCAACAGAATGA 20907       C          GC
                GA                   TCTCG TCTGTTGCCCAG  TGGA
                                     ||||| ||||||||||||  ||||
                                     AGAGT AGACAACGGGTC  ACCT
                                       A           TC
GAM1628  IRAK1    3'  TCCAGCCTGGGTGACAGAGCAA 9618      C      TG
                GA                   TCT GCTCTGT  CCCAGGCTGGA
                                     ||| |||||||  ||||||||||
                                     AGA CGAGACA  GGGTCCGACCT
                                       A      GT
GAM1628  IRAK4    3'  TCCAGCCTGGGTGACAGAGTGA 61847           TG
                GA                   TCTCGCTCTGT  CCCAGGCTGGA
                                     ||||||||||  ||||||||||
                                     AGAGTGAGACA  GGGTCCGACCT
                                           GT
GAM1628  ITGAL    3'  TCCAGCCTGGGCAACACAGCGA 11050         C
                GA                   TCTCGCT TGTTGCCCAGGCTGGA
                                     ||||||| ||||||||||||||||
                                     AGAGCGA ACAACGGGTCCGACCT
                                        C
GAM1628  KAI1     3'  TCCAGCCTGGGGGACAGAAAGA 11130      GC     G
                GA                   TCTC  TCTGTT CCCAGGCTGGA
                                     ||||  |||||| ||||||||||
                                     AGAG  AGACAG GGGTCCGACCT
                                       AA     G
GAM1628  KCNA7    3'  TCCAGCCTGGGCAACAGAGGGA 49905     G
                G                     CTC CTCTGTTGCCCAGGCTGGA
                                      ||| ||||||||||||||||||
                                      GAG GAGACAACGGGTCCGACCT
                                        G
GAM1628  KCNA7    3'  TCCAGCCTGGGCAGCAGAGC  49906
                                     GCTCTGTTGCCCAGGCTGGA
                                     ||||||||||||||||||||
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                                CGAGACGACGGGTCCGACCT

GAM1628  KCNJ5    3'  TCCAGCCTGGGCGACAGAGCGA 7978
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACAGCGGGTCCGACCT

GAM1628  KCNK3    3'  TCCAGCCTGGGTGACAGGGCAA 11178     C      TG
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGGGACA  GGGTCCGACCT
                                      A      GT
GAM1628  KCNK6    3'  TCCAGCCTGCGGGACAGAGTGA 17885          G  _
                GA                  TCTCGCTCTGTT CC CAGGCTGGA
                                    ||||||||||| || |||||||||
                                    AGAGTGAGACAG GG GTCCGACCT
                                          _  C
GAM1628  KIF1B    3'  TCCAGCCTGGGTGACAGAGCAA 31271     C      TG
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGAGACA  GGGTCCGACCT
                                      A      GT
GAM1628  KIF3B    3'  TCCAGCCTGGGTGACAGAGTGA 17810          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          GT
GAM1628  KLRG1    3'  TCCAGCCTGGGAGATAGAGCAA 20557     C      TG
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGAGATA  GGGTCCGACCT
                                      A      GA
GAM1628  KNSL1    3'  TCCAGCCTGGGCAACAGAGCAA 16949     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAACGGGTCCGACCT
                                      A
GAM1628  LAMC2    3'  TCCAGCCTGGGGAACAGAGCAA 19909     C      G
                GA                  TCT GCTCTGTT CCCAGGCTGGA
                                    ||| |||||||| ||||||||||
                                    AGA CGAGACAA GGGTCCGACCT
                                      A       G
GAM1628  LDLR     3'  CCTGGGCGACAGAGCGAGA    6733
                                    TCTCGCTCTGTTGCCCAGG
                                    |||||||||||||||||||
                                    AGAGCGAGACAGCGGGTCC

GAM1628  LDLR     3'  TCCAGCCTGGGCAACAGATGAA 6744      _  C
                GA                  TCT CG TCTGTTGCCCAGGCTGGA
                                    ||| || ||||||||||||||||||
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                                AGA GT AGACAACGGGTCCGACCT
                                  A  _
GAM1628  LDLR     3'  TCCAGCCTGGGCAACATAGTAA 6745      CG  C
                GA                  TCT  CT TGTTGCCCAGGCTGGA
                                    |||  || ||||||||||||||||
                                    AGA  GA ACAACGGGTCCGACCT
                                      AT  T
GAM1628  LILRB1   3'  TCCAGCCTGGCGACAGAGGGAG 22877      G         C
                A                    TCTC CTCTGTTGCC AGGCTGGA
                                     |||| |||||||||| ||||||||
                                     AGAG GAGACAGCGG TCCGACCT
                                       G         _
GAM1628  LPIN1    3'  TCCAGCCTGGGTGACAGAGTAA 67992     CG     TG
                GA                  TCT  CTCTGT  CCCAGGCTGGA
                                    |||  ||||||  ||||||||||
                                    AGA  GAGACA  GGGTCCGACCT
                                      AT     GT
GAM1628  LRRC2    3'  TCCAGCCTGGGCAACAGAGTGA 44759
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAACGGGTCCGACCT

GAM1628  LRRC2    3'  TCCAGCCTGGGTGACAGAGCCA 44760     C      TG
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGAGACA  GGGTCCGACCT
                                      C      GT
GAM1628  LRRC2    3'  TCCAGCCTGGGTGACAGAGTGA 45722           TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          GT
GAM1628  LUZP1    3'  TCCAGCCTGGGCAACAAGAGTG 54405        _
                A                    TCGCTCT GTTGCCCAGGCTGGA
                                     |||||||  ||||||||||||||
                                     AGTGAGA CAACGGGTCCGACCT
                                        A
GAM1628  LY94     3'  CCTGGGCGACAGAGCGAGA    17897
                                    TCTCGCTCTGTTGCCCAGG
                                    |||||||||||||||||
                                    AGAGCGAGACAGCGGGTCC

GAM1628  MAFF     3'  TCCAGCCTGGGCAACATAGC   25583     C
                                    GCT TGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||
                                    CGA ACAACGGGTCCGACCT
                                      T
GAM1628  MDM4     3'  TCCAGCCTGGGTGACAGCGCGA 11514       T    TG
                GA                  TCTCGC CTGT  CCCAGGCTGGA
                                    |||||| ||||  ||||||||||
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                                AGAGCG GACA  GGGTCCGACCT
                                  C    GT
GAM1628  MEN1     5'  TCCAGCCTGGGCGAAAGAGAAA 56361     CG    G
                GA                  TCT  CTCT TTGCCCAGGCTGGA
                                    |||  |||| ||||||||||||||
                                    AGA  GAGA AGCGGGTCCGACCT
                                      AA    A
GAM1628  MSH3     3'  TCCAGCTTGGGCAACAGAGCAA 11693     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAACGGGTTCGACCT
                                      A
GAM1628  MTMR8    3'  TCCAGCCTGAGCAACAGAGCGA 31917             C
                GA                  TCTCGCTCTGTTGC CAGGCTGGA
                                    |||||||||||||| |||||||||
                                    AGAGCGAGACAACG GTCCGACCT
                                            A
GAM1628  MTMR8    3'  TCCAGCCTGGGCGAAAGGGCAA 31918     C    G
                GA                  TCT GCTCT TTGCCCAGGCTGGA
                                    ||| ||||| ||||||||||||||
                                    AGA CGGGA AGCGGGTCCGACCT
                                      A    A
GAM1628  MYH11    3'  TCCAGCCTGGGCAACAGAG    11744
                                    CTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||
                                    GAGACAACGGGTCCGACCT

GAM1628  MYH11    3'  TCCAGCCTGGGCAACAGAG    11745
                                    CTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||
                                    GAGACAACGGGTCCGACCT

GAM1628  MYH11    3'  TCCAGCCTGGGCAACGTAGT   11746     C
                                    GCT TGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||
                                    TGA GCAACGGGTCCGACCT
                                      T
GAM1628  MYH11    3'  TCCAGCCTGGGCAACGTAGT   11747     C
                                    GCT TGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||
                                    TGA GCAACGGGTCCGACCT
                                      T
GAM1628  MYO1B    3'  TCCAGCCCGGGTGACAATACAA 25247     CGCTC   TG   A
                GA                  TCT    TGT  CCC GGCTGGA
                                    |||    |||  ||| |||||||
                                    AGA    ACA  GGG CCGACCT
                                      ACATA   GT   C
GAM1628  MYO1C    3'  TCCAGCCTGGGCAACAGAGCGA 61870
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
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                                AGAGCGAGACAACGGGTCCGACCT

GAM1628  NCOA6    5'  TCCAGCCCAGGCAACAGAGCGT 26849    T         CA
                GA                TC CGCTCTGTTGCC  GGCTGGA
                                  || |||||||||||  |||||||
                                  AG GCGAGACAACGG  CCGACCT
                                   T          AC
GAM1628  NESG1    5'  CCAGCCCAGGGCCAGAGCGA  25619        TT   A_
                                  TCGCTCTG  GCCC  GGCTGG
                                  ||||||||  ||||  ||||||
                                  AGCGAGAC  CGGG  CCGACC
                                       __   AC
GAM1628  NFKBIL2  3'  TCCAGCCTGGGCGACAGACCGA 26455      C
                GA                TCTCG TCTGTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||||||
                                  AGAGC AGACAGCGGGTCCGACCT
                                    C
GAM1628  NKX3A    3'  TCCAGCCTGGGCAACGAGCAAG 21617    C   T
                A                 TCT GCTC GTTGCCCAGGCTGGA
                                  ||| |||| ||||||||||||||
                                  AGA CGAG CAACGGGTCCGACCT
                                    A  _
GAM1628  NPHP1    3'  TCCAGCCTAGGCAACAAGAGTG 63150       _    C
                A                 TCGCTCT GTTGCC AGGCTGGA
                                  ||||||| |||||| ||||||||
                                  AGTGAGA CAACGG TCCGACCT
                                      A     A
GAM1628  NPHS1    3'  TCCAGCCTGGGCGACAGAGCGA 17374
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCCGACCT

GAM1628  NT5C2    3'  TCCAGCCTGGGCAACAAGA   25268    _
                                  TCT GTTGCCCAGGCTGGA
                                  ||| ||||||||||||||
                                  AGA CAACGGGTCCGACCT
                                    A
GAM1628  NUP62    3'  TCCAGCCTAGGCAACAGAG   25652         C
                                  CTCTGTTGCC AGGCTGGA
                                  |||||||||| ||||||||
                                  GAGACAACGG TCCGACCT
                                       A
GAM1628  OGG1     5'  TCCAGCCTAGGCGACAGAGTGA 34160            C
                GA                TCTCGCTCTGTTGCC AGGCTGGA
                                  |||||||||||||| ||||||||
                                  AGAGTGAGACAGCGG TCCGACCT
                                         A
GAM1628  OPA3     3'  CTAGCCTGGGCAACAGAGCAAG 47843     C
                A                 TCT GCTCTGTTGCCCAGGCTGG
                                  ||| ||||||||||||||||||
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                                AGA CGAGACAACGGGTCCGATC
                                  A
GAM1628 OPA3     3' TCCAGCCCGGGTGACAGAGCAA 47848     C      TG   A
                GA                TCT GCTCTGT  CCC GGCTGGA
                                  ||| |||||||  ||| |||||||
                                  AGA CGAGACA  GGG CCGACCT
                                    A      GT   C
GAM1628 OPTN     3' TCCAGCCTGGGTGACAGAGGGA 42053      G     TG
                GA                TCTC CTCTGT  CCCAGGCTGGA
                                  |||| ||||||  ||||||||||
                                  AGAG GAGACA  GGGTCCGACCT
                                    G     GT
GAM1628 P53AIP1  3' TCCAGCCTGGGCGACAGAGAGA 42340      G
                GA                TCTC CTCTGTTGCCCAGGCTGGA
                                  |||| ||||||||||||||||||
                                  AGAG GAGACAGCGGGTCCGACCT
                                    A
GAM1628 PA2G4    3' TCCAGCCTGGGTGACAGAATGA 71831       C    TG
                GA                TCTCG TCTGT  CCCAGGCTGGA
                                  ||||| |||||  ||||||||||
                                  AGAGT AGACA  GGGTCCGACCT
                                    A    GT
GAM1628 PAICS    3' TCCAACCTGGGCAGCAGAGCAA 22268     C           C
                GA                TCT GCTCTGTTGCCCAGG TGGA
                                  ||| |||||||||||||| ||||
                                  AGA CGAGACGACGGGTCC ACCT
                                    A            A
GAM1628 PCDH11X  3' TCCAGCCTGGGTGACAGAGCAA 28017     C      TG
                GA                TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A      GT
GAM1628 PCDH11Y  3' TCCAGCCTGGGTGACAGAGCAA 53169     C      TG
                GA                TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A      GT
GAM1628 PCDHB9   3' TCCAGCCTGGGCAATAAGAGC  39451      _
                                  GCTCT GTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||||
                                  CGAGA TAACGGGTCCGACCT
                                    A
GAM1628 PDCL     3' CCAACCTGGGCGACAGAG    19395           C
                                  CTCTGTTGCCCAGG TGG
                                  |||||||||||||| |||
                                  GAGACAGCGGGTCC ACC
                                            A
GAM1628 PDE4C    3' CCTGGGCAACATAGCAAGA   8101     C  C
                                  TCT GCT TGTTGCCCAGG
                                  ||| ||| ||||||||||
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                                AGA CGA ACAACGGGTCC
                                  A   T
GAM1628  PDE4C    3'  TCCAGCCTGGGCAACACAGCAA 8107      C   C
                GA                  TCT GCT TGTTGCCCAGGCTGGA
                                    ||| ||| ||||||||||||||||
                                AGA CGA ACAACGGGTCCGACCT
                                  A   C
GAM1628  PDE4C    3'  TCCAGCCTGGGGCTGACAGAGC 8108      C       _   _
                AAGA                  TCT GCTCTGTT GCCC AGGCTGGA
                                    ||| |||||||| |||| ||||||||
                                AGA CGAGACAG CGGG TCCGACCT
                                  A       T   G
GAM1628  PIK3CD   3'  TCCAAAACTCAACAGAGCCAGA 18501     C       CCC  GC_
                                TCT GCTCTGTTG   AG   TGGA
                                ||| |||||||||   ||   ||||
                                AGA CGAGACAAC   TC   ACCT
                                  C       ___  AAA
GAM1628  PIK3CG   3'  TCCAGCCTGGATAACAGAGCGA 12125           C
                GA                  TCTCGCTCTGTTG CCAGGCTGGA
                                    |||||||||||| ||||||||||
                                AGAGCGAGACAAT GGTCCGACCT
                                        A
GAM1628  PLA2G2D  3'  TCCAGCCTGGGCAACAGAGTGA 25723
                                TCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||
                                AGTGAGACAACGGGTCCGACCT

GAM1628  POLH     3'  TCCAGCCTGGGCAACAGAGCGA 22484
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                AGAGCGAGACAACGGGTCCGACCT

GAM1628  POLH     3'  TCCAGCCTGGGCAACAGAGCGA 22485
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                AGAGCGAGACAACGGGTCCGACCT

GAM1628  POLK     3'  CCAGCCTGAAGAGCGAGA     33100         GTTGCC
                                TCTCGCTCT     CAGGCTGG
                                |||||||||     ||||||||
                                AGAGCGAGA     GTCCGACC
                                    A_____
GAM1628  PPP1R12B 3'  TCCAGCCTGGGTGACAGAGCAA 50366     C      TG
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM1628  PRKY     3'  TCCAGCCTGGGTGACAGAGTGA 12384          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
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                                AGAGTGAGACA  GGGTCCGACCT
                                      GT
GAM1628  PRKY     3'  TCCAGGCTGGACGACAGAGCAA 12385     C       C    G
                GA                  TCT GCTCTGTTG CCAG CTGGA
                                    ||| ||||||||| |||| |||||
                                    AGA CGAGACAGC GGTC GACCT
                                      A        A   G
GAM1628  PSMB2    3'  TCCAGCCTGGCAACAGAGTGAG 12478             C
                A                    TCTCGCTCTGTTGCC AGGCTGGA
                                    |||||||||||||| ||||||||
                                    AGAGTGAGACAACGG TCCGACCT
                                                 _
GAM1628  PSMB2    3'  TCCAGCCTGGCTGACAGAGCAA 12479     C       GC
                GA                  TCT GCTCTGTT  CCAGGCTGGA
                                    ||| ||||||||  ||||||||||
                                    AGA CGAGACAG  GGTCCGACCT
                                      A        TC
GAM1628  PSMB9    3'  TCCAGCCTGGGAAACAGAGCGA 12509          G
                                    TCGCTCTGTT CCCAGGCTGGA
                                    |||||||||| ||||||||||
                                    AGCGAGACAA GGGTCCGACCT
                                          A
GAM1628  PSMB9    3'  TCCAGCCTGGGCGACAAAGCGA 12510        C
                GA                  TCTCGCT TGTTGCCCAGGCTGGA
                                    ||||||| ||||||||||||||||
                                    AGAGCGA ACAGCGGGTCCGACCT
                                       A
GAM1628  PSMD5    3'  CCTGGGCAACACAGCAAGA    18557     C   C
                                    TCT GCT TGTTGCCCAGG
                                    ||| ||| ||||||||||
                                    AGA CGA ACAACGGGTCC
                                      A   C
GAM1628  PTAFR    3'  TCTAGCCTGGCAACAGAGCGAG 8168             C
                A                    TCTCGCTCTGTTGCC AGGCTGGA
                                    |||||||||||||| ||||||||
                                    AGAGCGAGACAACGG TCCGATCT
                                                 _
GAM1628  PTGIS    3'  TCCAGCCTGGGCGACAGAGCAA 8229      C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAGCGGGTCCGACCT
                                      A
GAM1628  RABIF    3'  TCCAGCCTGGGCAACAGAGTGA 12730
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAACGGGTCCGACCT

GAM1628  RAD1     3'  TCCAGCCTAGGCAATAAGAGC  12647       _     C
                                    GCTCT GTTGCC AGGCTGGA
                                    ||||| |||||| ||||||||
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                                CGAGA TAACGG TCCGACCT
                                  A     A
GAM1628 RANBP2L1 3' TCCAGCTCGGGGAACAGAGCGA 51052          G   AG
            GA                    TCTCGCTCTGTT CCC  GCTGGA
                                  |||||||||||| |||  ||||||
                                  AGAGCGAGACAA GGG  CGACCT
                                        G   CT
GAM1628 RBBP5   3' TCCAGCCTAGGTGACAGAATGA 18579      C    TG  C
            GA                    TCTCG TCTGT  CC AGGCTGGA
                                  ||||| |||||  || ||||||||
                                  AGAGT AGACA  GG TCCGACCT
                                    A    GT  A
GAM1628 RBBP9   3' CCAGGGCAACACAGCAAGA   70687    C  C      A
                                  TCT GCT TGTTGCCC GG
                                  ||| ||| |||||||| ||
                                  AGA CGA ACAACGGG CC
                                    A  C       A
GAM1628 RBL1    3' TCCAGCCTGGGCAACAAGAGT  12789      _
                                  GCTCT GTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||||
                                  TGAGA CAACGGGTCCGACCT
                                    A
GAM1628 RBM3    3' TCCAGCCTGGGCAACAGCGAGA 71013        CT
                                  TCTCGCT  GTTGCCCAGGCTGGA
                                  |||||||  ||||||||||||||||
                                  AGAGCGA  CAACGGGTCCGACCT
                                          __
GAM1628 RFC2    3' CCAGCCTGGGCGACAGAG    12839
                                  CTCTGTTGCCCAGGCTGG
                                  ||||||||||||||||||
                                  GAGACAGCGGGTCCGACC

GAM1628 ROCK2   3' TCCAGCCTGGGCAGCTGAACAA 66625    CGC  T
            GA                    TCT   TC GTTGCCCAGGCTGGA
                                  |||   || ||||||||||||||||
                                  AGA   AG CGACGGGTCCGACCT
                                    ACA  T
GAM1628 SCAP2   3' TCCAGCCTGGGCGACAGAGTGA 15427
            GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAGCGGGTCCGACCT

GAM1628 SFRS2IP  5' TCCAGCCTGGGTGACAGAGTGA 17547          TG
            GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                  |||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                        GT
GAM1628 SIGLEC11 3' TCCAGCCTGGGCAACAGAGTGA 54657
            GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
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                                AGAGTGAGACAACGGGTCCGACCT

GAM1628  SIGLEC6   3'  CCAGCCTGGGCAACAGAGCGAG 60605
                A                TCTCGCTCTGTTGCCCAGGCTGG
                                 ||||||||||||||||||||||
                                 AGAGCGAGACAACGGGTCCGACC

GAM1628  SIM2      3'  TCCAGCCTGGGTAACAGAGTGA 18624
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  |||||||||||||||||||||||
                                  AGAGTGAGACAATGGGTCCGACCT

GAM1628  SLC14A2   3'  TCCAGCCTGGGCAACGGATTGA 24128       C
                GA                TCTCG TCTGTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||||||
                                  AGAGT AGGCAACGGGTCCGACCT
                                    T
GAM1628  SLC17A5   3'  TCCAGCCTGGGCGATGGAGCGA 25835
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  |||||||||||||||||||||||
                                  AGAGCGAGGTAGCGGGTCCGACCT

GAM1628  SLC26A4   3'  TCCAGCCTGGGCGACAGAGCAA 6530      C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM1628  SLC28A2   3'  TCCAGCCTGGGTGACAGAGCGA 16154          TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                       GT
GAM1628  SLC2A6    3'  TCCAGCCTGGGCAACGAGAGTG 34577        _
                A                 TCGCTCT GTTGCCCAGGCTGGA
                                  |||||||| ||||||||||||||
                                  AGTGAGA CAACGGGTCCGACCT
                                     G
GAM1628  SMG1      3'  TCCAGCCTGGGCAACAGAGCTA 31352     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||
                                  AGA CGAGACAACGGGTCCGACCT
                                    T
GAM1628  SRGAP1    5'  TCCAGCCTGGGCAACAGAGCGA 72721
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  |||||||||||||||||||||||
                                  AGAGCGAGACAACGGGTCCGACCT

GAM1628  STK38     5'  TCCAGCCTGGGCAACAAGAGCG 24401        _
                A                 TCGCTCT GTTGCCCAGGCTGGA
                                  |||||||| ||||||||||||||
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                                AGCGAGA CAACGGGTCCGACCT
                                   A
GAM1628  SULT2A1   3'  TCCAGCCTGGGTGACAGAGCGA 72232          TG
                GA                 TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   AGAGCGAGACA  GGGTCCGACCT
                                      GT
GAM1628  SWAP70    3'  TCCAGCTTGGGCAACAGAGTGA 71874
                GA                 TCTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGTGAGACAACGGGTTCGACCT

GAM1628  TADA2L   3'  TCCAGCCTGGGCAACAAAGTGA 56765        C
                GA                 TCTCGCT TGTTGCCCAGGCTGGA
                                   |||||||  ||||||||||||||||
                                   AGAGTGA ACAACGGGTCCGACCT
                                      A
GAM1628  TBX1      3'  TCCAGCCTGGGTGACAGAGTGA 55541          TG
                GA                 TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   AGAGTGAGACA  GGGTCCGACCT
                                      GT
GAM1628  TBX6      3'  TCCAGCCTAGGCAACACGAGC  55817     _     C
                                   GCTC TGTTGCC AGGCTGGA
                                   ||||  |||||||  ||||||||
                                   CGAG ACAACGG TCCGACCT
                                     C      A
GAM1628  TCF1      3'  CCAGCCTGGGCCTATGGAG   6783       T_
                                   CTCTGT  GCCCAGGCTGG
                                   ||||||  ||||||||||
                                   GAGGTA  CGGGTCCGACC
                                      TC
GAM1628  TCTA      3'  TCCAGCCTGGGCAACAGAGCAA 42503     C
                GA                 TCT GCTCTGTTGCCCAGGCTGGA
                                   |||  ||||||||||||||||||||
                                   AGA CGAGACAACGGGTCCGACCT
                                     A
GAM1628  TEM7      3'  TCCAGCCTGGGTGACAGAGCGA 40269          TG
                GA                 TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   AGAGCGAGACA  GGGTCCGACCT
                                      GT
GAM1628  TEM7      3'  TCCAGCCTGGGTGACAGAGTGA 40270          TG
                GA                 TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   AGAGTGAGACA  GGGTCCGACCT
                                      GT
GAM1628  TNFAIP6   3'  CTGGGCAACATAGCAAGA    60165     C   C
                                   TCT GCT TGTTGCCCAG
                                   |||  |||  ||||||||||
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                                AGA CGA ACAACGGGTC
                                  A   T
GAM1628  TNFRSF1B  3'  TCCAGCCTGAGCAACAGAGTGA 8402              C
                GA                TCTCGCTCTGTTGC CAGGCTGGA
                                  |||||||||||||| |||||||||
                                  AGAGTGAGACAACG GTCCGACCT
                                        A
GAM1628  TNFRSF1B  3'  TCCAGCCTGGGCGACAGAGCGA 8403
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCCGACCT

GAM1628  TNFSF10   3'  TCCAGCCTGGCGACAGAGCGAG 15094              C
                A                 TCTCGCTCTGTTGCC AGGCTGGA
                                  |||||||||||||| ||||||||
                                  AGAGCGAGACAGCGG TCCGACCT
                                           _
GAM1628  TNFSF15   3'  TCCAGCCTGGGTAACAAGAGC  18870       _
                                  GCTCT GTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||||
                                  CGAGA CAATGGGTCCGACCT
                                    A
GAM1628  TPM4      3'  TCCAGCCTGGTCGACAGAGTGA 13834            C
                GA                TCTCGCTCTGTTG CCAGGCTGGA
                                  |||||||||||| |||||||||
                                  AGAGTGAGACAGC GGTCCGACCT
                                        T
GAM1628  TPMT      3'  CCAGCCTGGGCAACAGAGCAAG 6307       C
                A                  TCT GCTCTGTTGCCCAGGCTGG
                                   ||| ||||||||||||||||||
                                   AGA CGAGACAACGGGTCCGACC
                                     A
GAM1628  TRIM14    3'  TCCAGCCTGGGCAATAGAGTGA 29516
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGATAACGGGTCCGACCT

GAM1628  TRIM14    3'  TCCAGCCTGGGGACAGAGCAAG 29517     C       G
                A                  TCT GCTCTGTT CCCAGGCTGGA
                                   ||| |||||||| ||||||||||
                                   AGA CGAGACAG GGGTCCGACCT
                                     A      _
GAM1628  TSN       3'  CCAGCCTGGGCAACAAAGTGAG 17297        C
                A                  TCTCGCT TGTTGCCCAGGCTGG
                                   ||||||| |||||||||||||||
                                   AGAGTGA ACAACGGGTCCGACC
                                       A
GAM1628  TSNAX     3'  TCCAGCCTGGGTAACAGAGCAA 21160     C
                GA                 TCT GCTCTGTTGCCCAGGCTGGA
                                   ||| ||||||||||||||||||
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                                AGA CGAGACAATGGGTCCGACCT
                                  A
GAM1628  UBE2B    3'  TCCAGCCTGGGTGACAGAGC   13938        TG
                                GCTCTGT  CCCAGGCTGGA
                                |||||||  ||||||||||
                                CGAGACA  GGGTCCGACCT
                                    GT
GAM1628  UBE2G2   3'  TCCAGCCTGGGCAACAGAGCGA 65495
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAACGGGTCCGACCT

GAM1628  UBE2G2   3'  TCCAGCCTGGGCAACAGAGTGA 65496
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAACGGGTCCGACCT

GAM1628  UC28     3'  TCCAGCCTGGGCAACAGGAGT  41590     _
                                GCTC TGTTGCCCAGGCTGGA
                                ||||  ||||||||||||||||
                                TGAG ACAACGGGTCCGACCT
                                  G
GAM1628  USP14    3'  TCCAGCCTGGGTGACAGAGAGA 18940    G     TG
                                TC CTCTGT  CCCAGGCTGGA
                                ||  ||||||  ||||||||||
                                AG GAGACA  GGGTCCGACCT
                                 A     GT
GAM1628  VHL      3'  CCAGCCTGGGAAACAAGAG   6841      _  G
                                CTCT GTT CCCAGGCTGG
                                ||||  |||  ||||||||||
                                GAGA CAA GGGTCCGACC
                                  A  A
GAM1628  VHL      3'  TCCAGCCTGGGGGACAGAGCAA 6876     C      G
              GA                  TCT GCTCTGTT CCCAGGCTGGA
                                  |||  ||||||||  ||||||||||
                                  AGA CGAGACAG GGGTCCGACCT
                                    A       G
GAM1628  VHL      3'  TCCAGCCTGTGTGACAGAGC   6877        TG C
                                GCTCTGT  C CAGGCTGGA
                                |||||||  | |||||||||
                                CGAGACA  G GTCCGACCT
                                    GT T
GAM1628  VPS41    3'  TCCAGCCTGGGCAACAAGAGC  27697      _
                                GCTCT GTTGCCCAGGCTGGA
                                |||||  ||||||||||||||||
                                CGAGA CAACGGGTCCGACCT
                                  A
GAM1628  WIG1     3'  TCCAGCCTGGGTGACAGAGCGA 96105          TG
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
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                                AGAGCGAGACA  GGGTCCGACCT
                                      GT
GAM1628  XT3      3'  TCCAGTCTGGGCGACAGAGCAA 39918     C
                GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                      ||| ||||||||||||||||||||
                                      AGA CGAGACAGCGGGTCTGACCT
                                        A
GAM1628  ZNF14    3'  TCCAGCCTGTGCGACAGAATGA 41058       C       C
                GA                    TCTCG TCTGTTGC CAGGCTGGA
                                      ||||| |||||||| |||||||||
                                      AGAGT AGACAGCG GTCCGACCT
                                        A       T
GAM1628  ZNF264   3'  TCCAGCCTGGGCAACAGAGCGA 14232
                GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                      ||||||||||||||||||||||||
                                      AGAGCGAGACAACGGGTCCGACCT

GAM1628  ZNF264   3'  TCCAGCCTGGGCAGCAGAGCGA 14233
                GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                      ||||||||||||||||||||||||
                                      AGAGCGAGACGACGGGTCCGACCT

GAM1628  ZNF36    3'  TCCAGCCTGGGTGACTAGC   95587     CT  TG
                                      GCT  GT  CCCAGGCTGGA
                                      |||  ||  ||||||||||
                                      CGA  CA  GGGTCCGACCT
                                        T_  GT
GAM1628  ZNF91    3'  CCTGGGCGACAGAGCGAGA   14280
                                      TCTCGCTCTGTTGCCCAGG
                                      |||||||||||||||||
                                      AGAGCGAGACAGCGGGTCC

GAM1628  AF020591  3'  TCCAGCCTGGGCAACAGAGCAA 27916     C
                GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                      ||| ||||||||||||||||||||
                                      AGA CGAGACAACGGGTCCGACCT
                                        A
GAM1628  ALTE     3'  TCCAGCCTGGAGGCCAGAGTGA 61006          _  GC
                GA                    TCTCGCTCTG TT  CCAGGCTGGA
                                      |||||||||| ||  ||||||||||
                                      AGAGTGAGAC GG  GGTCCGACCT
                                            C  A_
GAM1628  ALTE     3'  TCCAGCCTGGGCGACAAGAGCG 61007          _
                AGA                     TCTCGCTCT GTTGCCCAGGCTGGA
                                      |||||||||| ||||||||||||||||
                                      AGAGCGAGA CAGCGGGTCCGACCT
                                            A
GAM1628  AP1GBP1  3'  TCTGAGCGACAGAGCAAGA   24356     C        C
                                      TCT GCTCTGTTGC CAGG
                                      ||| |||||||||| ||||
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                                AGA CGAGACAGCG GTCT
                                  A         A
GAM1628  AP4S1    3'  TCCAATCTGGCAACAGAGCGAG 23965              C  GC
                 A                TCTCGCTCTGTTGCC AG  TGGA
                                  |||||||||||||||  ||  ||||
                                  AGAGCGAGACAACGG TC  ACCT
                                           _  TA
GAM1628  APOF     3'  TCCAGCCTGGGTGACAGAGCGA 9696            TG
                 GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GT
GAM1628  APXL2    3'  TCCAGCCTGGGCGACAGAGCAA 75686     C
                 GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM1628  ARNTL2   3'  CCAGCCTGGGCGACAGAGCGAG 39843
                 A                TCTCGCTCTGTTGCCCAGGCTGG
                                  |||||||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCCGACC

GAM1628  ARNTL2   3'  TCCAGTCTGGGCAACAGAGTGA 39858
                 GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  |||||||||||||||||||||||
                                  AGAGTGAGACAACGGGTCTGACCT

GAM1628  ASAHL    3'  TCTAGCCTGGGCAACAGAGCGA 64321
                 GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  |||||||||||||||||||||||
                                  AGAGCGAGACAACGGGTCCGATCT

GAM1628  ATP1B4   3'  TCCAGCCTGGGTGACAGAGTGA 24852           TG
                 GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                        GT
GAM1628  BANP     3'  TCCAGACTGTGCGACAGAGCGA 66805            C  G
                 GA                TCTCGCTCTGTTGC CAG CTGGA
                                  |||||||||||||| ||| |||||
                                  AGAGCGAGACAGCG GTC GACCT
                                           T  A
GAM1628  BIRC1    3'  TCCAGCCTGGGCAACAGAGCAA 16995     C
                 GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||
                                  AGA CGAGACAACGGGTCCGACCT
                                    A
GAM1628  BIVM     3'  TCCAGCCTGGGCAACAGGGCAA 35160     C
                 GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||
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                                AGA CGGGACAACGGGTCCGACCT
                                  A
GAM1628  BLOV1    3'  TCCAGCCTGGGCAACAAGAGCG 76799        _
                 A                 TCGCTCT GTTGCCCAGGCTGGA
                                   ||||||| ||||||||||||||||
                                   AGCGAGA CAACGGGTCCGACCT
                                      A
GAM1628  BLOV1    3'  TCCAGCCTGGGCGACAGAGCAA 76800     C
                 GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                     ||| ||||||||||||||||||||
                                     AGA CGAGACAGCGGGTCCGACCT
                                       A
GAM1628  BTN3A2   3'  TCCAGCCTGGGAGACAGAGCGA 23880          TG
                 GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                     ||||||||||  ||||||||||
                                     AGAGCGAGACA  GGGTCCGACCT
                                           GA
GAM1628  C12orf2  3'  TCCAGCCTGGGTAACAGAGTGA 83688
                 GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                     ||||||||||||||||||||||||
                                     AGAGTGAGACAATGGGTCCGACCT

GAM1628  C13orf1  3'  TCCAGCCTAGGCAACAGAGTGA 40372            C
                 GA                  TCTCGCTCTGTTGCC AGGCTGGA
                                     |||||||||||||| ||||||||
                                     AGAGTGAGACAACGG TCCGACCT
                                           A
GAM1628  C1orf33  3'  TCCAGCCTGGGCAACAGAGT  32987
                                     GCTCTGTTGCCCAGGCTGGA
                                     ||||||||||||||||||||
                                     TGAGACAACGGGTCCGACCT

GAM1628  C1orf34  3'  CCTGGGCGACAGAGCGAGA   61304
                                     TCTCGCTCTGTTGCCCAGG
                                     |||||||||||||||||||
                                     AGAGCGAGACAGCGGGTCC

GAM1628  C1QTNF2  3'  TCCAGCCTGGGCAACAGAGTGA 49977
                 GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                     ||||||||||||||||||||||||
                                     AGAGTGAGACAACGGGTCCGACCT

GAM1628  C20orf106 3'  TCCAGCCCAGGTGACAGAGTGA 55914          TG  CA
                 GA                  TCTCGCTCTGT  CC  GGCTGGA
                                     ||||||||||  ||  |||||||
                                     AGAGTGAGACA  GG  CCGACCT
                                           GT  AC
GAM1628  C20orf108 3'  TCCAGCCTGGGCGACAGAGGGA 55883      G
                 GA                  TCTC CTCTGTTGCCCAGGCTGGA
                                     |||| ||||||||||||||||||
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                                AGAG GAGACAGCGGGTCCGACCT
                                  G
GAM1628  C20orf12  3'  TCCAGCCTGGGCAACAAGAGC  36850      _
                                GCTCT GTTGCCCAGGCTGGA
                                ||||| ||||||||||||||||
                                CGAGA CAACGGGTCCGACCT
                                  A
GAM1628  C20orf142 3'  TCCAGCCTGAGCGACAGAGTGA 75289           C
              GA                  TCTCGCTCTGTTGC CAGGCTGGA
                                  |||||||||||||| |||||||||
                                  AGAGTGAGACAGCG GTCCGACCT
                                           A
GAM1628  C20orf154 3'  CTTGGGCAACATAGCAAGA   90049    C   C
                                  TCT GCT TGTTGCCCAGG
                                  ||| ||| ||||||||||
                                  AGA CGA ACAACGGGTTC
                                    A   T
GAM1628  C20orf172 3'  TCCAGCCTGAGCGACAGAGTGA 46768           C
              GA                  TCTCGCTCTGTTGC CAGGCTGGA
                                  |||||||||||||| |||||||||
                                  AGAGTGAGACAGCG GTCCGACCT
                                           A
GAM1628  C20orf177 3'  TCCAGCCTGGGCAACAAGAGGG 62841    G   _
              A                    TC CTCT GTTGCCCAGGCTGGA
                                  || |||| ||||||||||||||||
                                  AG GAGA CAACGGGTCCGACCT
                                    G   A
GAM1628  C20orf183 3'  TCCAGGCTGGGCGACAGAGCGA 48537               G
              GA                  TCTCGCTCTGTTGCCCAG CTGGA
                                  |||||||||||||||||| |||||
                                  AGAGCGAGACAGCGGGTC GACCT
                                           G
GAM1628  C20orf29  3'  TCCAGCCTGGGCAACAGAGTGA 37712
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAACGGGTCCGACCT


GAM1628  C21orf108 3'  TCCAGCCTAGGTGACAGAGCAA 90121    C     TG  C
              GA                  TCT GCTCTGT  CC AGGCTGGA
                                  ||| |||||||  || ||||||||
                                  AGA CGAGACA  GG TCCGACCT
                                    A      GT  A
GAM1628  C22orf19  3'  TCTGGACAACAGAGCAAGA   14831    C       C
                                  TCT GCTCTGTTG CCAGG
                                  ||| ||||||||| |||||
                                  AGA CGAGACAAC GGTCT
                                    A       A
GAM1628  C22orf20  3'  TCCAGCCTGGGCAACATGAGTG 48200       _
              A                    TCGCTC TGTTGCCCAGGCTGGA
                                  ||||||| ||||||||||||||||
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                                AGTGAG ACAACGGGTCCGACCT
                                   T
GAM1628  C6orf5    3'  TCCAGCCTGGGCAATAGAGTGA 32004
                GA                 TCTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGTGAGATAACGGGTCCGACCT

GAM1628  C8orf17   3'  CAGCCTGGGCAACAGAATGAGA 39990       C
                                   TCTCG TCTGTTGCCCAGGCTG
                                   ||||| ||||||||||||||||
                                   AGAGT AGACAACGGGTCCGAC
                                     A
GAM1628  C9orf5    3'  TCCAGCCTGGGTGAGAGAGTGA 50108          G TG
                GA                 TCTCGCTCT T  CCCAGGCTGGA
                                   |||||||||| |  ||||||||||
                                   AGAGTGAGA A  GGGTCCGACCT
                                        G GT
GAM1628  CAMKK2    5'  TCCAGCCTGGGCAACACAGAGA 22630      G  C
                GA                 TCTC CT TGTTGCCCAGGCTGGA
                                   |||| || ||||||||||||||||
                                   AGAG GA ACAACGGGTCCGACCT
                                     A  C
GAM1628  CAMKK2    5'  TCCAGCGTGGGCGACAGAGCGA 22631                G
                GA                 TCTCGCTCTGTTGCCCA GCTGGA
                                   |||||||||||||||| ||||||
                                   AGAGCGAGACAGCGGGT CGACCT
                                          G
GAM1628  CBCIP2    3'  TCCAGCCTGGGCGACAGAGCCA 52661     C
                GA                 TCT GCTCTGTTGCCCAGGCTGGA
                                   ||| ||||||||||||||||||||
                                   AGA CGAGACAGCGGGTCCGACCT
                                     C
GAM1628  CCR6      3'  TCCAGCCTGGGTGACAGAGCGA 16448           TG
                GA                 TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   AGAGCGAGACA  GGGTCCGACCT
                                        GT
GAM1628  CDT1      3'  TCCAGCCTGGGTGACAGAGCGA 78166           TG
                GA                 TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   AGAGCGAGACA  GGGTCCGACCT
                                        GT
GAM1628  CENTA2    3'  TCCAGCCTGGGTGACAGAGCGA 37868           TG
                GA                 TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   AGAGCGAGACA  GGGTCCGACCT
                                        GT
GAM1628  cerk      3'  TCCAGCCTGGGCAACAGAGGGA 43169      G
                GA                 TCTC CTCTGTTGCCCAGGCTGGA
                                   |||| ||||||||||||||||||
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                                AGAG GAGACAACGGGTCCGACCT
                                  G
GAM1628  CG012    5'  TCCAGCCCAGGTGACAGAGGGA 84166      G     TG  CA
                GA                  TCTC CTCTGT  CC  GGCTGGA
                                    |||| ||||||  ||  |||||||
                                    AGAG GAGACA  GG  CCGACCT
                                      G     GT  AC
GAM1628  CG012    3'  TCCAGCCTCGCCGACAAAGCGA 84167        C     CCC
                GA                  TCTCGCT TGTTG   AGGCTGGA
                                    ||||||| |||||   ||||||||
                                    AGAGCGA ACAGC   TCCGACCT
                                       A     CGC
GAM1628  CG012    5'  TCCAGCCTGGGCAACAGAACGA 84168       C
                GA                  TCTCG TCTGTTGCCCAGGCTGGA
                                    ||||| ||||||||||||||||||
                                    AGAGC AGACAACGGGTCCGACCT
                                      A
GAM1628  CGI-203  3'  TCCAGCCTGGGTGACAGAGTGA 40277           TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    |||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          GT
GAM1628  CHRFAM7A 3'  CCTGGGCGACAAAGCAAGA    96717     C   C
                                    TCT GCT TGTTGCCCAGG
                                    ||| ||| ||||||||||
                                    AGA CGA ACAGCGGGTCC
                                      A   A
GAM1628  CNNM1    3'  CCTAGGCAACAGAGCGAGA    40117             C
                                    TCTCGCTCTGTTGCC AGG
                                    |||||||||||||| |||
                                    AGAGCGAGACAACGG TCC
                                              A
GAM1628  CPR2     3'  TCCAGCCATACAGAACAGAGA  48838      GC_    TGCCCA
                                    TCTC   TCTGT     GGCTGGA
                                    ||||   |||||     |||||||
                                    AGAG   AGACA     CCGACCT
                                      ACA    TA____
GAM1628  CPR2     3'  TCCAGCCTGGGCGACAGAGTGA 48839
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    |||||||||||||||||||||||
                                    AGAGTGAGACAGCGGGTCCGACCT

GAM1628  CPR2     3'  TCCAGCCTGGGTAACAGAGCAA 48840     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||
                                    AGA CGAGACAATGGGTCCGACCT
                                      A
GAM1628  CRTAM    3'  TCCAGCCTGGGCGACAGAGGGA 39476      G
                GA                  TCTC CTCTGTTGCCCAGGCTGGA
                                    |||| ||||||||||||||||||
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                                AGAG GAGACAGCGGGTCCGACCT
                                  G
GAM1628  CSAD     3'  TCCAGGCTGGGCAACAGTACGA 32585       CT          G
                GA                  TCTCG  CTGTTGCCCAG CTGGA
                                    |||||  |||||||||||| |||||
                                    AGAGC  GACAACGGGTC GACCT
                                      AT          G
GAM1628  CXYorf1   3'  CCAGCCCAAACTGTGACAGGAG 82906      GCT    TG CCA___
                A                   TCTC   CTGT  C      GGCTGG
                                    ||||   ||||  |      ||||||
                                    AGAG   GACA  G      CCGACC
                                      ___    GT TCAAAC
GAM1628  CYB5-M    3'  CCTGGGCAACATAGCGAGA    96201         C
                                    TCTCGCT TGTTGCCCAGG
                                    |||||||  ||||||||||
                                    AGAGCGA ACAACGGGTCC
                                       T
GAM1628  D21S2056E 3'  TCCAGCCTGGGCAACGAGAGGG 14873      G   T
                A                   TCTC CTC GTTGCCCAGGCTGGA
                                    |||| ||| ||||||||||||||
                                    AGGG GAG CAACGGGTCCGACCT
                                      A  _
GAM1628  DCOHM     3'  TCCAGCCTGGGTGACGGAACGG 50537       C     TG
                GA                  TCTCG TCTGT  CCCAGGCTGGA
                                    |||||  |||||  ||||||||||
                                    AGGGC AGGCA  GGGTCCGACCT
                                      A     GT
GAM1628  DDX34     3'  TCCAGCCTGGTTGACAGAGCAA 28678      C       GC
                GA                  TCT GCTCTGTT  CCAGGCTGGA
                                    |||  ||||||||  ||||||||||
                                    AGA CGAGACAG  GGTCCGACCT
                                      A        TT
GAM1628  DEGS      3'  TCCACCCTGGGCAACAGAGCAA 59270      C            C
                GA                  TCT GCTCTGTTGCCCAGG TGGA
                                    |||  |||||||||||||| ||||
                                    AGA CGAGACAACGGGTCC ACCT
                                      A             C
GAM1628  DEGS      3'  TCCACCCTGGGCAACAGAGCAA 59271      C            C
                GA                  TCT GCTCTGTTGCCCAGG TGGA
                                    |||  |||||||||||||| ||||
                                    AGA CGAGACAACGGGTCC ACCT
                                      A             C
GAM1628  DIS3      3'  TCCAGCCTGGGTGACAGAACAA 30922      CGC     TG
                GA                  TCT   TCTGT  CCCAGGCTGGA
                                    |||   |||||  ||||||||||
                                    AGA   AGACA  GGGTCCGACCT
                                      ACA     GT
GAM1628  dJ383J4.3 3'  TCCAGCCTGGGCAACAAAGTGA 67498         C
                GA                  TCTCGCT TGTTGCCCAGGCTGGA
                                    |||||||  ||||||||||||||||
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                                AGAGTGA ACAACGGGTCCGACCT
                                   A
GAM1628  DKFZP434A0131 3'  TCCAGCCTGGGTGACAGAGCAA 39154     C      TG
            GA                   TCT GCTCTGT  CCCAGGCTGGA
                                 ||| |||||||  ||||||||||
                                 AGA CGAGACA  GGGTCCGACCT
                                   A      GT
GAM1628  DKFZP434B168 3'  TCCAGCCTGGGCGACAGAGCGA 31872
            GA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                 ||||||||||||||||||||||||
                                 AGAGCGAGACAGCGGGTCCGACCT

GAM1628  DKFZP434C171 3'  TCCAGCCCGGGTGACAGAGCAA 32199     C      TG   A
            GA                   TCT GCTCTGT  CCC GGCTGGA
                                 ||| |||||||  ||| |||||||
                                 AGA CGAGACA  GGG CCGACCT
                                   A      GT   C
GAM1628  DKFZp434E0519 3'  TCTGGGCAACACAGCAAGA    51001     C   C
                                 TCT GCT TGTTGCCCAGG
                                 ||| ||| ||||||||||
                                 AGA CGA ACAACGGGTCT
                                   A   C
GAM1628  DKFZp434E169 3'  CCTGGGCGACAGAGCGAGA    51076
                                 TCTCGCTCTGTTGCCCAGG
                                 |||||||||||||||||
                                 AGAGCGAGACAGCGGGTCC

GAM1628  DKFZP434F1735 3'  TCCAGCCTGGGCAGTATAGCAA 32117     C   C
            GA                   TCT GCT TGTTGCCCAGGCTGGA
                                 ||| ||| |||||||||||||||
                                 AGA CGA ATGACGGGTCCGACCT
                                   A   T
GAM1628  DKFZp434G171 3'  TCCAGCCTGGGAGACACAGCGA 80247        C   TG
            GA                   TCTCGCT TGT  CCCAGGCTGGA
                                 ||||||| |||  ||||||||||
                                 AGAGCGA ACA  GGGTCCGACCT
                                    C   GA
GAM1628  DKFZp434G171 3'  TCCAGCCTGGGCAACAAGAGGG 80248    G   _
            A                     TC CTCT GTTGCCCAGGCTGGA
                                 || |||| |||||||||||||||
                                 AG GAGA CAACGGGTCCGACCT
                                   G   A
GAM1628  DKFZP434I1735 3'  TCCAGCCTGGGCGACAGAGTGA 89173
            GA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                 ||||||||||||||||||||||||
                                 AGAGTGAGACAGCGGGTCCGACCT

GAM1628  DKFZP434K1421 3'  TCCAACCTGGGCAACAGAATGA 50468      C          C
            GA                   TCTCG TCTGTTGCCCAGG TGGA
                                 ||||| |||||||||||| ||||
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                                AGAGT AGACAACGGGTCC ACCT
                                  A           A
GAM1628  DKFZP434N1511 3'  TCCAGCCTGGGCAACAGAGCAA 93063     C
            GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAACGGGTCCGACCT
                                    A
GAM1628  DKFZP434N161 3'  CCTGGGCAACACAGCAAGA    79214     C   C
                                  TCT GCT TGTTGCCCAGG
                                  ||| ||| ||||||||||
                                  AGA CGA ACAACGGGTCC
                                    A   C
GAM1628  DKFZp547C176 3'  TCCAGCCTGGCGACAGAGCAAG 67806     C         C
            A                     TCT GCTCTGTTGCC AGGCTGGA
                                  ||| |||||||||| ||||||||
                                  AGA CGAGACAGCGG TCCGACCT
                                    A        _
GAM1628  DKFZp547G183 3'  TCCAGCCTGGGCGACAAGAGC  38649      _
                                  GCTCT GTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||||
                                  CGAGA CAGCGGGTCCGACCT
                                     A
GAM1628  DKFZp547I094 3'  TCCAGCCTGGGCGGCAGAGTGA 50566
            GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACGGCGGGTCCGACCT

GAM1628  DKFZP564A022 3'  TCCAGCCTGGGCAACAGAGTGA 48975
            GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAACGGGTCCGACCT

GAM1628  DKFZP564B1023 3'  TCCAGCCTGGACAACAGATTGA 49368      C      C
            GA                    TCTCG TCTGTTG CCAGGCTGGA
                                  ||||| ||||||| ||||||||||
                                  AGAGT AGACAAC GGTCCGACCT
                                     T      A
GAM1628  DKFZP564B1023 3'  TCCAGCCTGGGCAACAAGAGTG 49369       _
            A                      TCGCTCT GTTGCCCAGGCTGGA
                                  ||||||| ||||||||||||||||
                                  AGTGAGA CAACGGGTCCGACCT
                                      A
GAM1628  DKFZP564I0422 5'  TCCAGCCTCTGCCAGAAGA   49518    GC    TT  CC
                                  TC  TCTG  GC  AGGCTGGA
                                  ||  ||||  ||  ||||||||
                                  AG  AGAC  CG  TCCGACCT
                                   A_   __  TC
GAM1628  DKFZP564I0422 3'  TCCAGCCTGGGCAATGGAGTGA 49519
            GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
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                                AGAGTGAGGTAACGGGTCCGACCT

GAM1628  DKFZP564I052 3'  TCCAGGCTGGGCAACAGAGTGA 67286              G
            GA                  TCTCGCTCTGTTGCCCAG CTGGA
                                |||||||||||||||||| |||||
                                AGAGTGAGACAACGGGTC GACCT
                                      G
GAM1628  DKFZp564K142 3'  TCCAGCCTGAGTGATAGAGTGA 50436          TG C
            GA                  TCTCGCTCTGT  C CAGGCTGGA
                                |||||||||||  | |||||||||
                                AGAGTGAGATA  G GTCCGACCT
                                      GT A
GAM1628  DKFZp564K142 3'  TCCAGCCTGGCAACAGAGCGAG 50437            C
            A                   TCTCGCTCTGTTGCC AGGCTGGA
                                |||||||||||||| ||||||||
                                AGAGCGAGACAACGG TCCGACCT
                                                _
GAM1628  DKFZP564M182 3'  TCCAGCCTGATGACAGAGCAAG 78642     C       CC
            A                   TCT GCTCTGTTG  CAGGCTGGA
                                ||| |||||||||  |||||||||
                                AGA CGAGACAGT  GTCCGACCT
                                  A        A_
GAM1628  DKFZP564M182 3'  TCCAGCCTGGGCAACAGAGAGA 78643      G
            GA                  TCTC CTCTGTTGCCCAGGCTGGA
                                |||| ||||||||||||||||||
                                AGAG GAGACAACGGGTCCGACCT
                                  A
GAM1628  DKFZP564M182 3'  TCCAGCCTGGGCGGCAGAGC   78644
                                GCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||
                                CGAGACGGCGGGTCCGACCT

GAM1628  DKFZp566H0824 3'  TCCAGCCTGGGCAACAGAGCAA 34492     C
            GG                  TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                GGA CGAGACAACGGGTCCGACCT
                                  A
GAM1628  DKFZp566H0824 5'  TCCAGCCTGGGCGACAGAGCGA 34493
            GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||||
                                AGAGCGAGACAGCGGGTCCGACCT

GAM1628  DKFZP586D2223 3'  CCTGGGCAACATAGCGAGA    38288        C
                                TCTCGCT TGTTGCCCAGG
                                ||||||| ||||||||||
                                AGAGCGA ACAACGGGTCC
                                     T
GAM1628  DKFZP586D2223 3'  TCTAGCCTGGGCAACAGAGTGA 38297
            GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||||
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                                AGAGTGAGACAACGGGTCCGATCT

GAM1628  DKFZP586M1120 3'  TCCAGCCTGGGCAACAGAGTGA 49286
                                TCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||
                                AGTGAGACAACGGGTCCGACCT

GAM1628  DKFZP667O116 3'  CCTGGGCAACATAGCGAGA    95940        C
                                TCTCGCT TGTTGCCCAGG
                                ||||||| ||||||||||
                                AGAGCGA ACAACGGGTCC
                                     T
GAM1628  DKFZp727G131 3'  TCCAGCCTGGGCAACAGCGTGA 59698        T
                GA                TCTCGC CTGTTGCCCAGGCTGGA
                                  ||||||| |||||||||||||||||
                                  AGAGTG GACAACGGGTCCGACCT
                                     C
GAM1628  DKFZP761G1913 3'  TCCAGCCTGGGTGAAGGAGTGA 49699          G TG
                GA                TCTCGCTCT T  CCCAGGCTGGA
                                  |||||||||  |  ||||||||||
                                  AGAGTGAGG A  GGGTCCGACCT
                                       A GT
GAM1628  DRF1     3'  TCCAGCCTGGGCGATAGAGCTA 47757     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| |||||||||||||||||||
                                  AGA CGAGATAGCGGGTCCGACCT
                                    T
GAM1628  DRF1     3'  TCCAGCCTGGGTGACAGAGCGA 47758           TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                       GT
GAM1628  DSCR6    3'  TCCAGCCTGGGCAACAAGAGCG 39076        _
                A                  TCGCTCT GTTGCCCAGGCTGGA
                                   ||||||| ||||||||||||||
                                   AGCGAGA CAACGGGTCCGACCT
                                      A
GAM1628  ET       3'  CCAGCCTGGATGACAAG     44467    C   GC
                                CT TGTT  CCAGGCTGG
                                || ||||  |||||||||
                                GA ACAG  GGTCCGACC
                                 _   TA
GAM1628  EVI5     3'  TCCAACCTGGGCAACATGGCAA 20218     C  C         C
                GA                TCT GCT TGTTGCCCAGG TGGA
                                  ||| ||| |||||||||| ||||
                                  AGA CGG ACAACGGGTCC ACCT
                                    A  T         A
GAM1628  FADS1    3'  TCCAGCCTGGGCGACAGAGCAA 26386     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
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                                AGA CGAGACAGCGGGTCCGACCT
                                  A
GAM1628  FADS1    3'  TCCAGCCTGGGGTGATAGAACA 26387     CGC     TG  _
                  AGA                  TCT   TCTGT  CCC AGGCTGGA
                                |||   |||||  ||| ||||||||
                                AGA   AGATA  GGG TCCGACCT
                                  ACA     GT   G
GAM1628  FBXO26   3'  TCCAGCCTGGGTGAGAAAGCAA 46631     C   CTG TG
                  GA                   TCT GCT   T  CCCAGGCTGGA
                                ||| |||   |  ||||||||||
                                AGA CGA   A  GGGTCCGACCT
                                  A   AAG GT
GAM1628  FBXO27   3'  TCCAGCCTGGGCAACACAGCGA 75014        C
                  GA                   TCTCGCT TGTTGCCCAGGCTGGA
                                |||||||| ||||||||||||||||
                                AGAGCGA ACAACGGGTCCGACCT
                                    C
GAM1628  FBXO27   3'  TCCAGCCTGGGTGACAGAGCGA 75015           TG
                  GA                   TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      GT
GAM1628  FBXO6    3'  TCCAGCCTGGGTGACAGAGCGA 37997           TG
                  GA                   TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      GT
GAM1628  FBXO9    3'  CCTGGACAACATAGCAAGA   54244     C  C     C
                                TCT GCT TGTTG CCAGG
                                ||| ||| ||||| |||||
                                AGA CGA ACAAC GGTCC
                                  A  T    A
GAM1628  FBXO9    3'  TCCAGCATGGGCAACATAACAA 54254     CGCTC        G
                  GA                   TCT    TGTTGCCCA GCTGGA
                                |||    ||||||||| ||||||
                                AGA    ACAACGGGT CGACCT
                                  ACAAT        A
GAM1628  FBXO9    3'  TCCAGCCTGAGCAACACAGTGA 54255        C     C
                  GA                   TCTCGCT TGTTGC CAGGCTGGA
                                ||||||| |||||| |||||||||
                                AGAGTGA ACAACG GTCCGACCT
                                    C     A
GAM1628  FKBP14   3'  TCCAGCCTGGGTGACAGAGCAA 36070     C      TG
                  GA                   TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM1628  FKSG17   3'  TCCAGCCTGGGTGACAGAGTGA 50159           TG
                  GA                   TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
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                                AGAGTGAGACA  GGGTCCGACCT
                                      GT
GAM1628  FKSG43   5'  TCCAGCCTGGGTGACAGAGCAA 50163     C      TG
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGAGACA  GGGTCCGACCT
                                      A      GT
GAM1628  FKSG44   5'  TCCAGCCTGGGCGACAGAGCGA 49963
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    |||||||||||||||||||||||||
                                    AGAGCGAGACAGCGGGTCCGACCT

GAM1628  FKSG83   3'  TCCAGCCTGGGAGACAGCAAGA 50146    GCT    TG
                                    TC   CTGT  CCCAGGCTGGA
                                    ||   ||||  ||||||||||
                                    AG   GACA  GGGTCCGACCT
                                     AAC    GA
GAM1628  FLJ00060 3'  TCCAGCCTGGGCGATAGAGCAA 61755     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGATAGCGGGTCCGACCT
                                      A
GAM1628  FLJ10008 3'  TCCAGCCTGGGCGACACAGCAA 36193     C   C
                GA                  TCT GCT TGTTGCCCAGGCTGGA
                                    ||| ||| ||||||||||||||||
                                    AGA CGA ACAGCGGGTCCGACCT
                                      A   C
GAM1628  FLJ10043 3'  TCCAGCCTGGGTGACAGAGCGA 36237           TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGCGAGACA  GGGTCCGACCT
                                          GT
GAM1628  FLJ10058 3'  TCCAGCCTGGGCAACACAGTGA 36264         C
                GA                  TCTCGCT TGTTGCCCAGGCTGGA
                                    ||||||| ||||||||||||||||
                                    AGAGTGA ACAACGGGTCCGACCT
                                        C
GAM1628  FLJ10139 3'  TCCAGCCTGGGTGACAAAGTAA 36317     CG  C   TG
                GA                  TCT  CT TGT  CCCAGGCTGGA
                                    |||  || |||  ||||||||||
                                    AGA  GA ACA  GGGTCCGACCT
                                      AT  A   GT
GAM1628  FLJ10157 5'  CCAGCCTGGACCAGAAGA    36329    GC    TTGC
                                    TC  TCTG    CCAGGCTGG
                                    ||  ||||    |||||||||
                                    AG  AGAC    GGTCCGACC
                                     A_    CA__
GAM1628  FLJ10159 3'  CCATTTGGGAACAGAGCAAGA  36335     C       G     C
                                    TCT GCTCTGTT CCCAGG TGG
                                    ||| |||||||| |||||| |||
```

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                                AGA CGAGACAA GGGTTT ACC
                                  A       _     _
GAM1628  FLJ10244  3'  TCCAGCCTGGGCAAAAAGAGC  36406       G_
                                GCTCT  TTGCCCAGGCTGGA
                                |||||  ||||||||||||||
                                CGAGA  AACGGGTCCGACCT
                                   AA
GAM1628  FLJ10314  3'  CCAGCCTGCACAACAAG     36485    C     CC
                                CT TGTTG  CAGGCTGG
                                || |||||  ||||||||
                                GA ACAAC  GTCCGACC
                                  _    AC
GAM1628  FLJ10460  3'  TCCAACCTGGGTGATGGAGCAA 36623     C      TG      C
                GA                TCT GCTCTGT  CCCAGG TGGA
                                  ||| |||||||  |||||| ||||
                                  AGA CGAGGTA  GGGTCC ACCT
                                    A       GT      A
GAM1628  FLJ10520  3'  TCCAGCCTCGGTGACAGAGCAA 36710     C      TG  C
                GA                TCT GCTCTGT  CC AGGCTGGA
                                  ||| |||||||  || ||||||||
                                  AGA CGAGACA  GG TCCGACCT
                                    A       GT  C
GAM1628  FLJ10547  3'  TCCAGCCTGGGCTACAGAGCGA 36779           T
                GA                TCTCGCTCTGT GCCCAGGCTGGA
                                  |||||||||||| ||||||||||||
                                  AGAGCGAGACA CGGGTCCGACCT
                                        T
GAM1628  FLJ10597  3'  CCAGCCTGGGCTGACAGG    36835        _
                                  TCTGTT GCCCAGGCTGG
                                  |||||| ||||||||||
                                  GGACAG CGGGTCCGACC
                                     T
GAM1628  FLJ10607  3'  TCCAGCCTGGCGACAGAGAGAG 77646      G         C
                A                  TCTC CTCTGTTGCC AGGCTGGA
                                   |||| |||||||||| ||||||||
                                   AGAG GAGACAGCGG TCCGACCT
                                     A       _
GAM1628  FLJ10613  3'  TCTAGCCTGGGCAACAACACGA 39341     CTC
                                  TCG   TGTTGCCCAGGCTGGA
                                  |||   ||||||||||||||||
                                  AGC   ACAACGGGTCCGATCT
                                    ACA
GAM1628  FLJ10650  3'  TCCAGCCTGGGCGACAGAATGA 36903       C
                GA                TCTCG TCTGTTGCCCAGGCTGGA
                                  ||||| |||||||||||||||||
                                  AGAGT AGACAGCGGGTCCGACCT
                                    A
GAM1628  FLJ10704  3'  TCCAGCCTGGACGACAGAGTGA 36984           C
                GA                TCTCGCTCTGTTG CCAGGCTGGA
                                  |||||||||||| ||||||||||
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                                AGAGTGAGACAGC GGTCCGACCT
                                      A
GAM1628  FLJ10781  3'  TCCAGCCTGGGCAGCAGAGTGA 37176
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACGACGGGTCCGACCT

GAM1628  FLJ10803  3'  TCCAGCCTGGGCAACAGAGCAA 37209     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAACGGGTCCGACCT
                                      A
GAM1628  FLJ10826  3'  TCCAGCCTGGGCAACAAGAGTG 37250        _
                A                    TCGCTCT GTTGCCCAGGCTGGA
                                    ||||||| ||||||||||||||||
                                    AGTGAGA CAACGGGTCCGACCT
                                       A
GAM1628  FLJ10830  3'  TCCAGCCTGGGCGACAGAACGA 37267       C
                GA                  TCTCG TCTGTTGCCCAGGCTGGA
                                    ||||| ||||||||||||||||||
                                    AGAGC AGACAGCGGGTCCGACCT
                                      A
GAM1628  FLJ10901  3'  CCAGCCTGGGCTGGGGGAGA   37355      G   TGTT
                                    TCTC CTC    GCCCAGGCTGG
                                    |||| |||    ||||||||||
                                    AGAG GGG    CGGGTCCGACC
                                      G   T___
GAM1628  FLJ10936  3'  TCCAGCCTGGGCAACAGAGGGA 37450      G
                GA                  TCTC CTCTGTTGCCCAGGCTGGA
                                    |||| ||||||||||||||||||
                                    AGAG GAGACAACGGGTCCGACCT
                                      G
GAM1628  FLJ10989  3'  TCCAGCCTGGGTGACAAAGCAA 37507     C   C   TG
                GA                  TCT GCT TGT  CCCAGGCTGGA
                                    ||| ||| |||  ||||||||||
                                    AGA CGA ACA  GGGTCCGACCT
                                      A   A   GT
GAM1628  FLJ10998  3'  TCCAGCCTGGGTGACAGTGA   37523       CT  TG
                                    TCGCT  GT  CCCAGGCTGGA
                                    |||||  ||  ||||||||||
                                    AGTGA  CA  GGGTCCGACCT
                                      __  GT
GAM1628  FLJ11016  3'  CCTGGGCAACACAGCAAGA    37540     C   C
                                    TCT GCT TGTTGCCCAGG
                                    ||| ||| ||||||||||
                                    AGA CGA ACAACGGGTCC
                                      A   C
GAM1628  FLJ11036  3'  TCCAGCCTGGGCGACAGAGCAA 37556     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
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                              AGA CGAGACAGCGGGTCCGACCT
                                A
GAM1628  FLJ11126  3'  TCCAGCCTGGGTAACAGAGCGA 37655
             GA                 TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||
                                AGAGCGAGACAATGGGTCCGACCT

GAM1628  FLJ11149  3'  TCTGGGCAACATAGCGAGA   37689       C
                              TCTCGCT TGTTGCCCAGG
                              ||||||| ||||||||||
                              AGAGCGA ACAACGGGTCT
                                  T
GAM1628  FLJ11151  3'  TCCAGCCTGGGCAACAGAGCAA 68482     C
             GA                 TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||
                                AGA CGAGACAACGGGTCCGACCT
                                  A
GAM1628  FLJ11259  3'  TCCAGTCTGGGCAACAGAGTGA 37772
             GA                 TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||
                                AGAGTGAGACAACGGGTCTGACCT

GAM1628  FLJ11301  3'  TCCAGCCTGGGCGACAGAGTGA 37810
             GA                 TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||
                                AGAGTGAGACAGCGGGTCCGACCT

GAM1628  FLJ11577  3'  TCCAGCCTGGGCAACAAGAGTG 47960        _
             AGA                  TCTCGCTCT GTTGCCCAGGCTGGA
                                |||||||| ||||||||||||||
                                AGAGTGAGA CAACGGGTCCGACCT
                                    A
GAM1628  FLJ11700  3'  TCCAGCCTGGGCAACAGAACAA 46567     CGC
             GA                 TCT   TCTGTTGCCCAGGCTGGA
                                |||   ||||||||||||||||||
                                AGA   AGACAACGGGTCCGACCT
                                  ACA
GAM1628  FLJ11710  5'  TCCAGCCTGGGCAACAGAGCAA 46252     C
             GA                 TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||
                                AGA CGAGACAACGGGTCCGACCT
                                  A
GAM1628  FLJ11715  3'  TCCAGCCTGGGTGATAGAGTGA 44983          TG
             GA                 TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGAGATA  GGGTCCGACCT
                                    GT
GAM1628  FLJ11722  3'  TCCAGCCTGGCAACAGAGCAAG 47008     C         C
             G                  TCT GCTCTGTTGCC AGGCTGGA
                                ||| |||||||||| ||||||||
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                                GGA CGAGACAACGG TCCGACCT
                                  A       _
GAM1628  FLJ11722  3'  TCCAGCCTGGCCACAGAGCGAG 47009          T   C
             A                   TCTCGCTCTGT GCC AGGCTGGA
                                 |||||||||| ||| ||||||||
                                 AGAGCGAGACA CGG TCCGACCT
                                       C  _
GAM1628  FLJ11726  3'  TCCAGCCTGGGCGACAGAGCAG 47031    TC
             GA                    TC  GCTCTGTTGCCCAGGCTGGA
                                   ||  ||||||||||||||||||
                                   AG  CGAGACAGCGGGTCCGACCT
                                    GA
GAM1628  FLJ11800  3'  TCCAGCCTGGGCAACAGAG   47042
                                   CTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||
                                   GAGACAACGGGTCCGACCT

GAM1628  FLJ11827  3'  CCTGGGCAACATAGCAAGA   47681    C   C
                                   TCT GCT TGTTGCCCAGG
                                   ||| ||| ||||||||||
                                   AGA CGA ACAACGGGTCC
                                     A   T
GAM1628  FLJ11996  3'  TCCAACCTGGGCAACAGAGTAA 47069    CG          C
             GA                    TCT  CTCTGTTGCCCAGG TGGA
                                   |||  |||||||||||||| ||||
                                   AGA  GAGACAACGGGTCC ACCT
                                     AT           A
GAM1628  FLJ12056  3'  TCAGCCCGGGCAACAAGAGCGA 46823         _     A
             GA                    TCTCGCTCT GTTGCCC GGCTGG
                                   ||||||||| ||||||| ||||||
                                   AGAGCGAGA CAACGGG CCGACT
                                       A      C
GAM1628  FLJ12078  3'  TCCAGCCTGGGTGGCAGAGAGA 47086     G    TG
             GA                    TCTC CTCTGT  CCCAGGCTGGA
                                   |||| ||||||  ||||||||||
                                   AGAG GAGACG  GGGTCCGACCT
                                     A     GT
GAM1628  FLJ12190  3'  TCCAGCCTGGGCAACAGAGC   47572
                                   GCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||
                                   CGAGACAACGGGTCCGACCT

GAM1628  FLJ12294  3'  TCCAGCCTGGGTGACAGAGAGA 47721     G    TG
             GA                    TCTC CTCTGT  CCCAGGCTGGA
                                   |||| ||||||  ||||||||||
                                   AGAG GAGACA  GGGTCCGACCT
                                     A     GT
GAM1628  FLJ12298  3'  TCCAGCCTGGGCAACAGAGCGA 50600
             GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||||
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                                AGAGCGAGACAACGGGTCCGACCT

GAM1628  FLJ12331  3'  TCCAGCCTGAGCTACAGAGCAA 47114     C      T  C
                GA                  TCT GCTCTGT GC CAGGCTGGA
                                    ||| ||||||| || |||||||||
                                    AGA CGAGACA CG GTCCGACCT
                                      A      T  A
GAM1628  FLJ12363  3'  TCCAGCCTGGGCAACAAGAGAG 50643      G  C
                A                    TCTC CT TGTTGCCCAGGCTGGA
                                    |||| || ||||||||||||||||
                                    AGAG GA ACAACGGGTCCGACCT
                                      A  _
GAM1628  FLJ12586  3'  TCCAGCCTGGGTGACAGAGCGA 45212          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGCGAGACA  GGGTCCGACCT
                                          GT
GAM1628  FLJ12592  3'  CCTGGGCAACATAGCGAGA    50650        C
                                    TCTCGCT TGTTGCCCAGG
                                    ||||||| ||||||||||
                                    AGAGCGA ACAACGGGTCC
                                        T
GAM1628  FLJ12592  3'  TCCAGCCTGGGTGACCGAGTGA 50655        T  TG
                GA                  TCTCGCTC GT  CCCAGGCTGGA
                                    |||||||| ||  ||||||||||
                                    AGAGTGAG CA  GGGTCCGACCT
                                        C  GT
GAM1628  FLJ12618  3'  TCCAGCCTGGGTGACAGAGCAA 46508     C      TG
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGAGACA  GGGTCCGACCT
                                      A      GT
GAM1628  FLJ12666  3'  TCCAGCCTGGGCAACAAAACGA 45072       CTC
                GA                  TCTCG   TGTTGCCCAGGCTGGA
                                    |||||   ||||||||||||||||
                                    AGAGC   ACAACGGGTCCGACCT
                                       AAA
GAM1628  FLJ12671  3'  TCCAGCCTGGGTGACAAGAGTG 49112          _  TG
                AGA                  TCTCGCTCT GT  CCCAGGCTGGA
                                    ||||||||| ||  ||||||||||
                                    AGAGTGAGA CA  GGGTCCGACCT
                                         A  GT
GAM1628  FLJ12687  3'  TCCAGCCTGGGTGACAGAGTGA 46759          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          GT
GAM1628  FLJ12847  3'  TCCAGCCTGGGCAACAGAGT   45079
                                    GCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||
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                                TGAGACAACGGGTCCGACCT

GAM1628  FLJ12921  3'  TCCAGCCTGGGCGACGGAGCGA 46400
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGGCAGCGGGTCCGACCT

GAM1628  FLJ12949  3'  TCCAGCCTGGGCAACAAAGCAA 43727     C   C
                GA                TCT GCT TGTTGCCCAGGCTGGA
                                  ||| ||| ||||||||||||||||
                                  AGA CGA ACAACGGGTCCGACCT
                                    A   A
GAM1628  FLJ13117  3'  TCCAGCCTGGGAGACAGAGCAA 43811     C      TG
                GA                TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A       GA
GAM1628  FLJ13193  3'  TCCAGCCTGGCGACAGAGCGAG 50736              C
                A                 TCTCGCTCTGTTGCC AGGCTGGA
                                  ||||||||||||||| ||||||||
                                  AGAGCGAGACAGCGG TCCGACCT
                                                  _
GAM1628  FLJ13241  3'  TCCAGCCTGGGTGGCAGAGCCA 47656     C      TG
                GA                TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACG  GGGTCCGACCT
                                    C       GT
GAM1628  FLJ13352  3'  CTGGCCTGGGCAACAGAGCAAG 45053     C             TG
                A                 TCT GCTCTGTTGCCCAGGC  G
                                  ||| ||||||||||||||||  |
                                  AGA CGAGACAACGGGTCCG  C
                                    A              GT
GAM1628  FLJ13448  3'  TCCAGCCTGGGCAACAGAGGGA 47885      G
                GA                TCTC CTCTGTTGCCCAGGCTGGA
                                  |||| ||||||||||||||||||
                                  AGAG GAGACAACGGGTCCGACCT
                                    G
GAM1628  FLJ13456  3'  CCTGGGAAACAGAGCGAGA    66542            G
                                  TCTCGCTCTGTT CCCAGG
                                  ||||||||||| ||||||
                                  AGAGCGAGACAA GGGTCC
                                         A
GAM1628  FLJ13456  3'  TCCAGCCTGGACAACGGAGTGA 66563             C
                GA                TCTCGCTCTGTTG CCAGGCTGGA
                                  |||||||||||| ||||||||||
                                  AGAGTGAGGCAAC GGTCCGACCT
                                         A
GAM1628  FLJ13456  3'  TCCAGCCTGGGTGACAGAGTAA 66564     CG     TG
                GA                TCT  CTCTGT  CCCAGGCTGGA
                                  |||  ||||||  ||||||||||
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                                AGA  GAGACA  GGGTCCGACCT
                                  AT     GT
GAM1628  FLJ13544  3'  TCCAGCCTGGATGACAGAGTGA 47210          GC
                GA                  TCTCGCTCTGTT  CCAGGCTGGA
                                    ||||||||||||  ||||||||||
                                    AGAGTGAGACAG  GGTCCGACCT
                                          TA
GAM1628  FLJ13621  3'  TCCAGCCTGGGCGACAGAGCGA 47226
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    |||||||||||||||||||||||||
                                    AGAGCGAGACAGCGGGTCCGACCT

GAM1628  FLJ13659  3'  TCCAGCCTGGGCAACAAGAGTG 48036        _
                G                    TCGCTCT GTTGCCCAGGCTGGA
                                    |||||||  ||||||||||||||||
                                    GGTGAGA CAACGGGTCCGACCT
                                        A
GAM1628  FLJ13769  3'  TCCAGCCTGGGTGACAGAGCGA 47264          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||||  ||||||||||
                                    AGAGCGAGACA  GGGTCCGACCT
                                          GT
GAM1628  FLJ13848  3'  TCCAGCCTAGGCGACAGAGTGA 45831            C
                GA                  TCTCGCTCTGTTGCC AGGCTGGA
                                    ||||||||||||||| ||||||||
                                    AGAGTGAGACAGCGG TCCGACCT
                                           A
GAM1628  FLJ13902  3'  CCTGGGCAATAGAGCGAGA   45380
                                    TCTCGCTCTGTTGCCCAGG
                                    |||||||||||||||||||
                                    AGAGCGAGATAACGGGTCC

GAM1628  FLJ13952  3'  TCCAGCCTGGGCAACAAGAGTG 46021        _
                A                    TCGCTCT GTTGCCCAGGCTGGA
                                    |||||||  ||||||||||||||||
                                    AGTGAGA CAACGGGTCCGACCT
                                        A
GAM1628  FLJ14011  3'  TCCAGTCTGGGCAACAGAGCAA 42320     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    |||  ||||||||||||||||||||
                                    AGA CGAGACAACGGGTCTGACCT
                                      A
GAM1628  FLJ14100  3'  TCCAGCCTGGGCGACAAAGCAA 47340     C   C
                GA                  TCT GCT TGTTGCCCAGGCTGGA
                                    |||  |||  ||||||||||||||||
                                    AGA CGA ACAGCGGGTCCGACCT
                                      A   A
GAM1628  FLJ14117  3'  TCCAGCCTGGGCAACAGA    43233
                                    TCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||
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                                AGACAACGGGTCCGACCT

GAM1628  FLJ14117  3'  TCCAGCTTGGGCAACAGAGCAA 43235     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAACGGGTTCGACCT
                                    A
GAM1628  FLJ14154  3'  CCAGCCTGAGGAGGAGGGAGA  46226      G    GTTG  _
                                  TCTC CTCT    CC CAGGCTGG
                                  |||| ||||    || ||||||||
                                  AGAG GAGG    GG GTCCGACC
                                    G    A___  A
GAM1628  FLJ14251  3'  TCCAGCCTGGGTAACAGAGCGA 46491
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAATGGGTCCGACCT

GAM1628  FLJ14326  3'  TCCAGCTTGGGCAACGAGC    50784      T
                                  GCTC GTTGCCCAGGCTGGA
                                  |||| ||||||||||||||
                                  CGAG CAACGGGTTCGACCT
                                    _
GAM1628  FLJ14327  3'  TCCAGCCTGGACAACAGAGCTA 46688     C        C
                GA                TCT GCTCTGTTG CCAGGCTGGA
                                  ||| ||||||||| ||||||||||
                                  AGA CGAGACAAC GGTCCGACCT
                                    T        A
GAM1628  FLJ14327  3'  TCCAGCCTGGATAATAGAGTGA 46689            C
                GA                TCTCGCTCTGTTG CCAGGCTGGA
                                  |||||||||||||| ||||||||||
                                  AGAGTGAGATAAT GGTCCGACCT
                                          A
GAM1628  FLJ14345  3'  TCCAGCCTGGGCAACAAGAGTG 45662          _
                A                  TCGCTCT GTTGCCCAGGCTGGA
                                   ||||||| ||||||||||||||||
                                   AGTGAGA CAACGGGTCCGACCT
                                       A
GAM1628  FLJ14346  3'  CCTGGGCAACATAGCAAGA    47362     C   C
                                  TCT GCT TGTTGCCCAGG
                                  ||| ||| ||||||||||||
                                  AGA CGA ACAACGGGTCC
                                    A   T
GAM1628  FLJ14346  3'  TCCAGCCTGGGCAACAGAGCAA 47372     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAACGGGTCCGACCT
                                    A
GAM1628  FLJ14346  3'  TCCAGCCTGGGGGACAGAGCGA 47373            G
                GA                TCTCGCTCTGTT CCCAGGCTGGA
                                  |||||||||||| ||||||||||
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                                AGAGCGAGACAG GGGTCCGACCT
                                       G
GAM1628  FLJ14397  3'  TCCAGCCTGGGCAACAAGGGC  52333      _
                                GCTCT GTTGCCCAGGCTGGA
                                ||||| ||||||||||||||||
                                CGGGA CAACGGGTCCGACCT
                                  A
GAM1628  FLJ14397  3'  TCCAGCCTGGGTGACAGAGCAA 52335     C      TG
           GA                     TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM1628  FLJ14431  3'  CCTGAGCAACATAGCAAGA   52367     C  C     C
                                TCT GCT TGTTGC CAGG
                                ||| ||| |||||| ||||
                                AGA CGA ACAACG GTCC
                                  A  T     A
GAM1628  FLJ14457  3'  TCCAGCCTGGGAGACAGAGTGA 52413          TG
           GA                     TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                       GA
GAM1628  FLJ14466  3'  TCCAACCTGGGCAACAGAGGGA 52431      G          C
           GA                     TCTC CTCTGTTGCCCAGG TGGA
                                |||| |||||||||||||| ||||
                                AGAG GAGACAACGGGTCC ACCT
                                  G            A
GAM1628  FLJ14466  3'  TCCAGCCTGGGCAACAACAGTG 52432       C_
           A                       TCGCT  TGTTGCCCAGGCTGGA
                                ||||||  ||||||||||||||||
                                AGTGA  ACAACGGGTCCGACCT
                                   CA
GAM1628  FLJ14490  3'  TCCAGCCTGGGCAACAGAGCAA 52448     C
           GA                     TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGAGACAACGGGTCCGACCT
                                  A
GAM1628  FLJ14621  3'  TCCAGCCTGGGCAACAGAGC   52540
                                GCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||
                                CGAGACAACGGGTCCGACCT

GAM1628  FLJ14888  3'  CCTGGGCAACATAGCAAGA   52747     C  C
                                TCT GCT TGTTGCCCAGG
                                ||| ||| ||||||||||
                                AGA CGA ACAACGGGTCC
                                  A  T
GAM1628  FLJ20004  3'  TCCAGCCTAGGCAACAAGAGTG 34765        _     C
           A                       TCGCTCT GTTGCC AGGCTGGA
                                |||||||  ||||||  ||||||||
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                                AGTGAGA CAACGG TCCGACCT
                                   A     A
GAM1628  FLJ20004  3'  TCCAGCCTGGCAACAGAGCAAG 34766     C         C
             A                   TCT GCTCTGTTGCC AGGCTGGA
                                 ||| |||||||||| ||||||||
                                 AGA CGAGACAACGG TCCGACCT
                                   A         _
GAM1628  FLJ20004  3'  TCCAGCCTGGGCAACAGAGGGA 34767      G
             GA                    TCTC CTCTGTTGCCCAGGCTGGA
                                   |||| ||||||||||||||||||
                                   AGAG GAGACAACGGGTCCGACCT
                                     G
GAM1628  FLJ20004  3'  TCCAGCCTGGGTGACAGAGTGA 34768           TG
             GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   AGAGTGAGACA  GGGTCCGACCT
                                         GT
GAM1628  FLJ20006  3'  TCCAGCCTGGGCGATAGAGTGA 34788
             GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGTGAGATAGCGGGTCCGACCT

GAM1628  FLJ20013  3'  TCCAGCCTCGGTGACAGAGCAA 34803     C      TG  C
             GA                    TCT GCTCTGT  CC AGGCTGGA
                                   ||| |||||||  || ||||||||
                                   AGA CGAGACA  GG TCCGACCT
                                     A      GT  C
GAM1628  FLJ20019  3'  TCCAGCCTAGGTGACAGGGCAA 34816     C      TG  C
             GA                    TCT GCTCTGT  CC AGGCTGGA
                                   ||| |||||||  || ||||||||
                                   AGA CGGGACA  GG TCCGACCT
                                     A      GT  A
GAM1628  FLJ20045  3'  TCCAGCCTGGGTGAGAAGAGCG 34893        G_ TG
             A                     TCGCTCT  T  CCCAGGCTGGA
                                   |||||||  |  ||||||||||
                                   AGCGAGA  A  GGGTCCGACCT
                                      AG GT
GAM1628  FLJ20055  3'  TCCAGCTGGGCAACACAGCAAG 34914     C  C        G
             A                     TCT GCT TGTTGCCCAG CTGGA
                                   ||| ||| |||||||||| |||||
                                   AGA CGA ACAACGGGTC GACCT
                                     A  C         _
GAM1628  FLJ20059  3'  TCCAGCCTGGACAGCAGGAGCG 34930        _    C
             A                     TCGCTC TGTTG CCAGGCTGGA
                                   |||||| ||||| ||||||||||
                                   AGCGAG ACGAC GGTCCGACCT
                                      G    A
GAM1628  FLJ20069  3'  TCCAGCCTGGGGGACAGAGCAA 34957     C       G
             GA                    TCT GCTCTGTT CCCAGGCTGGA
                                   ||| |||||||| ||||||||||
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                                AGA CGAGACAG GGGTCCGACCT
                                  A       G
GAM1628  FLJ20084  3'  TCCAGCCTGGGCAACAGAGCGA 34999
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAACGGGTCCGACCT

GAM1628  FLJ20139  3'  TCCAGCCTGCGTGACAAAGTGA 35122        C   TG C
                GA                TCTCGCT TGT  C CAGGCTGGA
                                  ||||||| |||  | |||||||||
                                  AGAGTGA ACA  G GTCCGACCT
                                     A   GT C
GAM1628  FLJ20139  3'  TTGGGCAACAAAGCAAGA    35124     C   C
                                  TCT GCT TGTTGCCCAG
                                  ||| ||| ||||||||||
                                  AGA CGA ACAACGGGTT
                                    A   A
GAM1628  FLJ20170  3'  TCCAGCCTGGGTGACAGAGTGA 35166          TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                        GT
GAM1628  FLJ20211  3'  TCCAGCCTGGGCAACAGAGTGA 35266
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAACGGGTCCGACCT

GAM1628  FLJ20211  3'  TCCAGCCTGGGCGACAGAGTGA 35267
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAGCGGGTCCGACCT

GAM1628  FLJ20241  3'  TCCAGCCTGGACAACAGAGCGA 35291           C
                GA                TCTCGCTCTGTTG CCAGGCTGGA
                                  |||||||||||| ||||||||||
                                  AGAGCGAGACAAC GGTCCGACCT
                                        A
GAM1628  FLJ20280  3'  TCCAGCCTGGGTGACAGAGCGA 35334          TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GT
GAM1628  FLJ20306  3'  TCCAGCCTGGACGACTGAGTGA 35399        T   C
                GA                TCTCGCTC GTTG CCAGGCTGGA
                                  |||||||| |||| ||||||||||
                                  AGAGTGAG CAGC GGTCCGACCT
                                      T   A
GAM1628  FLJ20306  3'  TCCAGCCTGGCGACAGAGCAAG 35400     C         C
                A                  TCT GCTCTGTTGCC AGGCTGGA
                                   ||| |||||||||| ||||||||
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                                AGA CGAGACAGCGG TCCGACCT
                                  A        _
GAM1628  FLJ20340  3'  TCCAGCCTGGTGACAGAGCGAG 35460          TG  C
                 A                 TCTCGCTCTGT  CC AGGCTGGA
                                   ||||||||||  || ||||||||
                                   AGAGCGAGACA  GG TCCGACCT
                                         GT  _
GAM1628  FLJ20456  3'  TCCAGCCTGGGTAACAGAGCTA 35666     C
                 GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                     ||| ||||||||||||||||||||
                                     AGA CGAGACAATGGGTCCGACCT
                                       T
GAM1628  FLJ20546  3'  TCCAGCCTGGGCAACGAGCGA  35814       T
                                     TCGCTC GTTGCCCAGGCTGGA
                                     ||||||| ||||||||||||||||
                                     AGCGAG CAACGGGTCCGACCT
                                       _
GAM1628  FLJ20671  3'  TCCAGCCTGGGTGACAGAGCGA 35945          TG
                 GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                     ||||||||||  ||||||||||
                                     AGAGCGAGACA  GGGTCCGACCT
                                           GT
GAM1628  FLJ20694  3'  TCCAGCCTGGCGACAGAGCAAG 35979     C         C
                 A                   TCT GCTCTGTTGCC AGGCTGGA
                                     ||| |||||||||| ||||||||
                                     AGA CGAGACAGCGG TCCGACCT
                                       A        _
GAM1628  FLJ20700  3'  TCCAGCCTGGGCGACACAGCGA 36020        C
                 GA                  TCTCGCT TGTTGCCCAGGCTGGA
                                     ||||||| ||||||||||||||||
                                     AGAGCGA ACAGCGGGTCCGACCT
                                         C
GAM1628  FLJ20802  3'  TCCAGCCTGGGCGACAGAGCGA 36114
                 GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                     ||||||||||||||||||||||||
                                     AGAGCGAGACAGCGGGTCCGACCT

GAM1628  FLJ20825  3'  TCCAGCCTGGCCCACAGAGTGA 36148          TGC
                 GA                  TCTCGCTCTGT   CCAGGCTGGA
                                     ||||||||||   ||||||||||
                                     AGAGTGAGACA   GGTCCGACCT
                                           CCC
GAM1628  FLJ20825  3'  TCCAGCCTGGGCAACAAGAGCG 36149        _
                 A                   TCGCTCT GTTGCCCAGGCTGGA
                                     ||||||| ||||||||||||||||
                                     AGCGAGA CAACGGGTCCGACCT
                                         A
GAM1628  FLJ20972  3'  TCCAGCCTGGGCAACAAGAGAA 47389     CG   _
                 GA                  TCT  CTCT GTTGCCCAGGCTGGA
                                     |||  |||| ||||||||||||||
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                                AGA  GAGA CAACGGGTCCGACCT
                                  A_    A
GAM1628  FLJ21144  3'  TCCAGCCTGGGCAACAGAGTGA 43194
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAACGGGTCCGACCT

GAM1628  FLJ21240  3'  TCCAGCCTGGGCAAAAAGAGC  46268      G_
                                    GCTCT  TTGCCCAGGCTGGA
                                    |||||  ||||||||||||||
                                    CGAGA  AACGGGTCCGACCT
                                      AA
GAM1628  FLJ21369  3'  TCCAGCCTGGGTGACAGAGCAA 46056     C      TG
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    |||  |||||||  ||||||||||
                                    AGA CGAGACA  GGGTCCGACCT
                                      A      GT
GAM1628  FLJ21687  3'  TCCAGCCTGGGTGACAGAGCGA 46304          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGCGAGACA  GGGTCCGACCT
                                          GT
GAM1628  FLJ21870  3'  TCCAGCCTGGGCAACGGAG   43750
                                    CTCTGTTGCCCAGGCTGGA
                                    |||||||||||||||||
                                    GAGGCAACGGGTCCGACCT

GAM1628  FLJ22009  3'  TCCAGCTTGGGCGACAGAGCGA 60921
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACAGCGGGTTCGACCT

GAM1628  FLJ22054  3'  TCCAGCCTGGGCAACAGAGCAA 96053     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    |||  ||||||||||||||||||
                                    AGA CGAGACAACGGGTCCGACCT
                                      A
GAM1628  FLJ22316  3'  TCCAGCCTGGGCAACAGAGCCA 47619     C
                GG                  TCT GCTCTGTTGCCCAGGCTGGA
                                    |||  ||||||||||||||||||
                                    GGA CGAGACAACGGGTCCGACCT
                                      C
GAM1628  FLJ22415  3'  TCCAGCCTGGGTGACAAAGCAA 93121     C   C   TG
                GA                  TCT GCT TGT  CCCAGGCTGGA
                                    |||  |||  |||  ||||||||||
                                    AGA CGA ACA  GGGTCCGACCT
                                      A   A   GT
GAM1628  FLJ22474  3'  TCCAGCCTGGGCAACAGAGTGA 45618
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
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                                AGAGTGAGACAACGGGTCCGACCT

GAM1628  FLJ22644  3'  TCCAGCCTGGGCTACAGAGCGA 47703          T
                GA                TCTCGCTCTGT GCCCAGGCTGGA
                                  |||||||||||| ||||||||||||
                                  AGAGCGAGACA CGGGTCCGACCT
                                        T
GAM1628  FLJ22814  3'  TCCAACCTGGGTGACGAGTGAG 46731        T  TG     C
                A                 TCTCGCTC GT  CCCAGG TGGA
                                  |||||||| ||  |||||| ||||
                                  AGAGTGAG CA  GGGTCC ACCT
                                       _ GT     A
GAM1628  FLJ22814  3'  TCCAGCCTGGGTGACAGAGGGA 46732    G     TG
                                  TC CTCTGT  CCCAGGCTGGA
                                  || ||||||  ||||||||||||
                                  AG GAGACA  GGGTCCGACCT
                                   G     GT
GAM1628  FLJ23022  3'  TCCAGCCTGGGCGACAAGAGC  47499      _
                                  GCTCT GTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||||
                                  CGAGA CAGCGGGTCCGACCT
                                     A
GAM1628  FLJ23040  3'  TCCAGCCTGGGCAATAGAGCAA 47992     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGATAACGGGTCCGACCT
                                    A
GAM1628  FLJ23042  3'  CCTGAGCAACAGATCAAGA    47941     CGC       C
                                  TCT   TCTGTTGC CAGG
                                  |||   |||||||| ||||
                                  AGA   AGACAACG GTCC
                                    ACT       A
GAM1628  FLJ23042  3'  TCCAGCCTGGGCAACAAGAGTG 47949        _
                A                 TCGCTCT GTTGCCCAGGCTGGA
                                  ||||||| ||||||||||||||||
                                  AGTGAGA CAACGGGTCCGACCT
                                       A
GAM1628  FLJ23120  3'  TCCAGCCTGGGTGACGGAGAAA 86330     CG     TG
                GA                TCT  CTCTGT  CCCAGGCTGGA
                                  |||  ||||||  ||||||||||||
                                  AGA  GAGGCA  GGGTCCGACCT
                                    AA     GT
GAM1628  FLJ23185  3'  TCCAGCCTTGGCAACAAAGCAA 47522     C  C      C
                GA                TCT GCT TGTTGCC AGGCTGGA
                                  ||| ||| ||||||| ||||||||
                                  AGA CGA ACAACGG TCCGACCT
                                    A  A      T
GAM1628  FLJ23185  3'  TCCAGCCTTGGCAACAGAGTGA 47523            C
                GA                TCTCGCTCTGTTGCC AGGCTGGA
                                  |||||||||||||| ||||||||
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                                AGAGTGAGACAACGG TCCGACCT
                                        T
GAM1628  FLJ23209  3'  CCTGGGCAACATAGCAAGA   46586    C   C
                                TCT GCT TGTTGCCCAGG
                                ||| ||| ||||||||||
                                AGA CGA ACAACGGGTCC
                                  A   T
GAM1628  FLJ23229  3'  TCCAGCCTGGACAACAGAGCAA 47532    C       C
                GA                TCT GCTCTGTTG CCAGGCTGGA
                                ||| ||||||||| ||||||||||
                                AGA CGAGACAAC GGTCCGACCT
                                  A       A
GAM1628  FLJ23360  3'  TCCAGCCCGGGTGACAGAGCGA 43835          TG   A
                GA                TCTCGCTCTGT  CCC GGCTGGA
                                |||||||||||  ||| |||||||
                                AGAGCGAGACA  GGG CCGACCT
                                      GT   C
GAM1628  FLJ23447  3'  CTGGGCAACAGAGCAAGA    46132    C
                                TCT GCTCTGTTGCCCAG
                                ||| ||||||||||||||
                                AGA CGAGACAACGGGTC
                                  A
GAM1628  FLJ23499  3'  CCTGGGCAACATAGCAAGA   43132    C   C
                                TCT GCT TGTTGCCCAGG
                                ||| ||| ||||||||||
                                AGA CGA ACAACGGGTCC
                                  A   T
GAM1628  FLJ23499  3'  TCCAGCCTGGGCGACAAGAGCG 43140        _
                A                 TCGCTCT GTTGCCCAGGCTGGA
                                ||||||| ||||||||||||||||
                                AGCGAGA CAGCGGGTCCGACCT
                                    A
GAM1628  FLJ23537  3'  TCCAGCCTGGGCAACAAGAGGA 88921    G   _
                                TC CTCT GTTGCCCAGGCTGGA
                                || |||| ||||||||||||||||
                                AG GAGA CAACGGGTCCGACCT
                                 _   A
GAM1628  FLJ23556  3'  CTGGGCAACAAAGCAAGA    46439    C   C
                                TCT GCT TGTTGCCCAG
                                ||| ||| ||||||||||
                                AGA CGA ACAACGGGTC
                                  A   A
GAM1628  FLJ23556  3'  TCCAGCCTGGGCGACTGTGAGA 46455       TCT
                                TCTCGC   GTTGCCCAGGCTGGA
                                ||||||   ||||||||||||||||
                                AGAGTG   CAGCGGGTCCGACCT
                                   T__
GAM1628  FLJ23878  3'  TCCAGCCTGGGTGACAGGGCGA 59373          TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
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                                AGAGCGGGACA  GGGTCCGACCT
                                      GT
GAM1628  FLJ25006  3'  TCCAGCCTGAGCAACAGAGTGA 58789            C
                GA                  TCTCGCTCTGTTGC CAGGCTGGA
                                    |||||||||||||| |||||||||
                                    AGAGTGAGACAACG GTCCGACCT
                                          A
GAM1628  FLJ30092  3'  TCCAGCCTGGGCAACAGAGTGA 59342
                G                   CTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    GAGTGAGACAACGGGTCCGACCT

GAM1628  FLJ30681  3'  TCCAGCCTAGGCAACAGAGGGA 93440      G        C
                GA                  TCTC CTCTGTTGCC AGGCTGGA
                                    |||| |||||||||| ||||||||
                                    AGAG GAGACAACGG TCCGACCT
                                      G         A
GAM1628  FLJ31168  3'  TCCAGCCTGGGCGACAGAGCGA 59186
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACAGCGGGTCCGACCT

GAM1628  FLJ31455  3'  TCCAGCCTGGGCGACAGAGCCA 59291     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||
                                    AGA CGAGACAGCGGGTCCGACCT
                                      C
GAM1628  FLJ31455  3'  TCCAGCCTGGGTGACAGAGCAA 59292     C      TG
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGAGACA  GGGTCCGACCT
                                      A       GT
GAM1628  FLJ31952  3'  TCCAGCCTGGGCAACAGAGTGA 59050
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAACGGGTCCGACCT

GAM1628  FLJ32499  5'  TCCAGTGACCGACAGAGCAAGA 58782     C        CCCAG
                                    TCT GCTCTGTTG     GCTGGA
                                    ||| |||||||||     ||||||
                                    AGA CGAGACAGC     TGACCT
                                      A         CAG__
GAM1628  FLJ32915  5'  TCCAGCCTGGGCGACAAGAGCG 59437          _
                AGA                   TCTCGCTCT GTTGCCCAGGCTGGA
                                      ||||||||| ||||||||||||||
                                      AGAGCGAGA CAGCGGGTCCGACCT
                                           A
GAM1628  FRSB     3'  TCCAGCCTGGGTGACAGAGTGA 20293           TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
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                                AGAGTGAGACA  GGGTCCGACCT
                                      GT
GAM1628  FUSIP1    3'  TCCAGCCTGGGCAACAGAGTGA 55043
                GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                      ||||||||||||||||||||||||
                                      AGAGTGAGACAACGGGTCCGACCT

GAM1628  GALNT6    3'  CCAGCCTGAGCAACAAGAGCGA 24244        _    C
                                      TCGCTCT GTTGC CAGGCTGG
                                      ||||||| ||||| ||||||||
                                      AGCGAGA CAACG GTCCGACC
                                         A    A
GAM1628  GALNT6    3'  TCCAGCCTGGGCAACAGGTAAG 24252     CG T
                A                      TCT  C CTGTTGCCCAGGCTGGA
                                       |||  | ||||||||||||||||
                                       AGA  G GACAACGGGTCCGACCT
                                         AT _
GAM1628  GCN2      3'  CCAGCCTGAGCAACAAAGCAAG 63437     C   C     C
                A                      TCT GCT TGTTGC CAGGCTGG
                                       ||| ||| |||||| ||||||||
                                       AGA CGA ACAACG GTCCGACC
                                         A  A     A
GAM1628  GCN2      3'  TCCAGTCTGGGACAACAGAGCA 63440     C       _
                AGA                     TCT GCTCTGTTG CCCAGGCTGGA
                                        ||| ||||||||| ||||||||||
                                        AGA CGAGACAAC GGGTCTGACCT
                                          A        A
GAM1628  GGA2      3'  TCCAGCCTGGGCTACATAGTGA 57683        C   T
                GA                      TCTCGCT TGT GCCCAGGCTGGA
                                        ||||||| ||| ||||||||||||
                                        AGAGTGA ACA CGGGTCCGACCT
                                           T   T
GAM1628  GGA2      3'  TCCAGCCTGGGCTACATAGTGA 31172        C   T
                GA                      TCTCGCT TGT GCCCAGGCTGGA
                                        ||||||| ||| ||||||||||||
                                        AGAGTGA ACA CGGGTCCGACCT
                                           T   T
GAM1628  GLTP      3'  TCCAGCCTGGGCAACAAGAGCG 33588        _
                A                       TCGCTCT GTTGCCCAGGCTGGA
                                        ||||||| ||||||||||||||||
                                        AGCGAGA CAACGGGTCCGACCT
                                           A
GAM1628  GNB4      3'  TCCAGCCTAGGCGACAGAGTGA 41570              C
                GA                      TCTCGCTCTGTTGCC AGGCTGGA
                                        |||||||||||||| ||||||||
                                        AGAGTGAGACAGCGG TCCGACCT
                                                 A
GAM1628  GP5       3'  CCTGGGCGACAGAGCGAGA    16872
                                        TCTCGCTCTGTTGCCCAGG
                                        |||||||||||||||||||
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                                AGAGCGAGACAGCGGGTCC

GAM1628 GTPBP5   3' TCCAGCCTGAGCGACAGAGCAA 65981     C        C
           GA                    TCT GCTCTGTTGC CAGGCTGGA
                                 ||| |||||||||| |||||||||
                                 AGA CGAGACAGCG GTCCGACCT
                                   A         A
GAM1628 GTPBP5   3' TCCAGCCTGAGTGACAGAGCGA 65982           TG C
           GA                    TCTCGCTCTGT  C CAGGCTGGA
                                 |||||||||||  | |||||||||
                                 AGAGCGAGACA  G GTCCGACCT
                                       GT A
GAM1628 HCGIX    3' TCCAGCCTGGGTGACAGCAAGA 20716     GCT    TG
           G                     CTC   CTGT  CCCAGGCTGGA
                                 |||   ||||  ||||||||||||
                                 GAG   GACA  GGGTCCGACCT
                                   AAC    GT
GAM1628 HEI10    3' TCCAGCCTGGGCAACAGAGTGA 41299
           GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                 ||||||||||||||||||||||||
                                 AGAGTGAGACAACGGGTCCGACCT

GAM1628 HES2     3' TCCAGGCTGGGCGACAGAGCGA 39378              G
           GA                    TCTCGCTCTGTTGCCCAG CTGGA
                                 |||||||||||||||| |||||
                                 AGAGCGAGACAGCGGGTC GACCT
                                                G
GAM1628 HIC      3' TCCAGCCTGGGCAACAGAGCGA 68052
           GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                 ||||||||||||||||||||||||
                                 AGAGCGAGACAACGGGTCCGACCT

GAM1628 HIG2     3' CCAGCCTGGGCCACAGTGCAAG 26198     C  T    T
           A                      TCT GC CTGT GCCCAGGCTGG
                                  ||| || |||| ||||||||||
                                  AGA CG GACA CGGGTCCGACC
                                    A  T    C
GAM1628 HRH4     3' CCAGCCTGGCAACAGAGCAAGA 41530     C        C
                                 TCT GCTCTGTTGCC AGGCTGG
                                 ||| |||||||||| |||||||
                                 AGA CGAGACAACGG TCCGACC
                                   A         _
GAM1628 HSA250303 3' TCCAGCCTGGGCTACAGAGTGA 38023           T
           GA                    TCTCGCTCTGT GCCCAGGCTGGA
                                 |||||||||| ||||||||||||
                                 AGAGTGAGACA CGGGTCCGACCT
                                       T
GAM1628 HSD17B7  3' TCCAGCCTGGGTGACAGCGAGA 33484        CT  TG
                                 TCTCGCT  GT  CCCAGGCTGGA
                                 |||||||  ||  ||||||||||
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                                AGAGCGA  CA  GGGTCCGACCT
                                   __  GT
GAM1628  HSH2     3'  TCCAGCCTGGATGACAGAGTGA 52744           GC
                GA                  TCTCGCTCTGTT  CCAGGCTGGA
                                    ||||||||||||  ||||||||||
                                    AGAGTGAGACAG  GGTCCGACCT
                                       TA
GAM1628  HSMPP8   3'  TCCAGCCTGAGTGACAGAATGA 95141      C     TG C
                GA                  TCTCG TCTGT  C CAGGCTGGA
                                    |||||  |||||  | |||||||||
                                    AGAGT AGACA  G GTCCGACCT
                                      A     GT A
GAM1628  HSU79252  5'  TCCAGCCTGGGTGACAGAGTGA 26143          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||||  ||||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                       GT
GAM1628  HSU79266  3'  CCAGCCTGAGGAGGGAGCGTGA 26144    T     GTTG  _
                                    TC CGCTCT    CC CAGGCTGG
                                    || ||||||    || |||||||||
                                    AG GCGAGG    GG GTCCGACC
                                     T     GA__  A
GAM1628  HYPK     3'  TCCAGCCTGGGGGGAAAGAGTGA 33516        G  G
                                    TCGCTCT TT CCCAGGCTGGA
                                    ||||||| || ||||||||||||
                                    AGTGAGA AG GGGTCCGACCT
                                        A  G
GAM1628  ICAM4    3'  TCCAGCCTGGGGGGACAGAGC   9545          G
                                    GCTCTGTT CCCAGGCTGGA
                                    |||||||| ||||||||||||
                                    CGAGACAG GGGTCCGACCT
                                         G
GAM1628  ICAM4    3'  TCCAGCCTGGGGGGACAGAGC   9546          G
                                    GCTCTGTT CCCAGGCTGGA
                                    |||||||| ||||||||||||
                                    CGAGACAG GGGTCCGACCT
                                         G
GAM1628  IL-23R   3'  TCCAGCCTGGGCAACAAGAGC  59132       _
                                    GCTCT GTTGCCCAGGCTGGA
                                    ||||| |||||||||||||||
                                    CGAGA CAACGGGTCCGACCT
                                       A
GAM1628  IL10RB   3'  TCCAGCCTGGGTGACAAAGTGA 7129         C   TG
                GA                  TCTCGCT TGT  CCCAGGCTGGA
                                    ||||||| |||  ||||||||||||
                                    AGAGTGA ACA  GGGTCCGACCT
                                        A   GT
GAM1628  IMAGE:4907098 3'  TCCAGCCTGGGCGACAGAGCAA 57758     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
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                                AGA CGAGACAGCGGGTCCGACCT
                                  A
GAM1628  KBRAS2    3'  TCCAGCCTGGTCAACAGAGCAA 34628     C        C
                GA                TCT GCTCTGTTG CCAGGCTGGA
                                  ||| ||||||||| ||||||||||
                                AGA CGAGACAAC GGTCCGACCT
                                  A        T
GAM1628  KCNH6     3'  TCCAGCCTGGGTGACAGAGTGA 48576           TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  |||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      GT
GAM1628  KIAA0042  3'  TCCAGTCTGAGCAACAGAACGA 30239       C       C
                GA                TCTCG TCTGTTGC CAGGCTGGA
                                  ||||| |||||||| |||||||||
                                AGAGC AGACAACG GTCTGACCT
                                   A       A
GAM1628  KIAA0057  3'  TCCAGCCTGGACAACAAGAGCG 25424         _   C
                A                  TCGCTCT GTTG CCAGGCTGGA
                                  ||||||| |||| ||||||||||
                                AGCGAGA CAAC GGTCCGACCT
                                    A   A
GAM1628  KIAA0184  3'  TCCAGCCTGGGTGACAGCACGA 65815       CT    TG
                GA                TCTCG  CTGT  CCCAGGCTGGA
                                  ||||| ||||  ||||||||||||
                                AGAGC  GACA  GGGTCCGACCT
                                   AC   GT
GAM1628  KIAA0186  3'  TCCAGCCTGGGTGACAAAGTGA 41119        C   TG
                GA                TCTCGCT TGT  CCCAGGCTGGA
                                  ||||||| |||  ||||||||||||
                                AGAGTGA ACA  GGGTCCGACCT
                                    A  GT
GAM1628  KIAA0226  3'  TCCAGCCTGGGTGACAGAGTGA 64264           TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      GT
GAM1628  KIAA0336  3'  TCCAGCTCGGGGAACAGAGCGA 28324           G   AG
                GA                TCTCGCTCTGTT CCC  GCTGGA
                                  ||||||||||| |||  ||||||
                                AGAGCGAGACAA GGG  CGACCT
                                     G   CT
GAM1628  KIAA0355  3'  TCCAGCCTGGGTGACAGAGTGA 28710           TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      GT
GAM1628  KIAA0391  3'  CCTGGGCAACATAGCAAGA   28605     C   C
                                TCT GCT TGTTGCCCAGG
                                ||| ||| ||||||||||
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                                AGA CGA ACAACGGGTCC
                                  A   T
GAM1628  KIAA0391  3'  TCCAGCCTAGGTGACAGAGTGA 28621          TG  C
                GA                  TCTCGCTCTGT  CC AGGCTGGA
                                    ||||||||||  || ||||||||
                                    AGAGTGAGACA  GG TCCGACCT
                                          GT  A
GAM1628  KIAA0408  3'  TCCAGCCTGGGTGACAGAGTGA 28802          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          GT
GAM1628  KIAA0409  3'  TCCAGCCTGGCTGTGAGCCAAG 31682     C_   TGTT   C
                A                    TCT  GCTC    GCC AGGCTGGA
                                    |||  ||||    ||| ||||||||
                                    AGA  CGAG    CGG TCCGACCT
                                      AC    TGT_  _
GAM1628  KIAA0427  3'  CCAGCCTGGGAACACAGA    29375      TG_
                                    TCTGT   CCCAGGCTGG
                                    |||||   ||||||||||
                                    AGACA   GGGTCCGACC
                                       CAA
GAM1628  KIAA0431  3'  TCCAACCTGGGTAACAGGGCAA 31554     C           C
                GA                  TCT GCTCTGTTGCCCAGG TGGA
                                    ||| ||||||||||||||| ||||
                                    AGA CGGGACAATGGGTCC ACCT
                                      A            A
GAM1628  KIAA0445  5'  TCCAGCCTGTGTGACAGAGCAA 28642     C      TG C
                GA                  TCT GCTCTGT  C CAGGCTGGA
                                    ||| |||||||  | |||||||||
                                    AGA CGAGACA  G GTCCGACCT
                                      A      GT T
GAM1628  KIAA0446  5'  TCCAGCCTGGGCGACAGAGCGA 69460
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACAGCGGGTCCGACCT

GAM1628  KIAA0447  3'  TCCAGCCTGGGCAACAGGGCAA 72129     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGGGACAACGGGTCCGACCT
                                      A
GAM1628  KIAA0451  5'  TCAGCCTGGGCAACAGAGCAAG 29781     C
                A                    TCT GCTCTGTTGCCCAGGCTGG
                                    ||| ||||||||||||||||||
                                    AGA CGAGACAACGGGTCCGACT
                                      A
GAM1628  KIAA0472  3'  TCCAGCCTGGGCAACAGAGCGA 72367
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
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                                AGAGCGAGACAACGGGTCCGACCT

GAM1628  KIAA0472  3'  TCCAGCCTGGGCAGCAGAGCAA 72368     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACGACGGGTCCGACCT
                                    A
GAM1628  KIAA0472  3'  TCCAGCCTGGGCGACAGAGTGA 72369
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAGCGGGTCCGACCT

GAM1628  KIAA0475  3'  TCCAGCCTGGGAGACAGAGCGA 30130          TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GA
GAM1628  KIAA0514  3'  TCCAGCCTGGATGACGGAGCCA 28755     C       GC
                GA                TCT GCTCTGTT  CCAGGCTGGA
                                  ||| ||||||||  ||||||||||
                                  AGA CGAGGCAG  GGTCCGACCT
                                    C       TA
GAM1628  KIAA0547  3'  TCCAGCCTGGCAACAGAGCAAG 29600     C         C
                A                 TCT GCTCTGTTGCC AGGCTGGA
                                  ||| ||||||||||| ||||||||
                                  AGA CGAGACAACGG TCCGACCT
                                    A         _
GAM1628  KIAA0557  3'  TCCAGCCTGGTGATAGAACGAG 78576       C     TG  C
                A                 TCTCG TCTGT  CC AGGCTGGA
                                  ||||| |||||  || ||||||||
                                  AGAGC AGATA  GG TCCGACCT
                                     A    GT  _
GAM1628  KIAA0563  3'  TCCAGCCTGGGCGACAGAGCAA 29890     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM1628  KIAA0565  3'  TCCAACCTGGGCGACAGAGCAA 67441     C           C
                GA                TCT GCTCTGTTGCCCAGG TGGA
                                  ||| |||||||||||||| ||||
                                  AGA CGAGACAGCGGGTCC ACCT
                                    A            A
GAM1628  KIAA0565  3'  TCCAATCTGGGCAACATAGCAA 67442     C   C       GC
                GA                TCT GCT TGTTGCCCAG  TGGA
                                  ||| ||| ||||||||||  ||||
                                  AGA CGA ACAACGGGTC  ACCT
                                    A  T        TA
GAM1628  KIAA0643  3'  TCCAGCCTGGGTGACAGAGTGA 45980          TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
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                                AGAGTGAGACA  GGGTCCGACCT
                                      GT
GAM1628  KIAA0694  3'  TCCAGCCTGGGCAACAGAGTGA 72974
                GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                      ||||||||||||||||||||||||
                                      AGAGTGAGACAACGGGTCCGACCT

GAM1628  KIAA0701  5'  CAGTGAGCAACAGGACGAGA   70094      CT      C AG
                                      TCTCG  CTGTTGC C  GCTG
                                      |||||  |||||||  |  ||||
                                      AGAGC  GACAACG G  TGAC
                                        AG      A __
GAM1628  KIAA0738  3'  TCCAGCCTGGGGGACAGAGTGA 28887            G
                GA                    TCTCGCTCTGTT CCCAGGCTGGA
                                      |||||||||||| ||||||||||
                                      AGAGTGAGACAG GGGTCCGACCT
                                            G
GAM1628  KIAA0752  3'  TCCAGCCTGGGCAACGAGCGA  67635       T
                                      TCGCTC GTTGCCCAGGCTGGA
                                      ||||||| ||||||||||||||
                                      AGCGAG CAACGGGTCCGACCT
                                        _
GAM1628  KIAA0794  3'  TCCAGCCTGGGCGACAAAGCGA 81238      C
                                      TCGCT TGTTGCCCAGGCTGGA
                                      ||||| ||||||||||||||||
                                      AGCGA ACAGCGGGTCCGACCT
                                        A
GAM1628  KIAA0795  3'  TCCAGCCTGGTTGACAGAGTGA 47232           GC
                GA                    TCTCGCTCTGTT  CCAGGCTGGA
                                      ||||||||||||  ||||||||||
                                      AGAGTGAGACAG  GGTCCGACCT
                                            TT
GAM1628  KIAA0798  3'  TCCAGCCTGGGCAACAAGAGCG 28455        _
                A                      TCGCTCT GTTGCCCAGGCTGGA
                                      |||||||  ||||||||||||||||
                                      AGCGAGA CAACGGGTCCGACCT
                                          A
GAM1628  KIAA0831  3'  TCCAGCCTGGGCAACAAGAGCG 30655         _
                AGG                     TCTCGCTCT GTTGCCCAGGCTGGA
                                      |||||||||  ||||||||||||||||
                                      GGAGCGAGA CAACGGGTCCGACCT
                                            A
GAM1628  KIAA0853  3'  TCCAACCTAGGTGACAGAGCAA 31215     C      TG  C   C
                GA                    TCT GCTCTGT  CC AGG TGGA
                                      |||  |||||||  ||  |||  ||||
                                      AGA CGAGACA  GG TCC ACCT
                                        A      GT  A   A
GAM1628  KIAA0872  3'  TCCAGCCTGGGTGACAGAGTGA 30762           TG
                GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                      ||||||||||  ||||||||||
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                                AGAGTGAGACA  GGGTCCGACCT
                                      GT
GAM1628  KIAA0876  3'  TCCAGCCTGGGCAACAGAGCGA 65319
                GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                      ||||||||||||||||||||||||
                                      AGAGCGAGACAACGGGTCCGACCT

GAM1628  KIAA0884  3'  TCCAACCTGGGTAACAGAGTGA 70758                C
                GA                    TCTCGCTCTGTTGCCCAGG TGGA
                                      |||||||||||||||||| ||||
                                      AGAGTGAGACAATGGGTCC ACCT
                                            A
GAM1628  KIAA0889  3'  TCCAGCCTGGGTGACAGAGTGA 31786          TG
                GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                      ||||||||||  ||||||||||
                                      AGAGTGAGACA  GGGTCCGACCT
                                            GT
GAM1628  KIAA0894  3'  TCCAGCCTGGGTGACAGAGCGA 30342          TG
                GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                      ||||||||||  ||||||||||
                                      AGAGCGAGACA  GGGTCCGACCT
                                            GT
GAM1628  KIAA0907  3'  TCCAGCCTGGGCAATAGAGCAA 30882     C
                GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                      ||| ||||||||||||||||||||
                                      AGA CGAGATAACGGGTCCGACCT
                                        A
GAM1628  KIAA0907  3'  TCCAGCCTGGGCACTAGAGTGA 30883          T
                GA                    TCTCGCTCTG TGCCCAGGCTGGA
                                      ||||||||||| ||||||||||||
                                      AGAGTGAGAT ACGGGTCCGACCT
                                           C
GAM1628  KIAA0924  3'  TCCAGCCTGGGCAACAGAGCGA 30376
                GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                      ||||||||||||||||||||||||
                                      AGAGCGAGACAACGGGTCCGACCT

GAM1628  KIAA0961  3'  TCCAGCCTGGGCAACAAGAGC  30409       _
                                      GCTCT GTTGCCCAGGCTGGA
                                      |||||  ||||||||||||||
                                      CGAGA CAACGGGTCCGACCT
                                        A
GAM1628  KIAA0981  3'  TCCAGCCTGGGCAACAGAGCAA 62093     C
                GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                      ||| ||||||||||||||||||||
                                      AGA CGAGACAACGGGTCCGACCT
                                        A
GAM1628  KIAA1001  3'  TCCAGCCTGGGTGATGGAGCAA 31012     C      TG
                GA                    TCT GCTCTGT  CCCAGGCTGGA
                                      ||| |||||||  ||||||||||
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                                AGA CGAGGTA  GGGTCCGACCT
                                  A      GT
GAM1628  KIAA1032  3'  TCCAGCCTGGGCAACAGA    66732
                                TCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||
                                AGACAACGGGTCCGACCT

GAM1628  KIAA1086  3'  CCAGCCCAGACAACAGAGTGAG 71284             CCCA
                A                TCTCGCTCTGTTG   GGCTGG
                                ||||||||||||||   ||||||
                                AGAGTGAGACAAC   CCGACC
                                        AGAC
GAM1628  KIAA1086  3'  TCCAGCCTGGGCAACAGAAGAA 71289     _ GC
                GA                TCT C  TCTGTTGCCCAGGCTGGA
                                ||| |  ||||||||||||||||||
                                AGA G  AGACAACGGGTCCGACCT
                                  A A_
GAM1628  KIAA1086  3'  TCCAGCCTGGGTTACAGAGCGA 71290           T
                GA                TCTCGCTCTGT GCCCAGGCTGGA
                                ||||||||||| ||||||||||||
                                AGAGCGAGACA TGGGTCCGACCT
                                      T
GAM1628  KIAA1130  3'  CCTGGGCAACATAGCAAGA   63085     C   C
                                TCT GCT TGTTGCCCAGG
                                ||| ||| ||||||||||
                                AGA CGA ACAACGGGTCC
                                  A   T
GAM1628  KIAA1143  3'  CCAGCCTGGGCGACAAAGC   69233     C
                                GCT TGTTGCCCAGGCTGG
                                ||| ||||||||||||||
                                CGA ACAGCGGGTCCGACC
                                  A
GAM1628  KIAA1143  3'  TCCAGCCTGGGCAACAGAGTAA 69251     CG
                GA                TCT  CTCTGTTGCCCAGGCTGGA
                                |||  ||||||||||||||||||
                                AGA  GAGACAACGGGTCCGACCT
                                  AT
GAM1628  KIAA1160  3'  TCCAGCCTGGCGACAGAGTGAG 40762              C
                A                TCTCGCTCTGTTGCC AGGCTGGA
                                ||||||||||||||| ||||||||
                                AGAGTGAGACAGCGG TCCGACCT
                                                _
GAM1628  KIAA1164  3'  CCTGGGCAATAGAGCGAGA   70041
                                TCTCGCTCTGTTGCCCAGG
                                ||||||||||||||||||
                                AGAGCGAGATAACGGGTCC

GAM1628  KIAA1164  3'  TCCAGCCTGGGTGACAGAGGGA 70051      G     TG
                GA                TCTC CTCTGT  CCCAGGCTGGA
                                |||| ||||||  ||||||||||
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                                AGAG GAGACA  GGGTCCGACCT
                                  G     GT
GAM1628  KIAA1191  3'  TCCAGCCTGGGCGACAGAACGA 40336       C
                GA                TCTCG TCTGTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||||||
                                  AGAGC AGACAGCGGGTCCGACCT
                                    A
GAM1628  KIAA1202  3'  TCCATCCTGGGCAACAGAGTGA 72492                C
                GA                TCTCGCTCTGTTGCCCAGG TGGA
                                  |||||||||||||||||| ||||
                                  AGAGTGAGACAACGGGTCC ACCT
                                               T
GAM1628  KIAA1204  3'  CCTGGGCAACACAGCGAGA    69738        C
                                  TCTCGCT TGTTGCCCAGG
                                  ||||||| ||||||||||
                                  AGAGCGA ACAACGGGTCC
                                     C
GAM1628  KIAA1228  3'  TCCAGCCTGGGCAACAGAGTGA 65678
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAACGGGTCCGACCT

GAM1628  KIAA1253  3'  TCTAGCCTGGGCAACAGAGTAA 93550     CG
                GA                TCT  CTCTGTTGCCCAGGCTGGA
                                  |||  ||||||||||||||||||
                                  AGA  GAGACAACGGGTCCGATCT
                                    AT
GAM1628  KIAA1257  3'  TCCAGCCTGGGCAGCAGAGCAA 63419     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACGACGGGTCCGACCT
                                    A
GAM1628  KIAA1271  3'  TCCAACCTGGGTGAGAGAGCGA 70145          G TG      C
                GA                TCTCGCTCT T  CCCAGG TGGA
                                  ||||||||| |  |||||| ||||
                                  AGAGCGAGA A  GGGTCC ACCT
                                       G GT      A
GAM1628  KIAA1277  3'  TCCAGCCTGGACAACAGAGCAA 65086     C        C
                GA                TCT GCTCTGTTG CCAGGCTGGA
                                  ||| ||||||||| ||||||||||
                                  AGA CGAGACAAC GGTCCGACCT
                                    A         A
GAM1628  KIAA1328  3'  TCCAGCCTGGGTGACAGAGCAA 62334     C       TG
                GA                TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A       GT
GAM1628  KIAA1340  3'  TCCAGCCTGGGCGACAGTGCAA 69699     C  T
                GA                TCT GC CTGTTGCCCAGGCTGGA
                                  ||| || ||||||||||||||||
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                                AGA CG GACAGCGGGTCCGACCT
                                  A  T
GAM1628  KIAA1348  3'  TCCAGCCTGGGCAACAAGAGTG 69129        _
                A                TCGCTCT GTTGCCCAGGCTGGA
                                 ||||||| ||||||||||||||||
                                 AGTGAGA CAACGGGTCCGACCT
                                    A
GAM1628  KIAA1364  3'  TCCAGCCTGTGTGACAGAATGA 64359       C     TG C
                GA                 TCTCG TCTGT  C CAGGCTGGA
                                   ||||| |||||  | |||||||||
                                   AGAGT AGACA  G GTCCGACCT
                                     A     GT T
GAM1628  KIAA1423  3'  TCCAGCCTGGGTGTCAGAGCGA 62398           T
                GA                 TCTCGCTCTG TGCCCAGGCTGGA
                                   |||||||||| ||||||||||||
                                   AGAGCGAGAC GTGGGTCCGACCT
                                        T
GAM1628  KIAA1456  3'  CCTGGGCAACATAGCAAGA   67546     C   C
                                   TCT GCT TGTTGCCCAGG
                                   ||| ||| ||||||||||
                                   AGA CGA ACAACGGGTCC
                                     A   T
GAM1628  KIAA1456  3'  CCTGGGCAACATAGCAAGA   67547     C   C
                                   TCT GCT TGTTGCCCAGG
                                   ||| ||| ||||||||||
                                   AGA CGA ACAACGGGTCC
                                     A   T
GAM1628  KIAA1456  3'  TCCAACCTGGGCAACAAGAGTG 67568         _         C
                A                  TCGCTCT GTTGCCCAGG TGGA
                                   ||||||| |||||||||| ||||
                                   AGTGAGA CAACGGGTCC ACCT
                                      A         A
GAM1628  KIAA1456  5'  TCCAGCCTGGGTGACTGAGGGA 67569      G   T  TG
                GA                 TCTC CTC GT  CCCAGGCTGGA
                                   |||| ||| ||  ||||||||||
                                   AGAG GAG CA  GGGTCCGACCT
                                     G   T  GT
GAM1628  KIAA1486  3'  TCCAGCCTGGGTGACAGAGCGA 67979           TG
                GA                 TCTCGCTCTGT  CCCAGGCTGGA
                                   |||||||||||  ||||||||||
                                   AGAGCGAGACA  GGGTCCGACCT
                                        GT
GAM1628  KIAA1497  5'  TCCAGCCTGGGCGACAGAGCGA 68132
                GA                 TCTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGCGAGACAGCGGGTCCGACCT

GAM1628  KIAA1508  3'  TCCAGCCTGGGTGACAGAGCGA 62564           TG
                GA                 TCTCGCTCTGT  CCCAGGCTGGA
                                   |||||||||||  ||||||||||
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                                AGAGCGAGACA  GGGTCCGACCT
                                      GT
GAM1628  KIAA1554  3'  TCCAACCTGGGTGACAGAGTGA 96862          TG     C
                GA                  TCTCGCTCTGT  CCCAGG TGGA
                                    |||||||||||  |||||| ||||
                                    AGAGTGAGACA  GGGTCC ACCT
                                      GT     A
GAM1628  KIAA1559  3'  TCCAGCCTGGGTAACAGAGCAA 73461     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAATGGGTCCGACCT
                                      A
GAM1628  KIAA1559  3'  TCCAGCCTGGGTGACAGAGTGA 73462          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    |||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                      GT
GAM1628  KIAA1586  5'  CCTGGGCAACAGAGCAAGA   93938     C
                                    TCT GCTCTGTTGCCCAGG
                                    ||| ||||||||||||||
                                    AGA CGAGACAACGGGTCC
                                      A
GAM1628  KIAA1614  3'  TCCAGCCTGGGCAACAAGAGC  70668      _
                                    GCTCT GTTGCCCAGGCTGGA
                                    ||||| ||||||||||||||
                                    CGAGA CAACGGGTCCGACCT
                                       A
GAM1628  KIAA1630  3'  TCCAGCCTGGGTGACAGAGCAA 38657     C      TG
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGAGACA  GGGTCCGACCT
                                      A      GT
GAM1628  KIAA1641  3'  TCCAGCCTGAGCAACAGAGTGA 81022          C
                                    TCGCTCTGTTGC CAGGCTGGA
                                    |||||||||||| |||||||||
                                    AGTGAGACAACG GTCCGACCT
                                          A
GAM1628  KIAA1644  3'  TCCAGCCTGGGCAACAGAGTGA 86223
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAACGGGTCCGACCT

GAM1628  KIAA1649  3'  TCCAGCCTGTGCAACAGAGCGA 51248           C
                GG                  TCTCGCTCTGTTGC CAGGCTGGA
                                    |||||||||||||| |||||||||
                                    GGAGCGAGACAACG GTCCGACCT
                                            T
GAM1628  KIAA1656  5'  TCCAGCCTGGCAACAGAGTGAG 66385           C
                A                    TCTCGCTCTGTTGCC AGGCTGGA
                                    |||||||||||||| ||||||||
```

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                                AGAGTGAGACAACGG TCCGACCT
                                                _
GAM1628  KIAA1674  3'  TCCAGCCTGGGCGACAGAGCGA 69348
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  |||||||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCCGACCT

GAM1628  KIAA1715  3'  TCCAGCCTGGGCAACAAGAGTG 68691       _
                A                  TCGCTCT GTTGCCCAGGCTGGA
                                   |||||||  ||||||||||||||
                                   AGTGAGA CAACGGGTCCGACCT
                                      A
GAM1628  KIAA1727  3'  TCCAGCCTGGATGACAGAGTGA 64765           GC
                GA                TCTCGCTCTGTT  CCAGGCTGGA
                                  ||||||||||||  ||||||||||
                                  AGAGTGAGACAG  GGTCCGACCT
                                        TA
GAM1628  KIAA1771  3'  TCCAGCCTGGACAACAGAGT   79867         C
                                  GCTCTGTTG CCAGGCTGGA
                                  |||||||||  ||||||||||
                                  TGAGACAAC GGTCCGACCT
                                       A
GAM1628  KIAA1786  3'  CCAGCCCGGGTGACAGAGCGAG 66630          TG   A
                A                  TCTCGCTCTGT  CCC GGCTGG
                                   ||||||||||  ||| ||||||
                                   AGAGCGAGACA  GGG CCGACC
                                         GT   C
GAM1628  KIAA1829  3'  TCCAGCCTGGGCAACAAGAGCG 62656       _
                A                  TCGCTCT GTTGCCCAGGCTGGA
                                   |||||||  ||||||||||||||
                                   AGCGAGA CAACGGGTCCGACCT
                                      A
GAM1628  KIAA1871  3'  TCCAGCCTGGGCAACAAGTGCG 61911      T  _
                A                  TCGC CT GTTGCCCAGGCTGGA
                                   ||||  ||  ||||||||||||||
                                   AGCG GA CAACGGGTCCGACCT
                                     T  A
GAM1628  KIAA1872  3'  TCCAGCCTGGGAGACAGAGCAA 63620     C      TG
                GA                TCT GCTCTGT  CCCAGGCTGGA
                                  |||  |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A      GA
GAM1628  KIAA1872  3'  TCCAGCCTGGGCAACAAGAGC  63621       _
                                  GCTCT GTTGCCCAGGCTGGA
                                  |||||  ||||||||||||||
                                  CGAGA CAACGGGTCCGACCT
                                     A
GAM1628  KIAA1872  3'  TCCAGCCTGGGCGACAGAGCAA 63623     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  |||  ||||||||||||||||||
```

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                                AGA CGAGACAGCGGGTCCGACCT
                                  A
GAM1628  KIAA1879  3'  TCCAGCCTGGGAGACAGAGCAA 73946     C      TG
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGAGACA  GGGTCCGACCT
                                      A      GA
GAM1628  KIAA1948  3'  TCCAGCCTGGGTGACAGACCGA 83306      C     TG
                GA                  TCTCG TCTGT  CCCAGGCTGGA
                                    ||||| |||||  ||||||||||
                                    AGAGC AGACA  GGGTCCGACCT
                                      C     GT
GAM1628  KIAA1948  5'  TCCAGCCTGGGTGACAGAGTGA 83307          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          GT
GAM1628  KIAA1951  3'  TCCAGCCTGGGCGACAGAGTGA 74165
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAGCGGGTCCGACCT

GAM1628  KIAA1951  3'  TCCAGTCTGGGCAACAGTGCAA 74166     C  T
                GA                  TCT GC CTGTTGCCCAGGCTGGA
                                    ||| || ||||||||||||||||
                                    AGA CG GACAACGGGTCTGACCT
                                      A  T
GAM1628  KIAA1954  3'  TCCAGCCTGAGCAACAGAGCAA 78231     C        C
                GA                  TCT GCTCTGTTGC CAGGCTGGA
                                    ||| |||||||||| |||||||||
                                    AGA CGAGACAACG GTCCGACCT
                                      A         A
GAM1628  KIAA1958  3'  TCCAGCCTGGGCAACAAAGCTA 82792     C   C
                GA                  TCT GCT TGTTGCCCAGGCTGGA
                                    ||| ||| ||||||||||||||||
                                    AGA CGA ACAACGGGTCCGACCT
                                      T   A
GAM1628  KIAA1969  3'  TCCAGTTTGGCAACAGAGTGAG 79482             C
                A                    TCTCGCTCTGTTGCC AGGCTGGA
                                    ||||||||||||||| ||||||||
                                    AGAGTGAGACAACGG TTTGACCT

                                                _
GAM1628  KR18     3'  TCCAGCCTGGGCAACAAGA    53896     _
                                    TCT GTTGCCCAGGCTGGA
                                    ||| ||||||||||||||
                                    AGA CAACGGGTCCGACCT
                                      A
GAM1628  KR18     3'  TCCAGCCTGGGCACCAGGAACG 53898     C_    T
                A                    TCG  TCTG TGCCCAGGCTGGA
                                    |||  |||| ||||||||||||
```

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                                AGC  GGAC ACGGGTCCGACCT
                                  AA    C
GAM1628  KREMEN    3'  TCCAGCCTGAGCAGCAGAGCGG 50237             C
                GA                  TCTCGCTCTGTTGC CAGGCTGGA
                                    |||||||||||||| |||||||||
                                    AGGGCGAGACGACG GTCCGACCT
                                          A
GAM1628  KREMEN    3'  TCCAGTGTAGGCAACAGAGTGA 50238             CAG
                GA                  TCTCGCTCTGTTGCC   GCTGGA
                                    ||||||||||||||   ||||||
                                    AGAGTGAGACAACGG   TGACCT
                                          ATG
GAM1628  LANO      3'  TCCAGCCCGGGTGACAGAGCGA 47977           TG   A
                GA                  TCTCGCTCTGT  CCC GGCTGGA
                                    ||||||||||  ||| |||||||
                                    AGAGCGAGACA  GGG CCGACCT
                                          GT   C
GAM1628  LIAS      3'  TCCAGCCTGGGTGACAAGAGC  71169      _  TG
                                    GCTCT GT  CCCAGGCTGGA
                                    ||||| ||  ||||||||||
                                    CGAGA CA  GGGTCCGACCT
                                      A  GT
GAM1628  LIM       3'  TCCAGCCTGGGTGACAGAGTGA 22334           TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          GT
GAM1628  LIM       3'  TCCAGCCTGGTGACAGAGCAAG 22335     C      TG  C
                A                    TCT GCTCTGT  CC AGGCTGGA
                                    ||| |||||||  || ||||||||
                                    AGA CGAGACA  GG TCCGACCT
                                      A      GT  _
GAM1628  LIN-28    3'  TCCAGCCTGGTTACAGAGCGAG 45471           TGC
                A                    TCTCGCTCTGT   CCAGGCTGGA
                                    ||||||||||   ||||||||||
                                    AGAGCGAGACA   GGTCCGACCT
                                          TT_
GAM1628  LRG       3'  CCTGGGCGACAGAGCAAGA    54817     C
                                    TCT GCTCTGTTGCCCAGG
                                    ||| ||||||||||||||
                                    AGA CGAGACAGCGGGTCC
                                      A
GAM1628  LRRFIP1   3'  TCCAGCCTGGACAACAAGAGCG 17617        _   C
                A                    TCGCTCT GTTG CCAGGCTGGA
                                    ||||||| |||| ||||||||||
                                    AGCGAGA CAAC GGTCCGACCT
                                       A   A
GAM1628  LSR68     3'  TCCAGCCTGGGCGACAGAATGA 38559       C
                GA                  TCTCG TCTGTTGCCCAGGCTGGA
                                    ||||| ||||||||||||||||||
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                                AGAGT AGACAGCGGGTCCGACCT
                                  A
GAM1628  MACF1    3'  TCCAACTTGGGCAACAGACAGA 53433          ____      C
                GCGAGA                  TCTCGCTCTGT   TGCCCAGG TGGA
                                ||||||||||   |||||||| ||||
                                AGAGCGAGACA   ACGGGTTC ACCT
                                      GACA      A
GAM1628  MACF1    3'  TCCAGCCTGGGCAACAGACAGA 53435          ____
                GTGAGA                  TCTCGCTCTGT   TGCCCAGGCTGGA
                                ||||||||||   ||||||||||||
                                AGAGTGAGACA   ACGGGTCCGACCT
                                      GACA
GAM1628  MAWBP    3'  CCTGGGCAACACAGCGAGA   42382       C
                                TCTCGCT TGTTGCCCAGG
                                ||||||| ||||||||||
                                AGAGCGA ACAACGGGTCC
                                    C
GAM1628  MAWBP    3'  TCCAGCCTGGGCAACAGAGTAA 42388     CG
                GA                  TCT  CTCTGTTGCCCAGGCTGGA
                                |||  ||||||||||||||||||
                                AGA  GAGACAACGGGTCCGACCT
                                  AT
GAM1628  MCAM     3'  TCCAGCCTGGGCAACACAGCGA 22466       C
                GA                  TCTCGCT TGTTGCCCAGGCTGGA
                                ||||||| ||||||||||||||||
                                AGAGCGA ACAACGGGTCCGACCT
                                    C
GAM1628  METL     3'  TCCAGCCTGGGCAAAATAGCGA 37841       CTG
                GA                  TCTCGCT   TTGCCCAGGCTGGA
                                |||||||   ||||||||||||||
                                AGAGCGA   AACGGGTCCGACCT
                                    TAA
GAM1628  MGC10200  3'  TCCAGTCTGGGCAACAGAGCGA 59649
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGCGAGACAACGGGTCTGACCT

GAM1628  MGC10765  3'  TCCAGCCTAGGCGACAGAGCGA 44567            C
                GA                  TCTCGCTCTGTTGCC AGGCTGGA
                                |||||||||||||| ||||||||
                                AGAGCGAGACAGCGG TCCGACCT
                                        A
GAM1628  MGC10814  3'  TCCAGCCTGGGCAACAAGAGC  52025      _
                                GCTCT GTTGCCCAGGCTGGA
                                ||||| ||||||||||||||
                                CGAGA CAACGGGTCCGACCT
                                  A
GAM1628  MGC10814  5'  TCCAGCCTGGGCAACAGAGTGA 52027
                GG                  TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
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                                GGAGTGAGACAACGGGTCCGACCT

GAM1628  MGC10999  3'  CCAGCCTCAGCAACAAG     51191    C     CC
                                CT TGTTGC  AGGCTGG
                                || ||||||  |||||||
                                GA ACAACG  TCCGACC
                                  _     AC
GAM1628  MGC11386  3'  TCCAGCCTGGGCAACAGAGCGA 53072
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAACGGGTCCGACCT

GAM1628  MGC12972  3'  CCTGGGCAACATAGCAAGA    52052     C   C
                                  TCT GCT TGTTGCCCAGG
                                  ||| ||| ||||||||||
                                  AGA CGA ACAACGGGTCC
                                    A   T
GAM1628  MGC13008  3'  TCCAGCCTGGGCAACAGAATGA 52059       C
                GA                TCTCG TCTGTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||||||
                                  AGAGT AGACAACGGGTCCGACCT
                                     A
GAM1628  MGC13017  3'  TCCAGCCTAGGCAATAAGAGC  55578       _     C
                                  GCTCT GTTGCC AGGCTGGA
                                  ||||| |||||| ||||||||
                                  CGAGA TAACGG TCCGACCT
                                     A      A
GAM1628  MGC13053  3'  TCCAGCCTGGGCGACAGAGTGA 52114
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAGCGGGTCCGACCT

GAM1628  MGC13053  3'  TCCAGCCTGGGCGACAGCAAGA 52115    GCT
                                  TC   CTGTTGCCCAGGCTGGA
                                  ||   ||||||||||||||||
                                  AG   GACAGCGGGTCCGACCT
                                   AAC
GAM1628  MGC14126  3'  TCCAGCCTGGGCGATGAGC    52942      T
                                  GCTC GTTGCCCAGGCTGGA
                                  |||| ||||||||||||||
                                  CGAG TAGCGGGTCCGACCT
                                     _
GAM1628  MGC14407  3'  TCCAGCCTGGGTGACAGAGCAA 52977     C      TG
                GA                TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A      GT
GAM1628  MGC14436  3'  TCCAGCCTGGGTGACAGAACGA 52931       C    TG
                GA                TCTCG TCTGT  CCCAGGCTGGA
                                  ||||| |||||  ||||||||||
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                                AGAGC AGACA  GGGTCCGACCT
                                  A    GT
GAM1628  MGC14799  3'  TCCAGCCTGGGTGACAGTGAGA 51332       CT  TG
                                TCTCGCT  GT  CCCAGGCTGGA
                                |||||||  ||  ||||||||||||
                                AGAGTGA  CA  GGGTCCGACCT
                                   __  GT
GAM1628  MGC15397  3'  TCCAGCCTGGGTGATAGAGTGA 55556          TG
           GA                     TCTCGCTCTGT  CCCAGGCTGGA
                                |||||||||||  ||||||||||||
                                AGAGTGAGATA  GGGTCCGACCT
                                      GT
GAM1628  MGC15631  3'  TCCAGCCTGTGCAACAGAGCCA 52235     C        C
           GA                     TCT GCTCTGTTGC CAGGCTGGA
                                ||| ||||||||||| |||||||||
                                AGA CGAGACAACG GTCCGACCT
                                  C         T
GAM1628  MGC16037  3'  TCCAGCCTGGACAACAGAGTGG 52894           C
           GA                     TCTCGCTCTGTTG CCAGGCTGGA
                                |||||||||||||| ||||||||||
                                AGGGTGAGACAAC GGTCCGACCT
                                       A
GAM1628  MGC16175  3'  TCCAGCCTGGGCAATAGAGCAA 52279     C
           GA                     TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGAGATAACGGGTCCGACCT
                                  A
GAM1628  MGC16332  3'  TCCAGCCTGGTCAACAAAGCAA 57545     C   C    C
           GA                     TCT GCT TGTTG CCAGGCTGGA
                                ||| ||| ||||| ||||||||||
                                AGA CGA ACAAC GGTCCGACCT
                                  A   A    T
GAM1628  MGC16703  3'  TCCAGCCTGGGCAACAGAGCGA 73498
           GA                     TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGCGAGACAACGGGTCCGACCT

GAM1628  MGC20235  3'  TCCAGCCTGGGCAAAAGAGC   59562       G
                                GCTCT TTGCCCAGGCTGGA
                                ||||| ||||||||||||||
                                CGAGA AACGGGTCCGACCT
                                   A
GAM1628  MGC22805  3'  CCAGGGCAACACAGCGAGA    58699        C       A
                                TCTCGCT TGTTGCCC GG
                                ||||||| |||||||| ||
                                AGAGCGA ACAACGGG CC
                                    C       A
GAM1628  MGC23244  3'  TCCAGCCTGGGCGACAGAGTGA 58838
           GA                     TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
```

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                                AGAGTGAGACAGCGGGTCCGACCT

GAM1628  MGC2396   3'  CCAGCCTGGGCAATAAGAG   54558     _
                                CTCT GTTGCCCAGGCTGG
                                |||| ||||||||||||||
                                GAGA TAACGGGTCCGACC
                                  A
GAM1628  MGC2562   3'  CCACTAGGCAACAGAGCCAGA  51434    C        C  GC
                                TCT GCTCTGTTGCC AG  TGG
                                ||| |||||||||| ||  |||
                                AGA CGAGACAACGG TC  ACC
                                  C         A __
GAM1628  MGC2562   3'  TCCAGCCTGACGACAAAGCGAG 51449       C    CC
           A                     TCTCGCT TGTTG  CAGGCTGGA
                                |||||||  |||||  |||||||||
                                AGAGCGA ACAGC  GTCCGACCT
                                    A    A_
GAM1628  MGC2562   3'  TCCAGCCTGGAAGACCAAACGA 51450      CTCT   GC
           GA                    TCTCG   GTT  CCAGGCTGGA
                                |||||   |||  ||||||||||
                                AGAGC   CAG  GGTCCGACCT
                                  AAAC   AA
GAM1628  MGC2562   3'  TCCAGCCTGGGCGACAGAGC   51451
                                GCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||
                                CGAGACAGCGGGTCCGACCT

GAM1628  MGC2663   3'  TCCAGCCTGGGCGATGGAGTGA 44338
           GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGGTAGCGGGTCCGACCT

GAM1628  MGC26641  3'  TCCAGCCTGGGCAATAGGGCAA 59326    C
           GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||
                                AGA CGGGATAACGGGTCCGACCT
                                  A
GAM1628  MGC26877  5'  CCAGCCTGGGTGACAGAGCGAG 58890         TG
           A                     TCTCGCTCTGT  CCCAGGCTGG
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACC
                                      GT
GAM1628  MGC2731   3'  TCCAGCCTGGGCAATAAGAGCG 44164       _
           A                     TCGCTCT GTTGCCCAGGCTGGA
                                |||||||  ||||||||||||||
                                AGCGAGA TAACGGGTCCGACCT
                                    A
GAM1628  MGC29762  3'  TCCAGCCTGGGCAACAAGAGC  59148     _
                                GCTCT GTTGCCCAGGCTGGA
                                |||||  |||||||||||||||
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                                CGAGA CAACGGGTCCGACCT
                                  A
GAM1628  MGC29891  3'  TCCAGCCTGGGCAACAGAGCCA 58871     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAACGGGTCCGACCT
                                    C
GAM1628  MGC29937  3'  TCCAGCCTGGGCAACAAGAGTG 58734        _
                A                  TCGCTCT GTTGCCCAGGCTGGA
                                   ||||||| ||||||||||||||||
                                   AGTGAGA CAACGGGTCCGACCT
                                      A
GAM1628  MGC3101   5'  TCCAGCCTGGGTGACAGAGCGA 44105          TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GT
GAM1628  MGC3207   3'  TCCAGCCTGGGCAACAGAGCGA 63242
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAACGGGTCCGACCT

GAM1628  MGC4368   3'  CCTGGGCAACACAGCAAGA   44725    C  C
                                  TCT GCT TGTTGCCCAGG
                                  ||| ||| ||||||||||
                                  AGA CGA ACAACGGGTCC
                                    A   C
GAM1628  MGC4400   3'  CCTGGGCAACATAGCGAGA   52037       C
                                  TCTCGCT TGTTGCCCAGG
                                  ||||||| ||||||||||
                                  AGAGCGA ACAACGGGTCC
                                      T
GAM1628  MGC4562   3'  TCCAGCCTGGGCAACAGAGCGA 56743
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAACGGGTCCGACCT

GAM1628  MGC4663   3'  TCCAGCCTGGGCAACAGAGCCA 44791     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAACGGGTCCGACCT
                                    C
GAM1628  MGC4771   3'  TCCAGCCTGGGCAACAGAGTGA 52006
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAACGGGTCCGACCT

GAM1628  MGC4840   3'  TCCAGCCTGGCTGACAGAGCGA 72029          GC
                GA                TCTCGCTCTGTT  CCAGGCTGGA
                                  ||||||||||||  ||||||||||
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                                AGAGCGAGACAG  GGTCCGACCT
                                      TC
GAM1628  MGC5384   3'  TCCAGCCTGGGCGACAGAGTGA 49094
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAGCGGGTCCGACCT

GAM1628  MGC5457   3'  TCCAGCCTGGGTGACAGAGCGA 51943          TG
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GT
GAM1628  MKRN4     3'  CCAGCCTGGGTGACAGAGCGAG 48455          TG
              A                   TCTCGCTCTGT  CCCAGGCTGG
                                  ||||||||||  |||||||||
                                  AGAGCGAGACA  GGGTCCGACC
                                        GT
GAM1628  MOST2     5'  TCCAGCCTGGGCACCACAGCAA 40072     C   C  T
              GA                  TCT GCT TG TGCCCAGGCTGGA
                                  ||| ||| || ||||||||||||
                                  AGA CGA AC ACGGGTCCGACCT
                                    A   C  C
GAM1628  MRPL48    5'  TCCAGCCTGCGCAACAGAGCGA 32662            C
              GA                  TCTCGCTCTGTTGC CAGGCTGGA
                                  |||||||||||||| |||||||||
                                  AGAGCGAGACAACG GTCCGACCT
                                        C
GAM1628  MRPS10    3'  TCCAGCCTGGCGACAGAGCGAG 36822            C
              A                   TCTCGCTCTGTTGCC AGGCTGGA
                                  |||||||||||||||| ||||||||
                                  AGAGCGAGACAGCGG TCCGACCT
                                                  _
GAM1628  MRPS18B   3'  TCCAGCCTGGGTGACAGCTAGA 26755     C   CT  TG
                                  TCT GCT  GT  CCCAGGCTGGA
                                  ||| |||  ||  ||||||||||
                                  AGA CGA  CA  GGGTCCGACCT
                                    T  __  GT
GAM1628  My015     3'  TCCAGCCTGGGAGACAGAGCAA 67235     C      TG
              GA                  TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A      GA
GAM1628  NCBP2     3'  CTGGGCAACATAGCAAGA    24767     C   C
                                  TCT GCT TGTTGCCCAG
                                  ||| ||| ||||||||||
                                  AGA CGA ACAACGGGTC
                                    A   T
GAM1628  NDUFC2    3'  TCCAGCCTGGGTGACAAAGGAG 17038      G  C   TG
              A                   TCTC CT TGT  CCCAGGCTGGA
                                  |||| || |||  ||||||||||
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                                AGAG GA ACA  GGGTCCGACCT
                                  _ A   GT
GAM1628  NMNAT    3'  TCCAGCCTGGCGACAGAGCAAG 43292     C         C
             A                   TCT GCTCTGTTGCC AGGCTGGA
                                 ||| |||||||||| ||||||||
                                 AGA CGAGACAGCGG TCCGACCT
                                   A         _
GAM1628  NMNAT    3'  TCCAGCCTGGGCAAAAAAGC   43293     CTG
                                 GCT   TTGCCCAGGCTGGA
                                 |||   ||||||||||||||
                                 CGA   AACGGGTCCGACCT
                                   AAA
GAM1628  NMNAT    3'  TCCAGCCTGGGTGACAGAGCGA 43295          TG
             GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                 ||||||||||  ||||||||||
                                 AGAGCGAGACA  GGGTCCGACCT
                                       GT
GAM1628  NMT2     3'  TCCAGCCTGGGTGACAGAGCGT 17859    T       TG
             GA                    TC CGCTCTGT  CCCAGGCTGGA
                                 || ||||||||  ||||||||||
                                 AG GCGAGACA  GGGTCCGACCT
                                  T       GT
GAM1628  NPTXR    3'  TCCAGCCTGGGCAACAGAGCAA 27445     C
             GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                 ||| ||||||||||||||||||
                                 AGA CGAGACAACGGGTCCGACCT
                                   A
GAM1628  Nup43    3'  TCCAGCCTGGGCAAAAGAGC   45355      G
                                 GCTCT TTGCCCAGGCTGGA
                                 ||||| ||||||||||||||
                                 CGAGA AACGGGTCCGACCT
                                    A
GAM1628  NY-BR-1  3'  TCCAGCCTAGGTGACAGAGTGA 54853          TG  C
             GA                    TCTCGCTCTGT  CC AGGCTGGA
                                 ||||||||||  ||  ||||||||
                                 AGAGTGAGACA  GG TCCGACCT
                                       GT  A
GAM1628  OR51E2   3'  TCCAGCCTGGGCAACGGAGCAA 48521     C
             GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                 ||| ||||||||||||||||||
                                 AGA CGAGGCAACGGGTCCGACCT
                                   A
GAM1628  ORC6L    3'  TCCAGCCTGGGTGACAGAGCGA 27494          TG
             GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                 ||||||||||  ||||||||||
                                 AGAGCGAGACA  GGGTCCGACCT
                                       GT
GAM1628  ORC6L    3'  TCCAGCCTGGGTGACAGAGCGA 27495          TG
             GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                 ||||||||||  ||||||||||
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                                AGAGCGAGACA  GGGTCCGACCT
                                      GT
GAM1628  PAFAH2   3'  TCCAGCCTGGGTGACAGAGCAA 6508      C      TG
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGAGACA  GGGTCCGACCT
                                      A      GT
GAM1628  PB1      3'  TCCAGCCTGGGCAACAAGAGCG 36880        _
                A                    TCGCTCT GTTGCCCAGGCTGGA
                                    ||||||| ||||||||||||||
                                    AGCGAGA CAACGGGTCCGACCT
                                       A
GAM1628  PB1      3'  TCCAGCCTGGGCAACAGAGTGA 36881
                G                    CTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||
                                    GAGTGAGACAACGGGTCCGACCT

GAM1628  PDCD7    3'  TCCAGCCTGGGAGACAGAGCAA 72611     C      TG
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGAGACA  GGGTCCGACCT
                                      A      GA
GAM1628  PIWIL2   3'  TCCAGCCTGTTGACAAAGCAAG 36547     C   C    GCC
                A                    TCT GCT TGTT   CAGGCTGGA
                                    ||| ||| ||||   ||||||||
                                    AGA CGA ACAG   GTCCGACCT
                                      A   A    TT_
GAM1628  POFUT1   3'  TCCAGCCTGGGCAACAGAGCGA 70984
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACAACGGGTCCGACCT

GAM1628  POLYDOM  3'  TCCAGCCTGGGCAATGGAGAGA 44691     G
                G                    CTC CTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||
                                    GAG GAGGTAACGGGTCCGACCT
                                      A
GAM1628  PPP1R3B  3'  CCCGCCTGGGCAGCAGAGCGAG 45138                T
                A                    TCTCGCTCTGTTGCCCAGGC GG
                                    |||||||||||||||||| ||
                                    AGAGCGAGACGACGGGTCCG CC
                                             C
GAM1628  PRIC285  3'  TCCAGCCTGGGTGACAGAGCGA 62120          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGCGAGACA  GGGTCCGACCT
                                      GT
GAM1628  PRO0038  3'  TCCAGCCTGGGTGACAGACCGA 26931      C    TG
                GA                  TCTCG TCTGT  CCCAGGCTGGA
                                    ||||| |||||  ||||||||||
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                                AGAGC AGACA  GGGTCCGACCT
                                  C     GT
GAM1628  PRO0478  5'  TCCAGCCTAGGCAACAAGAGCG 27035        _     C
                A                  TCGCTCT GTTGCC AGGCTGGA
                                   ||||||| |||||| ||||||||
                                   AGCGAGA CAACGG TCCGACCT
                                     A     A
GAM1628  PRO0478  5'  TCCAGCCTGGACAACAGAGTGA 27036            C
                GA                   TCTCGCTCTGTTG CCAGGCTGGA
                                     |||||||||||| ||||||||||
                                     AGAGTGAGACAAC GGTCCGACCT
                                           A
GAM1628  PRO0478  3'  TCCAGCCTGGCAACAGAGCGAG 27037             C
                A                    TCTCGCTCTGTTGCC AGGCTGGA
                                     |||||||||||||| ||||||||
                                     AGAGCGAGACAACGG TCCGACCT
                                                 _
GAM1628  PRO0478  3'  TCCAGCCTGGGGGACAGAGCAA 27038     C       G
                GG                   TCT GCTCTGTT CCCAGGCTGGA
                                     ||| |||||||| ||||||||||
                                     GGA CGAGACAG GGGTCCGACCT
                                       A       G
GAM1628  PRO1048  5'  TCCAGCCTGGGTGACAGAGCGA 38119           TG
                GA                   TCTCGCTCTGT  CCCAGGCTGGA
                                     |||||||||||  ||||||||||
                                     AGAGCGAGACA  GGGTCCGACCT
                                           GT
GAM1628  PRO1386  3'  TCCAGCCTGGGCAACAGAGTGA 49218
                GA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                     ||||||||||||||||||||||||
                                     AGAGTGAGACAACGGGTCCGACCT

GAM1628  PRO1496  3'  TCCAACCTGGGTGACAGACCGA 38368      C    TG     C
                GA                   TCTCG TCTGT  CCCAGG TGGA
                                     ||||| |||||  |||||| ||||
                                     AGAGC AGACA  GGGTCC ACCT
                                       C    GT     A
GAM1628  PRO1942  5'  TCCAGCCTGGACAACAGAAAGA 38384      GC      C
                GA                   TCTC  TCTGTTG CCAGGCTGGA
                                     ||||  ||||||| ||||||||||
                                     AGAG  AGACAAC GGTCCGACCT
                                       AA      A
GAM1628  PRO2015  3'  TCCAGCCTGGGCCACACAGTGA 38166        C  T
                GA                   TCTCGCT TGT GCCCAGGCTGGA
                                     ||||||| ||| ||||||||||||
                                     AGAGTGA ACA CGGGTCCGACCT
                                        C  C
GAM1628  PRO2859  3'  TCCAGCCTGGGGAGACAGAGCG 38214           G_
                AGA                   TCTCGCTCTGTT  CCCAGGCTGGA
                                      ||||||||||||  ||||||||||
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                                AGAGCGAGACAG  GGGTCCGACCT
                                      AG
GAM1628  PRO2893   3'  TCCAACCTGGGCAATAAGAGC  38435      _       C
                                GCTCT GTTGCCCAGG TGGA
                                ||||| |||||||||| ||||
                                CGAGA TAACGGGTCC ACCT
                                   A         A
GAM1628  PRO2964   3'  CCAGCCTGGGCAAAAAGAG   38255     G_
                                CTCT  TTGCCCAGGCTGG
                                ||||  ||||||||||||
                                GAGA  AACGGGTCCGACC
                                  AA
GAM1628  PSR       3'  TCCAGCCTGGGTGACAGACCGA 65794      C    TG
                GA                TCTCG TCTGT  CCCAGGCTGGA
                                ||||| |||||  ||||||||||
                                AGAGC AGACA  GGGTCCGACCT
                                   C    GT
GAM1628  PTD012    3'  CCAGCTTGGGCAACATAGCAAG 26736     C   C
                A                  TCT GCT TGTTGCCCAGGCTGG
                                ||| ||| ||||||||||||||||
                                AGA CGA ACAACGGGTTCGACC
                                  A   T
GAM1628  PTK6      3'  TCCAGCCTGGGCGACAGAGCGA 21082
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGCGAGACAGCGGGTCCGACCT

GAM1628  PTRF      3'  TCCAGCCTGGGTGACAGAGTGA 64245          TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      GT
GAM1628  PTRF      3'  TCCATCCTAGGCAACAGAGTGA 64246           C   C
                GA                TCTCGCTCTGTTGCC AGG TGGA
                                |||||||||||||| ||| ||||
                                AGAGTGAGACAACGG TCC ACCT
                                        A   T
GAM1628  Rabip4R   3'  TCCAACCTGGGTGACAGAGCAA 36279     C      TG     C
                GA                TCT GCTCTGT  CCCAGG TGGA
                                ||| |||||||  |||||| ||||
                                AGA CGAGACA  GGGTCC ACCT
                                  A      GT     A
GAM1628  RHOBTB3   3'  TCCAGCCTGGGTGACAAGAGCG 30432        _ TG
                A                  TCGCTCT GT  CCCAGGCTGGA
                                ||||||| ||  ||||||||||
                                AGCGAGA CA  GGGTCCGACCT
                                    A  GT
GAM1628  RNO2      5'  TCCAGCCTAGACAACAGGGCAA 53941     C        CCC
                GG                TCT GCTCTGTTG   AGGCTGGA
                                ||| |||||||||   ||||||||
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                                GGA CGGGACAAC   TCCGACCT
                                  A        AGA
GAM1628  RNO2     5'  TCCAGCCTGGGCAACAAGAGCG 53942        _
                A                  TCGCTCT GTTGCCCAGGCTGGA
                                   ||||||| ||||||||||||||
                                   AGCGAGA CAACGGGTCCGACCT
                                     A
GAM1628  RoXaN    3'  TCCAGCCTGGGCTACAGAGTGA 47304          T
                GA                   TCTCGCTCTGT GCCCAGGCTGGA
                                     |||||||||||| ||||||||||||
                                     AGAGTGAGACA CGGGTCCGACCT
                                           T
GAM1628  RoXaN    3'  TCCAGCCTGAGAGACAGAATGA 34589       C     GCC
                GA                   TCTCG TCTGTT   CAGGCTGGA
                                     ||||| ||||||   |||||||||
                                     AGAGT AGACAG   GTCCGACCT
                                       A     AGA
GAM1628  Rpo1-2   3'  TCCAGCCTGGGCGACAGAATGA 39225       C
                GA                   TCTCG TCTGTTGCCCAGGCTGGA
                                     ||||| ||||||||||||||||||
                                     AGAGT AGACAGCGGGTCCGACCT
                                       A
GAM1628  Rpo1-2   3'  TCCAGCCTGGGTGACAGAGCAG 39226    TC      TG
                GA                   TC  GCTCTGT  CCCAGGCTGGA
                                     ||  |||||||  ||||||||||||
                                     AG  CGAGACA  GGGTCCGACCT
                                      GA      GT
GAM1628  RRP4     3'  TCCAGCCTGGGTGACAGAGCGA 27363          TG
                GA                   TCTCGCTCTGT  CCCAGGCTGGA
                                     ||||||||||||  ||||||||||||
                                     AGAGCGAGACA  GGGTCCGACCT
                                           GT
GAM1628  SAC2     3'  TCCAGCCTGGGGGACAGAGCAA 30728     C       G
                GA                   TCT GCTCTGTT CCCAGGCTGGA
                                     |||  |||||||| ||||||||||||
                                     AGA CGAGACAG GGGTCCGACCT
                                       A       G
GAM1628  SAMHD1   3'  TCCAGCCTGGGTGACAGAGTGA 61991          TG
                GA                   TCTCGCTCTGT  CCCAGGCTGGA
                                     ||||||||||||  ||||||||||||
                                     AGAGTGAGACA  GGGTCCGACCT
                                           GT
GAM1628  SC65     3'  TCCAGCCTGGGCGACAGAGCGA 22302
                GA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                     ||||||||||||||||||||||||||
                                     AGAGCGAGACAGCGGGTCCGACCT

GAM1628  SC65     3'  TCCAGCCTGGGCGACAGAGTGA 22303
                GA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                     ||||||||||||||||||||||||||
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                                AGAGTGAGACAGCGGGTCCGACCT

GAM1628  SCAND2   3'  TCCAGCCTGGGCGACAGAGTGA 54423
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAGCGGGTCCGACCT

GAM1628  SCAND2   3'  TCCAGCCTGGGCGACAGAGTGA 54424
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAGCGGGTCCGACCT

GAM1628  SCIN     3'  TCCAGCCTGGGCAACAGAG   53605
                                  CTCTGTTGCCCAGGCTGGA
                                  |||||||||||||||||||
                                  GAGACAACGGGTCCGACCT

GAM1628  SCN12A   3'  TCCAGCCTGGTGACAGAGTGAG 27083          TG  C
                A                  TCTCGCTCTGT  CC AGGCTGGA
                                   ||||||||||  || ||||||||
                                   AGAGTGAGACA  GG TCCGACCT
                                         GT  _
GAM1628  SCYA5    3'  TCCAGCCTGGGCGACAGAGCGA 12971
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCCGACCT

GAM1628  SCYA5    3'  TCCAGCCTGGGTGACAAAGTGA 12972        C   TG
                GA                TCTCGCT TGT  CCCAGGCTGGA
                                  |||||||  |||  ||||||||||
                                  AGAGTGA ACA  GGGTCCGACCT
                                     A   GT
GAM1628  SEMA3E   3'  CCTGGGCGACAGAGCGAGA   25806
                                  TCTCGCTCTGTTGCCCAGG
                                  |||||||||||||||||
                                  AGAGCGAGACAGCGGGTCC

GAM1628  SMA3     3'  TCCAGGAGATACAACAGAGGAG 23263      G       CCCAGG
                A                  TCTC CTCTGTTG     CTGGA
                                   |||| ||||||||      |||||
                                   AGAG GAGACAAC     GACCT
                                     _       ATAGAG
GAM1628  SMCR5    3'  TCTGGGCGACAGAGCAAGA   59251     C
                                  TCT GCTCTGTTGCCCAGG
                                  ||| ||||||||||||||
                                  AGA CGAGACAGCGGGTCT
                                    A
GAM1628  SNAPC1   3'  TCCAGCCTGGGCAACAGAGTGA 13279
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
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                                AGAGTGAGACAACGGGTCCGACCT

GAM1628  SPRY4    3'  TCCAGCCTGGGTGACAGAGCAA 49032     C      TG
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGAGACA  GGGTCCGACCT
                                      A      GT
GAM1628  SPRY4    3'  TCCAGCCTGGGTGACAGAGTGA 49033          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          GT
GAM1628  SPTLC2   3'  CCTGGGCAACACAGCAAGA   17989     C   C
                                    TCT GCT TGTTGCCCAGG
                                    ||| ||| ||||||||||
                                    AGA CGA ACAACGGGTCC
                                      A   C
GAM1628  SPTLC2   3'  TCCAGCCTGGGTGACAGAGTGA 18001          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          GT
GAM1628  SYAP1    3'  TCCAGCCTGGGTGATAGAGTGA 52475          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGATA  GGGTCCGACCT
                                          GT
GAM1628  SYT12    3'  CCAGCCTGAGCAATGGCAGGA  96376    TC   CT    C
                                    TC  GCT  GTTGC CAGGCTGG
                                    ||  |||  ||||| ||||||||
                                    AG  CGG  TAACG GTCCGACC
                                     GA  __    A
GAM1628  TADA3L   3'  TCCAGCCTGGGCAACAAGAGTG 22047        _
                A                    TCGCTCT GTTGCCCAGGCTGGA
                                    |||||||  ||||||||||||||
                                    AGTGAGA CAACGGGTCCGACCT
                                        A
GAM1628  TBPL1    5'  CCGGAACAACAAAGCAAGG    18009     C   C    CCCAGG
                                    TCT GCT TGTTG     CTGG
                                    ||| ||| |||||     ||||
                                    GGA CGA ACAAC     GGCC
                                      A   A    AA____
GAM1628  THEA     3'  TCCAGCCCAGGCAATAGAGTAA 66896     CG        CA
                GA                  TCT  CTCTGTTGCC  GGCTGGA
                                    |||  ||||||||||  |||||||
                                    AGA  GAGATAACGG  CCGACCT
                                      AT         AC
GAM1628  TIP47    3'  TCCAGCCTGGGGGACAAGAGTG 20608         _   G
                AGA                   TCTCGCTCT GTT CCCAGGCTGGA
                                    |||||||||  ||| ||||||||||
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                                AGAGTGAGA CAG GGGTCCGACCT
                                     A   G
GAM1628  TMG4     3'  TCCAGCCTGGGCGACAGAGCAA 44217     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAGCGGGTCCGACCT
                                      A
GAM1628  TOMM70A  3'  TCCAGCCTGGGCAATATAGCAA 29739     C   C
                GA                  TCT GCT TGTTGCCCAGGCTGGA
                                    ||| ||| ||||||||||||||||
                                    AGA CGA ATAACGGGTCCGACCT
                                      A   T
GAM1628  TRIAD3   3'  TCCAGCCTGAGCAACAAAAGC  96138     C_     C
                                    GCT  TGTTGC CAGGCTGGA
                                    |||  |||||| |||||||||
                                    CGA  ACAACG GTCCGACCT
                                      AA     A
GAM1628  TSGA2    3'  TCCAGCCTGGGTGGCAGAGCGA 55956          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGCGAGACG  GGGTCCGACCT
                                          GT
GAM1628  Ubc6p    5'  CCAGCCCAGGCAGGCGG     55191      CTGT    CA
                                    TCGCT    TGCC  GGCTGG
                                    |||||    ||||  ||||||
                                    GGCGG    ACGG  CCGACC
                                       ____    AC
GAM1628  UBCE7IP5  3'  TCCAGCCTGGGCGACGGAGTGA 30856
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGGCAGCGGGTCCGACCT

GAM1628  UST      3'  TCCAGCCTGGGTGACAGAGTGA 20354          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          GT
GAM1628  VIT1     5'  TCCAGCCTGGGTGGCAGAGTGA 38606          TG
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACG  GGGTCCGACCT
                                          GT
GAM1628  VPS4B    3'  TCCAGCCTGGGCGACTGA    18024    T
                                    TC GTTGCCCAGGCTGGA
                                    || |||||||||||||||
                                    AG CAGCGGGTCCGACCT
                                     T
GAM1628  WBSCR21  3'  TCCAGCCTAGGCAACAGAGCAA 49306     C          C
                GA                  TCT GCTCTGTTGCC AGGCTGGA
                                    ||| |||||||||| ||||||||
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                                AGA CGAGACAACGG TCCGACCT
                                  A         A
GAM1628  WBSCR23  3'  TCCAGCCTGGGCGACAAAGTGA 47443        C
             GA                   TCTCGCT TGTTGCCCAGGCTGGA
                                  ||||||| ||||||||||||||||
                                  AGAGTGA ACAGCGGGTCCGACCT
                                    A
GAM1628  WBSCR23  3'  TCCAGCCTGGGCGACAGAGCAA 47444     C
             GA                   TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM1628  WBSCR23  5'  TCCAGCCTGGGCGACAGAGCCA 47445     C
             GA                   TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    C
GAM1628  WBSCR23  3'  TCCAGCCTGGGTGATAGAGCAA 47446     C      TG
             GA                   TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGATA  GGGTCCGACCT
                                    A       GT
GAM1628  WIRE     3'  TCCAGCCTGGGCGACAGAGCCA 78907     C
             GA                   TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    C
GAM1628  WSB1     3'  TCCAACCTGGACAACAGAGCGA 56978           C     C
             GA                   TCTCGCTCTGTTG CCAGG TGGA
                                  |||||||||||| ||||| ||||
                                  AGAGCGAGACAAC GGTCC ACCT
                                          A     A
GAM1628  WSB1     3'  TCCAACCTGGACAACAGAGCGA 56979           C     C
             GA                   TCTCGCTCTGTTG CCAGG TGGA
                                  |||||||||||| ||||| ||||
                                  AGAGCGAGACAAC GGTCC ACCT
                                          A     A
GAM1628  YME1L1   3'  TCCAGCCTGGGCAACAGAGCAA 58439     C
             GA                   TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAACGGGTCCGACCT
                                    A
GAM1628  YME1L1   3'  TCCAGCCTGGGTGACAGAGTGA 58440          TG
             GA                   TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                        GT
GAM1628  ZAK      3'  CCTGGGCAAGAGAACAAGA   34103     CGC   G
                                  TCT   TCT TTGCCCAGG
                                  |||   ||| |||||||||
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                                AGA   AGA AACGGGTCC
                                  ACA   G
GAM1628  ZAK      3'  TCCAGCCTGGATGACAGAGTGA 34109            GC
                GA                  TCTCGCTCTGTT  CCAGGCTGGA
                                    ||||||||||||  ||||||||||
                                    AGAGTGAGACAG  GGTCCGACCT
                                          TA
GAM1628  ZFP106   3'  CCAGCCTGGGCGACAAGAG    42720      _
                                    CTCT GTTGCCCAGGCTGG
                                    |||| ||||||||||||||
                                    GAGA CAGCGGGTCCGACC
                                      A
GAM1628  ZFP106   3'  TCCAGCCTGGTGACAGAGTGAG 42742            TG  C
                A                    TCTCGCTCTGT  CC AGGCTGGA
                                    ||||||||||  ||  ||||||||
                                    AGAGTGAGACA  GG TCCGACCT
                                          GT  _
GAM1628  ZNF197   3'  TCCAGCCTGGGCAACAAGAGCG 23760          _
                A                    TCGCTCT GTTGCCCAGGCTGGA
                                    |||||||  ||||||||||||||||
                                    AGCGAGA CAACGGGTCCGACCT
                                       A
GAM1628  ZNF271   3'  TCCAGCCTGGGCAACAGAGTGA 96968
                GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAACGGGTCCGACCT

GAM1628  ZNF271   3'  TCCAGTCTGGGCAACAGAGCAA 96969     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    |||  ||||||||||||||||||||
                                    AGA CGAGACAACGGGTCTGACCT
                                      A
GAM1628  ZNF297B  3'  TCCAGCCTGCGCGACAGATCGA 26672       C       C
                GA                  TCTCG TCTGTTGC CAGGCTGGA
                                    |||||  ||||||||  |||||||||
                                    AGAGC AGACAGCG GTCCGACCT
                                       T       C
GAM1628  ZNF297B  5'  TCCAGCCTGGGCAACAAGAGC  26673       _
                                    GCTCT GTTGCCCAGGCTGGA
                                    |||||  ||||||||||||||||
                                    CGAGA CAACGGGTCCGACCT
                                      A
GAM1628  ZNF297B  5'  TCCAGCCTGGGCAACAGAGCAA 26675     C
                GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                    |||  ||||||||||||||||||||
                                    AGA CGAGACAACGGGTCCGACCT
                                      A
GAM1628  ZNF297B  5'  TCCAGCCTGGGTAAAAGAGTGA 26676          G
                GA                  TCTCGCTCT TTGCCCAGGCTGGA
                                    |||||||||  ||||||||||||||
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                                AGAGTGAGA AATGGGTCCGACCT
                                     A
GAM1628  ZNF333    3'  TCCAGCCTGGGCAACAGAGTGA 51595
                                TCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||
                                AGTGAGACAACGGGTCCGACCT

GAM1628  ZNF339    3'  TCCAGCCTGGGCAACAGAGTGG 41398
                                TCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||
                                GGTGAGACAACGGGTCCGACCT

GAM1628  LOC112687 3'  TCCAGCCTGGGCAACAGAGTGG 73243
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||
                                AGGGTGAGACAACGGGTCCGACCT

GAM1628  LOC112868 3'  TCCAGCCTGACCCCAGAGCAGA 73271     C     TTGCC
                                TCT GCTCTG    CAGGCTGGA
                                ||| ||||||    |||||||||
                                AGA CGAGAC    GTCCGACCT
                                  _     CCCA_
GAM1628  LOC113201 3'  TCCAGCTTGGGCACCAGAGCAA 57357     C     T
              GA                  TCT GCTCTG TGCCCAGGCTGGA
                                ||| |||||| ||||||||||||
                                AGA CGAGAC ACGGGTTCGACCT
                                  A     C
GAM1628  LOC113523 3'  TCCAGCCTGGGCGACAGGGCAA 73434     C
              GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGGGACAGCGGGTCCGACCT
                                  A
GAM1628  LOC114987 3'  TCCAGCCTGGGCAACAAGAGCG 59800        _
              A                   TCGCTCT GTTGCCCAGGCTGGA
                                |||||||| ||||||||||||||
                                AGCGAGA CAACGGGTCCGACCT
                                     A
GAM1628  LOC115129 3'  TCCAGCCTGAGCGACAGAGTAA 73629     CG        C
              GA                  TCT  CTCTGTTGC CAGGCTGGA
                                |||  ||||||||| |||||||||
                                AGA  GAGACAGCG GTCCGACCT
                                  AT        A
GAM1628  LOC115196 3'  TCCAGCCTGGGAGACAGAGCGA 73661           TG
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                       GA
GAM1628  LOC115273 3'  TCCAGCCTGGGCAACAGAGTGA 73754
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||
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                                AGAGTGAGACAACGGGTCCGACCT

GAM1628  LOC115761 3'  TCCAGTCTGGGCAACAGAGTGA 93398
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAACGGGTCTGACCT

GAM1628  LOC116113 3'  CCAGCCTGGGGGAAGGAG    93832     G  G
                                  CTCT TT CCCAGGCTGG
                                  |||| || ||||||||||
                                  GAGG AG GGGTCCGACC
                                    A  G
GAM1628  LOC116143 3'  TCCAGCCTGGGCAACTGAGCAA 74194     C    T
                GA                TCT GCTC GTTGCCCAGGCTGGA
                                  ||| |||| ||||||||||||||||
                                  AGA CGAG CAACGGGTCCGACCT
                                    A    T
GAM1628  LOC116236 3'  TCCAGCCTGGGCGACAGAGTAA 74248     CG
                GA                TCT  CTCTGTTGCCCAGGCTGGA
                                  |||  ||||||||||||||||||||
                                  AGA  GAGACAGCGGGTCCGACCT
                                    AT
GAM1628  LOC116349 3'  TCCAGCCTGGGCAACAGAGCGA 74281
                GG                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  GGAGCGAGACAACGGGTCCGACCT

GAM1628  LOC119504 5'  TCCAGCCTGGGCAACAAGAGGG 74449    G   _
                A                  TC CTCT GTTGCCCAGGCTGGA
                                   || |||| ||||||||||||||||
                                   AG GAGA CAACGGGTCCGACCT
                                    G   A
GAM1628  LOC120406 3'  TCCAGCCTGGGTGACAGAGCGA 76066          TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GT
GAM1628  LOC122704 3'  TCCAACCTGGGCGACAGGGCGA 74611                C
                GA                TCTCGCTCTGTTGCCCAGG TGGA
                                  |||||||||||||||||| ||||
                                  AGAGCGGGACAGCGGGTCC ACCT
                                              A
GAM1628  LOC124225 5'  CCAGCCTGAGAAACAAGC    74758     C    GCC
                                  GCT TGTT   CAGGCTGG
                                  ||| ||||   ||||||||
                                  CGA ACAA   GTCCGACC
                                    _    AGA
GAM1628  LOC126282 3'  TCCAGCCTGGGTGACAGAGCAA 74967     C      TG
                GA                TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
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                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM1628  LOC126669 3'  TCCAGCCTGAGTGACAGAGTGA 75951          TG C
                GA                TCTCGCTCTGT  C CAGGCTGGA
                                  |||||||||||  | |||||||||
                                  AGAGTGAGACA  G GTCCGACCT
                                        GT A
GAM1628  LOC127262 3'  TCCAGCCCGGGCGACAGAGCGA 76605              A
                GA                TCTCGCTCTGTTGCCC GGCTGGA
                                  |||||||||||||||| |||||||
                                  AGAGCGAGACAGCGGG CCGACCT
                                        C
GAM1628  LOC127428 3'  TCCAGCCTGGGCAACAGAGTGA 75163
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAACGGGTCCGACCT

GAM1628  LOC129880 3'  TCCAGCTTGGGCAACAGAGCAA 75409     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAACGGGTTCGACCT
                                    A
GAM1628  LOC130026 3'  TCCAGCCTAGGCAACAGAGCAA 57441     C          C
                GA                TCT GCTCTGTTGCC AGGCTGGA
                                  ||| |||||||||| ||||||||
                                  AGA CGAGACAACGG TCCGACCT
                                    A          A
GAM1628  LOC130535 3'  TCCAGCCTGGGCAACAAGAATG 76655     C  _
                A                  TCG TCT GTTGCCCAGGCTGGA
                                   ||| ||| ||||||||||||||||
                                   AGT AGA CAACGGGTCCGACCT
                                     A   A
GAM1628  LOC130535 3'  TCCAGCCTGGGTGACAGAGCAA 76656     C      TG
                GA                TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A      GT
GAM1628  LOC131965 3'  TCCAGCCTGGGCGACAGAGTGA 75528
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAGCGGGTCCGACCT

GAM1628  LOC133926 3'  TCCAGCCTGGGCGACAGAGCGA 75634
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCCGACCT

GAM1628  LOC134147 3'  TCCAGCCTGGACAACAGAGGGA 57967      G       C
                GA                TCTC CTCTGTTG CCAGGCTGGA
                                  |||| |||||||| ||||||||||
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                                AGAG GAGACAAC GGTCCGACCT
                                  G       A
GAM1628  LOC134265 3'  TCCAGCCTAAGCAAATAGCAAG 75657     C   CTG    CC
            A                    TCT GCT   TTGC  AGGCTGGA
                                 ||| |||   ||||  ||||||||
                                 AGA CGA   AACG  TCCGACCT
                                   A  TA_    AA
GAM1628  LOC135154 3'  TCCAGCCTGGGCAACAAGAGCG 75736        _
            A                    TCGCTCT GTTGCCCAGGCTGGA
                                 |||||||| ||||||||||||||
                                 AGCGAGA CAACGGGTCCGACCT
                                     A
GAM1628  LOC135818 3'  TCCAGCCTGGGCAATAGGGTAA 75749     CG
            GA                     TCT  CTCTGTTGCCCAGGCTGGA
                                   |||  ||||||||||||||||||
                                   AGA  GGGATAACGGGTCCGACCT
                                     AT
GAM1628  LOC137362 3'  TCCAGCCTGGGCAACAAGAGC  75787       _
                                   GCTCT GTTGCCCAGGCTGGA
                                   ||||| ||||||||||||||
                                   CGAGA CAACGGGTCCGACCT
                                     A
GAM1628  LOC138389 3'  TCCAGCCTGGGCAACAAGAGTG 76744        _
            A                    TCGCTCT GTTGCCCAGGCTGGA
                                 |||||||| ||||||||||||||
                                 AGTGAGA CAACGGGTCCGACCT
                                     A
GAM1628  LOC142937 3'  TCCAGCCTGGGCCACAGAACGA 57447      C     T
            GA                     TCTCG TCTGT GCCCAGGCTGGA
                                   ||||| ||||| ||||||||||||
                                   AGAGC AGACA CGGGTCCGACCT
                                     A     C
GAM1628  LOC142948 3'  TCCAGCCTGGGTGACAGAGCGA 83780          TG
            GG                     TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   GGAGCGAGACA  GGGTCCGACCT
                                         GT
GAM1628  LOC143196 3'  TCCAGCTTGGCAACAGAGCGAG 83805             C
            A                    TCTCGCTCTGTTGCC AGGCTGGA
                                 |||||||||||||| ||||||||
                                 AGAGCGAGACAACGG TTCGACCT
                                              _
GAM1628  LOC143310 3'  CCAGCCTGGGTGACAGAGCGAG 77040          TG
            A                    TCTCGCTCTGT  CCCAGGCTGG
                                 ||||||||||  ||||||||||
                                 AGAGCGAGACA  GGGTCCGACC
                                       GT
GAM1628  LOC143465 3'  TCCAGCCTGGGTGACGGAGTGA 83878          TG
            GA                     TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
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                                AGAGTGAGGCA  GGGTCCGACCT
                                      GT
GAM1628  LOC143888 3'  TCCAGCCTGGGTGACAGAGTGA 77175          TG
                GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                      |||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      GT
GAM1628  LOC143943 3'  TCCAGCCTGGGTGACAGAGCGA 83921          TG
                GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                      |||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      GT
GAM1628  LOC144289 3'  TCCAGCCTGGGTGACAGAGTGA 83962          TG
                GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                      |||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      GT
GAM1628  LOC144308 5'  TCCAGCCTGGGTGACAGAGC   83985       TG
                                GCTCTGT  CCCAGGCTGGA
                                |||||||  ||||||||||
                                CGAGACA  GGGTCCGACCT
                                   GT
GAM1628  LOC144465 3'  TCCAGCCTGGGCAACAAGAGC  77350       _
                                GCTCT GTTGCCCAGGCTGGA
                                |||||  ||||||||||||||
                                CGAGA CAACGGGTCCGACCT
                                  A
GAM1628  LOC144465 3'  TCCAGCCTGGGCAACAAGAGTG 77352        _
                A                    TCGCTCT GTTGCCCAGGCTGGA
                                     |||||||  ||||||||||||||
                                     AGTGAGA CAACGGGTCCGACCT
                                        A
GAM1628  LOC144481 3'  CCATCTTGGGCAACAGAATGAG 84015       C          C
                A                    TCTCG TCTGTTGCCCAGG TGG
                                     |||||  |||||||||||| |||
                                     AGAGT AGACAACGGGTTC ACC
                                       A          T
GAM1628  LOC144519 5'  TCCAGCCTGGGCGACAGAGTGA 77380
                GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                      ||||||||||||||||||||||||
                                      AGAGTGAGACAGCGGGTCCGACCT

GAM1628  LOC144563 3'  TCCAGCTTGGGCAACAGAGTAA 77405     CG
                GA                    TCT  CTCTGTTGCCCAGGCTGGA
                                      |||  ||||||||||||||||||
                                      AGA  GAGACAACGGGTTCGACCT
                                        AT
GAM1628  LOC144845 3'  TCCAGCCCGGGCGACAGAGCAA 57464     C          A
                GA                    TCT GCTCTGTTGCCC GGCTGGA
                                      ||| |||||||||||  |||||||
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                                AGA CGAGACAGCGGG CCGACCT
                                  A          C
GAM1628  LOC145216 3'  CCAGCCTAGCGACAGAGCAAGA 84219     C         CC
                                TCT GCTCTGTTGC  AGGCTGG
                                ||| ||||||||||  |||||||
                                AGA CGAGACAGCG  TCCGACC
                                  A         A_
GAM1628  LOC145231 3'  TCCAGCCTGAACAACATAACAA 84259     CGCTC     CC
              GA                  TCT    TGTTG  CAGGCTGGA
                                |||    |||||  |||||||||
                                AGA    ACAAC  GTCCGACCT
                                  ACAAT    AA
GAM1628  LOC145299 3'  CCTGGGCGACAGAGCGAGA    84275
                                TCTCGCTCTGTTGCCCAGG
                                |||||||||||||||||||
                                AGAGCGAGACAGCGGGTCC

GAM1628  LOC145333 3'  TCCAGCCTGGGCGACAGAGCGA 84304
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||||
                                AGAGCGAGACAGCGGGTCCGACCT

GAM1628  LOC145387 3'  TCCAGCCTGGGCGACAGAGAGA 84344      G
              GA                  TCTC CTCTGTTGCCCAGGCTGGA
                                |||| ||||||||||||||||||
                                AGAG GAGACAGCGGGTCCGACCT
                                  A
GAM1628  LOC145387 3'  TCCAGCCTGGGTGGCAGAGTGA 84345           TG
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGAGACG  GGGTCCGACCT
                                      GT
GAM1628  LOC145438 3'  TCCAGCCTGGGCGACAGAGCGA 84316
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||||
                                AGAGCGAGACAGCGGGTCCGACCT

GAM1628  LOC145453 3'  TCAGCCTGGGCAACAGAGTGAG 77670
              A                   TCTCGCTCTGTTGCCCAGGCTGG
                                |||||||||||||||||||||||
                                AGAGTGAGACAACGGGTCCGACT

GAM1628  LOC145482 3'  CCAGCCTGGGCGACAAGAG    77741      _
                                CTCT GTTGCCCAGGCTGG
                                |||| ||||||||||||||
                                GAGA CAGCGGGTCCGACC
                                  A
GAM1628  LOC145483 3'  TCCAGCCTGGGCAGCAGAGC   77758
                                GCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||
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                                CGAGACGACGGGTCCGACCT

GAM1628  LOC145608 5'  TCCAGCCTGGGTGACAGAGCAA 84386     C      TG
                GA                TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A       GT
GAM1628  LOC145609 3'  TCCAGCCTGGGTGACAGAGCAA 84370     C      TG
                GA                TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A       GT
GAM1628  LOC145663 3'  TCCAGCCTGGGCGACAGAGCTA 84430     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    T
GAM1628  LOC145757 3'  TCCAGCCTAGGTGACAGAGCGA 77942           TG  C
                GA                TCTCGCTCTGT  CC AGGCTGGA
                                  ||||||||||  || ||||||||
                                  AGAGCGAGACA  GG TCCGACCT
                                        GT  A
GAM1628  LOC145820 3'  TCCAGCCTGGGCGACAGAGCAA 77980     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM1628  LOC145945 5'  TCCAGCCTGAGCAACAGAGCAA 84571     C        C
                GA                TCT GCTCTGTTGC CAGGCTGGA
                                  ||| |||||||||| |||||||||
                                  AGA CGAGACAACG GTCCGACCT
                                    A          A
GAM1628  LOC145988 5'  TCCAGCCTGGAAGGCAGAGAGA 78072      G      GC
                GA                TCTC CTCTGTT  CCAGGCTGGA
                                  |||| |||||||  ||||||||||
                                  AGAG GAGACGG  GGTCCGACCT
                                     A       AA
GAM1628  LOC146059 3'  TCCAGTCTGGGTAACAGAGCGA 78090
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAATGGGTCTGACCT

GAM1628  LOC146229 3'  TCCAGCCTGGGCGACAGAGCGA 78317
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCCGACCT

GAM1628  LOC146540 3'  TCCAGCCTGGGCTACAAAGCAG 78530    TC   C   T
                GA                TC  GCT TGT GCCCAGGCTGGA
                                  ||  ||| ||| ||||||||||||
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                                AG  CGA ACA CGGGTCCGACCT
                                 GA   A   T
GAM1628  LOC146713 3'  TCCAGCCTGGGCAACAGAGC   84739
                                GCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||
                                CGAGACAACGGGTCCGACCT

GAM1628  LOC146713 3'  TCCAGCCTGGTCAACAGAGCAA 84741     C        C
           GA                     TCT GCTCTGTTG CCAGGCTGGA
                                ||| ||||||||| ||||||||||
                                AGA CGAGACAAC GGTCCGACCT
                                  A        T
GAM1628  LOC146728 5'  TCCAGACTGGACAACAGAGC   84772         C    G
                                GCTCTGTTG CCAG CTGGA
                                ||||||||| |||| |||||
                                CGAGACAAC GGTC GACCT
                                      A    A
GAM1628  LOC146728 3'  TCCAGCCTGGGAAGCAGAGTGA 84774           G
           GA                     TCTCGCTCTGTT CCCAGGCTGGA
                                |||||||||||| ||||||||||
                                AGAGTGAGACGA GGGTCCGACCT
                                       A
GAM1628  LOC146756 3'  TCCAGCCTGGGCGACAGAGCGA 84813
           GA                     TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||
                                AGAGCGAGACAGCGGGTCCGACCT

GAM1628  LOC146839 5'  TCCAGCCTGGGCAACATAGC   84853     C
                                GCT TGTTGCCCAGGCTGGA
                                ||| ||||||||||||||
                                CGA ACAACGGGTCCGACCT
                                  T
GAM1628  LOC146895 3'  TCCAGCCTGGGTGACAAGAGC  84874       _  TG
                                GCTCT GT  CCCAGGCTGGA
                                ||||| ||  ||||||||||
                                CGAGA CA  GGGTCCGACCT
                                   A  GT
GAM1628  LOC146901 3'  CAGCCTAGACAACAGAGCAAGA 84894     C        CCC
                                TCT GCTCTGTTG   AGGCTG
                                ||| |||||||||   ||||||
                                AGA CGAGACAAC   TCCGAC
                                  A        AGA
GAM1628  LOC146923 3'  TCCAGCCTGGGCGACAGAGTGA 78804
           GA                     TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||
                                AGAGTGAGACAGCGGGTCCGACCT

GAM1628  LOC146958 3'  TCCAGCCTGGGTGACACAGCGA 84946        C   TG
           GA                     TCTCGCT TGT  CCCAGGCTGGA
                                |||||||  |||  ||||||||||
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                                AGAGCGA ACA  GGGTCCGACCT
                                    C   GT
GAM1628  LOC146958 3'  TCCAGCCTGGGTGACAGAGCGA 84948          TG
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GT
GAM1628  LOC147063 5'  CCAGCCTGGGCAACAGAGTGAG 85016
              A                   TCTCGCTCTGTTGCCCAGGCTGG
                                  |||||||||||||||||||||||
                                  AGAGTGAGACAACGGGTCCGACC

GAM1628  LOC147071 3'  TCCAGCCTGGGCGACAGAGCAA 73373     C
              GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM1628  LOC147180 5'  TCCAGCCCGGGTGACAGAGTGA 85105         TG   A
                                  TCGCTCTGT  CCC GGCTGGA
                                  |||||||||  ||| |||||||
                                  AGTGAGACA  GGG CCGACCT
                                        GT   C
GAM1628  LOC147599 3'  TCCAGCCTGGGCAACAGAGAGA 85166    G
                                  TC CTCTGTTGCCCAGGCTGGA
                                  || ||||||||||||||||||
                                  AG GAGACAACGGGTCCGACCT
                                    A
GAM1628  LOC147622 3'  TCCAGCCTGGGTGACAGAGCTA 85172     C      TG
              GA                  TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    T      GT
GAM1628  LOC147649 3'  CCTGGGCGACAGAGCGAGA    79060
                                  TCTCGCTCTGTTGCCCAGG
                                  |||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCC

GAM1628  LOC147664 3'  TCCAGCCTGGGCAACGAGAG   79049      _
                                  CTCT GTTGCCCAGGCTGGA
                                  |||| ||||||||||||||
                                  GAGA CAACGGGTCCGACCT
                                    G
GAM1628  LOC147700 3'  TCCAGCCTGTGCAACAAGCGA  59886      C     C
                                  TCGCT TGTTGC CAGGCTGGA
                                  ||||| |||||| |||||||||
                                  AGCGA ACAACG GTCCGACCT
                                     _     T
GAM1628  LOC147727 5'  TCCAGCCTGGGCGATAGAGTGA 79139
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                  |||||||||||||||||||||||
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                                AGAGTGAGATAGCGGGTCCGACCT

GAM1628  LOC147727 5'  TCCAGTCTGGGCGACAGAGCGA 79140
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  |||||||||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCTGACCT

GAM1628  LOC147837 3'  CCAGCCTGGGCGACAGAGCCAG 79204     C
                A                  TCT GCTCTGTTGCCCAGGCTGG
                                   ||| ||||||||||||||||||
                                   AGA CGAGACAGCGGGTCCGACC
                                     C
GAM1628  LOC147837 3'  TCCAGCCTGGGCAGCAAGAGC  79209      _
                                   GCTCT GTTGCCCAGGCTGGA
                                   ||||| ||||||||||||||
                                   CGAGA CGACGGGTCCGACCT
                                      A
GAM1628  LOC147990 3'  TCCAGCCTGGGCAACAGAGC   85235
                                   GCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||
                                   CGAGACAACGGGTCCGACCT

GAM1628  LOC148166 3'  TCCAGCCTAGGCGACGGGGCAA 79424     C         C
                GA                TCT GCTCTGTTGCC AGGCTGGA
                                  ||| |||||||||| ||||||||
                                  AGA CGGGGCAGCGG TCCGACCT
                                    A          A
GAM1628  LOC148206 3'  TCCAGCCTGGGCCACAAGGCAA 79466     C  TC   T
                GA                TCT GC  TGT GCCCAGGCTGGA
                                  ||| ||  ||| ||||||||||||
                                  AGA CG  ACA CGGGTCCGACCT
                                    A  GA   C
GAM1628  LOC148397 3'  CCAGCCTGGGCAACAAGAGT   79565       _
                                   GCTCT GTTGCCCAGGCTGG
                                   ||||| ||||||||||||||
                                   TGAGA CAACGGGTCCGACC
                                      A
GAM1628  LOC148534 3'  TCCAGCCTGGGCGACAGAGCAA 79640     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM1628  LOC148758 5'  TCCAGCCTGGGCAACAAGAGC  79726      _
                                   GCTCT GTTGCCCAGGCTGGA
                                   ||||| ||||||||||||||
                                   CGAGA CAACGGGTCCGACCT
                                      A
GAM1628  LOC148809 3'  TCCAGCCTGGGCGACAGAGCAA 79762     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
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                                AGA CGAGACAGCGGGTCCGACCT
                                  A
GAM1628  LOC148809 5'  TCCAGCCTGGGTGACAGAGCAA 79763     C      TG
                 GA                TCT GCTCTGT  CCCAGGCTGGA
                                   ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM1628  LOC148823 3'  TCCAGCTTGGGCAACAGAGTGA 59896
                 GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                AGAGTGAGACAACGGGTTCGACCT

GAM1628  LOC148936 3'  TCCAGGTTGGGCAACAGAGCAA 85459     C           G
                 GA                TCT GCTCTGTTGCCCAG CTGGA
                                   ||| |||||||||||||| |||||
                                AGA CGAGACAACGGGTT GACCT
                                  A            G
GAM1628  LOC148938 3'  TCCAGGCTGGGCAACACAGCAA 85441     C   C        G
                 GA                TCT GCT TGTTGCCCAG CTGGA
                                   ||| ||| |||||||||| |||||
                                AGA CGA ACAACGGGTC GACCT
                                  A   C        G
GAM1628  LOC148946 5'  CCAACGGAAAACAGAGCGAGA  85465           GC  AGGC
                                TCTCGCTCTGTT  CC    TGG
                                ||||||||||||  ||    |||
                                AGAGCGAGACAA  GG    ACC
                                      AA  CA__
GAM1628  LOC149073 3'  TCCAGCCTGGGCAACAGTGTGA 85487       T
                 GA                TCTCGC CTGTTGCCCAGGCTGGA
                                   |||||| ||||||||||||||||
                                AGAGTG GACAACGGGTCCGACCT
                                    T
GAM1628  LOC149113 5'  CCAGCCTGGGCTACAAGAG    79905      _  T
                                CTCT GT GCCCAGGCTGG
                                |||| || ||||||||||
                                GAGA CA CGGGTCCGACC
                                  A  T
GAM1628  LOC149157 5'  TCCAGCCTGGTCCAGAGAGAAA 79943     CG    G   C_
                 GA                TCT  CTCT TTG  CCAGGCTGGA
                                   |||  |||| |||  ||||||||||
                                AGA  GAGA GAC  GGTCCGACCT
                                  AA    _   CT
GAM1628  LOC149175 3'  TCCAGCCTGGGCGACAGAGCGA 79957
                 GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                AGAGCGAGACAGCGGGTCCGACCT

GAM1628  LOC149194 5'  TCCAGCCTGGGCAACAAGAGC  79990       _
                                GCTCT GTTGCCCAGGCTGGA
                                ||||| ||||||||||||||
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                                CGAGA CAACGGGTCCGACCT
                                  A
GAM1628  LOC149271 3'  TCCAGCCTGGGCAACAAGAGTG 80012       _
                  A             TCGCTCT GTTGCCCAGGCTGGA
                                |||||||  ||||||||||||||||
                                AGTGAGA CAACGGGTCCGACCT
                                  A
GAM1628  LOC149464 3'  CCAGCCTGGGCAACAAGAG   85588     _
                                CTCT GTTGCCCAGGCTGG
                                ||||  ||||||||||||||
                                GAGA CAACGGGTCCGACC
                                  A
GAM1628  LOC149579 5'  TCCAGCCTGTGTGACAGAGCAA 71695     C      TG C
                  GA            TCT GCTCTGT  C CAGGCTGGA
                                |||  |||||||  | |||||||||
                                AGA CGAGACA  G GTCCGACCT
                                  A      GT T
GAM1628  LOC149606 3'  CCTGGGCAACATAGCGAGA   80258       C
                                TCTCGCT TGTTGCCCAGG
                                |||||||  ||||||||||||
                                AGAGCGA ACAACGGGTCC
                                    T
GAM1628  LOC149628 3'  TCCAGCCTGGGTGACAGAGCGA 80281          TG
                  GA            TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      GT
GAM1628  LOC149672 5'  TCCAGCCTGGGCAACAGAGTGA 80339
                  GA            TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||||
                                AGAGTGAGACAACGGGTCCGACCT

GAM1628  LOC149705 3'  TCCAGCCTGGGTGACGAGTGA  85787       T  TG
                                TCGCTC GT  CCCAGGCTGGA
                                ||||||  ||  ||||||||||||
                                AGTGAG CA  GGGTCCGACCT
                                   _  GT
GAM1628  LOC149711 3'  TCCAGCCTGGGTGACAGAGTGA 85856          TG
                  GA            TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      GT
GAM1628  LOC149952 3'  TCCAGCCTGGGCAATAGAGTGA 80372
                  GA            TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||||
                                AGAGTGAGATAACGGGTCCGACCT

GAM1628  LOC150095 3'  TCCAGCCTGGGCAACAGAGCGA 85996
                  GA            TCTCGCTCTGTTGCCCAGGCTGGA
                                |||||||||||||||||||||||||
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                                AGAGCGAGACAACGGGTCCGACCT

GAM1628  LOC150139 3'  CCTGAGCAACATAGCGAGA    80410        C     C
                                TCTCGCT TGTTGC CAGG
                                ||||||| |||||| ||||
                                AGAGCGA ACAACG GTCC
                                    T     A
GAM1628  LOC150139 3'  TCCAGCCTGGGTGACAGAGAGA 80413    G     TG
                                TC CTCTGT  CCCAGGCTGGA
                                || ||||||  ||||||||||
                                AG GAGACA  GGGTCCGACCT
                                 A     GT
GAM1628  LOC150142 5'  CCAGCCTGGGCAACAAAGTAAG 80404     CG  C
           A                     TCT  CT TGTTGCCCAGGCTGG
                                 |||  || ||||||||||||||
                                 AGA  GA ACAACGGGTCCGACC
                                   AT  A
GAM1628  LOC150174 3'  TCCAGCCTGGTCAACAGAGTGA 80441            C
           GA                      TCTCGCTCTGTTG CCAGGCTGGA
                                   |||||||||||| ||||||||||
                                   AGAGTGAGACAAC GGTCCGACCT
                                         T
GAM1628  LOC150185 3'  TCCAGCCTGGGTGACAGAGCGA 86070           TG
           GA                      TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   AGAGCGAGACA  GGGTCCGACCT
                                         GT
GAM1628  LOC150213 3'  TCCAGCCTGGTCAACAGAGTGA 75360            C
           GA                      TCTCGCTCTGTTG CCAGGCTGGA
                                   |||||||||||| ||||||||||
                                   AGAGTGAGACAAC GGTCCGACCT
                                         T
GAM1628  LOC150225 3'  TCCAGCCTGGGCGTCAGAGTGA 86206          T
           GA                      TCTCGCTCTG TGCCCAGGCTGGA
                                   |||||||||| ||||||||||||
                                   AGAGTGAGAC GCGGGTCCGACCT
                                        T
GAM1628  LOC150236 3'  TCCAGCCTGGTCAACAGAGTGA 80503            C
           GA                      TCTCGCTCTGTTG CCAGGCTGGA
                                   |||||||||||| ||||||||||
                                   AGAGTGAGACAAC GGTCCGACCT
                                         T
GAM1628  LOC150244 3'  TCCAGCCTGGGCGACAGAGCGA 80552
           GA                      TCTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGCGAGACAGCGGGTCCGACCT

GAM1628  LOC150245 3'  TCCAGCCTGGGTGACAGAATAA 86119     CGC    TG
           GA                      TCT   TCTGT  CCCAGGCTGGA
                                   |||   |||||  ||||||||||
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                                AGA   AGACA  GGGTCCGACCT
                                  ATA     GT
GAM1628  LOC150299 3'  TCCAGCCTGGCGACAGAGCAAG 86170     C         C
               A                   TCT GCTCTGTTGCC AGGCTGGA
                                   ||| |||||||||| ||||||||
                                   AGA CGAGACAGCGG TCCGACCT
                                     A         _
GAM1628  LOC150319 3'  TCCAGCCTGGGCAACAAGAGCG 80477         _
               A                   TCGCTCT GTTGCCCAGGCTGGA
                                   ||||||| |||||||||||||||
                                   AGCGAGA CAACGGGTCCGACCT
                                       A
GAM1628  LOC150358 3'  TCCAGCCTGGGCGACAGAGCGA 86101
               GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                     ||||||||||||||||||||||||
                                     AGAGCGAGACAGCGGGTCCGACCT

GAM1628  LOC150481 3'  TCCAGCCTGGTGACAGAGCAAG 80714     C      TG  C
               A                   TCT GCTCTGT  CC AGGCTGGA
                                   ||| |||||||  || ||||||||
                                   AGA CGAGACA  GG TCCGACCT
                                     A      GT  _
GAM1628  LOC150577 3'  TCCAGCCTGGATGACAGAGTGA 86260          GC
                                   TCGCTCTGTT  CCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   AGTGAGACAG  GGTCCGACCT
                                         TA
GAM1628  LOC150622 3'  TCCAGCCTGGGCAACAAGAGC  80768       _
                                   GCTCT GTTGCCCAGGCTGGA
                                   ||||| |||||||||||||||
                                   CGAGA CAACGGGTCCGACCT
                                      A
GAM1628  LOC150630 5'  TCCAGCCTGGGCAGCAGAGTGA 86307
               GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                     ||||||||||||||||||||||||
                                     AGAGTGAGACGACGGGTCCGACCT

GAM1628  LOC150889 3'  TCCAGCCTGCGGGACAGAGTGA 80819           G  _
               GA                    TCTCGCTCTGTT CC CAGGCTGGA
                                     |||||||||||| || |||||||||
                                     AGAGTGAGACAG GG GTCCGACCT
                                           _  C
GAM1628  LOC150960 3'  TCCAGCTTGGGCAACAAAGTGA 80879         C
               GA                    TCTCGCT TGTTGCCCAGGCTGGA
                                     ||||||| |||||||||||||||
                                     AGAGTGA ACAACGGGTTCGACCT
                                        A
GAM1628  LOC151196 3'  TCCAGCCTGGGCAACACAGCAA 86456     C   C
               GA                    TCT GCT TGTTGCCCAGGCTGGA
                                     ||| ||| ||||||||||||||||
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                                AGA CGA ACAACGGGTCCGACCT
                                  A   C
GAM1628  LOC151248 5'  CCTGGGCGACAGAGCGAGA    80992
                                TCTCGCTCTGTTGCCCAGG
                                ||||||||||||||||||
                                AGAGCGAGACAGCGGGTCC

GAM1628  LOC151248 3'  TCCAGCCCAGGTAACAGAGTGA 80998              CA
                  GA                TCTCGCTCTGTTGCC  GGCTGGA
                                ||||||||||||||  |||||||
                                AGAGTGAGACAATGG  CCGACCT
                                          AC
GAM1628  LOC151248 3'  TCCAGCCTGGTGACAGAGCGAG 80999           TG  C
                  A                 TCTCGCTCTGT  CC AGGCTGGA
                                ||||||||||  || ||||||||
                                AGAGCGAGACA  GG TCCGACCT
                                       GT  _
GAM1628  LOC151429 3'  TCCAGCCTGGGCGACAGAGCAA 86549     C
                  GA                TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGAGACAGCGGGTCCGACCT
                                  A
GAM1628  LOC151429 3'  TCCAGCCTGGGTGACAGAGCAA 86550     C      TG
                  GA                TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM1628  LOC151438 3'  CCTGGGCAACACAGCAAGA    86555     C   C
                                TCT GCT TGTTGCCCAGG
                                ||| ||| ||||||||||
                                AGA CGA ACAACGGGTCC
                                  A   C
GAM1628  LOC151446 3'  TCTGAACAACAGAGCAAGA    86575     C        CC
                                TCT GCTCTGTTG  CAGG
                                ||| |||||||||  ||||
                                AGA CGAGACAAC  GTCT
                                  A        AA
GAM1628  LOC151556 3'  TCCAGCCTGAGCAACAGAGCAA 81085     C        C
                  GA                TCT GCTCTGTTGC CAGGCTGGA
                                ||| |||||||||| |||||||||
                                AGA CGAGACAACG GTCCGACCT
                                  A         A
GAM1628  LOC151632 3'  TCCAGCCTGGGCAACAGAGTAA 86651     CG
                  GA                TCT  CTCTGTTGCCCAGGCTGGA
                                |||  ||||||||||||||||||
                                AGA  GAGACAACGGGTCCGACCT
                                  AT
GAM1628  LOC151720 3'  TCCAGCCTGGGCGACAGAGCGA 81158
                  GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
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                                AGAGCGAGACAGCGGGTCCGACCT

GAM1628  LOC151904 3'  TCCAGCCTGGGCAACAGAGCGA 81210
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAACGGGTCCGACCT

GAM1628  LOC152002 3'  TCCAGCCTGGACGACAGAGTGA 81268          C
                GA                TCTCGCTCTGTTG CCAGGCTGGA
                                  |||||||||||||| |||||||||
                                  AGAGTGAGACAGC GGTCCGACCT
                                        A
GAM1628  LOC152106 3'  TCCAGCCTGGTCGACAGAGTGA 70598          C
                GA                TCTCGCTCTGTTG CCAGGCTGGA
                                  |||||||||||||| |||||||||
                                  AGAGTGAGACAGC GGTCCGACCT
                                        T
GAM1628  LOC152271 3'  TCCAGCCTGGGCAACAGAGTAA 81365     CG
                GA                TCT  CTCTGTTGCCCAGGCTGGA
                                  |||  ||||||||||||||||||
                                  AGA  GAGACAACGGGTCCGACCT
                                    AT
GAM1628  LOC152283 3'  TCCAGCCTGGGCAACAAGAGTG 86875          _
                AGA                TCTCGCTCT GTTGCCCAGGCTGGA
                                  |||||||||  ||||||||||||||
                                  AGAGTGAGA CAACGGGTCCGACCT
                                       A
GAM1628  LOC152313 3'  TCCAGCCTGGGTGACAGAGCGA 86853          TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GT
GAM1628  LOC152316 3'  TCCAGCCTAGGCAACAGAGCGA 86794           C
                GA                TCTCGCTCTGTTGCC AGGCTGGA
                                  ||||||||||||||| ||||||||
                                  AGAGCGAGACAACGG TCCGACCT
                                        A
GAM1628  LOC152317 3'  TCCAGCCTGAGTGACAGA     86837       TG C
                                  TCTGT  C CAGGCTGGA
                                  |||||  | |||||||||
                                  AGACA  G GTCCGACCT
                                     GT A
GAM1628  LOC152426 3'  TCCAGCCTGGGCGACAGAGTGA 86902
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAGCGGGTCCGACCT

GAM1628  LOC152445 3'  TCCAGCCTGAGTGAGGAAGC   86964     _  G TG C
                                  GCT CT T  C CAGGCTGGA
                                  ||| || |  | |||||||||
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                                CGA GG A  G GTCCGACCT
                                  A  _ GT A
GAM1628  LOC152453 3'  TCCAGCCTGGGCAACAAGAGCG 81480        _
                A                TCGCTCT GTTGCCCAGGCTGGA
                                 ||||||| ||||||||||||||
                                 AGCGAGA CAACGGGTCCGACCT
                                    A
GAM1628  LOC152627 5'  TCCAGCCTGGATAAAAGAGCAA 81515     C    G   C
                GA               TCT GCTCT TTG CCAGGCTGGA
                                 ||| ||||| ||| ||||||||||
                                 AGA CGAGA AAT GGTCCGACCT
                                   A    A  A
GAM1628  LOC152627 3'  TCCAGCCTGGGCCACAGAGTGA 81516           T
                GA               TCTCGCTCTGT GCCCAGGCTGGA
                                 |||||||||| ||||||||||
                                 AGAGTGAGACA CGGGTCCGACCT
                                       C
GAM1628  LOC152804 3'  TCCAGCCTGGGCAACAGAGCGA 87088
                GG               TCTCGCTCTGTTGCCCAGGCTGGA
                                 ||||||||||||||||||||||||
                                 GGAGCGAGACAACGGGTCCGACCT

GAM1628  LOC152860 3'  CCAGCCTGGGCAGCAAGAG   81578     _
                                 CTCT GTTGCCCAGGCTGG
                                 |||| ||||||||||||||
                                 GAGA CGACGGGTCCGACC
                                   A
GAM1628  LOC152897 3'  CCAGCCTGGGAGACAGAGTGAG 81603          TG
                A                TCTCGCTCTGT  CCCAGGCTGG
                                 ||||||||||  ||||||||||
                                 AGAGTGAGACA  GGGTCCGACC
                                       GA
GAM1628  LOC153077 3'  TCCAGCCTGGGCTACAGAGCAA 87133     C      T
                GA               TCT GCTCTGT GCCCAGGCTGGA
                                 ||| ||||||| ||||||||||||
                                 AGA CGAGACA CGGGTCCGACCT
                                   A      T
GAM1628  LOC153146 3'  TCCAGCCTGGGTGACAGAGGGA 87148      G     TG
                GA               TCTC CTCTGT  CCCAGGCTGGA
                                 |||| ||||||  ||||||||||
                                 AGAG GAGACA  GGGTCCGACCT
                                   G     GT
GAM1628  LOC153243 5'  CCTGGAGCAGCAGAACAAGA   81662     CGC      _
                                 TCT   TCTGTTGC CCAGG
                                 |||   |||||||| |||||
                                 AGA   AGACGACG GGTCC
                                   ACA       A
GAM1628  LOC153338 3'  TCCAGCCTGGGTGACAGAGCAA 87198     C      TG
                GA               TCT GCTCTGT  CCCAGGCTGGA
                                 ||| |||||||  ||||||||||
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                                AGA CGAGACA  GGGTCCGACCT
                                  A      GT
GAM1628  LOC153561 3'  AGCCTGGGCAACAGAGTGAGA  81748
                                TCTCGCTCTGTTGCCCAGGCT
                                |||||||||||||||||||||
                                AGAGTGAGACAACGGGTCCGA

GAM1628  LOC153579 3'  CCAGCCTGGGCCCGCAGA    81767      T_
                                TCTGT  GCCCAGGCTGG
                                |||||  ||||||||||
                                AGACG  CGGGTCCGACC
                                   CC
GAM1628  LOC153579 3'  TCCAGCCTGGGCGACAGAGCGA 81774
                  GA              TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCCGACCT

GAM1628  LOC153642 3'  TCCAGCCTGGCAACAGAGTGAG 81793             C
                  A               TCTCGCTCTGTTGCC AGGCTGGA
                                  ||||||||||||||| ||||||||
                                  AGAGTGAGACAACGG TCCGACCT
                                                _
GAM1628  LOC153682 3'  TCCAGCCTGAGCGACAGAGCAA 87276     C        C
                  GA              TCT GCTCTGTTGC CAGGCTGGA
                                  ||| |||||||||| |||||||||
                                  AGA CGAGACAGCG GTCCGACCT
                                    A         A
GAM1628  LOC153688 3'  TCCAGCCTGGGCGACAGAGGGA 87333      G
                  GA              TCTC CTCTGTTGCCCAGGCTGGA
                                  |||| ||||||||||||||||||
                                  AGAG GAGACAGCGGGTCCGACCT
                                    G
GAM1628  LOC154403 5'  CCAGCCTGGGCTACAAGAG    81971      _  T
                                CTCT GT GCCCAGGCTGG
                                |||| || ||||||||||
                                GAGA CA CGGGTCCGACC
                                  A  T
GAM1628  LOC154739 5'  TCCAGCCTGGGCAACAGGTGAG 87443       T
                  A               TCTCGC CTGTTGCCCAGGCTGGA
                                  ||||||| |||||||||||||||||
                                  AGAGTG GACAACGGGTCCGACCT
                                                _
GAM1628  LOC154739 3'  TCCAGCCTGGGTGACAGAGTGA 87444           TG
                  GA              TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                        GT
GAM1628  LOC154791 3'  TCCAGCCTGGGCAACAAGAGC  82055      _
                                GCTCT GTTGCCCAGGCTGGA
                                |||||  ||||||||||||||
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                                CGAGA CAACGGGTCCGACCT
                                  A
GAM1628  LOC154877 3'  TCCAGCCTAGGTGATAGAGCAA 87576     C      TG  C
                GA                TCT GCTCTGT  CC AGGCTGGA
                                  ||| |||||||  || ||||||||
                                  AGA CGAGATA  GG TCCGACCT
                                    A       GT  A
GAM1628  LOC155006 3'  TCCAGCCTGGGCGGCAGAGCAA 82176     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACGGCGGGTCCGACCT
                                    A
GAM1628  LOC155054 3'  TCCAGCCTGGGTGACAGAGCAA 82206     C      TG
                GA                TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A       GT
GAM1628  LOC155072 3'  TCCAACCTGGGTGACAGAGCGA 87672          TG      C
                                  TCGCTCTGT  CCCAGG TGGA
                                  |||||||||  |||||| ||||
                                  AGCGAGACA  GGGTCC ACCT
                                       GT      A
GAM1628  LOC155072 3'  TCCAGCCTGGGTGACTGAGCGA 87673          T  TG
                GA                TCTCGCTC GT  CCCAGGCTGGA
                                  |||||||| ||  ||||||||||
                                  AGAGCGAG CA  GGGTCCGACCT
                                       T  GT
GAM1628  LOC155376 3'  TCCAGCCTGGGTGACAAAGCAA 82251     C   C   TG
                GA                TCT GCT TGT  CCCAGGCTGGA
                                  ||| ||| |||  ||||||||||
                                  AGA CGA ACA  GGGTCCGACCT
                                    A   A   GT
GAM1628  LOC157247 5'  CCTGGGCAACATAGCAAGA    82294     C   C
                                  TCT GCT TGTTGCCCAGG
                                  ||| ||| ||||||||||
                                  AGA CGA ACAACGGGTCC
                                    A   T
GAM1628  LOC157464 5'  TCCAGCCTGGGCAACGGGCGAG 87752        T
                A                  TCTCGC CTGTTGCCCAGGCTGGA
                                  ||||||| ||||||||||||||||
                                  AGAGCG GGCAACGGGTCCGACCT
                                       _
GAM1628  LOC157562 5'  TCCAGCCTGGGCAACATAGTGA 87776         C
                GA                TCTCGCT TGTTGCCCAGGCTGGA
                                  ||||||| ||||||||||||||||
                                  AGAGTGA ACAACGGGTCCGACCT
                                       T
GAM1628  LOC157657 3'  TCCAGCCTGGACAACACAGTGA 82437         C     C
                GA                TCTCGCT TGTTG CCAGGCTGGA
                                  ||||||| ||||| ||||||||||
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                                AGAGTGA ACAAC GGTCCGACCT
                                   C    A
GAM1628  LOC157660 3'  TCCAGCGTGGGCAACAGAGTGA 87807              G
              GA                  TCTCGCTCTGTTGCCCA GCTGGA
                                  ||||||||||||||||| ||||||
                                  AGAGTGAGACAACGGGT CGACCT
                                        G
GAM1628  LOC157737 3'  TCCAGCCTGGGCAACAGAGAGA 87846     G
              GA                  TCTC CTCTGTTGCCCAGGCTGGA
                                  |||| ||||||||||||||||||
                                  AGAG GAGACAACGGGTCCGACCT
                                    A
GAM1628  LOC157983 3'  TCCAGCCTGGCGACAGAGC   82543          C
                                  GCTCTGTTGCC AGGCTGGA
                                  |||||||||| ||||||||
                                  CGAGACAGCGG TCCGACCT

                                      _
GAM1628  LOC158088 3'  TCCAGCCTGGCGACAGAGCAAG 87978    C         C
              A                    TCT GCTCTGTTGCC AGGCTGGA
                                  ||| |||||||||| ||||||||
                                  AGA CGAGACAGCGG TCCGACCT
                                    A         _
GAM1628  LOC158160 3'  TCCAGCCTGGGTGACAGCGAGA 73476        CT  TG
                                  TCTCGCT  GT  CCCAGGCTGGA
                                  |||||||  ||  ||||||||||
                                  AGAGCGA  CA  GGGTCCGACCT
                                      __  GT
GAM1628  LOC158187 3'  TCCAGCCTGGGTGACAGAGCAA 87998    C      TG
              GA                  TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A      GT
GAM1628  LOC158191 3'  TCCAGCCTGGCGACAGAGCTAG 82682    C         C
              A                    TCT GCTCTGTTGCC AGGCTGGA
                                  ||| |||||||||| ||||||||
                                  AGA CGAGACAGCGG TCCGACCT
                                    T         _
GAM1628  LOC158235 3'  TCCAGCCTGGGCAACACAGAGA 88008     G  C
              GA                  TCTC CT TGTTGCCCAGGCTGGA
                                  |||| || ||||||||||||||||
                                  AGAG GA ACAACGGGTCCGACCT
                                    A  C
GAM1628  LOC158292 5'  TCCAGCCTGGGCAACAGAGCAA 88056    C
              GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAACGGGTCCGACCT
                                    A
GAM1628  LOC158292 5'  TCCAGCCTGGGCGACAGAGCGA 88057
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                  |||||||||||||||||||||||
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                                AGAGCGAGACAGCGGGTCCGACCT

GAM1628  LOC158337 3'  TCCAGCCTGGGTGACAGAGCGA 88112          TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GT
GAM1628  LOC158677 5'  TCCAGCCTGGGTGACAGAGCAA 88252     C      TG
                GA                TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A      GT
GAM1628  LOC158819 3'  TCCAGCCTGGGTGACAGAGCGA 88286          TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GT
GAM1628  LOC158987 3'  TCCAGCCTGGGCAACAGAGGGA 88334     G
                G                  CTC CTCTGTTGCCCAGGCTGGA
                                   ||| ||||||||||||||||||
                                   GAG GAGACAACGGGTCCGACCT
                                     G
GAM1628  LOC158987 3'  TCCAGCCTGGGCAACATAGTGA 88335        C
                GA                TCTCGCT TGTTGCCCAGGCTGGA
                                  ||||||| ||||||||||||||||
                                  AGAGTGA ACAACGGGTCCGACCT
                                      T
GAM1628  LOC158987 3'  TCCAGCCTGGGTGACAGAGCGA 88337          TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GT
GAM1628  LOC159053 3'  TCCAGCCTGGGCAACAGTGAGA 88377        CT
                                  TCTCGCT  GTTGCCCAGGCTGGA
                                  |||||||  ||||||||||||||||
                                  AGAGTGA  CAACGGGTCCGACCT
                                       __
GAM1628  LOC159110 3'  CCAGCCTGGGCAACAGAACAGG 82986     CGC
                A                  TCT   TCTGTTGCCCAGGCTGG
                                   |||   ||||||||||||||||
                                   AGG   AGACAACGGGTCCGACC
                                     ACA
GAM1628  LOC159116 3'  CCAGCCTGGGCAACAGAACAGG 82969     CGC
                A                  TCT   TCTGTTGCCCAGGCTGG
                                   |||   ||||||||||||||||
                                   AGG   AGACAACGGGTCCGACC
                                     ACA
GAM1628  LOC161823 3'  TCCAGCCTGGGCAACAGAGTGA 83176
                                  TCGCTCTGTTGCCCAGGCTGGA
                                  |||||||||||||||||||||
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                                AGTGAGACAACGGGTCCGACCT

GAM1628  LOC162962 3'  TCCAGCCTGGGTGACAGCGAGA 83260       CT  TG
                                TCTCGCT  GT  CCCAGGCTGGA
                                |||||||  ||  ||||||||||||
                                AGAGCGA  CA  GGGTCCGACCT
                                   __  GT
GAM1628  LOC170395 3'  TCAAGCCTGGGCAACAGAGTGA 76876                  G
              GA                  TCTCGCTCTGTTGCCCAGGCT GA
                                  ||||||||||||||||||||| ||
                                  AGAGTGAGACAACGGGTCCGA CT
                                                       A
GAM1628  LOC170395 3'  TCCAGCCTGGGCAACAAGAGC  76877      _
                                GCTCT GTTGCCCAGGCTGGA
                                |||||| ||||||||||||||||
                                CGAGA CAACGGGTCCGACCT
                                   A
GAM1628  LOC196047 5'  TCCAGCCTGGGTGACAGAGCGA 91167          TG
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||||  ||||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GT
GAM1628  LOC196540 3'  TCCAGCCTGGGTGACAGAGTGA 91208          TG
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||||  ||||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                        GT
GAM1628  LOC196761 3'  TCCAGCCTGGGCGATAGAGGGA 91121      G
              GA                  TCTC CTCTGTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||||||
                                  AGAG GAGATAGCGGGTCCGACCT
                                    G
GAM1628  LOC197196 3'  TCCAGCCTGGGCGACAAGAGCG 91306        _
              A                    TCGCTCT GTTGCCCAGGCTGGA
                                   ||||||| ||||||||||||||||
                                   AGCGAGA CAGCGGGTCCGACCT
                                      A
GAM1628  LOC197201 3'  TCCAGCCTGGGCAACACAGCAA 89288     C   C
              GA                  TCT GCT TGTTGCCCAGGCTGGA
                                  ||| ||| ||||||||||||||||
                                  AGA CGA ACAACGGGTCCGACCT
                                    A   C
GAM1628  LOC197319 3'  TCCAGCCTGGCAACAGAGTGAG 89329             C
              A                    TCTCGCTCTGTTGCC AGGCTGGA
                                   ||||||||||||||| ||||||||
                                   AGAGTGAGACAACGG TCCGACCT
                                                  _
GAM1628  LOC197362 3'  TCCAGCCTGGGTGACAGAGTGA 91312          TG
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||||  ||||||||||||
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                                AGAGTGAGACA  GGGTCCGACCT
                                      GT
GAM1628  LOC199729 3'  TCCAGCCAGGGCAACAGAGTGA 73397              A
                GA                    TCTCGCTCTGTTGCCC GGCTGGA
                                      ||||||||||||||| |||||||
                                      AGAGTGAGACAACGGG CCGACCT
                                         A
GAM1628  LOC199733 3'  TCCAACCTGGGCAACAGAGCCA 91443     C           C
                GA                    TCT GCTCTGTTGCCCAGG TGGA
                                      ||| |||||||||||||| ||||
                                      AGA CGAGACAACGGGTCC ACCT
                                        C           A
GAM1628  LOC199786 3'  TCCAGCCTGGGTGATGGGAGTG 89767         _  TG
                AGA                    TCTCGCTCT GT  CCCAGGCTGGA
                                       ||||||||| ||  ||||||||||
                                       AGAGTGAGG TA  GGGTCCGACCT
                                          G  GT
GAM1628  LOC199858 3'  TCCAGCCTGGGCGACAGAGCGA 89803
                GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                      ||||||||||||||||||||||||
                                      AGAGCGAGACAGCGGGTCCGACCT

GAM1628  LOC199923 3'  TCCAGCCTGGACGACAGAGCAA 89874     C       C
                GA                    TCT GCTCTGTTG CCAGGCTGGA
                                      ||| ||||||||| ||||||||||
                                      AGA CGAGACAGC GGTCCGACCT
                                        A       A
GAM1628  LOC199923 3'  TCCAGCCTGGGCAACTGAGC   89875      T
                                      GCTC GTTGCCCAGGCTGGA
                                      |||| ||||||||||||||
                                      CGAG CAACGGGTCCGACCT
                                        T
GAM1628  LOC200014 3'  TCCAGCCTGGGCGACAGAGCAA 89948     C
                GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                      ||| ||||||||||||||||||
                                      AGA CGAGACAGCGGGTCCGACCT
                                        A
GAM1628  LOC200251 3'  TCCAGCCTAGGCAACAAGAGC  90066      _     C
                                      GCTCT GTTGCC AGGCTGGA
                                      ||||| |||||| ||||||||
                                      CGAGA CAACGG TCCGACCT
                                         A     A
GAM1628  LOC200316 3'  TCCAGTTTGAGCAACAGATCAA 90194     CGC       C
                GA                    TCT   TCTGTTGC CAGGCTGGA
                                      |||   |||||||| |||||||||
                                      AGA   AGACAACG GTTTGACCT
                                        ACT       A
GAM1628  LOC200317 3'  TCCAGCCTGGGCAACAAGAGTG 90229        _
                A                      TCGCTCT GTTGCCCAGGCTGGA
                                       ||||||| ||||||||||||||||
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                                AGTGAGA CAACGGGTCCGACCT
                                   A
GAM1628  LOC200853 3'  TCCAGCCTGGGAGACAGAGCGA 90335         TG
                                TCGCTCTGT  CCCAGGCTGGA
                                |||||||||  ||||||||||
                                AGCGAGACA  GGGTCCGACCT
                                   GA
GAM1628  LOC200904 3'  TCTAGCCTGGGCAACAGAGTAA 91785     CG
            GA                    TCT  CTCTGTTGCCCAGGCTGGA
                                  |||  ||||||||||||||||||
                                  AGA  GAGACAACGGGTCCGATCT
                                    AT
GAM1628  LOC200918 3'  CCAGCCTGGGCGACAAGAG    90366      _
                                CTCT GTTGCCCAGGCTGG
                                |||| ||||||||||||||
                                GAGA CAGCGGGTCCGACC
                                   A
GAM1628  LOC200940 3'  TCCAGCCTGGGCGACAGAGTGA 90396
            GA                    TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAGCGGGTCCGACCT

GAM1628  LOC201173 3'  TCCAGCCTGGGCGACAGAGCAA 88694     C
            GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM1628  LOC201182 5'  TCCAGCCTGGTCAACAGAGCAA 91338     C        C
            GA                    TCT GCTCTGTTG CCAGGCTGGA
                                  ||| ||||||||| ||||||||||
                                  AGA CGAGACAAC GGTCCGACCT
                                    A        T
GAM1628  LOC201220 3'  TCCAGCCTGGGTGACAGAGCAA 88727     C       TG
            GA                    TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A      GT
GAM1628  LOC201564 3'  TCCAGCCTGGGCAACAAGAGC  81276       _
                                GCTCT GTTGCCCAGGCTGGA
                                ||||| ||||||||||||||
                                CGAGA CAACGGGTCCGACCT
                                   A
GAM1628  LOC201685 3'  TCAAGCCTGGACAACAGGGCAA 91846     C        C       G
            GA                    TCT GCTCTGTTG CCAGGCT GA
                                  ||| ||||||||| ||||||| ||
                                  AGA CGGGACAAC GGTCCGA CT
                                    A        A       A
GAM1628  LOC201868 5'  CCAGCCTGGGCTACAAGAG    90518      _  T
                                CTCT GT GCCCAGGCTGG
                                |||| || ||||||||||
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                                GAGA CA CGGGTCCGACC
                                  A  T
GAM1628  LOC201895 3'  TCCAGCCTAAGCAATAGAGCGA 90548           CC
                GA                TCTCGCTCTGTTGC  AGGCTGGA
                                  ||||||||||||||  ||||||||
                                  AGAGCGAGATAACG  TCCGACCT
                                        AA
GAM1628  LOC201911 3'  TCCAGCCTGGGCAACAAGAGC  91869      _
                                  GCTCT GTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||||
                                  CGAGA CAACGGGTCCGACCT
                                    A
GAM1628  LOC201931 3'  TCCAGCCTGGGCGACAGAGCGA 90569
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCCGACCT

GAM1628  LOC202020 3'  TCCAGCCCGGGCGACAGAGTGA 90603             A
                GA                TCTCGCTCTGTTGCCC GGCTGGA
                                  |||||||||||||||| |||||||
                                  AGAGTGAGACAGCGGG CCGACCT
                                        C
GAM1628  LOC202781 3'  TCCAGCCTGGACGATATAGCCA 91975     C   C     C
                GA                TCT GCT TGTTG CCAGGCTGGA
                                  ||| ||| ||||| ||||||||||
                                  AGA CGA ATAGC GGTCCGACCT
                                    C   T     A
GAM1628  LOC202781 3'  TCCAGCCTGGGCGACAGAGCGA 91976
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAGCGGGTCCGACCT

GAM1628  LOC202868 3'  TCCAACCTGGGTGACAGAGCGA 92009          TG      C
                                  TCGCTCTGT  CCCAGG TGGA
                                  |||||||||  |||||| ||||
                                  AGCGAGACA  GGGTCC ACCT
                                       GT      A
GAM1628  LOC202868 3'  TCCAGCCTGGGTGACAGAGCGA 92010           TG
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||||  ||||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                       GT
GAM1628  LOC203025 3'  TCCAGCCTGGGCAACAAGAGC  90749      _
                                  GCTCT GTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||||
                                  CGAGA CAACGGGTCCGACCT
                                    A
GAM1628  LOC203083 3'  TCCAGCCTGGGCAACAGAGTAA 92095     CG
                GA                TCT  CTCTGTTGCCCAGGCTGGA
                                  |||  ||||||||||||||||||
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                                AGA  GAGACAACGGGTCCGACCT
                                  AT
GAM1628  LOC203246 3'  CCTGGGCGACAGAACGAGA   90830      C
                                TCTCG TCTGTTGCCCAGG
                                ||||| ||||||||||||
                                AGAGC AGACAGCGGGTCC
                                   A
GAM1628  LOC203276 3'  TCCAGCCTGGGCAACAGAGTGA 92130
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAACGGGTCCGACCT

GAM1628  LOC203289 3'  TCCAGCCTGGCGACAGAGC   90870          C
                                GCTCTGTTGCC AGGCTGGA
                                |||||||||| ||||||||
                                CGAGACAGCGG TCCGACCT

                                   _
GAM1628  LOC203305 3'  TCCAGCCTGGGCAACAGAGTGA 92183
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAACGGGTCCGACCT

GAM1628  LOC203350 3'  CCTGGGGCAACATAGCGAGA   92235       C      _
                                TCTCGCT TGTTGCCC AGG
                                ||||||| |||||||| |||
                                AGAGCGA ACAACGGG TCC
                                    T       G
GAM1628  LOC203350 3'  TCCAGCCTGGATGACAGAGTGA 92250           GC
              GA                  TCTCGCTCTGTT  CCAGGCTGGA
                                  ||||||||||||  ||||||||||
                                  AGAGTGAGACAG  GGTCCGACCT
                                        TA
GAM1628  LOC203378 3'  TCCAGCCTGGGCGACAGAACAA 92303     CGC
              GA                  TCT   TCTGTTGCCCAGGCTGGA
                                  |||   ||||||||||||||||||
                                  AGA   AGACAGCGGGTCCGACCT
                                    ACA
GAM1628  LOC205327 3'  TCCAACCTGGGCAACATAGTGG 91072       C         C
              GA                  TCTCGCT TGTTGCCCAGG TGGA
                                  ||||||| |||||||||| ||||
                                  AGGGTGA ACAACGGGTCC ACCT
                                     T         A
GAM1628  LOC219347 3'  TCCAGCCTGGGCAACAGAGTGA 94581
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAACGGGTCCGACCT

GAM1628  LOC219540 3'  TCCAGCCTGGGCGACAGAGCGA 95247
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
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                                AGAGCGAGACAGCGGGTCCGACCT

GAM1628  LOC219627 3'  TCCAGCCTGGGCAACAAGCGA  93812       C
                                TCGCT TGTTGCCCAGGCTGGA
                                ||||| ||||||||||||||||
                                AGCGA ACAACGGGTCCGACCT
                                  _
GAM1628  LOC219627 3'  TCCAGCTGGGCGACAGAGCGAG 93813                 G
              A                  TCTCGCTCTGTTGCCCAG CTGGA
                                 |||||||||||||||| |||||
                                 AGAGCGAGACAGCGGGTC GACCT
                                       _
GAM1628  LOC219649 3'  TCCAGCCTAGGCAACAAGAGC  94557       _     C
                                GCTCT GTTGCC AGGCTGGA
                                ||||| |||||| ||||||||
                                CGAGA CAACGG TCCGACCT
                                   A     A
GAM1628  LOC219649 3'  TCCAGCCTGGGCGACAGAGTGA 94558
              GA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGTGAGACAGCGGGTCCGACCT

GAM1628  LOC219672 5'  TCCAGCCTGGGCAACAAGAGTG 92973        _
              A                  TCGCTCT GTTGCCCAGGCTGGA
                                 ||||||| |||||||||||||||
                                 AGTGAGA CAACGGGTCCGACCT
                                    A
GAM1628  LOC219722 5'  CCAGCCTGGGCAACAGAACAAG 94677     CGC
              A                  TCT   TCTGTTGCCCAGGCTGG
                                 |||   ||||||||||||||||
                                 AGA   AGACAACGGGTCCGACC
                                   ACA
GAM1628  LOC219722 5'  TCAGCCTGGACAACAGAGTGAG 94685            C
              A                  TCTCGCTCTGTTG CCAGGCTGG
                                 |||||||||||| ||||||||
                                 AGAGTGAGACAAC GGTCCGACT
                                         A
GAM1628  LOC219919 3'  TCCAGCCTGGGCAACAGAGTAA 94933     CG
              GA                   TCT  CTCTGTTGCCCAGGCTGGA
                                   |||  ||||||||||||||||||
                                   AGA  GAGACAACGGGTCCGACCT
                                     AT
GAM1628  LOC220038 3'  TCCAGCCTGGGCGATGGAGTGA 93377
              GA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGTGAGGTAGCGGGTCCGACCT

GAM1628  LOC220506 3'  TCCAGCCTGGGCAACAGAACAA 74521     CGC
              GA                   TCT   TCTGTTGCCCAGGCTGGA
                                   |||   ||||||||||||||||||
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                                AGA   AGACAACGGGTCCGACCT
                                  ACA
GAM1628  LOC220549 3'  TCCAGCCTGGGTGACAGAATGA 94511      C     TG
              GA                  TCTCG TCTGT  CCCAGGCTGGA
                                  ||||| |||||  ||||||||||
                                  AGAGT AGACA  GGGTCCGACCT
                                    A     GT
GAM1628  LOC220662 3'  TCCAGCCTGGGCAACACGAGCG 92831       _
              A                   TCGCTC TGTTGCCCAGGCTGGA
                                  |||||| ||||||||||||||||
                                  AGCGAG ACAACGGGTCCGACCT
                                    C
GAM1628  LOC220692 3'  TCCAGCTCGGGGAACAGAGCGA 92866           G   AG
              GA                  TCTCGCTCTGTT CCC  GCTGGA
                                  |||||||||||| |||  ||||||
                                  AGAGCGAGACAA GGG  CGACCT
                                         G   CT
GAM1628  LOC220776 3'  CCAGCCCAGAGTAAGAGAGCAG 68920     C     G    CCA_
              A                   TCT GCTCT TTGC    GGCTGG
                                  ||| ||||| ||||    ||||||
                                  AGA CGAGA AATG    CCGACC
                                    _    G    AGAC
GAM1628  LOC220906 3'  TCCAGCCTGGGCAACAAGCGA  93037      C
                                  TCGCT TGTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||||
                                  AGCGA ACAACGGGTCCGACCT
                                    _
GAM1628  LOC220906 3'  TCCAGCTGGGCGACAGAGCGAG 93038              G
              A                   TCTCGCTCTGTTGCCCAG CTGGA
                                  |||||||||||||||| |||||
                                  AGAGCGAGACAGCGGGTC GACCT
                                              _
GAM1628  LOC220992 3'  TCCAGCCTGGGCAACATAGCAA 93110     C   C
              GA                  TCT GCT TGTTGCCCAGGCTGGA
                                  ||| ||| ||||||||||||||||
                                  AGA CGA ACAACGGGTCCGACCT
                                    A   T
GAM1628  LOC221042 3'  TCCAGCCTGGGTGACAGAGCAA 94807     C      TG
              GA                  TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A      GT
GAM1628  LOC221069 3'  TCCAGCCTGGGCGACAGAGCAA 94821     C
              GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM1628  LOC221178 3'  TCCAGCCTGGGAGATACAGCGA 95176       C   TG
              GA                  TCTCGCT TGT  CCCAGGCTGGA
                                  ||||||| |||  ||||||||||
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                                AGAGCGA ATA  GGGTCCGACCT
                                   C   GA
GAM1628  LOC221271 3'  TCCAGCCTGGGCAACAGAGGGA 93530      G
              GA                  TCTC CTCTGTTGCCCAGGCTGGA
                                  |||| ||||||||||||||||||
                                  AGAG GAGACAACGGGTCCGACCT
                                    G
GAM1628  LOC221271 3'  TCCAGCCTGGGTGACAGAGCGA 93532          TG
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GT
GAM1628  LOC221288 3'  TCCAGCCTGGGCGACAGAGTGA 95263
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAGCGGGTCCGACCT

GAM1628  LOC221337 3'  TCCAGCCTGGGCAACAAGAGTG 93738        _
              A                    TCGCTCT GTTGCCCAGGCTGGA
                                  |||||||  ||||||||||||||
                                  AGTGAGA CAACGGGTCCGACCT
                                     A
GAM1628  LOC221410 3'  TCCAGCCTGGGTGACAGAGCGA 93699          TG
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        GT
GAM1628  LOC221477 3'  TCCAGCCTGGGCGACAGAGCGA 93776
                                  TCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||
                                  AGCGAGACAGCGGGTCCGACCT

GAM1628  LOC221490 3'  CCTAGGCGACAGAGCAAGA   95304     C        C
                                  TCT GCTCTGTTGCC AGG
                                  ||| |||||||||| |||
                                  AGA CGAGACAGCGG TCC
                                    A         A
GAM1628  LOC221543 3'  TCCAGCCTGGGCAACAAGAGTA 95386    CG   _
              AG                  CT  CTCT GTTGCCCAGGCTGGA
                                  ||  |||| ||||||||||||||
                                  GA  GAGA CAACGGGTCCGACCT
                                   AT    A
GAM1628  LOC221543 5'  TCCAGCCTGGGCGACAGAGCAA 95388     C
              GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM1628  LOC221641 5'  TCCAGCCTGGGTGGCAGAGCGA 95348          TG
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
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                                AGAGCGAGACG  GGGTCCGACCT
                                      GT
GAM1628  LOC221795 3'  TCCAGCCTGGGCAACAGAGTAA 94081     CG
                GA                TCT  CTCTGTTGCCCAGGCTGGA
                                  |||  ||||||||||||||||||
                                  AGA  GAGACAACGGGTCCGACCT
                                    AT
GAM1628  LOC221931 3'  CCAGAGCAACAGAGTGAGA    95630            CCAGG
                                  TCTCGCTCTGTTGC     CTGG
                                  ||||||||||||||     ||||
                                  AGAGTGAGACAACG     GACC
                                           A____
GAM1628  LOC221943 5'  TCCAGCCTGGGCGACAGAGCAA 95625     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM1628  LOC221954 5'  TCCAGCCTGGGCAACAGAGCGA 95651
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAACGGGTCCGACCT

GAM1628  LOC221954 5'  TCCAGCCTGGGTGACAGAGTAA 95652     CG     TG
                GA                TCT  CTCTGT  CCCAGGCTGGA
                                  |||  ||||||  ||||||||||
                                  AGA  GAGACA  GGGTCCGACCT
                                    AT     GT
GAM1628  LOC221954 5'  TCCAGCTTGGGCGACAGAGCAA 95653     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||
                                  AGA CGAGACAGCGGGTTCGACCT
                                    A
GAM1628  LOC222008 5'  TCCAGCCTGGGCTCCGCAGG   95659      T__
                                  TCTGT   GCCCAGGCTGGA
                                  |||||   ||||||||||||
                                  GGACG   CGGGTCCGACCT
                                     CCT
GAM1628  LOC222060 5'  TCCAGCCTGGGCGACAGAGCAA 95758     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||
                                  AGA CGAGACAGCGGGTCCGACCT
                                    A
GAM1628  LOC222160 3'  TCCAGCCTGGGCAGCAGAGGAA 95791     CG
                GA                TCT  CTCTGTTGCCCAGGCTGGA
                                  |||  ||||||||||||||||||
                                  AGA  GAGACGACGGGTCCGACCT
                                    AG
GAM1628  LOC222160 5'  TCCAGCCTGGGCGACAGAGCAA 95792     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||
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                                AGA CGAGACAGCGGGTCCGACCT
                                  A
GAM1628  LOC222182 3'  TCCAGCCTGGGCAATAGAGTGA 95862
                  GA             TCTCGCTCTGTTGCCCAGGCTGGA
                                 ||||||||||||||||||||||||
                                 AGAGTGAGATAACGGGTCCGACCT

GAM1628  LOC222865 3'  TCCAGCCTGAGTGACAGAGCGA 94450          TG C
                  GA             TCTCGCTCTGT  C CAGGCTGGA
                                 ||||||||||  | |||||||||
                                 AGAGCGAGACA  G GTCCGACCT
                                       GT A
GAM1628  LOC245771 5'  CCAGCCTGGGCTGGGGGAGA   94469     G   TGTT
                                 TCTC CTC    GCCCAGGCTGG
                                 |||| |||    ||||||||||
                                 AGAG GGG    CGGGTCCGACC
                                   G   T___
GAM1628  LOC253039 3'  TCCAGCCTGGGCGACAGAGCAA 97867     C
                  GA             TCT GCTCTGTTGCCCAGGCTGGA
                                 ||| ||||||||||||||||||||
                                 AGA CGAGACAGCGGGTCCGACCT
                                   A
GAM1628  LOC253532 3'  TCCAGCCTGGGTGACAAAGCAA 97740     C   C   TG
                  GA             TCT GCT TGT  CCCAGGCTGGA
                                 ||| ||| |||  ||||||||||
                                 AGA CGA ACA  GGGTCCGACCT
                                   A   A   GT
GAM1628  LOC253612 5'  TCCAGCCTAGGCAACAGAGTGA 98559              C
                  GA             TCTCGCTCTGTTGCC AGGCTGGA
                                 ||||||||||||||| ||||||||
                                 AGAGTGAGACAACGG TCCGACCT
                                           A
GAM1628  LOC253639 3'  TCCAGCCTGGGCGACAGAGTGA 97517
                  GA             TCTCGCTCTGTTGCCCAGGCTGGA
                                 ||||||||||||||||||||||||
                                 AGAGTGAGACAGCGGGTCCGACCT

GAM1628  LOC253778 5'  TCCAGCCTGGGCGACAGAGTGA 96527
                  GA             TCTCGCTCTGTTGCCCAGGCTGGA
                                 ||||||||||||||||||||||||
                                 AGAGTGAGACAGCGGGTCCGACCT

GAM1628  LOC253786 3'  TCCAGCCTGGGCAATAGAGCAA 98834     C
                  GA             TCT GCTCTGTTGCCCAGGCTGGA
                                 ||| ||||||||||||||||||||
                                 AGA CGAGATAACGGGTCCGACCT
                                   A
GAM1628  LOC253832 3'  TCCAGCCTGGGCGACGAGTGA  96593       T
                                 TCGCTC GTTGCCCAGGCTGGA
                                 ||||||| ||||||||||||||
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                                AGTGAG CAGCGGGTCCGACCT
                                      _
GAM1628  LOC253840 5'  TCCAGCCTGGGCAACAGAGCAA 97914     C
                GA                TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAACGGGTCCGACCT
                                    A
GAM1628  LOC253906 3'  CAGCCTGGGCAACAAAGTGAGA 98299        C
                                  TCTCGCT TGTTGCCCAGGCTG
                                  ||||||| |||||||||||||
                                  AGAGTGA ACAACGGGTCCGAC
                                      A
GAM1628  LOC254041 5'  CCTGGACGACAGAGCAAGA   96554     C       C
                                  TCT GCTCTGTTG CCAGG
                                  ||| ||||||||| |||||
                                  AGA CGAGACAGC GGTCC
                                    A       A
GAM1628  LOC254045 3'  CCATCTTGGGCAACAGAATGAG 98265       C           C
                A                  TCTCG TCTGTTGCCCAGG TGG
                                   ||||| |||||||||||| |||
                                   AGAGT AGACAACGGGTTC ACC
                                     A           T
GAM1628  LOC254100 3'  TCCAGCCTGGGCAACAGAGTGA 98160
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAACGGGTCCGACCT

GAM1628  LOC254176 3'  TCCAGCCTGGGCAACAGAGTAA 99176     CG
                GA                TCT  CTCTGTTGCCCAGGCTGGA
                                  |||  ||||||||||||||||||
                                  AGA  GAGACAACGGGTCCGACCT
                                    AT
GAM1628  LOC254243 3'  TCCAGCCTGGGCAACAGAGTGA 99269
                GA                TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAACGGGTCCGACCT

GAM1628  LOC254531 5'  TCCAGCCTGGGTGACAGAGCAA 96673     C      TG
                GA                TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A      GT
GAM1628  LOC254659 3'  TCCAGAGTGGGAAACAGAGCAA 96822     C       G    GG
                GA                TCT GCTCTGTT CCCA  CTGGA
                                  ||| |||||||| ||||  |||||
                                  AGA CGAGACAA GGGT  GACCT
                                    A       A   GA
GAM1628  LOC254756 3'  TCCAGCCTGGGCAATAGAGTAA 99212     CG
                GA                TCT  CTCTGTTGCCCAGGCTGGA
                                  |||  ||||||||||||||||||
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                                AGA  GAGATAACGGGTCCGACCT
                                  AT
GAM1628  LOC254808 3'  TCCAGCCTGGGCAACAGAGCAA 98810     C
                 GA                TCT GCTCTGTTGCCCAGGCTGGA
                                   ||| ||||||||||||||||||||
                                   AGA CGAGACAACGGGTCCGACCT
                                     A
GAM1628  LOC254875 3'  TCCAGCCTGGGTGACAAAGCAA 97785     C   C   TG
                 GA                TCT GCT TGT  CCCAGGCTGGA
                                   ||| ||| |||  ||||||||||
                                   AGA CGA ACA  GGGTCCGACCT
                                     A   A   GT
GAM1628  LOC255030 5'  TCCAGCCTGGGTGACAGAGCGA 99086          TG
                 GA                TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   AGAGCGAGACA  GGGTCCGACCT
                                         GT
GAM1628  LOC255031 3'  TCCAGCCTGGCTACAGAGTGAG 99044          T   C
                 A                 TCTCGCTCTGT GCC AGGCTGGA
                                   |||||||||| ||| ||||||||
                                   AGAGTGAGACA CGG TCCGACCT
                                         T   _
GAM1628  LOC255042 3'  TCCAGCCTGGGCAACAAGAGCG 97056        _
                 A                 TCGCTCT GTTGCCCAGGCTGGA
                                   ||||||| ||||||||||||||
                                   AGCGAGA CAACGGGTCCGACCT
                                       A
GAM1628  LOC255042 3'  TCCAGCCTGGGCGACGAGC    97057      T
                                   GCTC GTTGCCCAGGCTGGA
                                   |||| ||||||||||||||
                                   CGAG CAGCGGGTCCGACCT
                                     _
GAM1628  LOC255177 3'  TCCAGCCTAGGCAACAGAGTGA 98401             C
                 GA                TCTCGCTCTGTTGCC AGGCTGGA
                                   |||||||||||||| ||||||||
                                   AGAGTGAGACAACGG TCCGACCT
                                           A
GAM1628  LOC255196 3'  CCTGGGCAACAGAGCCAGA    98952     C
                                   TCT GCTCTGTTGCCCAGG
                                   ||| ||||||||||||||
                                   AGA CGAGACAACGGGTCC
                                     C
GAM1628  LOC255196 5'  TCCAACCTGGGCAGCACGAAGA 98966     _ CTC         C
                                   TCT CG   TGTTGCCCAGG TGGA
                                   ||| ||   |||||||||| ||||
                                   AGA GC   ACGACGGGTCC ACCT
                                     A ___          A
GAM1628  LOC255231 3'  TCCAGCCTGGGTGACAGAGTGA 97123          TG
                 GA                TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
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                                AGAGTGAGACA  GGGTCCGACCT
                                      GT
GAM1628  LOC255326 3'  TCCAGCCTGGGTGACAGAGCAA 98124     C      TG
              GA                  TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A       GT
GAM1628  LOC255328 3'  TCCAGCCTGGGTGATAAGAGC  98347       _  TG
                                  GCTCT GT  CCCAGGCTGGA
                                  ||||| ||  ||||||||||
                                  CGAGA TA  GGGTCCGACCT
                                     A  GT
GAM1628  LOC255463 3'  TCCAGCCTGGACAACATAGTGA 96543        C     C
              GA                  TCTCGCT TGTTG CCAGGCTGGA
                                  ||||||| ||||| ||||||||||
                                  AGAGTGA ACAAC GGTCCGACCT
                                      T     A
GAM1628  LOC255523 3'  TCCAGCCTGGGCAACAGAGCAA 96737     C
              GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAACGGGTCCGACCT
                                    A
GAM1628  LOC255565 5'  CCAGCCTGAGAAACAAGC     96802     C    GCC
                                  GCT TGTT   CAGGCTGG
                                  ||| ||||   ||||||||
                                  CGA ACAA   GTCCGACC
                                    _    AGA
GAM1628  LOC255671 3'  TCCAGCCTGGGTAACAGAGCAA 99076     C
              GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAATGGGTCCGACCT
                                    A
GAM1628  LOC255671 5'  TCCAGCCTGGGTGACAGAGTGA 99077           TG
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                        GT
GAM1628  LOC255792 5'  CCAGCCCAAGGCTAGAAGA   98469    GC    TT   CA_
                                  TC  TCTG  GCC   GGCTGG
                                  ||  ||||  |||   ||||||
                                  AG  AGAT  CGG   CCGACC
                                   A_   __   AAC
GAM1628  LOC256073 3'  CCTGGGCAACATAGCGAGA   98485        C
                                  TCTCGCT TGTTGCCCAGG
                                  ||||||| ||||||||||
                                  AGAGCGA ACAACGGGTCC
                                      T
GAM1628  LOC256207 3'  TCCAACCTGGGCGACAGAGCAA 96880     C            C
              GA                  TCT GCTCTGTTGCCCAGG TGGA
                                  ||| |||||||||||||| ||||
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                                AGA CGAGACAGCGGGTCC ACCT
                                  A           A
GAM1628  LOC256267 3'  CCAGCCTGGAAAACAAGT    98608     C   GC
                                GCT TGTT  CCAGGCTGG
                                ||| ||||  |||||||||
                                TGA ACAA  GGTCCGACC
                                  _   AA
GAM1628  LOC256267 5'  TCCAGCCTGGGAGACAGAGTGA 98613          TG
            GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      GA
GAM1628  LOC256515 3'  TCCAGCCTGGGCAACAGAGTAA 98218     CG
            GA                    TCT  CTCTGTTGCCCAGGCTGGA
                                |||  ||||||||||||||||||
                                AGA  GAGACAACGGGTCCGACCT
                                  AT
GAM1628  LOC256520 3'  TCCAGCCTGGGCGACAGAGCCA 97670     C
            GA                    TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGAGACAGCGGGTCCGACCT
                                  C
GAM1628  LOC256544 3'  TCCAGCCTGGCGACAGAGC    97934          C
                                GCTCTGTTGCC AGGCTGGA
                                ||||||||||| ||||||||
                                CGAGACAGCGG TCCGACCT
                                           _
GAM1628  LOC256594 3'  TCCAGCCTGGGCAACAGAGTAA 98868     CG
            GA                    TCT  CTCTGTTGCCCAGGCTGGA
                                |||  ||||||||||||||||||
                                AGA  GAGACAACGGGTCCGACCT
                                  AT
GAM1628  LOC256980 3'  TCCAGCCTGGTCGACAAGAGAG 96933      G  C    C
            A                     TCTC CT TGTTG CCAGGCTGGA
                                |||| || ||||| ||||||||||
                                AGAG GA ACAGC GGTCCGACCT
                                  A _    T
GAM1628  LOC257282 5'  TCAAGCCTGGGCAACAGAGCAA 98136     C             G
            GA                    TCT GCTCTGTTGCCCAGGCT GA
                                ||| |||||||||||||||| ||
                                AGA CGAGACAACGGGTCCGA CT
                                  A             A
GAM1628  LOC257397 3'  TCCAGCCTGGACAGCAGAACAA 97953     CGC      C
            GA                    TCT   TCTGTTG CCAGGCTGGA
                                |||   ||||||| ||||||||||
                                AGA   AGACGAC GGTCCGACCT
                                  ACA      A
GAM1628  LOC257596 3'  TCCAGCCTGGGCAACAAGAGTA 99789    CG   _
            AG                    CT  CTCT GTTGCCCAGGCTGGA
                                ||  |||| ||||||||||||||
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                              GA  GAGA CAACGGGTCCGACCT
                               AT    A
GAM1628  LOC257596 5'  TCCAGCCTGGGCGACAGAGCAA 99791     C
              GA                 TCT GCTCTGTTGCCCAGGCTGGA
                                 ||| ||||||||||||||||||||
                                 AGA CGAGACAGCGGGTCCGACCT
                                   A
GAM1628  LOC51145  3'  TCCAGCCTGGGCGACAGAGTGA 32928
              GA                 TCTCGCTCTGTTGCCCAGGCTGGA
                                 ||||||||||||||||||||||||
                                 AGAGTGAGACAGCGGGTCCGACCT

GAM1628  LOC51212  3'  TCCAGCCTGGGTGACAGAGCAA 33501     C      TG
              GA                 TCT GCTCTGT  CCCAGGCTGGA
                                 ||| |||||||  ||||||||||
                                 AGA CGAGACA  GGGTCCGACCT
                                   A       GT
GAM1628  LOC51279  3'  TCCAGCCTAAGCAACATAGTGA 33763       C      CC
                                 TCGCT TGTTGC  AGGCTGGA
                                 ||||| ||||||  ||||||||
                                 AGTGA ACAACG  TCCGACCT
                                    T      AA
GAM1628  LOC51279  3'  TCCAGCCTGCGGACAGACCAAG 33764     CGC     TG  _
              A                   TCT   TCTGT  CC CAGGCTGGA
                                  |||   |||||  || |||||||||
                                  AGA   AGACA  GG GTCCGACCT
                                    ACC     __  C
GAM1628  LOC51333  3'  TCCGGCCTGGGCAACAGAGGAA 34057     CG
              GA                 TCT  CTCTGTTGCCCAGGCTGGA
                                 |||  ||||||||||||||||||||
                                 AGA  GAGACAACGGGTCCGGCCT
                                   AG
GAM1628  LOC51336  3'  TCCAGCCTGGGTGACAGCGT   34078    T    TG
                                 GC CTGT  CCCAGGCTGGA
                                 || ||||  ||||||||||
                                 TG GACA  GGGTCCGACCT
                                  C    GT
GAM1628  LOC51652  3'  CCTGGGCAACATAGCAAGA    32700     C   C
                                 TCT GCT TGTTGCCCAGG
                                 ||| ||| ||||||||||
                                 AGA CGA ACAACGGGTCC
                                   A   T
GAM1628  LOC51759  3'  TCCAGCCTGGGCAACGAGC    73172      T
                                 GCTC GTTGCCCAGGCTGGA
                                 |||| ||||||||||||||
                                 CGAG CAACGGGTCCGACCT
                                    _
GAM1628  LOC57107  5'  CCAGCCTGGGCTGCTAGA     40182     _  T
                                 TCT GT GCCCAGGCTGG
                                 ||| || ||||||||||
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                              AGA CG CGGGTCCGACC
                                T  T
GAM1628 LOC63929 3' TCCAGCCTGGGTGACTGAGCAA 42285     C    T  TG
            GA                  TCT GCTC GT  CCCAGGCTGGA
                                ||| |||| ||  ||||||||||
                                AGA CGAG CA  GGGTCCGACCT
                                  A    T  GT
GAM1628 LOC64167 3' TCCAGCCTGGGTGACTGAGCGA 42543         T  TG
            GA                  TCTCGCTC GT  CCCAGGCTGGA
                                |||||||| ||  ||||||||||
                                AGAGCGAG CA  GGGTCCGACCT
                                    T  GT
GAM1628 LOC85479 5' TCCAGCCTGGGCGACAGAGCAA 53571     C
            GA                  TCT GCTCTGTTGCCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGAGACAGCGGGTCCGACCT
                                  A
GAM1628 LOC89890 3' TCCAGCCTGGATGACAGAGTGA 61209           GC
            GA                  TCTCGCTCTGTT  CCAGGCTGGA
                                ||||||||||||  ||||||||||
                                AGAGTGAGACAG  GGTCCGACCT
                                      TA
GAM1628 LOC90038 3' TCCAGCCTGGGCAACAGAGTGA 61813
            GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGACAACGGGTCCGACCT

GAM1628 LOC90072 3' TCCAGCCTGGGGAACAGAGCAA 61963     C       G
            GA                  TCT GCTCTGTT CCCAGGCTGGA
                                ||| |||||||| ||||||||||
                                AGA CGAGACAA GGGTCCGACCT
                                  A       G
GAM1628 LOC90072 5' TCCAGCCTGGGTGACAGAACAA 61964     CGC    TG
            GA                  TCT   TCTGT  CCCAGGCTGGA
                                |||   |||||  ||||||||||
                                AGA   AGACA  GGGTCCGACCT
                                  ACA    GT
GAM1628 LOC90092 3' TCCAGCCTGGCGACAAGAGCGA 62075          _    C
            GA                  TCTCGCTCT GTTGCC AGGCTGGA
                                |||||||| |||||| ||||||||
                                AGAGCGAGA CAGCGG TCCGACCT
                                    A    _
GAM1628 LOC90110 5' TCCAGCCTGGGCAACGGAGTGA 62182
            GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGGCAACGGGTCCGACCT

GAM1628 LOC90141 3' TCCAGCCTGGATGATAGAGCAA 62310     C       GC
            GA                  TCT GCTCTGTT  CCAGGCTGGA
                                ||| ||||||||  ||||||||||
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                                AGA CGAGATAG  GGTCCGACCT
                                  A       TA
GAM1628  LOC90155  5'  TCCAGCCTGGGCAACAAGAGTG 62368       _
              A                    TCGCTCT GTTGCCCAGGCTGGA
                                   ||||||| ||||||||||||||||
                                   AGTGAGA CAACGGGTCCGACCT
                                      A
GAM1628  LOC90233  3'  TCCAGCCCAGGCAACAGAGTGA 57197            CA
              GA                     TCTCGCTCTGTTGCC  GGCTGGA
                                     ||||||||||||||  |||||||
                                     AGAGTGAGACAACGG  CCGACCT
                                           AC
GAM1628  LOC90321  3'  TCCAACCTGGGTGACAGAGCGA 62938          TG     C
              GA                     TCTCGCTCTGT  CCCAGG TGGA
                                     ||||||||||  |||||| ||||
                                     AGAGCGAGACA  GGGTCC ACCT
                                           GT     A
GAM1628  LOC90393  5'  TCCAGCCTGGGTGACAGAGTGA 63309          TG
              GA                     TCTCGCTCTGT  CCCAGGCTGGA
                                     ||||||||||  ||||||||||
                                     AGAGTGAGACA  GGGTCCGACCT
                                           GT
GAM1628  LOC90538  3'  TCTGGGCAAAAAAGCGAGA   63902       CTG
                                     TCTCGCT   TTGCCCAGG
                                     |||||||   |||||||||
                                     AGAGCGA   AACGGGTCT
                                        AAA
GAM1628  LOC90573  5'  TCCAGCCTGGGCGACAGAGTGA 63962
              GA                     TCTCGCTCTGTTGCCCAGGCTGGA
                                     ||||||||||||||||||||||||
                                     AGAGTGAGACAGCGGGTCCGACCT

GAM1628  LOC90624  3'  TCCAGCCTGGGGGACAGAGTGA 64373           G
              GA                     TCTCGCTCTGTT CCCAGGCTGGA
                                     |||||||||||| ||||||||||
                                     AGAGTGAGACAG GGGTCCGACCT
                                           G
GAM1628  LOC90639  3'  TCCAGCCTGAGCAACAGAGCCG 64416     C        C
              GA                     TCT GCTCTGTTGC CAGGCTGGA
                                     ||| |||||||||| |||||||||
                                     AGG CGAGACAACG GTCCGACCT
                                       C         A
GAM1628  LOC90784  5'  TCCAGCCTGGGCAACAGAGTGA 64700
              GA                     TCTCGCTCTGTTGCCCAGGCTGGA
                                     ||||||||||||||||||||||||
                                     AGAGTGAGACAACGGGTCCGACCT

GAM1628  LOC90785  3'  TCCAGCCTGGGTGACAGAGCGA 64720          TG
              GA                     TCTCGCTCTGT  CCCAGGCTGGA
                                     ||||||||||  ||||||||||
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                                AGAGCGAGACA  GGGTCCGACCT
                                      GT
GAM1628  LOC90918  5'  TCCAGCCTAGGCAACAAGAGTG 65005       _     C
              A                  TCGCTCT GTTGCC AGGCTGGA
                                 ||||||| |||||| ||||||||
                                 AGTGAGA CAACGG TCCGACCT
                                    A     A
GAM1628  LOC91035  3'  TCCAGCCTGGACAACAAGAGC  65306      _   C
                                 GCTCT GTTG CCAGGCTGGA
                                 ||||| |||| ||||||||||
                                 CGAGA CAAC GGTCCGACCT
                                   A   A
GAM1628  LOC91056  3'  TCCAGCCTGGGCGACAGAGCAA 96410     C
              GG                   TCT GCTCTGTTGCCCAGGCTGGA
                                 ||| ||||||||||||||||||||
                                 GGA CGAGACAGCGGGTCCGACCT
                                   A
GAM1628  LOC91064  3'  TCCAGCGTGGGCGACAGAGCAA 65391     C          G
              GA                   TCT GCTCTGTTGCCCA GCTGGA
                                 ||| |||||||||||| ||||||
                                 AGA CGAGACAGCGGGT CGACCT
                                   A          G
GAM1628  LOC91250  5'  TCCAGCCTGAGTGACAGAGTGA 65921          TG C
              GA                   TCTCGCTCTGT  C CAGGCTGGA
                                 |||||||||||  | |||||||||
                                 AGAGTGAGACA  G GTCCGACCT
                                       GT A
GAM1628  LOC91250  5'  TCCAGCCTGGGCAACAGAGTGA 65922
              GA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                 ||||||||||||||||||||||||
                                 AGAGTGAGACAACGGGTCCGACCT

GAM1628  LOC91286  3'  TCCAGCCTGGACAACAGA    66061       C
                                 TCTGTTG CCAGGCTGGA
                                 ||||||| ||||||||||
                                 AGACAAC GGTCCGACCT
                                    A
GAM1628  LOC91380  3'  TCCAGCCTGGGTGACAGAGTGA 66454          TG
              GA                   TCTCGCTCTGT  CCCAGGCTGGA
                                 |||||||||||  ||||||||||
                                 AGAGTGAGACA  GGGTCCGACCT
                                       GT
GAM1628  LOC91442  3'  TCCAGCCTGGGCACCAGAGCGA 66648          T
              GA                   TCTCGCTCTG TGCCCAGGCTGGA
                                 |||||||||| ||||||||||||
                                 AGAGCGAGAC ACGGGTCCGACCT
                                       C
GAM1628  LOC91547  3'  TCCAGCCTGGGCGACAGAGCGA 67006
              GA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                 ||||||||||||||||||||||||
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                                AGAGCGAGACAGCGGGTCCGACCT

GAM1628 LOC91750 3' TCCAGCCTGGGCAACAGAGTGA 67657
              GA                  TCTCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAACGGGTCCGACCT

GAM1628 LOC91812 3' TCCAGCCTGGGCAACAGAACGA 67821      C
              GA                  TCTCG TCTGTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||||||
                                  AGAGC AGACAACGGGTCCGACCT
                                    A
GAM1628 LOC91813 3' TCCAGCCTGGGCAACAGAACGA 67848      C
              GA                  TCTCG TCTGTTGCCCAGGCTGGA
                                  ||||| ||||||||||||||||||
                                  AGAGC AGACAACGGGTCCGACCT
                                    A
GAM1628 LOC91862 3' TCCAGCCCAGGTGACAGAGCGA 54574          TG  CA
              GA                  TCTCGCTCTGT  CC  GGCTGGA
                                  ||||||||||  ||  |||||||
                                  AGAGCGAGACA  GG  CCGACCT
                                        GT  AC
GAM1628 LOC91963 5' TCCAGCCTGGGCAACAGAGTGA 68327
                                  TCGCTCTGTTGCCCAGGCTGGA
                                  ||||||||||||||||||||||
                                  AGTGAGACAACGGGTCCGACCT

GAM1628 LOC92078 3' TCCAGCCTGGGTGACAGAGTGA 68612          TG
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                        GT
GAM1628 LOC92223 3' TCCAGCCTGGGCAACAAGAGTG 69055        _
              A                    TCGCTCT GTTGCCCAGGCTGGA
                                  |||||||  ||||||||||||||
                                  AGTGAGA CAACGGGTCCGACCT
                                      A
GAM1628 LOC92228 3' CCAGCCTGGGCAACGGAGTGAG 69073
              A                    TCTCGCTCTGTTGCCCAGGCTGG
                                  ||||||||||||||||||||||
                                  AGAGTGAGGCAACGGGTCCGACC

GAM1628 LOC92267 3' TCCAGCCTGGGCAACAAGAGAG 69179     G  C
              A                    TCTC CT TGTTGCCCAGGCTGGA
                                  ||||  ||  ||||||||||||||
                                  AGAG GA ACAACGGGTCCGACCT
                                    A  _
GAM1628 LOC92299 3' TCCAGCCTGGCGACAAAGCGAG 69373       C      C
              A                    TCTCGCT TGTTGCC AGGCTGGA
                                  |||||||  |||||||  ||||||||
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                                AGAGCGA ACAGCGG TCCGACCT
                                   A     _
GAM1628  LOC92340  3'  TCCAGCCTAGTAATGGAGCAAG 69568     C        CC
                 A                  TCT GCTCTGTTGC  AGGCTGGA
                                    ||| ||||||||||  ||||||||
                                    AGA CGAGGTAATG  TCCGACCT
                                      A        A_
GAM1628  LOC92360  3'  TCCAGCCTGGGTGACAGAGCAA 69626     C      TG
                 GG                   TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    GGA CGAGACA  GGGTCCGACCT
                                      A      GT
GAM1628  LOC92405  3'  TCTAGCCTGGGCAACAGAGCAA 69718     C
                 GG                   TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||
                                    GGA CGAGACAACGGGTCCGATCT
                                      A
GAM1628  LOC92421  3'  TCCAGACTGGGCAACAGAGGGA 69729      G          G
                 GA                   TCTC CTCTGTTGCCCAG CTGGA
                                    |||| ||||||||||||| |||||
                                    AGAG GAGACAACGGGTC GACCT
                                      G          A
GAM1628  LOC92465  5'  TCCAGCCTGGGCGACAGAGCGA 69955
                 GA                   TCTCGCTCTGTTGCCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACAGCGGGTCCGACCT

GAM1628  LOC92465  5'  TCCAGTCTGGGCAACAGAGCAA 69956     C
                 GA                   TCT GCTCTGTTGCCCAGGCTGGA
                                    ||| ||||||||||||||||||
                                    AGA CGAGACAACGGGTCTGACCT
                                      A
GAM1628  LOC92466  3'  CCAGCCTGGAAAACAAGT    69964     C    GC
                                    GCT TGTT  CCAGGCTGG
                                    ||| ||||  |||||||||
                                    TGA ACAA  GGTCCGACC
                                      _    AA
GAM1628  LOC92466  5'  TCCAGCCTGGGAGACAGAGTGA 69969          TG
                 GA                   TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          GA
GAM1628  LOC92482  3'  CCAGCCTGGGCAACAGAGCAAG 70019     C
                 A                  TCT GCTCTGTTGCCCAGGCTGG
                                    ||| |||||||||||||||||
                                    AGA CGAGACAACGGGTCCGACC
                                      A
GAM1628  LOC92492  3'  TCCAGCCTGGATGACAGCGAGA 70083        CT   GC
                                    TCTCGCT  GTT  CCAGGCTGGA
                                    |||||||  |||  ||||||||||
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                                AGAGCGA  CAG  GGTCCGACCT
                                   __  TA
GAM1628  LOC92499  5'  CCTGGACGACAGAGCAAGA   70105    C       C
                                TCT GCTCTGTTG CCAGG
                                ||| ||||||||| |||||
                                AGA CGAGACAGC GGTCC
                                  A       A
GAM1628  LOC92568  3'  TCCAGCCTGGGTGACAGAGTGA 70331          TG
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      GT
GAM1628  LOC92573  3'  TCCAGCCTGGGTGACAGAGCGA 70379          TG
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      GT
GAM1628  LOC92659  3'  CCAGCCTGGGCGACAGAG    70609
                                CTCTGTTGCCCAGGCTGG
                                ||||||||||||||||||
                                GAGACAGCGGGTCCGACC

GAM1628  LOC92771  3'  CCTGAGCAACATAGCGAGA   54210       C     C
                                TCTCGCT TGTTGC CAGG
                                ||||||| |||||| ||||
                                AGAGCGA ACAACG GTCC
                                    T     A
GAM1628  LOC92771  3'  TCCAGCCTGGGCCACAGAATGA 54215      C     T
              GA                  TCTCG TCTGT GCCCAGGCTGGA
                                ||||| ||||| ||||||||||||
                                AGAGT AGACA CGGGTCCGACCT
                                  A    C
GAM1628  LOC92973  5'  TCCAGCCTGGGCAACAGAGTGA 71594
              GG                  TCTCGCTCTGTTGCCCAGGCTGGA
                                ||||||||||||||||||||||||
                                GGAGTGAGACAACGGGTCCGACCT

GAM1628  LOC93070  3'  TCCAGCCTGGGCAACAGAGGGA 71815     G
              GA                  TCTC CTCTGTTGCCCAGGCTGGA
                                |||| ||||||||||||||||||
                                AGAG GAGACAACGGGTCCGACCT
                                  G
GAM1628  LOC93132  3'  TCCAGCTCGGGCAACAAAGTGA 72000       C       AG
              GA                  TCTCGCT TGTTGCCC  GCTGGA
                                ||||||| ||||||||  ||||||
                                AGAGTGA ACAACGGG  CGACCT
                                   A       CT
GAM1628  LOC93613  3'  TCCAACCTGGGCGGCAGAGTGA 73082              C
              GA                  TCTCGCTCTGTTGCCCAGG TGGA
                                |||||||||||||||||| ||||
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                                AGAGTGAGACGGCGGGTCC ACCT
                                          A
GAM1628 LOC96597 5' CCAGCCTGGGCGACAAGAG   67449     _
                                CTCT GTTGCCCAGGCTGG
                                |||| |||||||||||||
                                GAGA CAGCGGGTCCGACC
                                  A
GAM1629 DLEC1    3' CATCTGGCCCTCCCTTG     24716      A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                   C    G  _
GAM1629 DLEC1    3' CATCTGGCCCTCCCTTG     24728      A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                   C    G  _
GAM1629 PIP5K1A  3' TATCCCACCCTGCCTTGATA  14520        A   CA  C
                                TATCAAGG AGGG  GG GTG
                                |||||||| ||||  || |||
                                ATAGTTCC TCCC  CC TAT
                                     G   A_  C
GAM1629 SOX11    3' ACCCACCCCCCCTTGGTA    13308        AA  CA  C
                                TATCAAGG  GGG  GG GT
                                ||||||||  |||  || ||
                                ATGGTTCC  CCC  CC CA
                                     CC   A_  _
GAM1629 CHL1     3' TGTTACCTTTCCTCAATA    22768     CA      CA
                                TAT  AGGAAGGG  GGCG
                                |||  ||||||||  ||||
                                ATA  TCCTTTCC  TTGT
                                  AC       A_
GAM1629 EPB41L1  3' CATTCTGCCCTTCCCTGA    71104     A        C
                                TCA GGAAGGGCAGG GTG
                                ||| |||||||||| |||
                                AGT CCTTCCCGTCT TAC
                                  C         _
GAM1629 FLJ00060 3' CATACCCCCTGCCCTCCTCTGA 61741     _   A     CGTG
                                TCA AGGA GGGCAGG   ATG
                                ||| |||| |||||||   |||
                                AGT TCCT CCCGTCC   TAC
                                  C   _      CCCA
GAM1629 FLJ10898 5' CACCACAGCCCTTTCTCAATA 60126     CA       AGGC
                                TAT  AGGAAGGGC   GTG
                                |||  |||||||||   |||
                                ATA  TCTTTCCCG   CAC
                                  AC       ACAC
GAM1629 FLJ22557 3' ATCATCCCATCCTTAATA    45581     C    A  CAGGC
                                TAT AAGGA GGG    GTGAT
                                ||| ||||| |||    |||||
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                                ATA TTCCT CCC     TACTA
                                  A     A  _____
GAM1629  KIAA0574  3'  CATCCCCTGCCCTCCCCTGA   69808     A  A       CGT
                                TCA GG AGGGCAGG   GATG
                                ||| || ||||||||   ||||
                                AGT CC TCCCGTCC   CTAC
                                  C  C       C__
GAM1629  KIAA0632  3'  CACCTCAGAAACCCTTCCTTGA 32071           CA___  C
                                TCAAGGAAGGG     GG GTG
                                ||||||||||     || |||
                                AGTTCCTTCCC     CT CAC
                                      AAAGA  C
GAM1629  KIAA1045  3'  CATCACATGTCCTTCC      71599          GGC
                                GGAAGGGCA   GTGATG
                                |||||||||   ||||||
                                CCTTCCTGT   CACTAC
                                     A__
GAM1629  KIAA1354  5'  CAGTGACTGCCTTCCCTTGATA 61572         A      G  _
                                TATCAAGG AGGGCAG CG TG
                                |||||||| ||||||| || ||
                                ATAGTTCC TTCCGTC GT AC
                                     C      A  G
GAM1629  MGC20460  5'  CACCGCCTCCTACCCTTCTT   54901         C___    _
                                AGGAAGGG    AGGCG TG
                                ||||||||    ||||| ||
                                TTCTTCCC    TCCGC AC
                                     ATCC     C
GAM1629  LOC158476 3'  CACGCCCGCCCCCCCCATTGA  88186      _ AA_    A
                                TCAA GG   GGGC GGCGTG
                                ||||  ||   ||||  ||||||
                                AGTT CC   CCCG CCGCAC
                                  A  CCC    C
GAM1629  LOC90459  3'  CACACCCGCCTAATTTTTG    63550       A_    A  C
                                CAAGGA  GGGC GG GTG
                                ||||||  ||||  ||  |||
                                GTTTTT  TCCG CC CAC
                                    AA    C  A
GAM1630  ADAR      5'  GGCGGGTCGGGCCGGGCA     32363       C       _
                                TGCCC GTCTGATT GCC
                                |||||  ||||||||  |||
                                ACGGG CGGGCTGG CGG
                                   C       G
GAM1630  APBA2     5'  CCTGTGGACAGACGGGGT     19740          A TG CA
                                GCCCCGTCTG T  C  AGG
                                ||||||||||  |  |  |||
                                TGGGGCAGAC G  G  TCC
                                     A GT __
GAM1630  APG5L     3'  TGGTCGTCATTGGCATGGGGT  17942       __  __    T
                                GCCCC  GTC  TGAT GCCA
                                |||||  |||  ||||  ||||
```

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                                TGGGG  CGG  ACTG TGGT
                                  TA   TT    C
GAM1630  ARF3     3'  TGATCTTAGGGGTTGGATGGGT 9782     C     TG   G  _
              CA                   TG CCCGTC  ATT CC AAGGTTG
                                || ||||||  ||| || |||||||
                                AC GGGTAG  TGG GG TTCTAGT
                                 T     GT   _  A
GAM1630  BCL7A    3'  CCCTTGGATCAGGCTGGGCA  40980      C      TG     TTG
                                TGCCC GTCTGAT  CCAAGG
                                ||||| |||||||  ||||||
                                ACGGG CGGACTA  GGTTCC
                                   T      __     CC
GAM1630  BTG3     3'  TGAAGTTAGATGGGCCA     23307    C         GC
                                TG CCCGTCTGATT  CA
                                || ||||||||||  ||
                                AC GGGTAGATTGA  GT
                                 C         A_
GAM1630  CD28     3'  GTGGTTAGTGGGTTAAACGGGG 21556        ____  G    _   AGGTTG
              TA                   TGCCCCGT    CT ATTG CCA
                                |||||||    || |||| |||
                                ATGGGGCA    GG TGAT GGT
                                     AATT  G    T     GT
GAM1630  CDH5     3'  CAGTTTTGCCTGAGAAGGGGCA 10148       G   GATT  C  GG
                                TGCCCC TCT    GC AA  TTG
                                |||||| |||    || ||  |||
                                ACGGGG AGA    CG TT  GAC
                                   A   GTC_  _  TT
GAM1630  CEP2     3'  TGGCTTTGCATCCTGGACGGGG 24198         AT_   C
                                CCCCGTCTG   TGC AAGGTTG
                                |||||||||   ||| |||||||
                                GGGGCAGGT   ACG TTTCGGT
                                     CCT   _
GAM1630  CLECSF5  3'  AATTTGTGTTTGAGATGGGGT  26038         GATT  _   GTTG
                                GCCCCGTCT    GC CAAG
                                |||||||||    || ||||
                                TGGGGTAGA    TG GTTT
                                     GTT_  T    AAT
GAM1630  CSF1R    3'  CAACTCCTCCATGGATGGGGC  19050         AT  CCAA
                                GCCCCGTCTG  TG   GGTTG
                                |||||||||  ||   |||||
                                CGGGGTAGGT  AC   TCAAC
                                     __  CTCC
GAM1630  DAG1     3'  CAACTTTGGTGCTCCAGGGT   16546     CGTCT  TT
                                GCCC    GA  GCCAAGGTTG
                                ||||    ||  ||||||||||
                                TGGG    CT  TGGTTTCAAC
                                  AC___  CG
GAM1630  DBT      3'  AACAAAATTAGGCCGGGCA    10355      C      GCCAAG
                                TGCCC GTCTGATT     GTT
                                ||||| ||||||||     |||
```

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                                ACGGG CGGATTAA     CAA
                                  C       AA____
GAM1630  DNAJB1   3'  CAATCTTGGCACACGTGGGGC  21564       TC  AT
                                GCCCCG  TG  TGCCAAGGTTG
                                ||||||  ||  ||||||||||
                                CGGGGT  AC  ACGGTTCTAAC
                                   GC  __
GAM1630  DUSP1    5'  GACGCGGGTCGGAGGGGCA   16625       G     _  CAAG
                                TGCCCC TCTGATT GC    GTT
                                |||||| ||||||| ||    |||
                                ACGGGG AGGCTGG CG    CAG
                                   _      G  ____
GAM1630  EDG6     3'  CAGTCTTGCGTGTGGATGGTGC 15020     C     AT   C   GT
           A                     TGC CCGTCTG  TGC AAG  TG
                                ||| |||||||  ||| |||  ||
                                ACG GGTAGGT  GCG TTC  AC
                                  T      GT  _  TG
GAM1630  EGLN2    5'  TGACTTTGGGCAGAGGGTGGGA 54923    C   GT  GA    _
           CA                     TG CCC  CT  TTGCC AAGGTTG
                                || |||  ||  ||||| |||||||
                                AC GGG  GG  GACGG TTTCAGT
                                 A  TG  A_    G
GAM1630  ELAC2    5'  CAGTTTTGGTGGAGACGGGC   36729     C    GA TG    GG
                                GCCC GTCT  T  CCAA  TTG
                                |||| ||||  |  ||||  |||
                                CGGG CAGA  G  GGTT  GAC
                                  _   __ GT   TT
GAM1630  EMD      5'  CGGTTTTGGTAGGCCCGGGC   5488      C_   GATT    GG
                                GCCC  GTCT   GCCAA  TTG
                                ||||  ||||   |||||  |||
                                CGGG  CGGA   TGGTT  GGC
                                  CC   ____    TT
GAM1630  FGF5     3'  CAACCTGAGTGGAGTCAGGTGA 53652      C GT     G  ___
           GGCA                    TGCC C  CTGATT CCA   AGGTTG
                                |||| |  |||||| |||   ||||||
                                ACGG G  GACTGA GGT   TCCAAC
                                  A TG     _  GAG
GAM1630  FGF5     3'  CAACCTGAGTGGAGTCAGGTGA 53653      C GT     G  ___
           GGCA                    TGCC C  CTGATT CCA   AGGTTG
                                |||| |  |||||| |||   ||||||
                                ACGG G  GACTGA GGT   TCCAAC
                                  A TG     _  GAG
GAM1630  GALGT    5'  CGGCTTTGCCCCGGGGCTGGGG 9419       _   GATT  C
           T                     GCCCC GTCT   GC AAGGTTG
                                ||||| ||||   || |||||||
                                TGGGG CGGG   CG TTTCGGC
                                  T   GCCC  _
GAM1630  INHBB    3'  TTCTTGGAGAGATGGGG     11013        GATTG     TT
                                CCCCGTCT    CCAAGG  G
                                ||||||||    ||||||  |
```

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                                GGGGTAGA    GGTTCT  T
                                    GA___     G
GAM1630  IPF1     3'  GCCCTGGCAGTTGAATGGGGC  5780        CT       A   TG
                                GCCCCGT  GATTGCCA GGT
                                |||||||  |||||||| |||
                                CGGGGTA  TTGACGGT CCG
                                    AG       C   C
GAM1630  KCNK1    5'  TGGCTTTGGCTTTGGCGGCGGC 11166     _    TGATT
                                GCC CCGTC    GCCAAGGTTG
                                ||| |||||    ||||||||||
                                CGG GGCGG    CGGTTTCGGT
                                  C    TTT__
GAM1630  KCNQ2    3'  CGGCCTTGGGTCCCGGTGGGGT 62047       T   ATTG
                                GCCCCG CTG    CCAAGGTTG
                                |||||| |||    |||||||||
                                TGGGGT GGC    GGTTCCGGC
                                   _  CCTG
GAM1630  KPNA1    5'  CGTCGAGGCTAGGCGGGGC    81132         ATT   AA GT
                                GCCCCGTCTG   GCC  G  TG
                                ||||||||||   |||  |  ||
                                CGGGGCGGAT   CGG  C  GC
                                     ___   AG TG
GAM1630  LDHB     5'  GGCGCTGTCAGACGGGGCA    11291           __
                                TGCCCCGTCTGAT  TGCC
                                ||||||||||||  ||||
                                ACGGGGCAGACTG  GCGG
                                      TC
GAM1630  LYN      5'  CAGCCCGCGGCAAGCGGGCGGG 11403         A    AA_
            GC                    GCCCCGTCTG TTGCC   GGTTG
                                ||||||||||| |||||   |||||
                                CGGGGCGGGC AACGG   CCGAC
                                     G    CGC
GAM1630  MBNL     3'  TAACCTAGTAATTGGGTGGG   41071     GT TG    CA
                                CCC  C  ATTGC  AGGTTG
                                |||  |  |||||  ||||||
                                GGG  G  TAATG  TCCAAT
                                  TG GT    A_
GAM1630  MNT      3'  GGCCTGACCGGACGGGGCA    40086          A  __
                                TGCCCCGTCTG TT  GCC
                                |||||||||||  ||  |||
                                ACGGGGCAGGC AG  CGG
                                      C  TC
GAM1630  MTNR1A   5'  TAACAAGTGGTCGGGCGGGC   21054      C      TG CAAG
                                GCCC GTCTGAT  C    GTTG
                                ||||  |||||||  |    ||||
                                CGGG CGGGCTG  G    CAAT
                                  _      GT AA__
GAM1630  NCOA4    3'  TAATCTTGGCAATTTTTGAC   19553     T__
                                GTC   GATTGCCAAGGTTG
                                |||   ||||||||||||||
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                                CAG   TTAACGGTTCTAAT
                                  TTT
GAM1630 NDRG1    3' TAACCTTTCGCCGAATGGGGCA 60311       C  ATT  C_
                                TGCCCCGT TG   GC  AAGGTTG
                                |||||||| ||   ||  |||||||
                                ACGGGGTA GC   CG  TTCCAAT
                                    A  ___  CT
GAM1630 NDUFA9   3' TGGTTTTGGCGTCTTTTGGGTC 18446    C   TCT  T     TT
            G                    TG CCCG   GAT GCCAAGG  G
                                || ||||   ||| |||||||  |
                                GC GGGT   CTG CGGTTTT  T
                                 T   TTT  _     GG
GAM1630 NFE2L1   5' TGGCCTTGGCTCCACAGGGT   13635     C  CT  TT
                                GCCC GT  GA  GCCAAGGTTG
                                |||| ||  ||  ||||||||||
                                TGGG CA  CT  CGGTTCCGGT
                                  A  C_  __
GAM1630 NPC1     3' TTGCCAGTTAGATGTGGCA    6055      C       C
                                TGCC CGTCTGATTG CAA
                                |||| |||||||||| |||
                                ACGG GTAGATTGAC GTT
                                  T        C
GAM1630 PCDHA1   3' CAGCTCTGCAGGATTGCATGGG 49410       C    GC_  AG
            GTA                   TGCCCCGT TGATT   CA  GTTG
                                |||||||| |||||   ||  ||||
                                ATGGGGTA GTTAG   GT  CGAC
                                    C    GAC  CT
GAM1630 PCDHA10  3' CAGCTCTGCAGGATTGCATGGG 38787       C    GC_  AG
            GTA                   TGCCCCGT TGATT   CA  GTTG
                                |||||||| |||||   ||  ||||
                                ATGGGGTA GTTAG   GT  CGAC
                                    C    GAC  CT
GAM1630 PCDHA11  3' CAGCTCTGCAGGATTGCATGGG 49858       C    GC_  AG
            GTA                   TGCCCCGT TGATT   CA  GTTG
                                |||||||| |||||   ||  ||||
                                ATGGGGTA GTTAG   GT  CGAC
                                    C    GAC  CT
GAM1630 PCDHA12  3' CAGCTCTGCAGGATTGCATGGG 38795       C    GC_  AG
            GTA                   TGCCCCGT TGATT   CA  GTTG
                                |||||||| |||||   ||  ||||
                                ATGGGGTA GTTAG   GT  CGAC
                                    C    GAC  CT
GAM1630 PCDHA13  3' CAGCTCTGCAGGATTGCATGGG 49866       C    GC_  AG
            GTA                   TGCCCCGT TGATT   CA  GTTG
                                |||||||| |||||   ||  ||||
                                ATGGGGTA GTTAG   GT  CGAC
                                    C    GAC  CT
GAM1630 PCDHA2   3' CAGCTCTGCAGGATTGCATGGG 38802       C    GC_  AG
            GTA                   TGCCCCGT TGATT   CA  GTTG
                                |||||||| |||||   ||  ||||
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                                ATGGGGTA GTTAG   GT  CGAC
                                    C    GAC  CT
GAM1630  PCDHA3   3'  CAGCTCTGCAGGATTGCATGGG 49803       C    GC_  AG
                GTA                 TGCCCCGT TGATT   CA  GTTG
                                    |||||||| |||||   ||  ||||
                                ATGGGGTA GTTAG   GT  CGAC
                                    C    GAC  CT
GAM1630  PCDHA4   3'  CAGCTCTGCAGGATTGCATGGG 38810       C    GC_  AG
                GTA                 TGCCCCGT TGATT   CA  GTTG
                                    |||||||| |||||   ||  ||||
                                ATGGGGTA GTTAG   GT  CGAC
                                    C    GAC  CT
GAM1630  PCDHA5   3'  CAGCTCTGCAGGATTGCATGGG 49810       C    GC_  AG
                GTA                 TGCCCCGT TGATT   CA  GTTG
                                    |||||||| |||||   ||  ||||
                                ATGGGGTA GTTAG   GT  CGAC
                                    C    GAC  CT
GAM1630  PCDHA6   3'  CAGCTCTGCAGGATTGCATGGG 38818       C    GC_  AG
                GTA                 TGCCCCGT TGATT   CA  GTTG
                                    |||||||| |||||   ||  ||||
                                ATGGGGTA GTTAG   GT  CGAC
                                    C    GAC  CT
GAM1630  PCDHA7   3'  CAGCTCTGCAGGATTGCATGGG 49823       C    GC_  AG
                GTA                 TGCCCCGT TGATT   CA  GTTG
                                    |||||||| |||||   ||  ||||
                                ATGGGGTA GTTAG   GT  CGAC
                                    C    GAC  CT
GAM1630  PCDHA8   3'  CAGCTCTGCAGGATTGCATGGG 38826       C    GC_  AG
                GTA                 TGCCCCGT TGATT   CA  GTTG
                                    |||||||| |||||   ||  ||||
                                ATGGGGTA GTTAG   GT  CGAC
                                    C    GAC  CT
GAM1630  PCDHA9   3'  CAGCTCTGCAGGATTGCATGGG 49834       C    GC_  AG
                GTA                 TGCCCCGT TGATT   CA  GTTG
                                    |||||||| |||||   ||  ||||
                                ATGGGGTA GTTAG   GT  CGAC
                                    C    GAC  CT
GAM1630  PCDHAC1  3'  CAGCTCTGCAGGATTGCATGGG 38777       C    GC_  AG
                GTA                 TGCCCCGT TGATT   CA  GTTG
                                    |||||||| |||||   ||  ||||
                                ATGGGGTA GTTAG   GT  CGAC
                                    C    GAC  CT
GAM1630  PCDHAC2  3'  CAGCTCTGCAGGATTGCATGGG 49875       C    GC_  AG
                GTA                 TGCCCCGT TGATT   CA  GTTG
                                    |||||||| |||||   ||  ||||
                                ATGGGGTA GTTAG   GT  CGAC
                                    C    GAC  CT
GAM1630  PLAU     3'  CAATCCTCACTGGGTGGGGT  69540      GT  GAT  CCA  _
                                GCCCC  CT   TG   AGG TTG
                                |||||  ||   ||   ||| |||
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                                TGGGG  GG   AC   TCC AAC
                                   TG  TC_  ___   T
GAM1630  POU4F1   3'  AGCCTTGAGGACTGGGGT    21757      _   GATTGC
                                GCCCC GTCT     CAAGGTT
                                ||||| ||||     |||||||
                                TGGGG CAGG     GTTCCGA
                                   T   A_____
GAM1630  PPFIA3   3'  CGACCTTGGGGGTGCGGGGC  61667       CTG   G
                                GCCCCGT   ATT CCAAGGTTG
                                |||||||   ||| |||||||||
                                CGGGGCG   TGG GGTTCCAGC
                                    ___   G
GAM1630  PRX      3'  AGCCCCTAGTCAGATGGGG   40889          CCAA   G
                                CCCCGTCTGATTG   GGTT
                                ||||||||||||    ||||
                                GGGGTAGACTGAT   CCGA
                                       CC__
GAM1630  PTGFRN   3'  TAGCTTTGGACCTGACCGGGT  67773     C   TGATTG
                                GCCC GTC     CCAAGGTTG
                                |||| |||     |||||||||
                                TGGG CAG     GGTTTCGAT
                                  C   TCCA__
GAM1630  PYGB     3'  CAGCCTTTTATTGAGTGGGGCA 12686       TC    TGCC
                                TGCCCCG  TGAT    AAGGTTG
                                |||||||  ||||    |||||||
                                ACGGGGT  GTTA    TTCCGAC
                                    GA    TT__
GAM1630  RAB5A    3'  GTGGTTTTTTTTTTTAAATGGG 16044       C   TT_______   AGGTTG
            GTA                   TGCCCCGT TGA       GCCA
                                |||||||| |||       ||||
                                ATGGGGTA ATT       TGGT
                                    A   TTTTTTTT      GT
GAM1630  RAD50    5'  CAATTTTGGTTGGACCCAATGG 20406       CTGATT__
            GGC                   GCCCCGT       GCCAAGGTTG
                                |||||||       ||||||||||
                                CGGGGTA       TGGTTTTAAC
                                    ACCCAGGT
GAM1630  RBBP6    3'  TAACCACCATTAATTAGTTGGG 73861       T      CCAA_
            GT                    GCCCCG CTGATTG    GGTTG
                                |||||| |||||||    |||||
                                TGGGGT GATTAAT    CCAAT
                                   T      TACCA
GAM1630  RRM2B    3'  TAATCTTGGTAAACCTCGGTGT 68436     C   TCTGA
            A                     TGC CCG    TTGCCAAGGTTG
                                ||| |||    ||||||||||||
                                ATG GGC    AATGGTTCTAAT
                                  T   TCCA_
GAM1630  RXRA     3'  CGGCTTTGCCGTTCAGATGGGG 12918          T  C
            C                     GCCCCGTCTGA TG CAAGGTTG
                                |||||||||| || ||||||||
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                                CGGGGTAGACT GC GTTTCGGC
                                      T  C
GAM1630  SECTM1   3'  GACCTTGGGTGGCGGGGC    13007       TGATTG
                                GCCCCGTC     CCAAGGTT
                                ||||||||     ||||||||
                                CGGGGCGG     GGTTCCAG
                                    TG____
GAM1630  SEPN1    3'  CAGCCTTGGCTCCATGGTGGC  66962    _   CT  TT
                                GCC CCGT  GA  GCCAAGGTTG
                                ||| ||||  ||  ||||||||||
                                CGG GGTA  CT  CGGTTCCGAC
                                  T   C_ __
GAM1630  SEPN1    3'  TGACCTCCAGACCAGATGGGGC 66982         A  GCCA
             A                   TGCCCCGTCTG TT    AGGTTG
                                ||||||||||| ||    ||||||
                                ACGGGGTAGAC AG    TCCAGT
                                      C  ACC_
GAM1630  SFTPC    3'  AGCTTTTGCAGACGGGCA    88878      C    ATTGCC
                                TGCCC GTCTG     AAGGTT
                                ||||| |||||     ||||||
                                ACGGG CAGAC     TTTCGA
                                  _    GT____
GAM1630  SFTPD    3'  AACTGGGGTGGGTGGGGCA   13037      GT  GATT   AA
                                TGCCCC  CT    GCC  GGTT
                                ||||||  ||    |||  ||||
                                ACGGGG  GG    TGG  TCAA
                                   TG  _____  GG
GAM1630  SLC35A3  3'  TGGTTTTTCACGATGGGGCA  25297        _   TT_
                                TGCCCCGTC TGA   GCCA
                                |||||||||  |||   ||||
                                ACGGGGTAG ACT   TGGT
                                     C   TTT
GAM1630  SLC7A4   3'  CTACCTGGGCAGTTGTGGTGGG 65818      GT _      A    TG
             GT                   GCCCC  C TGATTGCC AGGT
                                |||||  | ||||||||  ||||
                                TGGGG  G GTTGACGG TCCA
                                   TG T       G    TCG
GAM1630  SNAI1    3'  CAGCCTCCTGTTTGGTGGGGT  21121      GT T   TGCCA
                                GCCCC  C GAT     AGGTTG
                                |||||  | |||    ||||||
                                TGGGG  G TTG     TCCGAC
                                   TG T   TCC__
GAM1630  SORCS1   3'  CAACTTTGAGAGCAGTGGGGT  54679       T   A  GC
                                GCCCCG CTG TT  CAAGGTTG
                                ||||||  ||| ||  ||||||||
                                TGGGGT GAC AG  GTTTCAAC
                                   _  G  A_
GAM1630  SOX9     3'  CAACCTTGGCTAAATGGAGCA  6229      C    CTGATT
                                TGC CCGT     GCCAAGGTTG
                                |||  ||||     ||||||||||
```

```
                                ACG GGTA     CGGTTCCAAC
                                  A   AAT___
GAM1630  SWAP70   3'  AGCCTTTGTTAGGTGGGCA   71859     C GT    TGCC
                                TGCC C  CTGAT    AAGGTT
                                |||| |  |||||    ||||||
                                ACGG G  GATTG    TTCCGA
                                  _ TG    T___
GAM1630  SWAP70   3'  CAGCTTTGGGGGCCGGGCGTGG 71862     C     AT G
           T                     GCC CGTCTG  T CCAAGGTTG
                                ||| ||||||  | |||||||||
                                TGG GCGGGC  G GGTTTCGAC
                                  T     CG G
GAM1630  THY1     3'  CAGCCTCCAAGTCAGGTGGGGT 21895      GT     GCCA
                                GCCCC  CTGATT    AGGTTG
                                |||||  ||||||    ||||||
                                TGGGG  GACTGA    TCCGAC
                                   TG     ACC_
GAM1630  TPS1     3'  GGCGTGGTCAGCTGGGGC    61105       T    __
                                GCCCCG CTGAT  TGCC
                                |||||| |||||  ||||
                                CGGGGT GACTG  GCGG
                                   C     GT
GAM1630  WNT3A    3'  TGGCTCTGGGTGGGCGGGGCA  53612          ATT___
                                TGCCCCGTCTG     GCCA
                                ||||||||||      ||||
                                ACGGGGCGGGT     CGGT
                                      GGGTCT
GAM1630  ZNF217   3'  CAACTTTGAGCATCTCAGATGG 22542          T_  _
           GG                     CCCCGTCTGA  TGC CAAGGTTG
                                ||||||||||  ||| ||||||||
                                GGGGTAGACT  ACG GTTTCAAC
                                      CT   A
GAM1630  ZNF26    5'  TAACCTGATATCAGTGGGGTA  73340        T    TGCCA
                                TGCCCCG CTGAT     AGGTTG
                                ||||||| |||||     ||||||
                                ATGGGGT GACTA     TCCAAT
                                   _     TAG__
GAM1630  AMOT     3'  TGGAGAGTTGCATGGGGT    56549        C    G_
                                GCCCCGT TGATT  CCA
                                ||||||| |||||  |||
                                TGGGGTA GTTGA  GGT
                                   C     GA
GAM1630  AP4B1    5'  CGATCTGTGGGCGGGGCG    22732          ___
                                TGCCCCGTCT   GATTG
                                ||||||||||   |||||
                                GCGGGGCGGG   CTAGC
                                      TGT
GAM1630  BA108L7.2 3'  TGGCTTCAGTGGTGGGTGGGGC 49084        T  G  TG CA
           A                     TGCCCCG CT AT  C  AGGTTG
                                ||||||| || ||  |  ||||||
```

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                                ACGGGGT GG TG  G  TTCGGT
                                    _  G  GT AC
GAM1630  BAG5     5'  GACCTAGTCGGGAGGGGT    18039      GT     GCCA
                                GCCCC  CTGATT    AGGTT
                                |||||  ||||||    |||||
                                TGGGG  GGCTGA    TCCAG
                                  AG     _____
GAM1630  BET3     5'  GGCTAGGCGAGTGGGGCGGGGC 27718         G  _  A  GTTG
                                GCCCCGTCT ATT GCC AG
                                |||||||||  ||| ||| ||
                                CGGGGCGGG TGA CGG TC
                                     G   G   A  GGT
GAM1630  C20orf139 3'  TGACCTTGGGGTAGGCTGGGT  85922      C     ATTG
                                GCCC GTCTG    CCAAGGTTG
                                ||||  |||||    |||||||||
                                TGGG CGGAT    GGTTCCAGT
                                  T    GG__
GAM1630  C20orf48  3'  TGGTCTTGGCAATCATCTGTGC 46958     CC  TC         TT
            A                     TGC  CG  TGATTGCCAAGG  G
                                |||  ||  ||||||||||||  |
                                ACG  GT  ACTAACGGTTCT  T
                                  T_  CT          GG
GAM1630  C9orf7    3'  CAGCCTTGGCAGTGACTGGACA 34579    C  C   TG
                                TG CC GTC  ATTGCCAAGGTTG
                                || || |||  ||||||||||||
                                AC GG CAG  TGACGGTTCCGAC
                                 A  T  __
GAM1630  CAMKK1    5'  CAGCGAGGCGGTGGGGCGGGGC 51151         G     AAG
                                GCCCCGTCT ATTGCC   GTTG
                                |||||||||  ||||||   ||||
                                CGGGGCGGG TGGCGG   CGAC
                                     G     AG_
GAM1630  CG012     3'  TAATTTTGGTCTTGAGGGGCGG 84165        GATT__
            GG                    CCCCGTCT     GCCAAGGTTG
                                |||||||||     ||||||||||
                                GGGGCGGG     TGGTTTTAAT
                                    GAGTTC
GAM1630  DAZAP1    3'  AACCTTGGGGGGGGGGGGC    39044      G   GATTG
                                GCCCC TCT    CCAAGGTT
                                |||||  |||    ||||||||
                                CGGGG GGG    GGTTCCAA
                                  G   G_____
GAM1630  DDX33     3'  CCCCTGGTCAGAGGGGGT    39784      G    ATT    A  TTG
                                GCCCC TCTG   GCCA GG
                                |||||  ||||   ||||  ||
                                TGGGG AGAC   TGGT CC
                                  G    ____    C  CT
GAM1630  DJ159A19.3 5'  CAGCCGCGAGGTGGACGGGGC  32280         A_    CAA
                                GCCCCGTCTG  TTGC   GGTTG
                                ||||||||||  ||||   |||||
```

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                                CGGGGCAGGT  AGCG   CCGAC
                                      GG   ___
GAM1630  DKFZP434A0225 5'  CAACCGTCCGGGTGGGTGGGGC 95521      GT  GATT   AA___
                                GCCCC  CT    GCC    GGTTG
                                |||||  ||    |||    |||||
                                CGGGG  GG    TGG    CCAAC
                                   TG  _____  GCCTG
GAM1630  DKFZp434B1222 3'  CAATTTTGGCAATTTTAAAGG  34549    GTCT_
                                CC    GATTGCCAAGGTTG
                                ||    ||||||||||||||
                                GG    TTAACGGTTTTAAC
                                 AAATT
GAM1630  DKFZP434C171 3'  CATCTTGGTGCCACCTGGGCA  32186      CGTC  ATT     GT
                                TGCCC   TG   GCCAAG  TG
                                |||||   ||   ||||||  ||
                                ACGGG   AC   TGGTTC  AC
                                   TCC_  CG_     TG
GAM1630  DKFZP434K028 3'  TAGCCTTGAAGTTGGAAGGGGT 94862      G  TG   GC
                                GCCCC TC  ATT  CAAGGTTG
                                ||||| ||  |||  ||||||||
                                TGGGG AG  TGA  GTTCCGAT
                                   A  GT   A_
GAM1630  DKFZp434K1815 3'  CAGCTTTGGGCCGATGGGG   95916       TGATTG
                                CCCCGTC     CCAAGGTTG
                                |||||||     |||||||||
                                GGGGTAG     GGTTTCGAC
                                    CCG___
GAM1630  DKFZP564A022 3'  AACATGGCCGGGCGGGGT    48965         ATT   AG   G
                                GCCCCGTCTG   GCCA  GTT
                                ||||||||||   ||||  |||
                                TGGGGCGGGC   CGGT  CAA
                                      ___    A_
GAM1630  DNAJC5    3'  TGACTGCAGCCGGTCAGGTGGG 62143     C GT      _ CAA
            C                    GCC C  CTGATTG C   GGTTG
                                |||  |  |||||||  |   |||||
                                CGG G  GACTGGC G   TCAGT
                                  _ TG      C ACG
GAM1630  EAT2     3'  GACCATGCAGTCAGAGGGGCA  80051       G       CAA   G
                                TGCCCC TCTGATTGC   GGTT
                                ||||||  |||||||||   ||||
                                ACGGGG AGACTGACG   CCAG
                                   _       TA_
GAM1630  EMILIN-2  5'  GACCCGGGCAGGCGGGGC    50255        GATT   AA
                                GCCCCGTCT    GCC  GGTT
                                |||||||||    |||  ||||
                                CGGGGCGGA    CGG  CCAG
                                      _____  GC
GAM1630  FHOD2    5'  AACCACATTGGATGGGTCA   74259    C     TG  T CCAA
                                TG CCCGTC  AT G    GGTT
                                || ||||||  || |    ||||
```

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                                AC GGGTAG  TA C    CCAA
                                 T     GT  _ A___
GAM1630  FLJ10081  3'  CATCTTGGGCTGGATGGG    36288        ATTG    GT
                                CCCGTCTG   CCAAG  TG
                                ||||||||   |||||  ||
                                GGGTAGGT   GGTTC  AC
                                    CG__    TG
GAM1630  FLJ10521  3'  CAACTTTGGCAGCGCTCTGGGC 36717      CGTC  A
           A                     TGCCC   TG TTGCCAAGGTTG
                                |||||   || ||||||||||||
                                ACGGG   GC GACGGTTTCAAC
                                  TCTC  _
GAM1630  FLJ10620  3'  AGCTGCAGTTAGACGGGGT   36863           CAA   G
                                GCCCCGTCTGATTGC   GGTT
                                ||||||||||||||   ||||
                                TGGGGCAGATTGACG   TCGA
                                          ___
GAM1630  FLJ10751  3'  CAGCACGTGGTGGGTGGGGT   37273     GT  GATT   AG_
                                GCCCC  CT   GCCA   GTTG
                                |||||  ||   ||||   ||||
                                TGGGG  GG   TGGT   CGAC
                                  TG  _____   GCA
GAM1630  FLJ11101  3'  CAGTTTTTCCATGGACGGGGT  37611         AT  CC  GG
                                GCCCCGTCTG  TG  AA  TTG
                                ||||||||||  ||  ||  |||
                                TGGGGCAGGT  AC  TT  GAC
                                     __  CT  TT
GAM1630  FLJ11726  3'  CAGCCCCCAAAGTCGGATGGAG 47016    C        GCCAA
           CA                    TGC CCGTCTGATT    GGTTG
                                |||  ||||||||||    |||||
                                ACG GGTAGGCTGA    CCGAC
                                  A        AACCC
GAM1630  FLJ12132  5'  CGGCCGGACGCGGGCGGGGC   47099         ATTG  AA
                                GCCCCGTCTG   CC  GGTTG
                                ||||||||||   ||  |||||
                                CGGGGCGGGC   GG  CCGGC
                                     GCA_  __
GAM1630  FLJ12190  3'  AACACAGCGGATGGGGCA    47556          A   CCAAG
                                TGCCCCGTCTG TTG    GTT
                                ||||||||||| |||    |||
                                ACGGGGTAGGC GAC    CAA
                                     _   A____
GAM1630  FLJ12443  3'  GACCCGTGGGCAGGTGGGGCA  46144       GT   A TG CAA   G
                                TGCCCC  CTG T  C   GGTT
                                ||||||  ||| |  |   ||||
                                ACGGGG  GAC G  G   CCAG
                                   TG   G GT C__
GAM1630  FLJ12595  3'  CAATCCGAATCGTCATCAGATG 47146          T  CAA__  _
           GGGT                   GCCCCGTCTGAT GC    GG TTG
                                |||||||||||| ||    || |||
```

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                                TGGGGTAGACTA TG    CC AAC
                                      C  CTAAG  T
GAM1630  FLJ12806  5'  CGGCCTTGCTGGGGTAGGGGC  43390     GT  GATT  C
                                GCCCC  CT   GC AAGGTTG
                                ||||| ||   || |||||||
                                CGGGG  GG   CG TTCCGGC
                                   AT  GGT_  _
GAM1630  FLJ13265  3'  ATCTGGTGGTGGATGGGGT   46410       G  TG   A
                                GCCCCGTCT AT  CCA GGT
                                ||||||||| ||  ||| |||
                                TGGGGTAGG TG  GGT CTA
                                      _ GT   _
GAM1630  FLJ13615  5'  TGGCCTTGGCGGAGTTGGGG   47798     T  GA
                                CCCCG CT  TTGCCAAGGTTG
                                ||||| ||  ||||||||||||
                                GGGGT GA  GGCGGTTCCGGT
                                   T  __
GAM1630  FLJ13842  3'  CGGCCTTGGGCTAGGCGGGGT  45332        ATTG
                                GCCCCGTCTG   CCAAGGTTG
                                ||||||||||   |||||||||
                                TGGGGCGGAT   GGTTCCGGC
                                      CG__
GAM1630  FLJ13962  3'  CAACTCCCATCAGATGGGCCA  46317   C       TGCCAA
                                TG CCCGTCTGAT     GGTTG
                                || ||||||||||     |||||
                                AC GGGTAGACTA     TCAAC
                                 C        CCC___
GAM1630  FLJ14753  3'  TAATTTTTTTTTTGATGGGGT  51766       T  TTGCC
                                GCCCCGTC GA     AAGGTTG
                                |||||||| ||    |||||||
                                TGGGGTAG TT     TTTTAAT
                                     T  TTT__
GAM1630  FLJ20033  3'  TAGTCATTGAGTGGGGTA    34822       _ __
                                TGCCCCG TC  TGATTG
                                ||||||| ||  ||||||
                                ATGGGGT AG  ACTGAT
                                    G  TT
GAM1630  FLJ20306  5'  CGTCTTGCACGGGCAGGGT   35390     C    AT   C   GT
                                GCCC GTCTG  TGC AAG  TG
                                |||| |||||  ||| |||  ||
                                TGGG CGGGC  ACG TTC  GC
                                  A    __  _   TG
GAM1630  FLJ20345  3'  AGCCACTGTCAGATGGGCA   35493      C      TGCCAA
                                TGCCC GTCTGAT     GGTT
                                ||||| |||||||     ||||
                                ACGGG TAGACTG     CCGA
                                   _      TCA___
GAM1630  FLJ20457  5'  AGCACTGTAATTGGGGGGGGC  35668      G  TG    CAAG   G
                                GCCCC TC  ATTGC    GTT
                                ||||| ||  |||||    |||
```

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                                CGGGG GG  TAATG   CGA
                                  G  GT    TCA_  A
GAM1630  FLJ20464  5'  CAATATGAGGGCGATGGACGGG 35688         G     AAG__
            GCA                   TGCCCCGTCT ATTGCC    GTTG
                                  |||||||||| ||||||    ||||
                                  ACGGGGCAGG TAGCGG    TAAC
                                        _     GAGTA
GAM1630  FLJ20701  3'  CAGCTGTTATTGGATGGGCCA  36023    C     TG  T  CAA
                                  TG CCCGTC  AT GC   GGTTG
                                  || ||||||  || ||   |||||
                                  AC GGGTAG  TA TG   TCGAC
                                   C     GT  T  ___
GAM1630  FLJ21736  3'  CAATCAGCAGGATGTGGGTGGG 46779      GT  GA___    CAA
            GC                    GCCCC  CT    TTGC   GGTTG
                                  |||||  ||    ||||   |||||
                                  CGGGG  GG    GACG   CTAAC
                                     TG  TGTAG    A__
GAM1630  FLJ22419  5'  TAACCCAGGGTGGGGTGGGGT  45532      GT  G  TG  AA
                                  GCCCC  CT AT  CC  GGTTG
                                  |||||  || ||  ||  |||||
                                  TGGGG  GG TG  GG  CCAAT
                                     TG  G  __  AC
GAM1630  FLJ23519  3'  TGGCCTTGGGGTGCTGGTGGGG 50964       GT TGATTG
            CA                    TGCCCC  C     CCAAGGTTG
                                  ||||||  |     |||||||||
                                  ACGGGG  G     GGTTCCGGT
                                     TG TCGTGG
GAM1630  FLJ30213  3'  TAACTTTTGCCATTGGGTGGGG 59404      GT TG  T  C
            T                     GCCCC  C  AT GC AAGGTTG
                                  |||||  |  || || |||||||
                                  TGGGG  G  TA CG TTTCAAT
                                     TG GT  C  T
GAM1630  FLJ32865  3'  TGACTTTGGCCGCCATGGGGAC 58822    _     CTGATT
            A                     TG CCCCGT     GCCAAGGTTG
                                  || ||||||     ||||||||||
                                  AC GGGGTA     CGGTTTCAGT
                                   A     CCGC__
GAM1630  GMPPB    5'  GGCATAGCAGATGGGGCA    26224          AT_
                                  TGCCCCGTCTG   TGCC
                                  ||||||||||   ||||
                                  ACGGGGTAGAC   ACGG
                                        GAT
GAM1630  HAGE     5'  CGACGTCACGGTCAGGTGGTGC 38523     C  GT      CCAAG
            A                     TGC CC  CTGATTG    GTTG
                                  ||| ||  |||||||    ||||
                                  ACG GG  GACTGGC    CAGC
                                   T  TG      ACTG_
GAM1630  HRH4     3'  TAATTTTGATAAGACAGGGTA  41548       C    GATTGC
                                  TGCCC GTCT     CAAGGTTG
                                  ||||| ||||     ||||||||
```

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                                ATGGG CAGA     GTTTTAAT
                                   A   ATA___
GAM1630  HSF1     3'  TTCTTGGGGAGGCAGGGCA   19831      C   GAT G     TT
                                TGCCC GTCT   T CCAAGG  G
                                ||||| ||||   | ||||||  |
                                ACGGG CGGA   G GGTTCT  T
                                   A   ___ G     G
GAM1630  HSPC065  3'  TACTCTTCAGTTTGGTGGGGTA 27162       GT T    CC    TTG
                                TGCCCC  C GATTG  AAGG
                                ||||||  | |||||  ||||
                                ATGGGG  G TTGAC  TTCT
                                   TG T     __    CATT
GAM1630  HTR3A    5'  CAACCTTGGTGGCCCAGGGAGT 7876     _  GTCTGA TG
                                GC CCC     T  CCAAGGTTG
                                || |||     |  |||||||||
                                TG GGG     G  GGTTCCAAC
                                 A   ACCC__ GT
GAM1630  IL22R    3'  CGATCTGGCCTCAGACGGG    41471         TT    A
                                CCCGTCTGA  GCCA GGTTG
                                |||||||||  |||| |||||
                                GGGCAGACT  CGGT CTAGC
                                     C_   _
GAM1630  ILF3     3'  CAGCTACGGCTCAGGCGGGGCA 25231           TT   AA
                                TGCCCCGTCTGA  GCC  GGTTG
                                ||||||||||||  |||  |||||
                                ACGGGGCGGACT  CGG  TCGAC
                                      __   CA
GAM1630  IMAGE145052 3'  TAATTTTGGCAAAAGATTGGGT 27329      C    GA
            A                    TGCCC GTCT  TTGCCAAGGTTG
                                |||||  ||||  ||||||||||||
                                ATGGG TAGA  AACGGTTTTAAT
                                   T   A_
GAM1630  IMAGE3451454 3'  TGGTCTTCCTCTGGATGGGGC  54940         ____  TT
                                GCCCCGTCT    GA  GCCA
                                |||||||||    ||  ||||
                                CGGGGTAGG    CT  TGGT
                                     TCTC  TC
GAM1630  KIAA0040  5'  GGCGCTGTCAGACGGGGCA    28492           __
                                TGCCCCGTCTGAT  TGCC
                                ||||||||||||  ||||
                                ACGGGGCAGACTG  GCGG
                                      TC
GAM1630  KIAA0061  3'  TGGCTTTGGGGGTGATGAGGT  68839     C    TG   G
                                GCC CGTC  ATT CCAAGGTTG
                                ||| ||||  ||| |||||||||
                                TGG GTAG  TGG GGTTTCGGT
                                  A   __   G
GAM1630  KIAA0125  5'  TGACTTTGGCTAGGGATGGAGC 29578     C      GATT
            A                    TGC CCGTCT    GCCAAGGTTG
                                ||| ||||||    ||||||||||
```

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                                ACG GGTAGG   CGGTTTCAGT
                                  A     GAT_
GAM1630 KIAA0152 3' CATCTTGTGAGATGGGGGCA  28967      _   G TTGC   GT
                                TGCCCC GTCT A   CAAG  TG
                                |||||| |||| |   ||||  ||
                                ACGGGG TAGA T   GTTC  AC
                                   G   G ____   TG
GAM1630 KIAA0169 3' CAGTTTTGGTAATTCTGTGGT 73177    C  TCT       GG
                                GCC CG   GATTGCCAA  TTG
                                ||| ||   |||||||||  |||
                                TGG GT   TTAATGGTT  GAC
                                  T  C__       TT
GAM1630 KIAA0218 3' CAGCTTCTGGGTGGTGGGTGGG 29294      T  G  TG  AA__
            GT                    GCCCCG CT AT  CC   GGTTG
                                ||||||  ||  ||  ||   |||||
                                TGGGGT GG TG  GG   TCGAC
                                   _  G  GT  GTCT
GAM1630 KIAA0321 5' TAGCCTTGAAAGGCGGGGT   63063        GATTGC
                                GCCCCGTCT     CAAGGTTG
                                |||||||||     ||||||||
                                TGGGGCGGA     GTTCCGAT
                                     AA____
GAM1630 KIAA0326 3' CAGCCTTGAGATGGATGGG   64959       G   GC
                                CCCGTCT ATT  CAAGGTTG
                                |||||||  |||  ||||||||
                                GGGTAGG TAG  GTTCCGAC
                                   _   A_
GAM1630 KIAA0367 3' GGCCTCTAGTGAGGTGGGGT  67870     GT  G    CCA    G
                                GCCCC  CT ATTG   AGGTT
                                |||||  || ||||   |||||
                                TGGGG  GA TGAT   TCCGG
                                   TG  G    C__
GAM1630 KIAA0561 3' CAATCGGGGCTGGATGGGGCA 66467         ATT   AA
                                TGCCCCGTCTG   GCC  GGTTG
                                ||||||||||   |||  |||||
                                ACGGGGTAGGT   CGG  CTAAC
                                      ___   GG
GAM1630 KIAA0677 3' GATTTTGGGGTGGGGGGT    28531     G  TGATTG
                                GCCCC TC     CCAAGGTT
                                ||||| ||     ||||||||
                                TGGGG GG     GGTTTTAG
                                   _ TGG___
GAM1630 KIAA0819 3' TGAGCTAATCGGGGTGGGGT  64337     GT  _   _ _
                                GCCCC  CT GATT GC CA
                                |||||  || |||| || ||
                                TGGGG  GG CTAA CG GT
                                   TG  G    T  A
GAM1630 KIAA0831 3' TGATTTTGTTTGGGAGGGGT  30657     GT TG TTGC
                                GCCCC  C  A    CAAGGTTG
                                |||||  |  |   ||||||||
```

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                              TGGGG  G  T   GTTTTAGT
                                 AG GT T___
GAM1630  KIAA0979  3'  TGGTTATAATAGATGGGGCA  31141          ATT__
                              TGCCCCGTCTG    GCCA
                              ||||||||||    ||||
                              ACGGGGTAGAT    TGGT
                                    AATAT
GAM1630  KIAA1029  3'  GCCTTGGATGAGGCGGGGCA  24430         G  TG      TG
                              TGCCCCGTCT AT  CCAAGGT
                              |||||||||| ||  |||||||
                              ACGGGGCGGA TA  GGTTCCG
                                    G  __      T
GAM1630  KIAA1030  3'  GACCTTGGTAGTCACAGG   94980    GTC
                              CC   TGATTGCCAAGGTT
                              ||   ||||||||||||||
                              GG   ACTGATGGTTCCAG
                               AC_
GAM1630  KIAA1034  3'  CGGCCTGCTCTCAGGGTGGGGT 63129      GT _   TT  CA
                              GCCCC  C TGA  GC  AGGTTG
                              |||||  | |||  ||  ||||||
                              TGGGG  G ACT  CG  TCCGGC
                                 TG G   CT  __
GAM1630  KIAA1157  3'  TGGCTTTTGTCAGATGGAGT   72707    C       T___
                              GC CCGTCTGAT    GCCA
                              || |||||||||    ||||
                              TG GGTAGACTG    CGGT
                               A        TTTT
GAM1630  KIAA1173  5'  CGGTTTTGGCAGAGGGTGGGGC 40765      GT  GA      GG
                              GCCCC  CT  TTGCCAA  TTG
                              |||||  ||  |||||||  |||
                              CGGGG  GG  GACGGTT  GGC
                                 TG  A_      TT
GAM1630  KIAA1200  3'  TAATTTTCTTTCTGGGGGGGGGC 63041      G   _  TTGCC
                              GCCCC TCT GA     AAGGTTG
                              ||||| ||| ||    |||||||
                              CGGGG GGG CT     TTTTAAT
                                 G   T  TTC__
GAM1630  KIAA1257  3'  TGATAGTTAGGGTGGGGCA   63424       GT _     C
                              TGCCCC  C TGATTG CA
                              ||||||  | ||||||  ||
                              ACGGGG  G ATTGAT GT
                                  TG G      A
GAM1630  KIAA1332  3'  TTCTTGGTAGCTCCTGGGCA  71710       CGTCT  _       TT
                              TGCCC    GA TTGCCAAGG  G
                              |||||    || |||||||||  |
                              ACGGG    CT GATGGTTCT  T
                                 TC___  C       G
GAM1630  KIAA1485  3'  TAATCACTGCTGGGTGGGGT   90770      GT   ATT  CAA
                              GCCCC  CTG   GC   GGTTG
                              |||||  |||   ||   |||||
```

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                                TGGGG GGT  CG  CTAAT
                                  TG  ___ TCA
GAM1630 KIAA1514 3' TGGCCTTGGCACTGTGGGATG 39327     G __
                                CGTCT AT  TGCCAAGGTTG
                                ||||| ||  ||||||||||
                                GTAGG TG  ACGGTTCCGGT
                                   G  TC
GAM1630 KIAA1644 3' AACTTTGGTGGTTGTGGC   86215   _  TG
                                GTC TGAT  CCAAGGTT
                                ||| ||||  ||||||||
                                CGG GTTG  GGTTTCAA
                                  T   GT
GAM1630 KIAA1822 3' CAATTTTTCCATGGATGGGG  68180       AT  CC
                                CCCCGTCTG  TG  AAGGTTG
                                |||||||||  ||  |||||||
                                GGGGTAGGT  AC  TTTTAAC
                                     __ CT
GAM1630 KIAA1843 3' CAATAGATTTAGTCGAGTGGGG 62882      TC    CCAAG
            CA                    TGCCCCG  TGATTG   GTTG
                                |||||||  ||||||   ||||
                                ACGGGGT  GCTGAT   TAAC
                                   GA    TTAGA
GAM1630 KIAA1855 3' TGATCTTGGAGATGGGTGGGCA 93960     CGT  G  TG
                                TGCCC  CT AT  CCAAGGTTG
                                |||||  || ||  |||||||||
                                ACGGG  GG TA  GGTTCTAGT
                                   T__  G  GA
GAM1630 KIAA1941 3' TTACTTCTGGGCAGATGGGGT  75346       ATTG  _  TG
                                GCCCCGTCTG   CCA AGGT
                                ||||||||||   ||| ||||
                                TGGGGTAGAC   GGT TTCA
                                     G___  C   TTT
GAM1630 LIG-1   3' TAATTTTGGAGGGGGTGGGG  64614     GT  GATTG
                                CCCC  CT   CCAAGGTTG
                                ||||  ||   |||||||||
                                GGGG  GG   GGTTTTAAT
                                  TG  GGA__
GAM1630 LIMR    3' ATTTGATGTGCAATAGGGTGGG 36675     GT  G   _  AGGTTG
            GTA                   TGCCCC  CT ATTGC CA
                                ||||||  || ||||| ||
                                ATGGGG  GG TAACG GT
                                   TG  A   T  AGTTTAG
GAM1630 MESDC2  3' GATCTTAATTGTGATGGGGT  72914       _   CCA   G
                                GCCCCGTC TGATTG  AGGTT
                                |||||||| ||||||  |||||
                                TGGGGTAG GTTAAT  TCTAG
                                     T    ___   G
GAM1630 MGC13064 3' CAACAGCAGTCAGGAGGGGTA 51345     GT     CAAG
                                TGCCCC  CTGATTGC   GTTG
                                ||||||  ||||||||   ||||
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                                ATGGGG  GACTGACG   CAAC
                                   AG      A___
GAM1630 MGC13114 3' CGACCTTGGTCCAGTGGGC   51391    CGT   ATT
                                GCCC   CTG   GCCAAGGTTG
                                ||||   |||   ||||||||||
                                CGGG   GAC   TGGTTCCAGC
                                  T__   C__
GAM1630 MGC23918 3' TTCTTGGGCAGGGATGGGG   59192      GA   _   TT
                                CCCCGTCT  TTGCC AAGG  G
                                ||||||||  ||||| ||||  |
                                GGGGTAGG  GACGG TTCT  T
                                     __    G   G
GAM1630 MGC2615  3' AACCTTTGGCGGGGGGGTA   44321     G  TGATT   _
                                TGCCCC TC    GCCAA GGTT
                                ||||||  ||    ||||| ||||
                                ATGGGG GG    CGGTT CCAA
                                   G  _____    T
GAM1630 MGC2865  3' GATCGGCAGTTGGGAGGGGC   51460     GT TG    AA   G
                                GCCCC  C  ATTGCC  GGTT
                                |||||  |  ||||||  ||||
                                CGGGG  G  TGACGG  CTAG
                                   AG GT     __    G
GAM1630 MGC3040  3' AACCCTGGTCAGGTGAGGTA   67383    C GT   ATT   A   G
                                TGCC C  CTG   GCCA GGTT
                                |||| |  |||   |||| ||||
                                ATGG G  GAC   TGGT CCAA
                                  A TG  ___    C   G
GAM1630 MGC35558 3' CAGTCTTTGTCAGATGGGACA  59410   C       TGCC   GT
                                TG CCCGTCTGAT    AAG  TG
                                || ||||||||||    |||  ||
                                AC GGGTAGACTG    TTC  AC
                                 A        T___   TG
GAM1630 MGC4707  3' TAGCCTTGGTAATATGAAGGGT 44363    CG  TG
                                GCCC  TC  ATTGCCAAGGTTG
                                ||||  ||  ||||||||||||||
                                TGGG  AG  TAATGGTTCCGAT
                                  A_  TA
GAM1630 MRPL4    5' CAGCGCGGAGTCGGGCGGGG   32550         G  AAG
                                CCCCGTCTGATT CC   GTTG
                                ||||||||||| ||   ||||
                                GGGGCGGGCTGA GG   CGAC
                                      _ CG_
GAM1630 NT5C1B   5' TGAGCAATCAGATGAGGC    71750    C        _
                                GCC CGTCTGATTGC CA
                                ||| |||||||||| ||
                                CGG GTAGACTAACG GT
                                  A         A
GAM1630 OR2C3    3' GACCTTGGAAGACAGGGCA    75974     C   GATTG
                                TGCCC GTCT    CCAAGGTT
                                ||||| ||||    ||||||||
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                                ACGGG CAGA    GGTTCCAG
                                  A   A____
GAM1630 PCANAP7  5' CAACTTGTATCGAGTGGGCGGG 95009        GA  CCA_
            GCA                   TGCCCCGTCT  TTG   AGGTTG
                                  ||||||||||  |||   ||||||
                                  ACGGGGCGGG  AGC   TTCAAC
                                      TG  TATG
GAM1630 PCYT1B   3' CAGCTGAAGAGTTGGGCGAGGT 17922    C   TG  GCCAA
                                  GCC CGTC  ATT    GGTTG
                                  ||| ||||  |||    |||||
                                  TGG GCGG  TGA    TCGAC
                                    A   GT  GAAG_
GAM1630 PEG10    3' TAATTTTAAGTGGGTGGGGT  31205      T  G  GCC
                                  GCCCCG CT ATT   AAGGTTG
                                  |||||| || |||   |||||||
                                  TGGGGT GG TGA   TTTTAAT
                                     _ G  A__
GAM1630 PMAIP1   3' TGACCTGTGATTAGACTGGGC  41214     C     TG CA
                                  GCCC GTCTGAT  C  AGGTTG
                                  |||| |||||||  |  ||||||
                                  CGGG CAGATTA  G  TCCAGT
                                    T     GT __
GAM1630 PPP1R14C 3' TGGCCTTGTCCAAGGATGGGG 48930       GA  C_
                                  CCCCGTCT  TTG  CAAGGTTG
                                  ||||||||  |||  ||||||||
                                  GGGGTAGG  AAC  GTTCCGGT
                                      __  CT
GAM1630 PRAX-1   3' TGACCTTGGTCTCCAGGGGT  17660     GTCT  TT
                                  GCCCC   GA  GCCAAGGTTG
                                  |||||   ||  ||||||||||
                                  TGGGG   CT  TGGTTCCAGT
                                    AC__  C_
GAM1630 RGS7     5' TGACCTTGGCGGAGGAGGGCA  12866     CG  GA
                                  TGCCC  TCT  TTGCCAAGGTTG
                                  |||||  |||  ||||||||||||
                                  ACGGG  AGG  GGCGGTTCCAGT
                                     __  A_
GAM1630 RLUCL    5' TGTCTTGGCGTGGGCGTGGGC  55239     _    AT     TT
                                  GCCC CGTCTG  TGCCAAGG  G
                                  |||| ||||||  ||||||||  |
                                  CGGG GCGGGT  GCGGTTCT  T
                                    T     __      GG
GAM1630 RNF38    5' GGCCCGGTCGGTTGGGGC    43260      T    __
                                  GCCCCG CTGATT  GCC
                                  |||||| ||||||  |||
                                  CGGGGT GGCTGG  CGG
                                     T     CC
GAM1630 SEMA3B   5' TGATTGTGGCCAGGCGGGGCA  17345        ATT   AG
                                  TGCCCCGTCTG   GCCA  GTTG
                                  ||||||||||   ||||  ||||
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                                ACGGGGCGGAC  CGGT  TAGT
                                     ___   GT
GAM1630 SEMA4F   3' AGTTTGGGGATGGGGCA    16207        GATTG   GG
                                TGCCCCGTCT   CCAA  TT
                                ||||||||||   ||||  ||
                                ACGGGGTAGG   GGTT  GA
                                     _____   TT
GAM1630 SEMA5A   3' TAGCTTTGGTGAAACTGGGGT  15596      TCTGA TG
                                GCCCCG   T  CCAAGGTTG
                                ||||||   |  |||||||||
                                TGGGGT   A  GGTTTCGAT
                                   CAA__ GT
GAM1630 SH3BGRL2 3' CAGCCCCTGGGTGGGGTGGGGT 49675     GT  G  TG  A_
                                GCCCC  CT AT  CCA  GGTTG
                                |||||  || ||  |||  |||||
                                TGGGG  GG TG  GGT  CCGAC
                                   TG  G  __  CC
GAM1630 SLC11A1  3' CAGCCCAAGGGTGGGTGGGGT  60156     GT  GATT   AA__
                                GCCCC  CT   GCC   GGTTG
                                |||||  ||   |||   |||||
                                TGGGG  GG   TGG   CCGAC
                                   TG  _____  GAAC
GAM1630 SLC7A10  5' CGGCCGGCCGGACAGACGGGGC 39552         ATT_  AA
            A                   TGCCCCGTCTG   GCC  GGTTG
                                ||||||||||    |||  |||||
                                ACGGGGCAGAC   CGG  CCGGC
                                      AGGC  __
GAM1630 SP329    5' CAACTCCCATCAGATGGGCCA  48645    C       TGCCAA
                                TG CCCGTCTGAT     GGTTG
                                || ||||||||||     |||||
                                AC GGGTAGACTA     TCAAC
                                 C        CCC___
GAM1630 STX6     5' CAGCTGCGGGAACAGGCGGGGT 20611         A  G  AA
                                GCCCCGTCTG TT CC  GGTTG
                                |||||||||| || ||  |||||
                                TGGGGCGGAC AA GG  TCGAC
                                      _  G  CG
GAM1630 SUN1     3'  TAACTTTGGTTTAAAACAGGGT 47923      C  CTGATT
                                GCCC GT     GCCAAGGTTG
                                ||||  ||    ||||||||||
                                TGGG CA     TGGTTTCAAT
                                  A  AAATT_
GAM1630 SZF1     5'  GTGGTTCCAGTGGCAGATGGGG 32732         ATT_____   AGGTTG
            CA                    TGCCCCGTCTG       GCCA
                                  ||||||||||        ||||
                                  ACGGGGTAGAC       TGGT
                                        GGTGACCT      GT
GAM1630 TED      3'  GGCTTTGGGGAGATGGGC    32272      C   GAT G
                                GCCC GTCT   T CCAAGGTT
                                ||||  ||||   |  ||||||||
```

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                                CGGG TAGA   G GGTTTCGG
                                  _   ___ G
GAM1630  TIGA1    5'  TGACCCTGGTCGGGTGGGG   54855     GT   ATT   A
                                CCCC  CTG   GCCA GGTTG
                                ||||  |||   |||| |||||
                                GGGG  GGC   TGGT CCAGT
                                  TG  ___   C
GAM1630  TLN1     5'  CGGCGGGCCGGCGGGCGGGGC  21904         ATT   AAG
                                GCCCCGTCTG   GCC   GTTG
                                ||||||||||   |||   ||||
                                CGGGGCGGGC   CGG   CGGC
                                     GGC   G__
GAM1630  TRIM6    3'  TGACTTTGGTAGAGAGGTGCA  55188     C  G   GA
                                TGC CC TCT  TTGCCAAGGTTG
                                ||| || |||  ||||||||||||
                                ACG GG AGA  GATGGTTTCAGT
                                 T  _  __
GAM1630  TSPEAR   3'  CAACTGGGGTGGCCAGGTGGGG 59374      GT   A TG  AA
             C                   GCCCC  CTG T  CC  GGTTG
                                 |||||  ||| |  ||  |||||
                                 CGGGG  GAC G  GG  TCAAC
                                    TG   C GT  GG
GAM1630  UHRF2    5'  CGGCGCGGGCCGGGCGGGGC   73832         ATT   AAG
                                GCCCCGTCTG   GCC   GTTG
                                ||||||||||   |||   ||||
                                CGGGGCGGGC   CGG   CGGC
                                     ___   GCG
GAM1630  URG4     3'  AGCCCTGTCTGATGGGGCA   35924         T   TGCCAA
                                TGCCCCGTC GAT     GGTT
                                ||||||||| |||     ||||
                                ACGGGGTAG CTG     CCGA
                                     T   TC____
GAM1630  VIAAT    3'  TGTTTTGGGGGGAGGCGGGGT  55454         GA  G     TT
                                GCCCCGTCT  TT CCAAGG  G
                                |||||||||  || ||||||  |
                                TGGGGCGGA  GG GGTTTT  T
                                     G_  G     GG
GAM1630  WDR5B    3'  AATTTTGGCAGTTTGGTA    39343     CCGTCT
                                TGCC     GATTGCCAAGGTT
                                ||||     ||||||||||||
                                ATGG     TTGACGGTTTTAA
                                  T_____
GAM1630  WNT2B    3'  TGGCCAAAGTTAGATGGGACA  44681    C         ___
                                TG CCCGTCTGATT   GCCA
                                || ||||||||||   ||||
                                AC GGGTAGATTGA   CGGT
                                 A          AAC
GAM1630  ZIM3     5'  TGGCCTGATAGGATCAGGTGGG 54641      GT     GCCA_
             GC                   GCCCC  CTGATT    AGGTTG
                                  |||||  ||||||    ||||||
```

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                                CGGGG  GACTAG    TCCGGT
                                  TG     GATAG
GAM1630  ZNF282    3'  TGGCCTGGCACCGGGTGGGGT  90700      GT   AT    A
                                GCCCC  CTG  TGCCA GGTTG
                                |||||  |||  ||||| |||||
                                TGGGG  GGC  ACGGT CCGGT
                                  TG   C_    _
GAM1630  LOC115294 5'  TGACTTTGGCGTCCGCGGGG   73384       CT   T
                                CCCCGT  GAT GCCAAGGTTG
                                ||||||  ||| ||||||||||
                                GGGGCG  CTG CGGTTTCAGT
                                   C_   _
GAM1630  LOC122830 3'  CAACTTTCTTTTAATGGGGT   74628       C   TTGCC
                                GCCCCGT TGA    AAGGTTG
                                ||||||| |||    |||||||
                                TGGGGTA ATT    TTTCAAC
                                   _   TTC__
GAM1630  LOC128272 3'  GGCCTTGGCATTGAGGGCA   75244      CG  TGAT
                                TGCCC  TC    TGCCAAGGTT
                                |||||  ||    ||||||||||
                                ACGGG  AG    ACGGTTCCGG
                                  __   TT__
GAM1630  LOC128977 3'  AGCCAGGTCAGGCTGGGCA   75329      C    ATT   AA
                                TGCCC GTCTG   GCC  GGTT
                                ||||| |||||   |||  ||||
                                ACGGG CGGAC   TGG  CCGA
                                  T    ____   A_
GAM1630  LOC142964 5'  CAACTTCGGCATCAAATGGGGC 76968        C   T   A
            A                    TGCCCCGT TGAT GCC AGGTTG
                                ||||||||| |||| ||| ||||||
                                ACGGGGTA ACTA CGG TTCAAC
                                    A   _   C
GAM1630  LOC143308 5'  TGGTATGAATTAGACTGGGT   83840      C      ___
                                GCCC GTCTGAT   TGCCA
                                ||||  |||||||   |||||
                                TGGG CAGATTA   ATGGT
                                  T      AGT
GAM1630  LOC145463 3'  TAATTTTGGCAAAAGATTGGGT 71483      C    GA
            A                    TGCCC GTCT  TTGCCAAGGTTG
                                |||||  ||||  ||||||||||||
                                ATGGG TAGA  AACGGTTTTAAT
                                  T   A_
GAM1630  LOC145725 5'  GACAGGGTCGGGCGGGG     77883        ATT   AAG   G
                                CCCCGTCTG   GCC   GTT
                                |||||||||   |||   |||
                                GGGGCGGGC   TGG   CAG
                                    ___   GA_   A
GAM1630  LOC145732 5'  GACAGGGTCGGGCGGGG     77895        ATT   AAG   G
                                CCCCGTCTG   GCC   GTT
                                |||||||||   |||   |||
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                                GGGGCGGGC  TGG  CAG
                                    ___  GA_  A
GAM1630  LOC146988 5'  GCTGTGTTCGGTGGGGCA   84960      T   TT  CAA  TG
                                TGCCCCG CTGA  GC  GGT
                                ||||||| ||||  ||  |||
                                ACGGGGT GGCT  TG  TCG
                                    _   TG  ___  T
GAM1630  LOC149566 3'  TTCTTGGTCCCTGCAGGGCA  85655     C  CTGATT     TT
                                TGCCC GT    GCCAAGG  G
                                ||||| ||    |||||||  |
                                ACGGG CG    TGGTTCT  T
                                   A  TCCC__     G
GAM1630  LOC151009 5'  CGGCTTTGGCAGGTGTCGGGGG 86366      GTCTGA
             C                  GCCCC    TTGCCAAGGTTG
                                |||||    ||||||||||||
                                CGGGG    GACGGTTTCGGC
                                   GCTGTG
GAM1630  LOC152015 3'  CAATTTTGGCAATTTTAAAGG  68460   GTCT_
                                CC    GATTGCCAAGGTTG
                                ||    ||||||||||||||
                                GG    TTAACGGTTTTAAC
                                 AAATT
GAM1630  LOC152457 3'  CAGCCTAGGGTCAGACAGGGT  81486     C      TG  A
                                GCCC GTCTGAT  CC AGGTTG
                                |||| |||||||  || ||||||
                                TGGG CAGACTG  GG TCCGAC
                                   A      __ A
GAM1630  LOC153688 3'  TGGCCAATTGGACAGGGCA   87340     C   TG   _
                                TGCCC GTC  ATTG CCA
                                ||||| |||  |||| |||
                                ACGGG CAG  TAAC GGT
                                   A  GT   C
GAM1630  LOC154790 5'  CAGCCTTGGTAGCTAACATGGG 82037      C_  C  A
             CA                   TGCCC  GT TG TTGCCAAGGTTG
                                |||||  || || ||||||||||||
                                ACGGG  CA AT GATGGTTCCGAC
                                   TA  _  C
GAM1630  LOC155063 3'  TAGCTTGGGAGATAACGGGTGG 87647      GT   A___  G    GTTG
             GGT                   GCCCC  CTG   TT CCAAG
                                |||||  |||   || |||||
                                TGGGG  GGC   GA GGTTC
                                   TG   AATA  G    GAT
GAM1630  LOC157623 5'  CAATCTTGCATGTGGGTGGGG  82412     GT   AT   C
                                CCCC  CTG  TGC AAGGTTG
                                ||||  |||  ||| |||||||
                                GGGG  GGT  ACG TTCTAAC
                                   TG  GT  _
GAM1630  LOC157740 5'  TGGCCCGTGGGGCGGGGC   82468        G  T_
                                GCCCCGTCT AT  GCCA
                                |||||||| ||  ||||
```

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                                CGGGGCGGG TG  CGGT
                                     G  CC
GAM1630  LOC157858 5'  TGGTGCTGACGGATGGGGT   87898         AT__
                                GCCCCGTCTG   TGCCA
                                ||||||||||   |||||
                                TGGGGTAGGC   GTGGT
                                      AGTC
GAM1630  LOC158172 5'  GGCCTTGGCGACCGAGGT    83668    C  TCTGA
                                GCC CG    TTGCCAAGGTT
                                ||| ||    ||||||||||
                                TGG GC    AGCGGTTCCGG
                                  A  C____
GAM1630  LOC158314 3'  TGGCCTTGGTGAGCTCCCGTGG 88100    C  TCTGA TG
              T                  GCC CG    T  CCAAGGTTG
                                ||| ||    |  |||||||||
                                TGG GC    A  GGTTCCGGT
                                  T  CCTCG GT
GAM1630  LOC158377 5'  CATCTTGGCACGAGGGGGCA   88131      G  TGAT     GT
                                TGCCCC TC    TGCCAAG  TG
                                |||||| ||    |||||||  ||
                                ACGGGG AG    ACGGTTC  AC
                                   G  C___      TG
GAM1630  LOC163412 5'  CGGTTTTGGTGGCCGGGGTGGG 83012     GT  _ A TG   GG
              G                   CCCC  CT G T  CCAA  TTG
                                ||||  || | |  ||||  |||
                                GGGG  GG C G  GGTT  GGC
                                  TG  G C GT    TT
GAM1630  LOC169611 3'  CGGCTTTCTCTGCGGTGGGGTA 83646       T   ATTGCC
                                TGCCCCG CTG     AAGGTTG
                                ||||||| |||     |||||||
                                ATGGGGT GGC     TTTCGGC
                                   _  GTCTC_
GAM1630  LOC196957 5'  GACAGGGTCGGGCGGGG    89188        ATT   AAG   G
                                CCCCGTCTG   GCC   GTT
                                |||||||||   |||   |||
                                GGGGCGGGC   TGG   CAG
                                     ___   GA_   A
GAM1630  LOC196961 5'  GACAGGGTCGGGCGGGG    89202        ATT   AAG   G
                                CCCCGTCTG   GCC   GTT
                                |||||||||   |||   |||
                                GGGGCGGGC   TGG   CAG
                                     ___   GA_   A
GAM1630  LOC197138 5'  GACAGGGTCGGGCGGGG    89251        ATT   AAG   G
                                CCCCGTCTG   GCC   GTT
                                |||||||||   |||   |||
                                GGGGCGGGC   TGG   CAG
                                     ___   GA_   A
GAM1630  LOC200058 3'  CAGCCTTGGTATGGGGTGGGG 89958     GT  G  T
                                CCCC  CT AT GCCAAGGTTG
                                ||||  || || ||||||||||
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                                GGGG  GG TA TGGTTCCGAC
                                  TG  G  _
GAM1630  LOC200471 5'  CAACCTTGGTGGTTGCACGGG  91633      C    TG
                                CCCGT TGAT  CCAAGGTTG
                                ||||| ||||  |||||||||
                                GGGCA GTTG  GGTTCCAAC
                                   C    GT
GAM1630  LOC221103 5'  TGTTTTGGCAACCCTGGGTGT  94872    _   TCTGA       TT
                                GC CCCG    TTGCCAAGG  G
                                || ||||    |||||||||  |
                                TG GGGT    AACGGTTTT  T
                                 T   CCC__       GG
GAM1630  LOC221415 3'  TTTCCTGGGGGTTGAGGTGGGG 95502      GT  _   G   A  TTG
             C                   GCCCC  CT GATT CCA GG
                                ||||| || |||| ||| ||
                                CGGGG  GA TTGG GGT CC
                                   TG  G   G  _ TTTG
GAM1630  LOC221922 5'  TGGAACAGTCGGGAGGGGCA  94261      GT     __
                                TGCCCC  CTGATTG  CCA
                                ||||||  |||||||  |||
                                ACGGGG  GGCTGAC  GGT
                                   AG      AA
GAM1630  LOC221960 3'  TGTCTTGCTGGATGGGGACA  92728   _      ATT  C   TT
                                TG CCCCGTCTG   GC AAGG  G
                                || |||||||||   || ||||  |
                                AC GGGGTAGGT   CG TTCT  T
                                 A       ___  _   GG
GAM1630  LOC222031 3'  TGGTGGGCTGGACGGGGCA   95689         A_ TG
                                TGCCCCGTCTG  T  CCA
                                ||||||||||  |  |||
                                ACGGGGCAGGT  G  GGT
                                      CG GT
GAM1630  LOC222160 3'  TAGCCAGGCATTGGTGGGGCA  95788       T TG  T   AA
                                TGCCCCG C  AT GCC  GGTTG
                                ||||||| |  || |||  |||||
                                ACGGGGT G  TA CGG  CCGAT
                                   _ GT  _   A_
GAM1630  LOC222166 3'  TAGTGGAAAATATAGATGGGGT 95745         _  G_   AGGTTG
                                GCCCCGTCTG ATT  CCA
                                |||||||||| |||  |||
                                TGGGGTAGAT TAA  GGT
                                      A   AA   GAT
GAM1630  LOC222182 3'  TGGCTCAGGCCAGGCGGGGT   95864         ATT   AA
                                GCCCCGTCTG   GCC  GGTTG
                                ||||||||||   |||  |||||
                                TGGGGCGGAC   CGG  TCGGT
                                      ___   AC
GAM1630  LOC253071 5'  CAATTCAGTGGTCAGTGGGGT  97419      T    TG CAA
                                GCCCCG CTGAT  C   GGTTG
                                |||||| |||||  |   |||||
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                                TGGGGT GACTG  G   TTAAC
                                   _    GT AC_
GAM1630  LOC254419 5'  CAAGCTCAGTTGGGCTGGGT   99372     C   TG    CCA  G
                                GCCC GTC  ATTG   AG TTG
                                |||| |||  ||||   || |||
                                TGGG CGG  TGAC   TC AAC
                                  T  GT    ___  G
GAM1630  LOC254528 5'  CGACCCGGGGGTCGGGCGGGCC 96752    C         G  AA
            A                    TG CCCGTCTGATT CC  GGTTG
                                || ||||||||||| ||  |||||
                                AC GGGCGGGCTGG GG  CCAGC
                                 C         G  C_
GAM1630  LOC254636 5'  CAGCCACCAGGGTGGGCGGGGC 99469          GATT   AA___
            A                    TGCCCCGTCT    GCC    GGTTG
                                ||||||||||    |||    |||||
                                ACGGGGCGGG    TGG    CCGAC
                                      _____  GACCA
GAM1630  LOC254986 5'  TGACTTTGGCGTCCGCGGGG   97806       CT   T
                                CCCCGT  GAT GCCAAGGTTG
                                ||||||  ||| ||||||||||
                                GGGGCG  CTG CGGTTTCAGT
                                   C_  _
GAM1630  LOC256867 5'  AGTCTGGCGGTTGGAGGGGT   96510       G  TG      A GT G
                                GCCCC TC  ATTGCCA G  T
                                ||||| ||  ||||||| |  |
                                TGGGG AG  TGGCGGT C  A
                                  _ GT      _ TG A
GAM1630  LOC257058 5'  CAGCTTTGGTAGTTATACTTGG 99347     CC  C
            T                    GCC  GT TGATTGCCAAGGTTG
                                |||  || ||||||||||||||||
                                TGG  CA ATTGATGGTTTCGAC
                                  TT  T
GAM1630  LOC257095 5'  TAGCCTTGGCTGGGTGGGG   98722     GT   ATT
                                CCCC  CTG   GCCAAGGTTG
                                ||||  |||   ||||||||||
                                GGGG  GGT   CGGTTCCGAT
                                  TG  ___
GAM1630  LOC257396 5'  TAGTTTTGCTTCGCAGATGGGC 98923    C      ATT_  C  GG
            CG                    TG CCCGTCTG    GC AA  TTG
                                || ||||||||    || ||  |||
                                GC GGGTAGAC    CG TT  GAT
                                 C       GCTT  _  TT
GAM1630  LOC51622  3'  TGTCTTGCTGGATGGGGACA   32211    _       ATT  C    TT
                                TG CCCCGTCTG   GC AAGG  G
                                || |||||||||   || ||||  |
                                AC GGGGTAGGT   CG TTCT  T
                                 A        ___  _    GG
GAM1630  LOC54466  3'  CAATCTTGGTAGAGGATGGG   39172       GA
                                CCCGTCT  TTGCCAAGGTTG
                                |||||||  ||||||||||||
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                                GGGTAGG  GATGGTTCTAAC
                                   A_
GAM1630 LOC55974 3' AATTTTGGAGGTTGGGGT    38737     GTCT  TG
                                GCCCC   GAT  CCAAGGTT
                                |||||   |||  ||||||||
                                TGGGG   TTG  GGTTTTAA
                                  ____  GA
GAM1630 LOC63928 3' CAGTTTTTCCACGGATGGG   42268       AT  CC  GG
                                CCCGTCTG  TG  AA  TTG
                                ||||||||  ||  ||  |||
                                GGGTAGGC  AC  TT  GAC
                                   __  CT  TT
GAM1630 LOC90019 5' TGGCTGCTGCTAGTCAGATGGG 57539          _  CAA
           GTA                   TGCCCCGTCTGATT GC   GGTTG
                                ||||||||||||||  ||   |||||
                                ATGGGGTAGACTGA CG   TCGGT
                                      T  TCG
GAM1630 LOC90309 3' CAGCTTGAAGATGGGTGGGGTA 62871       T  G   GCCA
                                TGCCCCG CT ATT    AGGTTG
                                |||||||  || |||    ||||||
                                ATGGGGT GG TAG    TTCGAC
                                   _  G   AAG_
GAM1630 LOC90631 3' AACTGGTTGGAGGGGGCA    64391      G  TG   GCCAA
                                TGCCCC TC  ATT    GGTT
                                ||||||  ||  |||    ||||
                                ACGGGG AG  TGG    TCAA
                                   G  GT  _____
GAM1631 ANKTM1   3' GTGGCTTACTATTTCATTGT   24701        CA  AC
                                GCAATGGAAT  AG  AGTTAT
                                ||||||||||  ||  ||||||
                                TGTTACTTTA  TC  TCGGTG
                                   __  AT
GAM1631 APG5L    3' GTAACTGTTCATCTTTGTTGTT 17940      TG  ATCAA
           T                    AGGCAA  GA    GACAGTTAT
                                ||||||  ||    |||||||||
                                TTTGTT  TT    TTGTCAATG
                                   GT  CTAC_
GAM1631 APLP2    3' GTGACTGTTTTTGTTTTGTT   92544    TG   C
                                AA  GAAT AAGACAGTTAT
                                ||  |||| ||||||||||
                                TT  TTTG TTTTGTCAGTG
                                 GT   T
GAM1631 ATF7     3' GTGGCTGTTACCTTTTTGTTCC 23402     C  TG   TCAA
           T                    AGG AA  GAA   GACAGTTAT
                                |||  ||  |||   |||||||||
                                TCC TT  TTT   TTGTCGGTG
                                  _  GT   TCCA
GAM1631 BACE     3'  ATAATTCAGAGTGGTTTCACTG 58079      A      AGAC_
           CCT                    AGGCA TGGAATCA    AGTTAT
                                |||||  ||||||||    ||||||
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                                TCCGT ACTTTGGT    TTAATA
                                  C       GAGAC
GAM1631 BCLG    3' TAACTGTTGTCTGTGCCT    57808      A   ATCAA
                                AGGCA TGGA    GACAGTTA
                                ||||| ||||    ||||||||
                                TCCGT GTCT    TTGTCAAT
                                  _   G____
GAM1631 BCLG    3' TAACTGTTGTCTGTGCCT    57809      A   ATCAA
                                AGGCA TGGA    GACAGTTA
                                ||||| ||||    ||||||||
                                TCCGT GTCT    TTGTCAAT
                                  _   G____
GAM1631 BLNK    3' TGGACTTGTTCTATTGCCT   26161          T   A_
                                AGGCAATGGAA CAAG  CA
                                |||||||||| ||||  ||
                                TCCGTTATCTT GTTC  GT
                                     _   AG
GAM1631 C18orf2  3' ATAACTGGTACAGATTTTGTGT 49458     A TG    AAGA_
            TT                   AGGC A  GAATC    CAGTTAT
                                |||| |  |||||    |||||||
                                TTTG T  TTTAG    GTCAATA
                                  _ GT    ACATG
GAM1631 CACNG3   3' TATTGTCCCCATTGTCT    22568        AATCAA   GT
                                AGGCAATGG     GACA  TA
                                |||||||||     ||||  ||
                                TCTGTTACC     CTGT  AT
                                     C_____    TG
GAM1631 CDH12    3' GTACTTGCTTTGTTTTGTTGTT 15778       TG   C  A  T
            T                    AGGCAA  GAAT AAG CAG TAT
                                ||||||  |||| ||| ||| |||
                                TTTGTT  TTTG TTC GTT ATG
                                   GT   T  _  C
GAM1631 CLOCK    3' GTAACTTTTAGTGGTTCTGTGC 18115      A      AGAC_
            CT                   AGGCA TGGAATCA    AGTTAT
                                ||||| ||||||||    ||||||
                                TCCGT GTCTTGGT    TCAATG
                                  _       GATTT
GAM1631 COL19A1  3' TTGACTGTTTTGATTTTATTTC 10267    C             T
            TT                   AGG AATGGAATCAAGACAGTTA
                                ||| ||||||||||||||||||
                                TTC TTATTTTAGTTTTGTCAGT
                                  T              TG
GAM1631 DMD     3' TGGTTTGGTTTTTGTTGCTT   15728       TG  _   A
                                AGGCAA  GAA TCAAG CA
                                ||||||  ||| ||||| ||
                                TTCGTT  TTT GGTTT GT
                                   GT  T   G
GAM1631 DMD     3' TGGTTTGGTTTTTGTTGCTT   15729       TG  _   A
                                AGGCAA  GAA TCAAG CA
                                ||||||  ||| ||||| ||
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                                TTCGTT  TTT GGTTT GT
                                   GT   T    G
GAM1631  DYRK1A   5'  GTAATTGTCTTGCATCATTATC 9164     GC     AAT
            T                    AG  AATGG   CAAGACAGTTAT
                                 ||  |||||   ||||||||||||
                                 TC  TTACT   GTTCTGTTAATG
                                  TA     AC_
GAM1631  EGR2     3'  TGGCTGTATATTTATGCCT    6377       A    ATCAAG
                                 AGGCA TGGA     ACAGTTA
                                 ||||| ||||     |||||||
                                 TCCGT ATTT     TGTCGGT
                                   _    ATA___
GAM1631  ENC1     3'  GTGACTGTGTTTGCATTGTCT  14649         G  TCA G
                                 AGGCAATG AA   A ACAGTTAT
                                 |||||||| ||   | ||||||||
                                 TCTGTTAC TT   T TGTCAGTG
                                      G  ___ G
GAM1631  EPB41L2  3'  GTTTTGGTTTTGTTTTCT    9293      C  TG
                                 AGG AA  GAATCAAGAC
                                 ||| ||  ||||||||||
                                 TCT TT  TTTGGTTTTG
                                   T  GT
GAM1631  FBXL11   3'  ACTTTGTTTTATTTTGTTGTCT 25511        TG    C      TTAT
                                 AGGCAA  GAAT AAGACAG
                                 ||||||  |||| |||||||
                                 TCTGTT  TTTA TTTTGTT
                                    GT    _      TCAT
GAM1631  FPRL1    3'  GTAATTCCTCTGATTCTGTTTT 9395      C        A  C_
            CT                    AGG AATGGAATCA GA  AGTTAT
                                  ||| |||||||||| ||  ||||||
                                  TCT TTGTCTTAGT CT  TTAATG
                                    T         _ CC
GAM1631  FUT5     5'  ATAGCTGAGTGATATTCCATTG 10725         __    AGA
            T                     GCAATGGA  ATCA   CAGTTAT
                                  ||||||||  ||||   |||||||
                                  TGTTACCT  TAGT   GTCGATA
                                       TA   GA_
GAM1631  GABPA    3'  ATAACTGTTTCCCCTCTCTGCT 10747      AT   ATCA__
            GCTT                    AGGCA  GGA     AGACAGTTAT
                                    |||||  |||     ||||||||||
                                    TTCGT  TCT     TTTGTCAATA
                                      CG   CTCCCC
GAM1631  GJA5     3'  TGCTCTTGAATCTGTTGTCT   19167          A     _
                                  AGGCAATGGA TCAAGA CA
                                  ||||||||||| |||||| ||
                                  TCTGTTGTCT AGTTCT GT
                                        A     C
GAM1631  GRF2     3'  GTTTTCTGGTTTGGTTTTGTTT 19201     C  TG       A   TTAT
            TCT                     AGG AA  GAATCAAG CAG
                                    ||| ||  |||||||| |||
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                                TCT TT  TTTGGTTT GTC
                                  T  GT      G   TTTTGG
GAM1631  GRM1     3'  GACTTTGGTTCCATGTTT    7737       A       GAC
                                AGGCA TGGAATCAA   AGTT
                                ||||| |||||||||   ||||
                                TTTGT ACCTTGGTT   TCAG
                                   _       ____
GAM1631  HADHB    3'  GTGGTTGTTTTTGGTCTCTGTT 5742         _     _  TT
              GTC                   GGCAATGGA ATCAAGA CAG  AT
                                ||||||||| ||||||| |||  ||
                                CTGTTGTCT TGGTTTT GTT  TG
                                     C      T   GG
GAM1631  HAO1     3'  ATAGCAATCCCTTTTATTTCAT 34510          C  ___  CA
              TGCTT                  AGGCAATGGAAT AA   GA  GTTAT
                                ||||||||||| ||   ||  |||||
                                TTCGTTACTTTA TT   CT  CGATA
                                      T  TCC  AA
GAM1631  HPSE     3'  ATAACTGTCTGTTAATGCTTGC 22860       TGGAATCA
              TT                   AGGCAA       AGACAGTTAT
                                ||||||       ||||||||||
                                TTCGTT       TCTGTCAATA
                                   CGTAATTG
GAM1631  IFRD1    3'  GTAGCAGTGGTTATATTGCTT  60755        G    AGACA
                                AGGCAATG AATCA    GTTAT
                                |||||||| |||||    |||||
                                TTCGTTAT TTGGT    CGATG
                                    A    GA___
GAM1631  IL1RAP   3'  ATAGTTGTCATAGTTCTTGCCT 57067      AT    CAA   GT
                                AGGCA  GGAAT   GACA  TAT
                                |||||  |||||   ||||  |||
                                TCCGT  TCTTG   CTGT  ATA
                                  __    ATA   TG
GAM1631  IMMP2L   3'  TTGGGTTTTGATTTTGGTGCTT 51710      AT        AGTTAT
                                AGGCA  GGAATCAAGAC
                                |||||  ||||||||||
                                TTCGT  TTTTAGTTTTG
                                   GG         GGTTG
GAM1631  ING1     3'  ATGGCAGTGATTCTGTTTGCCT 19855       _      AGACA
                                AGGCAA TGGAATCA    GTTAT
                                |||||| ||||||||    |||||
                                TCCGTT GTCTTAGT    CGGTA
                                   T      GA___
GAM1631  JMJ      3'  GTGGTTGTCCGGTTTCTATGGC 18324     A    TCAA    TT
              CT                   AGGC ATGGAA   GACAG  AT
                                |||| ||||||   |||||  ||
                                TCCG TATCTT   CTGTT  TG
                                  G    TGGC    GG
GAM1631  KCNS2    3'  GTAGCTTAAATACTTTTGTTGC 68850       TG   TCAAGAC
              CT                   AGGCAA  GAA      AGTTAT
                                ||||||  |||      ||||||
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                                TCCGTT  TTT      TCGATG
                                   GT   CATAAAT
GAM1631  LMAN1    3'  ATAACTGTTTAAACATTG    19927      GAATCA
                                CAATG     AGACAGTTAT
                                ||||||     ||||||||||
                                GTTAC     TTTGTCAATA
                                  AAA___
GAM1631  MBNL     3'  GTGATTGTTTTTTAATTGCT   41070       GGAATC
                                GGCAAT     AAGACAGTTAT
                                ||||||     ||||||||||
                                TCGTTA     TTTTGTTAGTG
                                  ATT___
GAM1631  MCCC2    3'  ATGATTGTTTTGCTGGTTATGC 42404       A   AAT_
              TT                  AGGCA TGG    CAAGACAGTTAT
                                ||||| |||    ||||||||||||
                                TTCGT ATT    GTTTTGTTAGTA
                                  _  GGTC
GAM1631  MEIS1    3'  ATGACTGTGGAGTTCCATTCTT 11532     C       CAAG
                                AGG AATGGAAT    ACAGTTAT
                                ||| ||||||||    ||||||||
                                TTC TTACCTTG    TGTCAGTA
                                  _       AGG_
GAM1631  MEIS2    3'  ATGACTGTTTTGGTTCATCAGT 39723     AATG
                                GC    GAATCAAGACAGTTAT
                                ||    ||||||||||||||||
                                TG    CTTGGTTTTGTCAGTA
                                 ACTA
GAM1631  MYO10    3'  GTGTTGACTCCATTGTTT    25614          A    G
                                AGGCAATGGA TCAA AC
                                |||||||||| |||| ||
                                TTTGTTACCT AGTT TG
                                      C    G
GAM1631  NPY1R    3'  ATGACTAAGATTTTCTTGTCT  8062        TG     AAGAC
                                AGGCAA  GAATC     AGTTAT
                                ||||||  |||||     ||||||
                                TCTGTT  TTTAG     TCAGTA
                                   CT     AA___
GAM1631  PACE4    3'  ATAACTGTTCTCATTTTATTGC 11946           CAA
              T                   GGCAATGGAAT   GACAGTTAT
                                ||||||||||   |||||||||
                                TCGTTATTTTA   TTGTCAATA
                                      CTC
GAM1631  PFN2     3'  GTATTTGCTTCTATTGTTT    54887           T   _
                                AGGCAATGGAA CAAG AC
                                |||||||||| |||| ||
                                TTTGTTATCTT GTTT TG
                                      C    A
GAM1631  PFN2     3'  GTATTTGCTTCTATTGTTT    54888           T   _
                                AGGCAATGGAA CAAG AC
                                |||||||||| |||| ||
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                                TTTGTTATCTT GTTT TG
                                      C    A
GAM1631  PKNOX1   3'  ATAACTGTAGGACTTCTGTTTC 17098     C      _ AAG
              CT                    AGG AATGGAA TC   ACAGTTAT
                                    ||| ||||||| ||   ||||||||
                                    TCC TTGTCTT AG   TGTCAATA
                                      T      C  GA_
GAM1631  POLB     3'  ATGATTGTTTCTTCTTCATGCT 12195      A    ATCA
              T                     AGGCA TGGA    AGACAGTTAT
                                    ||||| ||||    ||||||||||
                                    TTCGT ACTT    TTTGTTAGTA
                                      _   CTTC
GAM1631  RABL2A   3'  TAGGGTTTTGTTTTTATTGTTT 23999          T     AGTTAT
                                    AGGCAATGGAA CAAGAC
                                    |||||||||| ||||||
                                    TTTGTTATTTT GTTTTG
                                          T     GGATA
GAM1631  RABL2A   3'  TAGGGTTTTGTTTTTATTGTTT 24000          T     AGTTAT
                                    AGGCAATGGAA CAAGAC
                                    |||||||||| ||||||
                                    TTTGTTATTTT GTTTTG
                                          T     GGATA
GAM1631  RABL2B   3'  TAGGGTTTTGTTTTTATTGTTT 23987          T     AGTTAT
                                    AGGCAATGGAA CAAGAC
                                    |||||||||| ||||||
                                    TTTGTTATTTT GTTTTG
                                          T     GGATA
GAM1631  RELN     3'  GTGGTTGTTTTTTCATTGT    95957         TCA     TT
                                    GCAATGGAA   AGACAG  AT
                                    |||||||||   ||||||  ||
                                    TGTTACTTT   TTTGTT  TG
                                          ___     GG
GAM1631  RGS16    3'  GTGATTGTCATAACATTGTTT  12872         GA  CAA
                                    AGGCAATG  AT   GACAGTTAT
                                    ||||||||  ||   |||||||||
                                    TTTGTTAC  TA   CTGTTAGTG
                                         AA  ___
GAM1631  RNMT     3'  ATGGTTGTATAATATTTCATTG 15048          CAAG_   TT
              T                     GCAATGGAAT    ACAG  AT
                                    ||||||||||    ||||  ||
                                    TGTTACTTTA    TGTT  TA
                                          TAATA   GG
GAM1631  RORB     3'  AAACAAGCTTGATTTCAGTGCT 23584       A        ACA   AT
              T                     AGGCA TGGAATCAAG   GTT
                                    ||||| ||||||||||   |||
                                    TTCGT ACTTTAGTTC   CAA
                                      G         GAA   AG
GAM1631  RPIP8    3'  GTGATTGTCTGTGTGTCTGTCT 22929       ATG  ATCA_
                                    AGGCA   GA    AGACAGTTAT
                                    |||||   ||    ||||||||||
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                                TCTGT  CT    TCTGTTAGTG
                                   ___ GTGTG
GAM1631  SHANK2   3' CTGCCTTGGTTCCATTTCCT  25527    C        A
                                AGG AATGGAATCAAG CAG
                                ||| |||||||||||| |||
                                TCC TTACCTTGGTTC GTC
                                  T         C
GAM1631  SIGLEC6  3' ATGGCTGTCTCCTCCTTGTGTC 60604     AT_  ATCA
            T                    AGGCA  GGA   AGACAGTTAT
                                |||||  |||  ||||||||||
                                TCTGT  CCT   TCTGTCGGTA
                                   GTT  CC__
GAM1631  SLC6A6   3' GTGTCTGATTTGATTTTACTGT 13186     A       A  T
            TT                    AGGCA TGGAATCAAG CAG TAT
                                ||||| |||||||||| ||| |||
                                TTTGT ATTTTAGTTT GTC GTG
                                   C        A  T
GAM1631  SORCS3   3' TACTGTTCTTGGTTTTATTGTT 31073            _   TAT
                                GGCAATGGAATCAAGA CAGT
                                |||||||||||||||| ||||
                                TTGTTATTTTGGTTCT GTCA
                                         T   TA
GAM1631  SPINT2   3' TGTTGAATTCCATTGCCT   63853          CAA
                                AGGCAATGGAAT  GACA
                                ||||||||||||  ||||
                                TCCGTTACCTTA  TTGT
                                      AG_
GAM1631  SRRM1    3' TAGTGTCTTGGTTTCACTGTTT 20698     A         GTTAT
                                AGGCA TGGAATCAAGACA
                                ||||| ||||||||||||
                                TTTGT ACTTTGGTTCTGT
                                   C          GATA
GAM1631  STARD4   3' TGTTTGGTTTTATTCCT    58249    C       A
                                AGG AATGGAATCA GACA
                                ||| |||||||||| ||||
                                TCC TTATTTTGGT TTGT
                                  _       _
GAM1631  STAU     3' ATGATCATTTGGTTCCATT   17193          ACA
                                AATGGAATCAAG  GTTAT
                                ||||||||||||  |||||
                                TTACCTTGGTTT  TAGTA
                                      AC_
GAM1631  TARDBP   3' TGTTTGGTTCTTTTGTTT   24792      T     A
                                AGGCAA GGAATCA GACA
                                |||||| ||||||| ||||
                                TTTGTT TCTTGGT TTGT
                                   T     _
GAM1631  TEM7     3' ATGAGATGCTTGGTTCTATT  40245          A  G_
                                AATGGAATCAAG CA  TTAT
                                |||||||||||| ||  ||||
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                                TTATCTTGGTTC GT  AGTA
                                      _ AG
GAM1631 TES      3'  ATAATTGTATCTTTCCATAGCT 72459      A     TCAAG
          T                    AGGC ATGGAA     ACAGTTAT
                               |||| ||||||     ||||||||
                               TTCG TACCTT     TGTTAATA
                                 A     TCTA_
GAM1631 TGFBR2   3'  ATAGCTGTTGCCCATTGACCT  13727     _     AATCAA
                               AGG CAATGG      GACAGTTAT
                               ||| ||||||      |||||||||
                               TCC GTTACC      TTGTCGATA
                                 A     CG____
GAM1631 TMEM1    3'  GTAACTGTAATTGGATGTTTAT 13805          _   AAG__
          TGTTT                   AGGCAATGGA ATC     ACAGTTAT
                               |||||||||| |||     ||||||||
                               TTTGTTATTT TAG     TGTCAATG
                                     G   GTTAA
GAM1631 TMEPAI   3'  ATGGCTGTTGTGCTGATTCCAA 39824       A       A___
          TGCTT                   AGGCA TGGAATCA    GACAGTTAT
                               ||||| ||||||||    |||||||||
                               TTCGT ACCTTAGT    TTGTCGGTA
                                  A       CGTG
GAM1631 TNFRSF10B 3'  ATAATTGGGGGTTTTGTTGTTT 15216       TG     AAGA
                               AGGCAA  GAATC    CAGTTAT
                               ||||||  |||||    |||||||
                               TTTGTT  TTTGG    GTTAATA
                                  GT     GG__
GAM1631 TSG      3'  ATAACTGTTCTTACTGATTTTA 40602           ___   _
          TTGCC                   GGCAATGGAATCA   AGA CAGTTAT
                               ||||||||||||||   ||| |||||||
                               CCGTTATTTTAGT   TCT GTCAATA
                                     CAT   T
GAM1631 WHSC1L1   3'  GGACTGTTTTTGGTTTTTTGTT 35501       T        _    AT
          T                    AGGCAA GGAATCAAGA CAGTT
                               |||||| |||||||||| |||||
                               TTTGTT TTTTGGTTTT GTCAG
                                  _         T     GT
GAM1631 ZNF132    5'  GTCTCCCTTATTCTGTTGCTT  14287           CA___
                               AGGCAATGGAAT     AGAC
                               ||||||||||||     ||||
                               TTCGTTGTCTTA     TCTG
                                     TTCCC
GAM1631 AKAP5     5'  TTTTGGTTCTTGTTGTTT     17955        _
                               AGGCAATG GAATCAAGA
                               |||||||| |||||||||
                               TTTGTTGT CTTGGTTTT
                                    T
GAM1631 ARL8      3'  ATTTCTGCTTGGTTGTGTTGTT 94810         G      A   TT
          T                    AGGCAATG AATCAAG CAG  AT
                               |||||||| ||||||| |||  ||
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                                TTTGTTGT TTGGTTC GTC  TA
                                    G      _  TT
GAM1631  ATP9A    3'  TGACTTGAATTTTGTTGTC   62740      TG   _   A
                                GGCAA  GAAT CAAG CA
                                |||||  |||| |||| ||
                                CTGTT  TTTA GTTC GT
                                   GT   A   A
GAM1631  BRPF3    3'  ATGACTGTCTGAAACTTATTTT 93924     C    AATCA
           CT                    AGG AATGG    AGACAGTTAT
                                ||| |||||    ||||||||||
                                TCT TTATT    TCTGTCAGTA
                                  T    CAAAG
GAM1631  C13orf1   3'  GTAATTGTCAGAGCATTTTGTT 40367       TG   CAA__
           GCCT                   AGGCAA  GAAT    GACAGTTAT
                                ||||||  ||||    |||||||||
                                TCCGTT  TTTA    CTGTTAATG
                                   GT   CGAGA
GAM1631  C1orf22   3'  GTTGTTGGATTTTATTGTTT   48043          AA__
                                AGGCAATGGAATC   GAC
                                ||||||||||||   |||
                                TTTGTTATTTTAG   TTG
                                       GTTG
GAM1631  C1orf9    3'  ATAACTGTTTTTAAACTTGCCT 33158       TGGAATC
                                AGGCAA      AAGACAGTTAT
                                ||||||      ||||||||||
                                TCCGTT      TTTTGTCAATA
                                   CAAAT__
GAM1631  C20orf103 3'  GTGATTGTCTTGGGAATGTTT  25327      ATGGAA
                                AGGCA     TCAAGACAGTTAT
                                |||||     ||||||||||||
                                TTTGT     GGTTCTGTTAGTG
                                  AAG___
GAM1631  C21orf108 3'  TAATTGTCTTGCACTGTCT    90119      A  GAAT
                                AGGCA TG    CAAGACAGTTA
                                ||||| ||    ||||||||||
                                TCTGT AC    GTTCTGTTAAT
                                  C  ____
GAM1631  C2F       3'  TGCAGTTTGGTTCCATGCTT   22011      A        ACA  TAT
                                AGGCA TGGAATCAAG   GT
                                ||||| |||||||||   ||
                                TTCGT ACCTTGGTTT   CG
                                  _        GA_  TT
GAM1631  CCT5      3'  ATAGCTGTTTGGTAACCATAGT 73032      A   A_   A
           TT                    AGGC ATGG  ATCA GACAGTTAT
                                |||| ||||  |||| |||||||||
                                TTTG TACC  TGGT TTGTCGATA
                                  A   AA   _
GAM1631  CDC14B    3'  ATGATTGTTAAGCCATTTTTGC 14772       ___   AATCAA
           CT                    AGGCA   ATGG     GACAGTTAT
                                |||||   ||||     |||||||||
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                                TCCGT   TACC     TTGTTAGTA
                                  TTT    GAA___
GAM1631  CHERP    3'  GTAATTTCTTGTGGATTTCATT 22133           ___    C
                GTTT                AGGCAATGGAATC   AAGA AGTTAT
                                    ||||||||||||   |||| ||||||
                                    TTTGTTACTTTAG   TTCT TTAATG
                                       GTG   _
GAM1631  CHSY1    3'  ATAGCTGTTTCATCATTGTCT  30563         AATCA
                                    AGGCAATGG    AGACAGTTAT
                                    |||||||||    ||||||||||
                                    TCTGTTACT    TTTGTCGATA
                                       AC___
GAM1631  CTPS2    3'  ATGGCTGAATAAAATTCCATTG 39565          CAAGA_
                T                    GCAATGGAAT     CAGTTAT
                                    ||||||||||     |||||||
                                    TGTTACCTTA     GTCGGTA
                                       AAATAA
GAM1631  DKFZp434A2417 3'  GTGATGATTACATTGCTT    66682        G    AG
                                    AGGCAATG AATCA  AC
                                    |||||||| |||||  ||
                                    TTCGTTAC TTAGT  TG
                                       A    AG
GAM1631  DKFZP434P0721 3'  ATAACTGTTTATAGTGGTTGTC 64456        GGAATCA
                T                    AGGCAAT      AGACAGTTAT
                                    |||||||      ||||||||||
                                    TCTGTTG      TTTGTCAATA
                                       GTGATA_
GAM1631  DKFZP564O1863 3'  TGGATTTGTTTCTGTTGTCT   69144          T   A_
                                    AGGCAATGGAA CAAG  CA
                                    |||||||||| ||||  ||
                                    TCTGTTGTCTT GTTT  GT
                                       T   AG
GAM1631  DKFZP586I2223 5'  GTGACTGTCCGTGTTTCTGTTC 55771     C      T  A_
                CT                   AGG AATGGAA CA  GACAGTTAT
                                    ||| ||||||| ||  |||||||||
                                    TCC TTGTCTT GT  CTGTCAGTG
                                      _      T  GC
GAM1631  DKFZp761J139 5'  ATGTCTCTTTAGTTTTGTTGTT 51101       TG   CA___    GTTAT
                T                    AGGCAA  GAAT    AGACA
                                    ||||||  ||||    |||||
                                    TTTGTT  TTTG    TCTGT
                                       GT   ATTTC    A
GAM1631  DKFZp762L0311 3'  GTCTGTTTGGTTTCTTGTCT   38673       T     A    TTAT
                                    AGGCAA GGAATCA GACAG
                                    |||||| ||||||| |||||
                                    TCTGTT CTTTGGT TTGTC
                                       _      _    TGG
GAM1631  DMTF1    5'  GTAGCTGATCCATCCGTTGTCT 41245          ATCAA  _
                                    AGGCAATGGA    GA CAGTTAT
                                    ||||||||||    || |||||||
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                                TCTGTTGCCT    CT GTCGATG
                                      AC___  A
GAM1631  ESDN     3'  TGACTGTTTTTTTTTGTT    56064    TG   TC
                                AA  GAA  AAGACAGTTA
                                ||  |||  ||||||||||
                                TT  TTT  TTTTGTCAGT
                                 GT   T_
GAM1631  FBXO9    5'  GTGACTGTTGAGAAATTTCACT 54253       A    __  AA
              GTTT                  AGGCA TGGAA  TC  GACAGTTAT
                                |||||  |||||  ||  |||||||||
                                TTTGT ACTTT  AG  TTGTCAGTG
                                   C    AA  AG
GAM1631  FEM-2    3'  ATGACTGTCTTCCCTATTCTT  28309     C    AATC
                                AGG AATGG    AAGACAGTTAT
                                ||| |||||    ||||||||||
                                TTC TTATC    TTCTGTCAGTA
                                  _    CC__
GAM1631  FIGN     3'  ATGACTGCCTTTTTATTGC    36575         TCA  A
                                GCAATGGAA   AG CAGTTAT
                                |||||||||   || |||||||
                                CGTTATTTT   TC GTCAGTA
                                      ___  C
GAM1631  FLJ10715 3'  ATAATTGTCATGTTTTGTTGCT 37014       TG   T  A
                                GGCAA  GAA CA GACAGTTAT
                                |||||  ||| || |||||||||
                                TCGTT  TTT GT CTGTTAATA
                                   GT   _  A
GAM1631  FLJ10933 3'  GTAGCAGATCTGTTTCTATTGT 37435          TCA   CA_
              TT                   AGGCAATGGAA   AGA   GTTAT
                                ||||||||||   |||   |||||
                                TTTGTTATCTT   TCT   CGATG
                                      TG_   AGA
GAM1631  FLJ10961 3'  ATAATTGTCTTGCCATTACTT  64222     C    AAT
                                AGG AATGG   CAAGACAGTTAT
                                ||| |||||   ||||||||||||
                                TTC TTACC   GTTCTGTTAATA
                                  A    ____
GAM1631  FLJ10983 3'  GTAATTGTTTTAATGTGTGCTT 37488       ATGGA  C
                                AGGCA     AT AAGACAGTTAT
                                |||||     || ||||||||||||
                                TTCGT     TA TTTTGTTAATG
                                   GTG__  A
GAM1631  FLJ13352 3'  GTGATGGTTTCAATGCCT    45056       A       AG
                                AGGCA TGGAATCA  AC
                                ||||| ||||||||  ||
                                TCCGT ACTTTGGT  TG
                                   A       AG
GAM1631  FLJ13456 3'  TAACTGTTATTGGTGCCT    66561       ATGGAA   _
                                AGGCA     TCAA GACAGTTA
                                |||||     |||| ||||||||
```

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                                TCCGT     GGTT TTGTCAAT
                                  _______   A
GAM1631  FLJ14166  3'  GTGGCTGTCTTGCCTTTGTTT  44991       T  AAT
                                AGGCAA GG   CAAGACAGTTAT
                                |||||| ||   ||||||||||||
                                TTTGTT CC   GTTCTGTCGGTG
                                   T  ___
GAM1631  FLJ14642  3'  TAGCTAGGTTCCATGTCT    52581       A      AAGAC
                                AGGCA TGGAATC     AGTTA
                                ||||| |||||||     |||||
                                TCTGT ACCTTGG     TCGAT
                                  _      A____
GAM1631  FLJ20081  3'  ATGATGCTAATTGATTTTATGC 34987       A       GACA_
           TT                    AGGCA TGGAATCAA     GTTAT
                                ||||| |||||||||     |||||
                                TTCGT ATTTTAGTT     TAGTA
                                  _       AATCG
GAM1631  FLJ20296  3'  ATAAATTTATTGATTCCATTGC 35363             GACAG
           TT                    AGGCAATGGAATCAA     TTAT
                                ||||||||||||||     ||||
                                TTCGTTACCTTAGTT     AATA
                                       ATTTA
GAM1631  FLJ20298  3'  ATGACTGTTTTGGTTCTAGCTT 35376      AA
                                AGGC  TGGAATCAAGACAGTTAT
                                ||||  ||||||||||||||||||
                                TTCG  ATCTTGGTTTTGTCAGTA
                                  __
GAM1631  FLJ20445  3'  TGATTTGTTTTCATTGTTT    35634          T    A
                                AGGCAATGGAA CAAG CA
                                |||||||||| |||| ||
                                TTTGTTACTTT GTTT GT
                                      T    A
GAM1631  FLJ20502  3'  ATAACTCAGGAGATTCCATGTC 35716       A      AAGAC
           T                     AGGCA TGGAATC     AGTTAT
                                ||||| |||||||     ||||||
                                TCTGT ACCTTAG     TCAATA
                                  _       AGGAC
GAM1631  FLJ20958  3'  GTAGCTCTGGGATTTTATCGCC 42310      A       A_   CA
           T                     AGGC ATGGAATC  AGA  GTTAT
                                |||| ||||||||  |||  |||||
                                TCCG TATTTTAG  TCT  CGATG
                                  C       GG  __
GAM1631  FLJ21791  3'  ATAATTGCTAAGATTTTGTTGG 62123    G   TG    A_  A
           TT                    AG CAA  GAATC  AG CAGTTAT
                                || |||  |||||  || |||||||
                                TT GTT  TTTAG  TC GTTAATA
                                 G   GT    AA  _
GAM1631  FLJ21934  3'  ATGACTGTTTTGATGATGTC   45695      ATGGA
                                GGCA     ATCAAGACAGTTAT
                                ||||     ||||||||||||||
```

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                                CTGT    TAGTTTTGTCAGTA
                                  AG___
GAM1631  FLJ22054  3'  TGCTTTGATTCCTTGTCT    96055       T      GA
                                AGGCAA GGAATCAA  CA
                                |||||| ||||||||  ||
                                TCTGTT CCTTAGTT  GT
                                   _       TC
GAM1631  FLJ22282  3'  ATAACCCATTGGTTCTTTGCCT 45963       T      GACA
                                AGGCAA GGAATCAA   GTTAT
                                |||||| ||||||||   |||||
                                TCCGTT TCTTGGTT   CAATA
                                   _       ACC_
GAM1631  FLJ22875  3'  GTAATTGTTTGATATATTTGTT 50912       TGGA   A
           T                     AGGCAA    ATCA GACAGTTAT
                                ||||||    |||| |||||||||
                                TTTGTT    TAGT TTGTTAATG
                                   TATA   _
GAM1631  FLJ23045  3'  ATGACTGTAGTCTTCCATGCTT 45551      A    TCAAG
                                AGGCA TGGAA    ACAGTTAT
                                ||||| |||||    ||||||||
                                TTCGT ACCTT    TGTCAGTA
                                   _    CTGA_
GAM1631  FLJ23309  3'  ATGACTGTTTTCATATTGCCT  46589       GAATC
                                AGGCAATG    AAGACAGTTAT
                                ||||||||    ||||||||||
                                TCCGTTAT    TTTTGTCAGTA
                                    AC___
GAM1631  FLJ25442  3'  GTGACTGTTCTAAATCCAGTGT 59498      A   ATCAA
           TT                    AGGCA TGGA    GACAGTTAT
                                ||||| ||||    |||||||||
                                TTTGT ACCT    TTGTCAGTG
                                   G   AAATC
GAM1631  FLJ30574  3'  ATAATTGTTAAAATCATTGCC  58894       AATCAA
                                GGCAATGG     GACAGTTAT
                                ||||||||     |||||||||
                                CCGTTACT     TTGTTAATA
                                    AAAA__
GAM1631  FLJ30678  3'  TAACTGCATTCTGTTGCC    58983         CAAGA
                                GGCAATGGAAT    CAGTTA
                                ||||||||||    ||||||
                                CCGTTGTCTTA    GTCAAT
                                      C_____
GAM1631  GABARAP   3'  GTGATTGTTTTGGTTTCTGTTC 24409    C     _
           C                     GG AATGGAA TCAAGACAGTTAT
                                || ||||||| ||||||||||||
                                CC TTGTCTT GGTTTTGTTAGTG
                                  _      T
GAM1631  GK001     3'  TGGCTGTGTGCCGTTGCTT   39884        AAT  AG
                                AGGCAATGG   CA  ACAGTTA
                                |||||||||   ||  |||||||
```

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                                TTCGTTGCC  GT  TGTCGGT
                                    ___ G_
GAM1631  GMFB     3'  AAATTGTATTTTATTGCTT   15937          CAAG     AT
                                AGGCAATGGAAT   ACAGTT
                                ||||||||||||  ||||||
                                TTCGTTATTTTA   TGTTAA
                                    _____     AG
GAM1631  GORASP2  3'  TAACTGCTGCTGTTGCTT    32035         AATCA  A
                                AGGCAATGG    AG CAGTTA
                                |||||||||    || ||||||
                                TTCGTTGTC    TC GTCAAT
                                   G_____ _
GAM1631  HDAC9-PENDING 3'  TGAATTGATTTATTGTCT    28843         G     GA
                                AGGCAATG AATCAA  CA
                                |||||||| ||||||  ||
                                TCTGTTAT TTAGTT  GT
                                    _     AA
GAM1631  HSH2     3'  CTGTTTGTTCTGTTGTCT    52740           CA
                                AGGCAATGGAAT  AGACAG
                                ||||||||||||  ||||||
                                TCTGTTGTCTTG  TTTGTC
                                    __
GAM1631  HSPC152  3'  ATGACTGTGTATTTTTGTTGAT 96154     _  TG   TCAAG
           CT                    AGG CAA  GAA    ACAGTTAT
                                ||| |||  |||    ||||||||
                                TCT GTT  TTT    TGTCAGTA
                                  A  GT   TATG_
GAM1631  IBTK     3'  AGTTGTGTCACCATTCTTGTTG 68098         _   CAA   GTTAT
           CTT                    AGGCAATG GAAT   GACA
                                ||||||||| ||||  ||||
                                TTCGTTGT CTTA   CTGT
                                    T   CCA    GTTGAT
GAM1631  KCNMB2   3'  TAACTGTTTTGTGTTGGTT   20689     G  AT
                                AAT GA  CAAGACAGTTA
                                ||| ||  ||||||||||||
                                TTG TT  GTTTTGTCAAT
                                  G  GT
GAM1631  KIAA0040 3'  GTGGCTGTCTCACCCTTGCTT  28493       T  AATCA
                                AGGCAA GG    AGACAGTTAT
                                |||||| ||    ||||||||||
                                TTCGTT CC    TCTGTCGGTG
                                   C  AC___
GAM1631  KIAA0090 3'  ATAATTGTAATTTCACTGCCT  89811       A     CAAG
                                AGGCA TGGAAT    ACAGTTAT
                                ||||| ||||||    ||||||||
                                TCCGT ACTTTA    TGTTAATA
                                   C     A___
GAM1631  KIAA0261 3'  GTGGCTGCCTTCTATTGTCT   68744          ATCA  A
                                AGGCAATGGA    AG CAGTTAT
                                ||||||||||    || |||||||
```

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                                TCTGTTATCT    TC GTCGGTG
                                      ____  C
GAM1631  KIAA0275  3'  GTAGCTGTTTTCTTTCCTTTTG 29331      T_   TC
              TT                   GGCAA  GGAA  AAGACAGTTAT
                                   |||||  ||||  ||||||||||
                                   TTGTT  CCTT  TTTTGTCGATG
                                     TT    TC
GAM1631  KIAA0280  3'  ATCTGGTTTTGTTTTGTTGTTT 93288      TG   T     AGTTAT
                                   AGGCAA  GAA CAAGAC
                                   ||||||  ||| ||||||
                                   TTTGTT  TTT GTTTTG
                                      GT   _     GTCTAA
GAM1631  KIAA0352  3'  GTTCATTTGATTTTGTTGCT   29827      TG      ___
                                   GGCAA  GAATCAA   GAC
                                   |||||  |||||||   |||
                                   TCGTT  TTTAGTT   TTG
                                     GT      TAC
GAM1631  KIAA0410  3'  ATGACTGTACCATTTATTGTTT 29422          ATCAAG
                                   AGGCAATGGA     ACAGTTAT
                                   ||||||||||     ||||||||
                                   TTTGTTATTT     TGTCAGTA
                                        ACCA__
GAM1631  KIAA0431  3'  TGACTTATTGTATTGCCT    31555        G   C   A
                                   AGGCAATG AAT AAG CA
                                   ||||||| ||| ||| ||
                                   TCCGTTAT TTA TTC GT
                                      G   _   A
GAM1631  KIAA0438  3'  ATAGCTGTTGTACTTTTTGCTT 29730       TGGAATCAA
                                   AGGCAA        GACAGTTAT
                                   ||||||        |||||||||
                                   TTCGTT        TTGTCGATA
                                     TTTCATG__
GAM1631  KIAA0459  3'  ATGGTTGTCTTGGTTTTCA    61644       _        TT
                                   TGGAA TCAAGACAG  AT
                                   |||||  |||||||||  ||
                                   ACTTT GGTTCTGTT  TA
                                     T        GG
GAM1631  KIAA0530  3'  TGGATGTTTTGATTTTACTGTT 71432       A           GTTAT
              T                     AGGCA TGGAATCAAGACA
                                   |||||  ||||||||||||||
                                   TTTGT ATTTTAGTTTTGT
                                     C            AGGTT
GAM1631  KIAA0601  3'  TGATTGTTGGCCGATGCCT    63173       A   AATCAA
                                   AGGCA TGG     GACAGTTA
                                   |||||  |||     ||||||||
                                   TCCGT GCC     TTGTTAGT
                                     A   GG_____
GAM1631  KIAA0618  3'  TGACTGGTCTTTATTGCCT    29861         GAATC    _
                                   AGGCAATG    AAGAC AGTTA
                                   ||||||||    ||||| |||||
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                                TCCGTTAT    TTCTG TCAGT
                                   _____    G
GAM1631  KIAA0620  3'  GTAGTGTCAGATTTTTGTTGCT 62814      TG   TCAA   G
              T                  AGGCAA  GAA   GACA TTAT
                                 ||||||  |||   |||| ||||
                                 TTCGTT  TTT   CTGT GATG
                                    GT   TAGA   _
GAM1631  KIAA0663  3'  GTCCATTTGATGCCATTGTTT  29789        A   ___
                                 AGGCAATGG ATCAA   GAC
                                 |||||||||| |||||   |||
                                 TTTGTTACC TAGTT   CTG
                                      G    TAC
GAM1631  KIAA0757  3'  TTGTTTTGTTTTGTTGTTT   21261      TG   T
                                 AGGCAA  GAA CAAGACAG
                                 ||||||  ||| ||||||||
                                 TTTGTT  TTT GTTTTGTT
                                    GT   _
GAM1631  KIAA0779  3'  GTGGTTGTTCTTGGGTTCTTTT 86910      T    _   _  TT
              GTCT                  AGGCAA GGAATC AAGA CAG  AT
                                 ||||||  |||||| |||| |||  ||
                                 TCTGTT TCTTGG TTCT GTT  TG
                                    T     G   T  GG
GAM1631  KIAA0820  3'  ATGACAGTAATTCTGTTGTCT  69588          CAAG  A
                                 AGGCAATGGAAT    AC GTTAT
                                 ||||||||||||    || |||||
                                 TCTGTTGTCTTA    TG CAGTA
                                       A___  A
GAM1631  KIAA0877  3'  ATAATTGTTGTGACTCTATGTT 62482      A   A  A
              T                  AGGCA TGGA TCA GACAGTTAT
                                 |||||  |||| ||| |||||||||
                                 TTTGT ATCT AGT TTGTTAATA
                                    _   C  G
GAM1631  KIAA0923  3'  ATGATTGTTTGCTAGATTTTGT 26706    C  TG    A___
              TTTCT                 AGG AA  GAATC    AGACAGTTAT
                                 |||  ||  |||||   ||||||||||
                                 TCT TT  TTTAG    TTTGTTAGTA
                                   T  GT    ATCG
GAM1631  KIAA0971  3'  ATAACTGTTCTTGTTTTGTT  30668    TG   T    _
                                 AA  GAA CAAGA CAGTTAT
                                 ||  ||| ||||| |||||||
                                 TT  TTT GTTCT GTCAATA
                                  GT   _    T
GAM1631  KIAA0978  3'  TGACCTTGGTTCTGTTGCT   70999           ACA   T
                                 GGCAATGGAATCAAG   GTTA
                                 ||||||||||||||   ||||
                                 TCGTTGTCTTGGTTC   CAGT
                                       ___
GAM1631  KIAA1033  3'  TAACTAGTTTACATTGCTT   65131        GAATCAA  _
                                 AGGCAATG      GAC AGTTA
                                 ||||||||      ||| |||||
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                                TTCGTTAC      TTG TCAAT
                                    AT_____   A
GAM1631  KIAA1041  3'  GTGGCCTGCTGTTTCTGTTGTC 30826          TCA  A  _
              T                  AGGCAATGGAA   AG CAG TTAT
                                 ||||||||||   || ||| ||||
                                 TCTGTTGTCTT   TC GTC GGTG
                                     TG_ _   C
GAM1631  KIAA1041  3'  TATAGCTGTTTTGAAACTGTTT 30831        G  _______
              TAATTGCTT              AGGCAAT GAA     TCAAGACAGTTAT   A
                                 |||||||  |||     ||||||||||||||   |
                                 TTCGTTA TTT     AGTTTTGTCGATA   T
                                    A   TGTCAA
GAM1631  KIAA1145  3'  ATGGCTGTCTCTCCTTTCATTG 66231          TCA_
              TC                   GGCAATGGAA    AGACAGTTAT
                                 ||||||||||    ||||||||||
                                 CTGTTACTTT    TCTGTCGGTA
                                     CCTC
GAM1631  KIAA1254  3'  ATAATGAGACTGATTCTGGTGT 70554      AT      AGACA
              CT                   AGGCA  GGAATCA    GTTAT
                                 |||||  |||||||    |||||
                                 TCTGT  TCTTAGT    TAATA
                                   GG      CAGAG
GAM1631  KIAA1432  3'  TGGCTAGATTTAGTTGTCT    67310        G    A  A
                                 AGGCAAT GAATC AG CA
                                 |||||||  |||||  ||  ||
                                 TCTGTTG TTTAG TC GT
                                    A    A  G
GAM1631  KIAA1706  3'  GTTGTTGTTTTGTATTTTGTTG 94369       TG   _      TT
              TTT                   AGGCAA  GAAT CAAGACAG  AT
                                 ||||||  ||||  ||||||||  ||
                                 TTTGTT  TTTA GTTTTGTT  TG
                                    GT    T      GT
GAM1631  KIAA1726  3'  GTAACTAGCCAGTCTGTTGTCT 67832          ATCAAGAC
                                 AGGCAATGGA       AGTTAT
                                 ||||||||||       ||||||
                                 TCTGTTGTCT       TCAATG
                                     GACCGA__
GAM1631  KIAA1795  5'  AAACTGTTTATTCTGTTGCTT  72612          CA       AT
                                 AGGCAATGGAAT  AGACAGTT
                                 ||||||||||||  ||||||||
                                 TTCGTTGTCTTA  TTTGTCAA
                                      __       AA
GAM1631  KIAA1944  3'  TGATTGTGAGTCATTGTCT    76083         AA  AAG
                                 AGGCAATGG  TC   ACAGTTA
                                 |||||||||  ||   |||||||
                                 TCTGTTACT  AG   TGTTAGT
                                     G_ ____
GAM1631  KIAA1954  3'  TAGCAGGATTCATTGCCT     78230         G    AAGACA
                                 AGGCAATG AATC     GTTA
                                 ||||||||  ||||     ||||
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                                TCCGTTAC TTAG     CGAT
                                    _   GA____
GAM1631  KIAA1966  3'  GTAGCGTGGTTGATGCTATTGT 56726        A    GA  _
             TT                   AGGCAATGG ATCAA  CA GTTAT
                                  ||||||||| |||||  || |||||
                                  TTTGTTATC TAGTT  GT CGATG
                                      G    G_  G
GAM1631  KRTHB5    3'  ATGACTGTCTATGGGTGCATTG 11247        GAA  _
             CCT                    AGGCAATG   TCA AGACAGTTAT
                                  ||||||||   ||| ||||||||||
                                  TCCGTTAC   GGT TCTGTCAGTA
                                      GTG   A
GAM1631  LANCL2    3'  ATGTTTCTTGGTGTTTGTTGTC 38617       TG  _      CAGTTAT
             T                    AGGCAA  GA ATCAAGA
                                  ||||||  || |||||||
                                  TCTGTT  TT TGGTTCT
                                     GT  G      TTGTA
GAM1631  LIM      3'  GTGATTGTTTCTGTTCATTGT  22333        ATCA
                                  GCAATGGA    AGACAGTTAT
                                  ||||||||    ||||||||||
                                  TGTTACTT    TTTGTTAGTG
                                      GTC_
GAM1631  MGC11242  3'  TGACTGTTTCTCATGCCT    44485      AT   ATCAA
                                  AGGCA  GGA    GACAGTTA
                                  |||||  |||    ||||||||
                                  TCCGT  TCT    TTGTCAGT
                                    AC  ______
GAM1631  MGC11324  3'  TTGTTTTGTTTTATTGTTT    52151          T
                                  AGGCAATGGAA CAAGACAG
                                  |||||||||||| ||||||||
                                  TTTGTTATTTT GTTTTGTT
                                             _
GAM1631  MGC5457   5'  GTCTTTTTGGTTTCACTGCCT  51942       A      ___
                                  AGGCA TGGAATCA   AGAC
                                  ||||| ||||||||   ||||
                                  TCCGT ACTTTGGT   TCTG
                                    C       TTT
GAM1631  MGC5590   3'  TGGCTACATTCCATTCCT    44150     C       CAAGAC
                                  AGG AATGGAAT     AGTTA
                                  ||| ||||||||     |||||
                                  TCC TTACCTTA     TCGGT
                                    _       CA____
GAM1631  MORF4     3'  GTAGAGTGTTTTATTGCCT    92471          T  AG__
                                  AGGCAATGGAA CA    AC
                                  |||||||||||| ||    ||
                                  TCCGTTATTTT GT    TG
                                         _ GAGA
GAM1631  MRG15     3'  GTAGAGTGTTTTATTGCCT    23286          T  AG__
                                  AGGCAATGGAA CA    AC
                                  |||||||||||| ||    ||
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                                TCCGTTATTTT GT    TG
                                      _ GAGA
GAM1631 MRPS35   3' TAAAGTGTTTTGATTTTATTTC 41821     C           G  AT
           T                   AGG AATGGAATCAAGACA TT
                               ||| |||||||||||||| ||
                               TCT TTATTTTAGTTTTGT AA
                                _           G  ATC
GAM1631 NIP30    3' GTTTGGGTTTTATTGCTT    46899           A
                               AGGCAATGGAATC AGAC
                               |||||||||||| ||||
                               TTCGTTATTTTGG TTTG
                                      G
GAM1631 NR4A3    3' GTAACTGTTTTGGTTGTGTTCT 23721    C   G
                               GG AATG AATCAAGACAGTTAT
                               || |||| ||||||||||||||
                               TC TTGT TTGGTTTTGTCAATG
                                _   G
GAM1631 OSR2     3' GTCTTTGTTTTGTTGTTT    54857       TG   C
                               AGGCAA  GAAT AAGAC
                               ||||||  |||| |||||
                               TTTGTT  TTTG TTCTG
                                  GT   T
GAM1631 PCDH10   3' GTCTGATTCTATTTCT     53102     C       A
                               AGG AATGGAATCA GAC
                               ||| |||||||||| |||
                               TCT TTATCTTAGT CTG
                                _       _
GAM1631 PDE1C    3' ATGACTGTCAATGCCGTTACTT 18462     C    AATCAA
                               AGG AATGG     GACAGTTAT
                               ||| |||||     |||||||||
                               TTC TTGCC     CTGTCAGTA
                                 A    GTAA__
GAM1631 PDGFC    3' GTGATGTTGTGGTTTTATTATC 33022    GC       A   G
           T                   AG  AATGGAATCA GACA TTAT
                               ||  |||||||||| |||| ||||
                               TC  TTATTTTGGT TTGT AGTG
                                TA        G   _
GAM1631 POLD3    3' TGGCTTGTGTTCTGTTCCT   93315     C      _   A
                               AGG AATGGAAT CAAG CA
                               ||| |||||||| |||| ||
                               TCC TTGTCTTG GTTC GT
                                _       T   G
GAM1631 PRO1489  3' ATAACTGTTACCGCCGTTCTT  38331     C    AATCAA
                               AGG AATGG     GACAGTTAT
                               ||| |||||     |||||||||
                               TTC TTGCC     TTGTCAATA
                                 _    GCCA__
GAM1631 PRO1600  3' GTCAGATTCTATTCTCT     26879     C       AA
                               AGG AATGGAATC  GAC
                               ||| |||||||||  |||
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                                TCT TTATCTTAG  CTG
                                  C       A_
GAM1631  RAP140   5'  ATGACTGTTAATTTCTTTGCCT 31508      T    CAA
                                AGGCAA GGAAT   GACAGTTAT
                                |||||| |||||   |||||||||
                                TCCGTT CTTTA   TTGTCAGTA
                                   T    A__
GAM1631  SAMSN1   5'  ATGACACGTTGATTTCTTGTTT 42410      T      GACA
                                AGGCAA GGAATCAA   GTTAT
                                |||||| ||||||||   |||||
                                TTTGTT CTTTAGTT   CAGTA
                                   _      GCA_
GAM1631  SCYA20   3'  ATAGCTGTAGGTTTTCTGTGTT 17179      A    TCAAG
            T                    AGGCA TGGAA    ACAGTTAT
                                |||||| |||||    |||||||||
                                TTTGT GTCTT    TGTCGATA
                                  _    TTGGA
GAM1631  SCYA28   3'  ATAGTTGTTTGGCTATTGCTT  39537        AATCA    GT
                                AGGCAATGG    AGACA  TAT
                                |||||||||    |||||  |||
                                TTCGTTATC    TTTGT  ATA
                                     GG___    TG
GAM1631  SDFR1    3'  ATGACTGTCTAAAGCATGCCT  25790      A  GAATCA
                                AGGCA TG     AGACAGTTAT
                                ||||| ||     ||||||||||
                                TCCGT AC     TCTGTCAGTA
                                  _ GAAA__
GAM1631  SLC6A14  3'  CAGAGTCTTGTTCTGTTGCCT  24305          T    AGTTAT
                                AGGCAATGGAA CAAGAC
                                |||||||||||| ||||||
                                TCCGTTGTCTT GTTCTG
                                     _     AGACT
GAM1631  SLK      3'  ATGGTTGTTTTGGAATTTTTGC 28889       TGGAA       TT
            TT                   AGGCAA    TCAAGACAG  AT
                                ||||||    |||||||||  ||
                                TTCGTT    GGTTTTGTT  TA
                                   TTTAA       GG
GAM1631  SPINLW1  3'  TTGGTTTGATTCCATGTTT   40234      A       A
                                AGGCA TGGAATCAAG CAG
                                ||||| |||||||||| |||
                                TTTGT ACCTTAGTTT GTT
                                  _        G
GAM1631  SPRY1    3'  GTGGCTGTTTTTTGTTTTTGTT 65634       T  ATC
            T                    AGGCAA GGA   AAGACAGTTAT
                                |||||| |||   ||||||||||||
                                TTTGTT TTT   TTTTGTCGGTG
                                  _  GTT
GAM1631  SPS      3'  ATAGCTGTTTGGTTTTGTT   25309    TG    A
                                AA  GAATCA GACAGTTAT
                                ||  |||||| |||||||||
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                                TT  TTTGGT TTGTCGATA
                                 GT     _
GAM1631  SYT6     3'  GTGGTTGTGAGGGTTTCTTGTT 79523       T     AAG    TT
                T                 AGGCAA GGAATC   ACAG  AT
                                  |||||| ||||||   ||||  ||
                                  TTTGTT CTTTGG   TGTT  TG
                                     _     GAG    GG
GAM1631  TMSNB    3'  ATGATGGGTGCTTCCATTGCTT 42076          T  AGACA
                                  AGGCAATGGAA CA     GTTAT
                                  |||||||||||| ||     ||||||
                                  TTCGTTACCTT GT     TAGTA
                                        C  GGG__
GAM1631  TOMM70A  3'  ATAATTGTCTGTGACTATTTTC 29734     C     AA   _
                T                 AGG AATGG  TCA AGACAGTTAT
                                  ||| |||||  ||| ||||||||||
                                  TCT TTATC  AGT TCTGTTAATA
                                   T    __  G
GAM1631  TPD52    3'  GTGATTGTTTTATTATTGTTT  18672         AATC
                                  AGGCAATGG    AAGACAGTTAT
                                  |||||||||    ||||||||||
                                  TTTGTTATT    TTTTGTTAGTG
                                       A___
GAM1631  TRIM4    3'  TTTCAGGTTTTGATTTTGTTAC 53410     C  TG        AGTTAT
                TT                  AGG AA  GAATCAAGAC
                                  ||| ||  ||||||||||
                                  TTC TT  TTTAGTTTTG
                                    A  GT        GACTTTG
GAM1631  UBE2G1   3'  ATAATTGTCAAGTTGTTGGCT  13951    G   TG AATCAA
                                  AG CAA  G     GACAGTTAT
                                  || |||  |     |||||||||
                                  TC GTT  T     CTGTTAATA
                                   G   GT GAA___
GAM1631  USP10    3'  GTGATTGTAACTTTATTGCC   64649         ATCAAG
                                  GGCAATGGA     ACAGTTAT
                                  |||||||||     ||||||||
                                  CCGTTATTT     TGTTAGTG
                                       CAA___
GAM1631  ZFP      3'  TAACTGTGGTTAATTGCCT    38472        GG    AAG
                                  AGGCAAT  AATC   ACAGTTA
                                  |||||||  ||||   |||||||
                                  TCCGTTA  TTGG   TGTCAAT
                                     A_   ___
GAM1631  ZNF347   3'  ATAAAATCTTTTATTCCATTGT 51819           C_   CAG
                TT                  AGGCAATGGAAT  AAGA   TTAT
                                  ||||||||||||  ||||   ||||
                                  TTTGTTACCTTA  TTCT   AATA
                                        TT    AA_
GAM1631  LOC120105 3'  GTAATTGTCACTTCTGTTG    76029         TCAA
                                  CAATGGAA    GACAGTTAT
                                  ||||||||    |||||||||
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                                GTTGTCTT   CTGTTAATG
                                    CA__
GAM1631  LOC120196 3'  GTAGCTGTTGTTATTTTAATGC 76060      A     CAA
             TT                   AGGCA TGGAAT   GACAGTTAT
                                  ||||| ||||||   |||||||||
                                  TTCGT ATTTTA   TTGTCGATG
                                    A     TTG
GAM1631  LOC122786 3'  ATGACTGTTTTCTCATGTGCCT 74620      ATG  ATC
                                  AGGCA   GA   AAGACAGTTAT
                                  |||||   ||   ||||||||||
                                  TCCGT   CT   TTTTGTCAGTA
                                    GTA  C__
GAM1631  LOC133688 3'  ATGATTGTACCTTTTTATTTGC 75603       _    TCAAG
             TT                   AGGCAA TGGAA     ACAGTTAT
                                  |||||| |||||     ||||||||
                                  TTCGTT ATTTT     TGTTAGTA
                                    T    TCCA_
GAM1631  LOC139065 5'  ATGACAATCTGATTTCATTCCT 76323     C        A  CA
                                  AGG AATGGAATCA GA  GTTAT
                                  ||| ||||||||| ||  |||||
                                  TCC TTACTTTAGT CT  CAGTA
                                    _        _ AA
GAM1631  LOC144512 5'  GTAACTGTTCTGCCATTTTCT  84040     C    AAT  AG
                                  AGG AATGG   CA  ACAGTTAT
                                  ||| |||||   ||  ||||||||
                                  TCT TTACC   GT  TGTCAATG
                                    T    ____ CT
GAM1631  LOC144512 3'  TGTCACTTGATTCCATTCTCT  84042     C         __
                                  AGG AATGGAATCAA  GACA
                                  ||| ||||||||||  ||||
                                  TCT TTACCTTAGTT  CTGT
                                    C         CA
GAM1631  LOC145231 3'  TGACTTAGTGTCATTGCCT    84261        GA  C   A
                                  AGGCAATG  AT AAG CA
                                  ||||||||  || ||| ||
                                  TCCGTTAC  TG TTC GT
                                       TG  A   A
GAM1631  LOC145773 3'  TAACTGTATTTTTGTGCCT    77963     A TG   TCAAG
                                  AGGC A  GAA     ACAGTTA
                                  |||| |  |||     |||||||
                                  TCCG T  TTT     TGTCAAT
                                    _ GT   TA____
GAM1631  LOC145824 5'  ATGATTGTTGTTGTCATCGTCT 77982      A    AATCAA
                                  AGGC ATGG      GACAGTTAT
                                  |||| ||||      |||||||||
                                  TCTG TACT      TTGTTAGTA
                                    C    GTTG__
GAM1631  LOC145842 5'  ATAACTGGAGAAATTTTGTTAC 77992     C  TG    CAAGA
             CT                   AGG AA  GAAT     CAGTTAT
                                  ||| ||  ||||     |||||||
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                                TCC TT  TTTA    GTCAATA
                                  A  GT   AAGAG
GAM1631  LOC146346 5'  ATGGCTTTTTTGGTTTTTTGTT 78386       T       C
                T                  AGGCAA GGAATCAAGA AGTTAT
                                   |||||| |||||||||| ||||||
                                   TTTGTT TTTTGGTTTT TCGGTA
                                     _        T
GAM1631  LOC146839 3'  GTGTTGTTTTGAATTATGCTT  84847      ATG  A       TT
                                   AGGCA   GA TCAAGACAG  AT
                                   |||||   || |||||||||  ||
                                   TTCGT   TT AGTTTTGTT  TG
                                     A__  A        GG
GAM1631  LOC148697 3'  ATGGTTGTCTGGTTTTGTTGTT 79674       TG     A    TT
                T                  AGGCAA  GAATCA GACAG  AT
                                   ||||||  |||||| |||||  ||
                                   TTTGTT  TTTGGT CTGTT  TA
                                     GT     _    GG
GAM1631  LOC150166 5'  TGTTTTGGTTTTTTGTTT    86046       T
                                   AGGCAA GGAATCAAGACA
                                   |||||| ||||||||||||
                                   TTTGTT TTTTGGTTTTGT
                                     _
GAM1631  LOC151443 5'  ATGGCCCAAGATTCCATTCCT  81043     C       AAGACA
                                   AGG AATGGAATC     GTTAT
                                   ||| |||||||||     |||||
                                   TCC TTACCTTAG     CGGTA
                                     _       AACC__
GAM1631  LOC151907 3'  TTTTGAATTCCATTGCTT    81213          _
                                   AGGCAATGGAAT CAAGA
                                   |||||||||||| |||||
                                   TTCGTTACCTTA GTTTT
                                           A
GAM1631  LOC151963 3'  TTCTGCCTCTGATTTCGTTGTT 81219           _  A   TTAT
                T                  AGGCAATGGAATCA AG CAG
                                   |||||||||||||| || |||
                                   TTTGTTGCTTTAGT TC GTC
                                           C  C   TTA
GAM1631  LOC152048 3'  GTAGCTGTAGCTAGGATTCTGT 86733      A      AAG___
                GTCT                AGGCA TGGAATC     ACAGTTAT
                                    ||||| |||||||     ||||||||
                                    TCTGT GTCTTAG     TGTCGATG
                                      _      GATCGA
GAM1631  LOC152200 3'  AGTTGCTTTCTTGATTTCATTT 86753     C          C   TAT
                TCT                   AGG AATGGAATCAAGA AGT
                                      ||| |||||||||||| |||
                                      TCT TTACTTTAGTTCT TCG
                                        T          T   TTGAT
GAM1631  LOC152343 3'  ATAACTGTCTTTGTTTCTTGCT 81419       T    C
                T                  AGGCAA GGAAT AAGACAGTTAT
                                   |||||| ||||| ||||||||||
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                                TTCGTT CTTTG TTCTGTCAATA
                                   _    T
GAM1631  LOC152627 5'  GTAATTGTTTTGGGGTGCC   81513     ATGGAA
                                GGCA     TCAAGACAGTTAT
                                ||||     ||||||||||||||
                                CCGT     GGTTTTGTTAATG
                                  GG____
GAM1631  LOC153931 3'  TGGCTGGTATCATTGCTT    81916        AATCAAGA
                                AGGCAATGG       CAGTTA
                                |||||||||       ||||||
                                TTCGTTACT       GTCGGT
                                     ATG_____
GAM1631  LOC155434 3'  GTAACTTTTTAATTCTGTTGTT 87692          C   C
            T                    AGGCAATGGAAT AAGA AGTTAT
                                ||||||||||||| ||||| ||||||
                                TTTGTTGTCTTA TTTT TCAATG
                                       A   _
GAM1631  LOC158156 3'  GTAGCTGTTATTTATTGT    82628        ATCAA
                                GCAATGGA    GACAGTTAT
                                ||||||||    |||||||||
                                TGTTATTT    TTGTCGATG
                                     A____
GAM1631  LOC158263 3'  ATGGCTGGTTTTCAATTGTCT  82726       G   TCAAGA
                                AGGCAAT GAA     CAGTTAT
                                ||||||| |||     |||||||
                                TCTGTTA CTT     GTCGGTA
                                    A   TTG___
GAM1631  LOC158293 3'  GCTTTTTGTTTTTGTTGCTT   82747       TG   T    C
                                AGGCAA  GAA CAAGA AGT
                                ||||||  ||| ||||| |||
                                TTCGTT  TTT GTTTT TCG
                                   GT   T    _
GAM1631  LOC158969 5'  GTAAATGATTTCGTTCCT    82938     C        AG_
                                AGG AATGGAATCA   AC
                                ||| ||||||||||   ||
                                TCC TTGCTTTAGT   TG
                                  _        AAA
GAM1631  LOC159250 5'  TTTTGTTTTGGTTTTGGTGTCT 88430      AT          TTAT
                                AGGCA  GGAATCAAGACAG
                                |||||  ||||||||||||||
                                TCTGT  TTTTGGTTTTGTT
                                   GG          TTG
GAM1631  LOC161102 5'  GTGGCTGTCTCCTCATGGCCT  88449     A    AATCA
                                AGGC ATGG     AGACAGTTAT
                                |||| ||||     ||||||||||
                                TCCG TACT     TCTGTCGGTG
                                  G    CC___
GAM1631  LOC162239 3'  ATAACTGTCAACTGTTTCATTG 83210          CAA_
            CTT                   AGGCAATGGAAT    GACAGTTAT
                                ||||||||||||    |||||||||
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                                TTCGTTACTTTG    CTGTCAATA
                                      TCAA
GAM1631  LOC165693 5'  TGATTGTTGGTCATTCCT    83492     C     AATCAA
                                AGG AATGG     GACAGTTA
                                ||| |||||     ||||||||
                                TCC TTACT     TTGTTAGT
                                  _    GG____
GAM1631  LOC169225 5'  GTGACTGTCGCACCTCTGTTTC 88626     C      ATCAA
              T                  AGG AATGGA     GACAGTTAT
                                 ||| ||||||     |||||||||
                                 TCT TTGTCT     CTGTCAGTG
                                   _     CCACG
GAM1631  LOC196337 3'  GTAACTGTCTGACGCTTTTGCC 89025       T  AA   A
              T                  AGGCAA GG  TCA GACAGTTAT
                                 |||||| ||  ||| |||||||||
                                 TCCGTT TC  AGT CTGTCAATG
                                    T  GC   _
GAM1631  LOC196478 5'  GTGATTGCACTTTCTATTGTTT 89068          TCAAGA
                                AGGCAATGGAA      CAGTTAT
                                ||||||||||      |||||||
                                TTTGTTATCTT      GTTAGTG
                                      TCAC__
GAM1631  LOC199221 3'  ATGGCTGTTCAACCCCACGTTG 81164        GAATCAA_
              TTT                  AGGCAATG       GACAGTTAT
                                   ||||||||       |||||||||
                                   TTTGTTGC       TTGTCGGTA
                                      ACCCCAAC
GAM1631  LOC200107 3'  ATAATTATCTGTGGTTCCTGTT 89981        _      _  C
              GCTT                    AGGCAAT GGAATCA AGA AGTTAT
                                      ||||||| ||||||| ||| ||||||
                                      TTCGTTG CCTTGGT TCT TTAATA
                                         T      G   A
GAM1631  LOC200470 5'  TGTTTGATTTTGTTTCCT    91643     C  TG     A
                                AGG AA  GAATCA GACA
                                ||| ||  |||||| ||||
                                TCC TT  TTTAGT TTGT
                                  T  GT     _
GAM1631  LOC200933 3'  TAATTGTCTCTTTTGTCT    91798       T   ATCAA
                                AGGCAA GGA     GACAGTTA
                                |||||| |||     ||||||||
                                TCTGTT TCT     CTGTTAAT
                                   T  ______
GAM1631  LOC201917 5'  GTGTTCACTTGCTTTTATTGTC 91874          T   ___   GTTAT
              T                  AGGCAATGGAA CAAG   ACA
                                 |||||||||||| ||||   |||
                                 TCTGTTATTTT GTTC   TGT
                                       C    ACT   G
GAM1631  LOC219686 3'  GTAGCTAAACATTTCATTGTC  92510          CAAGAC
                                GGCAATGGAAT     AGTTAT
                                ||||||||||      ||||||
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                                CTGTTACTTTA     TCGATG
                                      CAAA__
GAM1631  LOC219818 3'  ATGACTCCTACTCCATTGTTT  92536         ATCA  AC
                                AGGCAATGGA    AG  AGTTAT
                                ||||||||||    ||  ||||||
                                TTTGTTACCT    TC  TCAGTA
                                      CA__  C_
GAM1631  LOC220074 3'  ATGACTGGCTAATTTTGTTGTT 59962       TG    CA  A
                                GGCAA  GAAT  AG CAGTTAT
                                |||||  ||||  || |||||||
                                TTGTT  TTTA  TC GTCAGTA
                                   GT    A_  G
GAM1631  LOC220776 3'  TTGTTTGGTTTTGTTGTT    68938       TG     A
                                GGCAA  GAATCA GACAG
                                |||||  |||||| |||||
                                TTGTT  TTTGGT TTGTT
                                   GT     _
GAM1631  LOC221035 3'  ATAACTGTTACACTGTCCTTGT 94779       T   ATCAA_
              CT                  AGGCAA GGA     GACAGTTAT
                                |||||| |||     |||||||||
                                TCTGTT CCT     TTGTCAATA
                                   _   GTCACA
GAM1631  LOC221632 3'  ATGGCTGTTCTCCATTGTCT   95445         ATCAA
                                AGGCAATGGA    GACAGTTAT
                                ||||||||||    |||||||||
                                TCTGTTACCT    TTGTCGGTA
                                      C_____
GAM1631  LOC253019 3'  GTCCATTTGATGCCATTGTTT  97111         A    ___
                                AGGCAATGG ATCAA   GAC
                                ||||||||| |||||   |||
                                TTTGTTACC TAGTT   CTG
                                      G    TAC
GAM1631  LOC253263 3'  TAGCTGGCTTTCGTTGCTT    98817         ATCA  A
                                AGGCAATGGA    AG CAGTTA
                                ||||||||||    || ||||||
                                TTCGTTGCTT    TC GTCGAT
                                      _____  G
GAM1631  LOC253664 3'  TTTTGTTTTGTTTTGTTGTTT  96477       TG   T       TTAT
                                AGGCAA  GAA CAAGACAG
                                ||||||  ||| ||||||||
                                TTTGTT  TTT GTTTTGTT
                                   GT   _       TTT
GAM1631  LOC253933 3'  GTGGCTTCCTAGTTTTGTTGTC 97754       TG    CAA  C
              T                   AGGCAA  GAAT   GA AGTTAT
                                ||||||  ||||   || ||||||
                                TCTGTT  TTTG   CT TCGGTG
                                   GT    ATC  _
GAM1631  LOC253975 3'  GTCCATTTGATGCCATTGTTT  97687         A    ___
                                AGGCAATGG ATCAA   GAC
                                ||||||||| |||||   |||
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                                TTTGTTACC TAGTT   CTG
                                     G    TAC
GAM1631  LOC254018 3'  TGGCTCGATCTTCATTGCTT  98743         _  A  A
                                AGGCAATGGA ATC AG CA
                                |||||||||| ||| || ||
                                TTCGTTACTT TAG TC GT
                                     C  C  G
GAM1631  LOC254143 5'  GTAACTGTTCTGCCATTTTCT  98254    C    AAT  AG
                                AGG AATGG   CA  ACAGTTAT
                                ||| |||||   ||  ||||||||
                                TCT TTACC   GT  TGTCAATG
                                  T    ___  CT
GAM1631  LOC254143 3'  TGTCACTTGATTCCATTCTCT  98256    C        __
                                AGG AATGGAATCAA  GACA
                                ||| ||||||||||  ||||
                                TCT TTACCTTAGTT  CTGT
                                  C         CA
GAM1631  LOC255520 3'  ATGGCTGTTTTTAATTTTGTCT 97550       TGGAATC
                                AGGCAA      AAGACAGTTAT
                                ||||||      ||||||||||
                                TCTGTT      TTTTGTCGGTA
                                   TTAAT__
GAM1631  LOC255545 3'  TTTTGAATTCCATTGCTT    97416          _
                                AGGCAATGGAAT CAAGA
                                |||||||||| |||||
                                TTCGTTACCTTA GTTTT
                                      A
GAM1631  LOC255925 3'  GTGGCTTTCTAGTTCTGTTGTC 98236          CA  C
           T                    AGGCAATGGAAT  AGA AGTTAT
                                |||||||||||  ||| ||||||
                                TCTGTTGTCTTG  TCT TCGGTG
                                      A_  T
GAM1631  LOC51580  3'  TTGTTTTGTTTTATTGTTT   32434         T
                                AGGCAATGGAA CAAGACAG
                                |||||||||| ||||||||
                                TTTGTTATTTT GTTTTGTT
                                     _
GAM1631  LOC91796  3'  ATGGTTGTCTTCCCTTGTT   67785      T  ATCA    TT
                                GGCAA GGA   AGACAG  AT
                                ||||| |||   ||||||  ||
                                TTGTT CCT   TCTGTT  TA
                                   C  ____     GG
GAM1631  LOC91923  5'  CTATTTTGGCTTTGTTGCCT  68171      TG  AT   C
                                AGGCAA  GA  CAAGA AG
                                ||||||  ||  ||||| ||
                                TCCGTT  TT  GTTTT TC
                                   GT  CG   A
GAM1631  LOC92017  3'  ATGATTGTCTTGACTCTGCCT  68486      ATG  A
                                AGGCA   GA TCAAGACAGTTAT
                                |||||   || ||||||||||||
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                                TCCGT   CT AGTTCTGTTAGTA
                                  ___  C
GAM1631  LOC92876  5'  TGGCTTTTGTTTCCATTGCTT  71353          T   AC    T
                                AGGCAATGGAA CAAG  AGTTA
                                |||||||||||  ||||  |||||
                                TTCGTTACCTT GTTT  TCGGT
                                      T   __    T
GAM1632  COL19A1   3'  ACACAAACACAGCAAGTTTTA  10259         AC  AT
                                TAAAACTTG  GT  TTTGTGT
                                |||||||||  ||  |||||||
                                ATTTTGAAC  CA  AAACACA
                                     GA  C_
GAM1632  DDB2      3'  ACACATGGGATCAAGTCCTGCA 5453       AA     CGTA TT
                                TGTA  ACTTGA   T  TGTGT
                                ||||  ||||||   |  |||||
                                ACGT  TGAACT   G  ACACA
                                  CC     AG__ GT
GAM1632  GIPR      3'  ACACAAAACATCAAGTTCCACA 5709       AA      C  AT
                                TGT  AACTTGA GT  TTTGTGT
                                |||  ||||||| ||  |||||||
                                ACA  TTGAACT CA  AAACACA
                                  CC      A  __
GAM1632  PGGT1B    3'  ACACAAATTTTCAAGTTTACA  18475        A    CGTAT
                                TGTAAA CTTGA    TTTGTGT
                                ||||||| |||||    |||||||
                                ACATTT GAACT    AAACACA
                                   _    TTT__
GAM1633  ANXA6     3'  TAGATCCTGTCCACCTCCAC   15741       A      CAA
                                GTGGA GTGGGCAG   GATCTA
                                |||||| ||||||||   ||||||
                                CACCT CACCTGTC   CTAGAT
                                  C      ___
GAM1633  FOXE3     3'  TTTGCCCCCCCACCTCCAC    25167       A    CA
                                GTGGA GTGGG  GCAAG
                                |||||| |||||  |||||
                                CACCT CACCC  CGTTT
                                  C    CC
GAM1633  MEL       3'  ATTTGGCGCCCACTTCCAC    19326          A  A
                                GTGGAAGTGGGC GC AGAT
                                ||||||||||||| || ||||
                                CACCTTCACCCG CG TTTA
                                      _  G
GAM1633  P2RY1     3'  TAGAAATGCCCACATCCAC    11933       A      GCAAGA
                                GTGGA GTGGGCA     TCTA
                                |||||| |||||||     ||||
                                CACCT CACCCGT     AGAT
                                  A      AA____
GAM1633  WHSC1     3'  ATCTGCACTGCCCACTTC     30578          CA_
                                GAAGTGGGCAG   AGAT
                                ||||||||||   ||||
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                                CTTCACCCGTC   TCTA
                                      ACG
GAM1633  WHSC1    3'  ATCTGCACTGCCCACTTC    56665          CA_
                                GAAGTGGGCAG   AGAT
                                ||||||||||   ||||
                                CTTCACCCGTC   TCTA
                                      ACG
GAM1633  WHSC1    3'  ATCTGCACTGCCCACTTC    56676          CA_
                                GAAGTGGGCAG   AGAT
                                ||||||||||   ||||
                                CTTCACCCGTC   TCTA
                                      ACG
GAM1633  ZNF264   3'  AGATCTTGTTTTACACTCCCAT 14194      A    GGC
                                GTGG AGTG   AGCAAGATCT
                                |||| ||||   ||||||||||
                                TACC TCAC   TTGTTCTAGA
                                  C    ATT
GAM1633  ZNF80    5'  ATCTTGCTACTTCTCAC     24067     _    GGGC
                                GTG GAAGT    AGCAAGAT
                                ||| |||||    ||||||||
                                CAC CTTCA    TCGTTCTA
                                  T    _____
GAM1633  CRF      3'  TTTACTGCCCACCTCCGC     22914      A       C
                                GTGGA GTGGGCAG AAG
                                ||||| |||||||| |||
                                CGCCT CACCCGTC TTT
                                   C       A
GAM1633  DHRS2    5'  ATCTTGCTGCTGCTCAC     20525     GA  TG G
                                GTG  AG  G CAGCAAGAT
                                |||  ||  | |||||||||
                                CAC  TC  C GTCGTTCTA
                                  __  GT _
GAM1633  EPB41L4  3'  AGATCTTGTACCACCAC     42423     AAG   GCA
                                GTGG   TGG   GCAAGATCT
                                ||||   |||   |||||||||
                                CACC   ACC   TGTTCTAGA
                                  ___   A__
GAM1633  FLJ10520 3'  TTTGCCAACCCACTTCCAC   36715          CA_
                                GTGGAAGTGGG   GCAAG
                                ||||||||||   |||||
                                CACCTTCACCC   CGTTT
                                      AAC
GAM1633  FLJ10738 3'  CTTCCTGCCACACACTTCCAC 37058         ___    C
                                GTGGAAGTG   GGCAG AAG
                                |||||||||   ||||| |||
                                CACCTTCAC   CCGTC TTC
                                     ACA    C
GAM1633  HSPC047  3'  CTTGCTGCCCACATCCAC    27116      A
                                GTGGA GTGGGCAGCAAG
                                ||||| ||||||||||||
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                                CACCT CACCCGTCGTTC
                                   A
GAM1633 KIAA0295 3' TTTGCTGCCCACCTCTAC    68679      A
                                GTGGA GTGGGCAGCAAG
                                ||||| ||||||||||||
                                CATCT CACCCGTCGTTT
                                   C
GAM1633 KIAA0346 5' TAGCACTGCCCACCCCAC    68903     AA      CAAGAT
                                GTGG  GTGGGCAG     CTA
                                ||||  ||||||||     |||
                                CACC  CACCCGTC     GAT
                                  C_       AC____
GAM1633 KIAA0889 3' ATCCCTGTCTCCCAATTCCAC 31758       G   CA   A_
                                GTGGAA TGGG  GCA  GAT
                                |||||| ||||  |||  |||
                                CACCTT ACCC  TGT  CTA
                                    A   TC   CC
GAM1633 KIAA1016 3' AGTGTGGCCGCCAACTTCCAC 93381        G   A  AAGAT
                                GTGGAAGT GGC GC    CT
                                |||||||| ||| ||    ||
                                CACCTTCA CCG CG    GA
                                     A   C  GTGT_
GAM1633 KIAA1077 3' GTAAATCTTTCAACACACTTCC 73291        GGCAGC    C
             AC                   GTGGAAGTG     AAGAT TAC
                                |||||||||     ||||| |||
                                CACCTTCAC     TTCTA ATG
                                     ACAACT    A
GAM1633 KIAA1729 3' GTAGATCTTTGGTACCACTTC  90592       _  AGC
                                GAAGTGG GC   AAGATCTAC
                                ||||||| ||   |||||||||
                                CTTCACC TG   TTCTAGATG
                                    A  GT_
GAM1633 LMOD1    3' AGACCCTGCCCACCCCAT    25098      AA      CAAGA
                                GTGG  GTGGGCAG     TCT
                                ||||  ||||||||     |||
                                TACC  CACCCGTC     AGA
                                  C_       CC___
GAM1633 MGC14376 3' GCTTCACCGCCCTACTTCCAC  52917        _   _____
                                GTGGAAGT GGGC     AGC
                                |||||||| ||||     |||
                                CACCTTCA CCCG     TCG
                                     T    CCACT
GAM1633 SLC38A5  3' AGACTGGCCCACTTCC      54307         AGCA  A
                                GGAAGTGGGC    AG TCT
                                ||||||||||    || |||
                                CCTTCACCCG    TC AGA
                                     G___  _
GAM1633 SNTA1    3' TCCTGCTGCCCCCCTCCAC   13298      AGT      A
                                GTGGA   GGGCAGCA GA
                                |||||   |||||||| ||
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                                CACCT   CCCGTCGT CT
                                   CCC       C
GAM1633  LOC149876 3'  TCATTGCTGCCCCCCAC     80351      AAGT       _
                                GTGG    GGGCAGCAA GA
                                ||||    |||||||||| ||
                                CACC    CCCGTCGTT CT
                                  C___        A
GAM1633  LOC151361 3'  ATCTAAGTGCTGCCCACTCCCA 86500      A         ___
           T                     GTGG AGTGGGCAGCA   AGAT
                                |||| ||||||||||   ||||
                                TACC TCACCCGTCGT   TCTA
                                  C          GAA
GAM1633  LOC51107  3'  AGATCCCACCTGCCTGTCCAC  32606      AG      CAA_
                                GTGGA  TGGGCAG    GATCT
                                |||||  |||||||    |||||
                                CACCT  GTCCGTC    CTAGA
                                  __       CACC
GAM1633  LOC90072  3'  ATCCCTGTCTCCCAATTCCAC  61948       G    CA   A_
                                GTGGAA TGGG  GCA  GAT
                                |||||| ||||  |||  |||
                                CACCTT ACCC  TGT  CTA
                                   A    TC   CC
GAM1633  LOC90288  3'  ATCTTGCTCTGTTCCCAT    62771      A  TG GC
                                GTGG AG  G  AGCAAGAT
                                |||| ||  |  ||||||||
                                TACC TT  C  TCGTTCTA
                                  C  GT __
GAM1633  LOC90631  5'  GTCTGCTGCCCACTCCC     64395    A         A
                                GG AGTGGGCAGCA GAT
                                || ||||||||||| |||
                                CC TCACCCGTCGT CTG
                                 C          _
GAM1633  LOC90784  5'  TCCTGCCCCCACTTCCAC     64702           CA   A
                                GTGGAAGTGGG  GCA GA
                                ||||||||||  ||| ||
                                CACCTTCACCC  CGT CT
                                       C_  C
GAM1634  CERD4     3'  ACACTGCCTGATATGTGAG    24874       TTAAGG
                                CTCAC     CAGGCAGTGT
                                |||||     ||||||||||
                                GAGTG     GTCCGTCACA
                                   TATA__
GAM1634  DLST      3'  ATGCTGTTGGCCTCAAGCAAGG 10414       CA   A    AG
           AA                     TTCCT  CTT AGGC  GCAGTGT
                                |||||  ||| ||||  |||||||
                                AAGGA  GAA TCCG  TGTCGTA
                                   AC   C    GT
GAM1634  JAG1      3'  ACACTGCCTGCCTTAAGTGAGG 5809
           AA                     TTCCTCACTTAAGGCAGGCAGTGT
                                |||||||||||||||||||||||
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                                AAGGAGTGAATTCCGTCCGTCACA

GAM1634 KIF5A    3' ACACAAAGCCTTAAGCAGAAGA 18371     C  A_      AGGCA
             A                   TTC TC  CTTAAGGC     GTGT
                                 ||| ||  ||||||||     ||||
                                 AAG AG  GAATTCCG     CACA
                                   A  AC       AAA__
GAM1634 C1GALT1  3' ACACTGGAATCCCAGTGAGGAA 39753         TAA  CAGG
                                 TTCCTCACT   GG    CAGTGT
                                 |||||||||   ||    ||||||
                                 AAGGAGTGA   CC    GTCACA
                                       C__  TAAG
GAM1634 CASPR3   3' ACACTGTCATTGAAGTGAGGAA 46414         AAGGCA
                                 TTCCTCACTT     GGCAGTGT
                                 ||||||||||     ||||||||
                                 AAGGAGTGAA     CTGTCACA
                                       GTTA__
GAM1634 KIAA0542 3' ACACTGCCCACTCAGCGAGGAA 66659       A  TAA  CA
                                 TTCCTC CT   GG  GGCAGTGT
                                 |||||| ||   ||  ||||||||
                                 AAGGAG GA   TC  CCGTCACA
                                    C  C__  AC
GAM1634 KIAA0546 3' ACACTAAGAACCAAGTGGGGAA 71835         AA  CAGGC
                                 TTCCTCACTT  GG     AGTGT
                                 ||||||||||  ||     |||||
                                 AAGGGGTGAA  CC     TCACA
                                       __  AAGAA
GAM1634 KIAA1058 3' ACACTGCTTCCCTTATGTGAAG 83134     C    T    C
             AA                    TTC TCAC TAAGG AGGCAGTGT
                                   ||| |||| ||||| |||||||||
                                   AAG AGTG ATTCC TTCGTCACA
                                     A   T    C
GAM1634 KIAA1260 3' GCTCTCCTTAAGTGAAGAA    60671     C        CA
                                   TTC TCACTTAAGG  GGC
                                   ||| ||||||||||  |||
                                   AAG AGTGAATTCC  TCG
                                     A         TC
GAM1634 MKI67IP  3' ACACTGTTTGGTCAAGTTAAGG 51503       C_    AA  _
             AA                    TTCCT  ACTT  GGC AGGCAGTGT
                                   |||||  ||||  ||| |||||||||
                                   AAGGA  TGAA  CTG TTTGTCACA
                                     AT    __   G
GAM1634 PTBP2    3' ACATACGTGCCTTAAAAAGGAA 41328       CAC       GGCA
                                   TTCCT   TTAAGGCA    GTGT
                                   |||||   ||||||||    ||||
                                   AAGGA   AATTCCGT    TACA
                                     AA_       GCA_
GAM1634 LOC149650 3' ACACTGCCCTTTAAGAGA    80283     A      CA
                                   TC CTTAAGG  GGCAGTGT
                                   || |||||||  ||||||||
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                                AG GAATTTC  CCGTCACA
                                 A      __
GAM1634  LOC157909 5'  ACACCAGCAGTCAGTGAGGAA  82519         TAA   AG  A_
                                TTCCTCACT   GGC  GC  GTGT
                                |||||||||   |||  ||  ||||
                                AAGGAGTGA   CTG  CG  CACA
                                      ____  A_  AC
GAM1634  LOC158886 5'  CAAACCGTCAAGTGAGGAA   83721          AA   A  CAG
                                TTCCTCACTT  GGC GG   TG
                                ||||||||||  ||| ||   ||
                                AAGGAGTGAA  CTG CC   AC
                                      __   _  AA_
GAM1634  LOC254431 3'  CCGCCCAGAGTGAGGAG     98648          AA   A
                                TTCCTCACTT  GGC GG
                                ||||||||||  ||| ||
                                GAGGAGTGAG  CCG CC
                                      AC   _
GAM1634  LOC92906  3'  ACATATTTTGCCTTGAGT    57250           CA
                                ACTTAAGGCAGG  GTGT
                                ||||||||||||  ||||
                                TGAGTTCCGTTT  TACA
                                      TA
GAM1635  BMP1      3'  GTGCCCAGCCTGTGGAGA    21536    C        CCT
                                TC CCATAGGCTG   CAT
                                || ||||||||||   |||
                                AG GGTGTCCGAC   GTG
                                 A         CC_
GAM1635  CLASP1    5'  GCAAGAAGAAGCCTGTGAGGA  65894     C       GCC  A   C
                                TCC CATAGGCT   TC TCT GC
                                ||| ||||||||   || ||| ||
                                AGG GTGTCCGA   AG AGA CG
                                 A       ___  A   A
GAM1635  CLK2      3'  GCGAGATGAGCGCAGTGTG   8919     G    _
                                TA GCTGC CTCATCTCGC
                                || ||||| ||||||||||
                                GT TGACG GAGTAGAGCG
                                 G    C
GAM1635  DAP       3'  GCTGATGAGGCACCCATG    72947     A  C        TC
                                CAT GG TGCCTCATC  GC
                                ||| || |||||||||  ||
                                GTA CC ACGGAGTAG  CG
                                  C  _        T_
GAM1635  DIA1      3'  TGAGGCAGCCTTGGGGA     24650       T
                                TCCCCA AGGCTGCCTCA
                                ||||||  ||||||||||
                                AGGGGT TCCGACGGAGT
                                      _
GAM1635  TGM2      3'  GCAGGGTGGGCAGCCTATGGGG 17244             T    TC
                 G                   TCCCCATAGGCTGCC CATC  GC
                                ||||||||||||||| ||||  ||
```

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                                GGGGGTATCCGACGG GTGG  CG
                                      _   GA
GAM1635  VIPR2    3'  GCCGGGAGGCAGCCACAGGGA  14066     CATA       AT  C
                                TCCC   GGCTGCCTC  CT GC
                                ||||   |||||||||  || ||
                                AGGG   CCGACGGAG  GG CG
                                  ACA_       __  C
GAM1635  FLJ11259 3'  GCGAGACAAGAAGAATGGAGA  37768    C    AGG  GC  CA
                                TC CCAT   CT  CT  TCTCGC
                                || ||||   ||  ||  ||||||
                                AG GGTA   GA  GA  AGAGCG
                                 A   A__  A_  AC
GAM1635  FLJ13769 3'  GCGAGACAAGGCAGCTTTGG   47255     T       CA
                                CCA AGGCTGCCT  TCTCGC
                                ||| |||||||||  ||||||
                                GGT TTCGACGGA  AGAGCG
                                  _       AC
GAM1635  KIAA0481  5'  GCGAGATGTCAGCCCAAGGA   72321     CCATA    CCT
                                TCC    GGCTG   CATCTCGC
                                |||    |||||   ||||||||
                                AGG    CCGAC   GTAGAGCG
                                  AAC__    T__
GAM1635  NEIL2    3'  GGAAAAAGAAAGCCTATGGG   59570          GC  CA_
                                CCCATAGGCT  CT   TCT
                                ||||||||||  ||   |||
                                GGGTATCCGA  GA   AGG
                                      AA  AAA
GAM1635  TEX27    3'  GCGTGGAGGCAGCCATGGG    41951      A       ATCT
                                CCCAT GGCTGCCTC    CGC
                                ||||| |||||||||    |||
                                GGGTA CCGACGGAG    GCG
                                  _       GT__
GAM1635  LOC149267 3'  CGAGACGGTGCGAAGCCCAGAG 57477     CCATA    __  C  A
            GA                    TCC    GGCT  GC TC TCTCG
                                |||    ||||  || || |||||
                                AGG    CCGA  CG GG AGAGC
                                  AGAC_   AG  T  C
GAM1636  CCND2    3'  TCCCAGCAAATCATCGGGCCA  10055          CCACA  _  A
                                TGGCCTGATGAT    GC GG GA
                                ||||||||||||    || || ||
                                ACCGGGCTACTA    CG CC CT
                                      AA___  A  C
GAM1636  GCN5L2   5'  CTCCGCTGCGGGGGAGGCC   60529      GATGA   A
                                GGCCT    TCC CAGCGGAG
                                |||||    ||| ||||||||
                                CCGGA    GGG GTCGCCTC
                                   GG___   C
GAM1636  GJA5     3'  CTGACCAGATCATCAGCCA    19164      C       CACAG
                                TGGC TGATGATC    CGG
                                |||| ||||||||    |||
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                                ACCG ACTACTAG    GTC
                                  _      ACCA_
GAM1636 HIVEP3   3'  TCCCCGCTGTGGTTGGCAGCCA 44702     C  ATGAT       A
                                TGGC TG    CCACAGCGG GA
                                |||| ||    ||||||||| ||
                                ACCG AC    GGTGTCGCC CT
                                  _ GGTT_       C
GAM1636 HOXD1    5'  CCGCCGGTATATTAGGCCA   44696         AT  ACA
                                TGGCCTGATG  CC   GCGG
                                ||||||||||  ||   ||||
                                ACCGGATTAT  GG   CGCC
                                      AT  C__
GAM1636 SUFU     3'  CCTTGTGACCCATCAGGCCA   32934         ATC    C
                                TGGCCTGATG   CACAG GG
                                ||||||||||   ||||| ||
                                ACCGGACTAC   GTGTT CC
                                      CCA    _
GAM1636 DKFZP586J1624 3'  CTCCGCCCAGTCACCATCAGGC 32043          ATCCACA_
             CA                   TGGCCTGATG       GCGGAG
                                ||||||||||       ||||||
                                ACCGGACTAC       CGCCTC
                                      CACTGACC
GAM1636 KIAA1671  3'  CTTTGCTTATGAATCATCAGAC 66282    C       C  C_
             C                    GG CTGATGAT CA  AGCGGAG
                                || |||||||| ||  |||||||
                                CC GACTACTA GT  TCGTTTC
                                 A       A  AT
GAM1636 LOC159110 5'  TCTCCGCTGCCCCGGTCAACCA 82995     CCTGA    CA__
                                TGG    TGATC    CAGCGGAGA
                                |||    |||||   |||||||||
                                ACC    ACTGG    GTCGCCTCT
                                  A_____    CCCC
GAM1636 LOC159116 5'  TCTCCGCTGCCCCGGTCAACCA 82978     CCTGA    CA__
                                TGG    TGATC    CAGCGGAGA
                                |||    |||||   |||||||||
                                ACC    ACTGG    GTCGCCTCT
                                  A_____    CCCC
GAM1636 LOC165476 5'  CTCCGCTGCCTGCTCAGCCA   88550     C   TGATCCA
                                TGGC TGA      CAGCGGAG
                                |||| |||      ||||||||
                                ACCG ACT      GTCGCCTC
                                  _   CGTCC__
GAM1636 LOC200032 5'  CTGACCAGATCATCAGCCA    85475      C       CACAG
                                TGGC TGATGATC     CGG
                                |||| ||||||||     |||
                                ACCG ACTACTAG    GTC
                                  _       ACCA_
GAM1636 LOC219654 5'  CTCCGCTGCGGAGGGGGGCC   92932      GATGA   A
                                GGCCT     TCC CAGCGGAG
                                |||||     ||| ||||||||
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                                CCGGG    AGG GTCGCCTC
                                   GGG__  C
GAM1636 LOC255862 3'  TCAAATGTAGACTATCAGGCCA 96115         A  C  GCG
                                TGGCCTGATG TC ACA  GA
                                |||||||||| || |||  ||
                                ACCGGACTAT AG TGT  CT
                                      C  A  AAA
GAM1637 HAL     5'  GCCACTCCTGCATAAAGCTC  10903          TGAAAA
                                GAGCTTTATGC    GGTGGC
                                ||||||||||    ||||||
                                CTCGAAATACG    TCACCG
                                      TCC___
GAM1637 HMGN2   3'  GGCCACCTTGGCACAAAAGC  19809      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _  GG
GAM1637 NMI     5'  GGCCACCTCCTCAGGAAG   17436     ATG   AA
                                CTTT  CTGA  AGGTGGCC
                                ||||  ||||  ||||||||
                                GAAG  GACT  TCCACCGG
                                  ___   CC
GAM1637 PACE    3'  GGCCACCTCTCCAAGGGCTT  11944       A  CT  AAA
                                GAGCTTT TG  GA  GGTGGCC
                                ||||||| ||  ||  |||||||
                                TTCGGGA AC  CT  CCACCGG
                                   _ CT  ___
GAM1637 PYCR1   3'  CCACCTTCCTCTAGAGCTC  70639       TGCT  A_
                                GAGCTTTA   GA  AAGGTGG
                                ||||||||   ||  |||||||
                                CTCGAGAT   CT  TTCCACC
                                     _____  CC
GAM1637 SDC1    3'  GGCCACCTCCCCAGCATTCCAG 12991    TT_    AAA
            C                    GCT  ATGCTG  AGGTGGCC
                                |||  ||||||  ||||||||
                                CGA  TACGAC  TCCACCGG
                                  CCT    CCC
GAM1637 FLJ11560 5' GCCCAGGCCCAGCATAAAG   48008        AAAA  ___
                                CTTTATGCTG   GGT  GGC
                                ||||||||||   |||  |||
                                GAAATACGAC   CCG  CCG
                                     _____  GAC
GAM1637 KIAA0446 5' CCACCTTTTGAAGAGCTC    69446      ATGCTG
                                GAGCTTT    AAAAGGTGG
                                |||||||    |||||||||
                                CTCGAGA    TTTTCCACC
                                   AG_____
GAM1637 KIAA0971 3' GTTGTTCTCAGCATAAAGT   30677         AAA  TG
                                GCTTTATGCTGA  GG  GC
                                ||||||||||||  ||  ||
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                                TGAAATACGACT   TT  TG
                                      C__  GT
GAM1637 KIAA1393 3' GGCCACCTTGGCACAAAAGC  72574      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                   _ _  GG
GAM1637 KIAA1656 3' GGCCACCTCCTCCTAGAAGCC 66377   A    ATGCT  AA
                                G GCTTT    GA  AGGTGGCC
                                | |||||    ||  ||||||||
                                C CGAAG    CT  TCCACCGG
                                 _    ATC__  CC
GAM1637 KIAA1884 3' GCCACCTTCATCTACCAAGGCT 73728       ATGCT  A_
             C                   GAGCTTT    GA  AAGGTGGC
                                |||||||    ||  ||||||||
                                CTCGGAA    CT  TTCCACCG
                                    CCAT_  AC
GAM1637 PP3501   3' GGCCACCGTTGACAGCATAAAG 41683         AAAA_
                                CTTTATGCTG    GGTGGCC
                                ||||||||||    |||||||
                                GAAATACGAC    CCACCGG
                                      AGTTG
GAM1637 SDCCAG3  3' GGTGTTCTCAGCATGAAGCTC  22803           AAA  TG
                                GAGCTTTATGCTGA   GG  GCC
                                ||||||||||||||   ||  |||
                                CTCGAAGTACGACT   CT  TGG
                                       ____  TG
GAM1637 SP140    3' GGCCACCTCCATGCAGAAGC   24327      A   TGAAA
                                GCTTT TGC    AGGTGGCC
                                ||||| |||    ||||||||
                                CGAAG ACG    TCCACCGG
                                   _  TACC_
GAM1637 LOC148760 3' GGCCACCTTCTCCAACAAGCTC 85364       TA  CT  A
                                GAGCTT  TG  GA AAGGTGGCC
                                ||||||  ||  || |||||||||
                                CTCGAA  AC  CT TTCCACCGG
                                   CA  __  C
GAM1637 LOC150170 5' ACCTGTTTCACATAAAGC    80414        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                      _    G
GAM1637 LOC150175 5' ACCTGTTTCACATAAAGC    80453        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                      _    G
GAM1637 LOC150215 5' ACCTGTTTCACATAAAGC    80456        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
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                                CGAAATAC ACTTT TCCA
                                   _    G
GAM1637  LOC150218 5'  ACCTGTTTCACATAAAGC    80525        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                   _    G
GAM1637  LOC152065 3'  GGCCACCTTCTCCTTGGCAGGC 86737      TTA   ___  A
           TC                    GAGCT   TGCT   GA AAGGTGGCC
                                |||||   ||||   || |||||||||
                                CTCGG   ACGG   CT TTCCACCGG
                                   ___    TTC  C
GAM1637  LOC152267 3'  GGCCACCTTGGCACAAAAGC   61036      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                   _ _  GG
GAM1637  LOC158292 5'  CCTCTGGACCCAGCATAAGGCT 88046           AAAA_  T
           C                     GAGCTTTATGCTG    GG GG
                                ||||||||||||    || ||
                                CTCGGAATACGAC    TC CC
                                      CCAGG  T
GAM1637  LOC219997 3'  GCCACCTCTTCAGCCTC    93256    CTTTAT    A
                                GAG     GCTGAA AGGTGGC
                                |||     |||||| |||||||
                                CTC     CGACTT TCCACCG
                                  _______     C
GAM1637  LOC256269 3'  GGCCACCTTGGCACAAAAGC   96608      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                   _ _  GG
GAM1637  LOC91963  5'  GGCCACCTCCTCTGAGAAGC   68321      ATGCT  AA
                                GCTTT    GA  AGGTGGCC
                                |||||    ||  ||||||||
                                CGAAG    CT  TCCACCGG
                                   AGT__  CC
GAM1638  LTB       3'  CGGGCCTCTCTGGTACACG   24808    AA  G  A
                                CGT  TA CG AGAGGCCCG
                                |||  || || |||||||||
                                GCA  AT GT TCTCCGGGC
                                  C_  G  C
GAM1638  P114-RHO-GEF 3'  GCGGGCCTCTAGCTTCAGCCA  31671     GTAAT   GA
                                TGGC    AGC  AGAGGCCCGC
                                ||||    |||  ||||||||||
                                ACCG    TCG  TCTCCGGGCG
                                  ACT__  A_
GAM1638  LOC137593 3'  GCAGACCTCATAGCTGTTACAC 75795    C      GAA    CCC
           CA                    TGG GTAATAGC   GAGG   GC
                                ||| ||||||||   ||||   ||
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                                ACC CATTGTCG   CTCC   CG
                                  A       ATA    AGA
GAM1638  LOC255480 5'  GCGGGCCTCTTTCCAACCAGCC 98286      GTAATAGC
              A                    TGGC       GAAGAGGCCCGC
                                   ||||       ||||||||||||
                                   ACCG       TTTCTCCGGGCG
                                     ACCAACC_
GAM1639  SCAMP1    3'  GCTAAATAAATATTCTCC     18013     T     C
                                   GGA AATATT ATTTAGC
                                   ||| |||||| |||||||
                                   CCT TTATAA TAAATCG
                                     C     A
GAM1639  SCAMP1    3'  GCTAAATAAATATTCTCC     54501     T     C
                                   GGA AATATT ATTTAGC
                                   ||| |||||| |||||||
                                   CCT TTATAA TAAATCG
                                     C     A
GAM1639  NX-17     3'  TGAATATCAGCCCCTAATA    40706         ATA_
                                   TATTAGGG    ATATTCA
                                   ||||||||    |||||||
                                   ATAATCCC    TATAAGT
                                        CGAC
GAM1639  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
              TA                     TATTAGGGATAATATTCATTTAGC
                                   |||||||||||||||||||||||
                                   ATAATCCCTATTATAAGTAAATCG

GAM1640  CD4       3'  ACTGACCCTGTGCAGAACCTC  7042            TG    C
                                   GAGGTTTTGTAT  AGGG CAGT
                                   ||||||||||||  |||| ||||
                                   CTCCAAGACGTG  TCCC GTCA
                                           __    A
GAM1640  GLRX      3'  ACTGACCCTCAATTGTCCTCT  10802       TTTTGT       C
                                   AGAGG      ATTGAGGG CAGT
                                   |||||      |||||||| ||||
                                   TCTCC      TAACTCCC GTCA
                                     TGT___       A
GAM1640  GPR4      5'  ACTGACTCCATACATAACCTC  60572       T     T A   C
                                   GAGGTT TGTAT G GGG CAGT
                                   |||||| ||||| | ||| ||||
                                   CTCCAA ACATA C CTC GTCA
                                      T     _ _   A
GAM1640  RAB3A     3'  ACCAGCCACGGGCACAAGACCC 12696    A       A_   AG   CA
              CT                     AG GGTTTTGT  TTG  GGC  GT
                                   || ||||||||  |||  |||  ||
                                   TC CCAGAACA  GGC  CCG  CA
                                    C       CG   A_   AC
GAM1640  TCF8      3'  ACTGATTCCAACACAAAACCCC 48425    A       A   A  GC
              T                     AG GGTTTTGT TTG GG  CAGT
                                   || |||||||| ||| ||  ||||
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                                TC CCAAAACA AAC CT  GTCA
                                 C       C   _ TA
GAM1640  APCL     3'  ACTGGCCCCCAACATGACC    20810      T   AT  A
                                GGTT TGT  TG GGGCCAGT
                                |||| |||  || ||||||||
                                CCAG ACA  AC CCCGGTCA
                                  T   __  C
GAM1640  DKFZP434N1511 3'  ACTGGCCCCCAAGGTCAGCTCC 93048    TT   TA_   A
                                GG  TTG   TTG GGGCCAGT
                                ||  |||   ||| ||||||||
                                CC  GAC   AAC CCCGGTCA
                                 TC   TGG   C
GAM1640  DKFZP586H2123 3'  CCATATACAAAACCTCT     62611            TGA
                                AGAGGTTTTGTAT   GG
                                ||||||||||||   ||
                                TCTCCAAAACATA   CC
                                        TA_
GAM1640  FLJ12876  3'  ACTGGGAAAATACAAAAGCTCT 43083      G       GAGGG
                                AGAG TTTTGTATT     CCAGT
                                |||| |||||||||     |||||
                                TCTC AAAACATAA     GGTCA
                                  G        AAG__
GAM1640  FPGT     3'  CTAGATACAAAGACCTCT     15180          _    G
                                AGAGGTTTT GTATT AG
                                ||||||||| ||||| ||
                                TCTCCAGAA CATAG TC
                                     A    A
GAM1640  KIAA0280  3'  ACTGGCCCCAGGATGCAAACCC 93286    A  T      GA_
            CT                    AG GG TTTGTATT   GGGCCAGT
                                || || ||||||||   ||||||||
                                TC CC AAACGTAG   CCCGGTCA
                                 _ C       GAC
GAM1640  THEA     3'  ACTGGCCATAAGCAAAACCTCT 66865           ATTGAG
                                AGAGGTTTTGT     GGCCAGT
                                ||||||||||     |||||||
                                TCTCCAAAACG     CCGGTCA
                                      AATA__
GAM1640  LOC122830 3'  ACTAACATTTCACACAAAACCT 74627          AT    GCC_
                                AGGTTTTGT  TGAGG    AGT
                                |||||||||  |||||    |||
                                TCCAAAACA  ACTTT    TCA
                                     C_     ACAA
GAM1640  LOC257457 3'  TCCTCCAACACAAAACCCT    63316    A       A  _
                                AG GGTTTTGT TTG AGGG
                                || |||||||| ||| ||||
                                TC CCAAAACA AAC TCCT
                                 _       C   C
GAM1640  LOC91266  5'  ACTGGCCCCCAATTCCACTCT  66018      GTTTTGT    A
                                AGAG      ATTG GGGCCAGT
                                ||||      |||| ||||||||
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                                TCTC      TAAC CCCGGTCA
                                  ACCT___    C
GAM1640  LOC92344  3'  CCTCCAATAAAAACCTCT    69575         G     AG
                                AGAGGTTTT TATTG  GG
                                ||||||||| |||||  ||
                                TCTCCAAAA ATAAC  CC
                                     _    CT
GAM1641  EIF2B5    3'  GTGACCACCATCCAGGCT    62206           CAGACAG
                                AGCCTGGATGGTG      CAC
                                ||||||||||||      |||
                                TCGGACCTACCAC      GTG
                                       CA_____
GAM1641  MAFF      3'  AGCGCCGCCTCTGTGCCCAGGT 25571       ATG TG    CA__  A
                                GCCTGG   G  CAGA    GC CT
                                ||||||   |  ||||    || ||
                                TGGACC   C  GTCT    CG GA
                                   ___ GT    CCGC  C
GAM1641  RRM1      5'  GTGCTGTCTGGCTCCAACT    8283     A   T  _
                                GG TGG GC AGACAGCAC
                                || ||| || |||||||||
                                TC ACC CG TCTGTCGTG
                                 A   T  G
GAM1641  SAG       5'  GCGCTGCCCCTTCAGGCT    6773         T  T    ACA
                                AGCCTGGA GG GCAG   GC
                                |||||||| || ||||   ||
                                TCGGACTT CC CGTC   CG
                                     C  _    G__
GAM1641  C6orf26   3'  GTTCCTGCACCACCCAGG    48272       A       AC
                                CCTGG TGGTGCAG  AGC
                                ||||| ||||||||  |||
                                GGACC ACCACGTC  TTG
                                   C       C_
GAM1641  DKFZP564O0823 3'  GCCTTGCACCAGCCAGGC    60259        A       ACA
                                GCCTGG TGGTGCAG   GC
                                |||||| ||||||||   ||
                                CGGACC ACCACGTT   CG
                                   G       C__
GAM1641  KIAA1297  5'  AGTGCTGTTAACACCCATGGC  72628     TGGAT    CA
                                GCC    GGTG  GACAGCACT
                                |||    ||||  |||||||||
                                CGG    CCAC  TTGTCGTGA
                                  TAC__    AA
GAM1641  KIAA1881  3'  AGTGCTGTGGCATCCCAGGCT  97080        AT    AG
                                AGCCTGG  GGTGC  ACAGCACT
                                |||||||  |||||  ||||||||
                                TCGGACC  CTACG  TGTCGTGA
                                   __    G_
GAM1641  LEPROTL1  3'  AGTGCTGTCTCTGATTTCTAGG 31700         TGGTGC
            CT                   AGCCTGGA     AGACAGCACT
                                ||||||||     ||||||||||
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                                TCGGATCT     TCTGTCGTGA
                                     TTAGTC
GAM1641  USP24    3'  GTGCCGTATCATCAGACT    92794    C   G      AGACA
                                AG CTG ATGGTGC     GCAC
                                || ||| |||||||     ||||
                                TC GAC TACTATG     CGTG
                                 A   _      C____
GAM1641  LOC123905 5'  AGCGCGGGGCCACCATCCAG   74721          _ AGACA  A
                                CTGGATGGTG C     GC CT
                                |||||||||| |     || ||
                                GACCTACCAC G     CG GA
                                      C GGG__  C
GAM1641  LOC147166 5'  TGCCATCTCCAGGCTCCAGGCT 78897         TGG  C   CA
                                AGCCTGGA   TG AGA  GCA
                                ||||||||   || |||  |||
                                TCGGACCT   AC TCT  CGT
                                     CGG  C   AC
GAM1641  LOC148709 5'  GCAAGGTACACAGCCATCCAGG 79691           GCAG_  A__
           CT                    AGCCTGGATGGT     AC   GC
                                ||||||||||||     ||   ||
                                TCGGACCTACCG     TG   CG
                                      ACACA  GAA
GAM1641  LOC150378 3'  TTGTCTGCACCCCCCAAGC    80562    C   AT
                                GC TGG  GGTGCAGACAG
                                || |||  ||||||||||
                                CG ACC  CCACGTCTGTT
                                 A   CC
GAM1641  LOC152897 3'  TGCTGTCTGCAAAGTAGAGCT  81612     _   GATGG
                                AGC CTG     TGCAGACAGCA
                                ||| |||     ||||||||||
                                TCG GAT     ACGTCTGTCGT
                                  A   GAA__
GAM1641  LOC200918 3'  AGTGCTGCACATCATCCAGGT  90364           CAGA
                                GCCTGGATGGTG    CAGCACT
                                ||||||||||||    |||||||
                                TGGACCTACTAC    GTCGTGA
                                      AC__
GAM1641  LOC255189 5'  AGTGCTATCTGTTTGCCAAGGC 98375       GGA   __    C
           T                     AGCCT   TGGT  GCAGA AGCACT
                                |||||   ||||  ||||| ||||||
                                TCGGA   ACCG  TGTCT TCGTGA
                                   ___    TT    A
GAM1641  LOC256948 3'  GTGACCACCATCCAAGCT    96118     C       CAGACAG
                                AGC TGGATGGTG      CAC
                                ||| |||||||||      |||
                                TCG ACCTACCAC      GTG
                                  A        CA_____
GAM1641  LOC54466  5'  GCTCTACTGCACCACCCCAG   39175      A_      AC_
                                CTGG  TGGTGCAG   AGC
                                ||||  ||||||||   |||
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                                GACC  ACCACGTC   TCG
                                  CC       ATC
GAM1642  CNN3     3'  TCCTACAGCATAATCAAT    60038          G   A
                                ATTGATTGTGT GTG GA
                                |||||||||| ||| ||
                                TAACTAATACG CAT CT
                                      A   C
GAM1642  CTGF     3'  GATTCCCACCCAATTCAA    10338      TTG  T    A
                                TTGA   TG GGTG GAATC
                                ||||   || |||| |||||
                                AACT   AC CCAC CTTAG
                                  TA_ _    C
GAM1642  PTGIS    3'  GATTCTCACCTGCCTTCAAAGA 8212     A    TT   T
                                TC TTGA  GTG GGTGAGAATC
                                || ||||  ||| ||||||||||
                                AG AACT  CGT CCACTCTTAG
                                 A    TC  _
GAM1642  TEM7     3'  GGATTCTCAGTGTTAATAAT   40265       GT__ G
                                ATTGT    G TGAGAATCC
                                |||||    | |||||||||
                                TAATA    T ACTCTTAGG
                                   ATTG G
GAM1642  AKAP10   3'  GGATTCTTCAACACAGCCAATG 24222        AT     GGT
           A                     TCATTG  TGTGT   GAGAATCC
                                ||||||  |||||   ||||||||
                                AGTAAC  ACACA   TTCTTAGG
                                   CG    AC_
GAM1642  DKFZP434P0111 3'  GAATTTCACCAACCAACAA   67959     A   TG       A
                                TTG TTG  TGGTGAGA TC
                                ||| |||  |||||||| ||
                                AAC AAC  ACCACTTT AG
                                  _  CA       A
GAM1642  FLJ31952 3'  GATTCTCTTTAAAAATCAATGA 59047          GTG   T
                                TCATTGATT   TGG GAGAATC
                                |||||||||   ||| |||||||
                                AGTAACTAA   ATT CTCTTAG
                                      AA_   T
GAM1642  KIAA1715 3'  ATTCTCAGTGAGAATGCAATGA 68682        ATTGTG  G
                                TCATTG     TG TGAGAAT
                                ||||||     || |||||||
                                AGTAAC     GT ACTCTTA
                                   GTAAGA  G
GAM1642  KIAA1765 3'  GATTGTATATCCACACAATGAA 71133     G        TGAG__
           T                     ATT ATTGTGTGG     AATC
                                ||| |||||||||     ||||
                                TAA TAACACACC     TTAG
                                  G        TATATG
GAM1642  LOC147077 5'  GGACCCTCACCACGAATCTCAT 78852      T_   G        AA
           GA                     TCAT  GATT TGTGGTGAG  TCC
                                ||||  |||| |||||||||  |||
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                                AGTA  CTAA GCACCACTC  AGG
                                  CT   _       CC
GAM1642  LOC90906  3'  TCCCCATATAACCATTGA    64957     T  A      T
                                TCA TG TTGTGTGG GA
                                ||| || |||||||| ||
                                AGT AC AATATACC CT
                                  T  C       C
GAM1643  EPHA2     3'  CAGCCTTCGGACAGACAT    16674      CC   GCGG
                                ATGTC  TTC   GAAGGCTG
                                |||||  |||   ||||||||
                                TACAG  AGG   CTTCCGAC
                                  AC  ____
GAM1643  EPHB6     3'  ACACTGGTCCGAGAAGGGACAT 16713          G    AA  C
              G                  CATGTCCCTTC CGGG  GG TGT
                                ||||||||||| ||||  || |||
                                GTACAGGGAAG GCCT  TC ACA
                                      A   GG  _
GAM1643  PRPF31    3'  CTTCCCACTGAAGGGACA    32212         C_
                                TGTCCCTTCG  GGGAAG
                                ||||||||||  ||||||
                                ACAGGGAAGT  CCCTTC
                                      CA
GAM1643  RHO       3'  CAGCCTGAGAAGGGACAT    6767          GCGGGA
                                ATGTCCCTTC     AGGCTG
                                ||||||||||     ||||||
                                TACAGGGAAG     TCCGAC
                                      AG____
GAM1643  CHFR      3'  ACAGCCCCCTGAGGGAAGGGAC 37188         G__    AA
              G                   TGTCCCTTC   CGGG  GGCTGT
                                ||||||||||  ||||  ||||||
                                GCAGGGAAG   GTCC  CCGACA
                                     GGA   C_
GAM1643  MGC11352  3'  CACCTTCCTGGAACGTG     65426      CCCT  G      C
                                CATGT    TC CGGGAAGG TG
                                |||||    || |||||||| ||
                                GTGCA    AG GTCCTTCC AC
                                   _____  _       A
GAM1643  MGC2803   3'  ACAGCCTTCCCTGAGAGGAC   44085      C    C
                                GTCC TTCG GGGAAGGCTGT
                                |||| |||| ||||||||||
                                CAGG GAGT CCCTTCCGACA
                                  A    _
GAM1643  PRC1      3'  ACAGCCTTCCTCCTGAAGAGA  15625    C     C _
                                TC CTTCG G GGAAGGCTGT
                                || ||||| | ||||||||||
                                AG GAAGT C CCTTCCGACA
                                 A     C T
GAM1644  ABCE1     5'  GGGGATCGTTTTCTCCAGA    60261          C  CTG
                                TCTGGAGAAA TG   CCTC
                                |||||||||| ||   ||||
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                                AGACCTCTTT GC   GGGG
                                      T  TA_
GAM1644  AKAP13   3'  TGAGGCAGCTGCCTCCTGA   91257    T    AAACT
                                TC GGAG     GCTGCCTCA
                                || ||||     |||||||||
                                AG CCTC     CGACGGAGT
                                 T    CGT__
GAM1644  ALOX12B  5'  GGGCAGCAGCTTTTCCAGA   8537          A
                                TCTGGAGAA CTGCTGCCT
                                ||||||||| |||||||||
                                AGACCTTTT GACGACGGG
                                      C
GAM1644  BCL7A    3'  GAGGCGGCGTTACCTCCAGA   40984        A_   T
                                TCTGGAG  AAC GCTGCCTC
                                |||||||  ||| ||||||||
                                AGACCTC  TTG CGGCGGAG
                                    CA  _
GAM1644  CUTL1    3'  GAGCCCCAGTCTCTTCAGA   10348        A    CT  C
                                TCTGGAGA ACTG  GC TC
                                |||||||| ||||  || ||
                                AGACTTCT TGAC  CG AG
                                    C    CC  _
GAM1644  EFNA1    3'  TGGGGCAGCACTCCCCAGA   16666       A  AAC
                                TCTGG GA   TGCTGCCTCA
                                ||||| ||   ||||||||||
                                AGACC CT   ACGACGGGGT
                                   C  C__
GAM1644  EGR1     3'  TGAGCTTCGGTTCTCCAGA   10493        A   CT  C
                                TCTGGAGAA CTG  GC TCA
                                ||||||||| |||  || |||
                                AGACCTCTT GGC  CG AGT
                                      _  TT  _
GAM1644  FLT1     3'  TGAGGAGAGTTTTCTCCA    10664        _  G  G
                                TGGAGAAA CT CT CCTCA
                                |||||||| || || |||||
                                ACCTCTTT GA GA GGAGT
                                     T  _  _
GAM1644  FRK      5'  AGCCGGTAAGTCTCTCCAGG   10715        A  _   C
                                TCTGGAGA ACT GCTG CT
                                |||||||| ||| |||| ||
                                GGACCTCT TGA TGGC GA
                                    C   A   C
GAM1644  GPC6     5'  AGGCAGCAGCCTTCCCAG    20329      A  A_
                                CTGG GAA  CTGCTGCCT
                                |||| |||  |||||||||
                                GACC CTT  GACGACGGA
                                   _  CC
GAM1644  GUCA2B   3'  TGAGGCAGCCCAGCTCCTGA  24020    T    AAACT
                                TC GGAG     GCTGCCTCA
                                || ||||     |||||||||
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                                AG CCTC    CGACGGAGT
                                 T   GACC_
GAM1644  MYO7A    3'  GAGGCAGCAGTGGGTTCAGG   6032       GAA
                                TCTGGA   ACTGCTGCCTC
                                ||||||   ||||||||||
                                GGACTT   TGACGACGGAG
                                   GGG
GAM1644  NPY2R    3'  TGAACAGAAATTTCTCCAGG   8067         CTG   CC
                                TCTGGAGAAA   CTG  TCA
                                ||||||||||   |||  |||
                                GGACCTCTTT   GAC  AGT
                                     AAA   A_
GAM1644  OXTR     3'  TGAATAGACATTTCTCCA    8083        C  _   CC
                                TGGAGAAA TG CTG  TCA
                                ||||||||| || |||  |||
                                ACCTCTTT AC GAT  AGT
                                    _ A   A_
GAM1644  PPP2R4   3'  TGAGGCATGTCTTTCCAGA   61184        A  TGC
                                TCTGGAGA AC   TGCCTCA
                                |||||||| ||   |||||||
                                AGACCTTT TG   ACGGAGT
                                    C  T__
GAM1644  REV3L    5'  TGAGGAAGATTTCTCTCA    12825   _     CTG  G
                                TG GAGAAA   CT CCTCA
                                || ||||||   || |||||
                                AC CTCTTT   GA GGAGT
                                 T     A__  A
GAM1644  SURF5    3'  TGAGGCAGCATTTCCTCCA   56919      A  C
                                TGGAG AA TGCTGCCTCA
                                ||||| || ||||||||||
                                ACCTC TT ACGACGGAGT
                                   C  T
GAM1644  VANGL2   3'  TGAGACATCGGACTCTCCGGA  72095        AA   C  C
                                TCTGGAGA  CTG TG CTCA
                                ||||||||  ||| || ||||
                                AGGCCTCT  GGC AC GAGT
                                    CA   T  A
GAM1644  WARS     3'  GAGGCAGCAGCCCTCGAGG   67865     G   AAA
                                TCT GAG   CTGCTGCCTC
                                ||| |||   ||||||||||
                                GGA CTC   GACGACGGAG
                                  G   CC_
GAM1644  ZNF45    5'  GACTTGGCACTTCTCCAGA   14250        AC    CC
                                TCTGGAGAA  TGCTG  TC
                                |||||||||  |||||  ||
                                AGACCTCTT  ACGGT  AG
                                     C_    TC
GAM1644  BLR1     3'  TGAGGCAGGGAAGTCCCCAGG  53119      A  AA_  G
                                TCTGG GA   CT CTGCCTCA
                                ||||| ||   || ||||||||
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                                GGACC CT   GG GACGGAGT
                                   C  GAA  _
GAM1644  C20orf150 3'  TGAAGCCGAGCTCCTCCAGA   66017       AAACT   __  C
                                TCTGGAG    GCT  GC TCA
                                |||||||    |||  || |||
                                AGACCTC    CGA  CG AGT
                                    CT___   GC  A
GAM1644  C20orf4   3'  GGGCAGCAATCTCTCCAGG   31948       AAC
                                TCTGGAGA   TGCTGCCT
                                ||||||||   ||||||||
                                GGACCTCT   ACGACGGG
                                    CTA
GAM1644  C20orf7   3'  TGAATATGCACCTTCTCCAGA  44383       AC   TGCC
                                TCTGGAGAA  TGC    TCA
                                |||||||||  |||    |||
                                AGACCTCTT  ACG    AGT
                                     CC   TATA
GAM1644  C6orf26   3'  AGAAAGCAGCTTTCTCCA    48268       _    GC
                                TGGAGAAA CTGCT  CT
                                |||||||| |||||  ||
                                ACCTCTTT GACGA  GA
                                    C     AA
GAM1644  CASKIN1   3'  TGAGGCGGATTTCCCCAGA   40784      A    CTG
                                TCTGG GAAA   CTGCCTCA
                                ||||| ||||   ||||||||
                                AGACC CTTT   GGCGGAGT
                                   C    A__
GAM1644  CCR8      3'  TGAGGCAGATGCCTCTAGA   19041      AAACTG
                                TCTGGAG     CTGCCTCA
                                |||||||     ||||||||
                                AGATCTC     GACGGAGT
                                    CGTA__
GAM1644  CPGL2     5'  GAAGCCGCTTTGTTCTCCAGA  74884       ACT_  T  C
                                TCTGGAGAA    GC GC TC
                                |||||||||    || || ||
                                AGACCTCTT    CG CG AG
                                     GTTT  C  A
GAM1644  CSRP2BP   5'  TGAAGCAGCAGTGGGACCAG   70657     AGAA      C
                                CTGG    ACTGCTGC TCA
                                ||||    |||||||| |||
                                GACC    TGACGACG AGT
                                  AGGG       A
GAM1644  DGKD      3'  TGAAACAACACTTTCTCCAG   60113       C  C  CC
                                CTGGAGAAA TG TG  TCA
                                ||||||||| || ||  |||
                                GACCTCTTT AC AC  AGT
                                     C  A  AA
GAM1644  DKFZP434A043 3'  TGAGGTAGTAATTTCCTCAGA  31823     GA   C
                                TCTG  GAAA TGCTGCCTCA
                                ||||  |||| ||||||||||
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                                AGAC  CTTT ATGATGGAGT
                                  TC    A
GAM1644  DKFZP434P0111 3'  TGAGGGTGTCTTTCCAGA    67963        A  T  TG
                                TCTGGAGA AC GC  CCTCA
                                |||||||| || ||  |||||
                                AGACCTTT TG TG  GGAGT
                                    C  _  __
GAM1644  DKFZP586M1120 3'  TGAGGCAGCAGCTCCCAG    49287     A  AA
                                CTGG GA  CTGCTGCCTCA
                                |||| ||  ||||||||||
                                GACC CT  GACGACGGAGT
                                  _ C_
GAM1644  ERG-1    3'  TGAGACATGTTTCTCCAGG    42102          TGC  C
                                TCTGGAGAAAC   TG CTCA
                                ||||||||||   || ||||
                                GGACCTCTTTG   AC GAGT
                                      T__  A
GAM1644  FASTK    3'  TGAGGCAGAAGCTCCAGG    47690       AAACTG
                                TCTGGAG     CTGCCTCA
                                |||||||     ||||||||
                                GGACCTC     GACGGAGT
                                    GAA___
GAM1644  FLJ14855  5'  GGTTCCCAGTTTTCCAGA    53766        A   CT_
                                TCTGGAGAA CTG   GCC
                                ||||||||| |||   |||
                                AGACCTTTT GAC   TGG
                                      _  CCT
GAM1644  FLJ20249  3'  TGAGGAGTCCCTCCCAGA    80223      A  AACT   G
                                TCTGG GA    GCT CCTCA
                                ||||| ||    ||| |||||
                                AGACC CT    TGA GGAGT
                                  _  CCC_  _
GAM1644  FLJ20730  3'  TGAAGAAGCAGTTTCTCAGA   36053     G        GCC
                                TCTG AGAAACTGCT   TCA
                                |||| ||||||||||   |||
                                AGAC TCTTTGACGA   AGT
                                  _        AGA
GAM1644  FLJ21007  5'  TGAAGCTTGCACAAGCTCTCCA 48648        AAC__   T_  C
            GA                    TCTGGAGA    TGC  GC TCA
                                |||||||     |||  || |||
                                AGACCTCT    ACG  CG AGT
                                    CGAAC   TT  A
GAM1644  KIAA0652  3'  TGAGGCAGCAATCTTTGG    29125   TG   AAC
                                C  GAGA   TGCTGCCTCA
                                |  ||||   ||||||||||
                                G  TTCT   ACGACGGAGT
                                 GT   A__
GAM1644  KIAA1030  3'  GAGGCAGCAGTGAGCCGAGA   94981    _  AGAA
                                TCT GG    ACTGCTGCCTC
                                ||| ||    ||||||||||
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                                AGA CC    TGACGACGGAG
                                  G  GAG_
GAM1644  KIAA1086  3'  TGAGGCAGGGGGTCCCCA    71291     A  AA  G
                                TGG GA  CT CTGCCTCA
                                ||| ||  || ||||||||
                                ACC CT  GG GACGGAGT
                                  C  GG  _
GAM1644  KIAA1322  3'  TGAGATAGTTTTTCCAGA    73118           CTGC
                                TCTGGAGAAACTG   CTCA
                                ||||||||||||   ||||
                                AGACCTTTTTGAT   GAGT
                                       A___
GAM1644  KIAA1634  3'  GCATCAGTCTCTTCTCCAGA   64124         ___   C
                                TCTGGAGAA   ACTG TGC
                                |||||||||   |||| |||
                                AGACCTCTT   TGAC ACG
                                     CTC    T
GAM1644  KIAA1638  3'  TGAAACAACGGTGACCTCTCCA 47824        A___   C  CC
           GG                     TCTGGAGA    ACTG TG  TCA
                                ||||||||    |||| ||  |||
                                GGACCTCT    TGGC AC  AGT
                                    CCAG    A  AA
GAM1644  KIAA1771  5'  GGGTTACCAGACCTCTCCAGA  79866        AA_  CT_
                                TCTGGAGA   CTG   GCCT
                                ||||||||   |||   ||||
                                AGACCTCT   GAC   TGGG
                                    CCA   CAT
GAM1644  KIAA1894  3'  GAGGCAACCTTTGCCTTCTTCA 74285        ACT _______
           GA                     TCTGGAGAA   GC     TGCCTC
                                |||||||||   ||     ||||||
                                AGACTTCTT   CG     ACGGAG
                                    C__  TTTCCA
GAM1644  KIAA1937  3'  GAGGCAGTGTCCCCCAGG    74071      AGAA  T
                                TCTGG    AC GCTGCCTC
                                |||||    || ||||||||
                                GGACC    TG TGACGGAG
                                   CCC_  _
GAM1644  KIAA1985  3'  TGAAAAGCACTTTCTCCA    45018        C   GCC
                                TGGAGAAA TGCT   TCA
                                |||||||| ||||   |||
                                ACCTCTTT ACGA   AGT
                                    C    AA_
GAM1644  LCHN      3'  TGAGATGCTTTCTCCAGA    87480         CT  TGC
                                TCTGGAGAAA  GC   CTCA
                                ||||||||||  ||   ||||
                                AGACCTCTTT  CG   GAGT
                                      __  TA_
GAM1644  MGC13007  3'  CAGTTCAGTTATCTCCAGA   51277         _    __
                                TCTGGAGA AACTG  CTG
                                |||||||| |||||  |||
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                                AGACCTCT TTGAC  GAC
                                    A     TT
GAM1644  MGC16385  5'  TGAAGCAGCAGCTGGGCTAGG  59543      AGAAA      C
                                TCTGG    CTGCTGC TCA
                                |||||    ||||||| |||
                                GGATC    GACGACG AGT
                                   GGGTC      A
GAM1644  MGC26914  3'  TGAATAGACATTTCTCCA    59332        C  _   CC
                                TGGAGAAA TG CTG  TCA
                                |||||||| || |||  |||
                                ACCTCTTT AC GAT  AGT
                                    _ A   A_
GAM1644  PSKH1     3'  AGGCTCCAGCCTCTCCAGA   68791        AA   CT
                                TCTGGAGA  CTG  GCCT
                                ||||||||  |||  ||||
                                AGACCTCT  GAC  CGGA
                                    CC   CT
GAM1644  SPAF      3'  TGAAGCGATTTCTTTTTCCAGA 83521         CTGC_   C
                                TCTGGAGAAA     TGC TCA
                                ||||||||||     ||| |||
                                AGACCTTTTT     GCG AGT
                                     CTTTA   A
GAM1644  SUN1      3'  TGAGTTTCCCAGTTTCTACAGA 47926      G       CTGC_
                                TCTG AGAAACTG     CTCA
                                |||| ||||||||     ||||
                                AGAC TCTTTGAC     GAGT
                                  A       CCTTT
GAM1644  USP24     3'  TGAAAATGCTGTGTTCTCCAGA 92795         _  T  TGCC
                                TCTGGAGAA AC GC    TCA
                                ||||||||| || ||    |||
                                AGACCTCTT TG CG    AGT
                                     G  T  TAAA
GAM1644  LOC129831 5'  TGAGACAGCAGCGGTGGCAGA  75398      GAGAA      ___
                                TCTG    ACTGCTGC   CTCA
                                ||||    ||||||||   ||||
                                AGAC    TGGCGACG   GAGT
                                  GG___       ACA
GAM1644  LOC134637 3'  TGAGAACACCTTCTCCAGG    75693        AC  CTGC
                                TCTGGAGAA  TG    CTCA
                                |||||||||  ||    ||||
                                GGACCTCTT  AC    GAGT
                                     CC  AA__
GAM1644  LOC146420 3'  TGAACTTCCAGATTCTCCAGA  84653         A   CTGCC
                                TCTGGAGAA CTG     TCA
                                |||||||||| |||     |||
                                AGACCTCTT GAC     AGT
                                     A   CTTCA
GAM1644  LOC147711 5'  TGAGCAGGCAAGTCTCTTCAGA 79117         A   _   GC
                                TCTGGAGA ACT GCT  CTCA
                                |||||||| ||| |||  ||||
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                                AGACTTCT TGA CGG  GAGT
                                     C   A   AC
GAM1644  LOC148753 3'  TGAGACTCCATTTTCTCCAGG  85373         C  CTGC
                                TCTGGAGAAA TG    CTCA
                                |||||||||| ||    ||||
                                GGACCTCTTT AC    GAGT
                                      T  CTCA
GAM1644  LOC150290 3'  TGAGGCAGATGGTGCCCAGA   80592       AGAA   _
                                TCTGG    ACTG CTGCCTCA
                                |||||    |||| ||||||||
                                AGACC    TGGT GACGGAGT
                                   CG__    A
GAM1644  LOC153218 5'  TGAAATAGAACTTTTCCAGA   81658         ACTG   CC
                                TCTGGAGAA    CTG  TCA
                                |||||||||    |||  |||
                                AGACCTTTT    GAT  AGT
                                      CAA_   AA
GAM1644  LOC157570 5'  TGAGGCTTTTTCTTCAGA     82397          CTGCT
                                TCTGGAGAAA     GCCTCA
                                ||||||||||     ||||||
                                AGACTTCTTT     CGGAGT
                                      TT____
GAM1644  LOC197259 5'  TGAGGCAGTGGCCTCCGGA    89304        AAA TG
                                TCTGGAG   C  CTGCCTCA
                                |||||||   |  ||||||||
                                AGGCCTC   G  GACGGAGT
                                    C__ GT
GAM1644  LOC199923 3'  TGAGTTAGCCAGTTTCTTCAGA 89879           _   C
                                TCTGGAGAAACTG CTG CTCA
                                |||||||||||||| ||| ||||
                                AGACTTCTTTGAC GAT GAGT
                                        C   T
GAM1644  LOC200940 3'  TGAGGCAGGCGGATCTCCTGA  90398    T     AA   _
                                TC GGAGA  CTGC TGCCTCA
                                || |||||  |||| |||||||
                                AG CCTCT  GGCG ACGGAGT
                                 T    A_    G
GAM1644  LOC205327 3'  AGTCAATGTTTCTCCAGA     91067          TGC  C
                                TCTGGAGAAAC   TG CT
                                ||||||||||   || ||
                                AGACCTCTTTG   AC GA
                                      TA_  T
GAM1644  LOC221288 3'  TGAAGCAGCAGTATCTAGA    95264       GAA       C
                                TCTGGA   ACTGCTGC TCA
                                ||||||   |||||||| |||
                                AGATCT   TGACGACG AGT
                                   A__       A
GAM1644  LOC253254 5'  TGAGAAGAACTTCTTCAGA    98908         ACTG  GC
                                TCTGGAGAA    CT  CTCA
                                |||||||||    ||  ||||
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                                AGACTTCTT   GA  GAGT
                                     CAA_  A_
GAM1644  LOC256789 3'  TGAGGCTGTACTCTCTAGA   99312       AAC   T
                                TCTGGAGA   TGC GCCTCA
                                ||||||||   ||| ||||||
                                AGATCTCT   ATG CGGAGT
                                     C__   T
GAM1644  LOC257336 5'  GGGCCCTAGTCCTCCAGA    97900       AA   CT
                                TCTGGAG  ACTG  GCCT
                                |||||||  ||||  ||||
                                AGACCTC  TGAT  CGGG
                                    C_   CC
GAM1644  LOC91923  5'  AGAGTTCCAGTTTCTCCA    68169         CT  _
                                TGGAGAAACTG  GC CT
                                ||||||||||  || ||
                                ACCTCTTTGAC  TG GA
                                       CT  A
GAM1644  LOC92876  5'  AGAGTTCCAGTTTCTCCA    71346         CT  _
                                TGGAGAAACTG  GC CT
                                ||||||||||  || ||
                                ACCTCTTTGAC  TG GA
                                       CT  A
GAM1644  LOC93496  3'  TGAAACAGACTTACACTTCTTC 72863        ACTG____   CC
           AGA                    TCTGGAGAA      CTG  TCA
                                |||||||||      |||  |||
                                AGACTTCTT      GAC  AGT
                                     CACATTCA   AA
GAM1645  A1BG     3'  CCCAGGCTGGAGTGCAGTG   56285
                                CACTGCACTCCAGCCTGGG
                                ||||||||||||||||||
                                GTGACGTGAGGTCGGACCC

GAM1645  A1BG     3'  GTTGCCCAGGCTGGAGTGCAAT 56297     C           AG
           GG                     CCA TGCACTCCAGCCTGGG  AC
                                ||| ||||||||||||||  ||
                                GGT ACGTGAGGTCGGACCC  TG
                                  A            GT
GAM1645  AASS     3'  CCCAGGCTGGAGTGCAGTG   20459
                                CACTGCACTCCAGCCTGGG
                                ||||||||||||||||||
                                GTGACGTGAGGTCGGACCC

GAM1645  ABCB6    5'  TCCCGGGCCCAGAGCCAGCGG  20301    A   CA   CA_
                                CC CTG  CTC   GCCTGGGA
                                || |||  |||   ||||||||
                                GG GAC  GAG   CGGGCCCT
                                 C  C_   ACC
GAM1645  ACADSB   3'  GTCACCCAGGCTAGAGTGCAGT 9648          C       A
           GG                     CCACTGCACTC AGCCTGGG GAC
                                |||||||||| |||||||| |||
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                                GGTGACGTGAG TCGGACCC CTG
                                      A       A
GAM1645 ADAMTS4   3'  GTCGCCCAGGCTGGAGTGCAAT 18771     C            A
             GG                   CCA TGCACTCCAGCCTGGG GAC
                                  ||| |||||||||||||| |||
                                  GGT ACGTGAGGTCGGACCC CTG
                                    A             G
GAM1645 ADCY2     3'  TCAGGCCGGGTGCAGTGG    65653         T  A
                                  CCACTGCAC CC GCCTGG
                                  ||||||||| || ||||||
                                  GGTGACGTG GG CGGACT
                                       _ C
GAM1645 ADCY6     5'  GTCACCCAGGCTGGAGTGCAAT 31593     C            A
             GG                   CCA TGCACTCCAGCCTGGG GAC
                                  ||| |||||||||||||| |||
                                  GGT ACGTGAGGTCGGACCC CTG
                                    A             A
GAM1645 AHR       3'  CCCAAACTGGAGTGCAGTGG   9674             CC
                                  CCACTGCACTCCAG  TGGG
                                  ||||||||||||  ||||
                                  GGTGACGTGAGGTC  ACCC
                                        AA
GAM1645 AIM1      3'  TCTCAGGCTGGAGTGCAGTGG  93471
                                  CCACTGCACTCCAGCCTGGGA
                                  ||||||||||||||||||||
                                  GGTGACGTGAGGTCGGACTCT

GAM1645 ALDH1B1   3'  GTCGCCCAGGCTGGAGTGCAGT 7326                 A
             GG                   CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC CTG
                                           G
GAM1645 ALOX15    3'  CCCAGGCTGGAGTGCAGTGG   8543
                                  CCACTGCACTCCAGCCTGGG
                                  ||||||||||||||||||||
                                  GGTGACGTGAGGTCGGACCC

GAM1645 APAF1     3'  CCAGGCTGGAGTGCAGTGG    8583
                                  CCACTGCACTCCAGCCTGG
                                  |||||||||||||||||
                                  GGTGACGTGAGGTCGGACC

GAM1645 APAF1     3'  TCACCCAGGCTGGAGTGCAGTG 8592                 A
             G                     CCACTGCACTCCAGCCTGGG GA
                                  |||||||||||||||||| ||
                                  GGTGACGTGAGGTCGGACCC CT
                                           A
GAM1645 APAF1     3'  CCAGGCTGGAGTGCAGTGG   25965
                                  CCACTGCACTCCAGCCTGG
                                  |||||||||||||||||
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                                GGTGACGTGAGGTCGGACC

GAM1645  APAF1    3'  TCACCCAGGCTGGAGTGCAGTG 25983                 A
                G                    CCACTGCACTCCAGCCTGGG GA
                                     |||||||||||||||||||| ||
                                     GGTGACGTGAGGTCGGACCC CT
                                                          A
GAM1645  APM1     3'  CCAGGCTAGAGTGCAGTGG   17769          C
                                     CCACTGCACTC AGCCTGG
                                     |||||||||||  |||||||
                                     GGTGACGTGAG TCGGACC
                                           A
GAM1645  APM1     3'  CCCTGGCTGGAGTTCAGTGG  17776       C       T
                                     CCACTG ACTCCAGCC GGG
                                     ||||||  |||||||||  |||
                                     GGTGAC TGAGGTCGG CCC
                                        T        T
GAM1645  APM1     3'  GTCACCCAGGCTGGAGTACAGT 17789       C          A
                G                    CACTG ACTCCAGCCTGGG GAC
                                     |||||  ||||||||||||| |||
                                     GTGAC TGAGGTCGGACCC CTG
                                       A           A
GAM1645  APOL1    3'  GTCGCCAAGTTGGAGTGCAATG 14743     C         C   GA
                G                    CCA TGCACTCCAGC TGG  GAC
                                     ||| ||||||||||  |||  |||
                                     GGT ACGTGAGGTTG ACC  CTG
                                       A         A   G_
GAM1645  APPL     3'  GTTGCCCAGGCTGGAGTGCAGT 24954                 AG
                GG                     CCACTGCACTCCAGCCTGGG  AC
                                       ||||||||||||||||||  ||
                                       GGTGACGTGAGGTCGGACCC  TG
                                                          GT
GAM1645  AQP6     3'  GTTACCCAGGCTGGAGTGCAGT 9733                 A
                GG                     CCACTGCACTCCAGCCTGGG GAC
                                       |||||||||||||||||| |||
                                       GGTGACGTGAGGTCGGACCC TTG
                                                          A
GAM1645  AQP6     3'  GTTACCCAGGCTGGAGTGCAGT 55012                 A
                GG                     CCACTGCACTCCAGCCTGGG GAC
                                       |||||||||||||||||| |||
                                       GGTGACGTGAGGTCGGACCC TTG
                                                          A
GAM1645  ARCN1    3'  CCCAGGCTGGAATGCAATGG  9748      C   C
                                       CCA TGCA TCCAGCCTGGG
                                       ||| |||| ||||||||||
                                       GGT ACGT AGGTCGGACCC
                                         A   A
GAM1645  ATF5     3'  CTCTCGGCCGGGTGCAGTGG  24819         T  A   T
                                       CCACTGCAC CC GCC GGGAG
                                       |||||||| || ||| |||||
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                                GGTGACGTG GG CGG CTCTC
                                      _ C   _
GAM1645 ATM      3' GTCATTCGGGCTGGGCGCAGCG 5301     A    A T        A
             G                   CC CTGC C CCAGCCTGGG GAC
                                 || |||| | |||||||||| |||
                                 GG GACG G GGTCGGGCTT CTG
                                  C   C _        A
GAM1645 ATM      3' GTCATTCGGGCTGGGCGCAGCG 57137    A    A T        A
             G                   CC CTGC C CCAGCCTGGG GAC
                                 || |||| | |||||||||| |||
                                 GG GACG G GGTCGGGCTT CTG
                                  C   C _        A
GAM1645 ATP1B2   3' GTTGCCCAGGCTGGAGTGCAAT 9840      C            AG
             GG                   CCA TGCACTCCAGCCTGGG  AC
                                 ||| ||||||||||||||  ||
                                 GGT ACGTGAGGTCGGACCC  TG
                                   A            GT
GAM1645 ATP6V1A1 3' GTTGCCCAGGCTGGAGTGCAAT 9874      C            AG
             GG                   CCA TGCACTCCAGCCTGGG  AC
                                 ||| ||||||||||||||  ||
                                 GGT ACGTGAGGTCGGACCC  TG
                                   A            GT
GAM1645 ATP7A    3' CCCAGGCTGGAGTGCAGTGG   5318
                                 CCACTGCACTCCAGCCTGGG
                                 ||||||||||||||||||
                                 GGTGACGTGAGGTCGGACCC

GAM1645 AXL      3' GTCACCCAGGCTGGAGTGCAGT 9910                A
             GG                   CCACTGCACTCCAGCCTGGG GAC
                                 |||||||||||||||||| |||
                                 GGTGACGTGAGGTCGGACCC CTG
                                           A
GAM1645 AXL      3' GTCACCCAGGCTGGAGTGCAGT 41892               A
             GG                   CCACTGCACTCCAGCCTGGG GAC
                                 |||||||||||||||||| |||
                                 GGTGACGTGAGGTCGGACCC CTG
                                           A
GAM1645 BAZ2A    5' CCCAGGCTTGAGTGCAATG   26506    C      C
                                 CA TGCACTC AGCCTGGG
                                 || ||||||| ||||||||
                                 GT ACGTGAG TCGGACCC
                                  A      T
GAM1645 BCL10    3' TCGCCCAGGCTGGAGTGCAGTG 15374               A
             G                   CCACTGCACTCCAGCCTGGG GA
                                 |||||||||||||||||| ||
                                 GGTGACGTGAGGTCGGACCC CT
                                           G
GAM1645 BCL2     3' TCTTCCTGAAATGCAGTGG   7150         CTC  GCCT
                                 CCACTGCA   CA    GGGAGA
                                 ||||||||   ||    ||||||
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                                GGTGACGT   GT    CCTTCT
                                    AAA  ____
GAM1645 BDKRB1    5' GTCGGCCCAGACTGAAGTGCAG 7386          C  C     A_
              TGG                   CCACTGCACT CAG CTGGG  GAC
                                    |||||||||| ||| |||||  |||
                                    GGTGACGTGA GTC GACCC  CTG
                                      A  A     GG
GAM1645 BDP1      3' CCCAGGCAAGAGTGCAGTGG  37964           CA
                                    CCACTGCACTC  GCCTGGG
                                    ||||||||||  |||||||
                                    GGTGACGTGAG  CGGACCC
                                      AA
GAM1645 BRIP1     3' GTTGCCCAGGCTGGAATGCAGT 50212         C          AG
              GG                    CCACTGCA TCCAGCCTGGG  AC
                                    ||||||||  ||||||||||  ||
                                    GGTGACGT AGGTCGGACCC  TG
                                       A          GT
GAM1645 C7        3' GTTGCCCAGGCTGGAGCGCAGT 6988          A          AG
              GG                    CCACTGC CTCCAGCCTGGG  AC
                                    |||||||  ||||||||||  ||
                                    GGTGACG GAGGTCGGACCC  TG
                                       C          GT
GAM1645 CAMLG     3' GTTGCCCAGGCTAGAGTGCAAT 10006     C      C       AG
              GG                    CCA TGCACTC AGCCTGGG  AC
                                    |||  |||||||  ||||||||  ||
                                    GGT ACGTGAG TCGGACCC  TG
                                      A      A       GT
GAM1645 CASP10    3' CCCAGACTGGAGTGCAGGG   53221    A        C
                                    CC CTGCACTCCAG CTGGG
                                    ||  ||||||||||  |||||
                                    GG GACGTGAGGTC GACCC
                                     _         A
GAM1645 CASP10    3' CCCAGACTGGAGTGCAGGG   53253    A        C
                                    CC CTGCACTCCAG CTGGG
                                    ||  ||||||||||  |||||
                                    GG GACGTGAGGTC GACCC
                                     _         A
GAM1645 CASP2     3' GTCGCCCAGGCTGGAGGGCAGT 53295        A          A
              GG                    CCACTGC CTCCAGCCTGGG GAC
                                    |||||||  ||||||||||| |||
                                    GGTGACG GAGGTCGGACCC CTG
                                       G          G
GAM1645 CASP2     3' GTCGCCCAGGCTGGAGGGCAGT 53311        A          A
              GG                    CCACTGC CTCCAGCCTGGG GAC
                                    |||||||  ||||||||||| |||
                                    GGTGACG GAGGTCGGACCC CTG
                                       G          G
GAM1645 CASP2     3' GTCGCCCAGGCTGGAGGGCAGT 53348        A          A
              GG                    CCACTGC CTCCAGCCTGGG GAC
                                    |||||||  ||||||||||| |||
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                                GGTGACG GAGGTCGGACCC CTG
                                   G          G
GAM1645  CASP2    3'  GTCGCCCAGGCTGGAGGGCAGT 8719         A          A
                GG                  CCACTGC CTCCAGCCTGGG GAC
                                    ||||||| |||||||||||| |||
                                GGTGACG GAGGTCGGACCC CTG
                                   G          G
GAM1645  CASP8    3'  GTCGCCCAGGCTGGAGTGCAGT 8762                A
                GG                  CCACTGCACTCCAGCCTGGG GAC
                                    |||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                          G
GAM1645  CASP8    3'  GTCGCCCAGGCTGGAGTGCAGT 54083               A
                GG                  CCACTGCACTCCAGCCTGGG GAC
                                    |||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                          G
GAM1645  CASP8    3'  GTCGCCCAGGCTGGAGTGCAGT 54103               A
                GG                  CCACTGCACTCCAGCCTGGG GAC
                                    |||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                          G
GAM1645  CASP8    3'  GTCGCCCAGGCTGGAGTGCAGT 54119               A
                GG                  CCACTGCACTCCAGCCTGGG GAC
                                    |||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                          G
GAM1645  CBFA2T2  3'  GTCTCCCAGGCTGGAGTGCA  18715
                                TGCACTCCAGCCTGGGAGAC
                                ||||||||||||||||||
                                ACGTGAGGTCGGACCCTCTG

GAM1645  CCNF     3'  GTCTCCCCGGCTGGAGTGCAGT 10086             T
                GG                  CCACTGCACTCCAGCC GGGAGAC
                                    |||||||||||||| |||||||
                                GGTGACGTGAGGTCGG CCCTCTG
                                         C
GAM1645  CDC6     3'  GTTGCCCAGGCTGGAGTGCAAT 8827      C          AG
                GG                  CCA TGCACTCCAGCCTGGG  AC
                                    ||| ||||||||||||||  ||
                                GGT ACGTGAGGTCGGACCC  TG
                                   A            GT
GAM1645  CDH1     3'  TCGGCCAGGCTGGAGTGCAGTG 16409              GA
                G                    CCACTGCACTCCAGCCTGG  GA
                                     |||||||||||||||||  ||
                                GGTGACGTGAGGTCGGACC  CT
                                         GG
GAM1645  CDH17    3'  GTCGCCCAGGCTGGAGTACAGT 15788       C          A
                GG                  CCACTG ACTCCAGCCTGGG GAC
                                    |||||| |||||||||||| |||
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                                GGTGAC TGAGGTCGGACCC CTG
                                   A          G
GAM1645 CELSR3   3' GTCTCCCAGGCCGAAGGTCAG 9190     C   CCA_
                                CTG ACT    GCCTGGGAGAC
                                ||| |||    ||||||||||
                                GAC TGG    CGGACCCTCTG
                                  _   AAGC
GAM1645 CIAS1    5' CCTAGGCTGGAGTGCAGTGG  18094
                                CCACTGCACTCCAGCCTGGG
                                ||||||||||||||||||||
                                GGTGACGTGAGGTCGGATCC

GAM1645 CLECSF12 3' GTTACCCAGGCTGGAGTGCAGT 77218                A
             GG                   CCACTGCACTCCAGCCTGGG GAC
                                ||||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC TTG
                                           A
GAM1645 CLECSF12 3' GTTGCCCAGGCTGGAGTGCAAC 77220    AC           AG
             GG                   CC  TGCACTCCAGCCTGGG  AC
                                || |||||||||||||||  ||
                                GG  ACGTGAGGTCGGACCC  TG
                                 CA             GT
GAM1645 CMAR     5' CCCAGGCTGGAGTGCAGTG   19030
                                CACTGCACTCCAGCCTGGG
                                ||||||||||||||||||
                                GTGACGTGAGGTCGGACCC

GAM1645 CNGA1    5' CCCAGGCTGGAGTGCAGTGG  60237
                                CCACTGCACTCCAGCCTGGG
                                ||||||||||||||||||||
                                GGTGACGTGAGGTCGGACCC

GAM1645 CNN2     3' GTTGCCCAGGCTGGAGTGCAGT 16463                AG
             GG                   CCACTGCACTCCAGCCTGGG  AC
                                ||||||||||||||||||  ||
                                GGTGACGTGAGGTCGGACCC  TG
                                           GT
GAM1645 CNP      3' TTTCCCAAGCTGGAGTGCAGTG 53629            C
             G                    CCACTGCACTCCAGC TGGGAGA
                                |||||||||||||| |||||||
                                GGTGACGTGAGGTCG ACCCTTT
                                         A
GAM1645 CORO2B   5' GTTGCCCAAGCTGGAGTGCAGT 65175            C   AG
             GG                   CCACTGCACTCCAGC TGGG  AC
                                |||||||||||||| ||||  ||
                                GGTGACGTGAGGTCG ACCC  TG
                                         A   GT
GAM1645 COX15    3' GTTGCCCAGGCTGGAGTACAAT 55289     C  C         AG
             GG                   CCA TG ACTCCAGCCTGGG  AC
                                ||| || ||||||||||||  ||
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                                GGT AC TGAGGTCGGACCC  TG
                                  A A           GT
GAM1645 CPS1     3'  CCAGGCTGGAGTGCAGTGG   10287
                                CCACTGCACTCCAGCCTGG
                                ||||||||||||||||||
                                GGTGACGTGAGGTCGGACC

GAM1645 CR1      3'  GTCTCCCAGGCTGGAGTGCAGT 6950
              GG                  CCACTGCACTCCAGCCTGGGAGAC
                                  ||||||||||||||||||||||||
                                  GGTGACGTGAGGTCGGACCCTCTG

GAM1645 CRTAP    3'  CCCAGGCTGGAGTGCAATGG  22076     C
                                CCA TGCACTCCAGCCTGGG
                                ||| ||||||||||||||||
                                GGT ACGTGAGGTCGGACCC
                                  A
GAM1645 CSNK2A2  5'  GTCACCCAGGCTGGAGTGCAGT 10321                A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC CTG
                                        A
GAM1645 CST      5'  TCCAGAGCTGGAGTGCAGCGG  17965    A         _
                                CC CTGCACTCCAGC CTGGG
                                || |||||||||| |||||
                                GG GACGTGAGGTCG GACCT
                                 C          A
GAM1645 CTF1     3'  GTCGCCCAGGCTGGGGTGCAGT 9020                 A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||| |||
                                  GGTGACGTGGGGTCGGACCC CTG
                                        G
GAM1645 CTSB     5'  CTGGGCTGGTGTGCAGTGG   65362         T     TG
                                CCACTGCAC CCAGCC  G
                                ||||||||| ||||||  |
                                GGTGACGTG GGTCGG  C
                                     T     GT
GAM1645 CXCL16   3'  GTCATCCAGGCTGGAGTGCAGT 42177               GA
              GG                  CCACTGCACTCCAGCCTGG  GAC
                                  |||||||||||||||||  |||
                                  GGTGACGTGAGGTCGGACC  CTG
                                        TA
GAM1645 CYP1A2   3'  CCAGGCTGGAGTGCAGTGG   7506
                                CCACTGCACTCCAGCCTGG
                                ||||||||||||||||||
                                GGTGACGTGAGGTCGGACC

GAM1645 CYP1A2   3'  GTCACCCAGGTTGGAGTGCAGT 7524                A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||| |||
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                                GGTGACGTGAGGTTGGACCC CTG
                                          A
GAM1645  CYP1A2   3'  GTCTCCTAAGCTGGAGTGCAGT 7526            C
              GG                  CCACTGCACTCCAGC TGGGAGAC
                                  ||||||||||||||| ||||||||
                                  GGTGACGTGAGGTCG ATCCTCTG
                                          A
GAM1645  CYP2B6   3'  GTCTCCCAGGCTGGAGTGCTAT 7566     CT
              GG                  CCA  GCACTCCAGCCTGGGAGAC
                                  |||  ||||||||||||||||||
                                  GGT  CGTGAGGTCGGACCCTCTG
                                   AT
GAM1645  CYP2B6   3'  GTTGCCCAGGCTGGAGTGCAGT 7568               AG
              GG                  CCACTGCACTCCAGCCTGGG  AC
                                  ||||||||||||||||||  ||
                                  GGTGACGTGAGGTCGGACCC  TG
                                          GT
GAM1645  CYP4F3   3'  CCCAGGCTGGAGTGCGGTGG  8003
                                  CCACTGCACTCCAGCCTGGG
                                  ||||||||||||||||||
                                  GGTGGCGTGAGGTCGGACCC

GAM1645  CYP51    3'  GTTGCCCAGGCTGGAGTGCAGT 7621               AG
              GG                  CCACTGCACTCCAGCCTGGG  AC
                                  ||||||||||||||||||  ||
                                  GGTGACGTGAGGTCGGACCC  TG
                                          GT
GAM1645  CYP8B1   3'  CCCAGGCTGCAGTGCAGTGG  16536         C
                                  CCACTGCACT CAGCCTGGG
                                  |||||||||| |||||||||
                                  GGTGACGTGA GTCGGACCC
                                        C
GAM1645  DFFB     3'  CTCAGGCTGGAGTGCAGTG   88768
                                  CACTGCACTCCAGCCTGGG
                                  ||||||||||||||||||
                                  GTGACGTGAGGTCGGACTC

GAM1645  DFFB     3'  GTTGCCCAGGCTGGAGTGTAGT 88783               AG
              GG                  CCACTGCACTCCAGCCTGGG  AC
                                  ||||||||||||||||||  ||
                                  GGTGATGTGAGGTCGGACCC  TG
                                          GT
GAM1645  DHFR     3'  GTTGCCCAGGCTAGCATGCAAT 7656     C   CTCC      AG
              GG                  CCA TGCA   AGCCTGGG  AC
                                  ||| ||||   ||||||||  ||
                                  GGT ACGT   TCGGACCC  TG
                                    A  ACGA      GT
GAM1645  DISC1    3'  GTCACCCAAGTTGGAGTGCAGT 38514           C   A
              GG                  CCACTGCACTCCAGC TGGG GAC
                                  |||||||||||||| |||| |||
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                                GGTGACGTGAGGTTG ACCC CTG
                                        A   A
GAM1645  DNAH11   3'  CCTCTGCTGGAGTGCAGTG   15022          CT
                                CACTGCACTCCAGC  GGG
                                |||||||||||||  |||
                                GTGACGTGAGGTCG  TCC
                                        TC
GAM1645  DSC3     3'  CAGGCTGGAGTGCAGTGG    44615
                                CCACTGCACTCCAGCCTG
                                ||||||||||||||||||
                                GGTGACGTGAGGTCGGAC

GAM1645  DSC3     3'  CAGGCTGGAGTGCAGTGG    10435
                                CCACTGCACTCCAGCCTG
                                ||||||||||||||||||
                                GGTGACGTGAGGTCGGAC

GAM1645  DYRK1A   5'  TCCCGGCTGAAGTGCAGTGG   56081         C    T
                                CCACTGCACT CAGCC GGGA
                                |||||||||| ||||| ||||
                                GGTGACGTGA GTCGG CCCT
                                      A    _
GAM1645  EBI3     3'  TTGGGCTGGGCGCAGTGG    20442       A T    TG
                                CCACTGC C CCAGCC  G
                                ||||||| | ||||||  |
                                GGTGACG G GGTCGG  T
                                    C _     GT
GAM1645  EDG8     3'  GTCACCCAGGCTGGAGTGCAAT 79150     C           A
            GG                    CCA TGCACTCCAGCCTGGG GAC
                                ||| ||||||||||||||| |||
                                GGT ACGTGAGGTCGGACCC CTG
                                  A            A
GAM1645  EHD2     3'  GTCGCCCAGGCTGGAGTGCAGT 28228              A
            GG                    CCACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                        G
GAM1645  EIF2S3   3'  GTCACCCAGGCTGGAGTGCAGT 9213               A
            GG                    CCACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                        A
GAM1645  ENDOGL1  3'  TCCAGGCTGGAGTGCGGTGG   18826
                                CCACTGCACTCCAGCCTGGG
                                ||||||||||||||||||
                                GGTGGCGTGAGGTCGGACCT

GAM1645  EPB72    3'  GTTGCCCAGGCTGGAGTGCA   15880           AG
                                TGCACTCCAGCCTGGG  AC
                                ||||||||||||||  ||
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                                ACGTGAGGTCGGACCC  TG
                                      GT
GAM1645  F2RL2    3'  TCACCCAGACTGGCGTGCAGTG 15902        T   C    A
              G                  CCACTGCAC CCAG CTGGG GA
                                 ||||||||| |||| ||||| ||
                                 GGTGACGTG GGTC GACCC CT
                                       C   A    A
GAM1645  F2RL3    3'  GTTGCCCAGGCTGGAGTGCAGT 15526              AG
              GG                   CCACTGCACTCCAGCCTGGG  AC
                                   ||||||||||||||||||| ||
                                   GGTGACGTGAGGTCGGACCC  TG
                                         GT
GAM1645  F3       3'  GTTGCCCAGGCTGGAGTGCAGT 67680             AG
                                   ACTGCACTCCAGCCTGGG  AC
                                   |||||||||||||||| ||
                                   TGACGTGAGGTCGGACCC  TG
                                         GT
GAM1645  FABP2    3'  CTCAGGCTGGAATGTAGTGG  5533        C
                                   CCACTGCA TCCAGCCTGGG
                                   |||||||| ||||||||||
                                   GGTGATGT AGGTCGGACTC
                                       A
GAM1645  FANCC    3'  CCTGGCTGGGTGCAGTGG    71037        T    T
                                   CCACTGCAC CCAGCC GGG
                                   ||||||||| |||||| |||
                                   GGTGACGTG GGTCGG TCC
                                             _    _
GAM1645  FANCE    3'  GTCATCCAGGCTGGAGTGCAGT 41901             GA
              G                    CACTGCACTCCAGCCTGG  GAC
                                   |||||||||||||||| |||
                                   GTGACGTGAGGTCGGACC  CTG
                                         TA
GAM1645  FANCF    3'  CCCAGTCTGGAGTGCAGTGG  42978          C
                                   CCACTGCACTCCAG CTGGG
                                   |||||||||||| |||||
                                   GGTGACGTGAGGTC GACCC
                                         T
GAM1645  FCAR     3'  GTCACCCAGGCTGGAGTGCAGT 10592              A
              GG                   CCACTGCACTCCAGCCTGGG GAC
                                   |||||||||||||||||| |||
                                   GGTGACGTGAGGTCGGACCC CTG
                                          A
GAM1645  FCAR     3'  GTCACCCAGGCTGAAGTGCAGT 56580        C      A
              GG                   CCACTGCACT CAGCCTGGG GAC
                                   |||||||||| ||||||||| |||
                                   GGTGACGTGA GTCGGACCC CTG
                                         A      A
GAM1645  FCAR     3'  GTCACCCAGGCTGAAGTGCAGT 56596        C      A
              GG                   CCACTGCACT CAGCCTGGG GAC
                                   |||||||||| ||||||||| |||
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                                GGTGACGTGA GTCGGACCC CTG
                                    A       A
GAM1645  FCAR     3'  GTCACCCAGGCTGAAGTGCAGT 56608         C       A
                GG                  CCACTGCACT CAGCCTGGG GAC
                                    |||||||||| ||||||||| |||
                                    GGTGACGTGA GTCGGACCC CTG
                                        A       A
GAM1645  FCAR     3'  GTCACCCAGGCTGAAGTGCAGT 56620         C       A
                GG                  CCACTGCACT CAGCCTGGG GAC
                                    |||||||||| ||||||||| |||
                                    GGTGACGTGA GTCGGACCC CTG
                                        A       A
GAM1645  FCAR     3'  CCAAGGCTGGAGTGCAGTGG  56632             G
                                    CCACTGCACTCCAGCCT GG
                                    ||||||||||||||||| ||
                                    GGTGACGTGAGGTCGGA CC
                                          A
GAM1645  FCAR     3'  CCAAGGCTGGAGTGCAGTGG  56645             G
                                    CCACTGCACTCCAGCCT GG
                                    ||||||||||||||||| ||
                                    GGTGACGTGAGGTCGGA CC
                                          A
GAM1645  FCGR2A   3'  GTTACCCAGGCTGGAGTGCAGT 80031               A
                GG                  CCACTGCACTCCAGCCTGGG GAC
                                    |||||||||||||||||| |||
                                    GGTGACGTGAGGTCGGACCC TTG
                                           A
GAM1645  FCRH1    3'  CTCAATCTGGAATGCAGTGG  54724       C    CC
                                    CCACTGCA TCCAG  TGGG
                                    |||||||| |||||  ||||
                                    GGTGACGT AGGTC  ACTC
                                       A    TA
GAM1645  FEZ1     3'  TCGCCCAGGCTGGAGTGCAATG 42874     C           A
                G                    CCA TGCACTCCAGCCTGGG GA
                                    ||| ||||||||||||||| ||
                                    GGT ACGTGAGGTCGGACCC CT
                                      A             G
GAM1645  FGF2     3'  TCTAGGCCGGGTGCAGTGG   10623         T  A
                                    CCACTGCAC CC GCCTGGG
                                    |||||||| || |||||||
                                    GGTGACGTG GG CGGATCT
                                         _ C
GAM1645  FGF5     3'  GTCACCAGGCTGGAGTGCAGTG 16764               GA
                G                    CCACTGCACTCCAGCCTGG  GAC
                                    |||||||||||||||||  |||
                                    GGTGACGTGAGGTCGGACC  CTG
                                          A_
GAM1645  FGF5     3'  GTCACCAGGCTGGAGTGCAGTG 53668               GA
                G                    CCACTGCACTCCAGCCTGG  GAC
                                    |||||||||||||||||  |||
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                                GGTGACGTGAGGTCGGACC  CTG
                                      A_
GAM1645  FHL2     5'  GTCGCCCAGGCTGGAGTGCAGT 9370                A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC CTG
                                      G
GAM1645  FSHPRH1   5'  GTCACCCAGGCTGGAGTGCAGT 23069                 A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC CTG
                                      A
GAM1645  FUT1     3'  GTAGCCCAGGCCAGAGTGCAGT 5609           CA      AG
              GG                  CCACTGCACTC  GCCTGGG  AC
                                  ||||||||||  |||||||  ||
                                  GGTGACGTGAG  CGGACCC  TG
                                        AC      GA
GAM1645  FUT1     3'  GTTGCCCAGGCTGGAGTGCAGT 5611                AG
              GG                  CCACTGCACTCCAGCCTGGG  AC
                                  ||||||||||||||||||  ||
                                  GGTGACGTGAGGTCGGACCC  TG
                                      GT
GAM1645  G1P3     3'  TCCAGGCTAGAGTGCAGTGG   10744          C
                                  CCACTGCACTC AGCCTGGG
                                  |||||||||| ||||||||
                                  GGTGACGTGAG TCGGACCT
                                        A
GAM1645  G1P3     3'  TCCAGGCTAGAGTGCAGTGG   43455          C
                                  CCACTGCACTC AGCCTGGG
                                  |||||||||| ||||||||
                                  GGTGACGTGAG TCGGACCT
                                        A
GAM1645  G1P3     3'  TCCAGGCTAGAGTGCAGTGG   43459          C
                                  CCACTGCACTC AGCCTGGG
                                  |||||||||| ||||||||
                                  GGTGACGTGAG TCGGACCT
                                        A
GAM1645  G6PC     3'  TCACCCAGGCTGGAGTGGAGTG 5665       G          A
              G                    CCACT CACTCCAGCCTGGG GA
                                   ||||| |||||||||||||| ||
                                   GGTGA GTGAGGTCGGACCC CT
                                     G           A
GAM1645  GHR      3'  CCAGGCTAGAGTGCGGTGG    5695          C
                                  CCACTGCACTC AGCCTGG
                                  |||||||||| |||||||
                                  GGTGGCGTGAG TCGGACC
                                        A
GAM1645  GM2A     3'  GTCACCAGGCTGGAGTGCAGTG 68388               GA
              G                    CCACTGCACTCCAGCCTGG  GAC
                                   |||||||||||||||||  |||
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                                GGTGACGTGAGGTCGGACC  CTG
                                      A_
GAM1645  GNAI1    5'  CCGGCGGGAGTGCAGCGG    10820    A       A   T
                                CC CTGCACTCC GCC GG
                                || ||||||||| ||| ||
                                GG GACGTGAGG CGG CC
                                 C       G  _
GAM1645  GNE      3'  CCCAGGCTGGAGTGCAGTGG   19665
                                CCACTGCACTCCAGCCTGGG
                                ||||||||||||||||||||
                                GGTGACGTGAGGTCGGACCC

GAM1645  GNE      3'  CTTCCAGGCCGGGCACAGTGG  19668       CA T  A
                                CCACTG  C CC GCCTGGGAG
                                ||||||  | || |||||||||
                                GGTGAC  G GG CGGACCTTC
                                    AC _  C
GAM1645  GPR4     3'  GTTGCCCAGGCTGGAGTGCAGT 60581              AG
                                ACTGCACTCCAGCCTGGG  AC
                                |||||||||||||||||  ||
                                TGACGTGAGGTCGGACCC  TG
                                      GT
GAM1645  GPR56    5'  CAGGCTGGAGTGCAGTGG    20269
                                CCACTGCACTCCAGCCTG
                                ||||||||||||||||||
                                GGTGACGTGAGGTCGGAC

GAM1645  GPR81    3'  TCCCAGGCTGGAGTGCAGTGG  51757
                                CCACTGCACTCCAGCCTGGGA
                                |||||||||||||||||||||
                                GGTGACGTGAGGTCGGACCCT

GAM1645  GRAF     3'  CCATGGCCGGGTGCAGTGG   31227         T  A  _
                                CCACTGCAC CC GCC TGG
                                ||||||||| || ||| |||
                                GGTGACGTG GG CGG ACC
                                     _  C   T
GAM1645  GRAF     3'  GTGGCCCAGGCTGGAGTGCAGT 31244               AG
            GG                    CCACTGCACTCCAGCCTGGG  AC
                                  |||||||||||||||||||  ||
                                  GGTGACGTGAGGTCGGACCC  TG
                                        GG
GAM1645  GRINL1A  3'  GTCGCCCAGGCTGGAGTGCAGT 70067               A
            GG                    CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC CTG
                                        G
GAM1645  GRM6     3'  TTTCTTAGGCTGGAGTGCAGTG 7778
            G                     CCACTGCACTCCAGCCTGGGAGA
                                  |||||||||||||||||||||||
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                                GGTGACGTGAGGTCGGATTCTTT

GAM1645 HCS     3' CCAAGGCTGGAGTGCAGTGG  38971              G
                                CCACTGCACTCCAGCCT GG
                                |||||||||||||||| ||
                                GGTGACGTGAGGTCGGA CC
                                          A
GAM1645 HCS     3' CCCAGGCTGAGTACAGTGG   38974      C   C
                                CCACTG ACTC AGCCTGGG
                                |||||| |||| ||||||||
                                GGTGAC TGAG TCGGACCC
                                   A   _
GAM1645 HCS     3' GTTGCCCAGGCTGGAGTGCAAT 38991    C           AG
             GG                   CCA TGCACTCCAGCCTGGG  AC
                                ||| ||||||||||||||  ||
                                GGT ACGTGAGGTCGGACCC  TG
                                  A            GT
GAM1645 HK1     3' GTCCCCCACGTGTGAAGTGTAG 5748          C _ C   A
             TGG                   CCACTGCACT CA GC TGGG GAC
                                |||||||||| || || |||| |||
                                GGTGATGTGA GT TG ACCC CTG
                                     A  G  C   C
GAM1645 HK1     3' GTCCCCCACGTGTGAAGTGTAG 54261         C _ C   A
             TGG                   CCACTGCACT CA GC TGGG GAC
                                |||||||||| || || |||| |||
                                GGTGATGTGA GT TG ACCC CTG
                                     A  G  C   C
GAM1645 HK1     3' GTCCCCCACGTGTGAAGTGTAG 54264         C _ C   A
             TGG                   CCACTGCACT CA GC TGGG GAC
                                |||||||||| || || |||| |||
                                GGTGATGTGA GT TG ACCC CTG
                                     A  G  C   C
GAM1645 HK1     3' GTCCCCCACGTGTGAAGTGTAG 54267         C _ C   A
             TGG                   CCACTGCACT CA GC TGGG GAC
                                |||||||||| || || |||| |||
                                GGTGATGTGA GT TG ACCC CTG
                                     A  G  C   C
GAM1645 HK1     3' GTCCCCCACGTGTGAAGTGTAG 54270         C _ C   A
             TGG                   CCACTGCACT CA GC TGGG GAC
                                |||||||||| || || |||| |||
                                GGTGATGTGA GT TG ACCC CTG
                                     A  G  C   C
GAM1645 HLCS    5' GTCGTCCAGGCTGGAGTGCAGT 6417              GA
             GG                   CCACTGCACTCCAGCCTGG  GAC
                                |||||||||||||||||  |||
                                GGTGACGTGAGGTCGGACC  CTG
                                          TG
GAM1645 HMG20A  3' CCCAGGCTGGAGTGCGGTGG  37063
                                CCACTGCACTCCAGCCTGGG
                                ||||||||||||||||||
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                                GGTGGCGTGAGGTCGGACCC

GAM1645  HTR1D    3'  CCAGGCTGGAGTGTAGTGG   7842
                                CCACTGCACTCCAGCCTGG
                                ||||||||||||||||||
                                GGTGATGTGAGGTCGGACC

GAM1645  HTR1E    5'  GTCGCCCAGGCTGGAGTGCAG  7865                A
                                CTGCACTCCAGCCTGGG GAC
                                |||||||||||||||| |||
                                GACGTGAGGTCGGACCC CTG
                                      G
GAM1645  HUNK     3'  GTCACCCAGGCTGGAGTGCAGT 28190                 A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                ||||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                      A
GAM1645  HUS1     3'  CCCAGACTGGAGTGCAGTG   92738            C
                                CACTGCACTCCAG CTGGG
                                |||||||||||| |||||
                                GTGACGTGAGGTC GACCC
                                      A
GAM1645  HYAL4    5'  GTTGCCCAGGCTGGAGTGTAGT 25371                 AG
              GG                  CCACTGCACTCCAGCCTGGG  AC
                                |||||||||||||||||||  ||
                                GGTGATGTGAGGTCGGACCC  TG
                                      GT
GAM1645  ICAM1    3'  GTCACCCAGGCTGGAGTGCAGT 72041                 A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                ||||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                      A
GAM1645  IFIT4    3'  GTTTTTTGGCCGGGCGCAGTGG 71496        A T  A   T
                                CCACTGC C CC GCC GGGAGAC
                                ||||||| | || ||| |||||||
                                GGTGACG G GG CGG TTTTTTG
                                    C _  C   _
GAM1645  IGF1     3'  GTCCCCCAGGCTGGAGTGCAGT 7080                  A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                ||||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                      C
GAM1645  IGJ      5'  CCATGGCGCCGGAGCGCACGG  58959    AC   A    A__   _
                                CC  TGC CTCC   GCC TGG
                                ||  ||| ||||   ||| |||
                                GG  ACG GAGG   CGG ACC
                                 C_   C    CCG   T
GAM1645  IHPK2    3'  CCTGGAGCTGATGTGCAGTGG  62516          TC    _ TG
                                CCACTGCAC  CAGC C  GG
                                |||||||||  |||| |  ||
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                                GGTGACGTG  GTCG G  CC
                                     TA    A GT
GAM1645  IL11     3'  CCTAGGCTGGAGTGCAGTG   7180
                                CACTGCACTCCAGCCTGGG
                                ||||||||||||||||||
                                GTGACGTGAGGTCGGATCC

GAM1645  INMT     3'  GTCACCCAGGCTAGAGTGCAAT 23223     C      C       A
              GG                  CCA TGCACTC AGCCTGGG GAC
                                ||| ||||||| |||||||| |||
                                GGT ACGTGAG TCGGACCC CTG
                                  A      A       A
GAM1645  INMT     3'  GTCGCCCAGGCTGGAGTGCAGT 23225                A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                       G
GAM1645  ITGAM    3'  GTCACCCAGGCTGGAGTGCAAT 72315     C            A
              GG                  CCA TGCACTCCAGCCTGGG GAC
                                ||| |||||||||||||| |||
                                GGT ACGTGAGGTCGGACCC CTG
                                  A             A
GAM1645  JAK3     3'  GTTACCCAGGGTGGAGTGCAGT 5832            G     A
              GG                  CCACTGCACTCCA CCTGGG GAC
                                |||||||||||| |||||| |||
                                GGTGACGTGAGGT GGACCC TTG
                                       G     A
GAM1645  JRK      3'  CCAGGCTGGAGTGAAGTGG   87821       G
                                CCACT CACTCCAGCCTGG
                                ||||| ||||||||||||
                                GGTGA GTGAGGTCGGACC
                                   A
GAM1645  JRK      3'  TCTTCAAGCTGGGTGCAGTGG  87838         T    CTG
                                CCACTGCAC CCAGC   GGAGA
                                ||||||||| |||||   |||||
                                GGTGACGTG GGTCG   CTTCT
                                     _    AA_
GAM1645  KLRD1    3'  CTGCCCAGGCTGGAGCATAGTG 24708       CA         _
              G                   CCACTG  CTCCAGCCTGGG AG
                                ||||||  |||||||||||| ||
                                GGTGAT  GAGGTCGGACCC TC
                                   AC          G
GAM1645  KLRD1    3'  CTGCCCAGGCTGGAGCATAGTG 11213       CA         _
              G                   CCACTG  CTCCAGCCTGGG AG
                                ||||||  |||||||||||| ||
                                GGTGAT  GAGGTCGGACCC TC
                                   AC          G
GAM1645  KMO      3'  CCAGGCTGGAGTGCAGTGG   14840
                                CCACTGCACTCCAGCCTGG
                                |||||||||||||||||||
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                                GGTGACGTGAGGTCGGACC

GAM1645  LARS2    3'  CTCCCAGGCCTGCTGTGG    31694      T   CTCCA
                                CCAC GCA    GCCTGGGAG
                                |||| |||    |||||||||
                                GGTG CGT    CGGACCCTC
                                  T  C____
GAM1645  LILRA3   3'  GTCACCAGGCTGGAATGCAGTG 97021         C        GA
              G                  CCACTGCA TCCAGCCTGG  GAC
                                |||||||| ||||||||||  |||
                                GGTGACGT AGGTCGGACC  CTG
                                    A        A_
GAM1645  LLGL1    3'  GTCGCCCAGGCTGGAGTGCAGT 67421                A
              GG                   CCACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                       G
GAM1645  LNK      3'  CCGGGCTGGAGTGCAGTGG   19641
                                CCACTGCACTCCAGCCTGG
                                ||||||||||||||||||
                                GGTGACGTGAGGTCGGGCC

GAM1645  LTB4R    5'  GTCATTCAGGCTGGAGTGCAGT 7472                 A
              GG                   CCACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACTT CTG
                                       A
GAM1645  LYZ      3'  GTCGCCCAGGCTGGAGTGCAGT 5902                A
              GG                   CCACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                       G
GAM1645  LZTS1    3'  GTCCCCCAGGCTGGAGTGCAGT 41039               A
              GG                   CCACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                       C
GAM1645  MADD     5'  TCTCCCAGCGGGCGCCGCGG   56218      ACT_  A  C
                                CTGC    CC GC TGGGAGA
                                ||||    || || |||||||
                                GGCG    GG CG ACCCTCT
                                  CCGC  G  _
GAM1645  MAK      3'  TCCAGGCTGGAGTGCAGTGG   20954
                                CCACTGCACTCCAGCCTGGG
                                ||||||||||||||||||||
                                GGTGACGTGAGGTCGGACCT

GAM1645  MDM2     3'  GTTACCCAGGCTGGAGTGCAGT 23462                A
              GG                   CCACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||||| |||
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                                GGTGACGTGAGGTCGGACCC TTG
                                      A
GAM1645  MDM2     3'  GTTACCCAGGCTGGAGTGCAGT 23475                A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC TTG
                                      A
GAM1645  MDM2     3'  GTTACCCAGGCTGGAGTGCAGT 23488                A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC TTG
                                      A
GAM1645  MDM2     3'  GTTACCCAGGCTGGAGTGCAGT 23501                A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC TTG
                                      A
GAM1645  MDM2     3'  GTTACCCAGGCTGGAGTGCAGT 11500                A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC TTG
                                      A
GAM1645  MDM4     3'  GTCTCCCAGGCTGAAGTGCAGT 11512          C
              G                    CACTGCACT CAGCCTGGGAGAC
                                   ||||||||| ||||||||||||
                                   GTGACGTGA GTCGGACCCTCTG
                                       A
GAM1645  MEF2A    5'  CCCAGGCTGAAGTGCAGTGG  19997          C
                                  CCACTGCACT CAGCCTGGG
                                  |||||||||| |||||||||
                                  GGTGACGTGA GTCGGACCC
                                      A
GAM1645  MEFV     3'  GTCACCCAGGCTGGAGTGCAGT 5946                 A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC CTG
                                      A
GAM1645  MEFV     3'  GTGGCCCAGGCTGGAGTGCAGT 5948                 AG
              GG                  CCACTGCACTCCAGCCTGGG  AC
                                  |||||||||||||||||||  ||
                                  GGTGACGTGAGGTCGGACCC  TG
                                      GG
GAM1645  MHC2TA   3'  CCCACGCTGGAGTGCAGTG   5973           C
                                  CACTGCACTCCAGC TGGG
                                  |||||||||||||| ||||
                                  GTGACGTGAGGTCG ACCC
                                       C
GAM1645  MHC2TA   3'  GTTGCCCAGGCTGGCGTGCAGT 5994          T       AG
              GG                  CCACTGCAC CCAGCCTGGG  AC
                                  |||||||||| ||||||||||  ||
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                                GGTGACGTG GGTCGGACCC  TG
                                     C         GT
GAM1645  MLANA    3'  GTTGCCCAGGCTGGAGTGCAAT 19769     C           AG
                GG                    CCA TGCACTCCAGCCTGGG  AC
                                      ||| ||||||||||||||||  ||
                                      GGT ACGTGAGGTCGGACCC  TG
                                        A             GT
GAM1645  MME      3'  GTCTCCCAGTTATGAATCAGTG 24436       CAC  CAGC
                G                     CCACTG   TC    CTGGGAGAC
                                      ||||||   ||    |||||||||
                                      GGTGAC   AG    GACCCTCTG
                                         TA_  TATT
GAM1645  MME      3'  GTCTCCCAGTTATGAATCAGTG 24438       CAC  CAGC
                G                     CCACTG   TC    CTGGGAGAC
                                      ||||||   ||    |||||||||
                                      GGTGAC   AG    GACCCTCTG
                                         TA_  TATT
GAM1645  MME      3'  GTCTCCCAGTTATGAATCAGTG 24440       CAC  CAGC
                G                     CCACTG   TC    CTGGGAGAC
                                      ||||||   ||    |||||||||
                                      GGTGAC   AG    GACCCTCTG
                                         TA_  TATT
GAM1645  MME      3'  GTCTCCCAGTTATGAATCAGTG 8033        CAC  CAGC
                G                     CCACTG   TC    CTGGGAGAC
                                      ||||||   ||    |||||||||
                                      GGTGAC   AG    GACCCTCTG
                                         TA_  TATT
GAM1645  MPL      3'  CCAGACTGGAGTGCAGTGG    19345            C
                                      CCACTGCACTCCAG CTGG
                                      |||||||||||||| ||||
                                      GGTGACGTGAGGTC GACC
                                               A
GAM1645  MPL      3'  CCCAGGCTGCAGTGCAATGG   19350     C     C
                                      CCA TGCACT CAGCCTGGG
                                      ||| |||||| |||||||||
                                      GGT ACGTGA GTCGGACCC
                                        A     C
GAM1645  MRPL49   3'  GTTGCCCAGGGTGGAGTGCAGT 70171            G     AG
                GG                    CCACTGCACTCCA CCTGGG  AC
                                      |||||||||||| ||||||  ||
                                      GGTGACGTGAGGT GGACCC  TG
                                             G     GT
GAM1645  MTR      3'  CCCAGGCTGGAGTGCAGGG    6015     A
                                      CC CTGCACTCCAGCCTGGG
                                      || ||||||||||||||||
                                      GG GACGTGAGGTCGGACCC
                                       _
GAM1645  MYLK2    3'  CTCCTAGCTGGAGTGCCATGG  53585     CT        C
                                      CCA  GCACTCCAGC TGGGAG
                                      |||  |||||||||| ||||||
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                                GGT  CGTGAGGTCG ATCCTC
                                  AC        _
GAM1645  MYO10    3'  TTTGAGCTGGAGTGCTGCGG   25617    ACT        CT
                                CC   GCACTCCAGC  GGG
                                ||   ||||||||||  |||
                                GG   CGTGAGGTCG  TTT
                                 CGT         AG
GAM1645  NCOA6    5'  CCGAGGCTGGAGTGCAGTGG   26833              G
                                CCACTGCACTCCAGCCT GG
                                |||||||||||||||| ||
                                GGTGACGTGAGGTCGGA CC
                                           G
GAM1645  NCOA6    5'  GTCGCCCAGGCTGGAGTGCAGT 26845                A
                                ACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||| |||
                                TGACGTGAGGTCGGACCC CTG
                                           G
GAM1645  NCOA6IP  3'  CCCAGGCTGGAGTGCAGTG   46152
                                CACTGCACTCCAGCCTGGG
                                ||||||||||||||||||
                                GTGACGTGAGGTCGGACCC

GAM1645  NDRG3    3'  GTTACCCAGGCTGGAGTGCAAT 50125     C            A
              GG                  CCA TGCACTCCAGCCTGGG GAC
                                ||| |||||||||||||| |||
                                GGT ACGTGAGGTCGGACCC TTG
                                  A             A
GAM1645  NEU3     5'  GTCACCCAGGCTGGAGTGCAGT 22833                A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                           A
GAM1645  NONO     3'  GTCGCCCAGGCTGGAGTGTAGT 82892                A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||| |||
                                GGTGATGTGAGGTCGGACCC CTG
                                           G
GAM1645  NPR2L    3'  GTTACCCAGGCTGGAATACAGT 22598        CAC         A
              GG                  CCACTG   TCCAGCCTGGG GAC
                                ||||||   |||||||||| |||
                                GGTGAC   AGGTCGGACCC TTG
                                   ATA         A
GAM1645  NQO1     3'  GTTACCCAGGCTGGAGTGCAGT 8054                 A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC TTG
                                           A
GAM1645  NT5C2    5'  CTGCCCAGGCTGGAGTACAGTG 25263       C          _
                                CACTG ACTCCAGCCTGGG AG
                                ||||| |||||||||||| ||
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                                GTGAC TGAGGTCGGACCC TC
                                  A           G
GAM1645  ORC1L    3'  GTCGCCCAGGCTGGAGTGCAGT 15987                 A
                GG                  CCACTGCACTCCAGCCTGGG GAC
                                    |||||||||||||||||||| |||
                                    GGTGACGTGAGGTCGGACCC CTG
                                                 G
GAM1645  P2RY6    3'  CAGGGGGCGAAGTGCAGTGG   15994          ___  AG
                                    CCACTGCACT   CC  CCTG
                                    ||||||||||   ||  ||||
                                    GGTGACGTGA   GG  GGAC
                                          AGC  G_
GAM1645  PAICS    3'  GTCGCCCAGGCTGGAGTGCAGT 22267                 A
                GG                  CCACTGCACTCCAGCCTGGG GAC
                                    |||||||||||||||||||| |||
                                    GGTGACGTGAGGTCGGACCC CTG
                                                 G
GAM1645  PCDH1    5'  TCTCCCAGGCTGGCAGCATTGG 51579     C   ACT
                                    CCA TGC   CCAGCCTGGGAGA
                                    ||| |||   ||||||||||||
                                    GGT ACG   GGTCGGACCCTCT
                                      T   AC_
GAM1645  PCDHA9   3'  CCCAGGCTGGAGTACAGTGG   26617       C
                                    CCACTG ACTCCAGCCTGGG
                                    |||||| ||||||||||||
                                    GGTGAC TGAGGTCGGACCC
                                       A
GAM1645  PCDHA9   3'  GTTGCCCAGGCTGGAGTGCAGT 26625                 AG
                GG                  CCACTGCACTCCAGCCTGGG  AC
                                    |||||||||||||||||||  ||
                                    GGTGACGTGAGGTCGGACCC  TG
                                                 GT
GAM1645  PCDHB11  3'  CCCTGGCTGGAGTGCAATGG   38919     C          T
                                    CCA TGCACTCCAGCC GGG
                                    ||| |||||||||||| |||
                                    GGT ACGTGAGGTCGG CCC
                                      A          T
GAM1645  PCDHB16  3'  GTCACCCAGGCTGGAGTGCAGT 40909                 A
                GG                  CCACTGCACTCCAGCCTGGG GAC
                                    |||||||||||||||||||| |||
                                    GGTGACGTGAGGTCGGACCC CTG
                                                 A
GAM1645  PCDHB9   3'  GTCGCCCAGGCTGGAGTGCAGT 39450                 A
                GG                  CCACTGCACTCCAGCCTGGG GAC
                                    |||||||||||||||||||| |||
                                    GGTGACGTGAGGTCGGACCC CTG
                                                 G
GAM1645  PDCL     3'  GTCACCCAGGCTGGAGTACA   19400    C          A
                                    TG ACTCCAGCCTGGG GAC
                                    || |||||||||||| |||
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                                AC TGAGGTCGGACCC CTG
                                 A           A
GAM1645  PDE6B    3'  CCCAGGCTGGAGTGCCGTGG  6073      T
                                CCAC GCACTCCAGCCTGGG
                                |||| ||||||||||||||
                                GGTG CGTGAGGTCGGACCC
                                  C
GAM1645  PDZK1    5'  GTTGCCCAGGCTGGAGTGCAGT 12035              AG
              GG                  CCACTGCACTCCAGCCTGGG  AC
                                  ||||||||||||||||||||  ||
                                  GGTGACGTGAGGTCGGACCC  TG
                                                GT
GAM1645  PER2     3'  CCCAGGCTGGAGTGCAGTGG  43348
                                  CCACTGCACTCCAGCCTGGG
                                  ||||||||||||||||||||
                                  GGTGACGTGAGGTCGGACCC

GAM1645  PIGR     3'  GTCGCCCAGGCTGGAGTGCAGT 73009              A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC CTG
                                                G
GAM1645  PIK3C2B  3'  GTCGCCAGGCTGGAGTGTAGTG 12110              GA
              G                    CCACTGCACTCCAGCCTGG  GAC
                                  ||||||||||||||||||  |||
                                  GGTGATGTGAGGTCGGACC  CTG
                                                G_
GAM1645  PIK3CD   3'  GTTGCCCAGGCTGGAGTGCAGT 18499              AG
              GG                  CCACTGCACTCCAGCCTGGG  AC
                                  ||||||||||||||||||||  ||
                                  GGTGACGTGAGGTCGGACCC  TG
                                                GT
GAM1645  PKNOX1   3'  GTTGCCCAGGCTGGAGGGCAAT 17102     C   A        AG
              GG                  CCA TGC CTCCAGCCTGGG  AC
                                  ||| ||| ||||||||||||  ||
                                  GGT ACG GAGGTCGGACCC  TG
                                    A   G          GT
GAM1645  PMCHL1   3'  GTTGCCCAGGCTGGAGTGCAAT 49921     C           AG
              GG                  CCA TGCACTCCAGCCTGGG  AC
                                  ||| ||||||||||||||||  ||
                                  GGT ACGTGAGGTCGGACCC  TG
                                    A             GT
GAM1645  PON1     3'  GTTGCCCAGGCTGGAGTGCAGT 6540               AG
              GG                  CCACTGCACTCCAGCCTGGG  AC
                                  ||||||||||||||||||||  ||
                                  GGTGACGTGAGGTCGGACCC  TG
                                                GT
GAM1645  POU2AF1  3'  CCCAGGCTGGAGTACAATGG  21735     C  C
                                  CCA TG ACTCCAGCCTGGG
                                  ||| || ||||||||||||
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                                GGT AC TGAGGTCGGACCC
                                  A  A
GAM1645  PPEF2    3'  GTTGCCCAGGCTGGAGTGCATT 21779     C            AG
                GG                  CCA TGCACTCCAGCCTGGG  AC
                                    ||| ||||||||||||||||  ||
                                    GGT ACGTGAGGTCGGACCC  TG
                                      T             GT
GAM1645  PPID     3'  CCCAGGCTGGAGTGCGGTGG   88824
                                    CCACTGCACTCCAGCCTGGG
                                    ||||||||||||||||||||
                                    GGTGGCGTGAGGTCGGACCC

GAM1645  PPP1R12B  3'  CCCAGGCTGGAGTGCAGTGG   50383
                                    CCACTGCACTCCAGCCTGGG
                                    ||||||||||||||||||||
                                    GGTGACGTGAGGTCGGACCC

GAM1645  PPP1R12B  3'  TCCCAATTCCACCAGGTGCAGT 50396          CCAGCC___
                GG                  CCACTGCACT        TGGGA
                                    ||||||||||        |||||
                                    GGTGACGTGG        ACCCT
                                          ACCACCTTA
GAM1645  PRKR     3'  GTTGCCCAGGCTGGAGTGCAAT 12352    C            AG
                G                    CA TGCACTCCAGCCTGGG  AC
                                    || ||||||||||||||||  ||
                                    GT ACGTGAGGTCGGACCC  TG
                                     A             GT
GAM1645  PRKWNK3   3'  GTCACCCAGGTTGGAGTGCAGT 62238                A
                GG                  CCACTGCACTCCAGCCTGGG GAC
                                    |||||||||||||||||||| |||
                                    GGTGACGTGAGGTTGGACCC CTG
                                               A
GAM1645  PRKY     3'  TCTAGGCTAGGTGCAGTGG    12386          CC
                                    CCACTGCACT  AGCCTGGG
                                    ||||||||||  ||||||||
                                    GGTGACGTGG  TCGGATCT
                                          A_
GAM1645  PSEN1    5'  TCTGAACTGGAGTGGAGT    24623     G       CC
                                    ACT CACTCCAG  TGGG
                                    ||| ||||||||  ||||
                                    TGA GTGAGGTC  GTCT
                                      G       AA
GAM1645  PSMB2    3'  CCCAGGCTGGAGTGCTGTGG   12463      T
                                    CCAC GCACTCCAGCCTGGG
                                    |||| ||||||||||||||
                                    GGTG CGTGAGGTCGGACCC
                                      T
GAM1645  PSMD9    3'  CCCAGGCTGGAGTGCAGTG    12523
                                    CACTGCACTCCAGCCTGGG
                                    ||||||||||||||||||||
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                                GTGACGTGAGGTCGGACCC

GAM1645  PTGES    3'  GTTGCCCAAGCTGGAGTGAAGT 18072       G        C    AG
                GG                    CCACT CACTCCAGC TGGG  AC
                                      ||||| ||||||||| ||||  ||
                                      GGTGA GTGAGGTCG ACCC  TG
                                        A        A    GT
GAM1645  PTGIS    3'  CCCAGGCTGGAGTGCAATGG   8203      C
                                      CCA TGCACTCCAGCCTGGG
                                      ||| ||||||||||||||||
                                      GGT ACGTGAGGTCGGACCC
                                        A
GAM1645  PTGIS    3'  CTGCCCAGGCTAGAGTGCAGTG 8207            C       _
                G                     CCACTGCACTC AGCCTGGG AG
                                      |||||||||| |||||||| ||
                                      GGTGACGTGAG TCGGACCC TC
                                            A       G
GAM1645  RAB36    3'  GTCACCCAGGCTGGAGTGCAAT 18178     C             A
                GG                    CCA TGCACTCCAGCCTGGG GAC
                                      ||| |||||||||||||| |||
                                      GGT ACGTGAGGTCGGACCC CTG
                                        A             A
GAM1645  RAB36    3'  GTTGCCCAGGCTGGAGTGCAAT 18180     C             AG
                GG                    CCA TGCACTCCAGCCTGGG  AC
                                      ||| ||||||||||||||  ||
                                      GGT ACGTGAGGTCGGACCC  TG
                                        A             GT
GAM1645  RABL2A   3'  GTCGCCAGGCTGGAGTGCAGTG 26414                 GA
                G                     CCACTGCACTCCAGCCTGG  GAC
                                      ||||||||||||||||||  |||
                                      GGTGACGTGAGGTCGGACC  CTG
                                                 G_
GAM1645  RABL2B   3'  GTCGCCAGGCTGGAGTGCAGTG 23985                 GA
                G                     CCACTGCACTCCAGCCTGG  GAC
                                      ||||||||||||||||||  |||
                                      GGTGACGTGAGGTCGGACC  CTG
                                                 G_
GAM1645  RAI3     3'  GTCACCCAGGCTTGAGTGCAGT 15622           C       A
                GG                    CCACTGCACTC AGCCTGGG GAC
                                      |||||||||| |||||||| |||
                                      GGTGACGTGAG TCGGACCC CTG
                                            T       A
GAM1645  RARG     5'  CTCCCAGGCTGGGGCAGTGG   8262         A T
                                      CCACTGC C CCAGCCTGGGAG
                                      ||||||| | ||||||||||||
                                      GGTGACG G GGTCGGACCCTC
                                          _ _
GAM1645  RBBP9    3'  GTCTCCCAGGCTGGAGGTCAGT 70696        CA
                GG                    CCACTG  CTCCAGCCTGGGAGAC
                                      ||||||  ||||||||||||||||
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                                GGTGAC  GAGGTCGGACCCTCTG
                                   TG
GAM1645  RHD     3'  CCAGGCTGGAGTGCAGTG    32819
                                CACTGCACTCCAGCCTGG
                                ||||||||||||||||||
                                GTGACGTGAGGTCGGACC

GAM1645  RHD     3'  GTCACCCAGGCTAGAGTGCAAT 32836     C      C       A
             GG                   CCA TGCACTC AGCCTGGG GAC
                                ||| ||||||| |||||||| |||
                                GGT ACGTGAG TCGGACCC CTG
                                  A      A       A
GAM1645  RHD     3'  CCAGGCTGGAGTGCAGTG    33139
                                CACTGCACTCCAGCCTGG
                                ||||||||||||||||||
                                GTGACGTGAGGTCGGACC

GAM1645  RHD     3'  GTCACCCAGGCTAGAGTGCAAT 33148     C      C       A
             GG                   CCA TGCACTC AGCCTGGG GAC
                                ||| ||||||| |||||||| |||
                                GGT ACGTGAG TCGGACCC CTG
                                  A      A       A
GAM1645  RP2     3'  GTTGCCCAAGCTGGAGTGCAAT 23606     C        C    AG
             GG                   CCA TGCACTCCAGC TGGG  AC
                                ||| |||||||||| ||||  ||
                                GGT ACGTGAGGTCG ACCC  TG
                                  A         A   GT
GAM1645  RPH3AL   3'  GTTGCCCAGGCTGGGGTGCAGT 23741                AG
             GG                   CCACTGCACTCCAGCCTGGG  AC
                                ||||||||||||||||||  ||
                                GGTGACGTGGGGTCGGACCC  TG
                                        GT
GAM1645  RPP30    3'  CTCAGGCTGGAGTACAGTGG   22197       C
                                CCACTG ACTCCAGCCTGGG
                                |||||| ||||||||||||
                                GGTGAC TGAGGTCGGACTC
                                   A
GAM1645  RPP30    3'  GTCCCCCAGGCTGGAGTGCAGT 22207                A
             GG                   CCACTGCACTCCAGCCTGGG GAC
                                ||||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                        C
GAM1645  SAS     3'  GTTGCCCAGGCTGGAGTGCAAT 21107     C            AG
             GG                   CCA TGCACTCCAGCCTGGG  AC
                                ||| ||||||||||||||  ||
                                GGT ACGTGAGGTCGGACCC  TG
                                  A            GT
GAM1645  SCD     3'  CTCCCAGGCAAGCAGCTGG    18592     _    ACTCCA
                                CCA CTGC     GCCTGGGAG
                                ||| ||||     |||||||||
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                                GGT GACG     CGGACCCTC
                                  C    AA____
GAM1645  SEDL     3'  CAGGCTGGAGTGCAGTGG    28080
                                CCACTGCACTCCAGCCTG
                                ||||||||||||||||||
                                GGTGACGTGAGGTCGGAC

GAM1645  SEDL     3'  CAGGCTGTAGTGCAGTGG    28081          C
                                CCACTGCACT CAGCCTG
                                |||||||||| |||||||
                                GGTGACGTGA GTCGGAC
                                       T
GAM1645  SEDL     3'  CCAGGCTGGAGTGCAGTGG   28086
                                CCACTGCACTCCAGCCTGG
                                |||||||||||||||||||
                                GGTGACGTGAGGTCGGACC

GAM1645  SEDL     3'  TCCAGGCTGGAGTGCAATGG  28111     C
                                CCA TGCACTCCAGCCTGGG
                                ||| ||||||||||||||||
                                GGT ACGTGAGGTCGGACCT
                                  A
GAM1645  SEPN1    3'  CCCAGGCTGGAGTGCTATGG  66967     CT
                                CCA  GCACTCCAGCCTGGG
                                |||  ||||||||||||||
                                GGT  CGTGAGGTCGGACCC
                                  AT
GAM1645  SERPINB9 3'  GTCACCCAGGCTGGAGTGTAGT 16029                 A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||||| |||
                                  GGTGATGTGAGGTCGGACCC CTG
                                             A
GAM1645  SERPINB9 3'  GTCGCCCAGGCTGGAGTGCAGT 16031                  A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC CTG
                                             G
GAM1645  SH3BP2   3'  CCCAGGCTGGAGTGCAATG   13056    C
                                CA TGCACTCCAGCCTGGG
                                || ||||||||||||||||
                                GT ACGTGAGGTCGGACCC
                                  A
GAM1645  SH3BP2   3'  CCGAGGCTGGAGCACAGGG   13059    A   CA       G
                                CC CTG  CTCCAGCCT GG
                                || |||  ||||||||| ||
                                GG GAC  GAGGTCGGA CC
                                  _  AC        G
GAM1645  SHOX     3'  GTCACCCAGGCTGGAGCACACT 23522     C  CA          A
              GG                  CCA TG  CTCCAGCCTGGG GAC
                                  ||| ||  |||||||||||| |||
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                                GGT AC  GAGGTCGGACCC CTG
                                  C  AC          A
GAM1645  SIL      3'  GTAGCCCAGGCTGGAGTGCAAT 13161     C            AG
                GG                  CCA TGCACTCCAGCCTGGG  AC
                                    ||| ||||||||||||||||  ||
                                    GGT ACGTGAGGTCGGACCC  TG
                                      A             GA
GAM1645  SLA2     3'  CCCATGCTGGAGTGCAATGG   50885     C         C
                                    CCA TGCACTCCAGC TGGG
                                    ||| |||||||||| ||||
                                    GGT ACGTGAGGTCG ACCC
                                      A          T
GAM1645  SLC14A2  5'  GTCACCCAGGCTGGAGTACACT 24124     C  C          A
                GG                  CCA TG ACTCCAGCCTGGG GAC
                                    ||| || |||||||||||| |||
                                    GGT AC TGAGGTCGGACCC CTG
                                      C  A           A
GAM1645  SLC15A1  3'  TCCAGGCTGGAGTGCAATGG   18648     C
                                    CCA TGCACTCCAGCCTGGG
                                    ||| ||||||||||||||||
                                    GGT ACGTGAGGTCGGACCT
                                      A
GAM1645  SLC19A2  3'  CCCAGGCTGCAGTGCAGTGG   69550          C
                                    CCACTGCACT CAGCCTGGG
                                    |||||||||| |||||||||
                                    GGTGACGTGA GTCGGACCC
                                          C
GAM1645  SLC24A1  3'  GTTGCCCAGGCTGGTGTGCAAT 17567     C    T        AG
                GG                  CCA TGCAC CCAGCCTGGG  AC
                                    ||| ||||| ||||||||||  ||
                                    GGT ACGTG GGTCGGACCC  TG
                                      A    T         GT
GAM1645  SLC39A1  5'  CCCAGGCTGGAGTGCGGTGG   27808
                                    CCACTGCACTCCAGCCTGGG
                                    ||||||||||||||||||||
                                    GGTGGCGTGAGGTCGGACCC

GAM1645  SLC7A6   3'  CTTGGTAAAGTGCAGTGG    15640          CCA   T
                                    CCACTGCACT   GCC GG
                                    |||||||||   ||| ||
                                    GGTGACGTGA   TGG TC
                                          AA_   T
GAM1645  SMAC     5'  GTCGCCCAGGCTGGAGTGCAGT 58025                A
                GG                  CCACTGCACTCCAGCCTGGG GAC
                                    |||||||||||||||||||| |||
                                    GGTGACGTGAGGTCGGACCC CTG
                                                G
GAM1645  SMAC     5'  GTTGCCCAGGCTGAAGTGCAGT 58027          C        AG
                GG                  CCACTGCACT CAGCCTGGG  AC
                                    |||||||||| |||||||||  ||
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                                  GGTGACGTGA GTCGGACCC  TG
                                        A        GT
GAM1645  SMP1     3'  TCTCCCAAGGGGTGAGTGG   27475       G     AGCC
                                  CCACT CACTCC    TGGGAGA
                                  ||||| ||||||    |||||||
                                  GGTGA GTGGGG    ACCCTCT
                                    _     A___
GAM1645  SNX15    3'  GTCGCCCAGACTGGAGTGCAGT 74130             C     A
               GG                   CCACTGCACTCCAG CTGGG GAC
                                  |||||||||||||| ||||| |||
                                  GGTGACGTGAGGTC GACCC CTG
                                        A    G
GAM1645  SPN      3'  CCCAGGCTGGAGTGCAATG   13373    C
                                  CA TGCACTCCAGCCTGGG
                                  || ||||||||||||||||
                                  GT ACGTGAGGTCGGACCC
                                   A
GAM1645  SS18     3'  GTCGCCCAGGCTGGAGTGCAGT 20105                 A
               GG                   CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC CTG
                                              G
GAM1645  STAU     5'  GTCGCCCAGGCTGGAGTGCAGT 17202                  A
               GG                   CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC CTG
                                              G
GAM1645  TAF11    3'  CCTAGGCTGGAGTGCAGCGG   20117    A
                                  CC CTGCACTCCAGCCTGGG
                                  || ||||||||||||||||
                                  GG GACGTGAGGTCGGATCC
                                   C
GAM1645  TAL1     3'  CTCAGGCTGGAGTACAGTGG   13527       C
                                  CCACTG ACTCCAGCCTGGG
                                  |||||| ||||||||||||
                                  GGTGAC TGAGGTCGGACTC
                                     A
GAM1645  TAPBP    3'  CCCAGGCTGCAGTGCAGTGG   13556          C
                                  CCACTGCACT CAGCCTGGG
                                  |||||||||| |||||||||
                                  GGTGACGTGA GTCGGACCC
                                        C
GAM1645  TAPBP    3'  GTCGCCCAGGCTGGAGTGCAGT 13583                 A
               GG                   CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC CTG
                                              G
GAM1645  TAPBP    3'  GTTGCCCAGGCTGGAGTGCAGT 13585                 AG
               GG                   CCACTGCACTCCAGCCTGGG  AC
                                  ||||||||||||||||||||  ||
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                                GGTGACGTGAGGTCGGACCC  TG
                                          GT
GAM1645  TAT      3'  CCCATGCTGGAGTGCAGTGG   6253              C
                                CCACTGCACTCCAGC TGGG
                                |||||||||||||| ||||
                                GGTGACGTGAGGTCG ACCC
                                         T
GAM1645  TBXA2R   3'  GTCCCCCAGGCTGGAGTGCAGT 8364                  A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                ||||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                          C
GAM1645  TCF2     3'  CCCGAGCTGGAGTGCAGTGG   22404              C
                                CCACTGCACTCCAGC TGGG
                                |||||||||||||| ||||
                                GGTGACGTGAGGTCG GCCC
                                         A
GAM1645  TDGF1    3'  CCCAGGCTGGACTGCAATG    13654    C    C
                                CA TGCA TCCAGCCTGGG
                                || |||| ||||||||||
                                GT ACGT AGGTCGGACCC
                                 A    C
GAM1645  TEM7     3'  TCCTTGGCCAGGTGCAGTGG   40271          CCA   T
                                CCACTGCACT   GCC GGGA
                                |||||||||   ||| ||||
                                GGTGACGTGG   CGG TCCT
                                      AC_   T
GAM1645  TERF1    3'  GTTGCCCAGGCTGGAGTGCAGT 34399                AG
              GG                  CCACTGCACTCCAGCCTGGG  AC
                                |||||||||||||||||||  ||
                                GGTGACGTGAGGTCGGACCC  TG
                                          GT
GAM1645  TERF2    3'  GTCACCCAGGCTGGAGTGCAGT 20162                 A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                ||||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                          A
GAM1645  TIM3     3'  GTTGCCCAGGCTGGAGTGCAAT 52361     C           AG
              GG                  CCA TGCACTCCAGCCTGGG  AC
                                ||| ||||||||||||||  ||
                                GGT ACGTGAGGTCGGACCC  TG
                                  A             GT
GAM1645  TJP1     5'  TCCAGGCAGGAGTGCAGTGG   13767           A
                                CCACTGCACTCC GCCTGGG
                                |||||||||||| |||||||
                                GGTGACGTGAGG CGGACCT
                                       A
GAM1645  TLR5     5'  CCCAGGCTGGACTGCAGTG    13784        C
                                CACTGCA TCCAGCCTGGG
                                ||||||| ||||||||||
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                                GTGACGT AGGTCGGACCC
                                   C
GAM1645  TMC1     5'  GTTGCCCAGGCTGGAGTGCAGT 57711                AG
                 GG                  CCACTGCACTCCAGCCTGGG  AC
                                     ||||||||||||||||||||  ||
                                     GGTGACGTGAGGTCGGACCC  TG
                                           GT
GAM1645  TMC2     3'  GTCTCCTCTCTTGGAATGCATG 55804    C    C     CCT
                                     CA TGCA TCCAG   GGGAGAC
                                     || |||| |||||   |||||||
                                     GT ACGT AGGTT   TCCTCTG
                                      _   A    CTC
GAM1645  TMPRSS3  3'  GTTGCCCAGGCTGGAGTGCAGT 51522                AG
                 GG                  CCACTGCACTCCAGCCTGGG  AC
                                     ||||||||||||||||||||  ||
                                     GGTGACGTGAGGTCGGACCC  TG
                                           GT
GAM1645  TMPRSS3  3'  GTTGCCCAGGCTGGAGTGCAGT 51549                AG
                 GG                  CCACTGCACTCCAGCCTGGG  AC
                                     ||||||||||||||||||||  ||
                                     GGTGACGTGAGGTCGGACCC  TG
                                           GT
GAM1645  TMPRSS3  3'  GTTGCCCAGGCTGGAGTGCAGT 44032                AG
                 GG                  CCACTGCACTCCAGCCTGGG  AC
                                     ||||||||||||||||||||  ||
                                     GGTGACGTGAGGTCGGACCC  TG
                                           GT
GAM1645  TNFAIP2  3'  GTTGCCCAGGCTGGAGTGCAGT 21928                AG
                 GG                  CCACTGCACTCCAGCCTGGG  AC
                                     ||||||||||||||||||||  ||
                                     GGTGACGTGAGGTCGGACCC  TG
                                           GT
GAM1645  TNFRSF10B 3'  CCCAGGCTGGAGTGCAACGG   15221    AC
                                     CC  TGCACTCCAGCCTGGG
                                     ||  ||||||||||||||||
                                     GG  ACGTGAGGTCGGACCC
                                      CA
GAM1645  TNFRSF10B 3'  GTCTCCCAGGCTGGAGTGCAAT 15231     C
                 GG                  CCA TGCACTCCAGCCTGGGAGAC
                                     |||  ||||||||||||||||||||
                                     GGT ACGTGAGGTCGGACCCTCTG
                                       A
GAM1645  TNFRSF11A 3'  CCCAGGCTAGAGTGCAGTGG   15192          C
                                     CCACTGCACTC AGCCTGGG
                                     ||||||||||| ||||||||
                                     GGTGACGTGAG TCGGACCC
                                           A
GAM1645  TNFRSF1B  3'  CTCAGGCCAGGTGCAGTGG    8392          CCA
                                     CCACTGCACT   GCCTGGG
                                     |||||||||   |||||||
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                                GGTGACGTGG   CGGACTC
                                     AC_
GAM1645  TNFRSF9   3'  GTCACCCAGGCTGGAGTGCAGT 9585                A
              GG                   CCACTGCACTCCAGCCTGGG GAC
                                   |||||||||||||||||||| |||
                                   GGTGACGTGAGGTCGGACCC CTG
                                          A
GAM1645  TP53      3'  GTTGCCCAGGCTGGAGTGGAGT 6805       G          AG
              GG                   CCACT CACTCCAGCCTGGG  AC
                                   ||||| ||||||||||||||  ||
                                   GGTGA GTGAGGTCGGACCC  TG
                                     G           GT
GAM1645  TPMT      3'  CCCAACCTGGAGTGCAGTGG   6308             CC
                                   CCACTGCACTCCAG  TGGG
                                   ||||||||||||||  ||||
                                   GGTGACGTGAGGTC  ACCC
                                          CA
GAM1645  TRAF5     3'  GTCACCCAGGCTGGAGTACAGT 17281        C          A
              GG                   CCACTG ACTCCAGCCTGGG GAC
                                   ||||||| |||||||||||||| |||
                                   GGTGAC TGAGGTCGGACCC CTG
                                     A           A
GAM1645  TRPM6     3'  CCCAGGCTGGAGTGCAATG    35030    C
                                   CA TGCACTCCAGCCTGGG
                                   || ||||||||||||||||
                                   GT ACGTGAGGTCGGACCC
                                    A
GAM1645  TRPV1     3'  CCCAGGCTGGAATGCAGTGG   38693        C
                                   CCACTGCA TCCAGCCTGGG
                                   |||||||| ||||||||||
                                   GGTGACGT AGGTCGGACCC
                                        A
GAM1645  TRPV1     3'  GTTGCCCAGGCTGGAGTGCAGT 38704                AG
              GG                   CCACTGCACTCCAGCCTGGG  AC
                                   |||||||||||||||||||  ||
                                   GGTGACGTGAGGTCGGACCC  TG
                                          GT
GAM1645  TRPV1     3'  CCCAGGCTGGAATGCAGTGG   55665        C
                                   CCACTGCA TCCAGCCTGGG
                                   |||||||| ||||||||||
                                   GGTGACGT AGGTCGGACCC
                                        A
GAM1645  TRPV1     3'  GTTGCCCAGGCTGGAGTGCAGT 55686                AG
              GG                   CCACTGCACTCCAGCCTGGG  AC
                                   |||||||||||||||||||  ||
                                   GGTGACGTGAGGTCGGACCC  TG
                                          GT
GAM1645  TRPV1     3'  CCCAGGCTGGAATGCAGTGG   55709        C
                                   CCACTGCA TCCAGCCTGGG
                                   |||||||| ||||||||||
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                                GGTGACGT AGGTCGGACCC
                                    A
GAM1645  TRPV1    3'  GTTGCCCAGGCTGGAGTGCAGT 55720                AG
                GG                  CCACTGCACTCCAGCCTGGG  AC
                                    ||||||||||||||||||  ||
                                    GGTGACGTGAGGTCGGACCC  TG
                                          GT
GAM1645  TRPV1    3'  CCCAGGCTGGAATGCAGTGG   55740         C
                                    CCACTGCA TCCAGCCTGGG
                                    ||||||||  ||||||||||
                                    GGTGACGT AGGTCGGACCC
                                        A
GAM1645  TRPV1    3'  GTTGCCCAGGCTGGAGTGCAGT 55751                AG
                GG                  CCACTGCACTCCAGCCTGGG  AC
                                    ||||||||||||||||||  ||
                                    GGTGACGTGAGGTCGGACCC  TG
                                          GT
GAM1645  TUFT1    3'  GTCACCCAGGCTGGAGTGCAGT 39676              A
                                    ACTGCACTCCAGCCTGGG GAC
                                    ||||||||||||||||| |||
                                    TGACGTGAGGTCGGACCC CTG
                                          A
GAM1645  UGDH     3'  GTTGCCCAGGCTGGAGTGCAGT 14003                AG
                GG                  CCACTGCACTCCAGCCTGGG  AC
                                    ||||||||||||||||||  ||
                                    GGTGACGTGAGGTCGGACCC  TG
                                          GT
GAM1645  UMPS     3'  CCCAGGATGGAGTGCAGTGG   6329            G
                                    CCACTGCACTCCA CCTGGG
                                    ||||||||||||| ||||||
                                    GGTGACGTGAGGT GGACCC
                                        A
GAM1645  VENTX2   3'  GTCACCCAGGCTGGAGTGCAAT 27864    C           A
                G                    CA TGCACTCCAGCCTGGG GAC
                                    || |||||||||||||| |||
                                    GT ACGTGAGGTCGGACCC CTG
                                     A           A
GAM1645  VHL      3'  CCCAGGCTGGAGTGCAGAGG   6845    A
                                    CC CTGCACTCCAGCCTGGG
                                    || ||||||||||||||||
                                    GG GACGTGAGGTCGGACCC
                                     A
GAM1645  VIPR2    3'  GTCGCCCAGGCTGGAGTGCAGT 14074              A
                GG                  CCACTGCACTCCAGCCTGGG GAC
                                    |||||||||||||||||| |||
                                    GGTGACGTGAGGTCGGACCC CTG
                                          G
GAM1645  WBSCR1   3'  CTCTCTGGCTGGGTGCAGTG   50085        T    T
                                    CACTGCAC CCAGCC GGGAG
                                    |||||||| |||||| |||||
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                                GTGACGTG GGTCGG CTCTC
                                    _     T
GAM1645  WBSCR1   3'  CTCTCTGGCTGGGTGCAGTG   42481        T     T
                                CACTGCAC CCAGCC GGGAG
                                |||||||| |||||| |||||
                                GTGACGTG GGTCGG CTCTC
                                    _     T
GAM1645  XRCC2    3'  CTCCTAGAGTGCAGGG      19499    A       CAGCC
                                CC CTGCACTC    TGGGAG
                                || ||||||||    ||||||
                                GG GACGTGAG    ATCCTC
                                 _     _____
GAM1645  XRCC2    3'  GTCTCCCAGGCTGCTGGAGTGC 19508           ___
             AGTGG                  CCACTGCACTCCA   GCCTGGGAGAC
                                ||||||||||||   ||||||||||
                                GGTGACGTGAGGT   CGGACCCTCTG
                                       CGT
GAM1645  XRCC2    3'  GTCTCCCAGGCTGGAGTGCAGT 19510
             GG                   CCACTGCACTCCAGCCTGGGAGAC
                                |||||||||||||||||||||||
                                GGTGACGTGAGGTCGGACCCTCTG

GAM1645  YES1     3'  CCCAGGCTGGAGTGCAGTGG   19532
                                CCACTGCACTCCAGCCTGGG
                                ||||||||||||||||||
                                GGTGACGTGAGGTCGGACCC

GAM1645  ZNF133   5'  GTTGCCCAGGCTGGAGTGCAAT 14299     C            AG
             GG                   CCA TGCACTCCAGCCTGGG  AC
                                ||| ||||||||||||||  ||
                                GGT ACGTGAGGTCGGACCC  TG
                                  A            GT
GAM1645  ZNF157   3'  GTCACCCAGGCTGGAGTGCAAT 14337     C            A
             GG                   CCA TGCACTCCAGCCTGGG GAC
                                ||| |||||||||||||| |||
                                GGT ACGTGAGGTCGGACCC CTG
                                  A            A
GAM1645  ZNF253   3'  CCGAGGCTGGAGTGCAATG    41077    C          G
                                CA TGCACTCCAGCCT GG
                                || ||||||||||||| ||
                                GT ACGTGAGGTCGGA CC
                                 A          G
GAM1645  ZNF264   3'  GTCACCCAGGCTGGAGTGCAGT 14226               A
             GG                   CCACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                          A
GAM1645  ZNF264   3'  CCCACGCTGGAGTGCTGTG    14206     T        C
                                CAC GCACTCCAGC TGGG
                                ||| |||||||||| ||||
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                                GTG CGTGAGGTCG ACCC
                                  T         C
GAM1645  ZNF7     5'  GTCTCTCGGCCAGAACACGTGG 14174      _  CAC  CA   T
                                CCAC TG   TC  GCC GGGAGAC
                                |||| ||   ||  ||| |||||||
                                GGTG AC   AG  CGG CTCTCTG
                                  C  A__  AC   _
GAM1645  20D7-FC4  5'  GTCACCCAGGCTGGAGTGCAGT 61567                 A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC CTG
                                             A
GAM1645  AAK1     3'  CCTGGGCTGGAGTGCAGTGG  30520              TG
                                CCACTGCACTCCAGCC  GG
                                ||||||||||||||||  ||
                                GGTGACGTGAGGTCGG  CC
                                          GT
GAM1645  AGMAT    3'  GTCACCCAGGCTGGAGTGCAGT 45743                 A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC CTG
                                             A
GAM1645  AGMAT    3'  TCTTGGCTGGAGTGAGTGG   45744       G        T
                                CCACT CACTCCAGCC GGGA
                                ||||| |||||||||| ||||
                                GGTGA GTGAGGTCGG TTCT
                                  _         _
GAM1645  ANKRD6   3'  GTCACCCAGACTGGAGTGCAGT 30774             C     A
              GG                  CCACTGCACTCCAG CTGGG GAC
                                  |||||||||||||| ||||| |||
                                  GGTGACGTGAGGTC GACCC CTG
                                           A    A
GAM1645  AP1S3    3'  GTCACCCAGGCTGGAGTGCAGT 75429                  A
                                ACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||| |||
                                TGACGTGAGGTCGGACCC CTG
                                             A
GAM1645  AP3S2    3'  CCCAGGCTGGAGTGCTGTGG  20648      T
                                CCAC GCACTCCAGCCTGGG
                                |||| ||||||||||||||
                                GGTG CGTGAGGTCGGACCC
                                  T
GAM1645  APOL2    3'  CCCAGGATGGAGTGCAGTGG  48786            G
                                CCACTGCACTCCA CCTGGG
                                |||||||||||| ||||||
                                GGTGACGTGAGGT GGACCC
                                           A
GAM1645  APXL2    5'  GTCGCCAGGCTGGAGTGCAGTG 75684                 GA
              G                   CCACTGCACTCCAGCCTGG  GAC
                                  |||||||||||||||||  |||
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                                  GGTGACGTGAGGTCGGACC  CTG
                                        G_
GAM1645  ARHF     3'  CTCAGGCTAGAGTGCAGTGG   39266          C
                                  CCACTGCACTC AGCCTGGG
                                  |||||||||| ||||||||
                                  GGTGACGTGAG TCGGACTC
                                        A
GAM1645  ARHGAP11A 3'  GTCGTCCAGGCTGGAGTGCAGT 29458                GA
              GG                    CCACTGCACTCCAGCCTGG  GAC
                                  |||||||||||||||||  |||
                                  GGTGACGTGAGGTCGGACC  CTG
                                        TG
GAM1645  ARHGAP5   5'  GTTGCCCAGGCTGGAGTGCAAT 77605     C            AG
              GG                    CCA TGCACTCCAGCCTGGG  AC
                                  ||| ||||||||||||||  ||
                                  GGT ACGTGAGGTCGGACCC  TG
                                    A             GT
GAM1645  ASB16    3'  GTTGCCCAGGCTGGAGTGCAGT 55989                AG
              GG                    CCACTGCACTCCAGCCTGGG  AC
                                  ||||||||||||||||||  ||
                                  GGTGACGTGAGGTCGGACCC  TG
                                        GT
GAM1645  ASB16    5'  GTCGCCCAGGCTGGAGTGCAGT 70492                 A
              GG                    CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC CTG
                                        G
GAM1645  ASB16    3'  GTGGCCCAGGCTGAAGTGCAGT 70494          C       AG
              GG                    CCACTGCACT CAGCCTGGG  AC
                                  |||||||||| |||||||||  ||
                                  GGTGACGTGA GTCGGACCC  TG
                                      A        GG
GAM1645  ASE-1    3'  GTCACCCAGGCTGGAGTGCAGT 24991                A
              GG                    CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC CTG
                                        A
GAM1645  ASE-1    3'  GTCGCCCAGGTTGGAGTGCAGT 24993                A
              GG                    CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||| |||
                                  GGTGACGTGAGGTTGGACCC CTG
                                        G
GAM1645  ATP1B4   3'  GTCACCCAGGCTGGAGTGCAGT 24851                 A
              GG                    CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC CTG
                                        A
GAM1645  BA108L7.2 3'  CCCAGGCTGGAGTGCGATGG   49070     C
                                  CCA TGCACTCCAGCCTGGG
                                  ||| ||||||||||||||
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                                GGT GCGTGAGGTCGGACCC
                                  A
GAM1645 BAG5     3' CCCAGGCTGCAGTGCAGTGG  18035          C
                                CCACTGCACT CAGCCTGGG
                                |||||||||| |||||||||
                                GGTGACGTGA GTCGGACCC
                                      C
GAM1645 BIA2     3' CTTAAGGCTGGGTGCAGTGG  71794          T      GG
                                CCACTGCAC CCAGCCT  GAG
                                ||||||||| |||||||  |||
                                GGTGACGTG GGTCGGA  TTC
                                      _      A_
GAM1645 BMF      3' CTCCCAGGAAGAGTGCTGTGG  54281      T     CAG
                                CCAC GCACTC   CCTGGGAG
                                |||| ||||||   ||||||||
                                GGTG CGTGAG   GGACCCTC
                                  T     AA_
GAM1645 BNIP-S   3' GTCGCCAGGCTGGAGTGCAGTG 57095                GA
             G                   CCACTGCACTCCAGCCTGG  GAC
                                 ||||||||||||||||||  |||
                                 GGTGACGTGAGGTCGGACC  CTG
                                           G_
GAM1645 BTN3A1   3' CTAGGCTGGAGTGCAGTGG   23889
                                CCACTGCACTCCAGCCTGG
                                ||||||||||||||||||
                                GGTGACGTGAGGTCGGATC

GAM1645 BY55     5' GTCAACCAGGCCAGAGTGCAGT 60063          CA     GA
             G                   CACTGCACTC  GCCTGG  GAC
                                 ||||||||||  ||||||  |||
                                 GTGACGTGAG  CGGACC  CTG
                                       AC      AA
GAM1645 C(27)-3BETA-HSD 3' GTCACCCAGACTGGAGTGCAGT 48054             C     A
             GG                    CCACTGCACTCCAG CTGGG GAC
                                   |||||||||||||| ||||| |||
                                   GGTGACGTGAGGTC GACCC CTG
                                         A     A
GAM1645 C11orf17 3' GTTGCCCAGGCTGGAGTGCAGT 40588                AG
             GG                    CCACTGCACTCCAGCCTGGG  AC
                                   ||||||||||||||||||  ||
                                   GGTGACGTGAGGTCGGACCC  TG
                                            GT
GAM1645 C13orf1  3' GTCACCCAGGCTAGAGTGCAGT 40369          C       A
             GG                    CCACTGCACTC AGCCTGGG GAC
                                   |||||||||| |||||||| |||
                                   GGTGACGTGAG TCGGACCC CTG
                                         A       A
GAM1645 C14orf4  5' GTCTCGGCGTGGAACGCACGG  67920    AC   AC    _   TGG
                                CC  TGC  TCCA GCC   GAGAC
                                ||  |||  |||| |||   |||||
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                                GG  ACG  AGGT CGG   CTCTG
                                 C_   CA    G  ___
GAM1645  C16orf7   3'  CCCAGAAGAAGCTGGAGTGCA  18143          _____
                                TGCACTCCAGC    CTGGG
                                ||||||||||    |||||
                                ACGTGAGGTCG    GACCC
                                      AAGAA
GAM1645  C1orf24   3'  CCAAGGCTGGAGTGCAGTGG   54785              G
                                CCACTGCACTCCAGCCT GG
                                |||||||||||||||| ||
                                GGTGACGTGAGGTCGGA CC
                                           A
GAM1645  C1QTNF6   3'  GTTGCCCAGGCTAGAGTGCAGT 49995          C       AG
              GG                   CCACTGCACTC AGCCTGGG  AC
                                |||||||||| ||||||||  ||
                                GGTGACGTGAG TCGGACCC  TG
                                      A       GT
GAM1645  C20orf172 3'  TTTTGAGGCTGGGCGCAATGG  46770     C   A T      G
                                CCA TGC C CCAGCCT GGAG
                                ||| ||| | ||||||| ||||
                                GGT ACG G GGTCGGA TTTT
                                  A   C _      G
GAM1645  C20orf183 3'  TCCCAACTGGGTGCAGTGG    48539         T    CC
                                CCACTGCAC CCAG  TGGGA
                                |||||||| ||||  |||||
                                GGTGACGTG GGTC  ACCCT
                                      _    A_
GAM1645  C21orf25  3'  CCTGACGCTGGAGTGCGGTG   64290            CT_
                                CACTGCACTCCAGC   GGG
                                ||||||||||||||   |||
                                GTGGCGTGAGGTCG   TCC
                                         CAG
GAM1645  C21orf25  3'  GTTGCCCAGGCTGGAGTGCAAT 64300     C            AG
              GG                   CCA TGCACTCCAGCCTGGG  AC
                                ||| ||||||||||||||  ||
                                GGT ACGTGAGGTCGGACCC  TG
                                  A             GT
GAM1645  C21orf67  5'  GTCGCCCAGGCTGGAGCGCAAT 55233     C   A          A
              GG                   CCA TGC CTCCAGCCTGGG GAC
                                ||| ||| ||||||||||| |||
                                GGT ACG GAGGTCGGACCC CTG
                                  A   C          G
GAM1645  C22orf19  3'  TCCAGGCTGGAGTGCAGTGG   14828
                                CCACTGCACTCCAGCCTGGG
                                ||||||||||||||||||
                                GGTGACGTGAGGTCGGACCT

GAM1645  C22orf19  3'  TGGGCTGGGCACAGTGG     14837        CA T
                                CCACTG  C CCAGCCTG
                                ||||||  | ||||||||
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                                GGTGAC  G GGTCGGGT
                                   AC _
GAM1645  C3F      3'  CCCACGCTGGAATGCAGTGG   20475         C     C
                                CCACTGCA TCCAGC TGGG
                                |||||||| |||||| ||||
                                GGTGACGT AGGTCG ACCC
                                     A     C
GAM1645  C6orf31   3'  TCTCCCAGGCTCTTTCTGCAG  48385       CTCC_
                                CTGCA    AGCCTGGGAGA
                                |||||    ||||||||||
                                GACGT    TCGGACCCTCT
                                   CTTTC
GAM1645  C6orf33   3'  GTCGCCCAGGCTGGAGTGCAGT 56719                 A
              G                    CACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||| |||
                                GTGACGTGAGGTCGGACCC CTG
                                          G
GAM1645  C6orf5    3'  CCAGGCTGCAGTACAGTG    31979       C   C
                                CACTG ACT CAGCCTGG
                                ||||| ||| ||||||||
                                GTGAC TGA GTCGGACC
                                   A   C
GAM1645  C6orf5    3'  TCCAGGCTGGAGTGCAGTG    32005
                                CACTGCACTCCAGCCTGGG
                                ||||||||||||||||||
                                GTGACGTGAGGTCGGACCT

GAM1645  C6orf5    3'  TTTTTAGGCTGGGCGCAGTGG  32010         A T
                                CCACTGC C CCAGCCTGGGAG
                                ||||||| | ||||||||||||
                                GGTGACG G GGTCGGATTTTT
                                     C _
GAM1645  C9orf9    3'  CCCAGGCTGGAGTGCGGTGG   39014
                                CCACTGCACTCCAGCCTGGG
                                ||||||||||||||||||
                                GGTGGCGTGAGGTCGGACCC

GAM1645  C9orf9    3'  GTCTCCCAGGCTGGAGTGCAGT 39032
              GG                   CCACTGCACTCCAGCCTGGGAGAC
                                ||||||||||||||||||||||
                                GGTGACGTGAGGTCGGACCCTCTG

GAM1645  CACNG4    3'  TCCCAGGCAGAGTAAGCAG    27710      __    CA
                                CTGC  ACTC  GCCTGGGA
                                ||||  ||||  ||||||||
                                GACG  TGAG  CGGACCCT
                                   AA    A_
GAM1645  CAPN6     3'  TCAAGAGCTGGAGTTCAATG   27401    C  C       _  GG
                                CA TG ACTCCAGC CT  GA
                                || || |||||||| ||  ||
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                                GT AC TGAGGTCG GA  CT
                                 A  T       A  A_
GAM1645  CARD6    3'  GTTGCCCAGGCTGGAGTGCAAT 51849     C            AG
                GG                  CCA TGCACTCCAGCCTGGG  AC
                                    ||| ||||||||||||||  ||
                                    GGT ACGTGAGGTCGGACCC  TG
                                      A             GT
GAM1645  CDC14B   3'  TCCAGGCTGGAGTGCAGTGG   54011
                                    CCACTGCACTCCAGCCTGGG
                                    ||||||||||||||||||||
                                    GGTGACGTGAGGTCGGACCT

GAM1645  CEACAM8  3'  GTCGCCCAGGCTGGAGTGCAGT 10187                A
                GG                  CCACTGCACTCCAGCCTGGG GAC
                                    |||||||||||||||||| |||
                                    GGTGACGTGAGGTCGGACCC CTG
                                                 G
GAM1645  CHSY1    3'  GTTACCCAGGCTGGAATGCAGT 30572        C        A
                GG                  CCACTGCA TCCAGCCTGGG GAC
                                    |||||||| |||||||||| |||
                                    GGTGACGT AGGTCGGACCC TTG
                                       A         A
GAM1645  CIP29    3'  CCCAGCTGGAGTGCAGTGG   51373            C
                                    CCACTGCACTCCAGC TGGG
                                    |||||||||||||| ||||
                                    GGTGACGTGAGGTCG ACCC
                                                 _
GAM1645  CNNM4    3'  CTTCCACTGGGTGCAG     39865       T   CC
                                    CTGCAC CCAG  TGGGAG
                                    |||||| ||||  ||||||
                                    GACGTG GGTC  ACCTTC
                                      _   __
GAM1645  COLEC12  3'  GTTGCCCAGGCTGGAGTGCAGT 48619                AG
                GG                  CCACTGCACTCCAGCCTGGG  AC
                                    |||||||||||||||||  ||
                                    GGTGACGTGAGGTCGGACCC  TG
                                                 GT
GAM1645  CPSF2    3'  GTCACCCAGGCTGGAGTGCAGT 62280                A
                GG                  CCACTGCACTCCAGCCTGGG GAC
                                    |||||||||||||||||| |||
                                    GGTGACGTGAGGTCGGACCC CTG
                                                 A
GAM1645  CPSF2    3'  GTTGCCCAGACTGGAGTGCAAT 62282     C        C    AG
                GG                  CCA TGCACTCCAG CTGGG  AC
                                    ||| |||||||||| |||||  ||
                                    GGT ACGTGAGGTC GACCC  TG
                                      A         A    GT
GAM1645  CSAD     3'  CTTTGAGGCCGGGTGCAGTGG  32579         T  A   G
                                    CCACTGCAC CC GCCT GGAG
                                    |||||||| || |||| ||||
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                                GGTGACGTG GG CGGA TTTC
                                    _ C   G
GAM1645 ctm-1    3' TCTCCCAGGGCCAGAGACAGCA 75765     A__  CA  _
            G                    CTGC  CTC  GCC TGGGAGA
                                 ||||  |||  ||| |||||||
                                 GACG  GAG  CGG ACCCTCT
                                   ACA  AC  G
GAM1645 CXYorf1  5' TCTCCCAGCAGGTAGAGCAG  82921     A _ A C
                                 CTGC CT CC GC TGGGAGA
                                 |||| || || || |||||||
                                 GACG GA GG CG ACCCTCT
                                   A T A _
GAM1645 CYLC2    3' CCCTGGCTGGAGTTCAGTG   9032       C       T
                                 CACTG ACTCCAGCC GGG
                                 ||||| ||||||||| |||
                                 GTGAC TGAGGTCGG CCC
                                   T       T
GAM1645 DBR1     3' CCTAGACTGGAGTGCAATGG  33062     C       C
                                 CCA TGCACTCCAG CTGGG
                                 ||| |||||||||| |||||
                                 GGT ACGTGAGGTC GATCC
                                   A        A
GAM1645 DCOHM    3' CAGACTGGAGTGCAGTGG    50514           C
                                 CCACTGCACTCCAG CTG
                                 |||||||||||||| |||
                                 GGTGACGTGAGGTC GAC
                                          A
GAM1645 DCOHM    3' GTCGCCCAGGCTGGAGTGCAAT 50535    C           A
            GG                   CCA TGCACTCCAGCCTGGG GAC
                                 ||| |||||||||||||| |||
                                 GGT ACGTGAGGTCGGACCC CTG
                                   A            G
GAM1645 DDX31    3' TCCCTGGATGGAGTGCAGTCA  57614   C       G  T
                                 C ACTGCACTCCA CC GGGA
                                 | |||||||||| || ||||
                                 A TGACGTGAGGT GG CCCT
                                  C         A  T
GAM1645 DKFZp434A2417 3' GTTGCCCAGGCTGGAGGGCAAT 66685    C  A         AG
            GG                   CCA TGC CTCCAGCCTGGG  AC
                                 ||| ||| ||||||||||||  ||
                                 GGT ACG GAGGTCGGACCC  TG
                                   A  G          GT
GAM1645 DKFZP434B044 3' GTTGCCCAAGGTAGAGTGCAGT 49721          CA  _  AG
            GG                   CCACTGCACTC  GCCT GGG  AC
                                 ||||||||||  |||| |||  ||
                                 GGTGACGTGAG  TGGA CCC  TG
                                        A_   A  GT
GAM1645 DKFZP434B1727 3' GTTACCCAGGCTGGAGTACAGT 50480       C          A
            GG                   CCACTG ACTCCAGCCTGGG GAC
                                 |||||| |||||||||||| |||
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                                GGTGAC TGAGGTCGGACCC TTG
                                   A           A
GAM1645  DKFZp434C0923 3'  GTCACCCAGGCTGGAGTACAGT 34652       C          A
            GG                  CCACTG ACTCCAGCCTGGG GAC
                                |||||| |||||||||||||| |||
                                GGTGAC TGAGGTCGGACCC CTG
                                   A           A
GAM1645  DKFZP434C212 3'   GTTGCCCAGGCTGGAGTGCAAT 69499     C             AG
            GG                  CCA TGCACTCCAGCCTGGG  AC
                                ||| ||||||||||||||||  ||
                                GGT ACGTGAGGTCGGACCC  TG
                                  A             GT
GAM1645  DKFZP434D146 3'   GTCGCCCAGGCTAGAGTATAGT 32140       C   C       A
            GG                  CCACTG ACTC AGCCTGGG GAC
                                |||||| |||| |||||||| |||
                                GGTGAT TGAG TCGGACCC CTG
                                   A   A       G
GAM1645  DKFZp434E2220 5'  GTTGCCCAGGCTGGAGTGCAGT 34718                 AG
            GG                  CCACTGCACTCCAGCCTGGG  AC
                                |||||||||||||||||||  ||
                                GGTGACGTGAGGTCGGACCC  TG
                                          GT
GAM1645  DKFZP434F0318 3'  CCTAGGCTGGAGTTGCAGTGG  48749         _
                                CCACTGCA CTCCAGCCTGGG
                                |||||||| ||||||||||||
                                GGTGACGT GAGGTCGGATCC
                                   T
GAM1645  DKFZp434F1719 3'  GTTTCCCAGGCTGGAGTGCAAT 51017     C
            GG                  CCA TGCACTCCAGCCTGGGAGAC
                                ||| ||||||||||||||||||||
                                GGT ACGTGAGGTCGGACCCTTTG
                                  A
GAM1645  DKFZP434J037 3'   CCCAGGCTAGAGTGCAATGG   48943     C      C
                                CCA TGCACTC AGCCTGGG
                                ||| ||||||| ||||||||
                                GGT ACGTGAG TCGGACCC
                                  A      A
GAM1645  DKFZP564D166 3'   CCTAGGCCAGAGTGCAGTGG   48395          CA
                                CCACTGCACTC  GCCTGGG
                                ||||||||||  |||||||
                                GGTGACGTGAG  CGGATCC
                                      AC
GAM1645  DKFZP564G092 5'   CCCAGGCTGTAGTGCAGTGG   32156          C
                                CCACTGCACT CAGCCTGGG
                                |||||||||| |||||||||
                                GGTGACGTGA GTCGGACCC
                                      T
GAM1645  DKFZP564I122 3'   CCTAGGCTGGAGTGCAGTGG   63874
                                CCACTGCACTCCAGCCTGGG
                                ||||||||||||||||||||
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                                GGTGACGTGAGGTCGGATCC

GAM1645  DKFZP564K0322 3'  GTTGCCCAGGCTGGAGTGCAGT 50190                AG
            GG                  CCACTGCACTCCAGCCTGGG  AC
                                ||||||||||||||||||  ||
                                GGTGACGTGAGGTCGGACCC  TG
                                      GT
GAM1645  DKFZP564O0523 3'  GTTGCCCAGGCTGGAATGCAGT 50424        C        AG
            GG                  CCACTGCA TCCAGCCTGGG  AC
                                ||||||||| ||||||||||  ||
                                GGTGACGT AGGTCGGACCC  TG
                                    A         GT
GAM1645  DKFZP566I1024 3'  GTTGCCCAGGCTAGAGTGCACT 70652     C      C       AG
            GG                  CCA TGCACTC AGCCTGGG  AC
                                ||| ||||||| ||||||||  ||
                                GGT ACGTGAG TCGGACCC  TG
                                  C      A       GT
GAM1645  DKFZP761E2110 3'  CCTAGGCTGGAATGCAGTGG   48962        C
                                CCACTGCA TCCAGCCTGGG
                                ||||||||| ||||||||||
                                GGTGACGT AGGTCGGATCC
                                    A
GAM1645  DKFZp761H2121 5'  CTCTTTTGGAGTGCAG      57179          CCT
                                CTGCACTCCAG   GGGAG
                                ||||||||||   |||||
                                GACGTGAGGTT   TTCTC
                                      ___
GAM1645  DKFZp761J139 5'  GTCACCCAGGCTGGAGTGCAGT 51112                A
            GG                  CCACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                      A
GAM1645  DKFZp761N1114 3'  CCAGGCTGGAATGCAGTGG    79777        C
                                CCACTGCA TCCAGCCTGG
                                ||||||||| ||||||||||
                                GGTGACGT AGGTCGGACC
                                    A
GAM1645  DKFZp761O0113 5'  GTTGCCCAGGCTTGAGTGCAGT 37899          C       AG
            G                    CACTGCACTC AGCCTGGG  AC
                                ||||||||| ||||||||  ||
                                GTGACGTGAG TCGGACCC  TG
                                    T       GT
GAM1645  DKFZp762K222 5'  GTCTCCCGGGGACTGCAGCGG  71674    A    C   AGC
                                CC CTGCA TCC   CTGGGAGAC
                                || ||||| |||   |||||||||
                                GG GACGT AGG   GGCCCTCTG
                                  C    C  ___
GAM1645  DKFZp762P2111 3'  GTTGCCCAGGCTGGAGTGCAAT 87640     C             AG
            GG                  CCA TGCACTCCAGCCTGGG  AC
                                ||| ||||||||||||||  ||
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                                GGT ACGTGAGGTCGGACCC  TG
                                  A             GT
GAM1645  DKFZp762P2111 3'  TCTTCTGGAGTGAGTGG     87643       G       CCT
                                CCACT CACTCCAG   GGGA
                                ||||| ||||||||   ||||
                                GGTGA GTGAGGTC   TTCT
                                   _      ____
GAM1645  DLL1     5'  CCCAGGCTCGCGCGTGG     20050      _   ACTCC
                                CCAC TGC    AGCCTGGG
                                |||| |||    ||||||||
                                GGTG GCG    TCGGACCC
                                  C   C____
GAM1645  DMRTB1    3'  TCCAGGTGGCTGGAGCCAGCAG 66840      A__       TG__
                                CTGC   CTCCAGCC    GGA
                                ||||   ||||||||    |||
                                GACG   GAGGTCGG    CCT
                                  ACC       TGGA
GAM1645  DRIM     3'  CCCAAGGCGGAGTGCAGTG   27950          A   _
                                CACTGCACTCC GCCT GGG
                                |||||||||| |||| |||
                                GTGACGTGAGG CGGA CCC
                                      _   A
GAM1645  DSCR6    3'  GTCTCCCAGGCTGGAGTGCAGT 39073
                  G                  CACTGCACTCCAGCCTGGGAGAC
                                |||||||||||||||||||||||
                                GTGACGTGAGGTCGGACCCTCTG

GAM1645  EPS8R1   3'  CCCGAGAGGGTGCAGTGG    56529          CAGCC
                                CCACTGCACTC    TGGG
                                ||||||||||    ||||
                                GGTGACGTGGG    GCCC
                                      AGA__
GAM1645  EPS8R1   3'  CCCGAGAGGGTGCAGTGG    58295          CAGCC
                                CCACTGCACTC    TGGG
                                ||||||||||    ||||
                                GGTGACGTGGG    GCCC
                                      AGA__
GAM1645  EPS8R1   3'  CCCGAGAGGGTGCAGTGG    35302          CAGCC
                                CCACTGCACTC    TGGG
                                ||||||||||    ||||
                                GGTGACGTGGG    GCCC
                                      AGA__
GAM1645  EREG     3'  GTTGCCCAGGTTGGAGTGCAGT 9315                 AG
                  GG                 CCACTGCACTCCAGCCTGGG  AC
                                ||||||||||||||||||  ||
                                GGTGACGTGAGGTTGGACCC  TG
                                         GT
GAM1645  EVI5     3'  CCCAGGCTGGAGTGCTGTGG   20204      T
                                CCAC GCACTCCAGCCTGGG
                                |||| ||||||||||||||
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                                GGTG CGTGAGGTCGGACCC
                                  T
GAM1645  EVI5     3'  CTCAGGCTGGAGTGCAGTGG  20205
                                CCACTGCACTCCAGCCTGGG
                                ||||||||||||||||||||
                                GGTGACGTGAGGTCGGACTC

GAM1645  FADS1    3'  CAAGCTGGATGCAGTGG    26373        C     C
                                CCACTGCA TCCAGC TG
                                |||||||| |||||| ||
                                GGTGACGT AGGTCG AC
                                     _     A
GAM1645  FBP17    3'  TTCAGACTGGAGTGCAGTGG  73164             C
                                CCACTGCACTCCAG CTGGG
                                |||||||||||||| |||||
                                GGTGACGTGAGGTC GACTT
                                        A
GAM1645  FBXO26   3'  CTTGCAGCCAGGTGCAGTGG  46627          CCA  C  G
                                CCACTGCACT   GC TG GAG
                                ||||||||||   || || |||
                                GGTGACGTGG   CG AC TTC
                                     AC_  _  G
GAM1645  FER1L4   3'  GTCTCCCAGGTTGGAGTGCAGT 48132
                   GG             CCACTGCACTCCAGCCTGGGAGAC
                                  ||||||||||||||||||||||||
                                  GGTGACGTGAGGTTGGACCCTCTG

GAM1645  FER1L4   3'  GTCTCCCAGGTTGGAGTGCAGT 48133
                   GG             CCACTGCACTCCAGCCTGGGAGAC
                                  ||||||||||||||||||||||||
                                  GGTGACGTGAGGTTGGACCCTCTG

GAM1645  FKBP9    3'  GTCGCCAGGCTGGAGTGCAGTG 95722              GA
                   G               CCACTGCACTCCAGCCTGG  GAC
                                   ||||||||||||||||||  |||
                                   GGTGACGTGAGGTCGGACC  CTG
                                              G_
GAM1645  FLJ00024 5'  GTCACCCAGGCTGGAGTGCAAT 64502     C           A
                   GG             CCA TGCACTCCAGCCTGGG GAC
                                  ||| |||||||||||||| |||
                                  GGT ACGTGAGGTCGGACCC CTG
                                    A            A
GAM1645  FLJ00060 5'  GTCACCCAGGCTGGAGTGCAGT 61753               A
                   GG             CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC CTG
                                             A
GAM1645  FLJ10008 3'  CTCCCAGGGCACGGTGG    36186       CA TCCAG
                                  CCACTG  C    CCTGGGAG
                                  ||||||  |    ||||||||
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                                GGTGGC  G    GGACCCTC
                                   AC _____
GAM1645  FLJ10101  3'  GTGGCCCAGGCTGGAGTGCAGT 45604                AG
              GG                   CCACTGCACTCCAGCCTGGG  AC
                                   ||||||||||||||||||||  ||
                                   GGTGACGTGAGGTCGGACCC  TG
                                         GG
GAM1645  FLJ10232  3'  CCCAGGCTGGAGTGCGATGG   36376     C
                                   CCA TGCACTCCAGCCTGGG
                                   ||| ||||||||||||||||
                                   GGT GCGTGAGGTCGGACCC
                                     A
GAM1645  FLJ10297  3'  GTTGCCCAGGCTAGAGTGCAGT 36445          C       AG
              GG                   CCACTGCACTC AGCCTGGG  AC
                                   ||||||||||| ||||||||  ||
                                   GGTGACGTGAG TCGGACCC  TG
                                         A       GT
GAM1645  FLJ10298  3'  GTTGCCCAGGCTGGAGTGCAGT 36462               AG
                                   ACTGCACTCCAGCCTGGG  AC
                                   ||||||||||||||||||  ||
                                   TGACGTGAGGTCGGACCC  TG
                                         GT
GAM1645  FLJ10346  5'  GTCTCCCAGGCTGAAGTGCAGT 36529          C
              GG                   CCACTGCACT CAGCCTGGGAGAC
                                   |||||||||| ||||||||||||
                                   GGTGACGTGA GTCGGACCCTCTG
                                      A
GAM1645  FLJ10535  3'  GTCACCCAGGCTGGAGTGCAGT 36755                A
              GG                   CCACTGCACTCCAGCCTGGG GAC
                                   |||||||||||||||||||| |||
                                   GGTGACGTGAGGTCGGACCC CTG
                                         A
GAM1645  FLJ10560  3'  GTCGCCCAGGCTGGCGTGCAGT 36801          T       A
              GG                   CCACTGCAC CCAGCCTGGG GAC
                                   ||||||||| |||||||||| |||
                                   GGTGACGTG GGTCGGACCC CTG
                                      C        G
GAM1645  FLJ10583  3'  TCTCCCAGGCTCACTGCAG   36831      CTCC
                                   CTGCA   AGCCTGGGAGA
                                   |||||   ||||||||||
                                   GACGT   TCGGACCCTCT
                                     CAC_
GAM1645  FLJ10607  3'  CCCAGGCTAGAGCGCAGGG   77627   A   A   C
                                   CC CTGC CTC AGCCTGGG
                                   || |||| ||| ||||||||
                                   GG GACG GAG TCGGACCC
                                    _   C   A
GAM1645  FLJ10607  3'  CCCAGGCTGGAGTCCAGTGG   77628       C
                                   CCACTG ACTCCAGCCTGGG
                                   |||||| ||||||||||||
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                                GGTGAC TGAGGTCGGACCC
                                   C
GAM1645  FLJ10640  5'  CCTAGGCTGAGTGCAGTGG   39234          C
                                CCACTGCACTC AGCCTGGG
                                |||||||||| ||||||||
                                GGTGACGTGAG TCGGATCC
                                          _
GAM1645  FLJ10713  3'  GTTGCCCAGGCTGGAGTGCAGT 37006               AG
                GG                 CCACTGCACTCCAGCCTGGG  AC
                                   ||||||||||||||||||  ||
                                   GGTGACGTGAGGTCGGACCC  TG
                                             GT
GAM1645  FLJ10846  3'  GTCACCCAGGCTGGAGTGCAGT 37291               A
                GG                 CCACTGCACTCCAGCCTGGG GAC
                                   |||||||||||||||||| |||
                                   GGTGACGTGAGGTCGGACCC CTG
                                             A
GAM1645  FLJ10847  3'  CAGGCTGGAGTGCGGTGG    37298
                                CCACTGCACTCCAGCCTG
                                |||||||||||||||||
                                GGTGGCGTGAGGTCGGAC

GAM1645  FLJ10900  3'  CCGGGGCTGGAGCGGAGTG   37345     GCA      G
                                CACT   CTCCAGCCT GG
                                ||||   ||||||||| ||
                                GTGA   GAGGTCGGG CC
                                   GGC        G
GAM1645  FLJ10900  3'  CCGGGGCTGGAGCGGAGTG   66206     GCA      G
                                CACT   CTCCAGCCT GG
                                ||||   ||||||||| ||
                                GTGA   GAGGTCGGG CC
                                   GGC        G
GAM1645  FLJ10901  3'  CCCAGGCTGGAATGCTGT    37358    T   C
                                AC GCA TCCAGCCTGGG
                                || ||| ||||||||||
                                TG CGT AGGTCGGACCC
                                 T   A
GAM1645  FLJ10922  3'  GTTGCCCAGGCTGGAATGCAAT 37408     C   C        AG
                GG                 CCA TGCA TCCAGCCTGGG  AC
                                   ||| |||| ||||||||||  ||
                                   GGT ACGT AGGTCGGACCC  TG
                                     A   A         GT
GAM1645  FLJ10956  3'  CCCACATTGGAGTGCAGTGG  37463           CC
                                CCACTGCACTCCAG  TGGG
                                ||||||||||||||  ||||
                                GGTGACGTGAGGTT  ACCC
                                          AC
GAM1645  FLJ10989  3'  CTTTTAGGCTGGGTGCAGTGG 37501         T
                                CCACTGCAC CCAGCCTGGGAG
                                |||||||| ||||||||||||
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                                GGTGACGTG GGTCGGATTTTC
                                        _
GAM1645  FLJ11004  5' CCCAGACTGGAGTGCTGTGG  37531     T       C
                                CCAC GCACTCCAG CTGGG
                                |||| ||||||||| |||||
                                GGTG CGTGAGGTC GACCC
                                  T       A
GAM1645  FLJ11029  3' CCCAGCTGGGTGCAGTGG   61633       T    C
                                CCACTGCAC CCAGC TGGG
                                ||||||||| ||||| ||||
                                GGTGACGTG GGTCG ACCC
                                        _   _
GAM1645  FLJ11042  3' CTGGCCAGGTGCAGTGG    37563         CCA  T
                                CCACTGCACT  GCC GG
                                ||||||||||  ||| ||
                                GGTGACGTGG  CGG TC
                                     AC_  _
GAM1645  FLJ11467  3' GTCACCCAGGCTGGAGTACAGT 46977       C         A
           GG                     CCACTG ACTCCAGCCTGGG GAC
                                  |||||| |||||||||||| |||
                                  GGTGAC TGAGGTCGGACCC CTG
                                    A          A
GAM1645  FLJ11710  3' GTCTCCCAGGCTGGAGTGCAGT 46250
           GG                     CCACTGCACTCCAGCCTGGGAGAC
                                  ||||||||||||||||||||||||
                                  GGTGACGTGAGGTCGGACCCTCTG

GAM1645  FLJ11710  5' TTTGAGGCTGGATGCAGTGG  46256       C      G
                                CCACTGCA TCCAGCCT GGA
                                |||||||| |||||||| |||
                                GGTGACGT AGGTCGGA TTT
                                    _      G
GAM1645  FLJ11715  3' GTTGCCCAGGCTGGAGGGCAGT 44982       A         AG
           G                      CACTGC CTCCAGCCTGGG  AC
                                  |||||| ||||||||||||  ||
                                  GTGACG GAGGTCGGACCC  TG
                                    G          GT
GAM1645  FLJ11800  3' GTCACCCAGGCCGGAGTGCAGT 47041          A     A
           GG                     CCACTGCACTCC GCCTGGG GAC
                                  |||||||||||| ||||||| |||
                                  GGTGACGTGAGG CGGACCC CTG
                                       C      A
GAM1645  FLJ12363  3' GTCCCCCAGGCTGGAGTGCCGT 50640     T          A
           GG                     CCAC GCACTCCAGCCTGGG GAC
                                  |||| |||||||||||||| |||
                                  GGTG CGTGAGGTCGGACCC CTG
                                    C           C
GAM1645  FLJ12572  5' GTCACCCAGGCTGGAGTATAGT 43546       C         A
           GG                     CCACTG ACTCCAGCCTGGG GAC
                                  |||||| |||||||||||| |||
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                                GGTGAT TGAGGTCGGACCC CTG
                                   A           A
GAM1645  FLJ12581  3'  GTCGCCCAGGCTGGAGTGCAGT 46342                A
                GG                  CCACTGCACTCCAGCCTGGG GAC
                                    |||||||||||||||||||| |||
                                    GGTGACGTGAGGTCGGACCC CTG
                                          G
GAM1645  FLJ12649  3'  CCCAGGCTGCAGTGCAGTGG   45088          C
                                    CCACTGCACT CAGCCTGGG
                                    |||||||||| |||||||||
                                    GGTGACGTGA GTCGGACCC
                                          C
GAM1645  FLJ12666  3'  TTTGGGCTGGGCGCAGTGG    45075        A T     TG
                                    CCACTGC C CCAGCC  GG
                                    ||||||| | ||||||  ||
                                    GGTGACG G GGTCGG  TT
                                       C _     GT
GAM1645  FLJ12668  3'  GTTGCCCAGGCTGGAGTACAGT 47161        C          AG
                GG                  CCACTG ACTCCAGCCTGGG  AC
                                    ||||||| |||||||||||||  ||
                                    GGTGAC TGAGGTCGGACCC  TG
                                       A           GT
GAM1645  FLJ12747  3'  GTCACCCAGGCTGGAGTGCAAT 50671     C            A
                GG                  CCA TGCACTCCAGCCTGGG GAC
                                    ||| |||||||||||||| |||
                                    GGT ACGTGAGGTCGGACCC CTG
                                      A             A
GAM1645  FLJ12787  3'  TCGCCCAGGCTGGAGTACAGTG 50696       C          A
                                    CACTG ACTCCAGCCTGGG GA
                                    ||||| |||||||||||| ||
                                    GTGAC TGAGGTCGGACCC CT
                                       A           G
GAM1645  FLJ12876  3'  GTCACCCAGGCTGGAGTGCAGT 43099                A
                GG                  CCACTGCACTCCAGCCTGGG GAC
                                    |||||||||||||||||||| |||
                                    GGTGACGTGAGGTCGGACCC CTG
                                          A
GAM1645  FLJ12888  3'  GTTGCCCAGGCTAGAGTGCAGT 46892          C       AG
                GG                  CCACTGCACTC AGCCTGGG  AC
                                    |||||||||| ||||||||  ||
                                    GGTGACGTGAG TCGGACCC  TG
                                          A       GT
GAM1645  FLJ12903  3'  GTTGCCCAGGCTGGAGTGCAAT 43077     C            AG
                GG                  CCA TGCACTCCAGCCTGGG  AC
                                    ||| |||||||||||||||  ||
                                    GGT ACGTGAGGTCGGACCC  TG
                                      A             GT
GAM1645  FLJ12960  3'  GTCGCCCAGGCTGGAGTGCAGT 45305                A
                GG                  CCACTGCACTCCAGCCTGGG GAC
                                    ||||||||||||||||||||| |||
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                                GGTGACGTGAGGTCGGACCC CTG
                                      G
GAM1645  FLJ12973  3' GTTGCCCAGGCTGGAGTGCA  46643            AG
                                TGCACTCCAGCCTGGG  AC
                                ||||||||||||||||  ||
                                ACGTGAGGTCGGACCC  TG
                                      GT
GAM1645  FLJ12975  3' CCCAGGCTGGAGTGCAGTG   70190
                                CACTGCACTCCAGCCTGGG
                                ||||||||||||||||||
                                GTGACGTGAGGTCGGACCC

GAM1645  FLJ13072  5' GTCGGCCAGGCTGGAGTGCAGT 91396              GA
            GG                    CCACTGCACTCCAGCCTGG  GAC
                                ||||||||||||||||||  |||
                                GGTGACGTGAGGTCGGACC  CTG
                                      GG
GAM1645  FLJ13114  3' GTCGCCCAGGCTGGAATGCAGT 44908        C        A
            GG                    CCACTGCA TCCAGCCTGGG GAC
                                ||||||||| |||||||||| |||
                                GGTGACGT AGGTCGGACCC CTG
                                   A         G
GAM1645  FLJ13188  3' GTCACCCAGGCTAGAGTGCAGT 42194        C       A
                                ACTGCACTC AGCCTGGG GAC
                                ||||||||| |||||||| |||
                                TGACGTGAG TCGGACCC CTG
                                   A       A
GAM1645  FLJ13193  3' CCCAGGCTGGAGTACAGTGG  50718       C
                                CCACTG ACTCCAGCCTGGG
                                |||||| ||||||||||||
                                GGTGAC TGAGGTCGGACCC
                                  A
GAM1645  FLJ13197  3' GTTGCCCAGGCTGGAGTGCAGT 45183              AG
            GG                    CCACTGCACTCCAGCCTGGG  AC
                                ||||||||||||||||||  ||
                                GGTGACGTGAGGTCGGACCC  TG
                                      GT
GAM1645  FLJ13352  3' CAGGCTGGGTGCAATGG    45049    C    T
                                CCA TGCAC CCAGCCTG
                                ||| ||||| ||||||||
                                GGT ACGTG GGTCGGAC
                                  A    _
GAM1645  FLJ13441  3' TCTCCCAGGCAGGCCATGG   43919    CT  A  CCA
                                CCA  GC CT   GCCTGGGAGA
                                |||  || ||   ||||||||||
                                GGT  CG GA   CGGACCCTCT
                                  AC  _  ____
GAM1645  FLJ13448  3' TTTGGGCTGGGCACAGTGG   47888       CA T     TG
                                CCACTG  C CCAGCC  GG
                                ||||||  | ||||||  ||
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                                GGTGAC  G GGTCGG  TT
                                   AC _     GT
GAM1645  FLJ13456  3'  GTCGCCCAAGCTGGAGTGCAGT 66560            C    A
              GG                   CCACTGCACTCCAGC TGGG GAC
                                   ||||||||||||||| |||| |||
                                   GGTGACGTGAGGTCG ACCC CTG
                                            A   G
GAM1645  FLJ13590  5'  TCAGGCTTGAGTGCAGTGG   46209          C
                                   CCACTGCACTC AGCCTGG
                                   |||||||||| |||||||
                                   GGTGACGTGAG TCGGACT
                                          T
GAM1645  FLJ13909  5'  GTCCCCCAGGCTGGTGGC    47782    ACT       A
                                   GC   CCAGCCTGGG GAC
                                   ||   |||||||||| |||
                                   CG   GGTCGGACCC CTG
                                    GT_        C
GAM1645  FLJ13952  3'  GTTGCCCAGGCTGGAATGCAGT 46019        C        AG
              GG                   CCACTGCA TCCAGCCTGGG  AC
                                   |||||||| ||||||||||  ||
                                   GGTGACGT AGGTCGGACCC  TG
                                      A         GT
GAM1645  FLJ13984  5'  CCTAGGCTGGAGTGCAGTGG   45804
                                   CCACTGCACTCCAGCCTGGG
                                   ||||||||||||||||||
                                   GGTGACGTGAGGTCGGATCC

GAM1645  FLJ14326  3'  CTCAGGCTGGGTGCAGTGG    50769         T
                                   CCACTGCAC CCAGCCTGGG
                                   ||||||||| ||||||||||
                                   GGTGACGTG GGTCGGACTC
                                          _
GAM1645  FLJ14351  3'  GTCGCCCAGGCTGGAGTGCAGT 45650              A
              GG                   CCACTGCACTCCAGCCTGGG GAC
                                   |||||||||||||||||| |||
                                   GGTGACGTGAGGTCGGACCC CTG
                                            G
GAM1645  FLJ14442  3'  GTTACCCAGGCTAGAGTGTAGT 52390          C       A
              GG                   CCACTGCACTC AGCCTGGG GAC
                                   |||||||||| |||||||| |||
                                   GGTGATGTGAG TCGGACCC TTG
                                         A       A
GAM1645  FLJ14803  3'  CAGACTGGAGTGCAGTGG    52691            C
                                   CCACTGCACTCCAG CTG
                                   |||||||||||||| |||
                                   GGTGACGTGAGGTC GAC
                                            A
GAM1645  FLJ14950  3'  CCCAGGCTGAACTGCAGTGG   52787        CTC
                                   CCACTGCA   CAGCCTGGG
                                   ||||||||   |||||||||
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                                GGTGACGT   GTCGGACCC
                                    CAA
GAM1645  FLJ14957  3'  CCGAGGCTGGAGTGCAATGG   52814     C          G
                                CCA TGCACTCCAGCCT GG
                                ||| |||||||||||| ||
                                GGT ACGTGAGGTCGGA CC
                                  A           G
GAM1645  FLJ20034  3'  GTTGCCCAGGCTGGAGTACAAT 34854     C  C          AG
           GG                     CCA TG ACTCCAGCCTGGG  AC
                                ||| || |||||||||||||  ||
                                GGT AC TGAGGTCGGACCC  TG
                                  A  A           GT
GAM1645  FLJ20045  3'  GTTTCCCAGGCTGGAGTGCAGT 34891
           GG                     CCACTGCACTCCAGCCTGGGAGAC
                                ||||||||||||||||||||||||
                                GGTGACGTGAGGTCGGACCCTTTG

GAM1645  FLJ20079  3'  GTTGCCCAGGCTGGAGTGCAAT 34975     C            AG
           GG                     CCA TGCACTCCAGCCTGGG  AC
                                ||| ||||||||||||||  ||
                                GGT ACGTGAGGTCGGACCC  TG
                                  A             GT
GAM1645  FLJ20136  3'  GTCGCCCAGGCTGGAATGCAGT 35100         C         A
           GG                     CCACTGCA TCCAGCCTGGG GAC
                                |||||||| |||||||||| |||
                                GGTGACGT AGGTCGGACCC CTG
                                    A          G
GAM1645  FLJ20147  3'  GTTGCCCAGGCTAGAGTGCAG  35136         C       AG
                                CTGCACTC AGCCTGGG  AC
                                |||||||| ||||||||  ||
                                GACGTGAG TCGGACCC  TG
                                    A       GT
GAM1645  FLJ20257  3'  CTCCCAGGCTGGATGGCATGG  39486     C   AC
                                CCA TGC  TCCAGCCTGGGAG
                                ||| |||  ||||||||||||
                                GGT ACG  AGGTCGGACCCTC
                                  _  GT
GAM1645  FLJ20340  3'  CAGGCCAGGTGCAGTGG     35455          CCA
                                CCACTGCACT   GCCTG
                                ||||||||||   |||||
                                GGTGACGTGG   CGGAC
                                     AC_
GAM1645  FLJ20342  3'  GTCCCCCAGGCTGGAGTGGTGC 35467          ___          A
           AGTGG                  CCACTGCAC   TCCAGCCTGGG GAC
                                |||||||||   |||||||||| |||
                                GGTGACGTG   AGGTCGGACCC CTG
                                     GTG         C
GAM1645  FLJ20344  3'  GTCATCCAAACTGGAGTGCAGT 35487             CC   GA
           GG                     CCACTGCACTCCAG  TGG  GAC
                                ||||||||||||||  |||  |||
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                                GGTGACGTGAGGTC  ACC  CTG
                                      AA   TA
GAM1645  FLJ20452  3'  CTAAAGGCCAGGTGCAGTGG  35646        CCA   GGG
                                CCACTGCACT   GCCT   AG
                                ||||||||||  ||||  ||
                                GGTGACGTGG   CGGA   TC
                                     AC_    AA_
GAM1645  FLJ20511  3'  GTCACCCAGGCTGGAGTGCAGT 35780              A
           GG                    CCACTGCACTCCAGCCTGGG GAC
                                 |||||||||||||||||||| |||
                                 GGTGACGTGAGGTCGGACCC CTG
                                           A
GAM1645  FLJ20555  3'  CCCACAAGCCTGAGTGCAGTGG 35828         CA  C__
                                CCACTGCACTC  GC   TGGG
                                ||||||||||  ||   ||||
                                GGTGACGTGAG  CG   ACCC
                                      TC  AAC
GAM1645  FLJ20671  3'  GTTGCCCAGGCTGGAGTGCAGT 35944              AG
           GG                    CCACTGCACTCCAGCCTGGG  AC
                                 ||||||||||||||||||  ||
                                 GGTGACGTGAGGTCGGACCC  TG
                                           GT
GAM1645  FLJ20700  3'  CCCAGGCTGGAGTGCAGTGG  36004
                                CCACTGCACTCCAGCCTGGG
                                ||||||||||||||||||
                                GGTGACGTGAGGTCGGACCC

GAM1645  FLJ20813  3'  CCCAGGCTGGAGTGCAGTGG  36129
                                CCACTGCACTCCAGCCTGGG
                                ||||||||||||||||||
                                GGTGACGTGAGGTCGGACCC

GAM1645  FLJ21162  3'  TCTTGGGCTGGGTGCAGTGG  46377        T     TG
                                CCACTGCAC CCAGCC  GGA
                                |||||||| ||||||  |||
                                GGTGACGTG GGTCGG  TCT
                                     _     GT
GAM1645  FLJ21302  3'  GTCTCCCAGGCTGGACTGCAG  43513      C
                                CTGCA TCCAGCCTGGGAGAC
                                ||||| ||||||||||||||
                                GACGT AGGTCGGACCCTCTG
                                   C
GAM1645  FLJ21324  5'  CCCAGGCTGGCGTGCAGTGG  92851         T
                                CCACTGCAC CCAGCCTGGG
                                |||||||| ||||||||||
                                GGTGACGTG GGTCGGACCC
                                      C
GAM1645  FLJ21459  3'  GTCACCCAGGCTGGGGTGCAGT 44811              A
           GG                    CCACTGCACTCCAGCCTGGG GAC
                                 |||||||||||||||||||| |||
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                                GGTGACGTGGGGTCGGACCC CTG
                                                   A
GAM1645  FLJ21603  3'  GTCACCCAGGCTGGAGTACAGT 45776       C          A
                GG                  CCACTG ACTCCAGCCTGGG GAC
                                    |||||| |||||||||||||| |||
                                    GGTGAC TGAGGTCGGACCC CTG
                                      A           A
GAM1645  FLJ21777  3'  GTCACCCAGGCTGGAGTGCAAT 50848     C            A
                GG                  CCA TGCACTCCAGCCTGGG GAC
                                    ||| |||||||||||||||| |||
                                    GGT ACGTGAGGTCGGACCC CTG
                                     A             A
GAM1645  FLJ22167  5'  CTCAGGCTGCAGTGCAGTGG   44867          C
                                    CCACTGCACT CAGCCTGGG
                                    |||||||||| |||||||||
                                    GGTGACGTGA GTCGGACTC
                                          C
GAM1645  FLJ22316  5'  GTCTCCCAGGCTGGAGTGCAGT 47617
                GG                  CCACTGCACTCCAGCCTGGGAGAC
                                    |||||||||||||||||||||||||
                                    GGTGACGTGAGGTCGGACCCTCTG

GAM1645  FLJ22329  3'  GTCACCCAGGCTGGAGTGCAGT 45407                A
                GG                  CCACTGCACTCCAGCCTGGG GAC
                                    |||||||||||||||||| |||
                                    GGTGACGTGAGGTCGGACCC CTG
                                                   A
GAM1645  FLJ22531  5'  GTTACCCAGGCCGGAGTGCAGT 45374          A      A
                GG                  CCACTGCACTCC GCCTGGG GAC
                                    |||||||||||| ||||||| |||
                                    GGTGACGTGAGG CGGACCC TTG
                                          C      A
GAM1645  FLJ22644  3'  CTCAGCCTGGAGTGCAGTG    47699           C
                                    CACTGCACTCCAG CTGGG
                                    |||||||||||| |||||
                                    GTGACGTGAGGTC GACTC
                                           C
GAM1645  FLJ22794  3'  CCTGGGCTGGAGTACAGTGG   93243       C        TG
                                    CCACTG ACTCCAGCC  GG
                                    |||||| |||||||||  ||
                                    GGTGAC TGAGGTCGG  CC
                                       A        GT
GAM1645  FLJ22800  3'  GTCTCAAAAAAGGCTGGAGTAC 45993      C        GG___
                AGT                   ACTG ACTCCAGCCT     GAGAC
                                    |||| ||||||||||     |||||
                                    TGAC TGAGGTCGGA     CTCTG
                                      A         AAAAA
GAM1645  FLJ22814  3'  GTCCCCCAGGCTCCTGCACGG  46730    AC    CTCC       A
                                    CC  TGCA    AGCCTGGG GAC
                                    ||  ||||    |||||||| |||
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                                GG  ACGT    TCGGACCC CTG
                                 C_   CC__       C
GAM1645  FLJ22965  3'  CCCAGGATGGAGTGCAGTGG   42295           G
                                CCACTGCACTCCA CCTGGG
                                |||||||||||| ||||||
                                GGTGACGTGAGGT GGACCC
                                       A
GAM1645  FLJ22969  3'  CCTAGGCTGGAGTGCAGTGG   69199
                                CCACTGCACTCCAGCCTGGG
                                ||||||||||||||||||||
                                GGTGACGTGAGGTCGGATCC

GAM1645  FLJ23024  3'  GTCTCCCAGGCTAGAGTGCAAT 46846     C      C
                GG                CCA TGCACTC AGCCTGGGAGAC
                                ||| ||||||| ||||||||||||
                                GGT ACGTGAG TCGGACCCTCTG
                                  A      A
GAM1645  FLJ23040  3'  TCACCCAAGCCAGAGTGCAGTG 47991          CA  C    A
                G                 CCACTGCACTC  GC TGGG GA
                                ||||||||||  || |||| ||
                                GGTGACGTGAG  CG ACCC CT
                                       AC  A    A
GAM1645  FLJ23040  3'  TTTTGAGGCTGGGTGCAGTGG  47996         T      G
                                CCACTGCAC CCAGCCT GGAG
                                |||||||| ||||||| ||||
                                GGTGACGTG GGTCGGA TTTT
                                      _      G
GAM1645  FLJ23053  3'  CCCAGGCTGGAGTGCAGTGG   43554
                                CCACTGCACTCCAGCCTGGG
                                ||||||||||||||||||||
                                GGTGACGTGAGGTCGGACCC

GAM1645  FLJ23186  3'  CTTAGCTGGAGTGCGGTGG    61041           C
                                CCACTGCACTCCAGC TGGG
                                |||||||||||||| ||||
                                GGTGGCGTGAGGTCG ATTC
                                          _
GAM1645  FLJ23263  5'  GTCGCCCAGGCTGGAGTGCAGT 47804                A
                GG                CCACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                         G
GAM1645  FLJ23356  3'  CTGAGGCTGGAGTGCAGTG    50922           G
                                CACTGCACTCCAGCCT GG
                                |||||||||||||||| ||
                                GTGACGTGAGGTCGGA TC
                                       G
GAM1645  FLJ23392  3'  CTGAGGCTGGAGTGCAGTGG   45891            G
                                CCACTGCACTCCAGCCT GG
                                |||||||||||||||| ||
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                                GGTGACGTGAGGTCGGA TC
                                      G
GAM1645  FLJ23392  3'  GTCACCCAGACTGGAGTGCAGT 45905          C    A
                GG          CCACTGCACTCCAG CTGGG GAC
                            |||||||||||||| ||||| |||
                            GGTGACGTGAGGTC GACCC CTG
                                  A    A
GAM1645  FLJ23392  3'  GTCCCCCAGGCTGGAGTGCAGT 45908              A
                GG          CCACTGCACTCCAGCCTGGG GAC
                            |||||||||||||||||| |||
                            GGTGACGTGAGGTCGGACCC CTG
                                      C
GAM1645  FLJ23416  3'  GTTGCCCAGGCTGGAGTGCAGT 50936              AG
                GG          CCACTGCACTCCAGCCTGGG  AC
                            |||||||||||||||||  ||
                            GGTGACGTGAGGTCGGACCC  TG
                                      GT
GAM1645  FLJ23519  3'  GTCACCCAGGCTGGAGTGCAGT 50957              A
                GG          CCACTGCACTCCAGCCTGGG GAC
                            |||||||||||||||||| |||
                            GGTGACGTGAGGTCGGACCC CTG
                                      A
GAM1645  FLJ23556  3'  GTCGCCCAGGCTGGAGTGCAGT 46453              A
                GG          CCACTGCACTCCAGCCTGGG GAC
                            |||||||||||||||||| |||
                            GGTGACGTGAGGTCGGACCC CTG
                                      G
GAM1645  FLJ23563  3'  GTTGCCCAGGCTAGAGTGCAAT 68218     C     C      AG
                GG          CCA TGCACTC AGCCTGGG  AC
                            ||| ||||||| ||||||||  ||
                            GGT ACGTGAG TCGGACCC  TG
                              A      A       GT
GAM1645  FLJ25416  5'  CCCAGGCTGAAGTGCCATGG  59452     CT    C
                            CCA  GCACT CAGCCTGGG
                            |||  ||||| |||||||||
                            GGT  CGTGA GTCGGACCC
                              AC    A
GAM1645  FLJ25416  5'  CCCAGGCTGGAGTGCCATGG  59453     CT
                            CCA  GCACTCCAGCCTGGG
                            |||  ||||||||||||||
                            GGT  CGTGAGGTCGGACCC
                              AC
GAM1645  FLJ30532  3'  GTTGCCCAGGCTGGAGTACAGT 59226       C          AG
                GG          CCACTG ACTCCAGCCTGGG  AC
                            ||||||| ||||||||||||  ||
                            GGTGAC TGAGGTCGGACCC  TG
                               A          GT
GAM1645  FLJ31101  3'  GTCGCCCAGGCTGGAATGCAGT 36170        C         A
                GG          CCACTGCA TCCAGCCTGGG GAC
                            |||||||| |||||||||| |||
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                                GGTGACGT AGGTCGGACCC CTG
                                    A         G
GAM1645  FLJ31153  3'  GTCACCCAGACTGGAGTGCAGT 58752            C    A
           GG                    CCACTGCACTCCAG CTGGG GAC
                                 |||||||||||||| ||||| |||
                                 GGTGACGTGAGGTC GACCC CTG
                                       A    A
GAM1645  FLJ32499  3'  CCCAGTCTGGAGTGCAGTGG  58777            C
                                 CCACTGCACTCCAG CTGGG
                                 |||||||||||||| |||||
                                 GGTGACGTGAGGTC GACCC
                                       T
GAM1645  FLJ32762  3'  GTCTCCCAAACCTTCAGAGAGT 59486      GCA  C__  CC_
           GG                    CCACT  CTC  AG  TGGGAGAC
                                 |||||  |||  ||  ||||||||
                                 GGTGA  GAG  TC  ACCCTCTG
                                   ___  ACT  CAA
GAM1645  FLJ32783  3'  TCTCCCAGTTGCATAGTACAGT 59308      C  C__   C
           G                     CACTG ACT  CAGC TGGGAGA
                                 ||||| |||  |||| |||||||
                                 GTGAC TGA  GTTG ACCCTCT
                                   A  TAC   _
GAM1645  FLJ32865  3'  GTCACCCAGGCTGGAGTACAAT 58819    C  C         A
           G                     CA TG ACTCCAGCCTGGG GAC
                                 || || |||||||||||| |||
                                 GT AC TGAGGTCGGACCC CTG
                                  A  A          A
GAM1645  GAL3ST-4  3'  GTCCCCCAGGCTGGAGTGCAGT 45281              A
           GG                    CCACTGCACTCCAGCCTGGG GAC
                                 |||||||||||||||||| |||
                                 GGTGACGTGAGGTCGGACCC CTG
                                          C
GAM1645  GALNT6   3'  TTCAGGCTGGGCACAGTGG   24255       CA T
                                 CCACTG  C CCAGCCTGGG
                                 ||||||  | ||||||||||
                                 GGTGAC  G GGTCGGACTT
                                    AC _
GAM1645  GGA2     3'  CTCAGGCTGGAGTGCGGTGG  57664
                                 CCACTGCACTCCAGCCTGGG
                                 ||||||||||||||||||
                                 GGTGGCGTGAGGTCGGACTC

GAM1645  GGA2     3'  CTCAGGCTGGAGTGCGGTGG  31164
                                 CCACTGCACTCCAGCCTGGG
                                 ||||||||||||||||||
                                 GGTGGCGTGAGGTCGGACTC

GAM1645  GMPPB    5'  CCCAGGCTGGAGTGCGATGG  97442    C
                                 CCA TGCACTCCAGCCTGGG
                                 ||| ||||||||||||||
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                                GGT GCGTGAGGTCGGACCC
                                  A
GAM1645  GNG4     3'  GTCACCCAGGCTGGAGTGCAAT 16853     C            A
                 GG                 CCA TGCACTCCAGCCTGGG GAC
                                    ||| |||||||||||||| |||
                                    GGT ACGTGAGGTCGGACCC CTG
                                      A             A
GAM1645  GOLGA3   3'  GTTGCCCAGGCTGGAGTGCAGT 20895                AG
                 GG                 CCACTGCACTCCAGCCTGGG  AC
                                    ||||||||||||||||||  ||
                                    GGTGACGTGAGGTCGGACCC  TG
                                                GT
GAM1645  GP5      3'  GTGGCCCAGGCTGGCGTGCAGT 16882          T        AG
                 GG                 CCACTGCAC CCAGCCTGGG  AC
                                    |||||||| ||||||||||  ||
                                    GGTGACGTG GGTCGGACCC  TG
                                         C         GG
GAM1645  GR6      5'  GTCACCCAGGCTGGAATGCAGT 24748          C         A
                 GG                 CCACTGCA TCCAGCCTGGG GAC
                                    |||||||| |||||||||||| |||
                                    GGTGACGT AGGTCGGACCC CTG
                                       A         A
GAM1645  GREB1    3'  CTGCCCAGGCTGGAGTGCAATG 28567     C            _
                 G                   CCA TGCACTCCAGCCTGGG AG
                                    ||| |||||||||||||| ||
                                    GGT ACGTGAGGTCGGACCC TC
                                      A             G
GAM1645  GREB1    3'  GTCACCCAGGCTGGAGTGCAGT 28578                 A
                 GG                 CCACTGCACTCCAGCCTGGG GAC
                                    |||||||||||||||||| |||
                                    GGTGACGTGAGGTCGGACCC CTG
                                                A
GAM1645  GRWD     3'  GTCGCCCAGGCTGGAGTGCAGT 49787                A
                                    ACTGCACTCCAGCCTGGG GAC
                                    |||||||||||||||| |||
                                    TGACGTGAGGTCGGACCC CTG
                                                G
GAM1645  GTF2E1   3'  CCCAGGCTGGAGTGCAATGG   19795     C
                                    CCA TGCACTCCAGCCTGGG
                                    ||| ||||||||||||||
                                    GGT ACGTGAGGTCGGACCC
                                      A
GAM1645  GTPBG3   3'  CCCAGGCTGGAGTGCAGTGG   51893
                                    CCACTGCACTCCAGCCTGGG
                                    ||||||||||||||||||||
                                    GGTGACGTGAGGTCGGACCC

GAM1645  GTPBG3   3'  CCCAGGCTGGAGTTCAGTGG   51894        C
                                    CCACTG ACTCCAGCCTGGG
                                    |||||| ||||||||||||
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                                GGTGAC TGAGGTCGGACCC
                                   T
GAM1645 H-plk    5' CCAGGATGGAGTGCAGTGG   32377          G
                                CCACTGCACTCCA CCTGG
                                |||||||||||| |||||
                                GGTGACGTGAGGT GGACC
                                      A
GAM1645 H105E3   5' TCCGGGCCTGGAGTTCAGTGG 32491      C    _
                                CCACTG ACTCCAG CCTGGG
                                |||||| ||||||| ||||||
                                GGTGAC TGAGGTC GGGCCT
                                   T     C
GAM1645 H2AV     3' CCCAGACTGGAGTGCGATGG  57629    C       C
                                CCA TGCACTCCAG CTGGG
                                ||| |||||||||| |||||
                                GGT GCGTGAGGTC GACCC
                                  A        A
GAM1645 HCA4     3' GTCGCCCAGGCTGGAGTGCATT 78044    C           A
             GG                   CCA TGCACTCCAGCCTGGG GAC
                                ||| |||||||||||||| |||
                                GGT ACGTGAGGTCGGACCC CTG
                                  T           G
GAM1645 HRH4     3' CCCACGCAGGAGTGCAGTGG  41532         A C
                                CCACTGCACTCC GC TGGG
                                |||||||||||| || ||||
                                GGTGACGTGAGG CG ACCC
                                      A C
GAM1645 HRH4     3' GTCACCCAGGCTGGAGTGCAGT 41546             A
                                ACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||| |||
                                TGACGTGAGGTCGGACCC CTG
                                      A
GAM1645 HRH4     3' GTCTCCCAGGCTGGAGCGTAGT 41547      A
                                ACTGC CTCCAGCCTGGGAGAC
                                ||||| ||||||||||||||||
                                TGATG GAGGTCGGACCCTCTG
                                   C
GAM1645 HRK      5' CCCGGCGGCTGGAGCGCGGCGG 15071    A   A     __
                                CC CTGC CTCCAGCC  TGGG
                                || |||| ||||||||  ||||
                                GG GGCG GAGGTCGG  GCCC
                                 C   C       CG
GAM1645 HSA6591  5' GTCTCCCGGCGAAAGTGAG   73249    G   CCA  T
                                CT CACT   GCC GGGAGAC
                                || ||||   ||| |||||||
                                GA GTGA   CGG CCCTCTG
                                 _   AAG  _
GAM1645 HSC3     3' CTTAGCTGGGTGCAGTGG    59732         T   C
                                CCACTGCAC CCAGC TGGG
                                ||||||||| ||||| ||||
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                                GGTGACGTG GGTCG ATTC
                                      _   _
GAM1645 HSMPP8   3' GTTGCCCAGGCTGGAGTGCAAT 95140    C          AG
            GG                  CCA TGCACTCCAGCCTGGG  AC
                                ||| ||||||||||||||||  ||
                                GGT ACGTGAGGTCGGACCC  TG
                                  A            GT
GAM1645 HSNOV1   3' CAGAGTCTAGAGTGCAGTGG  34431         C _ _
                                CCACTGCACTC AG C CTG
                                |||||||||| || | |||
                                GGTGACGTGAG TC G GAC
                                      A  T A
GAM1645 HSPC065  3' GTCCCCAAGGCTGGAGTGCAGT 27160            _  A
            GG                  CCACTGCACTCCAGCCT GGG GAC
                                |||||||||||||||| ||| |||
                                GGTGACGTGAGGTCGGA CCC CTG
                                        A  _
GAM1645 HSPC065  3' GTCCCCCATGCTGGAGTGCAGT 27161            C   A
            GG                  CCACTGCACTCCAGC TGGG GAC
                                |||||||||||||| |||| |||
                                GGTGACGTGAGGTCG ACCC CTG
                                      T   C
GAM1645 ICK      3' GTCACCCAGGCTGGAGTGCAGT 30600              A
            GG                  CCACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                        A
GAM1645 IMPACT   3' CCTAGGCTGGAGTGCAGTGG  38004
                                CCACTGCACTCCAGCCTGGG
                                ||||||||||||||||||
                                GGTGACGTGAGGTCGGATCC

GAM1645 INPP5E   3' CCCAGCGCTGGAGTGCAG    73504          _
                                CTGCACTCCAGC CTGGG
                                |||||||||| |||||
                                GACGTGAGGTCG GACCC
                                      C
GAM1645 JAM1     3' GTCACCCAGGCTGGAGTGCAGT 58525              A
            GG                  CCACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                        A
GAM1645 JAM1     3' GTCACCCAGGCTGGAGTGCAGT 58552              A
            GG                  CCACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                        A
GAM1645 JAM1     3' GTCACCCAGGCTGGAGTGCAGT 58581              A
            GG                  CCACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||| |||
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                                GGTGACGTGAGGTCGGACCC CTG
                                          A
GAM1645 JAM1     3' GTCACCCAGGCTGGAGTGCAGT 34243              A
             GG                  CCACTGCACTCCAGCCTGGG GAC
                                 |||||||||||||||||||| |||
                                 GGTGACGTGAGGTCGGACCC CTG
                                          A
GAM1645 JM11     3' GTCACCAGGCTGGAGTGCAGCG 54371    A          GA
             G                   CC CTGCACTCCAGCCTGG  GAC
                                 || ||||||||||||||||  |||
                                 GG GACGTGAGGTCGGACC  CTG
                                  C            A_
GAM1645 KIAA0022 3' CCCAGGCTACAGTGCAGTGG   30278         CC
                                 CCACTGCACT  AGCCTGGG
                                 |||||||||  ||||||||
                                 GGTGACGTGA  TCGGACCC
                                       CA
GAM1645 KIAA0063 3' GTTGCCCAGGCTGGAGTGCAAT 30261     C           AG
             GG                  CCA TGCACTCCAGCCTGGG  AC
                                 ||| ||||||||||||||  ||
                                 GGT ACGTGAGGTCGGACCC  TG
                                   A            GT
GAM1645 KIAA0087 3' GTCACCCAGGCTGGAGTGCAGT 29347              A
             GG                  CCACTGCACTCCAGCCTGGG GAC
                                 |||||||||||||||||||| |||
                                 GGTGACGTGAGGTCGGACCC CTG
                                          A
GAM1645 KIAA0090 3' GTCACCCAGGCTGGAGAGCAGT 89818       A         A
             GG                  CCACTGC CTCCAGCCTGGG GAC
                                 ||||||| |||||||||||| |||
                                 GGTGACG GAGGTCGGACCC CTG
                                    A          A
GAM1645 KIAA0161 3' GTCCCCCAAGCTGGAGTACAAT 29206    C  C      C    A
             G                   CA TG ACTCCAGC TGGG GAC
                                 || || |||||||| |||| |||
                                 GT AC TGAGGTCG ACCC CTG
                                  A  A       A    C
GAM1645 KIAA0186 3' GTCACCCAGGCTGGGGTGCAGT 41113              A
             GG                  CCACTGCACTCCAGCCTGGG GAC
                                 |||||||||||||||||||| |||
                                 GGTGACGTGGGGTCGGACCC CTG
                                          A
GAM1645 KIAA0205 3' CCCAGGCTGTAGTGCAGTGG   30206         C
                                 CCACTGCACT CAGCCTGGG
                                 |||||||||| |||||||||
                                 GGTGACGTGA GTCGGACCC
                                       T
GAM1645 KIAA0210 5' GTCGCCCAGGCTGGAGTGCAGT 29172              A
             GG                  CCACTGCACTCCAGCCTGGG GAC
                                 |||||||||||||||||||| |||
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                                GGTGACGTGAGGTCGGACCC CTG
                                             G
GAM1645 KIAA0210 5' TCCAGGCTGGAGTATAATGG  29177    C  C
                                CCA TG ACTCCAGCCTGGG
                                ||| || ||||||||||||
                                GGT AT TGAGGTCGGACCT
                                  A  A
GAM1645 KIAA0391 3' TCTAGGCTGGAGTGCAATGG  28622    C
                                CCA TGCACTCCAGCCTGGG
                                ||| ||||||||||||||||
                                GGT ACGTGAGGTCGGATCT
                                  A
GAM1645 KIAA0410 3' GTCTCCCAGGCCTTCCCAGTCA 29428   C   CACTCCA
                                C ACTG      GCCTGGGAGAC
                                | ||||      ||||||||||
                                A TGAC      CGGACCCTCTG
                                 C   CCTTC__
GAM1645 KIAA0418 5' CTCAGGCTGGATTGCAGTGG  28294       C
                                CCACTGCA TCCAGCCTGGG
                                |||||||| ||||||||||
                                GGTGACGT AGGTCGGACTC
                                     T
GAM1645 KIAA0426 3' GTCGCCCAGGCTGGAGTGCAAT 28932    C           A
           GG                     CCA TGCACTCCAGCCTGGG GAC
                                ||| |||||||||||||| |||
                                GGT ACGTGAGGTCGGACCC CTG
                                  A             G
GAM1645 KIAA0435 3' TCAAGCACCAGAGTTGCAGTGG 29664       _  CA__  C
                                CCACTGCA CTC   GC TGG
                                |||||||| |||   || |||
                                GGTGACGT GAG   CG ACT
                                     T  ACCA  A
GAM1645 KIAA0441 3' TCACCCAGGCCAGAGTGTAGTG 29644         CA     A
           G                     CCACTGCACTC  GCCTGGG GA
                                |||||||||||  ||||||| ||
                                GGTGATGTGAG  CGGACCC CT
                                       AC      A
GAM1645 KIAA0446 5' GTCCCCCAGGCTGAGGCTGGGG 69455   ACT  A   C      A
                                CC   GC CTC AGCCTGGG GAC
                                ||   || ||| |||||||| |||
                                GG   CG GAG TCGGACCC CTG
                                 GGT  _  _       C
GAM1645 KIAA0446 5' GTCTCCTAGGCTGGAGTGCAGT 69457
           GG                     CCACTGCACTCCAGCCTGGGAGAC
                                |||||||||||||||||||||||
                                GGTGACGTGAGGTCGGATCCTCTG

GAM1645 KIAA0447 3' GTCACCCAGGCTGGAGTACAGT 72128       C          A
           GG                     CCACTG ACTCCAGCCTGGG GAC
                                |||||| ||||||||||||| |||
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                                GGTGAC TGAGGTCGGACCC CTG
                                   A           A
GAM1645  KIAA0450  5'  CCCCAGGCTGCAGGG      28345    A    CTCCA      A
                                CC CTGCA    GCCTGGG G
                                || |||||    ||||||| |
                                GG GACGT    CGGACCC C
                                 _    _____      C
GAM1645  KIAA0469  3'  GTCACCCAGGCTGGAGTGCAGT 29993                  A
             GG                   CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC CTG
                                             A
GAM1645  KIAA0469  3'  GTCACCCAGGCTGGAGTGCAGT 29994                  A
             GG                   CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC CTG
                                             A
GAM1645  KIAA0475  3'  GTTGCCCAGGCTGGAGTGCAGT 30128                  AG
             GG                   CCACTGCACTCCAGCCTGGG  AC
                                  ||||||||||||||||||||  ||
                                  GGTGACGTGAGGTCGGACCC  TG
                                             GT
GAM1645  KIAA0493  5'  CCCAAGCTGGAGTGCAGTG    64931              C
                                CACTGCACTCCAGC TGGG
                                |||||||||||||| ||||
                                GTGACGTGAGGTCG ACCC
                                      A
GAM1645  KIAA0495  3'  GTCACCCAGGCTGGAGTGCAAT 63273     C             A
             GG                   CCA TGCACTCCAGCCTGGG GAC
                                  ||| |||||||||||||| |||
                                  GGT ACGTGAGGTCGGACCC CTG
                                    A            A
GAM1645  KIAA0513  3'  CCCAAGTGGCGTGCAGTG    29024         T   G C
                                CACTGCAC CCA C TGGG
                                |||||||| ||| | ||||
                                GTGACGTG GGT G ACCC
                                     C   _ A
GAM1645  KIAA0513  3'  CCTGCAGAGTGCAGTG      29028          CA  CT
                                CACTGCACTC  GC  GGG
                                |||||||||  ||  |||
                                GTGACGTGAG  CG  TCC
                                     A_  __
GAM1645  KIAA0513  3'  GTTGCCCAGGCTGGAGTGCAGT 29048                  AG
             G                    CACTGCACTCCAGCCTGGG  AC
                                  ||||||||||||||||||  ||
                                  GTGACGTGAGGTCGGACCC  TG
                                             GT
GAM1645  KIAA0513  5'  TTTCCCAGGCTGGAGTGCAGAG 29060    A
             G                    CC CTGCACTCCAGCCTGGGAGA
                                  || ||||||||||||||||||
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                                GG GACGTGAGGTCGGACCCTTT
                                 A
GAM1645  KIAA0527  3'  CCCAGGCTGGAGTGCAGTG   97493
                                CACTGCACTCCAGCCTGGG
                                ||||||||||||||||||
                                GTGACGTGAGGTCGGACCC

GAM1645  KIAA0532  3'  GTCACCCAGGCTAGAGTACAGT 71325      C   C      A
              GG                  CCACTG ACTC AGCCTGGG GAC
                                  |||||| |||| |||||||| |||
                                  GGTGAC TGAG TCGGACCC CTG
                                     A   A      A
GAM1645  KIAA0544  3'  CTGCCCAGGCTGGAGTGCAGTG 71464                 _
              G                   CCACTGCACTCCAGCCTGGG AG
                                  |||||||||||||||||||| ||
                                  GGTGACGTGAGGTCGGACCC TC
                                           G
GAM1645  KIAA0555  3'  CCCATGCTGGAGTGCATTGG   29548     C         C
                                CCA TGCACTCCAGC TGGG
                                ||| |||||||||| ||||
                                GGT ACGTGAGGTCG ACCC
                                  T         T
GAM1645  KIAA0561  3'  CCCGGGCTGGAGTGCAGCGG   66469    A
                                CC CTGCACTCCAGCCTGGG
                                || ||||||||||||||||
                                GG GACGTGAGGTCGGGCCC
                                 C
GAM1645  KIAA0562  3'  CCTAGGCTGGAGTGCAGTGG   28819
                                CCACTGCACTCCAGCCTGGG
                                ||||||||||||||||||||
                                GGTGACGTGAGGTCGGATCC

GAM1645  KIAA0563  5'  CCCAGGCTGAAGTGCAGTG    29875          C
                                CACTGCACT CAGCCTGGG
                                ||||||||| |||||||||
                                GTGACGTGA GTCGGACCC
                                     A
GAM1645  KIAA0594  3'  GTTGCCCAGGCTGGAGTGCAGT 65517                  AG
              GG                  CCACTGCACTCCAGCCTGGG  AC
                                  |||||||||||||||||||  ||
                                  GGTGACGTGAGGTCGGACCC  TG
                                           GT
GAM1645  KIAA0599  3'  GTCACCCAGGCTGGAGTGCAAT 77698     C             A
              GG                  CCA TGCACTCCAGCCTGGG GAC
                                  ||| |||||||||||||| |||
                                  GGT ACGTGAGGTCGGACCC CTG
                                    A             A
GAM1645  KIAA0599  3'  GTCGCCCAGGCTGGAGCGCAGT 77700         A          A
              GG                  CCACTGC CTCCAGCCTGGG GAC
                                  ||||||| |||||||||||| |||
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                                GGTGACG GAGGTCGGACCC CTG
                                    C          G
GAM1645  KIAA0635  3'  TAGGCCGGGTGCAGTGG     28420          T  A
                                CCACTGCAC CC GCCTG
                                |||||||| || |||||
                                GGTGACGTG GG CGGAT
                                     _ C
GAM1645  KIAA0682  3'  CCGAGAGGGCTGGAGTGCAGTG 30018                ____
           G                    CCACTGCACTCCAGCCT    GG
                                |||||||||||||||||    ||
                                GGTGACGTGAGGTCGGG    CC
                                       AGAG
GAM1645  KIAA0737  3'  GTCACCCAGGCTGGAGTGCAGT 29817                  A
           GG                   CCACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                       A
GAM1645  KIAA0841  3'  GTTGCCCAAGTTGGAGTGCAGT 71903              C    AG
           GG                   CCACTGCACTCCAGC TGGG  AC
                                |||||||||||||| ||||  ||
                                GGTGACGTGAGGTTG ACCC  TG
                                       A   GT
GAM1645  KIAA0841  3'  GTTTCCCAGGCTGAAGTGCAGT 71905          C
           GG                   CCACTGCACT CAGCCTGGGAGAC
                                |||||||||| ||||||||||||
                                GGTGACGTGA GTCGGACCCTTTG
                                     A
GAM1645  KIAA0861  3'  GTCGCCCAGGCTGGAGTGCAGT 90359                A
           GG                   CCACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                       G
GAM1645  KIAA0889  3'  GTCCCCCAGGCTTGAGTGCAAT 31783    C      C       A
           G                    CA TGCACTC AGCCTGGG GAC
                                || ||||||| |||||||| |||
                                GT ACGTGAG TCGGACCC CTG
                                 A      T       C
GAM1645  KIAA0924  3'  CCCAGGCTAGAGTGCAGTGG   30358          C
                                CCACTGCACTC AGCCTGGG
                                |||||||||| ||||||||
                                GGTGACGTGAG TCGGACCC
                                       A
GAM1645  KIAA0924  3'  CCTGGGCTGGAGTGCAGTGG   30361             TG
                                CCACTGCACTCCAGCC  GG
                                |||||||||||||||  ||
                                GGTGACGTGAGGTCGG  CC
                                       GT
GAM1645  KIAA0924  3'  GTTGCCCAGGCTAGAGTGCAGT 30373          C       AG
           GG                   CCACTGCACTC AGCCTGGG  AC
                                |||||||||| ||||||||  ||
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                                GGTGACGTGAG TCGGACCC  TG
                                      A       GT
GAM1645  KIAA0930  3'  TTGGGGCTGGGCGCAGTGG   71078        A T      G
                                CCACTGC C CCAGCCT GG
                                ||||||| | ||||||| ||
                                GGTGACG G GGTCGGG TT
                                    C _      G
GAM1645  KIAA0931  3'  CTCAGGCTGGAGTGCAATGG  68009     C
                                CCA TGCACTCCAGCCTGGG
                                ||| ||||||||||||||||
                                GGT ACGTGAGGTCGGACTC
                                  A
GAM1645  KIAA0961  3'  CCCAGGCTGGCGTGCAGTGG  30397          T
                                CCACTGCAC CCAGCCTGGG
                                ||||||||| ||||||||||
                                GGTGACGTG GGTCGGACCC
                                      C
GAM1645  KIAA1001  3'  TTTAGGCTGGGCGCAGTGG   31018        A T
                                CCACTGC C CCAGCCTGGG
                                ||||||| | ||||||||||
                                GGTGACG G GGTCGGATTT
                                    C _
GAM1645  KIAA1017  3'  TGGGACTGGGTGCAGTGG    24272          T   _
                                CCACTGCAC CCAG CCTG
                                ||||||||| |||| ||||
                                GGTGACGTG GGTC GGGT
                                      _   A
GAM1645  KIAA1026  3'  CCCAGGATGGAGTGCAGTG   71734            G
                                CACTGCACTCCA CCTGGG
                                |||||||||||| ||||||
                                GTGACGTGAGGT GGACCC
                                      A
GAM1645  KIAA1028  3'  GTCACCCAAGCTGGAGTGCAGT 93591              C   A
            GG                    CCACTGCACTCCAGC TGGG GAC
                                ||||||||||||||| |||| |||
                                GGTGACGTGAGGTCG ACCC CTG
                                      A   A
GAM1645  KIAA1029  5'  CTCCCAGGCCATGCACCGG   24427    AC    CTCCA
                                CC  TGCA    GCCTGGGAG
                                ||  ||||    |||||||||
                                GG  ACGT    CGGACCCTC
                                  CC    AC___
GAM1645  KIAA1040  3'  GTCACCCAGGCTGGAATGCAGT 72691         C         A
            GG                    CCACTGCA TCCAGCCTGGG GAC
                                ||||||||| |||||||||| |||
                                GGTGACGT AGGTCGGACCC CTG
                                    A         A
GAM1645  KIAA1041  3'  GTTGCCCAGGCTGGAGTGCAGT 30829                AG
            GG                    CCACTGCACTCCAGCCTGGG  AC
                                |||||||||||||||||||  ||
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                                GGTGACGTGAGGTCGGACCC  TG
                                          GT
GAM1645  KIAA1045  3'  CCCTGAGGCTGGGCACAGTGG  71602       CA T     __
                                CCACTG  C CCAGCCT  GGG
                                ||||||  | |||||||  |||
                                GGTGAC  G GGTCGGA  CCC
                                   AC _      GT
GAM1645  KIAA1052  5'  CTCAGGCTGCAGTGCAGTGG   30941          C
                                CCACTGCACT CAGCCTGGG
                                |||||||||| |||||||||
                                GGTGACGTGA GTCGGACTC
                                      C
GAM1645  KIAA1054  3'  GTTGCCCAGGCTGGAGTGCAGT 68969                AG
            GG                    CCACTGCACTCCAGCCTGGG  AC
                                ||||||||||||||||||  ||
                                GGTGACGTGAGGTCGGACCC  TG
                                          GT
GAM1645  KIAA1110  3'  CTCCTGGGAGAGGCAGTG    62500       A   CAG  TG
                                CACTGC CTC   CC  GGAG
                                |||||| |||   ||  ||||
                                GTGACG GAG   GG  CCTC
                                   _  A__  GT
GAM1645  KIAA1128  3'  CCCAGGCTGGATTACAGTGG   68999       CAC
                                CCACTG   TCCAGCCTGGG
                                ||||||   ||||||||||
                                GGTGAC   AGGTCGGACCC
                                   ATT
GAM1645  KIAA1143  3'  GTCACCCAGGCTGGAGTGCAGT 69248                A
            GG                    CCACTGCACTCCAGCCTGGG GAC
                                ||||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                          A
GAM1645  KIAA1155  3'  GTCACCCAGGCTGGAGTGCAGT 62916                A
            GG                    CCACTGCACTCCAGCCTGGG GAC
                                ||||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                          A
GAM1645  KIAA1161  5'  GTCACCCAGGTTGGAGTGCAGT 82650                A
            GG                    CCACTGCACTCCAGCCTGGG GAC
                                ||||||||||||||||||| |||
                                GGTGACGTGAGGTTGGACCC CTG
                                          A
GAM1645  KIAA1169  5'  CCTGGGCTGGAGTCCAGTGG   35881       C        TG
                                CCACTG ACTCCAGCC  GG
                                |||||| |||||||||  ||
                                GGTGAC TGAGGTCGG  CC
                                   C        GT
GAM1645  KIAA1170  3'  GTTGCCCAAGCTGGAGTGCAAT 70422     C         C    AG
            GG                    CCA TGCACTCCAGC TGGG  AC
                                ||| ||||||||||| ||||  ||
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                                GGT ACGTGAGGTCG ACCC  TG
                                  A         A    GT
GAM1645  KIAA1185  3'  GTCGCCAGGCTGGAGTGCAGTG 63294              GA
              G                   CCACTGCACTCCAGCCTGG  GAC
                                  ||||||||||||||||||  |||
                                  GGTGACGTGAGGTCGGACC  CTG
                                           G_
GAM1645  KIAA1193  3'  GTCGCCAGGCTGGAGTGCAGTG 68277              GA
              G                   CCACTGCACTCCAGCCTGG  GAC
                                  ||||||||||||||||||  |||
                                  GGTGACGTGAGGTCGGACC  CTG
                                           G_
GAM1645  KIAA1198  3'  CCAAGCTGGACTGCAGTGG   64011        C     C
                                  CCACTGCA TCCAGC TGG
                                  ||||||||  ||||||  |||
                                  GGTGACGT AGGTCG ACC
                                       C     A
GAM1645  KIAA1198  3'  CCAGGCTGGAGTGCAGTGG   64016
                                  CCACTGCACTCCAGCCTGG
                                  ||||||||||||||||||
                                  GGTGACGTGAGGTCGGACC

GAM1645  KIAA1198  3'  CCCAGGCTGGAGTGCAGTGG  64020
                                  CCACTGCACTCCAGCCTGGG
                                  ||||||||||||||||||
                                  GGTGACGTGAGGTCGGACCC

GAM1645  KIAA1198  3'  CCCAGGCTGGAGTGCAGTGG  64021
                                  CCACTGCACTCCAGCCTGGG
                                  ||||||||||||||||||
                                  GGTGACGTGAGGTCGGACCC

GAM1645  KIAA1198  3'  GTTGCCCAGGCTGGAGTGCAGT 64057               AG
              GG                    CCACTGCACTCCAGCCTGGG  AC
                                    ||||||||||||||||||  ||
                                    GGTGACGTGAGGTCGGACCC  TG
                                             GT
GAM1645  KIAA1210  3'  GTTACCCAGATTGGAGTGCAGT 98081          GC    A
              GG                    CCACTGCACTCCA  CTGGG GAC
                                    ||||||||||||  ||||| |||
                                    GGTGACGTGAGGT  GACCC TTG
                                           TA    A
GAM1645  KIAA1254  3'  GTCAGCCAGGCTGGAGTGCAGT 70564             GA
              G                     CACTGCACTCCAGCCTGG  GAC
                                    ||||||||||||||||||  |||
                                    GTGACGTGAGGTCGGACC  CTG
                                             GA
GAM1645  KIAA1257  3'  GTCGCCCAGGCTGGAGTGCAGT 63411               A
              GG                    CCACTGCACTCCAGCCTGGG GAC
                                    ||||||||||||||||||| |||
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                                GGTGACGTGAGGTCGGACCC CTG
                                      G
GAM1645  KIAA1257  3'  GTTGCCCAGGCTGGAGTACAAT 63414     C  C          AG
              GG                  CCA TG ACTCCAGCCTGGG  AC
                                  ||| || ||||||||||||||  ||
                                  GGT AC TGAGGTCGGACCC  TG
                                    A  A           GT
GAM1645  KIAA1280  5'  CCAAGCTGGAGTACACGG    70276    AC  C       C
                                  CC  TG ACTCCAGC TGG
                                  ||  || ||||||||| |||
                                  GG  AC TGAGGTCG ACC
                                   C_  A       A
GAM1645  KIAA1280  5'  GTTGCCCAGGCTGGAGTGCAGT 70287                AG
              G                   CACTGCACTCCAGCCTGGG  AC
                                  ||||||||||||||||||  ||
                                  GTGACGTGAGGTCGGACCC  TG
                                        GT
GAM1645  KIAA1287  3'  GTTGCCCAGGCTGGAGTGCAGT 78941                AG
              GG                  CCACTGCACTCCAGCCTGGG  AC
                                  ||||||||||||||||||  ||
                                  GGTGACGTGAGGTCGGACCC  TG
                                        GT
GAM1645  KIAA1320  5'  CCCAGGCTGGAGTATAGTG    69836       C
                                  CACTG ACTCCAGCCTGGG
                                  ||||| ||||||||||||
                                  GTGAT TGAGGTCGGACCC
                                     A
GAM1645  KIAA1320  5'  GTCACCCAGGCTGGAGTGCAGT 69847                A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC CTG
                                        A
GAM1645  KIAA1373  3'  GTCGCCCAGGCTGGAGTGCAGT 71511                A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC CTG
                                        G
GAM1645  KIAA1404  3'  TTTTTAGGCTGGGCGCAGTGG  62697        A T
                                  CCACTGC C CCAGCCTGGGAG
                                  ||||||| | ||||||||||||
                                  GGTGACG G GGTCGGATTTTT
                                      C _
GAM1645  KIAA1443  3'  CCCAGGCTGTAGTGCAATGG   64568     C     C
                                  CCA TGCACT CAGCCTGGG
                                  ||| |||||| |||||||||
                                  GGT ACGTGA GTCGGACCC
                                    A     T
GAM1645  KIAA1456  3'  GTCGCCCAGGCTGGAGTGCACT 67567     C           A
              GG                  CCA TGCACTCCAGCCTGGG GAC
                                  ||| |||||||||||||| |||
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                                GGT ACGTGAGGTCGGACCC CTG
                                  C            G
GAM1645  KIAA1465  3'  GTCGCCAGGCTGGAGTGCAGTG 61508              GA
                 G                 CCACTGCACTCCAGCCTGG  GAC
                                   ||||||||||||||||||  |||
                                   GGTGACGTGAGGTCGGACC  CTG
                                          G_
GAM1645  KIAA1467  3'  GTCGCCCAGGCTGGAGTGCAGT 72076               A
                 GG                  CCACTGCACTCCAGCCTGGG GAC
                                     |||||||||||||||||| |||
                                     GGTGACGTGAGGTCGGACCC CTG
                                          G
GAM1645  KIAA1473  3'  CCCAGGCTGGAGTACAGTGG  71208       C
                                     CCACTG ACTCCAGCCTGGG
                                     |||||| ||||||||||||
                                     GGTGAC TGAGGTCGGACCC
                                        A
GAM1645  KIAA1497  5'  GTTGCCCAGGCTGGAGTGCAGT 68130              AG
                 GG                  CCACTGCACTCCAGCCTGGG  AC
                                     ||||||||||||||||||  ||
                                     GGTGACGTGAGGTCGGACCC  TG
                                          GT
GAM1645  KIAA1508  3'  GTCACCCAGGCTGGAGTGCA  62560            A
                                     TGCACTCCAGCCTGGG GAC
                                     |||||||||||||| |||
                                     ACGTGAGGTCGGACCC CTG
                                           A
GAM1645  KIAA1530  3'  CCCAGGCTGAGTGCAGTGG  68553          C
                                     CCACTGCACTC AGCCTGGG
                                     |||||||||| ||||||||
                                     GGTGACGTGAG TCGGACCC
                                          _
GAM1645  KIAA1530  3'  GTCGCCAGGCTGGAGTGCAATG 68569    C          GA
                 G                   CCA TGCACTCCAGCCTGG  GAC
                                     ||| ||||||||||||||  |||
                                     GGT ACGTGAGGTCGGACC  CTG
                                       A           G_
GAM1645  KIAA1559  3'  GTCCCCCAGGCTGGAGTGCAGT 73460              A
                 GG                  CCACTGCACTCCAGCCTGGG GAC
                                     |||||||||||||||||| |||
                                     GGTGACGTGAGGTCGGACCC CTG
                                          C
GAM1645  KIAA1571  3'  GTCTTGCCCAGGCTGGAGTGCA 61622                __
                 GTGG                  CCACTGCACTCCAGCCTGGG  AGAC
                                       ||||||||||||||||||  ||||
                                       GGTGACGTGAGGTCGGACCC  TCTG
                                          GT
GAM1645  KIAA1615  3'  CCTAGGCTGGAGTGCAGTGG  69273
                                     CCACTGCACTCCAGCCTGGG
                                     ||||||||||||||||||
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                                GGTGACGTGAGGTCGGATCC

GAM1645  KIAA1615  3'  GTCACCAGGCCGGAGTGCAGTG 69282          A     GA
                 G                  CCACTGCACTCC GCCTGG  GAC
                                    |||||||||||| ||||||  |||
                                    GGTGACGTGAGG CGGACC  CTG
                                           C     A_
GAM1645  KIAA1649  3'  CCAAGGCTGGAGTGCAGTGG  51223             G
                                    CCACTGCACTCCAGCCT GG
                                    ||||||||||||||||| ||
                                    GGTGACGTGAGGTCGGA CC
                                              A
GAM1645  KIAA1655  3'  GTTGCCCAGGCTGGAGTGCAGT 67201               AG
                 GG                   CCACTGCACTCCAGCCTGGG  AC
                                      |||||||||||||||||||  ||
                                      GGTGACGTGAGGTCGGACCC  TG
                                                GT
GAM1645  KIAA1668  3'  GTCGCCCAGGCTGGAGTGCAGT 67079               A
                 GG                   CCACTGCACTCCAGCCTGGG GAC
                                      |||||||||||||||||||| |||
                                      GGTGACGTGAGGTCGGACCC CTG
                                                G
GAM1645  KIAA1671  3'  CCAGGCTGGAATGCAGTGG   66272        C
                                    CCACTGCA TCCAGCCTGG
                                    |||||||| ||||||||||
                                    GGTGACGT AGGTCGGACC
                                          A
GAM1645  KIAA1671  3'  CTCAAGCTGGAGTGGAGTGG  66275      G       C
                                    CCACT CACTCCAGC TGGG
                                    ||||| ||||||||| ||||
                                    GGTGA GTGAGGTCG ACTC
                                       G        A
GAM1645  KIAA1712  3'  CCCAGGCTGGAGTGCACTGG  68152    C
                                    CCA TGCACTCCAGCCTGGG
                                    ||| ||||||||||||||||
                                    GGT ACGTGAGGTCGGACCC
                                      C
GAM1645  KIAA1712  3'  GTTGCCCAGGCTGGAGTGCA  68164             AG
                                    TGCACTCCAGCCTGGG  AC
                                    ||||||||||||||||  ||
                                    ACGTGAGGTCGGACCC  TG
                                              GT
GAM1645  KIAA1727  3'  GTCTCCCAGACTGGACTGCAGT 64763        C    C
                 GG                   CCACTGCA TCCAG CTGGGAGAC
                                      |||||||| ||||| |||||||||
                                      GGTGACGT AGGTC GACCCTCTG
                                           C     A
GAM1645  KIAA1751  3'  CCTAGGCTGGAGTGCAGTGG  72153
                                    CCACTGCACTCCAGCCTGGG
                                    ||||||||||||||||||||
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                              GGTGACGTGAGGTCGGATCC

GAM1645 KIAA1755 3' TCCAGGCTGGAGTGCAGTGG  62023
                              CCACTGCACTCCAGCCTGGG
                              ||||||||||||||||||||
                              GGTGACGTGAGGTCGGACCT

GAM1645 KIAA1784 3' CCTAGGCTGGAGTGCAGTGG  65746
                              CCACTGCACTCCAGCCTGGG
                              ||||||||||||||||||||
                              GGTGACGTGAGGTCGGATCC

GAM1645 KIAA1821 3' GTTGCCCAGGCTGGAGTGTAGT 72274                AG
             GG                 CCACTGCACTCCAGCCTGGG  AC
                              ||||||||||||||||||||  ||
                              GGTGATGTGAGGTCGGACCC  TG
                                       GT
GAM1645 KIAA1829 3' GTTGCCCAGGCTGGAGTGCAGT 62654                AG
             GG                 CCACTGCACTCCAGCCTGGG  AC
                              ||||||||||||||||||||  ||
                              GGTGACGTGAGGTCGGACCC  TG
                                       GT
GAM1645 KIAA1829 3' TCCAGGCTGGAATGCGGTG   62657       C
                              CACTGCA TCCAGCCTGGG
                              |||||||  ||||||||||
                              GTGGCGT AGGTCGGACCT
                                 A
GAM1645 KIAA1877 3' GTCGCCCAGGCTAGAGTGCAGT 66759          C      A
             GG                 CCACTGCACTC AGCCTGGG GAC
                              ||||||||||  ||||||||  |||
                              GGTGACGTGAG TCGGACCC CTG
                                    A      G
GAM1645 KIAA1908 5' CTCCCAGGCTGGGCTTTGTAG  73787      C__
                              CTGCA   TCCAGCCTGGGAG
                              |||||   ||||||||||||
                              GATGT   GGGTCGGACCCTC
                                 TTC
GAM1645 KIAA1922 5' GTTGCCCAGGCTGGAGTGCAAT 74004     C           AG
             GG                 CCA TGCACTCCAGCCTGGG  AC
                              |||  ||||||||||||||  ||
                              GGT ACGTGAGGTCGGACCC  TG
                                A            GT
GAM1645 KIAA1924 3' CCCAGGATGGAGTGCAGTGG  74043          G
                              CCACTGCACTCCA CCTGGG
                              ||||||||||||  ||||||
                              GGTGACGTGAGGT GGACCC
                                       A
GAM1645 KIAA1924 3' CCTAGGCTGGAATGCAGTGG  74044       C
                              CCACTGCA TCCAGCCTGGG
                              ||||||||  ||||||||||
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                                GGTGACGT AGGTCGGATCC
                                    A
GAM1645 KIAA1971 3' CCAGGCTGGGGTGCAGTGG   74673
                                CCACTGCACTCCAGCCTGG
                                ||||||||||||||||||
                                GGTGACGTGGGGTCGGACC

GAM1645 KIAA1971 3' GTCATCCAGGCTAGAGTGCAGT 74691          C      GA
            GG                  CCACTGCACTC AGCCTGG  GAC
                                |||||||||| |||||||  |||
                                GGTGACGTGAG TCGGACC  CTG
                                      A      TA
GAM1645 KIAA1971 3' GTCGCCCAGGCTGGGGTGCAGT 74693               A
            GG                  CCACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||| |||
                                GGTGACGTGGGGTCGGACCC CTG
                                        G
GAM1645 KIAA1975 5' GTCTCCCGGCCTGGAGTGCAGT 74427            C
            GG                  CCACTGCACTCCAG CTGGGAGAC
                                |||||||||||| |||||||||
                                GGTGACGTGAGGTC GGCCCTCTG
                                      C
GAM1645 KIAA1987 5' GTTGCCCAGGTTAGAGTGCAGT 89389          C      AG
            GG                  CCACTGCACTC AGCCTGGG  AC
                                |||||||||| ||||||||  ||
                                GGTGACGTGAG TTGGACCC  TG
                                      A      GT
GAM1645 LAMP3   3' GTCACCCAGGCTGGAGTACAGT 60210       C          A
            GG                  CCACTG ACTCCAGCCTGGG GAC
                                |||||| |||||||||||| |||
                                GGTGAC TGAGGTCGGACCC CTG
                                   A          A
GAM1645 LENG1   5' CCTGGGCCAGAGTGCAGCGG  85194   A      CA  TG
                                CC CTGCACTC  GCC  GG
                                || ||||||||  |||  ||
                                GG GACGTGAG  CGG  CC
                                 C       AC  GT
GAM1645 LIECG3  3' GTTGCCCAGGTTGGAGTGCAGT 88803               AG
            GG                  CCACTGCACTCCAGCCTGGG  AC
                                ||||||||||||||||||  ||
                                GGTGACGTGAGGTTGGACCC  TG
                                       GT
GAM1645 LY75    3' GTTGCCCAGGCTGGAGTACAAT 11398    C  C         AG
            GG                  CCA TG ACTCCAGCCTGGG  AC
                                ||| || ||||||||||||  ||
                                GGT AC TGAGGTCGGACCC  TG
                                  A A          GT
GAM1645 LZIC    3' TCCCCACTCATTGGAGTGAACA 51399    __      CC__   A
            G                    CTG  CACTCCAG    TGGG GA
                                ||| ||||||||   |||| ||
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                                GAC  GTGAGGTT    ACCC CT
                                  AA       ACTC   _
GAM1645  MAIL     3'  CCCAGGCTGGAGTACAGTGG   49471       C
                                CCACTG ACTCCAGCCTGGG
                                |||||| ||||||||||||
                                GGTGAC TGAGGTCGGACCC
                                   A
GAM1645  MAP-1    3'  GTCACCCAGGCTGGAGTGCAGT 42448               A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                            A
GAM1645  MCM10    3'  CCCTGGCTGGAGTGCAGT    38174            T
                                ACTGCACTCCAGCC GGG
                                |||||||||||||| |||
                                TGACGTGAGGTCGG CCC
                                      T
GAM1645  MEF-2    3'  CCCAGGCTGCTGGAGTGCCGTG 65019      T      ___
              G                   CCAC GCACTCCA   GCCTGGG
                                |||| ||||||||   |||||||
                                GGTG CGTGAGGT   CGGACCC
                                  C       CGT
GAM1645  MESDC2   3'  TTGGGCTGGGTACAGTGG    72928       C  T     TG
                                CCACTG AC CCAGCC  G
                                |||||| || ||||||  |
                                GGTGAC TG GGTCGG  T
                                   A  _     GT
GAM1645  MGC10200 3'  CAGGCTAGAGTGCAGTGG    59638          C
                                CCACTGCACTC AGCCTG
                                |||||||||| ||||||
                                GGTGACGTGAG TCGGAC
                                      A
GAM1645  MGC10818 3'  GTCGCCCAGGCTGGAGTACAAT 48304     C  C          A
              GG                  CCA TG ACTCCAGCCTGGG GAC
                                ||| || |||||||||||| |||
                                GGT AC TGAGGTCGGACCC CTG
                                  A  A          G
GAM1645  MGC11386 3'  CCTAGGCTGAAGCACAGTGG   53061       CA  C
                                CCACTG  CT CAGCCTGGG
                                ||||||  || |||||||||
                                GGTGAC  GA GTCGGATCC
                                   AC  A
GAM1645  MGC12466 3'  CTAGGCTGAAGTGTAGTGG    79796          C
                                CCACTGCACT CAGCCTGG
                                |||||||||| ||||||||
                                GGTGATGTGA GTCGGATC
                                      A
GAM1645  MGC13017 3'  TTTTTGGGCTGGGCACAGTGG  55584       CA T     TG
                                CCACTG  C CCAGCC  GGAG
                                ||||||  | ||||||  ||||
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                                GGTGAC  G GGTCGG  TTTT
                                  AC _     GT
GAM1645  MGC13138  3'  GTCACCCAGGCTGGAGTGCAGT 54160                A
            GG                    CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC CTG
                                        A
GAM1645  MGC13138  3'  GTTGCCCAGGCTGGAGTGCA  54162              AG
                                  TGCACTCCAGCCTGGG  AC
                                  ||||||||||||||||  ||
                                  ACGTGAGGTCGGACCC  TG
                                        GT
GAM1645  MGC13204  3'  GTTGCCCAGGCTGGAGTGCAGT 49632                AG
            GG                    CCACTGCACTCCAGCCTGGG  AC
                                  ||||||||||||||||||||  ||
                                  GGTGACGTGAGGTCGGACCC  TG
                                        GT
GAM1645  MGC14289  3'  GTTGCCCAGGCTGGAGTGCAGT 55593                AG
            G                      CACTGCACTCCAGCCTGGG  AC
                                  ||||||||||||||||||  ||
                                  GTGACGTGAGGTCGGACCC  TG
                                        GT
GAM1645  MGC14836  3'  GTTGCCCAGGCTGGAGTGCAGT 54176                AG
            GG                    CCACTGCACTCCAGCCTGGG  AC
                                  ||||||||||||||||||  ||
                                  GGTGACGTGAGGTCGGACCC  TG
                                        GT
GAM1645  MGC15606  5'  GTTGCCCAGGCTGGAGTACATT 59525     C  C          AG
            GG                    CCA TG ACTCCAGCCTGGG  AC
                                  ||| || ||||||||||||  ||
                                  GGT AC TGAGGTCGGACCC  TG
                                    T  A          GT
GAM1645  MGC1842   3'  GTTGCCCAGACTGGAGTGCAGT 66262             C    AG
            GG                    CCACTGCACTCCAG CTGGG  AC
                                  |||||||||||||| |||||  ||
                                  GGTGACGTGAGGTC GACCC  TG
                                        A    GT
GAM1645  MGC20235  3'  GTCTTACAGCTGGGTGCAGTGG 59559         T    C  GG
                                  CCACTGCAC CCAGC TG  AGAC
                                  ||||||||| ||||| ||  ||||
                                  GGTGACGTG GGTCG AC  TCTG
                                      _    _ AT
GAM1645  MGC20481  3'  TCTCGGGTCCAGAGCGAGCAG  63369     A__  CA_
                                  CTGC   CTC   GCCTGGGA
                                  ||||   |||   ||||||||
                                  GACG   GAG   TGGGCTCT
                                    AGC   ACC
GAM1645  MGC21675  3'  GTTGCCCAGGCTGGAGTGCAAT 54596     C           AG
            GG                    CCA TGCACTCCAGCCTGGG  AC
                                  ||| ||||||||||||||  ||
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                                GGT ACGTGAGGTCGGACCC  TG
                                  A             GT
GAM1645  MGC2474   3'  CCCAGGCTGGAATGCAGTGG   43956        C
                                CCACTGCA TCCAGCCTGGG
                                |||||||| ||||||||||
                                GGTGACGT AGGTCGGACCC
                                    A
GAM1645  MGC2474   3'  GTTGCCCAGGCTGGAGTGCAAT 43964     C            AG
           GG                     CCA TGCACTCCAGCCTGGG  AC
                                ||| ||||||||||||||||  ||
                                GGT ACGTGAGGTCGGACCC  TG
                                  A             GT
GAM1645  MGC2477   5'  CCCAGCTGGAGTGCAGTGG    44295            C
                                CCACTGCACTCCAGC TGGG
                                |||||||||||||| ||||
                                GGTGACGTGAGGTCG ACCC
                                                _
GAM1645  MGC2477   5'  CCCAGGGCTGGAGTGCAGTGG  44296             _
                                CCACTGCACTCCAGCC TGGG
                                |||||||||||||| ||||
                                GGTGACGTGAGGTCGG ACCC
                                      G
GAM1645  MGC2603   3'  GTCGCCAGGCTGGAGTGCAGTG 44082               GA
           G                     CCACTGCACTCCAGCCTGG  GAC
                                |||||||||||||||||  |||
                                GGTGACGTGAGGTCGGACC  CTG
                                    G_
GAM1645  MGC29891  3'  CCCAGGCTGGAGTGCGGTGG   58857
                                CCACTGCACTCCAGCCTGGG
                                ||||||||||||||||||
                                GGTGGCGTGAGGTCGGACCC

GAM1645  MGC29898  3'  GTTGCCCAGACTGGAGTGCAGT 59588            C    AG
           GG                     CCACTGCACTCCAG CTGGG  AC
                                |||||||||||| |||||  ||
                                GGTGACGTGAGGTC GACCC  TG
                                      A    GT
GAM1645  MGC3113   3'  GTTCCCCAGGCCGGAGTGCAGT 44063          A     AG
           GG                     CCACTGCACTCC GCCTGGG  AC
                                |||||||||||| |||||||  ||
                                GGTGACGTGAGG CGGACCC  TG
                                      C      CT
GAM1645  MGC32043  3'  CTCCTGTATCCAGAGATGCAGT 58662        _  CAGCCT_
           GG                     CCACTGCA CTC      GGGAG
                                |||||||| |||      |||||
                                GGTGACGT GAG      TCCTC
                                    A  ACCTATG
GAM1645  MGC3329   3'  TCTAGGCTGGAGTGCCGTGG   44251     T
                                CCAC GCACTCCAGCCTGGG
                                |||| ||||||||||||||
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                                GGTG CGTGAGGTCGGATCT
                                  C
GAM1645  MGC4248   3'  CCAGGCTGGGTGCAGTGG    51312        T
                                CCACTGCAC CCAGCCTGG
                                ||||||||| |||||||||
                                GGTGACGTG GGTCGGACC
                                         _
GAM1645  MGC4638   3'  GTCACCAGGCTGGAGTGCAGTG 49744             GA
                                CACTGCACTCCAGCCTGG  GAC
                                |||||||||||||||||  |||
                                GTGACGTGAGGTCGGACC  CTG
                                         A_
GAM1645  MGC5149   3'  GTCACCAGGCTAGAGTGCAGTG 72762         C     GA
           G                     CCACTGCACTC AGCCTGG  GAC
                                |||||||||| |||||||  |||
                                GGTGACGTGAG TCGGACC  CTG
                                      A     A_
GAM1645  MGC9912   3'  GTCGCCAGACTGGAGTGCAGTG 55609           C   GA
           G                     CCACTGCACTCCAG CTGG  GAC
                                |||||||||||| ||||  |||
                                GGTGACGTGAGGTC GACC  CTG
                                        A   G_
GAM1645  MKRN4     3'  GTCACCCAGGCTGGAGTGCAGT 48473               A
           GG                      CCACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                         A
GAM1645  MMPL1     3'  GTCCTCCAGGCTGGAGTGCAAT 15966    C          GA
           G                     CA TGCACTCCAGCCTGG  GAC
                                || |||||||||||||  |||
                                GT ACGTGAGGTCGGACC  CTG
                                 A           TC
GAM1645  MO25      5'  CAGGCGGAGTGCAGCGG     33285    A      A
                                CC CTGCACTCC GCCTG
                                || ||||||||| |||||
                                GG GACGTGAGG CGGAC
                                 C       _
GAM1645  moblak    3'  CCAGGCTGGAGTGCAGTGG    56391
                                CCACTGCACTCCAGCCTGG
                                ||||||||||||||||||
                                GGTGACGTGAGGTCGGACC

GAM1645  MOCS3     3'  GTTGCCCAGGCTGGAGTGTAGT 27935               AG
           GG                      CCACTGCACTCCAGCCTGGG  AC
                                ||||||||||||||||||  ||
                                GGTGATGTGAGGTCGGACCC  TG
                                         GT
GAM1645  MRAS      5'  CCGGGGCTGGAGCGCGCGG   25236    AC  A      G
                                CC  TGC CTCCAGCCT GG
                                ||  ||| ||||||||| ||
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                                GG  GCG GAGGTCGGG CC
                                 C_  C       G
GAM1645  MRPL20   3'  GTCACCCAGGCTGGAGTGCAAT 36208     C           A
                GG                  CCA TGCACTCCAGCCTGGG GAC
                                    ||| |||||||||||||| |||
                                    GGT ACGTGAGGTCGGACCC CTG
                                      A           A
GAM1645  MRPL35   3'  GTTGCCCAGGCTGGAGTGCAGT 34023               AG
                GG                  CCACTGCACTCCAGCCTGGG  AC
                                    ||||||||||||||||||  ||
                                    GGTGACGTGAGGTCGGACCC  TG
                                              GT
GAM1645  MRPL44   3'  CCCAGGCTGGACTGCAGTGG  43594       C
                                    CCACTGCA TCCAGCCTGGG
                                    |||||||| ||||||||||
                                    GGTGACGT AGGTCGGACCC
                                         C
GAM1645  MRPS27   3'  GTCACCCAGGCTGGAGTGCAGT 31333               A
                GG                  CCACTGCACTCCAGCCTGGG GAC
                                    |||||||||||||||||| |||
                                    GGTGACGTGAGGTCGGACCC CTG
                                              A
GAM1645  MT-ACT48 3'  TTTTTAGGCCAGGCACAGTGG  25611       CACT  A_
                                    CCACTG   CC  GCCTGGGAG
                                    ||||||   ||  |||||||||
                                    GGTGAC   GG  CGGATTTTT
                                       AC__  AC
GAM1645  MtFMT    3'  CCCAGGCTGGAATCCAGTGG  58333       CAC
                                    CCACTG   TCCAGCCTGGG
                                    ||||||   ||||||||||
                                    GGTGAC   AGGTCGGACCC
                                       CTA
GAM1645  MYO5C    3'  TCGCCAGGCTGGAGTGTAGTGG 38727                  _
                                    CCACTGCACTCCAGCCTGG GA
                                    |||||||||||||||||| ||
                                    GGTGATGTGAGGTCGGACC CT
                                              G
GAM1645  NAPG     5'  CCCAGGCTGGAGTGCAGTGG  98535
                                    CCACTGCACTCCAGCCTGGG
                                    ||||||||||||||||||
                                    GGTGACGTGAGGTCGGACCC

GAM1645  NDP52    3'  GTCACCCAGGCTGGCGTGCAAT 20676     C    T        A
                GG                  CCA TGCAC CCAGCCTGGG GAC
                                    ||| ||||| |||||||||| |||
                                    GGT ACGTG GGTCGGACCC CTG
                                      A    C         A
GAM1645  NDUFB1   5'  TCCCCCAGGCTGGAGTGTAGTG 17016               A
                G                    CCACTGCACTCCAGCCTGGG GA
                                    |||||||||||||||||| ||
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                                GGTGATGTGAGGTCGGACCC CT
                                                    C
GAM1645 NDUFC2   3' TCAGGCTGGAGTGCAGTGG   17037
                                CCACTGCACTCCAGCCTGG
                                ||||||||||||||||||
                                GGTGACGTGAGGTCGGACT

GAM1645 NINJ2    3' CTAGGCTGGAGTAAAATGG   33721     CTGC
                                CCA   ACTCCAGCCTGG
                                |||   ||||||||||||
                                GGT   TGAGGTCGGATC
                                  AAAA
GAM1645 NOSIP    5' CCTAGGCTGGAGTGCAATGG  32542     C
                                CCA TGCACTCCAGCCTGGG
                                ||| ||||||||||||||||
                                GGT ACGTGAGGTCGGATCC
                                  A
GAM1645 Nup43    3' GTCTTGCTCTGCTGGAGTGCGG 45353             CT _
             TGG                    CCACTGCACTCCAGC  GG GAGAC
                                ||||||||||||||  || |||||
                                GGTGGCGTGAGGTCG  TC TTCTG
                                        TC  G
GAM1645 NXN      3' GTCGCCCAGGCTGGAGTGCAGT 42680                A
             GG                   CCACTGCACTCCAGCCTGGG GAC
                                ||||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                                    G
GAM1645 OCT11    3' CCCAGGCTGGAGTGCAGTGG  27585
                                CCACTGCACTCCAGCCTGGG
                                ||||||||||||||||||||
                                GGTGACGTGAGGTCGGACCC

GAM1645 OR51E2   3' GTCACCAGGCTGGAGTGCAGTG 48516               GA
             G                   CCACTGCACTCCAGCCTGG  GAC
                                |||||||||||||||||  |||
                                GGTGACGTGAGGTCGGACC  CTG
                                                  A_
GAM1645 OSBPL2   3' GTTGCCCAGGCTGGAGTGCAAT 58492     C           AG
             GG                   CCA TGCACTCCAGCCTGGG  AC
                                ||| ||||||||||||||  ||
                                GGT ACGTGAGGTCGGACCC  TG
                                  A             GT
GAM1645 OSBPL2   3' GTTGCCCAGGCTGGAGTGCAAT 29906     C           AG
             GG                   CCA TGCACTCCAGCCTGGG  AC
                                ||| ||||||||||||||  ||
                                GGT ACGTGAGGTCGGACCC  TG
                                  A             GT
GAM1645 PASK     5' CTGAGGCTGGAGTGCAGTGG  31408             G
                                CCACTGCACTCCAGCCT GG
                                |||||||||||||||| ||
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                                GGTGACGTGAGGTCGGA TC
                                       G
GAM1645  PCBP3    3'  CCCATGCACCGGCATGCAGTGG 40443        CT  A__  C
                                CCACTGCA  CC   GC TGGG
                                ||||||||  ||   || ||||
                                GGTGACGT  GG   CG ACCC
                                     AC  CCA  T
GAM1645  PELI1    5'  GTCACCCAGGCTGGAGTGCAGT 40648              A
            GG                    CCACTGCACTCCAGCCTGGG GAC
                                ||||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                       A
GAM1645  PELI1    5'  GTCGCCCAGGCTGGAGTGCAGT 40650              A
            GG                    CCACTGCACTCCAGCCTGGG GAC
                                ||||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                       G
GAM1645  PELI1    5'  GTTGCCCAGGTTGGAGTGCAGT 40652              AG
            GG                    CCACTGCACTCCAGCCTGGG  AC
                                ||||||||||||||||||  ||
                                GGTGACGTGAGGTTGGACCC  TG
                                       GT
GAM1645  PI4KII   3'  TCTCCCATCAGTGCTGTGG   37954     T    CCAGCC
                                CCAC GCACT     TGGGAGA
                                ||||  |||||     |||||||
                                GGTG CGTGA     ACCCTCT
                                  T    CT_____
GAM1645  PIP3-E   3'  GTTGCCCAGGCTGGAGTGCAGT 67359              AG
            GG                    CCACTGCACTCCAGCCTGGG  AC
                                ||||||||||||||||||  ||
                                GGTGACGTGAGGTCGGACCC  TG
                                       GT
GAM1645  POFUT1   3'  GTCTCCCAGGCTGGAGTGCAGT 70981
            GG                    CCACTGCACTCCAGCCTGGGAGAC
                                ||||||||||||||||||||||||
                                GGTGACGTGAGGTCGGACCCTCTG

GAM1645  POLE3    3'  GTGGCCCAGGCTGGAGTGCAGT 34319               AG
            GG                    CCACTGCACTCCAGCCTGGG  AC
                                ||||||||||||||||||  ||
                                GGTGACGTGAGGTCGGACCC  TG
                                       GG
GAM1645  POLE3    3'  TCTCCCAGACTTGTGACTATGG 34322     CTG_  TCC  C
                                CCA   CAC   AG CTGGGAGA
                                |||   |||   || ||||||||
                                GGT   GTG   TC GACCCTCT
                                  ATCA  T__  A
GAM1645  PRO0365  5'  GTCGCCAGGCTGAAGTGCAGTG 26993          C       GA
            G                     CCACTGCACT CAGCCTGG  GAC
                                |||||||||| ||||||||  |||
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                                GGTGACGTGA GTCGGACC  CTG
                                     A       G_
GAM1645  PRO0456  3'  TTTAGGCTGGGTGCAGTGG   27011          T
                                CCACTGCAC CCAGCCTGGG
                                ||||||||| ||||||||||
                                GGTGACGTG GGTCGGATTT
                                     _
GAM1645  PRO0478  3'  TCCCAGCCTGGAATGCAGTGG  27040         C    C
                                CCACTGCA TCCAG CTGGGA
                                |||||||| ||||| ||||||
                                GGTGACGT AGGTC GACCCT
                                    A    C
GAM1645  PRO0611  3'  TCTTCTGGCTGGGCGCAGTGG  26861        A T    T
                                CCACTGC C CCAGCC GGGAGA
                                ||||||| | |||||| ||||||
                                GGTGACG G GGTCGG TCTTCT
                                    C _    _
GAM1645  PRO0902  3'  GTCACCCAGGCTGGAGTGTAGT 54969                A
           GG                     CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||||| |||
                                  GGTGATGTGAGGTCGGACCC CTG
                                           A
GAM1645  PRO1048  3'  CTGCCCAGGCTGGAGTACAGTG 38113        C          _
           G                      CCACTG ACTCCAGCCTGGG AG
                                  |||||| |||||||||||| ||
                                  GGTGAC TGAGGTCGGACCC TC
                                     A           G
GAM1645  PRO1386  3'  TCTGGCCAGGTGCAGTGG    49219          CCA   TG
                                CCACTGCACT   GCC  GGA
                                ||||||||||   |||  |||
                                GGTGACGTGG   CGG  TCT
                                     AC_   __
GAM1645  PRO1992  5'  GTCACCCAGACTGGAGTGCAGT 26910             C    A
           GG                     CCACTGCACTCCAG CTGGG GAC
                                  |||||||||||||| ||||| |||
                                  GGTGACGTGAGGTC GACCC CTG
                                           A    A
GAM1645  PRO1992  3'  GTCACCCAGGCTGGAGTGCAGT 26912                A
           GG                     CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC CTG
                                           A
GAM1645  PRO2955  3'  GTCCCCCAGGCTGAAGTGCAGC 38244    A      C       A
           GG                     CC CTGCACT CAGCCTGGG GAC
                                  || ||||||| ||||||||| |||
                                  GG GACGTGA GTCGGACCC CTG
                                   C      A       C
GAM1645  PSPH     3'  GTTGCCCAGGCTGGAGTGCAGT 17139                AG
           GG                     CCACTGCACTCCAGCCTGGG  AC
                                  ||||||||||||||||||||  ||
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                                GGTGACGTGAGGTCGGACCC  TG
                                      GT
GAM1645  PSR      3'  CCAAGGCCAGGTGCAGTGG   65781          CCA   G
                                CCACTGCACT   GCCT GG
                                ||||||||||   |||| ||
                                GGTGACGTGG   CGGA CC
                                     AC_   A
GAM1645  PSTPIP2   3'  GTCCCCCAGGCTGAAGTGCAGC 44661    A      C        A
              GG                  CC CTGCACT CAGCCTGGG GAC
                                  || ||||||| ||||||||| |||
                                  GG GACGTGA GTCGGACCC CTG
                                   C      A        C
GAM1645  PTD011    5'  CAGGCTGGAGTGCAGTGG    26759
                                CCACTGCACTCCAGCCTG
                                ||||||||||||||||||
                                GGTGACGTGAGGTCGGAC

GAM1645  RAB21     3'  GTCACCCAGGCTGGAGTGCACT 31097     C             A
              GG                  CCA TGCACTCCAGCCTGGG GAC
                                  ||| |||||||||||||| |||
                                  GGT ACGTGAGGTCGGACCC CTG
                                    C             A
GAM1645  RAB33B    3'  GTCTCCAGGCTGGAGTGCAGTG 49333                G
              G                   CCACTGCACTCCAGCCTGG AGAC
                                  |||||||||||||||||| ||||
                                  GGTGACGTGAGGTCGGACC TCTG
                                                  _
GAM1645  RAB39     3'  GTCACCCAGGCTGGAGTGCAGT 77125                 A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC CTG
                                        A
GAM1645  RAP140    3'  GTCGCCCAAGCTGGAGTACAGT 31523       C       C    A
              GG                  CCACTG ACTCCAGC TGGG GAC
                                  |||||| |||||||| |||| |||
                                  GGTGAC TGAGGTCG ACCC CTG
                                     A       A    G
GAM1645  RASSF2    3'  GTTTCCCAGGCTGGAGTGCAGT 29111
              GG                  CCACTGCACTCCAGCCTGGGAGAC
                                  ||||||||||||||||||||||||
                                  GGTGACGTGAGGTCGGACCCTTTG

GAM1645  RES4-25   3'  GTTGCCCAGGCTGGAGTGCAAT 65273     C             AG
              GG                  CCA TGCACTCCAGCCTGGG  AC
                                  ||| ||||||||||||||  ||
                                  GGT ACGTGAGGTCGGACCC  TG
                                    A             GT
GAM1645  RIL       3'  TCCTAGGCTCTGGGTGCAGT   14889          C_
                                ACTGCACTC  AGCCTGGGA
                                |||||||||  |||||||||
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                                TGACGTGGG  TCGGATCCT
                                     TC
GAM1645  RNF8     3'  GTTGCCCAAGCTGGAGTACAGT 15573      C       C    AG
                                ACTG ACTCCAGC TGGG  AC
                                |||| |||||||| ||||  ||
                                TGAC TGAGGTCG ACCC  TG
                                  A       A    GT
GAM1645  RNO2     5'  CCAAGGCTGGAGTGCAGGG   53928    A           G
                                CC CTGCACTCCAGCCT GG
                                || |||||||||||||| ||
                                GG GACGTGAGGTCGGA CC
                                 _           A
GAM1645  SARM     3'  TCCAGGCTGGAGGGCAGTG   31306       A
                                CACTGC CTCCAGCCTGGG
                                |||||| ||||||||||||
                                GTGACG GAGGTCGGACCT
                                   G
GAM1645  SCAMP-4  3'  GTCGCCCAGGCTGGAGTGCAGT 55354                  A
            GG                    CCACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                            G
GAM1645  SCAND2   3'  TCACCCAGGCTGGAGTGGAGTG 42145       G           A
            G                     CCACT CACTCCAGCCTGGG GA
                                ||||| ||||||||||||| ||
                                GGTGA GTGAGGTCGGACCC CT
                                   G            A
GAM1645  SCYA13   3'  TCAAGCTGGAGTACGTG     19431     T C       C
                                CAC G ACTCCAGC TGG
                                ||| | |||||||| |||
                                GTG C TGAGGTCG ACT
                                  _ A       A
GAM1645  SCYA16   3'  GTCACCCAGGCTGGAGTGCAGT 17177                  A
            GG                    CCACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                            A
GAM1645  SCYA22   3'  CCCACGCTGGAGTGCAATGG   92585     C         C
                                CCA TGCACTCCAGC TGGG
                                ||| ||||||||||| ||||
                                GGT ACGTGAGGTCG ACCC
                                  A          C
GAM1645  SCYA22   3'  GTCGCCCAGGCTGGAGTGCAGT 92606                  A
            GG                    CCACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                            G
GAM1645  SCYA22   3'  GTCTCCCAAGCCTGGCATGTGG 92607    TG  CT    _ C
                                C  CA  CCAG C TGGGAGAC
                                |  ||  |||| | ||||||||
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                                  G  GT  GGTC G ACCCTCTG
                                   GT  AC    C A
GAM1645  SCYA28   3'  CAGGCTGGAGGGCAGTGG    39538        A
                                  CCACTGC CTCCAGCCTG
                                  ||||||| ||||||||||
                                  GGTGACG GAGGTCGGAC
                                      G
GAM1645  SERF1B   3'  CCCAGGCTGGACTGCAGTGG   43693         C
                                  CCACTGCA TCCAGCCTGGG
                                  |||||||| ||||||||||
                                  GGTGACGT AGGTCGGACCC
                                       C
GAM1645  SERF1B   3'  GTCACCAGACTGGAGTGCAGTG 43702             C    GA
              G                    CCACTGCACTCCAG CTGG  GAC
                                  |||||||||||||| ||||  |||
                                  GGTGACGTGAGGTC GACC  CTG
                                            A    A_
GAM1645  SERF2    5'  CCCATGCTGGAGTACGGTGG   20488       C       C
                                  CCACTG ACTCCAGC TGGG
                                  |||||| |||||||| ||||
                                  GGTGGC TGAGGTCG ACCC
                                      A       T
GAM1645  SFXN2    3'  GTCGCCCAGGCTGGAATGCAGT 74384         C          A
              GG                    CCACTGCA TCCAGCCTGGG GAC
                                  |||||||| |||||||||| |||
                                  GGTGACGT AGGTCGGACCC CTG
                                       A          G
GAM1645  SIRPB1   3'  TTCCCAGGCTGGAGTGCAATG  21372    C
                                  CA TGCACTCCAGCCTGGGAG
                                  || ||||||||||||||||
                                  GT ACGTGAGGTCGGACCCTT
                                   A
GAM1645  SLC11A1  3'  CCAAGGCTGGAGTGCAGTGG   60157              G
                                  CCACTGCACTCCAGCCT GG
                                  |||||||||||||||| ||
                                  GGTGACGTGAGGTCGGA CC
                                             A
GAM1645  SLC12A8  3'  CCCAGGCTGGAGTCCAGTGG   45235       C
                                  CCACTG ACTCCAGCCTGGG
                                  |||||| ||||||||||||
                                  GGTGAC TGAGGTCGGACCC
                                      C
GAM1645  SLC16A4  3'  CCCAGGCTGGAGTGCAGTGG   17450
                                  CCACTGCACTCCAGCCTGGG
                                  ||||||||||||||||||||
                                  GGTGACGTGAGGTCGGACCC

GAM1645  SLC16A6  5'  GTCATTCAGGCAAGAGTGCAGT 17442          CA      A
                                  ACTGCACTC  GCCTGGG GAC
                                  |||||||||  ||||||| |||
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                                TGACGTGAG  CGGACTT CTG
                                     AA      A
GAM1645  SLC19A3   3'  TCAGAGGCTGGAGTGCAATGG  48251     C          GG
                                CCA TGCACTCCAGCCT  GA
                                ||| ||||||||||||  ||
                                GGT ACGTGAGGTCGGA  CT
                                  A           GA
GAM1645  SLC19A3   3'  TCTATGGGCCAGGTGCAGTGG  48253         CCA    GG
                                CCACTGCACT   GCCTG  AGA
                                ||||||||||   |||||  |||
                                GGTGACGTGG   CGGGT  TCT
                                     AC_    A_
GAM1645  SLC6A14   3'  CCTGGGCTGGAGTGCAGTGG   24307             TG
                                CCACTGCACTCCAGCC  GG
                                ||||||||||||||  ||
                                GGTGACGTGAGGTCGG  CC
                                        GT
GAM1645  SREC      3'  GTCCCCCAGGCTGGAGTGCAGT 14910               A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                  ||||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC CTG
                                           C
GAM1645  SS-56     3'  GTTGCCCAGGCTGGAGTGCAGT 60359               AG
              GG                  CCACTGCACTCCAGCCTGGG  AC
                                  |||||||||||||||||||  ||
                                  GGTGACGTGAGGTCGGACCC  TG
                                           GT
GAM1645  STAF65(gamma) 3'  GTCACCCAGGCTGGAGTGCAAT 30073     C            A
              GG                  CCA TGCACTCCAGCCTGGG GAC
                                  ||| ||||||||||||||| |||
                                  GGT ACGTGAGGTCGGACCC CTG
                                    A            A
GAM1645  STAM2     3'  GTCACCCAGGCTGGAGTGCAGT 20706               A
                                  ACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||| |||
                                  TGACGTGAGGTCGGACCC CTG
                                           A
GAM1645  SULT1C2   3'  GTCGCCCAGGCTGGAGTGCAGT 22720                 A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                  ||||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC CTG
                                           G
GAM1645  SUN1      3'  GTTGCCCAGGCTGGAGTGCAGT 47922               AG
              GG                  CCACTGCACTCCAGCCTGGG  AC
                                  |||||||||||||||||||  ||
                                  GGTGACGTGAGGTCGGACCC  TG
                                           GT
GAM1645  SYT12     5'  TCAGGCTGGAGTGCAGTGG   96388
                                CCACTGCACTCCAGCCTGG
                                |||||||||||||||||||
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                                GGTGACGTGAGGTCGGACT

GAM1645  SYT13    3'  GTTGCCCAGGCTGGAGTGCAGT 95105                AG
                GG                  CCACTGCACTCCAGCCTGGG  AC
                                    ||||||||||||||||||||  ||
                                    GGTGACGTGAGGTCGGACCC  TG
                                          GT
GAM1645  T54      3'  TCCCCCAGGCTGGTACCAG   32278     CACT       A
                                    CTG   CCAGCCTGGG GA
                                    |||   |||||||||| ||
                                    GAC   GGTCGGACCC CT
                                      CAT_        C
GAM1645  TADA3L   3'  GTCACCCAGGCTGGAGTGCAGT 56814                A
                GG                  CCACTGCACTCCAGCCTGGG GAC
                                    |||||||||||||||||||| |||
                                    GGTGACGTGAGGTCGGACCC CTG
                                          A
GAM1645  TCL6     5'  CTCAGGCTGGAATGCAGTGG   40470        C
                                    CCACTGCA TCCAGCCTGGG
                                    |||||||| ||||||||||
                                    GGTGACGT AGGTCGGACTC
                                       A
GAM1645  TCL6     5'  CTCAGGCTGGAATGCAGTGG   40508        C
                                    CCACTGCA TCCAGCCTGGG
                                    |||||||| ||||||||||
                                    GGTGACGT AGGTCGGACTC
                                       A
GAM1645  TCL6     5'  CCAGGCCAGAGTGCAGTGG   40528          CA
                                    CCACTGCACTC  GCCTGG
                                    ||||||||||  ||||||
                                    GGTGACGTGAG  CGGACC
                                          AC
GAM1645  TCL6     5'  CCAGGCCAGAGTGCAGTGG   40536          CA
                                    CCACTGCACTC  GCCTGG
                                    ||||||||||  ||||||
                                    GGTGACGTGAG  CGGACC
                                          AC
GAM1645  TCL6     5'  CTCAGGCTGGAATGCAGTGG   25904        C
                                    CCACTGCA TCCAGCCTGGG
                                    |||||||| ||||||||||
                                    GGTGACGT AGGTCGGACTC
                                       A
GAM1645  TCL6     5'  CTCAGGCTGGAATGCAGTGG   27756        C
                                    CCACTGCA TCCAGCCTGGG
                                    |||||||| ||||||||||
                                    GGTGACGT AGGTCGGACTC
                                       A
GAM1645  TERA     3'  GTTACCCAGGCTGGAGTGCAGT 41422                A
                GG                  CCACTGCACTCCAGCCTGGG GAC
                                    |||||||||||||||||||| |||
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                                GGTGACGTGAGGTCGGACCC TTG
                                           A
GAM1645  TGIF2    3'  CCCGGGCTGGAGTGCAGTGG  41743
                                CCACTGCACTCCAGCCTGGG
                                ||||||||||||||||||||
                                GGTGACGTGAGGTCGGGCCC

GAM1645  THEA     3'  GTTGCCCAGGCTGGAGTGCAGT 66894                AG
              G                  CACTGCACTCCAGCCTGGG  AC
                                 ||||||||||||||||||  ||
                                 GTGACGTGAGGTCGGACCC  TG
                                           GT
GAM1645  TOR1B    3'  GTCATCCAAGCTGGAGTGCAGT 27977             C   GA
              GG                   CCACTGCACTCCAGC TGG  GAC
                                   |||||||||||||| |||  |||
                                   GGTGACGTGAGGTCG ACC  CTG
                                         A   TA
GAM1645  TRIM16   3'  GTTGCCCAGGCTGGAGAGCAGT 22376         A          AG
              GG                   CCACTGC CTCCAGCCTGGG  AC
                                   |||||||  ||||||||||||  ||
                                   GGTGACG GAGGTCGGACCC  TG
                                      A          GT
GAM1645  TRIM35   3'  TCACCCAGGCTGGAGTACAGTG 61520        C          A
              G                    CCACTG ACTCCAGCCTGGG GA
                                   ||||||  ||||||||||||| ||
                                   GGTGAC TGAGGTCGGACCC CT
                                      A          A
GAM1645  TRIM5    3'  GTTCCCCAGGCTGGAGTGCAAT 53475     C            AG
              GG                   CCA TGCACTCCAGCCTGGG  AC
                                   |||  ||||||||||||||||  ||
                                   GGT ACGTGAGGTCGGACCC  TG
                                     A             CT
GAM1645  TRIM6    3'  GTCGCCCAGGCTGGAGTGCACT 55186     C            A
              GG                   CCA TGCACTCCAGCCTGGG GAC
                                   |||  |||||||||||||||  |||
                                   GGT ACGTGAGGTCGGACCC CTG
                                     C             G
GAM1645  TU12B1-TY 3'  CCCAGGCCGGAGTGCAATGG  33837     C       A
                                CCA TGCACTCC GCCTGGG
                                |||  ||||||||  |||||||
                                GGT ACGTGAGG CGGACCC
                                  A       C
GAM1645  TU12B1-TY 3'  CCCAGGCTGGAGTGCAGTGG  33838
                                CCACTGCACTCCAGCCTGGG
                                ||||||||||||||||||||
                                GGTGACGTGAGGTCGGACCC

GAM1645  TU12B1-TY 3'  CCCATTCTGGAGTGCAGTGG  33839            CC
                                CCACTGCACTCCAG  TGGG
                                ||||||||||||||  ||||
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                                GGTGACGTGAGGTC  ACCC
                                      TT
GAM1645  TUCAN    3'  GTTACCCAGGCTGGAGTGCAGT 30985                A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC TTG
                                        A
GAM1645  TUCAN    3'  TCTAGGCTGGAGTGCAGTGG  30991
                                  CCACTGCACTCCAGCCTGGG
                                  ||||||||||||||||||||
                                  GGTGACGTGAGGTCGGATCT

GAM1645  TUSP     3'  CCCAACTAGAGTGTAGTGG   40018          C  CC
                                  CCACTGCACTC AG  TGGG
                                  |||||||||| ||  ||||
                                  GGTGATGTGAG TC  ACCC
                                        A  A_
GAM1645  TXNL2    3'  CCAGGCTGGGCACAATGG    22579     C  CA T
                                  CCA TG  C CCAGCCTGG
                                  ||| ||  | |||||||||
                                  GGT AC  G GGTCGGACC
                                    A  AC _
GAM1645  TXNL2    3'  GTCACCCAGGCTGGAGTGCAGT 22585                A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC CTG
                                        A
GAM1645  UBF-fl   3'  GTCTCCCAGGCTAGAGTACCGT 52632      TGC    C
              GG                  CCAC   ACTC AGCCTGGGAGAC
                                  ||||   |||| ||||||||||||
                                  GGTG   TGAG TCGGACCCTCTG
                                    CCA    A
GAM1645  VDU1     3'  CCCAGGCTGGAGTGCTGTGG   31121      T
                                  CCAC GCACTCCAGCCTGGG
                                  |||| ||||||||||||||
                                  GGTG CGTGAGGTCGGACCC
                                    T
GAM1645  VPS33A   3'  GTCACCCAGACTAGAGTGCAGT 43615          C  C    A
              GG                  CCACTGCACTC AG CTGGG GAC
                                  |||||||||| || ||||| |||
                                  GGTGACGTGAG TC GACCC CTG
                                        A  A    A
GAM1645  WNT2B    3'  CTGAGGTGGAATGCAGTGG    44679        C   G  G
                                  CCACTGCA TCCA CCT GG
                                  |||||||| |||| ||| ||
                                  GGTGACGT AGGT GGA TC
                                      A   _  G
GAM1645  WNT2B    3'  CTGAGGTGGAATGCAGTGG    16082        C   G  G
                                  CCACTGCA TCCA CCT GG
                                  |||||||| |||| ||| ||
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                                GGTGACGT AGGT GGA TC
                                   A   _  G
GAM1645  ZNF17    3'  GTTGCCCAGACTAGAGTGCAGT 83276          C  C    AG
              GG                   CCACTGCACTC AG CTGGG  AC
                                   |||||||||||  || |||||  ||
                                   GGTGACGTGAG TC GACCC  TG
                                         A A    GT
GAM1645  ZNF197   3'  TGGGCTGGGTGCAGTGG     23763          T
                                   CCACTGCAC CCAGCCTG
                                   |||||||||  ||||||||
                                   GGTGACGTG GGTCGGGT
                                      _
GAM1645  ZNF338   3'  GTTTCCCAGGCTGGAGTGCAGT 42261
              GG                   CCACTGCACTCCAGCCTGGGAGAC
                                   ||||||||||||||||||||||||
                                   GGTGACGTGAGGTCGGACCCTTTG

GAM1645  ZNF339   3'  GTCACCCAGGCTGGAGTACAGT 41396        C          A
              GG                   CCACTG ACTCCAGCCTGGG GAC
                                   ||||||  |||||||||||||  |||
                                   GGTGAC TGAGGTCGGACCC CTG
                                      A          A
GAM1645  ZNF347   3'  CTGGCTGGGTGCAGTGG     51827          T     T
                                   CCACTGCAC CCAGCC GG
                                   |||||||||  ||||||  ||
                                   GGTGACGTG GGTCGG TC
                                      _     _
GAM1645  ZTL1     3'  CCCAGGCTGCAGTGCAGTG    44140          C
                                   CACTGCACT CAGCCTGGG
                                   |||||||||  |||||||||
                                   GTGACGTGA GTCGGACCC
                                         C
GAM1645  LOC112687 3'  CAGGCTGGGTGCAATGG     73226     C     T
                                   CCA TGCAC CCAGCCTG
                                   |||  |||||  ||||||||
                                   GGT ACGTG GGTCGGAC
                                     A    _
GAM1645  LOC112687 3'  GTCACCCAGGCTGGAGTGCAGT 73242                A
              GG                   CCACTGCACTCCAGCCTGGG GAC
                                   ||||||||||||||||||  |||
                                   GGTGACGTGAGGTCGGACCC CTG
                                            A
GAM1645  LOC112724 5'  GTCGCCAGGCTGGAATGCAGT  57306        C         GA
                                   ACTGCA TCCAGCCTGG  GAC
                                   ||||||  ||||||||||  |||
                                   TGACGT AGGTCGGACC  CTG
                                      A         G_
GAM1645  LOC112817 3'  GTCACCCAGGCTGGAGTGCAAT 57332     C             A
              GG                   CCA TGCACTCCAGCCTGGG GAC
                                   |||  ||||||||||||||  |||
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                                GGT ACGTGAGGTCGGACCC CTG
                                  A             A
GAM1645  LOC113675 5'  GTCACCCAGGCTGGAGTGCAGT 57382                 A
                  GG                CCACTGCACTCCAGCCTGGG GAC
                                    |||||||||||||||||| |||
                                    GGTGACGTGAGGTCGGACCC CTG
                                                A
GAM1645  LOC115196 3'  CCCAGGCTGGAGTCCAGTGG   73654       C
                                    CCACTG ACTCCAGCCTGGG
                                    |||||| ||||||||||||
                                    GGTGAC TGAGGTCGGACCC
                                       C
GAM1645  LOC115219 5'  GTCCCCCAGGCTGGAGTGCGAT 73705     C            A
                  GG                CCA TGCACTCCAGCCTGGG GAC
                                    ||| |||||||||||||| |||
                                    GGT GCGTGAGGTCGGACCC CTG
                                      A             C
GAM1645  LOC115343 5'  CTGAGAGCTGGAGTACAG    72532     C      _  G
                                    CTG ACTCCAGC CT GG
                                    ||| |||||||| || ||
                                    GAC TGAGGTCG GA TC
                                      A       A  G
GAM1645  LOC115648 3'  CCTGGCTGGAGTGCAGTGG    60020              T
                                    CCACTGCACTCCAGCC GGG
                                    |||||||||||||| |||
                                    GGTGACGTGAGGTCGG TCC
                                                 _
GAM1645  LOC116411 5'  TCCAGGCTGGAGTGCAGTGG   74303
                                    CCACTGCACTCCAGCCTGGG
                                    ||||||||||||||||||
                                    GGTGACGTGAGGTCGGACCT

GAM1645  LOC119504 5'  CCGCTGAGGTGCAGTGG     74444          TC    CT
                                    CCACTGCAC  CAGC  GG
                                    |||||||||  ||||  ||
                                    GGTGACGTG  GTCG  CC
                                          GA   __
GAM1645  LOC120114 3'  GTCACCCAGGCTAGAGTGCAAT 76050     C      C       A
                  GG                CCA TGCACTC AGCCTGGG GAC
                                    ||| ||||||| |||||||| |||
                                    GGT ACGTGAG TCGGACCC CTG
                                      A      A       A
GAM1645  LOC120224 5'  GTCACCCAGGCTGGAGTGCAAT 57893     C            A
                  GG                CCA TGCACTCCAGCCTGGG GAC
                                    ||| |||||||||||||| |||
                                    GGT ACGTGAGGTCGGACCC CTG
                                      A             A
GAM1645  LOC120526 3'  CCAGCTGGAGTGCAGTG     74463            C
                                    CACTGCACTCCAGC TGG
                                    |||||||||||||| |||
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                                GTGACGTGAGGTCG ACC
                                               _
GAM1645  LOC120939 3'  GTAGCCCAGGCTGGGATGCAAT 76769     C    CT         AG
                GG                    CCA TGCA  CCAGCCTGGG  AC
                                      ||| ||||  ||||||||||  ||
                                      GGT ACGT  GGTCGGACCC  TG
                                        A    AG         GA
GAM1645  LOC121219 3'  CTCCTGGAAGGCTGGAGCACA  74487    CA        ___
                                      TG  CTCCAGCCT   GGGAG
                                      ||  |||||||||   |||||
                                      AC  GAGGTCGGA   TCCTC
                                       AC        AGG
GAM1645  LOC121504 3'  CCGAGGCTGGAGTGCAGTGG   74543               G
                                      CCACTGCACTCCAGCCT GG
                                      |||||||||||||||| ||
                                      GGTGACGTGAGGTCGGA CC
                                                  G
GAM1645  LOC123591 5'  GTCCCCCAGGCTGGGACGGGG  76132    A   CAC         A
                                      CC CTG   TCCAGCCTGGG GAC
                                      || |||   |||||||||| |||
                                      GG GGC   GGGTCGGACCC CTG
                                       _  A__          C
GAM1645  LOC124602 3'  GTTTTTCAGGCTGGGCACAGTG 74790       CA T       GG
                                      CACTG  C CCAGCCTG  AGAC
                                      |||||  | ||||||||  ||||
                                      GTGAC  G GGTCGGAC  TTTG
                                         AC _       TT
GAM1645  LOC125268 3'  TCTCCCAGGCACGCATGG     76581     C   ACTCCA
                                      CCA TGC      GCCTGGGAGA
                                      ||| |||      ||||||||||
                                      GGT ACG      CGGACCCTCT
                                        _   CA____
GAM1645  LOC125268 3'  TCTCCCAGGTGCCACTGCAG   76582       CTCCA
                                      CTGCA     GCCTGGGAGA
                                      |||||     ||||||||||
                                      GACGT     TGGACCCTCT
                                         CACCG
GAM1645  LOC126133 3'  GTCACCCAGGCTGGAGCGCAGT 74915         A          A
                GG                    CCACTGC CTCCAGCCTGGG GAC
                                      ||||||| |||||||||||| |||
                                      GGTGACG GAGGTCGGACCC CTG
                                          C          A
GAM1645  LOC126364 3'  CCCAGGCTGGAGTGCAATG    76186    C
                                      CA TGCACTCCAGCCTGGG
                                      || ||||||||||||||||
                                      GT ACGTGAGGTCGGACCC
                                       A
GAM1645  LOC126661 3'  GTTGCCCAGGCTGGAGTGCAGT 75063                AG
                GG                    CCACTGCACTCCAGCCTGGG  AC
                                      ||||||||||||||||||||  ||
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                                GGTGACGTGAGGTCGGACCC  TG
                                      GT
GAM1645  LOC126669 3'  GTTGCCCAGGCTGGAGTGCAAT 75948     C            AG
                GG                  CCA TGCACTCCAGCCTGGG  AC
                                    ||| ||||||||||||||  ||
                                    GGT ACGTGAGGTCGGACCC  TG
                                      A             GT
GAM1645  LOC128077 3'  CCCAGGCTGGAGTGCAGTGG   75209
                                    CCACTGCACTCCAGCCTGGG
                                    ||||||||||||||||||||
                                    GGTGACGTGAGGTCGGACCC

GAM1645  LOC128077 3'  GTCGCCCAGGCTAGAGTGCAGT 75229          C       A
                GG                  CCACTGCACTC AGCCTGGG GAC
                                    |||||||||| |||||||| |||
                                    GGTGACGTGAG TCGGACCC CTG
                                          A       G
GAM1645  LOC128387 3'  GTTGCCCAGGCTGGAGTGCAAT 75259     C            AG
                GG                  CCA TGCACTCCAGCCTGGG  AC
                                    ||| ||||||||||||||  ||
                                    GGT ACGTGAGGTCGGACCC  TG
                                      A             GT
GAM1645  LOC128989 3'  GTCACCCAGGCTGGAGTGCAGT 75324                A
                GG                  CCACTGCACTCCAGCCTGGG GAC
                                    |||||||||||||||||| |||
                                    GGTGACGTGAGGTCGGACCC CTG
                                          A
GAM1645  LOC130813 3'  CCTAGGCTAGAGGGCAGTG    76270       A   C
                                    CACTGC CTC AGCCTGGG
                                    |||||| ||| ||||||||
                                    GTGACG GAG TCGGATCC
                                       G   A
GAM1645  LOC131308 3'  CTCAGGCTGGAGTGCAGTGG   75494
                                    CCACTGCACTCCAGCCTGGG
                                    ||||||||||||||||||||
                                    GGTGACGTGAGGTCGGACTC

GAM1645  LOC131965 3'  CAGGCTGGAGTGCAGTGG    75519
                                    CCACTGCACTCCAGCCTG
                                    ||||||||||||||||||
                                    GGTGACGTGAGGTCGGAC

GAM1645  LOC132241 5'  TTCCCAGGCTGGAGTGCAGTGG 75568
                                    CCACTGCACTCCAGCCTGGGAG
                                    |||||||||||||||||||||||
                                    GGTGACGTGAGGTCGGACCCTT

GAM1645  LOC133686 3'  CCCAGGCTGGACTGCAGTGG   75615          C
                                    CCACTGCA TCCAGCCTGGG
                                    |||||||| ||||||||||
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                                GGTGACGT AGGTCGGACCC
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GAM1645  LOC135154 3'  CCCAGGCTGGAGTGGAGTGG   75728      G
                                CCACT CACTCCAGCCTGGG
                                ||||| ||||||||||||||
                                GGTGA GTGAGGTCGGACCC
                                   G
GAM1645  LOC135293 3'  GTTGCCCAGGCTGAAGTGTAGT 76690          C       AG
              GG                   CCACTGCACT CAGCCTGGG  AC
                                ||||||||||| |||||||||  ||
                                GGTGATGTGA GTCGGACCC  TG
                                     A       GT
GAM1645  LOC135293 3'  TCTCCCAGGCTGGAGTGCAGTG 76692
              G                    CCACTGCACTCCAGCCTGGGAGA
                                ||||||||||||||||||||||||
                                GGTGACGTGAGGTCGGACCCTCT

GAM1645  LOC135398 3'  CCCAGCCTGGAATGTAGTGG   76468        C    C
                                CCACTGCA TCCAG CTGGG
                                |||||||| ||||| |||||
                                GGTGATGT AGGTC GACCC
                                     A    C
GAM1645  LOC135763 3'  GTCACCCAGGCTGGAGTGCAGT 57562                A
              GG                   CCACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                          A
GAM1645  LOC138050 5'  CCCAGGCTGGAGTGCGGTGG   75813
                                CCACTGCACTCCAGCCTGGG
                                ||||||||||||||||||||
                                GGTGGCGTGAGGTCGGACCC

GAM1645  LOC138199 3'  GTCTCCCAGGCCGGAGTGCAGT 75827           A
              GG                   CCACTGCACTCC GCCTGGGAGAC
                                |||||||||||| ||||||||||
                                GGTGACGTGAGG CGGACCCTCTG
                                     C
GAM1645  LOC138428 3'  CTTGGAGGCCGGGTGCAGTGG  75857         T  A    GG
                                CCACTGCAC CC GCCT  GAG
                                ||||||||| || ||||  |||
                                GGTGACGTG GG CGGA  TTC
                                     _ C    GG
GAM1645  LOC139422 5'  GTTGCCCAGACTGGAGTGCAGT 76355             C     AG
              GG                   CCACTGCACTCCAG CTGGG  AC
                                |||||||||||||| |||||  ||
                                GGTGACGTGAGGTC GACCC  TG
                                     A    GT
GAM1645  LOC142913 5'  CCCAGGCTGGAGTAGAGTG    76932      GC
                                CACT  ACTCCAGCCTGGG
                                ||||  ||||||||||||
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                                GTGA  TGAGGTCGGACCC
                                  GA
GAM1645  LOC143153 3'  GTCACCCAGGCTGGAGTGCAG  76982              A
                                CTGCACTCCAGCCTGGG GAC
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                                GACGTGAGGTCGGACCC CTG
                                       A
GAM1645  LOC143154 3'  GTCACCCAGGCTGGAGTGCAG  76993              A
                                CTGCACTCCAGCCTGGG GAC
                                |||||||||||||||| |||
                                GACGTGAGGTCGGACCC CTG
                                       A
GAM1645  LOC143187 3'  CCTGGCTGGAGTGGAGTGG   59757      G       T
                                CCACT CACTCCAGCC GGG
                                ||||| |||||||||| |||
                                GGTGA GTGAGGTCGG TCC
                                  G       _
GAM1645  LOC143241 5'  GTTGCCCAGGCTGGAGTGCAAT 57975     C           AG
            GG                    CCA TGCACTCCAGCCTGGG  AC
                                ||| ||||||||||||||  ||
                                GGT ACGTGAGGTCGGACCC  TG
                                  A             GT
GAM1645  LOC144248 5'  CCCAGGCTGGAGTGCAATGG   77251     C
                                CCA TGCACTCCAGCCTGGG
                                ||| ||||||||||||||
                                GGT ACGTGAGGTCGGACCC
                                  A
GAM1645  LOC144305 3'  GTTGCCCAGGCTGGAGTGCAGT 83975               AG
            GG                    CCACTGCACTCCAGCCTGGG  AC
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                                GGTGACGTGAGGTCGGACCC  TG
                                       GT
GAM1645  LOC144317 5'  CCCAGGCTGGAGTGCGATGG   77291     C
                                CCA TGCACTCCAGCCTGGG
                                ||| ||||||||||||||
                                GGT GCGTGAGGTCGGACCC
                                  A
GAM1645  LOC144519 5'  CCTGGGCTGGAGTGCAGTGG   77370           TG
                                CCACTGCACTCCAGCC  GG
                                ||||||||||||||  ||
                                GGTGACGTGAGGTCGG  CC
                                       GT
GAM1645  LOC144524 5'  GTTGCCCAAGCTGGAGTGCAAT 84061     C       C   AG
            GG                    CCA TGCACTCCAGC TGGG  AC
                                ||| |||||||||| ||||  ||
                                GGT ACGTGAGGTCG ACCC  TG
                                  A         A   GT
GAM1645  LOC144742 5'  CCTAGGCTGGAGTACAGTGG   77455       C
                                CCACTG ACTCCAGCCTGGG
                                |||||| ||||||||||||
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                                GGTGAC TGAGGTCGGATCC
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GAM1645  LOC144776 5'  CTCAGGCTGGAGTACAGTG    77489       C
                                CACTG ACTCCAGCCTGGG
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                                GTGAC TGAGGTCGGACTC
                                   A
GAM1645  LOC144776 5'  GTTGCCCAGGCTGGAGTGCAAT 77495     C             AG
                GG                 CCA TGCACTCCAGCCTGGG  AC
                                ||| ||||||||||||||  ||
                                GGT ACGTGAGGTCGGACCC  TG
                                  A             GT
GAM1645  LOC144817 5'  GTCGCCCAGGCTGGAGTGCAGT 77522                 A
                GG                 CCACTGCACTCCAGCCTGGG GAC
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GAM1645  LOC144871 3'  CCCAGGCTGGAGTGCAGGG    84123    A
                                CC CTGCACTCCAGCCTGGG
                                || ||||||||||||||||
                                GG GACGTGAGGTCGGACCC
                                 _
GAM1645  LOC145009 3'  GTCGCCCAGGCTGGAGTGCAGT 60980                 A
                GG                 CCACTGCACTCCAGCCTGGG GAC
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                                            G
GAM1645  LOC145082 3'  TCAGCCAAGTGCAGTGG     84199          CCA  C
                                CCACTGCACT   GC TGG
                                |||||||||   || |||
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                                      AC_  _
GAM1645  LOC145268 5'  CCCAGGCTGGAGCGAAGTG    77576      GCA
                                CACT   CTCCAGCCTGGG
                                ||||   ||||||||||||
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                                  AGC
GAM1645  LOC145387 3'  CCAAGGCCAGGTGCAGTGG    84332          CCA    G
                                CCACTGCACT   GCCT GG
                                |||||||||   |||| ||
                                GGTGACGTGG   CGGA CC
                                      AC_    A
GAM1645  LOC145725 3'  GTCACCAGGCTGGAGTACAGTG 77887       C          GA
                                CACTG ACTCCAGCCTGG  GAC
                                ||||| ||||||||||||  |||
                                GTGAC TGAGGTCGGACC  CTG
                                  A          A_
GAM1645  LOC145732 3'  GTCACCAGGCTGGAGTACAGTG 77899       C          GA
                                CACTG ACTCCAGCCTGG  GAC
                                ||||| ||||||||||||  |||
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                                GTGAC TGAGGTCGGACC  CTG
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GAM1645  LOC145757 3'  CCAGGGGGAGCTGGGATGCAGT 77924        CT    _____
                GG                CCACTGCA  CCAGC     CTGG
                                  ||||||||  |||||     ||||
                                  GGTGACGT  GGTCG     GACC
                                     AG     AGGGG
GAM1645  LOC145757 5'  CCCAGGCTGGAGTGCGGTGG   77927
                                  CCACTGCACTCCAGCCTGGG
                                  ||||||||||||||||||||
                                  GGTGGCGTGAGGTCGGACCC

GAM1645  LOC145757 5'  GTCGCCCAGGCTGGAGTGCAGT 77941                A
                GG                CCACTGCACTCCAGCCTGGG GAC
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                                  GGTGACGTGAGGTCGGACCC CTG
                                           G
GAM1645  LOC145813 5'  GTCACCCAGGCTGGAGTGCAAT 84512     C          A
                GG                CCA TGCACTCCAGCCTGGG GAC
                                  ||| |||||||||||||| |||
                                  GGT ACGTGAGGTCGGACCC CTG
                                    A             A
GAM1645  LOC145826 5'  TGGGAACTGGAGTGCATGG    84534     C       __
                                  CCA TGCACTCCAG  CCTG
                                  ||| ||||||||||  ||||
                                  GGT ACGTGAGGTC  GGGT
                                  _         AA
GAM1645  LOC146050 3'  GTCGTCCAGGCTGGAGTGCAGT 78121               GA
                GG                CCACTGCACTCCAGCCTGG  GAC
                                  ||||||||||||||||||  |||
                                  GGTGACGTGAGGTCGGACC  CTG
                                           TG
GAM1645  LOC146050 3'  GTTGCCCAGGCTGGAGTGCAAT 78124     C          AG
                GG                CCA TGCACTCCAGCCTGGG  AC
                                  ||| ||||||||||||||  ||
                                  GGT ACGTGAGGTCGGACCC  TG
                                    A             GT
GAM1645  LOC146138 3'  CTCCCATGAGAGTGCAG     84592        _ GCC
                                  CTGCACTC CA   TGGGAG
                                  |||||||| ||   ||||||
                                  GACGTGAG GT   ACCCTC
                                     A ___
GAM1645  LOC146159 3'  CAGGCCAGGTGCAGTGG     78174          CCA
                                  CCACTGCACT   GCCTG
                                  ||||||||||   |||||
                                  GGTGACGTGG   CGGAC
                                        AC_
GAM1645  LOC146229 3'  CCTAGGCTGGAGTACAGTGG   78273       C
                                  CCACTG ACTCCAGCCTGGG
                                  |||||| ||||||||||||
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                                GGTGAC TGAGGTCGGATCC
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GAM1645  LOC146229 3'  CCTAGGCTGGAGTGCAATGG   78274     C
                                CCA TGCACTCCAGCCTGGG
                                ||| ||||||||||||||||
                                GGT ACGTGAGGTCGGATCC
                                  A
GAM1645  LOC146229 3'  GTCGCCCAGGCTAGAGTGCAGT 78305          C       A
                GG                CCACTGCACTC AGCCTGGG GAC
                                  |||||||||| |||||||| |||
                                  GGTGACGTGAG TCGGACCC CTG
                                        A       G
GAM1645  LOC146229 3'  GTCGCCCAGGCTGGAGTGCAGT 78307                A
                GG                CCACTGCACTCCAGCCTGGG GAC
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                                           G
GAM1645  LOC146272 5'  CCAGCCAGGTGCAGTGG     78326          CCA  C
                                CCACTGCACT   GC TGG
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                                     AC_  _
GAM1645  LOC146336 3'  CCTGTCGCTGGAGTGCAGTGG  78368             C_
                                CCACTGCACTCCAGC  TGGG
                                ||||||||||||||  ||||
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GAM1645  LOC146346 5'  CCAGGCTGGAGTGCTGTGG    78391      T
                                CCAC GCACTCCAGCCTGG
                                |||| ||||||||||||||
                                GGTG CGTGAGGTCGGACC
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GAM1645  LOC146346 5'  GTTGCCCAGGCTGGAGTGCAGT 78408                AG
                GG                CCACTGCACTCCAGCCTGGG  AC
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                                  GGTGACGTGAGGTCGGACCC  TG
                                           GT
GAM1645  LOC146429 5'  GTCACCAGGCTGGAGTGCAGTG 84675                GA
                G                 CCACTGCACTCCAGCCTGG  GAC
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                                           A_
GAM1645  LOC146443 5'  CCCGGGCTGGAGTGCAGTGG   78442
                                CCACTGCACTCCAGCCTGGG
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GAM1645  LOC146455 3'  GTCGCCCAGGCTGGAGTGTAGT 78465                A
                GG                CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||| |||
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                                GGTGATGTGAGGTCGGACCC CTG
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GAM1645  LOC146603 5'  GTCGCCCAGGCTGGAGTGCAGT 78605                A
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                                      G
GAM1645  LOC146784 5'  CCCAGGCTGGAGTGCGGTGG   78709
                                  CCACTGCACTCCAGCCTGGG
                                  ||||||||||||||||||||
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GAM1645  LOC146839 3'  GTTGCCCAGGCTGGAGTGCAGT 84849               AG
              GG                  CCACTGCACTCCAGCCTGGG  AC
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GAM1645  LOC146894 3'  CTGCCCAGGCTGGAGTGCAGTG 59858                _
              G                    CCACTGCACTCCAGCCTGGG AG
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GAM1645  LOC146895 5'  GTCACCCAGGCTGGAGTGCAGT 84872                A
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GAM1645  LOC146901 3'  TCAGGCTGGAGTGCAGTGG   84912
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GAM1645  LOC146909 3'  GTCGCCCAGGCTGGAGTGCAGT 78780                A
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                                  |||||||||||||||||||| |||
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                                      G
GAM1645  LOC146909 3'  GTCGCCCAGGCTGGAGTGCAGT 78781                A
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GAM1645  LOC146952 5'  GTTGCCCAGGCTGGAATGCAGT 84934          C     AG
              GG                  CCACTGCA TCCAGCCTGGG  AC
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                                      A     GT
GAM1645  LOC147071 5'  CCCAGGCTGAAGTGCAATG   73357   C    C
                                  CA TGCACT CAGCCTGGG
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                                GT ACGTGA GTCGGACCC
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GAM1645  LOC147080 5'  GTCCGCCAGGCTGGAGTGCAGT 85050                GA
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                                                GC
GAM1645  LOC147166 3'  GTTGCCCAGGCTGGAGTGCAGT 78893                AG
                 GG                CCACTGCACTCCAGCCTGGG  AC
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                                                GT
GAM1645  LOC147276 3'  CCCACGCTGGAGTGCAATGG   78954     C         C
                                   CCA TGCACTCCAGC TGGG
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                                   GGT ACGTGAGGTCG ACCC
                                     A         C
GAM1645  LOC147429 5'  GTTGCCCAGGCTGGAATACAGT 78999       CAC         AG
                 GG                CCACTG   TCCAGCCTGGG  AC
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                                      ATA         GT
GAM1645  LOC147622 3'  GTCCCCTAGGCTGCAGTGCAGT 85171          C       A
                 GG                CCACTGCACT CAGCCTGGG GAC
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                                         C       C
GAM1645  LOC147660 3'  CTGCCCAGGCTAGAGTGCAATG 79028     C      C      _
                 G                  CCA TGCACTC AGCCTGGG AG
                                   ||| ||||||| |||||||| ||
                                   GGT ACGTGAG TCGGACCC TC
                                     A      A       G
GAM1645  LOC147694 3'  CCCAGGCTGGAGTGCAGTG    79093
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                                   ||||||||||||||||||
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GAM1645  LOC147817 3'  GTCGCCCAGGCTGGAGTGCAAT 79190     C            A
                 GG                CCA TGCACTCCAGCCTGGG GAC
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                                     A             G
GAM1645  LOC147841 3'  TCCAGTCTGGAGTGCAATGG   79231     C       C
                                   CCA TGCACTCCAG CTGGG
                                   ||| |||||||||| |||||
                                   GGT ACGTGAGGTC GACCT
                                     A         T
GAM1645  LOC147895 5'  CCTACGCTGGAGTGCAGTGG   85199             C
                                   CCACTGCACTCCAGC TGGG
                                   |||||||||||||| ||||
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                                GGTGACGTGAGGTCG ATCC
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GAM1645  LOC147990 3'  CCCAGGCTGGAGTGCGGTGG   85218
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GAM1645  LOC147990 3'  GTCACCCAGGCTAGAATGCAGT 85230        C  C       A
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                                     A  A       A
GAM1645  LOC148014 3'  CTCCAGCGGGAAGACAGTGG   79308       CAC   A  CTG
                                CCACTG   TCC GC   GGAG
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                                    AGA   G  A__
GAM1645  LOC148137 3'  CCCAGGCTGTAGTACAATGG   59091     C  C   C
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GAM1645  LOC148147 3'  GTCACCAGGCTGGAGTGCAGTG 79405                GA
              G                   CCACTGCACTCCAGCCTGG  GAC
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GAM1645  LOC148195 5'  CCTAGGCTGCAGTGCAGTGG   85278          C
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GAM1645  LOC148195 3'  TCCAGGCTGGTGTGCAGTG    85291         T
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GAM1645  LOC148198 3'  CCCAGGCTGGAGTACAGTGG   71224        C
                                CCACTG ACTCCAGCCTGGG
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GAM1645  LOC148443 3'  GTCACCCAGGCTGGGATGCAGT 79606         CT        A
              GG                  CCACTGCA  CCAGCCTGGG GAC
                                ||||||||  ||||||||||  |||
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                                     AG         A
GAM1645  LOC148645 5'  CCAAGGCTGGAATGCAGTGG   85329         C       G
                                CCACTGCA TCCAGCCT GG
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                                GGTGACGT AGGTCGGA CC
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GAM1645  LOC148709 5'  CTCAGGCTGGAGTGCGGTGG   79690
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GAM1645  LOC148887 5'  GTCGCCCAGGCTGGAGTGCAGT 85410                A
              GG                  CCACTGCACTCCAGCCTGGG GAC
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                                                G
GAM1645  LOC149132 5'  TCCAAGGCTGGAGTGTAGT    79926             G
                                ACTGCACTCCAGCCT GGA
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GAM1645  LOC149421 3'  GTCGCCCAGGCTGGAGGGCAGT 80150        A          A
              GG                  CCACTGC CTCCAGCCTGGG GAC
                                  ||||||| |||||||||||| |||
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                                     G          G
GAM1645  LOC149478 3'  TCGAGGCTGGAGTGTAGTGG   80178               G
                                CCACTGCACTCCAGCCT GG
                                |||||||||||||||| ||
                                GGTGATGTGAGGTCGGA CT
                                       G
GAM1645  LOC149506 3'  CCCAGGCTGTAGTGCAGTGG   85628          C
                                CCACTGCACT CAGCCTGGG
                                |||||||||| |||||||||
                                GGTGACGTGA GTCGGACCC
                                     T
GAM1645  LOC149506 3'  GTCGGCCAGGCTAGAGTGCAGT 85644           C      GA
              GG                  CCACTGCACTC AGCCTGG  GAC
                                  |||||||||| |||||||  |||
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                                      A       GG
GAM1645  LOC149577 3'  CCCAAGCTGGAGTGCAGTGG   85670              C
                                CCACTGCACTCCAGC TGGG
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                                GGTGACGTGAGGTCG ACCC
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GAM1645  LOC149577 3'  CCCAGGCTGGAGTGCGGTGG   85671
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GAM1645  LOC149692 3'  GTCACCCAGGCTGGAGTGCAGT 85743                A
              GG                  CCACTGCACTCCAGCCTGGG GAC
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                                GGTGACGTGAGGTCGGACCC CTG
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GAM1645  LOC149734 3'  CCCAGGCTGGAGTGTAGT    85793
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GAM1645  LOC149734 3'  GTCACCCAGGCTGGAGTGCAGT 85797                A
           GG                     CCACTGCACTCCAGCCTGGG GAC
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GAM1645  LOC150054 5'  GTCGCCCAGGCTGGAGTGCAGT 85978                A
           GG                     CCACTGCACTCCAGCCTGGG GAC
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GAM1645  LOC150225 3'  CTCAGGCTGGAGTGCAGTGG   86189
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GAM1645  LOC150290 3'  CCCATCCTAGAGTGCAGT    80587          C  CC
                                ACTGCACTC AG  TGGG
                                ||||||||| ||  ||||
                                TGACGTGAG TC  ACCC
                                      A  CT
GAM1645  LOC150397 3'  GTCGTCCAGGTTAGAGTGCAAT 80666     C      C      GA
           GG                     CCA TGCACTC AGCCTGG  GAC
                                ||| ||||||| |||||||  |||
                                GGT ACGTGAG TTGGACC  CTG
                                  A      A      TG
GAM1645  LOC150407 3'  TCCAGGCTAGAGTGCAGTGG   80645           C
                                CCACTGCACTC AGCCTGGG
                                |||||||||| ||||||||
                                GGTGACGTGAG TCGGACCT
                                       A
GAM1645  LOC150587 3'  CCCAAGCTGGAATGCGGTGG   86241         C     C
                                CCACTGCA TCCAGC TGGG
                                |||||||| |||||| ||||
                                GGTGGCGT AGGTCG ACCC
                                     A     A
GAM1645  LOC150696 3'  GTCACCCAGGCTGGAGTGTAGT 59166                A
           GG                     CCACTGCACTCCAGCCTGGG GAC
                                ||||||||||||||||||| |||
                                GGTGATGTGAGGTCGGACCC CTG
                                           A
GAM1645  LOC150889 3'  TCCAGGCCAGGTGCAGTGG    80820          CCA
                                CCACTGCACT   GCCTGGG
                                |||||||||   |||||||
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                                GGTGACGTGG   CGGACCT
                                      AC_
GAM1645  LOC150960 3'  GTCACCCAGGCTGGAGTGCAGT 80877                A
               GG                  CCACTGCACTCCAGCCTGGG GAC
                                   |||||||||||||||||||| |||
                                   GGTGACGTGAGGTCGGACCC CTG
                                         A
GAM1645  LOC151057 3'  GTCACCCAGGCTGGAGTGCAGT 86395                A
               GG                  CCACTGCACTCCAGCCTGGG GAC
                                   |||||||||||||||||||| |||
                                   GGTGACGTGAGGTCGGACCC CTG
                                         A
GAM1645  LOC151195 3'  TCCAGGCTGGAGTGCAGTGG   80970
                                   CCACTGCACTCCAGCCTGGG
                                   ||||||||||||||||||||
                                   GGTGACGTGAGGTCGGACCT

GAM1645  LOC151201 3'  CCCAGGCTGGAGTCCAATGG   86470     C  C
                                   CCA TG ACTCCAGCCTGGG
                                   ||| || ||||||||||||
                                   GGT AC TGAGGTCGGACCC
                                     A  C
GAM1645  LOC151201 3'  GTCACCAGGCTGGAGTGCAGTG 86482                GA
               G                    CCACTGCACTCCAGCCTGG  GAC
                                   ||||||||||||||||||  |||
                                   GGTGACGTGAGGTCGGACC  CTG
                                         A_
GAM1645  LOC151429 3'  TAGGCTGGGTGCAGTGG     86548          T
                                   CCACTGCAC CCAGCCTG
                                   |||||||| ||||||||
                                   GGTGACGTG GGTCGGAT

                                      _
GAM1645  LOC151475 5'  GTCATCCAGGCTGGAGTGCAGT 86601                GA
               GG                  CCACTGCACTCCAGCCTGG  GAC
                                   ||||||||||||||||||  |||
                                   GGTGACGTGAGGTCGGACC  CTG
                                         TA
GAM1645  LOC151475 5'  GTGGCCCAGGCTGGAGTGTAGT 86603                AG
               GG                  CCACTGCACTCCAGCCTGGG  AC
                                   ||||||||||||||||||  ||
                                   GGTGATGTGAGGTCGGACCC  TG
                                         GG
GAM1645  LOC151701 3'  GTCGCCCAGGCTGGAGTGCAGT 86679                A
                                   ACTGCACTCCAGCCTGGG GAC
                                   |||||||||||||||| |||
                                   TGACGTGAGGTCGGACCC CTG
                                         G
GAM1645  LOC151826 3'  GTCACCCAGGCTGGAGTGCAGT 81186                A
               GG                  CCACTGCACTCCAGCCTGGG GAC
                                   |||||||||||||||||||| |||
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                                GGTGACGTGAGGTCGGACCC CTG
                                           A
GAM1645  LOC151877 3'  CTCCCAAGCTGGAGTCCAGTGG 86696       C       C
                                CCACTG ACTCCAGC TGGGAG
                                |||||| |||||||| ||||||
                                GGTGAC TGAGGTCG ACCCTC
                                   C       A
GAM1645  LOC151979 5'  GTTGCCCAAGCTGGAATGCAGT 81254        C     C    AG
              GG                  CCACTGCA TCCAGC TGGG  AC
                                |||||||| |||||| ||||  ||
                                GGTGACGT AGGTCG ACCC  TG
                                    A     A   GT
GAM1645  LOC152137 3'  CAGGCTGGAGTGCAGTGG    81309
                                CCACTGCACTCCAGCCTG
                                ||||||||||||||||||
                                GGTGACGTGAGGTCGGAC

GAM1645  LOC152220 3'  CTCAGGCTGGAGTGCAGTG   86763
                                CACTGCACTCCAGCCTGGG
                                |||||||||||||||||||
                                GTGACGTGAGGTCGGACTC

GAM1645  LOC152282 5'  GTTGCCCAGGCTGGAGTATAGT 81407      C          AG
                                ACTG ACTCCAGCCTGGG  AC
                                |||| ||||||||||||  ||
                                TGAT TGAGGTCGGACCC  TG
                                  A           GT
GAM1645  LOC152300 3'  GTCACCCAGGCTGGAGTGCAGT 81389               A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                           A
GAM1645  LOC152343 3'  GTCACCCAGGCTGGAGTGCAGT 81432               A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                           A
GAM1645  LOC152445 3'  GTCTCCGAGGCTGGAATACGGT 86959       CAC       G
              GG                  CCACTG   TCCAGCCT GGAGAC
                                ||||||   |||||||| ||||||
                                GGTGGC   AGGTCGGA CCTCTG
                                   ATA       G
GAM1645  LOC152445 3'  GTTGCCCAGGCTGGAGTGCAGT 86962               AG
              GG                  CCACTGCACTCCAGCCTGGG  AC
                                |||||||||||||||||||  ||
                                GGTGACGTGAGGTCGGACCC  TG
                                           GT
GAM1645  LOC152485 3'  CTCCCAGGCTCTGCAG      81491       CTCC
                                CTGCA    AGCCTGGGAG
                                |||||    ||||||||||
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                                GACGT    TCGGACCCTC
                                  C___
GAM1645  LOC152620 3'  GTTGCCCAGGCTGGAGTGCAGT 60712                AG
                GG                  CCACTGCACTCCAGCCTGGG  AC
                                    ||||||||||||||||||||  ||
                                    GGTGACGTGAGGTCGGACCC  TG
                                                 GT
GAM1645  LOC152719 5'  CCCAGCCTGGAGTGCAGTGG   87019            C
                                    CCACTGCACTCCAG CTGGG
                                    |||||||||||||| |||||
                                    GGTGACGTGAGGTC GACCC
                                              C
GAM1645  LOC152719 5'  GTCGCCCAGGCTGGAATGCAGT 87041        C         A
                GG                  CCACTGCA TCCAGCCTGGG GAC
                                    |||||||| |||||||||| |||
                                    GGTGACGT AGGTCGGACCC CTG
                                       A         G
GAM1645  LOC152765 5'  CCTCTGCTGGAGTGAAACAG   81543     ___       CT
                                    CTG   CACTCCAGC  GGG
                                    |||   |||||||||  |||
                                    GAC   GTGAGGTCG  TCC
                                      AAA        TC
GAM1645  LOC152794 5'  GTTACCCAGGCTGGAGTGCAGT 81562                A
                GG                  CCACTGCACTCCAGCCTGGG GAC
                                    |||||||||||||||||||| |||
                                    GGTGACGTGAGGTCGGACCC TTG
                                                 A
GAM1645  LOC152804 3'  CAGGCTTGGAGTGCAGTGG    87075           _
                                    CCACTGCACTCCA GCCTG
                                    |||||||||||| |||||
                                    GGTGACGTGAGGT CGGAC
                                              T
GAM1645  LOC152851 3'  CCTAGGCTGGAGTGCAGTGG   81590
                                    CCACTGCACTCCAGCCTGGG
                                    ||||||||||||||||||||
                                    GGTGACGTGAGGTCGGATCC

GAM1645  LOC152925 3'  CCCAGGCTGGAGTGCAGGG    81617    A
                                    CC CTGCACTCCAGCCTGGG
                                    || ||||||||||||||||
                                    GG GACGTGAGGTCGGACCC
                                     _
GAM1645  LOC153077 3'  TCACCCAGGCTGGAGTGCAGTG 87132                A
                G                    CCACTGCACTCCAGCCTGGG GA
                                    |||||||||||||||||||| ||
                                    GGTGACGTGAGGTCGGACCC CT
                                                 A
GAM1645  LOC153688 3'  GTCACCCAGGCTGGAGTGCAAT 87329     C           A
                GG                  CCA TGCACTCCAGCCTGGG GAC
                                    ||| |||||||||||||| |||
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                                GGT ACGTGAGGTCGGACCC CTG
                                  A             A
GAM1645  LOC153811 5'  CCCAGGCAGGAGTGCAGTGG   81828           A
                                CCACTGCACTCC GCCTGGG
                                |||||||||||| |||||||
                                GGTGACGTGAGG CGGACCC
                                       A
GAM1645  LOC153811 3'  GTCGCCCAGACTGGAGTGCAGT 81847           C    A
                                ACTGCACTCCAG CTGGG GAC
                                |||||||||||| ||||| |||
                                TGACGTGAGGTC GACCC CTG
                                       A    G
GAM1645  LOC153811 3'  GTTGCCCAGACTGGAGTGCAGT 81849           C    AG
            GG                    CCACTGCACTCCAG CTGGG  AC
                                |||||||||||||| |||||  ||
                                GGTGACGTGAGGTC GACCC  TG
                                       A    GT
GAM1645  LOC153883 5'  CCCAGGCTGGAGTGCAGTGG   81892
                                CCACTGCACTCCAGCCTGGG
                                ||||||||||||||||||||
                                GGTGACGTGAGGTCGGACCC

GAM1645  LOC153910 5'  CCCAGTCTGGAGTGCAGTGG   81904           C
                                CCACTGCACTCCAG CTGGG
                                |||||||||||||| |||||
                                GGTGACGTGAGGTC GACCC
                                       T
GAM1645  LOC154007 3'  TCTACTGGCTGGAGTGCAGTGG 81933           TG_
                                CCACTGCACTCCAGCC   GGA
                                ||||||||||||||||   |||
                                GGTGACGTGAGGTCGG   TCT
                                       TCA
GAM1645  LOC154282 5'  GTCGCCAGGTTGGAGTGCAGTG 87412           GA
            G                    CCACTGCACTCCAGCCTGG  GAC
                                |||||||||||||||||  |||
                                GGTGACGTGAGGTTGGACC  CTG
                                       G_
GAM1645  LOC154726 5'  GTTGCCCAGGCTGGAGTGCAGT 82013           AG
            GG                    CCACTGCACTCCAGCCTGGG  AC
                                |||||||||||||||||||  ||
                                GGTGACGTGAGGTCGGACCC  TG
                                       GT
GAM1645  LOC154822 3'  CCAGGCTGGAGTGCAATG    87484    C
                                CA TGCACTCCAGCCTGG
                                || ||||||||||||||
                                GT ACGTGAGGTCGGACC
                                 A
GAM1645  LOC154877 3'  CCAGGCTGGAATGCCGTGG    87537     T  C
                                CCAC GCA TCCAGCCTGG
                                |||| ||| ||||||||||
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                                GGTG CGT AGGTCGGACC
                                  C   A
GAM1645  LOC154877 3'  GTCGCCCAGGGTGGAGTGCAGT 87569           G     A
                 GG                CCACTGCACTCCA CCTGGG GAC
                                   |||||||||||| |||||| |||
                                   GGTGACGTGAGGT GGACCC CTG
                                     G     G
GAM1645  LOC154877 3'  GTCTCGCAGGCCAGAGTGCAGT 87570          CA    G
                 GG                CCACTGCACTC  GCCTG GAGAC
                                   ||||||||||  ||||| |||||
                                   GGTGACGTGAG  CGGAC CTCTG
                                      AC    G
GAM1645  LOC154930 3'  CCAGGCTGGAGTGCACTGG   82089    C
                                   CCA TGCACTCCAGCCTGG
                                   ||| ||||||||||||||
                                   GGT ACGTGAGGTCGGACC
                                     C
GAM1645  LOC155376 3'  TTCAGGCTGGGTGCAGTGG   82253        T
                                   CCACTGCAC CCAGCCTGGG
                                   |||||||| ||||||||||
                                   GGTGACGTG GGTCGGACTT
                                          _
GAM1645  LOC157247 5'  CCCAGGGCTGGAGTGCAGTGG  82291             _
                                   CCACTGCACTCCAGCC TGGG
                                   |||||||||||||| ||||
                                   GGTGACGTGAGGTCGG ACCC
                                         G
GAM1645  LOC157506 3'  GTCACCAGGCTGGAGTGCAGT  82372             GA
                                   ACTGCACTCCAGCCTGG  GAC
                                   |||||||||||||||  |||
                                   TGACGTGAGGTCGGACC  CTG
                                        A_
GAM1645  LOC157562 5'  CCAGGCCAGGTGCAGTG     87773         CCA
                                   CACTGCACT   GCCTGG
                                   |||||||||   ||||||
                                   GTGACGTGG   CGGACC
                                      AC_
GAM1645  LOC158014 5'  GTCACCCAGGCTGGAGTGTAGT 82565               A
                 GG                CCACTGCACTCCAGCCTGGG GAC
                                   |||||||||||||||||| |||
                                   GGTGATGTGAGGTCGGACCC CTG
                                        A
GAM1645  LOC158288 3'  GTCCCCCAGGCTGAGTCA    88030    C   C      A
                                   TG ACTC AGCCTGGG GAC
                                   || |||| |||||||| |||
                                   AC TGAG TCGGACCC CTG
                                    _   _      C
GAM1645  LOC158310 5'  GTCGCCCAGGCTGGAGTGCAGT 88088               A
                 GG                CCACTGCACTCCAGCCTGGG GAC
                                   |||||||||||||||||| |||
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                                GGTGACGTGAGGTCGGACCC CTG
                                      G
GAM1645  LOC158402 5'  GTTGCCCAGGCTGGAGTGCAGT 88152              AG
              GG                  CCACTGCACTCCAGCCTGGG  AC
                                  ||||||||||||||||||||  ||
                                  GGTGACGTGAGGTCGGACCC  TG
                                      GT
GAM1645  LOC158476 3'  CCCAGCTTGAGTGCAGTGG   88189         C   C
                                  CCACTGCACTC AGC TGGG
                                  |||||||||| ||| ||||
                                  GGTGACGTGAG TCG ACCC
                                        T  _
GAM1645  LOC158476 3'  GTCGCCCAGGCTGGAGTGCAGT 88203              A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                  ||||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC CTG
                                      G
GAM1645  LOC158549 5'  GTCTCCCAGGCTGGAGTGCAGT 88228
              GG                  CCACTGCACTCCAGCCTGGGAGAC
                                  ||||||||||||||||||||||||
                                  GGTGACGTGAGGTCGGACCCTCTG

GAM1645  LOC158668 3'  GTTGCCCAGGCTGGAGTGCAAT 69905    C          AG
              GG                  CCA TGCACTCCAGCCTGGG  AC
                                  ||| ||||||||||||||  ||
                                  GGT ACGTGAGGTCGGACCC  TG
                                    A          GT
GAM1645  LOC159184 5'  TCTTCTTCTGGAGCAAGT   60683    GCA    CCT
                                  ACT  CTCCAG  GGGAGA
                                  |||  ||||||  ||||||
                                  TGA  GAGGTC  TCTTCT
                                    AC_    T__
GAM1645  LOC160646 3'  GTCACCCAGGCTGGAGTGCAGT 83120              A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                  ||||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC CTG
                                      A
GAM1645  LOC161829 3'  GTCACCCAGGCTGGAGTGTAGT 83193              A
              GG                  CCACTGCACTCCAGCCTGGG GAC
                                  ||||||||||||||||||| |||
                                  GGTGATGTGAGGTCGGACCC CTG
                                      A
GAM1645  LOC162427 3'  GTTGCCCAGGCTGGAGTGCAGT 83229              AG
              GG                  CCACTGCACTCCAGCCTGGG  AC
                                  ||||||||||||||||||||  ||
                                  GGTGACGTGAGGTCGGACCC  TG
                                      GT
GAM1645  LOC162962 3'  CCAGGCTGGAATGCAGTG   83254       C
                                  CACTGCA TCCAGCCTGG
                                  ||||||| ||||||||||
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                                GTGACGT AGGTCGGACC
                                    A
GAM1645  LOC165552 3'  CCCTCGCGGAGTGCGTGG    83378     T     A  CT
                                CCAC GCACTCC GC  GGG
                                |||| ||||||| ||  |||
                                GGTG CGTGAGG CG  CCC
                                  _      _  CT
GAM1645  LOC169611 3'  CCCGGGCTGGAATGCAATGG   83642    C   C
                                CCA TGCA TCCAGCCTGGG
                                ||| |||| ||||||||||
                                GGT ACGT AGGTCGGGCCC
                                  A   A
GAM1645  LOC170409 5'  CTCATAAGGGCTGGAGTGCTGT 83743     T         GG__
            GG                    CCAC GCACTCCAGCCT   GAG
                                |||| ||||||||||||   |||
                                GGTG CGTGAGGTCGGG   CTC
                                  T          AATA
GAM1645  LOC196047 5'  GTCTCCCAGGCTGGAGTGCA   91162
                                TGCACTCCAGCCTGGGAGAC
                                ||||||||||||||||||||
                                ACGTGAGGTCGGACCCTCTG

GAM1645  LOC196074 5'  CTGAGGCTGGAAACAGCGG   88969    A  CAC      G
                                CC CTG   TCCAGCCT GG
                                || |||   |||||||| ||
                                GG GAC   AGGTCGGA TC
                                 C  AA_       G
GAM1645  LOC196264 3'  GTCGCCAGGCTGGAGTGCAGTG 88992              GA
            G                    CCACTGCACTCCAGCCTGG  GAC
                                |||||||||||||||||  |||
                                GGTGACGTGAGGTCGGACC  CTG
                                             G_
GAM1645  LOC196411 3'  CCTGGGCTGGAATGCAGTGG   89045       C      TG
                                CCACTGCA TCCAGCC  GG
                                |||||||| |||||||  ||
                                GGTGACGT AGGTCGG  CC
                                     A      GT
GAM1645  LOC196529 3'  CCCAGGCTGGAGTGCAATG    89129    C
                                CA TGCACTCCAGCCTGGG
                                || ||||||||||||||||
                                GT ACGTGAGGTCGGACCC
                                 A
GAM1645  LOC196529 3'  GTTGCCCAGGCTGGAGTGCAAT 89138    C           AG
            G                    CA TGCACTCCAGCCTGGG  AC
                                || ||||||||||||||||  ||
                                GT ACGTGAGGTCGGACCC  TG
                                 A             GT
GAM1645  LOC196812 3'  CCTCTGCGGAGTGTAGTG    91123          A  CT
                                CACTGCACTCC GC  GGG
                                |||||||||| ||  |||
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                                GTGATGTGAGG CG  TCC
                                      _ TC
GAM1645  LOC196957 3'  GTCACCAGGCTGGAGTACAGTG 89193      C         GA
                                CACTG ACTCCAGCCTGG  GAC
                                ||||| ||||||||||||  |||
                                GTGAC TGAGGTCGGACC  CTG
                                   A          A_
GAM1645  LOC196961 3'  GTCACCAGGCTGGAGTACAGTG 89206      C         GA
                                CACTG ACTCCAGCCTGG  GAC
                                ||||| ||||||||||||  |||
                                GTGAC TGAGGTCGGACC  CTG
                                   A          A_
GAM1645  LOC197138 3'  GTCACCAGGCTGGAGTACAGTG 89255      C         GA
                                CACTG ACTCCAGCCTGG  GAC
                                ||||| ||||||||||||  |||
                                GTGAC TGAGGTCGGACC  CTG
                                   A          A_
GAM1645  LOC197358 3'  GTCACCCAGGCTGGAGTGCAGT 89441                 A
            GG                    CCACTGCACTCCAGCCTGGG GAC
                                ||||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                      A
GAM1645  LOC197358 3'  GTCGCCCAGGCTGGAGTGCAGT 89443                 A
            GG                    CCACTGCACTCCAGCCTGGG GAC
                                ||||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                      G
GAM1645  LOC199699 3'  GTCACCCAGGCTGGAGTGCAAT 89681     C           A
            GG                    CCA TGCACTCCAGCCTGGG GAC
                                ||| ||||||||||||||| |||
                                GGT ACGTGAGGTCGGACCC CTG
                                  A            A
GAM1645  LOC199699 3'  GTCGCCCAGGCTGGAGTGCAGT 89683                 A
            GG                    CCACTGCACTCCAGCCTGGG GAC
                                ||||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                      G
GAM1645  LOC199725 5'  CCTAGGCTGGATTGCAATGG   91414     C   C
                                CCA TGCA TCCAGCCTGGG
                                ||| |||| ||||||||||
                                GGT ACGT AGGTCGGATCC
                                  A   T
GAM1645  LOC199786 3'  CCCGGGCTGGAGTGCAGTGG   89746
                                CCACTGCACTCCAGCCTGGG
                                ||||||||||||||||||||
                                GGTGACGTGAGGTCGGGCCC

GAM1645  LOC199899 5'  TCTCAGGCTGGAGTACAGTGG  91472       C
                                CCACTG ACTCCAGCCTGGGA
                                |||||| ||||||||||||||
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                                GGTGAC TGAGGTCGGACTCT
                                   A
GAM1645  LOC199906 3'  TCCAGGCTGGAGTGCAGTGG   89860
                                CCACTGCACTCCAGCCTGGG
                                ||||||||||||||||||||
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GAM1645  LOC200014 3'  CCAGGCTGGAGTGCAGTGG    89926
                                CCACTGCACTCCAGCCTGG
                                |||||||||||||||||||
                                GGTGACGTGAGGTCGGACC

GAM1645  LOC200093 5'  TCTCCCAGCAGGTAGAGCAG   63777      A  _  A  C
                                CTGC CT CC GC TGGGAGA
                                |||| || || || |||||||
                                GACG GA GG CG ACCCTCT
                                  A  T  A  _
GAM1645  LOC200107 3'  CCAGGCTGGAGTGCAGTG     89982
                                CACTGCACTCCAGCCTGG
                                ||||||||||||||||||
                                GTGACGTGAGGTCGGACC

GAM1645  LOC200169 5'  GTCGTCCAGGCTGGAGTGCAGT 91560                GA
                                ACTGCACTCCAGCCTGG  GAC
                                ||||||||||||||||  |||
                                TGACGTGAGGTCGGACC  CTG
                                      TG
GAM1645  LOC200301 5'  TCGCCCAGGCTGGAGTACAGTG 90156       C          A
            G                    CCACTG ACTCCAGCCTGGG GA
                                ||||||  |||||||||||||  ||
                                GGTGAC TGAGGTCGGACCC CT
                                   A          G
GAM1645  LOC200310 3'  CCTAGGCTGGAGTGCAGTG    66323
                                CACTGCACTCCAGCCTGGG
                                ||||||||||||||||||
                                GTGACGTGAGGTCGGATCC

GAM1645  LOC200314 3'  CCAGGCTGGGGTGCAGTGG    91594
                                CCACTGCACTCCAGCCTGG
                                |||||||||||||||||||
                                GGTGACGTGGGGTCGGACC

GAM1645  LOC200860 3'  GTCACCCAGGCTGGAGTGCAGT 91756                A
            GG                     CCACTGCACTCCAGCCTGGG GAC
                                ||||||||||||||||||||  |||
                                GGTGACGTGAGGTCGGACCC CTG
                                      A
GAM1645  LOC200860 3'  TCCAGGCTGGAGTGCAATGG   91759     C
                                CCA TGCACTCCAGCCTGGG
                                |||  ||||||||||||||||
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                                GGT ACGTGAGGTCGGACCT
                                  A
GAM1645  LOC200982 3'  CAGGCTGGGCACAGTGG     91810        CA T
                                CCACTG  C CCAGCCTG
                                ||||||  | ||||||||
                                GGTGAC  G GGTCGGAC
                                   AC _
GAM1645  LOC201164 3'  GTGGCCCAGGCTGGAGTGCAGT 89501                 AG
              GG                   CCACTGCACTCCAGCCTGGG  AC
                                ||||||||||||||||||  ||
                                GGTGACGTGAGGTCGGACCC  TG
                                      GG
GAM1645  LOC201173 5'  CCCAGGCTGAAGTGCAATG    88677    C     C
                                CA TGCACT CAGCCTGGG
                                || |||||| |||||||||
                                GT ACGTGA GTCGGACCC
                                 A     A
GAM1645  LOC201220 5'  CCCAGGCTGAAGTGCAATG    88712    C     C
                                CA TGCACT CAGCCTGGG
                                || |||||| |||||||||
                                GT ACGTGA GTCGGACCC
                                 A     A
GAM1645  LOC201294 3'  CCAGGCCAGAGTGCAGTGG    89578          CA
                                CCACTGCACTC  GCCTGG
                                ||||||||||  ||||||
                                GGTGACGTGAG  CGGACC
                                      AC
GAM1645  LOC201294 3'  GTCGCCCAGGCTGGAGTGCAGT 89595                 A
              GG                   CCACTGCACTCCAGCCTGGG GAC
                                ||||||||||||||||||| |||
                                GGTGACGTGAGGTCGGACCC CTG
                                      G
GAM1645  LOC201411 3'  CCCAACCTGGAGTGCAATGG   63639     C        CC
                                CCA TGCACTCCAG  TGGG
                                ||| ||||||||||  ||||
                                GGT ACGTGAGGTC  ACCC
                                  A         CA
GAM1645  LOC201626 3'  GTTGCCCAGGCTGGAGTGCAAT 90438     C            AG
              GG                   CCA TGCACTCCAGCCTGGG  AC
                                ||| ||||||||||||||  ||
                                GGT ACGTGAGGTCGGACCC  TG
                                  A              GT
GAM1645  LOC201627 3'  GTTGCCCAGGCTGGAGTGCAAT 90459     C            AG
              GG                   CCA TGCACTCCAGCCTGGG  AC
                                ||| ||||||||||||||  ||
                                GGT ACGTGAGGTCGGACCC  TG
                                  A              GT
GAM1645  LOC201696 3'  GTTGCCCAGGCTGGAGTGCAAT 63827     C            AG
              GG                   CCA TGCACTCCAGCCTGGG  AC
                                ||| ||||||||||||||  ||
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                                GGT ACGTGAGGTCGGACCC  TG
                                  A             GT
GAM1645  LOC201702 5'  GTCACCCAGGCTGGAGTGCAAT 90473     C             A
                 GG                 CCA TGCACTCCAGCCTGGG GAC
                                    ||| |||||||||||||| |||
                                    GGT ACGTGAGGTCGGACCC CTG
                                      A             A
GAM1645  LOC201868 5'  TTGGGGCCAGGTGCAGTGG    90535          CCA    G
                                    CCACTGCACT   GCCT GG
                                    ||||||||||   |||| ||
                                    GGTGACGTGG   CGGG TT
                                          AC_    G
GAM1645  LOC202460 5'  GTCACCAGGCTGGAGTGCAGTG 90676                 GA
                 G                  CCACTGCACTCCAGCCTGG  GAC
                                    ||||||||||||||||||  |||
                                    GGTGACGTGAGGTCGGACC  CTG
                                             A_
GAM1645  LOC202908 5'  CAGGCTGGAGTACAGTGG     90714        C
                                    CCACTG ACTCCAGCCTG
                                    |||||| ||||||||||
                                    GGTGAC TGAGGTCGGAC
                                       A
GAM1645  LOC202908 5'  GTCACCCAGGCTGGAGTACAGT 90731        C           A
                 GG                 CCACTG ACTCCAGCCTGGG GAC
                                    |||||| |||||||||||| |||
                                    GGTGAC TGAGGTCGGACCC CTG
                                       A           A
GAM1645  LOC202908 5'  TCCAAGGCTGGAGTGTAGT    90733              G
                                    ACTGCACTCCAGCCT GGA
                                    |||||||||||||| |||
                                    TGATGTGAGGTCGGA CCT
                                            A
GAM1645  LOC202934 3'  GTCACCAGGCTGGAGTGCAGTG 92048                 GA
                 G                  CCACTGCACTCCAGCCTGG  GAC
                                    ||||||||||||||||||  |||
                                    GGTGACGTGAGGTCGGACC  CTG
                                             A_
GAM1645  LOC202934 3'  GTCACCCAGGCTGGAGTACAGT 92050        C           A
                 GG                 CCACTG ACTCCAGCCTGGG GAC
                                    |||||| |||||||||||| |||
                                    GGTGAC TGAGGTCGGACCC CTG
                                       A           A
GAM1645  LOC203197 3'  GTCACCCAGGCTGGAGTGCAGT 90816                  A
                 GG                 CCACTGCACTCCAGCCTGGG GAC
                                    |||||||||||||||||| |||
                                    GGTGACGTGAGGTCGGACCC CTG
                                             A
GAM1645  LOC203297 5'  GTCACCCAGGCTGGAGTGCAAT 75874     C             A
                 GG                 CCA TGCACTCCAGCCTGGG GAC
                                    ||| |||||||||||||| |||
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                                GGT ACGTGAGGTCGGACCC CTG
                                  A             A
GAM1645  LOC203350 3'  GTTGCCCAGGCTGGAGTGCAGT 92247                AG
                GG               CCACTGCACTCCAGCCTGGG  AC
                                 ||||||||||||||||||  ||
                                 GGTGACGTGAGGTCGGACCC  TG
                                        GT
GAM1645  LOC203369 3'  GTCTCCCAGGCTGGAGTGCAGT 90892
                GG               CCACTGCACTCCAGCCTGGGAGAC
                                 ||||||||||||||||||||||||
                                 GGTGACGTGAGGTCGGACCCTCTG

GAM1645  LOC203378 3'  GTCGCCCAGGCTGGAGAGCAGT 92297        A          A
                GG               CCACTGC CTCCAGCCTGGG GAC
                                 |||||||  ||||||||||||  |||
                                 GGTGACG GAGGTCGGACCC CTG
                                    A          G
GAM1645  LOC203397 3'  GTTTTTCAGGCTGGGCACAGTG 90903       CA T       GG
                                 CACTG  C CCAGCCTG  AGAC
                                 |||||  |  ||||||||  ||||
                                 GTGAC  G GGTCGGAC  TTTG
                                   AC _       TT
GAM1645  LOC204804 3'  GTCACCCAGGCTAGAGTGCAGT 91048           C       A
                GG               CCACTGCACTC AGCCTGGG GAC
                                 ||||||||||  ||||||||  |||
                                 GGTGACGTGAG TCGGACCC CTG
                                       A       A
GAM1645  LOC204804 3'  GTCTCCCAGGCTGGAGTACAGT 91050        C
                GG               CCACTG ACTCCAGCCTGGGAGAC
                                 ||||||  ||||||||||||||||
                                 GGTGAC TGAGGTCGGACCCTCTG
                                   A
GAM1645  LOC219294 3'  GTCACCCAGGCTGGAGTGCAG  94598                A
                                 CTGCACTCCAGCCTGGG GAC
                                 ||||||||||||||||  |||
                                 GACGTGAGGTCGGACCC CTG
                                       A
GAM1645  LOC219295 3'  GTCACCCAGGCTGGAGTGCAG  94589                A
                                 CTGCACTCCAGCCTGGG GAC
                                 ||||||||||||||||  |||
                                 GACGTGAGGTCGGACCC CTG
                                       A
GAM1645  LOC219529 5'  CCCAGCCTGGAGTGCAGTGG   94565             C
                                 CCACTGCACTCCAG CTGGG
                                 ||||||||||||| |||||
                                 GGTGACGTGAGGTC GACCC
                                       C
GAM1645  LOC219673 5'  CCCAGTCTGGAGTGCAGTGG   94621             C
                                 CCACTGCACTCCAG CTGGG
                                 ||||||||||||| |||||
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                                GGTGACGTGAGGTC GACCC
                                       T
GAM1645  LOC219673 5'  GTTGCCCAGGCTGGAGGGCAGT 94631        A          AG
                GG                CCACTGC CTCCAGCCTGGG  AC
                                  ||||||| ||||||||||||  ||
                                  GGTGACG GAGGTCGGACCC  TG
                                     G          GT
GAM1645  LOC219731 5'  GTCATCCAGGCTGGAGTGCAGT 94713                GA
                GG                CCACTGCACTCCAGCCTGG  GAC
                                  ||||||||||||||||||  |||
                                  GGTGACGTGAGGTCGGACC  CTG
                                        TA
GAM1645  LOC219735 3'  GTTGCCCAGGCTGGAGTGCAGT 94734                AG
                                  ACTGCACTCCAGCCTGGG  AC
                                  ||||||||||||||||||  ||
                                  TGACGTGAGGTCGGACCC  TG
                                        GT
GAM1645  LOC219894 3'  CCCAGGCTGGAGTGCAGTGG   94902
                                  CCACTGCACTCCAGCCTGGG
                                  ||||||||||||||||||||
                                  GGTGACGTGAGGTCGGACCC

GAM1645  LOC220074 3'  CCCAGCTGGAGTGCAGTGG    59970              C
                                  CCACTGCACTCCAGC TGGG
                                  |||||||||||||| ||||
                                  GGTGACGTGAGGTCG ACCC
                                        _
GAM1645  LOC220074 3'  GTCACCCAGGCTGGAGTGCAGT 59993                A
                GG                CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC CTG
                                        A
GAM1645  LOC220074 3'  CAGGCTGGAGTGCAGTGG     59966
                                  CCACTGCACTCCAGCCTG
                                  ||||||||||||||||||
                                  GGTGACGTGAGGTCGGAC

GAM1645  LOC220575 3'  GTCACCCAGGCCGGAGTGCAGT 76816          A    A
                GG                CCACTGCACTCC GCCTGGG GAC
                                  |||||||||||| ||||||| |||
                                  GGTGACGTGAGG CGGACCC CTG
                                        C     A
GAM1645  LOC220662 3'  CCCAGGCTGGAGTGCGGTGG   92814
                                  CCACTGCACTCCAGCCTGGG
                                  ||||||||||||||||||||
                                  GGTGGCGTGAGGTCGGACCC

GAM1645  LOC220662 3'  CTTGGCTGGATGCAGTGG     92817        C    T
                                  CCACTGCA TCCAGCC GG
                                  |||||||| ||||||| ||
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                                GGTGACGT AGGTCGG TC
                                    _      T
GAM1645  LOC220739 3'  TCAGGGGCCAGAGTGCAGGG   94530    A      CA    GG
                                CC CTGCACTC  GCCT  GA
                                || ||||||||  ||||  ||
                                GG GACGTGAG  CGGG  CT
                                 _       AC    GA
GAM1645  LOC221035 3'  GTCACCAGGCTGGAGTGCAGTG 94782                GA
              G                  CCACTGCACTCCAGCCTGG  GAC
                                 ||||||||||||||||||  |||
                                 GGTGACGTGAGGTCGGACC  CTG
                                           A_
GAM1645  LOC221060 3'  GTTGCCCAGGCTGGAGTGCAAT 94836     C             AG
              GG                   CCA TGCACTCCAGCCTGGG  AC
                                 ||| ||||||||||||||  ||
                                 GGT ACGTGAGGTCGGACCC  TG
                                   A             GT
GAM1645  LOC221271 3'  CTCAGGCTGGAGTGCAATG    93514    C
                                 CA TGCACTCCAGCCTGGG
                                 || ||||||||||||||
                                 GT ACGTGAGGTCGGACTC
                                  A
GAM1645  LOC221271 3'  TGGGCCGGGTGCAGTGG     93535         T  A
                                 CCACTGCAC CC GCCTG
                                 |||||||| || |||||
                                 GGTGACGTG GG CGGGT
                                       _ C
GAM1645  LOC221296 3'  GTCGCCCAGGTTGGAGTGCAGT 93616                A
              GG                   CCACTGCACTCCAGCCTGGG GAC
                                 |||||||||||||||||| |||
                                 GGTGACGTGAGGTTGGACCC CTG
                                           G
GAM1645  LOC221641 3'  TTCTAGGCCAGGCACAATGG   95351     C__   A  CCA
                                 CCA   TGC CT   GCCTGGGA
                                 |||   ||| ||   ||||||||
                                 GGT   ACG GA   CGGATCTT
                                   AAC   _  C__
GAM1645  LOC221663 5'  CCAAGGCTGGAGTGCAGTGG   95459              G
                                 CCACTGCACTCCAGCCT GG
                                 |||||||||||||||| ||
                                 GGTGACGTGAGGTCGGA CC
                                           A
GAM1645  LOC221773 3'  GTCTCCCAGGCTGGAGTGCAGT 92696
              G                   CACTGCACTCCAGCCTGGGAGAC
                                 |||||||||||||||||||||||
                                 GTGACGTGAGGTCGGACCCTCTG

GAM1645  LOC221814 5'  GTCGCCAAGCCAGAGTGCAGTG 95559          CA  C   GA
              G                   CCACTGCACTC  GC TGG  GAC
                                 ||||||||||  || |||  |||
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                                GGTGACGTGAG  CG ACC  CTG
                                      AC  A   G_
GAM1645  LOC221960 3'  CCCAGGCTGGAATGCAATGG   92724     C    C
                                CCA TGCA TCCAGCCTGGG
                                ||| |||| ||||||||||
                                GGT ACGT AGGTCGGACCC
                                  A   A
GAM1645  LOC221964 3'  GTCTCCCAGGCTGGACTGCAGT 95611         C
              GG                  CCACTGCA TCCAGCCTGGGAGAC
                                ||||||||| ||||||||||||||
                                GGTGACGT AGGTCGGACCCTCTG
                                     C
GAM1645  LOC222057 5'  TCCAAGGCTGGAGTGTAGT    94361              G
                                ACTGCACTCCAGCCT GGA
                                |||||||||||||| |||
                                TGATGTGAGGTCGGA CCT
                                        A
GAM1645  LOC222060 5'  CTCCCAGGTGAGGGCAGTGG   95753        A   CA
                                CCACTGC CTC  GCCTGGGAG
                                ||||||| |||  |||||||||
                                GGTGACG GAG  TGGACCCTC
                                   G   __
GAM1645  LOC222068 3'  GTCGCCCAGGCTGGAGTGCAAT 94279     C             A
              GG                  CCA TGCACTCCAGCCTGGG GAC
                                ||| |||||||||||||| |||
                                GGT ACGTGAGGTCGGACCC CTG
                                  A             G
GAM1645  LOC222070 5'  GTCTCCCAGGCTGGAGTGCAGT 95822
              GG                  CCACTGCACTCCAGCCTGGGAGAC
                                ||||||||||||||||||||||||
                                GGTGACGTGAGGTCGGACCCTCTG

GAM1645  LOC222112 5'  CTCCCAGGATGCTAGTGG    94378       _  CTCCAG
                                CCACT GCA     CCTGGGAG
                                ||||| |||     ||||||||
                                GGTGA CGT     GGACCCTC
                                   T   A_____
GAM1645  LOC222160 3'  TAGGCTGGGCGCAGTGG     95790        A T
                                CCACTGC C CCAGCCTG
                                ||||||| | ||||||||
                                GGTGACG G GGTCGGAT
                                   C _
GAM1645  LOC222189 5'  CTGAGAGCTGGAGTACAG    95834     C       _  G
                                CTG ACTCCAGC CT GG
                                ||| |||||||| || ||
                                GAC TGAGGTCG GA TC
                                  A       A  G
GAM1645  LOC245771 5'  GTCGCCCAGGCTGGAATGCAGT 94486       C         A
                                ACTGCA TCCAGCCTGGG GAC
                                |||||| |||||||||| |||
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                                TGACGT AGGTCGGACCC CTG
                                   A         G
GAM1645  LOC253142 3'  TCTCCCAAATGCTGAGCAG   99226     ACTC   C__
                                CTGC   CAGC   TGGGAGA
                                ||||   ||||  |||||||
                                GACG   GTCG   ACCCTCT
                                  A___   TAA
GAM1645  LOC253532 3'  TTCAGGCTGGGTGCAGTGG   97743         T
                                CCACTGCAC CCAGCCTGGG
                                ||||||||| ||||||||||
                                GGTGACGTG GGTCGGACTT
                                          _
GAM1645  LOC253612 5'  GTCTCCCAGGCTGGAGTGCGGT 98556
            GG                    CCACTGCACTCCAGCCTGGGAGAC
                                  ||||||||||||||||||||||||
                                  GGTGGCGTGAGGTCGGACCCTCTG

GAM1645  LOC253664 3'  GTTGCCCAGGCTGGAGTGCAGT 96474                AG
            GG                    CCACTGCACTCCAGCCTGGG  AC
                                  ||||||||||||||||||  ||
                                  GGTGACGTGAGGTCGGACCC  TG
                                            GT
GAM1645  LOC253779 3'  GTCACCCAGGTTGGAGTGCAGT 98926                A
            GG                    CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||| |||
                                  GGTGACGTGAGGTTGGACCC CTG
                                            A
GAM1645  LOC253805 3'  GTTGCCCAGGCTGGAGTGCAGT 98183                AG
            G                      CACTGCACTCCAGCCTGGG  AC
                                   ||||||||||||||||||  ||
                                   GTGACGTGAGGTCGGACCC  TG
                                             GT
GAM1645  LOC253868 5'  CCCAGGACTCTGAGTGCAG   97320         C_ _
                                CTGCACTC  AG CCTGGG
                                ||||||||  || ||||||
                                GACGTGAG  TC GGACCC
                                     TC  A
GAM1645  LOC254013 3'  CTCCCAGGCTGGAATGCAGTGG 96533         C
                                CCACTGCA TCCAGCCTGGGAG
                                |||||||| ||||||||||||
                                GGTGACGT AGGTCGGACCCTC
                                     A
GAM1645  LOC254013 3'  GTCGTCCAGGCTGGAGTGCAGT 96535               GA
            G                      CACTGCACTCCAGCCTGG  GAC
                                   ||||||||||||||||||  |||
                                   GTGACGTGAGGTCGGACC  CTG
                                             TG
GAM1645  LOC254082 5'  GTCGCCCAAGCTAGAGTGCAGT 98997           C  C   A
            GG                    CCACTGCACTC AGC TGGG GAC
                                  |||||||||| ||| |||| |||
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                                GGTGACGTGAG TCG ACCC CTG
                                      A  A   G
GAM1645  LOC254351 3'  TCCAGGCTGGAGTGCAATGG  96695    C
                                CCA TGCACTCCAGCCTGGG
                                ||| ||||||||||||||||
                                GGT ACGTGAGGTCGGACCT
                                  A
GAM1645  LOC254381 5'  CCGGGGCTGGAGCGCAGCGG  99326   A   A      G
                                CC CTGC CTCCAGCCT GG
                                || |||| ||||||||| ||
                                GG GACG GAGGTCGGG CC
                                 C   C       G
GAM1645  LOC254423 5'  TTTCCTGGGAGCACAATGG   99304    C  CA   AGCC
                                CCA TG  CTCC   TGGGAGA
                                ||| ||  ||||   |||||||
                                GGT AC  GAGG   GTCCTTT
                                  A  AC   ____
GAM1645  LOC254655 3'  GTCTCCCAGGCTGGAGTGCAGT 97225
            GG                    CCACTGCACTCCAGCCTGGGAGAC
                                ||||||||||||||||||||||||
                                GGTGACGTGAGGTCGGACCCTCTG

GAM1645  LOC254672 3'  GTTGCCCAGGCTGGAGTGCAAT 96299    C           AG
            GG                    CCA TGCACTCCAGCCTGGG  AC
                                ||| ||||||||||||||  ||
                                GGT ACGTGAGGTCGGACCC  TG
                                  A            GT
GAM1645  LOC254875 3'  TTCAGGCTGGGTGCAGTGG   97787        T
                                CCACTGCAC CCAGCCTGGG
                                ||||||||| ||||||||||
                                GGTGACGTG GGTCGGACTT
                                     _
GAM1645  LOC255027 5'  CCGGCTGCTGCAGTGCAGT   96775        C   __
                                ACTGCACT CAGC  CTGG
                                |||||||| ||||  ||||
                                TGACGTGA GTCG  GGCC
                                     C   TC
GAM1645  LOC255031 3'  CCCAGGCTAGAGTGCAGTGG  99033          C
                                CCACTGCACTC AGCCTGGG
                                |||||||||| ||||||||
                                GGTGACGTGAG TCGGACCC
                                       A
GAM1645  LOC255177 3'  GTTGCCCAGGCTGGAGTGCAAT 98400    C           AG
            GG                    CCA TGCACTCCAGCCTGGG  AC
                                ||| ||||||||||||||  ||
                                GGT ACGTGAGGTCGGACCC  TG
                                  A            GT
GAM1645  LOC255196 5'  CTCAGGCTGGAGTGCAGTG   98955
                                CACTGCACTCCAGCCTGGG
                                ||||||||||||||||||
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                                GTGACGTGAGGTCGGACTC

GAM1645  LOC255326 3'  TCTGGCCGGGTGCAGTGG    98126         T  A   TGGG
                                CCACTGCAC CC GCC    AGA
                                |||||||||  || |||    |||
                                GGTGACGTG GG CGG    TCT
                                      _  C   ____
GAM1645  LOC255458 5'  CCAGGCTGGAGTATAGTGG    98932       C
                                CCACTG ACTCCAGCCTGG
                                ||||||  ||||||||||||
                                GGTGAT TGAGGTCGGACC
                                   A
GAM1645  LOC255465 3'  GTCACCAGGCTGGAGTGCAGTG 99123                GA
              G                  CCACTGCACTCCAGCCTGG  GAC
                                 ||||||||||||||||||  |||
                                 GGTGACGTGAGGTCGGACC  CTG
                                        A_
GAM1645  LOC255465 3'  GTCACCCAGGCTGGAGTACAGT 99125       C          A
              GG                   CCACTG ACTCCAGCCTGGG GAC
                                   ||||||  |||||||||||| |||
                                   GGTGAC TGAGGTCGGACCC CTG
                                      A          A
GAM1645  LOC255620 5'  GTCTCCTACCTGCGGATGCAG  98875      C   A  C__
                                CTGCA TCC GC   TGGGAGAC
                                |||||  ||| ||   ||||||||
                                GACGT AGG CG   ATCCTCTG
                                   _   _  TCC
GAM1645  LOC255919 3'  CCAGGCTGGAGGGCAGTGG    96744        A
                                CCACTGC CTCCAGCCTGG
                                |||||||  ||||||||||
                                GGTGACG GAGGTCGGACC
                                   G
GAM1645  LOC255975 5'  TCCAAGGCTGGAGTGTAGT    97590              G
                                ACTGCACTCCAGCCT GGA
                                |||||||||||||| |||
                                TGATGTGAGGTCGGA CCT
                                        A
GAM1645  LOC256055 5'  TCTCCGTCAAGTGCAGT     97623         CCA  CTG
                                ACTGCACT   GC   GGAGA
                                ||||||||   ||   |||||
                                TGACGTGA   TG   CCTCT
                                   AC_  ___
GAM1645  LOC256158 5'  CCTGTGGCGCTGGAGTGCGTGG 99491      T        _ __
                                CCAC GCACTCCAGC CT  GGG
                                ||||  ||||||||||  ||  |||
                                GGTG CGTGAGGTCG GG  TCC
                                   _         C  TG
GAM1645  LOC256221 3'  CTCAGGCTGGAGTGCAGTGG   96908
                                CCACTGCACTCCAGCCTGGG
                                ||||||||||||||||||||
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                                GGTGACGTGAGGTCGGACTC

GAM1645  LOC256267 5'  CCCAGGTTCTAGAGTGCAGTGG 98609          C__
                                CCACTGCACTC   AGCCTGGG
                                ||||||||||   ||||||||
                                GGTGACGTGAG   TTGGACCC
                                      ATC
GAM1645  LOC256306 3'  CCCAGGCTGGAGTGCAGAGG   98510    A
                                CC CTGCACTCCAGCCTGGG
                                || ||||||||||||||||
                                GG GACGTGAGGTCGGACCC
                                 A
GAM1645  LOC256476 5'  GTCACCCAGGCTGGAGTGCATG 98625    C            A
                                CA TGCACTCCAGCCTGGG GAC
                                || |||||||||||||||| |||
                                GT ACGTGAGGTCGGACCC CTG
                                 _            A
GAM1645  LOC256878 5'  TCCAAGGCTGGAGTGTAGT    98691             G
                                ACTGCACTCCAGCCT GGA
                                |||||||||||||| |||
                                TGATGTGAGGTCGGA CCT
                                         A
GAM1645  LOC256923 5'  CCTGGGCTGGAGTGCAGTG    96846             TG
                                CACTGCACTCCAGCC  GG
                                |||||||||||||  ||
                                GTGACGTGAGGTCGG  CC
                                         GT
GAM1645  LOC256940 5'  CCAGTGCTGAAGTGCAGT     98245        C   _
                                ACTGCACT CAGC CTGG
                                |||||||| |||| ||||
                                TGACGTGA GTCG GACC
                                     A   T
GAM1645  LOC257054 5'  CCCAGGCTGGAGTGCAGTG    97371
                                CACTGCACTCCAGCCTGGG
                                ||||||||||||||||||
                                GTGACGTGAGGTCGGACCC

GAM1645  LOC257463 3'  TCCCCAGGCTGGAGTGCAATGG 71625    C            A
                                CCA TGCACTCCAGCCTGGG GA
                                ||| |||||||||||||| ||
                                GGT ACGTGAGGTCGGACCC CT
                                  A           _
GAM1645  LOC257465 3'  GTCTTCCAGGCTGGAGTGCAGT 82499
                  GG              CCACTGCACTCCAGCCTGGGAGAC
                                  ||||||||||||||||||||||||
                                  GGTGACGTGAGGTCGGACCTTCTG

GAM1645  LOC257486 3'  GTTACCCAGATTGGAGTGCAGT 69781          GC    A
                  GG              CCACTGCACTCCA  CTGGG GAC
                                  ||||||||||||  ||||| |||
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                                GGTGACGTGAGGT  GACCC TTG
                                       TA    A
GAM1645  LOC51031  5'  TCAGGCTGGAGTGCAGTGG   32711
                                CCACTGCACTCCAGCCTGG
                                ||||||||||||||||||
                                GGTGACGTGAGGTCGGACT

GAM1645  LOC51122  3'  CTAAGCTGGGTGCAGTGG    66197        T    C
                                CCACTGCAC CCAGC TGG
                                ||||||||| ||||| |||
                                GGTGACGTG GGTCG ATC
                                      _    A
GAM1645  LOC51193  5'  GTTACCCAGGCTGGAGGACAGT 33369      CA         A
           G                     CACTG  CTCCAGCCTGGG GAC
                                |||||  |||||||||||| |||
                                GTGAC  GAGGTCGGACCC TTG
                                   AG          A
GAM1645  LOC51193  3'  TCCAGGATGGAGTGCAGTGG   33370           G
                                CCACTGCACTCCA CCTGGG
                                |||||||||||| ||||||
                                GGTGACGTGAGGT GGACCT
                                       A
GAM1645  LOC51219  5'  GTCGCCCAGGCTGGAGTGCAAT 33550     C           A
           GG                     CCA TGCACTCCAGCCTGGG GAC
                                ||| |||||||||||||| |||
                                GGT ACGTGAGGTCGGACCC CTG
                                  A             G
GAM1645  LOC51336  3'  GTTACCCAGGCTGGAGTGCAAT 34076     C           A
           GG                     CCA TGCACTCCAGCCTGGG GAC
                                ||| |||||||||||||| |||
                                GGT ACGTGAGGTCGGACCC TTG
                                  A             A
GAM1645  LOC51622  3'  CCCAGGCTGGAATGCAATGG   32206     C   C
                                CCA TGCA TCCAGCCTGGG
                                ||| |||| ||||||||||
                                GGT ACGT AGGTCGGACCC
                                  A   A
GAM1645  LOC51696  3'  GTCACCCAGGCTGGAGTGCAGT 33087              A
                                ACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||| |||
                                TGACGTGAGGTCGGACCC CTG
                                       A
GAM1645  LOC55954  5'  GTCACCCAGGCTGGAGTGTAGT 39399              A
           GG                     CCACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||| |||
                                GGTGATGTGAGGTCGGACCC CTG
                                       A
GAM1645  LOC56181  5'  GTCACCCAGGTTGGAGTGCAGT 97283              A
           GG                     CCACTGCACTCCAGCCTGGG GAC
                                |||||||||||||||||| |||
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                                GGTGACGTGAGGTTGGACCC CTG
                                           A
GAM1645 LOC57107 3' GTTGCCCAGGCTGGAGTGCAAT 40193     C           AG
             GG                  CCA TGCACTCCAGCCTGGG  AC
                                 ||| ||||||||||||||  ||
                                 GGT ACGTGAGGTCGGACCC  TG
                                   A            GT
GAM1645 LOC57118 3' CTGGGCTGGGTGCAGTGG    40223         T     TG
                                 CCACTGCAC CCAGCC  G
                                 |||||||| ||||||  |
                                 GGTGACGTG GGTCGG  C
                                       _     GT
GAM1645 LOC57146 3' GTTGCCCAGGCTGGAGTGCAAC 40298    AC           AG
             GG                  CC  TGCACTCCAGCCTGGG  AC
                                 ||  ||||||||||||||  ||
                                 GG  ACGTGAGGTCGGACCC  TG
                                  CA            GT
GAM1645 LOC63929 3' TCAGGGCTGGGCACAGCGG   42284    A   CA T     GG
                                 CC CTG  C CCAGCCT  GA
                                 || |||  | |||||||  ||
                                 GG GAC  G GGTCGGG  CT
                                  C   AC _      A_
GAM1645 LOC81034 3' GTCGCCCAGGCTGGAGTGCAGT 48594               A
             GG                  CCACTGCACTCCAGCCTGGG GAC
                                 |||||||||||||||||| |||
                                 GGTGACGTGAGGTCGGACCC CTG
                                           G
GAM1645 LOC89231 3' GTTGCCCAGGCTGGAGTGCAAT 94301     C           AG
             GG                  CCA TGCACTCCAGCCTGGG  AC
                                 ||| ||||||||||||||  ||
                                 GGT ACGTGAGGTCGGACCC  TG
                                   A            GT
GAM1645 LOC89932 3' CCCAGGCTGGAGTACAATGG   61453     C  C
                                 CCA TG ACTCCAGCCTGGG
                                 ||| || ||||||||||||
                                 GGT AC TGAGGTCGGACCC
                                   A  A
GAM1645 LOC89932 3' GTTGCCCAGGCTGGAGGGCAAT 61473     C   A         AG
             GG                  CCA TGC CTCCAGCCTGGG  AC
                                 ||| ||| ||||||||||||  ||
                                 GGT ACG GAGGTCGGACCC  TG
                                   A   G          GT
GAM1645 LOC90141 3' CCTAAGCTGGAGTACAGTG    62302       C       C
                                 CACTG ACTCCAGC TGGG
                                 ||||| |||||||| ||||
                                 GTGAC TGAGGTCG ATCC
                                    A       A
GAM1645 LOC90155 3' TCCCAGGCTAGAGTGCAGTGG  62369           C
                                 CCACTGCACTC AGCCTGGGA
                                 |||||||||| |||||||||
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                                GGTGACGTGAG TCGGACCCT
                                      A
GAM1645 LOC90288 3' CCTAGGCTGGAGTGAAGTGG  62782     G
                                CCACT CACTCCAGCCTGGG
                                ||||| ||||||||||||||
                                GGTGA GTGAGGTCGGATCC
                                   A
GAM1645 LOC90288 3' GTCACCCAGGCTGGAGTGCAGT 62797              A
          GG                      CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC CTG
                                        A
GAM1645 LOC90333 3' GTCGCCCAGGTTGGAGTGCAGT 62962              A
          GG                      CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||||| |||
                                  GGTGACGTGAGGTTGGACCC CTG
                                        G
GAM1645 LOC90371 5' GTCACCCAGGCTGGAGTGCAGT 63165              A
          GG                      CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC CTG
                                        A
GAM1645 LOC90408 5' GTTACCCAGGCTGGAGTGCAGT 63346              A
          GG                      CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||||| |||
                                  GGTGACGTGAGGTCGGACCC TTG
                                        A
GAM1645 LOC90459 3' CCAGGATGGAGTGCAGTGG   63552          G
                                CCACTGCACTCCA CCTGG
                                |||||||||||| |||||
                                GGTGACGTGAGGT GGACC
                                   A
GAM1645 LOC90485 3' GTCACCCAGGCTAGAGTGCAGT 63707          C     A
          GG                      CCACTGCACTC AGCCTGGG GAC
                                  |||||||||| |||||||| |||
                                  GGTGACGTGAG TCGGACCC CTG
                                        A     A
GAM1645 LOC90485 3' GTCGCCCAGGCTGGAGTGCAGT 63708              A
          G                        CACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||||| |||
                                  GTGACGTGAGGTCGGACCC CTG
                                        G
GAM1645 LOC90557 5' CTGAGCCGGGGTGCAGTGG   57855          A  CT
                                CCACTGCACTCC GC  GG
                                |||||||||||| ||  ||
                                GGTGACGTGGGG CG  TC
                                   C  AG
GAM1645 LOC90591 3' GTCACCCAGGCTGGAGTGCAGT 64184              A
          GG                      CCACTGCACTCCAGCCTGGG GAC
                                  |||||||||||||||||||| |||
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                                GGTGACGTGAGGTCGGACCC CTG
                                           A
GAM1645 LOC90591 3' GTTGCCCAGGCTGGAGTGCAGT 64187              AG
           GG                  CCACTGCACTCCAGCCTGGG  AC
                               ||||||||||||||||||  ||
                               GGTGACGTGAGGTCGGACCC  TG
                                           GT
GAM1645 LOC90639 3' CAGGCTGGGCGCAGCGG    64406   A   A T
                               CC CTGC C CCAGCCTG
                               || |||| | ||||||||
                               GG GACG G GGTCGGAC
                                C   C _
GAM1645 LOC90999 3' GTTGCCCAGGCTGGAGTACAGT 65185       C         AG
           GG                  CCACTG ACTCCAGCCTGGG  AC
                               ||||||| ||||||||||||  ||
                               GGTGAC TGAGGTCGGACCC  TG
                                  A          GT
GAM1645 LOC91040 5' TCTCCCAGCAGGTAGAGCAG  65351     A _ A  C
                               CTGC CT CC GC TGGGAGA
                               |||| || || || |||||||
                               GACG GA GG CG ACCCTCT
                                 A  T  A  _
GAM1645 LOC91115 3' CCCAGGCTGGAGTGCTGTGG  65556     T
                               CCAC GCACTCCAGCCTGGG
                               |||| ||||||||||||||
                               GGTG CGTGAGGTCGGACCC
                                 T
GAM1645 LOC91115 3' GTCACCCAGGCTGGAGTGCAAT 65575    C          A
           GG                  CCA TGCACTCCAGCCTGGG GAC
                               ||| ||||||||||||||| |||
                               GGT ACGTGAGGTCGGACCC CTG
                                 A            A
GAM1645 LOC91115 3' GTTGCCCAGGCTGGAGTGCAAT 65577    C          AG
           GG                  CCA TGCACTCCAGCCTGGG  AC
                               ||| ||||||||||||||  ||
                               GGT ACGTGAGGTCGGACCC  TG
                                 A            GT
GAM1645 LOC91291 5' GTCGCCCAGACTAGAATGCAGT 66093       C  C  C   A
           GG                  CCACTGCA TC AG CTGGG GAC
                               |||||||| || || ||||| |||
                               GGTGACGT AG TC GACCC CTG
                                   A  A  A    G
GAM1645 LOC91373 3' GTTGCCCAGGCTGGAGTGAAGT 66419     G          AG
           GG                  CCACT CACTCCAGCCTGGG  AC
                               ||||| ||||||||||||||  ||
                               GGTGA GTGAGGTCGGACCC  TG
                                 A          GT
GAM1645 LOC91380 3' TCCAGGCTGGAGTTCAGTGG  66455      C
                               CCACTG ACTCCAGCCTGGG
                               |||||| ||||||||||||
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                                GGTGAC TGAGGTCGGACCT
                                   T
GAM1645  LOC91445  3'  CCCCCTCAGTGCAGTGG     61166          CC  CCT
                                CCACTGCACT  AG   GGG
                                ||||||||||  ||   |||
                                GGTGACGTGA  TC   CCC
                                      C_  C__
GAM1645  LOC91661  3'  CTCAGACCTAGAGTGCAGGG   57211    A       C  C_
                                CC CTGCACTC AG  CTGGG
                                || ||||||||| ||  |||||
                                GG GACGTGAG TC  GACTC
                                 _       A  CA
GAM1645  LOC91661  3'  GTCGGCCAGGCTGGAATGCAAT 57219     C    C         GA
            GG                    CCA TGCA TCCAGCCTGG  GAC
                                  ||| |||| ||||||||||  |||
                                  GGT ACGT AGGTCGGACC  CTG
                                    A   A         GG
GAM1645  LOC91893  3'  CCCAGGCGGGAGTGCAGTGG   68070           A
                                CCACTGCACTCC GCCTGGG
                                |||||||||||| |||||||
                                GGTGACGTGAGG CGGACCC
                                       G
GAM1645  LOC92148  5'  CCCAGGCTAGAGTGCAGTGG   68873           C
                                CCACTGCACTC AGCCTGGG
                                |||||||||| ||||||||
                                GGTGACGTGAG TCGGACCC
                                      A
GAM1645  LOC92267  3'  GTCCCCCAGGCTGGAGTGCCGT 69175      T            A
            GG                    CCAC GCACTCCAGCCTGGG GAC
                                  |||| |||||||||||||| |||
                                  GGTG CGTGAGGTCGGACCC CTG
                                    C            C
GAM1645  LOC92283  3'  CCCAGGCTGGAGTCCAGTGG   69301       C
                                CCACTG ACTCCAGCCTGGG
                                |||||| ||||||||||||
                                GGTGAC TGAGGTCGGACCC
                                   C
GAM1645  LOC92299  3'  TTAGGCTGGGCGCAGTGG     69376        A T
                                CCACTGC C CCAGCCTGG
                                ||||||| | |||||||||
                                GGTGACG G GGTCGGATT
                                    C _
GAM1645  LOC92303  3'  CCCGGGCTGGAGTGCAATGG   69389     C
                                CCA TGCACTCCAGCCTGGG
                                ||| ||||||||||||||
                                GGT ACGTGAGGTCGGGCCC
                                  A
GAM1645  LOC92466  5'  CCCAGGTTCTAGAGTGCAGTGG 69965           C__
                                CCACTGCACTC   AGCCTGGG
                                ||||||||||   ||||||||
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                                GGTGACGTGAG   TTGGACCC
                                      ATC
GAM1645 LOC92609 3' GTTGCCCAGGCTGGAGTGCATT 73210    C           AG
             G                   CA TGCACTCCAGCCTGGG  AC
                                 || ||||||||||||||||  ||
                                 GT ACGTGAGGTCGGACCC  TG
                                  T            GT
GAM1645 LOC92661 5' CCCAGGCTGGAGTGCAGTGG   70625
                                 CCACTGCACTCCAGCCTGGG
                                 ||||||||||||||||||||
                                 GGTGACGTGAGGTCGGACCC

GAM1645 LOC92697 5' CCCAGGCTGGAGTGCAGTGG   70808
                                 CCACTGCACTCCAGCCTGGG
                                 ||||||||||||||||||||
                                 GGTGACGTGAGGTCGGACCC

GAM1645 LOC92841 3' GTTGCCCAGGCTGGAGTGCAAT 71263     C           AG
             GG                    CCA TGCACTCCAGCCTGGG  AC
                                 ||| ||||||||||||||||  ||
                                 GGT ACGTGAGGTCGGACCC  TG
                                   A            GT
GAM1645 LOC93129 3' CCAGGCTGGAGTGTAGTG    71954
                                 CACTGCACTCCAGCCTGG
                                 ||||||||||||||||||
                                 GTGATGTGAGGTCGGACC

GAM1645 LOC93129 3' CTCCCAGGTAGTGAGT      71955     G   CCA
                                 ACT CACT   GCCTGGGAG
                                 ||| ||||   |||||||||
                                 TGA GTGA   TGGACCCTC
                                   _   ___
GAM1645 LOC93132 5' GTCACCAGGCTGGAGGGCAGTG 71998        A        GA
             G                    CCACTGC CTCCAGCCTGG  GAC
                                 ||||||| ||||||||||  |||
                                 GGTGACG GAGGTCGGACC  CTG
                                     G         A_
GAM1645 LOC93408 5' GTCGCCCAGGCTGGAGCGCAAT 57289     C  A         A
             GG                    CCA TGC CTCCAGCCTGGG GAC
                                 ||| ||| ||||||||||| |||
                                 GGT ACG GAGGTCGGACCC CTG
                                   A  C          G
GAM1645 LOC93613 5' TCCTGGCTTCTGGGCACAATGG 73083     C  CA   C__    T
                                 CCA TG  CTC   AGCC GGGA
                                 ||| ||  |||   |||| ||||
                                 GGT AC  GGG   TCGG TCCT
                                   A  AC   TCT   _
GAM1646 ARHGAP6  5' CCAGGCTACCGCCTCCTGGACC 8610          A  CAGCC
                                 GGTCCAGGA GC    AGCTTGG
                                 |||||||| ||    |||||||
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                                CCAGGTCCT CG    TCGGACC
                                    C  CCA__
GAM1646  ESRRA    3'  CCAAGCAGACTCCAGCCCCTGG 16718        AA  C__  CCA
              ACC                  GGTCCAGG  GC   AG   GCTTGG
                                |||||||| ||   ||  ||||||
                                CCAGGTCC  CG   TC   CGAACC
                                    C_  ACC  AGA
GAM1646  GSTM5    3'  AGCCTGACTCCCTGGACC    7798         A  C   CCA
                                GGTCCAGG AG CAG   GCT
                                |||||||| || |||   |||
                                CCAGGTCC TC GTC   CGA
                                    C  A   ___
GAM1646  JRK      3'  CCAAGCCAAGGCATGTCCCTGG 87818        AA  CA   A__
              GCC                  GGTCCAGG  GC  GCC   GCTTGG
                                |||||||| ||  |||   ||||||
                                CCGGGTCC  TG  CGG   CGAACC
                                    C_  TA   AAC
GAM1646  LMO2     5'  CCAAGAGGCCCAGCCCTCCAAA 19934     CCA   A_  CA_   AG
              CC                   GGT   GGA  GC   GCC  CTTGG
                                |||   |||  ||   |||  |||||
                                CCA   CCT  CG   CGG  GAACC
                                  AA_   CC  ACC   A_
GAM1646  MPP2     3'  CAAAGCTGGCCCCTGAACC   60515     C    AA     CAGC
                                GGT CAGG  GCCAGC    TTG
                                ||| ||||  ||||||    |||
                                CCA GTCC  CGGTCG    AAC
                                  A   C_     A___
GAM1646  PLAU     3'  CTGGGTGCTGGCTGCCCAGACC 69542      CA  A      CA   TG
                                GGTC  GG AGCCAGC  GCT  G
                                ||||  || |||||||  |||  |
                                CCAG  CC TCGGTCG  TGG  C
                                  AC  G      __   GT
GAM1646  RPH3AL   3'  CCAAGCTGGGAGCTCCTGGGCC 23731         A  CAG
                                GGTCCAGGA GC   CCAGCTTGG
                                |||||||| ||   |||||||||
                                CCGGGTCCT CG   GGTCGAACC
                                    _  AG_
GAM1646  SFTPA2   3'  CCAAACCCATCTTCCTGGACC  23626          CCAGCCAGC
                                GGTCCAGGAAG        TTGG
                                ||||||||||        ||||
                                CCAGGTCCTTC        AACC
                                      TACCCA___
GAM1646  TAL1     3'  CAAGCTGGCTGGGGTGGCC    13523    T   GGAAG
                                GG CCA     CCAGCCAGCTTG
                                || |||     ||||||||||||
                                CC GGT     GGTCGGTCGAAC
                                  _  GG___
GAM1646  VCP      3'  AGTGAGCTGGCCTGCCTGGACC 75886        AA_     CA
                                GGTCCAGG   GCCAGC  GCT
                                ||||||||   ||||||  |||
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                                CCAGGTCC  CGGTCG  TGA
                                    GTC    AG
GAM1646 AP4S1   3' CCATCCTCTGACTTCCTGGGCC 23964         C  CC  CT
                                GGTCCAGGAAG CAG  AG  TGG
                                |||||||||| ||| || |||
                                CCGGGTCCTTC GTC  TC  ACC
                                     A  __ CT
GAM1646 BART1   3' CCAAAATGACCTAACCCTCCTG 25036        AGCC_ C_ GC
           GACC                 GGTCCAGGA   AG  CA  TTGG
                                |||||||||   || ||  ||||
                                CCAGGTCCT   TC  GT  AACC
                                     CCCAA  CA  AA
GAM1646 CIB1    3' CCAAGCTGGCCCAGCCTGGAGC 22122   G    AAGCCA
                                G TCCAGG    GCCAGCTTGG
                                | ||||||    ||||||||||
                                C AGGTCC    CGGTCGAACC
                                 G    GACC__
GAM1646 CRA     3' CCAAGCTTCATGGTTCCTGGAC 22934         G  GCC
           C                     GGTCCAGGAA CCA  AGCTTGG
                                |||||||||| |||  |||||||
                                CCAGGTCCTT GGT  TCGAACC
                                     _  ACT
GAM1646 DKFZP434C128 3' CTGGCTGGCCTTCCTGGACC  65469         _
                                GGTCCAGGAAG CCAGCCAG
                                |||||||||| ||||||||
                                CCAGGTCCTTC GGTCGGTC
                                     C
GAM1646 FAM10A6  5' CAAGCCAGCACCTGGGCC   72781       AAGCCA  CA
                                GGTCCAGG    GC  GCTTG
                                ||||||||    ||  |||||
                                CCGGGTCC    CG  CGAAC
                                    A_____  AC
GAM1646 FLJ00024 3' CCTGGGGGCCGGCCACCTGGAC 64493       AA  A  AG  T
           C                     GGTCCAGG  GCC GCC  CT GG
                                |||||||  ||| |||  || ||
                                CCAGGTCC  CGG CGG  GG CC
                                    AC  C  G_  T
GAM1646 FLJ10052 3' CCAGGAGGCTGGCCTCCCAGCC 36247    CCA  A    AG
                                GGT  GGA GCCAGCC  CTTGG
                                |||  ||| |||||||  |||||
                                CCG  CCT CGGTCGG  GGACC
                                  AC_  C     A_
GAM1646 FLJ11181 3' TTGGCTGGCTCCCCGAAGCC  37719    CCA  A_
                                GGT  GG  AGCCAGCCAG
                                |||  ||  ||||||||||
                                CCG  CC  TCGGTCGGTT
                                  AAG  CC
GAM1646 FLJ13769 3' CCAAGCCACTCTCAGCTTCCTG 47248    TC     C_  CCA_
           ATCC                   GG  CAGGAAGC  AG   GCTTGG
                                || ||||||||  ||   ||||||
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                                CC  GTCCTTCG  TC    CGAACC
                                 TA       AC  TCAC
GAM1646  FLJ20450  3'  CCACGCCCGGGCCCCTGGACC  35638        AA   AGCCA  T
                                GGTCCAGG  GCC    GC TGG
                                ||||||||  |||    || |||
                                CCAGGTCC  CGG    CG ACC
                                    C_   GCC__  C
GAM1646  FLJ20542  3'  CCAAGGTGCTGCTGGTCTCCTG 50744         AG    __  G
            GACC                  GGTCCAGGA  CCAGC  CA CTTGG
                                ||||||||||  |||||  || |||||
                                CCAGGTCCT  GGTCG  GT GAACC
                                    CT    TC  G
GAM1646  FLJ21195  3'  CTGCTGGTCCCTGGACC     42703        AA     C
                                GGTCCAGG  GCCAGC AG
                                ||||||||  |||||| ||
                                CCAGGTCC  TGGTCG TC
                                    C_     _
GAM1646  FLJ21977  3'  CTGTAGCTGGCTCCCTAGCC   50869     CC   A      __
                                GGT  AGG AGCCAGC  CAG
                                |||  ||| |||||||  |||
                                CCG  TCC TCGGTCG  GTC
                                  A_   C      AT
GAM1646  FLJ22056  5'  CCAAGCTGGCCAGCGCCGACC  42831      CA  AA  CA
                                GGTC  GG  GC  GCCAGCTTGG
                                ||||  ||  ||  ||||||||||
                                CCAG  CC  CG  CGGTCGAACC
                                  __  G_  AC
GAM1646  FLJ22678  3'  CAAGCTGGCCCACTGGTCC   61116    T   GAAGCCA
                                GG CCAG      GCCAGCTTG
                                || ||||      |||||||||
                                CC GGTC      CGGTCGAAC
                                 T   ACC____
GAM1646  HUMNPIIY20 3'  GCCGCCTTCCTGGACC      84322          CCA  CA
                                GGTCCAGGAAG   GC  GC
                                ||||||||||   ||  ||
                                CCAGGTCCTTC   CG  CG
                                      ___  C_
GAM1646  JFC1     3'  CCAAGCCTCTCTCTCTGGACC  52838       GA  CC  CCA
                                GGTCCAG  AG  AG   GCTTGG
                                |||||||  ||  ||   ||||||
                                CCAGGTC  TC  TC   CGAACC
                                    TC  TC  ___
GAM1646  KIAA0337  3'  CCTCTACCTGACCCCCTGGACC 29476        AAGC   CC  CTT
                                GGTCCAGG    CAG  AG   GG
                                ||||||||    |||  ||   ||
                                CCAGGTCC    GTC  TC   CC
                                    CCCA   CA  T__
GAM1646  KIAA1000  3'  CCAGAGACAGCTCCCTGGACC  65880        A   CAGCCAG  _
                                GGTCCAGG AGC      CT TGG
                                |||||||| |||      || |||
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                                CCAGGTCC TCG      GA ACC
                                    C   ACA____  G
GAM1646  MGC11242  3'  CCTGTGACTACTCCCTGGACC  44482        A  CC  CCA  TT
                                GGTCCAGG AG  AG   GC  GG
                                |||||||| ||  ||   ||  ||
                                CCAGGTCC TC  TC   TG  CC
                                    C  A_  AG_  T_
GAM1646  MGC12679  3'  CCAAGCTGGCCGGCCCTAGCC  52183     CC   AA   A
                                GGT  AGG  GCC GCCAGCTTGG
                                |||  |||  ||| ||||||||||
                                CCG  TCC  CGG CGGTCGAACC
                                  A_  __   C
GAM1646  MGC19556  5'  GGACACTGGATTCCTGGACC   54341         G   ___
                                GGTCCAGGAA CCAG   CC
                                |||||||||| ||||   ||
                                CCAGGTCCTT GGTC   GG
                                     A    ACA
GAM1646  NCKX3     3'  CCAAGCCGGCCCAGCTGCACC  40724     C   GAAGCCA   A
                                GGT CAG      GCC GCTTGG
                                ||| |||      ||| |||||||
                                CCA GTC      CGG CGAACC
                                  C   GACC___   C
GAM1646  ORCTL4    3'  CTGAGGGCCAGGCCCCCAGACC 17833      CA  AA   A_   AG  TG
                                GGTC  GG  GCC  GCC  CT  G
                                ||||  ||  |||  |||  ||  |
                                CCAG  CC  CGG  CGG  GA  C
                                  A_  CC   AC   __  GT
GAM1646  P2RXL1    3'  CCAAGCTCTGCTCCCTGGATC  19557        A   C  CC
                                GGTCCAGG AGC AG  AGCTTGG
                                |||||||| ||| ||  |||||||
                                CTAGGTCC TCG TC  TCGAACC
                                    C   _  __
GAM1646  PINK1     3'  CCAAGCTGTGCGTTCTGGACC  51563         A  CAGC
                                GGTCCAGGA GC    CAGCTTGG
                                |||||||||  ||    ||||||||
                                CCAGGTCTT CG    GTCGAACC
                                     G  T___
GAM1646  QSCN6     3'  CCAGCCTCCAGCTCCTCAGACC 12567      C_   A  CAGCCA   T
                                GGTC  AGGA GC      GCT GG
                                ||||  |||| ||      ||| ||
                                CCAG  TCCT CG      CGA CC
                                  AC    _  ACCTC_   _
GAM1646  RNF40     3'  CCAAGGCTCTACTGGGTCCCTG 29363         AAG    CC_  _
           GACC                  GGTCCAGG   CCAG   AGC TTGG
                                ||||||||   ||||   ||| ||||
                                CCAGGTCC   GGTC   TCG AACC
                                    CTG    ATC   G
GAM1646  TREX1     5'  CCACTCTGCCAGCTTCCTGGAG 54380    G        CA  C  CT
           C                    G TCCAGGAAGC  GC AG  TGG
                                | ||||||||||  || ||  |||
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                                C AGGTCCTTCG  CG TC  ACC
                                 G         AC  _  TC
GAM1646  TREX1     5'  CCACTCTGCCAGCTTCCTGGAG 54387    G         CA  C  CT
              C                   G TCCAGGAAGC  GC AG  TGG
                                | ||||||||||  || ||  |||
                                C AGGTCCTTCG  CG TC  ACC
                                 G         AC  _  TC
GAM1646  LOC115574 3'  CCAGCCCCTGGCTTCCTGACC  73848      C         CCA   T
                                GGTC AGGAAGCCAG   GCT GG
                                |||| ||||||||||   ||| ||
                                CCAG TCCTTCGGTC   CGA CC
                                  _         CC_  _
GAM1646  LOC126695 3'  CTGACTGGGTTCCTGGACC    75957           G    C
                                GGTCCAGGAA CCAG CAG
                                |||||||||| |||| |||
                                CCAGGTCCTT GGTC GTC
                                      G    A
GAM1646  LOC149345 3'  CAAGCCAAGCCCTGGGCC     80081         AA  CAGCCA
                                GGTCCAGG  GC      GCTTG
                                ||||||||  ||      |||||
                                CCGGGTCC  CG      CGAAC
                                     __  AAC____
GAM1646  LOC149559 5'  CAACTGGCCGGCTTCCTGGCC  80253    T         A     C
                                GG CCAGGAAGCC GCCAG TTG
                                || |||||||||| ||||| |||
                                CC GGTCCTTCGG CGGTC AAC
                                  _         C     _
GAM1646  LOC160717 5'  CCAAGGAGAAGCTCCCTGGGCC 83128         A   CAGCCAG
                                GGTCCAGG AGC       CTTGG
                                |||||||| |||       |||||
                                CCGGGTCC TCG       GAACC
                                     C   AAGAG__
GAM1646  LOC163412 5'  CAGCCCCGCTTCCTGGACC    83011           CAGCCA   T
                                GGTCCAGGAAGC      GCT G
                                ||||||||||||      ||| |
                                CCAGGTCCTTCG      CGA C
                                       CCC___   _
GAM1646  LOC164633 3'  TTGGCCGGCTCCCTGGGCC    83425         A    A
                                GGTCCAGG AGCC GCCAG
                                |||||||| |||| |||||
                                CCGGGTCC TCGG CGGTT
                                     C    C
GAM1646  LOC200925 3'  CAACTGGCCGGCTTCCTGGCC  90374    T         A     C
                                GG CCAGGAAGCC GCCAG TTG
                                || |||||||||| ||||| |||
                                CC GGTCCTTCGG CGGTC AAC
                                  _         C     _
GAM1646  LOC221143 3'  CCAAACTGGAGCTGTCCCTGGC 95213    T    A__   CAG    C
              C                   GG CCAGG   AGC   CCAG TTGG
                                || |||||   |||   |||| ||||
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                                CC GGTCC   TCG   GGTC AACC
                                 _    CTG   A__    A
GAM1646  LOC256594 5'  CCAAACTTGGCTTCCTAGCC   98859     CC       GCC  C
                                GGT  AGGAAGCCA   AG TTGG
                                |||  |||||||||   || ||||
                                CCG  TCCTTCGGT   TC AACC
                                  A_       ___  A
GAM1646  LOC256789 3'  TGGACTGGCCTCCTGGACC    99313         A    _
                                GGTCCAGGA GCCAG CCA
                                ||||||||| ||||| |||
                                CCAGGTCCT CGGTC GGT
                                      C    A
GAM1647  ABR      3'  AGCGTCGTTTCCGGGCCCTCA  41993      A      CAC    C
                                TGAG GCCTGGAA   ATGAC CT
                                |||| ||||||||   ||||| ||
                                ACTC CGGGCCTT   TGCTG GA
                                  C       ___    C
GAM1647  DIAPH2    5'  CGTGTGTTGAGGCCCTC     23003     A   G  A
                                GAG GCCT GA CACATG
                                ||| |||| || ||||||
                                CTC CGGA TT GTGTGC
                                  C   G  _
GAM1647  MBL2     3'  AGGGTCATATCACTCAGGCCCT 5909      A     AACAC
             C                   GAG GCCTGG    ATGACCCT
                                ||| ||||||    ||||||||
                                CTC CGGACT    TACTGGGA
                                  C     CACTA
GAM1647  PFKFB4    3'  GGGGTCATTCCAGGCCCTC    17088     A      ACAC
                                GAG GCCTGGA    ATGACCCT
                                ||| |||||||    ||||||||
                                CTC CGGACCT    TACTGGGG
                                  C     ____
GAM1647  ARHGAP9   5'  TCTTGTGCCTCAGGCTCCCA   51663    A      AA    T
                                TG GAGCCTGG  CACA GA
                                || ||||||||  |||| ||
                                AC CTCGGACT  GTGT CT
                                 C       CC    T
GAM1647  C8orf14   5'  AGGAAGCTGTTCCAGGCCTCA  55081      A        CATGAC
                                TGAG GCCTGGAACA     CCT
                                |||| ||||||||||     |||
                                ACTC CGGACCTTGT     GGA
                                  _        CGAA__
GAM1647  CLDN6     3'  GTGTTGACTCAGACTCTCA    41337       C    ___
                                TGAGAG CTGG   AACAC
                                ||||||| ||||   |||||
                                ACTCTC GACT   TTGTG
                                   A   CAG
GAM1647  CLIPR-59  3'  GGATATGCATTCCAGGCTCCCA 32019    A        CA    A
                                TG GAGCCTGGAA  CATG CC
                                || ||||||||||  |||| ||
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                                AC CTCGGACCTT  GTAT GG
                                 C        AC   A
GAM1647  CMG2     3'  GTCATGTGTCCACACATTCA   55200     AGCC   A
                                TGAG   TGGA CACATGAC
                                ||||   |||| ||||||||
                                ACTT   ACCT GTGTACTG
                                  ACAC   _
GAM1647  DKFZp434D177 5'  AGGTTCCTGGTGACCCAGGCTC 51068          AA  AT_  C
           TCA                    TGAGAGCCTGG  CAC   GA CCT
                                ||||||||||  |||   || |||
                                ACTCTCGGACC  GTG   CT GGA
                                      CA   GTC  T
GAM1647  FLJ14440  3'  GTCATGTGTTTTCTTTCTCA   52370      CCT
                                TGAGAG   GGAACACATGAC
                                ||||||   ||||||||||||
                                ACTCTT   TTTTGTGTACTG
                                   TC_
GAM1647  KIAA1701  5'  AGGGCCATATAACTGGGCTTCA 68428     G   TG AACAC   A
                                TGA AGCC  G    ATG CCCT
                                ||| ||||  |    ||| ||||
                                ACT TCGG  C    TAC GGGA
                                  _   GT AATA_   C
GAM1647  KIAA1855  3'  AGGGGCTGTGCCCCAGGCTC   93946       AA   TGA
                                GAGCCTGG  CACA   CCCT
                                ||||||||  ||||   ||||
                                CTCGGACC  GTGT   GGGA
                                     CC    CG_
GAM1647  MRVI1    5'  AGGGTCTTCTCCAGGCTC    56093        ACACAT
                                GAGCCTGGA     GACCCT
                                |||||||||     ||||||
                                CTCGGACCT     CTGGGA
                                      CTT___
GAM1647  TRIM35   3'  AGGGCCACATGTTCCAGG    61513        CA  A
                                CCTGGAACA  TG CCCT
                                |||||||||  || ||||
                                GGACCTTGT  AC GGGA
                                      AC  C
GAM1647  LOC126767 3'  GGGGCAGTTCAGGCTCCCA   75961    A     G   ACA  A
                                TG GAGCCTG AAC   TG CCC
                                || ||||||| |||   || |||
                                AC CTCGGAC TTG   AC GGG
                                 C      _  ___  G
GAM1647  LOC133686 3'  GTCATGTGTTTCTTTCA     75620       CCTG
                                TGAGAG   GAACACATGAC
                                ||||||   ||||||||||||
                                ACTTTC   TTTGTGTACTG
                                     ____
GAM1647  LOC143308 5'  AGGCAGTCATCCCAGGCTCCA  83833    A      AACAC    __
                                TG GAGCCTGG    ATGAC  CCT
                                || ||||||||    |||||  |||
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                                AC CTCGGACC    TACTG  GGA
                                 _      C____    AC
GAM1647  LOC149910 3'  AGGGCCTCTGCCCAGGCTCTC  80354         AA  CATGA
                                GAGAGCCTGG  CA    CCCT
                                ||||||||||  ||    ||||
                                CTCTCGGACC  GT    GGGA
                                     C_  CTCC_
GAM1647  LOC200301 3'  CATGCTGTGGCTCTCA     90135        TGGA  _
                                TGAGAGCC    ACA CATG
                                ||||||||    ||| ||||
                                ACTCTCGG    TGT GTAC
                                     _____  C
GAM1647  LOC256957 3'  ATGCTTCTCAGGCTCCCA    96827    A     _  CA
                                TG GAGCCTG GAA  CAT
                                || ||||||| |||  |||
                                AC CTCGGAC CTT  GTA
                                 C      T   C_
GAM1647  LOC91266  5'  AGGGTCCCTTCTAGGCTCCCA  66019    A        CACAT
                                TG GAGCCTGGAA    GACCCT
                                || ||||||||||    ||||||
                                AC CTCGGATCTT    CTGGGA
                                 C        CC___
GAM1648  CDH12     3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM1648  GOCAP1    3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM1648  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090       T    AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                   _   GTCA_
GAM1648  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
            A                    TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM1648  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM1648  HMP19     3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
            TA                    TACA   TCC   GAAGAATAAG
                                ||||   |||   ||||||||||
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                              ATGT   AGG   TTTCTTATTC
                                AAA_  ATTG
GAM1648 KIAA1719 3' TCTGTCTTGGGAGTGGTGTA  68742           _
                              TACACCACTCCCAAGA AGA
                              |||||||||||||||| |||
                              ATGTGGTGAGGGTTCT TCT
                                       G
GAM1648 KIAA1853 3' TTTTTCTTGGAAGCAGTG   69929    CA  C
                              CAC  CT CCAAGAAGAA
                              |||  || ||||||||||
                              GTG  GA GGTTCTTTTT
                                AC  A
GAM1648 KIAA1877 3' CTTATTCTTCTGCCATGAGT  66748     CCA__
                              ACTC    AGAAGAATAAG
                              ||||    ||||||||||
                              TGAG    TCTTCTTATTC
                                TACCG
GAM1648 KIAA1906 3' CTTATTCTTCTTGACTTTTGG 73571    CTCC_
                              CCA    CAAGAAGAATAAG
                              |||    ||||||||||||
                              GGT    GTTCTTCTTATTC
                                TTTCA
GAM1648 OSBPL11  3' CTTAATTTCCCAAGAGTGGTG 43206       CCAA   AA
                              CACCACTC   GAAG  TAAG
                              ||||||||   ||||  ||||
                              GTGGTGAG   CTTT  ATTC
                                   AACC   A_
GAM1648 YME1L1   3' TCATTCTTGATGTGGTGTA   58438       TCC    _
                              TACACCAC   CAAGAA GA
                              ||||||||   ||||||  ||
                              ATGTGGTG   GTTCTT CT
                                   TA_    A
GAM1648 ZNF262   3' CTTATTTTGTTTGGGAGT    18723        A
                              ACTCCCAAG AGAATAAG
                              ||||||||| ||||||||
                              TGAGGGTTT TTTTATTC
                                   G
GAM1648 LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_    AAGA
                              TACACCAC   CCAAG   ATA
                              ||||||||   |||||   |||
                              ATGTGGTG   GGTTC   TGT
                                   CAA    GG__
GAM1649 SCAMP1   3' GCTAAATAAATATTCTCC    54500    T    C
                              GGA AATATT ATTTAGC
                              ||| |||||| |||||||
                              CCT TTATAA TAAATCG
                                C    A
GAM1649 SCAMP1   3' GCTAAATAAATATTCTCC    54501    T    C
                              GGA AATATT ATTTAGC
                              ||| |||||| |||||||
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                                CCT TTATAA TAAATCG
                                  C     A
GAM1649  NX-17    3'  TGAATATCAGCCCCTAATA   40706        ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM1649  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
           TA                    TATTAGGGATAATATTCATTTAGC
                                 ||||||||||||||||||||||||
                                 ATAATCCCTATTATAAGTAAATCG

GAM1650  ABCE1    5'  GGGGATCGTTTTCTCCAGA   60261         C  CTG
                                TCTGGAGAAA TG   CCTC
                                |||||||||| ||   ||||
                                AGACCTCTTT GC   GGGG
                                      T  TA_
GAM1650  AKAP13   3'  TGAGGCAGCTGCCTCCTGA   91257    T    AAACT
                                TC GGAG    GCTGCCTCA
                                || ||||    |||||||||
                                AG CCTC    CGACGGAGT
                                 T   CGT__
GAM1650  ALOX12B  5'  GGGCAGCAGCTTTTCCAGA   8537          A
                                TCTGGAGAA CTGCTGCCT
                                ||||||||| |||||||||
                                AGACCTTTT GACGACGGG
                                      C
GAM1650  BCL7A    3'  GAGGCGGCGTTACCTCCAGA   40984        A_   T
                                TCTGGAG  AAC GCTGCCTC
                                |||||||  ||| ||||||||
                                AGACCTC  TTG CGGCGGAG
                                    CA   _
GAM1650  CLDN3    3'  TGGGGCAGCTTCCCCAG     8961       A   ACT
                                CTGG GAA   GCTGCCTCA
                                |||| |||   |||||||||
                                GACC CTT   CGACGGGGT
                                  C   ____
GAM1650  CUTL1    3'  GAGCCCCAGTCTCTTCAGA   10348         A    CT  C
                                TCTGGAGA ACTG  GC TC
                                |||||||| ||||  || ||
                                AGACTTCT TGAC  CG AG
                                    C    CC  _
GAM1650  EFNA1    3'  TGGGGCAGCACTCCCCAGA   16666       A  AAC
                                TCTGG GA   TGCTGCCTCA
                                ||||| ||   ||||||||||
                                AGACC CT   ACGACGGGGT
                                  C  C__
GAM1650  EGR1     3'  TGAGCTTCGGTTCTCCAGA   10493         A   CT  C
                                TCTGGAGAA CTG  GC TCA
                                ||||||||| |||  || |||
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                                AGACCTCTT GGC  CG AGT
                                     _  TT  _
GAM1650  FLT1    3'  TGAGGAGAGTTTTCTCCA    10664       _  G  G
                                TGGAGAAA CT CT CCTCA
                                |||||||| || || |||||
                                ACCTCTTT GA GA GGAGT
                                    T  _  _
GAM1650  FRK     5'  AGCCGGTAAGTCTCTCCAGG  10715       A  _   C
                                TCTGGAGA ACT GCTG CT
                                |||||||| ||| |||| ||
                                GGACCTCT TGA TGGC GA
                                    C   A   C
GAM1650  GAB2    3'  GAGGCAGCATCTCCAGA    55405       AAC
                                TCTGGAGA  TGCTGCCTC
                                ||||||||  |||||||||
                                AGACCTCT  ACGACGGAG
                                     ___
GAM1650  GPC6    5'  AGGCAGCAGCCTTCCCAG    20329     A  A_
                                CTGG GAA  CTGCTGCCT
                                |||| |||  |||||||||
                                GACC CTT  GACGACGGA
                                  _  CC
GAM1650  GUCA2B  3'  TGAGGCAGCCCAGCTCCTGA  24020    T   AAACT
                                TC GGAG    GCTGCCTCA
                                || ||||    |||||||||
                                AG CCTC    CGACGGAGT
                                 T   GACC_
GAM1650  IL8RA   3'  TGAGGCAGGCACTGCCA     7153     _ AAAC  _
                                TGG AG   TGC TGCCTCA
                                ||| ||   ||| |||||||
                                ACC TC   ACG ACGGAGT
                                  G  ____  G
GAM1650  MADH6   5'  AGGCAGGGCTTTCCAGA     19972       AA TG
                                TCTGGAGA  C  CTGCCT
                                ||||||||  |  ||||||
                                AGACCTTT  G  GACGGA
                                     CG __
GAM1650  MYO7A   3'  GAGGCAGCAGTGGGTTCAGG  6032       GAA
                                TCTGGA  ACTGCTGCCTC
                                ||||||  ||||||||||
                                GGACTT  TGACGACGGAG
                                   GGG
GAM1650  NPY2R   3'  TGAACAGAAATTTCTCCAGG  8067        CTG  CC
                                TCTGGAGAAA  CTG  TCA
                                ||||||||||  |||  |||
                                GGACCTCTTT  GAC  AGT
                                      AAA  A_
GAM1650  OXTR    3'  TGAATAGACATTTCTCCA    8083        C  _  CC
                                TGGAGAAA TG CTG  TCA
                                |||||||| || |||  |||
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                                ACCTCTTT AC GAT  AGT
                                     _ A   A_
GAM1650  PPP2R4   3'  TGAGGCATGTCTTTCCAGA   61184        A  TGC
                                TCTGGAGA AC   TGCCTCA
                                |||||||| ||   |||||||
                                AGACCTTT TG   ACGGAGT
                                     C  T__
GAM1650  PRX      3'  GAGGCAGCCCTTCCAGA     40896       AAACT
                                TCTGGAG    GCTGCCTC
                                |||||||    ||||||||
                                AGACCTT    CGACGGAG
                                    CC___
GAM1650  REV3L    5'  TGAGGAAGATTTCTCTCA    12825    _     CTG  G
                                TG GAGAAA   CT CCTCA
                                || ||||||   || |||||
                                AC CTCTTT   GA GGAGT
                                 T     A__  A
GAM1650  SURF5    3'  TGAGGCAGCATTTCCTCCA   56919      A  C
                                TGGAG AA TGCTGCCTCA
                                ||||| || ||||||||||
                                ACCTC TT ACGACGGAGT
                                   C  T
GAM1650  VANGL2   3'  TGAGACATCGGACTCTCCGGA  72095        AA   C  C
                                TCTGGAGA  CTG TG CTCA
                                ||||||||  ||| || ||||
                                AGGCCTCT  GGC AC GAGT
                                     CA   T  A
GAM1650  WARS     3'  GAGGCAGCAGCCCTCGAGG   67865     G   AAA
                                TCT GAG   CTGCTGCCTC
                                ||| |||   ||||||||||
                                GGA CTC   GACGACGGAG
                                  G   CC_
GAM1650  ZNF45    5'  GACTTGGCACTTCTCCAGA   14250        AC    CC
                                TCTGGAGAA  TGCTG  TC
                                |||||||||  |||||  ||
                                AGACCTCTT  ACGGT  AG
                                     C_    TC
GAM1650  BLR1     3'  TGAGGCAGGGAAGTCCCCAGG  53119      A  AA_  G
                                TCTGG GA   CT CTGCCTCA
                                ||||| ||   || ||||||||
                                GGACC CT   GG GACGGAGT
                                   C  GAA  _
GAM1650  C20orf150 3'  TGAAGCCGAGCTCCTCCAGA   66017       AAACT  __  C
                                TCTGGAG    GCT  GC TCA
                                |||||||    |||  || |||
                                AGACCTC    CGA  CG AGT
                                    CT___   GC  A
GAM1650  C20orf4  3'  GGGCAGCAATCTCTCCAGG   31948        AAC
                                TCTGGAGA   TGCTGCCT
                                ||||||||   ||||||||
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                                GGACCTCT   ACGACGGG
                                    CTA
GAM1650  C20orf7   3'  TGAATATGCACCTTCTCCAGA  44383        AC   TGCC
                                TCTGGAGAA  TGC    TCA
                                |||||||||  |||    |||
                                AGACCTCTT  ACG    AGT
                                    CC   TATA
GAM1650  C6orf26   3'  AGAAAGCAGCTTTCTCCA    48268        _    GC
                                TGGAGAAA CTGCT  CT
                                |||||||| |||||  ||
                                ACCTCTTT GACGA  GA
                                    C    AA
GAM1650  CASKIN1   3'  TGAGGCGGATTTCCCCAGA   40784      A   CTG
                                TCTGG GAAA   CTGCCTCA
                                ||||| ||||   ||||||||
                                AGACC CTTT   GGCGGAGT
                                   C   A__
GAM1650  CCR8      3'  TGAGGCAGATGCCTCTAGA   19041       AAACTG
                                TCTGGAG     CTGCCTCA
                                |||||||     ||||||||
                                AGATCTC     GACGGAGT
                                    CGTA__
GAM1650  CPGL2     5'  GAAGCCGCTTTGTTCTCCAGA  74884        ACT_  T  C
                                TCTGGAGAA    GC GC TC
                                |||||||||    || || ||
                                AGACCTCTT    CG CG AG
                                     GTTT  C  A
GAM1650  CSRP2BP   5'  TGAAGCAGCAGTGGGACCAG   70657     AGAA      C
                                CTGG    ACTGCTGC TCA
                                ||||    |||||||| |||
                                GACC    TGACGACG AGT
                                  AGGG       A
GAM1650  DGKD      3'  TGAAACAACACTTTCTCCAG   60113        C  C  CC
                                CTGGAGAAA TG TG  TCA
                                ||||||||| || ||  |||
                                GACCTCTTT AC AC  AGT
                                     C  A  AA
GAM1650  DKFZP434A043 3'  TGAGGTAGTAATTTCCTCAGA  31823      GA    C
                                TCTG  GAAA TGCTGCCTCA
                                ||||  |||| ||||||||||
                                AGAC  CTTT ATGATGGAGT
                                  TC    A
GAM1650  DKFZP434P0111 3'  TGAGGGTGTCTTTCCAGA    67963        A  T  TG
                                TCTGGAGA AC GC  CCTCA
                                |||||||| || ||  |||||
                                AGACCTTT TG TG  GGAGT
                                     C  _  __
GAM1650  DKFZP586M1120 3'  TGAGGCAGCAGCTCCCAG    49287      A  AA
                                CTGG GA  CTGCTGCCTCA
                                |||| ||  ||||||||||
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                                GACC CT  GACGACGGAGT
                                  _  C_
GAM1650 ERG-1    3'  TGAGACATGTTTCTCCAGG   42102          TGC  C
                                TCTGGAGAAAC   TG CTCA
                                ||||||||||   || ||||
                                GGACCTCTTTG   AC GAGT
                                      T__  A
GAM1650 FASTK    3'  TGAGGCAGAAGCTCCAGG    22969       AAACTG
                                TCTGGAG     CTGCCTCA
                                |||||||     ||||||||
                                GGACCTC     GACGGAGT
                                   GAA___
GAM1650 FLJ14855 5'  GGTTCCCAGTTTTCCAGA    53766        A   CT_
                                TCTGGAGAA CTG   GCC
                                ||||||||| |||   |||
                                AGACCTTTT GAC   TGG
                                      _  CCT
GAM1650 FLJ20249 3'  TGAGGAGTCCCTCCCAGA    80223      A  AACT   G
                                TCTGG GA    GCT CCTCA
                                ||||| ||    ||| |||||
                                AGACC CT    TGA GGAGT
                                  _  CCC_  _
GAM1650 FLJ20730 3'  TGAAGAAGCAGTTTCTCAGA   36053     G        GCC
                                TCTG AGAAACTGCT   TCA
                                |||| ||||||||||   |||
                                AGAC TCTTTGACGA   AGT
                                  _        AGA
GAM1650 FLJ21007 5'  TGAAGCTTGCACAAGCTCTCCA 48648        AAC__   T_  C
           GA                    TCTGGAGA    TGC  GC TCA
                                ||||||||    |||  || |||
                                AGACCTCT    ACG  CG AGT
                                     CGAAC   TT  A
GAM1650 GPT2     3'  TGAGGCAGCAGCCTCTA     56772      AAA
                                TGGAG   CTGCTGCCTCA
                                |||||   ||||||||||
                                ATCTC   GACGACGGAGT
                                  C__
GAM1650 KIAA0542 3'  GGGGCAGCTCCTCCAGG     66665       AAACT
                                TCTGGAG    GCTGCCTC
                                |||||||    ||||||||
                                GGACCTC    CGACGGGG
                                   CT___
GAM1650 KIAA0652 3'  TGAGGCAGCAATCTTTGG    29125   TG   AAC
                                C  GAGA   TGCTGCCTCA
                                |  ||||   ||||||||||
                                G  TTCT   ACGACGGAGT
                                 GT   A__
GAM1650 KIAA1026 3'  GAGACGGCTTTTTCCA      71738        CT   C
                                TGGAGAAA  GCTG CTC
                                ||||||||  |||| |||
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                                ACCTTTTT  CGGC GAG
                                    __    A
GAM1650  KIAA1030  3'  GAGGCAGCAGTGAGCCGAGA   94981     _  AGAA
                                TCT GG    ACTGCTGCCTC
                                ||| ||    ||||||||||
                                AGA CC    TGACGACGGAG
                                  G  GAG_
GAM1650  KIAA1086  3'  TGAGGCAGGGGGTCCCCA    71291     A  AA  G
                                TGG GA  CT CTGCCTCA
                                ||| ||  || ||||||||
                                ACC CT  GG GACGGAGT
                                  C  GG  _
GAM1650  KIAA1322  3'  TGAGATAGTTTTTCCAGA    73118           CTGC
                                TCTGGAGAAACTG    CTCA
                                ||||||||||||    ||||
                                AGACCTTTTTGAT    GAGT
                                       A___
GAM1650  KIAA1634  3'  GCATCAGTCTCTTCTCCAGA   64124         ___    C
                                TCTGGAGAA   ACTG TGC
                                |||||||||   |||| |||
                                AGACCTCTT   TGAC ACG
                                     CTC    T
GAM1650  KIAA1638  3'  TGAAACAACGGTGACCTCTCCA 47824         A___    C  CC
           GG                     TCTGGAGA    ACTG TG  TCA
                                |||||||    |||| ||  |||
                                GGACCTCT    TGGC AC  AGT
                                     CCAG    A  AA
GAM1650  KIAA1771  5'  GGGTTACCAGACCTCTCCAGA  79866         AA_   CT_
                                TCTGGAGA   CTG   GCCT
                                ||||||||   |||   ||||
                                AGACCTCT   GAC   TGGG
                                     CCA   CAT
GAM1650  KIAA1831  5'  GGAGCAGTCTCTCCGGA     64525         A     G
                                TCTGGAGA ACTGCT CC
                                |||||||| |||||| ||
                                AGGCCTCT TGACGA GG
                                     C     _
GAM1650  KIAA1894  3'  GAGGCAACCTTTGCCTTCTTCA 74285         ACT _______
           GA                     TCTGGAGAA   GC     TGCCTC
                                |||||||||   ||     ||||||
                                AGACTTCTT   CG     ACGGAG
                                     C__  TTTCCA
GAM1650  KIAA1937  3'  GAGGCAGTGTCCCCCAGG    74071       AGAA  T
                                TCTGG    AC GCTGCCTC
                                |||||    || ||||||||
                                GGACC    TG TGACGGAG
                                   CCC_  _
GAM1650  KIAA1985  3'  TGAAAAGCACTTTCTCCA     45018         C    GCC
                                TGGAGAAA TGCT   TCA
                                |||||||| ||||   |||
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                                ACCTCTTT ACGA   AGT
                                    C    AA_
GAM1650 LCHN     3' TGAGATGCTTTCTCCAGA    87480        CT  TGC
                                TCTGGAGAAA  GC   CTCA
                                ||||||||||  ||   ||||
                                AGACCTCTTT  CG   GAGT
                                     __  TA_
GAM1650 MGC13007 3' CAGTTCAGTTATCTCCAGA   51277        _    __
                                TCTGGAGA AACTG  CTG
                                |||||||| |||||  |||
                                AGACCTCT TTGAC  GAC
                                    A    TT
GAM1650 MGC16385 5' TGAAGCAGCAGCTGGGCTAGG 59543      AGAAA      C
                                TCTGG    CTGCTGC TCA
                                |||||    ||||||| |||
                                GGATC    GACGACG AGT
                                   GGGTC      A
GAM1650 MGC26914 3' TGAATAGACATTTCTCCA    59332        C  _   CC
                                TGGAGAAA TG CTG  TCA
                                |||||||| || |||  |||
                                ACCTCTTT AC GAT  AGT
                                    _ A   A_
GAM1650 PSKH1    3' AGGCTCCAGCCTCTCCAGA   68791        AA   CT
                                TCTGGAGA  CTG  GCCT
                                ||||||||  |||  ||||
                                AGACCTCT  GAC  CGGA
                                    CC   CT
GAM1650 SEMA4G   5' GGGCAGCTGTCTCCAGA     35860        AACT
                                TCTGGAGA    GCTGCCT
                                ||||||||    |||||||
                                AGACCTCT    CGACGGG
                                    GT__
GAM1650 SPAF     3' TGAAGCGATTTCTTTTTCCAGA 83521         CTGC_   C
                                TCTGGAGAAA     TGC TCA
                                ||||||||||     ||| |||
                                AGACCTTTTT     GCG AGT
                                     CTTTA   A
GAM1650 SUN1     3' TGAGTTTCCCAGTTTCTACAGA 47926      G       CTGC_
                                TCTG AGAAACTG     CTCA
                                |||| ||||||||     ||||
                                AGAC TCTTTGAC     GAGT
                                  A       CCTTT
GAM1650 USP24    3' TGAAAATGCTGTGTTCTCCAGA 92795         _  T  TGCC
                                TCTGGAGAA AC GC    TCA
                                ||||||||| || ||    |||
                                AGACCTCTT TG CG    AGT
                                     G  T  TAAA
GAM1650 LOC123096 3' TGAGGCAGACACTCCAG     74654        AAAC  _
                                CTGGAG    TG CTGCCTCA
                                ||||||    || ||||||||
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                                GACCTC    AC GACGGAGT
                                   ____  A
GAM1650  LOC129831 5'  TGAGACAGCAGCGGTGGCAGA  75398     GAGAA      ___
                                TCTG    ACTGCTGC   CTCA
                                ||||    ||||||||  ||||
                                AGAC    TGGCGACG   GAGT
                                  GG___       ACA
GAM1650  LOC134637 3'  TGAGAACACCTTCTCCAGG   75693        AC  CTGC
                                TCTGGAGAA  TG   CTCA
                                |||||||||  ||   ||||
                                GGACCTCTT  AC   GAGT
                                     CC  AA__
GAM1650  LOC146420 3'  TGAACTTCCAGATTCTCCAGA  84653        A   CTGCC
                                TCTGGAGAA CTG    TCA
                                ||||||||| |||    |||
                                AGACCTCTT GAC    AGT
                                     A   CTTCA
GAM1650  LOC147711 5'  TGAGCAGGCAAGTCTCTTCAGA 79117        A  _   GC
                                TCTGGAGA ACT GCT  CTCA
                                |||||||| ||| |||  ||||
                                AGACTTCT TGA CGG  GAGT
                                     C   A   AC
GAM1650  LOC148753 3'  TGAGACTCCATTTTCTCCAGG  85373        C  CTGC
                                TCTGGAGAAA TG   CTCA
                                |||||||||| ||   ||||
                                GGACCTCTTT AC   GAGT
                                      T  CTCA
GAM1650  LOC150290 3'  TGAGGCAGATGGTGCCCAGA   80592      AGAA   _
                                TCTGG   ACTG CTGCCTCA
                                |||||   |||| ||||||||
                                AGACC   TGGT GACGGAGT
                                   CG__   A
GAM1650  LOC153218 5'  TGAAATAGAACTTTTCCAGA   81658        ACTG   CC
                                TCTGGAGAA   CTG  TCA
                                |||||||||   |||  |||
                                AGACCTTTT   GAT  AGT
                                     CAA_   AA
GAM1650  LOC157570 5'  TGAGGCTTTTTCTTCAGA    82397         CTGCT
                                TCTGGAGAAA    GCCTCA
                                ||||||||||    ||||||
                                AGACTTCTTT    CGGAGT
                                      TT___
GAM1650  LOC197259 5'  TGAGGCAGTGGCCTCCGGA   89304       AAA TG
                                TCTGGAG   C  CTGCCTCA
                                |||||||   |  ||||||||
                                AGGCCTC   G  GACGGAGT
                                    C__ GT
GAM1650  LOC199923 3'  TGAGTTAGCCAGTTTCTTCAGA 89879          _  C
                                TCTGGAGAAACTG CTG CTCA
                                |||||||||||| ||| ||||
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                                AGACTTCTTTGAC GAT GAGT
                                      C   T
GAM1650  LOC200940 3'  TGAGGCAGGCGGATCTCCTGA  90398    T    AA   _
                                TC GGAGA  CTGC TGCCTCA
                                || |||||  |||| |||||||
                                AG CCTCT  GGCG ACGGAGT
                                 T    A_   G
GAM1650  LOC201685 3'  AGGAGCTATTTTCCAGA     91834         ACT   G
                                TCTGGAGAA   GCT CCT
                                |||||||||   ||| |||
                                AGACCTTTT   CGA GGA
                                      AT_  _
GAM1650  LOC205327 3'  AGTCAATGTTTCTCCAGA    91067          TGC  C
                                TCTGGAGAAAC   TG CT
                                ||||||||||   || ||
                                AGACCTCTTTG   AC GA
                                       TA_  T
GAM1650  LOC221288 3'  TGAAGCAGCAGTATCTAGA   95264       GAA       C
                                TCTGGA   ACTGCTGC TCA
                                ||||||   |||||||| |||
                                AGATCT   TGACGACG AGT
                                   A__       A
GAM1650  LOC222057 3'  AGGTCAGCCTCTCCAGG     94345        AACT   _
                                TCTGGAGA    GCTG CCT
                                ||||||||    |||| |||
                                GGACCTCT    CGAC GGA
                                     C___    T
GAM1650  LOC253254 5'  TGAGAAGAACTTCTTCAGA   98908         ACTG  GC
                                TCTGGAGAA    CT  CTCA
                                |||||||||    ||  ||||
                                AGACTTCTT    GA  GAGT
                                      CAA_  A_
GAM1650  LOC256789 3'  TGAGGCTGTACTCTCTAGA   99312        AAC   T
                                TCTGGAGA   TGC GCCTCA
                                ||||||||   ||| ||||||
                                AGATCTCT   ATG CGGAGT
                                     C__   T
GAM1650  LOC257336 5'  GGGCCCTAGTCCTCCAGA    97900       AA    CT
                                TCTGGAG  ACTG  GCCT
                                |||||||  ||||  ||||
                                AGACCTC  TGAT  CGGG
                                   C_    CC
GAM1650  LOC91923  5'  AGAGTTCCAGTTTCTCCA    68169         CT  _
                                TGGAGAAACTG  GC CT
                                ||||||||||  || ||
                                ACCTCTTTGAC  TG GA
                                       CT  A
GAM1650  LOC92876  5'  AGAGTTCCAGTTTCTCCA    71346         CT  _
                                TGGAGAAACTG  GC CT
                                ||||||||||  || ||
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                                ACCTCTTTGAC  TG GA
                                      CT  A
GAM1650  LOC93496  3'  TGAAACAGACTTACACTTCTTC 72863         ACTG____   CC
              AGA                   TCTGGAGAA       CTG  TCA
                                    |||||||||       |||  |||
                                    AGACTTCTT       GAC  AGT
                                         CACATTCA   AA
GAM1651  CLECSF5  3'  CAAAAAGGCCTAGTCTGTT   26039       TCA      C
                                    AACAGG   AGGCCTT TTG
                                    ||||||   ||||||| |||
                                    TTGTCT   TCCGGAA AAC
                                       GA_      A
GAM1651  EGFL4    5'  CAAGAGCCGGGCCTGGCCTGT  62451         A    ___
                                    ACAGGTCA GGCCT   TCTTG
                                    ||||||||| |||||   |||||
                                    TGTCCGGT CCGGG   AGAAC
                                         _    CCG
GAM1651  EGFR     3'  CAAGAAGGCCTTCATGGCC    19084      ___
                                    GGTCA   AGGCCTTCTTG
                                    |||||   ||||||||||||
                                    CCGGT   TCCGGAAGAAC
                                       ACT
GAM1651  EMP1     3'  CAAGAAGGAGACCTTTTC    9236     C    AAGG
                                    GAA AGGTC    CCTTCTTG
                                    ||| |||||    ||||||||
                                    CTT TCCAG    GGAAGAAC
                                      T    A___
GAM1651  GOLGA5   3'  CAAGAAGGCCAATTGCCT    18851     T   __
                                    AGG CAA  GGCCTTCTTG
                                    ||| |||  ||||||||||
                                    TCC GTT  CCGGAAGAAC
                                      _  AA
GAM1651  HRH1     3'  CAAGAAAGTCAGACCTGTTT   7813          AA   C
                                    GAACAGGTC  GGC TTCTTG
                                    |||||||||  ||| ||||||
                                    TTTGTCCAG  CTG AAGAAC
                                         A_   A
GAM1651  PART1    3'  CAAGAAGGCCTGCCTCATC   33899    AC    CA
                                    GA  AGGT  AGGCCTTCTTG
                                    ||  ||||  ||||||||||
                                    CT  TCCG  TCCGGAAGAAC
                                     AC   __
GAM1651  POMZP3   5'  CAAGAAGGCTGTGCTGT     25276     GT  A
                                    ACAG  CA GGCCTTCTTG
                                    ||||  || ||||||||||
                                    TGTC  GT TCGGAAGAAC
                                      __ G
GAM1651  PRKY     3'  AAGGAACCTCACCTGTTC    12355        CA   CC
                                    GAACAGGT  AGG  TTCTT
                                    ||||||||  |||  |||||
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                                CTTGTCCA  TCC  AGGAA
                                    C_   A_
GAM1651  RHCE    3'  CAAGAAAAACAAGGCCTGTTC  40422        AAGGCC
                                GAACAGGTC     TTCTTG
                                |||||||||     ||||||
                                CTTGTCCGG     AAGAAC
                                    AACAAA
GAM1651  RHCE    3'  CAAGAAAAACAAGGCCTGTTC  57605        AAGGCC
                                GAACAGGTC     TTCTTG
                                |||||||||     ||||||
                                CTTGTCCGG     AAGAAC
                                    AACAAA
GAM1651  RHCE    3'  CAAGAAAAACAAGGCCTGTTC  57606        AAGGCC
                                GAACAGGTC     TTCTTG
                                |||||||||     ||||||
                                CTTGTCCGG     AAGAAC
                                    AACAAA
GAM1651  RHCE    3'  CAAGAAAAACAAGGCCTGTTC  57607        AAGGCC
                                GAACAGGTC     TTCTTG
                                |||||||||     ||||||
                                CTTGTCCGG     AAGAAC
                                    AACAAA
GAM1651  RHD     3'  CAAGAAAAACAAGGCCTGTTC  32818        AAGGCC
                                GAACAGGTC     TTCTTG
                                |||||||||     ||||||
                                CTTGTCCGG     AAGAAC
                                    AACAAA
GAM1651  RHD     3'  CAAGAAAAACAAGGCCTGTTC  33138        AAGGCC
                                GAACAGGTC     TTCTTG
                                |||||||||     ||||||
                                CTTGTCCGG     AAGAAC
                                    AACAAA
GAM1651  BCDO    3'  CAAAAAGACCTTGACCATG   34284   _      C   C
                                CA GGTCAAGG CTT TTG
                                || |||||||| ||| |||
                                GT CCAGTTCC GAA AAC
                                 A       A   A
GAM1651  C16orf5  5'  GGAGCCCTGCCTGTTC      26352        CA   C
                                GAACAGGT  AGG CTTC
                                ||||||||  ||| ||||
                                CTTGTCCG  TCC GAGG
                                    __   C
GAM1651  C9orf5   3'  CAGGAAACTTGACCTG      50104        GCC
                                CAGGTCAAG   TTCTTG
                                |||||||||   ||||||
                                GTCCAGTTC   AAGGAC
                                    A__
GAM1651  CPSF2    3'  CAAGAAGTATCTGCTTGACCTT 62265     C      GC____
             TC                   GAA AGGTCAAG     CTTCTTG
                                ||| ||||||||     |||||||
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                                CTT TCCAGTTC     GAAGAAC
                                  _      GTCTAT
GAM1651  CYYR1    3'  CAAGAGTTTCAGCCTGTTC   54759       CA    CT
                                GAACAGGT  AGGC  TCTTG
                                ||||||||  ||||  |||||
                                CTTGTCCG  TTTG  AGAAC
                                    AC   __
GAM1651  DKFZP586A011 3'  CAAGTGCTTCTTGACCCCTTC  31838     CA      CCTT
                                GAA  GGTCAAGG   CTTG
                                |||  ||||||||   ||||
                                CTT  CCAGTTCT   GAAC
                                  CC       TCGT
GAM1651  FLJ11101  3'  CAAGAAGGGAGACCTGTTT   37610        AAGG
                                GAACAGGTC   CCTTCTTG
                                |||||||||   ||||||||
                                TTTGTCCAG   GGAAGAAC
                                    AG__
GAM1651  FLJ14642  3'  CAAGAAGGCCCAGTTGTCCT   52572     T   ___
                                AGG CAA   GGCCTTCTTG
                                ||| |||   ||||||||||
                                TCC GTT   CCGGAAGAAC
                                  T   GAC
GAM1651  FLJ14665  3'  CAAGAAGGCAAGGCCTCC    52585   C    AAG
                                A AGGTC   GCCTTCTTG
                                | |||||   |||||||||
                                C TCCGG   CGGAAGAAC
                                 C    AA_
GAM1651  FLJ20054  5'  AAGGAGGTGCACTGTTC     39306       _  CAAG
                                GAACAG GT   GCCTTCTT
                                |||||| ||   ||||||||
                                CTTGTC CG   TGGAGGAA
                                   A  _____
GAM1651  FLJ20300  5'  CAAGCGGCTCCTGACCTG    35378       A_   TT
                                CAGGTCA  GGCC  CTTG
                                |||||||  ||||  ||||
                                GTCCAGT  TCGG  GAAC
                                    CC   C_
GAM1651  FLJ20548  3'  CAAGCTGGCCCCTGCCTGTTC  35817        CAA   TT
                                GAACAGGT   GGCC  CTTG
                                ||||||||   ||||  ||||
                                CTTGTCCG   CCGG  GAAC
                                    TCC    TC
GAM1651  KIAA0182  3'  CAAGAAGGCCTCTCTTGCTC   72497    A   TCA
                                GA CAGG   AGGCCTTCTTG
                                || ||||   ||||||||||
                                CT GTTC   TCCGGAAGAAC
                                 C   TC_
GAM1651  KIAA0515  3'  CAAAAAGGTCACCTGTTC    64543       CAA    C
                                GAACAGGT   GGCCTT TTG
                                ||||||||   |||||| |||
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                                CTTGTCCA  CTGGAA AAC
                                   ___    A
GAM1651 KIAA0618 5' CAAGAAGGCTGTGCTGT    29845    GT  A
                                ACAG  CA GGCCTTCTTG
                                ||||  || ||||||||||
                                TGTC  GT TCGGAAGAAC
                                  __ G
GAM1651 KIAA1508 5' AGAGACCCTACCTGTTC    62538      CA  CC
                                GAACAGGT  AGG  TTCT
                                ||||||||  |||  ||||
                                CTTGTCCA  TCC  GAGA
                                   __  CA
GAM1651 MGC2541  3' CAAGAAGGCCCAGTTGCC   55620   T  ___
                                GG CAA  GGCCTTCTTG
                                || |||  ||||||||||
                                CC GTT  CCGGAAGAAC
                                 _  GAC
GAM1651 MGC4643  3' CAAGAAGGTATCCTCTTC   52137   C  TCAAG
                                GAA AGG   GCCTTCTTG
                                ||| |||   |||||||||
                                CTT TCC   TGGAAGAAC
                                  C  TA___
GAM1651 TED      3' CAAGAAGACCCTTTGACT    32263      C__
                                GGTCAAGG  CTTCTTG
                                ||||||||  |||||||
                                TCAGTTTC  GAAGAAC
                                    CCA
GAM1651 TRIM40   3' AGAAGCTCTGACCTGTTC    57732       AG  C
                                GAACAGGTCA  GC TTCT
                                ||||||||||  || ||||
                                CTTGTCCAGT  CG AAGA
                                     CT  _
GAM1651 TRIP-Br2 3' AAGGAGGTATAACCTTTC    29256    C   CAAG
                                GAA AGGT   GCCTTCTT
                                ||| ||||   ||||||||
                                CTT TCCA   TGGAGGAA
                                  _   ATA_
GAM1651 LOC118611 5' CAGGGAGCCCTGGCCTGT   75994       A  C
                                ACAGGTCA GGC TTCTTG
                                |||||||| ||| ||||||
                                TGTCCGGT CCG AGGGAC
                                    C  _
GAM1651 LOC128916 5' CAAGAAGGCTGGTGCCCT   76296    T  A_
                                AGG CA  GGCCTTCTTG
                                ||| ||  ||||||||||
                                TCC GT  TCGGAAGAAC
                                  C  GG
GAM1651 LOC145663 5' CAAGAAGGCCCGTTGGAGTC  84414   ACAGG  __
                                GA   TCAA  GGCCTTCTTG
                                ||   ||||  ||||||||||
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                                CT    GGTT  CCGGAAGAAC
                                 GA___    GC
GAM1651  LOC201191 3'  CAAGACCTGGTCTTTGACCCAT 91342     CA       _  T__
              TC                  GAA  GGTCAAGG CC   TCTTG
                                  |||  |||||||| ||   |||||
                                  CTT  CCAGTTTC GG   AGAAC
                                    AC       T  TCC
GAM1651  LOC221495 3'  CAAGCTACCTACCTGTTC    95491        CA   CCTT
                                  GAACAGGT  AGG    CTTG
                                  ||||||||  |||    ||||
                                  CTTGTCCA  TCC    GAAC
                                       __   ATC_
GAM1651  LOC222681 5'  CAAGAAGGCCTGCCAGTTC    94426     A   CA
                                  GAAC GGT  AGGCCTTCTTG
                                  |||| |||  ||||||||||
                                  CTTG CCG  TCCGGAAGAAC
                                    A   __
GAM1651  LOC255811 5'  CAAGAAGGCCCGGAGTGACC   96306      A____
                                  GGTCA    GGCCTTCTTG
                                  |||||    ||||||||||
                                  CCAGT    CCGGAAGAAC
                                     GAGGC
GAM1651  LOC257507 5'  CAAGAAGGCCTGCCAGTTC    99613     A   CA
                                  GAAC GGT  AGGCCTTCTTG
                                  |||| |||  ||||||||||
                                  CTTG CCG  TCCGGAAGAAC
                                    A   __
GAM1651  LOC257625 5'  CAAGAAGGCCTGCCAGTTC    99733     A   CA
                                  GAAC GGT  AGGCCTTCTTG
                                  |||| |||  ||||||||||
                                  CTTG CCG  TCCGGAAGAAC
                                    A   __
GAM1651  LOC85865  5'  CAAGAAGGTTTCCTGGCC    95528      __
                                  GGTCA  AGGCCTTCTTG
                                  |||||  ||||||||||
                                  CCGGT  TTTGGAAGAAC
                                     CC
GAM1652  EPHA2    3'  CAGCCTTCGGACAGACAT    16674      CC   GCGG
                                  ATGTC  TTC    GAAGGCTG
                                  |||||  |||    ||||||||
                                  TACAG  AGG    CTTCCGAC
                                    AC   _____
GAM1652  EPHB6    3'  ACACTGGTCCGAGAAGGGACAT 16713          G    AA  C
              G                    CATGTCCCTTC CGGG  GG TGT
                                  ||||||||||| ||||  || |||
                                  GTACAGGGAAG GCCT  TC ACA
                                        A   GG  _
GAM1652  PRPF31   3'  CTTCCCACTGAAGGGACA    32212          C_
                                  TGTCCCTTCG  GGGAAG
                                  ||||||||||  ||||||
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                                ACAGGGAAGT  CCCTTC
                                      CA
GAM1652  RHO      3'  CAGCCTGAGAAGGGACAT    6767          GCGGGA
                                ATGTCCCTTC     AGGCTG
                                ||||||||||     ||||||
                                TACAGGGAAG     TCCGAC
                                      AG____
GAM1652  CHFR     3'  ACAGCCCCCTGAGGGAAGGGAC 37188         G__    AA
              G                  TGTCCCTTC   CGGG  GGCTGT
                                ||||||||||   ||||  ||||||
                                GCAGGGAAG   GTCC  CCGACA
                                      GGA   C_
GAM1652  MGC11352 3'  CAACCTTCCTGGAACGTG    65425       CCCT  G       C
                                CATGT    TC CGGGAAGG TG
                                |||||    || |||||||| ||
                                GTGCA    AG GTCCTTCC AC
                                   _____  _       A
GAM1652  MGC2803   3'  ACAGCCTTCCCTGAGAGGAC   44085      C    C
                                GTCC TTCG GGGAAGGCTGT
                                |||| |||| ||||||||||
                                CAGG GAGT CCCTTCCGACA
                                  A    _
GAM1652  PRC1      3'  ACAGCCTTCCTCCTGAAGAGA  15625    C     C _
                                TC CTTCG G GGAAGGCTGT
                                || ||||| | ||||||||||
                                AG GAAGT C CCTTCCGACA
                                 A     C T
GAM1652  LOC148089 3'  ACAGCCTTCCCGCAGG      79322     TC
                                CCT  GCGGGAAGGCTGT
                                |||  ||||||||||||
                                GGA  CGCCCTTCCGACA
                                   __
GAM1653  ADAM28    3'  GACTCAAGAAGGTTAACATTTT 41712          AGTG
              C                   GAAAATGTTAA    TTTGAGTC
                                ||||||||||    ||||||||
                                CTTTTACAATT    GAACTCAG
                                      GGAA
GAM1653  BCL3      3'  GACTCTGACCCCAGCATTCTCA 18991     A     AAAGT   T
                                TGA AATGTT     GTT GAGTC
                                ||| ||||||     ||| |||||
                                ACT TTACGA     CAG CTCAG
                                  C     CCC__   T
GAM1653  CCNK      5'  CTCCGGATTCTAACATTTTCA  77795          A   G TT
                                TGAAAATGTTA AGT T  GAG
                                |||||||||| ||| |  |||
                                ACTTTTACAAT TTA G  CTC
                                      C   _ GC
GAM1653  EPHB2     3'  GACACTTTGACATTTCCA    34346    A
                                TG AAATGTTAAAGTGTT
                                || ||||||||||||||
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                                AC TTTACAGTTTCACAG
                                 C
GAM1653  PYCS     3'  ACTCTTCTTTTTAGCATTCTCA 12679     A        TGTTT
                                TGA AATGTTAAAG     GAGT
                                ||| ||||||||||     ||||
                                ACT TTACGATTTT     CTCA
                                  C         TCTT_
GAM1653  SH3BP5   3'  GACTGCTTTTCTTTAACGTTTT 17918            TGTTTG
              CA                  TGAAAATGTTAAAG      AGTC
                                  ||||||||||||||      ||||
                                  ACTTTTGCAATTTC      TCAG
                                           TTTTCG
GAM1653  CD109    3'  GACTCTGTGTAACACTAACATT 56862    A      AA     T____
              TCCA                  TG AAATGTT  AGTGTT     GAGTC
                                  || |||||||  ||||||     |||||
                                  AC TTTACAA  TCACAA     CTCAG
                                   C       __       TGTGT
GAM1653  FLJ23045 3'  ACCCAAACACTGATGTTTACA  45550    A      AA       A
                                  TG AAATGTT  AGTGTTTG GT
                                  || |||||||  |||||||| ||
                                  AC TTTGTAG  TCACAAAC CA
                                   A       __        C
GAM1653  KIAA1577 3'  ACTCATCTTTACATTTTCA    65097          T    TGTT
                                  TGAAAATGT AAAG    TGAGT
                                  |||||||| ||||    |||||
                                  ACTTTTACA TTTC    ACTCA
                                        _    T____
GAM1653  LOC145134 5'  AACACTACAACATTTTCA     84207           AA
                                  TGAAAATGTT  AGTGTT
                                  ||||||||||  ||||||
                                  ACTTTTACAA  TCACAA
                                        CA
GAM1653  LOC146136 5'  GACTTTCTACTTTAACAGTTTC 73319       A         TTT
              A                    TGAAA TGTTAAAGTG   GAGTC
                                  ||||| ||||||||||   |||||
                                  ACTTT ACAATTTCAT   TTCAG
                                     G         CT_
GAM1653  LOC146181 3'  GACTTTCTACTTTAACAGTTTC 69150       A         TTT
              A                    TGAAA TGTTAAAGTG   GAGTC
                                  ||||| ||||||||||   |||||
                                  ACTTT ACAATTTCAT   TTCAG
                                     G         CT_
GAM1653  LOC146449 3'  GACTTTCTACTTTAACAGTTTC 61713       A         TTT
              A                    TGAAA TGTTAAAGTG   GAGTC
                                  ||||| ||||||||||   |||||
                                  ACTTT ACAATTTCAT   TTCAG
                                     G         CT_
GAM1653  LOC158402 3'  ACTCAAATAAACACTTTTCA   88139        _    AAAG
                                  TGAAAA TGTT    TGTTTGAGT
                                  |||||| ||||    |||||||||
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                                ACTTTT ACAA    ATAAACTCA
                                  C   ____
GAM1653  LOC197423 3'  GACTTTCTACTTTAACAGTTTC 78425      A        TTT
           A                     TGAAA TGTTAAAGTG   GAGTC
                                 ||||| ||||||||||   |||||
                                 ACTTT ACAATTTCAT   TTCAG
                                   G         CT_
GAM1653  LOC200014 3'  ACCCAAATCATTTTAAAATTTT 89912       G      _   A
           CA                     TGAAAAT TTAAAGTG TTTG GT
                                 ||||||| |||||||| |||| ||
                                 ACTTTTA AATTTTAC AAAC CA
                                    A       T   C
GAM1653  LOC220565 3'  GACTTTCTACTTTAACAGTTTC 92444      A        TTT
           A                     TGAAA TGTTAAAGTG   GAGTC
                                 ||||| ||||||||||   |||||
                                 ACTTT ACAATTTCAT   TTCAG
                                   G         CT_
GAM1654  ABP1     5'  GCAGAGCGAACTGGGAGCAGAG 63799         CCGC    C
                                 CTCTGTTCTT    CGCTC GC
                                 ||||||||||    ||||| ||
                                 GAGACGAGGG    GCGAG CG
                                       TCAA     A
GAM1654  AHCY     3'  GGCAACTGAGAAAGAACAGAG  7304          _ _ ____
                                 CTCTGTTCTT C C    GCC
                                 |||||||||| | |    |||
                                 GAGACAAGAA G G    CGG
                                       A A TCAA
GAM1654  BSN      3'  GGCAGAGGCAAGAGCAGAG    14387         CC   G  _
                                 CTCTGTTCTT  GCC CT CC
                                 ||||||||||  ||| || ||
                                 GAGACGAGAA  CGG GA GG
                                       __   A  C
GAM1654  CSE1L    5'  GCGGAGCGGCGGCAGGAGC    62513       _
                                 GTTCTT CCGCCGCTCCGC
                                 |||||| ||||||||||||
                                 CGAGGA GGCGGCGAGGCG
                                   C
GAM1654  EHD4     3'  AGTGGCAAAAAAATAGAG     58362        C  CC
                                 CTCTGTT TT  GCCGCT
                                 |||||||  ||  ||||||
                                 GAGATAA AA  CGGTGA
                                    A  AA
GAM1654  EIF2C1   3'  AGCCCAGCTGAAGAACAGA    25181          C  C__
                                 TCTGTTCTTC GC   GCT
                                 |||||||||| ||   |||
                                 AGACAAGAAG CG   CGA
                                       T  ACC
GAM1654  JUND     3'  GAGAGAAGAACAGAGT      19298           CGCCG
                                 ACTCTGTTCTTC    CTC
                                 ||||||||||||    |||
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                                TGAGACAAGAAG    GAG
                                      A____
GAM1654  KCNK4    3'  GCAGAGCAGCAGAGCAGG    33985       TCC  C    C
                                TCTGTTCT   GC GCTC GC
                                ||||||||   || |||| ||
                                GGACGAGA   CG CGAG CG
                                   ___  A    A
GAM1654  MYO1D    3'  GCGGAACAGCCCATCCAGCAGA 72249       CTTCC_  CGC
              GT                  ACTCTGTT     GC   TCCGC
                                ||||||||     ||   |||||
                                TGAGACGA     CG   AGGCG
                                   CCTACC  ACA
GAM1654  NUP62    3'  GGCAAAGCAGCACAGTGTGAAT 33786       TTCC___  C   CC
              AGA                 TCTGTTC      GC GCT  GCC
                                |||||||      || |||  |||
                                AGATAAG      CG CGA  CGG
                                   TGTGACA  A   AA
GAM1654  RABIF    3'  GGCATGTGCAGAAAAACAGAGT 12728       C   C  C  TCC
                                ACTCTGTT TTC GC GC   GCC
                                |||||||| ||| || ||   |||
                                TGAGACAA AAG CG TG   CGG
                                   A   A  _  TA_
GAM1654  RAX      3'  GCAGGGGAGGCGGAAAAATAGA 26466       C      G   _
              GT                  ACTCTGTT TTCCGCC CTCC GC
                                |||||||| ||||||| |||| ||
                                TGAGATAA AAGGCGG GGGG CG
                                   A      A   A
GAM1654  RBM10    3'  GGCAGGGAAGGACAGAGT    20247          __
                                ACTCTGTTCTTCC  GCC
                                ||||||||||||  |||
                                TGAGACAGGAAGG  CGG
                                      GA
GAM1654  RGS16    3'  GGCAGGGCCCAGGAGAACAAAG 12869     C     T  GCC   C
              T                   ACT TGTTCT CC   GCTC GCC
                                ||| |||||| ||   |||| |||
                                TGA ACAAGA GG   CGGG CGG
                                  A     _  ACC   A
GAM1654  ROM1     3'  GGAACAGCAAAGAACAGAGT   6165          CC  CGC
                                ACTCTGTTCTT  GC   TCC
                                ||||||||||  ||   |||
                                TGAGACAAGAA  CG   AGG
                                      A_  ACA
GAM1654  SLC21A2  3'  GCAAAGCAAGTGATGAAGCAGA 20084       _ TTC   C_   CC
              GT                  ACTCTGTT C   CGC  GCT  GC
                                |||||||| |   |||  |||  ||
                                TGAGACGA G   GTG  CGA  CG
                                   A TA_   AA   AA
GAM1654  SMARCA5  5'  AGCCCCGCGGAAGAGCAGA   14588          C__
                                TCTGTTCTTCCGC   GCT
                                ||||||||||||   |||
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                                AGACGAGAAGGCG  CGA
                                      CCC
GAM1654 SYNGR1   3' GGCAGAGCGGCAAGGACAGGG 17507        CC     C
                                CTCTGTTCTT GCCGCTC GCC
                                |||||||||| ||||||| |||
                                GGGACAGGAA CGGCGAG CGG
                                     __     A
GAM1654 TRAM     5' AGCAGCTGGGAAGAGCAGA  27451         __ C
                                TCTGTTCTTCC GC GCT
                                |||||||||| || |||
                                AGACGAGAAGG CG CGA
                                      GT A
GAM1654 VAT1     3' AGCAGGGAAGTACAGAGT   22088       T   GCC
                                ACTCTGT CTTCC  GCT
                                ||||||| |||||  |||
                                TGAGACA GAAGG  CGA
                                    T   GA_
GAM1654 CBX1     3' AGCAATGGAAAAGAACAGA  23308       __  CC
                                TCTGTTCT TCCG GCT
                                |||||||| |||| |||
                                AGACAAGA AGGT CGA
                                     AA  AA
GAM1654 CDC14A   5' GGCGGAGCAGCAGCTGCAGCAG 14786   _  TCTTCC C
                                CT CTGT    GC GCTCCGCC
                                || ||||    || ||||||||
                                GA GACG    CG CGAGGCGG
                                 C  TCGA__ A
GAM1654 CDC14A   5' GGCGGAGCAGCAGCTGCAGCAG 53964   _  TCTTCC C
                                CT CTGT    GC GCTCCGCC
                                || ||||    || ||||||||
                                GA GACG    CG CGAGGCGG
                                 C  TCGA__ A
GAM1654 CDC14A   5' GGCGGAGCAGCAGCTGCAGCAG 53966   _  TCTTCC C
                                CT CTGT    GC GCTCCGCC
                                || ||||    || ||||||||
                                GA GACG    CG CGAGGCGG
                                 C  TCGA__ A
GAM1654 DKFZp547I224 5' GATGGGGAAAAAACAGAG   39956      C_  G  C
                                CTCTGTT TTCC CCG TC
                                ||||||| |||| ||| ||
                                GAGACAA AAGG GGT AG
                                    AA  _  _
GAM1654 ECE2     3' GCAGGGAAAAGGAAGAACAGAG 28732         GCCG  C
           T                     ACTCTGTTCTTCC  CTC GC
                                ||||||||||||   ||| ||
                                TGAGACAAGAAGG  GGG CG
                                      AAAA  A
GAM1654 FLJ10648 3' CGAAGCAAACCAAGAACAGAG  36890        CCGCC  C
                                CTCTGTTCTT   GCT CG
                                ||||||||||   ||| ||
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                                GAGACAAGAA    CGA GC
                                      CCAAA   A
GAM1654  GRIN3A   3'  GCGGAGCAAGTGCCAAGCAGA  56783      CTTC   C_
                                TCTGTT   CGC  GCTCCGC
                                ||||||   |||  |||||||
                                AGACGA   GTG  CGAGGCG
                                   ACC_   AA
GAM1654  INE1     3'  GCAGGTGTTAGACGAAAGAACA 14757       C  CC__  T  _
            GA                    TCTGTTCTT CG   GC CC GC
                                ||||||||| ||   || || ||
                                AGACAAGAA GC   TG GG CG
                                     A  AGAT  T  A
GAM1654  KIAA0410 3'  GCAGAGCTTAAGAATAGA    29426       CCGCC   C
                                TCTGTTCTT    GCTC GC
                                |||||||||    |||| ||
                                AGATAAGAA    CGAG CG
                                     TT___    A
GAM1654  KIAA0872 3'  AGCGCGGAAGACAGAGT     30739       T      C
                                ACTCTGT CTTCCGC GCT
                                ||||||| ||||||| |||
                                TGAGACA GAAGGCG CGA
                                   _      _
GAM1654  KIAA0964 5'  GCGGAACGGCAGAGCGGG    30448       TCC    C
                                TCTGTTCT   GCCG TCCGC
                                ||||||||   |||| |||||
                                GGGCGAGA   CGGC AGGCG
                                     ___    A
GAM1654  KIAA1218 5'  AGCAGCACAAAAGAAACAGAGT 95958       _   CC__  C
                                ACTCTGTT CTT    GC GCT
                                |||||||| |||    || |||
                                TGAGACAA GAA    CG CGA
                                     A   AACA  A
GAM1654  KIAA1285 3'  AGCAAGGAGAACAGAGT     91978        T  GCC
                                ACTCTGTTCT CC   GCT
                                |||||||||| ||   |||
                                TGAGACAAGA GG   CGA
                                     _  AA_
GAM1654  KIAA1322 3'  GGCAGCCGAGAAGAACAGA   73112        _  CC   _
                                TCTGTTCTTC CG  GCT CC
                                |||||||||| ||  ||| ||
                                AGACAAGAAG GC  CGA GG
                                     A  __   C
GAM1654  KIAA1391 3'  AGTGGAGAAAAACAGAGT    67851       C   CG
                                ACTCTGTT TTC  CCGCT
                                |||||||| |||  |||||
                                TGAGACAA AAG  GGTGA
                                     A   A_
GAM1654  MGC13251 3'  AGCAGCCATAGAAAGGACAGA  52134       _ C___  C
                                TCTGTTCTT C    GC GCT
                                ||||||||| |    || |||
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                                AGACAGGAA G    CG CGA
                                     A ATAC  A
GAM1654  MYH7B    3'  GGCGGAGCAGCAGGCCAACA   71058      CTT  _  C
                                TGTT   CC GC GCTCCGCC
                                ||||   || || ||||||||
                                ACAA   GG CG CGAGGCGG
                                  CC_  A  A
GAM1654  NCOA2    3'  GGCAAGGAGAAGAGCAAAGT   22572     C       CG  GCT
                                ACT TGTTCTTC  CC   CC
                                ||| ||||||||  ||   ||
                                TGA ACGAGAAG  GG   GG
                                  A       A_  AAC
GAM1654  PTRF     3'  GGCAGTGGGGAAGACAGAG    64242       T    G    _
                                CTCTGT CTTCC CCGCT CC
                                |||||| ||||| ||||| ||
                                GAGACA GAAGG GGTGA GG
                                   _    _    C
GAM1654  RHOBTB2  3'  AGCAGGAGGAAAAGCAGAGT   61593        C   G  _
                                ACTCTGTT TTCC CC GCT
                                |||||||| |||| || |||
                                TGAGACGA AAGG GG CGA
                                     A   A  A
GAM1654  TAGAP    3'  AGACTGCAAGGAACAGAGT    55099          CC  CG_
                                ACTCTGTTCTT  GC   CT
                                ||||||||||  ||   ||
                                TGAGACAAGGA  CG   GA
                                       A_  TCA
GAM1654  VELI1    3'  AGTGTAAGAAGAATAAAGT    17417     C       CGC
                                ACT TGTTCTTC   CGCT
                                ||| ||||||||   ||||
                                TGA ATAAGAAG   GTGA
                                  A       AAT
GAM1654  LOC145783 5'  GCGGAGCGACGGAGACACAG   77949      TC    C
                                CTGT  TTCCG CGCTCCGC
                                ||||  ||||| ||||||||
                                GACA  GAGGC GCGAGGCG
                                   CA    A
GAM1654  LOC150157 3'  AGCAAATGGAAAAGAACAGA   86020         __   CC_
                                TCTGTTCT  TCCG   GCT
                                ||||||||  ||||   |||
                                AGACAAGA  AGGT   CGA
                                     AA    AAA
GAM1654  LOC151516 5'  GGCGGAGCTTCCAGAACAAAG  81068    C     TCCGCC
                                CT TGTTCT     GCTCCGCC
                                || ||||||     ||||||||
                                GA ACAAGA     CGAGGCGG
                                 A     CCTT__
GAM1654  LOC153769 3'  GGCGGAGCAGCATGAGAAAGA  81807     G    CC  C
                                TCT TTCTT  GC GCTCCGCC
                                ||| |||||  || ||||||||
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                                AGA AAGAG  CG CGAGGCGG
                                  _    TA  A
GAM1654  LOC161734 3'  GATGGGGAAAAAACAGAG    88467       C_   G   C
                                CTCTGTT  TTCC CCG TC
                                |||||||  |||| ||| ||
                                GAGACAA  AAGG GGT AG
                                    AA   _  _
GAM1654  LOC167026 5'  GGCGGAGCGGCGGGCGGA    88620      TCTT
                                TCTGT   CCGCCGCTCCGCC
                                |||||   ||||||||||||
                                AGGCG   GGCGGCGAGGCGG
                                  _____
GAM1654  LOC196890 3'  AGCAAATGGAAAAGAACAGA   91222        __   CC_
                                TCTGTTCT  TCCG   GCT
                                ||||||||  ||||   |||
                                AGACAAGA  AGGT   CGA
                                    AA    AAA
GAM1654  LOC200731 5'  AGCACTGAAGAACAGAGT    91688          CGCC
                                ACTCTGTTCTTC    GCT
                                ||||||||||||    |||
                                TGAGACAAGAAG    CGA
                                      TCA_
GAM1654  LOC221504 5'  CGGAGCGGCGGGGCAGGAG   94020     GTTC
                                CTCT    TTCCGCCGCTCCG
                                ||||    |||||||||||||
                                GAGG    GGGGCGGCGAGGC
                                  AC__
GAM1654  LOC221663 5'  GCAAAGCCCAGAACAGAGT   95462         TCCGCC   CC
                                ACTCTGTTCT     GCT  GC
                                ||||||||||     |||  ||
                                TGAGACAAGA     CGA  CG
                                     CC_____   AA
GAM1654  LOC256310 3'  GGCAGAGCAGCGGGAGCAGGAG 98102      GTT      C    C
                                CTCT   CTTCCGC GCTC GCC
                                ||||   ||||||| |||| |||
                                GAGG   GAGGGCG CGAG CGG
                                  AC_      A    A
GAM1654  LOC51762  3'  GGCCTAGCAAAAGAACAGA   33708         CCGCC   CC
                                TCTGTTCTT    GCT  GCC
                                |||||||||    |||  |||
                                AGACAAGAA    CGA  CGG
                                     AA___   TC
GAM1654  LOC91266  5'  GGCTGAGGAAAAACAGAGT   66024        ___    C
                                ACTCTGT   TCTTC GCC
                                |||||||   ||||| |||
                                TGAGACA   AGGAG CGG
                                    AAA    T
GAM1655  PPARGC1   3'  TGATACACCTACTACTCA    26085      G    A    _
                                TGAG AGTA GTGTA CA
                                |||| |||| ||||| ||
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                                ACTC TCAT CACAT GT
                                  A   C    A
GAM1655 C20orf140 3' ATCACATTAAGGCACCCACTC 58892     AA   AC_
                                GAGT  GTGT  AATGTGAT
                                |||| ||||  ||||||||
                                CTCA  CACG  TTACACTA
                                  CC   GAA
GAM1655 DQX1    3' ATCACATTAGATTATCCCTCA 56908     AG  GTGTAC
                                TGAGG  TAA    AATGTGAT
                                |||||  |||    ||||||||
                                ACTCC  ATT    TTACACTA
                                  CT   AGA___
GAM1655 FLJ20729 3' ATCACATTCCTAGCCCACTCTC 36081     G  AA  GTAC
            A                    TGAG AGT  GT   AATGTGAT
                                |||| |||  ||   ||||||||
                                ACTC TCA  CG   TTACACTA
                                  _  CC  ATCC
GAM1655 HABP2   3' TCACATCTTTATTCCTCA   15952         TGTACA
                                TGAGGAGTAAG    ATGTGA
                                ||||||||||     ||||||
                                ACTCCTTATTT    TACACT
                                      C_____
GAM1655 LOC222234 3' ATCACATTCAGTTTTCACTCCC 95899    A    A  TGTAC
            A                    TG GGAGT AG    AATGTGAT
                                || ||||| ||    ||||||||
                                AC CCTCA TT    TTACACTA
                                 _    C  TTGAC
GAM1655 LOC51194  3' TCACAAACCTATTCCTCA   33401        A T  ACAA
                                TGAGGAGTA G GT   TGTGA
                                ||||||||| | ||   |||||
                                ACTCCTTAT C CA   ACACT
                                     _ _  A___
GAM1656 ABCC11   5' TGGGGAGGGTGGTTAGAGAAGG 53688     G  GCA  TG
                                CCTT CT   AAC  CTTTTCTTG
                                |||| ||   |||  |||||||||
                                GGAA GA   TTG  GGGAGGGGT
                                  _ GA_  GT
GAM1656 ABCD1   3' GGGAAAGTAGATGTGGAGGG  5261     G TG  AA
                                CCTT C  CA  CTGCTTTTCT
                                |||| |  ||  ||||||||||
                                GGGA G  GT  GATGAAAGGG
                                  _ GT  A_
GAM1656 ABH     3' GAGGAAGGTAGAAGTGAG   60462    TG  GCAAA
                                CT  CT    CTGCTTTTCTT
                                ||  ||    |||||||||||
                                GA  GA    GATGGAAGGAG
                                 GT  A____
GAM1656 ABL1    3' CAAGGGAGGCAGTGGCTAGTGG 24606    TG  _  AA     TT
            GG                   CCT  CT GC  ACTGCTT  CTTG
                                |||  || ||  |||||||  ||||
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                                GGG  GA CG  TGACGGA  GAAC
                                  GT  T  G_      GG
GAM1656  ABR      3'  GGGGGAGGAGGCGGTCAGG   42006     T    AAA  G   TT
                                CCT GCTGC   CT CTT  CT
                                ||| |||||   || |||  ||
                                GGA TGGCG   GA GAG  GG
                                  C    ___  G   GG
GAM1656  ACN      5'  CGAGAAAAGGGGCGCTGCAGGG 31067       T  AAA  G
                                CCTTGC GC   CT CTTTTCTTG
                                |||||| ||   || |||||||||
                                GGGACG CG   GG GAAAAGAGC
                                   T  C__  G
GAM1656  ACTR1B   3'  CAAGGAGGGCGGGGCATGTTGG 71378     T  _   AAA
              G                  CCT GC TGC   CTGCTTTTCTTG
                                ||| || |||   ||||||||||||
                                GGG TG ACG   GGCGGGAGGAAC
                                  T  T   G__
GAM1656  ADAMTS1  3'  AGGAAGGGCTGGTGCAGGG   23747       T  AAACT
                                CCTTGC GC    GCTTTTCTT
                                |||||| ||    |||||||||
                                GGGACG TG    CGGGAAGGA
                                   _  GT___
GAM1656  ADD1     3'  TAGGGAAGGTATATCAGGAGGG 27210      G   CAAAC
                                CCTT CTG    TGCTTTTCTTG
                                |||| |||    ||||||||||||
                                GGGA GAC    ATGGAAGGGAT
                                  G   TAT__
GAM1656  ADD1     3'  TAGGGAAGGTATATCAGGAGGG 27211      G   CAAAC
                                CCTT CTG    TGCTTTTCTTG
                                |||| |||    ||||||||||||
                                GGGA GAC    ATGGAAGGGAT
                                  G   TAT__
GAM1656  ADORA1   3'  TGGGAGAGGCAGAAAGGGTAGG 7274        GCAAA
                                CTTGCT    CTGCTTTTCTTG
                                ||||||    ||||||||||||
                                GGATGG    GACGGAGAGGGT
                                   GAAA_
GAM1656  ADRA2B   3'  AGGGGGGCTGCTAGCAAGG   7294         _  AACT   TT
                                CCTTGCT GCA   GCTT  CT
                                ||||||| |||   ||||  ||
                                GGAACGA CGT   CGGG  GA
                                   T  _____   GG
GAM1656  ADRA2B   3'  GGGAGGGGTGGGCAGGGGGG  7298      G   AA   G
                                CCTT CTGC  ACT CTTTT
                                |||| ||||  ||| |||||
                                GGGG GACG  TGG GAGGG
                                  G   GG  G
GAM1656  AES      3'  TGGGAGGAGCAGGGTGAGGGTG 8527     TG  G_  AA
              GG                  CT  CT  CA  CTGCTTTTCTTG
                                ||  ||  ||  ||||||||||||
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                                GG  GG  GT  GACGAGGAGGGT
                                 GT  GA  GG
GAM1656 AGR2     3'  CAGGGAAAGCCTCTGGCAAG  22161       GCAAACT
                                CTTGCT      GCTTTTCTTG
                                ||||||      ||||||||||
                                GAACGG      CGAAAGGGAC
                                   TCTC___
GAM1656 ALDH8A1  3'  GGGGAAGGCTATGTGGTAAG  42916      TG  AACT       G
                                CTTGC  CA   GCTTTTCTT
                                |||||  ||   |||||||||
                                GAATG  GT   CGGAAGGGG
                                   GT  AT__
GAM1656 ALK      5'  CGGGGAGAGCGAAGGGTGAGG  73771     TG  GCAAAC
                                CCT  CT     TGCTTTTCTTG
                                |||  ||     ||||||||||
                                GGA  GG     GCGAGAGGGGC
                                  GT  GAA___
GAM1656 ALPL     3'  CGGGAAGAGCCACCTGGCAGGG 6648        GCAAACT
                                CCTTGCT      GCTTTTCTTG
                                |||||||      ||||||||||
                                GGGACGG      CGAGAAGGGC
                                    TCCAC__
GAM1656 ALPP     3'  CAAGGAGGCTCCTGGGGTGGGG 69407     TG  G  AACT    T
                                CCT  CT CA   GCTTT CTTG
                                |||  || ||   ||||| ||||
                                GGG  GG GT   CGGAG GAAC
                                  GT  G  CCT_    _
GAM1656 ALPPL2   3'  CAAGGAGGCTGCTGTGGTGGGG 69424     TG TG  AACT    T
                                CCT  C  CA   GCTTT CTTG
                                |||  |  ||   ||||| ||||
                                GGG  G  GT   CGGAG GAAC
                                  GT GT  CGT_    _
GAM1656 ALS2     3'  TAAGAAAAGCTTCCAGTAG   40883       CAAACT
                                TTGCTG     GCTTTTCTTG
                                ||||||     ||||||||||
                                GATGAC     CGAAAAGAAT
                                   CTT___
GAM1656 ALX3     3'  TAAGGAGGGTGTAAAGGCCAAG 22426      _  GCAA  T
              G                  CCTTG CT    AC GCTTTTCTTG
                                 |||||  ||    ||  ||||||||||
                                 GGAAC GG    TG TGGGAGGAAT
                                   C  AAA_  _
GAM1656 AMFR     3'  GGGAAGAGTGTGGGGGAGG   58041     G  G  A   G   TT
                                CCTT CT CA ACT CTT  C
                                |||| || || ||| |||  |
                                GGAG GG GT TGA GAA  G
                                  _  G  G   _   GG
GAM1656 AMFR     3'  GGGAAGAGTGTGGGGGAGG   58042     G  G  A   G   TT
                                CCTT CT CA ACT CTT  C
                                |||| || || ||| |||  |
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                                GGAG GG GT TGA GAA  G
                                  _ G G  _  GG
GAM1656  ANK1    3'  GAGGGCTTTTTGTGGCTGGG  40409    T  TG   CT
                                CCT GC  CAAA  GCTTTT
                                ||| ||  ||||  ||||||
                                GGG CG  GTTT  CGGGAG
                                  T  GT   TT
GAM1656  ANK1    3'  GAGGGCTTTTTGTGGCTGGG  40410    T  TG   CT
                                CCT GC  CAAA  GCTTTT
                                ||| ||  ||||  ||||||
                                GGG CG  GTTT  CGGGAG
                                  T  GT   TT
GAM1656  ANK1    3'  GAGGGCTTTTTGTGGCTGGG  40411    T  TG   CT
                                CCT GC  CAAA  GCTTTT
                                ||| ||  ||||  ||||||
                                GGG CG  GTTT  CGGGAG
                                  T  GT   TT
GAM1656  ANK1    3'  GAGGGCTTTTTGTGGCTGGG  40412    T  TG   CT
                                CCT GC  CAAA  GCTTTT
                                ||| ||  ||||  ||||||
                                GGG CG  GTTT  CGGGAG
                                  T  GT   TT
GAM1656  ANP32A  3'  CGAGAGGGGAAGAGTGTACTGG 21946     GC   AA  G
           GG                    CCTT  TGCA  CT CTTTTCTTG
                                ||||  ||||  || |||||||||
                                GGGG  ATGT  GA GGGGAGAGC
                                  TC   GA  A
GAM1656  ANXA6   3'  AGGAAGGGGCAGGGGTGGGG  15739    TG  GCAAA    _
                                CCT  CT    CTGCTT TTCTT
                                |||  ||    |||||| |||||
                                GGG  GG    GACGGG AAGGA
                                  GT  G____     G
GAM1656  AP1S1   3'  TGGGAGGGGTGGGGAGGGGGAG 55107     G  GCAAA TG
           G                     CCTT CT    C  CTTTTCTTG
                                |||| ||    |  |||||||||
                                GGAG GG    G  GGGGAGGGT
                                  G  GAGG_ GT
GAM1656  APBB1   3'  CAAGAGGAGCAGGAAGCAAGG  8599       GCAAA
                                CCTTGCT    CTGCTTTTCTTG
                                |||||||    ||||||||||||
                                GGAACGA    GACGAGGAGAAC
                                   AG___
GAM1656  AQP6    3'  CAGGGAGAGCAAGGGGCAAGG  54989      GCAAAC
                                CCTTGCT     TGCTTTTCTTG
                                |||||||     ||||||||||
                                GGAACGG     ACGAGAGGGAC
                                   GGA___
GAM1656  AQP6    3'  CAGGGAGGGCAGGGAGAGCAAG 54990      GCAAA
           G                     CCTTGCT    CTGCTTTTCTTG
                                |||||||    ||||||||||||
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                                GGAACGA    GACGGGAGGGAC
                                   GAGG_
GAM1656 AR      5' AAGAGAAGGGGAGGCGGGG   5270        GCAAA  G
                                CCTTGCT    CT CTTTTCTT
                                |||||||    || ||||||||
                                GGGGCGG    GG GAAGAGAA
                                   A____  G
GAM1656 ARHGAP6  5' CAAGGAGAGAGTGCAGGGAGG  26431     G    AACTG
                                CCTT CTGCA    CTTTTCTTG
                                |||| |||||    |||||||||
                                GGAG GACGT    GAGAGGAAC
                                  G    GA___
GAM1656 ARHGEF1  3' GGGAGGGGCCCAGCTGGG    17481     T   CAAACT
                                CCT GCTG     GCTTTTCTT
                                ||| ||||     |||||||||
                                GGG CGAC     CGGGGAGGG
                                  T   C_____
GAM1656 ASCL2    5' TGAGAAAGGCGACGGCGGCGG  18977       AAAC
                                TTGCTGC   TGCTTTTCTTG
                                |||||||   ||||||||||
                                GGCGGCG   GCGGAAAGAGT
                                   GCA_
GAM1656 ASH1     3' TGGGAAGGGTCCATCTGGGCAA 38090       GCAAACT
            GG                   CCTTGCT     GCTTTTCTTG
                                |||||||     |||||||||
                                GGAACGG     TGGGAAGGGT
                                   GTCTACC
GAM1656 ASIC4    3' TAGGGAAAGCCGGGTGGGG   38538    TG  GCAAACT
                                CCT  CT     GCTTTTCTTG
                                |||  ||     |||||||||
                                GGG  GG     CGAAAGGGAT
                                  GT  GC_____
GAM1656 ASIC4    5' TAGGGAGGGACAGGGCAGGGAG 38539     G   AAA  _
            G                    CCTT CTGC   CTG CTTTTCTTG
                                |||| ||||   ||| |||||||||
                                GGAG GACG   GAC GGGAGGGAT
                                  G   G__   A
GAM1656 ASS      3' GGGGGCAGCTGCGGTGGGG   5282     TG    AA    TT
                                CCT  CTGCA  CTGCTT  C
                                |||  |||||  ||||||  |
                                GGG  GGCGT  GACGGG  G
                                  GT    C_    GG
GAM1656 ASS      3' GGGGGGCAGCTGCGGTGGGG  5283     TG    AA    TT
                                CCT  CTGCA  CTGCTT  C
                                |||  |||||  ||||||  |
                                GGG  GGCGT  GACGGG  G
                                  GT    C_    GG
GAM1656 ATP1A2   3' AGGAAGAGGTTGCAGTGAG   7355    TG    ACTG
                                CT  CTGCAA   CTTTTCTT
                                ||  ||||||   ||||||||
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                                GA  GACGTT   GAGAAGGA
                                 GT     G___
GAM1656  ATP6V0A4  5'  GGGAGGGGCGCTGCGGGG    40552       T  AAACT
                                CCTTGC GC    GCTTTTCTT
                                |||||| ||    |||||||||
                                GGGGCG CG    CGGGGAGGG
                                   T _____
GAM1656  ATP8B2   5'  GGATTCCTGGTTTGCATGGGG  65840      C       GCTTT
                                CCTTG TGCAAACT    TCT
                                ||||| ||||||||    |||
                                GGGGT ACGTTTGG    AGG
                                   _       TCCTT
GAM1656  ATSV     3'  TGAGAAAATCCCATGGGGTGGG 16312     TG  G  AACTGC
             G                   CCT  CT CA     TTTTCTTG
                                |||  || ||     ||||||||
                                GGG  GG GT     AAAAGAGT
                                  GT  G  ACCCT_
GAM1656  BAZ1B    3'  TGGGAGGAGAGAGCGGCAG    51561       AAA  G
                                TTGCTGC   CT CTTTTCTTG
                                |||||||   || |||||||||
                                GACGGCG   GA GAGGAGGGT
                                   A__  _
GAM1656  BCL2L2   3'  CAAGGAAGGAGCGGAAGTAGGG 15754       GCAAA     __
                                CCTTGCT    CTGCTT  TTCTTG
                                |||||||    ||||||  ||||||
                                GGGATGA    GGCGAG  AGGAAC
                                   A_____     GA
GAM1656  BCL7A    3'  AGGAACGCTTTTTGGCGGGG   40977       TG    CT  T
                                CCTTGC  CAAA  GC TTTCT
                                ||||||  ||||  || |||||
                                GGGGCG  GTTT  CG AAGGA
                                   __    TT  C
GAM1656  BCL7A    3'  CAAGGGGAGTTGGCGCAGGTGA 40979     TG _   AAACT    TT
             GG                   CCT  C TGC    GCTT  CTTG
                                |||  | |||    ||||  ||||
                                GGA  G ACG    TGAG  GAAC
                                  GT G   CGGT_    GG
GAM1656  BCL7B    3'  CGAGAAGAGAGAGATGTGGAAG 9920      G TG  AACTG
             G                   CCTT C  CA    CTTTTCTTG
                                ||||  |  ||    |||||||||
                                GGAA G  GT    GAGAAGAGC
                                  _ GT  AGAGA
GAM1656  C20orf1  3'  TAAGGATCCCTTTGCTGTGAGG 25054     TG T    CTGCTT
                                CCT  C GCAAA     TTCTTG
                                |||  | |||||     ||||||
                                GGA  G CGTTT     AGGAAT
                                  GT T    CCCT__
GAM1656  CACNA1C  3'  CGGGGAGAGGAGGCGGCGAGG  7399          AAA  G
                                CCTTGCTGC   CT CTTTTCTTG
                                |||||||||   || |||||||||
```

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                                GGAGCGGCG  GA GAGAGGGGC
                                    ___ G
GAM1656 CACNA1S  5' CAGGGAAGGGAAAGCACTGGGG 5360     GC  AAACTG
                                CCTT TGC    CTTTTCTTG
                                |||| |||    |||||||||
                                GGGG ACG    GGAAGGGAC
                                  TC  AAAG__
GAM1656 CACNG1   3' TGGGGGAGGCAGAGCCAGCAGG 7413       CAAA    TT
                                CTTGCTG   CTGCTT CTTG
                                |||||||   ||||||  ||||
                                GGACGAC   GACGGA GGGT
                                    CGA_    GG
GAM1656 CACNG3   5' GGGAAGGGCGGGGTGAGG   22567    TG GCAAA
                                CCT CT    CTGCTTTTCTT
                                ||| ||    ||||||||||
                                GGA GG    GGCGGGAAGGG
                                 GT _____
GAM1656 CALM3    3' CAAGAGAGGCATTCCAGAAGG 19001     G  C AC
                                CCTT CTG AA TGCTTTTCTTG
                                |||| ||| ||  ||||||||||
                                GGAA GAC TT ACGGAGAGAAC
                                  _  C __
GAM1656 CAPN1    5' GGGAGGAGGGCGGGGAGG    19012     G   AAACTG
                                CCTT CTGC    CTTTTCTT
                                |||| ||||    ||||||||
                                GGAG GGCG    GAGGAGGG
                                  G   G_____
GAM1656 CAPN2    3' CAGGAAAAAAAAATGCAGGGAG 10010     G    AACTGC
            G                    CCTT CTGCA    TTTTCTTG
                                |||| |||||    ||||||||
                                GGAG GACGT    AAAAGGAC
                                  G    AAAAA_
GAM1656 CASP2    3' CGAGGAGAGTGATGCCGGTAA  53327      _ AAC
                                TTGCTG CA  TGCTTTTCTTG
                                |||||| ||  ||||||||||
                                AATGGC GT  GTGAGAGGAGC
                                   C  A__
GAM1656 CASP2    3' CGAGGAGAGTGATGCCGGTAA  53328      _ AAC
                                TTGCTG CA  TGCTTTTCTTG
                                |||||| ||  ||||||||||
                                AATGGC GT  GTGAGAGGAGC
                                   C  A__
GAM1656 CASP2    5' CGGGAAAAGCGGGAAATGGCGG 53329     AAA___
            C                    GCTGC    CTGCTTTTCTTG
                                |||||    ||||||||||||
                                CGGCG    GGCGAAAAGGGC
                                  GTAAAG
GAM1656 CASP4    5' CAAGAGAAGCAACGTATGGCAG 8724      GCAAAC
            G                    CTTGCT    TGCTTTTCTTG
                                ||||||    ||||||||||
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                                GGACGG     ACGAAGAGAAC
                                   TATGCA
GAM1656  CASP6    5'  AGGAAGAGGAGGGCAAGG    53360        GCAAA  G
                                CCTTGCT    CT CTTTTCTT
                                |||||||    || ||||||||
                                GGAACGG    GA GAGAAGGA
                                   ______ G
GAM1656  CBFA2T3  5'  CGGGAAAGGCAGTCCTGGTAGA 19015     TG    AA__
            GG                    CCT  CTGC    ACTGCTTTTCTTG
                                |||  ||||   ||||||||||||
                                GGA  GATG   TGACGGAAAGGGC
                                  __   GTCC
GAM1656  CCNB1    5'  AGGAGGGAGCAGTGCGGGG   50076       TGCAA      _
                                CCTTGC    ACTGCTTT TCTT
                                ||||||    |||||||| ||||
                                GGGGCG    TGACGAGG AGGA
                                   ______      G
GAM1656  CCND2    5'  CGGGGAAAGCAGGAGGGAGAGG 10050     G_  GCAAA
                                CCTT  CT    CTGCTTTTCTTG
                                ||||  ||    ||||||||||||
                                GGAG  GG    GACGAAAGGGGC
                                  AG  AG___
GAM1656  CCND3    3'  AGGGAAAATGCAGCAGGG    10059         AACTGC
                                CCTTGCTGCA     TTTTCTT
                                ||||||||||     |||||||
                                GGGACGACGT     AAAGGGA
                                     A_____
GAM1656  CCNG1    5'  CGGGGAGGGTGGTTACCGCTGA 15773     _  TGCA   TG
            GG                    CCTT GC    AAC  CTTTTCTTG
                                |||| ||    |||  |||||||||
                                GGAG CG    TTG  GGGAGGGGC
                                  T  CCA_   GT
GAM1656  CDK10    5'  CGAGAAGAGCACAAGCAGAGG  54833     TG    AAAC
                                CCT  CTGC    TGCTTTTCTTG
                                |||  ||||   ||||||||||
                                GGA  GACG    ACGAGAAGAGC
                                  __    AAC_
GAM1656  CDK3     3'  TGGGGAGAGCAAAGCACTAAGG 8843       C   AAAC
                                CCTTG TGC    TGCTTTTCTTG
                                ||||| |||    ||||||||||
                                GGAAT ACG    ACGAGAGGGGT
                                   C   AA__
GAM1656  CDKN1B   3'  GGGGAAGGGAGGGCAGGG    15793        GCAAA  G
                                CCTTGCT    CT CTTTTCTT
                                |||||||    || ||||||||
                                GGGACGG    GA GGAAGGGG
                                   ______ G
GAM1656  CDS1     5'  CGGGAGGGGCCTGCGCGGCGGC 8849     _      AAACT
            GG                    CC TTGCTGC    GCTTTTCTTG
                                || |||||||    ||||||||||
```

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                                GG GGCGGCG    CGGGGAGGGC
                                 C      CGTC_
GAM1656 CENTD2   5' CAGGGGGAGGGGAGTGTGAGG 31538    TG T  AAA  G   TT
                                CCT  C GC   CT CTT  CTTG
                                |||  | ||   || |||  ||||
                                GGA  G TG   GG GAG  GGAC
                                  GT _  A__  G   GG
GAM1656 CEP2    5' CAAGAGGAGGTTGAAGTGGCAT 23242    T   TG AAACTG
             GG                   CC TGC  C     CTTTTCTTG
                                || |||  |     |||||||||
                                GG ACG  G     GAGGAGAAC
                                 T   GT AAGTTG
GAM1656 CHD4    3'  GGGGAGGGGAGGGAGTGAGG   8876     TG  GCAAA  G
                                CCT  CT    CT CTTTTCTT
                                |||  ||    || ||||||||
                                GGA  GA    GA GGGAGGGG
                                  GT  GG___  G
GAM1656 CHGA    5'  AGGGGAGCTTGCGGGAGG    8878      G     ACT    TT
                                CCTT CTGCAA   GCTT  CT
                                |||| ||||||   ||||  ||
                                GGAG GGCGTT   CGAG  GA
                                  _     ___    GG
GAM1656 CHRNA4   3'  AAGAGGGGCGGGGCCAGG    7435      T   GCAAA
                                CCT GCT    CTGCTTTTCTT
                                ||| |||    ||||||||||
                                GGA CGG    GGCGGGGAGAA
                                  C  _____
GAM1656 CHRNE    3'  AGGGAGGCTGTAGCCAGG    5376      T     AACT    TT
                                CCT GCTGCA    GCTT  CT
                                ||| ||||||    ||||  ||
                                GGA CGATGT    CGGA  GA
                                  C     _____    GG
GAM1656 CHST6    3'  TGGGAAAGGTAGGAGGAGAGAA 41506      G  GCAAA_
             GG                   CCTT CT     CTGCTTTTCTTG
                                ||||  ||     ||||||||||||
                                GGAA GA     GATGGAAAGGGT
                                  _  GAGGAG
GAM1656 CHST6    3'  TGGGGAGGGCTGGGCAGCAAG  41507        AAACT
                                CTTGCTGC    GCTTTTCTTG
                                ||||||||    ||||||||||
                                GAACGACG    CGGGAGGGGT
                                    GGT__
GAM1656 CHST7    3'  GAGATGAAGTTTCCAGTAAGG  39579        C    GCT
                                CCTTGCTG AAACT   TTTC
                                |||||||| |||||   ||||
                                GGAATGAC TTTGA   AGAG
                                    C    AGT
GAM1656 CIS4     3'  GGGGAAGTGTCAGCAAGG    16168        CAA  T    TT
                                CCTTGCTG   AC GCTT  CT
                                ||||||||   || ||||  ||
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                                GGAACGAC   TG TGAA  GG
                                   ___  _   GG
GAM1656  CISH     3'  CAGGAAGAGCCAGCAAGAGCAA 26179        GCAAA  _
              GG                    CCTTGCT    CTG CTTTTCTTG
                                    |||||||    ||| |||||||||
                                    GGAACGA    GAC GAGAAGGAC
                                       GAAC_  C
GAM1656  CIT      3'  CAGGAGGGGCAGGTGGCTGAGG 70301      _  TG AAA
                                    CCTT GC  C   CTGCTTTTCTTG
                                    ||||  ||  |   ||||||||||||
                                    GGAG CG  G   GACGGGGAGGAC
                                      T  GT ___
GAM1656  CKAP1    5'  GGGAGGGGGAGGTGCCAGGG   73903      CT   AA  G
                                    CCTTG  GCA  CT CTTTTCTT
                                    |||||  |||  || ||||||||
                                    GGGAC  CGT  GA GGGGAGGG
                                      __  G_  G
GAM1656  CLN5     5'  TGAGGGGAGCGGTAGGGGAGG  22434      G  GCAA      TT
                                    CCTT CT    ACTGCTT  CTTG
                                    ||||  ||    |||||||  ||||
                                    GGAG GG    TGGCGAG  GAGT
                                      G  A___      GG
GAM1656  CLTCL1   3'  GAGGGAGTACCTGAGCAAGG   64422        G  A__   G
                                    CCTTGCT CA   ACT CTTT
                                    |||||||  ||   ||| ||||
                                    GGAACGA GT   TGA GGAG
                                       _  CCA   G
GAM1656  COL4A4   5'  GGGGAGGTGGCTGCGCAGGG   5405        T   AA TG   TT
                                    CCTTGC GCA  C  CTT  CT
                                    ||||||  |||  |  |||  ||
                                    GGGACG CGT  G  GGA  GG
                                       _  C_ GT   GG
GAM1656  COMP     3'  GAGAAGGGCTCAGAGAGG    5414      TG   CAAACT
                                    CCT  CTG     GCTTTTCTT
                                    |||  |||     |||||||||
                                    GGA  GAC     CGGGAAGAG
                                      GA   T_____
GAM1656  CORO1C   3'  TAGGGAGGGCGGAAAGGGAGG  27507      G  GCAAA
                                    CCTT CT    CTGCTTTTCTTG
                                    ||||  ||    ||||||||||||
                                    GGAG GA    GGCGGGAGGGAT
                                      G  AA___
GAM1656  CORO2B   5'  TGAGGGAGGCAGGGCTAGAGG  65176      GCT  AAA     TT
                                    CCTT   GC   CTGCTT  CTTG
                                    ||||   ||   ||||||  ||||
                                    GGAG   CG   GACGGA  GAGT
                                      AT_  G__     GG
GAM1656  CPE      5'  CGGGGAAGGTGAGGCGAGTAGA 10285     _   _  AAAC
              GG                    CCT TGCT GC    TGCTTTTCTTG
                                    ||| |||| ||    ||||||||||
```

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                                GGA ATGA CG   GTGGAAGGGGC
                                  G   G  GA__
GAM1656  CRY2     3'  CAGGAGGAGACCAGGTTGCAGT 72658   TG     A  __
                GG                  T  CTGCAA CTG  CTTTTCTTG
                                | ||||||| |||  |||||||||
                                G  GACGTT GAC  GAGGAGGAC
                                 GT     G   CA
GAM1656  CRYAA    3'  TGGGGGGAGCACCCTGAGGGCG 6367        G_  AAC    TT
                GGG                   CCTTGCT  CA   TGCTT  CTTG
                                ||||||| ||   |||||  ||||
                                GGGGCGG  GT   ACGAG  GGGT
                                    GA  CCC    GG
GAM1656  CSNK1D   5'  GAGGGGGGCGGAGCCGGG    10315     T   GCAAA     TT
                                CCT GCT    CTGCTT  CTT
                                ||| |||    ||||||  |||
                                GGG CGA    GGCGGG  GAG
                                  C  _____     GG
GAM1656  CSNK2A1  3'  CAGGGGAGGCAGGAAGAAAGGA 10317     G  GCAAA_     TT
                AGG                   CCTT CT     CTGCTT  CTTG
                                |||| ||     ||||||  ||||
                                GGAA GA     GACGGA  GGAC
                                  G  AAGAAG     GG
GAM1656  CSPG3    3'  TGAGGGAAGCACAAGTAGCAA  16520        AAAC    TT
                                TTGCTGC    TGCTT  CTTG
                                |||||||    |||||  ||||
                                AACGATG    ACGAA  GAGT
                                    AAC_    GG
GAM1656  CTMP     3'  CAGGAGGAAGAGGTTGCAGTGA 54948    TG     A  GC
                G                    CT  CTGCAA CT  TTTTCTTG
                                ||  ||||||  ||  ||||||||
                                GA  GACGTT GA  AGGAGGAC
                                 GT     G  GA
GAM1656  CTNS     3'  TGGGGAAGGCCTCACCCAGCGA 18224       CAAACT
                                TTGCTG     GCTTTTCTTG
                                ||||||     ||||||||||
                                AGCGAC     CGGAAGGGGT
                                    CCACTC
GAM1656  CUL5     3'  TGGGAAGGGTGAGGGTGGGGT  14433     G  AA  _
                                GCT CA  CT GCTTTTCTTG
                                ||| ||  || ||||||||||
                                TGG GT  GA TGGGAAGGGT
                                  G  GG  G
GAM1656  CYP27A1  5'  TGGGAGGAGCGAGGGAGCGAGC 7602      _  AAA  _
                                GCT GC   CT GCTTTTCTTG
                                ||| ||   || ||||||||||
                                CGA CG   GA CGAGGAGGGT
                                  G  AGG  G
GAM1656  DACH     3'  CAAGAGACTCTTGTAGCAG   55821         ACTGCT
                                TTGCTGCAA     TTTCTTG
                                |||||||||     |||||||
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                                GACGATGTT     AGAGAAC
                                     CTC___
GAM1656  DBT     3'  TAGGGGAGGCTGAAGCAGGAGG 10378     G   AAACT   TT
                                CCTT CTGC    GCTT  CTTG
                                |||| ||||    ||||  ||||
                                GGAG GACG    CGGA  GGAT
                                  _   AAGT_   GG
GAM1656  DBY     3'  AGGAAGGATTGTGCAGCAGG   17405        AACTG
                                CTTGCTGCA    CTTTTCT
                                |||||||||    |||||||
                                GGACGACGT    GGAAGGA
                                     GTTA_
GAM1656  DDX26    5'  CAGGAGGAGGCGGAGGCGGGG  25113       GCAAA     _
                                CCTTGCT    CTGCTTT TCTTG
                                |||||||    ||||||| |||||
                                GGGGCGG    GGCGGAG AGGAC
                                    A_____      G
GAM1656  DGCR2    3'  CAGGAAGAAGCTCTGGAGTGGG 18896     TG  G  AACT    _
             G                   CCT  CT CA    GCTTTT CTTG
                                 |||  || ||    |||||| ||||
                                 GGG  GA GT    CGAAGA GGAC
                                   GT  G  CT__     A
GAM1656  DIPA     3'  CAGGAGGGGCCGCTGGCATGG  23391    T   _  AAACT
                                CC TGCT GC    GCTTTTCTTG
                                || |||| ||    ||||||||||
                                GG ACGG CG    CGGGGAGGAC
                                 T   T  C____
GAM1656  DISC1    5'  CGGGAGGAGCTGGCAGCGGGG  38505        AAACT
                                CCTTGCTGC    GCTTTTCTTG
                                |||||||||    ||||||||||
                                GGGGCGACG    CGAGGAGGGC
                                     GT___
GAM1656  DLG4     3'  GAGGGAGGGTGGGGCAGGG   9081        G  AA  G   TT
                                CCTTGCT CA  CT CTT  C
                                ||||||| ||  || |||  |
                                GGGACGG GT  GA GGA  G
                                    G  GG  G
GAM1656  DLG4     5'  TAGGGAAAGAGAAGTGTAAGG  9087       T  AAA  G
                                CCTTGC GC   CT CTTTTCTTG
                                |||||| ||   || |||||||||
                                GGAATG TG   GA GAAAGGGAT
                                   _ AA_  _
GAM1656  DNM2     3'  CGAGGGGGGCGTGCTCTCGGGG 18233      CT_   AAC    TT
                                CCTTG   GCA   TGCTT  CTTG
                                |||||   |||   |||||  ||||
                                GGGGC   CGT   GCGGG  GAGC
                                  TCT   ___     GG
GAM1656  DNMT3B   3'  AGGAGAGGAGTGTGAAGCAAGG 23547       G  A   G     TG
                                CCTTGCT CA ACT CTTTTCT
                                ||||||| || ||| |||||||
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                                GGAACGA GT TGA GAGAGGA
                                    A  G   G      T
GAM1656  DPP4     3'  TAGGGAGAGAAGATAGCAGGG  10423        CAAA  G
                                CCTTGCTG    CT CTTTTCTTG
                                ||||||||    || |||||||||
                                GGGACGAT    GA GAGAGGGAT
                                    A___  A
GAM1656  DPYSL3   5'  GAGGAAGGCGCGGGCGAG    9125        _  AAACT
                                CTTGCT GC     GCTTTTCTT
                                |||||| ||     |||||||||
                                GAGCGG CG     CGGAAGGAG
                                   G  _____
GAM1656  DUX4     5'  CGGGGGGAGGAAGGCAGGGAGG 73195      G    AAACTG   TT
                                CCTT CTGC      CTT  CTTG
                                |||| ||||      |||  ||||
                                GGAG GACG      GAG  GGGC
                                  G    GAAG__   GG
GAM1656  DVL3     5'  CAAGAGGAGTCGCGGCGGCAAG 16637         AAACT
                                CTTGCTGC     GCTTTTCTTG
                                ||||||||     ||||||||||
                                GAACGGCG     TGAGGAGAAC
                                    GCGC_
GAM1656  DXS1283E 3'  CAAGAGAAGAAAACTTGTGCAG 71386       T    ACTG_
            GG                    CCTTGC GCAA     CTTTTCTTG
                                ||||||  ||||     |||||||||
                                GGGACG TGTT     GAAGAGAAC
                                   _    CAAAA
GAM1656  ECEL1    3'  CAGGAGGGGCCTGGAGCAGGG  17889        G  AACT
                                CCTTGCT CA    GCTTTTCTTG
                                |||||||  ||    ||||||||||
                                GGGACGA GT    CGGGGAGGAC
                                    G  C___
GAM1656  ECM2     3'  TAAGGAAAGCTGGCAGAAGG   9150       G    AAACT
                                CCTT CTGC     GCTTTTCTTG
                                |||| ||||     ||||||||||
                                GGAA GACG     CGAAAGGAAT
                                  _    GT___
GAM1656  EDAR     5'  AGGGAAAGCCCCTCGGCAAGG  42521         CAAACT       G
                                CCTTGCTG      GCTTTTCTT
                                ||||||||      |||||||||
                                GGAACGGC      CGAAAGGGA
                                    TCCC__
GAM1656  EDAR     5'  AGGTGAGTTTGCAATGAGG    42523      GC       _
                                CCTT  TGCAAACT GCTT
                                ||||  |||||||| ||||
                                GGAG  ACGTTTGA TGGA
                                  TA       G
GAM1656  EDNRA    5'  CGGGAGAAGCAGTGCCCAGGAG 64800      G   CAA
            G                     CCTT CTG   ACTGCTTTTCTTG
                                ||||  |||   ||||||||||||
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                                GGAG GAC   TGACGAAGAGGGC
                                  _   CCG
GAM1656  EFNA3    3'  GGGGGGGGAGAGATGGGGCGGG 18253       G  AA_  G   TT  TG
                G                  CCTTGCT CA   CT CTT  CT
                                   ||||||| ||   || |||  ||
                                   GGGGCGG GT   GA GGG  GG
                                       G  AGA  G   GG  T
GAM1656  EGFL4    3'  CAGGAGGAGCAGGGGCCAGCAG 62456    _     _ AAA
                TGG                  CC TTGCTG C   CTGCTTTTCTTG
                                   || |||||| |   ||||||||||||
                                   GG GACGAC G   GACGAGGAGGAC
                                    T     C GG_
GAM1656  EGFL5    3'  GGGAGAATGTTTGTGTAAGG   87916       T     TGC
                                   CCTTGC GCAAAC   TTTTCT
                                   |||||| ||||||   ||||||
                                   GGAATG TGTTTG   AGAGGG
                                      _     TA_
GAM1656  EGR3     3'  CGAGAGGGGGAGGGGGTAAGG  60303       GCAAA  G
                                   CCTTGCT    CT CTTTTCTTG
                                   |||||||    || |||||||||
                                   GGAATGG    GA GGGGAGAGC
                                       GG___  G
GAM1656  EIF4EBP1  3'  TGGGAGGAGTCCCACCAGCCAG 15852     T    CAAACT
                G                  CCT GCTG     GCTTTTCTTG
                                   ||| ||||     ||||||||||
                                   GGA CGAC     TGAGGAGGGT
                                     C    CACCC_
GAM1656  ELOVL4   5'  AGGAGAAGACGCAGCCGGG   42989     T    AAACTG
                                   CCT GCTGC     CTTTTCTT
                                   ||| |||||     ||||||||
                                   GGG CGACG     GAAGAGGA
                                     C    CA_____
GAM1656  ELOVL4   3'  TAAGAAAGAATTGCAGTAA   42991         ACTG   T
                                   TTGCTGCAA    CTTT CTTG
                                   |||||||||    |||| ||||
                                   AATGACGTT    GAAA GAAT
                                        AA__    _
GAM1656  EN2      5'  TAAGGGGAGGAGGGGCGGCGGG 9271         AAA  G   TT
                                   CTTGCTGC   CT CTT  CTTG
                                   ||||||||   || |||  ||||
                                   GGGCGGCG   GA GAG  GAAT
                                       GG_  G   GG
GAM1656  ENPP3    3'  AGGGAAGGCAGGTGGTGGG    18468    TG TG AAA        G
                                   CT  C  C   CTGCTTTTCTT
                                   ||  |  |   ||||||||||
                                   GG  G  G   GACGGAAGGGA
                                    GT GT ____
GAM1656  EPB49    3'  TGGGAGGGGCAGGAGGTGGGG  10530     TG  GCAAA
                                   CCT  CT    CTGCTTTTCTTG
                                   |||  ||    ||||||||||||
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                              GGG  GG    GACGGGGAGGGT
                                GT  AG___
GAM1656  EPHA8    3'  GAGGAGGTGTGTGAGCAGGG   40433       G  A  TG
                              CCTTGCT CA AC  CTTTTC
                              ||||||| || ||  ||||||
                              GGGACGA GT TG  GAGGAG
                                 _  G  TG
GAM1656  EPHB4    5'  CAGGGAGAGTCAGACCTGGGGG 16706     G  GCAAA  _
            GG                  CCTT CT    CTG CTTTTCTTG
                              |||| ||    ||| |||||||||
                              GGGG GG    GAC GAGAGGGAC
                                G  TCCA_   T
GAM1656  ESPN     5'  TGGGGAAGGCGCTGAGTGCGG  49703      AAC__
                              CTGCA    TGCTTTTCTTG
                              |||||    ||||||||||
                              GGCGT    GCGGAAGGGGT
                                 GAGTC
GAM1656  ETS1     5'  CAGGAGGAGCGGGCGCGCGGCG 19113        AAA_
            GG                  CTTGCTGC   CTGCTTTTCTTG
                              ||||||||   ||||||||||||
                              GGGCGGCG   GGCGAGGAGGAC
                                  CGCG
GAM1656  EXT2     5'  GGGAAAACACTGCAGCGG    6382         AAC  C
                              TTGCTGCA   TG TTTTCT
                              ||||||||   || ||||||
                              GGCGACGT   AC AAAGGG
                                  C__  A
GAM1656  EXTL3    3'  GGAAGTTTTACAGCAAGG    9335         C   CT    TT
                              CCTTGCTG AAA  GCTT  C
                              |||||||| |||  ||||  |
                              GGAACGAC TTT  TGAA  G
                                  A   __   GG
GAM1656  EXTL3    3'  TGGGGAGCTCCTAGTTTGTGGG 9339     G TG    ____   TT TTG
            GGG                   CTT C  CAAACT   GCTT  C
                              ||| |  ||||||   ||||  |
                              GGG G  GTTTGA   CGAG  G
                                G GT     TCCT   GG T
GAM1656  EZH1     3'  TGGGAGAGGCAGACGAGTGAG  10557    TG  GCAAA
                              CT  CT    CTGCTTTTCTTG
                              ||  ||    ||||||||||||
                              GA  GA    GACGGAGAGGGT
                               GT  GCA__
GAM1656  FANCG    5'  CGAGAGAAGCAGGGGAGCTCGG 17336       __  AAA_
            CGGGG                CCTTGCT  GC   CTGCTTTTCTTG
                              |||||||  ||   ||||||||||||
                              GGGGCGG  CG   GACGAAGAGAGC
                                  CT  AGGG
GAM1656  FBXW1B   5'  GGGGAGAGCGAGGCGGGG    25475       GCAAACT
                              CCTTGCT     GCTTTTCTT
                              |||||||     |||||||||
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                                GGGGCGG      CGAGAGGGG
                                   AG_____
GAM1656  FBXW1B   5'  GGGGAGAGCGAGGCGGGG    25476       GCAAACT
                                CCTTGCT      GCTTTTCTT
                                |||||||      |||||||||
                                GGGGCGG      CGAGAGGGG
                                   AG_____
GAM1656  FBXW1B   5'  GGGGAGAGCGAGGCGGGG    25477       GCAAACT
                                CCTTGCT      GCTTTTCTT
                                |||||||      |||||||||
                                GGGGCGG      CGAGAGGGG
                                   AG_____
GAM1656  FCAR     3'  CAGGAGGCAGCTGTTGCAGTGA 56563    TG     ACT  _
            G                    CT  CTGCAA   GCT TTTCTTG
                                ||  ||||||   ||| |||||||
                                GA  GACGTT   CGA GGAGGAC
                                 GT     GT_   C
GAM1656  FCAR     3'  CAGGAGGCAGCTGTTGCAGTGA 56564    TG     ACT  _
            G                    CT  CTGCAA   GCT TTTCTTG
                                ||  ||||||   ||| |||||||
                                GA  GACGTT   CGA GGAGGAC
                                 GT     GT_   C
GAM1656  FGF18    5'  CGAGGAGGGAGCAGCAGCAGCG 15257       AAA    __
                                TGCTGC   CTGCTT  TTCTTG
                                ||||||   ||||||  ||||||
                                GCGACG   GACGAG  AGGAGC
                                   AC_     GG
GAM1656  FGF18    5'  GGGAGGAGCCGCGCGGGG    15261       T  AAACT
                                CCTTGC GC    GCTTTTCTT
                                |||||| ||    |||||||||
                                GGGGCG CG    CGAGGAGGG
                                   _  C_____
GAM1656  FKRP     3'  TAAGGAGAGCATGAGAGAAGG  44438     G  G_  AAC
                                CCTT CT  CA   TGCTTTTCTTG
                                |||| ||  ||   ||||||||||
                                GGAA GA  GT   ACGAGAGGAAT
                                  _  GA  ___
GAM1656  FLG      3'  CAGGAGAAGCAGGCGCCAGGG  71447      C   AAA
                                CCTTG TGC   CTGCTTTTCTTG
                                ||||| |||   ||||||||||||
                                GGGAC GCG   GACGAAGAGGAC
                                   C  ___
GAM1656  FLI1     5'  CAGGGAGGGCCCAGGGCGCCAG 77106      C   AAACT
            GG                    CCTTG TGC    GCTTTTCTTG
                                ||||| |||    ||||||||||
                                GGGAC GCG    CGGGAGGGAC
                                   C   GGACC
GAM1656  FLT4     3'  CAAGAGGAGCATGAAAGTGGAC 10668      _ TG AAAC_
            AAGG                   CCTTG C  C    TGCTTTTCTTG
                                ||||| |  |    ||||||||||
```

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                                GGAAC G  G    ACGAGGAGAAC
                                  A GT AAAGT
GAM1656  FN14    3'  GGGGAGAGTTTGGAGGGG   34043    TG  G    G   TT
                                CCT  CT CAAACT CTT  C
                                |||  || |||||| |||  |
                                GGG  GA GTTTGA GAG  G
                                 __  G     _   GG
GAM1656  FOLR1   5'  CAAGGAGAAGGTGGAGTGAGG  34114    TG  G AA   GC
                                CCT  CT C  ACT  TTTTCTTG
                                |||  || |  |||  ||||||||
                                GGA  GA G  TGG  AGAGGAAC
                                 GT  G __   A_
GAM1656  FOXD2   5'  GGGAGAGGACGGGTGGGG   16790    TG TGCAAA  _
                                CCT  C     CTG CTTTTCTT
                                |||  |     ||| ||||||||
                                GGG  G     GGC GGAGAGGG
                                 GT _______  A
GAM1656  FOXE1   3'  GGGAGGAGGTGGGGCGAGG   16781       G  AACTG
                                CCTTGCT CA    CTTTTCTT
                                |||||||  ||    ||||||||
                                GGAGCGG GT    GAGGAGGG
                                   G  G____
GAM1656  FRAT2   3'  CAAGGTCACGGTTTGCTGTGGG 24899    TG T      CTTT
           G                     CCT  C GCAAACTG   TCTTG
                                |||  | ||||||||   |||||
                                GGG  G CGTTTGGC   GGAAC
                                 GT T       ACT_
GAM1656  FUT4    3'  TGAGGAGGGCAGTCCAAGAGGG 10724     G  GCAA
                                CCTT CT   ACTGCTTTTCTTG
                                ||||  ||   ||||||||||||
                                GGGA GA   TGACGGGAGGAGT
                                  _  ACC_
GAM1656  FXYD1   5'  GGGGGCCTTCTTTCAGCAGGG  41859       C   CT__
                                CCTTGCTG AAA   GCTTTT
                                ||||||||  |||   ||||||
                                GGGACGAC TTT   CGGGGG
                                    _  CTTC
GAM1656  FZD8    3'  CAGGAGGGGTGGGGAGGGGGGC 49872       GCAAA__ TG
           GAGG                  CCTTGCT     C  CTTTTCTTG
                                |||||||      |  |||||||||
                                GGAGCGG      G  GGGGAGGAC
                                   GGGGAGG GT
GAM1656  GADD45G  3'  AGGAGGGGCCCGGTGGCGGCAG 22953        AA  __      G
           GG                   CCTTGCTGC  ACT  GCTTTTCTT
                                |||||||||  |||  |||||||||
                                GGGACGGCG  TGG  CGGGGAGGA
                                   G_  CC       G
GAM1656  GADD45G  3'  CGGGGGGGGGCGCCTGGAGAGCG 22955       GCAAAC_    TT
           AGG                   CCTTGCT     TGCTT  CTTG
                                |||||||      |||||  ||||
```

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                                GGAGCGA     GCGGG  GGGC
                                   GAGGTCC    GG
GAM1656  GALNT2   3'  GGGAGGGGTCCTTTGCGGTGAG 16818   TG     CT      G
                                CT  CTGCAAA  GCTTTTCTT
                                ||  |||||||  |||||||||
                                GA  GGCGTTT  TGGGGAGGG
                                 GT      CC       G
GAM1656  GFRA2    3'  GGGAGAGCCCTTGTGGCGAGG  9466      TG   ACT      TG
                                CCTTGC  CAA   GCTTTTCT
                                ||||||  |||   ||||||||
                                GGAGCG  GTT   CGAGAGGG
                                   GT   CC_      T
GAM1656  GJA1     5'  TGAGGAAAGTACCAAACAGCAG 5715       AAAC___
            C                    GCTGC      TGCTTTTCTTG
                                |||||      ||||||||||
                                CGACG      ATGAAAGGAGT
                                   ACAAACC
GAM1656  GJB1     3'  TAAGAGGAGCAGAGGGCAGGG  60639       GCAAA
                                CCTTGCT    CTGCTTTTCTTG
                                |||||||    ||||||||||||
                                GGGACGG    GACGAGGAGAAT
                                   GA___
GAM1656  GJB1     5'  TGGGAAAGGGCAGCAGCAGCCA 60640     T    AAA    _
            GG                   CCT GCTGC   CTGCT TTTCTTG
                                ||| |||||   ||||| |||||||
                                GGA CGACG   GACGG AAAGGGT
                                  C    AC_    G
GAM1656  GLUL     3'  CAAGGGAAGTGGTTCTTAGATG 10806    TTG   CA   TG   TT
            G                    CC   CTG  AAC  CTT  CTTG
                                ||   |||  |||  |||  ||||
                                GG   GAT  TTG  GAA  GAAC
                                 TA_   TC   GT   GG
GAM1656  GNA15    5'  CAGGACCCAGTCTGCGGTGGGG 60586     TG    A   CTTT
                                CCT  CTGCA ACTG    TCTTG
                                |||  ||||| ||||    |||||
                                GGG  GGCGT TGAC    AGGAC
                                  GT    C    CC__
GAM1656  GPC1     3'  GAAGGGGTCCTGCAGGGGG    10859     G    A_   G   TT
                                CTT CTGCA  ACT CTT  C
                                ||| |||||  ||| |||  |
                                GGG GACGT  TGG GAA  G
                                  G    CC   G   G
GAM1656  GPR30    5'  CAGGAGAGGCGGCCCTGGTGGG 9491      TG  GCAAA
            G                    CCT  CT    CTGCTTTTCTTG
                                |||  ||    ||||||||||||
                                GGG  GG    GGCGGAGAGGAC
                                  GT  TCCC_
GAM1656  GPR48    5'  CGGGAGAGGCCGGCGCGGGAGG 38094      G    AAACT
                                CCTT CTGC    GCTTTTCTTG
                                |||| ||||    ||||||||||
```

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                                GGAG GGCG    CGGAGAGGGC
                                  _   CGGC_
GAM1656 GRIA1   5' CAAGGAAGGAACTGCAGGAGG 7709      G    AACTG
                                CCTT CTGCA    CTTTTCTTG
                                |||| |||||    |||||||||
                                GGAG GACGT    GGAAGGAAC
                                  _    CAA__
GAM1656 GRIN2C  3' AGGAGGGTGTGCTGTGGGG  7733     TG T  AAC
                                CCT  C GCA   TGCTTTTCT
                                |||  | |||   |||||||||
                                GGG  G CGT   GTGGGAGGA
                                  GT T  ____
GAM1656 GRM4    5' GGGAGAGGGTAGCAGCATGG  7752     T     AA  G
                                CC TGCTGC  ACT CTTTTCT
                                || ||||||  ||| |||||||
                                GG ACGACG  TGG GAGAGGG
                                 T     A_  _
GAM1656 GUCA2A  3' CGGGAGGAGCAGCCCGGGGAGG 70600     G   CAAA
                                CCTT CTG    CTGCTTTTCTTG
                                |||| |||    ||||||||||||
                                GGAG GGC    GACGAGGAGGGC
                                  G   CC__
GAM1656 GUCY1A3 5' CAGGAGGAGATCGCAGCAGGG  64225         AAACTG
                                CCTTGCTGC     CTTTTCTTG
                                |||||||||     |||||||||
                                GGGACGACG     GAGGAGGAC
                                     CTA___
GAM1656 GYS1    3' GAGAGGGGAGGGCAGGAGGG  89784     G    AAA  G
                                CCTT CTGC   CT CTTTT
                                |||| ||||   || |||||
                                GGGA GACG   GG GAGAG
                                  G    GGA  G
GAM1656 HADHB   3' GAGGGTTTGCAGTTGGG     5740      T        G
                                CCT GCTGCAAACT CTT
                                ||| |||||||||| |||
                                GGG TGACGTTTGG GAG
                                  T         _
GAM1656 HCFC1   3' TGGGGAGAGACTTTTGCGGGGA 71550      G      CTG
            GG                    CCTT CTGCAAA   CTTTTCTTG
                                |||| |||||||   |||||||||
                                GGAG GGCGTTT   GAGAGGGGT
                                  G      TCA
GAM1656 HCN4    5' GGGAGGAGGTGTAGCGCGG   19685    T     AACTG
                                CC TGCTGCA    CTTTTCTT
                                || |||||||    ||||||||
                                GG GCGATGT    GAGGAGGG
                                 C      G____
GAM1656 HIP12   3' CAGGAGGGGTGGGACCAGGCTG 66815     T   GCAAA TG
            GG                    CCT GCT    C  CTTTTCTTG
                                ||| |||    |  |||||||||
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                                GGG CGG    G  GGGGAGGAC
                                  T   ACCAG GT
GAM1656  HLA-E    3'  CGAGGAGGGCAGATCACGAGG  92674      C  CAAA
                                CCTTG TG    CTGCTTTTCTTG
                                ||||| ||    ||||||||||||
                                GGAGC AC    GACGGGAGGAGC
                                  _  TA__
GAM1656  HMGN1    5'  CGGGAGGAGTGGCAGCGGCAAG 18303         AAA TG
            G                    CCTTGCTGC   C  CTTTTCTTG
                                |||||||||   |  |||||||||
                                GGAACGGCG   G  GAGGAGGGC
                                     AC_ GT
GAM1656  HOXB13   3'  TGGGAGGAGCGAAAGTGGGG   22064     TG  GCAAAC
                                CCT  CT     TGCTTTTCTTG
                                |||  ||     ||||||||||
                                GGG  GA     GCGAGGAGGGT
                                  GT  AA____
GAM1656  HOXB5    3'  TAAGGGGCAGCAGTTGAGGTGG 10959     TG  GCA      _ TT
            GG                   CCT  CT   AACTGCT T  CTTG
                                |||  ||   ||||||| |  ||||
                                GGG  GG   TTGACGA G  GAAT
                                  GT  AG_      C GG
GAM1656  HOXC4    5'  TGGGGAGGGTGGGGATGGGAGG 28251      G  GCAAA TG
            G                    CCTT CT     C  CTTTTCTTG
                                ||||  ||     |  |||||||||
                                GGGA GG     G  GGGAGGGGT
                                  G  TAGG_ GT
GAM1656  HOXC6    3'  CGGGGAGGGCCGGAGCGGAGGG 16908      G    AAACT
                                CCTT CTGC     GCTTTTCTTG
                                ||||  ||||    ||||||||||
                                GGGA GGCG     CGGGAGGGGC
                                  _    AGGC_
GAM1656  HPCAL1   3'  GGGAAGGGTGGGGACGAGG    10968      _  GCAAA TG
                                CCTTG CT     C  CTTTTCTT
                                |||||  ||    |  ||||||||
                                GGAGC GG     G  GGGAAGGG
                                  A  _____ GT
GAM1656  HSPA1L   5'  CAGGGAGGGACGGGGTGGGG   99599     TG  GCAAA  _
                                CCT  CT    CTG CTTTTCTTG
                                |||  ||    ||| |||||||||
                                GGG  GG    GGC GGGAGGGAC
                                  GT  _____   A
GAM1656  IFNGR2   5'  TGGGGGGGGTCAGGAGGGGTGG 19851     TG  GCAAA  _   TT
            GG                   CCT  CT    CTG CTT  CTTG
                                |||  ||    ||| |||  ||||
                                GGG  GG    GAC GGG  GGGT
                                  GT  GGAG_   T   GG
GAM1656  IHPK3    3'  GAGACACGGCTTGCAGTGGGG  55096     TG     A   CT
                                CCT  CTGCAA CTG  TTTC
                                |||  |||||| |||  ||||
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                                GGG  GACGTT GGC  AGAG
                                  GT     C   AC
GAM1656  IL18R1   3'  GGAGGAGGGGCTGGCAGGG   15253        _  AAA  G   TT
                                CCTTGCT GC   CT CTT  C
                                ||||||| ||   || |||  |
                                GGGACGG CG   GA GGA  G
                                    T  GG_  _   GG
GAM1656  IL4R     3'  TGAGGAGAGTGGAACAGAAGG  6458       G   CAAA TG
                                CCTT CTG    C  CTTTTCTTG
                                |||| |||    |  |||||||||
                                GGAA GAC    G  GAGAGGAGT
                                  _   AA__ GT
GAM1656  INHA     5'  TGAGAAGGGTAGAAGAGGGTGG 11001     TG  GCAAA
              G                  CT  CT     CTGCTTTTCTTG
                                 ||  ||     ||||||||||||
                                GG  GG     GATGGGAAGAGT
                                 GT  GAGAA
GAM1656  ISLR     3'  TGGGAGAAGCCTCAGTGGTGG  19883    _ TG   CAAACT
                                CC T  CTG      GCTTTTCTTG
                                || |  |||      ||||||||||
                                GG G  GAC      CGAAGAGGGT
                                 T GT   TC____
GAM1656  ITGA2    3'  GGGGAGGTGCGGGGGGCAGGTA 11026        _   AAA    T     G
              GGG                  CCTTGC TGC   CTGC TTTCTT
                                   ||||||  |||   ||||  ||||||
                                   GGGATG ACG   GGCG GGAGGG
                                      G   GGG    T     GG
GAM1656  ITGB2    3'  TGAGGAGGGCTTGAGGTTGGTG 5800      TG   _ AAACT
              AGG                  CCT  CTG C     GCTTTTCTTG
                                   |||  ||| |     ||||||||||
                                   GGA  GGT G     CGGGAGGAGT
                                     GT   T GAGTT
GAM1656  JUN      3'  GGGAGGGGCGGCAGGAGGG    11104      G    AAAC
                                CCTT CTGC    TGCTTTTCTT
                                |||| ||||    ||||||||||
                                GGGA GACG    GCGGGGAGGG
                                  G   _____
GAM1656  KCNA6    5'  GAGGGGGCAGCAGGCGGGG    11137        GCAAA    T TT
                                CCTTGCT     CTGC T  CTT
                                |||||||     ||||  |  |||
                                GGGGCGG     GACG G  GAG
                                    AC___    _ GG
GAM1656  KCNC1    5'  CAGGGGGAGTTGGCGCCGGG   18327     T  T  AAACT    TT
                                CCT GC GC     GCTT  CTTG
                                ||| || ||     ||||  ||||
                                GGG CG CG     TGAG  GGAC
                                  C  _  GT___    GG
GAM1656  KCND2    5'  CGGGAAGGGCTACTTGGAAAGG 25382      GCTG   ACT
                                CCTT    CAA   GCTTTTCTTG
                                ||||    |||   ||||||||||
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                                GGAA   GTT  CGGGAAGGGC
                                  AG__  CAT
GAM1656  KCND2    5'  TGAGAAGGGTAGGTGTAAGG  25387      TGCAAA
                                CCTTGC    CTGCTTTTCTTG
                                ||||||    ||||||||||||
                                GGAATG    GATGGGAAGAGT
                                   TG____
GAM1656  KCNH2    3'  TGAGAGGGGCAGGGGCAGGG  5885       GCAAA
                                CCTTGCT   CTGCTTTTCTTG
                                |||||||   ||||||||||||
                                GGGACGG   GACGGGGAGAGT
                                   G____
GAM1656  KCNN3    5'  GAGGACATCTTTGGAGCGAGG  11184      G   C_  C
                                CCTTGCT CAAA  TG TTTTC
                                ||||||| ||||  || |||||
                                GGAGCGA GTTT  AC AGGAG
                                   G   CT  _
GAM1656  KCNQ2    3'  CAGGGGAGGCACAAAGGGCAGG 62045      GCAAAC    TT
                                CTTGCT    TGCTT  CTTG
                                ||||||    |||||  ||||
                                GGACGG    ACGGA  GGAC
                                   GAAAC_   GG
GAM1656  KIFC3    3'  CAAGGAGGGTTCCCGCAGCTGG 19889    T    AAACT
            G                   CCT GCTGC    GCTTTTCTTG
                                ||| |||||    ||||||||||
                                GGG CGACG    TGGGAGGAAC
                                  T    CCCT_
GAM1656  KIFC3    5'  GGGAGGGGCGCGAGCGGG    19891      _  AAACT
                                CTTGCT GC    GCTTTTCTT
                                |||||| ||    |||||||||
                                GGGCGA CG    CGGGGAGGG
                                   G  _____
GAM1656  KIFC3    3'  TGAGGAGGGCGGGAGTGTGGAG 19893    TG TG  AA_
            G                   CCT  C  CA   CTGCTTTTCTTG
                                |||  |  ||   ||||||||||||
                                GGA  G  GT   GGCGGGAGGAGT
                                  __ GT  GAG
GAM1656  KLF8     5'  AGGAAAAGCTGCAGGGGGG   24370     G    AACT
                                CCTT CTGCA   GCTTTTCTT
                                |||| |||||   |||||||||
                                GGGG GACGT   CGAAAAGGA
                                   G   _____
GAM1656  LAMC1    5'  TGAGGGAAGCGCGGAGGCGGGG 11273      GCAAAC    TT
                                CCTTGCT    TGCTT  CTTG
                                |||||||    |||||  ||||
                                GGGGCGG    GCGAA  GAGT
                                   AGGC__    GG
GAM1656  LAMC2    3'  TGGGGGCACTTGAGTTTTGGCA 19911       C   _____    CTTG
            AGG                   CCTTGCTG AAACT    GCTTTT
                                ||||||||| |||||    ||||||
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                                GGAACGGT TTTGA    CGGGGG
                                    _    GTTCA     T
GAM1656 LANGERIN 3' GGGAGGGGTGGGTAGAGAGG  32313    TG   AA  G
                                CCT  CTGC  ACT CTTTT
                                |||  ||||  ||| |||||
                                GGA  GATG  TGG GAGGG
                                  GA   GG  G
GAM1656 LARGE    3' TAGGGGGAGACATGCTGTAGGG 56931      T  AAC  _  TT
                                CCTTGC GCA   TG CTT  CTTG
                                |||||| |||   || |||  ||||
                                GGGATG CGT   AC GAG  GGAT
                                   T  ___  A  GG
GAM1656 LGR6     3' TGAGGGAAGTAAAGACAGTGAA 85358     _   CAAAC    TT
            GG                    CCTT GCTG    TGCTT  CTTG
                                |||| ||||    |||||  ||||
                                GGAA TGAC    ATGAA  GAGT
                                  G   AGAA_    GG
GAM1656 LIG1     3' CAGGGGAGGGGTGTGTGTGTGA 5879     TG _   A  G  TT  TG
            GG                    CCT  C TGCA ACT CTT  CT
                                |||  | |||| ||| |||  ||
                                GGA  G GTGT TGG GAG  GA
                                  GT T   G   G   GG  C
GAM1656 LIMK1    3' GGGGAGGTGCTGGGCAAGG   11339      __ AAACT   TT
                                CCTTGCT  GC    GCTT  CT
                                |||||||  ||    ||||  ||
                                GGAACGG  CG    TGGA  GG
                                   GT  _____   GG
GAM1656 LMAN1    3' AAGGAGGCTGTAGTAGAGG   19926    _     AA  G
                                CCT TGCTGCA  CT CTT
                                ||| |||||||  || |||
                                GGA ATGATGT  GA GAA
                                  G      CG  G
GAM1656 LMO4     5' CGGGAGGAGCGCGGGCGGGGGC 23182       ___  AAAC
            GGGG                   CCTTGCT   GC   TGCTTTTCTTG
                                |||||||   ||   ||||||||||
                                GGGGCGG   CG   GCGAGGAGGGC
                                   GGG  GGC_
GAM1656 LY6E     3' CAGGGAGACCGTGTCAGTAGGG 11380       _ AAC  C
                                CCTTGCTG CA   TG TTTTCTTG
                                |||||||| ||   || ||||||||
                                GGGATGAC GT   GC AGAGGGAC
                                   T  ___  C
GAM1656 MADD     5' GGGGAGGATGTCCTGCGGCGGG 56215        A_  TG   TT  TG
            G                    CCTTGCTGCA  AC  CTT  CT
                                |||||||||  ||  |||  ||
                                GGGGCGGCGT  TG  GGA  GG
                                     CC  TA   GG
GAM1656 MADH6    5' CGGGAGGCACTTTTGTGGAGGG 19975     G TG   C_    TT TTG
                                CCTT C  CAAA  TGCTT  C
                                |||| |  ||||  |||||  |
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                                GGGA G  GTTT  ACGGA  G
                                  _ GT    TC     GG C
GAM1656  MADH6    3'  GGGAGGGGCGGGTGGGAGG    19977      G TG AAA
                                CCTT C  C   CTGCTTTTCTT
                                |||| |  |   ||||||||||
                                GGAG G  G   GGCGGGGAGGG
                                  _ GT ___
GAM1656  MAF      5'  AGGAGGGGCCGGGGCGAGCGAG 19308        _  AAACT        G
             G                   CCTTGCT GC     GCTTTTCTT
                                 ||||||| ||     |||||||||
                                 GGAGCGA CG     CGGGGAGGA
                                    G  GGGC_        A
GAM1656  MAN2A1   5'  CGGGGAGGGCGGCAGGCCAGG  11434     T   GCAAA
                                CCT GCT     CTGCTTTTCTTG
                                ||| |||     ||||||||||||
                                GGA CGG     GGCGGGAGGGGC
                                  C   AC___
GAM1656  MAP3K7IP2 5'  TGGGAGAGGCGGCGGCGGCG   31356       AAA
                                TGCTGC   CTGCTTTTCTTG
                                ||||||   ||||||||||||
                                GCGGCG   GGCGGAGAGGGT
                                   GC_
GAM1656  MAP4     3'  TGGGAGGGGGTTGGGGTGGTTG 11452      _ TG A__    G   TT TTG
             AGG                  CCTTG C  C   AACT CTT  C
                                  ||||| |  |   |||| |||  |
                                  GGAGT G  G   TTGG GGA  G
                                     T GT GGG    G   GG T
GAM1656  MAP4     3'  TGGGAGGGGGTTGGGGTGGTTG 11453      _ TG A__    G   TT TTG
             AGG                  CCTTG C  C   AACT CTT  C
                                  ||||| |  |   |||| |||  |
                                  GGAGT G  G   TTGG GGA  G
                                     T GT GGG    G   GG T
GAM1656  MAPK8IP1  3'  TAGGGGAGGGTGGGGCAATGG  19583    _    G  AA  G    TCTTG
                                CC TTGCT CA  CT CTTT
                                || ||||| ||  || ||||
                                GG AACGG GT  GA GGGA
                                 T    G  GG  G    T
GAM1656  MAPRE3   3'  CGAGGGGGGCTTGGGGGCATGG 25597    T   _ G   ACT    TT
                                CC TGC T CAA   GCTT  CTTG
                                || ||| | |||   ||||  ||||
                                GG ACG G GTT   CGGG  GAGC
                                 T   G G   ___    GG
GAM1656  MASP1    3'  TGAGAGAAGCAGGGACAGGAGG 58220      G   CAAA
             G                   CCTT CTG    CTGCTTTTCTTG
                                 |||| |||    ||||||||||||
                                 GGGA GAC    GACGAAGAGAGT
                                   G   AGG_
GAM1656  MCM4     5'  GGGGAGGGCGTGGCGCGG    62581    T   TG AAACT
                                CC TGC  C    GCTTTTCTT
                                || |||  |    |||||||||
```

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                                GG GCG  G    CGGGAGGGG
                                 C  GT _____
GAM1656  MDFI    3'  TGGGGAGGGTGGGCCGGTGGGG 19984    TG  CAAA TG
                                CCT  CTG   C  CTTTTCTTG
                                |||  |||   |  |||||||||
                                GGG  GGC   G  GGGAGGGGT
                                  GT  CG__ GT
GAM1656  MDM4    3'  TAGGGGAGGTGTGGGGCGACAG 11513     C  AA_  T   TT
            GG                    CCTTG TGC  AC GCTT  CTTG
                                |||||  |||  ||  ||||  ||||
                                GGGAC GCG  TG TGGA  GGAT
                                   A  GGG  _   GG
GAM1656  MEN1    5'  GGGAGAGAGTGGGCGAGG   56355       G  AA  G   TT
                                CCTTGCT CA  CT CTT  C
                                |||||||  ||  ||  |||  |
                                GGAGCGG GT  GA GAG  G
                                    _  GA  _   GG
GAM1656  MGAT1   3'  AGGAGAGAGGTGCAGGGAGG   11550    G    AA  G
                                CCTT CTGCA  CT CTTTTCT
                                ||||  |||||  ||  |||||||
                                GGAG GACGT  GA GAGAGGA
                                  G    G_  _
GAM1656  MIC2    5'  AGGGGAGGCCGGGGCGGGG   11579       GCAAA  _  TT
                                CCTTGCT    CTG CTT  CTT
                                |||||||    |||  |||  |||
                                GGGGCGG    GGC GGA  GGA
                                    _____  C   GG
GAM1656  MMP19   5'  CAAGAAGAGTCCAGTGATAAGG 11617     CT  AAACT
                                CCTTG  GC    GCTTTTCTTG
                                |||||  ||    ||||||||||
                                GGAAT  TG    TGAGAAGAAC
                                   AG  ACC__
GAM1656  MMP19   5'  CAAGAAGAGTCCAGTGATAAGG 11618     CT  AAACT
                                CCTTG  GC    GCTTTTCTTG
                                |||||  ||    ||||||||||
                                GGAAT  TG    TGAGAAGAAC
                                   AG  ACC__
GAM1656  MN1     3'  CGAGAAAGGTGTGAGCCGAGG  11651     CT  AA  T
                                CCTTG  GC  AC GCTTTTCTTG
                                |||||  ||  ||  ||||||||||
                                GGAGC  CG  TG TGGAAAGAGC
                                   __  AG  _
GAM1656  MTF1    3'  TGGGAAAAGCGGGTGAGCAGGA 21052     G   AAA_
            GG                    CCTT CTGC   CTGCTTTTCTTG
                                ||||  ||||   ||||||||||||
                                GGAG GACG   GGCGAAAAGGGT
                                  _   AGTG
GAM1656  MTNR1B  3'  GGGAGAGAGTCTGCTGCAAGG  21057      T  A  G
                                CCTTGC GCA ACT CTTTTCT
                                ||||||  |||  |||  |||||||
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                                GGAACG CGT TGA GAGAGGG
                                   T  C  _
GAM1656 MXI1    5' CGAGAAGGGAGTGCGGAGAGG 56126    TG   AACTG
                                CCT CTGCA   CTTTTCTTG
                                ||| |||||   |||||||||
                                GGA GGCGT   GGGAAGAGC
                                  GA   GA___
GAM1656 MYEOV   5' TGGGAGAGGCCAAGTGAGTGGG 57850    TG G AACT
           G                     CCT CT CA   GCTTTTCTTG
                                ||| || ||   ||||||||||
                                GGG GA GT   CGGAGAGGGT
                                  GT _ GAAC
GAM1656 MYO1D   5' CGGGAGGAGCGGAAACTGTCGG 72244    T TGCAAA
           G                     CCT GC    CTGCTTTTCTTG
                                ||| ||    ||||||||||||
                                GGG TG    GGCGAGGAGGGC
                                  C TCAAA_
GAM1656 MYO1D   3' GAGGGAAGTAGAGGCTGGG   72247    T GCAAA    TT
                                CCT GCT   CTGCTT CTT
                                ||| |||   ||||||  |||
                                GGG CGG   GATGAA GAG
                                  T  A____    GG
GAM1656 MYOC    3' TGGGGGGAGCAGGCTGAAGG  6034     GCTG AA    TT
                                CCTT   CA CTGCTT CTTG
                                ||||   || ||||||  ||||
                                GGAA   GT GACGAG GGGT
                                  ____ CG    GG
GAM1656 MYOD1   5' AGGAGAGGGAGGGGTGGGG   65625    TG GCAAA G
                                CCT CT    CT CTTTTCTT
                                ||| ||    || ||||||||
                                GGG GG    GA GGAGAGGA
                                  GT G____  G
GAM1656 NDUFS2  5' CAGGAGAGGCAGAGAGTGAGG 17041    TG GCAAA
                                CCT CT    CTGCTTTTCTTG
                                ||| ||    ||||||||||||
                                GGA GA    GACGGAGAGGAC
                                  GT GA___
GAM1656 NEO1    5' CGGGAGCCGAGCTTGCAGCGAG 11771         ACT  __
           G                     CCTTGCTGCAA  GCTT TTCTTG
                                ||||||||||  ||||  ||||||
                                GGAGCGACGTT  CGAG GAGGGC
                                      ___   CC
GAM1656 NET1    3' AAGGGGAGCATCATAGGG    20766     C CAAAC    TT
                                CCTTG TG    TGCTT CTT
                                ||||| ||    |||||  |||
                                GGGAT AC    ACGAG GAA
                                   _ T____    GG
GAM1656 NEURL   3' GGGAAAGGGTGTGGCTGAGG  16132     _ TG AACTG
                                CCTT GC  CA    CTTTTCT
                                |||| ||  ||    |||||||
```

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                                GGAG CG  GT    GAAAGGG
                                  T  GT  GG___
GAM1656  NMB     5'  CGGGGAGGGCGGCGGGCGCGGG 74209       T  AAA
                 G                 CCTTGC GC   CTGCTTTTCTTG
                                   |||||| ||   ||||||||||||
                                   GGGGCG CG   GGCGGGAGGGGC
                                     _  GGC
GAM1656  NMI     5'  CGGGAAGGGCAGGCGCGCTGGG 17434     T  T  AAA
                                   CCT GC GC   CTGCTTTTCTTG
                                   ||| || ||   ||||||||||||
                                   GGG CG CG   GACGGGAAGGGC
                                    T  _  CG_
GAM1656  NR2F6   5'  GAGAGGGGTGCCCGGAGGG   19105     G   CAA   G
                                   CCTT CTG   ACT CTTTT
                                   |||| |||   ||| |||||
                                   GGGA GGC   TGG GAGAG
                                     _   CCG   G
GAM1656  NRXN2   5'  GGGGAGAGAGGCGCGAGG    57823       T  AAACTG
                                   CCTTGC GC     CTTTTCTT
                                   |||||| ||     ||||||||
                                   GGAGCG CG     GAGAGGGG
                                     _  GA____
GAM1656  NUMB    3'  CAAGAAGAGTGGTTTGTGCTCA 14977     T_  T     TG
                 GG                  CCT  GC GCAAAC  CTTTTCTTG
                                     |||  || ||||||  |||||||||
                                     GGA  CG TGTTTG  GAGAAGAAC
                                      CT  _     GT
GAM1656  NUP62   5'  CGGGAAAGGCAGTTGGAGAAG  25648     G  G   A
                                   CTT CT CAA CTGCTTTTCTTG
                                   ||| || ||| ||||||||||||
                                   GAA GA GTT GACGGAAAGGGC
                                     _  G  _
GAM1656  NYX     3'  GGCTTGAGTGTGTTTGTGGTAA 42905       TG    _    TTCTTG
                 GG                  CCTTGC  CAAAC TGCTT
                                     ||||||  ||||| |||||
                                     GGAATG  GTTTG GTGAG
                                       GT    T    TTCGGG
GAM1656  OGDH    3'  CGGGGGGAGCAGGAGGAGGAAA 92748     G  GCAAA     TT
                 GG                  CCTT CT    CTGCTT  CTTG
                                     |||| ||    ||||||  ||||
                                     GGAA GG    GACGAG  GGGC
                                      A  AGGAG     GG
GAM1656  OGG1    5'  CGGGAGAAGATAAGTCGCAAGG 34153       T  AAACTG
                                   CCTTGC GC     CTTTTCTTG
                                   |||||| ||     |||||||||
                                   GGAACG TG     GAAGAGGGC
                                     C  AATA__
GAM1656  OGG1    5'  CGGGAGAAGATAAGTCGCAAGG 34154       T  AAACTG
                                   CCTTGC GC     CTTTTCTTG
                                   |||||| ||     |||||||||
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                                GGAACG TG     GAAGAGGGC
                                   C  AATA__
GAM1656  OGG1     5'  CGGGAGAAGATAAGTCGCAAGG 34155       T  AAACTG
                                CCTTGC GC     CTTTTCTTG
                                |||||| ||     |||||||||
                                GGAACG TG     GAAGAGGGC
                                   C  AATA__
GAM1656  OVOL1    3'  CAAGAGAAGGGATGAGGCAAGG 17061       G  AA TG
                                CCTTGCT CA  C  CTTTTCTTG
                                ||||||| ||  |  |||||||||
                                GGAACGG GT  G  GAAGAGAAC
                                    A  AG __
GAM1656  OVOL1    5'  GGGAAGGCGGTGCAGCAGTGG  17072    _     AA
                                CC TTGCTGC  ACTGCTTTTCT
                                || |||||||  ||||||||||
                                GG GACGACG  TGGCGGAAGGG
                                 T      __
GAM1656  OXTR     3'  GGGAAGGGTGGTGCTAAG    8079      CT  AA  TG
                                CTTG  GC  AC  CTTTTCTT
                                ||||  ||  ||  ||||||||
                                GAAT  CG  TG  GGGAAGGG
                                  __  __  GT
GAM1656  PAPPA    5'  CAAGAAGGGTGAAGAAGCGA   11969      GCAAACT
                                TTGCT      GCTTTTCTTG
                                |||||      ||||||||||
                                AGCGA      TGGGAAGAAC
                                   AGAAG__
GAM1656  PCDHGA1  3'  CAGGAAGGGTGGGCCAGCCAGG 38836     T    CAAA TG
                                CCT GCTG    C  CTTTTCTTG
                                ||| ||||    |  |||||||||
                                GGA CGAC    G  GGGAAGGAC
                                  C    CG__ GT
GAM1656  PCDHGA10 3'  CAGGAAGGGTGGGCCAGCCAGG 50311     T    CAAA TG
                                CCT GCTG    C  CTTTTCTTG
                                ||| ||||    |  |||||||||
                                GGA CGAC    G  GGGAAGGAC
                                  C    CG__ GT
GAM1656  PCDHGA11 3'  CAGGAAGGGTGGGCCAGCCAGG 38843     T    CAAA TG
                                CCT GCTG    C  CTTTTCTTG
                                ||| ||||    |  |||||||||
                                GGA CGAC    G  GGGAAGGAC
                                  C    CG__ GT
GAM1656  PCDHGA12 3'  CAGGAAGGGTGGGCCAGCCAGG 50318     T    CAAA TG
                                CCT GCTG    C  CTTTTCTTG
                                ||| ||||    |  |||||||||
                                GGA CGAC    G  GGGAAGGAC
                                  C    CG__ GT
GAM1656  PCDHGA2  3'  CAGGAAGGGTGGGCCAGCCAGG 38850     T    CAAA TG
                                CCT GCTG    C  CTTTTCTTG
                                ||| ||||    |  |||||||||
```

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                                GGA CGAC   G  GGGAAGGAC
                                  C   CG__ GT
GAM1656  PCDHGA3  3' CAGGAAGGGTGGGCCAGCCAGG 50094    T   CAAA TG
                                CCT GCTG   C  CTTTTCTTG
                                ||| ||||   |  |||||||||
                                GGA CGAC   G  GGGAAGGAC
                                  C   CG__ GT
GAM1656  PCDHGA4  3' CAGGAAGGGTGGGCCAGCCAGG 38858    T   CAAA TG
                                CCT GCTG   C  CTTTTCTTG
                                ||| ||||   |  |||||||||
                                GGA CGAC   G  GGGAAGGAC
                                  C   CG__ GT
GAM1656  PCDHGA5  3' CAGGAAGGGTGGGCCAGCCAGG 50292    T   CAAA TG
                                CCT GCTG   C  CTTTTCTTG
                                ||| ||||   |  |||||||||
                                GGA CGAC   G  GGGAAGGAC
                                  C   CG__ GT
GAM1656  PCDHGA6  3' CAGGAAGGGTGGGCCAGCCAGG 38866    T   CAAA TG
                                CCT GCTG   C  CTTTTCTTG
                                ||| ||||   |  |||||||||
                                GGA CGAC   G  GGGAAGGAC
                                  C   CG__ GT
GAM1656  PCDHGA7  3' CAGGAAGGGTGGGCCAGCCAGG 50299    T   CAAA TG
                                CCT GCTG   C  CTTTTCTTG
                                ||| ||||   |  |||||||||
                                GGA CGAC   G  GGGAAGGAC
                                  C   CG__ GT
GAM1656  PCDHGA8  3' CAGGAAGGGTGGGCCAGCCAGG 26600    T   CAAA TG
                                CCT GCTG   C  CTTTTCTTG
                                ||| ||||   |  |||||||||
                                GGA CGAC   G  GGGAAGGAC
                                  C   CG__ GT
GAM1656  PCDHGA9  3' CAGGAAGGGTGGGCCAGCCAGG 50306    T   CAAA TG
                                CCT GCTG   C  CTTTTCTTG
                                ||| ||||   |  |||||||||
                                GGA CGAC   G  GGGAAGGAC
                                  C   CG__ GT
GAM1656  PCDHGB1  3' CAGGAAGGGTGGGCCAGCCAGG 38875    T   CAAA TG
                                CCT GCTG   C  CTTTTCTTG
                                ||| ||||   |  |||||||||
                                GGA CGAC   G  GGGAAGGAC
                                  C   CG__ GT
GAM1656  PCDHGB2  3' CAGGAAGGGTGGGCCAGCCAGG 50324    T   CAAA TG
                                CCT GCTG   C  CTTTTCTTG
                                ||| ||||   |  |||||||||
                                GGA CGAC   G  GGGAAGGAC
                                  C   CG__ GT
GAM1656  PCDHGB3  3' CAGGAAGGGTGGGCCAGCCAGG 38883    T   CAAA TG
                                CCT GCTG   C  CTTTTCTTG
                                ||| ||||   |  |||||||||
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                                GGA CGAC   G  GGGAAGGAC
                                  C   CG__ GT
GAM1656  PCDHGB4   3'  CAGGAAGGGTGGGCCAGCCAGG 50329    T   CAAA TG
                                CCT GCTG   C  CTTTTCTTG
                                ||| ||||   |  |||||||||
                                GGA CGAC   G  GGGAAGGAC
                                  C   CG__ GT
GAM1656  PCDHGB5   3'  CAGGAAGGGTGGGCCAGCCAGG 38890    T   CAAA TG
                                CCT GCTG   C  CTTTTCTTG
                                ||| ||||   |  |||||||||
                                GGA CGAC   G  GGGAAGGAC
                                  C   CG__ GT
GAM1656  PCDHGB6   3'  CAGGAAGGGTGGGCCAGCCAGG 38895    T   CAAA TG
                                CCT GCTG   C  CTTTTCTTG
                                ||| ||||   |  |||||||||
                                GGA CGAC   G  GGGAAGGAC
                                  C   CG__ GT
GAM1656  PCDHGB7   3'  CAGGAAGGGTGGGCCAGCCAGG 38899    T   CAAA TG
                                CCT GCTG   C  CTTTTCTTG
                                ||| ||||   |  |||||||||
                                GGA CGAC   G  GGGAAGGAC
                                  C   CG__ GT
GAM1656  PCDHGC3   3'  CAGGAAGGGTGGGCCAGCCAGG 51528    T   CAAA TG
                                CCT GCTG   C  CTTTTCTTG
                                ||| ||||   |  |||||||||
                                GGA CGAC   G  GGGAAGGAC
                                  C   CG__ GT
GAM1656  PCDHGC4   3'  CAGGAAGGGTGGGCCAGCCAGG 38905    T   CAAA TG
                                CCT GCTG   C  CTTTTCTTG
                                ||| ||||   |  |||||||||
                                GGA CGAC   G  GGGAAGGAC
                                  C   CG__ GT
GAM1656  PCDHGC5   3'  CAGGAAGGGTGGGCCAGCCAGG 51555    T   CAAA TG
                                CCT GCTG   C  CTTTTCTTG
                                ||| ||||   |  |||||||||
                                GGA CGAC   G  GGGAAGGAC
                                  C   CG__ GT
GAM1656  PCTK1     5'  CGAGGGGAGGGGGCAGTTGGG  53417    T    AAA  G   TT
                                CCT GCTGC   CT CTT  CTTG
                                ||| |||||  || |||  ||||
                                GGG TGACG   GG GAG  GAGC
                                  T    ____  G   GG
GAM1656  PCTK1     3'  GGGGAGGGTGAGGCAGGGCAGG 53419       __  AA_   G   TT TTG
            G                    CCTTGCT  GC   ACT CTT  C
                                ||||||| ||   ||| |||  |
                                GGGACGG  CG   TGG GAG  G
                                    GA  GAG   _   GG
GAM1656  PCTK1     3'  TGGGGAGGGTGAGGCAGGGCAG 53422       __  AA_   G   TT TTG
            GG                   CCTTGCT  GC   ACT CTT  C
                                ||||||| ||   ||| |||  |
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                                GGGACGG  CG   TGG GAG  G
                                   GA  GAG   _   GG T
GAM1656  PCTP     3'  TAGGAGGGGAAGTCTTCAGTAG 41372        CAA   G
              GG                   CCTTGCTG   ACT CTTTTCTTG
                                   ||||||||   ||| |||||||||
                                   GGGATGAC   TGA GGGGAGGAT
                                      TTC   A
GAM1656  PDGFB    3'  AGGAGAGTGTGTGGGCAGGG   12019       G  A  T
                                   CCTTGCT CA AC GCTTTTCT
                                   ||||||| || || ||||||||
                                   GGGACGG GT TG TGAGAGGA
                                      _  G  _
GAM1656  PDGFB    3'  AGGAGGGAGACTGTGGTAGGG  12020       TG  AA  G      TG
                                   CCTTGC  CA  CT CTTTTCT
                                   ||||||  ||  || |||||||
                                   GGGATG  GT  GA GGGAGGA
                                      GT  CA  _      T
GAM1656  PDK4     3'  AAAACAGTTTGCAGTAGG    99089            C
                                   CTTGCTGCAAACTG TTTT
                                   |||||||||||||| ||||
                                   GGATGACGTTTGAC AAAA
                                                  _
GAM1656  PHEMX    3'  CAGGGAGAGGAGGCGGCGAG   58139         AAA  G
                                   CTTGCTGC   CT CTTTTCTTG
                                   ||||||||   || |||||||||
                                   GAGCGGCG   GA GAGAGGGAC
                                      ____  G
GAM1656  PHKG1    3'  CAGGGAGGGCTAGGGGGCAGGT 21701     TG _   AAA  _
              GGGG                    CCT  C TGC   CT GCTTTTCTTG
                                   |||  | |||   || ||||||||||
                                   GGG  G ACG   GA CGGGAGGGAC
                                     GT G   GGG  T
GAM1656  PIGR     3'  TGGGAGAGCTGATTGCAGAAAG 73015      G     ACT       TG
              G                    CCTT CTGCAA   GCTTTTCT
                                   |||| ||||||   ||||||||
                                   GGAA GACGTT   CGAGAGGG
                                     A     AGT       T
GAM1656  PIK3C2B  3'  CAGGAGGGGGAAGAGGAGTGGG 12092     TG  GCAAA  G_
              G                    CCT  CT     CT  CTTTTCTTG
                                   |||  ||     ||  |||||||||
                                   GGG  GA     GA  GGGGAGGAC
                                     GT  GGA__  AG
GAM1656  PIM1     5'  CGAGAGGAGTCGGTGGCAGCGG 92685     _      AA   _
              CGG                    CC TTGCTGC  ACTG CTTTTCTTG
                                   || |||||||  |||| |||||||||
                                   GG GGCGACG  TGGC GAGGAGAGC
                                    C      G_    T
GAM1656  PIN1     3'  TAAGGAATTGACTTCAGCAGGG 21707         CAAACTGCT
                                   CCTTGCTG        TTTCTTG
                                   ||||||||        |||||||
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                                GGGACGAC       AAGGAAT
                                    TTCAGTT__
GAM1656 PIP5K1A  5'  TGAGGGAGGCCCGGAGGGGGCG 14521       GCAAACT_   TT
            GGG                   CCTTGCT      GCTT  CTTG
                                  |||||||      ||||  ||||
                                  GGGGCGG      CGGA  GAGT
                                    GGGAGGCC   GG
GAM1656 PITPN    5'  CGGGGAGAGCGGCCGGCGGGCA 21713    _    _  AAA
            GCGG                  CC TTGCT GC   CTGCTTTTCTTG
                                  || ||||| ||   ||||||||||||
                                  GG GACGG CG   GGCGAGAGGGGC
                                   C    G  GCC
GAM1656 PKP1     3'  AGGGAGGTTGGGGCGGGG    6107        G  AACT   TT
                                  CCTTGCT CA    GCTT  CT
                                  ||||||| ||    ||||  ||
                                  GGGGCGG GT    TGGA  GA
                                    G  ____    GG
GAM1656 PLA2G2D  3'  GGGAGAAGCCCAAGCAAGG   25719       GCAAACT
                                  CCTTGCT      GCTTTTCTT
                                  |||||||      |||||||||
                                  GGAACGA      CGAAGAGGG
                                    ACC____
GAM1656 PLAUR    5'  GGGAAGGAAGTTTGTGGCGGAG 12155     _ TG     G      TG
            G                     CCTT GC  CAAACT CTTTTCT
                                  |||| ||  |||||| |||||||
                                  GGAG CG  GTTTGA GGAAGGG
                                    G  GT     A      C
GAM1656 POLK     5'  CAGGAGGAGCGGAGAAAGGAGA 33099     TG  GCAAA
            GG                    CCT  CT    CTGCTTTTCTTG
                                  |||  ||    ||||||||||||
                                  GGA  GG    GGCGAGGAGGAC
                                   GA  AAAGA
GAM1656 POLR2E   3'  AGGAGAGGGCAGGGCAGGG   60593       GCAAA    _
                                  CCTTGCT    CTGCT TTTCTT
                                  |||||||    ||||| ||||||
                                  GGGACGG    GACGG AGAGGA
                                     _____    G
GAM1656 POP2     5'  TAGGAAAGGTGGAGTCGGTAGT 42408    TG   AA  __
            GAG                     CT  CTGC  ACT  GCTTTTCTTG
                                  ||  ||||  |||  ||||||||||
                                  GA  GATG  TGA  TGGAAAGGAT
                                   GT   GC   GG
GAM1656 POU2AF1  5'  TGGGGAGGGCTTGACACGGGG  21753      C  _  ACT
                                  CCTTG TG CAA   GCTTTTCTTG
                                  ||||| || |||   ||||||||||
                                  GGGGC AC GTT   CGGGAGGGGT
                                    _ A  ___
GAM1656 PPFIA3   3'  GAGAGGGGGAAGAAGCGGGG   61670       GCAAA  G
                                  CCTTGCT    CT CTTTTC
                                  |||||||    || ||||||
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                                GGGGCGA    GG GGAGAG
                                    AGAA_  G
GAM1656  PPP1R12B  5'  CGGGAGGAGTAAAGATGGCGGC 50354      AAAC__
                                GCTGC     TGCTTTTCTTG
                                |||||     ||||||||||
                                CGGCG     ATGAGGAGGGC
                                   GTAGAA
GAM1656  PPP3CA   5'  CAGCCGAGCGGTTTGCAGCGCG 8134     T           TT  TG
           G                     CC TGCTGCAAACTGCTT  CT
                                || ||||||||||||||  ||
                                GG GCGACGTTTGGCGAG  GA
                                 C            CC  C
GAM1656  PRAME    3'  AGGAAAACATGTTCAGTGAGG  21486     TG   CA  _  C      G
                                CCT  CTG  AAC TG TTTTCTT
                                |||  |||  ||| || |||||||
                                GGA  GAC  TTG AC AAAAGGA
                                  GT   __   T  _      G
GAM1656  PRKAG1   3'  AGGGAAGGTATGGGGGAGG   12280      G  G  AAC
                                CCTT CT CA   TGCTTTTCTT
                                |||| || ||   ||||||||||
                                GGAG GG GT   ATGGAAGGGA
                                  _  G  ___
GAM1656  PRKCN    3'  AAGAAAACTGAGGCAAGG    20561        G  AACTGC
                                CCTTGCT CA      TTTTCTT
                                |||||||  ||     |||||||
                                GGAACGG GT      AAAAGAA
                                    A  C_____
GAM1656  PSMB2    3'  CGGGAGAGGGAGGTTGCAGTGA 12468    TG     A  G
           G                     CT  CTGCAA CT CTTTTCTTG
                                ||  |||||| || |||||||||
                                GA  GACGTT GA GGAGAGGGC
                                 GT     G  G
GAM1656  PSMB9    5'  CGAGGAGAGCGGTGCCTTGCAG 12502       TGCAA
           GG                     CCTTGC    ACTGCTTTTCTTG
                                ||||||    ||||||||||||
                                GGGACG    TGGCGAGAGGAGC
                                   TTCCG
GAM1656  PSMB9    3'  CGGGAGGTAGAGTTTGCAGTGA 12503    TG       __    TT TTG
           G                     CT  CTGCAAACT  GCTT  C
                                ||  |||||||||  ||||  |
                                GA  GACGTTTGA  TGGA  G
                                 GT        GA    GG C
GAM1656  PTTG1IP  3'  CAGGGAAAGCAGCGTGCGGGGA 16347    G    AA
                                TT CTGCA  CTGCTTTTCTTG
                                || |||||  ||||||||||||
                                AG GGCGT  GACGAAAGGGAC
                                 G    GC
GAM1656  RAB5C    3'  AAGGGGGGGAGTGGGAGGG   60524      G  GCAA   G   TT
                                CCTT CT    ACT CTT  CTT
                                ||||  ||    |||  |||  |||
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                                GGGA GG    TGA GGG  GAA
                                  G ____   G   GG
GAM1656  RAD50    5'  CGGGGAAAGCAGCTGGTGTGGG 20407    TG T  AAA
                                CT  C GC   CTGCTTTTCTTG
                                ||  | ||   ||||||||||||
                                GG  G TG   GACGAAAGGGGC
                                 GT _  GTC
GAM1656  RAD52    3'  CAGGAAAAAGGTTGGAGCAAGG 57023        G   A  GC
                                CCTTGCT CAA CT  TTTTCTTG
                                |||||||  ||| ||  ||||||||
                                GGAACGA GTT GG  AAAAGGAC
                                    G   _  A_
GAM1656  RAD52    3'  CAGGAAAAAGGTTGGAGCAAGG 57024        G   A  GC
                                CCTTGCT CAA CT  TTTTCTTG
                                |||||||  ||| ||  ||||||||
                                GGAACGA GTT GG  AAAAGGAC
                                    G   _  A_
GAM1656  RANBP9   5'  CAGGAGAAGGAGTTGCAGCGGC 19716    _       A  G
              GG                  CC TTGCTGCAA CT CTTTTCTTG
                                ||  |||||||||  ||  |||||||||
                                GG GGCGACGTT GA GAAGAGGAC
                                 C        _  G
GAM1656  RENT1    5'  CGAGGGGAGCTGAGGCGCGGAG 12810     G    AAA  __    TT
              GG                  CCTT CTGC   CT  GCTT  CTTG
                                ||||  ||||   ||  ||||  ||||
                                GGGA GGCG   GA  CGAG  GAGC
                                  _    CG_  GT    GG
GAM1656  RERE     5'  CAGGAAAGGTCACGGCAGGG   25014        CAAACT
                                CCTTGCTG     GCTTTTCTTG
                                ||||||||     ||||||||||
                                GGGACGGC     TGGAAAGGAC
                                    AC____
GAM1656  RPE65    3'  CAAGGAAGTATCATGCAATAAG 6169        C    AAC     T
              G                   CCTTG TGCA   TGCTTT CTTG
                                |||||  ||||   ||||||  ||||
                                GGAAT ACGT   ATGAAG GAAC
                                  A    ACT     _
GAM1656  RPIP8    5'  CGGGAGGGGTGGGGGGGGCAGCG 22928         AAA_ TG
              GG                  CTTGCTGC    C  CTTTTCTTG
                                ||||||||   |  |||||||||
                                GGGCGACG   G  GGGGAGGGC
                                    GGGG GT
GAM1656  RRM2B    5'  GGGGGAGGCGGGGCCGGG    68435     T   GCAAA     TT
                                CCT GCT    CTGCTT  CTT
                                |||  |||    ||||||  |||
                                GGG CGG    GGCGGA  GGG
                                  C  _____     GG
GAM1656  RTN2     5'  CGGGAGGAGGAGGCGGCGAG   20052        AAA  G
                                CTTGCTGC   CT CTTTTCTTG
                                ||||||||   ||  |||||||||
```

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                                GAGCGGCG   GA GAGGAGGGC
                                   ___  G
GAM1656  RYR2     3'  TAAGAAAAGCAGTTTGCA    8291
                                TGCAAACTGCTTTTCTTG
                                ||||||||||||||||||
                                ACGTTTGACGAAAAGAAT

GAM1656  S100A11  5'  CGGGAAGGGCGTGGGTTGAGG  20054      CT  AA  T
                                CCTTG  GC  AC GCTTTTCTTG
                                |||||  ||  || ||||||||||
                                GGAGT  TG  TG CGGGAAGGGC
                                   __  GG  _
GAM1656  SCML1    3'  AAGAGAGGTATTATCAGGG   23108      CTGCAAAC
                                CCTTG       TGCTTTTCTT
                                |||||       ||||||||||
                                GGGAC       ATGGAGAGAA
                                   TATT____
GAM1656  SCN1A    3'  AAGTCGTGGTTTGCATGAGG   90266      C      TG TTTT
                                CCTTG TGCAAAC  C    CTT
                                ||||| |||||||  |    |||
                                GGAGT ACGTTTG  G    GAA
                                   _      GT CT__
GAM1656  SDC2     5'  GGGGAGGGAGGCGCGGCGCGG  67718    T     AAA  G   TT  TG
                                CC TGCTGC   CT CTT  CT
                                || ||||||   || |||  ||
                                GG GCGGCG   GA GGA  GG
                                 C     CG_  G   GG  C
GAM1656  SEPN1    3'  CAGGAGGGGCCAGGCTGCCAAG 66963      CT   AA   _
            G                    CCTTG  GCA  CTG CTTTTCTTG
                                |||||  |||  ||| |||||||||
                                GGAAC  CGT  GAC GGGGAGGAC
                                   __  CG   C
GAM1656  SERPINF2 3'  GGGGGGGGGCGCGGCTGGG    8123      T    AAACT    TT
                                CCT GCTGC    GCTT  CTT
                                ||| |||||    ||||  |||
                                GGG CGGCG    CGGG  GGG
                                  T    _____    GG
GAM1656  SGCA     3'  CAGGGAGAGGGGGTGGGGTGGG 5245      TG  G  AA  G
            G                    CCT  CT CA  CT CTTTTCTTG
                                |||  || ||  || |||||||||
                                GGG  GG GT  GG GAGAGGGAC
                                  GT  G  GG  _
GAM1656  SH3BP5   3'  TGGGAAAGGTGAATGCCAGTGG 17920     TG  _  AAC
            GG                    CCT  CTG CA   TGCTTTTCTTG
                                |||  ||| ||   ||||||||||
                                GGG  GAC GT   GTGGAAAGGGT
                                  GT   C  AA_
GAM1656  SHH      3'  GGGGGAGGGGCGCGGGAGGG   5756      G   AAA  G   TT
                                CCTT CTGC   CT CTT  CT
                                |||| ||||   || |||  ||
```

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                                GGGA GGCG   GG GAG  GG
                                  G   C__  G  GG
GAM1656 SIAT4C   3'  TGGGAAGAGCACTGGTGTGGGG 21860    TG T  AAAC
                                CCT  C GC   TGCTTTTCTTG
                                |||  | ||   ||||||||||
                                GGG  G TG   ACGAGAAGGGT
                                  GT _  GTC_
GAM1656 SIRT2    3'  TAGGGGGAGTCTGAGCCGGGAG 48363     G   CAAACT   TT
             GG                   CCTT CTG     GCTT  CTTG
                                |||| |||     ||||  ||||
                                GGGA GGC     TGAG  GGAT
                                  G   CGAGTC   GG
GAM1656 SLC14A1  3'  CAGGAGGAGGAGGCTGCAGTGA 32411    TG    AA  G
             G                    CT  CTGCA  CT CTTTTCTTG
                                ||  |||||  || |||||||||
                                GA  GACGT  GA GAGGAGGAC
                                 GT    CG  G
GAM1656 SLC25A17 5'  GGGAAAAGTGTGGCTGGG    22060    T  TG AAACT
                                CCT GC  C    GCTTTTCTT
                                ||| ||  |    |||||||||
                                GGG CG  G    TGAAAAGGG
                                  T  GT _____
GAM1656 SLC2A6   3'  CAGGAAGAGCAGTGTGATGGG  34567    TGCTG  A
                                CCT    CA ACTGCTTTTCTTG
                                |||    || ||||||||||||
                                GGG    GT TGACGAGAAGGAC
                                  TA___  G
GAM1656 SLC7A6   5'  GGGAGAGTTTATGTGGCCGAGG 15642      _ TG  AACT      TG
                                CCTTG C  CA   GCTTTTCT
                                |||||  |  ||   ||||||||
                                GGAGC G  GT   TGAGAGGG
                                   C GT  ATT_      T
GAM1656 SLIT2    5'  CGAGGAAGGAGGCGGCGGGG   17724        AAACTG
                                CCTTGCTGC     CTTTTCTTG
                                |||||||||     |||||||||
                                GGGGCGGCG     GGAAGGAGC
                                      GA____
GAM1656 SMAC     3'  GGGATGCCAGTTGTGGCAGGG  58004      TG   A   CTT
                                CCTTGC  CAA CTG   TTCT
                                ||||||  ||| |||   ||||
                                GGGACG  GTT GAC   AGGG
                                   GT   _   CGT
GAM1656 SORCS2   3'  TGGGAGAGGCTGAGGATGGCAG 40809       GCAAACT
             GG                   CCTTGCT      GCTTTTCTTG
                                |||||||      ||||||||||
                                GGGACGG      CGGAGAGGGT
                                    TAGGAGT
GAM1656 SOX10    5'  CGGGGGAGGCGGCCGAGGCGGC 23675       AAA__     TT
             G                    TGCTGC    CTGCTT  CTTG
                                ||||||    ||||||  ||||
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                                GCGGCG    GGCGGA  GGGC
                                   GAGCC     GG
GAM1656  SOX9     3'  TGAGGGAGGCTACCTGGAGGGG 6233      TG  G  AACT    TT
                                CCT  CT CA    GCTT  CTTG
                                |||  || ||    ||||  ||||
                                GGG  GA GT    CGGA  GAGT
                                  __  G  CCAT    GG
GAM1656  SP100    3'  GAGGGAACTGTGTAGACAAGG  13338      _    AACTG
                                CCTTG CTGCA    CTTTT
                                ||||| |||||    |||||
                                GGAAC GATGT    GGGAG
                                   A    GTCAA
GAM1656  SPAG6    5'  CGAGGAGGGCAGACGGCGGCGG 25848         AAA
              GG                   CCTTGCTGC   CTGCTTTTCTTG
                                |||||||||   ||||||||||||
                                GGGGCGGCG   GACGGGAGGAGC
                                     GCA
GAM1656  SPON2    5'  CGGGGAAGGTCGCTGGGCAGGG 25850       G  AACT
                                CCTTGCT CA    GCTTTTCTTG
                                ||||||| ||    ||||||||||
                                GGGACGG GT    TGGAAGGGGC
                                   _  CGC_
GAM1656  SPTBN2   5'  AAGGAGAGCGGAGCACAGG    23689     C   AAA
                                CTTG TGC   CTGCTTTTCTT
                                |||| |||   ||||||||||
                                GGAC ACG   GGCGAGAGGAA
                                  _   A__
GAM1656  SPTBN4   5'  CAGGGAGGGCGGTCGGTCGCGG 48155        AA___
              CGAG                  CTTGCTGC    ACTGCTTTTCTTG
                                ||||||||    ||||||||||||
                                GAGCGGCG    TGGCGGGAGGGAC
                                     CTGGC
GAM1656  SRRM1    3'  CAGGAAGAGCCAGTGGCAGC   20694      AA   _
                                GCTGC  ACTG CTTTTCTTG
                                |||||  |||| |||||||||
                                CGACG  TGAC GAGAAGGAC
                                   G_    C
GAM1656  STIM1    3'  GGGGAAGGGGTGGCTAAGG    60784     _  GCAA   G   TT
                                CCTT GCT    ACT CTT  CT
                                |||| |||    ||| |||  ||
                                GGAA CGG    TGG GAA  GG
                                  T  _____   G   GG
GAM1656  STX8     5'  CAGGAAGAGTCCGAGCGGCGGG 17945        AAACT
                                CTTGCTGC    GCTTTTCTTG
                                ||||||||    ||||||||||
                                GGGCGGCG    TGAGAAGGAC
                                     AGCC_
GAM1656  SUPT6H   3'  GGGAGGGGAGTGTGGCAGGG   61031       TG AA   G
                                CCTTGC  C  ACT CTTTTCT
                                ||||||  |  ||| |||||||
```

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                                GGGACG  G  TGA GGGAGGG
                                   GT __   G
GAM1656  SURF4    3'  CGGGAAGATGCCTTTGCAGGGA 53707     G     CT  _
                GG                  CCTT CTGCAAA  GC TTTTCTTG
                                    |||| |||||||  || ||||||||
                                    GGAG GACGTTT  CG AGAAGGGC
                                      G      C_  T
GAM1656  TAF7L    5'  AAGAGGAGTTTTTAGTGATGG  46512    _ TG   C    G
                                    CC T  CTG AAACT CTTTT
                                    || |  ||| ||||| |||||
                                    GG A  GAT TTTGA GAGAA
                                     T GT   T    G
GAM1656  TBL1X    5'  TGAGGAGGGCCGGCGGCGGGG  20140         AAACT
                                    CCTTGCTGC    GCTTTTCTTG
                                    |||||||||    ||||||||||
                                    GGGGCGGCG    CGGGAGGAGT
                                         GC___
GAM1656  TBX1     5'  CAGGGGGAGCGAGGAGGAAGG  55539     G  GCAAAC    TT
                                    CCTT CT     TGCTT  CTTG
                                    |||| ||     |||||  ||||
                                    GGAA GA     GCGAG  GGAC
                                      G  GGA___     GG
GAM1656  TBXA2R   5'  TAGGAATGGAGAGTCTGTAGCA 8366          A   G_  T
                AGG                  CCTTGCTGCA ACT  CT TTCTTG
                                     |||||||||| |||  || ||||||
                                     GGAACGATGT TGA  GG AAGGAT
                                          C   GA  T
GAM1656  TCF21    3'  CGGGGGGAGCGGGCCCCGGGAA 13642     G   CAAA     TT
                GG                   CCTT CTG    CTGCTT  CTTG
                                     |||| |||    ||||||  ||||
                                     GGAA GGC    GGCGAG  GGGC
                                       G   CCCG     GG
GAM1656  TCF21    3'  TGGGAAAGGCGCGCTCCCGGGG 13645      CT_  AAAC
                                     CCTTG   GC    TGCTTTTCTTG
                                     |||||   ||    ||||||||||
                                     GGGGC   CG    GCGGAAAGGGT
                                       CCT  C___
GAM1656  TCF3     3'  GGGAAGGGACGTCAGCAAGG   71273        CAA  TG      G
                                     CCTTGCTG   AC  CTTTTCTT
                                     ||||||||   ||  ||||||||
                                     GGAACGAC   TG  GGGAAGGG
                                          ___  CA
GAM1656  TCIRG1   5'  TGGGGGAGGCAGGGCAGGAGG  21205     G    AAA     TT
                                     CCTT CTGC   CTGCTT  CTTG
                                     |||| ||||   ||||||  ||||
                                     GGAG GACG   GACGGA  GGGT
                                       _   G__     GG
GAM1656  TCN2     5'  AGGAGAGCCTCAGCAGGG    6265         CAAACT
                                     CCTTGCTG     GCTTTTCT
                                     ||||||||     ||||||||
```

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                                GGGACGAC     CGAGAGGA
                                    TC____
GAM1656  TCOF1    5'  CGAGGGAAGTGGCGGGCGGGG  6268        GCAAA TG   TT
                                CCTTGCT    C  CTT  CTTG
                                |||||||    |  |||  ||||
                                GGGGCGG    G  GAA  GAGC
                                    GC___ GT   GG
GAM1656  TCTA     3'  CGGGGGTTCAGGGTTGGTAGCA 42494         AAA__   CT TT  TG
            GGG                   CCTTGCTGC    CTG  T  CT
                                |||||||||    |||  |  ||
                                GGGACGATG    GAC  G  GG
                                     GTTGG   TT GG  C
GAM1656  TEM5     3'  TGAGGGGAGTAGAGGGAGAGG  52305     TG  GCAAA     TT
                                CCT  CT    CTGCTT  CTTG
                                |||  ||    ||||||  ||||
                                GGA  GG    GATGAG  GAGT
                                  GA  GA___     GG
GAM1656  TFCP2    5'  CAAGAGGAGTGGGAGTGCGGGA 20165     G    AA_ TG
            G                    CTT CTGCA   C  CTTTTCTTG
                                |||  |||||   |  |||||||||
                                GAG GGCGT   G  GAGGAGAAC
                                  _    GAG GT
GAM1656  TFDP2    3'  AGAGGGGAGCTGTGTAGTGAGG 21889     TG    AACT    TT   G
                                CCT  CTGCA    GCTT  CTT
                                |||  |||||    ||||  |||
                                GGA  GATGT    CGAG  GAG
                                  GT    GT__    GG   AG
GAM1656  TMEM1    3'  TAGGGGAGGCGGGTGGGGGAGG 13806      G  G  AA     TT
            G                    CCTT CT CA  CTGCTT  CTTG
                                ||||  ||  ||  ||||||  ||||
                                GGGA GG GT  GGCGGA  GGAT
                                  G  G  G_     GG
GAM1656  TNFAIP2  3'  AGGAGGGAGAGTGCAGCCAGG  21919     T     AA  G
                                CCT GCTGCA  CT CTTTTCT
                                |||  ||||||  ||  |||||||
                                GGA CGACGT  GA GGGAGGA
                                  C     GA  _
GAM1656  TNFRSF6  5'  TGAGGGAAGCGGTTTACGAGT  5269      _ C        TT
                                GCT G AAACTGCTT  CTTG
                                |||  |  |||||||||  ||||
                                TGA C TTTGGCGAA  GAGT
                                  G A        GG
GAM1656  TNFSF11  3'  GGGAAAACTTGCAGCTAAGG   14914      _      ACTGC
                                CCTT GCTGCAA     TTTTCTT
                                ||||  |||||||    |||||||
                                GGAA CGACGTT     AAAAGGG
                                  T      C_____
GAM1656  TNFSF8   3'  AGGGAAGCAATGTAGTGTGG   8800     T      AAC     TT
                                CC TGCTGCA   TGCTT  CT
                                ||  |||||||  |||||  ||
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                                GG GTGATGT   ACGAA  GA
                                 T      A__     GG
GAM1656  TNS      3'  TGGGGAAGGGGCTTGTGGGGAG 42953      G TG   A  G   TT  TG
                 G                 CCTT C  CAA CT CTT  CT
                                   |||| |  ||| || |||  ||
                                   GGAG G  GTT GG GAA  GG
                                     G GT   C  G   GG  T
GAM1656  TRAM     5'  GGGAAGAGCAGAACCGGGG    27453      CTGCAAA
                                   CCTTG      CTGCTTTTCTT
                                   |||||      ||||||||||
                                   GGGGC      GACGAGAAGGG
                                     CAA____
GAM1656  TRAP100  3'  CAAGGGAAGCAGTGAGGAAAGA 29722       _ GCAA__      TT
                   TGAGG                 CCTTG CT     ACTGCTT  CTTG
                                   ||||| ||     |||||||  ||||
                                   GGAGT GA     TGACGAA  GAAC
                                     A  AAGGAG      GG
GAM1656  TRC8     5'  CAGGAGAGGAAGGAGGGCAGGG 24275        GCAAA  G
                                   CCTTGCT     CT CTTTTCTTG
                                   |||||||     || |||||||||
                                   GGGACGG     GA GGAGAGGAC
                                      GAG__  A
GAM1656  TREM2    3'  AGGAGAAGTCCCACCAGGG    39095      C  CAAACT
                                   CCTTG TG     GCTTTTCTT
                                   ||||| ||     |||||||||
                                   GGGAC AC     TGAAGAGGA
                                     C  CC____
GAM1656  TRIM     5'  TAGGAAAAAAGTTTGTAGGAGG 33507      G        GC
                                   CCTT CTGCAAACT  TTTTCTTG
                                   |||| |||||||||  ||||||||
                                   GGAG GATGTTTGA  AAAAGGAT
                                     _        A_
GAM1656  TRIM8    3'  GGGAAAGTGTCTGTGTCGAGG  48857       C    A  T
                                   CCTTG TGCA AC GCTTTTCT
                                   ||||| |||| || ||||||||
                                   GGAGC GTGT TG TGAAAGGG
                                     T    C  _
GAM1656  TRPV1    5'  GGGGAGGGAGGCAGCGCGG    55679     T     AAA  G   TT
                                   CC TGCTGC   CT CTT  CT
                                   || ||||||   || |||  ||
                                   GG GCGACG   GA GGA  GG
                                    C      ___  G   GG
GAM1656  TSN      3'  TGAGGAAAGCAGTTGAAATGAG 17307      GCTGCA
                   G                 CCTT      AACTGCTTTTCTTG
                                   ||||      ||||||||||||||
                                   GGAG      TTGACGAAAGGAGT
                                     TAAAG_
GAM1656  TSSC4    5'  AAGAGAGGTGTGGCGTGG    20326    T   TG AAACT
                                   CC TGC  C     GCTTTTCTT
                                   || |||  |     |||||||||
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                                GG GCG  G    TGGAGAGAA
                                 T  GT _____
GAM1656  TST     5'  CGAGGGGGGCGAGCGCCAGCGC 13874    T    CAAAC    TT
                GG                  CC TGCTG    TGCTT  CTTG
                                    || |||||    |||||  ||||
                                    GG GCGAC    GCGGG  GAGC
                                     C    CGCGA    GG
GAM1656  TULP1   3'  CAGGAGGAGCCCGGACGGCGGG 13902       CAAACT
                                    CTTGCTG     GCTTTTCTTG
                                    |||||||     ||||||||||
                                    GGGCGGC     CGAGGAGGAC
                                        AGGCC_
GAM1656  UBE2B   3'  TGAGAAAGGCACATATTGGAG  13941    G   AC__
                                    CT CAA    TGCTTTTCTTG
                                    || |||    ||||||||||
                                    GA GTT    ACGGAAAGAGT
                                     G   ATAC
GAM1656  UBE2I   5'  GAGGAGGGCGTGGGGAAGG    13961     G  G  AAC
                                    CCTT CT CA   TGCTTTTCTT
                                    |||| || ||   ||||||||||
                                    GGAA GG GT   GCGGGAGGAG
                                      _  G  ___
GAM1656  UFD1L   5'  GGGAGAGCGGTCGGCGGGG   73675        CAA
                                    CCTTGCTG   ACTGCTTTTCT
                                    ||||||||   ||||||||||
                                    GGGGCGGC   TGGCGAGAGGG
                                               ___
GAM1656  USP18   3'  AAGAGATTTTGCAATGAGG   64383     GC     CTG
                                    CCTT  TGCAAA   CTTTT
                                    ||||  ||||||   |||||
                                    GGAG  ACGTTT   GAGAA
                                      TA     TA_
GAM1656  USP18   3'  TGGGGAGAGCAGTGGCAGTGGG 64386    TG    AA
                                    CT  CTGC  ACTGCTTTTCTTG
                                    ||  ||||  ||||||||||||
                                    GG  GACG  TGACGAGAGGGGT
                                     GT    G_
GAM1656  VCX     5'  CGAGAGGGGTATATACAGGGAG 69700     G   CAAAC
                G                   CCTT CTG    TGCTTTTCTTG
                                    |||| |||    ||||||||||
                                    GGAG GAC    ATGGGGAGAGC
                                      G   ATAT_
GAM1656  VENTX2  3'  CAGGGAAAGCAGGGCAGCCGGG 27858     T    AAA
                                    CCT GCTGC   CTGCTTTTCTTG
                                    ||| |||||   ||||||||||||
                                    GGG CGACG   GACGAAAGGGAC
                                      C    G__
GAM1656  WDR10   5'  TAGGAGGAGCCCGAGCCGTAAG 37342       T  AAACT
                G                   CCTTGC GC    GCTTTTCTTG
                                    ||||||  ||    ||||||||||
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                                GGAATG CG    CGAGGAGGAT
                                   C  AGCC_
GAM1656  WHSC1L1   5'  CGGGAGAGGCGGCGGCGGCG   35497       AAA
                                TGCTGC   CTGCTTTTCTTG
                                ||||||   ||||||||||||
                                GCGGCG   GGCGGAGAGGGC
                                   GC_
GAM1656  WRN      5'  CGAGAAAGGCGAGCCGGGCCGG 6890      T   __  AAAC
            G                    CCT GCT  GC    TGCTTTTCTTG
                                 ||| |||  ||    ||||||||||
                                 GGG CGG  CG    GCGGAAAGAGC
                                   C   GC  A___
GAM1656  WRN      5'  CGGGGAGAGCGACGGCGGGG   6891         CAAAC
                                CCTTGCTG    TGCTTTTCTTG
                                ||||||||    ||||||||||
                                GGGGCGGC    GCGAGAGGGGC
                                    A____
GAM1656  XPNPEP2   3'  AAGAGGGAATGCGGTGAGG    14139     TG    AA  G
                                CCT  CTGCA  CT CTTTT
                                |||  |||||  || |||||
                                GGA  GGCGT  GG GAGAA
                                  GT    AA  _
GAM1656  XRCC5     3'  AGGAAAACCATGGGTAAGG    41240        G  AAC  C
                                CCTTGCT CA   TG TTTTCTT
                                ||||||| ||   || |||||||
                                GGAATGG GT   AC AAAAGGA
                                   _  ___  C
GAM1656  YY1      5'  CAGGGCGGGCGGTTGCGGCGAG 14151           A    TT
            G                    CCTTGCTGCAA CTGCT  TCTTG
                                 ||||||||||| |||||  |||||
                                 GGAGCGGCGTT GGCGG  GGGAC
                                       _    GC
GAM1656  ZIC1      5'  TGGGGGGGGCGGGGGAGGCCGG 14168     T   GCAAA     TT
            G                    CCT GCT    CTGCTT  CTTG
                                 ||| |||    ||||||  ||||
                                 GGG CGG    GGCGGG  GGGT
                                   C   AGGG_     GG
GAM1656  ZNF205    3'  AGGAAAGGGGGAGCGGGG     14369        GCAAA  G
                                CCTTGCT    CT CTTTTCTT
                                |||||||    || ||||||||
                                GGGGCGA    GG GGAAAGGA
                                   _____  G
GAM1656  ZNF205    5'  TGGGGGAGGCGGTACCTTCAGG 14371       CTGCAA      TT
            G                    CCTTG     ACTGCTT  CTTG
                                 |||||     |||||||  ||||
                                 GGGAC     TGGCGGA  GGGT
                                   TTCCA_      GG
GAM1656  ZNF278    5'  GGGAGGGGAGGTGGCAGG    50275       TG AAA  G
                                CTTGC  C   CT CTTTTCT
                                |||||  |   || |||||||
```

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                                GGACG  G   GA GGGAGGG
                                  GT ___  G
GAM1656  ZNF289    3'  TAGGGAAAGCGGAAGGTAGAAG 65933      G    AAA
             G                     CCTT CTGC   CTGCTTTTCTTG
                                   |||| ||||   ||||||||||||
                                   GGAA GATG   GGCGAAAGGGAT
                                     _    GAA
GAM1656  ZNF74     5'  CGGGAGGAGCGTGTGGCGGGG  14259       TG  AAC
                                   CCTTGC  CA   TGCTTTTCTTG
                                   ||||||  ||   ||||||||||
                                   GGGGCG  GT   GCGAGGAGGGC
                                     GT  ___
GAM1656  20D7-FC4  3'  GGGGGGGCCCCGTGGGCAGGG  61565       G  AACT    TT
                                   CCTTGCT CA    GCTT  CT
                                   |||||||  ||    ||||  ||
                                   GGGACGG GT    CGGG  GG
                                      _  GCCC    GG
GAM1656  AD-003    3'  TGGGGGGAGCTGGCAGCTGGG  26781     T    AAACT    TT
                                   CCT GCTGC     GCTT  CTTG
                                   ||| |||||     ||||  ||||
                                   GGG CGACG     CGAG  GGGT
                                     T    GT___    GG
GAM1656  AF9Q34    3'  TAAGAAGGGTGGGAGTGGGGC  51721     G  AA_ TG
                                   GCT CA   C  CTTTTCTTG
                                   ||| ||   |  |||||||||
                                   CGG GT   G  GGGAAGAAT
                                     G  GAG GT
GAM1656  AK5       3'  TGGGAGGGGCATGTCAGTAAG  24933        _  AAC
                                   CTTGCTG CA   TGCTTTTCTTG
                                   |||||||  ||   ||||||||||||
                                   GAATGAC GT   ACGGGGAGGGT
                                      T  ___
GAM1656  AKR1D1    3'  CGGGAGGAGGAGCTTGCAGTGA 21131     TG     A  G
             G                     CT  CTGCAA CT CTTTTCTTG
                                   ||  ||||||  || |||||||||
                                   GA  GACGTT GA GAGGAGGGC
                                    GT     C  G
GAM1656  AMOT      5'  GAGGAGGGGAGCAGCCGGG    56544     T    AAA  G
                                   CCT GCTGC   CT CTTTTC
                                   ||| |||||   || ||||||
                                   GGG CGACG   GG GAGGAG
                                     C    A__  G
GAM1656  ASB16     5'  CAAGGGAGGTAGTCGGGTCGAG 55974       _  GCAA      TT
             G                     CCTTG CT    ACTGCTT  CTTG
                                   |||||  ||    |||||||  ||||
                                   GGAGC GG    TGATGGA  GAAC
                                      T  GC__      GG
GAM1656  ASTN2     3'  GAGGATGGTTGCAGTGAGG    73559     TG     A   C
                                   CCT  CTGCAA CTG TTTTC
                                   |||  |||||| ||| |||||
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                                GGA  GACGTT GGT AGGAG
                                  GT     _  _
GAM1656 ATP6V0A1 3' CAGGAGGGGTGTCCTGGGCAGG 18983       G  A_  T
             G                   CCTTGCT CA  AC GCTTTTCTTG
                                 ||||||| ||  || ||||||||||
                                 GGGACGG GT  TG TGGGGAGGAC
                                    _  CC  _
GAM1656 BANP    5' AAGAGATTTTGCGCTGGG    66796    T  T    CTGCT
                                 CCT GC GCAAA    TTTCTT
                                 ||| || |||||    ||||||
                                 GGG CG CGTTT    AGAGAA
                                  T  _    T_____
GAM1656 BATF    3' CGGGGAGAGCAGAGCCTCGGGA 22146     G  CAAA_
             GG                   CCTT CTG    CTGCTTTTCTTG
                                 |||| |||    ||||||||||||
                                 GGAG GGC    GACGAGAGGGGC
                                   _  TCCGA
GAM1656 BFAR    3' AAGAGGGGTGAGGCAGGG    61418       GCAA  G
                                 CCTTGCT    ACT CTTTT
                                 |||||||    ||| |||||
                                 GGGACGG    TGG GAGAA
                                    AG__   G
GAM1656 BRD1    3' GGGGAAAGTAGGGTGGGT    28144    G  AA
                                 GCT CA  CTGCTTTTCTT
                                 ||| ||  ||||||||||
                                 TGG GT  GATGAAAGGGG
                                   _  GG
GAM1656 BRD2    3' TAGGAGAGCTGGCTCTGCAGTG 18800    TG    AA_  _      TG
             GGG                   CCT  CTGCA   CT GCTTTTCT
                                 |||  |||||   || ||||||||
                                 GGG  GACGT   GG CGAGAGGA
                                   GT    CTC  T       T
GAM1656 BTN3A2   3' TGAGGAGGGCGGATCACAAGG  23881      C  CAAA
                                 CCTTG TG    CTGCTTTTCTTG
                                 ||||| ||    ||||||||||||
                                 GGAAC AC    GGCGGGAGGAGT
                                    _  TA__
GAM1656 C11orf11 3' GGGGAAGGGTGTGGAGTGGGG  94880    TG  G  A   G   TT
                                 CCT  CT CA ACT CTT  CT
                                 |||  || || ||| |||  ||
                                 GGG  GA GT TGG GAA  GG
                                   GT  G  G   _   GG
GAM1656 C11orf16 3' AGGAAGGCACCTGTTGTGAGG  40591    TG T   AAC
                                 CCT  C GCA   TGCTTTTCT
                                 |||  | |||   |||||||||
                                 GGA  G TGT   ACGGAAGGA
                                   GT T   CC_
GAM1656 C11orf21 5' CAGGAAGGGGAGGGGCAGTGAG 27101    TG   AAA  G
             G                    CCT  CTGC   CT CTTTTCTTG
                                 |||  ||||   || |||||||||
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                                GGA  GACG   GA GGGAAGGAC
                                  GT   GG_  G
GAM1656  C11orf21  3'  GGGAGGGAAGGTGCGGTGGGG  27106     TG    AACTG      TG
                                CCT  CTGCA    CTTTTCT
                                |||  |||||    |||||||
                                GGG  GGCGT    GGGAGGG
                                  GT    GGAA_      T
GAM1656  C12orf22  5'  CGGGAGGAGGCAGCTGCGGCGG 48705          AA      _
              GG                  CCTTGCTGCA  CTGCTTT TCTTG
                                |||||||||  ||||||| |||||
                                GGGGCGGCGT  GACGGAG AGGGC
                                      C_      G
GAM1656  C12orf3   3'  AAGAGAAATGCAGTCAGG    40162     T     AACTGC
                                CCT GCTGCA     TTTTCTT
                                ||| ||||||     |||||||
                                GGA TGACGT     AAGAGAA
                                  C     A_____
GAM1656  C17orf26  5'  GAGAGAGTGGCAGCGGGG    58265         AA   G
                                CCTTGCTGC  ACT CTTTT
                                |||||||||  ||| |||||
                                GGGGCGACG  TGA GAGAG
                                     G_  _
GAM1656  C1orf16   3'  AGTCAGTGTGTAGCAAGG    29910          A   _
                                CCTTGCTGCA ACTG CT
                                |||||||||| |||| ||
                                GGAACGATGT TGAC GA
                                      G   T
GAM1656  C1orf2    5'  AGGGAGGGCCGAGCGAGG    22726        GCAAACT
                                CCTTGCT      GCTTTTCTT
                                |||||||      |||||||||
                                GGAGCGA      CGGGAGGGA
                                   GC_____
GAM1656  C20orf102 3'  TGGGGGAGGTGGGAGAGGCCGA 55512       _  GCAAA TG   TT
              GG                  CCTTG CT    C  CTT  CTTG
                                ||||| ||    |  |||  ||||
                                GGAGC GG    G  GGA  GGGT
                                  C  AGAG_ GT   GG
GAM1656  C20orf139 5'  GAGGAACGCTGGGCAGGG    85919        G  AACT  T
                                CCTTGCT CA    GC TTTCTT
                                ||||||| ||    || ||||||
                                GGGACGG GT    CG AAGGAG
                                   _ ____  C
GAM1656  C20orf160 3'  TGAGGAAGGCATGAAGAGTGGG 55527     TG  GCAAAC
                                CT  CT     TGCTTTTCTTG
                                ||  ||     ||||||||||
                                GG  GA     ACGGAAGGAGT
                                 GT  GAAGT_
GAM1656  C20orf178 3'  CGGGGGGAGGGGGGCGGGCGGG 75292         _  AAA  G   TT
              G                   CCTTGCT GC   CT CTT  CTTG
                                ||||||| ||   || |||  ||||
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                                GGGGCGG CG   GG GAG  GGGC
                                    G  G__  G   GG
GAM1656  C20orf29  3'  TGGGAGGCAGAGTTTGCAGTGA 37713    TG       __    TT TTG
             G                   CT  CTGCAAACT  GCTT  C
                                 ||  |||||||||  ||||  |
                                 GA  GACGTTTGA  CGGA  G
                                  GT        GA    GG T
GAM1656  C20orf54  3'  CAGGGAGAGATGATTTGCTGGT 54154     TG  _    CT  _
             GGGG                   CCT  CT GCAAA  G CTTTTCTTG
                                 |||  ||  |||||  |  |||||||||
                                 GGG  GG CGTTT  T GAGAGGGAC
                                   GT  T    AG A
GAM1656  C20orf60  3'  AGGAGGAGCCGCAGGAGG    54805      G    AAACT
                                 CCTT CTGC     GCTTTTCTT
                                 ||||  ||||     |||||||||
                                 GGAG GACG     CGAGGAGGA
                                   _    C_____
GAM1656  C20orf67  5'  GGGGAGGGCGAGGCGGAGG    42322     TG    AAAC
                                 CCT  CTGC    TGCTTTTCTT
                                 |||  ||||    ||||||||||
                                 GGA  GGCG    GCGGGAGGGG
                                   __    GA__
GAM1656  C21orf57  3'  CGGGAGGGGTGGAGGCTGCGGG 75299        T  AAA TG
             G                   CCTTGC GC   C  CTTTTCTTG
                                 ||||||  ||   |  |||||||||
                                 GGGGCG CG   G  GGGGAGGGC
                                    T  GA_ GT
GAM1656  C22orf19  3'  TAGGAGAAGCCAAAGGCAGCAG 14827        AAACT
                                 TTGCTGC     GCTTTTCTTG
                                 |||||||     ||||||||||
                                 GACGACG     CGAAGAGGAT
                                     GAAAC
GAM1656  C22orf5   3'  CGGGAGGGGTGGCCACACAGTG 25337     TG   CAAA_ TG
             GGG                    CCT  CTG    C  CTTTTCTTG
                                 |||  |||    |  |||||||||
                                 GGG  GAC    G  GGGGAGGGC
                                   GT   ACACC GT
GAM1656  C22orf5   3'  GGGGAAGGCAGTCCGGCAGGG  25345        CAA          G
                                 CCTTGCTG   ACTGCTTTTCTT
                                 ||||||||   ||||||||||||
                                 GGGACGGC   TGACGGAAGGGG
                                      C__
GAM1656  C22orf5   3'  TGGGGGGAGCTCAGTGGCAGGG 25347       TG AAACT    TT
                                 CCTTGC  C    GCTT  CTTG
                                 ||||||  |    ||||  ||||
                                 GGGACG  G    CGAG  GGGT
                                    GT ACT__    GG
GAM1656  C2F      3'  TGGGGGGGGTGGTGGTAGCG   22012       AA  TG   TT
                                 TGCTGC  AC  CTT  CTTG
                                 ||||||  ||  |||  ||||
```

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                                GCGATG  TG  GGG  GGGT
                                   G_  GT   GG
GAM1656  C6orf35   5'  AGGAGGAGGCGGTAGCGG    38044      AA       _
                                CTGC  ACTGCTTT TCTT
                                ||||  |||||||| ||||
                                GGCG  TGGCGGAG AGGA
                                  A_       G
GAM1656  C6orf37   5'  AGGAGGGGTCGCGGGGAGG    68091      G    AAACT
                                CCTT CTGC     GCTTTTCTT
                                |||| ||||     |||||||||
                                GGAG GGCG     TGGGGAGGA
                                  G    C____
GAM1656  CABP5     5'  CAAGAGAGGCAGGAAGAGGTGG 39561      _  TG AAA___
              CAAAGG                  CCTT GC  C      CTGCTTTTCTTG
                                ||||  ||  |     ||||||||||||
                                GGAA CG  G      GACGGAGAGAAC
                                  A  GT GAGAAG
GAM1656  CAMTA2    3'  CGGGGAGGGCTGCACGGCCGGG 61884     T    CAAACT
                                CCT GCTG      GCTTTTCTTG
                                |||  ||||      ||||||||||
                                GGG CGGC      CGGGAGGGGC
                                  C    ACGT__
GAM1656  CARHSP1   3'  GAGGAGACTTTGCGGGGAGG   27480      G      CTG
                                CCTT CTGCAAA   CTTTTC
                                |||| |||||||   ||||||
                                GGAG GGCGTTT   GAGGAG
                                  G      CA_
GAM1656  CASKIN1   3'  AGGGGAGGTCTGGGCAAGG    40781       G  AACT    TT
                                CCTTGCT CA    GCTT  CTT
                                |||||||  ||    ||||  |||
                                GGAACGG GT    TGGA  GGA
                                   _  C___    GG
GAM1656  CCR7      3'  AAGGAGGGTGAGTGCAAGG    10220       TGCAA   _
                                CCTTGC     ACT GCTTTTCTT
                                ||||||     ||| |||||||||
                                GGAACG     TGA TGGGAGGAA
                                   _____   G
GAM1656  CCRK      5'  TAGGAAAAGGCGCAGTGGGG   25078     TG    AAACTG
                                CCT  CTGC      CTTTTCTTG
                                |||  ||||      |||||||||
                                GGG  GACG      GAAAAGGAT
                                  GT    CG____
GAM1656  CCT5      3'  TGAGAAAACTATGTAGCAAG   73034         AAC  C
                                CTTGCTGCA   TG TTTTCTTG
                                |||||||||   || ||||||||
                                GAACGATGT   AT AAAAGAGT
                                     ___  C
GAM1656  CDC14B    5'  AGGAGGCGCTGTAGCGAGG    14771          AACT  T
                                CCTTGCTGCA    GC TTTCTT
                                ||||||||||    || ||||||
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                                GGAGCGATGT   CG GGAGGA
                                     ____ C
GAM1656 CDIPT    5' CGAGGGAGGTTGCGGGTAGGAA 21974     G   AAACT   TT
             GG                   CCTT CTGC    GCTT  CTTG
                                  |||| ||||    ||||  ||||
                                  GGAA GATG    TGGA  GAGC
                                    G   GGCGT   GG
GAM1656 CENTG1   3' TGGGGAGGGCGTTTTGGGGTAG 29360       G   C
             GG                   CCTTGCT CAAA TGCTTTTCTTG
                                  ||||||| |||| ||||||||||
                                  GGGATGG GTTT GCGGGAGGGGT
                                     G   T
GAM1656 CEZANNE  3' GGGGAAGGTTTGGTGTGTGGGG 39896    TG T   AACT      G
                                  CCT  C GCA   GCTTTTCTT
                                  |||  | |||   |||||||||
                                  GGG  G TGT   TGGAAGGGG
                                    GT _   GGTT       A
GAM1656 CGI-142  5' AGGAAGGGGAGCGGCTGGG   32689    T   AAAC G
                                  CCT GCTGC   T CTTTTCTT
                                  ||| |||||   | ||||||||
                                  GGG CGGCG   A GGGAAGGA
                                    T    ____ G
GAM1656 CGI-57   3' TAAGGGAAGTGGGGTGAGAGG  74310    TG  G  AA TG   TT
                                  CCT  CT CA  C  CTT  CTTG
                                  |||  || ||  |  |||  ||||
                                  GGA  GA GT  G  GAA  GAAT
                                    __ _  GG GT   GG
GAM1656 CHERP    3' CAGGAGGAGCATGTGCAGGAAG 22129     G    AAC
             G                    CCTT CTGCA   TGCTTTTCTTG
                                  |||| |||||   ||||||||||
                                  GGAA GACGT   ACGAGGAGGAC
                                    G    GT_
GAM1656 CHST3    5' CGGGGAGGGCGCCAGGCAGG   16236      GCAAAC
                                  CTTGCT     TGCTTTTCTTG
                                  ||||||     ||||||||||
                                  GGACGG     GCGGGAGGGGC
                                     ACC___
GAM1656 CLDN15   3' GGGGAAGGTGATGGGGCGGGG  57372       G  AAC       G
                                  CCTTGCT CA   TGCTTTTCTT
                                  ||||||| ||   ||||||||||
                                  GGGGCGG GT   GTGGAAGGGG
                                     G  A__
GAM1656 CLPTM1   3' CGAGGGGTGGGTTGGGCGGGG  8923       G   A TG T TT
                                  CCTTGCT CAA C  C T  CTTG
                                  ||||||| ||| |  | |  ||||
                                  GGGGCGG GTT G  G G  GAGC
                                     _  G GT _ GG
GAM1656 CLSTN3   5' GAGAAGTGCAGAGTGAAGG   28877     _  GCAAA   T
                                  CCTT GCT    CTGC TTTCTT
                                  |||| |||    |||| ||||||
```

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                                GGAA TGA    GACG GAAGAG
                                  G _____   T
GAM1656 CLTH    5' CGGGGGAAGGAGCCGGTGGGG 24131    TG  CAAA G  TT
                                CCT CTG   CT CTT CTTG
                                ||| |||   || ||| ||||
                                GGG GGC   GA GAA GGGC
                                  GT  C___ G  GG
GAM1656 CMRF-35H 5' CAAGAAAAGCAGAAGTCGGG  70935    T  GCAAA
                                CCT GCT   CTGCTTTTCTTG
                                ||| |||   ||||||||||||
                                GGG TGA   GACGAAAAGAAC
                                  C  A____
GAM1656 CRF     3' GGGAGAGGTCGCGGCGGCGGG 22913      AAACT      G
                                CTTGCTGC  GCTTTTCTT
                                ||||||||  |||||||||
                                GGGCGGCG  TGGAGAGGG
                                    GCGC_
GAM1656 CSPG5   3' AAGAAGAGAGGAAGCGGGG   22694      GCAAA G
                                CCTTGCT   CT CTTTTCTT
                                |||||||   || ||||||||
                                GGGGCGA   GA GAGAAGAA
                                   AG___ _
GAM1656 CSR1    3' CAAGGAAACCTTTGCGGGTGGG 33185    TG _   CTGC
            G                    CCT  CT GCAAA   TTTTCTTG
                                ||| || |||||  ||||||||
                                GGG  GG CGTTT  AAAGGAAC
                                  GT  G   CC__
GAM1656 CSRP2BP  3' TGAGAAAAGCGGCATGCAGT  70658      AA
                                GCTGCA  CTGCTTTTCTTG
                                ||||||  ||||||||||||
                                TGACGT  GGCGAAAAGAGT
                                   AC
GAM1656 CST9L   5' TGGGAAGAGCAAAGTCAGCGGT 55514     AA  __
                                GCTGC  ACT  GCTTTTCTTG
                                |||||  |||  ||||||||||
                                TGGCG  TGA  CGAGAAGGGT
                                   AC   AA
GAM1656 CSTL1   5' CAGGAAAGCCTATGTTGGTGAG 57119    TG  _ AACT      TG
            G                    CCT  CTG CA   GCTTTTCT
                                |||  ||| ||   ||||||||
                                GGA  GGT GT   CGAAAGGA
                                  GT   T  ATC_      C
GAM1656 D123    5' CAGGAGAGGGAAAGGCAGCAGC 21213   _     AAACTG
            GG                   CC TTGCTGC     CTTTTCTTG
                                || |||||||    |||||||||
                                GG GACGACG     GGAGAGGAC
                                 C      GAAAG_
GAM1656 DAZAP1  5' TGGGGAGGGCGACGGAGCGGG 39046      GCAAAC
                                CTTGCT     TGCTTTTCTTG
                                ||||||     ||||||||||
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                                GGGCGA     GCGGGAGGGGT
                                   GGCA__
GAM1656  DDX17    5'  CGAGAGAGGCGGCGACGGTGGC 48781    TG AAA__
                                GC  C    CTGCTTTTCTTG
                                ||  |    ||||||||||||
                                CG  G    GGCGGAGAGAGC
                                 GT GCAGC
GAM1656  DDX34    3'  TAGGAGGGGCGTTAGAGCCAGC 28677        _ A__   T
            AGGG                  CCTTGCTG C   AAC GCTTTTCTTG
                                ||||||||| |   ||| ||||||||||
                                GGGACGAC G   TTG CGGGGAGGAT
                                     C AGA   _
GAM1656  DDX34    3'  TGGGAAAGGCGGAGGTGCACAG 28682      C    AA_
            G                    CTTG TGCA   CTGCTTTTCTTG
                                |||| ||||   ||||||||||||
                                GGAC ACGT   GGCGGAAAGGGT
                                   _    GGA
GAM1656  DDX37    3'  GGGAGGGGGAGGGTGGGG    51988     TG  GCAAA  G
                                CCT  CT     CT CTTTTCTT
                                |||  ||     || ||||||||
                                GGG  GG     GA GGGGAGGG
                                  GT  _____  G
GAM1656  DDX39    3'  CAGGAGGAGCGGTGAGTGCGAG 20544       T  AA
                                CTTGC GC  ACTGCTTTTCTTG
                                |||||  ||  ||||||||||||
                                GAGCG TG  TGGCGAGGAGGAC
                                   _  AG
GAM1656  DGKZ     3'  AGGAGGGACAATGCGGCCAGG  14675     T     AAC  _      TG
                                CCT GCTGCA   TG CTTTTCT
                                ||| ||||||   || |||||||
                                GGA CGGCGT   AC GGGAGGA
                                  C     A__  A      C
GAM1656  DKFZP434C171 3'  TGGGGAAGGTGAGTGGTAGAGA 32202     TG    AA   _
            GG                    CCT  CTGC  ACT GCTTTTCTTG
                                |||  ||||  ||| ||||||||||
                                GGA  GATG  TGA TGGAAGGGGT
                                  GA   G_   G
GAM1656  DKFZP434H0820 5'  CGGGGGAAGCAGGGCGGGCCGG 64583     T   _  AAA     TT
            G                    CCT GCT GC   CTGCTT  CTTG
                                ||| ||| ||   ||||||  ||||
                                GGG CGG CG   GACGAA  GGGC
                                  C   G  G__     GG
GAM1656  DKFZP434I0714 5'  CGGGAAAGGTGGTGAGAGGGGC 86992      _   GCAA__  TG
            AAAGG                   CCTT GCT      AC  CTTTTCTTG
                                |||| |||     ||  |||||||||
                                GGAA CGG     TG  GGAAAGGGC
                                  A   GGAGAG  GT
GAM1656  DKFZp434I1117 3'  CGGGGAGGGCAGGAAGGGAGG  62844      G  GCAAA
                                CCTT CT     CTGCTTTTCTTG
                                |||| ||     ||||||||||||
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                                GGAG GA    GACGGGAGGGGC
                                  G  AG___
GAM1656  DKFZP434I2117 3'  AGGAGGGCTTGTGGGGAGG   49729     G TG   ACT
                                CCTT C  CAA   GCTTTTCT
                                |||| |  |||   ||||||||
                                GGAG G  GTT   CGGGAGGA
                                  G GT  ___
GAM1656  DKFZp434N035 3'  AAGGGGAGGTGCGCGAGG    51056       T   AACTG   TT
                                CCTTGC GCA    CTT  CTT
                                |||||| |||    |||  |||
                                GGAGCG CGT    GAG  GAA
                                   _  G____   GG
GAM1656  DKFZp434N035 3'  AGGAGAAGCTGCAGCAGG    51059         AACT       G
                                CTTGCTGCA   GCTTTTCTT
                                |||||||||   |||||||||
                                GGACGACGT   CGAAGAGGA
                                     ____
GAM1656  DKFZP434N178 3'  GGGGGAGGATGCGGAGGG    72401     G    AA  G   TT
                                CCTT CTGCA  CT CTT  C
                                |||| |||||  || |||  |
                                GGGA GGCGT  GA GGG  G
                                  _    AG  _   GG
GAM1656  DKFZp547J036 5'  TGGGGGGGGCCCAGGGAGCAGG 51124        GCAAACT   TT
           G                     CCTTGCT      GCTT  CTTG
                                |||||||      ||||  ||||
                                GGGACGA      CGGG  GGGT
                                    GGGACC_   GG
GAM1656  DKFZP564B167 5'  AGGGAAAGCCGCGGGAAGG   31836     G   AAACT
                                CCTT CTGC    GCTTTTCTT
                                |||| ||||    |||||||||
                                GGAA GGCG    CGAAAGGGA
                                  G   C____
GAM1656  DKFZP564C186 3'  TGGGGGAGGCAGTAGACACGGG 72845      C  CAA      TT
                                CTTG TG   ACTGCTT  CTTG
                                |||| ||   |||||||  ||||
                                GGGC AC   TGACGGA  GGGT
                                  _ AGA      GG
GAM1656  DKFZP566F2124 3'  CGGGGGGAGGGTTGTGGCAAG  32216      TG   A  G   TT
                                CTTGC  CAA CT CTT  CTTG
                                |||||  ||| || |||  ||||
                                GAACG  GTT GG GAG  GGGC
                                   GT  _ _   GG
GAM1656  DKFZP566G1424 5'  TGGGGGGGGCACCAGTGAGG   85947    TG   CAAAC    TT
                                CCT  CTG    TGCTT  CTTG
                                |||  |||    |||||  ||||
                                GGA  GAC    ACGGG  GGGT
                                  GT   C____    GG
GAM1656  DKFZP586B0923 5'  TGAGGAAAGCCAGGCAGTAGAG 94742     _     AAACT
           G                     CCT TGCTGC    GCTTTTCTTG
                                ||| ||||||    ||||||||||
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                                GGA ATGACG    CGAAAGGAGT
                                  G     GAC__
GAM1656  DKFZP586J1624 3'  AGGGAGGGCTGGGGCGGGG   32041        G  AACT
                                CCTTGCT CA    GCTTTTCTT
                                ||||||| ||    |||||||||
                                GGGGCGG GT    CGGGAGGGA
                                   G  _____
GAM1656  DKFZP586N0721 5'  AGGAAGAGCACACATGAGG    31826       C  CAAAC
                                CCTTG TG     TGCTTTTCTT
                                ||||| ||     ||||||||||
                                GGAGT AC     ACGAGAAGGA
                                   _  AC____
GAM1656  DKFZp761O17121 3'  CAGGAGAAGCTCCCCAGAGTAG 51131         GCAAACT
            GG                    CCTTGCT      GCTTTTCTTG
                                |||||||      ||||||||||
                                GGGATGA      CGAAGAGGAC
                                   GACCCCT
GAM1656  DKFZp762M136 3'  TAGGAGGAGCAGTGACCGGGG  65325      CTGCAA
                                CCTTG     ACTGCTTTTCTTG
                                |||||     ||||||||||||
                                GGGGC     TGACGAGGAGGAT
                                  CAG___
GAM1656  DNAM-1    5'  TAAGGGAGGGAGCAGCGGGG   22686         AAAC G   TT
                                CCTTGCTGC    T CTT  CTTG
                                |||||||||    | |||  ||||
                                GGGGCGACG    A GGA  GAAT
                                     _____ G   GG
GAM1656  DOC2B     3'  CGGGGAGGGCAAGGAGCTGGG  14560     T   GCAAAC
                                CCT GCT      TGCTTTTCTTG
                                ||| |||      ||||||||||
                                GGG CGA      ACGGGAGGGGC
                                  T   GGA___
GAM1656  DOK4      3'  TGGGAAGATGCCCCTGGGGTAG 36664        G  AACT  _
            GG                    CCTTGCT CA    GC TTTTCTTG
                                ||||||| ||    || ||||||||
                                GGGATGG GT    CG AGAAGGGT
                                   G  CCC_  T
GAM1656  DRAP1     5'  AAGAGGAGGGCACTAGGG    22243       C   AAACTG
                                CCTTG TGC     CTTTTCTT
                                ||||| |||     ||||||||
                                GGGAT ACG     GAGGAGAA
                                  C   G_____
GAM1656  EDR2      3'  TGGGAGGGGCAGAGAGGTAGG  61115       GCAAA
                                CTTGCT    CTGCTTTTCTTG
                                ||||||    ||||||||||||
                                GGATGG    GACGGGGAGGGT
                                   AGA__
GAM1656  EIF2S2    5'  TGGGAGAGGTATCGGCAGGG   15341        CAAAC
                                CCTTGCTG    TGCTTTTCTTG
                                ||||||||    ||||||||||
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                                GGGACGGC    ATGGAGAGGGT
                                   T____
GAM1656 EIF3S1   3' CAAGAAAAGCAGTTTGCAGCAA 63865
              GG                  CCTTGCTGCAAACTGCTTTTCTTG
                                  ||||||||||||||||||||||
                                  GGAACGACGTTTGACGAAAAGAAC
                                             T
GAM1656 EIF4B    3' AGGGGAGGGAGGTAGAAGG   76495     G   AAA G   TT
                                  CCTT CTGC   CT CTT  CTT
                                  |||| ||||   || |||  |||
                                  GGAA GATG   GA GGA  GGA
                                    _   ___ G   GG
GAM1656 ENDO180  3' GGCTCTGGTTTGGAGCAAGG  21268       G    ___
                                  CCTTGCT CAAACT   GCT
                                  ||||||| ||||||   |||
                                  GGAACGA GTTTGG   CGG
                                     G     TCT
GAM1656 EPLIN    5' CAGGAAAGGCGGCTTTTAGCCA 33449     T   C  A
              GG                  CCT GCTG AA CTGCTTTTCTTG
                                  ||| |||| || ||||||||||||
                                  GGA CGAT TT GGCGGAAAGGAC
                                    C   T  C
GAM1656 FADS2    3' TGAGAAGAGGAGGAGGTGGGG  16220     TG  GCAAA  G
                                  CCT  CT    CT CTTTTCTTG
                                  |||  ||    || |||||||||
                                  GGG  GG    GA GAGAAGAGT
                                    GT  AG___  G
GAM1656 FADS2    3' GGGGAAGGGGTGCAGGTGGGG  16216     TG _   AA   G   TT
                                  CCT  C TGC  ACT CTT  CT
                                  |||  | |||  ||| |||  ||
                                  GGG  G ACG  TGG GAA  GG
                                    GT G   __   G   GG
GAM1656 FASTK    5' GGGAGCGACCTGCGCAGGG   22968       T   AAC
                                  CCTTGC GCA   TGCTTTT
                                  |||||| |||   |||||||
                                  GGGACG CGT   GCGAGGG
                                     _   CCA
GAM1656 FASTK    5' TGGGAGAGGGAGGTGGTCGGG  22970     T  TG AAA  G
                                  CCT GC  C   CT CTTTTCTTG
                                  ||| ||  |   || |||||||||
                                  GGG TG  G   GA GGAGAGGGT
                                    C  GT ___  G
GAM1656 FLJ00060 5' TGAGAGAGGCAGAAGGATGGG  61756     TG  GCAAA
                                  CCT  CT    CTGCTTTTCTTG
                                  |||  ||    ||||||||||||
                                  GGG  GG    GACGGAGAGAGT
                                    TA  AA___
GAM1656 FLJ10140 3' GAGGGGACCTGCAGAGGG    36319      G    AACTG
                                  CCTT CTGCA     CTTTTC
                                  |||| |||||     ||||||
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                                GGGA GACGT    GGGGAG
                                  _    CCA__
GAM1656  FLJ10300  5'  CGAGAAAGAAAGCTGCAGTACG 36469    T     AA  GC
             G                   CC TGCTGCA  CT  TTTTCTTG
                                 || |||||||  ||  ||||||||
                                 GG ATGACGT  GA  GAAAGAGC
                                  C      C_  AA
GAM1656  FLJ10350  3'  CGAGAGGAGCAGCTGGCACGGG 97249     C   AAA
                                 CTTG TGC   CTGCTTTTCTTG
                                 |||| |||   ||||||||||||
                                 GGGC ACG   GACGAGGAGAGC
                                   _  GTC
GAM1656  FLJ10350  3'  CGGGAAAAGCACTTCCAGCAGC 97250        A__  C
             AGG                    CTTGCTGC   AA TGCTTTTCTTG
                                 ||||||||   || ||||||||||
                                 GGACGACG   TT ACGAAAAGGGC
                                      ACC  C
GAM1656  FLJ10350  3'  CGGGAAGAGGCGGAGCGGCAGC 97251      AAA_   _
                                 GCTGC    CTGC TTTTCTTG
                                 |||||    |||| ||||||||
                                 CGACG    GGCG AGAAGGGC
                                    GCGA   G
GAM1656  FLJ10508  5'  GGGAAAATTGTTTGCAGAAGG  36682     G      TGC
                                 CCTT CTGCAAAC   TTTTCT
                                 |||| ||||||||   ||||||
                                 GGAA GACGTTTG   AAAGGG
                                   _      TTA
GAM1656  FLJ10508  3'  GGGAGAGGCCCATGTGGCAGG  36683      TG  AACT      G
                                 CTTGC  CA    GCTTTTCTT
                                 |||||  ||    |||||||||
                                 GGACG  GT    CGGAGAGGG
                                    GT  ACC_
GAM1656  FLJ10540  5'  CAAGGGAGGCGACCGCGGAGGG 36765     G    AAAC    TT
                                 CCTT CTGC    TGCTT  CTTG
                                 |||| ||||    |||||  ||||
                                 GGGA GGCG    GCGGA  GAAC
                                   _    CCA_    GG
GAM1656  FLJ10540  5'  CAGGGAGGGCAGGTCAGTGGG  36766    TG   CAAA
                                 CT  CTG    CTGCTTTTCTTG
                                 ||  |||    ||||||||||||
                                 GG  GAC    GACGGGAGGGAC
                                  GT   TG__
GAM1656  FLJ10647  3'  GGGGAGGGGGCAGCATGCAGGG 36886       _   AAA  G   TT TTG
                                 CCTTGC TGC   CT CTT  C
                                 |||||| |||   || |||  |
                                 GGGACG ACG   GG GAG  G
                                    T   ACG  G   GG
GAM1656  FLJ10661  3'  CAAGAAGAAGCTGCGGGAAGG  36914     G    AACT     _
                                 CCTT CTGCA    GCTTTT CTTG
                                 |||| |||||    |||||| ||||
```

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                                GGAA GGCGT   CGAAGA GAAC
                                  G    ____     A
GAM1656 FLJ10761 3' CAGGAGAGGGAGTGGTGAGG  37126    TG  GCAA  G
                                CCT  CT   ACT CTTTTCTTG
                                |||  ||   ||| |||||||||
                                GGA  GG   TGA GGAGAGGAC
                                  GT  ____  G
GAM1656 FLJ10761 3' GGGGAAGGAGGCGGGGAGG  37132     G   AAA  G   TT
                                CCTT CTGC   CT CTT  CT
                                |||| ||||   || |||  ||
                                GGAG GGCG   GA GAA  GG
                                  G   ___ G   GG
GAM1656 FLJ10829 3' AGGGAAGGCCATGCCGGGG  37254     CT   AACT
                                CCTTG  GCA   GCTTTTCTT
                                |||||  |||   |||||||||
                                GGGGC  CGT   CGGAAGGGA
                                   __  AC__
GAM1656 FLJ10901 3' GGGGGAGGATGCAGGAGG   37369     G    AA  G
                                CCTT CTGCA  CT CTTT
                                |||| |||||  || ||||
                                GGAG GACGT  GA GGGG
                                  _    AG  G
GAM1656 FLJ11126 3' GAGAGAGAGTGATCTGGCGAGG 37651       GCAA_  G    CTTG
                                CCTTGCT    ACT CTTTT
                                |||||||    ||| |||||
                                GGAGCGG    TGA GAGAG
                                    TCTAG  _    AGT
GAM1656 FLJ11126 3' TGAGGGAAGTGGCAGCAGAGAG 37656    TG   AAA TG   TT
            G                    CCT  CTGC   C  CTT  CTTG
                                |||  ||||  |  |||  ||||
                                GGA  GACG   G  GAA  GAGT
                                  GA   AC_ GT   GG
GAM1656 FLJ11160 3' GAGAAGAGAGTGCAGGAGGG  37694     G    AA  G
                                CCTT CTGCA  CT CTTTTC
                                |||| |||||  || ||||||
                                GGGA GACGT  GA GAAGAG
                                  G    GA  _
GAM1656 FLJ11526 5' CGGGGGGAGCGAACTGTTGTGG 45255   T  TG  AC___   TT
            TGCGG                 CC TGC  CAA    TGCTT  CTTG
                                || |||  |||    |||||  ||||
                                GG GTG  GTT    GCGAG  GGGC
                                 C  GT   GTCAA    GG
GAM1656 FLJ11539 3' GGGGGGAGGCGGCGGAGG   45707     _   AAACTG   TT
                                CCTT GCTGC     CTT  CTT
                                |||| |||||     |||  |||
                                GGAG CGGCG     GAG  GGG
                                  G    _______  GG
GAM1656 FLJ11715 3' GGGAAAGTGCTCAGCAAGG   44981       CAAACT
                                CCTTGCTG     GCTTTTCT
                                ||||||||     ||||||||
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                                GGAACGAC     TGAAAGGG
                                    TCG___
GAM1656  FLJ12168  5'  TAGGAAAAGGAGGAGGCGGGG  45507       GCAAA  G
                                CCTTGCT    CT CTTTTCTTG
                                |||||||    || |||||||||
                                GGGGCGG    GA GAAAAGGAT
                                   AG___  G
GAM1656  FLJ12190  3'  GGGGAGAGGAGGCGCAAGG   47570      T  AAA  G
                                CCTTGC GC   CT CTTTTCTT
                                |||||| ||   || ||||||||
                                GGAACG CG   GA GAGAGGGG
                                   _ ___  G
GAM1656  FLJ12229  5'  GGGAGAGGCCTGGGTGAGG   46407    TG  G  AACT
                                CCT  CT CA    GCTTTTCTT
                                |||  || ||    |||||||||
                                GGA  GG GT    CGGAGAGGG
                                  GT  _  C___
GAM1656  FLJ12242  3'  GGGAGAGGCAGCAGAAGG    45502     G    AAAC
                                CCTT CTGC    TGCTTTTCTT
                                |||| ||||    ||||||||||
                                GGAA GACG    ACGGAGAGGG
                                   _    _____
GAM1656  FLJ12242  5'  GGGAAGGGCGAAGCGGGG    45501       GCAAACT
                                CCTTGCT      GCTTTTCTT
                                |||||||      |||||||||
                                GGGGCGA      CGGGAAGGG
                                   AG_____
GAM1656  FLJ12294  3'  GGGAAAGGTGGGGTTAGG    47717     T   GCAAA TG
                                CCT GCT     C  CTTTTCTT
                                ||| |||     |  ||||||||
                                GGA TGG     G  GGAAAGGG
                                  T   _____ GT
GAM1656  FLJ12298  5'  TGAGGAAAGGAGAGTGTGGAGA 50601     TG TG  AA  G
            GG                   CCT  C  CA  CT CTTTTCTTG
                                ||| |  ||  || |||||||||
                                GGA  G  GT  GA GAAAGGAGT
                                  GA GT  GA  G
GAM1656  FLJ12363  3'  TAGGAGAATAGTTGTGGTATGG 50641    T   TG   A   C
                                CC TGC  CAA CTG TTTTCTTG
                                || |||  ||| ||| ||||||||
                                GG ATG  GTT GAT AAGAGGAT
                                 T  GT  _  _
GAM1656  FLJ12595  5'  CAGGAGGAGTTTCAGTGTAAGG 47147       T  AAACT
                                CCTTGC GC    GCTTTTCTTG
                                |||||| ||    ||||||||||
                                GGAATG TG    TGAGGAGGAC
                                   _ ACTT_
GAM1656  FLJ12700  3'  CAGGGAAAGTGAAAGTTGCAAG 46653       T  AAACT
            G                    CCTTGC GC    GCTTTTCTTG
                                |||||| ||    ||||||||||
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                                GGAACG TG    TGAAAGGGAC
                                   T  AAAG_
GAM1656  FLJ12783  3'  AGGAAGGGGGAGGTATGGGG  49482      C   AAA  G
                                CCTTG TGC   CT CTTTTCT
                                ||||| |||   || |||||||
                                GGGGT ATG   GG GGAAGGA
                                   _  GA_  G
GAM1656  FLJ12783  3'  GAGAAGACCTTGGAGTAGGG  49486       G   ACTG
                                CCTTGCT CAA    CTTTTC
                                ||||||| |||    ||||||
                                GGGATGA GTT    GAAGAG
                                    G   CCA_
GAM1656  FLJ12800  3'  TGGGAAGCAGAGTTTGCAGTGA 43537    TG       __    TT TTG
           G                     CT  CTGCAAACT  GCTT  C
                                ||  |||||||||  ||||  |
                                GA  GACGTTTGA  CGAA  G
                                 GT        GA    GG T
GAM1656  FLJ12806  5'  GGGAGGGGACGGGGTGGGG   43392    TG  GCAAA  _
                                CCT  CT    CTG CTTTTCTT
                                |||  ||    ||| ||||||||
                                GGG  GG    GGC GGGGAGGG
                                  GT  _____   A
GAM1656  FLJ12960  5'  GAATGGTTTGTTGGCAGGG   45295        _     GC
                                CCTTGCTG CAAACT  TT
                                |||||||| ||||||  ||
                                GGGACGGT GTTTGG  AG
                                     T     TA
GAM1656  FLJ12973  3'  TAAGAAGAGTGTACTTTTAGTA 46644        CAAACT_
           AGG                    CCTTGCTG      GCTTTTCTTG
                                ||||||||      ||||||||||
                                GGAATGAT      TGAGAAGAAT
                                    TTTCATG
GAM1656  FLJ13031  3'  TAAGAAAGGAGCTCTGTGATGA 45513      CT   AACTG
           GG                     CCTTG  GCA    CTTTTCTTG
                                |||||  |||    |||||||||
                                GGAGT  TGT    GGAAAGAAT
                                   AG   CTCGA
GAM1656  FLJ13057  5'  CGGGGAAGGCTGGCGGCGGCGG 97365    _     AAACT
                                CC TTGCTGC    GCTTTTCTTG
                                || |||||||    ||||||||||
                                GG GGCGGCG    CGGAAGGGGC
                                 C      GT___
GAM1656  FLJ13057  5'  CGGGGAAGGCTGGCGGCGGCGG 42705    _     AAACT
                                CC TTGCTGC    GCTTTTCTTG
                                || |||||||    ||||||||||
                                GG GGCGGCG    CGGAAGGGGC
                                 C      GT___
GAM1656  FLJ13117  3'  AAGAGAGGCAATCAGGGGG   43799     G   CAAAC
                                CTT CTG    TGCTTTTCTT
                                ||| |||    ||||||||||
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                                GGG GAC    ACGGAGAGAA
                                  G  TA___
GAM1656  FLJ13158  3'  GGGAAAAAAATGCAGTGAAGG  46651     _    AACTGC
                                CCTT GCTGCA     TTTTCT
                                |||| ||||||     ||||||
                                GGAA TGACGT     AAAGGG
                                  G     AAAA__
GAM1656  FLJ13162  5'  CAGGGGGAGCCGTGAGTGAGG  47183    TG  G  AACT   TT
                                CCT  CT CA    GCTT  CTTG
                                |||  || ||    ||||  ||||
                                GGA  GA GT    CGAG  GGAC
                                  GT  _  GC__    GG
GAM1656  FLJ13181  5'  GGGAGGGGGGGTGGCAGTGG   48023   TG   AA   G
                                T  CTGC  ACT CTTTTCT
                                |  ||||  ||| |||||||
                                G  GACG  TGG GGGAGGG
                                 GT   G_  G
GAM1656  FLJ13224  3'  CGAGAGAACACTGCGGCGG   46024       AAC  C
                                TTGCTGCA   TG TTTTCTTG
                                ||||||||   || ||||||||
                                GGCGGCGT   AC AAGAGAGC
                                     C__  _
GAM1656  FLJ13693  3'  TGGGGAGAGTGGAAGAGGCAGG 46077       GCAAA TG
            G                    CCTTGCT    C  CTTTTCTTG
                                |||||||    |  |||||||||
                                GGGACGG    G  GAGAGGGGT
                                    AGAA_ GT
GAM1656  FLJ13962  3'  CGAGGAAAGCAGCTGTGAGAAA 46318     G  G  AA_
            GG                    CCTT CT CA   CTGCTTTTCTTG
                                |||| || ||   ||||||||||||
                                GGAA GA GT   GACGAAAGGAGC
                                  A  _  GTC
GAM1656  FLJ13984  5'  CGGGAGGGGCGCTGTGTCGAGG 45805      C    AAC
                                CCTTG TGCA   TGCTTTTCTTG
                                ||||| ||||   ||||||||||||
                                GGAGC GTGT   GCGGGGAGGGC
                                   T   C__
GAM1656  FLJ14050  3'  AAGGAGGGAGGAGTAGGG    60953       GCAAA  G
                                CCTTGCT    CT CTTTTCTT
                                |||||||    || ||||||||
                                GGGATGA    GG GGGAGGAA
                                    _____  A
GAM1656  FLJ14129  5'  TGGGGGAGGCGGCCCTGCAG   48816      AA_    TT
                                CTGCA   CTGCTT  CTTG
                                |||||   ||||||  ||||
                                GACGT   GGCGGA  GGGT
                                   CCC     GG
GAM1656  FLJ14146  3'  CAAGGGAGGCTGGGTAGCCAGG 45566    T    AAACT   TT
                                CCT GCTGC    GCTT  CTTG
                                ||| |||||    ||||  ||||
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                                GGA CGATG    CGGA  GAAC
                                  C    GGT__   GG
GAM1656  FLJ14213  3'  AGGAAAAGCTGCACTGGGG   46213     GC   AACT
                                CCTT  TGCA   GCTTTTCTT
                                ||||  ||||   |||||||||
                                GGGG  ACGT   CGAAAAGGA
                                  TC   ____
GAM1656  FLJ14280  5'  CAGGAGGAGTGGCTGAGGCAGG 46519       G  AA TG
            G                    CCTTGCT CA  C  CTTTTCTTG
                                |||||||  ||  |  |||||||||
                                GGGACGG GT  G  GAGGAGGAC
                                    A  C_ GT
GAM1656  FLJ14280  3'  TAAGAAAAGTAAATAGGCCGGG 46524    T   GCAAAC
                                CCT GCT     TGCTTTTCTTG
                                ||| |||     ||||||||||
                                GGG CGG     ATGAAAAGAAT
                                  C   ATAA__
GAM1656  FLJ14437  3'  TGAGAAGAGCTAGGCAGTAG   51800       AAACT
                                TTGCTGC    GCTTTTCTTG
                                |||||||    ||||||||||
                                GATGACG    CGAGAAGAGT
                                    GAT__
GAM1656  FLJ14490  5'  TGGGAGGAGCAGCGGCCTGCGG 52449       T_  AAA
            GG                    CCTTGC  GC   CTGCTTTTCTTG
                                ||||||  ||   ||||||||||||
                                GGGGCG  CG   GACGAGGAGGGT
                                    TC  GC_
GAM1656  FLJ14596  5'  GGGAGGGGAGCAGCTGGG    52518    T    AAAC G
                                CCT GCTGC    T CTTTTCT
                                ||| |||||    | |||||||
                                GGG CGACG    A GGGAGGG
                                  T    _____ G
GAM1656  FLJ14596  3'  GGGGGAAGCAGAGGCCAGG    52519    T   GCAAA     TT
                                CCT GCT    CTGCTT  CTT
                                ||| |||    ||||||  |||
                                GGA CGG    GACGAA  GGG
                                  C   A____     GG
GAM1656  FLJ14641  3'  CGAGAAGGGTGGATCATGAGG  52556      C  CAAA TG
                                CCTTG TG    C  CTTTTCTTG
                                |||||  ||   |  |||||||||
                                GGAGT AC    G  GGGAAGAGC
                                    _  TA__ GT
GAM1656  FLJ14735  3'  GAGAGGAGTGTATAGTATGG   52667    T    CAA   G
                                CC TGCTG   ACT CTTTTC
                                ||  |||||   ||| ||||||
                                GG ATGAT   TGA GGAGAG
                                  T    ATG   _
GAM1656  FLJ14816  3'  AAGAGAGCACTGTGGTGAGG   52706     TG TG  AAC     T   G
                                CCT  C  CA   TGCTTT CTT
                                |||  |  ||   |||||| |||
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                                GGA  G  GT   ACGAGA GAA
                                  GT GT  C__     _  G
GAM1656  FLJ14936  3'  CGAGAAAGGCATCGGAGCAAG  51128       GCAAAC
                                CTTGCT     TGCTTTTCTTG
                                ||||||     ||||||||||
                                GAACGA     ACGGAAAGAGC
                                   GGCT__
GAM1656  FLJ20006  5'  CAGGGAGGGCAGGAGAGCGCCG 34781     T  T  AAA_
           GG                    CCT GC GC    CTGCTTTTCTTG
                                ||| || ||    ||||||||||||
                                GGG CG CG    GACGGGAGGGAC
                                  C  _  AGAG
GAM1656  FLJ20060  3'  TGAGAAAAGTAGTACCTTGGG  34932     TGCTGCAA
                                CCT       ACTGCTTTTCTTG
                                |||       ||||||||||||
                                GGG       TGATGAAAAGAGT
                                  TTCCA___
GAM1656  FLJ20123  5'  TGAGGAGAGAGGAGCAGCAGG  35074        AAA  G
                                CTTGCTGC   CT CTTTTCTTG
                                ||||||||   || |||||||||
                                GGACGACG   GA GAGAGGAGT
                                     AG_  _
GAM1656  FLJ20174  3'  AAGAAAGGAGGCAGAAGG    35187      G    AAACTG
                                CCTT CTGC     CTTTTCTT
                                |||| ||||     ||||||||
                                GGAA GACG     GGAAAGAA
                                  _    GA_____
GAM1656  FLJ20195  3'  GGGAAGAGGGTATGCAAGG    35220       TGCAA   G
                                CCTTGC     ACT CTTTTCTT
                                ||||||     ||| ||||||||
                                GGAACG     TGG GAGAAGGG
                                   TA___   _
GAM1656  FLJ20195  3'  GGGGAAGGCGGGGCTAGG    35222     T   GCAAA
                                CCT GCT     CTGCTTTTCTT
                                ||| |||     ||||||||||
                                GGA CGG     GGCGGAAGGGG
                                  T  ______
GAM1656  FLJ20257  5'  TGGGGGGGGCGGGGGCAAG    39493       GCAAA     TT
                                CTTGCT    CTGCTT  CTTG
                                ||||||    ||||||  ||||
                                GAACGG    GGCGGG  GGGT
                                   G_____     GG
GAM1656  FLJ20296  3'  AGGGAGGTGTGGGGTAAGG    35362       G  AAC    TT
                                CCTTGCT CA   TGCTT  CT
                                ||||||| ||   |||||  ||
                                GGAATGG GT   GTGGA  GA
                                    G  ___     GG
GAM1656  FLJ20306  3'  TGGGAGGAGAAGGTTGCAGTGA 35403    TG     A  G
           G                     CT  CTGCAA CT CTTTTCTTG
                                ||  |||||| || |||||||||
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                                GA  GACGTT GA GAGGAGGGT
                                 GT     G  A
GAM1656  FLJ20320  5'  CAGGAGGGAGCTGTGGCCGAGG 35418      _ TG  AACT    _
                                CCTTG C  CA    GCTTT TCTTG
                                ||||| |  ||    ||||| |||||
                                GGAGC G  GT    CGAGG AGGAC
                                   C GT  ____     G
GAM1656  FLJ20333  5'  GGGAAAAGTGGCACTGAGG   35434     GC   AAAC
                                CCTT  TGC    TGCTTTTCTT
                                ||||  |||    ||||||||||
                                GGAG  ACG    GTGAAAAGGG
                                  TC  ____
GAM1656  FLJ20356  3'  CAAGGGAGTGGGTTTTGTGCAA 39138       T    __ TG T TT
            GG                    CCTTGC GCAAA  C  C T  CTTG
                                ||||||  |||||  |  | |  ||||
                                GGAACG TGTTT  G  G A  GAAC
                                   _    TG GT _ GG
GAM1656  FLJ20374  5'  AGGGGAGGGGCCTGGCGGCAGG 35548         AAA_  G   TT  TG
            G                     CCTTGCTGC    CT CTT  CT
                                |||||||||    || |||  ||
                                GGGACGGCG    GG GAG  GA
                                     GTCC  G   GG  C
GAM1656  FLJ20378  3'  CAGGAGAGGTGGGGTGGGG   35553     TG  GCAAA TG
                                CCT  CT    C  CTTTTCTTG
                                |||  ||    |  |||||||||
                                GGG  GG    G  GGAGAGGAC
                                  GT  _____ GT
GAM1656  FLJ20445  3'  TAGGAAAAGTAAATGGAGAGG  35633     TG  G  AAC
                                CCT  CT CA   TGCTTTTCTTG
                                |||  || ||   ||||||||||
                                GGA  GA GT   ATGAAAAGGAT
                                  __  G  AA_
GAM1656  FLJ20519  5'  CGAGGGGAGCGAAGGTAGGAGG 35797      G    AAAC    TT
                                CCTT CTGC    TGCTT  CTTG
                                |||| ||||    |||||  ||||
                                GGAG GATG    GCGAG  GAGC
                                   _    GAA_     GG
GAM1656  FLJ20559  5'  CAGGAGGAGCGTGGGGAAAGG  35832      G  G  AAC
                                CCTT CT CA   TGCTTTTCTTG
                                |||| || ||   ||||||||||
                                GGAA GG GT   GCGAGGAGGAC
                                  A  G  ___
GAM1656  FLJ20568  3'  TGGGAGGGGTGGGAGCATGG   35847    T    GCAAA TG
                                CC TGCT    C  CTTTTCTTG
                                || ||||    |  |||||||||
                                GG ACGA    G  GGGGAGGGT
                                 T   G____ GT
GAM1656  FLJ20605  3'  AAGGAAAGTATTAGAGGG    35869      G   CAAAC
                                CCTT CTG    TGCTTTTCTT
                                |||| |||    ||||||||||
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                                GGGA GAT     ATGAAAGGAA
                                  _   T_____
GAM1656  FLJ21240  3'  CAGGAGGTGGAGTTTGCAGTGA 46261    TG        G  _
              G                    CT  CTGCAAACT CT TTTCTTG
                                   ||  |||||||||| || |||||||
                                   GA  GACGTTTGA GG GGAGGAC
                                    GT        _  T
GAM1656  FLJ21324  5'  TGGGGAGGGTGGCTGTGGGAGG 92861      G TG  AA TG
                                   CCTT C  CA  C  CTTTTCTTG
                                   |||| |  ||  |  |||||||||
                                   GGAG G  GT  G  GGGAGGGGT
                                     _ GT  C_ GT
GAM1656  FLJ21369  3'  CGGGAGGAGCATCATGAGTAGG 46050       G  AAC
                                   CTTGCT CA   TGCTTTTCTTG
                                   |||||| ||   ||||||||||
                                   GGATGA GT   ACGAGGAGGGC
                                      _  ACT
GAM1656  FLJ21596  3'  CGAGGAGAGCCCTGGCTGAGG  46114     GCT  AAACT
                                   CCTT   GC    GCTTTTCTTG
                                   ||||   ||    ||||||||||
                                   GGAG   CG    CGAGAGGAGC
                                     T__  GTCC_
GAM1656  FLJ21687  3'  CGAGGAAGGCGCTGGCAGAGG  46296     TG    AAAC
                                   CCT  CTGC    TGCTTTTCTTG
                                   |||  ||||    ||||||||||
                                   GGA  GACG    GCGGAAGGAGC
                                     __    GTC_
GAM1656  FLJ21709  3'  GAGAAGGGTCTTCAGCTGGG   78480     T    CAA   G
                                   CCT GCTG   ACT CTTTTC
                                   ||| ||||   ||| ||||||
                                   GGG CGAC   TGG GAAGAG
                                     T    TTC   _
GAM1656  FLJ21742  3'  GGGAAGGGTGGGCTGAGG    50814      GCT  AAA TG
                                   CCTT   GC   C  CTTTTCTT
                                   ||||   ||   |  ||||||||
                                   GGAG   CG   G  GGGAAGGG
                                     T__  ____ GT
GAM1656  FLJ21777  5'  CAAGGGGAGCGCCCTAGCGGGG 50834         CAAAC    TT
                                   CCTTGCTG    TGCTT  CTTG
                                   ||||||||    |||||  ||||
                                   GGGGCGAT    GCGAG  GAAC
                                        CCC__     GG
GAM1656  FLJ22055  3'  CAAGAGGAGTACCCAGTTAGG  45847     T    CAAAC
                                   CCT GCTG    TGCTTTTCTTG
                                   ||| ||||    ||||||||||
                                   GGA TGAC    ATGAGGAGAAC
                                     T   CC____
GAM1656  FLJ22174  5'  TGGGGAAGGTGGGAAGGATCCA 41960         CAAA_____ TG
              GCGAGG                 CCTTGCTG       C  CTTTTCTTG
                                   ||||||||       |  |||||||||
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                                GGAGCGAC      G  GGAAGGGGT
                                    CTAGGAAG GT
GAM1656  FLJ22301  3'  GAGGGAGGCTTGCTGAGG    46179     GCT   ACT   TT
                                CCTT   GCAA   GCTT  CTT
                                ||||   ||||   ||||  |||
                                GGAG   CGTT   CGGA  GAG
                                  T__    ___    GG
GAM1656  FLJ22386  5'  TGGGGAGGGCGCTCGGCGGCG  45043       AAAC
                                TGCTGC    TGCTTTTCTTG
                                ||||||    ||||||||||
                                GCGGCG    GCGGGAGGGGT
                                   GCTC
GAM1656  FLJ22390  5'  CAAGGGGGTGCCGGTGAGCGAG 43030        G  AACT  _  TT
            G                    CCTTGCT CA    GC TT  CTTG
                                |||||||  ||    ||  ||  ||||
                                GGAGCGA GT    CG GG  GAAC
                                   _  GGC_  T  GG
GAM1656  FLJ22415  3'  CAAGGAAGGTAGCCGGGCATGG 93117    T   GCAAA
                                CC TGCT     CTGCTTTTCTTG
                                ||  ||||     ||||||||||||
                                GG ACGG     GATGGAAGGAAC
                                 T   GCC__
GAM1656  FLJ22688  3'  AGGAGGGGCTACAACAGGG    47821       C  CAAACT
                                CCTTG TG      GCTTTTCTT
                                |||||  ||     |||||||||
                                GGGAC AC      CGGGGAGGA
                                   A  AT_____
GAM1656  FLJ22795  3'  TGGGGAAGGCAGGGAGGGCAGG 47638       GCAAA
                                CTTGCT     CTGCTTTTCTTG
                                ||||||     ||||||||||||
                                GGACGG     GACGGAAGGGGT
                                   GAGG_
GAM1656  FLJ22940  5'  TGAGAGGGGCGGCCCTGGAG   44999    G  AA_
                                CT CA   CTGCTTTTCTTG
                                ||  ||   ||||||||||||
                                GA GT   GGCGGGGAGAGT
                                 G  CCC
GAM1656  FLJ23047  5'  TGAGAAAAGTTCCACAGAAGG  44935     G   CAAACT
                                CCTT CTG      GCTTTTCTTG
                                ||||  |||     ||||||||||
                                GGAA GAC      TGAAAAGAGT
                                  _   ACCT__
GAM1656  FLJ23119  3'  GGAAGCACTTGAGGTAGGG    45377       G   AC    TT
                                CCTTGCT CAA  TGCTT  C
                                |||||||  |||  |||||  |
                                GGGATGG GTT  ACGAA  G
                                   A   C_    GG
GAM1656  FLJ23121  5'  AGGAGGAGCTGGCGCAGG    45519      T  AAACT
                                CTTGC GC     GCTTTTCTT
                                |||||  ||    |||||||||
```

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                                GGACG CG    CGAGGAGGA
                                  _ GT___
GAM1656 FLJ23121 3' CAAGAAGAGCGGTTGAAGT   45521    GCA
                                GCT   AACTGCTTTTCTTG
                                |||   ||||||||||||||
                                TGA   TTGGCGAGAAGAAC
                                  AG_
GAM1656 FLJ23277 3' TAAGGGGGGTGGTGGGTGGGAG 50920     G TG AA  TG   TT
           GG                   CCTT C  C  AC  CTT  CTTG
                                ||||| |  |  ||  |||  ||||
                                GGGA G  G  TG  GGG  GAAT
                                  G GT GG  GT   GG
GAM1656 FLJ23436 3' CAGGGAGGGGGGGAGGGCAGGG  45462       GCAAA  G
                                CCTTGCT    CT CTTTTCTTG
                                |||||||    || |||||||||
                                GGGACGG    GG GGGAGGGAC
                                   GA___  G
GAM1656 FLJ23441 3' CAAGAAGAGGTACTTATAGCAA 45491       CAAACTG
           GG                   CCTTGCTG      CTTTTCTTG
                                ||||||||      |||||||||
                                GGAACGAT      GAGAAGAAC
                                   ATTCATG
GAM1656 FLJ23510 3' AAGAAAGATGTAGTAGGG    45621         AACTGC
                                CCTTGCTGCA     TTTTCTT
                                ||||||||||     |||||||
                                GGGATGATGT     GAAAGAA
                                   A_____
GAM1656 FLJ23598 5' CAGGGAAAGGGAAGCATGG   96505    T   GCAAACTG
                                CC TGCT       CTTTTCTTG
                                || ||||       |||||||||
                                GG ACGA       GAAAGGGAC
                                 T   AGG_____
GAM1656 FLJ25132 5' CGGGGAGGGCGGAGACGCAG  78652     AAA_
                                CTGC   CTGCTTTTCTTG
                                ||||   ||||||||||||
                                GACG   GGCGGGAGGGGC
                                  CAGA
GAM1656 FLJ30567 3' CAGGGAGAGAAAGCAGGTAGGG 59472       _  AAACTG
                                CCTTGC TGC     CTTTTCTTG
                                |||||| |||     |||||||||
                                GGGATG ACG     GAGAGGGAC
                                   G  AAA___
GAM1656 FLJ30791 5' GGGAGAGGCCAGTGTGGGAGG  59117     G TG  AACT       G
                                CCTT C  CA    GCTTTTCTT
                                |||| |  ||    |||||||||
                                GGAG G  GT    CGGAGAGGG
                                  _ GT  GAC_       G
GAM1656 FLJ31300 3' TGGGGGAAGTGGCCTCTGTCAG 58936      CT   AA__ TG   TT
           GG                   CCTTG  GCA    C  CTT  CTTG
                                |||||  |||    |  |||  ||||
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                                GGGAC  TGT   G  GAA  GGGT
                                  __   CTCC GT   GG
GAM1656  FLJ32356  3'  AGGGAAATCATGGGCAAGG   59014       G  AAC  C
                                CCTTGCT CA   TG TTTTCTT
                                ||||||| ||   || |||||||
                                GGAACGG GT   AC AAAGGGA
                                   _  ___  T
GAM1656  FLJ32468  3'  TGAGGGAAGCAGTCTCCTGCGG 59713      A___      TT
                                CTGCA   ACTGCTT  CTTG
                                |||||   |||||||  ||||
                                GGCGT   TGACGAA  GAGT
                                  CCTC      GG
GAM1656  FLJ32919  5'  CAGGAGGAGCGGCGTTCAGCCG 58696    T   CAAA
            GG                    CCT GCTG   CTGCTTTTCTTG
                                ||| ||||   ||||||||||||
                                GGG CGAC   GGCGAGGAGGAC
                                  C   TTGC
GAM1656  FLNC     3'  CAGGGAAGCCCTGAGTTTCTGG 9389        C    ____   TT  TG
            CGGGG                  CCTTGCTG AAACT   GCTT  CT
                                |||||||| |||||   ||||  ||
                                GGGGCGGT TTTGA   CGAA  GA
                                    C    GTCC   GG  C
GAM1656  FOXO3A   5'  GGGAGGGACCTGCGGCTGGG   9383     T    AACTG
                                CCT GCTGCA    CTTTTCT
                                ||| ||||||    |||||||
                                GGG CGGCGT    GGGAGGG
                                  T    CCA__
GAM1656  FTSJ3    3'  TAGGAGGAAGGGTGTGGCATGG 34936    T  TG  AA  GC
                                CC TGC  CA  CT  TTTTCTTG
                                || |||  ||  ||  ||||||||
                                GG ACG  GT  GA  AGGAGGAT
                                 T  GT  GG  __
GAM1656  FUBP3    3'  TGGGAGGGGCATTTTGTAG   64474       C
                                CTGCAAA TGCTTTTCTTG
                                ||||||| ||||||||||
                                GATGTTT ACGGGGAGGGT
                                    T
GAM1656  G4       3'  AGGAGGGCCAGTGCAGAAGG   92633     G    AACT
                                CCTT CTGCA   GCTTTTCT
                                |||| |||||   ||||||||
                                GGAA GACGT   CGGGAGGA
                                  _    GAC_
GAM1656  GABARAPL1 3'  TAGGGAAAGGGGACTTGTGGTA 49424     TG   A_  G
            G                   TTGC  CAA  CT CTTTTCTTG
                                ||||  |||  || |||||||||
                                GATG  GTT  GG GAAAGGGAT
                                  GT   CA  G
GAM1656  GABARAPL3 3'  TAGGGAAAGGGGACTTGTGGTA 51788    _   TG   A_  G
            GTGG                  CC TTGC  CAA  CT CTTTTCTTG
                                || ||||  |||  || |||||||||
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                                GG GATG  GTT  GG GAAAGGGAT
                                 T   GT   CA  G
GAM1656  GABBR1   3'  TGAGGGAGGACAGGCCAGTAGG 9413        CAAA  _  TT
             G                   CCTTGCTG   CTG CTT  CTTG
                                 ||||||||   ||| |||  ||||
                                 GGGATGAC   GAC GGA  GAGT
                                     CG__   A   GG
GAM1656  GABBR1   5'  TGGGGGAAGCGAGAGAGGAGGG 9415      G  GCAAAC    TT
                                 CCTT CT     TGCTT  CTTG
                                 |||| ||     |||||  ||||
                                 GGGA GA     GCGAA  GGGT
                                   G  GAGA__     GG
GAM1656  GALNT12  5'  GGGGGCGTCTGCGGCGAGG   45320         A  T
                                 CCTTGCTGCA AC GCTTTT
                                 |||||||||| || ||||||
                                 GGAGCGGCGT TG CGGGGG
                                       C  _
GAM1656  GALNT6   3'  TAGGGAAGGCAGCTGGGGGAGG 24251     G  G  AA
             G                   CCTT CT CA  CTGCTTTTCTTG
                                 |||| || ||  ||||||||||||
                                 GGGA GG GT  GACGGAAGGGAT
                                   G  G  C_
GAM1656  GDF11    3'  GGGGAAAGGGGAAGCAGGG   20559       GCAAA  G
                                 CCTTGCT    CT CTTTTCTT
                                 |||||||    || ||||||||
                                 GGGACGA    GG GAAAGGGG
                                     A_____  G
GAM1656  GMEB2    3'  TAGGGGGAGCCTGGGTGCAGCA 25668       AACT_   TT
             G                   TTGCTGCA    GCTT  CTTG
                                 ||||||||    ||||  ||||
                                 GACGACGT    CGAG  GGAT
                                     GGGTC   GG
GAM1656  GNB1L    3'  CGAGGAGGGCGGGCAGGGAGG  54865     G   AAA
                                 CCTT CTGC   CTGCTTTTCTTG
                                 |||| ||||   ||||||||||||
                                 GGAG GACG   GGCGGGAGGAGC
                                   G   ___
GAM1656  GORASP2  3'  CGGGAAAGGTGGTGGCGGGG   32034       GCAA  TG
                                 CCTTGCT    AC  CTTTTCTTG
                                 |||||||    ||  |||||||||
                                 GGGGCGG    TG  GGAAAGGGC
                                     _____  GT
GAM1656  GREB1    3'  GGGGGGGGAGTTGGCGGGG   28572       GCA   G   TT
                                 CCTTGCT   AACT CTT  CT
                                 |||||||   |||| |||  ||
                                 GGGGCGG   TTGA GGG  GG
                                     ___    G   GG
GAM1656  GRID1    3'  CAGGAGGGGCGACCAGATAAGG 69022      _  CAAAC
                                 CCTTG CTG    TGCTTTTCTTG
                                 ||||| |||    ||||||||||
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                                GGAAT GAC    GCGGGGAGGAC
                                  A  CA___
GAM1656 GRIN3A   5' GGGGGAGCCTGCAGGAGGG   56786     G    AACT   TT
                                CCTT CTGCA   GCTT  CT
                                |||| |||||   ||||  ||
                                GGGA GACGT   CGAG  GG
                                  G    C___   GG
GAM1656 GSK3A    5' CGGGGGAGGCGGCGGCAGCGGC 96979    _     AAA    TT
             GG                   CC TTGCTGC   CTGCTT  CTTG
                                || |||||||   ||||||  ||||
                                GG GGCGACG   GGCGGA  GGGC
                                 C      GC_    GG
GAM1656 H2AV     3' AAGAGAGGTTCCAGGAGGG   57624     G   CAAACT
                                CCTT CTG     GCTTTTCTT
                                |||| |||     |||||||||
                                GGGA GAC     TGGAGAGAA
                                  G  CT____
GAM1656 HCC-4    5' GGACCAGTTTGCGGTTAGG   57600     T        C
                                CCT GCTGCAAACTG TTT
                                ||| ||||||||||| |||
                                GGA TGGCGTTTGAC AGG
                                  T         C
GAM1656 HE3-BETA 5' GAGGGAGTCTGAGTAGGG    42558       G  A   G
                                CCTTGCT CA ACT CTTT
                                ||||||| || ||| ||||
                                GGGATGA GT TGA GGAG
                                    _ C   G
GAM1656 HEMGN    5' AGGAAGGTATTGCAGCAAG   37982         AC
                                CTTGCTGCAA  TGCTTTTCT
                                ||||||||||  |||||||||
                                GAACGACGTT  ATGGAAGGA
                                          __
GAM1656 HES6     5' CGAGGGGAGCGCGGACGGCTGG 38458     T   CAAAC    TT
             G                   CCT GCTG    TGCTT  CTTG
                                ||| ||||    |||||  ||||
                                GGG CGGC    GCGAG  GAGC
                                  T   AGGC_    GG
GAM1656 HGC6.1.1 3' CGGGAAGGGTCCCCCACAGCAA 27611       CAAACT
             G                   CTTGCTG     GCTTTTCTTG
                                |||||||     ||||||||||
                                GAACGAC     TGGGAAGGGC
                                    ACCCCC
GAM1656 HIP-55   3' GGAAGGGTCCTGAGCAGGG   26775       G  A_   G   TT
                                CCTTGCT CA  ACT CTT  CT
                                ||||||| ||  ||| |||  ||
                                GGGACGA GT  TGG GAA  GG
                                    _ CC   _   G
GAM1656 HIP-55   3' TGGATCATGGTGGTTTGGCAGC 26777         _   TG  TT__   TG
             AGGG                  CCTTGCTGC AAAC  CT    TCT
                                |||||||| ||||  ||    |||
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                                GGGACGACG TTTG  GG    AGG
                                     G   GT  TACT   T
GAM1656  HIRIP3   5'  TGAGAAAGGCAGCGTCGCGGG  14606      T  AAA
                                CTTGC GC   CTGCTTTTCTTG
                                ||||| ||   ||||||||||||
                                GGGCG TG   GACGGAAAGAGT
                                  C  C__
GAM1656  HMP19    3'  TAAGAAAACGTAGCTTCAGTGG 88862     TG   C  A   _
           GG                     CCT  CTG AA CTGC TTTTCTTG
                                ||| ||| || |||| ||||||||
                                GGG  GAC TT GATG AAAAGAAT
                                  GT   _  C    C
GAM1656  HNK-1ST  3'  TGAGGAGGGACAGAGAAGCAAG 17951        GCAAA   _
           G                      CCTTGCT    CTG CTTTTCTTG
                                |||||||    ||| |||||||||
                                GGAACGA    GAC GGGAGGAGT
                                    AGA__   A
GAM1656  HOOK2    3'  GGGGAGGGAGGGCGGGAGG    26160     G   AAA  G   TT
                                CCTT CTGC   CT CTT  CT
                                |||| ||||   || |||  ||
                                GGAG GGCG   GA GGA  GG
                                  _   G__  G   GG
GAM1656  HRIHFB2122 5'  CGAGAGGGGCGGCGGCGGCGGC 57618    _      AAA
           GG                     CC TTGCTGC   CTGCTTTTCTTG
                                || |||||||   ||||||||||||
                                GG GGCGGCG   GGCGGGGAGAGC
                                 C      GC_
GAM1656  HSA243666 3'  CAGGGAGGGAAGATGAGGTGGG 34556     TG  G  AA  G
           G                      CCT  CT CA  CT CTTTTCTTG
                                |||  || ||  || |||||||||
                                GGG  GG GT  GA GGGAGGGAC
                                  GT  A  A_  A
GAM1656  HSA6591   3'  TGAGAGGAGCAGGAGTGAGT   73250     G  AA_
                                GCT CA   CTGCTTTTCTTG
                                ||| ||   ||||||||||||
                                TGA GT   GACGAGGAGAGT
                                  _  GAG
GAM1656  HSJ1     3'  GGGGGCGTGTGTGTGGTGGGG  23084     TG TG  A  _
                                CCT  C  CA AC TGCTTTT
                                |||  |  || || |||||||
                                GGG  G  GT TG GCGGGGG
                                  GT GT  G  T
GAM1656  HSRNAFEV  5'  TAAGAGGGGCGGGGGCGGGG   34453        GCAAA
                                CCTTGCT    CTGCTTTTCTTG
                                |||||||    ||||||||||||
                                GGGGCGG    GGCGGGGAGAAT
                                    G____
GAM1656  HSU79303  3'  CGGGAGAGGCAGCGAGTGAAGG 26150      _  GCAAA
                                CCTT GCT    CTGCTTTTCTTG
                                |||| |||    ||||||||||||
```

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                                GGAA TGA    GACGGAGAGGGC
                                  G  GC___
GAM1656 HTMP10   3' TAAGGAGGGCAGTTCTGCGACG 53759    C  _
                                TG TGCA AACTGCTTTTCTTG
                                || |||| ||||||||||||||
                                GC GCGT TTGACGGGAGGAAT
                                 A   C
GAM1656 HYPE     5' GGGGAAGGCGGTTGGGGT    23961    G  A
                                GCT CAA CTGCTTTTCTT
                                ||| ||| ||||||||||
                                TGG GTT GGCGGAAGGGG
                                  G  _
GAM1656 IL18BP   3' TGGGGAAGGTAGGGTGTGAGC  20316    _  AA
                                GCT GCA  CTGCTTTTCTTG
                                ||| |||  ||||||||||||
                                CGA TGT  GATGGAAGGGGT
                                  G  GG
GAM1656 IMP-1    3' TGAGAAAGATGTTCCAGTGAGG 22606    TG  CA  TGC
                                CCT  CTG  AAC   TTTTCTTG
                                |||  |||  |||   |||||||||
                                GGA  GAC  TTG   GAAAGAGT
                                  GT   C_   TA_
GAM1656 INE1     5' CAAGGGAAGTCGGGGTGTCAGG 14756     CT   AA  _  TT
             G                   CCTTG  GCA  CTG CTT  CTTG
                                 |||||  |||  ||| |||  ||||
                                 GGGAC  TGT  GGC GAA  GAAC
                                    __  GG   T  GG
GAM1656 ITPK1    3' GAGGAGGGAGGCACAGGG    27232      C  AAACTG
                                CCTTG TGC     CTTTTCTT
                                ||||| |||     ||||||||
                                GGGAC ACG     GGGAGGAG
                                   _  GA____
GAM1656 JIK      5' GAGAGGAAGCGGCGGCGGCG   33263      AAA     _   G
                                TGCTGC   CTGCTTT TCTT
                                ||||||   ||||||| ||||
                                GCGGCG   GGCGAAG AGAG
                                   GC_      G
GAM1656 KATII    5' GGAGGGGGCGCGGCGAGG    33167       AAA  G   TT
                                CCTTGCTGC   CT CTT  C
                                |||||||||   || |||  |
                                GGAGCGGCG   GG GGA  G
                                     C__  G   GG
GAM1656 KCNJ9    5' TGGGGGGGGCGGTGTCAGGG   18369     CTGCAA     TT
                                CCTTG     ACTGCTT  CTTG
                                |||||     |||||||  ||||
                                GGGAC     TGGCGGG  GGGT
                                  TG_____      GG
GAM1656 KCNK13   5' CGAGGAGAGCAGGGGGAGTGGA 42151     G TG AAA__
             GGG                  CCTT C  C    CTGCTTTTCTTG
                                  |||| |  |    ||||||||||||
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                                GGGA G  G    GACGAGAGGAGC
                                  _ GT AGGGG
GAM1656  KIAA0033  3'  CAAGAAAGGACCCTTCAGCAAG 77083        CAAACTG
             G                   CCTTGCTG      CTTTTCTTG
                                 ||||||||      |||||||||
                                 GGAACGAC      GGAAAGAAC
                                     TTCCCA_
GAM1656  KIAA0061  3'  CAGGAAGAGTGGGCTCAGTGTG 68835    T    CAAA TG
             G                   CC TGCTG    C  CTTTTCTTG
                                 || |||||    |  |||||||||
                                 GG GTGAC    G  GAGAAGGAC
                                  T    TCG_ GT
GAM1656  KIAA0102  5'  CGGGAGAAGCGGTGGTAGCGGA 29247     _    AA
             GG                   CCTT GCTGC  ACTGCTTTTCTTG
                                 |||| |||||  ||||||||||||
                                 GGAG CGATG  TGGCGAAGAGGGC
                                   G    G_
GAM1656  KIAA0184  5'  TGAGGGGAGCTACGTAGCCGAG 65816      _   AAACT   TT
             G                   CCTTG CTGC    GCTT  CTTG
                                 ||||| ||||    ||||  ||||
                                 GGAGC GATG    CGAG  GAGT
                                   C    CAT__    GG
GAM1656  KIAA0210  3'  CAGGGAGAGCAGCCATGCCAGG 29150      CT   AA_
             G                   CCTTG  GCA   CTGCTTTTCTTG
                                 |||||  |||   ||||||||||||
                                 GGGAC  CGT   GACGAGAGGGAC
                                   __   ACC
GAM1656  KIAA0296  3'  TGGGGGAGGGAGCGCGTGCAGG 28779       _   AAA  G   TT
             G                   CCTTGC TGC   CT CTT  CTTG
                                 ||||||  |||   ||  |||  ||||
                                 GGGACG GCG   GA GGA  GGGT
                                    T   C__   G   GG
GAM1656  KIAA0321  3'  CAGGGGAGGCGGTGGGGGGTGG 63047     TG TG AA___      TT
             TGGGG                 CCT  C  C    ACTGCTT  CTTG
                                 |||  |  |    |||||||  ||||
                                 GGG  G  G    TGGCGGA  GGAC
                                   GT GT GGGGG      GG
GAM1656  KIAA0321  5'  GAGGGTCTTTGCAGCAGGG    63053          CT
                                 CCTTGCTGCAAA  GCTTTT
                                 ||||||||||||  ||||||
                                 GGGACGACGTTT  TGGGAG
                                        C_
GAM1656  KIAA0321  3'  TGGGGAGAGAAAAGGTGGCCAG 63065     T  TG AAACTG
             G                   CCT GC  C     CTTTTCTTG
                                 ||| ||  |     |||||||||
                                 GGA CG  G     GAGAGGGGT
                                   C  GT GAAAA_
GAM1656  KIAA0322  3'  AAGAGAAGTTTAGGAGGG    94327      G   CAAACT
                                 CCTT CTG     GCTTTTCTT
                                 |||| |||     |||||||||
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                                GGGA GAT     TGAAGAGAA
                                  G  T_____
GAM1656 KIAA0356 3' TGGGGAGGGCTTGGGCCTGTGA 66781     TG T_  AAACT
            GG                    CCT  C  GC    GCTTTTCTTG
                                  |||  |  ||    ||||||||||
                                  GGA  G  CG    CGGGAGGGGT
                                    GT TC  GGTT_
GAM1656 KIAA0431 3' TAAGAAAAAGTATCTAGCAAGG 31553        CAA   GC
                                  CCTTGCTG   ACT  TTTTCTTG
                                  ||||||||   |||  ||||||||
                                  GGAACGAT   TGA  AAAAGAAT
                                      CTA   __
GAM1656 KIAA0446 5' AAGGAAGGCCTGGCCAAGG   69434      CT  AAACT
                                  CCTTG  GC    GCTTTTCTT
                                  |||||  ||    |||||||||
                                  GGAAC  CG    CGGAAGGAA
                                    __  GTC__
GAM1656 KIAA0446 5' CAGGGGAATCATTGAAGTGAGG 69445     TG  G   AC  C  TT
                                  CCT  CT CAA  TG TT  CTTG
                                  |||  || |||  || ||  ||||
                                  GGA  GA GTT  AC AA  GGAC
                                    GT  A   __  T  GG
GAM1656 KIAA0449 3' TGGGAAGGGACAGCGGTGGG   34641    TG    AAAC  _
                                  CT  CTGC    TG CTTTTCTTG
                                  ||  ||||    || |||||||||
                                  GG  GGCG    AC GGGAAGGGT
                                   GT   _____  A
GAM1656 KIAA0470 3' TAGGAAAAAGCAGATTGTGGCA 29717     TG   A       _
            G                      TTGC  CAA CTGCTTTT CTTG
                                  ||||  ||| |||||||| ||||
                                  GACG  GTT GACGAAAA GGAT
                                    GT   A       A
GAM1656 KIAA0543 3' CAAGAGGAGTGTCCTGGTAGGG 69517        CAA  T
                                  CCTTGCTG   AC GCTTTTCTTG
                                  ||||||||   || ||||||||||
                                  GGGATGGT   TG TGAGGAGAAC
                                      CC_  _
GAM1656 KIAA0596 3' GAGAGGAGGGAGGTGCTGGG   63490    T  T  AAA  G
                                  CCT GC GC   CT CTTTTC
                                  ||| || ||   || ||||||
                                  GGG CG TG   GG GGAGAG
                                    T  _  GAG  A
GAM1656 KIAA0620 3' CAGGGAGGGTGGAGGGGAGG   62810     G  GCAAA TG
                                  CCTT CT    C  CTTTTCTTG
                                  |||| ||    |  |||||||||
                                  GGAG GG    G  GGGAGGGAC
                                    G  A____ GT
GAM1656 KIAA0648 3' TAAGGGAAGCAAGAGTAGGG   83544       GCAAAC    TT
                                  CCTTGCT     TGCTT  CTTG
                                  |||||||     |||||  ||||
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                                GGGATGA     ACGAA  GAAT
                                   GA____    GG
GAM1656  KIAA0662  3'  TGGGAGAGGCAGCTTGGTGGAG 82741     GCTG   A
             G                    CCTT    CAA CTGCTTTTCTTG
                                  ||||    ||| ||||||||||||
                                  GGAG    GTT GACGGAGAGGGT
                                    GTG_   C
GAM1656  KIAA0668  3'  CAAGAAGAGTGGGGAGCATGG  67119    T    GCAAA TG
                                  CC TGCT     C  CTTTTCTTG
                                  || ||||     |  |||||||||
                                  GG ACGA     G  GAGAAGAAC
                                   T    GG___ GT
GAM1656  KIAA0668  3'  GGGGAGGGTAGCAGTGGG    67124    TG    AAAC
                                  CT  CTGC    TGCTTTTCTT
                                  ||  ||||    ||||||||||
                                  GG  GACG    ATGGGAGGGG
                                   GT    ____
GAM1656  KIAA0672  5'  CGGGAGGAGTAGGCGGCGGC   30048      AAA
                                  GCTGC   CTGCTTTTCTTG
                                  |||||   ||||||||||||
                                  CGGCG   GATGAGGAGGGC
                                     GCG
GAM1656  KIAA0694  5'  TGGGAAGAGTGGGGGTGCAAG  72976      T  AAA TG
                                  CTTGC GC   C  CTTTTCTTG
                                  ||||| ||   |  |||||||||
                                  GAACG TG   G  GAGAAGGGT
                                     _  GG_ GT
GAM1656  KIAA0712  5'  CAAGAAAACTGCTGCTGCAGGG 28866       T   AACT  __
                                  CCTTGC GCA    GC  TTTTCTTG
                                  |||||| |||    ||  |||||||||
                                  GGGACG CGT    CG  AAAAGAAC
                                     T    _____  TC
GAM1656  KIAA0757  3'  GGAGAGGAGAGTTTGGGGCAGG 21259       G     G      G
             G                    CCTTGCT CAAACT CTTTTCTT
                                  ||||||| |||||| ||||||||
                                  GGGACGG GTTTGA GAGGAGAG
                                     G     _       GG
GAM1656  KIAA0759  3'  GGGAGAGGCAGAAGGGGGG   67889     G  GCAAA
                                  CCTT CT     CTGCTTTTCTT
                                  |||| ||     ||||||||||
                                  GGGG GA     GACGGAGAGGG
                                    G  A____
GAM1656  KIAA0763  3'  GGGAGGGGAGGCAGGAGG    30166     G    AAA  G
                                  CCTT CTGC   CT CTTTTCT
                                  |||| ||||   || |||||||
                                  GGAG GACG   GA GGGAGGG
                                    _    ___  G
GAM1656  KIAA0775  5'  AGGGAGAGGGGTACCAGGG   28948      CTGCAA   G
                                  CCTTG     ACT CTTTTCTT
                                  |||||     ||| ||||||||
```

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                                GGGAC     TGG GAGAGGGA
                                  CA____  G
GAM1656 KIAA0775 5' GAGGAGCTTGGCGGCGAGG   28955        AAACT
                                CCTTGCTGC    GCTTTTC
                                |||||||||    |||||||
                                GGAGCGGCG    CGAGGAG
                                     GTT__
GAM1656 KIAA0781 3' GGGAAAGGGCAGTGTGGGG   68059    TG TGCAA    _
                                CCT  C    ACTGCT TTTCTT
                                |||  |    |||||| ||||||
                                GGG  G    TGACGG AAAGGG
                                  GT _____     G
GAM1656 KIAA0789 5' CAGGAGGAGCCTTGGTGGCGAG 64428      TG AAACT
                                CTTGC  C    GCTTTTCTTG
                                |||||  |    ||||||||||
                                GAGCG  G    CGAGGAGGAC
                                   GT GTTC_
GAM1656 KIAA0790 5' AAGAAACGCCTTTGCAGTGGG  69255    TG     CT  T    G
                                CT  CTGCAAA  GC TTTCTT
                                ||  |||||||  || ||||||
                                GG  GACGTTT  CG AAAGAA
                                 GT     C_  C     G
GAM1656 KIAA0802 5' CGGGAAGGGCCTGTTGGCGGGG 63248       GCA   T_
                                CCTTGCT   AAC  GCTTTTCTTG
                                |||||||   |||  ||||||||||
                                GGGGCGG   TTG  CGGGAAGGGC
                                    ___   TC
GAM1656 KIAA0821 3' CAGGGAGGGAACCCTGGGCAGG 30603       G  AACTG
             G                   CCTTGCT CA    CTTTTCTTG
                                |||||||  ||    |||||||||
                                GGGACGG GT    GGGAGGGAC
                                   _  CCCAA
GAM1656 KIAA0821 3' TGGGGGAAGTGTAGTGAGG   30612    TG   AAACT   TT
                                CCT  CTGC    GCTT  CTTG
                                |||  ||||    ||||  ||||
                                GGA  GATG    TGAA  GGGT
                                  GT   _____   GG
GAM1656 KIAA0841 3' AGGGAAGGTGGGTGGCAGGG   71886      TG AAA TG      G
                                CCTTGC  C   C  CTTTTCTT
                                ||||||  |   |  ||||||||
                                GGGACG  G   G  GGAAGGGA
                                   GT ___ GT
GAM1656 KIAA0861 3' GGGAGAGGCGGTGTGGGG    90353    TG TGCAA
                                CCT  C    ACTGCTTTTCTT
                                |||  |    ||||||||||||
                                GGG  G    TGGCGGAGAGGG
                                  GT _____
GAM1656 KIAA0872 3' GGGGAGGCTGAGGCAGGG    30760       G  AACT   TT
                                CCTTGCT CA   GCTT  CT
                                |||||||  ||   ||||  ||
```

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                              GGGACGG GT   CGGA  GG
                                 A _____   GG
GAM1656 KIAA0893 5' CGGGAGGGGCGGACGTGAGAAG 31062     G  G  AA_
            G                    CCTT CT CA   CTGCTTTTCTTG
                                 |||| || ||   ||||||||||||
                                 GGAA GA GT   GGCGGGGAGGGC
                                   _ _  GCA
GAM1656 KIAA0912 3' CAGGGAAGGTAAGGAGTGAG   65040    TG  GCAAAC
                                 CT  CT     TGCTTTTCTTG
                                 ||  ||     ||||||||||
                                 GA  GA     ATGGAAGGGAC
                                  GT  GGA___
GAM1656 KIAA0935 3' GGGAAAAGCAGTGCGGAGGG   73098     G    AA
                                 CCTT CTGC  ACTGCTTTTCTT
                                 |||| ||||  ||||||||||||
                                 GGGA GGCG  TGACGAAAAGGG
                                   _   ___
GAM1656 KIAA0945 3' GGGAGAGGGTTGGGGGCAGGG  30903       GCA   G
                                 CCTTGCT   AACT CTTTTCT
                                 |||||||   |||| |||||||
                                 GGGACGG   TTGG GAGAGGG
                                    GGG   _
GAM1656 KIAA0976 5' CGAGAGGGGGCGACTTGCAGGA 30549     G     AC     _
            GG                     CCTT CTGCAA  TGCTTT TCTTG
                                 |||| ||||||  |||||| |||||
                                 GGAG GACGTT  GCGGGG AGAGC
                                   _     CA     G
GAM1656 KIAA0987 5' CGAGGGAGGTCACTGACAAGG  25507      CTG  AACT   TT
                                 CCTTG   CA    GCTT  CTTG
                                 |||||   ||    ||||  ||||
                                 GGAAC   GT    TGGA  GAGC
                                   A__  CAC_   GG
GAM1656 KIAA0992 3' CAGGAGAGGTAGCAAAGGCCAG 32717     T   GCAAA
            G                    CCT GCT    CTGCTTTTCTTG
                                 ||| |||    ||||||||||||
                                 GGA CGG    GATGGAGAGGAC
                                  C   AAAC_
GAM1656 KIAA1032 3' AGGGGGGGCCCTGGGCAAGG   66722       G  AACT   TT
                                 CCTTGCT CA    GCTT  CTT
                                 |||||||  ||    ||||  |||
                                 GGAACGG GT    CGGG  GGA
                                    _ CC__    GG
GAM1656 KIAA1042 5' GAGGAAGGCACGGGAGGG    31049     G   CAAAC
                                 CCTT CTG    TGCTTTTCTT
                                 |||| |||    ||||||||||
                                 GGGA GGC    ACGGAAGGAG
                                   G  _____
GAM1656 KIAA1042 5' GGGAGGGTGGCTGTGCGAGG   31052       T   AA TG
                                 CCTTGC GCA  C  CTTTTCT
                                 ||||||  |||  |  |||||||
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                                GGAGCG TGT  G  GGGAGGG
                                   _  C_ GT
GAM1656 KIAA1056 3' GGGAAGAGCTGAAGTGGGG   30316    TG  G  AACT
                                CCT  CT CA   GCTTTTCTT
                                |||  || ||   |||||||||
                                GGG  GA GT   CGAGAAGGG
                                  GT  A  ____
GAM1656 KIAA1058 3' GGGAAGAGGCAGGGCGGGG   83140       GCAAA   _
                                CCTTGCT    CTGC TTTTCTT
                                |||||||    |||| |||||||
                                GGGGCGG    GACG AGAAGGG
                                    _____   G
GAM1656 KIAA1061 3' AGGGGGGCCTCCTGTAGCAAG 71715        AACT   TT  TG
                                CTTGCTGCA   GCTT  CT
                                |||||||||   ||||  ||
                                GAACGATGT   CGGG  GA
                                     CCTC   GG  C
GAM1656 KIAA1110 3' TGGGAGAGGCAGTGAGCATGAG 62505     C   AA
                                CTTG TGC  ACTGCTTTTCTTG
                                |||| |||  ||||||||||||||
                                GAGT ACG  TGACGGAGAGGGT
                                  _  AG
GAM1656 KIAA1171 3' CAGGGAGGGTGGGAGCTGGAGG 89339     GCT  AAA TG
                                CCTT   GC   C  CTTTTCTTG
                                ||||   ||   |  |||||||||
                                GGAG   CG   G  GGGAGGGAC
                                  GT_  AG_ GT
GAM1656 KIAA1194 5' GAGGAGGGCGAGGCCGGGG   97636     CT  AAAC
                                CCTTG  GC   TGCTTTTCTT
                                |||||  ||   ||||||||||
                                GGGGC  CG   GCGGGAGGAG
                                  __  GA__
GAM1656 KIAA1202 3' AAGGAGCTGCAGCAAGG     72478        AACT  T TT
                                CCTTGCTGCA   GC T  CTT
                                ||||||||||   || |  |||
                                GGAACGACGT   CG A  GAA
                                     _____  _ GG
GAM1656 KIAA1211 5' TGGGAAGAGCTGGAACAGCAGG 69471       CAAACT
                                CTTGCTG     GCTTTTCTTG
                                |||||||     ||||||||||
                                GGACGAC     CGAGAAGGGT
                                    AAGGT_
GAM1656 KIAA1247 5' CGAGGGGAGCGCCCGGCCGGG 62508    T   CAAAC    TT
                                CCT GCTG    TGCTT  CTTG
                                ||| ||||    |||||  ||||
                                GGG CGGC    GCGAG  GAGC
                                  C   CC___    GG
GAM1656 KIAA1277 3' AGGGAGGGTGTGGAGAAGG   65069     G  G  AAC
                                CCTT CT CA   TGCTTTTCTT
                                |||| || ||   ||||||||||
```

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                                GGAA GA GT   GTGGGAGGGA
                                  _ G ___
GAM1656 KIAA1303 3' CAGGGGAGGCAGGTCCTTGGCG 66600       GCAAA_     TT
             AGG                  CCTTGCT     CTGCTT  CTTG
                                  |||||||     ||||||  ||||
                                  GGAGCGG     GACGGA  GGAC
                                     TTCCTG     GG
GAM1656 KIAA1319 3' GGGAGAGGGACTTTGGTAGGG  40790       GCAAA  G
                                  CCTTGCT     CT CTTTTCT
                                  |||||||     || |||||||
                                  GGGATGG     GG GAGAGGG
                                     TTTCA  _
GAM1656 KIAA1377 5' GGGAGGGGCCGAGCAGGAGG   67760      G    AAACT
                                  CCTT CTGC     GCTTTTCTT
                                  |||| ||||     |||||||||
                                  GGAG GACG     CGGGGAGGG
                                    _    AGC__
GAM1656 KIAA1434 5' TGGGGGGAGCGCTGGCGAGG   70214       _ AAACT    TT
                                  CCTTGCT GC     GCTT  CTTG
                                  ||||||| ||     ||||  ||||
                                  GGAGCGG CG     CGAG  GGGT
                                     T ______    GG
GAM1656 KIAA1465 3' GGGGGGGCGGATGGGCGGGG   61503       G  AA     TT
                                  CCTTGCT CA  CTGCTT  CT
                                  ||||||| ||  ||||||  ||
                                  GGGGCGG GT  GGCGGG  GG
                                     _ A_     GG
GAM1656 KIAA1494 5' GAGGGGGGCAGCAGAGAGG    68981     TG    AAAC    TT
                                  CCT  CTGC    TGCTT  CTT
                                  |||  ||||    |||||  |||
                                  GGA  GACG    ACGGG  GAG
                                    GA   _____     GG
GAM1656 KIAA1535 3' CAGGAGGAGTAGGAGGAGGCAG 80209       GCAAA
             GG                   CCTTGCT     CTGCTTTTCTTG
                                  |||||||     ||||||||||||
                                  GGGACGG     GATGAGGAGGAC
                                     AGGAG
GAM1656 KIAA1564 3' TGGGAGGGGCAGGGGAGATGTG 64595     TG TGCAAA_
             GGG                    CCT  C      CTGCTTTTCTTG
                                  |||  |      ||||||||||||
                                  GGG  G      GACGGGGAGGGT
                                    GT TAGAGGG
GAM1656 KIAA1602 3' CGAGGAAGGCAGAGTGGCCAGC 65239        __  AA
             GGGG                    CCTTGCTG  CA  CTGCTTTTCTTG
                                  ||||||||  ||  ||||||||||||
                                  GGGGCGAC  GT  GACGGAAGGAGC
                                     CG  GA
GAM1656 KIAA1604 5' CAAGAGGGGTGTGAGAGCGGCT 64892     T    AA__  T
             AGG                    CCT GCTGC    AC GCTTTTCTTG
                                  ||| |||||    || ||||||||||
```

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                                GGA CGGCG   TG TGGGGAGAAC
                                  T    AGAG  _
GAM1656  KIAA1607  3'  TAGGAAGAGAGAGGCAGCAGAG 64539    _    AAA  G
             G                   CCT TGCTGC  CT CTTTTCTTG
                                 ||| ||||||  || |||||||||
                                 GGA ACGACG  GA GAGAAGGAT
                                   G    GA_  _
GAM1656  KIAA1608  5'  CGGGGAGAGCGCCAGAGGG   46105    G  CAAAC
                                 CCTT CTG    TGCTTTTCTTG
                                 |||| |||    ||||||||||
                                 GGGA GAC    GCGAGAGGGGC
                                   _  C____
GAM1656  KIAA1615  5'  CGGGAGGAGCTCGCGGTGAGG  69276    TG   AAACT
                                 CCT  CTGC    GCTTTTCTTG
                                 |||  ||||    ||||||||||
                                 GGA  GGCG    CGAGGAGGGC
                                   GT   CT___
GAM1656  KIAA1649  3'  CGGGAGGCGGAGTTTGCAGTGA 51231    TG      __   TT TTG
             GG                   CCT  CTGCAAACT  GCTT  C
                                 |||  |||||||||  ||||  |
                                 GGA  GACGTTTGA  CGGA  G
                                   GT       GG   GG C
GAM1656  KIAA1668  3'  GAGAGGAGGAGTGATGGGG   67070   G  A_  G
                                 CT CA  ACT CTTTTCTT
                                 || ||  ||| ||||||||
                                 GG GT  TGA GAGGAGAG
                                  G  AG   G
GAM1656  KIAA1737  5'  CAGGGCTTTGGTTTGCTGTGAG 67936    TG T     ___    TCTTG
             G                   CCT  C GCAAACT   GCTTT
                                 |||  | |||||||   |||||
                                 GGA  G CGTTTGG   CGGGA
                                   GT T      TTT    C
GAM1656  KIAA1737  5'  TGAGGAGGGGGCTGCGTGTGGG 67949    TG _   AA  G    TTG
             G                   CCT  C TGCA  CT CTTTTC
                                 |||  | ||||  || ||||||
                                 GGG  G GCGT  GG GAGGAG
                                   GT T   CG  G     T
GAM1656  KIAA1742  3'  AGGAGGGGTTTTGGAGGGG   78136    TG  G   CT
                                 CCT  CT CAAA  GCTTTTCTT
                                 |||  || ||||  |||||||||
                                 GGG  GA GTTT  TGGGGAGGA
                                   __  G   __
GAM1656  KIAA1775  3'  AGGAAAGCAAATGTAGGTAAGG 53542      _   AAC      TG
                                 CCTTGC TGCA   TGCTTTTCT
                                 |||||| ||||   |||||||||
                                 GGAATG ATGT   ACGAAAGGA
                                    G   AA_       T
GAM1656  KIAA1819  5'  TAGGGGGGGCCTCTGGGGCGGG 70256      G  AACT   TT
             G                   CCTTGCT CA   GCTT  CTTG
                                 |||||||  ||   ||||  ||||
```

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                                GGGGCGG GT   CGGG  GGAT
                                   G  CTC_   GG
GAM1656  KIAA1862  3'  AGGGAGAGAGCTGCAGGG   69501      T  AAACTG
                                CCTTGC GC    CTTTTCTT
                                |||||| ||    ||||||||
                                GGGACG CG    GAGAGGGA
                                   T  A_____
GAM1656  KIAA1862  3'  CAGGAAGAACTGTGGGGTGGGG 69503    TG  G  AACTGC
                                CCT  CT CA    TTTTCTTG
                                |||  || ||    ||||||||
                                GGG  GG GT    AGAAGGAC
                                  GT  G  GTCA__
GAM1656  KIAA1870  3'  GGGGGAGGAAGCTTGGGTAAGG 50587      G   A  G_   TT  TG
                                CCTTGCT CAA CT  CTT  CT
                                ||||||| ||| ||  |||  ||
                                GGAATGG GTT GA  GAG  GG
                                   _  C  AG   GG  T
GAM1656  KIAA1871  3'  GAGAAAACCTTCAGCAAGG   61903       CAAACTGC
                                CCTTGCTG      TTTTCTT
                                ||||||||      |||||||
                                GGAACGAC      AAAAGAG
                                    TTCC_____
GAM1656  KIAA1881  3'  CAGGGGGAGGAAGGGTGGAGGG 97082    TG  G  AA  G_   TT
           G                     CCT  CT CA  CT  CTT  CTTG
                                |||  || ||  ||  |||  ||||
                                GGG  GA GT  GA  GAG  GGAC
                                  __  G  GG  AG   GG
GAM1656  KIAA1881  3'  TGAGACTGAGCAGTTTGCAGGG 97090    G          T_
           GG                     CTT CTGCAAACTGCTT  TCTTG
                                ||| ||||||||||||  |||||
                                GGG GACGTTTGACGAG  AGAGT
                                  G          TC
GAM1656  KIAA1887  5'  TGGGAGGGGCCCCCACGGTGGA 77280    _ TG   CAAACT
           GG                     CC T  CTG     GCTTTTCTTG
                                || |  |||     ||||||||||
                                GG G  GGC     CGGGGAGGGT
                                 A GT   ACCCC_
GAM1656  KIAA1913  5'  CAGGAGGAGTGGGTGGCAGG   74315      TG AAA TG
                                CTTGC  C   C  CTTTTCTTG
                                |||||  |   |  |||||||||
                                GGACG  G   G  GAGGAGGAC
                                   GT ___ GT
GAM1656  KIAA1938  3'  TAGGGGAGGTAGGATGGATGGG 93825    TGCTG  AA     TT
                                CCT    CA  CTGCTT  CTTG
                                |||    ||  ||||||  ||||
                                GGG    GT  GATGGA  GGAT
                                  TAG__  AG     GG
GAM1656  KIAA1938  3'  TGGGGGAGGTAGGACAGGGCTG 93826    T   GCAAA     TT
           GG                     CCT GCT    CTGCTT  CTTG
                                ||| |||    ||||||  ||||
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                                GGG CGG    GATGGA  GGGT
                                  T  GACAG     GG
GAM1656  KIAA1949  5'  TGGGGGAGGCAGGCGGTGG   99704   TG   AAA    TT
                                T  CTGC   CTGCTT  CTTG
                                |  ||||   ||||||  ||||
                                G  GGCG   GACGGA  GGGT
                                 GT   ___     GG
GAM1656  KIF1C    3'  TGGGAGAGGACTGAGAGTGAGG 61888     TG  G_  AACTG
                                CCT  CT  CA    CTTTTCTTG
                                |||  ||  ||    |||||||||
                                GGA  GA  GT    GGAGAGGGT
                                  GT  GA  CA___
GAM1656  KREMEN   3'  TGGGAGGCGGAGTTTGCAGTGA 50240    TG       __    TT TTG
             G                   CT  CTGCAAACT  GCTT  C
                                ||  |||||||||  ||||  |
                                GA  GACGTTTGA  CGGA  G
                                 GT       GG   GG T
GAM1656  LASP1    3'  AGGAAAAGACTGTGGGTGGGG  21572     TG  G  AACTG      G
                                CCT  CT CA    CTTTTCTT
                                |||  || ||    ||||||||
                                GGG  GG GT    GAAAAGGA
                                  GT  _  GTCA_       G
GAM1656  LGI4     3'  AGGGAGGGACAGCGGGAGG   58410     G    AAAC  _
                                CCTT CTGC    TG CTTTTCTT
                                ||||  ||||   ||  ||||||||
                                GGAG GGCG    AC GGGAGGGA
                                  _   _____  A
GAM1656  LIAS     3'  TGGGAGGGGGAGGTTGCAGTGA 71171    TG     A  G
             G                   CT  CTGCAA CT CTTTTCTTG
                                ||  ||||||  ||  |||||||||
                                GA  GACGTT GA GGGGAGGGT
                                 GT     G  G
GAM1656  LIM      3'  GGGAGGGAGAGGTTGCAGTGAG 22331    TG     A  G_     TG
                                CT  CTGCAA CT  CTTTTCT
                                ||  ||||||  ||  |||||||
                                GA  GACGTT GA  GGGAGGG
                                 GT     G  GA
GAM1656  LY6G5B   5'  AGGAAAGGGTAAGTGGGG    41401     TG  GCAA   G
                                CCT  CT    ACT CTTTTCT
                                |||  ||    ||| |||||||
                                GGG  GA    TGG GAAAGGA
                                  GT  A___   _
GAM1656  M96      5'  AGGGGAAGCGCCCACGGGG   24756      C  CAAAC    TT
                                CCTTG TG    TGCTT  CTT
                                |||||  ||    |||||  |||
                                GGGGC AC    GCGAA  GGA
                                   _  CC___     GG
GAM1656  MAFB     3'  AGGAAGAGAGCAACGAGG    19588      C   AAACTG
                                CCTTG TGC     CTTTTCTT
                                |||||  |||     ||||||||
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                                GGAGC ACG     GAGAAGGA
                                  A  A_____
GAM1656  MAN1C1   5'  CGGGGAGGGCTCGGCCGGAGGG 40173     G  _ AAACT
                                CCTT CTG C    GCTTTTCTTG
                                |||| ||| |    ||||||||||
                                GGGA GGC G    CGGGAGGGGC
                                  _  C GCT__
GAM1656  MAST205  5'  GAGAAGGCGAGGCGGCAGC   31359      AAA _    T  G
                                GCTGC  CT GCTTT CTT
                                |||||  || ||||| |||
                                CGACG  GA CGGAA GAG
                                  GCG  G    _
GAM1656  MBD2     3'  CAGGAAGAGCGAGTACAGCAAG 32334       CAA  _
                                CTTGCTG  ACT GCTTTTCTTG
                                |||||||  ||| ||||||||||
                                GAACGAC  TGA CGAGAAGGAC
                                    A__  G
GAM1656  MCF2L    3'  TGAGGAGAGCGGGGCACGGGG  61531      C  AAA
                                CCTTG TGC  CTGCTTTTCTTG
                                ||||| |||  ||||||||||||
                                GGGGC ACG  GGCGAGAGGAGT
                                  _  G__
GAM1656  MFN2     3'  TGAGAAAAGCAGTTTGGGTGA  30229   TG  G
                                T  CT CAAACTGCTTTTCTTG
                                |  || ||||||||||||||||
                                A  GG GTTTGACGAAAAGAGT
                                 GT  _
GAM1656  MGC10715 3'  CAGGGAGAATCTGCATGTGGGG 44496    TG _   AACTGC
                                CCT  C TGCA     TTTTCTTG
                                |||  | ||||     ||||||||
                                GGG  G ACGT     AGAGGGAC
                                  GT T   CTA___
GAM1656  MGC10955 3'  TGAGGGAGGCAGGGAAAGTAAG 52032       GCAAA     TT
                                CTTGCT    CTGCTT  CTTG
                                ||||||    ||||||  ||||
                                GAATGA    GACGGA  GAGT
                                   AAGG_     GG
GAM1656  MGC10999 3'  GAGGATTGCTTGAGGCGAGG   51196       G  ACT  TT   G
                                CCTTGCT CAA   GC  TTCTT
                                ||||||| |||   ||  |||||
                                GGAGCGG GTT   CG  AGGAG
                                    A  ___  TT
GAM1656  MGC11061 5'  AGGAGAAGACTTTGGTGGGG   51258    TG TG   CTG
                                CCT  C  CAAA   CTTTTCTT
                                |||  |  ||||   ||||||||
                                GGG  G  GTTT   GAAGAGGA
                                  GT __   CA_
GAM1656  MGC11335 3'  CAAGAGGGGCCAGCTCGGCTGA 48767     _   CAAA  _
            GG                   CCTT GCTG   CTG CTTTTCTTG
                                |||| ||||   ||| |||||||||
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                                GGAG CGGC    GAC GGGGAGAAC
                                  T    TC__   C
GAM1656 MGC1136  3' AGGGAAGGAGGCAGCTAGG   44037     T    AAA  G   TT
                                CCT GCTGC   CT CTT  CT
                                ||| |||||   || |||  ||
                                GGA CGACG   GA GAA  GA
                                  T    ____ G   GG
GAM1656 MGC1136  3' TGGGAGGGGACGGGGAGTGAGG 44039     TG  GCAAA  _
                                CCT  CT    CTG CTTTTCTTG
                                |||  ||    ||| |||||||||
                                GGA  GA    GGC GGGGAGGGT
                                  GT  GG___   A
GAM1656 MGC1203  5' GGGAGGAGAGGGCGGAGGG   44410     G    AAACTG
                                CCTT CTGC     CTTTTCTT
                                |||| ||||     ||||||||
                                GGGA GGCG     GAGGAGGG
                                  _    GGA___
GAM1656 MGC12760 3' AGGAACAGCTGAGTGAGG    52154     TG  G  AACT   T    G
                                CCT  CT CA    GCT TTCTT
                                |||  || ||    ||| |||||
                                GGA  GA GT    CGA AAGGA
                                  GT  _  _____   C    A
GAM1656 MGC12966 3' TGAGAAAGGATCCGAGCGGGG  52089       GCAAACTG
                                CCTTGCT       CTTTTCTTG
                                |||||||       |||||||||
                                GGGGCGA       GGAAAGAGT
                                    GCCTA___
GAM1656 MGC13102 3' CAGGAAGAGGGGAGCAGACAGG 51291      _    AAA  G
            G                    CCTTG CTGC   CT CTTTTCTTG
                                |||||  ||||   || |||||||||
                                GGGAC GACG   GG GAGAAGGAC
                                  A    A__  G
GAM1656 MGC14136 5' AGGAGGGGCGGGGCGATAGGG  52978      C   AAA        G
                                CCTTG TGC   CTGCTTTTCTT
                                |||||  |||   ||||||||||
                                GGGAT GCG   GGCGGGGAGGA
                                  A   G__
GAM1656 MGC14480 3' TGGGAAAGGCCTGGCCAGCAGG 59389       _ AAACT
                                CTTGCTG C     GCTTTTCTTG
                                |||||||  |    ||||||||||
                                GGACGAC G     CGGAAAGGGT
                                    C GTC__
GAM1656 MGC14859 3' TGGGAAGGGCGGCCTTGCTGGG 62608     TGCT    A_
                                CCT    GCAA  CTGCTTTTCTTG
                                |||    ||||  ||||||||||||
                                GGG    CGTT  GGCGGGAAGGGT
                                  T____    CC
GAM1656 MGC15548 5' AGGAAGGTGCGGGCGGGG    52221        _  AAACT
                                CCTTGCT GC     GCTTTTCT
                                |||||||  ||    ||||||||
```

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                                GGGGCGG CG    TGGAAGGA
                                   G _____
GAM1656 MGC16153 5' TAGGGGAAGTGGCCGGCTGCAG 52271      T  AAA TG   TT
           GG                    CCTTGC GC   C  CTT  CTTG
                                 |||||| ||   |  |||  ||||
                                 GGGACG CG   G  GAA  GGAT
                                    T  GCC GT   GG
GAM1656 MGC17299 3' TGAGGAGAGTAACTGCTGGCCA 58887    T  _  AAC
           GG                    CCT GCT GCA   TGCTTTTCTTG
                                 ||| ||| |||   ||||||||||
                                 GGA CGG CGT   ATGAGAGGAGT
                                   C   T   CA_
GAM1656 MGC20255 3' TGAGAAGGGTCAGATGGTAG   54544     AAA  _
                                 CTGC   CTG CTTTTCTTG
                                 ||||   ||| |||||||||
                                 GATG   GAC GGGAAGAGT
                                   GTA   T
GAM1656 MGC20496 3' TGAGGTTGTCAGTTTCCAGCAA 54532       C    _ TTT
           GG                    CCTTGCTG AAACTG C   TCTTG
                                 |||||||| |||||| |   |||||
                                 GGAACGAC TTTGAC G   GGAGT
                                     C     T TT_
GAM1656 MGC21738 5' GAGGGGAGCGCCGCGGGG    59577      T  AAACT   TT
                                 CCTTGC GC    GCTT  CTT
                                 |||||| ||    ||||  |||
                                 GGGGCG CG    CGAG  GAG
                                    C _____   GG
GAM1656 MGC2541  3' TGAGAAAAGCTGGAGAAGTGAG 55625    TG  GCAAACT
           G                     CCT  CT     GCTTTTCTTG
                                 |||  ||     ||||||||||
                                 GGA  GA     CGAAAAGAGT
                                   GT  AGAGGT_
GAM1656 MGC2601  3' GGGAGGGGCTGGTAGGAGGG  44097     G   AAACT
                                 CCTT CTGC    GCTTTTCTT
                                 |||| ||||    |||||||||
                                 GGGA GATG    CGGGGAGGG
                                   G   GT___
GAM1656 MGC26766 3' CAAGGGAAGAGGAGGAGCAGGG 59467       GCAAA  G   TT
                                 CCTTGCT    CT CTT  CTTG
                                 |||||||    || |||  ||||
                                 GGGACGA    GA GAA  GAAC
                                    GGAG_ _   GG
GAM1656 MGC2865  5' TAAGGGAGGCGGAGTGTGCGG  51461     AA__    TT
                                 CTGCA   CTGCTT  CTTG
                                 |||||   ||||||  ||||
                                 GGCGT   GGCGGA  GAAT
                                   GTGA    GG
GAM1656 MGC29891 3' TAAGAAGAAAACTATAGCAGGG 58869       CAAACTGC
                                 CCTTGCTG      TTTTCTTG
                                 ||||||||      ||||||||
```

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                                GGGACGAT       AGAAGAAT
                                    ATCAAA__
GAM1656  MGC4093   5'  GGGAGAGGCGCGAGCCAGG   48332     T  _  AAACT
                                CCT GCT GC     GCTTTTCTT
                                ||| ||| ||     |||||||||
                                GGA CGA CG     CGGAGAGGG
                                  C  G  _____
GAM1656  MGC4251   3'  TGAGAAGGGAGTATGGCAGGG  51469        CAA   G
                                CCTTGCTG   ACT CTTTTCTTG
                                ||||||||   ||| |||||||||
                                GGGACGGT   TGA GGGAAGAGT
                                    A__   _
GAM1656  MGC4415   3'  TGGGAAGAGTGAGGGTGGTTGG 49765     T  TG AAACT
           G                     CCT GC  C     GCTTTTCTTG
                                ||| ||  |     ||||||||||
                                GGG TG  G     TGAGAAGGGT
                                  T  GT GGAG_
GAM1656  MGC4562   3'  CAGGAAGAGGAGGTTGCAGTGA 56735    TG     A  G
           G                     CT  CTGCAA CT CTTTTCTTG
                                ||  |||||| || |||||||||
                                GA  GACGTT GA GAGAAGGAC
                                 GT     G  G
GAM1656  MGC4638   3'  AAGAGGGAGATGGGCAAGG   49731        G  AA  G  TT
                                CCTTGCT CA  CT CT  TCTT
                                ||||||| ||  || ||  ||||
                                GGAACGG GT  GA GG  AGAA
                                    _ A_  G  __
GAM1656  MGC5338   5'  GGGGAAGGGAGAGTAGGG    44153        GCAAA  G
                                CCTTGCT     CT CTTTTCTT
                                |||||||     || ||||||||
                                GGGATGA     GA GGAAGGGG
                                    ______  G
GAM1656  MGC5457   3'  TGAGGAAGGCAAATCACAAGG  51944       C  CAAAC
                                CCTTG TG    TGCTTTTCTTG
                                ||||| ||    ||||||||||
                                GGAAC AC    ACGGAAGGAGT
                                   _  TAA__
GAM1656  MGC5508   3'  GGGAGGGGCAGGGGTAAGG   44269        GCAAA
                                CCTTGCT     CTGCTTTTCTT
                                |||||||     |||||||||||
                                GGAATGG     GACGGGGAGGG
                                    G_____
GAM1656  MKP-7     3'  TAAGAAAGGTACAAATTGCTGA 67018      GCT    AC__
           GG                    CCTT   GCAA    TGCTTTTCTTG
                                ||||   ||||    ||||||||||||
                                GGAG   CGTT    ATGGAAAGAAT
                                  T__    AAAC
GAM1656  MKP-7     3'  TGAGAGAGGCTTTAGTGAGG   67019     TG   CAAACT
                                CCT  CTG     GCTTTTCTTG
                                |||  |||     ||||||||||
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                                GGA  GAT     CGGAGAGAGT
                                  GT   TT____
GAM1656  moblak   5'  CGAGAAGAGCAGAGCGGAGGG  56395      G    AAA
                                CCTT CTGC   CTGCTTTTCTTG
                                |||| ||||   ||||||||||||
                                GGGA GGCG   GACGAGAAGAGC
                                  _    A__
GAM1656  MOST2    5'  TGGGAGGAGGAGGTTGCAGTGA 40075    TG     A  G
            G                    CT  CTGCAA CT CTTTTCTTG
                                ||  |||||| || |||||||||
                                GA  GACGTT GA GAGGAGGGT
                                  GT     G  G
GAM1656  MRPL35   3'  CAGGAAGAGTAGAAATTGGGTG 34018    TG AAA____
            GT                   GC  C      CTGCTTTTCTTG
                                ||  |      ||||||||||||
                                TG  G      GATGAGAAGGAC
                                 GT GGTTAAA
GAM1656  MTCH1    3'  TAGGGAAGGTGAGGCGAGGTGG 27564     TG  GCAAA  _
            GG                   CCT  CT     CT GCTTTTCTTG
                                |||  ||     || ||||||||||
                                GGG  GG     GA TGGAAGGGAT
                                  GT  AGCG_  G
GAM1656  MTX2     5'  CGAGAGCCTCCGGGTTTGCGGT 22635    TG       _____     CTTG
            GG                   T  CTGCAAACT     GCTTTT
                                |  |||||||||     ||||||
                                G  GGCGTTTGG     CGAGAG
                                 GT        GCCTC     C
GAM1656  MVD      3'  TGAGAAAGGAGCTCAGTGGGG  11720     TG   CAAA  G
                                CCT  CTG    CT CTTTTCTTG
                                |||  |||    || |||||||||
                                GGG  GAC    GA GGAAAGAGT
                                  GT   TC__  _
GAM1656  MY014    3'  AAGAATGTTTGTGTGAGG    48878     TG T     TGCTT
                                CCT  C GCAAAC     TTCTT
                                |||  | ||||||     |||||
                                GGA  G TGTTTG     AAGAA
                                  GT _      T_____
GAM1656  MYH7B    3'  CAGGAGAGGCGGGAGGCTGAGG 71054      _   GCAAA
                                CCTT GCT     CTGCTTTTCTTG
                                |||| |||     ||||||||||||
                                GGAG CGG     GGCGGAGAGGAC
                                  T   AG___
GAM1656  MYT1L    5'  GAGAGGCTGTAGCCAAGG     67364       _     AA  G
                                CCTTG CTGCA  CT CTT
                                ||||| |||||  || |||
                                GGAAC GATGT  GA GAG
                                   C     CG  G
GAM1656  NASP     3'  CAGGAAAGGTGGTTCTTGAGT  68576     G   __  TG
                                GCT CAA  AC  CTTTTCTTG
                                ||| |||  ||  |||||||||
```

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                                TGA GTT  TG  GGAAAGGAC
                                  _  CT  GT
GAM1656  NBR2     3'  CGGGAGGAGTGGCAGCGGCCAG 20617     T     AAA TG
              G                    CCT GCTGC   C  CTTTTCTTG
                                   ||| |||||   |  |||||||||
                                   GGA CGGCG   G  GAGGAGGGC
                                     C     AC_ GT
GAM1656  NDRG4    3'  CGGGGGAAGGGTTGTGGCGGG  40379      TG   A  G   TT
                                   CTTGC  CAA CT CTT  CTTG
                                   |||||  ||| || |||  ||||
                                   GGGCG  GTT GG GAA  GGGC
                                      GT   _ _   GG
GAM1656  NDRG4    3'  CGGGGGAAGGGTTGTGGCGGG  40380      TG   A  G   TT
                                   CTTGC  CAA CT CTT  CTTG
                                   |||||  ||| || |||  ||||
                                   GGGCG  GTT GG GAA  GGGC
                                      GT   _ _   GG
GAM1656  NECL1    3'  AGGAAGGGTAAGGGGCAGGG   41324       GCAAAC
                                   CCTTGCT     TGCTTTTCTT
                                   |||||||     ||||||||||
                                   GGGACGG     ATGGGAAGGA
                                       GGA___
GAM1656  NEU4     3'  AAGGGGAGCAGCGGCTGGG   55789     T    AAAC    TT   G
                                   CCT GCTGC    TGCTT  CTT
                                   ||| |||||    |||||  |||
                                   GGG CGGCG    ACGAG  GAA
                                     T    _____    GG   G
GAM1656  NFKBIE   3'  TGAGAAAAGCACAAGCGGTGTA 17058     _     AAAC
              GG                     CCT TGCTGC    TGCTTTTCTTG
                                     ||| ||||||    ||||||||||
                                     GGA GTGGCG    ACGAAAAGAGT
                                       T     AAC_
GAM1656  NICE-1   5'  AGGGTCTGGTTTGTCGTGAGG  39319     TG T      __
                                   CCT  C GCAAACT  GCTTT
                                   |||  | |||||||  |||||
                                   GGA  G TGTTTGG  TGGGA
                                     GT C      TC
GAM1656  NMP200   3'  AGGAGGGCTTGTGCAGGG    27949       T   ACT
                                   CCTTGC GCAA   GCTTTTCT
                                   |||||| ||||   ||||||||
                                   GGGACG TGTT   CGGGAGGA
                                      _   ____
GAM1656  NTN4     5'  CAGGAGGAGGCGGCGGCGGCG  63581       AAA      _
                                   TGCTGC   CTGCTTT TCTTG
                                   ||||||   ||||||| |||||
                                   GCGGCG   GGCGGAG AGGAC
                                      GC_      G
GAM1656  NUCKS    3'  TAGGGAGGGTGGGCAATGGGG  43004      GC   AAA TG
                                   CCTT  TGC   C  CTTTTCTTG
                                   ||||  |||   |  |||||||||
```

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                                GGGG  ACG   G  GGGAGGGAT
                                  TA   ___ GT
GAM1656  NXN      3'  TGAGAAGAAAAATGTAGCTAAG 42683      _     AACTG     TTG
                 G                 CCTT GCTGCA     CTTTTC
                                   |||| ||||||     ||||||
                                   GGAA CGATGT     GAAGAG
                                     T      AAAAA      T
GAM1656  ODC-p    3'  TGGGAGAGGTGGGGAAGATGGC 54854       GCAAA__ TG
                 AGG                 CTTGCT      C  CTTTTCTTG
                                   ||||||      |  |||||||||
                                   GGACGG      G  GGAGAGGGT
                                      TAGAAGG GT
GAM1656  OR2C3    3'  GAGGAAGGCGGTCCAGAGG    75975     TG   CAA
                                   CCT  CTG   ACTGCTTTTCTT
                                   |||  |||   ||||||||||||
                                   GGA  GAC   TGGCGGAAGGAG
                                    __   C__
GAM1656  ORMDL2   3'  AGGAAGGCAGGTGAGGTAAGG  27194       GCAAA
                                   CCTTGCT    CTGCTTTTCT
                                   |||||||    ||||||||||
                                   GGAATGG    GACGGAAGGA
                                      AGTG_
GAM1656  ORMDL3   3'  AACTTGGAGTAGCTTGTAGTGG 74795     TG     A      TCTTG
                 GG                  CCT  CTGCAA CTGCTTT
                                   |||  |||||| |||||||
                                   GGG  GATGTT GATGAGG
                                     GT      C      TTCAAC
GAM1656  OSBPL10  5'  AAGAGAGGGTGGCAGAAGG    35521      G    AAACTG
                                   CCTT CTGC      CTTTTCTT
                                   |||| ||||      ||||||||
                                   GGAA GACG      GGAGAGAA
                                     _    GTG___
GAM1656  P450RAI-2 3'  GGGAAGGGCGTGGCAGGG    39576       TG AAACT
                                   CCTTGC  C     GCTTTTCTT
                                   ||||||  |     |||||||||
                                   GGGACG  G     CGGGAAGGG
                                      GT _____
GAM1656  P8       5'  TAGGAGAAGAAGAGAGGCAGGG 25676       GCAAA  G
                                   CCTTGCT     CT CTTTTCTTG
                                   |||||||     || |||||||||
                                   GGGACGG     GA GAAGAGGAT
                                      AGA__  A
GAM1656  PCYT2    3'  CAAGGTGCCTGGTTTGCAGCAG 12681           GCTTT
                 G                  CTTGCTGCAAACT     TCTTG
                                   ||||||||||||||     |||||
                                   GGACGACGTTTGG     GGAAC
                                           TCCGT
GAM1656  PEX16    3'  GGGAGGGGTGGGGCAGGG    55158       G AA   G   TT
                                   CCTTGCT C  ACT CTT  C
                                   |||||||  |  |||  |||  |
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                                GGGACGG G  TGG GAG  G
                                   G __  G  GG
GAM1656  PGRMC2   3'  TGAGGGAGGCGACCTGATCAGG 21979      CTG  AAC    TT
            G                   CCTTG  CA  TGCTT  CTTG
                                ||||||  ||  |||||  ||||
                                GGGAC  GT  GCGGA  GAGT
                                  TA_  CCA    GG
GAM1656  PIPPIN   3'  TGAGAGAGGGCTTGTTGGTGAG 80512     TG  _  ACTG
            G                   CCT  CTG CAA   CTTTTCTTG
                                |||  ||| |||   |||||||||
                                GGA  GGT GTT   GGAGAGAGT
                                 GT  T  CG__
GAM1656  PLCL2    5'  TGGGGGAAGACGGTGTCGGGG  68698      CTGCAA   _  TT
                                CCTTG     ACTG CTT  CTTG
                                |||||     |||| |||  ||||
                                GGGGC     TGGC GAA  GGGT
                                  TG____    A  GG
GAM1656  POF1B    3'  TGGGAAAAGGGGTGTGCGAGG  46773       TGCAA  G
                                CCTTGC    ACT CTTTTCTTG
                                ||||||    ||| |||||||||
                                GGAGCG    TGG GAAAAGGGT
                                   TG___  G
GAM1656  POF1B    3'  TGGGAGAAATATTTTGTAGCAG 46774         C  C
                                TTGCTGCAAA TG TTTTCTTG
                                |||||||||| || ||||||||
                                GACGATGTTT AT AAGAGGGT
                                      T  A
GAM1656  POLYDOM  3'  TGAGGAGGGTGGATCACGAGG  44693      C  CAAA TG
                                CCTTG TG   C  CTTTTCTTG
                                ||||| ||   |  |||||||||
                                GGAGC AC   G  GGGAGGAGT
                                  _  TA__ GT
GAM1656  PP3501   3'  TGGGAGGGGCTCACCTGTAGGG 41688       TGCAAACT
                                CCTTGC       GCTTTTCTTG
                                ||||||       ||||||||||
                                GGGATG       CGGGGAGGGT
                                   TCCACT__
GAM1656  PPFIA4   3'  GAGAAGTGTTGCAGGGAGG   70842      G     A T
                                CCTT CTGCAA C GCTTTTC
                                |||| |||||| | |||||||
                                GGAG GACGTT G TGAAGAG
                                  G    _ _
GAM1656  PPP1R13B 3'  CAAGGAGGGCGCTTCACTGAGG 31654     GC  CAAAC
                                CCTT  TG    TGCTTTTCTTG
                                ||||  ||    ||||||||||
                                GGAG  AC    GCGGGAGGAAC
                                  TC  TTC__
GAM1656  PPP1R13B 3'  CAGGAGGGGCCGCCACCAAGG  31655      C  CAAACT
                                CCTTG TG     GCTTTTCTTG
                                ||||| ||     ||||||||||
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                              GGAAC AC     CGGGGAGGAC
                                C  CGC___
GAM1656 PPP1R1B  5' GGGAGAGGCAGAGAGAGG    50793     TG  GCAAA
                              CCT  CT    CTGCTTTTCTT
                              |||  ||    ||||||||||
                              GGA  GA    GACGGAGAGGG
                               GA  _____
GAM1656 PRDM13   3' GGGAAGGGGCGGGGTGAGG   41513     TG  GCAAA    _
                              CCT  CT    CTGCTT TTCTT
                              |||  ||    |||||| |||||
                              GGA  GG    GGCGGG AAGGG
                               GT  _____     G
GAM1656 PRO0641  5' TGAGAAAAGCAAAGGCATAGAA 27068     GC_   AAAC
            GG                  CCTT   TGC   TGCTTTTCTTG
                              ||||   |||   ||||||||||
                              GGAA   ACG   ACGAAAAGAGT
                                GAT   GAA_
GAM1656 PRO1496  3' TGAGAGAAGTGGGAAAGAAGCA 38369    _    GCAAA_ TG
            ATGG                 CC TTGCT     C  CTTTTCTTG
                              || |||||     |  |||||||||
                              GG AACGA     G  GAAGAGAGT
                               T    AGAAAG GT
GAM1656 PRO1600  5' CGAGAAAAGTAAACATCTTTTA 26876        CAAAC____
            GCAAGG                CCTTGCTG       TGCTTTTCTTG
                              ||||||||       ||||||||||
                              GGAACGAT       ATGAAAAGAGC
                                  TTTCTACAA
GAM1656 PRO1880  5' AGGAAAGGAAAAGTGGTAAGG  26887       TG AAACTG      G
                              CCTTGC  C     CTTTTCTT
                              ||||||  |     ||||||||
                              GGAATG  G     GGAAAGGA
                                 GT AAAA__
GAM1656 PRO2266  3' CAGGAGAAGTAGGAGGTGA   38184   TG  GCAAA
                              T  CT    CTGCTTTTCTTG
                              |  ||    ||||||||||||
                              A  GG    GATGAAGAGGAC
                               GT  AG___
GAM1656 PRO2389  3' GGGAGGGGCATGGGTAAGG   64480       G  AAC
                              CCTTGCT CA   TGCTTTTCTT
                              |||||||  ||   ||||||||||
                              GGAATGG GT   ACGGGGAGGG
                                    _  ___
GAM1656 PRO2714  5' CAAGGGGAGCGGGATGTAAGAG 38192     GC    AA     TT
                              CTT  TGCA  CTGCTT  CTTG
                              |||  ||||  ||||||  ||||
                              GAG  ATGT  GGCGAG  GAAC
                                A_   AG     GG
GAM1656 PSK      5' CAGGAAGGGCGAAAGCCGAGG  32877      CT  AAAC
                              CCTTG  GC   TGCTTTTCTTG
                              |||||  ||   ||||||||||
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                                GGAGC  CG    GCGGGAAGGAC
                                  __  AAA_
GAM1656  PTPRR    5'  TGAGAAGCAGCTCTGGCAGCGG 56451         AAA__       TTG
                 GG                  CCTTGCTGC     CTGCTTTTC
                                     |||||||||     |||||||||
                                     GGGGCGACG     GACGAAGAG
                                        GTCTC        T
GAM1656  PURB     3'  AAGGGAGGCCGCAGAGGG    53784      G    AAACT    TT
                                     CCTT CTGC     GCTT  CTT
                                     |||| ||||     ||||  |||
                                     GGGA GACG     CGGA  GAA
                                       _    C____    GG
GAM1656  PYPAF6   5'  CAAGGAGACCTGGTGGCAGGG  59399       TG AAACTGC
                                     CCTTGC  C      TTTTCTTG
                                     ||||||  |      ||||||||
                                     GGGACG  G      AGAGGAAC
                                        GT GTCC___
GAM1656  QSCN6    3'  CAGGGAGGGCAGCCCCGGGCAG 12566    TG    AAA___
                 TGGG                  CT  CTGC     CTGCTTTTCTTG
                                     ||  ||||     ||||||||||||
                                     GG  GACG     GACGGGAGGGAC
                                      GT    GGCCCC
GAM1656  R32184_3  5'  TGAGGAGAGCGGCGGCTGCGAG 54200       T  AAA
                 G                   CCTTGC GC   CTGCTTTTCTTG
                                     ||||||  ||   ||||||||||||
                                     GGAGCG CG   GGCGAGAGGAGT
                                        T  GC_
GAM1656  RAB-R    3'  TGGGGAAGGTAGGGGAAAGATG 21392      _  GCAAA
                 AGG                   CCTTG CT     CTGCTTTTCTTG
                                     |||||  ||     ||||||||||||
                                     GGAGT GA     GATGGAAGGGGT
                                        A  AAGGG
GAM1656  Rab11-FIP2 5'  TGGGGAAGGTGGAGACAGGGGC 30459        GCAAA__ TG
                 GGGG                  CCTTGCT      C  CTTTTCTTG
                                     |||||||      |  |||||||||
                                     GGGGCGG      G  GGAAGGGGT
                                         GGACAGA GT
GAM1656  Rab11-FIP3 3'  GGGGAAGGACGGGTGGGCAAGG 28788        G  AA   _      G
                                     CCTTGCT CA  CTG CTTTTCTT
                                     ||||||| ||  ||| ||||||||
                                     GGAACGG GT  GGC GGAAGGGG
                                        _  G_   A
GAM1656  RAB17    3'  TGGGAAGGGCAGCTGGGGGCAG 42618    TG    AAA___
                 TGG                   T  CTGC     CTGCTTTTCTTG
                                     |  ||||     ||||||||||||
                                     G  GACG     GACGGGAAGGGT
                                      GT    GGGGTC
GAM1656  RAB3GAP  3'  AGGGAGGGAAGGTACCAGGG  67501       C   AAACTG
                                     CCTTG TGC     CTTTTCTT
                                     |||||  |||     ||||||||
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                                GGGAC ATG     GGGAGGGA
                                  C   GAA___
GAM1656  RABEX5   3'  GAGAGGTGTTTGTTGTGGGG  27961     TG T     T
                                CCT  C GCAAAC GCTTTTC
                                |||  | ||||||| |||||||
                                GGG  G TGTTTG TGGAGAG
                                  GT T     _
GAM1656  RBM14    3'  GGGGAAGCAACCTGCAGCTGAG 21994      _     AAC     TT  TG
             G                   CCTT GCTGCA   TGCTT  CT
                                |||| ||||||   |||||  ||
                                GGAG CGACGT   ACGAA  GG
                                  T     CCA     GG  T
GAM1656  RER1     3'  AAGGAGGATGCCGGCAAGG   23844         _  AA  G
                                CCTTGCTG CA  CT CTT
                                |||||||| ||  || |||
                                GGAACGGC GT  GA GAA
                                     C  AG  G
GAM1656  RGS7     5'  GGGAGGGGAGACGCCGCGGGG  12865       T  AAA  G
                                CCTTGC GC   CT CTTTTCT
                                |||||| ||   || |||||||
                                GGGGCG CG   GA GGGAGGG
                                   C  CA_  G
GAM1656  RIP60    5'  CAGGGAGAGGGCAGCATAAGG  26360     __     AAACTG
                                CCT  TGCTGC     CTTTTCTTG
                                |||  ||||||     |||||||||
                                GGA  ACGACG     GAGAGGGAC
                                  AT     G_____
GAM1656  RLUCL    3'  AGGAAGGGCTGAGGTGGGG   55238     TG  G  AACT
                                CCT  CT CA    GCTTTTCTT
                                |||  || ||    |||||||||
                                GGG  GG GT    CGGGAAGGA
                                  GT  A  ____
GAM1656  RNPS1    5'  CAGGAGGAGGTGGCGGCGGCG  55485       AAA TG   _
                                TGCTGC   C  CTTT TCTTG
                                ||||||   |  |||| |||||
                                GCGGCG   G  GGAG AGGAC
                                   GC_ GT    G
GAM1656  RNPS1    5'  TGAGGAAAGCAGGAGGAGGTGG 55488    _   TG AAA___
             CGGCGG                 CC TTGC  C     CTGCTTTTCTTG
                                || ||||  |     ||||||||||||
                                GG GGCG  G     GACGAAAGGAGT
                                 C    GT GAGGAG
GAM1656  RTP801   3'  AGGAAGGGGTGGGTGTCAGGG  39316      C   AA   G
                                CCTTG TGC  ACT CTTTTCT
                                ||||| |||  ||| |||||||
                                GGGAC GTG  TGG GGAAGGA
                                   T   GG  _
GAM1656  SCAMP5   3'  TAGGAGGGGCACACAGCTGGG  58062     T    CAAAC
                                CCT GCTG    TGCTTTTCTTG
                                ||| ||||    ||||||||||
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                                GGG CGAC    ACGGGGAGGAT
                                  T   AC___
GAM1656 SEC24D   5' CGGGAGAAGCGACCGCAGCGGG 29753        AAAC
                                CTTGCTGC   TGCTTTTCTTG
                                ||||||||   ||||||||||
                                GGGCGACG   GCGAAGAGGGC
                                    CCA_
GAM1656 SEC63L   5' GAGAAGAGCGAGGCGGAGG   24263    TG   AAAC
                                CCT CTGC   TGCTTTTCTT
                                ||| ||||   ||||||||||
                                GGA GGCG   GCGAGAAGAG
                                  __   GA__
GAM1656 SEEK1    5' TGGGAAGAATTGGTTTGCAGCC 26810    T       GC_
            AGG                   CCT GCTGCAAACT   TTTTCTTG
                                ||| ||||||||||   ||||||||
                                GGA CGACGTTTGG   AGAAGGGT
                                  C        TTA
GAM1656 SEMA6B   3' CAGGGGAGGCTTGGACGCCGGT 56659    TG  _ AAACT_   TT
            GGGG                  CCT  CTG C     GCTT  CTTG
                                ||| ||| |     ||||  ||||
                                GGG  GGC G     CGGA  GGAC
                                  GT   C CAGGTT    GG
GAM1656 SES2     3' CAGGAGGGGCGGGAGGCACCAG 49590      C   AAA
            GG                    CCTTG TGC   CTGCTTTTCTTG
                                ||||| |||   ||||||||||||
                                GGGAC ACG   GGCGGGGAGGAC
                                  C   GAG
GAM1656 SFXN5    5' CGGGAGAGGCAGCTGTGGCGGG 58649      TG  AA
            G                     CCTTGC  CA  CTGCTTTTCTTG
                                ||||||  ||  ||||||||||||
                                GGGGCG  GT  GACGGAGAGGGC
                                   GT  C_
GAM1656 SHANK3   3' CAGGAAGGGCGTGGACCAGGGA 66101     G   CAA_  T
            GG                    CCTT CTG    AC GCTTTTCTTG
                                |||| |||    || ||||||||||
                                GGAG GAC    TG CGGGAAGGAC
                                  G   CAGG  _
GAM1656 SIAT4B   5' AGGGAGGGCGTGGCAAGG    23632       TG AAACT
                                CCTTGC  C    GCTTTTCTT
                                ||||||  |    |||||||||
                                GGAACG  G    CGGGAGGGA
                                   GT _____
GAM1656 SLC1A7   3' GGGAAGGAGGTGCAGCCAGG   22882     T     AA  G   TT
                                CCT GCTGCA  CT CTT  C
                                ||| ||||||  || |||  |
                                GGA CGACGT  GA GAA  G
                                  C     G_  G   GG
GAM1656 SLC26A10 5' TAAGAAGGGGGTTGTGTGGAAG 56848     G TG  _   G
            G                     CCTT C  CA AACT CTTTTCTTG
                                ||||  |  ||  |||| |||||||||
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                                GGAA G  GT TTGG GGGAAGAAT
                                  _ GT  G   _
GAM1656 SLC2A12  5' GTGGTCGGGGCGGTTTGGTGGC 59740      TG _       TCTTG
           GGGG                   CCTTGC  C AAACTGCTTT
                                |||||| | ||||||||||
                                GGGGCG  G TTTGGCGGGG
                                   GT G        CTGGTGG
GAM1656 SLC34A1  3' TGGGGAAGGCCTGGTGTGGAAA 13209     G TG  AACT
           GG                   CCTT C  CA   GCTTTTCTTG
                                ||||| |  ||   ||||||||||
                                GGAA G  GT   CGGAAGGGGT
                                  A GT  GGTC
GAM1656 SLC39A3  3' GAGAAGGGCATGAAGCGAGG  58602       G  AAC       G
                                CCTTGCT CA   TGCTTTTCTT
                                ||||||| ||   ||||||||||
                                GGAGCGA GT   ACGGGAAGAG
                                   A ____
GAM1656 SNAPC4   3' CAAGAGAGGCAGCCAGAGGCCA 13286    T   GCAAA
           GG                   CCT GCT    CTGCTTTTCTTG
                                ||| |||    ||||||||||||
                                GGA CGG    GACGGAGAGAAC
                                  C   AGACC
GAM1656 SP329    5' CGAGGAAAGCAGCTGTGAGAAA 48646     G  G  AA_
           GG                   CCTT CT CA   CTGCTTTTCTTG
                                |||| || ||   ||||||||||||
                                GGAA GA GT   GACGAAAGGAGC
                                  A _  GTC
GAM1656 SPANXB1  5' AGGAGGGTATGCATAGGG    51623      C    AAC
                                CCTTG TGCA   TGCTTTTCT
                                ||||| ||||   |||||||||
                                GGGAT ACGT   ATGGGAGGA
                                  _   ____
GAM1656 SPR1     5' TAGGGAGAGCAGGCAGCTGGG  26813     T    AAA
                                CCT GCTGC   CTGCTTTTCTTG
                                ||| |||||   ||||||||||||
                                GGG CGACG   GACGAGAGGGAT
                                  T    ____
GAM1656 SR-A1    3' GGGGGAGGGTTGCTGCAGGG   70585       T   A  G   TT
                                CCTTGC GCAA CT CTT  CT
                                |||||| |||| || |||  ||
                                GGGACG CGTT GG GAG  GG
                                   T   _ _   GG
GAM1656 SREC     3' CAGGAAGGGTTGCCTGCAGGG  14898       T_  AACT
                                CCTTGC  GCA   GCTTTTCTTG
                                ||||||  |||   ||||||||||
                                GGGACG  CGT   TGGGAAGGAC
                                   TC  _____
GAM1656 SRPUL    5' TGAGAGGAGCAGAGAGGAAGG  27846     G  GCAAA
                                CCTT CT    CTGCTTTTCTTG
                                |||| ||    ||||||||||||
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                                GGAA GA    GACGAGGAGAGT
                                  G  GA___
GAM1656  SS-56    3'  GAGGGAAGCACGACAGGG    60352      C  CAAAC    TT
                                CCTTG TG    TGCTT  CTT
                                |||||  ||    |||||  |||
                                GGGAC GC    ACGAA  GAG
                                  A  _____    GG
GAM1656  SSBP3    5'  CGAGGAGAGCGCCAGCGAGCGA 36549       _  AAAC
                G                CTTGCT GC    TGCTTTTCTTG
                                |||||| ||   ||||||||||
                                GAGCGA CG    GCGAGAGGAGC
                                  G  ACC_
GAM1656  SSH3BP1  5'  CGAGAGGAAGCGATGCAGAGGG 19616      G    AAC    _
                                CCTT CTGCA   TGCTTT TCTTG
                                ||||  |||||   ||||||  |||||
                                GGGA GACGT   GCGAAG AGAGC
                                  _    A__     G
GAM1656  ST13     5'  TGGGAGGAGCCAGCGGCCGGG  15435     T    AAACT
                                CCT GCTGC    GCTTTTCTTG
                                |||  |||||    ||||||||||
                                GGG CGGCG    CGAGGAGGGT
                                  C    AC___
GAM1656  STC2     3'  TGGGGGAGGTGAACCAGGGAGG 14936      G   CAAACT   TT
                                CCTT CTG     GCTT  CTTG
                                ||||  |||     ||||  ||||
                                GGAG GAC     TGGA  GGGT
                                  G   CAAG__    GG
GAM1656  STIM2    3'  TGGGAGGAGCTGTTAGCAAGG  40864        CAA  T
                                CCTTGCTG   AC GCTTTTCTTG
                                ||||||||   || ||||||||||
                                GGAACGAT   TG CGAGGAGGGT
                                     ___  T
GAM1656  STK22D   3'  AGGAAGAGCAGCAGGAAGG    50142      G    AAAC
                                CCTT CTGC    TGCTTTTCTT
                                ||||  ||||    ||||||||||
                                GGAA GACG    ACGAGAAGGA
                                  G   _____
GAM1656  STMN4    3'  TGGGGGGAGGGGGGTGGCCAAG 48653       _ TG AAA  G   TT
                G                CCTTG C  C   CT CTT  CTTG
                                |||||  |  |   || |||  ||||
                                GGAAC G  G   GG GAG  GGGT
                                  C GT G__  G   GG
GAM1656  STOML1   3'  CAAGAAGAGGTCCCTGTGGCGA 17863      TG  AACTG
                                TTGC  CA    CTTTTCTTG
                                ||||  ||    |||||||||
                                AGCG  GT    GAGAAGAAC
                                  GT  CCCTG
GAM1656  SUI1     3'  TGAGAGGAGAGGATGGGGTAAG 20539       G  AA  G
                G                CCTTGCT CA  CT CTTTTCTTG
                                |||||||  ||  || |||||||||
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                                GGAATGG GT  GA GAGGAGAGT
                                   G  AG  _
GAM1656  SULT4A1   3'  TGAGGGAAGTCTGCCTGGTGAG 69018     TG  __   AACT    TT
              G                    CCT  CT  GCA    GCTT  CTTG
                                   |||  ||  |||    ||||  ||||
                                   GGA  GG  CGT    TGAA  GAGT
                                     GT  TC   C___    GG
GAM1656  SYT12     3'  CGGGGAAGGCCAGGGTGGAAGG 96378      G TG AAACT
                                   CCTT C  C     GCTTTTCTTG
                                   ||||  |  |    ||||||||||
                                   GGAA G  G     CGGAAGGGGC
                                     _ GT GGAC_
GAM1656  TAF5L     3'  CAGGAGAAGTGGCGCCGCAGGG 27720       T  AAA TG
                                   CCTTGC GC   C  CTTTTCTTG
                                   ||||||  ||   |  |||||||||
                                   GGGACG CG   G  GAAGAGGAC
                                      C  C__ GT
GAM1656  TAO1      5'  CAGGAAGGGCGAAAGCCGAGG  17716      CT  AAAC
                                   CCTTG  GC    TGCTTTTCTTG
                                   |||||  ||    ||||||||||
                                   GGAGC  CG    GCGGGAAGGAC
                                     __  AAA_
GAM1656  TEB4      3'  GGGAGTTGGGTTTCAGTGGGG  61285     TG   C    __
                                   CCT  CTG AAACT  GCTTTT
                                   |||  ||| |||||  ||||||
                                   GGG  GAC TTTGG  TGAGGG
                                     GT   _    GT
GAM1656  TJP2      5'  CAGGAGGAGTAGGAGCAGGAG  60328     G    AAA
                                   CTT CTGC   CTGCTTTTCTTG
                                   |||  ||||   ||||||||||||
                                   GAG GACG   GATGAGGAGGAC
                                     _   AG_
GAM1656  TLE4      3'  ACTGGAGAGTGGCTTGCAGTGG 68510     TG     A TG     TTG
              GG                     CCT  CTGCAA C  CTTTTC
                                   |||  ||||||  |  ||||||
                                   GGG  GACGTT G  GAGAGG
                                     GT     C GT     TCAA
GAM1656  TLE4      3'  GGGAAGGGCTGCGTCAAGG    68513      C    AACT
                                   CCTTG TGCA    GCTTTTCTT
                                   |||||  ||||    |||||||||
                                   GGAAC GCGT    CGGGAAGGG
                                     T   _____
GAM1656  TLK2      5'  CGGGAGGAGCGTGGAGCGCGG  78807    T    G  AAC
                                   CC TGCT CA   TGCTTTTCTTG
                                   ||  ||||  ||   ||||||||||
                                   GG GCGA GT   GCGAGGAGGGC
                                    C   G  ___
GAM1656  TMG3      3'  TGGGGAGGGTGGGGGTAGGG   44225       GCAAA TG
                                   CCTTGCT    C  CTTTTCTTG
                                   |||||||    |  |||||||||
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                                GGGATGG    G  GGGAGGGGT
                                   G____ GT
GAM1656  TMLHE    3'  GAGGGATAATTGCAGAAAGG  37048     G     ACTG
                                CCTT CTGCAA    CTTTT
                                |||| ||||||    |||||
                                GGAA GACGTT    GGGAG
                                  A      AATA
GAM1656  TNRC9    3'  CAAGGAGAGTGGCATAGGAGGG 71799      G   CAAA TG
                                CCTT CTG    C  CTTTTCTTG
                                |||| |||    |  |||||||||
                                GGGA GAT    G  GAGAGGAAC
                                  G   AC__ GT
GAM1656  TPRA40   5'  TGGGGAGGGTGGTTTACAGGGG 33488     TG   C    TG
                                CCT  CTG AAAC  CTTTTCTTG
                                |||  ||| ||||  |||||||||
                                GGG  GAC TTTG  GGGAGGGGT
                                  __   A   GT
GAM1656  TRAF3    5'  GGGAAGGGTGGCCACGGGG    13855      C  CAAA TG
                                CCTTG TG    C  CTTTTCTT
                                ||||| ||    |  ||||||||
                                GGGGC AC    G  GGGAAGGG
                                   _  C___ GT
GAM1656  TREX1    5'  AAGAAACCATTGTGTGGCAGGG 50603       TG  AAC  CT     G
                                CCTTGC  CA   TG  TTTCTT
                                ||||||  ||   ||  ||||||
                                GGGACG  GT   AC  AAAGAA
                                   GT  GTT  C_     G
GAM1656  TRIM26   3'  CAGGGAAAGGAAGGCAGCAGG  14343        AAACTG
                                CTTGCTGC     CTTTTCTTG
                                ||||||||     |||||||||
                                GGACGACG     GAAAGGGAC
                                    GAAG__
GAM1656  TTYH2    3'  AGGAAAGCTCTGCAGTGGGG   51974     TG    AACT
                                CCT  CTGCA    GCTTTTCT
                                |||  |||||    ||||||||
                                GGG  GACGT    CGAAAGGA
                                  GT    CT__
GAM1656  TTYH2    3'  AGGAGGGGAGTGGCAGTGAGG  51975     TG    AA   G
                                CCT  CTGC  ACT CTTTTCT
                                |||  ||||  ||| |||||||
                                GGA  GACG  TGA GGGAGGA
                                  GT   G_   G
GAM1656  TU3A     3'  AGGGGAGGAAGGGCAGGG    24177       GCAAA  G   TT
                                CCTTGCT    CT CTT  CTT
                                |||||||    || |||  |||
                                GGGACGG    GA GGA  GGA
                                   _____ A   GG
GAM1656  U2AF65   3'  GGGGAGGGTGGGGGCAGGG    24413       GCAAA TG
                                CCTTGCT    C  CTTTTCTT
                                |||||||    |  ||||||||
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                                GGGACGG    G  GGGAGGGG
                                   G____ GT
GAM1656  UAP1     5'  CGAGAGGGGCGGGGTGGCCGGG 13341     T  TG AAA
                                CCT GC  C   CTGCTTTTCTTG
                                ||| ||  |   ||||||||||||
                                GGG CG  G   GGCGGGGAGAGC
                                  C  GT G__
GAM1656  UBE2E1   3'  CAGGGAGGGTGGGAGTTGGTAA 13948       GCAAA TG
                                TTGCT    C  CTTTTCTTG
                                ||||||    |  |||||||||
                                AATGG    G  GGGAGGGAC
                                   TTGAG GT
GAM1656  UCK1     3'  AGGGGAGTGTTAGCAGCGAGG  49501         A  T   TT
                                CCTTGCTGC AAC GCTT  CT
                                |||||||||| ||| ||||  ||
                                GGAGCGACG TTG TGAG  GA
                                     A  _   GG
GAM1656  UHRF2    5'  CAGGGAAAGCGGCGCGGGCCGG 73829     T  _  AAA
              G                  CCT GCT GC   CTGCTTTTCTTG
                                ||| ||| ||   ||||||||||||
                                GGG CGG CG   GGCGAAAGGGAC
                                  C  G  C__
GAM1656  UPB1     3'  AGGGGGAGAGTGGCATGG    33344    T   GCAA   G   TT
                                CC TGCT    ACT CTT  CTT
                                || ||||    ||| |||  |||
                                GG ACGG    TGA GAG  GGA
                                 T   _____  _  GG
GAM1656  WDR13    5'  GAGAAGGGAAGGCGGAGGG   35841     G   AAACTG
                                CCTT CTGC     CTTTTCTT
                                |||| ||||     ||||||||
                                GGGA GGCG     GGGAAGAG
                                  _   GAA___
GAM1656  XT2      3'  GGGAAAGGCAGGGTCAGGG   42475      _ GCAAA
                                CCTTG CT    CTGCTTTTCTT
                                ||||| ||    ||||||||||
                                GGGAC GG    GACGGAAAGGG
                                   T _____
GAM1656  XYLT1    5'  TGGGAAAGGCCCCGGTGAGG   78418    TG   CAAACT
                                CCT  CTG     GCTTTTCTTG
                                |||  |||     ||||||||||
                                GGA  GGC     CGGAAAGGGT
                                  GT   CC____
GAM1656  YF13H12  3'  TGGGAGGAGAGGGCGGCAA   27455       AAACTG
                                TTGCTGC     CTTTTCTTG
                                |||||||     |||||||||
                                AACGGCG     GAGGAGGGT
                                    GGA___
GAM1656  YKT6     3'  GGGAAGGCTCTGTGGGAGGG   22641     G TG  AACT
                                CCTT C  CA    GCTTTTCT
                                |||| |  ||    ||||||||
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                                GGGA G  GT    CGGAAGGG
                                  G GT  CT__
GAM1656  ZDHHC1   5'  CGGGGAGGGTGGAAGGCCAGG  78210     T   GCAAA TG
                                CCT GCT     C  CTTTTCTTG
                                ||| |||     |  |||||||||
                                GGA CGG     G  GGGAGGGGC
                                  C   AA___ GT
GAM1656  ZDHHC2   5'  CAGGGGAGGCGGCCGGGCGGCG 33445         AAA_     TT
              GGG                  CCTTGCTGC    CTGCTT  CTTG
                                |||||||||    ||||||  ||||
                                GGGGCGGCG    GGCGGA  GGAC
                                     GGCC     GG
GAM1656  ZDHHC3   5'  AGGGGAAGGCAGCGGCGGCGGC 33928    _      AAA         G
              GG                   CC TTGCTGC   CTGCTTTTCTT
                                || |||||||   ||||||||||
                                GG GGCGGCG   GACGGAAGGGG
                                 C      GC_         AC
GAM1656  ZDHHC3   3'  TGAGAAGGGCAGGATCAGAAGG 33936     G   CAAA
                                CCTT CTG    CTGCTTTTCTTG
                                |||| |||    ||||||||||||
                                GGAA GAC    GACGGGAAGAGT
                                  _   TAG_
GAM1656  ZER6     5'  GGGGAAGGCAGGGCCGGG    64115     T   GCAAA
                                CCT GCT     CTGCTTTTCTT
                                ||| |||     ||||||||||
                                GGG CGG     GACGGAAGGGG
                                  C  _____
GAM1656  ZFP91    5'  GGGGAGCAGCGCCGAGG     54878      CT  AAA     TT
                                CCTTG  GC   CTGCTT  CTT
                                |||||  ||   ||||||  |||
                                GGAGC  CG   GACGAG  GGG
                                   __  C__     G
GAM1656  ZMPSTE24 3'  TAAGAAAGGTAATAGTTGGTAA 20731        GCAAAC
              GG                   CCTTGCT     TGCTTTTCTTG
                                |||||||     ||||||||||
                                GGAATGG     ATGGAAAGAAT
                                    TTGATA
GAM1656  ZNF228   3'  GAGAGGGGTTTCACGAGG    60600      C  C    G
                                CCTTG TG AAACT CTTTT
                                ||||| || ||||| |||||
                                GGAGC AC TTTGG GAGAG
                                  _ _    G
GAM1656  ZNF263   3'  GAGGGAGGTGCAGAGGCAGCAG 20426    _     AAA   _     G
              AGG                  CCT TGCTGC   CTGC TTTTCTT
                                ||| ||||||   |||| |||||||
                                GGA ACGACG   GACG GGAGGGA
                                  G     GA_   T      GT
GAM1656  ZNF334   5'  TAGGAAGGGCTGGCGGCGAG   36639        AAACT
                                CTTGCTGC    GCTTTTCTTG
                                ||||||||    ||||||||||
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                                GAGCGGCG    CGGGAAGGAT
                                    GT___
GAM1656  ZNF363    5'  GGGAGGGGTGTGCTAGAGAGG  73835    TG _  A  G
                                CCT  CT GCA ACT CTTTT
                                |||  || ||| ||| |||||
                                GGA  GA CGT TGG GAGGG
                                  GA  T   G   G
GAM1656  LOC112616 3'  AGGAGCTTTGCAGAGAGG    57293    TG     CT
                                CCT  CTGCAAA  GCTTTT
                                |||  |||||||  ||||||
                                GGA  GACGTTT  CGAGGA
                                  GA      __
GAM1656  LOC112724 5'  CGAGGGAGGTCTCATCGGCGGT 57302    TG   AAACT__   TT
             GAGG                   CCT  CTGC      GCTT  CTTG
                                |||  ||||      ||||  ||||
                                GGA  GGCG      TGGA  GAGC
                                  GT    GCTACTC    GG
GAM1656  LOC113201 5'  GAGGAGGGGGGGCGGGGAGG    57356     G    AAA  G
                                CCTT CTGC   CT CTTTTC
                                |||| ||||   || ||||||
                                GGAG GGCG   GG GAGGAG
                                  G    G__  G
GAM1656  LOC115051 3'  CAAGGAGGGTTTGGGTAGTAGG 60675         AAACT
                                CTTGCTGC    GCTTTTCTTG
                                ||||||||    ||||||||||
                                GGATGATG    TGGGAGGAAC
                                    GGTT_
GAM1656  LOC115129 5'  AGGAGACAGGTTGCAGTGAG   73603    TG     A   C
                                CT  CTGCAA CTG TTTTCT
                                ||  |||||| ||| ||||||
                                GA  GACGTT GAC AGAGGA
                                 GT     G   _
GAM1656  LOC115557 3'  GGGAGGGCTGGGGCAGGG    56822        G  AACT
                                CCTTGCT CA    GCTTTTCT
                                ||||||| ||    ||||||||
                                GGGACGG GT    CGGGAGGG
                                    G  _____
GAM1656  LOC115708 3'  CAGGAAGGGCGGCTGTGATGG  73913    _ TG T  AAAC
                                CC T  C GC    TGCTTTTCTTG
                                || |  | ||   ||||||||||
                                GG A  G CG    GCGGGAAGGAC
                                 T GT T  _____
GAM1656  LOC116071 3'  TGAGGAAGGACCCTGTGCAAGG 57421        T   AACTG
                                CCTTGC GCA     CTTTTCTTG
                                ||||||| |||    |||||||||
                                GGAACG TGT     GGAAGGAGT
                                   _   CCCA_
GAM1656  LOC116236 3'  TGAGAAGGGCGGCAGAGGCAGT 74249     TG    AAA__
             GGGG                   CCT  CTGC    CTGCTTTTCTTG
                                |||  ||||    ||||||||||||
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                                GGG  GACG    GGCGGGAAGAGT
                                  GT   GAGAC
GAM1656  LOC119559 3'  TGAGGGAACGGTTGGAGTGGGG 74455    TG  G   A   C  TT
                                CCT  CT CAA CTG TT  CTTG
                                |||  || ||| ||| ||  ||||
                                GGG  GA GTT GGC AA  GAGT
                                  GT  G   _   _  GG
GAM1656  LOC121219 5'  TGGGGGGAGCTGGTGGGTGAGG 74491    TG  G  AACT   TT
                                CCT  CT CA    GCTT  CTTG
                                |||  || ||    ||||  ||||
                                GGA  GG GT    CGAG  GGGT
                                  GT  _  GGT_   GG
GAM1656  LOC121344 5'  AGGAGGGGCTAAGGCGGGAGGG 74500     G   AAACT      G
                                CCTT CTGC    GCTTTTCTT
                                |||| ||||    |||||||||
                                GGGA GGCG    CGGGGAGGA
                                  G   GAAT_       G
GAM1656  LOC122553 3'  AGGGAACTCTGCAGCAGGG   74589         AACTGCT
                                CCTTGCTGCA      TTTCTT
                                ||||||||||      ||||||
                                GGGACGACGT      AAGGGA
                                     CTC_____
GAM1656  LOC123876 3'  CAGGAAGACTTGTGTGTGGGG  74715    TG T   AACTGC
                                CCT  C GCA     TTTTCTTG
                                |||  | |||     ||||||||
                                GGG  G TGT     AGAAGGAC
                                  GT _   GTTC__
GAM1656  LOC124045 3'  GGGGAGGGTACACCAGGG    76549      C  CAAAC
                                CCTTG TG    TGCTTTTCTT
                                |||||  ||    ||||||||||
                                GGGAC AC    ATGGGAGGGG
                                   C  ______
GAM1656  LOC124093 3'  CGAGAGGAGGCCAGGGCAGCCG 74722     T    AAA  __
            GG                    CCT GCTGC   CTG  CTTTTCTTG
                                ||| |||||   |||  |||||||||
                                GGG CGACG   GAC  GAGGAGAGC
                                  C    G__   CG
GAM1656  LOC124222 3'  CAAGGAGGGTGTCCAGGGCTAG 74744     T   GCAA  T
            G                     CCT GCT    AC GCTTTTCTTG
                                ||| |||    || ||||||||||
                                GGA CGG    TG TGGGAGGAAC
                                  T   GACC  _
GAM1656  LOC124222 3'  CAGGAGCGCTGGGTTCTGCAGC 74746          _   __  T    TG
            AGGG                    CCTTGCTGCA AACT  GC TTTCT
                                ||||||||||| ||||  || |||||
                                GGGACGACGT TTGG  CG GAGGA
                                     C    GT  C    C
GAM1656  LOC124460 3'  CAGGGAAGGCTTCTCAGAGGG  76557      G   CAAACT
                                CCTT CTG     GCTTTTCTTG
                                |||| |||     ||||||||||
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                              GGGA GAC     CGGAAGGGAC
                                _  TCTT__
GAM1656  LOC124602 3'  GGGAGGAGCAGCGAAAGG    74788     GC   AAAC
                              CCTT  TGC    TGCTTTTCTT
                              ||||  |||    ||||||||||
                              GGAA  GCG    ACGAGGAGGG
                                A_  ____
GAM1656  LOC125058 3'  TGAGGAAAGCAGAGACAGGAGA 60549     G_   CAAA
           GG                   CCTT  CTG    CTGCTTTTCTTG
                              ||||  |||    ||||||||||||
                              GGAG  GAC    GACGAAAGGAGT
                                AG   AGA_
GAM1656  LOC126282 3'  CAGGAGGAGGAGGTTGCAGTGA 74948    TG     A  G
           G                    CT  CTGCAA CT CTTTTCTTG
                              ||  |||||| || |||||||||
                              GA  GACGTT GA GAGGAGGAC
                               GT     G  G
GAM1656  LOC126302 3'  TGAGAGAAGCAAAAAAGTAAG  74983       GCAAAC
                              CTTGCT     TGCTTTTCTTG
                              ||||||     ||||||||||
                              GAATGA     ACGAAGAGAGT
                                 AAAA__
GAM1656  LOC126302 3'  TGAGGGAGGAAGGAGCACAAGG 74984       C   AAA  G   TT
                              CCTTG TGC   CT CTT  CTTG
                              ||||| |||   || |||  ||||
                              GGAAC ACG   GA GGA  GAGT
                                _  AG_  A   GG
GAM1656  LOC127534 3'  GAGGAGGGTGGCTGTGGGG    75970     TG T  AA   G
                              CCT  C GC  ACT CTTTTC
                              |||  | ||  ||| ||||||
                              GGG  G CG  TGG GAGGAG
                               GT T  G_  _
GAM1656  LOC127703 5'  GGGAGGGTAACTGCGGAGAGG  75179     TG    AAC
                              CCT  CTGCA   TGCTTTTCT
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                              GGA  GGCGT   ATGGGAGGG
                                GA    CA_
GAM1656  LOC129080 3'  CAAGGAGGGATAGAGGTACAAG 56791       C   AAA  _
           G                    CCTTG TGC   CTG CTTTTCTTG
                              ||||| |||   ||| |||||||||
                              GGAAC ATG   GAT GGGAGGAAC
                                _  GA_  A
GAM1656  LOC129138 3'  CAAGGAGATACTGCAGTGAG   57920    TG    AACTGC
                              CT  CTGCA     TTTTCTTG
                              ||  |||||     ||||||||
                              GA  GACGT     AGAGGAAC
                               GT    CAT___
GAM1656  LOC129566 5'  CGGGGGGAGCAAGCGGAGGAGG 76224      G_    AAAC    TT
                              CCTT  CTGC    TGCTT  CTTG
                              ||||  ||||    |||||  ||||
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                                GGAG  GGCG   ACGAG  GGGC
                                  GA   A___    GG
GAM1656  LOC130436 3'  TGAGGGAAGTAGTTGAAGCATG 75439   T   GCA      TT
             G                   CC TGCT   AACTGCTT  CTTG
                                 || ||||   ||||||||  ||||
                                 GG ACGA   TTGATGAA  GAGT
                                  T   AG_      GG
GAM1656  LOC131363 5'  TGATGCTGGCAGTTTCCAGCAG 76372       C       TT__  TTG
             GG                   CCTTGCTG AAACTGCT   TC
                                 |||||||| ||||||||   ||
                                 GGGACGAC TTTGACGG   AG
                                      C       TCGT  T
GAM1656  LOC131870 3'  CAGGAAGGGTAAGGAAGTGGCT 75508    T  TG AAA  _
             AGG                   CCT GC  C   CT GCTTTTCTTG
                                 ||| ||  |   || ||||||||||
                                 GGA CG  G   GA TGGGAAGGAC
                                   T  GT AAG  A
GAM1656  LOC131870 3'  AAGAGGAGTGGCCACAAGG   75505      C  CAAA TG
                                 CCTTG TG   C  CTTTTCTT
                                 ||||| ||   |  ||||||||
                                 GGAAC AC   G  GAGGAGAA
                                   _  C___ GT
GAM1656  LOC131870 3'  CAGGAAGGGCGGTATGGAAGGC 75507       G__  A
             AGG                   CTTGCT   CA ACTGCTTTTCTTG
                                 ||||||   || ||||||||||||
                                 GGACGG   GT TGGCGGGAAGGAC
                                    AAG  A
GAM1656  LOC132422 5'  TGAGGAGGGCTTTGGTGCGG   76404      AACT_
                                 CTGCA    GCTTTTCTTG
                                 |||||    ||||||||||
                                 GGCGT    CGGGAGGAGT
                                   GGTTT
GAM1656  LOC132625 5'  AAGAAGGGCACAGGCAGG    76425       GCAAAC
                                 CTTGCT     TGCTTTTCTT
                                 ||||||     ||||||||||
                                 GGACGG     ACGGGAAGAA
                                    AC____
GAM1656  LOC134265 3'  TGGGGAGGGAACAAGTAGAAGG 75658     G   AAACTG
                                 CCTT CTGC     CTTTTCTTG
                                 |||| ||||     |||||||||
                                 GGAA GATG     GGGAGGGGT
                                   _    AACAA_
GAM1656  LOC134701 5'  AGGGAGAGGGGCGGAGAGG   75695    TG   AAAC G
                                 CCT  CTGC   T CTTTTCTT
                                 |||  ||||   | ||||||||
                                 GGA  GGCG   G GAGAGGGA
                                   GA   _____ G
GAM1656  LOC138150 5'  GGGAGGGGCCTCAGCAGG    75820       CAAACT
                                 CTTGCTG     GCTTTTCTT
                                 |||||||     |||||||||
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                                GGACGAC     CGGGGAGGG
                                   TC____
GAM1656  LOC139341 5'  CAGGGAGAGGAGGGCGGGTGGG 75898     TG _  AAA  G
            G                   CCT  CT GC   CT CTTTTCTTG
                                |||  || ||   || |||||||||
                                GGG  GG CG   GA GAGAGGGAC
                                  GT  G  G__  G
GAM1656  LOC142955 5'  CAAGAGAAGCAGGCAAGAAGCG 76958      _   GCAAA_
            GAGG                  CCTT GCT     CTGCTTTTCTTG
                                |||| |||     ||||||||||||
                                GGAG CGA     GACGAAGAGAAC
                                  G   AGAACG
GAM1656  LOC143282 3'  TGGGGGAGGCGTGGGGAAGG   77025     G  G  AAC    TT
                                CCTT CT CA   TGCTT  CTTG
                                |||| || ||   |||||  ||||
                                GGAA GG GT   GCGGA  GGGT
                                  _  G  ___    GG
GAM1656  LOC143425 3'  GAGGACTGCTTGTGCCAAGG   89015      CT   AACT  TT    G
                                CCTTG  GCA    GC  TTCTT
                                |||||  |||    ||  |||||
                                GGAAC  CGT    CG  AGGAG
                                   __   GTT_  TC
GAM1656  LOC143666 3'  CGGGAGGAGCATGAAAGTGGAT 83883       _ TG AAAC_
            AAGG                  CCTTG C  C     TGCTTTTCTTG
                                |||||  |  |    ||||||||||
                                GGAAT G  G    ACGAGGAGGGC
                                   A GT AAAGT
GAM1656  LOC144079 5'  GAGAAAAAGACTGCAGAAAGG  77180     G    AA  GC
                                CCTT CTGCA  CT  TTTTC
                                |||| |||||  ||  |||||
                                GGAA GACGT  GA  AAGAG
                                  A    CA  AA
GAM1656  LOC144231 5'  CAAGAAAGACAGTGTATAAGG  83936      C   AA    CT
                                CCTTG TGC  ACTG  TTTCTTG
                                ||||| |||  ||||  |||||||
                                GGAAT ATG  TGAC  AAAGAAC
                                  _  __    AG
GAM1656  LOC144231 5'  GGGGGAAGGATGCAGAAGG   83941     G    AA  GC  TT
                                CCTT CTGCA  CT  TT  CT
                                |||| |||||  ||  ||  ||
                                GGAA GACGT  GA  AG  GG
                                  _    AG  __  GG
GAM1656  LOC144305 3'  GAGGAGGCTGGGGTGCAG    83971      AA _    T   G
                                CTGCA  CT GCTTT CTT
                                |||||  || ||||| |||
                                GACGT  GG CGGAG GAG
                                   GG  T    _
GAM1656  LOC144317 5'  TAGGAGGGGTGGAACCCAGCAG 77297      AAA___ TG
            C                   GCTGC     C  CTTTTCTTG
                                |||||     |  |||||||||
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                                CGACG     G  GGGGAGGAT
                                  ACCCAA GT
GAM1656  LOC144465 3'  TGAGGAGAGCAGGAAAGGCAGT 77354    _ TG    AAA__
           GGTGG                  CC T  CTGC     CTGCTTTTCTTG
                                || |  ||||    ||||||||||||
                                GG G  GACG    GACGAGAGGAGT
                                 T GT    GAAAG
GAM1656  LOC144473 5'  TGGGGAGGGATGTGATGTAGTA 83998         A_  TG_   TT  TG
           AG                   CTTGCTGCA  AC   CTT  CT
                                |||||||||  ||   |||  ||
                                GAATGATGT  TG   GGA  GG
                                     AG  TAG   GG  T
GAM1656  LOC144571 5'  TGGGAAGACCTGTTTGCAGAGA 84081     TG       TG__   TT TTG
           GG                   CCT  CTGCAAAC    CTT  C
                                |||  ||||||||    |||  |
                                GGA  GACGTTTG    GAA  G
                                  GA       TCCA   GG T
GAM1656  LOC144583 3'  CAGGAAAGGACTGGTAGACGGG 77414       _    AAACTG
           G                    CCTTG CTGC     CTTTTCTTG
                                |||||  ||||     |||||||||
                                GGGGC GATG     GGAAAGGAC
                                  A    GTCA__
GAM1656  LOC144845 5'  CAGGGGAAGCTGCAGTGTGG   57456    T      AACT    TT
                                CC TGCTGCA    GCTT  CTTG
                                || |||||||    ||||  ||||
                                GG GTGACGT    CGAA  GGAC
                                 T       _____   GG
GAM1656  LOC144845 3'  CGGGAGGCGGAGGTTGCAGTGA 57459     TG     A__     TT TTG
           GG                   CCT  CTGCAA   CTGCTT  C
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                                GGA  GACGTT   GGCGGA  G
                                  GT     GGA     GG C
GAM1656  LOC144866 5'  GGGAAGGGTGTGCACTGGGG   84138     GC    A   G   TT
                                CCTT  TGCA ACT CTT  C
                                ||||  |||| ||| |||  |
                                GGGG  ACGT TGG GAA  G
                                  TC    G   _   GG
GAM1656  LOC144871 3'  CAGGAAAAGTGAAATCAGAGAG 84121     TG   CAAACT
           G                    CCT  CTG     GCTTTTCTTG
                                |||  |||     ||||||||||
                                GGA  GAC     TGAAAAGGAC
                                  GA   TAAAG_
GAM1656  LOC145135 5'  GCAGGGAGAGCAGGGCCCCTCT 84205     TG TG  AA_______
           GTGGTGAGG               CCT  C  CA       CTGCTTTTCTTG   C
                                |||  |  ||      ||||||||||||  |
                                GGA  G  GT       GACGAGAGGGAC   G
                                  GT GT  CTCCCCGG
GAM1656  LOC145333 5'  GTGGGAAAAGCAGTTCACTTGG 84302         A_____
           CGGTAAG                 CTTGCTGC     AACTGCTTTTCTTG   T
                                ||||||||     ||||||||||||||  |
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                                GAATGGCG     TTGACGAAAAGGGT   G
                                    GTTCAC
GAM1656  LOC145644 5'  CGGGGAGGGCAAGAAGCAGG   65287       GCAAAC
                                CTTGCT     TGCTTTTCTTG
                                ||||||     ||||||||||
                                GGACGA     ACGGGAGGGGC
                                   AGA___
GAM1656  LOC145663 3'  CGGGAGGCGGAGCTTGTAGTGA 84422     TG     A__     TT TTG
           GG                     CCT  CTGCAA   CTGCTT  C
                                ||| ||||||   ||||||  |
                                GGA  GATGTT   GGCGGA  G
                                  GT     CGA     GG C
GAM1656  LOC145694 5'  CAGGGAAGGAAAGTGGGGAGG  84440      G TG AAACTG
                                CCTT C  C     CTTTTCTTG
                                |||| |  |     |||||||||
                                GGAG G  G     GGAAGGGAC
                                  G GT AAA___
GAM1656  LOC145717 3'  TGGGGAAGGCAGGGAGGGCAGG 67379       GCAAA
                                CTTGCT    CTGCTTTTCTTG
                                ||||||    ||||||||||||
                                GGACGG    GACGGAAGGGGT
                                   GAGG_
GAM1656  LOC145757 3'  CAGGGGGAGCTGGGATGCAGTG 77921    TG    AA  _   TT
           GG                     CT  CTGCA  CT GCTT  CTTG
                                ||  |||||  || ||||  ||||
                                GG  GACGT  GG CGAG  GGAC
                                 GT    AG  T   GG
GAM1656  LOC145780 5'  GGAAGGGTTTGCCAAGG     84494      CT      G   TT
                                CCTTG  GCAAACT CTT  C
                                |||||  ||||||| |||  |
                                GGAAC  CGTTTGG GAA  G
                                   __     _  GG
GAM1656  LOC145820 3'  CAAGAAACTTACATTTCAGTAA 77971        CAAACTGCT
           GG                     CCTTGCTG       TTTCTTG
                                ||||||||       |||||||
                                GGAATGAC       AAAGAAC
                                    TTTACATTC
GAM1656  LOC145824 5'  CAGGGAGATGTTTGCAGTGTGG 77984    T        TGC
                                CC TGCTGCAAAC   TTTTCTTG
                                || ||||||||||   ||||||||
                                GG GTGACGTTTG   AGAGGGAC
                                 T        T__
GAM1656  LOC145854 5'  CGGGAGGAGCGGCAGCGGCAAG 78007         AAA
           G                     CCTTGCTGC   CTGCTTTTCTTG
                                |||||||||   ||||||||||||
                                GGAACGGCG   GGCGAGGAGGGC
                                    AC_
GAM1656  LOC145873 3'  GGGAGAATGGGTGTAGGAGG   78013     G    AA  GC
                                CCTT CTGCA  CT  TTTTCT
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GAM1656  LOC145902 5'  CAGGGGGAGCTTCGGCAGGG   78020        CAAACT    TT
                                CCTTGCTG     GCTT  CTTG
                                ||||||||     ||||  ||||
                                GGGACGGC     CGAG  GGAC
                                    TT____    GG
GAM1656  LOC145946 5'  CGGGGAAGGAAGGGCATGAGG  84559      C   AAACTG
                                CCTTG TGC     CTTTTCTTG
                                ||||| |||     |||||||||
                                GGAGT ACG     GGAAGGGGC
                                  _  GGAA__
GAM1656  LOC146174 5'  GGGGGGAGCGGGGCGGGG    78201       GCAAA     TT
                                CCTTGCT    CTGCTT  CTT
                                |||||||    ||||||  |||
                                GGGGCGG    GGCGAG  GGG
                                    _____     GG
GAM1656  LOC146237 5'  CGAGAGAGGTGGTGCAGGCTGG 84608        _  AA__  TG
            CAGGG                CCTTGCT GC    AC  CTTTTCTTG
                                ||||||| ||    ||  |||||||||
                                GGGACGG CG    TG  GGAGAGAGC
                                   T  GACG  GT
GAM1656  LOC146307 3'  AGGGAGGACAGCTGCTGGCAGG 84636        _  AA  _  TT  TG
            G                   CCTTGCT GCA  CTG CTT  CT
                                ||||||| |||  ||| |||  ||
                                GGGACGG CGT  GAC GGA  GA
                                   T  C_  A  GG  C
GAM1656  LOC146332 3'  GGGAGAGGAGTGGGGAGG    78358      G  GCAA   G
                                CCTT CT    ACT CTTTTCT
                                ||||  ||    ||| |||||||
                                GGAG GG    TGA GAGAGGG
                                  G  ____   G
GAM1656  LOC146336 5'  CAGGAGAGGAAGGAGCGGCGGG 78365         AAA  G
                                CTTGCTGC   CT CTTTTCTTG
                                ||||||||   || |||||||||
                                GGGCGGCG   GA GGAGAGGAC
                                    AG_  A
GAM1656  LOC146562 5'  CAGGAGAGGCAGGACGCGCAAA 58252      _  T  AAA
            GG                   CCTT GC GC   CTGCTTTTCTTG
                                |||| || ||   ||||||||||||
                                GGAA CG CG   GACGGAGAGGAC
                                  A  _  CAG
GAM1656  LOC146562 5'  TGGGGGGGGCAGGAGAGGCAGG 58257       GCAAA     TT
                                CTTGCT    CTGCTT  CTTG
                                ||||||    ||||||  ||||
                                GGACGG    GACGGG  GGGT
                                   AGAG_     GG
GAM1656  LOC146774 3'  CAGGAGAAGTAAATAAATAAGG 78694       CTGCAAAC
                                CCTTG       TGCTTTTCTTG
                                |||||       ||||||||||
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                                GGAAT       ATGAAGAGGAC
                                  AAATAA__
GAM1656  LOC146909 3'  TGGGGAGAGCACTCTCAGCAGG 78788         CAAAC
             G                    CCTTGCTG     TGCTTTTCTTG
                                  ||||||||     ||||||||||
                                  GGGACGAC     ACGAGAGGGGT
                                     TCTC_
GAM1656  LOC147040 5'  CAGGGAAGGCGGCGCGGCCGGG 78832     T     AAA
                                  CCT GCTGC   CTGCTTTTCTTG
                                  ||| |||||   ||||||||||||
                                  GGG CGGCG   GGCGGAAGGGAC
                                    C     C__
GAM1656  LOC147080 3'  CGGGAGGCAGCAGTTGCAGTGA 85034     TG      A     _
             G                    CT  CTGCAA CTGCT TTTCTTG
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                                  GA  GACGTT GACGA GGAGGGC
                                   GT      _     C
GAM1656  LOC147093 5'  TGAGGAGAGCCCTGCAGTGGAG 85059     _ TG     AACT
             G                    CC T  CTGCA    GCTTTTCTTG
                                  || |  |||||    ||||||||||
                                  GG G  GACGT    CGAGAGGAGT
                                   A GT     CC__
GAM1656  LOC147343 5'  GGGAGAGGTGGAGGAGGG     85131       G  GCAAA TG
                                  CCTT CT     C  CTTTTCTT
                                  |||| ||     |  ||||||||
                                  GGGA GA     G  GGAGAGGG
                                    G  _____ GT
GAM1656  LOC147515 3'  AGGAAGGGGGAGTAGGAGGG   85146       G    AAA  G
                                  CCTT CTGC   CT CTTTTCT
                                  |||| ||||   || |||||||
                                  GGGA GATG   GG GGAAGGA
                                    G    A__  G
GAM1656  LOC147515 5'  TGGGGGCTAAGCTTGTGGTGAG 85152     TG TG   A  __      CTTG
             G                    CCT  C  CAA CT  GCTTTT
                                  |||  |  ||| ||  ||||||
                                  GGA  G  GTT GA  CGGGGG
                                    GT GT   C  AT      T
GAM1656  LOC147669 3'  CAGGAATTAGAGGTTGCAGTGA 85177     TG      A  G  T_
             GG                    CCT  CTGCAA CT CT  TTCTTG
                                  |||  |||||| || ||  ||||||
                                  GGA  GACGTT GA GA  AAGGAC
                                    GT      G  _  TT
GAM1656  LOC147727 5'  CAAGAAGAGCAAGGAAGGCCAG 79128     T   GCAAAC
             G                    CCT GCT      TGCTTTTCTTG
                                  ||| |||      ||||||||||
                                  GGA CGG      ACGAGAAGAAC
                                    C   AAGGA_
GAM1656  LOC147912 5'  CGAGAAGAGCGGGGAGTGGGG  79265     TG  GCAAA
                                  CCT  CT     CTGCTTTTCTTG
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                                GGG  GA    GGCGAGAAGAGC
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GAM1656  LOC147958 3'  GGAGCCGTGCGGCGGGG     88525         AACT    TT
                                CCTTGCTGCA    GCTT  C
                                ||||||||||    ||||  |
                                GGGGCGGCGT    CGAG  G
                                      GC__    G
GAM1656  LOC147990 3'  CGGGAGGAAGAGGTTGCAGTGA 85220    TG     A  GC
           G                     CT  CTGCAA CT  TTTTCTTG
                                ||  ||||||  ||  ||||||||
                                GA  GACGTT GA  AGGAGGGC
                                 GT     G  GA
GAM1656  LOC148014 3'  CGGGGAAAGGGGCTGCAGCGGA 79307      _     AA  G
           GG                    CCTT GCTGCA  CT CTTTTCTTG
                                ||||  ||||||  ||  |||||||||
                                GGAG CGACGT  GG GAAAGGGGC
                                  G     C_  G
GAM1656  LOC148066 3'  CAGGGAGGGGGGGTGCAATGAGG 79321      GC   AA   G
                                CCTT  TGC  ACT CTTTTCTTG
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                                GGAG  ACG  TGG GGGAGGGAC
                                  TA   __   G
GAM1656  LOC148147 5'  CAGGGAGAGTGAATACAGCTAG 79393     T    CAAACT
           G                     CCT GCTG     GCTTTTCTTG
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                                GGA CGAC     TGAGAGGGAC
                                 T   ATAAG_
GAM1656  LOC148413 3'  CAAGACAAGCAGGTTGCGGCAA 79578          A     T
           GG                    CCTTGCTGCAA CTGCTT TCTTG
                                ||||||||||| |||||| |||||
                                GGAACGGCGTT GACGAA AGAAC
                                      G     C
GAM1656  LOC148413 3'  TGAGGGGAGCCAGGGTGGGTGG 79582     TG  G  AA  _  TT
           GG                    CCT  CT CA  CTG CTT  CTTG
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                                GGG  GG GT  GAC GAG  GAGT
                                  GT  _  GG   C   GG
GAM1656  LOC148479 3'  TGGGGGAGGCACTGGCGGGAGG 79618     G    AAAC    TT
                                CCTT CTGC    TGCTT  CTTG
                                ||||  ||||    |||||  ||||
                                GGAG GGCG    ACGGA  GGGT
                                  _    GTC_     GG
GAM1656  LOC148490 5'  AGAGACAAAGGCGTTTGTGGCA 79619       TG     T    __    G
           AGG                    CCTTGC  CAAAC GCTTT  TCTT
                                ||||||  |||||  |||||  ||||
                                GGAACG  GTTTG CGGAA  AGAG
                                   GT     _     AC    AG
GAM1656  LOC148638 5'  CAGGAAAACAAGCTGAGTGAGG 79666     TG  G  AAC  C
                                CCT  CT CA   TG TTTTCTTG
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                                GGA  GA GT   AC AAAAGGAC
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GAM1656  LOC148697 3'  TAGGAAAAGTGGTCCAGCAAAG 79680      _    CAA  TG
                 G                 CCTT GCTG   AC  CTTTTCTTG
                                   |||| ||||   ||  |||||||||
                                   GGAA CGAC   TG  GAAAAGGAT
                                     A   C__  GT
GAM1656  LOC148753 3'  AGGGAAAGCTCAGCAAAGG    85368     _   CAAACT
                                   CCTT GCTG     GCTTTTCTT
                                   |||| ||||     |||||||||
                                   GGAA CGAC     CGAAAGGGA
                                     A   T_____
GAM1656  LOC148758 5'  TGAGAAGATGACACTTGAGCAG 79728       G   ACTG___     TTG
                 GG                CCTTGCT CAA      CTTTTC
                                   |||||||  |||      ||||||
                                   GGGACGA GTT      GAAGAG
                                      _  CACAGTA     T
GAM1656  LOC148918 5'  AGGAAAGGCCTGTAGAGGG    79816     G    AACT
                                   CCTT CTGCA    GCTTTTCTT
                                   |||| |||||    |||||||||
                                   GGGA GATGT    CGGAAAGGA
                                     _    C___
GAM1656  LOC149111 3'  TGGGAGAGGCCTGAGACGGAGA 79933     TG   CAAACT
                 GG                CCT  CTG     GCTTTTCTTG
                                   |||  |||     ||||||||||
                                   GGA  GGC     CGGAGAGGGT
                                     GA   AGAGTC
GAM1656  LOC149113 3'  CGAGGAGGGTGGATCACGAGG  79908      C  CAAA TG
                                   CCTTG TG    C  CTTTTCTTG
                                   ||||| ||    |  |||||||||
                                   GGAGC AC    G  GGGAGGAGC
                                     _  TA__ GT
GAM1656  LOC149182 5'  CAGGAAAGGCAGGCATGGGGGA 85532      G  G  AA_
                 AGG                 CCTT CT CA   CTGCTTTTCTTG
                                   |||| || ||   ||||||||||||
                                   GGAA GG GT   GACGGAAAGGAC
                                     G  G  ACG
GAM1656  LOC149194 3'  CAAGGAAAGTGGGGCTACCGAG 79980      CT_  AAA TG
                 G                 CCTTG   GC   C  CTTTTCTTG
                                   |||||   ||   |  |||||||||
                                   GGAGC   CG   G  GAAAGGAAC
                                     CAT  G__ GT
GAM1656  LOC149271 3'  CAGGAGGCAGAGTTTGCAGTGA 80000    TG       G  _
                 G                 CT  CTGCAAACT CT TTTCTTG
                                   ||  |||||||||  || |||||||
                                   GA  GACGTTTGA GA GGAGGAC
                                    GT        _  C
GAM1656  LOC149302 5'  TGAGGAGAGTAACTTTGGTCAG 80044      CTG   C_
                 GG                CCTTG   CAAA  TGCTTTTCTTG
                                   |||||   ||||  ||||||||||
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                                GGGAC  GTTT  ATGAGAGGAGT
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GAM1656  LOC149319 3'  TGAGAGAGGCATGGGGAAGG  80079     G  G  AAC
                                CCTT CT CA   TGCTTTTCTTG
                                |||| || ||   ||||||||||
                                GGAA GG GT   ACGGAGAGAGT
                                  _  G  ___
GAM1656  LOC149373 3'  TGAGAAGGGTGGAAGGTGCAGG 80094      T  AAA TG
                                CTTGC GC   C  CTTTTCTTG
                                |||||  ||   |  |||||||||
                                GGACG TG   G  GGGAAGAGT
                                  _  GAA GT
GAM1656  LOC149579 3'  AGGAACAGCTGAGTGAGG    71687     TG  G  AACT   T    G
                                CCT  CT CA    GCT TTCTT
                                |||  || ||    ||| |||||
                                GGA  GA GT    CGA AAGGA
                                  GT  _  _____   C
GAM1656  LOC149606 3'  CAGGGAGAGAAAAAGCAGGTAG 80257       _   AAACTG
            GG                    CCTTGC TGC     CTTTTCTTG
                                |||||| |||     |||||||||
                                GGGATG ACG     GAGAGGGAC
                                  G   AAAAA_
GAM1656  LOC149672 5'  GAGAATCGCTTGAAGTAGGG   80338       G   ACT  TT    G
                                CCTTGCT CAA   GC  TTCTT
                                ||||||| |||   ||  |||||
                                GGGATGA GTT   CG  AAGAG
                                    A   ___  CT
GAM1656  LOC149773 5'  TGGGAGGAGAAACGCGGCAGG  80293        AAACTG
                                CTTGCTGC     CTTTTCTTG
                                ||||||||     |||||||||
                                GGACGGCG     GAGGAGGGT
                                    CAAA__
GAM1656  LOC149832 5'  CAGGAGAAGATGGTTGTGGGG  85861     TG T  AAACTG
                                CCT  C GC     CTTTTCTTG
                                |||  | ||     |||||||||
                                GGG  G TG     GAAGAGGAC
                                  GT T  GTA___
GAM1656  LOC149832 5'  GGGGAGGGGGTTGTGGTAAGG  85867       TG   A  G   TT  TG
                                CCTTGC  CAA CT CTT  CT
                                ||||||  ||| || |||  ||
                                GGAATG  GTT GG GGA  GG
                                  GT   _  G   GG  C
GAM1656  LOC149992 5'  GGGAAGGGCGAGCAGCGGG   80378        AAAC        G
                                CTTGCTGC   TGCTTTTCTT
                                ||||||||   ||||||||||
                                GGGCGACG   GCGGGAAGGG
                                    A___
GAM1656  LOC149995 3'  AGGAAGGGGGAGTAGGAGGG  85980     G   AAA  G
                                CCTT CTGC   CT CTTTTCT
                                |||| ||||   || |||||||
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                                GGGA GATG   GG GGAAGGA
                                  G   A__  G
GAM1656  LOC149995 5'  CGGGGGCTAAGCTTGTGGTGGG 85983    TG TG   A __     CTTG
             G                    CCT  C  CAA CT  GCTTTT
                                  ||| |  ||| ||  ||||||
                                  GGG  G  GTT GA  CGGGGG
                                    GT GT   C  AT     C
GAM1656  LOC150095 5'  AGGGAAAGGGAGGCAGGG    85989       GCAAACTG
                                  CCTTGCT       CTTTTCTT
                                  |||||||       ||||||||
                                  GGGACGG       GAAAGGGA
                                     AGG_____
GAM1656  LOC150197 3'  CAGGAAGAGCCAGGCAGGGTGG 80419    TG_   AAACT
             G                    CCT   CTGC    GCTTTTCTTG
                                  |||   ||||    ||||||||||
                                  GGG   GACG    CGAGAAGGAC
                                    TGG    GAC__
GAM1656  LOC150208 3'  GGGAAGGACCTGCGGTACAGG  86077    _     AACTG
                                  CCT TGCTGCA    CTTTTCT
                                  ||| |||||||    |||||||
                                  GGA ATGGCGT    GGAAGGG
                                    C      CCA__
GAM1656  LOC150271 3'  TAAGACTTGGTTTCTGGTGAGG 86146    TG   C     CTTT
                                  CCT  CTG AAACTG    TCTTG
                                  |||  ||| ||||||    |||||
                                  GGA  GGT TTTGGT    AGAAT
                                    GT   C     TC__
GAM1656  LOC150271 3'  TGGGAGGGGCAGCCAGAGGG   86149     G   CAAA
                                  CCTT CTG    CTGCTTTTCTTG
                                  |||| |||    ||||||||||||
                                  GGGA GAC    GACGGGGAGGGT
                                    _   C___
GAM1656  LOC150280 3'  TAAGGAAAGCGGGTCAATAGGG 80524      C  CAAA
                                  CCTTG TG    CTGCTTTTCTTG
                                  ||||| ||    ||||||||||||
                                  GGGAT AC    GGCGAAAGGAAT
                                     A  TG__
GAM1656  LOC150295 5'  AGGAGAGGAGTTGTTGTGAGG  86153    TG T    A  G
                                  CCT  C GCAA CT CTTTTCT
                                  |||  | |||| || |||||||
                                  GGA  G TGTT GA GAGAGGA
                                    GT T    _  G
GAM1656  LOC150358 3'  CGGGAGGCAGAGTTTGCAGTGA 86095    TG        __    TT TTG
             G                    CT  CTGCAAACT  GCTT  C
                                  ||  |||||||||  ||||  |
                                  GA  GACGTTTGA  CGGA  G
                                    GT        GA    GG C
GAM1656  LOC150368 3'  TGAGAGGGGTGGGAAGATTGGG 80518    TG_  GCAAA TG
                                  CCT   CT    C  CTTTTCTTG
                                  |||   ||    |  |||||||||
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                                GGG  GA    G  GGGGAGAGT
                                  TTA  AG___ GT
GAM1656  LOC150596 3'  AGGGAAGGAAGTTTGGCAGGG  80748       TG     G      G
                                CCTTGC  CAAACT CTTTTCTT
                                ||||||  |||||| ||||||||
                                GGGACG  GTTTGA GGAAGGGA
                                   __     A
GAM1656  LOC150776 3'  CAAGAAAGGAAGGCAGTTGGG  63921     T    AAACTG
                                CCT GCTGC     CTTTTCTTG
                                ||| |||||     |||||||||
                                GGG TGACG     GGAAAGAAC
                                  T    GAA___
GAM1656  LOC150889 3'  CGGGAGGCAGACTTTGCAGTGA 80814    TG     __     TT TTG
            G                    CT  CTGCAAA  CTGCTT  C
                                ||  |||||||  ||||||  |
                                GA  GACGTTT  GACGGA  G
                                 GT      CA     GG C
GAM1656  LOC150933 5'  GAGGAGGGGTGGCAGAGG    86337    TG   AA   G
                                CCT  CTGC  ACT CTTTTC
                                |||  ||||  ||| ||||||
                                GGA  GACG  TGG GAGGAG
                                  __   G_  G
GAM1656  LOC151005 5'  GGGAAGGGCGAGCAGCGGG   80897       AAAC       G
                                CTTGCTGC   TGCTTTTCTT
                                ||||||||   ||||||||||
                                GGGCGACG   GCGGGAAGGG
                                    A___
GAM1656  LOC151124 5'  GGGGTGTCTGCAGCAAGG    86418         A  T
                                CCTTGCTGCA AC GCTTT
                                |||||||||| || |||||
                                GGAACGACGT TG TGGGG
                                     C  _
GAM1656  LOC151124 5'  TAGGGAGGGCGGGGGTTGTGGT 86420    TG TG   A__
            GAG                   CT  C  CAA   CTGCTTTTCTTG
                                ||  |  |||   ||||||||||||
                                GA  G  GTT   GGCGGGAGGGAT
                                 GT GT   GGG
GAM1656  LOC151178 5'  CAGGGAAAGTGGGGAGGAGGG  80954     G  GCAAA TG
                                CCTT CT    C  CTTTTCTTG
                                |||| ||    |  |||||||||
                                GGGA GA    G  GAAAGGGAC
                                  G  GG___ GT
GAM1656  LOC151188 5'  CGGGGAAGGCGAAAGGAGGG   80962     G  GCAAAC
                                CCTT CT     TGCTTTTCTTG
                                |||| ||     ||||||||||
                                GGGA GA     GCGGAAGGGGC
                                  G  AA____
GAM1656  LOC151188 5'  GGGAGGGAAGTTGTAGTACGG  80963    T      A  G      TG
                                CC TGCTGCAA CT CTTTTCT
                                || |||||||| || |||||||
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                                GG ATGATGTT GA GGGAGGG
                                 C       _ A      C
GAM1656  LOC151304 3'  CAGGGAGAGCTGACCATTGAGG 86498     GC  CAAACT
                                CCTT  TG     GCTTTTCTTG
                                ||||  ||     ||||||||||
                                GGAG  AC     CGAGAGGGAC
                                  TT  CAGT__
GAM1656  LOC151313 3'  GGGAAAGGCCCAGTGGCAGG   60907      TG AAACT       G
                                CTTGC  C    GCTTTTCTT
                                |||||  |    |||||||||
                                GGACG  G    CGGAAAGGG
                                   GT ACC__
GAM1656  LOC151446 3'  CAGGAGGGGGAGTTTGCAGTGA 86568    TG        G
              G                  CT  CTGCAAACT CTTTTCTTG
                                 ||  ||||||||| |||||||||
                                 GA  GACGTTTGA GGGGAGGAC
                                  GT        G
GAM1656  LOC151610 3'  CAGGAAATCCTTGCAGCAGGG  81091          ACTGCT
                                CCTTGCTGCAA     TTTCTTG
                                ||||||||||      |||||||
                                GGGACGACGTT     AAAGGAC
                                      CCT___
GAM1656  LOC152286 3'  CAGGGAGGGCGCAAAGCAGCAG 86803        AAAC
                                TTGCTGC    TGCTTTTCTTG
                                |||||||    ||||||||||
                                GACGACG    GCGGGAGGGAC
                                    AAAC
GAM1656  LOC153027 5'  CAGGAGGAGGTGGTGGCGGCG  68029       AA  TG   _
                                TGCTGC  AC  CTTT TCTTG
                                ||||||  ||  |||| |||||
                                GCGGCG  TG  GGAG AGGAC
                                   G_  GT   G
GAM1656  LOC153027 5'  TGAGGAAAGCAGGAGGAGGTGG 68032    _ TG TG AAA___
              TGGCGG                CC T  C  C     CTGCTTTTCTTG
                                || |  | |     ||||||||||||
                                GG G  G  G     GACGAAAGGAGT
                                 C GT GT GAGGAG
GAM1656  LOC153146 3'  TAAGAAAGGTGGCTGGGCACAA 87147      C   AAA_ TG
              GG                  CCTTG TGC    C  CTTTTCTTG
                                |||||  |||    |  |||||||||
                                GGAAC ACG    G  GGAAAGAAT
                                   _   GGTC GT
GAM1656  LOC153196 3'  TGGGGAGAGTGGGGAGAGGGG  87174     TG  GCAAA TG
                                CCT  CT     C  CTTTTCTTG
                                |||  ||     |  |||||||||
                                GGG  GA     G  GAGAGGGGT
                                  GA  GG___ GT
GAM1656  LOC153277 3'  CAAGGAGTAGATTGTGTGTGGG 87186     TG _     A       CTTG
              G                  CCT  C TGCAA CTGCTTTT
                                 |||  | ||||| ||||||||
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                                GGG  G GTGTT GATGAGGA
                                  GT T    A       AC
GAM1656  LOC153642 3'  CGGGAGGCAGCAGTTGCAGTGA 81786    TG     A    _
              G                    CT  CTGCAA CTGCT TTTCTTG
                                   ||  |||||| ||||| |||||||
                                   GA  GACGTT GACGA GGAGGGC
                                    GT     _    C
GAM1656  LOC153642 3'  TGAGGAAAGCAGATCACAAGG  81795      C  CAAA
                                   CCTTG TG    CTGCTTTTCTTG
                                   |||||| ||   ||||||||||||
                                   GGAAC AC    GACGAAAGGAGT
                                      _ TA__
GAM1656  LOC154403 3'  CGAGGAGGGTGGATCACGAGG  81974      C  CAAA TG
                                   CCTTG TG    C  CTTTTCTTG
                                   |||||| ||   |  |||||||||
                                   GGAGC AC    G  GGGAGGAGC
                                      _ TA__ GT
GAM1656  LOC154739 5'  AGGAGGGAATGCAGGGAGG    87428     G    AACTG
                                   CCTT CTGCA     CTTTTCT
                                   |||| |||||     |||||||
                                   GGAG GACGT     GGGAGGA
                                     G    AA___
GAM1656  LOC154739 5'  TGGGAAGAGTGAGCCAGGCAAG 87449       __  AA   G   TT TTG
                                   CTTGCT  GC  ACT CTT  C
                                   ||||||  ||  ||| |||  |
                                   GAACGG  CG  TGA GAA  G
                                       AC  AG  _   GG T
GAM1656  LOC154739 5'  TGGGAAGGGCAAAAGAGTGGG  87450    TG  GCAAAC
                                   CT  CT     TGCTTTTCTTG
                                   ||  ||     ||||||||||||
                                   GG  GA     ACGGGAAGGGT
                                    GT  GAAA__
GAM1656  LOC154834 3'  CGGGAGGAGCAGCACGCAAG   87494      _  AAAC
                                   CTTGC TGC    TGCTTTTCTTG
                                   ||||| |||    ||||||||||||
                                   GAACG ACG    ACGAGGAGGGC
                                      C  _____
GAM1656  LOC154992 3'  CGAGGAGGGTGGATCACGAGG  82135      C  CAAA TG
                                   CCTTG TG    C  CTTTTCTTG
                                   |||||| ||   |  |||||||||
                                   GGAGC AC    G  GGGAGGAGC
                                      _ TA__ GT
GAM1656  LOC155064 5'  CGGGGAAGGTAGGACTGGAAGG 82177      G  GCAAA
                                   CCTT CT     CTGCTTTTCTTG
                                   |||| ||     ||||||||||||
                                   GGAA GG     GATGGAAGGGGC
                                     _ TCAG_
GAM1656  LOC155064 5'  CGGGGGGAGGGGGCGGCACGG  82178    T     AAA  G   TT
                                   CC TGCTGC   CT CTT  CTTG
                                   || ||||||   || |||  ||||
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                                GG ACGGCG   GG GAG  GGGC
                                 C     ___  G   GG
GAM1656  LOC155376 3'  AGGAAGAGGTTGCAGTGAG   82238    TG     ACTG      G
                                CT  CTGCAA    CTTTTCTT
                                ||  ||||||    ||||||||
                                GA  GACGTT    GAGAAGGA
                                 GT     G___
GAM1656  LOC157381 3'  GGGGAAGGTATACTGGGCAGGG 87734        G  AAC        G
                                CCTTGCT CA   TGCTTTTCTT
                                |||||||  ||   ||||||||||
                                GGGACGG GT   ATGGAAGGGG
                                    _  CAT
GAM1656  LOC157624 5'  TGGGAGGAGTCCACCCTCTAGT 87793     TG   CAAACT__
              GGGG                  CCT  CTG       GCTTTTCTTG
                                |||  |||       ||||||||||
                                GGG  GAT       TGAGGAGGGT
                                  GT   CTCCCACC
GAM1656  LOC157657 3'  CAAGGGAAGTAAACAGCAAG   82431        CAAAC     TT
                                CTTGCTG     TGCTT  CTTG
                                |||||||     |||||  ||||
                                GAACGAC     ATGAA  GAAC
                                    AA___     GG
GAM1656  LOC157848 3'  AGGGAGAGGGGAGGCGGGG    82515        GCAAA  G
                                CCTTGCT     CT CTTTTCTT
                                |||||||     || ||||||||
                                GGGGCGG     GG GAGAGGGA
                                    A_____  G
GAM1656  LOC157922 5'  CAGGAGAGGTCTGTGGTGGG   87925    TG TG  AACT
                                CT  C  CA    GCTTTTCTTG
                                ||  |  ||    ||||||||||
                                GG  G  GT    TGGAGAGGAC
                                 GT GT  C___
GAM1656  LOC158055 3'  CGAGGGAGGCTGAGCGGTTGAG 82581       _    AAACT    TT
              G                  CCTTG CTGC     GCTT  CTTG
                                |||||  ||||     ||||  ||||
                                GGAGT GGCG     CGGA  GAGC
                                   T    AGT__    GG
GAM1656  LOC158301 3'  AGATCCTCAGTTTGCAGAAGG  82750      G        CTTT
                                CCTT CTGCAAACTG    TCT
                                ||||  ||||||||||    |||
                                GGAA GACGTTTGAC    AGA
                                   _         TCCT
GAM1656  LOC158373 5'  CAAGGAGAGTTCAATCGGTAGC 71597        AAACT__
              G                   TGCTGC       GCTTTTCTTG
                                ||||||       ||||||||||
                                GCGATG       TGAGAGGAAC
                                    GCTAACT
GAM1656  LOC158382 5'  GAGAGAGGAAGCAACGGGG    88125       C   AAACTG
                                CCTTG TGC     CTTTTCTT
                                |||||  |||     ||||||||
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                                GGGGC ACG     GGAGAGAG
                                  A  AA____
GAM1656  LOC158382 5'  GAGGATCGCTTGAGGCAAGG  88126       G  ACT  TT    G
                                CCTTGCT CAA  GC  TTCTT
                                ||||||| |||  ||  |||||
                                GGAACGG GTT  CG  AGGAG
                                   A  ___  CT
GAM1656  LOC158401 5'  AGGAAGAGATGCAGGAGG   82804     G    AACTG
                                CCTT CTGCA    CTTTTCTT
                                |||| |||||    ||||||||
                                GGAG GACGT    GAGAAGGA
                                  _    A____
GAM1656  LOC158490 3'  GAGAAGAAGCTGTGGGAAGG  82823     G TG  AA  G
                                CCTT C  CA  CT CTTTTC
                                |||| |  ||  || ||||||
                                GGAA G  GT  GA GAAGAG
                                  G GT  C_  A
GAM1656  LOC158572 3'  CGGGGGAGGGGGGCAGCAGG  82849       AAA  G   TT
                                CTTGCTGC   CT CTT  CTTG
                                ||||||||   || |||  ||||
                                GGACGACG   GG GGA  GGGC
                                    ___  G   GG
GAM1656  LOC158947 5'  AGCACTGTTTGCGGCGAGG   82929          __
                                CCTTGCTGCAAAC  TGCT
                                ||||||||||||  ||||
                                GGAGCGGCGTTTG  ACGA
                                       TC
GAM1656  LOC158956 5'  CGGGAGGAGTGGCAGCGGCCAG 67212    T    AAA TG
            G                   CCT GCTGC   C  CTTTTCTTG
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                                GGA CGGCG   G  GAGGAGGGC
                                  C    AC_ GT
GAM1656  LOC159036 3'  CAAGGGAAGTTTGATGGCAGG  88343       _  ACT   TT
                                CTTGCTG CAA   GCTT  CTTG
                                ||||||| |||   ||||  ||||
                                GGACGGT GTT   TGAA  GAAC
                                   A  ___    GG
GAM1656  LOC159110 3'  CAGGAGGCAGAGTTTGCAGTGA 82984    TG       G  _
            G                   CT  CTGCAAACT CT TTTCTTG
                                ||  ||||||||| || |||||||
                                GA  GACGTTTGA GA GGAGGAC
                                 GT        _  C
GAM1656  LOC159116 3'  CAGGAGGCAGAGTTTGCAGTGA 82967    TG       G  _
            G                   CT  CTGCAAACT CT TTTCTTG
                                ||  ||||||||| || |||||||
                                GA  GACGTTTGA GA GGAGGAC
                                 GT        _  C
GAM1656  LOC162545 3'  TGAGAGGGGCAGGAAGTGGGG  88506    TG  GCAAA
                                CCT  CT    CTGCTTTTCTTG
                                |||  ||    ||||||||||||
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                                GGG  GA    GACGGGGAGAGT
                                  GT  AG___
GAM1656  LOC162762 5'  TGAGAGAAGCGGTGTCTGTGAG 83252    TG TGCAA
                 G                 CCT  C    ACTGCTTTTCTTG
                                   |||  |    ||||||||||||
                                   GGA  G    TGGCGAAGAGAGT
                                     GT TCTG_
GAM1656  LOC163126 5'  CAGGGAAAGCCCGGCGGCGGCG 83317    _     AAACT
                 G                 CC TTGCTGC    GCTTTTCTTG
                                   ||  |||||||    ||||||||||
                                   GG GGCGGCG    CGAAAGGGAC
                                    C      GCC__
GAM1656  LOC163126 5'  CAGGGAAGGTCGGATGGCGGCG 83318      AAA  _
                                   TGCTGC   CTG CTTTTCTTG
                                   ||||||   ||| |||||||||
                                   GCGGCG   GGC GGAAGGGAC
                                      GTA   T
GAM1656  LOC163126 5'  CGGGGAAGGCGCGATGGCGGCG 83320      AAAC_
                                   TGCTGC    TGCTTTTCTTG
                                   ||||||    ||||||||||
                                   GCGGCG    GCGGAAGGGGC
                                      GTAGC
GAM1656  LOC163688 3'  CGGGGGAGGCCTGCCCGGGAAG 57749     G   CAAACT   TT
                 G                 CCTT CTG     GCTT  CTTG
                                   |||| |||     ||||  ||||
                                   GGAA GGC     CGGA  GGGC
                                     G   CCGTC_   GG
GAM1656  LOC164390 5'  CAGGAAGAGTTCGACACAGCGA 83400      CAAACT
                                   TTGCTG     GCTTTTCTTG
                                   ||||||     ||||||||||
                                   AGCGAC     TGAGAAGGAC
                                      ACAGCT
GAM1656  LOC164695 5'  CAGGGAAGGTTACTGTGCAGGG 83429      T   AACT
                                   CCTTGC GCA    GCTTTTCTTG
                                   ||||||  |||   ||||||||||
                                   GGGACG TGT    TGGAAGGGAC
                                      _   CAT_
GAM1656  LOC165476 5'  AGGGAGAGAGGCACAAGG    88549      C   AAACTG
                                   CCTTG TGC     CTTTTCTT
                                   |||||  |||     ||||||||
                                   GGAAC ACG     GAGAGGGA
                                     _   GA____
GAM1656  LOC165519 5'  TAGGAGAGGTCAGGTCAGTGG  83377   TG   CAAA  _
                                   T  CTG    CTG CTTTTCTTG
                                   |  |||    ||| |||||||||
                                   G  GAC    GAC GGAGAGGAT
                                    GT   TG__   T
GAM1656  LOC166042 5'  GGGAAAGGTTTGTAGAGAGG   83506    TG      TG
                                   CCT  CTGCAAAC  CTTTTCT
                                   |||  ||||||||  |||||||
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                                GGA  GATGTTTG  GAAAGGG
                                  GA       __
GAM1656  LOC166867 5'  CGGGAAGAGCGCAGCCAGCCGG 83553     T    CAAAC
                 G                 CCT GCTG     TGCTTTTCTTG
                                   ||| ||||     ||||||||||
                                   GGG CGAC     GCGAGAAGGGC
                                     C    CGAC_
GAM1656  LOC170393 5'  GGGAAGGGAGGCAGGAGG    83734      G    AAA  G
                                   CCTT CTGC   CT CTTTTCT
                                   |||| ||||   || |||||||
                                   GGAG GACG   GA GGAAGGG
                                     _    ___  G
GAM1656  LOC170394 5'  CAGGAGGAGCAAGAGGGAGAGG 83735      G_  GCAAAC
                                   CCTT  CT     TGCTTTTCTTG
                                   ||||  ||     ||||||||||
                                   GGAG  GG     ACGAGGAGGAC
                                     AG  AGA___
GAM1656  LOC196510 3'  AGGAAGAGTAGGACTGGGG    89090    G  AA_
                                   CT CA   CTGCTTTTCTT
                                   || ||   ||||||||||
                                   GG GT   GATGAGAAGGA
                                    G  CAG
GAM1656  LOC196510 3'  CAAGGGAAGCAAGTGGGTGTGA 89091     TG T  AA  _   TT
                 GG                  CCT  C GC  ACT GCTT  CTTG
                                     |||  | ||  ||| ||||  ||||
                                     GGA  G TG  TGA CGAA  GAAC
                                       GT _  GG   A    GG
GAM1656  LOC196759 5'  AAGAAAGGCACCTGCAAGG    88905       TGCAAAC
                                   CCTTGC      TGCTTTTCTT
                                   ||||||      ||||||||||
                                   GGAACG      ACGGAAAGAA
                                      TCC____
GAM1656  LOC196759 3'  CAAGAGGGAGGTTGAGGTGGGG 88909     TG  GCA   GC
                                   CCT  CT   AACT  TTTTCTTG
                                   |||  ||   ||||  ||||||||
                                   GGG  GG   TTGG  GGGAGAAC
                                     GT  AG_   A_
GAM1656  LOC196955 5'  TAGGAGAAGGAATCTGAGCAGG 77873        G  AACTG
                 G                 CCTTGCT CA     CTTTTCTTG
                                   ||||||| ||     |||||||||
                                   GGGACGA GT     GAAGAGGAT
                                      _  CTAAG
GAM1656  LOC197085 5'  CAGGAGAGGCTGCTGGAGAGG  89220     TG  _   AACT
                                   CCT  CT GCA    GCTTTTCTTG
                                   |||  || |||    ||||||||||
                                   GGA  GG CGT    CGGAGAGGAC
                                     GA  T  _____
GAM1656  LOC197115 5'  CAGGAGAGGCTGCTGGAGAGG  89225     TG  _   AACT
                                   CCT  CT GCA    GCTTTTCTTG
                                   |||  || |||    ||||||||||
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                                GGA  GG CGT    CGGAGAGGAC
                                  GA  T  ____
GAM1656  LOC197125 3'  CAAGGAGGGCAGAATAGGCAGA 89240     _   GCAAA
              GG                   CCT TGCT    CTGCTTTTCTTG
                                |||  ||||    ||||||||||||
                                GGA ACGG    GACGGGAGGAAC
                                  G   ATAA_
GAM1656  LOC197259 5'  AGGAAAGGGGGCGCAGGG    89298       T  AAA  G
                                CCTTGC GC   CT CTTTTCT
                                |||||| ||   || |||||||
                                GGGACG CG   GG GAAAGGA
                                   _ ___  G
GAM1656  LOC197285 3'  AGGAGGAGCTGTGGGGAGG   89151     G TG  AACT
                                CCTT C  CA   GCTTTTCTT
                                ||||  |  ||   |||||||||
                                GGAG G  GT   CGAGGAGGA
                                  G GT  ____
GAM1656  LOC197285 3'  TGGGAGAAGCTTCTAGAAGG   89155     G   CAAACT
                                CCTT CTG     GCTTTTCTTG
                                |||| |||     ||||||||||
                                GGAA GAT     CGAAGAGGGT
                                  _   CTT___
GAM1656  LOC199224 3'  CAGGGAGGGCCAGCCCAGCAGG 90405         CAAA  _
              G                   CCTTGCTG    CTG CTTTTCTTG
                                ||||||||    ||| |||||||||
                                GGGACGAC    GAC GGGAGGGAC
                                    CC__   C
GAM1656  LOC199799 3'  AAGAAGGGCCAGGGTGAGG    79251     TG  GCAAA  _
                                CCT  CT    CTG CTTTTCTT
                                |||  ||    ||| ||||||||
                                GGA  GG    GAC GGGAAGAA
                                  GT  ______   C
GAM1656  LOC199864 5'  AAGAAAGGCACCTGCAAGG    91455       TGCAAAC
                                CCTTGC      TGCTTTTCTT
                                ||||||      ||||||||||
                                GGAACG      ACGGAAAGAA
                                   TCC_____
GAM1656  LOC199886 3'  GGGAAGGCACTGTGGGAAGG   89825      G TG  AAC
                                CCTT C  CA   TGCTTTTCT
                                ||||  |  ||   |||||||||
                                GGAA G  GT   ACGGAAGGG
                                  G GT  C__
GAM1656  LOC199923 3'  CGAGAAAGGCGCCCTGGGGAAG 89870      G  G  AAC
              G                   CCTT CT CA   TGCTTTTCTTG
                                ||||  ||  ||   ||||||||||
                                GGAA GG GT   GCGGAAAGAGC
                                  _  G  CCC
GAM1656  LOC200220 3'  AGGAAGAGTAGGACTGGGG   90032    G  AA_
                                CT CA   CTGCTTTTCTT
                                ||  ||   ||||||||||
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                                GG GT   GATGAGAAGGA
                                 G  CAG
GAM1656  LOC200220 3'  CAAGGGAAGCAAGTGGGTGTGA 90034     TG T  AA   _    TT
              GG                  CCT  C GC  ACT GCTT  CTTG
                                  |||  | ||  ||| ||||  ||||
                                  GGA  G TG  TGA CGAA  GAAC
                                    GT _  GG   A    GG
GAM1656  LOC200317 3'  CAGGAGGCGGAGTTTGCAGTGA 90221     TG        G  _
              G                   CT  CTGCAAACT CT TTTCTTG
                                  ||  |||||||||| || |||||||
                                  GA  GACGTTTGA GG GGAGGAC
                                   GT         _  C
GAM1656  LOC200317 3'  CAGTGGGGCAGTTAGTGGTGGG 90222     TG TG A       TT  TG
              G                   CCT  C  C AACTGCTT  CT
                                  |||  |  | ||||||||  ||
                                  GGG  G  G TTGACGGG  GA
                                    GT GT A       GT  C
GAM1656  LOC200803 3'  GGGAGGGTGATGCAGGAGG    90299      G     AAC
                                  CCTT CTGCA   TGCTTTTCT
                                  |||| |||||   |||||||||
                                  GGAG GACGT   GTGGGAGGG
                                    _     A__
GAM1656  LOC200933 5'  AAGATTGGTTTCAGTGAGG    91788     TG   C    GCTTT
                                  CCT  CTG AAACT     TCTT
                                  |||  ||| |||||     ||||
                                  GGA  GAC TTTGG     AGAA
                                    GT   _     TT___
GAM1656  LOC200942 3'  TGAGAGAGGCATGGGGGTGAG  90381    TG  GCAAAC
                                  CT  CT     TGCTTTTCTTG
                                  ||  ||     ||||||||||
                                  GA  GG     ACGGAGAGAGT
                                   GT  GGGT__
GAM1656  LOC201158 3'  GAGGAAGGATGCGGTGAG    61086    TG    AACTG
                                  CT  CTGCA    CTTTTCTT
                                  ||  |||||    ||||||||
                                  GA  GGCGT    GGAAGGAG
                                   GT    A____
GAM1656  LOC201294 3'  GGGAGGAGCTGGGGTGGGG    89589     TG  G  AACT
                                  CCT  CT CA    GCTTTTCTT
                                  |||  || ||   |||||||||
                                  GGG  GG GT    CGAGGAGGG
                                    GT  G  ____
GAM1656  LOC201514 5'  CGGGGAGAGCTTCCCGGGAAGG 89634      G   CAAACT
                                  CCTT CTG     GCTTTTCTTG
                                  |||| |||     ||||||||||
                                  GGAA GGC     CGAGAGGGGC
                                    G   CCTT__
GAM1656  LOC201514 3'  TAAGGAGAGTGGCCGTGAG    89635    TG T  AAAC
                                  CT  C GC    TGCTTTTCTTG
                                  ||  | ||    ||||||||||
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                                GA  G CG    GTGAGAGGAAT
                                 GT C  ____
GAM1656  LOC201617 5'  CAAGGGAGGCACTAGCAAG   91822       CAAAC    TT
                                CTTGCTG    TGCTT  CTTG
                                |||||||    |||||  ||||
                                GAACGAT    ACGGA  GAAC
                                    C____    GG
GAM1656  LOC201868 3'  CGAGGAGGGTGGATCATGAGG  90522      C  CAAA TG
                                CCTTG TG    C  CTTTTCTTG
                                ||||| ||    |  |||||||||
                                GGAGT AC    G  GGGAGGAGC
                                   _  TA__ GT
GAM1656  LOC202134 3'  CAAGAAAAGTAACAGGCAAGG  91916       GCAAAC
                                CCTTGCT     TGCTTTTCTTG
                                |||||||     ||||||||||
                                GGAACGG     ATGAAAAGAAC
                                    ACA___
GAM1656  LOC202309 3'  GAGGGAGGACAGTGGAAGG    91941     G  GCAA   _   TT
                                CCTT CT    ACTG CTT  CTT
                                |||| ||    |||| |||  |||
                                GGAA GG    TGAC GGA  GAG
                                  _ ____    A   GG
GAM1656  LOC203246 3'  TGGGGAAGGTTGGCTGCCAAGG 90839      _ T  AAACT
                                CCTTG C GC     GCTTTTCTTG
                                ||||| | ||    ||||||||||
                                GGAAC G CG     TGGAAGGGGT
                                   C T  GT___
GAM1656  LOC203397 3'  GGGAGGAGCAGCGAAAGG    90901     GC   AAAC
                                CCTT  TGC    TGCTTTTCTT
                                ||||  |||    ||||||||||
                                GGAA  GCG    ACGAGGAGGG
                                  A_  ____
GAM1656  LOC204823 3'  TGGGAAGGGCTACATTAGTAAG 91061       CAAACT
                                CTTGCTG     GCTTTTCTTG
                                |||||||     ||||||||||
                                GAATGAT     CGGGAAGGGT
                                    TACAT_
GAM1656  LOC204845 5'  CAGGAAAGGGTAAGGGCGCAGG 91062       T  AAACTG
            G                    CCTTGC GC     CTTTTCTTG
                                ||||||  ||     |||||||||
                                GGGACG CG     GGAAAGGAC
                                   _  GGAATG
GAM1656  LOC205418 3'  CAGGAGGAGCTGACCCGGCTGG 92368     T    CAAACT
            G                    CCT GCTG     GCTTTTCTTG
                                |||  ||||     ||||||||||
                                GGG CGGC     CGAGGAGGAC
                                  T   CCAGT_
GAM1656  LOC219287 5'  TGGGAAAGGCATGAAGATGCAG 95218       TGCAAAC
            GG                    CCTTGC      TGCTTTTCTTG
                                ||||||      ||||||||||
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                                GGGACG      ACGGAAAGGGT
                                   TAGAAGT
GAM1656  LOC219347 5'  CAAGAAGAGTAGCCCAGGAGGG 94572      G   CAAA
                                CCTT CTG    CTGCTTTTCTTG
                                |||| |||    ||||||||||||
                                GGGA GAC    GATGAGAAGAAC
                                  G   CC__
GAM1656  LOC219401 5'  CAAGAGGGCAGCTGGTAGCAGG 94384          AAA      T
            G                    CCTTGCTGC   CTGCTTT CTTG
                                |||||||||   ||||||| ||||
                                GGGACGATG   GACGGGA GAAC
                                     GTC      _
GAM1656  LOC219654 5'  GGGGGAGGCGGCGGCAGCG    92938       AAA     TT
                                TGCTGC   CTGCTT  CTT
                                ||||||   ||||||  |||
                                GCGACG   GGCGGA  GGG
                                   GC_     GG
GAM1656  LOC219722 5'  TGGGAGGCAGAGGTTGCAGTGA 94689     TG     A__     TT TTG
            GG                   CCT  CTGCAA   CTGCTT  C
                                |||  ||||||   ||||||  |
                                GGA  GACGTT   GACGGA  G
                                  GT     GGA     GG T
GAM1656  LOC219800 5'  AAGAAAGGCAAGGCTGGG     94889     T   GCAAAC
                                CCT GCT      TGCTTTTCTT
                                ||| |||      ||||||||||
                                GGG CGG      ACGGAAAGAA
                                  T   A_____
GAM1656  LOC219842 3'  AGGAGCCCTGTGCAGCAGGG   94890          AACT
                                CCTTGCTGCA    GCTTTT
                                ||||||||||    ||||||
                                GGGACGACGT    CGAGGA
                                     GTCC
GAM1656  LOC219842 3'  GGGAGAAGTAAGGGCCAGG    94892     T   GCAAAC
                                CCT GCT      TGCTTTTCTT
                                ||| |||      ||||||||||
                                GGA CGG      ATGAAGAGGG
                                  C   GA____
GAM1656  LOC219848 3'  GGGAGAAGCAGGCTGGGG     93126    G  AA
                                CT CA  CTGCTTTTCTT
                                || ||  ||||||||||||
                                GG GT  GACGAAGAGGG
                                 G  CG
GAM1656  LOC219855 3'  TGGGGAGAGTAGAAAGAGGG   93144      G  GCAAA
                                CCTT CT     CTGCTTTTCTTG
                                |||| ||     ||||||||||||
                                GGGA GA     GATGAGAGGGGT
                                  _  AA___
GAM1656  LOC219917 3'  CGAGAAGAAGCTGCGGGAAGG  93165      G     AACT     _
                                CCTT CTGCA    GCTTTT CTTG
                                |||| |||||    |||||| ||||
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                                GGAA GGCGT    CGAAGA GAGC
                                  G    ____     A
GAM1656  LOC220020 3'  AAGAAAGGCCTAGGAAGG    95041      G   CAAACT
                                CCTT CTG     GCTTTTCTT
                                |||| |||     |||||||||
                                GGAA GAT     CGGAAAGAA
                                  G  C_____
GAM1656  LOC220370 3'  CAAGGGTGCTGTGCAGCAAGG  94394          AACT  TT
                                CCTTGCTGCA   GC  TTCTTG
                                ||||||||||   ||  ||||||
                                GGAACGACGT   CG  GGGAAC
                                      GT__  T_
GAM1656  LOC220537 3'  TGGGGAAGGCAGGGAGGGCAGG 92428        GCAAA
                                CTTGCT    CTGCTTTTCTTG
                                ||||||    ||||||||||||
                                GGACGG    GACGGAAGGGGT
                                   GAGG_
GAM1656  LOC220766 3'  TAGGAAAAAGCAGATTGTGGCA 92475      TG   A      _
             G                   TTGC  CAA CTGCTTTT CTTG
                                ||||  ||| |||||||| ||||
                                GACG  GTT GACGAAAA GGAT
                                  GT   A       A
GAM1656  LOC221218 3'  TGGGGAAGGCCAAGTGGGAGG  93419      G TG AAACT
                                CCTT C  C    GCTTTTCTTG
                                |||| |  |    ||||||||||
                                GGAG G  G    CGGAAGGGGT
                                  _ GT AAC__
GAM1656  LOC221300 3'  TGGGAAGGGTAGTTTCAAGAGG 93580      GC  C
                                CCTT  TG AAACTGCTTTTCTTG
                                ||||  || ||||||||||||||||
                                GGAG  AC TTTGATGGGAAGGGT
                                  A_  _
GAM1656  LOC221354 3'  CAAGACATGTTTGCAGTAA   94011          _  CTTT
                                TTGCTGCAAAC TG   TCTTG
                                |||||||||| ||   |||||
                                AATGACGTTTG AC   AGAAC
                                      T  ____
GAM1656  LOC221421 3'  GAGAAGAGCTGATGTAAGG   93891       TGCAAACT
                                CCTTGC       GCTTTTCTT
                                ||||||       |||||||||
                                GGAATG       CGAGAAGAG
                                   TAGT____
GAM1656  LOC221424 5'  CGGGGGGAGCCGGGCGGCAG   95272        AAACT   TT
                                TTGCTGC    GCTT  CTTG
                                |||||||    ||||  ||||
                                GACGGCG    CGAG  GGGC
                                    GGC__   GG
GAM1656  LOC221474 3'  CAGGAGGAGGAGGTTGCAGTGA 93992    TG     A  G
             G                   CT  CTGCAA CT CTTTTCTTG
                                ||  |||||| || |||||||||
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                                GA  GACGTT GA GAGGAGGAC
                                 GT     G  G
GAM1656  LOC221476 3'  TGGGGGAGGCAGGGACGAGGGA 93898      G  GCAAA_     TT
              AGG                  CCTT CT     CTGCTT  CTTG
                                |||| ||     ||||||  ||||
                                GGAA GG     GACGGA  GGGT
                                  G  AGCAGG     GG
GAM1656  LOC221479 3'  CAAGAGAAGTGGTGTACAGG   93843      C   AA  TG
                                CTTG TGC  AC  CTTTTCTTG
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                                GGAC ATG  TG  GAAGAGAAC
                                  _  __  GT
GAM1656  LOC221496 5'  CGGGAGGAGGCCCGGCCGCGGG 93637       T  AAACTG
              G                   CCTTGC GC     CTTTTCTTG
                                ||||||  ||     |||||||||
                                GGGGCG CG     GAGGAGGGC
                                   C  GCCCG_
GAM1656  LOC221550 3'  TGGGAGGAGGAGGTTGCAGTGA 93749    TG     A  G
              G                   CT  CTGCAA CT CTTTTCTTG
                                ||  |||||| || |||||||||
                                GA  GACGTT GA GAGGAGGGT
                                 GT     G  G
GAM1656  LOC221749 3'  AGGAGTATTTGCAGAAGG    93647      G      C
                                CCTT CTGCAAA TGCTTTT
                                |||| ||||||| |||||||
                                GGAA GACGTTT ATGAGGA
                                  _      _
GAM1656  LOC221749 5'  CGAGGGAGGAGGCGCGGGG   93649       T  AAACTG   TT
                                CCTTGC GC     CTT  CTTG
                                ||||||  ||     |||  ||||
                                GGGGCG CG     GGA  GAGC
                                   _  GA____   GG
GAM1656  LOC221755 5'  GGGAAAGACTTGCATCGGGG   94009      C     ACTG
                                CCTTG TGCAA    CTTTTCT
                                ||||| |||||    |||||||
                                GGGGC ACGTT    GAAAGGG
                                   T     CA__
GAM1656  LOC221953 5'  GGGAGAGGAGGCGTGGGG    94458     TG T  AAA  G
                                CCT  C GC   CT CTTTTCT
                                |||  | ||   || |||||||
                                GGG  G CG   GA GAGAGGG
                                  GT _  ___  G
GAM1656  LOC222008 5'  TAGGGAGGGCAGTGATCACGCA 95658       _  CAA
              AG                  CTTGC TG   ACTGCTTTTCTTG
                                ||||| ||   ||||||||||||
                                GAACG AC   TGACGGGAGGGAT
                                  C  TAG
GAM1656  LOC222160 3'  TGGGAGGCAGAGTTTGCAGTGA 95796    TG       __    TT TTG
              G                   CT  CTGCAAACT  GCTT  C
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                                GA  GACGTTTGA  CGGA  G
                                 GT       GA    GG T
GAM1656  LOC222258 5'  CAGGAAGAGCAACGAAGGTGAA 96039     _  GCAAAC
              GG                  CCTT GCT     TGCTTTTCTTG
                                  |||| |||     ||||||||||
                                  GGAA TGG     ACGAGAAGGAC
                                    G   AAGCA_
GAM1656  LOC222865 3'  CAGGAGGGGTTCATTTGCGTGG 94441     TG T    CT_
              GG                  CCT  C GCAAA   GCTTTTCTTG
                                  |||  | |||||   ||||||||||
                                  GGG  G CGTTT   TGGGGAGGAC
                                    GT _    ACT
GAM1656  LOC245771 3'  GGGGGAGGATGCAGGAGG    94484     G    AA  G
                                  CCTT CTGCA  CT CTTT
                                  |||| |||||  || ||||
                                  GGAG GACGT  GA GGGG
                                    _    AG  G
GAM1656  LOC253128 3'  CGAGAAGAGCAGTCATTAGGAA 96576     G   CAA
              GG                  CCTT CTG   ACTGCTTTTCTTG
                                  |||| |||   ||||||||||||
                                  GGAA GAT   TGACGAGAAGAGC
                                    G   TAC
GAM1656  LOC253148 5'  CAAGAGGAGCAAGAGCAAGG   98665       GCAAAC
                                  CCTTGCT     TGCTTTTCTTG
                                  |||||||     ||||||||||
                                  GGAACGA     ACGAGGAGAAC
                                     GA____
GAM1656  LOC253258 3'  CGGGAGGAGCATGAAAGTGGAT 98228      _ TG AAAC_
              AAGG                  CCTTG C  C    TGCTTTTCTTG
                                  |||||  |  |    ||||||||||
                                  GGAAT G  G    ACGAGGAGGGC
                                    A GT AAAGT
GAM1656  LOC253264 5'  TGGGAAAGGCAGGAGGGGAGG  96339     G  GCAAA
                                  CCTT CT    CTGCTTTTCTTG
                                  |||| ||    ||||||||||
                                  GGAG GG    GACGGAAAGGGT
                                    G  AG___
GAM1656  LOC253358 5'  GGGGAAGGTGCTTGGAGG    98033     GCT  AAACT
                                  CCTT   GC    GCTTTTCTT
                                  ||||   ||    |||||||||
                                  GGAG   CG    TGGAAGGGG
                                    GTT  _____
GAM1656  LOC253405 5'  CAAGGGAACGGGTGTGGAAGG  99370     G TG  AA   C  TT
                                  CCTT C  CA  CTG TT  CTTG
                                  |||| |  ||  ||| ||  ||||
                                  GGAA G  GT  GGC AA  GAAC
                                    _ GT  G_   _  GG
GAM1656  LOC253532 3'  AGGAAGAGGTTGCAGTGAG   97727    TG     ACTG      G
                                  CT  CTGCAA    CTTTTCTT
                                  ||  ||||||    ||||||||
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                                GA  GACGTT    GAGAAGGA
                                 GT     G___
GAM1656  LOC253539 3'  CAGGAGAGGCACAAGAATAAGG 97698       CTGCAAAC
                                CCTTG       TGCTTTTCTTG
                                |||||       ||||||||||
                                GGAAT       ACGGAGAGGAC
                                   AAGAAC__
GAM1656  LOC253681 5'  CAGGGAAGGCGGCGCGGCCGGG 96837     T    AAA
                                CCT GCTGC   CTGCTTTTCTTG
                                ||| |||||   ||||||||||||
                                GGG CGGCG   GGCGGAAGGGAC
                                  C    C__
GAM1656  LOC253868 3'  GGGGGAGGTGCACGGCAGGG   97326        CAA  TG   TT
                                CCTTGCTG   AC  CTT  CT
                                ||||||||   ||  |||  ||
                                GGGACGGC   TG  GAG  GG
                                     ACG  __   GG
GAM1656  LOC253943 5'  GGGGAGAGGCCCAGGCAGCGGC 97847    _      AAACT       G
            GG                    CC TTGCTGC     GCTTTTCTT
                                || |||||||     |||||||||
                                GG GGCGACG     CGGAGAGGG
                                 C      GACC_       GC
GAM1656  LOC253946 5'  CGAGGAGGGTTGCTAGTGG    96975    TG  _   AACT
                                T  CT GCA    GCTTTTCTTG
                                |  || |||    ||||||||||
                                G  GA CGT    TGGGAGGAGC
                                 GT  T  _____
GAM1656  LOC253981 3'  TGGGGGAGGCCAGTTACAAGG  97541      CTGCA    _   TT
                                CCTTG     AACTG CTT  CTTG
                                |||||     ||||| |||  ||||
                                GGAAC     TTGAC GGA  GGGT
                                   A_____     C   GG
GAM1656  LOC253982 3'  GGGAGAGGCTGGGGCAGGG    96774        G  AACT
                                CCTTGCT CA    GCTTTTCTT
                                ||||||| ||    |||||||||
                                GGGACGG GT    CGGAGAGGG
                                     G  _____
GAM1656  LOC254158 5'  TGGGAAACTGTCTTTGCAGCGG 98051          CT  T_
                                TTGCTGCAAA  GC  TTTCTTG
                                ||||||||||  ||  |||||||
                                GGCGACGTTT  TG  AAAGGGT
                                      C_  TC
GAM1656  LOC254266 3'  CAGGAGGAGGAGCTTGCAGTGA 99195    TG     A  G
            G                    CT  CTGCAA CT CTTTTCTTG
                                ||  |||||| || |||||||||
                                GA  GACGTT GA GAGGAGGAC
                                 GT     C  G
GAM1656  LOC254266 5'  TGAGGAAGGCAGACTTGGCGGG 99203       GCAAA
                                CTTGCT    CTGCTTTTCTTG
                                ||||||    ||||||||||||
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                                GGGCGG    GACGGAAGGAGT
                                   TTCA_
GAM1656  LOC254517 5'  CAGGAGAGGCTGCTGGAGAGG  96636    TG  _  AACT
                                CCT  CT GCA   GCTTTTCTTG
                                |||  || |||   ||||||||||
                                GGA  GG CGT   CGGAGAGGAC
                                  GA  T  _____
GAM1656  LOC254587 5'  GAGAGGAGCAGCAGCGGC    99525     AAA
                                GCTGC   CTGCTTTTCTT
                                |||||   ||||||||||
                                CGGCG   GACGAGGAGAG
                                   AC_
GAM1656  LOC254659 5'  CAGGAGAAGCAGCGAGCGAG   96818      GCAAA
                                CTTGCT    CTGCTTTTCTTG
                                ||||||    ||||||||||||
                                GAGCGA    GACGAAGAGGAC
                                   GC___
GAM1656  LOC254740 5'  TGAGGAAGGTGGTTTTGGTTAC 97967    TT_   C   TG
            GG                    CC   GCTG AAAC  CTTTTCTTG
                                ||   |||| ||||  |||||||||
                                GG   TGGT TTTG  GGAAGGAGT
                                 CAT   _   GT
GAM1656  LOC254875 3'  AGGAAGAGGTTGCAGTGAG   97771    TG    ACTG     G
                                CT  CTGCAA   CTTTTCTT
                                ||  ||||||   ||||||||
                                GA  GACGTT   GAGAAGGA
                                 GT    G___
GAM1656  LOC254901 5'  CAAGGAAAGAGAAGTGGGAGG  98003     G TG AAA  G
                                CCTT C  C   CT CTTTTCTTG
                                ||||  |  |   || |||||||||
                                GGAG G  G   GA GAAAGGAAC
                                  _ GT AA_  _
GAM1656  LOC254944 3'  CAGGAGGGGCGGTGGAGGGG   99002    TG  GCAA
                                CCT  CT   ACTGCTTTTCTTG
                                |||  ||   ||||||||||||
                                GGG  GG   TGGCGGGGAGGAC
                                  GA  _____
GAM1656  LOC254964 5'  CAGGAGAGGCTGCTGGAGAGG  96699    TG  _  AACT
                                CCT  CT GCA   GCTTTTCTTG
                                |||  || |||   ||||||||||
                                GGA  GG CGT   CGGAGAGGAC
                                  GA  T  _____
GAM1656  LOC255043 3'  AGGAGAGGCCTCGGGGAGG   97066     G  CAAACT
                                CCTT CTG     GCTTTTCTT
                                ||||  |||    |||||||||
                                GGAG GGC     CGGAGAGGA
                                  G  TC_____
GAM1656  LOC255102 5'  CGAGGGAGGCGGAAGTGCGGT  97802      AA_    TT
                                GCTGCA  CTGCTT  CTTG
                                ||||||  ||||||  ||||
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                                TGGCGT   GGCGGA  GAGC
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GAM1656  LOC255374 3'  GGGAGAAGGTTCGTGGGAGGG  97791     G TG A    GC
                                CCTT C  C AACT  TTTTCT
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                                GGGA G  G TTGG  AGAGGG
                                  G GT C    A_
GAM1656  LOC255452 3'  GGGAGAGAGACTGCGTGGGG   99398     TG T   AA  G
                                CCT  C GCA  CT CTTTTCT
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                                GGG  G CGT  GA GAGAGGG
                                  GT _   CA  _
GAM1656  LOC255463 5'  CAGGGAAGGCGGGCGCGGAGG  96539     TG    AAA
                                CCT  CTGC   CTGCTTTTCTTG
                                |||  ||||   ||||||||||||
                                GGA  GGCG   GGCGGAAGGGAC
                                  __    CG_
GAM1656  LOC255650 3'  TGGGGGGAGCAGAGGCAGGAGG 98528      G    AAA     TT
                                CCTT CTGC   CTGCTT  CTTG
                                |||| ||||   ||||||  ||||
                                GGAG GACG   GACGAG  GGGT
                                  _    GA_     GG
GAM1656  LOC255728 3'  CAAGAAAAGGTAGCCGGCAAGG 98584         CAAA    _
                                CCTTGCTG    CTGC TTTTCTTG
                                ||||||||    |||| ||||||||
                                GGAACGGC    GATG AAAAGAAC
                                     C___    G
GAM1656  LOC255737 5'  CAAGGAGGGTCCACGGCGGG   98006       CAAACT
                                CTTGCTG     GCTTTTCTTG
                                |||||||     ||||||||||
                                GGGCGGC     TGGGAGGAAC
                                    ACC___
GAM1656  LOC255749 3'  CAAGGAAGGCACAGGGTGGG   98192    TG  GCAAAC
                                CT  CT     TGCTTTTCTTG
                                ||  ||     ||||||||||
                                GG  GG     ACGGAAGGAAC
                                 GT  GAC___
GAM1656  LOC255974 5'  GGGGAGACACTGCAGAGGG    99344     G    AAC  _  TT
                                CCTT CTGCA   TG CTT  C
                                |||| |||||   || |||  |
                                GGGA GACGT   AC GAG  G
                                  _    C__  A   GG
GAM1656  LOC256283 5'  AGGAGAGGCCATGGGGAGG    98821     G  GCAAACT
                                CCTT CT      GCTTTTCTT
                                |||| ||      |||||||||
                                GGAG GG      CGGAGAGGA
                                  G  TAC_____
GAM1656  LOC256307 3'  CAAGGGAAGCACATGGTAGGG  98840       GCAAAC    TT
                                CCTTGCT     TGCTT  CTTG
                                |||||||     |||||  ||||
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                                GGGATGG     ACGAA  GAAC
                                    TAC___    GG
GAM1656  LOC256494 5'  CGGGAAGGGACGGCAGCGCGG  99093    T     AAACTG
                                CC TGCTGC     CTTTTCTTG
                                || ||||||     |||||||||
                                GG GCGACG     GGGAAGGGC
                                 C     GCA___
GAM1656  LOC256982 5'  CGGGGGAGGCGGGGCCAGAGGG 99055      G   CAAA     TT
                                CCTT CTG    CTGCTT  CTTG
                                |||| |||    ||||||  ||||
                                GGGA GAC    GGCGGA  GGGC
                                   _  CGG_     GG
GAM1656  LOC257095 5'  CGGGGAAGGCAGGTGAGTGTAG 98719       AA___
                                CTGCA    CTGCTTTTCTTG
                                |||||    ||||||||||||
                                GATGT    GACGGAAGGGGC
                                   GAGTG
GAM1656  LOC257408 5'  AGGGAGGCTGTGTCGCAGCGAG 97796         AA_  T    TT  TG
              G                     CCTTGCTGC   AC GCTT  CT
                                |||||||||   || ||||  ||
                                GGAGCGACG   TG CGGA  GA
                                      CTG  T    GG  C
GAM1656  LOC257449 3'  AGGAGGGGTTTTGGAGGGG    63372     TG  G    CT
                                CCT  CT CAAA  GCTTTTCTT
                                |||  || ||||  |||||||||
                                GGG  GA GTTT  TGGGGAGGA
                                  __  G   __
GAM1656  LOC257485 3'  CAAGAAAACCAGCTTGCAGCAA 66209           A   C
              GG                    CCTTGCTGCAA CTG TTTTCTTG
                                |||||||||||| ||| ||||||||
                                GGAACGACGTT GAC AAAAGAAC
                                      C   C
GAM1656  LOC257494 3'  CAGGGAAAGGAAGGCAGCAGG  99628         AAACTG
                                CTTGCTGC     CTTTTCTTG
                                ||||||||     |||||||||
                                GGACGACG     GAAAGGGAC
                                     GAAG__
GAM1656  LOC257495 3'  TGGGAGGAGGAGGTTGCAGTGA 99576    TG     A  G
              G                     CT  CTGCAA CT CTTTTCTTG
                                ||  |||||| || |||||||||
                                GA  GACGTT GA GAGGAGGGT
                                 GT     G  G
GAM1656  LOC257539 3'  CGAGGAGGGCAGATCACGAGG  99548       C  CAAA
                                CCTTG TG    CTGCTTTTCTTG
                                ||||| ||    ||||||||||||
                                GGAGC AC    GACGGGAGGAGC
                                   _  TA__
GAM1656  LOC257554 3'  AGGAGGGCCAGTGCAGAAGG   99529      G    AACT
                                CCTT CTGCA    GCTTTTCT
                                |||| |||||    ||||||||
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                                GGAA GACGT    CGGGAGGA
                                  _    GAC_
GAM1656  LOC257576 3'  TGGGAGGAGGAGGTTGCAGTGA 99713    TG     A  G
            G                    CT  CTGCAA CT CTTTTCTTG
                                 ||  |||||| || |||||||||
                                 GA  GACGTT GA GAGGAGGGT
                                  GT     G  G
GAM1656  LOC257578 3'  CGAGGAGGGCAGATCACGAGG  99660      C  CAAA
                                 CCTTG TG    CTGCTTTTCTTG
                                 |||||| ||    ||||||||||||
                                 GGAGC AC    GACGGGAGGAGC
                                   _  TA__
GAM1656  LOC257618 5'  CAGGGAGGGACGGGGTGGGG   99676    TG  GCAAA  _
                                 CCT  CT     CTG CTTTTCTTG
                                 |||  ||     ||| |||||||||
                                 GGG  GG     GGC GGGAGGGAC
                                   GT  ______   A
GAM1656  LOC51117  3'  TGAGAAGAGAGAAGTGGAGGG  32635     G TG AAA  G
                                 CCTT C  C   CT CTTTTCTTG
                                 |||| |  |   || |||||||||
                                 GGGA G  G   GA GAGAAGAGT
                                   _ GT AA_  _
GAM1656  LOC51133  5'  GGGGAAGGAGGGCGGCGAG    32789        AAA  G   TT
                                 CTTGCTGC   CT CTT  CT
                                 ||||||||   || |||  ||
                                 GAGCGGCG   GA GAA  GG
                                      G__  G   GG
GAM1656  LOC51157  5'  AGGAGTGGCAGGTGGTGGCGGG 33014       TG AAA    T    G
            G                    CCTTGC  C   CTGCT TTCTT
                                 ||||||  |   ||||| |||||
                                 GGGGCG  G   GACGG GAGGA
                                    GT GTG    T
GAM1656  LOC51308  3'  CAAGAAGAAGACCTCTGGCGGG 33959       GCAAACTG   _
            G                    CCTTGCT       CTTTT CTTG
                                 |||||||       ||||| ||||
                                 GGGGCGG       GAAGA GAAC
                                     TCTCCA__     A
GAM1656  LOC51619  3'  CAAGAGAAGCTGGCAGAGAGG  32567    TG   AAACT
                                 CCT  CTGC    GCTTTTCTTG
                                 |||  ||||    ||||||||||
                                 GGA  GACG    CGAAGAGAAC
                                   GA   GT___
GAM1656  LOC51667  3'  TGGGGAAGGTGTCCAGGGCAGG 32780       GCAA  T
            G                    CCTTGCT    AC GCTTTTCTTG
                                 |||||||    || ||||||||||
                                 GGGACGG    TG TGGAAGGGGT
                                     GACC  _
GAM1656  LOC55924  5'  GGAGCGCAGTTTCCAGTGGGG  39395    TG   C      T
                                 CCT  CTG AAACTGC TTTC
                                 |||  ||| ||||||| ||||
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                                GGG  GAC TTTGACG GAGG
                                  GT   C      C
GAM1656  LOC56834  5'  GGGGGAGGGTGGGGCGGGG   39752        G  AA  G
                                CCTTGCT CA  CT CTTT
                                ||||||| ||  || ||||
                                GGGGCGG GT  GA GGGG
                                    G  GG  G
GAM1656  LOC56961  5'  CAGGGGGAGGGGAGGGGCGGGG 63574        GCAAA  G   TT
                                CCTTGCT    CT CTT  CTTG
                                |||||||    || |||  ||||
                                GGGGCGG    GG GAG  GGAC
                                    GGA__  G   GG
GAM1656  LOC57795  5'  AAGGAGGGCTCTTGCAAGG   69863       TGCAAACT
                                CCTTGC       GCTTTTCTT
                                ||||||       |||||||||
                                GGAACG       CGGGAGGAA
                                   TTCT____
GAM1656  LOC58525  3'  GGGAGCATTTGGGTGGGG    79348     TG  G    C
                                CCT  CT CAAA TGCTTTT
                                |||  || |||| |||||||
                                GGG  GG GTTT ACGAGGG
                                  GT  _    _
GAM1656  LOC63928  5'  CGGGGGAGGCGTGGAAACGCGG 42269       TGCAA_  T    TT
           GG                   CCTTGC     AC GCTT  CTTG
                                ||||||     || ||||  ||||
                                GGGGCG     TG CGGA  GGGC
                                   CAAAGG  _    GG
GAM1656  LOC64167  3'  TGAGAAGGGCGGATCACGAGG  42544      C  CAAA
                                CCTTG TG    CTGCTTTTCTTG
                                ||||| ||    ||||||||||||
                                GGAGC AC    GGCGGGAAGAGT
                                  _  TA__
GAM1656  LOC83468  5'  GGGAAGAGCAGCGTGGAG    49343    G  AA
                                CT CA  CTGCTTTTCTT
                                || ||  ||||||||||
                                GA GT  GACGAGAAGGG
                                 G  GC
GAM1656  LOC84548  3'  CAGGAAGAGTGTGAGAACAGGG 71762      CTGCAA  T
                                CCTTG     AC GCTTTTCTTG
                                |||||     || ||||||||||
                                GGGAC     TG TGAGAAGGAC
                                  AAGAG_  _
GAM1656  LOC89894  5'  AGGAGGAGCCCAGCTGGG    61230     T   CAAACT
                                CCT GCTG     GCTTTTCTT
                                ||| ||||     |||||||||
                                GGG CGAC     CGAGGAGGA
                                  T   C_____
GAM1656  LOC90010  5'  GGGAAGGGCCCAGGTAGGG   61722       GCAAACT
                                CCTTGCT      GCTTTTCTT
                                |||||||      |||||||||
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                                GGGATGG      CGGGAAGGG
                                   ACC____
GAM1656 LOC90119 5' CGGGGAGGGCAGAGGGGTCAGG 62208      _ GCAAA
             G                    CCTTG CT    CTGCTTTTCTTG
                                  |||||| ||    ||||||||||||
                                  GGGAC GG    GACGGGAGGGGC
                                    T  GGA__
GAM1656 LOC90120 5' GGGAGGGGCCTCAGCAGG    62217       CAAACT
                                  CTTGCTG     GCTTTTCTT
                                  |||||||     |||||||||
                                  GGACGAC     CGGGGAGGG
                                     TC____
GAM1656 LOC90183 3' AGGAAGAGAGCAACGAGG    62403      C   AAACTG
                                  CCTTG TGC     CTTTTCTT
                                  ||||| |||     ||||||||
                                  GGAGC ACG     GAGAAGGA
                                     A   A_____
GAM1656 LOC90378 5' CAAGAGAGGTGGAGAAGAGCGA 63186       GCAAA TG
             G                    CTTGCT    C  CTTTTCTTG
                                  ||||||    |  |||||||||
                                  GAGCGA    G  GGAGAGAAC
                                     GAAGA GT
GAM1656 LOC90594 5' TAGGAGGAGCAGCGGTCTGTGG 64219     TG T_  AAA
             GG                     CCT  C  GC   CTGCTTTTCTTG
                                  |||  |  ||   ||||||||||||
                                  GGG  G  TG   GACGAGGAGGAT
                                    GT TC  GC_
GAM1656 LOC90673 3' CGGGGAGGGCGAAAAGGAAGG  64561     G  GCAAAC
                                  CCTT CT     TGCTTTTCTTG
                                  |||| ||     ||||||||||||
                                  GGAA GA     GCGGGAGGGGC
                                    G  AAA___
GAM1656 LOC90678 3' GGGAAGGCGTGTGGTGCAG    57203      A_  _
                                  CTGCA  AC TGCTTTTCT
                                  |||||  || |||||||||
                                  GACGT  TG GCGGAAGGG
                                     GG  T
GAM1656 LOC90678 3' GGGAAGGGAGCAGGAGGG    57204      G    AAAC G
                                  CCTT CTGC    T CTTTTCT
                                  |||| ||||    | |||||||
                                  GGGA GACG    A GGAAGGG
                                    G    ____ G
GAM1656 LOC90719 3' AAGAAAGTGGTGGGCAAGG    64606       GCAA  TG    T
                                  CCTTGCT    AC  CTTT CTT
                                  |||||||    ||  |||| |||
                                  GGAACGG    TG  GAAA GAA
                                     G___  GT    _
GAM1656 LOC91056 3' TAGGAAGGGCCTGCTAATAAGG 96409      CT_   AACT
                                  CCTTG   GCA   GCTTTTCTTG
                                  |||||   |||   ||||||||||
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                                GGAAT  CGT   CGGGAAGGAT
                                  AAT  C___
GAM1656 LOC91064 5' GGGAGGGTGGCAGCGGG    65388       AA  G  TT
                                CTTGCTGC  ACT CTT  C
                                ||||||||  ||| |||  |
                                GGGCGACG  TGG GAG  G
                                    G_  _  GG
GAM1656 LOC91097 5' GGGAGGGTGAGTGGGTGAGG  65463    TG  G  AAC
                                CCT  CT CA   TGCTTTTCT
                                |||  || ||   |||||||||
                                GGA  GG GT   GTGGGAGGG
                                  GT  _  GA_
GAM1656 LOC91149 5' CGAGGAAGGCTTGGCGTGGGG 65691    TG T  AAACT
                                CCT  C GC    GCTTTTCTTG
                                |||  | ||    ||||||||||
                                GGG  G CG    CGGAAGGAGC
                                  GT _  GTT__
GAM1656 LOC91319 3' AAGGGGAGCAGGGTTAGG    66189    T  GCAAA    TT
                                CCT GCT    CTGCTT  CTT
                                ||| |||    ||||||  |||
                                GGA TGG    GACGAG  GAA
                                  T  _____     GG
GAM1656 LOC91661 3' TGGGAGAAGCCCCCCTCAGCAG 57220       CAAACT
            G                    CTTGCTG     GCTTTTCTTG
                                |||||||     ||||||||||
                                GGACGAC     CGAAGAGGGT
                                    TCCCCC
GAM1656 LOC91663 5' CGGGGAGGGGAGGGGGCGGGG  57222       GCAAA  G
                                CCTTGCT    CT CTTTTCTTG
                                |||||||    || |||||||||
                                GGGGCGG    GA GGGAGGGGC
                                    GG___  G
GAM1656 LOC91695 3' CAGGAGGAACATGAGGTGAGG  67508    TG  G  AAC  C
                                CCT  CT CA   TG TTTTCTTG
                                |||  || ||   || ||||||||
                                GGA  GG GT   AC AGGAGGAC
                                  GT  A  ___  A
GAM1656 LOC91748 3' CGGGAGAAGCAGAGGCAAG   67638       GCAAA
                                CTTGCT    CTGCTTTTCTTG
                                ||||||    ||||||||||||
                                GAACGG    GACGAAGAGGGC
                                   A____
GAM1656 LOC91796 5' TGAGAGAAGTATAATTATCAGG 67790       CTGCAAAC
            G                    CCTTG       TGCTTTTCTTG
                                |||||       ||||||||||||
                                GGGAC       ATGAAGAGAGT
                                  TATTAAT_
GAM1656 LOC91807 5' CAAGGAGAGTCTGGGGCATGG  67810    T   G  AACT
                                CC TGCT CA    GCTTTTCTTG
                                || |||| ||    ||||||||||
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                              GG ACGG GT    TGAGAGGAAC
                               T   G  C___
GAM1656 LOC91828 5' GAGGAGGCGGTGCGGCGA    67859       AA      T  G
                              TTGCTGC  ACTGCTTT CTT
                              |||||||  |||||||| |||
                              AGCGGCG  TGGCGGAG GAG
                                 __      _
GAM1656 LOC92078 3' TAGGGAGAGTGGGAGGTAGGCA 68611    _  _  AAA TG
           GAGG                  CCT TGC TGC   C  CTTTTCTTG
                              ||| ||| |||   |  |||||||||
                              GGA ACG ATG   G  GAGAGGGAT
                                G   G   GAG GT
GAM1656 LOC92106 5' CGGGAAAGGCGGGGTGGGGAGG 57227     G TG AAA
                              CCTT C  C   CTGCTTTTCTTG
                              |||| |  |   ||||||||||||
                              GGAG G  G   GGCGGAAAGGGC
                                G GT G__
GAM1656 LOC92267 3' TAGGAGAATAGTTGTGGTATGG 69177    T   TG   A   C
                              CC TGC  CAA CTG TTTTCTTG
                              || |||  ||| ||| ||||||||
                              GG ATG  GTT GAT AAGAGGAT
                               T   GT   _  _
GAM1656 LOC92305 3' AGGGAAGGGGGTGGCTGGG    57231     T   GCAA   G
                              CCT GCT    ACT CTTTTCTT
                              ||| |||    ||| ||||||||
                              GGG CGG    TGG GGAAGGGA
                                T   _____   G
GAM1656 LOC92379 3' CAAGAAAGGCTCCAGTGTCAAG 69676      CT   AACT_
           G                   CCTTG  GCA    GCTTTTCTTG
                              |||||  |||    ||||||||||
                              GGAAC  TGT    CGGAAAGAAC
                                 __  GACCT
GAM1656 LOC92539 5' GGGGAGGTAGATGTGGCTGAGG 70223     _ TG  AA     TT  TG
                              CCTT GC  CA  CTGCTT  CT
                              |||| ||  ||  ||||||  ||
                              GGAG CG  GT  GATGGA  GG
                                T  GT  A_     GG  T
GAM1656 LOC92597 3' TAGGGAAAGTAGTTTTTTTGGA 70514     G  ____
           GC                   GCT CAA    ACTGCTTTTCTTG
                              ||| |||    ||||||||||||||
                              CGA GTT    TGATGAAAGGGAT
                                G   TTTT
GAM1656 LOC92661 5' GGGGAGGCCCATGTGCGTAAGG 70632       T   AACT_   TT  TG
                              CCTTGC GCA    GCTT  CT
                              |||||| |||    ||||  ||
                              GGAATG CGT    CGGA  GG
                                 _  GTACC    GG  C
GAM1656 LOC93132 5' GGGGAGGGTAACTGATGGCAAG 71996        _ AAC        G
           G                   CCTTGCTG CA   TGCTTTTCTT
                              |||||||| ||   ||||||||||
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                                GGAACGGT GT   ATGGGAGGGG
                                    A  CA_        G
GAM1656 LOC93259 5' GGGGAGGCCTGGGTAGGG    72290       G  AACT    TT
                                CCTTGCT CA    GCTT  CT
                                ||||||| ||    ||||  ||
                                GGGATGG GT    CGGA  GG
                                    _ C___    GG
GAM1656 LOC93320 3' CAAGAAGAAGCTGCGGGAAGG 72513     G    AACT    _
                                CCTT CTGCA    GCTTTT CTTG
                                |||| |||||    |||||| ||||
                                GGAA GGCGT    CGAAGA GAAC
                                  G    _____     A
GAM1657 SCAMP1   3' GCTAAATAAATATTCTCC    54500     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1657 SCAMP1   3' GCTAAATAAATATTCTCC    54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1657 NX-17    3' TGAATATCAGCCCCTAATA   40706        ATA_
                                TATTAGGG    ATATTCA
                                ||||||||    |||||||
                                ATAATCCC    TATAAGT
                                    CGAC
GAM1657 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
            TA                   TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM1658 DLEC1    3' CATCTGGCCCTCCCTTG     24717      A     A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                  C    G  _
GAM1658 DLEC1    3' CATCTGGCCCTCCCTTG     96278      A     A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                  C    G  _
GAM1658 PIP5K1A  3' TATCCCACCCTGCCTTGATA  14520        A    CA  C
                                TATCAAGG AGGG  GG GTG
                                |||||||| ||||  || |||
                                ATAGTTCC TCCC  CC TAT
                                    G   A_  C
GAM1658 SOX11    3' ACCCACCCCCCCTTGGTA    13308        AA   CA  C
                                TATCAAGG  GGG  GG GT
                                |||||||  |||  || ||
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                                ATGGTTCC  CCC  CC CA
                                    CC   A_ _
GAM1658 CHL1     3'  TGTTACCTTTCCTCAATA    22768     CA      CA
                                TAT  AGGAAGGG  GGCG
                                |||  ||||||||  ||||
                                ATA  TCCTTTCC  TTGT
                                  AC       A_
GAM1658 EPB41L1  3'  CATTCTGCCCTTCCCTGA    71104     A        C
                                TCA GGAAGGGCAGG GTG
                                ||| ||||||||||| |||
                                AGT CCTTCCCGTCT TAC
                                  C        _
GAM1658 FLJ00060 3'  CATACCCCCTGCCCTCCTCTGA 61741     _   A      CGTG
                                TCA AGGA GGGCAGG    ATG
                                ||| |||| |||||||    |||
                                AGT TCCT CCCGTCC    TAC
                                  C   _      CCCA
GAM1658 FLJ10898 5'  CACCACAGCCCTTTCTCAATA  60126     CA       AGGC
                                TAT  AGGAAGGGC    GTG
                                |||  |||||||||    |||
                                ATA  TCTTTCCCG    CAC
                                  AC        ACAC
GAM1658 FLJ22557 3'  ATCATCCCATCCTTAATA    45581     C    A   CAGGC
                                TAT AAGGA GGG     GTGAT
                                ||| ||||| |||     |||||
                                ATA TTCCT CCC     TACTA
                                  A    A  _____
GAM1658 KIAA0574 3'  CATCCCCTGCCCTCCCCTGA   69808     A  A      CGT
                                TCA GG AGGGCAGG   GATG
                                ||| || ||||||||   ||||
                                AGT CC TCCCGTCC   CTAC
                                  C  C       C__
GAM1658 KIAA0632 3'  CACCTCAGAAACCCTTCCTTGA 32071          CA___  C
                                TCAAGGAAGGG     GG GTG
                                ||||||||||     || |||
                                AGTTCCTTCCC     CT CAC
                                       AAAGA  C
GAM1658 KIAA1045 3'  CATCACATGTCCTTCC      71599         GGC
                                GGAAGGGCA   GTGATG
                                |||||||||   ||||||
                                CCTTCCTGT   CACTAC
                                     A__
GAM1658 KIAA1354 5'  CAGTGACTGCCTTCCCTTGATA 61572        A      G  _
                                TATCAAGG AGGGCAG CG TG
                                |||||||| ||||||| || ||
                                ATAGTTCC TTCCGTC GT AC
                                     C      A  G
GAM1658 MGC20460 5'  CACCGCCTCCTACCCTTCTT   54901        C___    _
                                AGGAAGGG    AGGCG TG
                                ||||||||    ||||| ||
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                                TTCTTCCC   TCCGC AC
                                    ATCC    C
GAM1658 LOC158476 3' CACGCCCGCCCCCCCCATTGA 88186     _ AA_   A
                                TCAA GG  GGGC GGCGTG
                                |||| ||  |||| ||||||
                                AGTT CC  CCCG CCGCAC
                                  A CCC   C
GAM1658 LOC90459 3' CACACCCGCCTAATTTTTG  63550      A_   A C
                                CAAGGA GGGC GG GTG
                                |||||| |||| || |||
                                GTTTTT TCCG CC CAC
                                   AA   C A
GAM1659 B4GALT2  3' GCGGCGACCAACCCCGCCA  48348   T AA   CCG
                                TG CG GTTGG  CGTCGT
                                || ||  |||||  ||||||
                                AC GC CAACC  GCGGCG
                                 C CC   A__
GAM1659 DKFZP434H132 5' CCAAGGACCAACTTCCACA  31929    C     _ GCGTCG
                                TGT GAAGTTGG CC    TGG
                                ||| |||||||| ||    |||
                                ACA CTTCAACC GG    ACC
                                  C      A A_____
GAM1659 KIAA1319  3' CCACATGTGCCCAACTTC   40788       C   C
                                GAAGTTGG CGCGT GTGG
                                |||||||| ||||| ||||
                                CTTCAACC GTGTA CACC
                                    C   _
GAM1659 MGC22014  3' ACATGGCCAACTTCAACA   65104    C       C
                                TGT GAAGTTGGCCG GT
                                ||| ||||||||||| ||
                                ACA CTTCAACCGGT CA
                                  A        A
GAM1659 LOC142964 5' GCCACAACCATAGCAACTTCGG 76969         GCCGC  C
           CA                   TGTCGAAGTTG    GT GTGGC
                                |||||||||||    || |||||
                                ACGGCTTCAAC    CA CACCG
                                      GATAC  A
GAM1660 MAP1A    3' GCTGTAACGGAGCCACCTCCAA 11441        AACA__  TT
           CTCT                 GGAGTTGGA    TT  TTACAGC
                                |||||||||    ||  |||||||
                                TCTCAACCT    AG  AATGTCG
                                   CCACCG  GC
GAM1660 RNF4     3' CTGCTCTTTTGTTTCCAACCC  12883    A       TTTTTTA
                                GG GTTGGAAACA     CAG
                                || ||||||||||     |||
                                CC CAACCTTTGT     GTC
                                 _       TTTCTC_
GAM1660 RRM1     5' CTGTCTGGCTCCAACTCC    8280         AA  TTTTTT
                                GGAGTTGGA  CA    ACAG
                                |||||||||  ||    ||||
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                                CCTCAACCT  GT     TGTC
                                     CG  C_____
GAM1660  SRGAP1   3'  CTGCCTAGAAAATGTTTCCATC 72715      T          __
             TCC                   GGAG TGGAAACATTTTTTA  CAG
                                   |||| ||||||||||||||  |||
                                   CCTC ACCTTTGTAAAAGAT  GTC
                                     T           CC
GAM1660  TM6SF2   3'  CTGTCACCATGCTCCAACTCC  72816        AA   TTTTT
                                   GGAGTTGGA  CAT    ACAG
                                   |||||||||  |||    ||||
                                   CCTCAACCT  GTA    TGTC
                                        C_   CCAC_
GAM1660  YWHAE    3'  AAAAATGTTTCCAACTCC    23135
                                   GGAGTTGGAAACATTTTT
                                   ||||||||||||||||||
                                   CCTCAACCTTTGTAAAAA

GAM1660  YWHAE    3'  GCTGTAAAAAATGTTTCCAACT 23136
             CC                    GGAGTTGGAAACATTTTTTACAGC
                                   |||||||||||||||||||||||||
                                   CCTCAACCTTTGTAAAAAATGTCG

GAM1660  LOC144017 3'  AAAAATGTCCCCATCTCC    83926      T   AA
                                   GGAG TGG  ACATTTTT
                                   |||| |||  ||||||||
                                   CCTC ACC  TGTAAAAA
                                     T   CC
GAM1660  LOC149506 5'  CTGTGGGGCTTGTTCCCAATCC 85633    AG    A    TT
             C                      GG  TTGG AACA  TTTTACAG
                                    ||  |||| ||||  ||||||||
                                    CC  AACC TTGT  GGGGTGTC
                                     CT    C    TC
GAM1660  LOC150498 3'  GCTGTAAAAAATGTTTCAAACT 80721      G
                                   AGTT GAAACATTTTTTACAGC
                                   |||| |||||||||||||||||
                                   TCAA CTTTGTAAAAAATGTCG
                                     A
GAM1660  LOC221405 5'  AAAAATACTTCCATCTCC    95503      T    AC
                                   GGAG TGGAA  ATTTTT
                                   |||| |||||  ||||||
                                   CCTC ACCTT  TAAAAA
                                     T    CA
GAM1660  LOC254556 3'  CTGCTCTTTTGTTTCCAACCC  96260    A        TTTTTTA
                                   GG GTTGGAAACA      CAG
                                   || ||||||||||      |||
                                   CC CAACCTTTGT      GTC
                                    _        TTTCTC_
GAM1661  BCAT1    5'  GGAGGTGGGCAGGAGCCAGTGA 66787          CAC  TG
                                   TCGCTGGCTCC   TT  TCTCC
                                   ||||||||||   ||  |||||
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                                AGTGACCGAGG  GG  GGAGG
                                     AC_  GT
GAM1661  CDX2     5'  GAGCCGCGAGGAGCCAGCGG  8851          CACT   __
                                TCGCTGGCTCC   TTGT  CTC
                                ||||||||||   ||||  |||
                                GGCGACCGAGG   AGCG  GAG
                                     ____   CC
GAM1661  CYP26A1  5'  GAAATGGAAAGCCAGTGA   7598         C_  C
                                TCGCTGGCT  CCA TTT
                                |||||||||  ||| |||
                                AGTGACCGA  GGT AAG
                                     AA  A
GAM1661  FCMD     3'  ACATAAGTGGGAACCAAAGA  23021    GC  C      _
                                TC  TGG TCCCACTT TGT
                                ||  ||| |||||||| |||
                                AG  ACC AGGGTGAA ACA
                                 AA  A       T
GAM1661  FOXD2    5'  AGAACCCTGGGAGCCAGGA   16783    G        CTTTG
                                TC CTGGCTCCCA    TCT
                                || ||||||||||    |||
                                AG GACCGAGGGT    AGA
                                 _        CCCA_
GAM1661  GGT1     5'  GGAGACAGAGAAACCAGC    19160      CTCCCA
                                GCTGG     CTTTGTCTCC
                                |||||     ||||||||||
                                CGACC     GAGACAGAGG
                                   AAA___
GAM1661  GGT1     5'  GGAGACAGAGAAACCAGC    26428      CTCCCA
                                GCTGG     CTTTGTCTCC
                                |||||     ||||||||||
                                CGACC     GAGACAGAGG
                                   AAA___
GAM1661  GRIA3    5'  GGAGGGGGTGTAAGAGCCAGCG 7712          C__    TG
           A                     TCGCTGGCTC   CACTT  TCTCC
                                ||||||||||   |||||  |||||
                                AGCGACCGAG   GTGGG  GGAGG
                                     AAT    __
GAM1661  GRIA3    5'  GGAGGGGGTGTAAGAGCCAGCG 24645         C__    TG
           A                     TCGCTGGCTC   CACTT  TCTCC
                                ||||||||||   |||||  |||||
                                AGCGACCGAG   GTGGG  GGAGG
                                     AAT    __
GAM1661  IFNAR2   3'  GGAAACAGGGAAGAGCCATCGA 7901      C     CCA     C
                                TCG TGGCTC   CTTTGT TCC
                                ||| ||||||   |||||| |||
                                AGC ACCGAG   GGGACA AGG
                                  T     AA_     A
GAM1661  NIPSNAP1 3'  GGAAAGGGATGGGAGCCAGGA  14660    G        _   G
                                TC CTGGCTCCCA CTTT TCT
                                || |||||||||| |||| |||
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                                AG GACCGAGGGT GGGA AGG
                                 _       A   A
GAM1661 OAS1    3' AGACAAAGCTCCTCAGTGA   34145       CTCCCA
                                TCGCTGG     CTTTGTCT
                                |||||||     ||||||||
                                AGTGACT     GAAACAGA
                                    CCTC__
GAM1661 PAK4    3' GGACTCGTGGGAGCAAGCGA  20828      G      TTT
                                TCGCT GCTCCCAC  GTCT
                                ||||| ||||||||  ||||
                                AGCGA CGAGGGTG  CAGG
                                   A       CT_
GAM1661 PMM2    3' GGAGGTAGTGGGAACCA     72563     C      TTG
                                TGG TCCCACT  TCTCC
                                ||| |||||||  |||||
                                ACC AGGGTGA  GGAGG
                                  A      T__
GAM1661 POU3F2  5' GGAGACAGAAAGAGCGAGCGA 20026      G   CCAC
                                TCGCT GCTC   TTTGTCTCC
                                ||||| ||||   |||||||||
                                AGCGA CGAG   AGACAGAGG
                                   G   AA__
GAM1661 SDS     3' AAGGTCGGCAGCCAGCGA    23377        _ C
                                TCGCTGGCT CC ACTTT
                                ||||||||| || |||||
                                AGCGACCGA GG TGGAA
                                      C  C
GAM1661 SEPN1   3' GGACTGCGGGAGCCAGCG    66976         ACTTT
                                CGCTGGCTCCC    GTCT
                                ||||||||||    ||||
                                GCGACCGAGGG    CAGG
                                       CGT__
GAM1661 SLC18A3 3' GAGCACCGAGGCCAGCGA    13213       TCCCA  T _
                                TCGCTGGC    CTT GT CTC
                                ||||||||    ||| || |||
                                AGCGACCG    GAG CA GAG
                                     _____  C  C
GAM1661 SLC2A1  3' GGGCCTGTGGGAGCCTGC    22516    T      TTT
                                GC GGCTCCCAC  GTCT
                                || |||||||||  ||||
                                CG CCGAGGGTG  CGGG
                                  T       TC_
GAM1661 SLC7A5  3' CAAGCCGGGAGCCAACGA    14462     C      AC
                                TCG TGGCTCCC  TTTG
                                ||| ||||||||  ||||
                                AGC ACCGAGGG  GAAC
                                  A       CC
GAM1661 SLC9A3R2 3' GAGACAGAGAGAGAGCGAGCGA 62102      G   CCA
                                TCGCT GCTC  CTTTGTCTC
                                ||||| ||||  |||||||||
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                                AGCGA CGAG   GAGACAGAG
                                   G    AGA
GAM1661  BCDO     5'  GGACAAGTGAGAGCCAGC    34286        C    T
                                GCTGGCTC CACTT GTCT
                                |||||||| ||||| ||||
                                CGACCGAG GTGAA CAGG
                                     A    _
GAM1661  C6.1A    3'  GGAGACAAAATGGGGAAAGATG 44535    _  GG T   C
              A                   TCG CT  C CCCA TTTGTCTCC
                                ||| ||  | |||| |||||||||
                                AGT GA  G GGGT AAACAGAGG
                                  A  AA _   A
GAM1661  CNNM1    3'  GAGACCCAACTGGGAGCCAGAG 40119    G        CTTT_
              A                   TC CTGGCTCCCA    GTCTC
                                || ||||||||||    |||||
                                AG GACCGAGGGT    CAGAG
                                 A         CAACC
GAM1661  DKFZP434E2135 3'  GAAGTTACACTAGAGCCAGCGA 48686          CC_____
                                TCGCTGGCTC       ACTTT
                                ||||||||||       |||||
                                AGCGACCGAG       TGAAG
                                      ATCACAT
GAM1661  DKFZp434O0515 5'  GAGATTGAGAGCCAGC      66511        C  CTTT
                                GCTGGCTC CA    GTCTC
                                |||||||| ||    |||||
                                CGACCGAG GT    TAGAG
                                     A _____
GAM1661  DKFZP564M182 3'  GGAGAGCAAGGAGCCAGC    78636         CACT  _
                                GCTGGCTCC    TTG TCTCC
                                |||||||||    ||| |||||
                                CGACCGAGG    AAC AGAGG
                                      _____  G
GAM1661  DKFZP727M111 5'  GAGACAAGCTGGAGCCAG    32059        CAC
                                CTGGCTCC   TTTGTCTC
                                ||||||||   ||||||||
                                GACCGAGG   GAACAGAG
                                     TC_
GAM1661  FLJ21596  3'  ACAAAATGGAGTGTAAGCGG   46111      G__    CAC
                                TCGCT   GCTCC   TTTGT
                                |||||   |||||   |||||
                                GGCGA   TGAGG   AAACA
                                   ATG    TA_
GAM1661  FLJ22378  3'  GGACGTGGCAGATGCCAGCGA  47597        _ __    TTT
                                TCGCTGGC TC  CCAC   GTCT
                                |||||||| ||  ||||   ||||
                                AGCGACCG AG  GGTG   CAGG
                                     T  AC   ___
GAM1661  GALNT12   3'  GAGACTGTGGAGCCAGGA    45318    G       C  TTT
                                TC CTGGCTCC AC   GTCTC
                                || |||||||| ||   |||||
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                                AG GACCGAGG TG   CAGAG
                                 _       _  T__
GAM1661 HELB     3'  GGAGACAAAATGAACATCG    54449    C  GCTCC  C
                                CG TG     CA TTTGTCTCC
                                || ||     || |||||||||
                                GC AC     GT AAACAGAGG
                                 T  AA___  A
GAM1661 HIC2     3'  AGTCGTGTGCAGGAGCCAGC   65857          __   TT  T
                                GCTGGCTCC  CAC  TG CT
                                |||||||||  |||  || ||
                                CGACCGAGG  GTG  GC GA
                                      AC   T_  T
GAM1661 HSPC156  5'  GGAGCCGGCGCGGGAGCCGCGA 27188      T      ACT   T
                                TCGC GGCTCCC   TTG CTCC
                                |||| |||||||   ||| ||||
                                AGCG CCGAGGG   GGC GAGG
                                  _      CGC   C
GAM1661 HT002    3'  GGAGACAAAGCAAGACCAG   26793      C  CCA
                                CTGG TC   CTTTGTCTCC
                                |||| ||   ||||||||||
                                GACC AG   GAAACAGAGG
                                  _ AAC
GAM1661 KCNH8    3'  AGAGTGTGAGGAGCCAGGGA   58903    G       ___
                                TC CTGGCTCC   CACTTT
                                || ||||||||   ||||||
                                AG GACCGAGG   GTGAGA
                                 G       AGT
GAM1661 KCNS1    3'  GGAGCATCCAACAGGAGTCAGC 11194         CACTT__  T
                                GCTGGCTCC      TG CTCC
                                |||||||||      || ||||
                                CGACTGAGG      AC GAGG
                                      ACAACCT  _
GAM1661 KIAA0215 5'  GGAGCCGGGCAGGAGCCGCGA  29084      T     CA  TT T
                                TCGC GGCTCC  CT  G CTCC
                                |||| ||||||  ||  | ||||
                                AGCG CCGAGG  GG  C GAGG
                                  _     AC  GC _
GAM1661 KIAA1483 3'  AGACAAAACAGGAGCCAG    70430         CAC
                                CTGGCTCC   TTTGTCT
                                ||||||||   |||||||
                                GACCGAGG   AAACAGA
                                     ACA
GAM1661 KIAA1580 5'  GGATGAGAAGAGCCAGCGA   69982          CCAC  TG
                                TCGCTGGCTC    TT  TCT
                                ||||||||||    ||  |||
                                AGCGACCGAG    GA  AGG
                                      AA__  GT
GAM1661 KIAA1656 3'  GGAGGGCGGTGGGAGCCAGT   66376            TTG
                                GCTGGCTCCCACT   TCTCC
                                ||||||||||||   |||||
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                                TGACCGAGGGTGG  GGAGG
                                       CG_
GAM1661 KIAA1814 3' GAGGACTGGGAGCCAGGA   70879   G       CTTTG
                                TC CTGGCTCCCA    TCTC
                                || ||||||||||    ||||
                                AG GACCGAGGGT    GGAG
                                 _       CA___
GAM1661 KIAA1822 3' GGAGCCGGGGTGGGAACCAGGA 68189   G   C       T
                                TC CTGG TCCCACTTTG CTCC
                                || |||| |||||||||| ||||
                                AG GACC AGGGTGGGGC GAGG
                                 _   A       C
GAM1661 LENG9    3' AGACAAAGCAGGAGCGTGC   75021   TG    CA
                                GC  GCTCC  CTTTGTCT
                                ||  |||||  ||||||||
                                CG  CGAGG  GAAACAGA
                                 TG    AC
GAM1661 MGC4643  3' GAGACAAAGTCTCAGC     52139     CTCCC
                                GCTGG    ACTTTGTCTC
                                |||||    ||||||||||
                                CGACT    TGAAACAGAG
                                  C____
GAM1661 MGC861   3' AGAGCTGGGCAGAAGCAGCGA  44131      G__ _   _
                                TCGCTG   CT CCCA CTTT
                                ||||||   || |||| ||||
                                AGCGAC   GA GGGT GAGA
                                   GAA  C   C
GAM1661 NFAT5    3' GAGACTCAGGTGAGCCAGC   57770       _ ACTTT
                                GCTGGCTC CC    GTCTC
                                |||||||| ||    |||||
                                CGACCGAG GG    CAGAG
                                     T  ACT__
GAM1661 NUCKS    3' GAGACTCGGAGCCAGTGA    43003         CACTTT
                                TCGCTGGCTCC     GTCTC
                                ||||||||||     |||||
                                AGTGACCGAGG     CAGAG
                                       CT____
GAM1661 p25      3' AGACATGCGGGAGCCAGGA   23822    G       ACTT
                                TC CTGGCTCCC    TGTCT
                                || |||||||||    |||||
                                AG GACCGAGGG    ACAGA
                                 _       CGT_
GAM1661 PLP1     3' GGAAACAAAGTGGAAGGAAAG  6759     GG  C_      C
                                CT  CT  CCACTTTGT TCC
                                ||  ||  ||||||||| |||
                                GA  GG  GGTGAAACA AGG
                                 AA  AA       A
GAM1661 RANBP1   5' GAGGCCGCGGAGCCAGCGA   12763         CACTTT
                                TCGCTGGCTCC     GTCTC
                                ||||||||||     |||||
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                                AGCGACCGAGG     CGGAG
                                      CGC___
GAM1661  RGS7     5'  GAGGGAGAGAGCCAGCGA    12864         CCAC   G
                                TCGCTGGCTC    TTT TCTC
                                ||||||||||    ||| ||||
                                AGCGACCGAG    AGA GGAG
                                      _____   G
GAM1661  SCYA14   5'  GAGACAAAAGAGGCCAGC    16051        CCCAC
                                GCTGGCT    TTTGTCTC
                                |||||||    ||||||||
                                CGACCGG    AAACAGAG
                                   AGA__
GAM1661  SCYA14   5'  GAGACAAAAGAGGCCAGC    53106        CCCAC
                                GCTGGCT    TTTGTCTC
                                |||||||    ||||||||
                                CGACCGG    AAACAGAG
                                   AGA__
GAM1661  SDCCAG3  3'  AGACATTGTCATAAAAGCCAGT 22799         CCC___  TT
            GA                    TCGCTGGCT     AC  TGTCT
                                |||||||||     ||  |||||
                                AGTGACCGA     TG  ACAGA
                                     AAATAC  TT
GAM1661  SLC37A1  3'  GAGAAGCAGAGAGCCAGCG   39091         CCA  TTG
                                CGCTGGCTC   CT   TCTC
                                |||||||||   ||   ||||
                                GCGACCGAG   GA   AGAG
                                     A__  CGA
GAM1661  WDR13    5'  GAGACAGAAGGAACCGGCGA   35842        C   CAC
                                TCGCTGG TCC   TTTGTCTC
                                |||||||  |||   ||||||||
                                AGCGGCC AGG   AGACAGAG
                                   A   A__
GAM1661  LOC112937 5'  GGAGAGGGGCGGAAGCCGC    93178    T    C  A    G
                                GC GGCT CC CTTT TCTCC
                                ||  ||||  ||  ||||  |||||
                                CG CCGA GG GGGG AGAGG
                                 _    A  C    _
GAM1661  LOC134701 5'  GGAGAGGGGCGGAGAGGCAGCG 75696       G   _  A    G
            A                    TCGCTG CTC CC CTTT TCTCC
                                ||||||  |||  ||  ||||  |||||
                                AGCGAC GAG GG GGGG AGAGG
                                   G   A  C    _
GAM1661  LOC145694 5'  GGAGGCGGCGGCAGCCAGCGA  84443         C  A  TT
                                TCGCTGGCT CC CT  GTCTCC
                                |||||||||  ||  ||  ||||||
                                AGCGACCGA GG GG  CGGAGG
                                     C  C  __
GAM1661  LOC146714 5'  GAGGCGGAAGACCAGCGA    84746        C  CCAC
                                TCGCTGG TC    TTTGTCTC
                                |||||||  ||    ||||||||
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                                AGCGACC AG    AGGCGGAG
                                    _ A___
GAM1661  LOC148089 3'  GGAACCGCGCATGGGAGCCAGC 79333          CTT_  TC
                                GCTGGCTCCCA    TG  TCC
                                ||||||||||    ||  |||
                                CGACCGAGGGT    GC  AGG
                                     ACGC  CA
GAM1661  LOC150935 3'  GAGCCTTGGGAGCCAGGA    80828    G        CTTT T
                                TC CTGGCTCCCA    G CTC
                                || ||||||||||    | |||
                                AG GACCGAGGGT    C GAG
                                 _        TC__ _
GAM1661  LOC151963 5'  AAAGCCTGGGAGCCTGCGA    81214      T       __
                                TCGC GGCTCCCA  CTTT
                                |||| ||||||||  ||||
                                AGCG CCGAGGGT  GAAA
                                  T       CC
GAM1661  LOC152283 5'  GGATGCTGAGGAAGCCAGCGA  86873         CCCA   T  C
                                TCGCTGGCT    CTT GT TCC
                                |||||||||    ||| || |||
                                AGCGACCGA    GAG CG AGG
                                     AG__   T  T
GAM1661  LOC152441 5'  GAGACAAAATGGGACCAG    86917      C    C
                                CTGG TCCCA TTTGTCTC
                                |||| ||||| ||||||||
                                GACC AGGGT AAACAGAG
                                  _    A
GAM1661  LOC157653 5'  GAACCGGGGAGCCAGCGA    82444           ACTTT  C
                                TCGCTGGCTCCC     GT TC
                                ||||||||||||    || ||
                                AGCGACCGAGGG     CA AG
                                     GC___  _
GAM1661  LOC158943 5'  GAGGCCGCGGAGCCAGCGA   61150          CACTTT
                                TCGCTGGCTCC     GTCTC
                                ||||||||||     |||||
                                AGCGACCGAGG     CGGAG
                                     CGC___
GAM1661  LOC163101 5'  GGACAATGAGAGCCAGC     83313         C  CT
                                GCTGGCTC CA  TTGTCT
                                |||||||| ||  ||||||
                                CGACCGAG GT  AACAGG
                                    A  __
GAM1661  LOC196759 5'  GAAGCTGGTGGGAGCCAGGA  88912    G         TT TC
                                TC CTGGCTCCCACT  G  TC
                                || ||||||||||||  |  ||
                                AG GACCGAGGGTGG  C  AG
                                 _          T_ GA
GAM1661  LOC199864 5'  GAAGCTGGTGGGAGCCAGGA  91459    G         TT TC
                                TC CTGGCTCCCACT  G  TC
                                || ||||||||||||  |  ||
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                                AG GACCGAGGGTGG  C  AG
                                 _         T_ GA
GAM1661  LOC202908 5'  GAGACAAAGACCAACGA     90723     C   CTCCCA
                                TCG TGG     CTTTGTCTC
                                ||| |||     |||||||||
                                AGC ACC     GAAACAGAG
                                  A   A_____
GAM1661  LOC206973 5'  GGAGATCTGGCACGGGGGCCAG 91111           A__  TT
           CGA                    TCGCTGGCTCCC   CT  GTCTCC
                                ||||||||||||   ||  ||||||
                                AGCGACCGGGGG   GG  TAGAGG
                                       CAC  TC
GAM1661  LOC220522 5'  GGAGACAGAGAAACCAGC    61142      CTCCCA
                                GCTGG     CTTTGTCTCC
                                |||||     ||||||||||
                                CGACC     GAGACAGAGG
                                   AAA___
GAM1661  LOC222057 5'  GAGACAAAGACCAGCGA     94353       CTCCCA
                                TCGCTGG     CTTTGTCTC
                                |||||||     |||||||||
                                AGCGACC     GAAACAGAG
                                    A_____
GAM1661  LOC222178 5'  GAAGAAGAAAAGCCAGTGA    95837        CCCA    G
                                TCGCTGGCT    CTTT TC
                                |||||||||    |||| ||
                                AGTGACCGA    GAAG AG
                                      AAA_    A
GAM1661  LOC255452 5'  GGAGCAGGGATGGAACCAGC   99396      C   CA    T
                                GCTGG TCC  CTTTG CTCC
                                ||||| |||  ||||| ||||
                                CGACC AGG  GGGAC GAGG
                                   A   TA    _
GAM1661  LOC256542 3'  GGAAACAAGGAGAGTCAGC    97291        CCA     C
                                GCTGGCTC   CTTTGT TCC
                                ||||||||   |||||| |||
                                CGACTGAG   GGAACA AGG
                                     A__     A
GAM1661  LOC256878 5'  GAGACAAAGACCAACGA     98687     C   CTCCCA
                                TCG TGG     CTTTGTCTC
                                ||| |||     |||||||||
                                AGC ACC     GAAACAGAG
                                  A   A_____
GAM1661  LOC57333  3'  GGAGGCAATAAAAGCCAGCG   74092        CCCACT
                                CGCTGGCT     TTGTCTCC
                                ||||||||     ||||||||
                                GCGACCGA     AACGGAGG
                                     AAAT__
GAM1661  LOC90625  3'  GGAGGGATGGGACCCAGC    64380      C    _  TTGT
                                GCTGG TCCCA CT    CTCC
                                ||||| ||||| ||    ||||
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                                CGACC AGGGT GG   GAGG
                                  C    A ____
GAM1662 ARAF1    5' TGGCACCTGCCCAGCCCCACCT 64647     ACAGA      TGC
             CA                    TGAG    GCTGGGCA  GCCA
                                ||||    ||||||||  ||||
                                ACTC    CGACCCGT  CGGT
                                  CACCC       CCA
GAM1662 FOS      5' TGCTCCTACCCAGCTCTGCTTC 19137     GA        CAT__
             A                     TGA  CAGAGCTGGG    GCG
                                ||| ||||||||||    |||
                                ACT  GTCTCGACCC    CGT
                                  TC        ATCCT
GAM1662 GPR81    3' TGGCGCATGCCTATAGTCTCA  51760       AGAGC
                                TGAGAC    TGGGCATGCGCCA
                                ||||||    ||||||||||||
                                ACTCTG    ATCCGTACGCGGT
                                   AT___
GAM1662 IL2RB    3' GGCACCAAGCTCTGTCCA    7943     A       G  CATGC
                                TG GACAGAGCT GG     GCC
                                || |||||||| ||     |||
                                AC CTGTCTCGA CC     CGG
                                 _       A  A____
GAM1662 KCNA7    3' TGGCACATGCCTGTGATCCCA  49909    A  CAGA  T      C
                                TG GA    GC GGGCATG GCCA
                                || ||    || ||||||| ||||
                                AC CT    TG TCCGTAC CGGT
                                 C  AG__  _      A
GAM1662 KIFC3    5' GCTCGCCCAGCCCTAGCTCA   19890     AC  A      AT
                                TGAG  AG GCTGGGC  GC
                                ||||  || |||||||  ||
                                ACTC  TC CGACCCG  CG
                                  GA  C      CT
GAM1662 MMP14    3' GCACCCCTCAAGCCTGTCTCA  18429         A   __   CA
                                TGAGACAG GCT  GGG  TGC
                                |||||||| |||  |||  |||
                                ACTCTGTC CGA  TCC  ACG
                                     _  AC   CC
GAM1662 NPHS1    3' TGGCGCATGCCTGTAGTCCCA  17376    A   AGA  T
                                TG GAC   GC GGGCATGCGCCA
                                || |||   || ||||||||||||
                                AC CTG   TG TCCGTACGCGGT
                                 C   A__  _
GAM1662 POLL     3' TGTCTGCCCAGCCCTCTCCCA  26094    A  C  A      T
                                TG GA AG GCTGGGCA GCG
                                || || || |||||||| |||
                                AC CT TC CGACCCGT TGT
                                 C  C  C       C
GAM1662 RBL1     3' TGGCGCATGCCTATAATC    12792    GC_
                                GA   TGGGCATGCGCCA
                                ||   ||||||||||||
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                                CT   ATCCGTACGCGGT
                                 AAT
GAM1662  SERPINH2  3'  GCTGCCTCCCCAGCTCTATCCC 8785     A  C       CAT  _
              A                   TG GA AGAGCTGGG   GC GC
                                  || || |||||||||   || ||
                                  AC CT TCTCGACCC   CG CG
                                   C  A       CTC  T
GAM1662  TNFSF10   3'  TGGCACATGCCTGTAGTCCCA  15096    A   AGA  T     C
                                  TG GAC   GC GGGCATG GCCA
                                  || |||   || ||||||| ||||
                                  AC CTG   TG TCCGTAC CGGT
                                   C  A__  _      A
GAM1662  XT3      3'  GCCCCAACTCTGTGCTCA    39916      _     C    CAT
                                  TGAG ACAGAG TGGG   GC
                                  |||| |||||| ||||   ||
                                  ACTC TGTCTC ACCC   CG
                                    G     A   ___
GAM1662  AF020591  3'  TGGCGCATACCTGTAGTCCCA  27917    A   AGA  T  C
                                  TG GAC   GC GGG ATGCGCCA
                                  || |||   || ||| ||||||||
                                  AC CTG   TG TCC TACGCGGT
                                   C  A__  _  A
GAM1662  BIRC1    3'  TGGCACATGCCTGTAGTCCCA  16996    A   AGA  T     C
                                  TG GAC   GC GGGCATG GCCA
                                  || |||   || ||||||| ||||
                                  AC CTG   TG TCCGTAC CGGT
                                   C  A__  _      A
GAM1662  C19orf7   3'  TGGCGCATGCCTGCTCCTGTC  61784       _  T
                                  GACAG AGC GGGCATGCGCCA
                                  ||||| ||| ||||||||||||
                                  CTGTC TCG TCCGTACGCGGT
                                     C  _
GAM1662  C8orf17   3'  TGGCACATGCCTGTAGTCCCA  40001    A   AGA  T     C
                                  TG GAC   GC GGGCATG GCCA
                                  || |||   || ||||||| ||||
                                  AC CTG   TG TCCGTAC CGGT
                                   C  A__  _      A
GAM1662  CARD14   3'  TGGCACATGAGGCCGGCTCT   54487        G__   C
                                  AGAGCTGG   CATG GCCA
                                  ||||||||   |||| ||||
                                  TCTCGGCC   GTAC CGGT
                                       GGA   A
GAM1662  DIO2     3'  CAGACCCAGCTCTGTTCCA   26549    AG        CA
                                  TG  ACAGAGCTGGG  TG
                                  ||  ||||||||||  ||
                                  AC  TGTCTCGACCC  AC
                                   CT         AG
GAM1662  DKFZp434E0519 3'  TGGCACATGCCTGTAGTCCCA  51004    A   AGA  T     C
                                  TG GAC   GC GGGCATG GCCA
                                  || |||   || ||||||| ||||
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                                AC CTG   TG TCCGTAC CGGT
                                 C  A__ _     A
GAM1662  DKFZP434J037 3'  TGGCGCGATCTCAGCTCACCTC 48958     ACA      CA
            A                    TGAG   GAGCTGGG  TGCGCCA
                                 ||||   ||||||||  |||||||
                                 ACTC   CTCGACTC  GCGCGGT
                                   CA_      TA
GAM1662  DKFZp727G131 3'  TGGCACATGCCTGCAGTCCCA  59700    A   AGA  T     C
                                 TG GAC   GC GGGCATG GCCA
                                 || |||   || ||||||| ||||
                                 AC CTG   CG TCCGTAC CGGT
                                  C  A__ _     A
GAM1662  FLJ10803  3'  TGGCACATGCCTGTAATCTCA  37212      CAGA  T     C
                                 TGAGA    GC GGGCATG GCCA
                                 |||||    || ||||||| ||||
                                 ACTCT    TG TCCGTAC CGGT
                                    AA__ _     A
GAM1662  FLJ11106  3'  CAGATCCAGACTCTGTCTCA   37620         _    CA
                                 TGAGACAGAG CTGGG  TG
                                 |||||||||| |||||  ||
                                 ACTCTGTCTC GACCT  AC
                                       A    AG
GAM1662  FLJ11539  3'  TGGACCCCCAGCTCCGTCTC   45709      A      CATGCG
                                 GAGAC GAGCTGGG     CCA
                                 ||||| ||||||||     |||
                                 CTCTG CTCGACCC     GGT
                                    C       CCA___
GAM1662  FLJ12618  3'  TGGCGCATGCCTGTAATCTCA  46511      CAGA  T
                                 TGAGA    GC GGGCATGCGCCA
                                 |||||    || ||||||||||||
                                 ACTCT    TG TCCGTACGCGGT
                                    AA__ _
GAM1662  FLJ13193  3'  TGGCGCATGCCTGTAGTCCCA  50740    A   AGA  T
                                 TG GAC   GC GGGCATGCGCCA
                                 || |||   || ||||||||||||
                                 AC CTG   TG TCCGTACGCGGT
                                  C  A__ _
GAM1662  FLJ13352  3'  TGGCACATGCCTGTAGTCCCA  45057    A   AGA  T     C
                                 TG GAC   GC GGGCATG GCCA
                                 || |||   || ||||||| ||||
                                 AC CTG   TG TCCGTAC CGGT
                                  C  A__ _     A
GAM1662  FLJ20004  3'  TGGCGCATGCCTTTAATCTCA  34770      CAGAGCT
                                 TGAGA      GGGCATGCGCCA
                                 |||||      ||||||||||||
                                 ACTCT      TCCGTACGCGGT
                                    AATT____
GAM1662  FLJ20337  5'  CGTGACCAACTTGTCTCA    35441        G  C   G
                                 TGAGACA AG TGG CATG
                                 ||||||| || ||| ||||
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                                ACTCTGT TC ACC GTGC
                                    _ A  A
GAM1662 FLJ20464 3' TGGCACATGCCTGTAATCTCA 35704     CAGA  T     C
                                TGAGA   GC GGGCATG GCCA
                                |||||   || ||||||| ||||
                                ACTCT   TG TCCGTAC CGGT
                                   AA__ _     A
GAM1662 FLJ23447 3' TGGCACATGCCTGTAGTCCCA 46134   A  AGA  T     C
                                TG GAC   GC GGGCATG GCCA
                                || |||   || ||||||| ||||
                                AC CTG   TG TCCGTAC CGGT
                                 C  A__ _     A
GAM1662 FLJ31455 3' TGGCGCATACCTGTAGTCCCA 59295   A  AGA  T  C
                                TG GAC   GC GGG ATGCGCCA
                                || |||   || ||| ||||||||
                                AC CTG   TG TCC TACGCGGT
                                 C  A__ _  A
GAM1662 FUSIP1   3' TGGCACATGCCTGTAATCTCA 55045     CAGA  T     C
                                TGAGA   GC GGGCATG GCCA
                                |||||   || ||||||| ||||
                                ACTCT   TG TCCGTAC CGGT
                                   AA__ _     A
GAM1662 GCN2     3' TGGCACATGCCTGTAGTCCCA 63441    A  AGA  T     C
                                TG GAC   GC GGGCATG GCCA
                                || |||   || ||||||| ||||
                                AC CTG   TG TCCGTAC CGGT
                                 C  A__ _     A
GAM1662 HSPC121  3' GCCACCCCAACCCTATCTCA  60468     C  AGC   CA  C
                                TGAGA AG   TGGG  TG GC
                                ||||| ||   ||||  || ||
                                ACTCT TC   ACCC  AC CG
                                   A  CCA   C_  C
GAM1662 IL10RB   3' TGGCGCATGCCTATAATC    7131     GC_
                                GA   TGGGCATGCGCCA
                                ||   ||||||||||||
                                CT   ATCCGTACGCGGT
                                 AAT
GAM1662 KBRAS2   3' CGATCCCAGCCCCATTTCA   34622      CAGA     C  G
                                TGAGA   GCTGGG AT CG
                                |||||   |||||| || ||
                                ACTTT   CGACCC TA GC
                                   ACCC     _ _
GAM1662 KIAA0074 3' GCGCCCTGAAGCTCCGTGCTCA 71852     _  A    __   CAT
                                TGAG AC GAGCT  GGG   GCGC
                                |||| || |||||  |||   ||||
                                ACTC TG CTCGA  TCC   CGCG
                                  G  C    AG  ___
GAM1662 KIAA0391 3' GCACATGCCTGTGGTCCCA   28613    A  AGA  T     C
                                TG GAC   GC GGGCATG GC
                                || |||   || ||||||| ||
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                                AC CTG   TG TCCGTAC CG
                                 C   G__ _      A
GAM1662 KIAA0449 3' GGCCCCCAGCTCCACTCA    34637     ACA      CATGC
                                TGAG   GAGCTGGG    GCC
                                ||||   ||||||||    |||
                                ACTC   CTCGACCC    CGG
                                  AC_      C____
GAM1662 KIAA0892 3' TGGCGCATGCCTGTAGTCCCA 71575    A   AGA  T
                                TG GAC   GC GGGCATGCGCCA
                                || |||   || ||||||||||||
                                AC CTG   TG TCCGTACGCGGT
                                 C   A__ _
GAM1662 KIAA1009 3' GGCCTCCAGCTCTATCCA    30319    A  C       CATGC
                                TG GA AGAGCTGGG    GCC
                                || || |||||||||    |||
                                AC CT TCTCGACCT    CGG
                                 _ A       C____
GAM1662 KIAA1030 3' TGGCACATGCCTATAGTCCCA 94988    A   AGAGC      C
                                TG GAC    TGGGCATG GCCA
                                || |||    |||||||| ||||
                                AC CTG    ATCCGTAC CGGT
                                 C   AT___       A
GAM1662 KIAA1614 3' TGGCGCATGCCTATAATC    70671    GC_
                                GA   TGGGCATGCGCCA
                                ||   ||||||||||||
                                CT   ATCCGTACGCGGT
                                 AAT
GAM1662 KIAA1940 3' TGGCGTCACTCCCTAGCTCTGT 80793    A         CA_ _
            CCCA                   TG GACAGAGCTGGG   TG CGCCA
                                || ||||||||||||   || |||||
                                AC CTGTCTCGATCC   AC GCGGT
                                 C          CTC  T
GAM1662 KIAA1979 3' TGGCACATGCCTGCCGTCTCA 89657       AGA  T     C
                                TGAGAC   GC GGGCATG GCCA
                                ||||||   || ||||||| ||||
                                ACTCTG   CG TCCGTAC CGGT
                                   C__ _      A
GAM1662 MGC14859 3' TGGCTGCTGCCCTCAGCTCCGC 62607     ACA    __    T _
            CTCA                   TGAG   GAGCT  GGGCA GC GCCA
                                ||||   |||||  ||||| || ||||
                                ACTC   CTCGA  CCCGT CG CGGT
                                  CGC    CT    _ T
GAM1662 MGC15873 5' TGACGCGGTGAACTCTGTCCA 53009    A     CTGG  A   C
                                TG GACAGAG    GC TGCG CA
                                || |||||||   || |||| ||
                                AC CTGTCTC    TG GCGC GT
                                 _      AAG_ _    A
GAM1662 MOST2    5' TGGCACATGCCTGTAGTCCCA 40074    A   AGA  T     C
                                TG GAC   GC GGGCATG GCCA
                                || |||   || ||||||| ||||
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                                AC CTG   TG TCCGTAC CGGT
                                 C  A__ _     A
GAM1662 PDE7B    5' GCAGGCTCGGCTCTGTCCCA  38950    A         A
                                TG GACAGAGCTGGGC TGC
                                || |||||||||||| |||
                                AC CTGTCTCGGCTCG ACG
                                 C          G
GAM1662 PSR      3' TGGCACATGCCTGTAGTCCCA 65796    A  AGA  T     C
                                TG GAC   GC GGGCATG GCCA
                                || |||   || ||||||| ||||
                                AC CTG   TG TCCGTAC CGGT
                                 C  A__ _     A
GAM1662 SERPINH1 3' GCTGCCTCCCCAGCTCTATCCC 16373    A  C       CAT  _
             A                   TG GA AGAGCTGGG   GC GC
                                || || |||||||||   || ||
                                AC CT TCTCGACCC   CG CG
                                 C  A       CTC  T
GAM1662 SMCR8    3' TGCTCACCCAGCTCTGCTC   59254    A       CAT
                                GAG CAGAGCTGGG   GCG
                                ||| ||||||||||   |||
                                CTC GTCTCGACCC   CGT
                                  _        ACT
GAM1662 TRIAD3   3' TGGCGCATGCCTATAATC    96143    GC_
                                GA   TGGGCATGCGCCA
                                ||   ||||||||||||
                                CT   ATCCGTACGCGGT
                                 AAT
GAM1662 TRIM4    3' GGCCTCCAGCTCCATCCA    53408    A  CA      CATGC
                                TG GA  GAGCTGGG    GCC
                                || ||  ||||||||    |||
                                AC CT  CTCGACCT    CGG
                                 _ AC       C____
GAM1662 WBSCR23  3' TGGCGCATGCCTATAGTCCCA 47452    A   AGAGC
                                TG GAC    TGGGCATGCGCCA
                                || |||    ||||||||||||
                                AC CTG    ATCCGTACGCGGT
                                 C  AT___
GAM1662 LOC115708 3' TGACGCACACCCCTGAGATCTC 73921      ___  AGCT   CA   C
             A                   TGAGA   CAG   GGG  TGCG CA
                                |||||   |||   |||  |||| ||
                                ACTCT   GTC   CCC  ACGC GT
                                   AGA  _____  AC   A
GAM1662 LOC126282 3' TGGCACATGCCTGTAGTCCCA  74971    A  AGA  T     C
                                TG GAC   GC GGGCATG GCCA
                                || |||   || ||||||| ||||
                                AC CTG   TG TCCGTAC CGGT
                                 C  A__ _     A
GAM1662 LOC130535 3' TGGCGCATGCCTGTGATCCCA  76660    A  CAGA  T
                                TG GA    GC GGGCATGCGCCA
                                || ||    || ||||||||||||
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                                AC CT    TG TCCGTACGCGGT
                                 C  AG__  _
GAM1662  LOC145871 5'  TGGCCTTACCCCCAGCCCTGGC 84554      A   A     CATGC_
                TCA                    TGAG CAG GCTGGG     GCCA
                                |||| ||| ||||||     ||||
                                ACTC GTC CGACCC     CGGT
                                  G   C     CCATTC
GAM1662  LOC146325 5'  GTGCCCGGCCCTGCCTCA    59848      A   A
                                TGAG CAG GCTGGGCAT
                                |||| ||| |||||||||
                                ACTC GTC CGGCCCGTG
                                  C   C
GAM1662  LOC146540 3'  TGGCACATGCCTGTAGTCCCA  78531    A   AGA  T      C
                                TG GAC   GC GGGCATG GCCA
                                || |||   || ||||||| ||||
                                AC CTG   TG TCCGTAC CGGT
                                 C   A__  _      A
GAM1662  LOC147160 5'  CGACTTGCCAGCTCTGTCT    85072           G  TG_
                                AGACAGAGCTGG CA   CG
                                |||||||||||| ||   ||
                                TCTGTCTCGACC GT   GC
                                       _  TCA
GAM1662  LOC147727 5'  TGGCACATGCCTGTAGTCCCA  79143    A   AGA  T      C
                                TG GAC   GC GGGCATG GCCA
                                || |||   || ||||||| ||||
                                AC CTG   TG TCCGTAC CGGT
                                 C   A__  _      A
GAM1662  LOC147837 3'  CGACAGAGCCAGACCCTGTCTC 79205         AG_   GCA  _
                A                TGAGACAG   CTGG   TG CG
                                ||||||||   ||||   || ||
                                ACTCTGTC   GACC   AC GC
                                     CCA    GAG  A
GAM1662  LOC148758 5'  TGGCGCATGCCTATAATC    79730    GC_
                                GA   TGGGCATGCGCCA
                                ||   ||||||||||||
                                CT   ATCCGTACGCGGT
                                 AAT
GAM1662  LOC197201 3'  TGGCACATGCCTGTAATCTCA  89291       CAGA  T      C
                                TGAGA    GC GGGCATG GCCA
                                |||||    || ||||||| ||||
                                ACTCT    TG TCCGTAC CGGT
                                   AA__  _      A
GAM1662  LOC202052 3'  TGGCACATGCCTGTAGTCCCA  91905    A   AGA  T      C
                                TG GAC   GC GGGCATG GCCA
                                || |||   || ||||||| ||||
                                AC CTG   TG TCCGTAC CGGT
                                 C   A__  _      A
GAM1662  LOC255146 3'  GCAGCTTCCAGCTCTGCCTCA  97345      A         CA_
                                TGAG CAGAGCTGGG   TGC
                                |||| ||||||||||   |||
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                                ACTC GTCTCGACCT   ACG
                                  C         TCG
GAM1662 LOC255397 5' GCATCCCCAGCTCCATCCCA  99367    A  CA      C
                                TG GA  GAGCTGGG ATGC
                                || ||  |||||||| ||||
                                AC CT  CTCGACCC TACG
                                 C  AC       C
GAM1662 LOC90573  3' TGGCACATGCCTGTAATCTCA  63963      CAGA  T     C
                                TGAGA    GC GGGCATG GCCA
                                ||||||    || ||||||| ||||
                                ACTCT    TG TCCGTAC CGGT
                                   AA__ _      A
GAM1662 LOC90785  3' TGGCACACACCTGTGTGTCCA  64722    A   GA  T   CA  C
                                TG GACA  GC GGG  TG GCCA
                                || ||||  || |||  || ||||
                                AC CTGT  TG TCC  AC CGGT
                                 _   G_ _   AC  A
GAM1662 LOC96597  3' TGGCACACGCCCAGCTGCGTCG 67472    A   AG      A  C
             CA                   TG GAC  AGCTGGGC TG GCCA
                                || |||  |||||||| || ||||
                                AC CTG  TCGACCCG AC CGGT
                                 G   CG       C  A
GAM1663 BGN      3' CCAGCCCCCCACCTCGGGTCCC 9923         C    CAGAGA
             T                    AGGGACCC AGGT     CTGG
                                |||||||| ||||     ||||
                                TCCCTGGG TCCA     GACC
                                     C    CCCCCC
GAM1663 BLMH     3' TCCAGTCTCCACCAGGAACCT  6361     GA  CCA   CA
                                AGG  CC   GGT  GAGACTGGA
                                |||  ||   |||  |||||||||
                                TCC  GG   CCA  CTCTGACCT
                                  AA  A__   C_
GAM1663 HSPA1B   5' CCAGTCTCAGAGCGGAGCCC   19273     AC  CAGG  A
                                GGG  CC    TC GAGACTGG
                                |||  ||    || ||||||||
                                CCC  GG    AG CTCTGACC
                                  GA  CG__  A
GAM1663 HTRA3    3' CCACCTGACCTGAGGCCCC    90577     A  C       AGAC
                                GGG CC CAGGTCAG    TGG
                                ||| || ||||||||    |||
                                CCC GG GTCCAGTC    ACC
                                  C  A       C___
GAM1663 HTRA3    3' CTGCCAGCCTGGGGTCCCT    90580           ___
                                AGGGACCCCAGGT   CAG
                                ||||||||||||   |||
                                TCCCTGGGGTCCG   GTC
                                       ACC
GAM1663 IL2RB    3' CCAGCTAACTCTGACCTGGGAG 7935       AC          A___
             CCCT                    AGGG  CCCAGGTCAGAG    CTGG
                                ||||  ||||||||||||   ||||
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                                TCCC  GGGTCCAGTCTC    GACC
                                  GA          AATC
GAM1663 LENG4    3'  CCTATGACCTGGGTCCCT    44417        C     GAGACT
                                AGGGACCC AGGTCA     GG
                                |||||||| ||||||     ||
                                TCCCTGGG TCCAGT     CC
                                    _     AT_____
GAM1663 LNK      3'  TCCTGCCCGGGGTCCCT     19652         A  T   A
                                AGGGACCCC GG CAG GA
                                ||||||||| || ||| ||
                                TCCCTGGGG CC GTC CT
                                     C  _   _
GAM1663 LY95     5'  CCAGTCTTCTCCAGGTGTCCC  17896      C  A  TCA
                                GGGAC CC GG   GAGACTGG
                                ||||| || ||   ||||||||
                                CCCTG GG CC   TTCTGACC
                                   T  A  TC_
GAM1663 MOG      3'  TCCAGTCTTCCACCTGGAAGCC 11676      ACC     CA
              CT                  AGGG   CCAGGT  GAGACTGGA
                                ||||   ||||||  |||||||||
                                TCCC   GGTCCA  TTCTGACCT
                                  GAA     CC
GAM1663 NESH     5'  CCAGTCTCCGACCCCATCCC   33570      CCCCA    A
                                GGGA    GGTC GAGACTGG
                                ||||    |||| ||||||||
                                CCCT    CCAG CTCTGACC
                                  ACC__    C
GAM1663 NFATC1   3'  CCAGCCCTTCTGGCACCCCT   21596      ACCCCAG      A__
                                AGGG      GTCAGAG   CTGG
                                ||||      |||||||   ||||
                                TCCC      CGGTCTT   GACC
                                  CA_____       CCC
GAM1663 RANBP3   3'  CCAACTATAGGCCTGGGACCCC 24641     AC       AG_  AC
                                GGG  CCCAGGTC   AG  TGG
                                |||  ||||||||   ||  |||
                                CCC  GGGTCCGG   TC  ACC
                                  CA       ATA  A_
GAM1663 RANBP3   3'  CCAACTATAGGCCTGGGACCCC 14633     AC       AG_  AC
                                GGG  CCCAGGTC   AG  TGG
                                |||  ||||||||   ||  |||
                                CCC  GGGTCCGG   TC  ACC
                                  CA       ATA  A_
GAM1663 RGS19IP1 3'  CCAGTCTGGCCGGGGTCCC    63169         A    GA
                                GGGACCCC GGTCA  GACTGG
                                |||||||| |||||  ||||||
                                CCCTGGGG CCGGT  CTGACC
                                     _    __
GAM1663 SIRT2    3'  CCAATCTCTTACAGCTCCCT   48360       CCCCAG  C    C
                                AGGGA     GT AGAGA TGG
                                |||||     || ||||| |||
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                                TCCCT     CA TCTCT ACC
                                   CGA___  T    A
GAM1663 SIRT2    3' CCAATCTCTTACAGCTCCCT  25286      CCCCAG  C    C
                                AGGGA     GT AGAGA TGG
                                |||||     || ||||| |||
                                TCCCT     CA TCTCT ACC
                                   CGA___  T    A
GAM1663 SREBF1   3' TCCTGACCTGAGGCTCCT    96078     GA  C      A
                                AGG  CC CAGGTCAG GA
                                |||  || |||||||| ||
                                TCC  GG GTCCAGTC CT
                                  TC  A      _
GAM1663 TEM5     3' CCAAGGTCTGACCTAGGGTTCC 52297       C      GA  _
                                GGGACCC AGGTCAGA  CT GG
                                ||||||| ||||||||  || ||
                                CCTTGGG TCCAGTCT  GA CC
                                     A       G_  A
GAM1663 TIMM17B  3' CCAGTTAGCCCTGGGACCCT  20690     AC     TCAGA
                                AGGG  CCCAGG    GACTGG
                                ||||  ||||||    ||||||
                                TCCC  GGGTCC    TTGACC
                                  A_     CGA__
GAM1663 ARHGDIG  3' CCTGCTCTGTCCCGGGACCCC 8620      AC   A  T    ACT
                                GGG  CCC GG CAGAG   GG
                                |||  ||| || |||||   ||
                                CCC  GGG CC GTCTC   CC
                                  CA   C  T    GT_
GAM1663 ATP5D    3' CCAGCTCCTGGGGTCCC     9859          TCAG  A
                                GGGACCCCAGG    AG CTGG
                                ||||||||||    || ||||
                                CCCTGGGGTCC    TC GACC
                                      ____  _
GAM1663 C17orf31 3' CCTTATCAACCTGGGTCCCT  34538        C    CA  GACT
                                AGGGACCC AGGT  GA    GG
                                |||||||| ||||  ||    ||
                                TCCCTGGG TCCA  CT    CC
                                     _    A_  ATT_
GAM1663 C2orf7   3' TCCAGCCTCCCCTACCCAGGGT 51274        CA   CA__   A
            CTCT                  AGGGACCC  GGT    GAG CTGGA
                                |||||||  |||    ||| |||||
                                TCTCTGGG  CCA    CTC GACCT
                                    AC   TCCC   C
GAM1663 CLIPR-59 5' CCAGTCTCCACTTTGGTCCC  32015       CC    CA
                                GGGACC  AGGT  GAGACTGG
                                ||||||  ||||  ||||||||
                                CCCTGG  TTCA  CTCTGACC
                                   T_    C_
GAM1663 CLIPR-59 3' TCCAGGGCGGACCTGGGGCCCC 32021     A        AGAGA
                                GGG CCCCAGGTC     CTGGA
                                ||| |||||||||     |||||
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                                CCC GGGGTCCAG    GACCT
                                  C       GCGG_
GAM1663  COL12A1   3'  CCAGTCTCTGACCCTTCCC   16470     CCCCA
                                GGGA    GGTCAGAGACTGG
                                ||||    ||||||||||||
                                CCCT    CCAGTCTCTGACC
                                  TC___
GAM1663  COL12A1   3'  CCAGTCTCTGACCCTTCCC   55534     CCCCA
                                GGGA    GGTCAGAGACTGG
                                ||||    ||||||||||||
                                CCCT    CCAGTCTCTGACC
                                  TC___
GAM1663  CYP2A7    5'  TCAGCTGCCCTGGGGTCCC   48354         T   AGA
                                GGGACCCCAGG CAG   CTGG
                                |||||||||| |||   ||||
                                CCCTGGGGTCC GTC   GACT
                                      C   ___
GAM1663  CYP2A7    5'  TCAGCTGCCCTGGGGTCCC   7542          T   AGA
                                GGGACCCCAGG CAG   CTGG
                                |||||||||| |||   ||||
                                CCCTGGGGTCC GTC   GACT
                                      C   ___
GAM1663  FASTK     3'  CCAGGATACCGGGGTCCC    47685        A   CAGAGA
                                GGGACCCC GGT     CTGG
                                |||||||| |||     ||||
                                CCCTGGGG CCA     GACC
                                    _   TAG___
GAM1663  FBXL9     3'  CCAGTCTCCAACCCTGGCCTT  25139     ACC    TCA_
                                AGGG   CCAGG    GAGACTGG
                                ||||   |||||    ||||||||
                                TTCC   GGTCC    CTCTGACC
                                  ___     CAAC
GAM1663  FLJ10874  3'  TCCAGAAAGAGTGACCTGGTGT 37330      C       GAGA__
            CCC                   GGGAC CCAGGTCA     CTGGA
                                |||||| ||||||||     |||||
                                CCCTG GGTCCAGT     GACCT
                                  T       GAGAAA
GAM1663  FLJ13241  3'  CCAGTCTCTCAGGCCTCCC   47649     CCCCA   __
                                GGGA    GGTC  AGAGACTGG
                                ||||    ||||  |||||||||
                                CCCT    CCGG  TCTCTGACC
                                  _____    AC
GAM1663  GIT1      3'  CCAACCTGTGTGCTGGGGTCCC 26720         GT  G  AC
                                GGGACCCCAG  CA AG  TGG
                                ||||||||||  || ||  |||
                                CCCTGGGGTC  GT TC  ACC
                                      GT  G  CA
GAM1663  HYPC      5'  CCAGCCCCTGGAACAGGGGTTC 65216         AGG_   AGA
            CT                    AGGGACCCC   TCAG   CTGG
                                |||||||||   ||||   ||||
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                                TCCTTGGGG   GGTC  GACC
                                     ACAA   CCC
GAM1663 KIAA0258 3' CCAGCCTCCTAGGATCCC   29466     C  C  TCAG  A
                                GGGA CC AGG   AG CTGG
                                |||| || |||   || ||||
                                CCCT GG TCC   TC GACC
                                  A  A  ____  C
GAM1663 KIAA0397 3' CCACGAGTGAACCTGGGGCCCC 62345    A      _  GAGAC
                                GGG CCCCAGGT CA    TGG
                                ||| |||||||| ||    |||
                                CCC GGGGTCCA GT    ACC
                                  C       A  GAGC_
GAM1663 KIAA0447 3' TCCAGTTTCCCTGCGGGCCCCT 72130     A  _   TCA
                                AGGG CCC CAGG  GAGACTGGA
                                |||| ||| ||||  |||||||||
                                TCCC GGG GTCC  CTTTGACCT
                                  C  C   ___
GAM1663 KIAA0449 5' CAGTTCCCTGGGGTCCCT   34634          TCAGA
                                AGGGACCCCAGG   GACTG
                                ||||||||||||   |||||
                                TCCCTGGGGTCC   TTGAC
                                      C____
GAM1663 KIAA0493 5' CCAGCCCGAGACGCCTGGGGTC 64930          CAGAGA__
           CC                   GGGACCCCAGGT       CTGG
                                ||||||||||||       ||||
                                CCCTGGGGTCCG       GACC
                                      CAGAGCCC
GAM1663 KIAA0674 3' TCAGACTGACCTGGGAGCCCT  61244     AC        AGA
                                AGGG  CCCAGGTCAG   CTGG
                                ||||  ||||||||||   ||||
                                TCCC  GGGTCCAGTC   GACT
                                  GA        A__
GAM1663 KIAA1130 5' CCAGTCCCCCACCTGGGGCGCC 63082    A_      CAGA
           C                    GGG  CCCCAGGT   GACTGG
                                |||  ||||||||   ||||||
                                CCC  GGGGTCCA   CTGACC
                                  GC       CCCC
GAM1663 KIAA1465 3' TCCAGCCCGGTGCCTGGGGCGC 61510    GA      CAGAGA
           CT                   AGG  CCCCAGGT     CTGGA
                                |||  ||||||||     |||||
                                TCC  GGGGTCCG     GACCT
                                  GC       TGGCCC
GAM1663 KIAA1719 3' TCTGTCTCCAACCTGGGGTCCC 68740          CA    T
           T                    AGGGACCCCAGGT  GAGAC GGA
                                ||||||||||||  ||||| |||
                                TCCCTGGGGTCCA  CTCTG TCT
                                      AC    _
GAM1663 KIAA1856 3' CCGGCCCAAGCCCAGGGTCCCT 94230       CA   CAGAGA
                                AGGGACCC  GGT     CTGG
                                ||||||||  |||     ||||
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                              TCCCTGGG CCG    GGCC
                                  AC  AACCC_
GAM1663 KIAA1924 3' TCCAGCTTCATGTGACCCTGGG 74059       CA   ____  A
            TCCCT                 AGGGACCC GGTCA   GAG CTGGA
                              |||||||| ||||| ||| |||||
                              TCCCTGGG CCAGT   TTC GACCT
                                  TC   GTAC  _
GAM1663 KIAA1949 5' CCAGTCTCCGGATCTCCC   93717    CCCCA  A_
                              GGGA   GGTC GAGACTGG
                              ||||   |||| ||||||||
                              CCCT   CTAG CTCTGACC
                                _____  GC
GAM1663 KIAA1949 5' CCAGTCTCCGGATCTCCC   99590    CCCCA  A_
                              GGGA   GGTC GAGACTGG
                              ||||   |||| ||||||||
                              CCCT   CTAG CTCTGACC
                                _____  GC
GAM1663 KIAA1949 5' CCAGTCTCCGGATCTCCC   99694    CCCCA  A_
                              GGGA   GGTC GAGACTGG
                              ||||   |||| ||||||||
                              CCCT   CTAG CTCTGACC
                                _____  GC
GAM1663 KIAA1978 3' CCAGCCGTGGGGCCCGGGGTCC 74890       A  AGAGA_
            CT                  AGGGACCCC GGTC    CTGG
                              ||||||||| ||||    ||||
                              TCCCTGGGG CCGG    GACC
                                  C   GGTGCC
GAM1663 LASP1   3' CCAGTCTCCAGGGACCCT   21576    A  CAGGTCA
                              AGGG CCC     GAGACTGG
                              |||| |||     ||||||||
                              TCCC GGG     CTCTGACC
                                A  AC_____
GAM1663 MAPK11  3' TTCTGGCCTAGGACCCCT   12314    AC  C
                              AGGG  CC AGGTCAGAG
                              ||||  || |||||||||
                              TCCC  GG TCCGGTCTT
                                CA  A
GAM1663 MAPK11  3' TTCTGGCCTAGGACCCCT   58102    AC  C
                              AGGG  CC AGGTCAGAG
                              ||||  || |||||||||
                              TCCC  GG TCCGGTCTT
                                CA  A
GAM1663 MGC14859 3' TCTCTGACTGGGGCCCCT   62604    A    G
                              AGGG CCCCAG TCAGAGA
                              |||| |||||| |||||||
                              TCCC GGGGTC AGTCTCT
                                C    _
GAM1663 MGC15438 5' CCAGTCTCACAAAGGCCCC   52850    A  CCAG  CA
                              GGG CC   GT  GAGACTGG
                              ||| ||   ||  ||||||||
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                                CCC GG   CA  CTCTGACC
                                  C  AAA_  __
GAM1663 NLI-IF   3'  TCCAACTGTTTCTGAAGCCCCT 41344     ACCCCAGG      ___
                                AGGG      TCAGAGAC   TGGA
                                ||||      ||||||||   ||||
                                TCCC      AGTCTTTG   ACCT
                                  CGA_____      TCA
GAM1663 NOLC1    3'  TCCAGTGGACCTGGGAACCCT  17637     AC      AGAG
                                AGGG  CCCAGGTC   ACTGGA
                                ||||  ||||||||   ||||||
                                TCCC  GGGTCCAG   TGACCT
                                  AA      G___
GAM1663 PRO2389  3'  CCAGTCAGCTTGGGTCCCT   64475       C   CAGA
                                AGGGACCC AGGT   GACTGG
                                |||||||| ||||   ||||||
                                TCCCTGGG TTCG   CTGACC
                                    _   A___
GAM1663 SHANK3   3'  CCAGCCTGAGCGGGGTTCC   66102       AGG   AGA
                                GGGACCCC   TCAG   CTGG
                                ||||||||   ||||   ||||
                                CCTTGGGG   AGTC   GACC
                                    CG_   C__
GAM1663 SMARCA4   3'  TCCAGTCTCGACCCCGAGCCCC 13248     ACCCCA   A
          T                      AGGG     GGTC GAGACTGGA
                                ||||     |||| |||||||||
                                TCCC     CCAG CTCTGACCT
                                  CGAGCC   _
GAM1663 SPIB     3'  CCACTTGTGCCTGGGGTCCCT  13355          CA   AC
                                AGGGACCCCAGGT  GAG  TGG
                                ||||||||||||  |||  |||
                                TCCCTGGGGTCCG  TTC  ACC
                                      TG   __
GAM1663 SYNGR4   5'  CCAGGGCTGGCCTGAAGCCC   25864     ACCC      AGA
                                GGG   CAGGTCAG   CTGG
                                |||   ||||||||   ||||
                                CCC   GTCCGGTC   GACC
                                  GAA_      GG_
GAM1663 T2BP     5'  CCAGTCTCCTCGATTCCC    70535     CCCCAG   A__
                                GGGA     GTC   GAGACTGG
                                ||||     |||   ||||||||
                                CCCT     TAG   CTCTGACC
                                  _______  CTC
GAM1663 TACR3    5'  TCCAGTCTTATCTGAAGACCC  8331     ACCC    CA
                                GGG   CAGGT  GAGACTGGA
                                |||   |||||  |||||||||
                                CCC   GTCTA  TTCTGACCT
                                  AGAA    __
GAM1663 TOMM40   3'  CCAGTGGGCCTGGGGTCCC   21482          AGAG
                                GGGACCCCAGGTC   ACTGG
                                ||||||||||||   |||||
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                                CCCTGGGGTCCGG   TGACC
                                      G___
GAM1663  TREX2    5'  TCCAACCTCTGACTGGCTGGTC 24233      __   G    AC
             CT                  GGGACC  CCAG TCAGAG  TGGA
                                 ||||||  |||| ||||||  ||||
                                 TCCTGG  GGTC AGTCTC  ACCT
                                    TC   _    CA
GAM1663  VPS4A    3'  CCAGCCACTGCCCCTGGGTCCC 26020       CA  T   AGA
             T                   AGGGACCC  GG CAG   CTGG
                                 ||||||||  || |||   ||||
                                 TCCCTGGG  CC GTC   GACC
                                      TC  C   ACC
GAM1663  LOC143287 3'  TCCGCTGTAACCCTAGGACCCC 83831    AC  C   T___   AGAC
                                 GGG  CC AGG   CAG   TGGA
                                 |||  || |||   |||   ||||
                                 CCC  GG TCC   GTC   GCCT
                                   CA  A   CAAT  ____
GAM1663  LOC147136 3'  CCAGTGAGAACTGACCTGAGTC 78862      CC      AG___
             CC                  GGGAC  CAGGTCAG    ACTGG
                                 |||||  ||||||||    |||||
                                 CCCTG  GTCCAGTC    TGACC
                                   A_       AAGAG
GAM1663  LOC147929 5'  TCCAGCAGCCTTGGGGTCCC   79273        _  CAGAGA
                                 GGGACCCCA GGT     CTGGA
                                 |||||||| |||     |||||
                                 CCCTGGGGT CCG     GACCT
                                      T   AC____
GAM1663  LOC149566 3'  TCCAGCCTGGATGACCTGGGAC 85654    AC       G__  A
             CCC                   GGG  CCCAGGTCA   AG CTGGA
                                 |||  |||||||||   || |||||
                                 CCC  GGGTCCAGT   TC GACCT
                                   CA       AGG  C
GAM1663  LOC149773 5'  CCAGTCTTCTGAGGCCCT    80291     A  C   GTCA
                                 AGGG CC CAG    GAGACTGG
                                 |||| || |||    ||||||||
                                 TCCC GG GTC    TTCTGACC
                                   _ A   ____
GAM1663  LOC152189 5'  TCCAGCCCCAGACCCGCCGGGG 81329        A___   AGAGA
             TCCCT                  AGGGACCCC    GGTC    CTGGA
                                 |||||||||   ||||    |||||
                                 TCCCTGGGG    CCAG    GACCT
                                      CCGC    ACCCC
GAM1663  LOC153196 5'  CCAGTCTCAGGGGTCACC    87166    _    AGGTCA
                                 GG GACCCC     GAGACTGG
                                 || ||||||     ||||||||
                                 CC CTGGGG     CTCTGACC
                                  A     A_____
GAM1663  LOC154807 5'  CTCTGCGACCTGGGGCCCT    87463     A       __
                                 AGGG CCCCAGGTC  AGAG
                                 ||||  |||||||||  ||||
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                                TCCC GGGGTCCAG  TCTC
                                  _       CG
GAM1663  LOC199958 3'  CCAGTCTCTGGCAACGCCCCT  91490     ACCCCAG
                                AGGG      GTCAGAGACTGG
                                ||||      ||||||||||||
                                TCCC      CGGTCTCTGACC
                                  CGCAA__
GAM1663  LOC201685 5'  CCAGTCTCATTGAATCCCT   91840      CCC   GTCA
                                AGGGA   CAG    GAGACTGG
                                |||||   |||    ||||||||
                                TCCCT   GTT    CTCTGACC
                                  AA_   A___
GAM1663  LOC204970 3'  CCAGCCGGAGCGTGGGGTCCC  90959         G  CAGAGA
                                GGGACCCCA GT      CTGG
                                |||||||||| ||      ||||
                                CCCTGGGGT CG      GACC
                                     G  AGGCC_
GAM1663  LOC221179 3'  CCAGTCTCTCCTCGGAGGCCCT 95193      A  _  _   TC
                                AGGG CC CC AGG  AGAGACTGG
                                |||| || || |||  |||||||||
                                TCCC GG GG TCC  TCTCTGACC
                                  _  A  C   __
GAM1663  LOC254105 3'  CCAGTCCAGGGCCTGGGCTCCC 96419      C       AGA
                                GGGA CCCAGGTC   GACTGG
                                |||| ||||||||   ||||||
                                CCCT GGGTCCGG   CTGACC
                                  C       GAC
GAM1663  LOC257185 5'  CCAGCATGCCAGGGGTCCC   98020        A  T  GAGA
                                GGGACCCC GG CA    CTGG
                                |||||||| || ||    ||||
                                CCCTGGGG CC GT    GACC
                                    A  _  AC__
GAM1663  LOC51161  3'  TCCTGACCTGAGGGCCCT    33046      A  _       A
                                AGGG CCC CAGGTCAG GA
                                |||| ||| |||||||| ||
                                TCCC GGG GTCCAGTC CT
                                  _   A       _
GAM1663  LOC91156  5'  CCAACTAAGGCCTGAGAGTCCC 65706       CC_     AG  AC
           T                     AGGGAC   CAGGTC  AG  TGG
                                ||||||   ||||||  ||  |||
                                TCCCTG   GTCCGG  TC  ACC
                                   AGA     AA  A_
GAM1664  A1BG     3'  TGAGACAGAATTTTGCTCT   56301         C  C
                                AGAGCAAGA TC GTCTCA
                                ||||||||| || ||||||
                                TCTCGTTTT AG CAGAGT
                                     A  A
GAM1664  AASS     3'  TGAGATGGAGTCTCGCTCTG   20463       A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
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                                GTCTCG TCTGAGGTAGAGT
                                   C
GAM1664 ADCY6    5' TGAGACGGAGTCTCACTCTG 31594      CA
                                CAGAG AGACTCCGTCTCA
                                ||||| ||||||||||||
                                GTCTC TCTGAGGCAGAGT
                                   AC
GAM1664 ADCY7    3' TGAGCCGTTCTTGCTCTG   8493        CTC T
                                CAGAGCAAGA  CG CTCA
                                |||||||||| || ||||
                                GTCTCGTTCT  GC GAGT
                                      T__ C
GAM1664 ALDH1B1  3' TGACACGGAGTCTCACTCTG 7329      CA      C
                                CAGAG AGACTCCGT TCA
                                ||||| ||||||||| |||
                                GTCTC TCTGAGGCA AGT
                                   AC       C
GAM1664 APM1     3' TGAGATGGAGTCTCACTCTG 17794     CA
                                CAGAG AGACTCCGTCTCA
                                ||||| ||||||||||||
                                GTCTC TCTGAGGTAGAGT
                                   AC
GAM1664 APOL1    3' TGAGACAGAGTCTTGCTCTG 14746        C
                                CAGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
                                GTCTCGTTCTGAG CAGAGT
                                      A
GAM1664 APPL     3' TGAGACAGAGTCTTGCTCTG 24959        C
                                CAGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
                                GTCTCGTTCTGAG CAGAGT
                                      A
GAM1664 ARCN1    3' TGAGATGGAGTCTCACTTTG 9759      CA
                                CAGAG AGACTCCGTCTCA
                                ||||| ||||||||||||
                                GTTTC TCTGAGGTAGAGT
                                   AC
GAM1664 ATP7A    3' TGAGACAGAGTCTTGTTTTG 5331        C
                                CAGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
                                GTTTTGTTCTGAG CAGAGT
                                      A
GAM1664 ATP8B2   3' TGAGATGGAGTCTCACTCT  65850     CA
                                AGAG AGACTCCGTCTCA
                                |||| ||||||||||||
                                TCTC TCTGAGGTAGAGT
                                  AC
GAM1664 BRIP1    3' TGAGACAGAGTCTTGGTCTG 50214     G      C
                                CAGA CAAGACTC GTCTCA
                                |||| |||||||| ||||||
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                                GTCT GTTCTGAG CAGAGT
                                  G       A
GAM1664  CDH17    3'  TGAGGTGGAGTCTTGCTCTG  15791            GT
                                CAGAGCAAGACTCC  CTCA
                                ||||||||||||||  ||||
                                GTCTCGTTCTGAGG  GAGT
                                        TG
GAM1664  CIAS1    5'  TGAGATGGAGTCTTGCTGTG  18103    G
                                CA AGCAAGACTCCGTCTCA
                                || ||||||||||||||||
                                GT TCGTTCTGAGGTAGAGT
                                 G
GAM1664  CR1      3'  TGAGATGGAGTCTGGCTCTG  6952        A
                                CAGAGC AGACTCCGTCTCA
                                ||||||| ||||||||||||
                                GTCTCG TCTGAGGTAGAGT
                                    G
GAM1664  CRTAP    3'  GAAGGGCAGTCTTCTCTG    22079      C     _  G_
                                CAGAG AAGACT CC  TC
                                ||||| |||||| ||  ||
                                GTCTC TTCTGA GG  AG
                                  _     C  GA
GAM1664  CRTAP    3'  TGAGATGGAGTCTCGCTCT   22085      A
                                AGAGC AGACTCCGTCTCA
                                ||||| ||||||||||||
                                TCTCG TCTGAGGTAGAGT
                                   C
GAM1664  CXCL16   3'  TGAGACGGAGTCTCGCTCTG  42182       A
                                CAGAGC AGACTCCGTCTCA
                                ||||||| ||||||||||||
                                GTCTCG TCTGAGGCAGAGT
                                    C
GAM1664  CYP2B6   3'  TGAGATGGAGTCTCACTCTG  7572       CA
                                CAGAG  AGACTCCGTCTCA
                                |||||  ||||||||||||
                                GTCTC  TCTGAGGTAGAGT
                                   AC
GAM1664  CYP2B6   3'  TGAAACTAAGCCTTGCTCTG  7571         A  CC  C
                                CAGAGCAAG CT  GT TCA
                                ||||||||| ||  || |||
                                GTCTCGTTC GA  CA AGT
                                      C  AT  A
GAM1664  CYP4F3   3'  TGAGATGGAGTCTCGCTCTG  8018        A
                                CAGAGC AGACTCCGTCTCA
                                ||||||| ||||||||||||
                                GTCTCG TCTGAGGTAGAGT
                                    C
GAM1664  CYP51    3'  TGAGATGGAGTCTCGCTCTG  7623        A
                                CAGAGC AGACTCCGTCTCA
                                ||||||| ||||||||||||
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                                GTCTCG TCTGAGGTAGAGT
                                   C
GAM1664 CYP8B1   3' TGAGACAGAGTCTTGCTCTG  16543          C
                                CAGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
                                GTCTCGTTCTGAG CAGAGT
                                      A
GAM1664 DISC1    3' TGAGATGGAGTCTCTCTCTG  38520      CA
                                CAGAG  AGACTCCGTCTCA
                                |||||  ||||||||||||
                                GTCTC  TCTGAGGTAGAGT
                                   TC
GAM1664 DSC3     3' TGAGACGGAGTCTCGCTCTG  44637      A
                                CAGAGC AGACTCCGTCTCA
                                ||||||| ||||||||||||
                                GTCTCG TCTGAGGCAGAGT
                                   C
GAM1664 DSC3     3' TGAGACGGAGTCTCGCTCTG  10447      A
                                CAGAGC AGACTCCGTCTCA
                                ||||||| ||||||||||||
                                GTCTCG TCTGAGGCAGAGT
                                   C
GAM1664 DSCR3    3' TGAGACGGAGTCTCAGTCTG  21325     GCA
                                CAGA   AGACTCCGTCTCA
                                ||||   ||||||||||||
                                GTCT   TCTGAGGCAGAGT
                                  GAC
GAM1664 EHD3     5' TGAGGAGGAGTCTTCCCCTG  28205    AGC      GT
                                CAG   AAGACTCC  CTCA
                                |||   ||||||||  ||||
                                GTC   TTCTGAGG  GAGT
                                  CCC       AG
GAM1664 F3       3' TGAGACGGAGTCTTGCTCTG  67683
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTCTGAGGCAGAGT

GAM1664 FANCF    3' TGAGATGGAGTCTCGCTCTG  42987      A
                                CAGAGC AGACTCCGTCTCA
                                ||||||| ||||||||||||
                                GTCTCG TCTGAGGTAGAGT
                                   C
GAM1664 FGF5     3' TGAGACAGAGTCTTGCTCTG  16766          C
                                CAGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
                                GTCTCGTTCTGAG CAGAGT
                                      A
GAM1664 FGF5     3' TGAGACAGAGTCTTGCTCTG  53670          C
                                CAGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
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                                GTCTCGTTCTGAG CAGAGT
                                      A
GAM1664 FUT1    3' TGAGACGGAGTCTTGCTCTG  5615
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTCTGAGGCAGAGT

GAM1664 GRAF    3' TGAGATGGAGTCTCACTCTG  31251      CA
                                CAGAG  AGACTCCGTCTCA
                                |||||  ||||||||||||
                                GTCTC  TCTGAGGTAGAGT
                                   AC
GAM1664 GRINL1A 3' TGAGATGGGGTCTTGCTCTG  70071
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTCTGGGGTAGAGT

GAM1664 HCS     3' TGAGACGGAGTTTCGCCCT   38993    A  A
                                AG GC AGACTCCGTCTCA
                                || || ||||||||||||
                                TC CG TTTGAGGCAGAGT
                                 C  C
GAM1664 HTR1D   3' TGAGACGGAGTCTTGCCCT   7850     A
                                AG GCAAGACTCCGTCTCA
                                || ||||||||||||||||
                                TC CGTTCTGAGGCAGAGT
                                 C
GAM1664 HUNK    3' TGAGACAGGGTCTTGCTCTG  28194          C
                                CAGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
                                GTCTCGTTCTGGG CAGAGT
                                      A
GAM1664 HUS1    3' TGAGACGGTCTCATTCTG    92743      CA   CT
                                CAGAG  AGA  CCGTCTCA
                                |||||  |||  ||||||||
                                GTCTT  TCT  GGCAGAGT
                                   AC  __
GAM1664 IGF1    3' TGAGATGGGGTCTCGCACTG  7086     A  A
                                CAG GC AGACTCCGTCTCA
                                ||| || ||||||||||||
                                GTC CG TCTGGGGTAGAGT
                                  A  C
GAM1664 IL11    3' TGAGATGGAGTCTCGCTCTG  7196       A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
                                GTCTCG TCTGAGGTAGAGT
                                    C
GAM1664 INMT    3' TGAGACGGAGTCTGGCTCTG  23229      A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
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                                GTCTCG TCTGAGGCAGAGT
                                   G
GAM1664 INMT    3' TGAGACGGAGTTTCGCTCTG  23230      A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
                                GTCTCG TTTGAGGCAGAGT
                                   C
GAM1664 INPP5A  3' GAGACGGGCACTCCCTCTG   19865     CA  AC
                                CAGAG  AG  TCCGTCTC
                                |||||  ||  ||||||||
                                GTCTC  TC  GGGCAGAG
                                   CC  AC
GAM1664 ITGAM   3' TGAGACGGAGTCTCGCTCTG  72316      A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
                                GTCTCG TCTGAGGCAGAGT
                                   C
GAM1664 JPH2    5' AGGCAGCCTTGCTCTG     96081       A  CC
                                CAGAGCAAG CT  GTCT
                                ||||||||| ||  ||||
                                GTCTCGTTC GA  CGGA
                                     C __
GAM1664 LILRA3  3' TGAGATGGAGTCTTGCTCTG  97022
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTCTGAGGTAGAGT

GAM1664 LLGL1   3' AGACGGAGTCTTGCTCTG    67409
                                CAGAGCAAGACTCCGTCT
                                ||||||||||||||||||
                                GTCTCGTTCTGAGGCAGA

GAM1664 LTB4R   5' TGAAATGGAGTCTCGCTCTG  7475       A       C
                                CAGAGC AGACTCCGT TCA
                                |||||| ||||||||| |||
                                GTCTCG TCTGAGGTA AGT
                                   C       A
GAM1664 LZTS1   3' TGAGACAGGGTCTTGCTCTG  41041          C
                                CAGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
                                GTCTCGTTCTGGG CAGAGT
                                      A
GAM1664 MDM2    3' TGAGACCGAGTCTTGCTCTG  23463          C
                                CAGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
                                GTCTCGTTCTGAG CAGAGT
                                      C
GAM1664 MDM2    3' TGAGACCGAGTCTTGCTCTG  23476          C
                                CAGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
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                                GTCTCGTTCTGAG CAGAGT
                                      C
GAM1664  MDM2     3'  TGAGACCGAGTCTTGCTCTG   23489          C
                                CAGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
                                GTCTCGTTCTGAG CAGAGT
                                      C
GAM1664  MDM2     3'  TGAGACCGAGTCTTGCTCTG   23503          C
                                CAGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
                                GTCTCGTTCTGAG CAGAGT
                                      C
GAM1664  MDM2     3'  TGAGACCGAGTCTTGCTCTG   11501          C
                                CAGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
                                GTCTCGTTCTGAG CAGAGT
                                      C
GAM1664  ME1      3'  TGAGACAATTTTGCTTCA    11529   A      CTCC
                                C GAGCAAGA   GTCTCA
                                | ||||||||   ||||||
                                A TTCGTTTT   CAGAGT
                                 C       AA__
GAM1664  MEFV     3'  TGAGACAAAGTTTTGCTCT   5953           CC
                                AGAGCAAGACT  GTCTCA
                                ||||||||||  ||||||
                                TCTCGTTTTGA  CAGAGT
                                      AA
GAM1664  MEFV     3'  TGAGACCAAATCTTGCTCTG  5954           CTCC
                                CAGAGCAAGA   GTCTCA
                                ||||||||||   ||||||
                                GTCTCGTTCT   CAGAGT
                                     AAAC
GAM1664  MHC2TA   3'  TGAACCACATCTTGCTCTG   5997           CTCC  C
                                CAGAGCAAGA   GT TCA
                                ||||||||||   || |||
                                GTCTCGTTCT   CA AGT
                                     ACAC  _
GAM1664  MRPL49   3'  TGAGACGGAGTCTCACTCTG  70174      CA
                                CAGAG  AGACTCCGTCTCA
                                |||||  ||||||||||||||
                                GTCTC  TCTGAGGCAGAGT
                                   AC
GAM1664  MYCL2    3'  TGAGACGGAGTCTCAACTCT  19382      CA_
                                AGAG   AGACTCCGTCTCA
                                ||||   ||||||||||||||
                                TCTC   TCTGAGGCAGAGT
                                  AAC
GAM1664  NAV2     3'  TGAGTGTGTCTTGTTCTG    60800          TC  T
                                CAGAGCAAGAC  CG CTCA
                                ||||||||||  || ||||
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                                GTCTTGTTCTG  GT GAGT
                                      T_  _
GAM1664  NCOA6    5'  TGAGATGAAGTCTTGCTCTG   26850          C
                                CAGAGCAAGACT CGTCTCA
                                |||||||||||| |||||||
                                GTCTCGTTCTGA GTAGAGT
                                       A
GAM1664  NONO     3'  GAGACGGAGTCTTACTCTG   82889      C
                                CAGAG AAGACTCCGTCTC
                                ||||| ||||||||||||
                                GTCTC TTCTGAGGCAGAG
                                   A
GAM1664  NPR2L    3'  TGAGACGGGGTCTCACTCTG   22600      CA
                                CAGAG  AGACTCCGTCTCA
                                |||||  ||||||||||||
                                GTCTC  TCTGGGGCAGAGT
                                   AC
GAM1664  NQO1     3'  TGAAGCAGTCTTGCTCTG    8058          CC TC
                                CAGAGCAAGACT  G  TCA
                                ||||||||||||  |  |||
                                GTCTCGTTCTGA  C  AGT
                                      __ GA
GAM1664  ORC1L    3'  TGAGACAGGGTCTTGCTCTG   15989          C
                                CAGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
                                GTCTCGTTCTGGG CAGAGT
                                       A
GAM1664  PCDHA9   3'  TGAGACGGAGTCGTTTTCTG   26626      CAA
                                CAGAG   GACTCCGTCTCA
                                |||||   ||||||||||||
                                GTCTT   CTGAGGCAGAGT
                                   TTG
GAM1664  PCDHB9   3'  TGAGACGGAGTCTCGCTCTG   39453       A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
                                GTCTCG TCTGAGGCAGAGT
                                    C
GAM1664  PDCL     3'  TGAGATGGAGTCTCGCTCTG   19401       A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
                                GTCTCG TCTGAGGTAGAGT
                                    C
GAM1664  PDE6B    3'  TGAGATGGAGTCTTGCTCTG   6080
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTCTGAGGTAGAGT

GAM1664  PIGR     3'  TGAGACGGAGTCTCTC      73014     CA
                                GAG  AGACTCCGTCTCA
                                |||  ||||||||||||
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                                CTC  TCTGAGGCAGAGT
                                  __
GAM1664  PIK3C2B  3'  GAGACGGAGTCTCGCCCTG   12099    A  A
                                CAG GC AGACTCCGTCTC
                                ||| || ||||||||||||
                                GTC CG TCTGAGGCAGAG
                                  C  C
GAM1664  PIK3CD   3'  TGAGATGGGGTCTTCCTCTG   18503     C
                                CAGAG AAGACTCCGTCTCA
                                ||||| ||||||||||||||
                                GTCTC TTCTGGGGTAGAGT
                                   C
GAM1664  PKNOX1   3'  TGAGACAGAGTTTTGCTCT   17103         C
                                AGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
                                TCTCGTTTTGAG CAGAGT
                                       A
GAM1664  PMCHL1   3'  TGAGATGGAGTCTCACTCTG   49923     CA
                                CAGAG  AGACTCCGTCTCA
                                |||||  ||||||||||||||
                                GTCTC  TCTGAGGTAGAGT
                                   AC
GAM1664  POU2AF1  3'  TGGGACGGAGTCTCACTC    21752    CA
                                GAG  AGACTCCGTCTCA
                                |||  ||||||||||||||
                                CTC  TCTGAGGCAGGGT
                                  AC
GAM1664  PPID     3'  TGAGATGGAGTCTTGCTCTG   88831
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTCTGAGGTAGAGT

GAM1664  PRKWNK3  3'  TGAGATGGAGTCTCTCTCTG   62241     CA
                                CAGAG  AGACTCCGTCTCA
                                |||||  ||||||||||||||
                                GTCTC  TCTGAGGTAGAGT
                                   TC
GAM1664  PTGES    3'  AGACAGAGTCTTGCTCTG    18052         C
                                CAGAGCAAGACTC GTCT
                                |||||||||||| ||||
                                GTCTCGTTCTGAG CAGA
                                       A
GAM1664  PTGIS    3'  TGAGATGGAGTCTCGCTCTG   8231      A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||||
                                GTCTCG TCTGAGGTAGAGT
                                   C
GAM1664  RABL2A   3'  TGAGACGGAGTCTCGCTCTG   26415     A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||||
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                                GTCTCG TCTGAGGCAGAGT
                                   C
GAM1664 RABL2B   3' TGAGACGGAGTCTCGCTCTG  23989      A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
                                GTCTCG TCTGAGGCAGAGT
                                   C
GAM1664 RAI3     3' TGAAACAGGATCTTGCTCTG  15623        C  _  C
                                CAGAGCAAGA TCC GT TCA
                                |||||||||| ||| || |||
                                GTCTCGTTCT AGG CA AGT
                                      _  A  A
GAM1664 RBBP9    3' TGAGACAGTGTCTTGCTCTG  70702         TCC
                                CAGAGCAAGAC  GTCTCA
                                ||||||||||   ||||||
                                GTCTCGTTCTG  CAGAGT
                                      TGA
GAM1664 RBM8A    3' TGAGATAGAGTCTTGCTGTG  18816   G       CG
                                CA AGCAAGACTC  TCTCA
                                || ||||||||||  |||||
                                GT TCGTTCTGAG  AGAGT
                                 G         AT
GAM1664 RHD      3' TGAAACGGAGTCTCACTCTG  32841     CA       C
                                CAGAG  AGACTCCGT TCA
                                |||||  ||||||||| |||
                                GTCTC  TCTGAGGCA AGT
                                   AC        A
GAM1664 RHD      3' TGAAACGGAGTCTCACTCTG  33151     CA       C
                                CAGAG  AGACTCCGT TCA
                                |||||  ||||||||| |||
                                GTCTC  TCTGAGGCA AGT
                                   AC        A
GAM1664 SAS      3' TGACACAGAGTCTTGCTCTG  21110         C  C
                                CAGAGCAAGACTC GT TCA
                                |||||||||||| || |||
                                GTCTCGTTCTGAG CA AGT
                                      A  C
GAM1664 SEDL     3' TGAGATGGAGTCTTGCTC    28112
                                GAGCAAGACTCCGTCTCA
                                ||||||||||||||||||
                                CTCGTTCTGAGGTAGAGT

GAM1664 SEDL     3' TGAGATGGAGTCTTGCTC    28113
                                GAGCAAGACTCCGTCTCA
                                ||||||||||||||||||
                                CTCGTTCTGAGGTAGAGT

GAM1664 SEDL     3' TGAGATGGAGTTTCGCTCTG  28114      A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
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                                GTCTCG TTTGAGGTAGAGT
                                   C
GAM1664  SEPN1    3'  TGAGACGGAGTCTTGCTCTG   66983
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTCTGAGGCAGAGT

GAM1664  SGPL1    3'  TGAGACAGCTTGAGCCTC    92982     ___   A  CC
                                GAG   CAAG CT  GTCTCA
                                |||   |||| ||  ||||||
                                CTC   GTTC GA  CAGAGT
                                  CGA   _ __
GAM1664  SHANK2   3'  TGAGACAGTCCTTTTGCTCT   25535       ___    CC
                                AGAGCAA   GACT  GTCTCA
                                |||||||   ||||  ||||||
                                TCTCGTT   CTGA  CAGAGT
                                    TTC   __
GAM1664  SHOX     3'  AGACAGAGTCTTGCTCTG    23512           C
                                CAGAGCAAGACTC GTCT
                                |||||||||||| ||||
                                GTCTCGTTCTGAG CAGA
                                       A
GAM1664  SHOX     3'  TGAGACAGAGACTTGCTTTG   6588         A   C
                                CAGAGCAAG CTC GTCTCA
                                |||||||| ||| ||||||
                                GTTTCGTTC GAG CAGAGT
                                     A   A
GAM1664  SIL      3'  TGAGACGGAGTTTTGCTCT    13165
                                AGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                TCTCGTTTTGAGGCAGAGT

GAM1664  SLA2     3'  TGAGACGGAGTCTTGCCCTG   50896     A
                                CAG GCAAGACTCCGTCTCA
                                ||| ||||||||||||||||
                                GTC CGTTCTGAGGCAGAGT
                                  C
GAM1664  SLC14A2  5'  TGAGACACAGTTTGCTCTG    24129       A    CC
                                CAGAGCA GACT  GTCTCA
                                ||||||| ||||  ||||||
                                GTCTCGT TTGA  CAGAGT
                                    _   CA
GAM1664  SLC15A1  3'  TGAGACAGAGTTTTGCTCT    18649           C
                                AGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
                                TCTCGTTTTGAG CAGAGT
                                       A
GAM1664  SS18     3'  TGAGATGGAGTCTTGCTCT    20106
                                AGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||
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                                TCTCGTTCTGAGGTAGAGT

GAM1664 TAF11    3' TGAGATAGGGTCTTGCTCT   20123          CG
                                AGAGCAAGACTC TCTCA
                                |||||||||||| |||||
                                TCTCGTTCTGGG AGAGT
                                       AT
GAM1664 TAPBP    3' TGAGACGGAGCTCACCTCT   13590     CA_ A
                                AGAG  AG CTCCGTCTCA
                                ||||  || ||||||||||
                                TCTC  TC GAGGCAGAGT
                                  CAC _
GAM1664 TAT      3' TGAGATGGAGTCTTGCTCTG  6262
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTCTGAGGTAGAGT

GAM1664 TBXA2R   3' AGACGGAGTCTCACTCTG    8338      CA
                                CAGAG AGACTCCGTCT
                                ||||| ||||||||||
                                GTCTC TCTGAGGCAGA
                                   AC
GAM1664 TBXA2R   3' AGACGGAGTCTTGCTCTG    8339
                                CAGAGCAAGACTCCGTCT
                                |||||||||||||||||
                                GTCTCGTTCTGAGGCAGA

GAM1664 TDGF1    3' TGAGACGGAGTCTCACTCTG  13664     CA
                                CAGAG AGACTCCGTCTCA
                                ||||| ||||||||||||
                                GTCTC TCTGAGGCAGAGT
                                   AC
GAM1664 TIM3     3' AGACGGTATAGGCTTGATCTG 52350     G   A ___
                                CAGA CAAG CT  CCGTCT
                                |||| |||| ||  ||||||
                                GTCT GTTC GA  GGCAGA
                                  A   G  TAT
GAM1664 TIM3     3' TGAGATGGAGTCTTGCTCTG  52364
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTCTGAGGTAGAGT

GAM1664 TMPRSS3  3' TGAGGTGGAGTCTCGCTCTG  51525      A     GT
                                CAGAGC AGACTCC  CTCA
                                |||||| |||||||  ||||
                                GTCTCG TCTGAGG  GAGT
                                   C      TG
GAM1664 TMPRSS3  3' TGAGGTGGAGTCTCGCTCTG  51552      A     GT
                                CAGAGC AGACTCC  CTCA
                                |||||| |||||||  ||||
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                                GTCTCG TCTGAGG  GAGT
                                   C      TG
GAM1664  TMPRSS3   3'  TGAGGTGGAGTCTCGCTCTG   44036       A      GT
                                CAGAGC AGACTCC  CTCA
                                |||||| |||||||  ||||
                                GTCTCG TCTGAGG  GAGT
                                   C      TG
GAM1664  TNFAIP2   3'  TGAGACAGGGTCTTGCTGTG   21930    G        C
                                CA AGCAAGACTC GTCTCA
                                || |||||||||| ||||||
                                GT TCGTTCTGGG CAGAGT
                                 G         A
GAM1664  TRIM9     5'  GAGACGGAGTCTCGCTCTG    31451       A
                                CAGAGC AGACTCCGTCTC
                                |||||| ||||||||||||
                                GTCTCG TCTGAGGCAGAG
                                   C
GAM1664  TRIM9     5'  TGAGACGGAGTTTCGCTCT    31463      A
                                AGAGC AGACTCCGTCTCA
                                ||||| |||||||||||||
                                TCTCG TTTGAGGCAGAGT
                                  C
GAM1664  UBE2G2    3'  TGAGATGGAGCCCTCTCTG    65498      CA  A_
                                CAGAG  AG  CTCCGTCTCA
                                |||||  ||  ||||||||||
                                GTCTC  TC  GAGGTAGAGT
                                  __  CC
GAM1664  USP6      5'  TGAGACGGAGCTGCCTC     92783     CA  A
                                GAG  AG CTCCGTCTCA
                                |||  || ||||||||||
                                CTC  TC GAGGCAGAGT
                                  CG  _
GAM1664  VENTX2    3'  TGAGACGGAGTGTTGCTCTG   27868        G
                                CAGAGCAA ACTCCGTCTCA
                                |||||||| ||||||||||
                                GTCTCGTT TGAGGCAGAGT
                                     G
GAM1664  VIPR2     3'  TGAGACGGAGTCTTGCTCTG   14076
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTCTGAGGCAGAGT

GAM1664  XRCC2     3'  AGACAGAGTCTTGCTCTG     19487           C
                                CAGAGCAAGACTC GTCT
                                |||||||||||| ||||
                                GTCTCGTTCTGAG CAGA
                                        A
GAM1664  YES1      3'  TGAGACGGAGTCTCGCTCTG   19546       A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
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                                GTCTCG TCTGAGGCAGAGT
                                   C
GAM1664 YY1      3' AGATGCTCTATCTTGCTCTG  14150        CTC__
                                CAGAGCAAGA    CGTCT
                                ||||||||||    |||||
                                GTCTCGTTCT    GTAGA
                                      ATCTC
GAM1664 ZNF133   5' TGAGACAGAGTCTTGCTCTG  14301          C
                                CAGAGCAAGACTC GTCTCA
                                |||||||||||||| ||||||
                                GTCTCGTTCTGAG CAGAGT
                                         A
GAM1664 ZNF157   3' TGAGATGGAGTCTCACTCTG  14339     CA
                                CAGAG  AGACTCCGTCTCA
                                |||||  ||||||||||||
                                GTCTC  TCTGAGGTAGAGT
                                   AC
GAM1664 ABLIM    3' TGAGACCAGCTCTTGCTT    11326       _ CC
                                GAGCAAGA CT  GTCTCA
                                |||||||| ||  ||||||
                                TTCGTTCT GA  CAGAGT
                                     C  C_
GAM1664 ABLIM    3' TGAGACCAGCTCTTGCTT    22987       _ CC
                                GAGCAAGA CT  GTCTCA
                                |||||||| ||  ||||||
                                TTCGTTCT GA  CAGAGT
                                     C  C_
GAM1664 AD022    3' AGTGTGGGTTTTGCCCTG    92646    A      _ T
                                CAG GCAAGACTC CG CT
                                ||| ||||||||| || ||
                                GTC CGTTTTGGG GT GA
                                  C       T _
GAM1664 ANAPC11  5' GAGACGGAGTTTCGTCATG   33632    GA  A
                                CA  GC AGACTCCGTCTC
                                ||  || ||||||||||||
                                GT  TG TTTGAGGCAGAG
                                 AC  C
GAM1664 ANKRD6   3' TGAGACAGGGTCTTGCTCTG  30775          C
                                CAGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
                                GTCTCGTTCTGGG CAGAGT
                                         A
GAM1664 AP3S2    3' TGAGGTGGAGTCTTGCTCTG  20658          GT
                                CAGAGCAAGACTCC  CTCA
                                ||||||||||||||  ||||
                                GTCTCGTTCTGAGG  GAGT
                                      TG
GAM1664 APOL2    3' TGAGATGGAGTCTCGCTCT   48795      A
                                AGAGC AGACTCCGTCTCA
                                ||||| ||||||||||||
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                                  TCTCG TCTGAGGTAGAGT
                                     C
GAM1664 ARHGAP5  5' TGAGACGGAATTTCACTTCA  77607   A  CA  C
                                  C GAG  AGA TCCGTCTCA
                                  | |||  ||| |||||||||
                                  A TTC  TTT AGGCAGAGT
                                   C  AC  A
GAM1664 ASB16    5' AGACGGGGTCTCACTCTG    70484     CA
                                  CAGAG  AGACTCCGTCT
                                  |||||  ||||||||||
                                  GTCTC  TCTGGGGCAGA
                                     AC
GAM1664 ASE-1    3' TGAGATGGAGTCTCGCTCTG  24997      A
                                  CAGAGC AGACTCCGTCTCA
                                  |||||| ||||||||||||
                                  GTCTCG TCTGAGGTAGAGT
                                     C
GAM1664 BNIP-S   3' TGAGACGGAGTCTCGCTCTG  57096      A
                                  CAGAGC AGACTCCGTCTCA
                                  |||||| ||||||||||||
                                  GTCTCG TCTGAGGCAGAGT
                                     C
GAM1664 BTN3A1   3' AGATGGAGTCTTACTCTG    23884     C
                                  CAGAG AAGACTCCGTCT
                                  ||||| ||||||||||||
                                  GTCTC TTCTGAGGTAGA
                                     A
GAM1664 C(27)-3BETA-HSD 3' TGAGACAGGGTCTTGCTCTG  48055          C
                                  CAGAGCAAGACTC GTCTCA
                                  |||||||||||||| ||||||
                                  GTCTCGTTCTGGG CAGAGT
                                        A
GAM1664 C1orf24  3' TGAGATGGAGTCTCGCTCTG  54797      A
                                  CAGAGC AGACTCCGTCTCA
                                  |||||| ||||||||||||
                                  GTCTCG TCTGAGGTAGAGT
                                     C
GAM1664 C1QTNF6  3' TGAGACAGAGTCTTGCTCTG  49997          C
                                  CAGAGCAAGACTC GTCTCA
                                  |||||||||||||| ||||||
                                  GTCTCGTTCTGAG CAGAGT
                                        A
GAM1664 C20orf39 3' TGAGATGGGCCTTACTCTG   46578     C  A T
                                  CAGAG AAG C CCGTCTCA
                                  ||||| ||| | ||||||||
                                  GTCTC TTC G GGTAGAGT
                                     A  C _
GAM1664 C21orf25 3' GAGATGGAGTTTCACTCTG   64294     CA
                                  CAGAG  AGACTCCGTCTC
                                  |||||  ||||||||||||
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                                GTCTC  TTTGAGGTAGAG
                                   AC
GAM1664  C22orf19  3'  TGAGACGGGGTCTTGCTCTG   14832
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTCTGGGGCAGAGT

GAM1664  C9orf9    3'  TGAGACGGAGTCTCGCTCTG   39038       A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
                                GTCTCG TCTGAGGCAGAGT
                                   C
GAM1664  C9orf9    3'  TGAGATGGAGTTTCACTCTG   39039      CA
                                CAGAG  AGACTCCGTCTCA
                                |||||  ||||||||||||
                                GTCTC  TTTGAGGTAGAGT
                                   AC
GAM1664  CEACAM8   3'  TGAGATGGAATCTCGCTCTG   10190       A   C
                                CAGAGC AGA TCCGTCTCA
                                |||||| ||| |||||||||
                                GTCTCG TCT AGGTAGAGT
                                   C   A
GAM1664  CENPH     3'  TGAGATGGAGTCTCGCTTTG   43573       A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
                                GTTTCG TCTGAGGTAGAGT
                                   C
GAM1664  CHSY1     3'  TGAGACGGAGTCTCACTCTG   30574      CA
                                CAGAG  AGACTCCGTCTCA
                                |||||  ||||||||||||
                                GTCTC  TCTGAGGCAGAGT
                                   AC
GAM1664  CIP29     3'  TGAGATGGAGTCTTGCTCTG   51383
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTCTGAGGTAGAGT

GAM1664  DGKD      3'  TGAGACGGAGCTGCTGCTG    60114     _    A A
                                CAG AGCA G CTCCGTCTCA
                                ||| |||| | ||||||||||
                                GTC TCGT C GAGGCAGAGT
                                  G   _ _
GAM1664  DKFZp434C0923 3'  GAGACAGGGTCTTGCTCTG    34649            C
                                CAGAGCAAGACTC GTCTC
                                |||||||||||| |||||
                                GTCTCGTTCTGGG CAGAG
                                        A
GAM1664  DKFZP434J037 3'  TGAGACGGAGTTTCGCTCT    48956       A
                                AGAGC AGACTCCGTCTCA
                                ||||| ||||||||||||
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                                TCTCG TTTGAGGCAGAGT
                                   C
GAM1664  DKFZp547M236 5'  TGAGACGGCACAGTCGCTCT  38662      AA   ___
                                AGAGC  GACT   CCGTCTCA
                                |||||  ||||   ||||||||
                                TCTCG  CTGA   GGCAGAGT
                                   __    CAC
GAM1664  DKFZP564G092 5'  TGAGACGGAGTTTCGCTCT   32169      A
                                AGAGC AGACTCCGTCTCA
                                ||||| ||||||||||||
                                TCTCG TTTGAGGCAGAGT
                                   C
GAM1664  DKFZp761J139 5'  TGAGACAGAGTTTTGCTCT   51114           C
                                AGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
                                TCTCGTTTTGAG CAGAGT
                                      A
GAM1664  DKFZp761J139 5'  TGAGACGGAGTTTATTCTCT  51115     CA_
                                AGAG   AGACTCCGTCTCA
                                ||||   ||||||||||||
                                TCTC   TTTGAGGCAGAGT
                                  TTA
GAM1664  DKFZp762L0311 3'  TGAGATGGAGTCTTGTTCTG  38676
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||
                                GTCTTGTTCTGAGGTAGAGT

GAM1664  EREG     3'  TGAGATGGAGTCTCGCTCTG  9320       A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
                                GTCTCG TCTGAGGTAGAGT
                                   C
GAM1664  FBP17     3'  TGAGACGGGAGTCTCGCTCT  73162      A     _
                                AGAGC AGACTCC GTCTCA
                                ||||| ||||||| ||||||
                                TCTCG TCTGAGG CAGAGT
                                   C      G
GAM1664  FLJ00060  5'  TGAGATGGAGGCTTGCTCTG  61757         A
                                CAGAGCAAG CTCCGTCTCA
                                ||||||||| ||||||||||
                                GTCTCGTTC GAGGTAGAGT
                                     G
GAM1664  FLJ10298  3'  GAGACAGAGTCTTGCTCTG   36457           C
                                CAGAGCAAGACTC GTCTC
                                |||||||||||| |||||
                                GTCTCGTTCTGAG CAGAG
                                      A
GAM1664  FLJ10535  3'  TGAGATGGAGTCTCACTCTG  36758      CA
                                CAGAG  AGACTCCGTCTCA
                                |||||  ||||||||||||
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                                GTCTC  TCTGAGGTAGAGT
                                   AC
GAM1664  FLJ10583  3'  TGAGGCAGGGTCTTGCTCTG  36832          C
                                CAGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
                                GTCTCGTTCTGGG CGGAGT
                                      A
GAM1664  FLJ10687  3'  TGAGACAGGGTCTTGCTCT   36954          C
                                AGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
                                TCTCGTTCTGGG CAGAGT
                                      A
GAM1664  FLJ10846  3'  TGAGACAGACAGAGTCTTGCTC 37293          C____
            TG                    CAGAGCAAGACTC    GTCTCA
                                |||||||||||||    ||||||
                                GTCTCGTTCTGAG    CAGAGT
                                      ACAGA
GAM1664  FLJ10853  3'  TGAGGGTGATCTTGCTCT    37320        C  CG
                                AGAGCAAGA TC  TCTCA
                                ||||||||| ||  |||||
                                TCTCGTTCT AG  GGAGT
                                     _ TG
GAM1664  FLJ10901  3'  TGAGATGGAGTCTCGCTCTG  37375       A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
                                GTCTCG TCTGAGGTAGAGT
                                   C
GAM1664  FLJ10956  3'  TGAGAAGGAGTCTTGCTCTG  37473          G
                                CAGAGCAAGACTCC TCTCA
                                |||||||||||||| |||||
                                GTCTCGTTCTGAGG AGAGT
                                      A
GAM1664  FLJ11004  5'  GGAAAGAGTCTTGCTCTG    37533          CG
                                CAGAGCAAGACTC  TCT
                                ||||||||||||  |||
                                GTCTCGTTCTGAG  AGG
                                      AA
GAM1664  FLJ11125  5'  GAGACAGTGTCTTGCTCTG   60323          TCC
                                CAGAGCAAGAC   GTCTC
                                ||||||||||   |||||
                                GTCTCGTTCTG   CAGAG
                                      TGA
GAM1664  FLJ11710  3'  TGAGACAGGATCTTGCTCTG  46253        C  _
                                CAGAGCAAGA TCC GTCTCA
                                |||||||||| ||| ||||||
                                GTCTCGTTCT AGG CAGAGT
                                     _  A
GAM1664  FLJ12409  3'  TGAGACGGAGTTTGCTCT    47774       A
                                AGAGCA GACTCCGTCTCA
                                |||||| ||||||||||||
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                                TCTCGT TTGAGGCAGAGT
                                      _
GAM1664  FLJ12581  3'  TGAGACGGAGTCTTGCTCTG   46344
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTCTGAGGCAGAGT

GAM1664  FLJ12649  3'  TGAGACGGAGTCTTGCCCTG   45097     A
                                CAG GCAAGACTCCGTCTCA
                                ||| ||||||||||||||||
                                GTC CGTTCTGAGGCAGAGT
                                  C
GAM1664  FLJ12668  3'  TGAGATGGAATATTGCTCTG   47163        GAC
                                CAGAGCAA   TCCGTCTCA
                                ||||||||   |||||||||
                                GTCTCGTT   AGGTAGAGT
                                     ATA
GAM1664  FLJ12847  3'  TGAGACGGAGTCCAGCCTG    45081     A  AA
                                CAG GC  GACTCCGTCTCA
                                ||| ||  ||||||||||||
                                GTC CG  CTGAGGCAGAGT
                                  _ AC
GAM1664  FLJ12876  3'  TGAGACGGAGTCTCGCTCTG   43102       A
                                CAGAGC AGACTCCGTCTCA
                                ||||||| ||||||||||||
                                GTCTCG TCTGAGGCAGAGT
                                   C
GAM1664  FLJ12960  3'  TGAGACGGAGCCTTGCTCTG   45307         A
                                CAGAGCAAG CTCCGTCTCA
                                ||||||||| ||||||||||
                                GTCTCGTTC GAGGCAGAGT
                                     C
GAM1664  FLJ13072  5'  TGAGACAGAGTCTTGCTCTG   91402           C
                                CAGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
                                GTCTCGTTCTGAG CAGAGT
                                       A
GAM1664  FLJ13114  3'  TGAGACGGAGTCTCACTCTG   44912      CA
                                CAGAG  AGACTCCGTCTCA
                                |||||  ||||||||||||
                                GTCTC  TCTGAGGCAGAGT
                                   AC
GAM1664  FLJ13188  3'  TGAGACAGAGCCTCGCTTGCTC 42198         A____   C
            TG                  CAGAGCAAG    CTC GTCTCA
                                |||||||||    ||| |||||||
                                GTCTCGTTC    GAG CAGAGT
                                     GCTCC   A
GAM1664  FLJ13197  3'  AGACGGAGTCTCACTCTG    45172      CA
                                CAGAG  AGACTCCGTCT
                                |||||  ||||||||||
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                                GTCTC  TCTGAGGCAGA
                                   AC
GAM1664  FLJ13441  3'  GGACAGCCTTGCTCTG     43915        A  CC
                                CAGAGCAAG CT  GTCT
                                ||||||||| ||  ||||
                                GTCTCGTTC GA  CAGG
                                     C  __
GAM1664  FLJ14442  3'  TGAGATGGAGTCTCACTCTG  52391      CA
                                CAGAG  AGACTCCGTCTCA
                                |||||  ||||||||||||
                                GTCTC  TCTGAGGTAGAGT
                                   AC
GAM1664  FLJ20045  3'  TGAGACGGAGTCTCGCTTTG  34895       A
                                CAGAGC AGACTCCGTCTCA
                                ||||||| ||||||||||||
                                GTTTCG TCTGAGGCAGAGT
                                    C
GAM1664  FLJ20136  3'  TGAGACCGAGTCTTGCTCTG  35104           C
                                CAGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
                                GTCTCGTTCTGAG CAGAGT
                                      C
GAM1664  FLJ20344  3'  TGAGACAGAGTCTTGCTCTG  35491           C
                                CAGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
                                GTCTCGTTCTGAG CAGAGT
                                      A
GAM1664  FLJ22965  3'  TGAGACAGAGTCTTGCTCT   42302           C
                                AGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
                                TCTCGTTCTGAG CAGAGT
                                      A
GAM1664  FLJ23024  3'  TGAGATGGAGTCTTGCTCTG  46849
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTCTGAGGTAGAGT

GAM1664  FLJ23040  3'  TGAGGGGGTTCTTGCTC     47994        CT  G
                                GAGCAAGA  CC TCTCA
                                ||||||||  || |||||
                                CTCGTTCT  GG GGAGT
                                     T_  G
GAM1664  FLJ23053  3'  TGAATGCTTTCTTGCTCT    43555        CTC   C
                                AGAGCAAGA   CGT TCA
                                |||||||||   ||| |||
                                TCTCGTTCT   GTA AGT
                                      TTC  _
GAM1664  FLJ23053  3'  TGAGATGGAGTCTTGCTCT   43556
                                AGAGCAAGACTCCGTCTCA
                                |||||||||||||||||||
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                                TCTCGTTCTGAGGTAGAGT

GAM1664  FLJ23263  5' TGAGACGGAGTCTCACTCTG  47805      CA
                                CAGAG AGACTCCGTCTCA
                                ||||| ||||||||||||
                                GTCTC TCTGAGGCAGAGT
                                   AC
GAM1664  FLJ23356  3' TGAGATGCGGTCTTGCTCTG  50926          C
                                CAGAGCAAGACT CGTCTCA
                                |||||||||||| |||||||
                                GTCTCGTTCTGG GTAGAGT
                                       C
GAM1664  FLJ23499  3' TGAGACGGTGCCATTGCTCT  43141       GACT_
                                AGAGCAA   CCGTCTCA
                                |||||||   ||||||||
                                TCTCGTT   GGCAGAGT
                                    ACCGT
GAM1664  FLJ23556  3' TGAGACGGAGTCTTGCTCTG  46458
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTCTGAGGCAGAGT

GAM1664  FLJ23556  3' TGAGATGGAGTTTTGCTCTG  46459
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTTTGAGGTAGAGT

GAM1664  FLJ31101  3' GAGACGGAGTCTTGCTCTG   36162
                                CAGAGCAAGACTCCGTCTC
                                |||||||||||||||||||
                                GTCTCGTTCTGAGGCAGAG

GAM1664  FLJ31101  3' TGAGATGGAGTCTCACTCTG  36171      CA
                                CAGAG AGACTCCGTCTCA
                                ||||| ||||||||||||
                                GTCTC TCTGAGGTAGAGT
                                   AC
GAM1664  FLJ31153  3' TGAGATGGAGTCTCGCTCTG  58755       A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
                                GTCTCG TCTGAGGTAGAGT
                                    C
GAM1664  FLJ32356  3' GACTCTGGACTTGCTCTG    59024       AC  ___
                                CAGAGCAAG  TCC  GTC
                                |||||||||  |||  |||
                                GTCTCGTTC  AGG  CAG
                                     __  TCT
GAM1664  GAL3ST-4  3' TGAAACGGAGTCTTGCTCTG  45283           C
                                CAGAGCAAGACTCCGT TCA
                                |||||||||||||||| |||
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                                GTCTCGTTCTGAGGCA AGT
                                        A
GAM1664  GNG4     3'  TGAGATGGAGTCTCGCTCTG   16855       A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||||
                                GTCTCG TCTGAGGTAGAGT
                                   C
GAM1664  GRWD     3'  TGAGACGGAGTCTTGGTCTG   49790      G
                                CAGA CAAGACTCCGTCTCA
                                |||| ||||||||||||||||
                                GTCT GTTCTGAGGCAGAGT
                                  G
GAM1664  H-plk    5'  TGAGATGGAGTCTTGCTGTG   32388    G
                                CA AGCAAGACTCCGTCTCA
                                || ||||||||||||||||||
                                GT TCGTTCTGAGGTAGAGT
                                 G
GAM1664  H-plk    5'  TGAGATGGTATCTCACTGTG   32389    G  CA   CT
                                CA AG  AGA  CCGTCTCA
                                || ||  |||  ||||||||
                                GT TC  TCT  GGTAGAGT
                                 G  AC   AT
GAM1664  HCA4     3'  TGAGACGGAGTCTTGCTCT    78046
                                AGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                TCTCGTTCTGAGGCAGAGT

GAM1664  HRH4     3'  TGAGACAGATTCTTGCTCTG   41549         C  C
                                CAGAGCAAGA TC GTCTCA
                                |||||||||| || ||||||
                                GTCTCGTTCT AG CAGAGT
                                      T  A
GAM1664  HRH4     3'  TGAGACAGCATCTTGCTCTG   41550         CTCC
                                CAGAGCAAGA   GTCTCA
                                ||||||||||   ||||||
                                GTCTCGTTCT   CAGAGT
                                      ACGA
GAM1664  HRH4     3'  TGAGATGGGGGTCTTGCTCTG  41551           _
                                CAGAGCAAGACTCC GTCTCA
                                |||||||||||||| ||||||
                                GTCTCGTTCTGGGG TAGAGT
                                        G
GAM1664  HSPC065  3'  TGAGATGGAGTCTTGCTCTG   27165
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTCTGAGGTAGAGT

GAM1664  JAM1     3'  AGACGGAGTCTCGCTCTG    58505       A
                                CAGAGC AGACTCCGTCT
                                |||||| ||||||||||
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                                GTCTCG TCTGAGGCAGA
                                   C
GAM1664  JAM1     3'  AGACGGAGTCTCGCTCTG    58533       A
                                CAGAGC AGACTCCGTCT
                                |||||| ||||||||||
                                GTCTCG TCTGAGGCAGA
                                   C
GAM1664  JAM1     3'  AGACGGAGTCTCGCTCTG    58560       A
                                CAGAGC AGACTCCGTCT
                                |||||| ||||||||||
                                GTCTCG TCTGAGGCAGA
                                   C
GAM1664  JAM1     3'  AGACGGAGTCTCGCTCTG    34212       A
                                CAGAGC AGACTCCGTCT
                                |||||| ||||||||||
                                GTCTCG TCTGAGGCAGA
                                   C
GAM1664  JM11     3'  GAGACGGAGTCTTGCTCTG   54359
                                CAGAGCAAGACTCCGTCTC
                                |||||||||||||||||||
                                GTCTCGTTCTGAGGCAGAG

GAM1664  KIAA0186 3'  TGAGATGGAGTCTTGTTCTG  41121
                                CAGAGCAAGACTCCGTCTCA
                                |||||||||||||||||||
                                GTCTTGTTCTGAGGTAGAGT

GAM1664  KIAA0210 5'  TGAGACGGACTCTCGCTCTG  29180       A   C
                                CAGAGC AGA TCCGTCTCA
                                |||||| ||| |||||||||
                                GTCTCG TCT AGGCAGAGT
                                   C   C
GAM1664  KIAA0391 3'  TGAGACAGAGTCTTGATCT   28623     G       C
                                AGA CAAGACTC GTCTCA
                                ||| |||||||| ||||||
                                TCT GTTCTGAG CAGAGT
                                  A       A
GAM1664  KIAA0426 3'  TGAGATGGAGTCTTGCTC    28936
                                GAGCAAGACTCCGTCTCA
                                ||||||||||||||||||
                                CTCGTTCTGAGGTAGAGT

GAM1664  KIAA0444 3'  AGGCAGGCTTGCTCTG      62994         A  CC
                                CAGAGCAAG CT  GTCT
                                ||||||||| ||  ||||
                                GTCTCGTTC GG  CGGA
                                      _ A_
GAM1664  KIAA0459 3'  TGAGACAGAGTCTTGCTTTG  61664           C
                                CAGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
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                                GTTTCGTTCTGAG CAGAGT
                                      A
GAM1664 KIAA0469 3' TGAGACAGGGTCTTGCTCTG  29998          C
                                CAGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
                                GTCTCGTTCTGGG CAGAGT
                                      A
GAM1664 KIAA0472 5' GAGACGGAGTCTCACTCTG   72352      CA
                                CAGAG  AGACTCCGTCTC
                                |||||  ||||||||||||
                                GTCTC  TCTGAGGCAGAG
                                   AC
GAM1664 KIAA0478 3' GAGACAGGGTCTTGCTCTG   30178          C
                                CAGAGCAAGACTC GTCTC
                                |||||||||||| |||||
                                GTCTCGTTCTGGG CAGAG
                                      A
GAM1664 KIAA0495 3' TGAGATGGAGTCTTGCCCTG  63275    A
                                CAG GCAAGACTCCGTCTCA
                                ||| ||||||||||||||||
                                GTC CGTTCTGAGGTAGAGT
                                  C
GAM1664 KIAA0555 3' TGAGATGGAGTCTTGCTCTG  29554
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTCTGAGGTAGAGT

GAM1664 KIAA0557 3' TGAGACGGGGCCTTGCTGTG  78577   G    A
                                CA AGCAAG CTCCGTCTCA
                                || |||||| ||||||||||
                                GT TCGTTC GGGGCAGAGT
                                  G     C
GAM1664 KIAA0562 3' TGAGACGGAGTCTTGCTCTG  28832
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTCTGAGGCAGAGT

GAM1664 KIAA0594 3' TGAGATGGAGTCTCACTCTG  65520      CA
                                CAGAG  AGACTCCGTCTCA
                                |||||  ||||||||||||
                                GTCTC  TCTGAGGTAGAGT
                                   AC
GAM1664 KIAA0599 3' TGAAACGGAGTCTTGCTCTG  77703           C
                                CAGAGCAAGACTCCGT TCA
                                |||||||||||||||| |||
                                GTCTCGTTCTGAGGCA AGT
                                      A
GAM1664 KIAA0861 3' GAGACGGAGTCTCGCTCTG   90347      A
                                CAGAGC AGACTCCGTCTC
                                |||||| ||||||||||||
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                                GTCTCG TCTGAGGCAGAG
                                   C
GAM1664  KIAA0931  3'  TGAGACGGAGTCTTGCTC    68020
                                GAGCAAGACTCCGTCTCA
                                ||||||||||||||||||
                                CTCGTTCTGAGGCAGAGT

GAM1664  KIAA0961  3'  TGAGACGGAGTCTCGCTCT   30413      A
                                AGAGC AGACTCCGTCTCA
                                ||||| ||||||||||||
                                TCTCG TCTGAGGCAGAGT
                                   C
GAM1664  KIAA1028  3'  TGAGACGGAGTGTTGCTCTG  93594        G
                                CAGAGCAA ACTCCGTCTCA
                                |||||||| ||||||||||
                                GTCTCGTT TGAGGCAGAGT
                                      G
GAM1664  KIAA1040  3'  TGAGACGGAGTCTCGCTCTG  72693       A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
                                GTCTCG TCTGAGGCAGAGT
                                   C
GAM1664  KIAA1041  3'  TGAGATGGAGTCTTGCCCTG  30833     A
                                CAG GCAAGACTCCGTCTCA
                                ||| ||||||||||||||||
                                GTC CGTTCTGAGGTAGAGT
                                  C
GAM1664  KIAA1128  3'  TGAGACAGAGTCTTGCTC    69013          C
                                GAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
                                CTCGTTCTGAG CAGAGT
                                      A
GAM1664  KIAA1185  3'  TGAGATGGAGTCTCGCTCTG  63296       A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
                                GTCTCG TCTGAGGTAGAGT
                                   C
GAM1664  KIAA1198  3'  TGAGCTGGAGTCTTACTCTG  64070      C       T
                                CAGAG AAGACTCCG CTCA
                                ||||| ||||||||| ||||
                                GTCTC TTCTGAGGT GAGT
                                   A       C
GAM1664  KIAA1254  3'  TGAGATGGAATCTTGCTTTG  70568         C
                                CAGAGCAAGA TCCGTCTCA
                                |||||||||| |||||||||
                                GTTTCGTTCT AGGTAGAGT
                                      A
GAM1664  KIAA1257  3'  GAGATGGAGTCTTGCTCTG   63403
                                CAGAGCAAGACTCCGTCTC
                                |||||||||||||||||||
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                                GTCTCGTTCTGAGGTAGAG

GAM1664 KIAA1257 3' TGAGACGGAGTTTTGCTCT   63422
                                AGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||
                                TCTCGTTTTGAGGCAGAGT

GAM1664 KIAA1257 3' TGAGATAGGGTCTTGCTCT   63423          CG
                                AGAGCAAGACTC  TCTCA
                                ||||||||||||  |||||
                                TCTCGTTCTGGG  AGAGT
                                      AT
GAM1664 KIAA1280 5' TGAGACAGGGTCTTGCTTTG  70292           C
                                CAGAGCAAGACTC GTCTCA
                                |||||||||||||| ||||||
                                GTTTCGTTCTGGG CAGAGT
                                      A
GAM1664 KIAA1287 3' TGAGGTGGAGTCTTCCCCTG  78943    AGC      GT
                                CAG   AAGACTCC  CTCA
                                |||   ||||||||  ||||
                                GTC   TTCTGAGG  GAGT
                                  CCC       TG
GAM1664 KIAA1320 5' TGAGATGGAGTCTCGCCCTG  69852    A  A
                                CAG GC AGACTCCGTCTCA
                                ||| || ||||||||||||
                                GTC CG TCTGAGGTAGAGT
                                  C  C
GAM1664 KIAA1393 3' GAGACAGGGTCTTGCTCTG   72571           C
                                CAGAGCAAGACTC GTCTC
                                |||||||||||||| |||||
                                GTCTCGTTCTGGG CAGAG
                                      A
GAM1664 KIAA1443 3' TGAGGTGGAGTCTTGCTCTG  64579           GT
                                CAGAGCAAGACTCC  CTCA
                                ||||||||||||||  ||||
                                GTCTCGTTCTGAGG  GAGT
                                      TG
GAM1664 KIAA1449 3' TGAGACCACAGGTTCTTGCTCT 40843         CT  ____
          G                      CAGAGCAAGA  CC   GTCTCA
                                ||||||||||  ||   ||||||
                                GTCTCGTTCT  GG   CAGAGT
                                     T_  ACAC
GAM1664 KIAA1467 3' TGAGACAGAGTTTTGCTCT   72079           C
                                AGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
                                TCTCGTTTTGAG CAGAGT
                                      A
GAM1664 KIAA1493 3' TGAGATGGAGTCTCACTCTG  64845      CA
                                CAGAG  AGACTCCGTCTCA
                                |||||  ||||||||||||
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                                GTCTC  TCTGAGGTAGAGT
                                   AC
GAM1664  KIAA1497  5'  AGACAGGGTCTTGCTCTG    68107          C
                                CAGAGCAAGACTC GTCT
                                |||||||||||| ||||
                                GTCTCGTTCTGGG CAGA
                                      A
GAM1664  KIAA1530  3'  TGAAATGGAATCTTGCTCTG  68572        C    C
                                CAGAGCAAGA TCCGT TCA
                                |||||||||| ||||| |||
                                GTCTCGTTCT AGGTA AGT
                                      A    A
GAM1664  KIAA1615  3'  TGAGATAGAGCCTTGCTCTG  69289        A  CG
                                CAGAGCAAG CTC  TCTCA
                                ||||||||| |||  |||||
                                GTCTCGTTC GAG  AGAGT
                                     C   AT
GAM1664  KIAA1617  3'  TGAGACAGGGTCTTGCTCTG  93086          C
                                CAGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
                                GTCTCGTTCTGGG CAGAGT
                                      A
GAM1664  KIAA1655  3'  AGACGGAGTCTCACTCTG    67172      CA
                                CAGAG  AGACTCCGTCT
                                |||||  ||||||||||
                                GTCTC  TCTGAGGCAGA
                                   AC
GAM1664  KIAA1671  3'  TGAGACACGGTCTTGCTCTG  66291         CC
                                CAGAGCAAGACT  GTCTCA
                                ||||||||||||  ||||||
                                GTCTCGTTCTGG  CAGAGT
                                      CA
GAM1664  KIAA1713  5'  TGAGACAACATTTTGTTCTG  72800        CTCC
                                CAGAGCAAGA   GTCTCA
                                ||||||||||   ||||||
                                GTCTTGTTTT   CAGAGT
                                      ACAA
GAM1664  KIAA1858  3'  TGAGATGGTCCACTCTG     67725     CAA  CT
                                CAGAG   GA  CCGTCTCA
                                |||||   ||  ||||||||
                                GTCTC   CT  GGTAGAGT
                                   AC_  __
GAM1664  KIAA1924  3'  TGAGAGAGAGCCTTGTTCTG  74060        A  CG
                                CAGAGCAAG CTC  TCTCA
                                ||||||||| |||  |||||
                                GTCTTGTTC GAG  AGAGT
                                     C  AG
GAM1664  KIAA1924  3'  TGAGATGGCATCTTGCTCTG  74061         CT
                                CAGAGCAAGA  CCGTCTCA
                                ||||||||||  ||||||||
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                                GTCTCGTTCT  GGTAGAGT
                                      AC
GAM1664  KIAA1971  3'  TGAGATGGAGTCTCACTCTG   74698      CA
                                CAGAG  AGACTCCGTCTCA
                                |||||  ||||||||||||||
                                GTCTC  TCTGAGGTAGAGT
                                   AC
GAM1664  KIAA1987  5'  TGAGACAGAGTTTTGCTCT   89394          C
                                AGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
                                TCTCGTTTTGAG CAGAGT
                                       A
GAM1664  KPNA6     3'  TGAGGAGAAAGTCCTTGCTCTG 25544        _  CCG_
                                CAGAGCAAG ACT    TCTCA
                                ||||||||| |||    |||||
                                GTCTCGTTC TGA    GGAGT
                                      C   AAGA
GAM1664  LAMP3     3'  TGAGACGGAGTTTCACTCT   60212     CA
                                AGAG  AGACTCCGTCTCA
                                ||||  ||||||||||||||
                                TCTC  TTTGAGGCAGAGT
                                  AC
GAM1664  MAIL      3'  GAGACAGGGTCTTGCTCTG   49474          C
                                CAGAGCAAGACTC GTCTC
                                |||||||||||| |||||
                                GTCTCGTTCTGGG CAGAG
                                       A
GAM1664  MGC10200  3'  TGAGACAGGATCTTGCTTTG  59650        C  _
                                CAGAGCAAGA TCC GTCTCA
                                |||||||||| ||| ||||||
                                GTTTCGTTCT AGG CAGAGT
                                      _  A
GAM1664  MGC13017  3'  TGAGACAGAGTCTTGCTCTG  55582          C
                                CAGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
                                GTCTCGTTCTGAG CAGAGT
                                       A
GAM1664  MGC13204  3'  TGAGATGTAATATTGCTCTG  49635       GACTC
                                CAGAGCAA    CGTCTCA
                                ||||||||    |||||||
                                GTCTCGTT    GTAGAGT
                                     ATAAT
GAM1664  MGC14289  3'  TGAGATGGTCTTGCTCTG    55595        CT
                                CAGAGCAAGA  CCGTCTCA
                                ||||||||||  ||||||||
                                GTCTCGTTCT  GGTAGAGT
                                            __
GAM1664  MGC14436  5'  GAGACGGGGTCTTGCCCTG   52927    A
                                CAG GCAAGACTCCGTCTC
                                ||| ||||||||||||||
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                                GTC CGTTCTGGGGCAGAG
                                  C
GAM1664 MGC14836 3' TGAGGCAGAGTCTTGCTCTG  54178          C
                                CAGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
                                GTCTCGTTCTGAG CGGAGT
                                       A
GAM1664 MGC1842  3' TGAGACGGAGACTCACTCTG  66265     CA A
                                CAGAG  AG CTCCGTCTCA
                                |||||  || ||||||||||
                                GTCTC  TC GAGGCAGAGT
                                   AC  A
GAM1664 MGC2474  3' TGAGACGGAGTTTTGCTCT   43968
                                AGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||
                                TCTCGTTTTGAGGCAGAGT

GAM1664 MGC2603  3' TGAGATGGAGTCTCGCTCTG  44084      A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
                                GTCTCG TCTGAGGTAGAGT
                                   C
GAM1664 MGC5302  5' TGAGACGGATTCGCTC     44254     AA C
                                GAGC  GA TCCGTCTCA
                                ||||  || |||||||||
                                CTCG  CT AGGCAGAGT
                                  __ T
GAM1664 MGC9912  3' TGAGATGGAGTCTTGCTCTG  55610
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||
                                GTCTCGTTCTGAGGTAGAGT

GAM1664 MMPL1    3' TGAGACGGGGCCTTATTCTG  15968     C  A
                                CAGAG AAG CTCCGTCTCA
                                ||||| ||| ||||||||||
                                GTCTT TTC GGGGCAGAGT
                                   A  C
GAM1664 MOCS3    3' TGAGATGGAATCTCTCTCTG  27936     CA  C
                                CAGAG  AGA TCCGTCTCA
                                |||||  ||| |||||||||
                                GTCTC  TCT AGGTAGAGT
                                   TC  A
GAM1664 MRPL20   3' GAGACGGAGTCTCGCGCTG   36202    A A
                                CAG GC AGACTCCGTCTC
                                ||| || ||||||||||||
                                GTC CG TCTGAGGCAGAG
                                  G  C
GAM1664 MRPL44   3' TGAGATGGAGTCTTACTCTG  43601     C
                                CAGAG AAGACTCCGTCTCA
                                ||||| ||||||||||||||
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                                GTCTC TTCTGAGGTAGAGT
                                   A
GAM1664  MYO5C    3'  TGAGACTCCGGAGTCTCGCTCT 38728      A     ___
                                AGAGC AGACTCC   GTCTCA
                                ||||| |||||||   ||||||
                                TCTCG TCTGAGG   CAGAGT
                                   C      CCT
GAM1664  NEIL2    3'  TGAGAGAGAGTCTTGCTCTG   59571           CG
                                CAGAGCAAGACTC  TCTCA
                                ||||||||||||  |||||
                                GTCTCGTTCTGAG  AGAGT
                                       AG
GAM1664  NFAT5    3'  TGAGATGGAGTCTTGCTCTG   57794
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTCTGAGGTAGAGT

GAM1664  NUBP2    3'  TGAGACGGGGGCGGCCTG    64891    A  AAGA
                                CAG GC    CTCCGTCTCA
                                ||| ||    ||||||||||
                                GTC CG    GGGGCAGAGT
                                  _ GCG_
GAM1664  Nup43    3'  TGAGGCAGAGTCTTGCTCTG   45358          C
                                CAGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
                                GTCTCGTTCTGAG CGGAGT
                                       A
GAM1664  NXN      3'  TGAGATGGAGTCTTGCTCTG   42684
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTCTGAGGTAGAGT

GAM1664  OR51E2   3'  TGAGATGGGGTCTCGCTCTG   48522      A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
                                GTCTCG TCTGGGGTAGAGT
                                   C
GAM1664  OSBPL2   3'  TGAGACGGAGTTTCACTCT    29908     CA
                                AGAG  AGACTCCGTCTCA
                                ||||  ||||||||||||
                                TCTC  TTTGAGGCAGAGT
                                  AC
GAM1664  OSBPL2   3'  TGAGACGGAGTTTCACTCT    58495     CA
                                AGAG  AGACTCCGTCTCA
                                ||||  ||||||||||||
                                TCTC  TTTGAGGCAGAGT
                                  AC
GAM1664  OSBPL3   3'  TGAGTGATCTTGTTCT       32078       C  CGT
                                AGAGCAAGA TC   CTCA
                                |||||||| ||   ||||
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                                TCTTGTTCT AG   GAGT
                                      _ T__
GAM1664  PELI1    5'  TGAAATGGAGTCTTGCTCTG   40657            C
                                CAGAGCAAGACTCCGT TCA
                                |||||||||||||||| |||
                                GTCTCGTTCTGAGGTA AGT
                                         A
GAM1664  PELI1    5'  TGAGACGGAGTCTCACTCTG   40659      CA
                                CAGAG  AGACTCCGTCTCA
                                |||||  ||||||||||||
                                GTCTC  TCTGAGGCAGAGT
                                   AC
GAM1664  PELI1    5'  TGAGATGGAGTCTTGCTCTG   40660
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTCTGAGGTAGAGT

GAM1664  PIP3-E   3'  AGACAGAGTCTTGCTCTG    67342          C
                                CAGAGCAAGACTC GTCT
                                |||||||||||| ||||
                                GTCTCGTTCTGAG CAGA
                                         A
GAM1664  POFUT1   3'  AGACAGGGCCTTGCTCTG    70968        A  C
                                CAGAGCAAG CTC GTCT
                                ||||||||| ||| ||||
                                GTCTCGTTC GGG CAGA
                                      C  A
GAM1664  PPIL2    3'  AGACAGGGTCTTGCTCTG    27539          C
                                CAGAGCAAGACTC GTCT
                                |||||||||||| ||||
                                GTCTCGTTCTGGG CAGA
                                         A
GAM1664  PRO0365  5'  TGAGATGGAGTCTTGCTCTG   26998
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTCTGAGGTAGAGT

GAM1664  PRO1992  5'  TGAGACTAGGTCTTGCTCTG   26913          CC
                                CAGAGCAAGACT  GTCTCA
                                ||||||||||||  ||||||
                                GTCTCGTTCTGG  CAGAGT
                                         AT
GAM1664  PSPH     3'  TGAGACAGAATCTTGCTCTG   17141        C  C
                                CAGAGCAAGA TC GTCTCA
                                |||||||||| || ||||||
                                GTCTCGTTCT AG CAGAGT
                                      A  A
GAM1664  RAB21    3'  TGAGACGGAGTCTCGCTCTG   31099       A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
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                                GTCTCG TCTGAGGCAGAGT
                                   C
GAM1664 RAB33B   3' TGAGATGGAGTCTCGCTCTG  49337      A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
                                GTCTCG TCTGAGGTAGAGT
                                   C
GAM1664 RBAK     3' AGATGGACTTGTTCTG     41270       AC
                                CAGAGCAAG  TCCGTCT
                                |||||||||  |||||||
                                GTCTTGTTC  AGGTAGA
                                     __
GAM1664 RES4-25  3' TGAGACGGAGTTTTGCTCT  65279
                                AGAGCAAGACTCCGTCTCA
                                |||||||||||||||||||
                                TCTCGTTTTGAGGCAGAGT

GAM1664 RNPC1    3' TGAGACGGTTCCTGCCTG   34412    A  A  CT
                                CAG GCA GA  CCGTCTCA
                                ||| ||| ||  ||||||||
                                GTC CGT CT  GGCAGAGT
                                  _  C  T_
GAM1664 SARM     3' GAGACAGGGTCTTGCTCTG  31292         C
                                CAGAGCAAGACTC GTCTC
                                |||||||||||| |||||
                                GTCTCGTTCTGGG CAGAG
                                      A
GAM1664 SAST     5' TGAGACGGTGCTAGCCCTG  63663    A  A  ACT
                                CAG GC AG   CCGTCTCA
                                ||| || ||   ||||||||
                                GTC CG TC   GGCAGAGT
                                  C  A  GT_
GAM1664 SCDGF-B  3' TGAGTCTCAGCCTTGCTTTG  48154       A  CCGT
                                CAGAGCAAG CT    CTCA
                                ||||||||| ||    ||||
                                GTTTCGTTC GA    GAGT
                                     C  CTCT
GAM1664 SCDGF-B  3' TGAGTCTCAGCCTTGCTTTG  53635       A  CCGT
                                CAGAGCAAG CT    CTCA
                                ||||||||| ||    ||||
                                GTTTCGTTC GA    GAGT
                                     C  CTCT
GAM1664 SERF1B   3' TGAGATGGAGTCTCACTCTG  43705     CA
                                CAGAG  AGACTCCGTCTCA
                                |||||  ||||||||||||
                                GTCTC  TCTGAGGTAGAGT
                                   AC
GAM1664 SFXN2    3' AGATGGAGTCTTGCTCTG    74372
                                CAGAGCAAGACTCCGTCT
                                ||||||||||||||||||
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                                GTCTCGTTCTGAGGTAGA

GAM1664  SIAT8C    5'  AGACAAGCCTTGCTCTG     32441          A  CC
                                CAGAGCAAG CT  GTCT
                                |||||||||  ||  ||||
                                GTCTCGTTC GA  CAGA
                                      C  A_
GAM1664  SLC16A4   3'  TGAGACGGAGTCTCGCTCT    17461       A
                                AGAGC AGACTCCGTCTCA
                                ||||| ||||||||||||||
                                TCTCG TCTGAGGCAGAGT
                                   C
GAM1664  SS-56     3'  TGACACGGAGTCTCACTCTG   60362       CA        C
                                CAGAG  AGACTCCGT TCA
                                |||||  |||||||||  |||
                                GTCTC  TCTGAGGCA AGT
                                   AC         C
GAM1664  STAF65(gamma) 3'  TGAGATGGAGTCTTGCTCTG   30074
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTCTGAGGTAGAGT

GAM1664  SULT1C2   3'  TGAGACGGAGTCTCGCTCTG   22723        A
                                CAGAGC AGACTCCGTCTCA
                                ||||||  ||||||||||||||
                                GTCTCG TCTGAGGCAGAGT
                                   C
GAM1664  TCL6      5'  TGAGACTGAGTCTTGCTCTG   25918           C
                                CAGAGCAAGACTC GTCTCA
                                ||||||||||||| ||||||
                                GTCTCGTTCTGAG CAGAGT
                                         T
GAM1664  TCL6      5'  TGAGACTGAGTCTTGCTCTG   27770           C
                                CAGAGCAAGACTC GTCTCA
                                ||||||||||||| ||||||
                                GTCTCGTTCTGAG CAGAGT
                                         T
GAM1664  TCL6      5'  TGAGACTGAGTCTTGCTCTG   40495           C
                                CAGAGCAAGACTC GTCTCA
                                ||||||||||||| ||||||
                                GTCTCGTTCTGAG CAGAGT
                                         T
GAM1664  TCL6      5'  TGAGACTGAGTCTTGCTCTG   40520           C
                                CAGAGCAAGACTC GTCTCA
                                ||||||||||||| ||||||
                                GTCTCGTTCTGAG CAGAGT
                                         T
GAM1664  TERA      3'  TGAGACGGAGTTTTGCTCT    41424
                                AGAGCAAGACTCCGTCTCA
                                |||||||||||||||||||
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                                TCTCGTTTTGAGGCAGAGT

GAM1664 THEA     3' TGAGACAGCCTTGCTCTG    66899        A  CC
                                CAGAGCAAG CT  GTCTCA
                                ||||||||| ||  ||||||
                                GTCTCGTTC GA  CAGAGT
                                    C  __
GAM1664 TRIM16   3' TGAGACGGAGTCTCGCACTG  22380     A  A
                                CAG GC AGACTCCGTCTCA
                                ||| || ||||||||||||||
                                GTC CG TCTGAGGCAGAGT
                                  A  C
GAM1664 TRIM6    3' TGAGATGGAATCTCGCTCTG  55189      A   C
                                CAGAGC AGA TCCGTCTCA
                                |||||| ||| |||||||||
                                GTCTCG TCT AGGTAGAGT
                                    C   A
GAM1664 TUCAN    3' TGAGATGGAGTCTCGCTCTG  30992      A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||||
                                GTCTCG TCTGAGGTAGAGT
                                    C
GAM1664 TUSP     3' TGAGACGGAGTCCCACTCT   40031     CAA
                                AGAG   GACTCCGTCTCA
                                ||||   ||||||||||||
                                TCTC   CTGAGGCAGAGT
                                  ACC
GAM1664 VDU1     3' TGAGACAGAGTCTTGCTTTG  31130          C
                                CAGAGCAAGACTC GTCTCA
                                |||||||||||||| ||||||
                                GTTTCGTTCTGAG CAGAGT
                                        A
GAM1664 VPS33A   3' TGAGACGGAGTCTTGCTCTG  43617
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTCTGAGGCAGAGT

GAM1664 ZNF17    3' TGAGACAGAATCTTGCTCTG  83278        C  C
                                CAGAGCAAGA TC GTCTCA
                                |||||||||| || ||||||
                                GTCTCGTTCT AG CAGAGT
                                      A  A
GAM1664 ZNF338   3' TGAGACGGAGTCTCGCTCTG  42263      A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
                                GTCTCG TCTGAGGCAGAGT
                                    C
GAM1664 ZTL1     3' TGAGAAAGAGTCTTGCTC    44144        CG
                                GAGCAAGACTC  TCTCA
                                ||||||||||  |||||
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                                CTCGTTCTGAG  AGAGT
                                      AA
GAM1664  LOC112687 3'  TGAGACGGAGTCTCGCCCTG   73244     A  A
                                CAG GC AGACTCCGTCTCA
                                ||| || ||||||||||||||
                                GTC CG TCTGAGGCAGAGT
                                  C  C
GAM1664  LOC116028 3'  AGAGAGCCTTGCTTTG      74094         A   CG
                                CAGAGCAAG CTC  TCT
                                ||||||||| |||  |||
                                GTTTCGTTC GAG  AGA
                                      C  __
GAM1664  LOC120114 3'  AGACAGAGTCTTGCTCTG     76035            C
                                CAGAGCAAGACTC GTCT
                                |||||||||||||| ||||
                                GTCTCGTTCTGAG CAGA
                                       A
GAM1664  LOC121219 5'  TGAGACGATCTTGCTTT      74490         CTC
                                AGAGCAAGA   CGTCTCA
                                |||||||||   |||||||
                                TTTCGTTCT   GCAGAGT
                                      A__
GAM1664  LOC124222 3'  TGGGGTCACGTCTTGCTCTG   74757           TCCG
                                CAGAGCAAGAC    TCTCA
                                ||||||||||    |||||
                                GTCTCGTTCTG    GGGGT
                                       CACT
GAM1664  LOC125988 5'  GAGACCGCAGCCCTTCTCTG   74898      C   A_  C  _
                                CAGAG AAG  CT CG TCTC
                                ||||| |||  || || ||||
                                GTCTC TTC  GA GC AGAG
                                   _   CC  C  C
GAM1664  LOC128077 3'  TGAGACGGAGTCTTGCTCTG   75233
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTCTGAGGCAGAGT

GAM1664  LOC128989 3'  TGAGACGGAGTCTTGCTCTG   75326
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTCTGAGGCAGAGT

GAM1664  LOC131583 5'  TGAGACTCTTTGCTCT       76383        _  CTCC
                                AGAGCAA GA    GTCTCA
                                ||||||| ||    ||||||
                                TCTCGTT CT    CAGAGT
                                     T  _____
GAM1664  LOC133686 3'  TGAGAACGGAGTCTTGCTTTG  75622              _
                                CAGAGCAAGACTCCGT CTCA
                                |||||||||||||||| ||||
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                                GTTTCGTTCTGAGGCA GAGT
                                      A
GAM1664  LOC135818 3'  TGAGACAGGGTTTTGCTCT   75751          C
                                AGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
                                TCTCGTTTTGGG CAGAGT
                                     A
GAM1664  LOC142820 5'  TGAGACGGAGTTTTGCCATG  76919    GA
                                CA  GCAAGACTCCGTCTCA
                                ||  ||||||||||||||||
                                GT  CGTTTTGAGGCAGAGT
                                 AC
GAM1664  LOC143187 3'  TGAGACAGAGTCTTGCCCTG  59765    A       C
                                CAG GCAAGACTC GTCTCA
                                ||| ||||||||| ||||||
                                GTC CGTTCTGAG CAGAGT
                                  C       A
GAM1664  LOC144248 5'  TGAGACGGAGTCTCGCTCT   77256      A
                                AGAGC AGACTCCGTCTCA
                                ||||| ||||||||||||
                                TCTCG TCTGAGGCAGAGT
                                   C
GAM1664  LOC144524 5'  TGAGACGGAGTTTTGCTCT   84068
                                AGAGCAAGACTCCGTCTCA
                                |||||||||||||||||||
                                TCTCGTTTTGAGGCAGAGT

GAM1664  LOC144667 3'  TGAGGCAGGGTCTTGCTCTG  84090          C
                                CAGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
                                GTCTCGTTCTGGG CGGAGT
                                     A
GAM1664  LOC144871 3'  TGAGACAGAATCTTGCTCTG  84130         C  C
                                CAGAGCAAGA TC GTCTCA
                                |||||||||| || ||||||
                                GTCTCGTTCT AG CAGAGT
                                      A  A
GAM1664  LOC145009 3'  TGAGATGGAGTCTCGCTCTG  60983      A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
                                GTCTCG TCTGAGGTAGAGT
                                   C
GAM1664  LOC146050 3'  GAGATGGAGTCTCACTCTG   78116      CA
                                CAGAG  AGACTCCGTCTC
                                |||||  ||||||||||||
                                GTCTC  TCTGAGGTAGAG
                                   AC
GAM1664  LOC146229 3'  AGATGGAGTCTCGCTCTG    78257      A
                                CAGAGC AGACTCCGTCT
                                |||||| ||||||||||
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                                GTCTCG TCTGAGGTAGA
                                   C
GAM1664  LOC146229 3'  TGAGACGGAGTCTCGCTCTG   78319       A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
                                GTCTCG TCTGAGGCAGAGT
                                   C
GAM1664  LOC146229 3'  TGAGATGGACTCTCACTCTG   78320      CA   C
                                CAGAG  AGA TCCGTCTCA
                                |||||  ||| |||||||||
                                GTCTC  TCT AGGTAGAGT
                                   AC   C
GAM1664  LOC146346 5'  TGAGATGGAGTCTCACTC    78411     CA
                                GAG  AGACTCCGTCTCA
                                |||  ||||||||||||
                                CTC  TCTGAGGTAGAGT
                                  AC
GAM1664  LOC146429 5'  TGAGATGGAGTCTCGCTCTG   84676       A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
                                GTCTCG TCTGAGGTAGAGT
                                   C
GAM1664  LOC146455 3'  GAGATGGAGTCTTACTCTG    78460      C
                                CAGAG AAGACTCCGTCTC
                                ||||| |||||||||||||
                                GTCTC TTCTGAGGTAGAG
                                   A
GAM1664  LOC146603 5'  TGAAACGGAGTCTCGCTCTG   78608       A        C
                                CAGAGC AGACTCCGT TCA
                                |||||| ||||||||| |||
                                GTCTCG TCTGAGGCA AGT
                                   C        A
GAM1664  LOC146839 3'  TGAGATGGAATCTCACTCTG   84856      CA   C
                                CAGAG  AGA TCCGTCTCA
                                |||||  ||| |||||||||
                                GTCTC  TCT AGGTAGAGT
                                   AC   A
GAM1664  LOC146909 3'  TGAGATGGAGTCTCGCTCTG   78785       A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
                                GTCTCG TCTGAGGTAGAGT
                                   C
GAM1664  LOC146909 3'  TGAGATGGAGTCTTACTCTG   78786      C
                                CAGAG AAGACTCCGTCTCA
                                ||||| |||||||||||||
                                GTCTC TTCTGAGGTAGAGT
                                   A
GAM1664  LOC146952 5'  TGAGACGGAGTCTGGCTCTG   84937       A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
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                                GTCTCG TCTGAGGCAGAGT
                                   G
GAM1664  LOC147166 3'  TGAGACGGAGTCTCGCACTG   78896     A  A
                                CAG GC AGACTCCGTCTCA
                                ||| || ||||||||||||||
                                GTC CG TCTGAGGCAGAGT
                                  A  C
GAM1664  LOC147622 3'  TGAGATGGAGTCTTGCTCT    85173
                                AGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||
                                TCTCGTTCTGAGGTAGAGT

GAM1664  LOC147694 3'  TGAGACAGAGTCTTGCTCTG   79109           C
                                CAGAGCAAGACTC GTCTCA
                                |||||||||||||| ||||||
                                GTCTCGTTCTGAG CAGAGT
                                         A
GAM1664  LOC147817 3'  TGAGACGGAGTCTTCCTCTG   79196      C
                                CAGAG AAGACTCCGTCTCA
                                ||||| ||||||||||||||
                                GTCTC TTCTGAGGCAGAGT
                                   C
GAM1664  LOC147817 3'  TGAGATGGAGTCTCGCTCTG   79197       A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
                                GTCTCG TCTGAGGTAGAGT
                                   C
GAM1664  LOC147990 3'  TGAGATAGGGTATTGCTCTG   85238        G   CG
                                CAGAGCAA ACTC  TCTCA
                                |||||||| ||||  |||||
                                GTCTCGTT TGGG  AGAGT
                                     A    AT
GAM1664  LOC147990 3'  TGAGATGGAGTCTCACTCTG   85239      CA
                                CAGAG  AGACTCCGTCTCA
                                |||||  ||||||||||||||
                                GTCTC  TCTGAGGTAGAGT
                                   AC
GAM1664  LOC148195 5'  TGAGAAATAATCTTGCTCTG   85294         CTCCG
                                CAGAGCAAGA     TCTCA
                                ||||||||||     |||||
                                GTCTCGTTCT     AGAGT
                                      AATAA
GAM1664  LOC148887 5'  TGAGACGGTGTCTCGCTCTG   85413       A   T
                                CAGAGC AGAC CCGTCTCA
                                |||||| |||| ||||||||
                                GTCTCG TCTG GGCAGAGT
                                   C   T
GAM1664  LOC149478 3'  TGAGACAGAGTCTTGCTCTG   80179           C
                                CAGAGCAAGACTC GTCTCA
                                |||||||||||||| ||||||
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                                GTCTCGTTCTGAG CAGAGT
                                      A
GAM1664  LOC149577 3'  TGAGATGGAGTCTCGCTTTG   85683       A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
                                GTTTCG TCTGAGGTAGAGT
                                   C
GAM1664  LOC149692 3'  AGATGGAGTCTCGCTCTG    85726       A
                                CAGAGC AGACTCCGTCT
                                |||||| ||||||||||
                                GTCTCG TCTGAGGTAGA
                                   C
GAM1664  LOC149703 5'  TGAGATAGAGTCTTGTTCTG  85826           CG
                                CAGAGCAAGACTC  TCTCA
                                ||||||||||||  |||||
                                GTCTTGTTCTGAG  AGAGT
                                      AT
GAM1664  LOC149711 3'  TGAGACGGAGTTTTGCTCT   85857
                                AGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||
                                TCTCGTTTTGAGGCAGAGT

GAM1664  LOC150166 5'  GGGCCAGTCTTGCCTG      86041    A      CC
                                CAG GCAAGACT  GTCT
                                ||| ||||||||  ||||
                                GTC CGTTCTGA  CGGG
                                  _      C_
GAM1664  LOC150225 3'  TGAGATAGAGTCTTGCTCTG  86207           CG
                                CAGAGCAAGACTC  TCTCA
                                ||||||||||||  |||||
                                GTCTCGTTCTGAG  AGAGT
                                      AT
GAM1664  LOC150397 3'  TGAGATGGAATCCCACTCTG  80669      CAA  C
                                CAGAG   GA TCCGTCTCA
                                |||||   || |||||||||
                                GTCTC   CT AGGTAGAGT
                                   ACC  A
GAM1664  LOC150407 3'  GAGAGAGGATCTTGCTCTG   80642         C   G_
                                CAGAGCAAGA TCC  TCTC
                                |||||||||| |||  ||||
                                GTCTCGTTCT AGG  AGAG
                                      _   AG
GAM1664  LOC150696 3'  TGAGACGGGGTCTCGCTCTG  59168       A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
                                GTCTCG TCTGGGGCAGAGT
                                   C
GAM1664  LOC150998 3'  AGAGAGCCTTTGCTCTG     86355        A_   CG
                                CAGAGCAAG  CTC  TCT
                                |||||||||  |||  |||
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                                GTCTCGTTT  GAG  AGA
                                     CC   __
GAM1664  LOC151201 3'  TGAGATGGAGTCTCACGCT   86490    A__
                                AGC   AGACTCCGTCTCA
                                |||   ||||||||||||||
                                TCG   TCTGAGGTAGAGT
                                  CAC
GAM1664  LOC151475 5'  TGAGACAGAGTCTTGCTCTG   86607          C
                                CAGAGCAAGACTC GTCTCA
                                |||||||||||||| ||||||
                                GTCTCGTTCTGAG CAGAGT
                                        A
GAM1664  LOC151701 3'  TGAGATGGAGTCTCGCTCTG   86682       A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||||
                                GTCTCG TCTGAGGTAGAGT
                                    C
GAM1664  LOC151826 3'  TGAGATGGAGTCTCACTCTG   81189      CA
                                CAGAG  AGACTCCGTCTCA
                                |||||  ||||||||||||||
                                GTCTC  TCTGAGGTAGAGT
                                   AC
GAM1664  LOC152137 3'  TGAGTTGGAGTCTCGCCCTG   81326     A  A      T
                                CAG GC AGACTCCG CTCA
                                ||| || |||||||| ||||
                                GTC CG TCTGAGGT GAGT
                                  C  C       T
GAM1664  LOC152245 3'  TGAAATGGAGTCTCGCTCTG   86785       A       C
                                CAGAGC AGACTCCGT TCA
                                |||||| ||||||||| |||
                                GTCTCG TCTGAGGTA AGT
                                    C        A
GAM1664  LOC152245 3'  TGAGATGGATTCTCGCTCTG   86786       A   C
                                CAGAGC AGA TCCGTCTCA
                                |||||| ||| |||||||||
                                GTCTCG TCT AGGTAGAGT
                                    C   T
GAM1664  LOC152282 5'  GGACAGAGTCTTGCCCTG    81406     A       C
                                CAG GCAAGACTC GTCT
                                ||| ||||||||| ||||
                                GTC CGTTCTGAG CAGG
                                  C        A
GAM1664  LOC152343 3'  TGAGATGGAGTCTTGCTGTG   81439    G
                                CA AGCAAGACTCCGTCTCA
                                || ||||||||||||||||
                                GT TCGTTCTGAGGTAGAGT
                                 G
GAM1664  LOC152445 3'  TGAGACGGAGTCTCGATCTG   86969     GCA
                                CAGA   AGACTCCGTCTCA
                                ||||   ||||||||||||
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                                GTCT   TCTGAGGCAGAGT
                                  AGC
GAM1664  LOC152445 3'  TGAGACGGGATCTTCCCCTG   86970     AGC    CT
                                CAG   AAGA  CCGTCTCA
                                |||   ||||  ||||||||
                                GTC   TTCT  GGCAGAGT
                                  CCC    AG
GAM1664  LOC152719 5'  TGAGACGGAGTCTCGCTCTG   87043       A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
                                GTCTCG TCTGAGGCAGAGT
                                   C
GAM1664  LOC152794 5'  TGAGACAGAGTCTTGGTCTG   81565     G       C
                                CAGA CAAGACTC GTCTCA
                                |||| |||||||| ||||||
                                GTCT GTTCTGAG CAGAGT
                                  G       A
GAM1664  LOC153688 3'  TGAGACGGAGTCTCACTCTG   87338      CA
                                CAGAG  AGACTCCGTCTCA
                                |||||  ||||||||||||
                                GTCTC  TCTGAGGCAGAGT
                                   AC
GAM1664  LOC157798 5'  TGAGACGGAGTCTTGCTGTG   87867    G
                                CA AGCAAGACTCCGTCTCA
                                || ||||||||||||||||
                                GT TCGTTCTGAGGCAGAGT
                                 G
GAM1664  LOC157858 5'  GAGACGGAATCTCACTCTG    87889      CA   C
                                CAGAG  AGA TCCGTCTC
                                |||||  ||| ||||||||
                                GTCTC  TCT AGGCAGAG
                                   AC   A
GAM1664  LOC158476 3'  AGACAGAGTCTTGCTCTG     88177           C
                                CAGAGCAAGACTC GTCT
                                |||||||||||| ||||
                                GTCTCGTTCTGAG CAGA
                                        A
GAM1664  LOC158476 3'  TGAGATGGAGTCTTGCTCTG   88209
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTCTGAGGTAGAGT

GAM1664  LOC158969 5'  TGGGGAAAGTCTTGCCTG     82939     A       CCG
                                CAG GCAAGACT   TCTCA
                                ||| ||||||||   |||||
                                GTC CGTTCTGA   GGGGT
                                  _       AA_
GAM1664  LOC160646 3'  TGAGACGGAGTCTCGGTCTG   83125      GCA
                                CAGA   AGACTCCGTCTCA
                                ||||   ||||||||||||
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                                GTCT   TCTGAGGCAGAGT
                                  GGC
GAM1664  LOC162962 3'  TGAGACGGAGTCTCTCTCTG   83261      CA
                                CAGAG  AGACTCCGTCTCA
                                |||||  ||||||||||||
                                GTCTC  TCTGAGGCAGAGT
                                   TC
GAM1664  LOC196529 3'  TGAGACGGAGTTTTCGCTCT   89144      _
                                AGAGC AAGACTCCGTCTCA
                                ||||| ||||||||||||||
                                TCTCG TTTTGAGGCAGAGT
                                   C
GAM1664  LOC197358 3'  TGAGATGGAGTCTCGCTCT    89448      A
                                AGAGC AGACTCCGTCTCA
                                ||||| ||||||||||||
                                TCTCG TCTGAGGTAGAGT
                                   C
GAM1664  LOC199699 3'  TGAGATGGAGTCTCGCTCTG   89686      A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
                                GTCTCG TCTGAGGTAGAGT
                                    C
GAM1664  LOC199725 5'  TGAGACGGAGTCACTCTG    91428      CAA
                                CAGAG   GACTCCGTCTCA
                                |||||   ||||||||||||
                                GTCTC   CTGAGGCAGAGT
                                   A__
GAM1664  LOC199786 3'  TGAGACTGAGTCTTGCTCTG   89769          C
                                CAGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
                                GTCTCGTTCTGAG CAGAGT
                                        T
GAM1664  LOC200314 3'  TGAGATGGAGTCTCCCTCTG   91605      CA
                                CAGAG  AGACTCCGTCTCA
                                |||||  ||||||||||||
                                GTCTC  TCTGAGGTAGAGT
                                   CC
GAM1664  LOC200316 3'  TGAGACGGAGTTTCACTCTG   90197      CA
                                CAGAG  AGACTCCGTCTCA
                                |||||  ||||||||||||
                                GTCTC  TTTGAGGCAGAGT
                                   AC
GAM1664  LOC200845 5'  TGAGATGGAGTCTCGCACTG   90320     A  A
                                CAG GC AGACTCCGTCTCA
                                ||| || ||||||||||||
                                GTC CG TCTGAGGTAGAGT
                                  A  C
GAM1664  LOC200860 3'  TGAGACGGGGTTTCGCTCT    91760      A
                                AGAGC AGACTCCGTCTCA
                                ||||| ||||||||||||
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                                TCTCG TTTGGGGCAGAGT
                                   C
GAM1664  LOC200860 3'  TGAGATAGTGTCTTGCTCTG  91761          TCC
                                CAGAGCAAGAC  GTCTCA
                                ||||||||||  ||||||
                                GTCTCGTTCTG  TAGAGT
                                      TGA
GAM1664  LOC200931 5'  GAGGCGGACTCTGCTCTG   90375       A  C
                                CAGAGCA GA TCCGTCTC
                                ||||||| || ||||||||
                                GTCTCGT CT AGGCGGAG
                                    _  C
GAM1664  LOC201164 3'  TGAGATGGAGTCTCACTCTG  89504      CA
                                CAGAG  AGACTCCGTCTCA
                                |||||  ||||||||||||
                                GTCTC  TCTGAGGTAGAGT
                                   AC
GAM1664  LOC201294 3'  TGAGACGGAGTCTCGCTCTG  89597       A
                                CAGAGC AGACTCCGTCTCA
                                ||||||| ||||||||||||
                                GTCTCG TCTGAGGCAGAGT
                                   C
GAM1664  LOC201294 3'  TGAGATGGAGTCTTGCTCTG  89598
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTCTGAGGTAGAGT

GAM1664  LOC202460 5'  TGAGATGGATTCTTGCTCTG  90679         C
                                CAGAGCAAGA TCCGTCTCA
                                |||||||||| |||||||||
                                GTCTCGTTCT AGGTAGAGT
                                      T
GAM1664  LOC202908 5'  GAGTGGAGTCTTGCTCTG   90726           T
                                CAGAGCAAGACTCCG CTC
                                |||||||||||||| |||
                                GTCTCGTTCTGAGGT GAG
                                                _
GAM1664  LOC202934 3'  TGAGATGGAATCTAGCTCTG  92056       A  C
                                CAGAGC AGA TCCGTCTCA
                                ||||||| ||| |||||||||
                                GTCTCG TCT AGGTAGAGT
                                   A  A
GAM1664  LOC203197 3'  TGAGATGGAGTCTTGCACTG  90820     A
                                CAG GCAAGACTCCGTCTCA
                                ||| ||||||||||||||||
                                GTC CGTTCTGAGGTAGAGT
                                  A
GAM1664  LOC203427 3'  GAGACAGGGTCTTGCTCTG   90920          C
                                CAGAGCAAGACTC GTCTC
                                |||||||||||| |||||
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                                GTCTCGTTCTGGG CAGAG
                                      A
GAM1664  LOC219562 5'  TGAGACGGAGCTGCCTC     92449     CA  A
                                GAG  AG CTCCGTCTCA
                                |||  || ||||||||||
                                CTC  TC GAGGCAGAGT
                                  CG  _
GAM1664  LOC219673 5'  TGAGACAGAGTCTTGCTCT    94636           C
                                AGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
                                TCTCGTTCTGAG CAGAGT
                                      A
GAM1664  LOC219735 3'  TGAGATGGAGTCTTGCTCTG   94737
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTCTGAGGTAGAGT

GAM1664  LOC219894 3'  TGAGATGGAGTCTTGCTCTG   94910
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTCTGAGGTAGAGT

GAM1664  LOC219940 3'  TGAGATTTCTTGCTCT      95005         CTCC
                                AGAGCAAGA    GTCTCA
                                |||||||||    ||||||
                                TCTCGTTCT    TAGAGT
                                     T___
GAM1664  LOC220064 3'  AGACGGAGTCTCACTCTG     95058       CA
                                CAGAG  AGACTCCGTCT
                                |||||  ||||||||||
                                GTCTC  TCTGAGGCAGA
                                   AC
GAM1664  LOC220074 3'  TGAGACGGAGTCTCACTCTG   59999       CA
                                CAGAG  AGACTCCGTCTCA
                                |||||  |||||||||||||
                                GTCTC  TCTGAGGCAGAGT
                                   AC
GAM1664  LOC220074 3'  TGAGACGGAGTCTCGCTCTG   60000        A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
                                GTCTCG TCTGAGGCAGAGT
                                    C
GAM1664  LOC221035 3'  TGAGACGGAGTCTTGCTCTG   94783
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTCTGAGGCAGAGT

GAM1664  LOC221060 3'  TGAGACAGAGTTTTGCCCT    94838    A        C
                                AG GCAAGACTC GTCTCA
                                || ||||||||| ||||||
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                                TC CGTTTTGAG CAGAGT
                                 C        A
GAM1664  LOC221751 5'  GAGACGCAGTTGCTCTG     93680        AG   C
                                CAGAGCA  ACT CGTCTC
                                |||||||  ||| ||||||
                                GTCTCGT  TGA GCAGAG
                                    __   C
GAM1664  LOC221962 3'  TGAGACGGGAAAATTGCTT    94244       GAC_
                                GAGCAA    TCCGTCTCA
                                ||||||    |||||||||
                                TTCGTT    GGGCAGAGT
                                   AAAA
GAM1664  LOC221975 5'  TGAGAGCGCTCCTTGCTCTG   94195         ACTC  _
                                CAGAGCAAG    CG TCTCA
                                |||||||||    || |||||
                                GTCTCGTTC    GC AGAGT
                                     CTC_  G
GAM1664  LOC245771 5'  TGAGATGGAGTCTCGCTCTG   94490       A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
                                GTCTCG TCTGAGGTAGAGT
                                   C
GAM1664  LOC253612 5'  TGAGATGGAGTCTCGCTCTG   98560       A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
                                GTCTCG TCTGAGGTAGAGT
                                   C
GAM1664  LOC253664 3'  TGATACGGAGTCTCGCTCTG   96475       A        C
                                CAGAGC AGACTCCGT TCA
                                |||||| ||||||||| |||
                                GTCTCG TCTGAGGCA AGT
                                   C        T
GAM1664  LOC253779 3'  TGAGATGGAGTCTTGCTCTG   98927
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTCTGAGGTAGAGT

GAM1664  LOC253805 3'  TGAGATGGAGACTCACTCTG   98188      CA  A
                                CAGAG  AG CTCCGTCTCA
                                |||||  || ||||||||||
                                GTCTC  TC GAGGTAGAGT
                                   AC  A
GAM1664  LOC254672 3'  TGAGATGGAGTCTCACTCTG   96301      CA
                                CAGAG  AGACTCCGTCTCA
                                |||||  ||||||||||||
                                GTCTC  TCTGAGGTAGAGT
                                   AC
GAM1664  LOC255196 5'  TGAGACAGAGTCTTGCTCT    98968          C
                                AGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
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                                TCTCGTTCTGAG CAGAGT
                                      A
GAM1664  LOC255465 3'  TGAGATGGAGTCTAGCTCTG   99130       A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
                                GTCTCG TCTGAGGTAGAGT
                                   A
GAM1664  LOC255497 3'  TGAGACGGAGCGTCGCTCTG   98991       AAGA
                                CAGAGC   CTCCGTCTCA
                                ||||||   ||||||||||
                                GTCTCG   GAGGCAGAGT
                                   CTGC
GAM1664  LOC255919 3'  AGACGGAGTCTCGCTCTG    96741       A
                                CAGAGC AGACTCCGTCT
                                |||||| ||||||||||
                                GTCTCG TCTGAGGCAGA
                                   C
GAM1664  LOC256221 3'  TGAGACGGAGTCTCGCTCTG   96921       A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
                                GTCTCG TCTGAGGCAGAGT
                                   C
GAM1664  LOC256267 5'  TGAGACAAGGTCTTGCTCTG   98615          CC
                                CAGAGCAAGACT  GTCTCA
                                ||||||||||||  ||||||
                                GTCTCGTTCTGG  CAGAGT
                                      AA
GAM1664  LOC256267 3'  TGAGATGGAGTCTCCCTCTG   98617      CA
                                CAGAG  AGACTCCGTCTCA
                                |||||  ||||||||||||
                                GTCTC  TCTGAGGTAGAGT
                                  CC
GAM1664  LOC256306 3'  TGAGATGGGAGTCTTGCTCTG  98522           _
                                CAGAGCAAGACTCC GTCTCA
                                |||||||||||||| ||||||
                                GTCTCGTTCTGAGG TAGAGT
                                      G
GAM1664  LOC257181 5'  TGAGACGGAGCTGCCTC     96230     CA  A
                                GAG  AG CTCCGTCTCA
                                |||  || ||||||||||
                                CTC  TC GAGGCAGAGT
                                  CG  _
GAM1664  LOC257463 3'  TGAGACAGGTTCTTGTTCT    71626        CT  _
                                AGAGCAAGA  CC GTCTCA
                                |||||||||  || ||||||
                                TCTTGTTCT  GG CAGAGT
                                      T_  A
GAM1664  LOC257465 3'  TGAGATGGAGTCTCACTCTG   82502      CA
                                CAGAG  AGACTCCGTCTCA
                                |||||  ||||||||||||
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                                GTCTC  TCTGAGGTAGAGT
                                   AC
GAM1664  LOC51031  5'  TGAGACTGAGTCTTGCTCTG  32712          C
                                CAGAGCAAGACTC GTCTCA
                                |||||||||||| ||||||
                                GTCTCGTTCTGAG CAGAGT
                                       T
GAM1664  LOC51696  3'  TGAGATGGAGTCTCACTCT  33092     CA
                                AGAG  AGACTCCGTCTCA
                                ||||  ||||||||||||
                                TCTC  TCTGAGGTAGAGT
                                   AC
GAM1664  LOC56181  5'  TGAGACGGAGTCTCGCTCTG  97287       A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
                                GTCTCG TCTGAGGCAGAGT
                                    C
GAM1664  LOC81034  3'  TGAGATGGAGTCTTGCTTTG  48598
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTTTCGTTCTGAGGTAGAGT

GAM1664  LOC90190  3'  TGAGACGGAATCTCCGTT    62434     A_  C
                                AGC  AGA TCCGTCTCA
                                |||  ||| |||||||||
                                TTG  TCT AGGCAGAGT
                                  CC   A
GAM1664  LOC90288  3'  TGAAACAAATCTTGCTCTG   62803         CTCC  C
                                CAGAGCAAGA    GT TCA
                                ||||||||||    || |||
                                GTCTCGTTCT    CA AGT
                                      AAA_  A
GAM1664  LOC90333  3'  TGAGATGGAGTCTTGCTCTG  62966
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTCTGAGGTAGAGT

GAM1664  LOC90371  5'  TGAGACGGAGTCTCGTTCTG  63167       A
                                CAGAGC AGACTCCGTCTCA
                                |||||| ||||||||||||
                                GTCTTG TCTGAGGCAGAGT
                                    C
GAM1664  LOC90459  3'  TGAGACAGAGTTTTTGCTC   63567        _  C
                                GAGCAAGA CTC GTCTCA
                                |||||||| ||| ||||||
                                CTCGTTTT GAG CAGAGT
                                     T   A
GAM1664  LOC90485  3'  TGAGACGGAGTCTTGCTCTG  63714
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
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                                GTCTCGTTCTGAGGCAGAGT

GAM1664 LOC90591 3' TGAGACGGAGTCTTGCTCTG  64194
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTCTGAGGCAGAGT

GAM1664 LOC91893 3' TGAGACGGAGTCTTGCTCTG  68081
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTCGTTCTGAGGCAGAGT

GAM1664 LOC92466 5' TGAGACAAGGTCTTGCTCTG  69971          CC
                                CAGAGCAAGACT GTCTCA
                                ||||||||||||  ||||||
                                GTCTCGTTCTGG CAGAGT
                                       AA
GAM1664 LOC92466 3' TGAGATGGAGTCTCCCTCTG  69973     CA
                                CAGAG AGACTCCGTCTCA
                                |||||  ||||||||||||
                                GTCTC TCTGAGGTAGAGT
                                   CC
GAM1664 LOC92661 5' TGAGATGGAGTCTTGTTCTG  70637
                                CAGAGCAAGACTCCGTCTCA
                                ||||||||||||||||||||
                                GTCTTGTTCTGAGGTAGAGT

GAM1664 LOC92710 5' TGAGCCTCTTTGCTCTG     70871       _ CTCC T
                                CAGAGCAA GA   G CTCA
                                |||||||| ||   | ||||
                                GTCTCGTT CT   C GAGT
                                     T  C___ _
GAM1664 LOC93132 5' TGAGATGGAGTCTCGCTCTG  72001      A
                                CAGAGC AGACTCCGTCTCA
                                ||||||  ||||||||||||
                                GTCTCG TCTGAGGTAGAGT
                                   C
GAM1664 LOC93206 3' TGAGACGGAGTTTCCCTCTG  72193     CA
                                CAGAG AGACTCCGTCTCA
                                |||||  ||||||||||||
                                GTCTC TTTGAGGCAGAGT
                                   CC
GAM1665 SLC13A4  3' CACCAGGAGCACACAACCCCAG 25859   AA   C      GAA
           A                     TC  GGGT GTGTGTTT  GTG
                                ||  |||| ||||||||  |||
                                AG  CCCA CACACGAG  CAC
                                 AC   A      GAC
GAM1665 ATP10B   3' CACTGGTCCACATAACCCTTGA 64104       CG   TTTGA
                                TCAAGGGT TGTG   AGTG
                                ||||||||  ||||   ||||
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                                AGTTCCCA  ACAC    TCAC
                                    AT   CTGG_
GAM1665  FLJ12076  3'  CACATTGCCACATGACCCTT  48021          TTT  A
                                AAGGGTCGTGTG  GA GTG
                                ||||||||||||  || |||
                                TTCCCAGTACAC  TT CAC
                                      CG_  A
GAM1665  KIAA0750  5'  CACTGCCGCACACGACTCCTGA 28304    A        TTGA
                                TCA GGGTCGTGTGT   AGTG
                                ||| ||||||||||   ||||
                                AGT CTCAGCACACG   TCAC
                                  C        CCG_
GAM1665  KIAA1485  3'  TAGACACACACCCCCTGA   90771    A  TC
                                TCA GGG  GTGTGTTTG
                                ||| |||  |||||||||
                                AGT CCC  CACACAGAT
                                  C  CA
GAM1665  LOC145608 5'  CACCCCAAATTACTGACCCTTG 84374         T  _   AA
             A                   TCAAGGGTCG GTG TTTG  GTG
                                 |||||||||| ||| ||||  |||
                                 AGTTCCCAGT CAT AAAC  CAC
                                       _  T   CC
GAM1666  DKFZP566B183 3'  AGAATTTTGATAGGGGTAGATA 31941    G    C   T_
                                TAT TACCCC ATTA  GTTTT
                                ||| |||||| ||||  |||||
                                ATA ATGGGG TAGT  TAAGA
                                  G    A   TT
GAM1666  FLJ10300  5'  GAAAACATCTCTGGGCCATA  36471    TACC   TT_
                                TATG   CCCA   ATGTTTTC
                                ||||   ||||   ||||||||
                                ATAC   GGGT   TACAAAAG
                                  C___   CTC
GAM1666  FLJ20694  3'  GGATATAATGGGGGCATACA  35976     __
                                TGTA  CCCCCATTATGTTT
                                ||||  ||||||||||||||
                                ACAT  GGGGGTAATATAGG
                                  AC
GAM1666  KIAA1466  3'  AAAATAGGTAATGGGGATAC  72403    C      __
                                GTA CCCCATTAT  GTTTT
                                ||| |||||||||  |||||
                                CAT GGGGTAATG  TAAAA
                                  A       GA
GAM1666  MGC29937  3'  GAAGAACATGGGGGACATA   58731     A     TATG
                                TATGT CCCCCAT   TTTTC
                                ||||| |||||||   |||||
                                ATACA GGGGGTA   AGAAG
                                   _     CA__
GAM1667  SCAMP1   3'  GCTAAATAAATATTCTCC    54500    T    C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
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                                CCT TTATAA TAAATCG
                                  C     A
GAM1667  SCAMP1    3'  GCTAAATAAATATTCTCC    54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1667  NX-17     3'  TGAATATCAGCCCCTAATA    40706         ATA_
                                TATTAGGG    ATATTCA
                                ||||||||    |||||||
                                ATAATCCC    TATAAGT
                                     CGAC
GAM1667  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
                TA                TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM1668  CRAT      3'  GGCCACCCACCAGGGCTCAGCT 7479      GT__       AA
                                AGC    CCCTGGTG  TGGCC
                                |||    ||||||||  |||||
                                TCG    GGGACCAC  ACCGG
                                  ACTC       CC
GAM1668  CRAT      3'  GGCCACCCACCAGGGCTCAGCT 15675     GT__       AA
                                AGC    CCCTGGTG  TGGCC
                                |||    ||||||||  |||||
                                TCG    GGGACCAC  ACCGG
                                  ACTC       CC
GAM1668  MNAT1     3'  GCTGAACCAGGGAGCTAGCA   11661     C   G      GAAT
                                TGC AGC TCCCTGGT    GGC
                                ||| ||| ||||||||    |||
                                ACG TCG AGGGACCA    TCG
                                  A   _       AG__
GAM1668  PLXNB3    3'  GCCACTGAGGGGAGCTGGCA   19408       G    GGTGAA
                                TGCCAGC TCCCT     TGGC
                                ||||||| |||||     ||||
                                ACGGTCG AGGGG     ACCG
                                     _    AGTC__
GAM1668  ZNF217    3'  GCCATTCGGAAGCTGGCA    22544       G   CTGGT
                                TGCCAGC TCC    GAATGGC
                                ||||||| |||    |||||||
                                ACGGTCG AGG    CTTACCG
                                    A  _____
GAM1668  ATF3      3'  GCCACAAGGACGCTGGC     15732         C  GTGAA
                                GCCAGCGTCC TG    TGGC
                                |||||||||| ||    ||||
                                CGGTCGCAGG AC    ACCG
                                     A  _____
GAM1668  KIAA0295  3'  GGCTCCCCAGGGACACTGG   68668      C       T  ATG
                                CCAG GTCCCTGG GA   GCC
                                |||| |||||||| ||   |||
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                                GGTC CAGGGACC CT   CGG
                                  A       C ___
GAM1668 KIAA1184 3' GCCATTCCTAAGAACACTG   42930     C  CCC   T
                                CAG GT   TGG GAATGGC
                                ||| ||   ||| |||||||
                                GTC CA   ATC CTTACCG
                                  A  AGA   _
GAM1668 MGC22014 5' GCCTGTGCCCAGAGACGCTGGC 65113          C    TGAAT
             A                   TGCCAGCGTC CTGG     GGC
                                ||||||||||| ||||     |||
                                ACGGTCGCAG GACC     CCG
                                      A    CGTGT
GAM1668 LOC144501 3' GCTCCCCAGAGACCTGACA   84031    C   C   C    T  ATG
                                TG CAG GTC CTGG GA   GC
                                || ||| ||| |||| ||   ||
                                AC GTC CAG GACC CT   CG
                                 A   _   A    C ___
GAM1668 LOC147791 5' GGCGTAACCAGAGACGCTGG   85190        C    GAATG
                                CCAGCGTC CTGGT     GCC
                                |||||||| |||||     |||
                                GGTCGCAG GACCA     CGG
                                     A     ATG__
GAM1668 LOC152405 5' CCAGTCAGGGACGCGGCA    81454      A        TGAA
                                TGCC GCGTCCCTGG    TGG
                                |||| ||||||||||    |||
                                ACGG CGCAGGGACT    ACC
                                  _         G___
GAM1668 LOC153577 3' GCCTGCAGGACGCTGGCA    87241          CTGG  AAT
                                TGCCAGCGTCC    TG   GGC
                                ||||||||||    ||   |||
                                ACGGTCGCAGG    AC   CCG
                                      _____  GT_
GAM1668 LOC197196 3' CCATCAACGGATGCTGACA   91300    C       CTGG   A
                                TG CAGCGTCC    TGA TGG
                                || ||||||||    ||| |||
                                AC GTCGTAGG    ACT ACC
                                 A       CA__   _
GAM1668 LOC255043 5' GCCAGCATGGACGCTGGCA   97071          CTG   AA
                                TGCCAGCGTCC   GTG  TGGC
                                ||||||||||   |||  ||||
                                ACGGTCGCAGG   TAC  ACCG
                                      ___   G_
GAM1668 LOC255743 5' CCAATCAGGGACCCAGCA    97601     CAGC       GAA
                                TGC    GTCCCTGGT   TGG
                                |||    |||||||||   |||
                                ACG    CAGGGACTA   ACC
                                  ACC_        ___
GAM1669 CDH12    3' CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
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                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM1669  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA       G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC        G
GAM1669  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT   98090      T   AGAAG
                                ACCAC CCCA    AATAAG
                                ||||| ||||    ||||||
                                TGGTG GGGT    TTATTC
                                   _   GTCA_
GAM1669  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877      CACTCCCA
           A                     TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM1669  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126        CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM1669  HMP19     3'  CTTATTCTTTGTTAGGAAAATG 88860     CCAC   CAA_
           TA                    TACA   TCC   GAAGAATAAG
                                ||||   |||   ||||||||||
                                ATGT   AGG   TTTCTTATTC
                                  AAA_   ATTG
GAM1669  KIAA1579  3'  TACTCTTAGTGGTGTA     37154        CCCAAG   A
                                TACACCACT     AAGA TA
                                |||||||||     |||| ||
                                ATGTGGTGA     TTCT AT
                                     _______   C
GAM1669  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA  68742             _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                          G
GAM1669  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM1669  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748      CCA__
                                ACTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM1669  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
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                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM1669 OSBPL11  3' CTTAATTTCCCAAGAGTGGTG 43206       CCAA   AA
                                CACCACTC   GAAG  TAAG
                                ||||||||   ||||  ||||
                                GTGGTGAG   CTTT  ATTC
                                    AACC   A_
GAM1669 YME1L1   3' TCATTCTTGATGTGGTGTA   58438       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                    TA_    A
GAM1669 YME1L1   3' TCATTCTTGATGTGGTGTA   27323       TCC    _
                                TACACCAC   CAAGAA GA
                                ||||||||   ||||||  ||
                                ATGTGGTG   GTTCTT CT
                                    TA_    A
GAM1669 ZNF262   3' CTTATTTTGTTTGGGAGT    18723        A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                     G
GAM1669 LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_    AAGA
                                TACACCAC   CCAAG   ATA
                                ||||||||   |||||   |||
                                ATGTGGTG   GGTTC   TGT
                                    CAA    GG__
GAM1670 FACL4    3' TGATTCAAAAAGTCACAG    16748       CC   GAC
                                CTGTGACTTT  TGGA   TCA
                                ||||||||||  ||||   |||
                                GACACTGAAA  ACTT   AGT
                                     A_    ___
GAM1670 FACL4    3' TGATTCAAAAAGTCACAG    43680       CC   GAC
                                CTGTGACTTT  TGGA   TCA
                                ||||||||||  ||||   |||
                                GACACTGAAA  ACTT   AGT
                                     A_    ___
GAM1670 MYH11    3' TGGGGAGAAAGTCACCGA    43435   T      CTGGAGA
                                TC GTGACTTTC      CTCA
                                || |||||||||      ||||
                                AG CACTGAAAG      GGGT
                                 C        AG_____
GAM1670 MYH11    3' TGGGGAGAAAGTCACCGA    43450   T      CTGGAGA
                                TC GTGACTTTC      CTCA
                                || |||||||||      ||||
                                AG CACTGAAAG      GGGT
                                 C        AG_____
GAM1670 MYH11    3' TGGGGAGAAAGTCACCGA    11751   T      CTGGAGA
                                TC GTGACTTTC      CTCA
                                || |||||||||      ||||
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                                AG CACTGAAAG      GGGT
                                 C       AG_____
GAM1670  NRXN1    3'  TGAATTAGAAAGTCACA     17826         C   AGAC
                                TGTGACTTTC TGG    TCA
                                |||||||||| |||    |||
                                ACACTGAAAG ATT    AGT
                                      _   A___
GAM1670  NRXN1    3'  TGAATTAGAAAGTCACA     57830         C   AGAC
                                TGTGACTTTC TGG    TCA
                                |||||||||| |||    |||
                                ACACTGAAAG ATT    AGT
                                      _   A___
GAM1670  WHSC1    3'  AGCCTTACGGGAAAGTCCAGA  30576      T        _   A
                                TCTG GACTTTCCTG GAG CT
                                |||| |||||||||| ||| ||
                                AGAC CTGAAAGGGC TTC GA
                                  _         A   C
GAM1670  WHSC1    3'  AGCCTTACGGGAAAGTCCAGA  56663      T        _   A
                                TCTG GACTTTCCTG GAG CT
                                |||| |||||||||| ||| ||
                                AGAC CTGAAAGGGC TTC GA
                                  _         A   C
GAM1670  WHSC1    3'  AGCCTTACGGGAAAGTCCAGA  56674      T        _   A
                                TCTG GACTTTCCTG GAG CT
                                |||| |||||||||| ||| ||
                                AGAC CTGAAAGGGC TTC GA
                                  _         A   C
GAM1670  ZNF195   3'  AGTCTCCAGAGCACA       24098      A  TTC
                                TGTG CT   CTGGAGACT
                                |||| ||   |||||||||
                                ACAC GA   GACCTCTGA
                                  _ ___
GAM1670  CDT6     3'  AGTCTCCAAGGAGCACA      41248      ACT    _
                                TGTG   TTCCT GGAGACT
                                ||||   ||||| |||||||
                                ACAC   GAGGA CCTCTGA
                                  ___     A
GAM1670  DKFZp434O0320 3'  GTGAACCCAGCAAGTCACAGG  84701          TC    AGAC
                                TCTGTGACTT  CTGG    TCAC
                                |||||||||  ||||    ||||
                                GGACACTGAA  GACC    AGTG
                                      C_    CA__
GAM1670  EDG2     3'  GTATTCCAAAAAAGTCATAGA  9177           CC    _
                                TCTGTGACTTT  TGGAG AC
                                ||||||||||  ||||| ||
                                AGATACTGAAA  ACCTT TG
                                       AA     A
GAM1670  EDG2     3'  GTATTCCAAAAAAGTCATAGA  55133          CC    _
                                TCTGTGACTTT  TGGAG AC
                                ||||||||||  ||||| ||
```

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                                AGATACTGAAA  ACCTT TG
                                      AA    A
GAM1670  FLJ10483  5'  TGAATGTCATGGAAGTCACA  36657        C  AGAC
                                TGTGACTTTC TGG   TCA
                                |||||||||| |||   |||
                                ACACTGAAGG ACT   AGT
                                     T  GTA_
GAM1670  FLJ12529  3'  GTAGGCAGGTAAAGTCACA   46089        _  GAG
                                TGTGACTTT CCTG  AC
                                ||||||||| ||||  ||
                                ACACTGAAA GGAC  TG
                                     T   GGA
GAM1670  LHFPL2    3'  TTCCAGGAAAGCACAGA    70503      A
                                TCTGTG CTTTCCTGGAG
                                |||||| ||||||||||
                                AGACAC GAAAGGACCTT
                                  _
GAM1670  MGC10946  5'  GAGTCGAAAACTCACAGA   48313      C_  CTGGA
                                TCTGTGA  TTTC   GACTC
                                |||||||  ||||   |||||
                                AGACACT  AAAG   CTGAG
                                    CA  _____
GAM1670  SLC26A7   3'  TGAGTTAAGGAAAGTCA    54513        GGA
                                TGACTTTCCT  GACTCA
                                ||||||||||  ||||||
                                ACTGAAAGGA  TTGAGT
                                     A__
GAM1670  LOC144703 5'  TGAGTCTCAGAACCACAGA   84098     ACT  CTG
                                TCTGTG  TTC  GAGACTCA
                                ||||||  |||  ||||||||
                                AGACAC  AAG  CTCTGAGT
                                   C__  A__
GAM1670  LOC149153 3'  TGAGTGGGGACAAGTCACAGA 85530        _  GGAG
                                TCTGTGACTT TCCT   ACTCA
                                |||||||||| ||||   |||||
                                AGACACTGAA AGGG   TGAGT
                                     C   G___
GAM1670  LOC151489 3'  TGAGAAGAAAAGTCACAGG   86609        C  GGAGA
                                TCTGTGACTTT CT    CTCA
                                |||||||||| ||    ||||
                                GGACACTGAAA GA    GAGT
                                     A  A____
GAM1670  LOC158431 3'  GAAATTTCAGGAAAACCACA  88166     AC       AC
                                TGTG  TTTCCTGGAG  TC
                                ||||  ||||||||||  ||
                                ACAC  AAAGGACTTT  AG
                                  CA        AA
GAM1670  LOC221583 3'  GTGAATAGCAGAATGTCACAGA 93760       T  C  GAGAC
                                TCTGTGAC TTC TG    TCAC
                                |||||||| ||| ||    ||||
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                                AGACACTG AAG AC     AGTG
                                     T   _  GATA_
GAM1670  LOC253675 3'  TGACTCTCAGGAAAATCAGA   98574      TGAC      G   C
                                TCTG    TTTCCTG AGA TCA
                                ||||    ||||||| ||| |||
                                AGAC    AAAGGAC TCT AGT
                                  TA__      _   C
GAM1670  LOC254835 5'  GTGAGTCTCCAGGAAGTCACAG 98711          T
            A                    TCTGTGACTT CCTGGAGACTCAC
                                ||||||||||| ||||||||||||
                                AGACACTGAA GGACCTCTGAGTG
                                      _
GAM1671  AKAP2    3'  GGCTGGTGCAGCCTACATGGC  24229       AAA    C  GT
                                GCCATG   GCTGC AT  GCC
                                ||||||   ||||| ||  |||
                                CGGTAC   CGACG TG  CGG
                                    ATC    _  GT
GAM1671  DGCR2    3'  GGCACATGGAACTTCACGGGT  18904    G  A    A CTG
                                AC CC TGAA G   CCATGTGCC
                                || || |||| |   |||||||||
                                TG GG ACTT C   GGTACACGG
                                 _ C    _ AA_
GAM1671  PPP1R12B  3'  GCACTTGGCTTTCACAAGC   50389    CA_    GCT    T
                                GC   TGAAA   GCCA GTGC
                                ||   |||||   |||| ||||
                                CG   ACTTT   CGGT CACG
                                 AAC     ____    T
GAM1671  RABIF    3'  GGCACATGGCCCCTCACAT    12727     AA  CT
                                ATG  AG  GCCATGTGCC
                                |||  ||  ||||||||||
                                TAC  TC  CGGTACACGG
                                  AC  CC
GAM1671  SLC2A3   3'  GGCACATGACAACTTTGCCAGC 23642    CATG    C  C
                                GC    AAAG TG CATGTGCC
                                ||    |||| || ||||||||
                                CG    TTTC AC GTACACGG
                                 ACCG    A  A
GAM1671  TAF4     3'  GGCACATGACATAGAAATGGC  13515      GAAAGC  C
                                GCCAT     TG CATGTGCC
                                |||||     || ||||||||
                                CGGTA     AC GTACACGG
                                   AAGAT_  A
GAM1671  WHSC1    3'  CACAACCTTTCATGTCGT    56692     C       CTGCCA
                                ACG CATGAAAG     TGTG
                                ||| ||||||||     ||||
                                TGC GTACTTTC     ACAC
                                  T       CA_____
GAM1671  A4GALT   3'  CACATGGTGCCATAGC     34298    C   AAA  T
                                GC ATG   GC GCCATGTG
                                || |||   || ||||||||
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                                CG TAC   CG TGGTACAC
                                 A  ___ _
GAM1671  C20orf149 3'  GCACTCGCTAGCTTTCCTG   44426    T     _  CAT
                                CA GAAAGCT GC   GTGC
                                || ||||||| ||   ||||
                                GT CTTTCGA CG   CACG
                                 C      T  CT_
GAM1671  CDC14B   3'  ACGACAGCCCTCATCGGCGT   53996      _   AA   CCA
                                ACGCC ATGA  GCTG   TGT
                                ||||| ||||  ||||   |||
                                TGCGG TACT  CGAC   GCA
                                   C   CC   A__
GAM1671  CECR2    3'  GGCATCACACACAGCTTTCTGG 49435     T      CCAT__
              C                  GCCA GAAAGCTG     GTGCC
                                |||| ||||||||      |||||
                                CGGT CTTTCGAC     TACGG
                                  _       ACACAC
GAM1671  CNNM1    3'  GCATTAAAGCTTTCATAAGGT  40122     __       GCCAT
                                GCC  ATGAAAGCT    GTGC
                                |||  |||||||||    ||||
                                TGG  TACTTTCGA    TACG
                                  AA        AAT__
GAM1671  FLJ10052 3'  GGCACATGGATCCATGGC    36249       AAAGCTG
                                GCCATG      CCATGTGCC
                                ||||||      |||||||||
                                CGGTAC      GGTACACGG
                                   CTA____
GAM1671  FLJ12484 3'  GGCACATGGTGAGCCACAGC   43176    CA  AAA  _
                                GC  TG   GCT GCCATGTGCC
                                ||  ||   ||| ||||||||||
                                CG  AC   CGA TGGTACACGG
                                 AC  ___   G
GAM1671  FLJ20758 3'  CACATGGTGAGGTCCATGGC   36078       AAA   __
                                GCCATG   GCT  GCCATGTG
                                ||||||   |||  ||||||||
                                CGGTAC   TGG  TGGTACAC
                                   C__   AG
GAM1671  FLJ21596 3'  GCACACTGTGCTCATGGCGT   46116         AA  T  CA
                                ACGCCATGA  GC GC  TGTGC
                                |||||||||  || ||  |||||
                                TGCGGTACT  CG TG  ACACG
                                     __  _  TC
GAM1671  KIAA0551 3'  GGCACTTATCTTCATGGCGT   67381          _____  C
                                ACGCCATGAA    AG TGCC
                                ||||||||||    || ||||
                                TGCGGTACTT    TC ACGG
                                     CTAT  _
GAM1671  KIAA0907 3'  GGCACATTGGTCTCATAGC    30878    C    AAGCT   _
                                GC ATGA     GCCA TGTGCC
                                || ||||     |||| ||||||
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                                CG TACT    TGGT ACACGG
                                 A   C____   T
GAM1671  KIAA1940  3'  GCACACCCAGCTCCCATGGCGT 80785       AA    CCA
                                ACGCCATG  AGCTG   TGTGC
                                ||||||||  |||||   |||||
                                TGCGGTAC  TCGAC   ACACG
                                    CC    CC_
GAM1671  PANX1     5'  GGCGCCGCGCAGCTTTCCCGAC 60805    CCAT       CAT
           G                     CG   GAAAGCTGC   GTGCC
                                ||   |||||||||  |||||
                                GC   CTTTCGACG   CGCGG
                                 AGCC       CGC
GAM1671  LOC124045 3'  GGCACATGGGACAGCCATGGC  76541      AAA   __
                                GCCATG   GCTG  CCATGTGCC
                                ||||||   ||||  |||||||||
                                CGGTAC   CGAC  GGTACACGG
                                   ___   AG
GAM1671  LOC143902 3'  CACATGGCAGAGGATGGC    77119      GAAAG
                                GCCAT    CTGCCATGTG
                                |||||    ||||||||||
                                CGGTA    GACGGTACAC
                                  GGA__
GAM1671  LOC144195 3'  GGCACATGACAACTTTGCCAGC 60986    CATG   C  C
                                GC   AAAG TG CATGTGCC
                                ||   |||| || ||||||||
                                CG   TTTC AC GTACACGG
                                 ACCG   A  A
GAM1671  LOC150319 3'  GGCACACAGCATGCGTGGCGT  80476       AAA   CCA
                                ACGCCATG   GCTG   TGTGCC
                                ||||||||   ||||   ||||||
                                TGCGGTGC   CGAC   ACACGG
                                    GTA    ___
GAM1671  LOC154860 5'  GCACAAGGCGCCCATGGCGT   87504       AAA  T   A
                                ACGCCATG   GC GCC TGTGC
                                ||||||||   || ||| |||||
                                TGCGGTAC   CG CGG ACACG
                                    C__  _   A
GAM1671  LOC202347 3'  GCACACAGCAGCTCATGGC   91947       AA    CA
                                GCCATGA  GCTGC  TGTGC
                                |||||||  |||||  |||||
                                CGGTACT  CGACG  ACACG
                                   __    AC
GAM1672  SCAMP1    3'  GCTAAATAAATATTCTCC    54500     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1672  SCAMP1    3'  GCTAAATAAATATTCTCC    54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
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                                CCT TTATAA TAAATCG
                                  C     A
GAM1672 NX-17    3' TGAATATCAGCCCCTAATA   40706        ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM1672 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
             TA                   TATTAGGGATAATATTCATTTAGC
                                  ||||||||||||||||||||||||
                                  ATAATCCCTATTATAAGTAAATCG

GAM1673 TRPV1    3' GTAAATGAAGCCCAGGAAAACA 38702    CACA   AG
                                TGT   CTGG  GCTTCATTTAC
                                |||   ||||  ||||||||||
                                ACA   GACC  CGAAGTAAATG
                                  AAAG   __
GAM1673 TRPV1    3' GTAAATGAAGCCCAGGAAAACA 55683    CACA   AG
                                TGT   CTGG  GCTTCATTTAC
                                |||   ||||  ||||||||||
                                ACA   GACC  CGAAGTAAATG
                                  AAAG   __
GAM1673 TRPV1    3' GTAAATGAAGCCCAGGAAAACA 55718    CACA   AG
                                TGT   CTGG  GCTTCATTTAC
                                |||   ||||  ||||||||||
                                ACA   GACC  CGAAGTAAATG
                                  AAAG   __
GAM1673 TRPV1    3' GTAAATGAAGCCCAGGAAAACA 55749    CACA   AG
                                TGT   CTGG  GCTTCATTTAC
                                |||   ||||  ||||||||||
                                ACA   GACC  CGAAGTAAATG
                                  AAAG   __
GAM1673 BCMP1    3' AAATGAAGGGTCTATATGACA  49533     CAC   GG
                                TGTCA   TGGA  CTTCATTT
                                |||||   ||||  ||||||||
                                ACAGT   ATCT  GAAGTAAA
                                  AT_   GG
GAM1673 KIAA0767  3' GTAAATAATCATTGCCAGTGTG 61257         AGGCTTC_
             AC                   GTCACACTGG      ATTTAC
                                  ||||||||||      ||||||
                                  CAGTGTGACC      TAAATG
                                      GTTACTAA
GAM1673 MGC4189   3' TAAATGAGCACAGTGCACA   51202    CA    GAG   T
                                TGT  CACTG   GCT CATTTA
                                |||  |||||   ||| ||||||
                                ACA  GTGAC   CGA GTAAAT
                                  C_    A__   _
GAM1673 PRO1596   3' TAAATGAATGAATGTGGCA   49221       CTGGAGGC
                                TGTCACA      TTCATTTA
                                |||||||      ||||||||
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                                ACGGTGT       AAGTAAAT
                                    AAGT____
GAM1673  SLC38A4   3'  TAAATGAACTTTTCAAATGACA 36347       CAC      C
                                TGTCA   TGGAGG TTCATTTA
                                |||||   |||||| ||||||||
                                ACAGT   ACTTTT AAGTAAAT
                                   AA_     C
GAM1673  LOC115795 3'  TAAATGAAACTGTGACA     73954        CTGGA GC
                                TGTCACA    G  TTCATTTA
                                |||||||    |  ||||||||
                                ACAGTGT    C  AAGTAAAT
                                    _____ A_
GAM1673  LOC152765 3'  ATGAAGCCTCCAGGTAACA    81541     C  A
                                TGT AC CTGGAGGCTTCAT
                                ||| || ||||||||||||
                                ACA TG GACCTCCGAAGTA
                                  A  _
GAM1673  LOC157381 3'  TAAATGAAGATTGAGTGTGCAC 87735     _     G  GG
             A                   TGT CACACT GA  CTTCATTTA
                                ||| |||||| ||  |||||||||
                                ACA GTGTGA TT  GAAGTAAAT
                                  C     G  A_
GAM1673  LOC200916 3'  TAAATGAAGTATACATGAGA   90373    A  C  GAG
                                TC CA TG   GCTTCATTTA
                                || || ||   ||||||||||
                                AG GT AC   TGAAGTAAAT
                                 A  _  ATA
GAM1673  LOC255177 3'  GGGCCCCACAGTGTGACA    98398          GA_
                                TGTCACACTG   GGCTT
                                ||||||||||   |||||
                                ACAGTGTGAC   CCGGG
                                      ACC
GAM1673  LOC90591  3'  GTAAATGAAGGGAATGTGA    64181       CTGGAGG
                                TCACA      CTTCATTTAC
                                |||||      ||||||||||
                                AGTGT      GAAGTAAATG
                                   AAGG___
GAM1674  DNAH9     5'  GTCTGCCATGGTTTTACA     9093     C      GCG     _
                                TG AAAACCA   TGGCGG C
                                || |||||||   |||||| |
                                AC TTTTGGT   ACCGTC G
                                 A      ___      T
GAM1674  DNASE1    5'  CGCCGCGCACGGCGCTGGTGCT 19071      AA       G________  GGCC
             GCA                   TGCA  ACCAGCGT       GC    G
                                ||||  ||||||||       ||   |
                                ACGT  TGGTCGCG       CG    C
                                  CG       GCAC___G  CCGG
GAM1674  DSCAM     5'  GGCCGCTGGCTGCGCA      9134      AAAAC    G
                                TGC     CAGC TGGCGGCC
                                |||     |||| ||||||||
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                                ACG    GTCG GTCGCCGG
                                  C____   _
GAM1674 HNF3A    5' CGCGGCCGCCCGTCGCTTCGCA 60458    AAAACCA  T
                                TGC     GCG GGCGGCCGCG
                                |||     ||| ||||||||||
                                ACG     TGC CCGCCGGCGC
                                  CTTCGC_  _
GAM1674 JUND     3' CGCGGCCGCCCCGTGTTGCA  19295     AACCA  T
                                TGCAA    GCG GGCGGCCGCG
                                |||||    ||| ||||||||||
                                ACGTT    TGC CCGCCGGCGC
                                   G____  C
GAM1674 PMM2     3' CGCAGCCTAGGCAGGCTCTGCA 72559    AAA  A  G  GC   C
                                TGCA   CC GC TG  GGC GCG
                                ||||   || || ||  ||| |||
                                ACGT   GG CG AT  CCG CGC
                                   CTC  A  G  __  A
GAM1674 ABIN-2   5' GCAGCTGCCGCGCTCTGCA   44459    AAACC        C
                                TGCA    AGCGTGGCGGC GC
                                ||||    |||||||||||  ||
                                ACGT    TCGCGCCGTCG CG
                                  C____         A
GAM1674 FLJ13052 3' GCGGCCTCCAGCTGCCGCA   43754    AAAAC   G   C
                                TGC    CAGC TGG GGCCGC
                                |||    |||| ||| ||||||
                                ACG    GTCG ACC CCGGCG
                                  CC___   _  T
GAM1674 FLJ14124 3' CGCGGCCGCGCCGGGCCTCGC  46355   AAAA_  A  GTG
                                GC    CC GC   GCGGCCGCG
                                ||    || ||   |||||||||
                                CG    GG CG   CGCCGGCGC
                                 CTCCG  C  ___
GAM1674 FLJ20255 5' CGCGGCAGCCGCCGTCCTTGCA 35300     AACCA  _   G
                                TGCAA    GCG TGGC GCCGCG
                                |||||    ||| |||| ||||||
                                ACGTT    TGC GCCG CGGCGC
                                   CC___   C   A
GAM1674 KIAA0211 5' CGCGGCCGAGACTCTGGCCTGC 28284     AAA   C  GG
            A                    TGCA   CCAG GT  CGGCCGCG
                                ||||   |||| ||  ||||||||
                                ACGT   GGTC CA  GCCGGCGC
                                  CC_   T  GA
GAM1674 KIAA0227 5' CGGCCGCCACGAAGCCTGCG   61347     AAACCAG
                                TGCA     CGTGGCGGCCG
                                ||||     ||||||||||
                                GCGT     GCACCGCCGGC
                                  CCGAA__
GAM1674 MAPK13   5' CGCAGCCGCCACGCCGGGGCCG 12318    AAAA  A       C
            C                    GC   CC GCGTGGCGGC GCG
                                ||   || |||||||||| |||
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                                CG    GG CGCACCGCCG CGC
                                 CCGG  C         A
GAM1674  OSBPL5    3'  CGCGGCGGCTGCAGGCCCTGCA 73062      AAA  AGC TG  G
                                TGCA   CC   G  GC GCCGCG
                                ||||   ||   |  || ||||||
                                ACGT   GG   C  CG CGGCGC
                                  CCC  A__ GT  G
GAM1674  PNMA1     5'  CGCAGCCGCCGCGACTTCGGCA 21219     AAAACCAG        C
                                TGC       CGTGGCGGC GCG
                                |||       ||||||||| |||
                                ACG       GCGCCGCCG CGC
                                  GCTTCA__        A
GAM1674  PSIP1     5'  CGCGGCCGCCCCCGCGCCGCCGC 41243     AAAACCA   T
              A                  TGC       GCG GGCGGCCGCG
                                |||       ||| ||||||||||
                                ACG       CGC CCGCCGGCGC
                                  CCGCCG_   C
GAM1674  SPRY4     3'  CGCTGTGGCCACGCTGGTT    49010           G  C
                                AACCAGCGTGGC GC GCG
                                |||||||||||| || |||
                                TTGGTCGCACCG TG CGC
                                       G  T
GAM1674  LOC148697 3'  GCCACGCTGTGTCTTGCA     79676       A  _
                                TGCAA AC CAGCGTGGC
                                ||||| || |||||||||
                                ACGTT TG GTCGCACCG
                                   C  T
GAM1674  LOC245806 5'  CGCGGAGCGCGCTGGCTTTGC  93541       A       G GG
                                GCAAA CCAGCGTG C  CCGCG
                                ||||| |||||||| |  |||||
                                CGTTT GGTCGCGC G  GGCGC
                                   C       _ A_
GAM1675  APBA1     3'  AAGAATCCACAAGGACCT     70472     C        _
                                AGG CTTTGTGGAT CTT
                                ||| |||||||||| |||
                                TCC GGAACACCTA GAA
                                  A         A
GAM1675  IGF1R     3'  GGACATGAAATTTACAAAGGGC 7908       _        C     _
              C                  GGCC TTTGTGGAT TTCATG CC
                                |||| ||||||||| |||||| ||
                                CCGG AAACATTTA AAGTAC GG
                                  G        _     A
GAM1675  NOS1      3'  GGGCACCAAGACCCCAAAGGCC 7097          T  A    CA
                                GGCCTTTG GG TCTT  TGCCC
                                |||||||| || ||||  |||||
                                CCGGAAAC CC AGAA  ACGGG
                                     _ C    CC
GAM1675  PMX1      5'  GGCACAGCACAAAGGCTT     23569           GAT  TCA
                                AGGCCTTTGTG   CT   TGCC
                                ||||||||||   ||   ||||
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                                TTCGGAAACAC   GA   ACGG
                                      ___  C__
GAM1675  RAB7L1    3'  GCATTTTCTTCCACAAAGAGCT 15407     _       TCTTC
                                GGC CTTTGTGGA     ATGC
                                ||| |||||||||     ||||
                                TCG GAAACACCT     TACG
                                  A        TCTTT
GAM1675  TEAD3     3'  GCAGGGGCCCTCAAAGGCC    13671        T  AT   CA
                                GGCCTTTG GG  CTT  TGC
                                |||||||| ||  |||  |||
                                CCGGAAAC CC  GGG  ACG
                                     T  CG   __
GAM1675  TRAF1     3'  GGGCACAAAGATGGGTGAAGGC 20177       TG GG     CA
               T                 GGCCTT  T  ATCTT  TGCCC
                                ||||||  |  |||||  |||||
                                TCGGAA  G  TAGAA  ACGGG
                                   GT GG     AC
GAM1675  WISP2     5'  CATAAAGACTCACAGGTC     15277      TT   GA    C
                                GGCCT  GTG  TCTT ATG
                                |||||  |||  |||| |||
                                CTGGA  CAC  AGAA TAC
                                  __  TC    A
GAM1675  CAP350    3'  GGGCATGAAAACAAAGAAATGC 29707     _____     GGATC
               C                 GGC    CTTTGT     TTCATGCCC
                                |||    ||||||     |||||||||
                                CCG    GAAACA     AAGTACGGG
                                  TAAA     A_____
GAM1675  CGRP-RCP  5'  GGACATCCGCAAAGACCT     27893     C         C
                                AGG CTTTGTGGAT TTC
                                ||| |||||||||| |||
                                TCC GAAACGCCTA AGG
                                  A         C
GAM1675  DGS-A     3'  GGGCACGAAGGGAGAGAGGCCT 86054         GTGGA     A
                                AGGCCTTT     TCTTC TGCCC
                                ||||||||     ||||| |||||
                                TCCGGAGA     GGAAG ACGGG
                                     GAG__     C
GAM1675  DKFZp586H0623 3'  GCATATCCCACAAGAGGCC    34501         _    ATCTTC
                                GGCCTTT GTGG      ATGC
                                ||||||| ||||      ||||
                                CCGGAGA CACC      TACG
                                   A    CTA___
GAM1675  H2AV      3'  GGGCATAGTTTCACAAAAGCTT 25760      C       T  TC
                                AGGC TTTGTGGA CT  ATGCCC
                                |||| |||||||| ||  ||||||
                                TTCG AAACACTT GA  TACGGG
                                  A       T  __
GAM1675  KCNH8     3'  GGGCATGAAGACTGAGCAAAGC 58908     C     GGA_
               T                 GGC TTTGT    TCTTCATGCCC
                                ||| |||||    ||||||||||
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                                TCG AAACG   AGAAGTACGGG
                                  _    AGTC
GAM1675 KIAA0258 3' GGGCATGAAAACAAGAGGTCT 29472       G GATC
                                AGGCCTTT TG   TTCATGCCC
                                |||||||| ||   |||||||||
                                TCTGGAGA AC   AAGTACGGG
                                    _ AA__
GAM1675 KIAA1937 5' GGCATGAAAATTCAGACCT   74072    C TTGT   C
                                AGG CT   GGAT TTCATGCC
                                ||| ||   |||| ||||||||
                                TCC GA   CTTA AAGTACGG
                                  A ____   A
GAM1675 PRO1777  3' GCACAAGCTTACAAAGTCCT  38373    C      AT  CA
                                AGG CTTTGTGG  CTT  TGC
                                ||| ||||||||  |||  |||
                                TCC GAAACATT  GAA  ACG
                                  T      C_  C_
GAM1675 PRO1843  5' CATGAAGAGGGCAAACCCT   38140    CC   GGA
                                AGG  TTTGT   TCTTCATG
                                |||  |||||   ||||||||
                                TCC  AAACG   AGAAGTAC
                                  C_    GG_
GAM1675 LOC149319 5' GGGCATGGCCTGCACAAAGGTC 80075         GATCT
            T                    AGGCCTTTGTG    TCATGCCC
                                ||||||||||    ||||||||
                                TCTGGAAACAC    GGTACGGG
                                      GTCC_
GAM1675 LOC197319 3' GGACATAAAAATTTTTGCAAGG 89323       T TG  TCTTC__  _
            CCT                   AGGCCTT G  GA      ATG CC
                                ||||||| |  ||      ||| ||
                                TCCGGAA C  TT      TAC GG
                                   _ GT  TTAAAAA   A
GAM1675 LOC253792 3' GGCCGACCCACAAAGAGCC   99025    _      A  TTCAT
                                GGC CTTTGTGG TC    GCC
                                ||| |||||||| ||    |||
                                CCG GAAACACC AG    CGG
                                  A       C  C____
GAM1675 LOC54466 5' GGCATGAAGACCCCCAACGC  39176   CT  T  A
                                GC  TTG GG TCTTCATGCC
                                ||  ||| || ||||||||||
                                CG  AAC CC AGAAGTACGG
                                  C_  C  C
GAM1675 LOC55901 5' GGACATGAGGAGACTAAAGACC 38543    C    TGGA      _
            T                    AGG CTTTG   TCTTCATG CC
                                ||| |||||   |||||||| ||
                                TCC GAAAT   AGGAGTAC GG
                                  A    CAG_      A
GAM1675 LOC56270 3' CATGAAGAAAAACGACCT   39503    CCT   GGA
                                AGG   TTGT   TCTTCATG
                                |||   ||||   ||||||||
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                                TCC  AGCA  AGAAGTAC
                                  ___   AAA
GAM1675 LOC91812 5' GGGCACATTTACACAAGGCC  67819      _    CTTCA
                                GGCCTT TGTGGAT   TGCCC
                                |||||| |||||||    |||||
                                CCGGAA ACATTTA   ACGGG
                                   C     C____
GAM1675 LOC91813 5' GGGCACATTTACACAAGGCC  67845      _    CTTCA
                                GGCCTT TGTGGAT   TGCCC
                                |||||| |||||||    |||||
                                CCGGAA ACATTTA   ACGGG
                                   C     C____
GAM1676 GALNT2   3' CCGCACACACAGATGCTCAGT  16814       C  _  AA
                                ACTGAGCA CTG GTG  TGG
                                |||||||| ||| |||  |||
                                TGACTCGT GAC CAC  GCC
                                     A  A  AC
GAM1676 NCSTN    3' CGCCCACAGTGCTCAGT    74135       CTG  AAT  C
                                ACTGAGCAC  GTG  GGC G
                                |||||||||  |||  ||| |
                                TGACTCGTG  CAC  CCG C
                                     A__  ___  A
GAM1676 PPP1R11  3' CCGGCAGCCCAGATGTTCAGT  41986       C   TGAATG
                                ACTGAGCA CTGG    GCCGG
                                |||||||| ||||    |||||
                                TGACTTGT GACC    CGGCC
                                     A   CGA___
GAM1676 GP5      3' CCTTCCCTCCAGGTGCCCAGT  16873     A     T__  T
                                ACTG GCACCTGG  GAA GG
                                |||| ||||||||  ||| ||
                                TGAC CGTGGACC  CTT CC
                                  C      TCC  _
GAM1676 HRH3     3' CCGGCCACTCTGTTTGCTCA  24316      CCTGGT  A
                                TGAGCA    GA TGGCCGG
                                ||||||    || |||||||
                                ACTCGT    CT ACCGGCC
                                   TTGT__  C
GAM1676 KIAA0574 3' CCAGCCACCCAGTGGACTCGGT 69809      __  CT   AA
                                ACTGAG  CAC  GGTG  TGG
                                ||||||  |||  ||||  |||
                                TGGCTC  GTG  CCAC  ACC
                                   AG   AC   CG
GAM1676 LOC145622 5' CCATCACCCAGGTGCTCAGT  77807          _  A
                                ACTGAGCACCTGG TGA TGG
                                |||||||||||| ||| |||
                                TGACTCGTGGACC ACT ACC
                                       C  _
GAM1676 LOC145622 5' CCATCAGCCAGGTGCTCAG   77808          GA
                                CTGAGCACCTGGT  ATGG
                                ||||||||||||  ||||
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                                GACTCGTGGACCG  TACC
                                      AC
GAM1676  LOC145622 5'  CCATCAGCCAGGTGCTCAG   77809          GA
                                CTGAGCACCTGGT  ATGG
                                ||||||||||||  ||||
                                GACTCGTGGACCG  TACC
                                      AC
GAM1676  LOC145622 5'  CCATCAGCCAGGTGCTCAG   77810          GA
                                CTGAGCACCTGGT  ATGG
                                ||||||||||||  ||||
                                GACTCGTGGACCG  TACC
                                      AC
GAM1676  LOC145622 5'  CCATCATCCAGGTGCTCAG   77811          _  A
                                CTGAGCACCTGG TGA TGG
                                ||||||||||| ||| |||
                                GACTCGTGGACC ACT ACC
                                      T  _
GAM1676  LOC145622 5'  TGTACGTCAGCCAGGTGCTCAG 77827          GA  GC
                                CTGAGCACCTGGT  ATG  CG
                                ||||||||||||  |||  ||
                                GACTCGTGGACCG  TGC  GT
                                      AC  AT
GAM1676  LOC145622 5'  TGTCTGTCAGCCAGGTGCTCAG 77828          GA   C
                                CTGAGCACCTGGT  ATGG CG
                                ||||||||||||  |||| ||
                                GACTCGTGGACCG  TGTC GT
                                      AC   T
GAM1676  LOC154995 5'  CGGCCTCCAGGTGCTCA    82104         TGAAT
                                TGAGCACCTGG    GGCCG
                                ||||||||||    |||||
                                ACTCGTGGACC    CCGGC
                                      T____
GAM1676  LOC155036 5'  CCAGCTGGCCAAGTGTTCAG  87611       C   GAA   C
                                CTGAGCAC TGGT  TGGC GG
                                |||||||| ||||  |||| ||
                                GACTTGTG ACCG  GTCG CC
                                     A   ___   A
GAM1676  LOC203248 3'  CCAGCCATTCATCGACAGTCAG 90842     G ACC        C
                                CTGA C  TGGTGAATGGC GG
                                |||| |  ||||||||||| ||
                                GACT G  GCTACTTACCG CC
                                  _ ACA         A
GAM1676  LOC221362 3'  CCAAAAGACACCAATGCTCAGT 95398       CC    AA___
                                ACTGAGCA  TGGTG    TGG
                                ||||||||  |||||    |||
                                TGACTCGT  ACCAC    ACC
                                     A_    AGAAA
GAM1676  LOC57821  5'  CCGGCCATCTCTGTGATCCCAG 41301    AG__  CT  T  A
                                CTG   CAC  GG GA TGGCCGG
                                |||   |||  || || |||||||
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                                GAC   GTG  TC CT ACCGGCC
                                  CCTA  __  T  _
GAM1677  BAI2     5'  GACATGCCTCACAGCTGATCA  9913     C   ACCA
                                TGA CGGC   AGGCATGTC
                                ||| ||||   |||||||||
                                ACT GTCG   TCCGTACAG
                                  A   ACAC
GAM1677  DDX10    3'  GACATGCTTTGTGCCATCA   16569    CC    C
                                TGA  GGCAC AAGGCATGTC
                                |||  ||||| ||||||||||
                                ACT  CCGTG TTTCGTACAG
                                  A_    _
GAM1677  FANCC    3'  ACATGCTTCGTGCCATCA    71028    CC    CA
                                TGA  GGCAC  AGGCATGT
                                |||  |||||  ||||||||
                                ACT  CCGTG  TTCGTACA
                                  A_    C_
GAM1677  HOXD4    5'  GCAGCCGGCGCTGGTCA     28261       A  AA   A
                                TGACCGGC CC  GGC TGT
                                |||||||| ||  ||| |||
                                ACTGGTCG GG  CCG ACG
                                     C  __  _
GAM1677  C1orf34  3'  ACATGTCTGGCACCTGTCA   61291     C  CA   A
                                TGAC GG  CCA GGCATGT
                                |||| ||  ||| |||||||
                                ACTG CC  GGT CTGTACA
                                  T  AC  _
GAM1677  C3orf4   5'  GTGTTTGGTGCGGTCA      39595       G      G
                                TGACCG CACCAAG CAT
                                |||||| ||||||| |||
                                ACTGGC GTGGTTT GTG

                                  _      _
GAM1677  ELF2     3'  ACATGCCTGTGTCACTCA    23448    CC    CA
                                TGA  GGCAC  AGGCATGT
                                |||  |||||  ||||||||
                                ACT  CTGTG  TCCGTACA
                                  CA    __
GAM1677  FLJ10895 3'  ACATGCCTTGGGAATGTTA   39358     CGGCA
                                TGAC    CCAAGGCATGT
                                ||||    ||||||||||
                                ATTG    GGTTCCGTACA
                                  TAAG_
GAM1677  FLJ14457 3'  GACATGCCTTGGCCTATAGTC  52406    C___  AC
                                GAC   GGC  CAAGGCATGTC
                                |||   |||  ||||||||||
                                CTG   CCG  GTTCCGTACAG
                                  ATAT  __
GAM1677  FLJ22301 3'  ATCCCCTGGAGCCGGTCA    46176       A  A  C
                                TGACCGGC CCA GG AT
                                |||||||| ||| || ||
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                                ACTGGCCG GGT CC TA
                                     A   C  C
GAM1677  FLJ22938  5'  GACATGCCTTCAGTCAGCC   45485    __ C_
                                GGC  AC  AAGGCATGTC
                                |||  ||  ||||||||||
                                CCG  TG  TTCCGTACAG
                                  AC  AC
GAM1677  FLJ23186  5'  ACACGCCTCTCAATGGTGCCG  61038       _____   A
                                CGGCACCA    AGGC TGT
                                ||||||||    |||| |||
                                GCCGTGGT    TCCG ACA
                                     AACTC   C
GAM1677  KIAA0429  5'  GATATTTCGGTGCCAGGCA   29242   A _    AA  C
                                TG CC GGCACC  GG ATGTC
                                || || ||||||  || |||||
                                AC GG CCGTGG  CT TATAG
                                 _ A     __ T
GAM1677  KIAA1271  3'  GACATGCCTTGGCTGAACC   70138   __ _
                                GG  CA CCAAGGCATGTC
                                ||  || ||||||||||||
                                CC  GT GGTTCCGTACAG
                                 AA  C
GAM1677  MADHIP    3'  GACAGCGCCTTGGTGCCGGT   24642          A_
                                ACCGGCACCAAGGC  TGTC
                                ||||||||||||||  ||||
                                TGGCCGTGGTTCCG  ACAG
                                      CG
GAM1677  MGC15631  3'  GACGTGCCCTGGTGACAGCC   52231    ____   A
                                GGC    ACCA GGCATGTC
                                |||    |||| ||||||||
                                CCG    TGGT CCGTGCAG
                                  ACAG    C
GAM1677  PASK      5'  GAGGTGGTCGATGCTGGTCA   31414       CCAA  _  G
                                TGACCGGCA    GGC AT TC
                                |||||||||    ||| || ||
                                ACTGGTCGT    CTG TG AG
                                     AG__    G  G
GAM1677  SSH3BP1   3'  ATGCTGGTGCTGGTCA      19615          AG
                                TGACCGGCACCA  GCAT
                                ||||||||||||  ||||
                                ACTGGTCGTGGT  CGTA
                                          __
GAM1677  TRAF4     3'  GACATGCCTTGGTGCCGGTCA  63319
                                TGACCGGCACCAAGGCATGTC
                                ||||||||||||||||||||
                                ACTGGCCGTGGTTCCGTACAG

GAM1677  LOC132573 5'  GACGTGCCTGGTGCCGGCCG   75573    A       A
                                TG CCGGCACCA GGCATGTC
                                || |||||||| ||||||||
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                                GC GGCCGTGGT CCGTGCAG
                                 C       _
GAM1677  LOC145824 5'  GACATGCCCCTTGAGGCTCA   77985   C   AC   __
                                C GGC  CAA  GGCATGTC
                                | |||  |||  ||||||||
                                A TCG  GTT  CCGTACAG
                                 C   GA   CC
GAM1677  LOC201304 3'  ACATACCCTGCTGGTCA     89602         CCAA  C
                                TGACCGGCA    GG ATGT
                                |||||||||    || ||||
                                ACTGGTCGT    CC TACA
                                      C___  A
GAM1677  LOC221288 3'  ACATGCCTTTGTTGAGT     95252    _    CC
                                AC CGGCA  AAGGCATGT
                                || |||||  |||||||||
                                TG GTTGT  TTCCGTACA
                                 A    __
GAM1678  HAL      5'  GCCACTCCTGCATAAAGCTC   10903          TGAAAA
                                GAGCTTTATGC     GGTGGC
                                ||||||||||      ||||||
                                CTCGAAATACG     TCACCG
                                      TCC___
GAM1678  HMGN2    3'  GGCCACCTTGGCACAAAAGC   19809      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                   _ _  GG
GAM1678  NMI      5'  GGCCACCTCCTCAGGAAG    17436     ATG   AA
                                CTTT   CTGA  AGGTGGCC
                                ||||   ||||  ||||||||
                                GAAG   GACT  TCCACCGG
                                   ___    CC
GAM1678  PACE     3'  GGCCACCTCTCCAAGGGCTT   11944       A  CT  AAA
                                GAGCTTT TG  GA   GGTGGCC
                                ||||||| ||  ||   |||||||
                                TTCGGGA AC  CT   CCACCGG
                                    _ CT  ___
GAM1678  PYCR1    3'  CCACCTTCCTCTAGAGCTC   70639       TGCT  A_
                                GAGCTTTA    GA  AAGGTGG
                                ||||||||    ||  |||||||
                                CTCGAGAT    CT  TTCCACC
                                      _____  CC
GAM1678  SDC1     3'  GGCCACCTCCCCAGCATTCCAG 12991     TT_     AAA
              C                  GCT   ATGCTG   AGGTGGCC
                                 |||   ||||||   ||||||||
                                 CGA   TACGAC   TCCACCGG
                                   CCT     CCC
GAM1678  FLJ11560 5'  GCCCAGGCCCAGCATAAAG   48008          AAAA   ___
                                CTTTATGCTG    GGT   GGC
                                ||||||||||    |||   |||
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                                GAAATACGAC   CCG  CCG
                                     ____  GAC
GAM1678 KIAA0446 5' CCACCTTTTGAAGAGCTC   69446      ATGCTG
                                GAGCTTT    AAAAGGTGG
                                |||||||    |||||||||
                                CTCGAGA    TTTTCCACC
                                   AG____
GAM1678 KIAA0971 3' GTTGTTCTCAGCATAAAGT  30677        AAA  TG
                                GCTTTATGCTGA  GG  GC
                                ||||||||||||  ||  ||
                                TGAAATACGACT  TT  TG
                                      C__  GT
GAM1678 KIAA1393 3' GGCCACCTTGGCACAAAAGC  72574     A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                  _ _  GG
GAM1678 KIAA1656 3' GGCCACCTCCTCCTAGAAGCC  66377   A    ATGCT  AA
                                G GCTTT    GA  AGGTGGCC
                                | |||||    ||  ||||||||
                                C CGAAG    CT  TCCACCGG
                                 _    ATC__  CC
GAM1678 KIAA1884 3' GCCACCTTCATCTACCAAGGCT 73728      ATGCT  A_
            C                    GAGCTTT    GA  AAGGTGGC
                                |||||||    ||  ||||||||
                                CTCGGAA    CT  TTCCACCG
                                   CCAT_  AC
GAM1678 PP3501   3' GGCCACCGTTGACAGCATAAAG 41683       AAAA_
                                CTTTATGCTG    GGTGGCC
                                ||||||||||    |||||||
                                GAAATACGAC    CCACCGG
                                     AGTTG
GAM1678 SDCCAG3  3' GGTGTTCTCAGCATGAAGCTC  22803         AAA  TG
                                GAGCTTTATGCTGA  GG  GCC
                                ||||||||||||||  ||  |||
                                CTCGAAGTACGACT  CT  TGG
                                      ____  TG
GAM1678 SP140    3' GGCCACCTCCATGCAGAAGC  24327     A  TGAAA
                                GCTTT TGC    AGGTGGCC
                                ||||| |||    ||||||||
                                CGAAG ACG    TCCACCGG
                                  _  TACC_
GAM1678 LOC148760 3' GGCCACCTTCTCCAACAAGCTC 85364      TA  CT  A
                                GAGCTT  TG  GA AAGGTGGCC
                                ||||||  ||  || |||||||||
                                CTCGAA  AC  CT TTCCACCGG
                                   CA  __  C
GAM1678 LOC150170 5' ACCTGTTTCACATAAAGC    80414       C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
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                                CGAAATAC ACTTT TCCA
                                    _    G
GAM1678  LOC150175 5'  ACCTGTTTCACATAAAGC    80453        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                    _    G
GAM1678  LOC150215 5'  ACCTGTTTCACATAAAGC    80456        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                    _    G
GAM1678  LOC150218 5'  ACCTGTTTCACATAAAGC    80525        C    _
                                GCTTTATG TGAAA AGGT
                                |||||||| ||||| ||||
                                CGAAATAC ACTTT TCCA
                                    _    G
GAM1678  LOC152065 3'  GGCCACCTTCTCCTTGGCAGGC 86737      TTA   ___  A
             TC                   GAGCT   TGCT   GA AAGGTGGCC
                                |||||   ||||   || |||||||||
                                CTCGG   ACGG   CT TTCCACCGG
                                   ___    TTC  C
GAM1678  LOC152267 3'  GGCCACCTTGGCACAAAAGC   61036      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                   _ _  GG
GAM1678  LOC158292 5'  CCTCTGGACCCAGCATAAGGCT 88046           AAAA_  T
             C                    GAGCTTTATGCTG     GG GG
                                ||||||||||||     || ||
                                CTCGGAATACGAC     TC CC
                                       CCAGG  T
GAM1678  LOC219997 3'  GCCACCTCTTCAGCCTC     93256     CTTTAT     A
                                GAG     GCTGAA AGGTGGC
                                |||     |||||| |||||||
                                CTC     CGACTT TCCACCG
                                  _______     C
GAM1678  LOC256269 3'  GGCCACCTTGGCACAAAAGC   96608      A  C  AA
                                GCTTT TG TG  AAGGTGGCC
                                ||||| || ||  |||||||||
                                CGAAA AC AC  TTCCACCGG
                                   _ _  GG
GAM1678  LOC91963  5'  GGCCACCTCCTCTGAGAAGC   68321      ATGCT  AA
                                GCTTT    GA  AGGTGGCC
                                |||||    ||  ||||||||
                                CGAAG    CT  TCCACCGG
                                   AGT__  CC
GAM1679  ABCC3     3'  TCTTTGACCACGTCATCGGGCC 39622          CCACAG
             A                    TGGCCTGATGAT     CGGAGA
                                ||||||||||||     ||||||
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                                ACCGGGCTACTG     GTTTCT
                                      CACCA_
GAM1679 ADAMTS3  3' TCTCTATAGATCGTCAGCTCA 27272    GC       CACAGC
                                TG  CTGATGATC     GGAGA
                                ||  |||||||||     |||||
                                AC  GACTGCTAG     TCTCT
                                 TC        ATA___
GAM1679 AIM1     3' TTTTTGAGACAGGATCTCAGGC 93474        T    ACAG_
             T                   GGCCTGA GATCC     CGGAGA
                                |||||||| |||||     ||||||
                                TCGGACT CTAGG     GTTTTT
                                    _     ACAGA
GAM1679 ALOX5AP  3' TCTCTGCTGAATATGGGGTT  9679       G   ATCCA
                                GGCCT ATG     CAGCGGAGA
                                ||||| |||     |||||||||
                                TTGGG TAT     GTCGTCTCT
                                   G   AA___
GAM1679 ANXA5    5' TTTCCGTTGCTTGGATCAGTC  8570      CTGA     __
                                GGC    TGATCCA  CAGCGGAGA
                                |||    |||||||  |||||||||
                                CTG    ACTAGGT  GTTGCCTTT
                                 _____      TC
GAM1679 ARHGEF12 3' TCTCTGCTGTCCAGTAGGCT  31648       A  ATCC
                                GGCCTG TG    ACAGCGGAGA
                                |||||| ||    ||||||||||
                                TCGGAT AC    TGTCGTCTCT
                                   G  C___
GAM1679 ASGR1    3' TTCTGCAGTTTGCAGGTTA   9806        ATGATCC  A
                                TGGCCTG      AC GCGGAG
                                |||||||      || ||||||
                                ATTGGAC      TG CGTCTT
                                    GTT____  A
GAM1679 CACNA1C  3' TCTGGGGATGGGCGTCGGGCC  7403         A   CAG_
                                GGCCTGATG TCCA    CGGA
                                ||||||||| ||||    ||||
                                CCGGGCTGC GGGT    GTCT
                                     _    AGGG
GAM1679 CD2AP    3' TTTCCAGCAGATTTCAGGCT   25082       T   CACA _
                                GGCCTGA GATC    GC GGAGA
                                ||||||| ||||    || |||||
                                TCGGACT TTAG    CG CCTTT
                                    _    A___  A
GAM1679 CELSR2   3' TCTTTGCTGTGATGTGGGT   9200       ATGATC
                                GCCTG     CACAGCGGAGA
                                |||||     ||||||||||
                                TGGGT     GTGTCGTTTCT
                                   GTA___
GAM1679 CNTFR    3' TCTCTGTTGCCACCATCAG   10240       ATCCA
                                CTGATG    CAGCGGAGA
                                ||||||    |||||||||
```

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                                GACTAC    GTTGTCTCT
                                   CACC_
GAM1679 CRH     3' TTTTTGTTGTGGTCTGAGCCA 7484      CTGAT  T
                                TGGC    GA CCACAGCGGAGA
                                ||||    || ||||||||||||
                                ACCG    CT GGTGTTGTTTTT
                                  AGT__ _
GAM1679 CYBB    3' TTCCAGATCATTAGGACA    76855    G       CACAGC
                                TG CCTGATGATC     GGAG
                                || ||||||||||     ||||
                                AC GGATTACTAG     CCTT
                                 A        A_____
GAM1679 DMRT2   3' CTTTGCTTCTTGTAGGCTA   22652       AT_  TCCAC
                                TGGCCTG   GA    AGCGGAG
                                |||||||   ||    |||||||
                                ATCGGAT   CT    TCGTTTC
                                    GTT  _____
GAM1679 DNCI1   3' TCTCTGCTGCTGTTGAGGTTA 92712      GA   CCA
                                TGGCCT  TGAT   CAGCGGAGA
                                ||||||  ||||   |||||||||
                                ATTGGA  GTTG   GTCGTCTCT
                                   __    TC_
GAM1679 DNMT3B  3' TTTTTGCTAATTTTTAGGCT   23551       T   CCAC
                                GGCCTGA GAT    AGCGGAGA
                                |||||||  |||    ||||||||
                                TCGGATT TTA    TCGTTTTT
                                    T   A___
GAM1679 DYRK1A  5' TTCTGCTGATTATCAG      56085        CAC
                                CTGATGATC   AGCGGAG
                                |||||||||   |||||||
                                GACTATTAG   TCGTCTT
                                     ___
GAM1679 FBXW7   3' TCTCCAGTGGTCATTGGGC   37591    TG    T   AGC
                                GCC  ATGA CCAC   GGAGA
                                |||  |||| ||||   |||||
                                CGG  TACT GGTG   CCTCT
                                  GT    _    A__
GAM1679 GALNT1  3' TTTTTGTTTGGTTTGTGGGCT  40403      G TG T   C
                                GGCCT A  A CCA AGCGGAGA
                                ||||| |  | ||| ||||||||
                                TCGGG T  T GGT TTGTTTTT
                                  _ GT T   _
GAM1679 HDAC4   3' TCTCTGACCACATCGTCAGG   21253        CCACAG
                                CCTGATGAT     CGGAGA
                                |||||||||     ||||||
                                GGACTGCTA     GTCTCT
                                     CACCA_
GAM1679 IL1RL2  3' TTTCTGCTGCAGGATGAGGCTA 60163       GATG   A_
                                TGGCCT    ATCC  CAGCGGAGA
                                ||||||    ||||  |||||||||
```

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                                ATCGGA   TAGG  GTCGTCTTT
                                   G___   AC
GAM1679 ITK     3'  TTTTTGCTCAAACCATCAGG   19887       ATCCAC
                                CCTGATG     AGCGGAGA
                                |||||||     ||||||||
                                GGACTAC     TCGTTTTT
                                    CAAAC_
GAM1679 KDR     3'  TCTCTGAATGATTATTAGCCA  11200     C      CACAG
                                TGGC TGATGATC    CGGAGA
                                |||| ||||||||    ||||||
                                ACCG ATTATTAG    GTCTCT
                                  _      TAA__
GAM1679 MAOA    3'  AAAGGCTGTGTCATTGGGCCA  5906      TG   TC    GGAGA
                                TGGCC  ATGA  CACAGC
                                |||||  ||||  ||||||
                                ACCGG  TACT  GTGTCG
                                   GT   __     GAAAT
GAM1679 MMP14   3'  TCTTCGTTGCTCAGTCAGTCA  18432     C   GATCCA
                                TGGC TGAT     CAGCGGAGA
                                |||| ||||     |||||||||
                                ACTG ACTG     GTTGCTTCT
                                  _   ACTC__
GAM1679 MPP2    3'  TCTTCGCTGCAGCGTCAGCCA  60523     C    ATCCA
                                TGGC TGATG    CAGCGGAGA
                                |||| |||||    |||||||||
                                ACCG ACTGC    GTCGCTTCT
                                  _    GAC__
GAM1679 MX1     3'  TCTCTGCTTATCCGTTAGCC   11723     C    ATCCAC
                                GGC TGATG     AGCGGAGA
                                ||| |||||     ||||||||
                                CCG ATTGC     TCGTCTCT
                                  _    CTAT__
GAM1679 MYB     3'  TTTTTGTTGTGGTACAACAG   60285     A  AT
                                CTG TG  CCACAGCGGAGA
                                ||| ||  ||||||||||||
                                GAC AC  GGTGTTGTTTTT
                                  A  AT
GAM1679 NT5C3   3'  TTTTTGTAATTTGGGTTATTAT 33662     C        CA__
            GCT                   GGC TGATGATCCA    GCGGAGA
                                ||| ||||||||||    |||||||
                                TCG ATTATTGGGT    TGTTTTT
                                  T         TTAA
GAM1679 OGDH    3'  TCTTTGCTGTGCCAAAGCAGGT 92753        ATGATC
            CA                  TGGCCTG     CACAGCGGAGA
                                |||||||     ||||||||||||
                                ACTGGAC     GTGTCGTTTCT
                                    GAAACC
GAM1679 OSR1    3'  TCTCTGTTGCTTCTATTGGCC  18839     TGAT  TCCA
                                GGCC   GA   CAGCGGAGA
                                ||||   ||   |||||||||
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                              CCGG   CT   GTTGTCTCT
                                TTAT  TC__
GAM1679 PCDH1    5' TTGTGCTTGTGAATTATTGGGT 51581      TG    C   _  G A
            TA                   TGGCC  ATGAT CACA GCG AG
                              ||||||  ||||| |||| ||| ||
                              ATTGG  TATTA GTGT CGT TT
                                 GT    A   T   G
GAM1679 PML      3' CTTTGGTCCTCAGGCCA     53803        T T  C
                              TGGCCTGA GA CCA AG
                              |||||||| || ||| ||
                              ACCGGACT CT GGT TC
                                   C  _  T
GAM1679 POLR2H   3' TCTCTGCCAAGTCACTCAGGTC 21722        _   CCACA
            A                    TGGCCTGA TGAT    GCGGAGA
                              |||||||| ||||    |||||||
                              ACTGGACT ACTG    CGTCTCT
                                   C   AAC__
GAM1679 POLS     3' TCTAAGTTGGGTCATCGTGTC  23782    C       CA  GG
                              GGC TGATGATCCA  GC  AGA
                              ||| ||||||||||  ||  |||
                              CTG GCTACTGGGT  TG  TCT
                                T        __ AA
GAM1679 PPP2R5C  3' TTTCCACGTGATTGTTACGCCA 12251     C   TG   C  AGC
                              TGGC TGA  ATC AC   GGAGA
                              |||| |||  ||| ||   |||||
                              ACCG ATT  TAG TG   CCTTT
                                C   GT   _  CA_
GAM1679 PRNP     3' TTTCTGCAATGTTATTATTGGC 6133      T     C_  CA
            T                    GGCC GATGAT  CA  GCGGAGA
                              |||| ||||||  ||  |||||||
                              TCGG TTATTA  GT  CGTCTTT
                                _     TT  AA
GAM1679 RAD21    3' TTTTTGTTGCTTATCGGGTT   21838         TCCA
                              GGCCTGATGA    CAGCGGAGA
                              ||||||||||    |||||||||
                              TTGGGCTATT    GTTGTTTTT
                                   C___
GAM1679 RAD51L1  3' TCTCTGCTAAAACATTTGGTT  56880     T   ATCCAC
                              GGCC GATG     AGCGGAGA
                              |||| ||||     ||||||||
                              TTGG TTAC     TCGTCTCT
                                T   AAAA__
GAM1679 RENT1    3' TTTCTGCGGGGCATCAGGCT   12820        AT  ACA
                              GGCCTGATG  CC   GCGGAGA
                              |||||||||  ||   |||||||
                              TCGGACTAC  GG   CGTCTTT
                                   GG  ___
GAM1679 RLN2     3' TCTTTGTTAGATATTAGGTC   18584        A  CAC
                              GGCCTGATG TC   AGCGGAGA
                              |||||||| ||   ||||||||
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                                CTGGATTAT AG   TTGTTTCT
                                     _ A__
GAM1679 RLN2     3' TCTTTGTTAGATATTAGGTC  18585        A  CAC
                                GGCCTGATG TC   AGCGGAGA
                                ||||||||| ||   ||||||||
                                CTGGATTAT AG   TTGTTTCT
                                     _ A__
GAM1679 S100B    3' TTCTGCTATATTAGGCC     21853         ATCCAC
                                GGCCTGATG     AGCGGAG
                                |||||||||     |||||||
                                CCGGATTAT     TCGTCTT
                                     A_____
GAM1679 SCN1A    3' TTTCTGTTGAGAAATAGGCTA 90269       ATGA  CA
                                TGGCCTG    TC  CAGCGGAGA
                                |||||||    ||  |||||||||
                                ATCGGAT    AG  GTTGTCTTT
                                    AA__  A_
GAM1679 SLC7A1   5' TCTTTGCTGCAAGATCGAGGCT 13199      GA    CA_
                                GGCCT  TGATC   CAGCGGAGA
                                |||||  |||||   |||||||||
                                TCGGA  GCTAG   GTCGTTTCT
                                   __    AAC
GAM1679 SORCS2   3' TCTCTGCTGTTTGGGTTGGGTT 40808      GAT    __
                                GGCCT   GATCC  ACAGCGGAGA
                                |||||   |||||  ||||||||||
                                TTGGG   TTGGG  TGTCGTCTCT
                                   ___    TT
GAM1679 SQSTM1   3' TTTCTGCTGGAAGCTGTCAGGC 15332        GATCCA
             T                   GGCCTGAT     CAGCGGAGA
                                 ||||||||     |||||||||
                                 TCGGACTG     GTCGTCTTT
                                     TCGAAG
GAM1679 TCP10    3' CTTTGTTGTTTGCAGGCCA   17237       ATGATCC
                                TGGCCTG      ACAGCGGAG
                                |||||||      |||||||||
                                ACCGGAC      TGTTGTTTC
                                    GTT____
GAM1679 TFG      5' TCTCGCTAGGCTTGTTGGGTCA 21382      TG TG T  AC   G
                                TGGCC  A  A CC  AGCG AGA
                                |||||  |  | ||  |||| |||
                                ACTGG  T  T GG  TCGC TCT
                                   GT GT C  A_   _
GAM1679 TMEPAI   3' TCTCCGTGAAGTCGTCAGCC  39830     C      CCACA
                                GGC TGATGAT    GCGGAGA
                                ||| |||||||    |||||||
                                CCG ACTGCTG    TGCCTCT
                                  _      AAG__
GAM1679 TRPM8    3' TCTCCAGTTGATCATTGGG   44209    TG     C  AGC
                                CC  ATGATC AC   GGAGA
                                ||  |||||| ||   |||||
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                                GG  TACTAG TG   CCTCT
                                 GT     T  A__
GAM1679  UNG      3'  TTTTTGCTGTTAGTCGGGTTA  56027         GATCC
                                TGGCCTGAT    ACAGCGGAGA
                                |||||||||    ||||||||||
                                ATTGGGCTG    TGTCGTTTTT
                                     AT___
GAM1679  VCP      3'  TTTCTGTTGTAGTTTGGGGC   75892     GAT   CC
                                GCCT   GAT  ACAGCGGAGA
                                ||||   |||  ||||||||||
                                CGGG   TTG  TGTTGTCTTT
                                  GT_   A_
GAM1679  ZNF261   3'  CTCTGCCATCTTAGGTT     18731        T   CCACA
                                GGCCTGA GAT    GCGGAG
                                |||||||  |||    ||||||
                                TTGGATT CTA    CGTCTC
                                    _   C____
GAM1679  ZNF265   3'  TCTTTGCTGCGTTTATGTAGGT 19578       _    TCCA
              T                  GGCCTG ATGA    CAGCGGAGA
                                 ||||||  ||||   |||||||||
                                 TTGGAT TATT    GTCGTTTCT
                                    G    TGC_
GAM1679  ZNF74    5'  TCTCGAGGATATATCGGGTT   14266         _    ACAGCG
                                GGCCTGATG ATCC     GAGA
                                |||||||||  ||||     ||||
                                TTGGGCTAT TAGG     CTCT
                                     A    AG____
GAM1679  ABCC13   3'  TTTTTGTTTAGATCATCAGGT  57813          CAC
                                GCCTGATGATC   AGCGGAGA
                                ||||||||||   ||||||||
                                TGGACTACTAG   TTGTTTTT
                                      AT_
GAM1679  AFAP     3'  TTTTGCTGCCTTCGGGTCA   41614        TGATCCA
                                TGGCCTGA      CAGCGGAG
                                ||||||||      ||||||||
                                ACTGGGCT      GTCGTTTT
                                     TCC____
GAM1679  AMOT     3'  TTTTTGTTGTTACACTGTTGGG 56551     TG  GATCC_
              T                  GCC  AT     ACAGCGGAGA
                                 |||  ||     ||||||||||
                                 TGG  TG     TGTTGTTTTT
                                   GT  TCACAT
GAM1679  BRD3     3'  TTTTGCTTTCATAGGTCA    24776        A   TCCAC
                                TGGCCTG TGA    AGCGGAG
                                |||||||  |||    |||||||
                                ACTGGAT ACT    TCGTTTT
                                    _   T____
GAM1679  C20orf3  3'  CTTCGTTGTGGTGGGG      68640     G TGAT
                                CCT A    CCACAGCGGAG
                                |||  |    ||||||||||
```

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                                GGG T    GGTGTTGCTTC
                                  G _____
GAM1679  C20orf46  5'  TTCTGCTTATGTTAGGGTA   37737    G     GATCCAC
                                TG CCTGAT      AGCGGAG
                                || ||||||      |||||||
                                AT GGATTG      TCGTCTT
                                 G     TAT_____
GAM1679  C5orf6    3'  CTCTGCTGTAGATTGGCT    33950      TGAT    C
                                GGCC    GATC ACAGCGGAG
                                ||||    |||| |||||||||
                                TCGG    TTAG TGTCGTCTC
                                  _____    A
GAM1679  C6.1A     3'  CTTCAGGATCTTGGGCTA    44531       TG T     ACAGC
                                TGGCC  A GATCC     GGAG
                                |||||  | |||||     ||||
                                ATCGG  T CTAGG     CTTC
                                   GT _     A_____
GAM1679  C6orf33   3'  TTTCTGTTCTGGGTTATTGGG  56724     TG       C
                                CC  ATGATCCA AGCGGAGA
                                ||  |||||||| ||||||||
                                GG  TATTGGGT TTGTCTTT
                                 GT       C
GAM1679  CKAP4     3'  TCTCTGCTTCTGCATTTGGTT  23348      T    ATCCAC
                                GGCC GATG      AGCGGAGA
                                |||| ||||      ||||||||
                                TTGG TTAC      TCGTCTCT
                                  T    GTCT__
GAM1679  CNOT7     3'  TCTCAGTTGGTTGTTAGGTT   26256        TG  CCA    G
                                GGCCTGA  AT   CAGC GAGA
                                |||||||  ||   |||| ||||
                                TTGGATT  TG   GTTG CTCT
                                    GT  ___    A
GAM1679  CSR1      3'  TTTCTGCTGGCCAGGTGGGCCA 33187        A_  ATCCA
                                TGGCCTG  TG     CAGCGGAGA
                                |||||||  ||     |||||||||
                                ACCGGGT  AC     GTCGTCTTT
                                    GG  CG___
GAM1679  DGKD      3'  CTCTCGAGTCATCAGGCTA    60104           CCACAG  _
                                TGGCCTGATGAT      CG GAG
                                ||||||||||||      || |||
                                ATCGGACTACTG      GC CTC
                                       A_____  T
GAM1679  DKFZP566G1424 3'  TCTTAGTGGTGGATCATCAGGT 85946              A  G
                                GCCTGATGATCCAC GC GAGA
                                |||||||||||||| || ||||
                                TGGACTACTAGGTG TG TTCT
                                         G  A
GAM1679  DKFZP586I2223 3'  TCTCTGTTTAAGTATCAGCTA  55775      C     ATCCAC
                                TGGC TGATG      AGCGGAGA
                                |||| |||||      ||||||||
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                                ATCG ACTAT     TTGTCTCT
                                  _    GAAT__
GAM1679  DKFZP586I2223 3'  TCTCTGTTTAAGTATCAGCTA  31881      C    ATCCAC
                                TGGC TGATG     AGCGGAGA
                                |||| |||||     ||||||||
                                ATCG ACTAT     TTGTCTCT
                                  _    GAAT__
GAM1679  DOK4     3'  TTTTTGTTGTTTTTTGGGTT   36667      TG T  TCC
                                GGCC  A GA   ACAGCGGAGA
                                ||||  | ||   ||||||||||
                                TTGG  T TT   TGTTGTTTTT
                                  GT T  ___
GAM1679  DRCTNNB1A 5'  TCTCCCGGCTGGGTTGTCAGTC 51811      C   TG T  A   __
           A                     TGGC TGA  A CC CAGC  GGAGA
                                |||| |||  | || ||||  |||||
                                ACTG ACT  T GG GTCG  CCTCT
                                  _  GT _  _   GC
GAM1679  EIF3S1   3'  CTTTGTTCTCTTAGGCT     63868        T  TCCAC
                                GGCCTGA GA    AGCGGAG
                                |||||||  ||    |||||||
                                TCGGATT CT    TTGTTTC
                                   _ C_____
GAM1679  FBXO30   3'  TTTTGTTATTGTTATGCCA    50492      C   TG  CCAC
                                TGGC TGA  AT    AGCGGAG
                                |||| |||  ||    |||||||
                                ACCG ATT  TA    TTGTTTT
                                  T  GT  _____
GAM1679  FKBP9    3'  TCTCCGTTTGTCGCCAGGCT   95724       A    CCAC
                                GGCCTG TGAT    AGCGGAGA
                                ||||||| ||||    ||||||||
                                TCGGAC GCTG    TTGCCTCT
                                   C    T___
GAM1679  FLJ00001  3'  TCTTTGCTCCTTGTCAGAGTT  82717     _    TG TCCAC
                                GGC CTGA  A    AGCGGAGA
                                ||| ||||  |    ||||||||
                                TTG GACT  T    TCGTTTCT
                                  A   GT CC___
GAM1679  FLJ10058  3'  TTTTTGTTGTCTGTGTTGAGTC 36269      CT    ATCC
           A                     TGGC  GATG    ACAGCGGAGA
                                ||||  ||||    ||||||||||
                                ACTG  TTGT    TGTTGTTTTT
                                  AG    GTC_
GAM1679  FLJ10379  3'  TCTTTGTTGACACAGTAGGGCT 36569       GA_  ATCCA
                                GGCCT   TG    CAGCGGAGA
                                |||||   ||    |||||||||
                                TCGGG   AC    GTTGTTTCT
                                  ATG  ACA__
GAM1679  FLJ10546  3'  TTTTTGTTGTTGTTGTTGGGCT 60187      TG TG  CC
                                GGCC  A  AT  ACAGCGGAGA
                                ||||  |  ||  ||||||||||
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                              TCGG  T  TG  TGTTGTTTTT
                                GT GT  T_
GAM1679  FLJ10925  5'  TTCTGCTGGTGTTGCGCT    37415    C   GATCCA
                              GGC TGAT     CAGCGGAG
                              ||| ||||     ||||||||
                              TCG GTTG     GTCGTCTT
                                C   TG____
GAM1679  FLJ11117  3'  CTCTGCTGCATGGGGCTA    37634      G  ATCCA
                              TGGCCT ATG    CAGCGGAG
                              |||||| |||    ||||||||
                              ATCGGG TAC    GTCGTCTC
                                 G  _____
GAM1679  FLJ11273  3'  TTTTTGTCACTTATTTCAGGTT 37778       TGATCCACA
           A                   TGGCCTGA       GCGGAGA
                              ||||||||       |||||||
                              ATTGGACT       TGTTTTT
                                   TTATTCAC_
GAM1679  FLJ13081  3'  TTTTTATGGGATCATCAG    46173         A  GC
                              CTGATGATCC CA  GGAGA
                              |||||||||| ||  |||||
                              GACTACTAGG GT  TTTTT
                                    _  A_
GAM1679  FLJ13154  3'  TCGGCTGTTGTGGGTTGCAGGT 45112       A         A_
           T                   GGCCTG TGATCCACAGCGG  GA
                              |||||| ||||||||||||  ||
                              TTGGAC GTTGGGTGTTGTC  CT
                                 _          GG  C
GAM1679  FLJ13197  3'  CTTCGATATCATTAGCT     45178     C     CCACAG
                              GGC TGATGAT     CGGAG
                              ||| |||||||     |||||
                              TCG ATTACTA     GCTTC
                                _      TA____
GAM1679  FLJ13204  3'  TCTGCCCCTGTGATTGGGCCA  45760      TG  GATC    C  _
                              TGGCC  AT    CACAG GG AGA
                              |||||  ||    ||||| || |||
                              ACCGG  TA    GTGTC CC TCT
                                 GT  _____    C  G
GAM1679  FLJ14855  3'  TTTTCGTTGGCTGGCAGGTT   53767      ATGAT  __
                              GGCCTG    CCA  CAGCGGAGA
                              ||||||    |||  |||||||||
                              TTGGAC    GGT  GTTGCTTTT
                                 _____  CG
GAM1679  FLJ20392  5'  TTTCTGCTGTGGCCTTAG    35578     TGAT
                              CTGA    CCACAGCGGAGA
                              ||||    ||||||||||||
                              GATT    GGTGTCGTCTTT
                                CC__
GAM1679  FLJ20699  3'  TCTCTGTTGTCTCATTGTGTT  35991     C     TCC
                              GGC TGATGA   ACAGCGGAGA
                              ||| ||||||   ||||||||||
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                                TTG GTTACT   TGTTGTCTCT
                                  T     C__
GAM1679  FLJ32865  3'  CTCCGTGTTGGTCAGGCT    58807       TGAT   CA
                                GGCCTGA    CCA  GCGGAG
                                |||||||    |||  ||||||
                                TCGGACT    GGT  TGCCTC
                                   _____   TG
GAM1679  G4        5'  TCTCTGCTGCGTGTTCGCGGGC 92642        A   TCCA_
            CA                    TGGCCTG TGA     CAGCGGAGA
                                |||||||  |||     |||||||||
                                ACCGGGC GCT     GTCGTCTCT
                                   _   TGTGC
GAM1679  gm117     3'  TGATATTGTGGGTTATTATGCC 79591      C           CGGAGA
            A                     TGGC TGATGATCCACAG
                                ||||  ||||||||||||
                                ACCG ATTATTGGGTGTT
                                  T           ATAGTT
GAM1679  HBOA      3'  TTTTTGATCTGTATTGGGCTA  23934      TG  GATCC   __
                                TGGCC  AT    ACAG  CGGAGA
                                |||||  ||    ||||  ||||||
                                ATCGG  TA    TGTC  GTTTTT
                                   GT  _____    TA
GAM1679  HCA4      3'  TTTTTGCTACATATTAAGGTCA 57747       GA    CCAC
                                TGGCCT  TGAT    AGCGGAGA
                                ||||||  ||||    ||||||||
                                ACTGGA  ATTA    TCGTTTTT
                                   __    TACA
GAM1679  HEI10     5'  CTCCGTTTTGGTGGGCT     41296       ATGAT   C
                                GGCCTG     CCA AGCGGAG
                                ||||||     ||| |||||||
                                TCGGGT     GGT TTGCCTC
                                   _____   T
GAM1679  HSPC195   5'  TCTCTGTTGTGGGCAGCAGGGC 81869       GA_  A
            CA                    TGGCCT   TG TCCACAGCGGAGA
                                ||||||   || ||||||||||||
                                ACCGGG   AC GGGTGTTGTCTCT
                                   ACG  _
GAM1679  ICK       3'  TTTCTTAGTAGGTCATTGGTT  33693      T      C  AGC
                                GGCC GATGATC AC   GGAGA
                                ||||  |||||| ||   |||||
                                TTGG TTACTGG TG   TCTTT
                                   _      A  AT_
GAM1679  KIAA0152  3'  TTTTCGCTGTGACTTGGGTC   28985      TG TGATC
                                GGCC  A    CACAGCGGAGA
                                ||||  |    ||||||||||
                                CTGG  T    GTGTCGCTTTT
                                  GT CA___
GAM1679  KIAA0205  3'  TCTCTGGAGCAGTCATTGGTT  30219      T     CCACAG
                                GGCC GATGAT     CGGAGA
                                ||||  ||||||     ||||||
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                              TTGG TTACTG     GTCTCT
                                _     ACGAG_
GAM1679 KIAA0349 3' TCTCTGTGGTCTGTTGGGTCA 93919      TG   AT     C
                              TGGCC  ATG  CCACAG GGA
                              |||||  |||  ||||||| |||
                              ACTGG  TGT  GGTGTC TCT
                                 GT   CT     _
GAM1679 KIAA0446 3' TCTTTGGAGGGGTTATTAGGTT 69462           ACAG
                              GGCCTGATGATCC    CGGAGA
                              ||||||||||||||   ||||||
                              TTGGATTATTGGG    GTTTCT
                                     GAG_
GAM1679 KIAA0449 3' TTTCTGCTGTTTCTGATGGGTC 34642       AT_  TCC
             A                 TGGCCTG   GA   ACAGCGGAGA
                              |||||||   ||   ||||||||||
                              ACTGGGT   CT   TGTCGTCTTT
                                  AGT  T__
GAM1679 KIAA0475 3' TTTTTGTTGTAAGTCAGG    30133       GATCC
                              CCTGAT    ACAGCGGAGA
                              ||||||    ||||||||||
                              GGACTG    TGTTGTTTTT
                                 AA___
GAM1679 KIAA0819 3' TTTCCGTTCTGTTTTGGGCCA  64339      TG TGATC  C
                              TGGCC  A    CA AGCGGAGA
                              |||||  |    || ||||||||
                              ACCGG  T    GT TTGCCTTT
                                 GT TT___  C
GAM1679 KIAA1007 3' TCTCTGTTGTACGTGTCAGTCT 95224     C     ATCC
             A                 TGG CTGATG    ACAGCGGAGA
                              |||  ||||||    ||||||||||
                              ATC GACTGT    TGTTGTCTCT
                                T     GCA_
GAM1679 KIAA1014 3' TTTCTGTTGTATCACAATCAGG 65962       GATCC_
             T                 GCCTGAT     ACAGCGGAGA
                              |||||||     ||||||||||
                              TGGACTA     TGTTGTCTTT
                                  ACACTA
GAM1679 KIAA1026 3' TTTTTGTTTGGTTCGTCGGTT  71747     T    T   C
                              GGCC GATGA CCA AGCGGAGA
                              |||| ||||| ||| ||||||||
                              TTGG CTGCT GGT TTGTTTTT
                                _     T   _
GAM1679 KIAA1054 3' TCTTTGCTGTGGGACTGGCC   68972     TGATGA
                              GGCC     TCCACAGCGGAGA
                              ||||     ||||||||||||||
                              CCGG     GGGTGTCGTTTCT
                                TCA___
GAM1679 KIAA1084 3' TTTTGAAATCTGGTTGTCAGGC 30506        TG   CACAG_    A
             CA                  TGGCCTGA  ATC     CGGAG
                              ||||||||  |||     |||||
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                              ACCGGACT  TGG     GTTTT
                                  GT   TCTAAA
GAM1679  KIAA1196  3'  TCTCTGGCTTCATCCTTGGGCC 62155      TG T   CCAC  _
            A                  TGGCC  A GAT    AGC GGAGA
                               ||||||  | |||   ||| |||||
                               ACCGG  T CTA    TCG TCTCT
                                  GT C   CT__   G
GAM1679  KIAA1209  3'  TTTTCGTTGTTTTCAGGT    61412       TGATCC
                               GCCTGA     ACAGCGGAGA
                               ||||||     ||||||||||
                               TGGACT     TGTTGCTTTT
                                  TT____
GAM1679  KIAA1363  3'  TTTTTGTTGTGTTTTTGGTTA  69793      TGAT  TC
                               TGGCC    GA  CACAGCGGAGA
                               |||||    ||  ||||||||||
                               ATTGG    TT  GTGTTGTTTTT
                                  T___  TT
GAM1679  KIAA1416  3'  TTTTTGCTGTGAAGGTCAAGCT 87759     C    GATC
                               GGC TGAT    CACAGCGGAGA
                               ||| ||||    ||||||||||
                               TCG ACTG    GTGTCGTTTTT
                                 A   GAA_
GAM1679  KIAA1430  3'  TCTTTGTTGCCACATGTCAGG  81651       GATCCA
                               CCTGAT     CAGCGGAGA
                               ||||||     |||||||||
                               GGACTG     GTTGTTTCT
                                  TACACC
GAM1679  KIAA1557  3'  TTTCTGCTGTGTCCTTAGG    61788      T  TC
                               CCTGA GA  CACAGCGGAGA
                               ||||| ||  ||||||||||
                               GGATT CT  GTGTCGTCTTT
                                  C  __
GAM1679  KIAA1673  3'  TTTTCGTATTGCCATCGGGTT  71333        ATC  CA
                               GGCCTGATG   CA  GCGGAGA
                               |||||||||   ||  |||||||
                               TTGGGCTAC   GT  TGCTTTT
                                    C__  TA
GAM1679  KIAA1712  3'  CTCCGTGTTGGTCAGGCT    68156       TGAT   CA
                               GGCCTGA    CCA  GCGGAG
                               |||||||    |||  ||||||
                               TCGGACT    GGT  TGCCTC
                                    ____   TG
GAM1679  KIAA1789  5'  CTTTGAAATGATTAGGTCA   67701         G  CCACAG
                               TGGCCTGAT AT     CGGAG
                               ||||||||| ||     |||||
                               ACTGGATTA TA     GTTTC
                                    G  AA____
GAM1679  KIAA1821  3'  TTTGGCCTGGGTGTTAGGTCA  72277         G    CA  G
                               TGGCCTGAT ATCCA  GC GAG
                               ||||||||| |||||  || |||
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                                ACTGGATTG TGGGT  CG TTT
                                      _    C_  G
GAM1679 KIAA1910 3' TCTCTGCTGCTTTTGTTGGTGC 73717    _ TG TG TCCA
            T                    GGC C  A  A   CAGCGGAGA
                                 ||| |  | |   |||||||||
                                 TCG G  T  T   GTCGTCTCT
                                   T GT GT TTC_
GAM1679 KIAA1949 5' TCTTTGTGCCGAGATTGTCAGT 99594   C   TG   CACA_
            CT                   GG CTGA  ATC    GCGGAGA
                                 || ||||  |||    |||||||
                                 TC GACT  TAG    TGTTTCT
                                  T   GT   AGCCG
GAM1679 KIF13B   3' TTTCTAGGAAGGTCTTTGGGTC 31575     TG T   CACAGC
            A                    TGGCC  A GATC     GGAGA
                                 |||||  | ||||     |||||
                                 ACTGG  T CTGG     TCTTT
                                    GT T   AAGGA_
GAM1679 KIF13B   3' TTTCTAGGAAGGTCTTTGGGTC 31576     TG T   CACAGC
            A                    TGGCC  A GATC     GGAGA
                                 |||||  | ||||     |||||
                                 ACTGG  T CTGG     TCTTT
                                    GT T   AAGGA_
GAM1679 LEC3     3' TTTTTAATGGGATTTTTAGGTC 31535       T    A  GC
            A                    TGGCCTGA GATCC CA  GGAGA
                                 |||||||| ||||| ||  |||||
                                 ACTGGATT TTAGG GT  TTTTT
                                       T    _ AA
GAM1679 MESDC2   3' TTCTGTTGTACTCAGGGCA   72927   G    TGATCC
                                 TG CCTGA     ACAGCGGAG
                                 || |||||     |||||||||
                                 AC GGACT     TGTTGTCTT
                                  G    CA____
GAM1679 MGC20253 3' TCTCTGTTGTGGTGGGCATAGG 58678     A  AT__
            T                    GCCTG TG   CCACAGCGGAGA
                                 ||||| ||   ||||||||||||
                                 TGGAT AC   GGTGTTGTCTCT
                                    _ GGGT
GAM1679 MGC2217  3' TCTTCATCTGGTCTTGGGTCA  44431     TG T  T   CAGC
                                 TGGCC  A GA CCA   GGAGA
                                 |||||  | || |||   |||||
                                 ACTGG  T CT GGT   CTTCT
                                    GT _  _   CTA_
GAM1679 NDST4    5' TTTTGCTGTACTCGGTC     42920     T  TGATCC
                                 GGCC GA     ACAGCGGAG
                                 |||| ||     |||||||||
                                 CTGG CT     TGTCGTTTT
                                    _ CA____
GAM1679 NLI-IF   3' TCTCTGCTGCCAAATTGGGCC  41346     TG  GATCCA
                                 GGCC  AT     CAGCGGAGA
                                 ||||  ||     |||||||||
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                                CCGG  TA     GTCGTCTCT
                                  GT  AACC__
GAM1679  OLIG1    3'  TTTCCGCTGTTCCTCAGCGGGC 97338       A   TCC
             C                     GGCCTG TGA   ACAGCGGAGA
                                   |||||| |||   ||||||||||
                                   CCGGGC ACT   TGTCGCCTTT
                                      G   CCT
GAM1679  PCDH20   3'  TTTTTGTTGTTGTTTAGGTT   43427       TGATCC
                                   GGCCTGA     ACAGCGGAGA
                                   |||||||     ||||||||||
                                   TTGGATT     TGTTGTTTTT
                                       TGT___
GAM1679  PJA1     3'  TTTTTGTTGCATGTTATGGGTC 42567       G    CCA
                                   GGCCT ATGAT   CAGCGGAGA
                                   ||||| |||||   |||||||||
                                   CTGGG TATTG   GTTGTTTTT
                                     _    TAC
GAM1679  PP1665   3'  TTGATGGGTCATGGGCCA    48644       G      _
                                   TGGCCT ATGATCCA CAG
                                   |||||| |||||||| |||
                                   ACCGGG TACTGGGT GTT
                                     _       A
GAM1679  PPP1R10  3'  TTTTGTGCAGGGTCTTGGGTTA 12234       TG T    ACA
                                   TGGCC  A GATCC   GCGGAG
                                   |||||  | |||||   ||||||
                                   ATTGG  T CTGGG   TGTTTT
                                      GT _    ACG
GAM1679  PPP1R3B  3'  TTCTGCTGTGTTTAGGACA   45149    G    TGATC
                                   TG CCTGA    CACAGCGGAG
                                   || |||||    ||||||||||
                                   AC GGATT    GTGTCGTCTT
                                    A    T_____
GAM1679  PRO0902  5'  TCTTTGGGTGGGGTGTTGGGCT 54972     TG   AT   AG
                                   GGCC  ATG  CCAC  CGGAGA
                                   ||||  |||  ||||  ||||||
                                   TCGG  TGT  GGTG  GTTTCT
                                     GT   GG   G_
GAM1679  SEC24A   3'  TTTTTGTTTTGTTTTAATGGGT 83570       A   TC  C
             TA                     TGGCCTG TGA  CA AGCGGAGA
                                    ||||||| |||  || ||||||||
                                    ATTGGGT ATT  GT TTGTTTTT
                                       A   TT  T
GAM1679  SH3BGRL2 3'  TTTTTGCTGCAGAATCAG    49681      GA  CA
                                   CTGAT  TC  CAGCGGAGA
                                   |||||  ||  |||||||||
                                   GACTA  AG  GTCGTTTTT
                                      __  AC
GAM1679  SLC2A12  3'  TTTCTGAGCAGGATATCAGGTT 59743         A   ACAG
             A                      TGGCCTGATG TCC    CGGAGA
                                    |||||||||| |||    ||||||
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                                ATTGGACTAT AGG   GTCTTT
                                      _  ACGA
GAM1679  SPRY4    3'  TTTCTGCTGTGGGTAACTGC  49041    CTGATG
                                GC     ATCCACAGCGGAGA
                                ||     ||||||||||||||
                                CG     TGGGTGTCGTCTTT
                                 TCAA__
GAM1679  STAG2    3'  TCTTTGCAAGCAGTCTTCAGGT 71089        T   CCACA
            TA                    TGGCCTGA GAT     GCGGAGA
                                ||||||||| |||    |||||||
                                ATTGGACT CTG     CGTTTCT
                                     T   ACGAA
GAM1679  TNFAIP3  3'  TTTCTGGTTGTTGTTGGGGCA 21912    G  TG   ATCC    _
                                TG CC  ATG    ACAGC GGAGA
                                || ||  |||    ||||| |||||
                                AC GG  TGT    TGTTG TCTTT
                                 G  GT  ____     G
GAM1679  TU12B1-TY 3'  CTCCATGGTGGTCAGGCT    33845       TGAT    AGC
                                GGCCTGA    CCAC   GGAG
                                |||||||    ||||   ||||
                                TCGGACT    GGTG   CCTC
                                    ____    GTA
GAM1679  WIT-1    5'  TCTTTGTTGTGGGTAACGTT   32399     __
                                GATG  ATCCACAGCGGAGA
                                ||||  ||||||||||||||
                                TTGC  TGGGTGTTGTTTCT
                                  AA
GAM1679  LOC115704 3'  CTCTGCTGAATCAGAGCT    73907     _    GATCCA
                                GGC CTGAT     CAGCGGAG
                                ||| |||||     ||||||||
                                TCG GACTA     GTCGTCTC
                                 A    A_____
GAM1679  LOC138649 5'  TTTGGGGGTGGATCGCGGGTT  75877       A       AG_
                                GGCCTG TGATCCAC   CGGA
                                |||||| ||||||||   ||||
                                TTGGGC GCTAGGTG   GTTT
                                    _       GGG
GAM1679  LOC139221 3'  TTCTGCTGTTGATGGGTTA    76331       GATG   C
                                TGGCCT    ATC ACAGCGGAG
                                ||||||    ||| |||||||||
                                ATTGGG    TAG TGTCGTCTT
                                    ____   T
GAM1679  LOC143286 5'  TCTTCAGCAGTGATTGTCAGCC 83849     C   TG   C  A  _
            A                    TGGC TGA  ATC AC GC GGAGA
                                |||| |||  ||| || || |||||
                                ACCG ACT  TAG TG CG CTTCT
                                  _  GT   _  A  A
GAM1679  LOC144161 3'  TTTCCGAAGTTGATTGGGCT   83935      GAT    C  AG
                                GGCCT   GATC AC  CGGAGA
                                |||||   |||| ||  ||||||
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                                TCGGG   TTAG TG  GCCTTT
                                  ___    T  AA
GAM1679  LOC145241 5'  TTTCTGGCTACTGTCAGGCT   63530        GATCCAC  _
                                GGCCTGAT      AGC GGAGA
                                ||||||||      ||| |||||
                                TCGGACTG      TCG TCTTT
                                    TCA____   G
GAM1679  LOC145623 3'  TTTCTGTTATCTTGTCAGTGTT 84399     _   TG TCCAC
                                GGC CTGA  A     AGCGGAGA
                                ||| ||||  |    ||||||||
                                TTG GACT  T    TTGTCTTT
                                  T   GT CTA__
GAM1679  LOC145739 3'  TCTCTGTTTGTTAATCATTAGT 77907    C       CC   _
              CT                  GG CTGATGAT  ACAG CGGAGA
                                || ||||||||  |||| ||||||
                                TC GATTACTA  TGTT GTCTCT
                                 T       AT   T
GAM1679  LOC145815 3'  TCCAGTGGATTGTTGGCCA   84523      T  TG     AGC
                                TGGCC GA  ATCCAC   GGA
                                ||||| ||  ||||||   |||
                                ACCGG TT  TAGGTG   CCT
                                  _ GT     A__
GAM1679  LOC145828 5'  TTTTTGCTTTGTCCTCATAGGT 84543        A   TC_  C
              TA                  TGGCCTG TGA   CA AGCGGAGA
                                ||||||| |||   || ||||||||
                                ATTGGAT ACT   GT TCGTTTTT
                                    _  CCT  T
GAM1679  LOC146184 5'  TTTTTGCTGTCACATTTAGGT  84598       TGATCC
                                GCCTGA     ACAGCGGAGA
                                ||||||     ||||||||||
                                TGGATT     TGTCGTTTTT
                                   TACAC_
GAM1679  LOC146481 5'  TTTCTTGTGGTCAGTTGGGTTA 78489      TG  GAT     C
                                TGGCC  AT   CCACAG GGAG
                                |||||  ||   |||||| ||||
                                ATTGG  TG   GGTGTT CTTT
                                  GT  ACT     _
GAM1679  LOC146794 3'  TCAATGTGGGGCATCAGGCCA  84825         AT    GCG
                                TGGCCTGATG  CCACA   GA
                                ||||||||||  |||||   ||
                                ACCGGACTAC  GGTGT   CT
                                     GG    AA_
GAM1679  LOC149077 3'  TCTCTGCTGTGGCAGTAGGT   79890      A  AT
                                GCCTG TG  CCACAGCGGAGA
                                ||||| ||  ||||||||||||
                                TGGAT AC  GGTGTCGTCTCT
                                  G  __
GAM1679  LOC149103 3'  CTTTGTTGGTATTGTGCCA    79938     CTG TG  CCA
                                TGGC   A  AT   CAGCGGAG
                                ||||   |  ||   ||||||||
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                                ACCG   T  TA   GTTGTTTC
                                  ___ GT  TG_
GAM1679  LOC149465 3'  TCTTTGCTGTTGGATCAGACCA 80194     CCTGA      _
                                TGG    TGATCCA CAGCGGAGA
                                |||    ||||||| |||||||||
                                ACC    ACTAGGT GTCGTTTCT
                                  AG___      T
GAM1679  LOC150622 3'  TTTCTGTTACATCCATTGAGGT 80771       _   ATCCAC
              CA                  TGGCCT GATG     AGCGGAGA
                                |||||| ||||     ||||||||
                                ACTGGA TTAC     TTGTCTTT
                                   G   CTACA_
GAM1679  LOC150848 5'  TCTTTGCTAATCTATTGGCC   86321      TGAT   CCAC
                                GGCC   GAT    AGCGGAGA
                                ||||   |||   ||||||||
                                CCGG   CTA    TCGTTTCT
                                  TTAT   A___
GAM1679  LOC151361 3'  TCTTTGCTGCCAGCCATCAGGT 86507        ATCCA
                                GCCTGATG    CAGCGGAGA
                                ||||||||    |||||||||
                                TGGACTAC    GTCGTTTCT
                                    CGACC
GAM1679  LOC151361 3'  TTCTGTATGTCTTAGGCCA    86509        T   CCACA
                                TGGCCTGA GAT    GCGGAG
                                |||||||| |||    ||||||
                                ACCGGATT CTG    TGTCTT
                                    _   TA___
GAM1679  LOC151405 5'  TTGATGGTATTAGGTTA     86515         AT   _
                                TGGCCTGATG  CCA CAG
                                ||||||||||  ||| |||
                                ATTGGATTAT  GGT GTT
                                    __   A
GAM1679  LOC151610 3'  TCTTTGCTGAATCCAGATGGGT 81099       GA_  ATCCA
              TA                  TGGCCT   TG    CAGCGGAGA
                                ||||||   ||    |||||||||
                                ATTGGG   AC    GTCGTTTCT
                                   TAG  CTAA_
GAM1679  LOC151827 5'  TCTTCGCTGGCCCGGCAGGCC  81193       ATGATCCA
                                GGCCTG       CAGCGGAGA
                                ||||||       |||||||||
                                CCGGAC       GTCGCTTCT
                                   GGCCCG__
GAM1679  LOC153196 5'  CTCCAGGACATCGGGCT     87169         A   ACAGC
                                GGCCTGATG TCC    GGAG
                                ||||||||| |||    ||||
                                TCGGGCTAC AGG    CCTC
                                    _   A____
GAM1679  LOC154222 3'  CTCTGTTCTTATCAGGGCA    87390    G       TCCAC
                                TG CCTGATGA    AGCGGAG
                                || ||||||||    |||||||
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                                AC GGACTATT    TTGTCTC
                                 G      C____
GAM1679  LOC158318 5'  TCTTTGTTGAAGACATTGGGC  88103    TG  A  CA
                                GCC  ATG TC  CAGCGGAGA
                                |||  ||| ||  |||||||||
                                CGG  TAC AG  GTTGTTTCT
                                  GT  _  AA
GAM1679  LOC158401 3'  TTCCGTTCACATTGGCC    82806    T   ATCCAC
                                GGCC GATG    AGCGGAG
                                |||| ||||    |||||||
                                CCGG TTAC    TTGCCTT
                                  _   AC____
GAM1679  LOC164121 5'  TCAAGGTGGGCGTCGGGCT   83050       A    AGCG
                                GGCCTGATG TCCAC   GA
                                ||||||||| |||||   ||
                                TCGGGCTGC GGGTG   CT
                                     _    GAA_
GAM1679  LOC196528 3'  TCTCAGGTGATCATCAGG    89109       C  AGCG
                                CCTGATGATC AC   GAGA
                                |||||||||| ||   ||||
                                GGACTACTAG TG   CTCT
                                     _  GA__
GAM1679  LOC200081 3'  TTTCCATGAGGTTATCGGACCA 89978    C     T  A  GC
                                TGG CTGATGA CC CA  GGAGA
                                ||| ||||||| || ||  |||||
                                ACC GGCTATT GG GT  CCTTT
                                  A     _ A  A_
GAM1679  LOC200268 3'  CTCTAGACTATTAGGCTA    90084       A  CACAGC
                                TGGCCTGATG TC    GGAG
                                |||||||||| ||    ||||
                                ATCGGATTAT AG    TCTC
                                     C  A_____
GAM1679  LOC201164 3'  TTCTGTTACTTCGGGTCA    89505       TGATCCAC
                                TGGCCTGA      AGCGGAG
                                ||||||||      |||||||
                                ACTGGGCT      TTGTCTT
                                    TCA_____
GAM1679  LOC201475 5'  TCTTTAAGTGTGGTCATCAGGT 89623        T   GC_
            CA                    TGGCCTGATGA CCACA  GGAGA
                                ||||||||||| |||||  |||||
                                ACTGGACTACT GGTGT  TTTCT
                                     _   GAA
GAM1679  LOC202404 5'  CTTTGTTGTGTTCAGCC    90650    C  TGATC
                                GGC TGA    CACAGCGGAG
                                ||| |||    ||||||||||
                                CCG ACT    GTGTTGTTTC
                                  _  T____
GAM1679  LOC202460 5'  TCTTTGTGACCTGTTGTTAGGC 90678      TG  CCACA
                                GCCTGA  AT    GCGGAGA
                                ||||||  ||    |||||||
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                                CGGATT  TG    TGTTTCT
                                   GT  TCCAG
GAM1679  LOC202934 5'  TTGAGGTGCATCATTAGGTT   92058          C   AG
                                GGCCTGATGAT CAC  CGG
                                |||||||||||  |||  |||
                                TTGGATTACTA GTG  GTT
                                      C   GA
GAM1679  LOC219654 3'  TTTCTGTTTCCCGTTATTGGGT 92944      TG    CCAC
           T                     GGCC  ATGAT    AGCGGAGA
                                ||||  |||||    ||||||||
                                TTGG  TATTG    TTGTCTTT
                                  GT    CCCT
GAM1679  LOC219690 3'  TCTCCTGCACCGGTTATTAAGC 94668      C       CACA  _
           CA                     TGGC TGATGATC    GC GGAGA
                                |||| ||||||||    || |||||
                                ACCG ATTATTGG    CG CCTCT
                                  A       CCA_  T
GAM1679  LOC220883 3'  TTTTTGATCTGTATTGGGCTA  92894      TG  GATCC   __
                                TGGCC  AT    ACAG  CGGAGA
                                |||||  ||    ||||  ||||||
                                ATCGG  TA    TGTC  GTTTTT
                                   GT  _____    TA
GAM1679  LOC221416 3'  CTCTGTCATCGTCAGGCT    95406          CCACA
                                GGCCTGATGAT    GCGGAG
                                ||||||||||    ||||||
                                TCGGACTGCTA    TGTCTC
                                      C____
GAM1679  LOC221687 3'  TCTTTGTTGTGTGATGCAGGT  93873      ATG  _
                                GCCTG   ATC CACAGCGGAGA
                                |||||   ||| ||||||||||
                                TGGAC   TAG GTGTTGTTTCT
                                   G__   T
GAM1679  LOC221975 3'  CTCTGCTTGTTATTGGTTA    94190      T     CCAC
                                TGGCC GATGAT    AGCGGAG
                                ||||| ||||||    |||||||
                                ATTGG TTATTG    TCGTCTC
                                   _     T___
GAM1679  LOC253263 3'  TTTCTGCCTCCCCTCTTTGGGT 98820      TG T  TCCACA
           TA                     TGGCC  A GA     GCGGAGA
                                |||||  | ||     |||||||
                                ATTGG  T CT     CGTCTTT
                                   GT T  CCCCTC
GAM1679  LOC254249 5'  TTTCTGTTGCAGAGTTAGGC   97189       GA  CA
                                GCCTGAT  TC  CAGCGGAGA
                                |||||||  ||  |||||||||
                                CGGATTG  AG  GTTGTCTTT
                                    __  AC
GAM1679  LOC254351 5'  CTCCGTGTTGGTCGGGCT    96687       TGAT   CA
                                GGCCTGA   CCA  GCGGAG
                                |||||||   |||  ||||||
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                                TCGGGCT   GGT  TGCCTC
                                    ____  TG
GAM1679  LOC255465 5'  TTGAGGTGCATCATTAGGTT  99132          C  AG
                                GGCCTGATGAT CAC  CGG
                                |||||||||| |||  |||
                                TTGGATTACTA GTG  GTT
                                     C  GA
GAM1679  LOC257554 5'  TCTCTGCTGCGTGTTCGCGGGC 99537       A  TCCA_
           CA                    TGGCCTG TGA    CAGCGGAGA
                                |||||| |||    |||||||||
                                ACCGGGC GCT    GTCGTCTCT
                                   _  TGTGC
GAM1679  LOC51696  3'  TTTTGTTGTAGTTAGG     33095       GATCC
                                CCTGAT    ACAGCGGAG
                                ||||||    |||||||||
                                GGATTG    TGTTGTTTT
                                   A____
GAM1679  LOC90408  5'  TTCTGCTGTGCCAGGGCT    63349      GATGATC
                                GGCCT     CACAGCGGAG
                                |||||     ||||||||||
                                TCGGG     GTGTCGTCTT
                                  ACC____
GAM1679  LOC91496  5'  TTTTTGTTGTTGTTTTTGGGCC 66814      TG T  CC
           A                     TGGCC  A GAT  ACAGCGGAGA
                                ||||| | |||  ||||||||||
                                ACCGG  T TTG  TGTTGTTTTT
                                   GT T  T_
GAM1679  LOC92231  3'  TCCATTGTGGCGTCATTAGGTT 69095          _    C  GA
           A                     TGGCCTGATGAT CCACAG GGA
                                |||||||||||| |||||| |||
                                ATTGGATTACTG GGTGTT CCT
                                     C    A
GAM1679  LOC92973  5'  TTTCTGCTGTATGACTTTGGTC 71596      TGATGATCC
           A                     TGGCC       ACAGCGGAGA
                                |||||       ||||||||||
                                ACTGG       TGTCGTCTTT
                                  TTTCAGTA_
GAM1680  ARF1     3'  TCCCACGGTTCCCAGGGGC   71199      CA  TG  TC
                                GCTCC  GGA  TGT  GGGA
                                |||||  |||  |||  ||||
                                CGGGG  CCT  GCA  CCCT
                                  AC   TG   __
GAM1680  ASB2     5'  CCCTTTCATCCTGGGACCTG  32874     C       TGTTC
                                CAG TCCCAGGATG    GGG
                                ||| ||||||||||    |||
                                GTC AGGGTCCTAC    CCC
                                  C        TTT__
GAM1680  BACE     5'  TCCCCAGCCCGCCCGGGAGCTG 58092       A  A  T  C
                                CAGCTCCC GG TG GTT GGGA
                                |||||||| || || ||| ||||
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                                GTCGAGGG CC GC CGA CCCT
                                    C _ C  C
GAM1680 BMP1    3' CTCAACACCCTGGGCAGCT  21529     _    AT   C
                                AGCT CCCAGG GTGTT GGG
                                |||| ||||||  ||||| |||
                                TCGA GGGTCC  CACAA CTC
                                  C     __   _
GAM1680 C21orf2 3' TCCCCAGCCCCCGGGAGCTG  18207       A ATGT  C
                                CAGCTCCC GG   GTT GGGA
                                |||||||| ||   ||| ||||
                                GTCGAGGG CC   CGA CCCT
                                    C C___  C
GAM1680 CELSR1  3' TCCCAGGTGGCCCGGGAGCTG 27279       A ATGTG TC
                                CAGCTCCC GG    T GGGA
                                |||||||| ||    | ||||
                                GTCGAGGG CC    G CCCT
                                    C GGT__ GA
GAM1680 EGFL4   5' TTCCCACGCTTCCTGGACACTG 62479    CTC    T   TC
                                CAG  CCAGGA GTGT GGGAA
                                |||  |||||| |||| |||||
                                GTC  GGTCCT CGCA CCCTT
                                  ACA    T  __
GAM1680 ENG     3' TGAACTCACCCTGGGAGC    5501         A T
                                GCTCCCAGG TG GTTCG
                                ||||||||| || |||||
                                CGAGGGTCC AC CAAGT
                                     C T
GAM1680 FCER2   3' TCCTCAGCACCCCAGGACCTG 10606    C  CA AT   C
                                CAG TCC GG GTGTT GGGA
                                ||| |||  ||  ||||| ||||
                                GTC AGG CC CACGA TCCT
                                  C  AC __    C
GAM1680 FCMD    3' TCCAGAGACATCCTGAGAGGC 23045   _ C      G  G
                                GC TC CAGGATGT TTC GGA
                                || || |||||||| ||| |||
                                CG AG GTCCTACA GAG CCT
                                 G A      _  A
GAM1680 GAB2    3' TCCCTAGCATTCCAGGAGC   25465     CA  T   C
                                GCTCC GGA GTGTT GGGA
                                |||||  ||| ||||| ||||
                                CGAGG CCT TACGA CCCT
                                   A_  _   T
GAM1680 GDF5    3' CTGGGTGGCACATCCCAAGAGC 6895     CCA     ___
                                GCTC  GGATGTGT  TCGG
                                ||||  ||||||||  ||||
                                CGAG  CCTACACG  GGTC
                                  AAC      GTG
GAM1680 LDHA    3' TTCCCAGTGAGTCACATCCTGG 19917          _  ___
            GA                  TCCCAGGATGTG TTC  GGGAA
                                |||||||||||| |||  |||||
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                                AGGGTCCTACAC GAG   CCCTT
                                      T   TGA
GAM1680  MAPK7    5'  TTCCCAGAGCTCCTGGGA    12310        TGT   _
                                TCCCAGGA   GTTC GGGAA
                                ||||||||   |||| |||||
                                AGGGTCCT   CGAG CCCTT
                                    ___    A
GAM1680  MHC2TA   3'  TCCCGAATAGCTGGGACT    5996     C     GATG
                                AG TCCCAG    TGTTCGGGA
                                || ||||||    |||||||||
                                TC AGGGTC    ATAAGCCCT
                                 _     G___
GAM1680  MTMR2    5'  CCCCTCACCCTGGGAGC     32909         AT   TTC
                                GCTCCCAGG  GTG   GGG
                                |||||||||  |||   |||
                                CGAGGGTCC  CAC   CCC
                                     __   TC_
GAM1680  MYBPC2   3'  TCCCCAACCTCCCAGGACTG   16972     C   CA   TGT   C
                                CAG TCC  GGA   GTT GGGA
                                ||| |||  |||   ||| ||||
                                GTC AGG  CCT   CAA CCCT
                                  _  AC   C__   C
GAM1680  NRGN     3'  CCCGCCGGGCTCCTGGGGCTG  21622      T      T  GTT_
                                CAGC CCCAGGA GT    CGGG
                                |||| ||||||| ||    ||||
                                GTCG GGGTCCT CG    GCCC
                                  _      _ GGCC
GAM1680  PTPRH    3'  TCCCAGACTCCTGGGTGCTG   12617     T      TGT  TC
                                CAGC CCCAGGA   GT  GGGA
                                |||| |||||||   ||  ||||
                                GTCG GGGTCCT   CA  CCCT
                                  T      ____  GA
GAM1680  RERE     3'  TCCCACTCTTCATCCTGGAAGT 25021     C       TGTTC_
                                GCT CCAGGATG      GGGA
                                ||| ||||||||      ||||
                                TGA GGTCCTAC      CCCT
                                  A       TTCTCA
GAM1680  SHOX     3'  TCCGGGCACCCCGGGAGCT    6586         A  AT
                                AGCTCCC GG  GTGTTCGGG
                                ||||||| ||  |||||||||
                                TCGAGGG CC  CACGGGCCT
                                    C  __
GAM1680  TAF15    3'  TCCCCAACCCTTGGAGCT     14471       C   ATGT   C
                                AGCTCC AGG    GTT GGGA
                                |||||| |||    ||| ||||
                                TCGAGG TCC    CAA CCCT
                                   T  _____   C
GAM1680  TMPRSS2  3'  TCCCCAAGACACATCCTAAAAG 20173    G  CCC        C__
            GTG                   CA CT   AGGATGTGTT   GGGA
                                || ||   ||||||||||   ||||
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                                GT GA   TCCTACACAG   CCCT
                                 G  AAA        AAC
GAM1680  USP6     5'  CCTGAACATCCCAGGAG     92781      CA     GT
                                CTCC  GGATGT  TCGGG
                                ||||  ||||||  |||||
                                GAGG  CCTACA  AGTCC
                                  AC     __
GAM1680  VDR      3'  CCCCAACTCCTGGAAGCTG    6340       C     TGT   C
                                CAGCT CCAGGA   GTT GGG
                                ||||| ||||||   ||| |||
                                GTCGA GGTCCT   CAA CCC
                                  A      ___   C
GAM1680  ZNF43    5'  CCCGGACATCCTGGAAGCTG   14247      C     TG
                                CAGCT CCAGGA  TGTTCGGG
                                ||||| ||||||  ||||||||
                                GTCGA GGTCCT  ACAGGCCC
                                  A     __
GAM1680  AGPAT1   3'  TCCCAGGCTCATCCTGGGAGCT 22178           T  TC
                                AGCTCCCAGGATG GT  GGGA
                                |||||||||||| ||  ||||
                                TCGAGGGTCCTAC CG  CCCT
                                       T  GA
GAM1680  AGPAT1   3'  TCCCAGGCTCATCCTGGGAGCT 22179           T  TC
                                AGCTCCCAGGATG GT  GGGA
                                |||||||||||| ||  ||||
                                TCGAGGGTCCTAC CG  CCCT
                                       T  GA
GAM1680  ATP6V1EL2 5'  CCCGTCATGGCCCCGGGTGC   55559    T   A  A_   TT
                                GC CCC GG  TGTG  CGGG
                                || ||| ||  ||||  ||||
                                CG GGG CC  GTAC  GCCC
                                 T   C  CG    T_
GAM1680  BAD      3'  CCCGCGATGCCCTGGGGGC    53353         AT    _
                                GCTCCCAGG  GTGTT CGGG
                                |||||||||  ||||| ||||
                                CGGGGGTCC  CGTAG GCCC
                                      __     C
GAM1680  BAD      3'  TTCCCACTGCCCTGGGCAGC   53355     _     AT T  TC
                                GCT CCCAGG  G GT  GGGAA
                                ||| ||||||  | ||  |||||
                                CGA GGGTCC  T CA  CCCTT
                                  C     CG _  __
GAM1680  BM039    5'  TCCCCACCTCCTGGGGC     38050    T      T   TTC
                                GC CCCAGGA GTG   GGGA
                                || |||||| |||   ||||
                                CG GGGTCCT CAC   CCCT
                                 _      C   ___
GAM1680  C14orf4  5'  TCCCCACGCCCTGGGCAGC    67922     _     A    TTC
                                GCT CCCAGG TGTG   GGGA
                                ||| |||||| ||||   ||||
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                                CGA GGGTCC GCAC   CCCT
                                  C     C   ___
GAM1680  C20orf46  5'  TTCCTGGGCCACTCCAGGAGCT 37736       CA  _  T
              G                    CAGCTCC  GGA TG GTTCGGGAA
                                   |||||||  ||| || |||||||||
                                   GTCGAGG  CCT AC CGGGTCCTT
                                      A_   C  _
GAM1680  C9orf7    3'  TCCCCACTGCCCTGGGTGC   34586    T    AT_  TTC
                                   GC CCCAGG   GTG   GGGA
                                   || ||||||   |||   ||||
                                   CG GGGTCC   CAC   CCCT
                                    T     CGT   ___
GAM1680  DKFZp762E1312 5'  CCGCACAGTCCTGGGAGC    37901          G   T
                                   GCTCCCAGGAT TGT CGG
                                   |||||||||| ||| |||
                                   CGAGGGTCCTG ACA GCC
                                         _   C
GAM1680  DNAL4     3'  TCCCCTTGCATCCTGGGAGC   20423            TTC
                                   GCTCCCAGGATGTG   GGGA
                                   ||||||||||||||   ||||
                                   CGAGGGTCCTACGT   CCCT
                                           TC_
GAM1680  FLJ10008  3'  TCCCAAGCCGTCTAGGAGC   36194      CA    T   C
                                   GCTCC  GGATG GTT GGGA
                                   |||||  ||||| ||| ||||
                                   CGAGG  TCTGC CGA CCCT
                                      A_    _   A
GAM1680  FLJ13188  3'  TCCCAAAGTTCTGGGAGT    42197          GTGTTC
                                   GCTCCCAGGAT     GGGA
                                   ||||||||||      ||||
                                   TGAGGGTCTTG     CCCT
                                         AAA___
GAM1680  FLJ14326  3'  TTCCCGAAGACCCTCGCTGGGA 50790          _  T_  G
              GCTG                    CAGCTCCCAG GA  GT TTCGGGAA
                                      |||||||||| ||  || ||||||||
                                      GTCGAGGGTC CT  CA AAGCCCTT
                                           G  CC  G
GAM1680  FLJ23356  5'  TTCCCGACCAGTCCCTGGGCGC 50927    T     ATG  T
                                   GC CCCAGG   TG TCGGGAA
                                   || ||||||   || |||||||
                                   CG GGGTCC   AC AGCCCTT
                                    C     CTG  C
GAM1680  GPR       5'  TCCCCGCCTCCCGGGCGC    24295    T   A   T   TTC
                                   GC CCC GGA GTG   GGGA
                                   || ||| ||| |||   ||||
                                   CG GGG CCT CGC   CCCT
                                    C   C   C   ___
GAM1680  HSZFP36   5'  CCCGGACACCTGGAAGCTG   64220      C    ATG
                                   CAGCT CCAGG   TGTTCGGG
                                   ||||| |||||   ||||||||
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                                GTCGA GGTCC   ACAGGCCC
                                  A    ___
GAM1680 HT002    3' TTCCCGAGGCCCCTACAAGC   26805    CCC   AT  G
                                GCT   AGG  GT TTCGGGAA
                                |||   |||  || ||||||||
                                CGA   TCC  CG GAGCCCTT
                                  ACA   C_  _
GAM1680 KCNK17   3' TTCCATCCACCCTAGAGGCTG  49595     CCC   AT   TTCG
                                CAGCT   AGG  GTG   GGAA
                                |||||   |||  |||   ||||
                                GTCGG   TCC  CAC   CCTT
                                  AGA   __   CTA_
GAM1680 KIAA0404 3' TCCTGAGCCTCCCAAGAGCTG  70216      CCA   TGT
                                CAGCTC   GGA   GTTCGGGA
                                ||||||   |||   ||||||||
                                GTCGAG   CCT   CGAGTCCT
                                   AAC   C__
GAM1680 KIAA0469 3' TTCCCGGGAGGCCCTGGGAGGT 30001    G       ATGTG
            G                    CA CTCCCAGG    TTCGGGAA
                                || ||||||||    ||||||||
                                GT GAGGGTCC    GGGCCCTT
                                 G       CGGA_
GAM1680 KIAA0476 5' CCCGGCGCCGCGGGAGCTG   30038        A_  A   GTT
                                CAGCTCCC  GG TGT   CGGG
                                ||||||||  || |||   ||||
                                GTCGAGGG  CC GCG   GCCC
                                    CG  _   ___
GAM1680 KIAA0561 3' TCCTTCCATCCTGGAGCTG   66486       C     TGTTC
                                CAGCTCC AGGATG    GGGA
                                ||||||| ||||||    ||||
                                GTCGAGG TCCTAC    TCCT
                                   _     CT___
GAM1680 KIAA0649 3' CCAGAGCACATCTGAAAACTG  29712    CTCCCA        G
                                CAG     GGATGTGTTC GG
                                |||     |||||||||| ||
                                GTC     TCTACACGAG CC
                                  AAAAG_         A
GAM1680 KIAA0775 3' CCCAAACACTCACTTTGAATGC 28951     __  CC  _  T    C
            TG                   CAGC  TC  AG GA GTGTT GGG
                                ||||  ||  || || ||||| |||
                                GTCG  AG  TC CT CACAA CCC
                                  TA  TT  A  _    A
GAM1680 KIAA0980 3' CTGGAGCCAGATCCTGGGAGCT 47997           G  _  G
            G                    CAGCTCCCAGGAT TG TTC GG
                                ||||||||||||| || ||| ||
                                GTCGAGGGTCCTA AC GAG TC
                                       G  C   G
GAM1680 KIAA1437 3' TCCCAGAACTCCCGGACAGC   61219    C_  A   TGT   _
                                GCT  CC GGA   GTTC GGGA
                                |||  || |||   |||| ||||
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                                CGA  GG CCT   CAAG CCCT
                                  CA  C  ___   A
GAM1680  KIAA1737  3'  TTCAGAACATCCTGGG     67951        GT  GG
                                CCCAGGATGT  TC  GAA
                                ||||||||||  ||  |||
                                GGGTCCTACA  AG  CTT
                                     __  A_
GAM1680  KIAA1938  3'  CCCGAATGCCTCCCTGGGAGGC 93821    _     AT_
                                GC TCCCAGG   GTGTTCGGG
                                || |||||||   |||||||||
                                CG AGGGTCC   CGTAAGCCC
                                 G      CTC
GAM1680  MGC4368   3'  TCCCCACCCCGTAGGAGCTG   44729       CA_  AT   TTC
                                CAGCTCC   GG  GTG   GGGA
                                |||||||   ||  |||   ||||
                                GTCGAGG   CC  CAC   CCCT
                                    ATG  C_   ___
GAM1680  MGC5576   3'  TTCCCAAAGGCCTGGGAGCT   44146        ATGTG  C
                                AGCTCCCAGG    TT GGGAA
                                ||||||||||    || |||||
                                TCGAGGGTCC    AA CCCTT
                                     GGA__  _
GAM1680  OLFM2     3'  CCCCCACCCCCAGGAGTTG   55168       CA  AT   TTC
                                CAGCTCC  GG  GTG   GGG
                                |||||||  ||  |||   |||
                                GTTGAGG  CC  CAC   CCC
                                    A_  CC   C__
GAM1680  P114-RHO-GEF 3'  TCCCGAACCCAGGGTCCTGGGA 31676     C       ___  T
           ACTG                  CAG TCCCAGGA   TG GTTCGGGA
                                |||  ||||||||   ||  ||||||||
                                GTC AGGGTCCT   AC CAAGCCCT
                                  A       GGG  C
GAM1680  PRO0386   5'  TTCTATTAACATCCTGAAGAAC 38303    C  C_      GTTCG
           T                   AG TC  CAGGATGT    GGAA
                                ||  ||  ||||||||    ||||
                                TC AG  GTCCTACA    TCTT
                                 A  AA       ATTA_
GAM1680  PRO0899   5'  TCCCAAAGTGCTGGGGGCT   38314        G  GTGTTC
                                AGCTCCCAG AT     GGGA
                                |||||||| ||     ||||
                                TCGGGGGTC TG     CCCT
                                     G  AAA___
GAM1680  PTGES2    3'  TTCCCAAGCCTCCCGGGACTG  47580     C   A   T  GTTC
                                CAG TCCC GGA GT    GGGAA
                                ||| |||| ||| ||    |||||
                                GTC AGGG CCT CG    CCCTT
                                  _   C   C  AA__
GAM1680  PTPNS1    3'  TCCCGTGTGGCATCTGGGAGC  55844        G   GTT_
                                GCTCCCAG ATGT    CGGGA
                                |||||||| ||||    |||||
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                                CGAGGGTC TACG   GCCCT
                                    _   GTGT
GAM1680  RAB35    3'  TCCCCACAGCCATTCTGGGAGC 23419          T  C__
              TG                  CAGCTCCCAGGATG GTT  GGGA
                                  |||||||||||||| |||  ||||
                                  GTCGAGGGTCTTAC CGA  CCCT
                                        _  CAC
GAM1680  RAP140   3'  TCCCGAATGGCTGGGACT   31525   C    GATG
                                  AG TCCCAG   TGTTCGGGA
                                  || ||||||   |||||||||
                                  TC AGGGTC   GTAAGCCCT
                                   _    G___
GAM1680  SEC10L1  5'  TCCCGCCCCTCCTGGGATCTG  22588    C     TGTGTT
                                  CAG TCCCAGGA    CGGGA
                                  ||| ||||||||     |||||
                                  GTC AGGGTCCT    GCCCT
                                    T      CCCC__
GAM1680  SPRY4    3'  TTCCGCGAGCACCCTGGGAACT 49038    C     AT     _
              G                    CAG TCCCAGG  GTGTTCG GGAA
                                  ||| |||||||  ||||||| ||||
                                  GTC AGGGTCC  CACGAGC CCTT
                                    A      __      G
GAM1680  SSTK     3'  TCCCCGCGATCCCGGGAGCTG  50173        A   _  TTC
                                  CAGCTCCC GGAT GTG   GGGA
                                  |||||||| |||| |||   ||||
                                  GTCGAGGG CCTA CGC   CCCT
                                       C   G  ___
GAM1680  STK29    5'  CCCCCACGTCCTAAAGCTG   88962     CCC      TTC
                                  CAGCT   AGGATGTG   GGG
                                  |||||   ||||||||   |||
                                  GTCGA   TCCTGCAC   CCC
                                     AA_      C__
GAM1680  LOC118978 5'  TCCCCGGTGCTCCTGGGGCT   76505    T     T TG TC
                                  AGC CCCAGGA G  T  GGGA
                                  ||| ||||||| |  |  ||||
                                  TCG GGGTCCT C  G  CCCT
                                    _      _ GT GC
GAM1680  LOC124842 3'  TCCCAGGACCTGGGAGCTG   76161          ATGTG  _
                                  CAGCTCCCAGG    TTC GGGA
                                  ||||||||||     ||| ||||
                                  GTCGAGGGTCC    AGG CCCT
                                         _____  A
GAM1680  LOC127281 3'  TCCCACCCCCGGGCAGCTG   75139      _  A  AT  GTTC
                                  CAGCT CCC GG  GT   GGGA
                                  ||||| ||| ||  ||   ||||
                                  GTCGA GGG CC  CA   CCCT
                                     C  _  CC  ____
GAM1680  LOC129433 5'  CCCAAGAGCTCCTGGGAGC   76221          TGT   __
                                  GCTCCCAGGA   GTTC  GGG
                                  |||||||||   ||||  |||
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                                CGAGGGTCCT  CGAG  CCC
                                      ___   AA
GAM1680  LOC145989 3'  TCCCAGCCCCCCAGGAGCTG  60296      CA  ATGT  C
                                CAGCTCC  GG   GTT GGGA
                                |||||||  ||   ||| ||||
                                GTCGAGG  CC   CGA CCCT
                                    AC  CC__  _
GAM1680  LOC149157 3'  CTGGATCACATTCTGAAAACTG 79940    CTCC      _
                                CAG   CAGGATGTG TTCGG
                                |||   ||||||||| |||||
                                GTC   GTCTTACAC AGGTC
                                  AAAA       T
GAM1680  LOC149276 3'  TCCCCAAACACACATCCTGGGA 85541           TC___
             GC                   GCTCCCAGGATGTGT    GGGA
                                |||||||||||||||    ||||
                                CGAGGGTCCTACACA    CCCT
                                         CAAAC
GAM1680  LOC149296 5'  TCCCCAGGTACCTGGGAGCT  80022        _  G  TTC
                                AGCTCCCAGG AT TG  GGGA
                                |||||||||| || ||  ||||
                                TCGAGGGTCC TG AC  CCCT
                                     A  G  ___
GAM1680  LOC149992 5'  TCCCGGGCCAAGCCTGGAAGCT 80379     C    A_  T
             G                    CAGCT CCAGG  TG GTTCGGGA
                                ||||| |||||  || ||||||||
                                GTCGA GGTCC  AC CGGGCCCT
                                   A    GA  _
GAM1680  LOC150271 5'  CCCCCACTCCCGGGTGCTG   86135    T  A  T  TTC
                                CAGC CCC GGA GTG  GGG
                                |||| ||| ||| |||  |||
                                GTCG GGG CCT CAC  CCC
                                  T  C  _  C__
GAM1680  LOC151176 3'  CTCAGGACCTCCTGGGAGC   86442        T  G  C
                                GCTCCCAGGA GT TT GGG
                                |||||||||| || || |||
                                CGAGGGTCCT CA GA CTC
                                     C  G  _
GAM1680  LOC154222 5'  TCCCAGGCTCCTGGGAAGC   87394    _    TGT  TC
                                GCT CCCAGGA  GT  GGGA
                                ||| |||||||  ||  ||||
                                CGA GGGTCCT  CG  CCCT
                                  A      ___  GA
GAM1680  LOC155066 5'  TCCCGCCGGGTCCCTGAACGC  82211   TCC   _  G  TT
                                GC  CAGG AT TG  CGGGA
                                ||  |||| || ||  |||||
                                CG  GTCC TG GC  GCCCT
                                 CAA   C  G  C_
GAM1680  LOC158814 3'  TTCCCGGGTTTCCCAGGAGC  82877     CA  TGT TT
                                GCTCC  GGA  G  CGGGAA
                                |||||  |||  |  ||||||
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                                CGAGG  CCT   T  GCCCTT
                                   AC   T__ GG
GAM1680  LOC163782 3'  TCCCCACACTTCCTGAAACTG  83038    CTCC    T   TC
                                CAG    CAGGA GTGT  GGGA
                                |||    ||||| ||||  ||||
                                GTC    GTCCT CACA  CCCT
                                  AAA_     T    C_
GAM1680  LOC196746 3'  CCCGAACCCTGGGGAGCTG   88899        _   ATGT
                                CAGCTCCC AGG    GTTCGGG
                                |||||||| |||    |||||||
                                GTCGAGGG TCC    CAAGCCC
                                     G  _____
GAM1680  LOC202020 5'  CCCGAACACTAAGCTTCCTGG  90597       T_____
                                CCAGGA     GTGTTCGGG
                                ||||||     |||||||||
                                GGTCCT     CACAAGCCC
                                    TCGAAT
GAM1680  LOC221511 3'  TTCCCGAGAATACCCTAAGA   92632    CC   A   G
                                TC  AGG TGT TTCGGGAA
                                ||  ||| ||| ||||||||
                                AG  TCC ATA GAGCCCTT
                                 AA   C   A
GAM1680  LOC254219 5'  CCCCCACGTTTCCTGAGGCTG  98320      CC    TG   TC
                                CAGCT  CAGGA  TGT  GGG
                                |||||  |||||  |||  |||
                                GTCGG  GTCCT  GCA  CCC
                                   A_    TT   CC
GAM1680  LOC256526 5'  CCCCCACGGCCTCTGGGAGC   99333        _ A_   TTC
                                GCTCCCAG G  TGTG   GGG
                                |||||||| |  ||||   |||
                                CGAGGGTC C  GCAC   CCC
                                     T CG    C__
GAM1680  LOC257459 5'  TCCAACCGCACATCCCGGAAGT 91531    A   C  A      TCG_
            CA                    C GCT CC GGATGTGT    GGA
                                | ||| || ||||||||    |||
                                A TGA GG CCTACACG    CCT
                                 C   A  C       CCAA
GAM1680  LOC257569 3'  TTCCCGAGAATACCCTAAGA   99667    CC   A   G
                                TC  AGG TGT TTCGGGAA
                                ||  ||| ||| ||||||||
                                AG  TCC ATA GAGCCCTT
                                 AA   C   A
GAM1680  LOC90288  3'  TCCCGAATAGCTGGGACT    62800    C     GATG
                                AG TCCCAG    TGTTCGGGA
                                || ||||||    |||||||||
                                TC AGGGTC    ATAAGCCCT
                                 _     G___
GAM1680  LOC91523  3'  TCCCCACTTCCTGGGAGT    57207         T   TTC
                                GCTCCCAGGA GTG   GGGA
                                |||||||||| |||   ||||
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                                TGAGGGTCCT CAC   CCCT
                                      T  ___
GAM1680  LOC92303  5'  CCCGGAGCATCTTAAGAGCTG  69388       CC      G
                                CAGCTC  AGGATGT TTCGGG
                                |||||||  ||||||| ||||||
                                GTCGAG  TTCTACG AGGCCC
                                   AA      _
GAM1680  LOC93444  3'  TCCCTGTGCATCCAGGAAGCTG 72826       C  A    TG TC
                                CAGCT CC GGATG  T  GGGA
                                ||||| || |||||  |  ||||
                                GTCGA GG CCTAC  G  CCCT
                                   A  A     GT T_
GAM1681  A1BG     3'  AGACAGGGTCTCACTGTGTT   56275          A   C
                                AACACGGTGA ACCC GTCT
                                |||||||||| |||| ||||
                                TTGTGTCACT TGGG CAGA
                                      C   A
GAM1681  A1BG     3'  AGAGATGGGGTTTCACCTTGTT 56277      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                   T
GAM1681  ADAMTS4  3'  AGAGACAGGGTTTCACCATGTT 18750      C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                   A        A
GAM1681  ADAMTS4  3'  AGAGACGGGGTTTCACCATGTT 18751      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                   A
GAM1681  ALOX15   3'  AGACGGGGCCTCACTATGTT   8539       CG    AA
                                AACA  GTGA  CCCCGTCT
                                ||||  ||||  ||||||||
                                TTGT  CACT  GGGGCAGA
                                   AT    CC
GAM1681  APAF1    3'  AGAGACGGGGTTTCACCATGTT 8579       C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                   A
GAM1681  APAF1    3'  AGAGACGGGGTTTCACCATGTT 25960      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                   A
GAM1681  APOL1    3'  AGAGATGGGGTTTCACCATGTT 14723      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
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                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  APPL     3'  AGAGACGGGGTTTCACCGTGTT 24942
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGAGA

GAM1681  ARCN1    3'  AGAGACGGGGTTTCACCGTGTT 9745
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGAGA

GAM1681  ATP7A    3'  AGAGACGGGGTTTCGCCATGTT 5314       C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCGCTTTGGGGCAGAGA
                                  A
GAM1681  AXL      3'  AGAGACAGGGTTTCACCATGTT 9900       C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  AXL      3'  AGAGACAGGGTTTCACCATGTT 41875      C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  BRIP1    3'  AGAGATGGGGTTTCACCATGTT 50202      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  C14orf1  3'  AGAGACGGGGTTTCACTCTGT  24163     C
                                ACA GGTGAAACCCCGTCTCT
                                ||| |||||||||||||||
                                TGT TCACTTTGGGGCAGAGA
                                  C
GAM1681  C7       3'  AGAGATGGGTTTCACCATGTT  6977       C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG TAGAGA
                                  A         _
GAM1681  CASP10   3'  AGAAACAGGAAACACCGTGTT  53212          AAAC  C  C
                                AACACGGTG    CC GT TCT
                                |||||||||    || || |||
                                TTGTGCCAC    GG CA AGA
                                     AAA_  A  A
GAM1681  CASP10   3'  AGATGGGGTTTCACTATGTT   53213      CG
                                AACA  GTGAAACCCCGTCT
                                ||||  ||||||||||||||
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                                TTGT  CACTTTGGGGTAGA
                                  AT
GAM1681  CASP10   3'  AGAAACAGGAAACACCGTGTT  53239         AAAC  C  C
                                AACACGGTG    CC GT TCT
                                |||||||||    || || |||
                                TTGTGCCAC    GG CA AGA
                                     AAA_  A  A
GAM1681  CASP10   3'  AGATGGGGTTTCACTATGTT   53240     CG
                                AACA  GTGAAACCCCGTCT
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGA
                                  AT
GAM1681  CASP2    3'  AGAGACAGGGTTTCACCATGTT 53285     C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  CASP2    3'  AGAGACAGGGTTTCACCATGTT 53301     C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  CASP2    3'  AGAGACAGGGTTTCACCATGTT 53319     C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  CASP2    3'  AGAGACAGGGTTTCACCATGTT 8704      C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  CASP8    3'  AGAGACAGGGTTTCACTGTGTT 8744            C
                                AACACGGTGAAACCC GTCTCT
                                |||||||||||||| ||||||
                                TTGTGTCACTTTGGG CAGAGA
                                        A
GAM1681  CASP8    3'  AGAGACAGGGTTTCACTGTGTT 54068           C
                                AACACGGTGAAACCC GTCTCT
                                |||||||||||||| ||||||
                                TTGTGTCACTTTGGG CAGAGA
                                        A
GAM1681  CASP8    3'  AGAGACAGGGTTTCACTGTGTT 54093           C
                                AACACGGTGAAACCC GTCTCT
                                |||||||||||||| ||||||
                                TTGTGTCACTTTGGG CAGAGA
                                        A
GAM1681  CASP8    3'  AGAGACAGGGTTTCACTGTGTT 54108           C
                                AACACGGTGAAACCC GTCTCT
                                |||||||||||||| ||||||
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                                TTGTGTCACTTTGGG CAGAGA
                                      A
GAM1681  CCNF     3'  AGAGACGGGATTTCACCATGTT 10066     C      C
                                AACA GGTGAAA CCCGTCTCT
                                |||| ||||||| |||||||||
                                TTGT CCACTTT GGGCAGAGA
                                  A      A
GAM1681  CDC6     3'  AGAGACAGGGTTTTACCATGTT 8816      C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCATTTTGGG CAGAGA
                                  A         A
GAM1681  CLECSF11  5'  AGAGATGGGGTTTCACTATGTT 56143      CG
                                AACA  GTGAAACCCCGTCTCT
                                ||||  ||||||||||||||||
                                TTGT  CACTTTGGGGTAGAGA
                                  AT
GAM1681  CLNS1A   3'  AGAGAGCTCCTTTCGCCATGTT 8920      C      CCCCG
                                AACA GGTGAAA     TCTCT
                                |||| |||||||     |||||
                                TTGT CCGCTTT     AGAGA
                                  A      CCTCG
GAM1681  CNGA1    5'  AGAGATGGGATTTCACCATGTT 60230      C      C
                                AACA GGTGAAA CCCGTCTCT
                                |||| ||||||| |||||||||
                                TTGT CCACTTT GGGTAGAGA
                                  A      A
GAM1681  CNN2     3'  AGAGATGGGGTTTCCCCATGTT 16451      C  T
                                AACA GG GAAACCCCGTCTCT
                                |||| || ||||||||||||||
                                TTGT CC CTTTGGGGTAGAGA
                                  A  C
GAM1681  CR1      3'  AGAGACGGGGTTTCACCATGTT 6936       C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  CRTAP    3'  AGAGACGGGGTTTTGCCATGTT 22074      C  TG
                                AACA GG  AAACCCCGTCTCT
                                |||| ||  |||||||||||||
                                TTGT CC  TTTGGGGCAGAGA
                                  A  GT
GAM1681  CTF1     3'  AGAGACGAGGTTTCGCCATGTT 9007       C        C
                                AACA GGTGAAACC CGTCTCT
                                |||| ||||||||| |||||||
                                TTGT CCGCTTTGG GCAGAGA
                                  A        A
GAM1681  CXCL16   3'  AGAGACGGGGTTTCACCATGTT 42160      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
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                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  CYP1A2   3'  AGAGACGAGGTTTCACTGTGTT 7497              C
                                AACACGGTGAAACC CGTCTCT
                                |||||||||||||| |||||||
                                TTGTGTCACTTTGG GCAGAGA
                                     A
GAM1681  CYP1A2   3'  AGAGACGGGTTTCACCATGTT  7498      C       C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A       _
GAM1681  CYP1A2   3'  AGATGGGGTTTCACCATGTT   7499      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM1681  CYP4F3   3'  AGAGGCGGGGTTTCGCCATGTT 7990      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| |||||||||||||||
                                TTGT CCGCTTTGGGGCGGAGA
                                  A
GAM1681  CYP51    3'  AGAGACGGGGGTTTCACTATGT 7608      CG       _
           T                     AACA  GTGAAACCCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT  CACTTTGGGG CAGAGA
                                  AT        G
GAM1681  DFFB     3'  AGAAACGGGGTTTCACCATGTT 88753     C          C
                                AACA GGTGAAACCCCGT TCT
                                |||| |||||||||||| |||
                                TTGT CCACTTTGGGGCA AGA
                                  A          A
GAM1681  DFFB     3'  AGAGACGGGGTTTCACCATGTT 88757     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  DHFR     3'  AGAGATGGGGTTTCACCATGTT 7637      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| |||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  DSC3     3'  AGAGACGGGGTTTCACTGTGTT 10433
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||
                                TTGTGTCACTTTGGGGCAGAGA

GAM1681  DSC3     3'  AGAGACGGGGTTTCACTGTGTT 44613
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||
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                                TTGTGTCACTTTGGGGCAGAGA

GAM1681  EHD2     3'  AGAGACGGGGTTTCACCATGTT 28213      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  EIF2S3   3'  AGAGACGGGGTTTCAGCATGTT 9204       CGG
                                AACA   TGAAACCCCGTCTCT
                                ||||   ||||||||||||||
                                TTGT   ACTTTGGGGCAGAGA
                                  ACG
GAM1681  ENDOGL1  3'  AGAGATGTGGTCTCGCCGTGT  18818          A   C
                                ACACGGTGA ACC CGTCTCT
                                ||||||||| ||| |||||||
                                TGTGCCGCT TGG GTAGAGA
                                     C   T
GAM1681  EPB72    3'  AGAGACGGGGTTTCACCATGTT 15868      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  F2RL2    3'  AGAGACGGGGTTTCACCATGTT 15892      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  F2RL3    3'  AGACGGAGTTTCACCATGTT   15488      C       C
                                AACA GGTGAAAC CCGTCT
                                |||| |||||||| ||||||
                                TTGT CCACTTTG GGCAGA
                                  A       A
GAM1681  FANCF     3'  AGAGACGGGGTTTCACCATG   42973    C
                                CA GGTGAAACCCCGTCTCT
                                || ||||||||||||||||
                                GT CCACTTTGGGGCAGAGA
                                 A
GAM1681  FCAR     3'  AGAGATGGGGTTTCACTGTGTT 56559
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||
                                TTGTGTCACTTTGGGGTAGAGA

GAM1681  FCAR     3'  AGAGATGGGGTTTCACTGTGTT 56589
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||
                                TTGTGTCACTTTGGGGTAGAGA

GAM1681  FCAR     3'  AGAGATGGGGTTTCACTGTGTT 56601
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||
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                                TTGTGTCACTTTGGGGTAGAGA

GAM1681  FCAR     3'  AGAGATGGGGTTTCACTGTGTT 56613
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||
                                TTGTGTCACTTTGGGGTAGAGA

GAM1681  FCAR     3'  AGACAGGGTTTCACCATGTT   56628      C         C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A         A
GAM1681  FCAR     3'  AGAGATGGGGTTTCACTGTGTT 10582
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||
                                TTGTGTCACTTTGGGGTAGAGA

GAM1681  FCGR2A   3'  AGAGACAGGGTTTCGCAATGTT 80024      CG        C
                                AACA  GTGAAACCC GTCTCT
                                ||||  ||||||||| ||||||
                                TTGT  CGCTTTGGG CAGAGA
                                  AA        A
GAM1681  FCRH1    3'  TAGAGACAAGATTTCACCGT   54732         CCCC     ___
                                ACGGTGAAA    GTCTCT   A
                                |||||||||    ||||||   |
                                TGCCACTTT    CAGAGA   T
                                     AGAA     ___
GAM1681  FEZ1     3'  AGAGATGGGAGTTTCACCATGT 42864      C       _
           T                     AACA GGTGAAAC CCCGTCTCT
                                ||||| |||||||| |||||||||
                                TTGT CCACTTTG GGGTAGAGA
                                  A       A
GAM1681  FGF5     3'  AGAGACGGGGTTTCACCATGTT 16757      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  FGF5     3'  AGAGACGGGGTTTCACCATGTT 53650      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  FSHPRH1  5'  AGAGACATTGGTCTCACTGTGT 23064          A   CC_
           T                     AACACGGTGA ACC   GTCTCT
                                |||||||||| |||   ||||||
                                TTGTGTCACT TGG   CAGAGA
                                     C   TTA
GAM1681  FUT1     3'  AGAGACAGGGTTTCACCATGTT 5581       C         C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
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                                TTGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  FUT1     3'  AGAGACGGGGTTTCATCGTGTT 5582
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||
                                TTGTGCTACTTTGGGGCAGAGA

GAM1681  G6PC     3'  AGAGATGGGATTTCATCATGTT 5651       C       C
                                AACA GGTGAAA CCCGTCTCT
                                |||| ||||||| |||||||||
                                TTGT CTACTTT GGGTAGAGA
                                  A      A
GAM1681  GHR      3'  AGAGACGGGGTTTCACCATGTT 5691       C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  GM2A     3'  AGAGATGGGGTTTCACCATGTT 68370      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  GNE      3'  GGACAGGGTTTCACCATGTT   19671      C         C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGG
                                  A         A
GAM1681  GPR4     3'  AGACAGGGTCTCACTGTGTT   60573          A    C
                                AACACGGTGA ACCC GTCT
                                |||||||||| |||| ||||
                                TTGTGTCACT TGGG CAGA
                                     C    A
GAM1681  GPR81    3'  AGAGACAGGGTTTTGCCATGTT 51736      C  TG     C
                                AACA GG  AAACCC GTCTCT
                                |||| ||  |||||| ||||||
                                TTGT CC  TTTGGG CAGAGA
                                  A  GT      A
GAM1681  GRM7     5'  AGAGATTGGGTTTCACCATGTT 7779       C         C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG TAGAGA
                                  A         T
GAM1681  HCS      3'  AGATGGTGTTTCACCATGTT   38963      C       C
                                AACA GGTGAAAC CCGTCT
                                |||| |||||||| ||||||
                                TTGT CCACTTTG GGTAGA
                                  A       T
GAM1681  HLCS     5'  AGAGGCGGGGGTTTCACCATG  6404     C         _
                                CA GGTGAAACCCC GTCTCT
                                || |||||||||| ||||||
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                                GT CCACTTTGGGG CGGAGA
                                 A          G
GAM1681  HTR1D    3'  AGACGGGGTTTCATCATGTT   7833       C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||||
                                TTGT CTACTTTGGGGCAGA
                                  A
GAM1681  HTR1E    5'  AGACGGGATTTCACCATGTT   7854       C      C
                                AACA GGTGAAA CCCGTCT
                                |||| ||||||| |||||||
                                TTGT CCACTTT GGGCAGA
                                  A      A
GAM1681  HUNK     3'  AGAAATGGGGTTTCGCCATGTT 28173      C           C
                                AACA GGTGAAACCCCGT TCT
                                |||| |||||||||||| |||
                                TTGT CCGCTTTGGGGTA AGA
                                  A           A
GAM1681  HUS1     3'  AGAGACAGGGTCTCACTGTGTT 92736          A    C
                                AACACGGTGA ACCC GTCTCT
                                |||||||||| |||| ||||||
                                TTGTGTCACT TGGG CAGAGA
                                     C    A
GAM1681  HYAL4    5'  AGAGATGGGGTTTCACCGTGTT 25361
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||
                                TTGTGCCACTTTGGGGTAGAGA

GAM1681  IGF1     3'  AGAGACGGGGTTTTACCATGTT 7059       C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCATTTTGGGGCAGAGA
                                  A
GAM1681  IL11     3'  AGAGACAGGGTTTCACCATGTT 7177       C         C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  IMPA2    5'  AGAGATGGGGCTTCGCCATG   96940    C     A
                                CA GGTGAA CCCCGTCTCT
                                || |||||| ||||||||||
                                GT CCGCTT GGGGTAGAGA
                                 A     C
GAM1681  INMT     3'  AGATATGGGGTTTCACCGTGTT 23206              C
                                AACACGGTGAAACCCCGT TCT
                                |||||||||||||||| |||
                                TTGTGCCACTTTGGGGTA AGA
                                        T
GAM1681  JAK3     3'  AGAGATGAGGTTTCACCATG   5822     C        C
                                CA GGTGAAACC CGTCTCT
                                || |||||||| |||||||
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                                GT CCACTTTGG GTAGAGA
                                 A        A
GAM1681  JRK      3'  AGAGACAGGGTCTCACTGTGTT 87815          A    C
                                AACACGGTGA ACCC GTCTCT
                                |||||||||| ||||| ||||||
                                TTGTGTCACT TGGG CAGAGA
                                     C    A
GAM1681  LLGL1    3'  AGAGATGGGGTTTCACCATGTT 67411      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  LNK      3'  AGAGACAGGGTTTCACCATGTT 19631      C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A        A
GAM1681  LTB4R    5'  AGAGACGGGGTTTCACCATGTT 7459       C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  LYZ      3'  AGAGACAGGGTTTCACCGTGTT 5891             C
                                AACACGGTGAAACCC GTCTCT
                                |||||||||||||| ||||||
                                TTGTGCCACTTTGGG CAGAGA
                                      A
GAM1681  MAK      3'  AGAGACAGGGTTTCACCATGTT 20940      C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A        A
GAM1681  MDM2     3'  AGAGACAGGGTTTCACCGTGTT 23456            C
                                AACACGGTGAAACCC GTCTCT
                                |||||||||||||| ||||||
                                TTGTGCCACTTTGGG CAGAGA
                                      A
GAM1681  MDM2     3'  AGAGACAGGGTTTCACCGTGTT 23469            C
                                AACACGGTGAAACCC GTCTCT
                                |||||||||||||| ||||||
                                TTGTGCCACTTTGGG CAGAGA
                                      A
GAM1681  MDM2     3'  AGAGACAGGGTTTCACCGTGTT 23482            C
                                AACACGGTGAAACCC GTCTCT
                                |||||||||||||| ||||||
                                TTGTGCCACTTTGGG CAGAGA
                                      A
GAM1681  MDM2     3'  AGAGACAGGGTTTCACCGTGTT 23495            C
                                AACACGGTGAAACCC GTCTCT
                                |||||||||||||| ||||||
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                                TTGTGCCACTTTGGG CAGAGA
                                      A
GAM1681  MDM2     3'  AGAGACAGGGTTTCACCGTGTT 11490            C
                                AACACGGTGAAACCC GTCTCT
                                |||||||||||||| ||||||
                                TTGTGCCACTTTGGG CAGAGA
                                      A
GAM1681  MEF2A    5'  AGAGATGGAGTTTCACCATGTT 19987     C       C
                                AACA GGTGAAAC CCGTCTCT
                                |||| |||||||| ||||||||
                                TTGT CCACTTTG GGTAGAGA
                                  A       A
GAM1681  MEFV     3'  AGACATGAGGTTTCATCATGTT 5923      C       C   C
                                AACA GGTGAAACC CGT TCT
                                |||| ||||||||| ||| |||
                                TTGT CTACTTTGG GTA AGA
                                  A       A   C
GAM1681  MEFV     3'  AGAGACGGGGGTTTCACCATGT 5925      C         _
                T                AACA GGTGAAACCCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGGG CAGAGA
                                  A         G
GAM1681  MHC2TA   3'  AGAGACAGGGTTTTGCCGTGTT 5967        TG     C
                                AACACGG  AAACCC GTCTCT
                                |||||||  |||||| ||||||
                                TTGTGCC  TTTGGG CAGAGA
                                    GT     A
GAM1681  MLANA    3'  AGAGACGGGGTTTCTCCATGTT 19758     C  T
                                AACA GG GAAACCCCGTCTCT
                                |||| || ||||||||||||||
                                TTGT CC CTTTGGGGCAGAGA
                                  A  T
GAM1681  MPL      3'  AGAGACAGGGTTTTGCCATGTT 19339     C  TG     C
                                AACA GG  AAACCC GTCTCT
                                |||| ||  |||||| ||||||
                                TTGT CC  TTTGGG CAGAGA
                                  A  GT     A
GAM1681  MRPL49   3'  AGAGATGGGGTTTCACCATGTT 70156     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  MTR      3'  AGAGACAGGATTTCACTGTGTT 6011           C  C
                                AACACGGTGAAA CC GTCTCT
                                |||||||||||| || ||||||
                                TTGTGTCACTTT GG CAGAGA
                                      A  A
GAM1681  NCOA6    5'  AGAGGCGGGGTTTCGCCATGTT 26823     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
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                                TTGT CCGCTTTGGGGCGGAGA
                                  A
GAM1681  NCOA6    5'  ATGGGGTTTCATCATGTT    26827      C
                                AACA GGTGAAACCCCGT
                                |||| ||||||||||||
                                TTGT CTACTTTGGGGTA
                                  A
GAM1681  NDRG3    3'  AGAGATGGAGTTTCACCATGTT 50114      C       C
                                AACA GGTGAAAC CCGTCTCT
                                |||| |||||||| ||||||||
                                TTGT CCACTTTG GGTAGAGA
                                  A       A
GAM1681  NQO1     3'  AGAGACGGCGTTTCACCATGTT 8042       C       C
                                AACA GGTGAAAC CCGTCTCT
                                |||| |||||||| ||||||||
                                TTGT CCACTTTG GGCAGAGA
                                  A       C
GAM1681  PCDHA9   3'  AGAGATGGGGTTTCACCGTGTT 26606
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||
                                TTGTGCCACTTTGGGGTAGAGA

GAM1681  PCDHA9   3'  AGAGATGGGGTTTCATCATGTT 26607      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CTACTTTGGGGTAGAGA
                                  A
GAM1681  PER2     3'  AGAGACAGGGTTTCACCATGTT 43342      C       C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  PIGR     3'  AGACAAAGTCTCACTGTGT    72983          A  CCC
                                ACACGGTGA AC   GTCT
                                ||||||||| ||   ||||
                                TGTGTCACT TG   CAGA
                                     C  AAA
GAM1681  PIGR     3'  AGAGACAGGGTTTCACCGTGTT 72987              C
                                AACACGGTGAAACCC GTCTCT
                                |||||||||||||| ||||||
                                TTGTGCCACTTTGGG CAGAGA
                                          A
GAM1681  PIGR     3'  AGAGACAGGGTTTCGCCATGTT 72988      C       C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCGCTTTGGG CAGAGA
                                  A         A
GAM1681  PIK3C2B  3'  AGAGACGGGGTTTCACCATGTT 12090      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
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                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  PIK3CD   3'  AGAGACGGGGGTTTCACCATGT 18484      C          _
                T                  AACA GGTGAAACCCC GTCTCT
                                   |||| |||||||||| ||||||
                                   TTGT CCACTTTGGGG CAGAGA
                                     A          G
GAM1681  POU2AF1  3'  AGAGACGGGGTTTCACCATGTT 21731      C
                                   AACA GGTGAAACCCCGTCTCT
                                   |||| ||||||||||||||||
                                   TTGT CCACTTTGGGGCAGAGA
                                     A
GAM1681  PRKR     3'  AGACAGGGTTTCACCATGTT   12338      C         C
                                   AACA GGTGAAACCC GTCT
                                   |||| |||||||||| ||||
                                   TTGT CCACTTTGGG CAGA
                                     A         A
GAM1681  PRKWNK3  3'  GGATGGGGTTTCACTATGTT   62234      CG
                                   AACA  GTGAAACCCCGTCT
                                   ||||  ||||||||||||||
                                   TTGT  CACTTTGGGGTAGG
                                     AT
GAM1681  PTGES    3'  AGAGACGGGTTCACCATGTT   18055      C     AC
                                   AACA GGTGAA  CCCGTCTCT
                                   |||| ||||||  |||||||||
                                   TTGT CCACTT  GGGCAGAGA
                                     A     __
GAM1681  PTGIS    3'  AGAGACGGGGTTTCCCCATGTT 8190       C  T
                                   AACA GG GAAACCCCGTCTCT
                                   |||| || ||||||||||||||
                                   TTGT CC CTTTGGGGCAGAGA
                                     A  C
GAM1681  PTGIS    3'  AGAGATGGGATTTCACCGT    8191          C
                                   ACGGTGAAA CCCGTCTCT
                                   |||||||||  |||||||||
                                   TGCCACTTT GGGTAGAGA
                                        A
GAM1681  RAB36    3'  AGAGAGAGGTTTCACCATGTT  18149      C         CCG
                                   AACA GGTGAAACC   TCTCT
                                   |||| |||||||||   |||||
                                   TTGT CCACTTTGG   AGAGA
                                     A         AG_
GAM1681  RAB36    3'  AGAGATGGGGTTTCTCCATGTT 18151      C  T
                                   AACA GG GAAACCCCGTCTCT
                                   |||| || ||||||||||||||
                                   TTGT CC CTTTGGGGTAGAGA
                                     A  T
GAM1681  RABL2A   3'  AGAGACGGGGTTTCACCATGTT 26404      C
                                   AACA GGTGAAACCCCGTCTCT
                                   |||| ||||||||||||||||
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                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  RABL2B   3'  AGAGACGGGGTTTCACCATGTT 23972      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  RBBP9    3'  AGAGACAGGGTTTCACCATGTT 70680      C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  RGS9     5'  AGACGGGGTTTTGTCATGTT   15168      C  TG
                                AACA GG  AAACCCCGTCT
                                |||| ||  ||||||||||
                                TTGT CT  TTTGGGGCAGA
                                  A  GT
GAM1681  RHD      3'  AGATGGGGTTTCACCATGTT   32806      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM1681  RHD      3'  AGATGGGGTTTCACCATGTT   33131      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM1681  RPH3AL   3'  AGAGATGGGGTTTCTCCATGTT 23726      C  T
                                AACA GG GAAACCCCGTCTCT
                                |||| || ||||||||||||||
                                TTGT CC CTTTGGGGTAGAGA
                                  A  T
GAM1681  RPP30    3'  AGAGACGGGGTTTCACCGTGTT 22191
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGAGA

GAM1681  SAS      3'  AGAGACAGGGTTTCACCATGTT 21095      C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  SCML2    3'  AGAGATGGGGTTTCTCCATGTT 21419      C  T
                                AACA GG GAAACCCCGTCTCT
                                |||| || ||||||||||||||
                                TTGT CC CTTTGGGGTAGAGA
                                  A  T
GAM1681  SERPINB9 3'  AGAGACGGGGTTTCACCGTGTT 16008
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||
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                                TTGTGCCACTTTGGGGCAGAGA

GAM1681  SH3BP2   3'  AGAGACGGGATTTTATCATGTT 13046      C      C
                                AACA GGTGAAA CCCGTCTCT
                                |||| ||||||| |||||||||
                                TTGT CTATTTT GGGCAGAGA
                                  A      A
GAM1681  SH3GL3   5'  AGAGATGGGTTTCACCATGTT  13101      C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG TAGAGA
                                  A        _
GAM1681  SHOX     3'  AGAGACGGCGTTTCACCGTGTT 6561             C
                                AACACGGTGAAAC CCGTCTCT
                                |||||||||||| ||||||||
                                TTGTGCCACTTTG GGCAGAGA
                                       C
GAM1681  SHOX     3'  AGAGATGGGGTTTGACCATGTT 23513      C   G
                                AACA GGT AAACCCCGTCTCT
                                |||| ||| ||||||||||||
                                TTGT CCA TTTGGGGTAGAGA
                                  A   G
GAM1681  SIGLEC11 3'  AGAGACAGGGTTTTGCCATGTT 54647      C  TG     C
                                AACA GG  AAACCC GTCTCT
                                |||| ||  |||||| ||||||
                                TTGT CC  TTTGGG CAGAGA
                                  A  GT      A
GAM1681  SIL      5'  AGACGGGGTTTCACCATGTT   13149      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM1681  SLC15A1  3'  AGAGATGGGGTTTCACCATGTT 18633      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  SLC3A2   5'  AGAGACGGGGTCTGACTGTGTT 11517         GAA
                                AACACGGT   ACCCCGTCTCT
                                ||||||||   ||||||||||
                                TTGTGTCA   TGGGGCAGAGA
                                    GTC
GAM1681  SLC3A2   5'  AGAGTTGGGGTCTCACTGTGTT 11518          A     T
                                AACACGGTGA ACCCCG CTCT
                                |||||||||| |||||| ||||
                                TTGTGTCACT TGGGGT GAGA
                                      C     T
GAM1681  SMAC     5'  AGAGATGGGGTTTCACCATGTT 58011      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
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                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  SNAP23   3'  AGAGACAGGGTTTCACCATGT  56334     C        C
                                ACA GGTGAAACCC GTCTCT
                                ||| |||||||||| ||||||
                                TGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  SNAP23   3'  AGAGACAGGGTTTCACCATGT  15135     C        C
                                ACA GGTGAAACCC GTCTCT
                                ||| |||||||||| ||||||
                                TGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  SNX15    3'  AGGGACGGGGTTACACCATGTT 74114     C    A
                                AACA GGTG AACCCCGTCTCT
                                |||| |||| ||||||||||||
                                TTGT CCAC TTGGGGCAGGGA
                                  A    A
GAM1681  SPN      3'  AGAGATGGGGTTTCACCATGTT 13364     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  SULT2B1  5'  AGGGGCGGGGTTTCACCATGTT 17221     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCGGGGA
                                  A
GAM1681  TAPBP    3'  AGAGACGGGGTTTCACCATGTT 13548     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  TAPBP    3'  AGAGACGGGGTTTCACCGTGTT 13549
                                AACACGGTGAAACCCCGTCTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGAGA

GAM1681  TAPBP    3'  AGAGACGGGGTTTCACCGTGTT 13550
                                AACACGGTGAAACCCCGTCTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGAGA

GAM1681  TAT      3'  AGAGACAGGGTTTCACCATGTT 6249      C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  TBXA2R   3'  AGAGACGGGGTTTCACCGTGTT 8342
                                AACACGGTGAAACCCCGTCTCT
                                ||||||||||||||||||||
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                                TTGTGCCACTTTGGGGCAGAGA

GAM1681 TDE1     5' GCTGGCAGTTACCACCGTGTT 23317        A_  __ C
                                AACACGGTG AAC CC GT
                                ||||||||| ||| || ||
                                TTGTGCCAC TTG GG CG
                                    CA  AC  T
GAM1681 TDGF1    3' AGAGATGGGGGTTTCACC    13650         _
                                GGTGAAACCCC GTCTCT
                                |||||||||| ||||||
                                CCACTTTGGGG TAGAGA
                                     G
GAM1681 TEM7     3' AGACAGGGTCTCACTGTGT   40241        A   C
                                ACACGGTGA ACCC GTCT
                                ||||||||| |||| ||||
                                TGTGTCACT TGGG CAGA
                                    C   A
GAM1681 TERF1    3' AGAGGCGGGGTTTCACCATG  34387   C
                                CA GGTGAAACCCCGTCTCT
                                || ||||||||||||||||
                                GT CCACTTTGGGGCGGAGA
                                 A
GAM1681 TERF2    3' AGAGACGGGGTTTCACCGTGTT 20144
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGAGA

GAM1681 TIM3     3' AGAGACAGGGTTTCACCATGTT 52351     C       C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A       A
GAM1681 TMPRSS3  3' AGAGACAGGGTTTCACCATGTT 44014     C       C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A       A
GAM1681 TMPRSS3  3' AGAGACAGGGTTTCACCATGTT 51511     C       C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A       A
GAM1681 TMPRSS3  3' AGAGACAGGGTTTCACCATGTT 51539     C       C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A       A
GAM1681 TNFRSF10B 3' AGAGACGGGGTTTCACCATGTT 15214    C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
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                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  TP53    3'  AGAGATGGGGTCTCACAGTGTT 6791       G   A
                                AACAC GTGA ACCCCGTCTCT
                                ||||| |||| ||||||||||
                                TTGTG CACT TGGGGTAGAGA
                                  A   C
GAM1681  TPMT    3'  AGACGGGGTTTCACCATGTT  6301      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM1681  TRAF5   3'  AGAGACGGAGTTTTGCCATGTT 17266     C  TG   C
                                AACA GG  AAAC CCGTCTCT
                                |||| ||  |||| ||||||||
                                TTGT CC  TTTG GGCAGAGA
                                  A  GT   A
GAM1681  TRPM6   3'  AGAGATGGGGTTTCACCATGTT 35022     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  TRPV1   3'  AGAGACGGGGTTTCACCATGTT 38685     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  TRPV1   3'  AGATATGGGGTTTCGCCATGTT 38686     C          C
                                AACA GGTGAAACCCCGT TCT
                                |||| |||||||||||| |||
                                TTGT CCGCTTTGGGGTA AGA
                                  A          T
GAM1681  TRPV1   3'  AGAGACGGGGTTTCACCATGTT 55655     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  TRPV1   3'  AGATATGGGGTTTCGCCATGTT 55656     C          C
                                AACA GGTGAAACCCCGT TCT
                                |||| |||||||||||| |||
                                TTGT CCGCTTTGGGGTA AGA
                                  A          T
GAM1681  TRPV1   3'  AGAGACGGGGTTTCACCATGTT 55701     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  TRPV1   3'  AGATATGGGGTTTCGCCATGTT 55702     C          C
                                AACA GGTGAAACCCCGT TCT
                                |||| |||||||||||| |||
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                                TTGT CCGCTTTGGGGTA AGA
                                  A           T
GAM1681  TRPV1    3'  AGAGACGGGGTTTCACCATGTT 55732      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  TRPV1    3'  AGATATGGGGTTTCGCCATGTT 55733      C           C
                                AACA GGTGAAACCCCGT TCT
                                |||| |||||||||||| |||
                                TTGT CCGCTTTGGGGTA AGA
                                  A           T
GAM1681  UGDH     3'  AGAGACAGGGTTTCACCATGT  13991     C         C
                                ACA GGTGAAACCC GTCTCT
                                ||| |||||||||| ||||||
                                TGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  VENTX2   3'  AGAAATGGGGTTTCACCATGTT 27851      C           C
                                AACA GGTGAAACCCCGT TCT
                                |||| |||||||||||| |||
                                TTGT CCACTTTGGGGTA AGA
                                  A           A
GAM1681  VHL      3'  AGACGGGGTTTCACCATGTT   6826       C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM1681  VHL      3'  AGAGACAGTGTTTCGCCATGTT 6829       C       CCC
                                AACA GGTGAAAC   GTCTCT
                                |||| ||||||||   ||||||
                                TTGT CCGCTTTG   CAGAGA
                                  A       TGA
GAM1681  VIPR2    3'  AGAGACAGGGTTTCACCATGTT 14057      C         C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  WBSCR5   5'  AGAGATGGAATTTCACCGTGTT 42106           CC
                                AACACGGTGAAA  CCGTCTCT
                                ||||||||||||  ||||||||
                                TTGTGCCACTTT  GGTAGAGA
                                      AA
GAM1681  WBSCR5   5'  AGAGATGGAATTTCACCGTGTT 51626           CC
                                AACACGGTGAAA  CCGTCTCT
                                ||||||||||||  ||||||||
                                TTGTGCCACTTT  GGTAGAGA
                                      AA
GAM1681  XRCC2    3'  AGAGACGGGGTTTCACCATGTT 19491      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
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                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  YES1     3'  AGAGACGCAGTTTCACCGTGTT 19527           CC
                                AACACGGTGAAAC  CGTCTCT
                                |||||||||||||  |||||||
                                TTGTGCCACTTTG  GCAGAGA
                                      AC
GAM1681  ZNF157   3'  AGACGGGTTTCACCATGTT   14322     C       C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A       _
GAM1681  ZNF264   3'  AGAGACGGGGTTTCACCATGTT 14193     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  ZNF74    5'  AGAGACGGGGTTTTGCCATGTT 14254     C  TG
                                AACA GG  AAACCCCGTCTCT
                                |||| ||  ||||||||||||
                                TTGT CC  TTTGGGGCAGAGA
                                  A  GT
GAM1681  AAK1     3'  AGAGATGGGGTTTCTCCATGTT 30513     C  T
                                AACA GG GAAACCCCGTCTCT
                                |||| || ||||||||||||||
                                TTGT CC CTTTGGGGTAGAGA
                                  A  T
GAM1681  ANKT     3'  AGAGACAGGGTCTCACTGTGTT 33456         A   C
                                AACACGGTGA ACCC GTCTCT
                                |||||||||| |||| ||||||
                                TTGTGTCACT TGGG CAGAGA
                                     C   A
GAM1681  AP3S2    3'  AGAGACAGGGTTTCACCATGTT 20642     C       C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A       A
GAM1681  APOL2    3'  AGACGGGGTTTCACTGTGTT   48785
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGTCACTTTGGGGCAGA

GAM1681  ARHF     3'  AGAGACAGGGTTTCACCATGTT 39261     C       C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A       A
GAM1681  ARHGAP11A 3'  AGAGACGGTTTCACCGTGTT  29441           CC
                                AACACGGTGAAACC  GTCTCT
                                ||||||||||||||  ||||||
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                                TTGTGCCACTTTGG  CAGAGA
                                          __
GAM1681  ARHGAP5   5'  AGAGATGGGGTTTCTCCATGTT 77594      C  T
                                AACA GG GAAACCCCGTCTCT
                                |||| || ||||||||||||||
                                TTGT CC CTTTGGGGTAGAGA
                                  A  T
GAM1681  ASB16     3'  AGACGGGGTCTCGCCATGTT   55969      C     A
                                AACA GGTGA ACCCCGTCT
                                |||| ||||| |||||||||
                                TTGT CCGCT TGGGGCAGA
                                  A     C
GAM1681  ASE-1     3'  AGAGACAGGGGTTTCACC     24965           _
                                GGTGAAACCCC GTCTCT
                                |||||||||| ||||||
                                CCACTTTGGGG CAGAGA
                                       A
GAM1681  ATP1B4    3'  AGACAGGGTTTCACCATGTT   24830      C         C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A         A
GAM1681  BA108L7.2 3'  AGAGATGGGGGTTTCACCATGT 49061      C         _
   T                             AACA GGTGAAACCCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGGG TAGAGA
                                  A         G
GAM1681  BAGE      3'  AGATGGAGTTTCACTGTGT    8637            C
                                ACACGGTGAAAC CCGTCT
                                |||||||||||| ||||||
                                TGTGTCACTTTG GGTAGA
                                       A
GAM1681  BNIP-S    3'  AGAGACGGGGTTTCACCATGTT 57086      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  BRAG      3'  AGAGATGGGGTCTCGCCGTGTT 30094          A
                                AACACGGTGA ACCCCGTCTCT
                                |||||||||| ||||||||||
                                TTGTGCCGCT TGGGGTAGAGA
                                     C
GAM1681  C11orf17  3'  AGAGACGGGGTTTAACCATGTT 40575      C   G
                                AACA GGT AAACCCCGTCTCT
                                |||| ||| ||||||||||||
                                TTGT CCA TTTGGGGCAGAGA
                                  A   A
GAM1681  C13orf1   3'  AGAGATGGGGTTTCACCATGTT 40348      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
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                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  C1orf24   3'  AGATGGGTTTTCACCATGTT   54779      C      C
                                AACA GGTGAAA CCCGTCT
                                |||| ||||||| |||||||
                                TTGT CCACTTT GGGTAGA
                                  A      T
GAM1681  C20orf142 3'  AGAGATGGGGTTTCTCCATGTT 75269      C  T
                                AACA GG GAAACCCCGTCTCT
                                |||| || ||||||||||||||
                                TTGT CC CTTTGGGGTAGAGA
                                  A  T
GAM1681  C6orf5    3'  AGAGACAGGGTTTCATATTG   31968    CG        C
                                CA  GTGAAACCC GTCTCT
                                ||  ||||||||| ||||||
                                GT  TACTTTGGG CAGAGA
                                 TA        A
GAM1681  C6orf5    3'  AGAGACAGGGTTTTGCCATGTT 31969      C  TG     C
                                AACA GG  AAACCC GTCTCT
                                |||| ||  |||||| ||||||
                                TTGT CC  TTTGGG CAGAGA
                                  A  GT     A
GAM1681  C9orf14   5'  ACGAGGTTTCACCCTGTT    87952      C        C
                                AACA GGTGAAACC CGT
                                |||| ||||||||| |||
                                TTGT CCACTTTGG GCA
                                  C        A
GAM1681  C9orf9    3'  AGAGACAGCGTTTCACCATGTT 39009      C       CCC
                                AACA GGTGAAAC   GTCTCT
                                |||| ||||||||   ||||||
                                TTGT CCACTTTG   CAGAGA
                                  A       CGA
GAM1681  CCRN4L    3'  AGAGACGGGGTTTCACCGTGTT 25066
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGAGA

GAM1681  CDC14B    3'  AGAGACGGAAGATGCCGTGTT  53985        GAAACC
                                AACACGGT     CCGTCTCT
                                ||||||||     ||||||||
                                TTGTGCCG     GGCAGAGA
                                     TAGAA_
GAM1681  CDC14B    3'  AGAGACAGGGTTTCACCATGTT 53999      C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A        A
GAM1681  CEACAM8   3'  AGAGACGGGGTTTCACTGTG   10176
                                CACGGTGAAACCCCGTCTCT
                                ||||||||||||||||||||
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                                GTGTCACTTTGGGGCAGAGA

GAM1681  CENPH    3'  AGAGACGGGGTTTCACCGTGTT 43564
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGAGA

GAM1681  CGI-96   3'  AGGGTGGATTTCATCGTGT   32290          CC   T
                                ACACGGTGAAA  CCG CTCT
                                ||||||||||  ||| ||||
                                TGTGCTACTTT  GGT GGGA
                                      A_  _
GAM1681  CHRAC1   3'  AGAGACGGGGTTCACCATGTT  34331     C     A
                                AACA GGTGAA CCCCGTCTCT
                                |||| |||||| ||||||||||
                                TTGT CCACTT GGGGCAGAGA
                                  A     _
GAM1681  CHSY1    3'  AGAGACGGGGTTTCACCATG   30561    C
                                CA GGTGAAACCCCGTCTCT
                                || ||||||||||||||||
                                GT CCACTTTGGGGCAGAGA
                                 A
GAM1681  CIP29    3'  AGAGACGGGGTTTCACCATGTT 51370      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  COLEC12  3'  AGAGAGGGGTTTCACAGTGTT  48604      G        G
                                AACAC GTGAAACCCC TCTCT
                                ||||| |||||||||| |||||
                                TTGTG CACTTTGGGG AGAGA
                                   A        _
GAM1681  CPSF2    3'  AGAGACAGGGTTTCACCATGTT 62260      C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A        A
GAM1681  CPSF2    3'  AGAGACGGGGTTTCTCCATGTT 62261      C  T
                                AACA GG GAAACCCCGTCTCT
                                |||| || ||||||||||||||
                                TTGT CC CTTTGGGGCAGAGA
                                  A  T
GAM1681  DBR1     3'  GACAGGGTTTCACCGTGTT   33064            C
                                AACACGGTGAAACCC GTC
                                ||||||||||||||| |||
                                TTGTGCCACTTTGGG CAG
                                      A
GAM1681  DCOHM    3'  AGAGATGGGGTTTCGCCATGTT 50506      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
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                                TTGT CCGCTTTGGGGTAGAGA
                                  A
GAM1681  DKFZp434A2417 3'  AGAGACGGGGTTTCTCCATGTT 66673      C  T
                                AACA GG GAAACCCCGTCTCT
                                |||| || ||||||||||||||
                                TTGT CC CTTTGGGGCAGAGA
                                  A  T
GAM1681  DKFZP434C212 3'   AGAAACGGGGTTTCACCATGTT 69480      C           C
                                AACA GGTGAAACCCCGT TCT
                                |||| |||||||||||| |||
                                TTGT CCACTTTGGGGCA AGA
                                  A           A
GAM1681  DKFZP434D146 3'   AGAGACAGGGTTTCATCATGTT 32131      C         C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CTACTTTGGG CAGAGA
                                  A         A
GAM1681  DKFZP434F0318 3'  AGAGACAGGGTTTCGCCATGTT 48743      C         C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCGCTTTGGG CAGAGA
                                  A         A
GAM1681  DKFZp434F1719 3'  AGAGATGGGATTTCGCCATGTT 51009      C      C
                                AACA GGTGAAA CCCGTCTCT
                                |||| ||||||| |||||||||
                                TTGT CCGCTTT GGGTAGAGA
                                  A      A
GAM1681  DKFZp547H025 3'   AGAGATGAGGTTTCACCATGTT 39766      C        C
                                AACA GGTGAAACC CGTCTCT
                                |||| ||||||||| |||||||
                                TTGT CCACTTTGG GTAGAGA
                                  A        A
GAM1681  DKFZP564O0423 3'  AGAGATGGGGTCTCACTATGTT 93339      CG    A
                                AACA  GTGA ACCCCGTCTCT
                                ||||  |||| ||||||||||
                                TTGT  CACT TGGGGTAGAGA
                                  AT    C
GAM1681  DKFZP586A0522 3'  AGACAGGGTCTCACTGTGTT   26725          A    C
                                AACACGGTGA ACCC GTCT
                                |||||||||| |||| ||||
                                TTGTGTCACT TGGG CAGA
                                      C    A
GAM1681  DKFZp761J139 5'   AGAGATGGGGTTTGACCATGTT 51096      C   G
                                AACA GGT AAACCCCGTCTCT
                                |||| ||| ||||||||||||
                                TTGT CCA TTTGGGGTAGAGA
                                  A   G
GAM1681  DKFZp761N1114 3'  AGAGACGGGATTTCACCGTGTT 79774            C
                                AACACGGTGAAA CCCGTCTCT
                                |||||||||||| |||||||||
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                                  TTGTGCCACTTT GGGCAGAGA
                                        A
GAM1681  DKFZp761O0113 5'  AGACGGGGTTTCTCCATGTT   37886      C  T
                                  AACA GG GAAACCCCGTCT
                                  |||| || ||||||||||||
                                  TTGT CC CTTTGGGGCAGA
                                    A  T
GAM1681  DKFZp762P2111 3'  AGAGACAGGGTTTCATCATGTT 87622      C         C
                                  AACA GGTGAAACCC GTCTCT
                                  |||| |||||||||| ||||||
                                  TTGT CTACTTTGGG CAGAGA
                                    A         A
GAM1681  DSCR6     3'  AGAGACTCGGTTTCACCATGTT 39057      C        CC
                                  AACA GGTGAAACC  GTCTCT
                                  |||| |||||||||  ||||||
                                  TTGT CCACTTTGG  CAGAGA
                                    A        CT
GAM1681  EREG      3'  AGAGGCGGGGTTTCACCATGTT 9299       C
                                  AACA GGTGAAACCCCGTCTCT
                                  |||| ||||||||||||||||
                                  TTGT CCACTTTGGGGCGGAGA
                                    A
GAM1681  ERO1L     3'  AGAGACAAGGTTTTGCTGTGTT 28154        TG     CC
                                  AACACGG  AAACC  GTCTCT
                                  |||||||  |||||  ||||||
                                  TTGTGTC  TTTGG  CAGAGA
                                      GT     AA
GAM1681  EVI5      3'  AGAGACAGGTGTCTCACTGTGT 20193          A  _  C
              T                    AACACGGTGA AC CC GTCTCT
                                  |||||||||| || || ||||||
                                  TTGTGTCACT TG GG CAGAGA
                                        C  T  A
GAM1681  EVI5      3'  AGAGATGGGGTTTCACCATGTT 20194      C
                                  AACA GGTGAAACCCCGTCTCT
                                  |||| ||||||||||||||||
                                  TTGT CCACTTTGGGGTAGAGA
                                    A
GAM1681  FBP17     3'  AGAGACAGGGTTTCACCGTGTT 73143             C
                                  AACACGGTGAAACCC GTCTCT
                                  |||||||||||||| ||||||
                                  TTGTGCCACTTTGGG CAGAGA
                                        A
GAM1681  FEM-2     3'  AGAGTGAAGTTTCACCATGT   28306     C       CC  T
                                  ACA GGTGAAAC  CG CTCT
                                  ||| ||||||||  || ||||
                                  TGT CCACTTTG  GT GAGA
                                    A       AA  _
GAM1681  FER1L4    3'  AGAGACAGGGTTTCACCATGTT 48110      C         C
                                  AACA GGTGAAACCC GTCTCT
                                  |||| |||||||||| ||||||
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                                TTGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  FKBP9    3'  AGAGACGGGGTTTCACCGTGTT 95712
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGAGA

GAM1681  FLJ00060 5'  AGAGATGGAATTTCACCATGTT 61732      C       CC
                                AACA GGTGAAA  CCGTCTCT
                                |||| |||||||  ||||||||
                                TTGT CCACTTT  GGTAGAGA
                                  A      AA
GAM1681  FLJ10298 3'  AGAGACGGGGTTTCACCATGTT 36453      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  FLJ10346 5'  AGAGGCAGGGTTTCACCATGTT 36519      C         C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CGGAGA
                                  A         A
GAM1681  FLJ10535 3'  AGAGATGGGGTTTCACCATGTT 36734      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  FLJ10560 3'  AGAGACGGGGTTTCACCGTGTT 36791
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGAGA

GAM1681  FLJ10713 3'  AGAGATGGGGTTTCACCATGTT 36994      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  FLJ10901 3'  AGAGATGGGGTTTCATCATGTT 37350      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CTACTTTGGGGTAGAGA
                                  A
GAM1681  FLJ10956 3'  AGACGGGGTTTCACCATGTT   37459      C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM1681  FLJ11193 3'  AGAGATGGGGTCTCACCATGTT 37743      C     A
                                AACA GGTGA ACCCCGTCTCT
                                |||| ||||| ||||||||||
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                                TTGT CCACT TGGGGTAGAGA
                                  A    C
GAM1681  FLJ12363  3'  ATGGGGTTTCACCATGTT    50627     C
                                AACA GGTGAAACCCCGT
                                |||| |||||||||||||
                                TTGT CCACTTTGGGGTA
                                  A
GAM1681  FLJ12581  3'  AGAGACAGGGTTTCACTGTGTT 46329            C
                                AACACGGTGAAACCC GTCTCT
                                |||||||||||||| ||||||
                                TTGTGTCACTTTGGG CAGAGA
                                       A
GAM1681  FLJ12649  3'  AGAGATAGGGTTTTACCATGTT 45084     C       CG
                                AACA GGTGAAACCC  TCTCT
                                |||| ||||||||||  |||||
                                TTGT CCATTTTGGG  AGAGA
                                  A         AT
GAM1681  FLJ12668  3'  AGAGATGAGGTTTCACCTTGTT 47152     C       C
                                AACA GGTGAAACC CGTCTCT
                                |||| ||||||||| |||||||
                                TTGT CCACTTTGG GTAGAGA
                                  T        A
GAM1681  FLJ12687  3'  AGAGACAGGGTTTCACCATGTT 46743     C       C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A        A
GAM1681  FLJ12876  3'  AGAGACGGGGTTTCACTGTG   43085
                                CACGGTGAAACCCCGTCTCT
                                ||||||||||||||||||||
                                GTGTCACTTTGGGGCAGAGA

GAM1681  FLJ12960  3'  AGAGATGGGGTTTCACCGT    45289
                                ACGGTGAAACCCCGTCTCT
                                ||||||||||||||||||
                                TGCCACTTTGGGGTAGAGA

GAM1681  FLJ12973  3'  AGAGATGGGGTTTCATCATGTT 46636     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CTACTTTGGGGTAGAGA
                                  A
GAM1681  FLJ12975  3'  AGACGGGGTTTCGCCTTGTT   70179     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCGCTTTGGGGCAGA
                                  T
GAM1681  FLJ13072  5'  AGAGACAGGGTTTCACCATGTT 91385     C       C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
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                                TTGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  FLJ13114  3'  AGAGATGGAGTTTCACCATGTT 44891      C       C
                                AACA GGTGAAAC CCGTCTCT
                                |||| |||||||| ||||||||
                                TTGT CCACTTTG GGTAGAGA
                                  A       A
GAM1681  FLJ13188  3'  AGAGACAGAGTTTTGCTGTGTT 42187        TG    CCC
                                AACACGG  AAAC   GTCTCT
                                |||||||  ||||   ||||||
                                TTGTGTC  TTTG   CAGAGA
                                   GT    AGA
GAM1681  FLJ13197  3'  AGAGACAAGAGTTTCACCATGT 45174      C       CCC_
           T                     AACA GGTGAAAC    GTCTCT
                                |||| ||||||||    ||||||
                                TTGT CCACTTTG    CAGAGA
                                  A       AGAA
GAM1681  FLJ13305  5'  AGATGGGGTTTCACCATGTT   91703     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM1681  FLJ13456  3'  AGAGACAGAGTTTCACTCTGT  66527     C       CCC
                                ACA GGTGAAAC   GTCTCT
                                ||| ||||||||   ||||||
                                TGT TCACTTTG   CAGAGA
                                  C       AGA
GAM1681  FLJ13590  5'  AGAGATGGCATCTCACTATGTT 46202      CG    AACC
                                AACA  GTGA    CCGTCTCT
                                ||||  ||||    ||||||||
                                TTGT  CACT    GGTAGAGA
                                  AT    CTAC
GAM1681  FLJ13769  5'  AGAGATGGGGTTTCACTATGTT 47239      CG
                                AACA  GTGAAACCCCGTCTCT
                                ||||  ||||||||||||||||
                                TTGT  CACTTTGGGGTAGAGA
                                  AT
GAM1681  FLJ14442  3'  AGAGATGGGGTTTTACCATGTT 52373      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCATTTTGGGGTAGAGA
                                  A
GAM1681  FLJ14950  3'  AGAGACAGGGTTTCACCATGTT 52781      C         C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  FLJ14957  3'  AGAGACGGGGTTTCACCATGTT 52808      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
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                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  FLJ20034  3' AGAGATGGGGTCTCTCCATGTT 34831     C  T  A
                                AACA GG GA ACCCCGTCTCT
                                |||| || || ||||||||||||
                                TTGT CC CT TGGGGTAGAGA
                                  A  T  C
GAM1681  FLJ20136  3' AGAGATGAGTTTCACCATGTT  35089     C       CC
                                AACA GGTGAAAC  CGTCTCT
                                |||| ||||||||  |||||||
                                TTGT CCACTTTG  GTAGAGA
                                  A       A_
GAM1681  FLJ20344  3' AGAGACAGGGTTTCACCATGTT 35476     C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  FLJ20507  3' AGAGACAGGGTTTCACCATGTT 35730     C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  FLJ20507  3' AGAGACAGGGTTTCACCATGTT 60839     C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  FLJ20511  3' AGAGGCGCAGTTTCACCGTGTT 35764           CC
                                AACACGGTGAAAC  CGTCTCT
                                ||||||||||||  |||||||
                                TTGTGCCACTTTG  GCGGAGA
                                      AC
GAM1681  FLJ20897  5' AGAGACGGGGTTTCAACGTGTT 51474       G
                                AACACG TGAAACCCCGTCTCT
                                |||||| ||||||||||||||||
                                TTGTGC ACTTTGGGGCAGAGA
                                   A
GAM1681  FLJ21302  3' AGAGACAGGGTTTCACCATGTT 43503     C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  FLJ21324  5' AGAGATGGGGTTTCACCATGTT 92838     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  FLJ21603  3' AGAGATGGGGTTTCACCCTGTT 45764     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
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                                TTGT CCACTTTGGGGTAGAGA
                                  C
GAM1681  FLJ22002  3'  AGAGATGAGGTTTCGCCATGTT 46191     C       C
                                AACA GGTGAAACC CGTCTCT
                                |||| ||||||||| |||||||
                                TTGT CCGCTTTGG GTAGAGA
                                  A       A
GAM1681  FLJ22167  5'  AGAGATGGGGTCTCACTGTGTT 44857         A
                                AACACGGTGA ACCCCGTCTCT
                                |||||||||| ||||||||||
                                TTGTGTCACT TGGGGTAGAGA
                                     C
GAM1681  FLJ22329  3'  AGAGACGGGGTTTCACCATGTT 45393     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  FLJ22529  3'  AGAGACAGGGTTTCATCATGTT 45939     C       C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CTACTTTGGG CAGAGA
                                  A       A
GAM1681  FLJ22684  3'  AGAGACAGGGTTTCACCATGTT 47465     C       C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A       A
GAM1681  FLJ22794  3'  AGAGACAGGGTTTCACCATGTT 93237     C       C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A       A
GAM1681  FLJ22969  3'  AGAGACAGGGTTTCACCATGTT 69197     C       C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A       A
GAM1681  FLJ23024  3'  AGAGACGGGGTTTCACCATGTT 46837     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| |||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  FLJ23392  3'  AGAGACAGGGTTTCACCATGTT 45878     C       C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A       A
GAM1681  FLJ23392  3'  AGAGACAGGGTTTCACCGTGTT 45879         C
                                AACACGGTGAAACCC GTCTCT
                                |||||||||||||| ||||||
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                                TTGTGCCACTTTGGG CAGAGA
                                          A
GAM1681  FLJ23392  3'  AGAGACGGGGTTTCACCGTGTT 45880
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGAGA

GAM1681  FLJ23519  3'  AGAGATGGGGTTTCACCGTGTT 50942
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||
                                TTGTGCCACTTTGGGGTAGAGA

GAM1681  FLJ23556  3'  AGAGACGGGGTTTCACCGTGTT 46425
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGAGA

GAM1681  FLJ25416  5'  AGATGGGGTTTCACCATGTT   59445      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                   A
GAM1681  FLJ31153  3'  AGAGATGGGGTTTCACCATG   58739    C
                                CA GGTGAAACCCCGTCTCT
                                || ||||||||||||||||
                                GT CCACTTTGGGGTAGAGA
                                  A
GAM1681  FLJ32865  3'  AGAGACGGGGTTTCTCCGTGTT 58799         T
                                AACACGG GAAACCCCGTCTCT
                                ||||||| ||||||||||||||
                                TTGTGCC CTTTGGGGCAGAGA
                                     T
GAM1681  FLJ32894  3'  AGAGATGGGATTTCACTGTGTT 58989             C
                                AACACGGTGAAA CCCGTCTCT
                                |||||||||||| |||||||||
                                TTGTGTCACTTT GGGTAGAGA
                                          A
GAM1681  GMPPB     5'  AGAGACAGGGTTTCACCAGGTT 97432     AC         C
                                AAC  GGTGAAACCC GTCTCT
                                |||  |||||||||| ||||||
                                TTG  CCACTTTGGG CAGAGA
                                  GA         A
GAM1681  GNG4      3'  AGACGGGGTTTCACCATGTT   16836      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                   A
GAM1681  GOLGA3    3'  ATGGGGTTTCACCATGTT    20880      C
                                AACA GGTGAAACCCCGT
                                |||| |||||||||||||
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                                TTGT CCACTTTGGGGTA
                                  A
GAM1681  GREB1    3'  AGAGACGGGGTTTCACCATGTT 28554      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  GRWD     3'  AGAGACGGGGTTTCACCATGTT 49774      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  GTF2E1   3'  AGAGGCAGGGTTTCACCATGTT 19790      C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CGGAGA
                                  A         A
GAM1681  GTPBG3   3'  AGAGACAAGGTTTCACCATGTT 51889      C        CC
                                AACA GGTGAAACC  GTCTCT
                                |||| |||||||||  ||||||
                                TTGT CCACTTTGG  CAGAGA
                                  A         AA
GAM1681  H2AV     3'  AGACGTGGGGTTTCACCATGTT 57626      C          TC
                                AACA GGTGAAACCCCG  TCT
                                |||| ||||||||||||  |||
                                TTGT CCACTTTGGGGT  AGA
                                  A           GC
GAM1681  HARS2    3'  AGAGACGGGGTTTTACCATGTT 55862      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCATTTTGGGGCAGAGA
                                  A
GAM1681  HCA4     3'  AGAGACGGGGTTTTGCCATGTT 78038      C  TG
                                AACA GG  AAACCCCGTCTCT
                                |||| ||  ||||||||||||
                                TTGT CC  TTTGGGGCAGAGA
                                  A  GT
GAM1681  HCGIV.9  3'  AGAGACAGGGTTTTTTGTTGTT 39129      _  T      C
                                AACA CGG GAAACCC GTCTCT
                                |||| ||| ||||||| ||||||
                                TTGT GTT TTTTGGG CAGAGA
                                  T  _      A
GAM1681  HRH4     3'  AGAGATGAAGTCTCACTGTGTT 41524          A  CC
                                AACACGGTGA AC  CGTCTCT
                                |||||||||| ||  |||||||
                                TTGTGTCACT TG  GTAGAGA
                                     C  AA
GAM1681  HSNOV1   3'  AGACATGGGGTTTCACCATGTT 34422      C          C
                                AACA GGTGAAACCCCGT TCT
                                |||| |||||||||||| |||
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                                TTGT CCACTTTGGGGTA AGA
                                  A          C
GAM1681  HSNOV1   3'  AGAGATGGGGTTTCGCCATGTT 34423     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCGCTTTGGGGTAGAGA
                                  A
GAM1681  HSPC065  3'  AGAGATGGGGTTTCACCATGTT 27132     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  HSPC065  3'  AGAGATGGGGTTTCACGATGTT 27133     CG
                                AACA  GTGAAACCCCGTCTCT
                                ||||  ||||||||||||||||
                                TTGT  CACTTTGGGGTAGAGA
                                  AG
GAM1681  HSPC232  3'  AGAGATGGGGTTCACCATGTT  33652     C     A
                                AACA GGTGAA CCCCGTCTCT
                                |||| |||||| ||||||||||
                                TTGT CCACTT GGGGTAGAGA
                                  A    _
GAM1681  HT002    3'  ACAGGGTTTCACCGTGTT    26782            C
                                AACACGGTGAAACCC GT
                                |||||||||||||| ||
                                TTGTGCCACTTTGGG CA
                                     A
GAM1681  ICK      3'  AGAGACGGGGTTTCACTGTGTT 30591
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||
                                TTGTGTCACTTTGGGGCAGAGA

GAM1681  JAM1     3'  AGAGACAGGGTTTCACCATGTT 34215     C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A        A
GAM1681  JAM1     3'  AGAGACAGGGTTTCACCATGTT 58506     C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A        A
GAM1681  JAM1     3'  AGAGACAGGGTTTCACCATGTT 58534     C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A        A
GAM1681  JAM1     3'  AGAGACAGGGTTTCACCATGTT 58561     C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
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                                TTGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  KIAA0063  3'  AGAGATGGGGTTTCTCCATGTT 30248      C  T
                                AACA GG GAAACCCCGTCTCT
                                |||| || ||||||||||||||
                                TTGT CC CTTTGGGGTAGAGA
                                  A  T
GAM1681  KIAA0161  3'  AGAGACGGGGTTTCACCATGTT 29190      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  KIAA0186  3'  AGAGACAGAGTTTTACCATGTT 41094      C       CCC
                                AACA GGTGAAAC   GTCTCT
                                |||| ||||||||   ||||||
                                TTGT CCATTTTG   CAGAGA
                                  A       AGA
GAM1681  KIAA0186  3'  AGATGGGGTTTCACCATGTT   41095      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM1681  KIAA0205  3'  AGAGATGGGGTTTCACCATGTT 30198      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  KIAA0210  5'  AGAGACGGAGGAGTTTCACCAT 29147      C      __ _
          GTT                   AACA GGTGAAA  CC CCGTCTCT
                                |||| |||||||  || ||||||||
                                TTGT CCACTTT  GG GGCAGAGA
                                  A       GA  A
GAM1681  KIAA0391  3'  AGAGACGGGTTTTCACCATGTT 28598      C      C
                                AACA GGTGAAA CCCGTCTCT
                                |||| ||||||| |||||||||
                                TTGT CCACTTT GGGCAGAGA
                                  A       T
GAM1681  KIAA0426  3'  AGAGACGGGGTTTCACCATGTT 28918      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  KIAA0441  3'  AGAGACGGGGTCTCACTGT    29622        A
                                ACGGTGA ACCCCGTCTCT
                                ||||||| ||||||||||
                                TGTCACT TGGGGCAGAGA
                                    C
GAM1681  KIAA0446  5'  AGAGACGGAGTCTCCCTATGTT 69440      CG T  A  C
                                AACA  G GA AC CCGTCTCT
                                ||||  | || || ||||||||
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                                TTGT  C CT TG GGCAGAGA
                                   AT C  C  A
GAM1681  KIAA0459  3'  AGAGACGGGGTTTCACCATGTT 61643      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                   A
GAM1681  KIAA0469  3'  AGAGACAGGGTCTTGCTGTGTT 29968        TG A    C
                                AACACGG  A ACCC GTCTCT
                                |||||||  | |||| ||||||
                                TTGTGTC  T TGGG CAGAGA
                                     GT C    A
GAM1681  KIAA0469  3'  AGAGACGGGATTTCACTGTGTT 29969           C
                                AACACGGTGAAA CCCGTCTCT
                                |||||||||||| |||||||||
                                TTGTGTCACTTT GGGCAGAGA
                                        A
GAM1681  KIAA0475  3'  AGGGTTTCGGGTTTCACCATGT 30109      C         CGT_
          T                      AACA GGTGAAACCC    CTCT
                                |||| ||||||||||    ||||
                                TTGT CCACTTTGGG    GGGA
                                   A         CTTT
GAM1681  KIAA0495  3'  AGAGATGGGATTTCACCATGTT 63256      C      C
                                AACA GGTGAAA CCCGTCTCT
                                |||| ||||||| |||||||||
                                TTGT CCACTTT GGGTAGAGA
                                   A      A
GAM1681  KIAA0513  5'  AGAGACAGGGTTTCGCCATGTT 29010      C         C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCGCTTTGGG CAGAGA
                                   A         A
GAM1681  KIAA0513  3'  AGAGATGGGGTTTCACCATG   29011    C
                                CA GGTGAAACCCCGTCTCT
                                || ||||||||||||||||
                                GT CCACTTTGGGGTAGAGA
                                  A
GAM1681  KIAA0513  3'  AGAGCCTTCTGTTTCACCGTG  29013           CCCGT_
                                CACGGTGAAAC      CTCT
                                ||||||||||      ||||
                                GTGCCACTTTG      GAGA
                                       TCTTCC
GAM1681  KIAA0527  3'  AGAGATGGAGTTTCACCATGTT 97485      C       C
                                AACA GGTGAAAC CCGTCTCT
                                |||| |||||||| ||||||||
                                TTGT CCACTTTG GGTAGAGA
                                   A       A
GAM1681  KIAA0555  3'  AGAGACAGGGTTTCACTATG   29544    CG        C
                                CA  GTGAAACCC GTCTCT
                                ||  ||||||||| ||||||
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                                GT  CACTTTGGG CAGAGA
                                 AT        A
GAM1681  KIAA0557  3'  AGAGATGGGGTTTCTCCATGTT 78543     C  T
                                AACA GG GAAACCCCGTCTCT
                                |||| || ||||||||||||||
                                TTGT CC CTTTGGGGTAGAGA
                                  A  T
GAM1681  KIAA0561  3'  AGACGGGGTTTCACCATGTT   66462     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM1681  KIAA0563  5'  AGAGGCGGAGTTTCGCCATGTT 29866     C       C
                                AACA GGTGAAAC CCGTCTCT
                                |||| |||||||| ||||||||
                                TTGT CCGCTTTG GGCGGAGA
                                  A       A
GAM1681  KIAA0599  3'  AGAGACGGGGTTTCGCCGTGTT 77685
                                AACACGGTGAAACCCCGTCTCT
                                ||||||||||||||||||||||
                                TTGTGCCGCTTTGGGGCAGAGA

GAM1681  KIAA0682  3'  AGACGGGGTTTCACCATGT    30011     C
                                ACA GGTGAAACCCCGTCT
                                ||| ||||||||||||||
                                TGT CCACTTTGGGGCAGA
                                  A
GAM1681  KIAA0682  3'  AGAGACTGGGTTTCACCATGT  30015     C        C
                                ACA GGTGAAACCC GTCTCT
                                ||| |||||||||| ||||||
                                TGT CCACTTTGGG CAGAGA
                                  A         T
GAM1681  KIAA0737  3'  AGAGACAGGGTTTCACCATGTT 29797     C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  KIAA0737  3'  AGAGATGGGGTCTCACTATGTT 29798     CG    A
                                AACA  GTGA ACCCCGTCTCT
                                ||||  |||| ||||||||||||
                                TTGT  CACT TGGGGTAGAGA
                                  AT    C
GAM1681  KIAA0798  3'  AGAGACGGGGTTTCACTGTGTT 28440
                                AACACGGTGAAACCCCGTCTCT
                                ||||||||||||||||||||||
                                TTGTGTCACTTTGGGGCAGAGA

GAM1681  KIAA0828  3'  AGAGACAGGGTTTCACTATGTT 82109     CG        C
                                AACA  GTGAAACCC GTCTCT
                                ||||  ||||||||| ||||||
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                                TTGT  CACTTTGGG CAGAGA
                                  AT        A
GAM1681  KIAA0831  3'  AGAGACGGGGGTTTTCACCATG 30626     C      __
              T                    ACA GGTGAAA  CCCCGTCTCT
                                   ||| |||||||  ||||||||||
                                   TGT CCACTTT  GGGGCAGAGA
                                     A       TG
GAM1681  KIAA0841  3'  ACGGGGTTTCATCATGTT     71885      C
                                   AACA GGTGAAACCCCGT
                                   |||| ||||||||||||
                                   TTGT CTACTTTGGGGCA
                                     A
GAM1681  KIAA0861  3'  AGAGACGGGGTTTCCCCGTGTT 90341         T
                                   AACACGG GAAACCCCGTCTCT
                                   ||||||| ||||||||||||||
                                   TTGTGCC CTTTGGGGCAGAGA
                                       C
GAM1681  KIAA0884  3'  AGAGGTGAGGTTTCACCATGTT 70745      C        C GT
                                   AACA GGTGAAACC C  CTCT
                                   |||| ||||||||| |  ||||
                                   TTGT CCACTTTGG G  GAGA
                                     A        A TG
GAM1681  KIAA0889  3'  AGACGGGGTTTCACCGTGTT   31751
                                   AACACGGTGAAACCCCGTCT
                                   ||||||||||||||||||||
                                   TTGTGCCACTTTGGGGCAGA

GAM1681  KIAA0931  3'  AGAGACGGGGTTTCACCATGTT 68004      C
                                   AACA GGTGAAACCCCGTCTCT
                                   |||| ||||||||||||||||
                                   TTGT CCACTTTGGGGCAGAGA
                                     A
GAM1681  KIAA0961  3'  AGATGGGGTTTCACCATGTT   30386      C
                                   AACA GGTGAAACCCCGTCT
                                   |||| ||||||||||||||
                                   TTGT CCACTTTGGGGTAGA
                                     A
GAM1681  KIAA1041  3'  AGAGATGGGGTTTCACCATGTT 30815      C
                                   AACA GGTGAAACCCCGTCTCT
                                   |||| ||||||||||||||||
                                   TTGT CCACTTTGGGGTAGAGA
                                     A
GAM1681  KIAA1054  3'  AGAGGTGGGGTTTCACCGTGTT 68958              GT
                                   AACACGGTGAAACCCC  CTCT
                                   ||||||||||||||||  ||||
                                   TTGTGCCACTTTGGGG  GAGA
                                             TG
GAM1681  KIAA1115  5'  AGAGACAGGGTTTCGCCATGTT 30686      C        C
                                   AACA GGTGAAACCC GTCTCT
                                   |||| |||||||||| ||||||
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                                TTGT CCGCTTTGGG CAGAGA
                                  A         A
GAM1681  KIAA1143  3'  AGAGACGGGGTTTCACTTTGTT 69228      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT TCACTTTGGGGCAGAGA
                                  T
GAM1681  KIAA1161  5'  AGAGATGGGGTTTACCATGTT  82635      C     A
                                AACA GGTGAA CCCCGTCTCT
                                |||| |||||| ||||||||||
                                TTGT CCATTT GGGGTAGAGA
                                  A     _
GAM1681  KIAA1170  3'  AGAAACAGGGTTTCACCATGTT 70407      C         C  C
                                AACA GGTGAAACCC GT TCT
                                |||| |||||||||| || |||
                                TTGT CCACTTTGGG CA AGA
                                  A         A  A
GAM1681  KIAA1198  3'  AGACGGGGTTTCACCGTGTT   63992
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGA

GAM1681  KIAA1198  3'  AGAGACAGTGTTTCACCATGTT 63993      C       CCC
                                AACA GGTGAAAC   GTCTCT
                                |||| ||||||||   ||||||
                                TTGT CCACTTTG   CAGAGA
                                  A       TGA
GAM1681  KIAA1198  3'  AGAGACGGGGTTTCACCATGTT 63994      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  KIAA1198  3'  AGAGACGGGGTTTCACCATGTT 63995      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  KIAA1198  3'  AGAGATGGGGTTTCACCATGTT 63996      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  KIAA1198  3'  AGAGATGGGGTTTCTCCATGTT 63997      C  T
                                AACA GG GAAACCCCGTCTCT
                                |||| || ||||||||||||||
                                TTGT CC CTTTGGGGTAGAGA
                                  A  T
GAM1681  KIAA1200  3'  AGAGACGGGGTTTCACCATGTT 63029      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
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                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  KIAA1209  3'  AGAGGCGGGGTTTCATCATGTT 61399     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CTACTTTGGGGCGGAGA
                                  A
GAM1681  KIAA1210  3'  AGAGACGGGGTTTCACCATGTT 98064     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  KIAA1254  3'  AGAGATGGGGTTTCACCATGTT 70550     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  KIAA1432  5'  AGAGGGCTTTCTTCGCCGTG  67300       AC___  G
                                CACGGTGAA    CCC TCT
                                |||||||||    ||| |||
                                GTGCCGCTT    GGG AGA
                                     CTTTC  _
GAM1681  KIAA1443  3'  AGAGACGGGTTTCATCATGTT  64565     C       C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CTACTTTGGG CAGAGA
                                  A       _
GAM1681  KIAA1456  3'  AGAGACGGGGTTTCACCGTGTT 67527
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGAGA

GAM1681  KIAA1465  3'  AGAGACGGGGTTTCACCATGTT 61485     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  KIAA1467  3'  AGAGACGGGGTTTCACCATGTT 72060     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  KIAA1493  3'  AGAGATGGGGTTTCACCTTGTT 64831     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  T
GAM1681  KIAA1497  5'  AGAGACAGGGTTTCACCATGTT 68110     C       C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
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                                TTGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  KIAA1508  3'  AGAAACAAGGTTTCACCATGTT 62537      C        CC  C
                                AACA GGTGAAACC  GT TCT
                                |||| |||||||||  || |||
                                TTGT CCACTTTGG  CA AGA
                                  A         AA  A
GAM1681  KIAA1530  3'  AGAGACGGGATTTCACTGTGTT 68543           C
                                AACACGGTGAAA CCCGTCTCT
                                |||||||||||| |||||||||
                                TTGTGTCACTTT GGGCAGAGA
                                       A
GAM1681  KIAA1530  3'  AGAGATGAGGTCTCACTGTGTT 68544          A   C
                                AACACGGTGA ACC CGTCTCT
                                |||||||||| ||| |||||||
                                TTGTGTCACT TGG GTAGAGA
                                      C   A
GAM1681  KIAA1571  3'  AGAGTTGGGGGTTTCACTATGT 61611      CG         GT_
           T                     AACA  GTGAAACCCC   CTCT
                                ||||  ||||||||||   ||||
                                TTGT  CACTTTGGGG   GAGA
                                  AT         GTT
GAM1681  KIAA1615  3'  AGAGACGGGATATCTCCGTGTT 69263        T  AAC
                                AACACGG GA   CCCGTCTCT
                                ||||||| ||   |||||||||
                                TTGTGCC CT   GGGCAGAGA
                                    T  ATA
GAM1681  KIAA1617  3'  AGAGACAGGGTTTCACCATGTT 93070      C         C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  KIAA1649  3'  AGAGATGAGGTTTCACCGTGTT 51213           C
                                AACACGGTGAAACC CGTCTCT
                                |||||||||||||| |||||||
                                TTGTGCCACTTTGG GTAGAGA
                                       A
GAM1681  KIAA1655  3'  AGAGACAGGTTTCACCATGTT  67173      C        CC
                                AACA GGTGAAACC  GTCTCT
                                |||| |||||||||  ||||||
                                TTGT CCACTTTGG  CAGAGA
                                  A         A_
GAM1681  KIAA1668  3'  AGAGACGGGGTTTCACCGTGTT 67057
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGAGA

GAM1681  KIAA1712  3'  AGAGACAGGGTTTCACCATGTT 68149      C         C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
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                                TTGT CCACTTTGGG CAGAGA
                                  A        A
GAM1681  KIAA1727  3'  AGAGATGGGATCTCACTATGTT 64749     CG    AAC
                                AACA  GTGA   CCCGTCTCT
                                ||||  ||||   |||||||||
                                TTGT  CACT   GGGTAGAGA
                                  AT    CTA
GAM1681  KIAA1737  3'  AGAAATGGGGTTTTACCGTGTT 67928              C
                                AACACGGTGAAACCCCGT TCT
                                |||||||||||||||||| |||
                                TTGTGCCATTTTGGGGTA AGA
                                          A
GAM1681  KIAA1751  3'  AGACACAGGGTTTCGCCATGTT 72149     C        C  C
                                AACA GGTGAAACCC GT TCT
                                |||| |||||||||| || |||
                                TTGT CCGCTTTGGG CA AGA
                                  A        A  C
GAM1681  KIAA1784  3'  AGAAACGGGGTTTCACCATGTT 65742     C          C
                                AACA GGTGAAACCCCGT TCT
                                |||| ||||||||||||| |||
                                TTGT CCACTTTGGGGCA AGA
                                  A          A
GAM1681  KIAA1821  3'  AGAGACAGGGTCTCACTGTGTT 72257         A   C
                                AACACGGTGA ACCC GTCTCT
                                |||||||||| |||| ||||||
                                TTGTGTCACT TGGG CAGAGA
                                     C   A
GAM1681  KIAA1877  3'  AGAGACAGGGTTTCACCGTGTT 66739             C
                                AACACGGTGAAACCC GTCTCT
                                |||||||||||||| ||||||
                                TTGTGCCACTTTGGG CAGAGA
                                          A
GAM1681  KIAA1971  3'  AGAGACAAGGTTTCGCTATGTT 74668     CG       CC
                                AACA  GTGAAACC  GTCTCT
                                ||||  ||||||||  ||||||
                                TTGT  CGCTTTGG  CAGAGA
                                  AT       AA
GAM1681  KIAA1971  3'  AGAGACGAGGTTTCACCGTGTT 74669           C
                                AACACGGTGAAACC CGTCTCT
                                |||||||||||||| |||||||
                                TTGTGCCACTTTGG GCAGAGA
                                          A
GAM1681  KIAA1975  5'  AGAGATGGGGTTTCACCATGTT 74410     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  KLK7      3'  AGAGACAGGGTTTCACCATGTT 58387     C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
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                                TTGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  KLK7     3'  AGAGACAGGGTTTCACCATGTT 18540      C         C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  LAMP3    3'  AGACGGGGTTTCACCATGTT   60194      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM1681  LIECG3   3'  AGAGGGGGGTCTCACTGTGTT  88795          A    G
                                AACACGGTGA ACCCC TCTCT
                                |||||||||| ||||| |||||
                                TTGTGTCACT TGGGG GGAGA
                                     C    _
GAM1681  LNIR     3'  AGAGATGGAGTCTCACTATGTT 48868      CG   A  C
                                AACA  GTGA AC CCGTCTCT
                                ||||  |||| || ||||||||
                                TTGT  CACT TG GGTAGAGA
                                  AT    C  A
GAM1681  LY75     3'  AGAGATGGGGTTTCACCATGTT 11384      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  MAP-1    3'  AGAGACGGGGTTTCACCATGTT 42434      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  MCLC     3'  AGAGATGGGGTTTCACCATGTT 31374      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  MEF-2    3'  AGAGACTGGGTTTCACCATGTT 65016      C         C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A         T
GAM1681  MGC10200 3'  AGAGATGGGGTTTCACCATGTT 59631      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  MGC11386 3'  AGAGATGGGGATCTCACTGTGT 53053          AA_
           T                     AACACGGTGA   CCCCGTCTCT
                                ||||||||||   ||||||||||
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                                TTGTGTCACT   GGGGTAGAGA
                                     CTA
GAM1681  MGC12518  3'  AGAGTGAGGGTTTCACCATGTT 64772      C         _  T
                                AACA GGTGAAACCC CG CTCT
                                |||| |||||||||| || ||||
                                TTGT CCACTTTGGG GT GAGA
                                  A         A  _
GAM1681  MGC15563  3'  AGAGATGGGATCTCACCATGTT 52857      C     AAC
                                AACA GGTGA   CCCGTCTCT
                                |||| |||||   |||||||||
                                TTGT CCACT   GGGTAGAGA
                                  A     CTA
GAM1681  MGC21675  3'  AGAGATGGGGTTTCACCATGTT 54582      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  MGC2474   3'  AGAGATGGGGTTTCACCATGTT 43944      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  MGC4766   5'  AGAGACGGGGTTTCACCGTGTT 49554
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGAGA

GAM1681  moblak    3'  AGAGACAGGGTTTCACCGTGTT 56383              C
                                AACACGGTGAAACCC GTCTCT
                                |||||||||||||| ||||||
                                TTGTGCCACTTTGGG CAGAGA
                                         A
GAM1681  MOCS3     3'  AGAGGGGGTTTCACCATGTT   27925      C         G
                                AACA GGTGAAACCCC TCT
                                |||| |||||||||| |||
                                TTGT CCACTTTGGGG AGA
                                  A         G
GAM1681  MRPS27    3'  AGAGATGGGGTTTCACCATGTT 31316      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  MtFMT     3'  AGAGATGGGGTTTCACCATGTT 58326      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  MYO5C     3'  AGACAGGTTTCACCATGTT    38711      C        CC
                                AACA GGTGAAACC  GTCT
                                |||| |||||||||  ||||
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                                TTGT CCACTTTGG  CAGA
                                  A       A_
GAM1681  NDP52    3'  AGAGACAGGGTTTCACTATGTT 20664     CG       C
                                AACA  GTGAAACCC GTCTCT
                                ||||  ||||||||| ||||||
                                TTGT  CACTTTGGG CAGAGA
                                  AT       A
GAM1681  NDUFC2   3'  AGAGACGGGGTTTCACCATGTT 17025     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  NINJ2    3'  AGAGACGGGGTTTCTCCATGTT 33717     C  T
                                AACA GG GAAACCCCGTCTCT
                                |||| || ||||||||||||
                                TTGT CC CTTTGGGGCAGAGA
                                  A  T
GAM1681  Nup43    3'  AGAGACGACAGGGTTTCACCAT 45341     C        ___
             GTT                  AACA GGTGAAACCC   CGTCTCT
                                |||| ||||||||||   |||||||
                                TTGT CCACTTTGGG   GCAGAGA
                                  A         ACA
GAM1681  Nup43    3'  AGATGGGGTTTCACTGTGTT   45342
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||
                                TTGTGTCACTTTGGGGTAGA

GAM1681  NXN      3'  AGAGATGGGGTTTCACCATGTT 42662     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  OCT11    3'  AGAGATGGGGTTTCACCATGTT 27579     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  OR51E2   3'  AGAGACAGAGTTTCACCATGTT 48502     C       CCC
                                AACA GGTGAAAC   GTCTCT
                                |||| ||||||||   ||||||
                                TTGT CCACTTTG   CAGAGA
                                  A       AGA
GAM1681  PASK     3'  AGAAACGGTAACTCGTGTT   31401       _ GAAACC   C
                                AACACG GT     CCGT TCT
                                |||||| ||     |||| |||
                                TTGTGC CA     GGCA AGA
                                   T  AT_____   A
GAM1681  PASK     5'  AGACGGGGTTTCTCCATGTT   31403     C  T
                                AACA GG GAAACCCCGTCT
                                |||| || ||||||||||||
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                                TTGT CC CTTTGGGGCAGA
                                  A  T
GAM1681  PELI1    5'  AGAGACGGGGTTTCACCATGTT 40621      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  PELI1    5'  AGATGGGGTTTCACCATGTT  40622      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM1681  PIP3-E   3'  AGAGACCGGGGTTTACCATGTT 67344      C     A    _
                                AACA GGTGAA CCCCG TCTCT
                                |||| |||||| ||||| |||||
                                TTGT CCATTT GGGGC AGAGA
                                  A     _    C
GAM1681  PIP5K1C  3'  AGAGACGGAAGCACGTGTGT  71295       _  AAACC
                                ACACG GTG     CCGTCTCT
                                ||||| |||     ||||||||
                                TGTGT CAC     GGCAGAGA
                                  G   GAA__
GAM1681  PRO0365  5'  AGAGACGGGGTTTCACTATGTT 26977      CG
                                AACA  GTGAAACCCCGTCTCT
                                ||||  ||||||||||||||||
                                TTGT  CACTTTGGGGCAGAGA
                                  AT
GAM1681  PRO0800  5'  AGACATCAGGTTTCATCATGTT 38348      C       CC__
                                AACA GGTGAAACC    GTCT
                                |||| |||||||||    ||||
                                TTGT CTACTTTGG    CAGA
                                  A        ACTA
GAM1681  PRO2955  3'  AGAGACAGGGTTTTACCATGTT 38233      C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCATTTTGGG CAGAGA
                                  A        A
GAM1681  PSPH     3'  AGAGACGGGGTTTGACCGTGTT 17129         G
                                AACACGGT AAACCCCGTCTCT
                                |||||||| ||||||||||||
                                TTGTGCCA TTTGGGGCAGAGA
                                    G
GAM1681  PSTPIP2  3'  AGAGACAGGGTTTTACCATGTT 44649      C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCATTTTGGG CAGAGA
                                  A        A
GAM1681  RAB21    3'  AGAGACGGGGTTTCACCAGGTT 31081     AC
                                AAC  GGTGAAACCCCGTCTCT
                                |||  ||||||||||||||||
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                                TTG  CCACTTTGGGGCAGAGA
                                  GA
GAM1681  RAB33B   3'  AGAGACGGGGTCTTGCTATGTT 49313      CG TG A
                                AACA  G  A ACCCCGTCTCT
                                ||||  |  | ||||||||||||
                                TTGT  C  T TGGGGCAGAGA
                                  AT GT C
GAM1681  RAB33B   3'  AGATGGGGTTTCACCATGTT   49315      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM1681  RAP140   3'  AGAGACAGGGTTTCACTGTGTT 31506              C
                                AACACGGTGAAACCC GTCTCT
                                |||||||||||||||| ||||||
                                TTGTGTCACTTTGGG CAGAGA
                                         A
GAM1681  RES4-25  3'  AGAGACGGGGTTTCTCCATGTT 65260      C  T
                                AACA GG GAAACCCCGTCTCT
                                |||| || ||||||||||||||
                                TTGT CC CTTTGGGGCAGAGA
                                  A  T
GAM1681  RNF8     3'  AGAGACAGGGTTTCACCATGTT 15559      C         C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  RNO2     5'  AGATGGGGTGTCACCATGTT   53916      C     A
                                AACA GGTGA ACCCCGTCT
                                |||| ||||| |||||||||
                                TTGT CCACT TGGGGTAGA
                                  A     G
GAM1681  SAMHD1   3'  AGAGACAAGGTTTTGCTCTGTT 61976      C  TG    CC
                                AACA GG  AAACC  GTCTCT
                                |||| ||  |||||  ||||||
                                TTGT TC  TTTGG  CAGAGA
                                  C  GT    AA
GAM1681  SCAMP-4  3'  AGATGGGGTTTCACCATGTT   55333      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM1681  SCYA16   3'  AGAGACGGGATTCTACCATGTT 17166      C    A  C
                                AACA GGTG AA CCCGTCTCT
                                |||| |||| || |||||||||
                                TTGT CCAT TT GGGCAGAGA
                                  A   C  A
GAM1681  SCYA22   3'  AGAGACGGGGTTTTGCCATGTT 92575      C  TG
                                AACA GG  AAACCCCGTCTCT
                                |||| ||  ||||||||||||
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                                TTGT CC  TTTGGGGCAGAGA
                                  A  GT
GAM1681  SCYA28   3'  AGACGGGGTTTCACCGTGTT  39536
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGA

GAM1681  SERF1B   3'  AGAGATGGGGTTTCACCATGTT 43686      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  SFXN2    3'  AGACGGGGTTTCACCATG    74369    C
                                CA GGTGAAACCCCGTCT
                                || ||||||||||||||
                                GT CCACTTTGGGGCAGA
                                 A
GAM1681  SIRPB1   3'  AGAGATGGGGTTTCTCCATGTT 21353      C  T
                                AACA GG GAAACCCCGTCTCT
                                |||| || ||||||||||||||
                                TTGT CC CTTTGGGGTAGAGA
                                  A  T
GAM1681  SLC11A1  3'  AGAGACGGGGTTTGCCATG   60155    C   G
                                CA GGT AAACCCCGTCTCT
                                || ||| ||||||||||||
                                GT CCG TTTGGGGCAGAGA
                                 A  _
GAM1681  SLC12A8  3'  AGACAGGGTTTCACCATGTT   45230     C        C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CCACTTTGGG CAGA
                                  A        A
GAM1681  SLC16A4  3'  AGAGGCGGGGTTTCACCATGTT 17445      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCGGAGA
                                  A
GAM1681  SLC19A3  3'  AGATGGGGTTTCACAATGTT   48233     CG
                                AACA  GTGAAACCCCGTCT
                                ||||  ||||||||||||||
                                TTGT  CACTTTGGGGTAGA
                                  AA
GAM1681  SLC2A10  3'  AGAGATGGGGTTTCACTGTGTT 48542
                                AACACGGTGAAACCCCGTCTCT
                                ||||||||||||||||||||||
                                TTGTGTCACTTTGGGGTAGAGA

GAM1681  SREC     3'  AGAGACAGGGTTTCACCATGTT 14897      C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
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                                  TTGT CCACTTTGGG CAGAGA
                                    A         A
GAM1681  SS-56     3'  AGAGACGGAGTTTCACCATGTT 60344       C       C
                                  AACA GGTGAAAC CCGTCTCT
                                  |||| |||||||| ||||||||
                                  TTGT CCACTTTG GGCAGAGA
                                    A       A
GAM1681  STAF65(gamma) 3'  AGAGATGAGGTTTCACCGTGTT 30058              C
                                  AACACGGTGAAACC CGTCTCT
                                  |||||||||||||| |||||||
                                  TTGTGCCACTTTGG GTAGAGA
                                          A
GAM1681  SULT1C2   3'  AGAGACGAGGTTTCACCGTGTT 22708               C
                                  AACACGGTGAAACC CGTCTCT
                                  |||||||||||||| |||||||
                                  TTGTGCCACTTTGG GCAGAGA
                                          A
GAM1681  SUN1      3'  AGAGACAGGGTTTCACTGTGTT 47907                C
                                  AACACGGTGAAACCC GTCTCT
                                  |||||||||||||| ||||||
                                  TTGTGTCACTTTGGG CAGAGA
                                          A
GAM1681  SYT13     3'  AGAGATGGGGTTTCACCATGTT 95091       C
                                  AACA GGTGAAACCCCGTCTCT
                                  |||| ||||||||||||||||
                                  TTGT CCACTTTGGGGTAGAGA
                                    A
GAM1681  TADA3L    3'  AGAGACGGGGTTTCACCGTGTT 56804
                                  AACACGGTGAAACCCCGTCTCT
                                  ||||||||||||||||||||||
                                  TTGTGCCACTTTGGGGCAGAGA

GAM1681  TBCC      3'  AGAGACGGGGTTTCGCCATGTT 13600       C
                                  AACA GGTGAAACCCCGTCTCT
                                  |||| ||||||||||||||||
                                  TTGT CCGCTTTGGGGCAGAGA
                                    A
GAM1681  TCL6      3'  AGAGACAGGGTTTCACCGTGTT 27752                C
                                  AACACGGTGAAACCC GTCTCT
                                  |||||||||||||| ||||||
                                  TTGTGCCACTTTGGG CAGAGA
                                          A
GAM1681  TCL6      5'  AGAGACGAGGTTTCACCATGTT 27753       C       C
                                  AACA GGTGAAACC CGTCTCT
                                  |||| ||||||||| |||||||
                                  TTGT CCACTTTGG GCAGAGA
                                    A       A
GAM1681  TCL6      3'  AGAGACAGGGTTTCACCGTGTT 25900               C
                                  AACACGGTGAAACCC GTCTCT
                                  |||||||||||||| ||||||
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                                TTGTGCCACTTTGGG CAGAGA
                                      A
GAM1681  TCL6     5'  AGAGACGAGGTTTCACCATGTT 25901      C        C
                                AACA GGTGAAACC CGTCTCT
                                |||| ||||||||| |||||||
                                TTGT CCACTTTGG GCAGAGA
                                  A        A
GAM1681  TCL6     5'  AGAGACGAGGTTTCACCATGTT 40460      C        C
                                AACA GGTGAAACC CGTCTCT
                                |||| ||||||||| |||||||
                                TTGT CCACTTTGG GCAGAGA
                                  A        A
GAM1681  TCL6     5'  AGAGACGAGGTTTCACCATGTT 40506      C        C
                                AACA GGTGAAACC CGTCTCT
                                |||| ||||||||| |||||||
                                TTGT CCACTTTGG GCAGAGA
                                  A        A
GAM1681  THEA     3'  AGAGACACTTTCACTGTGTT   66868           CCCC
                                AACACGGTGAAA   GTCTCT
                                ||||||||||||   ||||||
                                TTGTGTCACTTT   CAGAGA
                                      CA__
GAM1681  THEA     3'  AGATGGGGTTTCACTGTGTT   66869
                                AACACGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                TTGTGTCACTTTGGGGTAGA

GAM1681  TRIM16   3'  AGAGATGGGGTTTCACCATGTT 22361      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  TRIM5    3'  AGAGACGGGGTTTCCCCATGTT 53464      C  T
                                AACA GG GAAACCCCGTCTCT
                                |||| || ||||||||||||||
                                TTGT CC CTTTGGGGCAGAGA
                                  A  C
GAM1681  TRIM5    3'  AGAGACGGGGTTTCCCCATGTT 53537      C  T
                                AACA GG GAAACCCCGTCTCT
                                |||| || ||||||||||||||
                                TTGT CC CTTTGGGGCAGAGA
                                  A  C
GAM1681  TRIM6    3'  AGAGATAGGGTTTCACCGTGTT 55171             CG
                                AACACGGTGAAACCC  TCTCT
                                ||||||||||||||  |||||
                                TTGTGCCACTTTGGG  AGAGA
                                      AT
GAM1681  TU12B1-TY 3'  AGAGACGGGGTTTCACCATGTT 33822      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
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                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  TU12B1-TY 3'  AGAGATGGGGTTTCACCATGTT 33823      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  TUCAN    3'  AGAGACAGAGTTTTGCTATGTT 30964      CG TG    CCC
                                AACA  G  AAAC   GTCTCT
                                ||||  |  ||||   ||||||
                                TTGT  C  TTTG   CAGAGA
                                  AT GT    AGA
GAM1681  UBF-fl   3'  ATGGGGTTTTACCATGTT    52617      C
                                AACA GGTGAAACCCCGT
                                |||| ||||||||||||
                                TTGT CCATTTTGGGGTA
                                  A
GAM1681  VDU1     3'  AGAGATGGGGTTTCACCATGTT 31114      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  VPS33A   3'  ATGGTGTTTCACCATGTT    43607      C       C
                                AACA GGTGAAAC CCGT
                                |||| |||||||| ||||
                                TTGT CCACTTTG GGTA
                                  A       T
GAM1681  WBSCR23  3'  AGAGACGGGGTTTCACCATGTT 47413      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  ZF       3'  AGAGACGGGACCAGCTGCTG   41365    _   GAAAC
                                CA CGGT     CCCGTCTCT
                                || ||||     |||||||||
                                GT GTCG     GGGCAGAGA
                                 C    ACCA_
GAM1681  ZNF221   3'  ACGGGGTTTCACCGTGTT    26261
                                AACACGGTGAAACCCCGT
                                ||||||||||||||||||
                                TTGTGCCACTTTGGGGCA

GAM1681  ZNF338   3'  AGAGGCGGGGTTTCATCATGTT 42251      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CTACTTTGGGGCGGAGA
                                  A
GAM1681  ZTL1     3'  AGAGACGGGGCTTCATTCACC  44137       A____
                                GGTGAA     CCCCGTCTCT
                                ||||||     ||||||||||
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                                CCACTT    GGGGCAGAGA
                                   ACTTC
GAM1681  LOC112817 3'  AGAGATGGGGTTTCACCGTGTT 57313
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||
                                TTGTGCCACTTTGGGGTAGAGA

GAM1681  LOC113523 5'  AGAGACAGGGTTTCACCATGTT 73410     C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  LOC115219 5'  AGAGACGGGGTTTCATCATGTT 73686     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CTACTTTGGGGCAGAGA
                                  A
GAM1681  LOC115648 3'  AGACGGGGTTTCACCATGTT   60014     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM1681  LOC120114 3'  AGAGATGGGGTTTCACCATGTT 76036     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  LOC120224 5'  AGAGACAGGGTTTCACCATGTT 57882     C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  LOC120939 3'  AGAGGGGGTTTCACCATGTT   76754     C         G
                                AACA GGTGAAACCCC TCT
                                |||| |||||||||| |||
                                TTGT CCACTTTGGGG AGA
                                  A         G
GAM1681  LOC121504 3'  AGATACGGGGTTTCACCATGTT 74539     C          C
                                AACA GGTGAAACCCCGT TCT
                                |||| ||||||||||||| |||
                                TTGT CCACTTTGGGGCA AGA
                                  A           T
GAM1681  LOC124216 3'  AGAGATGGTTTCACCATGTT   74732     C       CC
                                AACA GGTGAAACC  GTCTCT
                                |||| |||||||||  ||||||
                                TTGT CCACTTTGG  TAGAGA
                                  A       __
GAM1681  LOC124871 3'  AGAGACGGGTCTCACTATGTT  74816     CG   AAC
                                AACA  GTGA   CCCGTCTCT
                                ||||  ||||   |||||||||
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                                TTGT  CACT   GGGCAGAGA
                                  AT    CT_
GAM1681  LOC126364 3'  AGAGATGGGGTTTCGCCATGTT 76180      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCGCTTTGGGGTAGAGA
                                  A
GAM1681  LOC126661 3'  AGAGATGGGGTTTCACCATGTT 75045      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  LOC128077 3'  AGAGACAGGGTTTCACCATGTT 75202      C         C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  LOC128077 3'  AGAGACGGGGTTTCACCATGTT 75203      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  LOC128989 3'  AGAGACGGGGTTTCACCATGTT 75310      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  LOC130813 3'  AGAGATGGGGTTTCTCCATGTT 76261      C  T
                                AACA GG GAAACCCCGTCTCT
                                |||| || ||||||||||||||
                                TTGT CC CTTTGGGGTAGAGA
                                  A  T
GAM1681  LOC132241 5'  AGAGAGTGGGTTTCACTATGTT 75552      CG        CG
                                AACA  GTGAAACCC  TCTCT
                                ||||  |||||||||  |||||
                                TTGT  CACTTTGGG  AGAGA
                                  AT        TG
GAM1681  LOC132625 3'  AGAGATGGGGTTTCACCATGTT 76430      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  LOC135154 3'  AGACAAGGTTTCACCATGTT   75717      C        CC
                                AACA GGTGAAACC  GTCT
                                |||| |||||||||  ||||
                                TTGT CCACTTTGG  CAGA
                                  A        AA
GAM1681  LOC135293 3'  AGAGACGGCATTTCACCATGTT 76677      C      CC
                                AACA GGTGAAA  CCGTCTCT
                                |||| |||||||  ||||||||
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                                TTGT CCACTTT  GGCAGAGA
                                  A      AC
GAM1681  LOC143153 3'  AGAGGTCTCTCACTGTGTT   76976         AACC  G
                                AACACGGTGA   CC TCT
                                ||||||||||   || |||
                                TTGTGTCACT   GG AGA
                                     CTCT  _
GAM1681  LOC143154 3'  AGAGGTCTCTCACTGTGTT   76987         AACC  G
                                AACACGGTGA   CC TCT
                                ||||||||||   || |||
                                TTGTGTCACT   GG AGA
                                     CTCT  _
GAM1681  LOC143187 3'  AGAGATGGAGTTTCACCATGTT 59751      C       C
                                AACA GGTGAAAC CCGTCTCT
                                |||| |||||||| ||||||||
                                TTGT CCACTTTG GGTAGAGA
                                  A       A
GAM1681  LOC143916 3'  AGAGATGGGGTTTCACCTTGTT 77134      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  T
GAM1681  LOC144114 5'  AGAGACGGGGGGTCCTG     83082     T  AA
                                CGG GA  CCCCGTCTCT
                                ||| ||  ||||||||||
                                GTC CT  GGGGCAGAGA
                                  _  GG
GAM1681  LOC144317 5'  AGAGACTGGGGTTTCTCCATGT 77288      C  T       _
           T                     AACA GG GAAACCCC GTCTCT
                                |||| || |||||||| ||||||
                                TTGT CC CTTTGGGG CAGAGA
                                  A  T       T
GAM1681  LOC144519 5'  AGAGACGGGGTTTTGCCATGTT 77367      C  TG
                                AACA GG  AAACCCCGTCTCT
                                |||| ||  ||||||||||||
                                TTGT CC  TTTGGGGCAGAGA
                                  A  GT
GAM1681  LOC144524 5'  AGAAACCGGGTTTCACCGTGTT 84048            C  C
                                AACACGGTGAAACCC GT TCT
                                |||||||||||||| || |||
                                TTGTGCCACTTTGGG CA AGA
                                       C  A
GAM1681  LOC144871 3'  AGAAATGGGGTTTCACTGTGTT 84116              C
                                AACACGGTGAAACCCCGT TCT
                                |||||||||||||||| |||
                                TTGTGTCACTTTGGGGTA AGA
                                        A
GAM1681  LOC145082 5'  AGAGACGAGGTTTTGCCATGTT 84180      C  TG     C
                                AACA GG  AAACC CGTCTCT
                                |||| ||  ||||| |||||||
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                                TTGT CC  TTTGG GCAGAGA
                                  A  GT    A
GAM1681  LOC145268 5'  AGAGACAGAGTTTCACCATGTT 77571      C       CCC
                                AACA GGTGAAAC   GTCTCT
                                |||| ||||||||   ||||||
                                TTGT CCACTTTG   CAGAGA
                                  A       AGA
GAM1681  LOC145453 5'  AGACAGGGTCTCACTGTGT    77651         A    C
                                ACACGGTGA ACCC GTCT
                                ||||||||| |||| ||||
                                TGTGTCACT TGGG CAGA
                                    C    A
GAM1681  LOC146050 3'  AGAGATGGGGTTTCACCATGTT 78096      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  LOC146050 3'  AGAGATGGGGTTTCTCCATGTT 78097      C  T
                                AACA GG GAAACCCCGTCTCT
                                |||| || ||||||||||||||
                                TTGT CC CTTTGGGGTAGAGA
                                  A  T
GAM1681  LOC146229 3'  AGAGACGGGGTTTCACCATGTT 78255      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  LOC146229 3'  AGAGACGGGGTTTTACCGTGTT 78256
                                AACACGGTGAAACCCCGTCTCT
                                ||||||||||||||||||||||
                                TTGTGCCATTTTGGGGCAGAGA

GAM1681  LOC146229 3'  AGTGACGGGGTTTCACCATGTT 78260      C            T
                                AACA GGTGAAACCCCGTC CT
                                |||| |||||||||||||| ||
                                TTGT CCACTTTGGGGCAG GA
                                  A            T
GAM1681  LOC146336 3'  AGACGGGGTCTCACCTGT     78363     C     A
                                ACA GGTGA ACCCCGTCT
                                ||| ||||| |||||||||
                                TGT CCACT TGGGGCAGA
                                  _     C
GAM1681  LOC146346 5'  AGAGACGGGGTTTCACCGTGTT 78385
                                AACACGGTGAAACCCCGTCTCT
                                ||||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGAGA

GAM1681  LOC146429 5'  AGACAGGGTTTCACCATG     84657     C        C
                                CA GGTGAAACCC GTCT
                                || |||||||||| ||||
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                                GT CCACTTTGGG CAGA
                                 A         A
GAM1681  LOC146603 5'  AGAGACGGGGTTTCACCGTGTT 78588
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGAGA

GAM1681  LOC146784 5'  AGAGATGGGGTTTCACCATGTT 78701      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  LOC146839 3'  AGAGACGGGGTTTCACCGTGTT 84835
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGAGA

GAM1681  LOC146894 3'  AGAGATGGGGTTTCACCATGTT 59849      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  LOC146901 3'  AGAGACGGGGTTTCACCATGTT 84886      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  LOC146909 3'  AGAGATGGGGTTTCACCGTGTT 78757
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||
                                TTGTGCCACTTTGGGGTAGAGA

GAM1681  LOC147054 3'  ATGGGGTTTCTCCATGTT     85001      C  T
                                AACA GG GAAACCCCGT
                                |||| || ||||||||||
                                TTGT CC CTTTGGGGTA
                                  A  T
GAM1681  LOC147071 5'  AGAGACGGAGTTTCACCATGTT 73349      C       C
                                AACA GGTGAAAC CCGTCTCT
                                |||| |||||||| ||||||||
                                TTGT CCACTTTG GGCAGAGA
                                  A       A
GAM1681  LOC147080 5'  AGAGACAAGGTTTCACCATGTT 85025      C        CC
                                AACA GGTGAAACC  GTCTCT
                                |||| |||||||||  ||||||
                                TTGT CCACTTTGG  CAGAGA
                                  A        AA
GAM1681  LOC147166 3'  AGAGATGGGGTTTCACCATGTT 78878      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
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                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  LOC147276 3'  AGAGACGGGGCTTCTCCATGTT 78950      C  T   A
                                AACA GG GAA CCCCGTCTCT
                                |||| || ||| ||||||||||
                                TTGT CC CTT GGGGCAGAGA
                                  A  T   C
GAM1681  LOC147429 3'  AGAGATGGGGTTTCACCATGTT 78987      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  LOC147694 3'  AGAGACGGGGTTTCACCGTGTT 79089
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGAGA

GAM1681  LOC147841 3'  AGAGATGGAGTTTCACCATG   79220    C       C
                                CA GGTGAAAC CCGTCTCT
                                || |||||||| ||||||||
                                GT CCACTTTG GGTAGAGA
                                 A       A
GAM1681  LOC148137 3'  AGAGACGGTGTTTCACTGTGTT 59086            C
                                AACACGGTGAAAC CCGTCTCT
                                |||||||||||| ||||||||
                                TTGTGTCACTTTG GGCAGAGA
                                        T
GAM1681  LOC148147 3'  AGAGATGAGGTTTCACCTTGTT 79384      C       C
                                AACA GGTGAAACC CGTCTCT
                                |||| ||||||||| |||||||
                                TTGT CCACTTTGG GTAGAGA
                                  T       A
GAM1681  LOC148189 5'  AGAGACGGGGTTTCACCATGTT 79445      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  LOC148887 5'  AGAGACAGGGTTTCACCATGTT 85391      C       C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A        A
GAM1681  LOC149171 5'  AGAGATGGGGTTTCTCCATGTT 79960      C  T
                                AACA GG GAAACCCCGTCTCT
                                |||| || ||||||||||||||
                                TTGT CC CTTTGGGGTAGAGA
                                  A  T
GAM1681  LOC149421 3'  AGAGACGGGGTTTCACCG    80138
                                CGGTGAAACCCCGTCTCT
                                ||||||||||||||||||
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                                GCCACTTTGGGGCAGAGA

GAM1681  LOC149478 3'  AGAGACGGGGGTTTCACCATGT 80163      C         _
                T                AACA GGTGAAACCCC GTCTCT
                                 |||| |||||||||| ||||||
                                 TTGT CCACTTTGGGG CAGAGA
                                   A          G
GAM1681  LOC149692 3'  AGAGACAGGGTTTCACCATGTT 85725      C         C
                                 AACA GGTGAAACCC GTCTCT
                                 |||| |||||||||| ||||||
                                 TTGT CCACTTTGGG CAGAGA
                                   A         A
GAM1681  LOC149703 5'  AGAGACGGGGTTTTGCCATGTT 85815      C  TG
                                 AACA GG  AAACCCCGTCTCT
                                 |||| ||  ||||||||||||
                                 TTGT CC  TTTGGGGCAGAGA
                                   A  GT
GAM1681  LOC149711 3'  AGAGATGGGGTTTTACCATGTT 85835      C
                                 AACA GGTGAAACCCCGTCTCT
                                 |||| ||||||||||||||||
                                 TTGT CCATTTTGGGGTAGAGA
                                   A
GAM1681  LOC149821 5'  AGACGGAGTTTCACCGTGTT   85927            C
                                 AACACGGTGAAAC CCGTCT
                                 |||||||||||| ||||||
                                 TTGTGCCACTTTG GGCAGA
                                        A
GAM1681  LOC150054 5'  ATGGGGTTTCCCATGTT     85967      C  T
                                 AACA GG GAAACCCCGT
                                 |||| || ||||||||||
                                 TTGT CC CTTTGGGGTA
                                   A  _
GAM1681  LOC150166 5'  AGAAATGGGGTTTCACCATGTT 86029      C           C
                                 AACA GGTGAAACCCCGT TCT
                                 |||| |||||||||||| |||
                                 TTGT CCACTTTGGGGTA AGA
                                   A           A
GAM1681  LOC150225 3'  AGAGACGGTTTCACCATGT    86179     C        CC
                                 ACA GGTGAAACC  GTCTCT
                                 ||| |||||||||  ||||||
                                 TGT CCACTTTGG  CAGAGA
                                   A       __
GAM1681  LOC150282 5'  AGAGATGGCGTTTCACCATGTT 80533      C        C
                                 AACA GGTGAAAC CCGTCTCT
                                 |||| |||||||| ||||||||
                                 TTGT CCACTTTG GGTAGAGA
                                   A       C
GAM1681  LOC150397 3'  AGAGACGCAGTTTCACCGTGTT 80650            CC
                                 AACACGGTGAAAC  CGTCTCT
                                 ||||||||||||  |||||||
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                                TTGTGCCACTTTG  GCAGAGA
                                      AC
GAM1681  LOC150630 5'  AGAGAGGGGGTTTCACCGTG   86284           G
                                CACGGTGAAACCCC TCTCT
                                |||||||||||||| |||||
                                GTGCCACTTTGGGG AGAGA
                                      G
GAM1681  LOC150696 3'  AGAGACGGGGTTTTGCCATGTT 59154     C  TG
                                AACA GG  AAACCCCGTCTCT
                                |||| ||  ||||||||||||
                                TTGT CC  TTTGGGGCAGAGA
                                  A  GT
GAM1681  LOC150960 3'  AGAGATGGGGTCTCACCCTGTT 80864     C    A
                                AACA GGTGA ACCCCGTCTCT
                                |||| ||||| ||||||||||
                                TTGT CCACT TGGGGTAGAGA
                                  C    C
GAM1681  LOC151050 5'  AGAGACAGAGTTTCACCATGTT 80915     C       CCC
                                AACA GGTGAAAC   GTCTCT
                                |||| ||||||||   ||||||
                                TTGT CCACTTTG   CAGAGA
                                  A       AGA
GAM1681  LOC151057 3'  AGAGACGGGGTTTCACCATGTT 86383     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  LOC151201 3'  AGAGACGGGGTTTCACCATGTT 86465     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  LOC151475 5'  AGAGACGAGGTTTCACCATGTT 86583     C       C
                                AACA GGTGAAACC CGTCTCT
                                |||| ||||||||| |||||||
                                TTGT CCACTTTGG GCAGAGA
                                  A       A
GAM1681  LOC151701 3'  AGAGACGGGGTTTCACCATGTT 86664     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  LOC151826 3'  AGAGACAGGGTTTCACCGTGTT 81175           C
                                AACACGGTGAAACCC GTCTCT
                                |||||||||||||| ||||||
                                TTGTGCCACTTTGGG CAGAGA
                                      A
GAM1681  LOC151979 5'  AGAGACGGGGTTTCACCATGTT 81244     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
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                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  LOC152137 3'  AGAGCGGGTTTCACCATGTT   81304      C         C T
                                AACA GGTGAAACCC G CTCT
                                |||| |||||||||| | ||||
                                TTGT CCACTTTGGG C GAGA
                                  A        _ _
GAM1681  LOC152343 3'  ACTGGGTTTCACCATGTT    81415      C         C
                                AACA GGTGAAACCC GT
                                |||| |||||||||| ||
                                TTGT CCACTTTGGG CA
                                  A         T
GAM1681  LOC152445 3'  AGAGACAGGGTTTCACCATGTT 86928      C         C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  LOC152620 3'  AGAGGCGGGGTTACACCATG   60702    C    A
                                CA GGTG AACCCCGTCTCT
                                || |||| ||||||||||||
                                GT CCAC TTGGGGCGGAGA
                                 A    A
GAM1681  LOC152719 5'  AGACGGGGTTTCACCATGTT   87012      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGCAGA
                                  A
GAM1681  LOC152719 5'  AGTGACGGGTTTCACCATGTT  87015      C         C   T
                                AACA GGTGAAACCC GTC CT
                                |||| |||||||||| ||| ||
                                TTGT CCACTTTGGG CAG GA
                                  A         _   T
GAM1681  LOC152794 5'  AGATGGGGTTTCATCATGTT   81552      C
                                AACA GGTGAAACCCCGTCT
                                |||| |||||||||||||||
                                TTGT CTACTTTGGGGTAGA
                                  A
GAM1681  LOC153077 3'  AGAGATGGGGCTTCACCATGTT 87106      C      A
                                AACA GGTGAA CCCCGTCTCT
                                |||| |||||| ||||||||||
                                TTGT CCACTT GGGGTAGAGA
                                  A      C
GAM1681  LOC153606 5'  AGAGATAGGGTTTCACCATGTT 87251      C         CG
                                AACA GGTGAAACCC  TCTCT
                                |||| ||||||||||  |||||
                                TTGT CCACTTTGGG  AGAGA
                                  A         AT
GAM1681  LOC153688 3'  AGAGACAGGATTTCATCGTGTT 87291            C  C
                                AACACGGTGAAA CC GTCTCT
                                |||||||||||| || ||||||
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                                TTGTGCTACTTT GG CAGAGA
                                      A  A
GAM1681  LOC153688 3'  AGAGACAGGGTTTCACCATGTT 87292      C         C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  LOC153883 5'  AGAAATGGGGTTTTACCATGTT 81885      C           C
                                AACA GGTGAAACCCCGT TCT
                                |||| |||||||||||| |||
                                TTGT CCATTTTGGGGTA AGA
                                  A           A
GAM1681  LOC153910 5'  AGAGACAGGGTTTTGCCATGTT 81901      C  TG     C
                                AACA GG  AAACCC GTCTCT
                                |||| ||  |||||| ||||||
                                TTGT CC  TTTGGG CAGAGA
                                  A  GT     A
GAM1681  LOC154282 5'  AGAGATGGTGTTTCACCATGTT 87396      C       C
                                AACA GGTGAAAC CCGTCTCT
                                |||| |||||||| ||||||||
                                TTGT CCACTTTG GGTAGAGA
                                  A       T
GAM1681  LOC154877 3'  AGAGTCGGGGTTTCACCATGTT 87524      C          T
                                AACA GGTGAAACCCCG CTCT
                                |||| |||||||||||| ||||
                                TTGT CCACTTTGGGGC GAGA
                                  A          T
GAM1681  LOC154930 3'  AGAGACAGGATTTTACTGTGTT 82086           C  C
                                AACACGGTGAAA CC GTCTCT
                                |||||||||||| || ||||||
                                TTGTGTCATTTT GG CAGAGA
                                      A  A
GAM1681  LOC155372 3'  AGAGACGGAATTTCACCATG   82257    C      CC
                                CA GGTGAAA  CCGTCTCT
                                || |||||||  ||||||||
                                GT CCACTTT  GGCAGAGA
                                 A      AA
GAM1681  LOC157247 5'  AGAGACGGGGTTTCACCAGTGT 82284      _
                                ACAC GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TGTG CCACTTTGGGGCAGAGA
                                  A
GAM1681  LOC157506 3'  AGAGACGGGGTTTCACCATGTT 82361      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  LOC157798 5'  AGAGACGGGGTTTCACCTTGTT 87852      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
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                                TTGT CCACTTTGGGGCAGAGA
                                  T
GAM1681  LOC157858 5'  AGAGACAGGGTTTCACTATGT  87882     CG        C
                                ACA  GTGAAACCC GTCTCT
                                |||  ||||||||| ||||||
                                TGT  CACTTTGGG CAGAGA
                                  AT        A
GAM1681  LOC158014 5'  AGAGACGGAGTTTCACCATGTT 82552      C        C
                                AACA GGTGAAAC CCGTCTCT
                                |||| |||||||| ||||||||
                                TTGT CCACTTTG GGCAGAGA
                                  A       A
GAM1681  LOC158310 5'  AGAGACAGGGTTTCACAATGTT 88074      CG        C
                                AACA  GTGAAACCC GTCTCT
                                ||||  ||||||||| ||||||
                                TTGT  CACTTTGGG CAGAGA
                                  AA        A
GAM1681  LOC158402 5'  AGAGGGGGGTTTCACCGTGTT  88140              G
                                AACACGGTGAAACCCC TCTCT
                                |||||||||||||||| |||||
                                TTGTGCCACTTTGGGG GGAGA
                                                 _
GAM1681  LOC158476 3'  AGAGACAGGGTTTCACCATGTT 88183      C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  LOC158549 5'  AGAGATAGGGGTTTCACCGTGT 88213               _
           T                     AACACGGTGAAACCCC GTCTCT
                                |||||||||||||||| ||||||
                                TTGTGCCACTTTGGGG TAGAGA
                                          A
GAM1681  LOC158629 5'  AGACAGGGTTTTGCTATGTT   88235      CG TG     C
                                AACA  G  AAACCC GTCT
                                ||||  |  |||||| ||||
                                TTGT  C  TTTGGG CAGA
                                  AT GT      A
GAM1681  LOC158668 3'  AGAGGTGGGGTTTCACCATG   69891    C         GT
                                CA GGTGAAACCCC  CTCT
                                ||  ||||||||||  ||||
                                GT CCACTTTGGGG  GAGA
                                  A          TG
GAM1681  LOC158865 5'  AGAGATGGGGACTTCACCGTGT 88302           A_
           T                     AACACGGTGAA  CCCCGTCTCT
                                ||||||||||  ||||||||||
                                TTGTGCCACTT  GGGGTAGAGA
                                       CA
GAM1681  LOC160646 3'  AGAGATGGGGCTTCACCATGTT 83101      C     A
                                AACA GGTGAA CCCCGTCTCT
                                |||| |||||| ||||||||||
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                                TTGT CCACTT GGGGTAGAGA
                                  A     C
GAM1681  LOC161829 3'  AGAGATGGGGTTTCACCATGTT 83179      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  LOC162427 3'  AGAAATGGGGTTTCACCATGTT 83219      C           C
                                AACA GGTGAAACCCCGT TCT
                                |||| |||||||||||| |||
                                TTGT CCACTTTGGGGTA AGA
                                  A           A
GAM1681  LOC169611 3'  AGAGACAGGGGTTTCACC     83635           _
                                GGTGAAACCCC GTCTCT
                                |||||||||| ||||||
                                CCACTTTGGGG CAGAGA
                                      A
GAM1681  LOC170082 5'  AGAGATGGGGTTTCACCATGTT 83436      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  LOC196047 5'  AGAGCCAGGGTTTCACCATGT  91142     C         CGT
                                ACA GGTGAAACCC   CTCT
                                ||| |||||||||   ||||
                                TGT CCACTTTGGG   GAGA
                                  A         ACC
GAM1681  LOC196411 3'  AGAGATGGGGTTTCACTATGTT 89037      CG
                                AACA  GTGAAACCCCGTCTCT
                                ||||  ||||||||||||||||
                                TTGT  CACTTTGGGGTAGAGA
                                  AT
GAM1681  LOC196529 3'  AGACAGGGTCTCACTGTGTT   89118          A   C
                                AACACGGTGA ACCC GTCT
                                |||||||||| |||| ||||
                                TTGTGTCACT TGGG CAGA
                                      C   A
GAM1681  LOC196529 3'  AGACAGGGTTTCACTACGTT   89120     AC        C
                                AAC  GGTGAAACCC GTCT
                                |||  |||||||||| ||||
                                TTG  TCACTTTGGG CAGA
                                  CA         A
GAM1681  LOC197358 3'  AGAGACGGGGTTTCATCATGTT 89413      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CTACTTTGGGGCAGAGA
                                  A
GAM1681  LOC197358 3'  AGAGATGGGGTTTCACCATGTT 89414      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
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                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  LOC199699 3'  AGACAGGGTTTCACCGTGTT   89663            C
                                AACACGGTGAAACCC GTCT
                                |||||||||||||| ||||
                                TTGTGCCACTTTGGG CAGA
                                     A
GAM1681  LOC199725 5'  AGAGACGGGATTTCACCATGTT 91409     C     C
                                AACA GGTGAAA CCCGTCTCT
                                |||| ||||||| |||||||||
                                TTGT CCACTTT GGGCAGAGA
                                  A     A
GAM1681  LOC199786 3'  AGAGACGGTGGTTTCACCATGT 89736     C       _
           T                     AACA GGTGAAACC CCGTCTCT
                                |||| ||||||||| ||||||||
                                TTGT CCACTTTGG GGCAGAGA
                                  A       T
GAM1681  LOC199786 3'  AGAGATGGGGTTTCACCATGTT 89737     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  LOC199906 3'  AGACAGGGTTTCATCATGTT   89841     C       C
                                AACA GGTGAAACCC GTCT
                                |||| |||||||||| ||||
                                TTGT CTACTTTGGG CAGA
                                  A       A
GAM1681  LOC200014 3'  AGAGACGGTGTTTCACCATGTT 89916     C       C
                                AACA GGTGAAAC CCGTCTCT
                                |||| |||||||| ||||||||
                                TTGT CCACTTTG GGCAGAGA
                                  A       T
GAM1681  LOC200169 5'  AGAGACGGAGTTTCACCATGTT 91550     C       C
                                AACA GGTGAAAC CCGTCTCT
                                |||| |||||||| ||||||||
                                TTGT CCACTTTG GGCAGAGA
                                  A       A
GAM1681  LOC200301 5'  AGAGACGGGGTTTCACCGTGTT 90133
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGAGA

GAM1681  LOC200310 3'  AGAGACGGGGTTTCACCATGTT 66319     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  LOC200316 3'  ACTGGGTTTCACCATGTT    90166     C       C
                                AACA GGTGAAACCC GT
                                |||| |||||||||| ||
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                                TTGT CCACTTTGGG CA
                                  A         T
GAM1681  LOC200316 5'  AGAGACGGGGTTTCTCCATGTT 90171      C  T
                                AACA GG GAAACCCCGTCTCT
                                |||| || ||||||||||||||
                                TTGT CC CTTTGGGGCAGAGA
                                  A  T
GAM1681  LOC200407 3'  AGAGACAGGGTTTTGCCATGTT 91625      C  TG      C
                                AACA GG  AAACCC GTCTCT
                                |||| ||  |||||| ||||||
                                TTGT CC  TTTGGG CAGAGA
                                  A  GT      A
GAM1681  LOC200845 5'  AGAGATGGGGTTTCACTATGTT 90310      CG
                                AACA  GTGAAACCCCGTCTCT
                                ||||  ||||||||||||||||
                                TTGT  CACTTTGGGGTAGAGA
                                  AT
GAM1681  LOC200860 3'  AGAGACGGGGTTTCTCCATGTT 91739      C  T
                                AACA GG GAAACCCCGTCTCT
                                |||| || ||||||||||||||
                                TTGT CC CTTTGGGGCAGAGA
                                  A  T
GAM1681  LOC201164 3'  AGAGACAGGGTTTCACCATGTT 89487      C         C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  LOC201173 5'  AGAGACGGAGTTTCACCATGTT 88668      C       C
                                AACA GGTGAAAC CCGTCTCT
                                |||| |||||||| ||||||||
                                TTGT CCACTTTG GGCAGAGA
                                  A       A
GAM1681  LOC201220 5'  AGAGATGGAGTTTCACCATGTT 88700      C       C
                                AACA GGTGAAAC CCGTCTCT
                                |||| |||||||| ||||||||
                                TTGT CCACTTTG GGTAGAGA
                                  A       A
GAM1681  LOC201294 3'  AGAGACGGGGTTTCACCATGTT 89573      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  LOC201411 3'  AGAGACAGGGTTTCACCATGTT 63635      C         C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A         A
GAM1681  LOC201627 3'  AGAGATGGGGTTTCTCCATGTT 90446      C  T
                                AACA GG GAAACCCCGTCTCT
                                |||| || ||||||||||||||
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                                TTGT CC CTTTGGGGTAGAGA
                                  A  T
GAM1681  LOC202460 5'  AGAGATGGGGTTTCACCATGT  90660     C
                                ACA GGTGAAACCCCGTCTCT
                                ||| ||||||||||||||||
                                TGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  LOC202908 5'  AGATGGGGTCTCACCCTGT    90705     C     A
                                ACA GGTGA ACCCCGTCT
                                ||| ||||| |||||||||
                                TGT CCACT TGGGGTAGA
                                  C     C
GAM1681  LOC203197 3'  AGAGATGGGGTTTCGCCATGTT 90800      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCGCTTTGGGGTAGAGA
                                  A
GAM1681  LOC203339 3'  AGAGATGGGGTTTCACCATGTT 92203      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  LOC203350 3'  AGAGACGGGGTTTCACCGTGTT 92227
                                AACACGGTGAAACCCCGTCTCT
                                ||||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGAGA

GAM1681  LOC203369 3'  ATGGGGTTTCACTGTGTT     90881
                                AACACGGTGAAACCCCGT
                                ||||||||||||||||||
                                TTGTGTCACTTTGGGGTA

GAM1681  LOC204804 3'  AGAGACAGGGTCTCACTGTGT  91031          A    C
                                ACACGGTGA ACCC GTCTCT
                                ||||||||| |||| ||||||
                                TGTGTCACT TGGG CAGAGA
                                      C    A
GAM1681  LOC204804 3'  AGAGATGAGGTTTCACCTTGTT 91032      C        C
                                AACA GGTGAAACC CGTCTCT
                                |||| ||||||||| |||||||
                                TTGT CCACTTTGG GTAGAGA
                                  T        A
GAM1681  LOC219445 5'  AGGGACGGGGTTTCACCGTGTT 93197
                                AACACGGTGAAACCCCGTCTCT
                                ||||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGGGA

GAM1681  LOC219673 5'  AGAAAAGGGGTTTCACCATGTT 94606      C          GTC
                                AACA GGTGAAACCCC   TCT
                                |||| ||||||||||   |||
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                                TTGT CCACTTTGGGG   AGA
                                  A          AAA
GAM1681  LOC219731 5'  AGAGACAGAGTTTCGTCATGTT 94697      C GT     CCC
                                AACA G  GAAAC   GTCTCT
                                |||| |  ||||||  ||||||
                                TTGT C  CTTTG   CAGAGA
                                  A TG     AGA
GAM1681  LOC219735 3'  AGAGACGGGGTTTCACCGTGTT 94723
                                AACACGGTGAAACCCCGTCTCT
                                ||||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGAGA

GAM1681  LOC219894 3'  AGAGATGGGGTTTCACCGTGTT 94895
                                AACACGGTGAAACCCCGTCTCT
                                ||||||||||||||||||||||
                                TTGTGCCACTTTGGGGTAGAGA

GAM1681  LOC220074 3'  AGAGACAAGGTTTCGCCATGTT 59957      C        CC
                                AACA GGTGAAACC  GTCTCT
                                |||| |||||||||  ||||||
                                TTGT CCGCTTTGG  CAGAGA
                                  A        AA
GAM1681  LOC220074 3'  AGAGACGGGGTTTCACCATGTT 59958      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  LOC220074 3'  AGAGATGGGGTTTCGCCATGTT 59959      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCGCTTTGGGGTAGAGA
                                  A
GAM1681  LOC221042 3'  AGAGACGGGGTTTGCTGTGTT  94792         G
                                AACACGGT AAACCCCGTCTCT
                                |||||||| ||||||||||||
                                TTGTGTCG TTTGGGGCAGAGA
                                     _
GAM1681  LOC221060 3'  AGACGGTGTTTCACCATGTT   94826      C       C
                                AACA GGTGAAAC CCGTCT
                                |||| |||||||| ||||||
                                TTGT CCACTTTG GGCAGA
                                  A       T
GAM1681  LOC221271 3'  AGAGGGGGTTTCATCATGTT   93493      C          G
                                AACA GGTGAAACCCC TCT
                                |||| |||||||||| |||
                                TTGT CTACTTTGGGG AGA
                                  A          G
GAM1681  LOC221296 3'  AGAGACGGGGTTTCACCATG   93603    C
                                CA GGTGAAACCCCGTCTCT
                                || ||||||||||||||||
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                                GT CCACTTTGGGGCAGAGA
                                 A
GAM1681  LOC221663 5'  AGAGACAAGGTTTCACTATGTT 95455     CG       CC
                                AACA  GTGAAACC  GTCTCT
                                ||||  ||||||||  ||||||
                                TTGT  CACTTTGG  CAGAGA
                                  AT       AA
GAM1681  LOC221964 3'  AGAGACAGGGTTTTGCCGTGTT 95599       TG     C
                                AACACGG  AAACCC GTCTCT
                                |||||||  |||||| ||||||
                                TTGTGCC  TTTGGG CAGAGA
                                   GT     A
GAM1681  LOC222068 3'  AGAGATGGGGTTTTACCATGTT 94266     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCATTTTGGGGTAGAGA
                                  A
GAM1681  LOC222070 5'  AGACGGTGTTTCACCATGTT   95805     C       C
                                AACA GGTGAAAC CCGTCT
                                |||| |||||||| ||||||
                                TTGT CCACTTTG GGCAGA
                                  A       T
GAM1681  LOC222224 5'  AGAGACAGGGTTTCACCATGTT 95869     C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A        A
GAM1681  LOC245771 5'  AGAGATGGGGTTTCATCATGTT 94464     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CTACTTTGGGGTAGAGA
                                  A
GAM1681  LOC253612 5'  AGAGACAGAGTTTTGCCATGTT 98542     C  TG   CCC
                                AACA GG  AAAC   GTCTCT
                                |||| ||  ||||   ||||||
                                TTGT CC  TTTG   CAGAGA
                                  A  GT    AGA
GAM1681  LOC253664 3'  AGAGATGGGGTTTCCCCATGTT 96454     C  T
                                AACA GG GAAACCCCGTCTCT
                                |||| || ||||||||||||||
                                TTGT CC CTTTGGGGTAGAGA
                                  A  C
GAM1681  LOC253666 3'  AGAGACGGGGTTTCACCATGTT 96759     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  LOC253981 3'  AGAGACGGGGTTTCACCG    97529
                                CGGTGAAACCCCGTCTCT
                                ||||||||||||||||||
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                                GCCACTTTGGGGCAGAGA

GAM1681  LOC254018 5'  AGAGATGGGGTTTCGCCATGTT 98735      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCGCTTTGGGGTAGAGA
                                  A
GAM1681  LOC254268 3'  AGAGATGGGGTTTCACCATGTT 97134      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGTAGAGA
                                  A
GAM1681  LOC254295 5'  AGAGACGGGGTTTCACCGTGTT 97887
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGAGA

GAM1681  LOC254351 5'  AGACGGGGTTTCTCCGTGTT   96679        T
                                AACACGG GAAACCCCGTCT
                                ||||||| ||||||||||||
                                TTGTGCC CTTTGGGGCAGA
                                    T
GAM1681  LOC254655 3'  AGAGACGGGGTTTCACCATGTT 97214      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  LOC255308 3'  AGAGACGGGGTTTCGGCATGTT 96174      CGG
                                AACA   TGAAACCCCGTCTCT
                                ||||   ||||||||||||||
                                TTGT   GCTTTGGGGCAGAGA
                                  ACG
GAM1681  LOC255465 3'  AGAGACGGGTTTCACCATGTT  99101      C         C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A        _
GAM1681  LOC255497 3'  AGAGACGGGGTTTCACCATGTT 98983      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  LOC256221 3'  AGAGACGGGGTTTCACCGTGTT 96906
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGAGA

GAM1681  LOC256306 3'  AGAGACGGGGTTTCACCATGTT 98504      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
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                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  LOC257465 3'  AGAGATGGTGTTTCACCATGTT 82487      C       C
                                AACA GGTGAAAC CCGTCTCT
                                |||| |||||||| ||||||||
                                TTGT CCACTTTG GGTAGAGA
                                  A       T
GAM1681  LOC257486 3'  AGAGACGGGGTTTCACCATGTT 69765      C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  LOC51008  5'  AGAGATGGGGTTTCTCCATGTT 32525      C  T
                                AACA GG GAAACCCCGTCTCT
                                |||| || ||||||||||||||
                                TTGT CC CTTTGGGGTAGAGA
                                  A  T
GAM1681  LOC51159  5'  AGAGACGGGATTTCACCATGTT 33027      C      C
                                AACA GGTGAAA CCCGTCTCT
                                |||| ||||||| |||||||||
                                TTGT CCACTTT GGGCAGAGA
                                  A      A
GAM1681  LOC51193  5'  AGACGGGGTTTCCCCATGTT   33356      C  T
                                AACA GG GAAACCCCGTCT
                                |||| || ||||||||||||
                                TTGT CC CTTTGGGGCAGA
                                  A  C
GAM1681  LOC51219  5'  AGACGGGGTTTCTCCATGT    33538     C  T
                                ACA GG GAAACCCCGTCT
                                ||| || ||||||||||||
                                TGT CC CTTTGGGGCAGA
                                  A  T
GAM1681  LOC51696  3'  AGAGACAGCGTTTCACCATGTT 33077      C       CCC
                                AACA GGTGAAAC   GTCTCT
                                |||| ||||||||   ||||||
                                TTGT CCACTTTG   CAGAGA
                                  A       CGA
GAM1681  LOC56181  5'  AGAGACAGGGCTTCACTGTGTT 97268           A   C
                                AACACGGTGAA CCC GTCTCT
                                |||||||||||| ||| ||||||
                                TTGTGTCACTT GGG CAGAGA
                                      C   A
GAM1681  LOC57107  3'  AGAGATGGGGTTTCACTATGTT 40178      CG
                                AACA  GTGAAACCCCGTCTCT
                                ||||  ||||||||||||||||
                                TTGT  CACTTTGGGGTAGAGA
                                  AT
GAM1681  LOC57146  3'  AGATGGGGTTTCACCATGTT   40288      C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
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                                TTGT CCACTTTGGGGTAGA
                                  A
GAM1681  LOC81034  3'  AGAAATGGGGTTTCACCATGTT 48580     C          C
                                AACA GGTGAAACCCCGT TCT
                                |||| |||||||||||||| |||
                                TTGT CCACTTTGGGGTA AGA
                                  A          A
GAM1681  LOC89231  3'  AGAGATGGGGTCTCACTATGTT 94291     CG   A
                                AACA  GTGA ACCCCGTCTCT
                                ||||  |||| ||||||||||
                                TTGT  CACT TGGGGTAGAGA
                                  AT   C
GAM1681  LOC89919  3'  AGAGACGGGGTTTCACCATGTT 61368     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  LOC89932  3'  AGAGACGGGGTTTCTCCATGTT 61441     C  T
                                AACA GG GAAACCCCGTCTCT
                                |||| || ||||||||||||||
                                TTGT CC CTTTGGGGCAGAGA
                                  A  T
GAM1681  LOC89932  3'  AGATGGGGTTTCACCATGTT   61442     C
                                AACA GGTGAAACCCCGTCT
                                |||| ||||||||||||||
                                TTGT CCACTTTGGGGTAGA
                                  A
GAM1681  LOC90288  3'  AGAGACGGGGTTTCACAGTGTT 62767      G
                                AACAC GTGAAACCCCGTCTCT
                                ||||| ||||||||||||||||
                                TTGTG CACTTTGGGGCAGAGA
                                   A
GAM1681  LOC90288  3'  AGAGGGAGTCTCACCGTGT    62768       A _  G
                                ACACGGTGA AC CCC TCT
                                ||||||||| || ||| |||
                                TGTGCCACT TG GGG AGA
                                     C  A  _
GAM1681  LOC90333  3'  AGAGACTGGGTTTCACCGTGTT 62956           C
                                AACACGGTGAAACCC GTCTCT
                                |||||||||||||| ||||||
                                TTGTGCCACTTTGGG CAGAGA
                                        T
GAM1681  LOC90459  3'  AGAGGCGGGGTTTCACCATGTT 63546     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCGGAGA
                                  A
GAM1681  LOC90485  3'  AGAGGCAGGGTTTCACCATGTT 63684     C       C
                                AACA GGTGAAACCC GTCTCT
                                |||| |||||||||| ||||||
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                                TTGT CCACTTTGGG CGGAGA
                                  A        A
GAM1681  LOC90485  3'  AGAGGCGGGGTTTCACCATGTT 63685     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCGGAGA
                                  A
GAM1681  LOC90591  3'  AGAGACGGAGTTTCATCGTGTT 64142          C
                                AACACGGTGAAAC CCGTCTCT
                                |||||||||||| ||||||||
                                TTGTGCTACTTTG GGCAGAGA
                                       A
GAM1681  LOC90591  3'  AGAGACGGGGCTTCACTATGTT 64143     CG    A
                                AACA  GTGAA CCCCGTCTCT
                                ||||  ||||| ||||||||||
                                TTGT  CACTT GGGGCAGAGA
                                  AT    C
GAM1681  LOC91012  5'  AGAGACAAGGTTTTGCCATGTT 65242     C  TG    CC
                                AACA GG  AAACC  GTCTCT
                                |||| ||  |||||  ||||||
                                TTGT CC  TTTGG  CAGAGA
                                  A  GT    AA
GAM1681  LOC91115  3'  AGAGATGGGGTTTCACTGTGTT 65541
                                AACACGGTGAAACCCCGTCTCT
                                ||||||||||||||||||||||
                                TTGTGTCACTTTGGGGTAGAGA

GAM1681  LOC91115  3'  AGAGATGGGGTTTCATCATGTT 65542     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CTACTTTGGGGTAGAGA
                                  A
GAM1681  LOC91250  5'  AGAGATGGGGTTTCATCATGTT 65902     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CTACTTTGGGGTAGAGA
                                  A
GAM1681  LOC91263  3'  AGAGGTGGGGGTCCCACTGTGT 65996        AAA_   GT
          T                      AACACGGTG    CCCC  CTCT
                                |||||||||    ||||  ||||
                                TTGTGTCAC    GGGG  GAGA
                                     CCTG    TG
GAM1681  LOC91291  5'  AGAGACAAGGTTTCACCCTGTT 66085     C       CC
                                AACA GGTGAAACC  GTCTCT
                                |||| |||||||||  ||||||
                                TTGT CCACTTTGG  CAGAGA
                                  C       AA
GAM1681  LOC91373  3'  AGAGATGGGGTTTGACCGTGTT 66405       G
                                AACACGGT AAACCCCGTCTCT
                                |||||||| ||||||||||||
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                                TTGTGCCA TTTGGGGTAGAGA
                                    G
GAM1681  LOC91561  5'  AGACGGGGTTTCTCCATGTT  67038     C  T
                                AACA GG GAAACCCCGTCT
                                |||| || ||||||||||||
                                TTGT CC CTTTGGGGCAGA
                                  A  T
GAM1681  LOC91893  3'  AGAGACGAGGTTTCACCGTGTT 68067           C
                                AACACGGTGAAACC CGTCTCT
                                |||||||||||||| |||||||
                                TTGTGCCACTTTGG GCAGAGA
                                       A
GAM1681  LOC92148  5'  AGAGACGGGGTTTCACCGTGTT 68871
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||||
                                TTGTGCCACTTTGGGGCAGAGA

GAM1681  LOC92303  3'  AGAGATGGGTTTCACCATGTT  69382     C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| ||||||||||| ||||||
                                TTGT CCACTTTGGG TAGAGA
                                  A       _
GAM1681  LOC92661  5'  AGAGGCGGGGTTTCACTGTGTT 70616
                                AACACGGTGAAACCCCGTCTCT
                                |||||||||||||||||||||||
                                TTGTGTCACTTTGGGGCGGAGA

GAM1681  LOC92689  3'  AGAGACAGGGTTTCACCATGTT 70770     C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| ||||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A        A
GAM1681  LOC92841  3'  AGAGACAGGGTTTCACCATGTT 71245     C        C
                                AACA GGTGAAACCC GTCTCT
                                |||| ||||||||||| ||||||
                                TTGT CCACTTTGGG CAGAGA
                                  A        A
GAM1681  LOC92841  3'  AGAGACGGGGTTTCACCATGTT 71246     C
                                AACA GGTGAAACCCCGTCTCT
                                |||| ||||||||||||||||
                                TTGT CCACTTTGGGGCAGAGA
                                  A
GAM1681  LOC93129  3'  AGAGACGGGGTTTCGCTGT   71953
                                ACGGTGAAACCCCGTCTCT
                                ||||||||||||||||||
                                TGTCGCTTTGGGGCAGAGA

GAM1681  LOC93349  3'  AGAGACGGGGTTTCACTATGTT 57262     CG
                                AACA  GTGAAACCCCGTCTCT
                                ||||  ||||||||||||||||
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                                TTGT  CACTTTGGGGCAGAGA
                                  AT
GAM1681  LOC93408  5'  AGAAACAGAGTTTCACCATGTT 57283     C       CCC  C
                                AACA GGTGAAAC   GT TCT
                                |||| ||||||||   || |||
                                TTGT CCACTTTG   CA AGA
                                  A       AGA  A
GAM1682  ITPR2    3'  AAAACAACCAAGTGCCAAG   11076        GGCC  C
                                CTTGGCACT    GT GTTTT
                                |||||||||    || |||||
                                GAACCGTGA    CA CAAAA
                                     AC__  A
GAM1682  MSF      3'  AAATGAGTGGCCAGCGCCAGG  89462       A      _
                                CTTGGC CTGGCCG TCGTTT
                                |||||| ||||||| ||||||
                                GGACCG GACCGGT AGTAAA
                                   C      G
GAM1682  SEMG1    3'  AAAGGATGGACCAATATCAAG  13012      CAC  _    G
                                CTTGG   TGG CCGTC TTT
                                |||||   ||| ||||| |||
                                GAACT   ACC GGTAG AAA
                                  ATA  A    G
GAM1682  TCF1     3'  AGCCTCGCAACCCGTGCCAAG  6781        T  C__  TC
                                CTTGGCAC GG   CG  GTT
                                |||||||| ||   ||  |||
                                GAACCGTG CC   GC  CGA
                                     C  AAC  TC
GAM1682  TCFL4    3'  AAAACAAGGTAGCCAGTGC   64205       CG  __
                                GCACTGGC  TC  GTTTT
                                ||||||||  ||  |||||
                                CGTGACCG  GG  CAAAA
                                     AT  AA
GAM1682  B3GALT1  5'  AAAACAAACTAGTGCCAAG   40941          CCGTC
                                CTTGGCACTGG    GTTTT
                                ||||||||||    |||||
                                GAACCGTGATC    CAAAA
                                      AAA__
GAM1682  C20orf42 3'  AAACACCTGCCAGTGTCAAG  35060          C_  C
                                CTTGGCACTGGC  GT GTTT
                                ||||||||||||  || ||||
                                GAACTGTGACCG  CA CAAA
                                      TC  _
GAM1682  FLJ23548 3'  AAAACTGTCCTGCTCAGTGCCA 45044         _  CGT_ _
            AG                   CTTGGCACTG GC    C GTTTT
                                ||||||||||  ||    |  |||||
                                GAACCGTGAC CG    G CAAAA
                                      T  TCCT T
GAM1682  GRIN3A   3'  AAGCGGAGCAAGTGCCAAG   56775        G  CG
                                CTTGGCACT GC  TCGTTT
                                |||||||||  ||  ||||||
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                                GAACCGTGA CG  GGCGAA
                                     A  A_
GAM1682  KIAA0546  3'  AAAACTAGTTTCCAAGTGCCAA 71834        _  CCGTC_
              G                   CTTGGCACT GG     GTTTT
                                  ||||||||| ||     |||||
                                  GAACCGTGA CC     CAAAA
                                     A  TTTGAT
GAM1682  KIAA1143  3'  AAAGCGACCACTGCCAAG    69223       C   CCG
                                  CTTGGCA TGG   TCGTTTT
                                  ||||||| |||   |||||||
                                  GAACCGT ACC   AGCGAAA
                                     C  ___
GAM1682  MGC3222   3'  AAAACACAGCCAGCCCAAG   44542      CA    C  C
                                  CTTGG  CTGGC GT GTTTT
                                  |||||  ||||| || |||||
                                  GAACC  GACCG CA CAAAA
                                     C_    A  _
GAM1682  RENT2     3'  AAAGTGATACCAGCCCAAG   55492      CA    CC
                                  CTTGG  CTGG  GTCGTTTT
                                  |||||  ||||  ||||||||
                                  GAACC  GACC  TAGTGAAA
                                     C_    A_
GAM1682  RENT2     3'  AAAGTGATACCAGCCCAAG   32064      CA    CC
                                  CTTGG  CTGG  GTCGTTTT
                                  |||||  ||||  ||||||||
                                  GAACC  GACC  TAGTGAAA
                                     C_    A_
GAM1682  SLC2A11   3'  AAAGGGGTGGCCAGAGCCAA   48691      A     GT G
                                  TTGGC CTGGCC  C TTTT
                                  ||||| ||||||  | ||||
                                  AACCG GACCGG  G GAAA
                                     A     TG G
GAM1682  WBSCR23   5'  AAAACGACAACCAATGCTGA   47402   TG   C   CC
                                  T  GCA TGG  GTCGTTTT
                                  |  ||| |||  ||||||||
                                  A  CGT ACC  CAGCAAAA
                                   GT   A   AA
GAM1682  LOC200014 5'  AGGCTGCGGCCAGTGCCAAG   89919            C
                                  CTTGGCACTGGCCGT GTTT
                                  |||||||||||||| ||||
                                  GAACCGTGACCGGCG CGGA
                                            T
GAM1683  BSN       3'  CCCAGCATCATGAGCAAG    14380         A  CTTCA  AA
                                  CTTGCTCAT GT    GC  GG
                                  ||||||||| ||    ||  ||
                                  GAACGAGTA TA    CG  CC
                                     C  _____  AC
GAM1683  CLCA2     3'  CCTTACACTTTGGCTATGAACA 22563     C       TTCAGC_
              A                    TTG TCATAGTC      AAGG
                                  ||| ||||||||      ||||
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                                AAC AGTATCGG      TTCC
                                  A       TTTCACA
GAM1683  CRY2     3'  CCTTGCTCCGTGAGCAA     72661         AGTCTTC
                                TTGCTCAT      AGCAAGG
                                ||||||||      |||||||
                                AACGAGTG      TCGTTCC
                                    CC_____
GAM1683  FADD     3'  TCCTCACTATGACACTGAGCAA 15126         TA   TTC  CA
             G                   CTTGCTCA  GTC   AG  AGGA
                                ||||||||  |||   ||  ||||
                                GAACGAGT  CAG   TC  TCCT
                                    CA   TA_  AC
GAM1683  HLCS     5'  TCCATTGAAGACTTGAACAAG  6421       C   T        CAA
                                CTTG TCA AGTCTTCAG   GGA
                                |||| ||| |||||||||   |||
                                GAAC AGT TCAGAAGTT   CCT
                                  A  _       A__
GAM1683  MEST     3'  CTGAAAGACCTATGAGCAA    70459          _   _
                                TTGCTCATAG TCTT CAG
                                |||||||||| |||| |||
                                AACGAGTATC AGAA GTC
                                     C    A
GAM1683  PCDH7    5'  CCCCGCTGCATGAGCAG     51616         A TCTT    AA
                                TTGCTCAT G    CAGC  GG
                                |||||||| |    ||||  ||
                                GACGAGTA C    GTCG  CC
                                    _ _____    CC
GAM1683  PCDH7    5'  CCCCGCTGCATGAGCAG     51619         A TCTT    AA
                                TTGCTCAT G    CAGC  GG
                                |||||||| |    ||||  ||
                                GACGAGTA C    GTCG  CC
                                    _ _____    CC
GAM1683  PCDH7    5'  CCCCGCTGCATGAGCAG     11987         A TCTT    AA
                                TTGCTCAT G    CAGC  GG
                                |||||||| |    ||||  ||
                                GACGAGTA C    GTCG  CC
                                    _ _____    CC
GAM1683  PLP2     5'  TCCTCGAAACCACGAGCAAG   12176         ATA  C   AGCA
                                CTTGCTC   GT TTC    AGGA
                                |||||||   || |||    ||||
                                GAACGAG   CA AAG    TCCT
                                    CAC  _   C___
GAM1683  PLXNA2   3'  TCCCTAAAGTTACTATGAGAAG 48003     G       __   C  CAA
                                CTT CTCATAGT  CTT AG   GGA
                                ||| ||||||||  ||| ||   |||
                                GAA GAGTATCA  GAA TC   CCT
                                  _       TT   A  ___
GAM1683  AP1GBP1  3'  CCTCAGACCAGTGAGCAA    24346         A_    TCAGCA
                                TTGCTCAT  GTCT     AGG
                                ||||||||  ||||     |||
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                                AACGAGTG CAGA    TCC
                                    AC   C_____
GAM1683 AP1GBP1  3' CCTCAGACCAGTGAGCAA   55438       A_   TCAGCA
                                TTGCTCAT GTCT    AGG
                                |||||||| ||||    |||
                                AACGAGTG CAGA    TCC
                                    AC   C_____
GAM1683 AP1GBP1  3' CCTCAGACCAGTGAGCAA   55444       A_   TCAGCA
                                TTGCTCAT GTCT    AGG
                                |||||||| ||||    |||
                                AACGAGTG CAGA    TCC
                                    AC   C_____
GAM1683 CAP350   3' CCTACTGAAGACTGGGC    29703      TA      CA
                                GCTCA GTCTTCAG AGG
                                ||||| |||||||| |||
                                CGGGT CAGAAGTC TCC
                                  __      A_
GAM1683 DDX34    3' TCCCTGCTGGAGACCAACAAG 28679     CTCATA       A
                                CTTG     GTCTTCAGCA GGA
                                ||||     |||||||||| |||
                                GAAC     CAGAGGTCGT CCT
                                  AAC___       C
GAM1683 DKFZP586G1122 3' CCGCAAAACTGTGAGCAA   61938          CTTCA  AA
                                TTGCTCATAGT    GC  GG
                                ||||||||||    ||  ||
                                AACGAGTGTCA    CG  CC
                                     AAA__  __
GAM1683 FAM10A6  3' CCTTGCTGAAGGAAAAGCAA  72782      CATAG
                                TTGCT    TCTTCAGCAAGG
                                |||||    ||||||||||||
                                AACGA    GGAAGTCGTTCC
                                  AAA__
GAM1683 FLJ10546 5' TGCAAAGACTATGAGCA    60184          CA
                                TGCTCATAGTCTT  GCA
                                |||||||||||||  |||
                                ACGAGTATCAGAA  CGT
                                     A_
GAM1683 FLJ10726 3' CTTAACTATGAGCAGG     37042          CTTCAGC
                                CTTGCTCATAGT      AAG
                                ||||||||||||      |||
                                GGACGAGTATCA      TTC
                                     A_______
GAM1683 KIAA0475 5' CCTTAATACATGAGCAAG   30115        A  C  CAGC
                                CTTGCTCAT GT TT   AAGG
                                ||||||||| || ||   ||||
                                GAACGAGTA CA AA   TTCC
                                     _ T  _____
GAM1683 KIAA1655 5' CCTCACTGTGGATGAGCAA  67179       TAG   T   CA
                                TTGCTCA   TCT CAG  AGG
                                |||||||   ||| |||  |||
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                                AACGAGT   AGG GTC  TCC
                                   ___   T   AC
GAM1683  MGC3077   3'  TCCTTGTTTTTAGACTAT    44128        TC_
                                ATAGTCT   AGCAAGGA
                                |||||||   ||||||||
                                TATCAGA   TTGTTCCT
                                    TTT
GAM1683  RAB40C    3'  CCTTGTTTGGGATTATGAACAA 41278     C        TC
                                TTG TCATAGTCT  AGCAAGG
                                ||| |||||||||  |||||||
                                AAC AGTATTAGG  TTGTTCC
                                  A        GT
GAM1683  SENP2     3'  CTGCTGAAGAGCAGG       76832        ATAGTC      A
                                CTTGCTC     TTCAGCA G
                                |||||||     ||||||| |
                                GGACGAG     AAGTCGT C
                                   _______      C
GAM1683  ST13      3'  CCTTGCTGAAGGAAAAGCAA   15431      CATAG
                                TTGCT    TCTTCAGCAAGG
                                |||||    ||||||||||||
                                AACGA    GGAAGTCGTTCC
                                   AAA__
GAM1683  LOC118491 5'  TCCTGTTGGAGAACTATGAGCA 74358           _       A
              AG                   CTTGCTCATAGT CTTCAGCA GGA
                                |||||||||||| |||||||| |||
                                GAACGAGTATCA GAGGTTGT CCT
                                      A       _
GAM1683  LOC125228 3'  CCTTTGGAAACTATGGGCAA   74863          C    GC
                                TTGCTCATAGT TTCA  AAGG
                                |||||||||||| ||||  ||||
                                AACGGGTATCA AGGT  TTCC
                                      A   __
GAM1683  LOC126751 3'  CCCTGCTGAGATTGAGCCAG   75072    T    TA   T    A
                                CT GCTCA  GTCT CAGCA GG
                                || |||||  |||| ||||| ||
                                GA CGAGT  TAGA GTCGT CC
                                 C    __   _    C
GAM1683  LOC144840 3'  CCTACTGAAGACTGGAG     77526     A        CA
                                CTC TAGTCTTCAG  AGG
                                ||| ||||||||||  |||
                                GAG GTCAGAAGTC  TCC
                                  _        A_
GAM1683  LOC149052 3'  CCTTGCTGAAGGAAAAGCAA   79872      CATAG
                                TTGCT    TCTTCAGCAAGG
                                |||||    ||||||||||||
                                AACGA    GGAAGTCGTTCC
                                   AAA__
GAM1683  LOC158886 3'  CCTTGCTGAAGGAAAAGCAA   83722      CATAG
                                TTGCT    TCTTCAGCAAGG
                                |||||    ||||||||||||
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                                AACGA    GGAAGTCGTTCC
                                  AAA__
GAM1683  LOC200197 3'  CCCTGCCGACATGAGCAA    90016        A   TTCA   A
                                TTGCTCAT GTC    GCA GG
                                |||||||| |||    ||| ||
                                AACGAGTA CAG    CGT CC
                                     _   C___   C
GAM1683  LOC219731 5'  CCAGGTTAAAACTATGAGGAAG 94699     G       C  C   AA
                                CTT CTCATAGT TT AGC  GG
                                ||| |||||||| || |||  ||
                                GAA GAGTATCA AA TTG  CC
                                  G       A  _   GA
GAM1683  LOC221178 3'  CCCTGCTGATGATGAGCAAG   95168         AGTCT     A
                                CTTGCTCAT     TCAGCA GG
                                |||||||||     |||||| ||
                                GAACGAGTA     AGTCGT CC
                                     GT___     C
GAM1683  LOC222407 5'  CCTACACTGAAAACAATGAGCA 95973         A  C     CA_
            A                    TTGCTCAT GT TTCAG   AGG
                                |||||||| || |||||   |||
                                AACGAGTA CA AAGTC   TCC
                                     A  A     ACA
GAM1683  LOC245718 3'  CCTTGCTGAAGGAAAAGCAA   92415       CATAG
                                TTGCT     TCTTCAGCAAGG
                                |||||     ||||||||||||
                                AACGA     GGAAGTCGTTCC
                                  AAA__
GAM1683  LOC256228 5'  CCTTGCTGAAGCAGGACAGCAA 97969       CATAGT
            G                    CTTGCT      CTTCAGCAAGG
                                ||||||      ||||||||||
                                GAACGA      GAAGTCGTTCC
                                   CAGGAC
GAM1684  ADAMTS4   3'  TAGAGACAGGGTTTCACCATGT 18772              C
            TG                     TAACATGGTGAAACCC GTCTCTA
                                |||||||||||||| |||||||
                                GTTGTACCACTTTGGG CAGAGAT
                                          A
GAM1684  ADAMTS4   3'  TAGAGACGGGGTTTCACCATGT 18773
            TG                     TAACATGGTGAAACCCCGTCTCTA
                                |||||||||||||||||||||||
                                GTTGTACCACTTTGGGGCAGAGAT

GAM1684  ADCY6     5'  TAGAGACGAGGTTTCACCATCT 40963     C         C
            TG                     TAA ATGGTGAAACC CGTCTCTA
                                ||| |||||||||| ||||||||
                                GTT TACCACTTTGG GCAGAGAT
                                  C          A
GAM1684  APAF1     3'  TAGAGACAGGGTCTCACTATGT 25980          A   C
            TG                     TAACATGGTGA ACCC GTCTCTA
                                |||||||||| |||| |||||||
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                                GTTGTATCACT TGGG CAGAGAT
                                      C    A
GAM1684  APAF1    3'  TAGAGACGGGGTTTCACCATGT 25981
                TG                  TAACATGGTGAAACCCCGTCTCTA
                                    ||||||||||||||||||||||||
                                    GTTGTACCACTTTGGGGCAGAGAT

GAM1684  APM1     3'  TAGAGACGGGGTTTCACCA   17791
                                    TGGTGAAACCCCGTCTCTA
                                    |||||||||||||||||||
                                    ACCACTTTGGGGCAGAGAT

GAM1684  APOL1    3'  TAGAGATGGGGTTTCACCATGT 14744
                TG                  TAACATGGTGAAACCCCGTCTCTA
                                    ||||||||||||||||||||||||
                                    GTTGTACCACTTTGGGGTAGAGAT

GAM1684  APPL     3'  TAGAGACGGGGTTTCACCGTGT 24957
                TA                  TAACATGGTGAAACCCCGTCTCTA
                                    ||||||||||||||||||||||||
                                    ATTGTGCCACTTTGGGGCAGAGAT

GAM1684  ARCN1    3'  TAGAGACGGGGTTTCACCGTGT 9758
                TG                  TAACATGGTGAAACCCCGTCTCTA
                                    ||||||||||||||||||||||||
                                    GTTGTGCCACTTTGGGGCAGAGAT

GAM1684  ATM      3'  TAGAGGTGGGGTTTCACCAT   5302            GT
                                    ATGGTGAAACCCC  CTCTA
                                    ||||||||||||  |||||
                                    TACCACTTTGGGG  GAGAT
                                          TG
GAM1684  ATP6V1A1  3'  TAGAAACGGGGTTTCACCAT   9875             C
                                    ATGGTGAAACCCCGT TCTA
                                    |||||||||||||| ||||
                                    TACCACTTTGGGGCA AGAT
                                          A
GAM1684  ATP7A    3'  TAGAGACGGGGTTTCGCCATGT 5330
                TG                  TAACATGGTGAAACCCCGTCTCTA
                                    ||||||||||||||||||||||||
                                    GTTGTACCGCTTTGGGGCAGAGAT

GAM1684  AXL      3'  TAGAGACAGGGTTTCACCATGT 41893            C
                TG                  TAACATGGTGAAACCC GTCTCTA
                                    ||||||||||||||| |||||||
                                    GTTGTACCACTTTGGG CAGAGAT
                                          A
GAM1684  BRIP1    3'  TAGAGATGGGGTTTCACCATGT 50213
                TG                  TAACATGGTGAAACCCCGTCTCTA
                                    ||||||||||||||||||||||||
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                                GTTGTACCACTTTGGGGTAGAGAT

GAM1684  C14orf1   3'  TAGAGACGGGGTTTCACTCTGT 24172     T
                                ACA GGTGAAACCCCGTCTCTA
                                ||| ||||||||||||||||||
                                TGT TCACTTTGGGGCAGAGAT
                                  C
GAM1684  C7       3'  TAGAGATGGGTTTCACCATGTT 6989              C
              G                  TAACATGGTGAAACCC GTCTCTA
                                 |||||||||||||||| |||||||
                                 GTTGTACCACTTTGGG TAGAGAT
                                                  _
GAM1684  CAMLG    3'  AGACAGGGTTTCTCCATGTTG  9994         T      C
                                 TAACATGG GAAACCC GTCT
                                 |||||||| ||||||| ||||
                                 GTTGTACC CTTTGGG CAGA
                                      T      A
GAM1684  CASP2    3'  TAGAGACAGGGTTTCACCATGT 8720              C
              TA                  TAACATGGTGAAACCC GTCTCTA
                                  |||||||||||||||| |||||||
                                  ATTGTACCACTTTGGG CAGAGAT
                                        A
GAM1684  CASP2    3'  TAGAGACAGGGTTTCACCATGT 8721              C
              TA                  TAACATGGTGAAACCC GTCTCTA
                                  |||||||||||||||| |||||||
                                  ATTGTACCACTTTGGG CAGAGAT
                                        A
GAM1684  CASP2    3'  TAGAGACAGGGTTTCACCATGT 53349             C
              TA                  TAACATGGTGAAACCC GTCTCTA
                                  |||||||||||||||| |||||||
                                  ATTGTACCACTTTGGG CAGAGAT
                                        A
GAM1684  CASP8    3'  TAGAGACAGGGTTTCACTGTGT 8764              C
              TA                  TAACATGGTGAAACCC GTCTCTA
                                  |||||||||||||||| |||||||
                                  ATTGTGTCACTTTGGG CAGAGAT
                                        A
GAM1684  CASP8    3'  TAGAGACAGGGTTTCACTGTGT 8765              C
              TA                  TAACATGGTGAAACCC GTCTCTA
                                  |||||||||||||||| |||||||
                                  ATTGTGTCACTTTGGG CAGAGAT
                                        A
GAM1684  CCNF     3'  TAGAGACGGGATTTCACCATGT 10087             C
              TG                  TAACATGGTGAAA CCCGTCTCTA
                                  |||||||||||| ||||||||||
                                  GTTGTACCACTTT GGGCAGAGAT
                                       A
GAM1684  CDC6     3'  TAGAGACAGGGTTTTACCATGT 8828              C
              TG                  TAACATGGTGAAACCC GTCTCTA
                                  |||||||||||||||| |||||||
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                                GTTGTACCATTTTGGG CAGAGAT
                                        A
GAM1684  CDH17    3'  TAGAGACGGGGTTTCGCCAT   15789
                                ATGGTGAAACCCCGTCTCTA
                                ||||||||||||||||||||
                                TACCGCTTTGGGGCAGAGAT

GAM1684  CNGA1    5'  TAGAGATGGGATTTCACCATGT 60244            C
              TG                  TAACATGGTGAAA CCCGTCTCTA
                                ||||||||||||| |||||||||
                                GTTGTACCACTTT GGGTAGAGAT
                                        A
GAM1684  COX15    3'  TAGAGAAGGGGTTTCACCA   55290          G
                                TGGTGAAACCCC TCTCTA
                                |||||||||||| ||||||
                                ACCACTTTGGGG AGAGAT
                                        A
GAM1684  CR1      3'  TAGAGACGGGGTTTCACCATGT 6951
              TA                  TAACATGGTGAAACCCCGTCTCTA
                                ||||||||||||||||||||||||
                                ATTGTACCACTTTGGGGCAGAGAT

GAM1684  CTF1     3'  TAGAGACGAGGTTTCGCCATGT 9021             C
              TG                  TAACATGGTGAAACC CGTCTCTA
                                ||||||||||||||| ||||||||
                                GTTGTACCGCTTTGG GCAGAGAT
                                        A
GAM1684  CXCL16   3'  TAGAGACGGGGTTTCACCATGT 42178
              TG                  TAACATGGTGAAACCCCGTCTCTA
                                ||||||||||||||||||||||||
                                GTTGTACCACTTTGGGGCAGAGAT

GAM1684  CYP1A2   3'  TAGAGACGAGGTTTCACTGTGT 69662            C
              TG                  TAACATGGTGAAACC CGTCTCTA
                                ||||||||||||||| ||||||||
                                GTTGTGTCACTTTGG GCAGAGAT
                                        A
GAM1684  CYP1A2   3'  TAGAGACGGGTTTCACCATGTT 69663            C
              G                   TAACATGGTGAAACCC GTCTCTA
                                ||||||||||||||| |||||||
                                GTTGTACCACTTTGGG CAGAGAT
                                        _
GAM1684  CYP1A2   3'  TGGGGTTTCACCATGTTG    7530
                                TAACATGGTGAAACCCCG
                                ||||||||||||||||||
                                GTTGTACCACTTTGGGGT

GAM1684  CYP4F3   3'  TAGAGGCGGGGTTTCGCCATGT 8014
              TA                  TAACATGGTGAAACCCCGTCTCTA
                                ||||||||||||||||||||||||
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                                ATTGTACCGCTTTGGGGCGGAGAT

GAM1684  DFFB     3'  TAGAAACGGGGTTTCACCATGT 88784                C
             TG                  TAACATGGTGAAACCCCGT TCTA
                                 |||||||||||||||||| ||||
                                 GTTGTACCACTTTGGGGCA AGAT
                                           A
GAM1684  DFFB     3'  TAGAGACGGGGTTTCACCATGT 88785
             TG                  TAACATGGTGAAACCCCGTCTCTA
                                 ||||||||||||||||||||||||
                                 GTTGTACCACTTTGGGGCAGAGAT

GAM1684  DHFR     3'  TAGAGATGGGGTTTCACCATGT 7657
             TG                  TAACATGGTGAAACCCCGTCTCTA
                                 ||||||||||||||||||||||||
                                 GTTGTACCACTTTGGGGTAGAGAT

GAM1684  DISC1    3'  TAGAGACAGGGCTTCACCATGT 38515           A   C
             TG                  TAACATGGTGAA CCC GTCTCTA
                                 |||||||||||| ||| |||||||
                                 GTTGTACCACTT GGG CAGAGAT
                                       C   A
GAM1684  DSC3     3'  TAGAGACGGGGTTTCACTGTGT 44635
             TA                  TAACATGGTGAAACCCCGTCTCTA
                                 ||||||||||||||||||||||||
                                 ATTGTGTCACTTTGGGGCAGAGAT

GAM1684  DSC3     3'  TAGAGACGGGGTTTCACTGTGT 44636
             TA                  TAACATGGTGAAACCCCGTCTCTA
                                 ||||||||||||||||||||||||
                                 ATTGTGTCACTTTGGGGCAGAGAT

GAM1684  DSCR3    3'  TAGAGACGGGGCTTCACCATCT 21323     C       A
             TG                  TAA ATGGTGAA CCCCGTCTCTA
                                 ||| |||||||| ||||||||||
                                 GTT TACCACTT GGGGCAGAGAT
                                   C       C
GAM1684  EHD2     3'  TAGAGACGGGGTTTCACCATGT 28229
             TG                  TAACATGGTGAAACCCCGTCTCTA
                                 ||||||||||||||||||||||||
                                 GTTGTACCACTTTGGGGCAGAGAT

GAM1684  EIF2S3   3'  TAGAGACGGGGTTTCAGCATGT 9214         G
             TG                  TAACATG TGAAACCCCGTCTCTA
                                 ||||||| ||||||||||||||||
                                 GTTGTAC ACTTTGGGGCAGAGAT
                                    G
GAM1684  EPB72    3'  TAGAGACGGGGTTTCACCATGT 15882
             TG                  TAACATGGTGAAACCCCGTCTCTA
                                 ||||||||||||||||||||||||
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                                GTTGTACCACTTTGGGGCAGAGAT

GAM1684  F2RL2    3'  TAGAGACGGGGTTTCACCATGT 15900
                TG                TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTACCACTTTGGGGCAGAGAT

GAM1684  F2RL3    3'  AGACGGAGTTTCACCATGTTG  15489          C
                                  TAACATGGTGAAAC CCGTCT
                                  |||||||||||||| ||||||
                                  GTTGTACCACTTTG GGCAGA
                                            A
GAM1684  FANCF    3'  TAGAGACGGGGTTTCACCATG  42986
                                  CATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||
                                  GTACCACTTTGGGGCAGAGAT

GAM1684  FCAR     3'  AGACAGGGTTTCACCATGTTG  10581            C
                                  TAACATGGTGAAACCC GTCT
                                  |||||||||||||||| ||||
                                  GTTGTACCACTTTGGG CAGA
                                            A
GAM1684  FCGR2A   3'  TAGAGACAGGGTTTCGCAATGT 80032       G       C
                TG                TAACAT GTGAAACCC GTCTCTA
                                  |||||| ||||||||| |||||||
                                  GTTGTA CGCTTTGGG CAGAGAT
                                     A        A
GAM1684  FCRH1    3'  TAGAGACAAGATTTCACCGTTT 54733     C       CCCC
                TG                TAA ATGGTGAAA    GTCTCTA
                                  ||| |||||||||    |||||||
                                  GTT TGCCACTTT    CAGAGAT
                                    T        AGAA
GAM1684  FEZ1     3'  TAGAGATGGGAGTTTCACCATG 18789                _
                TTG                TAACATGGTGAAAC CCCGTCTCTA
                                  |||||||||||||| ||||||||||
                                  GTTGTACCACTTTG GGGTAGAGAT
                                            A
GAM1684  FGF5     3'  TAGAGACGGGGTTTCACCATGT 16765
                TG                TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTACCACTTTGGGGCAGAGAT

GAM1684  FGF5     3'  TAGAGACGGGGTTTCACCATGT 53669
                TG                TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTACCACTTTGGGGCAGAGAT

GAM1684  FUT1     3'  TAGAGACAGGGTTTCACCATGT 5612             C
                TG                TAACATGGTGAAACCC GTCTCTA
                                  |||||||||||||||| |||||||
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                                GTTGTACCACTTTGGG CAGAGAT
                                        A
GAM1684  FUT1    3'  TAGAGACGAGGTCTTGTGAT  5613     G TG A  C
                                AT G  A ACC CGTCTCTA
                                || |  | ||| ||||||||
                                TA T  T TGG GCAGAGAT
                                 G GT C   A
GAM1684  FUT1    3'  TAGAGACGGGGTTTCATCGTGT 5614
           TA                    TAACATGGTGAAACCCCGTCTCTA
                                 ||||||||||||||||||||||||
                                 ATTGTGCTACTTTGGGGCAGAGAT

GAM1684  GHR     3'  AGAGACGGGGTTTCACCATGTT 5692
           G                     TAACATGGTGAAACCCCGTCTCT
                                 |||||||||||||||||||||||
                                 GTTGTACCACTTTGGGGCAGAGA

GAM1684  GM2A    3'  TAGAGATGGGGTTTCACCATGT 68389
           TG                    TAACATGGTGAAACCCCGTCTCTA
                                 ||||||||||||||||||||||||
                                 GTTGTACCACTTTGGGGTAGAGAT

GAM1684  GNE     3'  TAGTGGACAGGGTTTCACCATG 19680              C  _
           TTG                   TAACATGGTGAAACCC GTCT CTA
                                 |||||||||||||||| |||| |||
                                 GTTGTACCACTTTGGG CAGG GAT
                                        A   T
GAM1684  GPD2    3'  TAGAAACGACAAATCACCATGT 6395          AACCC  C
                                 ACATGGTGA    CGT TCTA
                                 |||||||||    ||| ||||
                                 TGTACCACT    GCA AGAT
                                      AAACA  A
GAM1684  GPR81   3'  TAGAGACAGGGTTTTGCCATGT 51756         TG     C
           TG                    TAACATGG  AAACCC GTCTCTA
                                 ||||||||  |||||| |||||||
                                 GTTGTACC  TTTGGG CAGAGAT
                                     GT     A
GAM1684  GRM6    3'  TAGAGACGAGGTCTCACTATGT 7770           A  C
           TG                    TAACATGGTGA ACC CGTCTCTA
                                 |||||||||||| ||| ||||||||
                                 GTTGTATCACT TGG GCAGAGAT
                                       C  A
GAM1684  GRM7    5'  TAGAGATTGGGTTTCACCATGT 7791              C
           TG                    TAACATGGTGAAACCC GTCTCTA
                                 |||||||||||||||| |||||||
                                 GTTGTACCACTTTGGG TAGAGAT
                                        T
GAM1684  HLCS    5'  TAGAGGCGGGGGTTTCACCATG 6419             _
                                 CATGGTGAAACCCC GTCTCTA
                                 |||||||||||||| |||||||
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                                GTACCACTTTGGGG CGGAGAT
                                      G
GAM1684  HTR1D    3'  AGACGGGGTTTCATCATGTTG  7836
                                TAACATGGTGAAACCCCGTCT
                                ||||||||||||||||||||
                                GTTGTACTACTTTGGGGCAGA

GAM1684  HTR1E    5'  TGGAGACGGGATTTCACCATGT 7867             C
            TG                    TAACATGGTGAAA CCCGTCTCTA
                                ||||||||||||| ||||||||||
                                GTTGTACCACTTT GGGCAGAGGT
                                      A
GAM1684  HUS1     3'  TAGAGACAGGGTCTCACTGTGT 92742          A   C
            TG                    TAACATGGTGA ACCC GTCTCTA
                                ||||||||||| |||| |||||||
                                GTTGTGTCACT TGGG CAGAGAT
                                      C   A
GAM1684  IGF1     3'  TAGAGACGGGGTTTTACCATGT 7081
            TG                    TAACATGGTGAAACCCCGTCTCTA
                                ||||||||||||||||||||||||
                                GTTGTACCATTTTGGGGCAGAGAT

GAM1684  IL11     3'  TAGAGACAGGGTTTCACCATGT 7194             C
            TG                    TAACATGGTGAAACCC GTCTCTA
                                ||||||||||||||| |||||||
                                GTTGTACCACTTTGGG CAGAGAT
                                      A
GAM1684  INMT     3'  TAGATATGGGGTTTCACCGTGT 23227              C
            TA                    TAACATGGTGAAACCCCGT TCTA
                                |||||||||||||||||| ||||
                                ATTGTGCCACTTTGGGGTA AGAT
                                      T
GAM1684  JRK      3'  TAGAGACAGGGTCTCACTGTGT 87834          A   C
            TG                    TAACATGGTGA ACCC GTCTCTA
                                ||||||||||| |||| |||||||
                                GTTGTGTCACT TGGG CAGAGAT
                                      C   A
GAM1684  LLGL1    3'  TAGAGATGGGGTTTCACCATGT 67423
            TA                    TAACATGGTGAAACCCCGTCTCTA
                                ||||||||||||||||||||||||
                                ATTGTACCACTTTGGGGTAGAGAT

GAM1684  LNK      3'  TAGAGACAGGGTTTCACCATGT 19651            C
            TG                    TAACATGGTGAAACCC GTCTCTA
                                |||||||||||||||| |||||||
                                GTTGTACCACTTTGGG CAGAGAT
                                      A
GAM1684  LTB4R    5'  TAGAGACGGGGTTTCACCATGT 7473
            TG                    TAACATGGTGAAACCCCGTCTCTA
                                ||||||||||||||||||||||||
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                                GTTGTACCACTTTGGGGCAGAGAT

GAM1684  LYZ      3'  TAGAGACAGGGTTTCACCGTGT 5903              C
                TA                    TAACATGGTGAAACCC GTCTCTA
                                      ||||||||||||||| |||||||
                                      ATTGTGCCACTTTGGG CAGAGAT
                                            A
GAM1684  MAK      3'  TAGAGACAGGGTTTCACCATGT 20952             C
                TG                    TAACATGGTGAAACCC GTCTCTA
                                      ||||||||||||||| |||||||
                                      GTTGTACCACTTTGGG CAGAGAT
                                            A
GAM1684  MDM2     3'  TAGAGACAGGGTTTCACCGTGT 23502              C
                TA                    TAACATGGTGAAACCC GTCTCTA
                                      ||||||||||||||| |||||||
                                      ATTGTGCCACTTTGGG CAGAGAT
                                            A
GAM1684  MEF2A    5'  TAGAGATGGAGTTTCACCATGT 20002              C
                TG                    TAACATGGTGAAAC CCGTCTCTA
                                      |||||||||||||| |||||||||
                                      GTTGTACCACTTTG GGTAGAGAT
                                            A
GAM1684  MEFV     3'  TAGAGACGGGGGTTTCACCATG 5949                _
                TTA                    TAACATGGTGAAACCCC GTCTCTA
                                      ||||||||||||||||| |||||||
                                      ATTGTACCACTTTGGGG CAGAGAT
                                             G
GAM1684  MICB     3'  AGAGACGGGGTTTCGCCA    21018
                                      TGGTGAAACCCCGTCTCT
                                      ||||||||||||||||||
                                      ACCGCTTTGGGGCAGAGA

GAM1684  MLANA    3'  TAGAGACGGGGTTTCTCCATGT 19771          T
                TG                    TAACATGG GAAACCCCGTCTCTA
                                      |||||||| ||||||||||||||
                                      GTTGTACC CTTTGGGGCAGAGAT
                                           T
GAM1684  MPL      3'  TAGAGACAGGGTTTTGCCATGT 19360         TG     C
                TG                    TAACATGG  AAACCC GTCTCTA
                                      ||||||||  |||||| |||||||
                                      GTTGTACC  TTTGGG CAGAGAT
                                           GT     A
GAM1684  MRPL49   3'  TAGAGATGGGGTTTCACCATGT 70172
                TG                    TAACATGGTGAAACCCCGTCTCTA
                                      ||||||||||||||||||||||||
                                      GTTGTACCACTTTGGGGTAGAGAT

GAM1684  MTR      3'  TAGAGACAGGATTTCACTGTGT 6027              C  C
                TA                    TAACATGGTGAAA CC GTCTCTA
                                      |||||||||||| || |||||||
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                                ATTGTGTCACTTT GG CAGAGAT
                                      A  A
GAM1684  MYCL2    3'  TAGAGATGGGGTTTCACCA   19380
                                TGGTGAAACCCCGTCTCTA
                                ||||||||||||||||||
                                ACCACTTTGGGGTAGAGAT

GAM1684  NCOA6IP  3'  TAGAGACGAGGTCCCACCATGT 46159          AA   C
           TG                     TAACATGGTG  ACC CGTCTCTA
                                ||||||||||  ||| ||||||||
                                GTTGTACCAC  TGG GCAGAGAT
                                     CC   A
GAM1684  NDRG3    3'  TAGAGATGGAGTTTCACCATGT 42770            C
           TG                     TAACATGGTGAAAC CCGTCTCTA
                                |||||||||||||| |||||||||
                                GTTGTACCACTTTG GGTAGAGAT
                                      A
GAM1684  NPR2L    3'  TAGAGACAGGGTTTCCCTATGT 22599         T      C
           TG                     TAACATGG GAAACCC GTCTCTA
                                ||||||||| ||||||| |||||||
                                GTTGTATC CTTTGGG CAGAGAT
                                    C      A
GAM1684  NQO1     3'  TAGAGACGGCGTTTCACCATGT 8055             C
           TG                     TAACATGGTGAAAC CCGTCTCTA
                                |||||||||||||| |||||||||
                                GTTGTACCACTTTG GGCAGAGAT
                                      C
GAM1684  ORC1L    3'  TAGAGACAGGGCTTCACCATGT 15988           A   C
           TG                     TAACATGGTGAA CCC GTCTCTA
                                |||||||||||| ||| |||||||
                                GTTGTACCACTT GGG CAGAGAT
                                      C   A
GAM1684  PCDHA9   3'  TAGAGATGGGGTTTCACCGTGT 49852
           TA                     TAACATGGTGAAACCCCGTCTCTA
                                ||||||||||||||||||||||||
                                ATTGTGCCACTTTGGGGTAGAGAT

GAM1684  PCDHB11  3'  TAGAGACGGATCGTCACCAT   38930        AACC
                                ATGGTGA    CCGTCTCTA
                                |||||||    |||||||||
                                TACCACT    GGCAGAGAT
                                    GCTA
GAM1684  PCDHB11  3'  TAGAGACGGGGTTTCACCACGT 38931      A
           TG                     TAAC TGGTGAAACCCCGTCTCTA
                                ||||| ||||||||||||||||||
                                GTTG ACCACTTTGGGGCAGAGAT
                                  C
GAM1684  PER2     3'  TAGAGACAGGGTTTCACCATGT 43360            C
           TG                     TAACATGGTGAAACCC GTCTCTA
                                ||||||||||||||| |||||||
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                                GTTGTACCACTTTGGG CAGAGAT
                                       A
GAM1684  PIGR     3'  TAGAGACAGGGTTTCACCGTGT 73010              C
                TA                  TAACATGGTGAAACCC GTCTCTA
                                    |||||||||||||||| |||||||
                                    ATTGTGCCACTTTGGG CAGAGAT
                                       A
GAM1684  PIGR     3'  TAGAGACAGGGTTTCGCCATGT 73011              C
                TG                  TAACATGGTGAAACCC GTCTCTA
                                    |||||||||||||||| |||||||
                                    GTTGTACCGCTTTGGG CAGAGAT
                                       A
GAM1684  PIK3C2B  3'  TAGAGACGGGGTTTCACCATGT 12111
                TG                  TAACATGGTGAAACCCCGTCTCTA
                                    ||||||||||||||||||||||||
                                    GTTGTACCACTTTGGGGCAGAGAT

GAM1684  PIK3CD   3'  TAGAGACGGGGGTTTCACCATG 18500                _
                TTG                  TAACATGGTGAAACCCC GTCTCTA
                                    |||||||||||||||| |||||||
                                    GTTGTACCACTTTGGGG CAGAGAT
                                       G
GAM1684  POU2AF1  3'  TAGAGACGGGGTTTCACCATGT 21751
                TG                  TAACATGGTGAAACCCCGTCTCTA
                                    ||||||||||||||||||||||||
                                    GTTGTACCACTTTGGGGCAGAGAT

GAM1684  PPID     3'  TAGAGATGGGGTTTCACCAT  88829
                                    ATGGTGAAACCCCGTCTCTA
                                    ||||||||||||||||||
                                    TACCACTTTGGGGTAGAGAT

GAM1684  PPT2     3'  AGAGACGGGGTTTTAGTA    18943    G
                                    TG TGAAACCCCGTCTCT
                                    || ||||||||||||||
                                    AT ATTTTGGGGCAGAGA
                                     G
GAM1684  PRKR     3'  AGACAGGGTTTCACCATGTTG  12341              C
                                    TAACATGGTGAAACCC GTCT
                                    |||||||||||||||| ||||
                                    GTTGTACCACTTTGGG CAGA
                                       A
GAM1684  PSMB2    3'  TAGAGACAGGGTCTCACCATGT 12477         A    C
                                    ACATGGTGA ACCC GTCTCTA
                                    ||||||||| |||| |||||||
                                    TGTACCACT TGGG CAGAGAT
                                          C    A
GAM1684  PSMD9    3'  TAGAGACAGGGTCTCCCTGTGT 12530         T  A    C
                TG                  TAACATGG GA ACCC GTCTCTA
                                    |||||||| || |||| |||||||
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                                GTTGTGTC CT TGGG CAGAGAT
                                    C C    A
GAM1684  PTGIS    3'  TAGAGACGGGGTTTCCCCATGT 8225          T
                TG                  TAACATGG GAAACCCCGTCTCTA
                                    |||||||| ||||||||||||||
                                    GTTGTACC CTTTGGGGCAGAGAT
                                        C
GAM1684  PTGIS    3'  TAGAGATGGGATTTCACCGT   8226          C
                                    ATGGTGAAA CCCGTCTCTA
                                    ||||||||| ||||||||||
                                    TGCCACTTT GGGTAGAGAT
                                        A
GAM1684  RAB36    3'  TAGAGAGAGGTTTCACCATGTT 18182              CCG
                A                    TAACATGGTGAAACC   TCTCTA
                                    ||||||||||||||   ||||||
                                    ATTGTACCACTTTGG   AGAGAT
                                           AG_
GAM1684  RABL2A   3'  TAGAGACGGGGTTTCACCATGT 23998
                TG                  TAACATGGTGAAACCCCGTCTCTA
                                    ||||||||||||||||||||||||
                                    GTTGTACCACTTTGGGGCAGAGAT

GAM1684  RABL2B   3'  TAGAGACGGGGTTTCACCATGT 23986
                TG                  TAACATGGTGAAACCCCGTCTCTA
                                    ||||||||||||||||||||||||
                                    GTTGTACCACTTTGGGGCAGAGAT

GAM1684  RBBP9    3'  TAGAGACAGGGTTTCACCATGT 70697              C
                TG                  TAACATGGTGAAACCC GTCTCTA
                                    |||||||||||||||| |||||||
                                    GTTGTACCACTTTGGG CAGAGAT
                                           A
GAM1684  RGS9     5'  AGACGGGGTTTTGTCATGTTG  15171         TG
                                    TAACATGG  AAACCCCGTCT
                                    ||||||||  ||||||||||
                                    GTTGTACT  TTTGGGGCAGA
                                        GT
GAM1684  RHD      3'  AGATGGGGTTTCACCATGTTG  32811
                                    TAACATGGTGAAACCCCGTCT
                                    |||||||||||||||||||||
                                    GTTGTACCACTTTGGGGTAGA

GAM1684  RHD      3'  AGATGGGGTTTCACCATGTTG  32812
                                    TAACATGGTGAAACCCCGTCT
                                    |||||||||||||||||||||
                                    GTTGTACCACTTTGGGGTAGA

GAM1684  RPP30    3'  AGAGACGGGGTTTCACCGTGTT 22192
                A                    TAACATGGTGAAACCCCGTCTCT
                                    |||||||||||||||||||||||
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                                ATTGTGCCACTTTGGGGCAGAGA

GAM1684  SAS      3'  TAGAGACAGGGTTTCACCATGT 21108              C
                TA                   TAACATGGTGAAACCC GTCTCTA
                                     |||||||||||||||| |||||||
                                     ATTGTACCACTTTGGG CAGAGAT
                                                A
GAM1684  SEDL     3'  TAGAGACAGGGTTTCACCAT  28107            C
                                     ATGGTGAAACCC GTCTCTA
                                     |||||||||||| |||||||
                                     TACCACTTTGGG CAGAGAT
                                                A
GAM1684  SEDL     3'  TAGAGACAGGGTTTCACCAT  28108            C
                                     ATGGTGAAACCC GTCTCTA
                                     |||||||||||| |||||||
                                     TACCACTTTGGG CAGAGAT
                                                A
GAM1684  SEDL     3'  TAGAGACGGGGTTTCGCTAT  28109
                                     ATGGTGAAACCCCGTCTCTA
                                     ||||||||||||||||||
                                     TATCGCTTTGGGGCAGAGAT

GAM1684  SEPN1    3'  TAGAGATGGGGTTTCACCAT  66981
                                     ATGGTGAAACCCCGTCTCTA
                                     ||||||||||||||||||
                                     TACCACTTTGGGGTAGAGAT

GAM1684  SERPINB9 3'  TAGAGACGGGGTTTCACCGTGT 16033
                TA                   TAACATGGTGAAACCCCGTCTCTA
                                     ||||||||||||||||||||||||
                                     ATTGTGCCACTTTGGGGCAGAGAT

GAM1684  SERPINB9 3'  TAGAGACGGGGTTTCGCCA   16034
                                     TGGTGAAACCCCGTCTCTA
                                     ||||||||||||||||||
                                     ACCGCTTTGGGGCAGAGAT

GAM1684  SH3BP2   3'  CGGGGTTTCACCATGTTG    13063
                                     TAACATGGTGAAACCCCG
                                     |||||||||||||||||
                                     GTTGTACCACTTTGGGGC

GAM1684  SH3BP2   3'  TAGAGACGGGATTTTATCATGT 13086              C
                TG                   TAACATGGTGAAA CCCGTCTCTA
                                     |||||||||||| ||||||||||
                                     GTTGTACTATTTT GGGCAGAGAT
                                                A
GAM1684  SH3GL3   5'  TAGAGATGGGTTTCACCATGTT 13115               C
                G                    TAACATGGTGAAACCC GTCTCTA
                                     |||||||||||||||| |||||||
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                                GTTGTACCACTTTGGG TAGAGAT
                                                 _
GAM1684  SHOX     3'  TAGAGACGGGATCTTGCTTTG  6584     T  TG AAC
                                CA GG  A   CCCGTCTCTA
                                || ||  |  ||||||||||
                                GT TC  T   GGGCAGAGAT
                                 T  GT CTA
GAM1684  SIGLEC11  3'  TAGAGACAGGGTTTTGCCATGT 54656        TG     C
            T                    AACATGG  AAACCC GTCTCTA
                                |||||||  |||||| |||||||
                                TTGTACC  TTTGGG CAGAGAT
                                    GT     A
GAM1684  SIL      5'  GAGACGGGGTTTCACCATGTTG 13156
                                TAACATGGTGAAACCCCGTCTC
                                ||||||||||||||||||||||
                                GTTGTACCACTTTGGGGCAGAG

GAM1684  SLA2     3'  TAGACATGGGGTTTCACCA   50893            C
                                TGGTGAAACCCCGT TCTA
                                |||||||||||||| ||||
                                ACCACTTTGGGGTA AGAT
                                         C
GAM1684  SLC14A2  5'  TAGAGACGGGGTTTCACCA   24127
                                TGGTGAAACCCCGTCTCTA
                                |||||||||||||||||
                                ACCACTTTGGGGCAGAGAT

GAM1684  SLC15A1  3'  TAGAGATGGGGTTTCACCATGT 18647
            TA                   TAACATGGTGAAACCCCGTCTCTA
                                |||||||||||||||||||||||
                                ATTGTACCACTTTGGGGTAGAGAT

GAM1684  SLC3A2   5'  TAGAGACGGGGTCTGACTGTGT 11525         GAA
            TA                   TAACATGGT   ACCCCGTCTCTA
                                |||||||||  ||||||||||||
                                ATTGTGTCA   TGGGGCAGAGAT
                                     GTC
GAM1684  SMAC     5'  TAGAGATGGGGTTTCACCATGT 58007
            TG                   TAACATGGTGAAACCCCGTCTCTA
                                |||||||||||||||||||||||
                                GTTGTACCACTTTGGGGTAGAGAT

GAM1684  SNAP23   3'  TAGAGACAGGGTTTCACCATGT 15143            C
                                ACATGGTGAAACCC GTCTCTA
                                |||||||||||||| |||||||
                                TGTACCACTTTGGG CAGAGAT
                                         A
GAM1684  SPN      3'  TAGAGATGGGGTTTCACCATGT 13380
            TG                   TAACATGGTGAAACCCCGTCTCTA
                                |||||||||||||||||||||||
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                                GTTGTACCACTTTGGGGTAGAGAT

GAM1684  SULT2B1   5'  TAGGGGCGGGGTTTCACCATGT 17228
                TG                TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTACCACTTTGGGGCGGGGAT

GAM1684  TAPBP     3'  TAGAGACGGGGTTTCACCATGT 13586
                TG                TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTACCACTTTGGGGCAGAGAT

GAM1684  TAPBP     3'  TAGAGACGGGGTTTCACCGTGT 13587
                TA                TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  ATTGTGCCACTTTGGGGCAGAGAT

GAM1684  TAPBP     3'  TAGAGACGGGGTTTCACCGTGT 13588
                TA                TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  ATTGTGCCACTTTGGGGCAGAGAT

GAM1684  TAT       3'  TAGAGACAGGGTTTCACCATGT 6259              C
                TA                TAACATGGTGAAACCC GTCTCTA
                                  |||||||||||||||| |||||||
                                  ATTGTACCACTTTGGG CAGAGAT
                                        A
GAM1684  TBXA2R    3'  TAGAGACGGGGTTTCACCGTGT 8365
                TG                TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTGCCACTTTGGGGCAGAGAT

GAM1684  TDGF1     3'  TAGAGATGGGGGTTTCACCAT  13662          _
                                  ATGGTGAAACCCC GTCTCTA
                                  |||||||||||| |||||||
                                  TACCACTTTGGGG TAGAGAT
                                        G
GAM1684  TERF1     3'  TAGAGGCGGGGTTTCACCATG  34402
                                  CATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||
                                  GTACCACTTTGGGGCGGAGAT

GAM1684  TERF2     3'  TAGAGACGGGGTTTCACCGTGT 20163
                TA                TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  ATTGTGCCACTTTGGGGCAGAGAT

GAM1684  TES       3'  TAGAGACAGGTTTTCACCATGT 72466           C  C
                TA                TAACATGGTGAAA CC GTCTCTA
                                  |||||||||||| || |||||||
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                                ATTGTACCACTTT GG CAGAGAT
                                      T  A
GAM1684  TIM3     3'  TAGAGACAGGGTTTCACCATGT 52362            C
           TG                   TAACATGGTGAAACCC GTCTCTA
                                |||||||||||||||| |||||||
                                GTTGTACCACTTTGGG CAGAGAT
                                      A
GAM1684  TMPRSS3  3'  TAGAGACAGGGTTTCACCATGT 44033            C
           TG                   TAACATGGTGAAACCC GTCTCTA
                                |||||||||||||||| |||||||
                                GTTGTACCACTTTGGG CAGAGAT
                                      A
GAM1684  TNFRSF10B 3'  TAGAGACGGGGTTTCACCATGT 15232
           TG                   TAACATGGTGAAACCCCGTCTCTA
                                ||||||||||||||||||||||||
                                GTTGTACCACTTTGGGGCAGAGAT

GAM1684  TNFRSF11A 3'  AGAGACACGGTCCCACCATGTT 15186         AA   CC
           A                    TAACATGGTG  ACC  GTCTCT
                                ||||||||||  |||  ||||||
                                ATTGTACCAC  TGG  CAGAGA
                                      CC   CA
GAM1684  TNFRSF9   3'  AGATGGCATTTCACCATGTTG  9578           CC
                                TAACATGGTGAAA  CCGTCT
                                ||||||||||||  ||||||
                                GTTGTACCACTTT  GGTAGA
                                      AC
GAM1684  TPMT     3'  TGGAGACGGGGTTTCACCATGT 6321
           TG                   TAACATGGTGAAACCCCGTCTCTA
                                ||||||||||||||||||||||||
                                GTTGTACCACTTTGGGGCAGAGGT

GAM1684  TRAF5    3'  TAGAGACGGAGTTTTGCCATGT 17283        TG   C
           TG                   TAACATGG  AAAC CCGTCTCTA
                                ||||||||  |||| |||||||||
                                GTTGTACC  TTTG GGCAGAGAT
                                     GT   A
GAM1684  TRIM9    5'  TAGAGACGGGGTTTCACCAT   31461
                                ATGGTGAAACCCCGTCTCTA
                                ||||||||||||||||||
                                TACCACTTTGGGGCAGAGAT

GAM1684  TRPM6    3'  TAGAGATGGGGTTTCACCATGT 35036
           TG                   TAACATGGTGAAACCCCGTCTCTA
                                ||||||||||||||||||||||||
                                GTTGTACCACTTTGGGGTAGAGAT

GAM1684  TRPV1    3'  TAGAGACGGGGTTTCACCATGT 55687
           TG                   TAACATGGTGAAACCCCGTCTCTA
                                ||||||||||||||||||||||||
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                                GTTGTACCACTTTGGGGCAGAGAT

GAM1684  TRPV1    3'  TAGAGACGGGGTTTCACCATGT 55688
                TG                TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTACCACTTTGGGGCAGAGAT

GAM1684  TUFT1    3'  TAGAGATGGGGTTTCACCAT  39677
                                  ATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||
                                  TACCACTTTGGGGTAGAGAT

GAM1684  UGDH     3'  TAGAGACAGGGTTTCACCATGT 14004          C
                                  ACATGGTGAAACCC GTCTCTA
                                  |||||||||||||| |||||||
                                  TGTACCACTTTGGG CAGAGAT
                                        A
GAM1684  VENTX2   3'  TAGAAATGGGGTTTCACCATGT 27866            C
                TA                TAACATGGTGAAACCCCGT TCTA
                                  |||||||||||||||||| ||||
                                  ATTGTACCACTTTGGGGTA AGAT
                                        A
GAM1684  VHL      3'  TGGAGACGGGGTTTCACCATGT 6881
                TG                TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTACCACTTTGGGGCAGAGGT

GAM1684  VIPR2    3'  TAGAGACAGGGTTTCACCATGT 14075          C
                TA                TAACATGGTGAAACCC GTCTCTA
                                  |||||||||||||||| |||||||
                                  ATTGTACCACTTTGGG CAGAGAT
                                        A
GAM1684  WHSC1    3'  TAGAGACAGGGTTTCGCCAT  24687          C
                                  ATGGTGAAACCC GTCTCTA
                                  |||||||||||| |||||||
                                  TACCGCTTTGGG CAGAGAT
                                        A
GAM1684  XRCC2    3'  TAGAGACGGGGTTTCACCATGT 19511
                TG                TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTACCACTTTGGGGCAGAGAT

GAM1684  YES1     3'  TAGAGACGCAGTTTCACCGTGT 19545          CC
                TA                TAACATGGTGAAAC  CGTCTCTA
                                  ||||||||||||||  ||||||||
                                  ATTGTGCCACTTTG  GCAGAGAT
                                        AC
GAM1684  ZNF133   5'  TAGAGACGGAGTTTCAGCAT  14300    G    C
                                  ATG TGAAAC CCGTCTCTA
                                  ||| |||||| |||||||||
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                                TAC ACTTTG GGCAGAGAT
                                  G     A
GAM1684  ZNF157   3'  AGACGGGTTTCACCATGTTG   14325              C
                                TAACATGGTGAAACCC GTCT
                                |||||||||||||||| ||||
                                GTTGTACCACTTTGGG CAGA
                                                 _
GAM1684  ZNF264   3'  TAGAGACGGGGTTTCACCATCT 14229     C
           TG                     TAA ATGGTGAAACCCCGTCTCTA
                                  ||| ||||||||||||||||||||
                                GTT TACCACTTTGGGGCAGAGAT
                                  C
GAM1684  ZNF264   3'  TAGAGACGGGGTTTCACCATGT 14230
           TG                     TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                GTTGTACCACTTTGGGGCAGAGAT

GAM1684  ZNF74    5'  TAGAGACGGGGTTTTGCCATGT 14264        TG
           T                      AACATGG  AAACCCCGTCTCTA
                                  |||||||  ||||||||||||||
                                TTGTACC  TTTGGGGCAGAGAT
                                    GT
GAM1684  ANKT     3'  TAGAGACAGGGTCTCACTGTGT 33459          A   C
           TG                     TAACATGGTGA ACCC GTCTCTA
                                  |||||||||||| |||| |||||||
                                GTTGTGTCACT TGGG CAGAGAT
                                      C   A
GAM1684  AP3S2    3'  TAGAGACAGGGTTTCACCATGT 20657             C
           TG                     TAACATGGTGAAACCC GTCTCTA
                                  |||||||||||||||| |||||||
                                GTTGTACCACTTTGGG CAGAGAT
                                     A
GAM1684  ARHF     3'  TAGAGACAGGGTTTCACCATGT 39277             C
           TG                     TAACATGGTGAAACCC GTCTCTA
                                  |||||||||||||||| |||||||
                                GTTGTACCACTTTGGG CAGAGAT
                                     A
GAM1684  ASE-1    3'  TAGAGACAGGGGTTTCACCAT  24995          _
                                ATGGTGAAACCCC GTCTCTA
                                |||||||||||| |||||||
                                TACCACTTTGGGG CAGAGAT
                                     A
GAM1684  ASE-1    3'  TAGAGATGGGGTTTCACCACGT 24996     A
           TA                     TAAC TGGTGAAACCCCGTCTCTA
                                  |||| ||||||||||||||||||
                                ATTG ACCACTTTGGGGTAGAGAT
                                  C
GAM1684  ATP1B4   3'  GGAGACAGGGTTTCACCATGTT 24847             C
           G                      TAACATGGTGAAACCC GTCTCT
                                  |||||||||||||||| ||||||
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                                GTTGTACCACTTTGGG CAGAGG
                                       A
GAM1684  BA108L7.2 3'  AGAGATGGGGGTTTCACCATGT 49062                    _
            TG                   TAACATGGTGAAACCCC GTCTCT
                                 |||||||||||||||| ||||||
                                 GTTGTACCACTTTGGGG TAGAGA
                                       G
GAM1684  BNIP-S    3'  TAGAGACGGGGTTTCACCATGT 57109
            TG                   TAACATGGTGAAACCCCGTCTCTA
                                 ||||||||||||||||||||||||
                                 GTTGTACCACTTTGGGGCAGAGAT

GAM1684  C11orf17  3'  TAGAGACGGGGTTTAACCATGT 40589          G
            TG                   TAACATGGT AAACCCCGTCTCTA
                                 |||||||| ||||||||||||||
                                 GTTGTACCA TTTGGGGCAGAGAT
                                      A
GAM1684  C13orf1   3'  TAGAGATGGGGTTTCACCATGT 40370
            TG                   TAACATGGTGAAACCCCGTCTCTA
                                 ||||||||||||||||||||||||
                                 GTTGTACCACTTTGGGGTAGAGAT

GAM1684  C1orf34   3'  TAGAGACAGGGTCTTGCTATGT 61321         TG A   C
            TG                   TAACATGG  A ACCC GTCTCTA
                                 ||||||||  | |||| |||||||
                                 GTTGTATC  T TGGG CAGAGAT
                                     GT C   A
GAM1684  C1QTNF6   3'  TAGAGATGGGGTTTCACCAT   49996
                                 ATGGTGAAACCCCGTCTCTA
                                 ||||||||||||||||||||
                                 TACCACTTTGGGGTAGAGAT

GAM1684  C21orf25  3'  TAGAAATGGAGTCTCACCATGT 64301           A  C   C
            TG                   TAACATGGTGA AC CCGT TCTA
                                 |||||||||| || |||| ||||
                                 GTTGTACCACT TG GGTA AGAT
                                       C A   A
GAM1684  C3F       3'  TAGAAACGGGATTTCACCACGT 20482      A      C    C
            TG                   TAAC TGGTGAAA CCCGT TCTA
                                 |||| |||||||| ||||| ||||
                                 GTTG ACCACTTT GGGCA AGAT
                                   C       A    A
GAM1684  C6orf33   3'  TAGAGACAGGGTTTTGCCACGT 56721      A   TG     C
            TG                   TAAC TGG  AAACCC GTCTCTA
                                 |||| |||  |||||| |||||||
                                 GTTG ACC  TTTGGG CAGAGAT
                                   C  GT     A
GAM1684  C6orf5    3'  TAGAGACAGGGTTTCATATTG  32002    TG       C
                                 CA  GTGAAACCC GTCTCTA
                                 ||  ||||||||| |||||||
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                                GT  TACTTTGGG CAGAGAT
                                 TA        A
GAM1684  C6orf5   3'  TAGAGACAGGGTTTTGCCATGT 32003         TG     C
                TG                TAACATGG  AAACCC GTCTCTA
                                  |||||||| ||||||| |||||||
                                  GTTGTACC  TTTGGG CAGAGAT
                                      GT     A
GAM1684  C9orf9   3'  TAGAGACAGCGTTTCACCATGT 39036             CCC
                TA                TAACATGGTGAAAC  GTCTCTA
                                  ||||||||||||||  |||||||
                                  ATTGTACCACTTTG  CAGAGAT
                                        CGA
GAM1684  C9orf9   3'  TAGAGACGGGGCTTCACCACGT 39037      A      A
                TG                TAAC TGGTGAA CCCCGTCTCTA
                                  |||| ||||||| ||||||||||
                                  GTTG ACCACTT GGGGCAGAGAT
                                    C      C
GAM1684  CCRN4L   3'  TAGAGACGGGGTTTCACCGTGT 25074
                TA                TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||||
                                  ATTGTGCCACTTTGGGGCAGAGAT

GAM1684  CDC14B   3'  TAGAGACAGGGTTTCACCATGT 53992              C
                TG                TAACATGGTGAAACCC GTCTCTA
                                  |||||||||||||||| |||||||
                                  GTTGTACCACTTTGGG CAGAGAT
                                        A
GAM1684  CEACAM8  3'  TAGAGACGGGGTTTCACTGTG  10188
                                  CATGGTGAAACCCCGTCTCTA
                                  |||||||||||||||||||||
                                  GTGTCACTTTGGGGCAGAGAT

GAM1684  CENPH    3'  TAGAGACGGGGTTTCACCGTGT 43572
                TG                TAACATGGTGAAACCCCGTCTCTA
                                  |||||||||||||||||||||||||
                                  GTTGTGCCACTTTGGGGCAGAGAT

GAM1684  CHRAC1   3'  TAGAGACGGGGTTCACCATGTT 34338           A
                G                 TAACATGGTGAA CCCCGTCTCTA
                                  |||||||||||| ||||||||||
                                  GTTGTACCACTT GGGGCAGAGAT
                                          _
GAM1684  CHSY1    3'  TAGAGACGGGGTTTCACCATG  30573
                                  CATGGTGAAACCCCGTCTCTA
                                  |||||||||||||||||||||
                                  GTACCACTTTGGGGCAGAGAT

GAM1684  CIP29    3'  TAGAGACGGGGTTTCACCATGT 51381
                TG                TAACATGGTGAAACCCCGTCTCTA
                                  |||||||||||||||||||||||||
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                                GTTGTACCACTTTGGGGCAGAGAT

GAM1684  COLEC12   3'  TAGAAACAGGGTCTTGCTATGT 48620        TG A    C  C
            TG                    TAACATGG  A ACCC GT TCTA
                                  ||||||||  | |||| || ||||
                                  GTTGTATC  T TGGG CA AGAT
                                      GT C    A  A
GAM1684  CPSF2     3'  TAGAGACAGGGTTTCACCATGT 62283              C
            TG                    TAACATGGTGAAACCC GTCTCTA
                                  |||||||||||||||| |||||||
                                  GTTGTACCACTTTGGG CAGAGAT
                                           A
GAM1684  CPSF2     3'  TAGAGACGGGGTTTCTCCATGT 62284         T
            TG                    TAACATGG GAAACCCCGTCTCTA
                                  ||||||||| ||||||||||||||
                                  GTTGTACC CTTTGGGGCAGAGAT
                                      T
GAM1684  DKFZp434A2417 3'  TAGAGACGGGGTTTCTCCATGT 66686         T
            TG                    TAACATGG GAAACCCCGTCTCTA
                                  |||||||| |||||||||||||||
                                  GTTGTACC CTTTGGGGCAGAGAT
                                      T
GAM1684  DKFZP434C212 3'  TAGAAACGGGGTTTCACCATGT 69500                C
            TG                    TAACATGGTGAAACCCCGT TCTA
                                  |||||||||||||||||| ||||
                                  GTTGTACCACTTTGGGGCA AGAT
                                           A
GAM1684  DKFZP434D146 3'  TAGAGACAGGGTTTCATCATGT 32141              C
            TG                    TAACATGGTGAAACCC GTCTCTA
                                  |||||||||||||||| |||||||
                                  GTTGTACTACTTTGGG CAGAGAT
                                           A
GAM1684  DKFZP434F0318 3'  TAGAGACAGGGTTTCGCCATGT 48764              C
            TG                    TAACATGGTGAAACCC GTCTCTA
                                  |||||||||||||||| |||||||
                                  GTTGTACCGCTTTGGG CAGAGAT
                                           A
GAM1684  DKFZP434J037 3'  TAGAGACAGGGTTTCTCCATGT 48954         T      C
            TG                    TAACATGG GAAACCC GTCTCTA
                                  |||||||| ||||||| |||||||
                                  GTTGTACC CTTTGGG CAGAGAT
                                      T      A
GAM1684  DKFZp547H025 3'  TAGAGATGAGGTTTCACCATGT 39778              C
            TG                    TAACATGGTGAAACC CGTCTCTA
                                  |||||||||||||| ||||||||
                                  GTTGTACCACTTTGG GTAGAGAT
                                           A
GAM1684  DKFZP564G092 5'  TAGAGACAGGATTTCACCATGT 32167             C  C
            TG                    TAACATGGTGAAA CC GTCTCTA
                                  |||||||||||| || |||||||
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                                GTTGTACCACTTT GG CAGAGAT
                                      A  A
GAM1684  DKFZp761N1114 3'  TAGAGACGGGATTTCACCGTGT 79791           C
           TA                  TAACATGGTGAAA CCCGTCTCTA
                               |||||||||||| ||||||||||
                               ATTGTGCCACTTT GGGCAGAGAT
                                      A
GAM1684  DKFZp762P2111 3'  TAGAGACAGGGTTTCATCATGT 87641            C
           TG                  TAACATGGTGAAACCC GTCTCTA
                               |||||||||||||||| |||||||
                               GTTGTACTACTTTGGG CAGAGAT
                                      A
GAM1684  DRIM     3'  TAGAAACAGGATTTCGCCATGT 27957          C  C  C
           TG                  TAACATGGTGAAA CC GT TCTA
                               |||||||||||| || || ||||
                               GTTGTACCGCTTT GG CA AGAT
                                      A  A  A
GAM1684  DSCR6    3'  TAGAGACTCGGTTTCACCATGT 39075           CC
           TG                  TAACATGGTGAAACC  GTCTCTA
                               |||||||||||||||  |||||||
                               GTTGTACCACTTTGG  CAGAGAT
                                      CT
GAM1684  EREG     3'  TAGAGGCGGGGTTTCACCATGT 9318
           TG                  TAACATGGTGAAACCCCGTCTCTA
                               ||||||||||||||||||||||||
                               GTTGTACCACTTTGGGGCGGAGAT

GAM1684  ERO1L    3'  TAGAGACAAGGTTTTGCTGTGT 28162        TG    CC
           TG                  TAACATGG  AAACC  GTCTCTA
                               ||||||||  |||||  |||||||
                               GTTGTGTC  TTTGG  CAGAGAT
                                   GT    AA
GAM1684  EVI5     3'  TAGAGATGGGGTTTCACCATGT 20215
           TG                  TAACATGGTGAAACCCCGTCTCTA
                               ||||||||||||||||||||||||
                               GTTGTACCACTTTGGGGTAGAGAT

GAM1684  FBP17    3'  TAGAGACAGGGTTTCACCGTGT 73159            C
           TG                  TAACATGGTGAAACCC GTCTCTA
                               |||||||||||||||| |||||||
                               GTTGTGCCACTTTGGG CAGAGAT
                                      A
GAM1684  FER1L4   3'  TAGAGACAGGGTTTCACCATGT 48137            C
           TG                  TAACATGGTGAAACCC GTCTCTA
                               |||||||||||||||| |||||||
                               GTTGTACCACTTTGGG CAGAGAT
                                      A
GAM1684  FKBP9    3'  TAGAGACGGGGTTTCACCGTGT 95723
           TG                  TAACATGGTGAAACCCCGTCTCTA
                               ||||||||||||||||||||||||
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                                GTTGTGCCACTTTGGGGCAGAGAT

GAM1684  FLJ00060  5'  TAGAGATGGAATTTCACCATGT 61754          CC
              TA                 TAACATGGTGAAA  CCGTCTCTA
                                 ||||||||||||  |||||||||
                                 ATTGTACCACTTT  GGTAGAGAT
                                       AA
GAM1684  FLJ10298  3'  TAGAGACGGGGTTTCACCATGT 36463
              TG                 TAACATGGTGAAACCCCGTCTCTA
                                 ||||||||||||||||||||||||
                                 GTTGTACCACTTTGGGGCAGAGAT

GAM1684  FLJ10346  5'  TAGAGGCAGGGTTTCACCATGT 36531            C
              TG                 TAACATGGTGAAACCC GTCTCTA
                                 ||||||||||||||| |||||||
                                 GTTGTACCACTTTGGG CGGAGAT
                                       A
GAM1684  FLJ10535  3'  TAGAGATGGGGTTTCACCATGT 36756
              TG                 TAACATGGTGAAACCCCGTCTCTA
                                 ||||||||||||||||||||||||
                                 GTTGTACCACTTTGGGGTAGAGAT

GAM1684  FLJ10560  3'  TAGAGACGGGGTTTCACCGTGT 36802
              TA                 TAACATGGTGAAACCCCGTCTCTA
                                 ||||||||||||||||||||||||
                                 ATTGTGCCACTTTGGGGCAGAGAT

GAM1684  FLJ10713  3'  TAGAGATGGGGTTTCACCATGT 37007
              TG                 TAACATGGTGAAACCCCGTCTCTA
                                 ||||||||||||||||||||||||
                                 GTTGTACCACTTTGGGGTAGAGAT

GAM1684  FLJ10846  3'  TAGAGACAGGGTCTCACCATGT 37292          A   C
              TA                 TAACATGGTGA ACCC GTCTCTA
                                 |||||||||| |||| |||||||
                                 ATTGTACCACT TGGG CAGAGAT
                                       C   A
GAM1684  FLJ10922  3'  TAGAGACGGGGTTTTGTC    37409    TG
                                 GG  AAACCCCGTCTCTA
                                 ||  |||||||||||||
                                 CT  TTTGGGGCAGAGAT
                                  GT
GAM1684  FLJ10956  3'  TGGAGACGGGGTTTCACCATGT 37474
              TG                 TAACATGGTGAAACCCCGTCTCTA
                                 ||||||||||||||||||||||||
                                 GTTGTACCACTTTGGGGCAGAGGT

GAM1684  FLJ11193  3'  TAGAGATGGGGTCTCACCATGT 37752          A
              TA                 TAACATGGTGA ACCCCGTCTCTA
                                 |||||||||| ||||||||||||
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                                ATTGTACCACT TGGGGTAGAGAT
                                      C
GAM1684  FLJ12363  3'  TGGGGTTTCACCATGTTG    50645
                                TAACATGGTGAAACCCCG
                                ||||||||||||||||||
                                GTTGTACCACTTTGGGGT

GAM1684  FLJ12581  3'  TAGAGACAGGGTTTCACTGTGT 46343             C
           TA                     TAACATGGTGAAACCC GTCTCTA
                                ||||||||||||||| |||||||
                                ATTGTGTCACTTTGGG CAGAGAT
                                      A
GAM1684  FLJ12687  3'  TAGAGACAGGGTTTCACCATGT 46757             C
           TG                     TAACATGGTGAAACCC GTCTCTA
                                ||||||||||||||| |||||||
                                GTTGTACCACTTTGGG CAGAGAT
                                      A
GAM1684  FLJ12747  3'  TAGAGACAGGGTATCTCCATGT 50672        T A   C
           TG                     TAACATGG GA ACCC GTCTCTA
                                |||||||| || |||| |||||||
                                GTTGTACC CT TGGG CAGAGAT
                                     T A   A
GAM1684  FLJ12787  3'  TAGAGACGGGGTTTCACC    50695
                                GGTGAAACCCCGTCTCTA
                                ||||||||||||||||||
                                CCACTTTGGGGCAGAGAT

GAM1684  FLJ12876  3'  TAGAGACGGGGTTTCACTGTG  43100
                                CATGGTGAAACCCCGTCTCTA
                                ||||||||||||||||||||
                                GTGTCACTTTGGGGCAGAGAT

GAM1684  FLJ12903  3'  TAGAGACAGGATTTCTCCATGT 43078        T   C  C
           TG                     TAACATGG GAAA CC GTCTCTA
                                |||||||| |||| || |||||||
                                GTTGTACC CTTT GG CAGAGAT
                                     T   A  A
GAM1684  FLJ12975  3'  AGACGGGGTTTCGCCTTGTTG  70182      T
                                TAACA GGTGAAACCCCGTCT
                                ||||| ||||||||||||||
                                GTTGT CCGCTTTGGGGCAGA
                                   T
GAM1684  FLJ13072  5'  TAGAGACAGGGTTTCACCATGT 91397             C
           TG                     TAACATGGTGAAACCC GTCTCTA
                                ||||||||||||||| |||||||
                                GTTGTACCACTTTGGG CAGAGAT
                                      A
GAM1684  FLJ13114  3'  TAGAGATGGAGTTTCACCATGT 44910           C
           TA                     TAACATGGTGAAAC CCGTCTCTA
                                ||||||||||||| |||||||||
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                                ATTGTACCACTTTG GGTAGAGAT
                                       A
GAM1684  FLJ13188  3'  TAGAGACAGAGTTTTGCTGTGT 42196        TG    CCC
                TG                TAACATGG  AAAC   GTCTCTA
                                  ||||||||  ||||   |||||||
                                  GTTGTGTC  TTTG   CAGAGAT
                                      GT    AGA
GAM1684  FLJ13197  3'  TAGAGACAAGAGTTTCACCATG 45187            CCC_
                TTG                TAACATGGTGAAAC    GTCTCTA
                                   ||||||||||||||    |||||||
                                   GTTGTACCACTTTG    CAGAGAT
                                         AGAA
GAM1684  FLJ13305  5'  TGGGGTTTCACCATGTTG    91717
                                  TAACATGGTGAAACCCCG
                                  |||||||||||||||||
                                  GTTGTACCACTTTGGGGT

GAM1684  FLJ13456  3'  TAGAGACAGAGTTTCACTCTGT 66562     T       CCC
                                  ACA GGTGAAAC   GTCTCTA
                                  |||  ||||||||   |||||||
                                  TGT TCACTTTG   CAGAGAT
                                    C       AGA
GAM1684  FLJ13952  3'  TAGAGACGGGTTTCACCACGTT 46020      A         C
                G                  TAAC TGGTGAAACCC GTCTCTA
                                   ||||  ||||||||||| |||||||
                                   GTTG ACCACTTTGGG CAGAGAT
                                     C         _
GAM1684  FLJ14950  3'  TAGAGACAGGGTTTCACCATGT 52797              C
                TG                 TAACATGGTGAAACCC GTCTCTA
                                   |||||||||||||||| |||||||
                                   GTTGTACCACTTTGGG CAGAGAT
                                          A
GAM1684  FLJ14957  3'  TAGAGACGGGGTTTCACCATGT 52826
                TG                 TAACATGGTGAAACCCCGTCTCTA
                                   ||||||||||||||||||||||||
                                   GTTGTACCACTTTGGGGCAGAGAT

GAM1684  FLJ20079  3'  TAGAGACAGGGTTTCTCCATGT 34977        T      C
                TG                 TAACATGG GAAACCC GTCTCTA
                                   ||||||||  |||||||  |||||||
                                   GTTGTACC CTTTGGG CAGAGAT
                                       T      A
GAM1684  FLJ20136  3'  TAGAGATGAGTTTCACCATGTT 35103             CC
                G                  TAACATGGTGAAAC  CGTCTCTA
                                   ||||||||||||||  ||||||||
                                   GTTGTACCACTTTG  GTAGAGAT
                                          A_
GAM1684  FLJ20344  3'  TAGAGACAGGGTTTCACCATGT 35488              C
                TG                 TAACATGGTGAAACCC GTCTCTA
                                   |||||||||||||||| |||||||
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                                GTTGTACCACTTTGGG CAGAGAT
                                      A
GAM1684  FLJ20507  3'  TAGAGACAGGGTTTCACCATGT 35750              C
                TG                  TAACATGGTGAAACCC GTCTCTA
                                    |||||||||||||||| |||||||
                                    GTTGTACCACTTTGGG CAGAGAT
                                      A
GAM1684  FLJ20511  3'  TAGAGGCGCAGTTTCACCGTGT 35783             CC
                TA                  TAACATGGTGAAAC  CGTCTCTA
                                    ||||||||||||||  ||||||||
                                    ATTGTGCCACTTTG  GCGGAGAT
                                      AC
GAM1684  FLJ20700  3'  TAGAGACGGGTTTCACCATATT 36019     C          C
                G                   TAA ATGGTGAAACCC GTCTCTA
                                    ||| |||||||||||| |||||||
                                    GTT TACCACTTTGGG CAGAGAT
                                     A          _
GAM1684  FLJ20897  5'  TAGAGACGGGGTTTCAACGTGT 51478         G
                TG                  TAACATG TGAAACCCCGTCTCTA
                                    ||||||| ||||||||||||||||
                                    GTTGTGC ACTTTGGGGCAGAGAT
                                       A
GAM1684  FLJ21302  3'  TAGAGACAGGGTTTCACCATGT 43514              C
                TG                  TAACATGGTGAAACCC GTCTCTA
                                    |||||||||||||||| |||||||
                                    GTTGTACCACTTTGGG CAGAGAT
                                      A
GAM1684  FLJ21324  5'  TAGAGATGGGGTTTCACCATGT 92859
                TG                  TAACATGGTGAAACCCCGTCTCTA
                                    ||||||||||||||||||||||||
                                    GTTGTACCACTTTGGGGTAGAGAT

GAM1684  FLJ21603  3'  TAGAGATGGGGTTTCACCCTGT 45777        T
                TA                  TAACA GGTGAAACCCCGTCTCTA
                                    ||||| ||||||||||||||||
                                    ATTGT CCACTTTGGGGTAGAGAT
                                       C
GAM1684  FLJ22329  3'  TAGAGACGGGGTTTCACCATGT 45408
                TG                  TAACATGGTGAAACCCCGTCTCTA
                                    ||||||||||||||||||||||||
                                    GTTGTACCACTTTGGGGCAGAGAT

GAM1684  FLJ22529  3'  TAGAGACAGGGTTTCACCA   45952           C
                                    TGGTGAAACCC GTCTCTA
                                    |||||||||| |||||||
                                    ACCACTTTGGG CAGAGAT
                                       A
GAM1684  FLJ22529  3'  TAGAGACAGGGTTTCATCATGT 45953             C
                TG                  TAACATGGTGAAACCC GTCTCTA
                                    |||||||||||||||| |||||||
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                                GTTGTACTACTTTGGG CAGAGAT
                                      A
GAM1684  FLJ22684  3'  TAGAGACAGGGTTTCACCATGT 47472            C
              TG                 TAACATGGTGAAACCC GTCTCTA
                                 ||||||||||||||| |||||||
                                 GTTGTACCACTTTGGG CAGAGAT
                                      A
GAM1684  FLJ22794  3'  TAGAGACAGGGTTTCACCATGT 93253            C
              TG                 TAACATGGTGAAACCC GTCTCTA
                                 ||||||||||||||| |||||||
                                 GTTGTACCACTTTGGG CAGAGAT
                                      A
GAM1684  FLJ22969  3'  TAGAGACAGGGTTTCACCATGT 69216            C
              TG                 TAACATGGTGAAACCC GTCTCTA
                                 ||||||||||||||| |||||||
                                 GTTGTACCACTTTGGG CAGAGAT
                                      A
GAM1684  FLJ23024  3'  TAGAGACGGGGTTTCACCATGT 46848
              TG                 TAACATGGTGAAACCCCGTCTCTA
                                 ||||||||||||||||||||||||
                                 GTTGTACCACTTTGGGGCAGAGAT

GAM1684  FLJ23392  3'  TAGAGACAGGGTTTCACCATGT 45909            C
              TG                 TAACATGGTGAAACCC GTCTCTA
                                 ||||||||||||||| |||||||
                                 GTTGTACCACTTTGGG CAGAGAT
                                      A
GAM1684  FLJ23392  3'  TAGAGACAGGGTTTCACCGTGT 45910            C
              TA                 TAACATGGTGAAACCC GTCTCTA
                                 ||||||||||||||| |||||||
                                 ATTGTGCCACTTTGGG CAGAGAT
                                      A
GAM1684  FLJ23392  3'  TAGAGACGGGGTTTCACCGTGT 45911
              TA                 TAACATGGTGAAACCCCGTCTCTA
                                 ||||||||||||||||||||||||
                                 ATTGTGCCACTTTGGGGCAGAGAT

GAM1684  FLJ23519  3'  TAGAGATGGGGTTTCACCGTGT 50961
              TA                 TAACATGGTGAAACCCCGTCTCTA
                                 ||||||||||||||||||||||||
                                 ATTGTGCCACTTTGGGGTAGAGAT

GAM1684  FLJ23556  3'  AGAGACGGGGTTTCACCGTGTT 46426
              A                   TAACATGGTGAAACCCCGTCTCT
                                  ||||||||||||||||||||||||
                                  ATTGTGCCACTTTGGGGCAGAGA

GAM1684  FLJ23556  3'  TAGAGACCGGGCTTCACCATGT 46454          A  C
              TG                 TAACATGGTGAA CCC GTCTCTA
                                 |||||||||||| ||| |||||||
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                                GTTGTACCACTT GGG CAGAGAT
                                      C   C
GAM1684  FLJ25416  5'  TGGGGTTTCACCATGTTG    59457
                                TAACATGGTGAAACCCCG
                                ||||||||||||||||||
                                GTTGTACCACTTTGGGGT

GAM1684  FLJ30532  3'  TAGAGACAGGATTTCACTATGT 59227            C  C
              TG                  TAACATGGTGAAA CC GTCTCTA
                                  ||||||||||||| || |||||||
                                  GTTGTATCACTTT GG CAGAGAT
                                        A  A
GAM1684  FLJ31101  3'  AGACGGGGGATTTCACCATGTT 36156            __
              G                   TAACATGGTGAAA  CCCCGTCT
                                  ||||||||||||  ||||||||
                                  GTTGTACCACTTT  GGGGCAGA
                                        AG
GAM1684  FLJ31153  3'  TAGAGATGGGGTTTCACCATG  58753
                                CATGGTGAAACCCCGTCTCTA
                                |||||||||||||||||||||
                                GTACCACTTTGGGGTAGAGAT

GAM1684  FLJ32865  3'  TAGAGACGGGGTTTCTCCGTGT 58820         T
              TG                  TAACATGG GAAACCCCGTCTCTA
                                  ||||||||  ||||||||||||||
                                  GTTGTGCC CTTTGGGGCAGAGAT
                                       T
GAM1684  GGA2      3'  TAGAGACAGGATTTCACCATGT 57679            C  C
              TG                  TAACATGGTGAAA CC GTCTCTA
                                  ||||||||||||| || |||||||
                                  GTTGTACCACTTT GG CAGAGAT
                                        A  A
GAM1684  GGA2      3'  TAGAGACAGGATTTCACCATGT 57680            C  C
              TG                  TAACATGGTGAAA CC GTCTCTA
                                  ||||||||||||| || |||||||
                                  GTTGTACCACTTT GG CAGAGAT
                                        A  A
GAM1684  GMPPB     5'  TAGAGACAGGGTTTCACCAGGT 97460      A         C
              TG                  TAAC TGGTGAAACCC GTCTCTA
                                  |||| |||||||||| |||||||
                                  GTTG ACCACTTTGGG CAGAGAT
                                    G         A
GAM1684  GNG4      3'  AGACGGGGTTTCACCATGTTG  16839
                                TAACATGGTGAAACCCCGTCT
                                |||||||||||||||||||||
                                GTTGTACCACTTTGGGGCAGA

GAM1684  GOLGA3    3'  ATGGGGTTTCACCATGTTG   20881
                                TAACATGGTGAAACCCCGT
                                |||||||||||||||||||
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                                GTTGTACCACTTTGGGGTA

GAM1684  GREB1    3'  TAGAGACGGGGTTTCACCATGT 28579
                TA                TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  ATTGTACCACTTTGGGGCAGAGAT

GAM1684  GRWD     3'  TAGAGACGGGGTTTCACCATGT 49788
                TG                TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTACCACTTTGGGGCAGAGAT

GAM1684  GTF2E1   3'  TAGAGGCAGGGTTTCACCATGT 19805             C
                TA                TAACATGGTGAAACCC GTCTCTA
                                  |||||||||||||||| |||||||
                                  ATTGTACCACTTTGGG CGGAGAT
                                        A
GAM1684  GTPBG3   3'  TAGAGACAAGGTTTCACCATGT 51907            CC
                TG                TAACATGGTGAAACC  GTCTCTA
                                  ||||||||||||||  |||||||
                                  GTTGTACCACTTTGG  CAGAGAT
                                        AA
GAM1684  H2AV     3'  TAGACGTGGGGTTTCACCATGT 57635             TC
                TG                TAACATGGTGAAACCCCG  TCTA
                                  ||||||||||||||||  ||||
                                  GTTGTACCACTTTGGGGT  AGAT
                                        GC
GAM1684  HARS2    3'  TAGAGACGGGGTTTTACCATGT 55869
                TA                TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  ATTGTACCATTTTGGGGCAGAGAT

GAM1684  HCA4     3'  TAGAGACGGGGTTTTGCCATGT 57745         TG
                TG                TAACATGG  AAACCCCGTCTCTA
                                  ||||||||  ||||||||||||||
                                  GTTGTACC  TTTGGGGCAGAGAT
                                     GT
GAM1684  HCGIV.9  3'  TAGAGACAGGGTTTTTTGTTGT 39135       TGGT      C
                TG                TAACA    GAAACCC GTCTCTA
                                  |||||    ||||||| |||||||
                                  GTTGT    TTTTGGG CAGAGAT
                                    TGTT      A
GAM1684  HSNOV1   3'  TAGACATGGGGTTTCACCATGT 34441               C
                TG                TAACATGGTGAAACCCCGT TCTA
                                  |||||||||||||||||| ||||
                                  GTTGTACCACTTTGGGGTA AGAT
                                        C
GAM1684  HSPC065  3'  TAGAGATGGGGTTTCACCATGT 27163
                TG                TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
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                              GTTGTACCACTTTGGGGTAGAGAT

GAM1684 ICK      3' TAGAGACGGGGTTTCACTGTGT 33692
           TA                 TAACATGGTGAAACCCCGTCTCTA
                              ||||||||||||||||||||||||
                              ATTGTGTCACTTTGGGGCAGAGAT

GAM1684 JAM1     3' TAGAGACAGGGTTTCACCATGT 34245          C
           TG                 TAACATGGTGAAACCC GTCTCTA
                              |||||||||||||||| |||||||
                              GTTGTACCACTTTGGG CAGAGAT
                                       A
GAM1684 JAM1     3' TAGAGACAGGGTTTCACCATGT 34246          C
           TG                 TAACATGGTGAAACCC GTCTCTA
                              |||||||||||||||| |||||||
                              GTTGTACCACTTTGGG CAGAGAT
                                       A
GAM1684 JM11     3' TAGAGACAAGGTTTCACCAT  54373        CC
                              ATGGTGAAACC  GTCTCTA
                              ||||||||||  |||||||
                              TACCACTTTGG  CAGAGAT
                                    AA
GAM1684 KIAA0022 3' TAGAGACGGGGTTTCGCCAT  30284
                              ATGGTGAAACCCCGTCTCTA
                              ||||||||||||||||||
                              TACCGCTTTGGGGCAGAGAT

GAM1684 KIAA0161 3' TAGAGACGGGGTTTCACCATGT 29209
           TG                 TAACATGGTGAAACCCCGTCTCTA
                              ||||||||||||||||||||||||
                              GTTGTACCACTTTGGGGCAGAGAT

GAM1684 KIAA0186 3' TAGAGACAGAGTTTTACCATGT 41116          CCC
           TG                 TAACATGGTGAAAC  GTCTCTA
                              ||||||||||||||  |||||||
                              GTTGTACCATTTTG  CAGAGAT
                                       AGA
GAM1684 KIAA0186 3' TGGGGTTTCACCATGTTG    41123
                              TAACATGGTGAAACCCCG
                              |||||||||||||||||
                              GTTGTACCACTTTGGGGT

GAM1684 KIAA0205 3' TAGAGATGGGGTTTCACCATGT 30217
           TG                 TAACATGGTGAAACCCCGTCTCTA
                              ||||||||||||||||||||||||
                              GTTGTACCACTTTGGGGTAGAGAT

GAM1684 KIAA0210 5' TAGAGACGGAGGAGTTTCACCA 29174          __ _
           TGTTG                 TAACATGGTGAAA  CC CCGTCTCTA
                              ||||||||||||  || |||||||||
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                                GTTGTACCACTTT  GG GGCAGAGAT
                                      GA  A
GAM1684  KIAA0210  5'  TAGAGACGGGGTTTCACTAT   29175
                                ATGGTGAAACCCCGTCTCTA
                                ||||||||||||||||||||
                                TATCACTTTGGGGCAGAGAT

GAM1684  KIAA0391  3'  TAGAGACGGGTTTTCACCATGT 28618            C
                TG                TAACATGGTGAAA CCCGTCTCTA
                                ||||||||||||| |||||||||
                                GTTGTACCACTTT GGGCAGAGAT
                                      T
GAM1684  KIAA0426  3'  TAGAGACGGGGTTTCACCATGT 28934
                TG                TAACATGGTGAAACCCCGTCTCTA
                                ||||||||||||||||||||||||
                                GTTGTACCACTTTGGGGCAGAGAT

GAM1684  KIAA0441  3'  TAGAGACGGGGTCTCACTGT   29641        A
                                ATGGTGA ACCCCGTCTCTA
                                |||||||  ||||||||||||
                                TGTCACT TGGGGCAGAGAT
                                   C
GAM1684  KIAA0446  5'  TAGAGACGGAGTCTCCCTATGT 69459         T  A  C
                TG                TAACATGG GA AC CCGTCTCTA
                                |||||||| || || |||||||||
                                GTTGTATC CT TG GGCAGAGAT
                                     C  C  A
GAM1684  KIAA0451  3'  AGAATCATTTCACCAGTTA    29761      A       CCCCG
                                TAAC TGGTGAAA     TCT
                                ||||  ||||||||     |||
                                ATTG ACCACTTT     AGA
                                  _       ACTA_
GAM1684  KIAA0459  3'  TAGAGACGGGGTTTCACCATGT 61660
                TA                TAACATGGTGAAACCCCGTCTCTA
                                ||||||||||||||||||||||||
                                ATTGTACCACTTTGGGGCAGAGAT

GAM1684  KIAA0469  3'  TAGAGACAGGGTCTTGCTGTGT 29996         TG A    C
                TA                TAACATGG  A ACCC GTCTCTA
                                ||||||||  | |||| |||||||
                                ATTGTGTC  T TGGG CAGAGAT
                                     GT C    A
GAM1684  KIAA0469  3'  TAGAGACGGGATTTCACTGTGT 29997            C
                TA                TAACATGGTGAAA CCCGTCTCTA
                                |||||||||||| |||||||||
                                ATTGTGTCACTTT GGGCAGAGAT
                                      A
GAM1684  KIAA0472  5'  TAGAGACGGGGTCTCCCCAT   72366      T  A
                                ATGG GA ACCCCGTCTCTA
                                |||| || ||||||||||||
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                                TACC CT TGGGGCAGAGAT
                                  C  C
GAM1684  KIAA0475  3'  AGGGTTTCGGGTTTCACCATGT 30110              CGT_
              TG                  TAACATGGTGAAACCC    CTCT
                                  ||||||||||||||||    ||||
                                  GTTGTACCACTTTGGG    GGGA
                                        CTTT
GAM1684  KIAA0478  3'  TAGAGACAGGGTCTCGCCATGT 30183          A    C
              TG                  TAACATGGTGA ACCC GTCTCTA
                                  |||||||||||| |||| |||||||
                                  GTTGTACCGCT TGGG CAGAGAT
                                        C    A
GAM1684  KIAA0495  3'  TAGAGATGGGATTTCACCATGT 63274            C
              TG                  TAACATGGTGAAA CCCGTCTCTA
                                  |||||||||||||| ||||||||||
                                  GTTGTACCACTTT GGGTAGAGAT
                                        A
GAM1684  KIAA0513  5'  TAGAGACAGGGTTTCGCCATGT 29049              C
              TG                  TAACATGGTGAAACCC GTCTCTA
                                  |||||||||||||||| |||||||
                                  GTTGTACCGCTTTGGG CAGAGAT
                                        A
GAM1684  KIAA0513  3'  TAGAGATGGGGTTTCACCATG  29050
                                  CATGGTGAAACCCCGTCTCTA
                                  |||||||||||||||||||||
                                  GTACCACTTTGGGGTAGAGAT

GAM1684  KIAA0527  3'  TAGAGATGGAGTTTCACCATGT 97501            C
              TG                  TAACATGGTGAAAC CCGTCTCTA
                                  |||||||||||||| |||||||||
                                  GTTGTACCACTTTG GGTAGAGAT
                                        A
GAM1684  KIAA0544  3'  TAGAGAAGGGATTTCACCATGT 71476            C   G
              TG                  TAACATGGTGAAA CCC TCTCTA
                                  |||||||||||| ||| ||||||
                                  GTTGTACCACTTT GGG AGAGAT
                                        A   A
GAM1684  KIAA0555  3'  TAGAGACAGGGTTTCACTATG  60745            C
                                  CATGGTGAAACCC GTCTCTA
                                  |||||||||||| |||||||
                                  GTATCACTTTGGG CAGAGAT
                                        A
GAM1684  KIAA0561  3'  AGACGGGGTTTCACCATGTTG  66463
                                  TAACATGGTGAAACCCCGTCT
                                  |||||||||||||||||||||
                                  GTTGTACCACTTTGGGGCAGA

GAM1684  KIAA0562  3'  TAGAGACGGGGTTTCACCAT   28830
                                  ATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||
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                                TACCACTTTGGGGCAGAGAT

GAM1684  KIAA0599  3'  TAGAGACGGGGTTTCGCCGTGT 77701
                TG                TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTGCCGCTTTGGGGCAGAGAT

GAM1684  KIAA0682  3'  TAGAGACTGGGTTTCACCATGT 30028          C
                                  ACATGGTGAAACCC GTCTCTA
                                  |||||||||||||| |||||||
                                  TGTACCACTTTGGG CAGAGAT
                                        T
GAM1684  KIAA0720  3'  TAGAGACGGCATTTCACCAT  62992       CC
                                  ATGGTGAAA  CCGTCTCTA
                                  |||||||||  |||||||||
                                  TACCACTTT  GGCAGAGAT
                                      AC
GAM1684  KIAA0737  3'  TAGAGACAGGGTTTCACCATGT 29820          C
                TG                TAACATGGTGAAACCC GTCTCTA
                                  |||||||||||||||| |||||||
                                  GTTGTACCACTTTGGG CAGAGAT
                                        A
GAM1684  KIAA0798  3'  TAGAGACGGGGTTTCACTGTGT 28454
                TG                TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTGTCACTTTGGGGCAGAGAT

GAM1684  KIAA0828  3'  TAGAGACAGGGTTTCACTATGT 82120          C
                TG                TAACATGGTGAAACCC GTCTCTA
                                  |||||||||||||||| |||||||
                                  GTTGTATCACTTTGGG CAGAGAT
                                        A
GAM1684  KIAA0831  3'  TAGAGACGGGGGTTTTCACCAT 30654          __
                GTTG                TAACATGGTGAAA  CCCCGTCTCTA
                                    ||||||||||||  ||||||||||||
                                    GTTGTACCACTTT  GGGGCAGAGAT
                                          TG
GAM1684  KIAA0861  3'  TAGAGACGGGGTTTCCCCGTGT 90360        T
                TA                TAACATGG GAAACCCCGTCTCTA
                                  ||||||||  ||||||||||||||||
                                  ATTGTGCC CTTTGGGGCAGAGAT
                                      C
GAM1684  KIAA0884  3'  TAGAGGTGAGGTTTCACCATGT 70757          C GT
                TG                TAACATGGTGAAACC C  CTCTA
                                  |||||||||||||||  |  |||||
                                  GTTGTACCACTTTGG G  GAGAT
                                        A TG
GAM1684  KIAA0924  3'  AGAGATGGGGTTTCACCAT   30351
                                  ATGGTGAAACCCCGTCTCT
                                  |||||||||||||||||||
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                              TACCACTTTGGGGTAGAGA

GAM1684  KIAA0931  3'  TAGAGACGGGGTTTCACCATGT 68017
              TG                TAACATGGTGAAACCCCGTCTCTA
                                ||||||||||||||||||||||||
                                GTTGTACCACTTTGGGGCAGAGAT

GAM1684  KIAA0961  3'  TGGGGTTTCACCATGTTG    30414
                              TAACATGGTGAAACCCCG
                              |||||||||||||||||
                              GTTGTACCACTTTGGGGT

GAM1684  KIAA1026  3'  TAGAGATGAGATTTCACCATGT 71744          CCC
              TG                TAACATGGTGAAA  CGTCTCTA
                                ||||||||||||  ||||||||
                                GTTGTACCACTTT  GTAGAGAT
                                      AGA
GAM1684  KIAA1041  3'  TAGAGATGGGGTTTCACCATGT 30830
              TG                TAACATGGTGAAACCCCGTCTCTA
                                ||||||||||||||||||||||||
                                GTTGTACCACTTTGGGGTAGAGAT

GAM1684  KIAA1115  5'  TAGAGACAGGGTTTCGCCATGT 30697            C
              TG                TAACATGGTGAAACCC GTCTCTA
                                ||||||||||||||| |||||||
                                GTTGTACCGCTTTGGG CAGAGAT
                                      A
GAM1684  KIAA1143  3'  TAGAGACGGGGTTTCACTTTGT 69249      T
              TA                TAACA GGTGAAACCCCGTCTCTA
                                ||||| ||||||||||||||||||
                                ATTGT TCACTTTGGGGCAGAGAT
                                  T
GAM1684  KIAA1170  3'  TAGAAACAGGGTTTCACCATGT 70423           C  C
              TA                TAACATGGTGAAACCC GT TCTA
                                |||||||||||||||| || ||||
                                ATTGTACCACTTTGGG CA AGAT
                                      A  A
GAM1684  KIAA1185  3'  TAGAGACGGGGTTTCACCATTT 63295    C
              TG                TAA ATGGTGAAACCCCGTCTCTA
                                ||| ||||||||||||||||||||
                                GTT TACCACTTTGGGGCAGAGAT
                                  T
GAM1684  KIAA1198  3'  CGGGGTTTCACCGTGTTA    64030
                              TAACATGGTGAAACCCCG
                              |||||||||||||||||
                              ATTGTGCCACTTTGGGGC

GAM1684  KIAA1198  3'  TAGAGACAGTGTTTCACCATGT 64061          CCC
              TG                TAACATGGTGAAAC  GTCTCTA
                                ||||||||||||||  |||||||
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                                GTTGTACCACTTTG   CAGAGAT
                                      TGA
GAM1684  KIAA1198  3'  TAGAGACGGGGTTTCACCATGT 64062
              TG                  TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTACCACTTTGGGGCAGAGAT

GAM1684  KIAA1198  3'  TAGAGACGGGGTTTCACCATGT 64063
              TG                  TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTACCACTTTGGGGCAGAGAT

GAM1684  KIAA1198  3'  TAGAGATGGGGTTTCACCATGT 64064
              TG                  TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTACCACTTTGGGGTAGAGAT

GAM1684  KIAA1200  3'  TAGAGACGGGGTTTCACCATGT 63042
              TG                  TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTACCACTTTGGGGCAGAGAT

GAM1684  KIAA1210  3'  TAGAGACGGGGTTTCACCATGT 98082
              TG                  TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTACCACTTTGGGGCAGAGAT

GAM1684  KIAA1254  3'  TAGAGATGGGGTTTCACCATGT 70565
              TG                  TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTACCACTTTGGGGTAGAGAT

GAM1684  KIAA1257  3'  TAGAGACAAGGTCTTGCTATGT 63415        TG A   CC
              TG                  TAACATGG  A ACC  GTCTCTA
                                  ||||||||  | |||  |||||||
                                  GTTGTATC  T TGG  CAGAGAT
                                       GT C   AA
GAM1684  KIAA1257  3'  TAGAGACGAGGTTTCTCCAT   63416      T     C
                                  ATGG GAAACC CGTCTCTA
                                  |||| |||||| ||||||||
                                  TACC CTTTGG GCAGAGAT
                                    T     A
GAM1684  KIAA1443  3'  TAGAGACGGGTTTCATCATGTT 64578              C
              A                    TAACATGGTGAAACCC GTCTCTA
                                  ||||||||||||||| |||||||
                                  ATTGTACTACTTTGGG CAGAGAT
                                                 _
GAM1684  KIAA1456  3'  CGGGGTTTCACCGTGTTA    67548
                                  TAACATGGTGAAACCCCG
                                  |||||||||||||||||
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                                ATTGTGCCACTTTGGGGC

GAM1684  KIAA1465  3'  TAGAGACGGGGTTTCACCATGT 61509
              TG                  TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTACCACTTTGGGGCAGAGAT

GAM1684  KIAA1467  3'  TAGAGACGGGGTTTCACCATGT 72077
              TG                  TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTACCACTTTGGGGCAGAGAT

GAM1684  KIAA1497  5'  ATAGAGACAGGGTTTCACCATG 68112            C     ___
              TTG                  TAACATGGTGAAACCC GTCTCTA   T
                                  |||||||||||||||| |||||||   |
                                  GTTGTACCACTTTGGG CAGAGAT   A
                                        A     __
GAM1684  KIAA1508  3'  TAGAAACAAGGTTTCACCATGT 62561            CC  C
              TG                  TAACATGGTGAAACC  GT TCTA
                                  ||||||||||||||  || ||||
                                  GTTGTACCACTTTGG  CA AGAT
                                        AA  A
GAM1684  KIAA1530  3'  TAGAGACGGGATTTCACTGTGT 68571           C
              TG                  TAACATGGTGAAA CCCGTCTCTA
                                  ||||||||||||| ||||||||||
                                  GTTGTGTCACTTT GGGCAGAGAT
                                        A
GAM1684  KIAA1615  3'  TAGATATGGAGTTTCACCACGT 69285     A      C   C
              TG                  TAAC TGGTGAAAC CCGT TCTA
                                  |||| ||||||||| |||| ||||
                                  GTTG ACCACTTTG GGTA AGAT
                                    C       A   T
GAM1684  KIAA1617  3'  TAGAGACAGGGTTTCACCATGT 93083            C
              TG                  TAACATGGTGAAACCC GTCTCTA
                                  |||||||||||||||| |||||||
                                  GTTGTACCACTTTGGG CAGAGAT
                                        A
GAM1684  KIAA1655  3'  TAGAGACAGGTTTCACCATGTT 67202            CC
              G                    TAACATGGTGAAACC  GTCTCTA
                                  ||||||||||||||  |||||||
                                  GTTGTACCACTTTGG  CAGAGAT
                                        A_
GAM1684  KIAA1668  3'  TAGAGACGGGGTTTCACCGTGT 67080
              TA                  TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  ATTGTGCCACTTTGGGGCAGAGAT

GAM1684  KIAA1671  3'  AGAGACAAGGGTCTTACCA   66268      A   C_
                                  TGGTGA ACCC  GTCTCT
                                  |||||| ||||  ||||||
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                                ACCATT TGGG  CAGAGA
                                  C    AA
GAM1684  KIAA1712  3'  TAGAGACAGGGTTTCACCATGT 68165              C
             TG                   TAACATGGTGAAACCC GTCTCTA
                                  ||||||||||||||| |||||||
                                  GTTGTACCACTTTGGG CAGAGAT
                                        A
GAM1684  KIAA1712  3'  TAGAGACAGGGTTTCTCCGTGT 68166         T      C
             TG                   TAACATGG GAAACCC GTCTCTA
                                  |||||||| ||||||| |||||||
                                  GTTGTGCC CTTTGGG CAGAGAT
                                     T      A
GAM1684  KIAA1784  3'  TAGAAACGGGGTTTCACCATGT 65755               C
             TG                   TAACATGGTGAAACCCCGT TCTA
                                  |||||||||||||||||| ||||
                                  GTTGTACCACTTTGGGGCA AGAT
                                        A
GAM1684  KIAA1821  3'  TAGAGACAGGGTCTCACTGTGT 72275          A    C
             TG                   TAACATGGTGA ACCC GTCTCTA
                                  |||||||||| |||| |||||||
                                  GTTGTGTCACT TGGG CAGAGAT
                                     C    A
GAM1684  KIAA1829  3'  TAGAGACGGGGTTTCACCA    62655
                                  TGGTGAAACCCCGTCTCTA
                                  |||||||||||||||||
                                  ACCACTTTGGGGCAGAGAT

GAM1684  KIAA1877  3'  TAGAGACAGGGTTTCACCGTGT 66761              C
             TA                   TAACATGGTGAAACCC GTCTCTA
                                  |||||||||||||||| |||||||
                                  ATTGTGCCACTTTGGG CAGAGAT
                                        A
GAM1684  KIAA1971  3'  TAGAGACAAGGTTTCGCTATGT 74694             CC
             TG                   TAACATGGTGAAACC  GTCTCTA
                                  |||||||||||||||  |||||||
                                  GTTGTATCGCTTTGG  CAGAGAT
                                        AA
GAM1684  KIAA1971  3'  TAGAGACGAGGTTTCACCGTGT 74695              C
             TA                   TAACATGGTGAAACC CGTCTCTA
                                  |||||||||||||||| ||||||||
                                  ATTGTGCCACTTTGG GCAGAGAT
                                        A
GAM1684  KIAA1971  3'  TAGAGATGAGAGTTTCACACA  74696    _      CC_
                                  TG GTGAAAC   CGTCTCTA
                                  || |||||||   ||||||||
                                  AC CACTTTG   GTAGAGAT
                                   A       AGA
GAM1684  KIAA1975  5'  TAGAGATGGGGTTTCACCATGT 74429
             TA                   TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
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                                ATTGTACCACTTTGGGGTAGAGAT

GAM1684  KIAA1987  5'  GAAACGAGGTTTCACCAT    89382          C   C
                                ATGGTGAAACC CGT TC
                                |||||||||| ||| ||
                                TACCACTTTGG GCA AG
                                      A   A
GAM1684  KLK7      3'  TAGAGACAGGGTTTCACCATGT 18548              C
              TG                  TAACATGGTGAAACCC GTCTCTA
                                  |||||||||||||| |||||||
                                  GTTGTACCACTTTGGG CAGAGAT
                                        A
GAM1684  LAMP3     3'  AGACGGGGTTTCACCATGTTG  60195
                                  TAACATGGTGAAACCCCGTCT
                                  ||||||||||||||||||||
                                  GTTGTACCACTTTGGGGCAGA

GAM1684  LY75      3'  TAGAGATGGGGTTTCACCATGT 11399
              TG                  TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTACCACTTTGGGGTAGAGAT

GAM1684  MAP-1     3'  TAGAGACGGGGTTTCACCATGT 42451
              TG                  TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTACCACTTTGGGGCAGAGAT

GAM1684  MCLC      3'  TAGAGATGGGGTTTCACCATGT 31386
              TG                  TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTACCACTTTGGGGTAGAGAT

GAM1684  MCM10     3'  GACAGGGTCTCACTATGT    38176          A   C
                                  ACATGGTGA ACCC GTC
                                  ||||||||| |||| |||
                                  TGTATCACT TGGG CAG
                                        C   A
GAM1684  MEF-2     3'  TAGAGACTGGGTTTCACCATGT 65031              C
              TG                  TAACATGGTGAAACCC GTCTCTA
                                  |||||||||||||| |||||||
                                  GTTGTACCACTTTGGG CAGAGAT
                                        T
GAM1684  MGC10200  3'  TGGGGTTTCACCATGTTG    59651
                                  TAACATGGTGAAACCCCG
                                  |||||||||||||||||
                                  GTTGTACCACTTTGGGGT

GAM1684  MGC12518  3'  TAGAGTGAGGGTTTCACCATGT 64781              _  T
              TG                  TAACATGGTGAAACCC CG CTCTA
                                  |||||||||||||| || |||||
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                                GTTGTACCACTTTGGG GT GAGAT
                                      A _
GAM1684  MGC15563  3'  TAGAGATGGGATCTCACCATGT 52863          AAC
            TG                  TAACATGGTGA  CCCGTCTCTA
                                |||||||||||  ||||||||||
                                GTTGTACCACT  GGGTAGAGAT
                                     CTA
GAM1684  MGC21675  3'  TAGAGATGGGGTTTCACCATGT 54598
            TG                  TAACATGGTGAAACCCCGTCTCTA
                                ||||||||||||||||||||||||
                                GTTGTACCACTTTGGGGTAGAGAT

GAM1684  MGC2474   3'  TAGAGATGGGGTTTCACCATGT 43965
            TG                  TAACATGGTGAAACCCCGTCTCTA
                                ||||||||||||||||||||||||
                                GTTGTACCACTTTGGGGTAGAGAT

GAM1684  MGC2603   3'  TAGAGACGAGGTTTCACCAT   44083          C
                                ATGGTGAAACC CGTCTCTA
                                |||||||||||  ||||||||
                                TACCACTTTGG GCAGAGAT
                                     A
GAM1684  MGC3113   3'  TAGAGACAGGGTTTCGCCA    44064          C
                                TGGTGAAACCC GTCTCTA
                                |||||||||||  |||||||
                                ACCGCTTTGGG CAGAGAT
                                     A
GAM1684  MGC4766   5'  TAGAGACGGGGTTTCACCGTGT 49564
            TA                  TAACATGGTGAAACCCCGTCTCTA
                                ||||||||||||||||||||||||
                                ATTGTGCCACTTTGGGGCAGAGAT

GAM1684  MGC5149   3'  AGAGATGGGGTTTCACCA     72750
                                TGGTGAAACCCCGTCTCT
                                ||||||||||||||||
                                ACCACTTTGGGGTAGAGA

GAM1684  MKRN4     3'  TAGAAACGGGGTTTCACCAT   48475            C
                                ATGGTGAAACCCCGT TCTA
                                ||||||||||||||  ||||
                                TACCACTTTGGGGCA AGAT
                                      A
GAM1684  MLZE      5'  TAGAGACAGGGTTTCACCATCT 49454     C         C
            TG                  TAA ATGGTGAAACCC GTCTCTA
                                |||  ||||||||||| |||||||
                                GTT TACCACTTTGGG CAGAGAT
                                  C          A
GAM1684  moblak    3'  TAGAGACAAGATTTCACCATGT 56409          CCCC
            TG                  TAACATGGTGAAA    GTCTCTA
                                ||||||||||||    |||||||
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                                GTTGTACCACTTT    CAGAGAT
                                      AGAA
GAM1684  moblak    3'  TAGAGACAGGGTTTCACCGTGT 56410              C
             TA                   TAACATGGTGAAACCC GTCTCTA
                                  ||||||||||||||| |||||||
                                  ATTGTGCCACTTTGGG CAGAGAT
                                        A
GAM1684  MOCS3     3'  AGAGGGGGTTTCACCATGTT  27924              G
                                  AACATGGTGAAACCCC TCT
                                  ||||||||||||||| |||
                                  TTGTACCACTTTGGGG AGA
                                        G
GAM1684  MRPS27    3'  TAGAGATGGGGTTTCACCATGT 31334
             TG                   TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTACCACTTTGGGGTAGAGAT

GAM1684  MtFMT     3'  TAGAGATGGGGTTTCACCATGT 58339
             TG                   TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTACCACTTTGGGGTAGAGAT

GAM1684  NDP52     3'  TAGAGACAGGGTTTCACTATGT 20677              C
             TG                   TAACATGGTGAAACCC GTCTCTA
                                  ||||||||||||||| |||||||
                                  GTTGTATCACTTTGGG CAGAGAT
                                        A
GAM1684  NDUFC2    3'  TAGAGACGGGGTTTCACCATGT 17036
             TG                   TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTACCACTTTGGGGCAGAGAT

GAM1684  NINJ2     3'  TAGAGACGGGGTTTCTCCATGT 33731          T
             TG                   TAACATGG GAAACCCCGTCTCTA
                                  |||||||| ||||||||||||||
                                  GTTGTACC CTTTGGGGCAGAGAT
                                       T
GAM1684  Nup43     3'  TAGAGACGACAGGGTTTCACCA 45354                ___
             TGTTG                  TAACATGGTGAAACCC   CGTCTCTA
                                  ||||||||||||||||   ||||||||
                                  GTTGTACCACTTTGGG   GCAGAGAT
                                        ACA
GAM1684  NXN       3'  TAGAGATGGGGTTTCACCATGT 42681
             TG                   TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTACCACTTTGGGGTAGAGAT

GAM1684  OCT11     3'  TAGAGATGGGGTTTCACCATGT 27594
             TG                   TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
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                                GTTGTACCACTTTGGGGTAGAGAT

GAM1684  OR51E2   3'  TAGAGACAGAGTTTCACCATGT 48520            CCC
            TG                  TAACATGGTGAAAC  GTCTCTA
                                |||||||||||||  |||||||
                                GTTGTACCACTTTG  CAGAGAT
                                      AGA
GAM1684  PELI1    5'  TAGAGACGGGGTTTCACCATGT 40654
            TG                  TAACATGGTGAAACCCCGTCTCTA
                                ||||||||||||||||||||||||
                                GTTGTACCACTTTGGGGCAGAGAT

GAM1684  PELI1    5'  TGGGGTTTCACCATGTTG    40662
                                TAACATGGTGAAACCCCG
                                |||||||||||||||||
                                GTTGTACCACTTTGGGGT

GAM1684  PRO0365  5'  TAGAGACGGGGTTTCACTATGT 26996
            TG                  TAACATGGTGAAACCCCGTCTCTA
                                ||||||||||||||||||||||||
                                GTTGTATCACTTTGGGGCAGAGAT

GAM1684  PRO2955  3'  TAGAGACAGGGTTTTACCATGT 38245             C
            TG                  TAACATGGTGAAACCC GTCTCTA
                                ||||||||||||||| |||||||
                                GTTGTACCATTTTGGG CAGAGAT
                                      A
GAM1684  PSPH     3'  TAGAGACGGGGTTTGACCGTGT 17140          G
            TA                  TAACATGGT AAACCCCGTCTCTA
                                |||||||| ||||||||||||||
                                ATTGTGCCA TTTGGGGCAGAGAT
                                    G
GAM1684  PSTPIP2  3'  TAGAGACAGGGTTTTACCATGT 44662             C
            TG                  TAACATGGTGAAACCC GTCTCTA
                                ||||||||||||||| |||||||
                                GTTGTACCATTTTGGG CAGAGAT
                                      A
GAM1684  RAB21    3'  TAGAGACGGGGTTTCACCAGGT 31098      A
            TA                  TAAC TGGTGAAACCCCGTCTCTA
                                |||| ||||||||||||||||||
                                ATTG ACCACTTTGGGGCAGAGAT
                                  G
GAM1684  RAB33B   3'  AGATGGGGTTTCACCATGTTG  49316
                                TAACATGGTGAAACCCCGTCT
                                |||||||||||||||||||||
                                GTTGTACCACTTTGGGGTAGA

GAM1684  RAB33B   3'  TAGAGACGGGGTCTTGCTATGT 49335         TG A
            TG                  TAACATGG  A ACCCCGTCTCTA
                                ||||||||  | ||||||||||||
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                                GTTGTATC  T TGGGGCAGAGAT
                                    GT C
GAM1684  RAI      5'  TAGAGACAGGGTTCTTACCATG 22857          _     C
             TTG                    TAACATGGTGA AACCC GTCTCTA
                                    |||||||||||  ||||| |||||||
                                    GTTGTACCATT TTGGG CAGAGAT
                                          C     A
GAM1684  RAP140    3'  TAGAGACAGGGTTTCACTGTGT 31524              C
             TA                     TAACATGGTGAAACCC GTCTCTA
                                    ||||||||||||||| |||||||
                                    ATTGTGTCACTTTGGG CAGAGAT
                                             A
GAM1684  RES4-25   3'  TAGAGACGGGGTTTCTCCATGT 65274         T
             TG                     TAACATGG GAAACCCCGTCTCTA
                                    ||||||||  ||||||||||||||
                                    GTTGTACC CTTTGGGGCAGAGAT
                                       T
GAM1684  RNF8      3'  TAGAGACAGGGTTTCACCATGT 15574              C
             TG                     TAACATGGTGAAACCC GTCTCTA
                                    |||||||||||||||  |||||||
                                    GTTGTACCACTTTGGG CAGAGAT
                                             A
GAM1684  SCAMP-4   3'  AGATGGGGTTTCACCATGTTG  55334
                                    TAACATGGTGAAACCCCGTCT
                                    ||||||||||||||||||||
                                    GTTGTACCACTTTGGGGTAGA

GAM1684  SCYA16    3'  TAGAGACGGGATTCTACCATGT 17178          A  C
             TG                     TAACATGGTG AA CCCGTCTCTA
                                    ||||||||||  ||  ||||||||||
                                    GTTGTACCAT TT GGGCAGAGAT
                                          C  A
GAM1684  SCYA22    3'  TAGAGACAGGTTTCACCAT    92609           CC
                                    ATGGTGAAACC  GTCTCTA
                                    ||||||||||  |||||||
                                    TACCACTTTGG  CAGAGAT
                                          A_
GAM1684  SCYA22    3'  TAGAGACGAGGCTTCACCATGT 92610           A  C
             TG                     TAACATGGTGAA CC CGTCTCTA
                                    ||||||||||||  ||  ||||||||
                                    GTTGTACCACTT GG GCAGAGAT
                                          C  A
GAM1684  SCYA22    3'  TAGAGACGGGGTTTTGCCATGT 92611         TG
             TA                     TAACATGG  AAACCCCGTCTCTA
                                    ||||||||  |||||||||||||||
                                    ATTGTACC  TTTGGGGCAGAGAT
                                       GT
GAM1684  SERF1B    3'  TAGAGATGGGGTTTCACCATGT 43703
             TG                     TAACATGGTGAAACCCCGTCTCTA
                                    ||||||||||||||||||||||||||
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                                GTTGTACCACTTTGGGGTAGAGAT

GAM1684  SFXN2    3'  TGGAGACGGGGTTTCACCATG  74386
                                CATGGTGAAACCCCGTCTCTA
                                |||||||||||||||||||||
                                GTACCACTTTGGGGCAGAGGT

GAM1684  SLC11A1  3'  AGAGACGGGGTTTGCCATG    60154       G
                                CATGGT AAACCCCGTCTCT
                                ||||||| ||||||||||||
                                GTACCG TTTGGGGCAGAGA
                                   _
GAM1684  SLC12A8  3'  TGGAGACAGGGTTTCACCATGT 45246              C
                TG                TAACATGGTGAAACCC GTCTCTA
                                  ||||||||||||||| |||||||
                                  GTTGTACCACTTTGGG CAGAGGT
                                        A
GAM1684  SLC16A4  3'  TAGAGGCGGGGTTTCACCATGT 17460
                TA                TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  ATTGTACCACTTTGGGGCGGAGAT

GAM1684  SREC     3'  TAGAGACAGGGTTTCACCATGT 14911              C
                TA                TAACATGGTGAAACCC GTCTCTA
                                  ||||||||||||||| |||||||
                                  ATTGTACCACTTTGGG CAGAGAT
                                        A
GAM1684  SS-56    3'  TAGAGACGGAGTTTCACCATGT 60360             C
                TA                TAACATGGTGAAAC CCGTCTCTA
                                  |||||||||||||| |||||||||
                                  ATTGTACCACTTTG GGCAGAGAT
                                       A
GAM1684  SULT1C2  3'  TAGAGACGAGGTTTCACCGTGT 22721              C
                TA                TAACATGGTGAAACC CGTCTCTA
                                  |||||||||||||| ||||||||
                                  ATTGTGCCACTTTGG GCAGAGAT
                                       A
GAM1684  SUN1     3'  TAGAGACAGGGTTTCACTGTGT 47924              C
                TG                TAACATGGTGAAACCC GTCTCTA
                                  ||||||||||||||| |||||||
                                  GTTGTGTCACTTTGGG CAGAGAT
                                        A
GAM1684  SYT13    3'  TAGAGATCTCTTCACCAT     95106         ACCCC
                                  ATGGTGAA     GTCTCTA
                                  ||||||||     |||||||
                                  TACCACTT     TAGAGAT
                                     CTC__
GAM1684  SYT13    3'  TAGAGATGGGGTTTCACCATGT 95107
                TG                TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
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                                GTTGTACCACTTTGGGGTAGAGAT

GAM1684  TADA3L   3'  TAGAGACGGGGTTTCACCGTGT 22046
              TA                 TAACATGGTGAAACCCCGTCTCTA
                                 ||||||||||||||||||||||||
                                 ATTGTGCCACTTTGGGGCAGAGAT

GAM1684  TBCC     3'  TAGAGACGGGGTTTCGCCATGT 13605
              TG                 TAACATGGTGAAACCCCGTCTCTA
                                 ||||||||||||||||||||||||
                                 GTTGTACCGCTTTGGGGCAGAGAT

GAM1684  TCL6     3'  TAGAGACAGGGTTTCACCGTGT 40491             C
              TA                 TAACATGGTGAAACCC GTCTCTA
                                 |||||||||||||||| |||||||
                                 ATTGTGCCACTTTGGG CAGAGAT
                                           A
GAM1684  TCL6     5'  TAGAGACGAGGTTTCACCATGT 40492             C
              TG                 TAACATGGTGAAACC CGTCTCTA
                                 |||||||||||||| ||||||||
                                 GTTGTACCACTTTGG GCAGAGAT
                                           A
GAM1684  TERA     3'  TAGAGACGGGGTTTCACCACGT 41423      A
              TG                 TAAC TGGTGAAACCCCGTCTCTA
                                 |||| ||||||||||||||||||
                                 GTTG ACCACTTTGGGGCAGAGAT
                                   C
GAM1684  TGIF2    3'  TAGAGACGGGGTTTCACCATCT 41759     C
              TG                 TAA ATGGTGAAACCCCGTCTCTA
                                 ||| ||||||||||||||||||||
                                 GTT TACCACTTTGGGGCAGAGAT
                                   C
GAM1684  TLK1     3'  AGAAACAGGAATACCATGTTA  25432          AAAC  C  C
                                 TAACATGGTG    CC GT TCT
                                 ||||||||||    || || |||
                                 ATTGTACCAT    GG CA AGA
                                       AA__  A  A
GAM1684  TRIM16   3'  TAGAGATGGGGTTTCACCATGT 22377
              TG                 TAACATGGTGAAACCCCGTCTCTA
                                 ||||||||||||||||||||||||
                                 GTTGTACCACTTTGGGGTAGAGAT

GAM1684  TRIM5    3'  TAGAGACGGGGTTTCCCCATGT 53476         T
              TG                 TAACATGG GAAACCCCGTCTCTA
                                 ||||||||| ||||||||||||||
                                 GTTGTACC CTTTGGGGCAGAGAT
                                      C
GAM1684  TRIM5    3'  TAGAGACGGGGTTTCCCCATGT 53477         T
              TG                 TAACATGG GAAACCCCGTCTCTA
                                 ||||||||| ||||||||||||||
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                                GTTGTACC CTTTGGGGCAGAGAT
                                    C
GAM1684  TU12B1-TY 3'  TAGAGACGGGGTTTCACCATGT 33860
            TG                   TAACATGGTGAAACCCCGTCTCTA
                                 ||||||||||||||||||||||||
                                 GTTGTACCACTTTGGGGCAGAGAT

GAM1684  TU12B1-TY 3'  TAGAGATGGGGTTTCACCATGT 33861
            TG                   TAACATGGTGAAACCCCGTCTCTA
                                 ||||||||||||||||||||||||
                                 GTTGTACCACTTTGGGGTAGAGAT

GAM1684  TUCAN    3'  TAGAGACAGAGTTTTGCTATGT 30988        TG   CCC
            TG                   TAACATGG  AAAC   GTCTCTA
                                 ||||||||  ||||   |||||||
                                 GTTGTATC  TTTG   CAGAGAT
                                     GT    AGA
GAM1684  TUCAN    3'  TAGAGACAGGGTTTCACCATTT 30989     C         C
            TG                   TAA ATGGTGAAACCC GTCTCTA
                                 ||| ||||||||||| |||||||
                                 GTT TACCACTTTGGG CAGAGAT
                                   T          A
GAM1684  UBCE7IP5  3'  TAGAGACAAGGTCTTGCTATGT 30851        TG A   CC
            TG                   TAACATGG  A ACC  GTCTCTA
                                 ||||||||  | |||  |||||||
                                 GTTGTATC  T TGG  CAGAGAT
                                     GT C   AA
GAM1684  VDU1     3'  TAGAGATGGGGTTTCACCATGT 31128
            TG                   TAACATGGTGAAACCCCGTCTCTA
                                 ||||||||||||||||||||||||
                                 GTTGTACCACTTTGGGGTAGAGAT

GAM1684  WBSCR23   3'  TAGAGACGGGGTTTCACCATGT 47441
            TG                   TAACATGGTGAAACCCCGTCTCTA
                                 ||||||||||||||||||||||||
                                 GTTGTACCACTTTGGGGCAGAGAT

GAM1684  ZNF221    3'  ACGGGGTTTCACCGTGTTA    26264
                                 TAACATGGTGAAACCCCGT
                                 ||||||||||||||||||
                                 ATTGTGCCACTTTGGGGCA

GAM1684  ZTL1     3'  TAGAGACGGGGCTTCATTCACC 43521        A____
            A                    TGGTGAA    CCCCGTCTCTA
                                 |||||||    ||||||||||
                                 ACCACTT    GGGGCAGAGAT
                                     ACTTC
GAM1684  LOC113523 5'  AGAGACAGGGTTTCACCATGTT 73411              C
            A                    TAACATGGTGAAACCC GTCTCT
                                 |||||||||||||||| ||||||
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                                ATTGTACCACTTTGGG CAGAGA
                                      A
GAM1684  LOC115219 5'  TAGAGACGGGGTTTCATCATGT 73707
              TG                  TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTACTACTTTGGGGCAGAGAT

GAM1684  LOC115509 3'  AGACAGGGTTTCAATTTCCA   73843     ____      C
                                  TGG    TGAAACCC GTCT
                                  |||    |||||||| ||||
                                  ACC    ACTTTGGG CAGA
                                    TTTA       A
GAM1684  LOC115648 3'  TGGAGACGGGGTTTCACCATGT 60033
              TG                  TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTACCACTTTGGGGCAGAGGT

GAM1684  LOC119392 3'  TAGAGACTGGGTTTCACCACGT 59817      A         C
              TG                  TAAC TGGTGAAACCC GTCTCTA
                                  |||| |||||||||| |||||||
                                  GTTG ACCACTTTGGG CAGAGAT
                                    C         T
GAM1684  LOC120114 3'  TAGAGATGGGGTTTCACCATGT 76051
              TG                  TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTACCACTTTGGGGTAGAGAT

GAM1684  LOC120224 5'  TAGAGACAGGGTTTCACCATGT 57894             C
              T                    AACATGGTGAAACCC GTCTCTA
                                  ||||||||||||||| |||||||
                                  TTGTACCACTTTGGG CAGAGAT
                                        A
GAM1684  LOC121504 3'  TAGATACGGGGTTTCACCATGT 74553               C
              TG                  TAACATGGTGAAACCCCGT TCTA
                                  |||||||||||||||||| ||||
                                  GTTGTACCACTTTGGGGCA AGAT
                                       T
GAM1684  LOC121551 3'  AGTTGGAGGACTTCACCGT    74557        A_ _   T
                                  ATGGTGAA  CC CCG CT
                                  ||||||||  || ||| ||
                                  TGCCACTT  GG GGT GA
                                     CA  A   T
GAM1684  LOC126661 3'  TAGAGACAGGTTTTCACCATGT 75064           C  C
              TG                  TAACATGGTGAAA CC GTCTCTA
                                  ||||||||||||| || |||||||
                                  GTTGTACCACTTT GG CAGAGAT
                                        T  A
GAM1684  LOC126661 3'  TAGAGATGGGGTTTCACCATGT 75065
              TG                  TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
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                                GTTGTACCACTTTGGGGTAGAGAT

GAM1684  LOC128077 3'  TAGAGACAGGGTTTCACCATGT 75231              C
                  TG                TAACATGGTGAAACCC GTCTCTA
                                    ||||||||||||||| |||||||
                                    GTTGTACCACTTTGGG CAGAGAT
                                          A
GAM1684  LOC128077 3'  TAGAGACGGGGTTTCACCATGT 75232
                  TA                TAACATGGTGAAACCCCGTCTCTA
                                    ||||||||||||||||||||||||
                                    ATTGTACCACTTTGGGGCAGAGAT

GAM1684  LOC128989 3'  TAGAGACGGGGTTTCACCATGT 75325
                  TG                TAACATGGTGAAACCCCGTCTCTA
                                    ||||||||||||||||||||||||
                                    GTTGTACCACTTTGGGGCAGAGAT

GAM1684  LOC132625 3'  TAGAGATGGGGTTTCACCATGT 76444
                  TG                TAACATGGTGAAACCCCGTCTCTA
                                    ||||||||||||||||||||||||
                                    GTTGTACCACTTTGGGGTAGAGAT

GAM1684  LOC135154 3'  AGACAAGGTTTCACCATGTTA  75720            CC
                                    TAACATGGTGAAACC  GTCT
                                    |||||||||||||||  ||||
                                    ATTGTACCACTTTGG  CAGA
                                          AA
GAM1684  LOC135293 3'  TAGAGACGGCATTTCACCATGT 76691            CC
                  TG                TAACATGGTGAAA  CCGTCTCTA
                                    ||||||||||||||  |||||||||
                                    GTTGTACCACTTT  GGCAGAGAT
                                          AC
GAM1684  LOC143187 3'  TAGAGATGGAGTTTCACCATGT 59764              C
                  TG                TAACATGGTGAAAC CCGTCTCTA
                                    |||||||||||||| |||||||||
                                    GTTGTACCACTTTG GGTAGAGAT
                                          A
GAM1684  LOC144519 5'  TAGAGACGGGGTTTTGCCATGT 77379          TG
                  TG                TAACATGG  AAACCCCGTCTCTA
                                    ||||||||  ||||||||||||||
                                    GTTGTACC  TTTGGGGCAGAGAT
                                        GT
GAM1684  LOC144524 5'  TAGAAACCGGGTTTCACCGTGT 84064              C  C
                  TA                TAACATGGTGAAACCC GT TCTA
                                    |||||||||||||||| || ||||
                                    ATTGTGCCACTTTGGG CA AGAT
                                          C  A
GAM1684  LOC144742 5'  TAGAGACAGGTTTTCACCATGT 77467              C  C
                  TG                TAACATGGTGAAA CC GTCTCTA
                                    |||||||||||||| || |||||||
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                                GTTGTACCACTTT GG CAGAGAT
                                      T  A
GAM1684  LOC145009 3'  TAGAGACAGGGTTTCACT    60981          C
                                GGTGAAACCC GTCTCTA
                                |||||||||| |||||||
                                TCACTTTGGG CAGAGAT
                                     A
GAM1684  LOC145082 5'  TAGAGACGAGGTTTTGCCATGT 84194        TG    C
           TG                    TAACATGG  AAACC CGTCTCTA
                                |||||||| ||||| ||||||||
                                GTTGTACC  TTTGG GCAGAGAT
                                   GT    A
GAM1684  LOC145268 5'  TAGAGACAGAGTTTCACCATGT 77586            CCC
           TG                    TAACATGGTGAAAC   GTCTCTA
                                |||||||||||||   |||||||
                                GTTGTACCACTTTG   CAGAGAT
                                      AGA
GAM1684  LOC145622 3'  TAGAGAGGGGGTTTCACCACGT 77825      A         G
           TG                    TAAC TGGTGAAACCCC TCTCTA
                                |||| ||||||||||| ||||||
                                GTTG ACCACTTTGGGG AGAGAT
                                  C          G
GAM1684  LOC146050 3'  TAGAGATGGGGTTTCACCATGT 78125
           TG                    TAACATGGTGAAACCCCGTCTCTA
                                |||||||||||||||||||||||
                                GTTGTACCACTTTGGGGTAGAGAT

GAM1684  LOC146229 3'  TAGACACAGGGTTTCACCAT   78309          C  C
                                ATGGTGAAACCC GT TCTA
                                |||||||||||| || ||||
                                TACCACTTTGGG CA AGAT
                                      A  C
GAM1684  LOC146229 3'  TAGAGACGGGGTTTCACCATGT 78310
           TG                    TAACATGGTGAAACCCCGTCTCTA
                                |||||||||||||||||||||||
                                GTTGTACCACTTTGGGGCAGAGAT

GAM1684  LOC146229 3'  TAGAGACGGGGTTTTACCGTGT 78311
           TA                    TAACATGGTGAAACCCCGTCTCTA
                                |||||||||||||||||||||||
                                ATTGTGCCATTTTGGGGCAGAGAT

GAM1684  LOC146229 3'  TAGTGACGGGGTTTCACCATGT 78312              T
           TG                    TAACATGGTGAAACCCCGTC CTA
                                |||||||||||||||||| |||
                                GTTGTACCACTTTGGGGCAG GAT
                                     T
GAM1684  LOC146346 5'  TAGAGACAGGATTTCATCATGT 78409          C  C
           TG                    TAACATGGTGAAA CC GTCTCTA
                                |||||||||||| || |||||||
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                                GTTGTACTACTTT GG CAGAGAT
                                      A  A
GAM1684  LOC146346 5'  TAGAGACGGGGTTTCACCGTGT 78410
                  TG                   TAACATGGTGAAACCCCGTCTCTA
                                       ||||||||||||||||||||||||
                                       GTTGTGCCACTTTGGGGCAGAGAT

GAM1684  LOC146429 5'  AGACAGGGTTTCACCATG    84656           C
                                       CATGGTGAAACCC GTCT
                                       |||||||||||| ||||
                                       GTACCACTTTGGG CAGA
                                             A
GAM1684  LOC146603 5'  TAGAGACGGGGTTTCACCGTGT 78606
                  TA                   TAACATGGTGAAACCCCGTCTCTA
                                       ||||||||||||||||||||||||
                                       ATTGTGCCACTTTGGGGCAGAGAT

GAM1684  LOC146784 5'  TAGAGATGGGGTTTCACCATGT 78718
                  TG                   TAACATGGTGAAACCCCGTCTCTA
                                       ||||||||||||||||||||||||
                                       GTTGTACCACTTTGGGGTAGAGAT

GAM1684  LOC146839 3'  TAGAGACGGGGTTTCACCGTGT 84852
                  TA                   TAACATGGTGAAACCCCGTCTCTA
                                       ||||||||||||||||||||||||
                                       ATTGTGCCACTTTGGGGCAGAGAT

GAM1684  LOC146894 3'  TAGAGATGGGGTTTCACCATGT 59864
                  TG                   TAACATGGTGAAACCCCGTCTCTA
                                       ||||||||||||||||||||||||
                                       GTTGTACCACTTTGGGGTAGAGAT

GAM1684  LOC146901 3'  AGAGACGGGGTTTCACCATGTT 84887
                  G                    TAACATGGTGAAACCCCGTCTCT
                                       |||||||||||||||||||||||
                                       GTTGTACCACTTTGGGGCAGAGA

GAM1684  LOC146909 3'  TAGAGATGGGGTTTCACCGTGT 78783
                  TA                   TAACATGGTGAAACCCCGTCTCTA
                                       ||||||||||||||||||||||||
                                       ATTGTGCCACTTTGGGGTAGAGAT

GAM1684  LOC146952 5'  TAGAGACAGGGTTTCACCA    84935           C
                                       TGGTGAAACCC GTCTCTA
                                       |||||||||| |||||||
                                       ACCACTTTGGG CAGAGAT
                                             A
GAM1684  LOC147071 5'  TAGAGACGGAGTTTCACCATGT 73371             C
                  TG                   TAACATGGTGAAAC CCGTCTCTA
                                       |||||||||||||| |||||||||
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                                GTTGTACCACTTTG GGCAGAGAT
                                      A
GAM1684  LOC147080 5'  TAGAGACAAGGTTTCACCATGT 85051              CC
              TA                  TAACATGGTGAAACC  GTCTCTA
                                  ||||||||||||||  |||||||
                                  ATTGTACCACTTTGG  CAGAGAT
                                        AA
GAM1684  LOC147166 3'  TAGAGATGGGGTTTCACCATGT 78894
              TG                  TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTACCACTTTGGGGTAGAGAT

GAM1684  LOC147276 3'  TAGAGACGGGGCTTCTCCATGT 78969        T   A
              TG                  TAACATGG GAA CCCCGTCTCTA
                                  ||||||||| ||| ||||||||||
                                  GTTGTACC CTT GGGGCAGAGAT
                                       T   C
GAM1684  LOC147429 3'  TAGAGATGGGGTTTCACCATGT 79001
              TA                  TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  ATTGTACCACTTTGGGGTAGAGAT

GAM1684  LOC147694 3'  TAGAGACGGGGTTTCACCGTGT 79108
              TA                  TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  ATTGTGCCACTTTGGGGCAGAGAT

GAM1684  LOC147817 3'  TAGAGACAGGGCTTCACCATGT 79191           A   C
              TG                  TAACATGGTGAA CCC GTCTCTA
                                  ||||||||||||| ||| |||||||
                                  GTTGTACCACTT GGG CAGAGAT
                                        C   A
GAM1684  LOC147817 3'  TAGAGACGGAGTTTCACCAT   79192          C
                                  ATGGTGAAAC CCGTCTCTA
                                  |||||||||| |||||||||
                                  TACCACTTTG GGCAGAGAT
                                       A
GAM1684  LOC147990 3'  TAGAGACGGGGTTTCAGCAT   85234     G
                                  ATG TGAAACCCCGTCTCTA
                                  ||| ||||||||||||||||
                                  TAC ACTTTGGGGCAGAGAT
                                    G
GAM1684  LOC148189 5'  TAGAGACGGGGTTTCACCATGT 79454
              TG                  TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTACCACTTTGGGGCAGAGAT

GAM1684  LOC148195 3'  TAGAGACAGGTTTCACCA    85290          CC
                                  TGGTGAAACC  GTCTCTA
                                  |||||||||  |||||||
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                                ACCACTTTGG  CAGAGAT
                                    A_
GAM1684  LOC148443 3'  AGACACAGGGTCTCACCATGTT 79597          A    C  C
              G                  TAACATGGTGA ACCC GT TCT
                                 |||||||||||  |||| || |||
                                 GTTGTACCACT TGGG CA AGA
                                     C    A  C
GAM1684  LOC148709 3'  TAGAGACAGGGTTTCTCCATGT 79700         T      C
              TG                   TAACATGG GAAACCC GTCTCTA
                                   ||||||||  |||||||  |||||||
                                   GTTGTACC CTTTGGG CAGAGAT
                                       T      A
GAM1684  LOC148887 5'  TAGAGACAGGGTTTCACCATGT 85412              C
              TG                   TAACATGGTGAAACCC GTCTCTA
                                   ||||||||||||||||  |||||||
                                   GTTGTACCACTTTGGG CAGAGAT
                                          A
GAM1684  LOC149421 3'  TAGAGACGGGGTTTCACCG    80151
                                   TGGTGAAACCCCGTCTCTA
                                   ||||||||||||||||||
                                   GCCACTTTGGGGCAGAGAT

GAM1684  LOC149478 3'  TAGAGACGGGGGTTTCACCATG 80177                _
              TTG                   TAACATGGTGAAACCCC GTCTCTA
                                    ||||||||||||||||  |||||||
                                    GTTGTACCACTTTGGGG CAGAGAT
                                          G
GAM1684  LOC149506 3'  TAGAGACGAGGGTTCACCACGT 85647      A      A  _
              TG                    TAAC TGGTGAA CCC CGTCTCTA
                                    ||||  |||||||  |||  ||||||||
                                    GTTG ACCACTT GGG GCAGAGAT
                                      C      _  A
GAM1684  LOC149692 3'  TAGAGACAGGGTTTCACCATGT 85744              C
              TG                    TAACATGGTGAAACCC GTCTCTA
                                    ||||||||||||||||  |||||||
                                    GTTGTACCACTTTGGG CAGAGAT
                                          A
GAM1684  LOC149692 3'  TAGAGACGAGTTTTCACCATGT 85745           CCC
              TG                    TAACATGGTGAAA   CGTCTCTA
                                    ||||||||||||   ||||||||
                                    GTTGTACCACTTT   GCAGAGAT
                                        TGA
GAM1684  LOC149703 5'  TAGAGACGGGGGTTTTGCCATGT 85824        TG
              TG                    TAACATGG  AAACCCCGTCTCTA
                                    ||||||||  ||||||||||||||
                                    GTTGTACC  TTTGGGGCAGAGAT
                                       GT
GAM1684  LOC149821 5'  AGACGGAGTTTCACCGTGTTA  85928             C
                                    TAACATGGTGAAAC CCGTCT
                                    ||||||||||||| ||||||
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                                ATTGTGCCACTTTG GGCAGA
                                      A
GAM1684  LOC150166 5'  TAGAAATGGGGTTTCACCATGT 86044                C
              TG                  TAACATGGTGAAACCCCGT TCTA
                                  |||||||||||||||||| ||||
                                  GTTGTACCACTTTGGGGTA AGAT
                                       A
GAM1684  LOC150282 5'  TAGAGATGGCGTTTCACCATGT 80545             C
              TG                  TAACATGGTGAAAC CCGTCTCTA
                                  |||||||||||||| |||||||||
                                  GTTGTACCACTTTG GGTAGAGAT
                                      C
GAM1684  LOC150696 3'  TAGAGACGGGGTTTTGCCATGT 59167         TG
              TG                  TAACATGG  AAACCCCGTCTCTA
                                  ||||||||  ||||||||||||||
                                  GTTGTACC  TTTGGGGCAGAGAT
                                     GT
GAM1684  LOC151050 5'  TAGAGACAGAGTTTCACCATGT 80921             CCC
              TG                  TAACATGGTGAAAC   GTCTCTA
                                  ||||||||||||||   |||||||
                                  GTTGTACCACTTTG   CAGAGAT
                                      AGA
GAM1684  LOC151057 3'  TAGAGACGGGGTTTCACCATGT 86398
              TG                  TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTACCACTTTGGGGCAGAGAT

GAM1684  LOC151201 3'  TAGAGACGAGGTTTCAGTTTGT 86486       TGG       C
              TG                  TAACA   TGAAACC CGTCTCTA
                                  |||||   ||||||| ||||||||
                                  GTTGT   ACTTTGG GCAGAGAT
                                    TTG      A
GAM1684  LOC151201 3'  TAGAGACGGGGTTTCACCATGT 86487
              TG                  TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTACCACTTTGGGGCAGAGAT

GAM1684  LOC151475 5'  TAGAGACGAGGTTTCACCATGT 86604             C
              TG                  TAACATGGTGAAACC CGTCTCTA
                                  |||||||||||||| ||||||||
                                  GTTGTACCACTTTGG GCAGAGAT
                                       A
GAM1684  LOC151701 3'  TAGAGACGGGGTTTCACCATGT 86680
              TG                  TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTACCACTTTGGGGCAGAGAT

GAM1684  LOC151826 3'  TAGAGACAGGGTTTCACCGTGT 81187             C
              TG                  TAACATGGTGAAACCC GTCTCTA
                                  ||||||||||||||| |||||||
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                                GTTGTGCCACTTTGGG CAGAGAT
                                      A
GAM1684  LOC151979 5'  TAGAGACGGGGTTTCACCATGT 81255
              TA                 TAACATGGTGAAACCCCGTCTCTA
                                 ||||||||||||||||||||||||
                                 ATTGTACCACTTTGGGGCAGAGAT

GAM1684  LOC152137 3'  AGAGCGGGTTTCACCATGTTG  81307            C T
                                 TAACATGGTGAAACCC G CTCT
                                 ||||||||||||||||| | ||||
                                 GTTGTACCACTTTGGG C GAGA
                                       _ _
GAM1684  LOC152300 3'  TAGAGACAGGGTTTCACCAT   81391          C
                                 ATGGTGAAACCC GTCTCTA
                                 |||||||||||| |||||||
                                 TACCACTTTGGG CAGAGAT
                                       A
GAM1684  LOC152343 3'  TAGCGACTGGGTTTCACCATGT 81434            C   T
              TG                 TAACATGGTGAAACCC GTC CTA
                                 |||||||||||||||| ||| |||
                                 GTTGTACCACTTTGGG CAG GAT
                                       T   C
GAM1684  LOC152445 3'  TAGAGACAGGGTTTCACCATGT 86963            C
              TA                 TAACATGGTGAAACCC GTCTCTA
                                 |||||||||||||||| |||||||
                                 ATTGTACCACTTTGGG CAGAGAT
                                       A
GAM1684  LOC152719 5'  GAGACGGGGTTTCACCATGTTG 87030
                                 TAACATGGTGAAACCCCGTCTC
                                 ||||||||||||||||||||||
                                 GTTGTACCACTTTGGGGCAGAG

GAM1684  LOC152719 5'  TAGTGACGGGTTTCACCATGTT 87042            C   T
              A                  TAACATGGTGAAACCC GTC CTA
                                 |||||||||||||||| ||| |||
                                 ATTGTACCACTTTGGG CAG GAT
                                       _   T
GAM1684  LOC152851 3'  TAGAGACAGGATTTCACTATGT 81595          C  C
              TG                 TAACATGGTGAAA CC GTCTCTA
                                 |||||||||||| || |||||||
                                 GTTGTATCACTTT GG CAGAGAT
                                       A  A
GAM1684  LOC153077 3'  TAGAGATGGGGCTTCACCATGT 87129          A
              TG                 TAACATGGTGAA CCCCGTCTCTA
                                 |||||||||||| ||||||||||
                                 GTTGTACCACTT GGGGTAGAGAT
                                       C
GAM1684  LOC153606 5'  TAGAGATAGGGTTTCACCATGT 87261            CG
              TG                 TAACATGGTGAAACCC  TCTCTA
                                 ||||||||||||||||  ||||||
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                                GTTGTACCACTTTGGG  AGAGAT
                                      AT
GAM1684  LOC153688 3'  TAGAGACAGGATTTCATCGTGT 87331           C  C
              TG                 TAACATGGTGAAA CC GTCTCTA
                                 |||||||||||||| || |||||||
                                 GTTGTGCTACTTT GG CAGAGAT
                                       A  A
GAM1684  LOC153688 3'  TAGAGACAGGGTTTCACCATGT 87332             C
              TG                 TAACATGGTGAAACCC GTCTCTA
                                 |||||||||||||||| |||||||
                                 GTTGTACCACTTTGGG CAGAGAT
                                       A
GAM1684  LOC153811 3'  TAGAAACGAGGTTTCACCACGT 81850      A        C   C
              TG                 TAAC TGGTGAAACC CGT TCTA
                                 |||| |||||||||| ||| ||||
                                 GTTG ACCACTTTGG GCA AGAT
                                   C         A   A
GAM1684  LOC153811 3'  TAGAGACAGAGCTTCTCCATGT 81851         T   ACCCC
              TG                 TAACATGG GAA     GTCTCTA
                                 |||||||| |||     |||||||
                                 GTTGTACC CTT     CAGAGAT
                                     T   CGAGA
GAM1684  LOC153910 5'  TAGAGACAGGGTTTTGCCATGT 81911         TG     C
              TG                 TAACATGG  AAACCC GTCTCTA
                                 ||||||||  |||||| |||||||
                                 GTTGTACC  TTTGGG CAGAGAT
                                     GT     A
GAM1684  LOC154007 3'  TAGAGACAGGATCTCACTATGT 81929          AAC  C
              T                   AACATGGTGA   CC GTCTCTA
                                 ||||||||||   || |||||||
                                 TTGTATCACT   GG CAGAGAT
                                      CTA  A
GAM1684  LOC154282 5'  TAGAGATGGTGTTTCACCATGT 87413            C
              TG                 TAACATGGTGAAAC CCGTCTCTA
                                 |||||||||||||| |||||||||
                                 GTTGTACCACTTTG GGTAGAGAT
                                       T
GAM1684  LOC154877 3'  TAGAGACAGGATCTCACTATGT 87573          AAC  C
              TG                 TAACATGGTGA   CC GTCTCTA
                                 ||||||||||   || |||||||
                                 GTTGTATCACT   GG CAGAGAT
                                      CTA  A
GAM1684  LOC154877 3'  TAGAGTCGGGGTTTCACCATGT 87574              T
              TG                 TAACATGGTGAAACCCCG CTCTA
                                 |||||||||||||||| |||||
                                 GTTGTACCACTTTGGGGC GAGAT
                                       T
GAM1684  LOC154877 3'  TGGAGACAGGGTCTCACCATGT 87583          A    C
              TG                 TAACATGGTGA ACCC GTCTCTA
                                 |||||||||| |||| |||||||
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                                GTTGTACCACT TGGG CAGAGGT
                                      C    A
GAM1684  LOC154930 3'  TAGAGACAGGATTTTACTGTGT 82097            C  C
                TG                    TAACATGGTGAAA CC GTCTCTA
                                      ||||||||||||| || |||||||
                                      GTTGTGTCATTTT GG CAGAGAT
                                        A  A
GAM1684  LOC155372 3'  TAGAGACGGAATTTCACCATG  82261          CC
                                      CATGGTGAAA  CCGTCTCTA
                                      ||||||||||  |||||||||
                                      GTACCACTTT  GGCAGAGAT
                                         AA
GAM1684  LOC157247 5'  TAGAGACGGGGTTTCACCAGTG 82307      _
                TT                    AACA TGGTGAAACCCCGTCTCTA
                                      |||| ||||||||||||||||||
                                      TTGT ACCACTTTGGGGCAGAGAT
                                        G
GAM1684  LOC157506 3'  TAGAGACGGGGTTTCACCATGT 82373
                TG                    TAACATGGTGAAACCCCGTCTCTA
                                      ||||||||||||||||||||||||
                                      GTTGTACCACTTTGGGGCAGAGAT

GAM1684  LOC157556 5'  AGAGACGGGGACATGT      87778       GTGAAA
                                      ACATG     CCCCGTCTCT
                                      |||||     ||||||||||
                                      TGTAC     GGGGCAGAGA
                                        A_____
GAM1684  LOC157623 3'  AGAGATGGAGTTTCACCAT    82407          C
                                      ATGGTGAAAC CCGTCTCT
                                      |||||||||| ||||||||
                                      TACCACTTTG GGTAGAGA
                                         A
GAM1684  LOC157798 5'  TAGAGACGGGGTTTCACCTTGT 87864       T
                TG                    TAACA GGTGAAACCCCGTCTCTA
                                      ||||| ||||||||||||||||||
                                      GTTGT CCACTTTGGGGCAGAGAT
                                        T
GAM1684  LOC157858 5'  TAGAGACAGGGTTTCACTATGT 87896            C
                                      ACATGGTGAAACCC GTCTCTA
                                      |||||||||||||| |||||||
                                      TGTATCACTTTGGG CAGAGAT
                                           A
GAM1684  LOC158014 5'  TAGAGACGGAGTTTCACCATGT 82568            C
                TA                    TAACATGGTGAAAC CCGTCTCTA
                                      |||||||||||||| |||||||||
                                      ATTGTACCACTTTG GGCAGAGAT
                                           A
GAM1684  LOC158310 5'  TAGAGACAGGGTTTCACAATGT 88090       G       C
                TG                    TAACAT GTGAAACCC GTCTCTA
                                      |||||| ||||||||| |||||||
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                                GTTGTA CACTTTGGG CAGAGAT
                                   A        A
GAM1684  LOC158476 3'  TAGAGACAGGGTTTCACCAT   88204           C
                                ATGGTGAAACCC GTCTCTA
                                |||||||||||| |||||||
                                TACCACTTTGGG CAGAGAT
                                      A
GAM1684  LOC158476 3'  TAGAGACAGGGTTTCACCATGT 88205              C
                TG                TAACATGGTGAAACCC GTCTCTA
                                |||||||||||||||| |||||||
                                GTTGTACCACTTTGGG CAGAGAT
                                      A
GAM1684  LOC158629 5'  AGACAGGGTTTTGCTATGTTA  88238        TG     C
                                TAACATGG  AAACCC GTCT
                                ||||||||  |||||| ||||
                                ATTGTATC  TTTGGG CAGA
                                   GT     A
GAM1684  LOC158668 3'  TAGAGGTGGGGTTTCACCATG  69907             GT
                                CATGGTGAAACCCC  CTCTA
                                ||||||||||||||  |||||
                                GTACCACTTTGGGG  GAGAT
                                      TG
GAM1684  LOC160646 3'  TAGAGATGGGGCTTCACCATGT 83121            A
                TG                TAACATGGTGAA CCCCGTCTCTA
                                |||||||||||| ||||||||||
                                GTTGTACCACTT GGGGTAGAGAT
                                      C
GAM1684  LOC161829 3'  TAGAGATGGGGTTTCACCATGT 83195
                TG                TAACATGGTGAAACCCCGTCTCTA
                                ||||||||||||||||||||||||
                                GTTGTACCACTTTGGGGTAGAGAT

GAM1684  LOC162427 3'  TAGAAATGGGGTTTCACCATGT 83230               C
                TG                TAACATGGTGAAACCCCGT TCTA
                                |||||||||||||||||| ||||
                                GTTGTACCACTTTGGGGTA AGAT
                                      A
GAM1684  LOC169611 3'  TAGAGACAGGATTTCACCATGT 83660           C  C
                TG                TAACATGGTGAAA CC GTCTCTA
                                |||||||||||| || |||||||
                                GTTGTACCACTTT GG CAGAGAT
                                      A  A
GAM1684  LOC169611 3'  TAGAGACAGGGGTTTCACCACG 83661      A         _
                TTG                TAAC TGGTGAAACCCC GTCTCTA
                                |||| |||||||||||| |||||||
                                GTTG ACCACTTTGGGG CAGAGAT
                                  C          A
GAM1684  LOC170082 5'  TAGAGATGGGGTTTCACCATGT 83449
                TA                TAACATGGTGAAACCCCGTCTCTA
                                |||||||||||||||||||||||||
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                                ATTGTACCACTTTGGGGTAGAGAT

GAM1684  LOC196047 5'  TAGAGCCAGGGTTTCACCATGT 91165            CGT
                                ACATGGTGAAACCC   CTCTA
                                ||||||||||||||   |||||
                                TGTACCACTTTGGG   GAGAT
                                      ACC
GAM1684  LOC196264 3'  TAGAGACGGGGTTTCACCATTT 88994     C
            TG                    TAA ATGGTGAAACCCCGTCTCTA
                                ||| ||||||||||||||||||||
                                GTT TACCACTTTGGGGCAGAGAT
                                  T
GAM1684  LOC197358 3'  TAGAGACGGGGTTTCATCATGT 89444
            TG                    TAACATGGTGAAACCCCGTCTCTA
                                ||||||||||||||||||||||||
                                GTTGTACTACTTTGGGGCAGAGAT

GAM1684  LOC197358 3'  TAGAGATGGGGTTTCACCATGT 89445
            TG                    TAACATGGTGAAACCCCGTCTCTA
                                ||||||||||||||||||||||||
                                GTTGTACCACTTTGGGGTAGAGAT

GAM1684  LOC199699 3'  AGACAGGGTTTCACCGTGTTA  89666              C
                                TAACATGGTGAAACCC GTCT
                                |||||||||||||||| ||||
                                ATTGTGCCACTTTGGG CAGA
                                      A
GAM1684  LOC199699 3'  TAGAGACAGAGTTTCACCAT   89684          CCC
                                ATGGTGAAAC   GTCTCTA
                                |||||||||   |||||||
                                TACCACTTTG   CAGAGAT
                                    AGA
GAM1684  LOC199725 5'  TAGAGACGGGATTTCACCATGT 91426            C
            TG                    TAACATGGTGAAA CCCGTCTCTA
                                |||||||||||| ||||||||||
                                GTTGTACCACTTT GGGCAGAGAT
                                      A
GAM1684  LOC199786 3'  TAGAGACAAGGTCTCGCTATG  89764         A  CC
                                CATGGTGA ACC  GTCTCTA
                                |||||||| |||  |||||||
                                GTATCGCT TGG  CAGAGAT
                                    C   AA
GAM1684  LOC199786 3'  TAGAGACGGTGGTTTCACCATG 89765                _
            TTG                    TAACATGGTGAAACC CCGTCTCTA
                                |||||||||||||| |||||||||
                                GTTGTACCACTTTGG GGCAGAGAT
                                      T
GAM1684  LOC199786 3'  TAGAGATGGGGTTTCACCATGT 89766
            TG                    TAACATGGTGAAACCCCGTCTCTA
                                ||||||||||||||||||||||||
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                                GTTGTACCACTTTGGGGTAGAGAT

GAM1684  LOC199906 3'  AGACAGGGTTTCATCATGTTG  89844              C
                                TAACATGGTGAAACCC GTCT
                                ||||||||||||||| ||||
                                GTTGTACTACTTTGGG CAGA
                                   A
GAM1684  LOC200014 3'  TAGAGACGGTGTTTCACCATGT 89946              C
              TG                  TAACATGGTGAAAC CCGTCTCTA
                                ||||||||||||| |||||||||
                                GTTGTACCACTTTG GGCAGAGAT
                                   T
GAM1684  LOC200169 5'  TAGAGACGGAGTTTCACCATGT 91561              C
              TG                  TAACATGGTGAAAC CCGTCTCTA
                                ||||||||||||| |||||||||
                                GTTGTACCACTTTG GGCAGAGAT
                                   A
GAM1684  LOC200301 5'  TAGAGACGGGGGTTTCACCGTGT 90152
              TA                  TAACATGGTGAAACCCCGTCTCTA
                                ||||||||||||||||||||||||
                                ATTGTGCCACTTTGGGGCAGAGAT

GAM1684  LOC200310 3'  TAGAGACGGGGGTTTCACCATGT 66334
              TG                  TAACATGGTGAAACCCCGTCTCTA
                                ||||||||||||||||||||||||
                                GTTGTACCACTTTGGGGCAGAGAT

GAM1684  LOC200314 3'  TAGAGATGGGGGTTTCACCACGT 91601      A
              TG                  TAAC TGGTGAAACCCCGTCTCTA
                                |||| ||||||||||||||||||
                                GTTG ACCACTTTGGGGTAGAGAT
                                  C
GAM1684  LOC200316 5'  TAGAGACGGGGGTTTCTCCATGT 90192         T
              TG                  TAACATGG GAAACCCCGTCTCTA
                                ||||||||| ||||||||||||||
                                GTTGTACC CTTTGGGGCAGAGAT
                                     T
GAM1684  LOC200316 3'  TAGTGACTGGGTTTCACCATGT 90193              C   T
              TG                  TAACATGGTGAAACCC GTC CTA
                                ||||||||||||||| ||| |||
                                GTTGTACCACTTTGGG CAG GAT
                                      T   T
GAM1684  LOC200407 3'  TAGAGACAGGGTTTTGCCATGT 91631         TG     C
              TG                  TAACATGG  AAACCC GTCTCTA
                                ||||||||  |||||| |||||||
                                GTTGTACC  TTTGGG CAGAGAT
                                     GT     A
GAM1684  LOC200860 3'  TAGAGACGGGGGTTTCTCCATGT 91758         T
              TA                  TAACATGG GAAACCCCGTCTCTA
                                ||||||||| ||||||||||||||
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                                ATTGTACC CTTTGGGGCAGAGAT
                                    T
GAM1684  LOC201164 3'  TAGAGACAGGGTTTCACCATGT 89502              C
                TG                TAACATGGTGAAACCC GTCTCTA
                                  |||||||||||||||| |||||||
                                  GTTGTACCACTTTGGG CAGAGAT
                                     A
GAM1684  LOC201173 5'  TAGAGACGGAGTTTCACCATGT 88692             C
                TG                TAACATGGTGAAAC CCGTCTCTA
                                  |||||||||||||| ||||||||
                                  GTTGTACCACTTTG GGCAGAGAT
                                     A
GAM1684  LOC201220 5'  TAGAGATGGAGTTTCACCATGT 88725             C
                TG                TAACATGGTGAAAC CCGTCTCTA
                                  |||||||||||||| ||||||||
                                  GTTGTACCACTTTG GGTAGAGAT
                                     A
GAM1684  LOC201294 3'  TAGAGACGGGGTTTCACCATGT 89596
                TG                TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTACCACTTTGGGGCAGAGAT

GAM1684  LOC201411 3'  TAGAGACAGGGTTTCACCATGT 63647              C
                TG                TAACATGGTGAAACCC GTCTCTA
                                  |||||||||||||||| |||||||
                                  GTTGTACCACTTTGGG CAGAGAT
                                     A
GAM1684  LOC201696 3'  TAGAGACGAGGTTTCTCCATGT 63829        T     C
                T                  AACATGG GAAACC CGTCTCTA
                                  ||||||| |||||| ||||||||
                                  TTGTACC CTTTGG GCAGAGAT
                                     T     A
GAM1684  LOC202460 5'  TAGAGATGGGGTTTCACCATGT 90677
                                  ACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||
                                  TGTACCACTTTGGGGTAGAGAT

GAM1684  LOC202934 3'  TAGAGACAGGGTTTCACCACGT 92052      A         C
                TG                TAAC TGGTGAAACCC GTCTCTA
                                  |||| |||||||||| |||||||
                                  GTTG ACCACTTTGGG CAGAGAT
                                    C         A
GAM1684  LOC203339 3'  TAGAGATGGGGTTTCACCATGT 92218
                T                  AACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  TTGTACCACTTTGGGGTAGAGAT

GAM1684  LOC203350 3'  TAGAGACGGGGTTTCACCGTGT 92249
                TG                TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
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                                GTTGTGCCACTTTGGGGCAGAGAT

GAM1684  LOC204804 3'  TAGAGACAGGGTCTCACTGTGT 91052         A    C
                                ACATGGTGA ACCC GTCTCTA
                                ||||||||| |||| |||||||
                                TGTGTCACT TGGG CAGAGAT
                                      C    A
GAM1684  LOC219445 5'  TAGAGACGGTGTTTCACCAT   93216          C
                                ATGGTGAAAC CCGTCTCTA
                                |||||||||| |||||||||
                                TACCACTTTG GGCAGAGAT
                                      T
GAM1684  LOC219445 5'  TAGGGACGGGGTTTCACCGTGT 93217
                   TA             TAACATGGTGAAACCCCGTCTCTA
                                ||||||||||||||||||||||||
                                ATTGTGCCACTTTGGGGCAGGGAT

GAM1684  LOC219673 3'  AGACAGGGTCTCACTATGTTG  94607          A    C
                                TAACATGGTGA ACCC GTCT
                                |||||||||| |||| ||||
                                GTTGTATCACT TGGG CAGA
                                      C    A
GAM1684  LOC219673 5'  TAGAAAAGGGGTTTCACCATGT 94633              GTC
                   TG             TAACATGGTGAAACCCC   TCTA
                                |||||||||||||||   ||||
                                GTTGTACCACTTTGGGG   AGAT
                                      AAA
GAM1684  LOC219731 5'  TAGAGACAGAGTTTCGTCATGT 94715        GT    CCC
                   TG             TAACATG  GAAAC   GTCTCTA
                                |||||||  |||||   |||||||
                                GTTGTAC  CTTTG   CAGAGAT
                                   TG    AGA
GAM1684  LOC219735 3'  TAGAGACGGGGTTTCACCGTGT 94735
                   TA             TAACATGGTGAAACCCCGTCTCTA
                                ||||||||||||||||||||||||
                                ATTGTGCCACTTTGGGGCAGAGAT

GAM1684  LOC219894 3'  TAGAGATGGGGTTTCACCGTGT 94909
                   TA             TAACATGGTGAAACCCCGTCTCTA
                                ||||||||||||||||||||||||
                                ATTGTGCCACTTTGGGGTAGAGAT

GAM1684  LOC220074 3'  TAGAGACAAGGTTTCGCCATGT 59995             CC
                   TG             TAACATGGTGAAACC  GTCTCTA
                                |||||||||||||||  |||||||
                                GTTGTACCGCTTTGG  CAGAGAT
                                      AA
GAM1684  LOC220074 3'  TAGAGACGGGGTTTCACCATGT 59996
                   TA             TAACATGGTGAAACCCCGTCTCTA
                                ||||||||||||||||||||||||
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                                ATTGTACCACTTTGGGGCAGAGAT

GAM1684  LOC221060 3'  AGACGGTGTTTCACCATGTTA  94827            C
                                TAACATGGTGAAAC CCGTCT
                                ||||||||||||| ||||||
                                ATTGTACCACTTTG GGCAGA
                                      T
GAM1684  LOC221271 3'  TAGAGAGGGGGTTTCATCATGT 93527              G
              TA                  TAACATGGTGAAACCCC TCTCTA
                                ||||||||||||||| ||||||
                                ATTGTACTACTTTGGGG AGAGAT
                                      G
GAM1684  LOC221296 3'  TAGAGACGGGGTTTCACCATG  93617
                                CATGGTGAAACCCCGTCTCTA
                                |||||||||||||||||||
                                GTACCACTTTGGGGCAGAGAT

GAM1684  LOC221663 5'  TAGAGACAAGGTTTCACTATGT 95469             CC
              TG                  TAACATGGTGAAACC  GTCTCTA
                                |||||||||||||  |||||||
                                GTTGTATCACTTTGG  CAGAGAT
                                      AA
GAM1684  LOC222031 3'  TAGAGACGAGGTTTCAACATGT 95685        G      C
              TG                  TAACATG TGAAACC CGTCTCTA
                                ||||||| ||||||| ||||||||
                                GTTGTAC ACTTTGG GCAGAGAT
                                    A      A
GAM1684  LOC222224 5'  TAGAGACAGGGTTTCACCATGT 95877              C
              TG                  TAACATGGTGAAACCC GTCTCTA
                                |||||||||||||||| |||||||
                                GTTGTACCACTTTGGG CAGAGAT
                                      A
GAM1684  LOC253612 5'  TAGAGACAGAGTTTTGCCATGT 98558         TG   CCC
              TG                  TAACATGG  AAAC   GTCTCTA
                                ||||||||  ||||  |||||||
                                GTTGTACC  TTTG   CAGAGAT
                                    GT    AGA
GAM1684  LOC253666 3'  TAGAGACGGGGTTTCACCATGT 96765
              T                   AACATGGTGAAACCCCGTCTCTA
                                |||||||||||||||||||||||
                                TTGTACCACTTTGGGGCAGAGAT

GAM1684  LOC253786 5'  AGATCTGGGCTTCACCAT    98827        A   C_
                                ATGGTGAA CCC  GTCT
                                |||||||| |||  ||||
                                TACCACTT GGG  TAGA
                                    C   TC
GAM1684  LOC253842 5'  TAGAAACATTGTTTCACCACGT 99243      A       CCC  C
              TA                  TAAC TGGTGAAAC   GT TCTA
                                |||| |||||||||   || ||||
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                                ATTG ACCACTTTG   CA AGAT
                                  C        TTA  A
GAM1684  LOC253943 3'  TGGTGGATTTCACCAGTTA    97850      A      _ _
                                TAAC TGGTGAAA CC CCG
                                |||| |||||||| || |||
                                ATTG ACCACTTT GG GGT
                                  _       A  T
GAM1684  LOC253981 3'  AGAGACGGGGTATCACTA     97528       A
                                TGGTGA ACCCCGTCTCT
                                |||||| ||||||||||
                                ATCACT TGGGGCAGAGA
                                   A
GAM1684  LOC254018 5'  TAGAGATGGGGTTTCGCCATGT 98742
                TA                TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  ATTGTACCGCTTTGGGGTAGAGAT

GAM1684  LOC254268 3'  TAGAGATGGGGTTTCACCATGT 97145
                TG                TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTACCACTTTGGGGTAGAGAT

GAM1684  LOC254295 5'  TAGAGACGGGGTTTCACCGTGT 97896
                TA                TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  ATTGTGCCACTTTGGGGCAGAGAT

GAM1684  LOC254532 5'  TAGAGACAGGGTTTCTCCATGT 98460         T      C
                TG                TAACATGG GAAACCC GTCTCTA
                                  |||||||| ||||||| |||||||
                                  GTTGTACC CTTTGGG CAGAGAT
                                     T      A
GAM1684  LOC254655 3'  TAGAGACGGGGTTTCACCATGT 97226
                TG                TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTACCACTTTGGGGCAGAGAT

GAM1684  LOC255308 3'  TAGAGACGGGGTTTCGGCATGT 96179        G
                TG                TAACATG TGAAACCCCGTCTCTA
                                  ||||||| ||||||||||||||||
                                  GTTGTAC GCTTTGGGGCAGAGAT
                                     G
GAM1684  LOC255465 3'  TAGAGACGGGTTTCACCATGTT 99127              C
                G                 TAACATGGTGAAACCC GTCTCTA
                                  |||||||||||||||| |||||||
                                  GTTGTACCACTTTGGG CAGAGAT
                                                 _
GAM1684  LOC255497 3'  TAGAGACGGGGTTTCACCATGT 98990
                TG                TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
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                                GTTGTACCACTTTGGGGCAGAGAT

GAM1684  LOC255927 5'  TAGAGACGGGGTTTCACCATCT 97713     C
                 TG                TAA ATGGTGAAACCCCGTCTCTA
                                   ||| ||||||||||||||||||||
                                   GTT TACCACTTTGGGGCAGAGAT
                                     C
GAM1684  LOC256221 3'  TAGAGACGGGGTTTCACCGTGT 96919
                 TA                TAACATGGTGAAACCCCGTCTCTA
                                   ||||||||||||||||||||||||
                                   ATTGTGCCACTTTGGGGCAGAGAT

GAM1684  LOC256306 3'  TAGAGACGGGGTTTCACCATGT 98520
                 TG                TAACATGGTGAAACCCCGTCTCTA
                                   ||||||||||||||||||||||||
                                   GTTGTACCACTTTGGGGCAGAGAT

GAM1684  LOC257465 3'  TAGAGATGGTGTTTCACCATGT 82500            C
                 TG                TAACATGGTGAAAC CCGTCTCTA
                                   |||||||||||||| |||||||||
                                   GTTGTACCACTTTG GGTAGAGAT
                                            T
GAM1684  LOC257486 3'  TAGAGACGGGGTTTCACCATGT 69782
                 TG                TAACATGGTGAAACCCCGTCTCTA
                                   ||||||||||||||||||||||||
                                   GTTGTACCACTTTGGGGCAGAGAT

GAM1684  LOC51159  5'  TAGAGACGGGATTTCACCATGT 33034           C
                 TG                TAACATGGTGAAA CCCGTCTCTA
                                   |||||||||||||| ||||||||||
                                   GTTGTACCACTTT GGGCAGAGAT
                                            A
GAM1684  LOC51200  3'  TAGAGACAGGGTTTCTCCATGT 33440        T      C
                 TG                TAACATGG GAAACCC GTCTCTA
                                   |||||||| ||||||| |||||||
                                   GTTGTACC CTTTGGG CAGAGAT
                                        T      A
GAM1684  LOC51696  3'  TAGAGACAGCGTTTCACCATGT 33091            CCC
                 TA                TAACATGGTGAAAC   GTCTCTA
                                   ||||||||||||||   |||||||
                                   ATTGTACCACTTTG   CAGAGAT
                                            CGA
GAM1684  LOC56181  5'  TAGAGACAGGGCTTCACTGTGT 97285          A   C
                 TA                TAACATGGTGAA CCC GTCTCTA
                                   |||||||||||| ||| |||||||
                                   ATTGTGTCACTT GGG CAGAGAT
                                            C   A
GAM1684  LOC57146  3'  AGATGGGGTTTCACCATGTTG  40289
                                   TAACATGGTGAAACCCCGTCT
                                   |||||||||||||||||||||
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                                GTTGTACCACTTTGGGGTAGA

GAM1684  LOC81034  3'  TAGAAATGGGGTTTCACCATGT 48596                C
              TA                  TAACATGGTGAAACCCCGT TCTA
                                  |||||||||||||||||| ||||
                                  ATTGTACCACTTTGGGGTA AGAT
                                            A
GAM1684  LOC89919  3'  TAGAGACGGGGTTTCACCATGT 61382
              TA                  TAACATGGTGAAACCCCGTCTCTA
                                  |||||||||||||||||||||||||
                                  ATTGTACCACTTTGGGGCAGAGAT

GAM1684  LOC89932  3'  TAGAGACGGGGTTTCTCCATGT 61474          T
              TG                  TAACATGG GAAACCCCGTCTCTA
                                  ||||||||| ||||||||||||||
                                  GTTGTACC CTTTGGGGCAGAGAT
                                       T
GAM1684  LOC89932  3'  TGGGGTTTCACCATGTTG    61477
                                  TAACATGGTGAAACCCCG
                                  |||||||||||||||||
                                  GTTGTACCACTTTGGGGT

GAM1684  LOC90288  3'  TAGAGACGGGGTTTCACAGTGT 62798        G
              TA                  TAACAT GTGAAACCCCGTCTCTA
                                  |||||| ||||||||||||||||
                                  ATTGTG CACTTTGGGGCAGAGAT
                                     A
GAM1684  LOC90288  3'  TAGAGATGGGGTTTCACCAT   62799
                                  ATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||
                                  TACCACTTTGGGGTAGAGAT

GAM1684  LOC90333  3'  TAGAGACTGGGTTTCACCGTGT 62965              C
              TA                  TAACATGGTGAAACCC GTCTCTA
                                  |||||||||||||| |||||||
                                  ATTGTGCCACTTTGGG CAGAGAT
                                            T
GAM1684  LOC90459  3'  TAGAGGCGGGGTTTCACCATGT 63564
              TG                  TAACATGGTGAAACCCCGTCTCTA
                                  |||||||||||||||||||||||||
                                  GTTGTACCACTTTGGGGCGGAGAT

GAM1684  LOC90485  3'  TAGAGGCAGGGTTTCACCATGT 63711              C
              TG                  TAACATGGTGAAACCC GTCTCTA
                                  |||||||||||||| |||||||
                                  GTTGTACCACTTTGGG CGGAGAT
                                            A
GAM1684  LOC90485  3'  TAGAGGCGGGGTTTCACCATGT 63712
              TG                  TAACATGGTGAAACCCCGTCTCTA
                                  |||||||||||||||||||||||||
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                                GTTGTACCACTTTGGGGCGGAGAT

GAM1684  LOC90591  3'  TAGAGACGGAGTTTCATCGTGT 64188            C
                TA                TAACATGGTGAAAC CCGTCTCTA
                                  |||||||||||||| |||||||||
                                  ATTGTGCTACTTTG GGCAGAGAT
                                        A
GAM1684  LOC90591  3'  TAGAGACGGGGCTTCACTATGT 64189           A
                TG                TAACATGGTGAA CCCCGTCTCTA
                                  |||||||||||| ||||||||||
                                  GTTGTATCACTT GGGGCAGAGAT
                                        C
GAM1684  LOC91291  5'  TAGAGACAAGGTTTCACCCTGT 66094      T       CC
                TG                TAACA GGTGAAACC  GTCTCTA
                                  ||||| |||||||||  |||||||
                                  GTTGT CCACTTTGG  CAGAGAT
                                     C        AA
GAM1684  LOC91893  3'  TAGAGACGAGGTTTCACCGTGT 68080            C
                TA                TAACATGGTGAAACC CGTCTCTA
                                  |||||||||||||| ||||||||
                                  ATTGTGCCACTTTGG GCAGAGAT
                                        A
GAM1684  LOC92148  5'  CGGGGTTTCACCGTGTTA    68877
                                  TAACATGGTGAAACCCCG
                                  |||||||||||||||||
                                  ATTGTGCCACTTTGGGGC

GAM1684  LOC92267  3'  TAGAGATGGGGTTTCACCAT   69176
                                  ATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||
                                  TACCACTTTGGGGTAGAGAT

GAM1684  LOC92303  3'  TAGAGATGGGTTTCACCATGTT 69397            C
                G                  TAACATGGTGAAACCC GTCTCTA
                                  |||||||||||||| |||||||
                                  GTTGTACCACTTTGGG TAGAGAT
                                                  _
GAM1684  LOC92689  3'  TAGAGACAGGGTTTCACCATGT 70780            C
                TG                TAACATGGTGAAACCC GTCTCTA
                                  |||||||||||||| |||||||
                                  GTTGTACCACTTTGGG CAGAGAT
                                        A
GAM1684  LOC92841  3'  TAGAGACAGGGTTTCACCATGT 71264            C
                TG                TAACATGGTGAAACCC GTCTCTA
                                  |||||||||||||| |||||||
                                  GTTGTACCACTTTGGG CAGAGAT
                                        A
GAM1684  LOC92841  3'  TAGAGACGGGGTTTCACCATGT 71265
                TA                TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
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                                ATTGTACCACTTTGGGGCAGAGAT

GAM1684 LOC93129 3' TAGAGACGGGGTTTCGCTGTTC 71958   C
                                A ATGGTGAAACCCCGTCTCTA
                                | ||||||||||||||||||||
                                C TGTCGCTTTGGGGCAGAGAT
                                 T
GAM1684 LOC93349 3' TAGAGACGGGGTTTCACTATGT 57275
           TG                     TAACATGGTGAAACCCCGTCTCTA
                                  ||||||||||||||||||||||||
                                  GTTGTATCACTTTGGGGCAGAGAT

GAM1684 LOC93408 5' TAGAAACAGAGTTTCACCATGT 57290           CCC  C
           TG                     TAACATGGTGAAAC   GT TCTA
                                  ||||||||||||||   || ||||
                                  GTTGTACCACTTTG   CA AGAT
                                           AGA  A
GAM1685 CDH15    3' CCCATGCGGGTCACCTCCC    18214        _ ___
                                  GGGAGGTG CT   ATGGG
                                  |||||||| ||   |||||
                                  CCCTCCAC GG   TACCC
                                       T  GCG
GAM1685 EPB49    3' CCCACCCAGCCCTCCCATA    10524        T   A__
                                  TATGGGAGG GCT   TGGG
                                  ||||||||| |||   ||||
                                  ATACCCTCC CGA   ACCC
                                       _   CCC
GAM1685 CORO1A   3' CCCATCCACTCACCTCCCAT   23956         CT___
                                  ATGGGAGGTG    ATGGG
                                  ||||||||||    |||||
                                  TACCCTCCAC    TACCC
                                       TCACC
GAM1685 FER1L3   3' TTTATGCCCACAACCATTGCTA 26524      G __   GCTA
           TA                     TATGG A  GGT    TGGGCATAAA
                                  ||||| |  |||   ||||||||||
                                  ATATC T  CCA    ACCCGTATTT
                                     G TA   AC__
GAM1685 FLJ31762 3' CCCATAACTAACACCTCCCA   58762         C____
                                  TGGGAGGTG    TATGGG
                                  |||||||||    ||||||
                                  ACCCTCCAC    ATACCC
                                       AATCA
GAM1685 MGC12435 5' TTTATGCCCAGATTCCCCCTAT 49494       A  TGCTA
           A                      TATGGG GG    TGGGCATAAA
                                  ||||||  ||    ||||||||||
                                  ATATCC CC    ACCCGTATTT
                                     C  TTAG_
GAM1685 MGC13017 3' TTATGCCCATAATAATCCCA   55583      GG  C
                                  TGGGA  TG TATGGGCATAA
                                  |||||  || ||||||||||
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                                ACCCT  AT ATACCCGTATT
                                   A_  A
GAM1685  SDCCAG43  3'  TCCACACCCACTTCCTATA   70896          CTA_
                                TATGGGAGGTG   TGGG
                                ||||||||||   ||||
                                ATATCCTTCAC   ACCT
                                      CCAC
GAM1685  LOC219700 5'  TCCACAGGCACCTCCTATA   94659           A_
                                TATGGGAGGTGCT  TGGG
                                ||||||||||||  ||||
                                ATATCCTCCACGG  ACCT
                                       AC
GAM1685  LOC222029 5'  TCTATGGAGCAGCTCCCATA  95694        G   __
                                TATGGGAG TGCT  ATGGG
                                ||||||||| ||||  |||||
                                ATACCCTC ACGA  TATCT
                                     G   GG
GAM1686  AGRN     3'  CCAGGCAGCCGTGCTGCA    79584        CA   _
                                TGCAGCAC  GCTGC TGG
                                ||||||||  ||||| |||
                                ACGTCGTG  CGACG ACC
                                     C_    G
GAM1686  ALEX1    5'  CTGCCTCAGAGCCGGCCCGCA  33974     AGCA  A   G   GA
                                TGC   CC GCT CTG  GCAG
                                |||   || ||| |||  ||||
                                ACG   GG CGA GAC  CGTC
                                  CCC_  C   _   TC
GAM1686  AP1B1    3'  CCACCGACTGGCAGCTGCA   8516        A_   C  C
                                TGCAGC  CCAG TG TGG
                                ||||||  |||| || |||
                                ACGTCG  GGTC GC ACC
                                   AC   A  C
GAM1686  ATM      3'  CTGCCGGGTAGCTGGGGCTACA 57144    C   A       GGA
                                TG AGC CCAGCTGCT   GCAG
                                || ||| |||||||||   ||||
                                AC TCG GGTCGATGG   CGTC
                                 A   G        GC_
GAM1686  BDP1     3'  CTGCCGGGTAGCTGGGACTACA 37966    C  CA       GGA
                                TG AG  CCAGCTGCT   GCAG
                                || ||  |||||||||   ||||
                                AC TC  GGTCGATGG   CGTC
                                 A  AG        GC_
GAM1686  CAPON    5'  CTGCTCTGGGGCCGGCGCCGC  64659    A  A  A   G TG
                                GC GC CC GCT C  GAGCAG
                                || || || ||| |  ||||||
                                CG CG GG CGG G  CTCGTC
                                 C  C  C   _ GT
GAM1686  CTF1     3'  CCAGCAGCTGGGACTACA    9009     C  CA
                                TG AG  CCAGCTGCTGG
                                || ||  ||||||||||
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                                AC TC  GGTCGACGACC
                                 A  AG
GAM1686  DDB2     3'  CTGCTCCAGAGTTGGTGACACA 5456     CAG       G
                                TG   CACCAGCT CTGGAGCAG
                                ||   |||||||| |||||||||
                                AC   GTGGTTGA GACCTCGTC
                                 ACA       _
GAM1686  ENDOGL1  3'  CTGCCCCCTGAGCAGCTGGGAC 18823    C  CA       ___  A
              TACA                   TG AG  CCAGCTGCT   GG GCAG
                                || ||  |||||||||   || ||||
                                AC TC  GGTCGACGA   CC CGTC
                                 A  AG        GTC  C
GAM1686  FCRH1    3'  CTGCTGAGTAGCTGGGACTACA 54726    C  CA       GG
                                TG AG  CCAGCTGCT  AGCAG
                                || ||  |||||||||  |||||
                                AC TC  GGTCGATGA  TCGTC
                                 A  AG        G_
GAM1686  FTH1     5'  GCTCCAGCGCCGCGCA      68713     A  ACCA  T
                                TGC GC    GC GCTGGAGC
                                ||| ||    || ||||||||
                                ACG CG    CG CGACCTCG
                                  _  C___  _
GAM1686  GAB2     3'  CCACAGCTGGTGCTCA      55404     C         C
                                TG AGCACCAGCTG TGG
                                || ||||||||||| |||
                                AC TCGTGGTCGAC ACC
                                 _         _
GAM1686  GAB2     3'  CCACAGCTGGTGCTCA      25457     C         C
                                TG AGCACCAGCTG TGG
                                || ||||||||||| |||
                                AC TCGTGGTCGAC ACC
                                 _         _
GAM1686  HTR4     3'  GCCCTGGCTGTGCTGCA     7885          C    GCT  A
                                TGCAGCAC AGCT   GG GC
                                |||||||| ||||   || ||
                                ACGTCGTG TCGG   CC CG
                                     _    T__  _
GAM1686  KLHL3    3'  TTCCAAGCAGGTGCTGCA    88855         A   GC
                                TGCAGCACC GCT  TGGAG
                                ||||||||| |||  |||||
                                ACGTCGTGG CGA  ACCTT
                                      A  __
GAM1686  LPIN1    3'  CTGCTCCAGCAAGTAGCT    67987     ACCA  _
                                AGC    GCT GCTGGAGCAG
                                |||    ||| ||||||||||
                                TCG    TGA CGACCTCGTC
                                  A___   A
GAM1686  MAD2L2   3'  GCCTAGGGCAGTGCTGCA    22018         CA   G    A
                                TGCAGCAC  GCT CTGG GC
                                ||||||||  ||| |||| ||
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                                ACGTCGTG  CGG GATC CG
                                   A_  _   _
GAM1686 MPST    3' TGCCCACCTGGTGCTG     41210        CTGC  A
                                CAGCACCAG   TGG GCA
                                |||||||||   ||| |||
                                GTCGTGGTC   ACC CGT
                                   C___  _
GAM1686 MSF     3' GCCCCCACTGGGCTGCA    89466      A   C  CT  A
                                TGCAGC CCAG TG  GG GC
                                |||||| |||| ||  || ||
                                ACGTCG GGTC AC  CC CG
                                   _   _ C_ _
GAM1686 OLFM1   3' GTATTTGCAGCTGGAACTGCA 27345     CA      TG A
                                TGCAG  CCAGCTGC  G GC
                                |||||  ||||||||  | ||
                                ACGTC  GGTCGACG  T TG
                                   AA       TT A
GAM1686 PTPN18  3' CTGCCGAGTAGCTGGGACTACA 27650   C  CA      GGA
                                TG AG  CCAGCTGCT   GCAG
                                || ||  |||||||||   ||||
                                AC TC  GGTCGATGA   CGTC
                                 A  AG        GC_
GAM1686 RPS18   5' CCGCCGCTTGTGCTGCA    42880       C   T  T
                                TGCAGCAC AGC GC GG
                                |||||||| ||| || ||
                                ACGTCGTG TCG CG CC
                                     T   C  _
GAM1686 SBF1    3' CTGGTCCAGCCAGCGGCTGCA 66069      ACCA   _    G
                                TGCAGC    GCTG CTGGA CAG
                                ||||||    |||| ||||| |||
                                ACGTCG    CGAC GACCT GTC
                                   G___    C    G
GAM1686 SCGB1A1 3' CTGCTCCAGCCTCTGCCGCT  13983    AC   CT
                                AGC  CAG  GCTGGAGCAG
                                |||  |||  ||||||||||
                                TCG  GTC  CGACCTCGTC
                                  CC   TC
GAM1686 SLC8A2  5' CTGCTCCAGGCTGTAGCCGCA 66934    A  AC   TG
                                TGC GC  CAGC  CTGGAGCAG
                                ||| ||  ||||  |||||||||
                                ACG CG  GTCG  GACCTCGTC
                                  C  AT   __
GAM1686 STARD5  3' GCTCCCTCAGTCCTGTGCTGCA 48318       CA_   CT
                                TGCAGCAC   GCTG  GGAGC
                                ||||||||   ||||  |||||
                                ACGTCGTG   TGAC  CCTCG
                                     TCC    TC
GAM1686 TARBP2  3' CTGCAGGAGCTGGTGGTGCA  57004     G      G  G
                                TGCA CACCAGCT CTG AG
                                |||| |||||||| ||| ||
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                                ACGT GTGGTCGA GAC TC
                                  G       G   G
GAM1686 ARHGAP8  3' CTGCCCCAGCCCTCTGGTGT  35201       CT_    A
                                GCACCAG   GCTGG GCAG
                                |||||||   ||||| ||||
                                TGTGGTC   CGACC CGTC
                                    TCC     C
GAM1686 BCKDK    3' CTGCTCCACACACTGCTGCA  60494       CCAGC  C
                                TGCAGCA    TG TGGAGCAG
                                |||||||    || ||||||||
                                ACGTCGT    AC ACCTCGTC
                                    CAC__ _
GAM1686 C11orf21 3' CTGAGATGGCAACTGGCACCGG 27103    AGCA_   C    GAG
             CA                   TGC    CCAG TGCTG   CAG
                                |||    |||| |||||   |||
                                ACG    GGTC ACGGT   GTC
                                  GCCAC    A    AGA
GAM1686 C14orf3  5' CTGCCGGGCGGCTGGCACT   25049    CA       GGA
                                AG  CCAGCTGCT   GCAG
                                ||  |||||||||   ||||
                                TC  GGTCGGCGG   CGTC
                                 AC        GC_
GAM1686 CDCA4    3' CTGCTCTGTTAGACTGGTGCTG 36086         _   CT
                                CAGCACCAG CTG  GGAGCAG
                                ||||||||| |||  |||||||
                                GTCGTGGTC GAT  TCTCGTC
                                     A   TG
GAM1686 CITED2   5' CTGCCCCAGCGGCCGCTGCG   21401       ACCA       A
                                TGCAGC    GCTGCTGG GCAG
                                ||||||    |||||||| ||||
                                GCGTCG    CGGCGACC CGTC
                                   C___       C
GAM1686 COPS7B   3' CTGGGGCAGCTGGCACTCA    42999    C  CA       GG
                                TG AG  CCAGCTGCT  AG
                                || ||  |||||||||  ||
                                AC TC  GGTCGACGG  TC
                                 _ AC        GG
GAM1686 CXYorf1  3' CCATCGTACAGTGGTGCTGCA  82908         G   C____
                                TGCAGCACCA CTG    TGG
                                |||||||||| |||    |||
                                ACGTCGTGGT GAC    ACC
                                      _   ATGCT
GAM1686 CXYorf1  5' TGCTCCAGAGCGCCTGCA    82922      CACCA   G
                                TGCAG    GCT CTGGAGCA
                                |||||    ||| ||||||||
                                ACGTC    CGA GACCTCGT
                                  CG___  _
GAM1686 D2S448   3' CTGCTCCAACAGCCAAATGC   73890     GCACCA    C
                                GCA     GCTG TGGAGCAG
                                |||     |||| ||||||||
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                                CGT     CGAC ACCTCGTC
                                  AAAC__   A
GAM1686  FER1L4   3'  CTGCTCTGTGCAGCTGGCCCGC 48119    AGCA      _
              A                    TGC   CCAGCTGC TGGAGCAG
                                   |||   |||||||| ||||||||
                                   ACG   GGTCGACG GTCTCGTC
                                     CCC_      T
GAM1686  FLJ10604 3'  CTCCAGCTTTCTGGTGTCACA 36858   CA     CT_
                                   TG  GCACCAG   GCTGGAG
                                   ||  |||||||   |||||||
                                   AC  TGTGGTC   CGACCTC
                                    AC      TTT
GAM1686  FLJ10640 5'  CCGAGTAGCTGGGACTACA   39232   C  CA      _
                                   TG AG  CCAGCTGCT GG
                                   || ||  |||||||||| ||
                                   AC TC  GGTCGATGA CC
                                    A  AG        G
GAM1686  FLJ11125 5'  CCACGTAGCTGGGGCTACA   60322   C   A     _
                                   TG AGC CCAGCTGC TGG
                                   || ||| |||||||| |||
                                   AC TCG GGTCGATG ACC
                                    A   G       C
GAM1686  FLJ11280 5'  CTGGAAGGCAGCTGGCACTGGC 37786    _  CA       GGAG
              A                    TGC AG  CCAGCTGCT    CAG
                                   ||| ||  |||||||||    |||
                                   ACG TC  GGTCGACGG    GTC
                                     G  AC        AAG_
GAM1686  FLJ12581 3'  CCGAGCAGCTGGGACTACA   46334   C  CA      _
                                   TG AG  CCAGCTGCT GG
                                   || ||  |||||||||| ||
                                   AC TC  GGTCGACGA CC
                                    A  AG        G
GAM1686  FLJ12697 3'  GCCCCAGCAGCCCCCGCGCA   94158    A  ACCA      A
                                   TGC GC    GCTGCTGG GC
                                   ||| ||    |||||||| ||
                                   ACG CG    CGACGACC CG
                                     _  CCCC       C
GAM1686  FLJ13710 3'  CTGCCCCATCCCTGGTGCT    46098       CTGC   A
                                   AGCACCAG    TGG GCAG
                                   ||||||||    ||| ||||
                                   TCGTGGTC    ACC CGTC
                                        CCT_   C
GAM1686  FLJ14681 5'  CTGCCTGGGGCGGTGCTGCA   52595        A   G TG A
                                   TGCAGCACC GCT C  G GCAG
                                   ||||||||| ||| |  | ||||
                                   ACGTCGTGG CGG G  C CGTC
                                         _  _ GT _
GAM1686  FLJ14871 3'  TCAGCAATGGTGCTGCA     52731         GC
                                   TGCAGCACCA  TGCTGG
                                   ||||||||||  ||||||
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                                ACGTCGTGGT  ACGACT
                                     A_
GAM1686  FLJ20150  3'  CTGCTCCAGCTGTTCACATGCA 35140     GCACC   T
                                TGCA    AGC GCTGGAGCAG
                                ||||    ||| ||||||||||
                                ACGT    TTG CGACCTCGTC
                                  ACAC_   T
GAM1686  FLJ30678  5'  CTGCCCCAGCAGCGGCCTG   58981    CA  A      A
                                CAG  CC GCTGCTGG GCAG
                                |||  || |||||||| ||||
                                GTC  GG CGACGACC CGTC
                                  C_ _       C
GAM1686  HCA112    3'  CTGCTCCAGCAGCACTTGC   38082    CCA
                                GCA   GCTGCTGGAGCAG
                                |||   ||||||||||||
                                CGT   CGACGACCTCGTC
                                  TCA
GAM1686  HEMK      3'  CTGTCGGGGCAGCTGGGGCCAC 32956   CA  A       GGA
                A                  TG  GC CCAGCTGCT   GCAG
                                ||  || |||||||||   ||||
                                AC  CG GGTCGACGG   TGTC
                                 AC  G        GGC
GAM1686  ITGB8     5'  CTGCTCCGCAGACGGGGCTGCA 11055       A  AG_   T
                                TGCAGC CC   CTGC GGAGCAG
                                |||||| ||   |||| |||||||
                                ACGTCG GG   GACG CCTCGTC
                                   _  GCA   _
GAM1686  KIAA0084  5'  GCTCCAGCGGCTGCTGT     68709       CCA
                                GCAGCA   GCTGCTGGAGC
                                ||||||   ||||||||||
                                TGTCGT   CGGCGACCTCG
                                   ___
GAM1686  KIAA0290  3'  CTGCCCCAGCTCTACACTGC   66716     CACC  CT    A
                                GCAG    AG  GCTGG GCAG
                                ||||    ||  ||||| ||||
                                CGTC    TC  CGACC CGTC
                                  ACA_  T_    C
GAM1686  KIAA0415  3'  GCCCAGGCCAGCTGGTGCT   94163          __    A
                                AGCACCAGCTG  CTGG GC
                                ||||||||||  |||| ||
                                TCGTGGTCGAC  GACC CG
                                     CG    _
GAM1686  KIAA0453  3'  CTGCCCTGTGGGCTGGTGCTTC 69605    C       _ TG T  A
                A                  TG AGCACCAG C  C GG GCAG
                                || ||||||||  |  | ||  ||||
                                AC TCGTGGTC G  G CC CGTC
                                 T       G GT T  _
GAM1686  KIAA0532  3'  CCAAGCAGCTGGGACTACA   71319    C  CA       _
                                TG AG  CCAGCTGCT GG
                                || ||  |||||||||  ||
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                                AC TC  GGTCGACGA CC
                                 A  AG        A
GAM1686  KIAA0720  3'  CTCTAGTAGCTGGAACTGCA   62981       CA
                                TGCAG  CCAGCTGCTGGAG
                                |||||  ||||||||||||||
                                ACGTC  GGTCGATGATCTC
                                   AA
GAM1686  KIAA0934  3'  CTGCCCCAGTGTGACCCTGCA  64883      CACCA  T    A
                                TGCAG    GC GCTGG GCAG
                                |||||    || ||||| ||||
                                ACGTC    TG TGACC CGTC
                                   CCAG_ _    C
GAM1686  KIAA1160  3'  CTGCAGACACAGGCTGGTGCTG 40756           GC  GA_
             CA                   TGCAGCACCAGCT  TG   GCAG
                                |||||||||||||  ||   ||||
                                ACGTCGTGGTCGG  AC   CGTC
                                       AC  AGA
GAM1686  KIAA1169  5'  CCAAGCAGCTGGAACTACA   35878    C  CA       _
                                TG AG  CCAGCTGCT GG
                                || ||  |||||||||  ||
                                AC TC  GGTCGACGA CC
                                 A  AA        A
GAM1686  KIAA1464  3'  CTCGGGACAGCTGTGTGCTGCA 68818         _     _  G
                                TGCAGCAC CAGCTG CT GAG
                                ||||||||  ||||||  ||  |||
                                ACGTCGTG GTCGAC GG CTC
                                     T     A  G
GAM1686  KIAA1465  3'  CTGCCTAGTAGCTGGGACTACA 61494    C  CA         A
                                TG AG  CCAGCTGCTGG GCAG
                                || ||  ||||||||||| ||||
                                AC TC  GGTCGATGATC CGTC
                                 A  AG         _
GAM1686  KIAA1671  3'  CTGCTCCAACCTGGTGCTG    66281         CTGC
                                CAGCACCAG    TGGAGCAG
                                |||||||||    ||||||||
                                GTCGTGGTC    ACCTCGTC
                                     CA__
GAM1686  KIAA1821  3'  CTGCCTGAGTAGCTGGGACTAC 72264    C  CA       _  A
             A                    TG AG  CCAGCTGCT GG GCAG
                                || ||  ||||||||| || ||||
                                AC TC  GGTCGATGA TC CGTC
                                 A  AG        G  _
GAM1686  MGC1842   5'  CTGCTCCAGGATGGTGCTGCA  66254         GCTG
                                TGCAGCACCA   CTGGAGCAG
                                ||||||||||   |||||||||
                                ACGTCGTGGT   GACCTCGTC
                                     AG__
GAM1686  MGC3178   3'  CTGCTCTGGCCCTGGTGTGCA  48718     G     CT  TG
                                TGCA CACCAG  GC  GAGCAG
                                |||| ||||||  ||  ||||||
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                                ACGT GTGGTC  CG  CTCGTC
                                  _     C_  GT
GAM1686  MGC34923  5'  CCAGCAGCTGGTGCTCA     59195    C
                                TG AGCACCAGCTGCTGG
                                || ||||||||||||||
                                AC TCGTGGTCGACGACC
                                 _
GAM1686  moblak    3'  CCAGCAGCTGGGACTACA    56389    C  CA
                                TG AG  CCAGCTGCTGG
                                || ||  ||||||||||
                                AC TC  GGTCGACGACC
                                 A  AG
GAM1686  NDRG4     3'  CTGGGCCCAGCTGGTGCTGTA 40381           CT  AG
                                TGCAGCACCAGCTG  GG  CAG
                                ||||||||||||||  ||  |||
                                ATGTCGTGGTCGAC  CC  GTC
                                        __  GG
GAM1686  NDRG4     3'  CTGGGCCCAGCTGGTGCTGTA 43578           CT  AG
                                TGCAGCACCAGCTG  GG  CAG
                                ||||||||||||||  ||  |||
                                ATGTCGTGGTCGAC  CC  GTC
                                        __  GG
GAM1686  NR4A3     5'  CCGGTGCAGCGCGGCGCCGCA 23718     A  A  A_    __
                                TGC GC CC  GCTGC  TGG
                                ||| || ||  |||||  |||
                                ACG CG GG  CGACG  GCC
                                  C  C  CG    TG
GAM1686  NSAP1     5'  CTGCCTCAGCCAGTAGCGCA  22086     A  ACCA   _  GA
                                TGC GC    GCTG CTG  GCAG
                                ||| ||    |||| |||  ||||
                                ACG CG    TGAC GAC  CGTC
                                  _ A___    C   TC
GAM1686  PDCD5     5'  CTGCTCCAGCGCTGACGC    17483    AC    T
                                GC  CAGC GCTGGAGCAG
                                ||  |||| ||||||||||
                                CG  GTCG CGACCTCGTC
                                 CA   _
GAM1686  PDZD2     5'  CTCCTCTACCAGTGGCTGCA  81720       ACCA   C    C
                                TGCAGC    GCTG TGGAG AG
                                ||||||    |||| ||||| ||
                                ACGTCG    TGAC ATCTC TC
                                   G___    C    C
GAM1686  PPP1R16B  3'  TTCCAAAGCAGGTGCTGCA   62042         A   GC
                                TGCAGCACC GCT  TGGAG
                                ||||||||| |||  |||||
                                ACGTCGTGG CGA  ACCTT
                                     A  A_
GAM1686  PSIP2     5'  CTGCGGCAGCTGGTGGCGCA  53781     AG         G
                                TGC  CACCAGCTGCTG AG
                                |||  |||||||||||| ||
```

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                                ACG  GTGGTCGACGGC TC
                                  CG          G
GAM1686  RAB40C    3'  CTGCCCACAGCACTGGTGCTCA 41279    C       C    GA_
                                TG AGCACCAG TGCTG   GCAG
                                || |||||||| |||||   ||||
                                AC TCGTGGTC ACGAC   CGTC
                                 _      _    ACC
GAM1686  RAB40C    3'  CTGCCCCAGCAGCCCCTCTGCA 41280      CACCA      A
                                TGCAG    GCTGCTGG GCAG
                                |||||    |||||||| ||||
                                ACGTC    CGACGACC CGTC
                                   TCCC_      C
GAM1686  SFXN5     3'  CTGCCAGCCGCTGGTGC     58652        T   GA
                                GCACCAGC GCTG  GCAG
                                |||||||| ||||  ||||
                                CGTGGTCG CGAC  CGTC
                                     C   __
GAM1686  SIMRP7    3'  CTGCTCCAGCAGACCATCTGCA 93972      CACCAG
                                TGCAG     CTGCTGGAGCAG
                                |||||     ||||||||||||
                                ACGTC     GACGACCTCGTC
                                   TACCA_
GAM1686  ZNF297B   5'  CTGTTGCGGCAGCTGAGGCTAC 82704    C   AC       G
            A                    TG AGC  CAGCTGCTG AGCAG
                                || |||  |||||||| |||||
                                AC TCG  GTCGACGGC TTGTC
                                 A  GA       G
GAM1686  LOC123242 5'  CTGAGGCCCAGCTGGTGCTG  76114          CT  AG_
                                CAGCACCAGCTG  GG   CAG
                                ||||||||||||  ||   |||
                                GTCGTGGTCGAC  CC   GTC
                                      __ GGA
GAM1686  LOC126603 5'  TGCTTCGCTGATCCTGCA    75914      CAC    TGCT
                                TGCAG   CAGC    GGAGCA
                                |||||   ||||    ||||||
                                ACGTC   GTCG    CTTCGT
                                   CTA   _____
GAM1686  LOC127841 5'  CTGCTCCCCAGCAGCTGGTGC  75186          __
                                GCACCAGCTGCT  GGAGCAG
                                ||||||||||||  |||||||
                                CGTGGTCGACGA  CCTCGTC
                                      CC
GAM1686  LOC130074 3'  CCACAGCTGGTGCTGCA     76624           C
                                TGCAGCACCAGCTG TGG
                                ||||||||||||| |||
                                ACGTCGTGGTCGAC ACC
                                          _
GAM1686  LOC132166 3'  CCAGCCGCTGGTGTGCA     75535      G      T
                                TGCA CACCAGC GCTGG
                                |||| ||||||| |||||
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                                ACGT GTGGTCG CGACC
                                  _      C
GAM1686  LOC132332 5'  CTGCCCTTGACTGGTGCTCA   76666    C       CTGCT  A
                                TG AGCACCAG     GG GCAG
                                || ||||||||     || ||||
                                AC TCGTGGTC     CC CGTC
                                 _       AGTT_  _
GAM1686  LOC142820 3'  GCTCCAGCTGCACTGCA     76916       CACCA  T
                                TGCAG     GC GCTGGAGC
                                |||||     || ||||||||
                                ACGTC     CG CGACCTCG
                                   A____  T
GAM1686  LOC143785 5'  CCAGACGCTGGTGTGCA     77102      G      TG
                                TGCA CACCAGC  CTGG
                                |||| |||||||  ||||
                                ACGT GTGGTCG  GACC
                                  _      CA
GAM1686  LOC146229 3'  CCAAGTAGCTGGGACTACA    78267    C  CA       _
                                TG AG  CCAGCTGCT GG
                                || ||  |||||||||  ||
                                AC TC  GGTCGATGA CC
                                 A  AG        A
GAM1686  LOC146268 3'  CTCTGGCTGGTGCTGC      78338           GCT
                                GCAGCACCAGCT   GGAG
                                ||||||||||||   ||||
                                CGTCGTGGTCGG   TCTC
                                       ___
GAM1686  LOC147080 5'  CCGAGCAGCTGGGACTACA    85031    C  CA       _
                                TG AG  CCAGCTGCT GG
                                || ||  |||||||||  ||
                                AC TC  GGTCGACGA CC
                                 A  AG        G
GAM1686  LOC147160 5'  CTGCTCCAGCACGTGTGC     85075      CA  _
                                GCAC  GC TGCTGGAGCAG
                                ||||  || ||||||||||||
                                CGTG  TG ACGACCTCGTC
                                  __  C
GAM1686  LOC148089 3'  CCGGCAGCTAGTGGCA      79329     AG   C
                                TGC  CAC AGCTGCTGG
                                |||  ||| |||||||||
                                ACG  GTG TCGACGGCC
                                  __   A
GAM1686  LOC150166 5'  CTGCTCCAGCAGCCGGGCCTGC 86037       CA  A
            A                    TGCAG  CC GCTGCTGGAGCAG
                                |||||  || ||||||||||||
                                ACGTC  GG CGACGACCTCGTC
                                   CG  C
GAM1686  LOC151178 5'  CTTGCAGCTGAAGCTGCA     80959       AC      T
                                TGCAGC  CAGCTGC GG
                                ||||||  ||||||| ||
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                                ACGTCG  GTCGACG TC
                                   AA      T
GAM1686  LOC151568 5'  CTGCTCCGGCATCCAGCGCTGC 57495      ACCAGC
                                GCAGC     TGCTGGAGCAG
                                |||||     ||||||||||
                                CGTCG     ACGGCCTCGTC
                                  CGACCT
GAM1686  LOC153205 5'  CTGCTCCTGACACGTGCTGCA  87157        CAGCTGCT
                                TGCAGCAC       GGAGCAG
                                ||||||||       |||||||
                                ACGTCGTG       CCTCGTC
                                    CACAGT__
GAM1686  LOC154084 3'  CTGCCCCAGTAGCATCTGCA   87377      CACCA       A
                                TGCAG     GCTGCTGG GCAG
                                |||||     |||||||| ||||
                                ACGTC     CGATGACC CGTC
                                  TA___       C
GAM1686  LOC154813 5'  CCACCAATGGTGCTGCA     82057          GC  C
                                TGCAGCACCA  TG TGG
                                ||||||||||  || |||
                                ACGTCGTGGT  AC ACC
                                     A_  C
GAM1686  LOC155006 3'  CTGCTCTGCCCTGATGTGCA   82168      G  C   CT  T
                                TGCA CA CAG  GC GGAGCAG
                                |||| || |||  || |||||||
                                ACGT GT GTC  CG TCTCGTC
                                  _  A   C_  _
GAM1686  LOC166129 5'  CTGCTCCAAGCAGCAGCGGCTG 88609       ACCA     _
            CA                    TGCAGC    GCTGCT GGAGCAG
                                |||||||   ||||||| |||||||
                                ACGTCG    CGACGA CCTCGTC
                                   GCGA     A
GAM1686  LOC196500 5'  GCTCCAGCGCCCTGCCGC    89084    A   CCA  T
                                GC GCA   GC GCTGGAGC
                                || |||   || ||||||||
                                CG CGT   CG CGACCTCG
                                 C   CC_  _
GAM1686  LOC200093 3'  CCATTGTACAGTGGTGCTGCA  63765          G   C____
                                TGCAGCACCA CTG     TGG
                                |||||||||| |||     |||
                                ACGTCGTGGT GAC     ACC
                                     _   ATGTT
GAM1686  LOC200093 5'  TGCTCCAGGGCGCCTGCA    63778      CACCA   G
                                TGCAG     GCT CTGGAGCA
                                |||||     ||| ||||||||
                                ACGTC     CGG GACCTCGT
                                  CG___   _
GAM1686  LOC253001 5'  CTGAGGCCCAGCTGGTGCTG   97993          CT  AG_
                                CAGCACCAGCTG  GG   CAG
                                ||||||||||||  ||   |||
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                                GTCGTGGTCGAC  CC   GTC
                                      __  GGA
GAM1686  LOC254266 5'  CCACCGTGCTGGTGCTCA    99196    C       _  C
                                TG AGCACCAGC TG TGG
                                || |||||||| || |||
                                AC TCGTGGTCG GC ACC
                                 _       T  C
GAM1686  LOC255189 5'  GCTCCCCCATTGTGCTGCA   98376        C  C  CT
                                TGCAGCAC AG TG  GGAGC
                                |||||||| || ||  |||||
                                ACGTCGTG TT AC  CCTCG
                                     _ _  CC
GAM1686  LOC255738 5'  CTGCCCACGTGGCTGGCATTGC 98629      CA    TG _   A
            A                    TGCAG  CCAGC  C TGG GCAG
                                |||||  |||||  | ||| ||||
                                ACGTT  GGTCG  G ACC CGTC
                                   AC    GT C  _
GAM1686  LOC91040  3'  CCATCGTACAGTGGTGCTGCA  65339         G   C____
                                TGCAGCACCA CTG    TGG
                                |||||||||| |||    |||
                                ACGTCGTGGT GAC    ACC
                                      _  ATGCT
GAM1686  LOC91040  5'  TGCTCCAGAGCGCCTGCA    65353      CACCA   G
                                TGCAG    GCT CTGGAGCA
                                |||||    ||| ||||||||
                                ACGTC    CGA GACCTCGT
                                   CG___  _
GAM1687  MAGEC1    3'  CCAAACACACCACATTGGGA   19595        __  ACG
                                TCCCAATGT  TG   TTGG
                                |||||||||  ||   ||||
                                AGGGTTACA  AC   AACC
                                     CC  ACA
GAM1687  TST       3'  CCCTCTCTCTGTCAACACTGG  13873     A      TT  CC
                                CCA TGTTGACG  GG  AGGG
                                ||| ||||||||  ||  ||||
                                GGT ACAACTGT  CT  TCCC
                                  C       CT  C_
GAM1687  ATIP1     3'  CCCTGCATGTGTCAACATTGTG 40772    C        TTG  C
            A                    TC CAATGTTGACG   GC AGGG
                                || ||||||||||   || ||||
                                AG GTTACAACTGT   CG TCCC
                                 T         GTA  _
GAM1687  DKFZp547I224 3'  CCCCACTGTCAACATT      39954          T   CCA
                                AATGTTGACG TGG   GG
                                |||||||||| |||   ||
                                TTACAACTGT ACC   CC
                                      C  ___
GAM1687  FLJ12704  3'  CTTGGCAAGCACCAACATTGAG 47169    C       AC   G
            A                    TC CAATGTTG  GTT GCCAGG
                                || ||||||||  ||| ||||||
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                                AG GTTACAAC  CGA CGGTTC
                                 A       CA   A
GAM1687  SH3BGRL3  3'  CCCAGCCAAGCATTGGGG    49258         TGACG    CA
                                TCCCAATGT    TTGGC  GG
                                |||||||||    |||||  ||
                                GGGGTTACG    AACCG  CC
                                      _____     AC
GAM1687  LOC146378 3'  CCCGGGGTTGTCAGCACTGGGA 78419      A       TTG   A_
                                TCCCA TGTTGACG   GCC  GGG
                                ||||| ||||||||   |||  |||
                                AGGGT ACGACTGT   TGG  CCC
                                   C       ___   GG
GAM1687  LOC149414 5'  CCCCGGCCAAGAAGCACCGGG  85570     AA   GACG     A
                                CCC  TGTT    TTGGCC GGG
                                |||  ||||    |||||| |||
                                GGG  ACGA    AACCGG CCC
                                  CC    AG__     C
GAM1687  LOC149684 5'  CCCTGGCCTGGAAAACAGTAGG 85762     CAA    GACGTT
              A                  TCC   TGTT     GGCCAGGG
                                |||   ||||     ||||||||
                                AGG   ACAA     CCGGTCCC
                                  ATG    AAGGT_
GAM1687  LOC165104 5'  CCCTGGCCATCCACACTGAGG  83351    _ A   T  CGT
                                CC CA TGT GA   TGGCCAGGG
                                || || ||| ||   |||||||||
                                GG GT ACA CT   ACCGGTCCC
                                 A  C   C  ___
GAM1688  ABCD3    3'  CAAAGTCCTTAACATGCCAG   12662     A   C_      C
                                CTG CAT  TGAGGACT TG
                                ||| |||  |||||||| ||
                                GAC GTA  ATTCCTGA AC
                                  C   CA       A
GAM1688  ADRA2A   5'  GCAGAGTCCGCGCCCCAGC    7291       ACATC  A
                                GCTG     TG GGACTCTGC
                                ||||     || |||||||||
                                CGAC     GC CCTGAGACG
                                   CCC__  G
GAM1688  ADSS     3'  GCATATTCCAGTGTCAGC     72234        T   A   CTC
                                GCTGACA CTG GGA   TGC
                                ||||||| ||| |||   |||
                                CGACTGT GAC CTT   ACG
                                      _   _   AT_
GAM1688  ARHG     5'  GCAAAAAGGCTCAGATGTCA   77090          GA  C__
                                TGACATCTGAG  CT   TGC
                                ||||||||||  ||   |||
                                ACTGTAGACTC  GA   ACG
                                       G_  AAA
GAM1688  BRCA1    3'  CAGAGCCCCAGAGTCAGC    24544        A    A  A
                                GCTGAC TCTG GG CTCTG
                                |||||| |||| || |||||
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                                CGACTG AGAC CC GAGAC
                                   _   C  _
GAM1688 CACNA1C  5' CAGAGTCTTTCTCTTCAGC   7397      CATCT
                                GCTGA    GAGGACTCTG
                                |||||    ||||||||||
                                CGACT    TTTCTGAGAC
                                   TCTC_
GAM1688 DYRK1A   3' CAGAGTCCTGTAGCTAGC    56074     ACAT  _
                                GCTG   CTG AGGACTCTG
                                ||||   ||| ||||||||||
                                CGAT   GAT TCCTGAGAC
                                  C___  G
GAM1688 FGF18    5' CAGAGTCTGCAGCAGC      54450     ACAT  A
                                GCTG   CTG GGACTCTG
                                ||||   ||| ||||||||
                                CGAC   GAC TCTGAGAC
                                  _____  G
GAM1688 FGF18    5' CAGAGTCTGCAGCAGC      15256     ACAT  A
                                GCTG   CTG GGACTCTG
                                ||||   ||| ||||||||
                                CGAC   GAC TCTGAGAC
                                  _____  G
GAM1688 GFPT2    3' GCATTCATCTCAGATGTGAGC  18842     G       ACTC
                                GCT ACATCTGAGG   TGC
                                ||| ||||||||||   |||
                                CGA TGTAGACTCT   ACG
                                  G        ACTT
GAM1688 GPR30    3' GCAGGGTCCAAAGGCCAGC   9492      ACA  GA
                                GCTG   TCT  GGACTCTGC
                                ||||   |||  |||||||||
                                CGAC   GGA  CCTGGGACG
                                  C__   AA
GAM1688 IL15     5' CAGAAATCAATGTTAGC     6970        C  GGAC
                                GCTGACAT TGA   TCTG
                                |||||||| |||   ||||
                                CGATTGTA ACT   AGAC
                                    _  AA__
GAM1688 KAI1     5' GCAGAGTCCTCCCTGCTGC   11124    TGA  TCT
                                GC   CA   GAGGACTCTGC
                                ||   ||   ||||||||||
                                CG   GT   CTCCTGAGACG
                                 TC_  CC_
GAM1688 KNSL1    3' GCAAAATCAGATGTCAGC    16948         GGACTC
                                GCTGACATCTGA     TGC
                                ||||||||||||     |||
                                CGACTGTAGACT     ACG
                                       AAA___
GAM1688 LAMC1    3' GCAAAGTTTTCACGTCA     11266     ATC      C
                                TGAC   TGAGGACT TGC
                                ||||   |||||||| |||
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                                ACTG   ACTTTTGA ACG
                                  C__       A
GAM1688 MFNG    3' GCAGAATCCAGGGTCTGCAGC  11545     AC_   GA  C
                                GCTG   ATCT  GGA TCTGC
                                ||||   ||||  ||| |||||
                                CGAC   TGGG  CCT AGACG
                                  GTC    A_   A
GAM1688 OGDH    3' CAGAGTCTGTGTGTAGC     92745     A  CTGA
                                GCTG CAT    GGACTCTG
                                |||| |||    ||||||||
                                CGAT GTG    TCTGAGAC
                                  _   TG__
GAM1688 RFX2    3' CAGAAGGTACTAATGTCAGC   7154        CTG  GA_ _
                                GCTGACAT   AG   CT CTG
                                ||||||||   ||   || |||
                                CGACTGTA   TC   GA GAC
                                     A__  ATG  A
GAM1688 RPS6KA5  3' CAGGTTTTCCAGATGTCTGC   17648    T      _    T
                                GC GACATCTG AGGAC CTG
                                || |||||||| ||||| |||
                                CG CTGTAGAC TTTTG GAC
                                 T       C    _
GAM1688 SLC18A1  5' CAGAATCCTCAGATAACAG    13210     AC       C
                                CTG  ATCTGAGGA TCTG
                                |||  ||||||||| ||||
                                GAC  TAGACTCCT AGAC
                                  AA        A
GAM1688 SPON1    3' GCAGAGGAGTAGTGTCAGC    63121       T   AGGA
                                GCTGACA CTG    CTCTGC
                                ||||||| |||    ||||||
                                CGACTGT GAT    GAGACG
                                   _   GAG_
GAM1688 ARTN    3' GCAGAGTCCCACTAGCCAGC   15614     ACATC  A
                                GCTG    TG GGACTCTGC
                                ||||    || |||||||||
                                CGAC    AC CCTGAGACG
                                  CGATC  _
GAM1688 ARTN    3' GCAGAGTCCCACTAGCCAGC   55110     ACATC  A
                                GCTG    TG GGACTCTGC
                                ||||    || |||||||||
                                CGAC    AC CCTGAGACG
                                  CGATC  _
GAM1688 ARTN    3' GCAGAGTCCCACTAGCCAGC   55118     ACATC  A
                                GCTG    TG GGACTCTGC
                                ||||    || |||||||||
                                CGAC    AC CCTGAGACG
                                  CGATC  _
GAM1688 ARTN    3' GCAGAGTCCCACTAGCCAGC   55138     ACATC  A
                                GCTG    TG GGACTCTGC
                                ||||    || |||||||||
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                                CGAC    AC CCTGAGACG
                                  CGATC  _
GAM1688 BICD2    3' GCATGTGTCTAATGTCAGC   70912       CTGA   TC_
                                GCTGACAT   GGAC  TGC
                                ||||||||   ||||  |||
                                CGACTGTA   TCTG  ACG
                                    A___   TGT
GAM1688 BLZF1    3' GCAGAGTTGAATAGATGCAGC 14754     A    AG_
                                GCTG CATCTG  GACTCTGC
                                |||| ||||||  ||||||||
                                CGAC GTAGAT  TTGAGACG
                                  _    AAG
GAM1688 C20orf126 3' GCAGAGTCCTGCACCAGGC   48733    GACATC  _
                                GCT     TG AGGACTCTGC
                                |||     || ||||||||||
                                CGG     AC TCCTGAGACG
                                  ACC___  G
GAM1688 CGI-127  3' GCAGAGTCTGTCTGCAGC    32675     A  TCTGA
                                GCTG CA    GGACTCTGC
                                |||| ||    |||||||||
                                CGAC GT    TCTGAGACG
                                  _ CTG__
GAM1688 CHST8    5' GCAGAGTCCCCGCTGCTGC   42693    TGA  TC  A
                                GC   CA  TG GGACTCTGC
                                ||   ||  || |||||||||
                                CG   GT  GC CCTGAGACG
                                 TC_  C_  C
GAM1688 DDX28    5' GCAACCTCGGATACCAGC    37789     AC      ACTC
                                GCTG  ATCTGAGG   TGC
                                ||||  ||||||||   |||
                                CGAC  TAGGCTCC   ACG
                                  CA       A___
GAM1688 DKFZP547E2110 3' CAGAGTTTAGAATATCAG    92625     CA_    GG
                                CTGA   TCTGA  ACTCTG
                                ||||   |||||  ||||||
                                GACT   AGATT  TGAGAC
                                  ATA    __
GAM1688 DKFZp762K2015 3' GCAGATGTTCACCAATGTCAGC 72891        C  A_   _
                                GCTGACAT TG  GGAC TCTGC
                                ||||||| ||  |||| |||||
                                CGACTGTA AC  CTTG AGACG
                                    _ CA   T
GAM1688 EFA6R    3' GCAGAGTCCTTACTTTATCGC  31636    T  CATC_
                                GC GA    TGAGGACTCTGC
                                || ||    ||||||||||||
                                CG CT    ATTCCTGAGACG
                                 _ ATTTC
GAM1688 FLJ11151  3' CAGAGTTTAGTCAACGTAGC   68472     ACATC   __
                                GCTG    TGA  GGACTCTG
                                ||||    |||  ||||||||
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                                CGAT    ACT  TTTGAGAC
                                  GCA__   GA
GAM1688  FLJ14525  3'  CAGGGATCCTCAGAATCAGC   52478      CA      _
                                GCTGA  TCTGAGGA CTCTG
                                |||||  |||||||| |||||
                                CGACT  AGACTCCT GGGAC
                                   A_       A
GAM1688  FLJ20671  3'  GCAGAGTCCCATGGACAGC    35941     A_  TC  A
                                GCTG  CA  TG GGACTCTGC
                                ||||  ||  || |||||||||
                                CGAC  GT  AC CCTGAGACG
                                  AG  __  _
GAM1688  FLJ21736  3'  GCAGAGTCCCAGCACGGCAGC  46784     ACAT_   A
                                GCTG    CTG GGACTCTGC
                                ||||    ||| |||||||||
                                CGAC    GAC CCTGAGACG
                                  GGCAC   _
GAM1688  FLJ22332  5'  CAGAGCCTTTTCAGACCCAGC  45636     ACA    ___  A
                                GCTG   TCTGA   GG CTCTG
                                ||||   |||||   || |||||
                                CGAC   AGACT   CC GAGAC
                                  CC_    TTT  _
GAM1688  FLJ23392  3'  CAAAGCCTATGTCAGC      45883        CTG   A  C
                                GCTGACAT   AGG CT TG
                                ||||||||   ||| || ||
                                CGACTGTA   TCC GA AC
                                     ___   _  A
GAM1688  FLJ32865  3'  CAAAGCCCTAGGGTTCCAGC   58802     AC   G   A  C
                                GCTG  ATCT AGG CT TG
                                ||||  |||| ||| || ||
                                CGAC  TGGG TCC GA AC
                                  CT   A   C  A
GAM1688  HELO1     3'  CAGAGTCCCGTAGATGAGC   41795     GA     A_
                                GCT  CATCTG  GGACTCTG
                                |||  ||||||  ||||||||
                                CGA  GTAGAT  CCTGAGAC
                                  __     GC
GAM1688  HSH2      3'  CAGAGCTATGGGTGTCAGC   52736          A  A
                                GCTGACATCTG GG CTCTG
                                |||||||||||  || |||||
                                CGACTGTGGGT TC GAGAC
                                      A  _
GAM1688  KIAA0376  3'  GCCCTGCCCAGATGTCAGC   66214          A  ACTCT
                                GCTGACATCTG GG    GC
                                |||||||||||  ||    ||
                                CGACTGTAGAC CC    CG
                                      _  GTCC_
GAM1688  KIAA0802  3'  CAAAGTCCTCAGTGGGC     63246     GA  T       C
                                GCT  CA CTGAGGACT TG
                                |||  ||  |||||||||  ||
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                                CGG  GT GACTCCTGA AC
                                  __ _       A
GAM1688 KIAA1467 3' GCAGAAAATTCAATGTTAGC  72069        C   GAC
                                GCTGACAT TGAG  TCTGC
                                |||||||| ||||  |||||
                                CGATTGTA ACTT  AGACG
                                     _   AAA
GAM1688 KIAA1674 3' GCATGGTCTCAGATGCCA   69344   A      G  C
                                TG CATCTGAG ACT TGC
                                || |||||||| ||| |||
                                AC GTAGACTC TGG ACG
                                 C       _  T
GAM1688 KIAA1922 5' GCTGGGTCTCAGATGCA    73998   A      G   T
                                TG CATCTGAG ACTC GC
                                || |||||||| |||| ||
                                AC GTAGACTC TGGG CG
                                 _       _   T
GAM1688 LPAAT-gamma1 5' TGGAGTCAGATGTGAGC    39698    G    GAG
                                GCT ACATCT  GACTCTG
                                ||| ||||||  |||||||
                                CGA TGTAGA  CTGAGGT
                                  G    ___
GAM1688 MCJ     5' GCAGAGTCCACTGGATCTGC  26018   T  CA  GA_
                                GC GA  TCT  GGACTCTGC
                                || ||  |||  |||||||||
                                CG CT  AGG  CCTGAGACG
                                 T  __  TCA
GAM1688 MGC12760 3' CAGAGTCAGCTGCAGC     52156    A  T  GAG
                                GCTG CA CT  GACTCTG
                                |||| || ||  |||||||
                                CGAC GT GA  CTGAGAC
                                  _ C  ___
GAM1688 MKRN4   3' CAGAGTCCCACTCTGTCA    48454     TC_  A
                                TGACA  TG GGACTCTG
                                |||||  || ||||||||
                                ACTGT  AC CCTGAGAC
                                   CTC  _
GAM1688 MOST2   3' AGGGCACAGAATGTCAGC    40052       _  AGGA
                                GCTGACAT CTG   CTCT
                                |||||||| |||   ||||
                                CGACTGTA GAC   GGGA
                                     A  AC__
GAM1688 NKIR    3' GCAGCCTTCAGATGCCAG    58137    A      ACT
                                CTG CATCTGAGG  CTGC
                                ||| |||||||||  ||||
                                GAC GTAGACTTC  GACG
                                  C       C__
GAM1688 OS4     3' CAGAGTCCCCAGAACTCA    20383    CA   A
                                TGA  TCTG GGACTCTG
                                |||  |||| ||||||||
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                                ACT  AGAC CCTGAGAC
                                  CA    C
GAM1688  PPP1R12C  3'  GCAGAGTCCCCAGGAGC     34693     GACA    A
                                GCT    TCTG GGACTCTGC
                                |||    |||| |||||||||
                                CGA    GGAC CCTGAGACG
                                 _____    C
GAM1688  PRDX1     3'  AGACTTCAGATTCAGC      11956       C       AC
                                GCTGA ATCTGAGG  TCT
                                ||||| ||||||||  |||
                                CGACT TAGACTTC  AGA
                                  _       __
GAM1688  PRO1777   3'  CAAAGTCCTCAGAGTTGC    38371    T   A        C
                                GC GAC TCTGAGGACT TG
                                || ||| ||||||||||  ||
                                CG TTG AGACTCCTGA AC
                                 _  _         A
GAM1688  PRSC      3'  GCAAAGTTCTTTAGATATCA   22703     C       _  C
                                TGA ATCTGAGGA CT TGC
                                ||| |||||||||  ||  |||
                                ACT TAGATTTCT GA ACG
                                  A        T  A
GAM1688  SEC15B    3'  CGCAAAGTCCAATATTAAGATG 67262          GA_____     C  ___
              TCAGC                  GCTGACATCT      GGACT TGC   G
                                ||||||||||      |||||  |||   |
                                CGACTGTAGA      CCTGA ACG   C
                                      ATTATAA     A  ___
GAM1688  SEMA3B    5'  CAGAGTCCAGGGCAGC      17344      ACA   GA
                                GCTG   TCT  GGACTCTG
                                ||||   |||  ||||||||
                                CGAC   GGG  CCTGAGAC
                                  ___   A_
GAM1688  Spir-1    3'  CAGAGATGCCGATGTCAGC    65328         TGA  A__
                                GCTGACATC   GG   CTCTG
                                |||||||||   ||   |||||
                                CGACTGTAG   CC   GAGAC
                                     ___ GTA
GAM1688  SPTLC2    3'  GCAAATTCAAATGTCAGT     17993         C    GACTC
                                GCTGACAT TGAG     TGC
                                |||||||| ||||     |||
                                TGACTGTA ACTT     ACG
                                     A    AA___
GAM1688  SYT13     3'  CAGAACATCTTAGATGTCAGC  95098            AC_
                                GCTGACATCTGAGG   TCTG
                                ||||||||||||||   ||||
                                CGACTGTAGATTCT   AGAC
                                       ACA
GAM1688  T2BP      3'  GCAGATCAGGATGTCAGC     70537          GAG  C
                                GCTGACATCT   GA TCTGC
                                ||||||||||   ||  |||||
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                                CGACTGTAGG  CT AGACG
                                     A__  _
GAM1688  WAP1     3'  GCAGAGTTTTCCAAACATCAG  80340     CATCT_
                                CTGA     GAGGACTCTGC
                                ||||     ||||||||||
                                GACT     CTTTTGAGACG
                                  ACAAAC
GAM1688  ZDHHC2   3'  CAGAGTCCAGGTGGCCTGC   33444    TGA_    GA
                                GC   CATCT  GGACTCTG
                                ||   |||||  ||||||||
                                CG   GTGGA  CCTGAGAC
                                 TCCG    __
GAM1688  ZNF317   3'  CAGATCAGCAGATGTCA     72473        AG  C
                                TGACATCTG  GA TCTG
                                |||||||||  || ||||
                                ACTGTAGAC  CT AGAC
                                     GA  _
GAM1688  LOC129052 5'  GCAGCCACCAGGTGTCAGC   76311          A_  ACT
                                GCTGACATCTG  GG   CTGC
                                ||||||||||  ||   ||||
                                CGACTGTGGAC  CC   GACG
                                     CA  ____
GAM1688  LOC129285 3'  CAGAAGTTGATGTCGGC     75368        TGAG   _
                                GCTGACATC    GACT CTG
                                |||||||||    |||| |||
                                CGGCTGTAG    TTGA GAC
                                     _____    A
GAM1688  LOC132332 3'  GCAGAGTGAAGGCATGTCAG   76667       _  GAGG
                                CTGACAT CT    ACTCTGC
                                |||||||  ||    |||||||
                                GACTGTA GG    TGAGACG
                                   C  AAG_
GAM1688  LOC143451 5'  CAGAATCCTGAGGTGTCA    77068        G   C
                                TGACATCT AGGA TCTG
                                |||||||| |||| ||||
                                ACTGTGGA TCCT AGAC
                                     G    A
GAM1688  LOC145125 5'  CAGAATCCTGAGGTGTCA    77544        G   C
                                TGACATCT AGGA TCTG
                                |||||||| |||| ||||
                                ACTGTGGA TCCT AGAC
                                     G    A
GAM1688  LOC145694 5'  GCAGAGAGGAGATGCAGC    84442     A    GAGGA
                                GCTG CATCT    CTCTGC
                                |||| |||||    ||||||
                                CGAC GTAGA    GAGACG
                                  _    GGA__
GAM1688  LOC147343 5'  GCAGATACTTCTCAGATATCA  85128    C       C__
                                TGA ATCTGAGGA   TCTGC
                                ||| |||||||||   |||||
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                                ACT TAGACTCTT   AGACG
                                  A       CAT
GAM1688  LOC148545 3'  GCAGAGTCCATGCTGTGAGC   79643    G   TCTGA
                                GCT ACA    GGACTCTGC
                                ||| |||    |||||||||
                                CGA TGT    CCTGAGACG
                                  G   CGTA_
GAM1688  LOC148545 3'  GCAGGAGACAGCATGTCAGC   79644       _   AGGAC
                                GCTGACAT CTG    TCTGC
                                |||||||| |||    |||||
                                CGACTGTA GAC    GGACG
                                    C   AGA__
GAM1688  LOC148709 5'  GCAGAGTCGGGCGTCCGC    79693    T   AT  GAG
                                GC GAC  CT   GACTCTGC
                                || |||  ||   ||||||||
                                CG CTG  GG   CTGAGACG
                                 C   CG  ___
GAM1688  LOC149271 5'  GCAAAGCCTCCTATGTCGGC   80005       CT    A  C
                                GCTGACAT  GAGG CT TGC
                                ||||||||  |||| || |||
                                CGGCTGTA  CTCC GA ACG
                                    TC    _  A
GAM1688  LOC149579 3'  CAGAGTCAGCTGCAGC      71689      A  T  GAG
                                GCTG CA CT   GACTCTG
                                |||| || ||   |||||||
                                CGAC GT GA   CTGAGAC
                                  _  C  ___
GAM1688  LOC150197 3'  GCAGAGTTGGGGACTCAGC   80424      CA   GAG
                                GCTGA  TCT   GACTCTGC
                                |||||  |||   ||||||||
                                CGACT  AGG   TTGAGACG
                                   C_   GG_
GAM1688  LOC150271 3'  GCAGAGGGCAGATGCAGC    86139      A     AGGA
                                GCTG CATCTG    CTCTGC
                                |||| ||||||    ||||||
                                CGAC GTAGAC    GAGACG
                                  _     GG__
GAM1688  LOC150819 5'  GCAGAGTCCAGCTGCAGC    86309      A  T  GA
                                GCTG CA CT  GGACTCTGC
                                |||| || ||  |||||||||
                                CGAC GT GA  CCTGAGACG
                                  _  C  __
GAM1688  LOC153688 3'  GCAGAGTCCTGGGTGACCAGC  87319      A_    G
                                GCTG  CATCT AGGACTCTGC
                                ||||  ||||| ||||||||||
                                CGAC  GTGGG TCCTGAGACG
                                  CA    _
GAM1688  LOC154215 3'  CAGATGACTTCAGTATGTCAGC 81954        _     AC_
                                GCTGACAT CTGAGG   TCTG
                                |||||||| ||||||   ||||
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                                CGACTGTA GACTTC   AGAC
                                     T     AGT
GAM1688  LOC157273 3'  GCAAAGTTTCTCAGATATCTGC 87723    T  C       _  C
                                GC GA ATCTGAGGA CT TGC
                                || || ||||||||| || |||
                                CG CT TAGACTCTT GA ACG
                                 T  A       T  A
GAM1688  LOC222112 3'  GCAGCATCGGATGTCAGC    94379          GGACT
                                GCTGACATCTGA    CTGC
                                ||||||||||||    ||||
                                CGACTGTAGGCT    GACG
                                       AC___
GAM1688  LOC254440 5'  CAGAATCCTGAGGTGTCA    98847        G   C
                                TGACATCT AGGA TCTG
                                |||||||| |||| ||||
                                ACTGTGGA TCCT AGAC
                                     G   A
GAM1688  LOC254479 5'  GCAGAAGCAGCAGAGTCAGC  98871       A   AGGAC
                                GCTGAC TCTG    TCTGC
                                |||||| ||||    |||||
                                CGACTG AGAC    AGACG
                                   _   GACGA
GAM1688  LOC51028  3'  GCAGAACCCTCAGAGTT    32693     A     AC
                                GAC TCTGAGG  TCTGC
                                ||| |||||||  |||||
                                TTG AGACTCC  AGACG
                                  _     CA
GAM1688  LOC92340  3'  GCAGAGCAGGACAGATGTCA  69563        AGGA_
                                TGACATCTG    CTCTGC
                                |||||||||    ||||||
                                ACTGTAGAC    GAGACG
                                      AGGAC
GAM1688  LOC92539  5'  GCAGAGTCCTCAGTATCCAGT  70220     ACAT
                                GCTG   CTGAGGACTCTGC
                                ||||   ||||||||||||
                                TGAC   GACTCCTGAGACG
                                  CTAT
GAM1689  ABP1      5'  GCAGAGCGAACTGGGAGCAGAG 63799         CCGC    C
                                CTCTGTTCTT   CGCTC GC
                                ||||||||||   ||||| ||
                                GAGACGAGGG   GCGAG CG
                                      TCAA    A
GAM1689  AHCY      3'  GGCAACTGAGAAAGAACAGAG  7304         _ _ ____
                                CTCTGTTCTT C C   GCC
                                |||||||||| | |   |||
                                GAGACAAGAA G G   CGG
                                      A A TCAA
GAM1689  BSN       3'  GGCAGAGGCAAGAGCAGAG   14387         CC  G  _
                                CTCTGTTCTT  GCC CT CC
                                |||||||||  ||| || ||
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                                GAGACGAGAA  CGG GA GG
                                    __   A  C
GAM1689  CSE1L    5'  GCGGAGCGGCGGCAGGAGC    62513       _
                                GTTCTT CCGCCGCTCCGC
                                |||||| ||||||||||||
                                CGAGGA GGCGGCGAGGCG
                                   C
GAM1689  EHD4     3'  AGTGGCAAAAAAATAGAG     58362        C  CC
                                CTCTGTT TT  GCCGCT
                                ||||||| ||  ||||||
                                GAGATAA AA  CGGTGA
                                    A  AA
GAM1689  EIF2C1   3'  AGCCCAGCTGAAGAACAGA    25181          C  C__
                                TCTGTTCTTC GC   GCT
                                |||||||||| ||   |||
                                AGACAAGAAG CG   CGA
                                      T  ACC
GAM1689  KCNK4    3'  GCGAGCAGCAGAGCAGG     33986        TCC  C    C
                                TCTGTTCT   GC GCTC GC
                                ||||||||   || |||| ||
                                GGACGAGA   CG CGAG CG
                                    ___  A    A
GAM1689  MYO1D    3'  GCGGAACAGCCCATCCAGCAGA 72249         CTTCC_  CGC
           GT                    ACTCTGTT     GC   TCCGC
                                 |||||||      ||   |||||
                                 TGAGACGA     CG   AGGCG
                                     CCTACC  ACA
GAM1689  NUP62    3'  GGCAAAGCAGCACAGTGTGAAT 25650        TTCC___  C   CC
           AGA                     TCTGTTC      GC GCT  GCC
                                   |||||||      || |||  |||
                                   AGATAAG      CG CGA  CGG
                                      TGTGACA  A   AA
GAM1689  RABIF    3'  GGCATGTGCAGAAAAACAGAGT 12728         C   C  C  TCC
                                 ACTCTGTT TTC GC GC   GCC
                                 ||||||| ||| || ||   |||
                                 TGAGACAA AAG CG TG   CGG
                                     A   A  _  TA_
GAM1689  RAX      3'  GCAGGGGAGGCGGAAAAATAGA 26466         C      G   _
           GT                      ACTCTGTT TTCCGCC CTCC GC
                                   ||||||| ||||||| |||| ||
                                   TGAGATAA AAGGCGG GGGG CG
                                       A      A   A
GAM1689  RBM10    3'  GGCAGGGAAGGACAGAGT    20247           __
                                 ACTCTGTTCTTCC  GCC
                                 |||||||||||||  |||
                                 TGAGACAGGAAGG  CGG
                                        GA
GAM1689  RGS16    3'  GGCAGGGCCCAGGAGAACAAAG 12869     C     T  GCC    C
           T                      ACT TGTTCT CC   GCTC GCC
                                  ||| |||||| ||   |||| |||
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                                TGA ACAAGA GG   CGGG CGG
                                  A     _ ACC    A
GAM1689 ROM1     3' GGAACAGCAAAGAACAGAGT   6165          CC  CGC
                                ACTCTGTTCTT  GC   TCC
                                ||||||||||  ||   |||
                                TGAGACAAGAA  CG   AGG
                                      A_  ACA
GAM1689 SLC21A2  3' GCAAAGCAAGTGATGAAGCAGA 20084        _ TTC   C_   CC
             GT                   ACTCTGTT C   CGC  GCT  GC
                                ||||||||  |   |||  |||  ||
                                TGAGACGA G   GTG  CGA  CG
                                    A TA_   AA   AA
GAM1689 SMARCA5  5' AGCCCCGCGGAAGAGCAGA    14588           C__
                                TCTGTTCTTCCGC   GCT
                                ||||||||||||   |||
                                AGACGAGAAGGCG   CGA
                                       CCC
GAM1689 SYNGR1   3' GGCAGAGCGGCAAGGACAGGG  17507         CC      C
                                CTCTGTTCTT  GCCGCTC GCC
                                ||||||||||  |||||||  |||
                                GGGACAGGAA  CGGCGAG CGG
                                      __      A
GAM1689 TRAM     5' AGCAGCTGGGAAGAGCAGA    27451          __ C
                                TCTGTTCTTCC  GC GCT
                                ||||||||||  ||  |||
                                AGACGAGAAGG  CG CGA
                                      GT  A
GAM1689 VAT1     3' AGCAGGGAAGTACAGAGT     22088        T    GCC
                                ACTCTGT CTTCC   GCT
                                |||||||  |||||   |||
                                TGAGACA GAAGG   CGA
                                    T    GA_
GAM1689 CBX1     3' AGCAATGGAAAAGAACAGA    23308         __   CC
                                TCTGTTCT  TCCG  GCT
                                ||||||||  ||||  |||
                                AGACAAGA  AGGT  CGA
                                     AA    AA
GAM1689 CDC14A   5' GGCGGAGCAGCAGCTGCAGCAG 53966    _   TCTTCC  C
                                CT CTGT     GC GCTCCGCC
                                ||  ||||     ||  ||||||||
                                GA GACG     CG CGAGGCGG
                                 C   TCGA__  A
GAM1689 CDC14A   5' GGCGGAGCAGCAGCTGCAGCAG 14786    _   TCTTCC  C
                                CT CTGT     GC GCTCCGCC
                                ||  ||||     ||  ||||||||
                                GA GACG     CG CGAGGCGG
                                 C   TCGA__  A
GAM1689 DKFZp547I224 5' GATGGGGAAAAAACAGAG    39956        C_   G   C
                                CTCTGTT  TTCC CCG TC
                                |||||||  |||| ||| ||
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                                GAGACAA  AAGG GGT AG
                                   AA   _  _
GAM1689  ECE2     3'  GCAGGGAAAAGGAAGAACAGAG 28732          GCCG   C
              T                    ACTCTGTTCTTCC    CTC GC
                                   ||||||||||||    ||| ||
                                   TGAGACAAGAAGG    GGG CG
                                       AAAA   A
GAM1689  FLJ10648 3'  CGAAGCAAACCAAGAACAGAG  36890        CCGCC   C
                                   CTCTGTTCTT     GCT CG
                                   ||||||||||     ||| ||
                                   GAGACAAGAA     CGA GC
                                       CCAAA   A
GAM1689  GRIN3A   3'  GCGGAGCAAGTGCCAAGCAGA  56783      CTTC   C_
                                   TCTGTT    CGC  GCTCCGC
                                   ||||||    |||  |||||||
                                   AGACGA    GTG  CGAGGCG
                                      ACC_   AA
GAM1689  INE1     3'  GCAGGTGTTAGACGAAAGAACA 14757        C  CC__  T  _
              GA                     TCTGTTCTT CG    GC CC GC
                                   |||||||||  ||    ||  ||  ||
                                   AGACAAGAA GC    TG GG CG
                                        A  AGAT  T  A
GAM1689  KIAA0410 3'  GCAGAGCTTAAGAATAGA    29426        CCGCC    C
                                   TCTGTTCTT     GCTC GC
                                   |||||||||     ||||  ||
                                   AGATAAGAA     CGAG CG
                                         TT____    A
GAM1689  KIAA0964 5'  GCGGAACGGCAGAGCGGG    30448        TCC    C
                                   TCTGTTCT   GCCG TCCGC
                                   ||||||||   ||||  |||||
                                   GGGCGAGA   CGGC AGGCG
                                        ____    A
GAM1689  KIAA1218 5'  AGCAGCACAAAAGAAACAGAGT 95958         _   CC__  C
                                   ACTCTGTT CTT    GC GCT
                                   |||||||| |||    ||  |||
                                   TGAGACAA GAA    CG CGA
                                        A   AACA  A
GAM1689  KIAA1322 3'  GGCAGCCGAGAAGAACAGA    73112          _  CC   _
                                   TCTGTTCTTC CG  GCT CC
                                   ||||||||||  ||  |||  ||
                                   AGACAAGAAG GC  CGA GG
                                         A  __   C
GAM1689  KIAA1391 3'  AGTGGAGAAAAACAGAGT    67851        C   CG
                                   ACTCTGTT TTC  CCGCT
                                   ||||||||  |||  |||||
                                   TGAGACAA AAG  GGTGA
                                        A   A_
GAM1689  MGC13251 3'  AGCAGCCATAGAAAGGACAGA  52134         _ C____  C
                                   TCTGTTCTT C    GC GCT
                                   |||||||||  |    ||  |||
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                                AGACAGGAA G    CG CGA
                                     A ATAC  A
GAM1689  MYH7B     3'  GGCGGAGCAGCAGGCCAACA   71058      CTT  _  C
                                TGTT   CC GC GCTCCGCC
                                ||||   || || ||||||||
                                ACAA   GG CG CGAGGCGG
                                  CC_  A  A
GAM1689  NCOA2     3'  GGCAAGGAGAAGAGCAAAGT   22572     C       CG  GCT
                                ACT TGTTCTTC  CC   CC
                                ||| ||||||||  ||   ||
                                TGA ACGAGAAG  GG   GG
                                  A       A_  AAC
GAM1689  PTRF      3'  GGCAGTGGGGAAGACAGAG    64242       T    G    _
                                CTCTGT CTTCC CCGCT CC
                                |||||| ||||| ||||| ||
                                GAGACA GAAGG GGTGA GG
                                   _    _    C
GAM1689  RHOBTB2   3'  AGCAGGAGGAAAAGCAGAGT   61593        C   G  _
                                ACTCTGTT TTCC CC GCT
                                |||||||| |||| || |||
                                TGAGACGA AAGG GG CGA
                                     A   A  A
GAM1689  TAGAP     3'  AGACTGCAAGGAACAGAGT    55099          CC  CG_
                                ACTCTGTTCTT  GC   CT
                                ||||||||||  ||   ||
                                TGAGACAAGGA  CG   GA
                                      A_  TCA
GAM1689  VELI1     3'  AGTGTAAGAAGAATAAAGT    17417     C       CGC
                                ACT TGTTCTTC   CGCT
                                ||| ||||||||   ||||
                                TGA ATAAGAAG   GTGA
                                  A       AAT
GAM1689  LOC145783 5'  GCGGAGCGACGGAGACACAG   77949      TC    C
                                CTGT  TTCCG CGCTCCGC
                                ||||  ||||| ||||||||
                                GACA  GAGGC GCGAGGCG
                                  CA    A
GAM1689  LOC150157 3'  AGCAAATGGAAAAGAACAGA   86020         __   CC_
                                TCTGTTCT  TCCG   GCT
                                ||||||||  ||||   |||
                                AGACAAGA  AGGT   CGA
                                     AA    AAA
GAM1689  LOC151516 5'  GGCGGAGCTTCCAGAACAAAG  81068    C     TCCGCC
                                CT TGTTCT     GCTCCGCC
                                || ||||||     ||||||||
                                GA ACAAGA     CGAGGCGG
                                 A     CCTT__
GAM1689  LOC153769 3'  GGCGGAGCAGCATGAGAAAGA  81807     G    CC  C
                                TCT TTCTT  GC GCTCCGCC
                                ||| |||||  || ||||||||
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                                AGA AAGAG  CG CGAGGCGG
                                  _    TA  A
GAM1689  LOC161734 3'  GATGGGGAAAAAACAGAG    88467       C_   G   C
                                CTCTGTT  TTCC CCG TC
                                |||||||  |||| ||| ||
                                GAGACAA  AAGG GGT AG
                                    AA   _  _
GAM1689  LOC167026 5'  GGCGGAGCGGCGGGCGGA    88620      TCTT
                                TCTGT   CCGCCGCTCCGCC
                                |||||   ||||||||||||
                                AGGCG   GGCGGCGAGGCGG
                                  _____
GAM1689  LOC196890 3'  AGCAAATGGAAAAGAACAGA   91222        __   CC_
                                TCTGTTCT  TCCG   GCT
                                ||||||||  ||||   |||
                                AGACAAGA  AGGT   CGA
                                     AA    AAA
GAM1689  LOC200731 5'  AGCACTGAAGAACAGAGT    91688          CGCC
                                ACTCTGTTCTTC    GCT
                                ||||||||||||    |||
                                TGAGACAAGAAG    CGA
                                       TCA_
GAM1689  LOC221504 5'  CGGAGCGGCGGGGCAGGAG   94020     GTTC
                                CTCT    TTCCGCCGCTCCG
                                ||||    |||||||||||||
                                GAGG    GGGGCGGCGAGGC
                                  AC__
GAM1689  LOC221663 5'  GCAAAGCCCAGAACAGAGT   95462         TCCGCC   CC
                                ACTCTGTTCT     GCT  GC
                                ||||||||||     |||  ||
                                TGAGACAAGA     CGA  CG
                                      CC_____   AA
GAM1689  LOC256310 3'  GGCAGAGCAGCGGGAGCAGGAG 98102      GTT      C    C
                                CTCT   CTTCCGC GCTC GCC
                                ||||   ||||||| |||| |||
                                GAGG   GAGGGCG CGAG CGG
                                  AC_      A    A
GAM1689  LOC51762  3'  GGCCTAGCAAAAGAACAGA   33708         CCGCC   CC
                                TCTGTTCTT    GCT  GCC
                                |||||||||    |||  |||
                                AGACAAGAA    CGA  CGG
                                     AA___   TC
GAM1689  LOC91266  5'  GGCTGAGGAAAAACAGAGT   66024        ___    C
                                ACTCTGT   TCTTC GCC
                                |||||||   ||||| |||
                                TGAGACA   AGGAG CGG
                                    AAA    T
GAM1690  DIAPH2    3'  AGCCTGTTTTGTCAATGTA   23002       C     GT C
                                TACAT GACAAG  G GCT
                                ||||| ||||||  | |||
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                                ATGTA CTGTTT  T CGA
                                   A     TG C
GAM1690  GAPD     3'  AGCCGCACCTTGTCATGTA   10755      C        _
                                TACAT GACAAGGTGCG CT
                                ||||| |||||||||||| ||
                                ATGTA CTGTTCCACGC GA
                                   _         C
GAM1690  HEBP1    3'  GCATCCTTCTCATTGATGTA  32573       C___   _
                                TACATCGA   AAGG TGC
                                ||||||||   |||| |||
                                ATGTAGTT   TTCC ACG
                                     ACTC   T
GAM1690  SLC1A3   3'  AGCATTACTTTGTAGATGTA  16060      G      C_
                                TACATC ACAAGGTG  GCT
                                |||||| ||||||||  |||
                                ATGTAG TGTTTCAT  CGA
                                   A       TA
GAM1690  SLC6A3   3'  AGCGCACCTCGCCGTGTCTTGT 8311     TC   _____
            G                    TACA  GACA    AGGTGCGCT
                                ||||  ||||    |||||||||
                                GTGT  CTGT    TCCACGCGA
                                  T_   GCCGC
GAM1690  ZIC3     3'  AGCATTACACTTGTGAATGTA  14170     CG    _  C_
                                TACAT  ACAAG GTG  GCT
                                |||||  ||||| |||  |||
                                ATGTA  TGTTC CAT  CGA
                                   AG    A   TA
GAM1690  FLJ10925 5'  AGTGCGACTACTCGATGTA   37411       CA  G
                                TACATCGA  AG TGCGCT
                                ||||||||  || ||||||
                                ATGTAGCT  TC GCGTGA
                                     CA  A
GAM1690  KIAA0556 3'  CGCATCTATATGCATCGATGTA 69646       __ ___
                                TACATCGA  CA   AGGTGCG
                                |||||||  ||   |||||||
                                ATGTAGCT  GT   TCTACGC
                                     AC  ATA
GAM1690  KIAA1058 3'  AGCGCATCCCTGTCATGTA   83135     C   A  _
                                TACAT GACA GG TGCGCT
                                ||||| |||| || ||||||
                                ATGTA CTGT CC ACGCGA
                                   _   C  T
GAM1690  KIAA1677 3'  AGTGTTCTTTGTCGATGTA   67662          T
                                TACATCGACAAGG GCGCT
                                |||||||||||| |||||
                                ATGTAGCTGTTTC TGTGA
                                        T
GAM1690  PLU-1    3'  AGCGATTGATTGATGTA     22770       CAA  G
                                TACATCGA   GGT CGCT
                                ||||||||   ||| ||||
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                                ATGTAGTT  TTA GCGA
                                    AG_  _
GAM1690  PLU-1     3'  AGCGATTGATTGATGTA     88805        CAA  G
                                TACATCGA  GGT CGCT
                                ||||||||  ||| ||||
                                ATGTAGTT  TTA GCGA
                                    AG_  _
GAM1690  LOC136345 3'  AGCAGTGAAGGTTGATGTA   76709         AAGG  _
                                TACATCGAC   TGC GCT
                                |||||||||   ||| |||
                                ATGTAGTTG   GTG CGA
                                     GAA_  A
GAM1690  LOC149664 3'  GGTGTCCTGTCGAGTGTA    80288     _    A  T
                                TACA TCGACA GG GCGCT
                                |||| |||||| || |||||
                                ATGT AGCTGT CC TGTGG
                                  G     _ _
GAM1690  LOC155032 5'  AGCAGTGAAGGTTGATGTA   87589         AAGG  _
                                TACATCGAC   TGC GCT
                                |||||||||   ||| |||
                                ATGTAGTTG   GTG CGA
                                     GAA_  A
GAM1690  LOC197196 3'  AGTGTGTGCTTGTCGATGTA  91295          _ TG
                                TACATCGACAAG G  CGCT
                                ||||||||||||  |  ||||
                                ATGTAGCTGTTC T  GTGA
                                       G GT
GAM1690  LOC221929 3'  AGTCCGGCCTTGTCAATG    94233     C      _ C
                                CAT GACAAGGT G GCT
                                |||  |||||||  | |||
                                GTA CTGTTCCG C TGA
                                  A       G C
GAM1691  CDC42     3'  GGAAGTTAATTTCTAACTTCTT 10141      A     TTGGC
                                AAGAA TTAGAG    ACTTCC
                                |||||  ||||||    ||||||
                                TTCTT AATCTT    TGAAGG
                                   C     TAAT_
GAM1691  GPR81     3'  GCCAACTCTAGCTCCTTT    51751      AAA
                                AAAG   TTAGAGTTGGC
                                ||||   ||||||||||
                                TTTC   GATCTCAACCG
                                  CTC
GAM1691  HDAC5     3'  GAAATGCCTTAATTTC      58298        AGTT   C
                                GAAATTAG    GGCA TTC
                                ||||||||    |||| |||
                                CTTTAATT    CCGT AAG
                                     ____   A
GAM1691  KRTHB1    3'  GAAGTGCTCAGCTACTTCTCC  11244   A   ATTAG   _
                                A AGAA     AGTTG GCACTTC
                                | ||||     ||||| |||||||
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                                C TCTT    TCGAC CGTGAAG
                                 C   CA___    T
GAM1691  NIPSNAP1  3'  GAAGTAGTTTCTGATTTC    14659        TTG  _
                                GAAATTAGAG   GC ACTTC
                                ||||||||||   || |||||
                                CTTTAGTCTT   TG TGAAG
                                     ___  A
GAM1691  PIP5K1A   3'  GGAACCGGACTCTTAATTTC   14519      _   _ CAC
                                GAAATTA GAGTT GG   TTCC
                                |||||||  ||||| ||   ||||
                                CTTTAAT CTCAG CC   AAGG
                                    T    G  ___
GAM1691  PRCP      3'  GGAAGTGAGAGCCATTTCTTT  18530      TAGA   GG
                                AAAGAAAT   GTT  CACTTCC
                                ||||||||   |||  |||||||
                                TTTCTTTA   CGA  GTGAAGG
                                     C___   GA
GAM1691  WHSC1     3'  AGTTCAGACTCTAACTTCTCC  30577   A   A      GGC
                                A AGAA TTAGAGTT   ACT
                                | |||| ||||||||   |||
                                C TCTT AATCTCAG   TGA
                                 C   C       ACT
GAM1691  WHSC1     3'  AGTTCAGACTCTAACTTCTCC  56664   A   A      GGC
                                A AGAA TTAGAGTT   ACT
                                | |||| ||||||||   |||
                                C TCTT AATCTCAG   TGA
                                 C   C       ACT
GAM1691  WHSC1     3'  AGTTCAGACTCTAACTTCTCC  56675   A   A      GGC
                                A AGAA TTAGAGTT   ACT
                                | |||| ||||||||   |||
                                C TCTT AATCTCAG   TGA
                                 C   C       ACT
GAM1691  BM-002    3'  GTGATCTGTAATTTCTTT    34009        G  TTGG
                                AAAGAAATTA AG    CAC
                                |||||||||| ||    |||
                                TTTCTTTAAT TC    GTG
                                     G  TA__
GAM1691  DD96      3'  GGAAATGGCCCTAATTTCT   20464       AGTT   AC_
                                AGAAATTAG    GGC   TTCC
                                |||||||||    |||   ||||
                                TCTTTAATC    CCG   AAGG
                                     _____   GTA
GAM1691  DIS3      3'  GGAAACCTGTTTAATTTCTTT  30920         GTT  CAC
                                AAAGAAATTAGA   GG   TTCC
                                ||||||||||||   ||   ||||
                                TTTCTTTAATTT   CC   AAGG
                                     GT_  A__
GAM1691  DKFZp762A227 3'  GGAAGTGTGTCAACTATTTCTT 26883        TAG    __
            T                    AAAGAAAT   AGTTG  GCACTTCC
                                 ||||||||   |||||  ||||||||
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                                TTTCTTTA  TCAAC  TGTGAAGG
                                   ___    TG
GAM1691  DKFZp762A227 3'  GGAAGTGTGTCAACTATTTCTT 34699       TAG   __
           T                    AAAGAAAT  AGTTG  GCACTTCC
                                |||||||| |||||  ||||||||
                                TTTCTTTA  TCAAC  TGTGAAGG
                                   ___    TG
GAM1691  FLJ10330 3'  GGAAGTGCCTTTGTAATT   36509     G  TT
                                AATTA AG  GGCACTTCC
                                ||||| ||  |||||||||
                                TTAAT TT  CCGTGAAGG
                                  G  T_
GAM1691  FLJ22548 3'  GAAGTACCATGATTTCTTT   42633       GAGT  C
                                AAAGAAATTA   TGG ACTTC
                                ||||||||||   ||| |||||
                                TTTCTTTAGT   ACC TGAAG
                                    ____  A
GAM1691  JAM1    3'  GGAAGTGCCACTGGGATCCCTC 34233    A__  AG  T
           T                    AGA  ATT  AGT GGCACTTCC
                                |||  |||  ||| |||||||||
                                TCT  TAG  TCA CCGTGAAGG
                                  CCC  GG  _
GAM1691  JAM1    3'  GGAAGTGCCACTGGGATCCCTC 58498    A__  AG  T
           T                    AGA  ATT  AGT GGCACTTCC
                                |||  |||  ||| |||||||||
                                TCT  TAG  TCA CCGTGAAGG
                                  CCC  GG  _
GAM1691  JAM1    3'  GGAAGTGCCACTGGGATCCCTC 58519    A__  AG  T
           T                    AGA  ATT  AGT GGCACTTCC
                                |||  |||  ||| |||||||||
                                TCT  TAG  TCA CCGTGAAGG
                                  CCC  GG  _
GAM1691  JAM1    3'  GGAAGTGCCACTGGGATCCCTC 58547    A__  AG  T
           T                    AGA  ATT  AGT GGCACTTCC
                                |||  |||  ||| |||||||||
                                TCT  TAG  TCA CCGTGAAGG
                                  CCC  GG  _
GAM1691  JAM1    3'  GGAAGTGCCACTGGGATCCCTC 58576    A__  AG  T
           T                    AGA  ATT  AGT GGCACTTCC
                                |||  |||  ||| |||||||||
                                TCT  TAG  TCA CCGTGAAGG
                                  CCC  GG  _
GAM1691  KIAA0335 3'  GAAGTACCTTGATTTAATTTTT 29671        GTT_  C
           T                    AAGAAATTAGA   GG ACTTC
                                ||||||||||   || |||||
                                TTTTTTAATTT   CC TGAAG
                                     AGTT  A
GAM1691  KIAA1354 3'  GAAGTGCATCCTAATCCTTT  61575     AA   AGTTG
                                AAAG  ATTAG   GCACTTC
                                ||||  |||||   |||||||
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                                TTTC  TAATC    CGTGAAG
                                  C_    CTA__
GAM1691  MRPS10   3'  GAAGTGCTTCATTTTCTTT   36819       TTA  GTT
                                AAAGAAA   GA   GGCACTTC
                                |||||||   ||   ||||||||
                                TTTCTTT   CT   TCGTGAAG
                                   TA_  ___
GAM1691  MSTP031  5'  AGGTGGCTCTAAATTC     50166     A      TGG
                                GAA TTAGAGT   CACTT
                                ||| |||||||   |||||
                                CTT AATCTCG   GTGGA
                                  A     ___
GAM1691  MUF1     5'  AAGTGTGCTAATTTCTT     97240          AGTTG
                                AAGAAATTAG    GCACTT
                                ||||||||||    ||||||
                                TTCTTTAATC    TGTGAA
                                      G____
GAM1691  PEG10    3'  AAATGCTGATTTCTTT      31195         AGAGTT    C
                                AAAGAAATT     GGCA TT
                                |||||||||     |||| ||
                                TTTCTTTAG     TCGT AA
                                      _______   A
GAM1691  R3HDM    3'  GGAAATGCCATTCAAATGCCTC 31717    A  AA   A    T    C
           C                     A AG  ATT GAGT GGCA TTCC
                                | ||  ||| |||| |||| ||||
                                C TC  TAA CTTA CCGT AAGG
                                 C  CG   A    _    A
GAM1691  SH3BGRL2 3'  AAGTACCAAAGCTTCTTTCT   49674      TT  AG    C
                                AGAAA  AG  TTGG ACTT
                                |||||  ||  |||| ||||
                                TCTTT  TC  AACC TGAA
                                   CT  GA    A
GAM1691  LOC144584 5'  GAAATGCCAGAAGATTTTTT   67588        AGAG     C
                                AAGAAATT    TTGGCA TTC
                                ||||||||    |||||| |||
                                TTTTTTAG    GACCGT AAG
                                     AA__     A
GAM1691  LOC197125 3'  GGAAGCTGGTTCTACCTCTT   89242     AAT    TT   AC
                                AAGA   TAGAG  GGC  TTCC
                                ||||   |||||  |||  ||||
                                TTCT   ATCTT  TCG  AAGG
                                  CC_    GG   __
GAM1691  LOC203232 5'  GAACTGGCAACTCTAATTT    71918          G  C
                                AAATTAGAGTTG CA TTC
                                |||||||||||| || |||
                                TTTAATCTCAAC GT AAG
                                       G  C
GAM1691  LOC222224 3'  GGAAGTGCTGAATATTCTCTTT 95873       _   TAGAG TG
                                AAAGA AAT     T  GCACTTCC
                                ||||| |||     |  ||||||||
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                                TTTCT TTA    A  CGTGAAGG
                                  C   TA___ GT
GAM1691  LOC253890 5'  GAAGTGCTCTAACTTTTCT   97384     ATTA    __
                                AGAA   GAGTT  GGCACTTC
                                ||||   |||||  ||||||||
                                TCTT   TTCAA  TCGTGAAG
                                  ____    TC
GAM1691  LOC254428 3'  GGAAACACAGCTCTAACCTC   97197    AA       GCAC
                                GA  TTAGAGTTG   TTCC
                                ||  |||||||||   ||||
                                CT  AATCTCGAC   AAGG
                                 CC       ACA_
GAM1691  LOC256308 3'  TGCAACTCTAATTCTCTT    97546     _        G
                                AAGA AATTAGAGTTG CA
                                |||| |||||||||| ||
                                TTCT TTAATCTCAAC GT
                                  C        _
GAM1691  LOC51696  3'  AAGTGCTAAGTTTCT      33073      TAGAG
                                AGAAAT    TTGGCACTT
                                ||||||    |||||||||
                                TCTTTG    AATCGTGAA
                                  _____
GAM1691  LOC90538  3'  AAGTGGAACCCTAATTTCTCC  63891   A       A   GG
                                A AGAAATTAG GTT  CACTT
                                | |||||||| |||  |||||
                                C TCTTTAATC CAA  GTGAA
                                 C       C   G_
GAM1692  AQP6     3'  AGCTGCTTCTGACCCTGCA   54982    C  TAG  C
                                TGC AG   CG AAGCAGCT
                                ||| ||   || ||||||||
                                ACG TC   GT TTCGTCGA
                                  _  CCA  C
GAM1692  BMP1     3'  AGCCGCCTGTGCTGGTA    21526     GTA    A  A
                                TGCCA   GCGCA GC GCT
                                |||||   ||||| || |||
                                ATGGT   CGTGT CG CGA
                                   ___    C  C
GAM1692  CCBP2    5'  AGCTGCTATTGAACACGGCA   8932     A  AG_  CA
                                TGCC GT   CG  AGCAGCT
                                |||| ||   ||  |||||||
                                ACGG CA   GT  TCGTCGA
                                  _  CAA  TA
GAM1692  FAAH     3'  AGCTGCTTGCTTTAGG     44449    AG   C
                                CC  TAG GCAAGCAGCT
                                ||  ||| ||||||||||
                                GG  ATT CGTTCGTCGA
                                 __   T
GAM1692  FCMD     3'  AGCTGCTTGGTGGGACAGC   23023    CA  AG   _
                                GC  GT  CGC AAGCAGCT
                                ||  ||  ||| ||||||||
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                                CG  CA  GTG TTCGTCGA
                                 A_  GG   G
GAM1692 HSPB3    5' AGCTGCTTCAACTGGTA    21949       AGCGC
                                TGCCAGT    AAGCAGCT
                                |||||||    ||||||||
                                ATGGTCA    TTCGTCGA
                                   AC___
GAM1692 LDB3     3' AGCTGCTCCTGCTGCTGGCA  76923         CA
                                TGCCAGTAGCG  AGCAGCT
                                ||||||||||  |||||||
                                ACGGTCGTCGT  TCGTCGA
                                      CC
GAM1692 MAPK14   3' AGCTGCTTGTGGGCCCGG    8974    A_ AG
                                CC  GT  CGCAAGCAGCT
                                ||  ||  ||||||||||
                                GG  CG  GTGTTCGTCGA
                                 CC  G_
GAM1692 MAPK14   3' AGCTGCTTGTGGGCCCGG    58123   A_ AG
                                CC  GT  CGCAAGCAGCT
                                ||  ||  ||||||||||
                                GG  CG  GTGTTCGTCGA
                                 CC  G_
GAM1692 MAPK14   3' AGCTGCTTGTGGGCCCGG    58129   A_ AG
                                CC  GT  CGCAAGCAGCT
                                ||  ||  ||||||||||
                                GG  CG  GTGTTCGTCGA
                                 CC  G_
GAM1692 PTPRD    5' AGCTGCTCGCGCACGCTGCTGC 56113   C     ____ A
           CA                    TG CAGTAGC   GC AGCAGCT
                                || |||||||   || |||||||
                                AC GTCGTCG   CG TCGTCGA
                                 C     CACG  C
GAM1692 PTPRD    5' AGCTGCTCGCGCACGCTGCTGC 56114   C     ____ A
           CA                    TG CAGTAGC   GC AGCAGCT
                                || |||||||   || |||||||
                                AC GTCGTCG   CG TCGTCGA
                                 C     CACG  C
GAM1692 PTPRD    5' AGCTGCTCGCGCACGCTGCTGC 56115   C     ____ A
           CA                    TG CAGTAGC   GC AGCAGCT
                                || |||||||   || |||||||
                                AC GTCGTCG   CG TCGTCGA
                                 C     CACG  C
GAM1692 PTPRD    5' AGCTGCTCGCGCACGCTGCTGC 12604   C     ____ A
           CA                    TG CAGTAGC   GC AGCAGCT
                                || |||||||   || |||||||
                                AC GTCGTCG   CG TCGTCGA
                                 C     CACG  C
GAM1692 PVT1     3' AGCTGCTTGGCACGTGGC    66174    _ A  G
                                GCCA GT GC CAAGCAGCT
                                |||| || || |||||||||
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                                CGGT CA CG GTTCGTCGA
                                  G  _  _
GAM1692 UBE4A    3'  AGCTTAAGGCCACTACTGGTA  17729         C_  AAGC
                                TGCCAGTAG  GC   AGCT
                                |||||||||  ||   ||||
                                ATGGTCATC  CG   TCGA
                                     AC  GAAT
GAM1692 BAG4     3'  AGCTGCTTCTTACCAGCA    18046     CA   CGC
                                TGC  GTAG   AAGCAGCT
                                |||  ||||   ||||||||
                                ACG  CATT   TTCGTCGA
                                  AC   C__
GAM1692 DKFZP564G092 5'  AGCTGCTTCCTCTGGTA     32153       T  CGC
                                TGCCAG AG   AAGCAGCT
                                ||||||  ||  ||||||||
                                ATGGTC TC   TTCGTCGA
                                   _  C__
GAM1692 FLJ12572  3'  AGCTGCTTGGTGTTCTAC    43540      __  _
                                GTAG  CGC AAGCAGCT
                                ||||  ||| ||||||||
                                CATC  GTG TTCGTCGA
                                  TT   G
GAM1692 FLJ13725  5'  AGCTGCTTCTTCTGTCA     68827    C   T  CGC
                                TG CAG AG   AAGCAGCT
                                ||  ||| ||  ||||||||
                                AC GTC TC   TTCGTCGA
                                 T   T  ____
GAM1692 FLJ20548  3'  CTGTGCTCTGCTGGCA      35818         C  AA
                                TGCCAGTAG GC  GCAG
                                |||||||||  ||  ||||
                                ACGGTCGTC CG  TGTC
                                     T  __
GAM1692 HSPC155   3'  AGCTGCTTCCTCTGGTA     33519       T  CGC
                                TGCCAG AG   AAGCAGCT
                                ||||||  ||  ||||||||
                                ATGGTC TC   TTCGTCGA
                                   _  C__
GAM1692 ILF2      3'  AGCTGCCTGCTACTGG      67486         CAA
                                CCAGTAGCG   GCAGCT
                                |||||||||   ||||||
                                GGTCATCGT   CGTCGA
                                     C__
GAM1692 KIAA0937  3'  AGCTGCTTGCTGTTAGGC    93221     AG   _
                                GCC  TAGC GCAAGCAGCT
                                |||  |||| ||||||||||
                                CGG  ATTG CGTTCGTCGA
                                  __   T
GAM1692 KIAA0964  5'  AGCTGCTTCCTGCCGGCA    30445      A   CGC
                                TGCC GTAG   AAGCAGCT
                                ||||  ||||  ||||||||
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                                ACGG CGTC   TTCGTCGA
                                  C   C__
GAM1692 KIAA1023 3' AGCTGTGGGGGCTGCTGGCA  34673        GCAA
                                TGCCAGTAGC   GCAGCT
                                ||||||||||   ||||||
                                ACGGTCGTCG   TGTCGA
                                     GGGG
GAM1692 KIAA1032 3' AGCTGCTTGAGACTTGGC    66720    _ AGCG
                                GCCA GT   CAAGCAGCT
                                |||| ||   |||||||||
                                CGGT CA   GTTCGTCGA
                                  T  GA__
GAM1692 KIAA1160 3' AGCTGGGCGTACTGGCA     40750       G  AAG
                                TGCCAGTA CGC   CAGCT
                                |||||||| |||   |||||
                                ACGGTCAT GCG   GTCGA
                                    _  G__
GAM1692 KIAA1228 5' AGCTGCCCGGGCTGCTGGC   65666       GCAA
                                GCCAGTAGC   GCAGCT
                                |||||||||   ||||||
                                CGGTCGTCG   CGTCGA
                                     GGCC
GAM1692 MAFB    3' AGCTGCTTTGCTGCCCGG    19587    A_    C
                                CC  GTAGCG AAGCAGCT
                                ||  |||||| ||||||||
                                GG  CGTCGT TTCGTCGA
                                 CC     _
GAM1692 MGC15606 3' AGCTGCTATTCCTACTGGC   59519       CGCA
                                GCCAGTAG   AGCAGCT
                                ||||||||   |||||||
                                CGGTCATC   TCGTCGA
                                    CTTA
GAM1692 MGC23427 3' AGCTGCTTGCATGCGTTACT  58973        ____
                                AGTAGCGCA   AGCAGCT
                                |||||||||   |||||||
                                TCATTGCGT   TCGTCGA
                                     ACGT
GAM1692 MGC5508  3' AGCTGCTTCGGGGCCATGCA  44263    CA_  AG  C
                                TGC   GT  CG AAGCAGCT
                                |||   ||  || ||||||||
                                ACG   CG  GC TTCGTCGA
                                  TAC  GG  _
GAM1692 NTSR2    3' AGCTGCTTAGTCACCTGGCA  25632      TA_  GC
                                TGCCAG   GC  AAGCAGCT
                                ||||||   ||  ||||||||
                                ACGGTC   TG  TTCGTCGA
                                   CAC  A_
GAM1692 PEX16    3' AGCTGCTTGCCTCGGCA     55156     AGT  C
                                TGCC   AG GCAAGCAGCT
                                ||||   || ||||||||||
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                                ACGG   TC CGTTCGTCGA
                                  C__  _
GAM1692  phorbolin-1 3'  AGCCGAGATTGCGCTACTGCA  90202     C        GCA__
                                TGC AGTAGCGCAA     GCT
                                ||| ||||||||||     |||
                                ACG TCATCGCGTT     CGA
                                  _         AGAGC
GAM1692  SEMA4F    3'  AGCTGCTTTCTCTGGC      16205       T  CGC
                                GCCAG AG   AAGCAGCT
                                ||||| ||   ||||||||
                                CGGTC TC   TTCGTCGA
                                   _ T__
GAM1692  VPS4B     3'  AGCTGAGATCGCGCTACTGCA  18017     C       AAG__
                                TGC AGTAGCGC     CAGCT
                                ||| ||||||||     |||||
                                ACG TCATCGCG     GTCGA
                                  _       CTAGA
GAM1692  LOC126520 5'  AGCGGCCTGCGCTACCTGCA   75023     CA       A  A
                                TGC  GTAGCGCA GC GCT
                                |||  |||||||| || |||
                                ACG  CATCGCGT CG CGA
                                  TC       C  G
GAM1692  LOC128272 3'  AGCTGCTCCTGCTGGCA     75239          CGCA
                                TGCCAGTAG    AGCAGCT
                                |||||||||    |||||||
                                ACGGTCGTC    TCGTCGA
                                     C___
GAM1692  LOC130074 3'  AGCTGCTTGGGTGCAGC     76622     CA   G G
                                GC  GTA C CAAGCAGCT
                                ||  ||| | |||||||||
                                CG  CGT G GTTCGTCGA
                                 A_   _ G
GAM1692  LOC145757 5'  AGCTGGGCCCTGCTGGCA     77914          C  AAG
                                TGCCAGTAG GC   CAGCT
                                ||||||||| ||   |||||
                                ACGGTCGTC CG   GTCGA
                                     C  G__
GAM1692  LOC149670 5'  AGCTGCTTGTCCTGGCA     80301        TAGC
                                TGCCAG    GCAAGCAGCT
                                ||||||    ||||||||||
                                ACGGTC    TGTTCGTCGA
                                   C___
GAM1692  LOC154282 5'  AGCTGCTTGCCAGTGTGCA   87399     _  GTAGC
                                TGC CA     GCAAGCAGCT
                                ||| ||     ||||||||||
                                ACG GT     CGTTCGTCGA
                                  T  GAC__
GAM1692  LOC159053 3'  AGCTGAGATCACGCTACTGCA  88359     C      CAAG__
                                TGC AGTAGCG      CAGCT
                                ||| |||||||      |||||
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                                ACG TCATCGC     GTCGA
                                  _     ACTAGA
GAM1692  LOC196738 3'  AGCTGCTTCTATCATAGCA   88884    CA__   CGC
                                TGC   GTAG   AAGCAGCT
                                |||   ||||   ||||||||
                                ACG   TATC   TTCGTCGA
                                  ATAC   ___
GAM1692  LOC203350 3'  AGCTGTGATCGCGCTACTGCA  92228    C      AA__
                                TGC AGTAGCGC   GCAGCT
                                ||| ||||||||   ||||||
                                ACG TCATCGCG   TGTCGA
                                  _      CTAG
GAM1692  LOC203504 3'  AGCTGCTTCCCTACTGG     92316       CGC
                                CCAGTAG   AAGCAGCT
                                |||||||   ||||||||
                                GGTCATC   TTCGTCGA
                                    CC_
GAM1692  LOC221103 5'  AGCTGCTTCTCTTGGCA     94869      T  CGC
                                TGCCAG AG   AAGCAGCT
                                |||||| ||   ||||||||
                                ACGGTT TC   TTCGTCGA
                                   C  ___
GAM1692  LOC90183  3'  AGCTGCTTTGCTGCCCGG    62402    A_     C
                                CC  GTAGCG AAGCAGCT
                                ||  |||||| ||||||||
                                GG  CGTCGT TTCGTCGA
                                 CC     _
GAM1692  LOC91750  3'  AGCTGCTTGCGGACAGG     67645    A  AG
                                CC GT  CGCAAGCAGCT
                                || ||  ||||||||||
                                GG CA  GCGTTCGTCGA
                                 A  G_
GAM1693  DCTN4     3'  GTAATATATGTGATGCAGTG   68395      _  T
                                CACTG ATT TATATATTAC
                                ||||| ||| ||||||||||
                                GTGAC TAG GTATATAATG
                                   G   T
GAM1693  FER1L4    3'  GGTAATAAGATCAGT       48129          ATAT
                                ACTGATTTTAT    TACC
                                ||||||||||    ||||
                                TGACTAGAATA    ATGG
                                      ____
GAM1693  LOC145660 3'  ACAGGGTGACTAAAGTCA    77840        TATA     C
                                TGATTTTA    TTACCC GT
                                ||||||||    |||||| ||
                                ACTGAAAT    AGTGGG CA
                                    C___      A
GAM1693  LOC202460 5'  GATATACAAAAATCAGTG    90672          A_
                                CACTGATTTT  TATATT
                                ||||||||||  ||||||
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                                GTGACTAAAA  ATATAG
                                      AC
GAM1694  ADCY1    5'  ATCCCAGTGCACAGCCCAGGAG 94337      CAGA  A  G TG
                                CTCC    CT GT G  CTGGGAT
                                ||||    || || |  |||||||
                                GAGG    GA CA C  GACCCTA
                                  ACCC  _  _ GT
GAM1694  ANKH     3'  CCCAACACTTTGGGAG      55066        ACTAGT    C
                                CTCCCAG     GGTG TGGG
                                |||||||     |||| ||||
                                GAGGGTT     TCAC ACCC
                                   _______   A
GAM1694  EN1      5'  CCCTCACTACTGCCTAGGA   9248      C  AC       CT
                                TCC AG  TAGTGGTG  GGG
                                ||| ||  ||||||||  |||
                                AGG TC  GTCATCAC  CCC
                                  A  C_       T_
GAM1694  IL13RA1  3'  CCCAGCAATTTGGGAG      9568         CTAGTGG
                                CTCCCAGA      TGCTGGG
                                ||||||||      |||||||
                                GAGGGTTT      ACGACCC
                                    A_______
GAM1694  MKI67    3'  ATCCCAGTGACCAGCCACAGGA 11589      CAGACTAG   _
           G                     CTCC       TGGT GCTGGGAT
                                ||||       |||| ||||||||
                                GAGG       ACCA TGACCCTA
                                  ACACCG__    G
GAM1694  NFKBIL2  3'  CCCAACACTTTGGGAG      26448        ACTAGT    C
                                CTCCCAG     GGTG TGGG
                                |||||||     |||| ||||
                                GAGGGTT     TCAC ACCC
                                   _______   A
GAM1694  NPHP1    3'  CCCAACACTTTGGGAG      63141        ACTAGT    C
                                CTCCCAG     GGTG TGGG
                                |||||||     |||| ||||
                                GAGGGTT     TCAC ACCC
                                   _______   A
GAM1694  PPP1R12B 3'  CCCAGCACTTCAGGAG      50382      CA  CTAGT
                                CTCC  GA    GGTGCTGGG
                                ||||  ||    |||||||||
                                GAGG  CT    TCACGACCC
                                  A_  ______
GAM1694  RFC2     3'  CCCAACACTTTGGGAG      12840        ACTAGT    C
                                CTCCCAG     GGTG TGGG
                                |||||||     |||| ||||
                                GAGGGTT     TCAC ACCC
                                   _______   A
GAM1694  RFNG     3'  CCCAGCACTTGCGCACCTGGGA 89559        ACTA   _
                                TCCCAG    GTG GTGCTGGG
                                ||||||    ||| ||||||||
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                              AGGGTC   CGT CACGACCC
                                 CACG  T
GAM1694 RFP     3' ATCCCAGTTTTCCGTCTGGGA 22507       TAGT T__
                              TCCCAGAC   GG  GCTGGGAT
                              ||||||||   ||  ||||||||
                              AGGGTCTG   CC  TGACCCTA
                                 ____ TTT
GAM1694 TCTA    3' CCCAACACTTTGGGAG     42491       ACTAGT   C
                              CTCCCAG    GGTG TGGG
                              |||||||    |||| ||||
                              GAGGGTT    TCAC ACCC
                                 _______  A
GAM1694 TNFSF15 3' CCCAACACTTTGGGAG     18865       ACTAGT   C
                              CTCCCAG    GGTG TGGG
                              |||||||    |||| ||||
                              GAGGGTT    TCAC ACCC
                                 _______  A
GAM1694 TPM4    3' CCCAACACTTTGGGAG     13831       ACTAGT   C
                              CTCCCAG    GGTG TGGG
                              |||||||    |||| ||||
                              GAGGGTT    TCAC ACCC
                                 _______  A
GAM1694 TSN     3' CCCAGCACACTGGGAG     17298       ACTAGTG
                              CTCCCAG    GTGCTGGG
                              |||||||    ||||||||
                              GAGGGTC    CACGACCC
                                 A_______
GAM1694 WHSC1   3' CCCAGCACGTGGGTCTAAAGAG 30581    CC_   AGTG
                              CTC  AGACT  GTGCTGGG
                              |||  |||||  ||||||||
                              GAG  TCTGG  CACGACCC
                                AAA   GTG_
GAM1694 WHSC1   3' CCCAGCACGTGGGTCTAAAGAG 56668    CC_   AGTG
                              CTC  AGACT  GTGCTGGG
                              |||  |||||  ||||||||
                              GAG  TCTGG  CACGACCC
                                AAA   GTG_
GAM1694 WHSC1   3' CCCAGCACGTGGGTCTAAAGAG 56679    CC_   AGTG
                              CTC  AGACT  GTGCTGGG
                              |||  |||||  ||||||||
                              GAG  TCTGG  CACGACCC
                                AAA   GTG_
GAM1694 WNT5B   3' ATCCTGGCCACTAGGCCAAGAG 51959    CCAGA    GT  TG
                              CTC   CTAGTG  GC  GGAT
                              |||   ||||||  ||  ||||
                              GAG   GATCAC  CG  CCTA
                                AACCG    __  GT
GAM1694 WNT5B   3' ATCCTGGCCACTAGGCCAAGAG 48524    CCAGA    GT  TG
                              CTC   CTAGTG  GC  GGAT
                              |||   ||||||  ||  ||||
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                                GAG    GATCAC  CG  CCTA
                                  AACCG     __  GT
GAM1694  ACAA2    5'  ATCCCAGCGTGTCTCAATCTGG 93422      CT_  TGG
                                CCAGA   AG   TGCTGGGAT
                                ||||||  ||  |||||||||
                                GGTCT   TC   GCGACCCTA
                                   AAC  TGT
GAM1694  C20orf175 3'  CCCAACACTTTGGGAG      55923       ACTAGT    C
                                CTCCCAG     GGTG TGGG
                                |||||||     |||| ||||
                                GAGGGTT     TCAC ACCC
                                   _______   A
GAM1694  C5orf6   3'  CCCAGCACTGCTGTTGGGA   33949       AC   TG
                                TCCCAG  TAG  GTGCTGGG
                                ||||||  |||  ||||||||
                                AGGGTT  GTC  CACGACCC
                                   __   GT
GAM1694  C8orf13   3'  CCCAGGGTGACAGCCTGGGAG  82473       A  A  GG G
                                CTCCCAG CT GT  T CTGGG
                                ||||||| || ||  | |||||
                                GAGGGTC GA CA  G GACCC
                                    C  _  GT G
GAM1694  CG012    5'  CCCAACACTTTGGGAG      84151       ACTAGT    C
                                CTCCCAG     GGTG TGGG
                                |||||||     |||| ||||
                                GAGGGTT     TCAC ACCC
                                   _______   A
GAM1694  DKFZP564M182 3'  ATCCCAGCACACCTCGTGGGA  78616      _  CTA   G
                                TCCCA GA   GTG TGCTGGGAT
                                ||||| ||   ||| |||||||||
                                AGGGT CT   CAC ACGACCCTA
                                   G  C__   _
GAM1694  DKFZP586J1624 3'  ATCCCAGCACACAGGCCTGGG  32042      A  A   G
                                CCCAG CT GTG TGCTGGGAT
                                ||||| || ||| |||||||||
                                GGGTC GG CAC ACGACCCTA
                                   C  A  _
GAM1694  DKFZp761N0624 3'  ATCCCAGATTTGTTGTCTGGGA 51159        T  TG TG
                                TCCCAGAC AG  G  CTGGGAT
                                ||||||| ||  |  |||||||
                                AGGGTCTG TT  T  GACCCTA
                                    _  GT TA
GAM1694  FADS1    3'  TCCCAACACTTTTGGGAG    26388        CTAGT    C
                                CTCCCAGA    GGTG TGGGA
                                ||||||||    |||| |||||
                                GAGGGTTT    TCAC ACCCT
                                   ______   A
GAM1694  FBXO26   3'  CCCAGCACTTCAGGAG     46625     CA  CTAGT
                                CTCC  GA    GGTGCTGGG
                                ||||  ||    |||||||||
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                              GAGG  CT    TCACGACCC
                                A_ _____
GAM1694  FLJ10460  3'  CCCAACACTTTGGGAG     36613       ACTAGT   C
                              CTCCCAG     GGTG TGGG
                              |||||||     |||| ||||
                              GAGGGTT     TCAC ACCC
                                 _______  A
GAM1694  FLJ12761  3'  TCAGTGTCCACCAGTTGGA   44925     CA   A   _
                              TCC  GACT GTGG TGCTGG
                              |||  |||| |||| ||||||
                              AGG  TTGA CACC GTGACT
                                __   C   T
GAM1694  FLJ13193  3'  CCCAACACTTTGGGAG     50715       ACTAGT   C
                              CTCCCAG     GGTG TGGG
                              |||||||     |||| ||||
                              GAGGGTT     TCAC ACCC
                                 _______  A
GAM1694  FLJ14326  3'  CCCAGCAATTTGGGAG     50765        CTAGTGG
                              CTCCCAGA      TGCTGGG
                              ||||||||      |||||||
                              GAGGGTTT      ACGACCC
                                 A_______
GAM1694  FLJ14525  3'  ATCCCAGTTGGCACAGCCTGGG 52477      A  A   GT_
                              CCCAG CT GTG   GCTGGGAT
                              ||||| || |||   ||||||||
                              GGGTC GA CAC   TGACCCTA
                                 C  _   GGT
GAM1694  FLJ20139  3'  CCCAACACTTTGGGAG     35115       ACTAGT   C
                              CTCCCAG     GGTG TGGG
                              |||||||     |||| ||||
                              GAGGGTT     TCAC ACCC
                                 _______  A
GAM1694  FLJ21240  3'  CCCAACACTTTGGGAG     46262       ACTAGT   C
                              CTCCCAG     GGTG TGGG
                              |||||||     |||| ||||
                              GAGGGTT     TCAC ACCC
                                 _______  A
GAM1694  FLJ21657  3'  CCCAACACTTTGGGAG     42796       ACTAGT   C
                              CTCCCAG     GGTG TGGG
                              |||||||     |||| ||||
                              GAGGGTT     TCAC ACCC
                                 _______  A
GAM1694  FLJ22615  3'  CCCATCCTAATCTGGGAG    69037        C   T   CT
                              CTCCCAGA TAG GGTG  GG
                              |||||||| ||| ||||  ||
                              GAGGGTCT ATC CTAC  CC
                                 A  _   __
GAM1694  FLJ22944  3'  CCCACCACTAATTTGAGA    47868    C   C       CT
                              TC CAGA TAGTGGTG  GG
                              || |||| ||||||||  ||
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                                AG GTTT ATCACCAC  CC
                                 A   A      __
GAM1694  GNB4     3'  CCCAGCAATTTGGGAG      41566        CTAGTGG
                                CTCCCAGA      TGCTGGG
                                ||||||||      |||||||
                                GAGGGTTT      ACGACCC
                                    A_______
GAM1694  GPT2     3'  TCCAGGCACCACCTGAGA    56771    C   ACTA      G
                                TC CAG    GTGGTGCT GGA
                                || |||    |||||||| |||
                                AG GTC    CACCACGG CCT
                                 A  _____       A
GAM1694  HSPC171  3'  CCCAGCACCAGAGCACAATGAG 27199     CCAGA_  AG
                                CTC     CT  TGGTGCTGGG
                                |||     ||  ||||||||||
                                GAG     GA  ACCACGACCC
                                  TAACAC  G_
GAM1694  KIAA0420 3'  CCCAACACTTTGGGAG      64085        ACTAGT    C
                                CTCCCAG     GGTG TGGG
                                |||||||     |||| ||||
                                GAGGGTT     TCAC ACCC
                                    _______   A
GAM1694  KIAA0794 3'  CCCAACACTTTGGGAG      81229        ACTAGT    C
                                CTCCCAG     GGTG TGGG
                                |||||||     |||| ||||
                                GAGGGTT     TCAC ACCC
                                    _______   A
GAM1694  KIAA0894 3'  CCCAGCAATTTGGGAG      30331         CTAGTGG
                                CTCCCAGA      TGCTGGG
                                ||||||||      |||||||
                                GAGGGTTT      ACGACCC
                                    A_______
GAM1694  KIAA1204 3'  CCCAACACTTTGGGAG      69737        ACTAGT    C
                                CTCCCAG     GGTG TGGG
                                |||||||     |||| ||||
                                GAGGGTT     TCAC ACCC
                                    _______   A
GAM1694  KIAA1244 3'  ATCCCAGCACTTACTTTGGGAG 72440         CTAGT
                                CTCCCAGA    GGTGCTGGGAT
                                ||||||||    ||||||||||||
                                GAGGGTTT    TCACGACCCTA
                                    CAT__
GAM1694  KIAA1554 3'  CCCAGCTACCTGGGAG      96855        GACTAGT  _
                                CTCCCA      GGT GCTGGG
                                ||||||      ||| ||||||
                                GAGGGT      CCA CGACCC
                                    ________  T
GAM1694  KIAA1560 5'  ATCCCAGCACATGATTTGGGA  64847        CTA   G
                                TCCCAGA   GTG TGCTGGGAT
                                |||||||   ||| |||||||||
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                                AGGGTTT   TAC ACGACCCTA
                                   AG_  _
GAM1694 KIAA1908 5' CCCAGCACACAGCCCTGAGG  73783   _  A_ A  G
                                CC CAG  CT GTG TGCTGGG
                                || |||  || ||| |||||||
                                GG GTC  GA CAC ACGACCC
                                 A  CC  _  _
GAM1694 MGC15827 3' CCCAGCGCAGTCCCGGGAG   52873     A_   AGTG
                                CTCCC  GACT   GTGCTGGG
                                |||||  ||||   ||||||||
                                GAGGG  CTGA   CGCGACCC
                                   CC   _____
GAM1694 MGC16332 3' CCCAACACTTTGGGAG     57544      ACTAGT   C
                                CTCCCAG     GGTG TGGG
                                |||||||     |||| ||||
                                GAGGGTT     TCAC ACCC
                                   _______  A
GAM1694 MGC29762 3' CCCAGCTACCTGGGAG     59143      GACTAGT  _
                                CTCCCA      GGT GCTGGG
                                ||||||      ||| ||||||
                                GAGGGT      CCA CGACCC
                                   ________ T
GAM1694 NCBP2    3' CCCAACACTTTGGGAG     24766      ACTAGT   C
                                CTCCCAG     GGTG TGGG
                                |||||||     |||| ||||
                                GAGGGTT     TCAC ACCC
                                   _______  A
GAM1694 PDCD7    3' CCCAACACTTTGGGAG     72600      ACTAGT   C
                                CTCCCAG     GGTG TGGG
                                |||||||     |||| ||||
                                GAGGGTT     TCAC ACCC
                                   _______  A
GAM1694 PNMA5    3' CCCAGCGCAGTTCCAGGAG  73970    CA_   AGTG
                                CTCC   GACT   GTGCTGGG
                                ||||   ||||   ||||||||
                                GAGG   TTGA   CGCGACCC
                                  ACC   _____
GAM1694 PRO2964  3' CCCAGCAATTTGGGAG     38256      CTAGTGG
                                CTCCCAGA    TGCTGGG
                                ||||||||    |||||||
                                GAGGGTTT    ACGACCC
                                   A_______
GAM1694 RHOBTB1  3' TCCCAGCATTATCCAGGG   93095    AGACTA
                                CCC    GTGGTGCTGGGA
                                |||    ||||||||||||
                                GGG    TATTACGACCCT
                                  ACC___
GAM1694 RoXaN    3' CCCAGCAATTTGGGAG     47281      CTAGTGG
                                CTCCCAGA    TGCTGGG
                                ||||||||    |||||||
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                                GAGGGTTT      ACGACCC
                                   A_______
GAM1694  SAC2     3'  CCCAACACTTTGGGAG      30726        ACTAGT    C
                                CTCCCAG     GGTG TGGG
                                |||||||     |||| ||||
                                GAGGGTT     TCAC ACCC
                                   _______  A
GAM1694  SDC3     3'  ATCCCTGCCACCAGTCTGGG   28462         A    GCT
                                CCCAGACT GTGGT   GGGAT
                                |||||||| |||||   |||||
                                GGGTCTGA CACCG   CCCTA
                                   C    T__
GAM1694  SPTLC2   3'  CCCAACACTTTGGGAG      17987        ACTAGT    C
                                CTCCCAG     GGTG TGGG
                                |||||||     |||| ||||
                                GAGGGTT     TCAC ACCC
                                   _______  A
GAM1694  UQCR     3'  CCCAACACTTTGGGAG      23356        ACTAGT    C
                                CTCCCAG     GGTG TGGG
                                |||||||     |||| ||||
                                GAGGGTT     TCAC ACCC
                                   _______  A
GAM1694  VAMP4    5'  CCCAGCACCGCCAGCCCGGGAG 61029       AGA  A
                                CTCCC   CT GTGGTGCTGGG
                                |||||   || ||||||||||||
                                GAGGG   GA CGCCACGACCC
                                   CCC  C
GAM1694  ZNF271   3'  CCCAACACTTTGGGAG      96962        ACTAGT    C
                                CTCCCAG     GGTG TGGG
                                |||||||     |||| ||||
                                GAGGGTT     TCAC ACCC
                                   _______  A
GAM1694  ZNF347   3'  CCCAACACTTTGGGAG      51822        ACTAGT    C
                                CTCCCAG     GGTG TGGG
                                |||||||     |||| ||||
                                GAGGGTT     TCAC ACCC
                                   _______  A
GAM1694  LOC124801 3'  TCCAGAGCCACTAGCCCAGGA  74814     CAGA      G
                                TCC    CTAGTGGT CTGGG
                                |||    |||||||| |||||
                                AGG    GATCACCG GACCT
                                  ACCC       A
GAM1694  LOC138241 3'  CCCAACACTTTGGGAG      75833        ACTAGT    C
                                CTCCCAG     GGTG TGGG
                                |||||||     |||| ||||
                                GAGGGTT     TCAC ACCC
                                   _______  A
GAM1694  LOC139522 5'  CCCAGCACCTCAAGGAG     76362      CA  CTAGT
                                CTCC  GA    GGTGCTGGG
                                ||||  ||    |||||||||
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                                GAGG  CT    CCACGACCC
                                  AA  _____
GAM1694  LOC144453 3'  CCACAGTCCAGTGTGAGA    77329    C  G   AGT  T   _
                                TC CA ACT   GG GCTG GG
                                || || |||   || |||| ||
                                AG GT TGA   CC TGAC CC
                                 A  G  ___  _    A
GAM1694  LOC144486 3'  CCCAGCACGCTGGGAG      84003       ACTAGTG
                                CTCCCAG      GTGCTGGG
                                |||||||      ||||||||
                                GAGGGTC      CACGACCC
                                   G_______
GAM1694  LOC145483 3'  CCCAACACTTTGGGAG      77754       ACTAGT   C
                                CTCCCAG     GGTG TGGG
                                |||||||     |||| ||||
                                GAGGGTT     TCAC ACCC
                                   _______   A
GAM1694  LOC146332 3'  CCCAACACTTTGGGAG      78354       ACTAGT   C
                                CTCCCAG     GGTG TGGG
                                |||||||     |||| ||||
                                GAGGGTT     TCAC ACCC
                                   _______   A
GAM1694  LOC147664 3'  CCCAACACTTTGGGAG      79046       ACTAGT   C
                                CTCCCAG     GGTG TGGG
                                |||||||     |||| ||||
                                GAGGGTT     TCAC ACCC
                                   _______   A
GAM1694  LOC147700 3'  CCCAACACTTTGGGAG      59881       ACTAGT   C
                                CTCCCAG     GGTG TGGG
                                |||||||     |||| ||||
                                GAGGGTT     TCAC ACCC
                                   _______   A
GAM1694  LOC149146 5'  CCCCACCCCCATCTGGGAG   79939        CTAGT   CT
                                CTCCCAGA    GGTG  GGG
                                ||||||||    ||||  |||
                                GAGGGTCT    CCAC  CCC
                                   ACCC_   __
GAM1694  LOC149650 3'  CCGGCGCCCTAGCCTGGGA   80285      A   T
                                TCCCAG CTAG GGTGCTGG
                                |||||| |||| ||||||||
                                AGGGTC GATC CCGCGGCC
                                   C   _
GAM1694  LOC150622 3'  CCCAACACTTTGGGAG      80759       ACTAGT   C
                                CTCCCAG     GGTG TGGG
                                |||||||     |||| ||||
                                GAGGGTT     TCAC ACCC
                                   _______   A
GAM1694  LOC152002 3'  CCCAACACTTTGGGAG      81266       ACTAGT   C
                                CTCCCAG     GGTG TGGG
                                |||||||     |||| ||||
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                                GAGGGTT     TCAC ACCC
                                   _______   A
GAM1694  LOC152106 3'  CCCAACACTTTGGGAG      70592       ACTAGT   C
                                CTCCCAG     GGTG TGGG
                                |||||||     |||| ||||
                                GAGGGTT     TCAC ACCC
                                   _______   A
GAM1694  LOC152627 5'  CCCAGCAATTTGGGAG      81507       CTAGTGG
                                CTCCCAGA     TGCTGGG
                                ||||||||     |||||||
                                GAGGGTTT     ACGACCC
                                   A_______
GAM1694  LOC153077 3'  CCCAGCAATTTGGGAG      87118       CTAGTGG
                                CTCCCAGA     TGCTGGG
                                ||||||||     |||||||
                                GAGGGTTT     ACGACCC
                                   A_______
GAM1694  LOC154739 3'  CCCAGCAATTTGGGAG      87435       CTAGTGG
                                CTCCCAGA     TGCTGGG
                                ||||||||     |||||||
                                GAGGGTTT     ACGACCC
                                   A_______
GAM1694  LOC158987 3'  CCCAACACTTTGGGAG      88321       ACTAGT   C
                                CTCCCAG     GGTG TGGG
                                |||||||     |||| ||||
                                GAGGGTT     TCAC ACCC
                                   _______   A
GAM1694  LOC196047 3'  ATCCCAGCACTTGGCCCAGGG  91145     AGA_  GT
                                CCC   CTA  GGTGCTGGGAT
                                |||   |||  ||||||||||
                                GGG   GGT  TCACGACCCTA
                                  ACCC  __
GAM1694  LOC197319 3'  CCCAACACTTTGGGAG      89317       ACTAGT   C
                                CTCCCAG     GGTG TGGG
                                |||||||     |||| ||||
                                GAGGGTT     TCAC ACCC
                                   _______   A
GAM1694  LOC200470 3'  CCCAACACTTTGGGAG      91640       ACTAGT   C
                                CTCCCAG     GGTG TGGG
                                |||||||     |||| ||||
                                GAGGGTT     TCAC ACCC
                                   _______   A
GAM1694  LOC200731 3'  CCCAGCAATTTGGGAG      91695       CTAGTGG
                                CTCCCAGA     TGCTGGG
                                ||||||||     |||||||
                                GAGGGTTT     ACGACCC
                                   A_______
GAM1694  LOC203276 3'  CCCAGCAATTTGGGAG      92116       CTAGTGG
                                CTCCCAGA     TGCTGGG
                                ||||||||     |||||||
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                                GAGGGTTT      ACGACCC
                                   A_______
GAM1694  LOC203305 3'  CCCAGCAATTTGGGAG      92169        CTAGTGG
                                CTCCCAGA      TGCTGGG
                                ||||||||      |||||||
                                GAGGGTTT      ACGACCC
                                   A_______
GAM1694  LOC220370 3'  CCCAACACTCTGGGAG      94397        CTAGTG  C
                                CTCCCAGA     GTG TGGG
                                ||||||||     ||| ||||
                                GAGGGTCT     CAC ACCC
                                   _______  A
GAM1694  LOC220906 3'  CCCAACACTTTGGGAG      93033        ACTAGT  C
                                CTCCCAG     GGTG TGGG
                                |||||||     |||| ||||
                                GAGGGTT     TCAC ACCC
                                   _______  A
GAM1694  LOC254243 3'  CCCAGCAATTTGGGAG      99255        CTAGTGG
                                CTCCCAGA      TGCTGGG
                                ||||||||      |||||||
                                GAGGGTTT      ACGACCC
                                   A_______
GAM1694  LOC255463 3'  CCCAACACTTTGGGAG      96540        ACTAGT  C
                                CTCCCAG     GGTG TGGG
                                |||||||     |||| ||||
                                GAGGGTT     TCAC ACCC
                                   _______  A
GAM1694  LOC257354 3'  CCCAACACTTTGGGAG      96787        ACTAGT  C
                                CTCCCAG     GGTG TGGG
                                |||||||     |||| ||||
                                GAGGGTT     TCAC ACCC
                                   _______  A
GAM1694  LOC57118  3'  CCCAACACTTTGGGAG      40218        ACTAGT  C
                                CTCCCAG     GGTG TGGG
                                |||||||     |||| ||||
                                GAGGGTT     TCAC ACCC
                                   _______  A
GAM1694  LOC89958  3'  ATCCCAGCACTTGAGGCCAGGA 61581      CAGA  AGT
            G                    CTCC   CT  GGTGCTGGGAT
                                ||||   ||  ||||||||||||
                                GAGG   GA  TCACGACCCTA
                                  ACCG  GT_
GAM1694  LOC90038  3'  CCCAGCAATTTGGGAG      61798        CTAGTGG
                                CTCCCAGA      TGCTGGG
                                ||||||||      |||||||
                                GAGGGTTT      ACGACCC
                                   A_______
GAM1694  LOC90139  3'  CCCAGCACCTGGCCCAGGA   56266     CAGA  GT
                                TCC   CTA  GGTGCTGGG
                                |||   |||  |||||||||
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                                AGG   GGT  CCACGACCC
                                  ACCC  __
GAM1694  LOC91408  5'  CCTGCCGCCACTAGCACTAAGA 66514    CC  A_      CT
             G                    CTC  AG  CTAGTGGTG  GGG
                                  |||  ||  |||||||||  |||
                                  GAG  TC  GATCACCGC  TCC
                                    AA  AC       CG
GAM1694  LOC91963  5'  TCCCAGCACTTATGGGAG    68328      GACTAGT
                                  CTCCCA     GGTGCTGGGA
                                  ||||||     ||||||||||
                                  GAGGGT     TCACGACCCT
                                     AT_____
GAM1694  LOC92661  5'  CCCAGCAATTTGGGAG      70624       CTAGTGG
                                  CTCCCAGA     TGCTGGG
                                  ||||||||     |||||||
                                  GAGGGTTT     ACGACCC
                                      A_______
GAM1695  ATP6V0C   3'  CCCCAGTAGTTGGTCTTGTA  88658        CTG  _  A
                                  TACAAGATCA   ACT CTG GG
                                  ||||||||||   ||| ||| ||
                                  ATGTTCTGGT   TGA GAC CC
                                       ___   T   C
GAM1695  DLX4      3'  GTCCCCAGAACCCTTGGTCTTG 57114       CTGAC   A
                                  CAAGATCA     TCTG GGAC
                                  ||||||||     |||| ||||
                                  GTTCTGGT     AGAC CCTG
                                       TCCCA    C
GAM1695  MNT       3'  TCCTCAGAGGCTGAGCCTGTA  40089     AGA   CTGA
                                  TACA   TCA    CTCTGAGGA
                                  ||||   |||    |||||||||
                                  ATGT   AGT    GAGACTCCT
                                    CCG   CG__
GAM1695  TCF2      3'  GTCCCCAGAACCAGCTGCAGAT 6617     AGAT  _  AC   A
             G                     CA    CA CTG  TCTG GGAC
                                  ||    || |||  |||| ||||
                                  GT    GT GAC  AGAC CCTG
                                   AGAC  C   CA    C
GAM1695  VNN1      3'  TCCTCAGAGCAATTCTCTGTA  17423      _  TCAC  A
                                  TACA AGA    TG CTCTGAGGA
                                  |||| |||    || |||||||||
                                  ATGT TCT    AC GAGACTCCT
                                    C   TA__  _
GAM1695  BMF       5'  CCTCAGAGTCAAACTTTGTG   54280       ATCAC
                                  TACAAG     TGACTCTGAGG
                                  ||||||     ||||||||||
                                  GTGTTT     ACTGAGACTCC
                                     CAA__
GAM1695  DDX33     3'  GTCCTCAGTGCGTGACCCTGT  39786     AGA    T ACT
                                  ACA   TCAC G   CTGAGGAC
                                  |||   |||| |   ||||||||
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                                TGT   AGTG C   GACTCCTG
                                  CCC    _ GT_
GAM1695  FLJ20364  3'  CCTCAGAGCCATGTATTTG   35528     AT  C  A
                                CAAG  CA TG CTCTGAGG
                                ||||  || || ||||||||
                                GTTT  GT AC GAGACTCC
                                  AT  _  C
GAM1695  HMGN4     3'  TCCTTTCCCCAGTGATTTGTA  22034     A       ACTCT
                                TACA GATCACTG     GAGGA
                                |||| ||||||||     |||||
                                ATGT TTAGTGAC     TTCCT
                                  _       CCCT_
GAM1695  KIAA0449  3'  TCCCCAGCACTCATGATCTTG  34639        C   CT_   A
                                CAAGATCA TGA   CTG GGA
                                |||||||| |||   ||| |||
                                GTTCTAGT ACT   GAC CCT
                                     _  CAC   C
GAM1695  KIAA1061  3'  GTCCTCAGAGTGCATTTCCTG  71723    A  TCAC  _
                                CA GA    TG ACTCTGAGGAC
                                || ||    || ||||||||||
                                GT CT    AC TGAGACTCCTG
                                 C  TT__  G
GAM1695  KIAA1535  3'  GTCCTCAGCTCAAGAATCCTGT 80214     A   CAC   CT
           A                     TACA GAT   TGA  CTGAGGAC
                                |||| |||   |||  ||||||||
                                ATGT CTA   ACT  GACTCCTG
                                  C   AGA   C_
GAM1695  LCHN      3'  TCCTCAGAGTATGTCTTG    87478       CACTG
                                CAAGAT     ACTCTGAGGA
                                ||||||     ||||||||||
                                GTTCTG     TGAGACTCCT
                                   TA___
GAM1695  MAGEH1    3'  TCATAATCTATGATCTTGTA   26772         CT  CTC
                                TACAAGATCA  GA   TGA
                                ||||||||||  ||   |||
                                ATGTTCTAGT  CT   ACT
                                      AT  AAT
GAM1695  LOC154789 5'  TCCTCAGAGCTCTCCTGTG   82034     A  TCACT  _
                                TACA GA     GA CTCTGAGGA
                                |||| ||     || |||||||||
                                GTGT CT     CT GAGACTCCT
                                  C  _____  C
GAM1695  LOC197201 3'  TCCTCAGAAGGTATTTGTA   89289       ATC   GAC
                                TACAAG   ACT   TCTGAGGA
                                ||||||   |||   ||||||||
                                ATGTTT   TGG   AGACTCCT
                                   A__   A__
GAM1695  LOC255193 3'  CCTCAGAGTCAGGCCTGTA   97103     AGATCA
                                TACA     CTGACTCTGAGG
                                ||||     ||||||||||||
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                                ATGT     GACTGAGACTCC
                                  CCG___
GAM1695 LOC96597 5' TCCCCAGAATTCTCTTGT    67468      TCACT C_   A
                                ACAAGA    GA  TCTG GGA
                                ||||||    ||  |||| |||
                                TGTTCT    CT  AGAC CCT
                                   _____  TA   C
GAM1696 CENPB    5' GCATCATCCTCAAGGAGAAGG  70116    G      __   CA
                                CCT CTCCTTGA  ATGA  GC
                                ||| ||||||||  ||||  ||
                                GGA GAGGAACT  TACT  CG
                                  A       CC   A_
GAM1696 COL19A1  3' GCTCTTCAAGGAGCAG      10262          T  CA
                                CTGCTCCTTGAA GA  GC
                                ||||||||||| ||  ||
                                GACGAGGAACTT CT  CG
                                         _  __
GAM1696 GPRK2L   3' CGCCAGGAAGGAGCATGTG   96111    C      GAA  ACA
                                CAC TGCTCCTT   TG   GCG
                                ||| ||||||||   ||   |||
                                GTG ACGAGGAA   AC   CGC
                                  T      GG_  ___
GAM1696 ICA1     3' CTGTCCCCACAGCAGGTG    42512       CCT  AAT
                                CACCTGCT   TG   GACAG
                                ||||||||   ||   |||||
                                GTGGACGA   AC   CTGTC
                                     C__  CC_
GAM1696 MTBP     3' GCTTTATTCAAAGAATAG    42128    C  C      C
                                CTG TC TTGAATGA AGC
                                ||| || |||||||| |||
                                GAT AG AACTTATT TCG
                                  A  A      _
GAM1696 PCTK3    5' GCGCCGGGTATAAGGAGCAAAG 73329    __      A  GACA
            G                    CCT  GCTCCTTG AT    GCGC
                                |||  |||||||| ||    ||||
                                GGA  CGAGGAAT TG    CGCG
                                  AA       A  GGC_
GAM1696 WHSC1    3' CGCCACTCTGAAGAGTAGGTG  56693        CTT_  A  ACA
                                CACCTGCTC   GA TG   GCG
                                |||||||||   || ||   |||
                                GTGGATGAG   CT AC   CGC
                                     AAGT  C  ___
GAM1696 ARGBP2   5' GCAGGTCTGAAAAAGCAGGTG  14590       CC  GAAT   A_
                                CACCTGCT  TT   GAC  GC
                                ||||||||  ||   |||  ||
                                GTGGACGA  AA   CTG  CG
                                     A_  AGT_   GA
GAM1696 DKFZP434H132 5' CGCTGTCGGAGGAGCGGG    31930          GAA
                                CCTGCTCCTT   TGACAGCG
                                ||||||||||   ||||||||
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                                GGGCGAGGAG  GCTGTCGC
                                    ___
GAM1696 FLJ13195 3' GCTATCCAAGGAGCAAGTG   43550    C      AAT  C
                                CAC TGCTCCTTG  GA AGC
                                ||| |||||||||  || |||
                                GTG ACGAGGAAC  CT TCG
                                  A      ___  A
GAM1696 FLJ14594 3' GCACCATCAGGAGCAGG     52505       T  A  ACA
                                CCTGCTCCT GA TG  GC
                                ||||||||| || ||  ||
                                GGACGAGGA CT AC  CG
                                     _ _ CA_
GAM1696 FLVCR    5' GCGCCACCGGGGAAGGAGCGGT 26761     T     GAA  ACA
            G                    CACC GCTCCTT  TG  GCGC
                                |||| |||||||  ||  ||||
                                GTGG CGAGGAA  GC  CGCG
                                  _     GGG  CAC
GAM1696 KIAA0172 5' GCGCCACGTGGAAAAGCAGGTG 65597       CC  GA  ACA
                                CACCTGCT  TT  ATG  GCGC
                                ||||||||  ||  |||  ||||
                                GTGGACGA  AG  TGC  CGCG
                                    AA  G_  AC_
GAM1696 MGC10772 5' GCGCCATGGGAAGGAGCGGG  48293        GA_  ACA
                                CCTGCTCCTT  ATG  GCGC
                                ||||||||||  |||  ||||
                                GGGCGAGGAA  TAC  CGCG
                                     GGG  ___
GAM1696 PRKWNK2  3' GCGCTGCAGCCCAAGGAGCAG 92198        AA_  A
                                CTGCTCCTTG  TG CAGCGC
                                ||||||||||  || ||||||
                                GACGAGGAAC  AC GTCGCG
                                     CCG  _
GAM1696 PSKH1    5' GCACTGCCTTCAGAGCAGGT  68798       CT   TGA  C
                                ACCTGCTC  TGAA  CAG GC
                                ||||||||  ||||  ||| ||
                                TGGACGAG  ACTT  GTC CG
                                    __  CC_  A
GAM1696 TNFRSF19L 3' GCACTGTGTACAGGAGCAGG  52835       T A  G   C
                                CCTGCTCCT G AT ACAG GC
                                ||||||||| | || |||| ||
                                GGACGAGGA C TG TGTC CG
                                     _ A  _   A
GAM1696 LOC115708 3' GCGCTGCGGAGAGGAGCGG   73917       GAA  A
                                CTGCTCCTT  TG CAGCGC
                                |||||||||  || ||||||
                                GGCGAGGAG  GC GTCGCG
                                     AG_  _
GAM1696 LOC125297 5' GCGCGGGCATCAAGGAGGAGG  74867    G      A  ACA
                                CCT CTCCTTGA TG  GCGC
                                ||| ||||||| ||  ||||
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                                GGA GAGGAACT AC   CGCG
                                  G       _ GGG
GAM1696  LOC146756 3'  GCTGATCAAAGGAGCAGG    84808         GAA  _
                                CCTGCTCCTT   TGA CAGC
                                ||||||||||   ||| ||||
                                GGACGAGGAA   ACT GTCG
                                      ____   A
GAM1696  LOC149706 5'  GCACTGTTTGAAGAGGAGCAG  85805        GAAT    C
                                CTGCTCCTT    GACAG GC
                                |||||||||    ||||| ||
                                GACGAGGAG    TTGTC CG
                                     AAGT    A
GAM1696  LOC157922 3'  CATTCCCAGGAGCAGGTG    87926          T_
                                CACCTGCTCCT  GAATG
                                ||||||||||  |||||
                                GTGGACGAGGA  CTTAC
                                      CC
GAM1696  LOC196337 5'  CGCTCCAAGAGGCAGGTG    89023       TC   AATGAC
                                CACCTGC  CTTG     AGCG
                                |||||||  ||||     ||||
                                GTGGACG  GAAC     TCGC
                                    GA   C_____
GAM1696  LOC221271 3'  CGCTATCATTTGACATGTG   93511    C  CTCC TG    C
                                CAC TG    T  AATGA AGCG
                                ||| ||    |  ||||| ||||
                                GTG AC    A  TTACT TCGC
                                  T  _____ GT    A
GAM1697  IRS1     3'  CCATAGATGGTTCTCAATTGTA 19874     C        TGAAC
                                TACA ATTGAGAACC    ATGG
                                |||| ||||||||||    ||||
                                ATGT TAACTCTTGG    TACC
                                  _        TAGA_
GAM1697  SERPINF1  3'  CCTGTAAGGTTTCAATG     12038        A   GA   T
                                CATTGAGA CCT  ACA GG
                                |||||||| |||  ||| ||
                                GTAACTTT GGA  TGT CC
                                     _   A_   _
GAM1697  HSA243396 3'  CCATGTTCAGCAATGTCAATG  37844       GAAC_
                                CATTGA    CTGAACATGG
                                ||||||    ||||||||||
                                GTAACT    GACTTGTACC
                                   GTAAC
GAM1697  KIAA1387  3'  CAGGAATTTTCAATATGTA   71444      C       __
                                TACA ATTGAGAA  CCTG
                                |||| ||||||||  ||||
                                ATGT TAACTTTT  GGAC
                                  A       AA
GAM1697  MGC16063  3'  TTCAAATTCCAATGTGTA    54930         A   CC
                                TACACATTG GAA  TGAA
                                |||||||| |||  ||||
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                                ATGTGTAAC CTT  ACTT
                                      _  AA
GAM1697  SMCR8    3'  CCATGCTCAGGTTTGACTATGT 59253      TGA_       A
                                ACAT   GAACCTGA CATGG
                                ||||   |||||||| |||||
                                TGTA   TTTGGACT GTACC
                                  TCAG       C
GAM1697  UPLC1    3'  CCATGCTAGGCCCCAATGT   35227       AGAA   AA
                                ACATTG   CCTG  CATGG
                                ||||||   ||||  |||||
                                TGTAAC   GGAT  GTACC
                                   CCC_   C_
GAM1697  ZNF334   3'  CCATAAGTCAACCCTCAATGT  36637        AACC   AC_
                                ACATTGAG   TGA   ATGG
                                ||||||||   |||   ||||
                                TGTAACTC   ACT   TACC
                                     CCA_  GAA
GAM1697  LOC145082 3'  TATGGAATGCCCTTAATGTGTA 84196          AACCTGAA
                                TACACATTGAG       CATG
                                ||||||||||        ||||
                                ATGTGTAATTC       GTAT
                                      CCGTAAG_
GAM1697  LOC157723 3'  CCAAGTAAGGTTCTCAAATGT  82465       _      GA  A
                                ACATT GAGAACCT  AC TGG
                                ||||| ||||||||  || |||
                                TGTAA CTCTTGGA  TG ACC
                                   A       A_  A
GAM1697  LOC219988 5'  CCATGTTCGGCCCCCAATG   93262       AGAAC
                                CATTG    CTGAACATGG
                                |||||    ||||||||||
                                GTAAC    GGCTTGTACC
                                   CCCC_
GAM1698  ASNS     5'  CTGTAGACTGCAAGACTCATCA 56762        C  ATCACT
                                TGATGAG TC     GTCTACAG
                                ||||||| ||     ||||||||
                                ACTACTC AG     CAGATGTC
                                    _  AACGT_
GAM1698  FCMD     3'  TGGAAGATGAGCTCACCA    23049    A        ACTG
                                TG TGAGCTCATC    TCTA
                                || ||||||||||    ||||
                                AC ACTCGAGTAG    AGGT
                                 C         A___
GAM1698  PPARGC1  3'  CTGCAGACACTGTGGGTAGCCC 26077       A   CA   __    A
            ATCA                    TGATG GCT  TCAC  TGTCT CAG
                                ||||| |||  ||||  ||||| |||
                                ACTAC CGA  GGTG  ACAGA GTC
                                   C   TG   TC    C
GAM1698  FLJ20689  3'  CTGCAGAAACTCAGACAGCTCA 35961         CATCACTG_   A
            TCA                   TGATGAGCT        TCT CAG
                                |||||||||        ||| |||
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                                ACTACTCGA        AGA GTC
                                     CAGACTCAA   C
GAM1698  FLJ20689  3'  CTGCAGAAACTCAGACAGCTCA 36210         CATCACTG_   A
              TCA                    TGATGAGCT        TCT CAG
                                |||||||||        ||| |||
                                ACTACTCGA        AGA GTC
                                     CAGACTCAA   C
GAM1698  FLJ31890  3'  CTGTAGACATCCAAAAGCTCAC 92985     A     CATCAC
              A                     TG TGAGCT     TGTCTACAG
                                || ||||||     |||||||||
                                AC ACTCGA     ACAGATGTC
                                 _     AAACCT
GAM1698  KIAA0342  3'  TGTCTACAGCTGCTTGCTGAGC 71144          T A_________   TCTA
              TCATCA                   TGATGAGCTCA C        CTG    CA
                                |||||||||||| |        |||    ||
                                ACTACTCGAGT G        GAC    GT
                                      C TTCGTC___   ATCT
GAM1698  STK3     3'  ACTGTAATAAGCTCATCA     74100         C  C  T
                                TGATGAGCT AT AC GT
                                ||||||||| || || ||
                                ACTACTCGA TA TG CA
                                     A  A  T
GAM1698  LOC146136 5'  CTGCAGACAGTGATGAAGGCCA 73317     A  __         A
              T                     ATG GC  TCATCACTGTCT CAG
                                ||| ||  |||||||||||| |||
                                TAC CG  AGTAGTGACAGA GTC
                                  _ GA          C
GAM1698  LOC146439 5'  GCAGGTGACATGAGCTCTCCA  78450    AT      __   _
                                TG  GAGCTCA  TCAC TGT
                                ||  |||||||  |||| |||
                                AC  CTCGAGT  AGTG ACG
                                 CT      AC    G
GAM1698  LOC220565 3'  CTGCAGACAGTGATGAAGGCCA 92442     A  __         A
              T                     ATG GC  TCATCACTGTCT CAG
                                ||| ||  |||||||||||| |||
                                TAC CG  AGTAGTGACAGA GTC
                                  _ GA          C
GAM1698  LOC90520  3'  AGAACAGTGATAAAGCCACCA  63833    A  A   C_      _
                                TG TG GCT  ATCACTGT CT
                                || || |||  |||||||| ||
                                AC AC CGA  TAGTGACA GA
                                 C  _   AA       A
GAM1699  MADH3    3'  GTCTCAGGCAGCACCACA    20921          CAT
                                TGTGGTGCTGTC   GGAC
                                ||||||||||||   ||||
                                ACACCACGACGG   TCTG
                                       AC_
GAM1699  NRAP     3'  TGCCCATGGACATGGTGCAC   21620      ____       A
                                GTGC    TGTCCATGG CA
                                ||||    ||||||||| ||
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                                CACG    ACAGGTACC GT
                                  TGGT        C
GAM1699  PVR      3'  TGTCTGTCTCCAGCACCCA   22496    T      TCC
                                TG GGTGCTG   ATGGACA
                                || |||||||   |||||||
                                AC CCACGAC   TGTCTGT
                                 _      CTC
GAM1699  SEL1L    3'  TTTGTCCATGGTAGCCCA    18610    T    T
                                TGG GCTG CCATGGACAAA
                                ||| |||| ||||||||||
                                ACC CGAT GGTACCTGTTT
                                  _   _
GAM1699  STK24    3'  GTCCAGGGACACACACA     14550     G  C    A
                                TGTG TG TGTCC TGGAC
                                |||| || ||||| |||||
                                ACAC AC ACAGG ACCTG
                                  _ _    G
GAM1699  TLL1     3'  TGTCCATGAGCATACAACA   25879    G   C  TC
                                TGT GTG TG  CATGGACA
                                ||| ||| ||  ||||||||
                                ACA CAT AC  GTACCTGT
                                  A  _ GA
GAM1699  DKFZP434I092 3'  TGTCTGCCCACAGCAGCCA   68414    _     CCA
                                TGG TGCTGT   TGGACA
                                ||| ||||||   ||||||
                                ACC ACGACA   GTCTGT
                                  G     CCC
GAM1699  FLJ14437 3'  TTTGCCCATAAAATACACCTCA 51801    T   C   CC_   A
                                TG GGTG TGT   ATGG CAAA
                                || |||| |||   |||| ||||
                                AC CCAC ATA   TACC GTTT
                                 T   _  AAA   C
GAM1699  FLJ22479 3'  TGTTTGTCTCACAATCACCACA 46608       C_  CCAT
                                TGTGGTG  TGT   GGACAAACA
                                |||||||  |||   |||||||||
                                ACACCAC  ACA   TCTGTTTGT
                                    TA  C___
GAM1699  FLJ31812 3'  TGTTCCTGAAAGCACCACA   59310        GTC  T
                                TGTGGTGCT   CA GGACA
                                |||||||||   || |||||
                                ACACCACGA   GT CTTGT
                                     AA_  C
GAM1699  ITPK1    3'  TTTGAGATCAGAGAGCACCACA 27235        G  CATGGA
                                TGTGGTGCT TC     CAAA
                                ||||||||| ||     ||||
                                ACACCACGA AG     GTTT
                                     G  ACTAGA
GAM1699  KIAA0819 3'  TGCCCACCCCAGCATCACA   64338         TCCA   A
                                TGTGGTGCTG    TGG CA
                                ||||||||||    ||| ||
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                                ACACTACGAC   ACC GT
                                     CCC_  C
GAM1699 KIAA1913 5' TGCTCAGGACAGCACACA   74322     G      A  GA
                                TGTG TGCTGTCC TG  CA
                                |||| |||||||| ||  ||
                                ACAC ACGACAGG AC  GT
                                  _      _ TC
GAM1699 LYPLA3   3' TCCACCCTGGCCAGCACCCA  25564    T     T  ___
                                TG GGTGCTG CCA   TGGA
                                || ||||||| |||   ||||
                                AC CCACGAC GGT   ACCT
                                 _     C   CCC
GAM1699 MAP-1    5' GTCCCTCCAGACAGTACCACA 42449          CAT__
                                TGTGGTGCTGTC    GGAC
                                ||||||||||||    ||||
                                ACACCATGACAG    CCTG
                                       ACCTC
GAM1699 MKNK1    3' GTTTATACAACACCAC     14878      C   CC
                                GTGGTG TGT  ATGGAC
                                |||||| |||  ||||||
                                CACCAC ACA  TATTTG
                                   A  __
GAM1699 SUCLA2   3' TGTTTATCTTCAGCACCA   15244       TCC
                                TGGTGCTG   ATGGACA
                                ||||||||   |||||||
                                ACCACGAC   TATTTGT
                                     TTC
GAM1699 LOC125268 3' TCCATGAGACAGCACCCA   76580    T      _
                                TG GGTGCTGTC CATGGA
                                || |||||||| ||||||
                                AC CCACGACAG GTACCT
                                 _       A
GAM1699 LOC203042 5' TTCAGCAGACAGCACCGCA  92072          CA_
                                TGTGGTGCTGTC   TGGA
                                ||||||||||||   ||||
                                ACGCCACGACAG   ACTT
                                       ACG
GAM1699 LOC219672 3' TGTCCATGGAGGCCCA     92976    T  G
                                TGG GCT TCCATGGACA
                                ||| ||| ||||||||||
                                ACC CGG AGGTACCTGT
                                  _  _
GAM1699 LOC221122 3' TCTGAAGACAGCACACA    95087     G     CA
                                TGTG TGCTGTC  TGGA
                                |||| |||||||  ||||
                                ACAC ACGACAG  GTCT
                                  _      AA
GAM1699 LOC81501 3' TGTTCCAAACAAACCACA    48634      GC   CCA   _
                                TGTGGT  TGT   TGGA CA
                                ||||||  |||   |||| ||
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                                ACACCA  ACA   ACCT GT
                                   A_  A__    T
GAM1699  LOC92181  3'  TCCATGAAGGACAGCACCA   68949          ___
                                TGGTGCTGTCC   ATGGA
                                ||||||||||   |||||
                                ACCACGACAGG   TACCT
                                      AAG
GAM1700  ABCB9     3'  TCCGAGCCCAGGCCTGCAGC   39516       A       G
                                GCTGCAG GCCTGGGCT GGA
                                ||||||| ||||||||| |||
                                CGACGTC CGGACCCGA CCT
                                   _       G
GAM1700  ACP2      3'  GCTCCCCAGCCCATGGACAG   9656      CAGAG _       A
                                CTG    CC TGGGCTGGG AGC
                                |||    || ||||||||| |||
                                GAC    GG ACCCGACCC TCG
                                  A____  T       C
GAM1700  AKR1A1    3'  GCCTCCCTTCCAGCTCTGCAGC 21373         C   CT   A
                                GCTGCAGAGC TGGG  GGGA GC
                                |||||||||| ||||  |||| ||
                                CGACGTCTCG ACCT  CCCT CG
                                      _   T_   C
GAM1700  APRT      3'  GCCTCCCAGCCCAACATCTCCA 6665      C   GCC        A
            GC                    GCTG AGA   TGGGCTGGGA GC
                                |||| |||   |||||||||| ||
                                CGAC TCT   ACCCGACCCT CG
                                  C   ACA        C
GAM1700  AQP2      5'  CCCCGCAGGGCTCTGCAGC    6668           GG  T
                                GCTGCAGAGCCT  GC GGG
                                ||||||||||||  || |||
                                CGACGTCTCGGG  CG CCC
                                      A_  C
GAM1700  ATF4      5'  TGGAAGCGCACCAGGCTCTGCA 9812           _______  GGGA
            GC                    GCTGCAGAGCCTGG     GCT    A
                                ||||||||||||||     |||   |
                                CGACGTCTCGGACC     CGA    T
                                      ACG___   AGGG
GAM1700  BLAME     3'  GCTTCAGCCCCAGACCCTGCAG 39654       AGC    _ GG
                                CTGCAG   CTGGG CT  GAAGC
                                ||||||   ||||| ||  |||||
                                GACGTC   GACCC GA  CTTCG
                                   CCA    C __
GAM1700  BST1      3'  CCCTCCTCCAGCCCTGCAGC   16338       A  C    CT_
                                GCTGCAG GC TGGG   GGG
                                ||||||| || ||||   |||
                                CGACGTC CG ACCT   CCC
                                   C _    CCT
GAM1700  CD5       3'  TCCCGGAGACCTCTGCAGC    27223         CCTGGG
                                GCTGCAGAG     CTGGGA
                                |||||||||     ||||||
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                                CGACGTCTC     GGCCCT
                                     CAGA__
GAM1700 CD63     5' CCTTGGGAAGCCCAGGCCCGGC 10115      AGA       _____
              AGC                   GCTGC   GCCTGGGCT    GGG
                                    |||||   |||||||||    |||
                                    CGACG   CGGACCCGA    TCC
                                       GCC       AGGGT
GAM1700 CIT      3' CCCAGCGTCATCTCCCCAGC   70302     CA   CC  _
                                    GCTG  GAG  TGG GCTGGG
                                    ||||  |||  ||| ||||||
                                    CGAC  CTC  ACT CGACCC
                                      CC   T_   G
GAM1700 CLU      3' GCCCCCCAGAGAGAGCTCTGCA 10212        _ GGG    AA
                                    TGCAGAGC CT   CTGGG  GC
                                    |||||||| ||   |||||  ||
                                    ACGTCTCG GA   GACCC  CG
                                         A  GA_    CC
GAM1700 COL4A3   5' CTCGCCCAGGCTCTGAGC    49383     G         T
                                    GCT CAGAGCCTGGGC GGG
                                    ||| ||||||||||| |||
                                    CGA GTCTCGGACCCG CTC
                                      _         _
GAM1700 COL4A3   5' CTCGCCCAGGCTCTGAGC    49387     G         T
                                    GCT CAGAGCCTGGGC GGG
                                    ||| ||||||||||| |||
                                    CGA GTCTCGGACCCG CTC
                                      _         _
GAM1700 COL4A3   5' CTCGCCCAGGCTCTGAGC    5401      G         T
                                    GCT CAGAGCCTGGGC GGG
                                    ||| ||||||||||| |||
                                    CGA GTCTCGGACCCG CTC
                                      _         _
GAM1700 CSF3     3' GCTCCCCAGCCCTGGCTCTGCA 7485          T       A
                                    TGCAGAGCC GGGCTGGG AGC
                                    ||||||||| |||||||| |||
                                    ACGTCTCGG CCCGACCC TCG
                                         T       C
GAM1700 DKK1     5' GCTCCCGGACCCTGACTCTGCA 25295         CCT   _     A
              GC                    GCTGCAGAG   GGG CTGGGA GC
                                    |||||||||   ||| |||||| ||
                                    CGACGTCTC   CCC GGCCCT CG
                                         AGT   A     _
GAM1700 DMRT2    3' CTCAGTTCAAGCCCTGAAGC   22651     G   A  C
                                    GCT CAG GC TGGGCTGGG
                                    ||| ||| || |||||||||
                                    CGA GTC CG ACTTGACTC
                                      A   C  A
GAM1700 DNMT3A   5' GCCCCCCAGCCCCGCGCAGC   42882      AGA  CT       AA
                                    GCTGC   GC  GGGCTGGG  GC
                                    |||||   ||  ||||||||  ||
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                                CGACG  CG  CCCGACCC  CG
                                   ___ C_      CC
GAM1700  DRG2    3'  CTCCCAGCCCCCTGCA     9129       AGCCT       A
                                TGCAG    GGGCTGGGA G
                                |||||    ||||||||| |
                                ACGTC    CCCGACCCT C
                                   C_____       C
GAM1700  EGR1    5'  CCCTGCCCCAGCCTCCGCAGC  10489      A  C    _ T
                                GCTGC GAG CTGGG C GGG
                                ||||| ||| ||||| | |||
                                CGACG CTC GACCC G CCC
                                   C  C    C T
GAM1700  EN2     3'  CCGCCCAGGCCCGCAGC     9254       AGA      T
                                GCTGC  GCCTGGGC GG
                                |||||  |||||||| ||
                                CGACG  CGGACCCG CC
                                   CC_      _
GAM1700  EPHB2   3'  CCCCCAGGTCTGCAGC     34344        G     CT
                                GCTGCAGA CCTGGG  GG
                                |||||||| ||||||  ||
                                CGACGTCT GGACCC  CC
                                      _     __
GAM1700  EPHB2   3'  CCCCCAGGTCTGCAGC     16697        G     CT
                                GCTGCAGA CCTGGG  GG
                                |||||||| ||||||  ||
                                CGACGTCT GGACCC  CC
                                      _     __
GAM1700  EPM2A   3'  TGGAAGCGCCTCCAGACTATGC 20237       G  C   ________   GGGA
            AGC                    GCTGCA AG CTGG      GCT    A
                                |||||| || ||||      |||    |
                                CGACGT TC GACC      CGA    T
                                   A  A    TCCG___   AGGG
GAM1700  FAAH    3'  CTCCCAGCCTCCGCAG      44451      A  GCCTG      A
                                CTGC GA    GGCTGGGA G
                                |||| ||    ||||||||| |
                                GACG CT    CCGACCCT C
                                  C  _____       C
GAM1700  FUT6    5'  CCGTGGCCCAGCCTCTGCA   5635         C      _
                                TGCAGAG CTGGGCTG GG
                                ||||||| |||||||| ||
                                ACGTCTC GACCCGGT CC
                                    C       G
GAM1700  GAS     5'  CCTCCCAGCTCTGCAG      7690          C    CT
                                CTGCAGAGC TGGG  GG
                                ||||||||| ||||  ||
                                GACGTCTCG ACCC  CC
                                      _   T_
GAM1700  GORASP1 3'  CTTCCCTTAACTCTGTAGC   49954          CCTGGGCT
                                GCTGCAGAG       GGGAAG
                                |||||||||       ||||||
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                                CGATGTCTC      CCCTTC
                                     AATT____
GAM1700 HIVEP2   3' GCTCCCCAGCTCTTCCTGTCAG 23073     _  AGCCT      A
            C                    GCTG CAG    GGGCTGGG AGC
                                 |||| |||    |||||||| |||
                                 CGAC GTC    CTCGACCC TCG
                                   T  CTT__      C
GAM1700 HSF4     5' CCCTCTGCGGACTCTGCAGC  60485        _ TG  CT
                                 GCTGCAGAG CC  GG  GGG
                                 ||||||||| ||  ||  |||
                                 CGACGTCTC GG  TC  CCC
                                      A  CG  T_
GAM1700 HTRA3    5' CCCGGCGCCCGGCCCCGCAGC  90579      AGA  T  _
                                 GCTGC   GCC GG GCTGGG
                                 |||||   ||| || ||||||
                                 CGACG   CGG CC CGGCCC
                                    CCC   C  G
GAM1700 IL2RB    3' CTCTCCAGCCCTGCAGC     7937       GAGCCT     GA
                                 GCTGCA     GGGCTGG  AG
                                 ||||||     |||||||  ||
                                 CGACGT     CCCGACC  TC
                                      _______      TC
GAM1700 KRT3     3' GCTCCCCAAGAACGCGGCTCTG 55104    T      _ GG  _  A
            CGC                    GC GCAGAGCC TG  CT GGG AGC
                                 || ||||||| ||  || ||| |||
                                 CG CGTCTCGG GC  GA CCC TCG
                                  _      C  AA  A   C
GAM1700 LNK      3' CCCCCAGGCTCACAGC      19638      CA       CT
                                 GCTG  GAGCCTGGG  GG
                                 ||||  |||||||||  ||
                                 CGAC  CTCGGACCC  CC
                                   A_       __
GAM1700 MAD      5' GCTCCATAGCGGGCTCCACAGC 11417      CA     GG   _  A
                                 GCTG  GAGCCT  GCTG GGA GC
                                 ||||  ||||||  |||| ||| ||
                                 CGAC  CTCGGG  CGAT CCT CG
                                   AC     __    A  _
GAM1700 MAP2K2   5' CTCGGCCCAGGCCCGCAGC   48405      AGA
                                 GCTGC   GCCTGGGCTGGG
                                 |||||   ||||||||||||
                                 CGACG   CGGACCCGGCTC
                                    CC_
GAM1700 MUC4     3' GCCCCCCAGCCTTCACTGACAG 57156     _  AGCCT      AA
            C                    GCTG CAG    GGGCTGGG  GC
                                 |||| |||    ||||||||  ||
                                 CGAC GTC    TCCGACCC  CG
                                   A  ACT__       CC
GAM1700 NFATC2   5' CCCTCGCCCCCGGCCCCGCAGC 25625      AGA  T_   T_
                                 GCTGC   GCC  GGGC  GGG
                                 |||||   |||  ||||  |||
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                                CGACG  CGG  CCCG  CCC
                                  CCC  CC   CT
GAM1700 NGFR    3' GCTCCCCAGCCCAGGGTTCCCC 11799     CA_   _      A
            CAGC                  GCTG  GAGCC TGGGCTGGG AGC
                                |||| |||||  ||||||||| |||
                                CGAC  CTTGG ACCCGACCC TCG
                                  CCC   G       C
GAM1700 PAK4    3' CTCTCCAGCCCCTGCAGC   20826       AGCCT     GA
                                GCTGCAG   GGGCTGG  AG
                                |||||||   |||||||  ||
                                CGACGTC   CCCGACC  TC
                                   _____     TC
GAM1700 PFKFB4  3' CTCCCAGGGCTTTGCAGC   17084         TGGG     A
                                GCTGCAGAGCC   CTGGGA G
                                ||||||||||   ||||||  |
                                CGACGTTTCGG   GACCCT C
                                    ____     C
GAM1700 PIM2    5' GCCCCCCAGCCCTGGCTCCCCA 60655     CA    T      AA
            GC                    GCTG  GAGCC GGGCTGGG  GC
                                |||| |||||  ||||||||  ||
                                CGAC  CTCGG CCCGACCC  CG
                                  CC    T       CC
GAM1700 PRKG2   3' CTCCCCAGCTCTCAGC     21823     C    C   CT
                                GCTG AGAGC TGGG  GGG
                                |||| |||||  ||||  |||
                                CGAC TCTCG ACCC  CTC
                                  _    _   __
GAM1700 PTGS2   5' CTCCTTCAGCTCCACAGC    8246      CA   C  GCT   A
                                GCTG  GAGC TGG   GGGA G
                                ||||  |||| |||   |||| |
                                CGAC  CTCG ACT   TCCT C
                                  AC   _  ___    C
GAM1700 PX19    5' CCTCCCAGGCTCCGCA     26015     A       CT
                                TGC GAGCCTGGG  GGG
                                |||  |||||||||  |||
                                ACG CTCGGACCC  TCC
                                  C       __
GAM1700 RARA    3' GCCCCCCAGTTCTCCTCCTCAG 8254      CA   CCT      AA
            C                     GCTG  GAG   GGGCTGGG  GC
                                ||||  |||   ||||||||  ||
                                CGAC  CTC   CTTGACCC  CG
                                  TC   CT_      CC
GAM1700 SLC30A3 3' CTCAGCCCCAGACTCTCAGC   14397     C   C    _
                                GCTG AGAG CTGGG CTGGG
                                |||| |||| ||||| |||||
                                CGAC TCTC GACCC GACTC
                                  _   A    C
GAM1700 SLC35A2 3' CCCCCAGCCCCTGCCAGC    20179     _  AGCCT      AA
                                GCTG CAG    GGGCTGGG  G
                                |||| |||    ||||||||  |
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                                CGAC GTC    CCCGACCC  C
                                  C _____       CC
GAM1700 SLC38A3  3' CCCTGCCCAGACTCTTCAGC  23372     C   C     T
                                GCTG AGAG CTGGGC GGG
                                |||| |||| |||||| |||
                                CGAC TCTC GACCCG CCC
                                  T   A     T
GAM1700 SLC6A12  5' GCTTCCCAACCCACCACACAGC 13194     CAGAGCC   C
                                GCTG      TGGG TGGGAAGC
                                ||||      |||| ||||||||
                                CGAC      ACCC ACCCTTCG
                                  ACACC__   A
GAM1700 SNAP25   5' CCCAGCCCAGGCGCCCAGC   13269     CAGA
                                GCTG   GCCTGGGCTGGG
                                ||||   ||||||||||||
                                CGAC   CGGACCCGACCC
                                  CCG_
GAM1700 SNAP25   5' CCCAGCCCAGGCGCCCAGC   56423     CAGA
                                GCTG   GCCTGGGCTGGG
                                ||||   ||||||||||||
                                CGAC   CGGACCCGACCC
                                  CCG_
GAM1700 STXBP1   3' CTCCCCAGCCCTGCACGC    13474   _   GAGCCT      A
                                GC TGCA     GGGCTGGG AG
                                || ||||     |||||||| ||
                                CG ACGT     CCCGACCC TC
                                 C  _______       C
GAM1700 TESK1    5' CCCAAGCCCAGGCCCTGCGC  21885   T   A       _
                                GC GCAG GCCTGGGCT GGG
                                || |||| ||||||||| |||
                                CG CGTC CGGACCCGA CCC
                                 _   C       A
GAM1700 TGFB1    5' CCCCCCCCGGCTCTGAGC    7252     G     T  CT
                                GCT CAGAGCC GGG  GGG
                                ||| ||||||| |||  |||
                                CGA GTCTCGG CCC  CCC
                                  _     _  CC
GAM1700 TIMP3    3' TCCATGCTCAGGCTCTCAGC  6291      C        _
                                GCTG AGAGCCTGGGC TGGG
                                |||| |||||||||| ||||
                                CGAC TCTCGGACTCG ACCT
                                  _         T
GAM1700 TLX1     5' CTCCCAGCCCCTGCTAGC    19818   _   AGCCT       A
                                GCT GCAG    GGGCTGGGA G
                                ||| ||||    ||||||||| |
                                CGA CGTC    CCCGACCCT C
                                  T  _____       C
GAM1700 TNFRSF11A 3' CTCCTCAAACTCGCAGC    15193      A  CC   CT
                                GCTGC GAG  TGGG  GGG
                                ||||| |||  ||||  |||
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                                CGACG CTC  ACTC  CTC
                                  _  AA   __
GAM1700  UBTF     3'  CCCAGGCCAGGACTCTGCAGC  27253         _    G
                                GCTGCAGAG CCTGG CTGGG
                                ||||||||| ||||| |||||
                                CGACGTCTC GGACC GACCC
                                    A    G
GAM1700  ALOXE3   5'  CTACCCAGCCCCGCAGC     41559      AGAGCCT      A
                                GCTGC      GGGCTGGG AG
                                |||||      |||||||| ||
                                CGACG      CCCGACCC TC
                                  C_______       A
GAM1700  APELIN   5'  CCTCCCGAGCTCTGCGC     34264    T      C    CT
                                GC GCAGAGC TGGG  GGG
                                || ||||||| ||||  |||
                                CG CGTCTCG GCCC  TCC
                                 _      A   __
GAM1700  ARFRP1   3'  CTGGCCCAGGCCCTGCAGC    13693        A       TG
                                GCTGCAG GCCTGGGC  G
                                ||||||| ||||||||  |
                                CGACGTC CGGACCCG  C
                                    C       GT
GAM1700  C20orf100 3'  TCCCACCAGACTCTGCAG    52879        C    GC
                                CTGCAGAG CTGG  TGGGA
                                |||||||| ||||  |||||
                                GACGTCTC GACC  ACCCT
                                    A   __
GAM1700  C20orf110 3'  GCTCCCCAGCCCCCTGCCTG   80363     A  CT_      A
                                CAG GC   GGGCTGGG AGC
                                ||| ||   |||||||| |||
                                GTC CG   CCCGACCC TCG
                                  _ TCC       C
GAM1700  C20orf151 3'  CCTGCACCAGGGTCCACAGC   90094      CA  G    _  T
                                GCTG  GA CCTGG GC GGG
                                ||||  || ||||| || |||
                                CGAC  CT GGACC CG TCC
                                  AC  G    A  _
GAM1700  C20orf177 3'  GCTTCCCAACTCTCTCCAAGC  62836     GCA   CCT   C
                                GCT   GAG   GGG TGGGAAGC
                                |||   |||   ||| ||||||||
                                CGA   CTC   CTC ACCCTTCG
                                  AC_   T__   A
GAM1700  CARD11   5'  CCCCTCCCGGCCCTGCAGC   51572       A   T   CT
                                GCTGCAG GCC GGG  GGG
                                ||||||| ||| |||  |||
                                CGACGTC CGG CCC  CCC
                                    C   _   TC
GAM1700  CCR7     3'  CCCTCCCAGGCTCTCA      10222    C       CT
                                TG AGAGCCTGGG  GGG
                                || ||||||||||  |||
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                                AC TCTCGGACCC  CCC
                                 _        T_
GAM1700  CD36L1    3'  GCCCCCCAGCCCCACAGCCTGA 19744     G   A  CT__       AA
              GC                   GCT CAG GC    GGGCTGGG  GC
                                  ||| ||| ||    |||||||  ||
                                  CGA GTC CG    CCCGACCC  CG
                                   _  _  ACAC       CC
GAM1700  CDC14B    3'  GCCCCCCAGCCCAGTTACTGCA 54006       AGC        AA
              G                    CTGCAG   CTGGGCTGGG  GC
                                  ||||||   ||||||||||  ||
                                  GACGTC   GACCCGACCC  CG
                                     ATT         CC
GAM1700  CKAP4     5'  GCCTCCCAGCCCGCGGCCCGAG 23347     GCAGA  _        A
              C                    GCT     GCC TGGGCTGGGA GC
                                  |||     ||| ||||||||||  ||
                                  CGA     CGG GCCCGACCCT CG
                                    GCC__   C         C
GAM1700  CYP2S1    3'  CTCCCCTGGATCTGCAGC    48370        G  T   CT
                                  GCTGCAGA CC GGG  GGG
                                  ||||||||  ||  |||  |||
                                  CGACGTCT GG CCC  CTC
                                       A  T   __
GAM1700  DCAMKL1   5'  CCCCCAGCCCTGCAGC      17600       GAGCCT       AA
                                  GCTGCA     GGGCTGGG  G
                                  ||||||     ||||||||  |
                                  CGACGT     CCCGACCC  C
                                     _______       CC
GAM1700  DJ102H19.4 5'  GCTCCCCACCTGGCTCTCAGC  42241      C     T   C    A
                                  GCTG AGAGCC GGG TGGG AGC
                                  |||| |||||| ||| |||| |||
                                  CGAC TCTCGG TCC ACCC TCG
                                    _     _  _    C
GAM1700  DKFZP434C171 3'  GCTTCAGCCCCAGGCCCTAAGC 32192      GC  A      _  GG
                                  GCT  AG GCCTGGG CT  GAAGC
                                  |||  || |||||| ||  |||||
                                  CGA  TC CGGACCC GA  CTTCG
                                    A_  C      C  __
GAM1700  DKFZp434N0650 5'  CCTCCCCGGGCTGTGCAGC    51053        G       CT
                                  GCTGCA AGCCTGGG  GG
                                  |||||| ||||||||  ||
                                  CGACGT TCGGGCCC  CC
                                     G       CT
GAM1700  DKFZP434P0111 3'  CCCAGCCCCTGCAGC       67953        AGCCT
                                  GCTGCAG    GGGCTGGG
                                  |||||||    ||||||||
                                  CGACGTC    CCCGACCC
                                             _____
GAM1700  DKFZp761G2113 3'  TGGAAGCGCCTCCAGCCTCTAC 70471      C    C   _______   GGGA
              AGC                    GCTG AGAG CTGG      GCT    A
                                  |||| |||| ||||      |||    |
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                                CGAC TCTC GACC      CGA   T
                                  A   C   TCCG___   AGGG
GAM1700  FLJ10052  3'  GCCTCCCAGCCCAGATAGCTCA 36248   A   ___       A
             GC                   GC GAGC   CTGGGCTGGGA GC
                                || ||||  |||||||||| ||
                                CG CTCG   GACCCGACCCT CG
                                 A   ATA        C
GAM1700  FLJ11413  3'  CTTCCTAAAGATCTACAGC   44956     C   GC  GGGC
                                GCTG AGA  CT   TGGGAAG
                                |||| |||  ||   |||||||
                                CGAC TCT  GA   ATCCTTC
                                  A  A_  A___
GAM1700  FLJ11560  5'  GCCCCCCAGCCCAGGCCCAGC  48009     CAGA        AA
                                GCTG   GCCTGGGCTGGG  GC
                                ||||   ||||||||||||  ||
                                CGAC   CGGACCCGACCC  CG
                                  C___         CC
GAM1700  FLJ11743  3'  CCTGCGCCAGGTCTGCAGC   44842       G   _  T
                                GCTGCAGA CCTGG GC GGG
                                |||||||| ||||| || |||
                                CGACGTCT GGACC CG TCC
                                    _   G  _
GAM1700  FLJ12154  5'  CTTTCACAGACCCTACAGC   41956     CAGAGCCT  _  _
                                GCTG      GGG CTG GGAAG
                                ||||      ||| ||| |||||
                                CGAC      CCC GAC CTTTC
                                  AT_______  A  A
GAM1700  FLJ12891  5'  CCCCCCAGTCCTGCAGC    46923       AG C   CT
                                GCTGCAG  C TGGG  GGG
                                |||||||  | ||||  |||
                                CGACGTC  G ACCC  CCC
                                   CT _   __
GAM1700  FLJ13725  3'  GCCTCCCAGCCTCGGCTCAGC  68831    A    T      A
                                GC GAGCC GGGCTGGGA GC
                                || ||||| ||||||||| ||
                                CG CTCGG TCCGACCCT CG
                                 A    C       C
GAM1700  FLJ20234  5'  GCTTCCCAGCCCAGCTGGGGC  35287    G   AGC
                                GCT CAG   CTGGGCTGGGAAGC
                                ||| |||   |||||||||||||
                                CGG GTC   GACCCGACCCTTCG
                                  G  ___
GAM1700  FLJ21240  5'  CCTCCCTGGCCCTGAGC    46265    G   A   T   CT
                                GCT CAG GCC GGG  GGG
                                ||| ||| ||| |||  |||
                                CGA GTC CGG CCC  TCC
                                  _  C   T  __
GAM1700  FLJ22969  3'  TCCCAGCCCCTTCCAAGC   69219    GCA   CCT
                                GCT   GAG   GGGCTGGGA
                                |||   |||   |||||||||
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                                CGA  TTC  CCCGACCCT
                                  ACC  ___
GAM1700 GSK3A    5' CCCGGGCAGCCCGAGCCCCGCA 96978      AGA  C    ____
             GC                   GCTGC  GC TGGGCT   GGG
                                |||||  || ||||||   |||
                                CGACG  CG GCCCGA   CCC
                                   CCC  A    CGGG
GAM1700 HIF3A    3' CCCAGCTTTCTTTCTACAG   42652    C   CCT
                                CTG AGAG  GGGCTGGG
                                ||| ||||  ||||||||
                                GAC TCTT  TTCGACCC
                                  A   TCT
GAM1700 HUMZD58C02 3' CCGGGCCCAGGCCCCTCAGC  80575    C  A_      G
                                GCTG AG  GCCTGGGCT GG
                                |||| ||  |||||||||| ||
                                CGAC TC  CGGACCCGG CC
                                  _  CC       G
GAM1700 KCND1    5' CCTCCCCCAGATAACTCTCAGC 18341    C   C___    CT
                                GCTG AGAG   CTGGG  GGG
                                |||| ||||   |||||  |||
                                CGAC TCTC   GACCC  TCC
                                  _   AATA    CC
GAM1700 KIAA0161  5' CCTCCCCCAGCTCTGCAG    29196       C   CT
                                CTGCAGAGC TGGG  GGG
                                ||||||||| ||||  |||
                                GACGTCTCG ACCC  TCC
                                     _   CC
GAM1700 KIAA0280  3' CTTCCCAGAACCCTGCTGC   93298    AGCCT  __
                                GCAG    GGG  CTGGGAAG
                                ||||    |||  ||||||||
                                CGTC    CCC  GACCCTTC
                                  GT___   AA
GAM1700 KIAA0445  3' GCTTCCCAGCAACACCTGCAGT 28641       AGCCTGG
                                GCTGCAG     GCTGGGAAGC
                                |||||||     ||||||||||
                                TGACGTC     CGACCCTTCG
                                   CACAA__
GAM1700 KIAA0544  3' CCCGTCCCAGGCTCTGCA    71461          C
                                TGCAGAGCCTGGG TGGG
                                |||||||||||| ||||
                                ACGTCTCGGACCC GCCC
                                       T
GAM1700 KIAA0553  3' GCCTTTCACCCAGGCTCTCAGC 70449    C       C  GG A
                                GCTG AGAGCCTGGG TG  A GC
                                |||| |||||||||| ||  | ||
                                CGAC TCTCGGACCC AC  T CG
                                  _        _ TT C
GAM1700 KIAA0792  3' TGGAAGCGCTTCCAGCTCTGCA 28769        C  ________  GGGA
             GC                   GCTGCAGAGC TGG     GCT   A
                                |||||||||| |||      |||   |
```

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                                CGACGTCTCG ACC      CGA   T
                                      _  TTCG___   AGGG
GAM1700 KIAA1111 3' CAGATAACCCTGGCCCTACAGC 97943     C A   T  ____
                                GCTG AG GCC GGG    CTG
                                |||| || ||| |||    |||
                                CGAC TC CGG CCC    GAC
                                  A  C   T   AATA
GAM1700 KIAA1754 3' TCCAGTCTGCAGGCTCTGAGC  63935     G       __
                                GCT CAGAGCCTG  GGCTGGG
                                ||| |||||||||  |||||||
                                CGA GTCTCGGAC  CTGACCT
                                  _       GT
GAM1700 KIAA1821 3' CCCAGGTGTCCCAGCTCCACAG 72262      CA    C   ____
             C                   GCTG  GAGC TGGG    CTGGG
                                ||||  |||| ||||    |||||
                                CGAC  CTCG ACCC    GACCC
                                  AC    _   TGTG
GAM1700 KIAA1854 3' CTCCCCTGCCCCTGCAGC    72204       AGCCT   T  A
                                GCTGCAG    GGGC GGG AG
                                |||||||    |||| ||| ||
                                CGACGTC    CCCG CCC TC
                                     _____   T   C
GAM1700 KIAA1904 3' GCCTCCCAGCCAGGCCAG    73872     CAGA     G     A
                                CTG    GCCTGG CTGGGA GC
                                |||    |||||| |||||| ||
                                GAC    CGGACC GACCCT CG
                                 ____     _     C
GAM1700 LGI3     3' CCCCCCCTACTCTGCAGC    58395         CCT   CT
                                GCTGCAGAG   GGG  GGG
                                |||||||||   |||  |||
                                CGACGTCTC   CCC  CCC
                                     AT_  C_
GAM1700 LIPG     3' GCTCCCCAGCTCACTCTCTGAA 21232     G    CC       A
             GC                   GCT CAGAG  TGGGCTGGG AGC
                                ||| |||||  ||||||||| |||
                                CGA GTCTC  ACTCGACCC TCG
                                  A    TC       C
GAM1700 LYPLA3   3' CTGGGCCCTGGCCCCGCAGC   25561      AGA   T    G
                                GCTGC   GCC GGGCT GG
                                |||||   ||| ||||| ||
                                CGACG   CGG CCCGG TC
                                   CCC   T    G
GAM1700 MEIS3    3' TGGAAGCGCCTCCAGGCTCTGA 78873     G       _______  GGGA
             GC                   GCT CAGAGCCTGG      GCT    A
                                ||| ||||||||||      |||   |
                                CGA GTCTCGGACC      CGA    T
                                  _        TCCG___   AGGG
GAM1700 MGC14161 5' CCTGGTCCAGGGTCCGCAGC   52908      A  G      TG
                                GCTGC GA CCTGGGC  GG
                                ||||| || |||||||  ||
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                                CGACG CT GGACCTG  CC
                                  C  G      GT
GAM1700  MGC15548  5'  GCCTCCCAGCCCAGAGCCCAGC 52223      CAGA  _         A
                                GCTG   GC CTGGGCTGGGA GC
                                ||||   || ||||||||||| ||
                                CGAC   CG GACCCGACCCT CG
                                  C___  A         C
GAM1700  MGC3113   3'  CCTGTGCTCCCGGCTCCGCA  44061     A    T  _  _
                                TGC GAGCC GG GC TGGG
                                ||| ||||| || || ||||
                                ACG CTCGG CC CG GTCC
                                  C    C  T  T
GAM1700  MGC9564   3'  CCAGCCCAAACTGCACAGC   55618     __   AGCC
                                GCT  GCAG   TGGGCTGG
                                |||  ||||   ||||||||
                                CGA  CGTC   ACCCGACC
                                  CA   AA__
GAM1700  MOT8      5'  GCTCCCCAGCCCTTTGCTGCGC 38730    T   AGCCT      A
                                GC GCAG    GGGCTGGG AGC
                                || ||||    |||||||| |||
                                CG CGTC    CCCGACCC TCG
                                 _   GTTT_      C
GAM1700  OS4       5'  CCCCGCCCAGGCCCCCCAGC   20387     CAGA      T
                                GCTG   GCCTGGGC GGG
                                ||||   |||||||| |||
                                CGAC   CGGACCCG CCC
                                  CCCC       C
GAM1700  OVCOV1    3'  CTCCCCAGCCTGCTGCCAGC   32517     _  AGCC      A
                                GCTG CAG   TGGGCTGGG AG
                                |||| |||   ||||||||| ||
                                CGAC GTC   GTCCGACCC TC
                                  C  ____       C
GAM1700  OVCOV1    3'  CTTCCCAGGCTCTGACAGC   32518     _        CT
                                GCTG CAGAGCCTGGG  GG
                                |||| ||||||||||  ||
                                CGAC GTCTCGGACCC  TC
                                  A         T_
GAM1700  Rab11-FIP3 5'  CTGGGAAGCGCTTCACAGGCTC 28784      A     _ ________  GGGA
           CGCGGC                 GCTGC GAGCCTG G      GCT   AG
                                ||||| ||||||| |      |||   ||
                                CGGCG CTCGGAC C      CGA   TC
                                  C      A TTCG___   AGGG
GAM1700  RAB11B    3'  CCCCCCGGGCTCTCAGC     74334      C        CT
                                GCTG AGAGCCTGGG  GGG
                                |||| ||||||||||  |||
                                CGAC TCTCGGGCCC  CCC
                                  _       __
GAM1700  RAI15     3'  GCTTCCCAATGAGCACTCAGCA 67245      A  CCTGGGC
           GC                   GCTGC GAG      TGGGAAGC
                                ||||| |||      ||||||||
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                                CGACG CTC      ACCCTTCG
                                   A  ACGAGTA
GAM1700  RASD2    3'  CTTCTCTCCCAGCCCTGCA   27461      A  C   CT
                                TGCAG GC TGGG  GGGAAG
                                |||||| || ||||  ||||||
                                ACGTC CG ACCC  CTCTTC
                                   C  _   T_
GAM1700  RBPMS    5'  TCCAGCTCCAGCCCCACAGC   23438     CAGA  C  _
                                GCTG   GC TGG GCTGGG
                                ||||   || ||| ||||||
                                CGAC   CG ACC CGACCT
                                  ACCC  _  T
GAM1700  SARM     3'  CTTCCCCAGCCCCTCAGC    31288     C  AGCCT      _
                                GCTG AG    GGGCTGGG AAG
                                |||| ||    |||||||| |||
                                CGAC TC    CCCGACCC TTC
                                  _ _____      C
GAM1700  SNAP29   3'  CTTCCCTTTACAGTCTGCAGC  17712       GC   GGCT
                                GCTGCAGA  CTG   GGGAAG
                                ||||||||  |||   ||||||
                                CGACGTCT  GAC   CCCTTC
                                    __  ATTT
GAM1700  SPTLC2   3'  CTGGCCCTGGCTCCGCAGC   17992      A    T   TG
                                GCTGC GAGCC GGGC  G
                                ||||| ||||| ||||  |
                                CGACG CTCGG CCCG  C
                                   C    T   GT
GAM1700  STOML1   3'  TGGCCCAGGCTCTAAGC     17865     GC
                                GCT  AGAGCCTGGGCTG
                                |||  ||||||||||||
                                CGA  TCTCGGACCCGGT
                                  A_
GAM1700  VPS16    5'  GCTTCCCAGCTGCCGTCTGCA  42932       __  CTG
                                TGCAGA  GC   GGCTGGGAAGC
                                ||||||  ||   ||||||||||
                                ACGTCT  CG   TCGACCCTTCG
                                   GC  ___
GAM1700  WBSCR21  3'  CCCAGGCTTCAAGTCTCTGCAG 49300        C  ___  G
            C                    GCTGCAGAG CT   GG CTGGG
                                |||||||| ||   || |||||
                                CGACGTCTC GA   TC GACCC
                                     T  ACT  G
GAM1700  ZFP100   5'  GCTTCCCACAGCCCTGCCAGC  70587     CAGA  CT    __
                                GCTG   GC  GGGCT  GGGAAGC
                                ||||   ||  |||||  |||||||
                                CGAC   CG  CCCGA  CCCTTCG
                                  _____ T_    CA
GAM1700  LOC112868 3'  GCTTCCCAGAGACCCCTCTGAG 73269     G    CCT  ___
            C                    GCT CAGAG   GGG   CTGGGAAGC
                                ||| |||||   |||   |||||||||
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                                CGA GTCTC   CCC   GACCCTTCG
                                  _    ___   AGA
GAM1700  LOC113655 5'  TCCCAGCCTCGCAGC      57375      A  GCCTG
                                GCTGC GA    GGCTGGGA
                                ||||| ||    ||||||||
                                CGACG CT    CCGACCCT
                                  _ _____
GAM1700  LOC114987 5'  CCCAGCTCCAGCCCCGCAGC   59793      AGA  C  _
                                GCTGC   GC TGG GCTGGG
                                |||||   || ||| ||||||
                                CGACG   CG ACC CGACCC
                                   CCC  _   T
GAM1700  LOC123643 5'  CTCCCCAGCCCTCAGCAGC   76528      A  GCCT      A
                                GCTGC GA    GGGCTGGG AG
                                ||||| ||    |||||||| ||
                                CGACG CT    CCCGACCC TC
                                   A  ____       C
GAM1700  LOC126364 3'  GCTTCCCAGCCTGTCTACTGTA 76194      _  CCT
                                TGCAG AG   GGGCTGGGAAGC
                                ||||| ||   ||||||||||||
                                ATGTC TC   TCCGACCCTTCG
                                   A  TG_
GAM1700  LOC138150 5'  CTCAGCAGGCTCCCAGC     75819      CA     GG
                                GCTG  GAGCCT  GCTGGG
                                ||||  ||||||  ||||||
                                CGAC  CTCGGA  CGACTC
                                  C_     __
GAM1700  LOC143920 5'  TGGAAGCGCACCAGGCTCTGCA 77117            _______  GGGA
            GC                    GCTGCAGAGCCTGG     GCT    A
                                ||||||||||||||     |||   |
                                CGACGTCTCGGACC     CGA    T
                                       ACG___   AGGG
GAM1700  LOC144308 3'  CTCAGCCCGGGCCCCACAGC   83979      CAGA
                                GCTG    GCCTGGGCTGGG
                                ||||    ||||||||||||
                                CGAC    CGGGCCCGACTC
                                  ACCC
GAM1700  LOC145748 3'  GCTCGTCCTCAGCCCAAAGCCT 84474      A  C_     _  __
            GCA                   TGCAG GC  TGGGCTG GGA  AGC
                                ||||| ||  ||||||| |||  |||
                                ACGTC CG  ACCCGAC CCT  TCG
                                  _ AA      T   GC
GAM1700  LOC146657 5'  TGGAAGCGCACCAGGCTCTGCA 61080            _______  GGGA
            GC                    GCTGCAGAGCCTGG     GCT    A
                                ||||||||||||||     |||   |
                                CGACGTCTCGGACC     CGA    T
                                       ACG___   AGGG
GAM1700  LOC147160 5'  CCCACCAGGCTCCGCAGC     85069      A      GC
                                GCTGC GAGCCTGG  TGGG
                                ||||| ||||||||  ||||
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                                CGACG CTCGGACC  ACCC
                                  C       __
GAM1700  LOC147645 3'  CTGGGAAGCACCTCCAAGCCTC 79067         _ C  ________  GGGA
                TGCAGC                  GCTGCAGAG C TGG      GCT    AG
                                |||||||||  | |||      |||    ||
                                CGACGTCTC G ACC      CGA    TC
                                    C A   TCCA___   AGGG
GAM1700  LOC149069 5'  CCCATTCTTCCCAGGCTCCCAG 79883      CA       C____
                C                   GCTG  GAGCCTGGG    TGGG
                                ||||  |||||||||    ||||
                                CGAC  CTCGGACCC    ACCC
                                  C_       TTCTT
GAM1700  LOC150933 3'  CCAGGGCCCAGTCCCTGCAGC  86336       AGC      G_
                                GCTGCAG   CTGGGCT  GG
                                |||||||   |||||||  ||
                                CGACGTC   GACCCGG  CC
                                    CCT      GA
GAM1700  LOC151178 5'  CTTCCCAGCCTCCACAGC    80957     CA  GCCTG
                                GCTG  GA    GGCTGGGAAG
                                ||||  ||    ||||||||||
                                CGAC  CT    CCGACCCTTC
                                  AC  _____
GAM1700  LOC151534 5'  CTCCCCAGCTCCCGCAGC    57484      AGAGCCT      A
                                GCTGC      GGGCTGGG AG
                                |||||      |||||||| ||
                                CGACG      CTCGACCC TC
                                   CC_____       C
GAM1700  LOC151623 5'  CTTCCCAGCCCCACTCCCCGCA 86633      A__   CCT
                G                   CTGC   GAG   GGGCTGGGAAG
                                ||||   |||   ||||||||||||
                                GACG   CTC   CCCGACCCTTC
                                  CCC   AC_
GAM1700  LOC152485 3'  CCTCCCAGGCTCTGCAG     81490            CT
                                CTGCAGAGCCTGGG  GGG
                                ||||||||||||||  |||
                                GACGTCTCGGACCC  TCC
                                        __
GAM1700  LOC153443 3'  GCTTTCTCACCCCAGGCTCTGC 81688             C  _
                AGC                   GCTGCAGAGCCTGGG TG GGAAGC
                                ||||||||||||||| || ||||||
                                CGACGTCTCGGACCC AC CTTTCG
                                        C  T
GAM1700  LOC157586 5'  GCCTCCCAGCCCCGGCGCACGC 82401    _  AGA   T       A
                                GC TGC   GCC GGGCTGGGA GC
                                || |||   ||| |||||||||  ||
                                CG ACG   CGG CCCGACCCT CG
                                 C  ___   C       C
GAM1700  LOC158056 5'  CCCCCAGCCCCTGCCGC     82586    T   AGCCT       AA
                                GC GCAG    GGGCTGGG  G
                                || ||||    ||||||||  |
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                                CG CGTC    CCCGACCC  C
                                 C  _____      CC
GAM1700  LOC158067 3'  GCCCCCCAGCCTCGGCACAGC  83625     CAGA  T      AA
                                GCTG   GCC GGGCTGGG  GC
                                ||||   ||| ||||||||  ||
                                CGAC   CGG TCCGACCC  CG
                                  A___  C       CC
GAM1700  LOC169611 3'  CTTACCCAGGCTCACACAGC  83647     CA_       C
                                GCTG  GAGCCTGGG TGGG
                                ||||  ||||||||| ||||
                                CGAC  CTCGGACCC ATTC
                                  ACA       _
GAM1700  LOC199986 5'  TCCCAGAGGCTCTGAGC    91513     G       GGG
                                GCT CAGAGCCT  CTGGGA
                                ||| ||||||||  ||||||
                                CGA GTCTCGGA  GACCCT
                                  _      ___
GAM1700  LOC199992 3'  CCCAGCAGGCCCTCAGC    89903     C  A   GG
                                GCTG AG GCCT  GCTGGG
                                |||| || ||||  ||||||
                                CGAC TC CGGA  CGACCC
                                  _ C   __
GAM1700  LOC201252 5'  CCACCCCAGGCTCCCCAGC   89550     CA       C
                                GCTG  GAGCCTGGG TGG
                                ||||  ||||||||| |||
                                CGAC  CTCGGACCC ACC
                                  CC       C
GAM1700  LOC201965 5'  CTTCCCAGGCCCCACCAGC   90574     CAGAGCCT   _
                                GCTG       GGGC TGGGAAG
                                ||||       |||| |||||||
                                CGAC       CCCG ACCCTTC
                                  CAC_____   G
GAM1700  LOC203068 5'  GCCTCCCAGCCCCGGCGCACGC 90756    _  AGA  T      A
                                GC TGC   GCC GGGCTGGGA GC
                                || |||   ||| |||||||||  ||
                                CG ACG   CGG CCCGACCCT CG
                                 C  ___  C       C
GAM1700  LOC219920 5'  TTTGGCCCAGACCTGCAGC   94965       AGC     TG
                                GCTGCAG  CTGGGC  GG
                                |||||||  ||||||  ||
                                CGACGTC  GACCCG  TT
                                   CA_     GT
GAM1700  LOC221962 3'  TCCCAGCCCCACTCCCCGCAG  94243     A__  CCT
                                CTGC   GAG   GGGCTGGGA
                                ||||   |||   |||||||||
                                GACG   CTC   CCCGACCCT
                                  CCC   AC_
GAM1700  LOC253027 5'  CTCCCCAGCTCTGCA      98766        C   CT
                                TGCAGAGC TGGG  GGG
                                |||||||| ||||  |||
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                                ACGTCTCG ACCC  CTC
                                   _   __
GAM1700  LOC253150 3'  CCGGGCCCGGGCCCTGCA    97256      A       G
                                TGCAG GCCTGGGCT GG
                                ||||| ||||||||| ||
                                ACGTC CGGGCCCGG CC
                                   C       G
GAM1700  LOC253216 3'  GCCTCCCAGCCTGGCTGAAGC  96630    GCAG    T       A
                                GCT    AGCC GGGCTGGGA GC
                                |||    |||| ||||||||| ||
                                CGA    TCGG TCCGACCCT CG
                                  AG__   _       C
GAM1700  LOC253767 3'  CCCTCTGCGGACTCTGCAGC   96056        _ TG  CT
                                GCTGCAGAG CC  GG  GGG
                                ||||||||| ||  ||  |||
                                CGACGTCTC GG  TC  CCC
                                      A  CG  T_
GAM1700  LOC254531 5'  TCTCAGCCCTGCAGC       96674       GAGCCT
                                GCTGCA     GGGCTGGGA
                                ||||||     |||||||||
                                CGACGT     CCCGACTCT
                                   _______
GAM1700  LOC255043 3'  GCCTCCCAGCCCAGCCCAGC   97072      CAGA  C       A
                                GCTG    GC TGGGCTGGGA GC
                                ||||    || |||||||||| ||
                                CGAC    CG ACCCGACCCT CG
                                  C___  _        C
GAM1700  LOC255461 5'  TCCCAGCCCCACTCCCCGCAG  99142     A__   CCT
                                CTGC   GAG   GGGCTGGGA
                                ||||   |||   |||||||||
                                GACG   CTC   CCCGACCCT
                                  CCC   AC_
GAM1700  LOC255516 5'  TCCCAGCCCCACTCCCCGCAG  99156     A__   CCT
                                CTGC   GAG   GGGCTGGGA
                                ||||   |||   |||||||||
                                GACG   CTC   CCCGACCCT
                                  CCC   AC_
GAM1700  LOC256338 5'  CCTCCCAGGCTCCGCA      96251     A       CT
                                TGC GAGCCTGGG  GGG
                                ||| |||||||||  |||
                                ACG CTCGGACCC  TCC
                                  C       __
GAM1700  LOC90120  5'  CTCAGCAGGCTCCCAGC     62212      CA     GG
                                GCTG  GAGCCT  GCTGGG
                                ||||  ||||||  ||||||
                                CGAC  CTCGGA  CGACTC
                                  C_     __
GAM1700  LOC91179  3'  CCGGGCCCAGGCCCCTCAGC   65764     C  A_       G
                                GCTG AG  GCCTGGGCT GG
                                |||| ||  |||||||| ||
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                                CGAC TC  CGGACCCGG CC
                                  _ CC       G
GAM1700 LOC92841 5' TCCCAGCCCTCGGCCCAGC   71266     CAGA  T_
                                GCTG   GCC  GGGCTGGGA
                                ||||   |||  |||||||||
                                CGAC   CGG  CCCGACCCT
                                  C___   CT
GAM1700 LOC93587 5' CTTCCCTGTCAACTCTTCAGC  73041     C   CCTG  T
                                GCTG AGAG   GGC GGGAAG
                                |||| ||||   ||| ||||||
                                CGAC TCTC   CTG CCCTTC
                                  T   AA__  T
GAM1701 ADCY6    5' GGTCTTGAACTCCTGACCTTGT 40961            A
           GA                     TCACAAGGTCAGGAG TCGAGACC
                                  |||||||||||||| ||||||||
                                  AGTGTTCCAGTCCTC AGTTCTGG
                                           A
GAM1701 APAF1    3' GGTCTCGATCTCTTGACCTCAT 25978     CA
           GA                     TCA  AGGTCAGGAGATCGAGACC
                                  |||  ||||||||||||||||||
                                  AGT  TCCAGTTCTCTAGCTCTGG
                                    AC
GAM1701 APM1     3' GGTCTCGAACTCCTGACCTTGT 17788            A
           GA                     TCACAAGGTCAGGAG TCGAGACC
                                  |||||||||||||| ||||||||
                                  AGTGTTCCAGTCCTC AGCTCTGG
                                           A
GAM1701 APOL1    3' CGGTCTCGATCTCCTGACCTCT 14737     CA              ___
           TGA                     TCA  AGGTCAGGAGATCGAGACC   G
                                  |||  ||||||||||||||||||  |
                                  AGT  TCCAGTCCTCTAGCTCTGG   C
                                    TC              __
GAM1701 APPL     3' TCTCGATCTCCTGACCTCATGA 24958     CA
                                  TCA  AGGTCAGGAGATCGAGA
                                  |||  ||||||||||||||||
                                  AGT  TCCAGTCCTCTAGCTCT
                                    AC
GAM1701 ATP8B2   3' GTCTTGAATTCCTGACCTCCTG 65845     CA        A
           A                       TCA  AGGTCAGGAG TCGAGAC
                                  |||  |||||||||| |||||||
                                  AGT  TCCAGTCCTT AGTTCTG
                                    CC         A
GAM1701 BAZ2B    5' GGTCTCGATCTCCTGACCTTGT 26522
           GA                     TCACAAGGTCAGGAGATCGAGACC
                                  ||||||||||||||||||||||
                                  AGTGTTCCAGTCCTCTAGCTCTGG

GAM1701 BLAME    3' GGCCTCAATCCAGTCTTGAT   39655        ___  C   A
                                  GTCAGGA   GAT GAG CC
                                  |||||||   ||| ||| ||
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                                TAGTTCT   CTA CTC GG
                                    GAC   A   C
GAM1701  BRIP1    3'  GGTCTCGAACTCCTGGCCTCGT 50210      A        A
              GA                    TCAC AGGTCAGGAG TCGAGACC
                                    |||| |||||||||| ||||||||
                                    AGTG TCCGGTCCTC AGCTCTGG
                                      C         A
GAM1701  BSN      3'  GTCCTCCACATGACCTTGTGA  14388           ___    ATCGA
                                    TCACAAGGTCA   GGAG    GAC
                                    ||||||||||   ||||    |||
                                    AGTGTTCCAGT   CCTC    CTG
                                          ACA   _____
GAM1701  CASP2    3'  GGTCTTGATCTCCTGACCTCAT 53341     CA
              GA                    TCA  AGGTCAGGAGATCGAGACC
                                    |||  ||||||||||||||||||
                                    AGT  TCCAGTCCTCTAGTTCTGG
                                      AC
GAM1701  CASP2    3'  GGTCTTGATCTCCTGACCTCAT 53342     CA
              GA                    TCA  AGGTCAGGAGATCGAGACC
                                    |||  ||||||||||||||||||
                                    AGT  TCCAGTCCTCTAGTTCTGG
                                      AC
GAM1701  CASP2    3'  GGTCTTGATCTCCTGACCTCAT 53343     CA
              GA                    TCA  AGGTCAGGAGATCGAGACC
                                    |||  ||||||||||||||||||
                                    AGT  TCCAGTCCTCTAGTTCTGG
                                      AC
GAM1701  CASP8    3'  GGTCTTGATCTCCTGACCTCGT 8758       A
              GA                    TCAC AGGTCAGGAGATCGAGACC
                                    |||| ||||||||||||||||||
                                    AGTG TCCAGTCCTCTAGTTCTGG
                                      C
GAM1701  CASP8    3'  GGTCTTGATCTCCTGACCTCGT 8759       A
              GA                    TCAC AGGTCAGGAGATCGAGACC
                                    |||| ||||||||||||||||||
                                    AGTG TCCAGTCCTCTAGTTCTGG
                                      C
GAM1701  CDC6     3'  GGTCTTGAACTCCTGACC    8825          A
                                    GGTCAGGAG TCGAGACC
                                    ||||||||| ||||||||
                                    CCAGTCCTC AGTTCTGG
                                         A
GAM1701  COL18A1  3'  CTCTCCCCTGACCTGTGA    48342       A      A  TC
                                    TCACA GGTCAGG GA  GAG
                                    ||||| ||||||| ||  |||
                                    AGTGT CCAGTCC CT  CTC
                                      _      C __
GAM1701  CR1      3'  GGTCTGGATCTCCTGACCTCGT 6947       A          G
              GA                    TCAC AGGTCAGGAGATC AGACC
                                    |||| |||||||||||| |||||
```

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                                AGTG TCCAGTCCTCTAG TCTGG
                                  C           G
GAM1701  CXCL16   3'  GGTCTCGAACTCCTGACCTGGT 42175      A         A
                GA                TCAC AGGTCAGGAG TCGAGACC
                                  |||| |||||||||| ||||||||
                                AGTG TCCAGTCCTC AGCTCTGG
                                  G         A
GAM1701  CYP1A2   3'  GGTCTCCATCTCTTGACCTCGT 69660      A          C
                GA                TCAC AGGTCAGGAGAT GAGACC
                                  |||| |||||||||||| ||||||
                                AGTG TCCAGTTCTCTA CTCTGG
                                  C           C
GAM1701  DSC3     3'  GGTCTCGATCTCCTGACCTCGT 44631      A
                GA                TCAC AGGTCAGGAGATCGAGACC
                                  |||| ||||||||||||||||||
                                AGTG TCCAGTCCTCTAGCTCTGG
                                  C
GAM1701  DSC3     3'  GGTCTCGATCTCCTGACCTCGT 44632      A
                GA                TCAC AGGTCAGGAGATCGAGACC
                                  |||| ||||||||||||||||||
                                AGTG TCCAGTCCTCTAGCTCTGG
                                  C
GAM1701  DSCR3    3'  GGTCTTGAACTCCTGACCTCGT 21321      A         A
                GA                TCAC AGGTCAGGAG TCGAGACC
                                  |||| |||||||||| ||||||||
                                AGTG TCCAGTCCTC AGTTCTGG
                                  C         A
GAM1701  FANCF    3'  GGTCTCAAACACCTGACCTTGT 42984             AGATC
                GA                TCACAAGGTCAGG    GAGACC
                                  ||||||||||||     ||||||
                                AGTGTTCCAGTCC    CTCTGG
                                        ACAAA
GAM1701  FEZ1     3'  GGTCTCGAACTCCTGACCTGGT 18787      A         A
                GA                TCAC AGGTCAGGAG TCGAGACC
                                  |||| |||||||||| ||||||||
                                AGTG TCCAGTCCTC AGCTCTGG
                                  G         A
GAM1701  FGF5     3'  GGTCTCAATCCTGGCCTCTTGA 53665     CA        GATC
                                TCA  AGGTCAGGA   GAGACC
                                |||  |||||||||   ||||||
                                AGT  TCCGGTCCT   CTCTGG
                                  TC        AA__
GAM1701  FGF5     3'  GGTCTCAATCCTGGCCTCTTGA 53666     CA        GATC
                                TCA  AGGTCAGGA   GAGACC
                                |||  |||||||||   ||||||
                                AGT  TCCGGTCCT   CTCTGG
                                  TC        AA__
GAM1701  FUT1     3'  GGTCTCGATCTCCTGACCTCGT 5606       A
                GA                TCAC AGGTCAGGAGATCGAGACC
                                  |||| ||||||||||||||||||
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                                AGTG TCCAGTCCTCTAGCTCTGG
                                  C
GAM1701  FUT1     3'  GGTCTCGATCTCCTGACCTTGT 5607
                                ACAAGGTCAGGAGATCGAGACC
                                ||||||||||||||||||||||
                                TGTTCCAGTCCTCTAGCTCTGG

GAM1701  GHR      3'  GGTCTCGAGTCTCCTGACCTCG 5706       A          _
            TGA                    TCAC AGGTCAGGAGA TCGAGACC
                                |||| |||||||||| ||||||||
                                AGTG TCCAGTCCTCT AGCTCTGG
                                  C         G
GAM1701  GM2A     3'  GGTCTCGATCTCTTGACCTCGT 68385      A
            GA                     TCAC AGGTCAGGAGATCGAGACC
                                |||| ||||||||||||||||||
                                AGTG TCCAGTTCTCTAGCTCTGG
                                  C
GAM1701  HCS      3'  GGTCTTGGACTCCTGACCTCGT 38989      A        A
            GA                     TCAC AGGTCAGGAG TCGAGACC
                                |||| |||||||||| ||||||||
                                AGTG TCCAGTCCTC GGTTCTGG
                                  C        A
GAM1701  HLCS     5'  GGTTTCGAACTCCTGACCTCGT 6414       A        A
            GA                     TCAC AGGTCAGGAG TCGAGACC
                                |||| |||||||||| ||||||||
                                AGTG TCCAGTCCTC AGCTTTGG
                                  C        A
GAM1701  HTR1D    3'  GGTCTCGATCTCTTGACCTCGT 7848       A
            GA                     TCAC AGGTCAGGAGATCGAGACC
                                |||| ||||||||||||||||||
                                AGTG TCCAGTTCTCTAGCTCTGG
                                  C
GAM1701  HTR1E    5'  GGTCTTGAACCCCCGACCTCGG 7864     ACA    A  AGA
            A                     TC   AGGTC GG   TCGAGACC
                                ||   ||||| ||   ||||||||
                                AG   TCCAG CC   AGTTCTGG
                                 GC_    C  CCA
GAM1701  IGF1     3'  CTCAAACTCCTGACCTTGTGA  7071              ATC
                                TCACAAGGTCAGGAG   GAG
                                ||||||||||||||   |||
                                AGTGTTCCAGTCCTC   CTC
                                        AAA
GAM1701  IMPA2    5'  GGTCTTGAAGTCCTGACCT    96948         GA
                                AGGTCAGGA  TCGAGACC
                                |||||||||  ||||||||
                                TCCAGTCCT  AGTTCTGG
                                     GA
GAM1701  INMT     3'  GGTCTCGATCTCCTGACCTGGT 23221      A
            GA                     TCAC AGGTCAGGAGATCGAGACC
                                |||| ||||||||||||||||||
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                                AGTG TCCAGTCCTCTAGCTCTGG
                                  G
GAM1701 LCP1    5' GTCACTTCCTGCCTTGTGA  11284       T    ATCGA
                                TCACAAGG CAGGAG    GAC
                                |||||||| ||||||    |||
                                AGTGTTCC GTCCTT    CTG
                                     _     CA___
GAM1701 LYZ     3' GGTCTCGATCTCCTGACCTTGT 5899
            GA                    TCACAAGGTCAGGAGATCGAGACC
                                  ||||||||||||||||||||||||
                                  AGTGTTCCAGTCCTCTAGCTCTGG

GAM1701 MAD1L1  3' CTGGGTTCCTCACCTTGTGA  88871       C   G  G
                                TCACAAGGT AGGA ATC AG
                                ||||||||| |||| ||| ||
                                AGTGTTCCA TCCT TGG TC
                                     C   _  G
GAM1701 MDM2    3' GGTCTCGATCTCCTGACCTCGT 11497     A
            GA                    TCAC AGGTCAGGAGATCGAGACC
                                  |||| ||||||||||||||||||
                                  AGTG TCCAGTCCTCTAGCTCTGG
                                    C
GAM1701 MGEA5   3' GTCTCTTAACTGCACCTTGTGA 25225       _  GA  TC
                                TCACAAGGT CAG  GA  GAGAC
                                ||||||||| |||  ||  |||||
                                AGTGTTCCA GTC  TT  CTCTG
                                     C  AA  __
GAM1701 MPL     3' GGTCTCGATATCTGATCTCGTG 19357     A      AG
            A                     TCAC AGGTCAGG  ATCGAGACC
                                  |||| ||||||||  |||||||||
                                  AGTG TCTAGTCT  TAGCTCTGG
                                    C       A_
GAM1701 MTR     3' GGTCTTGATCTCCCGACCTCGT 6023      A    A
            GA                    TCAC AGGTC GGAGATCGAGACC
                                  |||| ||||| ||||||||||||
                                  AGTG TCCAG CCTCTAGTTCTGG
                                    C    C
GAM1701 NONO    3' TCTTGAACTCCTGACCTCGTGA 82894     A       A
                                TCAC AGGTCAGGAG TCGAGA
                                |||| |||||||||| ||||||
                                AGTG TCCAGTCCTC AGTTCT
                                  C        A
GAM1701 PCDHA9  3' GGTCTCGAACTCCTGACCTTGT 49849           A
            GA                    TCACAAGGTCAGGAG TCGAGACC
                                  |||||||||||||| ||||||||
                                  AGTGTTCCAGTCCTC AGCTCTGG
                                           A
GAM1701 PCDHA9  3' GGTCTCGATCTCCTGACCTCAT 49850    CA
            GA                    TCA  AGGTCAGGAGATCGAGACC
                                  |||  ||||||||||||||||||
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                                AGT  TCCAGTCCTCTAGCTCTGG
                                  AC
GAM1701  PIGR     3'  GGTCTCGATCTCCTGACCTCGT 73005      A
                GA                  TCAC AGGTCAGGAGATCGAGACC
                                    |||| ||||||||||||||||||
                                    AGTG TCCAGTCCTCTAGCTCTGG
                                      C
GAM1701  PIK3C2B  3'  GGTCTCGATCTCTTGACCTCGT 12107      A
                GA                  TCAC AGGTCAGGAGATCGAGACC
                                    |||| ||||||||||||||||||
                                    AGTG TCCAGTTCTCTAGCTCTGG
                                      C
GAM1701  PMCHL1   3'  GGTCTGGAACTCCTGACCTCGT 49918      A        A  G
                GA                  TCAC AGGTCAGGAG TC AGACC
                                    |||| |||||||||| || |||||
                                    AGTG TCCAGTCCTC AG TCTGG
                                      C        A  G
GAM1701  POU2AF1  3'  GGTCTCGAACTCCTGACCTTGT 21748             A
                GA                  TCACAAGGTCAGGAG TCGAGACC
                                    |||||||||||||| ||||||||
                                    AGTGTTCCAGTCCTC AGCTCTGG
                                             A
GAM1701  PPID     3'  GGTCTTGAACTCCTGACCTTGT 88826             A
                GA                  TCACAAGGTCAGGAG TCGAGACC
                                    |||||||||||||| ||||||||
                                    AGTGTTCCAGTCCTC AGTTCTGG
                                             A
GAM1701  PRKWNK3  3'  GGTCTCAAACTCCTAACCTTGT 62235        C    ATC
                GA                  TCACAAGGT AGGAG   GAGACC
                                    ||||||||| |||||   ||||||
                                    AGTGTTCCA TCCTC   CTCTGG
                                         A    AAA
GAM1701  PRPSAP1  3'  GGTCTCGACCCTGGACCTCCTG 12405     CA    _  AGA
                A                    TCA  AGGTC AGG   TCGAGACC
                                    |||  ||||| |||   ||||||||
                                    AGT  TCCAG TCC   AGCTCTGG
                                      CC    G  C__
GAM1701  PRY      3'  GGCCTCCAATTCTGACCTT   60893         GATC  A
                                    AAGGTCAGGA   GAG CC
                                    ||||||||||   ||| ||
                                    TTCCAGTCTT   CTC GG
                                         AAC_  C
GAM1701  PTGIS    3'  GGTCTCGAACTCCTGACCTCGT 8220      A        A
                GA                  TCAC AGGTCAGGAG TCGAGACC
                                    |||| |||||||||| ||||||||
                                    AGTG TCCAGTCCTC AGCTCTGG
                                      C        A
GAM1701  PTGIS    3'  GGTCTTGATCTCCTGAGCTCGT 8221      A  G
                GA                  TCAC AG TCAGGAGATCGAGACC
                                    |||| || ||||||||||||||||
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                                AGTG TC AGTCCTCTAGTTCTGG
                                  C  G
GAM1701  RAB36    3'  GGTCTCGATGATCTGACCTCGT 18175      A       AG
                GA                TCAC AGGTCAGG  ATCGAGACC
                                  |||| ||||||||  |||||||||
                                  AGTG TCCAGTCT  TAGCTCTGG
                                    C       AG
GAM1701  RABL2A   3'  GGTCTCGATCTCCTCACCTCGT 26412      A   C
                GA                TCAC AGGT AGGAGATCGAGACC
                                  |||| |||| ||||||||||||||
                                  AGTG TCCA TCCTCTAGCTCTGG
                                    C   C
GAM1701  RABL2B   3'  GGTCTCGATCTCCTCACCTCGT 23983      A   C
                GA                TCAC AGGT AGGAGATCGAGACC
                                  |||| |||| ||||||||||||||
                                  AGTG TCCA TCCTCTAGCTCTGG
                                    C   C
GAM1701  RAD50    5'  GATCCTCCTGACCCTGAGA   20409    A  A       _
                                  TC CA GGTCAGGAG ATC
                                  || || ||||||||| |||
                                  AG GT CCAGTCCTC TAG
                                   A  C        C
GAM1701  RPP30    3'  GGTCTCAATCTCCTGACCT   22205            C
                                  AGGTCAGGAGAT GAGACC
                                  |||||||||||| ||||||
                                  TCCAGTCCTCTA CTCTGG
                                        A
GAM1701  SEDL     3'  GGTCTTGAACTCCTGACCTCGT 28105      A        A
                GA                TCAC AGGTCAGGAG TCGAGACC
                                  |||| |||||||||| ||||||||
                                  AGTG TCCAGTCCTC AGTTCTGG
                                    C         A
GAM1701  SEDL     3'  GGTCTTGAACTCCTGACCTCGT 28106      A        A
                GA                TCAC AGGTCAGGAG TCGAGACC
                                  |||| |||||||||| ||||||||
                                  AGTG TCCAGTCCTC AGTTCTGG
                                    C         A
GAM1701  SERPINB9 3'  GGTGTCGATCTCCTGACCTCGT 16026      A            G
                GA                TCAC AGGTCAGGAGATCGA ACC
                                  |||| ||||||||||||||| |||
                                  AGTG TCCAGTCCTCTAGCT TGG
                                    C             G
GAM1701  SH3GL3   5'  GGTCTCGATCTCCTGACCTCGT 13113      A
                GA                TCAC AGGTCAGGAGATCGAGACC
                                  |||| ||||||||||||||||||
                                  AGTG TCCAGTCCTCTAGCTCTGG
                                    C
GAM1701  SLC15A1  3'  GGTCTCGATCTCTTGACCTGGT 18644      A
                GA                TCAC AGGTCAGGAGATCGAGACC
                                  |||| ||||||||||||||||||
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                                AGTG TCCAGTTCTCTAGCTCTGG
                                  G
GAM1701  SNAP23   3'  GGTCTTGGACTCCTGACGTCGT 15142      AAG       A
             GA                   TCAC   GTCAGGAG TCGAGACC
                                  ||||   |||||||| ||||||||
                                  AGTG   CAGTCCTC GGTTCTGG
                                    CTG       A
GAM1701  TAPBP    3'  GGTCTCGATCTCCTAACCTGGT 13577      A    C
             GA                   TCAC AGGT AGGAGATCGAGACC
                                  |||| |||| ||||||||||||||
                                  AGTG TCCA TCCTCTAGCTCTGG
                                    G   A
GAM1701  TAPBP    3'  GGTCTCGATCTCCTGACCTTGT 13578
             GA                   TCACAAGGTCAGGAGATCGAGACC
                                  ||||||||||||||||||||||||
                                  AGTGTTCCAGTCCTCTAGCTCTGG

GAM1701  TCIRG1   3'  CTCCTTCCTGACCTCTG     21204    _        ATC
                                  CA AGGTCAGGAG   GAG
                                  || ||||||||||   |||
                                  GT TCCAGTCCTT   CTC
                                   C         C__
GAM1701  TDGF1    3'  GGTCTCGAACTCTGACCTTGTG 13660           G  A
             A                     TCACAAGGTCAG AG TCGAGACC
                                  |||||||||||| || ||||||||
                                  AGTGTTCCAGTC TC AGCTCTGG
                                        _  A
GAM1701  TERF2    3'  GGTCTCGATCTCCTGACCTCGT 20159      A
             GA                   TCAC AGGTCAGGAGATCGAGACC
                                  |||| ||||||||||||||||||
                                  AGTG TCCAGTCCTCTAGCTCTGG
                                    C
GAM1701  TES      3'  GGTCTCAAACTCCTGACCT    72463          ATC
                                  AGGTCAGGAG   GAGACC
                                  ||||||||||   ||||||
                                  TCCAGTCCTC   CTCTGG
                                       AAA
GAM1701  TIM3     3'  GGTCTCAAACTCCTGACCTCAT 52359     CA        ATC
             GA                   TCA  AGGTCAGGAG   GAGACC
                                  |||  ||||||||||   ||||||
                                  AGT  TCCAGTCCTC   CTCTGG
                                    AC         AAA
GAM1701  TP53BP2  5'  GGTCTCGATCTCCTGACCTTGT 19465
             GA                   TCACAAGGTCAGGAGATCGAGACC
                                  ||||||||||||||||||||||||
                                  AGTGTTCCAGTCCTCTAGCTCTGG

GAM1701  TRPM6    3'  GGTCTCAAACTCCTGACCT    35035          ATC
                                  AGGTCAGGAG   GAGACC
                                  ||||||||||   ||||||
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                                TCCAGTCCTC   CTCTGG
                                     AAA
GAM1701  UGDH     3'  GGTCTCAATCTCCTGACCTTGT 14001              C
                GA                TCACAAGGTCAGGAGAT GAGACC
                                  |||||||||||||||| ||||||
                                  AGTGTTCCAGTCCTCTA CTCTGG
                                        A
GAM1701  VENTX2   3'  GGTCTCAAACTCCTGACCCTGT 27863       A       ATC
                GA                TCACA GGTCAGGAG   GAGACC
                                  ||||| |||||||||   ||||||
                                  AGTGT CCAGTCCTC   CTCTGG
                                    C        AAA
GAM1701  VHL      3'  GGTCTTGATCTCCTGACCTTGT 6871
                GA                TCACAAGGTCAGGAGATCGAGACC
                                  ||||||||||||||||||||||||
                                  AGTGTTCCAGTCCTCTAGTTCTGG

GAM1701  VIPR2    3'  GGTCTCGATCTCCTGACCTCGT 14072      A
                GA                TCAC AGGTCAGGAGATCGAGACC
                                  |||| ||||||||||||||||||
                                  AGTG TCCAGTCCTCTAGCTCTGG
                                    C
GAM1701  WHSC1    3'  GGTCTTGAACTCCTGACCTCGT 24683      A        A
                GA                TCAC AGGTCAGGAG TCGAGACC
                                  |||| |||||||||| ||||||||
                                  AGTG TCCAGTCCTC AGTTCTGG
                                    C         A
GAM1701  WHSC1    5'  GGTCTTGAACTCCTGACCTTGT 24684              A
                GA                TCACAAGGTCAGGAG TCGAGACC
                                  |||||||||||||| ||||||||
                                  AGTGTTCCAGTCCTC AGTTCTGG
                                        A
GAM1701  YES1     3'  GGTCTCGATCTCCTGACCTTGT 19542
                GA                TCACAAGGTCAGGAGATCGAGACC
                                  ||||||||||||||||||||||||
                                  AGTGTTCCAGTCCTCTAGCTCTGG

GAM1701  ZNF264   3'  GGTCTCAAACTCCTGACCTTGT 14221             ATC
                GA                TCACAAGGTCAGGAG   GAGACC
                                  ||||||||||||||   ||||||
                                  AGTGTTCCAGTCCTC   CTCTGG
                                        AAA
GAM1701  ZNF264   3'  GGTCTTGAACTCTTGACCTCAT 14222     CA       A
                GA                TCA  AGGTCAGGAG TCGAGACC
                                  |||  |||||||||| ||||||||
                                  AGT  TCCAGTTCTC AGTTCTGG
                                    AC         A
GAM1701  APOL2    3'  GGTCTCCATCTCCTGACCTCGT 48793      A         C
                GA                TCAC AGGTCAGGAGAT GAGACC
                                  |||| ||||||||||| ||||||
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                                AGTG TCCAGTCCTCTA CTCTGG
                                  C          C
GAM1701  ARHF     3'  GGTCTTGAACTCCTGACCTCGT 39275      A        A
                GA                  TCAC AGGTCAGGAG TCGAGACC
                                    |||| |||||||||| ||||||||
                                    AGTG TCCAGTCCTC AGTTCTGG
                                      C        A
GAM1701  ARHGAP11A 3'  GGTCTCGATCTCCTGACCTTGT 29452
                GA                  TCACAAGGTCAGGAGATCGAGACC
                                    ||||||||||||||||||||||||
                                    AGTGTTCCAGTCCTCTAGCTCTGG

GAM1701  ASE-1    3'  CGGTCTCGATCTCCTGACCTCC 24977     CA              ___
                TGA                  TCA  AGGTCAGGAGATCGAGACC   G
                                    |||  ||||||||||||||||||  |
                                    AGT  TCCAGTCCTCTAGCTCTGG   C
                                      CC             __
GAM1701  ASE-1    3'  GGTCTCGAACTCCTGACCTCGT 24987      A        A
                GA                  TCAC AGGTCAGGAG TCGAGACC
                                    |||| |||||||||| ||||||||
                                    AGTG TCCAGTCCTC AGCTCTGG
                                      C        A
GAM1701  ATP6V0A1  3'  GACCTGACCCGACCTTGTG    18987          A __ A
                                    CACAAGGTC GG  AG TC
                                    ||||||||| ||  || ||
                                    GTGTTCCAG CC  TC AG
                                          C  AG  C
GAM1701  BAG5     3'  GGTCTCGAACTCCTGACCTCGT 18043      A        A
                GA                  TCAC AGGTCAGGAG TCGAGACC
                                    |||| |||||||||| ||||||||
                                    AGTG TCCAGTCCTC AGCTCTGG
                                      C        A
GAM1701  BAGE     3'  GATCTCCTGACCTCGTGA     8640       A
                                    TCAC AGGTCAGGAGATC
                                    |||| ||||||||||||
                                    AGTG TCCAGTCCTCTAG
                                      C
GAM1701  BAGE     3'  GGTCTCGATCTCCTGACCTCGT 8641       A
                GA                  TCAC AGGTCAGGAGATCGAGACC
                                    |||| ||||||||||||||||||
                                    AGTG TCCAGTCCTCTAGCTCTGG
                                      C
GAM1701  BMF      3'  CTGGATCCTGACCTGT      54282     A       GA  G
                                    ACA GGTCAGGA  TC AG
                                    ||| ||||||||  || ||
                                    TGT CCAGTCCT  AG TC
                                      _       __  G
GAM1701  BNIP-S   3'  GGTCTCGATCTCTTGACCTCGT 57107      A
                GA                  TCAC AGGTCAGGAGATCGAGACC
                                    |||| ||||||||||||||||||
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                                AGTG TCCAGTTCTCTAGCTCTGG
                                  C
GAM1701  BTN3A1    3'  GGTCTCGATCTCTTGACCTCAT 23894     CA
                GA                TCA  AGGTCAGGAGATCGAGACC
                                  |||  ||||||||||||||||||
                                  AGT  TCCAGTTCTCTAGCTCTGG
                                    AC
GAM1701  C11orf17  3'  GGTCTCGATCTCTTGACCTCGT 40585      A
                GA                TCAC AGGTCAGGAGATCGAGACC
                                  ||||| ||||||||||||||||||
                                  AGTG TCCAGTTCTCTAGCTCTGG
                                    C
GAM1701  C13orf1   3'  GGTCTCAAACTCCTGACCTCAT 40366     CA        ATC
                GA                TCA  AGGTCAGGAG   GAGACC
                                  |||  ||||||||||   ||||||
                                  AGT  TCCAGTCCTC   CTCTGG
                                    AC         AAA
GAM1701  C6orf5    3'  GGTCTCGAACTCCTGACCTTGT 32000              A
                GA                TCACAAGGTCAGGAG TCGAGACC
                                  |||||||||||||| ||||||||
                                  AGTGTTCCAGTCCTC AGCTCTGG
                                           A
GAM1701  C9orf9    3'  GGTCTCAATCTCCTGACCTCAT 39030     CA          C
                GA                TCA  AGGTCAGGAGAT GAGACC
                                  |||  |||||||||||| ||||||
                                  AGT  TCCAGTCCTCTA CTCTGG
                                    AC           A
GAM1701  CEACAM8   3'  GGTCTCAATCTCCTGACTTCAT 10184     CA          C
                GG                TCA  AGGTCAGGAGAT GAGACC
                                  |||  |||||||||||| ||||||
                                  GGT  TTCAGTCCTCTA CTCTGG
                                    AC           A
GAM1701  DKFZP434C212 3'  CTCAATCTCCTGACCTCGTGA  69485      A          C
                                  TCAC AGGTCAGGAGAT GAG
                                  |||| |||||||||||| |||
                                  AGTG TCCAGTCCTCTA CTC
                                    C           A
GAM1701  DKFZP564O0523 3'  GGTCTCGAACTCCTGACCTTGT 50422              A
                GA                TCACAAGGTCAGGAG TCGAGACC
                                  |||||||||||||| ||||||||
                                  AGTGTTCCAGTCCTC AGCTCTGG
                                           A
GAM1701  DKFZp761J139 5'  GGTCTCGATATCCTGACCTTGT 51109            G
                GA                TCACAAGGTCAGGA ATCGAGACC
                                  |||||||||||||| |||||||||
                                  AGTGTTCCAGTCCT TAGCTCTGG
                                           A
GAM1701  DKFZp761N1114 3'  GGTCTTGATCTCCTGACCTCAT 79789     CA
                GA                TCA  AGGTCAGGAGATCGAGACC
                                  |||  ||||||||||||||||||
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                                AGT  TCCAGTCCTCTAGTTCTGG
                                  AC
GAM1701  DKFZp762E1511 3'  GTCTGTCTCCTGCCCCATGA   60251     CAA  T       CG
                                TCA   GG CAGGAGAT  AGAC
                                |||   || ||||||||  ||||
                                AGT   CC GTCCTCTG  TCTG
                                  ACC  _       __
GAM1701  DRCTNNB1A 3'  GCTCCCCTGACTTTATGA    51810     C        AGATC   A
                                TCA AAGGTCAGG     GAG C
                                ||| |||||||||     ||| |
                                AGT TTTCAGTCC     CTC G
                                  A        C____   _
GAM1701  FLJ00060  5'  GGTCTTTATCTCCTGACCTCAT 61750      CA          C
            GA                    TCA  AGGTCAGGAGAT GAGACC
                                ||||  |||||||||||| ||||||
                                AGT  TCCAGTCCTCTA TTCTGG
                                  AC           T
GAM1701  FLJ10298  3'  GGTCTCAAACTCCTGACCTAGT 36461       A         ATC
            GA                    TCAC AGGTCAGGAG   GAGACC
                                |||| ||||||||||   ||||||
                                AGTG TCCAGTCCTC   CTCTGG
                                  A         AAA
GAM1701  FLJ10560  3'  GGTCTCGATCTCCTGACCTCGT 36798      A
            GA                    TCAC AGGTCAGGAGATCGAGACC
                                |||| ||||||||||||||||||
                                AGTG TCCAGTCCTCTAGCTCTGG
                                  C
GAM1701  FLJ11126  3'  GTCTGAATCCTGACCCCTTGA  37653     CAA       GA  G
                                TCA   GGTCAGGA  TC AGAC
                                |||   ||||||||  || ||||
                                AGT   CCAGTCCT  AG TCTG
                                  TCC       A_  _
GAM1701  FLJ12581  3'  GGTCTCGATCTCCTGACCTTGT 46339
            GA                    TCACAAGGTCAGGAGATCGAGACC
                                ||||||||||||||||||||||||
                                AGTGTTCCAGTCCTCTAGCTCTGG

GAM1701  FLJ12876  3'  GATCTCCTGACCTCGTGA    43094      A
                                TCAC AGGTCAGGAGATC
                                |||| ||||||||||||
                                AGTG TCCAGTCCTCTAG
                                  C
GAM1701  FLJ12876  3'  GGTCTCGATCTCCTGACCTCGT 43096      A
            GA                    TCAC AGGTCAGGAGATCGAGACC
                                |||| ||||||||||||||||||
                                AGTG TCCAGTCCTCTAGCTCTGG
                                  C
GAM1701  FLJ12960  3'  GGTCTCGATCTCCTGACCTCAT 45303     CA
            GA                    TCA  AGGTCAGGAGATCGAGACC
                                |||  ||||||||||||||||||
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                                AGT  TCCAGTCCTCTAGCTCTGG
                                  AC
GAM1701  FLJ12975  3'  TCTCGAACTCCTGACCTCATGA 70198     CA        A
                                TCA  AGGTCAGGAG TCGAGA
                                |||  |||||||||| ||||||
                                AGT  TCCAGTCCTC AGCTCT
                                  AC         A
GAM1701  FLJ14346  5'  GTCTCGATCTCTGTCCTGTGG  47371      A  T   G
                                TCACA GG CAG AGATCGAGAC
                                ||||| || ||| ||||||||||
                                GGTGT CC GTC TCTAGCTCTG
                                   _  T  _
GAM1701  FLJ14442  3'  GGTCTCAAACTTCTGACCTCGT 52388      A        ATC
            GA                    TCAC AGGTCAGGAG   GAGACC
                                |||| ||||||||||   ||||||
                                AGTG TCCAGTCTTC   CTCTGG
                                  C         AAA
GAM1701  FLJ20045  3'  TCTCGAACTCCTGACCTCGTGA 34894      A        A
                                TCAC AGGTCAGGAG TCGAGA
                                |||| |||||||||| ||||||
                                AGTG TCCAGTCCTC AGCTCT
                                  C         A
GAM1701  FLJ20097  3'  GGTCTCTATCTCCTGACCTCGT 35048      A         C
            GA                    TCAC AGGTCAGGAGAT GAGACC
                                |||| |||||||||||| ||||||
                                AGTG TCCAGTCCTCTA CTCTGG
                                  C          T
GAM1701  FLJ20136  3'  GTCTCGAACTCCTGACCTTGTG 35101             A
            A                     TCACAAGGTCAGGAG TCGAGAC
                                |||||||||||||| |||||||
                                AGTGTTCCAGTCCTC AGCTCTG
                                          A
GAM1701  FLJ20511  3'  GGTCTCGATCTCCTGACCTCGT 35778      A
            GA                    TCAC AGGTCAGGAGATCGAGACC
                                |||| ||||||||||||||||||
                                AGTG TCCAGTCCTCTAGCTCTGG
                                  C
GAM1701  FLJ20700  3'  GGTCTCGAACTCCTGACCTCAT 36018     CA        A
            GA                    TCA  AGGTCAGGAG TCGAGACC
                                |||  |||||||||| ||||||||
                                AGT  TCCAGTCCTC AGCTCTGG
                                  AC         A
GAM1701  FLJ20813  3'  GGTCTCAAACTCCTGACCTCAT 36133     CA        ATC
            GA                    TCA  AGGTCAGGAG   GAGACC
                                |||  ||||||||||   ||||||
                                AGT  TCCAGTCCTC   CTCTGG
                                  AC         AAA
GAM1701  FLJ21302  3'  GGTCTCGAACGCCTGACCTCAT 43512     CA       AGA
            GA                    TCA  AGGTCAGG   TCGAGACC
                                |||  ||||||||   ||||||||
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                                AGT  TCCAGTCC   AGCTCTGG
                                  AC       GCA
GAM1701  FLJ21603  3'  TCTCAATCTCCTGACCTCGTGA 45781      A          C
                                TCAC AGGTCAGGAGAT GAGA
                                |||| |||||||||||| ||||
                                AGTG TCCAGTCCTCTA CTCT
                                  C          A
GAM1701  FLJ22167  5'  GGTCTCGATCTCCTGACCTCGT 44877      A
           GA                     TCAC AGGTCAGGAGATCGAGACC
                                |||| ||||||||||||||||||||
                                AGTG TCCAGTCCTCTAGCTCTGG
                                  C
GAM1701  FLJ22635  3'  GTCTCAATCCCAGGCTCCTCTT 47674      ____  A  A   C
           G                     CAAG    GTC GG GAT GAGAC
                                ||||    ||| || ||| |||||
                                GTTC    CGG CC CTA CTCTG
                                  TCCT   A  _   A
GAM1701  FLJ22794  3'  GGTCTCGAACTCCTGACCTCGT 93252      A        A
           GA                     TCAC AGGTCAGGAG TCGAGACC
                                |||| |||||||||| ||||||||
                                AGTG TCCAGTCCTC AGCTCTGG
                                  C         A
GAM1701  FLJ23392  3'  GGTCTCGATCTCCTGACCTCGT 45901      A
           GA                     TCAC AGGTCAGGAGATCGAGACC
                                |||| ||||||||||||||||||||
                                AGTG TCCAGTCCTCTAGCTCTGG
                                  C
GAM1701  FLJ23519  3'  GGTCTTGATATCCTGACCTCGT 50955      A       G
           GA                     TCAC AGGTCAGGA ATCGAGACC
                                |||| ||||||||| |||||||||
                                AGTG TCCAGTCCT TAGTTCTGG
                                  C        A
GAM1701  FLJ23556  3'  GATCTCCTGACCTTGTGA    46444
                                TCACAAGGTCAGGAGATC
                                ||||||||||||||||||
                                AGTGTTCCAGTCCTCTAG

GAM1701  FLJ30532  3'  GGTCTCAAGCTCCTGACCT    59224          ATC
                                AGGTCAGGAG   GAGACC
                                |||||||||   ||||||
                                TCCAGTCCTC   CTCTGG
                                     GAA
GAM1701  FLJ31101  3'  GGTCTTGAACTCCTGACCTCAT 36167     CA        A
           GA                     TCA  AGGTCAGGAG TCGAGACC
                                |||  |||||||||| ||||||||
                                AGT  TCCAGTCCTC AGTTCTGG
                                  AC         A
GAM1701  FLJ32894  3'  GGTCTCGAACTCCTGACCTCGG 59001    ACA        A
           GA                     TC   AGGTCAGGAG TCGAGACC
                                ||   |||||||||| ||||||||
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                                AG   TCCAGTCCTC AGCTCTGG
                                 GGC         A
GAM1701  GNG4     3'  GGTCTCAAACTCCTGACCTCGT 16851       A         ATC
                GA                  TCAC AGGTCAGGAG   GAGACC
                                    |||| ||||||||||   ||||||
                                    AGTG TCCAGTCCTC   CTCTGG
                                      C         AAA
GAM1701  GOLGA3   3'  GGTCTCGATCTCCTGACCT    20893
                                    AGGTCAGGAGATCGAGACC
                                    ||||||||||||||||||
                                    TCCAGTCCTCTAGCTCTGG

GAM1701  GREB1    3'  GGTCTCGATCTCCTGACCTCGT 28575       A
                GA                  TCAC AGGTCAGGAGATCGAGACC
                                    |||| ||||||||||||||||||
                                    AGTG TCCAGTCCTCTAGCTCTGG
                                      C
GAM1701  GTF2E1   3'  TCTCGATCTCCTGACCTCATGA 19806      CA
                                    TCA  AGGTCAGGAGATCGAGA
                                    |||  |||||||||||||||
                                    AGT  TCCAGTCCTCTAGCTCT
                                      AC
GAM1701  HARS2    3'  GGTCTCGATCTCCTGCCCTGGT 55868       A   T
                GA                  TCAC AGG CAGGAGATCGAGACC
                                    |||| ||| ||||||||||||||
                                    AGTG TCC GTCCTCTAGCTCTGG
                                      G   C
GAM1701  HSPC065  3'  GGTCTCGAACTCCTGACCTCAT 27157      CA         A
                GA                  TCA  AGGTCAGGAG TCGAGACC
                                    |||  |||||||||| ||||||||
                                    AGT  TCCAGTCCTC AGCTCTGG
                                      AC         A
GAM1701  HT002    3'  GGTCTCGATCTCCTGACCTCGT 26800       A
                GA                  TCAC AGGTCAGGAGATCGAGACC
                                    |||| ||||||||||||||||||
                                    AGTG TCCAGTCCTCTAGCTCTGG
                                      C
GAM1701  ICK      3'  GGCCTCGATCTCCTGACCTCGT 33690       A            A
                GA                  TCAC AGGTCAGGAGATCGAG CC
                                    |||| |||||||||||||| ||
                                    AGTG TCCAGTCCTCTAGCTC GG
                                      C             C
GAM1701  JAM1     3'  GGTCTCAAACTCCTGACCTCTT 34237      CA         ATC
                GA                  TCA  AGGTCAGGAG   GAGACC
                                    |||  ||||||||||   ||||||
                                    AGT  TCCAGTCCTC   CTCTGG
                                      TC         AAA
GAM1701  JAM1     3'  GGTCTCAAACTCCTGACCTCTT 34238      CA         ATC
                GA                  TCA  AGGTCAGGAG   GAGACC
                                    |||  ||||||||||   ||||||
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                                AGT  TCCAGTCCTC   CTCTGG
                                  TC         AAA
GAM1701  JM11     3'  GGTCTTGAACTCTTGACCTCGT 54366      A         A
              GA                  TCAC AGGTCAGGAG TCGAGACC
                                  |||| |||||||||| ||||||||
                                  AGTG TCCAGTTCTC AGTTCTGG
                                    C         A
GAM1701  KIAA0087 3'  GGTCTTGAACTCCTGACCTTGT 29345             A
              GG                  TCACAAGGTCAGGAG TCGAGACC
                                  |||||||||||||| ||||||||
                                  GGTGTTCCAGTCCTC AGTTCTGG
                                           A
GAM1701  KIAA0426 3'  GGTCTCGAACTCCTGACCTTGT 28930             A
              GA                  TCACAAGGTCAGGAG TCGAGACC
                                  |||||||||||||| ||||||||
                                  AGTGTTCCAGTCCTC AGCTCTGG
                                           A
GAM1701  KIAA0459 3'  GGTCTCAAACTCCTGACCTTGT 61657             ATC
              GA                  TCACAAGGTCAGGAG   GAGACC
                                  ||||||||||||||   ||||||
                                  AGTGTTCCAGTCCTC   CTCTGG
                                           AAA
GAM1701  KIAA0469 3'  GGTCTGGATCTCCTGACCTTGT 29989               G
              GA                  TCACAAGGTCAGGAGATC AGACC
                                  |||||||||||||||| |||||
                                  AGTGTTCCAGTCCTCTAG TCTGG
                                             G
GAM1701  KIAA0472 5'  GGTCTTGAACTCCTGACCT    72361          A
                                  AGGTCAGGAG TCGAGACC
                                  |||||||||| ||||||||
                                  TCCAGTCCTC AGTTCTGG
                                        A
GAM1701  KIAA0495 3'  GGTCTCGAACTACTGACCTCGT 63270      A      G  A
              GA                  TCAC AGGTCAG AG TCGAGACC
                                  |||| ||||||| || ||||||||
                                  AGTG TCCAGTC TC AGCTCTGG
                                    C      A  A
GAM1701  KIAA0557 3'  GGTCTTGAACTCCCGACCTTGT 78574          A    A
              GA                  TCACAAGGTC GGAG TCGAGACC
                                  |||||||||| |||| ||||||||
                                  AGTGTTCCAG CCTC AGTTCTGG
                                        C    A
GAM1701  KIAA0561 3'  GGTCTCGAACTCCTGACCTCAT 66485     CA         A
              GA                  TCA  AGGTCAGGAG TCGAGACC
                                  |||  |||||||||| ||||||||
                                  AGT  TCCAGTCCTC AGCTCTGG
                                    AC         A
GAM1701  KIAA0562 3'  GGTCTCAAACTCCTGACCTTGT 28829             ATC
              GA                  TCACAAGGTCAGGAG   GAGACC
                                  ||||||||||||||   ||||||
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                                AGTGTTCCAGTCCTC   CTCTGG
                                      AAA
GAM1701  KIAA0594  3'  GGTCTCGAACTCCTGACCTTGT 65514            A
              GA                TCACAAGGTCAGGAG TCGAGACC
                                |||||||||||||| ||||||||
                                AGTGTTCCAGTCCTC AGCTCTGG
                                      A
GAM1701  KIAA0737  3'  GGTCTCGAACTCCTGACCTCAT 29815     CA       A
              GA                TCA  AGGTCAGGAG TCGAGACC
                                |||  |||||||||| ||||||||
                                AGT  TCCAGTCCTC AGCTCTGG
                                  AC        A
GAM1701  KIAA0831  5'  GGTCTTGATCTCCTAACCTCTT 30651     CA   C
              GA                TCA  AGGT AGGAGATCGAGACC
                                |||  |||| ||||||||||||||
                                AGT  TCCA TCCTCTAGTTCTGG
                                  TC   A
GAM1701  KIAA0861  3'  GGTCTCGATCTCCTGACCTCGT 90355      A
              GA                TCAC AGGTCAGGAGATCGAGACC
                                |||| ||||||||||||||||||
                                AGTG TCCAGTCCTCTAGCTCTGG
                                  C
GAM1701  KIAA0924  3'  GGTCTCAAACTCCTGACCTTGT 30368            ATC
              GA                TCACAAGGTCAGGAG   GAGACC
                                ||||||||||||||   ||||||
                                AGTGTTCCAGTCCTC   CTCTGG
                                      AAA
GAM1701  KIAA1068  3'  GGCCTTCCACCCTGACCTTG   31687          AGATC   A
                                CAAGGTCAGG    GAG CC
                                ||||||||||    ||| ||
                                GTTCCAGTCC    TTC GG
                                     CACC_   C
GAM1701  KIAA1143  3'  GGTCTCAATCTCCTGACCTCAT 69246     CA         C
              GA                TCA  AGGTCAGGAGAT GAGACC
                                |||  |||||||||||| ||||||
                                AGT  TCCAGTCCTCTA CTCTGG
                                  AC          A
GAM1701  KIAA1161  5'  GTCTCAAACTCCTGACCTAGTG 82651      A        ATC
              A                 TCAC AGGTCAGGAG   GAGAC
                                |||| ||||||||||   |||||
                                AGTG TCCAGTCCTC   CTCTG
                                  A         AAA
GAM1701  KIAA1185  3'  GGTCTTGATCTCTTGACCTCAT 63292     CA
              GA                TCA  AGGTCAGGAGATCGAGACC
                                |||  ||||||||||||||||||
                                AGT  TCCAGTTCTCTAGTTCTGG
                                  AC
GAM1701  KIAA1198  3'  GGTCTCAATCTCCTGACCTTGT 64052              C
              GA                TCACAAGGTCAGGAGAT GAGACC
                                |||||||||||||||| ||||||
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                                AGTGTTCCAGTCCTCTA CTCTGG
                                          A
GAM1701  KIAA1198  3'  GGTCTCGCCCTCCTGACCTTGT 64053              AT
             GA                  TCACAAGGTCAGGAG  CGAGACC
                                 ||||||||||||||  |||||||
                                 AGTGTTCCAGTCCTC  GCTCTGG
                                          CC
GAM1701  KIAA1198  3'  GTCTTGATCTCCTGACCTCGTG 64055      A
             A                    TCAC AGGTCAGGAGATCGAGAC
                                  |||| ||||||||||||||||||
                                  AGTG TCCAGTCCTCTAGTTCTG
                                    C
GAM1701  KIAA1209  3'  GGTCTCGAACTCCTGATCTCAT 61407     CA         A
             GA                   TCA  AGGTCAGGAG TCGAGACC
                                  |||  |||||||||| ||||||||
                                  AGT  TCTAGTCCTC AGCTCTGG
                                    AC         A
GAM1701  KIAA1210  3'  GGTCTTGATCTCCTGACCTCGT 98078      A
             GA                   TCAC AGGTCAGGAGATCGAGACC
                                  |||| ||||||||||||||||||
                                  AGTG TCCAGTCCTCTAGTTCTGG
                                    C
GAM1701  KIAA1257  3'  GGTCTTGAACTCCTGACCTCGT 63407      A         A
             GA                   TCAC AGGTCAGGAG TCGAGACC
                                  |||| |||||||||| ||||||||
                                  AGTG TCCAGTCCTC AGTTCTGG
                                    C         A
GAM1701  KIAA1260  3'  GATCAACTTCTGACCCTGTGA  60669       A       ___
                                  TCACA GGTCAGGA   GATC
                                  ||||| ||||||||   ||||
                                  AGTGT CCAGTCTT   CTAG
                                     C       CAA
GAM1701  KIAA1328  5'  TCTCGATTTTCTGACCTCGTGA 62335      A
                                  TCAC AGGTCAGGAGATCGAGA
                                  |||| ||||||||||||||||
                                  AGTG TCCAGTCTTTTAGCTCT
                                    C
GAM1701  KIAA1373  3'  GGTCTCGAATTCCTGACCTCTG 71509     _         A
                                  CA AGGTCAGGAG TCGAGACC
                                  || |||||||||| ||||||||
                                  GT TCCAGTCCTT AGCTCTGG
                                    C         A
GAM1701  KIAA1443  3'  GATCTCCTGACCTCATGA    64572     CA
                                  TCA  AGGTCAGGAGATC
                                  |||  ||||||||||||
                                  AGT  TCCAGTCCTCTAG
                                    AC
GAM1701  KIAA1443  3'  GGTCTTGATCTCCTGACCTCAT 64577     CA
             GA                   TCA  AGGTCAGGAGATCGAGACC
                                  |||  ||||||||||||||||||
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                                AGT  TCCAGTCCTCTAGTTCTGG
                                  AC
GAM1701  KIAA1456  3'  GGTCTCGATCTCCTGACGTCGT 67565      AAG
             GA                   TCAC   GTCAGGAGATCGAGACC
                                  ||||   ||||||||||||||||
                                AGTG   CAGTCCTCTAGCTCTGG
                                  CTG
GAM1701  KIAA1467  3'  GGTCACGAACTCCTGACCT    72074          A   A
                                AGGTCAGGAG TCG GACC
                                |||||||||| ||| ||||
                                TCCAGTCCTC AGC CTGG
                                     A   A
GAM1701  KIAA1497  5'  GGTCTCGAACTCCTGACCTCAT 68126     CA         A
             GA                   TCA  AGGTCAGGAG TCGAGACC
                                  |||  |||||||||| ||||||||
                                AGT  TCCAGTCCTC AGCTCTGG
                                  AC         A
GAM1701  KIAA1530  3'  GGTCTTGATCTCTTGACCTCGT 68564      A
             GA                   TCAC AGGTCAGGAGATCGAGACC
                                  |||| ||||||||||||||||||
                                AGTG TCCAGTTCTCTAGTTCTGG
                                  C
GAM1701  KIAA1571  3'  GGTCTCAAACTCCTGACCTTGT 61620              ATC
             GG                   TCACAAGGTCAGGAG   GAGACC
                                  ||||||||||||||   ||||||
                                GGTGTTCCAGTCCTC   CTCTGG
                                     AAA
GAM1701  KIAA1615  3'  GTCTCGATTTCCTGACCTTGTG 69283
             A                     TCACAAGGTCAGGAGATCGAGAC
                                   |||||||||||||||||||||
                                AGTGTTCCAGTCCTTTAGCTCTG

GAM1701  KIAA1668  3'  GATCTCCTGACCTTGTGA    67072
                                TCACAAGGTCAGGAGATC
                                ||||||||||||||||
                                AGTGTTCCAGTCCTCTAG

GAM1701  KIAA1668  3'  GGTCTCGATCTCCTGACCTTGT 67076
             GA                   TCACAAGGTCAGGAGATCGAGACC
                                  ||||||||||||||||||||||
                                AGTGTTCCAGTCCTCTAGCTCTGG

GAM1701  KIAA1877  3'  GGTCTCGATCTCCTGACCTTGT 66756
             GA                   TCACAAGGTCAGGAGATCGAGACC
                                  ||||||||||||||||||||||
                                AGTGTTCCAGTCCTCTAGCTCTGG

GAM1701  KIAA1898  3'  CTTGGCCCTGACCTCAGGA   74313    ACA      AGA
                                TC   AGGTCAGG   TCGAG
                                ||   ||||||||   |||||
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                                AG   TCCAGTCC   GGTTC
                                 GAC       C__
GAM1701  KIAA1971  3'  GGTCTCGATCTTCTGACCTCGT 74685      A
             GA                   TCAC AGGTCAGGAGATCGAGACC
                                  |||| ||||||||||||||||||
                                  AGTG TCCAGTCTTCTAGCTCTGG
                                    C
GAM1701  KIAA1971  3'  GGTCTTGAACTCCTGACCTCGT 74686      A        A
             GA                   TCAC AGGTCAGGAG TCGAGACC
                                  |||| |||||||||| ||||||||
                                  AGTG TCCAGTCCTC AGTTCTGG
                                    C        A
GAM1701  KIAA1975  5'  GGTCTCGATCTCCTGACCTCGT 74424      A
             GA                   TCAC AGGTCAGGAGATCGAGACC
                                  |||| ||||||||||||||||||
                                  AGTG TCCAGTCCTCTAGCTCTGG
                                    C
GAM1701  KLHL6     3'  GGTCTTGAACGCCTGACCTTGT 56174            AGA
             GA                   TCACAAGGTCAGG   TCGAGACC
                                  ||||||||||||   ||||||||
                                  AGTGTTCCAGTCC   AGTTCTGG
                                        GCA
GAM1701  MEF-2     3'  GGTCTCAAACTCCTGACCTCGT 65027      A        ATC
             GA                   TCAC AGGTCAGGAG   GAGACC
                                  |||| ||||||||||   ||||||
                                  AGTG TCCAGTCCTC   CTCTGG
                                    C        AAA
GAM1701  MGC12518  3'  GGTCTCGAACGCCTGACCTCGT 64779     A       AGA
             G                     CAC AGGTCAGG   TCGAGACC
                                  ||| ||||||||   ||||||||
                                  GTG TCCAGTCC   AGCTCTGG
                                    C       GCA
GAM1701  MGC13523  5'  CGTCCCTGAGCCTTGTGA     54169         _    A  T
                                  TCACAAGG TCAGG GA CG
                                  |||||||| ||||| || ||
                                  AGTGTTCC AGTCC CT GC
                                       G    _ _
GAM1701  MGC20255  3'  GTCCACGGTTCCTGACCT     54542         G    A_
                                  AGGTCAGGA ATCG  GAC
                                  ||||||||| ||||  |||
                                  TCCAGTCCT TGGC  CTG
                                       _    AC
GAM1701  MGC2477   5'  GGTCTCGAACTCCTGACCTCGT 44309      A        A
             GA                   TCAC AGGTCAGGAG TCGAGACC
                                  |||| |||||||||| ||||||||
                                  AGTG TCCAGTCCTC AGCTCTGG
                                    C        A
GAM1701  MGC2603   3'  GGTCTCCATCTCCTGACCTCCT 44078     CA         C
             GA                   TCA  AGGTCAGGAGAT GAGACC
                                  |||  |||||||||||| ||||||
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                                AGT  TCCAGTCCTCTA CTCTGG
                                  CC          C
GAM1701  MGC4638   3'  GGTCTCAATCTCTTGACCTCTT 49739     CA          C
            GA                    TCA  AGGTCAGGAGAT GAGACC
                                  |||  |||||||||||| ||||||
                                  AGT  TCCAGTTCTCTA CTCTGG
                                    TC          A
GAM1701  MGC4766   5'  GATCTCCTGACCTCGTGA    49559      A
                                  TCAC AGGTCAGGAGATC
                                  |||| ||||||||||||
                                  AGTG TCCAGTCCTCTAG
                                    C
GAM1701  MGC4766   5'  GGTCTCGATCTCCTGACCTCGT 49562      A
            GA                    TCAC AGGTCAGGAGATCGAGACC
                                  |||| ||||||||||||||||||
                                  AGTG TCCAGTCCTCTAGCTCTGG
                                    C
GAM1701  MGC5149   3'  GGTCTCGATCTCAACCTCGTGA 72760      A   CAG
                                  TCAC AGGT   GAGATCGAGACC
                                  |||| ||||   ||||||||||||
                                  AGTG TCCA   CTCTAGCTCTGG
                                    C   A__
GAM1701  MLZE      5'  TCTTGAACTCCTGACCTCGGGA 49455    ACA        A
                                  TC   AGGTCAGGAG TCGAGA
                                  ||   |||||||||| ||||||
                                  AG   TCCAGTCCTC AGTTCT
                                   GGC         A
GAM1701  moblak    3'  GGTCTTGATCTCCTGACCTTGT 56407
            GA                    TCACAAGGTCAGGAGATCGAGACC
                                  |||||||||||||||||||||||
                                  AGTGTTCCAGTCCTCTAGTTCTGG

GAM1701  MOCS3     3'  GGTCTCGAACTCCTGACCTCGT 27933      A        A
            GA                    TCAC AGGTCAGGAG TCGAGACC
                                  |||| |||||||||| ||||||||
                                  AGTG TCCAGTCCTC AGCTCTGG
                                    C         A
GAM1701  MRPS27    3'  GGTCTCAACCTCCTGACCT    31331          ATC
                                  AGGTCAGGAG   GAGACC
                                  ||||||||||   ||||||
                                  TCCAGTCCTC   CTCTGG
                                       CAA
GAM1701  MtFMT     3'  GGTCTCGAACTCCTGACCTTGT 58337              A
            GA                    TCACAAGGTCAGGAG TCGAGACC
                                  |||||||||||||| ||||||||
                                  AGTGTTCCAGTCCTC AGCTCTGG
                                            A
GAM1701  MYO5C     3'  GGCCTCGATCTCTTGACCTCGT 38722      A            A
            GA                    TCAC AGGTCAGGAGATCGAG CC
                                  |||| ||||||||||||||| ||
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                                AGTG TCCAGTTCTCTAGCTC GG
                                  C            C
GAM1701  NDUFC2   3'  GGTCTCAATCTCTTGACCTTGT 17034              C
                GA                TCACAAGGTCAGGAGAT GAGACC
                                  |||||||||||||||| ||||||
                                  AGTGTTCCAGTTCTCTA CTCTGG
                                           A
GAM1701  Nup43    3'  GGTCTTGAACTGACCTCATGA  45352    CA     GAGA
                                  TCA  AGGTCAG   TCGAGACC
                                  |||  |||||||   ||||||||
                                  AGT  TCCAGTC   AGTTCTGG
                                    AC      A___
GAM1701  OCT11    3'  GGTCTTGAACTCCTGACCTCCT 27593    CA       A
                GA                TCA  AGGTCAGGAG TCGAGACC
                                  |||  |||||||||| ||||||||
                                  AGT  TCCAGTCCTC AGTTCTGG
                                    CC        A
GAM1701  OR51E2   3'  GGTCTCGATCTCCTGACCTTGT 48514
                GA                TCACAAGGTCAGGAGATCGAGACC
                                  ||||||||||||||||||||||||
                                  AGTGTTCCAGTCCTCTAGCTCTGG

GAM1701  PRO0365  5'  GTCTTGATCTCCTGACCTCATG 26994    CA
                A                  TCA  AGGTCAGGAGATCGAGAC
                                  |||  ||||||||||||||||
                                  AGT  TCCAGTCCTCTAGTTCTG
                                    AC
GAM1701  PRO0899  5'  GGTCTCAATCTCCTGGGCC   38313     _     C
                                  GGTC AGGAGAT GAGACC
                                  |||| ||||||| ||||||
                                  CCGG TCCTCTA CTCTGG
                                    G      A
GAM1701  PSPH     3'  GGTCTTGATCTCCTGACCTTGT 17136
                GA                TCACAAGGTCAGGAGATCGAGACC
                                  ||||||||||||||||||||||||
                                  AGTGTTCCAGTCCTCTAGTTCTGG

GAM1701  RAB21    3'  GGTCTCGATCTCCTGACCTTGT 31095
                GA                TCACAAGGTCAGGAGATCGAGACC
                                  ||||||||||||||||||||||||
                                  AGTGTTCCAGTCCTCTAGCTCTGG

GAM1701  RAB33B   3'  GGTCTCGATCTCTTGACCTCAT 49331    CA
                GA                TCA  AGGTCAGGAGATCGAGACC
                                  |||  ||||||||||||||||||
                                  AGT  TCCAGTTCTCTAGCTCTGG
                                    AC
GAM1701  RAI17    3'  GGTTTGACCCCTGACCT     92906        AGA  G
                                  AGGTCAGG   TC AGACC
                                  ||||||||   || |||||
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                                TCCAGTCC   AG TTTGG
                                    CC_  _
GAM1701  RAP140   3'  GGTCTTGATCTCCTGACCTCAT 31520     CA
             GA                   TCA  AGGTCAGGAGATCGAGACC
                                  |||  ||||||||||||||||||
                                  AGT  TCCAGTCCTCTAGTTCTGG
                                    AC
GAM1701  RASSF2   3'  GGTCTTGAACTCCTGACCTCGT 29106      A         A
             GA                   TCAC AGGTCAGGAG TCGAGACC
                                  ||||  ||||||||||  ||||||||
                                  AGTG TCCAGTCCTC AGTTCTGG
                                    C         A
GAM1701  SERF1B   3'  GGTCTCCATCTCCTGACCTCGT 43700      A          C
             GA                   TCAC AGGTCAGGAGAT GAGACC
                                  ||||  ||||||||||||  ||||||
                                  AGTG TCCAGTCCTCTA CTCTGG
                                    C           C
GAM1701  SFRS5    3'  GGTCTCGATCCCGGACC     23624      A  A
                                  GGTC GG GATCGAGACC
                                  ||||  ||  ||||||||||
                                  CCAG CC CTAGCTCTGG
                                    G  _
GAM1701  SLC12A8  3'  GGTCTCGAACTCCTGACCTCGT 45243      A         A
             GA                   TCAC AGGTCAGGAG TCGAGACC
                                  ||||  ||||||||||  ||||||||
                                  AGTG TCCAGTCCTC AGCTCTGG
                                    C         A
GAM1701  SLC16A4  3'  GGTCTCCATCTCCTGACCTCGT 17456      A          C
             GA                   TCAC AGGTCAGGAGAT GAGACC
                                  ||||  ||||||||||||  ||||||
                                  AGTG TCCAGTCCTCTA CTCTGG
                                    C           C
GAM1701  SREC     3'  GGTCTCGATCTCCTGACCTCGT 14908      A
             GA                   TCAC AGGTCAGGAGATCGAGACC
                                  ||||  ||||||||||||||||||
                                  AGTG TCCAGTCCTCTAGCTCTGG
                                    C
GAM1701  SS-56    3'  GGTCTCGATCTCCTGACCTCAT 60356     CA
             GA                   TCA  AGGTCAGGAGATCGAGACC
                                  |||  ||||||||||||||||||
                                  AGT  TCCAGTCCTCTAGCTCTGG
                                    AC
GAM1701  SULT1C2  3'  TCTCGATCTCCTGACCCCATGA 22722     CAA
                                  TCA   GGTCAGGAGATCGAGA
                                  |||   ||||||||||||||||
                                  AGT   CCAGTCCTCTAGCTCT
                                    ACC
GAM1701  SUN1     3'  GGTCTCGATTTCCTGACCTAGT 47917      A
             GA                   TCAC AGGTCAGGAGATCGAGACC
                                  ||||  ||||||||||||||||||
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                                AGTG TCCAGTCCTTTAGCTCTGG
                                  A
GAM1701  TADA3L   3'  GGTCTCGATCTCCTGACCTCGT 22043      A
              GA                  TCAC AGGTCAGGAGATCGAGACC
                                  |||| ||||||||||||||||||
                                  AGTG TCCAGTCCTCTAGCTCTGG
                                    C
GAM1701  TCL6     3'  CTCCATCTCCTGACCTCGTGA  40471      A          C
                                  TCAC AGGTCAGGAGAT GAG
                                  |||| |||||||||||| |||
                                  AGTG TCCAGTCCTCTA CTC
                                    C          C
GAM1701  TGIF2    3'  GGTCTTGGAACTCCTGACCTCG 41756      A         A_
              TGA                   TCAC AGGTCAGGAG  TCGAGACC
                                  |||| ||||||||||  ||||||||
                                  AGTG TCCAGTCCTC  GGTTCTGG
                                    C         AA
GAM1701  TRIM16   3'  TCTCAAACTCCTGACCTCGTGA 22379      A         ATC
                                  TCAC AGGTCAGGAG   GAGA
                                  |||| ||||||||||   ||||
                                  AGTG TCCAGTCCTC   CTCT
                                    C         AAA
GAM1701  TU12B1-TY 3'  GGTCTCGAACTCCTGACCT   33859          A
                                  AGGTCAGGAG TCGAGACC
                                  |||||||||| ||||||||
                                  TCCAGTCCTC AGCTCTGG
                                       A
GAM1701  TUCAN    3'  GGTCTCGATCTCCTGACCTCAT 30983     CA
              GA                    TCA  AGGTCAGGAGATCGAGACC
                                  |||  ||||||||||||||||||
                                  AGT  TCCAGTCCTCTAGCTCTGG
                                    AC
GAM1701  YKT6     3'  GTCTCAGTGGTCCTGACC    22643         G_  C
                                  GGTCAGGA  AT GAGAC
                                  ||||||||  || |||||
                                  CCAGTCCT  TG CTCTG
                                       GG  A
GAM1701  LOC112687 3'  GGTCCCAAACTCCTGACCTCAT 73239    CA         ATCGA
              G                     CA  AGGTCAGGAG    GACC
                                  ||  ||||||||||    ||||
                                  GT  TCCAGTCCTC    CTGG
                                    AC         AAACC
GAM1701  LOC113523 5'  GGTCTCGATCTCCTGACCTCGT 73430      A
              GA                    TCAC AGGTCAGGAGATCGAGACC
                                  |||| ||||||||||||||||||
                                  AGTG TCCAGTCCTCTAGCTCTGG
                                    C
GAM1701  LOC113523 3'  GGTCTTGAACTCCTGACCT    73431          A
                                  AGGTCAGGAG TCGAGACC
                                  |||||||||| ||||||||
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                                TCCAGTCCTC AGTTCTGG
                                      A
GAM1701  LOC115219 5'  GTCTCAAACTCCTGACGTCGTG 73706      AAG       ATC
                 A                    TCAC   GTCAGGAG   GAGAC
                                      ||||   ||||||||   |||||
                                      AGTG   CAGTCCTC   CTCTG
                                        CTG       AAA
GAM1701  LOC120114 3'  GGTCTCAAACTCCTGACCTCGT 76048    A        ATC
                                      AC AGGTCAGGAG   GAGACC
                                      || ||||||||||   ||||||
                                      TG TCCAGTCCTC   CTCTGG
                                       C         AAA
GAM1701  LOC124216 3'  GTCTCAAACTCCTGACCTCGTG 74740      A        ATC
                 A                    TCAC AGGTCAGGAG   GAGAC
                                      |||| ||||||||||   |||||
                                      AGTG TCCAGTCCTC   CTCTG
                                        C         AAA
GAM1701  LOC126669 3'  GGTCTCAAACTCCTGACCT    75943          ATC
                                      AGGTCAGGAG   GAGACC
                                      ||||||||||   ||||||
                                      TCCAGTCCTC   CTCTGG
                                            AAA
GAM1701  LOC128077 3'  GGTCTCCATCTCCTGACCTCGT 75226      A          C
                 GA                     TCAC AGGTCAGGAGAT GAGACC
                                      |||| ||||||||||| ||||||
                                      AGTG TCCAGTCCTCTA CTCTGG
                                        C           C
GAM1701  LOC128439 3'  CGATCTCCGACTCCTGA     58135     CAA    A
                                      TCA   GGTC GGAGATCG
                                      |||   |||| ||||||||
                                      AGT   TCAG CCTCTAGC
                                        CC_   _
GAM1701  LOC133686 3'  GGTCTCGAACTCCTGACCTTGT 75618              A
                 GA                     TCACAAGGTCAGGAG TCGAGACC
                                      |||||||||||||| ||||||||
                                      AGTGTTCCAGTCCTC AGCTCTGG
                                            A
GAM1701  LOC143187 3'  GGTCTCGATCTCTTAACCTTGT 59763          C
                 GA                     TCACAAGGT AGGAGATCGAGACC
                                      |||||||| ||||||||||||||
                                      AGTGTTCCA TTCTCTAGCTCTGG
                                          A
GAM1701  LOC144871 3'  GATCTCCTGACCTTGTGA     84126
                                      TCACAAGGTCAGGAGATC
                                      ||||||||||||||||||
                                      AGTGTTCCAGTCCTCTAG

GAM1701  LOC144871 3'  GGTCTTGATCTCCTGACCTTGT 84128
                 GA                     TCACAAGGTCAGGAGATCGAGACC
                                      ||||||||||||||||||||||||
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                                AGTGTTCCAGTCCTCTAGTTCTGG

GAM1701  LOC145009 3'  GGTCTTGAACTCCTGACCTCGT 60978      A        A
              GA                 TCAC AGGTCAGGAG TCGAGACC
                                 |||| |||||||||| ||||||||
                                 AGTG TCCAGTCCTC AGTTCTGG
                                   C         A
GAM1701  LOC145622 3'  GGTCTCGATCTCTTGACGTCGT 77823      AAG
              GA                 TCAC   GTCAGGAGATCGAGACC
                                 ||||   ||||||||||||||||
                                 AGTG   CAGTTCTCTAGCTCTGG
                                   CTG
GAM1701  LOC146229 3'  GGTCTCGATCTCCTGCCCTCGT 78300      A   T
              GA                 TCAC AGG CAGGAGATCGAGACC
                                 |||| ||| ||||||||||||||
                                 AGTG TCC GTCCTCTAGCTCTGG
                                   C   C
GAM1701  LOC146346 5'  GGTCTCCATCTCCTGACCTCAT 78402      CA          C
              GA                 TCA  AGGTCAGGAGAT GAGACC
                                 |||  |||||||||||| ||||||
                                 AGT  TCCAGTCCTCTA CTCTGG
                                   AC          C
GAM1701  LOC146429 5'  GATCTCCTGACCTCATGA    84667     CA
                                 TCA  AGGTCAGGAGATC
                                 |||  ||||||||||||
                                 AGT  TCCAGTCCTCTAG
                                   AC
GAM1701  LOC146429 5'  GGTCTCGATCTCCTGACCTCAT 84673      CA
              GA                 TCA  AGGTCAGGAGATCGAGACC
                                 |||  ||||||||||||||||||
                                 AGT  TCCAGTCCTCTAGCTCTGG
                                   AC
GAM1701  LOC146455 3'  TCTTGAACTCCTGACCTCGTGA 78468      A        A
                                 TCAC AGGTCAGGAG TCGAGA
                                 |||| |||||||||| ||||||
                                 AGTG TCCAGTCCTC AGTTCT
                                   C         A
GAM1701  LOC146603 5'  GGTCTTGATCTCCTGACCTCAT 78601      CA
              GA                 TCA  AGGTCAGGAGATCGAGACC
                                 |||  ||||||||||||||||||
                                 AGT  TCCAGTCCTCTAGTTCTGG
                                   AC
GAM1701  LOC146784 5'  GGTCTTGAACCCCTGACCTCAT 78717      CA       AGA
              GA                 TCA  AGGTCAGG   TCGAGACC
                                 |||  ||||||||   ||||||||
                                 AGT  TCCAGTCC   AGTTCTGG
                                   AC       CCA
GAM1701  LOC146839 3'  GGTCTGGATCTCCTGACCTCGT 84845      A          G
              GA                 TCAC AGGTCAGGAGATC AGACC
                                 |||| |||||||||||| |||||
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                                AGTG TCCAGTCCTCTAG TCTGG
                                  C           G
GAM1701  LOC146894 3'  GGTCTTGAACTCCTGACCT    59863          A
                                AGGTCAGGAG TCGAGACC
                                |||||||||| ||||||||
                                TCCAGTCCTC AGTTCTGG
                                     A
GAM1701  LOC146952 5'  GGTCTCAAACTCCTGACCT    84932          ATC
                                AGGTCAGGAG   GAGACC
                                ||||||||||   ||||||
                                TCCAGTCCTC   CTCTGG
                                     AAA
GAM1701  LOC147080 5'  GGTTTCGATCTCCTGACCTTGT 85046
                 GA               TCACAAGGTCAGGAGATCGAGACC
                                |||||||||||||||||||||||
                                AGTGTTCCAGTCCTCTAGCTTTGG

GAM1701  LOC147166 3'  TCTCAAACTTCTGACCTCGTGA 78895      A         ATC
                                TCAC AGGTCAGGAG   GAGA
                                |||| ||||||||||   ||||
                                AGTG TCCAGTCTTC   CTCT
                                  C         AAA
GAM1701  LOC147429 3'  GGTCTCGATTTCCTGACCTTGT 78997
                 GA               TCACAAGGTCAGGAGATCGAGACC
                                |||||||||||||||||||||||
                                AGTGTTCCAGTCCTTTAGCTCTGG

GAM1701  LOC147694 3'  GATCTCCTGACCTTGTGA     79098
                                TCACAAGGTCAGGAGATC
                                ||||||||||||||||||
                                AGTGTTCCAGTCCTCTAG

GAM1701  LOC147694 3'  GGTCCTGATCTCCTGACCTTGT 79102                A
                 GA               TCACAAGGTCAGGAGATCG GACC
                                |||||||||||||||||| ||||
                                AGTGTTCCAGTCCTCTAGT CTGG
                                          C
GAM1701  LOC147817 3'  GGTCTCAAACTCCTGACCTT   79187          ATC
                                AAGGTCAGGAG   GAGACC
                                ||||||||||   ||||||
                                TTCCAGTCCTC   CTCTGG
                                     AAA
GAM1701  LOC147990 3'  TCTCGAACTCCTGACCTTGTGA 85237              A
                                TCACAAGGTCAGGAG TCGAGA
                                ||||||||||||||| ||||||
                                AGTGTTCCAGTCCTC AGCTCT
                                          A
GAM1701  LOC148137 3'  GGTCTCCTGACCTCGTGA     59108      A
                                TCAC AGGTCAGGAGATC
                                |||| ||||||||||||
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                                AGTG TCCAGTCCTCTGG
                                  C
GAM1701  LOC148147 3'  CGGTCTCGATCTCCTGACCTTC 79396     C              ___
                 TGA                TCA AAGGTCAGGAGATCGAGACC   G
                                |||| ||||||||||||||||||||   |
                                AGT TTCCAGTCCTCTAGCTCTGG   C
                                  C                ___
GAM1701  LOC148189 5'  GGTCTCAATCTCTTGACCTCGT 79453    A          C
                                AC AGGTCAGGAGAT GAGACC
                                || ||||||||||||| ||||||
                                TG TCCAGTTCTCTA CTCTGG
                                 C          A
GAM1701  LOC149421 3'  GGTCTCGATCTCCTGACCTCGT 80148      A
                 GA                 TCAC AGGTCAGGAGATCGAGACC
                                |||| ||||||||||||||||||||
                                AGTG TCCAGTCCTCTAGCTCTGG
                                  C
GAM1701  LOC149821 5'  GATCTCCTGACCTCGTGA    85933      A
                                TCAC AGGTCAGGAGATC
                                |||| |||||||||||||
                                AGTG TCCAGTCCTCTAG
                                  C
GAM1701  LOC149821 5'  GGTCTCGATCTCCTGACCTCGT 85936      A
                 GA                 TCAC AGGTCAGGAGATCGAGACC
                                |||| ||||||||||||||||||||
                                AGTG TCCAGTCCTCTAGCTCTGG
                                  C
GAM1701  LOC150225 3'  GGTCTCAAACTCCTGACCT    86198          ATC
                                AGGTCAGGAG   GAGACC
                                ||||||||||   ||||||
                                TCCAGTCCTC   CTCTGG
                                     AAA
GAM1701  LOC150630 5'  GGTCTCGATCTCCTGACCTCGT 86306      A
                 GA                 TCAC AGGTCAGGAGATCGAGACC
                                |||| ||||||||||||||||||||
                                AGTG TCCAGTCCTCTAGCTCTGG
                                  C
GAM1701  LOC151057 3'  GGTCTCGAACTCCTGACCTTGT 86392             A
                 GA                 TCACAAGGTCAGGAG TCGAGACC
                                |||||||||||||| ||||||||
                                AGTGTTCCAGTCCTC AGCTCTGG
                                       A
GAM1701  LOC151201 3'  GGTCTCAAACTCTTGACCTCGT 86480      A        ATC
                 GA                 TCAC AGGTCAGGAG   GAGACC
                                |||| ||||||||||   ||||||
                                AGTG TCCAGTTCTC   CTCTGG
                                  C        AAA
GAM1701  LOC151701 3'  GGTCTCGAACTCCTGACCT    86678          A
                                AGGTCAGGAG TCGAGACC
                                |||||||||| ||||||||
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                                TCCAGTCCTC AGCTCTGG
                                     A
GAM1701  LOC151979 5'  GTGTCGATCTCCTGACCTCATG 81252     CA           G
              A                   TCA  AGGTCAGGAGATCGA AC
                                  |||  |||||||||||||| ||
                                  AGT  TCCAGTCCTCTAGCT TG
                                    AC            G
GAM1701  LOC152300 3'  GGTCTCGAACTACTGACCTCGT 81387      A      G  A
              GA                    TCAC AGGTCAG AG TCGAGACC
                                  |||| ||||||| || ||||||||
                                  AGTG TCCAGTC TC AGCTCTGG
                                    C      A  A
GAM1701  LOC152343 3'  TCTTGAACTTCTGACCTTGTGA 81438             A
                                  TCACAAGGTCAGGAG TCGAGA
                                  |||||||||||||| ||||||
                                  AGTGTTCCAGTCTTC AGTTCT
                                         A
GAM1701  LOC152445 3'  GGTCTCGATCTCCTGACCTCGT 86958      A
              GA                    TCAC AGGTCAGGAGATCGAGACC
                                  |||| ||||||||||||||||||
                                  AGTG TCCAGTCCTCTAGCTCTGG
                                    C
GAM1701  LOC152719 5'  GGTCTCAATCTCCTGACCTCGT 87039      A          C
              GA                    TCAC AGGTCAGGAGAT GAGACC
                                  |||| ||||||||||| ||||||
                                  AGTG TCCAGTCCTCTA CTCTGG
                                    C          A
GAM1701  LOC153811 3'  GGTCTCAAACTCCTGACCT    81841          ATC
                                  AGGTCAGGAG   GAGACC
                                  ||||||||||   ||||||
                                  TCCAGTCCTC   CTCTGG
                                       AAA
GAM1701  LOC154282 5'  GGTCTCAATCTCTTGACCTTGT 87410              C
              GA                    TCACAAGGTCAGGAGAT GAGACC
                                  |||||||||||||||| ||||||
                                  AGTGTTCCAGTTCTCTA CTCTGG
                                         A
GAM1701  LOC154877 3'  GGTCTCGAACTCCTGACCTT   87567          A
                                  AAGGTCAGGAG TCGAGACC
                                  |||||||||| ||||||||
                                  TTCCAGTCCTC AGCTCTGG
                                       A
GAM1701  LOC155061 3'  GGCCTCCACAGACCTTGTGA   82191          A__    AT
                                  TCACAAGGTC   GGAG  C
                                  |||||||||   ||||  |
                                  AGTGTTCCAG   CCTC  G
                                       ACA    CG
GAM1701  LOC157798 5'  TCTCGATCTCTTGATCTCGTGA 87865      A
                                  TCAC AGGTCAGGAGATCGAGA
                                  |||| |||||||||||||||
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                                AGTG TCTAGTTCTCTAGCTCT
                                  C
GAM1701  LOC158549 5'  GGTCTCGATCTCCTGACCTGGT 88226      A
                GA               TCAC AGGTCAGGAGATCGAGACC
                                 |||| ||||||||||||||||||
                                 AGTG TCCAGTCCTCTAGCTCTGG
                                   G
GAM1701  LOC158668 3'  GGTCTCCAACTCCTGACTTCAT 69902     CA        ATC
                GA               TCA  AGGTCAGGAG   GAGACC
                                 |||  ||||||||||   ||||||
                                 AGT  TTCAGTCCTC   CTCTGG
                                   AC         AAC
GAM1701  LOC159160 3'  GGCCTCCAATTCTGACCTT    61154          GATC   A
                                 AAGGTCAGGA    GAG CC
                                 ||||||||||    ||| ||
                                 TTCCAGTCTT    CTC GG
                                       AAC_   C
GAM1701  LOC170082 5'  GGTCTCGATCTCCTGACCTCGT 83446      A
                GA               TCAC AGGTCAGGAGATCGAGACC
                                 |||| ||||||||||||||||||
                                 AGTG TCCAGTCCTCTAGCTCTGG
                                   C
GAM1701  LOC196264 3'  GGTCTCAATCCCCTGACCTCGT 88990      A       A   C
                GA               TCAC AGGTCAGG GAT GAGACC
                                 |||| |||||||| ||| ||||||
                                 AGTG TCCAGTCC CTA CTCTGG
                                   C       C   A
GAM1701  LOC196411 3'  GGTCTCGAACTCCTGACCTCGT 89049      A        A
                GA               TCAC AGGTCAGGAG TCGAGACC
                                 |||| |||||||||| ||||||||
                                 AGTG TCCAGTCCTC AGCTCTGG
                                   C         A
GAM1701  LOC196707 3'  GGCCTCCCTGAGCCTTGTGA   88925          _    _ AT
                                 TCACAAGG TCAGG AG  C
                                 |||||||| ||||| ||  |
                                 AGTGTTCC AGTCC TC  G
                                      G    C  CG
GAM1701  LOC199699 3'  GGTCTCTATCTCCTGACCTCGT 89678      A          C
                GA               TCAC AGGTCAGGAGAT GAGACC
                                 |||| ||||||||||| ||||||
                                 AGTG TCCAGTCCTCTA CTCTGG
                                   C           T
GAM1701  LOC199725 5'  GGTCTCGAACTCCTGACCTCGT 91424      A        A
                GA               TCAC AGGTCAGGAG TCGAGACC
                                 |||| |||||||||| ||||||||
                                 AGTG TCCAGTCCTC AGCTCTGG
                                   C         A
GAM1701  LOC199786 3'  GGTCTTGAACTCCTGACCTCAT 89759     CA        A
                GA               TCA  AGGTCAGGAG TCGAGACC
                                 |||  |||||||||| ||||||||
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                                AGT  TCCAGTCCTC AGTTCTGG
                                  AC          A
GAM1701  LOC200014 3'  GGTCTCGAACTCCTGACCTCAT 89940     CA          A
                GA               TCA  AGGTCAGGAG TCGAGACC
                                 |||  |||||||||| ||||||||
                                AGT  TCCAGTCCTC AGCTCTGG
                                  AC          A
GAM1701  LOC200301 5'  GGTTTCGATCTCCTCACCTCGC 90149     ACA    C
                GA               TC   AGGT AGGAGATCGAGACC
                                 ||   |||| ||||||||||||||
                                AG   TCCA TCCTCTAGCTTTGG
                                  CGC    C
GAM1701  LOC200310 3'  GGTCTCGAACTCCTGACCTCGT 66332      A          A
                GA               TCAC AGGTCAGGAG TCGAGACC
                                 |||| |||||||||| ||||||||
                                AGTG TCCAGTCCTC AGCTCTGG
                                  C          A
GAM1701  LOC200316 5'  GGTCTCGAACTCCTGACCTCGT 90189      A          A
                GA               TCAC AGGTCAGGAG TCGAGACC
                                 |||| |||||||||| ||||||||
                                AGTG TCCAGTCCTC AGCTCTGG
                                  C          A
GAM1701  LOC200845 5'  GGTCTTGAACTCCTGACCTGGT 90319      A          A
                GA               TCAC AGGTCAGGAG TCGAGACC
                                 |||| |||||||||| ||||||||
                                AGTG TCCAGTCCTC AGTTCTGG
                                  G          A
GAM1701  LOC201294 3'  GGTCTCAATCTCTTGACCTCCT 89593     CA           C
                GA               TCA  AGGTCAGGAGAT GAGACC
                                 |||  |||||||||||| ||||||
                                AGT  TCCAGTTCTCTA CTCTGG
                                  CC           A
GAM1701  LOC202460 5'  GGTCTCGAACTCTTGACCTTGT 90674               A
                GA               TCACAAGGTCAGGAG TCGAGACC
                                 |||||||||||||| ||||||||
                                AGTGTTCCAGTTCTC AGCTCTGG
                                           A
GAM1701  LOC202934 3'  TCTCGAACTCCTGACCTCGTGA 92055      A          A
                                TCAC AGGTCAGGAG TCGAGA
                                |||| |||||||||| ||||||
                                AGTG TCCAGTCCTC AGCTCT
                                  C          A
GAM1701  LOC203339 3'  GGTCTTTATCTCCTGCCCTTGT 92217          T        C
                GA               TCACAAGG CAGGAGAT GAGACC
                                 |||||||| |||||||| ||||||
                                AGTGTTCC GTCCTCTA TTCTGG
                                     C        T
GAM1701  LOC203350 3'  GGTCTTGTACTCCTGACCTTGT 92245               AT
                GA               TCACAAGGTCAGGAG  CGAGACC
                                 ||||||||||||||  |||||||
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                                AGTGTTCCAGTCCTC  GTTCTGG
                                        AT
GAM1701  LOC203369 3'  GATCTCCTGACCTCGTGA    90888      A
                                TCAC AGGTCAGGAGATC
                                |||| ||||||||||||
                                AGTG TCCAGTCCTCTAG
                                  C
GAM1701  LOC203369 3'  GGTCTCGATCTCCTGACCTCGT 90890      A
              GA                  TCAC AGGTCAGGAGATCGAGACC
                                |||| ||||||||||||||||||
                                AGTG TCCAGTCCTCTAGCTCTGG
                                  C
GAM1701  LOC219445 5'  GGTCTCGATCTCCTGACGTCGT 93211      AAG
              GA                  TCAC   GTCAGGAGATCGAGACC
                                ||||   ||||||||||||||||
                                AGTG   CAGTCCTCTAGCTCTGG
                                  CTG
GAM1701  LOC219445 5'  GGTCTCGGACCCTTGACCTTGT 93212            AGA
              GA                  TCACAAGGTCAGG   TCGAGACC
                                ||||||||||||   ||||||||
                                AGTGTTCCAGTTC   GGCTCTGG
                                      CCA
GAM1701  LOC219735 3'  TCTCGATCTCCTGACCTCGTGA 94736      A
                                TCAC AGGTCAGGAGATCGAGA
                                |||| ||||||||||||||||
                                AGTG TCCAGTCCTCTAGCTCT
                                  C
GAM1701  LOC219894 3'  GGTCTTGATCTCCTGACCTCAT 94907     CA
              GA                  TCA  AGGTCAGGAGATCGAGACC
                                |||  ||||||||||||||||||
                                AGT  TCCAGTCCTCTAGTTCTGG
                                  AC
GAM1701  LOC220074 3'  GGTCTCCATCTCCTGACCTTGT 59988              C
              GA                  TCACAAGGTCAGGAGAT GAGACC
                                |||||||||||||||| ||||||
                                AGTGTTCCAGTCCTCTA CTCTGG
                                      C
GAM1701  LOC221296 3'  GGTCTCGAACCCCGATCTCGTG 93614      A    A  AGA
              A                   TCAC AGGTC GG   TCGAGACC
                                |||| ||||| ||   ||||||||
                                AGTG TCTAG CC   AGCTCTGG
                                  C    C  CA_
GAM1701  LOC253666 3'  GTCTCCATCTCTTGACCTCGTG 96764      A          C
              A                   TCAC AGGTCAGGAGAT GAGAC
                                |||| |||||||||||| |||||
                                AGTG TCCAGTTCTCTA CTCTG
                                  C          C
GAM1701  LOC253805 3'  GGTCTCGAACTCCTGACCT    98182          A
                                AGGTCAGGAG TCGAGACC
                                |||||||||| ||||||||
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                                TCCAGTCCTC AGCTCTGG
                                      A
GAM1701  LOC253842 5'  GGTCTCCATCTCCTGACCTCGT 99239      A          C
                GA                TCAC AGGTCAGGAGAT GAGACC
                                  |||| |||||||||||| ||||||
                                  AGTG TCCAGTCCTCTA CTCTGG
                                    C          C
GAM1701  LOC253981 3'  GGTCTCGATCTCCTGACCTCGT 97539      A
                GA                TCAC AGGTCAGGAGATCGAGACC
                                  |||| ||||||||||||||||||
                                  AGTG TCCAGTCCTCTAGCTCTGG
                                    C
GAM1701  LOC254018 5'  GGTCTGGATCTCCTGACCTCGT 98741      A          G
                GA                TCAC AGGTCAGGAGATC AGACC
                                  |||| |||||||||||| |||||
                                  AGTG TCCAGTCCTCTAG TCTGG
                                    C          G
GAM1701  LOC254249 5'  GGTCTTGATCTCCTGACCTCGT 97186      A
                GA                TCAC AGGTCAGGAGATCGAGACC
                                  |||| ||||||||||||||||||
                                  AGTG TCCAGTCCTCTAGTTCTGG
                                    C
GAM1701  LOC254295 5'  GGTCTCGATTTCCTGACCTCGT 97894      A
                GA                TCAC AGGTCAGGAGATCGAGACC
                                  |||| ||||||||||||||||||
                                  AGTG TCCAGTCCTTTAGCTCTGG
                                    C
GAM1701  LOC254672 3'  GGTCTGGAACTCCTGACCCTGT 96296       A       A  G
                GA                TCACA GGTCAGGAG TC AGACC
                                  ||||| ||||||||| || |||||
                                  AGTGT CCAGTCCTC AG TCTGG
                                     C        A  G
GAM1701  LOC255146 3'  CGGGCTCCTCACCTTGTGA   97344          C     AT
                                  TCACAAGGT AGGAG  CG
                                  ||||||||| |||||  ||
                                  AGTGTTCCA TCCTC  GC
                                        C     GG
GAM1701  LOC255465 3'  TCTCGAACTCCTGACCTCGTGA 99129      A        A
                                  TCAC AGGTCAGGAG TCGAGA
                                  |||| |||||||||| ||||||
                                  AGTG TCCAGTCCTC AGCTCT
                                    C         A
GAM1701  LOC256221 3'  GTCTCGATCTCCTGACCTCGTG 96918      A
                A                  TCAC AGGTCAGGAGATCGAGAC
                                  |||| |||||||||||||||||
                                  AGTG TCCAGTCCTCTAGCTCTG
                                    C
GAM1701  LOC257486 3'  GGTCTTGATCTCTTGACCTCGT 69778      A
                GA                TCAC AGGTCAGGAGATCGAGACC
                                  |||| ||||||||||||||||||
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                                AGTG TCCAGTTCTCTAGTTCTGG
                                  C
GAM1701  LOC51159  5'  GGTCTCCGTCTCCTGACCTCGT 33033      A          C
                GA                TCAC AGGTCAGGAGAT GAGACC
                                  |||| |||||||||||| ||||||
                                  AGTG TCCAGTCCTCTG CTCTGG
                                    C          C
GAM1701  LOC51696  3'  GGTCTAGATCTCCTGACCTTGT 33086               G
                GA                TCACAAGGTCAGGAGATC AGACC
                                  |||||||||||||||||| |||||
                                  AGTGTTCCAGTCCTCTAG TCTGG
                                             A
GAM1701  LOC56181  5'  GGTCTCGCTCTCCTGACCTCGT 97280      A         T
                GA                TCAC AGGTCAGGAGA CGAGACC
                                  |||| |||||||||| |||||||
                                  AGTG TCCAGTCCTCT GCTCTGG
                                    C          C
GAM1701  LOC81034  3'  GGTCTCAATCTCCTGACCTTGT 48592               C
                GA                TCACAAGGTCAGGAGAT GAGACC
                                  |||||||||||||||| ||||||
                                  AGTGTTCCAGTCCTCTA CTCTGG
                                             A
GAM1701  LOC89919  3'  GTCTCGATCTCCGGACCTCATG 61378     CA     A
                A                  TCA  AGGTC GGAGATCGAGAC
                                   |||  ||||| ||||||||||||
                                   AGT  TCCAG CCTCTAGCTCTG
                                     AC     G
GAM1701  LOC89932  3'  GGTCTCGAACTTCTGACCT    61470          A
                                  AGGTCAGGAG TCGAGACC
                                  |||||||||| ||||||||
                                  TCCAGTCTTC AGCTCTGG
                                        A
GAM1701  LOC90288  3'  GGTCTCGATCTCCTGACTTCAT 62794     CA
                GA                TCA  AGGTCAGGAGATCGAGACC
                                  |||  ||||||||||||||||||
                                  AGT  TTCAGTCCTCTAGCTCTGG
                                    AC
GAM1701  LOC90485  3'  GGTCTCGATCTCCTGACTTCGT 63705    A
                                  AC AGGTCAGGAGATCGAGACC
                                  || ||||||||||||||||||
                                  TG TTCAGTCCTCTAGCTCTGG
                                   C
GAM1701  LOC90591  3'  GGTCTCAATCTCCTGACCTCGT 64179      A          C
                GA                TCAC AGGTCAGGAGAT GAGACC
                                  |||| |||||||||||| ||||||
                                  AGTG TCCAGTCCTCTA CTCTGG
                                    C          A
GAM1701  LOC91115  3'  GGTCAATCTCCTGACCTTGTGA 65572               CGA
                                  TCACAAGGTCAGGAGAT   GACC
                                  |||||||||||||||||   ||||
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                                AGTGTTCCAGTCCTCTA  CTGG
                                        A__
GAM1701  LOC91115  3'  GGTCTCCAACTCCTGACCT   65573        ATC
                                AGGTCAGGAG  GAGACC
                                ||||||||||  ||||||
                                TCCAGTCCTC  CTCTGG
                                     AAC
GAM1701  LOC91308  3'  GATCACTCCTGACCACGTGA  66167    AA     __
                                TCAC  GGTCAGGA  GATC
                                ||||  ||||||||  ||||
                                AGTG  CCAGTCCT  CTAG
                                  CA      CA
GAM1701  LOC91373  3'  GGTCTCGATCTCCTGACCTCGT 66417     A
           GA                     TCAC AGGTCAGGAGATCGAGACC
                                ||||| ||||||||||||||||||
                                AGTG TCCAGTCCTCTAGCTCTGG
                                  C
GAM1701  LOC92148  5'  GGTCTCGATCTCCTGACCTTGT 68885
           GA                     TCACAAGGTCAGGAGATCGAGACC
                                ||||||||||||||||||||||||
                                AGTGTTCCAGTCCTCTAGCTCTGG

GAM1701  LOC92661  5'  GGTCTCGATCTCTTGATCTCAT 70634    CA
           GA                     TCA  AGGTCAGGAGATCGAGACC
                                |||  ||||||||||||||||||
                                AGT  TCTAGTTCTCTAGCTCTGG
                                  AC
GAM1701  LOC92689  3'  GGTCTCGATCTCCTGACCTCGT 70779     A
           GA                     TCAC AGGTCAGGAGATCGAGACC
                                ||||| ||||||||||||||||||
                                AGTG TCCAGTCCTCTAGCTCTGG
                                  C
GAM1701  LOC93349  3'  GGTCTCGAACTCCTGACCTCAT 57274    CA       A
           GA                     TCA  AGGTCAGGAG TCGAGACC
                                |||  |||||||||| ||||||||
                                AGT  TCCAGTCCTC AGCTCTGG
                                  AC       A
GAM1701  LOC93356  3'  ATCTTCCTGACCTTGTGA   72548          _
                                TCACAAGGTCAGGA GAT
                                |||||||||||||| |||
                                AGTGTTCCAGTCCT CTA
                                       T
GAM1702  CDKN1A    5'  AGAGCCGAGCCAAGCGTGCC  55265       CGAA  TC   C
                                GGCACGCT   CT  CGGC CT
                                ||||||||   ||  |||| ||
                                CCGTGCGA   GA  GCCG GA
                                     ACC_  __   A
GAM1702  DKFZp761A052 5'  GGCCGGAACAAGCGTAGC   73377   _   CGAAC
                                GC ACGCT   TTCCGGCC
                                || |||||   ||||||||
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                                CG TGCGA    AAGGCCGG
                                 A    AC___
GAM1702 KIAA0415 3' GGCTCAGCCCGGCGTGCCA   94167       T  AA  TCC
                                TGGCACGC CG  CT   GGCC
                                |||||||| ||  ||   ||||
                                ACCGTGCG GC  GA   TCGG
                                     _  CC  C__
GAM1702 PDE4DIP  5' AGAGCCGGAAGCCCGCTGACC  28402    _  C  TCGAA      C
                                GG CA GC    CTTCCGGC CT
                                || || ||    |||||||| ||
                                CC GT CG    GAAGGCCG GA
                                 A  _  CCC__      A
GAM1702 SCYB14   5' GGCCGGAAGGCGCGCC      18088     A   TCGAA      C
                                GGC CGC    CTTCCGGC C
                                ||| |||    |||||||| |
                                CCG GCG    GAAGGCCG G
                                  C  _____      A
GAM1702 LOC144100 3' AGGGCCGGAGCAGGAGCATGCT 77183      C    GAAC
              A                  TGGCA GCTC    TTCCGGCCCT
                                 ||||| ||||    ||||||||||
                                 ATCGT CGAG    GAGGCCGGGA
                                    A    GAC_
GAM1702 LOC145934 5' AGGGCCGGAGAAGCGAGCGGCC 84558      A     AAC
              A                  TGGC CGCTCG   TTCCGGCCCT
                                 |||| ||||||   ||||||||||
                                 ACCG GCGAGC   GAGGCCGGGA
                                   _     GAA
GAM1702 LOC148696 5' AGGGCCGAGAAGGCGCGTGCCA 85344        TCGAA   _
                                TGGCACGC     CTTC CGGCCCT
                                ||||||||     |||| |||||||
                                ACCGTGCG     GAAG GCCGGGA
                                     CG___    A
GAM1702 LOC253263 3' AGGGCCGGCTCGTGAACAGCCA 98813      ACGCT_   ACTT
                                TGGC     CGA    CCGGCCCT
                                ||||     |||    ||||||||
                                ACCG     GCT    GGCCGGGA
                                  ACAAGT   C___
GAM1702 LOC254559 5' AGGGCGCGTGGTTCGGCGTGCC 98380        T     TC  _
              A                  TGGCACGC CGAACT  CG GCCCT
                                 ||||||| ||||||  || |||||
                                 ACCGTGCG GCTTGG  GC CGGGA
                                     _     T_  G
GAM1702 LOC256444 5' AGGGCCGGAGAAGCGAGCGGCC 98382      A     AAC
              A                  TGGC CGCTCG   TTCCGGCCCT
                                 |||| ||||||   ||||||||||
                                 ACCG GCGAGC   GAGGCCGGGA
                                   _     GAA
GAM1703 ENAM     3' AGGATGCTGAATGAGCCACCAC 49926     AA    C__
              T                  AGT  TGGC   TTCAGCATCCT
                                 |||  ||||   ||||||||||
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                                TCA  ACCG   AAGTCGTAGGA
                                  CC    AGT
GAM1703  LASS2    3'  AGAATGACTGAACCATTACT   68305        CC    _  C
                                AGTAATGG  TTCAG CAT CT
                                ||||||||  ||||| ||| ||
                                TCATTACC  AAGTC GTA GA
                                    __    A   A
GAM1703  C20orf162 5'  AGGACACTGAAGGCCTGGC    55496    AAT       CA
                                GT   GGCCTTCAG  TCCT
                                ||   |||||||||  ||||
                                CG   CCGGAAGTC  AGGA
                                 GT_       AC
GAM1703  CBX6     3'  GGATGCTGAAGAATCCATT    27420      C__
                                AATGG   CTTCAGCATCC
                                |||||   ||||||||||
                                TTACC   GAAGTCGTAGG
                                   TAA
GAM1703  DKFZP566K0524 3'  GATGTGGCCATTATTA      69877          TTCA
                                TAGTAATGGCC    GCATC
                                ||||||||||    |||||
                                ATTATTACCGG    TGTAG
                                      ____
GAM1703  KIAA1463  3'  AGGCCTGAAAGGCCATTACTA  72735           _  CAT
                                TAGTAATGGCCTT CAG   CCT
                                ||||||||||||| |||   |||
                                ATCATTACCGGAA GTC   GGA
                                       A   C__
GAM1703  PPP2R3A   3'  ATGTTGAAAACAATTACTA    12238       GGCC
                                TAGTAAT    TTCAGCAT
                                |||||||    ||||||||
                                ATCATTA    AAGTTGTA
                                    ACAA
GAM1703  RICH1    3'  GAACCTGGAGGCCACCACTA   36480      AA        CA
                                TAGT  TGGCCTTCAG  TC
                                ||||  ||||||||||  ||
                                ATCA  ACCGGAGGTC  AG
                                  CC         CA
GAM1703  LOC133088 5'  AGGACATGAAGCCATTATTATA 75585           C    GCA
                                TATAGTAATGGC TTCA   TCCT
                                ||||||||||| ||||   ||||
                                ATATTATTACCG AAGT   AGGA
                                       _    AC_
GAM1703  LOC151323 3'  GATGCTGAACGGCCACAC    81025    AA    _
                                GT  TGGCC TTCAGCATC
                                ||  ||||| |||||||||
                                CA  ACCGG AAGTCGTAG
                                 C_    C
GAM1703  LOC92181  3'  GCTTAGAAGGTCACTACTATA  68947        A       __
                                TATAGTA TGGCCTTC  AGC
                                ||||||| ||||||||  |||
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                                ATATCAT ACTGGAAG  TCG
                                    C       AT
GAM1704  LOC91585  5'  TTGAGGACAAGGCCTAG     67161     C   A  AAGA
                                CTA GCC TG    TCCTCAA
                                ||| ||| ||    |||||||
                                GAT CGG AC    AGGAGTT
                                  C   A  ____
GAM1705  SNAI2     3'  CTCAGGTGCCTTAAAAAGT    13240     C    C   AC
                                AC TTTTG GGC  ACCTGAG
                                || ||||| |||  |||||||
                                TG AAAAT CCG  TGGACTC
                                 A    T  __
GAM1705  BRPF3     3'  CAGATGGCAAGAGGTC      93926         GGCA  C
                                GACCTTTTGC    CA CTG
                                ||||||||||    || |||
                                CTGGAGAACG    GT GAC
                                      ____  A
GAM1705  CSMD1     3'  TCAAATGTGTCAGGGTCTT   53787        TTGC     CC
                                AAGACCTT    GGCACA  TGA
                                ||||||||    ||||||  |||
                                TTCTGGGA    CTGTGT  ACT
                                     ____      AA
GAM1705  FLJ10204  3'  CTCAAATGCCCATAAAAGGT  36356        C_    CACC
                                ACCTTTTG  GGCA    TGAG
                                ||||||||  ||||    ||||
                                TGGAAAAT  CCGT    ACTC
                                    AC    AA__
GAM1705  FLJ10874  5'  TCAGGTGTGCCGAAGCTCT   37328     C   TTG
                                AGA CTT   CGGCACACCTGA
                                ||| |||   ||||||||||||
                                TCT GAA   GCCGTGTGGACT
                                  C   ___
GAM1705  FLJ12800  5'  CAAGTGTCTGACTCGCAAAGGC 43525    AC       C____    C
             CCT                  AG  CTTTTGCGG    ACAC TG
                                ||  |||||||||    |||| ||
                                TC  GGAAACGCT    TGTG AC
                                 CC       CAGTC    A
GAM1705  KIAA0939  3'  CAAGTGAGCTGCAAGAGG    62709          A   C
                                CCTTTTGCGGC CAC TG
                                |||||||||| ||| ||
                                GGAGAACGTCG GTG AC
                                      A   A
GAM1705  MVD       3'  CAGGTGTCAGGAGAGGTC    11715        GCGGC
                                GACCTTTT    ACACCTG
                                ||||||||    |||||||
                                CTGGAGAG    TGTGGAC
                                    GAC__
GAM1705  SRPK1     3'  CTCAGGTGTTCTATAAACAGTC 13405     CT    CG C
                                GAC  TTTG  G ACACCTGAG
                                |||  ||||  | |||||||||
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                                CTG  AAAT  C TGTGGACTC
                                  AC    AT T
GAM1705  UPK1A    3'  CTCAGGTGTGCCCTGAAA    23785      C
                                TTTTG GGCACACCTGAG
                                ||||| ||||||||||||
                                AAAGT CCGTGTGGACTC
                                   C
GAM1705  VEGFC    3'  TCATCTGCAAAAGGCCT     19475    A        CACACC
                                AG CCTTTTGCGG     TGA
                                || ||||||||||     |||
                                TC GGAAAACGTC     ACT
                                 C         T_____
GAM1705  LOC136319 5'  GGTGGCCGCAAAAGAACTT   75772     AC         A
                                AAG  CTTTTGCGGC CACC
                                |||  |||||||||| ||||
                                TTC  GAAAACGCCG GTGG
                                  AA         _
GAM1705  LOC143677 3'  CAGGGGCAAAAGGCTCT     83894     _       GGCACA
                                AGA CCTTTTGC      CCTG
                                ||| ||||||||      ||||
                                TCT GGAAAACG      GGAC
                                  C       G_____
GAM1705  LOC146330 5'  CAGGTGTGCAAGGCCT      78377    A    TTGCG
                                AG CCTT     GCACACCTG
                                || ||||     |||||||||
                                TC GGAA     CGTGTGGAC
                                 C    _____
GAM1705  LOC150406 3'  CTCAGGTGTGCCCGCGGGA    80672         _
                                TTTTGCGG CACACCTGAG
                                |||||||| ||||||||||
                                AGGGCGCC GTGTGGACTC
                                     C
GAM1705  LOC151361 3'  CTCACACCCACAGAAGGTCTT  86503           C  CACACC
                                AAGACCTTTTG GG      TGAG
                                |||||||||| ||      ||||
                                TTCTGGAAGAC CC      ACTC
                                       A  CAC___
GAM1705  LOC201771 5'  TCAATCCGTAAAAAGTCTT    70519       C       CACACC
                                AAGAC TTTTGCGG      TGA
                                ||||| ||||||||      |||
                                TTCTG AAAATGCC      ACT
                                   A       TA____
GAM1705  LOC204970 3'  TCAGGTGCGCCCAGACCGT    90969     CT    C   A
                                AC  TTTG GGC CACCTGA
                                ||  |||| ||| |||||||
                                TG  AGAC CCG GTGGACT
                                 CC    _   C
GAM1705  LOC221191 3'  CAGGTGTGGGAAGGTC      95219         GCGG
                                GACCTTTT    CACACCTG
                                ||||||||    ||||||||
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                                CTGGAAGG   GTGTGGAC
                                    ____
GAM1705 LOC256158 5' CAGGTATCGGATAAAGGTTT  99483       TG_  CAC
                                AGACCTTT  CGG  ACCTG
                                ||||||||  |||  |||||
                                TTTGGAAA  GCT  TGGAC
                                    TAG  A__
GAM1706 ADAM12   3' TTCACTCTTCAAATGCCT   14426          _
                                AGGCATTTGAAGA TGAA
                                |||||||||||| ||||
                                TCCGTAAACTTCT ACTT
                                       C
GAM1706 CHST1    3' CACCTCATCTTCGTGTC    14693     TT     AA
                                GGCAT  GAAGATGA  TG
                                |||||  ||||||||  ||
                                CTGTG  CTTCTACT  AC
                                  __      CC
GAM1706 CNTN3    3' TTTCATTTAATTCAAATGCT  67272       GATG
                                GGCATTTGAA   AAATGAAA
                                ||||||||||   ||||||||
                                TCGTAAACTT   TTTACTTT
                                     AA__
GAM1706 FGA      3' TCTGTATTCCCAAATGCCT   41852       AA   AAAT
                                AGGCATTTG  GATG   GA
                                |||||||||  ||||   ||
                                TCCGTAAAC  TTAT   CT
                                     CC   GT__
GAM1706 GTF2F1   3' TTCTGGAATCTTCAGATGCCT 10896         GAAAT
                                AGGCATTTGAAGAT   GAA
                                ||||||||||||||   |||
                                TCCGTAGACTTCTA   CTT
                                       AGGT_
GAM1706 H4FH     3' TTTCATTTTCAACCAAAGGCC 14515    AT____
                                GGC    TTGAAGATGAAA
                                |||    ||||||||||||
                                CCG    AACTTTTACTTT
                                  GAAACC
GAM1706 MGAT4B   5' TTTCCACTTCAGATGCCT   55028         AT
                                AGGCATTTGAAG  GAAA
                                ||||||||||||  ||||
                                TCCGTAGACTTC  CTTT
                                       AC
GAM1706 MSN      3' CACTTGATTTTGCAAATGCC  60880       _   G  A
                                GGCATTTG AAGAT AA TG
                                |||||||| ||||| || ||
                                CCGTAAAC TTTTA TT AC
                                     G   G  C
GAM1706 PLEK     3' TCATTTTATCAAATCCT    12167    C    AGA
                                AGG ATTTGA   TGAAATGA
                                ||| ||||||   ||||||||
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                                TCC TAAACT   ATTTTACT
                                  _    ___
GAM1706  PPEF1    5'  TTCATTTCCTTTGAAACACCT  21781    CA_  TG   AT
                                AGG   TT  AAG  GAAATGAA
                                |||   ||  |||  ||||||||
                                TCC   AA  TTC  CTTTACTT
                                  ACA  GT   __
GAM1706  RNF26    5'  CAGCCCATCTTCAAAACCT   50133    CA       AAA
                                AGG  TTTGAAGATG   TG
                                |||  ||||||||||   ||
                                TCC  AAACTTCTAC   AC
                                  A_        CCG
GAM1706  C(27)-3BETA-HSD 3'  CATTGTTTTTCAAAGGCCT   48049     A      TGA
                                AGGC TTTGAAGA   AATG
                                ||||  ||||||||   ||||
                                TCCG AAACTTTT   TTAC
                                  G       TG_
GAM1706  CALN1    3'  TTTTATTCCAAATGCCT     49673        AA
                                AGGCATTTG  GATGAAA
                                |||||||||  |||||||
                                TCCGTAAAC  TTATTTT
                                     C_
GAM1706  DEFA3    3'  TCATCTCAAATAAATGCCT    19069        A___
                                AGGCATTTG    AGATGA
                                |||||||||    ||||||
                                TCCGTAAAT    TCTACT
                                     AAAC
GAM1706  DKFZP434N014 3'  CAGCCCATCCCCAGATGCCT   61227        AA   AAA
                                AGGCATTTG  GATG   TG
                                |||||||||  ||||   ||
                                TCCGTAGAC  CTAC   AC
                                     CC    CCG
GAM1706  DKFZP564O1664 3'  TTTTCATTTCAACTGAAAATGC 48671        GA  A
            TT                    AGGCATTT  AG TGAAATGAAAA
                                |||||||||  || ||||||||||
                                TTCGTAAA  TC ACTTTACTTTT
                                     AG  A
GAM1706  FLJ11618  3'  TTCACCCCATTTCCAAGTGCC  42628        A    AAA
                                GGCATTTG AGATG   TGAA
                                |||||||| |||||   ||||
                                CCGTGAAC TTTAC   ACTT
                                     C    CCC
GAM1706  FLJ20360  3'  TTTTCATTTTAAACAAGATGCC 92511        GAAGA
            T                    AGGCATTT    TGAAATGAAAA
                                ||||||||    ||||||||||
                                TCCGTAGA    ATTTTACTTTT
                                     ACAA_
GAM1706  FLJ31737  3'  TTTCATCTTCCATCAATGCCT  59352        T___
                                AGGCATT    GAAGATGAAA
                                |||||||    ||||||||||
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                                TCCGTAA   CTTCTACTTT
                                   CTAC
GAM1706  FUBP1    3'  TTTCACTTTCCAAATGCCT   15334        _  A
                                AGGCATTTG AAG TGAAA
                                ||||||||| ||| |||||
                                TCCGTAAAC TTT ACTTT
                                    C  C
GAM1706  KIAA0377 3'  CATATCATCCCCAAGTGCC   28499       AA   A
                                GGCATTTG  GATGA ATG
                                ||||||||  ||||| |||
                                CCGTGAAC  CTACT TAC
                                    CC    A
GAM1706  KIAA0547 3'  TTTCATTCTACAAGTGCCT   29604        A  _
                                AGGCATTTG AGA TGAAA
                                ||||||||| ||| |||||
                                TCCGTGAAC TCT ACTTT
                                    A  T
GAM1706  KIAA0819 3'  ATTCCATCTTCAAACCCC    64329    CA       A
                                GG  TTTGAAGATG AAT
                                ||  |||||||||| |||
                                CC  AAACTTCTAC TTA
                                 CC        C
GAM1706  KIAA0993 3'  TTTTCATTTCAAATAAATACCT 64825    C    AAGA
                                AGG ATTTG   TGAAATGAAAA
                                ||| |||||   ||||||||||
                                TCC TAAAT   ACTTTACTTTT
                                  A    AA__
GAM1706  KIAA1076 3'  TCATTTTAACAAACGCC    66128    A   AAGA
                                GGC TTTG   TGAAATGA
                                ||| ||||   ||||||||
                                CCG AAAC   ATTTTACT
                                  C   A___
GAM1706  KIAA1238 3'  TTTCATTTACAAATCCT    71636    C    A
                                AGG ATTTG AGATGAAA
                                ||| ||||| ||||||||
                                TCC TAAAC TTTACTTT
                                  _    A
GAM1706  KIAA1613 3'  TCATTTCACAAATCCAGCCT  65443     ___    AAGA
                                AGGC  ATTTG   TGAAATGA
                                ||||  |||||   ||||||||
                                TCCG  TAAAC   ACTTTACT
                                  ACC   ____
GAM1706  KIAA1677 3'  TTTTCACTTTATATCTCAAATG 67668       AG_   A
            CC                   GGCATTTGA  ATGAA TGAAAA
                                ||||||||||  ||||| ||||||
                                CCGTAAACT  TATTT ACTTTT
                                    CTA    C
GAM1706  KIAA1754 3'  TCATTCCATCAGATGC     63934       AGA  A
                                GCATTTGA  TG AATGA
                                ||||||||  || |||||
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                                CGTAGACT   AC TTACT
                                     ___  C
GAM1706 KLF12    3'  CATTTCATCTCATGTCC     24360    C  T   A
                                GG AT TGA GATGAAATG
                                || || ||| |||||||||
                                CC TG ACT CTACTTTAC
                                 _  T   _
GAM1706 MGC15668 3'  CATTTCATCAGTGCCT      52242        TGAA
                                AGGCATT    GATGAAATG
                                |||||||    |||||||||
                                TCCGTGA    CTACTTTAC
                                     ____
GAM1706 MGC27277 3'  TTTCATCTATCAAATACT    59364    C     _
                                GG ATTTGA AGATGAAA
                                || |||||| ||||||||
                                TC TAAACT TCTACTTT
                                 A     A
GAM1706 MRVI1    3'  CATCTCATTTTCAATAACT    56094    GCAT        A
                                AG    TTGAAGATGA ATG
                                ||    |||||||||| |||
                                TC    AACTTTTACT TAC
                                 AAT_         C
GAM1706 MRVI1    3'  CATCTCATTTTCAATAACT    21380    GCAT        A
                                AG    TTGAAGATGA ATG
                                ||    |||||||||| |||
                                TC    AACTTTTACT TAC
                                 AAT_         C
GAM1706 NAALAD2  3'  TTTCATCTGCAAAGCCT     19614     A    A
                                AGGC TTTG AGATGAAA
                                |||| |||| ||||||||
                                TCCG AAAC TCTACTTT
                                  _    G
GAM1706 P5-1     3'  TTTTCATCTCATGATGGATGCT 22891      TT AAG    A
                                GGCAT  G   ATGA ATGAAAA
                                |||||  |   |||| |||||||
                                TCGTA  T   TACT TACTTTT
                                   GG AG_    C
GAM1706 PSR      3'  TTCTGCATCCTCAAATGCC    65797         A    AAAT
                                GGCATTTGA GATG    GAA
                                ||||||||| ||||    |||
                                CCGTAAACT CTAC    CTT
                                     C    GT__
GAM1706 SLC26A8  3'  TCATTTCACCTTCAGC      57804    ATT    A
                                GC   TGAAG TGAAATGA
                                ||   ||||| ||||||||
                                CG   ACTTC ACTTTACT
                                 ___     C
GAM1706 SLC26A8  3'  TCATTTCACCTTCAGC      54770    ATT    A
                                GC   TGAAG TGAAATGA
                                ||   ||||| ||||||||
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                                CG   ACTTC ACTTTACT
                                 ___     C
GAM1706  TACTILE   3'  TCTTTCATCTCCAAACGCCT   20595      A    A       T
                                AGGC TTTG AGATGAAA GA
                                |||| |||| |||||||| ||
                                TCCG AAAC TCTACTTT CT
                                  C   C       _
GAM1706  WNT8A     3'  CATTTCATCTTTCCT       55256     CATTT
                                AGG     GAAGATGAAATG
                                |||     ||||||||||||
                                TCC     TTTCTACTTTAC
                                 _____
GAM1706  LOC122830 3'  TTTCATTTCTTAAAATGCTT   74633         GAAGAT
                                AGGCATTT     GAAATGAAA
                                ||||||||     |||||||||
                                TTCGTAAA     CTTTACTTT
                                     ATT___
GAM1706  LOC145098 3'  TTTCTTTCCAAATGCCT     77540          A   T
                                AGGCATTTG AGA GAAA
                                ||||||||| ||| ||||
                                TCCGTAAAC TTT CTTT
                                     C   _
GAM1706  LOC146895 5'  CAGATCATCTTACAAATGCCT  84861          _      AA
                                AGGCATTTG AAGATGA  TG
                                ||||||||| |||||||  ||
                                TCCGTAAAC TTCTACT  AC
                                     A      AG
GAM1706  LOC149271 5'  TTTTCATTTGCAAAGCAAAGCC 80015      A    AAGA  _
           T                     AGGC TTTG    TG AAATGAAAA
                                |||| ||||    || |||||||||
                                TCCG AAAC    AC TTTACTTTT
                                  _    GAA_  G
GAM1706  LOC149386 5'  TTCAAGTACACTTCAAATACCT 85566     C       A  AAA_
                                AGG ATTTGAAG TG    TGAA
                                ||| |||||||| ||    ||||
                                TCC TAAACTTC AC    ACTT
                                  A       _  ATGA
GAM1706  LOC200609 5'  TTTCATTTCACTTCTATCCT   91672     C  TT    A
                                AGG AT  GAAG TGAAATGAAA
                                ||| ||  |||| ||||||||||
                                TCC TA  CTTC ACTTTACTTT
                                  _  T_   _
GAM1706  LOC220081 3'  TCTGGCATCCACCAAATGCCT  93405         AA_   AAAT
                                AGGCATTTG   GATG    GA
                                |||||||||   ||||    ||
                                TCCGTAAAC   CTAC    CT
                                     CAC    GGT_
GAM1707  ABCD3     3'  AATTAAATTGGGCTTCAA     12660          T  C
                                TTGAAGCCCA TT AGTT
                                |||||||||| || ||||
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                                AACTTCGGGT AA TTAA
                                      T  A
GAM1707  FUT8     3'  AACTGACATAGGCTTCAA    16810        C  T
                                TTGAAGCC AT TCAGTT
                                |||||||| || ||||||
                                AACTTCGG TA AGTCAA
                                     A  C
GAM1707  GABRA6   3'  TTATGAGGATGAAATGGGTTCA 7694       G       GTTAA
              A                  TTGAA CCCATTTCA    ATAA
                                |||||  |||||||||    ||||
                                AACTT GGGTAAAGT    TATT
                                   _       AGGAG
GAM1707  GLI3     3'  TAACTGAGATGTGTTTCAA   5719        C
                                TTGAAGC CATTTCAGTTA
                                ||||||| ||||||||||
                                AACTTTG GTAGAGTCAAT
                                     T
GAM1707  PRKAR2B  3'  ATTTTGGGAAACAGGTTTCAA  12284        CA   AGTT
                                TTGAAGCC  TTTC   AAAT
                                ||||||||  ||||   ||||
                                AACTTTGG  AAAG   TTTA
                                     AC   GGT_
GAM1707  SMARCA2  3'  TGACCAAATGGGCCTCAA    13243     A      CA
                                TTGA GCCCATTT  GTTA
                                |||| ||||||||  ||||
                                AACT CGGGTAAA  CAGT
                                   C       C_
GAM1707  TAZ      3'  TATTTAACTTGAGCTTTAA   31921       C  TTTC
                                TTGAAGC CA   AGTTAAATA
                                ||||||| ||   |||||||||
                                AATTTCG GT   TCAATTTAT
                                     A  ____
GAM1707  DKFZP434G1415 3'  TTATTTAAACTCATGGGCTTCA 49270          TTCAG
              G                  TTGAAGCCCAT    TTAAATAA
                                ||||||||||    ||||||||
                                GACTTCGGGTA    AATTTATT
                                      CTCA_
GAM1707  KIAA1219  3'  TATCTAGTGAAATGGGCT    62029          G  A
                                AGCCCATTTCA TTA ATA
                                |||||||||| ||| |||
                                TCGGGTAAAGT GAT TAT
                                      _  C
GAM1707  KIAA1918  3'  TTAAGTTGAAAAAGCTTCAA   73541       CCA    _
                                TTGAAGC   TTTCAG TTAA
                                |||||||   |||||| ||||
                                AACTTCG   AAAGTT AATT
                                     AA_     G
GAM1707  MESDC2   3'  ACTGCTTAATAGGCTTCAA   72904        C  T__
                                TTGAAGCC ATT   CAGT
                                |||||||| |||   ||||
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                                AACTTCGG TAA   GTCA
                                     A   TTC
GAM1707  PRO2577   3'  AACTAAAAAGGCTTCAA     38423         CA   C
                                TTGAAGCC  TTT AGTT
                                ||||||||  ||| ||||
                                AACTTCGG  AAA TCAA
                                     AA  _
GAM1707  TTTY9     3'  TTAATGAATGGGCTTCAA    50023           CA
                                TTGAAGCCCATTT  GTTAA
                                ||||||||||||  |||||
                                AACTTCGGGTAAG  TAATT
                                       __
GAM1707  LOC166824 3'  TAACTGAAATAAGCTTGAA   83550    G    CC
                                TT AAGC  ATTTCAGTTA
                                || ||||  ||||||||||
                                AA TTCG  TAAAGTCAAT
                                 G   AA
GAM1707  LOC93206  5'  TTATTTAACTCATGGGAGCCTC 72194     AG__    TTC
              AG                  TTGA   CCCAT   AGTTAAATAA
                                ||||   |||||  ||||||||||
                                GACT   GGGTA   TCAATTTATT
                                  CCGA    C__
GAM1708  MYO1D     3'  CGGCAGAACCCACCAAGTGC   72243      A       C___
                                GCAC TGGTGGGT    CCG
                                |||| ||||||||    |||
                                CGTG ACCACCCA    GGC
                                  A       AGAC
GAM1708  SH3BP4    3'  CGCCAATCATCCCACCAT    27999         TCCC
                                ATGGTGGG    GATTGGCG
                                ||||||||    ||||||||
                                TACCACCC    CTAACCGC
                                     TA__
GAM1708  ABHD2     3'  CAGGGGGCACCCACCATG    23793          _   GA
                                CATGGTGGGT CCC  TTG
                                |||||||||| |||  |||
                                GTACCACCCA GGG  GAC
                                      C   G_
GAM1708  BCoR      3'  CAAGCTGGACCCACCATGT   40887           CGA
                                ACATGGTGGGTCC   TTG
                                ||||||||||||   |||
                                TGTACCACCCAGG   AAC
                                       TCG
GAM1708  FLJ12488  3'  CCGATTGGCGCAAGGCCCACCA 49157     C        _________  GATT
              TATGC                 GCA ATGGTGGGTC       CC    GG
                                ||| ||||||||||       ||    ||
                                CGT TACCACCCGG       GG    CC
                                  A        AAC___GC  TTAG
GAM1708  FLJ20856  5'  GTTAAGCACCCACCATGTGC   47865           CCCGA
                                GCACATGGTGGGT    TTGGC
                                ||||||||||||    |||||
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                                CGTGTACCACCCA    AATTG
                                      CG___
GAM1708 NXPH3    3' CCAATGGACACCCACCGTGTGC 66340          C_ G
                                GCACATGGTGGGT  CC ATTGG
                                |||||||||||||  || |||||
                                CGTGTGCCACCCA  GG TAACC
                                      CA  _
GAM1708 LOC145453 3' CCAACCAGGATGCTTCACCATG 77656        ___   CGA
                                CATGGTGG   GTCC   TTGG
                                ||||||||   ||||   ||||
                                GTACCACT   TAGG   AACC
                                     TCG    ACC
GAM1708 LOC150935 5' CGGACACCCACCACGTGC    80825      A      C_
                                GCAC TGGTGGGT  CCG
                                |||| ||||||||  |||
                                CGTG ACCACCCA  GGC
                                  C       CA
GAM1708 LOC56270  3' CGCCACAGCACCCACCACCTGC 39504     CA      CCCGAT
                                GCA  TGGTGGGT     TGGCG
                                |||  ||||||||     |||||
                                CGT  ACCACCCA     ACCGC
                                 CC       CGAC__
GAM1709 ADCY8    5' GGACATGCCTTTCTCCACGTCC 8502     A   A     __  CA
            GC                    GC GGAC TGGAGAA  GTA  TCC
                                || |||| |||||||  |||  |||
                                CG CCTG ACCTCTT  CGT  AGG
                                 _   C      TC   AC
GAM1709 AKT2     5' GTGCCTCCTGCATGTCCTGCT  9677          G  AA_
                                AGCAGGACATG AG   GTAC
                                ||||||||||| ||   ||||
                                TCGTCCTGTAC TC   CGTG
                                      G  CTC
GAM1709 APOBEC2  3' TACTTCTCATGCTGT      23280      GA   G
                                GCAG  CATG AGAAGTA
                                ||||  |||| |||||||
                                TGTC  GTAC TCTTCAT
                                  __   _
GAM1709 GPD1     3' GCTTTCTCCATATCCTCT    60397    C   C      _
                                AG AGGA ATGGAGAA GT
                                || |||| |||||||| ||
                                TC TCCT TACCTCTT CG
                                 _   A       T
GAM1709 HMGN2    3' TGTCTGCCCATGTCCTGC    19810          AGA  T
                                GCAGGACATGG   AG ACA
                                ||||||||||   || |||
                                CGTCCTGTACC   TC TGT
                                      CG_  _
GAM1709 MCM4     3' GCTCCCTGCATGTCCTGCT   62579          G  A_
                                AGCAGGACATG AG  AGT
                                |||||||||| ||  |||
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                                TCGTCCTGTAC TC  TCG
                                      G  CC
GAM1709  MEN1     3'  GGATGTACTAAAATGTATCCT  95013      C   GAGA
                                AGGA ATG    AGTACATCC
                                |||| |||    |||||||||
                                TCCT TGT    TCATGTAGG
                                  A   AAAA
GAM1709  MTL5     3'  GATGTGGCAACCCATGCCCCCT 18199    CA  A    AGAAG
                                AG  GG CATGG    TACATC
                                ||  || |||||    ||||||
                                TC  CC GTACC    GTGTAG
                                 CC  _    CAACG
GAM1709  MTMR3    5'  GCCTCGCCATGTCCTGCT    41164          A  A
                                AGCAGGACATGG GA GT
                                |||||||||||| || ||
                                TCGTCCTGTACC CT CG
                                      G  C
GAM1709  PCDH9    3'  TGCTTCTCCACAGCCTGCT   83697       ACA
                                AGCAGG   TGGAGAAGTA
                                ||||||   ||||||||||
                                TCGTCC   ACCTCTTCGT
                                   GAC
GAM1709  SLC39A1  3'  GCCTCTCCAGTCCTGCT     27813        A     A
                                AGCAGGAC TGGAGA GT
                                |||||||| |||||| ||
                                TCGTCCTG ACCTCT CG
                                    _     C
GAM1709  SLC6A8   3'  GGATGCACTTCCCGCACCT   20073     ACA  A    A
                                AGG   TGG GAAGT CATCC
                                |||   ||| ||||| |||||
                                TCC   GCC CTTCA GTAGG
                                  AC_  _    C
GAM1709  AD-020   3'  ACTTCTCCATTCCCTGCT    39713       AC
                                AGCAGG  ATGGAGAAGT
                                ||||||  ||||||||||
                                TCGTCC  TACCTCTTCA
                                   CT
GAM1709  AD-020   3'  ACTTCTCCATTCCCTGCT    60090       AC
                                AGCAGG  ATGGAGAAGT
                                ||||||  ||||||||||
                                TCGTCC  TACCTCTTCA
                                   CT
GAM1709  ALDH9    3'  GTTCCTTCTCCATTCCCACT  7348     CA  C       T_
                                AG  GGA ATGGAGAAG  AC
                                ||  ||| |||||||||  ||
                                TC  CCT TACCTCTTC  TG
                                 AC  _       CT
GAM1709  ARHGEF4  3'  GATGGCGCCCTGTCCTGC    53372        T  AGAA  A
                                GCAGGACA GG    GT CATC
                                |||||||| ||    || ||||
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                                CGTCCTGT CC    CG GTAG
                                    _ CG__  _
GAM1709  DDR1     3'  GGACACACTCTCATGTCC     26560        G   A  ACA
                                GGACATG AGA GT   TCC
                                ||||||| ||| ||   |||
                                CCTGTAC TCT CA   AGG
                                    _  _ CAC
GAM1709  DDR1     3'  GGACACACTCTCATGTCC     26562        G   A  ACA
                                GGACATG AGA GT   TCC
                                ||||||| ||| ||   |||
                                CCTGTAC TCT CA   AGG
                                    _  _ CAC
GAM1709  DDR1     3'  GGACACACTCTCATGTCC     10477        G   A  ACA
                                GGACATG AGA GT   TCC
                                ||||||| ||| ||   |||
                                CCTGTAC TCT CA   AGG
                                    _  _ CAC
GAM1709  FLJ20150 3'  GTCCTCCCCCATGTCCTGC    35145          AGA  T
                                GCAGGACATGG   AG AC
                                ||||||||||   || ||
                                CGTCCTGTACC   TC TG
                                     CCC  C
GAM1709  FLJ23259 3'  TGATTTCCCATGTCCTACT    45638    C       A    A
                                AG AGGACATGG GAAGT CA
                                || ||||||||| ||||| ||
                                TC TCCTGTACC CTTTA GT
                                 A       _    _
GAM1709  GAL3ST2  3'  GCTGCCTCCATGTCCTGC     53484          A_
                                GCAGGACATGGAG  AGT
                                ||||||||||||  |||
                                CGTCCTGTACCTC  TCG
                                      CG
GAM1709  GMEB2    3'  GCTCCTCCAGGTCCTGCT     25664        A    A
                                AGCAGGAC TGGAG AGT
                                |||||||| ||||| |||
                                TCGTCCTG ACCTC TCG
                                    G    C
GAM1709  HMG17L1  3'  TGTCTGCCCATGTCCTGCT    41049          AGA  T
                                AGCAGGACATGG   AG ACA
                                ||||||||||   || |||
                                TCGTCCTGTACC   TC TGT
                                     CG_  _
GAM1709  HNRPA3   3'  GGATATATACCCATGTCT     20453        AGAA  C
                                GGACATGG    GTA ATCC
                                ||||||||    ||| ||||
                                TCTGTACC    TAT TAGG
                                    CA__   A
GAM1709  KIAA0441 3'  GGATGTACCACCACACCCAGCT 29636     A  ACA   AGAA
                                AGC GG   TGG    GTACATCC
                                ||| ||   |||    ||||||||
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                                TCG CC   ACC    CATGTAGG
                                  A  CAC   AC__
GAM1709  KIAA0522  3'  GTCCTCCTCCCCATGTCCT   72426         A  __  T
                                AGGACATGG GA  AG AC
                                ||||||||| ||  || ||
                                TCCTGTACC CT  TC TG
                                     C  CC  C
GAM1709  KIAA1393  3'  TGTCTGCCCATGTCCTGC    72576          AGA  T
                                GCAGGACATGG   AG ACA
                                ||||||||||   || |||
                                CGTCCTGTACC   TC TGT
                                      CG_  _
GAM1709  KIAA1922  3'  ATGTGGCATCATGTCCTGC    73987          AGAAG
                                GCAGGACATGG    TACAT
                                ||||||||||    |||||
                                CGTCCTGTACT    GTGTA
                                      ACG__
GAM1709  LOC113220 5'  GGATGTACCATCTGCCCTTCT  57359    C   A  TG  GAA
                                AG AGG CA  GA   GTACATCC
                                || ||| ||  ||   ||||||||
                                TC TCC GT  CT   CATGTAGG
                                 T   C  __  AC_
GAM1709  LOC143153 3'  GGCTGTTCTCCATCTCCCGCT  76980    A   C      AGT   T
                                AGC GGA ATGGAGA   ACA CC
                                ||| ||| |||||||   ||| ||
                                TCG CCT TACCTCT   TGT GG
                                  C   C       ___   C
GAM1709  LOC145540 3'  TGTCTGCCCATGTCCTGC    77779          AGA  T
                                GCAGGACATGG   AG ACA
                                ||||||||||   || |||
                                CGTCCTGTACC   TC TGT
                                      CG_  _
GAM1709  LOC148915 3'  TGTCTGCCCATGTCCTGC    79810          AGA  T
                                GCAGGACATGG   AG ACA
                                ||||||||||   || |||
                                CGTCCTGTACC   TC TGT
                                      CG_  _
GAM1709  LOC150166 5'  GATATACTTCTTTCTTGCT   86038        CATG       C
                                AGCAGGA    GAGAAGTA ATC
                                |||||||    |||||||| |||
                                TCGTTCT    TTCTTCAT TAG
                                    ____        A
GAM1709  LOC150580 3'  TGTCTGCCCATGTCCTGC    61068          AGA  T
                                GCAGGACATGG   AG ACA
                                ||||||||||   || |||
                                CGTCCTGTACC   TC TGT
                                      CG_  _
GAM1709  LOC152212 3'  TGTCTGCCCATGTCCTGC    83712          AGA  T
                                GCAGGACATGG   AG ACA
                                ||||||||||   || |||
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                                CGTCCTGTACC   TC TGT
                                      CG_  _
GAM1709  LOC152300 3'  ATGCACTTGTCCTGTT      81380         TGGAGA   A
                                AGCAGGACA     AGT CAT
                                |||||||||     ||| |||
                                TTGTCCTGT     TCA GTA
                                      _______  C
GAM1709  LOC153346 5'  ATGCACTAGCTGTCCTGT    87203         TG AGA   A
                                GCAGGACA  G   AGT CAT
                                ||||||||  |   ||| |||
                                TGTCCTGT  C   TCA GTA
                                     __ GA_   C
GAM1709  LOC153811 3'  GGACATACCATCTTGTCCTGCT 81839         T   GAA   CA
                                AGCAGGACA GGA   GTA  TCC
                                ||||||||| |||   |||  |||
                                TCGTCCTGT TCT   CAT  AGG
                                      _   AC_   AC
GAM1709  LOC154807 5'  GATGGCGGCTCCCGTCCTGCT  87464         AT    AA  A
                                AGCAGGAC  GGAG  GT CATC
                                ||||||||  ||||  || ||||
                                TCGTCCTG  CCTC  CG GTAG
                                     C_    GG  _
GAM1709  LOC196453 5'  ATGACATTTCATGTCCCACT   92341    CA        AA  A
                                AG  GGACATGGAG  GT CAT
                                ||  ||||||||||  || |||
                                TC  CCTGTACTTT  CA GTA
                                 AC         A_  _
GAM1709  LOC221468 3'  ACTTCTCCATAGTCCTGCT    60003         _
                                AGCAGGAC ATGGAGAAGT
                                |||||||| ||||||||||
                                TCGTCCTG TACCTCTTCA
                                     A
GAM1709  LOC254000 3'  TGTCTGCCCATGTCCTGC     96615          AGA  T
                                GCAGGACATGG   AG ACA
                                ||||||||||   || |||
                                CGTCCTGTACC   TC TGT
                                      CG_  _
GAM1709  LOC257153 5'  GGCTGTTTCTCACATCCTGC   97467       CA  _    GT   T
                                GCAGGA  TG GAGAA  ACA CC
                                ||||||  || |||||  ||| ||
                                CGTCCT  AC CTCTT  TGT GG
                                   __  A    __   C
GAM1709  LOC88584  3'  GATTATCTGCCCATGTCCTGC  61102          AGA  TAC
                                GCAGGACATGG   AG   ATC
                                ||||||||||   ||   |||
                                CGTCCTGTACC   TC   TAG
                                      CG_  TAT
GAM1710  ABCA1     5'  AGGAGAAAGAGACGCAAACACA 19733       G        CCAA
             A                   TTGTGT TGTGTTTCT    TCCT
                                ||||||  |||||||||    ||||
```

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                                AACACA ACGCAGAGA    AGGA
                                   A        AAG_
GAM1710  ABCB4    5'  AGGATGCAGAGGCACAGCACAA 38755       G        CCA
                                TTGTGT TGTGTTTCT   ATCCT
                                |||||| |||||||||   |||||
                                AACACG ACACGGAGA   TAGGA
                                   _        CG_
GAM1710  ABCB4    5'  GGATGAACATGCAAACAA    38762      G        C
                                TTGT TGTGTGTTT TCC
                                |||| ||||||||| |||
                                AACA ACGTACAAG AGG
                                  A        T
GAM1710  ABCB4    5'  GGGATCTACAGGATGAACATGC 38763         C   A____
            A                    TGTGTGTTT TCC     ATCCT
                                |||||||||| |||     |||||
                                ACGTACAAG AGG     TAGGG
                                      T   ACATC
GAM1710  ACAA1    3'  GGCTGGAGGCGCTACGCAG    9635         T    TT     AT
                                TTGTGTG GTGT  CTCCA  CC
                                ||||||| ||||  |||||  ||
                                GACGCAT CGCG  GAGGT  GG
                                   _   __    C_
GAM1710  ACAT1    5'  GGGGTTGGGGAGGAGGCCGC   5237      T  G_
                                GTG GT  TTTCTCCAATCCT
                                ||| ||  ||||||||||||||
                                CGC CG  GGAGGGGTTGGGG
                                  _  GA
GAM1710  ACE2     3'  AGGATTGAGAATGGCATGCAT  41727         GT     C
                                GTGTGTGT  TTCTC AATCCT
                                ||||||||  ||||| ||||||
                                TACGTACG  AAGAG TTAGGA
                                     GT    _
GAM1710  ACLY     5'  GGAAGAAGCGCCGCGCACG    65686         _      _
                                TGTGTGTG TGTTTCT CC
                                |||||||| ||||||| ||
                                GCACGCGC GCGAAGA GG
                                     C      A
GAM1710  ADAM11   3'  GGACTGCAGGGGAGGCCACGTG 41492     TG   T       AA___   T
            CAG                    TTG  TGTG GTTTCTCC    TCC
                                |||  |||| ||||||||    |||
                                GAC  GCAC CGGAGGGG    AGG
                                  GT   _       ACGTC
GAM1710  ADAM23   3'  GGAACAACACACACACAA    15100           TC
                                TTGTGTGTGTGTT  TCC
                                ||||||||||||  |||
                                AACACACACACAA  AGG
                                        CA
GAM1710  ADAMTS8  5'  GGGGTTAACGTGGGTCCACGCG 23853         TT   CC___
            TA                   TGTGTGTG  TCT    AATCCT
                                |||||||  |||    ||||||
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                                ATGCGCAC  GGG    TTGGGG
                                    CT   TGCAA
GAM1710  ADCY7    3'  AGGATTTCTCAGACACATGCAC 8488          CTCC
                                GTGTGTGTGTTT   AATCCT
                                ||||||||||||   ||||||
                                CACGTACACAGA   TTAGGA
                                    CTCT
GAM1710  ADCY9    3'  GGGGTGCGAAGGGGGCATGTCA 8507      T TG   TT  CCA__
           CGA                   TTGTG G  TGT  CT    ATCCT
                                |||||  |  |||  ||    |||||
                                AGCAC T  ACG  GG    TGGGG
                                  _ GT   GG  AAGCG
GAM1710  ADORA2B  3'  AGGATTGACAAATATATTTATG 7280    TG  T      CTC
           A                     T  TG GTGTGTTT   CAATCCT
                                |  || ||||||||   |||||||
                                A  AT TATATAAA   GTTAGGA
                                 GT  T       CA_
GAM1710  AGL      5'  ACCTGGGGCGAGTGCGCGCACG 7211        TG  _    ATCCT
                                TGTGTGTG  TTT CTCCA
                                ||||||||  ||| |||||
                                GCACGCGC  GAG GGGGT
                                    GT   C    CCA
GAM1710  AGL      5'  GGGGCGAGTGCGCGCACGG   7216         TG  _
                                TTGTGTGTG  TTT CTCC
                                |||||||||  ||| ||||
                                GGCACGCGC  GAG GGGG
                                     GT   C
GAM1710  AKT1     3'  GGGGTGGCAGGCACACAG    18963       G   TT
                                TTGTGTGT TGT  CTCC
                                |||||||| |||  ||||
                                GACACACG ACG  GGGG
                                    G   GT
GAM1710  AMELY    3'  TGGGATGACACAAGCACACAA  8555         __    TC   AATCCT
                                TTGTGTGT  GTGTT  TCC
                                ||||||||  |||||  |||
                                AACACACG  CACAG  GGG
                                    AA    TA     TC
GAM1710  AMMECR1  5'  GGGTCGGAAACGCTGCGTGG   31723   TG   T      CCA
                                T  TGTG GTGTTTCT   ATCC
                                |  |||| ||||||||   ||||
                                G  GCGT CGCAAAGG   TGGG
                                 GT   _      C__
GAM1710  ANGPT1   5'  AGGGTCTAGAATATGTACACGC 58413        TG _   CCA
           AG                    TTGTGTGTG  T TTCT   ATCCT
                                |||||||||  | ||||   |||||
                                GACGCACAT  A AAGA   TGGGA
                                    GT T    TC_
GAM1710  ANGPT1   3'  GGAAAAATAAACACACAA    58415       G    C
                                TTGTGTGT TGTTT TCC
                                |||||||| ||||| |||
```

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                                AACACACA ATAAA AGG
                                    A    A
GAM1710 APAF1    3' GGGACTACAGGTGTGCGCACAT 25975       TG T  CCAA
                                GTGTGTG  T TCT   TCCT
                                |||||||  | |||   ||||
                                TACACGC  G GGA   AGGG
                                   GT T  CATC
GAM1710 APP      5' GCACGCGGAGGAGCGTGCGCGG 6662    G   TG      AATCCT
           GG                    TT TGTG  TGTTTCTCC
                                || ||||  |||||||||
                                GG GCGC  GCGAGGAGG
                                 G   GT       CGCACGA
GAM1710 ARF4L    3' AGGACTGTGGAGACGTAAATGT 70386    TG G      TC  A
           AA                    TTG  T TGTGTTTC  CA TCCT
                                |||  | ||||||||  || ||||
                                AAT  A ATGCAGAG  GT AGGA
                                  GT A       GT  C
GAM1710 ASB2     5' GGGCGTGGGGGGCACAGGTACA 32876      TG    TT T   AT
           G                     TTGTG  TGTGT  C CCA  CCT
                                |||||  |||||  | |||  |||
                                GACAT  ACACG  G GGT  GGG
                                   GG    GG _   GC
GAM1710 ATP6V1C1 3' GGAAAAAATATATATATA    9891           C_
                                TGTGTGTGTGTTT  TCC
                                ||||||||||||  |||
                                ATATATATATAAA  AGG
                                       AA
GAM1710 ATP7B    3' GGACATGGAAATATTTATATAA 5335        T       CCAA
                                TTGTGTG GTGTTTCT    TCC
                                ||||||| ||||||||    |||
                                AATATAT TATAAAGG    AGG
                                   T       TAC_
GAM1710 AVPR1A   5' GGAGGGAGCGCGCCGCGA    7382       T       _
                                TTGTG GTGTGTTTC TCC
                                ||||| ||||||||| |||
                                AGCGC CGCGCGAGG AGG
                                   _       G
GAM1710 AXIN1    3' GGGGCACGGGAAGCACGTACCC 61540    T          CAA
           AA                    TTG GTGTGTGTTTCTC   TCCT
                                ||| ||||||||||||   ||||
                                AAC CATGCACGAAGGG   GGGG
                                  C           CAC
GAM1710 B3GALT2  3' GGATGAACAATGTATACAA   15031       TG _   C
                                TTGTGTG  T GTTT TCC
                                |||||||  | |||| |||
                                AACATAT  A CAAG AGG
                                   GT A   T
GAM1710 BAPX1    3' GGAGAGCGCACACCCAG     8645     T       T
                                TTG GTGTGTGTT CTCC
                                ||| ||||||||| ||||
```

```
                                GAC CACACGCGA GAGG
                                  C       _
GAM1710 BAT4     5' GGGCATTGTGGGGGCGTTATGT 53743     TG  TGT  TT TC   _
                AA                  TTG  TG   GT  C  CAAT CCT
                                    |||  ||   ||  |  |||| |||
                                    AAT  AT   CG  G  GTTA GGG
                                      GT  TG_  GG GT    C   A
GAM1710 BCL9     5' GGAAAAAGGCATACAGGCAG   16320      G       C__
                                    TTGT TGTGTGTTT   TCC
                                    |||| |||||||||   |||
                                    GACG ACATACGGA   AGG
                                      G        AAA
GAM1710 BCRP2    3' AGGCCCCATAAGACACACACAT 63068    TG         CTCCAAT
                GA                  T  TGTGTGTGTTT      CCT
                                    |  ||||||||||       |||
                                    A  ACACACACAGA      GGA
                                     GT         ATACCCC
GAM1710 BDKRB2   3' GGGGTGAACTCACGCACAG    7112          T   _
                                    TTGTGTGTG GTTT CTCC
                                    ||||||||| |||| ||||
                                    GACACGCAC CAAG GGGG
                                          T   T
GAM1710 BIN1     5' GGGGCTGGGAGCGCGGCGCGCA 16289         _    T T   AT
                A                    TTGTGTGT GTGTT C CCA  CCT
                                     |||||||| ||||| | |||  |||
                                     AACGCGCG CGCGA G GGT  GGG
                                        G    _ _   CG
GAM1710 BIN3     3' GGAGGGCACGCGGGCAA     38579      G       T
                                    TTGT TGTGTGTT CTCC
                                    |||| |||||||| ||||
                                    AACG GCGCACGG GAGG
                                      G       _
GAM1710 BMP4     3' AGGATAGACAGATATACACAC  8658            C  CA
                                    GTGTGTGTGTTT TC  ATCCT
                                    ||||||||||| ||  |||||
                                    CACACATATAGA AG  TAGGA
                                           C  A_
GAM1710 BMP4     5' AGGCGAGAGAGACGCAGACGCA 8659        G         CAAT
                G                    TTGTGT TGTGTTTCTC    CCT
                                     ||||||  ||||||||||    |||
                                     GACGCA ACGCAGAGAG    GGA
                                        G         AGC_
GAM1710 BMP7     3' AGGAAAAAAAAAACAACGCATAA 9944          G    CTCCAA
                                    TTGTGTGT TGTTT      TCCT
                                    ||||||||  |||||      ||||
                                    AATACGCA ACAAA      AGGA
                                         _     AAAAA_
GAM1710 BMPR1B   5' GGGAGCCGGGAGCGCACGCGCG 8665              CCAA
                G                    TTGTGTGTGTGTTTCT    TCCT
                                     ||||||||||||||||    ||||
```

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                                GGCGCGCACGCGAGGG    AGGG
                                        CCG_
GAM1710  C11orf13  3'  GGGACAGGAGATGCATGGACA  14429     G    T    AA
                                TGT TGTGT TCTCC  TCCT
                                ||| ||||| |||||  ||||
                                ACA GTACG AGAGG  AGGG
                                  G    T    AC
GAM1710  C18orf2   3'  TGGGAAAAACAGACAGTGCA   49463     _  G    C   AATCCT
                                TGTG TGT TGTTT TCC
                                |||| ||| ||||| |||
                                ACGT ACA ACAAA AGG
                                  G  G    A  G  TC
GAM1710  C1orf1    3'  GGGAGCACAGGAGGTGTGCTAC 8681      T TG T    AA___
             A                   TGTG G  T TCTCC    TCCT
                                |||| |  | |||||    ||||
                                ACAT C  G GGAGG    AGGG
                                  _ GT T    ACACG
GAM1710  C1orf1    3'  GGTTCAGAAATGGGCACATAA  8682        G     ___
                                TTGTGTGT TGTTTCT   CC
                                |||||||| |||||||   ||
                                AATACACG GTAAAGA   GG
                                     G      CTT
GAM1710  C1QG      3'  GGGGTGGGGAGATATATAAATA 63152     G          AT  T
             A                   TTGT TGTGTGTTTCTCCA  CC
                                |||| ||||||||||||||  ||
                                AATA ATATATAGAGGGGT  GG
                                  A            GG
GAM1710  C2        3'  AGGATGCCAGAGGCAGCGCACA 5349         _     CCA
             CAA                   TTGTGTGTG TGTTTCT   ATCCT
                                |||||||| |||||||   |||||
                                AACACACGC ACGGAGA   TAGGA
                                     G      CCG
GAM1710  C6        5'  AGGACAAAGGCAGTATGCACAC 96120        TT  _  AA__
             G                   TGTGTGTGT  CT CC    TCCT
                                |||||||||  || ||    ||||
                                GCACACGTA  GA GG    AGGA
                                     T_  C  AAAC
GAM1710  CACNA1B   5'  GGGCCGGGGATGCACGCG    7394        T    AA
                                TGTGTGT TCTCC  TCC
                                ||||||| |||||  |||
                                GCGCACG AGGGG  GGG
                                   T    CC
GAM1710  CALB1     3'  GGGAGCACCAGATGACACATAA 18209       _______
                                TTGTGTGT     GTGTTTCT
                                ||||||||     ||||||||
                                AATACACA     CACGAGGG
                                     GTAGAC
GAM1710  CAPON     5'  GGCAGGGGCGCCGCGCAG    64661       T   TT  _
                                TTGTGTG GTGT  CT CC
                                ||||||| ||||  || ||
```

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                                GACGCGC CGCG  GA GG
                                    _   GG  C
GAM1710  CASP2    3'  GGGCTTGTGATATGCACGTGG  8714    TG       TCTC   T
                                T  TGTGTGTGTT    CAA CCT
                                |  ||||||||||    ||| |||
                                G  GCACGTATAG    GTT GGG
                                 GT        T___   C
GAM1710  CASP2    3'  GGGCTTGTGATATGCACGTGG  53338   TG       TCTC   T
                                T  TGTGTGTGTT    CAA CCT
                                |  ||||||||||    ||| |||
                                G  GCACGTATAG    GTT GGG
                                 GT        T___   C
GAM1710  CASP7    5'  GGAAGGGATACATGACAA    54033     G     TT  _
                                TTGT TGTGTGT  CT CC
                                |||| |||||||  || ||
                                AACA GTACATA  GA GG
                                   _      GG  A
GAM1710  CD3Z     3'  GGAAGACGCAACACATGG    7424    TG    _    C
                                T  TGTGT GTGTTT TCC
                                |  ||||| ||||||| |||
                                G  ACACA CGCAGA AGG
                                 GT    A     _
GAM1710  CDKN2B   3'  AGGGTTTTCTGAGGGAAAGTGC 55311   TG    TG G_ TT   C___
            ATATGA                T  TGTG  T  T  CTC    AATCCT
                                |  ||||  |  |  |||    ||||||
                                A  ATAC  G  A  GAG    TTGGGA
                                 GT    GT AA GG   TCTT
GAM1710  CELSR2   3'  GGACAAAGCCACACGCAG    9196         T    C_
                                TTGTGTGTG GTTT  TCC
                                |||||||||  ||||  |||
                                GACGCACAC CGAA  AGG
                                      _   AC
GAM1710  CENPB    5'  GGAGAAGGCGCTGCGCATAG   70118        _   _
                                TTGTGTGT GTGT TTCTCC
                                |||||||| |||| ||||||
                                GATACGCG CGCG AAGAGG
                                     T   G
GAM1710  CENTD1   3'  GCATTGGAGAGGTTGTGTACAC 58277       TG _ TT      CCT
            AG                    TTGTGTG  T G  TCTCCAAT
                                |||||||  | |  ||||||||
                                GACACAT  G T  AGAGGTTA
                                    GT T GG       CG
GAM1710  CENTD2   5'  GGGGTCAGGAGTCACGTGTA   58273    TG    TTT    A_
                                TG  TGTG   CTCC  ATCCT
                                ||  ||||   ||||  |||||
                                AT  GCAC   GAGG  TGGGG
                                 GT    T__    AC
GAM1710  CHAC     3'  TTGGGAAGCATATTACAG    53958      T       T
                                TTGTG GTGTGTTTC CCAA
                                ||||| |||||||| ||||
```

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                                GACAT TATACGAAG GGTT
                                  _       _
GAM1710 CHS1     5' GGGAGAGGGGGAGTGCGCGGCG 5382      G    TG      AA
                                TGT TGTG  TTTCTCC  TCCT
                                ||| ||||  |||||||  ||||
                                GCG GCGC  GAGGGGG  AGGG
                                  _   GT       AG
GAM1710 CISH     3' GGGAGAGGGGAGGTGTCACACA 59669        T TG      AA
              A                  TTGTGTG G  TTTCTCC  TCCT
                                ||||||| |  |||||||  ||||
                                AACACAC T  GGAGGGG  AGGG
                                    _ GT      AG
GAM1710 CLECSF5  3' GGGGCACGGAATAAGCACATAG 26041         G     TCCAA
                                TTGTGTGT TGTTTC     TCC
                                |||||||| ||||||     |||
                                GATACACG ATAAGG     GGG
                                     A     CACG_
GAM1710 COL5A1   3' GGGGTTGGGGGAGGGACTGCCA 5410      T   T  G      _
              G                  TTG GTG GT TTTCTCC AATCCT
                                ||| ||| || ||||||| ||||||
                                GAC CGT CA GGAGGGG TTGGGG
                                  _  _ G      G
GAM1710 COX10    3' TGGGGGTACACATACACAG    8950            T
                                TTGTGTGTGTGT TCTCCA
                                |||||||||||| ||||||
                                GACACATACACA GGGGGT
                                       T
GAM1710 COX11    3' GGAGAAATATTGTACAA     16486       TGT
                                TTGTG   GTGTTTCTCC
                                |||||   ||||||||||
                                AACAT   TATAAAGAGG
                                   GT_
GAM1710 CREM     3' AGGATGTGGAATGCAGCGTGA  10299    TG   G       TCCA
                                T  TGT TGTGTTTC    ATCCT
                                |  ||| ||||||||    |||||
                                A  GCG ACGTAAGG    TAGGA
                                 GT   _       TG__
GAM1710 CRK      5' GGGGCCGGAGGGGCGCGCGCG  60546         TT    AA
                                TGTGTGTGT  CTCC  TCCT
                                |||||||||  ||||  ||||
                                GCGCGCGCG  GAGG  GGGG
                                     GG    CC
GAM1710 CRYBA4   3' GGCACGGAGGAGCGCATGCG   10305             AAT  T
                                TGTGTGTGTTTCTCC   CC
                                ||||||||||||||   ||
                                GCGTACGCGAGGAGG   GG
                                         CAC
GAM1710 CSRP1    3' AGGCAGAGAGGCATGCAGGCG  15810     G          CAAT
                                TGT TGTGTGTTTCTC    CCT
                                ||| ||||||||||||    |||
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                                GCG ACGTACGGAGAG   GGA
                                  G          AC__
GAM1710 CTNNA2   3' GGGGCACTGGAAGCACAATACG 16523      G       CCAA
                                TGTGT TGTGTTTCT   TCCT
                                ||||| |||||||||   ||||
                                GCATA ACACGAAGG   GGGG
                                   _       TCAC
GAM1710 CTNNA2   3' GGTTGGCAGGTATATGCATA  16524        T  _
                                TGTGTGTGT TCT CCAATC
                                ||||||||| ||| ||||||
                                ATACGTATA GGA GGTTGG
                                      T  C
GAM1710 CTSL     3' TAGGACTTGACTGGGGATGGCG 10346   TG       _     A_____
            CATGCATGG               T  TGTGTGTGTT TCTCCA     TCCT  A
                                | |||||||||| ||||||     ||||  |
                                G  ACGTACGCGG AGGGGT     AGGA  T
                                 GT        T     CAGTTC
GAM1710 CTSL2    5' AGGGTGCCTGCGCACGTGCGA  9024     TG     TTCTCCA
                                TTG  TGTGTGT      ATCCT
                                |||  |||||||      |||||
                                AGC  GCACGCG      TGGGA
                                  GT      TCCG___
GAM1710 CXCL1    3' AGGCAGGGGAATGTATGTGCAC 9495      TG  GT_     AAT
            A                    TGTG  TGT   TTCTCC   CCT
                                |||| |||  ||||||  |||
                                ACAC  GTA   AAGGGG   GGA
                                  GT   TGT     AC_
GAM1710 CYLN2    3' AGGCCACACAGAGACACATAC  14087          CCAAT_
                                GTGTGTGTTTCT     CCT
                                ||||||||||||     |||
                                CATACACAGAGA     GGA
                                      CACACC
GAM1710 DAAM2    3' GGGATGGGGGGCTGTGTGTGG  93904   TG  TG  T  TT T   A
                                T  TG  TG GT  C CCA TCCT
                                |  ||  || ||  | ||| ||||
                                G  GT  GT CG  G GGT AGGG
                                 GT  GT  _  GG _  _
GAM1710 DBCCR1   3' GGGAGAAGGGAGAAAGCATATG 28242          G      AA__
            CAA                    TTGTGTGTGT TTTCTCC    TCCT
                                |||||||||| |||||||    ||||
                                AACGTATACG AAAGAGG    AGGG
                                      _      GAAG
GAM1710 DCX      5' GGGAGGGGATGCACACAT    6893         T    AA
                                GTGTGTGT TCTCC  TCCT
                                |||||||| |||||  ||||
                                TACACACG AGGGG  AGGG
                                     T    __
GAM1710 DDB2     3' AGGCCTTGGAGCCCACACAT   5454        TTT     T_
                                GTGTGTG   CTCCAA  CCT
                                |||||||   ||||||  |||
```

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                                TACACAC   GAGGTT  GGA
                                   CC_     CC
GAM1710  DDX3     5'  GGAAAGGGGAGCGAATGCGTAA 9058         G     T  AA
                                TTGTGTGT TGTTTC CC  TCC
                                |||||||| |||||| ||  |||
                                AATGCGTA GCGAGG GG  AGG
                                    A     _  AA
GAM1710  DDX3     3'  GGTTGGAAATATGTACATAA   9060        TG    TC
                                TTGTGTG  TGTT  TCCAATC
                                |||||||  ||||  |||||||
                                AATACAT  ATAA  AGGTTGG
                                   GT   __
GAM1710  DGAT2    5'  GGAATGGGCACACAGCAA    51775      G      TTCT   A
                                TTGT TGTGTGT    CCA TCC
                                |||| |||||||    ||| |||
                                AACG ACACACG    GGT AGG
                                  _      _____  A
GAM1710  DGAT2    5'  GGGACCACCAGGGAATGGGCAC 51776         G      CCAA__
            ACAG                    TTGTGTGT TGTTTCT     TCCT
                                |||||||| |||||||     ||||
                                GACACACG GTAAGGG     AGGG
                                    G      ACCACC
GAM1710  DGCR2    3'  AGGGCTTCAGAAACATGCATA  18895           CCAA
                                TGTGTGTGTTTCT    TCCT
                                ||||||||||||    ||||
                                ATACGTACAAAGA    GGGA
                                      CTTC
GAM1710  DGKB     3'  GGGCCATGGAACACATATGC   94109           TCCAA   T
                                GTGTGTGTGTTTC    TCC
                                ||||||||||||    |||
                                CGTATACACAAGG    GGG
                                      TACC_
GAM1710  DGKI     3'  AGGAGCTGGGAAGTGCCACATG 17522    TG    T TG    T   A_
            G                    T  TGTG G  TTTC CCA  TCCT
                                |  |||| |  |||| |||  ||||
                                G  ACAC C  GAAG GGT  AGGA
                                 GT   _ GT   _   CG
GAM1710  DHCR7    5'  GGGGCCGAGGTGTGCGCAGGA  9066     G     TG    TCCAA
                                TT TGTGTG  TTTC    TCC
                                || ||||||  ||||    |||
                                AG ACGCGT  GGAG    GGG
                                 G     GT    CCG__
GAM1710  DHFR     3'  GGAGCAGTATGTACACAG    7652         TG    T
                                TTGTGTG  TGTT CTCC
                                |||||||  |||| ||||
                                GACACAT  ATGA GAGG
                                    GT    C
GAM1710  DIAPH2   3'  AGGATTGGGTTGATGGTACA   24586      TGT   TC
                                TGTG   GTT  TCCAATCCT
                                ||||   |||  |||||||||
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                                ACAT   TAG  GGGTTAGGA
                                  GG_   TT
GAM1710  DKC1     5'  GGACCGGGCGGCACGCACGCG  9078          TT T  AA
                                TGTGTGTGTGT  C CC  TCC
                                ||||||||||  | ||  |||
                                GCGCACGCACG  G GG  AGG
                                      GC _  CC
GAM1710  DLK1     5'  GGAGAGCGCAGCGCGCAG    15177        _     T
                                TTGTGTG TGTGTT CTCC
                                ||||||| |||||| ||||
                                GACGCGC ACGCGA GAGG
                                    G     _
GAM1710  DMPK     5'  GGACAGGCAGACATGCAG    16615         G     C
                                TTGTGTGT TGTTT TCC
                                |||||||| ||||| |||
                                GACGTACA ACGGA AGG
                                     G    C
GAM1710  DPEP1    3'  GGGACAGTTCAGGACACACACA 16621            CTCCAA_
              CAG                   TTGTGTGTGTGTTT      TCCT
                                ||||||||||||||       ||||
                                GACACACACACAGG      AGGG
                                       ACTTGAC
GAM1710  DSCAM    5'  AGGTGTGCAGGAGCGCAGCGCG 9132        _       C  AT
              CG                    TGTGTG TGTGTTTCT CA  CCT
                                |||||| |||||||| ||  |||
                                GCGCGC ACGCGAGGA GT  GGA
                                   G        C  GT
GAM1710  DSCAM    5'  GGCGCCCGGGAGCAGGTGTGCA 9135       TG G      CCAAT  T
              G                     TTGTG  T TGTTTCT    CC
                                |||||  | |||||||    ||
                                GACGT  G ACGAGGG    GG
                                   GT G      CCCGC
GAM1710  DUSP7    5'  AGGAGCTGGAGGCGCGCGGCG  66039     G      TT    A_
                                TGT TGTGTGT  CTCCA  TCCT
                                ||| |||||||  |||||  ||||
                                GCG GCGCGCG  GAGGT  AGGA
                                  _      ___     CG
GAM1710  DUT      3'  AGGATGTGGGTTATACACAT   10460         TT T   _
                                GTGTGTGT  C CCA ATCCT
                                ||||||||  | ||| |||||
                                TACACATA  G GGT TAGGA
                                     TT _   G
GAM1710  DUX4     5'  GGCCACGGAGGAGCCACACGCA 73197          T       AAT_  T
              G                     TTGTGTGTG GTTTCTCC    CC
                                |||||||||| ||||||||    ||
                                GACGCACAC CGAGGAGG    GG
                                      _       CACC
GAM1710  ECEL1    3'  GGGGCAGGCATGCACCCG    17891    T        _
                                TG GTGTGTGTTT CTCC
                                || ||||||||| ||||
```

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                                GC CACGTACGGA GGGG
                                 C        C
GAM1710  ECM2     3'  GGCAGAAGGGTGTGCATAA   9149        TG G    _
                                TTGTGTG  T TTTCT CC
                                |||||||  | ||||| ||
                                AATACGT  G GAAGA GG
                                    GT G    C
GAM1710  EDG8     3'  AGGATGAGGGAATGGCATGCGC 79145         GT    CA
              AA                  TTGTGTGTGT  TTCTC  ATCCT
                                |||||||||  |||||  |||||
                                AACGCGTACG  AAGGG  TAGGA
                                      GT    AG
GAM1710  EEF2     3'  GGGAAAGGAACACGCGGGTAG  96232     TG        CCAA
                                TTG  TGTGTGTTTCT   TCCT
                                |||  ||||||||||   ||||
                                GAT  GCGCACAAGGA   AGGG
                                  GG         A___
GAM1710  EGLN2    3'  AGGTGCCAGGAGGAGCATGGGT 54911   TG G        AAT__
              GT                  G  T TGTGTTTCTCC    CCT
                                |  | ||||||||||    |||
                                T  G GTACGAGGAGG    GGA
                                 GT G         ACCGT
GAM1710  EGLN2    3'  AGGTGCCAGGAGGAGCATGGGT 54912   TG G        AAT__
              GT                  G  T TGTGTTTCTCC    CCT
                                |  | ||||||||||    |||
                                T  G GTACGAGGAGG    GGA
                                 GT G         ACCGT
GAM1710  EHD2     3'  GGAGAGGGCACCTACACAG   28224       T    _
                                TTGTGTG GTGTT TCTCC
                                ||||||| ||||| |||||
                                GACACAT CACGG AGAGG
                                    C    G
GAM1710  EHD4     3'  TGGAGAAATGCGCATGGGG   58365    G
                                TT TGTGTGTGTTTCTCCA
                                || ||||||||||||||
                                GG GTACGCGTAAAGAGGT
                                 G
GAM1710  EHF      3'  GGGAAAAAACGTACACAG    25126         G   CT
                                TTGTGTGTGT TTT  CC
                                |||||||||| |||  ||
                                GACACATGCA AAA  GG
                                      A   AG
GAM1710  EIF4E    3'  AGGATCCAGGAATATGACACAA 10504       G       CCA
                                TTGTGT TGTGTTTCT   ATCCT
                                |||||| |||||||||   |||||
                                AACACA GTATAAGGA   TAGGA
                                   _       CC_
GAM1710  ELAC2    5'  AGGGCACGGGAAACGCGGGCG  36728     G        CAA
                                TGT TGTGTTTCTC   TCCT
                                ||| ||||||||||   ||||
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                                GCG GCGCAAAGGG   GGGA
                                  G         CAC
GAM1710  ELK1     5'  GGGGCGGTGGGGCCGCGTATGG 19089    TG     T  TT T  AA
                                T  TGTGTG GT  C CC  TCC
                                |  |||||| ||  | ||  |||
                                G  ATGCGC CG  G GG  GGG
                                 GT     _  GG T  CG
GAM1710  EMX2     5'  GGGCGGCGGAGGCAGCGTGCG  88955    TG   G      _  AA
                                TG  TGT TGTTTCT CC  TCC
                                ||  ||| ||||||| ||  |||
                                GC  GCG ACGGAGG GG  GGG
                                 GT   _      C  C_
GAM1710  EN1      5'  AGGGGGAGGGACGCGGGTGCG  9246     TG G    TT    AA
                                TG  T TGTGT  CTCC  TCCT
                                ||  | |||||  ||||  ||||
                                GC  G GCGCA  GAGG  GGGA
                                 GT G    GG   __
GAM1710  EN2      3'  GGGACAGCCAGGGGGTGTGCCC 9261      T TG T    AA____
              ACG                   TGTG G  T TCTCC     TCCT
                                |||| |  | |||||     ||||
                                GCAC C  G GGGGG     AGGG
                                  C GT T    ACCGAC
GAM1710  EPHA1    3'  CTGGGGTTAATATATATACA  19099          T_   AATCCT
                                TGTGTGTGTGTT  CTCC
                                ||||||||||||  ||||
                                ACATATATATAA  GGGG
                                      TT      TCC
GAM1710  EPHA8    3'  GGCTGGAGGCACATGTGG    40437   TG     GTTT    AT
                                T  TGTGTGT    CTCCA  CC
                                |  |||||||    |||||  ||
                                G  GTACACG    GAGGT  GG
                                 GT      ____     C_
GAM1710  EPHB1    3'  GGGAAACCAAATATATAA    16694        GT_    T
                                TTGTGTGT   GTTTC CC
                                ||||||||   ||||| ||
                                AATATATA   CAAAG GG
                                     AAC    _
GAM1710  ESRRBL1  3'  GACAGGAGAAAGTGTATGTAA  36324     TG  TG G      AA
                                TTG  TG  T TTTCTCC  TC
                                |||  ||  | |||||||  ||
                                AAT  AT  G AAAGAGG  AG
                                  GT  GT _      AC
GAM1710  ETS1     5'  GGGCAGGAGGAGCGGGCGCGCG 19115        G       AA   T
                                TGTGTGT TGTTTCTCC  TCC
                                ||||||| |||||||||  |||
                                GCGCGCG GCGAGGAGG  GGG
                                     G        AC
GAM1710  EVPL     3'  TAGGAGCCAGTGGGGAAGTGCG 10544    TG  TG       A____
              TGT                   G  TG  TTTCTCCA    TCCT   A
                                |  ||  ||||||||    ||||   |
```

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                                T  GC  GAAGGGGT    AGGA   T
                                 GT  GT      GACCG
GAM1710  EYA1     3'  AGCATGAGGCAGCACGTGCACA 6695       TG     _    CAATCCT
             A                    TTGTG  TGTGTT TCTC
                                  |||||  ||||||  ||||
                                  AACAC  GCACGA GGAG
                                     GT     C    TACGA
GAM1710  F2RL1    5'  TGGGGAGGCGCGCAGCAG    60267     G
                                  TTGT TGTGTGTTTCTCCA
                                  ||||  ||||||||||||||
                                  GACG ACGCGCGGAGGGGT
                                    _
GAM1710  F7       3'  GGATGCACAGAGATATGCACAC 5525             CCA_   T
             A                    TGTGTGTGTGTTTCT   ATCC
                                  ||||||||||||||    ||||
                                  ACACACGTATAGAGA   TAGG
                                           CACG
GAM1710  FACL4    3'  GGGATTGATTTTAAAATGTACA 16746    TG   TG   CTC___
             TGTA                   TG  TGTG  TTT     CAATCCT
                                  ||  ||||  |||     |||||||
                                  AT  ACAT  AAA     GTTAGGG
                                   GT   GT   ATTTTA
GAM1710  FBN2     3'  GGATTGCCATATGTGCAA    10578     TG     TTTCTC
                                  TTG  TGTGTG     CAATCC
                                  |||  ||||||     ||||||
                                  AAC  GTATAC     GTTAGG
                                    GT     C_____
GAM1710  FBXL5    5'  TAGGAGTTCAAAATGCATGAGC 25137      G       ____    AATCCT
             AG                     TTGT TGTGTGTTT    CTCC
                                  ||||  |||||||||    ||||
                                  GACG GTACGTAAA    GAGG
                                    A        ACTT    A   TC
GAM1710  FCN2     3'  GGACTGGGCCACGTACAA     15919         T  TTCT   A
                                  TTGTGTGTG GT    CCA TCC
                                  |||||||||  ||    |||  |||
                                  AACATGCAC CG    GGT AGG
                                       _  ____   C
GAM1710  FCN2     3'  GGACTGGGCCACGTACAA     15920         T  TTCT   A
                                  TTGTGTGTG GT    CCA TCC
                                  |||||||||  ||    |||  |||
                                  AACATGCAC CG    GGT AGG
                                       _  ____   C
GAM1710  FGF12    3'  GTGTAAGAGAAGGCACATACAT 41062           _    CAATCCT
             AG                     TTGTGTGTGTGT TTCTC
                                  ||||||||||||  |||||
                                  GATACATACACG AAGAG
                                         G     AATGTGA
GAM1710  FGFR1    3'  GGAAAAGAAATTGCATGCAG   7022          T     CCAA
                                  TTGTGTGTG GTTTCT    TCC
                                  |||||||||  ||||||    |||
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                                GACGTACGT TAAAGA    AGG
                                      _     AA__
GAM1710  FGFR2    5'  GGGCGAGGGAGCGCGCGCG    5564         G TT   CAA
                                TGTGTGTGT T  CTC   TCC
                                |||||||||  |  |||   |||
                                GCGCGCGCG A  GAG   GGG
                                      _ GG   C__
GAM1710  FGFRL1   3'  CCCTGGACACACACACACAG   41909          TTC    ATCCT
                                TTGTGTGTGTGT   TCCA
                                ||||||||||||   ||||
                                GACACACACACA   AGGT
                                       C__    CCCC
GAM1710  FN1      3'  GGGATCAATAGGAAAGCATATG 10708          G    CCA_
            CAG                    TTGTGTGTGT TTTCT    ATCCT
                                ||||||||||  |||||    |||||
                                GACGTATACG AAGGA    TAGGG
                                       A     TAAC
GAM1710  FNTB     3'  AGGAGCTCAGAGATGCAGCATG 10711    TG   G       CCAA
            A                   T  TGT TGTGTTTCT    TCCT
                                |  |||  |||||||||    ||||
                                A  ACG ACGTAGAGA    AGGA
                                GT   _       CTCG
GAM1710  FXR2     3'  AGGAGCTAGTGGAGGGGTGTGT 17958      G GT TG TT     A____
            AACAG                  TTGT T  G  T  CTCCA     TCCT
                                ||||  |  |  |  |||||     ||||
                                GACA A  T  G  GAGGT     AGGA
                                  _ TG GT GG     GATCG
GAM1710  G1P3     3'  AGGATTACAAGCATGCGCCGA  43451     T        CTCC
                                TTG GTGTGTGTTT    AATCCT
                                |||  ||||||||||    ||||||
                                AGC CGCGTACGAA    TTAGGA
                                  _        CA__
GAM1710  G6PD     5'  GGGATGCGGGAGCACTACGCG  6389        T       CCA
                                TGTGTG GTGTTTCT   ATCCT
                                ||||||  ||||||||   |||||
                                GCGCAT CACGAGGG   TAGGG
                                   _       CG_
GAM1710  GAA      5'  GGGCGGCCAGGGCGCGCGTGCG 5670       TG    T  ___  AA   T
            CG                    TGTG  TGTGT TCT   CC  TCC
                                ||||  |||||  |||   ||  |||
                                GCGC  GCGCG GGG   GG  GGG
                                   GT    C   ACC  C_
GAM1710  GABPA    5'  ACCCGGAGAGACGCTGCACGTG 10746    TG    _        AATCCT
            G                     T  TGTGT GTGTTTCTCC
                                |  |||||  ||||||||||
                                G  GCACG CGCAGAGAGG
                                 GT    T        CCCA
GAM1710  GABRE    3'  TGGGGAAATATGTAAATAA   18292      G  TG
                                TTGT TG  TGTTTCTCCA
                                ||||  ||  ||||||||||
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                                AATA AT  ATAAAGGGGT
                                  A  GT
GAM1710  GABRE    3'  TGGGGAAATATGTAAATAA   18293     G  TG
                                TTGT TG  TGTTTCTCCA
                                |||| ||  ||||||||||
                                AATA AT  ATAAAGGGGT
                                  A  GT
GAM1710  GAD1     3'  AGGAACAGAGTATATATGTACA 7696      TG    TT   CAA
              G                  TTGTG  TGTGT  CTC   TCCT
                                 |||||  |||||  |||   ||||
                                 GACAT  ATATA  GAG   AGGA
                                    GT    T_   ACA
GAM1710  GAN      5'  GGGCCGGGCGGGCGCGCGCGCA 42120          TC   AA   T
              G                  TTGTGTGTGTGTT  TCC  TCC
                                 ||||||||||||  |||  |||
                                 GACGCGCGCGCGG  GGG  GGG
                                        GC   CC
GAM1710  GAS1     3'  GGAGGAAGCAAGCATGTGG   10760   TG    G    _
                                 T  TGTGT TGTTTC TCC
                                 |  ||||| ||||||  |||
                                 G  GTACG ACGAAG AGG
                                  GT    A     G
GAM1710  GCMB     3'  GGGACATAATAGCAGTGTGCAT 17646        TG  T  CCAA__
              GCAG                  TTGTGTGTG  TT CT     TCCT
                                    |||||||||  || ||     ||||
                                    GACGTACGT  GA GA     AGGG
                                         GT  C  TAATAC
GAM1710  GCNT3    3'  GGGGCAAGAGCATGTACAA   17644      TG   G  _
                                 TTGTG  TGT TTT CTCC
                                 |||||  ||| ||| ||||
                                 AACAT  ACG GAA GGGG
                                    GT   A   C
GAM1710  GDF5     3'  GGCAGGAGCATCTACACAG   6897        T      _
                                 TTGTGTG GTGTTTCT CC
                                 ||||||| |||||||| ||
                                 GACACAT TACGAGGA GG
                                     C       C
GAM1710  GFAP     3'  CTGGGATGGCACTAGGCATACA 10781         ___    TC   AATCCT
              A                   TTGTGTGT   GTGTT  TCC
                                  ||||||||   |||||  |||
                                  AACATACG   CACGG  GGG
                                       GAT    TA     TCC
GAM1710  GGT2     5'  AGATTGGGAGGGACACACTGCG 74082      T     TT   _   CT
                                 TGTG GTGTGT  CTCC AATC
                                 |||| ||||||  |||| ||||
                                 GCGT CACACA  GAGG TTAG
                                   _     GG   G   A
GAM1710  GJA1     3'  AGGATTCAGTAGTACACATACA 5711            T  CC
              A                   TTGTGTGTGTGTT CT  AATCCT
                                  |||||||||||| ||  ||||||
```

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                                AACATACACATGA GA  TTAGGA
                                       T  C_
GAM1710  GLP1R    3'  GGAAGGGACACACACACA    10796          TT  _
                                TGTGTGTGTGT  CT CC
                                ||||||||||  || ||
                                ACACACACACA  GA GG
                                      GG  A
GAM1710  GLRA3    3'  TGGAGGATTGTACATATAA   60700        GT T
                                TTGTGTGT  G TTCTCCA
                                ||||||||  | |||||||
                                AATATACA  T AGGAGGT
                                     TG T
GAM1710  GLRX     3'  GGATCAGAGGCACAAGTGCAG  10803     TG G       CCA
                                TTG  T TGTGTTTCT   ATCC
                                |||  | |||||||||   ||||
                                GAC  G ACACGGAGA   TAGG
                                  GT A        C__
GAM1710  GLRX2    3'  AGGATGTTTTAAATACATGCAT 32678           CTCCA
                                GTGTGTGTGTTT    ATCCT
                                ||||||||||||    |||||
                                TACGTACATAAA    TAGGA
                                       TTTTG
GAM1710  GNAQ     5'  AGGCGGGAGGGTGTGTGTGCGC 10824      TG  TG _     AAT
           G                     TGTG  TG  T TTCTCC   CCT
                                ||||  ||  | ||||||   |||
                                GCGC  GT  G GGGAGG   GGA
                                  GT  GT T     GC_
GAM1710  GNB1     3'  GGGGCCAAGCACATGCGGGG   10838    G         __
                                TT TGTGTGTGTTT  CTCC
                                || ||||||||||  ||||
                                GG GCGTACACGAA  GGGG
                                 G         CC
GAM1710  GNE      3'  GGGATTGCGGGCACATGCAC   19673          TT  C
                                GTGTGTGTGT  CT CAATCCT
                                ||||||||||  || |||||||
                                CACGTACACG  GG GTTAGGG
                                       __  C
GAM1710  GNLY     5'  GGGGAGATGACATACAA     22231         G
                                TTGTGTGT TGTTTCTCC
                                |||||||| |||||||||
                                AACATACA GTAGAGGGG
                                       _
GAM1710  GP1BA    3'  GGGGTTGGAGGGGTAAGGAACA 5723        GTG_  TT
           CAG                    TTGTGT    TG  TCTCCAATCCT
                                ||||||    ||  ||||||||||||
                                GACACA    AT  GGAGGTTGGGG
                                    AGGA  GG
GAM1710  GP1BB    3'  AGGACCATGGGGCACAATGCG  6392       G     TT TCCAA
                                TGTGT TGTGT  C     TCCT
                                ||||| |||||  |    ||||
```

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                                GCGTA ACACG  G    AGGA
                                  _    GG TACC_
GAM1710  GPR75    5'  GGAGGAGGGGCGCGCTGCG   23287     T    TT   AA
                                TGTG GTGTGT  CTCC  TCC
                                |||| ||||||  ||||  |||
                                GCGT CGCGCG  GAGG  AGG
                                  _     GG   __
GAM1710  GPR84    3'  GGTGAAATAACACATGTGG   40159   TG     _    T
                                T  TGTGTGT GTTTC CC
                                |  ||||||| ||||| ||
                                G  GTACACA TAAAG GG
                                 GT      A    T
GAM1710  GRM1     5'  GGGCGTCTTGGGGGTGCGCGCC 7742     T    T     ____   T
            G                    TG GTGTGT TCTCCAA    TCC
                                || |||||| |||||||    |||
                                GC CGCGCG GGGGGTT    GGG
                                 _     T      CTGC
GAM1710  GSBS     3'  GGAAAAGTAGATACGCAA    92732        G    C
                                TTGTGTGT TGTTT TCC
                                |||||||| ||||| |||
                                AACGCATA ATGAA AGG
                                     G    A
GAM1710  GTF2F1   5'  GGGATCGAGGGACGCGCACGC  10892         TT   CA
                                GTGTGTGTGT  CTC  ATCCT
                                ||||||||||  |||  |||||
                                CGCACGCGCA  GAG  TAGGG
                                      GG   C_
GAM1710  HDAC4    5'  AGGCTGAGGAGATGCGGCGCG  21242      G      TC  AT
                                TGTGT TGTGTTTC  CA  CCT
                                ||||| ||||||||  ||  |||
                                GCGCG GCGTAGAG  GT  GGA
                                  _       GA  C_
GAM1710  HEM1     3'  AGGGCGTGGGGCCACATGTGTG 19235   TG  TG   TTT    A_
            A                    T  TG  TGTG   CTCCA  TCCT
                                |  ||  ||||   |||||  ||||
                                A  GT  ACAC   GGGGT  GGGA
                                 GT  GT   C__    GC
GAM1710  HEPH     5'  GGATGACTCATACACAG     29650         T   TC
                                TTGTGTGTG GTT  TCC
                                |||||||| |||  |||
                                GACACATAC CAG  AGG
                                      T   T_
GAM1710  HIVEP2   3'  GGGGTGCAGCAACATGTGCACA 23075      TG     T  CCA
            G                    TTGTG  TGTGTT CT   ATCCT
                                |||||  |||||| ||   |||||
                                GACAC  GTACAA GA   TGGGG
                                  GT     C  CG_
GAM1710  HLX1     3'  AGGGCAGGAGACGCAGCGTGG  41982   TG   G   TT    AA
                                T  TGT TGTG  TCTCC  TCCT
                                |  ||| ||||  |||||  ||||
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                                G  GCG ACGC  AGAGG  GGGA
                                 GT  _  __    AC
GAM1710 HNMT    3'  AGGTAGAGAGACCACATGCAG  23553        T     CAAT
                                TTGTGTGTG GTTTCTC   CCT
                                ||||||||| |||||||   |||
                                GACGTACAC CAGAGAG   GGA
                                      _     AT__
GAM1710 HNRPDL  3'  GGGATTGGCATACGTGTTCACA 19603      T TG  TTCT
             G                   TTGTG G  TGT   CCAATCCT
                                 ||||| |  |||   ||||||||
                                 GACAC T  GCA   GGTTAGGG
                                    T GT  TAC_
GAM1710 HNRPF   3'  TGGGAAGCATCAAATAGACACA 18306       _______     T  AATCCT
             CG                   TGTGTGT     GTGTTTC CC
                                  |||||||     ||||||| ||
                                  GCACACA     TACGAAG GG
                                     GATAAAC     _    TC
GAM1710 HNRPK   3'  TTGGGGGGGGGGAAGGGCGTGCA 49195   TG  G     AA  T
                                TG  TGT TTTCTCC  TCC
                                ||  ||| |||||||  |||
                                AC  GCG GAAGGGG  GGG
                                 GT  G     GG  TTG
GAM1710 HNRPK   3'  TTGGGGGGGGGGAAGGGCGTGCA 49196   TG  G     AA  T
                                TG  TGT TTTCTCC  TCC
                                ||  ||| |||||||  |||
                                AC  GCG GAAGGGG  GGG
                                 GT  G     GG  TTG
GAM1710 HOXD10  3'  AGGATTGGAGAGGGGGCACC  10962   T   G  _
                                G GTGT TT TCTCCAATCCT
                                | |||| || ||||||||||
                                C CACG GG AGAGGTTAGGA
                                _   G  G
GAM1710 HPS4    5'  AGGCATGGAAATATACAT    42225        TC   AT
                                GTGTGTGTT  TCCA  CCT
                                |||||||||  ||||  |||
                                TACATATAA  AGGT  GGA
                                     __    AC
GAM1710 HS3ST3A1  5'  GGCCACAGGGGCGCACGGCGA  21274     G     TT  ____
                                TTGT TGTGTGT  CT   CC
                                |||| |||||||  ||   ||
                                AGCG GCACGCG  GA   GG
                                   _     GG  CACC
GAM1710 HSD3B1  3'  AGGATGACAGAGATGTGCATGT 7830   TG   TG    CCA
             GG                   T  TGTG  TGTTTCT   ATCCT
                                  |  ||||  |||||||   |||||
                                  G  GTAC  GTAGAGA   TAGGA
                                  GT   GT     CAG
GAM1710 HSD3B2  3'  AGGATGACAGAGATGTGCATGT 5773   TG   TG    CCA
             GG                   T  TGTG  TGTTTCT   ATCCT
                                  |  ||||  |||||||   |||||
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                                G  GTAC  GTAGAGA   TAGGA
                                 GT    GT      CAG
GAM1710  ICMT     3'  GGATTTGAGCATATACA     25735        TTT   C
                                TGTGTGTG   CTC AATCC
                                ||||||||   ||| |||||
                                ACATATAC   GAG TTAGG
                                     ___   T
GAM1710  IER3     3'  AGGTGATGGAGATGTGTACGTA 54480       TG T     AT_
                                TGTGTG  T TCTCCA   CCT
                                ||||||  | ||||||   |||
                                ATGCAT  G AGAGGT   GGA
                                   GT T     AGT
GAM1710  IER3     3'  AGGTGATGGAGATGTGTACGTA 15318       TG T     AT_
                                TGTGTG  T TCTCCA   CCT
                                ||||||  | ||||||   |||
                                ATGCAT  G AGAGGT   GGA
                                   GT T     AGT
GAM1710  IER5     3'  GGTCAGAAGTACTACACAG    33746        T       CCAAT
                                TTGTGTG GTGTTTCT     CC
                                ||||||| ||||||||     ||
                                GACACAT CATGAAGA     GG
                                    _       CT___
GAM1710  IKBKAP   5'  GGACAGAGACGCGTGCGCAA   71152       TG        CCAA
                                TTGTG  TGTGTTTCT    TCC
                                |||||  |||||||||    |||
                                AACGC  GCGCAGAGA    AGG
                                   GT        C___
GAM1710  IL12B    3'  GGGAACGCAAGAGATACTTACA 10991    TG    T      CCAA_
            TGG                    T  TGTG GTGTTTCT     TCCT
                                |  |||| ||||||||     ||||
                                G  ACAT CATAGAGA     AGGG
                                 GT    T       ACGCA
GAM1710  IL20RA   5'  AGGTCGCCTGGAGCGTGGCACG 27799        GTTT     AT___
            CA                   TGTGTGT    CTCCA     CCT
                                |||||||    |||||    |||
                                ACGCACG    GAGGT    GGA
                                    GTGC    CCGCT
GAM1710  IL20RA   5'  GGGTAGCCGGGGGAGCGCGCGT 27802    G GT          A___    T
            GGGG                    TT T  GTGTGTTTCTCC    ATCC
                                || |  ||||||||||||    ||||
                                GG G  CGCGCGAGGGGG    TGGG
                                 G TG           CCGA
GAM1710  IL22RA2  3'  TGAGGAGATACATATCAG     54776     T         TC
                                TTG GTGTGTGTTTC  CA
                                ||| ||||||||||  ||
                                GAC TATACATAGAG  GT
                                  _         GA
GAM1710  IL8      3'  GGAGAATATACAAATAG     96112      G       T
                                TTGT TGTGTGTT CTCC
                                |||| |||||||| ||||
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                                GATA ACATATAA GAGG
                                  A      _
GAM1710 IPF1     5' GGGAGTGGGAACGCCACACAG 5781        T    T T   A
                                TTGTGTG GTGTT C CCA TCCT
                                ||||||| ||||| | ||| ||||
                                GACACAC CGCAA G GGT AGGG
                                   _    _ _  G
GAM1710 ISLR     3' AGGATTGGGGGAATGGAGC   19881    G_
                                GT  TGTTTCTCCAATCCT
                                ||  ||||||||||||||
                                CG  GTAAGGGGGTTAGGA
                                 AG
GAM1710 ITGB4    5' GGACGGGCGCACAGCAG     5808      G      TC
                                TTGT TGTGTGTT  TCC
                                |||| ||||||||  |||
                                GACG ACACGCGG  AGG
                                  _       GC
GAM1710 ITSN2    3' GGGGCTGAGGGAGCACCATGCA 39463       T     TC  AT
              G                  TTGTGTG GTGTTTC  CA  CCT
                                 ||||||| |||||||  ||  |||
                                 GACGTAC CACGAGG  GT  GGG
                                    _     GA  CG
GAM1710 JMJ      3' GGGATAGGAGACACACGCGCAC 18323          T    A
              A                  TGTGTGTGTGT TCTCC ATCCT
                                 |||||||||| ||||| |||||
                                 ACACGCGCACA AGAGG TAGGG
                                       C    A
GAM1710 JRK      5' AGGCAGGAGGTGCAGCGTGT  87817   TG  G  T    AAT
                                 G  TGT TGT TCTCC   CCT
                                 |  ||| ||| |||||   |||
                                 T  GCG ACG GGAGG   GGA
                                  GT   _  T    AC_
GAM1710 JRK      3' GGCAGGAGGGCATGTGCAG   87830    TG    G    _
                                 TTG  TGTGT TTTCT CC
                                 |||  ||||| ||||| ||
                                 GAC  GTACG GAGGA GG
                                   GT    G    C
GAM1710 JUN      3' AGGGTTGGGGAGGGGCGGCAGG 11099    G  G  G
              A                  TT TGT TGT TTTCTCCAATCCT
                                 || ||| ||| ||||||||||||
                                 AG ACG GCG GGAGGGGTTGGGA
                                  G   _  G
GAM1710 JUNB     3' GGAAAAGAAACACGCAC     11105          CCAA
                                 GTGTGTGTTTCT   TCC
                                 ||||||||||||   |||
                                 CACGCACAAAGA   AGG
                                       AA__
GAM1710 JUND     3' GGGGCTCCGAGGGGGCGCACGT 19300     _     G TT   CAA_
              CAA                   TTG TGTGTGT T  CTC   TCCT
                                 ||| ||||||| |  |||   ||||
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                                AAC GCACGCG G  GAG    GGGG
                                  T      _ GG   CCTC
GAM1710  KCNK1    5'  GGGGCGGGCGGGCGCGCG    11164        G    _
                                TGTGTGT TGTTT CTCC
                                ||||||| ||||| ||||
                                GCGCGCG GCGGG GGGG
                                    G    C
GAM1710  KCNK4    3'  GGACGAGGAGAGCGTGCATA   33988      TG   T   AA_
                                TGTG  TGTT CTCC   TCC
                                ||||  |||| ||||   |||
                                ATAC  GCGA GAGG   AGG
                                  GT    _    AGC
GAM1710  KCNS3    3'  GCTGACTGAGACGACATGCATG 11196     TG       _   CAATCCT
            TAA                   TTG  TGTGTGTT TCTC
                                ||| ||||||||| ||||
                                AAT  ACGTACAG AGAG
                                  GT       C   TCAGTCGA
GAM1710  KIAA0857 3'  GATGGAGCAGAGGAGCGCCACA 67254       T       CAA   T
            CA                    TGTGTG GTGTTTCTC   TCC
                                |||||| |||||||||   |||
                                ACACAC CGCGAGGAG   AGG
                                  _       ACG   TAGG
GAM1710  KLHL2    3'  GGTAGAAGCACCGTGTAG    24338     TG  T      _
                                TTG  TG GTGTTTCT CC
                                |||  || |||||||| ||
                                GAT  GC CACGAAGA GG
                                  GT  _       T
GAM1710  KLHL3    5'  AGGATCCCCGAGTGCATACACA 88842         TG   CTCCA
            G                     TTGTGTGTG  TTT    ATCCT
                                |||||||||  |||    |||||
                                GACACATAC  GAG    TAGGA
                                     GT   CCCC_
GAM1710  LAMP1    3'  GGCTTGGGGATTGTACACG    19904       TT_     T
                                TGTGTG   TCTCCAA CC
                                ||||||   ||||||| ||
                                GCACAT   AGGGGTT GG
                                   GTT      C
GAM1710  LASS2    3'  AGGGTAGGAGGAGGGTGCACAT 68306        TG G      A
            AA                    TTGTGTG  T TTTCTCC ATCCT
                                |||||||  | ||||||| |||||
                                AATACAC  G GAGGAGG TGGGA
                                    GT G      A
GAM1710  LDHB     5'  GATTCAGACACATATATACAA  11288           T   CC
                                TTGTGTGTGTGT TCT  AATC
                                |||||||||||| |||  ||||
                                AACATATATACA AGA  TTAG
                                       C   C_
GAM1710  LDHB     5'  GGCGCCGGAGGAGACGCACGCA 11290          G      AAT_  T
            G                     TTGTGTGTGT TTTCTCC    CC
                                |||||||||| |||||||    ||
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                                GACGCACGCA GAGGAGG   GG
                                      _      CCGC
GAM1710  LIPE     3'  GGGAGGGGGACGCGCACACACA 19302          T    AA
                                TGTGTGTGTGT TCTCC  TCCT
                                |||||||||| |||||  ||||
                                ACACACACGCG AGGGG  AGGG
                                      C    G_
GAM1710  LRP6     3'  GGGAATACTGGAGATATTTGTA 11365    GT T  T    A___
              CA                  TGT  G GT TCTCCA   TCCT
                                |||  | || ||||||   ||||
                                ACA  T TA AGAGGT   AGGG
                                  TG T  T     CATA
GAM1710  LRP8     3'  GGGGAAATGGCATACGCAA   34457          _
                                TTGTGTGTGT GTTTCTCC
                                |||||||||| ||||||||
                                AACGCATACG TAAAGGGG
                                      G
GAM1710  LTA      3'  TGAGAGGGCATGCGCACAA   6992           T  _
                                TTGTGTGTGTGTT CTC CA
                                |||||||||||| ||| ||
                                AACACGCGTACGG GAG GT
                                       _  A
GAM1710  LYAAT1   3'  GGGGTGGCAGACACGCAG    55309        G   TT
                                TTGTGTGT TGT  CTCC
                                |||||||| |||  ||||
                                GACGCACA ACG  GGGG
                                     G   GT
GAM1710  MADH3    3'  ATTGGGAGGTGCGTGTTCAG   20919     T TG  TG    T
                                TTG G  TG  TTTC CCAAT
                                ||| |  ||  |||| |||||
                                GAC T  GC  GGAG GGTTA
                                  T GT  GT   _
GAM1710  MAP1B    5'  GGAGGGGGAGGCGGCGCGCG   20964        G       AA   T
                                TGTGTGT TGTTTCTCC  TCC
                                ||||||| |||||||||  |||
                                GCGCGCG GCGGAGGGG  AGG
                                     _       G_   C
GAM1710  MAPK12   5'  GGGGGAGGGGCCGTGCGCAG   12938      TG  T  TT    AA
                                TTGTG  TG GT  CTCC  TCC
                                |||||  || ||  ||||  |||
                                GACGC  GC CG  GAGG  GGG
                                   GT  _  GG   __
GAM1710  MAPK4    3'  GGAGACCACATGTGTGCACAG  12303       ____    TT
                                TTGTGT    GTGTG  TCTCC
                                ||||||    |||||  |||||
                                GACACG    TACAC  AGAGG
                                    TGTG    C_
GAM1710  MDM1     3'  GGGGTGTTCATAGAAGCAGTGT 39682       TG G      CCA___
              GCAG                  TTGTG  T TGTTTCT     ATCCT
                                |||||  | |||||||     |||||
```

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                                GACGT  G ACGAAGA     TGGGG
                                   GT _      TACTTG
GAM1710  MEIS2    3'  GGGAAAAGGAAACACACGCA  39726          CCAA
                                TGTGTGTGTTTCT    TCCT
                                ||||||||||||    ||||
                                ACGCACACAAAGG    AGGG
                                      AAA_
GAM1710  MEN1     5'  GGGAAACGAGTGCTGCACACAG 56354        T  TT   CAA
                                TTGTGTGTG GT  CTC   TCCT
                                |||||||||  ||  |||   ||||
                                GACACACGT CG  GAG   AGGG
                                     _ T_   CAA
GAM1710  MEST     5'  GGCCTCAGGAAGCGCATGCGCA 70461            CCAAT  T
           A                     TTGTGTGTGTGTTTCT     CC
                                ||||||||||||||||     ||
                                AACGCGTACGCGAAGG     GG
                                      ACTCC
GAM1710  MET      5'  GGGAGGCGCGGAGCGCGCGTGT 71771    TG        TCCAA
                                G  TGTGTGTTTC     TCCT
                                |  ||||||||||     ||||
                                T  GCGCGCGAGG     AGGG
                                 GT        CGCGG
GAM1710  MGAT1    3'  GGGAGAAGGGGACATATTTGTG 11555    TG  T     TT  CCAA
           G                     T  TG GTGTGT  CT    TCCT
                                |  || ||||||  ||    ||||
                                G  GT TATACA  GG    AGGG
                                 GT  T     GG  AAG_
GAM1710  MGAT3    3'  AGGATTGGGGAAGAGAGCCTGC 11559      T  GTG
           AG                      TTGTG GT   TTTCTCCAATCCT
                                |||||  ||   ||||||||||||
                                GACGT CG   GAAGGGGTTAGGA
                                   C  AGA
GAM1710  MGEA5    5'  AGGAGCCGGAGGGGCGCACAC  25216        TT    AA_
                                GTGTGTGT  CTCC   TCCT
                                ||||||||  ||||   ||||
                                CACACGCG  GAGG   AGGA
                                     GG    CCG
GAM1710  MLLT3    5'  AGGAGGGGGGGGTACCACACAA 16958        T   TT    AA
                                TTGTGTG GTG  TCTCC  TCCT
                                |||||||  |||  |||||  ||||
                                AACACAC CAT  GGGGG  AGGA
                                     _  GG    G_
GAM1710  MLLT3    3'  GGACGAATGCATATTCAA    16960     T        C
                                TTG GTGTGTGTTT TCC
                                |||  ||||||||||  |||
                                AAC TATACGTAAG AGG
                                  T         C
GAM1710  MLLT4    3'  GGCCCTGAGAGATGCCACGTGA 21039    TG    T       CAAT
                                T  TGTG GTGTTTCTC    CC
                                |  ||||  |||||||||    ||
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                                A  GCAC CGTAGAGAG    GG
                                 GT    _        TCCC
GAM1710  MMP16    3'  GGGAGATTTGGAATACACATGC 21048             TCCAA
                AG                    TTGTGTGTGTGTTTC     TCCT
                                      ||||||||||||||     ||||
                                      GACGTACACATAAGG     AGGG
                                               TTTAG
GAM1710  MMP19    5'  GGAAGGAGACATGTGACATGG  11633    TG  _ TG      CCAA
                                      T  TGT G  TGTTTCT    TCC
                                      |  ||| |  |||||||    |||
                                      G  ACA T  ACAGAGG    AGG
                                       GT   G GT      A___
GAM1710  MN1      5'  GGCCGGAGGCGCGCCGCG    11656      T         __
                                      TGTG GTGTGTTTCT  CC
                                      |||| ||||||||||  ||
                                      GCGC CGCGCGGAGG  GG
                                        _         CC
GAM1710  MSF      5'  GGGGCGGGGGCGCAGCGCGCG  89467        G   T     AA
                                      TGTGTGT TGT TCTCC  TCC
                                      ||||||| ||| |||||  |||
                                      GCGCGCG ACG GGGGG  GGG
                                          _  C    CG
GAM1710  MSR1     3'  AGGGTAATAGAAATGCATACCA 11702     T          CCA
                G                     TTG GTGTGTGTTTCT   ATCCT
                                      |||  ||||||||||||   |||||
                                      GAC CATACGTAAAGA   TGGGA
                                        _          TAA
GAM1710  MSX1     5'  GGGGCGGGAGGCGCGCGCGGGA 11711    G           CAA
                                      TT TGTGTGTGTTTCTC   TCC
                                      ||  ||||||||||||||   |||
                                      AG GCGCGCGCGGAGGG   GGG
                                       G            CG_
GAM1710  MTCP1    5'  GGAGGAGCGCTACATGG     27244    TG    T
                                      T  TGTG GTGTTTCTCC
                                      |  ||||  ||||||||||
                                      G  ACAT CGCGAGGAGG
                                       GT    _
GAM1710  MUCDHL   3'  GGTGGGGACACAGCACAG    88644       G     TT  _
                                      TTGTGT TGTGT  CT CC
                                      ||||||  |||||  ||  ||
                                      GACACG ACACA  GG GG
                                          _    GG  T
GAM1710  MUCDHL   3'  GGTGGGGGCACAGCACAG    88645       G     TT  _
                                      TTGTGT TGTGT  CT CC
                                      ||||||  |||||  ||  ||
                                      GACACG ACACG  GG GG
                                          _    GG  T
GAM1710  MUCDHL   3'  GGTGGGGGCACAGCACAG    88646       G     TT  _
                                      TTGTGT TGTGT  CT CC
                                      ||||||  |||||  ||  ||
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                                GACACG ACACG  GG GG
                                   _    GG  T
GAM1710  MXI1    3'  GGGTCAGAAGAGTTGTGCACGC 56130       TG GT   _ CA   T
                AG                  TTGTGTG  T  TTCT C  ATCC
                                    |||||||  |  |||| |  ||||
                                    GACGCAC  G  GAGA G  TGGG
                                       GT TT    A AC
GAM1710  MXI1    3'  GGGTCAGAAGAGTTGTGCACGC 56131       TG GT   _ CA   T
                AG                  TTGTGTG  T  TTCT C  ATCC
                                    |||||||  |  |||| |  ||||
                                    GACGCAC  G  GAGA G  TGGG
                                       GT TT    A AC
GAM1710  MYF6    3'  GGGAAGGAGACACATTCACAA  11736      T        CCAA
                                    TTGTG GTGTGTTTCT    TCCT
                                    |||||  ||||||||||   ||||
                                    AACAC TACACAGAGG    AGGG
                                       T        A___
GAM1710  MYO1A   3'  GGAGGGGGCACCATGCAG    19387       T    TT _
                                    TTGTGTG GTGT  C TCC
                                    |||||||  ||||  |  |||
                                    GACGTAC CACG  G AGG
                                       _    GG G
GAM1710  NAB2    5'  GGAAGAGGGCAGCACGCAG    21059       _   G  TC
                                    TTGTGTG TGT TT  TCC
                                    |||||||  |||  ||  |||
                                    GACGCAC ACG GA  AGG
                                       G   G  GA
GAM1710  NFIA    5'  GGCGGAGGCGGGCGCGCG    70886       G      _
                                    TGTGTGT TGTTTCT CC
                                    |||||||  |||||||  ||
                                    GCGCGCG GCGGAGG GG
                                       G      C
GAM1710  NFIL3   3'  GGATTGGTGACAAACACA    19390      G    TCT
                                    TGTGT TGTT   CCAATCC
                                    |||||  ||||   |||||||
                                    ACACA ACAG   GGTTAGG
                                       A    T__
GAM1710  NGFR    5'  GGGGCGCTGGAGCGCAGCGCAG 11802       G       TCCAA
                                    TTGTGT TGTGTTTC     TCC
                                    ||||||  ||||||||    |||
                                    GACGCG ACGCGAGG     GGG
                                       _       TCGCG
GAM1710  NIPSNAP1  3'  GGGGCAGGAGACAGACACGTAA 14661        G  TT    AA
                                    TTGTGTGT TG  TCTCC  TCCT
                                    ||||||||  ||  |||||  ||||
                                    AATGCACA AC  AGAGG  GGGG
                                       G  __     AC
GAM1710  NKX3A   3'  GGGAGCAAGAGGTGTGCACACC 21614     T    TG T    CAA_
                AA                  TTG GTGTG  T TCTC    TCCT
                                    |||  |||||  | ||||    ||||
```

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                                AAC CACAC  G GGAG    AGGG
                                  _    GT T    AACG
GAM1710  NLGN1    3'  GGAGGAATATTATGTGA     30699    TG    T
                                T  TGTG GTGTTTCTCC
                                |  |||| ||||||||||
                                A  GTAT TATAAGGAGG
                                 GT   _
GAM1710  NLGN3    3'  AGATCCAGGAACACATGCACA  39117              CCA   CT
                                TGTGTGTGTGTTTCT   ATC
                                ||||||||||||||   |||
                                ACACGTACACAAGGA   TAG
                                          CC_   A
GAM1710  NOC4     3'  GGGATCAGGGTAGACACG    21375        _   CA
                                TGTGTTT CTC  ATCCT
                                |||||||  |||  |||||
                                GCACAGA GGG  TAGGG
                                     T   AC
GAM1710  NONO     3'  AGGTCACAGGCAGCGTACATAC 82882           T  CCAAT
                 G                TGTGTGTGTGTT CT     CCT
                                |||||||||||  ||     |||
                                GCATACATGCGA GG     GGA
                                       C  ACACT
GAM1710  NOVA1    3'  AGGATTGGAAATTATAAACA   22417     G    TTTC
                                TGT TGTG    TCCAATCCT
                                |||  ||||    |||||||||
                                ACA ATAT    AGGTTAGGA
                                  A    TAA_
GAM1710  NPHP1    3'  GGGAAAACATATTTGCAA     63146       T       CT
                                TTGTG GTGTGTTT  CC
                                |||||  ||||||||  ||
                                AACGT TATACAAA  GG
                                   T       AG
GAM1710  NPM1     3'  TGGGAGACAAAAATACACATGT 11824    TG        ____     AATCCT
                 GA                T  TGTGTGTGTT    TCTCC
                                |  ||||||||||    |||||
                                A  GTACACATAA    AGAGG
                                 GT         AAAC     G   TC
GAM1710  NPR1     3'  GGGTTGGGGGCCTGTATGC    88742      GT TT
                                GTGT  G  TCTCCAATCC
                                ||||  |  ||||||||||
                                CGTA  T  GGGGGTTGGG
                                   TG CC
GAM1710  NR2C2    5'  ATCCTGAGGTAACACGTACACA 13845           _   CAATCCT
                 G                 TTGTGTGTGTGTT TCTC
                                ||||||||||||| ||||
                                GACACATGCACAA GGAG
                                        T    TCCTA
GAM1710  NRF1     3'  GGGGTGGGTCAGAGATGTGCTT 60750       T TG      __  A
                 GCAA                  TTGTG G  TGTTTCT  CC ATCCT
                                |||||  |  |||||||  ||  |||||
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                                AACGT C  GTAGAGA  GG TGGGG
                                   T GT      CT  G
GAM1710  NRXN3    3'  GGACACACACACACACAG    58074          TTC
                                TTGTGTGTGTGT   TCC
                                ||||||||||||  |||
                                GACACACACACA   AGG
                                      CAC
GAM1710  OA1      3'  AGGGTTCATGCACACACG    6056         TTCTCC
                                TGTGTGTGT     AATCCT
                                |||||||||     ||||||
                                GCACACACG     TTGGGA
                                     TAC___
GAM1710  OAS2     3'  AGGATGTTGAGCAGCATGTGT  11867   TG     T   CA_
                                G  TGTGTT CTC   ATCCT
                                |  ||||||  |||   |||||
                                T  GTACGA GAG   TAGGA
                                 GT     C   TTG
GAM1710  OAS3     3'  GGGAGTTGGGACATGCATGC   21655         TT TCCAA
                                GTGTGTGTGT  C    TCCT
                                ||||||||||  |    ||||
                                CGTACGTACA  G    AGGG
                                     GG TTG__
GAM1710  OAS3     3'  TTCTTATGGAAAAATACACACG 21661           C    ATCCT
            CAA                   TTGTGTGTGTGTTT TCCA
                                ||||||||||||||  ||||
                                AACGCACACATAAA AGGT
                                       A   ATTCTTG
GAM1710  OPCML    3'  GGGGTTGGGGGCGGGGTGGGCA 11900     G  TG  _
                                TGT TG  TT TCTCCAATCCT
                                |||  ||  ||  ||||||||||
                                ACG GT  GG GGGGGTTGGGG
                                  G  GG  C
GAM1710  OPRD1    5'  GGGGCGGCCGGGGCGCGGCACG 8069        _    TT T_  AA   T
            CG                    TGTGTGT GTGT  C  CC  TCC
                                |||||||  ||||  |  ||  |||
                                GCGCACG CGCG  G  GG  GGG
                                     G    GG CC  CG
GAM1710  OSBP     5'  GGGGCGGGGACGCTGCGCG    11917       T  T    AA
                                TGTGTG GT TCTCC  TCC
                                ||||||  ||  |||||  |||
                                GCGCGT CG AGGGG  GGG
                                     _  C     CG
GAM1710  OSM      3'  GGCGCTGGGAGGTGTACACGGA 40450    G     TG    T   AT_  T
            G                     TT TGTGTG  TTTC CCA   CC
                                ||  ||||||  ||||  |||   ||
                                GA GCACAT  GGAG GGT   GG
                                 G     GT    _   CGC
GAM1710  OSR1     5'  GGGGTGGGGAGACGCGCGGCGA 18837      G           AT
                                TTGT TGTGTGTTTCTCCA  CC
                                ||||  ||||||||||||||  ||
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                                AGCG GCGCGCAGAGGGGT  GG
                                  _           GG
GAM1710  OSR1     3'  GGTGGAACAGCACGTAA     18838        G     T
                                TTGTGTGT TGTTTC CC
                                |||||||| |||||| ||
                                AATGCACG ACAAGG GG
                                    _     T
GAM1710  OTOR     3'  GGGGATGCATATAACAG     39755      G      T
                                TTGT TGTGTGT TCTCC
                                |||| ||||||| |||||
                                GACA ATATACG AGGGG
                                  _      T
GAM1710  OTOR     3'  GGGGTTGGAGGTGGCAGATA   39756     G   _
                                TGT TGTT TCTCCAATCCT
                                ||| |||| ||||||||||
                                ATA ACGG GGAGGTTGGGG
                                  G   T
GAM1710  OTX1     3'  GGCGGGAACGCTGTACATAG   28057       GT_      _
                                TTGTGT   GTGTTTCT CC
                                ||||||   |||||||| ||
                                GATACA   CGCAAGGG GG
                                   TGT       C
GAM1710  OVOL1    3'  GGCAAGGAGAGGCACACATGT  17071    TG          AAT  T
                                G  TGTGTGTTTCTCC   CC
                                |  ||||||||||||   ||
                                T  ACACACGGAGAGG   GG
                                 GT           AAC
GAM1710  OXTR     5'  GGGCCGGGAGCGCACGCGTCA  8080     _          CCAA
                                TG TGTGTGTGTTTCT    TCC
                                || ||||||||||||    |||
                                AC GCGCACGCGAGGG    GGG
                                 T          CC__
GAM1710  P2RY2    5'  GGAGAAGCGCAGCGCAG     11936       G
                                TTGTGT TGTGTTTCTCC
                                |||||| ||||||||||
                                GACGCG ACGCGAAGAGG
                                   _
GAM1710  PACE4    5'  GGGGCGGGAACGCGCCGCG    11952      T       CCAA
                                TGTG GTGTGTTTCT    TCC
                                |||| ||||||||||    |||
                                GCGC CGCGCAAGGG    GGG
                                  _        CG__
GAM1710  PAH      3'  AGGATATGAGTACATACTCA   6062     T     TT   CA
                                TG GTGTGT  CTC  ATCCT
                                || ||||||  |||  |||||
                                AC CATACA  GAG  TAGGA
                                 T     T_  TA
GAM1710  PATE     3'  GGGGTTGGAGAATAAAAGCA   57153     GTG    T
                                TGT   TGTT CTCCAATCCT
                                |||   |||| ||||||||||
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                                ACG   ATAA GAGGTTGGGG
                                  AAA   _
GAM1710  PCTK1    3'  GGGGTTGGGTTCCTGAATGCAC 53421       T       C____
              CATAA                   TTGTG GTGTGTTT     TCCAATCCT
                                |||||| ||||||||     |||||||||
                                AATAC CACGTAAG     GGGTTGGGG
                                  _       TCCTT
GAM1710  PDE4B    5'  GGGGTTGGGGGGGAAACTTGGCA 12014      GT_  G TT
              C                    GTGT   GT T  CTCCAATCCT
                                ||||   || |  ||||||||||
                                CACG   CA A  GGGGTTGGGG
                                  GTT  A GG
GAM1710  PDGFRA   3'  AGGGTTGGAATTCAACCACGCA 21693        T  GTTTC
              G                    TTGTGTG GT     TCCAATCCT
                                ||||||| ||     |||||||||
                                GACGCAC CA     AGGTTGGGA
                                  _  ACTTA
GAM1710  PDGFRB   3'  AGGGCACTTGGAGCACACGCA  66579           TCCAA
                                TGTGTGTGTTTC     TCCT
                                ||||||||||||     ||||
                                ACGCACACGAGG     GGGA
                                     TTCAC
GAM1710  PER2     3'  GGATGAATGCACACGCAG     43354             C
                                TTGTGTGTGTGTTT TCC
                                |||||||||||||| |||
                                GACGCACACGTAAG AGG
                                     T
GAM1710  PFKFB4   3'  GGGATATTCTTGAAGCCACACA 17087    TG     T     TCCA__
              TGG                    T  TGTGTG GTTTC      ATCCT
                                |  |||||| |||||      |||||
                                G  ACACAC CGAAG      TAGGG
                                 GT     _     TTCTTA
GAM1710  PIG8     3'  AGGAATATTGGGTGCTGCATAT 18078         T  TT T   ___
              AG                     TTGTGTGTG GT  C CCAA   TCCT
                                |||||||||  ||  | ||||   ||||
                                GATATACGT CG  G GGTT   AGGA
                                     _  T_ _    ATA
GAM1710  PITPNB   3'  GGAGCTTAGGCGCACATGGAA  25702    G         ___
                                TT TGTGTGTGTTT   CTCC
                                ||  ||||||||||   ||||
                                AA GTACACGCGGA   GAGG
                                  G          TTC
GAM1710  PITX1    3'  GGGCGCGGAGGACGCACGCG   12140          T   AAT
                                TGTGTGTGTT CTCC   CCT
                                |||||||||| ||||   |||
                                GCGCACGCAG GAGG   GGG
                                     _    CGC
GAM1710  PITX2    3'  GTTGCAAGGACACATACACAA  6160             CTC
                                TTGTGTGTGTGTTT   CAAT
                                ||||||||||||||   ||||
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                                AACACATACACAGG  GTTG
                                      AAC
GAM1710  PLCG2    5'  GGGACGCGGGCTGCGCGCGCG  72881        TT  CAA
                                TGTGTGTGT  CTC  TCCT
                                |||||||||  |||  ||||
                                GCGCGCGCG  GGG  AGGG
                                    TC  CGC
GAM1710  PNUTL2   3'  GGATGCAGGAGATGCTACACAA 55374       T      CCA
                                TTGTGTG GTGTTTCT  ATCC
                                |||||||  ||||||||  ||||
                                AACACAT CGTAGAGG  TAGG
                                    _      ACG
GAM1710  PNUTL2   3'  GGATGCAGGAGATGCTACACAA 55375       T      CCA
                                TTGTGTG GTGTTTCT  ATCC
                                |||||||  ||||||||  ||||
                                AACACAT CGTAGAGG  TAGG
                                    _      ACG
GAM1710  POU4F1   3'  GGGACCAAGGAACTATGTACAA 21764      TG  T    CCAA
                                TTGTG  TG GTTTCT   TCCT
                                |||||  ||  ||||||   ||||
                                AACAT  AT CAAGGA   AGGG
                                   GT  _     ACC_
GAM1710  PPP1R3D  3'  AGGGTGGTGGGGTAGGTGCATG 21791   TG  TG G  TT  T  A
           G                    T  TG  T TG  TC CA TCCT
                                |  ||  | ||  || ||| ||||
                                G  AC  G AT  GG GGT GGGA
                                 GT  GT G  GG  T  _
GAM1710  PPP2R4   3'  GGGAGCACTGAGAAGCACAGCA 61181       G       CAA__
           CAG                    TTGTGT TGTGTTTCTC    TCCT
                                ||||||  ||||||||||    ||||
                                GACACG ACACGAAGAG    AGGG
                                    _       TCACG
GAM1710  PPT2     3'  TGGGAGGCGCATCTGCAG    18952     GT       T
                                TTGT  GTGTGTTTC CCA
                                ||||  |||||||| |||
                                GACG  TACGCGGAG GGT
                                  TC       _
GAM1710  PRAME    3'  GGCTTGGGAAGTACATGTAGGA 21487    G  TG      T   T
                                TT TG  TGTGTTTC CCAA CC
                                || ||  |||||||| |||| ||
                                AG AT  ACATGAAG GGTT GG
                                 G  GT       _   C
GAM1710  PRDM2    3'  GGGAATGGGGACGGTGTAT   32419     TG  _     A
                                GTG  TT TCTCCA TCCT
                                |||  || |||||| ||||
                                TAT  GG AGGGGT AGGG
                                  GT  C     A
GAM1710  PRDM2    5'  TTGGGGAGGTAAATATATGA  32421    TG    G  TT
                                T  TGTGT TG  TCTCCAA
                                |  |||||  ||  |||||||
```

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                                A  ATATA AT  AGGGGTT
                                 GT     A  GG
GAM1710  PRKWNK3   3'  AGGTTTCGAGACTTACATAT   62223        TT    C  T
                                GTGTGTG  TCTC AA CCT
                                |||||||  |||| || |||
                                TATACAT  AGAG TT GGA
                                    TC    C  T
GAM1710  PRNP      3'  AGGTCTTTGAAATATGCATGTA 6131     TG         TCCAAT
                                TG  TGTGTGTTTC     CCT
                                ||  ||||||||||     |||
                                AT  ACGTATAAAG     GGA
                                 GT         TTTCT_
GAM1710  PROC      3'  GGGACATTAAAGGGACATGTAA 6135      G  TG   TT  CCAA__
              CAA                  TTGT TG  TGT  CT     TCCT
                                |||| ||  |||  ||     ||||
                                AACA AT  ACA  GA     AGGG
                                  _  GT   GG  AATTAC
GAM1710  PSAP      3'  TGGGGGAATGAACGCACAG   69889         G
                                TTGTGTGT TGTTTCTCCA
                                |||||||| ||||||||||
                                GACACGCA GTAAGGGGGT
                                    A
GAM1710  PSEN1     5'  GGGGCGGCGGGGAAGCGTATAC 24621             AA__
                                GTGTGTGTTTCTCC    TCCT
                                ||||||||||||||   ||||
                                CATATGCGAAGGGG    GGGG
                                       CGGC
GAM1710  PSG1      5'  GGAGAACACACAAGCAG     23579      G       T
                                TTGT TGTGTGTT CTCC
                                |||| |||||||| ||||
                                GACG ACACACAA GAGG
                                  A      _
GAM1710  PSG11     5'  GGAGAACATGCACGCAG     12450           T
                                TTGTGTGTGTGTT CTCC
                                |||||||||||| ||||
                                GACGCACGTACAA GAGG
                                                _
GAM1710  PSG2      5'  GGAGAACACACAGGCAG     49189      G       T
                                TTGT TGTGTGTT CTCC
                                |||| |||||||| ||||
                                GACG ACACACAA GAGG
                                  G      _
GAM1710  PSG3      5'  GGAGAACACGCAGGCAG     41017      G       T
                                TTGT TGTGTGTT CTCC
                                |||| |||||||| ||||
                                GACG ACGCACAA GAGG
                                  G      _
GAM1710  PSG4      5'  GGAGAACACACAAGCAG     12443      G       T
                                TTGT TGTGTGTT CTCC
                                |||| |||||||| ||||
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                                GACG ACACACAA GAGG
                                  A      _
GAM1710  PSG6     5'  GGAGAACACACAGACAG     12447      G       T
                                TTGT TGTGTGTT CTCC
                                |||| |||||||| ||||
                                GACA ACACACAA GAGG
                                  G      _
GAM1710  PSG9     5'  GGAGAACACACAGGCAG     12449      G       T
                                TTGT TGTGTGTT CTCC
                                |||| |||||||| ||||
                                GACG ACACACAA GAGG
                                  G      _
GAM1710  PTGFR    3'  AGGAGTGAGAGAGATGTGTACA 8177        TG      _  A
             TA                   TGTGTG  TGTTTCTC CA TCCT
                                |||||| ||||||| || ||||
                                ATACAT  GTAGAGAG GT AGGA
                                   GT       A  G
GAM1710  PTGS1    5'  GGGCAGTGTGCGAGGCGCACGC 55476             TC_  AT_
             ACAG                  TTGTGTGTGTGTTTC   CA   CCT
                                |||||||||||||||   ||   |||
                                GACACGCACGCGGAG   GT   GGG
                                        CGT  GAC
GAM1710  PTGS2    3'  GGGAATTTGGGTTGTGTATGCG 8248        TG TT T   __
                                TGTGTG  T  C CCAA  TCCT
                                |||||| |  | ||||  ||||
                                GCGTAT  G  G GGTT  AGGG
                                   GT TT _    TA
GAM1710  PTK2B    3'  GGGGTGGGGAGGTGTCACATGG 15908    TG    T TG      AT
                                T  TGTG G  TTTCTCCA  CC
                                |  |||| |  ||||||||  ||
                                G  ACAC T  GGAGGGGT  GG
                                 GT    _ GT       GG
GAM1710  PTP4A2   3'  AGGGTAGAAGAGAGACATCGTG 14437     TG  T       CA__
             CAA                   TTG  TG GTGTTTCTC    ATCCT
                                |||  || |||||||||    |||||
                                AAC  GC TACAGAGAG    TGGGA
                                  GT  _        AAGA
GAM1710  PTPN11   5'  AGGATGCTTTGGACACTGTGCG 55494    TG  TG _     CTCCA
             TGG                   T  TG  T GTGTTT     ATCCT
                                |  ||  | ||||||     |||||
                                G  GC  G CACAGG     TAGGA
                                 GT  GT T     TTTCG
GAM1710  PTPN11   5'  AGGCCTGGAGGGGGGTCTGTGC 55495      TG  __ G TT    AT
             GCG                   TGTG  TG  T T  CTCCA  CCT
                                ||||  ||  | |  |||||  |||
                                GCGC  GT  G G  GAGGT  GGA
                                  GT  CT G GG    CC
GAM1710  PTPN2    5'  GGCGGGGCGCGGCGCGCAG   12581         _    TT T
                                TTGTGTGT GTGT  C CC
                                |||||||| ||||  | ||
```

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                                GACGCGCG CGCG  G GG
                                     G    GG C
GAM1710  PTPRJ    3'  AGGGCATGAAGCTGCATATGA  12618   TG     T    TCCAA
                                T  TGTGTG GTTTC    TCCT
                                |  |||||| |||||    ||||
                                A  ATACGT CGAAG    GGGA
                                 GT     _    TAC__
GAM1710  RAD9     5'  GGGCCGGCAGGGGCGGTGCGCG 17159     TG G   TT  _  AA   T
                                TGTG  T TGT  CT CC  TCC
                                ||||  | |||  || ||  |||
                                GCGC  G GCG  GA GG  GGG
                                  GT _   GG  C  CC
GAM1710  RAGE     5'  AGGGTGACAGGGACACAACATG 27250   TG   G    TT  CCA
              G                  T  TGT TGTGT  CT   ATCCT
                                |  ||| |||||  ||   |||||
                                G  ACA ACACA  GA   TGGGA
                                 GT   _    GG  CAG
GAM1710  RAI2     5'  GGGGTTCTCCACGCACACAG   41716          TTT__
                                TTGTGTGTGTG    CTCC
                                ||||||||||    ||||
                                GACACACGCAC    GGGG
                                      CTCTT
GAM1710  RALBP1   3'  GGTGGGAACTGCACACAA    23278         T    _
                                TTGTGTGTG GTTTCT CC
                                ||||||||| |||||| ||
                                AACACACGT CAAGGG GG
                                      _     T
GAM1710  RAMP3    3'  GGGGTTCCCAGGAGCCATGCGT 20728   TG     T     CC_
              GG                   T  TGTGTG GTTTCT   AATCCT
                                |  |||||| ||||||   ||||||
                                G  GCGTAC CGAGGA   TTGGGG
                                 GT     _     CCC
GAM1710  RANBP3   5'  AGGCTGCCGGGGATGCTGCACA 24629       T  T    AAT__
                                TGTGTG GT TCTCC    CCT
                                |||||| || |||||    |||
                                ACACGT CG AGGGG    GGA
                                    _ T    CCGTC
GAM1710  RASGRP1  3'  AGGGCCAAAGAGGTATAGTATA 20416       _   TT   CCAA
              CAA                  TTGTGTG TGTG  TCT    TCCT
                                |||||||  ||||  |||   ||||
                                AACATAT ATAT  AGA    GGGA
                                     G   GG   AACC
GAM1710  RASGRP2  3'  GGGATATGAGGGTGGCATGCA  20631       TT  _ _
                                TGTGTGT  CTC CA ATCCT
                                |||||||  ||| || |||||
                                ACGTACG  GGG GT TAGGG
                                     GT   A  A
GAM1710  RBP3     3'  TGGAGGTGTGTATATATA    12796        TG T
                                TGTGTGTG  T TCTCCA
                                ||||||||  | ||||||
```

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                                ATATATAT  G GGAGGT
                                    GT T
GAM1710  RDS     3'  GGGCCCAGGGACACCCACACAG 6151        T   TT  CCAA
                                TTGTGTG GTGT  CT   TCC
                                ||||||| ||||  ||   |||
                                GACACAC CACA  GA   GGG
                                    C   GG  CCC_
GAM1710  RENT1   3'  AGGCCGCGTAGAGGCATGCACC 12807    T         CCAAT_
           G                     TG GTGTGTGTTTCT     CCT
                                || ||||||||||||     |||
                                GC CACGTACGGAGA     GGA
                                _          TGCGCC
GAM1710  RGS16   3'  GGTTTAGGAAACATGTGGATAA 12871     G  TG      CC
                                TTGT TG  TGTTTCT  AATC
                                |||| ||  |||||||  ||||
                                AATA GT  ACAAAGG  TTGG
                                  G  GT      AT
GAM1710  RGS6    5'  GGGTGTGAAGCGCACACCGA   16280     T         TCCA
                                TTG GTGTGTGTTTC   ATCC
                                ||| ||||||||||    ||||
                                AGC CACACGCGAAG   TGGG
                                 _         TG__
GAM1710  RPA3    5'  AGGATGTGAAGACAATGCACAG 12902        G    C  CA
                                TTGTGTGT TGTTT TC  ATCCT
                                |||||||| ||||| ||  |||||
                                GACACGTA ACAGA AG  TAGGA
                                    _    _  TG
GAM1710  RPP30   3'  AGGAGAGAGGATACACATGTAA 22193     TG       T   CAA
                                TTG  TGTGTGTT CTC   TCCT
                                |||  |||||||| |||   ||||
                                AAT  ACACATAG GAG   AGGA
                                  GT       _   AG_
GAM1710  RPS20   5'  GGTCAGGAAGCCCGCGCGCAA  8278          T     ___
                                TTGTGTGTG GTTTCT   CC
                                ||||||||| ||||||   ||
                                AACGCGCGC CGAAGG   GG
                                    C      ACT
GAM1710  RPS6KA5  3'  GGGATCCATCTGAGATGCATGC 17650           TCCA__
                                GTGTGTGTTTC     ATCCT
                                ||||||||||      |||||
                                CGTACGTAGAG     TAGGG
                                     TCTACC
GAM1710  RRAD    3'  GGGCCCACAGAGATGCATGCGC 16049             CCAAT
           AG                    TTGTGTGTGTGTTTCT    CCT
                                ||||||||||||||||    |||
                                GACGCGTACGTAGAGA    GGG
                                     CACCC
GAM1710  RRM2    5'  AGGGTCGGAGGCATGGCACAG  8284        G    TT   A
                                TTGTGT TGTGT  CTCC ATCCT
                                |||||| |||||  |||| |||||
```

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                                GACACG GTACG  GAGG TGGGA
                                  _    __    C
GAM1710 RSN     3'  GGAAAAAAACATACACAA    12914          G   C
                                TTGTGTGTGT TTT TCC
                                |||||||||| ||| |||
                                AACACATACA AAA AGG
                                     A   A
GAM1710 RXRB    3'  TGGAGGAGCACACATCCAA   42032     TG
                                TTG  TGTGTGTTTCTCCA
                                |||  ||||||||||||||
                                AAC  ACACACGAGGAGGT
                                  CT
GAM1710 S100A5  5'  GGGATTGGGGACGTGTGTGC  12931    TG  TG T
                                G  TG  T TCTCCAATCCT
                                |  ||  | ||||||||||
                                C  GT  G AGGGGTTAGGG
                                 GT  GT C
GAM1710 SCAMP3  5'  GGGTTAGAGGTATCACGTGG  54518   TG   T   TT   CC
                                T  TGTG GTG  TCT  AATCC
                                |  |||| |||  |||  |||||
                                G  GCAC TAT  AGA  TTGGG
                                 GT   _  GG  __
GAM1710 SCML2   3'  GGGGTGACGATGGAACTATGTA 21429        TG _    _ CA_
             TATAG                 TTGTGTG  T GTTTC TC   ATCCT
                                |||||||  | ||||| ||   |||||
                                GATATAT  A CAAGG AG   TGGGG
                                     GT T    T  CAG
GAM1710 SCN1A   5'  TCCTTGGAGGAACATAGTATA  90268     _          TCCT
                                TGTG TGTGTTTCTCCAA
                                |||| ||||||||||||
                                ATAT ATACAAGGAGGTT
                                   G          CCTT
GAM1710 SCN3A   3'  TTGGGCAAATATATATATAG  23621             C
                                TTGTGTGTGTGTTT TCCAA
                                |||||||||||||| |||||
                                GATATATATATAAA GGGTT
                                          C
GAM1710 SCNN1G  3'  GGGGCCTGGGCATGCGCAGGA  8304     G        ___
                                TT TGTGTGTGTTT   CTCC
                                || ||||||||||   ||||
                                AG ACGCGTACGGG   GGGG
                                  G         TCC
GAM1710 SERPINB9 5' GGCTCGGAGCGCGGCACG    16023      G      T__
                                TGTGT TGTGTTTC   CC
                                ||||| ||||||||   ||
                                GCACG GCGCGAGG   GG
                                   _       CTC
GAM1710 SFRP5   5'  AGGGCCGGGGGCGCACGCCG  13031    T      TT   AA
                                TG GTGTGTGT  CTCC  TCCT
                                || ||||||||  ||||  ||||
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                                GC CGCACGCG  GGGG  GGGA
                                 _      __    CC
GAM1710  SH3BP4   5'  AGGAGCCGGCGGGGACGCCATG 27998       T   TT  _  AA_
            CGA                   TTGTGTG GTGT  CT CC   TCCT
                                  ||||||| ||||  || ||   ||||
                                  AGCGTAC CGCA  GG GG   AGGA
                                     _   GG  C  CCG
GAM1710  SH3GL1   3'  GGGGCGCAGAGATGAGCACACA 13096       G      CCAA   T
            G                    TTGTGTGT TGTTTCT    TCC
                                 |||||||| |||||||    |||
                                 GACACACG GTAGAGA    GGG
                                     A      CGCG
GAM1710  SIM1     3'  AGGATCTCTGAAACATATTTAT 18618      T       TCCA
            AG                    TTGTG GTGTGTTTC    ATCCT
                                  ||||| |||||||||    |||||
                                  GATAT TATACAAAG    TAGGA
                                     T        TCTC
GAM1710  SIP      3'  GGGGTTGACACATGAACAG    27734      G       T_
                                  TTGT TGTGTGTT  CTCC
                                  |||| ||||||||  ||||
                                  GACA GTACACAG  GGGG
                                    A       TT
GAM1710  SLA      3'  GGAGAAAACACAATGTATAG   23114       TG _     _
                                  TTGTG  T GTGTTT CTCC
                                  |||||  | |||||| ||||
                                  GATAT  A CACAAA GAGG
                                     GT A     A
GAM1710  SLC22A12  5'  TGGGAGGTGGGCACACAG    58693        G  TT  T
                                  TTGTGTGT TG  TC CCA
                                  |||||||| ||  || |||
                                  GACACACG GT  AG GGT
                                       G  GG  _
GAM1710  SLC22A5   3'  AGGAATGTGAGAAGCATATGC  13226           _  A
                                  GTGTGTGTTTCTC CA TCCT
                                  |||||||||||| || ||||
                                  CGTATACGAAGAG GT AGGA
                                           T  A
GAM1710  SLC24A1   3'  GGTTGGGATAGGCGCACGA    17563        G    TCT
                                  TTGTGTGT TGTT   CCAATC
                                  |||||||| ||||   ||||||
                                  AGCACGCG ATAG   GGTTGG
                                       G   ___
GAM1710  SLC25A11  5'  GGGAGAGCTGGAGGGGCGTGCG 14535      TG   TT    A___
            CGC                   GTGTG  TGT  CTCCA    TCCT
                                  |||||  |||  |||||    ||||
                                  CGCGC  GCG  GAGGT    AGGG
                                     GT   GG    CGAG
GAM1710  SLC2A2   3'  AGGCAAATTGGAAATACACAGA 6217    TG G       TC     ___
            TGA                   T  T TGTGTGTT  TCCAAT   CCT
                                  |  | ||||||||  ||||||   |||
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                                A  A ACACATAA  AGGTTA   GGA
                                 GT G       __      AAC
GAM1710 SLC2A3   3'  GGGATTGGCCGCTTGGCACATG 23643      G       TCT___
            ACAA                  TTGT TGTGTGTT     CCAATCCT
                                |||| ||||||||      ||||||||
                                AACA GTACACGG     GGTTAGGG
                                  _       TTCGCC
GAM1710 SLC39A1  3'  AGGAATATGGGGACATGGACAT 27806    TG   G    TT  CCAA
            GG                    T  TGT TGTGT  CT    TCCT
                                |  ||| |||||  ||    ||||
                                G  ACA GTACA  GG    AGGA
                                 GT   G    GG  TATA
GAM1710 SLC7A5   3'  GCTGCCGGAGGAGCATGCGCAG 14467    G            AATCCT
            AG                    TT TGTGTGTGTTTCTCC
                                || ||||||||||||||
                                GA ACGCGTACGAGGAGG
                                 G            CCGTCGG
GAM1710 SLC8A2   3'  AGGAGCGGGTGGGTGTGCGCGC 66932         TG  TC   AA
            AA                    TTGTGTGTG  TT  TCC  TCCT
                                |||||||||  ||  |||  ||||
                                AACGCGCGT  GG  GGG  AGGA
                                     GT  GT   CG
GAM1710 SLIT2    5'  GGGCGGTGGGAGGCGTGTGC   17725     TG     T   AT_
                                GTG  TGTTTC CCA   CCT
                                |||  |||||| |||   |||
                                CGT  GCGGAG GGT   GGG
                                  GT     _  GGC   A
GAM1710 SMAC     5'  AGGAGGAGGGACACGGCATGG  57994    TG   G    TT   AA
                                T  TGT TGTGT  CTCC  TCCT
                                |  ||| |||||  ||||  ||||
                                G  ACG GCACA  GAGG  AGGA
                                 GT   _    GG   __
GAM1710 SMARCD2  3'  AGGTATGGGGTATGTGCATGTG 13260    TG    TG   TT    AT
            G                     T  TGTG  TGT  CTCCA  CCT
                                |  ||||  |||  |||||  |||
                                G  GTAC  GTA  GGGGT  GGA
                                 GT   GT   T_    AT
GAM1710 SNAPAP   3'  GGGGCCCCAGGAAACCTACACA 25846         T     CCAA_
            CAG                     TTGTGTGTG GTTTCT     TCCT
                                |||||||| ||||||    ||||
                                GACACACAT CAAAGG     GGGG
                                     C     ACCCC
GAM1710 SNX9     3'  GGTCCGGGAAGCGTATCATAA  33123       T         CAAT
                                TTGTG GTGTGTTTCTC    CC
                                ||||| ||||||||||    ||
                                AATAC TATGCGAAGGG    GG
                                  _         CCT_
GAM1710 SORCS2   5'  GGGGGACGCGACGCACAA    40805         _    TT
                                TTGTGTGT GTGT  CTC
                                |||||||| ||||  |||
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                                AACACGCA CGCA  GGG
                                     G    GG
GAM1710  SORCS3   3'  TGCAGAAAGCATGCACAA    31074          G    C
                                TTGTGTGTGT TTTCT CA
                                |||||||||| ||||| ||
                                AACACGTACG AAAGA GT
                                      _    C
GAM1710  SPINT2   5'  GTTGGGAGGTGTAGCGCG    63852      G  TG   T
                                TGTGT TG  TTTC CCAAT
                                ||||| ||  |||| |||||
                                GCGCG AT  GGAG GGTTG
                                   _ GT   _
GAM1710  SPN      3'  AGGCTGGAGTGCAATGCACGA  13368        G   TT    AT
                                TTGTGTGT TGT  CTCCA  CCT
                                |||||||| |||  |||||  |||
                                AGCACGTA ACG  GAGGT  GGA
                                     _  T_    C_
GAM1710  SPOCK    5'  AGGCAGAAAGGAGTGCCTGCAC 63470       T TG    CCAAT
              AG                  TTGTGTG G  TTTCT    CCT
                                |||||||  |  |||||    |||
                                GACACGT C  GAGGA    GGA
                                    C GT    AAGAC
GAM1710  SPON1    3'  GGGGTTCAGAGGAGTATGTACA 63122     TG      C_
                                TGTG  TGTTTCTC  AATCCT
                                ||||  ||||||||  ||||||
                                ACAT  ATGAGGAG  TTGGGG
                                  GT       AC
GAM1710  SQLE     3'  GGAAGAGGATATATATAG    13390         G  TC
                                TTGTGTGTGT TT  TCC
                                |||||||||| ||  |||
                                GATATATATA GA  AGG
                                      G  GA
GAM1710  SSRP1    5'  GGGACGCGGGGCCGCGCACGCG 13420         TTT   AA_
                                TGTGTGTGTG   CTCC   TCCT
                                ||||||||||   ||||  ||||
                                GCGCACGCGC   GGGG   AGGG
                                      C__    CGC
GAM1710  STAC     3'  AGGACATGAGACATAGATACAG 13422      G      TCCAA
                                TTGTGT TGTGTTTC    TCCT
                                |||||| ||||||||    ||||
                                GACATA ATACAGAG    AGGA
                                    G       TAC__
GAM1710  STC1     3'  AGGTTATGAAACATATCATGG  13454   TG  T      TCCAAT
                                T  TG GTGTGTTTC     CCT
                                |  || |||||||||     |||
                                G  AC TATACAAAG     GGA
                                 GT  _       TATT__
GAM1710  STX1A    3'  AGGCAGGGAGATGCATGCG   17205       T    AAT
                                TGTGTGT TCTCC   CCT
                                ||||||| |||||   |||
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                                GCGTACG AGAGG   GGA
                                    T    GAC
GAM1710  SUDD    3'  GGATGAAAGGTATATATAA   15158        TG   _
                                TTGTGTGTG  TTTC TCC
                                |||||||||  |||| |||
                                AATATATAT  AAAG AGG
                                     GG   T
GAM1710  TARBP2   5'  GGGCGAGCCACGCACGCAG   16072         T  _
                                TTGTGTGTGTG TTC TCC
                                |||||||||||| ||| |||
                                GACGCACGCAC GAG GGG
                                      C  C
GAM1710  TARDBP   3'  GAAAAGGAGAGAGCGCGTGCAG 24788    TG    G     AATCCT
                                TTG  TGTGT TTTCTCC
                                |||  ||||| |||||||
                                GAC  GCGCG AGAGAGG
                                  GT    _     AAAAGA
GAM1710  TBX1    3'  AGGAGGTCAAGTGTGCATGCAA 55537        TG  CT  AA
                                TTGTGTGTG  TTT  CC  TCCT
                                |||||||||  |||  ||  ||||
                                AACGTACGT  GAA  GG  AGGA
                                     GT  CT  __
GAM1710  TCF2    3'  AGGATGAAAGGAGTGAATGTAT 6609      TG  _   A___
           A                     TGTG  TTT CTCC   ATCCT
                                ||||  ||| ||||   |||||
                                ATAT  AAG GAGG   TAGGA
                                  GT  T   AAAG
GAM1710  TCTA    5'  GGGGTTAGGTGCGCGTGCGCG  42502     TG    T  CC
                                TGTG  TGTGT TCT  AATCCT
                                ||||  ||||| |||  ||||||
                                GCGC  GCGCG GGA  TTGGGG
                                  GT    T  __
GAM1710  THBD    5'  AGATGAAAGAGGGCTGCACGCG 6274    TG     GT    CA__  CT
           TGG                    T  TGTGTGT  TTCTC   ATC
                                |  |||||||  |||||   |||
                                G  GCGCACG  GGGAG   TAG
                                 GT     TC    AAAG  A
GAM1710  THBS1   3'  GGAGGGCGCATACCCGA    13747    T      T
                                TTG GTGTGTGTT CTCC
                                ||| ||||||||| ||||
                                AGC CATACGCGG GAGG
                                  C       _
GAM1710  THBS1   3'  GGTGAAACTTACATACAA    13748        T    T
                                TTGTGTGTG GTTTC CC
                                ||||||||| ||||| ||
                                AACATACAT CAAAG GG
                                     T    T
GAM1710  TJP1    5'  AGATGCTGAGGAGTCCATGTGC 13759    TG   TG    CA_  CT
           AG                     TTG  TGTG  TTTCTC  ATC
                                |||  ||||  ||||||  |||
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                                GAC  GTAC  GAGGAG   TAG
                                  GT   CT    TCG   A
GAM1710  TMEFF1   5'  GGGAAGATAAAACAGGCACATA 14892       G    CTCCAA
            A                    TTGTGTGT TGTTT     TCCT
                                 |||||||| |||||     ||||
                                 AATACACG ACAAA     AGGG
                                     G    ATAGA_
GAM1710  TNC      5'  GGGAACTCGGGGGAACGCGCAC 10977   TG          AA__
            GTGG                   T  TGTGTGTGTTTCTCC   TCCT
                                 |  ||||||||||||||   ||||
                                 G  GCACGCGCAAGGGGG   AGGG
                                  GT           CTCA
GAM1710  TNFRSF10D 3'  AGGGTCGTTTTAGGCCACATGC 15201       T   CTCCA_
            G                    TGTGTGTG GTTT     ATCCT
                                 |||||||| ||||     |||||
                                 GCGTACAC CGGA     TGGGA
                                     _   TTTTGC
GAM1710  TNFRSF8   3'  AGGGCCTTCAGACGTGTATGCA 8795       TG    CTCCAA
            A                    TTGTGTG  TGTTT     TCCT
                                 |||||||  |||||     ||||
                                 AACGTAT  GCAGA     GGGA
                                     GT    CTTCC_
GAM1710  TNXB     5'  GGGGTTGGGGACAGAGCAGGTG 51635    TG G   GTT_
            CAG                   TTG  T TGT    TCTCCAATCCT
                                  |||  | |||   ||||||||||
                                  GAC  G ACG    AGGGGTTGGGG
                                    GT G   AGAC
GAM1710  TOMM22   3'  GGCGGGACATGCACACAA    40012          TT T
                                 TTGTGTGTGTGT  C CC
                                 ||||||||||||  | ||
                                 AACACACGTACA  G GG
                                       GG C
GAM1710  TOMM22   3'  GTTGTTGGGGCGGGACATGCAC 40013           __      CCT
            ACAA                   TTGTGTGTGTGTTT  CTCCAAT
                                   ||||||||||||||  |||||||
                                   AACACACGTACAGG  GGGGTTG
                                         GC      TTGA
GAM1710  TPM1     3'  GGGGTGGGGAAAACACATACAA 6296         G       AT
                                 TTGTGTGTGT TTTCTCCA  CC
                                 |||||||||| ||||||||  ||
                                 AACATACACA AAAGGGGT  GG
                                       _       GG
GAM1710  TPX1     5'  GGTGAGAGGGGCGCGCAGCAG  13844      G      TT  _  AT
                                 TTGT TGTGTGT  CTC CA  CC
                                 |||| |||||||  ||| ||  ||
                                 GACG ACGCGCG  GAG GT  GG
                                   _      GG   A  __
GAM1710  TRAF5    3'  GGGTCTGAAGGTGTATATACAA 17279        TG   C  CA
                                 TTGTGTGTG  TTT TC  ATCC
                                 |||||||||  ||| ||  ||||
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                                AACATATAT  GGA AG  TGGG
                                     GT   _  TC
GAM1710  TRAP240   3'  GTTGCAGAGTACATGTACA   18875     TG  _   C
                                TGTG  TGT TTCT CAAT
                                |||| ||| |||| ||||
                                ACAT  ACA GAGA GTTG
                                  GT   T   C
GAM1710  TRH     3'  GGGGTGGGACTGAAGCGTTGTG 24054      TG GT_    __  A
           TGCAA                  TTGTG  T   GTTTC  TCC ATCCT
                                |||||  |  |||||  ||| |||||
                                AACGT  G   CGAAG  AGG TGGGG
                                   GT TTG    TC   G
GAM1710  TRH     3'  TTGGAGAAGCATATGTAGGG   24055    G  TG
                                TT TG  TGTGTTTCTCCAA
                                || ||  ||||||||||||
                                GG AT  ATACGAAGAGGTT
                                 G  GT
GAM1710  TRHDE    3'  GGATGGGCATTATGCAA     26315       T     TC
                                TTGTGTG GTGTT  TCC
                                ||||||| |||||  |||
                                AACGTAT TACGG  AGG
                                    _    GT
GAM1710  TRIM9    5'  AGGCGAGAGGCGTACGTGTA   31443    TG         CAAT
                                TG  TGTGTGTTTCTC   CCT
                                ||  ||||||||||||   |||
                                AT  GCATGCGGAGAG   GGA
                                 GT          C___
GAM1710  TRPM6    3'  GGGTTGGGGGGGGATACAT    35034       G TT
                                GTGTGT T  CTCCAATCC
                                |||||| |  |||||||||
                                TACATA G  GGGGTTGGG
                                   _ GG
GAM1710  TSG     3'  GGTCATATGAGAAGCAGGTGCG 40605      TG G       CAAT__  T
           CAG                    TTGTG  T TGTTTCTC     CC
                                |||||  | ||||||||     ||
                                GACGC  G ACGAAGAG     GG
                                   GT G       TATACT
GAM1710  TSPY     3'  AGGCGAAAGGAGATCATACAT  82999       TT    AAT__
                                GTGTGTG  TCTCC    CCT
                                |||||||  |||||    |||
                                TACATAC  AGAGG    GGA
                                    T_    AAAGC
GAM1710  TUFT1    3'  GGAGGGAATGTACATTCAG   39675    T    TG   _
                                TTG GTGTG  TTTC TCC
                                ||| |||||  |||| |||
                                GAC TACAT  AAGG AGG
                                  T    GT   G
GAM1710  TXNRD1   3'  AGGGCATCGAAGGGATGCATCC 13920   TG  TG    TT  _ CAA_
           ATGA                   T  TG  TGTGT  CT C    TCCT
                                |  ||  |||||  || |   ||||
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                                A  AC  ACGTA  GA G    GGGA
                                 GT  CT     GG  A CTAC
GAM1710  UBASH3A   3'  GGCAGAAACCATGTGCAG    39050     TG    T     _
                                TTG  TGTG GTTTCT CC
                                |||  |||| |||||| ||
                                GAC  GTAC CAAAGA GG
                                  GT    _     C
GAM1710  UBE2L6    3'  GGGACAGTGGAGCATATGGGTG 16162    TG G        TCCAA
             G                   T  T TGTGTGTTTC     TCCT
                                |  | ||||||||||     ||||
                                G  G GTATACGAGG     AGGG
                                 GT G         TGAC_
GAM1710  UCP3      3'  GGGGTGCTATGACATGCAAGTG 13981    TG G       TCTCCA
             A                   T  T TGTGTGTT      ATCCT
                                |  | ||||||||      |||||
                                A  G ACGTACAG      TGGGG
                                 GT A       TATCG_
GAM1710  UFD1L     3'  TGGAGAAGCAAACATGTGA    73676    TG     G
                                T  TGTGT TGTTTCTCCA
                                |  ||||| ||||||||||
                                A  GTACA ACGAAGAGGT
                                 GT     A
GAM1710  UPF3A     3'  GGGATAAACTAGATATAGCATA 43733         _      CTCCA
             CAG                   TTGTGTG TGTGTTT     ATCCT
                                |||||||  |||||||     |||||
                                GACATAC ATATAGA     TAGGG
                                     G      TCAAA
GAM1710  USP11     5'  TGGGAGGCATACTGCAG     17386       T       T
                                TTGTG GTGTGTTTC CCA
                                |||||  ||||||||| |||
                                GACGT CATACGGAG GGT
                                   _       _
GAM1710  VCP       3'  GGGACCAGGGGTGCGCCCACAG 75890       T   TG TT  CCAA
                                TTGTG GTG  T  CT    TCCT
                                |||||  |||  |  ||    ||||
                                GACAC CGC  G  GA    AGGG
                                   C   GT GG  CC__
GAM1710  VCX       5'  GGGATCGCGAGAGGGGTATATA 69703          TG     CA_
             CAG                   TTGTGTGTG  TTTCTC   ATCCT
                                |||||||||  ||||||   |||||
                                GACATATAT  GGAGAG   TAGGG
                                     GG      CGC
GAM1710  VSNL1     3'  GGCAGAAATGTGCTGCAA     14083       T TG      _
                                TTGTG G  TGTTTCT CC
                                |||||  |  |||||||  ||
                                AACGT C  GTAAAGA GG
                                   _ GT      C
GAM1710  WNT14     3'  AGGGTGCAGGCATTGCACACG  14134         _    CTCCA
                                TGTGTGTG TGTTT     ATCCT
                                ||||||||  |||||     |||||
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                                GCACACGT ACGGA    TGGGA
                                    T    CG___
GAM1710  WNT14    3'  GGGGTACAGGCATTGCACACAG 14136        _   ___
                                TTGTGTGTG TGTTT  CTCC
                                ||||||||| |||||  ||||
                                GACACACGT ACGGA  GGGG
                                    T    CAT
GAM1710  WNT7A    5'  GGCGCGGAGCGCGCGGACG   17321    G       T__
                                TGT TGTGTGTTTC  CC
                                ||| ||||||||||  ||
                                GCA GCGCGCGAGG  GG
                                  G       CGC
GAM1710  WSX1     3'  AGGCTAGAGGGATGCTCATGCA 17913       T   TT  CAAT
           G                     TTGTGTG GTGT  CTC   CCT
                                ||||||| ||||  |||   |||
                                GACGTAC CGTA  GAG   GGA
                                    T   GG  ATC_
GAM1710  XDH      3'  GGAGGAACATACCACAG     6350       T
                                TTGTG GTGTGTTTCTCC
                                ||||| ||||||||||||
                                GACAC CATACAAGGAGG
                                  _
GAM1710  XPC      3'  AGGCAAACTGAGGCAGCATGCA 17331        _    TCCAAT
           CG                    TGTGTGTG TGTTTC     CCT
                                |||||||| ||||||     |||
                                GCACGTAC ACGGAG     GGA
                                    G     TCAAAC
GAM1710  ZFHX1B   3'  AGGAACTTGAAGTGATGCATGT 29605   TG  TG    T  C  __
           GTGA                    T  TG  TGTGTT CT CAA  TCCT
                                |  ||  |||||| || |||  ||||
                                A  GT  ACGTAG GA GTT  AGGA
                                 GT  GT     T  A   CA
GAM1710  ZHX1     3'  GGAAATCAGAAATGTTTATACA 24289       T TG    CCAA   T
           G                     TTGTGTG G  TTTCT   TCC
                                ||||||| |  |||||   |||
                                GACATAT T  AAAGA   AGG
                                    T GT    CTAA
GAM1710  ZIC3     3'  GGCAAGAGGCCATATATAG    14173        T    __
                                TTGTGTGTG GTTTCT  CC
                                |||||||| ||||||  ||
                                GATATATAC CGGAGA  GG
                                    _     AC
GAM1710  ZNF10    3'  AGGCATTAAAATATGTACACAA 31816       TG    CTCC  _
                                TTGTGTG  TGTTT   AAT CCT
                                |||||||  |||||   ||| |||
                                AACACAT  ATAAA   TTA GGA
                                    GT    A___   C
GAM1710  ZNF140   3'  GGAAAGAATACATATCCAA   14313    TG       C_
                                TTG  TGTGTGTTT  TCC
                                |||  |||||||||  |||
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                                AAC  ATACATAAG  AGG
                                  CT        AA
GAM1710  ZNF146   5'  TTGGGAGATCATACACAG    24080         T    T
                                TTGTGTGTG GTTTC CCAA
                                ||||||||| ||||| ||||
                                GACACATAC TAGAG GGTT
                                      _    _
GAM1710  ZNF266   3'  GGAAGGATACACATGGAG    89691    G        TC
                                TT TGTGTGTGTT  TCC
                                || ||||||||||  |||
                                GA GTACACATAG  AGG
                                 G         GA
GAM1710  ZNF278   5'  GGAGAGAGTGGCGCGCAG    50273        GTG
                                TTGTGTGT   TTTCTCC
                                ||||||||   |||||||
                                GACGCGCG   AGAGAGG
                                     GTG
GAM1710  ZNF43    3'  GGAAAAAGGTATATACACAA   14249          TT C__
                                TTGTGTGTGTG  T   TCC
                                ||||||||||  |   |||
                                AACACATATAT  A   AGG
                                      GG AAA
GAM1710  ABCA5    5'  AGGATTGGATTTATGTATGTCC 38533     TG    TG TTC
            AG                    TTG  TGTG  T   TCCAATCCT
                                ||| ||||  |   |||||||||
                                GAC  GTAT  A   AGGTTAGGA
                                  CT    GT TTT
GAM1710  ACAS2L   5'  AGGACTCCGGGGTGGGCGCG   68644        _    AA__
                                TGTGTTT CTCC    TCCT
                                ||||||| ||||    ||||
                                GCGCGGG GGGG    AGGA
                                    T    CCTC
GAM1710  AD024    3'  AGTTTTAGGGTACATGTGCACA 40710      TG    TT   C  TC
            A                     TTGTG  TGTGT  CTC AA  CT
                                |||||  |||||  ||| ||  ||
                                AACAC  GTACA  GGG TT  GA
                                   GT    T_   A  TT
GAM1710  AF9Q34   3'  GGACCCAGGCGCTGCATACAG  51719         _     C__
                                TTGTGTGT GTGTTT   TCC
                                ||||||| ||||||   |||
                                GACATACG CGCGGA   AGG
                                     T     CCC
GAM1710  AK5      3'  AGGTGTCTGGAAATCATGCATG 24928    TG     T     CCAAT
            G                     T  TGTGTG GTTTCT    CCT
                                |  |||||| ||||||    |||
                                G  ACGTAC TAAAGG    GGA
                                 GT     _     TCTGT
GAM1710  AKAP5    5'  AGGATTAGAGATGTATGTA   17954    TG  TG    CC
                                TG  TG  TTTCT  AATCCT
                                ||  ||  |||||  ||||||
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                                AT  AT  AGAGA  TTAGGA
                                 GT  GT    __
GAM1710 AKT3     3'  AGGGTGGTGGCGTGCATATGTA 19605     TG    TG T  T   A
             A                    TTG  TGTG  T TC CCA TCCT
                                  |||  ||||  | || ||| ||||
                                  AAT  ATAC  G GG GGT GGGA
                                    GT    GT C  T   _
GAM1710 AKT3     3'  GGGATATATATATATATATATA 19608           TTCTCCA
             A                    TTGTGTGTGTGT      ATCCT
                                  ||||||||||||      |||||
                                  AATATATATATA      TAGGG
                                         TATATA_
GAM1710 ALK7     3'  GGAAGAAATATATTACAA    76244       T        _
                                  TTGTG GTGTGTTTCT CC
                                  ||||| ||||||||| ||
                                  AACAT TATATAAAGA GG
                                     _        A
GAM1710 ALS2CR12 3'  AGGGTTTTCTTGAGAAAATGCA 58244          G     C____
             TATAA                   TTGTGTGTGT TTTCTC     AATCCT
                                  |||||||||| ||||||     ||||||
                                  AATATACGTA AAAGAG     TTGGGA
                                         _     TTCTT
GAM1710 APOL3    3'  GGAGGTGAGCCATACACA    27575        T   T  AA
                                  TGTGTGTG TTC CC  TCC
                                  |||||||| ||| ||  |||
                                  ACACATAC GAG GG  AGG
                                       C   T  __
GAM1710 APXL2    5'  AGGGTTGGGGAGGAAAGGAACA 75670   TG   GTGTG_
             TGG                     T  TGT     TTTCTCCAATCCT
                                  |  |||     ||||||||||||
                                  G  ACA     GGAGGGGTTGGGA
                                   GT   AGGAAA
GAM1710 ARHE     3'  AGTGATGAGAAGTGAATACATG 18974    TG    G GT    CA  _
             G                    T  TGTGT T  TTCTC  ATC CT
                                  |  ||||| |  |||||  ||| ||
                                  G  ACATA G  AAGAG  TAG GA
                                   GT     A TG     __   T
GAM1710 ARHGAP4  3'  GGGATGGGGCCGTGCACACAG  9796        TG  TTT    A
                                  TTGTGTG  TG   CTCCA TCCT
                                  |||||||  ||   ||||| ||||
                                  GACACAC  GC   GGGGT AGGG
                                       GT  C__    _
GAM1710 ARHGEF16 5'  GGAGGAAACGTGGGCACAA    27821       G GT    _
                                  TTGTGT T  GTTTC TCC
                                  ||||||  |  ||||| |||
                                  AACACG G  CAAAG AGG
                                     G TG    G
GAM1710 ARHU     5'  AGGGCCGGGGACGCGCCCGCA  41358     T    T    AA
                                  TGTG GTGT TCTCC  TCCT
                                  |||| |||| |||||  ||||
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                                ACGC CGCG AGGGG  GGGA
                                  C    C     CC
GAM1710 ARS2     5'  TGGGGTGACGCAGGCGCAG   32483       G     T    AATCCT
                                TTGTGT TGTGTT CTCC
                                |||||| |||||| ||||
                                GACGCG ACGCAG GGGG
                                   G     T      TC
GAM1710 ATIP1    3'  GGAGGAACGTGGGCACAA    40774       G GT
                                TTGTGT T  GTTTCTCC
                                |||||| |  ||||||||
                                AACACG G  CAAGGAGG
                                   G TG
GAM1710 ATP6M8-9 3'  GGGACATTTTGAGGCATGAATA 20467       G       TCCAA_
           TAA                    TTGTGT TGTGTTTC     TCCT
                                |||||| ||||||||     ||||
                                AATATA GTACGGAG     AGGG
                                   A       TTTTAC
GAM1710 ATP6V1B2 3'  GGGGTTGGGGGAGTCAGCAT   9886      GTG
                                GTGT   TTTCTCCAATCCT
                                ||||   ||||||||||||
                                TACG   GAGGGGGTTGGGG
                                  ACT
GAM1710 B3GNT5   3'  AGGAGATGTAGAAAAATGTGTA 50248      TG   G    C  A_
           CAA                    TTGTG  TGT TTTCT CA  TCCT
                                |||||  ||| ||||| ||  ||||
                                AACAT  GTA AAAGA GT  AGGA
                                   GT   A    T  AG
GAM1710 BA526D8.4 5' AGGGTTTATGCAGGAATATGCA 70905          C ____
           C                     GTGTGTGTTTCT CA   ATCCT
                                |||||||||||| ||   |||||
                                CACGTATAAGGA GT   TGGGA
                                      C  ATT
GAM1710 BBP      5'  GGACTGGGTACATGCATAT    50139         TT T   A
                                GTGTGTGTGT  C CCA TCC
                                ||||||||||  | ||| |||
                                TATACGTACA  G GGT AGG
                                      T_ _   C
GAM1710 BCoR     3'  AGGTTGCTTGGAAATGTACATA 40886       TG    C__    CT
                                TGTGTG  TTTCT   CAATC
                                ||||||  |||||   |||||
                                ATACAT  AAAGG   GTTGG
                                   GT    TTC    A
GAM1710 BHC80    5'  GGGGGATATGATATGCAG    34015        _   TT
                                TTGTGTGT GTGT  CTC
                                |||||||| ||||  |||
                                GACGTATA TATA  GGG
                                     G   GG
GAM1710 BIRC2    5'  GGGAAAGAAGCCTGCATATAA  67780         T     CCAA
                                TTGTGTGTG GTTTCT    TCCT
                                ||||||||| ||||||    ||||
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                                AATATACGT CGAAGA    AGGG
                                     C     A___
GAM1710 BNIP-S    5'  AGGTAAGAGAAGCATCTGTATA 57099      GT T        CAAT
              G                   TTGT  G GTGTTTCTC    CCT
                                  ||||  | |||||||||    |||
                                  GATA  T TACGAAGAG    GGA
                                    TG C        AAT_
GAM1710 BRD2      5'  GGGGTGGGGGGGGAAGCGGGCAC 18797    TG     G        A__
              GTGA                  T  TGTGT TGTTTCTCC   ATCCT
                                  |  ||||| |||||||||   |||||
                                  A  GCACG GCGAAGGGG   TGGGG
                                   GT     G        GGG
GAM1710 BSPECV    3'  GGGTGAAGAGGAGACGTGTTAC 34046      T TG     _  CA_    T
              G                   TGTG G  TGTTTC TC   ATCC
                                  |||| |  |||||| ||   ||||
                                  GCAT T  GCAGAG AG   TGGG
                                    _ GT     G  AAG
GAM1710 C1orf9    3'  GAGGTAATACATATGTGA    33161    TG        _
                                  T  TGTGTGTGTT TCTC
                                  |  |||||||||| ||||
                                  A  GTATACATAA GGAG
                                   GT         T
GAM1710 C1QTNF6   3'  AGGCGGGGAGAGATGTGTACAT 49986        TG        AAT
              AG                    TTGTGTG  TGTTTCTCC   CCT
                                  |||||||  |||||||||   |||
                                  GATACAT  GTAGAGAGG   GGA
                                      GT        GGC
GAM1710 C1QTNF7   3'  GGCGGAAACATCACATACAA   50005         _      _
                                  TTGTGTGTG TGTTTCT CC
                                  |||||||||| ||||||| ||
                                  AACATACAC ACAAAGG GG
                                        T      C
GAM1710 C20orf140 3'  GGAAGGAGGAACGCTGCACAG  58893        T        AA
                                  TTGTGTG GTGTTTCTCC  TCC
                                  ||||||| ||||||||||  |||
                                  GACACGT CGCAAGGAGG  AGG
                                     _         A_
GAM1710 C20orf172 3'  GGAAAGAGAAGCATGCAACAA  46767      G          CAA
                                  TTGT TGTGTGTTTCTC   TCC
                                  |||| ||||||||||||   |||
                                  AACA ACGTACGAAGAG   AGG
                                    _          AA_
GAM1710 C20orf18  5'  GGGACAGCGAGGCACACACAGG 49181    G          TCCAA
              G                    TT TGTGTGTGTTTC     TCCT
                                  || ||||||||||||     ||||
                                  GG ACACACACGGAG     AGGG
                                   G          CGAC_
GAM1710 C20orf28  3'  GGGGTTGGGGGGCACGGTACGC 31846       _    TT T
                                  GTGTGT GTGT  C CCAATCCT
                                  |||||| ||||  | ||||||||
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                                CGCATG CACG  G GGTTGGGG
                                   G   GG _
GAM1710  C20orf51  3'  GGAGACCAGGCGCGCCATGG  42288   TG  T     ___
                                T  TG GTGTGTT   TCTCC
                                |  || |||||||   |||||
                                G  AC CGCGCGG   AGAGG
                                 GT  _      ACC
GAM1710  C21orf100 3'  GGGGAAATGTGGACACAG    59506       G  TG
                                TTGTGT TG  TTTCTCC
                                ||||||| ||  |||||||
                                GACACA GT  AAAGGGG
                                   G  GT
GAM1710  C21orf57  3'  GGGAGCCGGGGTCGCACACG  75300        TT   AA_
                                TGTGTGT  CTCC   TCCT
                                |||||||  ||||   ||||
                                GCACACG  GGGG   AGGG
                                    CT   CCG
GAM1710  C21orf62  5'  GAGTGGACGCACATACAG    39464            _
                                TTGTGTGTGTGTTT CTC
                                |||||||||||||| |||
                                GACATACACGCAGG GAG
                                         T
GAM1710  C21orf62  5'  TGGGGACATGCAACAA      39465      G     TT
                                TTGT TGTGTG  TCTCCA
                                |||| ||||||  ||||||
                                AACA ACGTAC  AGGGGT
                                  _     ___
GAM1710  C22orf5   3'  GGAAGAAATCTATATATGA   25342    TG     T     _
                                T  TGTGTG GTTTCT CC
                                |  |||||| |||||| ||
                                A  ATATAT TAAAGA GG
                                 GT     C     A
GAM1710  C22orf5   3'  GGCAGAGGCCTGCATGTGG   25343    TG     T     _
                                T  TGTGTG GTTTCT CC
                                |  |||||| |||||| ||
                                G  GTACGT CGGAGA GG
                                 GT     C     C
GAM1710  C22orf5   3'  GGGACGGGAACATGTGCCCGA  25344     T TG       CCAA
                                TTG G  TGTGTTTCT    TCCT
                                |||  |  |||||||||    ||||
                                AGC C  GTACAAGGG    AGGG
                                  C GT        C____
GAM1710  C2F       3'  GGGGTGGTGGTAGCGGCACATA 22010           TT  _  ___
            CACAA                   TTGTGTGTGTGT  CT CCA  ATCCT
                                |||||||||||  || |||  |||||
                                AACACATACACG  GA GGT  TGGGG
                                       GC  T   GG
GAM1710  C6.1A     3'  GGAACAGACACATACGTCAA   44534      _         C_
                                TTG TGTGTGTGTTT  TCC
                                ||| ||||||||||  |||
```

```
                                AAC GCATACACAGA  AGG
                                  T         CA
GAM1710  C6orf33   5'  GGCTGGGCTACGCGCACG    56717        TTC    AT
                                TGTGTGTGT   TCCA  CC
                                |||||||||   ||||  ||
                                GCACGCGCA   GGGT  GG
                                     TC_    CG
GAM1710  CAMKK1    3'  GGGGTGCTGGAGCGCGTGCA   51154    TG      TCCA
                                TG  TGTGTTTC    ATCCT
                                ||  ||||||||    |||||
                                AC  GCGCGAGG    TGGGG
                                 GT       TCG_
GAM1710  CAMP-GEFII 3'  GGATGAGATGTGCTACAA    23810      T TG     _
                                TTGTG G  TGTTTC TCC
                                ||||| |  |||||| |||
                                AACAT C  GTAGAG AGG
                                   _ GT     T
GAM1710  CAMTA2    3'  AGGGCCGAAGGGGAGGTGGTGT 61880       TG _ TT    AA___
            ACATA                   TGTGTG  T G  TCTCC    TCCT
                                |||||| | |  |||||    ||||
                                ATACAT  G T  AGGGG    GGGA
                                    GT G GG    AAGCC
GAM1710  CAP350    3'  AGGAAATGAGTGTGTGCACCAA 29702     T    TG TT   CAA
                                TTG GTGTG  T  CTC   TCCT
                                ||| |||||  |  |||   ||||
                                AAC CACGT  G  GAG   AGGA
                                  _    GT T_   TAA
GAM1710  CAP350    3'  GGTTAGAAGCATGATACAA    29708       G       __
                                TTGTGT TGTGTTTCT  CC
                                |||||| |||||||||  ||
                                AACATA GTACGAAGA  GG
                                   _       TT
GAM1710  CAPS2     3'  GGGGTGCTCAATATGCATATAG 71128           TCTCCA
                                TTGTGTGTGTGTT     ATCCT
                                ||||||||||||      |||||
                                GATATACGTATAA     TGGGG
                                        CTCG__
GAM1710  CARD9     3'  GGAGGAGCTGCACGCACAG    54478          _
                                TTGTGTGTGT GTTTCTCC
                                |||||||||| ||||||||
                                GACACGCACG CGAGGAGG
                                      T
GAM1710  CASP9     3'  GGGATTTTTGGCTACACACAA  8775          T   TCTCC
                                TTGTGTGTG GTT     AATCCT
                                ||||||||| |||     ||||||
                                AACACACAT CGG     TTAGGG
                                     _  TTT__
GAM1710  CBLN1     5'  GGCGGCGGACGTGCGCACG    16368       TG    _ _
                                TGTGTG  TGTTT CT CC
                                ||||||  ||||| || ||
```

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                                GCACGC  GCAGG GG GG
                                   GT    C  C
GAM1710  CBLN1    5'  GGGGCTCCGGGAACACAGCGCG 16370      G       CCAA
                                TGTGT TGTGTTTCT   TCCT
                                ||||| |||||||||   ||||
                                GCGCG ACACAAGGG   GGGG
                                  _       CCTC
GAM1710  CBX1     5'  AGGCGTGAGGAGGCGCATACG  23309          TC  AT
                                TGTGTGTGTTTC  CA  CCT
                                ||||||||||||  ||  |||
                                GCATACGCGGAG  GT  GGA
                                       GA  GC
GAM1710  CCR5     3'  AGGAGGGAGGTATTCGTGCA   6960     TG  T  T    AA
                                TG  TG GT TCTCC  TCCT
                                ||  || || |||||  ||||
                                AC  GC TA GGAGG  AGGA
                                 GT  T  T    G_
GAM1710  CCR7     3'  GGGATGACATGCACTCAG    10225     T       TC
                                TTG GTGTGTGTT  TCC
                                ||| |||||||||  |||
                                GAC CACGTACAG  GGG
                                  T       TA
GAM1710  CD109    3'  GGGGTTGCAGGGATGGTGTACA 56863      TG G   TT  C
            A                    TTGTG  T TGT  CT CAATCCT
                                 |||||  | |||  || |||||||
                                 AACAT  G GTA  GA GTTGGGG
                                    GT _   GG  C
GAM1710  CDC14A   3'  TGGGGCTTTAAAATACAGCATG 53968       _     _____   AATCCT
            CAG                    TTGTGTG TGTGTTT    CTCC
                                   |||||||  |||||||    ||||
                                   GACGTAC ACATAAA    GGGG
                                      G      ATTTC      TC
GAM1710  CDC16    5'  AGGGTGCAGGAGGCGCGCGC   15335          CCA
                                   GTGTGTGTTTCT   ATCCT
                                   ||||||||||||   |||||
                                   CGCGCGCGGAGG   TGGGA
                                          ACG
GAM1710  CDIPT    5'  AGGTTCCCGGAAGCCACGCGCA 21972         T     CCAAT
            G                      TTGTGTGTG GTTTCT    CCT
                                   |||||||||  ||||||    |||
                                   GACGCGCAC CGAAGG    GGA
                                        _     CCCTT
GAM1710  CEACAM8  5'  GGAGAACACGCAGGCAG     10183      G       T
                                   TTGT TGTGTGTT CTCC
                                   |||| |||||||| ||||
                                   GACG ACGCACAA GAGG
                                     G       _
GAM1710  CECR7    3'  AGGATTGGGGAGGTGGATGC   80445      G  TT
                                   GTGT TG  TCTCCAATCCT
                                   |||| ||  ||||||||||
```

```
                                CGTA GT  AGGGGTTAGGA
                                  G  GG
GAM1710 CEP3     5'  GGGATCGGGAGAGGTGGGCGCA 22248        G  TT    A_
             CGA                   TTGTGTGT TG  TCTCC  ATCCT
                                |||||||| ||  |||||  |||||
                                AGCACGCG GT  AGAGG  TAGGG
                                    G  GG    GC
GAM1710 CGI-142  5'  AGGCCCGCGGGGAGCGCGGCGC 32690       G        CAAT_
             AA                   TTGTGT TGTGTTTCTC    CCT
                                |||||| ||||||||||    |||
                                AACGCG GCGCGAGGGG    GGA
                                   _       CGCCC
GAM1710 CGI-96   3'  GGGCTGGGAGCATGTGTGTGCA 32294    TG  TG  _  T  AT
                                TG  TG  TGT TTC CCA  CC
                                ||  ||  ||| ||| |||  ||
                                AC  GT  GTA GAG GGT  GG
                                 GT  GT   C  _  CG
GAM1710 CGI-96   3'  TTCCTGATGGAATGCGCACACA 32297            TC  ATCCT
             G                    TTGTGTGTGTGTTTC  CA
                                |||||||||||||||  ||
                                GACACACGCGTAAGG  GT
                                         TA  CCTTC
GAM1710 CGR11    3'  GGGCAGGGGAAATGTACGC    22691      TG      AA
                                GTGTG  TTTCTCC  TCC
                                |||||  |||||||  |||
                                CGCAT  AAAGGGG  GGG
                                   GT      AC
GAM1710 CHERP    3'  AGGCTCCAGGAGGAGCATGTGC 22127    G  TG        AAT__
             AGGA                   TT TG  TGTGTTTCTCC    CCT
                                || ||  ||||||||||    |||
                                AG AC  GTACGAGGAGG    GGA
                                 G  GT         ACCTC
GAM1710 CHK      3'  GGGAAGACGAAATATAGTGCAA 8887      TG G      _  CAA
                                TTG  T TGTGTTTC TC   TCCT
                                |||  | ||||||| ||   ||||
                                AAC  G ATATAAAG AG   AGGG
                                  GT _       C  A__
GAM1710 CHRFAM7A 3'  GGGTAAGGAACAATGCACACAG 96722          _    CCA
                                TTGTGTGTGT GTTTCT   ATCC
                                |||||||||| ||||||   ||||
                                GACACACGTA CAAGGA   TGGG
                                     A     A__
GAM1710 CLSTN1   5'  AGGAGCCCGGGAGCGCGCGTAG 30783    G          CCAA
             GG                   TT TGTGTGTGTTTCT    TCCT
                                || ||||||||||||    ||||
                                GG ATGCGCGCGAGGG    AGGA
                                 G          CCCG
GAM1710 CLSTN1   3'  AGGATGGGGGGTACTGTGTA   30784    TG  T  T    A
                                TG  TG GT TCTCC ATCCT
                                ||  || || ||||| |||||
```

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                                AT  GT CA GGGGG TAGGA
                                 GT  _ T    G
GAM1710  CLSTN2   3'  AGGAATTAGAAGCATATTTGCA 42398      T        CCAA
              A                   TTGTG GTGTGTTTCT    TCCT
                                  ||||| ||||||||||    ||||
                                  AACGT TATACGAAGA    AGGA
                                    T         TTA_
GAM1710  CLSTN3   3'  GGGGCCCCGGGTGTACATATAT 28880          TT   CCAA
              AA                   TTGTGTGTGTG  TCT    TCCT
                                   ||||||||||  |||    ||||
                                   AATATATACAT  GGG    GGGG
                                         GT   CCCC
GAM1710  CREB-H   3'  AGGACCCGGGAAATACACACAG 51866    G           CAA
              AG                   TT TGTGTGTGTTTCTC   TCCT
                                   || ||||||||||||||   ||||
                                   GA ACACACATAAAGGG   AGGA
                                    G            CCC
GAM1710  CREB-H   3'  GCAAAGAGCAGACACACATACA 51878            _   CAATCCT
              G                    TTGTGTGTGTGTTT CTC
                                   |||||||||||||| |||
                                   GACATACACACAGA GAG
                                           C   AAACGA
GAM1710  CREB3    3'  GGGCTCAAACACACCACAA    22068       T       C__
                                   TTGTG GTGTGTTT   TCC
                                   ||||| ||||||||   |||
                                   AACAC CACACAAA   GGG
                                     _       CTC
GAM1710  CRMP5    5'  GGCCCCCGAGCGAGCGCGCGTG 39704     TG        _   CAAT_  T
              CAG                    TTG  TGTGTGTTT CTC     CC
                                     |||  ||||||||| |||     ||
                                     GAC  GCGCGCGAG GAG     GG
                                      GT        C   CCCCC
GAM1710  CSMD1    5'  AGGGTTGGTGCAAATGTACA   53786      TG   CT_
                                   TGTG  TTT   CCAATCCT
                                   ||||  |||   ||||||||
                                   ACAT  AAA   GGTTGGGA
                                     GT   CGT
GAM1710  CTPS2    3'  AGGATGGCAGGGAACATGC    39563           __   A
                                   GTGTGTTTCT  CCA TCCT
                                   ||||||||||  ||| ||||
                                   CGTACAAGGG  GGT AGGA
                                         AC   _
GAM1710  CXYorf1  5'  AGGGCATCAGACACAGGTACAG 82902       TG       CTCCAA
                                   TTGTG  TGTGTTT     TCCT
                                   |||||  |||||||     ||||
                                   GACAT  ACACAGA     GGGA
                                     GG      CTAC__
GAM1710  DDX39    3'  AGGTCCTCTGGGAAGTGTCGCA 20543        T TG    T   AT___
              CAA                    TTGTGTG G  TTTC CCA     CCT
                                     ||||||| |  |||| |||     |||
```

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                                AACACGC T  GAAG GGT    GGA
                                   _ GT   _  CTCCT
GAM1710 DEPP     3' AGGGCTGGGAATTGCGCATGTG 23804   TG     GT  T  AT
           A                    T  TGTGTGT  TTC CCA  CCT
                                |  |||||||  ||| |||  |||
                                A  GTACGCG  AAG GGT  GGA
                                 GT      TT  _  CG
GAM1710 DGS-A    3' GGAGCGGGCAGTGCACACAA  86052        _   _
                                TTGTGTGTG TGTTT CTCC
                                ||||||||| ||||| ||||
                                AACACACGT ACGGG GAGG
                                     G    C
GAM1710 DJ102H19.4 5' GGGATTGGGGTGCAAGTGCACA 42242      TG G  TT
           G                    TTGTG  T TGT  CTCCAATCCT
                                |||||  | |||  ||||||||||
                                GACAC  G ACG  GGGGTTAGGG
                                   GT A  T_
GAM1710 dJ309H15.1 3' GGGAAAAGGGGCAGCATGTGG  57571   TG   G  TT  CCAA
                                T  TGTGT TGT  CT   TCCT
                                |  ||||| |||  ||   ||||
                                G  GTACG ACG  GA   AGGG
                                 GT    _  GG  AA__
GAM1710 DKFZP434C171 3' GGGGTTGGGGGGGAGTGTGGACA 32195     G  TG G TT
           A                    TTGT TG  T T  CTCCAATCCT
                                |||| ||  | |  ||||||||||
                                AACA GT  G A  GGGGTTGGGG
                                  G  GT _ GG
GAM1710 DKFZP434C212 3' AGGTCAAGAAATCCATGTACAG 69481     TG  TG   CCAAT
                                TTGTG  TG  TTTCT   CCT
                                |||||  ||  |||||   |||
                                GACAT  AC  AAAGA   GGA
                                   GT  CT   ACT__
GAM1710 DKFZP434F1735 5' GGCAGGAACAGGCATGCAG   32116       G    _
                                TTGTGTGT TGTTTCT CC
                                |||||||| ||||||| ||
                                GACGTACG ACAAGGA GG
                                     G     C
GAM1710 DKFZP434G072 5' GGGAAAATAAACACACCACAA  50501     T     CTCCAA
                                TTGTG GTGTGTTT     TCCT
                                ||||| ||||||||     ||||
                                AACAC CACACAAA     AGGG
                                   _       TAAA__
GAM1710 DKFZP434G1415 3' AGGAAGAGAAGCTATATGCAA  49268        T     CAA
                                TTGTGTGTG GTTTCTC   TCCT
                                ||||||||| |||||||   ||||
                                AACGTATAT CGAAGAG   AGGA
                                     _     A__
GAM1710 DKFZP434I092 3' AGGATGGAATCAAACAATATGC 68411       G   C__   A
           AA                    TTGTGTGT TGTTT   TCCA TCCT
                                ||||||||| |||||   |||| ||||
```

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                                AACGTATA ACAAA   AGGT AGGA
                                     _    CTA   _
GAM1710  DKFZp434J1015 3'  GGGGCTGAAACAGCACACG   94211       G     TCCAA
                                TGTGTGT TGTTTC    TCC
                                ||||||| ||||||    |||
                                GCACACG ACAAAG    GGG
                                     _    TCG__
GAM1710  DKFZP434K0427 3'  GGAAGAAAATACACGACAA   50499     _     G    _
                                TTGT GTGTGT TTTCT CC
                                |||| |||||| ||||| ||
                                AACA CACATA AAAGA GG
                                  G     _    A
GAM1710  DKFZp434K2435 3'  AGGTAGAGAAGCCGTGCATGA  51044   TG  TG  T      CAAT
                                T  TG  TG GTTTCTC    CCT
                                |  ||  || |||||||    |||
                                A  AC  GC CGAAGAG    GGA
                                 GT  GT  _      AT__
GAM1710  DKFZp434N035 3'  AGGCGGCGCGGGAGCGCGCGCA 51060            ___  AAT
                                TGTGTGTGTTTCT   CC   CCT
                                ||||||||||||   ||   |||
                                ACGCGCGCGAGGG   GG   GGA
                                       CGC  C__
GAM1710  DKFZp547D155 3'  AGGGCAATGAGTGTGCACATAC 70943         TG TT   CAA_
            AA                   TTGTGTGTG  T  CTC    TCCT
                                |||||||||  |  |||    ||||
                                AACATACAC  G  GAG    GGGA
                                     GT T_   TAAC
GAM1710  DKFZp547D155 3'  AGGTTCAAGGGAGCGTGCACCA 70944     T   TG      CCAAT
            G                    TTG GTG  TGTTTCT     CCT
                                ||| |||  |||||||     |||
                                GAC CAC  GCGAGGG     GGA
                                  _  GT      AACTT
GAM1710  DKFZp547D155 3'  TGGGGCAGTGTGCATGCAA    70951         TG  T
                                TTGTGTGTG  TT CTCCA
                                |||||||||  || |||||
                                AACGTACGT  GA GGGGT
                                     GT  C
GAM1710  DKFZP547E1010 3'  GGGTTGGTTTATACTGCAA    32175      T    TTTCT
                                TTGTG GTGTG     CCAATCC
                                |||||| |||||     |||||||
                                AACGT CATAT     GGTTGGG
                                   _     TT___
GAM1710  DKFZp547G183 3'  AGGAAATGAGACAGCACGTGA  38638    TG    G     TCCAA
                                T  TGTGT TGTTTC     TCCT
                                |  ||||| ||||||     ||||
                                A  GCACG ACAGAG     AGGA
                                 GT     _      TAA__
GAM1710  DKFZp547G183 3'  GGGGCAACTGAGTCATGCGCG  38648         T____   T
                                TGTGTGTG     GTT CTCC
                                ||||||||     ||| ||||
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                                GCGCGTAC    CAA GGGG
                                    TGAGT   C
GAM1710  DKFZp547H236 5'  GGGGCCGGGGTCCATGCGCG   79249       TTT   AA
                                TGTGTGTG  CTCC  TCCT
                                ||||||||  ||||  ||||
                                GCGCGTAC  GGGG  GGGG
                                    CT_   CC
GAM1710  DKFZp547H236 5'  GGGGTGGGGGGGCGCGCGC   79250       TT    AT  T
                                GTGTGTGT  CTCCA  CC
                                ||||||||  |||||  ||
                                CGCGCGCG  GGGGT  GG
                                    GG    GG
GAM1710  DKFZp547I224 3'  GGATCAAATTCACACATAA   39958        T   C_
                                TTGTGTGTG GTTT  TCC
                                |||||||| ||||  |||
                                AATACACAC TAAA  AGG
                                     T    CT
GAM1710  DKFZp547I224 5'  GGGGCAGGGCACACACAA    39959        G  T
                                TTGTGTGTGT TT CTCC
                                |||||||||| || ||||
                                AACACACACG GA GGGG
                                     G  C
GAM1710  DKFZp547O146 5'  GGGGTTGGGGAGACTATGTCGC 39967    _   T
                                GTG TGTG GTTTCTCCAATCCT
                                ||| |||| ||||||||||||||
                                CGC GTAT CAGAGGGGTTGGGG
                                  T   _
GAM1710  DKFZP564C1940 5'  GGGACGAGAAGTGCGTGTATGA 26745   TG  TG  TG    CAA
                                T  TG  TG  TTTCTC   TCCT
                                |  ||  ||  ||||||   ||||
                                A  AT  GC  GAAGAG   AGGG
                                 GT  GT  GT    C__
GAM1710  DKFZP564F0522 3'  GGAAGAAATGCACTACAA    69138      T       _
                                TTGTG GTGTGTTTCT CC
                                ||||| |||||||||| ||
                                AACAT CACGTAAAGA GG
                                   _        A
GAM1710  DKFZP564K247 5'  GGACTGGGTGCGCCTGCA    26766     T   TT T   A
                                TGTG GTGT  C CCA TCC
                                |||| ||||  | ||| |||
                                ACGT CGCG  G GGT AGG
                                  C   T_ _  C
GAM1710  DKFZP564O0823 3'  GAAAGGGAGAGGCATGTACG   60257     TG       AA_
                                TGTG  TGTTTCTCC   TC
                                ||||  |||||||||   ||
                                GCAT  ACGGAGAGG   AG
                                  GT        GAA
GAM1710  DKFZP566I1024 3'  AGGATTGCAAACACACAAACAA 70646     G       CTC
                                TTGT TGTGTGTTT   CAATCCT
                                |||| |||||||||   |||||||
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                                AACA ACACACAAA   GTTAGGA
                                  A        C__
GAM1710  DKFZP566K1924 5'  GGGATTGTGGTGCGTAAACA   74200     G     TT TC
                                TGT TGTGT  C  CAATCCT
                                ||| |||||  |  |||||||
                                ACA ATGCG  G  GTTAGGG
                                  A    T_ GT
GAM1710  DKFZP586F1318 5'  AGGAATTGAGACACATTTACAG 32248       T        TCCAA
                                TTGTG GTGTGTTTC     TCCT
                                ||||| |||||||||     ||||
                                GACAT TACACAGAG     AGGA
                                   T        TTA__
GAM1710  DKFZP727G051 5'  GGGAAAGAGAGAGGCTGTGTGT 70011    TG  TG _  G     CAA
            GG                    T  TG  T GT TTTCTC   TCCT
                                |  ||  | || ||||||   ||||
                                G  GT  G CG AGAGAG   AGGG
                                 GT  GT T  G     AA_
GAM1710  DKFZp761D0614 3'  AGGGTTTTAGATGTGTACACA  88944       TG T   CC
                                TGTGTG  T TCT  AATCCT
                                ||||||  | |||  ||||||
                                ACACAT  G AGA  TTGGGA
                                   GT T   TT
GAM1710  DKFZP761I2123 3'  GGCGGGGACACGCTCACAG    49548      T     TT  _
                                TTGTG GTGTGT  CT CC
                                ||||| ||||||  || ||
                                GACAC CGCACA  GG GG
                                   T     GG  C
GAM1710  DKFZp761K1423 3'  AGGATTTAAAATATGTATATGA 37934    TG    TG    CTCC
                                T  TGTG  TGTTT    AATCCT
                                |  ||||  |||||    ||||||
                                A  ATAT  ATAAA    TTAGGA
                                 GT    GT    AT__
GAM1710  DKFZp761N0624 3'  AGGAGGCAAAGCCACGCGTGG  51158    TG     T    CT  AA
                                T  TGTGTG GTTT  CC  TCCT
                                |  |||||| ||||  ||  ||||
                                G  GCGCAC CGAA  GG  AGGA
                                 GT     _    AC  __
GAM1710  DKFZp761P1010 3'  GGGGTTGGAGGAGAACTATAAC 37944     GTGT  G
            G                    TGT    GT TTTCTCCAATCCT
                                |||    || ||||||||||||||
                                GCA    CA GAGGAGGTTGGGG
                                  ATAT  A
GAM1710  DKFZp762K2015 3'  GGAGAGAATAGCACATGCAA   72893          G__
                                TTGTGTGTGT   TTTCTCC
                                ||||||||||   |||||||
                                AACGTACACG   AGAGAGG
                                      ATA
GAM1710  DKFZp762K222 5'  GGGGCTGGGAAAATGTGCGCA  71672      TG    CT   AT
                                TGTG  TGTTT  CCA  CCT
                                ||||  |||||  |||  |||
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                                ACGC  GTAAA  GGT  GGG
                                  GT    AG   CG
GAM1710  DNAJB11   3'  AGGAGCAAAAGAAACACAATAT 33305       G       CCAA_
             AG                   TTGTGT TGTGTTTCT     TCCT
                                  |||||| |||||||||     ||||
                                  GATATA ACACAAAGA     AGGA
                                    _       AAACG
GAM1710  DNAJC6    3'  AGGATTTCTGGATTTATACGTA 29490        TT   CC_
                                  TGTGTGTG  TCT   AATCCT
                                  ||||||||  |||   ||||||
                                  ATGCATAT  AGG   TTAGGA
                                       TT   TCT
GAM1710  DRIL2     3'  TGGGAGACACCGCGCG      22356       T      T
                                  TGTGTG GTGTTTC CCA
                                  |||||| ||||||| |||
                                  GCGCGC CACAGAG GGT
                                    _      _
GAM1710  DRIM      5'  GGGGCTCAAGCCGCACGTGA   27955    TG     T   ___
                                  T  TGTGTG GTTT   CTCC
                                  |  |||||| ||||   ||||
                                  A  GCACGC CGAA   GGGG
                                   GT     _    CTC
GAM1710  DUSP14    3'  GGGACATAAAGGGAATGCATAC 23819            CCAA__
             AT                    GTGTGTGTGTTTCT     TCCT
                                   ||||||||||||||     ||||
                                   TACATACGTAAGGG     AGGG
                                         AAATAC
GAM1710  DZIP1     5'  AGGGTTCTGGGTGCACGC    30701       T   CC
                                  GTGTGT TCT  AATCCT
                                  |||||| |||  ||||||
                                  CGCACG GGG  TTGGGA
                                     T   TC
GAM1710  DZIP1     5'  GGGGTTCTAGGGACGTATAC   30704        TT  CC
                                  GTGTGTGT  CT  AATCCT
                                  ||||||||  ||  ||||||
                                  CATATGCA  GA  TTGGGG
                                       GG  TC
GAM1710  EAT2      3'  GGGAGTGATGGAGATGCATACA 80054       T     A___
                                  TGTGTGT TCTCCA    TCCT
                                  ||||||| ||||||    ||||
                                  ACATACG AGAGGT    AGGG
                                     T     AGTG
GAM1710  EBNA1BP2  5'  AGGTGTGGGACGTGCGTGCGG  23345    TG  TG   TCT   AT
                                  TTG  TG  TGTT   CCA  CCT
                                  |||  ||  ||||   |||  |||
                                  GGC  GC  GCAG   GGT  GGA
                                    GT  GT   ___   GT
GAM1710  EDG2      5'  GGGGTGTTTGGGGGCGCGCGTG 9176     TG     TT  CCA_
             CGA                    TTG  TGTGTGT  CT    ATCCT
                                    |||  |||||||  ||    |||||
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                                AGC  GCGCGCG  GG    TGGGG
                                  GT      GG  TTTG
GAM1710  EFS2     5'  GGGAGGCCGCGGGGACAGCACG 20777        G   TT  CCAA__
              CAG                    TTGTGTGT TGT  CT     TCCT
                                |||||||| |||  ||     ||||
                                GACGCACG ACA  GG     AGGG
                                    _  GG  CGCCGG
GAM1710  EIF4ENIF1 3'  AGGGTTCTGAGGAAATAAATGT 39527      TG G     TC __
              ATAG                   TTGTG  T TGTTTC  CA  ATCCT
                                ||||||  | ||||||  ||  |||||
                                GATAT  A ATAAAG  GT  TGGGA
                                   GT A     GA  CT
GAM1710  EIF5     5'  GTATTGGGGAAACATAGCATAC 10509        _          CCT
              AA                     TTGTGTG TGTGTTTCTCCAAT
                                ||||||| ||||||||||||||
                                AACATAC ATACAAAGGGGTTA
                                    G           TG
GAM1710  ELAC1    3'  AGGCCCATTGAGATACACAGCA 92618      G        TCCAAT
              A                      TTGT TGTGTGTTTC     CCT
                                |||| ||||||||||     |||
                                AACG ACACATAGAG     GGA
                                  _        TTACCC
GAM1710  ELF1     3'  GGACTTGGGGGGGGTTGCATAC 71951         TG TT    _  T
              AA                     TTGTGTGTG  T  CTCCAA TCC
                                |||||||||  |  |||||| |||
                                AACATACGT  G  GGGGTT AGG
                                     TG GG     C
GAM1710  EML4     3'  GTAATAGGAGAAATATAAATAC 39324       G        AATCCT
              AG                     TTGTGT TGTGTTTCTCC
                                ||||||| ||||||||||
                                GACATA ATATAAAGAGG
                                   A         ATAATGA
GAM1710  EPN2     3'  GGGATTTTTAACAAACATGCAC 31042         CTCC__
                                GTGTGTGTTT     AATCCT
                                ||||||||||     ||||||
                                CACGTACAAA     TTAGGG
                                     CAATTT
GAM1710  EPN3     5'  GGAGGCAAACGCACGCGGGA   36090    G       __
                                TT TGTGTGTGTT  TCTCC
                                || ||||||||||  |||||
                                AG GCGCACGCAA  GGAGG
                                  G         AC
GAM1710  ERAP140  3'  GGGTATATAGAGATATATGTGT 75706    TG        CCA_   T
                                G  TGTGTGTTTCT    ATCC
                                |  ||||||||||    ||||
                                T  GTATATAGAGA    TGGG
                                 GT          TATA
GAM1710  ERO1L    3'  AGGATTATCAAATTCATATATG 28155    TG     T    CTCC
              A                      T  TGTGTG GTTT    AATCCT
                                |  |||||| ||||    ||||||
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                                A  ATATAC TAAA    TTAGGA
                                 GT     T    CTA_
GAM1710  ESDN     5'  GGTGAGGAGCGCGGCGCG    56059       G         CAAT
                                TGTGT TGTGTTTCTC    CC
                                ||||| ||||||||||    ||
                                GCGCG GCGCGAGGAG    GG
                                   _        T___
GAM1710  EZF-2    3'  GGGGTTGGGGGAGGCAGCGGGT 37679    TG G   G       _
              GA                  T  T TGT TGTTTCTCC AATCCT
                                | | ||| ||||||||| ||||||
                                A  G GCG ACGGAGGGG TTGGGG
                                 GT G   _        G
GAM1710  EZFIT    5'  GGCCTCGGGGAGACGGCGTGCA 41379     TG   G       AAT_  T
              G                   TTG  TGT TGTTTCTCC    CC
                                |||  ||| |||||||||    ||
                                GAC  GCG GCAGAGGGG    GG
                                  GT   _       CTCC
GAM1710  FABP7    5'  GGGACACTGGAGGGGTGTGTTT 9345       TG  TG TT    A__
              GCAA                  TTGTG  TG  T  CTCCA   TCCT
                                |||||  ||  |  |||||   ||||
                                AACGT  GT  G  GAGGT   AGGG
                                   TT  GT GG    CAC
GAM1710  FBL      3'  AGGATTGCGAGAGATGTGTGT  9322    TG  TG     _
                                G  TG  TTTCTC CAATCCT
                                |  ||  |||||| |||||||
                                T  GT  AGAGAG GTTAGGA
                                 GT  GT     C
GAM1710  FBXO24   3'  TGGGAGGCCCTGGACATGCTGC 25150      T      _____     AATCCT
              AG                    TTGTG GTGTGTT     TCTCC
                                |||||  |||||||     |||||
                                GACGT  CGTACAG     GGAGG
                                   _      GTCCC     G   TC
GAM1710  FBXO9    3'  GGTGAAATGTGCATACAG    54252        TG     T
                                TTGTGTG  TGTTTC CC
                                |||||||  |||||| ||
                                GACATAC  GTAAAG GG
                                    GT     T
GAM1710  FER1L4   3'  GGGGTTGGAGCATGACAAGCA  48126     G    T__
                                TGT TGTT   CTCCAATCCT
                                ||| ||||   ||||||||||
                                ACG ACAG   GAGGTTGGGG
                                  A    TAC
GAM1710  FHX      3'  AGGGTAGGATCATACATGCAA  37919          TTTC   A
                                TTGTGTGTGTG    TCC ATCCT
                                ||||||||||    ||| |||||
                                AACGTACATAC    AGG TGGGA
                                       T___   A
GAM1710  FLJ00024 3'  GGGTTGGGGTCGCCCGCG    64499      T  TT
                                TGTG GT  CTCCAATCC
                                |||| ||  |||||||||
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                                GCGC CG  GGGGTTGGG
                                  C  CT
GAM1710  FLJ10094  3'  GGGTTGGTCCCGCACGCA    36297        TTTCT
                                TGTGTGTG    CCAATCC
                                ||||||||    |||||||
                                ACGCACGC    GGTTGGG
                                     CCT__
GAM1710  FLJ10193  3'  GGGTCTCGGAATGGGCGCATAA 57361        G     TCCA
                                TTGTGTGT TGTTTC    ATCC
                                |||||||| ||||||    ||||
                                AATACGCG GTAAGG    TGGG
                                     G     CTC_
GAM1710  FLJ10335  3'  GGAAAAAATACATATATAG    36511           C_
                                TTGTGTGTGTGTTT  TCC
                                ||||||||||||||  |||
                                GATATATACATAAA  AGG
                                        AA
GAM1710  FLJ10483  3'  GGGATATTCATAAGCATATATC 36655     T        CTCCA_
           AA                     TTG GTGTGTGTTT      ATCCT
                                ||| ||||||||||      |||||
                                AAC TATATACGAA      TAGGG
                                  _         TACTTA
GAM1710  FLJ10490  3'  GGGATGCAGGACAGACACACAG 36670        G    T  CCA
                                TTGTGTGT TGTT CT   ATCCT
                                |||||||| |||| ||   |||||
                                GACACACA ACAG GA   TAGGG
                                     G    _  CG_
GAM1710  FLJ10520  5'  AGGAAGAAGGGGACACTTGTAC 36698      GT T    TT  CCAA
           AA                     TTGT  G GTGT  CT    TCCT
                                ||||  | ||||  ||    ||||
                                AACA  T CACA  GG    AGGA
                                  TG T    GG  AAGA
GAM1710  FLJ10563  5'  GGACTTGAGCAGGCACGCG    36805        G     C__
                                TGTGTGT TGTTT   TCC
                                ||||||| |||||   |||
                                GCGCACG ACGAG   AGG
                                     G     TTC
GAM1710  FLJ10563  5'  GGGAAGAGAGAGTGCGCGCG   36806        TG G      CAA
                                TGTGTG  T TTTCTC   TCCT
                                ||||||  | ||||||   ||||
                                GCGCGC  G AGAGAG   AGGG
                                   GT _      A__
GAM1710  FLJ10597  3'  GGGAAGTGGGGAGCATGGCGCA 36838        G       T   A_
           A                      TTGTGT TGTGTTTC CCA  TCCT
                                |||||| |||||||| |||  ||||
                                AACGCG GTACGAGG GGT  AGGG
                                   _       _  GA
GAM1710  FLJ10597  3'  GGGGTTGGGGGAGTAGTGGGGC 36839        GTG__
           ACGG                     TTGTGT    TGTTTCTCCAATCCT
                                ||||||    ||||||||||||||||
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                                GGCACG    ATGAGGGGGTTGGGG
                                   GGGTG
GAM1710  FLJ10620  3'  GGGGTTGGTTTCCTGTATATAT 36864        TTTCT__
             AT                  GTGTGTGTG      CCAATCCT
                                 |||||||||      ||||||||
                                 TATATATAT      GGTTGGGG
                                     GTCCTTT
GAM1710  FLJ10647  3'  GGAGGGGGCAGCATGCA     36885        T   AA
                                 TGTGTGTT CTCC  TCC
                                 |||||||| ||||  |||
                                 ACGTACGA GGGG  AGG
                                     C   G_
GAM1710  FLJ10648  3'  GGCTTTAGAAATATATACCAG  36893     T         ____
                                 TTG GTGTGTGTTTCT   CC
                                 ||| ||||||||||||   ||
                                 GAC CATATATAAAGA   GG
                                   _         TTTC
GAM1710  FLJ10726  3'  TGTAGAGTGCATATACAG    37044        TG  T  C
                                 TTGTGTGTG  TT CT CA
                                 |||||||||  || || ||
                                 GACATATAC  GA GA GT
                                     GT  _  T
GAM1710  FLJ10743  3'  GGATGAGGCATGGGTATAG   37087      TG      _
                                 TTGTG  TGTGTTTC TCC
                                 |||||  |||||||| |||
                                 GATAT  GTACGGAG AGG
                                    GG       T
GAM1710  FLJ10829  5'  GGGATTACAGGCACGTGCCAA  37260     T TG      CTCC
                                 TTG G  TGTGTTT    AATCCT
                                 ||| |  |||||||    ||||||
                                 AAC C  GCACGGA    TTAGGG
                                   _ GT      CA__
GAM1710  FLJ10856  3'  GGGATTTTGGAGTATGTACATG 37325   TG    TG  TTT    __
             A                    T  TGTG  TG   CTCCA  ATCCT
                                  |  ||||  ||   |||||  |||||
                                  A  ACAT  AT   GAGGT  TAGGG
                                  GT    GT  ___     TT
GAM1710  FLJ10874  3'  GGAGGAACAGCATGTAA     37326     TG   G
                                 TTG  TGT TGTTTCTCC
                                 |||  ||| |||||||||
                                 AAT  ACG ACAAGGAGG
                                   GT   _
GAM1710  FLJ10891  3'  AGGATTGGGCCAGGCGTGT   37338   TG   G  TTTC
                                 G  TGT TG    TCCAATCCT
                                 |  ||| ||    |||||||||
                                 T  GCG AC    GGGTTAGGA
                                  GT   G  C___
GAM1710  FLJ11017  3'  GGGATTGGGGAGGCTGGCCA  37545    T  GT
                                 TG GT  GTTTCTCCAATCCT
                                 || ||  ||||||||||||||
```

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                                AC CG  CGGAGGGGTTAGGG
                                 _ GT
GAM1710  FLJ11042  3'  AGGTTACAGAGAAAAGTATATG 37561    TG   TG    CAAT_
            TAA                   TTG  TGTG  TTTCTC    CCT
                                ||| ||||  ||||||    |||
                                AAT  ATAT  AAAGAG    GGA
                                  GT   GA    ACATT
GAM1710  FLJ11151  3'  AGGAAAAGTGGGAATGTATGCA 68468   G    TG    CCAA_
            GAG                   TT TGTGTG  TTTCT    TCCT
                                || ||||||  |||||    ||||
                                GA ACGTAT  AAGGG    AGGA
                                 G     GT    TGAAA
GAM1710  FLJ11218  3'  GGGAAAAAATACACACACACAA 37759          TTCTCCAA
                                TTGTGTGTGTGT       TCCT
                                ||||||||||||       ||||
                                AACACACACACA       AGGG
                                       TAAAAA__
GAM1710  FLJ11320  3'  GGGAGTGGGGGACACACACA   37830        TT T   A
                                TGTGTGTGT  C CCA TCCT
                                |||||||||  | ||| ||||
                                ACACACACA  G GGT AGGG
                                     GG _   G
GAM1710  FLJ11539  3'  AGGAGAGGGGGACGCGCGCGGG 45705    G       TT T  AA
            G                    TT TGTGTGTGT  C CC  TCCT
                                || |||||||||  | ||  ||||
                                GG GCGCGCGCA  G GG  AGGA
                                 G       GG _  AG
GAM1710  FLJ11618  3'  GGGAGAGGGGCGTGTGCATGG  42625   TG   TG   TT   CAA
                                T  TGTG  TGT  CTC   TCCT
                                |  ||||  |||  |||   ||||
                                G  ACGT  GCG  GAG   AGGG
                                 GT   GT   GG   ____
GAM1710  FLJ11700  3'  GGATGCAGACACACCATGG   46564   TG  T      CTCCA
                                T  TG GTGTGTTT    ATCC
                                |  || ||||||||    ||||
                                G  AC CACACAGA    TAGG
                                 GT  _       CG____
GAM1710  FLJ12056  3'  AGGATTGGGTCCCACATA    46815       TTT T
                                TGTGTG   C CCAATCCT
                                ||||||   | ||||||||
                                ATACAC   G GGTTAGGA
                                    CCT _
GAM1710  FLJ12221  3'  AGGGTTGGGGAAGTCCTCGC   63218     TGTG
                                GTG   TTTCTCCAATCCT
                                |||   ||||||||||||
                                CGC   GAAGGGGTTGGGA
                                  TCCT
GAM1710  FLJ12221  3'  GGGGTTGGGGGACACAGACGCG 63222       G    TT T
            A                    TTGTGT TGTGT  C CCAATCCT
                                ||||||  |||||  | ||||||||
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                                AGCGCA ACACA  G GGTTGGGG
                                   G    GG _
GAM1710  FLJ12294  3'  GGTTAAGAAATTATACATGCG  47719          _    CC
                                TGTGTGTGTG TTTCT  AATC
                                |||||||||| |||||  ||||
                                GCGTACATAT AAAGA  TTGG
                                      T    A_
GAM1710  FLJ12294  3'  GTTAGGAGAAAGACATACATAA 47720          G      AATCCT
                                TTGTGTGTGT TTTCTCC
                                |||||||||| |||||||
                                AATACATACA AAAGAGG
                                      G      ATTGA
GAM1710  FLJ12529  3'  AGGATTGGAGAGGCACAT    46082
                                GTGTGTTTCTCCAATCCT
                                ||||||||||||||||||
                                TACACGGAGAGGTTAGGA

GAM1710  FLJ12529  3'  GGAAAAATATATATAGAA    46087    G        C
                                TT TGTGTGTGTTT TCC
                                || |||||||||| |||
                                AA ATATATATAAA AGG
                                 G         A
GAM1710  FLJ12568  3'  TGGGGTTGGACTTAAAAACACA 47144            C____
           CATACAA               TTGTGTGTGTGTTT    TCCAATCCT   G
                                |||||||||||||    |||||||||  |
                                AACATACACACAAA    AGGTTGGGG   T
                                      AATTC
GAM1710  FLJ12610  5'  GGGCAGGAAAGCGTGCGTGCG  45861    TG  TG    C   AA
                                TG  TG  TGTTT TCC  TCC
                                ||  ||  ||||| |||  |||
                                GC  GC  GCGAA AGG  GGG
                                 GT  GT    _   AC
GAM1710  FLJ12649  3'  GGGCACACAGAAATGCACACA  45095           CCAAT
                                TGTGTGTGTTTCT    CCT
                                ||||||||||||    |||
                                ACACACGTAAAGA    GGG
                                       CACAC
GAM1710  FLJ12687  5'  AGGGTTGGCTGCGCGTGCGGCG 46745    _ TG    TTCT
                                TGT G  TGTGT    CCAATCCT
                                ||| |  |||||   ||||||||
                                GCG C  GCGCG    GGTTGGGA
                                  G GT    TC__
GAM1710  FLJ12704  5'  GGAGTAAATACACAGATAA   47170     G       _
                                TTGT TGTGTGTTT CTCC
                                |||| ||||||||| ||||
                                AATA ACACATAAA GAGG
                                  G       T
GAM1710  FLJ12783  3'  AGGCAGCTGAGAGGCAGCGTGC 49483    TG   G      CAAT_
           AG                   TTG  TGT TGTTTCTC    CCT
                                |||  ||| ||||||||    |||
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                                GAC  GCG ACGGAGAG    GGA
                                  GT  _      TCGAC
GAM1710  FLJ12875  3'  GTTGGAGGTCACATACACAG  44919         TT
                                TTGTGTGTGTG  TCTCCAAT
                                ||||||||||  ||||||||
                                GACACATACAC  GGAGGTTG
                                      T_
GAM1710  FLJ12895  5'  GGTCCCGGGGATGCAGCGCG  43927     G  T   AAT_
                                TGTGT TGT TCTCC   CC
                                ||||| ||| |||||   ||
                                GCGCG ACG AGGGG   GG
                                   _  T    CCCT
GAM1710  FLJ12969  5'  GGCTGGGCCCATGCACAG   43411       T  TTCT  AT
                                TTGTGTGTG GT   CCA  CC
                                |||||||| ||   |||  ||
                                GACACGTAC CG   GGT  GG
                                     C  ____  CG
GAM1710  FLJ12975  3'  AGGCTGGAGTGCAGTGCACAA  70184     TG G  TT   AT
                                TTGTG  T TGT  CTCCA  CCT
                                |||||  | |||  |||||  |||
                                AACAC  G ACG  GAGGT  GGA
                                   GT _  T_   C_
GAM1710  FLJ13063  5'  GGGGCGGGGCACGGCACGA   72300      _   G TT
                                TTGTGT GTGT T  CTCC
                                ||||||  ||||  |  ||||
                                AGCACG CACG G  GGGG
                                    G   G GC
GAM1710  FLJ13153  3'  GTACTGGGAAATGGGCATACAG 45924       G    T  ATCCT
                                TTGTGTGT TGTTTC CCA
                                ||||||||  ||||||  |||
                                GACATACG GTAAAG GGT
                                     G    _  CATGA
GAM1710  FLJ13153  3'  TACTGGGAAATGGGCATACAG  45925       G    T  ATCCT
                                TTGTGTGT TGTTTC CCA
                                ||||||||  ||||||  |||
                                GACATACG GTAAAG GGT
                                     G    _  CATG
GAM1710  FLJ13195  3'  GGGAAAAGAAATACATAT   43551         CCAA
                                GTGTGTGTTTCT   TCCT
                                ||||||||||||   ||||
                                TATACATAAAGA   AGGG
                                      AA__
GAM1710  FLJ13197  3'  AATTTGAAGAAGTGTGTGCACA 45169     TG  TG   C  TCCT
           A                    TTGTG  TG  TTTCT CAA
                                |||||  ||  ||||| |||
                                AACAC  GT  GAAGA GTT
                                   GT  GT   A  TAAG
GAM1710  FLJ13291  3'  GGGGCCAAGAAACAATATATAT 50741   TG    _    CCAA  T
           GA                    T  TGTGTGT GTTTCT   TCC
                                |  ||||||| ||||||   |||
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                                A  ATATATA CAAAGA    GGG
                                 GT      A     ACCG
GAM1710  FLJ13305  5'  GGGGTGGATGAACATGCACCGA 91715     T        C    AT
                                TTG GTGTGTGTTT TCCA  CC
                                ||| |||||||||| ||||  ||
                                AGC CACGTACAAG AGGT  GG
                                  _        T   GG
GAM1710  FLJ13315  3'  GGACTGAGCACATGCCAA    47198     T        C_
                                TTG GTGTGTGTTT  TCC
                                ||| ||||||||||  |||
                                AAC CGTACACGAG  AGG
                                  _        TC
GAM1710  FLJ13322  5'  GGGAGTTGGAGATGTGCAC    45632     TG T     _
                                GTG  T TCTCCAA TCCT
                                |||  | ||||||| ||||
                                CAC  G AGAGGTT AGGG
                                  GT T      G
GAM1710  FLJ13391  5'  GGTTGGGAGAGATATGTAGCG  50747     G  TG       AAT
                                TGT TG  TGTTTCTCC   CC
                                ||| ||  |||||||||   ||
                                GCG AT  ATAGAGAGG   GG
                                  _ GT       GTT
GAM1710  FLJ13646  3'  GATGAAGGAGACATATAT    45029          CCA
                                GTGTGTGTTTCT   ATC
                                ||||||||||||   |||
                                TATATACAGAGG   TAG
                                       AAG
GAM1710  FLJ13782  3'  GGAGATTGATATATGTACAA   46702      TG     __
                                TTGTG  TGTGTT  TCTCC
                                |||||  ||||||  |||||
                                AACAT  ATATAG  AGAGG
                                   GT     TT
GAM1710  FLJ13842  3'  AGGATTCACAGATTCACATACG 45331        TT   CC_
                                TGTGTGTG  TCT   AATCCT
                                ||||||||  |||   ||||||
                                GCATACAC  AGA   TTAGGA
                                     TT   CAC
GAM1710  FLJ13855  3'  AGTTGAGGAAATATATGCACAG 43844            TC   CCT
                                TTGTGTGTGTGTTTC  CAAT
                                ||||||||||||||  ||||
                                GACACGTATATAAAG  GTTG
                                         GA   A
GAM1710  FLJ13855  3'  GAGTTGAGGAAATATATGCACA 43851            TC   CCT
            G                    TTGTGTGTGTGTTTC  CAAT
                                ||||||||||||||  ||||
                                GACACGTATATAAAG  GTTG
                                         GA   AG
GAM1710  FLJ13902  3'  GGGAAGGCCTGGGTGTGTGCAC 45381      TG  TG   CT_  AA
            AA                   TTGTG  TG  TTT   CC  TCCT
                                |||||  ||  |||   ||  ||||
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                              AACAC  GT  GGG   GG  AGGG
                                 GT  GT   TCC  A_
GAM1710  FLJ13940  5'  GTTGGAATGCATACACA     47310         TTC
                              TGTGTGTGT   TCCAAT
                              |||||||||   ||||||
                              ACACATACG   AGGTTG
                                   TA_
GAM1710  FLJ14100  3'  AGGAAGGGAGCGTGCTTGCAG  47327      T TG  TTT    AA
                              TTGTG G  TG   CTCC  TCCT
                              ||||| |  ||   ||||  ||||
                              GACGT C  GC   GAGG  AGGA
                                 T GT  ____   GA
GAM1710  FLJ14124  3'  GGCAGGTGCGCACACGTGA   46359   TG       T   _
                              T  TGTGTGTGT TCT CC
                              |  |||||||||| ||| ||
                              A  GCACACGCG GGA GG
                               GT        T   C
GAM1710  FLJ14124  5'  TGGAGGAGCTCGTGCACG    46361     TG  T
                              TGTG  TG GTTTCTCCA
                              ||||  || |||||||||
                              GCAC  GC CGAGGAGGT
                                 GT  T
GAM1710  FLJ14166  3'  GGGTTGGGGGACACATTG    44989    T     TT T
                              G GTGTGT  C CCAATCC
                              | ||||||  | |||||||
                              G TACACA  G GGTTGGG
                               T     GG _
GAM1710  FLJ14393  5'  GGTTACAGAGAGTCGCACACGT 52306   TG      T    CAAT_  T
            GG                   T  TGTGTGTG TTCTC     CC
                              |  |||||||| |||||     ||
                              G  GCACACGC GAGAG     GG
                               GT       T    ACATT
GAM1710  FLJ14440  3'  GGGATTGGAGAAAGACAAATGT 52369   TG   G   G
            GG                   T  TGT TGT TTTCTCCAATCCT
                              |  ||| ||| ||||||||||||
                              G  GTA ACA AAAGAGGTTAGGG
                               GT   A   G
GAM1710  FLJ14566  5'  GGAGGGCGGCACACACATGG   52501   TG       __
                              T  TGTGTGTGTT  TCTCC
                              |  ||||||||||  |||||
                              G  ACACACACGG  GGAGG
                               GT        CG
GAM1710  FLJ14906  3'  GGAAAGAGATATGTAAACAA   52762     G  TG     CCAA
                              TTGT TG  TGTTTCT    TCC
                              |||| ||  |||||||    |||
                              AACA AT  ATAGAGA    AGG
                                 A  GT      A___
GAM1710  FLJ20126  3'  AGGGTATGGAGAGATGGTATAC 35076        TGT       _
            AG                   TTGTGTG   GTTTCTCCA ATCCT
                              |||||||   ||||||||| |||||
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                                GACATAT   TAGAGAGGT TGGGA
                                   GG_       A
GAM1710  FLJ20184  3' AGGATTATGTGAGATAACACGT 35197   TG    G     TCC_
             GG                  T  TGTGT TGTTTC    AATCCT
                                 |  ||||| ||||||    ||||||
                                 G  GCACA ATAGAG    TTAGGA
                                  GT    _     TGTA
GAM1710  FLJ20202  3' TGGGAGAATTTGGGCAGCGCGT 35236   TG    G  _____     AATCCT
             GA                  T  TGTGT TGT     TTCTCC
                                 |  ||||| |||     ||||||
                                 A  GCGCG ACG     AAGAGG
                                  GT    _  GGTTT     G   TC
GAM1710  FLJ20207  3' AGGGTTGGAGAGTGGCTTAAGT 35239   TG GTGT  GT
             GG                  T  T    GT  TTCTCCAATCCT
                                 |  |    ||  ||||||||||||
                                 G  G    CG  GAGAGGTTGGGA
                                  GT AATT  GT
GAM1710  FLJ20232  3' AGGAAGAGAGCACACAGATAA  39182     G       T   CAA
                                 TTGT TGTGTGTT CTC   TCCT
                                 |||| |||||||| |||   ||||
                                 AATA ACACACGA GAG   AGGA
                                   G       _  A__
GAM1710  FLJ20257  5' AGGGTGGTGGCGGAGTGCGCAT 39480        TG   T  __
             GCG                   TGTGTGTG  TTTC CCA  ATCCT
                                 ||||||||  |||| |||  |||||
                                 GCGTACGC  GAGG GGT  TGGGA
                                      GT   C   GG
GAM1710  FLJ20257  5' GGGGTCGGCGCACGCGCGG   39490           T_
                                 TTGTGTGTGTGTT  CTCC
                                 ||||||||||||  ||||
                                 GGCGCGCACGCGG  GGGG
                                         CT
GAM1710  FLJ20274  3' AGGAAAGGAAAATATGCAT   63323          C   AA
                                 GTGTGTGTTT TCC  TCCT
                                 ||||||||| |||  ||||
                                 TACGTATAAA AGG  AGGA
                                       _   AA
GAM1710  FLJ20288  5' GGATCCAGAGACACAGGCACGA 45447       G       CCA
                                 TTGTGT TGTGTTTCT   ATCC
                                 ||||||  |||||||||  ||||
                                 AGCACG ACACAGAGA   TAGG
                                    G        CC_
GAM1710  FLJ20303  3' TTCTTGGGGAAGTGTGTTATAA 35382      TGT TG       TCCT
                                 TTGTG   G  TTTCTCCAA
                                 |||||   |  |||||||||
                                 AATAT   T  GAAGGGGTT
                                    TG_ GT       CTTA
GAM1710  FLJ20320  3' GATCTGGGGGCACAGTATA   35426     _    TT    _
                                 TGTG TGTGT  CTCCA ATC
                                 |||| |||||  ||||| |||
```

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                                ATAT ACACG  GGGGT TAG
                                  G    __    C
GAM1710  FLJ20356  3'  CAAATGGAGGCACGAACGCAG  39137      G    TT    ATCCT
                                TTGTGT TGTGT  CTCCA
                                |||||| |||||  |||||
                                GACGCA GCACG  GAGGT
                                   A    __    AAACG
GAM1710  FLJ20366  3'  GGGGTATAGAAAGCATGCTCAT 35530   TG  T      _  CCA
           GA                    T  TG GTGTGTTT CT   ATCCT
                                |  || |||||||| ||   |||||
                                A  AC CGTACGAA GA   TGGGG
                                 GT  T       A  TA_
GAM1710  FLJ20421  3'  AGGATTGGTGGAGACTATGCAT 35613   TG     T     _
           GG                    T  TGTGTG GTTTCT CCAATCCT
                                |  |||||| |||||| ||||||||
                                G  ACGTAT CAGAGG GGTTAGGA
                                 GT     _     T
GAM1710  FLJ20485  3'  GATTAGAAAACGTACACA    39294          C  C
                                TGTGTGTGTTT TC AATC
                                |||||||||||| || ||||
                                ACACATGCAAA AG TTAG
                                       _  A
GAM1710  FLJ20531  5'  AGGCCCGGGAGGCGCAGGCGCA 35800       G        CAAT
           G                     TTGTGT TGTGTTTCTC    CCT
                                |||||| ||||||||||    |||
                                GACGCG ACGCGGAGGG    GGA
                                   G         CCC_
GAM1710  FLJ20539  5'  GGGTGCGGGAGATGCCGTGCG  35804    TG  T       _  A
                                TG  TG GTGTTTCTC CA TCC
                                ||  || |||||||| || |||
                                GC  GC CGTAGAGGG GT GGG
                                 GT  _        C  _
GAM1710  FLJ20555  5'  GGCCCGGAAGCGCTCGCGCAG  35829        T      ___
                                TTGTGTG GTGTTTCT   CC
                                ||||||| ||||||||   ||
                                GACGCGC CGCGAAGG   GG
                                     T       CCC
GAM1710  FLJ20605  3'  GGGAATATGAAAGTATATATAT 35872           _    TCCAA
           AA                    TTGTGTGTGTG TTTC     TCCT
                                |||||||||| ||||    ||||
                                AATATATATAT AAAG     AGGG
                                       G    TATA_
GAM1710  FLJ20666  3'  AGGAAAAGAAAGCACATACAG  35927          G    CCAA
                                TTGTGTGTGT TTTCT    TCCT
                                |||||||||| |||||    ||||
                                GACATACACG AAAGA    AGGA
                                       _    AA__
GAM1710  FLJ20727  3'  GGACAAATGTGCACATAG    36047        TG    C
                                TTGTGTG  TGTTT TCC
                                |||||||  ||||| |||
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                                GATACAC  GTAAA AGG
                                    GT    C
GAM1710  FLJ20752  5'  GGCTGGAAGCGCGCATGC    39305           __
                                GTGTGTGTGTTTCT  CC
                                ||||||||||||||  ||
                                CGTACGCGCGAAGG  GG
                                       TC
GAM1710  FLJ20772  3'  GGGACACATGGGATCCACGTGC 36088    TG   TT  T   A___
           G                    TG  TGTG  TC CCA    TCCT
                                ||  ||||  || |||    ||||
                                GC  GCAC  AG GGT    AGGG
                                 GT   CT  _   ACAC
GAM1710  FLJ20856  3'  AGGATTTGAGACAATATGTATA 47862      TG   _   C
                                TGTG  TGTT TCTC AATCCT
                                ||||  |||| |||| ||||||
                                ATAT  ATAA AGAG TTAGGA
                                  GT   C   T
GAM1710  FLJ20871  5'  GGATGGAATACGCCATGA    42266   TG  T       _
                                T  TG GTGTGTTTC TCC
                                |  || |||||||| |||
                                A  AC CGCATAAGG AGG
                                 GT  _       T
GAM1710  FLJ21032  3'  AGGTCAGAAGAGAGATATACAA 46617      G         CAAT__
           CAG                    TTGT TGTGTGTTTCTC     CCT
                                ||||  ||||||||||||     |||
                                GACA ACATATAGAGAG     GGA
                                  _          AAGACT
GAM1710  FLJ21126  3'  AGGAAATGGATATGCACATAT  91927        TTC   A_
                                GTGTGTGT   TCCA  TCCT
                                ||||||||   ||||  ||||
                                TATACACG   AGGT  AGGA
                                     TAT    AA
GAM1710  FLJ21276  3'  AGGGTGGGAGGGATGCACGCG  45257         TT   A
                                TGTGTGTGT  CTCC ATCCT
                                |||||||||  ||||  |||||
                                GCGCACGTA  GAGG TGGGA
                                      GG   G
GAM1710  FLJ21290  3'  GGACAAAACACACACACA    47397           C_
                                TGTGTGTGTGTTT  TCC
                                ||||||||||||  |||
                                ACACACACACAAA  AGG
                                       AC
GAM1710  FLJ21459  3'  AGGAAGTGGGGTGCACAGCA   44799     G    TT    A_
                                TGT TGTGT  CTCCA  TCCT
                                |||  |||||  |||||  ||||
                                ACG ACACG  GGGGT  AGGA
                                  _    T_    GA
GAM1710  FLJ21511  5'  GGGAACGAGGGGCGCGGACGCA 47646       G    TT   CAA
           G                    TTGTGT TGTGT  CTC   TCCT
                                ||||||  |||||  |||   ||||
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                                GACGCA GCGCG  GAG   AGGG
                                   G    GG   CA_
GAM1710  FLJ21596  3'  GGGAAAGGTAGAGGCCTGTGCG 46119      TG  T     _  AA
            CAG                    TTGTG  TG GTTTCT CC  TCCT
                                   |||||  || ||||||  ||  ||||
                                   GACGC  GT CGGAGA GG  AGGG
                                      GT  C     T  AA
GAM1710  FLJ21615  5'  GGGAAGAAAAGAAATATGTACA 50811    G    TG      CCAA_
            GAA                    TT TGTG  TGTTTCT    TCCT
                                   ||  ||||  |||||||    ||||
                                   AA ACAT  ATAAAGA    AGGG
                                    G   GT     AAAGA
GAM1710  FLJ21736  3'  AGGAACCGGGGCTGCGCGCA   46777       TT    AA_
                                   TGTGTGT  CTCC   TCCT
                                   |||||||  ||||   ||||
                                   ACGCGCG  GGGG   AGGA
                                       TC    CCA
GAM1710  FLJ21777  5'  AGGGCGAGGAGCAGCGCGCAG  50833        G      CAA
                                   TTGTGTGT TGTTTCTC   TCCT
                                   ||||||||  ||||||||   ||||
                                   GACGCGCG ACGAGGAG   GGGA
                                        _       C__
GAM1710  FLJ21877  3'  GGGATTGGGATGGGGGTATGTG 42200   TG    TT   ___
            T                       G  TGTG  TCT   CCAATCCT
                                    |  ||||  |||   ||||||||
                                    T  GTAT  GGG   GGTTAGGG
                                     GT    GG   TAG
GAM1710  FLJ21952  5'  GGCACATGGAAATGTGCGCACA 42855       TG      CCAAT  T
            G                       TTGTGTG  TGTTTCT    CC
                                    |||||||  |||||||    ||
                                    GACACGC  GTAAAGG    GG
                                        GT      TACAC
GAM1710  FLJ22055  3'  GGGGTTGGAGCCCCCATATA   45850       TTT_
                                    TGTGTG   CTCCAATCCT
                                    ||||||   ||||||||||
                                    ATATAC   GAGGTTGGGG
                                       CCCC
GAM1710  FLJ22127  3'  GGGTATGAATCGTGCACACAG  43202       TG  T   TCCA
                                    TTGTGTG  TG TTC    ATCC
                                    |||||||  ||  |||    ||||
                                    GACACAC  GC AAG    TGGG
                                        GT  T   TA__
GAM1710  FLJ22127  5'  TGGAGAGACAAGTGTGCAG    43204      TG G
                                    TTGTG  T TGTTTCTCCA
                                    |||||  |  ||||||||||
                                    GACGT  G ACAGAGAGGT
                                       GT A
GAM1710  FLJ22169  3'  GGGTAGGGACCGTGTACAG    44234      TG  T  TT  CCA
                                    TTGTG  TG GT  CT   ATCC
                                    |||||  ||  ||  ||   ||||
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                                GACAT  GC CA  GA   TGGG
                                   GT  _  GG  ___
GAM1710  FLJ22644  3'  AGACTGGGAAACATACACATA  47696            T   A  CT
                                TGTGTGTGTGTTTC CCA TC
                                |||||||||||||| ||| ||
                                ATACACATACAAAG GGT AG
                                       _  C  A
GAM1710  FLJ22672  3'  TAGGGTCTGAGAGGGGAGATGC 46600             A_____
            ATGCG                  TGTGTGTGTTTCTCC     ATCCT   A
                                |||||||||||||||     |||||  |
                                GCGTACGTAGAGGGG     TGGGA   T
                                       AGAGTC
GAM1710  FLJ22746  5'  GGGTGGCCAGGAGCACGTGT   45919   TG       __  A  T
                                G  TGTGTTTCT  CCA TCC
                                |  |||||||||  ||| |||
                                T  GCACGAGGA  GGT GGG
                                 GT        CC  _
GAM1710  FLJ23018  3'  AGGAAATTGAGATGGATGTACA 46078      TG G     TCCAA
            A                   TTGTG  T TGTTTC     TCCT
                                |||||  | ||||||     ||||
                                AACAT  A GTAGAG     AGGA
                                   GT G     TTAA_
GAM1710  FLJ23027  3'  GGGACTTGGGGATACAGCGTGA 50913   TG   GTG   T     _
                                T  TGT   TGT TCTCCAA TCCT
                                |  |||   ||| ||||||| ||||
                                A  GCG   ACA AGGGGTT AGGG
                                 GT  ___   T      C
GAM1710  FLJ23231  3'  AGGATTGGTTCTGGCCCATGCA 47603       T   TCT_
                                TGTGTG GTT    CCAATCCT
                                ||||||| |||    ||||||||
                                ACGTAC CGG    GGTTAGGA
                                    C   TCTT
GAM1710  FLJ23375  5'  GGCTCCCGGGAGCGCCGCGCG  46951       T      CCAAT
                                TGTGTG GTGTTTCT     CC
                                |||||| ||||||||     ||
                                GCGCGC CGCGAGGG     GG
                                    _       CCCTC
GAM1710  FLJ23441  3'  GGCAGAGACACTGCACATGA   45492   TG    _      _
                                T  TGTGT GTGTTTCT CC
                                |  ||||| |||||||| ||
                                A  ACACG CACAGAGA GG
                                 GT     T       C
GAM1710  FLJ23590  3'  AGGATGAAATGGGAGACATATG 45363     T          CA___
            CCCAG                  TTG GTGTGTGTTTCTC     ATCCT
                                ||| ||||||||||||     |||||
                                GAC CGTATACAGAGGG     TAGGA
                                  C           TAAAG
GAM1710  FLJ32356  3'  AGTGACTGGGGACACAGGTGCA 59015     TG G    TT     A  _
            G                   TTG  T TGTG  TCTCCA TC CT
                                |||  | ||||  |||||| || ||
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                                GAC  G ACAC  AGGGGT AG GA
                                  GT G   __     C  T
GAM1710  FLJ32356  3'  GGGGAACGTCACGTGCAA    59026     TG   _
                                TTG  TGTG TGTTTCTC
                                |||  |||| ||||||||
                                AAC  GCAC GCAAGGGG
                                  GT    T
GAM1710  FLJ32468  3'  TGTGCGTTGGGGATGCATGCGA 59716      G      T       CCT
           CAG                    TTGT TGTGTGT TCTCCAAT
                                |||| ||||||| ||||||||
                                GACA GCGTACG AGGGGTTG
                                  _      T       CGTGTT
GAM1710  FRAT1    3'  GGGGCTAGGGAGACGCCATGTG 19690    TG    T       CAA
           A                     T  TGTG GTGTTTCTC   TCCT
                                |  |||| |||||||||   ||||
                                A  GTAC CGCAGAGGG   GGGG
                                 GT   _        ATC
GAM1710  FUK      5'  AGGACCCAGAGAAGCGTGTGGG 59622      G  TG       CAA_
           CAG                    TTGT TG  TGTTTCTC    TCCT
                                |||| ||  ||||||||    ||||
                                GACG GT  GCGAAGAG    AGGA
                                  G  GT       ACCC
GAM1710  FYCO1    5'  GGCAGGAGACATACAGACAA   44774      G         __
                                TTGT TGTGTGTTTCT  CC
                                |||| ||||||||||  ||
                                AACA ACATACAGAGG  GG
                                  G          AC
GAM1710  G0S2     3'  GGGAGAGACAGAGGGGGCGCGC 32308           TT _  CAA___
           GCACAG                   TTGTGTGTGTGT  C TC     TCCT
                                ||||||||||||  | ||     ||||
                                GACACGCGCGCG  G AG     AGGG
                                       GG G  ACAGAG
GAM1710  GABARAPL1 3'  GGGGTAGGGGAGGGGTGTGTGT 49421       _____ TG G      A
           GCGCGA                   TTGTGT    G  T TTTCTCC ATCCT
                                ||||||    |  | ||||||| |||||
                                AGCGCG    T  G GGAGGGG TGGGG
                                    TGTG GT G      A
GAM1710  GABARAPL3 3'  GGGGTAGGGGAGGGGTGTGTGT 51785    TG  TG  TG TT    A__
           GTGA                     T  TG  TG  T  CTCC   ATCCT
                                |  ||  ||  |  ||||   |||||
                                A  GT  GT  G  GAGG   TGGGG
                                 GT  GT  GT GG    GGA
GAM1710  GBTS1    3'  AGGGTTGTGTCCAACATACACG 59719    G        TCTC_
           GAA                      TT TGTGTGTGTT     CAATCCT
                                || ||||||||||     |||||||
                                AA GCACATACAA     GTTGGGA
                                 G         CCTGT
GAM1710  GDAP2    3'  GGAGGAAGTGTGTCACAG    35126       _  TG G
                                TTGTG TG  T TTTCTCC
                                ||||| ||  | |||||||
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                                GACAC GT  G AAGGAGG
                                   T  GT _
GAM1710  GENX-3414 3'  AGGACTGTGAAGTACAGGCACA 15455       G       TC  A
              G                    TTGTGT TGTGTTTC  CA TCCT
                                   |||||| ||||||||  || ||||
                                   GACACG ACATGAAG  GT AGGA
                                      G       T_  C
GAM1710  GMEB2    3'  GTTGGGAACATGCACCCG    25667    T       T T
                                   TG GTGTGTGTT C CCAAT
                                   || |||||||| | |||||
                                   GC CACGTACAA G GGTTG
                                    C       _ _
GAM1710  GMNN     5'  AGGCGGCAGGAAGTGGGTACGC 32471       TG GT    __  AAT
              AG                    TTGTGTG  T  TTCT  CC   CCT
                                   |||||||  |  ||||  ||   |||
                                   GACGCAT  G  AAGG  GG   GGA
                                       GG TG    AC  C__
GAM1710  GMPPB    5'  GGCGTTGGGAGTGCGCGGCAG  97454     G    TG  T T    _
                                   TTGT TGTG  TT C CCAAT CC
                                   |||| ||||  || | ||||| ||
                                   GACG GCGC  GA G GGTTG GG
                                     _   GT  _ _    C
GAM1710  GOLPH3   3'  GGGATTCCCTAATATGTATAC  42392      TG    TCTCC
                                   GTGTG  TGTT    AATCCT
                                   |||||  ||||    ||||||
                                   CATAT  ATAA    TTAGGG
                                      GT    TCCC_
GAM1710  GPR105   3'  AGGATATTAGATACATGC    30268         CTCCA
                                   GTGTGTGTTT    ATCCT
                                   ||||||||||    |||||
                                   CGTACATAGA    TAGGA
                                         TTA__
GAM1710  GPR108   3'  GGCGGGGGCGCGGGCACAG   69629       G    TT  _
                                   TTGTGT TGTGT  CT CC
                                   |||||| |||||  || ||
                                   GACACG GCGCG  GG GG
                                      G    GG  C
GAM1710  GPR108   3'  GGGGTTGGGGTCTACACG    69632       TTT
                                   TGTGTG   CTCCAATCCT
                                   ||||||   ||||||||||
                                   GCACAT   GGGGTTGGGG
                                      CT_
GAM1710  GRID1    3'  AGGTGAGAAGCATAAGTGTAA  69020     TG G        CAAT
                                   TTG  T TGTGTTTCTC   CCT
                                   |||  | ||||||||||   |||
                                   AAT  G ATACGAAGAG   GGA
                                     GT A        T____
GAM1710  GRM5     3'  GGGAAGCAGTGCGTGTGA    63244     TG   _
                                   TTG  TGTG TGTTTCTC
                                   |||  |||| ||||||||
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                                AGT  GCGT ACGAAGGG
                                  GT    G
GAM1710  GRO3     3'  AGGGTAAGGGAATGTATGTACA 63183       TG GT_     CA
                CA                  TGTGTG  T   TTCTC  ATCCT
                                    ||||||  |   |||||  |||||
                                    ACACAT  A   AAGGG  TGGGA
                                       GT TGT     AA
GAM1710  GTF2E1   3'  GGGAGGTGGGAGCGTGTGTGGA 19801    G GT TG      _  AA
                A                    TT T  G  TGTTTCT CC  TCCT
                                     || |  |  ||||||| ||  ||||
                                     AA G  T  GCGAGGG GG  AGGG
                                      G TG GT      T  __
GAM1710  GTPBG3   3'  GGGATTACAGGCATGTGCCAG  51900     T TG      CTCC
                                    TTG G  TGTGTTT    AATCCT
                                    ||| |  |||||||    ||||||
                                    GAC C  GTACGGA    TTAGGG
                                      _ GT      CA__
GAM1710  GTPBP5   3'  AGGAGTGGAAGGAGACGTGTGC 65965     TG   G  TC    A
                                    GTG  TGT TT  TCCA TCCT
                                    |||  ||| ||  |||| ||||
                                    CGT  GCA AG  AGGT AGGA
                                      GT   G  GA    G
GAM1710  GTPBP5   3'  GGGGTTGGGGTGCCCATAACG  65979     G    T  TT
                                    TGT TGTG GT  CTCCAATCCT
                                    ||| |||| ||  ||||||||||
                                    GCA ATAC CG  GGGGTTGGGG
                                      _    C  T_
GAM1710  GW112    3'  TTGGAGCATATGTGCAA     22216     TG     TTT
                                    TTG  TGTGTG   CTCCAA
                                    |||  ||||||   ||||||
                                    AAC  GTATAC   GAGGTT
                                      GT     ____
GAM1710  H2AFA    3'  TGCTGGAATACACATACGA    41086             TC
                                    TTGTGTGTGTGTTTC  CA
                                    ||||||||||||||  ||
                                    AGCATACACATAAGG  GT
                                              TC
GAM1710  H2AFJ    3'  GGAACAAAATGCATATATGG   37381    TG         C__
                                    T  TGTGTGTGTTT   TCC
                                    |  ||||||||||   |||
                                    G  ATATACGTAAA   AGG
                                     GT          ACA
GAM1710  H2AV     3'  AGGCCTTTGAAATGGATACATG 25755    TG    G     TCCAAT
                A                    T  TGTGT TGTTTC      CCT
                                     |  ||||| ||||||      |||
                                     A  ACATA GTAAAG     GGA
                                     GT    G     TTTCC_
GAM1710  H2BFB    3'  GGAGAAATGAATGCATAA     41087         G
                                    TTGTGTGT TGTTTCTCC
                                    |||||||| |||||||||
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                                AATACGTA GTAAAGAGG
                                    A
GAM1710 H2BFQ    3' AGGTCATGGGAAATGGCATACG 60076       G     T  AT_
                                TGTGTGT TGTTTC CCA   CCT
                                ||||||| |||||| |||   |||
                                GCATACG GTAAAG GGT   GGA
                                   _     _   ACT
GAM1710 HAND2    5' AGGGCGCGGCGGGGCTGCGCGC 42024         _  TT T  AA_
           ACGA                   TTGTGTGTGT GT  C CC   TCCT
                                ||||||||||  ||  | ||   ||||
                                AGCACGCGCG CG  G GG   GGGA
                                     T  GG C  CGC
GAM1710 HCA4     3' AGGATTGGGGGAAGGGAGAACG 57738     GTGTGTG
           A                    TTGT      TTTCTCCAATCCT
                                ||||      ||||||||||||
                                AGCA      AAGGGGGTTAGGA
                                  AGAGGG_
GAM1710 HDAC9-PENDING 5' GGGAAGAGAGGCACAGACACAG 28842       G        CAA
                                TTGTGT TGTGTTTCTC   TCCT
                                |||||| ||||||||||   ||||
                                GACACA ACACGGAGAG   AGGG
                                   G        A__
GAM1710 HDCMA18P  5' AGGATGAGGATGAACGCACA   34089        C   A_
                                TGTGTGTTT TCC  ATCCT
                                ||||||||| |||  |||||
                                ACACGCAAG AGG  TAGGA
                                     T   AG
GAM1710 HERC3    3' AGGATTAAAAATATATATACAG 28234           CTCC
                                TTGTGTGTGTGTTT    AATCCT
                                ||||||||||||||    ||||||
                                GACATATATATAAA    TTAGGA
                                       AA__
GAM1710 HIF1AN   3' AGGGCACGGGCAAACACATA   62667        C   AA_
                                TGTGTGTTT TCC   TCCT
                                ||||||||| |||   ||||
                                ATACACAAA GGG   GGGA
                                     C   CAC
GAM1710 HIRIP3   3' GGGACCCTTGATACATGTACAA 14605      TG     TCTCCAA
                                TTGTG  TGTGTT      TCCT
                                |||||  ||||||      ||||
                                AACAT  ACATAG      AGGG
                                   GT     TTCCC__
GAM1710 HMP19    3' AGGAAGGCACGGGACAGGCATG 88857   TG    G   TT T__  AA
           TGA                    T  TGTGT TGT  C   CC  TCCT
                                |  ||||| |||  |   ||  ||||
                                A  GTACG ACA  G   GG  AGGA
                                 GT    G   GG CAC  A_
GAM1710 HNK-1ST  3' GGAGGAAGCATCACACAG    17949        T     _
                                TTGTGTG GTGTTTC TCC
                                ||||||| ||||||| |||
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                                GACACAC TACGAAG AGG
                                   _     G
GAM1710 HS6ST1   5' GGGCCGGAGCGCGGGCGCG   17848      G      __
                                TGTGT TGTGTTTC  TCC
                                ||||| ||||||||  |||
                                GCGCG GCGCGAGG  GGG
                                   G       CC
GAM1710 HSAJ1454 3' AGGATAACAGAGAGATACCACA 34252   TG   T       CA__
             TGG                   T  TGTG GTGTTTCTC    ATCCT
                                |  |||| |||||||||   |||||
                                G  ACAC CATAGAGAG    TAGGA
                                 GT   _       ACAA
GAM1710 HSPB7    5' GGGAAACAAAACACACAA    27784        G_     T
                                TTGTGTGT  TGTTTC CC
                                ||||||||  ||||||  ||
                                AACACACA  ACAAAG GG
                                     AA     _
GAM1710 HSSEXGENE 5' AGGCCGTGGGGACGTGCGAGCG 34420     G  TG T     AT_
                                TGT TG  T TCTCCA   CCT
                                ||| ||  | ||||||   |||
                                GCG GC  G AGGGGT   GGA
                                  A  GT C     GCC
GAM1710 HSZFP36  5' GGGAAATGAAGTCATACATGTG 64221    TG      _   TCCAA
             A                   T  TGTGTGTG TTTC     TCCT
                                |  |||||||| ||||    ||||
                                A  GTACATAC GAAG     AGGG
                                 GT       T    TAA__
GAM1710 HYPE     5' GGGGTTCTGACAGCTGCGCGCG 23962         T   _  TCC
             A                   TTGTGTGTG GTT TC   AATCCT
                                |||||||||  ||| ||   ||||||
                                AGCGCGCGT CGA AG   TTGGGG
                                     _   C  TC_
GAM1710 IBTK     3' TGGGAGACACATAAGCAA     68099      G        T
                                TTGT TGTGTGTTTC CCA
                                ||||  ||||||||||  |||
                                AACG ATACACAGAG GGT
                                  A        _
GAM1710 IGF2AS   3' GGGGTGGAGGGTGCACACGA   33531        TG GTT     AT
                                TTGTGTG  T   TCTCCA  CC
                                |||||||  |   ||||||  ||
                                AGCACAC  G   GGAGGT  GG
                                    GT ___     GG
GAM1710 IL17D    3' GGACCAAAGGGATGCACAGGCG 57121     G      TT  CCAA   T
                                TGT TGTGTGT  CT    TCC
                                ||| |||||||  ||    |||
                                GCG ACACGTA  GA    AGG
                                  G      GG  AACC
GAM1710 IMAGE:4907098 5' GGACGAGGCGCGCGCGGAG    57756    G          _
                                TT TGTGTGTGTTTC TCC
                                || ||||||||||| |||
```

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                                GA GCGCGCGCGGAG AGG
                                 G          C
GAM1710  IMAGE:4907098 3'  GGGAGCCTGTGGAGGCAGGTGT 57757    GT TG G     TC  A__
             GTAG                  TT  G  T TGTTTC  CA   TCCT
                                || |  | ||||||  ||   ||||
                                GA  T  G ACGGAG  GT   AGGG
                                 TG GT G     GT  CCG
GAM1710  ING4     3'  GGACTGGGGCATAGCATGG   60429   TG   G   TTT    A
                                T  TGT TGTG   CTCCA TCC
                                |  ||| ||||   ||||| |||
                                G  ACG ATAC   GGGGT AGG
                                 GT   _   ___    C
GAM1710  ITM3     3'  GGGCTTCAGAAGTATCTGCACA 48893       GT       CCAA   T
             A                    TTGTGT  GTGTTTCT    TCC
                                ||||||  ||||||||    |||
                                AACACG  TATGAAGA    GGG
                                    TC       CTTC
GAM1710  ITPK1    3'  AGGGTTGGGGAGAAGCCTCTGC 27226       TGT  G
             AG                    TTGTG   GT TTTCTCCAATCCT
                                ||||||   || ||||||||||||||
                                GACGT   CG AGAGGGGTTGGGA
                                   CTC  A
GAM1710  ITPK1    3'  GGGAGGTGAGGGGGTGTGCGTAT 27233    TG     TG TT   CAA
             GG                    T  TGTGTG  T  CTC   TCCT
                                |  ||||||  |  |||   ||||
                                G  ATGCGT  G  GAG   AGGG
                                 GT     GT GG   TGG
GAM1710  KCNG3    5'  GGGAGGTGAGCGGCGCGCGCG  56662         TT   CAA
                                TGTGTGTGT  CTC   TCCT
                                |||||||||  |||   ||||
                                GCGCGCGCG  GAG   AGGG
                                     GC   TGG
GAM1710  KCNH7    3'  AGGATGTAAATATACATA     53836          CTCCA
                                TGTGTGTGTTT     ATCCT
                                ||||||||||     |||||
                                ATACATATAAA     TAGGA
                                      TG___
GAM1710  KCNMB2   3'  GGGATTTTAAAGCTATGTGCAC 20687       TG   _    CTCC
             AG                    TTGTG  TGT GTTT    AATCCT
                                |||||  ||| ||||    ||||||
                                GACAC  GTA CGAA    TTAGGG
                                   GT   T    ATT_
GAM1710  KIAA0084 5'  GGAGGGACAGACACACGA    68710         G   TT
                                TTGTGTGT TGT  CTCC
                                ||||||||  |||  ||||
                                AGCACACA ACA  GAGG
                                     G   GG
GAM1710  KIAA0141 3'  TTGGGAAACATGTGCCAG    29397     T TG       T
                                TTG G  TGTGTTTC CCAA
                                |||  |  ||||||||  ||||
```

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                              GAC C  GTACAAAG GGTT
                                _ GT      _
GAM1710 KIAA0143 3' AGGAACTGGGTGTGCACACG   65408       TTC   A_
                              TGTGTGT   TCCA  TCCT
                              |||||||   ||||  ||||
                              GCACACG   GGGT  AGGA
                                  TGT   CA
GAM1710 KIAA0170 3' AGGATTGGGGTATATTGATACA 28388      GT   TT
           A                   TTGTGT  GTGT  CTCCAATCCT
                              ||||||  ||||  ||||||||||
                              AACATA  TATA  GGGGTTAGGA
                                 GT   T_
GAM1710 KIAA0186 3' GGGAAGGAAGGACACACAT   41111       TC   AA
                              GTGTGTGTT  TCC  TCCT
                              |||||||||  |||  ||||
                              TACACACAG  AGG  AGGG
                                   GA   A_
GAM1710 KIAA0266 5' GGGATTGGAGTTGTGGAGTGTA 41642     G   TG  _____
           TGGCAG                TTGT TGTG  TTT    CTCCAATCCT
                              ||||  ||||  |||    ||||||||||
                              GACG GTAT  GAG    GAGGTTAGGG
                                _   GT   GTGTT
GAM1710 KIAA0284 3' GGCGGGGGTGAGCGCACG    63804        _   AAT
                              TGTGTGTTT CTCC   CC
                              |||||||| ||||   ||
                              GCACGCGAG GGGG   GG
                                   T   GC_
GAM1710 KIAA0296 3' GGGGGAGGGAGCGCGTGCAG  28778    TG    G TT   AA
                              TTG  TGTGT T  CTCC  TCC
                              |||  ||||| |  ||||  |||
                              GAC  GCGCG A  GAGG  GGG
                                GT    _ GG   __
GAM1710 KIAA0296 5' TTGGGAAGCTTGTGCACAG   28780     TG  T    T
                              TTGTG  TG GTTTC CCAA
                              |||||  || ||||| ||||
                              GACAC  GT CGAAG GGTT
                                 GT  T    _
GAM1710 KIAA0316 3' GGAGAGCACATATGCAA     70246          T
                              TTGTGTGTGTGTT CTCC
                              |||||||||||| ||||
                              AACGTATACACGA GAGG
                                           _
GAM1710 KIAA0321 3' AGGACCACAGGATGGATATGCA 63044       TC   AA___
                              TGTGTGTT  TCC    TCCT
                              ||||||||  |||    ||||
                              ACGTATAG  AGG    AGGA
                                   GT   ACACC
GAM1710 KIAA0322 3' AGGATTGACAAAAGCTGTGCAT 94329   TG  TG  T   CTC_
           GA                   T  TG  TG GTTT    CAATCCT
                              |  ||  || ||||   |||||||
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                              A  AC  GT CGAA   GTTAGGA
                               GT  GT  _   AACA
GAM1710  KIAA0335  3'  GGACCCAGAGGCAGTGCATAA  29672      TG G     CCAA
                              TTGTG  T TGTTTCT   TCC
                              |||||  | |||||||   |||
                              AATAC  G ACGGAGA   AGG
                                 GT _     CCC_
GAM1710  KIAA0339  3'  GGAGAAGCGCTACGTGCAG   71965    TG  _
                              TTG  TGT GTGTTTCTCC
                              |||  ||| ||||||||||
                              GAC  GCA CGCGAAGAGG
                                GT   T
GAM1710  KIAA0349  3'  AGAGTTGGGGGACACACATGCA 93913          TT T   TC
            G                  TTGTGTGTGTGT  C CCAA  CT
                              ||||||||||||  | ||||  ||
                              GACGTACACACA  G GGTT  GA
                                     GG _   GA
GAM1710  KIAA0349  3'  GTTGGGGGACACACATGCAG   93918          TT T
                              TTGTGTGTGTGT  C CCAAT
                              ||||||||||||  | |||||
                              GACGTACACACA  G GGTTG
                                     GG _
GAM1710  KIAA0397  3'  CCCCCTTGGAGGAGCTGTGTAT 62347      TG _       TCCT
            GCG                  TGTGTG  T GTTTCTCCAA
                              ||||||  | ||||||||||
                              GCGTAT  G CGAGGAGGTT
                                 GT T        CCCCCA
GAM1710  KIAA0429  3'  GGGATTGGGGGGAGGGCCATGG 29243    G   T  G     _
            GA                   TT TGTG GT TTTCTCC AATCCT
                              || |||| || ||||||| ||||||
                              AG GTAC CG GAGGGGG TTAGGG
                               G   _ G     G
GAM1710  KIAA0431  3'  GGGAGTTATGGAAACGTGCCTA 31551    TG  T TG     CCAA_
            TGA                  T  TG G  TGTTTCT    TCCT
                              |  || |  |||||||    ||||
                              A  AT C  GCAAAGG    AGGG
                               GT  C GT      TATTG
GAM1710  KIAA0435  5'  AGGTTTTGGAGGCATACATGG  29657   TG     GTTT     T_
                              T  TGTGTGT   CTCCAA  CCT
                              |  |||||||   ||||||  |||
                              G  ACATACG   GAGGTT  GGA
                               GT      ____     TT
GAM1710  KIAA0450  3'  GGAGGGACATACACGGAG    28362    G       TT
                              TT TGTGTGTGT  CTCC
                              || |||||||||  ||||
                              GA GCACATACA  GAGG
                               G       GG
GAM1710  KIAA0450  3'  GGAGGGAGGGACATACACG   28363        TT   AA
                              TGTGTGTGT  CTCC  TCC
                              |||||||||  ||||  |||
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                                GCACATACA  GAGG  AGG
                                     GG   G_
GAM1710  KIAA0476  5'  GGGGTTGGGGGAGTAGAGAAAG 30041    GTGTG_
              CG                   TGT     TGTTTCTCCAATCCT
                                   |||     ||||||||||||||
                                   GCG     ATGAGGGGGTTGGGG
                                     AAAGAG
GAM1710  KIAA0553  3'  GGAGGTGAGCACATTTACAG   70450      T      __
                                   TTGTG GTGTGTTT  CTCC
                                   ||||| ||||||||  ||||
                                   GACAT TACACGAG  GAGG
                                      T       TG
GAM1710  KIAA0603  3'  GGTGGAAACATTTATGTAA    29836     TG  T      _
                                   TTG  TG GTGTTTCT CC
                                   |||  || ||||||||  ||
                                   AAT  AT TACAAAGG GG
                                     GT  T       T
GAM1710  KIAA0616  3'  AGGCTCAGGGGAGGGGCGCGCA 47312    TG      G      AAT_
              TGG                    T  TGTGTGT TTTCTCC    CCT
                                   |  |||||||  |||||||    |||
                                   G  ACGCGCG GGAGGGG    GGA
                                    GT      G      ACTC
GAM1710  KIAA0618  3'  GGGGTGAGCTGAGCATGCATGG 29857    TG      GTTT   CA
                                   T  TGTGTGT    CTC  ATCCT
                                   |  |||||||    |||  |||||
                                   G  ACGTACG    GAG  TGGGG
                                    GT      AGTC   __
GAM1710  KIAA0637  5'  GGGCCGAGGTAATGCACA     29923         _    CAA
                                   TGTGTGTT TCTC   TCC
                                   ||||||||  ||||   |||
                                   ACACGTAA GGAG   GGG
                                        T    CC_
GAM1710  KIAA0643  3'  AGGTGTGGAGGGGCATGCCTGT 45970    TG  T      TT     AT
              GG                     T  TG GTGTGT  CTCCA  CCT
                                   |  ||  ||||||  |||||  |||
                                   G  GT CGTACG  GAGGT  GGA
                                    GT  C      GG     GT
GAM1710  KIAA0644  3'  GGAGAAGGCTGCATGCAA     29726         TG
                                   TTGTGTGTG  TTTCTCC
                                   |||||||||  |||||||
                                   AACGTACGT  GAAGAGG
                                        CG
GAM1710  KIAA0649  5'  GGGACGTGGGACGCGGGCGCAG 29715        G     TT TCCAA
                                   TTGTGT TGTGT  C     TCCT
                                   ||||||  |||||  |     ||||
                                   GACGCG GCGCA  G     AGGG
                                      G     GG TGC__
GAM1710  KIAA0677  3'  AGGATTGGAGGGCTTCACACCA 28528     T     TGT
              A                      TTG GTGTG   TTCTCCAATCCT
                                   ||| |||||   ||||||||||||
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                                AAC CACAC   GGGAGGTTAGGA
                                  _    TTC
GAM1710 KIAA0705 3' AGGCCTGGGAGCATGGACGTGG 25482   TG   G     T T   AT
                                T  TGT TGTGTT C CCA  CCT
                                |  ||| |||||| | |||  |||
                                G  GCA GTACGA G GGT  GGA
                                 GT   G     _ _   CC
GAM1710 KIAA0711 5' AGGCGGGGGAGCAGCGTGTGA  30147     TG   G       AAT
                                TTG  TGT TGTTTCTCC   CCT
                                |||  ||| |||||||||   |||
                                AGT  GCG ACGAGGGGG   GGA
                                  GT   _       C__
GAM1710 KIAA0721 3' AGGAGGTCTGAACACACACAG  41649         GTT__    AATCCT
                                TTGTGTGTGT    TCTCC
                                ||||||||||    |||||
                                GACACACACA    GGAGG
                                      AGTCT    A   T
GAM1710 KIAA0721 3' TAGGAGGTCTGAACACACACAG 41656         GTT__    AATCCT
                                TTGTGTGTGT    TCTCC
                                ||||||||||    |||||
                                GACACACACA    GGAGG
                                      AGTCT    A   TC
GAM1710 KIAA0731 5' GGGCGGGGGGGGGACGCACGC   67481        TT   AAT
                                GTGTGTGT  CTCC   CCT
                                ||||||||  ||||  |||
                                CGCACGCA  GGGG   GGG
                                     GG   GGC
GAM1710 KIAA0776 3' GAGAGAGAACACATGCAA    65450         G_
                                TTGTGTGTGT  TTTCTC
                                ||||||||||  ||||||
                                AACGTACACA  AGAGAG
                                      AG
GAM1710 KIAA0781 3' AGGACTCCAGAGGTGTCACACG 68055   TG    _ TT   CCAA
           TGG                    T  TGTGTG TG  TCT    TCCT
                                |  |||||| ||  |||   ||||
                                G  GCACAC GT  AGA    AGGA
                                 GT     T  GG   CCTC
GAM1710 KIAA0789 3' AGGTTAATTGGAGACACCATGT 64426   TG   T   TT      ___
           GG                     T  TGTG GTG  TCTCCAAT   CCT
                                |  |||| |||  ||||||||   |||
                                G  GTAC CAC  AGAGGTTA   GGA
                                 GT   _  __       ATT
GAM1710 KIAA0790 5' GGGGCCGCCGGGGCATGCAGCG 69257     _     TT TCCAA
           CG                     TGTG TGTGTGT  C     TCCT
                                ||||  |||||||  |    ||||
                                GCGC ACGTACG  G    GGGG
                                  G      GG CCGCC
GAM1710 KIAA0843 3' AGGAATGAGAAAGTGTGCGTGA 30795   TG    TG G     CAA
                                T  TGTG  T TTTCTC   TCCT
                                |  ||||  | ||||||   ||||
```

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                                A  GCGT  G AAAGAG   AGGA
                                 GT    GT _     TA_
GAM1710  KIAA0869  3'  GGGATTCAGAGGTGCATCCACG 71421      TG  TG    CC
                                TGTG  TG  TTTCT  AATCCT
                                ||||  ||  |||||  ||||||
                                GCAC  AC  GGAGA  TTAGGG
                                  CT  GT    C_
GAM1710  KIAA0876  3'  AGGAGCCAGCGGGACGCCGCAC 65313         _   TT TCCAA_
              GCG                  TGTGTGTG TGT  C      TCCT
                                |||||||| |||  |     ||||
                                GCGCACGC GCA  G     AGGA
                                     C   GG CGACCG
GAM1710  KIAA0894  3'  GGGATTCTTCAAATATATGCAG 30339    G         CTCC
              AG                   TT TGTGTGTGTTT    AATCCT
                                || ||||||||||    ||||||
                                GA ACGTATATAAA    TTAGGG
                                 G         CTTC
GAM1710  KIAA0918  3'  TGGGAAACATTTGTGTAA    73522     TG  T      T
                                TTG  TG GTGTTTC CCA
                                |||  || |||||| |||
                                AAT  GT TACAAAG GGT
                                  GT  T      _
GAM1710  KIAA0980  3'  GGGGCTGGGGGGAATATGCATGT 47998    TG           AT
                                G  TGTGTGTTTCTCCA  CCT
                                |  ||||||||||||||  |||
                                T  ACGTATAAGGGGGT  GGG
                                 GT            CG
GAM1710  KIAA0984  3'  GGGATGGATGAGGTAACACACA 66141         G  TT  _    A
              G                    TTGTGTGT TG  TC TCCA TCCT
                                |||||||| ||  || |||| ||||
                                GACACACA AT  AG AGGT AGGG
                                     _ GG  T    _
GAM1710  KIAA1001  3'  AGGGTTAAATAAAGGCATACAT 30999    TG      G   CTCC
              GA                   T  TGTGTGT TTT    AATCCT
                                |  ||||||| |||    ||||||
                                A  ACATACG AAA    TTGGGA
                                 GT      G   TAAA
GAM1710  KIAA1013  5'  GGGGTCGGGGCTGCACGTACG  90306         TT    A
                                TGTGTGTGT  CTCC ATCCT
                                |||||||||  |||| |||||
                                GCATGCACG  GGGG TGGGG
                                     TC    C
GAM1710  KIAA1014  5'  AGGGTCCGAGGCGCTTGCGCAA 65959         T      TCCA
                                TTGTGTG GTGTTTC    ATCCT
                                |||||||| |||||||    |||||
                                AACGCGT CGCGGAG    TGGGA
                                    T      CC__
GAM1710  KIAA1014  3'  GGGCAAGAGTGTATGCATACAA 65960           TTT   CAA
                                TTGTGTGTGTG   CTC   TCC
                                ||||||||||   |||   |||
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                                AACATACGTAT  GAG  GGG
                                     GT_  AAC
GAM1710 KIAA1016 5' GGGGTCTGGAGCGCGCGC   93388      TTT   _
                                GTGTGTG  CTCCA ATCCT
                                |||||||  ||||| |||||
                                CGCGCGC  GAGGT TGGGG
                                    ___   C
GAM1710 KIAA1025 3' GGGGTTGACTTTCGCAATGTAT 64678     TG _  TTTCTC
           AG                    TTGTG  T GTG    CAATCCT
                                |||||  | |||    |||||||
                                GATAT  A CGC    GTTGGGG
                                  GT A  TTTCA_
GAM1710 KIAA1032 3' AGGCCTGGGGAACAGCACGTGC 66721    TG   GT     AT
           GA                    TTG  TGTGT  TTCTCCA  CCT
                                |||  |||||  |||||||  |||
                                AGC  GCACG  AAGGGGT  GGA
                                  GT    AC     CC
GAM1710 KIAA1032 3' GGGGTTGGGGAGATCTGCA   66729    GT
                                TGT  GTTTCTCCAATCCT
                                |||  |||||||||||||
                                ACG  TAGAGGGGTTGGGG
                                  TC
GAM1710 KIAA1034 3' GGAGAAGACATGTTGCAA    63132     _ TG  G
                                TTGT G  TGT TTTCTCC
                                ||||  |  ||| |||||||
                                AACG T  ACA GAAGAGG
                                  T GT  _
GAM1710 KIAA1056 3' AGGAAAGAGTGGGGGTACATGC 30308      T    A____
                                GTGTGT TCTCCA    TCCT
                                |||||| ||||||    ||||
                                CGTACA GGGGGT    AGGA
                                   T     GAGAA
GAM1710 KIAA1058 3' GGAAAGGAGTATATTTACA   83139     T   TT   AA
                                TGTG GTGT  CTCC  TCC
                                |||| ||||  ||||  |||
                                ACAT TATA  GAGG  AGG
                                  T   T_   AA
GAM1710 KIAA1085 3' AGGGTGATAAATACATGTATAA 40731     TG     C  CA
                                TTGTG  TGTGTTT TC  ATCCT
                                |||||  ||||||| ||  |||||
                                AATAT  ACATAAA AG  TGGGA
                                  GT     T __
GAM1710 KIAA1100 3' AGGGTTGGGGGTCTGTGCTCA  30438   T TG  TT
                                TG G  TG  TCTCCAATCCT
                                || |  ||  ||||||||||
                                AC C  GT  GGGGGTTGGGA
                                 T GT  CT
GAM1710 KIAA1116 3' AGGTATTTGAGGAGCACAATAC 30303      G       C  _
           AG                    TTGTGT TGTGTTTCTC AAT CCT
                                |||||| |||||||||| ||| |||
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                                GACATA ACACGAGGAG TTA GGA
                                  _       T  T
GAM1710 KIAA1117 3' AGGCTGGGAAACGTATTATAA 61771     T      T  AT
                                TTGTG GTGTGTTTC CCA  CCT
                                ||||| ||||||||| |||  |||
                                AATAT TATGCAAAG GGT  GGA
                                  _       _  C_
GAM1710 KIAA1157 5' AGGCTCTGGGAGCCGCGCGCG 72695       T    CCAAT
                                TGTGTGTG GTTTCT    CCT
                                |||||||| ||||||    |||
                                GCGCGCGC CGAGGG    GGA
                                     _    TCTC_
GAM1710 KIAA1190 3' GGGATTGGGGGGACTGGGGAGG 71653      GTGT___  TT
           CGCAG                TTGTGT     GT  CTCCAATCCT
                                ||||||     ||  ||||||||||
                                GACGCG     CA  GGGGTTAGGG
                                   GAGGGGT  GG
GAM1710 KIAA1191 3' AGGGCCTGGAACGCCTGTGCG 40329    TG  T     TCCAA
                                TG  TG GTGTTTC    TCCT
                                ||  || |||||||    ||||
                                GC  GT CGCAAGG    GGGA
                                 GT  C     TCC__
GAM1710 KIAA1200 3' AGGGTGAGGGTACATATGTGA  63030   TG      TTT  CA
                                T  TGTGTGTG  CTC  ATCCT
                                |  ||||||||  |||  |||||
                                A  GTATACAT  GGG  TGGGA
                                 GT       ___  AG
GAM1710 KIAA1209 3' GGGGTGGGGATGTATATAACGA 61405     G    TT    AT
                                TTGT TGTGTG  TCTCCA  CC
                                |||| ||||||  ||||||  ||
                                AGCA ATATAT  AGGGGT  GG
                                  _    GT    GG
GAM1710 KIAA1277 3' GGGGTTCAGGAATATGTATCTA 65083    T  TG     CC
           A                     TTG GTG  TGTTTCT  AATCCT
                                ||| |||  |||||||  ||||||
                                AAT TAT  ATAAGGA  TTGGGG
                                  C  GT     C_
GAM1710 KIAA1303 3' GCACCTGGGGGCACACACATGC 66606         T    ATCCT
           AG                     TTGTGTGTGTGT TCTCCA
                                ||||||||||| ||||||
                                GACGTACACACA GGGGGT
                                       C     CCACGG
GAM1710 KIAA1320 3' AGGAAGTAGGAACATGCATACA 69831           CCAA
                                TGTGTGTGTGTTTCT   TCCT
                                ||||||||||||||   ||||
                                ACATACGTACAAGGA   AGGA
                                       TGA_
GAM1710 KIAA1321 3' AGGATGCTTCAGGCCCATGTAC 62898     TG  T   CTCCA
           AA                     TTGTG  TG GTTT    ATCCT
                                |||||  || ||||    |||||
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                                AACAT  AC CGGA    TAGGA
                                   GT  C   CTTCG
GAM1710  KIAA1322  3'  AGGCTGCAGGTGCACACGTGG  73108   TG    TG   CTC  AT
                                T  TGTGTG  TTT   CA  CCT
                                |  ||||||  |||   ||  |||
                                G  GCACAC  GGA   GT  GGA
                                 GT     GT   C__  C_
GAM1710  KIAA1374  3'  GGGATTATGTATGATATATATA 61915          TCTCC_
            TA                   TGTGTGTGTGTT     AATCCT
                                ||||||||||||     ||||||
                                ATATATATATAG     TTAGGG
                                       TATGTA
GAM1710  KIAA1387  5'  GGAGAGTGGGTGTATGCGCG   71445        TG ___
                                TGTGTGTG  T   TTCTCC
                                ||||||||  |   ||||||
                                GCGCGTAT  G   GAGAGG
                                     GT GGT
GAM1710  KIAA1430  5'  AGGTGAGGGGCGCGCGAGCG   81649    G      TT   CAAT
                                TGT TGTGTGT  CTC    CCT
                                ||| |||||||  |||    |||
                                GCG GCGCGCG  GAG    GGA
                                  A      GG   T___
GAM1710  KIAA1465  3'  GGGAAGGGGAGGGGCGCGGCGC 61501       G    TT    AA_
            G                    TGTGT TGTGT  CTCC   TCCT
                                ||||| |||||  ||||   ||||
                                GCGCG GCGCG  GAGG   AGGG
                                   _    GG    GGA
GAM1710  KIAA1494  3'  GGGAAACCAAACATACAA    68982         GT_    T
                                TTGTGTGT   GTTTC CC
                                ||||||||   ||||| ||
                                AACATACA   CAAAG GG
                                     AAC    _
GAM1710  KIAA1494  3'  TGGGAAATACATAATAA     68984      G        T
                                TTGT TGTGTGTTTC CCA
                                |||| ||||||||| |||
                                AATA ATACATAAAG GGT
                                   _       _
GAM1710  KIAA1497  3'  AGGCAATAGAAATATGTATAT  68111       TG      CCAAT
                                GTGTG  TGTTTCT    CCT
                                |||||  |||||||    |||
                                TATAT  ATAAAGA    GGA
                                   GT      TAAC_
GAM1710  KIAA1508  3'  AGGTATGTGGGAAGCATGTGTA 62539    TG        _  AT
                                TG  TGTGTTTCTC CA  CCT
                                ||  |||||||||| ||  |||
                                AT  GTACGAAGGG GT  GGA
                                 GT        T  AT
GAM1710  KIAA1530  3'  CTGGGGTTCAGCACGGACGGAA 68557     TG  TG     _  _______
            TGTGTGTGCAG              TTG  TG  TGTTTC TCC     AATCCT   GG
                                |||  ||  |||||| |||     ||||||   ||
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                              GAC  GT  GTAAGG AGG     TTGGGG   TC
                                GT  GT     C   CACGAC
GAM1710  KIAA1549  3'  GGGATTGAGACTGGTACGTGTA 69875      TG     TC  _
            CGA                  TTGTG  TGTGTT  TC CAATCCT
                              |||||  ||||||  || |||||||
                              AGCAT  GCATGG  AG GTTAGGG
                                 GT     TC  A
GAM1710  KIAA1554  3'  AGGACTCAGAGCACATACA   96851          T  CCAA
                              TGTGTGTGTT CT    TCCT
                              ||||||||||  ||    ||||
                              ACATACACGA GA    AGGA
                                    _  CTC_
GAM1710  KIAA1643  3'  GGTGGAGTACATATGCATAG   65156           TT    AT
                              TTGTGTGTGTGT  CTCCA  CC
                              ||||||||||||  |||||  ||
                              GATACGTATACA  GAGGT  GG
                                     T_    __
GAM1710  KIAA1649  3'  GGGATGCCTGGAGGCATATATC 51246     TG         CCA_
            CAG                  TTG  TGTGTGTTTCT   ATCCT
                              |||  ||||||||||    |||||
                              GAC  ATATACGGAGG    TAGGG
                                CT          TCCG
GAM1710  KIAA1666  5'  TGGGAGGCACAGCGCAG     65854       G       T
                              TTGTGT TGTGTTTC CCA
                              ||||||| |||||||| |||
                              GACGCG ACACGGAG GGT
                                 _      _
GAM1710  KIAA1691  5'  GGGCCCAGGAGCGCGCGGATGA 94134    TG G         CCAA
                              T  T TGTGTGTTTCT    TCC
                              |  | ||||||||||    |||
                              A  A GCGCGCGAGGA    GGG
                               GT G          CCC_
GAM1710  KIAA1695  3'  GGGGTTGGGGAGACTTGATAT  47832      GT_
                              GTGT   GTTTCTCCAATCCT
                              ||||   ||||||||||||||
                              TATA   CAGAGGGGTTGGGG
                                GTT
GAM1710  KIAA1789  5'  GGAGAACACTGTATACAG     67704       GT_    T
                              TTGTGT   GTGTT CTCC
                              ||||||   ||||| ||||
                              GACATA   CACAA GAGG
                                 TGT    _
GAM1710  KIAA1804  3'  AGGGTAGAGAAATATATAC    70345           CA
                              GTGTGTGTTTCTC  ATCCT
                              ||||||||||||  |||||
                              CATATATAAAGAG  TGGGA
                                     A_
GAM1710  KIAA1828  5'  GGGTGTGAAACTGTGCACAG   74207      TG  T    TCCA
                              TTGTG  TG GTTTC    ATCC
                              |||||  ||  |||||    ||||
```

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                                GACAC  GT CAAAG   TGGG
                                  GT  _    TG__
GAM1710  KIAA1838  5'  AGGGTGCAGCGGGCGCGTCTGC 65368     TG     _ CCA
            G                    TGTG  TGTGTTT CT   ATCCT
                                 ||||  ||||||| ||   |||||
                                 GCGT  GCGCGGG GA   TGGGA
                                   CT     C  CG_
GAM1710  KIAA1870  3'  AGGAAAGACAGAAGTGTATATA 50580       TG    CCAA_
            TA                   TGTGTGTG  TTTCT    TCCT
                                 ||||||||  |||||    ||||
                                 ATATATAT  GAAGA    AGGA
                                     GT    CAGAA
GAM1710  KIAA1870  5'  GGGAAGATGAACCCGCATGCAG 50586        T   C  CAA
                                 TTGTGTGTG GTTT TC   TCCT
                                 |||||||||| |||| ||   ||||
                                 GACGTACGC CAAG AG   AGGG
                                      C   T  A__
GAM1710  KIAA1871  3'  AGGGTTGGGATTACCGGCATGA 61893   TG   GT   TT  T
                                 T  TGT  GTG  TC CCAATCCT
                                 |  |||  |||  || ||||||||
                                 A  ACG  CAT  AG GGTTGGGA
                                  GT   GC   T_ _
GAM1710  KIAA1910  3'  GGGGCTGGAGGGGCGTGTACCC 73716    T   TG   TT    AT
            AA                   TTG GTG  TGT  CTCCA  CCT
                                 ||| |||  |||  |||||  |||
                                 AAC CAT  GCG  GAGGT  GGG
                                   C   GT   GG    CG
GAM1710  KIAA1911  5'  AGGGCTGAAGAGGAGCGTTGCG 73887      GTG      __ AT
            CAA                    TTGTGT   TGTTTCTC  CA  CCT
                                   ||||||   ||||||||  ||  |||
                                   AACGCG   GCGAGGAG  GT  GGA
                                      TT_      AA  CG
GAM1710  KIAA1912  5'  GGAGCGCGGGCGCGCGCGCG   73760          ___
                                 TGTGTGTGTGTTT   CTCC
                                 ||||||||||||   ||||
                                 GCGCGCGCGCGGG   GAGG
                                         CGC
GAM1710  KIAA1925  5'  GGGAAGGGTGCATGTGCGCG   93714     TG    TTCT  AA
                                 TGTG  TGTGT    CC  TCCT
                                 ||||  |||||    ||  ||||
                                 GCGC  GTACG    GG  AGGG
                                   GT    T___  GA
GAM1710  KIAA1938  3'  AGGGTTTAGGAGGGTGTGTATG 93816   TG  TG _     __
            T                    G  TG  T TTCTCC  AATCCT
                                 |  ||  | ||||||  ||||||
                                 T  AT  G GGGAGG  TTGGGA
                                  GT  GT T     AT
GAM1710  KIAA1940  5'  AGGAGCTGGAGGAGCGCGCG   80775          A_
                                 TGTGTGTTTCTCCA  TCCT
                                 ||||||||||||||  ||||
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                                GCGCGCGAGGAGGT AGGA
                                      CG
GAM1710 KIF13B   3' GGGACAGGGGGCAGGTGTGTGA 31571   TG TG G  TT   AA
                                T TG T TGT CTCC TCCT
                                | || | ||| |||| ||||
                                A GT G ACG GGGG AGGG
                                 GT GT G __   AC
GAM1710 KIR3DS1  3' GGAGGTGACATACGCATAA  27981          _
                                TTGTGTGTGTGTT TCTCC
                                |||||||||||| |||||
                                AATACGCATACAG GGAGG
                                      T
GAM1710 KLF5     3' GGGGTGAAGGGGAGTGTGTGCA 9962    TG TG    CA_
                                TG TG TTTCTC ATCCT
                                || || |||||| |||||
                                AC GT GAGGGG TGGGG
                                 GT GT    AAG
GAM1710 KLK12    3' GGGGTGAGAGAAGTGTGCA  39467    TG    CA
                                TGTG TTTCTC ATCCT
                                |||| |||||| |||||
                                ACGT GAAGAG TGGGG
                                  GT    AG
GAM1710 L3MBTL   3' GGAAGAAGCACATAGGTAA  70088    TG       _
                                TTG TGTGTGTTTCT CC
                                ||| |||||||||| ||
                                AAT ATACACGAAGA GG
                                 GG        A
GAM1710 L3MBTL   3' GGTCACACAGAGGCCTGCATGC 70089        T    CCAAT_ T
            AA                   TTGTGTGTG GTTTCT    CC
                                ||||||||| ||||||    ||
                                AACGTACGT CGGAGA    GG
                                     C    CACACT
GAM1710 LAMB4    3' AGGAAGTCAGAATTCATACACA 82080        TGT   CCAA
            G                    TTGTGTGTG  TTCT   TCCT
                                |||||||||  ||||  ||||
                                GACACATAC  AAGA   AGGA
                                     TT_   CTGA
GAM1710 LCE      3' GGCACAAGGAATCACACGTGG 44261   TG    T   ____
                                T TGTGTG GTTTCT   CC
                                | |||||| ||||||   ||
                                G GCACAC TAAGGA   GG
                                 GT    _    ACAC
GAM1710 LCP      5' AGGAGGCTGGGAAACGCGAGCG 27476      G       CAA_
            CAG                   TTGTGT TGTGTTTCTC   TCCT
                                |||||| ||||||||||   ||||
                                GACGCG GCGCAAAGGG   AGGA
                                   A        TCGG
GAM1710 LHX6     3' GGGAAAACACACACACGG    27643          CT
                                TTGTGTGTGTGTTT  CC
                                |||||||||||||  ||
```

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                                GGCACACACACAAA  GG
                                      AG
GAM1710  LHX6     3'  GGGCTCAGGCTACACACGA   27644         T   C__
                                TTGTGTGTG GTTT   TCC
                                ||||||||| ||||   |||
                                AGCACACAT CGGA   GGG
                                     _   CTC
GAM1710  LHX6     3'  GGGGAAAACACACACACG    27645          _
                                TGTGTGTGTGTTT CTCC
                                |||||||||||| ||||
                                GCACACACACAAA GGGG
                                      A
GAM1710  LIN-28   3'  GGGTTCCAGGGAGACACACAAG 45470     G         C__    T
              CGA                  TTGT TGTGTGTTTCTC   AATCC
                                |||| ||||||||||   |||||
                                AGCG ACACACAGAGGG   TTGGG
                                  A          ACC
GAM1710  LOXL4    3'  GGACCAAAATACACAGCAG    50860     G       C__
                                TTGT TGTGTGTTT   TCC
                                |||| |||||||||   |||
                                GACG ACACATAAA   AGG
                                  _        ACC
GAM1710  LSM10    5'  GGAAGGAATGTCGCGTGCAA   52870     TG   _     _
                                TTG  TGTG TGTTTCT CC
                                |||  |||| ||||||| ||
                                AAC  GCGC GTAAGGA GG
                                  GT   T      A
GAM1710  LW-1     5'  AGGACCAGAATGTGCACATGCA 60884         TG _   CCAA
              G                   TTGTGTGTG  T TTCT    TCCT
                                |||||||||  | ||||   ||||
                                GACGTACAC  G AAGA    AGGA
                                     GT T    CC__
GAM1710  LW-1     5'  AGGACCAGAATGTGCACATGCA 60885         TG _   CCAA
              G                   TTGTGTGTG  T TTCT    TCCT
                                |||||||||  | ||||   ||||
                                GACGTACAC  G AAGA    AGGA
                                     GT T    CC__
GAM1710  MAP3K3   3'  GGGGCTGGGAACAGTGTGCAA  11543      TG G    T T   AT
                                TTGTG  T TGTT C CCA  CCT
                                |||||  | |||| | |||  |||
                                AACGT  G ACAA G GGT  GGG
                                  GT _    _ _   CG
GAM1710  MBLL39   3'  AGGAGGCAAGGCAAATGCATAG 59256        G    CT  AA
                                TTGTGTGT TGTTT  CC  TCCT
                                |||||||| |||||  ||  ||||
                                GATACGTA ACGGA  GG  AGGA
                                     A    AC  __
GAM1710  MDS028   3'  AGGATAGGGAATATGCATTACA 38062       _         CCA
              G                   TTGTG TGTGTGTTTCT   ATCCT
                                ||||| ||||||||||   |||||
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                                GACAT ACGTATAAGGG   TAGGA
                                   T         A__
GAM1710  MESDC1    3'  GGCAGGGCCATGCACGCAA    42902          TT   _
                                TTGTGTGTGTG  TCT CC
                                ||||||||||  ||| ||
                                AACGCACGTAC  GGA GG
                                      CG   C
GAM1710  MGC10999  5'  GGGGCCAGAGCTGCGCGTGG   51200   TG     T   ___
                                T  TGTGTG GTTT   CTCC
                                |  |||||| ||||   ||||
                                G  GCGCGT CGAG   GGGG
                                 GT      _    ACC
GAM1710  MGC11352  3'  GGGAGGTGGCAGGCATGCA    65435        G   _    AATCCT
                                TGTGTGT TGTT TCTCC
                                |||||||  |||| |||||
                                ACGTACG ACGG GGAGG
                                     G    T    G   T
GAM1710  MGC12679  3'  GGGTCGGCGCATGCGCACGA   52184           TTCT  A
                                TTGTGTGTGTGT    CC ATCC
                                ||||||||||||    || ||||
                                AGCACGCGTACG    GG TGGG
                                       C___  C
GAM1710  MGC13008  5'  GGGCCAGGGCGCACCACG     52058      T       C__
                                TGTG GTGTGTTT   TCC
                                ||||  ||||||||   |||
                                GCAC CACGCGGG   GGG
                                   _       ACC
GAM1710  MGC13057  5'  GGAGGTAAACACTACACGTGA  51284    TG    _    __
                                T  TGTGT GTGTT  TCTCC
                                |  |||||  |||||  |||||
                                A  GCACA CACAA  GGAGG
                                 GT     T    AT
GAM1710  MGC13159  5'  AGGATTTACCAGAAACATGCGT 53035    TG         CC__
            GTA                    TG  TGTGTGTTTCT    AATCCT
                                ||  ||||||||||    ||||||
                                AT  GCGTACAAAGA    TTAGGA
                                 GT          CCAT
GAM1710  MGC13159  5'  GGTGAGGCGCGCACCAA      53039     T         T
                                TTG GTGTGTGTTTC CC
                                |||  ||||||||||  ||
                                AAC CACGCGCGGAG GG
                                   _         T
GAM1710  MGC13168  3'  GAATGGGAGGCATGTATGC    52186       TG     T   A
                                GTGTG  TGTTTC CCA TC
                                |||||  ||||||  |||  ||
                                CGTAT  ACGGAG GGT AG
                                   GT      _   A
GAM1710  MGC14161  5'  AGGAGCCTGGAGCGCGAGTACA 52906       TG       TCCAA
            G                    TTGTG  TGTGTTTC     TCCT
                                |||||  ||||||||     ||||
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                                GACAT  GCGCGAGG    AGGA
                                   GA      TCCG_
GAM1710  MGC14421  5'  AGGATTAAGTGAGACATGGTAT 52962      GT_     TCC_
             ATAA                  TTGTGT   GTGTTTC   AATCCT
                                |||||||  |||||||  |||||||
                                AATATA   TACAGAG   TTAGGA
                                   TGG      TGAA
GAM1710  MGC14859  3'  AGGGTATGGGGCATGTGCCCAG 62597    T TG    TT TCCA
                                TTG G  TGTGT  C    ATCCT
                                ||| |  |||||  |    |||||
                                GAC C  GTACG  G    TGGGA
                                  C GT     GG TA__
GAM1710  MGC15435  3'  AGGAATTGGGGTGGCACACG   51394       TT      _
                                TGTGTGT  CTCCAAT CCT
                                |||||||  ||||||| |||
                                GCACACG  GGGGTTA GGA
                                    GT      A
GAM1710  MGC15504  5'  GGAAAACATGCGCCCAA     52220     T       C
                                TTG GTGTGTGTTT TCC
                                ||| |||||||||| |||
                                AAC CGCGTACAAA AGG
                                  C        _
GAM1710  MGC15631  5'  GGGATGCAGAGCACATGCCG   52234    T       T  CCA
                                TG GTGTGTGTT CT   ATCCT
                                || |||||||| ||   |||||
                                GC CGTACACGA GA   TAGGG
                                 _       _ CG_
GAM1710  MGC15873  3'  GGACACAGACACACACAGAG   53008    G        C__
                                TT TGTGTGTGTTT   TCC
                                || ||||||||||   |||
                                GA ACACACACAGA   AGG
                                 G         CAC
GAM1710  MGC15906  5'  GGGCGAGGGTGACATACA    52887       GT    CAA
                                TGTGTGT  TTCTC   TCC
                                |||||||  |||||  |||
                                ACATACA  GGGAG   GGG
                                    GT    C__
GAM1710  MGC16491  3'  GGGGTTGAGGTGGGCAGTATAC 54740       _   TC  _
             A                   TGTGTG TGTT  TC CAATCCT
                                ||||||| ||||  || |||||||
                                ACATAT ACGG  GG GTTGGGG
                                   G   GT  A
GAM1710  MGC17303  3'  GGGAGAGGCTGGGGGCACCCAT 58234   TG   T   TT __  AA
             GTGG                  T  TGTG GTGT  CT  CC  TCCT
                                |  |||| ||||  ||  ||  ||||
                                G  GTAC CACG  GG  GG  AGGG
                                 GT   C   GG  TC  AG
GAM1710  MGC18079  3'  AGGCACTGCAGGGGTGTCACAC 59030       T TG TT  C  AT_
             AG                   TTGTGTG G  T  CT CA   CCT
                                ||||||| |  |  || ||   |||
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                                GACACAC T  G  GA GT   GGA
                                   _ GT GG  C  CAC
GAM1710  MGC19780  5'  GGGAAGTTGGACGCATGCGC  59363        TTTC   __
                                GTGTGTGTG   TCCAA  TCCT
                                |||||||||   |||||  ||||
                                CGCGTACGC   AGGTT  AGGG
                                    ____    GA
GAM1710  MGC20255  3'  GGACAAGTGTGCATGCAG   54539        TG   C
                                TTGTGTGTG  TTT TCC
                                |||||||||  ||| |||
                                GACGTACGT  GAA AGG
                                     GT   C
GAM1710  MGC20255  3'  GGACAAGTGTGCATGCAG   54540        TG   C
                                TTGTGTGTG  TTT TCC
                                |||||||||  ||| |||
                                GACGTACGT  GAA AGG
                                     GT   C
GAM1710  MGC21738  3'  GGAGAAGGCATATGACAG   59578     _    G
                                TTGT GTGTGT TTTCTCC
                                |||| ||||||| |||||||
                                GACA TATACG GAAGAGG
                                  G    _
GAM1710  MGC2306   3'  GGAATAAAACCTACACACAA  51953        T   C__
                                TTGTGTGTG GTTT   TCC
                                |||||||||  ||||   |||
                                AACACACAT CAAA   AGG
                                     C   ATA
GAM1710  MGC23884  3'  AGGATACTGAAATACACACAT  59334          TCCA
                                GTGTGTGTGTTTC   ATCCT
                                ||||||||||||   |||||
                                TACACACATAAAG   TAGGA
                                       TCA_
GAM1710  MGC2452   5'  AGGAGTGTCGGAGCACATGTGT 51963   TG  TG      TC  A
           GG                    T  TG  TGTGTTTC  CA TCCT
                                 |  ||  ||||||||  || ||||
                                 G  GT  ACACGAGG  GT AGGA
                                  GT  GT       CT  G
GAM1710  MGC2452   5'  GGGAGCCTTGAAGATACGTGCA 51965    TG    G   TCCAA
           A                      TTG  TGTGT TTTC    TCCT
                                  |||  ||||| ||||    ||||
                                  AAC  GCATA GAAG    AGGG
                                    GT    _   TTCCG
GAM1710  MGC2487   5'  AGGAGCAGAGGAGCACACAGAT 43975   TG G         CAA
           GA                     T  T TGTGTGTTTCTC   TCCT
                                  |  | ||||||||||||   ||||
                                  A  A ACACACGAGGAG   AGGA
                                  GT G          ACG
GAM1710  MGC2488   3'  GGAAAGAAGCATGTAGCAA   44090     G  TG     CCAA
                                TTGT TG  TGTTTCT   TCC
                                |||| ||  |||||||   |||
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                                AACG AT  ACGAAGA   AGG
                                  _ GT     A___
GAM1710 MGC2555  5' GGGCTGGACACGCAGCG    52291    G    TTTC   AT
                                TGT TGTGTG   TCCA  CC
                                ||| ||||||   ||||  ||
                                GCG ACGCAC   AGGT  GG
                                  _    ____   CG
GAM1710 MGC2628  3' AGGAGACGGGTGTTACACGCA 44195       TTT  CAA
                                TGTGTGTG  CTC  TCCT
                                ||||||||  |||  ||||
                                ACGCACAT  GGG  AGGA
                                    TGT  CAG
GAM1710 MGC2628  3' GGGATGCTGGAGGCATGCCTGC 44199     T       CCA
              AG                  TTGTG GTGTGTTTCT  ATCCT
                                  ||||| ||||||||||  |||||
                                  GACGT CGTACGGAGG  TAGGG
                                     C        TCG
GAM1710 MGC2721  3' GGGGTTGGTCTGAAGCCTGCAC 52189       T    T__
              GCG                   TGTGTGTG GTTTC  CCAATCCT
                                  |||||||| |||||  ||||||||
                                  GCGCACGT CGAAG  GGTTGGGG
                                     C    TCT
GAM1710 MGC2747  3' AGGGTTTCAGGAGCGTTTATGT 44324    TG  TG     CC
              AA                  TTG  TG  TGTTTCT  AATCCT
                                  |||  ||  |||||||  ||||||
                                  AAT  AT  GCGAGGA  TTGGGA
                                    GT  TT     CT
GAM1710 MGC29937 3' GAACATGGGGGACATATATATA 58730         TT T   ATCCT
                                TGTGTGTGTGT  C CCA
                                ||||||||||  | |||
                                ATATATATACA  G GGT
                                      GG _   ACAAGA
GAM1710 MGC29956 3' GGGGTTGGTCTGCTTTGTGTAT 58924   TG  TG  T_  TTCT
              GG                  T  TG  TG  GT   CCAATCCT
                                  |  ||  ||  ||   ||||||||
                                  G  AT  GT  CG   GGTTGGGG
                                   GT  GT  TT  TCT_
GAM1710 MGC3123  3' AGGACACAGGAGGCAAGTATGC 44341      TG     CCAA
              G                    TGTGTG  TGTTTCT   TCCT
                                  ||||||  |||||||   ||||
                                  GCGTAT  ACGGAGG   AGGA
                                     GA      ACAC
GAM1710 MGC3178  3' GGGAATAAGCACATACAG    48720        GT_  T
                                TTGTGTGTGT   TTC CC
                                ||||||||||   ||| ||
                                GACATACACG   AAG GG
                                      AAT  _
GAM1710 MGC33630 3' AGGACTTTGGGTGTGTGTGCAT 59003      TG TTC    __
                                GTGTG  T   TCCAA  TCCT
                                |||||  |   |||||  ||||
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                                TACGT  G   GGGTT  AGGA
                                  GT TGT    TC
GAM1710  MGC34869  3'  TGGGGTGACAATGTATATATGC 58720        _____   T   AATCCT
             AA                   TTGTGTGTG    TGTT CTCC
                                  |||||||||    |||| ||||
                                  AACGTATAT    ACAG GGGG
                                       ATGTA   T      TC
GAM1710  MGC4238   3'  GGACCGAGACACAGACATGG   51306   TG   G      __
                                  T  TGT TGTGTTTC  TCC
                                  |  ||| ||||||||  |||
                                  G  ACA ACACAGAG  AGG
                                   GT   G      CC
GAM1710  MGC4607   5'  GGGCCGCGGGAGCCGCACGCG  49542        T     CCAA
                                  TGTGTGTG GTTTCT    TCC
                                  ||||||||| ||||||    |||
                                  GCGCACGC CGAGGG    GGG
                                       _     CGCC
GAM1710  MGC4737   5'  GTTGGAAGCGTGCATCAA    49651     T   TG    TC
                                  TTG GTG  TGTT  TCCAAT
                                  ||| |||  ||||  ||||||
                                  AAC TAC  GCGA  AGGTTG
                                    _  GT   __
GAM1710  MGC5139   5'  GGGATGGAAGAGACAGTGTGTG 74574    TG  TG G      _  A
             G                    T  TG  T TGTTTCT CCA TCCT
                                  |  ||  | ||||||| ||| ||||
                                  G  GT  G ACAGAGA GGT AGGG
                                   GT  GT _      A  _
GAM1710  MGC7036   5'  AGGCCCAAGAGTCGCGTGCGCG 59615      TG    T    CCAAT
                                  TGTG  TGTG TTCT    CCT
                                  ||||  |||| ||||    |||
                                  GCGC  GCGC GAGA    GGA
                                    GT    T   ACCC_
GAM1710  MGC9753   3'  GGGTTAGGGGAACGTGTGTGC  54197   TG  TG      C    T
                                  G  TG  TGTTTCTC AATCC
                                  |  ||  |||||||| |||||
                                  C  GT  GCAAGGGG TTGGG
                                   GT  GT       A
GAM1710  MGEA6     3'  AGGATATTGAGATGTACTACAG 21011      T   TG    TCCA
                                  TTGTG GTG  TTTC    ATCCT
                                  ||||| |||  ||||    |||||
                                  GACAT CAT  AGAG    TAGGA
                                    _  GT    TTA_
GAM1710  MIG-6     5'  GGACGGACATGCGCGGGA    39000    G        TC
                                  TT TGTGTGTGTT  TCC
                                  || ||||||||||  |||
                                  AG GCGCGTACAG  AGG
                                   G         GC
GAM1710  MIL1      3'  GGGAATCTTCGAAATATGTACA 31726        TG     TCCAA_
             CAG                    TTGTGTG  TGTTTC     TCCT
                                  |||||||  ||||||     ||||
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                                GACACAT  ATAAAG     AGGG
                                   GT     CTTCTA
GAM1710 MLZE    5'  AGGCTGGAGTGCAGCGCATGG  49445   TG    G   TT    AT
                                T  TGTGT TGT  CTCCA  CCT
                                |  ||||| |||  |||||  |||
                                G  ACGCG ACG  GAGGT  GGA
                                 GT    _   T_    C_
GAM1710 MPPE1   3'  GGGATTATGTGTATACATAA  43819         TG TTCTCC
                                TTGTGTGTG  T     AATCCT
                                |||||||||  |     ||||||
                                AATACATAT  G     TTAGGG
                                      GT TA____
GAM1710 MPZL1   5'  TGGGGAGCGCGGCGTGG     15539   TG   G       T
                                T  TGT TGTGTTTC CCA
                                |  ||| ||||||||| |||
                                G  GCG GCGCGAGG GGT
                                 GT  _       _
GAM1710 MRPS18B  3'  GGGACTAGGAGATAATGTGTAT 26753     TG  TG   _    AA_
            GTAG                   TTG  TG  TGTT TCTCC   TCCT
                                |||  ||  |||| |||||   ||||
                                GAT  AT  GTAA AGAGG   AGGG
                                  GT  GT    T    ATC
GAM1710 MRPS2   3'  GGGTGAGCGACATGTGCA    32632    TG     T   CA
                                TG  TGTGTT CTC  ATCC
                                ||  |||||| |||  ||||
                                AC  GTACAG GAG  TGGG
                                 GT     C   __
GAM1710 MSTP031  5'  AGGGTTGCATAACAGCATGTAA 50165     TG   G    TCTC
                                TTG  TGT TGTT    CAATCCT
                                |||  ||| ||||   |||||||
                                AAT  ACG ACAA    GTTGGGA
                                  GT   _    TAC_
GAM1710 MYL9    3'  AGGCCAGGAGAAGTGCGTGCCG 60611     T TG  TG      AAT
            A                    TTG G  TG  TTTCTCC   CCT
                                ||| |  ||  |||||||   |||
                                AGC C  GC  GAAGAGG   GGA
                                  _ GT  GT      ACC
GAM1710 MYO5C   3'  GGTAGGAATAATACATGA    38723   TG    G      _
                                T  TGTGT TGTTTCT CC
                                |  ||||| ||||||| ||
                                A  ACATA ATAAGGA GG
                                 GT    _      T
GAM1710 NICE-1   3'  GGGATTCGAGAGCCATGCGTGG 39320   TG     T   T   C
                                T  TGTGTG GTT CTC AATCCT
                                |  |||||| ||| ||| ||||||
                                G  GCGTAC CGA GAG TTAGGG
                                 GT     _   _   C
GAM1710 NIR1    5'  GGGGCGGGGGCGCGGGCGCG   49166      G    TT    AA
                                TGTGT TGTGT  CTCC  TCC
                                ||||| |||||  ||||  |||
```

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                                GCGCG GCGCG  GGGG  GGG
                                  G    __   CG
GAM1710  NIR1     5'  GGGAAGCGCGAGGAGCGCGCGT 49165          CAA__
                A                  TGTGTGTGTTTCTC    TCCT
                                   ||||||||||||||    ||||
                                   ATGCGCGCGAGGAG    AGGG
                                         CGCGA
GAM1710  NOL5A    3'  GGGAGGTGGGGCATACCATAG  22139     T     TT T  AA
                                   TTGTG GTGTGT  C CC  TCCT
                                   ||||| ||||||  | ||  ||||
                                   GATAC CATACG  G GG  AGGG
                                     _     GG T  __
GAM1710  NUDT3    5'  GGGGCGCGCGCGCACGCG    22952          TT_
                                   TGTGTGTGTGT   CTCC
                                   ||||||||||   ||||
                                   GCGCACGCGCG   GGGG
                                         CGC
GAM1710  NUP54    5'  GGATTTAATACACAGCAG    60726     G      TCTCC
                                   TTGT TGTGTGTT    AATCC
                                   |||| ||||||||    |||||
                                   GACG ACACATAA    TTAGG
                                     _      T_____
GAM1710  NXPH2    3'  GGAAATGAGGGATACATATGTA 73094    TG     TT   CAA   T
                                   TG  TGTGTGT  CTC   TCC
                                   ||  |||||||  |||   |||
                                   AT  ATACATA  GAG   AGG
                                    GT      GG   TAA
GAM1710  NYD-SP15 3'  GGAAGAAGCATACAAGTGG   48847   TG G        _
                                   T  T TGTGTGTTTCT CC
                                   |  | ||||||||||| ||
                                   G  G ACATACGAAGA GG
                                    GT A         A
GAM1710  OATPRP4  3'  TTGATTGGAAAAATGTATGTGC 48986    TG   TG   C     CT
                AG                   TTG  TGTG  TTT TCCAATC
                                     |||  ||||  ||| |||||||
                                     GAC  GTAT  AAA AGGTTAG
                                       GT   GT   A     TTT
GAM1710  OAZ2     3'  AGGAAGAGGAATATATAGCAA  11872     G         CAA
                                   TTGT TGTGTGTTTCTC   TCCT
                                   |||| ||||||||||||   ||||
                                   AACG ATATATAAGGAG   AGGA
                                     _         A__
GAM1710  OAZIN    5'  AGGGCCTAGGAGAAGTGCTGTA 32435      TGT TG     AA__
                TAG                  TTGTG   G  TTTCTCC    TCCT
                                     |||||   |  |||||||    ||||
                                     GATAT   C  GAAGAGG    GGGA
                                       GT_ GT      ATCC
GAM1710  OBSCN    3'  GGAGTCCCAGGACACACACA   71191          _____
                                   TGTGTGTGTTT    CTCC
                                   ||||||||||     ||||
```

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                                ACACACACAGG    GAGG
                                     ACCCT
GAM1710 OBTP    5' GGAAGACCACACATGCAG   34666          T TC
                                TTGTGTGTGTG T  TCC
                                |||||||||| |  |||
                                GACGTACACAC A  AGG
                                     C GA
GAM1710 OLIG1   3' GTTGAAGAGCTACATACG   97337        T   C
                                TGTGTGTG TTCT CAAT
                                |||||||| |||| ||||
                                GCATACAT GAGA GTTG
                                    C   A
GAM1710 OPRL1   5' GGAGGTTGCAGAAGTACCGTAC 8072        T      C   _
           AG                     TTGTGTG GTGTTTCT CAATC CT
                                |||||||| |||||||| ||||| ||
                                GACATGC CATGAAGA GTTGG GG
                                   _     C    A
GAM1710 OSBPL10 5' GGGGTGGGGAGTGACGTGCA  35524   TG   T   A_
                                TG  TGTT CTCC  ATCCT
                                ||  |||| ||||  |||||
                                AC  GCAG GAGG  TGGGG
                                 GT   T   GG
GAM1710 OSBPL1A 5' GGCCGAGCGCACAGCAG    55490     G       CT
                                TTGT TGTGTGTTT  CC
                                |||| |||||||||  ||
                                GACG ACACGCGAG  GG
                                   _       CC
GAM1710 OSRF    3' GGGTTGGAGAAATTAGCAC   60270     GTGT
                                GTGT   GTTTCTCCAATCC
                                ||||   ||||||||||||
                                CACG   TAAAGAGGTTGGG
                                  AT__
GAM1710 P450RAI-2 3' GGGAGGTAGAAACCTGTGTGTG 39577   TG  TG  T    _ AA
           G                     T  TG  TG GTTTCT CC  TCCT
                                |  ||  || ||||||  ||  ||||
                                G  GT  GT CAAAGA GG  AGGG
                                 GT  GT  C     T __
GAM1710 P5-1    3' AGGATGGAAGGAGTGCAATGTA 22889    TG G  TG    _  A
           G                     TTG  T TG  TTTCT CCA TCCT
                                |||  | ||  ||||| ||| ||||
                                GAT  A AC  GAGGA GGT AGGA
                                  GT _  GT    A  _
GAM1710 PABPC5  3' GGGGAAAACATATGTGA    55934   TG     G
                                T  TGTGTGT TTTCTCC
                                |  ||||||| |||||||
                                A  GTATACA AAAGGGG
                                 GT     _
GAM1710 PADI1   3' AGGTCACTGAGACATGCACA  62698          TCCAAT
                                TGTGTGTGTTTC    CCT
                                ||||||||||||    |||
```

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                                ACACGTACAGAG     GGA
                                      TCACT_
GAM1710  PAIP1    3'  AGGATTGCTTGTAAATATGCAT 67474     TG       CTC__
             GTAA                  TTG  TGTGTGTTT     CAATCCT
                                ||| |||||||||    |||||||
                                AAT  ACGTATAAA    GTTAGGA
                                  GT        TGTTC
GAM1710  PCDH20   3'  GGGAAATAGATATATACATACA 43423          T   CCAA
                                TGTGTGTGTGT TCT    TCCT
                                |||||||||||| |||    ||||
                                ACATACATATA AGA    AGGG
                                      T   TAA_
GAM1710  PCMF     3'  AGGAAGAGAGAAAATATATATG 73955    TG      G     CAA
             A                   T  TGTGTGT TTTCTC   TCCT
                                |  ||||||| ||||||   ||||
                                A  ATATATA AAAGAG   AGGA
                                 GT      _     AGA
GAM1710  PDCD6    3'  GGGAATGGAGCACAGGTGCAG  60274     TG G    TTT     A
                                TTG  T TGTG   CTCCA TCCT
                                |||  | ||||   ||||| ||||
                                GAC  G ACAC   GAGGT AGGG
                                  GT G   ___     A
GAM1710  PDCD7    5'  CCTTGGCGAAGTGCGCGCGCGA 72603         TG    T    TCCT
                                TTGTGTGTG  TTTC CCAA
                                |||||||||  |||| ||||
                                AGCGCGCGC  GAAG GGTT
                                      GT    C    CCG
GAM1710  PDE10A   3'  AGGAAGAGAGAAGCAAACATGT 22842     TG   G       CAA
             AG                    TTG  TGT TGTTTCTC   TCCT
                                |||  ||| |||||||||   ||||
                                GAT  ACA ACGAAGAG   AGGA
                                  GT   A       AGA
GAM1710  PDE11A   5'  GGGGTGAACATGTGCAGGA   34256    G  TG      _
                                TT TG  TGTGTTT CTCC
                                || ||  ||||||| ||||
                                AG AC  GTACAAG GGGG
                                 G  GT      T
GAM1710  PF1      5'  GGGGTTGGGGGGGCCGGAGCAG 96833    G   G_  T  TT
             AG                    TT TGT  TG GT  CTCCAATCCT
                                || |||  || ||  ||||||||||
                                GA ACG  GC CG  GGGGTTGGGG
                                 G   AG  _  GG
GAM1710  PGRMC2   3'  GGGAGGTGGGGGTACACATCA  21978    T     T     A_
                                TG GTGTGT TCTCCA  TCCT
                                || |||||| ||||||  ||||
                                AC TACACA GGGGGT  AGGG
                                  _     T     GG
GAM1710  PI15     3'  GGGAACATGGGCATGTATATA  32458       TG   TTCT   A__
                                TGTGTG  TGT    CCA   TCCT
                                ||||||  |||    |||   ||||
```

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                                ATATAT  ACG   GGT   AGGG
                                   GT  _____  ACA
GAM1710  PIK3C2G  5'  GGAAGATATATGCGTCAG    17094    _        C
                                TTG TGTGTGTGTTT TCC
                                ||| |||||||||| |||
                                GAC GCGTATATAGA AGG
                                  T        _
GAM1710  PIP5K2A  3'  GGGTGAGTGTGTGCGCGC    18519       TG TT   CA
                                GTGTGTG  T  CTC  ATCC
                                |||||||  |  |||  ||||
                                CGCGCGT  G  GAG  TGGG
                                    GT T_  __
GAM1710  PITPNM   5'  AGGAGCGGAGGCCGCGCGCG   18142        T  TT    AA
                                TGTGTGTG GT  CTCC  TCCT
                                |||||||| ||  ||||  ||||
                                GCGCGCGC CG  GAGG  AGGA
                                     _ __    CG
GAM1710  PKNOX2   3'  GGGGTTGGAGAAGGTGCTACAT 92529      T TG _
                                GTGTG G  T TTCTCCAATCCT
                                ||||| |  | ||||||||||||
                                TACAT C  G AAGAGGTTGGGG
                                   _ GT G
GAM1710  PLA2G12  5'  GGGAAGGAGGCGTGGATATGG  48778   TG   G GT  TT    AA
                                T  TGT T  GT  CTCC  TCCT
                                |  ||| |  ||  ||||  ||||
                                G  ATA G  CG  GAGG  AGGG
                                 GT   G TG  __    A_
GAM1710  PLXNC1   5'  GGAGCCCGAGCGCGCGCAGGA  20456    G         ___
                                TT TGTGTGTGTTT   CTCC
                                || ||||||||||   ||||
                                AG ACGCGCGCGAG   GAGG
                                 G         CCC
GAM1710  PM5      5'  GGGGTCGAAGCGCGCGTGC   27382   TG        TCCA
                                G  TGTGTGTTTC    ATCCT
                                |  ||||||||||    |||||
                                C  GCGCGCGAAG    TGGGG
                                 GT         C___
GAM1710  PMX2B    3'  GGAAAAGGCACACACACA    15384           C_
                                TGTGTGTGTGTTT  TCC
                                ||||||||||||  |||
                                ACACACACACGGA  AGG
                                        AA
GAM1710  POLR2D   3'  GGGAGACGGAAGAAGCACGCCA 17843   TG  T        _  AA_
            TGG                    T  TG GTGTGTTTCT CC   TCCT
                                |  || ||||||||||  ||   ||||
                                G  AC CGCACGAAGA GG   AGGG
                                 GT  _         A  CAG
GAM1710  PP1628   5'  GGGGCTGGGAGCACACACGC   48079          T T   AT
                                GTGTGTGTGTT C CCA  CCT
                                |||||||||| | |||  |||
```

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                                CGCACACACGA G GGT  GGG
                                      _ _  CG
GAM1710 PP3501   3' GGATGAGACCTGCACGCAA   41682        T   _
                                TTGTGTGTG GTTTC TCC
                                ||||||||| ||||| |||
                                AACGCACGT CAGAG AGG
                                     C    T
GAM1710 PPP1R14C 3' GGAAAAAGGAAGCACTGTGTAG 48928    TG  T      CCAA
                                TTG  TG GTGTTTCT   TCC
                                |||  || ||||||||   |||
                                GAT  GT CACGAAGG   AGG
                                  GT _      AAAA
GAM1710 PPP1R1B  5' GGCAGAGACACACGCGGAG   50792   G         _
                                TT TGTGTGTGTTTCT CC
                                || ||||||||||||| ||
                                GA GCGCACACAGAGA GG
                                 G          C
GAM1710 PRC1     3' CTTTGTTGGGGGTATGCATGTA 15627   TG  TG    T      CCT
            TGA                   T  TG  TGTGT TCTCCAAT
                                | ||  ||||| ||||||||
                                A  AT  ACGTA GGGGGTTG
                                 GT  GT    T      TTTCC
GAM1710 PRDM10   3' TTGGAAAACATGTATGTAG   39980    TG  TG    C
                                TTG  TG  TGTTT TCCAA
                                |||  ||  ||||| |||||
                                GAT  AT  ACAAA AGGTT
                                  GT  GT   _
GAM1710 PRDM8    5' GGACTCCGGGGAAATACGCACG 39974    G          AA__  T
            GGG                    TT TGTGTGTGTTTCTCC   TCC
                                || ||||||||||||||   |||
                                GG GCACGCATAAAGGGG   AGG
                                 G           CCTC
GAM1710 PRKWNK2  3' ATTGGGGAGTGTATCTGCAA  92191     GT  TG   T
                                TTGT  GTG  TTTC CCAAT
                                ||||  |||  |||| |||||
                                AACG  TAT  GAGG GGTTA
                                  TC  GT   _
GAM1710 PRO0097  5' GAGGCAAACACGTGTGCGA   26934      TG    __
                                TTGTG  TGTGTT  TCTC
                                |||||  ||||||  ||||
                                AGCGT  GCACAA  GGAG
                                   GT     AC
GAM1710 PRO1598  5' AGGGTTGGGGAGGTATCAGCCA 38127    T  GT   TT
            A                   TTG GT  GTG  TCTCCAATCCT
                                ||| ||  |||  ||||||||||
                                AAC CG  TAT  AGGGGTTGGGA
                                  _ AC   GG
GAM1710 PRO1905  3' TCCCTGGGAAGCGCACATACA  38381          T   ATCCT
                                TGTGTGTGTGTTTC CCA
                                |||||||||||||| |||
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                                ACATACACGCGAAG GGT
                                      _  CCCTA
GAM1710 PRO2000  5' TAGGATTTTCTTAAGAAATGTT 26917       _ TG   CC____
            ACACATAG               TTGTGTGT G  TTTCT    AATCCT  A
                                |||||||| |  |||||    ||||||  |
                                GATACACA T  AAAGA    TTAGGA  T
                                    T GT    ATTCTT
GAM1710 PRO2012  3' TGGGGAACGGTATACACGA   38390        TGT
                                TTGTGTGTG  TTCTCCA
                                |||||||||  |||||||
                                AGCACATAT  AAGGGGT
                                     GGC
GAM1710 PRO2015  3' AGGGTTGGAGAAGTGTGC    38155    TG
                                GTG  TTTCTCCAATCCT
                                |||  ||||||||||||
                                CGT  GAAGAGGTTGGGA
                                  GT
GAM1710 PRO2714  3' GGGGCCAGGCATGCCTGCGA  38194     T     __
                                TTGTG GTGTGTTT  CTCC
                                ||||| ||||||||  ||||
                                AGCGT CGTACGGA  GGGG
                                   C      CC
GAM1710 PRO2893  3' GGGCAGTGAAATGCATCCACGA 38434     TG      TCCAA
                                TTGTG  TGTGTTTC    TCC
                                |||||  ||||||||    |||
                                AGCAC  ACGTAAAG    GGG
                                   CT      TGAC_
GAM1710 PRO2955  3' GGGGTGGTTGAATATATATATA 38241          CT  AT  T
                                TGTGTGTGTGTTT  CCA  CC
                                ||||||||||||  |||  ||
                                ATATATATATAAG  GGT  GG
                                       TT   GG
GAM1710 PRRG2    3' AGGGCGGGGGGCATATTTGCAA 8158      T    TT   CAA
                                TTGTG GTGTGT  CTC   TCCT
                                ||||| ||||||  |||   ||||
                                AACGT TATACG  GGG   GGGA
                                   T     GG  C__
GAM1710 PRSC     3' AGGGTACACGAGCACAACGTGC 22702    TG  _    CTCCA
            AG                   TTG  TGT GTGTTT    ATCCT
                                |||  ||| ||||||    |||||
                                GAC  GCA CACGAG    TGGGA
                                  GT   A     CACA_
GAM1710 PS-PLA1  3' AGGATTCAATAGAAACATGTAC 32474    G   TG     CC__
            AGGG                  TT TGTG  TGTTTCT    AATCCT
                                || ||||  |||||||   ||||||
                                GG ACAT  ACAAAGA    TTAGGA
                                 G   GT     TAAC
GAM1710 PTGES2   3' GGGACTGGGACATGTTTGCAA  47578     T TG   TCT   A
                                TTGTG G  TGTT   CCA TCCT
                                ||||| |  ||||   ||| ||||
```

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                                AACGT T  ACAG   GGT AGGG
                                  T GT    ___   C
GAM1710  PV1      3'  AGGATGCAGGGATATGCTCACA 49372      T     TT  CCA
              G                    TTGTG GTGTGT  CT   ATCCT
                                   ||||| ||||||  ||   |||||
                                   GACAC CGTATA  GA   TAGGA
                                     T     GG  CG_
GAM1710  QKI      5'  GGGGCGGGCGAGCGCGCG    66050         C   AA
                                   TGTGTGTTT TCC  TCC
                                   ||||||||| |||  |||
                                   GCGCGCGAG GGG  GGG
                                         C   CG
GAM1710  RAB10    3'  GGTGGAAGCATGTGCAGGA    86354    G  TG       _
                                   TT TG  TGTGTTTCT CC
                                   || ||  ||||||||| ||
                                   AG AC  GTACGAAGG GG
                                    G  GT        T
GAM1710  Rab11-FIP3 5'  AGGGCAGCTGAGGCGCGGTGCG 28783     TG G       TCCAA
              A                    TTG  T TGTGTTTC     TCCT
                                   |||  | ||||||||     ||||
                                   AGC  G GCGCGGAG     GGGA
                                     GT _       TCGAC
GAM1710  RAB35    3'  AGGCACTGTGGGGAGTGCATGC 23411       TG     _  AT_
                                   GTGTG  TTTCTC CA   CCT
                                   |||||  |||||| ||   |||
                                   CGTAC  GAGGGG GT   GGA
                                      GT     T  CAC
GAM1710  RAB40C   3'  GGGTGCGAGGAGGAGCATGCAC 41283             A___    T
              G                    TGTGTGTGTTTCTCC    ATCC
                                   ||||||||||||||    ||||
                                   GCACGTACGAGGAGG    TGGG
                                            AGCG
GAM1710  RAB6B    5'  GGGAGTCAGGGACGCGCGCA   33876         TT  CCAA
                                   TGTGTGTGT  CT    TCCT
                                   |||||||||  ||    ||||
                                   ACGCGCGCA  GA    AGGG
                                         GG  CTG_
GAM1710  RAB6C    5'  GGGAAGCCGAAGCGCCGCGCG  50487       T      TCCAA
                                   TGTGTG GTGTTTC     TCCT
                                   |||||| |||||||     ||||
                                   GCGCGC CGCGAAG     AGGG
                                      _       CCGA_
GAM1710  RAD52B   5'  GGGAATATGAGGGCATGTGCG  89601    TG     T   CAA_
                                   TG  TGTGTT CTC    TCCT
                                   ||  |||||| |||    ||||
                                   GC  GTACGG GAG    AGGG
                                    GT      _  TATA
GAM1710  RBM12    5'  GGGGCGGAGGCACTCGCGCG   21284       T    TT    AA
                                   TGTGTG GTGT  CTCC  TCC
                                   |||||| ||||  ||||  |||
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                                GCGCGC CACG  GAGG  GGG
                                   T   __   CG
GAM1710  REV1L    5'  GGGGTTGGTTGCCGCGAGCGTG 33320   TG  G   TTTCT
                 G                  T  TGT TGTG    CCAATCCT
                                    |  ||| ||||    ||||||||
                                    G  GCG GCGC    GGTTGGGG
                                     GT   A   CGTT_
GAM1710  RHOBTB2  3'  AGGAAGTAGGAATGAGTGCACG 61595     TG G     CCAA
                                    TGTG  T TGTTTCT   TCCT
                                    ||||  | |||||||   ||||
                                    GCAC  G GTAAGGA   AGGA
                                      GT A     TGA_
GAM1710  RIL      3'  AGGTCTGGGATGCTGCGTGCG  14884   TG   T  T  T   AT
                                    TG  TGTG GT TC CCA  CCT
                                    ||  |||| || || |||  |||
                                    GC  GCGT CG AG GGT  GGA
                                     GT   _ T _  CT
GAM1710  RNF2     3'  GGGGTTAGGTACATTCACAA   24257     T    TT __
                                    TTGTG GTGTG  T  CTCC
                                    ||||| |||||  |  ||||
                                    AACAC TACAT  A  GGGG
                                       T    GG TT
GAM1710  RNF38    3'  AGGGTTGTTGGTAATAAATGTA 43256   TG  TG G   _  TC
                 TGA                  T  TG  T TGTT TC  CAATCCT
                                    |  ||  | |||| ||  |||||||
                                    A  AT  A ATAA GG  GTTGGGA
                                     GT  GT A   T  TT
GAM1710  RNPC1    5'  GGTCGGGAGCGCAGCGCG    34411     G      __
                                    TGTGT TGTGTTTCT  CC
                                    ||||| |||||||||  ||
                                    GCGCG ACGCGAGGG  GG
                                       _       CT
GAM1710  RP4-622L5 3'  GGACAGGATATACAGACG    39427    G    TTTC   AA
                                    TGT TGTGTG   TCC  TCC
                                    ||| ||||||   |||  |||
                                    GCA ACATAT   AGG  AGG
                                      G    _____  AC
GAM1710  RPH3A    3'  GGGGTTGGGGAGACGTTTACA  30935     TG
                                    TGTG  TGTTTCTCCAATCCT
                                    ||||  ||||||||||||||
                                    ACAT  GCAGAGGGGTTGGGG
                                      TT
GAM1710  RPL10L   5'  GGACGAGGGGCAACGTATATAA 55801        _  TT   CAA
                                    TTGTGTGTGT GT  CTC   TCC
                                    |||||||||| ||  |||  |||
                                    AATATATGCA CG  GAG   AGG
                                          A  GG   C__
GAM1710  RTP801   5'  AGGCCAAGGGGGAGGTGCGAGC 39317   TG   G  TG     AAT__
                 GTGG                  T  TGT TG  TTTCTCC    CCT
                                    |  ||| ||  |||||||    |||
```

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                                G  GCG GC  GGAGGGG    GGA
                                 GT   A  GT     GAACC
GAM1710  RYBP     5'  GGACAGGAGCACTGCACAG   60175       T      CCAA
                                TTGTGTG GTGTTTCT   TCC
                                ||||||| ||||||||   |||
                                GACACGT CACGAGGA   AGG
                                    _      C___
GAM1710  S164     5'  GATGAAGAAGATGCATACGA  61432         G    CCA
                                TTGTGTGTGT TTTCT   ATC
                                |||||||||| |||||   |||
                                AGCATACGTA GAAGA   TAG
                                      _    AG_
GAM1710  SBBI31   3'  AGGATAAAAGCATATATAC   26729          CTCCA
                                GTGTGTGTGTTT    ATCCT
                                ||||||||||||    |||||
                                CATATATACGAA    TAGGA
                                       AA___
GAM1710  SCYA28   3'  GGGATTGCAGGTGTGCGCCA  39545   T   TG T   C
                                TG GTG  T TCT CAATCCT
                                || |||  | ||| |||||||
                                AC CGC  G GGA GTTAGGG
                                 _  GT T   C
GAM1710  SE57-1   3'  GGGTCTGAAATTCATACATGA  48168   TG     T    TCCA
                                T  TGTGTG GTTTC    ATCC
                                |  |||||| |||||    ||||
                                A  ACATAC TAAAG    TGGG
                                 GT     T    TC__
GAM1710  SEC22A   3'  GGGATAAGGAGGGAACATATCA 25799      _    G TT    A_
            TAA                    TTGTG TGTGT T  CTCC  ATCCT
                                |||||| ||||| |  ||||  ||||||
                                AATAC ATACA A  GAGG  TAGGG
                                   T    _ GG    AA
GAM1710  SEC61A1  3'  GGGGCCTGGGGGTGCGTGCA   26230    TG   T     A_
                                TG  TGT TCTCCA  TCCT
                                ||  ||| ||||||  ||||
                                AC  GCG GGGGGT  GGGG
                                 GT   T     CC
GAM1710  SEMA4G   5'  GGAAAAAAGGAAGCACACGCA  35859           CCAA_
                                TGTGTGTGTTTCT    TCC
                                ||||||||||||    |||
                                ACGCACACGAAGG    AGG
                                       AAAAA
GAM1710  Sfmbt    5'  AGCGATCGAGCGAGCGCGCGCG 33349            _  CA  _
            CGA                    TTGTGTGTGTGTTT CTC  ATC CT
                                |||||||||||||| |||  ||| ||
                                AGCGCGCGCGCGAG GAG  TAG GA
                                       C  C_  C
GAM1710  SIAT8A   5'  GGGGCCGAAGAAGCGTGCGTGC 13145    TG  TG     CCAA
            G                     TG  TG  TGTTTCT    TCCT
                                ||  ||  |||||||    ||||
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                                GC  GC  GCGAAGA   GGGG
                                 GT  GT      AGCC
GAM1710 SLC11A1   3' GGATGTGGAGGGGGCGCGTGCA 60159    TG    G TT   _   T
             G                    TTG  TGTGT T  CTCCA ATCC
                                  |||  ||||| |  ||||| |||||
                                  GAC  GCGCG G  GAGGT TAGG
                                    GT    _ GG    G
GAM1710 SLC21A11  5' GGGGCGGGGACAGCACGCA   65096       _    AA
                                  TGTGTGTT TCTCC  TCC
                                  ||||||||| |||||  |||
                                  ACGCACGA AGGGG  GGG
                                       C    CG
GAM1710 SLC21A14  5' GGGAGCTGAGATGCACGTCA   34297   _    T   CAA
                                  TG TGTGT TCTC   TCCT
                                  || ||||| ||||   ||||
                                  AC GCACG AGAG   AGGG
                                   T    T   TCG
GAM1710 SLC26A10  5' AGGAGCAGAGGAGGCATGAGCA 56838   TG   G      _ CAA
             TGG                    T  TGT TGTGTTTC TC   TCCT
                                  |  ||| |||||||| ||   ||||
                                  G  ACG GTACGGAG AG   AGGA
                                   GT   A       G  ACG
GAM1710 SLC2A10   5' GGCGGGGGATGCGCGCCCG   48558    T     T    AAT
                                  TG GTGTGT TCTCC   CC
                                  || |||||| |||||   ||
                                  GC CGCGCG AGGGG   GG
                                   C     T    GC_
GAM1710 SLC37A1   3' AGGGTGGGGGGGGTGCACAGGT 39086    TG    TG TT    A
             AG                     TTG  TGTG  T  CTCC ATCCT
                                  |||  ||||  |  |||| |||||
                                  GAT  ACAC  G  GGGG TGGGA
                                    GG   GT GG   G
GAM1710 SLC38A4   3' GGGCAGACATACATATGA    36345   TG        C
                                  T  TGTGTGTGTTT TCC
                                  |  ||||||||||| |||
                                  A  ATACATACAGA GGG
                                   GT         C
GAM1710 SLI      3' GGCGGAGACACGGACATGA    79283   TG   G      _
                                  T  TGT TGTGTTTCT CC
                                  |  ||| |||||||| ||
                                  A  ACA GCACAGAGG GG
                                   GT   G       C
GAM1710 SMARCA4   5' AGGCGGGCGGGCGCGCGCGCGA 13245           TC   AAT
                                  TTGTGTGTGTGTT  TCC   CCT
                                  ||||||||||||  |||   |||
                                  AGCGCGCGCGCGG  GGG   GGA
                                         GC   C__
GAM1710 SMARCA4   5' GGGAGCCGGCGAGCGCGCGCGC 13246           T T  AA_
             AG                     TTGTGTGTGTGTT C CC   TCCT
                                  ||||||||||||| | ||   ||||
```

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                                GACGCGCGCGCGA G GG   AGGG
                                       _ C  CCG
GAM1710  SMT3H2   3'  AGGGTATAGGGTAGCACATGT  23655   TG     T   CA_
                                G  TGTGTT CTC   ATCCT
                                |  |||||| |||   |||||
                                T  ACACGA GGG   TGGGA
                                 GT     T   ATA
GAM1710  SNAP91   5'  GGGGCACCGGGGCTGCGCGCG  29937       TT    AA__
                                TGTGTGT  CTCC    TCCT
                                |||||||  ||||    ||||
                                GCGCGCG  GGGG    GGGG
                                    TC    CCAC
GAM1710  SP2      3'  AGGGTTGGGGGCAATGATGAGC 13328   TG    G   ____
             ATATGA                  T  TGTGT TGTT    TCTCCAATCCT
                                |  ||||| ||||    ||||||||||
                                A  ATACG GTAG    GGGGGTTGGGA
                                 GT    A    TAAC
GAM1710  SPRY1    5'  AGGATTTCAGATGCATGCCA   65630    T     T   CC
                                TG GTGTGT TCT  AATCCT
                                || |||||| |||  ||||||
                                AC CGTACG AGA  TTAGGA
                                 _     T   CT
GAM1710  SR-BP1   3'  GGGAACAAATGAGACACATATA 20789          TCCAA_
                                TGTGTGTGTTTC     TCCT
                                ||||||||||||     ||||
                                ATATACACAGAG     AGGG
                                      TAAACA
GAM1710  SRF      5'  GGACAGGGGGCGCTGCGCGCG  13395       _   TT    AA
                                TGTGTGT GTGT  CTCC  TCC
                                |||||||  ||||  ||||  |||
                                GCGCGCG CGCG  GGGG  AGG
                                    T   __    AC
GAM1710  SSTK     3'  GGGAGCTGGAGGCGCATGCGCA 50170          TT    A_
                                TGTGTGTGTGT  CTCCA  TCCT
                                ||||||||||  |||||  ||||
                                ACGCGTACGCG  GAGGT  AGGG
                                      __    CG
GAM1710  SSTK     3'  GGGCCAGGGCGGCGCACGCGCA 50171          TT   CAA   T
             A                   TTGTGTGTGTGT  CTC   TCC
                                ||||||||||||  |||   |||
                                AACGCGCACGCG  GGG   GGG
                                      GC   ACC
GAM1710  STARD7   3'  GGGATGTGGATGGATGTGTGCA 39745       TG    TC   _
             TAA                   TTGTGTG  TGTT  TCCA ATCCT
                                |||||||  ||||  |||| |||||
                                AATACGT  GTAG  AGGT TAGGG
                                    GT   GT   G
GAM1710  STATI2   5'  GGGGCGGGTGCGCAGACAA   96193     G   TG   _
                                TTGT TGTG  TTT CTCC
                                |||| ||||  ||| ||||
```

```
                                AACA ACGC  GGG GGGG
                                  G   GT   C
GAM1710  STC2     3'  GGGGGGATGTCACACGCAG   14935        _  TT
                                TTGTGTGTG TGT  CTCC
                                ||||||||| |||  ||||
                                GACGCACAC GTA  GGGG
                                     T   GG
GAM1710  STIM2    5'  GGGATTGGTATGCGAGCGAATG 40860     TG  G    CT___
           TGCGA                  TTG  TGT TGTTT    CCAATCCT
                                |||  ||| |||||    ||||||||
                                AGC  GTA GCGAG    GGTTAGGG
                                  GT   A    CGTAT
GAM1710  STIM2    5'  GGGGCGGGGGGGATGCGCCGCG  40861     T     TT   AA
                                TGTG GTGTGT  CTCC  TCC
                                |||| ||||||  ||||  |||
                                GCGC CGCGTA  GGGG  GGG
                                  _     GG   CG
GAM1710  STIP-1   3'  GGAAAAAAGCATATGCATAA   70239           C__
                                TTGTGTGTGTGTTT   TCC
                                ||||||||||||||   |||
                                AATACGTATACGAA   AGG
                                      AAA
GAM1710  STK22B   3'  GGGGTTGGGGGGGCATGGTGCAG 54867     TG G     TT T
                                TTG  T TGTGT  C CCAATCCT
                                |||  | |||||  | ||||||||
                                GAC  G GTACG  G GGTTGGGG
                                  GT _    GG _
GAM1710  STX1B2   3'  GGAGGCCCAGGTACACACAG   54620         __ TT
                                TTGTGTGTG  TG  TCTCC
                                |||||||||  ||  |||||
                                GACACACAT  AC  GGAGG
                                     GG  CC
GAM1710  SV2      3'  AGGGTAATTTCAGCGGATGCAC 29956           _  CCA___
           ACACAA                  TTGTGTGTGTGTTT CT     ATCCT
                                |||||||||||||| ||     |||||
                                AACACACACGTAGG GA     TGGGA
                                      C  CTTTAA
GAM1710  SV2B     3'  AGGTCACTGGGGGACAATGTAC 29948      TG G   TT T   AT__
           AG                    TTGTG  T TGT  C CCA    CCT
                                |||||  | |||  | |||    |||
                                GACAT  A ACA  G GGT    GGA
                                   GT _   GG _   CACT
GAM1710  SYNPO2   3'  AGGATTGTTGGAATGTATATA  72385      TG    TC
                                TGTGTG  TTTC  CAATCCT
                                ||||||  ||||  |||||||
                                ATATAT  AAGG  GTTAGGA
                                   GT    TT
GAM1710  TACTILE  5'  AGGCCGGTAGAGGCACTGCACA 20580       T      _  AAT
           A                     TTGTGTG GTGTTTCT CC   CCT
                                |||||||  |||||||  ||   |||
```

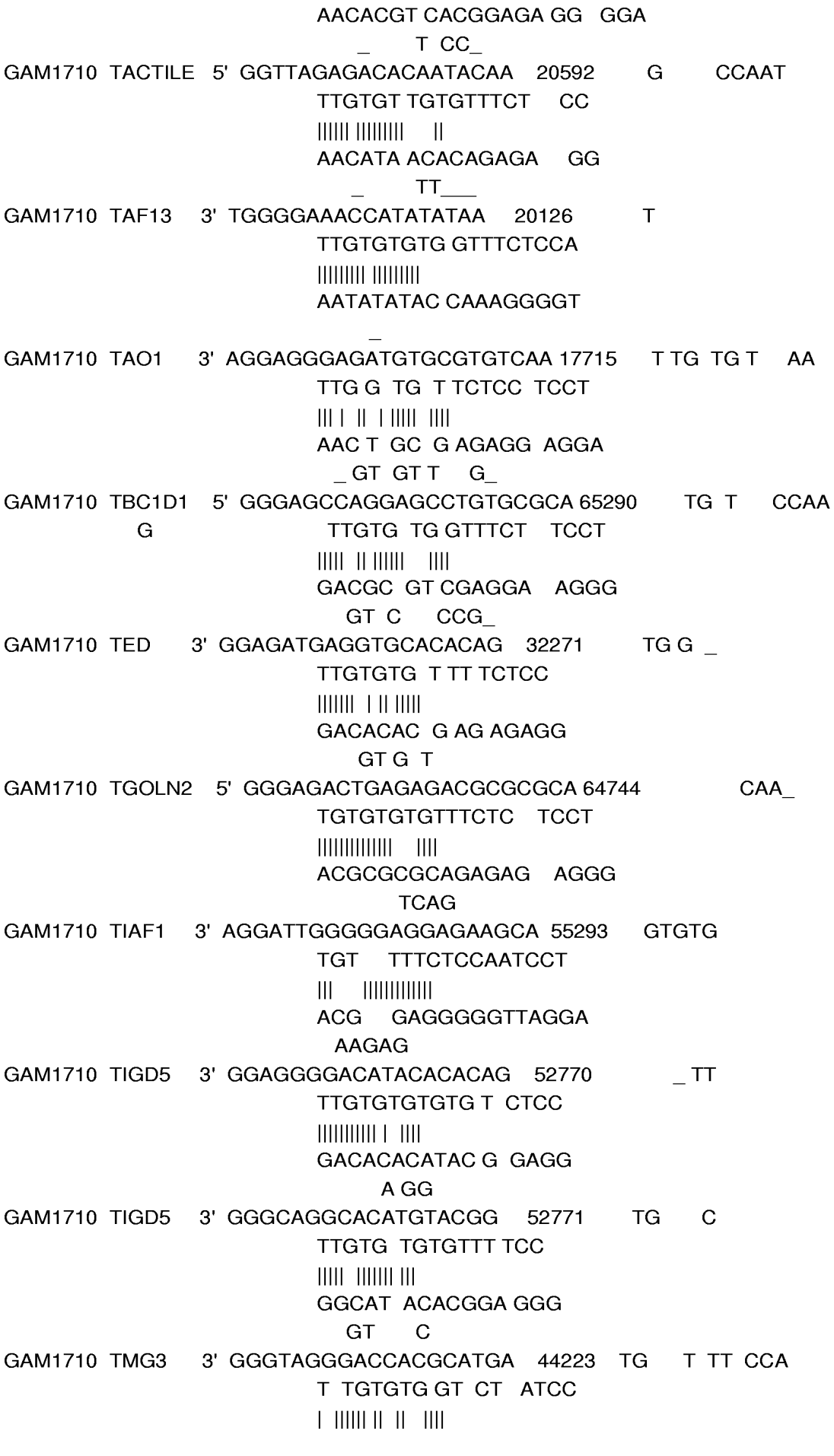
AACACGT CACGGAGA GG GGA
_ T CC_
GAM1710 TACTILE 5' GGTTAGAGACACAATACAA 20592 G CCAAT
TTGTGT TGTGTTTCT CC
AACATA ACACAGAGA GG
_ TT___
GAM1710 TAF13 3' TGGGGAAACCATATATAA 20126 T
TTGTGTGTG GTTTCTCCA
AATATATAC CAAAGGGGT
_
GAM1710 TAO1 3' AGGAGGGAGATGTGCGTGTCAA 17715 T TG TG T AA
TTG G TG T TCTCC TCCT
AAC T GC G AGAGG AGGA
_ GT GT T G_
GAM1710 TBC1D1 5' GGGAGCCAGGAGCCTGTGCGCA 65290 TG T CCAA
G TTGTG TG GTTTCT TCCT
GACGC GT CGAGGA AGGG
GT C CCG_
GAM1710 TED 3' GGAGATGAGGTGCACACAG 32271 TG G _
TTGTGTG T TT TCTCC
GACACAC G AG AGAGG
GT G T
GAM1710 TGOLN2 5' GGGAGACTGAGAGACGCGCGCA 64744 CAA_
TGTGTGTGTTTCTC TCCT
ACGCGCGCAGAGAG AGGG
TCAG
GAM1710 TIAF1 3' AGGATTGGGGGAGGAGAAGCA 55293 GTGTG
TGT TTTCTCCAATCCT
ACG GAGGGGGTTAGGA
AAGAG
GAM1710 TIGD5 3' GGAGGGGACATACACACAG 52770 _ TT
TTGTGTGTGTG T CTCC
GACACACATAC G GAGG
A GG
GAM1710 TIGD5 3' GGGCAGGCACATGTACGG 52771 TG C
TTGTG TGTGTTT TCC
GGCAT ACACGGA GGG
GT C
GAM1710 TMG3 3' GGGTAGGGACCACGCATGA 44223 TG T TT CCA
T TGTGTG GT CT ATCC

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                                A  ACGCAC CA  GA   TGGG
                                 GT     _  GG  ___
GAM1710  TMG4     5'  GGGGCTGCTGGAACATGTGCGG 44215    G  TG      TC  AT
                   GG                  TT TG  TGTGTTTC  CA  CCT
                                       || ||  ||||||||  ||  |||
                                       GG GC  GTACAAGG  GT  GGG
                                        G  GT       TC  CG
GAM1710  TMPRSS5  5'  GGGATACAGGGAGGGGCCATGT 48496     TG   T  TT   A___
                   GCGA                  TTG  TGTG GT  CTCC   ATCCT
                                         |||  |||| ||  ||||   |||||
                                         AGC  GTAC CG  GAGG   TAGGG
                                          GT   _  GG   GACA
GAM1710  TNRC5    5'  GGTTGCTCGGAGGCACGTGTGC 22701      TG       C__    CT
                   AG                    TTGTG  TGTGTTTCT   CAATC
                                         |||||  |||||||||   |||||
                                         GACGT  GCACGGAGG   GTTGG
                                            GT        CTC
GAM1710  TOSO     3'  AGGGTTGGGTCTTACACAAATA 19567      G     TTT T
                   G                     TTGT TGTGTG   C CCAATCCT
                                         ||||  ||||||   |  ||||||||
                                         GATA ACACAT   G GGTTGGGA
                                           A     TCT _
GAM1710  TPRA40   5'  GGGATTGGGTCGTGACCTGTGT 33487    TG  T   TC__
                                         G  TG GTT    TCCAATCCT
                                         |  ||  |||    |||||||||
                                         T  GT CAG    GGGTTAGGG
                                          GT  C   TGCT
GAM1710  TRAF2    3'  GGGGTTGGGGGGCAGCCAGGCAC 41238       G  T   _
                   AG                    TTGTGT TG GTT TCTCCAATCCT
                                         ||||||  ||  |||  ||||||||||
                                         GACACG AC CGA GGGGGTTGGGG
                                            G  _   C
GAM1710  TRAF3    3'  GGCGGGAGGAGCCACGCGTGA  13853    TG     T      AAT
                                         T  TGTGTG GTTTCTCC   CC
                                         |  ||||||  ||||||||   ||
                                         A  GCGCAC CGAGGAGG   GG
                                          GT     _       GC_
GAM1710  TRAF3    5'  GGCGGGAGGAGCCACGCGTGA  13854    TG     T      AAT
                                         T  TGTGTG GTTTCTCC   CC
                                         |  ||||||  ||||||||   ||
                                         A  GCGCAC CGAGGAGG   GG
                                          GT     _       GC_
GAM1710  TReP-132 3'  GGGGTTGGGGGAATAAATA    54272     G
                                         TGT TGTTTCTCCAATCCT
                                         |||  ||||||||||||||
                                         ATA ATAAGGGGGTTGGGG
                                           A
GAM1710  TReP-132 3'  GGGGTTGGGGGAATAAATA    54273     G
                                         TGT TGTTTCTCCAATCCT
                                         |||  ||||||||||||||
```

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                                ATA ATAAGGGGGTTGGGG
                                  A
GAM1710  TRIM26   3'  GGATCCAGACATACACG     14350          CTCCA
                                TGTGTGTGTTT    ATCC
                                ||||||||||    ||||
                                GCACATACAGA    TAGG
                                     CC___
GAM1710  TRIM29   3'  AGGATTGGAGAGGAGACA    25005     G_
                                TGT  TTTCTCCAATCCT
                                |||  ||||||||||||
                                ACA  GGAGAGGTTAGGA
                                  GA
GAM1710  TRIM29   3'  AGGATTGGAGAGGAGACA    25006     G_
                                TGT  TTTCTCCAATCCT
                                |||  ||||||||||||
                                ACA  GGAGAGGTTAGGA
                                  GA
GAM1710  TRIM29   3'  GGGGTTGGGGAGGGAGACATCC 25009    TG   G __
            A                    TG  TGT TT  TCTCCAATCCT
                                ||  |||  ||  ||||||||||
                                AC  ACA AG  AGGGGTTGGGG
                                 CT   G  GG
GAM1710  TRIM29   3'  GGGGTTGGGGAGGGAGACATCC 25010    TG   G __
            A                    TG  TGT TT  TCTCCAATCCT
                                ||  |||  ||  ||||||||||
                                AC  ACA AG  AGGGGTTGGGG
                                 CT   G  GG
GAM1710  TSCOT    3'  AGGGTTACAGGGAGGCTGCACA 53510         T      C__
            CAG                    TTGTGTGTG GTTTCTC   AATCCT
                                |||||||||  |||||||   ||||||
                                GACACACGT CGGAGGG   TTGGGA
                                     _      ACA
GAM1710  TSPAN-3  5'  GGGGCTGCGGGGAGCGCCGCGC 20370        T       _  AT
            AG                     TTGTGTG GTGTTTCTC CA  CCT
                                |||||||  |||||||||  ||  |||
                                GACGCGC CGCGAGGGG GT  GGG
                                     _       C  CG
GAM1710  TSSC1    5'  GGGCGCTGGGAACACGCCCGCG 13871       T        CCAA   T
            A                    TTGTG GTGTGTTTCT    TCC
                                |||||  ||||||||||    |||
                                AGCGC CGCACAAGGG    GGG
                                   C         TCGC
GAM1710  TTTY12   5'  GGGGTTAAAGACAGGAATATGG 50028       G       CC_____
            CACAA                   TTGTGT TGTGTTTCT      AATCCT
                                ||||||  |||||||||     ||||||
                                AACACG GTATAAGGA     TTGGGG
                                     _       CAGAAA
GAM1710  TUB      3'  GGGAGAGGAAGCACACTGCAG  13896       T        CCAA
                                TTGTG GTGTGTTTCT    TCCT
                                |||||  ||||||||||    ||||
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                                GACGT CACACGAAGG    AGGG
                                  _        AG__
GAM1710 U2AF65    3'  AGGGGACTGGGGAAGTGCGCAC 24410         TG       A
             ACAG                   TTGTGTGTG  TTTCTCCA TCCT
                                ||||||||| ||||||| ||||
                                GACACACGC  GAAGGGGT AGGG
                                    GT       C    GAG
GAM1710 U2AF65    3'  GGGACTGGGGAAGTGCGCACAC 24412         TG       A
             AG                   TTGTGTGTG  TTTCTCCA TCCT
                                ||||||||| ||||||| ||||
                                GACACACGC  GAAGGGGT AGGG
                                    GT       C
GAM1710 UBP1      3'  GGGATTGGATTTTACCATATGA 27993    TG    T   TTTC
                                T  TGTG GTG    TCCAATCCT
                                |  |||| |||    |||||||||
                                A  ATAC CAT    AGGTTAGGG
                                 GT    _  TTT_
GAM1710 USP28     3'  GGATTAGGTGGGCACATA     40873         CT  _
                                TGTGTGTTT  CC AATCC
                                |||||||||  || |||||
                                ATACACGGG  GG TTAGG
                                     T_  A
GAM1710 VIAAT     3'  GGGAGGCGGGGTGCATTTGCG  55452      T   TG TT T  AA
                                TGTG GTG  T  C CC  TCCT
                                |||| |||  |  | ||  ||||
                                GCGT TAC  G  G GG  AGGG
                                  T   GT GG C  __
GAM1710 WAC       3'  TGGGAAGCCATGTGTAA     34035     TG    T     T
                                TTG  TGTG GTTTC CCA
                                |||  |||| ||||| |||
                                AAT  GTAC CGAAG GGT
                                  GT    _     _
GAM1710 WASPIP    3'  GGGAGTGGGAATATGCGTGTGT 14084    TG  TG    _   T   A
             GG                     T  TG  TGTGT TTC CCA TCCT
                                |  ||  ||||| ||| ||| ||||
                                G  GT  GCGTA AAG GGT AGGG
                                 GT  GT     T   _   G
GAM1710 WBP11     3'  AGGATATGTGGGAAGAATATGT 33314       TG   G     _ _
             ACAA                   TTGTG  TGT TTTCTC CA ATCCT
                                |||||  ||| |||||| || |||||
                                AACAT  ATA GAAGGG GT TAGGA
                                   GT   A     T  A
GAM1710 WBSCR17   3'  GGTTAGGGTGCACATATA    82218         TT   C
                                TGTGTGTGT  CTC AATC
                                |||||||||  ||| ||||
                                ATATACACG  GGG TTGG
                                     T_   A
GAM1710 X123      3'  GGGCATTCAGGAGTAAATGCAC 70481         _    __   _
             A                    TGTGTGTTT CTCC  AAT CCT
                                |||||||||  ||||  ||| |||
```

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                                ACACGTAAA GAGG  TTA GGG
                                     T   AC  C  A
GAM1710 YAP1    5' GGGTCAGGGGGTGCGCGTCG  21463   _   T   A_
                                TG TGTGT TCTCC  ATCC
                                || ||||| |||||  ||||
                                GC GCGCG GGGGG  TGGG
                                 T    T    AC
GAM1710 ZDHHC5  3' GGAGGGATACATATACGG   93186         TT
                                TTGTGTGTGTGT  CTCC
                                ||||||||||||  ||||
                                GGCATATACATA  GAGG
                                      GG
GAM1710 ZDHHC5  5' GGCGGGAGCGCGCGGCAG   93187     G       _
                                TTGT TGTGTGTTTCT CC
                                |||| |||||||||| ||
                                GACG GCGCGCGAGGG GG
                                  _        C
GAM1710 ZDHHC5  3' TGGGAAAATGAGGGAGGGATAC 93191         TT   AA_____
           ATATACG                TGTGTGTGTGT  CTCC     TCCT  G
                                ||||||||||  ||||     ||||  |
                                GCATATACATA  GAGG     AGGG  T
                                      GG   GAGTAAA
GAM1710 ZF5128  3' AGGTGAGAGGGATGCAGGCATG 27574   TG  G    TT  _ AT
           G                    T  TGT TGTGT  CTC CA  CCT
                                |  ||| |||||  ||| ||  |||
                                G  ACG ACGTA  GAG GT  GGA
                                 GT   G    GG   A __
GAM1710 ZIC4    3' GGGAAATGGGGACATGTGTCAA 50541    T TG   TT    A_
                                TTG G  TGTG  TCTCCA  TCCT
                                ||| |  ||||  ||||||  ||||
                                AAC T  GTAC  AGGGGT  AGGG
                                  _ GT   __     AA
GAM1710 ZNF197  3' GGGCATGGGGGCACACACCG  23757   T      TT    AT
                                TG GTGTGTGT  CTCCA  CCT
                                || ||||||||  |||||  |||
                                GC CACACACG  GGGGT  GGG
                                 _      __     AC
GAM1710 ZNF297  3' GGGAATAAGGAGCACGATGCAA 19572       G       CCAA
                                TTGTGT TGTGTTTCT   TCCT
                                |||||| |||||||||   ||||
                                AACGTA GCACGAGGA   AGGG
                                   _       ATA_
GAM1710 ZNF338  3' GGGGTTGGAATTAAATGCAT  42259        C__
                                GTGTGTTT   TCCAATCCT
                                ||||||||   |||||||||
                                TACGTAAA   AGGTTGGGG
                                     TTA
GAM1710 ZNF396  3' GGAGAGATGTACCACAG    76169      T   TG
                                TTGTG GTG  TTTCTCC
                                ||||| |||  |||||||
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                                GACAC CAT  AGAGAGG
                                  _  GT
GAM1710  LOC113091 5'  GGGAAGCTGGGGGTGGATGCAT 73314       __     A__
                                GTGTGTT  TCTCCA   TCCT
                                |||||||  ||||||   ||||
                                TACGTAG  GGGGGT   AGGG
                                   GT     CGA
GAM1710  LOC113220 3'  GGATGAAATACATGAATAA    57358      G       _
                                TTGT TGTGTGTTTC TCC
                                |||| |||||||||| |||
                                AATA GTACATAAAG AGG
                                  A        T
GAM1710  LOC115749 5'  GGATAAGAATGCACTACAA    73950      T      T  CCA
                                TTGTG GTGTGTT CT   ATCC
                                ||||| ||||||| ||   ||||
                                AACAT CACGTAA GA   TAGG
                                  _     _ A__
GAM1710  LOC118786 5'  TGAAGAAGCAGATACACAA    76011        G      C
                                TTGTGTGT TGTTTCT CA
                                |||||||| ||||||| ||
                                AACACATA ACGAAGA GT
                                     G      A
GAM1710  LOC120105 3'  GGTGCAGAGACGACGCACATAG 76028         _     C  AT
                                TTGTGTGTGT GTTTCT CA  CC
                                |||||||||| |||||| ||  ||
                                GATACACGCA CAGAGA GT  GG
                                      G     C  __
GAM1710  LOC120196 3'  GGTGATTTTGAGGAGCACATGC 76059              C_   _
            ATAA                   TTGTGTGTGTGTTTCTC  AATC CT
                                |||||||||||||||  |||| ||
                                AATACGTACACGAGGAG  TTAG GG
                                           TT    T
GAM1710  LOC120224 3'  GGGATTTTTAAACATACTATAA 57890      T      CTCC
                                TTGTG GTGTGTTT    AATCCT
                                ||||| ||||||||    ||||||
                                AATAT CATACAAA    TTAGGG
                                  _       TTT_
GAM1710  LOC121536 3'  GGGGTAAAGAGCTATATACATG 74527    TG      T    CCA
            A                    T  TGTGTGTG TTCT   ATCCT
                                |  |||||||| ||||   |||||
                                A  ACATATAT GAGA   TGGGG
                                 GT       C    AA_
GAM1710  LOC121838 5'  AGGCACCAGAGGGTACACACGC 76510         _    CAAT_
            A                    TGTGTGTGT TTCTC     CCT
                                |||||||||| |||||     |||
                                ACGCACACA GGGAG     GGA
                                      T     ACCAC
GAM1710  LOC122210 5'  GGGACCCCGAAATGCACACG   74579           TCCAA
                                TGTGTGTGTTTC     TCCT
                                ||||||||||||     ||||
```

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                                GCACACGTAAAG    AGGG
                                      CCCC_
GAM1710  LOC122726 5'  AGGCTTGGGAAGATACACATGC 76102           CT   T
              AA                  TTGTGTGTGTGTTT  CCAA CCT
                                  ||||||||||||||  |||| |||
                                  AACGTACACATAGA  GGTT GGA
                                        AG    C
GAM1710  LOC122726 5'  GGGAAGATACACATGCAA    76104           CT
                                  TTGTGTGTGTGTTT  CC
                                  ||||||||||||||  ||
                                  AACGTACACATAGA  GG
                                        AG
GAM1710  LOC123316 5'  GGCGGGAGGCGCACAGCG    76123    G         CAAT
                                  TGT TGTGTGTTTCTC    CC
                                  ||| ||||||||||||    ||
                                  GCG ACACGCGGAGGG    GG
                                    _         C___
GAM1710  LOC123691 5'  GGGGCTTTGAGCATACGTCA   76138    _       ____
                                  TG TGTGTGTTT    CTCC
                                  || |||||||||    ||||
                                  AC GCATACGAG    GGGG
                                    T       TTTC
GAM1710  LOC124460 5'  GCTCTGAGAGGCAGCACACACA 76565         _      CAATCCT
              G                   TTGTGTGTG TGTTTCTC
                                  |||||||||| ||||||||
                                  GACACACAC ACGGAGAG
                                        G       TCTCG
GAM1710  LOC125434 3'  AGGTCTGTGTGAAACACACATG 74870   TG         TC_  AT
              TGG                   T  TGTGTGTGTTTC   CA  CCT
                                  |  ||||||||||||   ||  |||
                                  G  GTACACACAAAG   GT  GGA
                                   GT          TGT  CT
GAM1710  LOC126129 5'  GGGATTGGACATATGCAAGCG  74918    G      TTC
                                  TGT TGTGTGT   TCCAATCCT
                                  ||| |||||||   |||||||||
                                  GCG ACGTATA   AGGTTAGGG
                                    A      C__
GAM1710  LOC126257 5'  GGAGCGGGAGCGTGTGTGCAG  74934    TG  TG     CCAA
                                  TTG  TG  TGTTTCT    TCC
                                  |||  ||  |||||||    |||
                                  GAC  GT  GCGAGGG    AGG
                                    GT  GT      CG__
GAM1710  LOC126432 5'  AGGTGTGCAGAGATGTCTATGC 75020       T TG    C  AT
              G                   TGTGTG G  TTTCT CA  CCT
                                  ||||||  |  |||||  ||  |||
                                  GCGTAT T  AGAGA GT  GGA
                                      C GT    C  GT
GAM1710  LOC126520 5'  GGGCTCGGGCCGCGTGTACAG  75025      TG   TTT   CAA
                                  TTGTG  TGTG   CTC   TCC
                                  |||||  ||||   |||   |||
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                                GACAT  GCGC   GGG   GGG
                                   GT    C__   CTC
GAM1710  LOC126917 5'  GGTGAAGCGCGAGCGCGA    75096       G       T
                                TTGTGT TGTGTTTC CC
                                |||||| |||||||| ||
                                AGCGCG GCGCGAAG GG
                                   A       T
GAM1710  LOC128102 3'  AGGATGACAGAGATGTGCATGT 75990   TG    TG      CCA
            GG                    T  TGTG  TGTTTCT   ATCCT
                                |  ||||  |||||||   ||||||
                                G  GTAC  GTAGAGA   TAGGA
                                 GT    GT      CAG
GAM1710  LOC128338 3'  GGGATTGGGGAAAGGTTCACAG 75252    G    TG G
            AA                    TT TGTG  T TTTCTCCAATCCT
                                || ||||  | ||||||||||||||
                                AA ACAC  G AAAGGGGTTAGGG
                                 G    TT G
GAM1710  LOC128989 3'  AGTTGCACAGACACACACACAC 75311           T   C__    CCT
            AG                    TTGTGTGTGTGT TCT   CAAT
                                |||||||||||| |||   ||||
                                GACACACACACA AGA   GTTG
                                      C   CAC    A
GAM1710  LOC129450 5'  GGGATTGATTTGGGGCCATGTA 75381       TG  T  TT TC__
            CAA                   TTGTG  TG GT  C    CAATCCT
                                |||||  || ||  |   |||||||
                                AACAT  AC CG  G    GTTAGGG
                                   GT  _  GG TTTA
GAM1710  LOC129676 5'  GGCAAGGAGCATGCACACAG   76235             __
                                TTGTGTGTGTGTTTCT  CC
                                ||||||||||||||||  ||
                                GACACACGTACGAGGA  GG
                                          AC
GAM1710  LOC130574 3'  TTGGAAGAATACATGCATGA   75462    TG        TC
                                T  TGTGTGTGTT  TCCAA
                                |  ||||||||||  |||||
                                A  ACGTACATAA  AGGTT
                                 GT         GA
GAM1710  LOC130814 3'  AGGATACCAAGGCAAGCATACA 75484     TG       _  CCA__
            TGTAG                   TTG  TGTGTGTTT CT     ATCCT
                                |||  |||||||||  ||     |||||
                                GAT  ACATACGAA GG     TAGGA
                                  GT        C  AACCA
GAM1710  LOC131827 3'  GGAGGAGCATATAGCAA     75502      G
                                TTGT TGTGTGTTTCTCC
                                |||| ||||||||||||
                                AACG ATATACGAGGAGG
                                   _
GAM1710  LOC131870 3'  GGATCTGAGAGATGATACATGA 75510    TG    G       CA
                                T  TGTGT TGTTTCTC  ATCC
                                |  ||||| ||||||||  ||||
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                                A  ACATA GTAGAGAG  TAGG
                                 GT    _       TC
GAM1710  LOC132671 3'  GGAGCCAAGCACATATAC    59840          __
                                GTGTGTGTGTTT  CTCC
                                ||||||||||||  ||||
                                CATATACACGAA  GAGG
                                      CC
GAM1710  LOC133619 3'  GGTGGAAATTCATGTGCAG   56421    TG   T    _
                                TTG  TGTG GTTTCT CC
                                |||  |||| ||||||  ||
                                GAC  GTAC TAAAGG GG
                                  GT   T     T
GAM1710  LOC135763 3'  AGGTCAAGAAAGACACACACG  57554        G    CCAAT
                                TGTGTGTGT TTTCT    CCT
                                |||||||||  |||||    |||
                                GCACACACA AAAGA    GGA
                                      G    ACT__
GAM1710  LOC136069 5'  AGGAAGTGGAGTGGACACACG  76472        _    A_
                                TGTGTGTTT CTCCA  TCCT
                                |||||||||  |||||  ||||
                                GCACACAGG GAGGT  AGGA
                                      T    GA
GAM1710  LOC136337 3'  GGGCTATGAGTCATACACATGG 76719   TG      T   TCCAA
                                T  TGTGTGTG TTC    TCC
                                |  ||||||||  |||    |||
                                G  ACACATAC GAG    GGG
                                 GT       T   TATC_
GAM1710  LOC138046 3'  GGTAAGGGAAACACTATATACA 75810        _       CAAT  T
            A                    TTGTGTGT GTGTTTCTC    CC
                                |||||||| |||||||||    ||
                                AACATATA CACAAAGGG    GG
                                     T       AAT_
GAM1710  LOC138639 3'  GGGACTCCACAGGGATATTCGT 75884    TG  T    TT  CCAA__
            GCAG                   TTG  TG GTGT  CT     TCCT
                                |||  || ||||  ||     ||||
                                GAC  GC TATA  GA     AGGG
                                  GT  T    GG  CACCTC
GAM1710  LOC138649 3'  GGGATTCACGGGCGCACACACA 75875         T   CC_
            CA                   TGTGTGTGTGT TCT   AATCCT
                                ||||||||||| |||   ||||||
                                ACACACACACG GGG   TTAGGG
                                      C   CAC
GAM1710  LOC139231 3'  GTTGTTAGGAATGCATAC    75896          C_
                                GTGTGTGTTTCT  CAAT
                                ||||||||||||  ||||
                                CATACGTAAGGA  GTTG
                                      TT
GAM1710  LOC142955 5'  GGGAACACAAGGCACACATATA 76962          CTCCAA
                                TGTGTGTGTGTTT     TCCT
                                ||||||||||||      ||||
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                                ATATACACACGGA     AGGG
                                      ACACA_
GAM1710  LOC143038 3'  GGAATAAAACACACCACAA   76972      T      C__
                                TTGTG GTGTGTTT   TCC
                                ||||| ||||||||   |||
                                AACAC CACACAAA   AGG
                                   _       ATA
GAM1710  LOC143187 3'  GGGGCGGCAGGGACAGCATGTA 59762     TG   G   TT  _  AA   T
            A                    TTG  TGT TGT  CT CC  TCC
                                 |||  ||| |||  || ||  |||
                                 AAT  ACG ACA  GA GG  GGG
                                   GT   _   GG  C  CG
GAM1710  LOC143287 3'  GGCGAGGCTCACACACAG    83829         T    T
                                TTGTGTGTG GTTTC CC
                                ||||||||| ||||| ||
                                GACACACAC CGGAG GG
                                      T    C
GAM1710  LOC143916 5'  AGTTTTAGGGTACATATGTACA 77137      TG    TT   C  TC
            A                    TTGTG  TGTGT  CTC AA  CT
                                 |||||  |||||  ||| ||  ||
                                 AACAT  ATACA  GGG TT  GA
                                    GT    T_   A  TT
GAM1710  LOC144017 3'  AGGAGGCGAGACGTGCGCCCG  83927    T   TG     T  AA
                                TG GTG  TGTTTC CC  TCCT
                                || |||  |||||| ||  ||||
                                GC CGC  GCAGAG GG  AGGA
                                 C   GT     C  __
GAM1710  LOC144195 3'  GGGATTGGCCGCTTGGCACATG 60987      G       TCT___
            ACAA                   TTGT TGTGTGTT     CCAATCCT
                                   |||| ||||||||     ||||||||
                                   AACA GTACACGG     GGTTAGGG
                                     _       TTCGCC
GAM1710  LOC144202 3'  GGGAGACAAAAGTATACACGTG 77227    TG        _____    AATCCT
            A                    T  TGTGTGTGTT    TCTCC
                                 |  ||||||||||    |||||
                                 A  GCACATATGA    AGAGG
                                  GT         AAAC     G   T
GAM1710  LOC144231 5'  GGGATTAAGTGAGATGACGCAT 83940    TG     _   C___
            GTA                    TG  TGTGTT TCTC    AATCCT
                                   ||  |||||| ||||    ||||||
                                   AT  ACGCAG AGAG    TTAGGG
                                    GT     T    TGAA
GAM1710  LOC144266 5'  GGAAAGAAATCACACATGG    77266    TG     T     CCAA
                                T  TGTGTG GTTTCT    TCC
                                |  |||||| ||||||    |||
                                G  ACACAC TAAAGA    AGG
                                 GT     _     A___
GAM1710  LOC144348 5'  GGCTCGGAGGCGCACCTGTGA  77302    TG  T     TT    AAT
                                T  TG GTGTGT  CTCC   CC
                                |  || ||||||  ||||   ||
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                              A  GT CACGCG  GAGG   GG
                               GT  C     __    CTC
GAM1710  LOC144453 3'  AGGAATCTGAAAAACATACATG 77328   TG      G    TCCAA
              A                 T  TGTGTGT TTTC     TCCT
                              |  ||||||| ||||     ||||
                              A  ACATACA AAAG     AGGA
                               GT      A    TCTA_
GAM1710  LOC144519 3'  GGAGAAATATTGCATAA     77376        T
                              TTGTGTG GTGTTTCTCC
                              ||||||| |||||||||
                              AATACGT TATAAAGAGG
                                    _
GAM1710  LOC144699 3'  TGGGGTATTATATATATACA   77438          TT__    AATCCT
                              TGTGTGTGTGT    CTCC
                              ||||||||||    ||||
                              ACATATATATA    GGGG
                                     TTAT      TC
GAM1710  LOC144817 5'  AGGGTCTCCAGAGCACACGACA 77504      G        CTCCA
              A                 TTGT TGTGTGTTT     ATCCT
                              |||| |||||||||     |||||
                              AACA GCACACGAG     TGGGA
                                _        ACCTC
GAM1710  LOC144845 5'  AGGGCAGGGTGCACACACACA  57452          TT T  AA
                              TGTGTGTGTGT  C CC  TCCT
                              ||||||||||  | ||  ||||
                              ACACACACACG  G GG  GGGA
                                     T_ _  AC
GAM1710  LOC145258 3'  GGGGTCAGGGCGCGCACAG    77563          G  T_
                              TTGTGTGTGT TT  CTCC
                              |||||||||| ||  ||||
                              GACACGCGCG GA  GGGG
                                    G  CT
GAM1710  LOC145317 3'  GGGAACCAACCACACATGCAG  84283          T____   T
                              TTGTGTGTGTG     TTC CC
                              ||||||||||     ||| ||
                              GACGTACACAC     AAG GG
                                     CAACC  _
GAM1710  LOC145368 3'  GGGATGCCTTGGGGTTCGTGCA 77616      TG  TTT    ____
              CA                  TGTG  TG   CTCCA    ATCCT
                              ||||  ||   |||||   |||||
                              ACAC  GC   GGGGT    TAGGG
                                GT  TT_    TCCG
GAM1710  LOC145468 3'  GGCGGGCATGCACGCAA     74254           T T
                              TTGTGTGTGTGTT C CC
                              |||||||||||| | ||
                              AACGCACGTACGG G GG
                                      _ C
GAM1710  LOC145468 3'  GGGGTTGGGGGGGGACATCGGAA 74255    G  T    G TT
                              TT TG GTGT T  CTCCAATCCT
                              || || |||| |  ||||||||||
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                                AA GC TACA G  GGGGTTGGGG
                                 G  _   _ GG
GAM1710  LOC145501 3'  GGGAGCCCTGGAAATGTGCATA 77772      TG      CCAA_
              T                   GTGTG  TGTTTCT     TCCT
                                  |||||  |||||||     ||||
                                  TATAC  GTAAAGG     AGGG
                                    GT      TCCCG
GAM1710  LOC145508 3'  TGGAGATGTGCATATATAA   77777        TG T
                                  TTGTGTGTG  T TCTCCA
                                  |||||||||  | ||||||
                                  AATATATAC  G AGAGGT
                                        GT T
GAM1710  LOC145566 5'  GGGAATCTTGGACATGCACACA 77790        TTC    ___
              CA                    TGTGTGTGT   TCCAA   TCCT
                                  |||||||||   |||||   ||||
                                  ACACACACG   AGGTT   AGGG
                                        TAC     CTA
GAM1710  LOC145624 5'  AGGATGCATGTGGATCATATGC 84400        TT  TC  ___
              A                    TGTGTGTG  TC  CA   ATCCT
                                  ||||||||  ||  ||   |||||
                                  ACGTATAC  AG  GT   TAGGA
                                       T_  GT  ACG
GAM1710  LOC145663 3'  GAGAGATTGTACATGCAG    84424        GT_
                                  TTGTGTGT   GTTTCTC
                                  ||||||||   |||||||
                                  GACGTACA   TAGAGAG
                                       TGT
GAM1710  LOC145693 3'  AGGCGTGCGAGGGGCACACGCC 77853     T      TT   _  AT
              CAA                    TTG GTGTGTGT  CTC CA  CCT
                                  |||  ||||||||  |||  ||  |||
                                  AAC CGCACACG  GAG GT  GGA
                                    C       GG   C  GC
GAM1710  LOC145693 3'  GGACTGGGATACGTACCA    77855    T     T  T   A
                                  TG GTGTGT TC CCA TCC
                                  ||  ||||||  ||  |||  |||
                                  AC CATGCA AG GGT AGG
                                   _     T  _   C
GAM1710  LOC145717 5'  GGGGTGGCTGGGGCTACGTGCA 67376     TG    T  TT T_   AT  T
              G                    TTG  TGTG GT  C  CCA  CC
                                  |||  ||||  ||  |  |||  ||
                                  GAC  GCAT CG  G  GGT  GG
                                    GT    _  GG TC   GG
GAM1710  LOC145757 3'  GGGAAATGGAGGACATGTGT   77938    TG     T    A_
                                  G  TGTGTT CTCCA  TCCT
                                  |  ||||||  |||||  ||||
                                  T  GTACAG GAGGT  AGGG
                                   GT      _     AA
GAM1710  LOC145757 3'  TGGGGAGACAGGCATGTGA    77944    TG    G
                                  T  TGTGT TGTTTCTCCA
                                  |  |||||  ||||||||||
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                                A  GTACG ACAGAGGGGT
                                 GT     G
GAM1710  LOC145815 3'  GGGATGGAATGGATGCACCGCA 84520       T       C_    A
              A                   TTGTG GTGTGTTT  TCCA TCCT
                                  ||||| ||||||||  |||| ||||
                                  AACGC CACGTAGG  AGGT AGGG
                                     _       TA    _
GAM1710  LOC145828 5'  AGGCCTGGGAGGTGCACAT    84536       TG    T   AT
                                  GTGTG  TTTC CCA  CCT
                                  |||||  |||| |||  |||
                                  TACAC  GGAG GGT  GGA
                                     GT    _  CC
GAM1710  LOC146108 5'  GGGATGCAGGGCGCGCGGACAG 78151       G       T  CCA
                                  TTGT TGTGTGTT CT   ATCCT
                                  |||| |||||||| ||   |||||
                                  GACA GCGCGCGG GA   TAGGG
                                    G       _ CG_
GAM1710  LOC146136 5'  GGTAGAAGCACTATGTGA    73320    TG    T       _
                                  T  TGTG GTGTTTCT CC
                                  |  |||| |||||||| ||
                                  A  GTAT CACGAAGA GG
                                   GT    _       T
GAM1710  LOC146138 5'  AGGATGTGGCACATATATAC   84588          TTCT   _
                                  GTGTGTGTGT    CCA ATCCT
                                  ||||||||||    ||| |||||
                                  CATATATACA    GGT TAGGA
                                        C___   G
GAM1710  LOC146138 3'  GGGATTGGATTAATACAT    84594        TC
                                  GTGTGTT  TCCAATCCT
                                  |||||||  |||||||||
                                  TACATAA  AGGTTAGGG
                                      TT
GAM1710  LOC146220 3'  GGGATCCCCGGGCGCGCGCGC  84601           CTCCA
                                  GTGTGTGTGTTT     ATCCT
                                  ||||||||||||     |||||
                                  CGCGCGCGCGGG     TAGGG
                                         CCCC_
GAM1710  LOC146227 5'  GGACGAGCACACATACAG     78216             C
                                  TTGTGTGTGTGTTT TCC
                                  |||||||||||||| |||
                                  GACATACACACGAG AGG
                                           C
GAM1710  LOC146268 3'  AGGACTCAGATCTACACACA   78332         TT   CCAA
                                  TGTGTGTG  TCT    TCCT
                                  ||||||||  |||    ||||
                                  ACACACAT  AGA    AGGA
                                       CT   CTC_
GAM1710  LOC146272 5'  AGGGTTGGGGAGGGGCACA    78325       G
                                  TGTGT TTTCTCCAATCCT
                                  ||||| ||||||||||||
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                                ACACG GGAGGGGTTGGGA
                                   G
GAM1710  LOC146332 5'  GGGGCAGGCGGGCGCACAG   78360        G    _
                                TTGTGTGT TGTTT CTCC
                                |||||||| ||||| ||||
                                GACACGCG GCGGA GGGG
                                     G    C
GAM1710  LOC146337 3'  GGAGGAGACGCAAACACAA   84642       G      _
                                TTGTGT TGTGTTTC TCC
                                |||||| |||||||| |||
                                AACACA ACGCAGAG AGG
                                   A       G
GAM1710  LOC146455 3'  AGGTCACAGGCAACGTACATAC 78456           T  CCAAT
            G                    TGTGTGTGTGTT CT     CCT
                                |||||||||||| ||     |||
                                GCATACATGCAA GG     GGA
                                       C  ACACT
GAM1710  LOC146513 3'  CTGGGAGGTCCCAGGCTGTGTG 84702       _____ G  TT_    AATCCT
            CACAG                  TTGTGT    GT TG   TCTCC
                                ||||||    || ||   |||||
                                GACACG    CG AC   GGAGG
                                   TGTGT  G  CCT    G   TCC
GAM1710  LOC146517 3'  GGAAGAATATACGGATAG    78507     G       TC
                                TTGT TGTGTGTT  TCC
                                |||| ||||||||  |||
                                GATA GCATATAA  AGG
                                  G       GA
GAM1710  LOC146520 5'  AGGAGGAGGGATGCCACACAG  78513       T    TT    AA
                                TTGTGTG GTGT  CTCC  TCCT
                                ||||||| ||||  ||||  ||||
                                GACACAC CGTA  GAGG  AGGA
                                   _   GG   __
GAM1710  LOC146656 3'  TAGGAGCCAGTGGGGAAGTGCG 78668   TG  TG      A____
            TGT                  G  TG  TTTCTCCA    TCCT   A
                                |  ||  ||||||||    ||||   |
                                T  GC  GAAGGGGT    AGGA   T
                                 GT  GT       GACCG
GAM1710  LOC146667 5'  GGGATTGGAGCAGGCAGCATGT 84715   TG    G    _
            GG                   T  TGTGT TGTTT CTCCAATCCT
                                |  ||||| ||||| ||||||||||
                                G  GTACG ACGGA GAGGTTAGGG
                                 GT    _    C
GAM1710  LOC146713 3'  GGGTTTTGGGTGGTGTGTGCAC 84737      TG  TG TT T    T_
            AA                   TTGTG  TG  T  C CCAA  CCT
                                |||||  ||  |  | ||||  |||
                                AACAC  GT  G  G GGTT  GGG
                                   GT  GT GT _   TT
GAM1710  LOC146723 5'  GGGAACTAAGAAACTACACACG 78683         T     CCAA
            A                    TTGTGTGTG GTTTCT    TCCT
                                |||||||| ||||||    ||||
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                                AGCACACAT CAAAGA    AGGG
                                      _     ATCA
GAM1710  LOC146728 5'  GGAGATTAGACATGCACAGAA  84768    G        ___
                                TT TGTGTGTGTT   TCTCC
                                || ||||||||||   |||||
                                AA ACACGTACAG   AGAGG
                                 G         ATT
GAM1710  LOC146988 5'  GGGGTGGGAGGTGTACGTAGAA 84961    G     TG    T   AT
                                TT TGTGTG  TTTC CCA  CC
                                || ||||||  |||| |||  ||
                                AA ATGCAT  GGAG GGT  GG
                                 G     GT    _  GG
GAM1710  LOC147004 3'  GGGATTGCTGTGCATATATAT  84969          TTCTC
                                GTGTGTGTGT    CAATCCT
                                ||||||||||    |||||||
                                TATATATACG    GTTAGGG
                                      TGTC_
GAM1710  LOC147011 5'  AGGGTTGGACTTCACGCA    78830       TTTC
                                TGTGTG   TCCAATCCT
                                ||||||   |||||||||
                                ACGCAC   AGGTTGGGA
                                   TTC_
GAM1710  LOC147229 3'  GGGGCTGGGAGGCACAGATGCA 78925       G       T   AT
            G                    TTGTGT TGTGTTTC CCA  CCT
                                ||||||| |||||||| |||  |||
                                GACGTA ACACGGAG GGT  GGG
                                   G       _  CG
GAM1710  LOC147276 5'  GGGATTTCCTAAGTGTATACAT 78967        TG   CTCC
            A                    TGTGTGTG  TTT    AATCCT
                                ||||||||  |||   ||||||
                                ATACATAT  GAA    TTAGGG
                                     GT   TCCT
GAM1710  LOC147341 5'  GGGGTGAGGGGGAGTGGGTGTG 85121    TG  TG G GT     A_
            TGA                    T  TG  T T  TTCTCC  ATCCT
                                |  ||  | |  ||||||  |||||
                                A  GT  G G  AGGGGG  TGGGG
                                 GT  GT G TG     AG
GAM1710  LOC147495 3'  AGGTGTAGATATGTATATACAA 85141         TG T   C  AT
                                TTGTGTGTG  T TCT CA  CCT
                                |||||||||  | ||| ||  |||
                                AACATATAT  A AGA GT  GGA
                                     GT T   T  __
GAM1710  LOC147639 5'  GGGGCCCAAGTGTGCACCCAG  79012     T    TG   ___
                                TTG GTGTG  TTT   CTCC
                                ||| |||||  |||   ||||
                                GAC CACGT  GAA   GGGG
                                  C    GT   CCC
GAM1710  LOC147859 5'  GGCCGGAGTACACGCGTACAA  88517           TT    AAT
                                TTGTGTGTGTGT  CTCC   CC
                                ||||||||||||  ||||   ||
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                                AACATGCGCACA  GAGG   GG
                                      T_    CC_
GAM1710  LOC147929 5'  ACACGTGCAGAGACGCACACAC 79271              C  ATCCT
              AG                    TTGTGTGTGTGTTTCT CA
                                    |||||||||||||||| ||
                                    GACACACACGCAGAGA GT
                                          C  GCACAG
GAM1710  LOC148147 3'  GGGGTTGGAGCCCCCACACAGA 79403    G     TGTTT
              G                     TT TGTGTG    CTCCAATCCT
                                    || ||||||    ||||||||||
                                    GA ACACAC    GAGGTTGGGG
                                     G     CCCC_
GAM1710  LOC148195 3'  AGGAAAAATAAATGCACAG   85268        G    C   AATCCT
                                    TTGTGTGT TGTTT TCC
                                    |||||||| ||||| |||
                                    GACACGTA ATAAA AGG
                                         A     A   A   T
GAM1710  LOC148343 5'  AGGAGGAGGACCACATGCGCAG 79537          T     AA
                                    TTGTGTGTGTG TTCTCC  TCCT
                                    |||||||||| ||||||  ||||
                                    GACGCGTACAC AGGAGG  AGGA
                                          C     __
GAM1710  LOC148418 3'  GGACAAGATGCGCACAGGG   79593    G        C_
                                    TT TGTGTGTGTTT  TCC
                                    || ||||||||||  |||
                                    GG ACACGCGTAGA  AGG
                                     G         AC
GAM1710  LOC148479 3'  GGTAGAAACTGTACATAG    79616        TGT     _
                                    TTGTGTG   GTTTCT CC
                                    |||||||   |||||| ||
                                    GATACAT   CAAAGA GG
                                        GT_     T
GAM1710  LOC148645 3'  AGGAACAAAGTCACATGCAG   85328          ____
                                    TTGTGTGTG    TGTTTCT
                                    |||||||||    |||||||
                                    GACGTACAC    ACAAGGA
                                          TGAA
GAM1710  LOC148645 3'  GGGGTTGTAGAGTAATATGTAA 85337     TG   GTGT    C
                                    TTG  TGT    TTCT CAATCCT
                                    |||  |||    |||| |||||||
                                    AAT  ATA    GAGA GTTGGGG
                                      GT   AT__    T
GAM1710  LOC148758 5'  GGGAAGGAAGACACGTATGTGA 79724    TG         C   AA
                                    T  TGTGTGTGTTT TCC  TCCT
                                    |  |||||||||| |||  ||||
                                    A  GTATGCACAGA AGG  AGGG
                                     GT          _  A_
GAM1710  LOC148824 3'  GGGATCACAGAACATGTGCAC  85381     TG     T  CCA
                                    GTG  TGTGTT CT   ATCCT
                                    |||  |||||| ||   |||||
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                                CAC  GTACAA GA   TAGGG
                                  GT     _ CAC
GAM1710  LOC148946 3'  AGGAGGGGAGAGACACACAGAT 85463      G          AA
                 AA                 TTGT TGTGTGTTTCTCC  TCCT
                                    |||| ||||||||||||  ||||
                                    AATA ACACACAGAGAGG  AGGA
                                      G          GG
GAM1710  LOC148946 5'  GGGAGAAATAGGAGCGCACACA 85471    TG          CCAA_
                 TGG                  T  TGTGTGTGTTTCT    TCCT
                                    |  ||||||||||||    ||||
                                    G  ACACACGCGAGGA    AGGG
                                     GT          TAAAG
GAM1710  LOC149171 5'  GGATTACAGGCATGCACA    79969          CTCC
                                    TGTGTGTGTTT    AATCC
                                    ||||||||||    |||||
                                    ACACGTACGGA    TTAGG
                                          CA__
GAM1710  LOC149194 3'  AGGGTTGGAGGTGGGGAACACG 79978       GTGTGTT
                 A                  TTGTGT      TCTCCAATCCT
                                    ||||||      ||||||||||
                                    AGCACA      GGAGGTTGGGA
                                       AGGGGT_
GAM1710  LOC149271 5'  GGGATTATAGGAGCTGCGTGTG 80010    TG  TG  _     CC
                 TGG                  T  TG  TGT GTTTCT  AATCCT
                                    |  ||  ||| ||||||  ||||||
                                    G  GT  GCG CGAGGA  TTAGGG
                                     GT  GT   T     TA
GAM1710  LOC149332 5'  GGGAGAAGAAACAACATGTGTG 85550    TG  TG  _     CCAA
                 A                  T  TG  TGT GTTTCT    TCCT
                                    |  ||  ||| ||||||    ||||
                                    A  GT  ACA CAAAGA    AGGG
                                     GT  GT   A     AG__
GAM1710  LOC149351 5'  GGCGGGAGCCCGCGCGTGG    80087    TG     T     _
                                    T  TGTGTG GTTTCT CC
                                    |  |||||| |||||| ||
                                    G  GCGCGC CGAGGG GG
                                     GT     C     C
GAM1710  LOC149420 3'  AGTGGGAGAAGATACATACACA 80152             _    AATCCT
                 G                  TTGTGTGTGTGTTT CTCC
                                    |||||||||||||| ||||
                                    GACACATACATAGA GAGG
                                           A    GTGA
GAM1710  LOC149420 3'  GGAGAAGATACATACACAG    80156             _
                                    TTGTGTGTGTGTTT CTCC
                                    |||||||||||||| ||||
                                    GACACATACATAGA GAGG
                                           A
GAM1710  LOC149464 3'  GGGGTCTGGCAGCACATGTA   85597    TG     TCT  _
                                    TG  TGTGTT   CCA ATCCT
                                    ||  ||||||   ||| |||||
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                                AT  ACACGA   GGT TGGGG
                                 GT     C__   C
GAM1710  LOC149478 5'  TGCAGGAGCGCTGCGTGG    80180    TG    T       C
                                T  TGTG GTGTTTCT CA
                                |  |||| |||||||| ||
                                G  GCGT CGCGAGGA GT
                                 GT    _       C
GAM1710  LOC149603 3'  GGGGTTGGAGGAGCGAGGAGCA 71175      GTGTG
              G                   TTGT     TGTTTCTCCAATCCT
                                  ||||     ||||||||||||||
                                  GACG     GCGAGGAGGTTGGGG
                                    AGGA_
GAM1710  LOC149672 3'  AGGACCAACAGGAATAACGCAT 80334    TG      _      CCAA_
              GTGG                   T  TGTGTGT GTTTCT     TCCT
                                  |  ||||||| ||||||     ||||
                                  G  GTACGCA TAAGGA     AGGA
                                   GT      A      CAACC
GAM1710  LOC149803 3'  GGAAGGAACGTACAAGTAA    80359     TG         _
                                  TTG  TGTGTGTTTCT CC
                                  |||  |||||||||| ||
                                  AAT  ACATGCAAGGA GG
                                    GA          A
GAM1710  LOC149832 5'  GGGAGTTGGGGCACGTGTGTGT 85866     TG  TG   TT     _
              AA                    TTG  TG  TGT  CTCCAA TCCT
                                  |||  ||  |||  |||||| ||||
                                  AAT  GT  GCA  GGGGTT AGGG
                                    GT  GT   C_     G
GAM1710  LOC149837 5'  GGAGGTGGACACATGAGCAG   85899      G       __
                                  TTGT TGTGTGTT  TCTCC
                                  |||| ||||||||  |||||
                                  GACG GTACACAG  GGAGG
                                    A       GT
GAM1710  LOC149844 5'  GGGATCACGCAGGGGCGCGCGC 80346          TT  CCA__
              A                     TGTGTGTGT  CT     ATCCT
                                  |||||||||  ||    |||||
                                  ACGCGCGCG  GA     TAGGG
                                        GG  CGCAC
GAM1710  LOC150113 5'  GGGAAGAGACGCGTGCACACAG 88569        TG   T    CAA
                                  TTGTGTG  TGT TCTC   TCCT
                                  |||||||  ||| ||||   ||||
                                  GACACAC  GCG AGAG   AGGG
                                      GT   C    A__
GAM1710  LOC150142 5'  AGGGCCGAGCGTGTATGCACAA 80399          TG TT   CAA
                                  TTGTGTGTG  T  CTC   TCCT
                                  |||||||||  |  |||   ||||
                                  AACACGTAT  G  GAG   GGGA
                                        GT C_   CC_
GAM1710  LOC150155 3'  GGCGGGCATGCACGCAA     71414             T T
                                  TTGTGTGTGTGTT C CC
                                  ||||||||||||| | ||
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                                AACGCACGTACGG G GG
                                       _ C
GAM1710  LOC150155 3'  GGGGTTGGGGGGGGACATCGGAA 71416    G  T    G TT
                                TT TG GTGT T  CTCCAATCCT
                                || || |||| |  ||||||||||
                                AA GC TACA G  GGGGTTGGGG
                                 G  _   _ GG
GAM1710  LOC150157 5'  GGGGCCATCAAGAGGCTGCACG 86026   TG     T     CCAA__
              TGA                 T  TGTGTG GTTTCT     TCCT
                                |  |||||| ||||||      ||||
                                A  GCACGT CGGAGA     GGGG
                                 GT     _     ACTACC
GAM1710  LOC150203 3'  CATGCTGGGAGATATGCAGACA 61135     G        T   ATCCT
              G                  TTGT TGTGTGTTTC CCA
                                |||| |||||||||| |||
                                GACA ACGTATAGAG GGT
                                   G         _   CGTACG
GAM1710  LOC150407 3'  AGGACACCAGGAAGAGCGTGCA 80636     TG    TC   AA___
              CA                   TGTG  TGTT  TCC     TCCT
                                ||||  ||||  |||     ||||
                                ACAC  GCGA  AGG     AGGA
                                   GT    GA   ACCAC
GAM1710  LOC150481 3'  AGGGTCGGGGGGCACGGCACAA  80691       G     TT    A
                                TTGTGT TGTGT  CTCC ATCCT
                                |||||| |||||  |||| |||||
                                AACACG GCACG  GGGG TGGGA
                                   _     __    C
GAM1710  LOC150481 3'  GAGAAGTACAATGTACAG     80703       TG _
                                TTGTG  T GTGTTTCTC
                                |||||  | |||||||||
                                GACAT  A CATGAAGAG
                                    GT A
GAM1710  LOC150519 3'  AGGGTTTAGAGGAGACACAGAC 80728       G        CC__
              ACAA                  TTGTGT TGTGTTTCT    AATCCT
                                |||||| |||||||||    ||||||
                                AACACA ACACAGAGG    TTGGGA
                                    G        AGAT
GAM1710  LOC150538 5'  GGGAAGGGGAGATGTGTGCA   80740      TG       AA
                                TGTG  TGTTTCTCC  TCCT
                                ||||  |||||||||  ||||
                                ACGT  GTAGAGGGG  AGGG
                                   GT        A_
GAM1710  LOC150630 5'  AGGATTCAGGGGATGCACAGGT 86287    TG G      TT  CC
              GG                    T  T TGTGTGT  CT  AATCCT
                                |  | |||||||  ||  ||||||
                                G  G ACACGTA  GG  TTAGGA
                                 GT G      GG  AC
GAM1710  LOC150946 3'  GGATCCAGGGGAGATGCATGTG 86349    G  TG         A__    T
              GAA                   TT TG  TGTGTTTCTCC   ATCC
                                || ||  ||||||||||   ||||
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                                AA GT  ACGTAGAGGGG   TAGG
                                 G  GT         ACC
GAM1710  LOC150967 3'  AGGGTTGGGACTTCAACACA   80881      GTGTT  T
                                TGTGT     TC CCAATCCT
                                ||||||     || ||||||||
                                ACACA     AG GGTTGGGA
                                   ACTTC  _
GAM1710  LOC150967 5'  GGGAGGAGGTGTGCGTGCACA  80885      TG  TG T    AA
                                TGTG  TG  T TCTCC  TCCT
                                ||||  ||  | |||||  ||||
                                ACAC  GC  G GGAGG  AGGG
                                  GT  GT T    __
GAM1710  LOC150967 5'  GGGAGGGAGGAGTACAGACATG 80886   TG   G         AA
              G                   T  TGT TGTGTTTCTCC  TCCT
                                |  ||| ||||||||||  ||||
                                G  ACA ACATGAGGAGG  AGGG
                                 GT   G         G_
GAM1710  LOC150967 3'  GGGATTGAACTAGACACACACA 80887          CTC_
                                TGTGTGTGTTT    CAATCCT
                                ||||||||||    |||||||
                                ACACACACAGA    GTTAGGG
                                      TCAA
GAM1710  LOC151009 5'  GGGGTGGGCAGGGGCGCGGGTG 86372     TG G     TT  _  A
              CAG                   TTG  T TGTGT  CT CC ATCCT
                                |||  | |||||  || || |||||
                                GAC  G GCGCG  GA GG TGGGG
                                  GT G    GG  C  G
GAM1710  LOC151009 5'  GGGTGCAGAGGAGCGCGTGCG  86373    TG        CA_    T
                                TG  TGTGTTTCTC   ATCC
                                ||  ||||||||||   ||||
                                GC  GCGCGAGGAG   TGGG
                                 GT         ACG
GAM1710  LOC151009 5'  TGGAAGGCGTGCGCGCAG    86376        TG    C
                                TTGTGTG  TGTTT TCCA
                                |||||||  ||||| ||||
                                GACGCGC  GCGGA AGGT
                                    GT    _
GAM1710  LOC151146 5'  GATTTAGGGGTGCATGGGCAG  80938      G    TG TT  CC
                                TTGT TGTG  T  CT  AATC
                                |||| ||||  |  ||  ||||
                                GACG GTAC  G  GA  TTAG
                                  G    GT GG  T_
GAM1710  LOC151278 3'  GGAGGGAGCATGCGGCAG    81011      _     G TT
                                TTGT GTGTGT T  CTCC
                                |||| ||||||  |  ||||
                                GACG CGTACG A  GAGG
                                  G     _ GG
GAM1710  LOC151361 3'  GGAAGGCAGGCGCACGA     86505        G    C
                                TTGTGTGT TGTTT TCC
                                ||||||||  ||||| |||
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                                AGCACGCG ACGGA AGG
                                    G    _
GAM1710  LOC151429 5'  GGGGTGGGGGGTGCGGCATACA 86544        G  T    A
              G                  TTGTGTGT TGT TCTCC ATCCT
                                 |||||||| ||| ||||| |||||
                                 GACATACG GCG GGGGG TGGGG
                                     _  T    G
GAM1710  LOC151512 5'  AGGACACAGAAGCATGCG    86612          CCAA
                                 TGTGTGTTTCT    TCCT
                                 ||||||||||    ||||
                                 GCGTACGAAGA    AGGA
                                      CAC_
GAM1710  LOC151534 5'  TTGGGAGACGCAGTGCAG    57489     TG G      T
                                 TTG  T TGTGTTTC CCAA
                                 |||  | ||||||| ||||
                                 GAC  G ACGCAGAG GGTT
                                   GT _      _
GAM1710  LOC151643 3'  GGAACCAGAGGTTATATACA   81140        TT    CAA_
                                 TGTGTGTG  TCTC    TCC
                                 ||||||||  ||||    |||
                                 ACATATAT  GGAG    AGG
                                     T_    ACCA
GAM1710  LOC151701 3'  GGGACTGGGGATGCGTCACA   86675     _  T     A
                                 TGTG TGT TCTCCA TCCT
                                 |||| ||| |||||| ||||
                                 ACAC GCG AGGGGT AGGG
                                   T  T     C
GAM1710  LOC151742 3'  TGTAGAGTCACATATATGA    58347    TG      T    C
                                 T  TGTGTGTG TTCT CA
                                 |  |||||||| |||| ||
                                 A  ATATACAC GAGA GT
                                  GT       T    T
GAM1710  LOC151816 5'  TGGGGAGCCCATACACAG     86688         T    T
                                 TTGTGTGTG GTTTC CCA
                                 ||||||||| ||||| |||
                                 GACACATAC CGAGG GGT
                                      C    _
GAM1710  LOC151827 5'  CGGACTGTAAGTGCGCGCGCG  81192        TG   CTC  A   T
                                 TGTGTGTG  TTT   CA TCC
                                 ||||||||  |||   || |||
                                 GCGCGCGC  GAA   GT AGG
                                     GT   T__  C   CG
GAM1710  LOC151877 3'  AGGGTTATCACAGGAACACTAT 86691     TG  T      CC___
              GTAG                  TTG  TG GTGTTTCT     AATCCT
                                 |||  || ||||||||     ||||||
                                 GAT  AT CACAAGGA     TTGGGA
                                   GT _       CACTA
GAM1710  LOC152217 3'  GGGGTCATTCCGGGCACTGCGC 92870        _     CTCCA_
              GCG                   TGTGTGT GTGTTT     ATCCT
                                 |||||||  ||||||     |||||
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                                GCGCGCG CACGGG     TGGGG
                                    T     CCTTAC
GAM1710  LOC152286 3'  TGGAGAGGCCATGCGCAA    86814         T
                                TTGTGTGTG GTTTCTCCA
                                ||||||||| |||||||||
                                AACGCGTAC CGGAGAGGT
                                        _
GAM1710  LOC152316 3'  GATGAGAGACAACATGTGA   86792   TG    G       CA
                                T  TGTGT TGTTTCTC  ATC
                                |  ||||| ||||||||  |||
                                A  GTACA ACAGAGAG  TAG
                                 GT    _      __
GAM1710  LOC152345 3'  GGAAAAACACGCCCACAG    81446      T       C
                                TTGTG GTGTGTTT TCC
                                ||||| |||||||| |||
                                GACAC CGCACAAA AGG
                                   C       A
GAM1710  LOC152445 5'  AGGGTTGGCCTGCCATGTGT   86934   TG    T  TTCT
                                G  TGTG GT    CCAATCCT
                                |  |||| ||    ||||||||
                                T  GTAC CG    GGTTGGGA
                                 GT    _  TCC_
GAM1710  LOC152445 5'  GGGGTCAAAGGATGCACAACAG 86956     G       T  CCA
                                TTGT TGTGTGTT CT   ATCCT
                                |||| |||||||| ||   |||||
                                GACA ACACGTAG GA   TGGGG
                                   _       _ AAC
GAM1710  LOC152453 5'  GGAGAAGGTGCACAGCAG    81476     G    TG _
                                TTGT TGTG  T TTCTCC
                                |||| ||||  | ||||||
                                GACG ACAC  G AAGAGG
                                   _    GT G
GAM1710  LOC152503 3'  AGCATGGGGAGGCTCACACACA 86975         T       ATCCT
            G                    TTGTGTGTG GTTTCTCCA
                                ||||||||| |||||||||
                                GACACACAC CGGAGGGGT
                                      T        ACGA
GAM1710  LOC152580 5'  AGGTCTCTGAGATGCAACACAA 86982       G       TCCAAT
                                TTGTGT TGTGTTTC     CCT
                                |||||| ||||||||     |||
                                AACACA ACGTAGAG     GGA
                                   _       TCTCT_
GAM1710  LOC152620 3'  GGATTACAGGCACACACA    60710          CTCC
                                TGTGTGTGTTT    AATCC
                                ||||||||||    |||||
                                ACACACACGGA    TTAGG
                                       CA__
GAM1710  LOC152687 5'  AGATACGAGAAATGTGGACATG 81528   TG   G  TG     CA   CT
            A                    T  TGT TG  TTTCTC  ATC
                                |  ||| ||  ||||||  |||
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                                A  ACA GT  AAAGAG  TAG
                                 GT   G  GT     CA   A
GAM1710  LOC152762 3'  GGGAACTGGAGTGTGCGAGCG  81535     G  TG TT    A_
                                TGT TG  T  CTCCA  TCCT
                                ||| ||  |  |||||  ||||
                                GCG GC  G  GAGGT  AGGG
                                  A  GT T_    CA
GAM1710  LOC152915 5'  GGGCTGGGACACATACAGGG   67585    G        TCT   AT
                                TT TGTGTGTGTT   CCA  CC
                                || ||||||||||   |||  ||
                                GG ACATACACAG   GGT  GG
                                 G         ___   CG
GAM1710  LOC152915 5'  GGGGTTGGGGACAGGACAT    67586     G  _
                                GTGT TT TCTCCAATCCT
                                |||| || ||||||||||
                                TACA GA AGGGGTTGGGG
                                  G  C
GAM1710  LOC153232 5'  GGACGAGACACGCATCAG     87184     T         _
                                TTG GTGTGTGTTTC TCC
                                ||| ||||||||||| |||
                                GAC TACGCACAGAG AGG
                                  _         C
GAM1710  LOC153277 3'  GGGTACAGAGACACCATGCAG  87189        T       CCA
                                TTGTGTG GTGTTTCT   ATCC
                                ||||||| ||||||||   ||||
                                GACGTAC CACAGAGA   TGGG
                                    _       CA_
GAM1710  LOC153505 3'  GGGACAGGGACGCGCGCCCAG  81706     T       TT  CCAA
                                TTG GTGTGTGT  CT    TCCT
                                ||| ||||||||  ||    ||||
                                GAC CGCGCGCA  GA    AGGG
                                  C       GG  C___
GAM1710  LOC153577 3'  AGGAAAATAAAATTCATACATA 87236         T    CTCCAA
            A                    TTGTGTGTG GTTT      TCCT
                                |||||||||  ||||      ||||
                                AATACATAC TAAA      AGGA
                                     T    ATAAA_
GAM1710  LOC153579 3'  GGAGTCGGGCGGATGCGCAA   81772         G    __
                                TTGTGTGT TGTTT  CTCC
                                |||||||| |||||  ||||
                                AACGCGTA GCGGG  GAGG
                                    G    CT
GAM1710  LOC153768 5'  AGGACTGAATGAGATCATGCGC 57498    TG       TT   ___  A
            ATGG                   T  TGTGTGTG  TCTC   CA TCCT
                                |  ||||||||  ||||   || ||||
                                G  ACGCGTAC  AGAG   GT AGGA
                                 GT       T_    TAA  C
GAM1710  LOC153931 3'  GGGAAGATAGAAACACACACAT 81915              CCAA
            A                    TGTGTGTGTGTTTCT    TCCT
                                ||||||||||||||    ||||
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                                ATACACACACAAAGA   AGGG
                                      TAGA
GAM1710  LOC154822 3'  AGGCTGGAGTGCAATGTGCAA  87483    TG  G  TT   AT
                                TTG  TGT TGT  CTCCA  CCT
                                |||  ||| |||  |||||  |||
                                AAC  GTA ACG  GAGGT  GGA
                                  GT  _  T_   C_
GAM1710  LOC154822 5'  GGAAGAAGATGCTGCATACAG  87487       _    _ _
                                TTGTGTGT GTGTTT CT CC
                                |||||||| |||||| || ||
                                GACATACG CGTAGA GA GG
                                     T    A  A
GAM1710  LOC154834 3'  AGGATAGGATGAGATGTGCATG 87490   TG   TG    _  A
           TGA                    T  TGTG  TGTTTC TCC ATCCT
                                |  ||||  |||||| ||| |||||
                                A  GTAC  GTAGAG AGG TAGGA
                                 GT   GT    T  A
GAM1710  LOC154834 3'  AGGGCGTTCGGGAGGAGCAGCA 87492       G       AA____
           CGCAA                   TTGTGTGT TGTTTCTCC    TCCT
                                |||||||| |||||||||     ||||
                                AACGCACG ACGAGGAGG    GGGA
                                     _       GCTTGC
GAM1710  LOC154860 5'  AGGATACACACAGACGCGCGCG 87500        T  CCA___
           CGC                    GTGTGTGTGT TCT    ATCCT
                                |||||||||| |||     |||||
                                CGCGCGCGCG AGA    TAGGA
                                      C  CACACA
GAM1710  LOC155066 3'  AGGAGTGGGAAGCAACACGCAG 82208       G    T  A
                                TTGTGTGT TGTTTC CCA TCCT
                                |||||||| |||||| ||| ||||
                                GACGCACA ACGAAG GGT AGGA
                                     _    _  G
GAM1710  LOC157254 5'  AGGAGGCGGGAGCCGTGTGCGA 82309     TG  T    _ AA
                                TTGTG  TG GTTTCT CC  TCCT
                                |||||  || |||||| ||  ||||
                                AGCGT  GC CGAGGG GG  AGGA
                                   GT  _    C  __
GAM1710  LOC157273 3'  AGGAAAAGAGATAGCACATATA 87717        GTT   CAA
           G                     TTGTGTGTGT   TCTC   TCCT
                                ||||||||||   ||||  ||||
                                GATATACACG   AGAG   AGGA
                                      AT_   AAA
GAM1710  LOC157623 5'  GGGGCCCACAGAAACATAATGC 82414      G       CCAA_
           AA                     TTGTGT TGTGTTTCT    TCCT
                                ||||||| |||||||||    ||||
                                AACGTA ATACAAAGA    GGGG
                                   _       CACCC
GAM1710  LOC157638 3'  GGGGTTGGGGGAAAGTTCG   82425    TGTG
                                TG   TTTCTCCAATCCT
                                ||   ||||||||||||
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                                GC    AAGGGGGTTGGGG
                                 TTGA
GAM1710  LOC157737 5'  GGAGAGAAGTTACGTATAA    87845         TG_
                                TTGTGTGTG   TTTCTCC
                                |||||||||   |||||||
                                AATATGCAT   AGAGAGG
                                     TGA
GAM1710  LOC158117 3'  TGGAGAAGACATATGTGG    82614    TG      G
                                T  TGTGTGT TTTCTCCA
                                |  ||||||| ||||||||
                                G  GTATACA GAAGAGGT
                                 GT      _
GAM1710  LOC158187 3'  AGGGTGCGCAAATGCACAT    87984          CTCCA
                                GTGTGTGTTT     ATCCT
                                ||||||||||     |||||
                                TACACGTAAA     TGGGA
                                      CGCG_
GAM1710  LOC158337 5'  AGGAATGGAGTATATATGT    88105    TG     TT     A
                                G  TGTGT  CTCCA TCCT
                                |  |||||  ||||| ||||
                                T  ATATA  GAGGT AGGA
                                 GT     T_     A
GAM1710  LOC158427 3'  AGGTTCCAAGAAACACATACGC 58350              CCAAT
           AG                     TTGTGTGTGTGTTTCT     CCT
                                ||||||||||||||||     |||
                                GACGCATACACAAAGA     GGA
                                      ACCTT
GAM1710  LOC158696 3'  GGTAGAGATGTGCCATAG     82860       T TG      _
                                TTGTG G  TGTTTCT CC
                                ||||| |  ||||||| ||
                                GATAC C  GTAGAGA GG
                                   _ GT      T
GAM1710  LOC158798 5'  GGGATGCCCAATACATACCAG  82875     T        TCTCCA
                                TTG GTGTGTGTT      ATCCT
                                ||| |||||||||      |||||
                                GAC CATACATAA      TAGGG
                                  _        CCCG__
GAM1710  LOC158987 3'  GGGTGTGGGGGCATGTGCCAG  88331     T TG     TT TC  A
                                TTG G  TGTGT  C  CA TCC
                                ||| |  |||||  |  || |||
                                GAC C  GTACG  G  GT GGG
                                  _ GT     GG GT  _
GAM1710  LOC159036 3'  AGGACTTGGAGTGTGTATGCAT 88341    TG      TG TT     _
           GA                     T  TGTGTG  T  CTCCAA TCCT
                                |  ||||||  |  |||||| ||||
                                A  ACGTAT  G  GAGGTT AGGA
                                 GT      GT T_      C
GAM1710  LOC159091 3'  TGGAGAAACACACACATCAA   57980     _
                                TTG TGTGTGTGTTTCTCCA
                                ||| ||||||||||||||||
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                                AAC ACACACACAAAGAGGT
                                  T
GAM1710  LOC159982 5'  AGGCCGGGGGAACGTGCGAGCA 88431      G  TG        AAT
                 G                 TTGT TG  TGTTTCTCC   CCT
                                   |||| ||  |||||||||   |||
                                   GACG GC  GCAAGGGGG   GGA
                                     A  GT        CC_
GAM1710  LOC160484 3'  AGGAACGAGAAAGACGCGCGCA 83090          G     CAA
                 A                 TTGTGTGTGT TTTCTC   TCCT
                                   |||||||||| ||||||   ||||
                                   AACGCGCGCA AAAGAG   AGGA
                                         G     CA_
GAM1710  LOC161635 5'  GGGGTTGGCATCCCCCACATAC 98356         TGTTTCT
                 G                 TGTGTGTG      CCAATCCT
                                   ||||||||      ||||||||
                                   GCATACAC      GGTTGGGG
                                       CCCCTAC
GAM1710  LOC162617 5'  GTTGGAAACACAGTGCAA    83251     TG G     TC
                                   TTG  T TGTGTT  TCCAAT
                                   |||  | ||||||  ||||||
                                   AAC  G ACACAA  AGGTTG
                                     GT _     __
GAM1710  LOC163026 5'  AGGTATGCCGGAAACAAATACG 83281    TG     G      CCA  _
                 TGA                 T  TGTGT TGTTTCT   AT CCT
                                   |  ||||| |||||||   || |||
                                   A  GCATA ACAAAGG   TA GGA
                                    GT    A      CCG  T
GAM1710  LOC163250 5'  AGGGGACGGACGCGCGCACAG  88529           TC   AAT
                                   TTGTGTGTGTGTT  TCC   CCT
                                   ||||||||||||  |||   |||
                                   GACACGCGCGCAG  AGG   GGA
                                         GC  ___
GAM1710  LOC163250 5'  GGACGGACGCGCGCACAG    88530           TC
                                   TTGTGTGTGTGTT  TCC
                                   ||||||||||||  |||
                                   GACACGCGCGCAG  AGG
                                         GC
GAM1710  LOC163590 3'  AGGATAAAGATCTATACAT    59508        TT   CCA
                                   GTGTGTG  TCT   ATCCT
                                   |||||||  |||   |||||
                                   TACATAT  AGA   TAGGA
                                      CT   AA_
GAM1710  LOC163682 5'  GGGCAGGCAGGCACGCAG    88411         G    C
                                   TTGTGTGT TGTTT TCC
                                   |||||||| ||||| |||
                                   GACGCACG ACGGA GGG
                                      G    C
GAM1710  LOC164173 3'  CCTAGGAAACATTAGATCATAT 83052          _______      CCAATCCT
                 ACAG                TTGTGTGTG     TGTTTCT
                                   |||||||||     |||||||
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                                GACATATAC     ACAAAGG
                                      TAGATT      A   TCCT
GAM1710  LOC164397 5'  GGAGAAGTGGACATACAA    83410        G GT
                                TTGTGTGT T  TTCTCC
                                |||||||| |  ||||||
                                AACATACA G  AAGAGG
                                     G TG
GAM1710  LOC165614 5'  GGGACTTAGGAGTGGTACGCA  83483        TT   _ _
                                TGTGTGT  CTCC AA TCCT
                                |||||||  |||| || ||||
                                ACGCATG  GAGG TT AGGG
                                    GT    A  C
GAM1710  LOC166793 5'  AGTCCCAGAGACAATACGCGTG 59917     TG       _    CAATCCT
            TGA                    TTG  TGTGTGTT TCTC
                                |||  |||||||| ||||
                                AGT  GCGCATAA AGAG
                                  GT       C    ACCCTGA
GAM1710  LOC166842 5'  AGGTTGAATTGGAGGGGCACAC 83551        TT      ____
            AT                    GTGTGTGT  CTCCAAT    CCT
                                ||||||||  |||||||    |||
                                TACACACG  GAGGTTA    GGA
                                     GG      AGTT
GAM1710  LOC166968 3'  AGGATCCCGGAACTGCGTGTGC 83558      TG  _    TCCA
            AG                    TTGTG  TGT GTTTC    ATCCT
                                |||||  ||| |||||    |||||
                                GACGT  GCG CAAGG    TAGGA
                                   GT   T    CCC_
GAM1710  LOC168448 3'  AGGAATTAAAGACACACACACA 83580            CTCCAA
            G                     TTGTGTGTGTGTTT     TCCT
                                ||||||||||||||     ||||
                                GACACACACACAGA     AGGA
                                        AATTA_
GAM1710  LOC169270 3'  GGACAAACATACTACAG     83613       T       C
                                TTGTG GTGTGTTT TCC
                                ||||| |||||||| |||
                                GACAT CATACAAA AGG
                                   _       C
GAM1710  LOC170106 5'  GGGGTTGGAGGAGCTGACAGGA 83453    G   GTGT
                                TT TGT    GTTTCTCCAATCCT
                                || |||    ||||||||||||||
                                AG ACA    CGAGGAGGTTGGGG
                                 G   GT__
GAM1710  LOC196047 5'  GGAAGAGGCATCGCATGG    91157    TG    T       _
                                T  TGTG GTGTTTCT CC
                                |  |||| |||||||| ||
                                G  ACGC TACGGAGA GG
                                 GT    _       A
GAM1710  LOC196418 5'  GGCTCGGAGGCGCACCTGTGA  89052    TG  T     TT    AAT
                                T  TG GTGTGT  CTCC   CC
                                |  || ||||||  ||||   ||
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                                A  GT CACGCG  GAGG   GG
                                 GT  C     __    CTC
GAM1710  LOC196484 3'  AGGCCTGGGGGGGGTGCACATC 63535     T    TG TT    AAT_
              AA                  TTG GTGTG  T  CTCC    CCT
                                ||| |||||  |  ||||    |||
                                AAC TACAC  G  GGGG    GGA
                                  _    GT GG    GTCC
GAM1710  LOC196528 3'  GGAGAAGACACATGCACA    89107           _
                                TGTGTGTGTGTTT CTCC
                                |||||||||||| ||||
                                ACACGTACACAGA GAGG
                                       A
GAM1710  LOC196540 3'  GGCGGGAGGAGCATGGACACAG 91206       G         AAT
                                TTGTGT TGTGTTTCTCC   CC
                                |||||| ||||||||||   ||
                                GACACA GTACGAGGAGG   GG
                                   G         GC_
GAM1710  LOC196759 3'  AGGGCTGAAAGAGGTGTAACAT 88908       G  TG    C_  AT
              AA                  TTGTGT TG  TTTCT  CA  CCT
                                |||||| ||  |||||  ||  |||
                                AATACA AT  GGAGA  GT  GGA
                                   _ GT    AA  CG
GAM1710  LOC196890 5'  GGGGCCATCAAGAGGCTGCACG 91227    TG     T     CCAA__
              TGA                   T  TGTGTG GTTTCT     TCCT
                                |  |||||| ||||||     ||||
                                A  GCACGT CGGAGA     GGGG
                                 GT     _     ACTACC
GAM1710  LOC197285 3'  GGGTCGAGATTGCACGCG    89153       T_   CA
                                TGTGTGT  TCTC  ATCC
                                |||||||  ||||  ||||
                                GCGCACG  AGAG  TGGG
                                    TT    C_
GAM1710  LOC197336 5'  TGCAGGGACACACACGGGG    59924    G       TT  C
                                TT TGTGTGTGT  CT CA
                                || |||||||||  || ||
                                GG GCACACACA  GA GT
                                 G        GG  C
GAM1710  LOC199692 3'  GGTTTGGAAGCACCATACAG   59927       T    TC    T
                                TTGTGTG GTGTT  TCCAA CC
                                |||||||  |||||  ||||| ||
                                GACATAC CACGA  AGGTT GG
                                   _    ___    T
GAM1710  LOC199714 3'  GGACCCCCAGGACCACGCGCAC 89701          T   CCAA_  T
              G                    TGTGTGTGTG TTCT     TCC
                                |||||||||| ||||     |||
                                GCACGCGCAC AGGA     AGG
                                      C    CCCCC
GAM1710  LOC199745 3'  GGAAAGACATTATACGTGG   89719    TG     _    C
                                T  TGTGTG TGTTT TCC
                                |  |||||| ||||| |||
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                                G  GCATAT ACAGA AGG
                                 GT     T    A
GAM1710  LOC199796 5'  GGGGCCTATCGGAGCATGCTGC 74924      T       TCCAA_
              AG                  TTGTG GTGTGTTTC     TCCT
                                  ||||| |||||||||     ||||
                                  GACGT CGTACGAGG     GGGG
                                    _       CTATCC
GAM1710  LOC199906 3'  AGGTAGAGAGAGAAAGTGCATG 89845      TG G_     CAAT
              CG                  TGTGTG  T  TTTCTC    CCT
                                  ||||||  |  ||||||   |||
                                  GCGTAC  G  AGAGAG    GGA
                                     GT AA     AGAT
GAM1710  LOC199906 3'  GGGGTGAGGGATGCAATGCG   89856      G    TT   CA
                                  TGTGT TGTGT  CTC  ATCCT
                                  ||||| |||||  |||  |||||
                                  GCGTA ACGTA  GAG  TGGGG
                                    _    GG   __
GAM1710  LOC200058 3'  GGAGAAAGCACATGCCAA    89962     T       _
                                  TTG GTGTGTGTTT CTCC
                                  ||| |||||||||| ||||
                                  AAC CGTACACGAA GAGG
                                    _        A
GAM1710  LOC200093 5'  AGGGCATCAGACACAGGTACAG 63760      TG      CTCCAA
                                  TTGTG  TGTGTTT     TCCT
                                  |||||  |||||||     ||||
                                  GACAT  ACACAGA     GGGA
                                     GG      CTAC__
GAM1710  LOC200197 3'  AGGATTAAAAGAGATACTTGTG 90012     TG  T      CC_
              CAA                   TTG  TG GTGTTTCT   AATCCT
                                  |||  || ||||||||   ||||||
                                  AAC  GT CATAGAGA   TTAGGA
                                    GT  T       AAA
GAM1710  LOC200317 3'  AGGGCATAGCAGGAGCACAGGC 90219    TG   G       CCAA__
              GTGG                    T  TGT TGTGTTTCT     TCCT
                                  |  ||| |||||||||     ||||
                                  G  GCG ACACGAGGA     GGGA
                                   GT   G       CGATAC
GAM1710  LOC200382 3'  GGAAAAGAAATAAGCACATAG  90236        G      CCAA
                                  TTGTGTGT TGTTTCT    TCC
                                  |||||||| |||||||    |||
                                  GATACACG ATAAAGA    AGG
                                       A      AA__
GAM1710  LOC200382 3'  GGGGCCAGACTTACATGTGG   90238    TG     T   __
                                  T  TGTGTG GTTT  CTCC
                                  |  |||||| ||||  ||||
                                  G  GTACAT CAGA  GGGG
                                   GT     T    CC
GAM1710  LOC200627 3'  GGCGGGGATACATAATAA     90262      G      TT  _
                                  TTGT TGTGTGT  CT CC
                                  |||| |||||||  || ||
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                                AATA ATACATA  GG GG
                                  _     GG  C
GAM1710  LOC200742 3'  GGAGTGAGCCATGTGCAA    90287     TG    T   _
                                TTG  TGTG GTTT CTCC
                                |||  |||| |||| ||||
                                AAC  GTAC CGAG GAGG
                                  GT   _    T
GAM1710  LOC200853 5'  GGGAGTATTGAGGAAATGCATG 90332           TC  ___
              CG                  TGTGTGTGTTTC  CAA   TCCT
                                |||||||||||  |||   ||||
                                GCGTACGTAAAG  GTT   AGGG
                                       GA   ATG
GAM1710  LOC200862 5'  AGGGCGGGCCAGGGGGCGCACA 91764         TT  ___  AA
              CG                  TGTGTGTGT  CT   CC  TCCT
                                |||||||||  ||   ||  ||||
                                GCACACGCG  GG   GG  GGGA
                                     GG  ACC  GC
GAM1710  LOC200862 5'  GGGCCAGGGGGCGCACACGGGG 91767    G       TT  CCAA
                                TT TGTGTGTGT  CT    TCC
                                || |||||||||  ||    |||
                                GG GCACACGCG  GG    GGG
                                 G       GG  ACC_
GAM1710  LOC201161 5'  GGGCGGCGGGGGGCGCGCGCA   89507         TT  _  AA
                                TGTGTGTGT  CT CC  TCC
                                |||||||||  || ||  |||
                                ACGCGCGCG  GG GG  GGG
                                     GG  C  C_
GAM1710  LOC201181 5'  GGGGTTGGGGGGGCAGGGCAGCA 89515     G   G_   TT T
              G                  TTGT TGT  TGT  C CCAATCCT
                                |||| |||  |||  | ||||||||
                                GACG ACG  ACG  G GGTTGGGG
                                  _   GG   GG _
GAM1710  LOC201229 3'  GGATGTGGCACATGACAG    89521      G       TCTCCA
                                TTGT TGTGTGTT      ATCC
                                ||||  ||||||||      ||||
                                GACA GTACACGG      TAGG
                                  _       TG____
GAM1710  LOC201626 5'  GGCAGACACGTACGCGCAG    90434           T   _
                                TTGTGTGTGTGT TCT CC
                                |||||||||||| ||| ||
                                GACGCGCATGCA AGA GG
                                       C   C
GAM1710  LOC201626 3'  GGGATTACAGGCGTGCGCCAA  90435     T   TG    CTCC
                                TTG GTG  TGTTT    AATCCT
                                ||| |||  |||||    ||||||
                                AAC CGC  GCGGA    TTAGGG
                                  _  GT    CA__
GAM1710  LOC201685 3'  TGGGGAAATAAACATACAG    91849         G
                                TTGTGTGT TGTTTCTCCA
                                ||||||||  ||||||||||
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                                GACATACA ATAAAGGGGT
                                     A
GAM1710  LOC201696 3'  GGGATTACAGGCATGCGC    63822          CTCC
                                GTGTGTGTTT    AATCCT
                                ||||||||||    ||||||
                                CGCGTACGGA    TTAGGG
                                      CA__
GAM1710  LOC201780 5'  GGGACGGCGAGAGGCACGCGGC 90484     G          CAA_
              G                  TGT TGTGTGTTTCTC    TCCT
                                ||| ||||||||||||    ||||
                                GCG GCGCACGGAGAG    AGGG
                                  _          CGGC
GAM1710  LOC202018 3'  GGGGTGTTTGAGGCGTATGGGT 90611    TG G        TCCA
              GG                   T  T TGTGTGTTTC    ATCCT
                                |  | ||||||||||    |||||
                                G  G GTATGCGGAG    TGGGG
                                 GT G         TTTG
GAM1710  LOC202025 5'  AGTGTGGCAGAGGCACACGTGC 91883     TG         _   ATCCT
              AG                   TTG  TGTGTGTTTCT CCA
                                |||  |||||||||||| |||
                                GAC  GCACACGGAGA GGT
                                  GT          C   GTGA
GAM1710  LOC202025 5'  GGCAGAGGCACACGTGCAG    91889     TG         _
                                TTG  TGTGTGTTTCT CC
                                |||  |||||||||||| ||
                                GAC  GCACACGGAGA GG
                                  GT          C
GAM1710  LOC202047 3'  TTTTGGGGGACCATGTGTGCAG 91893      TG    T      TCCT
                                TTGTG  TGTG TTCTCCAA
                                |||||  |||| ||||||||
                                GACGT  GTAC AGGGGGTT
                                   GT    C       TTA
GAM1710  LOC202050 3'  AGGAAAGGAAGCATGGTATATA 90624       GT_      CCAA
              A                   TTGTGT   GTGTTTCT    TCCT
                                ||||||   ||||||||    ||||
                                AATATA   TACGAAGG    AGGA
                                    TGG       AA__
GAM1710  LOC202052 3'  GGCAGGAGCATGGGCACGA    91900       G        _
                                TTGTGT TGTGTTTCT CC
                                |||||| |||||||| ||
                                AGCACG GTACGAGGA GG
                                    G        C
GAM1710  LOC202126 3'  GGGCGGGGCCACGCACAG    91909         T  TT _
                                TTGTGTGTG GT  C TCC
                                ||||||||| ||  | |||
                                GACACGCAC CG  G GGG
                                      _ GG C
GAM1710  LOC202284 5'  AGGTGGGGGGGACATATCACAG  91930      T     TT     AT
                                TTGTG GTGTGT  CTCCA  CCT
                                ||||| ||||||  |||||  |||
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                                GACAC TATACA  GGGGT  GGA
                                  _     GG    __
GAM1710  LOC202451 5'  GGGATTGGATTCTATACAGCAG 91957     G     TTTC
                                TTGT TGTGTG   TCCAATCCT
                                |||| ||||||   |||||||||
                                GACG ACATAT   AGGTTAGGG
                                  _     CTT_
GAM1710  LOC202460 5'  ATTGGGAACTATGCATGCGA   90667          T   T
                                TTGTGTGTGTG TTC CCAAT
                                |||||||||| ||| |||||
                                AGCGTACGTAT AAG GGTTA
                                       C   _
GAM1710  LOC203052 3'  AGGAAAAGGGACACATACG    92074         TT  CCAA
                                TGTGTGTGT  CT    TCCT
                                |||||||||  ||    ||||
                                GCATACACA  GA    AGGA
                                     GG  AA__
GAM1710  LOC203078 3'  AGGAAAACTAGAATATATATAT 90786           CTCCAA
            A                    TGTGTGTGTGTTT     TCCT
                                ||||||||||||      ||||
                                ATATATATATAAG     AGGA
                                       ATCAAA
GAM1710  LOC203275 3'  TGGAGAAGACATATGTGG    90858    TG      G
                                T  TGTGTGT TTTCTCCA
                                |  ||||||| ||||||||
                                G  GTATACA GAAGAGGT
                                 GT      _
GAM1710  LOC203339 5'  GGAGGATATGACACGCGA    92212         _    T
                                TTGTGTGT GTGTT CTCC
                                |||||||| ||||| ||||
                                AGCGCACA TATAG GAGG
                                     G    _
GAM1710  LOC203339 5'  GGAGGATATGACACGCGA    92213         _    T
                                TTGTGTGT GTGTT CTCC
                                |||||||| ||||| ||||
                                AGCGCACA TATAG GAGG
                                     G    _
GAM1710  LOC203339 5'  GGGGTGATATGACTACATACAT 92216    TG      _   TCTCCA
            GG                    T  TGTGTGT GTT     ATCCT
                                |  ||||||| |||     |||||
                                G  ACATACA CAG     TGGGG
                                 GT      T   TATAG_
GAM1710  LOC203636 3'  GGGAGGCGCTGGAGCGTGTGCG 90978    G   TG     TCCAA_
            GAG                    TT TGTG  TGTTTC     TCCT
                                || ||||  ||||||     ||||
                                GA GCGT  GCGAGG     AGGG
                                 G   GT     TCGCGG
GAM1710  LOC203636 3'  GGGGTGGGGGGGCACACGGGCA 90980     G      TT    AT  T
            G                    TTGT TGTGTGT  CTCCA  CC
                                |||| |||||||  |||||  ||
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                                GACG GCACACG  GGGGT  GG
                                  G      GG    GG
GAM1710  LOC205418 5'  AGGCCTTGGGGGGCATGCACGG 92366    G       TT T   T_
                GG                  TT TGTGTGTGT  C CCAA  CCT
                                || |||||||||  | ||||  |||
                                GG GCACGTACG  G GGTT  GGA
                                 G       GG _   CC
GAM1710  LOC205952 5'  GGGGAAATGCATAAATGG    92399   TG G
                                T  T TGTGTGTTTCTCC
                                |  | ||||||||||||||
                                G  A ATACGTAAAGGGG
                                 GT A
GAM1710  LOC219295 3'  TGGGAGATGCCATACAG     94591        T      T
                                TTGTGTG GTGTTTC CCA
                                ||||||| ||||||| |||
                                GACATAC CGTAGAG GGT
                                    _      _
GAM1710  LOC219529 3'  AGGTGAATTGGGGGTGCATATA 94562         T       ___
                C                    GTGTGTGT TCTCCAAT   CCT
                                |||||||| ||||||||   |||
                                CATATACG GGGGGTTA   GGA
                                     T       AGT
GAM1710  LOC219627 3'  AGGACATGGGGCTATGCATA   93795        TT    A_
                                TGTGTGT  CTCCA  TCCT
                                |||||||  |||||  ||||
                                ATACGTA  GGGGT  AGGA
                                     TC     AC
GAM1710  LOC219688 5'  CTGGGGTTTGCACGGCGAGCGC 94640         _____   TT_   AATCCT
                ACGA                 TTGTGTGT    GTGT   CTCC
                                ||||||||    ||||  ||||
                                AGCACGCG    CACG   GGGG
                                     AGCGG    TTT      TCC
GAM1710  LOC219690 3'  GGGGTTGGGCTGCTGCCACGA  94666      T   T  TTC
                                TTGTG GTG GT   TCCAATCCT
                                ||||| ||| ||   |||||||||
                                AGCAC CGT CG   GGGTTGGGG
                                   _   _  TC_
GAM1710  LOC219927 3'  GGGCTGGACATGCAGACAG    93168      G     TTTC    AT
                                TTGT TGTGTG    TCCA  CC
                                |||| ||||||    ||||  ||
                                GACA ACGTAC    AGGT  GG
                                  G      ____    CG
GAM1710  LOC219942 3'  GGGGTGAGCGGGGCGCGGCGTG 94995    TG   G    TT TCCA
                G                    T  TGT TGTGT  C    ATCCT
                                |  ||| |||||  |    |||||
                                G  GCG GCGCG  G    TGGGG
                                 GT   _     GG CGAG
GAM1710  LOC219972 3'  GGGATTGGGGAGAGGGAACA   93279     GTG_
                                TGT    TTTCTCCAATCCT
                                |||    ||||||||||||
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                                ACA    AGAGGGGTTAGGG
                                  AGGG
GAM1710  LOC220032 3'  GGAGTGACTGTGCATATAA    93332        TG _   T
                                TTGTGTG  T GTT CTCC
                                |||||||  | ||| ||||
                                AATATAC  G CAG GAGG
                                    GT T   T
GAM1710  LOC220073 3'  AGGCCTGGGGGTGCACATCA   95071    T     T     AT
                                TG GTGTGT TCTCCA  CCT
                                || |||||| ||||||  |||
                                AC TACACG GGGGGT  GGA
                                  _     T     CC
GAM1710  LOC220446 5'  GGGGTAGAGAAACCTGCATATA 94404          T      CA
             A                   TTGTGTGTG GTTTCTC  ATCCT
                                |||||||||| |||||||  |||||
                                AATATACGT CAAAGAG  TGGGG
                                      C      A_
GAM1710  LOC220537 3'  AGGAAGAGAAATGCAACGTGT  92419    TG   _       CAA
                                G  TGT GTGTTTCTC   TCCT
                                |  ||| |||||||||   ||||
                                T  GCA CGTAAAGAG   AGGA
                                 GT   A        A__
GAM1710  LOC220565 3'  GGTAGAAGCACTATGTGA    92446    TG    T      _
                                T  TGTG GTGTTTCT CC
                                |  |||| |||||||| ||
                                A  GTAT CACGAAGA GG
                                 GT    _       T
GAM1710  LOC220729 3'  AGGAGTCACGGGGCGCGCACGC 72049           TT TCCAA
                                GTGTGTGTGT  C     TCCT
                                ||||||||||  |     ||||
                                CGCACGCGCG  G     AGGA
                                      GG CACTG
GAM1710  LOC220793 3'  GGAAAAGAAATAAGCACATAG  61010         G      CCAA
                                TTGTGTGT TGTTTCT    TCC
                                |||||||| |||||||    |||
                                GATACACG ATAAAGA    AGG
                                     A      AA__
GAM1710  LOC221061 3'  GGGACATTAAGAAACCGCACGT 94842    TG     T     CCAA_
             GA                   T  TGTGTG GTTTCT     TCCT
                                |  |||||| ||||||     ||||
                                A  GCACGC CAAAGA     AGGG
                                 GT     _     ATTAC
GAM1710  LOC221140 3'  GGAGGGCATGCATGTGG     95146    TG        T
                                T  TGTGTGTGTT CTCC
                                |  |||||||||| ||||
                                G  GTACGTACGG GAGG
                                 GT        _
GAM1710  LOC221154 3'  AGGATAAAACAAATACATATGG 95190    G         CTCCA
             GA                   TT TGTGTGTGTTT     ATCCT
                                || ||||||||||     |||||
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                                AG GTATACATAAA     TAGGA
                                 G          CAAAA
GAM1710  LOC221294 5'  AGGATTGGGATTTCTGTTGCAA 93457       TGTGTGTT  T
                                TTGTG       TC CCAATCCT
                                |||||       || ||||||||
                                AACGT       AG GGTTAGGA
                                   TGTCTTT_  _
GAM1710  LOC221294 5'  GGCAGAGGCATATGGCAA     93458      G         _
                                TTGT TGTGTGTTTCT CC
                                |||| ||||||||||| ||
                                AACG GTATACGGAGA GG
                                   _         C
GAM1710  LOC221303 5'  GGGTCCGGAGGTGCGGGTGCG  93553    TG G   T     A_
                                TG  T TGT TCTCC  ATCC
                                ||  | ||| |||||  ||||
                                GC  G GCG GGAGG  TGGG
                                 GT G   T     CC
GAM1710  LOC221354 3'  GGGAGGCAAGACATGTTTGCAG 94016       T TG     CT  AA
                                TTGTG G  TGTTT  CC  TCCT
                                ||||| |  |||||  ||  ||||
                                GACGT T  ACAGA  GG  AGGG
                                   T GT     AC  __
GAM1710  LOC221362 3'  GGGATGTGCAAGCACATATGGA 95401    G         CTCCA
            G                    TT TGTGTGTGTTT     ATCCT
                                || ||||||||||     |||||
                                GA GTATACACGAA     TAGGG
                                 G          CGTG_
GAM1710  LOC221405 3'  GGGAGGAGATGTGTGTACA    95508      TG  TT     AA
                                TGTG  TG  TCTCC  TCCT
                                ||||  ||  |||||  ||||
                                ACAT  GT  AGAGG  AGGG
                                  GT  GT    __
GAM1710  LOC221543 5'  AGGGGAGGGGTGTACGAACAG  95360      G    TG TT    AAT
                                TTGT TGTG  T  CTCC   CCT
                                |||| ||||  |  ||||   |||
                                GACA GCAT  G  GAGG   GGA
                                  A    GT GG   ___
GAM1710  LOC221683 5'  TTGGGGAGTGTACGCTCAA    95335     T    TG    T
                                TTG GTGTG  TTTC CCAA
                                |||  |||||  |||| ||||
                                AAC CGCAT  GAGG GGTT
                                  T    GT   _
GAM1710  LOC221687 3'  AGGATGAGAATAGTATACATGG 93867    TG     TGT     CA
                                T  TGTGTG   TTCTC  ATCCT
                                |  ||||||   |||||  |||||
                                G  ACATAT   AAGAG  TAGGA
                                 GT     GAT    __
GAM1710  LOC221749 5'  TGGGAGCCCTTGGCGGGGGCAT 93652     TG      TT  _   ____
            GCGTGCGA                TTG  TGTGTGT  CT CCAA    TCCT   G
                                |||  |||||||  || ||||   ||||   |
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                                AGC  GCGTACG  GG GGTT    AGGG   T
                                  GT      GG  C    CCCG
GAM1710  LOC221766 3'  GGCCGGAGACACACGCCGTGG  95421    TG  T     T    AAT
                                T  TG GTGTGT TCTCC   CC
                                |  || |||||| |||||   ||
                                G  GC CGCACA AGAGG   GG
                                 GT  _     C    CC_
GAM1710  LOC221773 5'  AGGACCCCGGGCGCGGGCGCG  92693       G      CTCCAA
                                TGTGT TGTGTTT     TCCT
                                |||||| |||||||      ||||
                                GCGCG GCGCGGG     AGGA
                                   G      CCCC__
GAM1710  LOC221849 3'  AGGGTTTTGGACAAACATAT   94090         C    __
                                GTGTGTTT TCCA  ATCCT
                                |||||||| ||||  |||||
                                TATACAAA AGGT  TGGGA
                                     C    TT
GAM1710  LOC221922 5'  GGGTCGGGAGGCGCATCCGTGG 94260    TG  TG       T  A
                                T  TG  TGTGTTTC CC ATCC
                                |  ||  |||||||| || ||||
                                G  GC  ACGCGGAG GG TGGG
                                 GT  CT       _  C
GAM1710  LOC221931 3'  GGGATGAAATGAGGTGTGTGCT 95634     T TG  TG    TCCA_
            CAG                   TTG G  TG  TTTC     ATCCT
                                ||| |  ||  ||||     |||||
                                GAC C  GT  GGAG     TAGGG
                                  T GT  GT    TAAAG
GAM1710  LOC222134 5'  AGGGTTGGAGAAAAGCCCG    95798    T  G
                                TG GT TTTCTCCAATCCT
                                || || ||||||||||||
                                GC CG AAAGAGGTTGGGA
                                 C  A
GAM1710  LOC222346 3'  GGACACAGGAGATGTATGAACA 94381     G    TT     AA__   T
                                TGT TGTG  TCTCC    TCC
                                ||| ||||  |||||    |||
                                ACA GTAT  AGAGG    AGG
                                  A    GT     ACAC
GAM1710  LOC245726 5'  GGGGCCGGGCCGCGCGTGA    74586    TG     T    __
                                T  TGTGTG GTTT  CTCC
                                |  |||||| ||||  ||||
                                A  GCGCGC CGGG  GGGG
                                 GT      _    CC
GAM1710  LOC245727 5'  GGGGTGGCTGGGGCTACGTGCA 92760     TG    T  TT T_   AT  T
            G                    TTG  TGTG GT  C  CCA  CC
                                |||  |||| ||  |  |||  ||
                                GAC  GCAT CG  G  GGT  GG
                                  GT    _  GG TC   GG
GAM1710  LOC245744 3'  GGAGGGGGCAGCGCGCA     92787         T    AA
                                TGTGTGTT CTCC  TCC
                                |||||||| ||||  |||
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                                ACGCGCGA GGGG  AGG
                                    C   G_
GAM1710  LOC245744 3'  GGGAACGGGGGAGGGGCGATGC 92788   TG    _ G     AA_
              ATGG                   T  TGTGT GT TTTCTCC   TCCT
                                |  ||||| || |||||||   ||||
                                G  ACGTA CG GGAGGGG   AGGG
                                 GT    G G      GCA
GAM1710  LOC253070 3'  GGGCAGGAGTGTGTGCGCGTGG 98788   TG     TG TT   AA
                                T  TGTGTG  T  CTCC  TCC
                                |  ||||||  |  ||||  |||
                                G  GCGCGT  G  GAGG  GGG
                                 GT     GT T_   AC
GAM1710  LOC253128 3'  GGACAGAAGTGCACAACAA   96577     G   TG    CCAA
                                TTGT TGTG  TTTCT    TCC
                                |||| ||||  |||||    |||
                                AACA ACAC  GAAGA    AGG
                                   _   GT    C___
GAM1710  LOC253165 5'  AGGGCCGGGCGTGACGCGCG   98596       TC_   AA
                                TGTGTGTTT   TCC  TCCT
                                ||||||||   |||  ||||
                                GCGCGCAG   GGG  GGGA
                                     TGC   CC
GAM1710  LOC253227 5'  GGTAAGAAGCCACATGCAA    99371        T     __
                                TTGTGTGTG GTTTCT  CC
                                |||||||| ||||||  ||
                                AACGTACAC CGAAGA  GG
                                      _     AT
GAM1710  LOC253289 5'  GGGGCAAGGAGCACGTGGCAG  97765     GTG       CCAA
                                TTGT   TGTGTTTCT    TCC
                                ||||   |||||||||    |||
                                GACG   GCACGAGGA    GGG
                                  GT_       ACG_
GAM1710  LOC253358 5'  GGGGCGAATGCACGCGGGA    98034    G        _
                                TT TGTGTGTGTTT CTCC
                                || ||||||||||| ||||
                                AG GCGCACGTAAG GGGG
                                 G         C
GAM1710  LOC253430 5'  AGGTGGCCGGGCACATGTACG  97972     TG     CT   AT
                                TGTG  TGTGTTT  CCA  CCT
                                ||||  |||||||  |||  |||
                                GCAT  ACACGGG  GGT  GGA
                                  GT      CC   __
GAM1710  LOC253436 3'  GGAAAGAGCGCATGCGTAA    98111           C_
                                TTGTGTGTGTGTTT  TCC
                                ||||||||||||||  |||
                                AATGCGTACGCGAG  AGG
                                        AA
GAM1710  LOC253612 5'  GGGATTACAGGAGCATGCCACA 98554      T        CC
              A                  TTGTG GTGTGTTTCT  AATCCT
                                |||||| ||||||||||  ||||||
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                                AACAC CGTACGAGGA  TTAGGG
                                  _       CA
GAM1710  LOC253634 5'  GGTTGAGGACGCGCGCGTGA  98416   TG       T  C
                                T  TGTGTGTGTT CTC AATC
                                |  |||||||||| ||| ||||
                                A  GCGCGCGCAG GAG TTGG
                                 GT       _  _
GAM1710  LOC253712 5'  GGAGGTTGGGAGGCTATGTGTG 98727   TG  TG  T    T    _
            A                    T  TG  TG GTTTC CCAATC CT
                                |  ||  || ||||| |||||| ||
                                A  GT  AT CGGAG GGTTGG GG
                                 GT  GT  _    _     A
GAM1710  LOC253868 3'  GGGGAGGTGCACGGCAG    97325     G   TG
                                TTGT TGTG  TTTCTCC
                                |||| ||||  |||||||
                                GACG GCAC  GGAGGGG
                                  _   GT
GAM1710  LOC253943 5'  GGGAAGAGGAGCGTGCAAGCG  97846    G  TG      CAA
                                TGT TG  TGTTTCTC   TCCT
                                ||| ||  ||||||||   ||||
                                GCG AC  GCGAGGAG   AGGG
                                  A  GT       A__
GAM1710  LOC254016 3'  AGTGATGGAGACATGCAC    98698       TT    A  _
                                GTGTGTG  TCTCCA TC CT
                                |||||||  |||||| || ||
                                CACGTAC  AGAGGT AG GA
                                    __     _  T
GAM1710  LOC254128 3'  TGGAGGAGCTTGTGTGCG    97361     TG  T
                                TGTG  TG GTTTCTCCA
                                ||||  || |||||||||
                                GCGT  GT CGAGGAGGT
                                  GT  T
GAM1710  LOC254186 5'  GTTGGAAACACAGTGCAA    98002    TG G    TC
                                TTG  T TGTGTT  TCCAAT
                                |||  | ||||||  ||||||
                                AAC  G ACACAA  AGGTTG
                                  GT _     __
GAM1710  LOC254381 5'  GGGTCTGGAGGCACAATGCG   99332      G    TT   _
                                TGTGT TGTGT  CTCCA ATCC
                                ||||| |||||  ||||| ||||
                                GCGTA ACACG  GAGGT TGGG
                                  _    __    C
GAM1710  LOC254707 5'  AGGATGTGGGAGCACCGCACG  99340       T     TC  A
                                TGTGTG GTGTTTC  CA TCCT
                                ||||||| |||||||  || ||||
                                GCACGC CACGAGG  GT AGGA
                                   _      GT  _
GAM1710  LOC254778 3'  GGACAAAGCACTATATATAA   97834        _    C_
                                TTGTGTGT GTGTTT  TCC
                                |||||||| ||||||  |||
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                                AATATATA CACGAA  AGG
                                     T     AC
GAM1710  LOC255017 5'  GGGTTAGAGGTATCACGTGG  96271   TG   T  TT  CC
                                T  TGTG GTG  TCT  AATCC
                                |  |||| |||  |||  |||||
                                G  GCAC TAT  AGA  TTGGG
                                 GT   _  GG  __
GAM1710  LOC255031 5'  GGACACAGGGGACAATACACG  99038        _    AA__
                                TGTGTGTT TCTCC    TCC
                                |||||||| |||||    |||
                                GCACATAA AGGGG    AGG
                                     C    ACAC
GAM1710  LOC255031 5'  GGGAGAGAAGAAGCGCAGGCAC 99039       G       CCAA
            AG                    TTGTGT TGTGTTTCT    TCCT
                                |||||| |||||||||    ||||
                                GACACG ACGCGAAGA    AGGG
                                   G        AGAG
GAM1710  LOC255040 3'  GGGAAGCCGAGTCCGCGCGCG  98127        TTT   CAA_
                                TGTGTGTG   CTC    TCCT
                                ||||||||   |||    ||||
                                GCGCGCGC   GAG    AGGG
                                     CT_   CCGA
GAM1710  LOC255041 3'  GGGAAGCCGAGTCCGCGCGCG  98128        TTT   CAA_
                                TGTGTGTG   CTC    TCCT
                                ||||||||   |||    ||||
                                GCGCGCGC   GAG    AGGG
                                     CT_   CCGA
GAM1710  LOC255045 3'  GATGAAGGAGACATATAT    97959          CCA
                                GTGTGTGTTTCT   ATC
                                ||||||||||||   |||
                                TATATACAGAGG   TAG
                                       AAG
GAM1710  LOC255121 5'  CGGGTGAAGATGGGGAGACAGT 99420      TG G        _____    T
            GCGCG                  TGTG  T TGTTTCTCCA    ATCC    G
                                ||||  | ||||||||||    ||||    |
                                GCGC  G ACAGAGGGGT    TGGG    C
                                  GT _        AGAAG      T
GAM1710  LOC255158 3'  GACTGGGAGACACATTATAA   97881      T       T   A
                                TTGTG GTGTGTTTC CCA TC
                                ||||| ||||||||| ||| ||
                                AATAT TACACAGAG GGT AG
                                   _        _  C
GAM1710  LOC255249 5'  GGGATCGCGAGAGGTGTATATA 99296         TG     CA_
            CAG                   TTGTGTGTG  TTTCTC   ATCCT
                                |||||||||  ||||||   |||||
                                GACATATAT  GGAGAG   TAGGG
                                     GT     CGC
GAM1710  LOC255270 5'  GGGATTGGGGACGTGTGTGC   96244    TG  TG T
                                G  TG  T TCTCCAATCCT
                                |  ||  | ||||||||||
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                                C  GT  G AGGGGTTAGGG
                                 GT  GT C
GAM1710  LOC255285 3'  GGAGAAGACGCGCGGACAG    98015      G        _
                                TTGT TGTGTGTTT CTCC
                                |||| ||||||||| ||||
                                GACA GCGCGCAGA GAGG
                                  G        A
GAM1710  LOC255446 3'  AGGATATGCCGAGTGCACGTAT 98937          TG   CTC  _
           AA                     TTGTGTGTG  TTT   CA ATCCT
                                |||||||||  |||   || |||||
                                AATATGCAC  GAG   GT TAGGA
                                     GT   CC_  A
GAM1710  LOC255455 5'  GGCTGAGGTGCTACACG     97971        T  T    C AT
                                TGTGTG GT TCTC A  CC
                                |||||| || |||| |  ||
                                GCACAT CG GGAG T  GG
                                   _ T    _ CG
GAM1710  LOC255621 3'  AGGCTTGAGAGGCATACAAATG 98885    TG G          C  T
           A                     T  T TGTGTGTTTCTC AA CCT
                                |  | ||||||||||||| || |||
                                A  A ACATACGGAGAG TT GGA
                                 GT A          _  C
GAM1710  LOC255645 3'  AGGGTGGGGGGGCGCGGACGCAG 98473        G     TT T   A
                                TTGTGT TGTGT  C CCA TCCT
                                |||||| |||||  | ||| ||||
                                GACGCA GCGCG  G GGT GGGA
                                   G    GG _  _
GAM1710  LOC255650 3'  GGGAAGGAGGAGCGTGTGTGT  98526    TG  TG       AA
                                G  TG  TGTTTCTCC  TCCT
                                |  ||  |||||||||  ||||
                                T  GT  GCGAGGAGG  AGGG
                                 GT  GT       A_
GAM1710  LOC255652 3'  GGATGGAACACAGGCATGG    98531    TG   G      _
                                T  TGT TGTGTTTC TCC
                                |  ||| ||||||||| |||
                                G  ACG ACACAAGG AGG
                                 GT   G       T
GAM1710  LOC255728 3'  GGAGAATACATGCAGAG      98585     G        T
                                TT TGTGTGTGTT CTCC
                                || ||||||||||| ||||
                                GA ACGTACATAA GAGG
                                  G        _
GAM1710  LOC255728 3'  GGGAAGAGGAGAATACATGCA  98586           T    AA_
                                TGTGTGTGTT CTCC   TCCT
                                |||||||||| ||||   ||||
                                ACGTACATAA GAGG   AGGG
                                      _    AGA
GAM1710  LOC255809 3'  GGGAGAGGGGACACAGGCATGG 98582    TG   G    TT     AA
                                T  TGT TGTG  TCTCC  TCCT
                                |  ||| ||||  |||||  ||||
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                                G  ACG ACAC  AGGGG  AGGG
                                 GT   G   __    AG
GAM1710  LOC255849 3'  AGGCAGATGGAATGTACATGTG 98190   TG    TG   _ CAAT
              A                   T  TGTGTG  TTTC TC   CCT
                                  |  ||||||  |||| ||   |||
                                  A  GTACAT  AAGG AG   GGA
                                   GT     GT   T  AC__
GAM1710  LOC256158 5'  AGGATTGGCCGGTGCAGACGTG 99477   TG   G  TG  TCT
              G                   T  TGT TG  TT   CCAATCCT
                                  |  ||| ||  ||   ||||||||
                                  G  GCA AC  GG   GGTTAGGA
                                   GT   G  GT  CC_
GAM1710  LOC256158 5'  GGACTCCGGGATGTACACATGC 99502          TT   CAA_  T
              GA                    TTGTGTGTGTG  TCTC   TCC
                                  ||||||||||  ||||   |||
                                  AGCGTACACAT  AGGG   AGG
                                        GT   CCTC
GAM1710  LOC256160 5'  GGGACGGCGAGAGGCACGCGGC 97564     G         CAA_
              G                   TGT TGTGTGTTTCTC   TCCT
                                  ||| ||||||||||||   ||||
                                  GCG GCGCACGGAGAG   AGGG
                                    _         CGGC
GAM1710  LOC256283 5'  AGGAGTGGAGAGTGTGCAT   98822      TG  T    A
                                  GTGTG  TT CTCCA TCCT
                                  |||||  || ||||| ||||
                                  TACGT  GA GAGGT AGGA
                                     GT  _    G
GAM1710  LOC256401 3'  AGGAATTAAAGACACACACACA 97717            CTCCAA
              G                   TTGTGTGTGTGTTT     TCCT
                                  ||||||||||||||     ||||
                                  GACACACACACAGA     AGGA
                                          AATTA_
GAM1710  LOC256950 3'  TGCAGAAATACACTACAG    97159      T        C
                                  TTGTG GTGTGTTTCT CA
                                  ||||| |||||||||| ||
                                  GACAT CACATAAAGA GT
                                     _        C
GAM1710  LOC257044 5'  TGTGGGAAATACACGGCAG   97264     G         _
                                  TTGT TGTGTGTTTCTC CA
                                  |||| |||||||||||| ||
                                  GACG GCACATAAAGGG GT
                                    _         T
GAM1710  LOC257062 5'  GGAGAATTTATATACAG     97078         TGT
                                  TTGTGTGTG   TTCTCC
                                  |||||||||   ||||||
                                  GACATATAT   AAGAGG
                                        TT_
GAM1710  LOC257346 5'  GGGATTTTAAAAGGAAGTGCAC 98288   TG G   TG    CC____
              AGATGG                T  T TGTG  TTTCT     AATCCT
                                  |  | ||||  |||||     ||||||
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                                G  A ACAC  GAAGG     TTAGGG
                                 GT G    GT    AAAATT
GAM1710  LOC257357 5'  GGATTCTAACTGCACATGA   97341   TG     T   TCTCC
                                T  TGTGTG GTT    AATCC
                                |  |||||| |||    |||||
                                A  ACACGT CAA    TTAGG
                                 GT     _   TC___
GAM1710  LOC257426 3'  GGGGTTGGGGAGCCACACA   67220       T
                                TGTGTG TTCTCCAATCCT
                                |||||| ||||||||||||
                                ACACAC GAGGGGTTGGGG
                                    C
GAM1710  LOC257428 5'  AGGATGATACTAGAGGCATGTT 95931   TG  T TG      CCA___
              TATGG                  T  TG G  TGTTTCT     ATCCT
                                |  || |  |||||||     |||||
                                G  AT T  ACGGAGA     TAGGA
                                 GT  T GT      TCATAG
GAM1710  LOC257494 3'  GGATCCAGACATACACG     99635          CTCCA
                                TGTGTGTGTTT    ATCC
                                ||||||||||    ||||
                                GCACATACAGA    TAGG
                                      CC___
GAM1710  LOC257596 5'  AGGGGAGGGGTGTACGAACAG  99763     G    TG TT    AAT
                                TTGT TGTG  T  CTCC   CCT
                                |||| ||||  |  ||||   |||
                                GACA GCAT  G  GAGG   GGA
                                  A   GT GG   ___
GAM1710  LOC51055  5'  GGACAAAGCAGCGCACAG    32477        G    C_
                                TTGTGTGT TGTTT  TCC
                                |||||||| |||||  |||
                                GACACGCG ACGAA  AGG
                                     _    AC
GAM1710  LOC51103  5'  TGCGGGAGGTATACGCCAA   63446     T      TT   _
                                TTG GTGTGTG  TCTC CA
                                ||| |||||||  |||| ||
                                AAC CGCATAT  AGGG GT
                                  _      GG   C
GAM1710  LOC51134  5'  GGGTTGCAAGGAGCGTGCGTGC 32793    TG  TG     C_     T
              G                   TG  TG  TGTTTCT  CAATCC
                                ||  ||  |||||||  ||||||
                                GC  GC  GCGAGGA  GTTGGG
                                 GT  GT      AC
GAM1710  LOC51141  3'  GGGGTGTGAGTATGTGTGCACA 69147       TG   TT   CA
                                TGTGTG  TGT  CTC  ATCCT
                                ||||||  |||  |||  |||||
                                ACACGT  GTA  GAG  TGGGG
                                    GT   T_   TG
GAM1710  LOC51141  3'  GGGTGGATGAATACATA     69148         C    AT
                                TGTGTGTTT TCCA  CC
                                |||||||| ||||  ||
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                                ATACATAAG AGGT  GG
                                     T    GG
GAM1710  LOC51161  3'  AGGAATTCAGGATGCATACA   33038       T   CC  _
                                TGTGTGT TCT  AAT CCT
                                ||||||| |||  ||| |||
                                ACATACG AGG  TTA GGA
                                    T   AC   A
GAM1710  LOC51161  3'  GGGAAGAGGGAAGCACGCACA  33042           CAA
                                TGTGTGTGTTTCTC   TCCT
                                ||||||||||||||   ||||
                                ACACGCACGAAGGG   AGGG
                                         AGA
GAM1710  LOC51161  3'  GGGATGCAGGGGTAGTGTATGC 33043       TG  T    A__
           A                     TGTGTG  TT CTCC   ATCCT
                                ||||||  || ||||   |||||
                                ACGTAT  GA GGGG   TAGGG
                                   GT  T    ACG
GAM1710  LOC51213  3'  AGAATGGAGGTAATACATACAT 33505           _     A  CT
           AG                     TTGTGTGTGTGTT TCTCCA TC
                                ||||||||||||| |||||| ||
                                GATACATACATAA GGAGGT AG
                                       T     A  A
GAM1710  LOC51236  3'  GGCAGAGGTGGGCGCATAG    33624        G  TT  _
                                TTGTGTGT TG  TCT CC
                                |||||||| ||  ||| ||
                                GATACGCG GT  AGA GG
                                     G  GG   C
GAM1710  LOC51334  5'  GGACGGGGGCACGCAGCAG    34060     G      TT  CCAA
                                TTGT TGTGTGT  CT    TCC
                                |||| |||||||  ||    |||
                                GACG ACGCACG  GG    AGG
                                  _      GG  C___
GAM1710  LOC51339  3'  GAGGGGCACCACATACAA     34094         _  TT
                                TTGTGTGTG TGT  CTC
                                |||||||| |||  |||
                                AACATACAC ACG  GAG
                                     C   GG
GAM1710  LOC51604  3'  AGGTGATGGGGTGTGCTACACA 32511        T TG TT    AT_
           G                     TTGTGTG G  T  CTCCA   CCT
                                ||||||| |  |  |||||   |||
                                GACACAT C  G  GGGGT   GGA
                                   _ GT T_     AGT
GAM1710  LOC51652  3'  AGGTTCAGGGGGTACATGTGCA 32699    TG    T    AAT_
                                TG  TGTGT TCTCC    CCT
                                ||  ||||| |||||    |||
                                AC  GTACA GGGGG    GGA
                                 GT    T    ACTT
GAM1710  LOC51762  3'  TGGAGACACATGCAGGA     33710    G      TT
                                TT TGTGTGTG  TCTCCA
                                || ||||||||  ||||||
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                                AG ACGTACAC  AGAGGT
                                 G       __
GAM1710  LOC55901  3'  GGAGGAAGTAACACACAG    38544         GTG
                                TTGTGTGT   TTTCTCC
                                ||||||||   |||||||
                                GACACACA   AAGGAGG
                                    ATG
GAM1710  LOC56270  3'  GGAGTGAACAAGTGTGCAG   39508       TG G    _
                                TTGTG  T TGTTT CTCC
                                |||||  | ||||| ||||
                                GACGT  G ACAAG GAGG
                                   GT A    T
GAM1710  LOC56920  3'  AGGGTGATGCAAGCATGCCGCA 39794       T       CTCCA
            G                    TTGTG GTGTGTTT     ATCCT
                                |||||| ||||||||     |||||
                                GACGC CGTACGAA     TGGGA
                                  _       CGTAG
GAM1710  LOC56959  5'  GGTCAGAGACACACGGCAA   82812      G         __
                                TTGT TGTGTGTTTCT  CC
                                |||| ||||||||||  ||
                                AACG GCACACAGAGA  GG
                                  _         CT
GAM1710  LOC58525  3'  GGGGCCGGGCACACTACAG   79350       T       __
                                TTGTG GTGTGTTT  CTCC
                                ||||| ||||||||  ||||
                                GACAT CACACGGG  GGGG
                                  _       CC
GAM1710  LOC63904  3'  GGGGTTGGAGTTTTGAACGTA  42211       GTGTTT
                                TGTGT     CTCCAATCCT
                                |||||     ||||||||||
                                ATGCA     GAGGTTGGGG
                                   AGTTTT
GAM1710  LOC84524  3'  GGAATAGGAGAGGAGCATATAT 51657    TG      G      AA_   T
            GG                    T  TGTGTGT TTTCTCC   TCC
                                |  ||||||| |||||||   |||
                                G  ATATACG GGAGAGG   AGG
                                 GT      A      ATA
GAM1710  LOC85479  5'  GGAGAAACAATGCATGG     53569    TG     G
                                T  TGTGT TGTTTCTCC
                                |  ||||| |||||||||
                                G  ACGTA ACAAAGAGG
                                 GT    _
GAM1710  LOC89932  5'  GGAAGGAGCACCCACACG     61468       T       _
                                TGTGTG GTGTTTCT CC
                                |||||| |||||||| ||
                                GCACAC CACGAGGA GG
                                   C       A
GAM1710  LOC89941  3'  GGGGCCGGGGAGCACAGGTGT  57852    TG G        CAA   T
                                G  T TGTGTTTCTC   TCC
                                |  | ||||||||||   |||
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                                T  G ACACGAGGGG   GGG
                                 GT G        CCG
GAM1710  LOC90141  3'  GGGGCAAGAGACATGTTTGCAG 62307      T TG      CCAA
                                TTGTG G  TGTTTCT    TCC
                                |||||| |  |||||||    |||
                                GACGT T  ACAGAGA    GGG
                                   T GT      ACG_
GAM1710  LOC90190  3'  GGGGTTGGAGAAGAACCAT    62429     T  G
                                GTG GT TTTCTCCAATCCT
                                ||| || ||||||||||||
                                TAC CA GAAGAGGTTGGGG
                                  _  A
GAM1710  LOC90246  5'  GGTTCAGGAGAAATATGCGTGT 62588    TG          AAT_  T
                                G  TGTGTGTTTCTCC    CC
                                |  ||||||||||||    ||
                                T  GCGTATAAAGAGG    GG
                                 GT           ACTT
GAM1710  LOC90342  5'  GGGGTGGTCTGGAGTGCGCTGC 63016      T   TG    T__   AT  T
            AG                    TTGTG GTG  TTTC   CCA  CC
                                ||||| |||  ||||   |||  ||
                                GACGT CGC  GAGG   GGT  GG
                                   _  GT    TCT   GG
GAM1710  LOC90639  3'  GGGATGGGAAGGAGCATACG   64414          _  A
                                TGTGTGTTTCT CC ATCCT
                                |||||||||| || |||||
                                GCATACGAGGA GG TAGGG
                                       A  G
GAM1710  LOC90750  5'  AGGGCATGAAGCACCGTGTGCA 64625      TG  _     TCCAA
            G                     TTGTG  TG TGTTTC     TCCT
                                |||||  || ||||||     ||||
                                GACGT  GC ACGAAG     GGGA
                                   GT  C     TAC__
GAM1710  LOC90777  3'  GGTGGTTGGGAAGTGTATATAT 64668        TG    T     _
            A                     TGTGTGTG  TTTC CCAATC CT
                                ||||||||  |||| |||||| ||
                                ATATATAT  GAAG GGTTGG GG
                                     GT   _     T  A
GAM1710  LOC90841  3'  AGGCCTGGAGCACAACATGTGG 64862   TG    _  TTT    AT
                                T  TGTGT GTG   CTCCA  CCT
                                |  ||||| |||   |||||  |||
                                G  GTACA CAC   GAGGT  GGA
                                 GT    A  ___     CC
GAM1710  LOC90841  3'  GGGCACGTTAGGAACATGCGC  64871          CCAAT_
                                GTGTGTGTTTCT     CCT
                                ||||||||||||     |||
                                CGCGTACAAGGA     GGG
                                       TTGCAC
GAM1710  LOC90850  5'  GGGGCGCCGAGGGGCGGCGCGC 64882        G   TT   CAA_
            G                     TGTGTGT TGT  CTC    TCCT
                                |||||||  |||  |||    ||||
```

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                                GCGCGCG GCG  GAG    GGGG
                                   _  GG   CCGC
GAM1710  LOC90906  5'  GGATGAACACATCACAG     64954       T       C
                                TTGTG GTGTGTTT TCC
                                ||||| |||||||| |||
                                GACAC TACACAAG AGG
                                   _       T
GAM1710  LOC90906  5'  GGCTAGAGGAACATGCAC     64955            CAAT
                                GTGTGTGTTTCTC    CC
                                ||||||||||||    ||
                                CACGTACAAGGAG    GG
                                        ATC_
GAM1710  LOC91040  5'  AGGGCATCAGACACAGGTACAG 65333       TG      CTCCAA
                                TTGTG  TGTGTTT     TCCT
                                |||||  |||||||     ||||
                                GACAT  ACACAGA     GGGA
                                   GG      CTAC__
GAM1710  LOC91069  3'  AGGTCTGGGGGAGTGCACATCA 65396     T     TG       AT
            A                    TTG GTGTG  TTTCTCCA  CCT
                                ||| |||||  ||||||||  |||
                                AAC TACAC  GAGGGGGT  GGA
                                  _    GT       CT
GAM1710  LOC91170  5'  GGAGGAGCCACATACGA     65734          T
                                TTGTGTGTG GTTTCTCC
                                |||||||| ||||||||
                                AGCATACAC CGAGGAGG
                                         _
GAM1710  LOC91252  3'  GGGACTCCTGGAGCAGGCACAT 65939         G      TCCAA
            AG                    TTGTGTGT TGTTTC     TCCT
                                |||||||| ||||||     ||||
                                GATACACG ACGAGG     AGGG
                                     G     TCCTC
GAM1710  LOC91301  5'  GGGGTTGGAGAGGGGAGCCAT  66150     T  GTG
                                GTG GT   TTTCTCCAATCCT
                                ||| ||   ||||||||||||
                                TAC CG   GGAGAGGTTGGGG
                                  _ AGG
GAM1710  LOC91355  5'  GTTGGAAGTGCATGGACAG    66310      G    TG  TC
                                TTGT TGTG  TT  TCCAAT
                                |||| ||||  ||  ||||||
                                GACA GTAC  GA  AGGTTG
                                   G    GT  __
GAM1710  LOC91445  3'  AGGAAAGGGGAAACCCACATGT 61162    TG     T       AA
            GA                    T  TGTGTG GTTTCTCC  TCCT
                                |  |||||| ||||||||  ||||
                                A  GTACAC CAAAGGGG  AGGA
                                 GT     C       AA
GAM1710  LOC91517  3'  GGGGTTCCATGAGAGGTGTGTG 66914      G GT TG     C___
            ACAG                    TTGT T  G  TTTCTC    AATCCT
                                |||| |  |  ||||||    ||||||
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                              GACA G  T  GGAGAG    TTGGGG
                                _ TG GT     TACC
GAM1710  LOC91548  5'  GAGAAATGACACGTATGA    67009    TG      _
                              T  TGTGTGT GTTTCTC
                              |  ||||||| |||||||
                              A  ATGCACA TAAAGAG
                               GT      G
GAM1710  LOC91582  3'  GGAGGATTTACACACAG     67143          TGT
                              TTGTGTGTG   TTCTCC
                              |||||||||   ||||||
                              GACACACAT   AGGAGG
                                    TT_
GAM1710  LOC91650  3'  AGGAACTTAAACATATTTACAA 67393       T       CTCCAA
                              TTGTG GTGTGTTT     TCCT
                              ||||| ||||||||     ||||
                              AACAT TATACAAA     AGGA
                                 T       TTCA__
GAM1710  LOC91694  3'  GGGGTTGGGTAGTGTGTGTGTA 67506    TG GT TG  T T
                              TG  T  G  TT C CCAATCCT
                              ||  |  |  || | ||||||||
                              AT  G  T  GA G GGTTGGGG
                               GT TG GT  T _
GAM1710  LOC91796  5'  TAGGATTTCAAAAGGGGAGGGC 67787   TG  TG   G     _______
            GTGTATGA               T  TG  TGT TTTCTCC     AATCCT   A
                              |  ||  ||| |||||||     ||||||  |
                              A  AT  GCG GGAGGGG     TTAGGA   T
                               GT  GT   _      AAAACT
GAM1710  LOC91907  3'  AGGCAATAGAAATATGTATAT  68100       TG      CCAAT
                              GTGTG  TGTTTCT     CCT
                              |||||  |||||||     |||
                              TATAT  ATAAAGA     GGA
                                 GT      TAAC_
GAM1710  LOC91923  3'  GGGATAGCATTAGGAGATATAC 68175            CCA____
            GTA                  TGTGTGTGTTTCT      ATCCT
                              ||||||||||||||      |||||
                              ATGCATATAGAGG      TAGGG
                                      ATTACGA
GAM1710  LOC91963  5'  GGGGTGATCGAGGGCGCGCGCA 68322           T   CA__
            T                   GTGTGTGTGTT CTC    ATCCT
                              ||||||||||| |||    |||||
                              TACGCGCGCGG GAG    TGGGG
                                     _   CTAG
GAM1710  LOC92148  5'  GGTGAGATAAGCATGCAG     68886        G     T
                              TTGTGTGT TGTTTC CC
                              |||||||| |||||| ||
                              GACGTACG ATAGAG GG
                                   A     T
GAM1710  LOC92230  5'  CTGGGAGGCAGGCAGGCATGCA 69085        G   __     AATCCT
                              TGTGTGT TGTT  TCTCC
                              ||||||| ||||  |||||
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                                ACGTACG ACGG  GGAGG
                                   G   AC    G  TCC
GAM1710 LOC92497 5' GGGGCAGGAGGCGTGCACGA  70097     TG  GTTT   AA
                                TTGTG  TGT   CTCC  TCCT
                                |||||  |||   ||||  ||||
                                AGCAC  GCG   GAGG  GGGG
                                  GT  ____   AC
GAM1710 LOC92539 3' GGAAGGAATACACAGCAA    70222     G       _
                                TTGT TGTGTGTTTCT CC
                                |||| |||||||||| ||
                                AACG ACACATAAGGA GG
                                  _        A
GAM1710 LOC92719 3' GGGAAGGGGGGGTATATGTGTA  70904   TG    T    AA
                                TG  TGTGT TCTCC  TCCT
                                ||  ||||| |||||  ||||
                                AT  GTATA GGGGG  AGGG
                                 GT    T    GA
GAM1710 LOC93109 3' GGGGCCTTGGGTCACACACA  71922       TTTC   __
                                TGTGTGTG   TCCAA  TCCT
                                ||||||||   |||||  ||||
                                ACACACAC   GGGTT  GGGG
                                     T___    CC
GAM1710 LOC93190 3' AGGGTTGGACAAGCTTGTGCG  72097   TG  T   C
                                TG  TG GTTT TCCAATCCT
                                ||  || |||| |||||||||
                                GC  GT CGAA AGGTTGGGA
                                 GT  T   C
GAM1710 LOC93206 3' GGGAAGATATAATATGCAG   72192       _    CT
                                TTGTGTGT GTGTTT  CC
                                ||||||||| ||||||  ||
                                GACGTATA TATAGA  GG
                                     A     AG
GAM1710 LOC93268 3' AGGTGGTAGGAACATGTGGACA 72377     G  TG     _  AT
            A                    TTGT TG  TGTTTCT CCA  CCT
                                ||||  ||  |||||||  |||  |||
                                AACA GT  ACAAGGA GGT  GGA
                                  G  GT      T  __
GAM1710 LOC93349 3' GCACTTGGGAAATAGCACATGC 57269        _    T   TCCT
            AG                    TTGTGTGTG TGTTTC CCAA
                                |||||||||  |||||| ||||
                                GACGTACAC ATAAAG GGTT
                                     G     _   CACGA
GAM1710 LOC93349 3' GGGATTGGAATGCAATGGCGCG 57271      GTG   TTC
            A                    TTGTGT   TGT   TCCAATCCT
                                ||||||   |||   |||||||||
                                AGCGCG   ACG   AGGTTAGGG
                                   GTA   TA_
GAM1710 LOC93432 5' GGAGAGATACAGCATAG     72809      G
                                TTGTGT TGTGTTTCTCC
                                ||||||  ||||||||||
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                                GATACG ACATAGAGAGG
                                   _
GAM1710 LOC93622 3' GGTGGAAGCATTGTGCACAG  57730      GT_     _
                                TTGTGT  GTGTTTCT CC
                                ||||||  |||||||| ||
                                GACACG  TACGAAGG GG
                                   TGT      T
GAM1710 LOC94431 5' GGGATTTCAAATATGCGTGCA 69152   TG      CTCC
                                TG TGTGTGTTT   AATCCT
                                || |||||||||  ||||||
                                AC GCGTATAAA   TTAGGG
                                 GT      CT__
GAM1710 LOC95244 5' GGGATCGCGAGAGGTGTATATA 61069       TG    CA_
            CAG                   TTGTGTGTG TTTCTC  ATCCT
                                |||||||||| ||||||  |||||
                                GACATATAT GGAGAG  TAGGG
                                     GT    CGC
GAM1710 LOC96573 3' GGTTGGAAGCATATGTGGGG  63873   G TG    TC
                                TT TG TGTGTT TCCAATC
                                || || |||||| |||||||
                                GG GT ATACGA AGGTTGG
                                 G GT    __
GAM1710 LOC96652 3' GGGGTGGGGGAATGTGTAC   66081    TG      AT
                                GTG TGTTTCTCCA CC
                                ||| |||||||||| ||
                                CAT GTAAGGGGGT GG
                                  GT       GG
GAM1711 CXorf6   3' CATATTTGAAAATTTTGTAAAT 19703    __   _
            GG                    CCGT ACGGA TTTTCAAATATG
                                |||| ||||| ||||||||||||
                                GGTA TGTTT AAAAGTTTATAC
                                  AA   T
GAM1711 RAB5B    3' CATATTTGAAAACATTGCGG  12707     CGGA
                                CCGTA   TTTTCAAATATG
                                |||||   ||||||||||||
                                GGCGT   AAAAGTTTATAC
                                   TAC_
GAM1712 NCAM2    3' AATACTTCAAATCATATCCTCA 16999       C_   TCG
                                TGAGGATATG TTGG  GGTATT
                                |||||||||| ||||  ||||||
                                ACTCCTATAC AACT  TCATAA
                                     TA   ___
GAM1712 MPZL1    3' AATACCTAGAACATATCCTCA 15536       C GGTC
                                TGAGGATATG TT   GGGTATT
                                |||||||||| ||   |||||||
                                ACTCCTATAC AG   TCCATAA
                                     A A___
GAM1713 ABCB4    5' CTTTGGACTTAGCAAAGCA   38758   G   G  A AAA
                                TG TTTG TAA G  TCCAAAG
                                || |||| ||| |  |||||||
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                                AC AAAC ATT C   AGGTTTC
                                 G   G  _ ____
GAM1713 B4GALT5  3' TCTTTGTTTTTCCCCAAACCA 17693       TAAA   TC
                                TGGTTTGG   GAAA  CAAAGA
                                ||||||||   ||||  ||||||
                                ACCAAACC   CTTT  GTTTCT
                                    C___   TT
GAM1713 CAMK4    3' CTTTGGATTTCTTCACAAGGCA 9988    G   GTA
                                TG TTTG   AAGAAATCCAAAG
                                || ||||   ||||||||||||
                                AC GAAC   TTCTTTAGGTTTC
                                 G   AC_
GAM1713 DSC1     5' CTCCGGACTGTCTTCCAAACCA 44604       TA   AA_  AA
                                TGGTTTGG  AAGA   TCC  AG
                                ||||||||  ||||   |||  ||
                                ACCAAACC  TTCT   AGG  TC
                                    __    GTC   CC
GAM1713 IGF1     5' TCTCTGGATTTCCTTTTGCT   7084       __      A
                                GGTAAA  GAAATCCA AGA
                                ||||||  |||||||| |||
                                TCGTTT  CTTTAGGT TCT
                                   TC       C
GAM1713 KNSL1    3' CTTTTTATTTTTCACCAAACCA 16945       AA     CC
                                TGGTTTGGT  AGAAAT  AAAG
                                |||||||||  ||||||  ||||
                                ACCAAACCA  TTTTTA  TTTC
                                    C_     TT
GAM1713 PDGFRA   3' TCTTTGGACTTCTGAAGAGACC 21696      GGTAA   A
            A                    TGGTTT    AGAA TCCAAAGA
                                ||||||    |||| ||||||||
                                ACCAGA    TCTT AGGTTTCT
                                   GAAG_   C
GAM1713 CHI3L2   3' CTTTGGATCTCTCTTCCAA   15673     TAA  A
                                TTGG   AGA ATCCAAAG
                                ||||   ||| ||||||||
                                AACC   TCT TAGGTTTC
                                  TTC   C
GAM1713 CNK1     3' TCCTTGGCAGTTCTCCCCCAAA 21969       TAA   AT_   A
            CCA                   TGGTTTGG   AGAA   CCAA GA
                                ||||||||   ||||   |||| ||
                                ACCAAACC   TCTT   GGTT CT
                                    CCC    GAC    C
GAM1713 DKFZP566J2046 3'  TCTTCGGAAAACATTTTATCAA 49140           AAA__  A
            ACCA                  TGGTTTGGTAAAG    TCC AAGA
                                ||||||||||||||    ||| ||||
                                ACCAAACTATTTT    AGG TTCT
                                       ACAAA   C
GAM1713 FLJ21438  5' TCTTTGGGGTGCCAACAAACCA 62201       GTAAAGAAA
                                TGGTTTG       TCCAAAGA
                                |||||||       ||||||||
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                                ACCAAAC       GGGTTTCT
                                   AACCGTG__
GAM1713 HTCD37   3' TCTTTGGATCCCTCTGTCCCA 68302    TT  TAA  AA
                                TGG  TGG   AG  ATCCAAAGA
                                |||  |||   ||  |||||||||
                                ACC  GTC   TC  TAGGTTTCT
                                  CT   ___  CC
GAM1713 KIAA0481 3' TTGGACTTCTTTGTGTGTCCA 72327    TTTGG     A
                                TGG    TAAAGAA TCCAA
                                |||    ||||||| |||||
                                ACC    GTTTCTT AGGTT
                                  TGTGT      C
GAM1713 KIAA1163 3' TCTTTGGACTCCTCAGAAACC 79655     GGTAAA  AA
                                GGTTT     GA  TCCAAAGA
                                |||||     ||  ||||||||
                                CCAAA     CT  AGGTTTCT
                                   GACTC_  C_
GAM1713 KIAA1719 3' TCTCTGGACCTCTGCTAAGC   68737      AA   AA   A
                                GTTTGGT  AGA  TCCA AGA
                                |||||||  |||  |||| |||
                                CGAATCG  TCT  AGGT TCT
                                   __  CC   C
GAM1713 MIG2     3' CTTTGCCTTACCAGACCA    72859         AGAAATC
                                TGGTTTGGTAA      CAAAG
                                ||||||||||       |||||
                                ACCAGACCATT      GTTTC
                                      CC_____
GAM1713 RNP24    3' TCTTTGGATTCCTTCAGTCTA  23329     T   TAA  A
                                TGG TTGG   AG AATCCAAAGA
                                ||| ||||   || ||||||||||
                                ATC GACT   TC TTAGGTTTCT
                                  T    ___  C
GAM1713 SDC3     3'  TCTCTGGATTTCTTCTCCCAAC 28483     T  TA        A
                                GTT GG  AAGAAATCCA AGA
                                ||| ||  ||||||||||| |||
                                CAA CC  TTCTTTAGGT TCT
                                  C  TC         C
GAM1713 TBPL1    3'  CTTTGGATTTTATTCCAAACC  18010       T  A
                                GGTTTGG AA GAAATCCAAAG
                                ||||||| || ||||||||||
                                CCAAACC TT TTTTAGGTTTC
                                   _  A
GAM1713 LOC115207 3'  TCTTTGGACCTCCTGAACCG   57400      TG TAAA  AA
                                TGGTT  G    GA  TCCAAAGA
                                |||||  |    ||  ||||||||
                                GCCAA  C    CT  AGGTTTCT
                                   GT _____  CC
GAM1713 LOC122704 3'  TCTCTGGATTTCTTTTCTATCA 74612     T_  T        A
             CC                    GGT  TGG AAAGAAATCCA AGA
                                |||  ||| ||||||||||| |||
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                                CCA  ATC TTTCTTTAGGT TCT
                                  CT   T         C
GAM1713  LOC122886 3'  TCCTTGGACCTCTTACCAAACC 76107          A  AA     A
             A                    TGGTTTGGTAA GA  TCCAA GA
                                  |||||||||||  ||  |||||  ||
                                  ACCAAACCATT CT  AGGTT CT
                                        _  CC    C
GAM1713  LOC256248 5'  TCTTTGGATGTGGTTCACCAAC 98030       T  _  AGAA
             CA                    TGGTT GGT AA    ATCCAAAGA
                                   |||||  |||  ||    |||||||||
                                   ACCAA CCA TT    TAGGTTTCT
                                     _  C  GGTG
GAM1713  LOC256790 5'  CTTCTGGGCTTTACCAGACCA  96492           AAA   _
                                   TGGTTTGGTAAAG   TCCA AAG
                                   ||||||||||||||   |||||  |||
                                   ACCAGACCATTTC   GGGT TTC
                                          ___    C
GAM1713  LOC256880 5'  TGGAGAGTCCCTACCAAGCCA  98890          AA  AA_
                                   TGGTTTGGTA  GA   TCCA
                                   ||||||||||  ||   ||||
                                   ACCGAACCAT  CT   AGGT
                                         CC  GAG
GAM1713  LOC51301  5'  TCTCTAGACCTCTGCCCAAACC 33910         TAA   AA  CAA
             A                    TGGTTTGG   AGA  TC   AGA
                                  ||||||||   |||  ||   |||
                                  ACCAAACC   TCT  AG   TCT
                                       CG_   CC  ATC
GAM1713  LOC92935  3'  TCTTTGTGCCTCCTTCCAAACC 71518         T  A  AATC
             A                    TGGTTTGG AA GA    CAAAGA
                                  ||||||||  ||  ||    ||||||
                                  ACCAAACC TT CT    GTTTCT
                                       _  C  CCGT
GAM1714  HHIP      3'  AATTTTCTGTCTGTAATCACTA 42750       A  C     TGA
                                  TAGT GA TACAG   GGAAAATT
                                  ||||  ||  |||||   ||||||||
                                  ATCA CT ATGTC   TCTTTTAA
                                    _  A    TG_
GAM1714  FLJ23510  3'  ATTTTCCCCATGCTACTA    45623        ACTACA   A
                                  TAGTAG     GTG GGAAAAT
                                  ||||||     |||  |||||||
                                  ATCATC     TAC CCTTTTA
                                     G_____   C
GAM1714  KIAA1915  3'  TTTTTTTCTACTGCCTACTA   73674        ACTA   _
                                  TAGTAG    CAGT GAGGAAAA
                                  ||||||    ||||  ||||||||
                                  ATCATC    GTCA CTTTTTTT
                                     C___    T
GAM1714  MGC10940  3'  TCTGCTGTGTCTACTA      51185         T    GA
                                  TAGTAGAC ACAGT  GGA
                                  ||||||||  |||||  |||
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                                ATCATCTG TGTCG  TCT
                                   _    __
GAM1714  PRO1430   3'  TTTTGGCTATAGTCTATTA   38359         C   G
                                TAGTAGACTA AGT AGGA
                                |||||||||| ||| ||||
                                ATTATCTGAT TCG TTTT
                                     A   G
GAM1714  LOC145231 5'  TTTCTTCACAGTCTCCTA    84263     T    ACA
                                TAG AGACT   GTGAGGAAA
                                ||| |||||   |||||||||
                                ATC TCTGA   CACTTCTTT
                                  C    ___
GAM1714  LOC149134 5'  ATTTTCTTGGTGTCTAC     85515       T  AGTGA
                                GTAGAC AC    GGAAAAT
                                |||||| ||    |||||||
                                CATCTG TG    TCTTTTA
                                   _ GT___
GAM1715  LHX2      5'  CACCCCACCAGGCAACCCCTGA 17734     A   C  G  TT   AA
                                TCA GGGT GT TG  GTG  GTG
                                ||| |||| || ||  |||  |||
                                AGT CCCA CG AC  CAC  CAC
                                  C   A  G __  CC
GAM1715  NCOA6     5'  CATAACACAGACCCCTGA    26830     A    G
                                TCA GGGTC TGTGTTGTG
                                ||| ||||| |||||||||
                                AGT CCCAG ACACAATAC
                                  C   _
GAM1715  P4HB      3'  CAGAACCACGACCCTTGA    8086           T   G
                                TCAAGGGTCGTG GTT TG
                                |||||||||||| ||| ||
                                AGTTCCCAGCAC CAA AC
                                      _  G
GAM1715  SLC21A3   3'  ACCCCACAACAGGCCCT     18652       GTG      AA
                                AGGGTC   TGTTGTG  GT
                                ||||||   |||||||  ||
                                TCCCGG   ACAACAC  CA
                                   ___      CC
GAM1715  ATP10B    3'  CACTGGTCCACATAACCCTTGA 64104         CG    TTGTGA
                                TCAAGGGT  TGTG     AGTG
                                ||||||||  ||||     ||||
                                AGTTCCCA  ACAC     TCAC
                                    AT    CTGG__
GAM1715  KIAA0750  5'  CACTGCCGCACACGACTCCTGA 28304     A         T  GA
                                TCA GGGTCGTGTGT GT  AGTG
                                ||| |||||||||| ||  ||||
                                AGT CTCAGCACACG CG  TCAC
                                  C         C __
GAM1715  KIAA1485  3'  CACCCCAGCATAGACACACACC 90763     A   TC     _    AA___
             CCCTGA                 TCA GGG  GTGTGT TGTG    GTG
                                ||| |||  |||||| ||||    |||
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                                AGT CCC  CACACA ATAC    CAC
                                  C  CA    G   GACCC
GAM1715  LOC145608 5'  CACCCCAAATTACTGACCCTTG 84374         T  TTG  AA
              A                   TCAAGGGTCG GTG  TG  GTG
                                  |||||||||| |||  ||  |||
                                  AGTTCCCAGT CAT  AC  CAC
                                        _  TAA  CC
GAM1716  HADHB    3'  CTGAGCTTTTCAATAATCAGTT 5739          C    T
              T                   AAGCTGATTA TGAAGA GTTCAG
                                  |||||||||| |||||| ||||||
                                  TTTGACTAAT ACTTTT CGAGTC
                                        A    _
GAM1716  LAPTM5   3'  TGTCATTCAACAATTAGCT   23140        AC   _
                                  AGCTGATT  TGAA GATG
                                  ||||||||  |||| ||||
                                  TCGATTAA  ACTT CTGT
                                       CA   A
GAM1716  OAS3     3'  CTGAACATCCCTTCTCTGCT  21651     T  TTACT  __
                                  AGC GA    GAA  GATGTTCAG
                                  ||| ||    |||  |||||||||
                                  TCG CT    CTT  CTACAAGTC
                                    T _____  CC
GAM1716  KIAA0630  5'  TGAGCTTCAGCAATCAGCT   90952        A    GAT
                                  AGCTGATT CTGAA   GTTCA
                                  |||||||| |||||  |||||
                                  TCGACTAA GACTT   CGAGT
                                       C   ___
GAM1716  KIAA1076  3'  CTGTTTAACTCCAGCATCAGCT 66122        TA   A  A  TT
              T                   AAGCTGAT  CTG AG TG  CAG
                                  ||||||||  ||| || ||  |||
                                  TTCGACTA  GAC TC AT  GTC
                                       C_   C  A  TT
GAM1716  MGC5306   3'  ACGTTGCTAGCAATCAGCTT   44371        A   AA
                                  AAGCTGATT CTG  GATGT
                                  ||||||||| |||  |||||
                                  TTCGACTAA GAT  TTGCA
                                       C   CG
GAM1716  PIF1     3'  CTGAACATCCCTCCTTTCAGGC 61676     _  TTACT  A_
              T                   AGC TGA    GA  GATGTTCAG
                                  ||| |||    ||  |||||||||
                                  TCG ACT    CT  CTACAAGTC
                                    G  TTC__  CC
GAM1716  LOC158038 3'  CTGGGGATCTCAGTAAT     82575        A   G
                                  ATTACTGA GAT TTCAG
                                  |||||||| ||| |||||
                                  TAATGACT CTA GGGTC
                                       _  G
GAM1716  LOC197287 3'  CTGATAATTCATTAATCAGCTT 61545         C   GATGT
                                  AAGCTGATTA TGAA    TCAG
                                  |||||||||| ||||    ||||
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                                TTCGACTAAT ACTT    AGTC
                                     T   AAT__
GAM1716 LOC253482 5' CTGAACATCTCCTTCCCAGC  97869     ATTACT  A
                                GCTG     GA GATGTTCAG
                                ||||     || |||||||||
                                CGAC     CT CTACAAGTC
                                  CCTTC_  _
GAM1717 CBFA2T1   3' CATTCTGGCAGTTTTGACA   16360         A  __
                                TGTCAAGACT CC  GATG
                                |||||||||| ||  ||||
                                ACAGTTTTGA GG  TTAC
                                     C  TC
GAM1717 STAT1    5' TAACCTCGACAGTCTTGGCA  24615         AC   T
                                TGTCAAGACT  CGA GGTTA
                                ||||||||||  ||| |||||
                                ACGGTTCTGA  GCT CCAAT
                                     CA  _
GAM1717 DKFZp434F1719 3' ACCTTGGACAGTAGTCTTGAC  51008          ____   T
                                GTCAAGACTA   CCGA GGT
                                ||||||||||   |||| |||
                                CAGTTCTGAT   GGTT CCA
                                     GACA   _
GAM1717 FLJ10038  3' TAACCATCAGCTTTGATA   36216       GA  ACC
                                TGTCAA  CT   GATGGTTA
                                ||||||  ||   ||||||||
                                ATAGTT  GA   CTACCAAT
                                   TC  ___
GAM1717 GW112    3' GTAACCATCGTTATAGACA   22215     AAGAC  C
                                TGTC    TA CGATGGTTAC
                                ||||    || ||||||||||
                                ACAG    AT GCTACCAATG
                                  AT___  T
GAM1717 KIAA0157  5' TAACCATCAGCCTTGTTCA   50752    T_   A  ACC
                                TG  CAAG CT   GATGGTTA
                                ||  |||| ||   ||||||||
                                AC  GTTC GA   CTACCAAT
                                 TT   C  ___
GAM1717 KIAA0844  3' GTTCCAGTAATCTTGGCA    30896        C   CGA   TT
                                TGTCAAGA TAC   TGG  AC
                                |||||||| |||   |||  ||
                                ACGGTTCT ATG   ACC  TG
                                     A  ___   TC
GAM1717 KIAA1894  3' TAACTCTGTGAACAGTCTTGAC 74286         AC_  AT_
                                GTCAAGACT   CG   GGTTA
                                |||||||||   ||   |||||
                                CAGTTCTGA   GT   TCAAT
                                     CAA  GTC
GAM1717 TRIM29   3' ACCTCTCAGTGTCTTGACA   25003         T  C  T_
                                TGTCAAGAC AC GA  GGT
                                |||||||| || ||  |||
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                                ACAGTTCTG TG CT  CCA
                                     _ A  CT
GAM1717  LOC144266 5'  TAATTATGGTAATTTTGACA   77270        C    G
                                TGTCAAGA TACC ATGGTTA
                                |||||||| |||| |||||||
                                ACAGTTTT ATGG TATTAAT
                                    A   _
GAM1717  LOC151602 3'  CATTTTAATGGTCTTGACA    81105          CC__
                                TGTCAAGACTA    GATG
                                ||||||||||    ||||
                                ACAGTTCTGGT    TTAC
                                      AATT
GAM1717  LOC152179 5'  TAATCATTGTAGTCCATGACA  86744      A_     C
                                TGTCA  GACTAC GATGGTTA
                                |||||  |||||| ||||||||
                                ACAGT  CTGATG TTACTAAT
                                   AC     _
GAM1718  ANKRD6    3'  CAACAGCTGTGGGAAAAACTAA 30769       __        A
                                TTGGTT  TTCCACAGCT TTG
                                ||||||  |||||||||| |||
                                AATCAA  AGGGTGTCGA AAC
                                    AA         C
GAM1718  DKFZP761C169 3'  CAATATGAAGAAAACCAAGA   68417          CA  GC
                                TCTTGGTTTTC  CA  TATTG
                                ||||||||||  ||  |||||
                                AGAACCAAAAG  GT  ATAAC
                                      AA  __
GAM1718  FLJ21939  3'  CAATAGTACAAAAACCAACATA 42649     C       CCACA
                                TAT TTGGTTTT    GCTATTG
                                ||| ||||||||    |||||||
                                ATA AACCAAAA    TGATAAC
                                  C       ACA__
GAM1718  HSPC133   3'  AGAATGGAAAATCAAGATA    27183            CAG
                                TATCTTGGTTTTCCA   CT
                                ||||||||||||||   ||
                                ATAGAACTAAAAGGT   GA
                                      AA_
GAM1718  KIAA0705  3'  AGCTATGGAAGAACCAAAATA  25481     C       _  C
                                TAT TTGGTTTT CCA AGCT
                                ||| |||||||| ||| ||||
                                ATA AACCAAGA GGT TCGA
                                  A       A  A
GAM1718  KIAA1881  3'  CAATGCTAGAAAACCAAG    97081          CAC   T
                                CTTGGTTTTC   AGC ATTG
                                ||||||||||   ||| ||||
                                GAACCAAAAG   TCG TAAC
                                      A__  _
GAM1718  MYT1      5'  CAATAGCTGTGGGGAAAGA    16975      GGT TT
                                TCTT   T  CCACAGCTATTG
                                ||||   |  ||||||||||||
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                                AGAA  A  GGTGTCGATAAC
                                  ___ GG
GAM1718  NDUFA3   3'  CAATAAAAATGTGAAAACCAA  17007        C  GC__
                                TTGGTTTTC ACA   TATTG
                                ||||||||| |||   |||||
                                AACCAAAAG TGT   ATAAC
                                     _  AAAA
GAM1718  LOC150113 5'  CAATGGTCAGAAAACCAA    88564        CACA
                                TTGGTTTTC   GCTATTG
                                |||||||||   |||||||
                                AACCAAAAG   TGGTAAC
                                     AC__
GAM1718  LOC253820 3'  CAATAGCTGTGAAAAGAAC   97422      C__
                                GTTTT  CACAGCTATTG
                                |||||  ||||||||||
                                CAAGA  GTGTCGATAAC
                                   AAA
GAM1719  CD8A     3'  ATCTCCTGTTAATATGGTGTA  10095        __   A
                                TACACCAT  TGGCA GGAGAT
                                ||||||||  ||||| ||||||
                                ATGTGGTA  ATTGT CCTCTA
                                     TA   _
GAM1719  HEPH     5'  GATCTCCTCATCACAAAAGTAA 29649   C  ACCAT  CA
           TG                    CA TAC    TGG  AGGAGATC
                                || |||    |||  ||||||||
                                GT ATG    ACT  TCCTCTAG
                                 A  AAAAC  AC
GAM1719  MLLT2    3'  CTTTCTGCCAATGAACAGTG  21029     ACAC      AG
                                CACT   CATTGGCA  GAG
                                ||||   ||||||||  |||
                                GTGA   GTAACCGT  TTC
                                  CAA_      CT
GAM1719  NCOA6    3'  ATCTCCTAATGATGTATTG   26826   C   C   GGCA
                                CA TACA CATT   AGGAGAT
                                || |||| ||||   |||||||
                                GT ATGT GTAA   TCCTCTA
                                 T   A   ____
GAM1719  PKIA     3'  ATCTCCTTGCAATCATGTG   23342     CC   G
                                TACA  ATTG CAAGGAGAT
                                ||||  |||| |||||||||
                                GTGT  TAAC GTTCCTCTA
                                  AC   _
GAM1719  RAD21    3'  GATCTCCTTTTCCAGTGCTG  21836   C    C_
                                CA CATTGG  AAGGAGATC
                                || ||||||  |||||||||
                                GT GTGACC  TTCCTCTAG
                                 C     TT
GAM1719  SDHC     3'  GATCTCCTTGGAGCAGTAG   69912     ACCA  GG
                                CTAC   TT  CAAGGAGATC
                                ||||   ||  ||||||||||
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                                GATG   AG  GTTCCTCTAG
                                  ACG_ __
GAM1719  TRIM37   3'  ATCTCCTTTTTGGAGTATGT  31622   _  A  TTGGC
                                AC TAC CCA    AAGGAGAT
                                || ||| |||    ||||||||
                                TG ATG GGT    TTCCTCTA
                                 T  A  TT___
GAM1719  FLJ21140 3'  GATCTCCTTTAGAGGGCACAGT 45837    ACA  A  GGC
           G                     CACT  CC TT  AAGGAGATC
                                ||||  || ||  |||||||||
                                GTGA  GG AG  TTCCTCTAG
                                  CAC  G  AT_
GAM1719  KIAA0159 3'  ATCTCCTTGTTTTCTAATG  30138     ____
                                CATTGG   CAAGGAGAT
                                ||||||   |||||||||
                                GTAATC   GTTCCTCTA
                                   TTTT
GAM1719  KIAA1975 5'  CCACCAATAGTGATAGTG   74417     _  C   CAA
                                CACTA CAC ATTGG  GG
                                ||||| ||| |||||  ||
                                GTGAT GTG TAACC  CC
                                  A  A   A__
GAM1719  MDS031   3'  GATCTCCTCTCACAGTGGT  38066      GCA_
                                ACCATTG   AGGAGATC
                                |||||||   ||||||||
                                TGGTGAC   TCCTCTAG
                                    ACTC
GAM1719  PER3     3'  ATCTCCTTTCAAAGTAGTG  34173      ACCA   C
                                CACTAC   TTGG AAGGAGAT
                                ||||||   |||| ||||||||
                                GTGATG   AACT TTCCTCTA
                                   A___   _
GAM1719  LOC145453 3'  CTTGCCAATGGTGGAGTG   77661     A
                                CACT CACCATTGGCAAG
                                |||| ||||||||||||
                                GTGA GTGGTAACCGTTC
                                  G
GAM1719  LOC148824 3'  TTTTGCCAATAATGTGTA   85382     C__
                                TACAC  ATTGGCAAGG
                                |||||  ||||||||||
                                ATGTG  TAACCGTTTT
                                   TAA
GAM1719  LOC220662 3'  ATCTCCTTTACCAATAGGTAGT 92806     ACC   C_
                                ACTAC  ATTGG  AAGGAGAT
                                |||||  |||||  ||||||||
                                TGATG  TAACC  TTCCTCTA
                                  GA_    AT
GAM1719  LOC253827 3'  GATCTCCTCTGCAGTGTAG   96573      CATTG  _
                                CTACAC   GCA AGGAGATC
                                ||||||   ||| ||||||||
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                                GATGTG    CGT TCCTCTAG
                                   A____  C
GAM1720 C18orf1  3' AGTTGTCAGCTCATGCTT   60860     _ T  TT
                                AAGC TG GCT  GACAACT
                                |||| || |||  |||||||
                                TTCG AC CGA  CTGTTGA
                                  T T  __
GAM1720 CCND1    3' TAAAGCACAGCTGTAGT    54960       A
                                ACTACA GCTGTGCTTTG
                                |||||| ||||||||||
                                TGATGT CGACACGAAAT
                                   _
GAM1720 DSG1     3' GAAGCAGCAGCTTGTAGT   10450         _
                                ACTACAAGCTG TGCTTT
                                |||||||||| ||||||
                                TGATGTTCGAC ACGAAG
                                      G
GAM1720 FCER1A   3' TTGTCAAACACAGCTTG    10597        C
                                CAAGCTGTG TTTGACAA
                                |||||||| ||||||||
                                GTTCGACAC AAACTGTT
                                   _
GAM1720 GLS      3' AGTTACCAATGCTAGCTTGTG 30461        T T  AC
                                TACAAGCTG GC TTG  AACT
                                |||||||| || |||  ||||
                                GTGTTCGAT CG AAC  TTGA
                                      _ T  CA
GAM1720 HTR2C    3' TCAGGGCAAGCTCATAG    7873     CA   G
                                CTA  AGCT TGCTTTGA
                                |||  |||| ||||||||
                                GAT  TCGA ACGGGACT
                                  AC   _
GAM1720 ITGA6    3' TAGAACACAGTTTGTAGT   5792           C
                                ACTACAAGCTGTG TTTG
                                |||||||||||| ||||
                                TGATGTTTGACAC AGAT
                                      A
GAM1720 LUZP1    5' TGTCAAAGAAGATTGTGGT  54407       GCTGTG
                                ACTACAA     CTTTGACA
                                |||||||     ||||||||
                                TGGTGTT     GAAACTGT
                                    AGAA__
GAM1720 PKD2     3' TGTCAAAGGGCTTCTGAGT  60721     A  A CT  G
                                ACT CA G  GT CTTTGACA
                                ||| || |  || ||||||||
                                TGA GT C  CG GAAACTGT
                                  _ _ TT  G
GAM1720 PVR      3' TGTTAGGCTCACAGTTACAGT 22497     ACA      C_
                                ACT   AGCTGTG  TTTGACA
                                |||   |||||||  |||||||
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                                TGA   TTGACAC  GGATTGT
                                  CA_      TC
GAM1720  APOF     3'  GTTATGCACGCTTGTAGT    9695          T    TT
                                ACTACAAGC GTGC  TGAC
                                ||||||||| ||||  ||||
                                TGATGTTCG CACG  ATTG
                                     _   T_
GAM1720  C1QR1    3'  TTTTAGCACAGTTCATAGT   24873     CA       TT
                                ACTA  AGCTGTGCT  GA
                                ||||  |||||||||  ||
                                TGAT  TTGACACGA  TT
                                  AC        TT
GAM1720  CREB-H   3'  TGGGGGAGGCACAGCTCATAG  51880     CA        GA_
                                CTA  AGCTGTGCTTT   CA
                                |||  ||||||||||   ||
                                GAT  TCGACACGGAG   GT
                                  AC          GGG
GAM1720  FIGN     3'  TGTCACAGAGCAGGCTGTAG   97364      A   G    __
                                CTACA GCT TGCTT  TGACA
                                ||||| ||| |||||  |||||
                                GATGT CGG ACGAG  ACTGT
                                   _  _     AC
GAM1720  KIAA0630 3'  TGTCAAAGTATTTGGAGT    90955     A   GCT
                                ACT CAA   GTGCTTTGACA
                                ||| |||   ||||||||||
                                TGA GTT   TATGAAACTGT
                                  G  ____
GAM1720  PEG10    3'  TTGCCAAAGCACAGTTTGAG   31208    A          A
                                CT CAAGCTGTGCTTTG CAA
                                || ||||||||||||| |||
                                GA GTTTGACACGAAAC GTT
                                  _           C
GAM1720  LOC143310 5'  TCAAGACAGCTTGAG       77051    A       G   T
                                CT CAAGCTGT CTT GA
                                || |||||||| ||| ||
                                GA GTTCGACA GAA CT
                                  _       _  _
GAM1720  LOC154813 3'  GTTGAAGTCACAGCTTACAG   82058    AC       _   TG
                                CT  AAGCTGTG CTT  AC
                                ||  |||||||| |||  ||
                                GA  TTCGACAC GAA  TG
                                  CA       T   GT
GAM1720  LOC197319 3'  AGATGGGAAGCACAGATTGCAG 89312     A   G       GA  A
            T                    ACT CAA CTGTGCTTT  CA CT
                                ||| ||| |||||||||  || ||
                                TGA GTT GACACGAAG  GT GA
                                  C   A        G_  A
GAM1720  LOC200488 5'  AGTTGTCAAAACATTTCTT   91647     CT   C
                                AAG  GTG TTTGACAACT
                                |||  ||| ||||||||||
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                                TTC  TAC AAACTGTTGA
                                  TT   A
GAM1720  LOC203335 3'  AGTTGTCAAAATATGTT     90874     T   C
                                AGC GTG TTTGACAACT
                                ||| ||| ||||||||||
                                TTG TAT AAACTGTTGA
                                  _   A
GAM1720  LOC253263 3'  TGCAACACAGTTTGTAG     98818           CT   A
                                CTACAAGCTGTG  TTG CA
                                ||||||||||||  ||| ||
                                GATGTTTGACAC  AAC GT
                                      __   _
GAM1721  DLEC1     3'  CATCTGGCCCTCCCTTG     24716      A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                   C    G  _
GAM1721  DLEC1     3'  CATCTGGCCCTCCCTTG     24728      A    A  C
                                CAAGG AGGGC GG GTG
                                ||||| ||||| || |||
                                GTTCC TCCCG TC TAC
                                   C    G  _
GAM1721  PIP5K1A   3'  TATCCCACCCTGCCTTGATA   14520        A   CA  C
                                TATCAAGG AGGG  GG GTG
                                |||||||| ||||  || |||
                                ATAGTTCC TCCC  CC TAT
                                     G   A_  C
GAM1721  SOX11     3'  ACCCACCCCCCCTTGGTA    13308        AA   CA  C
                                TATCAAGG  GGG  GG GT
                                ||||||||  |||  || ||
                                ATGGTTCC  CCC  CC CA
                                     CC   A_  _
GAM1721  CHL1      3'  TGTTACCTTTCCTCAATA     22768     CA      CA
                                TAT  AGGAAGGG  GGCG
                                |||  ||||||||  ||||
                                ATA  TCCTTTCC  TTGT
                                  AC       A_
GAM1721  EPB41L1   3'  CATTCTGCCCTTCCCTGA     71104     A        C
                                TCA GGAAGGGCAGG GTG
                                ||| ||||||||||| |||
                                AGT CCTTCCCGTCT TAC
                                  C          _
GAM1721  FLJ00060  3'  CATACCCCCTGCCCTCCTCTGA 61741     _   A     CGTG
                                TCA AGGA GGGCAGG    ATG
                                ||| |||| |||||||    |||
                                AGT TCCT CCCGTCC    TAC
                                  C    _      CCCA
GAM1721  FLJ10898  5'  CACCACAGCCCTTTCTCAATA  60126     CA       AGGC
                                TAT  AGGAAGGGC    GTG
                                |||  |||||||||    |||
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                                ATA  TCTTTCCCG   CAC
                                  AC       ACAC
GAM1721  FLJ22557  3'  ATCATCCCATCCTTAATA   45581    C    A  CAGGC
                                TAT AAGGA GGG    GTGAT
                                ||| ||||| |||    |||||
                                ATA TTCCT CCC    TACTA
                                  A    A  _____
GAM1721  KIAA0574  3'  CATCCCCTGCCCTCCCCTGA  69808    A  A      CGT
                                TCA GG AGGGCAGG   GATG
                                ||| || ||||||||   ||||
                                AGT CC TCCCGTCC   CTAC
                                  C  C       C__
GAM1721  KIAA0632  3'  CACCTCAGAAACCCTTCCTTGA 32071          CA___  C
                                TCAAGGAAGGG    GG GTG
                                ||||||||||    || |||
                                AGTTCCTTCCC    CT CAC
                                      AAAGA  C
GAM1721  KIAA1045  3'  CATCACATGTCCTTCC      71599         GGC
                                GGAAGGGCA   GTGATG
                                |||||||||   ||||||
                                CCTTCCTGT   CACTAC
                                     A__
GAM1721  KIAA1354  5'  CAGTGACTGCCTTCCCTTGATA 61572        A      G  _
                                TATCAAGG AGGGCAG CG TG
                                |||||||| ||||||| || ||
                                ATAGTTCC TTCCGTC GT AC
                                     C      A  G
GAM1721  MGC20460  5'  CACCGCCTCCTACCCTTCTT   54901        C___    _
                                AGGAAGGG    AGGCG TG
                                ||||||||    ||||| ||
                                TTCTTCCC    TCCGC AC
                                     ATCC    C
GAM1721  LOC158476 3'  CACGCCCGCCCCCCCCATTGA  88186     _  AA_   A
                                TCAA GG   GGGC GGCGTG
                                |||| ||   |||| ||||||
                                AGTT CC   CCCG CCGCAC
                                  A  CCC    C
GAM1721  LOC90459  3'  CACACCCGCCTAATTTTTG    63550       A_   A  C
                                CAAGGA  GGGC GG GTG
                                ||||||  |||| || |||
                                GTTTTT  TCCG CC CAC
                                   AA   C  A
GAM1722  CDH12    3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                     AA___   AC
GAM1722  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
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                                ATGTG  GAGGGTTCTT TTA
                                  AC         G
GAM1722  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT    98090       T    AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||     ||||||
                                TGGTG GGGT     TTATTC
                                  _    GTCA_
GAM1722  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
           A                     TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                  TACTCCC_
GAM1722  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM1722  HMP19     3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
           TA                    TACA    TCC    GAAGAATAAG
                                ||||    |||    ||||||||||
                                ATGT    AGG    TTTCTTATTC
                                  AAA_   ATTG
GAM1722  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68742             _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                         G
GAM1722  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
                                GTG  GA GGTTCTTTTT
                                  AC  A
GAM1722  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748      CCA__
                                ACTC     AGAAGAATAAG
                                ||||     ||||||||||
                                TGAG     TCTTCTTATTC
                                  TACCG
GAM1722  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     CTCC_
                                CCA     CAAGAAGAATAAG
                                |||     ||||||||||||
                                GGT     GTTCTTCTTATTC
                                  TTTCA
GAM1722  OSBPL11   3'  CTTAATTTCCCAAGAGTGGTG  43206         CCAA    AA
                                CACCACTC    GAAG  TAAG
                                ||||||||    ||||  ||||
                                GTGGTGAG    CTTT  ATTC
                                     AACC    A_
GAM1722  YME1L1    3'  TCATTCTTGATGTGGTGTA    58438         TCC     _
                                TACACCAC   CAAGAA GA
                                ||||||||   |||||| ||
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                                ATGTGGTG  GTTCTT CT
                                    TA_    A
GAM1722 ZNF262   3' CTTATTTTGTTTGGGAGT   18723        A
                                ACTCCCAAG AGAATAAG
                                ||||||||| ||||||||
                                TGAGGGTTT TTTTATTC
                                    G
GAM1722 LOC91960 3' TGTGGCTTGGAACGTGGTGTA 68294       TC_   AAGA
                                TACACCAC  CCAAG   ATA
                                ||||||||  |||||   |||
                                ATGTGGTG  GGTTC   TGT
                                    CAA   GG__
GAM1723 AF1Q     3' GGTGCTGATGAATCTGC    23332        AAGCCA
                                GCAGATTCA    GGCACC
                                |||||||||    ||||||
                                CGTCTAAGT    TCGTGG
                                    AG____
GAM1723 ALOX5AP  3' TGACCGTGGCCCCAAATTTGCT 9680        CAAA  _ _
                                AGCAGATT   GCCA GG CA
                                ||||||||   |||| || ||
                                TCGTTTAA   CGGT CC GT
                                    ACCC   G  A
GAM1723 ATP8B2   3' GTGCCTGGCTTGGTCTG    65846      CA
                                CAGATT  AAGCCAGGCAC
                                ||||||  ||||||||||
                                GTCTGG  TTCGGTCCGTG
                                  __
GAM1723 B4GALT1  3' TGGTGCCTGGCCCCAGTCTTA 9473   C    CAAA
                                G AGATT   GCCAGGCACCA
                                | |||||   ||||||||||
                                A TCTGA   CGGTCCGTGGT
                                 T   CCC_
GAM1723 C7orf2   3' TGGTTTCTTGGCTTTAAGTCCA 42638    CA   C      C_
          CTG                    CAG  GATT AAAGCCAGG  ACCA
                                |||  |||| |||||||||  ||||
                                GTC  CTGA TTTCGGTTC  TGGT
                                  AC   A       TT
GAM1723 C8orf1   3' TGCCTGGCTTGGTGTCTGGC  16346   _   TCA
                                GC AGAT   AAGCCAGGCA
                                || ||||   ||||||||||
                                CG TCTG   TTCGGTCCGT
                                 G   TGG
GAM1723 CD74     3' TGGTGCCTGGCTCTTTCGTC  16382    TCAA_
                                GAT    AGCCAGGCACCA
                                |||    ||||||||||||
                                CTG    TCGGTCCGTGGT
                                  CTTTC
GAM1723 COL5A3   3' TGGTGCTGAGGCTTTGAAGC  32320   AGA      A_
                                GC   TTCAAAGCC  GGCACCA
                                ||   |||||||||  |||||||
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                              CG  AAGTTTCGG  TCGTGGT
                               ___       AG
GAM1723  CYP2B6   3'  TGTTCCTTCAAATCTGCTG   7574        CA  CCA
                              CAGCAGATT  AAG  GGCA
                              |||||||||  |||  ||||
                              GTCGTCTAA  TTC  TTGT
                                   AC  C__
GAM1723  DAPK1    5'  GGCGCCTGGGAGGGATCTGC  18227       AAAG    A
                              GCAGATTC   CCAGGC CC
                              ||||||||   |||||| ||
                              CGTCTAGG   GGTCCG GG
                                   GAG_    C
GAM1723  EXTL3    5'  GCCAGAACTTAAAATCTGCTG 9334        CA  CCA_
                              CAGCAGATT  AAG   GGC
                              |||||||||  |||   |||
                              GTCGTCTAA  TTC   CCG
                                   AA  AAGA
GAM1723  FBXL3A   3'  GTTTGCTCTGTAATCTGCT   25132       _ A  C
                              AGCAGATT CA AGC AGGC
                              |||||||| || ||| ||||
                              TCGTCTAA GT TCG TTTG
                                   T  C  _
GAM1723  KLHL3    3'  GGTGTTTCTTGAATTGCT    88851      A   AGCC
                              AGCAG TTCAA   AGGCACC
                              ||||| |||||   |||||||
                              TCGTT AAGTT   TTTGTGG
                                 _   C___
GAM1723  MYH4     5'  TGTCTGCTTTGAGCCTGC    34474     AT     C
                              GCAG  TCAAAGC AGGCA
                              ||||  ||||||| |||||
                              CGTC  AGTTTCG TCTGT
                                CG     _
GAM1723  PRex1    3'  TGGTGCCTGGCCTTCGGCT   40827     A  TTCAAA
                              AGC GA     GCCAGGCACCA
                              ||| ||     ||||||||||
                              TCG CT     CGGTCCGTGGT
                                G  TC____
GAM1723  PRKY     3'  TGGCATTGCTCAAATCTGCTG  12389       ____  A
                              CAGCAGATT   CAA GCCA
                              |||||||||   ||| ||||
                              GTCGTCTAA   GTT CGGT
                                   ACTC  A
GAM1723  TNFSF4   3'  GGTACCTGACTACCATTTGCTG 13914       TCAA  C   C
                              CAGCAGAT   AG CAGG ACC
                              ||||||||   || |||| |||
                              GTCGTTTA   TC GTCC TGG
                                   CCA_  A   A
GAM1723  C19orf7  3'  GTGCCTGGCCTCAGACTCTGT  61782     T  AAA_
                              GCAGA TC   GCCAGGCAC
                              ||||| ||   |||||||||
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                                TGTCT AG   CGGTCCGTG
                                   C  ACTC
GAM1723  DKFZp547I224 5'  GTCATTTGAATCTGCT     39960          GCCA
                                AGCAGATTCAAA   GGC
                                ||||||||||||  |||
                                TCGTCTAAGTTT   CTG
                                      A___
GAM1723  DOCK3    3'  GCCTCTCTGAGTCTGC      67098        A  CC
                                GCAGATTCA AG  AGGC
                                |||||||||  ||  ||||
                                CGTCTGAGT TC  TCCG
                                     C  __
GAM1723  FLJ11539 3'  GTCACTTTAAATCTGCTG    45708        C   CCA
                                CAGCAGATT AAAG   GGC
                                |||||||||  ||||  |||
                                GTCGTCTAA TTTC   CTG
                                     A   A__
GAM1723  FLJ12303 3'  GGTACCTAGTAATTTGCTG   73086        CAAA  C   C
                                CAGCAGATT   GC AGG ACC
                                |||||||||   ||  |||  |||
                                GTCGTTTAA   TG TCC TGG
                                     ____  A   A
GAM1723  FLJ13102 3'  TGGCTCTACCTTGGATCTGCT  46537         _____
                                AGCAGATTCAA    AGCCA
                                ||||||||||    |||||
                                TCGTCTAGGTT    TCGGT
                                      CCATC
GAM1723  FLJ13940 3'  TGGTGCCTGGGAGTGACCTG  47311    AT   AAG
                                CAG  TCA   CCAGGCACCA
                                |||  |||   ||||||||||
                                GTC  AGT   GGTCCGTGGT
                                  C_   GAG
GAM1723  FLJ14596 5'  GGTGCCTGGGACCCAGCTG   52520     AGAT  AAAG
                                CAGC   TC   CCAGGCACC
                                ||||   ||   |||||||||
                                GTCG   AG   GGTCCGTGG
                                  ACCC  ____
GAM1723  KIAA0089 3'  CCACTCTGAAGTCTGCTG    70505        _  A  CCA
                                CAGCAGATT CA AG   GG
                                |||||||||  ||  ||   ||
                                GTCGTCTGA GT TC   CC
                                     A  C  A__
GAM1723  KIAA0102 3'  GTCTCCTTGATCTGCTG     29248        CA   CC
                                CAGCAGATT  AAG  AGGC
                                |||||||||  |||  ||||
                                GTCGTCTAG  TTC  TCTG
                                     __   C_
GAM1723  KIAA0254 3'  TGTTGCTTTGAATCTGCTG   29285           CA
                                CAGCAGATTCAAAGC  GGCA
                                ||||||||||||||  ||||
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                                GTCGTCTAAGTTTCG  TTGT
                                      __
GAM1723 KIAA0515 3' TGGTGCCTGGCTCCCCGCCTG 64559    ATTCAA
                                CAG     AGCCAGGCACCA
                                |||     ||||||||||||
                                GTC     TCGGTCCGTGGT
                                  CGCCCC
GAM1723 KIAA0882 3' GTACCTGGCTTGAAGCCTAGT 83536   _ A_    A     C
                                GC AG  TTCAA GCCAGG AC
                                || ||  ||||| |||||| ||
                                TG TC  AAGTT CGGTCC TG
                                 A  CG    _     A
GAM1723 KIAA0997 3' TTTGTGTAAATCTGCTG     30890        CAAA  _
                                CAGCAGATT    GC CAGG
                                |||||||||    || ||||
                                GTCGTCTAA    TG GTTT
                                      A___  T
GAM1723 KIAA1297 5' GTACTGTCTTCGGATCTGC   72644        A   C   GC
                                GCAGATTC AAG CAG  AC
                                |||||||| ||| |||  ||
                                CGTCTAGG TTC GTC  TG
                                     C   T   A_
GAM1723 KIAA1423 3' GCACTGCTGAATCTGT      62393        AA  C  _
                                GCAGATTCA  GC AG GC
                                |||||||||  || || ||
                                TGTCTAAGT  CG TC CG
                                      __  _  A
GAM1723 KIAA1987 3' TGGTGCCCGGCGGCCTTCCTCT 89395     CA  TTCAAA   A
            G                    CAG  GA     GCC GGCACCA
                                |||  ||     ||| |||||||
                                GTC  CT     CGG CCGTGGT
                                  TC  TCCGG_  C
GAM1723 MGC21636 5' TGGCGTTTAAATGTGCTG    59502      G   C   _
                                CAGCA ATT AAA GCCA
                                ||||| ||| ||| ||||
                                GTCGT TAA TTT CGGT
                                   G   A   G
GAM1723 MGC26610 5' GTGCCTGGCCAGGGGCTCTG   58963      _   AAA
                                CAGA TTC   GCCAGGCAC
                                |||| |||   |||||||||
                                GTCT GGG   CGGTCCGTG
                                  C   GAC
GAM1723 PRO0365  5' TGGTGCCTGGCCCTTATTTGTT 27000        TCAAA
                                AGCAGAT    GCCAGGCACCA
                                |||||||    ||||||||||||
                                TTGTTTA    CGGTCCGTGGT
                                    TTCC_
GAM1723 PTPN3    3' TGGTGCCTAACCTGGATTAGT  12589    A     AAGCC
                                GC GATTCA    AGGCACCA
                                || ||||||    ||||||||
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                                TG TTAGGT    TCCGTGGT
                                 A    CCAA_
GAM1723 SCAMP-4  3' TGGTGCCTAGCTGAGTCCTCGC 55358     A__     AA  C
            TG                   CAGC   GATTCA  GC AGGCACCA
                                 ||||   ||||||  || ||||||||
                                 GTCG   CTGAGT  CG TCCGTGGT
                                   CTC     __ A
GAM1723 SENP7    3' GTGCTTGTCAAATTTGCTG   40674        CAAAGC
                                 CAGCAGATT     CAGGCAC
                                 |||||||||     |||||||
                                 GTCGTTTAA     GTTCGTG
                                      ACT___
GAM1723 XAT2     3' GTACCTGGCTTCAGAGTC    57979      A_      C
                                 GATTC  AAGCCAGG AC
                                 |||||  |||||||| ||
                                 CTGAG  TTCGGTCC TG
                                    AC       A
GAM1723 ZFP106   3' GTCTACCTTTACATCTGCTG  42738       TC    CC
                                 CAGCAGAT  AAAG  AGGC
                                 ||||||||  ||||  ||||
                                 GTCGTCTA  TTTC  TCTG
                                      CA    CA
GAM1723 LOC133418 3' CCTGGCTTCCTGGTATCT    75595     _   __
                                 AGAT TCA  AAGCCAGG
                                 |||| |||  ||||||||
                                 TCTA GGT  TTCGGTCC
                                   T   CC
GAM1723 LOC147808 5' GGTGCCTGATGACTGC     85198     AT   AAGC
                                 GCAG  TCA    CAGGCACC
                                 ||||  |||    ||||||||
                                 CGTC  AGT    GTCCGTGG
                                   __   A___
GAM1723 LOC152627 5' TGATGCCTGGCTTCAAATCT  81517      CA       C
                                 AGATT  AAGCCAGGCA CA
                                 |||||  |||||||||| ||
                                 TCTAA  TTCGGTCCGT GT
                                    AC        A
GAM1723 LOC163682 5' GGTGCCTGGGACCTGC     88413     AT  AAAG
                                 GCAG  TC    CCAGGCACC
                                 ||||  ||    |||||||||
                                 CGTC  AG    GGTCCGTGG
                                   C_  _____
GAM1723 LOC197257 5' GTGCCTGGCTATGGCCCGACTG 89305     CAGAT   A
                                 CAG     TCA AGCCAGGCAC
                                 |||     ||| ||||||||||
                                 GTC     GGT TCGGTCCGTG
                                   AGCCC   A
GAM1723 LOC200953 5' TGGTGCCTGGCTTCCTGC    91806     ATTCA
                                 GCAG     AAGCCAGGCACCA
                                 ||||     ||||||||||||
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                                CGTC    TTCGGTCCGTGGT
                                  C____
GAM1723  LOC203276 3'  GGTGCCCAAGGATCTGCT    92128        AAAGCCA
                                AGCAGATTC     GGCACC
                                |||||||||     ||||||
                                TCGTCTAGG     CCGTGG
                                    AAC____
GAM1723  LOC203305 3'  GGTGCCCAAGAATCTGCT    92181        AAAGCCA
                                AGCAGATTC     GGCACC
                                |||||||||     ||||||
                                TCGTCTAAG     CCGTGG
                                    AAC____
GAM1723  LOC254243 3'  GGTGCCCAAGGATCTGCT    99267        AAAGCCA
                                AGCAGATTC     GGCACC
                                |||||||||     ||||||
                                TCGTCTAGG     CCGTGG
                                    AAC____
GAM1723  LOC256267 5'  GTCTGGCTTCAAATCTCT    98612    C    CA
                                AG AGATT  AAGCCAGGC
                                || |||||  |||||||||
                                TC TCTAA  TTCGGTCTG
                                 _    AC
GAM1723  LOC256789 3'  GGAGGGCTTTGTATCTGCTG   99309        T      AGGCA
                                CAGCAGAT CAAAGCC    CC
                                |||||||| |||||||    ||
                                GTCGTCTA GTTTCGG    GG
                                    T      GA___
GAM1723  LOC90038  3'  GGTGCCCAAGGATCTGCT    61811        AAAGCCA
                                AGCAGATTC     GGCACC
                                |||||||||     ||||||
                                TCGTCTAGG     CCGTGG
                                    AAC____
GAM1723  LOC92466  5'  GTCTGGCTTCAAATCTCT    69968    C    CA
                                AG AGATT  AAGCCAGGC
                                || |||||  |||||||||
                                TC TCTAA  TTCGGTCTG
                                 _    AC
GAM1724  ASTN     3'  GGAGGGGTCAACACTTTCA   69872      ACC_   ATT
                                TGAAAG   GACC   CTTCC
                                ||||||   ||||   |||||
                                ACTTTC   CTGG   GGAGG
                                   ACAA   ___
GAM1724  AXL      3'  CAGGGGATGGACGATCTCCCA  41878    AA   C  A    CTT
                                TG  AGA CG CCATT   CCCTG
                                ||  ||| || |||||   |||||
                                AC  TCT GC GGTAG   GGGAC
                                 CC   A  A    ___
GAM1724  AXL      3'  CAGGGGATGGACGATCTCCCA  9902     AA   C  A    CTT
                                TG  AGA CG CCATT   CCCTG
                                ||  ||| || |||||   |||||
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                                AC  TCT GC GGTAG   GGGAC
                                 CC   A  A    ___
GAM1724  HADHSC    3'  AGGAGGTCGGTTTTCA      19226      A       A
                                TGAA GACCGACC TTCT
                                |||| |||||||| ||||
                                ACTT TTGGCTGG AGGA
                                   _       _
GAM1724  RANBP3    3'  AGGCACAGAGTCGGTCTCCCA  24636    AA       CAT   TC_
                                TG  AGACCGAC   TCT   CCT
                                ||  ||||||||   |||   |||
                                AC  TCTGGCTG   AGA   GGA
                                 CC        ___   CAC
GAM1724  SIM2      3'  AGAAAGGAATGGCCTTTCA   24796       ACCGA       CC
                                TGAAAG    CCATTCTT  CT
                                ||||||    ||||||||  ||
                                ACTTTC    GGTAAGGA  GA
                                   C____       AA
GAM1724  TRPV1     3'  CAGTTTGGATGGTCAGTCT   38690      C       TTCC
                                AGAC GACCATTC    CTG
                                |||| ||||||||    |||
                                TCTG CTGGTAGG    GAC
                                  A       TTT_
GAM1724  TRPV1     3'  CAGTTTGGATGGTCAGTCT   55661      C       TTCC
                                AGAC GACCATTC    CTG
                                |||| ||||||||    |||
                                TCTG CTGGTAGG    GAC
                                  A       TTT_
GAM1724  TRPV1     3'  CAGTTTGGATGGTCAGTCT   55706      C       TTCC
                                AGAC GACCATTC    CTG
                                |||| ||||||||    |||
                                TCTG CTGGTAGG    GAC
                                  A       TTT_
GAM1724  TRPV1     3'  CAGTTTGGATGGTCAGTCT   55737      C       TTCC
                                AGAC GACCATTC    CTG
                                |||| ||||||||    |||
                                TCTG CTGGTAGG    GAC
                                  A       TTT_
GAM1724  ARHF      3'  GGGAAGAACAGTCGGCTCCCA  39271    AA  A    CA
                                TG  AG CCGAC  TTCTTCCC
                                ||  || |||||  ||||||||
                                AC  TC GGCTG  AAGAAGGG
                                 CC  _    AC
GAM1724  BOP       5'  GAAGACTGATAGTCTTTCA   86229        CGAC  T
                                TGAAAGAC    CA TCTTC
                                ||||||||    || |||||
                                ACTTTCTG    GT AGAAG
                                     ATA_  C
GAM1724  DKFZp434E0519 3'  AGGGGAGTGATCTTTCA     50983        C  ACCATT
                                TGAAAGA CG     CTTCCCT
                                ||||||| ||     |||||||
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                                ACTTTCT GT     GAGGGGA
                                   A _______
GAM1724 DPYSL4   3' CAGGGAAGTTTTGCGATCCTTT 22226     A  C  ACCATT
            A                    TGAA GA CG     CTTCCCTG
                                 |||| || ||     ||||||||
                                 ATTT CT GC     GAAGGGAC
                                   C  A  GTTTT_
GAM1724 FLJ14440 3' CAGGGAAGAGAAACATCCTTCA 52368     A  CCGACCA
                                 TGAA GA      TTCTTCCCTG
                                 |||| ||      ||||||||||
                                 ACTT CT      GAGAAGGGAC
                                   C  ACAAA__
GAM1724 FLJ20392 5' CAGGGAAGAATATGGAACCTTC 35575     AGA_   ACC
            A                    TGAA   CCG   ATTCTTCCCTG
                                 ||||   |||   ||||||||||||
                                 ACTT   GGT   TAAGAAGGGAC
                                   CCAA   A__
GAM1724 KIAA0618 3' CAGGGAAGAACCATTCATTCA  29847     A  CCGACCA
                                 TGAA GA      TTCTTCCCTG
                                 |||| ||      ||||||||||
                                 ACTT CT      AAGAAGGGAC
                                   A  TACC___
GAM1724 KIAA1301  3' CAGGGAACAACCCAACCGTCTT 66945       CGACCATTC_
            TCA                    TGAAAGAC        TTCCCTG
                                   ||||||||        |||||||
                                   ACTTTCTG        AAGGGAC
                                      CCAACCCAAC
GAM1724 PDZD2    5' CAGGGAAGAAGGGGGCCGCTC  81718    C  A_  A_
                                 GA CG  CC  TTCTTCCCTG
                                 || ||  ||  ||||||||||
                                 CT GC  GG  AAGAAGGGAC
                                  C  CG  GG
GAM1724 PRSS25   5' CAGGGAGGAGTCGGCCTCCCG  26029    AA  A    CAT
                                 TG  AG CCGAC   TCTTCCCTG
                                 ||  || |||||   |||||||||
                                 GC  TC GGCTG   AGGAGGGAC
                                  CC  C    ___
GAM1724 PRSS25   5' CAGGGAGGAGTCGGCCTCCCG  59672    AA  A    CAT
                                 TG  AG CCGAC   TCTTCCCTG
                                 ||  || |||||   |||||||||
                                 GC  TC GGCTG   AGGAGGGAC
                                  CC  C    ___
GAM1724 LOC112817 3' CAGGAAAGTGACACTGGTCTTT 57318         ACCATT   C
            CA                     TGAAAGACCG     CTT CCTG
                                   ||||||||||     ||| ||||
                                   ACTTTCTGGT     GAA GGAC
                                         CACAGT   A
GAM1724 LOC147118 3' CAGGGAAGCTTCCTCGGTCT   85061       CCATT
                                 AGACCGA    CTTCCCTG
                                 |||||||    ||||||||
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                                TCTGGCT    GAAGGGAC
                                    CCTTC
GAM1724  LOC151195 3'  CAGGAAAGAATGGGACCTTGTC 80967     CGA___       C
                                GAC     CCATTCTT CCTG
                                |||     |||||||| ||||
                                CTG     GGTAAGAA GGAC
                                  TTCCAG       A
GAM1724  LOC158055 3'  CAGGGAAGAGCCGCGGCCTT   82578     A   ACCA
                                AAG CCG    TTCTTCCCTG
                                ||| |||    ||||||||||
                                TTC GGC    GAGAAGGGAC
                                  C   GCC_
GAM1724  LOC203100 3'  GAAAAATGGATGGTTATCA    90791     AA    A    C
                                TGA  GACCG CCATT TTC
                                |||  ||||| ||||| |||
                                ACT  TTGGT GGTAA AAG
                                  A_    A    A
GAM1724  LOC256691 3'  GAATGAATGCAGTCTTTCA    97922        CGAC    _
                                TGAAAGAC    CATTC TTC
                                ||||||||    ||||| |||
                                ACTTTCTG    GTAAG AAG
                                     AC__     T
GAM1725  ACATN    5'  GACTGGCTCCCGGCTTCAG    17596        AGTG   CA   A
                                TTGAAGCC    GGG  CCA TC
                                ||||||||    |||  ||| ||
                                GACTTCGG    CCC  GGT AG
                                     _____  TC   C
GAM1725  B3GALT2   3'  GTGTCTCAGGCTCAA       15032      A   AG
                                TTGA GCC  TGGGGCAC
                                |||| |||  ||||||||
                                AACT CGG  ACTCTGTG
                                  _   __
GAM1725  CD164    3'  GGACTAGTGCAGAGGCTTTAA  21197        AGTGGG    CAA
                                TTGAAGCC     GCAC   TCC
                                ||||||||     ||||   |||
                                AATTTCGG     CGTG   AGG
                                     AGA___    ATC
GAM1725  DRG2     3'  TGGTTAGTGGCTTCAA      9131          G  GGGC
                                TTGAAGCCA TG    ACCA
                                |||||||| ||    ||||
                                AACTTCGGT AT    TGGT
                                     G  _____
GAM1725  HPS4     3'  ATTGGTGCCACAAGCTTC    42226       CAG  G
                                GAAGC   TG GGCACCAAT
                                |||||   || |||||||||
                                CTTCG   AC CCGTGGTTA
                                   A__  A
GAM1725  SDPR     5'  GACTGGTGCCCTGAGCTCCAA  17400     A   CAG        A
                                TTG AGC   TGGGGCACCA TC
                                |||  |||   |||||||||| ||
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                                AAC TCG   GTCCCGTGGT AG
                                  C   A__         C
GAM1725 C5orf6   3' GATTGGCTGTGCCAGCTTC   33954      CAG   G  _
                                GAAGC   TGG GCA CCAATC
                                |||||   ||| ||| ||||||
                                CTTCG   ACC TGT GGTTAG
                                   ___   G   C
GAM1725 C8orf17  3' GGACCACACTGGCTGCAA    39998     A      G  CA
                                TTG AGCCAGTG GG  CC
                                ||| |||||||| ||  ||
                                AAC TCGGTCAC CC  GG
                                  G       A  A_
GAM1725 CABP5    5' GACTGGTGCCCTGCGAGCTCCA 39562    A   CA TG       A
                                TG AGC  G  GGGCACCA TC
                                || |||  |  |||||||| ||
                                AC TCG  C  CCCGTGGT AG
                                 C   AG GT       C
GAM1725 FLJ13940 3' GGACTGGTGCCCCACAGGCTTT 47309         A         A
             AA                   TTGAAGCC GTGGGGCACCA TCC
                                |||||||| |||||||||| |||
                                AATTTCGG CACCCCGTGGT AGG
                                     A         C
GAM1725 KCNMB2   3' ATTGGTGGACTGGTTTCAA   20684          GGGG
                                TTGAAGCCAGT    CACCAAT
                                ||||||||||    |||||||
                                AACTTTGGTCA    GTGGTTA
                                      G___
GAM1725 KIAA0530 3' GATTGGTGTATAGCTTTAA   71431        CAGTGGG
                                TTGAAGC      GCACCAATC
                                |||||||      |||||||||
                                AATTTCG      TGTGGTTAG
                                   ATA____
GAM1725 KIAA1522 3' GGATTGGCCTTCCTGTGCCTCA 65607     A  _   TG    AC
             A                    TTGA GC CAG  GGGC  CAATCC
                                |||| || |||  ||||  ||||||
                                AACT CG GTC  TCCG  GTTAGG
                                  C  T   CT    __
GAM1725 KIAA1853 3' GGATGCCCCACTAGTCCAA   69924     AA  C       _
                                TTG  GC AGTGGGGCA CC
                                |||  || |||||||| ||
                                AAC  TG TCACCCCGT GG
                                  C_  A        A
GAM1725 LOXL4    3' GATTGGTCTAAACTTCAA    50859       CCAG   GGC
                                TTGAAG   TGG   ACCAATC
                                ||||||   |||   |||||||
                                AACTTC   ATC   TGGTTAG
                                   AA__   ____
GAM1725 LSR7     5' GGACCGGCCCTGCCCCCGGCTT 38280         AGT     ___  AA
             CAA                   TTGAAGCC   GGGGCA   CC  TCC
                                |||||||   ||||||   ||  |||
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                                AACTTCGG  CCCCGT  GG AGG
                                    C__    CCC CC
GAM1725 PLK     3' GGACTGGTGCCCTCCTCACT  18525   CC TG     A
                                AG AG GGGCACCA TCC
                                || || |||||||| |||
                                TC TC CCCGTGGT AGG
                                 AC CT      C
GAM1725 STK22D  3' GGTCCCCACTGGCCGCAA   50145    AA       C
                                TTG GCCAGTGGGG ACC
                                ||| |||||||||| |||
                                AAC CGGTCACCCC TGG
                                  GC       _
GAM1725 LOC124871 3' TGCTGCCCCACCAGCTTCAG  74818       CA      C
                                TTGAAGC GTGGGGCA CA
                                ||||||| |||||||| ||
                                GACTTCG CACCCCGT GT
                                    AC      C
GAM1725 LOC157349 3' GACTGGCTGCTGGCTCCGA   82341    A    TG GGCA  A
                                TTG AGCCAG G   CCA TC
                                ||| |||||| |   ||| ||
                                AGC TCGGTC C   GGT AG
                                  C    GT ____  C
GAM1725 LOC222550 5' GGATCAATATCGTGCTGGCTT 96018       G CACCA
                                AAGCCAGTG GG    ATCC
                                ||||||||| ||    ||||
                                TTCGGTCGT CT    TAGG
                                     G ATAAC
GAM1726 PIP5K1A  3' TATCCCACCCTGCCTTGATA  14520       A  CA C
                                TATCAAGG AGGG GG GTG
                                |||||||| |||| || |||
                                ATAGTTCC TCCC CC TAT
                                    G  A_ C
GAM1726 SOX11   3' ACCCACCCCCCCTTGGTA   13308       AA  CA C
                                TATCAAGG GGG GG GT
                                |||||||| ||| || ||
                                ATGGTTCC CCC CC CA
                                    CC  A_ _
GAM1726 CHL1    3' TGTTACCTTTCCTCAATA   22768    CA     CA
                                TAT AGGAAGGG GGCG
                                ||| |||||||| ||||
                                ATA TCCTTTCC TTGT
                                  AC      A_
GAM1726 EPB41L1  3' CATTCTGCCCTTCCCTGA   71104    A       C
                                TCA GGAAGGGCAGG GTG
                                ||| |||||||||| |||
                                AGT CCTTCCCGTCT TAC
                                  C       _
GAM1726 FLJ00060 3' CATACCCCCTGCCCTCCTCTGA 61741    _   A     CGTG
                                TCA AGGA GGGCAGG   ATG
                                ||| |||| |||||||   |||
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                                AGT TCCT CCCGTCC    TAC
                                  C   _      CCCA
GAM1726  FLJ10898  5'  CACCACAGCCCTTTCTCAATA  60126     CA       AGGC
                                TAT  AGGAAGGGC    GTG
                                |||  |||||||||    |||
                                ATA  TCTTTCCCG    CAC
                                  AC        ACAC
GAM1726  FLJ22557  3'  ATCATCCCATCCTTAATA    45581     C    A   CAGGC
                                TAT AAGGA GGG    GTGAT
                                ||| ||||| |||    |||||
                                ATA TTCCT CCC    TACTA
                                  A    A  _____
GAM1726  KIAA0574  3'  CATCCCCTGCCCTCCCCTGA   69808     A  A      CGT
                                TCA GG AGGGCAGG   GATG
                                ||| || ||||||||   ||||
                                AGT CC TCCCGTCC   CTAC
                                  C  C       C__
GAM1726  KIAA0632  3'  CACCTCAGAAACCCTTCCTTGA 32071          CA___  C
                                TCAAGGAAGGG     GG GTG
                                ||||||||||     || |||
                                AGTTCCTTCCC     CT CAC
                                      AAAGA  C
GAM1726  KIAA1354  5'  CAGTGACTGCCTTCCCTTGATA 61572        A      G  _
                                TATCAAGG AGGGCAG CG TG
                                |||||||| ||||||| || ||
                                ATAGTTCC TTCCGTC GT AC
                                     C      A  G
GAM1726  MGC20460  5'  CACCGCCTCCTACCCTTCTT   54901        C___    _
                                AGGAAGGG    AGGCG TG
                                ||||||||    ||||| ||
                                TTCTTCCC    TCCGC AC
                                     ATCC     C
GAM1726  LOC158476 3'  CACGCCCGCCCCCCCCATTGA  88186     _  AA_   A
                                TCAA GG   GGGC GGCGTG
                                |||| ||   |||| ||||||
                                AGTT CC   CCCG CCGCAC
                                  A  CCC    C
GAM1726  LOC90459  3'  CACACCCGCCTAATTTTTG    63550       A_   A  C
                                CAAGGA  GGGC GG GTG
                                ||||||  |||| || |||
                                GTTTTT  TCCG CC CAC
                                   AA    C  A
GAM1727  AQP2      3'  CTTGGGGGTTCTGGGAATGATG 6669     C       AG AGAA
                                CA CATTCCCA  A    TAAG
                                || ||||||||  |    ||||
                                GT GTAAGGGT  T    GTTC
                                 A       CT GGGG
GAM1727  GRLF1     3'  CTCCTTGGGAACGTGTA     79258       CA       A
                                TACAC  TTCCCAAG AG
                                |||||  |||||||| ||
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                                ATGTG  AAGGGTTC TC
                                  C_       C
GAM1727  MLANA    3'  CTCCTTTGGAATGGTGTA    19762          C   A
                                TACACCATTCC AAG AG
                                |||||||||| ||| ||
                                ATGTGGTAAGG TTC TC
                                      T   C
GAM1727  CHIC1    3'  CTTATTCTTTATAATGGT    82900       CCCAA
                                ACCATT    GAAGAATAAG
                                ||||||    ||||||||||
                                TGGTAA    TTTCTTATTC
                                   TA___
GAM1727  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CATTCCCA
           A                     TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM1727  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCATT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                     AGACG___
GAM1727  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860      CCA    CAA_
           TA                    TACA   TTCC    GAAGAATAAG
                                ||||   ||||    ||||||||||
                                ATGT   AAGG    TTTCTTATTC
                                  AA_    ATTG
GAM1727  HYPH     3'  CTTATTCTATTGACAGACATGG 96568        _ C__   GA
           TGTA                    TACACCAT TC   CAA  AGAATAAG
                                |||||||| ||   |||  ||||||||
                                ATGTGGTA AG   GTT  TCTTATTC
                                     C  ACA   A_
GAM1727  KIAA1579  3'  TACTCTTAGTGGTGTA     37154         CCCAAG    A
                                TACACCATT     AAGA TA
                                |||||||||     |||| ||
                                ATGTGGTGA     TTCT AT
                                     _______   C
GAM1727  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68742              _
                                TACACCATTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                          G
GAM1727  KIAA1877  3'  CTTATTCTTCTGCCATGAGT   66748      CCA__
                                ATTC    AGAAGAATAAG
                                ||||    ||||||||||
                                TGAG    TCTTCTTATTC
                                  TACCG
GAM1727  KIAA1906  3'  CTTATTCTTCTTGACTTTTGG  73571     TTCC_
                                CCA    CAAGAAGAATAAG
                                |||    ||||||||||||
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                                GGT    GTTCTTCTTATTC
                                  TTTCA
GAM1727 SR-BP1   3' ATTCTTCCTTTGGGGGTATG  20786   CC      __
                                CA  ATTCCCAA  GAAGAAT
                                ||  ||||||||  |||||||
                                GT  TGGGGGTT  CTTCTTA
                                 A_       TC
GAM1727 LOC90148 3' CTTATTCTTGCTGAGAATG   62340      C  AG
                                CATTC CA  AAGAATAAG
                                |||||  ||  |||||||||
                                GTAAG GT  TTCTTATTC
                                   A  CG
GAM1728 CYP4F3   3' ATTTTCAAAGTAAGTCTCTGCC 7994     T    A
             CT                   AG GCAGA ACTTACTTTGAAAGT
                                || |||||  ||||||||||||||||
                                TC CGTCT TGAATGAAACTTTTA
                                 C    C
GAM1728 GAS11    3' CTTCTCAGAGTGCCCCGCACT  9428       AGAAACT      _
                                AGTGC      TACTTTGA AAG
                                |||||      |||||||| |||
                                TCACG      GTGAGACT TTC
                                   CCCC___       C
GAM1728 ITPKB    3' TTCCTGAAGTCTCTGCATT   11070        A   ACTTT
                                AGTGCAGA ACTT     GAA
                                |||||||| ||||     |||
                                TTACGTCT TGAA     CTT
                                     C   GTC__
GAM1728 MYH11    3' CTTTCTACAGTTTTGCAC    11740        A  TACTTT
                                GTGCAGAA CT     GAAAG
                                |||||||| ||     |||||
                                CACGTTTT GA     CTTTC
                                     _  CAT___
GAM1728 MYH11    3' CTTTCTACAGTTTTGCAC    43431        A  TACTTT
                                GTGCAGAA CT     GAAAG
                                |||||||| ||     |||||
                                CACGTTTT GA     CTTTC
                                     _  CAT___
GAM1728 PIK3R1   3' ACCTTCAGAATAAGCTTCCCCA 69133     CA  A   C     A
             C                   GTG  GAA CTTA TTTGAA GT
                                |||  ||| |||| |||||| ||
                                CAC  CTT GAAT AGACTT CA
                                  CC   C    A     C
GAM1728 PLS1     3' ACTTTTCTGTAAGTTTCTATAC 12179      C        TTT
             T                    AGTG AGAAACTTAC   GAAAGT
                                |||| ||||||||||   ||||||
                                TCAT TCTTTGAATG   TTTTCA
                                  A         TC_
GAM1728 SERPINA4 3' CTCTTGGAGCAAGTTTCTGCCT 21704    T        A   TG A
                                AG GCAGAAACTT CTT  A AG
                                || ||||||||||  |||  | ||
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                                TC CGTCTTTGAA GAG  T TC
                                 _        C   GT C
GAM1728  DKFZp434G179 3'  ACTTTCAAAGTCTCCTACACT  80888      C  AAACTT
                                AGTG AG      ACTTTGAAAGT
                                |||| ||      ||||||||||
                                TCAC TC      TGAAACTTTCA
                                  A  CTC___
GAM1728  DKFZP434I1735 3'  TCTAGTGTAAATTATCTGCACT 89174         _  C    TTT_
                                AGTGCAGA AA TTAC    GA
                                |||||||| || ||||    ||
                                TCACGTCT TT AATG    CT
                                     A  A    TGAT
GAM1728  DKFZp761K1423 3'  ACCTTCAAAGTTTTCTCCAC   37933     C     CTT       A
                                GTG AGAAA   ACTTTGAA GT
                                ||| |||||   |||||||| ||
                                CAC TCTTT   TGAAACTT CA
                                  C    ___       C
GAM1728  FLJ12650  3'  CTTTCTGCAGTTTCTGACT    44822     G       TACTTT
                                AGT CAGAAACT     GAAAG
                                ||| ||||||||     |||||
                                TCA GTCTTTGA     CTTTC
                                  _       CGT___
GAM1728  FLJ20281  5'  ACTTTCAAAGTAAATTGGTCTG 92620      AAC__
                                CAGA     TTACTTTGAAAGT
                                ||||     ||||||||||||
                                GTCT     AATGAAACTTTCA
                                   GGTTA
GAM1728  KIAA0170  3'  ACTTTGGGCAAGTCTCTGTACT 28387         A    A   TG
                                AGTGCAGA ACTT CTT  AAAGT
                                |||||||| |||| |||  |||||
                                TCATGTCT TGAA GGG  TTTCA
                                     C    C   __
GAM1728  REG-IV    3'  TCAGGAGTAAGCTTCTAGAC   50218    GC    A      _
                                GT  AGAA CTTACTT TGA
                                ||  |||| ||||||| |||
                                CA  TCTT GAATGAG ACT
                                 GA    C      G
GAM1728  ROBO2     3'  ACTTTTATGTTTAAATTTTGCA 63153          ACTT_  TT
              CT                   AGTGCAGAA     AC  TGAAAGT
                                |||||||||     ||  |||||||
                                TCACGTTTT     TG  ATTTTCA
                                     AAATT  T_
GAM1728  SH3BGRL   3'  CATAGTAAGTTTCACACT     62621      CA        T
                                AGTG  GAAACTTACT TG
                                ||||  |||||||||| ||
                                TCAC  CTTTGAATGA AC
                                  A_         T
GAM1728  LOC203378 3'  CAAAGCAAGACTCTGCACT    92279         AA   A
                                AGTGCAGA  CTT CTTTG
                                ||||||||  ||| |||||
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                                TCACGTCT  GAA GAAAC
                                    CA   C
GAM1728  LOC203508 3'  AGGTAATAAAGTTCTGCACT   90936        AC___
                                AGTGCAGAA    TTACTT
                                |||||||||    ||||||
                                TCACGTCTT    AATGGA
                                     GAAAT
GAM1729  ADAR     3'  CCTCTCTCCTTTAGATGACAGA 8481        GC_   A
           C                     GTTTGTCG   AAAG AGAGAGG
                                ||||||||   |||| |||||||
                                CAGACAGT   TTTC TCTCTCC
                                    AGA   C
GAM1729  ADAR     3'  CCTCTCTCCTTTAGATGACAGA 32349       GC_   A
           C                     GTTTGTCG   AAAG AGAGAGG
                                ||||||||   |||| |||||||
                                CAGACAGT   TTTC TCTCTCC
                                    AGA   C
GAM1729  ADAR     3'  CCTCTCTCCTTTAGATGACAGA 32357       GC_   A
           C                     GTTTGTCG   AAAG AGAGAGG
                                ||||||||   |||| |||||||
                                CAGACAGT   TTTC TCTCTCC
                                    AGA   C
GAM1729  CHES1    3'  CCCTCTTCTTTGTTTTGGAC   19026    ___        A
                                GTC   GGCAAAGAAGAG GG
                                |||   |||||||||||| ||
                                CAG   TTGTTTCTTCTC CC
                                  GTT         _
GAM1729  IARS     5'  CCTCTCTTCCCTGCAGGAT   26417     G_   AA
                                GTC  GCA  GAAGAGAGG
                                |||  |||  |||||||||
                                TAG  CGT  CTTCTCTCC
                                  GA   CC
GAM1729  KCNMB1   3'  CCTCCCTTCTTTGTTTGA    15958     _      A
                                TCGG CAAAGAAG GAGG
                                |||| |||||||| ||||
                                AGTT GTTTCTTC CTCC
                                  T       C
GAM1729  LIMD1    3'  CTCTCTTCCCATCAAAT     27259      TC  CAAA
                                GTTTG  GG   GAAGAGAG
                                |||||  ||   ||||||||
                                TAAAC  CC   CTTCTCTC
                                  TA  _____
GAM1729  OVOL1    5'  CCTCTCTTCTCCACCAAGC   17065      TC  CAA
                                GTTTG  GG   AGAAGAGAGG
                                |||||  ||   ||||||||||
                                CGAAC  CC   TCTTCTCTCC
                                  CA  ___
GAM1729  PCDH11X  5'  CTCTCCTCTCCCAAACTT    28012       TC  CAA   A
                                AAGTTTG  GG   AGA GAGAG
                                |||||||  ||   ||| |||||
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                                TTCAAAC  CC   TCT CTCTC
                                   __ ___  C
GAM1729  PCDH11X  5'  CTCTCCTCTCCCAAACTT    53135       TC  CAA   A
                                AAGTTTG  GG   AGA GAGAG
                                |||||||  ||   ||| |||||
                                TTCAAAC  CC   TCT CTCTC
                                   __ ___  C
GAM1729  PCDH11X  5'  CTCTCCTCTCCCAAACTT    53142       TC  CAA   A
                                AAGTTTG  GG   AGA GAGAG
                                |||||||  ||   ||| |||||
                                TTCAAAC  CC   TCT CTCTC
                                   __ ___  C
GAM1729  PCDH11Y  5'  CTCTCCTCTCCCAAACTT    53179       TC  CAA   A
                                AAGTTTG  GG   AGA GAGAG
                                |||||||  ||   ||| |||||
                                TTCAAAC  CC   TCT CTCTC
                                   __ ___  C
GAM1729  PCDH11Y  5'  CTCTCCTCTCCCAAACTT    53187       TC  CAA   A
                                AAGTTTG  GG   AGA GAGAG
                                |||||||  ||   ||| |||||
                                TTCAAAC  CC   TCT CTCTC
                                   __ ___  C
GAM1729  PIM2     3'  CCTCCTACTACCACCACACAAA 60653        C_  CAA_  A  A
           CTT                   AAGTTTGT  GG    AG AG GAGG
                                |||||||| ||    || || ||||
                                TTCAAACA  CC    TC TC CTCC
                                    CA  ACCA  A  _
GAM1729  PKLR     3'  CCTCTCTTCTCTATTCCTGAC  6106       C  ___
                                GTCGG AA   AGAAGAGAGG
                                ||||| ||   ||||||||||
                                CAGTC TT   TCTTCTCTCC
                                  C  ATC
GAM1729  PSG1     3'  CTATTTTGCAAACAAACTT   23578        CG     A
                                AAGTTTGT  GCAAAG AG
                                ||||||||  |||||| ||
                                TTCAAACA  CGTTTT TC
                                    AA     A
GAM1729  ACTR1A   3'  CCTCCCTTCTCTTAGCCCAAGC 63650      TC  _ _    A
                                GTTTG  GGC AA AGAAG GAGG
                                |||||  ||| || ||||| ||||
                                CGAAC  CCG TT TCTTC CTCC
                                  __  A  C    C
GAM1729  DKFZp434A2417 5'  CCTGATTCCCGCCGACAGAC   66678         AAA   GAG
                                GTTTGTCGGC   GAA   AGG
                                ||||||||||   |||   |||
                                CAGACAGCCG   CTT   TCC
                                     CC_   AG_
GAM1729  FLJ10210 5'  CCCCTCCTCCTGACAAAC    36359        CAAA  A   A
                                GTTTGTCGG    GA GAG GG
                                |||||||||    || ||| ||
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                                CAAACAGTC   CT CTC CC
                                    ____ C  C
GAM1729 FLJ10970 3' CTTCTTTAACGACAAACTT   37478        GC
                                AAGTTTGTCG  AAAGAAG
                                ||||||||||  |||||||
                                TTCAAACAGC  TTTCTTC
                                     AA
GAM1729 KIAA0843 3' CCTCTCTTCTCCTCTCCAAAC 30797     TC  CAA
                                GTTTG  GG   AGAAGAGAGG
                                |||||  ||   ||||||||||
                                CAAAC  CT   TCTTCTCTCC
                                   CT  CC_
GAM1729 KIAA1870 5' CTCTCTTCTCCCAAGACT    52899     GTC  CAA
                                AGTTT   GG   AGAAGAGAG
                                |||||   ||   |||||||||
                                TCAGA   CC   TCTTCTCTC
                                   AC_  ___
GAM1729 SGP28    3' CCTCTCTTCTCTTTGACAAAAC 21347      _    CAA
             TT                  AAGTTT GTCGG   AGAAGAGAGG
                                 |||||| |||||   ||||||||||
                                 TTCAAA CAGTT   TCTTCTCTCC
                                    A    TC_
GAM1729 ZAK      3'  TCCCTTCCCCACTGACAAACTT 56948         CAAA   A
                                 AAGTTTGTCGG    GAAG GA
                                 ||||||||||    |||| ||
                                 TTCAAACAGTC    CTTC CT
                                       ACCC    C
GAM1729 ZFP36L2   5'  CCTCTCCTCTCGCCCCCCGGCA 23531          CAA___   A
             AACTT                  AAGTTTGTCGG     AGA GAGAGG
                                    ||||||||||      ||| ||||||
                                    TTCAAACGGCC     TCT CTCTCC
                                       CCCCGC   C
GAM1729 LOC157623 5' CCTCTCTTCTTTACAGATT    82413       CGGC
                                 AGTTTGT    AAAGAAGAGAGG
                                 |||||||    ||||||||||||
                                 TTAGACA    TTTCTTCTCTCC
                                      ____
GAM1729 LOC55885  3'  CCCTCTTCCGAGTTGCCCACAA 38441        C    A___     A
             ACTT                   AAGTTTGT GGCAA    GAAGAG GG
                                    |||||||| |||||    |||||| ||
                                    TTCAAACA CCGTT    CTTCTC CC
                                       C     GAGC     _
GAM1729 LOC57862  3'  CCTCTCTTCCCACTGCAAATTT 41321        T   CAAA
                                 AAGTTTG CGG    GAAGAGAGG
                                 |||||||  |||    |||||||||
                                 TTTAAAC GTC    CTTCTCTCC
                                    _   ACC_
GAM1729 LOC90841  3'  CCTCTCTTCCTTCTTTCAACCT 64866     T   TC  C  A
             T                   AAG TTG  GG AA GAAGAGAGG
                                 ||| |||  || || |||||||||
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                                TTC AAC  TC TT CTTCTCTCC
                                  C   TT  _  C
GAM1730  CDKN1A    5'  AGGCCGAGCCAAGCGTGCC    55266        CGAA  TC    C
                                GGCACGCT    CT  CGGC CT
                                |||||||||    ||  |||| ||
                                CCGTGCGA    GA  GCCG GA
                                     ACC_  ___    A
GAM1730  DKFZp761A052 5'  GGCCGGAACAAGCGTAGC     73377    _     CGAAC
                                GC ACGCT     TTCCGGCC
                                || |||||     ||||||||
                                CG TGCGA     AAGGCCGG
                                 A    AC____
GAM1730  KIAA0415  3'  GGCTCAGCCCGGCGTGCCA    94167        T  AA  TCC
                                TGGCACGC CG  CT   GGCC
                                |||||||| ||  ||   ||||
                                ACCGTGCG GC  GA   TCGG
                                     _  CC  C__
GAM1730  PDE4DIP   5'  AGAGCCGGAAGCCCGCTGACC  97172    _  C  TCGAA       C
                                GG CA GC     CTTCCGGC CT
                                || || ||     |||||||| ||
                                CC GT CG     GAAGGCCG GA
                                 A  _  CCC__       A
GAM1730  SCYB14    5'  GGCCGGAAGGCGCGCC      18088     A   TCGAA       C
                                GGC CGC     CTTCCGGC C
                                ||| |||     |||||||| |
                                CCG GCG     GAAGGCCG G
                                  C  ______        A
GAM1730  LOC144100 3'  AGGGCCGGAGCAGGAGCATGCT 77183       C    GAAC
              A                   TGGCA GCTC    TTCCGGCCCT
                                |||||| ||||    ||||||||||
                                ATCGT CGAG    GAGGCCGGGA
                                   A    GAC_
GAM1730  LOC145934 5'  AGGGCCGGAGAAGCGAGCGGCC 84558      A     AAC
              A                   TGGC CGCTCG   TTCCGGCCCT
                                |||| ||||||   ||||||||||
                                ACCG GCGAGC   GAGGCCGGGA
                                   _     GAA
GAM1730  LOC148696 5'  AGGGCCGAGAAGGCGCGTGCCA 85344         TCGAA   _
                                TGGCACGC     CTTC CGGCCCT
                                ||||||||     |||| |||||||
                                ACCGTGCG     GAAG GCCGGGA
                                     CG____    A
GAM1730  LOC253263 3'  AGGGCCGGCTCGTGAACAGCCA 98813      ACGCT_   ACTT
                                TGGC     CGA    CCGGCCCT
                                ||||     |||    ||||||||
                                ACCG     GCT    GGCCGGGA
                                  ACAAGT   C____
GAM1730  LOC254559 5'  AGGGCGCGTGGTTCGGCGTGCC 98380         T     TC  _
              A                   TGGCACGC CGAACT  CG GCCCT
                                ||||||| ||||||  || |||||
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                                ACCGTGCG GCTTGG  GC CGGGA
                                     _     T_  G
GAM1730  LOC256444 5'  AGGGCCGGAGAAGCGAGCGGCC 98382      A     AAC
              A                   TGGC CGCTCG   TTCCGGCCCT
                                  |||| ||||||   ||||||||||
                                  ACCG GCGAGC   GAGGCCGGGA
                                    _     GAA
GAM1731  SLC25A15  3'  CAAGTGGAAATGAGGAACGGAA 27289     ATCA  AG   CC
                                  TTC    CC  TCA  TCCACTTG
                                  |||    ||  |||  ||||||||
                                  AAG    GG  AGT  AGGTGAAC
                                    GCAA  __   AA
GAM1731  FLJ12581  3'  CAAGTACGAATTGGTGATGAA  46331          CACC  C_
                                  TTCATCACCAGT    TC  ACTTG
                                  ||||||||||||    ||  |||||
                                  AAGTAGTGGTTA    AG  TGAAC
                                        _____  CA
GAM1731  KIAA1193  3'  GAGGTGACTGATGAGAA     68272     A   C
                                  TTC TCA CAGTCACCTC
                                  ||| ||| ||||||||||
                                  AAG AGT GTCAGTGGAG
                                    _   A
GAM1731  LOC113523 3'  CAAGTACATGGGACTGGTGAT  73412          A  TCC_
                                  ATCACCAGTC CC    ACTTG
                                  |||||||||| ||    |||||
                                  TAGTGGTCAG GG    TGAAC
                                        _  TACA
GAM1731  LOC147976 3'  CAAGTAAAGGAGCAAGTGATGG 79286        CA  CA   CC
              A                   TTCATCAC  GT  CCT  ACTTG
                                  ||||||||  ||  |||  |||||
                                  AGGTAGTG  CG  GGA  TGAAC
                                       AA  A_   AA
GAM1731  LOC149705 3'  GGAGATGATAGTGATGAA    85784         CA    C
                                  TTCATCAC  GTCA CTCC
                                  ||||||||  |||| ||||
                                  AAGTAGTG  TAGT GAGG
                                       A_    A
GAM1731  LOC149722 5'  CAAGTGGAGGGTGAGCAAGATG 85750       ACCAG    _
              AA                    TTCATC    TCACC TCCACTTG
                                    ||||||    ||||| ||||||||
                                    AAGTAG    AGTGG AGGTGAAC
                                       AACG_    G
GAM1731  LOC153688 3'  CAAGTGGAGGTGGTCGTAAGTG 87297      CAG___
              A                    TCAC     TCACCTCCACTTG
                                   ||||     ||||||||||||
                                   AGTG     GGTGGAGGTGAAC
                                     AATGCT
GAM1731  LOC256021 3'  GTGAAGGTGACAGTGATGAA  98280         CA      C
                                  TTCATCAC  GTCACCT CAC
                                  ||||||||  ||||||| |||
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                                AAGTAGTG  CAGTGGA GTG
                                   A_      A
GAM1732 ICMT     3'  AGGTGAGACGCTGGCTTCA   25733       G       CGAT
                                TGAAGC AGCGTCTT    GCCT
                                |||||| ||||||||    ||||
                                ACTTCG TCGCAGAG    TGGA
                                   G       _____
GAM1732 PCSK5    5'  GCGGAGGACGCCCGCCCCA   21674    AA  A       GA
                                TG  GCG GCGTCTTC  TGC
                                ||  ||| ||||||||  |||
                                AC  CGC CGCAGGAG  GCG
                                 CC   C       __
GAM1732 RFP      5'  AGGCATCGGCCCGGCCACTC   22506     C_   T__
                                GAG  GTC   TCGATGCCT
                                |||  |||   |||||||||
                                CTC  CGG   GGCTACGGA
                                  AC   CCC
GAM1732 DKFZP566K023 3'  AGGCATCATTCTAACTTCA   31924       CG  C  CTTC
                                TGAAG  AG GT    GATGCCT
                                |||||  || ||    |||||||
                                ACTTC  TC TA    CTACGGA
                                   AA  T  _____
GAM1732 FER1L4   3'  AGGAGACAGACGTTCACTTCA  48111       C       TCGATG
                                TGAAG GAGCGTCT     CCT
                                ||||| ||||||||     |||
                                ACTTC CTTGCAGA     GGA
                                   A       CAGA__
GAM1732 FLJ11126 3'  TAGGCATCGTGGAACCAGCTCC 37654    A   GAGCG   T
             A                    TG AGC     TCT CGATGCCTA
                                || |||     ||| |||||||||
                                AC TCG     AGG GCTACGGAT
                                 C   ACCA_   T
GAM1732 KIAA1229 3'  TAGGCATCACGCTACCTGACTT 62759       _ ____     CTTC
             CA                   TGAAG CG   AGCGT    GATGCCTA
                                ||||| ||   |||||   ||||||||
                                ACTTC GT   TCGCA    CTACGGAT
                                   A  CCA    _____
GAM1733 ACVRL1   5'  TTTATTAGGAGGGAGTGGTG   5240          AAGAAG
                                CACCACTCCC      AATAAG
                                ||||||||||      ||||||
                                GTGGTGAGGG      TTATTT
                                     AGGA__
GAM1733 BCL11B   3'  TTTGTTTTTGGGGTGGGGGGTG 57582       A_  __       G  TAAG
             TG                   TACACC  CT  CCCAAGAA AA
                                ||||||  ||  |||||||| ||
                                GTGTGG  GG  GGGTTTTT TT
                                   GG  TG       G  T
GAM1733 C18orf1  3'  CTTCGTGTGGGAGTGGTGTG   60865           A__
                                TACACCACTCCCA   GAAG
                                ||||||||||||   ||||
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                                GTGTGGTGAGGGT  CTTC
                                       GTG
GAM1733 ITPR3    3' CTTGTTTTTCTCCTTTTGGTGT 11085       CTCCCA
             A                  TACACCA     AGAAGAATAAG
                                |||||||     ||||||||||
                                ATGTGGT     TCTTTTTGTTC
                                   TTTCC_
GAM1733 KCNAB1   3' GTTTGTTTTTTTTTGAAGGGGG 61585          ____
             TGGTGTG               TACACCACTCCC   AAGAAGAATAAG  T
                                |||||||||||   ||||||||||||  |
                                GTGTGGTGGGGG   TTTTTTTTGTTT  G
                                       AAGT
GAM1733 KRAS2    3' CTTATTTTTCTTACCAAGTGTG 54123    C  CCC_
                                CAC ACT   AAGAAGAATAAG
                                ||| |||   ||||||||||||
                                GTG TGA   TTCTTTTTATTC
                                  _  ACCA
GAM1733 KRAS2    3' CTTATTTTTCTTACCAAGTGTG 54124    C  CCC_
                                CAC ACT   AAGAAGAATAAG
                                ||| |||   ||||||||||||
                                GTG TGA   TTCTTTTTATTC
                                  _  ACCA
GAM1733 LIFR     3' TTTGTTTTTTTTGGTTGGTTG  11315   C  CTC
                                A ACCA  CCAAGAAGAATAAG
                                | ||||  ||||||||||||||
                                G TGGT  GGTTTTTTTTGTTT
                                 T   T__
GAM1733 MEN1     5' CTTGTTTTTTTCCTTTTGGTG  56348     CTCCCA
                                CACCA     AGAAGAATAAG
                                |||||     ||||||||||
                                GTGGT     TTTTTTTGTTC
                                   TTTCC_
GAM1733 MLLT7    3' TTGTGCCTGGGAGTGTGTG    21043    _     AGAAGA
                                CAC CACTCCCA     ATAA
                                ||| ||||||||     ||||
                                GTG GTGAGGGT     TGTT
                                  T       CCG___
GAM1733 SIAH1    3' TTTGTTTTTGCCGTGGGAGTGT 13128    _     AG__
             GTG                  CAC CACTCCCA    AAGAATAAG
                                ||| ||||||||   |||||||||
                                GTG GTGAGGGT    TTTTTGTTT
                                  T       GCCG
GAM1733 SLC7A6   3' TTTGTTTTTGTGGTGGGTGCTG 15646     C   _  AG
             TG                   TACA CACTC CCA  AAGAATAAG
                                |||| ||||| |||  |||||||||
                                GTGT GTGGG GGT  TTTTTGTTT
                                  C    T  G_
GAM1733 STAT6    5' ATTTTTCTTTTTGGTGGTGGTG 13448       TC        TAAG
                                CACCAC  CCAAGAAGAA
                                ||||||  ||||||||||
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                                GTGGTG  GGTTTTTCTT
                                   GT        TTTAT
GAM1733  TCF8     3'  CTTGTTTTTTTAAGAGTGTGTG 48429     _    CCA
                                CAC CACTC   AGAAGAATAAG
                                ||| |||||   ||||||||||
                                GTG GTGAG   TTTTTTTGTTC
                                  T    AA_
GAM1733  B3GNT7   3'  TTGTTCTTGGCTGGTGGGTG   71685     A    C_     G
                                TAC CCACT  CCAAGAA AA
                                ||| |||||  ||||||| ||
                                GTG GGTGG  GGTTCTT TT
                                  _    TC      G
GAM1733  BCDO     3'  TTATTCTTTCTGTGGGTG    34287      C  AG
                                CACTC CA  AAGAATAA
                                ||||| ||  ||||||||
                                GTGGG GT  TTCTTATT
                                   T  CT
GAM1733  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
              A                  TACAC       AGAAGAATAAG
                                 |||||       ||||||||||||
                                 ATGTG       TCTTCTTATTC
                                    TACTCCC_
GAM1733  EPN2     3'  TTTATTTTTCTTTGACTCGTGT 31046      CAC  CC
              G                  TACAC   TC  AAGAAGAATAAG
                                 |||||   ||  ||||||||||||
                                 GTGTG   AG  TTCTTTTTATTT
                                    CTC  T_
GAM1733  FLJ13855 3'  GGGTATTTTTCTTGGGGGTGGA 43853     A              AG
              GTA                   TAC CCACTCCCAAGAAGAATA
                                 ||| ||||||||||||||||||
                                 ATG GGTGGGGGTTCTTTTTAT
                                   A              GGGA
GAM1733  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                 TACACCACT       GAATAAG
                                 |||||||||       |||||||
                                 ATGTGGTGA       TTTATTC
                                       AGACG___
GAM1733  FLJ32865  3'  TTTGTTGGGGGTGGGGTG    58824     A        G
                                 TAC CCACTCCCAA AAG
                                 ||| |||||||||| |||
                                 GTG GGTGGGGGTT TTT
                                   G         G
GAM1733  GRP3     3'  TTGTTCTTCTTGGTGTG     31742     TC
                                 CAC  CCAAGAAGAATAA
                                 |||  ||||||||||||
                                 GTG  GGTTCTTCTTGTT
                                   T_
GAM1733  HAND1    3'  TTTGTTCTTCGAATCGTGGTG  17880       TCCCAA
                                 CACCAC     GAAGAATAAG
                                 ||||||     ||||||||||
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                                GTGGTG     CTTCTTGTTT
                                   CTAAG_
GAM1733  KIAA0562  3'  TTTGTTTTGCGGGGGTGGTG   28834          AAGA
                                CACCACTCCC    AGAATAAG
                                ||||||||||    ||||||||
                                GTGGTGGGGG    TTTTGTTT
                                     CG__
GAM1733  KIAA0871  5'  TTTATTTTTTTGGTGTGTGTGT 31023      _  TC        ATAAG
              G                   TACAC CAC  CCAAGAAGA
                                ||||| |||  |||||||||
                                GTGTG GTG  GGTTTTTTT
                                   T  T_       ATTT
GAM1733  KIAA0970  3'  TTTGTTTTTTTTGTTAGGGTG  30622      A  CC
                                CACC CT  CAAGAAGAATAAG
                                |||| ||  ||||||||||||
                                GTGG GA  GTTTTTTTTGTTT
                                  _  TT
GAM1733  KIAA1240  3'  TTTATTTTTAGGGAGTGGGTA  67297      A       AAG
                                TAC CCACTCCC   AAGAATAAG
                                ||| ||||||||   |||||||||
                                ATG GGTGAGGG   TTTTTATTT
                                  _       A__
GAM1733  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68742             _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                        G
GAM1733  KIAA1750  3'  TTTATTTTTTTGTTCTAGGTGT 68815        ACTCCCA
              G                   TACACC      AGAAGAATAAG
                                ||||||      ||||||||||||
                                GTGTGG      TTTTTTTATTT
                                   ATCTTG_
GAM1733  MAP2K3    3'  CTTGTTTTTCTTGCATGGT    59686      CTCC
                                ACCA    CAAGAAGAATAAG
                                ||||    ||||||||||||||
                                TGGT    GTTCTTTTTGTTC
                                  AC__
GAM1733  MLN64     3'  CTTGTTGGGGAGTGGGTG     96062      A       _  G
                                TAC CCACTCCC AA AAG
                                ||| |||||||| || |||
                                GTG GGTGAGGG TT TTC
                                  _       G  G
GAM1733  NY-REN-41 3'  TTTGTTTTTCTATCCTGGTGG  55564       CCCA_
                                CCACT     AGAAGAATAAG
                                |||||     ||||||||||||
                                GGTGG     TCTTTTTGTTT
                                   TCCTA
GAM1733  PRO1489   5'  TTTGTTTTTCGTGTGTGTGTG  38334      _  TCCCAA
                                TACAC CAC     GAAGAATAAG
                                ||||| |||     ||||||||||
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                                GTGTG GTG     CTTTTTGTTT
                                  T   TG____
GAM1733  SEC15L   3'  TTTGTTCTACTTGGGTGGT   72731     CT     A
                                ACCA  CCCAAG AGAATAAG
                                ||||  |||||| ||||||||
                                TGGT  GGGTTC TCTTGTTT
                                  __     A
GAM1733  SHAPY    3'  TTTGTTCTTTTTGGAACTGTG  57915     TC__
                                CAC    CCAAGAAGAATAAG
                                |||    ||||||||||||||
                                GTG    GGTTTTTCTTGTTT
                                 TCAA
GAM1733  STAM2    3'  GTTTTTCTTCCTGCAATGTGGT 20707        TCC_  A     TAAG
            GTG                   TACACCAC    CA GAAGAA
                                ||||||||    || ||||||
                                GTGTGGTG    GT CTTCTT
                                     TAAC  C     TTTGT
GAM1733  TUBGCP3  3'  TTTATTTTTTTTTAGTGTTGTA 21982     C    CCC
                                TACA CACT   AAGAAGAATAAG
                                |||| ||||   ||||||||||||
                                ATGT GTGA   TTTTTTTTATTT
                                  T    T__
GAM1733  ZNF220   3'  CTTGTTTTTTTACCACCTGGTG 23157      CTCCCA
                                CACCA     AGAAGAATAAG
                                |||||     ||||||||||
                                GTGGT     TTTTTTTGTTC
                                   CCACCA
GAM1733  LOC121219 5'  TTGTTCTATGGGTGGGTG    74493     ACT    AGA
                                CACC   CCCA   AGAATAA
                                ||||   ||||   |||||||
                                GTGG   GGGT   TCTTGTT
                                  GT_    A__
GAM1733  LOC143146 3'  TTTGTTGGAGGTGGTGTA    60767        TC    G
                                TACACCAC  CCAA AAG
                                ||||||||  |||| |||
                                ATGTGGTG  GGTT TTT
                                     GA    G
GAM1733  LOC146445 3'  TTGTTCTTTGTGTGGTTG    84687    C    TCCCAA
                                A ACCAC     GAAGAATAA
                                | |||||     |||||||||
                                G TGGTG     TTTCTTGTT
                                 T    TG____
GAM1733  LOC150174 3'  TTTATTTTTTTTTACAATGGTG 80444      CTCCC
                                CACCA     AAGAAGAATAAG
                                |||||     ||||||||||||
                                GTGGT     TTTTTTTTATTT
                                   AACAT
GAM1733  LOC150213 3'  TTTATTTTTTTTACAATGGTG  75363      CTCCC
                                CACCA     AAGAAGAATAAG
                                |||||     ||||||||||||
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                                GTGGT    TTTTTTTTATTT
                                   AACA_
GAM1733  LOC150236 3'  TTTATTTTTTTTACAATGGTG  80505      CTCCC
                                CACCA    AAGAAGAATAAG
                                |||||    ||||||||||||
                                GTGGT    TTTTTTTTATTT
                                   AACA_
GAM1733  LOC154084 3'  CTTGTTTTTTTAGTAGGTGTG  87378      _  CCCA
                                TACACC ACT    AGAAGAATAAG
                                |||||| |||    ||||||||||||
                                GTGTGG TGA    TTTTTTTGTTC
                                   A  ____
GAM1733  LOC170261 3'  TTTATTCTTTGTGAAAGTGGT  83472      CC  A
                                ACCACT  CA GAAGAATAAG
                                ||||||  || ||||||||||
                                TGGTGA  GT TTTCTTATTT
                                   AA  G
GAM1733  LOC199692 3'  CTTGTTCTTCTGCTGTAGTGTG 59926      C  TCCCA
                                TACAC AC     AGAAGAATAAG
                                ||||| ||     ||||||||||||
                                GTGTG TG     TCTTCTTGTTC
                                   A  TCG__
GAM1733  LOC203414 3'  CTTGTCAACTGGGGGTGATGTG 90913      C       A AA  A
                                TACA CACTCCCA G  GA TAAG
                                |||| |||||||| |  || ||||
                                GTGT GTGGGGGT C  CT GTTC
                                  A       _ AA  _
GAM1733  LOC222256 3'  TTTTTCTTGTGGTGT      95915        TCCC
                                ACACCAC    AAGAAGAA
                                |||||||    ||||||||
                                TGTGGTG    TTCTTTTT
                                     ____
GAM1733  LOC257051 3'  TTTATTCTTTGTGAAAGTGGT  98054      CC  A
                                ACCACT  CA GAAGAATAAG
                                ||||||  || ||||||||||
                                TGGTGA  GT TTTCTTATTT
                                   AA  G
GAM1733  LOC92303  3'  TTATTTTTTTTGAGGTGG    69400      CC
                                CCACT  CAAGAAGAATAA
                                |||||  ||||||||||||
                                GGTGG  GTTTTTTTTATT
                                   A_
GAM1734  DGCR2     3'  GGGGCCGGTCAGACACGTAG   18906    T     CA   CTCTT
                                CT CGTGTC  ACC     GCCCT
                                || ||||||  |||    |||||
                                GA GCACAG  TGG     CGGGG
                                 T     AC   C____
GAM1734  HMGE      3'  GGCAAGAGAGTTGAAACAT    73105      C_   C
                                GTGT  CAAC CTCTTGCC
                                ||||  |||| ||||||||
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                                TACA  GTTG GAGAACGG
                                  AA   A
GAM1734  PIK4CB   3'  GGCAAGAAACACGAAG     12132        CCAACCC
                                CTTCGTGT     TCTTGCC
                                ||||||||     |||||||
                                GAAGCACA     AGAACGG
                                   A_______
GAM1734  ARG99    3'  AGGGCAAGAAGGTCTGAGAGG  50010     GTG  CA   C
                                CTTC   TC  ACC TCTTGCCCT
                                ||||   ||  ||| |||||||||
                                GGAG   AG  TGG AGAACGGGA
                                  ___  TC   A
GAM1734  FLJ10748 3'  GCGAGAATTGGACATGAAG   37102          CCC
                                CTTCGTGTCCAA   TCTTGC
                                ||||||||||||   ||||||
                                GAAGTACAGGTT   AGAGCG
                                      A__
GAM1734  FLJ13441 3'  GAGTGGAGTCATACACGAAG   43913        CCA  _  T
                                CTTCGTGT   AC CC CTT
                                ||||||||   || || |||
                                GAAGCACA   TG GG GAG
                                     TAC  A  T
GAM1734  KIAA0239 5'  AGGGCAAGAAGAGTGACTCGAA 31615      T   CA  C  _
           G                     CTTCG GTC  AC CT CTTGCCCT
                                ||||| |||  || || ||||||||
                                GAAGC CAG  TG GA GAACGGGA
                                   T   __  A  A
GAM1734  KIAA0435 3'  AGGACAGTGATTAGACACGAAG 29656         C  CCC  _  C
                                CTTCGTGTC AA   TC TTG CCT
                                |||||||||  ||   || ||| |||
                                GAAGCACAG TT   AG GAC GGA
                                     A  ___  T   A
GAM1734  KIAA0976 3'  AGGGCAAGAATTCACACGTAG  30547    T    CCAACCC
                                CT CGTGT      TCTTGCCCT
                                ||  |||||      |||||||||
                                GA GCACA      AGAACGGGA
                                 T    CTTA___
GAM1734  KIAA1036 3'  AGGGCAAGAGGCTGCAGGAAG  30484     G   CCAAC
                                CTTC TGT    CCTCTTGCCCT
                                ||||  |||    ||||||||||
                                GAAG ACG    GGAGAACGGGA
                                  G   TC___
GAM1734  KIAA1456 5'  GGCAAGAGAATTGCTTGAA    67560     TGTC   CC
                                TTCG    CAA  CTCTTGCC
                                ||||    |||  ||||||||
                                AAGT    GTT  GAGAACGG
                                  TC__   AA
GAM1734  PRO2037  3'  GGCAAGAGGATTGCTTGA    38396     TGTC   C
                                TCG    CAA CCTCTTGCC
                                |||    ||| |||||||||
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                                AGT   GTT GGAGAACGG
                                  TC__  A
GAM1734  SERF2    5'  AGGATGGCTGACACGAAG    20487        CAA  C
                                CTTCGTGTC   CC TCTT
                                |||||||||   || ||||
                                GAAGCACAG   GG AGGA
                                     TC_  T
GAM1734  SLC38A4  5'  GCAAGTTGGACAGAAG     36342     G      CCTC
                                CTTC TGTCCAAC   TTGC
                                |||| ||||||||   ||||
                                GAAG ACAGGTTG   AACG
                                  _     _____
GAM1734  SSH2     3'  GGAAGCAGGTTGGACAGAA   62892     G      CT   G
                                TTC TGTCCAACC  CTT CC
                                ||| |||||||||  ||| ||
                                AAG ACAGGTTGG  GAA GG
                                  _       AC  _
GAM1734  TBX21    3'  CAAGAAAGTCTTGGGCATGAAG 26247          CC __
                                CTTCGTGTCCAA  C  TCTTG
                                ||||||||||||  |  |||||
                                GAAGTACGGGTT  G  AGAAC
                                       CT AA
GAM1734  LOC148764 5'  CAAGAGGGCCTTGTGCAAGA   79733    G  TC  __
                                TC TG  CAA  CCCTCTTG
                                || ||  |||  ||||||||
                                AG AC  GTT  GGGAGAAC
                                 A  GT   CC
GAM1734  LOC149876 5'  AGAGCAAGAAGGCGTACACGAG 80350        CCA  _  _    C
            G                    CTTCGTGT   AC CCT CTTGC CT
                                ||||||||   || ||| ||||| ||
                                GGAGCACA   TG GGA GAACG GA
                                     ___  C   A    A
GAM1734  LOC167829 5'  AGGGCAAGAAAGTCAGCAC   83571     CCA  CC
                                GTGT   AC  TCTTGCCCT
                                ||||   ||  |||||||||
                                CACG   TG  AGAACGGGA
                                  AC_  AA
GAM1734  LOC199786 3'  AGGTGTACAGGATGGAACACGA 89741        _  AC   CT   _
            AG                   CTTCGTGT CCA  CCT  TGC CCT
                                ||||||| |||  |||  ||| |||
                                GAAGCACA GGT  GGA  ATG GGA
                                     A  A_  C_  T
GAM1734  LOC96810  3'  GGCAAGAGGAACCAGAAG    71086     G  TCCAAC      C
                                CTTC TG     CCTCTTGC C
                                |||| ||     |||||||| |
                                GAAG AC     GGAGAACG G
                                  _ CAA___       A
GAM1735  DSC3     3'  TACAATTAGGTCTTTGTCA   10445     TGC
                                TGAT   AGACCTAATTGTA
                                ||||   ||||||||||||
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                              ACTG  TCTGGATTAACAT
                                TT_
GAM1735 DSC3    3' TACAATTAGGTCTTTGTCA  44633    TGC
                              TGAT  AGACCTAATTGTA
                              ||||  ||||||||||||
                              ACTG  TCTGGATTAACAT
                                TT_
GAM1735 POU4F1  3' ACAATTAGGTCTCACTCTGGT 21755    T T C
                              ACCA GA TG AGACCTAATTGT
                              |||| || || ||||||||||||
                              TGGT CT AC TCTGGATTAACA
                                _ C _
GAM1735 SULT1C2 3' ACATTTTCTACAATCATG   22704      C  CCT T
                              CATGATTG AGA  AA TGT
                              |||||||| |||  || |||
                              GTACTAAC TCT  TT ACA
                                   A  ___ T
GAM1735 LOC118851 5' TACAATCAGGGCAAACAATGGT 76017     GA_  AGA  A
                              ACCAT  TTGC  CCT ATTGTA
                              |||||  ||||  ||| ||||||
                              TGGTA  AACG  GGA TAACAT
                                 ACA  ___  C
GAM1735 LOC201799 3' TACAATTGTTTTCTGAATCAT 90493     G   CC_
                              ATGATT CAGA  TAATTGTA
                              |||||| ||||  ||||||||
                              TACTAA GTCT  GTTAACAT
                                _  TTT
GAM1735 LOC257101 5' ACAATTAGGTTGTTGTCATAGG 98692   _   T   A
                              CC ATGAT GCAG CCTAATTGT
                              || ||||| |||| |||||||||
                              GG TACTG TGTT GGATTAACA
                               A   T  _
GAM1736 ADD3    3' TTCTCCATAATATCTGTTA  34169    G  C   AACC
                              TAA AGA ATTG   TGGAGAA
                              ||| ||| ||||   |||||||
                              ATT TCT TAAT   ACCTCTT
                                G  A  ____
GAM1736 ASIC4   3' TCTCCAGGCCCAGCTCCCCTCT 38540    ACA__  AA
                              AGAG   TTG CCTGGAGA
                              ||||   |||  ||||||||
                              TCTC   GAC  GGACCTCT
                                CCCTC  CC
GAM1736 ATP12A  3' CTCCCTTCCTATGTCTCT   9815       T_  CCT
                              AGAGACAT  GAA  GGAG
                              ||||||||  |||  ||||
                              TCTCTGTA  CTT  CCTC
                                   TC  C__
GAM1736 CD79A   3' CTTCTCCAGGCCAGGCCTC  10121    ACA  AA
                              GAG  TTG  CCTGGAGAAG
                              |||  |||  ||||||||||
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                                CTC  GAC  GGACCTCTTC
                                  CG_  C_
GAM1736  CD79A    3'  CTTCTCCAGGCCAGGCCTC   41487    ACA  AA
                                GAG  TTG  CCTGGAGAAG
                                |||  |||  ||||||||||
                                CTC  GAC  GGACCTCTTC
                                  CG_  C_
GAM1736  CYP1A2   3'  CTTCTCCAGCCTCGGCCTC   7513     ACA  AC
                                GAG  TTGA  CTGGAGAAG
                                |||  ||||  |||||||||
                                CTC  GGCT  GACCTCTTC
                                  C__   CC
GAM1736  EPB72    3'  CTTCTCCAGGTCATATGTGCCT 15872     AG   _  A
           TA                     TAAG  ACAT TGA CCTGGAGAAG
                                ||||  |||| ||| ||||||||||
                                ATTC  TGTA ACT GGACCTCTTC
                                  CG   T  _
GAM1736  EPHB3    3'  CTTCTCCAGGCCTGTGTTCCCT 16703    ___   TGAA
           C                     GAG  ACAT   CCTGGAGAAG
                                |||  ||||   ||||||||||
                                CTC  TGTG   GGACCTCTTC
                                  CCT   TCC_
GAM1736  IGFBP4   3'  CTTCCCCAGGTCCTTCCTTT  9553     ACATT  A   A
                                AGAG    GA CCTGG GAAG
                                ||||    || ||||| ||||
                                TTTC    CT GGACC CTTC
                                  CTTC_ _    C
GAM1736  LCP1     3'  TCTCCAGGCATTAGCCCTC   11286    ACA  A_
                                GAG  TTGA  CCTGGAGA
                                |||  ||||  ||||||||
                                CTC  GATT  GGACCTCT
                                  CC_  AC
GAM1736  MMP25    5'  TCTCCAGGCCCGGATCTC   42699     CA  AA
                                GAGA  TTG  CCTGGAGA
                                ||||  |||  ||||||||
                                CTCT  GGC  GGACCTCT
                                  A_  CC
GAM1736  NKX3A    3'  TTCCCCAGGGTGTCTC     21619      TGAA   A
                                GAGACAT   CCTGG GAA
                                |||||||   ||||| |||
                                CTCTGTG   GGACC CTT
                                    ____   C
GAM1736  PITX3    3'  CTTCTCCAGGCTTCCCCTCCCT 18522    ACATT_  _
           C                     GAG    GAA CCTGGAGAAG
                                |||    ||| ||||||||||
                                CTC    CTT GGACCTCTTC
                                  CCTCCC  C
GAM1736  PLAT     3'  TCTCCAGGAATGCCTC     53398    A   GAA
                                GAG CATT  CCTGGAGA
                                ||| ||||  ||||||||
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                                CTC GTAA   GGACCTCT
                                  C   ___
GAM1736 PLAT     3'  TCTCCAGGAATGCCTC      8119      A   GAA
                                GAG CATT   CCTGGAGA
                                ||| ||||   ||||||||
                                CTC GTAA   GGACCTCT
                                  C   ___
GAM1736 PXN      3'  CTCCAAAGGTCTGATGTCTC   12671        GA   __
                                GAGACATT  ACCT  GGAG
                                ||||||||  ||||  ||||
                                CTCTGTAG  TGGA  CCTC
                                     TC   AA
GAM1736 RECQL5   3'  CTTCTCCAAACTGCTGTCTCT  16200        TTGAACC
                                AGAGACA      TGGAGAAG
                                |||||||      ||||||||
                                TCTCTGT      ACCTCTTC
                                    CGTCAA_
GAM1736 SLC6A8   3'  TCTCCAGGCTCTGCTCT     20077      A  TT  A
                                AGAG CA  GA CCTGGAGA
                                |||| ||  || ||||||||
                                TCTC GT  CT GGACCTCT
                                  _ __  C
GAM1736 SUFU     3'  CTCCAGGTCCCTGGTGCT    32935    A    A__
                                AG CATTG   ACCTGGAG
                                || |||||   ||||||||
                                TC GTGGT   TGGACCTC
                                 _    CCC
GAM1736 SVIL     5'  TCCCCAGGCTGAAGTGTCCTC  41708    _    GAA_    A
                                GAG ACATT    CCTGG GA
                                ||| |||||    ||||| ||
                                CTC TGTGA    GGACC CT
                                  C    AGTC    C
GAM1736 WASF3    3'  TTTTAGTTTAATGTCTC     22817          C
                                GAGACATTGAAC TGGAG
                                |||||||||||| |||||
                                CTCTGTAATTTG ATTTT
                                             _
GAM1736 APELIN   3'  CTTCTCCAGGTCCCCTC     34266     ACATT  A
                                GAG    GA CCTGGAGAAG
                                |||    || ||||||||||
                                CTC    CT GGACCTCTTC
                                  CC___  _
GAM1736 APXL2    3'  TTCTCCAAAGTGTTCTC     75687     _   GAACC
                                GAGA CATT    TGGAGAA
                                |||| ||||    |||||||
                                CTCT GTGA    ACCTCTT
                                  T   A____
GAM1736 BHLHB2   5'  TCTCCAGGGCAGTCCTC     14766     AC   AA
                                GAG  ATTG  CCTGGAGA
                                |||  ||||  ||||||||
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                                CTC  TGAC  GGACCTCT
                                  C_   G_
GAM1736 C1orf19   3'  CTTTTGTTAATGTCTCT     68749          ACCT
                                AGAGACATTGA    GGAG
                                ||||||||||    ||||
                                TCTCTGTAATT    TTTC
                                      GT__
GAM1736 CBARA1    3'  TCTCCAGGATGGGCCTCT    21397     A__   TGAA
                                AGAG   CAT    CCTGGAGA
                                ||||   |||    ||||||||
                                TCTC   GTA    GGACCTCT
                                  CGG  ____
GAM1736 CCR6      5'  CTCTGGGGAGTTCAATGCCTCT 49400      A      ___  TG
                                AGAG CATTGAA   CC  GAG
                                |||| |||||||   ||  |||
                                TCTC GTAACTT   GG  CTC
                                  C      GAG  GT
GAM1736 ctm-1     3'  TCTCCAGGTTCGGAGTTTC    75764      A
                                GAGAC TTGAACCTGGAGA
                                ||||| |||||||||||||
                                CTTTG GGCTTGGACCTCT
                                   A
GAM1736 DKFZp434F142 3'  TCTCCAGGCCCAGCTCTT    51036      ACA   AA
                                AAGAG   TTG  CCTGGAGA
                                |||||   |||  ||||||||
                                TTCTC   GAC  GGACCTCT
                                   ___   CC
GAM1736 DKFZp434F142 3'  TCTCCAGGCCCATCTCTTG    51037       CAT  AA
                                TAAGAGA   TG  CCTGGAGA
                                |||||||   ||  ||||||||
                                GTTCTCT   AC  GGACCTCT
                                    ___  CC
GAM1736 DKFZp434F142 3'  TCTCCAGGCTTTTCTC      51038      CATT  _
                                GAGA    GAA CCTGGAGA
                                ||||    ||| ||||||||
                                CTCT    TTT GGACCTCT
                                  _____  C
GAM1736 DKFZP761G1913 3'  CTTCCCACACCACCATGTCTCT 49696         TGAACC_  A
                                AGAGACAT      TGG GAAG
                                ||||||||      ||| ||||
                                TCTCTGTA      ACC CTTC
                                     CCACCAC  _
GAM1736 DKFZp761N1114 3'  CTTAATAGTCCAAAGTCTCTTA 79784         A  A  CTG_
                                TAAGAGAC TTG AC    GAG
                                |||||||| ||| ||    |||
                                ATTCTCTG AAC TG    TTC
                                     A  C  ATAA
GAM1736 FLJ10120  3'  CTTCTCCAAGGGCGCGCCTTCT 36306     CAT  AA_  _
                                AGA   TG   CCT GGAGAAG
                                |||   ||   ||| |||||||
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                                TCT   GC   GGA CCTCTTC
                                  TCC  GCG   A
GAM1736  FLJ10706  5'  TTCTCCAGGCTCTTTTC     36987      CATT  A
                                GAGA    GA CCTGGAGAA
                                ||||    || |||||||||
                                CTTT    CT GGACCTCTT
                                  T___  C
GAM1736  FLJ10948  3'  TCTCCAGACTTCCATTTCTTCA 37455    A    C  T   C_
                                A GAGA AT GAA  CTGGAGA
                                | |||| || |||  |||||||
                                A TTCT TA CTT  GACCTCT
                                 C    T  C   CA
GAM1736  FLJ12704  3'  CTTCTCCAGGCCAATCATCCTT 47167      A  C_   AA
              A                  TAAG GA  ATTG  CCTGGAGAAG
                                |||| ||  ||||  ||||||||||
                                ATTC CT  TAAC  GGACCTCTTC
                                  _  AC   C_
GAM1736  KIAA0352  3'  TTCTCCAGATTGTCTCT     29830        TTGAAC
                                AGAGACA     CTGGAGAA
                                |||||||     ||||||||
                                TCTCTGT     GACCTCTT
                                   TA____
GAM1736  KIAA0700  3'  CTTCTCCAGGCCTCTCTC    72520      CATT  A_
                                GAGA   GA  CCTGGAGAAG
                                ||||   ||  ||||||||||
                                CTCT   CT  GGACCTCTTC
                                  ____  CC
GAM1736  KIAA0789  5'  CTTCTCCAAGTGCTATTCTC   64430      C  TGA  C
                                GAGA AT   AC TGGAGAAG
                                |||| ||   || ||||||||
                                CTCT TA   TG ACCTCTTC
                                  _  TCG  A
GAM1736  KIAA0876  3'  CTTCTCCAGGTGCCTCTC    65317      CATTGA
                                GAGA     ACCTGGAGAAG
                                ||||     ||||||||||
                                CTCT     TGGACCTCTTC
                                  CCG___
GAM1736  MRVI1    5'  CTTCTCCAGGCTCACATGCTT  56096     A  _  A
                                GAG CAT TGA CCTGGAGAAG
                                ||| ||| ||| ||||||||||
                                TTC GTA ACT GGACCTCTTC
                                  _  C  C
GAM1736  NFASC    3'  CTCCAGACCCAATGTCTCT   70853         AAC
                                AGAGACATTG   CTGGAG
                                ||||||||||   ||||||
                                TCTCTGTAAC   GACCTC
                                     CCA
GAM1736  ShrmL    5'  TTCTCCAAACCTCTCTT     40854       CA  GAACC
                                AAGAGA  TT    TGGAGAA
                                ||||||  ||    |||||||
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                                TTCTCT  AA    ACCTCTT
                                   CC  _____
GAM1736  TGIF2LY   3'  CTTCTCCAGAACTTGTGTCTC  58318       TGAAC
                                GAGACAT    CTGGAGAAG
                                |||||||    |||||||||
                                CTCTGTG    GACCTCTTC
                                    TTCAA
GAM1736  LOC120772 3'  TCCCCGTGTCCCCAATGTCTTC 74470   A       A__  C   A
             A                   A GAGACATTG   AC TGG GA
                                 | |||||||||   || ||| ||
                                 A TTCTGTAAC   TG GCC CT
                                 C       CCC  T   C
GAM1736  LOC125704 5'  CTTCTCCAGCTTCCCGCCCCTC 74878     ACATT_   C
                                GAG     GAA CTGGAGAAG
                                |||     ||| |||||||||
                                CTC     CTT GACCTCTTC
                                  CCCGCC   C
GAM1736  LOC144121 3'  TCCCCGTGTCCCCAATGTCTTC 77192   A       A__  C   A
             A                   A GAGACATTG   AC TGG GA
                                 | |||||||||   || ||| ||
                                 A TTCTGTAAC   TG GCC CT
                                 C       CCC  T   C
GAM1736  LOC145968 3'  CTTCTCCAAATGATGTTATCTT 84577       _      AACC
             A                   TAAGA GACATTG    TGGAGAAG
                                 ||||| |||||||    ||||||||
                                 ATTCT TTGTAGT    ACCTCTTC
                                    A      AA__
GAM1736  LOC146488 3'  TCTCCAGGCTCTGCTCT     71364      A  TT  A
                                AGAG CA  GA CCTGGAGA
                                |||| ||  || ||||||||
                                TCTC GT  CT GGACCTCT
                                  _ __  C
GAM1736  LOC146894 3'  TCCCCAGGTTCTCCTCTTG    59866       ACATT       A
                                TAAGAG     GAACCTGG GA
                                ||||||     |||||||| ||
                                GTTCTC     CTTGGACC CT
                                    CT___       C
GAM1736  LOC147694 3'  TTCCCCAGAAATGTCTC      79111        GAAC    A
                                GAGACATT    CTGG GAA
                                ||||||||    |||| |||
                                CTCTGTAA    GACC CTT
                                     A___    C
GAM1736  LOC148113 3'  CTTCTCCAGACAGCCCCCTC   79373     ACA_   AAC
                                GAG    TTG   CTGGAGAAG
                                |||    |||   |||||||||
                                CTC    GAC   GACCTCTTC
                                  CCCC   A__
GAM1736  LOC148181 3'  TCTCCAGGCTCAGCTC      79438     ACA    A
                                GAG   TTGA CCTGGAGA
                                |||   |||| ||||||||
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                                CTC   GACT GGACCTCT
                                  ___   C
GAM1736  LOC149132 5'  TCTCCAGGCCCAGAACTTT   79927     ACA   AA
                                AGAG   TTG  CCTGGAGA
                                ||||   |||  ||||||||
                                TTTC   GAC  GGACCTCT
                                  AA_   CC
GAM1736  LOC149132 5'  TCTCCAGGCCCAGAACTTT   79928     ACA   AA
                                AGAG   TTG  CCTGGAGA
                                ||||   |||  ||||||||
                                TTTC   GAC  GGACCTCT
                                  AA_   CC
GAM1736  LOC151657 5'  CTTCTCTGTGCCTCAATGTCTT 86654    A        ACCT_
             CA                   A GAGACATTGA     GGAGAAG
                                | ||||||||||     |||||||
                                A TTCTGTAACT     TCTCTTC
                                 C         CCGTG
GAM1736  LOC170063 3'  CCACTCAATGTTCTTA     88598       A     ACC
                                TAAGAG CATTGA   TGG
                                |||||| ||||||   |||
                                ATTCTT GTAACT   ACC
                                   _     C__
GAM1736  LOC222057 3'  TCTCCAGGCCCAGCTCTT    94362      ACA   AA
                                AAGAG   TTG  CCTGGAGA
                                |||||   |||  ||||||||
                                TTCTC   GAC  GGACCTCT
                                  ___   CC
GAM1736  LOC222183 3'  TCTCCAGGCCAGGCTCTC    95831     CA   AA
                                GAGA  TTG  CCTGGAGA
                                ||||  |||  ||||||||
                                CTCT  GAC  GGACCTCT
                                  CG   C_
GAM1736  LOC223009 5'  TCTCCAGGCCCAGCCTCT    96035     ACA   AA
                                AGAG   TTG  CCTGGAGA
                                ||||   |||  ||||||||
                                TCTC   GAC  GGACCTCT
                                  C__   CC
GAM1736  LOC253024 5'  CTTCTCTGGTCAACATCTCTTG 99460       CA    A  T
                                TAAGAGA  TTGA CC GGAGAAG
                                |||||||  |||| || |||||||
                                GTTCTCT  AACT GG TCTCTTC
                                   AC   _ _
GAM1736  LOC255975 5'  TCTCCAGGCCCAGAACTTT   97592     ACA   AA
                                AGAG   TTG  CCTGGAGA
                                ||||   |||  ||||||||
                                TTTC   GAC  GGACCTCT
                                  AA_   CC
GAM1736  LOC255975 3'  TCTCCAGGCCCAGCTCTT    97593     ACA   AA
                                AAGAG   TTG  CCTGGAGA
                                |||||   |||  ||||||||
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                                TTCTC   GAC  GGACCTCT
                                  ___   CC
GAM1736  LOC256867 3'  TCCCCGTGTCCCCAATGTCTTC 96517   A       A__  C   A
             A                   A GAGACATTG   AC TGG GA
                                 | |||||||||   || ||| ||
                                 A TTCTGTAAC   TG GCC CT
                                  C       CCC  T   C
GAM1736  LOC90936  5'  CTTCTCCATGGACACGTCTGTC 65056     T_  AA_  _
                                 GACA  TG   CC TGGAGAAG
                                 ||||  ||   || ||||||||
                                 CTGT  GC   GG ACCTCTTC
                                   CT  ACA  T
GAM1737  ALDH3A2   3'  GACAGAGCAGGGCAGGCA    69800       G      C
                                 TGCCTGC CCTGCTC TGTT
                                 ||||||| ||||||| ||||
                                 ACGGACG GGACGAG ACAG
                                        _      _
GAM1737  FANCC     3'  TGACAGGCCACAGGAGCAGACA 71051    C    G    CT_
                                 TG CTGC CCTG   CCTGTTA
                                 || |||| ||||   |||||||
                                 AC GACG GGAC   GGACAGT
                                  A    A    ACC
GAM1737  GYPA      3'  TGATAACAAAGCAGCAAGGCA  88840      GC  C    CC
                                 TGCCT  GC TGCT  TGTTATCA
                                 |||||  || ||||  ||||||||
                                 ACGGA  CG ACGA  ACAATAGT
                                    A_  _    A_
GAM1737  LFG       5'  GAGGAAGGAAGAGACGCAGGCA 77237        C  GC    GTTA
                                 TGCCTGCG CT  TCCT    TC
                                 |||||||| ||  ||||    ||
                                 ACGGACGC GA  AGGA    AG
                                      A  GA    AGG_
GAM1737  PKIB      3'  TGATAACAGAAACATCTTTAGG 51640      CGCC  CTC
                                 CCTG    TG   CTGTTATCA
                                 ||||    ||   |||||||||
                                 GGAT    AC   GACAATAGT
                                   TTCT  AAA
GAM1737  PSEN1     3'  TGAGGAAGAGCAGGCACCAGCA 24624     C  C_       CTGTTA
                                 TGC TG  GCCTGCTC      TCA
                                 ||| ||  ||||||||      |||
                                 ACG AC  CGGACGAG      AGT
                                   _ CA       AAGG__
GAM1737  RFP       5'  GGGGGGCACAGGCGCAGGCA    22511          __
                                 TGCCTGCGCCT  GCTCCT
                                 ||||||||||  ||||||
                                 ACGGACGCGGA  CGGGGG
                                        CA
GAM1737  WBSCR14   3'  TGACCACAGCAGGGCAGGCA   53095        G      CCT
                                 TGCCTGC CCTGCT   GTTA
                                 ||||||| ||||||   ||||
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                                ACGGACG GGACGA   CAGT
                                   _     CAC
GAM1737 ALDH5A1   3' CAGAGCAGGCACAGCA      8413      C  C       C
                                TGC TG GCCTGCTC TG
                                ||| || |||||||| ||
                                ACG AC CGGACGAG AC
                                  _ A       _
GAM1737 GTPBP5    3' GGCAGAGCGGCGCAGGCA     65977          T    C
                                TGCCTGCGCC GCTC TGTT
                                |||||||||| |||| ||||
                                ACGGACGCGG CGAG ACGG

                                   _   _
GAM1737 H17       3' TGGCTGGGCAGGCACAGGCA   34515       C     T  T
                                TGCCTG GCCTGC CC GTTA
                                |||||| |||||| || ||||
                                ACGGAC CGGACG GG CGGT
                                    A     _ T
GAM1737 KIAA0648  3' TGATAACAAAATAACGAAGGCA 83545       G  CCTGCTCC
                                TGCCT CG       TGTTATCA
                                ||||| ||       ||||||||
                                ACGGA GC       ACAATAGT
                                   A  AATAAA__
GAM1737 KIAA1550  3' AGCAAGCAGGCCAGGCA     67148       C      CC
                                TGCCTG GCCTGCT  TGTT
                                |||||| |||||||  ||||
                                ACGGAC CGGACGA  ACGA

                                   _     __
GAM1737 KIAA1550  3' AGCAAGCAGGCCAGGCA     67149       C      CC
                                TGCCTG GCCTGCT  TGTT
                                |||||| |||||||  ||||
                                ACGGAC CGGACGA  ACGA

                                   _     __
GAM1737 KIAA1550  3' AGCAAGCAGGCCAGGCA     67150       C      CC
                                TGCCTG GCCTGCT  TGTT
                                |||||| |||||||  ||||
                                ACGGAC CGGACGA  ACGA

                                   _     __
GAM1737 MGC10334  5' GCAGAGCAGAGCAGGCA     48320        GC     C
                                TGCCTGC  CTGCTC TGT
                                |||||||  |||||| |||
                                ACGGACG  GACGAG ACG
                                    A_     _
GAM1737 LOC132166 3' GGTGGAAGGAAGCACAGGCA  75538       C  CTGC    G
                                TGCCTG GC    TCCT TTATC
                                |||||| ||    |||| |||||
                                ACGGAC CG    AGGA GGTGG
                                   A  A___    A
GAM1737 LOC135570 5' CAGGAGGCGCAGGCA       76471          TGC
                                TGCCTGCGCC   TCCTG
                                ||||||||||   |||||
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                                ACGGACGCGG   AGGAC
                                     ___
GAM1737  LOC149319 5'  TGACACAGGCAGGGCAGGCA   80078       G     CC
                                TGCCTGC CCTGCT  TGTTA
                                ||||||| ||||||  |||||
                                ACGGACG GGACGG  ACAGT
                                    _     AC
GAM1737  LOC152317 5'  CAGGAGAGCAGGGCAGGCA    86824       G    __
                                TGCCTGC CCTGC  TCCTG
                                ||||||| |||||  |||||
                                ACGGACG GGACG  AGGAC
                                    _    AG
GAM1737  LOC221641 5'  TGATAACAAAATAGCCAGGCA  95350       C  CTGCTCC
                                TGCCTG GC      TGTTATCA
                                |||||| ||      ||||||||
                                ACGGAC CG      ACAATAGT
                                   _ ATAAA__
GAM1737  LOC255031 5'  CGGGAGAGAAGAAGCGCAGGCA 99034         _____  G
                                TGCCTGCGC    CT CTCCTG
                                |||||||||    || ||||||
                                ACGGACGCG    GA GAGGGC
                                      AAGAA  _
GAM1737  LOC255104 3'  AACAGAGCAGGCGCAGGTA    97127            C
                                TGCCTGCGCCTGCTC TGTT
                                |||||||||||||| ||||
                                ATGGACGCGGACGAG ACAA
                                                _
GAM1738  CD28      3'  TCCCTGACGTTTAGTAGCATG  21559         T   AT__  A
                                CATGCTACT AGAC    GG GA
                                ||||||||| ||||    || ||
                                GTACGATGA TTTG    CC CT
                                      _   CAGT  _
GAM1738  CDC23     3'  CTCCATGTAAAGAACAGCACGT 17409    A   A__   AG
                                AC TGCT   CTT  ACATGGAG
                                || ||||   |||  ||||||||
                                TG ACGA   GAA  TGTACCTC
                                 C   CAA  A_
GAM1738  CRYBB1    5'  CTCCAGCAGGAAGTAGCAAGT  10306    A       AGACA
                                AC TGCTACTT     TGGAG
                                || ||||||||     |||||
                                TG ACGATGAA     ACCTC
                                 A       GGACG
GAM1738  CSPG3     3'  CTCCATGTCTGTTACTCACTTT 16518     CA  CTACT
              C                  GAA  TG     TAGACATGGAG
                                 |||  ||     ||||||||||
                                 CTT  AC     GTCTGTACCTC
                                   TC  TCATT
GAM1738  PRKCN     3'  TCTGCTGCTAAATATGCATGTT 20564         _ C    A  _
              C                  GAACATGC TA TTAG CA TGGA
                                 |||||||| || |||| || ||||
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                                CTTGTACG AT AATC GT GTCT
                                     T  A    _  C
GAM1738  FLJ20079  3'  TCATTTCCCAATAGCATGTTC  34978          CTTA  C
                                GAACATGCTA    GA ATGG
                                ||||||||||    || ||||
                                CTTGTACGAT    CT TACT
                                      AACC  T
GAM1738  KIAA0447  3'  TCTCCATGCCCAAGTCGGTTTC 72132     CAT  _   AGA
                                GAA   GCT ACTT   CATGGAGA
                                |||   ||| ||||   ||||||||
                                CTT   TGG TGAA   GTACCTCT
                                  ___   C    CCC
GAM1738  SH3BGRL3  3'  CTCCATGTAAAGGCAACATTC  49259     CA_   ACTTAG
                                GAA   TGCT     ACATGGAG
                                |||   ||||     ||||||||
                                CTT   ACGG     TGTACCTC
                                  ACA    AAA___
GAM1738  SMT3H2    3'  CTCCATTAGTGGCATGCTC    23659    A       TAGAC
                                GA CATGCTACT     ATGGAG
                                || |||||||||     ||||||
                                CT GTACGGTGA     TACCTC
                                 C        T_____
GAM1738  LOC112868 3'  CTCCACATGCCAGGTAAGTAGC 73267          GA___  __
            A                    TGCTACTTA     CA  TGGAG
                                |||||||||     ||  |||||
                                ACGATGAAT     GT  ACCTC
                                      GGACC  AC
GAM1738  LOC150358 3'  TCCCAGTGTTAGTAGCAT    86102         TA   _   A
                                ATGCTACT  GACA TGG GA
                                ||||||||  |||| ||| ||
                                TACGATGA  TTGT ACC CT
                                     __    G   C
GAM1738  LOC154547 3'  CTCCATTAGTGGCATGCTC    76569    A       TAGAC
                                GA CATGCTACT     ATGGAG
                                || |||||||||     ||||||
                                CT GTACGGTGA     TACCTC
                                 C        T_____
GAM1738  LOC158997 3'  CTCCATTAGTGGCATGCTC    82952    A       TAGAC
                                GA CATGCTACT     ATGGAG
                                || |||||||||     ||||||
                                CT GTACGGTGA     TACCTC
                                 C        T_____
GAM1738  LOC200953 5'  CTCCATGTCTTCAGCTTGTTC  91802      T   ACTT
                                GAACA GCT    AGACATGGAG
                                ||||| |||    ||||||||||
                                CTTGT CGA    TCTGTACCTC
                                   T   CT__
GAM1738  LOC221561 3'  CTCCATTAGTGGCATGCTC    93753    A       TAGAC
                                GA CATGCTACT     ATGGAG
                                || |||||||||     ||||||
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                                CT GTACGGTGA     TACCTC
                                 C        T____
GAM1738  LOC257591 3'  CTCCATTAGTGGCATGCTC   99673    A        TAGAC
                                GA CATGCTACT     ATGGAG
                                || |||||||||     ||||||
                                CT GTACGGTGA     TACCTC
                                 C        T____
GAM1739  EIF2B5    3'  GTGACCACCATCCAGGCT    62206            CAGACAG
                                AGCCTGGATGGTG      CAC
                                ||||||||||||       |||
                                TCGGACCTACCAC      GTG
                                       CA_____
GAM1739  MAFF      3'  AGCGCCGCCTCTGTGCCCAGGT 25571        ATG TG    CA__  A
                                GCCTGG   G  CAGA    GC CT
                                ||||||   |  ||||    || ||
                                TGGACC   C  GTCT    CG GA
                                   ___ GT    CCGC  C
GAM1739  RRM1      5'  GTGCTGTCTGGCTCCAACT    8283     A   T  _
                                GG TGG GC AGACAGCAC
                                || ||| || |||||||||
                                TC ACC CG TCTGTCGTG
                                 A   T  G
GAM1739  SAG       5'  GCGCTGCCCCTTCAGGCT    6773         T  T    ACA
                                AGCCTGGA GG GCAG   GC
                                |||||||| || ||||   ||
                                TCGGACTT CC CGTC   CG
                                     C  _    G__
GAM1739  C6orf26   3'  GTTCCTGCACCACCCAGG    48272       A       AC
                                CCTGG TGGTGCAG  AGC
                                ||||| ||||||||  |||
                                GGACC ACCACGTC  TTG
                                   C       C_
GAM1739  DKFZP564O0823 3'  GCCTTGCACCAGCCAGGC    60259        A       ACA
                                GCCTGG TGGTGCAG   GC
                                |||||| ||||||||   ||
                                CGGACC ACCACGTT   CG
                                   G       C__
GAM1739  KIAA1297  5'  AGTGCTGTTAACACCCATGGC  72628     TGGAT    CA
                                GCC    GGTG  GACAGCACT
                                |||    ||||  |||||||||
                                CGG    CCAC  TTGTCGTGA
                                  TAC__    AA
GAM1739  KIAA1881  3'  AGTGCTGTGGCATCCCAGGCT  97080        AT    AG
                                AGCCTGG  GGTGC  ACAGCACT
                                |||||||  |||||  ||||||||
                                TCGGACC  CTACG  TGTCGTGA
                                   __    G_
GAM1739  LEPROTL1  3'  AGTGCTGTCTCTGATTTCTAGG 31700         TGGTGC
              CT                  AGCCTGGA     AGACAGCACT
                                  ||||||||     ||||||||||
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                                TCGGATCT     TCTGTCGTGA
                                     TTAGTC
GAM1739  USP24    3'  GTGCCGTATCATCAGACT    92794    C   G      AGACA
                                AG CTG ATGGTGC     GCAC
                                || ||| |||||||     ||||
                                TC GAC TACTATG     CGTG
                                 A   _      C_____
GAM1739  LOC123905 5'  AGCGCGGGGCCACCATCCAG   74721          _ AGACA  A
                                CTGGATGGTG C     GC CT
                                |||||||||| |     || ||
                                GACCTACCAC G     CG GA
                                      C GGG__  C
GAM1739  LOC147166 5'  TGCCATCTCCAGGCTCCAGGCT 78897         TGG  C   CA
                                AGCCTGGA   TG AGA  GCA
                                ||||||||   || |||  |||
                                TCGGACCT   AC TCT  CGT
                                     CGG  C   AC
GAM1739  LOC148709 5'  GCAAGGTACACAGCCATCCAGG 79691           GCAG_  A__
             CT                   AGCCTGGATGGT    AC   GC
                                ||||||||||||    ||   ||
                                TCGGACCTACCG    TG   CG
                                       ACACA  GAA
GAM1739  LOC150378 3'  TTGTCTGCACCCCCCAAGC    80562    C   AT
                                GC TGG  GGTGCAGACAG
                                || |||  ||||||||||
                                CG ACC  CCACGTCTGTT
                                 A   CC
GAM1739  LOC152897 3'  TGCTGTCTGCAAAGTAGAGCT  81612     _  GATGG
                                AGC CTG    TGCAGACAGCA
                                ||| |||    ||||||||||
                                TCG GAT    ACGTCTGTCGT
                                  A   GAA__
GAM1739  LOC200918 3'  AGTGCTGCACATCATCCAGGT  90364          CAGA
                                GCCTGGATGGTG   CAGCACT
                                ||||||||||||   |||||||
                                TGGACCTACTAC   GTCGTGA
                                       AC__
GAM1739  LOC255189 5'  AGTGCTATCTGTTTGCCAAGGC 98375      GGA   __    C
             T                    AGCCT   TGGT  GCAGA AGCACT
                                |||||  ||||  ||||| ||||||
                                TCGGA   ACCG  TGTCT TCGTGA
                                   ___   TT    A
GAM1739  LOC256948 3'  GTGACCACCATCCAAGCT    96118     C       CAGACAG
                                AGC TGGATGGTG      CAC
                                ||| |||||||||      |||
                                TCG ACCTACCAC      GTG
                                  A       CA_____
GAM1739  LOC54466  5'  GCTCTACTGCACCACCCCAG   39175     A_      AC_
                                CTGG  TGGTGCAG   AGC
                                ||||  ||||||||   |||
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                                GACC  ACCACGTC   TCG
                                  CC       ATC
GAM1740  SCAMP1   3'  GCTAAATAAATATTCTCC    18013     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1740  SCAMP1   3'  GCTAAATAAATATTCTCC    54501     T     C
                                GGA AATATT ATTTAGC
                                ||| |||||| |||||||
                                CCT TTATAA TAAATCG
                                  C     A
GAM1740  NX-17    3'  TGAATATCAGCCCCTAATA    40706         ATA_
                                TATTAGGG    ATATTCA
                                ||||||||    |||||||
                                ATAATCCC    TATAAGT
                                     CGAC
GAM1740  LOC161589 3'  GCTAAATGAATATTATCCCTAA 83159
              TA                  TATTAGGGATAATATTCATTTAGC
                                ||||||||||||||||||||||||
                                ATAATCCCTATTATAAGTAAATCG

GAM1741  ACK1     3'  GCCCTGGGTGACAGACTGGGA  20514       C          _
                                TCTCG TCTGTCACCCAGG C
                                ||||| |||||||||||| |
                                AGGGT AGACAGTGGGTCC G
                                   C           C
GAM1741  ADAM12   3'  TTTAGCTTGGGAAAGGTGG    14428      T  GTCA
                                TCGC CT    CCCAGGCTGGA
                                |||| ||    ||||||||||
                                GGTG GA    GGGTTCGATTT
                                  _  AA__
GAM1741  ADAM17   3'  ACTCCAGCCTGGGTGACAGAGT 41840
              GAGA                  TCTCGCTCTGTCACCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGACAGTGGGTCCGACCT
                                                CAC
GAM1741  ADAM17   3'  ACTCCAGCCTGGGTGACAGAGT 41841
              GAGA                  TCTCGCTCTGTCACCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGACAGTGGGTCCGACCT
                                                CAC
GAM1741  ADAMTS13 3'  CAGCTGGCAGAGCGAGA     58150            CCCAG
                                TCTCGCTCTGTCA    GCTG
                                ||||||||||||    ||||
                                AGAGCGAGACGGT    CGAC
                                                 _____
GAM1741  ADAT1    3'  TCCAGCCTGGGTGATAGAGCAA 24919     C
              GA                    TCT GCTCTGTCACCCAGGCTGGA
                                ||| ||||||||||||||||||||
```

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                                AGA CGAGATAGTGGGTCCGACCT
                                  A
GAM1741  ADCY2    3'  ACTCCAGCCTGGGTGACAGAGC 65642
                 GAGA                  TCTCGCTCTGTCACCCAGGCTGGA
                                       ||||||||||||||||||||||||
                                       AGAGCGAGACAGTGGGTCCGACCT
                                                  CAC
GAM1741  AIRE     3'  TCCAGTCTGGTCGGCAAGAGTG 7246          _  AC
                 AGA                   TCTCGCTCT GTC  CCAGGCTGGA
                                       |||||||||  |||  ||||||||||
                                       AGAGTGAGA CGG  GGTCTGACCT
                                            A   CT
GAM1741  AK1      3'  TCCAGCCTGGGTGACAGAGCAA 6641      C
                 GA                    TCT GCTCTGTCACCCAGGCTGGA
                                       |||  ||||||||||||||||||||
                                       AGA CGAGACAGTGGGTCCGACCT
                                         A
GAM1741  ALDH3A2  3'  TTCAGCTTGGGCAACAGAGCAA 69804     C      CA
                 GA                    TCT GCTCTGT  CCCAGGCTGGA
                                       |||  |||||||  ||||||||||
                                       AGA CGAGACA  GGGTTCGACTT
                                         A       AC
GAM1741  ALDH3B1  3'  TCCGGCCTGGGTGACAGAAGGA 93162      GC
                 GG                    TCTC  TCTGTCACCCAGGCTGGA
                                       ||||  ||||||||||||||||||
                                       GGAG  AGACAGTGGGTCCGGCCT
                                         GA
GAM1741  ALDH8A1  3'  TTCAGCCTGGGGGATACAGTGA 42917        C    A
                 GA                    TCTCGCT TGTC CCCAGGCTGGA
                                       |||||||  ||||  ||||||||||
                                       AGAGTGA ATAG GGGTCCGACTT
                                           C    G
GAM1741  ALPP     3'  ACTGCAGCCTGGGCGACAGAGC 69403            A        GA
                 GAGA                  TCTCGCTCTGTC CCCAGGCTG
                                       ||||||||||| |||||||||
                                       AGAGCGAGACAG GGGTCCGAC
                                              C        GTCAC
GAM1741  AMN      3'  TCCGGTGAGGGGAGGGTGAGG  48922         TG  A   AG
                                       TCTCGCTC  TC CCC  GCTGGA
                                       ||||||||  || |||  ||||||
                                       GGAGTGGG  AG GGG  TGGCCT
                                            __  _  AG
GAM1741  ANKH     3'  TCCAGCCTGGGTGACAAGAGC  55074       _
                                       GCTCT GTCACCCAGGCTGGA
                                       |||||  ||||||||||||||||
                                       CGAGA CAGTGGGTCCGACCT
                                         A
GAM1741  AOC3     3'  CGGCCTAGTGGGGAGGGG    14959     G   G   CC   TG
                                       CTC CTCT TCAC  AGGC  G
                                       |||  ||||  ||||  ||||  |
```

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                                GGG GAGG GGTG  TCCG  C
                                  _   _    A_    GT
GAM1741  APAF1    3'  TCCAGCCTGGGTGACATAGCAA 25984     C   C
                 GA                  TCT GCT TGTCACCCAGGCTGGA
                                     ||| ||| ||||||||||||||||
                                     AGA CGA ACAGTGGGTCCGACCT
                                       A   T
GAM1741  APOL1    3'  CTCCAGCCTGGGTGACAGAGCG 14739
                 AGA                   TCTCGCTCTGTCACCCAGGCTGGA
                                     ||||||||||||||||||||||||
                                     AGAGCGAGACAGTGGGTCCGACCT
                                                 CA
GAM1741  ARHGEF12 3'  TTCGGATAGTGGCAGGGGTGGG 31651         _     CCAGG
                 G                   TCTCGCTC TGTCAC     CTGGA
                                     |||||||| ||||||     |||||
                                     GGGGTGGG ACGGTG     GGCTT
                                         G     ATA__
GAM1741  ASIC4    3'  TGAGCTTGGAGGGTGGGA    38541          GTCAC      GGA
                                     TCTCGCTCT    CCAGGCT
                                     |||||||||    |||||||
                                     AGGGTGGGA    GGTTCGA
                                           _____      GTC
GAM1741  ATF4     5'  TTTGGATTGGTGGGGTGCGG  9814     T    TG   C_
                                     TC CGCTC  TCA  CCAGG
                                     || |||||  |||  |||||
                                     GG GTGGG  GGT  GGTTT
                                      C    GT   TA
GAM1741  ATF7     3'  TTTAGTTTAACCATCAGGGCAG 23406     C     TCACCC
                 A                   TCT GCTCTG     AGGCTGGA
                                     ||| ||||||     ||||||||
                                     AGA CGGGAC     TTTGATTT
                                       _     TACCAA
GAM1741  ATM      3'  TCCAGCCTGGGAGACAGAGCGA 5303            A
                 GA                    TCTCGCTCTGTC CCCAGGCTGGA
                                     |||||||||||| ||||||||||
                                     AGAGCGAGACAG GGGTCCGACCT
                                            A
GAM1741  ATM      3'  TCCAGCCTGGGTGACAAGAGCG 5304         _
                 A                    TCGCTCT GTCACCCAGGCTGGA
                                     |||||||| ||||||||||||||
                                     AGCGAGA CAGTGGGTCCGACCT
                                        A
GAM1741  ATP1A2   3'  TCCAGCCTGGGCGAAAGGGTGA 7369          G  A
                 GA                    TCTCGCTCT TC CCCAGGCTGGA
                                     ||||||||| || ||||||||||
                                     AGAGTGGGA AG GGGTCCGACCT
                                          A  C
GAM1741  BAK1     3'  CTGGGCTTGGGGTGTGGGGTGG 93629         TG CA       GGA
                 GG                    TCTCGCTC  T  CCCAGGCT
                                     ||||||||  |  ||||||||
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                                GGGGTGGG  G  GGGTTCGG
                                    GT TG       GTCT
GAM1741  BAK1     3'  TTCAGCCAAATGCAGGGAGGGG 93636      G     CACCCA
                                TCTC CTCTGT      GGCTGGA
                                |||| ||||||      |||||||
                                GGGG GGGACG      CCGACTT
                                  A     TAAA__
GAM1741  BCL2L2   3'  CTCAGGTGATAGGGAGAGG   15758      G        CA
                                TCTC CTCTGTCACC  GG
                                |||| ||||||||||  ||
                                GGAG GGGATAGTGG  TC
                                  A         AC
GAM1741  BCL7A    3'  CTGGGGGTGGGGTGGGG     40982         TG  A
                                TCTCGCTC  TC CCCAG
                                ||||||||  || |||||
                                GGGGTGGG  GG GGGTC
                                    GT  _
GAM1741  BCL9     3'  TTAGTCTTTGGGGCAAG     16325    C    A  C_
                                CT TGTC CC  AGGCTGG
                                || |||| ||  |||||||
                                GA ACGG GG  TCTGATT
                                 _    _  TT
GAM1741  BHMT2    3'  ACTTCAGCCTGGGTGACAGAGT 34725
                   GAGA                 TCTCGCTCTGTCACCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGACAGTGGGTCCGACTT
                                                CAC
GAM1741  BRCA1    5'  TCCAGCCTGGGCGACAGAGCGA 24576           A
                   GA                   TCTCGCTCTGTC CCCAGGCTGGA
                                ||||||||||||| ||||||||||
                                AGAGCGAGACAG GGGTCCGACCT
                                      C
GAM1741  C1orf1   3'  TCCAGCCTAGGCGACAGAGTGA 8683            A  C
                   GA                   TCTCGCTCTGTC CC AGGCTGGA
                                ||||||||||||  || ||||||||
                                AGAGTGAGACAG GG TCCGACCT
                                      C  A
GAM1741  C5R1     3'  TCTAGCCTGGGTGACCGAGGGA 9977       G   T
                   GG                   TCTC CTC GTCACCCAGGCTGGA
                                |||| ||| ||||||||||||||||
                                GGAG GAG CAGTGGGTCCGATCT
                                  G   C
GAM1741  C8orf1   3'  CTGGGGGTGGGGTGAGG     16345         TG  A
                                TCTCGCTC  TC CCCAG
                                ||||||||  || |||||
                                GGAGTGGG  GG GGGTC
                                    GT  _
GAM1741  CA12     3'  ACTCTAGCCTGGGTGACAGAGC 8686
                   GAGA                 TCTCGCTCTGTCACCCAGGCTGGA
                                ||||||||||||||||||||||||
```

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                                AGAGCGAGACAGTGGGTCCGATCT
                                     CAC
GAM1741 CACNA1D  3' TCTGGCCTCAGGTGGGGCGCAG 7404     _    TGT   C_   TG
           G                  TCT CGCTC  CACC  AGGC  GA
                              ||| |||||  ||||  ||||  ||
                              GGA GCGGG  GTGG  TCCG  CT
                                C    ___    AC   GT
GAM1741 CAPN11   3' CTAGCCCAGGAGGGTGGGG   23912        GTCA  CA
                              TCTCGCTCT   CC  GGCTGG
                              |||||||||   ||  ||||||
                              GGGGTGGGA   GG  CCGATC
                                    ____ AC
GAM1741 CARKL    3' TCCAGCCTGGGTGACAGAGCAA 26109     C
           GA                   TCT GCTCTGTCACCCAGGCTGGA
                              ||| ||||||||||||||||||||
                              AGA CGAGACAGTGGGTCCGACCT
                                A
GAM1741 CASP10   3' TCCAGCTTGGGCAACAGGGCGA 53264          CA
           GA                   TCTCGCTCTGT  CCCAGGCTGGA
                              ||||||||||  ||||||||||
                              AGAGCGGGACA  GGGTTCGACCT
                                    AC
GAM1741 CASP10   3' TCCAGCTTGGGCAACAGGGCGA 53265          CA
           GA                   TCTCGCTCTGT  CCCAGGCTGGA
                              ||||||||||  ||||||||||
                              AGAGCGGGACA  GGGTTCGACCT
                                    AC
GAM1741 CASP3    3' TTTAGTTTGTATGCCAAGTGAG 16356       C  T  CC
           A                   TCTCGCT TG CA  CAGGCTGGA
                              |||||||  ||  ||  |||||||||
                              AGAGTGA AC GT  GTTTGATTT
                                 _  C  AT
GAM1741 CASP6    3' TCCAGCCTGGGCAACGAGTGA  53366       T  CA
                              TCGCTC GT  CCCAGGCTGGA
                              ||||||  ||  ||||||||||
                              AGTGAG CA  GGGTCCGACCT
                                 _  AC
GAM1741 CASP8    3' TCAAGCTTGGGTGACAGAGCAA 8766      C            G
           GA                   TCT GCTCTGTCACCCAGGCT GA
                              ||| |||||||||||||||  ||
                              AGA CGAGACAGTGGGTTCGA CT
                                A             A
GAM1741 CASP8    3' TCAAGCTTGGGTGACAGAGCAA 8767      C            G
           GA                   TCT GCTCTGTCACCCAGGCT GA
                              ||| |||||||||||||||  ||
                              AGA CGAGACAGTGGGTTCGA CT
                                A             A
GAM1741 CCND1    3' TCTGTCGTGATGGGGCAAGG  54961     C        C_
                              TCT GCTCTGTCAC  CAGG
                              ||| ||||||||||  ||||
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                                GGA CGGGGTAGTG  GTCT
                                  A         CT
GAM1741  CCNF     3'  GCCACCCTGGGTGGGGTGTGG  10078    T    TGT      C   A
                                TC CGCTC   CACCCAGG TGG
                                || |||||   |||||||| |||
                                GG GTGGG   GTGGGTCC ACC
                                 T    ____       C   GG
GAM1741  CD28     3'  TCCAGCCTGGGCGACAGAGTGA 21558           A
              GA                  TCTCGCTCTGTC CCCAGGCTGGA
                                ||||||||||| ||||||||||
                                AGAGTGAGACAG GGGTCCGACCT
                                       C
GAM1741  CD68     3'  TCCAGCCTGGGCGACAGAGCCA 60508     C       A
              GA                  TCT GCTCTGTC CCCAGGCTGGA
                                ||| |||||||| ||||||||||
                                AGA CGAGACAG GGGTCCGACCT
                                  C       C
GAM1741  CDC23    3'  TTCAGCCTTTATCTAGATGAGG 17410      C    TCACCC
                                TCTCG TCTG     AGGCTGGA
                                ||||| ||||     ||||||||
                                GGAGT AGAT     TCCGACTT
                                   _    CTATT_
GAM1741  CDC42    3'  CTGGGGGTAGGGTGGGG     10138         GT A
                                TCTCGCTCT  C CCCAG
                                |||||||||  | |||||
                                GGGGTGGGA  G GGGTC
                                      TG _
GAM1741  CDK2     3'  AGGGCTGTGATTGAGTGAGG   10153        T    CCA    GGA
                                TCTCGCTC GTCAC   GGCT
                                |||||||| |||||   ||||
                                GGAGTGAG TAGTG   TCGG
                                     T    ____   GAC
GAM1741  CDKN2D   3'  TCAGGCATGGGGGGTGGGG   10160        TGTCA    G  _
                                TCTCGCTC    CCCA GC TGG
                                ||||||||    |||| || |||
                                GGGGTGGG    GGGT CG ACT
                                     ______   A  G
GAM1741  CEACAM5  3'  TCCAGTCTGGCAACAGAGCAAG 16425     C      CAC
              A                   TCT GCTCTGT   CCAGGCTGGA
                                ||| |||||||   ||||||||||
                                AGA CGAGACA   GGTCTGACCT
                                  A      AC_
GAM1741  CEBPA    3'  TCTGGCTGTGGGGCGGG     16432         T  C
                                CTCGCTCTG CA CCAGG
                                ||||||||| || |||||
                                GGGCGGGGT GT GGTCT
                                      _ C
GAM1741  CELSR2   3'  GCTGTGATGTGGGTGGGG    9195          _     CCA
                                TCTCGCTC TGTCAC   GGC
                                |||||||| ||||||   |||
```

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                                GGGGTGGG GTAGTG   TCG
                                     T    ___
GAM1741  CELSR3   3'  CCGAAGGGTAGGGTGGGA    9185         GTC    AGGC
                                TCTCGCTCT   ACCC    TGG
                                |||||||||   ||||    |||
                                AGGGTGGGA   TGGG    GCC
                                     ___    AA__
GAM1741  CENTD2   3'  TCCAGTCTGGGCTGAGTGGGG  31542        TGTCA
                                TCTCGCTC    CCCAGGCTGGA
                                ||||||||    ||||||||||
                                GGGGTGAG    GGGTCTGACCT
                                     TC___
GAM1741  CHRNA4   3'  TCCAGCCAGGGGTGGGGATGGG 7439       C   G     A_
            G                    TCTCG TCT TCACCC  GGCTGGA
                                |||||  ||| ||||||  |||||||
                                GGGGT AGG GGTGGG  CCGACCT
                                  _  _     GA
GAM1741  CHRNB4   3'  CCTGGGTTGTGGGGTGAGA   7448         TG C
                                TCTCGCTC  T ACCCAGG
                                ||||||||  | |||||||
                                AGAGTGGG  G TGGGTCC
                                     GT T
GAM1741  CLASP1   3'  TTTGGGGGTGGGGTGGGG    65899        TG  A
                                TCTCGCTC  TC CCCAGG
                                ||||||||  || ||||||
                                GGGGTGGG  GG GGGTTT
                                     GT  _
GAM1741  COPA     3'  TCCAGCCTGGGTGACAGAGCAA 16480     C
            GA                    TCT GCTCTGTCACCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGAGACAGTGGGTCCGACCT
                                  A
GAM1741  CPM      3'  TCCAGCTTGGGCAACAGAGTAA 60411     CG     CA
            GA                    TCT  CTCTGT  CCCAGGCTGGA
                                |||  ||||||  ||||||||||
                                AGA  GAGACA  GGGTTCGACCT
                                  AT     AC
GAM1741  CPT2     3'  TCCGGCCTGGGCGACAGAGCGA 5429            A
            GA                    TCTCGCTCTGTC CCCAGGCTGGA
                                ||||||||||| ||||||||||
                                AGAGCGAGACAG GGGTCCGGCCT
                                       C
GAM1741  CREBL1   3'  TCAGTTGTGGGGTGGGTG    16499       TGTCA   _
                                CGCTC    CCCA GGCTGG
                                |||||    |||| ||||||
                                GTGGG    GGGT TTGACT
                                   TG___    G
GAM1741  CRMP1    3'  TTTAGTTGGTGCTGATGGAGGG 8973       G       C__    G
            AGG                   TCTC CTCTGTCA   CCAG CTGGA
                                |||| ||||||||   |||| |||||
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                                GGAG GAGGTAGT   GGTT GATTT
                                  G       CGT   _
GAM1741  CTSS     3'  TCCAGCCTGGATGACAGAGTGG 15822    T        C
              A                    TC CGCTCTGTCA CCAGGCTGGA
                                   || |||||||||| ||||||||||
                                   AG GTGAGACAGT GGTCCGACCT
                                    _        A
GAM1741  CYP2A6   3'  TCTGGTGGGCGGGGCCAGG   7536      C       AC
                                   TCT GCTCTGTC  CCAGG
                                   ||| ||||||||  |||||
                                   GGA CGGGGCGG  GGTCT
                                     C       GT
GAM1741  CYP4F3   3'  CCAGCCTGGGGGAGGGGGA   8001      G    GTCA
                                   TCTC CTCT    CCCAGGCTGG
                                   |||| ||||    ||||||||||
                                   AGGG GAGG    GGGTCCGACC
                                     G   _____
GAM1741  CYP4F3   3'  TCCAGCCTGGGTGAAAGAGCTA 8015      C    G
              GA                   TCT GCTCT TCACCCAGGCTGGA
                                   ||| ||||| ||||||||||||||
                                   AGA CGAGA AGTGGGTCCGACCT
                                     T    A
GAM1741  CYP4F3   3'  TCTGTGAGTGGAAGAGTGGGG  8016         GT   C__
                                   TCTCGCTCT  CAC   CAGG
                                   |||||||||  |||   ||||
                                   GGGGTGAGA  GTG   GTCT
                                        AG   AGT
GAM1741  DAPP1    3'  TCTAGCCTGGGTGACAGAGTCA 27683     C
              GA                   TCT GCTCTGTCACCCAGGCTGGA
                                   ||| ||||||||||||||||||||
                                   AGA TGAGACAGTGGGTCCGATCT
                                     C
GAM1741  DBN1     5'  TCCGGGCGGGGACGGGGCGGGG 56022           A   AGG
                                   TCTCGCTCTGTC CCC   CTGGA
                                   |||||||||||| |||   |||||
                                   GGGGCGGGGCAG GGG   GGCCT
                                          _  CG_
GAM1741  DBT      3'  TCCAGCCTGGGCGACAGAGCAA 10379     C       A
              GA                   TCT GCTCTGTC CCCAGGCTGGA
                                   ||| |||||||| ||||||||||
                                   AGA CGAGACAG GGGTCCGACCT
                                     A       C
GAM1741  DBT      3'  TCCAGCCTGGGTGGCAGAGC   10380
                                   GCTCTGTCACCCAGGCTGGA
                                   ||||||||||||||||||||
                                   CGAGACGGTGGGTCCGACCT

GAM1741  DBT      3'  TCCAGTATGGGTGACAGAGTGA 10382              G
              GA                   TCTCGCTCTGTCACCCA GCTGGA
                                   |||||||||||||||| ||||||
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                                AGAGTGAGACAGTGGGT TGACCT
                                          A
GAM1741  DCLRE1C   3'  TCTAGTCTGGGTGACAGAGCAA 42824     C
            GA                    TCT GCTCTGTCACCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGTGGGTCTGATCT
                                    A
GAM1741  DEFB103   5'  TCCAGTCTCAGCGTGGGGTGA  38491       TG CACCC
                                  TCGCTC  T    AGGCTGGA
                                  |||||| |    ||||||||
                                  AGTGGG  G    TCTGACCT
                                     GT CGAC_
GAM1741  DFFA      3'  TCCAGCCTGGGCAACAGAGCGA 16598          CA
            GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        AC
GAM1741  DHFR      5'  TCCGGCGAGACATGGCAGGGCA 7658      C       CCCAG_
            AGG                     TCT GCTCTGTCA     GCTGGA
                                  ||| |||||||||     ||||||
                                  GGA CGGGACGGT     CGGCCT
                                    A        ACAGAG
GAM1741  DLG4      3'  TCCAGCCTGTTGGAGGGGGGA  9089      G   G   CC
                                  TCTC CTCT TCA  CAGGCTGGA
                                  |||| |||| |||  |||||||||
                                  AGGG GGGA GGT  GTCCGACCT
                                    _   _   T_
GAM1741  DMC1      3'  TCCAGCCTAGGTGACAGAGTGA 23947             C
            GA                    TCTCGCTCTGTCACC AGGCTGGA
                                  |||||||||||||| ||||||||
                                  AGAGTGAGACAGTGG TCCGACCT
                                          A
GAM1741  DNASE2    3'  TTCAGCCTGGGTGACAGAATGA 9102       C
            GA                    TCTCG TCTGTCACCCAGGCTGGA
                                  ||||| ||||||||||||||||||
                                  AGAGT AGACAGTGGGTCCGACTT
                                    A
GAM1741  DNM2      3'  TGGGTGGTGGTGGCGGGG    18236        _ TG
                                  TCTCGCT C  TCACCCA
                                  ||||||| |  |||||||
                                  GGGGCGG G  GGTGGGT
                                      T GT
GAM1741  DOCK1     3'  TTCAGTTCTCACCATGGAGTGA 9107          CACCCA
            G                      CTCGCTCTGT     GGCTGGA
                                  ||||||||||     |||||||
                                  GAGTGAGGTA     TTGACTT
                                        CCACTC
GAM1741  DPP6      5'  TCTGGAGCGGGGTGGGGAGTGG 56326         G     AGG_ TG
            GA                    TCTCGCTCT TCACCC    C  GA
                                  ||||||||| ||||||    |  ||
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                                AGGGTGAGG GGTGGG   G  CT
                                      _     GCGA GT
GAM1741  DSC1     3'  TCCAGCCTGGGCAACAAGAGCG 44606       _  CA
             A                   TCGCTCT GT  CCCAGGCTGGA
                                 ||||||| ||  ||||||||||
                                 AGCGAGA CA  GGGTCCGACCT
                                     A  AC
GAM1741  DSC1     3'  TCCAGCCTGGGCAACAAGAGCG 18243       _  CA
             A                   TCGCTCT GT  CCCAGGCTGGA
                                 ||||||| ||  ||||||||||
                                 AGCGAGA CA  GGGTCCGACCT
                                     A  AC
GAM1741  DSCAM    5'  TCCGGCCGCAGCGTGGGGCGCG 9136    T    TG CACCCA
             G                   TC CGCTC  T     GGCTGGA
                                 || |||||  |     |||||||
                                 GG GCGGG  G     CCGGCCT
                                  C    GT CGACG_
GAM1741  DVL3     3'  TCCAGCCTGGGTGACAGAGTGA 16651
             GA                    TCTCGCTCTGTCACCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGTGAGACAGTGGGTCCGACCT

GAM1741  DYRK1A   3'  TGTTTTGGGTGGGAGGGTGGGA 56083         G       CTGGA
                                 TCTCGCTCT TCACCCAGG
                                 |||||||| |||||||||
                                 AGGGTGGGA GGTGGGTTT
                                      G        TGTT
GAM1741  DYRK1A   3'  TTGTTTTGGGTGGGAGGGTGGG 56087         G       CTGGA
             A                   TCTCGCTCT TCACCCAGG
                                 |||||||| |||||||||
                                 AGGGTGGGA GGTGGGTTT
                                      G        TGTTT
GAM1741  EGFL4    3'  TCCAACCTGGGTGACAGAGCGA 62475              C
             GA                    TCTCGCTCTGTCACCCAGG TGGA
                                   |||||||||||||||||| ||||
                                   AGAGCGAGACAGTGGGTCC ACCT
                                              A
GAM1741  EGFL5    3'  TCCAGCCTGGGCGACAGAGCAA 87921     C       A
             GA                    TCT GCTCTGTC CCCAGGCTGGA
                                   ||| |||||||| ||||||||||
                                   AGA CGAGACAG GGGTCCGACCT
                                     A       C
GAM1741  EIF2C1   3'  TTTGGCCTTCTAAGCAGATTGG 25202      C    CACCC    TG
             GA                    TCTCG TCTGT    AGGC  GA
                                   ||||| |||||    ||||  ||
                                   AGGGT AGACG    TCCG  TT
                                     T    AATCT    GT
GAM1741  ELK1     3'  TCTGATTGTGGTGGGGTGGGG  19090        TG   C__
                                 TCTCGCTC  TCAC   CAGG
                                 ||||||||  ||||   ||||
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                                GGGGTGGG  GGTG   GTCT
                                    GT    TTA
GAM1741  ENC1     3'  TTTGGTTGTGCTGATAGGGTAA 14654     CG       CCCA   TG
              GG                    TCT  CTCTGTCA    GGC  GA
                                ||| ||||||||   ||| ||
                                GGA  GGGATAGT    TTG  TT
                                  AT       CGTG   GT
GAM1741  ENPP3    3'  TCCAGAGCCTGGGTGACAGAGC 73331     C            __
              AAGA                   TCT GCTCTGTCACCCAGGCT  GGA
                                ||| ||||||||||||||||  |||
                                AGA CGAGACAGTGGGTCCGA  CCT
                                  A              GA
GAM1741  EXTL3    3'  TCTGTGTGGTGGAGCCAGG   9337     C    TG    C
                                TCT GCTC  TCAC CAGG
                                ||| ||||  |||| ||||
                                GGA CGAG  GGTG GTCT
                                  C    GT    T
GAM1741  F2R      3'  TCCAGCCTGGGCAACAGAGCAA 10573     C      CA
              GA                    TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A      AC
GAM1741  F2RL3    3'  TCCAGCCTGGGCAACAGAGCAA 15527     C      CA
              GA                    TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A      AC
GAM1741  FANCC     3'  TCCAGCCTGGGCAACAGAGCGA 71049          CA
              GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      AC
GAM1741  FCAR     3'  TCCAGCCTGGGTGACAGAACGA 56582       C
              GA                    TCTCG TCTGTCACCCAGGCTGGA
                                ||||| ||||||||||||||||||
                                AGAGC AGACAGTGGGTCCGACCT
                                   A
GAM1741  FCAR     3'  TCCAGCCTGGGTGACAGAACGA 56583       C
              GA                    TCTCG TCTGTCACCCAGGCTGGA
                                ||||| ||||||||||||||||||
                                AGAGC AGACAGTGGGTCCGACCT
                                   A
GAM1741  FCMD     3'  TTCAGCCTGGGCGATAGAGCAA 23051     C       A
              GA                    TCT GCTCTGTC CCCAGGCTGGA
                                ||| |||||||| ||||||||||
                                AGA CGAGATAG GGGTCCGACTT
                                  A       C
GAM1741  FGF2     3'  TCCAGCCTAGGCAACAGAGTGA 10622          CA  C
              GA                    TCTCGCTCTGT  CC AGGCTGGA
                                ||||||||||  || ||||||||
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                                AGAGTGAGACA  GG TCCGACCT
                                      AC  A
GAM1741  FGFR1    3'  TCCAGCCTGGGTGACAGAGTGA 7023
                G                  CTCGCTCTGTCACCCAGGCTGGA
                                   ||||||||||||||||||||||
                                   GAGTGAGACAGTGGGTCCGACCT

GAM1741  FGFR2    3'  TCCAGCCTTGGCGACAGAGCGA 5566           A  C
                GA                   TCTCGCTCTGTC CC AGGCTGGA
                                     |||||||||||| || ||||||||
                                     AGAGCGAGACAG GG TCCGACCT
                                           C  T
GAM1741  FGFR3    3'  TCCAGCCTGCCCCGGAGCTGGA 5571      C     TCACC
                                     TCT GCTCTG    CAGGCTGGA
                                     ||| ||||||    |||||||||
                                     AGG CGAGGC    GTCCGACCT
                                       T     CCC__
GAM1741  FKBP10   3'  TTTGGGGCTGAGGGGTGGGA  41941         GTCA_
                                     TCTCGCTCT    CCCAGG
                                     |||||||||    ||||||
                                     AGGGTGGGG    GGGTTT
                                           AGTCG
GAM1741  FLNA     3'  TTTGGTTCTGGGAGGGGTGAGG 9387          GTCA     _ TG
                                     TCTCGCTCT    CCCAGG C  GA
                                     |||||||||    |||||| |  ||
                                     GGAGTGGGG    GGGTCT G  TT
                                           A___      T GT
GAM1741  FLRT2    5'  TCCAGCCTAAGCAACAGAGCAA 26004     C      CACCC
                GA                     TCT GCTCTGT    AGGCTGGA
                                       ||| |||||||    |||||||||
                                       AGA CGAGACA    TCCGACCT
                                         A      ACGAA
GAM1741  FMN2     3'  TTCAGCTGACCTGAGAGTGGGA 80132         TG   CCCA
                                       TCTCGCTC  TCA    GGCTGGA
                                       ||||||||  |||    |||||||
                                       AGGGTGAG  AGT    TCGACTT
                                             __  CCAG
GAM1741  FSTL3    3'  TCTAGCCTGGGTGAGTACGGAG 20739       ___
                                       CTCTG   TCACCCAGGCTGGA
                                       |||||   ||||||||||||||
                                       GAGGC   AGTGGGTCCGATCT
                                          ATG
GAM1741  FSTL3    3'  TCTAGCCTGGGTGAGTACGGAG 20740    G    ___
                GG                     C CTCTG   TCACCCAGGCTGGA
                                       | |||||   ||||||||||||||
                                       G GAGGC   AGTGGGTCCGATCT
                                        G    ATG
GAM1741  FSTL3    3'  TCTAGCCTGGGTGAGTACGGAG 20741    G    ___
                GG                     C CTCTG   TCACCCAGGCTGGA
                                       | |||||   ||||||||||||||
```

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                                G GAGGC  AGTGGGTCCGATCT
                                 G    ATG
GAM1741  FSTL3   3' TCTAGCCTGGGTGAGTATGGAG 20742  G   ___
          GG                     C CTCTG  TCACCCAGGCTGGA
                                | |||||  ||||||||||||||
                                G GAGGT  AGTGGGTCCGATCT
                                 G    ATG
GAM1741  FSTL3   3' TCTAGCCTGGGTGAGTATGGAG 20743  G   ___
          GG                     C CTCTG  TCACCCAGGCTGGA
                                | |||||  ||||||||||||||
                                G GAGGT  AGTGGGTCCGATCT
                                 G    ATG
GAM1741  FSTL3   3' TCTAGCCTGGGTGAGTATGGAG 20744  G   ___
          GG                     C CTCTG  TCACCCAGGCTGGA
                                | |||||  ||||||||||||||
                                G GAGGT  AGTGGGTCCGATCT
                                 G    ATG
GAM1741  FSTL3   3' TCTAGCCTGGGTGAGTATGGAG 20745  G   ___
          GG                     C CTCTG  TCACCCAGGCTGGA
                                | |||||  ||||||||||||||
                                G GAGGT  AGTGGGTCCGATCT
                                 G    ATG
GAM1741  FSTL3   3' TCTAGCCTGGGTGTGTACGGAG 20746    ___
                                CTCTGT  CACCCAGGCTGGA
                                ||||||  ||||||||||||
                                GAGGCA  GTGGGTCCGATCT
                                   TGT
GAM1741  FSTL3   3' TCTAGCCTGGGTGTGTACGGAG 20747    ___
                                CTCTGT  CACCCAGGCTGGA
                                ||||||  ||||||||||||
                                GAGGCA  GTGGGTCCGATCT
                                   TGT
GAM1741  FSTL3   3' TCTAGCCTGGGTGTGTATGGAG 20748    ___
                                CTCTGT  CACCCAGGCTGGA
                                ||||||  ||||||||||||
                                GAGGTA  GTGGGTCCGATCT
                                   TGT
GAM1741  FSTL3   3' TCTAGCCTGGGTGTGTATGGAG 20749    ___
                                CTCTGT  CACCCAGGCTGGA
                                ||||||  ||||||||||||
                                GAGGTA  GTGGGTCCGATCT
                                   TGT
GAM1741  FSTL3   3' TCTAGCCTGGGTGTGTATGGAG 20750    ___
                                CTCTGT  CACCCAGGCTGGA
                                ||||||  ||||||||||||
                                GAGGTA  GTGGGTCCGATCT
                                   TGT
GAM1741  FSTL3   3' TCTAGTCTGGGTGTGTACGGAG 20751    ___
                                CTCTGT  CACCCAGGCTGGA
                                ||||||  ||||||||||||
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                                GAGGCA  GTGGGTCTGATCT
                                   TGT
GAM1741  GABRE    3'  GTTGGGGGGGTGGATAGGGTGGG 18288          _   AGG TG A
                 G                  TCTCGCTCTGTC ACCC  C  G
                                    |||||||||||| ||||  | |
                                    GGGGTGGGATAG TGGG  G  T
                                          G   G__ GT GT
GAM1741  GABRE    3'  GTTGGGGGGGTGGATAGGGTGGG 18289          _   AGG TG A
                 G                  TCTCGCTCTGTC ACCC  C  G
                                    |||||||||||| ||||  | |
                                    GGGGTGGGATAG TGGG  G  T
                                          G   G__ GT GT
GAM1741  GABRE    3'  TTGGGGGGGTGGATAGGGTGGGG 18294          _   AGG TG A
                                    TCTCGCTCTGTC ACCC  C  G
                                    |||||||||||| ||||  | |
                                    GGGGTGGGATAG TGGG  G  T
                                          G   G__ GT G
GAM1741  GABRE    3'  TTGGGGGGGTGGATAGGGTGGGG 18295          _   AGG TG A
                                    TCTCGCTCTGTC ACCC  C  G
                                    |||||||||||| ||||  | |
                                    GGGGTGGGATAG TGGG  G  T
                                          G   G__ GT G
GAM1741  GADD45B  3'  TCCACTCGGGGGTGGAGTGAGA 32247        TG  A  AG C
                                    TCTCGCTC  TC CCC  G TGGA
                                    ||||||||  || |||  | ||||
                                    AGAGTGAG  GG GGG  C ACCT
                                         GT  _   CT _
GAM1741  GALNT7   3'  TCCAACCTGGGTGACAGAGTGA 55090              C
                 GA                   TCTCGCTCTGTCACCCAGG TGGA
                                      |||||||||||||||||| ||||
                                      AGAGTGAGACAGTGGGTCC ACCT
                                                 A
GAM1741  GAN      5'  TCCAGCTTCTGCTCAGAGCGCG 42123     _      TCACCC
                 GA                   TCT CGCTCTG     AGGCTGGA
                                      ||| |||||||     ||||||||
                                      AGG GCGAGAC     TTCGACCT
                                        C      TCGTC_
GAM1741  GAS1     5'  TCTCGGGTGGGAGAGCGGGA   10764         G     _
                                    TCTCGCTCT TCACCC AGG
                                    ||||||||| |||||| |||
                                    AGGGCGAGA GGTGGG TCT
                                          G     C
GAM1741  GAS7     3'  TCCAGCTTGGGTGACAGAGCAA 20859     C
                 GA                   TCT GCTCTGTCACCCAGGCTGGA
                                      ||| ||||||||||||||||||||
                                      AGA CGAGACAGTGGGTTCGACCT
                                        A
GAM1741  GAS7     3'  TCTGGGGGGTGGGGTGAGG    14671         TG  A
                                    TCTCGCTC  TC CCCAGG
                                    ||||||||  || ||||||
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                                GGAGTGGG  GG GGGTCT
                                    GT  _
GAM1741  GCH1     3'  TTTGGGTTATGATGGGGCAAGA 5681      C       ___
                                TCT GCTCTGTC   ACCCAGG
                                ||| ||||||||   |||||||
                                AGA CGGGGTAG   TGGGTTT
                                  A       TAT
GAM1741  GCN5L1   5'  CCAGCTTCCGGAGCCGGA    9436      C     TCACCC
                                TCT GCTCTG     AGGCTGG
                                ||| ||||||     |||||||
                                AGG CGAGGC     TTCGACC
                                  C     C_____
GAM1741  GFAP     3'  TTGGTTTTTATGAGGTGGGA   10787       CTG   CCC    TG
                                TCTCGCT   TCA   AGGC  GA
                                |||||||   |||   ||||  ||
                                AGGGTGG   AGT   TTTG  TT
                                    ___   ATT    GT
GAM1741  GHR      3'  TTTGGGGGAGTGACAGGATGGG 5707       CT      _  AGG TG
              G                  TCTCG  CTGTCAC CC   C  GA
                                 |||||  ||||||| ||   |  ||
                                 GGGGT  GACAGTG GG   G  TT
                                   AG      A  G__ GT
GAM1741  GP2      3'  TCCAGCCTGGGCAACAGAGCAA 9483      C       CA
              GA                 TCT GCTCTGT  CCCAGGCTGGA
                                 ||| |||||||  ||||||||||
                                 AGA CGAGACA  GGGTCCGACCT
                                   A      AC
GAM1741  GPC4     3'  TTTCTTGGGGGATGGGGTGGGG 9357             A     CTGGA
                                 TCTCGCTCTGTC CCCAGG
                                 ||||||||||| ||||||
                                 GGGGTGGGGTAG GGGTTC
                                        G     TTTT
GAM1741  GPC6     5'  TCGGCTTGAGGGGCAAGG    20334    TC    A  _
                                 C  TGTC CC CAGGCTGG
                                 |  |||| || ||||||||
                                 G  ACGG GG GTTCGGCT
                                  GA    _  A
GAM1741  GRAF     3'  TCCAGCCTGGGTGACAGAGCCA 31248     C
              GA                 TCT GCTCTGTCACCCAGGCTGGA
                                 ||| ||||||||||||||||||
                                 AGA CGAGACAGTGGGTCCGACCT
                                   C
GAM1741  GRIN2B   3'  TTGGGCCTGGCTGGGTGGGA   7732         TGTCAC      G
                                 TCTCGCTC     CCAGGCT GA
                                 ||||||||     ||||||| ||
                                 AGGGTGGG     GGTCCGG TT
                                      TC____       G
GAM1741  GRM3     5'  TCCAGTTTGGAAATGAGAGAG  7748      G   C__
                                 CTCT TCA   CCAGGCTGGA
                                 |||| |||   ||||||||||
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                                GAGA AGT   GGTTTGACCT
                                  G   AAA
GAM1741  GRM6     3'  TCCAGCCTGGGTGACAGAGCGA 7771
                 GA                TCTCGCTCTGTCACCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGCGAGACAGTGGGTCCGACCT
                                                      C
GAM1741  GTF2F1   3'  TCCAGCCTGGGTGACAGAATGA 10893     C
                                   TCG TCTGTCACCCAGGCTGGA
                                   ||| ||||||||||||||||||
                                   AGT AGACAGTGGGTCCGACCT
                                     A
GAM1741  HD       3'  CGGTGGGTGGAGTCAGG     10913     C    TGT    AG  TG
                                   TCT GCTC   CACCC  GC  G
                                   ||| ||||   |||||  ||  |
                                   GGA TGAG   GTGGG  TG  C
                                     C    ___     __  GT
GAM1741  HDAC6    3'  TCCAGCCTGTACCTTGGATGAG 21280       C    TCACC
                 G                  TCTCG TCTG     CAGGCTGGA
                                    |||||| ||||    |||||||||
                                    GGAGT AGGT     GTCCGACCT
                                      _    TCCAT
GAM1741  HEPH     5'  TCAGTGTGGTAGATGAGA    29652       C    TCAC   G
                                   TCTCG TCTG    CCA GCTGG
                                   ||||| ||||    ||| |||||
                                   AGAGT AGAT    GGT TGACT
                                     _    ____   G
GAM1741  HIP1     3'  ACTCCGGCCTGGGTGACAGAGT 19245
                 GAGA                  TCTCGCTCTGTCACCCAGGCTGGA
                                       ||||||||||||||||||||||||
                                       AGAGTGAGACAGTGGGTCCGGCCT
                                                    CAC
GAM1741  HIP1     3'  TCCAGCCTGAGTGACAGAGCGA 19264             C
                 GA                  TCTCGCTCTGTCAC CAGGCTGGA
                                     |||||||||||||| |||||||||
                                     AGAGCGAGACAGTG GTCCGACCT
                                               A
GAM1741  HKE4     3'  TTGGGGGGATGGGGTGGGA    23715           A_
                                   TCTCGCTCTGTC  CCCAG
                                   ||||||||||||  |||||
                                   AGGGTGGGGTAG  GGGTT
                                          GG
GAM1741  HLA-E    3'  TCCAGCCTGGGTGACAGGGTGA 92677
                                   TCGCTCTGTCACCCAGGCTGGA
                                   ||||||||||||||||||||||
                                   AGTGGGACAGTGGGTCCGACCT

GAM1741  HMGA2    3'  TCTGGGGTGGGGTGGGGTGGGG 14458         TG CA    GG TG
                                   TCTCGCTC  T  CCCA  C  GA
                                   ||||||||  |  ||||  |  ||
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                                GGGGTGGG  G  GGGT  G  CT
                                    GT __    GG GT
GAM1741  HNRPH1   3'  TCCAGTATGAGTGGTGGATGGG 19813      C  TG   C  G
           G                     TCTCG TC  TCAC CA GCTGGA
                                 |||||| ||  |||| || |||||||
                                 GGGGT AG  GGTG GT TGACCT
                                   _ GT    A  A
GAM1741  HOXB6    3'  CCGGCGCAGACAGGCGGGG   60538       T    ACCCAG
                                 TCTCGC CTGTC     GCTGG
                                 |||||| |||||     |||||
                                 GGGGCG GACAG     CGGCC
                                    _    ACG___
GAM1741  HRH1     3'  TCCAGCCTGGGCAACAGAGCAA 7828      C      CA
           GA                      TCT GCTCTGT  CCCAGGCTGGA
                                 ||| |||||||  ||||||||||
                                 AGA CGAGACA  GGGTCCGACCT
                                   A      AC
GAM1741  HS3ST2   3'  CAAGATGCTCTGGGTGGTGGGA 21276      CT TG      _  TGGA
           TGGGA                   TCTCG  C  TCACCCAG GC
                                 |||||  |  |||||||| ||
                                 AGGGT  G  GGTGGGTC CG
                                   AG GT       T  TAGAACT
GAM1741  HSD17B1  5'  TTTGGCTCAGAACAGGGTGGGG 6431          CACCCA   TG
                                 TCTCGCTCTGT     GGC  GA
                                 ||||||||||     |||  ||
                                 GGGGTGGGACA     TCG  TT
                                       AGAC__   GT
GAM1741  HSPA1L   5'  TTTGCAGGGAGGGACGGGGTGG 99601          AC_  AG  TGGA
           GG                      TCTCGCTCTGTC   CC  GC
                                 ||||||||||||   ||  ||
                                 GGGGTGGGGCAG   GG  CG
                                       GGA  GA  TTT
GAM1741  HSPA5    3'  TCCAGCCTGGCGACAAGAGTGA 19290         _  AC
           GA                      TCTCGCTCT GTC  CCAGGCTGGA
                                 |||||||| |||  ||||||||||
                                 AGAGTGAGA CAG  GGTCCGACCT
                                      A  C_
GAM1741  HTLF     5'  TCAGCCTGGGAAGTGAGG    10975       CTGTCA
                                 TCTCGCT     CCCAGGCTGG
                                 |||||||     ||||||||||
                                 GGAGTGA     GGGTCCGACT
                                    A_____
GAM1741  HUNK     3'  TCCAGCTTAGGTGGCAAAGTGA 28192       C      C
           GA                      TCTCGCT TGTCACC AGGCTGGA
                                 ||||||| ||||||| ||||||||
                                 AGAGTGA ACGGTGG TTCGACCT
                                    A      A
GAM1741  IAPP     3'  ACTCCAGCCTGGGTGGCAGAGT 6433
           GAGA                    TCTCGCTCTGTCACCCAGGCTGGA
                                 |||||||||||||||||||||||||
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                                AGAGTGAGACGGTGGGTCCGACCT
                                                    CAC
GAM1741  ICAM1    3'  CTAGCCTGATGAGAGGGGA   72036    G   G  CC
                                TC CTCT TCA  CAGGCTGG
                                || |||| |||  ||||||||
                                AG GGGA AGT  GTCCGATC
                                 _   G   A_
GAM1741  ICOS     3'  TCTGTGTGTGGGGTGGGG    24925          T  C
                                TCTCGCTCTG CAC CAGG
                                |||||||||| ||| ||||
                                GGGGTGGGGT GTG GTCT
                                       _  T
GAM1741  ID1      3'  TCCAGCCTGGGGCTGAGGCTGA 70574      _  T  GTCA
              GG                  TCTC GC CT    CCCAGGCTGGA
                                |||| || ||    ||||||||||
                                GGAG CG GA    GGGTCCGACCT
                                  T  _  GTCG
GAM1741  IFIT4    3'  TCCAGCCTGGGCAACAGAGCAA 71497     C      CA
              GA                  TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A       AC
GAM1741  IL10     3'  TCCAGCCTGGGTGACAGAGCAA 6929      C
              GA                  TCT GCTCTGTCACCCAGGCTGGA
                                ||| ||||||||||||||||||
                                AGA CGAGACAGTGGGTCCGACCT
                                  A
GAM1741  IL13RA1  3'  TCTAGCCTGGGTGACAGAGCAA 9576      C
              GA                  TCT GCTCTGTCACCCAGGCTGGA
                                ||| ||||||||||||||||||
                                AGA CGAGACAGTGGGTCCGATCT
                                  A
GAM1741  IL17R    3'  ACTGCAGCCTGGATGACAGAGC 27547           C       GA
              GAGA                  TCTCGCTCTGTCA CCAGGCTG
                                |||||||||||| ||||||||
                                AGAGCGAGACAGT GGTCCGAC
                                       A       GTCAC
GAM1741  IL1R1    3'  TCTAGCCTGGCAACAGAGCAAG 7925      C      CAC
              A                   TCT GCTCTGT   CCAGGCTGGA
                                ||| |||||||   ||||||||||
                                AGA CGAGACA   GGTCCGATCT
                                  A      AC_
GAM1741  IL26     3'  CGGCTGGATTTGTGTGTGGAGT 37858         TG _  ________  AGGCT
              GGGA                  TCTCGCTC  T CAC       CC    G
                                ||||||||  | |||      ||    |
                                AGGGTGAG  G GTG      GG    C
                                     GT T   TTT   A  TCGGA
GAM1741  IL2RA    3'  TCCAGCCTGGGCAACAGAGCAA 6453      C      CA
              GA                  TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
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                                AGA CGAGACA  GGGTCCGACCT
                                  A      AC
GAM1741  IRAK1    3'  TCCAGCCTGGGTGACAGAGCAA 9618      C
                GA                  TCT GCTCTGTCACCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAGTGGGTCCGACCT
                                      A
GAM1741  IRAK4    3'  ACTCCAGCCTGGGTGACAGAGT 61837
                GAGA                  TCTCGCTCTGTCACCCAGGCTGGA
                                      |||||||||||||||||||||||||
                                      AGAGTGAGACAGTGGGTCCGACCT
                                                  CAC
GAM1741  ITGA5    3'  TTAGCCTGCAGTGTGAGG    61936       T   TCACC
                                      TCTCGC CTG    CAGGCTGG
                                      |||||| |||    ||||||||
                                      GGAGTG GAC    GTCCGATT
                                         T  _____
GAM1741  ITGAL    3'  TCCAGCCTGGGCAACACAGCGA 11050        C   CA
                GA                    TCTCGCT TGT  CCCAGGCTGGA
                                      ||||||| |||  ||||||||||||
                                      AGAGCGA ACA  GGGTCCGACCT
                                         C   AC
GAM1741  ITPKB    3'  GCTGGGGGGTGGAGGGTGGGA   11067         G     A_
                                      TCTCGCTCT TCACCC  GGC
                                      |||||||||| ||||||  |||
                                      AGGGTGGGA GGTGGG  TCG
                                            _     GG
GAM1741  JMJ      3'  TCTCGGTGGGGGGGTGGGG    18325         G    C
                                      TCTCGCTCT TCACC AGG
                                      |||||||||| ||||| |||
                                      GGGGTGGGG GGTGG TCT
                                            _    C
GAM1741  JPH2     5'  TCTGGCTGGTGGAGTCGGG   96086      _  TG   C
                                      CTCG CTC  TCA CCAGG
                                      |||| |||  ||| |||||
                                      GGGC GAG  GGT GGTCT
                                        T   GT   C
GAM1741  KCNA7    3'  TCCAGCCTGGGCAACAGAGGGA 49904    G     CA
                                      TC CTCTGT  CCCAGGCTGGA
                                      || ||||||  ||||||||||||
                                      AG GAGACA  GGGTCCGACCT
                                       G     AC
GAM1741  KCNJ5    3'  TCCAGCCTGGGCGACAGAGCGA 7978             A
                GA                    TCTCGCTCTGTC CCCAGGCTGGA
                                      |||||||||||| ||||||||||||
                                      AGAGCGAGACAG GGGTCCGACCT
                                              C
GAM1741  KCNK3    3'  TCCAGCCTGGGTGACAGGGCAA 11178     C
                GA                    TCT GCTCTGTCACCCAGGCTGGA
                                      ||| ||||||||||||||||||||
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                                AGA CGGGACAGTGGGTCCGACCT
                                  A
GAM1741  KCNK6    3'  TCCAGCCTGCGGGACAGAGTGA 17885          A  _
                GA                  TCTCGCTCTGTC CC CAGGCTGGA
                                    |||||||||||| || |||||||||
                                    AGAGTGAGACAG GG GTCCGACCT
                                          _  C
GAM1741  KIF1B    3'  TCCAGCCTGGGTGACAGAGCAA 31271     C
                GA                  TCT GCTCTGTCACCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAGTGGGTCCGACCT
                                      A
GAM1741  KIF3B    3'  ATTCCAGCCTGGGTGACAGAGT 17802
                GAGA                  TCTCGCTCTGTCACCCAGGCTGGA
                                    |||||||||||||||||||||||||
                                    AGAGTGAGACAGTGGGTCCGACCT
                                                TAC
GAM1741  KLHL3    3'  TCTGGTCTCACTATGAAGTGGG 88853        CT  CACCC    TG
                G                    TCTCGCT  GT    AGGC  GA
                                    |||||||  ||    ||||  ||
                                    GGGGTGA  TA    TCTG  CT
                                       AG  TCAC_   GT
GAM1741  KLRG1    3'  TCCAGCCTGGGAGATAGAGCAA 20557     C       A
                GA                  TCT GCTCTGTC CCCAGGCTGGA
                                    ||| |||||||| ||||||||||
                                    AGA CGAGATAG GGGTCCGACCT
                                      A       A
GAM1741  KNSL1    3'  TCCAGCCTGGGCAACAGAGCAA 16949     C      CA
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGAGACA  GGGTCCGACCT
                                      A      AC
GAM1741  KNSL2    3'  TCTATGTATCGGGTGAGGGGTG 74289          G     AG_  _
                GGA                   TCTCGCTCT TCACCC   GC TGGA
                                    ||||||||| ||||||   || ||||
                                    AGGGTGGGG AGTGGG   TG ATCT
                                         _     CTA  T
GAM1741  LAMC2    3'  TCCAGCCTGGGGAACAGAGCAA 19909     C      CA
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGAGACA  GGGTCCGACCT
                                      A      AG
GAM1741  LDLR     3'  TCTGGCCTGGGCGACAGAGCGA 6746            A      TG
                GA                  TCTCGCTCTGTC CCCAGGC  GA
                                    |||||||||||| |||||||  ||
                                    AGAGCGAGACAG GGGTCCG  CT
                                          C      GT
GAM1741  LEF1     5'  TCGGCCTCGGGGCGGGCG    33227     T    A  C
                                    CGC CTGTC CC AGGCTGG
                                    ||| ||||| || |||||||
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                                GCG GGCGG GG TCCGGCT
                                  _    _ C
GAM1741 LEP      3' TCCGGCCTGATGACAGAGCGAG 5870           CC
                A                  TCTCGCTCTGTCA CAGGCTGGA
                                   |||||||||||| |||||||||
                                   AGAGCGAGACAGT GTCCGGCCT
                                          A_
GAM1741 LFG      3' ATAGCCAGGATAGGGCGGGA 77229          ACCCA   GA
                                   TCTCGCTCTGTC   GGCTG
                                   |||||||||||    |||||
                                   AGGGCGGGATAG   CCGAT
                                          GA___   AC
GAM1741 LFG      3' TTTGGCCTGGGTGGGGCTGGG 77244    _   TGT      TG
                                   CTC GCTC  CACCCAGGC GA
                                   ||| ||||  ||||||||| ||
                                   GGG CGGG  GTGGGTCCG TT
                                     T  ___       GT
GAM1741 LIF      3' TCCAGTCTGAGAGCAGGGGAGG 11308     G    CACC
                                   TCTC CTCTGT   CAGGCTGGA
                                   |||| ||||||   |||||||||
                                   GGAG GGGACG   GTCTGACCT
                                     _    AGA_
GAM1741 LILRB1   3' TCCAGCCTGGCGACAGAGGGAG 22877     G     AC
                A                  TCTC CTCTGTC  CCAGGCTGGA
                                   |||| |||||||  ||||||||||
                                   AGAG GAGACAG  GGTCCGACCT
                                     G     C_
GAM1741 LIMD1    3' TCCAGCTCAGTGTGGGGCGTGG 27264    T     T  CCA
                                   TC CGCTCTG CAC  GGCTGGA
                                   || ||||||| |||  |||||||
                                   GG GCGGGGT GTG  TCGACCT
                                    T      _  AC_
GAM1741 LPIN1    3' TCCAGCCTGGGTGACAGAGTAA 67992    CG
                GA                   TCT  CTCTGTCACCCAGGCTGGA
                                   |||  ||||||||||||||||||
                                   AGA  GAGACAGTGGGTCCGACCT
                                     AT
GAM1741 LRRC2    3' CCTCCAGCCTGGGTGACAGAGT 44743
                GAGA                   TCTCGCTCTGTCACCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGTGAGACAGTGGGTCCGACCT
                                            CCC
GAM1741 LRRC2    3' TCCAGCCTGGGCAACAGAGTGA 44759          CA
                GA                   TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   AGAGTGAGACA  GGGTCCGACCT
                                         AC
GAM1741 LRRC2    3' TCCAGCCTGGGTGACAGAGCCA 44760    C
                GA                   TCT GCTCTGTCACCCAGGCTGGA
                                   ||| ||||||||||||||||||
```

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                                AGA CGAGACAGTGGGTCCGACCT
                                  C
GAM1741 LTB     3'  TGGGGCCGTGATGGTGGGGTGA 11371        TG  CCCA   GGA
                GG                  TCTCGCTC  TCA   GGCT
                                    ||||||||  |||   ||||
                                    GGAGTGGG  GGT   CCGG
                                       GT   AGTG   GGTT
GAM1741 LUZP1   3'  TCCAGCCTGGGCAACAAGAGTG 54405       _  CA
                A                    TCGCTCT GT  CCCAGGCTGGA
                                    |||||||  ||  ||||||||||
                                    AGTGAGA CA  GGGTCCGACCT
                                       A  AC
GAM1741 LY64    3'  TCCGCATGTGGAAGAGTGGGA  19949        GT  CCAG  T
                                    TCTCGCTCT  CAC   GC GGA
                                    |||||||||  |||   || |||
                                    AGGGTGAGA  GTG   CG CCT
                                         AG   TA__  _
GAM1741 LY94    3'  TTGAGCCTGGGCGACAGAGCGA 17898          A      G
                GA                  TCTCGCTCTGTC CCCAGGCT GA
                                    ||||||||||| |||||||| ||
                                    AGAGCGAGACAG GGGTCCGA TT
                                          C       G
GAM1741 LZTS1   3'  TCTGCAGATGTGCGGAGCGGGA 41040         T  CCAG  T
                                    TCTCGCTCTG CAC   GC GGA
                                    |||||||||| |||   || |||
                                    AGGGCGAGGC GTG   CG TCT
                                          _  TAGA  _
GAM1741 MADH2   5'  GGCCTGGGGGCGGGGCGGGA  20916          A
                                    TCTCGCTCTGTC CCCAGGCT
                                    |||||||||||| ||||||||
                                    AGGGCGGGGCGG GGGTCCGG
                                                _
GAM1741 MADH2   3'  TTAGTTTGCATAGATGAGG   20918      C    CACC
                                    TCTCG TCTGT   CAGGCTGG
                                    ||||| |||||   ||||||||
                                    GGAGT AGATA   GTTTGATT
                                       _    C___
GAM1741 MAFF    3'  TTTAGCCTTTTTAGATTGAGA  25588      C   TCACCC
                                    TCTCG TCTG    AGGCTGGA
                                    ||||| ||||    ||||||||
                                    AGAGT AGAT    TCCGATTT
                                       T   TTT___
GAM1741 MAP3K14  3'  TCCAGCCTGGGTCAGAAGGGGT 15548        G  __
                GGG                 CTCGCTCT TC  ACCCAGGCTGGA
                                    ||||||||  ||  ||||||||||||
                                    GGGTGGGG AG  TGGGTCCGACCT
                                       A  AC
GAM1741 MATN4   3'  TCCGGCTTGGGCTGTCGGGGCG 48358    T     T  _
                GA                  TC CGCTCTG CA CCCAGGCTGGA
                                    || ||||||| || ||||||||||
```

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                                AG GCGGGGC GT GGGTTCGGCCT
                                 _      T  C
GAM1741  MBD4     3'  TCCAGTCTGGATGACAGAGAGA 15389      G       C
                GA                TCTC CTCTGTCA CCAGGCTGGA
                                  |||| |||||||| ||||||||||
                                  AGAG GAGACAGT GGTCTGACCT
                                    A       A
GAM1741  MCL1     3'  TTTAGTGAAGATGGTAGGGTGG 41991     T     GT  CCCAG
                A                  TC CGCTCT  CA     GCTGGA
                                  || ||||||  ||     ||||||
                                  AG GTGGGA  GT     TGATTT
                                   _     TG  AGAAG
GAM1741  MCM4     3'  TCCAGCCTCAGCAATAGAGTGA 62583           CACCC
                GA                TCTCGCTCTGT     AGGCTGGA
                                  ||||||||||     ||||||||
                                  AGAGTGAGATA     TCCGACCT
                                        ACGAC
GAM1741  MDM4     3'  TCCAGCCTGGGTGACAGCGCGA 11514        T
                GA                TCTCGC CTGTCACCCAGGCTGGA
                                  |||||| ||||||||||||||||
                                  AGAGCG GACAGTGGGTCCGACCT
                                     C
GAM1741  MECP2    3'  TCTAGCCCTGCCCGGATGGAGC 18414           ACC_   _
                GGGG                  TCTCGCTCTGTC    CAGG CTGGA
                                  ||||||||||    |||| |||||
                                  GGGGCGAGGTAG    GTCC GATCT
                                        GCCC    C
GAM1741  MHC2TA   3'  ATAGCCTAGGTGACAGAGTGAG 5968             C     GA
                A                  TCTCGCTCTGTCACC AGGCTG
                                  |||||||||||||| ||||||
                                  AGAGTGAGACAGTGG TCCGAT
                                           A     AT
GAM1741  MKPX     5'  CCGCGAGGGCGGAGTGGGG    39877          TCA   AG  T
                                  TCTCGCTCTG   CCC  GC GG
                                  ||||||||||   |||  || ||
                                  GGGGTGAGGC   GGG  CG CC
                                        ____   AG  _
GAM1741  MMP11    3'  TCCTGCAGGGGGATGGGGTGGG 21046           A   AG  T
                G                  TCTCGCTCTGTC CCC  GC GGA
                                  |||||||||||| |||  || |||
                                  GGGGTGGGGTAG GGG  CG CCT
                                        _   GA  T
GAM1741  MOG      3'  TCTAGCCGGAGTGACAGAGTAA 11677     CG       _ A
                GA                  TCT  CTCTGTCAC CC GGCTGGA
                                  |||  ||||||||| || |||||||
                                  AGA  GAGACAGTG GG CCGATCT
                                    AT        A  _
GAM1741  MSH3     3'  TCCAGCTTGGGCAACAGAGCAA 11693     C      CA
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
```

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                                AGA CGAGACA  GGGTTCGACCT
                                  A      AC
GAM1741  MTMR8    3'  TCCAGCCTGAGCAACAGAGCGA 31917          CACC
                GA                  TCTCGCTCTGT   CAGGCTGGA
                                    ||||||||||    |||||||||
                                    AGAGCGAGACA   GTCCGACCT
                                          ACGA
GAM1741  MTMR8    3'  TCCAGCCTGGGCGAAAGGGCAA 31918     C    G  A
                GA                  TCT GCTCT TC CCCAGGCTGGA
                                    ||| ||||| || ||||||||||
                                    AGA CGGGA AG GGGTCCGACCT
                                      A    A  C
GAM1741  MUC4     5'  CTGGTGGGGTAGTGGGGTGGGG 37878          TC   AG  TG A
                                    TCTCGCTCTG  ACCC  GC  G
                                    |||||||||  ||||  ||  |
                                    GGGGTGGGGT  TGGG  TG  C
                                          GA   G_  GT C
GAM1741  MYO10    3'  TCTGAGGGAAGGTGAGGGAGTG 25615         G    CAGG  _
                GGA                   TCTCGCTCT TCACC   CT GGA
                                    |||||||||  |||||   || |||
                                    AGGGTGAGG AGTGG   GA TCT
                                         G    AAGG  G
GAM1741  MYO1C    3'  TCCAGCCTGGGCAACAGAGCGA 61870          CA
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGCGAGACA  GGGTCCGACCT
                                          AC
GAM1741  NAV2     3'  TCCGTGAGAGTGAGTGACGGAG 60798           C  GG  ___
                TGAGA                 TCTCGCTCTGTCAC CA  CT   GGA
                                    |||||||||||||| ||  ||   |||
                                    AGAGTGAGGCAGTG GT  GA   CCT
                                           A  GA  GTG
GAM1741  NAV2     3'  TTCATTAGGGGTGGGGTGGGA  60801        TGT    AGGC
                                    TCTCGCTC   CACCC    TGGA
                                    ||||||||   |||||    ||||
                                    AGGGTGGG   GTGGG    ACTT
                                         ___     GATT
GAM1741  NCAM2    5'  TCCGGTCTCTCTCCAGGGCTGG 17004     C     TCACCC
                A                    TCT GCTCTG     AGGCTGGA
                                    ||| ||||||     ||||||||
                                    AGG CGGGAC     TCTGGCCT
                                      T     CTCTC_
GAM1741  NDRG1    3'  TCCAGCCTTCCAGGTGGCGTGA 60312       TCT     C___
                GA                    TCTCGC   GTCACC    AGGCTGGA
                                    ||||||   ||||||    ||||||||
                                    AGAGTG   CGGTGG    TCCGACCT
                                       ___     ACCT
GAM1741  NFIA     5'  TCAGCTCATGGAGCGG      70889          CACCCA
                                    TCGCTCTGT     GGCTGG
                                    |||||||||     ||||||
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                                GGCGAGGTA     TCGACT
                                    C_____
GAM1741  NFKBIL2   3'  TCCAGCCTGGGCGACAGACCGA 26455      C     A
            GA                    TCTCG TCTGTC CCCAGGCTGGA
                                  ||||| |||||| ||||||||||
                                  AGAGC AGACAG GGGTCCGACCT
                                    C     C
GAM1741  NIPSNAP1  3'  TCCAGTGGCTAGAGGTGGGGTG 14663        TG  AC___  AG
            GGA                   TCTCGCTC  TC    CC  GCTGGA
                                  |||||||| ||    ||  ||||||
                                  AGGGTGGG  GG    GG  TGACCT
                                      GT  AGATC  __
GAM1741  NKX3A    3'  TCCAGCCTGGGCAACGAGCAAG 21617     C    T  CA
            A                     TCT GCTC GT  CCCAGGCTGGA
                                  ||| |||| ||  ||||||||||
                                  AGA CGAG CA  GGGTCCGACCT
                                    A   _  AC
GAM1741  NPHS1    3'  TCCAGCCTGGGCGACAGAGCGA 17374           A
            GA                    TCTCGCTCTGTC CCCAGGCTGGA
                                  |||||||||||| ||||||||||
                                  AGAGCGAGACAG GGGTCCGACCT
                                         C
GAM1741  NPTX1    3'  TTTGGCCTCCCGGAGTGCAGA  11843     _      TCACCC    TG
                                  TCT CGCTCTG     AGGC  GA
                                  ||| |||||||     ||||  ||
                                  AGA GTGAGGC     TCCG  TT
                                    C      CC_____    GT
GAM1741  NR1I2    3'  TTCAGTCTGTAGGGAGTGA    15305        GTCACC
                                  TCGCTCT     CAGGCTGGA
                                  |||||||     |||||||||
                                  AGTGAGG     GTCTGACTT
                                      GAT___
GAM1741  NRXN2    3'  TGGTGGGGTTGGGTGGGA     57826         TGTC    AG  TG
                                  TCTCGCTC    ACCC  GC  G
                                  ||||||||    ||||  ||  |
                                  AGGGTGGG    TGGG  TG  T
                                      T___    G_  GT
GAM1741  OGG1     5'  TCCAGCCTAGGCGACAGAGTGA 34160           A  C
            GA                    TCTCGCTCTGTC CC AGGCTGGA
                                  |||||||||||| || ||||||||
                                  AGAGTGAGACAG GG TCCGACCT
                                         C  A
GAM1741  OPA3     3'  TCCAGCCCGGGTGACAGAGCAA 47848     C          A
            GA                    TCT GCTCTGTCACCC GGCTGGA
                                  ||| |||||||||||| |||||||
                                  AGA CGAGACAGTGGG CCGACCT
                                    A           C
GAM1741  OPCML    3'  TCCAGCTTGAATGAGTGGGGTT 11901       _    _  CC
            GGGG                    TCTCG CTCTG TCA  CAGGCTGGA
                                  ||||| ||||| |||  |||||||||
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                                GGGGT GGGGT AGT  GTTCGACCT
                                  T    G  AA
GAM1741  OPRD1    3'  TCTGGTTTGGGGCGAGGCAGAG 8070        A___     TG
                                CTCTGTC   CCCAGGC  GA
                                |||||||   |||||||  ||
                                GAGACGG   GGGTTTG  CT
                                   AGCG      GT
GAM1741  OPTN     3'  TCCAGCCTGGGTGACAGAGGGA 42053     G
           GA                     TCTC CTCTGTCACCCAGGCTGGA
                                |||| ||||||||||||||||||
                                AGAG GAGACAGTGGGTCCGACCT
                                  G
GAM1741  P53AIP1  3'  TCCAGCCTGGGCGACAGAGAGA 42340     G     A
           GA                     TCTC CTCTGTC CCCAGGCTGGA
                                |||| ||||||| ||||||||||
                                AGAG GAGACAG GGGTCCGACCT
                                  A      C
GAM1741  PA2G4    3'  TCCAGCCTGGGTGACAGAATGA 71831      C
           GA                     TCTCG TCTGTCACCCAGGCTGGA
                                ||||| ||||||||||||||||||
                                AGAGT AGACAGTGGGTCCGACCT
                                   A
GAM1741  PACSIN1  3'  TCCAGCCTGAGACATCAGGGGA 93886     G    TCACC_
           GA                     TCTC CTCTG     CAGGCTGGA
                                |||| |||||     |||||||||
                                AGAG GGGAC     GTCCGACCT
                                  _    TACAGA
GAM1741  PCDH11X  3'  TCCAGCCTGGGTGACAGAGCAA 28017     C
           GA                     TCT GCTCTGTCACCCAGGCTGGA
                                ||| ||||||||||||||||||
                                AGA CGAGACAGTGGGTCCGACCT
                                  A
GAM1741  PCDH11Y  3'  TCCAGCCTGGGTGACAGAGCAA 53169     C
           GA                     TCT GCTCTGTCACCCAGGCTGGA
                                ||| ||||||||||||||||||
                                AGA CGAGACAGTGGGTCCGACCT
                                  A
GAM1741  PCDH7    5'  TCTGGCCCCTTCCGACAGAGCG 11993          ACCCA_  TG
           GGG                    TCTCGCTCTGTC     GGC  GA
                                ||||||||||||     |||  ||
                                GGGGCGAGACAG     CCG  CT
                                      CCTTCC   GT
GAM1741  PDE4C    3'  TCCAGCCTGGGGCTGACAGAGC 8108      C       __
           AAGA                    TCT GCTCTGTCA  CCCAGGCTGGA
                                ||| |||||||||  ||||||||||
                                AGA CGAGACAGT  GGGTCCGACCT
                                  A        CG
GAM1741  PHF1     3'  CCAAGAGTGGGGAGTGGGG   44389        TGTCA   GG  _
                                TCTCGCTC    CCCA  CT GG
                                ||||||||    ||||  || ||
```

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                                GGGGTGAG    GGGT  GA CC
                                     _____   GA  A
GAM1741  PHF1    3'  CCAGAGTGGGGAGTGGGG    44390        TGTCA   GG  _
                                TCTCGCTC    CCCA  CT GG
                                ||||||||    ||||  || ||
                                GGGGTGAG    GGGT  GA CC
                                     _____   GA  A
GAM1741  PHKB    3'  CACCAGCCTGGGTGACAGAGCG 6096                  A
           AGA                    TCTCGCTCTGTCACCCAGGCTGG
                                ||||||||||||||||||||||
                                AGAGCGAGACAGTGGGTCCGACC
                                          ACA
GAM1741  PHLDA3  3'  TTCGGCCTAAGGTGGTGGGGGT 25696       _ TG    C_
           GAGG                   TCTCGCT C  TCACC  AGGCTGGA
                                ||||||| |  |||||  ||||||||
                                GGAGTGG G  GGTGG  TCCGGCTT
                                    G GT    AA
GAM1741  PIAS3   3'  CCAGTATGACAGAGGAGG    21444      G      CCCAG
                                TCTC CTCTGTCA    GCTGG
                                |||| ||||||||    |||||
                                GGAG GAGACAGT    TGACC
                                  _       A____
GAM1741  PIK3CG  3'  TCCAGCCTGGATAACAGAGCGA 12125          CAC
           GA                     TCTCGCTCTGT   CCAGGCTGGA
                                ||||||||||   ||||||||||
                                AGAGCGAGACA   GGTCCGACCT
                                      ATA
GAM1741  PIM1    3'  CCGGGGGTGGGGGGTGGGG   92683        G     AGG
                                TCTCGCTCT TCACCC   CTGG
                                |||||||| ||||||   ||||
                                GGGGTGGGG GGTGGG   GGCC
                                     _    ___
GAM1741  PITPNB  3'  TCTGGCCTGCGTGCGGTGAGG  25703       CT T   C    TG
                                TCTCGCT  G CAC CAGGC  GA
                                |||||||  | ||| |||||  ||
                                GGAGTGG  C GTG GTCCG  CT
                                   __ _  C    GT
GAM1741  PLA2G2D  3'  TCCAGCCTGGGCAACAGAGTGA 25723         CA
                                TCGCTCTGT  CCCAGGCTGGA
                                |||||||||  ||||||||||
                                AGTGAGACA  GGGTCCGACCT
                                     AC
GAM1741  PML     3'  TCTGGTGGGCAGAGAGGGA   53806     G      AC
                                TCTC CTCTGTC  CCAGG
                                |||| |||||||  |||||
                                AGGG GAGACGG  GGTCT
                                  A      GT
GAM1741  PMM2    3'  TCTAGTTTCTCAGGGATGGAGC 72565          A  C___
           GAGA                   TCTCGCTCTGTC CC    AGGCTGGA
                                ||||||||||| ||    ||||||||
```

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                                AGAGCGAGGTAG GG    TTTGATCT
                                      _ ACTC
GAM1741  POLH     3'  TCCAGCCTGGGCAACAGAGCGA 22484          CA
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        AC
GAM1741  POLH     3'  TCCAGCCTGGGCAACAGAGCGA 22485          CA
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        AC
GAM1741  POLK     3'  CCAGCCTGAAGAGCGAGA    33100          GTCACC
                                  TCTCGCTCT     CAGGCTGG
                                  |||||||||     ||||||||
                                  AGAGCGAGA     GTCCGACC
                                        A_____
GAM1741  POU4F1   3'  TTCGGGGGAGTGGGGAGTGGGG 21768          G   _ AGG
                                  TCTCGCTCT TCAC CC   CTGGA
                                  ||||||||| |||| ||   |||||
                                  GGGGTGAGG GGTG GG   GGCTT
                                        _   A  G__
GAM1741  PPP1R12B 3'  TCCAGCCTGGGTGACAGAGCAA 50366     C
              GA                  TCT GCTCTGTCACCCAGGCTGGA
                                  ||| ||||||||||||||||||
                                  AGA CGAGACAGTGGGTCCGACCT
                                    A
GAM1741  PPP2R4   3'  TCCAGTCTGGTTTTGAGAGCAG 61183      _    GTCAC
              GGG                   TCTC GCTCT    CCAGGCTGGA
                                  |||| |||||    ||||||||||
                                  GGGG CGAGA    GGTCTGACCT
                                    A    GTTTT
GAM1741  PPP5C    3'  CCTCGGGGTGGGGTGGGG    21809         TG  A  C
                                  TCTCGCTC  TC CC AGG
                                  ||||||||  || || |||
                                  GGGGTGGG  GG GG TCC
                                       GT  _  C
GAM1741  PRKACA   3'  TGGTCGGGGGGGGTGGGA     12272         GTCA   A   TG
                                  TCTCGCTCT   CCC GGC  G
                                  |||||||||   ||| |||  |
                                  AGGGTGGGG   GGG CTG  T
                                        ____  _  GT
GAM1741  PRKY     3'  CTCCAGCCTGGGTGACAGAGTG 12373
              AGA                   TCTCGCTCTGTCACCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAGTGGGTCCGACCT
                                              CC
GAM1741  PSMB2    3'  TCCAGCCTGGCAACAGAGTGAG 12478          CAC
              A                    TCTCGCTCTGT   CCAGGCTGGA
                                  ||||||||||   ||||||||||
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                                AGAGTGAGACA   GGTCCGACCT
                                      AC_
GAM1741  PSMB2    3'  TCCAGCCTGGCTGACAGAGCAA 12479     C       C
                GA                    TCT GCTCTGTCA CCAGGCTGGA
                                      ||| ||||||||| ||||||||||
                                      AGA CGAGACAGT GGTCCGACCT
                                        A       C
GAM1741  PSMB9    3'  TCCAGCCTGGGAAACAGAGCGA 12509         CA
                                      TCGCTCTGT  CCCAGGCTGGA
                                      |||||||||  ||||||||||
                                      AGCGAGACA  GGGTCCGACCT
                                           AA
GAM1741  PSMB9    3'  TCCAGCCTGGGCGACAAAGCGA 12510       C   A
                GA                    TCTCGCT TGTC CCCAGGCTGGA
                                      |||||||| |||| ||||||||||
                                      AGAGCGA ACAG GGGTCCGACCT
                                          A   C
GAM1741  PSMB9    3'  TCCAGTCTGGACGACAGAGTGA 12511          AC
                GA                    TCTCGCTCTGTC  CCAGGCTGGA
                                      ||||||||||||  ||||||||||
                                      AGAGTGAGACAG  GGTCTGACCT
                                            CA
GAM1741  PTAFR    3'  TCTAGCCTGGCAACAGAGCGAG 8168          CAC
                A                     TCTCGCTCTGT   CCAGGCTGGA
                                      ||||||||||   ||||||||||
                                      AGAGCGAGACA   GGTCCGATCT
                                            AC_
GAM1741  PTGES    3'  TCTGGCTCAGGTGTGGGTGGGA 18074       TGT   CA   TG
                                      TCTCGCTC   CACC  GGC  GA
                                      ||||||||   ||||  |||  ||
                                      AGGGTGGG   GTGG  TCG  CT
                                           T__    AC   GT
GAM1741  PTGIS    3'  TCCAGCCTGGGCGACAGAGCAA 8229      C       A
                GA                    TCT GCTCTGTC CCCAGGCTGGA
                                      ||| |||||||| ||||||||||
                                      AGA CGAGACAG GGGTCCGACCT
                                        A       C
GAM1741  PTGIS    3'  TCTAGCTTTAGCTGGAGGGAGA 8230      G   _ CACCC
                                      TCTC CTCT GT     AGGCTGGA
                                      |||| |||| ||     ||||||||
                                      AGAG GAGG CG     TTCGATCT
                                        G    T  AT___
GAM1741  PTGIS    3'  TTCAGGAGCTGACAGAGCCAGA 8236      C       CCCAGG
                                      TCT GCTCTGTCA     CTGGA
                                      ||| |||||||||     |||||
                                      AGA CGAGACAGT     GACTT
                                        C       CGAG__
GAM1741  PTK2     3'  TCTAGCCTTCCACCAGCAGCGA 20034       _  TCACCC
                GG                    TCTCGCT CTG     AGGCTGGA
                                      ||||||| |||     ||||||||
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                                GGAGCGA GAC     TCCGATCT
                                    C   CACCT_
GAM1741  PTPN23   5'  CCGGCACGAAGGGGCGGGG   64473         G  ACCCAG
                                TCTCGCTCT TC     GCTGG
                                |||||||||  ||     |||||
                                GGGGCGGGG AG     CGGCC
                                    A  CA____
GAM1741  PTPRF    5'  TCCAGCTCGGGTGGCGGTGGCG 56141        _       AG
           GGA                    TCTCGCT CTGTCACCC  GCTGGA
                                |||||||  |||||||||  ||||||
                                AGGGCGG GGCGGTGGG  CGACCT
                                    T        CT
GAM1741  PTPRO    3'  TTCAGCTTCAAAGTAGAGTAGA 48415     C     TCACCC
                                TCT GCTCTG     AGGCTGGA
                                ||| ||||||     ||||||||
                                AGA TGAGAT     TTCGACTT
                                  _     GAAAC_
GAM1741  PTPRO    3'  TTCAGCTTCAAAGTAGAGTAGA 48416     C     TCACCC
                                TCT GCTCTG     AGGCTGGA
                                ||| ||||||     ||||||||
                                AGA TGAGAT     TTCGACTT
                                  _     GAAAC_
GAM1741  PTPRS    3'  CCGGGGTGGGGGGTGGGG    12629         G     A
                                TCTCGCTCT TCACCC GG
                                |||||||||  ||||||  ||
                                GGGGTGGGG GGTGGG CC
                                    _     G
GAM1741  PUM1     3'  TCTAGTCTCAAGTATAGCGAGA 28647        CTGTCACCC
                                TCTCGCT        AGGCTGGA
                                |||||||        ||||||||
                                AGAGCGA        TCTGATCT
                                    TATGAAC__
GAM1741  PUNC     3'  TCCAGAGGGTGGACGGAGCGGG 91232           _    AGG
             G                   TCTCGCTCTGTC ACCC   CTGGA
                                ||||||||||||  ||||   |||||
                                GGGGCGAGGCAG TGGG   GACCT
                                    G    A__
GAM1741  PXF      3'  TCCGTAAGTTGCAGAGTGAGG  12658          C  CCAG  T
                                TCTCGCTCTGT AC    GC GGA
                                ||||||||||  ||    ||  |||
                                GGAGTGAGACG TG    TG CCT
                                    T  AA__  _
GAM1741  PXN      3'  TCTGTGGGGTGGGGTGGGG    12676         TG  A  _
                                TCTCGCTC  TC CC CAGG
                                ||||||||  ||  ||  ||||
                                GGGGTGGG  GG GG GTCT
                                    GT  _  T
GAM1741  PYGM     5'  TTCGGTGGGGGTGGAGTGAGG  20038         TG  A   AG
                                TCTCGCTC  TC CCC  GCTGGA
                                ||||||||  ||  |||  ||||||
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                                GGAGTGAG  GG GGG  TGGCTT
                                    GT  _  __
GAM1741  RAB30    3'  TCCAGTCTGGAGTTGGAGCAAG 27940     C     TC  _
            G                    TCT GCTCTG  AC CCAGGCTGGA
                                 ||| ||||||  || ||||||||||
                                 GGA CGAGGT  TG GGTCTGACCT
                                   A     __ A
GAM1741  RAB5C    3'  TTTGGTTTGGGCGGTGGGGCAG 60528     C    TG  A      TG
            A                    TCT GCTC  TC CCCAGGC  GA
                                 ||| ||||  || |||||||  ||
                                 AGA CGGG  GG GGGTTTG  TT
                                   _   GT  C      GT
GAM1741  RAB7L1   3'  TTCAGCCTGGGCAACAAGAGTG 15415        _  CA
            A                    TCGCTCT GT  CCCAGGCTGGA
                                 |||||||  ||  ||||||||||
                                 AGTGAGA CA  GGGTCCGACTT
                                     A  AC
GAM1741  RAB7L1   3'  TTCAGCCTGGGTGACAGAGAAG 15416     CG
            GA                     TCT  CTCTGTCACCCAGGCTGGA
                                   |||  ||||||||||||||||||
                                   AGG  GAGACAGTGGGTCCGACTT
                                     AA
GAM1741  RABIF    3'  TCCAGCCTGGGCAACAGAGTGA 12730          CA
            GA                     TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   AGAGTGAGACA  GGGTCCGACCT
                                        AC
GAM1741  RAD21    3'  TTCAGTTTCTTCAGAGTGG   21837        TCACCC
                                   TCGCTCTG     AGGCTGGA
                                   ||||||||     ||||||||
                                   GGTGAGAC     TTTGACTT
                                       TTC___
GAM1741  RAD50    3'  ATCCTGGGGGTGGTGGTGGGGT 56819        TG  _____     CTGGA
            GGGG                   TCTCGCTC  TCA    CCCAGG
                                   ||||||||  |||    ||||||
                                   GGGGTGGG  GGT    GGGTCC
                                       GT   GGTGG     T   AG
GAM1741  RBBP5    3'  TCCAGCCTAGGTGACAGAATGA 18579      C       C
            GA                     TCTCG TCTGTCACC AGGCTGGA
                                   ||||| ||||||||| ||||||||
                                   AGAGT AGACAGTGG TCCGACCT
                                     A       A
GAM1741  RBBP9    3'  TCCATCCTGGGTGATGGAGCGA 70698              C
                                   TCGCTCTGTCACCCAGG TGGA
                                   |||||||||||||||| ||||
                                   AGCGAGGTAGTGGGTCC ACCT
                                             T
GAM1741  RBM3     3'  TCCAGCCTGGGCAACAGCGAGA 71013        CT  CA
                                   TCTCGCT  GT  CCCAGGCTGGA
                                   |||||||  ||  ||||||||||
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                                AGAGCGA  CA  GGGTCCGACCT
                                   __  AC
GAM1741  RFX1     3'  TCCAGCCTCAGCCAGGGCAGGG 12852      _     TCACCC
                A                   TCTC GCTCTG     AGGCTGGA
                                    |||| ||||||     ||||||||
                                    AGGG CGGGAC     TCCGACCT
                                      A     CGAC__
GAM1741  RGS2     3'  TCAGCCTGGGTGTTCAGG    12862      T_
                                    TCTG  CACCCAGGCTGG
                                    ||||  ||||||||||||
                                    GGAC  GTGGGTCCGACT
                                      TT
GAM1741  RGS3     5'  TCCAGCCTCTCTCCAGAGTGG  56317        TCACCC
                                    TCGCTCTG     AGGCTGGA
                                    ||||||||     ||||||||
                                    GGTGAGAC     TCCGACCT
                                         CTCTC_
GAM1741  RNMT     3'  TTTAGCCTGCATGGCAGGGAGA 15060      G       CC
                GG                    TCTC CTCTGTCA  CAGGCTGGA
                                    |||| ||||||||  |||||||||
                                    GGAG GGGACGGT  GTCCGATTT
                                      A       AC
GAM1741  RPH3AL   3'  TCAGCTTGAGGAGCTGGGA   23743      _    GTCACC
                                    TCTC GCTCT     CAGGCTGG
                                    |||| |||||     ||||||||
                                    AGGG CGAGG     GTTCGACT
                                      T    A_____
GAM1741  RREB1    3'  TTGGCTGTTGAGGAGTGAGA   12912        G   CCCA   TG
                                    TCTCGCTCT TCA    GGC  GA
                                    ||||||||| |||    |||  ||
                                    AGAGTGAGG AGT    TCG  TT
                                         _   TG__   GT
GAM1741  RXRA     3'  TCTGGTTGAAGGTGGGGTGGGG 12924        TGT    CA_   TG
                                    TCTCGCTC   CACC   GGC  GA
                                    ||||||||   ||||   |||  ||
                                    GGGGTGGG   GTGG   TTG  CT
                                         ___    AAG   GT
GAM1741  SCAP2    3'  TCCAGCCTGGGCGACAGAGTGA 15427           A
                GA                    TCTCGCTCTGTC CCCAGGCTGGA
                                    |||||||||||| ||||||||||
                                    AGAGTGAGACAG GGGTCCGACCT
                                           C
GAM1741  SCN4A    3'  TCTGGGCATGGCAGGGCCAGG  6208      C       __
                                    TCT GCTCTGTCA  CCCAGG
                                    ||| |||||||||  ||||||
                                    GGA CGGGACGGT  GGGTCT
                                      C        AC
GAM1741  SCN4A    3'  TTTGGCCTGGGGGGAGGTCAGA  6211     C  T  G  A      TG
                                    TCT GC CT TC CCCAGGC  GA
                                    ||| || || || |||||||  ||
```

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                                AGA TG GA GG GGGTCCG  TT
                                  C  _  _  _      GT
GAM1741  SFRP1    3'  CCCGGGGGCAGGGTGGGG    13025          A   A
                                TCTCGCTCTGTC CCC GG
                                |||||||||||| ||| ||
                                GGGGTGGGACGG GGG CC
                                       _   C
GAM1741  SFRS2IP  5'  ACTCCAGCCTGGGTGACAGAGT 17534
            GAGA                  TCTCGCTCTGTCACCCAGGCTGGA
                                |||||||||||||||||||||||||
                                AGAGTGAGACAGTGGGTCCGACCT
                                            CAC
GAM1741  SH3BP2   3'  TTCAGCCTGCCTGGGGTGAGA  13090        GTCACC
                                TCTCGCTCT     CAGGCTGGA
                                |||||||||     |||||||||
                                AGAGTGGGG     GTCCGACTT
                                     TCC___
GAM1741  SHANK2   3'  CCAGCAGGGTAAAGCGGGA   25524       CTGTC    AG
                                TCTCGCT    ACCC  GCTGG
                                |||||||    ||||  |||||
                                AGGGCGA    TGGG  CGACC
                                    AA___    A_
GAM1741  SHC1     3'  TCTGGGAGGGCGGGGTGGGG   13124          A_
                                TCTCGCTCTGTC  CCCAGG
                                ||||||||||||  ||||||
                                GGGGTGGGGCGG  GGGTCT
                                      GA
GAM1741  SIGLEC11 3'  TCCAGCCTGGGCAACAGAGTGA 54657          CA
            GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||||  ||||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      AC
GAM1741  SIM2     3'  TCCAGCCTGGGTAACAGAGTGA 18624          C
            GA                    TCTCGCTCTGT ACCCAGGCTGGA
                                ||||||||||||| ||||||||||||
                                AGAGTGAGACA TGGGTCCGACCT
                                      A
GAM1741  SLC14A2  3'  TCCAGCCTGGGCAACGGATTGA 24128      C    CA
            GA                    TCTCG TCTGT  CCCAGGCTGGA
                                |||||| |||||  ||||||||||||
                                AGAGT AGGCA  GGGTCCGACCT
                                   T     AC
GAM1741  SLC17A5  3'  TCCAGCCTGGGCGATGGAGCGA 25835          A
            GA                    TCTCGCTCTGTC CCCAGGCTGGA
                                |||||||||||| ||||||||||||
                                AGAGCGAGGTAG GGGTCCGACCT
                                      C
GAM1741  SLC25A15 3'  TCCAGACTGGGTGACACAGCGA 27296        C        G
            GA                    TCTCGCT TGTCACCCAG CTGGA
                                ||||||| |||||||||| |||||
```

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                                AGAGCGA ACAGTGGGTC GACCT
                                    C         A
GAM1741  SLC26A4   3'  TCCAGCCTGGGCGACAGAGCAA 6530      C       A
                GA                    TCT GCTCTGTC CCCAGGCTGGA
                                ||| |||||||| ||||||||||
                                AGA CGAGACAG GGGTCCGACCT
                                  A       C
GAM1741  SLC28A2   3'  CTCCAGCCTGGGTGACAGAGCG 16150
                AGA                    TCTCGCTCTGTCACCCAGGCTGGA
                                |||||||||||||||||||||||
                                AGAGCGAGACAGTGGGTCCGACCT
                                                CA
GAM1741  SLC2A3    3'  TCTAGCCTGGGCCACAGGGCGA 23647           CA
                GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                |||||||||||  ||||||||||
                                AGAGCGGGACA  GGGTCCGATCT
                                      CC
GAM1741  SLC2A6    3'  TCCAGCCTGGGCAACGAGAGTG 34577        _ CA
                A                     TCGCTCT GT  CCCAGGCTGGA
                                ||||||| ||  ||||||||||
                                AGTGAGA CA  GGGTCCGACCT
                                    G  AC
GAM1741  SLC31A1   3'  TCCAGCCTGGGTGACAAGAGTG 10279        _
                A                     TCGCTCT GTCACCCAGGCTGGA
                                ||||||| ||||||||||||||
                                AGTGAGA CAGTGGGTCCGACCT
                                    A
GAM1741  SLC4A10   5'  CCGGCTAAGCAGAGCGAG    42153          CACCCA
                                CTCGCTCTGT     GGCTGG
                                ||||||||||     ||||||
                                GAGCGAGACG     TCGGCC
                                      AA____
GAM1741  SMARCB1   3'  TCGGGTGGGGGTGGAGTGGGG  66188         TG  A   AG   G
                                TCTCGCTC  TC CCC  GCT GA
                                ||||||||  || |||  ||| ||
                                GGGGTGAG  GG GGG  TGG CT
                                     GT  _   __   G
GAM1741  SMCX      5'  TCCGGTTTGTTGTGGTGTGGGG 16090       T   T  CC
                                TCTCGC CTG CA  CAGGCTGGA
                                |||||| ||| ||  |||||||||
                                GGGGTG GGT GT  GTTTGGCCT
                                   T   _  T_
GAM1741  SMG1      3'  TCCAGCCTGGGCAACAGAGCTA 31352     C      CA
                GA                    TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  T      AC
GAM1741  SPAG8     3'  CTGGGTGGTGGAGGGGGG    25840      G   TG
                                TCTC CTC  TCACCCAG
                                |||| |||  ||||||||
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                                GGGG GAG  GGTGGGTC
                                  G   GT
GAM1741  SPAG8    3'  TCTGGCTTGGGGAGAGTGGGA  25844        TG  A      TG
                                TCTCGCTC  TC CCCAGGC  GA
                                ||||||||  || |||||||  ||
                                AGGGTGAG  AG GGGTTCG  CT
                                     __  _      GT
GAM1741  SPAG8    3'  TTGGGGGCAGAGCGGGG     25845           A
                                TCTCGCTCTGTC CCCAG
                                |||||||||||| |||||
                                GGGGCGAGACGG GGGTT
                                          _
GAM1741  SPK      3'  TCGGGGCTGGGGGACGGGGCGG 17873           A    G  G
            GG                    TCTCGCTCTGTC CCCAG CT GA
                                  |||||||||||| ||||| || ||
                                  GGGGCGGGGCAG GGGTC GG CT
                                        G    G  G
GAM1741  SRGAP1   5'  TCCAGCCTGGGCAACAGAGCGA 72721          CA
            GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        AC
GAM1741  SRGAP1   3'  TTCGGTTCCATGTGGAGCGGGG 72725          T  CCCA
                                TCTCGCTCTG CA    GGCTGGA
                                |||||||||| ||    |||||||
                                GGGGCGAGGT GT    TTGGCTT
                                     _  ACC_
GAM1741  SRGAP2   3'  ATTCGGGGAAGAGAGGTGGGGT 75106        TG  A_____   A  CTGGA
            GGGG                    TCTCGCTC  TC     CCC GG
                                    ||||||||  ||     ||| ||
                                    GGGGTGGG  GG     GGG CT
                                       GT  AGAGAA   G  T   AG
GAM1741  SSRP1    3'  TTTGGGGAGAGATAGGGTGGGA 13421           A___
                                TCTCGCTCTGTC   CCCAGG
                                ||||||||||||   ||||||
                                AGGGTGGGATAG   GGGTTT
                                       AGAG
GAM1741  STAC     3'  GTACTGGCCTGGGTGACAGAGC 13428    TC           TG A
            AGGA                    TC  GCTCTGTCACCCAGGC  G
                                    ||  ||||||||||||||||  |
                                    AG  CGAGACAGTGGGTCCG  C
                                     GA             GT ATGG
GAM1741  STC1     3'  TCTGGCAAATGATGATGGGGTG 13464          CCCAG_  TG
            GGA                     TCTCGCTCTGTCA     GC  GA
                                    ||||||||||||||     ||  ||
                                    AGGGTGGGGTAGT     CG  CT
                                          AGTAAA  GT
GAM1741  STK38    5'  TCCAGCCTGGGCAACAAGAGCG 24401        _  CA
            A                      TCGCTCT GT  CCCAGGCTGGA
                                   |||||||  ||  ||||||||||
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                                AGCGAGA CA  GGGTCCGACCT
                                   A  AC
GAM1741  SULT2A1   3'  ACTCCAGCCTGGGTGACAGAGC 72222
            GAGA                  TCTCGCTCTGTCACCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAGTGGGTCCGACCT
                                        CAC
GAM1741  SUPT6H    3'  TTCAGTTTGGGGCAGGAGGGAG 61033      G    GTCA
            A                   TCTC CTCT    CCCAGGCTGGA
                                |||| ||||    ||||||||||
                                AGAG GAGG    GGGTTTGACTT
                                  G    ACG_
GAM1741  SWAP70    3'  TCCAGCTTGGGCAACAGAGTGA 71874           CA
            GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTTCGACCT
                                        AC
GAM1741  TADA2L    3'  TCCAGCCTGGGCAACAAAGTGA 56765        C   CA
            GA                    TCTCGCT TGT  CCCAGGCTGGA
                                  |||||||  |||  ||||||||||
                                  AGAGTGA ACA  GGGTCCGACCT
                                     A   AC
GAM1741  TAF1C     3'  TTGGTGAGGGTGGAGTGAGG   20267        TGT    AG  TG
                                  TCTCGCTC   CACCC  GC  GA
                                  ||||||||   |||||  ||  ||
                                  GGAGTGAG   GTGGG  TG  TT
                                       ___     AG  GT
GAM1741  TBX1      3'  ACTCCAGCCTGGGTGACAGAGT 55536
            GAGA                  TCTCGCTCTGTCACCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAGTGGGTCCGACCT
                                        CAC
GAM1741  TBX2      3'  TCTGGTCTTCCAGCGAGGTGGG 21144       TC   CACCC    TG
            A                     TCTCGC  TGT    AGGC  GA
                                  ||||||  |||    ||||  ||
                                  AGGGTG  GCG    TCTG  CT
                                     GA   ACCT_   GT
GAM1741  TCF7      3'  TCCAGTCTGGGTAACAGGGAGA 13625      G T    C
                                  TCTC C CTGT ACCCAGGCTGGA
                                  |||| | |||| ||||||||||||
                                  AGAG G GACA TGGGTCTGACCT
                                    _ _    A
GAM1741  TCTA      3'  TCCAGCCTGGGCAACAGAGCAA 42503      C      CA
            GA                    TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A      AC
GAM1741  TEM7      3'  CTCCAGCCTGGGTGACAGAGCG 40255
            AGA                    TCTCGCTCTGTCACCCAGGCTGGA
                                   ||||||||||||||||||||||||
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                                AGAGCGAGACAGTGGGTCCGACCT
                                      CA
GAM1741  TEM7     3'  CTCCAGCCTGGGTGACAGAGTG 40256
            AGA                  TCTCGCTCTGTCACCCAGGCTGGA
                                 ||||||||||||||||||||||||
                                 AGAGTGAGACAGTGGGTCCGACCT
                                      CA
GAM1741  TM7SF3   3'  TCCAGCTTGGGTGACAGAG   60395
                                 CTCTGTCACCCAGGCTGGA
                                 ||||||||||||||||||
                                 GAGACAGTGGGTTCGACCT

GAM1741  TMEM2    3'  TCCAGTTTGATACAGAATGGGG 26339      C    CACC
                                 TCTCG TCTGT   CAGGCTGGA
                                 ||||| |||||   |||||||||
                                 GGGGT AGACA   GTTTGACCT
                                    A    TA__
GAM1741  TNFRSF10C 3'  TCCTCAACTGGGTGACAAGGGT 15205        _       GCT_
            GAGG                  TCTCGCTCT GTCACCCAG   GGA
                                 |||||||||| |||||||||   |||
                                 GGAGTGGGA CAGTGGGTC   CCT
                                      A       AACT
GAM1741  TNFRSF1B  3'  TCCAGCCTGAGCAACAGAGTGA 8402          CACC
            GA                    TCTCGCTCTGT   CAGGCTGGA
                                 ||||||||||    |||||||||
                                 AGAGTGAGACA   GTCCGACCT
                                       ACGA
GAM1741  TNFRSF1B  3'  TCCAGCCTGGGCGACAGAGCGA 8403          A
            GA                    TCTCGCTCTGTC CCCAGGCTGGA
                                 ||||||||||||| ||||||||||
                                 AGAGCGAGACAG GGGTCCGACCT
                                       C
GAM1741  TNFSF10   3'  TCCAGCCTGGCGACAGAGCGAG 15094          AC
            A                     TCTCGCTCTGTC  CCAGGCTGGA
                                 ||||||||||||  ||||||||||
                                 AGAGCGAGACAG  GGTCCGACCT
                                       C_
GAM1741  TPM4     3'  TCCAGCCTGGTCGACAGAGTGA 13834          AC
            GA                    TCTCGCTCTGTC  CCAGGCTGGA
                                 ||||||||||||  ||||||||||
                                 AGAGTGAGACAG  GGTCCGACCT
                                       CT
GAM1741  TRIM14   3'  TCCAGCCTGGGCAATAGAGTGA 29516          CA
            GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                 ||||||||||||  ||||||||||||
                                 AGAGTGAGATA  GGGTCCGACCT
                                       AC
GAM1741  TRIM9    5'  TCTAGCCTGGGCAACAAGAGTG 31462        _ CA
            A                     TCGCTCT GT  CCCAGGCTGGA
                                 |||||||  ||  ||||||||||||
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                                AGTGAGA CA  GGGTCCGATCT
                                    A  AC
GAM1741  TRPM8    3'  TCCAGCCGGGGTGACAGAGTGA 44208              A
                GA                  TCTCGCTCTGTCACCC GGCTGGA
                                    |||||||||||||||| |||||||
                                    AGAGTGAGACAGTGGG CCGACCT
                                          G
GAM1741  TSNAX    3'  TCCAGCCTGGGTAACAGAGCAA 21160     C      C
                GA                  TCT GCTCTGT ACCCAGGCTGGA
                                    ||| ||||||| ||||||||||||
                                    AGA CGAGACA TGGGTCCGACCT
                                      A      A
GAM1741  UBE2B    3'  TCCAGCCTGGGTGACAGAGC   13938
                                    GCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||
                                    CGAGACAGTGGGTCCGACCT

GAM1741  UBE2G2   3'  TCCAGCCTGGGCAACAGAGCGA 65495           CA
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGCGAGACA  GGGTCCGACCT
                                          AC
GAM1741  UBE2G2   3'  TCCAGCCTGGGCAACAGAGTGA 65496           CA
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          AC
GAM1741  UBE2L3   3'  TCTGGTCTGTGCAGAAGTGGGG 13965        _    CACC     TG
                                    TCTCGCT CTGT    CAGGC  GA
                                    ||||||| ||||    |||||  ||
                                    GGGGTGA GACG    GTCTG  CT
                                        A   T___     GT
GAM1741  USP14    3'  TCCAGCCTGGGTGACAGAGAGA 18940    G
                                    TC CTCTGTCACCCAGGCTGGA
                                    || ||||||||||||||||||
                                    AG GAGACAGTGGGTCCGACCT
                                     A
GAM1741  VAPB     3'  TCTGGTCATGTGGAGGTGGGG  17630       T  G    CCA   TG
                                    TCTCGC CT TCAC   GGC  GA
                                    |||||| || ||||   |||  ||
                                    GGGGTG GA GGTG   CTG  CT
                                       _ _    TA_   GT
GAM1741  VDR      3'  TTCAGGAAAACTGACAGAGGAG 6348       G       CCCAGG
                G                    TCTC CTCTGTCA     CTGGA
                                    |||| ||||||||     |||||
                                    GGAG GAGACAGT     GACTT
                                      _       CAAAAG
GAM1741  VHL      3'  CCAGCCTTTTTAGGGCAGA   6842      C     TCACCC
                                    TCT GCTCTG     AGGCTGG
                                    ||| ||||||     |||||||
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                                AGA CGGGAT     TCCGACC
                                  _     TTT___
GAM1741  VHL     3'  TCCAGCCTGGGAAACAAGAGTG 6875        _  CA
                A                  TCGCTCT GT  CCCAGGCTGGA
                                   ||||||| ||  ||||||||||
                                   AGTGAGA CA  GGGTCCGACCT
                                      A  AA
GAM1741  VHL     3'  TCCAGCCTGGGGGACAGAGCAA 6876     C      A
                GA                   TCT GCTCTGTC CCCAGGCTGGA
                                     ||| |||||||| ||||||||||
                                     AGA CGAGACAG GGGTCCGACCT
                                       A       G
GAM1741  VHL     3'  TCTAACCTGGGCGACAGAGTGA 6879           A     C
                GA                   TCTCGCTCTGTC CCCAGG TGGA
                                     |||||||||||| |||||| ||||
                                     AGAGTGAGACAG GGGTCC ATCT
                                            C     A
GAM1741  WHSC1   3'  CCAGTTCTACAGAGTGAGA   24656          CACCC  _
                                     TCTCGCTCTGT    AGG CTGG
                                     ||||||||||     ||| ||||
                                     AGAGTGAGACA    TCT GACC
                                            _____  T
GAM1741  WHSC1   3'  CCAGTTCTACAGAGTGAGA   24657          CACCC  _
                                     TCTCGCTCTGT    AGG CTGG
                                     ||||||||||     ||| ||||
                                     AGAGTGAGACA    TCT GACC
                                            _____  T
GAM1741  WHSC1   3'  CCAGTTCTACAGAGTGAGA   24658          CACCC  _
                                     TCTCGCTCTGT    AGG CTGG
                                     ||||||||||     ||| ||||
                                     AGAGTGAGACA    TCT GACC
                                            _____  T
GAM1741  WIG1    3'  CTCCAGCCTGGGTGACAGAGCG 96101
                AGA                    TCTCGCTCTGTCACCCAGGCTGGA
                                       ||||||||||||||||||||||||
                                       AGAGCGAGACAGTGGGTCCGACCT
                                                 CA
GAM1741  WNT10B  3'  TCAGCAGGAAGGGTGGGA    14129         G  ACCCAG
                                     TCTCGCTCT TC     GCTGG
                                     |||||||| ||     |||||
                                     AGGGTGGGA AG     CGACT
                                          _ GA____
GAM1741  XT3     3'  TCCAGTCTGGGCGACAGAGCAA 39918     C      A
                GA                   TCT GCTCTGTC CCCAGGCTGGA
                                     ||| |||||||| ||||||||||
                                     AGA CGAGACAG GGGTCTGACCT
                                       A       C
GAM1741  ZNF124  5'  TTCAGGAACTAATAGAGCGAGA 14285          CACCCAGG
                                     TCTCGCTCTGT       CTGGA
                                     ||||||||||        |||||
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                                AGAGCGAGATA       GACTT
                                      ATCAAG__
GAM1741  ZNF137   3'  CCGGCAGGCGGGGCGAG     14309          ACCCAG
                                CTCGCTCTGTC     GCTGG
                                ||||||||||      |||||
                                GAGCGGGGCGG     CGGCC
                                      A_____
GAM1741  ZNF14    3'  TCCAGCCTGTGCGACAGAATGA 41058      C     ACC
            GA                    TCTCG TCTGTC   CAGGCTGGA
                                ||||| ||||||   |||||||||
                                AGAGT AGACAG   GTCCGACCT
                                   A     CGT
GAM1741  ZNF217   3'  TTGGGTTGGGTGGGGCGGGA   22551        TGT      G TG
                                TCTCGCTC   CACCCAG C  GA
                                ||||||||   ||||||| |  ||
                                AGGGCGGG   GTGGGTT G  TT
                                     ___      G GT
GAM1741  ZNF264   3'  TCCAGCCTGGGCAACAGAGCGA 14232          CA
            GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      AC
GAM1741  ZNF264   3'  TCCAGCCTGGGCAGCAGAGCGA 14233          CA
            GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACG  GGGTCCGACCT
                                      AC
GAM1741  ZNF36    3'  TCCAGCCTGGGTGACTAGC    95587     CT
                                GCT  GTCACCCAGGCTGGA
                                |||  ||||||||||||||
                                CGA  CAGTGGGTCCGACCT
                                  T_
GAM1741  ZNF91    3'  TCAAGCCTGGGCGACAGAGCGA 14283          A       G
            GA                    TCTCGCTCTGTC CCCAGGCT GA
                                ||||||||||| |||||||| ||
                                AGAGCGAGACAG GGGTCCGA CT
                                      C       A
GAM1741  ACYP2    5'  TCCGGGACCGGTGACAGGCGCG 57406       _       CA  __
            GGG                    TCTCGC TCTGTCACC  GG  CTGGA
                                ||||||  |||||||||  ||  |||||
                                GGGGCG GGACAGTGG  CC  GGCCT
                                   C        __  AG
GAM1741  AF020591 3'  TCCAGCCTGGGCAACAGAGCAA 27916     C      CA
            GA                    TCT GCTCTGT  CCCAGGCTGGA
                                |||  |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A      AC
GAM1741  AKAP10   3'  TCAGCGGAACAGGGTGAGA    24223          CA  CAG
                                TCTCGCTCTGT  CC   GCTGG
                                ||||||||||  ||   |||||
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                                AGAGTGGGACA  GG   CGACT
                                      A_  ___
GAM1741  AKR1D1   3'  TCCGGCCTGGGTGAAAGAGCGA 21134          G
            GA                    TCTCGCTCT TCACCCAGGCTGGA
                                  ||||||||| ||||||||||||||
                                  AGAGCGAGA AGTGGGTCCGGCCT
                                      A
GAM1741  ALTE     3'  TCCAGCCTGGAGGCCAGAGTGA 61006          _  AC
            GA                    TCTCGCTCTG TC  CCAGGCTGGA
                                  |||||||||| ||  ||||||||||
                                  AGAGTGAGAC GG  GGTCCGACCT
                                      C  A_
GAM1741  ALTE     3'  TCCAGCCTGGGCGACAAGAGCG 61007          _  A
            AGA                    TCTCGCTCT GTC CCCAGGCTGGA
                                   ||||||||| ||| ||||||||||
                                   AGAGCGAGA CAG GGGTCCGACCT
                                      A  C
GAM1741  AP1GBP1  3'  TCCGGTCTGAGCGACAGAGCAA 24355     C       ACC
            GA                    TCT GCTCTGTC   CAGGCTGGA
                                  ||| ||||||||   |||||||||
                                  AGA CGAGACAG   GTCTGGCCT
                                    A       CGA
GAM1741  APOF     3'  ATTCCAGCCTGGGTGACAGAGC 9689
            GAGA                    TCTCGCTCTGTCACCCAGGCTGGA
                                    |||||||||||||||||||||||||
                                    AGAGCGAGACAGTGGGTCCGACCT
                                                TAC
GAM1741  APOL6    3'  TCCAGTCTGGGTGTCAGAATGA 48375       C    T
            GA                    TCTCG TCTG CACCCAGGCTGGA
                                  ||||| |||| ||||||||||||
                                  AGAGT AGAC GTGGGTCTGACCT
                                    A    T
GAM1741  APXL2    3'  TCCAGCCTGGGCGACAGAGCAA 75686     C       A
            GA                    TCT GCTCTGTC CCCAGGCTGGA
                                  ||| |||||||| ||||||||||
                                  AGA CGAGACAG GGGTCCGACCT
                                    A       C
GAM1741  ARHGAP11A 5'  TCCGGCGGCCAGGCTAGGGCGG 29459          _   AC_  AG
            GG                    TCTCGCTCT GTC   CC  GCTGGA
                                  ||||||||| |||   ||  ||||||
                                  GGGGCGGGA CGG   GG  CGGCCT
                                      T   ACC  __
GAM1741  ARNTL2   3'  CCAGCCTGGGCGACAGAGCGAG 39843           A        A
            A                     TCTCGCTCTGTC CCCAGGCTGG
                                  |||||||||||| ||||||||||
                                  AGAGCGAGACAG GGGTCCGACC
                                        C         C
GAM1741  ARNTL2   3'  TCCAGTCTGGGCAACAGAGTGA 39858           CA
            GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                  |||||||||||  ||||||||||||
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                                AGAGTGAGACA  GGGTCTGACCT
                                      AC
GAM1741  ASAHL    3'  TCTAGCCTGGGCAACAGAGCGA 64321          CA
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGCGAGACA  GGGTCCGATCT
                                          AC
GAM1741  ATIP1    3'  TTCAGTCTGACTGTGGGGGTGG 40777         GT  CC
                GG                  TCTCGCTCT  CA  CAGGCTGGA
                                    |||||||||  ||  |||||||||
                                    GGGGTGGGG  GT  GTCTGACTT
                                         GT  CA
GAM1741  ATP1B4   3'  ATTCCAGCCTGGGTGACAGAGT 24835
                GAGA                  TCTCGCTCTGTCACCCAGGCTGGA
                                      ||||||||||||||||||||||||
                                      AGAGTGAGACAGTGGGTCCGACCT
                                                TAC
GAM1741  BA108L7.2 3'  TCTGGCTTCAGTGGTGGGTGGG 49081       T TG    CC    TG
                G                    TCTCGC C  TCAC  AGGC  GA
                                     |||||| |  ||||  ||||  ||
                                     GGGGTG G  GGTG  TTCG  CT
                                        _ GT    AC    GT
GAM1741  BA108L7.2 3'  TTCAGTGGTGGGTGGGGCAGGG 49085       __     G_
                                     CTCTGT  CACCCA  GCTGGA
                                     ||||||  ||||||  ||||||
                                     GGGACG  GTGGGT  TGACTT
                                        GG     GG
GAM1741  BANP     3'  TCCAGACTGTGCGACAGAGCGA 66805          ACC   G
                GA                  TCTCGCTCTGTC   CAG CTGGA
                                    ||||||||||||   ||| |||||
                                    AGAGCGAGACAG   GTC GACCT
                                          CGT   A
GAM1741  BFAR     3'  TTCAGCCTGGGTGACAGAGGGA 61427      G
                GA                  TCTC CTCTGTCACCCAGGCTGGA
                                    |||| ||||||||||||||||||
                                    AGAG GAGACAGTGGGTCCGACTT
                                      G
GAM1741  BIRC1    3'  TCCAGCCTGGGCAACAGAGCAA 16995     C      CA
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGAGACA  GGGTCCGACCT
                                      A       AC
GAM1741  BIVM     3'  TCCAGCCTGGGCAACAGGGCAA 35160     C      CA
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGGGACA  GGGTCCGACCT
                                      A       AC
GAM1741  BLOV1    3'  TCCAGCCTGGGCAACAAGAGCG 76799        _  CA
                A                    TCGCTCT GT  CCCAGGCTGGA
                                     |||||||  ||  ||||||||||
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                                AGCGAGA CA  GGGTCCGACCT
                                   A  AC
GAM1741  BLOV1    3'  TCCAGCCTGGGCGACAGAGCAA 76800     C       A
                GA                  TCT GCTCTGTC CCCAGGCTGGA
                                    ||| |||||||| ||||||||||
                                    AGA CGAGACAG GGGTCCGACCT
                                      A       C
GAM1741  BTN3A2   3'  TCCAGCCTGGGAGACAGAGCGA 23880           A
                GA                  TCTCGCTCTGTC CCCAGGCTGGA
                                    |||||||||||| ||||||||||
                                    AGAGCGAGACAG GGGTCCGACCT
                                           A
GAM1741  BUCS1    3'  TTTAGTCTCCCCACTATGGTGA 54762        CT_  CACCC
                GG                  TCTCGCT   GT    AGGCTGGA
                                    |||||||   ||    ||||||||
                                    GGAGTGG   CA    TCTGATTT
                                       TAT  CCCC_
GAM1741  C12orf2  3'  TCCAGCCTGGGTAACAGAGTGA 83688          C
                GA                  TCTCGCTCTGT ACCCAGGCTGGA
                                    |||||||||||| ||||||||||||
                                    AGAGTGAGACA TGGGTCCGACCT
                                           A
GAM1741  C12orf3  3'  TTCAGCCTGCAGCAGAGGAGG  40168      G     CACC
                                    TCTC CTCTGT    CAGGCTGGA
                                    |||| ||||||    |||||||||
                                    GGAG GAGACG    GTCCGACTT
                                      _      AC__
GAM1741  C13orf1  3'  TCCAGCCTAGGCAACAGAGTGA 40372          CA  C
                GA                  TCTCGCTCTGT  CC AGGCTGGA
                                    ||||||||||  || ||||||||
                                    AGAGTGAGACA  GG TCCGACCT
                                           AC  A
GAM1741  C17orf31 3'  TCCAGTGGAGACAGGGCAGGG  34544    TC       A  CAG
                                    TC  GCTCTGTC CC   GCTGGA
                                    ||  |||||||| ||   ||||||
                                    GG  CGGGACAG GG   TGACCT
                                     GA       A ___
GAM1741  C1orf2   5'  TCCAGTGCCCGTGGTGGGGAGG 96268      G   TG    CCAG
                GA                  TCTC CTC  TCAC    GCTGGA
                                    |||| |||  ||||    ||||||
                                    AGGG GGG  GGTG    TGACCT
                                      A  GT    CCCG
GAM1741  C1orf22  3'  CGGCTGGATTTAGTAGTGGAGT 48040          TC _________  AGGCT
                GGGG                  TCTCGCTCTG  AC       CC    G
                                    ||||||||||  ||       ||    |
                                    GGGGTGAGGT  TG       GG    C
                                          GA  ATTT   A  TCGGA
GAM1741  C1orf24  3'  TCCAGCTTGGGCGACGGAGTGA 54795           A
                GA                  TCTCGCTCTGTC CCCAGGCTGGA
                                    ||||||||||||| ||||||||||
```

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                                AGAGTGAGGCAG GGGTTCGACCT
                                      C
GAM1741  C1orf34   3'  GCCTTAGCCTGGGCGACAGAGC 61314          A        A
            GAGA                   TCTCGCTCTGTC CCCAGGCTGG
                                   |||||||||||| ||||||||||
                                   AGAGCGAGACAG GGGTCCGATT
                                         C         CCGA
GAM1741  C1QTNF2   3'  TCCAGCCTGGGCAACAGAGTGA 49977          CA
            GA                     TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   AGAGTGAGACA  GGGTCCGACCT
                                         AC
GAM1741  C20orf106 3'  TCCAGCCCAGGTGACAGAGTGA 55914            CA
            GA                     TCTCGCTCTGTCACC  GGCTGGA
                                   ||||||||||||||  |||||||
                                   AGAGTGAGACAGTGG  CCGACCT
                                           AC
GAM1741  C20orf108 3'  TCCAGCCTGGGCGACAGAGGGA 55883      G      A
            GA                     TCTC CTCTGTC CCCAGGCTGGA
                                   |||| ||||||| ||||||||||
                                   AGAG GAGACAG GGGTCCGACCT
                                     G      C
GAM1741  C20orf142 3'  TCCAGCCTGAGCGACAGAGTGA 75289          ACC
            GA                     TCTCGCTCTGTC   CAGGCTGGA
                                   ||||||||||   |||||||||
                                   AGAGTGAGACAG   GTCCGACCT
                                         CGA
GAM1741  C20orf172 3'  TCCAGCCTGAGCGACAGAGTGA 46768          ACC
            GA                     TCTCGCTCTGTC   CAGGCTGGA
                                   ||||||||||   |||||||||
                                   AGAGTGAGACAG   GTCCGACCT
                                         CGA
GAM1741  C20orf177 3'  TCAGTTTGCAAGAGCAGGA   62840    TC    GTCACC
                                   TC  GCTCT     CAGGCTGG
                                   ||  |||||     ||||||||
                                   AG  CGAGA     GTTTGACT
                                    GA    AC____
GAM1741  C20orf177 3'  TCCAGCCTGGGCAACAAGAGGG 62841    G   _  CA
            A                       TC CTCT GT  CCCAGGCTGGA
                                   ||  ||||  ||  ||||||||||
                                   AG GAGA CA  GGGTCCGACCT
                                    G   A  AC
GAM1741  C20orf177 3'  TTGCTTGGGGTGAGGGGCGGGA 62842          G    _   TGGA
                                   TCTCGCTCT TCACCC AGGC
                                   |||||||||  ||||||  ||||
                                   AGGGCGGGG AGTGGG TTCG
                                         _     G    TTT
GAM1741  C20orf183 3'  TCCAGGCTGGGCGACAGAGCGA 48537          A    G
            GA                     TCTCGCTCTGTC CCCAG CTGGA
                                   ||||||||||||  |||||  |||||
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                                AGAGCGAGACAG GGGTC GACCT
                                      C     G
GAM1741  C20orf29  3'  TCCAGCCTGGGCAACAGAGTGA 37712          CA
              GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          AC
GAM1741  C20orf42  3'  TTTGGTTTGTTAGAGGTGGGA  35065       _   TCACC     TG
                                    TCTCGC TCTG     CAGGC  GA
                                    ||||||  ||||     |||||  ||
                                    AGGGTG AGAT     GTTTG  TT
                                       G    T____     GT
GAM1741  C21orf108 3'  TCCAGCCTAGGTGACAGAGCAA 90121     C          C
              GA                    TCT GCTCTGTCACC AGGCTGGA
                                    |||  ||||||||||| ||||||||
                                    AGA CGAGACAGTGG TCCGACCT
                                      A          A
GAM1741  C21orf25  3'  TTTGGCCTGACGCTGGAGTGCG 64309     T     _  CACC     TG
              G                     TC CGCTCT GT    CAGGC  GA
                                    || ||||||  ||    |||||  ||
                                    GG GTGAGG CG    GTCCG  TT
                                     C      T  CA__     GT
GAM1741  C21orf57  5'  TTAGTCTCCCAAGCGAGA     75301        C  TCACCC
                                    TCTCGCT TG      AGGCTGG
                                    |||||||  ||     |||||||
                                    AGAGCGA AC      TCTGATT
                                        _  CC_____
GAM1741  C22orf19  3'  TCCGGCCTGGGCAACGTAGTGA 14829         C   CA
              GA                    TCTCGCT TGT  CCCAGGCTGGA
                                    |||||||  |||  ||||||||||
                                    AGAGTGA GCA  GGGTCCGGCCT
                                        T   AC
GAM1741  C22orf19  3'  TCCGGCTTGGGCGAGAGTGAGA 14830         TG  A
                                    TCTCGCTC  TC CCCAGGCTGGA
                                    ||||||||  || ||||||||||
                                    AGAGTGAG  AG GGGTTCGGCCT
                                         __  C
GAM1741  C22orf20  3'  TCCAGCCTGGGCAACATGAGTG 48200        _   CA
              A                     TCGCTC TGT  CCCAGGCTGGA
                                    ||||||  |||  ||||||||||
                                    AGTGAG ACA  GGGTCCGACCT
                                       T   AC
GAM1741  C3orf4    3'  CCAGTTCAGCCGGGCGAGG    39590         T  CACCCA
                                    TCTCGCTC GT      GGCTGG
                                    ||||||||  ||     ||||||
                                    GGAGCGGG CG      TTGACC
                                         C  AC_____
GAM1741  C5orf5    3'  TCGGGGGGTGGGGGGTGAGG   33944          G     AGG TG
                                    TCTCGCTCT TCACCC   C  GA
                                    |||||||||  ||||||   |  ||
```

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                                GGAGTGGGG GGTGGG   G  CT
                                      _     G__ GT
GAM1741  C6orf5   3'  TCCAGCCTGGGCAATAGAGTGA 32004          CA
            GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                  |||||||||||  ||||||||||
                                  AGAGTGAGATA  GGGTCCGACCT
                                        AC
GAM1741  C6orf5   3'  TCTAGCTTGGGAGACAGAGCGA 32006           A
            GA                    TCTCGCTCTGTC CCCAGGCTGGA
                                  |||||||||||| ||||||||||
                                  AGAGCGAGACAG GGGTTCGATCT
                                        A
GAM1741  C8orf2   3'  TCTAGCTTGGGCAATAGAGCAA 24157     C      CA
            GG                    TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  GGA CGAGATA  GGGTTCGATCT
                                    A       AC
GAM1741  C9orf5   3'  TCCAGCCTGGGTGAGAGAGTGA 50108          G
            GA                    TCTCGCTCT TCACCCAGGCTGGA
                                  |||||||||  ||||||||||||||
                                  AGAGTGAGA AGTGGGTCCGACCT
                                       G
GAM1741  CAMKK2   5'  TCCAGCGTGGGCGACAGAGCGA 22631           A    G
            GA                    TCTCGCTCTGTC CCCA GCTGGA
                                  |||||||||||| |||| ||||||
                                  AGAGCGAGACAG GGGT CGACCT
                                        C    G
GAM1741  CBCIP2   3'  TCCAGCCTGGGCGACAGAGCCA 52661     C       A
            GA                    TCT GCTCTGTC CCCAGGCTGGA
                                  ||| ||||||||  ||||||||||
                                  AGA CGAGACAG GGGTCCGACCT
                                    C       C
GAM1741  CCR5     3'  TGGGCTGGGGGTGGGGTGGGA  6964          TG  A    G
                                  TCTCGCTC  TC CCCAG CTG
                                  ||||||||  || ||||| |||
                                  AGGGTGGG  GG GGGTC GGT
                                       GT  _     G
GAM1741  CCR5     3'  TTTGGTTTGGAAGTGAGGGTCA 6965      C    TG   __     TG
            GA                    TCT GCTC  TCAC  CCAGGC  GA
                                  ||| ||||  ||||  ||||||  ||
                                  AGA TGGG  AGTG  GGTTTG  TT
                                    C    __    AA     GT
GAM1741  CCR6     3'  ACTCCAGCCTGGGTGACAGAGC 16436
            GAGA                    TCTCGCTCTGTCACCCAGGCTGGA
                                  |||||||||||||||||||||||
                                  AGAGCGAGACAGTGGGTCCGACCT
                                                CAC
GAM1741  CDA08    3'  TCTGGCTTGAAAAAATAGGGGA 48635      G     CACC_    TG
            GA                    TCTC CTCTGT    CAGGC  GA
                                  |||| ||||||    |||||  ||
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                                AGAG GGGATA    GTTCG  CT
                                  _     AAAAA    GT
GAM1741  CDKL2    5'  TTGGGGACAGAGTGAGG     15472          A
                                TCTCGCTCTGTC CCCAG
                                |||||||||||| |||||
                                GGAGTGAGACAG GGGTT
                                          _
GAM1741  CDT1     3'  TCCAGCCTGGGTGACAGAGCGA 78166
                GA                TCTCGCTCTGTCACCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAGTGGGTCCGACCT

GAM1741  CENTA2   3'  ATTCCAGCCTGGGTGACAGAGC 37865
                GAGA                TCTCGCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACAGTGGGTCCGACCT
                                              TAC
GAM1741  CENTA2   3'  CTTAGCCTGGGTGACAGAGTGA 37867                A
                GA                TCTCGCTCTGTCACCCAGGCTGG
                                  |||||||||||||||||||||||
                                  AGAGTGAGACAGTGGGTCCGATT
                                            CA
GAM1741  cerk     3'  TCCAGCCTGGGCAACAGAGGGA 43169      G     CA
                GA                TCTC CTCTGT  CCCAGGCTGGA
                                  |||| ||||||  ||||||||||
                                  AGAG GAGACA  GGGTCCGACCT
                                    G     AC
GAM1741  CG012    5'  TCCAGCCCAGGTGACAGAGGGA 84166      G        CA
                GA                TCTC CTCTGTCACC  GGCTGGA
                                  |||| ||||||||||  |||||||
                                  AGAG GAGACAGTGG  CCGACCT
                                    G         AC
GAM1741  CG012    3'  TCCAGCCTCGCCGACAAAGCGA 84167        C    ACCC
                GA                TCTCGCT TGTC    AGGCTGGA
                                  ||||||| ||||    ||||||||
                                  AGAGCGA ACAG    TCCGACCT
                                     A    CCGC
GAM1741  CG012    5'  TCCAGCCTGGGCAACAGAACGA 84168      C     CA
                GA                TCTCG TCTGT  CCCAGGCTGGA
                                  ||||| |||||  ||||||||||
                                  AGAGC AGACA  GGGTCCGACCT
                                    A     AC
GAM1741  CG012    3'  TGGTCTTGAGGGGCGGGG    84172         G  CCC    TG
                                  TCTCGCTCT TCA   AGGC  G
                                  ||||||||| |||   ||||  |
                                  GGGGCGGGG AGT   TCTG  T
                                     _  ____   GT
GAM1741  CGI-203  3'  ACTCCAGCCTGGGTGACAGAGT 40275
                GAGA                TCTCGCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||||||
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                                AGAGTGAGACAGTGGGTCCGACCT
                                      CAA
GAM1741  CHST3    3'  TTGGCCTGGGTGGTAGAGGAGA 16247     G   GT       TG A
                                TCTC CTCT  CACCCAGGC  G
                                |||| ||||  |||||||||  |
                                AGAG GAGA  GTGGGTCCG  T
                                  _   TG       GT C
GAM1741  CIC      3'  TCCAGTTTGGGGCGGAATGAGG 31370      C    CA
                                TCTCG TCTGT  CCCAGGCTGGA
                                ||||| |||||  ||||||||||
                                GGAGT AGGCG  GGGTTTGACCT
                                  A   __
GAM1741  CINP     5'  CCGGTGGGGTGGGCGGGG    51925       CTGT    AG
                                TCTCGCT   CACCC  GCTGG
                                |||||||   |||||  |||||
                                GGGGCGG   GTGGG  TGGCC
                                    ____   G_
GAM1741  CLDN4    3'  TGTGGTGGTGGAGTGGGG    8957        TG   _
                                TCTCGCTC  TCACC CA
                                ||||||||  ||||| ||
                                GGGGTGAG  GGTGG GT
                                     GT    T
GAM1741  CLSTN1   3'  GCTTGGTGGTAGGGCAGGA   30790    TC    GT   C
                                TC  GCTCT  CACC AGGC
                                ||  |||||  |||| ||||
                                AG  CGGGA  GTGG TTCG
                                 GA    TG   _
GAM1741  CLSTN2   3'  TTCATGGTGGGTGGAGTGGGG  42403       TGT    GGC
                                TCTCGCTC   CACCCA   TGGA
                                ||||||||   ||||||   ||||
                                GGGGTGAG   GTGGGT   ACTT
                                    ___     GGT
GAM1741  COE2     3'  TCCAGCCTGGGTGACAGAG   64910
                                CTCTGTCACCCAGGCTGGA
                                ||||||||||||||||||
                                GAGACAGTGGGTCCGACCT

GAM1741  COL4A3BP  5'  TCCGGCGCAGCTGAGGGAGCGG 20342         G   CCCAG
           GG                   TCTCGCTCT TCA    GCTGGA
                                |||||||| |||    ||||||
                                GGGGCGAGG AGT    CGGCCT
                                     G   CGACG
GAM1741  CPR2     3'  TCCAGCCTGGGCGACAGAGTGA 48839          A
           GA                   TCTCGCTCTGTC CCCAGGCTGGA
                                ||||||||||| ||||||||||
                                AGAGTGAGACAG GGGTCCGACCT
                                       C
GAM1741  CPR2     3'  TCCAGCCTGGGTAACAGAGCAA 48840    C     C
           GA                   TCT GCTCTGT ACCCAGGCTGGA
                                ||| ||||||| ||||||||||||
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                                AGA CGAGACA TGGGTCCGACCT
                                  A      A
GAM1741  CRTAM     3'  TCCAGCCTGGGCGACAGAGGGA 39476      G      A
                GA                  TCTC CTCTGTC CCCAGGCTGGA
                                    |||| ||||||| ||||||||||
                                    AGAG GAGACAG GGGTCCGACCT
                                      G      C
GAM1741  CSEN      3'  TCTGGGCTGGCAGAGGGGA   26462      G      _
                                    TCTC CTCTGTCA CCCAGG
                                    |||| |||||||| ||||||
                                    AGGG GAGACGGT GGGTCT
                                      _      C
GAM1741  CXYorf1   3'  CCAGCTCTGCAGGGTGGGG   82907          TCACC  _
                                    TCTCGCTCTG    CAG GCTGG
                                    ||||||||||    ||| |||||
                                    GGGGTGGGAC    GTC CGACC
                                          _____  T
GAM1741  CXYorf1   3'  TCCGGCCTCCCCAGCGCGGGG  82920       T   TCACCC
                                    TCTCGC CTG     AGGCTGGA
                                    |||||| |||     ||||||||
                                    GGGGCG GAC     TCCGGCCT
                                       C   CCC___
GAM1741  CYP2A7    3'  TCTGGTGGGCGGGGCCAGG    48355     C       AC
                                    TCT GCTCTGTC  CCAGG
                                    ||| ||||||||  |||||
                                    GGA CGGGGCGG  GGTCT
                                      C       GT
GAM1741  D21S2056E 3'  TCCAGCCTGGGCAACGAGAGGG 14873      G   T  CA
                A                    TCTC CTC GT  CCCAGGCTGGA
                                    |||| ||| ||  ||||||||||
                                    AGGG GAG CA  GGGTCCGACCT
                                      A   _  AC
GAM1741  DAPK2     3'  TCCAGTCTGGGTGACAGAGAGA 27516      G
                GA                  TCTC CTCTGTCACCCAGGCTGGA
                                    |||| ||||||||||||||||||
                                    AGAG GAGACAGTGGGTCTGACCT
                                      A
GAM1741  DARS      3'  TCCAGTGTGGATGACAGAGCGA 9051             C   G
                GA                  TCTCGCTCTGTCA CCA GCTGGA
                                    |||||||||||| ||| ||||||
                                    AGAGCGAGACAGT GGT TGACCT
                                           A   G
GAM1741  DCOHM     3'  TCCAGCCTGGGTGACGGAACGG 50537       C
                GA                  TCTCG TCTGTCACCCAGGCTGGA
                                    ||||| ||||||||||||||||||
                                    AGGGC AGGCAGTGGGTCCGACCT
                                      A
GAM1741  DDX34     3'  TCCAGCCTGGTTGACAGAGCAA 28678      C       C
                GA                  TCT GCTCTGTCA CCAGGCTGGA
                                    ||| ||||||||| ||||||||||
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                                AGA CGAGACAGT GGTCCGACCT
                                  A       T
GAM1741  DGKD     3'  TTCAGCTTGGGGTGTGAGTGAG 60115        TGTCA
                 A                 TCTCGCTC    CCCAGGCTGGA
                                   ||||||||    ||||||||||
                                   AGAGTGAG    GGGTTCGACTT
                                       TGTG_
GAM1741  DIS3     3'  TCCAGCCTGGGTGACAGAACAA 30922     CGC
                 GA                  TCT   TCTGTCACCCAGGCTGGA
                                   |||   ||||||||||||||||||
                                   AGA   AGACAGTGGGTCCGACCT
                                     ACA
GAM1741  DIS3     3'  TTCAGCCTGGATGATGAGAGTG 30928         _   C
                 AGA                   TCTCGCTCT GTCA CCAGGCTGGA
                                   ||||||||| |||| ||||||||||
                                   AGAGTGAGA TAGT GGTCCGACTT
                                       G   A
GAM1741  DJ122O8.2 3'  ACTTCAGCCTGGGTGACAGAGT 40391
                 GAGA                  TCTCGCTCTGTCACCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGTGAGACAGTGGGTCCGACTT
                                                CAC
GAM1741  DJ159A19.3 5'  TCGGCGTGGGAGAGCGAGA   32283        GTCA   G
                                   TCTCGCTCT   CCCA GCTGG
                                   |||||||||   |||| |||||
                                   AGAGCGAGA   GGGT CGGCT
                                         ____   G
GAM1741  DJ37E16.5 3'  TCCAGTTCTGCACCGGGGTGGG 40099          TCACC   _
                 G                   TCTCGCTCTG    CAGG CTGGA
                                   ||||||||||    |||| |||||
                                   GGGGTGGGGC    GTCT GACCT
                                       CAC__   T
GAM1741  dJ383J4.3 3'  TCCAGCCTGGGCAACAAAGTGA 67498       C   CA
                 GA                  TCTCGCT TGT  CCCAGGCTGGA
                                   |||||||  |||  ||||||||||
                                   AGAGTGA ACA  GGGTCCGACCT
                                      A   AC
GAM1741  DKFZP434A0131 3'  TCCAGCCTGGGTGACAGAGCAA 39154     C
                 GA                  TCT GCTCTGTCACCCAGGCTGGA
                                   ||| ||||||||||||||||||||
                                   AGA CGAGACAGTGGGTCCGACCT
                                     A
GAM1741  DKFZP434B168 3'  TCCAGCCTGGGCGACAGAGCGA 31872           A
                 GA                  TCTCGCTCTGTC CCCAGGCTGGA
                                   |||||||||||| ||||||||||
                                   AGAGCGAGACAG GGGTCCGACCT
                                         C
GAM1741  DKFZP434C171 3'  TCCAGCCCGGGTGACAGAGCAA 32199     C         A
                 GA                  TCT GCTCTGTCACCC GGCTGGA
                                   ||| ||||||||||| |||||||
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                                AGA CGAGACAGTGGG CCGACCT
                                  A          C
GAM1741  DKFZp434E0519 3'  TCCGGCCTGGGCGAGAGTGAGA 51000        TG  A
                                TCTCGCTC  TC CCCAGGCTGGA
                                ||||||||  || ||||||||||
                                AGAGTGAG  AG GGGTCCGGCCT
                                    __  C
GAM1741  DKFZp434E169 3'  CCAGCCTGGGCGACAGAGCGAG 51074          A        A
           A                     TCTCGCTCTGTC CCCAGGCTGG
                                ||||||||||| ||||||||||
                                AGAGCGAGACAG GGGTCCGACC
                                      C         G
GAM1741  DKFZp434E2220 5'  TCCAGCCTGGGCGACAGGGTGA 34720          A
           GA                    TCTCGCTCTGTC CCCAGGCTGGA
                                ||||||||||| ||||||||||
                                AGAGTGGGACAG GGGTCCGACCT
                                      C
GAM1741  DKFZP434F091 5'  TTCAGCTTGGGGAGAGAGGGG  31899     G    G  A
                                CTC CTCT TC CCCAGGCTGGA
                                ||| |||| || ||||||||||
                                GGG GAGA AG GGGTTCGACTT
                                  _   G  _
GAM1741  DKFZp434G171 3'  TCCAGCCTGGGAGACACAGCGA 80247        C    A
           GA                    TCTCGCT TGTC CCCAGGCTGGA
                                ||||||| |||| ||||||||||
                                AGAGCGA ACAG GGGTCCGACCT
                                    C    A
GAM1741  DKFZp434G171 3'  TCCAGCCTGGGCAACAAGAGGG 80248     G    _  CA
           A                     TC CTCT GT  CCCAGGCTGGA
                                || |||| ||  ||||||||||
                                AG GAGA CA  GGGTCCGACCT
                                 G    A  AC
GAM1741  DKFZP434I1735 3'  TCCAGCCTGGGCGACAGAGTGA 89173          A
           GA                    TCTCGCTCTGTC CCCAGGCTGGA
                                ||||||||||| ||||||||||
                                AGAGTGAGACAG GGGTCCGACCT
                                      C
GAM1741  DKFZP434N1511 3'  TCCAGCCTGGGCAACAGAGCAA 93063     C       CA
           GA                    TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A       AC
GAM1741  DKFZP434P0721 3'  TCCAGAAACATGGCAGAGCAGA 64467     C        CCCAGG
                                TCT GCTCTGTCA      CTGGA
                                ||| |||||||||      |||||
                                AGA CGAGACGGT      GACCT
                                  _        ACAAA_
GAM1741  DKFZP434P211 3'  TCCAGCCTGGTCGACAGAGTGA 28031          AC
                                TCGCTCTGTC  CCAGGCTGGA
                                ||||||||||  ||||||||||
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                                AGTGAGACAG  GGTCCGACCT
                                      CT
GAM1741  DKFZp547C176 3'  TCCAGCCTGGCGACAGAGCAAG 67806     C       AC
            A                  TCT GCTCTGTC  CCAGGCTGGA
                               ||| ||||||||  ||||||||||
                               AGA CGAGACAG  GGTCCGACCT
                                 A       C_
GAM1741  DKFZp547I094 3'  TCCAGCCTGGGCGGCAGAGTGA 50566           A
            GA                 TCTCGCTCTGTC CCCAGGCTGGA
                               |||||||||||| ||||||||||
                               AGAGTGAGACGG GGGTCCGACCT
                                      C
GAM1741  DKFZP564A022 3'  TCCAGCCTGGGCAACAGAGTGA 48975          CA
            GA                 TCTCGCTCTGT  CCCAGGCTGGA
                               ||||||||||  ||||||||||
                               AGAGTGAGACA  GGGTCCGACCT
                                      AC
GAM1741  DKFZP564B1023 3'  TCCAGCCTGGACAACAGATTGA 49368      C    CAC
            GA                 TCTCG TCTGT   CCAGGCTGGA
                               ||||| |||||   ||||||||||
                               AGAGT AGACA   GGTCCGACCT
                                  T    ACA
GAM1741  DKFZP564B1023 3'  TCCAGCCTGGGCAACAAGAGTG 49369       _  CA
            A                  TCGCTCT GT  CCCAGGCTGGA
                               ||||||| ||  ||||||||||
                               AGTGAGA CA  GGGTCCGACCT
                                   A  AC
GAM1741  DKFZP564C1940 5'  TCTGGCCTGGGAGCTGGCGA   26746      CT  CA      TG
                               TCGCT  GT  CCCAGGC  GA
                               |||||  ||  |||||||  ||
                               AGCGG  CG  GGGTCCG  CT
                                  T_  A_      GT
GAM1741  DKFZP564I0422 3'  TCCAGCCTGGGCAATGGAGTGA 49519          CA
            GA                 TCTCGCTCTGT  CCCAGGCTGGA
                               ||||||||||  ||||||||||
                               AGAGTGAGGTA  GGGTCCGACCT
                                      AC
GAM1741  DKFZP564I122 3'  TCTAGCCTGGGTGACAGTGTGA 63881       T
            GA                 TCTCGC CTGTCACCCAGGCTGGA
                               ||||||| ||||||||||||||||
                               AGAGTG GACAGTGGGTCCGATCT
                                  T
GAM1741  DKFZp564K142 3'  TCCAGCCTGAGTGATAGAGTGA 50436           C
            GA                 TCTCGCTCTGTCAC CAGGCTGGA
                               |||||||||||||| |||||||||
                               AGAGTGAGATAGTG GTCCGACCT
                                      A
GAM1741  DKFZp564K142 3'  TCCAGCCTGGCAACAGAGCGAG 50437          CAC
            A                  TCTCGCTCTGT   CCAGGCTGGA
                               ||||||||||   ||||||||||
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                                AGAGCGAGACA   GGTCCGACCT
                                      AC_
GAM1741  DKFZP564M182 3'  CTGTAGCCTGGGTGACAGTGTG 78627       T           GA
            AGA                   TCTCGC CTGTCACCCAGGCTG
                                  |||||| |||||||||||||||
                                  AGAGTG GACAGTGGGTCCGAT
                                     T             GTCG
GAM1741  DKFZP564M182 3'  TCCAGCCTGATGACAGAGCAAG 78642     C       CC
            A                  TCT GCTCTGTCA  CAGGCTGGA
                               ||| |||||||||  |||||||||
                               AGA CGAGACAGT  GTCCGACCT
                                 A        A_
GAM1741  DKFZP564M182 3'  TCCAGCCTGGGCAACAGAGAGA 78643     G     CA
            GA                   TCTC CTCTGT  CCCAGGCTGGA
                                 |||| ||||||  ||||||||||
                                 AGAG GAGACA  GGGTCCGACCT
                                   A      AC
GAM1741  DKFZp566H0824 3'  TCCAGCCTGGGCAACAGAGCAA 34492     C      CA
            GG                   TCT GCTCTGT  CCCAGGCTGGA
                                 ||| |||||||  ||||||||||
                                 GGA CGAGACA  GGGTCCGACCT
                                   A       AC
GAM1741  DKFZp566H0824 5'  TCCAGCCTGGGCGACAGAGCGA 34493          A
            GA                   TCTCGCTCTGTC CCCAGGCTGGA
                                 |||||||||||| ||||||||||
                                 AGAGCGAGACAG GGGTCCGACCT
                                       C
GAM1741  DKFZP586C1324 3'  TCAAGTCTGGGCGACAGGGTGA 70361          A       G
            GA                   TCTCGCTCTGTC CCCAGGCT GA
                                 |||||||||||| |||||||| ||
                                 AGAGTGGGACAG GGGTCTGA CT
                                       C       A
GAM1741  DKFZP586D2223 3'  TCTAGCCTGGGCAACAGAGTGA 38297          CA
            GA                   TCTCGCTCTGT  CCCAGGCTGGA
                                 ||||||||||  ||||||||||
                                 AGAGTGAGACA  GGGTCCGATCT
                                       AC
GAM1741  DKFZP586D2223 3'  TTCAGCCTGGGTGACAGAGCAA 38300     C
            GA                   TCT GCTCTGTCACCCAGGCTGGA
                                 ||| ||||||||||||||||||||
                                 AGA CGAGACAGTGGGTCCGACTT
                                   A
GAM1741  DKFZP586M1120 3'  TCCAGCCTGGGCAACAGAGTGA 49286         CA
                                 TCGCTCTGT  CCCAGGCTGGA
                                 |||||||||  ||||||||||
                                 AGTGAGACA  GGGTCCGACCT
                                       AC
GAM1741  DKFZp727G131 3'  TCCAGCCTGGGCAACAGCGTGA 59698       T   CA
            GA                   TCTCGC CTGT  CCCAGGCTGGA
                                 |||||| ||||  ||||||||||
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                                AGAGTG GACA  GGGTCCGACCT
                                   C    AC
GAM1741  DKFZP761G1913 3'  TCCAGCCTGGGTGAAGGAGTGA 49699          G
            GA                    TCTCGCTCT TCACCCAGGCTGGA
                                  ||||||||| ||||||||||||||
                                  AGAGTGAGG AGTGGGTCCGACCT
                                     A
GAM1741  DKFZp761N0624 3'  TCTAGCCTTGAAAATGGAGTGA 51161          CACCC
                                  TCGCTCTGT    AGGCTGGA
                                  |||||||||    ||||||||
                                  AGTGAGGTA    TCCGATCT
                                     AAAGT
GAM1741  DKFZp761O17121 3'  TCCAGCCTGTAGGGGAGTGA   51135        GTCA __
                                  TCGCTCT   CC  CAGGCTGGA
                                  |||||||   ||  |||||||||
                                  AGTGAGG   GG  GTCCGACCT
                                     ____  AT
GAM1741  DLAT     5'  TCTGGCCTGGGGAGCGGGTGGA 68086    T  T   CA     TG
                                  TC CGC CTGT  CCCAGGC  GA
                                  || ||| ||||  |||||||  ||
                                  AG GTG GGCG  GGGTCCG  CT
                                   _  _   AG      GT
GAM1741  DRF1     3'  ACTCCAGCCTGGGTGACAGAGC 47731
            GAGA                    TCTCGCTCTGTCACCCAGGCTGGA
                                    |||||||||||||||||||||||||
                                    AGAGCGAGACAGTGGGTCCGACCT
                                                 CAC
GAM1741  DRF1     3'  TCCAGCCTGGGCGATAGAGCTA 47757     C       A
            GA                     TCT GCTCTGTC CCCAGGCTGGA
                                   ||| |||||||| ||||||||||
                                   AGA CGAGATAG GGGTCCGACCT
                                     T       C
GAM1741  DRIL2    3'  CTCAGCCTGCAGGGTGTGG    22347    T      TCACC       A
                                   TC CGCTCTG    CAGGCTGG
                                   || |||||||    ||||||||
                                   GG GTGGGAC    GTCCGACT
                                    T      _____       CC
GAM1741  DSCR6    3'  TCCAGCCTGGGCAACAAGAGCG 39076        _ CA
            A                       TCGCTCT GT  CCCAGGCTGGA
                                    ||||||| ||  ||||||||||||
                                    AGCGAGA CA  GGGTCCGACCT
                                       A  AC
GAM1741  DXS1357E  5'  TCCGGCCGCGGTATGAGGGGCG 20435          GTC_  CA
            GGG                     TCTCGCTCT   ACC  GGCTGGA
                                    |||||||||   |||  |||||||
                                    GGGGCGGGG   TGG  CCGGCCT
                                       AGTA  CG
GAM1741  EIF2S1   3'  TCGAGCCTGGGTGACAGGGCAA 15848     C            G
            GA                      TCT GCTCTGTCACCCAGGCT GA
                                    ||| |||||||||||||||| ||
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                                AGA CGGGACAGTGGGTCCGA CT
                                  A             G
GAM1741  ESDN     5'  TCCGGCCTGGGGTCTCGGCGCG 56063       T   TCA_
                GG                  CTCGC CTG    CCCAGGCTGGA
                                    ||||| |||    ||||||||||
                                    GGGCG GGC    GGGTCCGGCCT
                                      C   TCTG
GAM1741  ET       3'  TCCAGCCTGGATGACAAGAGTG 44474        _    C
                A                    TCGCTCT GTCA CCAGGCTGGA
                                    ||||||| |||| ||||||||||
                                    AGTGAGA CAGT GGTCCGACCT
                                       A   A
GAM1741  FADS1    3'  TCCAGCCTGGGCGACAGAGCAA 26386     C       A
                GA                  TCT GCTCTGTC CCCAGGCTGGA
                                    ||| |||||||| ||||||||||
                                    AGA CGAGACAG GGGTCCGACCT
                                      A       C
GAM1741  FBXO26   3'  TCCAGCCTGGGTGAGAAAGCAA 46631     C   CTG
                GA                  TCT GCT   TCACCCAGGCTGGA
                                    ||| |||   ||||||||||||||
                                    AGA CGA   AGTGGGTCCGACCT
                                      A   AAG
GAM1741  FBXO27   3'  ACTCCAGCCTGGGTGACAGAGC 74998
                GAGA                  TCTCGCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACAGTGGGTCCGACCT
                                                CAC
GAM1741  FBXO27   3'  TCCAGCCTGGGCAACACAGCGA 75014        C   CA
                GA                  TCTCGCT TGT  CCCAGGCTGGA
                                    ||||||| |||  ||||||||||
                                    AGAGCGA ACA  GGGTCCGACCT
                                       C   AC
GAM1741  FBXO6    3'  ACTCCAGCCTGGGTGACAGAGC 37985
                GAGA                  TCTCGCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACAGTGGGTCCGACCT
                                                CAC
GAM1741  FBXO9    3'  TCCAGCCTGAGCAACACAGTGA 54255        C   CACC
                GA                  TCTCGCT TGT    CAGGCTGGA
                                    ||||||| |||    |||||||||
                                    AGAGTGA ACA    GTCCGACCT
                                       C   ACGA
GAM1741  FEM1B    5'  TCCGGCCTGAGGCCCGGGGCGG 31680         TCA _
                                    TCGCTCTG   CC CAGGCTGGA
                                    ||||||||   || |||||||||
                                    GGCGGGGC   GG GTCCGGCCT
                                         CC_  A
GAM1741  FKBP14   3'  TCCAGCCTGGGTGACAGAGCAA 36070     C
                GA                  TCT GCTCTGTCACCCAGGCTGGA
                                    ||| ||||||||||||||||||||
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                                AGA CGAGACAGTGGGTCCGACCT
                                  A
GAM1741  FKSG17   3'  TCCAGCCTGGGTGACAGAGTGA 50159
                GA                  TCTCGCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAGTGGGTCCGACCT

GAM1741  FKSG43   5'  TCCAGCCTGGGTGACAGAGCAA 50163     C
                GA                  TCT GCTCTGTCACCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAGTGGGTCCGACCT
                                      A
GAM1741  FKSG44   5'  TCCAGCCTGGGCGACAGAGCGA 49963           A
                GA                  TCTCGCTCTGTC CCCAGGCTGGA
                                    |||||||||||| ||||||||||
                                    AGAGCGAGACAG GGGTCCGACCT
                                           C
GAM1741  FLJ00007 3'  TCTGGCCTAAGGTAGGGGAGG  71784     G    GT ACCC    TG
                                    TCTC CTCT  C    AGGC  GA
                                    |||| ||||  |    ||||  ||
                                    GGAG GGGA  G    TCCG  CT
                                      _    TG AA__    GT
GAM1741  FLJ00060 3'  TCCAGCCTGGGCGATAGAGCAA 61755     C       A
                GA                  TCT GCTCTGTC CCCAGGCTGGA
                                    ||| |||||||| ||||||||||
                                    AGA CGAGATAG GGGTCCGACCT
                                      A       C
GAM1741  FLJ10043 3'  CTCCAGCCTGGGTGACAGAGCG 36233
                AGA                   TCTCGCTCTGTCACCCAGGCTGGA
                                      ||||||||||||||||||||||||
                                      AGAGCGAGACAGTGGGTCCGACCT
                                                  CA
GAM1741  FLJ10058 3'  TCCAGCCTGGGCAACACAGTGA 36264        C   CA
                GA                  TCTCGCT TGT  CCCAGGCTGGA
                                    ||||||| |||  ||||||||||
                                    AGAGTGA ACA  GGGTCCGACCT
                                       C   AC
GAM1741  FLJ10097 3'  CCAGACTCACAGAGTGGGG    69035          CACCC  G
                                    TCTCGCTCTGT     AG CTGG
                                    ||||||||||     || ||||
                                    GGGGTGAGACA     TC GACC
                                          C_____  A
GAM1741  FLJ10139 3'  TCCAGCCTGGGTGACAAAGTAA 36317     CG  C
                GA                  TCT  CT TGTCACCCAGGCTGGA
                                    |||  || ||||||||||||||||
                                    AGA  GA ACAGTGGGTCCGACCT
                                      AT  A
GAM1741  FLJ10201 3'  TCCAGCCCTGGTGACAGAGGAG 36355      G        CA
                A                    TCTC CTCTGTCACC  GGCTGGA
                                     |||| ||||||||||  |||||||
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                                AGAG GAGACAGTGG  CCGACCT
                                  _        TC
GAM1741  FLJ10276  3'  CGGCTGGATTCAGTGAGGGGGT 36421        G   _________  AGGCT
                GGGA                TCTCGCTCT TCAC       CC    G
                                    ||||||||| ||||       ||    |
                                    AGGGTGGGG AGTG       GG    C
                                       G   ACTT   A  TCGGA
GAM1741  FLJ10460  3'  TCCAACCTGGGTGATGGAGCAA 36623     C           C
                GA                  TCT GCTCTGTCACCCAGG TGGA
                                    ||| |||||||||||||| ||||
                                    AGA CGAGGTAGTGGGTCC ACCT
                                      A            A
GAM1741  FLJ10520  3'  TCCAGCCTCGGTGACAGAGCAA 36710     C         C
                GA                  TCT GCTCTGTCACC AGGCTGGA
                                    ||| |||||||||| ||||||||
                                    AGA CGAGACAGTGG TCCGACCT
                                      A         C
GAM1741  FLJ10525  5'  TCCGGCCTGTGTGTGGCGCGAG 36724       T   T   C
                G                   TCTCGC CTG CAC CAGGCTGGA
                                    |||||| ||| ||| |||||||||
                                    GGAGCG GGT GTG GTCCGGCCT
                                       C   _   T
GAM1741  FLJ10546  3'  TTTGGTCTCTTTTGGTGGGGTG 60186        TG   CCC_   TG
                GGG                 TCTCGCTC  TCA   AGGC  GA
                                    ||||||||  |||   ||||  ||
                                    GGGGTGGG  GGT   TCTG  TT
                                         GT   TTTC   GT
GAM1741  FLJ10547  3'  TCCAGCCTGGGCTACAGAGCGA 36779          CA
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGCGAGACA  GGGTCCGACCT
                                          TC
GAM1741  FLJ10607  3'  TCCAGCCTGGCGACAGAGAGAG 77646      G      AC
                A                    TCTC CTCTGTC  CCAGGCTGGA
                                    ||||  |||||||  ||||||||||
                                    AGAG GAGACAG  GGTCCGACCT
                                      A      C_
GAM1741  FLJ10650  3'  TCCAGCCTGGGCGACAGAATGA 36903      C     A
                GA                  TCTCG TCTGTC CCCAGGCTGGA
                                    |||||  ||||||  ||||||||||
                                    AGAGT AGACAG GGGTCCGACCT
                                      A     C
GAM1741  FLJ10704  3'  TCCAGCCTGGACGACAGAGTGA 36984          AC
                GA                  TCTCGCTCTGTC  CCAGGCTGGA
                                    ||||||||||||  ||||||||||
                                    AGAGTGAGACAG  GGTCCGACCT
                                          CA
GAM1741  FLJ10709  3'  TCTGGCTCACAGGGGGAGGGTG 36989        G  A   A___   TG
                AGG                 TCTCGCTCT TC CCC    GGC  GA
                                    ||||||||| || |||    |||  ||
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                                GGAGTGGGA GG GGG   TCG  CT
                                    _ _  ACAC  GT
GAM1741  FLJ10761  3'  TCTTGGTGATGGGTGGGG   37133      T      C
                                TCTCGC CTGTCACC AGG
                                ||||||| |||||||| |||
                                GGGGTG GGTAGTGG TCT
                                   _      T
GAM1741  FLJ10781  3'  TCCAGCCTGGGCAGCAGAGTGA 37176          CA
           GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGAGACG  GGGTCCGACCT
                                      AC
GAM1741  FLJ10803  3'  TCCAGCCTGGGCAACAGAGCAA 37209    C      CA
           GA                    TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A       AC
GAM1741  FLJ10826  3'  TCCAGCCTGGGCAACAAGAGTG 37250       _ CA
           A                     TCGCTCT GT  CCCAGGCTGGA
                                ||||||| ||  ||||||||||
                                AGTGAGA CA  GGGTCCGACCT
                                    A  AC
GAM1741  FLJ10830  3'  TCCAGCCTGGGCGACAGAACGA 37267      C     A
           GA                    TCTCG TCTGTC CCCAGGCTGGA
                                ||||| |||||| ||||||||||
                                AGAGC AGACAG GGGTCCGACCT
                                   A     C
GAM1741  FLJ10936  3'  TCCAGCCTGGGCAACAGAGGGA 37450     G     CA
           GA                    TCTC CTCTGT  CCCAGGCTGGA
                                |||| ||||||  ||||||||||
                                AGAG GAGACA  GGGTCCGACCT
                                  G     AC
GAM1741  FLJ10986  5'  TCTGGTGGACCAGAGTGGGG  37492          _ AC
                                TCTCGCTCTG TC  CCAGG
                                |||||||||| ||  |||||
                                GGGGTGAGAC AG  GGTCT
                                      C  GT
GAM1741  FLJ10989  3'  TCCAGCCTGGGTGACAAAGCAA 37507    C   C
           GA                    TCT GCT TGTCACCCAGGCTGGA
                                ||| ||| ||||||||||||||||
                                AGA CGA ACAGTGGGTCCGACCT
                                  A   A
GAM1741  FLJ10998  3'  TCCAGCCTGGGTGACAGTGA   37523      CT
                                TCGCT  GTCACCCAGGCTGGA
                                |||||  ||||||||||||||||
                                AGTGA  CAGTGGGTCCGACCT
                                   __
GAM1741  FLJ11000  3'  TCTAGCTTCAGGAGGGTGGGG  37528         GTCA  C_
                                TCTCGCTCT   CC  AGGCTGGA
                                |||||||||   ||  ||||||||
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                                GGGGTGGGA   GG  TTCGATCT
                                     ____  AC
GAM1741  FLJ11036  3'  TCCAGCCTGGGCGACAGAGCAA 37556    C      A
            GA                   TCT GCTCTGTC CCCAGGCTGGA
                                 ||| |||||||| ||||||||||
                                 AGA CGAGACAG GGGTCCGACCT
                                   A       C
GAM1741  FLJ11042  3'  TCCAGTTTGGACTACAGAGTGA 37566          CAC
            GA                   TCTCGCTCTGT  CCAGGCTGGA
                                 ||||||||||  ||||||||||
                                 AGAGTGAGACA  GGTTTGACCT
                                       TCA
GAM1741  FLJ11106  3'  TCCAGCCTGGGTGACAGATCCA 37626    CGC
            GA                   TCT  TCTGTCACCCAGGCTGGA
                                 |||  ||||||||||||||||||
                                 AGA  AGACAGTGGGTCCGACCT
                                   CCT
GAM1741  FLJ11116  3'  TTTGGCCTCTTACTAGGGGGGA 83476    G   TCACCC   TG
                                 TCTC CTCTG    AGGC  GA
                                 |||| |||||    ||||  ||
                                 AGGG GGGAT    TCCG  TT
                                   _   CATTC_  GT
GAM1741  FLJ11126  3'  TCCAGCCTGGGTAACAGAGCGA 37655          C
            GA                   TCTCGCTCTGT ACCCAGGCTGGA
                                 |||||||||| ||||||||||
                                 AGAGCGAGACA TGGGTCCGACCT
                                       A
GAM1741  FLJ11151  3'  TCCAGCCTGGGCAACAGAGCAA 68482    C     CA
            GA                   TCT GCTCTGT  CCCAGGCTGGA
                                 ||| |||||||  ||||||||||
                                 AGA CGAGACA  GGGTCCGACCT
                                   A      AC
GAM1741  FLJ11259  3'  TCCAGTCTGGGCAACAGAGTGA 37772          CA
            GA                   TCTCGCTCTGT  CCCAGGCTGGA
                                 ||||||||||  ||||||||||
                                 AGAGTGAGACA  GGGTCTGACCT
                                       AC
GAM1741  FLJ11301  3'  TCCAGCCTGGGCGACAGAGTGA 37810          A
            GA                   TCTCGCTCTGTC CCCAGGCTGGA
                                 |||||||||||| ||||||||||
                                 AGAGTGAGACAG GGGTCCGACCT
                                       C
GAM1741  FLJ11413  3'  TCTGGCCTGTGGCAGGGCCGGG 44959      _       CC   TG
            A                    TCTCG CTCTGTCAC  AGGC  GA
                                 ||||| |||||||||  ||||  ||
                                 AGGGC GGGACGGTG  TCCG  CT
                                   C        __   GT
GAM1741  FLJ11577  3'  TCCAGCCTGGGCAACAAGAGTG 47960        _ CA
            AGA                    TCTCGCTCT GT  CCCAGGCTGGA
                                 |||||||||  ||  ||||||||||
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                                AGAGTGAGA CA  GGGTCCGACCT
                                     A  AC
GAM1741  FLJ11710  5'  TCCAGCCTGGGCAACAGAGCAA 46252     C      CA
                GA                   TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A       AC
GAM1741  FLJ11715  3'  ACTCCAGCCTGGGTGATAGAGT 44973
                GAGA                   TCTCGCTCTGTCACCCAGGCTGGA
                                |||||||||||||||||||||||||
                                AGAGTGAGATAGTGGGTCCGACCT
                                              CAC
GAM1741  FLJ11722  3'  TCCAGCCTGGCAACAGAGCAAG 47008     C      CAC
                G                    TCT GCTCTGT   CCAGGCTGGA
                                ||| |||||||   ||||||||||
                                GGA CGAGACA   GGTCCGACCT
                                  A       AC_
GAM1741  FLJ11722  3'  TCCAGCCTGGCCACAGAGCGAG 47009           CAC
                A                    TCTCGCTCTGT   CCAGGCTGGA
                                ||||||||||   ||||||||||
                                AGAGCGAGACA   GGTCCGACCT
                                      CC_
GAM1741  FLJ11726  3'  TCCAGCCTGGGCGACAGAGCAG 47031    TC       A
                GA                   TC  GCTCTGTC CCCAGGCTGGA
                                ||  |||||||| ||||||||||
                                AG  CGAGACAG GGGTCCGACCT
                                 GA       C
GAM1741  FLJ11996  3'  TCCAGCTTGGGTGACAGAGCAA 47070     C
                GA                   TCT GCTCTGTCACCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGAGACAGTGGGTTCGACCT
                                  A
GAM1741  FLJ12056  3'  TCCAGCCTGCTTCAGGAGGGAG 46825      G    GTCACC
                G                    TCTC CTCT      CAGGCTGGA
                                |||| ||||      |||||||||
                                GGAG GAGG      GTCCGACCT
                                  G    ACTTC_
GAM1741  FLJ12078  3'  TCCAGCCTGGGTGGCAGAGAGA 47086      G
                GA                   TCTC CTCTGTCACCCAGGCTGGA
                                |||| ||||||||||||||||||||
                                AGAG GAGACGGTGGGTCCGACCT
                                  A
GAM1741  FLJ12294  3'  TCCAGCCTGGGTGACAGAGAGA 47721      G
                GA                   TCTC CTCTGTCACCCAGGCTGGA
                                |||| ||||||||||||||||||||
                                AGAG GAGACAGTGGGTCCGACCT
                                  A
GAM1741  FLJ12298  3'  TCCAGCCTGGGCAACAGAGCGA 50600           CA
                GA                   TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
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                                AGAGCGAGACA  GGGTCCGACCT
                                      AC
GAM1741  FLJ12331  3'  TCCAGCCTGAGCTACAGAGCAA 47114     C      CACC
                GA                    TCT GCTCTGT    CAGGCTGGA
                                      ||| |||||||    |||||||||
                                      AGA CGAGACA    GTCCGACCT
                                        A       TCGA
GAM1741  FLJ12363  3'  TCCAGCCTGGGCAACAAGAGAG 50643      G  C   CA
                A                      TCTC CT TGT  CCCAGGCTGGA
                                       |||| || |||  ||||||||||
                                       AGAG GA ACA  GGGTCCGACCT
                                         A _   AC
GAM1741  FLJ12409  3'  TCTAGCTTTGATGGCGAAGTGA 47773        C     CCC
                GA                    TCTCGCT TGTCA   AGGCTGGA
                                      ||||||| |||||   ||||||||
                                      AGAGTGA GCGGT   TTCGATCT
                                         A     AGT
GAM1741  FLJ12448  3'  TCTAGCCTAAGCAATGGAGCAA 43481     C      CACCC
                GA                    TCT GCTCTGT     AGGCTGGA
                                      ||| |||||||     ||||||||
                                      AGA CGAGGTA     TCCGATCT
                                        A       ACGAA
GAM1741  FLJ12484  3'  TCTGGGGATGGTGGGTGGGG   70230        __     A
                                      TCTCGCT  CTGTC CCCAGG
                                      |||||||  ||||| ||||||
                                      GGGGTGG  GGTAG GGGTCT
                                         GT    _
GAM1741  FLJ12586  3'  ACTCCAGCCTGGGTGACAGAGC 45203
                GAGA                      TCTCGCTCTGTCACCCAGGCTGGA
                                          ||||||||||||||||||||||||
                                          AGAGCGAGACAGTGGGTCCGACCT
                                                    CAC
GAM1741  FLJ12592  3'  TCCAGCCTGGGTGACCGAGTGA 50655         T
                GA                    TCTCGCTC GTCACCCAGGCTGGA
                                      |||||||| ||||||||||||||
                                      AGAGTGAG CAGTGGGTCCGACCT
                                         C
GAM1741  FLJ12606  3'  ACTTCAGCCTGGGTGACAGAGT 46059
                GAGA                      TCTCGCTCTGTCACCCAGGCTGGA
                                          ||||||||||||||||||||||||
                                          AGAGTGAGACAGTGGGTCCGACTT
                                                    CAC
GAM1741  FLJ12618  3'  TCCAGCCTGGGTGACAGAGCAA 46508     C
                GA                    TCT GCTCTGTCACCCAGGCTGGA
                                      ||| ||||||||||||||||||||
                                      AGA CGAGACAGTGGGTCCGACCT
                                        A
GAM1741  FLJ12650  3'  TTCGGAGGAGTGGGGCGGGGCG 44827          CA    GG___
                GGG                     TCTCGCTCTGT  CCCA     CTGGA
                                        ||||||||||  ||||     |||||
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                                GGGGCGGGGCG  GGGT    GGCTT
                                      __   GAGGA
GAM1741  FLJ12660  3'  TCCAGCCTGGTCAATGGAGTGC 47900    T      CAC
              GA                  TC CGCTCTGT   CCAGGCTGGA
                                  || ||||||||   ||||||||||
                                  AG GTGAGGTA   GGTCCGACCT
                                   C       ACT
GAM1741  FLJ12671  3'  TCCAGCCTGGGTGACAAGAGTG 49112        _
              AGA                   TCTCGCTCT GTCACCCAGGCTGGA
                                  |||||||||  ||||||||||||||
                                  AGAGTGAGA CAGTGGGTCCGACCT
                                        A
GAM1741  FLJ12687  3'  CTCCAGCCTGGGTGACAGAGTG 46749
              AGA                   TCTCGCTCTGTCACCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAGTGGGTCCGACCT
                                              CA
GAM1741  FLJ12800  3'  TCCAGGCTGGGCGACAGAGTGA 43534          A    G
              GA                    TCTCGCTCTGTC CCCAG CTGGA
                                  |||||||||||| ||||| |||||
                                  AGAGTGAGACAG GGGTC GACCT
                                        C    G
GAM1741  FLJ12875  3'  TTTAGTGCAAGACAGATGGGG  44921      C     ACCCAG
                                  TCTCG TCTGTC     GCTGGA
                                  ||||| ||||||     ||||||
                                  GGGGT AGACAG     TGATTT
                                     _     AACG__
GAM1741  FLJ12891  3'  TTGGCGGGGGGGTGGAGCGGGG  46934       TG  A   AG  TG
                                  TCTCGCTC  TC CCC  GC  G
                                  ||||||||  || |||  ||  |
                                  GGGGCGAG  GG GGG  CG  T
                                       GT  _   G_  GT
GAM1741  FLJ12921  3'  TCCAGCCTGGGCGACGGAGCGA 46400          A
              GA                    TCTCGCTCTGTC CCCAGGCTGGA
                                  |||||||||||| ||||||||||
                                  AGAGCGAGGCAG GGGTCCGACCT
                                        C
GAM1741  FLJ13117  3'  TCCAGCCTGGGAGACAGAGCAA 43811    C      A
              GA                    TCT GCTCTGTC CCCAGGCTGGA
                                  ||| |||||||| ||||||||||
                                  AGA CGAGACAG GGGTCCGACCT
                                    A       A
GAM1741  FLJ13193  3'  TCCAGCCTGGCGACAGAGCGAG 50736          AC
              A                     TCTCGCTCTGTC  CCAGGCTGGA
                                  ||||||||||||  ||||||||||
                                  AGAGCGAGACAG  GGTCCGACCT
                                        C_
GAM1741  FLJ13241  3'  TCCAGCCTGGGTGGCAGAGCCA 47656    C
              GA                    TCT GCTCTGTCACCCAGGCTGGA
                                  ||| ||||||||||||||||||||
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                                AGA CGAGACGGTGGGTCCGACCT
                                  C
GAM1741  FLJ13262  3'  TTAGTCCCGGTGGAGCGG    46697       TGT    CA
                                TCGCTC   CACC  GGCTGG
                                ||||||   ||||  ||||||
                                GGCGAG   GTGG  CTGATT
                                   ___    CC
GAM1741  FLJ13265  3'  TCTGTATCTGGTGGTGGATGGG 46413      C  TG    C   CT_
           G                     TCTCG TC  TCACC AGG   GGA
                                ||||| ||  ||||| |||   |||
                                GGGGT AG  GGTGG TCT   TCT
                                   _ GT    _  ATG
GAM1741  FLJ13273  5'  TCCAGCTCGGACTGGGCGGGA  45724        T   ACCCA
                                TCTCGCTC GTC    GGCTGGA
                                |||||||| |||    |||||||
                                AGGGCGGG CAG    TCGACCT
                                     T  GC___
GAM1741  FLJ13390  3'  TCCATCCTGGGTCACAGAGTGA 42840          C      C
           GA                    TCTCGCTCTGT ACCCAGG TGGA
                                ||||||||||| ||||||| ||||
                                AGAGTGAGACA TGGGTCC ACCT
                                      C      T
GAM1741  FLJ13448  3'  TCCAGCCTGGGCAACAGAGGGA 47885     G     CA
           GA                    TCTC CTCTGT  CCCAGGCTGGA
                                |||| ||||||  ||||||||||
                                AGAG GAGACA  GGGTCCGACCT
                                  G     AC
GAM1741  FLJ13456  3'  TCCAGCCTGGACAACGGAGTGA 66563          CAC
           GA                    TCTCGCTCTGT   CCAGGCTGGA
                                ||||||||||   ||||||||||
                                AGAGTGAGGCA   GGTCCGACCT
                                      ACA
GAM1741  FLJ13456  3'  TCCAGCCTGGGTGACAGAGTAA 66564     CG
           GA                    TCT  CTCTGTCACCCAGGCTGGA
                                |||  ||||||||||||||||||
                                AGA  GAGACAGTGGGTCCGACCT
                                  AT
GAM1741  FLJ13544  3'  TCCAGCCTGGATGACAGAGTGA 47210           C
           GA                    TCTCGCTCTGTCA CCAGGCTGGA
                                |||||||||||| ||||||||||
                                AGAGTGAGACAGT GGTCCGACCT
                                       A
GAM1741  FLJ13611  3'  TCTAGCCTGAGCGACAGAGTGA 46868          ACC
           GA                    TCTCGCTCTGTC   CAGGCTGGA
                                ||||||||||||   |||||||||
                                AGAGTGAGACAG   GTCCGATCT
                                      CGA
GAM1741  FLJ13615  5'  TCGGCCTTGGCGGAGTTGGGG  47797       _      CCC    TG
                                TCTCG CTCTGTCA   AGGC  GA
                                ||||| ||||||||   ||||  ||
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                                GGGGT GAGGCGGT   TCCG  CT
                                  T       ___    GT
GAM1741  FLJ13621  3'  TCCAGCCTGGGCGACAGAGCGA 47226           A
                GA                  TCTCGCTCTGTC CCCAGGCTGGA
                                    |||||||||||| ||||||||||
                                    AGAGCGAGACAG GGGTCCGACCT
                                          C
GAM1741  FLJ13769  3'  ACTCCAGCCTGGGTGACAGAGC 47237
                GAGA                  TCTCGCTCTGTCACCCAGGCTGGA
                                      ||||||||||||||||||||||||
                                      AGAGCGAGACAGTGGGTCCGACCT
                                            CAC
GAM1741  FLJ13769  3'  TCCAGCAGTCTGGGCGACAGAG 47263           A    ___
                TGAGA                  TCTCGCTCTGTC CCCAG   GCTGGA
                                       |||||||||||| |||||   ||||||
                                       AGAGTGAGACAG GGGTC   CGACCT
                                             C     TGA
GAM1741  FLJ13848  3'  TCCAGCCTAGGCGACAGAGTGA 45831           A  C
                GA                  TCTCGCTCTGTC CC AGGCTGGA
                                    |||||||||||| || ||||||||
                                    AGAGTGAGACAG GG TCCGACCT
                                          C  A
GAM1741  FLJ13952  3'  TCCAGCCTGGGCAACAAGAGTG 46021        _  CA
                A                   TCGCTCT GT  CCCAGGCTGGA
                                    ||||||| ||  ||||||||||
                                    AGTGAGA CA  GGGTCCGACCT
                                        A  AC
GAM1741  FLJ13984  3'  TCCAAACTGGGTGACATGGTGA 45812        C         GC
                GA                  TCTCGCT TGTCACCCAG  TGGA
                                    ||||||| ||||||||||  ||||
                                    AGAGTGG ACAGTGGGTC  ACCT
                                        T         AA
GAM1741  FLJ14011  3'  TCCAGTCTGGGCAACAGAGCAA 42320     C      CA
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGAGACA  GGGTCTGACCT
                                      A       AC
GAM1741  FLJ14117  3'  TCCAGCTTGGGCAACAGAGCAA 43235     C      CA
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGAGACA  GGGTTCGACCT
                                      A       AC
GAM1741  FLJ14124  3'  TATGCCTGTGGTGGAGCTGGG  46360     C    TGT   _    TGGA
                                    TCT GCTC   CACC CAGGC
                                    ||| ||||   |||| |||||
                                    GGG CGAG   GTGG GTCCG
                                      T    ___    T    TATT
GAM1741  FLJ14154  3'  TCCGATGCAGGGGTGGGGTGGG 46235         TGT    AG  __
                G                   TCTCGCTC   CACCC  GC  TGGA
                                    ||||||||   |||||  ||  ||||
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                                GGGGTGGG  GTGGG  CG  GCCT
                                   ___    GA  TA
GAM1741  FLJ14166  3'  TTAGTTTGGGGTTGGGGGA   44994    G   TGTCA
                                TC CTC    CCCAGGCTGG
                                || |||    ||||||||||
                                AG GGG    GGGTTTGATT
                                 G  TTG__
GAM1741  FLJ14166  3'  TTTAGTTTGGGGTTGGGG    44995      TCA
                                CTCTG  CCCAGGCTGGA
                                |||||  ||||||||||
                                GGGGT  GGGTTTGATTT
                                   TG_
GAM1741  FLJ14251  3'  TCCAGCCTGGGTAACAGAGCGA 46491          C
                   GA             TCTCGCTCTGT ACCCAGGCTGGA
                                  |||||||||| ||||||||||
                                  AGAGCGAGACA TGGGTCCGACCT
                                        A
GAM1741  FLJ14251  3'  TCCAGCCTTGGTGACAGAGTGA 46492            C
                   GA             TCTCGCTCTGTCACC AGGCTGGA
                                  |||||||||||||| ||||||||
                                  AGAGTGAGACAGTGG TCCGACCT
                                         T
GAM1741  FLJ14327  3'  TCCAGCCTGGACAACAGAGCTA 46688    C     CAC
                   GA             TCT GCTCTGT   CCAGGCTGGA
                                  ||| |||||||   ||||||||||
                                  AGA CGAGACA   GGTCCGACCT
                                    T      ACA
GAM1741  FLJ14327  3'  TCCAGCCTGGATAATAGAGTGA 46689          CAC
                   GA             TCTCGCTCTGT   CCAGGCTGGA
                                  ||||||||||   ||||||||||
                                  AGAGTGAGATA   GGTCCGACCT
                                        ATA
GAM1741  FLJ14345  3'  TCCAGCCTGGGCAACAAGAGTG 45662       _  CA
                   A               TCGCTCT GT  CCCAGGCTGGA
                                  ||||||| ||  ||||||||||
                                  AGTGAGA CA  GGGTCCGACCT
                                      A  AC
GAM1741  FLJ14346  3'  TCCAGCCTGGGCAACAGAGCAA 47372    C     CA
                   GA             TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A      AC
GAM1741  FLJ14346  3'  TCCAGCCTGGGGGACAGAGCGA 47373          A
                   GA             TCTCGCTCTGTC CCCAGGCTGGA
                                  |||||||||||| ||||||||||
                                  AGAGCGAGACAG GGGTCCGACCT
                                         G
GAM1741  FLJ14397  3'  TCCAGCCTGGGTGACAGAGCAA 52335    C
                   GA             TCT GCTCTGTCACCCAGGCTGGA
                                  ||| ||||||||||||||||||||
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                                AGA CGAGACAGTGGGTCCGACCT
                                  A
GAM1741  FLJ14457  3'  TCCAGCCTGGGAGACAGAGTGA 52413           A
                GA                  TCTCGCTCTGTC CCCAGGCTGGA
                                    |||||||||||| ||||||||||
                                    AGAGTGAGACAG GGGTCCGACCT
                                           A
GAM1741  FLJ14490  3'  TCCAGCCTGGGCAACAGAGCAA 52448     C      CA
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGAGACA  GGGTCCGACCT
                                      A       AC
GAM1741  FLJ20004  3'  ACTCCAGCCTGGGTGACAGAGT 34743
                GAGA                  TCTCGCTCTGTCACCCAGGCTGGA
                                      ||||||||||||||||||||||||
                                      AGAGTGAGACAGTGGGTCCGACCT
                                                  CAC
GAM1741  FLJ20004  3'  TCCAGCCTGGCAACAGAGCAAG 34766     C      CAC
                A                    TCT GCTCTGT   CCAGGCTGGA
                                     ||| |||||||   ||||||||||
                                     AGA CGAGACA   GGTCCGACCT
                                       A       AC_
GAM1741  FLJ20004  3'  TCCAGCCTGGGCAACAGAGGGA 34767      G      CA
                GA                  TCTC CTCTGT  CCCAGGCTGGA
                                    |||| ||||||  ||||||||||
                                    AGAG GAGACA  GGGTCCGACCT
                                      G      AC
GAM1741  FLJ20006  3'  TCCAGCCTGGGCGATAGAGTGA 34788           A
                GA                  TCTCGCTCTGTC CCCAGGCTGGA
                                    |||||||||||| ||||||||||
                                    AGAGTGAGATAG GGGTCCGACCT
                                           C
GAM1741  FLJ20013  3'  TCCAGCCTCGGTGACAGAGCAA 34803     C          C
                GA                  TCT GCTCTGTCACC AGGCTGGA
                                    ||| |||||||||| ||||||||
                                    AGA CGAGACAGTGG TCCGACCT
                                      A          C
GAM1741  FLJ20019  3'  TCCAGCCTAGGTGACAGGGCAA 34816     C          C
                GA                  TCT GCTCTGTCACC AGGCTGGA
                                    ||| |||||||||| ||||||||
                                    AGA CGGGACAGTGG TCCGACCT
                                      A          A
GAM1741  FLJ20045  3'  TCCAGCCTGGGTGAGAAGAGCG 34893         G_
                A                    TCGCTCT  TCACCCAGGCTGGA
                                     |||||||  ||||||||||||||
                                     AGCGAGA  AGTGGGTCCGACCT
                                        AG
GAM1741  FLJ20059  3'  TCCAGCCTGGACAGCAGGAGCG 34930         _  CAC
                A                    TCGCTC TGT   CCAGGCTGGA
                                     |||||| |||   ||||||||||
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                                AGCGAG ACG   GGTCCGACCT
                                   G   ACA
GAM1741  FLJ20069  3'  TCCAGCCTGGGGGACAGAGCAA 34957     C       A
                GA                  TCT GCTCTGTC CCCAGGCTGGA
                                    ||| |||||||| ||||||||||
                                    AGA CGAGACAG GGGTCCGACCT
                                      A       G
GAM1741  FLJ20081  3'  CCTGGGTGACAGAATGAGA    34990       C
                                    TCTCG TCTGTCACCCAGG
                                    ||||| ||||||||||||
                                    AGAGT AGACAGTGGGTCC
                                       A
GAM1741  FLJ20084  3'  TCCAGCCTGGGCAACAGAGCGA 34999           CA
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGCGAGACA  GGGTCCGACCT
                                          AC
GAM1741  FLJ20130  3'  TCCAGTTGAATCATAGGGTGA  35084          CACCCA
                                    TCGCTCTGT     GGCTGGA
                                    |||||||||     |||||||
                                    AGTGGGATA     TTGACCT
                                         CTAAG_
GAM1741  FLJ20139  3'  TCCAGCCTGCGTGACAAAGTGA 35122        C     C
                GA                  TCTCGCT TGTCAC CAGGCTGGA
                                    ||||||| |||||| |||||||||
                                    AGAGTGA ACAGTG GTCCGACCT
                                       A     C
GAM1741  FLJ20170  3'  TCCAGCCTGGGTGACAGAGTGA 35166
                GA                  TCTCGCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAGTGGGTCCGACCT

GAM1741  FLJ20211  3'  TCCAGCCTGGGCAACAGAGTGA 35266           CA
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          AC
GAM1741  FLJ20211  3'  TCCAGCCTGGGCGACAGAGTGA 35267            A
                GA                  TCTCGCTCTGTC CCCAGGCTGGA
                                    |||||||||||| ||||||||||
                                    AGAGTGAGACAG GGGTCCGACCT
                                          C
GAM1741  FLJ20241  3'  TCCAGCCTGGACAACAGAGCGA 35291           CAC
                GA                  TCTCGCTCTGT   CCAGGCTGGA
                                    ||||||||||   |||||||||
                                    AGAGCGAGACA   GGTCCGACCT
                                          ACA
GAM1741  FLJ20280  3'  CTCCAGCCTGGGTGACAGAGCG 35328
                AGA                   TCTCGCTCTGTCACCCAGGCTGGA
                                      ||||||||||||||||||||||||
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                                AGAGCGAGACAGTGGGTCCGACCT
                                      CA
GAM1741  FLJ20306  3'  TCCAGCCTGGACGACTGAGTGA 35399        T   AC
            GA                  TCTCGCTC GTC  CCAGGCTGGA
                                |||||||| |||  ||||||||||
                                AGAGTGAG CAG  GGTCCGACCT
                                    T   CA
GAM1741  FLJ20306  3'  TCCAGCCTGGCGACAGAGCAAG 35400     C       AC
            A                   TCT GCTCTGTC  CCAGGCTGGA
                                ||| ||||||||  ||||||||||
                                AGA CGAGACAG  GGTCCGACCT
                                  A       C_
GAM1741  FLJ20337  3'  TTTGGTAGTGGAGGGTGGGG   35445         G   __
                                TCTCGCTCT TCAC  CCAGG
                                ||||||||| ||||  |||||
                                GGGGTGGGA GGTG  GGTTT
                                      _   AT
GAM1741  FLJ20456  3'  TCCAGCCTGGGTAACAGAGCTA 35666     C      C
            GA                  TCT GCTCTGT ACCCAGGCTGGA
                                ||| ||||||| ||||||||||||
                                AGA CGAGACA TGGGTCCGACCT
                                  T      A
GAM1741  FLJ20546  3'  TCCAGCCTGGGCAACGAGCGA  35814       T  CA
                                TCGCTC GT  CCCAGGCTGGA
                                |||||| ||  ||||||||||
                                AGCGAG CA  GGGTCCGACCT
                                    _ AC
GAM1741  FLJ20625  3'  TCTGGCCAGGGATGGGGTGGGG 35899           A  CA   TG
                                TCTCGCTCTGTC CC  GGC  GA
                                |||||||||||| ||  |||  ||
                                GGGGTGGGGTAG GG  CCG  CT
                                      _ A_   GT
GAM1741  FLJ20640  5'  TCCAGCCTGCGCCTGGGGTTGG 35918     C    GTCACC
            A                   TCT GCTCT     CAGGCTGGA
                                ||| |||||     |||||||||
                                AGG TGGGG     GTCCGACCT
                                  T    TCCGC_
GAM1741  FLJ20671  3'  TTCCAGCCTGGGTGACAGAGCG 35947
            AGA                   TCTCGCTCTGTCACCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGCGAGACAGTGGGTCCGACCT
                                      TA
GAM1741  FLJ20686  3'  TCCAGCTTGGGTGACAGAGTGA 35957
            GA                    TCTCGCTCTGTCACCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGACAGTGGGTTCGACCT

GAM1741  FLJ20694  3'  TCCAGCCTGGCGACAGAGCAAG 35979     C       AC
            A                   TCT GCTCTGTC  CCAGGCTGGA
                                ||| ||||||||  ||||||||||
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                                AGA CGAGACAG  GGTCCGACCT
                                  A       C_
GAM1741  FLJ20700  3'  TCCAGCCTGGGCGACACAGCGA 36020        C    A
                GA                  TCTCGCT TGTC CCCAGGCTGGA
                                    ||||||| |||| ||||||||||
                                    AGAGCGA ACAG GGGTCCGACCT
                                       C    C
GAM1741  FLJ20700  5'  TTCGGCCTGGGCTGGGTGG    36021        TGTCA
                                    TCGCTC    CCCAGGCTGGA
                                    ||||||    ||||||||||
                                    GGTGGG    GGGTCCGGCTT
                                       TC___
GAM1741  FLJ20783  3'  CTTCAGCCTGGGTGACAGAGTG 36100
                GA                  TCTCGCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAGTGGGTCCGACTT
                                                CA
GAM1741  FLJ20802  3'  TCCAGCCTGGGCGACAGAGCGA 36114           A
                GA                  TCTCGCTCTGTC CCCAGGCTGGA
                                    |||||||||||| ||||||||||
                                    AGAGCGAGACAG GGGTCCGACCT
                                          C
GAM1741  FLJ20813  3'  TCTAGCCTGGGGAATAGAGTGA 36136          CA
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGATA  GGGTCCGATCT
                                          AG
GAM1741  FLJ20825  3'  TCCAGCCTGGCCCACAGAGTGA 36148          CAC
                GA                  TCTCGCTCTGT   CCAGGCTGGA
                                    ||||||||||   ||||||||||
                                    AGAGTGAGACA   GGTCCGACCT
                                          CCC
GAM1741  FLJ20825  3'  TCCAGCCTGGGCAACAAGAGCG 36149        _  CA
                A                    TCGCTCT GT  CCCAGGCTGGA
                                    |||||||  ||  ||||||||||
                                    AGCGAGA CA  GGGTCCGACCT
                                       A  AC
GAM1741  FLJ21144  3'  TCCAGCCTGGGCAACAGAGTGA 43194          CA
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          AC
GAM1741  FLJ21162  3'  TCCAGCCTGGGAAATAGAGTGA 46376          CA
                G                    CTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    GAGTGAGATA  GGGTCCGACCT
                                          AA
GAM1741  FLJ21369  3'  TCCAGCCTGGGTGACAGAGCAA 46056     C
                GA                  TCT GCTCTGTCACCCAGGCTGGA
                                    ||| ||||||||||||||||||||
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                                AGA CGAGACAGTGGGTCCGACCT
                                  A
GAM1741  FLJ21415  3'  CCAGCCTGGGTGAGGAG     45684      G
                                CTCT TCACCCAGGCTGG
                                |||| ||||||||||||
                                GAGG AGTGGGTCCGACC
                                 _
GAM1741  FLJ21551  3'  GCAACCTGGGTGACAGAGCGAG 46038                C  GA
                  A                TCTCGCTCTGTCACCCAGG TG
                                |||||||||||||||||| ||
                                AGAGCGAGACAGTGGGTCC AC
                                          A  GT
GAM1741  FLJ21603  3'  TCCAGTCTGGACCACAGAGTGA 45779           CAC
                  GA               TCTCGCTCTGT   CCAGGCTGGA
                                |||||||||||   ||||||||||
                                AGAGTGAGACA   GGTCTGACCT
                                      CCA
GAM1741  FLJ21687  3'  ACTCCAGCCTGGGTGACAGAGC 46286
                  GAGA                TCTCGCTCTGTCACCCAGGCTGGA
                                |||||||||||||||||||||||||
                                AGAGCGAGACAGTGGGTCCGACCT
                                          CAC
GAM1741  FLJ22009  3'  TCCAGCTTGGGCGACAGAGCGA 60921           A
                  GA               TCTCGCTCTGTC CCCAGGCTGGA
                                |||||||||||| ||||||||||
                                AGAGCGAGACAG GGGTTCGACCT
                                      C
GAM1741  FLJ22054  3'  TCCAGCCTGGGCAACAGAGCAA 96053     C      CA
                  GA               TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A      AC
GAM1741  FLJ22056  3'  TCCAGCCCCTGAAGTTGGAGTG 42836          ___  CCCA
                  GGG                TCTCGCTCTG   TCA    GGCTGGA
                                |||||||||   |||   |||||||
                                GGGGTGAGGT   AGT    CCGACCT
                                      TGA   CC__
GAM1741  FLJ22167  3'  ACCCTAGCTTGGGTGGCAGAGC 44855     C             A
                  AAGA                TCT GCTCTGTCACCCAGGCTGG
                                ||| ||||||||||||||||||
                                AGA CGAGACGGTGGGTTCGATC
                                  A              CCAC
GAM1741  FLJ22313  3'  TCCACCCTGGGCGACAGAGTGA 42582           A     C
                  GA               TCTCGCTCTGTC CCCAGG TGGA
                                |||||||||||| |||||| ||||
                                AGAGTGAGACAG GGGTCC ACCT
                                      C     C
GAM1741  FLJ22316  3'  TCCAGCCTGGGCAACAGAGCCA 47619     C      CA
                  GG               TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
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                                GGA CGAGACA  GGGTCCGACCT
                                  C      AC
GAM1741  FLJ22316  3'  TTTGGTTGTGGGGCGGG     47622         T  C
                                CTCGCTCTG CA CCAGG
                                ||||||||| || |||||
                                GGGCGGGGT GT GGTTT
                                     _  T
GAM1741  FLJ22415  3'  TCCAGCCTGGGTGACAAAGCAA 93121     C   C
           GA                     TCT GCT TGTCACCCAGGCTGGA
                                ||| ||| ||||||||||||||||
                                AGA CGA ACAGTGGGTCCGACCT
                                  A   A
GAM1741  FLJ22474  3'  TCCAGCCTGGGCAACAGAGTGA 45618           CA
           GA                     TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      AC
GAM1741  FLJ22644  3'  TCCAGCCTGGGCTACAGAGCGA 47703           CA
           GA                     TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      TC
GAM1741  FLJ22671  3'  TTCAGTGCCTGGTGGGGCAGGG 46316        AC_     __
                                CTCTGTC   CCAGGC  TGGA
                                |||||||   ||||||  ||||
                                GGGACGG   GGTCCG  ACTT
                                    GGT     TG
GAM1741  FLJ22692  3'  TTCAGCCTGGGTGACAGAAAGA 47486      GC
           GA                     TCTC  TCTGTCACCCAGGCTGGA
                                ||||  ||||||||||||||||||
                                AGAG  AGACAGTGGGTCCGACTT
                                  AA
GAM1741  FLJ22814  3'  TCCAACCTGGGTGACGAGTGAG 46731         T        C
           A                      TCTCGCTC GTCACCCAGG TGGA
                                |||||||| ||||||||| ||||
                                AGAGTGAG CAGTGGGTCC ACCT
                                     _        A
GAM1741  FLJ22814  3'  TCCAGCCTGGGTGACAGAGGGA 46732    G
                                TC CTCTGTCACCCAGGCTGGA
                                || ||||||||||||||||||
                                AG GAGACAGTGGGTCCGACCT
                                 G
GAM1741  FLJ22865  5'  TCCAGTCTGGCCGGGCGGGG   47786        AC_
                                CTCTGTC   CCAGGCTGGA
                                |||||||   ||||||||||
                                GGGGCGG   GGTCTGACCT
                                    GCC
GAM1741  FLJ22965  3'  TCTAGCCTGGGCGACAGAGTGA 42301           A
           GA                     TCTCGCTCTGTC CCCAGGCTGGA
                                ||||||||||| ||||||||||
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                                AGAGTGAGACAG GGGTCCGATCT
                                       C
GAM1741  FLJ23040  3'  TCCAGCCTGGGCAATAGAGCAA 47992     C      CA
                GA                    TCT GCTCTGT  CCCAGGCTGGA
                                      ||| |||||||  ||||||||||
                                      AGA CGAGATA  GGGTCCGACCT
                                        A      AC
GAM1741  FLJ23042  3'  TCCAGCCTGGGCAACAAGAGTG 47949        _  CA
                A                      TCGCTCT GT  CCCAGGCTGGA
                                       ||||||| ||  ||||||||||
                                       AGTGAGA CA  GGGTCCGACCT
                                          A  AC
GAM1741  FLJ23120  3'  TCCAGCCTGGGTGACGGAGAAA 86330     CG
                GA                    TCT  CTCTGTCACCCAGGCTGGA
                                      |||  ||||||||||||||||||
                                      AGA  GAGGCAGTGGGTCCGACCT
                                        AA
GAM1741  FLJ23185  3'  TCCAGCCTTGGCAACAGAGTGA 47523          CA  C
                GA                    TCTCGCTCTGT  CC AGGCTGGA
                                      ||||||||||  || ||||||||
                                      AGAGTGAGACA  GG TCCGACCT
                                            AC  T
GAM1741  FLJ23229  3'  TCCAGCCTGGACAACAGAGCAA 47532     C      CAC
                GA                    TCT GCTCTGT   CCAGGCTGGA
                                      ||| |||||||   ||||||||||
                                      AGA CGAGACA   GGTCCGACCT
                                        A      ACA
GAM1741  FLJ23251  3'  TTTGGCCTTTTGGAGTGGGG   46103         TCACCC    TG
                                      TCTCGCTCTG     AGGC  GA
                                      ||||||||||     ||||  ||
                                      GGGGTGAGGT     TCCG  TT
                                            TT____    GT
GAM1741  FLJ23277  3'  TAAGGGGGGTGGTGGGTGGGA  50918       T TG     AGG  GGA
                                      TCTCGC C  TCACCC   CT
                                      |||||| |  ||||||   ||
                                      AGGGTG G  GGTGGG   GA
                                         _ GT     GG_  ATT
GAM1741  FLJ23360  3'  CCAGCCTCGTGGCGTGGGA   43827       TCT    CC
                                      TCTCGC   GTCAC  AGGCTGG
                                      ||||||   |||||  |||||||
                                      AGGGTG   CGGTG  TCCGACC
                                         ___     C_
GAM1741  FLJ23360  3'  TCCAGCCCGGGTGACAGAGCGA 43835              A
                GA                    TCTCGCTCTGTCACCC GGCTGGA
                                      |||||||||||||||| |||||||
                                      AGAGCGAGACAGTGGG CCGACCT
                                               C
GAM1741  FLJ23499  3'  ACTTTAGCCTGGGTGACAGAGC 43122
                GAGA                    TCTCGCTCTGTCACCCAGGCTGGA
                                        ||||||||||||||||||||||||
```

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                                AGAGCGAGACAGTGGGTCCGATTT
                                      CAC
GAM1741  FLJ23499  3'  TCCAGCCTGGGCGACAAGAGCG 43140       _  A
              A                TCGCTCT GTC CCCAGGCTGGA
                               ||||||| ||| ||||||||||
                               AGCGAGA CAG GGGTCCGACCT
                                  A  C
GAM1741  FLJ23878  3'  TCCAGCCTGGGTGACAGGGCGA 59372
              GA                 TCTCGCTCTGTCACCCAGGCTGGA
                               ||||||||||||||||||||||||
                               AGAGCGGGACAGTGGGTCCGACCT
                                      A
GAM1741  FLJ25006  3'  TCCAGCCTGAGCAACAGAGTGA 58789          CACC
              GA                 TCTCGCTCTGT   CAGGCTGGA
                               ||||||||||   |||||||||
                               AGAGTGAGACA   GTCCGACCT
                                     ACGA
GAM1741  FLJ25012  3'  CTGCAGCCTGGGTGGCAGAGTG 58709                GA
              AGA                TCTCGCTCTGTCACCCAGGCTG
                               |||||||||||||||||||||
                               AGAGTGAGACGGTGGGTCCGAC
                                      GTCA
GAM1741  FLJ30092  3'  TCCAGCCTGGGCAACAGAGTGA 59342          CA
              G                  CTCGCTCTGT  CCCAGGCTGGA
                               |||||||||  ||||||||||
                               GAGTGAGACA  GGGTCCGACCT
                                     AC
GAM1741  FLJ30294  5'  TCGGTCTCAGGCAAGGTGGGG  58898       TC   ACCC   TG
                               TCTCGC  TGTC   AGGC  GA
                               ||||||  ||||   ||||  ||
                               GGGGTG  ACGG   TCTG  CT
                                  GA   AC__   GT
GAM1741  FLJ30655  5'  TTCAGTCTCTCACCAGGGCCAG 58956     C     TCACCC
              G                  TCT GCTCTG     AGGCTGGA
                               ||| ||||||     ||||||||
                               GGA CGGGAC     TCTGACTT
                                 C     CACTC_
GAM1741  FLJ30681  3'  TTCAGTTAAAAAGGGGTGGGG  93443         GTCACCCA
                               TCTCGCTCT       GGCTGGA
                               |||||||||       |||||||
                               GGGGTGGGG       TTGACTT
                                     AAAAA___
GAM1741  FLJ31168  3'  TCCAGCCTGGGCGACAGAGCGA 59186           A
              GA                 TCTCGCTCTGTC CCCAGGCTGGA
                               |||||||||||| ||||||||||
                               AGAGCGAGACAG GGGTCCGACCT
                                      C
GAM1741  FLJ31455  3'  TCCAGCCTGGGCGACAGAGCCA 59291     C       A
              GA                 TCT GCTCTGTC CCCAGGCTGGA
                               ||| |||||||| ||||||||||
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                                AGA CGAGACAG GGGTCCGACCT
                                  C       C
GAM1741  FLJ31455  3'  TCCAGCCTGGGTGACAGAGCAA 59292     C
                GA                  TCT GCTCTGTCACCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAGTGGGTCCGACCT
                                      A
GAM1741  FLJ31890  5'  TTTGGTCTTACGCCCTAGGGTG 92988          TCACCC_   TG
                GGG                   TCTCGCTCTG      AGGC  GA
                                      ||||||||||      ||||  ||
                                      GGGGTGGGAT      TCTG  TT
                                           CCCGCAT    GT
GAM1741  FLJ31952  3'  TCCAGCCTGGGCAACAGAGTGA 59050          CA
                GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                      ||||||||||  ||||||||||
                                      AGAGTGAGACA  GGGTCCGACCT
                                            AC
GAM1741  FLJ32499  5'  TCCAGTGACCGACAGAGCAAGA 58782     C       ACCCAG
                                      TCT GCTCTGTC      GCTGGA
                                      ||| ||||||||      ||||||
                                      AGA CGAGACAG      TGACCT
                                        A       CCAG__
GAM1741  FLJ32865  3'  TTGGGGGTGGGGTGGGG     58823         TG  A
                                      TCTCGCTC  TC CCCAG
                                      ||||||||  || |||||
                                      GGGGTGGG  GG GGGTT
                                           GT  _
GAM1741  FLJ32915  5'  TCCAGCCTGGGCGACAAGAGCG 59437          _   A
                AGA                     TCTCGCTCT GTC CCCAGGCTGGA
                                        ||||||||| ||| ||||||||||
                                        AGAGCGAGA CAG GGGTCCGACCT
                                             A   C
GAM1741  FREQ     5'  CCGGCCCGGGGGGGGCGGGG    27368         GTCA   A
                                      TCTCGCTCT    CCC GGCTGG
                                      |||||||||    ||| ||||||
                                      GGGGCGGGG    GGG CCGGCC
                                           _____   C
GAM1741  FRSB     3'  CCTCCAGCCTGGGTGACAGAGT 20290
                GAGA                    TCTCGCTCTGTCACCCAGGCTGGA
                                        ||||||||||||||||||||||||
                                        AGAGTGAGACAGTGGGTCCGACCT
                                                  CCC
GAM1741  FUSIP1    3'  TCCAGCCTGGGCAACAGAGTGA 55043          CA
                GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                      ||||||||||  ||||||||||
                                      AGAGTGAGACA  GGGTCCGACCT
                                            AC
GAM1741  GABARAPL1 3'  TTTGGGATTTTGTGGGGTGGGA 49428         TG CA___
                                      TCTCGCTC  T     CCCAGG
                                      ||||||||  |     ||||||
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                                AGGGTGGG  G    GGGTTT
                                    GT TTTTA
GAM1741  GALNT6   3'  TCCAGCCTGGGCAACAGGTAAG 24252    CG T   CA
            A                    TCT  C CTGT  CCCAGGCTGGA
                                 |||  | ||||  ||||||||||
                                 AGA  G GACA  GGGTCCGACCT
                                   AT _   AC
GAM1741  GGA2     3'  TCCAGCCTGGGCTACATAGTGA 57682       C   CA
            GA                     TCTCGCT TGT  CCCAGGCTGGA
                                   |||||||  |||  ||||||||||
                                   AGAGTGA ACA  GGGTCCGACCT
                                      T   TC
GAM1741  GGA2     3'  TCCAGCCTGGGCTACATAGTGA 57683       C   CA
            GA                     TCTCGCT TGT  CCCAGGCTGGA
                                   |||||||  |||  ||||||||||
                                   AGAGTGA ACA  GGGTCCGACCT
                                      T   TC
GAM1741  GIOT-3   5'  TTGGCCTCCGGTGGGCGAGA   33220       CTGT   C_   TG
                                   TCTCGCT   CACC  AGGC  GA
                                   |||||||   ||||  ||||  ||
                                   AGAGCGG   GTGG  TCCG  TT
                                      ____   CC   GT
GAM1741  GIT1     3'  TCTGGAGTTTTGAGGGGTGAGG 26723         GTC__  _
                                   TCTCGCTCT    AC CCAGG
                                   |||||||||    || |||||
                                   GGAGTGGGG    TG GGTCT
                                       AGTTT  A
GAM1741  GLTP     3'  TCCAGCCTGGGCAACAAGAGCG 33588        _  CA
            A                      TCGCTCT GT  CCCAGGCTGGA
                                   |||||||  ||  ||||||||||
                                   AGCGAGA CA  GGGTCCGACCT
                                      A  AC
GAM1741  GNB4     3'  TCCAGCCTAGGCGACAGAGTGA 41570           A  C
            GA                     TCTCGCTCTGTC CC AGGCTGGA
                                   ||||||||||||  ||  ||||||||
                                   AGAGTGAGACAG GG TCCGACCT
                                         C  A
GAM1741  GP5      3'  TCTAGCCTGGGCGACAGAGCGA 16883           A
            GA                     TCTCGCTCTGTC CCCAGGCTGGA
                                   ||||||||||||  ||||||||||
                                   AGAGCGAGACAG GGGTCCGATCT
                                         C
GAM1741  GR6      5'  CTGGGTGGCTGGGTGGGG    24745         T
                                   TCTCGCTC GTCACCCAG
                                   ||||||||  |||||||||
                                   GGGGTGGG CGGTGGGTC
                                      T
GAM1741  GR6      3'  TTTGGATGATAAGAGTGAGG   24755         _   C
                                   TCTCGCTCT GTCA CCAGG
                                   |||||||||  ||||  |||||
```

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                                GGAGTGAGA TAGT GGTTT
                                     A   A
GAM1741  GS3955   5'  TTTGGTCTCGGGGTAGGGGGAG 41629     G   GT A  C   TG
            A                    TCTC CTCT  C CC AGGC  GA
                                 |||| ||||  | || ||||  ||
                                 AGAG GGGA  G GG TCTG  TT
                                   G   TG _  C   GT
GAM1741  GTPBP5   3'  TCCAGCCTGAGCGACAGAGCAA 65981     C       ACC
            GA                   TCT GCTCTGTC   CAGGCTGGA
                                 ||| ||||||||   |||||||||
                                 AGA CGAGACAG   GTCCGACCT
                                   A       CGA
GAM1741  GTPBP5   3'  TCCAGCCTGAGTGACAGAGCGA 65982            C
            GA                   TCTCGCTCTGTCAC CAGGCTGGA
                                 |||||||||||||| |||||||||
                                 AGAGCGAGACAGTG GTCCGACCT
                                        A
GAM1741  GTSE1    3'  TCCAGCCTGGGCACCAATGTGA 33565       TC  TCA
            GA                   TCTCGC  TG   CCCAGGCTGGA
                                 ||||||  ||   ||||||||||
                                 AGAGTG  AC   GGGTCCGACCT
                                    TA  CAC
GAM1741  HARS2    3'  TCCAGCCTCTCCCTGGGGCCAG 55870     C    GTCACCC
            G                    TCT GCTCT      AGGCTGGA
                                 ||| |||||      ||||||||
                                 GGA CGGGG      TCCGACCT
                                   C    TCCCTC_
GAM1741  HCGIX    3'  TCCAGCCTGGGTGACAGCAAGA 20717      GCT
            GA                   TCTC   CTGTCACCCAGGCTGGA
                                 ||||   ||||||||||||||||
                                 AGAG   GACAGTGGGTCCGACCT
                                   AAC
GAM1741  HEI10    3'  TCCAGCCTGGGCAACAGAGTGA 41299          CA
            GA                   TCTCGCTCTGT  CCCAGGCTGGA
                                 ||||||||||  ||||||||||
                                 AGAGTGAGACA  GGGTCCGACCT
                                       AC
GAM1741  HES2     3'  TCCAGGCTGGGCGACAGAGCGA 39378          A    G
            GA                   TCTCGCTCTGTC CCCAG CTGGA
                                 |||||||||||| ||||| |||||
                                 AGAGCGAGACAG GGGTC GACCT
                                       C    G
GAM1741  HES6     3'  TTCAGATGTGGTGGGGTAGGG  38460     CG   TG   CCAGG
                                 TCT  CTC  TCAC    CTGGA
                                 |||  |||  ||||    |||||
                                 GGG  GGG  GGTG    GACTT
                                   AT   GT   TA___
GAM1741  HIC      3'  TCCAGCCTGGGCAACAGAGCGA 68052          CA
            GA                   TCTCGCTCTGT  CCCAGGCTGGA
                                 ||||||||||  ||||||||||
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                                AGAGCGAGACA  GGGTCCGACCT
                                      AC
GAM1741  HIC2     3'  TTTGTGGGGCGGGGCGGGA   65876          A  _
                                TCTCGCTCTGTC CC CAGG
                                |||||||||||| || ||||
                                AGGGCGGGGCGG GG GTTT
                                      _  T
GAM1741  HOMER-3  3'  TCCGGCCTGGGATGCGGGCCAG 17907     C  T   CA
           G                     TCT GC CTGT  CCCAGGCTGGA
                                ||| || ||||  ||||||||||
                                GGA CG GGCG  GGGTCCGGCCT
                                  C  _   TA
GAM1741  HSA250303 3'  TCCAGCCTGGGCTACAGAGTGA 38023          CA
           GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      TC
GAM1741  HSC3     3'  TCCAGCTTGGGTGACAAAGTAA 59734     CG  C
           GA                    TCT  CT TGTCACCCAGGCTGGA
                                |||  || ||||||||||||||||
                                AGA  GA ACAGTGGGTTCGACCT
                                  AT  A
GAM1741  HSH2     3'  TCCAGCCTGGATGACAGAGTGA 52744            C
           GA                    TCTCGCTCTGTCA CCAGGCTGGA
                                |||||||||||| ||||||||||
                                AGAGTGAGACAGT GGTCCGACCT
                                      A
GAM1741  HSJ001348 3'  TTCAGTATTGATGGGGAGGGA  62861      G       CCCAG
                                TCTC CTCTGTCA     GCTGGA
                                |||| ||||||||     ||||||
                                AGGG GGGGTAGT     TGACTT
                                  A       TA___
GAM1741  HSJ1     3'  GGCCTGGGTGGCGGGTGGGG   23083       T
                                TCTCGC CTGTCACCCAGGCT
                                |||||| ||||||||||||||
                                GGGGTG GGCGGTGGGTCCGG
                                      _
GAM1741  HSMPP8   3'  TCCAGCCTGAGTGACAGAATGA 95141       C       C
           GA                    TCTCG TCTGTCAC CAGGCTGGA
                                ||||| |||||||| |||||||||
                                AGAGT AGACAGTG GTCCGACCT
                                   A       A
GAM1741  HSPC043  3'  TCCAGCCTGGGTGACAGTGAG  68353       CT
                                CTCGCT  GTCACCCAGGCTGGA
                                ||||||  ||||||||||||||||
                                GAGTGA  CAGTGGGTCCGACCT
                                      __
GAM1741  HSPC072  3'  TCTAGCCTGCTGGAGGATGAGA 27173       C   GT  CC
                                TCTCG TCT  CA  CAGGCTGGA
                                ||||| |||  ||  |||||||||
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                                AGAGT AGG  GT  GTCCGATCT
                                  _   AG  C_
GAM1741  HSU79252  5'  AGTCCAGCCTGGGTGACAGAGT 26141
              GAGA                  TCTCGCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAGTGGGTCCGACCT
                                          GAG
GAM1741  HYPK      3'  TCCAGCCTGGGGGAAAGAGTGA 33516        G  A
                                    TCGCTCT TC CCCAGGCTGGA
                                    ||||||| || ||||||||||
                                    AGTGAGA AG GGGTCCGACCT
                                       A  G
GAM1741  IL10RB    3'  TCCAGCCTGGGTGACAAAGTGA 7129         C
              GA                    TCTCGCT TGTCACCCAGGCTGGA
                                    ||||||| ||||||||||||||||
                                    AGAGTGA ACAGTGGGTCCGACCT
                                       A
GAM1741  IMAGE:4907098 3'  TCCAGCCTGGGCGACAGAGCAA 57758     C       A
              GA                    TCT GCTCTGTC CCCAGGCTGGA
                                    ||| |||||||| ||||||||||
                                    AGA CGAGACAG GGGTCCGACCT
                                      A       C
GAM1741  INE1      3'  TCCAGCCTGTGTGATGGAGAGA 14760      G       C
              GA                    TCTC CTCTGTCAC CAGGCTGGA
                                    |||| ||||||||| |||||||||
                                    AGAG GAGGTAGTG GTCCGACCT
                                      A       T
GAM1741  JDD1      5'  CTAGGTGACGGGGCGAGA     63914              C
                                    TCTCGCTCTGTCACC AG
                                    |||||||||||||| ||
                                    AGAGCGGGGCAGTGG TC
                                             A
GAM1741  JDD1      3'  TCCAGCCTGGGTGATGGAG    63919
                                    CTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||
                                    GAGGTAGTGGGTCCGACCT

GAM1741  KALI      3'  TCCAGTCTGGGTGACAGAGTGA 54697
              GA                    TCTCGCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAGTGGGTCTGACCT

GAM1741  KBRAS2    3'  TCCAGCCTGGTCAACAGAGCAA 34628     C       CAC
              GA                    TCT GCTCTGT   CCAGGCTGGA
                                    ||| |||||||   ||||||||||
                                    AGA CGAGACA   GGTCCGACCT
                                      A       ACT
GAM1741  KCNH6     3'  ACTCCAGCCTGGGTGACAGAGT 48566
              GAGA                  TCTCGCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||||||
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                                AGAGTGAGACAGTGGGTCCGACCT
                                      CAC
GAM1741 KCNJ9    3' GGGAAATGGAGGGTGGGG    18368         G  ___
                                TCTCGCTCT TCA   CCC
                                ||||||||| |||   |||
                                GGGGTGGGA GGT   GGG
                                    _  AAA
GAM1741 KIAA0014 3' CCAGCCCTACAGGGCGAGG   28539          CACCCA
                                TCTCGCTCTGT     GGCTGG
                                ||||||||||      ||||||
                                GGAGCGGGACA     CCGACC
                                    TC_____
GAM1741 KIAA0042 3' TCCAGTCTGAGCAACAGAACGA 30239      C    CACC
           GA                     TCTCG TCTGT    CAGGCTGGA
                                |||||  |||||    |||||||||
                                AGAGC AGACA    GTCTGACCT
                                   A     ACGA
GAM1741 KIAA0057 3' TCCAGCCTGGACAACAAGAGCG 25424       _  CAC
           A                      TCGCTCT GT   CCAGGCTGGA
                                |||||||  ||   ||||||||||
                                AGCGAGA CA   GGTCCGACCT
                                    A  ACA
GAM1741 KIAA0061 3' TTGGGGGTGATGAGGTGGGG   68840        CT      AGG TG
                                TCTCGCT  GTCACCC   C  GA
                                |||||||  |||||||   |  ||
                                GGGGTGG  TAGTGGG   G  TT
                                    AG      ___ GT
GAM1741 KIAA0125 5' TTTGGCTAGGGATGGAGCAGA  29583     C       A  CA   TG
                                TCT GCTCTGTC CC  GGC  GA
                                ||| ||||||| ||  |||  ||
                                AGA CGAGGTAG GG  TCG  TT
                                  _       _ A_   GT
GAM1741 KIAA0184 3' TCCAGCCTGGGTGACAGCACGA 65815       CT
           GA                     TCTCG  CTGTCACCCAGGCTGGA
                                |||||  ||||||||||||||||
                                AGAGC  GACAGTGGGTCCGACCT
                                   AC
GAM1741 KIAA0186 3' TCCAGCCTGGGTGACAAAGTGA 41119        C
           GA                     TCTCGCT TGTCACCCAGGCTGGA
                                |||||||  ||||||||||||||||
                                AGAGTGA ACAGTGGGTCCGACCT
                                    A
GAM1741 KIAA0218 3' ATTCAGCTTCTGGGTGGTGGGT 29292        T TG       __
           GGGG                     TCTCGC C  TCACCCAG  GCTGGA   T
                                ||||||  |  ||||||||  ||||||   |
                                GGGGTG G  GGTGGGTC  CGACTT   A
                                   _ GT       TT
GAM1741 KIAA0226 3' TCCAGCCTGGGTGACAGAGTGA 64264
           GA                     TCTCGCTCTGTCACCCAGGCTGGA
                                |||||||||||||||||||||||||
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                                AGAGTGAGACAGTGGGTCCGACCT

GAM1741  KIAA0247  3'  TTTGTGGTGACGGAGGGGA   29080     G       _
                                TCTC CTCTGTCACC CAGG
                                |||| |||||||||| ||||
                                AGGG GAGGCAGTGG GTTT
                                  _       T
GAM1741  KIAA0252  3'  CTCCAGTCTGGGTGACAGAGTG 63454
                AGA                 TCTCGCTCTGTCACCCAGGCTGGA
                                |||||||||||||||||||||||||
                                AGAGTGAGACAGTGGGTCTGACCT
                                          CA
GAM1741  KIAA0317  5'  TCTTGGTGGGAGAGTGGGG   29749        G   C
                                TCTCGCTCT TCACC AGG
                                ||||||||| ||||| |||
                                GGGGTGAGA GGTGG TCT
                                     G    T
GAM1741  KIAA0337  3'  TCCAGTCATGATCGGGTGGGG  29482        T   CCCA
                                TCTCGCTC GTCA   GGCTGGA
                                |||||||| ||||   |||||||
                                GGGGTGGG TAGT   CTGACCT
                                    C   A___
GAM1741  KIAA0355  3'  ACTCCAGCCTGGGTGACAGAGT 28696
                GAGA                TCTCGCTCTGTCACCCAGGCTGGA
                                |||||||||||||||||||||||||
                                AGAGTGAGACAGTGGGTCCGACCT
                                          CAC
GAM1741  KIAA0391  3'  CTCTAGCCTGGGTGACAGAGCG 28609
                AGA                 TCTCGCTCTGTCACCCAGGCTGGA
                                |||||||||||||||||||||||||
                                AGAGCGAGACAGTGGGTCCGATCT
                                          CA
GAM1741  KIAA0391  3'  TCCAGCCTAGGTGACAGAGTGA 28621            C
                GA                  TCTCGCTCTGTCACC AGGCTGGA
                                |||||||||||||| ||||||||
                                AGAGTGAGACAGTGG TCCGACCT
                                       A
GAM1741  KIAA0408  3'  ACTCCAGCCTGGGTGACAGAGT 28791
                GAGA                TCTCGCTCTGTCACCCAGGCTGGA
                                |||||||||||||||||||||||||
                                AGAGTGAGACAGTGGGTCCGACCT
                                          CAC
GAM1741  KIAA0427  3'  TCTGAGAGTGGCGAGTGGGG  29392        T   C__
                                TCTCGCTC GTCAC  CAGG
                                |||||||| |||||  ||||
                                GGGGTGAG CGGTG  GTCT
                                   _    AGA
GAM1741  KIAA0445  5'  TCCAGCCTGTGTGACAGAGCAA 28642     C       C
                GA                  TCT GCTCTGTCAC CAGGCTGGA
                                ||| |||||||||| |||||||||
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                                AGA CGAGACAGTG GTCCGACCT
                                  A         T
GAM1741  KIAA0446  5'  TCCAGCCTGGGCGACAGAGCGA 69460           A
                GA                  TCTCGCTCTGTC CCCAGGCTGGA
                                    |||||||||||| ||||||||||
                                    AGAGCGAGACAG GGGTCCGACCT
                                          C
GAM1741  KIAA0447  3'  TCCAGCCTGGGCAACAGGGCAA 72129     C      CA
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGGGACA  GGGTCCGACCT
                                      A      AC
GAM1741  KIAA0450  3'  TTAGAAGGGTGAAGAGTGAGG  28378         G     AGG
                                    TCTCGCTCT TCACCC   CTGG
                                    |||||||| ||||||   ||||
                                    GGAGTGAGA AGTGGG   GATT
                                          _     AA_
GAM1741  KIAA0451  3'  TTCAGCCTCCCAACAGGGCAGA 29785     _      CACCC
                GA                  TCTC GCTCTGT     AGGCTGGA
                                    |||| |||||||     ||||||||
                                    AGAG CGGGACA     TCCGACTT
                                      A      ACCC_
GAM1741  KIAA0451  5'  TTCAGCCTGGGCAACAGAGCAA 29786     C      CA
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGAGACA  GGGTCCGACTT
                                      A      AC
GAM1741  KIAA0472  3'  TCCAGCCTGGGCAACAGAGCGA 72367          CA
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGCGAGACA  GGGTCCGACCT
                                          AC
GAM1741  KIAA0472  3'  TCCAGCCTGGGCAGCAGAGCAA 72368     C      CA
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGAGACG  GGGTCCGACCT
                                      A      AC
GAM1741  KIAA0472  3'  TCCAGCCTGGGCGACAGAGTGA 72369          A
                GA                  TCTCGCTCTGTC CCCAGGCTGGA
                                    |||||||||||| ||||||||||
                                    AGAGTGAGACAG GGGTCCGACCT
                                          C
GAM1741  KIAA0472  3'  TCCATATTGTGTCAGAGTGGGA 72370          T   CCAGGC
                                    TCTCGCTCTG CAC      TGGA
                                    |||||||||| |||     ||||
                                    AGGGTGAGAC GTG      ACCT
                                          T   TTAT__
GAM1741  KIAA0475  3'  TCCAGCCTGGGAGACAGAGCGA 30130          A
                GA                  TCTCGCTCTGTC CCCAGGCTGGA
                                    |||||||||||| ||||||||||
```

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                                AGAGCGAGACAG GGGTCCGACCT
                                       A
GAM1741  KIAA0493  5'  TCAGAGTGGCAGAGGAGA    64937     G       CCAGG
                                TCTC CTCTGTCAC    CTGG
                                |||| |||||||||    ||||
                                AGAG GAGACGGTG    GACT
                                  _       A____
GAM1741  KIAA0493  5'  TCTGGTTTTGGAGTAGAGA    64939     _     TCAC
                                TCTC GCTCTG    CCAGG
                                |||| ||||||    |||||
                                AGAG TGAGGT    GGTCT
                                  A     TTT_
GAM1741  KIAA0513  3'  TTTAGAGAAATGTCAGAGCGAG 29058          T  CCCAGG
                   G                TCTCGCTCTG CA     CTGGA
                                |||||||||| ||     |||||
                                GGAGCGAGAC GT     GATTT
                                       T  AAAGA_
GAM1741  KIAA0514  3'  TCCAGCCTGGATGACGGAGCCA 28755     C       C
                   GA                 TCT GCTCTGTCA CCAGGCTGGA
                                ||| ||||||||| ||||||||||
                                AGA CGAGGCAGT GGTCCGACCT
                                  C        A
GAM1741  KIAA0514  3'  TCCAGTTTGAGCAAGAGGAGG  28756      G    GTCACC
                                TCTC CTCT     CAGGCTGGA
                                |||| ||||     |||||||||
                                GGAG GAGA     GTTTGACCT
                                  _    ACGA__
GAM1741  KIAA0515  5'  TCCGGCGCCTCCGGCAAGAGCG 64556          _   ACCCAG
                   GGA                 TCTCGCTCT GTC     GCTGGA
                                ||||||||| |||     ||||||
                                AGGGCGAGA CGG     CGGCCT
                                       A   CCTCCG
GAM1741  KIAA0543  3'  CCAGATGGTGGAGCTGGG    69518     C    TGT    CAGG
                                TCT GCTC   CACC    CTGG
                                ||| ||||   ||||    ||||
                                GGG CGAG   GTGG    GACC
                                  T    ____    TA__
GAM1741  KIAA0547  3'  TCCAGCCTGGCAACAGAGCAAG 29600     C      CAC
                   A                  TCT GCTCTGT   CCAGGCTGGA
                                ||| |||||||   ||||||||||
                                AGA CGAGACA   GGTCCGACCT
                                  A      AC_
GAM1741  KIAA0547  3'  TCCTGCCTGGTTGACAGAGTGA 29601           C      T
                   GA                 TCTCGCTCTGTCA CCAGGC GGA
                                |||||||||||| |||||| |||
                                AGAGTGAGACAGT GGTCCG CCT
                                       T     T
GAM1741  KIAA0563  5'  CCGGCAGGGCAGGATGGGA   29876      CT    ACCCAG
                                TCTCG  CTGTC     GCTGG
                                |||||  |||||     |||||
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                                AGGGT  GACGG     CGGCC
                                  AG    GA____
GAM1741  KIAA0563  3'  TCCAGCCTGGGCGACAGAGCAA 29890     C       A
                GA                  TCT GCTCTGTC CCCAGGCTGGA
                                    ||| |||||||| ||||||||||
                                    AGA CGAGACAG GGGTCCGACCT
                                      A       C
GAM1741  KIAA0607  3'  TCTGGCCTGGCTGGAGCCAGG  72955     C     TCAC     TG
                                    TCT GCTCTG    CCAGGC  GA
                                    ||| ||||||    ||||||  ||
                                    GGA CGAGGT    GGTCCG  CT
                                      C     C___      GT
GAM1741  KIAA0618  3'  ACAGGGGGGTGAGGAGTGGGG  29839         G     AGG   GA
                                    TCTCGCTCT TCACCC   CTG
                                    |||||||| ||||||   |||
                                    GGGGTGAGG AGTGGG   GAC
                                          _     GG_   AT
GAM1741  KIAA0635  3'  TCCAGCCTGGGTGACAGAGT   28421
                                    GCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||
                                    TGAGACAGTGGGTCCGACCT

GAM1741  KIAA0643  3'  ACTCCAGCCTGGGTGACAGAGT 45969
                GAGA                  TCTCGCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAGTGGGTCCGACCT
                                                 CAC
GAM1741  KIAA0664  3'  TTTAGTTTGGGGCGGGACGGGA 64945      CT    CA
                                    TCTCG  CTGT  CCCAGGCTGGA
                                    |||||  ||||  ||||||||||
                                    AGGGC  GGCG  GGGTTTGATTT
                                      AG    __
GAM1741  KIAA0682  3'  TGGGCTGGGGGGCGGGGCGGGG 33010           A     G
                                    TCTCGCTCTGTC CCCAG CTG
                                    |||||||||||| ||||| |||
                                    GGGGCGGGGCGG GGGTC GGT
                                           G     G
GAM1741  KIAA0694  3'  CGGCCAGGCATGGTGGGG    72967        C    ACCCA   TG
                                    TCTCGCT TGTC     GGC  G
                                    ||||||| ||||     |||  |
                                    GGGGTGG ACGG     CCG  C
                                        T    A____    GT
GAM1741  KIAA0694  3'  TCCAGCCTGGGCAACAGAGTGA 72974           CA
                GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                      ||||||||||  ||||||||||
                                      AGAGTGAGACA  GGGTCCGACCT
                                            AC
GAM1741  KIAA0738  3'  TCCAGCCTGGGGGACAGAGTGA 28887           A
                GA                    TCTCGCTCTGTC CCCAGGCTGGA
                                      |||||||||||| ||||||||||
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                                AGAGTGAGACAG GGGTCCGACCT
                                       G
GAM1741  KIAA0752  3'  TCCAGCCTGGGCAACGAGCGA  67635       T  CA
                                TCGCTC GT  CCCAGGCTGGA
                                |||||| ||  ||||||||||
                                AGCGAG CA  GGGTCCGACCT
                                   _  AC
GAM1741  KIAA0795  3'  TCCAGCCTGGTTGACAGAGTGA 47232            C
              GA                  TCTCGCTCTGTCA CCAGGCTGGA
                                  |||||||||||| ||||||||||
                                  AGAGTGAGACAGT GGTCCGACCT
                                         T
GAM1741  KIAA0798  3'  TCCAGCCTGGGCAACAAGAGCG 28455        _  CA
              A                    TCGCTCT GT  CCCAGGCTGGA
                                   ||||||| ||  ||||||||||
                                   AGCGAGA CA  GGGTCCGACCT
                                      A  AC
GAM1741  KIAA0821  3'  TTTAGTTTCCTGGGCAGGGAGG 30613      G    TCA    ___
              GG                   TCTC CTCTG   CCCAGG   CTGGA
                                   |||| |||||   ||||||   |||||
                                   GGGG GGGAC   GGGTCC   GATTT
                                     A    ___      TTT
GAM1741  KIAA0830  3'  TTAGACTTGACAGAGGAGA   70273      G       CCC  G
                                TCTC CTCTGTCA   AG CTGG
                                |||| ||||||||   || ||||
                                AGAG GAGACAGT   TC GATT
                                  _      ___  A
GAM1741  KIAA0831  3'  TCCAGCCTGGGCAACAAGAGCG 30655          _  CA
              AGG                   TCTCGCTCT GT  CCCAGGCTGGA
                                    ||||||||| ||  ||||||||||
                                    GGAGCGAGA CA  GGGTCCGACCT
                                       A  AC
GAM1741  KIAA0872  3'  ACTCCAGCCTGGGTGACAGAGT 30734
              GAGA                    TCTCGCTCTGTCACCCAGGCTGGA
                                      ||||||||||||||||||||||||
                                      AGAGTGAGACAGTGGGTCCGACCT
                                                CAC
GAM1741  KIAA0876  3'  TCCAGCCTGGGCAACAGAGCGA 65319           CA
              GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGCGAGACA  GGGTCCGACCT
                                          AC
GAM1741  KIAA0884  3'  TCCAACCTGGGTAACAGAGTGA 70758           C      C
              GA                    TCTCGCTCTGT ACCCAGG TGGA
                                    |||||||||| ||||||| ||||
                                    AGAGTGAGACA TGGGTCC ACCT
                                          A      A
GAM1741  KIAA0889  3'  CTCCAGCCTGGGTGACAGAGTG 31773
              AGA                     TCTCGCTCTGTCACCCAGGCTGGA
                                      ||||||||||||||||||||||||
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                                AGAGTGAGACAGTGGGTCCGACCT
                                      CA
GAM1741  KIAA0889  3'  TCCAGCCTGGGTGACAGACTAA 31785     CGC
            GA                  TCT   TCTGTCACCCAGGCTGGA
                                |||   ||||||||||||||||||
                                AGA   AGACAGTGGGTCCGACCT
                                  ATC
GAM1741  KIAA0889  5'  TCCAGCCTGGGTGACATATCAA 31787     CGCTC
            GA                  TCT    TGTCACCCAGGCTGGA
                                |||    ||||||||||||||||
                                AGA    ACAGTGGGTCCGACCT
                                  ACTAT
GAM1741  KIAA0894  3'  ACTCCAGCCTGGGTGACAGAGC 30322
            GAGA                  TCTCGCTCTGTCACCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGCGAGACAGTGGGTCCGACCT
                                      CAC
GAM1741  KIAA0907  3'  TCCAGCCTGGGCAATAGAGCAA 30882     C      CA
            GA                  TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGATA  GGGTCCGACCT
                                  A      AC
GAM1741  KIAA0907  3'  TCCAGCCTGGGCACTAGAGTGA 30883          TCA
            GA                  TCTCGCTCTG   CCCAGGCTGGA
                                |||||||||   ||||||||||
                                AGAGTGAGAT   GGGTCCGACCT
                                     CAC
GAM1741  KIAA0912  3'  CTCCAGCCTGGGTGACAGAGTG 65042
            AGG                   TCTCGCTCTGTCACCCAGGCTGGA
                                ||||||||||||||||||||||||
                                GGAGTGAGACAGTGGGTCCGACCT
                                      CA
GAM1741  KIAA0916  5'  CCGGGGTGGCGGGGTTAGA    31187     C          A
                                TCT GCTCTGTCACCC GG
                                ||| |||||||||||  ||
                                AGA TGGGGCGGTGGG CC
                                  T          G
GAM1741  KIAA0924  3'  TCCAGCCTGGGCAACAGAGCGA 30376          CA
            GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                     AC
GAM1741  KIAA0930  3'  TCAGAGGTGAGGGGCGGGA    71075         G    CAGG
                                TCTCGCTCT TCACC    CTGG
                                |||||||| |||||    ||||
                                AGGGCGGGG AGTGG    GACT
                                     _    A___
GAM1741  KIAA0930  3'  TCTAGCCTGGGCAACGAGAGCG 71076        _  CA
            A                    TCGCTCT GT  CCCAGGCTGGA
                                |||||||  ||  ||||||||||
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                                AGCGAGA CA  GGGTCCGATCT
                                   G  AC
GAM1741  KIAA0953  3'  TTCAGCCTAGGTGACAGAGTGA 67335            C
            GA                   TCTCGCTCTGTCACC AGGCTGGA
                                 |||||||||||||||| ||||||||
                                 AGAGTGAGACAGTGG TCCGACTT
                                        A
GAM1741  KIAA0981  3'  TCCAGCCTGGGCAACAGAGCAA 62093     C      CA
            GA                   TCT GCTCTGT  CCCAGGCTGGA
                                 ||| |||||||  ||||||||||
                                 AGA CGAGACA  GGGTCCGACCT
                                   A      AC
GAM1741  KIAA1001  3'  TCCAGCCTGGGTGATGGAGCAA 31012     C
            GA                   TCT GCTCTGTCACCCAGGCTGGA
                                 ||| ||||||||||||||||||||
                                 AGA CGAGGTAGTGGGTCCGACCT
                                   A
GAM1741  KIAA1001  3'  TCTAGCCTGAGGGACAGAGTGA 31014           A  _
            GA                   TCTCGCTCTGTC CC CAGGCTGGA
                                 |||||||||||| || |||||||||
                                 AGAGTGAGACAG GG GTCCGATCT
                                        _  A
GAM1741  KIAA1029  3'  TCTGGAGTCTGGCAAGCGGGG  24434        C   __  _
                                 TCTCGCT TGTC  AC CCAGG
                                 ||||||| ||||  || |||||
                                 GGGGCGA ACGG  TG GGTCT
                                    _   TC  A
GAM1741  KIAA1030  3'  TCCAGCCTGGGTGACAGAG   94985
                                 CTCTGTCACCCAGGCTGGA
                                 ||||||||||||||||||
                                 GAGACAGTGGGTCCGACCT

GAM1741  KIAA1056  3'  TCCGGCCTGGGTGACAGAGCCA 30317     C
            GA                   TCT GCTCTGTCACCCAGGCTGGA
                                 ||| ||||||||||||||||||||
                                 AGA CGAGACAGTGGGTCCGGCCT
                                   C
GAM1741  KIAA1086  3'  TCCAGCCTGGGTTACAGAGCGA 71290           C
            GA                   TCTCGCTCTGT ACCCAGGCTGGA
                                 ||||||||||| ||||||||||||
                                 AGAGCGAGACA TGGGTCCGACCT
                                       T
GAM1741  KIAA1130  3'  TCCTGCCTGGGTGACAGAGCGA 63100                T
            GA                   TCTCGCTCTGTCACCCAGGC GGA
                                 |||||||||||||||||| |||
                                 AGAGCGAGACAGTGGGTCCG CCT
                                          T
GAM1741  KIAA1143  3'  TCCAGCCTGGGCAACAGAGTAA 69251     CG     CA
            GA                   TCT  CTCTGT  CCCAGGCTGGA
                                 |||  ||||||  ||||||||||
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                                AGA  GAGACA  GGGTCCGACCT
                                  AT     AC
GAM1741  KIAA1157  3'  TTTATGGCAGTGGTGGAGTGAG 72708        TG   __  GGCTGGA
                 G                 TCTCGCTC  TCAC  CCA
                                   ||||||||  ||||  |||
                                   GGAGTGAG  GGTG  GGT
                                       GT    AC   ATTT
GAM1741  KIAA1160  3'  TCCAGCCTGGCGACAGAGTGAG 40762           AC
                 A                 TCTCGCTCTGTC  CCAGGCTGGA
                                   ||||||||||||  ||||||||||
                                   AGAGTGAGACAG  GGTCCGACCT
                                         C_
GAM1741  KIAA1164  3'  TCCAGCCTGGGTGACAGAGGGA 70051      G
                 GA                TCTC CTCTGTCACCCAGGCTGGA
                                   ||||  ||||||||||||||||||
                                   AGAG GAGACAGTGGGTCCGACCT
                                     G
GAM1741  KIAA1191  3'  TCCAGCCTGGGCGACAGAACGA 40336      C     A
                 GA                TCTCG TCTGTC CCCAGGCTGGA
                                   |||||  ||||||  ||||||||||
                                   AGAGC AGACAG GGGTCCGACCT
                                     A     C
GAM1741  KIAA1203  3'  TTTAGTTCATTGGTAGGGTTGG 72090     C    GT  CCCA
                 G                 TCT GCTCT  CA    GGCTGGA
                                   |||  |||||  ||    |||||||
                                   GGG TGGGA  GT    TTGATTT
                                     T    TG  TAC_
GAM1741  KIAA1228  3'  TCCAGCCTGGGCAACAGAGTGA 65678          CA
                 GA                TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   AGAGTGAGACA  GGGTCCGACCT
                                         AC
GAM1741  KIAA1253  3'  TCTAGCCTGGGCAACAGAGTAA 93550     CG     CA
                 GA                TCT  CTCTGT  CCCAGGCTGGA
                                   |||  ||||||  ||||||||||
                                   AGA  GAGACA  GGGTCCGATCT
                                     AT     AC
GAM1741  KIAA1255  3'  TCTGGCTTGTGTGCTGGATGAG 67747      C   T  C    TG
                 G                 TCTCG TCTG CAC CAGGC  GA
                                   |||||  ||||  |||  |||||  ||
                                   GGAGT AGGT GTG GTTCG  CT
                                     _   C   T    GT
GAM1741  KIAA1257  3'  TCCAGCCTGGGCAGCAGAGCAA 63419     C      CA
                 GA                TCT GCTCTGT  CCCAGGCTGGA
                                   |||  |||||||  ||||||||||
                                   AGA CGAGACG  GGGTCCGACCT
                                     A      AC
GAM1741  KIAA1266  3'  TTTGGCCTAGAGGTGTGGAGTG 66704          T   C__   TG
                 AGA                TCTCGCTCTG CACC   AGGC  GA
                                   |||||||||  ||||   ||||  ||
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                                AGAGTGAGGT GTGG   TCCG  TT
                                      _   AGA    GT
GAM1741  KIAA1271  3'  TCCAACCTGGGTGAGAGAGCGA 70145         G        C
                GA                  TCTCGCTCT TCACCCAGG TGGA
                                    ||||||||| ||||||||| ||||
                                    AGAGCGAGA AGTGGGTCC ACCT
                                       G        A
GAM1741  KIAA1271  3'  TCCAGCCTGGGCGACAGAGTGG 70146          A
                                    TCGCTCTGTC CCCAGGCTGGA
                                    |||||||||| ||||||||||
                                    GGTGAGACAG GGGTCCGACCT
                                          C
GAM1741  KIAA1276  3'  AACCAGCCTGGGTGACAGAGGG 67025      G              A
                AGA                   TCTC CTCTGTCACCCAGGCTGG
                                    |||| ||||||||||||||||||
                                    AGAG GAGACAGTGGGTCCGACC
                                      G               AAC
GAM1741  KIAA1277  3'  TCCAGCCTGGACAACAGAGCAA 65086     C      CAC
                GA                  TCT GCTCTGT   CCAGGCTGGA
                                    ||| |||||||   ||||||||||
                                    AGA CGAGACA   GGTCCGACCT
                                      A       ACA
GAM1741  KIAA1297  5'  TTTGGCTGCCCCATGGAGGAGA 72646      G     CACCCA   TG
                                    TCTC CTCTGT      GGC  GA
                                    |||| ||||||      |||  ||
                                    AGAG GAGGTA      TCG  TT
                                      _     CCCCG_   GT
GAM1741  KIAA1322  3'  TCCAGCCTGCACAGTAGAGTGA 73117          TCACC
                GG                  TCTCGCTCTG    CAGGCTGGA
                                    ||||||||||    |||||||||
                                    GGAGTGAGAT    GTCCGACCT
                                          GACAC
GAM1741  KIAA1328  3'  TCCAGCCTGGGTGACAGAGCAA 62334     C
                GA                  TCT GCTCTGTCACCCAGGCTGGA
                                    ||| ||||||||||||||||||||
                                    AGA CGAGACAGTGGGTCCGACCT
                                      A
GAM1741  KIAA1348  3'  TCCAGCCTGGGCAACAAGAGTG 69129        _ CA
                A                    TCGCTCT GT  CCCAGGCTGGA
                                    ||||||| ||  ||||||||||
                                    AGTGAGA CA  GGGTCCGACCT
                                       A  AC
GAM1741  KIAA1364  3'  TCCAGCCTGGGAGATGGTGAGA 64358        CT   A
                                    TCTCGCT  GTC CCCAGGCTGGA
                                    |||||||  ||| ||||||||||
                                    AGAGTGG  TAG GGGTCCGACCT
                                       __   A
GAM1741  KIAA1364  3'  TCCAGCCTGTGTGACAGAATGA 64359       C       C
                GA                  TCTCG TCTGTCAC CAGGCTGGA
                                    ||||| |||||||| |||||||||
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                                AGAGT AGACAGTG GTCCGACCT
                                  A       T
GAM1741  KIAA1377  3'  CCAGCCTGGGTGACAGTGTGAG 67757       T            A
            A                    TCTCGC CTGTCACCCAGGCTGG
                                 |||||| ||||||||||||||||
                                 AGAGTG GACAGTGGGTCCGACC
                                    T
GAM1741  KIAA1423  3'  TCCAGCCTGGGTGTCAGAGCGA 62398          T
            GA                     TCTCGCTCTG CACCCAGGCTGGA
                                   |||||||||| ||||||||||||
                                   AGAGCGAGAC GTGGGTCCGACCT
                                        T
GAM1741  KIAA1456  5'  TCCAGCCTGGGTGACTGAGGGA 67569      G   T
            GA                     TCTC CTC GTCACCCAGGCTGGA
                                   |||| ||| ||||||||||||||
                                   AGAG GAG CAGTGGGTCCGACCT
                                     G   T
GAM1741  KIAA1458  3'  TTTAGTCTTCATGGGGTTGGA  69573     C      CACCC
                                   TCT GCTCTGT     AGGCTGGA
                                   ||| |||||||     ||||||||
                                   AGG TGGGGTA     TCTGATTT
                                     T      CT___
GAM1741  KIAA1473  3'  TCCGTCCTGGGTGACAAAGTGA 71213        C          C
            GA                     TCTCGCT TGTCACCCAGG TGGA
                                   ||||||| |||||||||| ||||
                                   AGAGTGA ACAGTGGGTCC GCCT
                                       A          T
GAM1741  KIAA1486  3'  ACTCCAGCCTGGGTGACAGAGC 67966
            GAGA                     TCTCGCTCTGTCACCCAGGCTGGA
                                     ||||||||||||||||||||||||
                                     AGAGCGAGACAGTGGGTCCGACCT
                                                CAC
GAM1741  KIAA1497  5'  TCCAGCCTGGGCGACAGAGCGA 68132            A
            GA                     TCTCGCTCTGTC CCCAGGCTGGA
                                   |||||||||||| ||||||||||
                                   AGAGCGAGACAG GGGTCCGACCT
                                          C
GAM1741  KIAA1508  3'  CTCCAGCCTGGGTGACAGAGCG 62548
            AGA                      TCTCGCTCTGTCACCCAGGCTGGA
                                     ||||||||||||||||||||||||
                                     AGAGCGAGACAGTGGGTCCGACCT
                                                CA
GAM1741  KIAA1522  5'  TCTGGAGAGGCAGGGTGGGA   65611           AC_
                                   TCTCGCTCTGTC   CCAGG
                                   ||||||||||||   |||||
                                   AGGGTGGGACGG   GGTCT
                                          AGA
GAM1741  KIAA1554  3'  TCCAACCTGGGTGACAGAGTGA 96862                C
            GA                     TCTCGCTCTGTCACCCAGG TGGA
                                   |||||||||||||||||| ||||
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                                AGAGTGAGACAGTGGGTCC ACCT
                                          A
GAM1741  KIAA1559  3'  ACTCCAGCCTGGGTGACAGAGT 73441
              GAGA                TCTCGCTCTGTCACCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAGTGGGTCCGACCT
                                          CAC
GAM1741  KIAA1559  3'  TCCAGCCTGGGTAACAGAGCAA 73461     C      C
              GA                  TCT GCTCTGT ACCCAGGCTGGA
                                  ||| ||||||| ||||||||||||
                                  AGA CGAGACA TGGGTCCGACCT
                                    A      A
GAM1741  KIAA1582  5'  TCCAGCCTGGAGTGCAGGAGGG 65993     G    GT  _
              GG                  CTC CTCT  CAC CCAGGCTGGA
                                  ||| ||||  ||| ||||||||||
                                  GGG GAGG  GTG GGTCCGACCT
                                    G    AC   A
GAM1741  KIAA1586  5'  ACTCCAGCTTGGGTGACAGAGC 93934
              GAGA                TCTCGCTCTGTCACCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAGTGGGTTCGACCT
                                          CAC
GAM1741  KIAA1594  3'  CTGCAGTCTGAGTGACAGAGTG 72551            C      GA
              AGA                 TCTCGCTCTGTCAC CAGGCTG
                                  |||||||||||||| |||||||
                                  AGAGTGAGACAGTG GTCTGAC
                                        A      GTCA
GAM1741  KIAA1630  3'  TCCAGCCTGGGTGACAGAGCAA 38657     C
              GA                  TCT GCTCTGTCACCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGTGGGTCCGACCT
                                    A
GAM1741  KIAA1644  3'  TCCAGCCTGGGCAACAGAGTGA 86223          CA
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                       AC
GAM1741  KIAA1649  5'  ACTTCAGCCTGGGTGACAGAGT 51210
              GAGA                TCTCGCTCTGTCACCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAGTGGGTCCGACTT
                                          CAC
GAM1741  KIAA1649  3'  CCAGGCTGGCAGAGCTGGA   51225     C     TCAC   G
                                  TCT GCTCTG   CCAG CTGG
                                  ||| ||||||   |||| ||||
                                  AGG CGAGAC   GGTC GACC
                                    T     ____   G
GAM1741  KIAA1649  3'  CCAGGCTGGCAGAGCTGGA   51226     C     TCAC   G
                                  TCT GCTCTG   CCAG CTGG
                                  ||| ||||||   |||| ||||
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                                AGG CGAGAC    GGTC GACC
                                  T     _____   G
GAM1741  KIAA1649  3'  TCCAGCCTGTGCAACAGAGCGA 51248          CACC
                GG                  TCTCGCTCTGT    CAGGCTGGA
                                    ||||||||||    |||||||||
                                    GGAGCGAGACA    GTCCGACCT
                                          ACGT
GAM1741  KIAA1656  5'  TCCAGCCTGGCAACAGAGTGAG 66385          CAC
                A                   TCTCGCTCTGT   CCAGGCTGGA
                                    ||||||||||   ||||||||||
                                    AGAGTGAGACA   GGTCCGACCT
                                          AC_
GAM1741  KIAA1674  3'  TCCAGCCTGGGCGACAGAGCGA 69348           A
                GA                  TCTCGCTCTGTC CCCAGGCTGGA
                                    |||||||||||| ||||||||||
                                    AGAGCGAGACAG GGGTCCGACCT
                                          C
GAM1741  KIAA1715  3'  TCCAGCCTGGGCAACAAGAGTG 68691        _ CA
                A                   TCGCTCT GT  CCCAGGCTGGA
                                    |||||||  ||  ||||||||||
                                    AGTGAGA CA  GGGTCCGACCT
                                       A  AC
GAM1741  KIAA1718  3'  TTTGGGGGGTGATGGGGAGGGG 64980      G         AGG TG
                                    TCTC CTCTGTCACCC   C  GA
                                    |||| ||||||||||   |  ||
                                    GGGG GGGGTAGTGGG   G  TT
                                      A          G__ GT
GAM1741  KIAA1724  3'  TCCAGCCAGAGTGACAGAGCAA 67622     C         CCA
                GA                  TCT GCTCTGTCAC   GGCTGGA
                                    ||| ||||||||||   |||||||
                                    AGA CGAGACAGTG   CCGACCT
                                      A         AGA
GAM1741  KIAA1727  3'  TCCAGCCTGGATGACAGAGTGA 64765           C
                GA                  TCTCGCTCTGTCA CCAGGCTGGA
                                    |||||||||||| ||||||||||
                                    AGAGTGAGACAGT GGTCCGACCT
                                          A
GAM1741  KIAA1735  3'  CCAGTTTCCAAAGCGAGA    89001        C  TCACCC
                                    TCTCGCT TG     AGGCTGG
                                    |||||||  ||     |||||||
                                    AGAGCGA AC     TTTGACC
                                       A  C_____
GAM1741  KIAA1786  3'  CCAGCCCGGGTGACAGAGCGAG 66630             A     A
                A                   TCTCGCTCTGTCACCC GGCTGG
                                    |||||||||||||||| ||||||
                                    AGAGCGAGACAGTGGG CCGACC
                                          C     C
GAM1741  KIAA1795  3'  TTTGGTCTCACCAACAAGTGAG 72619        C   CACCC    TG
                G                   TCTCGCT TGT    AGGC  GA
                                    |||||||  |||    ||||  ||
```

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                                GGAGTGA ACA    TCTG  TT
                                   _  ACCAC    GT
GAM1741  KIAA1811  3'  TCTGCGGGGTGGGGTGGGG   65422        TG  A  _
                                TCTCGCTC  TC CC CAGG
                                ||||||||  || || ||||
                                GGGGTGGG  GG GG GTCT
                                   GT  _  C
GAM1741  KIAA1821  3'  GAGGTGTTTTGGGGGTGGGGCG 72267        TG  A     CTGGA
           AGG                    TCTCGCTC  TC CCCAGG
                                ||||||||  || ||||||
                                GGAGCGGG  GG GGGTTT
                                   GT  _     TGTGGAGA
GAM1741  KIAA1821  3'  TTTGGCCTGGGTGTTAGGTCAG 72278     C  T   T       TG
           A                     TCT GC CTG CACCCAGGC  GA
                                ||| || ||| |||||||||  ||
                                AGA TG GAT GTGGGTCCG  TT
                                  C  _   T        GT
GAM1741  KIAA1829  3'  TCCAGCCTGGGCAACAAGAGCG 62656        _  CA
           A                     TCGCTCT GT  CCCAGGCTGGA
                                |||||||  ||  ||||||||||
                                AGCGAGA CA  GGGTCCGACCT
                                   A  AC
GAM1741  KIAA1841  3'  CCTAGCCTGGGTGACAGAGCAA 80850     C             A
           GA                     TCT GCTCTGTCACCCAGGCTGG
                                ||| ||||||||||||||||||
                                AGA CGAGACAGTGGGTCCGATC
                                  A               CT
GAM1741  KIAA1870  3'  TTCAGCCTGGATGACAGAGTGA 50590           C
           GA                     TCTCGCTCTGTCA CCAGGCTGGA
                                ||||||||||||| ||||||||||
                                AGAGTGAGACAGT GGTCCGACTT
                                        A
GAM1741  KIAA1871  3'  TCCAGCCTGGGCAACAAGTGCG 61911      T  _  CA
           A                     TCGC CT GT  CCCAGGCTGGA
                                ||||  ||  ||  ||||||||||
                                AGCG GA CA  GGGTCCGACCT
                                  T  A  AC
GAM1741  KIAA1872  3'  TCCAGCCTGGGAGACAGAGCAA 63620     C      A
           GA                     TCT GCTCTGTC CCCAGGCTGGA
                                |||  ||||||||  ||||||||||
                                AGA CGAGACAG GGGTCCGACCT
                                  A       A
GAM1741  KIAA1872  3'  TCCAGCCTGGGCGACAGAGCAA 63623     C      A
           GA                     TCT GCTCTGTC CCCAGGCTGGA
                                |||  ||||||||  ||||||||||
                                AGA CGAGACAG GGGTCCGACCT
                                  A       C
GAM1741  KIAA1879  3'  TCCAGCCTGGGAGACAGAGCAA 73946     C      A
           GA                     TCT GCTCTGTC CCCAGGCTGGA
                                |||  ||||||||  ||||||||||
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                                AGA CGAGACAG GGGTCCGACCT
                                  A       A
GAM1741  KIAA1922  5'  TCTAGTCTCCTTTTAGAGATGA 74008      _    TCACCC
                GA                  TCTCG CTCTG     AGGCTGGA
                                    ||||| |||||     ||||||||
                                    AGAGT GAGAT     TCTGATCT
                                      A     TTTCC_
GAM1741  KIAA1938  3'  CGGCGGGATAGGGGAGG     93823      G      A  CAG  TG
                                    TCTC CTCTGTC CC   GC  G
                                    |||| ||||||| ||   ||  |
                                    GGAG GGGATAG GG   CG  C
                                      _      _ ____  GT
GAM1741  KIAA1948  5'  ACTCCAGCCTGGGTGACAGAGT 83289
                GAGA                  TCTCGCTCTGTCACCCAGGCTGGA
                                    |||||||||||||||||||||||||
                                    AGAGTGAGACAGTGGGTCCGACCT
                                                 CAC
GAM1741  KIAA1948  3'  TCCAGCCTGGGTGACAGACCGA 83306       C
                GA                  TCTCG TCTGTCACCCAGGCTGGA
                                    ||||| ||||||||||||||||||
                                    AGAGC AGACAGTGGGTCCGACCT
                                      C
GAM1741  KIAA1950  3'  GGAGTGACGAGGGCGGGG     94184          _    _
                                    TCTCGCTCT GTCAC CC
                                    ||||||||| ||||| ||
                                    GGGGCGGGA CAGTG GG
                                         G     A
GAM1741  KIAA1951  3'  TCCAGCCTGGGCGACAGAGTGA 74165           A
                GA                  TCTCGCTCTGTC CCCAGGCTGGA
                                    |||||||||||| ||||||||||
                                    AGAGTGAGACAG GGGTCCGACCT
                                           C
GAM1741  KIAA1954  3'  TCCAGCCTGAGCAACAGAGCAA 78231     C      CACC
                GA                  TCT GCTCTGT    CAGGCTGGA
                                    ||| |||||||    |||||||||
                                    AGA CGAGACA    GTCCGACCT
                                      A       ACGA
GAM1741  KIAA1957  3'  TCCGTGCATGTGGCCAGGGCGG 76219          _   CCAG  _
                GG                  TCTCGCTCTG TCAC    GC TGGA
                                    |||||||||| ||||    || ||||
                                    GGGGCGGGAC GGTG    CG GCCT
                                         C    TA__  T
GAM1741  KIAA1969  3'  TCCAGTTTGGCAACAGAGTGAG 79482           CAC
                A                    TCTCGCTCTGT   CCAGGCTGGA
                                    ||||||||||||   ||||||||||
                                    AGAGTGAGACA   GGTTTGACCT
                                           AC_
GAM1741  KIAA1979  3'  TCCAGCATGGGTGATGGAGAGA 89655      G          G
                GA                  TCTC CTCTGTCACCCA GCTGGA
                                    |||| |||||||||||| ||||||
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                                AGAG GAGGTAGTGGGT CGACCT
                                  A          A
GAM1741  KLHL6    3'  TCTAGTCCCAAGAAGGGTGAGG 56176          G  ACCCA
                                TCTCGCTCT TC     GGCTGGA
                                ||||||||| ||     |||||||
                                GGAGTGGGA AG     CTGATCT
                                     _  AACC_
GAM1741  KREMEN   3'  TCCAGCCTGAGCAGCAGAGCGG 50237           CACC
              GA                  TCTCGCTCTGT    CAGGCTGGA
                                ||||||||||    |||||||||
                                AGGGCGAGACG    GTCCGACCT
                                      ACGA
GAM1741  LANO     3'  TCCAGCCCGGGTGACAGAGCGA 47977              A
              GA                  TCTCGCTCTGTCACCC GGCTGGA
                                ||||||||||||||| |||||||
                                AGAGCGAGACAGTGGG CCGACCT
                                       C
GAM1741  LGI3     3'  TCAGTGGACCGGGTGGGG     58398         T   ACCCAG
                                TCTCGCTC GTC     GCTGG
                                |||||||| |||     |||||
                                GGGGTGGG CAG     TGACT
                                     C   G_____
GAM1741  LIAS     3'  TCCAGCCTGGGTGACAAGAGC  71169       _
                                GCTCT GTCACCCAGGCTGGA
                                ||||| ||||||||||||||
                                CGAGA CAGTGGGTCCGACCT
                                   A
GAM1741  LIM      3'  ACTCCAGCCTGGGTGACAGAGT 22310
              GAGA                  TCTCGCTCTGTCACCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGACAGTGGGTCCGACCT
                                           CAC
GAM1741  LIN-28   3'  TCCAGCCTGGTTACAGAGCGAG 45471           CAC
              A                   TCTCGCTCTGT   CCAGGCTGGA
                                ||||||||||   ||||||||||
                                AGAGCGAGACA   GGTCCGACCT
                                      TT_
GAM1741  LRG      3'  TCTAGCCTGGGCGACAGAGCAA 54826     C       A
              GA                    TCT GCTCTGTC CCCAGGCTGGA
                                ||| ||||||||  ||||||||||
                                AGA CGAGACAG GGGTCCGATCT
                                  A       C
GAM1741  LRRFIP1  3'  TCCAGCCTGGACAACAAGAGCG 17617        _  CAC
              A                   TCGCTCT GT   CCAGGCTGGA
                                |||||||  ||   ||||||||||
                                AGCGAGA CA   GGTCCGACCT
                                    A  ACA
GAM1741  LSR68    3'  TCCAGCCTGGGCGACAGAATGA 38559       C      A
              GA                    TCTCG TCTGTC CCCAGGCTGGA
                                ||||| |||||| ||||||||||
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                                AGAGT AGACAG GGGTCCGACCT
                                  A     C
GAM1741  LUC7L    3'  TCTGGTGGGGATGGGGCTGGG  36367     C       A   AG  TG
                                TCT GCTCTGTC CCC  GC  GA
                                ||| |||||||| |||  ||  ||
                                GGG CGGGGTAG GGG  TG  CT
                                  T       _  __  GT
GAM1741  LW-1     5'  TCGGCTAGGACAGGGTGGA   60888    T       ACCCA   TG
                                TC CGCTCTGTC    GGC  GA
                                || |||||||||    |||  ||
                                AG GTGGGACAG    TCG  CT
                                 _       GA___   GT
GAM1741  LW-1     5'  TCTGGCTAGGACAGGGTGGA   32892    T       ACCCA   TG
                                TC CGCTCTGTC    GGC  GA
                                || |||||||||    |||  ||
                                AG GTGGGACAG    TCG  CT
                                 _       GA___   GT
GAM1741  MACF1    3'  TCCAGCCTGGGCAACAGACAGA 53435           A____
              GTGAGA                  TCTCGCTCTGTC    CCCAGGCTGGA
                                ||||||||||||    ||||||||||||
                                AGAGTGAGACAG    GGGTCCGACCT
                                      ACAAC
GAM1741  MAWBP    3'  TCCAGCCTGGGCAACAGAGTAA 42388     CG     CA
              GA                  TCT  CTCTGT  CCCAGGCTGGA
                                |||  ||||||  ||||||||||||
                                AGA  GAGACA  GGGTCCGACCT
                                  AT     AC
GAM1741  MBIP     5'  TTGGTGGTGGTGGTGGTGGGG  33896       _ TG    CAG  TG A
                                TCTCGCT C  TCACC   GC  G
                                ||||||| |  |||||   ||  |
                                GGGGTGG G  GGTGG   TG  T
                                    T GT     ___  GT C
GAM1741  MCAM     3'  TCCAGCCTGGGCAACACAGCGA 22466       C   CA
              GA                  TCTCGCT TGT  CCCAGGCTGGA
                                ||||||| |||  ||||||||||||
                                AGAGCGA ACA  GGGTCCGACCT
                                    C   AC
GAM1741  MCC2     3'  TCCAGGGCCTGATGGGGTGTGG 72529    T       CCCA   __
                                TC CGCTCTGTCA   GGCT  GGA
                                || ||||||||||   ||||  |||
                                GG GTGGGGTAGT   CCGG  CCT
                                 T        ____   GA
GAM1741  MCM10    3'  TTCAGTTTATATATAGAGAGAG 38182     G     CACCC
              A                   TCTC CTCTGT    AGGCTGGA
                                |||| ||||||    ||||||||
                                AGAG GAGATA    TTTGACTT
                                  A     TATA_
GAM1741  MEF-2    3'  TTTAGTGGGCTTTGGCAGGGCG 65034           ___  AG
              GGG                   TCTCGCTCTGTCA   CCC  GCTGGA
                                ||||||||||||   |||  ||||||
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                                GGGGCGGGACGGT  GGG  TGATTT
                                       TTC  __
GAM1741  MESDC2   3'  TCCAGCCTGGATGACGGGATGA 72924      CT     C
            GA                   TCTCG  CTGTCA CCAGGCTGGA
                                 |||||  |||||| ||||||||||
                                 AGAGT  GGCAGT GGTCCGACCT
                                   AG     A
GAM1741  METL     3'  TCCAGCCTGGGCAAAATAGCGA 37841        CTGTCA
            GA                   TCTCGCT     CCCAGGCTGGA
                                 |||||||     ||||||||||||
                                 AGAGCGA     GGGTCCGACCT
                                    TAAAAC
GAM1741  MGC10200 3'  TCCAGTCTGGGCAACAGAGCGA 59649          CA
            GA                   TCTCGCTCTGT  CCCAGGCTGGA
                                 ||||||||||||  ||||||||||||
                                 AGAGCGAGACA  GGGTCTGACCT
                                       AC
GAM1741  MGC10765 3'  TCCAGCCTAGGCGACAGAGCGA 44567           A  C
            GA                   TCTCGCTCTGTC CC AGGCTGGA
                                 ||||||||||||| || ||||||||
                                 AGAGCGAGACAG GG TCCGACCT
                                       C  A
GAM1741  MGC10771 3'  TCCAGCCTGGCTGACAGTGAGA 44716       CT    C
                                 TCTCGCT  GTCA CCAGGCTGGA
                                 |||||||  ||||  ||||||||||
                                 AGAGTGA  CAGT GGTCCGACCT
                                    __    C
GAM1741  MGC10814 5'  TCCAGCCTGGGCAACAGAGTGA 52027          CA
            GG                   TCTCGCTCTGT  CCCAGGCTGGA
                                 ||||||||||||  ||||||||||||
                                 GGAGTGAGACA  GGGTCCGACCT
                                       AC
GAM1741  MGC11266 5'  TCTGGCCTGGGTGAGCTAGA   44491     C    TGTC       TG
                                 TCT GCTC    ACCCAGGC  GA
                                 ||| ||||    ||||||||  ||
                                 AGA CGAG    TGGGTCCG  CT
                                   T   ____       GT
GAM1741  MGC11316 3'  CGCTGGATTTAGTGCTGGGGTG 53046          T  _________  AGGCT
            GGA                   TCTCGCTCTG CAC       CC     G
                                  |||||||||| |||       ||     |
                                  AGGGTGGGGT GTG       GG     C
                                        C   ATTT   A  TCGG
GAM1741  MGC11386 3'  TCCAGCCTGGGCAACAGAGCGA 53072          CA
            GA                   TCTCGCTCTGT  CCCAGGCTGGA
                                 ||||||||||||  ||||||||||||
                                 AGAGCGAGACA  GGGTCCGACCT
                                       AC
GAM1741  MGC12921 5'  TTGGAGCTGGGTGGCAGAGGAG 64518      G          G_ TG A
            A                    TCTC CTCTGTCACCCAG  C  G
                                 |||| ||||||||||||  |  |
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                                AGAG GAGACGGTGGGTC  G  T
                                  _          GA GT
GAM1741  MGC12945  3'  TCCAGCCTAGGCATGGTGAGA  51269       C    ACCC
                                TCTCGCT TGTC    AGGCTGGA
                                ||||||| ||||    ||||||||
                                AGAGTGG ACGG    TCCGACCT
                                    T   A___
GAM1741  MGC13008  3'  TCCAGCCTGGGCAACAGAATGA 52059      C    CA
           GA                     TCTCG TCTGT  CCCAGGCTGGA
                                ||||| |||||  ||||||||||
                                AGAGT AGACA  GGGTCCGACCT
                                  A     AC
GAM1741  MGC13053  3'  TCCAGCCTGGGCGACAGAGTGA 52114          A
           GA                     TCTCGCTCTGTC CCCAGGCTGGA
                                |||||||||||| ||||||||||
                                AGAGTGAGACAG GGGTCCGACCT
                                       C
GAM1741  MGC13090  3'  TCTGGCCTTGGAGCAGGTCGGG 52125      CT   CA  C   TG
           A                     TCTCG  CTGT  CC AGGC  GA
                                |||||  ||||  || ||||  ||
                                AGGGC  GACG  GG TCCG  CT
                                  TG   A_  T   GT
GAM1741  MGC13090  3'  TTTGGATGCGGGGTGAGG    52126         T  C
                                TCTCGCTCTG CA CCAGG
                                |||||||||| || |||||
                                GGAGTGGGGC GT GGTTT
                                     _ A
GAM1741  MGC14136  3'  GCCGTGCAGGGTGGGA     52979         T   CCA
                                TCTCGCTCTG CAC   GGC
                                |||||||||| |||   |||
                                AGGGTGGGAC GTG   CCG
                                     _  ____
GAM1741  MGC14289  3'  TTGGGGATGGGGTGGGA     55597          A
                                TCTCGCTCTGTC CCCAG
                                |||||||||||| |||||
                                AGGGTGGGGTAG GGGTT
                                     _
GAM1741  MGC14407  3'  TCCAGCCTGGGTGACAGAGCAA 52977     C
           GA                     TCT GCTCTGTCACCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGAGACAGTGGGTCCGACCT
                                  A
GAM1741  MGC14436  3'  TCCAGCCTGGGTGACAGAACGA 52931      C
           GA                     TCTCG TCTGTCACCCAGGCTGGA
                                ||||| ||||||||||||||||||
                                AGAGC AGACAGTGGGTCCGACCT
                                  A
GAM1741  MGC15397  3'  ACTCCAGCCTGGGTGATAGAGT 55548
           GAGA                    TCTCGCTCTGTCACCCAGGCTGGA
                                ||||||||||||||||||||||||
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                                AGAGTGAGATAGTGGGTCCGACCT
                                      CAC
GAM1741  MGC15631  3'  TCCAGCCTGTGCAACAGAGCCA 52235     C      CACC
            GA                  TCT GCTCTGT    CAGGCTGGA
                                ||| |||||||    |||||||||
                                AGA CGAGACA    GTCCGACCT
                                  C       ACGT
GAM1741  MGC16037  3'  TCCAGCCTGGACAACAGAGTGG 52894          CAC
            GA                  TCTCGCTCTGT   CCAGGCTGGA
                                ||||||||||   ||||||||||
                                AGGGTGAGACA   GGTCCGACCT
                                      ACA
GAM1741  MGC16175  3'  TCCAGCCTGGGCAATAGAGCAA 52279     C      CA
            GA                  TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGATA  GGGTCCGACCT
                                  A       AC
GAM1741  MGC16384  3'  GTAGCCTGGGTGACAAAGTGAG 54937        C           GA
            A                    TCTCGCT TGTCACCCAGGCTG
                                 ||||||| |||||||||||||
                                 AGAGTGA ACAGTGGGTCCGAT
                                     A           GT
GAM1741  MGC16703  3'  TCCAGCCTGGGCAACAGAGCGA 73498          CA
            GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      AC
GAM1741  MGC23244  3'  TCCAGCCTGGGCGACAGAGTGA 58838          A
            GA                  TCTCGCTCTGTC CCCAGGCTGGA
                                ||||||||||| ||||||||||
                                AGAGTGAGACAG GGGTCCGACCT
                                      C
GAM1741  MGC2396   3'  TCCAGCCTGGGCAATAAGAGTG 54562        GTCA_
            A                    TCGCTCT    CCCAGGCTGGA
                                 |||||||    ||||||||||
                                 AGTGAGA    GGGTCCGACCT
                                     ATAAC
GAM1741  MGC2452   5'  TCCAGTTACAGCGGCAGGAGCG 51968         _   ACCCA
            GGA                   TCTCGCTC TGTC    GGCTGGA
                                  ||||||| ||||    |||||||
                                  AGGGCGAG ACGG    TTGACCT
                                      G   CGACA
GAM1741  MGC2488   3'  TTTGGCTTACTCTTTGGATGAG 44093      C   TCACCC   TG
            A                    TCTCG TCTG     AGGC  GA
                                 ||||| ||||     ||||  ||
                                 AGAGT AGGT     TTCG  TT
                                    _   TTCTCA   GT
GAM1741  MGC2562   3'  TCCAGCCTGACGACAAAGCGAG 51449        C   ACC
            A                    TCTCGCT TGTC   CAGGCTGGA
                                 ||||||| ||||   |||||||||
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                                AGAGCGA ACAG   GTCCGACCT
                                   A    CA_
GAM1741  MGC2663   3'  TCCAGCCTGGGCGATGGAGTGA 44338          A
            GA                   TCTCGCTCTGTC CCCAGGCTGGA
                                 |||||||||||| ||||||||||
                                 AGAGTGAGGTAG GGGTCCGACCT
                                       C
GAM1741  MGC26641  3'  TCCAGCCTGGGCAATAGGGCAA 59326     C      CA
            GA                   TCT GCTCTGT  CCCAGGCTGGA
                                 ||| |||||||  ||||||||||
                                 AGA CGGGATA  GGGTCCGACCT
                                   A      AC
GAM1741  MGC2668   3'  TCCAGCAGCTGTGGTGGGGGAG 61196      G    _  __
                                 CTCT TCACC CAG  GCTGGA
                                 |||| ||||| |||  ||||||
                                 GAGG GGTGG GTC  CGACCT
                                   G    T   GA
GAM1741  MGC26877  5'  ACCCAGCCTGGGTGACAGAGCG 58889                  A
            AGA                   TCTCGCTCTGTCACCCAGGCTGG
                                  ||||||||||||||||||||||
                                  AGAGCGAGACAGTGGGTCCGACC
                                              CAA
GAM1741  MGC2731   3'  TCCAGCCTGGGCAATAAGAGCG 44164        GTCA_
            A                     TCGCTCT     CCCAGGCTGGA
                                  |||||||     ||||||||||
                                  AGCGAGA     GGGTCCGACCT
                                     ATAAC
GAM1741  MGC29891  3'  TCCAGCCTGGCGACACAGTGAG 58870        C    AC
            A                     TCTCGCT TGTC  CCAGGCTGGA
                                  ||||||| ||||  ||||||||||
                                  AGAGTGA ACAG  GGTCCGACCT
                                     C    C_
GAM1741  MGC29891  3'  TCCAGCCTGGGCAACAGAGCCA 58871     C      CA
            GA                    TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    C      AC
GAM1741  MGC29937  3'  TCCAGCCTGGGCAACAAGAGTG 58734        _  CA
            A                     TCGCTCT GT  CCCAGGCTGGA
                                  ||||||| ||  ||||||||||
                                  AGTGAGA CA  GGGTCCGACCT
                                     A  AC
GAM1741  MGC3101   5'  ACTCCAGCCTGGGTGACAGAGC 44099
            GAGA                    TCTCGCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACAGTGGGTCCGACCT
                                                CAC
GAM1741  MGC3103   3'  TCTGGCCTCCAGACCAGGGTAA 44066     CG    _  ACCC    TG
            GG                    TCT  CTCTG TC    AGGC  GA
                                  |||  ||||| ||    ||||  ||
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                                GGA  GGGAC AG    TCCG  CT
                                  AT     C  ACC_    GT
GAM1741  MGC3207   3'  TCCAGCCTGGGCAACAGAGCGA 63242          CA
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGCGAGACA  GGGTCCGACCT
                                          AC
GAM1741  MGC35558  3'  TCTAGTCTGAAAGGAGCGCAGG 59420     _     GTCACC
                                    TCT CGCTCT     CAGGCTGGA
                                    ||| ||||||     |||||||||
                                    GGA GCGAGG     GTCTGATCT
                                      C     AAA___
GAM1741  MGC4248   3'  TCCAGCCTGGGTGACTGAG    51319     T
                                    CTC GTCACCCAGGCTGGA
                                    ||| ||||||||||||||
                                    GAG CAGTGGGTCCGACCT
                                      T
GAM1741  MGC4309   3'  TTCAGCTTGAATTGATGGGGAG 44369      G       CC_
                GGA                   TCTC CTCTGTCA   CAGGCTGGA
                                    |||| ||||||||   |||||||||
                                    AGGG GGGGTAGT   GTTCGACTT
                                      A       TAA
GAM1741  MGC4342   3'  TCCGGCCCCAGTGTGGTGGGCG 44518       T TG    CCA__
                AGG                   TCTCGC C  TCAC     GGCTGGA
                                    |||||| |  ||||     |||||||
                                    GGAGCG G  GGTG     CCGGCCT
                                       _ GT    TGACC
GAM1741  MGC4562   3'  TCCAGCCTGGGCAACAGAGCGA 56743          CA
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGCGAGACA  GGGTCCGACCT
                                          AC
GAM1741  MGC4663   3'  TCCAGCCTGGGCAACAGAGCCA 44791     C       CA
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGAGACA  GGGTCCGACCT
                                      C       AC
GAM1741  MGC4730   3'  TTCAGTAAGTCCGTGATGGAGC 64916     C        CCAG__
                TAGA                  TCT GCTCTGTCAC      GCTGGA
                                    ||| ||||||||||      ||||||
                                    AGA CGAGGTAGTG      TGACTT
                                      T         CCTGAA
GAM1741  MGC4771   3'  TCCAGCCTGGGCAACAGAGTGA 52006          CA
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                          AC
GAM1741  MGC4840   3'  TCCAGCACCCTGGGCGACAGAG 72028           A    ___
                TGAGA                   TCTCGCTCTGTC CCCAG   GCTGGA
                                    |||||||||||| |||||   ||||||
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                                AGAGTGAGACAG GGGTC   CGACCT
                                      C     CCA
GAM1741  MGC4840   3'  TCCAGCCTGGCTGACAGAGCGA 72029           C
            GA                   TCTCGCTCTGTCA CCAGGCTGGA
                                 |||||||||||| ||||||||||
                                 AGAGCGAGACAGT GGTCCGACCT
                                       C
GAM1741  MGC5384   3'  TCCAGCCTGGGCGACAGAGTGA 49094           A
            GA                   TCTCGCTCTGTC CCCAGGCTGGA
                                 |||||||||||| ||||||||||
                                 AGAGTGAGACAG GGGTCCGACCT
                                       C
GAM1741  MGC5457   3'  ACTCCAGCCTGGGTGACAGAGC 51932
            GAGA                   TCTCGCTCTGTCACCCAGGCTGGA
                                 ||||||||||||||||||||||||
                                 AGAGCGAGACAGTGGGTCCGACCT
                                          CAC
GAM1741  MGC5627   3'  CCAGATGGTGGAGCCAGG    44277    C   TGT   CAGG
                                 TCT GCTC   CACC    CTGG
                                 ||| ||||   ||||    ||||
                                 GGA CGAG   GTGG    GACC
                                   C    ___    TA__
GAM1741  MGC7036   3'  TTGGCCTGGGCCAGTGAGA   59620       CTGTCA      TG
                                 TCTCGCT     CCCAGGC  GA
                                 |||||||     |||||||  ||
                                 AGAGTGA     GGGTCCG  TT
                                      CC____      GT
GAM1741  MKRN4     3'  CCCAGCCTGGGTGACAGAGCGA 48457                 A
            GA                   TCTCGCTCTGTCACCCAGGCTGG
                                 |||||||||||||||||||||||
                                 AGAGCGAGACAGTGGGTCCGACC
                                          CT
GAM1741  MRPL48    5'  TCCAGCCTGCGCAACAGAGCGA 32662          CACC
            GA                   TCTCGCTCTGT    CAGGCTGGA
                                 ||||||||||    |||||||||
                                 AGAGCGAGACA    GTCCGACCT
                                       ACGC
GAM1741  MRPS10    3'  TCCAGCCTGGCGACAGAGCGAG 36822           AC
            A                    TCTCGCTCTGTC  CCAGGCTGGA
                                 ||||||||||||  ||||||||||
                                 AGAGCGAGACAG  GGTCCGACCT
                                       C_
GAM1741  MRPS18B   3'  TCCAGCCTGGGTGACAGCTAGA 26755    GCT
                                 TC   CTGTCACCCAGGCTGGA
                                 ||   ||||||||||||||||
                                 AG   GACAGTGGGTCCGACCT
                                  ATC
GAM1741  MSI2      5'  TTTGGGGGTGGGGGGGCGGGG  58048         G     AGG TG
                                 TCTCGCTCT TCACCC   C  GA
                                 |||||||| ||||||   |  ||
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                                GGGGCGGGG GGTGGG   G  TT
                                      G      ___ GT
GAM1741  MT-ACT48  3'  TCCAGTCTGGGTGACAGCAAGA 25610     GCT
                                TC   CTGTCACCCAGGCTGGA
                                ||   ||||||||||||||||
                                AG   GACAGTGGGTCTGACCT
                                 AAC
GAM1741  MY014     5'  TCCGGCTGCCAGGCAGGGCGAG 48881           ACCCA
                                CTCGCTCTGTC     GGCTGGA
                                ||||||||||     |||||||
                                GAGCGGGACGG     TCGGCCT
                                       ACCG_
GAM1741  My015     3'  TCCAGCCTGGGAGACAGAGCAA 67235      C       A
              GA                    TCT GCTCTGTC CCCAGGCTGGA
                                ||| |||||||| ||||||||||
                                AGA CGAGACAG GGGTCCGACCT
                                  A       A
GAM1741  N4BP2     3'  TCAGCCTGGGTGACAGAGCAAG 36943     C               A
              A                     TCT GCTCTGTCACCCAGGCTGG
                                ||| ||||||||||||||||||
                                AGA CGAGACAGTGGGTCCGACT
                                  A
GAM1741  NDUFC2    3'  TCCAGCCTGGGTGACAAAGGAG 17038      G  C
              A                     TCTC CT TGTCACCCAGGCTGGA
                                |||| || ||||||||||||||||
                                AGAG GA ACAGTGGGTCCGACCT
                                  _ A
GAM1741  NK4       5'  TCAGGCTGGTGGGGTGGGG    16159          TCAC    G
                                TCTCGCTCTG    CCAG CTGG
                                ||||||||||    |||| ||||
                                GGGGTGGGGT    GGTC GACT
                                      _____    G
GAM1741  NKX2C     3'  TCCGGGCCTGGTAGGGACGGGG 59910         AC__      _
                                CTCTGTC    CCAGGCT GGA
                                |||||||    ||||||| |||
                                GGGGCAG    GGTCCGG CCT
                                     GGAT      G
GAM1741  NMNAT     3'  ACTCCAGCCTGGGTGACAGAGC 43275
              GAGA                    TCTCGCTCTGTCACCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGCGAGACAGTGGGTCCGACCT
                                                CAC
GAM1741  NMNAT     3'  TCCAGCCTGGCGACAGAGCAAG 43292      C       AC
              A                     TCT GCTCTGTC  CCAGGCTGGA
                                ||| ||||||||  ||||||||||
                                AGA CGAGACAG  GGTCCGACCT
                                  A       C_
GAM1741  NMT1      3'  TCCAGTCTGTGTGTAGGGAGAG 41152      G    T   C
              A                     TCTC CTCTG CAC CAGGCTGGA
                                |||| ||||| ||| |||||||||
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                                AGAG GGGAT GTG GTCTGACCT
                                  A    _  T
GAM1741  NMT2     3'  TCCAGCCTGGGTGACAGAGCGT 17859    T
                GA                TC CGCTCTGTCACCCAGGCTGGA
                                  || ||||||||||||||||||||
                                  AG GCGAGACAGTGGGTCCGACCT
                                   T
GAM1741  NPTXR    3'  TCCAGCCTGGGCAACAGAGCAA 27445     C      CA
                GA                TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A      AC
GAM1741  NR4A3    3'  TAGGCATTGGGGGATGGGGTGG 23722           A    _  GGA
                GA                TCTCGCTCTGTC CCCAG GCT
                                  |||||||||||| ||||| |||
                                  AGGGTGGGGTAG GGGTT CGG
                                         G    A  ATT
GAM1741  NSE1     5'  TTCGGCTCGGGGGTAGAGCGGA  59679    T      TCA  AG
                                  TC CGCTCTG   CCC  GCTGGA
                                  || |||||||   |||  |||||||
                                  AG GCGAGAT   GGG  CGGCTT
                                   _      G__   CT
GAM1741  NY-BR-1  3'  TCCAGCCTAGGTGACAGAGTGA 54853             C
                GA                TCTCGCTCTGTCACC AGGCTGGA
                                  |||||||||||||| ||||||||
                                  AGAGTGAGACAGTGG TCCGACCT
                                          A
GAM1741  OBTP     3'  TCCAGCCTGCAAACTCAGAGGG 34669     G    TCACC_
                GG                CTC CTCTG      CAGGCTGGA
                                  ||| |||||      |||||||||
                                  GGG GAGAC      GTCCGACCT
                                    G     TCAAAC
GAM1741  OR51E2   3'  TCCAGCCTGGGCAACGGAGCAA 48521     C      CA
                GA                TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGGCA  GGGTCCGACCT
                                    A      AC
GAM1741  ORC6L    3'  CTCCAGCCTGGGTGACAGAGCG 27490
                AGA                TCTCGCTCTGTCACCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGCGAGACAGTGGGTCCGACCT
                                             CA
GAM1741  ORC6L    3'  TCCAGCCTGGGTGACAGAGCGA 27494
                GA                TCTCGCTCTGTCACCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAGTGGGTCCGACCT

GAM1741  ORCTL3   3'  TCCAGGGCCCATGCAGGGTGAG 16193          T  CCCA   __
                G                 TCTCGCTCTG CA    GGCT  GGA
                                  |||||||||| ||    ||||  |||
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                                GGAGTGGGAC GT    CCGG  CCT
                                      _  AC__    GA
GAM1741  OS4      3'  TCCAGTTTCACCGTGTGTTAGG 20395          T   CC____
              GTGAGG                   TCTCGCTCTG CAC      AGGCTGGA
                                |||||||||| |||     ||||||||
                                GGAGTGGGAT GTG     TTTGACCT
                                      T   TGCCAC
GAM1741  P11      3'  TTTGGTTTTTTCCAGAGTTAGA 21217     C     TCACCC    TG
                                TCT GCTCTG     AGGC  GA
                                ||| ||||||     ||||  ||
                                AGA TGAGAC     TTTG  TT
                                  T     CTTT__    GT
GAM1741  P114-RHO-GEF 3'  TCTAGCTTCAGCCAGGGCGGG  31677          TCACCC
                                CTCGCTCTG     AGGCTGGA
                                |||||||||     ||||||||
                                GGGCGGGAC     TTCGATCT
                                      CGAC__
GAM1741  p25      3'  CCGGTCTGTGGGGACGAG    23829     T   A  _
                                CTC GTC CC CAGGCTGG
                                ||| ||| || ||||||||
                                GAG CAG GG GTCTGGCC
                                  _   G  T
GAM1741  PAFAH2    3'  ATCTGGGACCTTGATGGAGTGG 6494              ____      CTGGA
              GG                    TCTCGCTCTGTCA    CCCAGG
                                ||||||||||||    ||||||
                                GGGGTGAGGTAGT    GGGTCT
                                        TCCA         AG
GAM1741  PAFAH2    3'  TCCAGCCTGGGTGACAGAGCAA 6508      C
              GA                    TCT GCTCTGTCACCCAGGCTGGA
                                ||| ||||||||||||||||||
                                AGA CGAGACAGTGGGTCCGACCT
                                  A
GAM1741  PASK     5'  TCTGCATCGTGGTGGGGCCAGG 31422     C    TG    CCAG  T
                                TCT GCTC  TCAC    GC GGA
                                ||| ||||  ||||    || |||
                                GGA CGGG  GGTG    CG TCT
                                  C    GT    CTA_  _
GAM1741  PASK     5'  TTCGGCTTCTATCCAGAGTCAG 31425     C     TCACCC
              A                     TCT GCTCTG     AGGCTGGA
                                ||| ||||||     ||||||||
                                AGA TGAGAC     TTCGGCTT
                                  C     CTATC_
GAM1741  PB1      3'  TCCAGCCTGGGCAACAAGAGCG 36880        _  CA
              A                     TCGCTCT GT  CCCAGGCTGGA
                                |||||||  ||  ||||||||||
                                AGCGAGA CA  GGGTCCGACCT
                                    A  AC
GAM1741  PB1      3'  TCCAGCCTGGGCAACAGAGTGA 36881          CA
              G                     CTCGCTCTGT  CCCAGGCTGGA
                                |||||||||  ||||||||||
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                                GAGTGAGACA  GGGTCCGACCT
                                      AC
GAM1741  PB1      3'  TTAGTTACTGGGGGTGGGG   36882     TG  A    __
                                CTC  TC CCCAG  GCTGG
                                |||  || |||||  |||||
                                GGG  GG GGGTC  TGATT
                                  GT  _    AT
GAM1741  PDCD7    3'  TCCAGCCTGGGAGACAGAGCAA 72611     C       A
            GA                    TCT GCTCTGTC CCCAGGCTGGA
                                |||  |||||||| ||||||||||
                                AGA CGAGACAG GGGTCCGACCT
                                  A       A
GAM1741  PDE1C    5'  TCCGGTTCTGTGGCGGGTGCGA 18465       _       CCA
            GA                    TCTCGC TCTGTCAC   GGCTGGA
                                ||||||  ||||||||   |||||||
                                AGAGCG GGGCGGTG   TTGGCCT
                                   T       TC_
GAM1741  PDE2A    5'  TCCAGGCAGCGGGGACAGGGCG 12006          A   AG_  _
            AGG                     TCTCGCTCTGTC CCC   GC TGGA
                                ||||||||||||  |||   ||  ||||
                                GGAGCGGGACAG GGG   CG ACCT
                                      _  CGA  G
GAM1741  PDP      3'  GCAGCAGGGTGGCAGGGCAGA  38031     C         AG    GA
                                TCT GCTCTGTCACCC  GCTG
                                |||  ||||||||||||  ||||
                                AGA CGGGACGGTGGG  CGAC
                                  _          A_    GT
GAM1741  PGGT1B   3'  TTAGATTGGGAGGGTGGGG   18477         GTCA    G
                                TCTCGCTCT    CCCAG CTGG
                                |||||||||    ||||| ||||
                                GGGGTGGGA    GGGTT GATT
                                      _____    A
GAM1741  PGS1     3'  TCCAGTCTGGGTGTCCCAGCGA 44594       CTGT
            G                     CTCGCT    CACCCAGGCTGGA
                                ||||||    ||||||||||||||
                                GAGCGA    GTGGGTCTGACCT
                                   CCCT
GAM1741  PIP5K1C  3'  TCCATGGCAGGACAGAGCGGGA 71310          AC_   GGC
                                TCTCGCTCTGTC   CCA   TGGA
                                ||||||||||||   |||   ||||
                                AGGGCGAGACAG   GGT   ACCT
                                      GAC   ____
GAM1741  PKNOX2   3'  TCTAGCTTTTTTGGCGTGAGA  92534       TCT    CCC
                                TCTCGC   GTCA   AGGCTGGA
                                ||||||   ||||   ||||||||
                                AGAGTG   CGGT   TTCGATCT
                                   ____   TTT
GAM1741  PM5      5'  TCTGGCGGCGGCGGTGGGGCGG 27384         TG  A  CAG  TG
            GG                      TCTCGCTC  TC CC   GC  GA
                                ||||||||  || ||   ||  ||
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                                GGGGCGGG  GG GG   CG  CT
                                    GT  C  CGG  GT
GAM1741  POFUT1    3'  TCCAGCCTGGGCAACAGAGCGA 70984          CA
            GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                       AC
GAM1741  POLYDOM   3'  TCCAGCCTGGGCAATGGAGAGA 44692      G     CA
            GG                    TCTC CTCTGT  CCCAGGCTGGA
                                  ||||| ||||||  ||||||||||
                                  GGAG GAGGTA  GGGTCCGACCT
                                    A     AC
GAM1741  PP1628    5'  TCTGGCCTGGCCTCTGGGCTGG 48081      _    TGTCAC     TG
            GG                    TCTC GCTC     CCAGGC  GA
                                  |||| ||||     ||||||  ||
                                  GGGG CGGG     GGTCCG  CT
                                    T    TCTCC_     GT
GAM1741  PP591     5'  TCCAGCCTGGGTGACAGAG   48150
                                  CTCTGTCACCCAGGCTGGA
                                  ||||||||||||||||||
                                  GAGACAGTGGGTCCGACCT

GAM1741  PPP1R10   3'  TCCAGTCTGGGGAGGAGAGAGA 12232      G    G  A
                                  TCTC CTCT TC CCCAGGCTGGA
                                  |||| |||| || ||||||||||
                                  AGAG GAGG AG GGGTCTGACCT
                                    A   _ _
GAM1741  PPP1R3B   3'  TTCAGCCTGAGCGACAGAGTGA 45148          ACC
                                  TCGCTCTGTC   CAGGCTGGA
                                  ||||||||||   |||||||||
                                  AGTGAGACAG   GTCCGACTT
                                       CGA
GAM1741  PRIC285   3'  ACTCCAGCCTGGGTGACAGAGC 62105
            GAGA                    TCTCGCTCTGTCACCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAGTGGGTCCGACCT
                                                CAC
GAM1741  PRKWNK2   3'  CCAGCCTCCCAGGTGGGG    92193       T   TCACCC
                                  TCTCGC CTG     AGGCTGG
                                  |||||| |||     |||||||
                                  GGGGTG GAC     TCCGACC
                                     _   CC_____
GAM1741  PRO0038   3'  TCCAGCCTGGGTGACAGACCGA 26931       C
            GA                    TCTCG TCTGTCACCCAGGCTGGA
                                  |||||| ||||||||||||||||||
                                  AGAGC AGACAGTGGGTCCGACCT
                                    C
GAM1741  PRO0478   5'  TCCAGCCTGGACAACAGAGTGA 27036          CAC
            GA                    TCTCGCTCTGT   CCAGGCTGGA
                                  ||||||||||   ||||||||||
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                                AGAGTGAGACA   GGTCCGACCT
                                      ACA
GAM1741  PRO0478  3'  TCCAGCCTGGCAACAGAGCGAG 27037          CAC
            A                  TCTCGCTCTGT   CCAGGCTGGA
                               ||||||||||   ||||||||||
                               AGAGCGAGACA   GGTCCGACCT
                                     AC_
GAM1741  PRO0478  3'  TCCAGCCTGGGGGACAGAGCAA 27038     C       A
            GG                   TCT GCTCTGTC CCCAGGCTGGA
                               ||| |||||||| ||||||||||
                               GGA CGAGACAG GGGTCCGACCT
                                 A       G
GAM1741  PRO1048  5'  TCCAGCCTGGGTGACAGAGCGA 38119
            GA                   TCTCGCTCTGTCACCCAGGCTGGA
                               |||||||||||||||||||||||
                               AGAGCGAGACAGTGGGTCCGACCT

GAM1741  PRO1048  3'  TCCAGGCCTGGGTGACAGTGCG 38120       T          _
            AGA                   TCTCGC CTGTCACCCAGGC TGGA
                               |||||| |||||||||||| ||||
                               AGAGCG GACAGTGGGTCCG ACCT
                                  T          G
GAM1741  PRO1386  3'  TCCAGCCTGGGCAACAGAGTGA 49218          CA
            GA                   TCTCGCTCTGT  CCCAGGCTGGA
                               ||||||||||  ||||||||||
                               AGAGTGAGACA  GGGTCCGACCT
                                     AC
GAM1741  PRO1496  3'  TCCAACCTGGGTGACAGACCGA 38368      C          C
            GA                   TCTCG TCTGTCACCCAGG TGGA
                               ||||| |||||||||||| ||||
                               AGAGC AGACAGTGGGTCC ACCT
                                  C          A
GAM1741  PRO1584  5'  TGGTGGGGGGGTGGGGTGGGG  38336        TG  A   AG
                               TCTCGCTC  TC CCC  GCTG
                               ||||||||  || |||  ||||
                               GGGGTGGG  GG GGG  TGGT
                                    GT  _   G_
GAM1741  PRO2015  3'  TCCAGCCTGGGCCACACAGTGA 38166       C   CA
            GA                   TCTCGCT TGT  CCCAGGCTGGA
                               |||||||  |||  ||||||||||
                               AGAGTGA ACA  GGGTCCGACCT
                                  C   CC
GAM1741  PRO2389  3'  TCCAGCCCCATATAGGGTGA  64482         CACCCA
                               TCGCTCTGT     GGCTGGA
                               |||||||||     |||||||
                               AGTGGGATA     CCGACCT
                                     TACC__
GAM1741  PRO2859  3'  TCCAGCCTGGGGAGACAGAGCG 38214          A_
            AGA                   TCTCGCTCTGTC  CCCAGGCTGGA
                               ||||||||||||  ||||||||||
```

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                                AGAGCGAGACAG  GGGTCCGACCT
                                      AG
GAM1741  PRPF4    3'  TCTAGCCTGTGTGACAGAGCAA 17470     C        C
                GA                    TCT GCTCTGTCAC CAGGCTGGA
                                      ||| |||||||||| |||||||||
                                      AGA CGAGACAGTG GTCCGATCT
                                        A         T
GAM1741  PRRG1    5'  TCCGCGAGTAGCGGAGCGGGA  8153           TC  CCAG  T
                                      TCTCGCTCTG  AC    GC GGA
                                      ||||||||||  ||    || |||
                                      AGGGCGAGGC  TG    CG CCT
                                            GA  AG__  _
GAM1741  PSR      3'  TCCAGCCTGGGTGACAGACCGA 65794       C
                GA                    TCTCG TCTGTCACCCAGGCTGGA
                                      ||||| ||||||||||||||||||
                                      AGAGC AGACAGTGGGTCCGACCT
                                        C
GAM1741  PTK6     3'  TCCAGCCTGGGCGACAGAGCGA 21082            A
                GA                    TCTCGCTCTGTC CCCAGGCTGGA
                                      |||||||||||| ||||||||||
                                      AGAGCGAGACAG GGGTCCGACCT
                                            C
GAM1741  PTPRU    3'  TGGTTGGGTGGGTGGGA     20325        CTGT      G TG
                                      TCTCGCT    CACCCAG C  G
                                      |||||||    ||||||| |  |
                                      AGGGTGG    GTGGGTT G  T
                                         _____      _ GT
GAM1741  PTRF     3'  CTCCAGCCTGGGTGACAGAGTG 64237
                AGA                     TCTCGCTCTGTCACCCAGGCTGGA
                                      ||||||||||||||||||||||||
                                      AGAGTGAGACAGTGGGTCCGACCT
                                                  CA
GAM1741  RAB35    3'  TGGAGCCACGGGATGGGGTGGG 23420            A  CA    GGA
                G                      TCTCGCTCTGTC CC  GGCT
                                      |||||||||||| ||  ||||
                                      GGGGTGGGGTAG GG  CCGA
                                            _  CA    GGTT
GAM1741  Rabip4R  3'  TCCAACCTGGGTGACAGAGCAA 36279     C            C
                GA                    TCT GCTCTGTCACCCAGG TGGA
                                      ||| |||||||||||||| ||||
                                      AGA CGAGACAGTGGGTCC ACCT
                                        A             A
GAM1741  RAD51    3'  TCCAGCCAGGGTGACAGAGTGA 56833              A
                GA                    TCTCGCTCTGTCACCC GGCTGGA
                                      |||||||||||||||| |||||||
                                      AGAGTGAGACAGTGGG CCGACCT
                                                A
GAM1741  RASGRP4  3'  TCTGGTGGTGGAGTGGG     54747        TG    C
                                      CTCGCTC  TCACC AGG
                                      |||||||  ||||| |||
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                                GGGTGAG  GGTGG TCT
                                   GT    _
GAM1741  RERG     3'  TCTAGTTTCTGTTTGAAGTGAG 53003        CTG   CC  __
            G                   TCTCGCT   TCA  CAG  GCTGGA
                                |||||||   |||  |||  ||||||
                                GGAGTGA   AGT  GTC  TGATCT
                                   ___   TT   TT
GAM1741  RERG     3'  TCTGGCCTCTAATAGGTTGGGA 53004      CT    CACCC    TG
                                TCTCG  CTGT    AGGC  GA
                                |||||  ||||    ||||  ||
                                AGGGT  GATA    TCCG  CT
                                   TG    ATC__    GT
GAM1741  RFX4     3'  TCTAGCCTTAGTGATACAGTGA 12858        C     CC
            GA                    TCTCGCT TGTCAC  AGGCTGGA
                                  |||||||  ||||||  ||||||||
                                  AGAGTGA ATAGTG  TCCGATCT
                                     C     AT
GAM1741  RHOBTB3  3'  TCCAGCCTGGGTGACAAGAGCG 30432        _
            A                     TCGCTCT GTCACCCAGGCTGGA
                                  |||||||  ||||||||||||||||
                                  AGCGAGA CAGTGGGTCCGACCT
                                     A
GAM1741  RNO2     5'  TCCAGCCTAGACAACAGGGCAA 53941     C      CACCC
            GG                    TCT GCTCTGT     AGGCTGGA
                                  |||  |||||||     ||||||||
                                  GGA CGGGACA     TCCGACCT
                                    A       ACAGA
GAM1741  RNO2     5'  TCCAGCCTGGGCAACAAGAGCG 53942        _  CA
            A                     TCGCTCT GT  CCCAGGCTGGA
                                  |||||||  ||  ||||||||||
                                  AGCGAGA CA  GGGTCCGACCT
                                     A  AC
GAM1741  RoXaN    3'  TCCAGCCTGAGAGACAGAATGA 47303       C     ACC
            GA                    TCTCG TCTGTC   CAGGCTGGA
                                  |||||  ||||||   |||||||||
                                  AGAGT AGACAG   GTCCGACCT
                                     A      AGA
GAM1741  RoXaN    3'  TCCAGCCTGGGCTACAGAGTGA 47304          CA
            GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                        TC
GAM1741  Rpo1-2   3'  TCCAGCCTGGGCGACAGAATGA 39225       C     A
            GA                    TCTCG TCTGTC CCCAGGCTGGA
                                  |||||  ||||||  ||||||||||
                                  AGAGT AGACAG GGGTCCGACCT
                                     A      C
GAM1741  Rpo1-2   3'  TCCAGCCTGGGTGACAGAGCAG 39226    TC
            GA                    TC  GCTCTGTCACCCAGGCTGGA
                                  ||  ||||||||||||||||||||
```

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                                AG  CGAGACAGTGGGTCCGACCT
                                 GA
GAM1741  RRP4     3'  TCCAGCCTGGGTGACAGAGCGA 27363
                GA                 TCTCGCTCTGTCACCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGCGAGACAGTGGGTCCGACCT

GAM1741  SAC2     3'  TCCAGCCTGGGGGACAGAGCAA 30728     C       A
                GA                 TCT GCTCTGTC CCCAGGCTGGA
                                   ||| |||||||| ||||||||||
                                   AGA CGAGACAG GGGTCCGACCT
                                     A       G
GAM1741  SAD1     3'  CTAGCTTCAGCAGGGCAGA    64723     C      CACCC
                                   TCT GCTCTGT     AGGCTGG
                                   ||| |||||||     |||||||
                                   AGA CGGGACG     TTCGATC
                                     _       AC___
GAM1741  SAMHD1   3'  ACTCCAGCCTGGGTGACAGAGT 61972
                GAGA                 TCTCGCTCTGTCACCCAGGCTGGA
                                     ||||||||||||||||||||||||
                                     AGAGTGAGACAGTGGGTCCGACCT
                                                  CAC
GAM1741  SC65     3'  TCCAGCCTGGGCGACAGAGCGA 22302           A
                GA                   TCTCGCTCTGTC CCCAGGCTGGA
                                     |||||||||||| ||||||||||
                                     AGAGCGAGACAG GGGTCCGACCT
                                                C
GAM1741  SC65     3'  TCCAGCCTGGGCGACAGAGTGA 22303           A
                GA                   TCTCGCTCTGTC CCCAGGCTGGA
                                     |||||||||||| ||||||||||
                                     AGAGTGAGACAG GGGTCCGACCT
                                                C
GAM1741  SCAMP5   3'  TCTGGCCTGGGGTCGGGTGA   58063      T   TCA      TG
                                   TCGC CTG   CCCAGGC  GA
                                   |||| |||   |||||||  ||
                                   AGTG GGC   GGGTCCG  CT
                                     _   TG_      GT
GAM1741  SCAMP5   3'  TCTTGGTGGTGGGTGGGA    58064       T TG    C
                                   TCTCGC C  TCACC AGG
                                   |||||| |  ||||| |||
                                   AGGGTG G  GGTGG TCT
                                      _ GT     T
GAM1741  SCAMP5   3'  TTCAGGTTAGGCAGGGTGGGA  58067           ACCC  G
                                   TCTCGCTCTGTC    AG CTGGA
                                   ||||||||||||    || |||||
                                   AGGGTGGGACGG    TT GACTT
                                          A___  G
GAM1741  SCAND2   3'  TCCAGCCTGGGCGACAGAGTGA 54423           A
                GA                   TCTCGCTCTGTC CCCAGGCTGGA
                                     |||||||||||| ||||||||||
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                                AGAGTGAGACAG GGGTCCGACCT
                                      C
GAM1741  SCAND2   3'  TCCAGCCTGGGCGACAGAGTGA 54424          A
            GA                  TCTCGCTCTGTC CCCAGGCTGGA
                                |||||||||||| ||||||||||
                                AGAGTGAGACAG GGGTCCGACCT
                                      C
GAM1741  SCAND2   3'  TTGAGCCTGGGCGACAGAGTGA 54426          A      G
            GA                  TCTCGCTCTGTC CCCAGGCT GA
                                |||||||||||| |||||||| ||
                                AGAGTGAGACAG GGGTCCGA TT
                                      C      G
GAM1741  SCDGF-B  3'  TTTAGTTTAAGGAGGGTGAGA  53636        GTCA  C_
                                TCTCGCTCT   CC  AGGCTGGA
                                |||||||||   ||  ||||||||
                                AGAGTGGGA   GG  TTTGATTT
                                     ____  AA
GAM1741  SCYA5    3'  TCCAGCCTGGGCGACAGAGCGA 12971          A
            GA                  TCTCGCTCTGTC CCCAGGCTGGA
                                |||||||||||| ||||||||||
                                AGAGCGAGACAG GGGTCCGACCT
                                      C
GAM1741  SCYA5    3'  TCCAGCCTGGGTGACAAAGTGA 12972       C
            GA                  TCTCGCT TGTCACCCAGGCTGGA
                                ||||||| ||||||||||||||||
                                AGAGTGA ACAGTGGGTCCGACCT
                                   A
GAM1741  SCYD1    3'  TCTGGCAGCTCAGAGAGGGTGG 92561        G  ACCCAG  TG
            GA                  TCTCGCTCT TC     GC  GA
                                ||||||||| ||     ||  ||
                                AGGGTGGGA AG     CG  CT
                                     G  ACTCGA  GT
GAM1741  SEMA3E   3'  TCCGGCCTGGGCGACAGAGCGA 25812          A
            GA                  TCTCGCTCTGTC CCCAGGCTGGA
                                |||||||||||| ||||||||||
                                AGAGCGAGACAG GGGTCCGGCCT
                                      C
GAM1741  SEMA5A   3'  TCCATCCTGGGTGACAGAGAGA 15599     G          C
            GA                  TCTC CTCTGTCACCCAGG TGGA
                                |||| |||||||||||||| ||||
                                AGAG GAGACAGTGGGTCC ACCT
                                  A           T
GAM1741  SERF2    5'  TTCAGCCGCAGAGGGGCGGGA  20492        GTCACCCA
                                TCTCGCTCT       GGCTGGA
                                |||||||||       |||||||
                                AGGGCGGGG       CCGACTT
                                     AGACG___
GAM1741  SFXN5    3'  TCTGGCCTGGGAAAAGGGCAGG 58659    TC    GTCA     TG
            A                    TC  GCTCT   CCCAGGC  GA
                                 ||  |||||   |||||||  ||
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                                AG  CGGGA   GGGTCCG  CT
                                 GA    AAA_     GT
GAM1741  SGKL     3'  TTCAGCCTGGGTGCCACAGCGA 26065       C  T
              GA                  TCTCGCT TG CACCCAGGCTGGA
                                  ||||||| || ||||||||||||
                                  AGAGCGA AC GTGGGTCCGACTT
                                     C  C
GAM1741  ShrmL    3'  TTTAGTTTTTAACAGGCTGAGG 40856     _ T   CACCC
                                  TCTC GC CTGT    AGGCTGGA
                                  |||| || ||||    ||||||||
                                  GGAG CG GACA    TTTGATTT
                                    T _   ATT__
GAM1741  SLC2A4RG  3'  TTTACTTGGGGTGGGGGGGCGG 39634        G    _  C
              GG                  TCTCGCTCT TCACCC AGG TGGA
                                  ||||||||| |||||| ||| ||||
                                  GGGGCGGGG GGTGGG TTC ATTT
                                       G    G  _
GAM1741  SLC37A1   5'  CCAGCCTGTGGGAGCGG    39087      TGTCA _
                                  TCGCTC    CC CAGGCTGG
                                  ||||||    || ||||||||
                                  GGCGAG    GG GTCCGACC
                                     _____  T
GAM1741  SLC7A11   3'  TCCAGCCTGGGTGACAAAGTCA 27532    C  C
              GA                  TCT GCT TGTCACCCAGGCTGGA
                                  ||| ||| ||||||||||||||||
                                  AGA TGA ACAGTGGGTCCGACCT
                                    C  A
GAM1741  SLIT1    5'  TCTGGCTCGCGAGCGGGA    13234       T  CAC
                                  TCTCGCTC GT   CCAGG
                                  |||||||| ||   |||||
                                  AGGGCGAG CG   GGTCT
                                       _ CTC
GAM1741  SMA3     3'  TCCAGCCTGGGTGACAGAGC   23262
                                  GCTCTGTCACCCAGGCTGGA
                                  ||||||||||||||||||||
                                  CGAGACAGTGGGTCCGACCT

GAM1741  SMAP-5   3'  ATCCAGCCTGGGTGACAGGGTG 48655
              AGA                   TCTCGCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGGGACAGTGGGTCCGACCT
                                                AC
GAM1741  SMARCF1   3'  TCCAGCTCCCATGGAGGGTGGG 21192        G   CCCA
              G                    TCTCGCTCT TCA    GGCTGGA
                                   |||||||| |||    |||||||
                                   GGGGTGGGA GGT    TCGACCT
                                        _  ACCC
GAM1741  SMCR5    3'  CCGGTTTCAGGGGTGAGA    59248         GTCACCC
                                  TCTCGCTCT      AGGCTGG
                                  |||||||||      |||||||
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                                AGAGTGGGG      TTTGGCC
                                     AC_____
GAM1741  SMCR7    3'  TTTAGTTTTCTTGCTGAGCGGG 58242        T T  CCC
            A                    TCTCGCTC G CA   AGGCTGGA
                                 |||||||| | ||   ||||||||
                                 AGGGCGAG C GT   TTTGATTT
                                      T _  TCT
GAM1741  SNAPC1   3'  TCCAGCCTGGGCAACAGAGTGA 13279          CA
            GA                     TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   AGAGTGAGACA  GGGTCCGACCT
                                         AC
GAM1741  SNPH     3'  TTTGGTGGATGTGACAGGGCTG 28911     C        __  AG  TG
            GG                     TCT GCTCTGTCAC  CC  GC  GA
                                   ||| ||||||||||  ||  ||  ||
                                   GGG CGGGACAGTG  GG  TG  TT
                                     T         TA  __  GT
GAM1741  SNRK     3'  TCTGAGGTGACGGACTGAGA   35284      C       _
                                   TCTCG TCTGTCACC CAGG
                                   ||||| ||||||||| ||||
                                   AGAGT AGGCAGTGG GTCT
                                      C        A
GAM1741  SNX11    5'  TCTGGCTATATGGTGGGGCGCG 26175    T    TG   CCCA   TG
            G                      TC CGCTC  TCA    GGC  GA
                                   || |||||  |||    |||  ||
                                   GG GCGGG  GGT    TCG  CT
                                    C     GT   ATA_   GT
GAM1741  SPRY4    3'  ACTCCAGCCTGGGTGACAGAGT 48990
            GAGA                       TCTCGCTCTGTCACCCAGGCTGGA
                                       ||||||||||||||||||||||||
                                       AGAGTGAGACAGTGGGTCCGACCT
                                                  CAC
GAM1741  SPRY4    3'  TCCAGCCTGGGTGACAGAGCAA 49032     C
            GA                     TCT GCTCTGTCACCCAGGCTGGA
                                   ||| ||||||||||||||||||
                                   AGA CGAGACAGTGGGTCCGACCT
                                     A
GAM1741  SPTLC2   3'  ACTCCAGCCTGGGTGACAGAGT 17975
            GAGA                       TCTCGCTCTGTCACCCAGGCTGGA
                                       ||||||||||||||||||||||||
                                       AGAGTGAGACAGTGGGTCCGACCT
                                                  CAC
GAM1741  SPTLC2   3'  TCCAGCCTTGGCGACAGAGGGA 18002      G      A  C
            GA                     TCTC CTCTGTC CC AGGCTGGA
                                   |||| ||||||| || ||||||||
                                   AGAG GAGACAG GG TCCGACCT
                                     G      C  T
GAM1741  SPTLC2   3'  TCTAGCCTGGGTGACAGAGC   18003
                                   GCTCTGTCACCCAGGCTGGA
                                   ||||||||||||||||||||
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                                CGAGACAGTGGGTCCGATCT

GAM1741  SSR3     3'  GCCTGGGTGGCAAGGGTGAGA  24036          _
                                TCTCGCTCT GTCACCCAGGC
                                ||||||||| ||||||||||
                                AGAGTGGGA CGGTGGGTCCG
                                     A
GAM1741  STI2     3'  TCCTTACTCCTGGGTGGGGAGT 90407          G        CT___
              GGGA                    TCTCGCTCT TCACCCAGG     GGA
                                ||||||||| |||||||||     |||
                                AGGGTGAGG GGTGGGTCC     CCT
                                     _        TCATT
GAM1741  STI2     3'  TTTGTGGGATGGGGTGAGG    90410           A  _
                                TCTCGCTCTGTC CC CAGG
                                |||||||||||| || ||||
                                GGAGTGGGGTAG GG GTTT
                                      _ T
GAM1741  STK38L   5'  CCCGGGGGGCGGGGCGAGG     69687           A   A
                                TCTCGCTCTGTC CCC GG
                                |||||||||||| ||| ||
                                GGAGCGGGGCGG GGG CC
                                      _  C
GAM1741  SUN1     3'  TTGGTTTAAAACAGGGTGA   47928         CACCC    TG
                                TCGCTCTGT    AGGC  GA
                                |||||||||    ||||  ||
                                AGTGGGACA    TTTG  TT
                                     AAA__    GT
GAM1741  SYAP1    3'  CTCCAGCCTGGGTGATAGAGTG 52471
              AGA                    TCTCGCTCTGTCACCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGATAGTGGGTCCGACCT
                                           CA
GAM1741  SYNE-2   3'  TTTGGCCACGGCGGGGGTGGGG 31478         GT A  CA   TG
                                TCTCGCTCT  C CC  GGC  GA
                                |||||||||  | ||  |||  ||
                                GGGGTGGGG  G GG  CCG  TT
                                     __ C  CA   GT
GAM1741  SYT13    3'  TTTGGGGGGGGCGGGGCGGGG  95112           A   AGG TG
                                TCTCGCTCTGTC CCC   C  GA
                                |||||||||||| |||   |  ||
                                GGGGCGGGGCGG GGG   G  TT
                                      _   G__ GT
GAM1741  SZF1     5'  TCTGGTTCCAGTGGCAGATGGG 32733      C       CCA   TG
              G                     TCTCG TCTGTCAC   GGC  GA
                                ||||| ||||||||   |||  ||
                                GGGGT AGACGGTG   TTG  CT
                                   _       ACC   GT
GAM1741  TA-LRRP  3'  CACCAGCCTGGGTGACAGAGCA 31709     C              A
              AGA                    TCT GCTCTGTCACCCAGGCTGG
                                ||| ||||||||||||||||||
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                                AGA CGAGACAGTGGGTCCGACC
                                  A               ACA
GAM1741  TA-PP2C   3'  TTTGGTAGACGCGGTGGGG   58407       C   AC
                                TCTCGCT TGTC  CCAGG
                                ||||||| ||||  |||||
                                GGGGTGG GCAG  GGTTT
                                    C   AT
GAM1741  TADA3L    3'  TCCAGCCTGGGCAACAAGAGTG 22047       _  CA
           A                     TCGCTCT GT  CCCAGGCTGGA
                                ||||||| ||  ||||||||||
                                AGTGAGA CA  GGGTCCGACCT
                                    A  AC
GAM1741  TBL1Y     5'  TCAGCCTGGAAGGCGAGG    53864       T  GTCAC
                                TCTCGC CT    CCAGGCTGG
                                |||||| ||    |||||||||
                                GGAGCG GA    GGTCCGACT
                                   _ A____
GAM1741  TBX19     3'  TCCAGCCTGGGTGGTAGA    18923     GT
                                TCT  CACCCAGGCTGGA
                                |||  ||||||||||||
                                AGA  GTGGGTCCGACCT
                                  TG
GAM1741  TED      3'  TCTGGTCTGCTGTGTGGGTTGG 32276      CT  T  C_    TG
           GG                    TCTCG  CTG CAC  CAGGC  GA
                                ||||| ||| |||  ||||| ||
                                GGGGT  GGT GTG  GTCTG  CT
                                   TG  _  TC    GT
GAM1741  TERA     3'  TTTAGTTTTAGTAGAGACGGGG 41427      _   GTC  CC
                                TCTCG CTCT   AC  AGGCTGGA
                                ||||| ||||  ||  ||||||||
                                GGGGC GAGA   TG  TTTGATTT
                                   A   ___  AT
GAM1741  TGIF2    3'  TCTGGCTTTTAGTAGAGACGGG 41760      _    TCACCC   TG
           G                     TCTCG CTCTG     AGGC  GA
                                ||||| |||||     ||||  ||
                                GGGGC GAGAT     TTCG  CT
                                   A    GATT__   GT
GAM1741  THEA     3'  TCCAGCCTGGGTGACAGAGTGA 66898
                                TCGCTCTGTCACCCAGGCTGGA
                                ||||||||||||||||||||||
                                AGTGAGACAGTGGGTCCGACCT

GAM1741  TIP47    3'  TCCAGCCTGGGGGGACAAGAGTG 20608        _  A
           AGA                    TCTCGCTCT GTC CCCAGGCTGGA
                                ||||||||| ||| ||||||||||
                                AGAGTGAGA CAG GGGTCCGACCT
                                     A  G
GAM1741  TMG4     3'  TCCAGCCTGGGCGACAGAGCAA 44217     C       A
           GA                     TCT GCTCTGTC CCCAGGCTGGA
                                ||| |||||||| ||||||||||
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                                AGA CGAGACAG GGGTCCGACCT
                                  A       C
GAM1741  TNRC4    3'  TTTGGCCTTTGTGAGGGAGCGA 24194        G   CC   TG
                GG                  TCTCGCTCT TCAC  AGGC  GA
                                    ||||||||| ||||  ||||  ||
                                    GGAGCGAGG AGTG  TCCG  TT
                                        G   TT   GT
GAM1741  TP53INP1  3'  ACTGAATCTGGTGATGGGGTGG 53866            C  CTGGA
                GG                  TCTCGCTCTGTCACC AGG
                                    |||||||||||||| |||
                                    GGGGTGGGGTAGTGG TCT
                                           _  AAGTCAT
GAM1741  TP53INP1  3'  TCTGGTGATGGGGTGGGG    53872            C
                                    TCTCGCTCTGTCACC AGG
                                    |||||||||||||| |||
                                    GGGGTGGGGTAGTGG TCT
                                           _
GAM1741  TRAP150   3'  TTGGTGTGTGGGGTGGGG    18873         T  _
                                    TCTCGCTCTG CAC CCAG
                                    |||||||||| ||| ||||
                                    GGGGTGGGGT GTG GGTT
                                          _  T
GAM1741  TRIM29    3'  TCTGGCGATGGAGTGTGG    25012    T       AC
                                    TC CGCTCTGTC  CCAGG
                                    || |||||||||  |||||
                                    GG GTGAGGTAG  GGTCT
                                     T       C_
GAM1741  TSGA2     3'  TCCAGCCTGGGTGGCAGAGCGA 55955
                GA                  TCTCGCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACGGTGGGTCCGACCT

GAM1741  UBCE7IP5  3'  TCCAGCCTGGGAGCCCCTGGAG 30854        ____  CA
                TGG                   TCGCTCT   GT  CCCAGGCTGGA
                                      |||||||   ||  ||||||||||
                                      GGTGAGG   CG  GGGTCCGACCT
                                          TCCC  A_
GAM1741  UBCE7IP5  3'  TCCAGCCTGGGCGACGGAGTGA 30856          A
                GA                  TCTCGCTCTGTC CCCAGGCTGGA
                                    |||||||||||| ||||||||||
                                    AGAGTGAGGCAG GGGTCCGACCT
                                           C
GAM1741  UBE2E1    5'  GCGGGGTGGGGTGGGG      13949        TGT    AG
                                    TCTCGCTC   CACCC  GC
                                    ||||||||   |||||  ||
                                    GGGGTGGG   GTGGG  CG
                                         ___     G_
GAM1741  USP19     3'  CGGTGGGAGAGGGTGGGG    90402         G  A  CAG  TG
                                    TCTCGCTCT TC CC   GC  G
                                    ||||||||| || ||   ||  |
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                                GGGGTGGGA AG GG   TG  C
                                     G  _  ___  GT
GAM1741  UST      3'  CTCCAGCCTGGGTGACAGAGTG 20352
              AGA                    TCTCGCTCTGTCACCCAGGCTGGA
                                     ||||||||||||||||||||||||
                                     AGAGTGAGACAGTGGGTCCGACCT
                                                CA
GAM1741  VIT1     5'  CTCCAGCCTGGGTGGCAGAGTG 38603
              AGA                    TCTCGCTCTGTCACCCAGGCTGGA
                                     ||||||||||||||||||||||||
                                     AGAGTGAGACGGTGGGTCCGACCT
                                                CA
GAM1741  VPS4B    3'  CCAGCCTGGGCGCCGAGA    18020       CTCT  CA
                                     TCTCG    GT  CCCAGGCTGG
                                     |||||    ||  ||||||||||
                                     AGAGC    CG  GGGTCCGACC
                                       _____  C_
GAM1741  WBSCR22  3'  TCTGCGGAGGTGGGGTGGGA   34471          TG  A  _
                                     TCTCGCTC  TC CC CAGG
                                     ||||||||  || || ||||
                                     AGGGTGGG  GG GG GTCT
                                          GT  A  C
GAM1741  WBSCR23  3'  TCCAGCCTGGGCGACAAAGTGA 47443          C    A
              GA                     TCTCGCT TGTC CCCAGGCTGGA
                                     |||||||  |||| ||||||||||
                                     AGAGTGA ACAG GGGTCCGACCT
                                        A    C
GAM1741  WBSCR23  3'  TCCAGCCTGGGCGACAGAGCAA 47444     C       A
              GA                     TCT GCTCTGTC CCCAGGCTGGA
                                     |||  ||||||||  ||||||||||
                                     AGA CGAGACAG GGGTCCGACCT
                                       A       C
GAM1741  WBSCR23  5'  TCCAGCCTGGGCGACAGAGCCA 47445     C       A
              GA                     TCT GCTCTGTC CCCAGGCTGGA
                                     |||  ||||||||  ||||||||||
                                     AGA CGAGACAG GGGTCCGACCT
                                       C       C
GAM1741  WBSCR23  3'  TCCAGCCTGGGTGATAGAGCAA 47446     C
              GA                     TCT GCTCTGTCACCCAGGCTGGA
                                     |||  ||||||||||||||||||||
                                     AGA CGAGATAGTGGGTCCGACCT
                                       A
GAM1741  WIRE     3'  TCCAGCCTGGGCGACAGAGCCA 78907     C       A
              GA                     TCT GCTCTGTC CCCAGGCTGGA
                                     |||  ||||||||  ||||||||||
                                     AGA CGAGACAG GGGTCCGACCT
                                       C       C
GAM1741  YAP1     3'  TTTAGCTTAGGGGGAGGGTGGG 21468          G  A  C
              A                      TCTCGCTCT TC CC AGGCTGGA
                                     |||||||||  || || ||||||||
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                                AGGGTGGGA GG GG TTCGATTT
                                     G _ A
GAM1741  YME1L1   3'  ACTCCAGCCTGGGTGACAGAGT 58418
            GAGA                    TCTCGCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAGTGGGTCCGACCT
                                          CAC
GAM1741  YME1L1   3'  CTCCAGCCTGGGTGACAGAGTG 58431
            AGA                     TCTCGCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAGTGGGTCCGACCT
                                          CA
GAM1741  YME1L1   3'  TCCAGCCTGGGCAACAGAGCAA 58439     C      CA
            GA                      TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGAGACA  GGGTCCGACCT
                                      A       AC
GAM1741  ZAK      3'  TCCAGCCTGGATGACAGAGTGA 34109            C
            GA                      TCTCGCTCTGTCA CCAGGCTGGA
                                    |||||||||||| ||||||||||
                                    AGAGTGAGACAGT GGTCCGACCT
                                          A
GAM1741  ZDHHC1   5'  CCAGCCTGCTGGAGCCGGA   78208     C     TCACC
                                    TCT GCTCTG    CAGGCTGG
                                    ||| ||||||    ||||||||
                                    AGG CGAGGT    GTCCGACC
                                      C     C____
GAM1741  ZDHHC1   3'  TCTGGCTTAGCTGGGCCGAGA  78212      _  T  CACCC   TG
                                    TCTCG CTC GT    AGGC  GA
                                    ||||| ||| ||    ||||  ||
                                    AGAGC GGG CG    TTCG  CT
                                       C  T  A____   GT
GAM1741  ZDHHC3   3'  TTTAGCTTTTGCTTGGGGTGGG 33937          TCACCC
            G                       TCTCGCTCTG     AGGCTGGA
                                    ||||||||||     ||||||||
                                    GGGGTGGGGT     TTCGATTT
                                          TCGTT_
GAM1741  ZFP106   3'  TCCAGCCTGGGCGACAAGAGTG 42741        _  A
            A                       TCGCTCT GTC CCCAGGCTGGA
                                    ||||||| ||| ||||||||||
                                    AGTGAGA CAG GGGTCCGACCT
                                       A  C
GAM1741  ZNF197   3'  TCCAGCCTGGGCAACAAGAGCG 23760        _  CA
            A                       TCGCTCT GT  CCCAGGCTGGA
                                    ||||||| ||  ||||||||||
                                    AGCGAGA CA  GGGTCCGACCT
                                       A  AC
GAM1741  ZNF271   3'  TCCAGCCTGGGCAACAGAGTGA 96968          CA
            GA                      TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
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                                AGAGTGAGACA  GGGTCCGACCT
                                      AC
GAM1741  ZNF271    3'  TCCAGTCTGGGCAACAGAGCAA 96969     C      CA
                GA                    TCT GCTCTGT  CCCAGGCTGGA
                                      ||| |||||||  ||||||||||
                                      AGA CGAGACA  GGGTCTGACCT
                                        A       AC
GAM1741  ZNF297    5'  TCTGGCCGCCGAGTGAGGGGCG 19573         G    CCA__   TG
                GGG                     TCTCGCTCT TCAC     GGC  GA
                                      |||||||||| ||||     |||  ||
                                      GGGGCGGGG AGTG     CCG  CT
                                           _    AGCCG   GT
GAM1741  ZNF297B   3'  TCCAGCCTGCGCGACAGATCGA 26672       C      ACC
                GA                    TCTCG TCTGTC   CAGGCTGGA
                                      ||||| ||||||   |||||||||
                                      AGAGC AGACAG   GTCCGACCT
                                        T     CGC
GAM1741  ZNF297B   5'  TCCAGCCTGGGCAACAGAGCAA 26675     C      CA
                GA                    TCT GCTCTGT  CCCAGGCTGGA
                                      ||| |||||||  ||||||||||
                                      AGA CGAGACA  GGGTCCGACCT
                                        A       AC
GAM1741  ZNF297B   5'  TCCAGCCTGGGTAAAAGAGTGA 26676         GTC
                GA                    TCTCGCTCT   ACCCAGGCTGGA
                                      |||||||||   ||||||||||||
                                      AGAGTGAGA   TGGGTCCGACCT
                                           AAA
GAM1741  ZNF333    3'  TCCAGCCTGGGCAACAGAGTGA 51595         CA
                                      TCGCTCTGT  CCCAGGCTGGA
                                      |||||||||  ||||||||||
                                      AGTGAGACA  GGGTCCGACCT
                                           AC
GAM1741  ZNF339    3'  TCCAGCCTGGGCAACAGAGTGG 41398         CA
                                      TCGCTCTGT  CCCAGGCTGGA
                                      |||||||||  ||||||||||
                                      GGTGAGACA  GGGTCCGACCT
                                           AC
GAM1741  ZNF33A    3'  GCAGCCTGGGTGACAGAATGAG 92997       C             GA
                A                     TCTCG TCTGTCACCCAGGCTG
                                      ||||| ||||||||||||||||
                                      AGAGT AGACAGTGGGTCCGAC
                                        A             GT
GAM1741  LOC112687 3'  TCCAGCCTGGGCAACAGAGTGG 73243           CA
                GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                      ||||||||||  ||||||||||
                                      AGGGTGAGACA  GGGTCCGACCT
                                           AC
GAM1741  LOC112817 5'  CGGCTTCAGAGCTGGGA     57323      _     TCACCC    TG
                                      TCTC GCTCTG     AGGC  G
                                      |||| ||||||     ||||  |
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                                AGGG CGAGAC     TTCG  C
                                  T     _______    GT
GAM1741  LOC112868 3'  TCCAGCCTGACCCCAGAGCAGA 73271     C     TCACC
                                TCT GCTCTG     CAGGCTGGA
                                ||| ||||||     |||||||||
                                AGA CGAGAC     GTCCGACCT
                                  _     CCCA_
GAM1741  LOC112868 3'  TCCAGTTTACAAACAGTGTGGG 73272       T    CACCC
                G                TCTCGC CTGT     AGGCTGGA
                                ||||||| ||||     |||||||||
                                GGGGTG GACA     TTTGACCT
                                   T    AACA_
GAM1741  LOC113201 3'  TCCAGCTTGGGCACCAGAGCAA 57357     C     TCA
                GA                 TCT GCTCTG   CCCAGGCTGGA
                                ||| ||||||   ||||||||||||
                                AGA CGAGAC   GGGTTCGACCT
                                  A      CAC
GAM1741  LOC113523 3'  TCCAGCCTGGGCGACAGGGCAA 73434     C       A
                GA                 TCT GCTCTGTC CCCAGGCTGGA
                                ||| |||||||| ||||||||||||
                                AGA CGGGACAG GGGTCCGACCT
                                  A       C
GAM1741  LOC114987 3'  TCCAGCCTGGGCAACAAGAGCG 59800        _  CA
                A                 TCGCTCT GT  CCCAGGCTGGA
                                ||||||| ||  ||||||||||||
                                AGCGAGA CA  GGGTCCGACCT
                                    A  AC
GAM1741  LOC114987 3'  TTTGGAATGGCCAGAGTGAGG  59803          TCAC   GG TG
                                TCTCGCTCTG    CCA  C  GA
                                ||||||||||    |||  |  ||
                                GGAGTGAGAC    GGT  G  TT
                                      C___    AA GT
GAM1741  LOC115129 3'  TCCAGCCTGAGCGACAGAGTAA 73629     CG      ACC
                GA                 TCT  CTCTGTC   CAGGCTGGA
                                |||  |||||||   |||||||||
                                AGA  GAGACAG   GTCCGACCT
                                  AT      CGA
GAM1741  LOC115196 3'  TCCAGCCTGGGAGACAGAGCGA 73661           A
                GA                 TCTCGCTCTGTC CCCAGGCTGGA
                                |||||||||||| ||||||||||||
                                AGAGCGAGACAG GGGTCCGACCT
                                      A
GAM1741  LOC115273 3'  TCCAGCCTGGGCAACAGAGTGA 73754          CA
                GA                 TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      AC
GAM1741  LOC115648 3'  ATCTGGGTTTGTAGTGGAGTGG 60017        TG C____      CTGGA
                GG                 TCTCGCTC  T     ACCCAGG
                                ||||||||  |     |||||||
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                                GGGGTGAG  G     TGGGTCT
                                   GT ATGTT         AG
GAM1741  LOC115708 3'  CCTGGGTGGCCAGAGTGGGA   73914          _
                                TCTCGCTCTG TCACCCAGG
                                |||||||||| |||||||||
                                AGGGTGAGAC GGTGGGTCC
                                      C
GAM1741  LOC115757 3'  CCCATCCTGGGTGACAGAGTGA 73952                C   A
            GA                    TCTCGCTCTGTCACCCAGG TGG
                                  |||||||||||||||||| |||
                                  AGAGTGAGACAGTGGGTCC ACC
                                           T   CC
GAM1741  LOC115761 3'  TCCAGTCTGGGCAACAGAGTGA 93398           CA
            GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCTGACCT
                                        AC
GAM1741  LOC116143 3'  TCCAGCCCTGGCGACAGAGTGA 74193           A  CA
            GA                    TCTCGCTCTGTC CC  GGCTGGA
                                  ||||||||||| ||  |||||||
                                  AGAGTGAGACAG GG  CCGACCT
                                        C  TC
GAM1741  LOC116143 3'  TCCAGCCTGGGCAACTGAGCAA 74194     C    T  CA
            GA                    TCT GCTC GT  CCCAGGCTGGA
                                  ||| |||| ||  ||||||||||
                                  AGA CGAG CA  GGGTCCGACCT
                                    A    T  AC
GAM1741  LOC116228 3'  TCTAGCCTAGGTGACAGAGTGA 74231             C
            GA                    TCTCGCTCTGTCACC AGGCTGGA
                                  |||||||||||||| ||||||||
                                  AGAGTGAGACAGTGG TCCGATCT
                                        A
GAM1741  LOC116236 3'  TCCAGCCTGGGCGACAGAGTAA 74248     CG      A
            GA                    TCT  CTCTGTC CCCAGGCTGGA
                                  |||  ||||||| ||||||||||
                                  AGA  GAGACAG GGGTCCGACCT
                                    AT      C
GAM1741  LOC116349 3'  TCCAGCCTGGGCAACAGAGCGA 74281           CA
            GG                    TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  GGAGCGAGACA  GGGTCCGACCT
                                        AC
GAM1741  LOC119504 5'  TCCAGCCTGGGCAACAAGAGGG 74449    G   _  CA
            A                      TC CTCT GT  CCCAGGCTGGA
                                   || |||| ||  ||||||||||
                                   AG GAGA CA  GGGTCCGACCT
                                    G   A  AC
GAM1741  LOC120406 3'  TCCAGCCTGGGTGACAGAGCGA 76066
            GA                    TCTCGCTCTGTCACCCAGGCTGGA
                                  ||||||||||||||||||||||||
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                                AGAGCGAGACAGTGGGTCCGACCT

GAM1741  LOC120526 5'  TCGGCCGACAGCAGGCGAGG   74467       __    ACCCA   TG
                                TCTCGCT  CTGTC    GGC  GA
                                |||||||  |||||    |||  ||
                                GGAGCGG  GACAG    CCG  CT
                                    AC    _____   GT
GAM1741  LOC122704 3'  TCCAACCTGGGCGACAGGGCGA 74611          A     C
           GA                     TCTCGCTCTGTC CCCAGG TGGA
                                |||||||||||| |||||| ||||
                                AGAGCGGGACAG GGGTCC ACCT
                                       C     A
GAM1741  LOC123591 3'  TCAGCAGGGTAGAGTGTGG   76133    T     GTC    AG
                                TC CGCTCT   ACCC  GCTGG
                                || ||||||   ||||  |||||
                                GG GTGAGA   TGGG  CGACT
                                 T     ___   A_
GAM1741  LOC124801 3'  AGAGCTTTGGGGGTGGGGTGGG 74811        TG  A    _  GGA
           G                     TCTCGCTC  TC CCCAG GCT
                                ||||||||  || ||||| |||
                                GGGGTGGG  GG GGGTT CGA
                                    GT  _    T   GAT
GAM1741  LOC124842 3'  TCCAGCTTGGGGTCAGGTGGG  76160      T   TCA
                                CTCGC CTG   CCCAGGCTGGA
                                ||||| |||   ||||||||||
                                GGGTG GAC   GGGTTCGACCT
                                   _   TG_
GAM1741  LOC124976 3'  TCTGGTGCGGGGGTGGGGTGGG 74844        TG  A   AG  TG
           G                     TCTCGCTC  TC CCC  GC  GA
                                ||||||||  || |||  ||  ||
                                GGGGTGGG  GG GGG  TG  CT
                                    GT  _   CG  GT
GAM1741  LOC125228 5'  CCAGCCTGCGCGGCGGGA    74862       C  TCACC
                                TCTCGCT TG    CAGGCTGG
                                ||||||| ||    ||||||||
                                AGGGCGG GC    GTCCGACC
                                    C  _____
GAM1741  LOC125929 3'  CTAGCCAATGGAGTGTGA    76173    T      CACCCA
                                TC CGCTCTGT     GGCTGG
                                || ||||||||     ||||||
                                AG GTGAGGTA     CCGATC
                                 T      A_____
GAM1741  LOC126031 5'  GCAGAATGTGGGGGGTGGGG   74902        GTCA  _  GG   GA
                                TCTCGCTCT   CC CA  CTG
                                |||||||||   || ||  |||
                                GGGGTGGGG   GG GT  GAC
                                     ____  T  AA   GT
GAM1741  LOC126282 3'  TCCAGCCTGGGTGACAGAGCAA 74967     C
           GA                     TCT GCTCTGTCACCCAGGCTGGA
                                ||| ||||||||||||||||||
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                                AGA CGAGACAGTGGGTCCGACCT
                                  A
GAM1741  LOC126353 3'  CCAGTCTGAGGGAGGAG     74989      G  A  _
                                CTCT TC CC CAGGCTGG
                                |||| || || ||||||||
                                GAGG AG GG GTCTGACC
                                  _  _  A
GAM1741  LOC126669 3'  TCCAGCCTGAGTGACAGAGTGA 75951             C
           GA                     TCTCGCTCTGTCAC CAGGCTGGA
                                |||||||||||||| |||||||||
                                AGAGTGAGACAGTG GTCCGACCT
                                        A
GAM1741  LOC126917 3'  TTCAGAAATGTGGTGGGTGGGG 75101        T TG    CCAGG
                                TCTCGC C  TCAC     CTGGA
                                |||||| |  ||||     |||||
                                GGGGTG G  GGTG     GACTT
                                   _ GT    TAAA_
GAM1741  LOC127262 3'  TCCAGCCCGGGCGACAGAGCGA 76605           A   A
           GA                     TCTCGCTCTGTC CCC GGCTGGA
                                |||||||||||| ||| |||||||
                                AGAGCGAGACAG GGG CCGACCT
                                      C   C
GAM1741  LOC127428 3'  TCCAGCCTGGGCAACAGAGTGA 75163           CA
           GA                     TCTCGCTCTGT  CCCAGGCTGGA
                                |||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      AC
GAM1741  LOC129303 3'  TCGGTGGAGGTGGAGTGGG    75377        TG  A  CAG  TG
                                CTCGCTC  TC CC   GC  GA
                                |||||||  || ||   ||  ||
                                GGGTGAG  GG GG   TG  CT
                                    GT  A  ___  GT
GAM1741  LOC129880 3'  TCCAGCTTGGGCAACAGAGCAA 75409     C      CA
           GA                     TCT GCTCTGT  CCCAGGCTGGA
                                ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTTCGACCT
                                  A      AC
GAM1741  LOC130535 3'  TCCAGCCTGGGTGACAGAGCAA 76656     C
           GA                     TCT GCTCTGTCACCCAGGCTGGA
                                ||| ||||||||||||||||||||
                                AGA CGAGACAGTGGGTCCGACCT
                                  A
GAM1741  LOC130617 5'  TCCGGTAACCCGGGCTGGGCGG 57938         T   ACCCAG
           GG                     TCTCGCTC GTC      GCTGGA
                                |||||||| |||      ||||||
                                GGGGCGGG CGG      TGGCCT
                                     T   GCCCAA
GAM1741  LOC131744 3'  TCCAGCCTGGGTGACAGAGTGA 76392
                                TCGCTCTGTCACCCAGGCTGGA
                                ||||||||||||||||||||||
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                                AGTGAGACAGTGGGTCCGACCT

GAM1741  LOC131965 3'  TCCAGCCTGGGCGACAGAGTGA 75528           A
                GA                TCTCGCTCTGTC CCCAGGCTGGA
                                  |||||||||||| |||||||||||
                                  AGAGTGAGACAG GGGTCCGACCT
                                        C
GAM1741  LOC133926 3'  TCCAGCCTGGGCGACAGAGCGA 75634           A
                GA                TCTCGCTCTGTC CCCAGGCTGGA
                                  |||||||||||| |||||||||||
                                  AGAGCGAGACAG GGGTCCGACCT
                                        C
GAM1741  LOC134147 3'  TCCAGCCTGGACAACAGAGGGA 57967     G     CAC
                GA                TCTC CTCTGT   CCAGGCTGGA
                                  |||| ||||||   ||||||||||
                                  AGAG GAGACA   GGTCCGACCT
                                    G     ACA
GAM1741  LOC134147 3'  TCTAGCCTGGGCAGCAGAGTGA 57968          CA
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACG  GGGTCCGATCT
                                        AC
GAM1741  LOC135154 3'  TCCAGCCTGGGCAACAAGAGCG 75736       _  CA
                A                  TCGCTCT GT  CCCAGGCTGGA
                                   |||||||  ||  ||||||||||
                                   AGCGAGA CA  GGGTCCGACCT
                                       A  AC
GAM1741  LOC135818 3'  TCCAGCCTGGGCAATAGGGTAA 75749     CG     CA
                GA                TCT  CTCTGT  CCCAGGCTGGA
                                  |||  ||||||  ||||||||||
                                  AGA  GGGATA  GGGTCCGACCT
                                    AT     AC
GAM1741  LOC136442 3'  TTTGGTTTTGGCGGGGAGAGG  55261     G      CCC    TG
                                  TCTC CTCTGTCA   AGGC  GA
                                  |||| ||||||||   ||||  ||
                                  GGAG GGGGCGGT   TTTG  TT
                                    A       ___    GT
GAM1741  LOC138241 5'  TCCAGCCTACTAGCGGGCGGGG 75838       T   CACCC
                                  TCTCGC CTGT     AGGCTGGA
                                  ||||||| ||||    ||||||||
                                  GGGGCG GGCG     TCCGACCT
                                     _    ATCA_
GAM1741  LOC138389 3'  TCCAGCCTGGGCAACAAGAGTG 76744       _  CA
                A                  TCGCTCT GT  CCCAGGCTGGA
                                   |||||||  ||  ||||||||||
                                   AGTGAGA CA  GGGTCCGACCT
                                       A  AC
GAM1741  LOC138428 3'  ACTCCAGTCTGGGTGACAGAGT 75852
                GAGA                 TCTCGCTCTGTCACCCAGGCTGGA
                                     ||||||||||||||||||||||||
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                                AGAGTGAGACAGTGGGTCTGACCT
                                        CAC
GAM1741  LOC139422 3'  ATTCTAGCCTGGGTGACAGAGC 76342
                GAGA                TCTCGCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACAGTGGGTCCGATCT
                                        TAC
GAM1741  LOC142779 3'  GCAGCCTGGTGACAGAGTGAGA 76907          C     GA
                                    TCTCGCTCTGTCACC AGGCTG
                                    ||||||||||||||| ||||||
                                    AGAGTGAGACAGTGG TCCGAC
                                          _     GT
GAM1741  LOC142927 3'  TCTAGCCTGGGTGACAGAACGA 76952      C
                GA                  TCTCG TCTGTCACCCAGGCTGGA
                                    ||||| |||||||||||||||||
                                    AGAGC AGACAGTGGGTCCGATCT
                                       A
GAM1741  LOC142937 3'  TCCAGCCTGGGCCACAGAACGA 57447      C    CA
                GA                  TCTCG TCTGT  CCCAGGCTGGA
                                    ||||| |||||  ||||||||||
                                    AGAGC AGACA  GGGTCCGACCT
                                       A    CC
GAM1741  LOC142948 3'  ACTCCAGCCTGGGTGACAGAGC 83771
                GAGG                TCTCGCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    GGAGCGAGACAGTGGGTCCGACCT
                                        CAC
GAM1741  LOC142955 5'  TCTGGCATGTGGCAGGGTGA   76966          CCAG  TG
                                    TCGCTCTGTCAC    GC  GA
                                    ||||||||||||    ||  ||
                                    AGTGGGACGGTG    CG  CT
                                          TA__  GT
GAM1741  LOC143196 3'  TCCAGCTTGGCAACAGAGCGAG 83805          CAC
                A                    TCTCGCTCTGT   CCAGGCTGGA
                                    ||||||||||   ||||||||||
                                    AGAGCGAGACA   GGTTCGACCT
                                        AC_
GAM1741  LOC143310 3'  ACCCCAGCCTGGGTGACAGAGC 77031                A
                GAGA                TCTCGCTCTGTCACCCAGGCTGG
                                    |||||||||||||||||||||||
                                    AGAGCGAGACAGTGGGTCCGACC
                                        CCAC
GAM1741  LOC143465 3'  CTCCAGCCTGGGTGACGGAGTG 83872
                AGA                 TCTCGCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGGCAGTGGGTCCGACCT
                                        CA
GAM1741  LOC143677 3'  TTTGGTTTTTGTTTTGAGGGGG 83900        G   CC_  __  TG
                TGGGG                TCTCGCTCT TCA   CAG  GC  GA
                                    |||||||| |||   |||  ||  ||
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                                GGGGTGGGG AGT   GTT  TG  TT
                                     G   TTT   TT  GT
GAM1741  LOC143888 3'  CTCCAGCCTGGGTGACAGAGTG 77169
              AGA                  TCTCGCTCTGTCACCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGTGAGACAGTGGGTCCGACCT
                                         CA
GAM1741  LOC143916 5'  TTGGCACTGGTGGTAGTGGGG  77150        CTG    C  _  TG
                                   TCTCGCT   TCACC AG GC  GA
                                   |||||||   ||||| || ||  ||
                                   GGGGTGA   GGTGG TC CG  TT
                                      T__     _  A  GT
GAM1741  LOC143943 3'  ACTCCAGCCTGGGTGACAGAGC 83909
              GAGA                 TCTCGCTCTGTCACCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGCGAGACAGTGGGTCCGACCT
                                         CAC
GAM1741  LOC144289 3'  CTCCAGCCTGGGTGACAGAGTG 83958
              AGA                  TCTCGCTCTGTCACCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGTGAGACAGTGGGTCCGACCT
                                         CA
GAM1741  LOC144308 5'  TCCAGCCTGGGTGACAGAGC   83985
                                   GCTCTGTCACCCAGGCTGGA
                                   ||||||||||||||||||
                                   CGAGACAGTGGGTCCGACCT

GAM1741  LOC144465 3'  TCCAGCCTGGGCAACAAGAGTG 77352        _  CA
              A                     TCGCTCT GT  CCCAGGCTGGA
                                   |||||||  ||  ||||||||||
                                   AGTGAGA CA  GGGTCCGACCT
                                      A  AC
GAM1741  LOC144519 5'  TCCAGCCTGGGCGACAGAGTGA 77380           A
              GA                     TCTCGCTCTGTC CCCAGGCTGGA
                                   ||||||||||| ||||||||||
                                   AGAGTGAGACAG GGGTCCGACCT
                                         C
GAM1741  LOC144524 3'  TCCAGCCTGGGTGACAGAGTGG 84066
              GA                     TCTCGCTCTGTCACCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGGGTGAGACAGTGGGTCCGACCT
                                         C
GAM1741  LOC144563 3'  TCCAGCTTGGGCAACAGAGTAA 77405     CG     CA
              GA                     TCT  CTCTGT  CCCAGGCTGGA
                                   |||  ||||||  ||||||||||
                                   AGA  GAGACA  GGGTTCGACCT
                                     AT     AC
GAM1741  LOC144583 3'  TCCAGCCCGAGTGACAGAATGA 77422       C       CCA
              GG                     TCTCG TCTGTCAC   GGCTGGA
                                   |||||  ||||||||   |||||||
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                                GGAGT AGACAGTG   CCGACCT
                                  A       AGC
GAM1741  LOC144667 3'  TCTGGGAAATGCATGGGGTGGG 84089          _ ___     CTGGA
            A                    TCTCGCTCTGT CA   CCCAGG
                                 |||||||||||  ||   ||||||
                                 AGGGTGGGGTA GT   GGGTCT
                                       C  AAA        A
GAM1741  LOC145231 3'  TCCAGCCTGGGTGACAGTGTGA 84260      T
                                 TCGC CTGTCACCCAGGCTGGA
                                 |||| ||||||||||||||||
                                 AGTG GACAGTGGGTCCGACCT
                                   T
GAM1741  LOC145299 3'  TCCGGCCTGGGCGACAGAGCGA 84279           A
            GA                   TCTCGCTCTGTC CCCAGGCTGGA
                                 ||||||||||| ||||||||||
                                 AGAGCGAGACAG GGGTCCGGCCT
                                       C
GAM1741  LOC145333 3'  TCCAGCCTGGGCGACAGAGCGA 84304           A
            GA                   TCTCGCTCTGTC CCCAGGCTGGA
                                 ||||||||||| ||||||||||
                                 AGAGCGAGACAG GGGTCCGACCT
                                       C
GAM1741  LOC145387 3'  CTCCAGCCTGGGTGGCAGAGTG 84334
            AGA                   TCTCGCTCTGTCACCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACGGTGGGTCCGACCT
                                        CA
GAM1741  LOC145387 3'  TCCAGCCTGGGCGACAGAGAGA 84344      G      A
            GA                   TCTC CTCTGTC CCCAGGCTGGA
                                 |||| ||||||| ||||||||||
                                 AGAG GAGACAG GGGTCCGACCT
                                   A      C
GAM1741  LOC145438 3'  TCCAGCCTGGGCGACAGAGCGA 84316           A
            GA                   TCTCGCTCTGTC CCCAGGCTGGA
                                 ||||||||||| ||||||||||
                                 AGAGCGAGACAG GGGTCCGACCT
                                       C
GAM1741  LOC145438 3'  TCTAGCCTGGGTGACAGAGTGA 84318
            GA                   TCTCGCTCTGTCACCCAGGCTGGA
                                 ||||||||||||||||||||||||
                                 AGAGTGAGACAGTGGGTCCGATCT

GAM1741  LOC145438 3'  TCTGGCTTTTAAAATGGGATGA 84319      CT   CACCC   TG
            GG                   TCTCG  CTGT    AGGC  GA
                                 |||||  ||||    ||||  ||
                                 GGAGT  GGTA    TTCG  CT
                                   AG   AAATT   GT
GAM1741  LOC145453 3'  TTCAGCCTGGGCAACAGAGTGA 77674           CA
            GA                   TCTCGCTCTGT  CCCAGGCTGGA
                                 ||||||||||  ||||||||||
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                                AGAGTGAGACA  GGGTCCGACTT
                                      AC
GAM1741  LOC145482 3'  TCCAGCCTGGGCGACAAGAGTG 77747        _   A
                A                TCGCTCT GTC CCCAGGCTGGA
                                 ||||||| ||| ||||||||||
                                 AGTGAGA CAG GGGTCCGACCT
                                    A   C
GAM1741  LOC145608 5'  TCCAGCCTGGGTGACAGAGCAA 84386     C
                GA                 TCT GCTCTGTCACCCAGGCTGGA
                                   ||| ||||||||||||||||||||
                                   AGA CGAGACAGTGGGTCCGACCT
                                     A
GAM1741  LOC145609 3'  TCCAGCCTGGGTGACAGAGCAA 84370     C
                GA                 TCT GCTCTGTCACCCAGGCTGGA
                                   ||| ||||||||||||||||||||
                                   AGA CGAGACAGTGGGTCCGACCT
                                     A
GAM1741  LOC145663 3'  TCCAGCCTGGGCGACAGAGCTA 84430     C       A
                GA                 TCT GCTCTGTC CCCAGGCTGGA
                                   ||| |||||||| ||||||||||
                                   AGA CGAGACAG GGGTCCGACCT
                                     T       C
GAM1741  LOC145757 3'  TCCAGCCTAGGTGACAGAGCGA 77942              C
                GA                 TCTCGCTCTGTCACC AGGCTGGA
                                   |||||||||||||| ||||||||
                                   AGAGCGAGACAGTGG TCCGACCT
                                          A
GAM1741  LOC145820 3'  TCCAGCCTGGGCGACAGAGCAA 77980     C       A
                GA                 TCT GCTCTGTC CCCAGGCTGGA
                                   ||| |||||||| ||||||||||
                                   AGA CGAGACAG GGGTCCGACCT
                                     A       C
GAM1741  LOC145945 5'  TCCAGCCTGAGCAACAGAGCAA 84571     C      CACC
                GA                 TCT GCTCTGT    CAGGCTGGA
                                   ||| |||||||    |||||||||
                                   AGA CGAGACA    GTCCGACCT
                                     A       ACGA
GAM1741  LOC145988 5'  TCCAGCCTGGAAGGCAGAGAGA 78072      G      AC
                GA                 TCTC CTCTGTC  CCAGGCTGGA
                                   |||| |||||||  ||||||||||
                                   AGAG GAGACGG  GGTCCGACCT
                                     A       AA
GAM1741  LOC145989 3'  TCTGCCAGGGTGGTGGTGGCGG 60298        _ TG     A   T
                GG                 TCTCGCT C  TCACCC GGC GGA
                                   ||||||| |  |||||| ||| |||
                                   GGGGCGG G  GGTGGG CCG TCT
                                      T GT      A   _
GAM1741  LOC146059 3'  TCCAGTCTGGGTAACAGAGCGA 78090           C
                GA                 TCTCGCTCTGT ACCCAGGCTGGA
                                   ||||||||||| ||||||||||||
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                                AGAGCGAGACA TGGGTCTGACCT
                                      A
GAM1741  LOC146108 5'  TCTAGTCTGGGCTCTGGCAGAG 78153        ___
                                CTCTGTCA   CCCAGGCTGGA
                                ||||||||   ||||||||||
                                GAGACGGT   GGGTCTGATCT
                                    CTC
GAM1741  LOC146229 3'  TCCAGCCTGGGCGACAGAGCGA 78317           A
           GA                     TCTCGCTCTGTC CCCAGGCTGGA
                                  ||||||||||| ||||||||||
                                  AGAGCGAGACAG GGGTCCGACCT
                                        C
GAM1741  LOC146443 5'  TTCAGTTTGTAAGTAGTGAGA  78448       _ GTCACC
                                TCTCGCT CT     CAGGCTGGA
                                ||||||| ||     |||||||||
                                AGAGTGA GA     GTTTGACTT
                                    T  AT____
GAM1741  LOC146475 5'  CGGCCTCCGGAGCTGGGA    84689     _    TCACCC   TG
                                TCTC GCTCTG     AGGC  G
                                |||| ||||||     ||||  |
                                AGGG CGAGGC     TCCG  C
                                  T     C_____   GT
GAM1741  LOC146488 5'  CCAAGGTGGCAGAGTCAGG   71355     C        CAGGC
                                TCT GCTCTGTCACC    TGG
                                ||| ||||||||||    |||
                                GGA TGAGACGGTGG    ACC
                                  C         A____
GAM1741  LOC146713 3'  TCCAGCCTGGTCAACAGAGCAA 84741     C      CAC
           GA                     TCT GCTCTGT   CCAGGCTGGA
                                  ||| |||||||   ||||||||||
                                  AGA CGAGACA   GGTCCGACCT
                                    A       ACT
GAM1741  LOC146728 3'  TCCAGCCTGGGAAGCAGAGTGA 84774           CA
           GA                     TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACG  GGGTCCGACCT
                                        AA
GAM1741  LOC146756 3'  TCCAGCCTGGGCGACAGAGCGA 84813           A
           GA                     TCTCGCTCTGTC CCCAGGCTGGA
                                  ||||||||||| ||||||||||
                                  AGAGCGAGACAG GGGTCCGACCT
                                        C
GAM1741  LOC146895 3'  TCCAGCCTGGGTGACAAGAGC  84874      _
                                GCTCT GTCACCCAGGCTGGA
                                ||||| ||||||||||||||
                                CGAGA CAGTGGGTCCGACCT
                                   A
GAM1741  LOC146901 3'  TCCAGTTTGGGCAACAGAATGA 84913      C    CA
           GG                     TCTCG TCTGT  CCCAGGCTGGA
                                  ||||| |||||  ||||||||||
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                                GGAGT AGACA  GGGTTTGACCT
                                   A     AC
GAM1741  LOC146923 3'  TCCAGCCTGGGCGACAGAGTGA 78804            A
                GA                  TCTCGCTCTGTC CCCAGGCTGGA
                                    |||||||||||| ||||||||||
                                    AGAGTGAGACAG GGGTCCGACCT
                                          C
GAM1741  LOC146953 5'  TCCAGCCCACCCCAGGGGCGGG 78822          GTCACCCA
                G                   TCTCGCTCT       GGCTGGA
                                    |||||||||       |||||||
                                    GGGGCGGGG       CCGACCT
                                         ACCCCAC_
GAM1741  LOC146958 3'  TCCAGCCTGGGTGACACAGCGA 84946        C
                GA                  TCTCGCT TGTCACCCAGGCTGGA
                                    ||||||| ||||||||||||||||
                                    AGAGCGA ACAGTGGGTCCGACCT
                                       C
GAM1741  LOC146958 3'  TCCAGCCTGGGTGACAGAGCGA 84947
                GA                  TCTCGCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACAGTGGGTCCGACCT
                                                C
GAM1741  LOC147043 3'  TTTAGTTTTGCTTACAGAGCAG 88505     C      CACCC
                A                   TCT GCTCTGT     AGGCTGGA
                                    ||| |||||||     ||||||||
                                    AGA CGAGACA     TTTGATTT
                                    _       TTCGT
GAM1741  LOC147057 3'  CTGGGCGACAGAGTGAGA     84983            A
                                    TCTCGCTCTGTC CCCAG
                                    |||||||||||| |||||
                                    AGAGTGAGACAG GGGTC
                                          C
GAM1741  LOC147071 5'  CCGGCAGGGCAGGATGGGA    73358       CT     ACCCAG
                                    TCTCG  CTGTC     GCTGG
                                    |||||  |||||     |||||
                                    AGGGT  GACGG     CGGCC
                                       AG     GA____
GAM1741  LOC147071 3'  TCCAGCCTGGGCGACAGAGCAA 73373     C       A
                GA                  TCT GCTCTGTC CCCAGGCTGGA
                                    ||| |||||||| ||||||||||
                                    AGA CGAGACAG GGGTCCGACCT
                                      A       C
GAM1741  LOC147077 3'  CGGCTTGCGGCGCGAGG      78847        T   TCACC     TG
                                    TCTCGC CTG     CAGGC  G
                                    |||||| |||     |||||  |
                                    GGAGCG GGC     GTTCG  C
                                       C  _____     GT
GAM1741  LOC147080 3'  TCCAGCTTAGGTGACAGAGTGA 85052              C
                GA                  TCTCGCTCTGTCACC AGGCTGGA
                                    |||||||||||||| ||||||||
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                                AGAGTGAGACAGTGG TTCGACCT
                                      A
GAM1741  LOC147180 5'  TCCAGCCCGGGTGACAGAGTGA 85105            A
                                TCGCTCTGTCACCC GGCTGGA
                                ||||||||||||| |||||||
                                AGTGAGACAGTGGG CCGACCT
                                      C
GAM1741  LOC147229 5'  TCTAGGAGAGGGACAGAGTGGG 78927          A  CAGG
           A                    TCTCGCTCTGTC CC    CTGGA
                                |||||||||||| ||    |||||
                                AGGGTGAGACAG GG    GATCT
                                      _  AGAG
GAM1741  LOC147229 5'  TTGGTCTGGGACACGGTGGG   78929       C   CA      TG
                                CTCGCT TGT  CCCAGGC  GA
                                |||||| |||  |||||||  ||
                                GGGTGG ACA  GGGTCTG  TT
                                   C   __       GT
GAM1741  LOC147599 3'  TCCAGCCTGGGCAACAGAGAGA 85166    G     CA
                                TC CTCTGT  CCCAGGCTGGA
                                || ||||||  ||||||||||
                                AG GAGACA  GGGTCCGACCT
                                 A     AC
GAM1741  LOC147622 3'  TCCAGCCTGGGTGACAGAGCTA 85172     C
           GA                     TCT GCTCTGTCACCCAGGCTGGA
                                ||| ||||||||||||||||||
                                AGA CGAGACAGTGGGTCCGACCT
                                  T
GAM1741  LOC147649 3'  TCCAGAGCCTGGGCGACAGAGC 79064           A       __
           GAGA                     TCTCGCTCTGTC CCCAGGCT  GGA
                                |||||||||||| ||||||||  |||
                                AGAGCGAGACAG GGGTCCGA  CCT
                                      C       GA
GAM1741  LOC147660 3'  TCCAGGCTGGGCGACAGAGTGA 79032           A    G
           GA                     TCTCGCTCTGTC CCCAG CTGGA
                                |||||||||||| ||||| |||||
                                AGAGTGAGACAG GGGTC GACCT
                                      C     G
GAM1741  LOC147664 3'  TCCAGCCTGGGCAACGAGAGGG 79050      G   _  CA
           GA                     TCTC CTCT GT  CCCAGGCTGGA
                                |||| |||| ||  ||||||||||
                                AGGG GAGA CA  GGGTCCGACCT
                                  _    G  AC
GAM1741  LOC147669 3'  TCCAGCCTGGGTGACAAGGGAA 85186     _ G  C
           GA                     TCT C CT TGTCACCCAGGCTGGA
                                ||| | || ||||||||||||||||
                                AGA G GA ACAGTGGGTCCGACCT
                                  A G  _
GAM1741  LOC147727 5'  TCCAGCCTGGGCGATAGAGTGA 79139           A
           GA                     TCTCGCTCTGTC CCCAGGCTGGA
                                |||||||||||| ||||||||||
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                                AGAGTGAGATAG GGGTCCGACCT
                                      C
GAM1741  LOC147727 5'  TCCAGTCTGGGCGACAGAGCGA 79140           A
                  GA                  TCTCGCTCTGTC CCCAGGCTGGA
                                      |||||||||||| ||||||||||
                                      AGAGCGAGACAG GGGTCTGACCT
                                            C
GAM1741  LOC147741 3'  TCCAGCCTGGCGACTGAGCGAG 79144        T   AC
                  A                   TCTCGCTC GTC  CCAGGCTGGA
                                      |||||||| |||  ||||||||||
                                      AGAGCGAG CAG  GGTCCGACCT
                                           T   C_
GAM1741  LOC147791 5'  CCAGCTGCCAGGGGCGAGG    85189         GTCACCCA
                                      TCTCGCTCT       GGCTGG
                                      |||||||||       ||||||
                                      GGAGCGGGG       TCGACC
                                            ACCG____
GAM1741  LOC147949 3'  TTCAGTCTTATTTATAGTGTGG 79280       T    CACCC
                  GA                  TCTCGC CTGT     AGGCTGGA
                                      |||||| ||||     ||||||||
                                      AGGGTG GATA     TCTGACTT
                                         T    TTTAT
GAM1741  LOC148089 3'  CCAGGATGGCAGAGCCAGG    79327     C       C  AGGC
                                      TCT GCTCTGTCA CC    TGG
                                      ||| ||||||||| ||    |||
                                      GGA CGAGACGGT GG    ACC
                                        C        A _____
GAM1741  LOC148166 5'  TCAGTTTGGGAAGAGGAGA    79423     G    GTCA
                                      TCTC CTCT    CCCAGGCTGG
                                      |||| ||||    ||||||||||
                                      AGAG GAGA    GGGTTTGACT
                                        _    A____
GAM1741  LOC148166 3'  TCCAGCCTAGGCGACGGGGCAA 79424     C       A  C
                  GA                  TCT GCTCTGTC CC AGGCTGGA
                                      ||| |||||||| || ||||||||
                                      AGA CGGGGCAG GG TCCGACCT
                                        A       C  A
GAM1741  LOC148198 3'  TCCATCCTGGGTGACAAAGTGA 71228        C         C
                  GA                  TCTCGCT TGTCACCCAGG TGGA
                                      ||||||| |||||||||| ||||
                                      AGAGTGA ACAGTGGGTCC ACCT
                                         A         T
GAM1741  LOC148254 3'  CCAGCCTGGGAGACGGGG    79501        A
                                      CTCTGTC CCCAGGCTGG
                                      ||||||| ||||||||||
                                      GGGGCAG GGGTCCGACC
                                         A
GAM1741  LOC148343 3'  CCAGCCTGGGCGACAGGGTGAG 79540           A        A
                  A                   TCTCGCTCTGTC CCCAGGCTGG
                                      |||||||||||| ||||||||||
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                                AGAGTGGGACAG GGGTCCGACC
                                      C
GAM1741  LOC148534 3'  TCCAGCCTGGGCGACAGAGCAA 79640     C       A
                GA                TCT GCTCTGTC CCCAGGCTGGA
                                  ||| |||||||| ||||||||||
                                  AGA CGAGACAG GGGTCCGACCT
                                    A       C
GAM1741  LOC148710 3'  TGGGTGGTGATGGAGGAGG    85352      G        CAG   GGA
                                  TCTC CTCTGTCACC   GCT
                                  |||| ||||||||||   |||
                                  GGAG GAGGTAGTGG   TGG
                                    _        ___  GTG
GAM1741  LOC148775 5'  TCCAGGGCCCTGGCGGGGC    85379       TCAC    ___
                                  GCTCTG    CCAGG   CTGGA
                                  ||||||    |||||   |||||
                                  CGGGGC    GGTCC   GACCT
                                     _____     CGG
GAM1741  LOC148809 3'  TCCAGCCTGGGCGACAGAGCAA 79762     C       A
                GA                TCT GCTCTGTC CCCAGGCTGGA
                                  ||| |||||||| ||||||||||
                                  AGA CGAGACAG GGGTCCGACCT
                                    A       C
GAM1741  LOC148809 5'  TCCAGCCTGGGTGACAGAGCAA 79763     C
                GA                TCT GCTCTGTCACCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGTGGGTCCGACCT
                                    A
GAM1741  LOC148823 3'  TCCAGCTTGGGCAACAGAGTGA 59896           CA
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTTCGACCT
                                        AC
GAM1741  LOC148872 3'  TTCGGCCGCGCGCGGGCGGGG  85384       T    CACCCA
                                  TCTCGC CTGT     GGCTGGA
                                  |||||| ||||     |||||||
                                  GGGGCG GGCG     CCGGCTT
                                     _   CGCG__
GAM1741  LOC149073 3'  TCCAGCCTGGGCAACAGTGTGA 85487       T    CA
                GA                TCTCGC CTGT  CCCAGGCTGGA
                                  |||||| ||||  ||||||||||
                                  AGAGTG GACA  GGGTCCGACCT
                                     T    AC
GAM1741  LOC149113 3'  TCAGCCTGGGCGACCGAGA    79918      CTCT   A
                                  TCTCG    GTC CCCAGGCTGG
                                  |||||    ||| ||||||||||
                                  AGAGC    CAG GGGTCCGACT
                                     _____   C
GAM1741  LOC149175 3'  TCCAGCCTGGGCGACAGAGCGA 79957           A
                GA                TCTCGCTCTGTC CCCAGGCTGGA
                                  |||||||||||| ||||||||||
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                                AGAGCGAGACAG GGGTCCGACCT
                                       C
GAM1741  LOC149271 3'  TCCAGCCTGGGCAACAAGAGTG 80012       _  CA
              A                 TCGCTCT GT  CCCAGGCTGGA
                                ||||||| ||  ||||||||||
                                AGTGAGA CA  GGGTCCGACCT
                                    A  AC
GAM1741  LOC149297 5'  TCCGGCTACGGGGCGGGGCCGG 85544     C       A  CA
              G                 TCT GCTCTGTC CC  GGCTGGA
                                ||| |||||||| ||  |||||||
                                GGG CGGGGCGG GG  TCGGCCT
                                  C       _  CA
GAM1741  LOC149373 3'  CCAGTGTAGGAGGGTGGGA    80092         GTCA  CAG
                                TCTCGCTCT    CC   GCTGG
                                |||||||||    ||   |||||
                                AGGGTGGGA    GG   TGACC
                                     ____  ATG
GAM1741  LOC149386 3'  CGGAGCTGGGGAGTGGGA     85555        TGTCA    G_ TG
                                TCTCGCTC     CCCAG  C  G
                                ||||||||     |||||  |  |
                                AGGGTGAG     GGGTC  G  C
                                     _____     GA GT
GAM1741  LOC149464 5'  TTCAGCTTGGGTGACAGAGCCA 85602     C
              GA                  TCT GCTCTGTCACCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGTGGGTTCGACTT
                                    C
GAM1741  LOC149506 3'  TCTATGGGGGGTGGGGCGAGG  85650         TG  A   GGC
                                TCTCGCTC  TC CCCA   TGGA
                                ||||||||  || ||||   ||||
                                GGAGCGGG  GG GGGT   ATCT
                                     GT  G   ___
GAM1741  LOC149579 5'  TCCAGCCTGTGTGACAGAGCAA 71695     C        C
              GA                  TCT GCTCTGTCAC CAGGCTGGA
                                  ||| |||||||||| |||||||||
                                  AGA CGAGACAGTG GTCCGACCT
                                    A         T
GAM1741  LOC149628 3'  ACTCCAGCCTGGGTGACAGAGC 80272
              GAGA                  TCTCGCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACAGTGGGTCCGACCT
                                                CAC
GAM1741  LOC149668 5'  GTCTGCCTGGGTGTGGGGTGAG 85702          T       T  A
              G                   TCTCGCTCTG CACCCAGGC GG
                                  |||||||||| ||||||||| ||
                                  GGAGTGGGGT GTGGGTCCG CT
                                       _       T  GT
GAM1741  LOC149672 5'  TCCAGCCTGGGCAACAGAGTGA 80339          CA
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
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                                AGAGTGAGACA  GGGTCCGACCT
                                      AC
GAM1741  LOC149705 3'  TCCAGCCTGGGTGACGAGTGA  85787       T
                                TCGCTC GTCACCCAGGCTGGA
                                |||||| ||||||||||||||||
                                AGTGAG CAGTGGGTCCGACCT
                                  _
GAM1741  LOC149707 3'  TCTAGCCTGGGTGACAGAATGA 80299       C
              GA                  TCTCG TCTGTCACCCAGGCTGGA
                                  ||||| ||||||||||||||||||
                                  AGAGT AGACAGTGGGTCCGATCT
                                    A
GAM1741  LOC149711 3'  ACTCCAGCCTGGGTGACAGAGT 85834
              GAGA                  TCTCGCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAGTGGGTCCGACCT
                                                CAC
GAM1741  LOC149721 5'  TTCAGGGGATGGCAGAGCTGGG 80322     C       _  AGG
                                TCT GCTCTGTCA CCC   CTGGA
                                ||| ||||||||| |||   |||||
                                GGG CGAGACGGT GGG   GACTT
                                  T       A  ___
GAM1741  LOC149952 3'  TCCAGCCTGGGCAATAGAGTGA 80372           CA
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                  |||||||||||  ||||||||||
                                  AGAGTGAGATA  GGGTCCGACCT
                                      AC
GAM1741  LOC150095 3'  TCCAGCCTGGGCAACAGAGCGA 85996           CA
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                  |||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                      AC
GAM1741  LOC150139 3'  TCCAGCCTGGGTGACAGAGAGA 80413     G
                                TC CTCTGTCACCCAGGCTGGA
                                || ||||||||||||||||||
                                AG GAGACAGTGGGTCCGACCT
                                 A
GAM1741  LOC150142 5'  ACTCCAGCTTGGGTGACAGAGT 80397
              GAGA                  TCTCGCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAGTGGGTTCGACCT
                                                CAC
GAM1741  LOC150174 3'  TCCAGCCTGGTCAACAGAGTGA 80441           CAC
              GA                    TCTCGCTCTGT   CCAGGCTGGA
                                    ||||||||||   ||||||||||
                                    AGAGTGAGACA   GGTCCGACCT
                                        ACT
GAM1741  LOC150185 3'  ACTCCAGCCTGGGTGACAGAGC 86058
              GAGA                  TCTCGCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||||||
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                                AGAGCGAGACAGTGGGTCCGACCT
                                        CAC
GAM1741  LOC150197 3'  TCCAGGCCCTGGCAGGTGGGG  80427      T     CCCA  _
                                TCTCGC CTGTCA    GGC TGGA
                                |||||| ||||||    ||| ||||
                                GGGGTG GACGGT    CCG ACCT
                                   _     C___   G
GAM1741  LOC150213 3'  TCCAGCCTGGTCAACAGAGTGA 75360          CAC
            GA                    TCTCGCTCTGT   CCAGGCTGGA
                                |||||||||||   ||||||||||
                                AGAGTGAGACA   GGTCCGACCT
                                      ACT
GAM1741  LOC150225 3'  TCCAGCCTGGGCGTCAGAGTGA 86206          TCA
            GA                    TCTCGCTCTG   CCCAGGCTGGA
                                |||||||||   ||||||||||
                                AGAGTGAGAC   GGGTCCGACCT
                                      TGC
GAM1741  LOC150236 3'  TCCAGCCTGGTCAACAGAGTGA 80503          CAC
            GA                    TCTCGCTCTGT   CCAGGCTGGA
                                |||||||||||   ||||||||||
                                AGAGTGAGACA   GGTCCGACCT
                                      ACT
GAM1741  LOC150244 3'  TCCAGCCTGGGCGACAGAGCGA 80552           A
            GA                    TCTCGCTCTGTC CCCAGGCTGGA
                                |||||||||||| ||||||||||
                                AGAGCGAGACAG GGGTCCGACCT
                                      C
GAM1741  LOC150245 3'  TCCAGCCTGGGTGACAGAATAA 86119     CGC
            GA                    TCT   TCTGTCACCCAGGCTGGA
                                |||   ||||||||||||||||||
                                AGA   AGACAGTGGGTCCGACCT
                                  ATA
GAM1741  LOC150299 3'  TCCAGCCTGGCGACAGAGCAAG 86170     C       AC
            A                     TCT GCTCTGTC  CCAGGCTGGA
                                |||| ||||||||  ||||||||||
                                AGA CGAGACAG  GGTCCGACCT
                                  A       C_
GAM1741  LOC150319 3'  TCCAGCCTGGGCAACAAGAGCG 80477        _  CA
            A                     TCGCTCT GT  CCCAGGCTGGA
                                |||||||  ||  ||||||||||
                                AGCGAGA CA  GGGTCCGACCT
                                    A  AC
GAM1741  LOC150358 3'  TCCAGCCTGGGCGACAGAGCGA 86101           A
            GA                    TCTCGCTCTGTC CCCAGGCTGGA
                                |||||||||||| ||||||||||
                                AGAGCGAGACAG GGGTCCGACCT
                                      C
GAM1741  LOC150372 3'  TTGGCCCAAGGGAGGGTGGGG  80624         GTCA  A__   TG
                                TCTCGCTCT    CCC   GGC  GA
                                |||||||||    |||   |||  ||
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                                GGGGTGGGA   GGG  CCG  TT
                                    ____  AAC  GT
GAM1741  LOC150577 3'  TCCAGCCTGGATGACAGAGTGA 86260          C
                                TCGCTCTGTCA CCAGGCTGGA
                                |||||||||| ||||||||||
                                AGTGAGACAGT GGTCCGACCT
                                    A
GAM1741  LOC150606 3'  TCTAGTTTGATTAGGAGCTAGA 86274    C    GTCACC
                                TCT GCTCT     CAGGCTGGA
                                ||| |||||     |||||||||
                                AGA CGAGG     GTTTGATCT
                                  T    ATTA__
GAM1741  LOC150630 5'  TCCAGCCTGGGCAGCAGAGTGA 86307          CA
           GA                     TCTCGCTCTGT  CCCAGGCTGGA
                                |||||||||||  ||||||||||
                                AGAGTGAGACG  GGGTCCGACCT
                                    AC
GAM1741  LOC150848 5'  TTTGGCAACAGGCACGGGTGAG 86322        _   ACCCAG  TG
           G                     TCTCGCTC TGTC     GC  GA
                                |||||||| ||||     ||  ||
                                GGAGTGGG ACGG     CG  TT
                                    C   ACAA__  GT
GAM1741  LOC150889 3'  TCCAGCCTGCGGGACAGAGTGA 80819          A  _
           GA                     TCTCGCTCTGTC CC CAGGCTGGA
                                |||||||||||| || |||||||||
                                AGAGTGAGACAG GG GTCCGACCT
                                    _  C
GAM1741  LOC150960 3'  TCCAGCTTGGGCAACAAAGTGA 80879       C   CA
           GA                     TCTCGCT TGT  CCCAGGCTGGA
                                |||||||| |||  ||||||||||||
                                AGAGTGA ACA  GGGTTCGACCT
                                   A   AC
GAM1741  LOC150998 3'  GCAGCCTGGGTGACAGAGCAAG 86359    C             GA
           A                     TCT GCTCTGTCACCCAGGCTG
                                ||| ||||||||||||||||||
                                AGA CGAGACAGTGGGTCCGAC
                                  A              GT
GAM1741  LOC151005 5'  CTAGTCTTGTCAGGGCGG    80896        T  CCC
                                TCGCTCTG CA   AGGCTGG
                                |||||||| ||   |||||||
                                GGCGGGAC GT   TCTGATC
                                    T  ____
GAM1741  LOC151040 3'  TCCGGGGACTGTTGTGGGGTGG 80908         T  CC   G__
           GG                     TCTCGCTCTG CA  CAG   CTGGA
                                |||||||||| ||  |||   |||||
                                GGGGTGGGGT GT  GTC   GGCCT
                                    _  T_   AGG
GAM1741  LOC151057 3'  TCTGAGGCTGGGGCGGGGTGGG 86399          CA    G  _
           G                     TCTCGCTCTGT  CCCAG CT GGA
                                ||||||||||  ||||| || |||
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                                GGGGTGGGGCG  GGGTC GA TCT
                                     __    G  G
GAM1741  LOC151248 3'  TCCAGCCCAGGTAACAGAGTGA 80998          C   CA
                GA                TCTCGCTCTGT ACC  GGCTGGA
                                  |||||||||| |||  |||||||
                                  AGAGTGAGACA TGG  CCGACCT
                                       A   AC
GAM1741  LOC151248 5'  TCCCGCCTGGGCGACAGAGCGA 81000           A      T
                GA                TCTCGCTCTGTC CCCAGGC GGA
                                  |||||||||||| ||||||| |||
                                  AGAGCGAGACAG GGGTCCG CCT
                                       C      C
GAM1741  LOC151429 5'  CCTGGTGGGCGGGGTGGGG    86533           AC
                                  TCTCGCTCTGTC  CCAGG
                                  ||||||||||||  |||||
                                  GGGGTGGGGCGG  GGTCC
                                       GT
GAM1741  LOC151429 3'  TCCAGCCTGGGCGACAGAGCAA 86549     C       A
                GA                TCT GCTCTGTC CCCAGGCTGGA
                                  ||| |||||||| ||||||||||
                                  AGA CGAGACAG GGGTCCGACCT
                                    A       C
GAM1741  LOC151429 3'  TCCAGCCTGGGTGACAGAGCAA 86550     C
                GA                TCT GCTCTGTCACCCAGGCTGGA
                                  ||| ||||||||||||||||||
                                  AGA CGAGACAGTGGGTCCGACCT
                                    A
GAM1741  LOC151556 3'  TCCAGCCTGAGCAACAGAGCAA 81085     C      CACC
                GA                TCT GCTCTGT    CAGGCTGGA
                                  ||| |||||||    |||||||||
                                  AGA CGAGACA    GTCCGACCT
                                    A       ACGA
GAM1741  LOC151556 5'  TCTGGTTGGAGTTGGAGGGTGA 81086          G  _ _   G TG
                GA                TCTCGCTCT TCA C CCAG C  GA
                                  ||||||||| ||| | |||| |  ||
                                  AGAGTGGGA GGT G GGTT G  CT
                                       _   T A    _ GT
GAM1741  LOC151602 3'  CTCCAGCTTGGGTGACAGAGCG 81109
                AGA                TCTCGCTCTGTCACCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGCGAGACAGTGGGTTCGACCT
                                             CA
GAM1741  LOC151632 3'  TCCAGCCTGGGCAACAGAGTAA 86651     CG     CA
                GA                TCT  CTCTGT  CCCAGGCTGGA
                                  |||  ||||||  ||||||||||
                                  AGA  GAGACA  GGGTCCGACCT
                                    AT     AC
GAM1741  LOC151658 5'  TCTGGAGTGCTGTGGTGGAGTG 86656    T    TG   C_  GG TG
                GA                TC CGCTC  TCAC  CA  C  GA
                                  || |||||  ||||  ||  |  ||
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                                AG GTGAG  GGTG  GT  G  CT
                                 _    GT    TC  GA GT
GAM1741  LOC151720 3'  TCCAGCCTGGGCGACAGAGCGA 81158          A
                GA                TCTCGCTCTGTC CCCAGGCTGGA
                                  |||||||||||| ||||||||||
                                  AGAGCGAGACAG GGGTCCGACCT
                                        C
GAM1741  LOC151904 3'  TCCAGCCTGGGCAACAGAGCGA 81210          CA
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  |||||||||||  ||||||||||
                                  AGAGCGAGACA  GGGTCCGACCT
                                        AC
GAM1741  LOC152002 3'  TCCAGCCTGGACGACAGAGTGA 81268          AC
                GA                TCTCGCTCTGTC  CCAGGCTGGA
                                  ||||||||||||  ||||||||||
                                  AGAGTGAGACAG  GGTCCGACCT
                                        CA
GAM1741  LOC152106 3'  TCCAGCCTGGTCGACAGAGTGA 70598          AC
                GA                TCTCGCTCTGTC  CCAGGCTGGA
                                  ||||||||||||  ||||||||||
                                  AGAGTGAGACAG  GGTCCGACCT
                                        CT
GAM1741  LOC152263 3'  TCCAGCCAGGATGACAGAGCAA 86860     C       C  A
                GA                TCT GCTCTGTCA CC GGCTGGA
                                  ||| |||||||| || |||||||
                                  AGA CGAGACAGT GG CCGACCT
                                    A       A  A
GAM1741  LOC152271 3'  TCCAGCCTGGGCAACAGAGTAA 81365     CG     CA
                GA                TCT  CTCTGT  CCCAGGCTGGA
                                  |||  ||||||  ||||||||||||
                                  AGA  GAGACA  GGGTCCGACCT
                                    AT     AC
GAM1741  LOC152283 3'  TCCAGCCTGGGCAACAAGAGTG 86875          _  CA
                AGA                TCTCGCTCT GT  CCCAGGCTGGA
                                   |||||||||  ||  ||||||||||
                                   AGAGTGAGA CA  GGGTCCGACCT
                                         A  AC
GAM1741  LOC152313 5'  CGCTGGATCGTGTGGTGGGGCG 86849        TG  _________  AGGCT
                GGG                 TCTCGCTC  TCAC       CC    G
                                    ||||||||  ||||       ||    |
                                    GGGGCGGG  GGTG       GG    C
                                       GT    TGCT   A  TCGG
GAM1741  LOC152313 3'  CTCCAGCCTGGGTGACAGAGCG 86851
                AGA                 TCTCGCTCTGTCACCCAGGCTGGA
                                    |||||||||||||||||||||||||
                                    AGAGCGAGACAGTGGGTCCGACCT
                                                CA
GAM1741  LOC152316 3'  TCCAGCCTAGGCAACAGAGCGA 86794          CA  C
                GA                TCTCGCTCTGT  CC AGGCTGGA
                                  ||||||||||  || ||||||||
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                                AGAGCGAGACA  GG TCCGACCT
                                      AC  A
GAM1741  LOC152426 3'  TCCAGCCTGGGCGACAGAGTGA 86902           A
              GA                  TCTCGCTCTGTC CCCAGGCTGGA
                                  |||||||||||| ||||||||||
                                  AGAGTGAGACAG GGGTCCGACCT
                                       C
GAM1741  LOC152445 3'  TCCAGTCTGGGTAAGAAGAGTG 86966       GTC_
              A                   TCGCTCT    ACCCAGGCTGGA
                                  |||||||    ||||||||||||
                                  AGTGAGA    TGGGTCTGACCT
                                     AGAA
GAM1741  LOC152453 3'  ACTCCAGCTTGGGTGACAGAGT 81461
              GAGA                  TCTCGCTCTGTCACCCAGGCTGGA
                                  |||||||||||||||||||||||||
                                  AGAGTGAGACAGTGGGTTCGACCT
                                            CAC
GAM1741  LOC152453 3'  CTCCAGCTTGGGTGACAGAGCG 81472
              AGA                   TCTCGCTCTGTCACCCAGGCTGGA
                                  |||||||||||||||||||||||||
                                  AGAGCGAGACAGTGGGTTCGACCT
                                            CA
GAM1741  LOC152453 3'  TCCAGCCTGGGCAACAAGAGCG 81480       _  CA
              A                   TCGCTCT GT  CCCAGGCTGGA
                                  ||||||| ||  ||||||||||
                                  AGCGAGA CA  GGGTCCGACCT
                                     A  AC
GAM1741  LOC152627 5'  TCCAGCCTGGATAAAAGAGCAA 81515     C     GTCAC
              GA                    TCT GCTCT     CCAGGCTGGA
                                  ||| |||||     ||||||||||
                                  AGA CGAGA     GGTCCGACCT
                                    A     AAATA
GAM1741  LOC152627 3'  TCCAGCCTGGGCCACAGAGTGA 81516           CA
              GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                        CC
GAM1741  LOC152641 3'  TCTAGTTCCCGGTGGAATGAG  81520     TG_    CA_
                                  CTC   TCACC   GGCTGGA
                                  |||   |||||   |||||||
                                  GAG   GGTGG   TTGATCT
                                    TAA     CCC
GAM1741  LOC152804 3'  TCCAGCCTGGGCAACAGAGCGA 87088           CA
              GG                    TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  GGAGCGAGACA  GGGTCCGACCT
                                        AC
GAM1741  LOC152804 3'  TCCGGCCTGGGGACAAGAGCAA 87089     C     _   A
              GA                    TCT GCTCT GTC CCCAGGCTGGA
                                  ||| ||||| ||| ||||||||||
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                                AGA CGAGA CAG GGGTCCGGCCT
                                  A    A  _
GAM1741  LOC152860 3'  TCCAGCCTGGGCAGCAAGAGTG 81582       _  CA
                  A                TCGCTCT GT  CCCAGGCTGGA
                                   ||||||| ||  ||||||||||
                                   AGTGAGA CG  GGGTCCGACCT
                                      A  AC
GAM1741  LOC152897 3'  TCCCAGCCTGGGAGACAGAGTG 81610          A        A
                  AGA               TCTCGCTCTGTC CCCAGGCTGG
                                   |||||||||||| ||||||||||
                                   AGAGTGAGACAG GGGTCCGACC
                                         A         CTA
GAM1741  LOC153077 3'  TCCAGCCTGGGCTACAGAGCAA 87133     C      CA
                  GA                TCT GCTCTGT  CCCAGGCTGGA
                                   ||| |||||||  ||||||||||
                                   AGA CGAGACA  GGGTCCGACCT
                                     A       TC
GAM1741  LOC153146 3'  TCCAGCCTGGGTGACAGAGGGA 87148      G
                  GA                TCTC CTCTGTCACCCAGGCTGGA
                                   |||| ||||||||||||||||||
                                   AGAG GAGACAGTGGGTCCGACCT
                                     G
GAM1741  LOC153338 3'  TCCAGCCTGGGTGACAGAGCAA 87198     C
                  GA                TCT GCTCTGTCACCCAGGCTGGA
                                   ||| ||||||||||||||||||
                                   AGA CGAGACAGTGGGTCCGACCT
                                     A
GAM1741  LOC153505 5'  TCTAGTGCTGGGTGTGGAGTGA 81708          T      _
                  GG                TCTCGCTCTG CACCCAG GCTGGA
                                   |||||||||| ||||||| ||||||
                                   GGAGTGAGGT GTGGGTC TGATCT
                                         _      G
GAM1741  LOC153577 5'  TCTGGAGCGGGCAGAGCGGGG  87244          AC__
                                   TCTCGCTCTGTC    CCAGG
                                   ||||||||||||    |||||
                                   GGGGCGAGACGG    GGTCT
                                         GCGA
GAM1741  LOC153579 3'  TCCAGCCTGGGCGACAGAGCGA 81774          A
                  GA                TCTCGCTCTGTC CCCAGGCTGGA
                                   |||||||||||| ||||||||||
                                   AGAGCGAGACAG GGGTCCGACCT
                                         C
GAM1741  LOC153642 3'  TCCAGCCTGGCAACAGAGTGAG 81793          CAC
                  A                 TCTCGCTCTGT   CCAGGCTGGA
                                   ||||||||||   ||||||||||
                                   AGAGTGAGACA   GGTCCGACCT
                                         AC_
GAM1741  LOC153682 3'  TCCAGCCTGAGCGACAGAGCAA 87276     C      ACC
                  GA                TCT GCTCTGTC   CAGGCTGGA
                                   ||| ||||||||   |||||||||
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                                AGA CGAGACAG   GTCCGACCT
                                  A       CGA
GAM1741  LOC153688 3'  TCCAGCCTGGGCGACAGAGGGA 87333      G      A
                GA                TCTC CTCTGTC CCCAGGCTGGA
                                  |||| ||||||| ||||||||||
                                  AGAG GAGACAG GGGTCCGACCT
                                    G      C
GAM1741  LOC153688 3'  TCTGAGTGGTGGTGGAGGGTGG 87337         G    CAG  _
                GG                TCTCGCTCT TCACC   GCT GGA
                                  ||||||||| |||||   ||| |||
                                  GGGGTGGGA GGTGG   TGA TCT
                                       _    TGG   G
GAM1741  LOC153727 3'  TCTAGCCTGGGTGACAGAGAGA 87364      G
                GA                TCTC CTCTGTCACCCAGGCTGGA
                                  |||| ||||||||||||||||||
                                  AGAG GAGACAGTGGGTCCGATCT
                                    A
GAM1741  LOC154089 3'  TTTAGTCTGGGTGACAGAGCAA 81949     C
                GA                TCT GCTCTGTCACCCAGGCTGGA
                                  ||| ||||||||||||||||||
                                  AGA CGAGACAGTGGGTCTGATTT
                                    A
GAM1741  LOC154386 3'  TCCAGCAGGGGAGGGGTGGGA  81990         G  A   AG
                                  TCTCGCTCT TC CCC  GCTGGA
                                  ||||||||| || |||  ||||||
                                  AGGGTGGGG AG GGG  CGACCT
                                       _ _   A_
GAM1741  LOC154403 3'  TCAGCCTGGGCGACCGAGA    81983       CTCT   A
                                  TCTCG    GTC CCCAGGCTGG
                                  |||||    ||| ||||||||||
                                  AGAGC    CAG GGGTCCGACT
                                     _____   C
GAM1741  LOC154739 5'  TCCAGCCTGGGCAACAGGTGAG 87443        T    CA
                A                  TCTCGC CTGT  CCCAGGCTGGA
                                  |||||| ||||  ||||||||||
                                  AGAGTG GACA  GGGTCCGACCT
                                     _    AC
GAM1741  LOC154739 3'  TCCAGCCTGGGTGACAGAGTGA 87444
                GA                TCTCGCTCTGTCACCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGTGAGACAGTGGGTCCGACCT

GAM1741  LOC154834 3'  TCCAGTCTTCTGGGGTGGGG   87497         GTCACCC
                                  TCTCGCTCT      AGGCTGGA
                                  |||||||||      ||||||||
                                  GGGGTGGGG      TCTGACCT
                                        TCT_____
GAM1741  LOC154877 3'  TCCAGCCTAGGTGATAGAGCAA 87576     C         C
                GA                TCT GCTCTGTCACC AGGCTGGA
                                  ||| |||||||||| ||||||||
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                                AGA CGAGATAGTGG TCCGACCT
                                  A          A
GAM1741  LOC154992 3'  TTCAGCCTGGGTGACCAAG    82145    CT
                                CT  GTCACCCAGGCTGGA
                                ||  ||||||||||||||
                                GA  CAGTGGGTCCGACTT
                                 AC
GAM1741  LOC155006 3'  TCCAGCCTGGGCGGCAGAGCAA 82176     C       A
           GA                     TCT GCTCTGTC CCCAGGCTGGA
                                ||| |||||||| ||||||||||
                                AGA CGAGACGG GGGTCCGACCT
                                  A       C
GAM1741  LOC155054 3'  TCCAGCCTGGGTGACAGAGCAA 82206     C
           GA                     TCT GCTCTGTCACCCAGGCTGGA
                                ||| ||||||||||||||||||
                                AGA CGAGACAGTGGGTCCGACCT
                                  A
GAM1741  LOC155072 3'  TCCAACCTGGGTGACAGAGCGA 87672               C
                                TCGCTCTGTCACCCAGG TGGA
                                |||||||||||||||| ||||
                                AGCGAGACAGTGGGTCC ACCT
                                           A
GAM1741  LOC155072 3'  TCCAGCCTGGGTGACTGAGCGA 87673         T
           GA                     TCTCGCTC GTCACCCAGGCTGGA
                                |||||||| ||||||||||||||
                                AGAGCGAG CAGTGGGTCCGACCT
                                     T
GAM1741  LOC155376 3'  ACTCCAGTCTGGGTGACAGAGT 82236
           GAGA                     TCTCGCTCTGTCACCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGACAGTGGGTCTGACCT
                                              CAC
GAM1741  LOC155376 3'  TCCAGCCTGGGTGACAAAGCAA 82251     C   C
           GA                     TCT GCT TGTCACCCAGGCTGGA
                                ||| ||| ||||||||||||||||
                                AGA CGA ACAGTGGGTCCGACCT
                                  A   A
GAM1741  LOC157464 5'  TCCAGCCTGGGCAACGGGCGAG 87752       T    CA
           A                      TCTCGC CTGT  CCCAGGCTGGA
                                ||||||| ||||  ||||||||||||
                                AGAGCG GGCA  GGGTCCGACCT
                                   _    AC
GAM1741  LOC157562 5'  TCCAGCCTGGGCAACATAGTGA 87776        C   CA
           GA                     TCTCGCT TGT  CCCAGGCTGGA
                                ||||||| |||  ||||||||||||
                                AGAGTGA ACA  GGGTCCGACCT
                                     T   AC
GAM1741  LOC157567 5'  TCCAGCTGCTCGGCCGGGGCGA 82394          TCA  CA__
           GA                     TCTCGCTCTG   CC    GGCTGGA
                                ||||||||||   ||    |||||||
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                                AGAGCGGGGC   GG    TCGACCT
                                      C__  CTCG
GAM1741  LOC157657 3'  TCCAGCCTGGACAACACAGTGA 82437        C   CAC
            GA                   TCTCGCT TGT   CCAGGCTGGA
                                 ||||||| |||   ||||||||||
                                 AGAGTGA ACA   GGTCCGACCT
                                    C   ACA
GAM1741  LOC157663 3'  TGCAGCAGGGTGGCAGGGTCAG 82456     C          AG    GA
            G                    TCT GCTCTGTCACCC  GCTG
                                 ||| ||||||||||||  ||||
                                 GGA TGGGACGGTGGG  CGAC
                                   C          A_    GTT
GAM1741  LOC157737 3'  TCCAGCCTGGGCAACAGAGAGA 87846      G     CA
            GA                   TCTC CTCTGT  CCCAGGCTGGA
                                 |||| ||||||  ||||||||||
                                 AGAG GAGACA  GGGTCCGACCT
                                   A      AC
GAM1741  LOC157848 3'  CCAGCTGTTGGGGCGGGG     82517        A  CA_
                                 CTCTGTC CC   GGCTGG
                                 ||||||| ||   ||||||
                                 GGGGCGG GG   TCGACC
                                    _  TTG
GAM1741  LOC158088 3'  TCCAGCCTGGCGACAGAGCAAG 87978     C       AC
            A                    TCT GCTCTGTC  CCAGGCTGGA
                                 ||| ||||||||  ||||||||||
                                 AGA CGAGACAG  GGTCCGACCT
                                   A       C_
GAM1741  LOC158187 3'  TCCAGCCTGGGTGACAGAGCAA 87998     C
            GA                   TCT GCTCTGTCACCCAGGCTGGA
                                 ||| ||||||||||||||||||||
                                 AGA CGAGACAGTGGGTCCGACCT
                                   A
GAM1741  LOC158191 3'  TCCAGCCTGGCGACAGAGCTAG 82682     C       AC
            A                    TCT GCTCTGTC  CCAGGCTGGA
                                 ||| ||||||||  ||||||||||
                                 AGA CGAGACAG  GGTCCGACCT
                                   T       C_
GAM1741  LOC158292 5'  TCCAGCCTGGGCAACAGAGCAA 88056     C      CA
            GA                   TCT GCTCTGT  CCCAGGCTGGA
                                 ||| |||||||  ||||||||||
                                 AGA CGAGACA  GGGTCCGACCT
                                   A      AC
GAM1741  LOC158292 5'  TCCAGCCTGGGCGACAGAGCGA 88057           A
            GA                   TCTCGCTCTGTC CCCAGGCTGGA
                                 ||||||||||| ||||||||||
                                 AGAGCGAGACAG GGGTCCGACCT
                                        C
GAM1741  LOC158337 3'  ATTCCAGCCTGGGTGACAGAGC 88107
            GAGA                   TCTCGCTCTGTCACCCAGGCTGGA
                                   ||||||||||||||||||||||||
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                                AGAGCGAGACAGTGGGTCCGACCT
                                      TAC
GAM1741  LOC158434 3'  TCTAGCCTGGGTGACAAAGTGA 88163        C
                GA                TCTCGCT TGTCACCCAGGCTGGA
                                  ||||||| ||||||||||||||||
                                  AGAGTGA ACAGTGGGTCCGATCT
                                     A
GAM1741  LOC158677 5'  TCCAGCCTGGGTGACAGAGCAA 88252     C
                GA                TCT GCTCTGTCACCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGTGGGTCCGACCT
                                    A
GAM1741  LOC158819 3'  ACTCCAGCCTGGGTGACAGAGC 88263
                GAGA                TCTCGCTCTGTCACCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAGTGGGTCCGACCT
                                        CAC
GAM1741  LOC158987 3'  TCCAGCCTGGGCAACAGAGGGA 88333    G     CA
                                  TC CTCTGT  CCCAGGCTGGA
                                  || ||||||  ||||||||||||
                                  AG GAGACA  GGGTCCGACCT
                                   G     AC
GAM1741  LOC158987 3'  TCCAGCCTGGGCAACATAGTGA 88335        C   CA
                GA                TCTCGCT TGT  CCCAGGCTGGA
                                  ||||||| |||  ||||||||||||
                                  AGAGTGA ACA  GGGTCCGACCT
                                     T   AC
GAM1741  LOC158987 3'  TCCAGCCTGGGTGACAGAGCGA 88336
                GA                TCTCGCTCTGTCACCCAGGCTGGA
                                  ||||||||||||||||||||||||
                                  AGAGCGAGACAGTGGGTCCGACCT
                                        C
GAM1741  LOC159036 3'  TCCAGCCTGGGCGACAGAGTGA 88351           A
                GG                TCTCGCTCTGTC CCCAGGCTGGA
                                  |||||||||||| ||||||||||
                                  GGAGTGAGACAG GGGTCCGACCT
                                        C
GAM1741  LOC159053 3'  TCCAGCCTGGGCAACAGTGAGA 88377        CT  CA
                                  TCTCGCT  GT  CCCAGGCTGGA
                                  |||||||  ||  ||||||||||||
                                  AGAGTGA  CA  GGGTCCGACCT
                                     __  AC
GAM1741  LOC159053 3'  TCCTGCTTGGGCGACAGAGTGA 88378           A      T
                GA                TCTCGCTCTGTC CCCAGGC GGA
                                  |||||||||||| ||||||| |||
                                  AGAGTGAGACAG GGGTTCG CCT
                                        C      T
GAM1741  LOC161823 3'  TCCAGCCTGGGCAACAGAGTGA 83176         CA
                                  TCGCTCTGT  CCCAGGCTGGA
                                  |||||||||  ||||||||||||
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                                AGTGAGACA  GGGTCCGACCT
                                     AC
GAM1741  LOC164395 5'  TCTAGCAGAAACGTGACGGGGC 83404     C        CCAG__
            TGGA                    TCT GCTCTGTCAC      GCTGGA
                                ||| ||||||||||      ||||||
                                AGG CGGGGCAGTG      CGATCT
                                  T         CAAAGA
GAM1741  LOC165283 3'  TCCAGGATGCACAGAGTGAGA  88548           CACC  GG
                                TCTCGCTCTGT    CA  CTGGA
                                ||||||||||    ||  |||||
                                AGAGTGAGACA    GT  GACCT
                                      C___  AG
GAM1741  LOC196047 5'  ACTCCAGCCTGGGTGACAGAGC 91140
            GAGA                    TCTCGCTCTGTCACCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGCGAGACAGTGGGTCCGACCT
                                           CAC
GAM1741  LOC196529 3'  TCTAGCCTGGGTGACAAGAGC  89141       _
                                GCTCT GTCACCCAGGCTGGA
                                ||||| ||||||||||||||
                                CGAGA CAGTGGGTCCGATCT
                                   A
GAM1741  LOC196540 3'  GCTCCAGCCTGGGTGACAGAGT 91203
            GAGA                    TCTCGCTCTGTCACCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGACAGTGGGTCCGACCT
                                           CGC
GAM1741  LOC196761 3'  TCCAGCCTGGGCGATAGAGGGA 91121      G      A
            GA                      TCTC CTCTGTC CCCAGGCTGGA
                                |||| ||||||| ||||||||||
                                AGAG GAGATAG GGGTCCGACCT
                                  G      C
GAM1741  LOC197132 3'  TCCAGCTTGGGAGACAAGAGCG 89230        _  A
            A                       TCGCTCT GTC CCCAGGCTGGA
                                ||||||| ||| ||||||||||
                                AGCGAGA CAG GGGTTCGACCT
                                    A  A
GAM1741  LOC197196 3'  TCCAGCCTGGGCGACAAGAGCG 91306        _  A
            A                       TCGCTCT GTC CCCAGGCTGGA
                                ||||||| ||| ||||||||||
                                AGCGAGA CAG GGGTCCGACCT
                                    A  C
GAM1741  LOC197201 3'  TCTAGCCTGGGCAACAAGAGTG 89290        _  CA
            A                       TCGCTCT GT  CCCAGGCTGGA
                                ||||||| ||  ||||||||||
                                AGTGAGA CA  GGGTCCGATCT
                                    A  AC
GAM1741  LOC197319 3'  TCCAGCCTGGCAACAGAGTGAG 89329           CAC
            A                       TCTCGCTCTGT   CCAGGCTGGA
                                ||||||||||   ||||||||||
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                                AGAGTGAGACA   GGTCCGACCT
                                      AC_
GAM1741  LOC197362 3'  TTCCAGCCTGGGTGACAGAGTG 91313
              AGA                   TCTCGCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAGTGGGTCCGACCT
                                          TA
GAM1741  LOC199221 3'  CCCGGGTGGCAGAGTCGGA    81166     C          A
                                    TCT GCTCTGTCACCC GG
                                    ||| |||||||||||| ||
                                    AGG TGAGACGGTGGG CC
                                      C          C
GAM1741  LOC199676 3'  TCCAGCCTGGGAGACAGAGTTA 91362     C       A
              GA                    TCT GCTCTGTC CCCAGGCTGGA
                                    ||| |||||||| ||||||||||
                                    AGA TGAGACAG GGGTCCGACCT
                                      T       A
GAM1741  LOC199725 3'  TCTGACTGTGATAGGGTGA    91427           C__
                                    TCGCTCTGTCAC   CAGG
                                    ||||||||||||   ||||
                                    AGTGGGATAGTG   GTCT
                                           TCA
GAM1741  LOC199733 5'  TCCGGTGCCGACGGAGCCGGG  91444     C       ACCCAG
                                    TCT GCTCTGTC      GCTGGA
                                    ||| ||||||||      ||||||
                                    GGG CGAGGCAG      TGGCCT
                                      C       CCG___
GAM1741  LOC199745 5'  TTCGTCACGTGACGAGGGCGGG 89721          _     CCA   TGGA
              A                      TCTCGCTCT GTCAC   GGC
                                    |||||||||| |||||   |||
                                    AGGGCGGGA CAGTG   CTG
                                          G     CA_   CTT
GAM1741  LOC199786 3'  TCCAGCCTGGGTGATGGGAGTG 89767          _
              AGA                     TCTCGCTCT GTCACCCAGGCTGGA
                                    |||||||||| ||||||||||||||||
                                    AGAGTGAGG TAGTGGGTCCGACCT
                                          G
GAM1741  LOC199858 3'  TCCAGCCTGGGCGACAGAGCGA 89803            A
              GA                      TCTCGCTCTGTC CCCAGGCTGGA
                                    |||||||||||| ||||||||||
                                    AGAGCGAGACAG GGGTCCGACCT
                                           C
GAM1741  LOC199923 3'  TCCAGCCTGGACGACAGAGCAA 89874     C       AC
              GA                      TCT GCTCTGTC  CCAGGCTGGA
                                    ||| ||||||||  ||||||||||
                                    AGA CGAGACAG  GGTCCGACCT
                                      A       CA
GAM1741  LOC200014 3'  TCCAGCCTGGGCGACAGAGCAA 89948     C       A
              GA                      TCT GCTCTGTC CCCAGGCTGGA
                                    ||| |||||||| ||||||||||
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                                AGA CGAGACAG GGGTCCGACCT
                                  A       C
GAM1741  LOC200014 3'  TTTAGTGGGTCACAGAGCGGGA 89949          C    AG
                                TCTCGCTCTGT ACCC  GCTGGA
                                |||||||||||| ||||  ||||||
                                AGGGCGAGACA TGGG  TGATTT
                                      C   __
GAM1741  LOC200058 3'  GCAGCCTTGGTATGGGGTGGGG 89960          C  C     GA
                                TCTCGCTCTGT ACC AGGCTG
                                |||||||||||| ||| ||||||
                                GGGGTGGGGTA TGG TCCGAC
                                      _  T     GA
GAM1741  LOC200093 3'  CCAGCTCTGCAGGGTGGGG   63764          TCACC  _
                                TCTCGCTCTG    CAG GCTGG
                                ||||||||||    ||| |||||
                                GGGGTGGGAC    GTC CGACC
                                      _____  T
GAM1741  LOC200227 3'  TCTAGCCTGGGTGACAGAATGA 90044      C
            GA                    TCTCG TCTGTCACCCAGGCTGGA
                                |||||| ||||||||||||||||||
                                AGAGT AGACAGTGGGTCCGATCT
                                   A
GAM1741  LOC200269 3'  TCTGGCCTCCCTGGCGGGGTGG 90077          CCC    TG
                                TCGCTCTGTCA   AGGC  GA
                                ||||||||||   ||||  ||
                                GGTGGGGCGGT   TCCG  CT
                                      CCC    GT
GAM1741  LOC200301 5'  TCTGGAACTAACAGAGTGAGA  90157          CAC__
                                TCTCGCTCTGT    CCAGG
                                ||||||||||    |||||
                                AGAGTGAGACA    GGTCT
                                      ATCAA
GAM1741  LOC200317 3'  TCCAGCCTGGGCAACAAGAGTG 90229       _  CA
            A                    TCGCTCT GT  CCCAGGCTGGA
                                ||||||| ||  ||||||||||
                                AGTGAGA CA  GGGTCCGACCT
                                    A  AC
GAM1741  LOC200728 3'  TCCATCCTGGGTGACAGAGCAA 91687     C          C
            GA                    TCT GCTCTGTCACCCAGG TGGA
                                ||| |||||||||||||| ||||
                                AGA CGAGACAGTGGGTCC ACCT
                                  A           T
GAM1741  LOC200731 3'  ATCCAGCCCCAGCTGGGTGACA 91691              _____
            GAGTGAGA                TCTCGCTCTGTCACCCA    GGCTGGA  T
                                ||||||||||||||||    |||||||  |
                                AGAGTGAGACAGTGGGT    CCGACCT  A
                                      CGACC
GAM1741  LOC200734 3'  TCCAGTTTGGAAAAGGAGCAGA 90282      _    GTCAC
            GA                    TCTC GCTCT    CCAGGCTGGA
                                |||| |||||    ||||||||||
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                                AGAG CGAGG     GGTTTGACCT
                                  A     AAAA_
GAM1741  LOC200853 3'  TCAGCCTGGGAGGTTGAG    90334     TG  A
                                CTC  TC CCCAGGCTGG
                                |||  || ||||||||||
                                GAG  GG GGGTCCGACT
                                  TT  A
GAM1741  LOC200853 3'  TCCAGCCTGGGAGACAGAGCGA 90335          A
                                TCGCTCTGTC CCCAGGCTGGA
                                |||||||||| ||||||||||
                                AGCGAGACAG GGGTCCGACCT
                                      A
GAM1741  LOC200904 3'  TCTAGCCTGGGCAACAGAGTAA 91785     CG      CA
              GA                  TCT  CTCTGT  CCCAGGCTGGA
                                |||  ||||||  ||||||||||
                                AGA  GAGACA  GGGTCCGATCT
                                  AT      AC
GAM1741  LOC200918 3'  TCCAGCCTGGGCGACAAGAGTG 90370        _  A
              A                   TCGCTCT GTC CCCAGGCTGGA
                                ||||||| ||| ||||||||||
                                AGTGAGA CAG GGGTCCGACCT
                                    A  C
GAM1741  LOC200939 3'  TCCAGTCTGGGTGAGACCTGAG 91800       CTCTG
              G                   TCTCG     TCACCCAGGCTGGA
                                |||||     ||||||||||||||
                                GGAGT     AGTGGGTCTGACCT
                                   CCAG_
GAM1741  LOC200940 3'  TCCAGCCTGGGCGACAGAGTGA 90396          A
              GA                  TCTCGCTCTGTC CCCAGGCTGGA
                                |||||||||||| ||||||||||
                                AGAGTGAGACAG GGGTCCGACCT
                                      C
GAM1741  LOC201102 5'  TCCGGGGCCTGGCGGGCCGGG  89472     T   AC      __
                                CTC GTC  CCAGGCT  GGA
                                ||| |||  |||||||  |||
                                GGG CGG  GGTCCGG  CCT
                                  C   GC      GG
GAM1741  LOC201173 5'  CCGGCAGGGCAGGATGGGA    88678       CT     ACCCAG
                                TCTCG  CTGTC     GCTGG
                                |||||  |||||     |||||
                                AGGGT  GACGG     CGGCC
                                   AG    GA____
GAM1741  LOC201173 3'  TCCAGCCTGGGCGACAGAGCAA 88694     C       A
              GA                  TCT GCTCTGTC CCCAGGCTGGA
                                ||| |||||||| ||||||||||
                                AGA CGAGACAG GGGTCCGACCT
                                  A       C
GAM1741  LOC201182 5'  TCCAGCCTGGTCAACAGAGCAA 91338     C      CAC
              GA                  TCT GCTCTGT   CCAGGCTGGA
                                ||| |||||||   ||||||||||
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                                AGA CGAGACA   GGTCCGACCT
                                  A      ACT
GAM1741  LOC201220 5'  CCGGCAGGGCAGGATGGGA   88713      CT    ACCCAG
                                TCTCG  CTGTC     GCTGG
                                |||||  |||||     |||||
                                AGGGT  GACGG     CGGCC
                                   AG    GA____
GAM1741  LOC201220 3'  TCCAGCCTGGGTGACAGAGCAA 88727     C
            GA                    TCT GCTCTGTCACCCAGGCTGGA
                                ||| ||||||||||||||||||
                                AGA CGAGACAGTGGGTCCGACCT
                                  A
GAM1741  LOC201252 3'  TCTAGCCTGAGTGACAGAGCAG 89556     C        C
            A                     TCT GCTCTGTCAC CAGGCTGGA
                                ||| |||||||||| |||||||||
                                AGA CGAGACAGTG GTCCGATCT
                                  _        A
GAM1741  LOC201562 3'  TTTGGGGGGCAGGGTGGGG    90417           A
                                TCTCGCTCTGTC CCCAGG
                                |||||||||||| ||||||
                                GGGGTGGGACGG GGGTTT
                                          _
GAM1741  LOC201627 3'  TCCAGCTTGGGTGACACAGTGA 90463        C
            GA                    TCTCGCT TGTCACCCAGGCTGGA
                                ||||||| ||||||||||||||||
                                AGAGTGA ACAGTGGGTTCGACCT
                                    C
GAM1741  LOC201689 3'  ACTCCAGCCTGGGTGACAGGGT 67728
            GAGA                    TCTCGCTCTGTCACCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGGGACAGTGGGTCCGACCT
                                             CAC
GAM1741  LOC201705 3'  TCCAGCCTGGGTGACAGAGTCA 91856     C
            GA                    TCT GCTCTGTCACCCAGGCTGGA
                                ||| ||||||||||||||||||
                                AGA TGAGACAGTGGGTCCGACCT
                                  C
GAM1741  LOC201868 3'  TTAGCCTGGGCGACCGAGA    90534      CTCT   A
                                TCTCG    GTC CCCAGGCTGG
                                |||||    ||| ||||||||||
                                AGAGC    CAG GGGTCCGATT
                                   _____   C
GAM1741  LOC201895 3'  TCCAGCCTAAGCAATAGAGCGA 90548          CACCC
            GA                    TCTCGCTCTGT     AGGCTGGA
                                ||||||||||     ||||||||
                                AGAGCGAGATA     TCCGACCT
                                      ACGAA
GAM1741  LOC201931 3'  TCCAGCCTGGGCGACAGAGCGA 90569           A
            GA                    TCTCGCTCTGTC CCCAGGCTGGA
                                |||||||||||| ||||||||||
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                                AGAGCGAGACAG GGGTCCGACCT
                                      C
GAM1741  LOC202020 3'  TCCAGCCCGGGCGACAGAGTGA 90603          A   A
                GA                TCTCGCTCTGTC CCC GGCTGGA
                                  |||||||||||| ||| |||||||
                                  AGAGTGAGACAG GGG CCGACCT
                                      C   C
GAM1741  LOC202781 3'  TCCAGCCTGGGCGACAGAGCGA 91976          A
                GA                TCTCGCTCTGTC CCCAGGCTGGA
                                  |||||||||||| ||||||||||
                                  AGAGCGAGACAG GGGTCCGACCT
                                      C
GAM1741  LOC202868 3'  CTCCAGCCTGGGTGACAGAGCG 92001
                AGA                TCTCGCTCTGTCACCCAGGCTGGA
                                   ||||||||||||||||||||||||
                                   AGAGCGAGACAGTGGGTCCGACCT
                                             CA
GAM1741  LOC202868 3'  TCCAACCTGGGTGACAGAGCGA 92009             C
                                  TCGCTCTGTCACCCAGG TGGA
                                  |||||||||||||||| ||||
                                  AGCGAGACAGTGGGTCC ACCT
                                        A
GAM1741  LOC203083 3'  TCCAGCCTGGGCAACAGAGTAA 92095     CG     CA
                GA                TCT  CTCTGT  CCCAGGCTGGA
                                  |||  ||||||  ||||||||||
                                  AGA  GAGACA  GGGTCCGACCT
                                    AT     AC
GAM1741  LOC203260 3'  CCTGGGAGGTGGGGCGGGG   90849        TG  A
                                  TCTCGCTC  TC CCCAGG
                                  ||||||||  || ||||||
                                  GGGGCGGG  GG GGGTCC
                                       GT  A
GAM1741  LOC203276 3'  TCCAGCCTGGGCAACAGAGTGA 92130          CA
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                        AC
GAM1741  LOC203276 3'  TCCAGCCTGGGTGACACAGTGA 92131        C
                GA                TCTCGCT TGTCACCCAGGCTGGA
                                  |||||||  ||||||||||||||||
                                  AGAGTGA ACAGTGGGTCCGACCT
                                     C
GAM1741  LOC203305 3'  TCCAGCCTGGGCAACAGAGTGA 92183          CA
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                        AC
GAM1741  LOC203305 3'  TCCAGCCTGGGTGACACAGTGA 92184        C
                GA                TCTCGCT TGTCACCCAGGCTGGA
                                  |||||||  ||||||||||||||||
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                                AGAGTGA ACAGTGGGTCCGACCT
                                    C
GAM1741  LOC203350 3'  TCCAGCCTGGATGACAGAGTGA 92250          C
                GA                TCTCGCTCTGTCA CCAGGCTGGA
                                  ||||||||||||| ||||||||||
                                  AGAGTGAGACAGT GGTCCGACCT
                                        A
GAM1741  LOC203378 3'  TCCTGCCTGGGTGACACAGCGA 92305      C       T
                GA                TCTCGCT TGTCACCCAGGC GGA
                                  ||||||| |||||||||||| |||
                                  AGAGCGA ACAGTGGGTCCG CCT
                                    C         T
GAM1741  LOC203504 5'  TTTGGTGGGCAAGTGGGG   92327      C   AC
                                  TCTCGCT TGTC  CCAGG
                                  ||||||| ||||  |||||
                                  GGGGTGA ACGG  GGTTT
                                    _   GT
GAM1741  LOC206962 5'  TCCAAGATGGCGGCGGGGCGGG 91109          AC  GGC
                G                 TCTCGCTCTGTC  CCA   TGGA
                                  ||||||||||||  |||   ||||
                                  GGGGCGGGGCGG  GGT   ACCT
                                        C_   AGA
GAM1741  LOC219347 3'  TCCAGCCTGGGCAACAGAGTGA 94581          CA
                GA                TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||  ||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                        AC
GAM1741  LOC219540 3'  TCCAGCCTGGGCGACAGAGCGA 95247          A
                GA                TCTCGCTCTGTC CCCAGGCTGGA
                                  |||||||||||| ||||||||||
                                  AGAGCGAGACAG GGGTCCGACCT
                                        C
GAM1741  LOC219627 3'  TCCAGCCTGGGCAACAAGCGA  93812      C   CA
                                  TCGCT TGT  CCCAGGCTGGA
                                  ||||| |||  ||||||||||
                                  AGCGA ACA  GGGTCCGACCT
                                    _   AC
GAM1741  LOC219627 3'  TCCAGCTGGGCGACAGAGCGAG 93813          A   G
                A                 TCTCGCTCTGTC CCCAG CTGGA
                                  |||||||||||| ||||| |||||
                                  AGAGCGAGACAG GGGTC GACCT
                                        C    _
GAM1741  LOC219649 3'  TCCAGCCTGGGCGACAGAGTGA 94558          A
                GA                TCTCGCTCTGTC CCCAGGCTGGA
                                  |||||||||||| ||||||||||
                                  AGAGTGAGACAG GGGTCCGACCT
                                        C
GAM1741  LOC219672 5'  TCCAGCCTGGGCAACAAGAGTG 92973       _  CA
                A                 TCGCTCT GT  CCCAGGCTGGA
                                  ||||||| ||  ||||||||||
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                                AGTGAGA CA  GGGTCCGACCT
                                   A  AC
GAM1741  LOC219722 5'  TTCAGCCTGGACAACAGAGTGA 94691          CAC
                GA                 TCTCGCTCTGT   CCAGGCTGGA
                                   ||||||||||   ||||||||||
                                   AGAGTGAGACA   GGTCCGACTT
                                         ACA
GAM1741  LOC219842 5'  TCTGGCTTGGTGAGATGGGGGA 94893     G      AC_     TG
                GG                 TCTC CTCTGTC   CCAGGC  GA
                                   |||| |||||||   ||||||  ||
                                   GGAG GGGGTAG   GGTTCG  CT
                                     _      AGT     GT
GAM1741  LOC219899 5'  CCGGCGGCCAGAGTGGGG    93130          TCA  CAG
                                   TCTCGCTCTG   CC   GCTGG
                                   ||||||||||   ||   |||||
                                   GGGGTGAGAC   GG   CGGCC
                                         C__  ___
GAM1741  LOC219919 3'  TCCAGCCTGGGCAACAGAGTAA 94933     CG     CA
                GA                 TCT  CTCTGT  CCCAGGCTGGA
                                   |||  ||||||  ||||||||||
                                   AGA  GAGACA  GGGTCCGACCT
                                     AT     AC
GAM1741  LOC219920 5'  TCTGGCCTGGGGGCCAGGGCAG 94964    TC     _ A      TG
                GA                 TC  GCTCTG TC CCCAGGC  GA
                                   ||  |||||| || |||||||  ||
                                   AG  CGGGAC GG GGGTCCG  CT
                                    GA     C  _      GT
GAM1741  LOC220038 3'  TCCAGCCTGGGCGATGGAGTGA 93377           A
                GA                 TCTCGCTCTGTC CCCAGGCTGGA
                                   |||||||||||| ||||||||||
                                   AGAGTGAGGTAG GGGTCCGACCT
                                         C
GAM1741  LOC220045 5'  TTCAGAGTTGGAGGGGTGGGG  95039          GTCAC    G_
                                   TCTCGCTCT    CCAG  CTGGA
                                   |||||||||    ||||  |||||
                                   GGGGTGGGG    GGTT  GACTT
                                         A____    GA
GAM1741  LOC220070 3'  TCCAGCCTGGAAAACGGAGTGA 59942           CAC
                GA                 TCTCGCTCTGT   CCAGGCTGGA
                                   ||||||||||   ||||||||||
                                   AGAGTGAGGCA   GGTCCGACCT
                                         AAA
GAM1741  LOC220431 5'  TCCAGTGTGCATGCCAGAGTGG 95997          T  CC  G
                GG                 TCTCGCTCTG CA  CA GCTGGA
                                   |||||||||| ||  || ||||||
                                   GGGGTGAGAC GT  GT TGACCT
                                         C  AC  G
GAM1741  LOC220549 3'  TCCAGCCTGGGTGACAGAATGA 94511       C
                GA                 TCTCG TCTGTCACCCAGGCTGGA
                                   ||||| ||||||||||||||||||
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                                AGAGT AGACAGTGGGTCCGACCT
                                   A
GAM1741  LOC220662 3'  TCCAGCCTGGGCAACACGAGCG 92831       _   CA
                  A                 TCGCTC TGT  CCCAGGCTGGA
                                    |||||| |||  ||||||||||
                                    AGCGAG ACA  GGGTCCGACCT
                                       C   AC
GAM1741  LOC220739 3'  GCTTGTGGCAGGGGTGAGA    94524         _     CC
                                    TCTCGCTC TGTCAC  AGGC
                                    |||||||| ||||||  ||||
                                    AGAGTGGG ACGGTG  TTCG
                                         G     __
GAM1741  LOC220906 3'  TCCAGCCTGGGCAACAAGCGA  93037       C   CA
                                    TCGCT TGT  CCCAGGCTGGA
                                    ||||| |||  ||||||||||
                                    AGCGA ACA  GGGTCCGACCT
                                       _   AC
GAM1741  LOC220906 3'  TCCAGCTGGGCGACAGAGCGAG 93038           A    G
                  A                 TCTCGCTCTGTC CCCAG CTGGA
                                    |||||||||||| ||||| |||||
                                    AGAGCGAGACAG GGGTC GACCT
                                           C    _
GAM1741  LOC221002 3'  TCTGGTCCTGGGTGGAGCAGGA 93111    TC    TGT      _ TG
                                    TC  GCTC   CACCCAGG C  GA
                                    ||  ||||   |||||||| |  ||
                                    AG  CGAG   GTGGGTCC G  CT
                                     GA   ____       T GT
GAM1741  LOC221042 3'  TCCAGCCTGGGTGACAGAGCAA 94807     C
                  GA                  TCT GCTCTGTCACCCAGGCTGGA
                                      ||| ||||||||||||||||||||
                                      AGA CGAGACAGTGGGTCCGACCT
                                        A
GAM1741  LOC221069 3'  TCCAGCCTGGGCGACAGAGCAA 94821     C       A
                  GA                  TCT GCTCTGTC CCCAGGCTGGA
                                      ||| |||||||| ||||||||||
                                      AGA CGAGACAG GGGTCCGACCT
                                        A       C
GAM1741  LOC221178 3'  TCCAGCCTGGGAGATACAGCGA 95176        C    A
                  GA                  TCTCGCT TGTC CCCAGGCTGGA
                                      ||||||| |||| ||||||||||
                                      AGAGCGA ATAG GGGTCCGACCT
                                         C    A
GAM1741  LOC221271 3'  ACTCCAGCCTGGGTGACAGAGC 93489
                  GAGA                  TCTCGCTCTGTCACCCAGGCTGGA
                                        ||||||||||||||||||||||||
                                        AGAGCGAGACAGTGGGTCCGACCT
                                                    CAC
GAM1741  LOC221271 3'  TCCAGCCTGGGCAACAGAGGGA 93530      G     CA
                  GA                  TCTC CTCTGT  CCCAGGCTGGA
                                      |||| ||||||  ||||||||||
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                                AGAG GAGACA  GGGTCCGACCT
                                  G      AC
GAM1741  LOC221288 3'  TCCAGCCTGGGCGACAGAGTGA 95263           A
                GA                  TCTCGCTCTGTC CCCAGGCTGGA
                                    |||||||||||| ||||||||||
                                    AGAGTGAGACAG GGGTCCGACCT
                                          C
GAM1741  LOC221337 3'  TCCAGCCTGGGCAACAAGAGTG 93738       _  CA
                A                    TCGCTCT GT  CCCAGGCTGGA
                                    ||||||| ||  ||||||||||
                                    AGTGAGA CA  GGGTCCGACCT
                                       A  AC
GAM1741  LOC221410 3'  CTCCAGCCTGGGTGACAGAGCG 93695
                AGA                   TCTCGCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACAGTGGGTCCGACCT
                                                CA
GAM1741  LOC221421 3'  TCTGGCCTCAGCCATGGGGCGA 93896          CACCC    TG
                GA                  TCTCGCTCTGT    AGGC  GA
                                    ||||||||||     ||||  ||
                                    AGAGCGGGGTA    TCCG  CT
                                          CCGAC    GT
GAM1741  LOC221474 3'  ACTCTAGCCTGGGTGACAGAGC 93985
                GAGA                  TCTCGCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACAGTGGGTCCGATCT
                                                CAC
GAM1741  LOC221477 3'  TCCAGCCTGGGCGACAGAGCGA 93776          A
                                    TCGCTCTGTC CCCAGGCTGGA
                                    |||||||||| ||||||||||
                                    AGCGAGACAG GGGTCCGACCT
                                          C
GAM1741  LOC221489 3'  TCCAGCCTGGGTGATAAGAGTG 95290        _
                A                    TCGCTCT GTCACCCAGGCTGGA
                                    ||||||| ||||||||||||||
                                    AGTGAGA TAGTGGGTCCGACCT
                                       A
GAM1741  LOC221491 3'  CCATGGTGATGGGGCCAGA    93655     C        CAGGC
                                    TCT GCTCTGTCACC     TGG
                                    ||| ||||||||||     |||
                                    AGA CGGGGTAGTGG     ACC
                                      C          T_____
GAM1741  LOC221543 5'  TCCAGCCTGGGCGACAGAGCAA 95388     C       A
                GA                  TCT GCTCTGTC CCCAGGCTGGA
                                    ||| |||||||| ||||||||||
                                    AGA CGAGACAG GGGTCCGACCT
                                      A       C
GAM1741  LOC221550 3'  TCCAGTCTGGTTGACAGAGTGA 93748           C
                GA                  TCTCGCTCTGTCA CCAGGCTGGA
                                    |||||||||||| ||||||||||
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                                AGAGTGAGACAGT GGTCTGACCT
                                       T
GAM1741  LOC221641 3'  ACACTAGCCTGGGTGACAGAGC 95336     C              A
                AAGA                    TCT GCTCTGTCACCCAGGCTGG
                                ||| ||||||||||||||||||
                                AGA CGAGACAGTGGGTCCGATC
                                  A               ACAC
GAM1741  LOC221641 5'  ACTCCAGCCTGGGTGGCAGAGC 95340
                GAGA                    TCTCGCTCTGTCACCCAGGCTGGA
                                |||||||||||||||||||||||
                                AGAGCGAGACGGTGGGTCCGACCT
                                              CAC
GAM1741  LOC221787 3'  GAAGGCTGGGTGACAGAGTGAG 94062                G  GGA
                G                        TCTCGCTCTGTCACCCAG CT
                                |||||||||||||||| ||
                                GGAGTGAGACAGTGGGTC GA
                                           G  AGA
GAM1741  LOC221795 3'  TCCAGCCTGGGCAACAGAGTAA 94081     CG     CA
                GA                      TCT  CTCTGT  CCCAGGCTGGA
                                |||  ||||||  ||||||||||
                                AGA  GAGACA  GGGTCCGACCT
                                  AT     AC
GAM1741  LOC221935 3'  CCAGTCTGAAAGGTGAGG     94199       T  GTCACC
                                TCTCGC CT     CAGGCTGG
                                |||||| ||     ||||||||
                                GGAGTG GA     GTCTGACC
                                   _  AA_____
GAM1741  LOC221943 5'  TCCAGCCTGGGCGACAGAGCAA 95625     C       A
                GA                      TCT GCTCTGTC CCCAGGCTGGA
                                ||| |||||||| ||||||||||
                                AGA CGAGACAG GGGTCCGACCT
                                  A       C
GAM1741  LOC221954 5'  TCCAGCCTGGGCAACAGAGCGA 95651           CA
                GA                      TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGCGAGACA  GGGTCCGACCT
                                      AC
GAM1741  LOC221954 5'  TCCAGCCTGGGTGACAGAGTAA 95652     CG
                GA                      TCT  CTCTGTCACCCAGGCTGGA
                                |||  ||||||||||||||||||
                                AGA  GAGACAGTGGGTCCGACCT
                                  AT
GAM1741  LOC221954 5'  TCCAGCTTGGGCGACAGAGCAA 95653     C       A
                GA                      TCT GCTCTGTC CCCAGGCTGGA
                                ||| |||||||| ||||||||||
                                AGA CGAGACAG GGGTTCGACCT
                                  A       C
GAM1741  LOC222060 5'  TCCAGCCTGGGCGACAGAGCAA 95758     C       A
                GA                      TCT GCTCTGTC CCCAGGCTGGA
                                ||| |||||||| ||||||||||
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                                AGA CGAGACAG GGGTCCGACCT
                                  A       C
GAM1741  LOC222066 3'  ACTCCAGCTTGGGTGACAGAGT 94308
                  GAGA                  TCTCGCTCTGTCACCCAGGCTGGA
                                |||||||||||||||||||||||
                                AGAGTGAGACAGTGGGTTCGACCT
                                           CAC
GAM1741  LOC222160 3'  CCAGCCTGGGCAGCAGAG    95779       CA
                                CTCTGT  CCCAGGCTGG
                                ||||||  |||||||||
                                GAGACG  GGGTCCGACC
                                   AC
GAM1741  LOC222160 5'  TCCAGCCTGGGCGACAGAGCAA 95792     C       A
                  GA                  TCT GCTCTGTC CCCAGGCTGGA
                                ||| ||||||| ||||||||||
                                AGA CGAGACAG GGGTCCGACCT
                                  A       C
GAM1741  LOC222166 3'  GCTGTGGCAGACTGGGG     95740       C       CCA
                                TCTCG TCTGTCAC   GGC
                                ||||| |||||||   |||
                                GGGGT AGACGGTG   TCG
                                  C      ___
GAM1741  LOC222182 3'  TCCAGCCTGGGCAATAGAGTGA 95862           CA
                  GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                |||||||||||  ||||||||||
                                AGAGTGAGATA  GGGTCCGACCT
                                      AC
GAM1741  LOC222256 3'  TCTAGCCTGGGTGACAAAGCAA 95912     C   C
                  GA                  TCT GCT TGTCACCCAGGCTGGA
                                ||| ||| ||||||||||||||||
                                AGA CGA ACAGTGGGTCCGATCT
                                  A   A
GAM1741  LOC222865 3'  TCCAGCCTGAGTGACAGAGCGA 94450             C
                  GA                  TCTCGCTCTGTCAC CAGGCTGGA
                                |||||||||||||| |||||||||
                                AGAGCGAGACAGTG GTCCGACCT
                                        A
GAM1741  LOC245812 3'  TCTGGGGTGGAGGGTGGGG    95571         G     _
                                TCTCGCTCT TCACCC AGG
                                ||||||||| |||||| |||
                                GGGGTGGGA GGTGGG TCT
                                      _     G
GAM1741  LOC253039 3'  TCCAGCCTGGGCGACAGAGCAA 97867     C       A
                  GA                  TCT GCTCTGTC CCCAGGCTGGA
                                ||| ||||||| ||||||||||
                                AGA CGAGACAG GGGTCCGACCT
                                  A       C
GAM1741  LOC253071 5'  TTCAGTGGTCAGTGGGGTGGGA 97420         TG C_   CAG
                                TCTCGCTC  T  ACC   GCTGGA
                                ||||||||  |  |||   ||||||
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                                AGGGTGGG  G  TGG   TGACTT
                                    GT AC  ___
GAM1741  LOC253314 3'  TACTTTGGGGGATGGGGCGGGA 97614          A     CTGGA
                                TCTCGCTCTGTC CCCAGG
                                |||||||||||| ||||||
                                AGGGCGGGGTAG GGGTTT
                                      G     CATT
GAM1741  LOC253532 3'  TCCAGCCTGGGTGACAAAGCAA 97740     C   C
              GA                  TCT GCT TGTCACCCAGGCTGGA
                                  ||| ||| ||||||||||||||||
                                  AGA CGA ACAGTGGGTCCGACCT
                                    A   A
GAM1741  LOC253532 3'  TCCAGTCTGGGTGACAGCGTGA 97741       T
              GA                  TCTCGC CTGTCACCCAGGCTGGA
                                  |||||| ||||||||||||||||
                                  AGAGTG GACAGTGGGTCTGACCT
                                     C
GAM1741  LOC253612 5'  TCCAGCCTAGGCAACAGAGTGA 98559          CA  C
              GA                  TCTCGCTCTGT  CC AGGCTGGA
                                  ||||||||||  ||  ||||||||
                                  AGAGTGAGACA  GG TCCGACCT
                                        AC  A
GAM1741  LOC253639 3'  TCCAGCCTGGGCGACAGAGTGA 97517          A
              GA                  TCTCGCTCTGTC CCCAGGCTGGA
                                  |||||||||||| ||||||||||
                                  AGAGTGAGACAG GGGTCCGACCT
                                        C
GAM1741  LOC253778 5'  TCCAGCCTGGGCGACAGAGTGA 96527          A
              GA                  TCTCGCTCTGTC CCCAGGCTGGA
                                  |||||||||||| ||||||||||
                                  AGAGTGAGACAG GGGTCCGACCT
                                        C
GAM1741  LOC253786 3'  TCCAGCCTGGGCAATAGAGCAA 98834     C      CA
              GA                  TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGATA  GGGTCCGACCT
                                    A       AC
GAM1741  LOC253832 3'  TCCAGCCTGGGCGACGAGTGA  96593       T   A
                                TCGCTC GTC CCCAGGCTGGA
                                |||||| ||| ||||||||||
                                AGTGAG CAG GGGTCCGACCT
                                   _  C
GAM1741  LOC253840 5'  TCCAGCCTGGGCAACAGAGCAA 97914     C      CA
              GA                  TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A       AC
GAM1741  LOC253868 3'  TTCAGCTTTGTGAGTGGGGCGA 97330          _   CC
              GG                  TCTCGCTCTG TCAC  AGGCTGGA
                                  |||||||||| ||||  ||||||||
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                                GGAGCGGGGT AGTG  TTCGACTT
                                      G    T_
GAM1741  LOC253906 3'  TTGAGCTTGGGTGACAGAGTAA 98301     CG            G
                GA                    TCT  CTCTGTCACCCAGGCT GA
                                      |||  |||||||||||||||| ||
                                      AGA  GAGACAGTGGGTTCGA TT
                                        AT             G
GAM1741  LOC253926 3'  GCAGCCAGTGACAGAGGAGA   96594      G       CCA     GA
                                      TCTC CTCTGTCAC   GGCTG
                                      |||| |||||||||   |||||
                                      AGAG GAGACAGTG   CCGAC
                                        _       A__     GA
GAM1741  LOC253980 5'  CCGGGTGGTGCGAGCGAGA    96770         _ GT     A
                                      TCTCGCTC T  CACCC GG
                                      |||||||| |  ||||| ||
                                      AGAGCGAG G  GTGGG CC
                                           C TG    _
GAM1741  LOC254100 3'  TCCAGCCTGGGCAACAGAGTGA 98160           CA
                GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                      ||||||||||  ||||||||||
                                      AGAGTGAGACA  GGGTCCGACCT
                                            AC
GAM1741  LOC254176 3'  TCCAGCCTGGGCAACAGAGTAA 99176     CG     CA
                GA                    TCT  CTCTGT  CCCAGGCTGGA
                                      |||  ||||||  ||||||||||
                                      AGA  GAGACA  GGGTCCGACCT
                                        AT     AC
GAM1741  LOC254243 3'  TCCAGCCTGGGCAACAGAGTGA 99269           CA
                GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                      ||||||||||  ||||||||||
                                      AGAGTGAGACA  GGGTCCGACCT
                                            AC
GAM1741  LOC254243 3'  TCCAGCCTGGGTGACACAGTGA 99270         C
                GA                    TCTCGCT TGTCACCCAGGCTGGA
                                      |||||||  ||||||||||||||||
                                      AGAGTGA ACAGTGGGTCCGACCT
                                           C
GAM1741  LOC254423 3'  TCTGGTCTGGCTGAAGAATGGG 99303       C   G   C      TG
                A                      TCTCG TCT TCA CCAGGC  GA
                                      |||||  |||  |||  ||||||  ||
                                      AGGGT AGA AGT GGTCTG  CT
                                        A   _   C      GT
GAM1741  LOC254531 5'  TCCAGCCTGGGTGACAGAGCAA 96673     C
                GA                    TCT GCTCTGTCACCCAGGCTGGA
                                      |||  ||||||||||||||||||||
                                      AGA CGAGACAGTGGGTCCGACCT
                                        A
GAM1741  LOC254756 3'  TCCAGCCTGGGCAATAGAGTAA 99212     CG     CA
                GA                    TCT  CTCTGT  CCCAGGCTGGA
                                      |||  ||||||  ||||||||||
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                                AGA  GAGATA  GGGTCCGACCT
                                  AT      AC
GAM1741  LOC254808 3'  TCCAGCCTGGGCAACAGAGCAA 98810     C      CA
                GA                TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||
                                AGA CGAGACA  GGGTCCGACCT
                                  A       AC
GAM1741  LOC254875 3'  TCCAGCCTGGGTGACAAAGCAA 97785     C   C
                GA                TCT GCT TGTCACCCAGGCTGGA
                                  ||| ||| ||||||||||||||||
                                AGA CGA ACAGTGGGTCCGACCT
                                  A   A
GAM1741  LOC254875 3'  ACTCCAGTCTGGGTGACAGAGT 97769
                GAGA                TCTCGCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                AGAGTGAGACAGTGGGTCTGACCT
                                          CAC
GAM1741  LOC255030 5'  CTCCAGCCTGGGTGACAGAGCG 99084
                AGA                 TCTCGCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                AGAGCGAGACAGTGGGTCCGACCT
                                          CA
GAM1741  LOC255031 3'  TCCAGCCTGGCTACAGAGTGAG 99044          CAC
                A                 TCTCGCTCTGT   CCAGGCTGGA
                                  ||||||||||   |||||||||
                                AGAGTGAGACA   GGTCCGACCT
                                      TC_
GAM1741  LOC255042 3'  ACTCTAGCCTGGGTGACAGAGT 97028
                GAGA                TCTCGCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                AGAGTGAGACAGTGGGTCCGATCT
                                          CAC
GAM1741  LOC255042 3'  TCCAGCCTGGGCAACAAGAGCG 97056       _  CA
                A                 TCGCTCT GT  CCCAGGCTGGA
                                  ||||||| ||  ||||||||||
                                AGCGAGA CA  GGGTCCGACCT
                                    A  AC
GAM1741  LOC255177 3'  TCCAGCCTAGGCAACAGAGTGA 98401          CA  C
                GA                TCTCGCTCTGT  CC AGGCTGGA
                                  ||||||||||  || ||||||||
                                AGAGTGAGACA  GG TCCGACCT
                                      AC  A
GAM1741  LOC255177 3'  TTTGGTTGTCTCTTGATGGGGG 98405     G      CCCA__  TG
                AGG                 TCTC CTCTGTCA     GGC  GA
                                    |||| ||||||||     |||  ||
                                GGAG GGGGTAGT     TTG  TT
                                  _       TCTCTG   GT
GAM1741  LOC255231 3'  ACTCCAGCCTGGGTGACAGAGT 97114
                GAGA                TCTCGCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||||||
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                                AGAGTGAGACAGTGGGTCCGACCT
                                        CAC
GAM1741  LOC255252 3'  TCCAGCGTGGGTGACAGAGTGA 96710              G
            GA                   TCTCGCTCTGTCACCCA GCTGGA
                                 |||||||||||||||| ||||||
                                 AGAGTGAGACAGTGGGT CGACCT
                                        G
GAM1741  LOC255271 5'  TCCGGTGCGGGCGGAGTCGGA  97244     C     TCA   AG
                                 TCT GCTCTG   CCC  GCTGGA
                                 ||| ||||||   |||  ||||||
                                 AGG TGAGGC   GGG  TGGCCT
                                   C     ___   CG
GAM1741  LOC255326 3'  TCCAGCCTGGGTGACAGAGCAA 98124     C
            GA                   TCT GCTCTGTCACCCAGGCTGGA
                                 ||| ||||||||||||||||||
                                 AGA CGAGACAGTGGGTCCGACCT
                                   A
GAM1741  LOC255328 3'  TCCAGCCTGGGTGATAAGAGC  98347       _
                                 GCTCT GTCACCCAGGCTGGA
                                 ||||| ||||||||||||||
                                 CGAGA TAGTGGGTCCGACCT
                                    A
GAM1741  LOC255463 3'  TCCAGCCTGGACAACATAGTGA 96543        C   CAC
            GA                   TCTCGCT TGT   CCAGGCTGGA
                                 ||||||| |||   ||||||||||
                                 AGAGTGA ACA   GGTCCGACCT
                                     T   ACA
GAM1741  LOC255523 3'  TCCAGCCTGGGCAACAGAGCAA 96737     C      CA
            GA                   TCT GCTCTGT  CCCAGGCTGGA
                                 ||| |||||||  ||||||||||
                                 AGA CGAGACA  GGGTCCGACCT
                                   A       AC
GAM1741  LOC255671 5'  ACTCCAGCCTGGGTGACAGAGT 99061
            GAGA                   TCTCGCTCTGTCACCCAGGCTGGA
                                 |||||||||||||||||||||||
                                 AGAGTGAGACAGTGGGTCCGACCT
                                        CAC
GAM1741  LOC255671 3'  TCCAGCCTGGGTAACAGAGCAA 99076     C      C
            GA                   TCT GCTCTGT ACCCAGGCTGGA
                                 ||| ||||||| ||||||||||||
                                 AGA CGAGACA TGGGTCCGACCT
                                   A       A
GAM1741  LOC255862 3'  TGGTCTTCATGGACGAGA    96116       C    CACCC    TG
                                 TCTCG TCTGT     AGGC  G
                                 ||||| |||||     ||||  |
                                 AGAGC AGGTA     TCTG  T
                                    _     CT___     GT
GAM1741  LOC255937 3'  TCCATCCTGGGTGACAGAGCAA 97684     C            C
            GA                   TCT GCTCTGTCACCCAGG TGGA
                                 ||| |||||||||||||| ||||
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                                AGA CGAGACAGTGGGTCC ACCT
                                  A            T
GAM1741  LOC255971 3'  ACTACAGCCTGGGTGACAGAGC 98304     C             GA
                AAGA                TCT GCTCTGTCACCCAGGCTG
                                ||| ||||||||||||||||||
                                AGA CGAGACAGTGGGTCCGAC
                                  A              ATCAC
GAM1741  LOC256158 5'  TCGGGCAGTGGCAGAGGAGG  99517     G       CCAG  G
                                TCTC CTCTGTCAC    GCT GA
                                |||| |||||||||    ||| ||
                                GGAG GAGACGGTG    CGG CT
                                  _       A___   G
GAM1741  LOC256267 5'  TCCAGCCTGGGAGACAGAGTGA 98613           A
                GA                  TCTCGCTCTGTC CCCAGGCTGGA
                                ||||||||||| ||||||||||
                                AGAGTGAGACAG GGGTCCGACCT
                                      A
GAM1741  LOC256494 5'  CTAGGCTGGCAGGGCGA     99094        TCAC   G
                                TCGCTCTG    CCAG CTGG
                                ||||||||    |||| ||||
                                AGCGGGAC    GGTC GATC
                                    _____   G
GAM1741  LOC256515 3'  TCCAGCCTGGGCAACAGAGTAA 98218     CG     CA
                GA                  TCT  CTCTGT  CCCAGGCTGGA
                                |||  ||||||  ||||||||||
                                AGA  GAGACA  GGGTCCGACCT
                                  AT     AC
GAM1741  LOC256520 3'  TCCAGCCTGGGCGACAGAGCCA 97670     C      A
                GA                  TCT GCTCTGTC CCCAGGCTGGA
                                ||| |||||||| ||||||||||
                                AGA CGAGACAG GGGTCCGACCT
                                  C       C
GAM1741  LOC256594 3'  TCCAGCCTGGGCAACAGAGTAA 98868     CG     CA
                GA                  TCT  CTCTGT  CCCAGGCTGGA
                                |||  ||||||  ||||||||||
                                AGA  GAGACA  GGGTCCGACCT
                                  AT     AC
GAM1741  LOC256790 5'  TCCCCAAGGTGACGGGTTGAGG 96494      CT      CA  CT
                                TCTCG  CTGTCACC  GG  GGA
                                |||||  ||||||||  ||  |||
                                GGAGT  GGCAGTGG  CC  CCT
                                   TG       AA  __
GAM1741  LOC257054 5'  TCCGGCCTGGTGACCGATGGGA 97378      C  T     C
                                TCTCG TC GTCACC AGGCTGGA
                                ||||| || |||||| ||||||||
                                AGGGT AG CAGTGG TCCGGCCT
                                   _ C     _
GAM1741  LOC257222 5'  TTTGGTCTGTTGCGGGATAGAG 99447     C      A ____     TG
                TAGA                TCT GCTCTGTC CC    CAGGC  GA
                                ||| |||||||| ||    |||||  ||
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                                AGA TGAGATAG GG    GTCTG  TT
                                  _       _ CGTT     GT
GAM1741  LOC257443 3'  TTTAGTCTTCATGGGGTTGGA  97548     C      CACCC
                                TCT GCTCTGT     AGGCTGGA
                                ||| |||||||     ||||||||
                                AGG TGGGGTA     TCTGATTT
                                  T      CT___
GAM1741  LOC257473 3'  TCTGGCTTAGCTGGGCCGAGA  96808      _  T  CACCC    TG
                                TCTCG CTC GT     AGGC  GA
                                ||||| ||| ||     ||||  ||
                                AGAGC GGG CG     TTCG  CT
                                   C   T  A____    GT
GAM1741  LOC257479 5'  CCGGTCCGCGCGGCGGGG    97986        C   CACCCA
                                TCTCGCT TGT     GGCTGG
                                ||||||| |||     ||||||
                                GGGGCGG GCG     CTGGCC
                                    C   C_____
GAM1741  LOC257495 3'  TCCAGTCTGGTTGACAGAGTGA 99575            C
              GA                  TCTCGCTCTGTCA CCAGGCTGGA
                                ||||||||||||| ||||||||||
                                AGAGTGAGACAGT GGTCTGACCT
                                        T
GAM1741  LOC257539 3'  TCCAGCCTGGGTGACAGGGTGA 99551
                                TCGCTCTGTCACCCAGGCTGGA
                                ||||||||||||||||||||||
                                AGTGGGACAGTGGGTCCGACCT

GAM1741  LOC257576 3'  TCCAGTCTGGTTGACAGAGTGA 99712            C
              GA                  TCTCGCTCTGTCA CCAGGCTGGA
                                ||||||||||||| ||||||||||
                                AGAGTGAGACAGT GGTCTGACCT
                                        T
GAM1741  LOC257578 3'  TCCAGCCTGGGTGACAGGGTGA 99663
                                TCGCTCTGTCACCCAGGCTGGA
                                ||||||||||||||||||||||
                                AGTGGGACAGTGGGTCCGACCT

GAM1741  LOC257596 5'  TCCAGCCTGGGCGACAGAGCAA 99791     C       A
              GA                  TCT GCTCTGTC CCCAGGCTGGA
                                ||| |||||||| ||||||||||
                                AGA CGAGACAG GGGTCCGACCT
                                  A       C
GAM1741  LOC257618 5'  TTGCAGGGAGGGACGGGGTGGG 99677            AC_  AG  TGGA
              G                   TCTCGCTCTGTC   CC  GC
                                ||||||||||||   ||  ||
                                GGGGTGGGGCAG   GG  CG
                                       GGA  GA  TTT
GAM1741  LOC51075  3'  TTGGCTGTGACTGGGTGGGG  32555         T    CCA   TG
                                TCTCGCTC GTCAC   GGC  GA
                                |||||||| |||||   |||  ||
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                                GGGGTGGG CAGTG   TCG  TT
                                     T    ___   GT
GAM1741  LOC51145  3'  TCCAGCCTGGGCGACAGAGTGA 32928          A
                GA                   TCTCGCTCTGTC CCCAGGCTGGA
                                     |||||||||||| ||||||||||
                                     AGAGTGAGACAG GGGTCCGACCT
                                           C
GAM1741  LOC51212  3'  TCCAGCCTGGGTGACAGAGCAA 33501     C
                GA                   TCT GCTCTGTCACCCAGGCTGGA
                                     ||| ||||||||||||||||||||
                                     AGA CGAGACAGTGGGTCCGACCT
                                       A
GAM1741  LOC51336  3'  TCCAGCCTGGGTGACAGCGTAA 34079     CG T
                GA                   TCT  C CTGTCACCCAGGCTGGA
                                     |||  | ||||||||||||||||
                                     AGA  G GACAGTGGGTCCGACCT
                                       AT C
GAM1741  LOC51667  3'  CCAGTTTGGACTGATGGG    32774       C_
                                     TCTGTCA  CCAGGCTGG
                                     |||||||  |||||||||
                                     GGGTAGT  GGTTTGACC
                                        CA
GAM1741  LOC54466  3'  TCTGGTCTGGAGGGGGCAGGG  39178       AC__     TG
                                     CTCTGTC    CCAGGC  GA
                                     |||||||    ||||||  ||
                                     GGGACGG    GGTCTG  CT
                                        GGGA     GT
GAM1741  LOC57118  3'  TCCAGCCTGGGTGACAGATTGA 40228      C
                GA                   TCTCG TCTGTCACCCAGGCTGGA
                                     |||||| ||||||||||||||||||
                                     AGAGT AGACAGTGGGTCCGACCT
                                       T
GAM1741  LOC58504  3'  TCCAGCCTTGTATGGAGTTAGA 41407     C      C  CC
                                     TCT GCTCTGT AC  AGGCTGGA
                                     ||| ||||||| ||  ||||||||
                                     AGA TGAGGTA TG  TCCGACCT
                                       T      _  T_
GAM1741  LOC58525  3'  TCTAGCAGCCAGGCAGGGCGA  79353         ACCCAG
                                     TCGCTCTGTC     GCTGGA
                                     ||||||||||     ||||||
                                     AGCGGGACGG     CGATCT
                                          ACCGA_
GAM1741  LOC58525  3'  TCTGGGGCCCTGGAGGGTGGGG 79354         GTCAC    ___ TG
                                     TCTCGCTCT    CCAGG   C  GA
                                     |||||||||    |||||  |  ||
                                     GGGGTGGGA    GGTCC   G  CT
                                          _____    CGG GT
GAM1741  LOC59346  5'  TCCAGAACTGGTAGAGCCGGG  41574     C     TCAC    G_
                                     TCT GCTCTG    CCAG  CTGGA
                                     ||| ||||||    ||||  |||||
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                                GGG CGAGAT    GGTC  GACCT
                                  C     ____    AA
GAM1741  LOC63929  3'  TCCAGCCTGGGTGACTGAGCAA 42285     C    T
              GA                  TCT GCTC GTCACCCAGGCTGGA
                                  ||| |||| ||||||||||||||||
                                  AGA CGAG CAGTGGGTCCGACCT
                                    A    T
GAM1741  LOC64167  3'  TCCAGCCTGGGTGACTGAGCGA 42543         T
              GA                  TCTCGCTC GTCACCCAGGCTGGA
                                  |||||||| ||||||||||||||||
                                  AGAGCGAG CAGTGGGTCCGACCT
                                      T
GAM1741  LOC81558  3'  TTCAGCTGCTGGCAGAGGGAGG 48681      G       CCCA
                                  TCTC CTCTGTCA    GGCTGGA
                                  |||| ||||||||    |||||||
                                  GGAG GAGACGGT    TCGACTT
                                    G       CG__
GAM1741  LOC85479  5'  TCCAGCCTGGGCGACAGAGCAA 53571     C       A
              GA                  TCT GCTCTGTC CCCAGGCTGGA
                                  ||| |||||||| ||||||||||||
                                  AGA CGAGACAG GGGTCCGACCT
                                    A       C
GAM1741  LOC89890  3'  TCCAGCCTGGATGACAGAGTGA 61209             C
              GA                  TCTCGCTCTGTCA CCAGGCTGGA
                                  |||||||||||||| |||||||||||
                                  AGAGTGAGACAGT GGTCCGACCT
                                        A
GAM1741  LOC90038  3'  TCCAGCCTGGGCAACAGAGTGA 61813           CA
              GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                  ||||||||||||  ||||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                       AC
GAM1741  LOC90038  3'  TCCAGCCTGGGTGACACAGTGA 61814         C
              GA                  TCTCGCT TGTCACCCAGGCTGGA
                                  ||||||| ||||||||||||||||
                                  AGAGTGA ACAGTGGGTCCGACCT
                                     C
GAM1741  LOC90072  3'  TCCAGCCTGGGGAACAGAGCAA 61963     C      CA
              GA                  TCT GCTCTGT  CCCAGGCTGGA
                                  ||| |||||||  ||||||||||||
                                  AGA CGAGACA  GGGTCCGACCT
                                    A      AG
GAM1741  LOC90072  5'  TCCAGCCTGGGTGACAGAACAA 61964     CGC
              GA                  TCT   TCTGTCACCCAGGCTGGA
                                  |||   ||||||||||||||||||
                                  AGA   AGACAGTGGGTCCGACCT
                                    ACA
GAM1741  LOC90072  5'  TCCAGCCTGGGTGACATATCAA 61965     CGCTC
              GA                  TCT     TGTCACCCAGGCTGGA
                                  |||     ||||||||||||||||
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                                AGA    ACAGTGGGTCCGACCT
                                  ACTAT
GAM1741  LOC90092  3'  TCCAGCCTGGCGACAAGAGCGA 62075        _  AC
                GA                  TCTCGCTCT GTC  CCAGGCTGGA
                                    ||||||||| |||  ||||||||||
                                    AGAGCGAGA CAG  GGTCCGACCT
                                       A  C_
GAM1741  LOC90110  5'  TCCAGCCTGGGCAACGGAGTGA 62182          CA
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||| ||||||||||
                                    AGAGTGAGGCA  GGGTCCGACCT
                                          AC
GAM1741  LOC90139  3'  TTTGGTCTGGGCTCAGTGGGA  56271       CT TCA      TG
                                    TCTCGCT  G   CCCAGGC  GA
                                    ||||||| |   ||||||| ||
                                    AGGGTGA  C   GGGTCTG  TT
                                       CT ___      GT
GAM1741  LOC90141  3'  TCCAGCCTGGATGATAGAGCAA 62310     C       C
                GA                  TCT GCTCTGTCA CCAGGCTGGA
                                    ||| ||||||||| ||||||||||
                                    AGA CGAGATAGT GGTCCGACCT
                                      A        A
GAM1741  LOC90155  5'  TCCAGCCTGGGCAACAAGAGTG 62368       _ CA
                A                    TCGCTCT GT  CCCAGGCTGGA
                                    ||||||| ||  ||||||||||
                                    AGTGAGA CA  GGGTCCGACCT
                                       A  AC
GAM1741  LOC90321  3'  CTCCAGCTTGGGTGACAGAGCG 62933
                AGA                   TCTCGCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACAGTGGGTTCGACCT
                                                CA
GAM1741  LOC90321  3'  TCCAACCTGGGTGACAGAGCGA 62938               C
                GA                  TCTCGCTCTGTCACCCAGG TGGA
                                    |||||||||||||||||| ||||
                                    AGAGCGAGACAGTGGGTCC ACCT
                                              A
GAM1741  LOC90393  5'  CTCCAGCCTGGGTGACAGAGTG 63307
                AGA                   TCTCGCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAGTGGGTCCGACCT
                                                CA
GAM1741  LOC90459  5'  TCGGGCTCTGCAGAGTGAGA   63566         TCACC  _  G
                                    TCTCGCTCTG    CAG GCT GA
                                    ||||||||||    ||| ||| ||
                                    AGAGTGAGAC    GTC CGG CT
                                          _____  T  G
GAM1741  LOC90538  3'  TCCAGTCTGGGTGAAAGAGCGA 63900         G
                GA                  TCTCGCTCT TCACCCAGGCTGGA
                                    ||||||||| ||||||||||||||
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                                AGAGCGAGA AGTGGGTCTGACCT
                                     A
GAM1741  LOC90573  5'  TCCAGCCTGGGCGACAGAGTGA 63962          A
                GA                  TCTCGCTCTGTC CCCAGGCTGGA
                                    |||||||||||| ||||||||||
                                    AGAGTGAGACAG GGGTCCGACCT
                                       C
GAM1741  LOC90591  3'  TCCAGCGGCGACAGAGCAAGA  64190    C      A  CAG
                                    TCT GCTCTGTC CC   GCTGGA
                                    ||| |||||||| ||   ||||||
                                    AGA CGAGACAG GG   CGACCT
                                      A       C ___
GAM1741  LOC90591  3'  TTCAGCCTGGGCAACAAGAGTG 64197       _  CA
                A                    TCGCTCT GT  CCCAGGCTGGA
                                    ||||||| ||  ||||||||||
                                    AGTGAGA CA  GGGTCCGACTT
                                        A  AC
GAM1741  LOC90624  3'  TCCAGCCTGGGGGACAGAGTGA 64373          A
                GA                  TCTCGCTCTGTC CCCAGGCTGGA
                                    |||||||||||| ||||||||||
                                    AGAGTGAGACAG GGGTCCGACCT
                                       G
GAM1741  LOC90631  3'  TCGGCTTCCAGAGTTGGG    64396    C     TCACCC
                                    TCT GCTCTG     AGGCTGG
                                    ||| ||||||     |||||||
                                    GGG TGAGAC     TTCGGCT
                                      T     C_____
GAM1741  LOC90639  3'  TCCAGCCTGAGCAACAGAGCCG 64416    C      CACC
                GA                  TCT GCTCTGT    CAGGCTGGA
                                    ||| |||||||    |||||||||
                                    AGG CGAGACA    GTCCGACCT
                                      C      ACGA
GAM1741  LOC90784  5'  TCCAGCCTGGGCAACAGAGTGA 64700          CA
                GA                  TCTCGCTCTGT  CCCAGGCTGGA
                                    ||||||||||  ||||||||||
                                    AGAGTGAGACA  GGGTCCGACCT
                                       AC
GAM1741  LOC90784  5'  TCCAGCTCGGGTGACAAGAGTG 64701        _     AG
                AGA                  TCTCGCTCT GTCACCC  GCTGGA
                                    |||||||| |||||||  ||||||
                                    AGAGTGAGA CAGTGGG  CGACCT
                                       A      CT
GAM1741  LOC90785  3'  ATTCCAGCCTGGGTGACAGAGC 64709
                GAGA                  TCTCGCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGCGAGACAGTGGGTCCGACCT
                                                TAC
GAM1741  LOC90841  5'  TCCAGCCTGGGTGATAGAGCTG 64873    C
                GA                  TCT GCTCTGTCACCCAGGCTGGA
                                    ||| ||||||||||||||||||
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                                AGG CGAGATAGTGGGTCCGACCT
                                  T
GAM1741 LOC90918 5' TCTGGGGACTGTGGTGGGG   65006       CT_  A    CTGGA
                                TCTCGCT  GTC CCCAGG
                                |||||||  ||| ||||||
                                GGGGTGG  CAG GGGTCT
                                    TGT  _       A
GAM1741 LOC91040 3' CCAGCTCTGCAGGGTGGGG   65338         TCACC  _
                                TCTCGCTCTG    CAG GCTGG
                                ||||||||||    ||| |||||
                                GGGGTGGGAC    GTC CGACC
                                      _____  T
GAM1741 LOC91040 3' TCTGGCCTCCCCAGCGTGGGG 65352      T  TCACCC   TG
                                TCTCGC CTG     AGGC  GA
                                |||||| |||     ||||  ||
                                GGGGTG GAC     TCCG  CT
                                   C  CCC___   GT
GAM1741 LOC91056 3' TCCAGCCTGGGCGACAGAGCAA 96410    C       A
            GG                    TCT GCTCTGTC CCCAGGCTGGA
                                ||| |||||||| ||||||||||
                                GGA CGAGACAG GGGTCCGACCT
                                  A       C
GAM1741 LOC91250 5' TCCAGCCTGAGTGACAGAGTGA 65921            C
            GA                    TCTCGCTCTGTCAC CAGGCTGGA
                                |||||||||||||| |||||||||
                                AGAGTGAGACAGTG GTCCGACCT
                                     A
GAM1741 LOC91250 5' TCCAGCCTGGGCAACAGAGTGA 65922          CA
            GA                    TCTCGCTCTGT  CCCAGGCTGGA
                                ||||||||||  ||||||||||
                                AGAGTGAGACA  GGGTCCGACCT
                                      AC
GAM1741 LOC91380 3' CTCCAGCCTGGGTGACAGAGTG 66446
            AGA                    TCTCGCTCTGTCACCCAGGCTGGA
                                ||||||||||||||||||||||||
                                AGAGTGAGACAGTGGGTCCGACCT
                                           CA
GAM1741 LOC91442 3' TCCAGCCTGGGCACCAGAGCGA 66648         TCA
            GA                    TCTCGCTCTG   CCCAGGCTGGA
                                ||||||||||   ||||||||||
                                AGAGCGAGAC   GGGTCCGACCT
                                     CAC
GAM1741 LOC91496 5' TTCAGCCATGGATGAGGAGTGG 66812        G  C  _
            GA                    TCTCGCTCT TCA CCA GGCTGGA
                                ||||||||| ||| ||| |||||||
                                AGGGTGAGG AGT GGT CCGACTT
                                     _  A  A
GAM1741 LOC91547 3' TCCAGCCTGGGCGACAGAGCGA 67006          A
            GA                    TCTCGCTCTGTC CCCAGGCTGGA
                                ||||||||||| ||||||||||
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                                AGAGCGAGACAG GGGTCCGACCT
                                      C
GAM1741 LOC91660 3' GCAATCTGGGTTACGGAGTGAG 67403          C     GC  GA
           A                    TCTCGCTCTGT ACCCAG  TG
                                |||||||||| |||||| ||
                                AGAGTGAGGCA TGGGTC  AC
                                      T     TA  GT
GAM1741 LOC91750 3' TCCAGCCTGGGCAACAGAGTGA 67657          CA
           GA                     TCTCGCTCTGT  CCCAGGCTGGA
                                  |||||||||| ||||||||||
                                  AGAGTGAGACA  GGGTCCGACCT
                                       AC
GAM1741 LOC91796 5' TCCAGCCAGGGGATAGAGCGAG 67788           A  A
           A                    TCTCGCTCTGTC CCC GGCTGGA
                                |||||||||||| ||| |||||||
                                AGAGCGAGATAG GGG CCGACCT
                                      _  A
GAM1741 LOC91812 3' TCCAGCCTGGGCAACAGAACGA 67821       C    CA
           GA                     TCTCG TCTGT  CCCAGGCTGGA
                                  ||||| |||||  ||||||||||
                                  AGAGC AGACA  GGGTCCGACCT
                                    A    AC
GAM1741 LOC91813 3' TCCAGCCTGGGCAACAGAACGA 67848       C    CA
           GA                     TCTCG TCTGT  CCCAGGCTGGA
                                  ||||| |||||  ||||||||||
                                  AGAGC AGACA  GGGTCCGACCT
                                    A    AC
GAM1741 LOC91862 3' TCCAGCCCAGGTGACAGAGCGA 54574             CA
           GA                     TCTCGCTCTGTCACC  GGCTGGA
                                  ||||||||||||||  |||||||
                                  AGAGCGAGACAGTGG  CCGACCT
                                       AC
GAM1741 LOC91963 5' TCCAGCCTGGGCAACAGAGTGA 68327          CA
                                  TCGCTCTGT  CCCAGGCTGGA
                                  |||||||||  ||||||||||
                                  AGTGAGACA  GGGTCCGACCT
                                      AC
GAM1741 LOC91963 3' TCTAGCTTGGGTGACAGAGCAA 68329     C
           GA                     TCT GCTCTGTCACCCAGGCTGGA
                                  ||| ||||||||||||||||||||
                                  AGA CGAGACAGTGGGTTCGATCT
                                    A
GAM1741 LOC92078 3' ACTCCAGCCTGGGTGACAGAGT 68586
           GAGA                     TCTCGCTCTGTCACCCAGGCTGGA
                                    ||||||||||||||||||||||||
                                    AGAGTGAGACAGTGGGTCCGACCT
                                          CAC
GAM1741 LOC92140 5' CTGGCGGCGGCGGAGTGAGG  68824           A  CAG  TG
                                  TCTCGCTCTGTC CC   GC  G
                                  |||||||||||| ||   ||  |
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                                GGAGTGAGGCGG GG   CG  C
                                      C  ___  GT
GAM1741  LOC92181  5'  CCGGAGGTGGCGGACGAGG   68944      C       CAGG
                                TCTCG TCTGTCACC   CTGG
                                ||||| |||||||||   ||||
                                GGAGC AGGCGGTGG   GGCC
                                  _       A___
GAM1741  LOC92223  3'  TCCAGCCTGGGCAACAAGAGTG 69055       _  CA
              A                  TCGCTCT GT  CCCAGGCTGGA
                                 ||||||| ||  ||||||||||
                                 AGTGAGA CA  GGGTCCGACCT
                                    A  AC
GAM1741  LOC92267  3'  TCCAGCCTGGGCAACAAGAGAG 69179     G  C   CA
              A                  TCTC CT TGT  CCCAGGCTGGA
                                 |||| || |||  ||||||||||
                                 AGAG GA ACA  GGGTCCGACCT
                                   A  _   AC
GAM1741  LOC92270  5'  TCCAGCTTGGGTGACAGAGTGA 69190
              G                  CTCGCTCTGTCACCCAGGCTGGA
                                 |||||||||||||||||||||||
                                 GAGTGAGACAGTGGGTTCGACCT

GAM1741  LOC92299  3'  CTGCAGCCTAGGTGACAGAGCG 69367             C     GA
              AGA                  TCTCGCTCTGTCACC AGGCTG
                                   ||||||||||||||| ||||||
                                   AGAGCGAGACAGTGG TCCGAC
                                            A     GTCA
GAM1741  LOC92299  3'  TCCAGCCTGGCGACAAAGCGAG 69373       C    AC
              A                  TCTCGCT TGTC  CCAGGCTGGA
                                 ||||||| ||||  ||||||||||
                                 AGAGCGA ACAG  GGTCCGACCT
                                    A   C_
GAM1741  LOC92340  3'  TCCAGCCTAGTAATGGAGCAAG 69568     C      C  CC
              A                  TCT GCTCTGT AC  AGGCTGGA
                                 ||| ||||||| ||  ||||||||
                                 AGA CGAGGTA TG  TCCGACCT
                                   A      A  A_
GAM1741  LOC92360  3'  TCCAGCCTGGGTGACAGAGCAA 69626     C
              GG                   TCT GCTCTGTCACCCAGGCTGGA
                                   ||| ||||||||||||||||||||
                                   GGA CGAGACAGTGGGTCCGACCT
                                     A
GAM1741  LOC92405  3'  TCTAGCCTGGGCAACAGAGCAA 69718     C      CA
              GG                   TCT GCTCTGT  CCCAGGCTGGA
                                   ||| |||||||  ||||||||||
                                   GGA CGAGACA  GGGTCCGATCT
                                     A      AC
GAM1741  LOC92421  5'  TCCGGTCTGGGTCCCCGAGA   69730      CTCTGTC
                                TCTCG      ACCCAGGCTGGA
                                |||||      ||||||||||||
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                                AGAGC      TGGGTCTGGCCT
                                  CCC____
GAM1741  LOC92465  5'  TCCAGCCTGGGCGACAGAGCGA 69955           A
                GA                  TCTCGCTCTGTC CCCAGGCTGGA
                                    |||||||||||| ||||||||||
                                    AGAGCGAGACAG GGGTCCGACCT
                                          C
GAM1741  LOC92465  5'  TCCAGTCTGGGCAACAGAGCAA 69956     C      CA
                GA                  TCT GCTCTGT  CCCAGGCTGGA
                                    ||| |||||||  ||||||||||
                                    AGA CGAGACA  GGGTCTGACCT
                                      A       AC
GAM1741  LOC92466  5'  TCCAGCCTGGGAGACAGAGTGA 69969           A
                GA                  TCTCGCTCTGTC CCCAGGCTGGA
                                    |||||||||||| ||||||||||
                                    AGAGTGAGACAG GGGTCCGACCT
                                          A
GAM1741  LOC92492  3'  TCCAGCCTGGATGACAGCGAGA 70083        CT    C
                                    TCTCGCT  GTCA CCAGGCTGGA
                                    |||||||  |||| ||||||||||
                                    AGAGCGA  CAGT GGTCCGACCT
                                       __    A
GAM1741  LOC92539  3'  TCTAGCTTGGAAGGGGGAGGGA 70224     G    G  AC
                                    TC CTCT TC  CCAGGCTGGA
                                    || |||| ||  ||||||||||
                                    AG GAGG GG  GGTTCGATCT
                                     G    G  AA
GAM1741  LOC92568  3'  ATCTGGGGACTGTTGTGGGGTG 70324          _______  A      CTGGA
                GGA                   TCTCGCTCT      GTC CCCAGG
                                    |||||||||      ||| ||||||
                                    AGGGTGGGG      CAG GGGTCT
                                         TGTTGT  _        AG
GAM1741  LOC92568  3'  CTCCAGCCTGGGTGACAGAGTG 70328
                AGA                   TCTCGCTCTGTCACCCAGGCTGGA
                                    |||||||||||||||||||||||||
                                    AGAGTGAGACAGTGGGTCCGACCT
                                                CA
GAM1741  LOC92573  3'  ACTCCAGCCTGGGTGACAGAGC 70365
                GAGA                   TCTCGCTCTGTCACCCAGGCTGGA
                                    |||||||||||||||||||||||||
                                    AGAGCGAGACAGTGGGTCCGACCT
                                                CAC
GAM1741  LOC92661  5'  TCATGATGGGTGGCAGAGCAAG 70635     C           GGC   A
                A                    TCT GCTCTGTCACCCA   TGG
                                    ||| ||||||||||||   |||
                                    AGA CGAGACGGTGGGT   ACT
                                      A            AGT
GAM1741  LOC92710  5'  TCTGGTCACCAAGGCTGGGCGG 70870         T   ACCCA   TG
                GA                    TCTCGCTC GTC     GGC  GA
                                    |||||||| |||     |||  ||
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                                AGGGCGGG CGG    CTG  CT
                                     T   AACCA   GT
GAM1741  LOC92771  3'  TCCAGCCTGGGCCACAGAATGA 54215      C    CA
              GA                   TCTCG TCTGT  CCCAGGCTGGA
                                   ||||| |||||  ||||||||||
                                   AGAGT AGACA  GGGTCCGACCT
                                     A     CC
GAM1741  LOC92973  5'  TCCAGCCTGGGCAACAGAGTGA 71594          CA
              GG                   TCTCGCTCTGT  CCCAGGCTGGA
                                   ||||||||||  ||||||||||
                                   GGAGTGAGACA  GGGTCCGACCT
                                         AC
GAM1741  LOC93070  3'  TCCAGCCTGGGCAACAGAGGGA 71815      G    CA
              GA                   TCTC CTCTGT  CCCAGGCTGGA
                                   |||| ||||||  ||||||||||
                                   AGAG GAGACA  GGGTCCGACCT
                                     G     AC
GAM1741  LOC93132  5'  ACCGTAGCCTGGGTGATAAGAG 71972          _          GA
              TGAGA                  TCTCGCTCT GTCACCCAGGCTG
                                   |||||||| ||||||||||||
                                   AGAGTGAGA TAGTGGGTCCGAT
                                        A           GCCAC
GAM1741  LOC93190  3'  TCCAGCCTTGGTGACAGAGTGA 72100            C
              GA                   TCTCGCTCTGTCACC AGGCTGGA
                                   |||||||||||||| ||||||||
                                   AGAGTGAGACAGTGG TCCGACCT
                                          T
GAM1741  LOC93613  3'  TCCAACCTGGGCGGCAGAGTGA 73082          A    C
              GA                   TCTCGCTCTGTC CCCAGG TGGA
                                   |||||||||||| |||||| ||||
                                   AGAGTGAGACGG GGGTCC ACCT
                                         C     A
GAM1741  LOC96597  5'  TCCAGCCCCTGATGGGGCAGA  67466    C       CCCA
                                   TCT GCTCTGTCA   GGCTGGA
                                   ||| |||||||||   |||||||
                                   AGA CGGGGTAGT   CCGACCT
                                     _       CC__
GAM1741  LOC96597  5'  TCGGACCCTGATGGGGTGGA  67470    T       CCCA _ TG
                                   TC CGCTCTGTCA   GG C  GA
                                   || ||||||||||   || |  ||
                                   AG GTGGGGTAGT   CC G  CT
                                     _       C___  A GT
GAM1742  SCAMP1    3'  GCTAAATAAATATTCTCC    54500    T    C
                                   GGA AATATT ATTTAGC
                                   ||| |||||| |||||||
                                   CCT TTATAA TAAATCG
                                     C     A
GAM1742  SCAMP1    3'  GCTAAATAAATATTCTCC    54501    T    C
                                   GGA AATATT ATTTAGC
                                   ||| |||||| |||||||
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                                CCT TTATAA TAAATCG
                                  C     A
GAM1742 NX-17    3' TGAATATCAGCCCCTAATA   40706        ATA_
                                TATTAGGG   ATATTCA
                                ||||||||   |||||||
                                ATAATCCC   TATAAGT
                                    CGAC
GAM1742 LOC161589 3' GCTAAATGAATATTATCCCTAA 83159
              TA                  TATTAGGGATAATATTCATTTAGC
                                  ||||||||||||||||||||||||
                                  ATAATCCCTATTATAAGTAAATCG

GAM1743 DTR      3' ATCCCCACAATCTGGCTTAGTG 10452     G_ _      CA
              C                   GCG  AA CCAGATTG  GGGAT
                                  |||  || ||||||||  |||||
                                  CGT  TT GGTCTAAC  CCCTA
                                    GA  C       AC
GAM1743 SHANK2   3' ATCCCTGTCCATTGATTCCACT 56552    C   C   ATT
                                  AG GGAA CAG   GCAGGGAT
                                  || |||| |||   ||||||||
                                  TC CCTT GTT   TGTCCCTA
                                   A   A   ACC
GAM1743 BCL2L1   3' ATCCCCAGGGGTCCCAGCCAC  57584    A  _  A   AGAT  CA
                                  GT GC GG ACC    TG  GGGAT
                                  || || || |||    ||  |||||
                                  CA CG CC TGG    AC  CCCTA
                                   C  A  C   GG__  __
GAM1743 FLJ12121 3' ATCCCTGCAGCCTGCCACTAC  47089     C  AAC   AT
                                  GTAG GG   CAG  TGCAGGGAT
                                  |||| ||   |||  |||||||||
                                  CATC CC   GTC  ACGTCCCTA
                                    A ___   CG
GAM1743 FLJ13315 3' TCCCTGTAGTCCCAGCTAC    47199      _  AACCA
                                  GTAGC GG    GATTGCAGGGA
                                  ||||| ||    ||||||||||
                                  CATCG CC    CTGATGTCCCT
                                     A _____
GAM1743 KIAA0441  3' CCCTGTAATCCCAGCTAC     29630      _  AACCA
                                  GTAGC GG    GATTGCAGGG
                                  ||||| ||    |||||||||
                                  CATCG CC    CTAATGTCCC
                                     A _____
GAM1743 RAB3D    5' CCCTGCAGGCGGCGCCCCCTAC 16259     C_  AA  AGA
                                  GTAG  GG  CC   TTGCAGGG
                                  ||||  ||  ||   ||||||||
                                  CATC  CC  GG   GACGTCCC
                                    CC  GC  CG_
GAM1743 Rpo1-2   3' CCCTGTAGTCCCAGCTAC    39217      _  AACCA
                                  GTAGC GG    GATTGCAGGG
                                  ||||| ||    |||||||||
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                                CATCG CC    CTGATGTCCC
                                  A _____
GAM1743  LOC112609 3'  GTTCTAATCTGGCCCTGCCAC  73200    A   AA     GCA
                                GT GCGG  CCAGATT   GGGAT
                                || ||||  |||||||   |||||
                                CA CGTC  GGTCTAA   TCTTG
                                 C   CC     ___
GAM1743  LOC135892 3'  TCCCCATGGTTCCTGCCAC   75763    A _     GATTGCA
                                GT GC GGAACCA      GGGA
                                || || |||||||      ||||
                                CA CG CCTTGGT      CCCT
                                 C  T      AC_____
GAM1743  LOC145553 5'  TCCCTGCATCTCCCGC      57467      AACC   T
                                GCGG    AGAT GCAGGGA
                                ||||    |||| |||||||
                                CGCC    TCTA CGTCCCT
                                  C___   _
GAM1743  LOC151178 3'  ATCCAAAGCAATCTGGTCACAC 80951    A___        AG_
            C                    GG    ACCAGATTGC   GGAT
                                ||   ||||||||||   ||||
                                CC   TGGTCTAACG   CCTA
                                 ACAC        AAA
GAM1743  LOC152627 5'  CCCTGTAATCCCAGCTAC    81508      _ AACCA
                                GTAGC GG    GATTGCAGGG
                                ||||| ||    ||||||||||
                                CATCG CC    CTAATGTCCC
                                  A _____
GAM1743  LOC196957 5'  ATCCCTGCCCTTGCGGCTACCA 89185     C  AA_  A_  TT
            CTAC                   GTAG GG   CC  GA  GCAGGGAT
                                |||| ||   ||  ||  ||||||||
                                CATC CC   GG  TT  CGTCCCTA
                                  A  ATC  CG  CC
GAM1743  LOC196961 5'  ATCCCTGCCCTTGCGGCTACCA 89199     C  AA_  A_  TT
            CTAC                   GTAG GG   CC  GA  GCAGGGAT
                                |||| ||   ||  ||  ||||||||
                                CATC CC   GG  TT  CGTCCCTA
                                  A  ATC  CG  CC
GAM1743  LOC197138 5'  ATCCCTGCCCTTGCGGCTACCA 89248     C  AA_  A_  TT
            CTAC                   GTAG GG   CC  GA  GCAGGGAT
                                |||| ||   ||  ||  ||||||||
                                CATC CC   GG  TT  CGTCCCTA
                                  A  ATC  CG  CC
GAM1744  CBFA2T3   3'  TGCCCCTCTCCGAAAGAAGA   19020      AGAG       AA
                                TTTTC    TCGGAGAGG  CA
                                |||||    |||||||||  ||
                                AGAAG    AGCCTCTCC  GT
                                  AA__        CC
GAM1744  DHFR      3'  TTGTTCCCCCTCCCTCTGAAAA 7662          TC    A_
            A                    TTTTTCAGAG  GGAG  GGAACAA
                                ||||||||||  ||||  |||||||
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                                AAAAAGTCTC  CCTC  CCTTGTT
                                      __    CC
GAM1744  GRAF     3'  TCACTGCCACTCTGAAAAA   31247          C  AG  _
                                TTTTTCAGAGT GG  AG GA
                                |||||||||||  ||  || ||
                                AAAAAGTCTCA CC  TC CT
                                      _  G_  A
GAM1744  NKX3A    3'  TCACTGAATATCAACTCTGAAA 21616          _______   A
              GA                  TTTTTCAGAG      TCGG GA
                                |||||||||||      |||| ||
                                AGAAAGTCTC      AGTC CT
                                     AACTATA    A
GAM1744  PKHD1    3'  TCCTCTTTCTCCTAAAAA    57718      CA   TC
                                TTTTT  GAG  GGAGAGGA
                                |||||  |||  ||||||||
                                AAAAA  CTC  TTTCTCCT
                                   TC  __
GAM1744  POLR2H   3'  TGCCCCTCCCCTTTTTGTAAAA 21723      _    TC  A   AA
              A                   TTTTT CAGAG  GG GAGG  CA
                                ||||| |||||  || ||||  ||
                                AAAAA GTTTT  CC CTCC  GT
                                   T    TC  _   CC
GAM1744  PPM1D    3'  TGTTCCTCATGTTGCTGAAAAA 14628        AGT  GA
                                TTTTTCAG   CG  GAGGAACA
                                ||||||||   ||  ||||||||
                                AAAAAGTC   GT  CTCCTTGT
                                     GTT  A_
GAM1744  TTC3     3'  TTGTTCCCCTTTTCTGTTTGAA 13889         GT    ___
              AAA                   TTTTTCAGA  CGGAGA   GGAACAA
                                |||||||||  ||||||   |||||||
                                AAAAAGTTT  GTCTTT   CCTTGTT
                                     __     TCC
GAM1744  YWHAZ    3'  CTCCCCACCCTGAAAAA     14155        A  C  A
                                TTTTTCAG GT GG GAG
                                |||||||| || || |||
                                AAAAAGTC CA CC CTC
                                     C  C  _
GAM1744  C8orf13  3'  CCATCCCATATTCTGAAAAA   82472          C_  A  _
                                TTTTTCAGAGT  GG GA GG
                                ||||||||||  || || ||
                                AAAAAGTCTTA  CC CT CC
                                      TA  _  A
GAM1744  CNOT3    5'  CTGTCCTGCTCTGAAAAA    27984          C   G
                                TTTTTCAGAGT GGA AG
                                |||||||||| ||| ||
                                AAAAAGTCTCG CCT TC
                                      T   G
GAM1744  FLJ10040 3'  TGTTCAGAACTCTGAAAA    36222          CGGAGAG
                                TTTTCAGAGT      GAACA
                                |||||||||      |||||
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                                  AAAAGTCTCA      CTTGT
                                        AGA____
GAM1744  FLJ21140  3'  TTGCTCCTTCTGACTCTGTAAA 45838      T        G    A
              A                    TTTT CAGAGTCGGA AGGA CAA
                                  |||| |||||||||| |||| |||
                                  AAAA GTCTCAGTCT TCCT GTT
                                    T        _    C
GAM1744  FLJ32421  5'  CTGAACCGACTCTGAGAAA   59119            AGA
                                  TTTTTCAGAGTCGG   GG
                                  ||||||||||||||   ||
                                  AAAGAGTCTCAGCC   TC
                                        AAG
GAM1744  KIAA0830  3'  TTGTGGCCATCTCTGAAAAA   70274          TC  AGAGGA
                                  TTTTTCAGAG  GG     ACAA
                                  ||||||||||  ||     ||||
                                  AAAAAGTCTC  CC     TGTT
                                        TA  GG____
GAM1744  KIAA0894  3'  TCACCACACTCTGAAAAA    30341          C_  A
                                  TTTTTCAGAGT  GG GA
                                  ||||||||||  || ||
                                  AAAAAGTCTCA  CC CT
                                        CA  A
GAM1744  KIAA1037  3'  TCCCCAGCCCTGAAAAA     31138        A  C  AGA
                                  TTTTTCAG GT GG   GGA
                                  |||||||| || ||   |||
                                  AAAAAGTC CG CC   CCT
                                       C  A  ___
GAM1744  MGC11034  3'  TTCTTCTACTCTGAAAAA    49578          C
                                  TTTTTCAGAGT GGAGAG
                                  |||||||||| ||||||
                                  AAAAAGTCTCA CTTCTT
                                        T
GAM1744  P450RAI-2 3'  CCCTCCGCCCTGAAAAA     39571        A T    A
                                  TTTTTCAG G CGGAG GG
                                  |||||||| | ||||| ||
                                  AAAAAGTC C GCCTC CC
                                       C _    _
GAM1744  STAG2    3'  TTCCCCTACCCTGAAGAA    71090        A  C  AGA
                                  TTTTTCAG GT GG   GGAA
                                  |||||||| || ||   ||||
                                  AAGAAGTC CA CC   CCTT
                                       C  T  ___
GAM1744  VANGL1   3'  CTGTCCACCCTGAAAAA     58043        A  C   G
                                  TTTTTCAG GT GGA AG
                                  |||||||| || ||| ||
                                  AAAAAGTC CA CCT TC
                                       C  _   G
GAM1744  LOC132671 3'  CCTTAGAGACTTTGAAAAA   59839          GGA
                                  TTTTTCAGAGTC   GAGG
                                  ||||||||||||   ||||
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                                AAAAAGTTTCAG   TTCC
                                      AGA
GAM1744  LOC148089 3'  TGTCCCCAATCCACTCCAGAAA 79337      A_   C  GA_ A
              A                    TTTTC  GAGT GGA   GG ACA
                                   ||||| |||| |||   || |||
                                   AAAAG  CTCA CCT   CC TGT
                                      AC   _   AAC  C
GAM1744  LOC150225 3'  CCGCCCCCGGCTCTGCAAAA   86188     T       AGA_
                                   TTTT CAGAGTCGG    GG
                                   |||| |||||||||    ||
                                   AAAA GTCTCGGCC    CC
                                     C       CCCG
GAM1744  LOC200895 3'  TTGTTCCCCCTCCCTCTGAGAA 90336         TC    A_
              A                    TTTTTCAGAG  GGAG  GGAACAA
                                   ||||||||||  ||||  |||||||
                                   AAAGAGTCTC  CCTC  CCTTGTT
                                         __    CC
GAM1744  LOC220549 5'  TTCCTCTTATTACTGTAAAA   94512     T   AGTCG
                                   TTTT CAG    GAGAGGAA
                                   |||| |||    ||||||||
                                   AAAA GTC    TTCTCCTT
                                     T   ATTA_
GAM1744  LOC220827 3'  TGCCCCTTTCCTGAAAAA    92883       GAGTC      AA
                                   TTTTTCA    GGAGAGG  CA
                                   |||||||    |||||||  ||
                                   AAAAAGT    CCTTTCC  GT
                                        _____      CC
GAM1744  LOC256073 5'  TTCCTCTCCTGAAGAA      98491       GAGTC
                                   TTTTTCA    GGAGAGGAA
                                   |||||||    |||||||||
                                   AAGAAGT    CCTCTCCTT
                                        _____
GAM1744  LOC93550  3'  TTGTTCGACTCTAAAAGA    72979      C       G
                                   TTTTT AGAGTCGGA AG
                                   ||||| ||||||||| ||
                                   AGAAA TCTCAGCTT TT
                                      A       G
GAM1745  CYP4F3    3'  AAAGAAAAGAAAATCCCT    7986         _ GGC
                                   GGGGATTT CT   TCTTT
                                   |||||||| ||   |||||
                                   TCCCTAAA GA   AGAAA
                                        A  AA_
GAM1745  DYRK2     3'  AAGAAAGAGGGTTGAAAATCCT 22412        CT       CC
              C                     GGGGATTT  GGCTCTTT  TCTT
                                   ||||||||  ||||||||  ||||
                                   CTCCTAAA  TTGGGAGA  AGAA
                                        AG       A_
GAM1745  TEM8      3'  AAGAAGAAAGAAAGAAATCCC  50818         GGC     C
                                   GGGATTTCT   TCTTTC TCTT
                                   |||||||||   |||||| ||||
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                                CCCTAAAGA   AGAAAG AGAA
                                     A__     A
GAM1745  AD-003    3'  AGAGGAAGGAAACACCCC    26778     ATTTC  GC
                                GGGG    TG  TCTTTCCTCT
                                ||||    ||  ||||||||||
                                CCCC    AC  AGGAAGGAGA
                                  _____  AA
GAM1745  C15orf12  3'  AGGAAAAACTGGAAATCCCC   37475         TG CTC
                                GGGGATTTC  G   TTTCCT
                                |||||||||  |   ||||||
                                CCCCTAAAG  C   AAAGGA
                                     GT AA_
GAM1745  FLJ23189  3'  AAGAACTGGACCAAAAATCTCC 47525         C   C   TTCC
                                GGGGATTT TGG TCT    TCTT
                                |||||||| ||| |||    ||||
                                CCTCTAAA ACC AGG    AGAA
                                     A   _   TCA_
GAM1745  KIAA0057  3'  AAGAGGAAAAAACCATTCTC   25394      TTTC   CTC
                                GGGGA    TGG   TTTCCTCTT
                                |||||    |||   |||||||||
                                CTCTT    ACC   AAAGGAGAA
                                   _____   AAA
GAM1745  KIAA1853  5'  AAGAAGAAAAAGAAGAAATCC  69915         GG  C    C
                                GGATTTCT  CT TTTC TCTT
                                ||||||||  || |||| ||||
                                CCTAAAGA  GA AAAG AGAA
                                     A_  A    A
GAM1745  KIAA1922  3'  AGAGGAAAAAAAATCGCC    73981    G    CTGGCTC
                                GG GATTT       TTTCCTCT
                                || |||||       ||||||||
                                CC CTAAA       AAAGGAGA
                                 G     AA_____
GAM1745  KIAA1958  3'  AGAGAAAGGAGAATCCCC    82771        TCTGG     C
                                GGGGATT     CTCTTT CTCT
                                |||||||     |||||| ||||
                                CCCCTAA     GAGGAA GAGA
                                   _____       A
GAM1745  MGC5466   3'  AAAGGGCAGAAATCACC     73435    G       G
                                GG GATTTCTG CTCTTT
                                || |||||||| ||||||
                                CC CTAAAGAC GGGAAA
                                 A       _
GAM1745  LOC134265 3'  AAGAGGAAAGAAGGAAAATCCC 75650      A     GGC
                                GGGG TTTCT   TCTTTCCTCTT
                                |||| |||||   ||||||||||||
                                CCCT AAAGG   AGAAAGGAGAA
                                  A    A__
GAM1745  LOC151009 3'  AGGAAAAGCCAGAATCCCC    86363        T     C
                                GGGGATT CTGGCT TTTCCT
                                ||||||| |||||| ||||||
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                                CCCCTAA GACCGA AAAGGA
                                      _     _
GAM1745  LOC151391 3'  AAGGCTGGAAGAGCAGAAATCC 86510          G      C_
              CC                    GGGGATTTCTG CTCTTTC  TCTT
                                    |||||||||||| |||||||  ||||
                                    CCCCTAAAGAC GAGAAGG  GGAA
                                          _      TC
GAM1745  LOC154881 3'  AAGAAGAAAGAGCATCTTCTCT 82065       TTTCTG       C
              CC                    GGGGA     GCTCTTTC TCTT
                                    |||||     |||||||| ||||
                                    CCTCT     CGAGAAAG AGAA
                                       CTTCTA       A
GAM1745  LOC196047 5'  AAGAGGAAAAAGCCAAAGA   91134     C    C
                                    TTT TGGCT TTTCCTCTT
                                    ||| ||||| |||||||||
                                    AGA ACCGA AAAGGAGAA
                                      A     A
GAM1745  LOC256830 5'  AAGAAGAAAGAGAGAATCTCC  96194        T  GG      C
                                    GGGGATT CT  CTCTTTC TCTT
                                    |||||||  ||  ||||||| ||||
                                    CCTCTAA GA  GAGAAAG AGAA
                                       _ __       A
GAM1746  ABCB11    3'  CACACATGACGCACCAGT    14974          _    _
                                    ACTGGTGCG CATG GTG
                                    ||||||||| |||| |||
                                    TGACCACGC GTAC CAC
                                         A    A
GAM1746  DLG5      5'  GGCCATCCAGCTGCAGCACCAG 83818         _   __   _
              T                      ACTGGTGC GCA  TGG TGGCC
                                    ||||||||  |||  |||  |||||
                                    TGACCACG CGT  ACC ACCGG
                                         A   CG   T
GAM1746  HTR2C     5'  GCGCAGCTCAGCGCACCG     7872          A  GT   CA
                                    TGGTGCGC TG  GGC  CGC
                                    |||||||  ||  |||  |||
                                    GCCACGCG AC  TCG  GCG
                                       _  __   AC
GAM1746  ICAM2     3'  GCATGGCCACCACCACGGT    7891       G  CGCA       C
                                    ACTG TG    TGGTGGCCA GC
                                    ||||  ||    |||||||||  ||
                                    TGGC AC    ACCACCGGT CG
                                      _  C___         A
GAM1746  ITGAL     3'  GGCGTGGTGGCACACACCTGT  11047     T    CGCA  _  G
                                    AC GGTG    TG GT GCCACGCC
                                    ||  ||||    ||  ||  ||||||||
                                    TG CCAC    AC CG TGGTGCGG
                                     T    _____  A  G
GAM1746  KCNQ1     5'  CGTGGGTGCGCGCCA       5841           GGTGG
                                    TGGTGCGCAT     CCACG
                                    ||||||||||     |||||
```

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                                ACCGCGCGTG    GGTGC
                                      _____
GAM1746 PKD2    5' GCGCGGCGCCGCGCACC    60718       AT   G A
                                GGTGCGC  GGTG CC CGC
                                |||||||  |||| || |||
                                CCACGCG  CCGC GG GCG
                                   __   _ C
GAM1746 RBM3    5' GCGTGGCCACCAAGCCCC   71011    TGC  A
                                GG   GC TGGTGGCCACGC
                                ||   || ||||||||||||
                                CC   CG ACCACCGGTGCG
                                 C__  A
GAM1746 ABHD2   3' GGCACCCACCATGCACACCTGT 23796    T   C       CCAC
                                AC GGTG GCATGGTGG    GCC
                                || |||| |||||||||    |||
                                TG CCAC CGTACCACC    CGG
                                 T   A       CA__
GAM1746 CRTAM   3' GGCGTAGTGGTGCGCACCTGT  39474    T       GGTG  C
                                AC GGTGCGCAT    GC ACGCC
                                || |||||||||    || |||||
                                TG CCACGCGTG    TG TGCGG
                                 T       G___  A
GAM1746 D21S2056E 3' CGTGGCCAGGCACAGT      14864      G   GCATGG
                                ACTG TGC     TGGCCACG
                                |||| |||     ||||||||
                                TGAC ACG     ACCGGTGC
                                  _  G_____
GAM1746 DKFZP434K2235 3' TGGCCACCTGACCTGT      84500    T   GCG  T
                                AC GGT   CA GGTGGCCA
                                || |||   || ||||||||
                                TG CCA   GT CCACCGGT
                                 T  ___  _
GAM1746 DKFZP434P211 3' GCATGGCCATTGACCCAGT    28028      TG  CATG     C
                                ACTGG  CG    GTGGCCA GC
                                |||||  ||    ||||||| ||
                                TGACC  GT    TACCGGT CG
                                   CA  _____      A
GAM1746 FKBP14   3' GGCGTGGTGGTGCACACCTGT  36068    T   C   GGTG
                                AC GGTG GCAT    GCCACGCC
                                || |||| ||||    ||||||||
                                TG CCAC CGTG    TGGTGCGG
                                 T   A   G___
GAM1746 FLJ10116 5' GGCGCGGTGGCCGCGCCCCAG  36304      T   AT   G   A
                                CTGG GCGC  GGT GCC CGCC
                                |||| ||||  ||| ||| ||||
                                GACC CGCG  CCG TGG GCGG
                                  C    __  G   C
GAM1746 FLJ11301  3' GGCGTGGTGGCGCGCACCTGT  37807    T     ATG  G
                                AC GGTGCGC   GT GCCACGCC
                                || |||||||   || ||||||||
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                              TG CCACGCG   CG TGGTGCGG
                               T     ___ G
GAM1746  FLJ13448  3' GGCGTGGTGGCACACACCTGT  47883    T   CGCA _ G
                              AC GGTG   TG GT GCCACGCC
                              || ||||   || || ||||||||
                              TG CCAC   AC CG TGGTGCGG
                               T   _____ A  G
GAM1746  FLJ14011  3' GGCGTGGTGGTGCGCACCTGT  42318    T      GGTG
                              AC GGTGCGCAT   GCCACGCC
                              || |||||||||   ||||||||
                              TG CCACGCGTG   TGGTGCGG
                               T      G___
GAM1746  FLJ20211  3' GGCATGGTGATGCGCACC    35263        GGTG   C
                              GGTGCGCAT   GCCA GCC
                              |||||||||   |||| |||
                              CCACGCGTA   TGGT CGG
                                    G___   A
GAM1746  FLJ20306  3' GGCGTGGTGGCACGCACCTGT  35396    T    CATG  G
                              AC GGTGCG   GT GCCACGCC
                              || ||||||   || ||||||||
                              TG CCACGC   CG TGGTGCGG
                               T    A___ G
GAM1746  FLJ20802  3' GGCATGGTGGTGTGCGCACCTG 36111    T       G  G   C
            T                  AC GGTGCGCATG TG CCA GCC
                              || |||||||||| || ||| |||
                              TG CCACGCGTGT GT GGT CGG
                               T       G  _  A
GAM1746  HGC6.1.1  3' GCGTGGCCGAGTCACACAGT   27612     _   C  ATGG
                              ACTG GTG GC   TGGCCACGC
                              |||| ||| ||   |||||||||
                              TGAC CAC TG   GCCGGTGCG
                                A   _  A___
GAM1746  KIAA0821  3' GCCACGCCACCAGCCACACGCA 30608       CA   T________   CAC
            CCAG                 CTGGTGCG  TGG      GGC   GC
                              |||||||  |||      |||   ||
                              GACCACGC  ACC      CCG   CG
                                   AC   GACCAIII   CAC
GAM1746  KIAA1871  3' GGCATGAGCCACTGCACCAG   61908       GCAT     _  C
                              CTGGTGC   GGTGGC CA GCC
                              |||||||   |||||| || |||
                              GACCACG   TCACCG GT CGG
                                   _____     A  A
GAM1746  PACSIN2   3' GGCACAGATTGATGCGCACCAG 24299          GG___  _
            T                  ACTGGTGCGCAT    TG GCC
                              ||||||||||||    || |||
                              TGACCACGCGTA    AC CGG
                                     GTTAG  A
GAM1746  PP1057    5' GGCCACCCAGCACCAGT     49254        GCAT
                              ACTGGTGC   GGTGGCC
                              ||||||||   |||||||
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                                TGACCACG   CCACCGG
                                    AC__
GAM1746 PP3501   3' GGCGCGGCCACCCACGCACC  41684      CAT     A
                                GGTGCG  GGTGGCC CGCC
                                ||||||  ||||||| ||||
                                CCACGC  CCACCGG GCGG
                                   AC_     C
GAM1746 TEX27    3' GGCATGGCCACCACGTGACGCT 41953     _  A       C
                                GGTG CGC TGGTGGCCA GCC
                                |||| ||| ||||||||| |||
                                TCGC GTG ACCACCGGT CGG
                                  A  C       A
GAM1746 WBSCR21  3' GGCGTGGTGGTGCACACCTGT  49305   T   C   GGTG
                                AC GGTG GCAT   GCCACGCC
                                || |||| ||||   ||||||||
                                TG CCAC CGTG   TGGTGCGG
                                 T   A   G___
GAM1746 WSB1     3' GGCGTGGTGGTGCACACCTGT  56976   T   C   GGTG
                                AC GGTG GCAT   GCCACGCC
                                || |||| ||||   ||||||||
                                TG CCAC CGTG   TGGTGCGG
                                 T   A   G___
GAM1746 WSB1     3' GGCGTGGTGGTGCACACCTGT  56992   T   C   GGTG
                                AC GGTG GCAT   GCCACGCC
                                || |||| ||||   ||||||||
                                TG CCAC CGTG   TGGTGCGG
                                 T   A   G___
GAM1746 WWP1     5' TGGCCACTGCTTCACCA    81262     C_  TG
                                TGGTG  GCA  GTGGCCA
                                |||||  |||  |||||||
                                ACCAC  CGT  CACCGGT
                                   TT  __
GAM1746 ZDHHC3   3' GGCATGGCCACTCAGACACAAG 33933    G  CGCA _     C
             T                   ACT GTG   TG GTGGCCA GCC
                                 ||| |||   || ||||||| |||
                                 TGA CAC   AC CACCGGT CGG
                                   A  AG__  T     A
GAM1746 ZNF297B  3' GGCGTGGTGGCGCACACCTGT  26663   T   C  ATG  G
                                AC GGTG GC   GT GCCACGCC
                                || |||| ||   || ||||||||
                                TG CCAC CG   CG TGGTGCGG
                                 T   A  ___  G
GAM1746 LOC112703 5' GCACTCACCCCTCGCGCACCAG 73878        AT  T  CCAC_
             T                   ACTGGTGCGC  GG GG    GC
                                 ||||||||||  || ||    ||
                                 TGACCACGCG  CC CC    CG
                                       CT  _  ACTCA
GAM1746 LOC113828 3' GCGCAGGTCGCACACTGCACCA 57386        CATG    A_
             GT                   ACTGGTGCG   GTGGCC  CGC
                                 |||||||||   ||||||  |||
```

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                                TGACCACGT   CGCTGG  GCG
                                    CACA    AC
GAM1746  LOC115129 3'  GGCGTGGTGGCACACACCCGT  73623   T   CGCA  _  G
                                AC GGTG   TG GT GCCACGCC
                                || ||||   || || ||||||||
                                TG CCAC   AC CG TGGTGCGG
                                 C   ____  A  G
GAM1746  LOC125268 3'  CGTGGCCATGTGCACACAG   76575    _     TGG
                                CTG GTGCGCA  TGGCCACG
                                ||| |||||||  ||||||||
                                GAC CACGTGT  ACCGGTGC
                                  A     ___
GAM1746  LOC132617 5'  GCACAGGCCTGGCACCAGT   76418       G  TGGT   AC_
                                ACTGGTGC CA   GGCC   GC
                                |||||||| ||   ||||  ||
                                TGACCACG GT   CCGG   CG
                                    _ ____    ACA
GAM1746  LOC150174 3'  GCATGGCCATTGACCCAGT   80437     TG  CATG     C
                                ACTGG  CG   GTGGCCA GC
                                |||||  ||   ||||||| ||
                                TGACC  GT   TACCGGT CG
                                   CA ____     A
GAM1746  LOC150213 3'  GCATGGCCATTGACCCAGT   75356     TG  CATG     C
                                ACTGG  CG   GTGGCCA GC
                                |||||  ||   ||||||| ||
                                TGACC  GT   TACCGGT CG
                                   CA ____     A
GAM1746  LOC150236 3'  GCATGGCCATTGACCCAGT   80501     TG  CATG     C
                                ACTGG  CG   GTGGCCA GC
                                |||||  ||   ||||||| ||
                                TGACC  GT   TACCGGT CG
                                   CA ____     A
GAM1746  LOC153572 5'  GCGCGGCCTACCCGTACCAG  87232       CAT  _   A
                                CTGGTGCG   GGT GGCC CGC
                                ||||||||   ||| |||| |||
                                GACCATGC   CCA CCGG GCG
                                    ___  T   C
GAM1746  LOC158226 3'  GGCCACACCCGCGCACCAG   82696       ATG_
                                CTGGTGCGC   GTGGCC
                                |||||||||   ||||||
                                GACCACGCG   CACCGG
                                    CCCA
GAM1746  LOC162952 5'  CGTGACCAGCGCCCGCACC   83262      CA  G   C
                                GGTGCG  TG TGG CACG
                                ||||||  || ||| ||||
                                CCACGC  GC ACC GTGC
                                   CC  G   A
GAM1746  LOC163682 5'  CGTGGCCAAGCACCAG     88403       GCATGG
                                CTGGTGC     TGGCCACG
                                |||||||     ||||||||
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                                GACCACG     ACCGGTGC
                                   A_____
GAM1746  LOC164537 5'  CGTGGCCCGGGGCCACCAGT   88574       C  ATGGT
                                ACTGGTG GC    GGCCACG
                                ||||||| ||    |||||||
                                TGACCAC CG    CCGGTGC
                                   _ GGGC_
GAM1746  LOC196489 3'  TGGCCACCGTGTTCCCAG    89078     TGC
                                CTGG   GCATGGTGGCCA
                                ||||   ||||||||||||
                                GACC   TGTGCCACCGGT
                                  CT_
GAM1746  LOC199786 3'  GGCGTGGCAGTGCACACCTGT  89757    T    C    GGTG
                                AC GGTG GCAT    GCCACGCC
                                || |||| ||||    ||||||||
                                TG CCAC CGTG    CGGTGCGG
                                 T    A    A___
GAM1746  LOC220514 3'  GGCACAGATTGATGCGCACCAG 61076           GG___ _
            T                    ACTGGTGCGCAT     TG GCC
                                ||||||||||||     || |||
                                TGACCACGCGTA     AC CGG
                                      GTTAG  A
GAM1746  LOC256158 5'  GGCGTGGCCACACTCAACACCA 99508       CGCATG
            G                    CTGGTG     GTGGCCACGCC
                                ||||||     ||||||||||
                                GACCAC     CACCGGTGCGG
                                   AACTCA
GAM1747  RHD      3'  ACACATAAACACCATTTAGTC  32799    ACG    ATA
                                GA   GGATG   TTTATGTGT
                                ||   |||||   |||||||||
                                CT   TTTAC   AAATACACA
                                 GA_    CAC
GAM1747  RHD      3'  ACACATAAACACCATTTAGTC  32800    ACG    ATA
                                GA   GGATG   TTTATGTGT
                                ||   |||||   |||||||||
                                CT   TTTAC   AAATACACA
                                 GA_    CAC
GAM1747  FLJ22059  3'  ACACATAAAGGTGCCCCCCCA  43051     AAC   ATGATA
                                TGG   GGG     TTTATGTGT
                                |||   |||     |||||||||
                                ACC   CCC     AAATACACA
                                  CC_   GTGG__
GAM1747  LOC113146 3'  ACATATGGAGCACCCCATCCC  73332       ATA___
                                GGGATG     TTTATGTGT
                                ||||||     |||||||||
                                CCCTAC     AGGTATACA
                                   CCCACG
GAM1748  FLRT3    3'  TTGTAGTATAAGCACAGG    26122      ACAC   CCGC
                                CCTG    TGC    TACTACAA
                                ||||    |||    ||||||||
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                                GGAC   ACG   ATGATGTT
                                  _____  AAT_
GAM1748 MAN2A2   3' CTTGGTCAGAGTGGGCAGTGCC 21509     A        ACTA_
            AGG                   CCTG CACTGCCCGCT    CAAG
                                  |||| ||||||||||    ||||
                                  GGAC GTGACGGGTGA    GTTC
                                    C         GACTG
GAM1748 T       3' TGCAGTAGCGGTGCTGTCCCAG 13509    AC  T  _      A
                                  CTG  AC GC CCGCTACT CA
                                  |||  || || |||||||| ||
                                  GAC  TG CG GGCGATGA GT
                                    CC  T  T       C
GAM1748 WTAP     3' TGTAGTAGTTTCAGTGTTAG  18141         CCC
                                  CTGACACTG   GCTACTACA
                                  |||||||||   |||||||||
                                  GATTGTGAC   TGATGATGT
                                       TT_
GAM1748 GMPPA    5' CTTGCAGTAGCGGGCGGCAG  72648    ACA         A
                                  CTG   CTGCCCGCTACT CAAG
                                  |||   |||||||||||| ||||
                                  GAC   GGCGGGCGATGA GTTC
                                    ___          C
GAM1748 KIAA0379 5' CTTGTAGTGAGGAAGCAGTTCA 68715      C    __ GC
            GG                    CCTGA ACTGC  CC  TACTACAAG
                                  ||||| |||||  ||  |||||||||
                                  GGACT TGACG  GG  GTGATGTTC
                                    _    AA  A_
GAM1748 KIAA0964 3' AGCCCTGGGCAGTGTCAGG   30444           ___
                                  CCTGACACTGCCC   GCT
                                  ||||||||||||   |||
                                  GGACTGTGACGGG   CGA
                                         TCC
GAM1748 MVD      3' CTTGCTGTGGGGCAGTGCAGG  11717     A      GC   TA
                                  CCTG CACTGCCC  TAC  CAAG
                                  |||| ||||||||  |||  ||||
                                  GGAC GTGACGGG  GTG  GTTC
                                    _       __   TC
GAM1748 WDR13    3' GGCAGCGGGCAGCTCCAGG   35843     ACA       A
                                  CCTG   CTGCCCGCT CT
                                  ||||   ||||||||| ||
                                  GGAC   GACGGGCGA GG
                                    CTC        C
GAM1748 LOC145980 5' AGTGCCGGGCAGTTCAGG    84579      C       C
                                  CCTGA ACTGCCCG TACT
                                  ||||| |||||||| ||||
                                  GGACT TGACGGGC GTGA
                                    _       C
GAM1748 LOC148397 3' AGTGCCAGGCAGTGTCAGG   79558           C_  T
                                  CCTGACACTGCC  GC ACT
                                  ||||||||||||  || |||
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                                GGACTGTGACGG  CG TGA
                                      AC  _
GAM1748  LOC150605 5'  TGTTTCTGGGCAGTGCAGG    86264      A       CTACT
                                CCTG CACTGCCCG     ACA
                                |||| |||||||||     |||
                                GGAC GTGACGGGT     TGT
                                  _       CTT__
GAM1748  LOC162333 5'  TAGTAGTGGGCAACATCA     88501     CAC
                                TGA   TGCCCGCTACTA
                                |||   ||||||||||||
                                ACT   ACGGGTGATGAT
                                  ACA
GAM1748  LOC199907 3'  TGTACATGGGCAGTATCAG    89832      C       CTAC
                                CTGA ACTGCCCG    TACA
                                |||| ||||||||    ||||
                                GACT TGACGGGT    ATGT
                                   A       AC__
GAM1748  LOC203246 3'  TTGTAGTAGACAGCCAGG     90840     ACACT  CCG
                                CCTG    GC   CTACTACAA
                                ||||    ||   |||||||||
                                GGAC    CG   GATGATGTT
                                  _____  ACA
GAM1748  LOC220753 3'  CTTGTAGAGGTGGGCAGTCCAG 94533     AC        A
                                CTG  ACTGCCCGCT CTACAAG
                                |||  |||||||||| |||||||
                                GAC  TGACGGGTGG GATGTTC
                                  C_         A
GAM1749  GRIN2A    3'  CCCCAAGAACTCCAGGC     7721      C      GA  TGTA
                                GCC GGAGTTT  TG    GGG
                                ||| |||||||  ||    |||
                                CGG CCTCAAG  AC    CCC
                                  A      A_  ____
GAM1749  MLLT3     5'  CCCCAGCAAACCTCCGGGC    16959        _    A  TGTA
                                GCCCGGAG TTTG TG    GGG
                                |||||||| |||| ||    |||
                                CGGGCCTC AAAC AC    CCC
                                     C    G  ____
GAM1749  MN1       3'  CCCTACACACTAGACTCCG    11650         A
                                CGGAGTTTG TGTGTAGGG
                                ||||||||| |||||||||
                                GCCTCAGAT ACACATCCC
                                      C
GAM1749  POR       3'  CCCCACAGACTCCGG       95840          A  TGTA
                                CCGGAGTTTG TG    GGG
                                |||||||||| ||    |||
                                GGCCTCAGAC AC    CCC
                                     _  _____
GAM1749  LOC255328 3'  TTATCATCAAACCCCAGGC    98353     C  A       T
                                GCC GG GTTTGATG GTAG
                                ||| || |||||||| ||||
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                                CGG CC CAAACTAC TATT
                                  A  C      _
GAM1750  ARF3     3'  CCACCCACCCCTGACA      9771       AA    A   _
                                TGTCA  GGGG TGGG GG
                                ||||||  |||| |||| ||
                                ACAGT  CCCC ACCC CC
                                  ___   _    A
GAM1750  ASCL1    3'  ACTCCCATCACCTCTAACA    73133     CAA   G
                                TGT   AGG GATGGGGGT
                                |||   ||| |||||||||
                                ACA   TCC CTACCCTCA
                                  ATC   A
GAM1750  CELL     3'  ACTCCCATCTCCCCCGACA    10166      AAA
                                TGTC   GGGGATGGGGGT
                                ||||   ||||||||||||
                                ACAG   CCTCTACCCTCA
                                  CCC
GAM1750  MSF      3'  TCCCCACCCCTTCGACA      89469      A     A
                                TGTC AAGGGG TGGGGG
                                |||| |||||| ||||||
                                ACAG TTCCCC ACCCCT
                                  C     _
GAM1750  PPIF     3'  TGTCACCCACCCCTTGTCA    20377    T   A    ATGG
                                TG CAA GGGG    GGGTGACA
                                || ||| ||||    ||||||||
                                AC GTT CCCC    CCCACTGT
                                 T   _    A___
GAM1750  CLIPR-59  3'  ATGTCATTGTTCCCCATTTAAC 32012     C   _     TG G
              A                  TGT AAA GGGGA  G GGTGACAT
                                ||| ||| |||||  | ||||||||
                                ACA TTT CCCCT  T TTACTGTA
                                  A  A     __ G
GAM1750  DCTN2    3'  ATCCCCATCCCATTTGACA    22148        G
                                TGTCAAA GGGATGGGGGT
                                |||||||  ||||||||||
                                ACAGTTT CCCTACCCCTA
                                     A
GAM1750  DCTN2    3'  ATCCCCATCCCATTTGACA    71615        G
                                TGTCAAA GGGATGGGGGT
                                |||||||  ||||||||||
                                ACAGTTT CCCTACCCCTA
                                     A
GAM1750  DIO2     5'  CCCCCACCCCCTTTATCA     26550     TC      A
                                TG  AAAGGGG TGGGGG
                                ||  |||||||  ||||||
                                AC  TTTCCCC ACCCCC
                                 TA      C
GAM1750  DUSP10   5'  TCCCCACCACCCCTGACA     59231       AA    A   _   T
                                TGTCA  GGGG TGG GGG GA
                                |||||  |||| ||| ||| ||
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                                ACAGT  CCCC ACC CCC CT
                                  __   _  A  _
GAM1750  FLJ10898  5'  ACTCCCTCCCCTTTAACA    60122    C      T
                                TGT AAAGGGGA GGGGGT
                                ||| |||||||| ||||||
                                ACA TTTCCCCT CCCTCA
                                  A      _
GAM1750  FLJ21919  5'  TCACCCCTTACCTCGAC    43738    AAA   AT
                                GTC  GGGG  GGGGGTGA
                                |||  ||||  ||||||||
                                CAG  CTCC  TCCCCACT
                                  ___   AT
GAM1750  KIAA0354  5'  CGTTCCCACCTCCTCTGACA  30189     A   A   GG
                                TGTCA AGGGG TGGG  TG
                                ||||| ||||| ||||  ||
                                ACAGT TCCTC ACCC  GC
                                   C    C   TT
GAM1750  KIAA1280  5'  TTCCCATCCACCCTGACA    70296     AA  _
                                TGTCA  GG GGATGGGGG
                                |||||  || |||||||||
                                ACAGT  CC CCTACCCTT
                                   C_  A
GAM1750  KIAA1332  3'  TCACCTTGCCACCCTGACA   71707     AAG  A  __
                                TGTCA  GGG TGG  GGGTGA
                                |||||  ||| |||  ||||||
                                ACAGT  CCC ACC  TCCACT
                                  ___  _  GT
GAM1750  RNF10    5'  CGCCGCCACCGCCTCCGACA  30159    AA  _ A  G
                                TGTC  AGG GG TGG GGTG
                                ||||  ||| || ||| ||||
                                ACAG  TCC CC ACC CCGC
                                  CC  G  _  G
GAM1750  LOC149606 3'  CGCCACCCCATCCTTGGCA  80260     AAG      __
                                TGTCA  GGGATGGGG  GTG
                                |||||  |||||||||  |||
                                ACGGT  TCCTACCCC  CGC
                                  ___       AC
GAM1750  LOC155038 3'  CACCACACCCCTGTGACA   82182     A   A  GG
                                TGTCA AGGGG TG  GGTG
                                ||||| ||||| ||  ||||
                                ACAGT TCCCC AC  CCAC
                                   G   _ A_
GAM1750  LOC89932  5'  GCCAGCCCATCTCCTCTGACA  61465     A       __
                                TGTCA AGGGGATGGG  GGT
                                ||||| ||||||||||  |||
                                ACAGT TCCTCTACCC  CCG
                                   C        GA
GAM1751  ALOX12B   5'  CAGCTGGGCTCCGCTGGG   8535        AG A   _
                                CCCAGTGGA  G TCTA CTG
                                |||||||||  | |||| |||
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                                GGGTCGCCT  C GGGT GAC
                                   __ _   C
GAM1751  COL1A1   3'  CAGCCCCTCACTGGGTT    5392         AA  ATCTA
                                AACCCAGTGG  GG    CTG
                                ||||||||||  ||    |||
                                TTGGGTCACT  CC    GAC
                                   CC  _____
GAM1751  KIF3C    3'  CGGAAGTCCCTCCACTGG    11205        A   T  A
                                CCAGTGGA GGA CT CTG
                                |||||||| ||| || |||
                                GGTCACCT CCT GA GGC
                                    C   _ A
GAM1751  KRT6B    3'  ATCAATACCTGTTCCACTG   19898        __   ATC  C
                                CAGTGGA  AGG   TA TGAT
                                |||||||  |||   || ||||
                                GTCACCT  TCC   AT ACTA
                                   TG   ___  A
GAM1751  PDE7A    3'  ATCTTGTACCTTCCACTAAGTT 66133     CC       ATC   T_
                                AAC  AGTGGAAGG   TAC  GAT
                                |||  |||||||||   |||  |||
                                TTG  TCACCTTCC   ATG  CTA
                                  AA        ___   TT
GAM1751  PKP2     3'  CAGTAGATACCGGCCACAGG   17107    A    AA  _
                                CC GTGG  GG ATCTACTG
                                || ||||  || ||||||||
                                GG CACC  CC TAGATGAC
                                 A   GG  A
GAM1751  RALBP1   3'  CAGCAAAGGCCTTCTCACTGGG 23272         _    A   A__
            TT                   AACCCAGTG GAAGG TCT   CTG
                                |||||||||  |||||  |||   |||
                                TTGGGTCAC CTTCC GGA   GAC
                                    T    _  AAC
GAM1751  SCN8A    3'  TAGTCCCTTGCACTGGGT    27217        G    AT
                                ACCCAGTG AAGG  CTA
                                ||||||||  ||||  |||
                                TGGGTCAC TTCC  GAT
                                    G    CT
GAM1751  SLC22A2  5'  CAGGAGCCGCCTGCCACTGGG  60278        A   AT_  A
                                CCCAGTGG AGG   CT CTG
                                ||||||||  |||   || |||
                                GGGTCACC TCC   GA GAC
                                    G   GCC  G
GAM1751  DKFZP727G051 3'  CAGCTGTCCCTCCACTGG    70002        A    CTA
                                CCAGTGGA GGAT   CTG
                                ||||||||  ||||   |||
                                GGTCACCT CCTG   GAC
                                    C    TC_
GAM1751  DSCR1L1  3'  ATCAAGTAATTCCTTCACTAGG 20624     C    G    TC   _
            TT                   AACC AGTG AAGGA  TACT GAT
                                ||||  ||||  |||||  ||||  |||
```

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                                TTGG TCAC TTCCT  ATGA CTA
                                  A   _    TA   A
GAM1751  FLJ11320  3'  CAGCAGATCCCCAGGGG    37827    AG  AA    A
                                CCC  TGG  GGATCT CTG
                                |||  |||  |||||| |||
                                GGG  ACC  CCTAGA GAC
                                  G_  __    C
GAM1751  KIAA0286  3'  CAGTTTTTTTTCCACCGTGTT  68856    CCA      TCT
                                AAC  GTGGAAGGA  ACTG
                                |||  |||||||||  ||||
                                TTG  CACCTTTTT  TGAC
                                  TGC      TT_
GAM1751  MGC13105  3'  ATCTTGGCTCCTTCCATAGG  71968   A      T  CT
                                CC GTGGAAGGA CTA  GAT
                                || |||||||| |||  |||
                                GG TACCTTCCT GGT  CTA
                                 A       C  T_
GAM1751  MRPS18C   3'  ATCAGTTCTGAGTTCCACTGG  32680       GGATCT
                                CCAGTGGAA    ACTGAT
                                |||||||||    ||||||
                                GGTCACCTT    TGACTA
                                     GAGTCT
GAM1751  LOC144811 3'  ATCAATAGATCCTGTTACT   84107     A      C
                                AGTGG AGGATCTA TGAT
                                ||||| |||||||| ||||
                                TCATT TCCTAGAT ACTA
                                   G      A
GAM1751  LOC200276 3'  ATCAGTAGATAAAAACTGTGTT 90104    C   GGAAGG
                                AAC CAGT     ATCTACTGAT
                                ||| ||||     ||||||||||
                                TTG GTCA     TAGATGACTA
                                  T   AAAA__
GAM1751  LOC203078 5'  CAGCGACGCTTCTACTGGG   90788        GA  TA
                                CCCAGTGGAAG  TC  CTG
                                ||||||||||  ||  |||
                                GGGTCATCTTC  AG  GAC
                                      GC  C_
GAM1751  LOC254057 5'  CAGCAGCTGGCCGCTGGG    98778       AA  AT  A
                                CCCAGTGG  GG  CT CTG
                                ||||||||  ||  || |||
                                GGGTCGCC  TC  GA GAC
                                    GG  __  C
GAM1752  CENTD2    5'  CTGGCCGGAGCTGTGGGA    58272       CAGA   A  A
                                TTCCACAGC    TTTG CCA G
                                |||||||||    |||| ||| |
                                AGGGTGTCG    AGGC GGT C
                                     _____    C  C
GAM1752  E2F3      3'  GCCTGACGGATGGGCTGTAGAA 10468    C     AG    AC  A
                                TTC ACAGCC  ATTTG  CA GC
                                ||| ||||||  |||||  || ||
```

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                                AAG TGTCGG  TAGGC  GT CG
                                  A     G_    A_  C
GAM1752  HEM1     5'  GCCTGTGAGTATCTGTCTGTGG 19239        C    TTGAC  A
                AA                  TTCCACAG CAGAT    CA GC
                                    |||||||| |||||    || ||
                                    AAGGTGTC GTCTA    GT CG
                                       T    TGAGT  C
GAM1752  MGAT5    5'  GCCTGGTCAAGGGCTCTG    11569    C   AGA      A
                                    CA AGCC   TTTGACCA GC
                                    || ||||   |||||||| ||
                                    GT TCGG   GAACTGGT CG
                                     C   ___       C
GAM1752  PCDH11X  3'  CTGTAATCTGGCAATGGAA   53128      CA      TGACCA
                                    TTCCA  GCCAGATT    AG
                                    |||||  ||||||||    ||
                                    AAGGT  CGGTCTAA    TC
                                       AA      TG____
GAM1752  PCDH11Y  3'  CTGTAATCTGGCAATGGAA   53161      CA      TGACCA
                                    TTCCA  GCCAGATT    AG
                                    |||||  ||||||||    ||
                                    AAGGT  CGGTCTAA    TC
                                       AA      TG____
GAM1752  PCDH11Y  3'  CTGTAATCTGGCAATGGAA   53180      CA      TGACCA
                                    TTCCA  GCCAGATT    AG
                                    |||||  ||||||||    ||
                                    AAGGT  CGGTCTAA    TC
                                       AA      TG____
GAM1752  PIK3R3   3'  GCTTGACCCTGAGCCTGTGGAA 61707        _ _  ATTTGAC
                                    TTCCACAG C CAG      CAAGC
                                    |||||||| | |||      |||||
                                    AAGGTGTC G GTC      GTTCG
                                       C A  CCA____
GAM1752  PRKCABP  5'  GCCTGGCCGGGACCCGGCTGTG 25748         AGA_   A  A
                GGA                   TTCCACAGCC   TTTG CCA GC
                                    ||||||||||   |||| ||| ||
                                    AGGGTGTCGG   GGGC GGT CG
                                       CCCA   C   C
GAM1752  T      3'  GCTTACAGATGAACCCAACTGT 13507        CCAG____    ACC
                GGAG                  TTCCACAG      ATTTG   AAGC
                                    ||||||||      |||||  ||||
                                    GAGGTGTC      TAGAC   TTCG
                                       AACCCAAG    A__
GAM1752  VIPR1    3'  CTTATCTCTCTGTGCTGTGGAA 17312        _   TTT  CC
                                    TTCCACAGC CAGA   GA  AAG
                                    ||||||||| ||||   ||  |||
                                    AAGGTGTCG GTCT   CT  TTC
                                       T    CT_  A_
GAM1752  XRCC3    3'  TTACATCTGGCTGGAA     19523      CA     T
                                    TTCCA  GCCAGAT TGA
                                    |||||  ||||||| |||
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                                AAGGT  CGGTCTA ATT
                                  __      C
GAM1752  YWHAG    3'  GCTCGGCAGGTGGCTGTGGGA  25944          GA    A  A
                                TTCCACAGCCA  TTTG CC AGC
                                ||||||||||  |||| || |||
                                AGGGTGTCGGT  GGAC GG TCG
                                      __   _ C
GAM1752  ZNF266   5'  TTTGATGATCTGGCTGTGGA   89693            TGAC
                                TCCACAGCCAGATT    CAAG
                                ||||||||||||||    ||||
                                AGGTGTCGGTCTAG    GTTT
                                        TA__
GAM1752  ARHU     3'  GCCTGGCTTACCTATCTGTGGA 41361         CC  ATT  _   A
           A                     TTCCACAG  AG   TGA CCA GC
                                ||||||||  ||   ||| ||| ||
                                AAGGTGTC  TC   ATT GGT CG
                                     TA  C__   C   C
GAM1752  C20orf28 3'  GCCTGGTCGAGGGCCCTGGAA  31845      CA   AGA       A
                                TTCCA  GCC   TTTGACCA GC
                                |||||  |||   |||||||| ||
                                AAGGT  CGG   GAGCTGGT CG
                                   CC  ___      C
GAM1752  CNNM4    5'  GCTTGGTCAACGTGAGCCGCGG 39868      ACA  _  GAT
           GA                    TTCC   GC CA   TTGACCAAGC
                                ||||   || ||   ||||||||||
                                AGGG   CG GT   AACTGGTTCG
                                  CGC  A  GC_
GAM1752  DKFZp761N1114 3'  CTGAGAATCTGGCTGGAA    79783      CA       GACCA
                                TTCCA  GCCAGATTT    AG
                                |||||  |||||||||    ||
                                AAGGT  CGGTCTAAG    TC
                                   __       AG___
GAM1752  FLJ10204  3'  CTTGGTCTCAAGATGTGGAA   36357       GCCA  TTT
                                TTCCACA   GA   GACCAAG
                                |||||||   ||   |||||||
                                AAGGTGT   CT   CTGGTTC
                                    AGAA  ___
GAM1752  FLJ11539  3'  TTAAATCTGCTGCAGAA     45710     CA   C
                                TTC  CAGC AGATTTGA
                                |||  |||| ||||||||
                                AAG  GTCG TCTAAATT
                                  AC   _
GAM1752  FLJ12056  3'  TCATCTTCTGGCTGTGGAA   46824           TT_
                                TTCCACAGCCAGA   TGA
                                ||||||||||||   |||
                                AAGGTGTCGGTCT   ACT
                                        TCT
GAM1752  FLJ13149  5'  GCCTGGTCAAATCTGTGAGGA  41831     A  GC         A
                                TCC CA  CAGATTTGACCA GC
                                ||| ||  ||||||||||| ||
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                                AGG GT  GTCTAAACTGGT CG
                                  A __          C
GAM1752  FLJ20084  3'  GCTTGGCCAATGACTGTGGAG  34997        C  GAT   A
                                TTCCACAG CA   TTG CCAAGC
                                |||||||| ||   ||| ||||||
                                GAGGTGTC GT   AAC GGTTCG
                                    A ___   C
GAM1752  FLJ20392  5'  GCCTGGCCAAATCTGAAATAGG 35576     ACAGC       A   A
              A                  TCC     CAGATTTG CCA GC
                                |||     |||||||| ||| ||
                                AGG     GTCTAAAC GGT CG
                                  ATAAA       C   C
GAM1752  FLJ21940  3'  TCAGAACTCTTAGCTGTGGAA  43387         C_   __
                                TTCCACAGC  AGA  TTTGA
                                |||||||||  |||  |||||
                                AAGGTGTCG  TCT  AGACT
                                     AT   CA
GAM1752  KIAA0237  3'  CTGGTCTGGCTGGGAA      29221      A     GATTT    A
                                TTCC CAGCCA    GACCA G
                                |||| ||||||    ||||| |
                                AAGG GTCGGT    CTGGT C
                                  _     _____    C
GAM1752  KIAA0596  3'  CTTGAGCCAGCTGTGGGA    63488         CAGATT  AC_
                                TTCCACAGC     TG   CAAG
                                |||||||||     ||   ||||
                                AGGGTGTCG     AC   GTTC
                                      _______ CGA
GAM1752  KIAA0773  3'  CTTGGTGTGGCTGTGGAG    28723          GATTTG
                                TTCCACAGCCA     ACCAAG
                                ||||||||||      ||||||
                                GAGGTGTCGGT     TGGTTC
                                     G_____
GAM1752  KIAA0789  5'  GCTTGGTCTTCAGCTGGGGAA  64433      A   CA  TTT
                                TTCC CAGC  GA   GACCAAGC
                                |||| ||||  ||   ||||||||
                                AAGG GTCG  CT   CTGGTTCG
                                  G   A_  T__
GAM1752  L3MBTL    3'  CTTCACCTCACTGTGGAA    70084        CCA  TT   CCA
                                TTCCACAG   GA  TGA   AG
                                ||||||||   ||  |||   ||
                                AAGGTGTC   CT  ACT   TC
                                    A__  CC   ___
GAM1752  NUDEL     3'  CTTGGTCACTGGATGCAGAA  48697     CA  G    ATT
                                TTC  CA CCAG   TGACCAAG
                                |||  || ||||   ||||||||
                                AAG  GT GGTC   ACTGGTTC
                                  AC  A   ___
GAM1752  SAST      5'  GCTCCCTTCATCTGGCTATGG  63662     C      TT   CCA_
                                CCA AGCCAGA  TGA    AGC
                                ||| |||||||  |||    |||
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                                GGT TCGGTCT  ACT    TCG
                                  A      __   TCCC
GAM1752  SLC26A8   5'  CTCAGTCAGTATCTGTGGAA   57803        CCAGAT    CA
                                TTCCACAG     TTGAC  AG
                                ||||||||     |||||  ||
                                AAGGTGTC     GACTG  TC
                                     TAT___     AC
GAM1752  SNURF     3'  CTTGGTATCCATGACTGTGGAG 20261        C  GATTTG
                                TTCCACAG CA      ACCAAG
                                |||||||| ||      ||||||
                                GAGGTGTC GT      TGGTTC
                                     A  ACCTA_
GAM1752  TMG3      3'  GCCTGGCCTGGGGGCTGTGGGA 44222          AGATTTGA   A
                                TTCCACAGCC       CCA GC
                                ||||||||||       ||| ||
                                AGGGTGTCGG       GGT CG
                                      GGGTCC__   C
GAM1752  LOC158956 3'  CTTGGTTACTGTGCTGTG    67213       _  ATT
                                CACAGC CAG   TGACCAAG
                                |||||| |||   ||||||||
                                GTGTCG GTC   ATTGGTTC
                                   T  ____
GAM1752  LOC159199 5'  GCTTGGTCCAGAGGCCAGGAA  83063      ACA   AGA   _
                                TTCC   GCC   TTTG ACCAAGC
                                ||||   |||   |||| |||||||
                                AAGG   CGG   AGAC TGGTTCG
                                  AC_  ____   C
GAM1752  LOC83693  3'  TCAAATCTGCTATGGAA     49607       C   C
                                TTCCA AGC AGATTTGA
                                ||||| ||| ||||||||
                                AAGGT TCG TCTAAACT
                                   A  _
GAM1753  CBFA2T2   3'  CCGGATGGCCATCTGTCC    18707     G          AG
                                GGA CAGATGGCCATC  TGG
                                ||| ||||||||||||  |||
                                CCT GTCTACCGGTAG  GCC
                                  _         __
GAM1753  EGFL4     3'  CCAAGATGGCCAGCCGCCC    62458    A  AGA       AG
                                GG GC   TGGCCATC  TGG
                                || ||   ||||||||  |||
                                CC CG   ACCGGTAG  ACC
                                 _  CCG       A_
GAM1753  FXYD6     3'  CCACATGGCCATCTGCTCC    42089             CA
                                GGAGCAGATGGCCAT  GTGG
                                ||||||||||||||  ||||
                                CCTCGTCTACCGGTA  CACC
                                                 __
GAM1753  GFAP      3'  CCACCTGGTGGCCTCTGCCC   10778    A    T       _
                                GG GCAGA GGCCATCAG TGG
                                || ||||| |||||||| |||
```

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                                CC CGTCT CCGGTGGTC ACC
                                 _    _       C
GAM1753 IHPK3    5' CCACCACCACCATCTGCCGCC  55092    A_      CCATCA   C
                                GG  GCAGATGG     GTGG GG
                                ||  ||||||||     |||| ||
                                CC  CGTCTACC     CACC CC
                                 GC       AC____    A
GAM1753 PRELP    3' CGCCACCGGATCTGCTCT    12257         GG  ATCA
                                GGAGCAGAT  CC    GTGGCG
                                |||||||||  ||    ||||||
                                TCTCGTCTA  GG    CACCGC
                                     __ C___
GAM1753 SYNGR1   3' CCACAGTGACCGCCTGCCC   17496    A   A  C   CA
                                GG GCAG TGG CAT  GTGG
                                || |||| ||| |||  ||||
                                CC CGTC GCC GTG  CACC
                                 _   C   A   A_
GAM1753 CORO1B   3' CCACTGCCCAGCCCTCTGCTCC 40318        T   CAT_
                                GGAGCAGA GGC    CAGTGG
                                |||||||| |||    ||||||
                                CCTCGTCT CCG    GTCACC
                                     C   ACCC
GAM1753 DKFZP564A1164 3' CCAAGATGGCCATATACTCC   71535     CAG       AG
                                GGAG   ATGGCCATC  TGG
                                ||||   |||||||||  |||
                                CCTC   TACCGGTAG  ACC
                                  ATA       A_
GAM1753 FLJ10432 3' CCACACGGCCATCTGCCC    39349    A       ATCA
                                GG GCAGATGGCC    GTGG
                                || ||||||||||    ||||
                                CC CGTCTACCGG    CACC
                                 _        CA__
GAM1753 FLJ14486 3' CGCCACTAGACCACGCTCC   52435      AGA   CCA  _
                                GGAGC   TGG   TC AGTGGCG
                                |||||   |||   || |||||||
                                CCTCG   ACC   AG TCACCGC
                                   C__   ___  A
GAM1753 FLJ20511 3' CCGCTGACCACCTCTCC     35768     C  A   CCA
                                GGAG AG TGG   TCAGTGG
                                |||| || |||   |||||||
                                CCTC TC ACC   AGTCGCC
                                  _ C   ___
GAM1753 KIAA1145 3' CCACCACTCCCGCCATCTGCTG 66233   G       CATC    C
           C                     G AGCAGATGGC    AGTGG GG
                                | ||||||||||    ||||| ||
                                C TCGTCTACCG    TCACC CC
                                 G        CCC_    A
GAM1753 KIAA1196 3' CCGCCTTGTGACCATCTGTCCC 62148    AG     C  T   T
                                GG  CAGATGG CA CAG GGCGG
                                ||  ||||||| || ||| |||||
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                                CC  GTCTACC GT GTT CCGCC
                                 CT      A  _  _
GAM1753  KIAA1271  3'  CCACCCATCTGTTCC      70132          CCATCA
                                GGAGCAGATGG     GTGG
                                ||||||||||     ||||
                                CCTTGTCTACC     CACC
                                        _______
GAM1753  PIGQ     3'  CCACAGCCAGCCATCTGCTCT  16103          CATCA
                                GGAGCAGATGGC    GTGG
                                ||||||||||||    ||||
                                TCTCGTCTACCG    CACC
                                      ACCGA
GAM1753  PP1201   3'  CCACATGTGGCCATCTGCTCC  42455            CA
                                GGAGCAGATGGCCAT  GTGG
                                ||||||||||||||  ||||
                                CCTCGTCTACCGGTG  CACC
                                       TA
GAM1753  SLPI     3'  CCACTGATATCCTCC      13237     CA   GGCC
                                GGAG  GAT   ATCAGTGG
                                ||||  |||   ||||||||
                                CCTC  CTA   TAGTCACC
                                  __  _____
GAM1753  TRIM26   3'  CCACTGGTAGCCACCTCC    14344     CAGA   C
                                GGAG   TGGC ATCAGTGG
                                ||||   |||| ||||||||
                                CCTC   ACCG TGGTCACC
                                  C___   A
GAM1753  LOC144698 5'  CCGCCACTCTGCCACCAGCTCC 77433      AGA   CATC
                                GGAGC   TGGC   AGTGGCGG
                                |||||   ||||   ||||||||
                                CCTCG   ACCG   TCACCGCC
                                   ACC   TC__
GAM1753  LOC146723 3'  CCAAAAGCCATCTGCTCC    78676          CATCAG
                                GGAGCAGATGGC     TGG
                                ||||||||||||     |||
                                CCTCGTCTACCG     ACC
                                      AAA___
GAM1753  LOC150837 3'  CCACCTATAACCATCTGCTC   80801         CC  CA
                                GAGCAGATGG  AT  GTGG
                                ||||||||||  ||  ||||
                                CTCGTCTACC  TA  CACC
                                     AA  TC
GAM1753  LOC151102 3'  CCACACTGGCCCATCTGCTCC  86408          _  TCA
                                GGAGCAGATGG CCA   GTGG
                                |||||||||||| |||   ||||
                                CCTCGTCTACC GGT   CACC
                                      C   CA_
GAM1753  LOC157773 5'  CATTGTGATGGCCATCTGCCC  82507    A          __
                                GG GCAGATGGCCATCA  GTG
                                || ||||||||||||||  |||
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                                CC CGTCTACCGGTAGT  TAC
                                 _           GT
GAM1753  LOC221490 5'  CCCACTCCATCTGCCC      95302    A      CCATC    C
                                GG GCAGATGG    AGTGG G
                                || ||||||||    ||||| |
                                CC CGTCTACC    TCACC C
                                 _      _____    A
GAM1753  LOC254423 3'  CCACCAAAGGGCCTCTGCTCC  99300        T   ATCAG   C
                                GGAGCAGA GGCC    TGG GG
                                |||||||| ||||    ||| ||
                                CCTCGTCT CCGG    ACC CC
                                     _   GAA__   A
GAM1753  LOC257054 5'  CCACCAGCACCGTCTGCTCC   97369          CCATCA
                                GGAGCAGATGG     GTGG
                                ||||||||||     ||||
                                CCTCGTCTGCC     CACC
                                       ACGAC_
GAM1753  LOC257494 3'  CCACTGGTAGCCACCTCC    99629     CAGA   C
                                GGAG   TGGC ATCAGTGG
                                ||||   |||| ||||||||
                                CCTC   ACCG TGGTCACC
                                  C___   A
GAM1754  ELF3     3'  TGACCTTGACCTTGACCAA   16685      T   GAT  AAA
                                TTGGT CAAGG   GG   GTCA
                                ||||| |||||   ||   ||||
                                AACCA GTTCC   TC   CAGT
                                   _    AGT  ___
GAM1754  JAK2     3'  TGACCTTCATTCTGAGACCAA  18318      CAA      AA
                                TTGGTT   GGGATGGA  GTCA
                                ||||||   ||||||||  ||||
                                AACCAG   TCTTACTT  CAGT
                                   AG_       C_
GAM1754  SLC10A2   5'  ACTCTCTGTCTTGACCAA    6590       CAA      A
                                TTGGTT   GGGATGGA AGT
                                ||||||   |||||||| |||
                                AACCAG   TTCTGTCT TCA
                                   ___       C
GAM1754  FLJ10803  3'  GTGACTTTCAGTTAAAGCCAA  37205      CAAGG   G
                                TTGGTT    GAT GAAAGTCAC
                                ||||||    ||| |||||||||
                                AACCGA    TTG CTTTCAGTG
                                   AA___   A
GAM1754  KIAA1958  5'  GTGACTTTGAACCCCAAACC   82788     CAA   ATGG
                                GGTT   GGG    AAAGTCAC
                                ||||   |||    ||||||||
                                CCAA   CCC    TTTCAGTG
                                  A__   CAAG
GAM1754  MARCKS    3'  ACTTTCCACCCTGCCCA     11411     TTCA   A
                                TGG    AGGG TGGAAAGT
                                |||    |||| ||||||||
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                                ACC   TCCC ACCTTTCA
                                  CG__  _
GAM1754 TUB     5' GTGGGACCATCCCTTAAACC  13898     C       AAAG
                                GGTT AAGGGATGG   TCAC
                                |||| |||||||||   ||||
                                CCAA TTCCCTACC   GGTG
                                  A       AG__
GAM1754 LOC80298 3' ACTTTTACCTTGAACCA    48062         GATG
                                TGGTTCAAGG   GAAAGT
                                ||||||||||   ||||||
                                ACCAAGTTCC   TTTTCA
                                     A___
GAM1755 EIF4G1   3' GCTGGTGGGGCCGGGGACCTG 18255       A      T  ATT
                                CAGGTCC CCGGCCCC AC  GC
                                ||||||| |||||||| ||  ||
                                GTCCAGG GGCCGGGG TG  CG
                                   _      _ GT_
GAM1755 GRM1    3' GCAATGTAATGTCAAATTGACC 7738       CACC_  CCC
             TG                   CAGGTC   GGC  TACATTGC
                                ||||||   |||  ||||||||
                                GTCCAG   CTG  ATGTAACG
                                   TTAAA  TA_
GAM1755 NORE1    3' GCTCGGAGAGCCGGTGGGCCTG 49526          CC  ACATT
                                CAGGTCCACCGGC  CT   GC
                                ||||||||||||  ||   ||
                                GTCCGGGTGGCCG  GA   CG
                                      A_  GGCT_
GAM1755 RNF7    3' TAGGAGCCGATGGATCTG   27274       C   C
                                CAGGTCCA CGGC CCTA
                                |||||||| |||| ||||
                                GTCTAGGT GCCG GGAT
                                    A   A
GAM1755 RNPEPL1  3' CAGAGACCTGTGGACCTG   37214       C  CCC  ACA
                                CAGGTCCAC GG  CT  TTG
                                ||||||||| ||  ||  |||
                                GTCCAGGTG CC  GA  GAC
                                     T  A__  ___
GAM1755 BICD2   3' TGTGGGACCAGCTGGACCTG  70917       CC_  CC
                                CAGGTCCA  GG  CCTACA
                                ||||||||  ||  ||||||
                                GTCCAGGT  CC  GGGTGT
                                    CGA  A_
GAM1755 C20orf51 5' TGGAGGGGGCCGGGGACC   42290     A       A_
                                GGTCC CCGGCCCCT  CA
                                ||||| |||||||||  ||
                                CCAGG GGCCGGGGG  GT
                                   _       AG
GAM1755 GMPPB   5' CAACGTGCTGGTGGACC    97438         CCCT  A
                                GGTCCACCGGC   AC TTG
                                ||||||||||   || |||
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                                CCAGGTGGTCG    TG AAC
                                      ____ C
GAM1755 HSPC072  3' TGTGGGTGCCAGTGGACCTG  27174        C  C
                                CAGGTCCAC GGC CCTACA
                                ||||||||| ||| ||||||
                                GTCCAGGTG CCG GGGTGT
                                     A  T
GAM1755 LCHN     3' TAGGAGCCATGTGGACCTG   87477        C_  C
                                CAGGTCCAC  GGC CCTA
                                |||||||||  ||| ||||
                                GTCCAGGTG  CCG GGAT
                                     TA  A
GAM1755 RHOBTB2  3' GCAACACAGGGGCCTGGCCT  61601    T  CC     ACA
                                AGG CCA  GGCCCCT   TTGC
                                ||| |||  |||||||   ||||
                                TCC GGT  CCGGGGA   AACG
                                  _  __      CAC
GAM1755 VMP      3' GCAATATAATGGGTGGACTCA 55763   A      GGCCCC  C
                                C GGTCCACC     TA ATTGC
                                | ||||||||     || |||||
                                A TCAGGTGG     AT TAACG
                                 C       GTA___  A
GAM1755 LOC151056 5' AGGAGGCTGGTGGACCTG    80923           _
                                CAGGTCCACCGGCC CCT
                                |||||||||||||| |||
                                GTCCAGGTGGTCGG GGA
                                      A
GAM1755 LOC157697 5' GCAATGTAAACTGCAGACC   82463     CAC   CCCC
                                GGTC   CGG    TACATTGC
                                ||||   |||    ||||||||
                                CCAG   GTC    ATGTAACG
                                  AC_   AA__
GAM1755 LOC202934 3' CAATGGATAAATCAATGGACCT 92028        CC  CCCCTA
             G                   CAGGTCCA  GG     CATTG
                                 ||||||||  ||     |||||
                                 GTCCAGGT  CT     GTAAC
                                      AA  AAATAG
GAM1755 LOC254381 5' AGGGGAAAACTGGTGGACCTG  99322          _____
                                CAGGTCCACCGG    CCCCT
                                ||||||||||||   |||||
                                GTCCAGGTGGTC    GGGGA
                                      AAAA
GAM1755 LOC255465 3' CAATGGATAAATCAATGGACCT 99104        CC  CCCCTA
             G                   CAGGTCCA  GG     CATTG
                                 ||||||||  ||     |||||
                                 GTCCAGGT  CT     GTAAC
                                      AA  AAATAG
GAM1755 LOC92719  5' GCTCGGGGGGCCGGGGACC    70903      A       ACATT
                                GGTCC CCGGCCCCT    GC
                                ||||| |||||||||    ||
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                                CCAGG GGCCGGGGG    CG
                                  _       GCT__
GAM1756  DKFZp547I224 3'  CCCCCACTGTCAACATT    39955         T  CCAG  C
                                AATGTTGACG TGG   GG G
                                |||||||||| |||   || |
                                TTACAACTGT ACC   CC C
                                    C  ____  A
GAM1756  MGC20253  3'  ACACCCTGGAAGGTCAACAT  58672       G  GG    C
                                ATGTTGAC TT  CCAGGG GT
                                |||||||| ||  |||||| ||
                                TACAACTG AA  GGTCCC CA
                                    G  __     A
GAM1756  MGC5391  3'  TGGCCAACATCCACACTG   52197   A  T  C
                                CA TGT GA GTTGGCCA
                                || ||| || ||||||||
                                GT ACA CT CAACCGGT
                                 C  C  A
GAM1756  LOC92912  3'  GCAGCCAAGTCAACATCA   71407   A      G    CAGG
                                C ATGTTGAC TTGGC   GC
                                | |||||||| |||||   ||
                                A TACAACTG AACCG   CG
                                C       _    A___
GAM1757  C18orf1  3'  TCAGCTGGAGAAAGAAACCA  60872    CTG  G_
                                TGG  CT  CTCCAGCTGA
                                |||  ||  ||||||||||
                                ACC  GA  GAGGTCGACT
                                  AAA  AA
GAM1757  HMGCR   3'  TCAGCTTTCAGAGCCAGTG   7806        G  CTCC
                                CACTGGCT CTG   AGCTGA
                                |||||||| |||   ||||||
                                GTGACCGA GAC   TCGACT
                                    _  TT__
GAM1757  KCNQ1   3'  CAGTCCCAGCAGCCAGCCA   5839       _   CCA
                                TGGCTG CTGCT  GCTG
                                |||||| |||||  ||||
                                ACCGAC GACGA  TGAC
                                   C    CCC
GAM1757  MAGEL2   5'  CAGCTGGAGCAGCCCTTTCAG  39328    CT__
                                CTGG   GCTGCTCCAGCTG
                                ||||   ||||||||||||||
                                GACT   CGACGAGGTCGAC
                                  TTCC
GAM1757  ODF2    5'  TCAGCGACCAGCAGCCAG    11887         C  CA
                                CTGGCTGCTG TC  GCTGA
                                |||||||||| ||  |||||
                                GACCGACGAC AG  CGACT
                                    C  __
GAM1757  RAD23A   3'  CAGCTCTCTGCAGCCAGACGGA 18564    A_      TGCTCC
                                TCC  CTGGCTGC     AGCTG
                                |||  ||||||||     |||||
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                                AGG  GACCGACG     TCGAC
                                  CA       TCTC__
GAM1757  SLC22A2   3'  TCAACCTAGGTCTACAGCCAGT 60281          C  CT  _  C_
              GGA                    TCCACTGGCTG TG  CC AG  TGA
                                |||||||||||  ||  || ||  |||
                                AGGTGACCGAC AT  GG TC  ACT
                                       _  CT  A  CA
GAM1757  ARHGEF15  3'  TCAGGACAGAGCAGCCAATG   30955    C       G  CCAG
                                CA TGGCTGCT CT    CTGA
                                || ||||||||  ||    ||||
                                GT ACCGACGA GA    GACT
                                 A       _  CAG_
GAM1757  BMF       3'  CAGCTGGGTGTCAGCCACGGA  54278     AC     C   T
                                TCC  TGGCTG TGC CCAGCTG
                                |||  ||||||  ||| |||||||
                                AGG  ACCGAC GTG GGTCGAC
                                  C_     T  _
GAM1757  CALCYON   5'  CTGCAGCAGCTGCCAGTGGA   32321         T     C
                                TCCACTGGC GCTGCT CAG
                                |||||||||  ||||||  |||
                                AGGTGACCG CGACGA GTC
                                      T     C
GAM1757  Di-Ras2   3'  CAGCTGGGTAGCAGCCAG    34610           T
                                CTGGCTGCTGC CCAGCTG
                                ||||||||||  |||||||
                                GACCGACGATG GGTCGAC
                                           _
GAM1757  FLJ10748  5'  TCAGCCAGAGGCAGCAGCAGTG 37104         G      _  CA
              GA                     TCCACTG CTGCTGC TC  GCTGA
                                |||||||  |||||||  ||  |||||
                                AGGTGAC GACGACG AG  CGACT
                                     _      G  AC
GAM1757  FLJ10748  3'  TCAGCTCCTGTTAGCAACCAGT 37105         C    _ TCC
              GGA                    TCCACTGG TGCTG C   AGCTGA
                                |||||||| |||||  |   ||||||
                                AGGTGACC ACGAT G   TCGACT
                                     A     T TCC
GAM1757  FLJ20718  5'  CAGCTGAGCAGCAGCAACGGA  36041     ACTG        C
                                TCC    GCTGCTGCTC AGCTG
                                |||    ||||||||||  |||||
                                AGG    CGACGACGAG TCGAC
                                  CAA_         _
GAM1757  HRK       3'  CAGCCGGAGCGAGCAACAG    15070     GC   _    A
                                CTG  TGCT GCTCC GCTG
                                |||  ||||  |||||  ||||
                                GAC  ACGA CGAGG CGAC
                                  A_   G    C
GAM1757  KIAA0443  5'  CAACTGAAGAGCAGCCAGAGGA 28853     A       G  C   C
                                TCC CTGGCTGCT CT CAG TG
                                ||| |||||||||  || ||| ||
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                                AGG GACCGACGA GA GTC AC
                                  A       _ A  A
GAM1757 KIAA0493 5' CAGCTGACACAGCCAGTG    64927        C  CTC
                                CACTGGCTG TG   CAGCTG
                                ||||||||| ||   ||||||
                                GTGACCGAC AC   GTCGAC
                                     _ A__
GAM1757 KIAA0628 3' TCAGCTGGAACAGTGGGGACAG 29535    G__ TG   C
                                CTG   C  CTG TCCAGCTGA
                                |||   |  ||| |||||||||
                                GAC   G  GAC AGGTCGACT
                                  AGG GT   A
GAM1757 KIAA0632 3' TCAGCCAGAGCAGCCA     32073        G  CCA
                                TGGCTGCT CT   GCTGA
                                |||||||| ||   |||||
                                ACCGACGA GA   CGACT
                                     _ C__
GAM1757 KIAA0830 3' CAGAGTAGAACAGCAGCCAG   70267         C  CAG_
                                CTGGCTGCTG TC    CTG
                                |||||||||| ||    |||
                                GACCGACGAC AG    GAC
                                      A  ATGA
GAM1757 KIAA1023 3' CAGCTGGAGGGCTCCAGGGA   34676     A   CT   G
                                TCC CTGG  GCT CTCCAGCTG
                                ||| ||||  ||| |||||||||
                                AGG GACC  CGG GAGGTCGAC
                                  _    T_  _
GAM1757 PCNT2    3' CAGCTGGAGCATTTTCTATGGA 21228     C   CTGC
                                TCCA TGG    TGCTCCAGCTG
                                |||| |||    ||||||||||
                                AGGT ATC    ACGAGGTCGAC
                                  _   TTTT
GAM1757 POU2F1   5' TCAGCCGCGGCGGCAGCAGCAG 12211     __       _ A__
             CAG                   CTG  GCTGCTGCT CC   GCTGA
                                |||  ||||||||| ||   |||||
                                GAC  CGACGACGG GG   CGACT
                                  GA        C  CGC
GAM1757 PTPRT    5' CAGCCGCGCGCACAGCCAGCGG 56487    A      C   TCCA_
                                CC CTGGCTG TGC     GCTG
                                || ||||||| |||     ||||
                                GG GACCGAC ACG     CGAC
                                 C       _   CGCGC
GAM1757 SLIT1    3' CAGCCGCTGCAGCAGCGGA    13230     ACTG       TCCA
                                TCC    GCTGCTGC    GCTG
                                |||    ||||||||    ||||
                                AGG    CGACGACG    CGAC
                                  _____       TCGC
GAM1757 SNPH     3' CAGCTGGAGAATCCACCAG    28900      C  CTG_
                                CTGG TG    CTCCAGCTG
                                |||| ||    |||||||||
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                                GACC AC    GAGGTCGAC
                                  _  CTAA
GAM1757  SSH-3    3'  CAGCCAGGCCAGGCAACCAGTG 35789       C    GCT  A_
             G                   CCACTGG TGCT   CC  GCTG
                                 ||||||| ||||   ||  ||||
                                 GGTGACC ACGG   GG  CGAC
                                    A    ACC  AC
GAM1757  SSH-3    3'  CAGCCAGGCCAGGCAACCAGTG 37416       C    GCT  A_
             G                   CCACTGG TGCT   CC  GCTG
                                 ||||||| ||||   ||  ||||
                                 GGTGACC ACGG   GG  CGAC
                                    A    ACC  AC
GAM1757  TREX1    5'  CAGCTGGAACAAGAGGTGG    54379      GG  GC  C
                                 CCACT  CT  TG TCCAGCTG
                                 |||||  ||  || ||||||||
                                 GGTGG  GA  AC AGGTCGAC
                                   A_  __  A
GAM1757  TREX1    5'  CAGCTGGAACAAGAGGTGG    54386      GG  GC  C
                                 CCACT  CT  TG TCCAGCTG
                                 |||||  ||  || ||||||||
                                 GGTGG  GA  AC AGGTCGAC
                                   A_  __  A
GAM1757  LOC146350 5'  TGAGAGCAGCACCCAGTGGA   84650        C       _
                                 TCCACTGG TGCTGCTC CA
                                 |||||||| |||||||| ||
                                 AGGTGACC ACGACGAG GT
                                      C       A
GAM1757  LOC146802 3'  TCAGGCCGGCAGCAGCAGCAG  78728     G       _  A  _
                                 CTG CTGCTGCT CC GC TGA
                                 ||| |||||||| || || |||
                                 GAC GACGACGA GG CG ACT
                                   _       C  C  G
GAM1757  LOC149296 5'  CAGCTTATGGGCAGCAGCCAGT 80020             C__
                                 ACTGGCTGCTGCTC   AGCTG
                                 ||||||||||||||   |||||
                                 TGACCGACGACGGG   TCGAC
                                          TAT
GAM1757  LOC150370 3'  CAACTGAGCAGCCATGGA    86122      C       GCTC   C
                                 TCCA TGGCTGCT    CAG TG
                                 |||| ||||||||    ||| ||
                                 AGGT ACCGACGA    GTC AC
                                   _       _____   A
GAM1757  LOC150946 3'  CAGCTGGAGCTGCACAGCTGGA 86346      _  GC   T
                                 TCCA CTG  TGC GCTCCAGCTG
                                 |||| |||  ||| ||||||||||
                                 AGGT GAC  ACG CGAGGTCGAC
                                   C   __   T
GAM1757  LOC155179 3'  CAGCTGGAGGGCTCCAGGGA   82224     A   CT   G
                                 TCC CTGG  GCT CTCCAGCTG
                                 ||| ||||  ||| |||||||||
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                                AGG GACC  CGG GAGGTCGAC
                                  _   T_  _
GAM1757  LOC158863 3'  CAGCTGGATTGGCCAGTG    88295        CTGC
                                CACTGGCTG   TCCAGCTG
                                |||||||||   ||||||||
                                GTGACCGGT   AGGTCGAC
                                     T___
GAM1757  LOC167147 5'  TCAGGAATGACAGCAGCCAG  83560        C  CAG_
                                CTGGCTGCTG TC   CTGA
                                |||||||||| ||   ||||
                                GACCGACGAC AG   GACT
                                      _ TAAG
GAM1757  LOC197414 3'  CAGCTGGAGCTCCCGGTG    89456      CTGCT
                                CACTGG    GCTCCAGCTG
                                ||||||    ||||||||||
                                GTGGCC    CGAGGTCGAC
                                   CT___
GAM1757  LOC201685 5'  TCAGAATAAGAAAGCAGCCAGC 91847    CA       GC  CAG__
           AGA                    TC  CTGGCTGCT  TC    CTGA
                                || |||||||||  ||    ||||
                                AG  GACCGACGA  AG    GACT
                                 AC       A_  AATAA
GAM1757  LOC202181 3'  CAGCCAATGCCAAGACAGTGGA 90635      G  GCT  TCCA
                                TCCACTG CT   GC   GCTG
                                ||||||| ||   ||   ||||
                                AGGTGAC GA   CG   CGAC
                                    A  AC_  TAAC
GAM1757  LOC203232 3'  CAGCCGGGGCAGCCAGCAGT   71916     G  _     A
                                ACTG CTG CTGCTCC GCTG
                                |||| ||| ||||||| ||||
                                TGAC GAC GACGGGG CGAC
                                  _  C      C
GAM1757  LOC205011 3'  CAGCTGGAGTGCCGCCAGCAGG 92330     A_    T  T
           A                     TCC  CTGGC GC GCTCCAGCTG
                                |||  ||||| || ||||||||||
                                AGG  GACCG CG TGAGGTCGAC
                                  AC    C  _
GAM1757  LOC245806 5'  CAGCTGGATTCCGAGCCGCGGA 93540     AC    GCTGC
                                TCC  TGGCT    TCCAGCTG
                                |||  |||||    ||||||||
                                AGG  GCCGA    AGGTCGAC
                                  C_    GCCTT
GAM1757  LOC253228 3'  TCAGCTGGAACTGGCCCGACAG 97638     GCT_  GC_
                                CTG   GCT   TCCAGCTGA
                                |||   |||   |||||||||
                                GAC   CGG   AGGTCGACT
                                  AGCC   TCA
GAM1757  LOC253891 3'  CAGCTGGAGCAGGGTTGCGGT  96063     __  G
                                ACTG  GCT CTGCTCCAGCTG
                                ||||  ||| ||||||||||||
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                                TGGC  TGG GACGAGGTCGAC
                                  GT  _
GAM1757  LOC253936 3'  CAGCCGGGGCAGCCAGCAGT   96318     G  _     A
                                ACTG CTG CTGCTCC GCTG
                                |||| ||| ||||||| ||||
                                TGAC GAC GACGGGG CGAC
                                  _  C      C
GAM1757  LOC256044 5'  CAGCTGGACCTAGCTCAGCGGA 98007     A  _   CTGC
                                TCC CTG GCTG    TCCAGCTG
                                ||| ||| ||||    ||||||||
                                AGG GAC CGAT    AGGTCGAC
                                  C  T   CC__
GAM1758  F13A1    3'  CCAGATATATAGAAGGACTGC  92709          TC___
                                GCAGTCCTTCT    TCTGG
                                ||||||||||     |||||
                                CGTCAGGAAGA    AGACC
                                       TATAT
GAM1758  KCNN3    5'  GCCAAAGAGAGGACTGGAG    11186     G      CT   C
                                CTC CAGTCCTT  TCT TGGC
                                ||| ||||||||  ||| ||||
                                GAG GTCAGGAG  AGA ACCG
                                  _       __  A
GAM1758  LANCL1   3'  GCCAGAGAAGACTTGATCACAG 21331     CGCA   CT_
           T                     ACT    GTC   TCTTCTCTGGC
                                 |||    |||   ||||||||||
                                 TGA    TAG   AGAAGAGACCG
                                   CAC_   TTC
GAM1758  LPIN2    5'  GCCAGAGAAGAAAAAGAACAGT 28432     AG_  C__
           G                     CGC   TC   TTCTTCTCTGGC
                                 |||   ||   ||||||||||||
                                 GTG   AG   AAGAAGAGACCG
                                   ACA  AAA
GAM1758  PART1    3'  GCCAGAGAAAAATCACAGC   33901    A  CC  C
                                GC GT  TT TTCTCTGGC
                                || ||  || |||||||||
                                CG CA  AA AAGAGACCG
                                 A  CT  A
GAM1758  BRD2     5'  GGCCAATGGAGGAGCTACGA   18795     C  TC      TC
                                TCG AG  CTTCTTC  TGGCC
                                ||| ||  |||||||  |||||
                                AGC TC  GAGGAGG  ACCGG
                                  A  __      TA
GAM1758  C1QTNF7  3'  GGCCAGAGAAGCTTTTACGC   50004    A  CCTT_
                                GC GT    CTTCTCTGGCC
                                || ||    ||||||||||
                                CG CA    GAAGAGACCGG
                                 _ TTTTC
GAM1758  DKFZp761G2113 3'  GCCAAGCTGGAGGACCGCGA   70467      A      TT  C
                                TCGC GTCCTTC  CT TGGC
                                |||| |||||||  || ||||
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                                AGCG CAGGAGG  GA ACCG
                                  C      TC  _
GAM1758  FLJ20436  5'  GCCAGAGAAGAAAGATGGGGT  35625      G  G  C
                                ACTC CA TC TTCTTCTCTGGC
                                |||| || || ||||||||||||
                                TGGG GT AG AAGAAGAGACCG
                                  _  _  A
GAM1758  FLJ22037  5'  GCTGGAAGAAGAACTAGA    95535    GC   C       CT
                                TC  AGT CTTCTTCT  GGC
                                ||  ||| ||||||||  |||
                                AG  TCA GAAGAAGG  TCG
                                 A_   A       __
GAM1758  FLJ22195  3'  GCCAGAGTAAGTGCAAGT    43108     C   GTCCTT   _
                                ACT GCA     CTT CTCTGGC
                                ||| |||     ||| |||||||
                                TGA CGT     GAA GAGACCG
                                  A  _______   T
GAM1758  HEMK      3'  GGCCAAAGCCAGAGACTCGA   32960     C    CT   T_  C
                                TCG AGTC  TCT  CT TGGCC
                                ||| ||||  |||  || |||||
                                AGC TCAG  AGA  GA ACCGG
                                  _   __  CC  A
GAM1758  KHSRP     3'  GCCAGAGAAGATAGCGAG    14881       AGTCCT
                                CTCGC     TCTTCTCTGGC
                                |||||     ||||||||||
                                GAGCG     AGAAGAGACCG
                                   AT____
GAM1758  KIAA0321  5'  GGCTGTCCAAGAAGGACTAAAG 63058     CGC        CTC
              T                  ACT   AGTCCTTCTT   TGGCC
                                |||   ||||||||||   |||||
                                TGA   TCAGGAAGAA   GTCGG
                                  AA_        CCT
GAM1758  KIAA0427  5'  GCCAGAGGAACCCCGAGT    29382       CA  CCTTC
                                ACTCG  GT    TTCTCTGGC
                                |||||  ||    |||||||||
                                TGAGC  CA    AGGAGACCG
                                   CC  _____
GAM1758  MGC10731  3'  GGCCAGAGAAGGCCCACCCGCG 48844       A_  CCT
              AG                   CTCGC  GT   TCTTCTCTGGCC
                                |||||  ||   ||||||||||||
                                GAGCG  CA   GGAAGAGACCGG
                                   CC  CCC
GAM1758  NAV1      5'  GCCAGAGAAGAAGGAGGTATCG 40323     ____  AG
              GAG                   CTC    GC  TCCTTCTTCTCTGGC
                                |||    ||  ||||||||||||||||
                                GAG    TG  AGGAAGAAGAGACCG
                                  GCTA  G_
GAM1758  NUP54     5'  CCAGCTGATAAATACTGCGAGT 60724         CCTTCT  T_
                                ACTCGCAGT     TC  CTGG
                                |||||||||     ||  ||||
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                                TGAGCGTCA     AG  GACC
                                     TAAAT_  TC
GAM1758  PP2447    3'  GGCATCGAGAAGAACTGGAG   48100     G   CCT      TG_
                                CTC CAGT   TCTTCTC   GCC
                                ||| ||||   |||||||   |||
                                GAG GTCA   AGAAGAG   CGG
                                  _   ___      CTA
GAM1758  RENT2     3'  GCCAGAGAAGAAACGGGT    32067      CAGTCC
                                ACTCG     TTCTTCTCTGGC
                                |||||     ||||||||||||
                                TGGGC     AAGAAGAGACCG
                                  A_____
GAM1758  LOC128954 5'  GCCAGAGAGCAGAACATGC    76304     _  C  T  T
                                GCA GT CT CT CTCTGGC
                                ||| || || || |||||||
                                CGT CA GA GA GAGACCG
                                  A  A  C  _
GAM1758  LOC145173 3'  AGCGAAAAAGGACTGAAAG    77559    CG       C   T
                                CT  CAGTCCTT TTC CT
                                ||  |||||||| ||| ||
                                GA  GTCAGGAA AAG GA
                                 AA       A   C
GAM1758  LOC147398 3'  GCCAGAGAAGTGACCGGC    60925    A_   CTT
                                GC  GTC   CTTCTCTGGC
                                ||  |||   ||||||||||
                                CG  CAG   GAAGAGACCG
                                 GC   T__
GAM1758  LOC148166 5'  GCCTTGGAGAAACCACGAG    79418     CA  CC     TCT
                                CTCG  GT  TTCTTC   GGC
                                ||||  ||  ||||||   |||
                                GAGC  CA  AAGAGG   CCG
                                  AC  __     TT_
GAM1758  LOC148645 3'  CCAGACTGGAGAACCACAGC   85330    A  CC     __
                                GC GT  TTCTTC  TCTGG
                                || ||  ||||||  |||||
                                CG CA  AAGAGG  AGACC
                                 A  CC     TC
GAM1758  LOC148894 3'  CCAGAGAAAGCTGCAGGT    85418    TC    CCTTC
                                AC  GCAGT    TTCTCTGG
                                ||  |||||    ||||||||
                                TG  CGTCG    AAGAGACC
                                 GA    A____
GAM1758  LOC168667 3'  GCCAATGAAGGACTGCAGT    94335     C        TTCTC
                                ACT GCAGTCCTTC    TGGC
                                ||| ||||||||||    ||||
                                TGA CGTCAGGAAG    ACCG
                                  _        TA___
GAM1758  LOC200488 5'  GGCCAGAGAAGGGGTTCT    91653    TC
                                AG  CTTCTTCTCTGGCC
                                ||  ||||||||||||||
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                                TC  GGGGAAGAGACCGG
                                 TT
GAM1758  LOC221336 3'  CCAGAGAATTTCTGCCAGT   93890     C    TCCTTC
                                ACT GCAG     TTCTCTGG
                                ||| ||||     ||||||||
                                TGA CGTC     AAGAGACC
                                  C    TTT___
GAM1758  LOC256218 3'  GGCCTACCTGAAGAAGAACCAC 96885      CA  C      TCT__
            GAG                   CTCG  GT CTTCTTC    GGCC
                                ||||  || |||||||    ||||
                                GAGC  CA GAAGAAG    CCGG
                                  AC  A      TCCAT
GAM1759  CDH12    3'  CTTATCATTTAAAGTGGTGTA  15777         CCCAA   GA
                                TACACCACT    GAA  ATAAG
                                |||||||||    |||  |||||
                                ATGTGGTGA    TTT  TATTC
                                      AA___   AC
GAM1759  GOCAP1   3'  ATTGTTCTTGGGAGCAGTGTA  43007      CA        G
                                TACAC  CTCCCAAGAA AAT
                                |||||  |||||||||| |||
                                ATGTG  GAGGGTTCTT TTA
                                   AC         G
GAM1759  DKFZp434N2435 5'  CTTATTACTGTGGGGTGGT    98090       T    AGAAG
                                ACCAC CCCA     AATAAG
                                ||||| ||||     ||||||
                                TGGTG GGGT     TTATTC
                                   _    GTCA_
GAM1759  DKFZP564I122 3'  CTTATTCTTCTCCCTCATGTGT 63877       CACTCCCA
            A                    TACAC       AGAAGAATAAG
                                |||||       ||||||||||
                                ATGTG       TCTTCTTATTC
                                   TACTCCC_
GAM1759  FLJ21791  3'  CTTATTTGCAGAAGTGGTGTA  62126         CCCAAGAA
                                TACACCACT       GAATAAG
                                |||||||||       |||||||
                                ATGTGGTGA       TTTATTC
                                      AGACG___
GAM1759  HMP19    3'  CTTATTCTTTGTTAGGAAAATG 88860      CCAC   CAA_
            TA                    TACA    TCC    GAAGAATAAG
                                ||||    |||    ||||||||||
                                ATGT    AGG    TTTCTTATTC
                                  AAA_   ATTG
GAM1759  KIAA1719  3'  TCTGTCTTGGGAGTGGTGTA   68742             _
                                TACACCACTCCCAAGA AGA
                                |||||||||||||||| |||
                                ATGTGGTGAGGGTTCT TCT
                                           G
GAM1759  KIAA1853  3'  TTTTTCTTGGAAGCAGTG    69929     CA  C
                                CAC  CT CCAAGAAGAA
                                |||  || ||||||||||
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